QUANTITATIVE ANALYSIS OF INTACT PROTEINS AND RNAS CARRIED BY IMMUNOSUPPRESSIVE EXOSOMES

by

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Dissertation submitted to the Faculty of the Graduate School of the
University of Maryland, College Park, in partial fulfillment
of the requirements for the degree of
Doctor of Philosophy
2016

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Appendix 4.1. Results of data processing for the analysis of the mRNA, miRNA and protein cargo

Experimental Design mRNA transcript isoforms

Sample ID	Condition	Batch	Inflammation condition	Sample type	Library type
HPGL0681	exo_polya_Infl	a	Infl	exo	large
HPGL0682	exo_polya_Conv	a	Conv	exo	large
HPGL0683	exo_polya_Infl	b	Infl	exo	large
HPGL0684	exo_polya_Conv	b	Conv	exo	large
HPGL0685	cell_polya_Infl	a	Infl	cell	large
HPGL0686	cell_polya_Conv	a	Conv	cell	large
HPGL0687	cell_polya_Infl	b	Infl	cell	large
HPGL0688	cell_polya_Conv	b	Conv	cell	large
HPGL0522	cell_polya_Infl	z	Infl	cell	large
HPGL0526	exo_polya_Infl	z	Infl	exo	large
HPGL0527	exo_polya_Infl	z	Infl	exo	large

Experimental Design miRNAs

Sample ID	Condition	Batch	Inflammation condition	Sample type	Library type
HPGL0673	exo_mirna_Infl	a	Infl	exo	small
HPGL0674	exo_mirna_Conv	a	Conv	exo	small
HPGL0675	exo_mirna_Infl	b	Infl	exo	small
HPGL0676	exo_mirna_Conv	b	Conv	exo	small
HPGL0677	cell_mirna_Infl	a	Infl	cell	small
HPGL0678	cell_mirna_Conv	a	Conv	cell	small
HPGL0679	cell_mirna_Infl	b	Infl	cell	small
HPGL0680	cell_mirna_Conv	b	Conv	cell	small
HPGL0523	cell_mirna_Infl	z	Infl	cell	small
HPGL0524	cell_mirna_Cell_after_exo_release	z	Cell_after_exo_release	cell	small
HPGL0525	exo_mirna_Infl	z	Infl	exo	small
HPGL0555	exo_mirna_Infl	z	Infl	exo	small
HPGL0556	cell_mirna_Infl	z	Infl	cell	small
HPGL0557	cell_mirna_Infl	z	Infl	cell	small
HPGL0558	cell_mirna_Cell_after_exo_release	z	Cell_after_exo_release	cell	small
HPGL0559	cell_mirna_Cell_after_exo_release	z	Cell_after_exo_release	cell	small
HPGL0560	exo_mirna_Infl	z	Infl	exo	small

Raw Reads mRNA transcript isoforms

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000000001	ENSMUSG00000000001	3	108107280	108146146	-1	12	14	20	163	15	13	2426	8854	4250	1256	2328		Q9DC51
ENSMUST00000000003	ENSMUSG00000000003	X	77837901	77853623	-1	0	0	12	0	0	0	0	0	0	0	0	Q3UV89	O08976
ENSMUST00000000010	ENSMUSG00000020875	11	96271457	96276595	1	0	0	13	413	33	17	0	0	0	0	0		P20615
ENSMUST00000000028	ENSMUSG00000000028	16	18780447	18811987	-1	0	13	11	5	3	0	87	136	34	13	26	Q3UI99	Q9Z1X9
ENSMUST00000000033	ENSMUSG00000048583	7	142650766	142666816	-1	0	0	0	0	6	0	0	1	2	3	0		P09535
ENSMUST00000000049	ENSMUSG00000000049	11	108343354	108414396	1	5	2	6	2	1	1	1	0	0	97	0		Q01339
ENSMUST00000000058	ENSMUSG00000000058	6	17281185	17289115	1	1	1	6	43	1	2	15	18	11	47	5		Q9WVC3
ENSMUST00000000080	ENSMUSG00000000078	13	5861489	5870393	1	26	16	82	93	40	22	2710	15604	5628	1010	5060	Q8BPQ2	
ENSMUST00000000087	ENSMUSG00000000085	4	120405281	120530186	1	0	0	20	15	0	0	65	153	135	0	0		Q8K214
ENSMUST00000000090	ENSMUSG00000000088	9	57521232	57532424	1	4	2	3	72	3	1	625	2201	665	297	290		P12787
ENSMUST00000000094	ENSMUSG00000061689	2	156613705	156764363	1	2	2	2	2	7	1	13	29	13	0	14	I1E4X0	
ENSMUST00000000095	ENSMUSG00000000093	11	85832551	85841948	1	24	22	30	586	46	11	1	3	1	4	10		Q60707
ENSMUST00000000096	ENSMUSG00000000094	11	85886422	85916097	1	0	28	76	3	35	0	0	0	0	0	0		P70325
ENSMUST00000000109	ENSMUSG00000055022	15	92051165	92341967	1	6	16	16	0	21	12	0	0	0	0	0		P12960
ENSMUST00000000122	ENSMUSG00000000120	11	95568818	95587735	-1	82	40	183	497	136	63	0	1	0	3	14	Q8CFT3	
ENSMUST00000000127	ENSMUSG00000000125	11	103774150	103817957	1	12	14	39	183	28	13	0	0	0	0	0	A2A649	P17553
ENSMUST00000000128	ENSMUSG00000000126	11	59306928	59333552	1	17	0	0	133	20	16	0	0	0	1	1	J3JS28	
ENSMUST00000000129	ENSMUSG00000000127	17	63896018	64139494	1	5	11	3	11	4	0	87	264	164	215	102		P70451
ENSMUST00000000137	ENSMUSG00000020152	11	20062304	20112913	-1	18	20	37	34	23	17	5922	20465	10564	7784	5465	Q5SW83	P61161
ENSMUST00000000145	ENSMUSG00000020333	11	54303798	54364756	1	2	0	0	15	0	0	0	5	0	0	0	Q5F2C5	
ENSMUST00000000153	ENSMUSG00000000149	5	140758408	140830431	-1	19	18	37	68	37	17	361	306	296	94	373		P27600
ENSMUST00000000161	ENSMUSG00000000157	16	96422288	96443619	-1	19	10	21	7	0	0	0	185	74	0	32		Q3UV74
ENSMUST00000000163	ENSMUSG00000000159	16	96361668	96525580	1	6	0	0	0	5	1	0	0	0	2	0	A0A0B4J1E1	
ENSMUST00000000171	ENSMUSG00000000167	9	50617321	50625000	1	0	0	0	9	0	0	0	8	0	4	0		Q8CHR9
ENSMUST00000000175	ENSMUSG00000000171	9	50596338	50603849	-1	8	5	29	8	12	4	990	2947	1067	2078	759		Q9CXV1
ENSMUST00000000186	ENSMUSG00000000182	6	127072902	127081408	1	24	14	63	182	26	6	0	0	0	0	0	Q3U1V5	Q9EPC2
ENSMUST00000000187	ENSMUSG00000000183	6	127015586	127028187	1	18	12	19	18	15	6	0	0	0	0	0		P21658
ENSMUST00000000188	ENSMUSG00000000184	6	127125162	127152193	-1	36	37	100	114	55	27	98	308	168	38	481	Q4FK45	P30280
ENSMUST00000000193	ENSMUSG00000035385	11	82035571	82037453	1	10	2	18	2	2	1	7	115	10	185	20	Q5SVU3	P10148
ENSMUST00000000194	ENSMUSG00000035352	11	82101845	82103400	1	2	2	0	3	0	0	0	0	0	104	9	Q545B5	Q62401
ENSMUST00000000199	ENSMUSG00000062661	2	31245823	31295989	1	27	17	128	86	39	24	8	18	6	1	40		Q8BNY6
ENSMUST00000000201	ENSMUSG00000000197	14	123276641	123627144	-1	34	20	31	86	23	19	0	0	0	0	0	E9QLE4	
ENSMUST00000000206	ENSMUSG00000000202	11	114791217	114795945	-1	0	0	0	153	0	0	0	0	0	0	0		Q9DB72
ENSMUST00000000208	ENSMUSG00000000204	11	83175186	83190221	1	0	0	38	0	15	15	6319	38966	11104	5850	14592	Q3UV66	
ENSMUST00000000219	ENSMUSG00000000214	7	142892752	142931128	-1	0	0	16	31	10	6	0	0	0	0	0		P24529
ENSMUST00000000220	ENSMUSG00000000215	7	142678656	142699510	-1	2	0	3	0	0	0	0	0	0	0	0	Q5EEX1	P01326
ENSMUST00000000221	ENSMUSG00000000216	7	121734479	121768475	1	23	10	26	40	24	9	0	0	0	0	0		Q9WU39
ENSMUST00000000228						8	0	27	53	6	6	0	0	0	0	0		
ENSMUST00000000253	ENSMUSG00000000247	2	38339281	38369733	1	12	2	7	278	21	10	0	0	0	0	0	Q543C6	Q9Z0S2
ENSMUST00000000254	ENSMUSG00000000248	6	128934381	128984707	1	0	1	0	0	0	0	6	7	7	0	11		Q9D676
ENSMUST00000000260	ENSMUSG00000000253	13	45507444	45546382	1	8	4	18	91	21	2	17	22	9	7	7		Q9DCZ1
ENSMUST00000000266	ENSMUSG00000026535	1	173962568	173982744	-1	7	7	10	6	8	13	30	488	52	382	123		Q9R002
ENSMUST00000000275	ENSMUSG00000038257	8	55940460	56125429	1	12	4	1	4	8	6	0	0	0	0	0	G5E811	
ENSMUST00000000284	ENSMUSG00000000275	11	88999376	89020293	1	35	33	132	95	57	25	0	20	2	1	0	Q5SU71	
ENSMUST00000000285	ENSMUSG00000000276	11	89035179	89066850	-1	0	0	0	0	0	0	13	0	13	9	0		Q9R1C6
ENSMUST00000000287	ENSMUSG00000000278	11	88924020	88955465	-1	15	9	34	27	21	6	122	335	112	138	432		Q920A5
ENSMUST00000000291	ENSMUSG00000000282	11	74830920	74845725	1	46	19	100	536	66	23	1189	1641	1211	84	971		O08789
ENSMUST00000000299	ENSMUSG00000000290	10	77530252	77565708	1	24	8	65	32	17	8	20978	33201	26094	3778	18907	Q542I8	
ENSMUST00000000304	ENSMUSG00000000295	10	31313382	31328204	1	6	0	3	31	0	0	0	63	29	344	23		Q3SXD3
ENSMUST00000000305	ENSMUSG00000000296	10	31332380	31445921	-1	5	3	1	28	5	2	1	0	0	36	4		O54818
ENSMUST00000000310	ENSMUSG00000000301	11	59970614	60046489	-1	0	0	0	0	2	3	3	6	5	12	4		Q61907
ENSMUST00000000312	ENSMUSG00000000303	8	106603351	106670246	1	28	38	52	129	31	24	97	326	193	14	204		
ENSMUST00000000314	ENSMUSG00000000305	2	179442431	179899373	1	51	40	141	68	62	28	0	0	0	0	1		P39038
ENSMUST00000000317	ENSMUSG00000000308	2	121357714	121363737	1	8	0	0	24	23	14	0	0	0	0	0	Q545N7	P30275
ENSMUST00000000326	ENSMUSG00000000317	11	70224128	70229798	-1	26	19	70	20	27	12	0	1	0	0	0	Q5BKP3	O88282
ENSMUST00000000327	ENSMUSG00000000318	11	70156197	70170834	1	3	0	0	0	4	0	0	26	6	4	59	F8WHB7	
ENSMUST00000000329	ENSMUSG00000000320	11	70241457	70255353	-1	44	60	189	62	61	35	19	23	26	56	114	A2CF85	P39655
ENSMUST00000000335	ENSMUSG00000000326	16	18406886	18426852	-1	0	0	0	1	1	0	41	64	32	34	85		O88587
ENSMUST00000000342	ENSMUSG00000020676	11	82057823	82062955	1	9	8	14	10	8	4	0	0	0	1	0		P48298
ENSMUST00000000348	ENSMUSG00000000339	3	116488963	116508208	-1	7	0	0	112	10	11	115	318	182	102	152		Q9D7H3
ENSMUST00000000349	ENSMUSG00000000340	3	116513070	116549981	1	40	29	84	280	47	28	18	69	49	94	54		P53395
ENSMUST00000000356	ENSMUSG00000000346	15	100615628	100620731	1	23	12	22	41	20	14	11545	23294	10863	7855	8303		Q9DCP9
ENSMUST00000000365	ENSMUSG00000000355	X	38600578	38613426	1	0	0	0	0	0	0	135	539	113	187	54		Q9DB27
ENSMUST00000000369	ENSMUSG00000000359	2	152626951	152635198	1	10	4	13	139	17	9	0	6	1	0	3		O35929
ENSMUST00000000384	ENSMUSG00000000374	10	78186725	78244642	-1	36	33	69	30	47	19	1208	1695	1758	130	1359	F8VQF9	
ENSMUST00000000388	ENSMUSG00000000378	11	6546887	6596744	1	6	0	0	20	13	1	329	752	585	117	517		Q8K2Y9
ENSMUST00000000394	ENSMUSG00000000384	11	6615598	6626067	-1	15	0	64	11	6	0	436	418	346	16	200		Q91YM4
ENSMUST00000000395	ENSMUSG00000000385	16	97564684	97611195	-1	18	20	53	52	25	10	0	0	0	1	0		Q9JIQ8
ENSMUST00000000402	ENSMUSG00000000392	2	62500943	62574075	-1	0	0	0	0	0	0	0	0	1	3	0		P97321
ENSMUST00000000412	ENSMUSG00000000402	X	166523007	166585720	-1	75	55	352	135	64	27	1	3	4	0	2		Q9JJZ5
ENSMUST00000000421	ENSMUSG00000000411	4	129489014	129491022	-1	12	4	15	30	10	8	0	14	11	1	10		Q9D2E1
ENSMUST00000000430	ENSMUSG00000000420	18	24205344	24286818	1	0	0	21	78	24	0	22	0	22	0	22		O08912
ENSMUST00000000445	ENSMUSG00000000435	10	107482908	107486134	-1	9	10	18	9	20	8	0	0	0	0	0	A2RSK4	P24699
ENSMUST00000000449	ENSMUSG00000000439	6	115601902	115622624	1	24	14	16	79	17	16	79	128	112	42	101		Q9ERV1
ENSMUST00000000450	ENSMUSG00000000440	6	115360951	115490399	1	0	4	0	1	0	5	4	0	0	0	3	Q6GU14	
ENSMUST00000000451	ENSMUSG00000000441	6	115618067	115676635	-1	0	0	0	0	0	0	1141	3084	2309	255	1640		Q99N57
ENSMUST00000000466	ENSMUSG00000028494	4	86648386	86670060	-1	8	7	31	26	7	4	3098	11615	2600	7153	2284		P43883
ENSMUST00000000476	ENSMUSG00000029231	5	75152292	75198215	1	8	14	0	6	11	6	1	1	2	25	96		P26618
ENSMUST00000000500	ENSMUSG00000000489	15	79995900	80014808	-1	18	9	53	135	50	15	7	4	2	6	15		
ENSMUST00000000505	ENSMUSG00000029730	5	138164583	138172422	-1	22	13	42	44	27	10	415	458	307	126	305	Q3U4T8	Q61881
ENSMUST00000000514	ENSMUSG00000026315	1	107590006	107610484	1	187	89	471	103	99	25	8	57	27	108	54		O08800
ENSMUST00000000542	ENSMUSG00000000530	15	101128522	101145336	1	21	0	0	30	18	16	29	138	380	36	0		Q61288
ENSMUST00000000543	ENSMUSG00000000531	15	101224207	101232755	1	93	54	407	258	93	33	5	4	1	1	9		Q9JJA9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000000544	ENSMUSG00000000532	15	101174067	101213679	1	41	25	110	52	49	26	2189	2989	3210	168	1670	Q3TZF1	Q61271
ENSMUST00000000572	ENSMUSG00000000560	5	70957597	71095849	-1	19	11	16	207	19	16	0	0	0	0	0	A0A0H2UKB5	
ENSMUST00000000573	ENSMUSG00000074340	3	105973711	105987423	1	7	2	25	11	2	7	320	1332	636	438	487	Q54AJ4	Q62010
ENSMUST00000000574	ENSMUSG00000000562	3	105870858	105908926	1	30	30	100	36	33	29	504	1230	696	608	345	Q3U4C5	
ENSMUST00000000579	ENSMUSG00000000567	11	112782224	112787760	1	21	35	151	641	52	17	0	1	0	1	12		Q04887
ENSMUST00000000590	ENSMUSG00000032050	9	52047150	52088737	1	0	0	0	35	0	0	0	7	60	22	18		P26043
ENSMUST00000000594	ENSMUSG00000000581	11	17257579	17269176	1	2	3	9	8	4	0	230	388	132	609	93		O35473
ENSMUST00000000608	ENSMUSG00000000594	11	55098115	55113029	1	28	20	70	69	55	21	4898	10380	4713	2278	4495	Q5F1Z8	Q60648
ENSMUST00000000619	ENSMUSG00000000605	7	7282316	7299511	-1	35	28	187	77	37	23	310	1263	574	183	449		Q61418
ENSMUST00000000631	ENSMUSG00000000617	11	50850685	50866208	1	27	25	20	134	35	33	14	25	25	0	20		Q5NCH9
ENSMUST00000000632	ENSMUSG00000044807	11	50811086	50827724	-1	0	5	9	12	5	1	0	3	1	0	1		Q571J5
ENSMUST00000000641	ENSMUSG00000000627	6	82911885	82939769	-1	42	40	157	216	48	25	90	155	63	4	82		Q9Z123
ENSMUST00000000642	ENSMUSG00000000628	6	82725025	82774454	-1	51	29	38	180	55	16	536	1071	949	82	787		O08528
ENSMUST00000000645	ENSMUSG00000000631	11	77763246	77865980	1	0	0	0	0	0	0	0	0	0	0	0	K3W4L0	
ENSMUST00000000646	ENSMUSG00000000632	11	77930800	77979048	1	6	0	0	0	0	2	0	0	0	0	0		Q7TSK2
ENSMUST00000000674	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	12	54	14	21	0		Q99M96
ENSMUST00000000687	ENSMUSG00000000673	17	83831356	83846790	-1	11	4	24	14	12	8	221	329	136	50	144		Q78JT3
ENSMUST00000000696	ENSMUSG00000000682	4	134082448	134095082	-1	3	8	12	22	11	9	14228	31144	10313	46373	5696		Q64389
ENSMUST00000000704	ENSMUSG00000000690	11	96292476	96301569	1	0	0	0	0	0	0	0	0	0	0	0		P09023
ENSMUST00000000707	ENSMUSG00000000693	6	83034173	83052562	1	16	0	46	27	33	5	5	14	0	5	36		Q9Z175
ENSMUST00000000717	ENSMUSG00000000701	12	105176358	105181143	1	10	8	18	6	12	6	0	0	0	0	0	Q3UT92	P56845
ENSMUST00000000718	ENSMUSG00000079007	12	105202422	105206993	1	10	4	19	10	8	7	0	0	0	0	0		P56844
ENSMUST00000000724	ENSMUSG00000000708	17	53566861	53672720	1	18	16	9	114	35	14	354	1506	733	152	615	B2RR30	Q9JHD1
ENSMUST00000000727	ENSMUSG00000000711	10	128677193	128696268	-1	27	24	37	126	47	21	4381	8274	4673	881	3022	B2RPS1	P61021
ENSMUST00000000746	ENSMUSG00000000730	10	78041947	78063622	1	0	0	42	11	16	6	0	0	0	0	0	A3EWM2	Q9CWR8
ENSMUST00000000755	ENSMUSG00000000739	8	123142847	123158315	-1	0	0	11	0	12	0	0	0	0	0	0	Q91X36	
ENSMUST00000000756	ENSMUSG00000000740	8	123102350	123105244	1	5	21	20	516	27	12	1814	3364	1650	5530	1422		P47963
ENSMUST00000000759	ENSMUSG00000000743	8	123204264	123212763	-1	31	14	101	35	43	20	3876	3791	2212	725	1540		Q921W0
ENSMUST00000000767	ENSMUSG00000000751	11	75298166	75348324	-1	0	0	0	0	0	0	234	350	240	133	293	Q5SWN2	
ENSMUST00000000769	ENSMUSG00000000753	11	75409769	75422701	-1	8	6	12	7	14	5	0	0	0	5	0		P97298
ENSMUST00000000776	ENSMUSG00000000759	8	12614277	12672248	-1	0	4	0	61	15	0	97	250	254	73	217		P58854
ENSMUST00000000783	ENSMUSG00000000766	10	6758506	7038198	1	0	1	0	3	0	1	0	0	0	0	0		P42866
ENSMUST00000000793	ENSMUSG00000000776	14	70438748	70443471	-1	16	0	0	216	14	3	0	19	10	0	51		Q91WD1
ENSMUST00000000804	ENSMUSG00000000787	X	13280970	13294052	1	8	7	11	24	11	10	1969	6283	2951	3358	2417	Q3TQX5	Q62167
ENSMUST00000000808	ENSMUSG00000000791	8	70808449	70821424	1	12	16	38	163	36	14	26	18	35	4	29		Q60837
ENSMUST00000000809	ENSMUSG00000000792	8	70882889	70892757	-1	24	16	69	210	44	21	0	1	0	0	1	G3X8P5	
ENSMUST00000000811	ENSMUSG00000000794	3	89520164	89675132	1	21	15	59	374	37	23	126	266	162	5	65		P58391
ENSMUST00000000821	ENSMUSG00000000804	11	84984442	85140161	-1	7	2	0	0	10	0	140	802	605	158	754	F6XDW8	
ENSMUST00000000828	ENSMUSG00000000811	6	89643988	89675529	1	10	12	26	41	8	8	17	21	19	7	23	G3X8P6	
ENSMUST00000000834	ENSMUSG00000000817	1	161780689	161788495	-1	6	7	11	8	17	10	3	15	1	11	7	Q544E9	P41047
ENSMUST00000000844	ENSMUSG00000000827	2	181497142	181517966	1	0	0	4	0	0	0	68	549	128	50	23	Q3TAI4	
ENSMUST00000000881	ENSMUSG00000000861	11	24078056	24174123	1	0	0	7	30	3	0	9	18	18	4	24		Q9QYE3
ENSMUST00000000889	ENSMUSG00000000869	11	53602982	53618669	-1	1	0	1	0	0	0	1	0	0	6	2		P07750
ENSMUST00000000894	ENSMUSG00000027490	2	154559407	154569892	-1	104	52	227	160	46	26	0	0	57	27	62	Q9CYB4	
ENSMUST00000000895	ENSMUSG00000027489	2	154544399	154558890	-1	0	4	0	26	0	0	0	0	0	0	0		Q9D6J4
ENSMUST00000000896	ENSMUSG00000000876	2	154585758	154603708	-1	95	108	390	115	89	45	319	523	330	82	186		Q9JJW0
ENSMUST00000000901	ENSMUSG00000000881	X	100767722	100818410	1	16	16	14	174	8	0	0	0	0	0	0	Q52KF7	
ENSMUST00000000904	ENSMUSG00000000884	16	18498768	18566679	1	13	9	52	0	37	12	0	0	0	0	0	F8WH35	
ENSMUST00000000910	ENSMUSG00000000889	2	27165233	27183200	1	33	22	71	34	47	19	0	0	0	0	0		Q64237
ENSMUST00000000924	ENSMUSG00000000901	10	75923222	75932502	-1	14	0	18	42	27	9	0	2	0	0	0	Q3UQT3	Q02853
ENSMUST00000000925	ENSMUSG00000000902	10	75896769	75921617	-1	0	0	3	78	12	0	57	121	76	0	68	Q6ZWP4	Q9Z0H3
ENSMUST00000000926	ENSMUSG00000000903	10	75943057	75949657	1	0	3	2	0	3	4	5	10	3	44	5	Q61243	
ENSMUST00000000939	ENSMUSG00000000915	5	123973628	124005558	1	29	15	96	116	37	24	1428	1694	1355	124	1022		Q9JKY5
ENSMUST00000000940	ENSMUSG00000000916	5	135369953	135376805	1	5	2	17	27	6	0	27	57	30	0	34		Q8K4F6
ENSMUST00000000958	ENSMUSG00000000934	15	75657035	75678800	-1	22	13	23	59	30	13	7	10	4	14	11		Q8R4U6
ENSMUST00000000964	ENSMUSG00000029844	6	52155590	52158317	-1	21	17	53	72	15	8	0	0	0	0	0	B9EHK7	
ENSMUST00000000984	ENSMUSG00000000958	14	54369442	54417780	-1	7	7	49	27	12	11	379	847	284	79	334		Q9Z1K8
ENSMUST00000000985	ENSMUSG00000000959	14	54360841	54369673	1	23	15	40	71	26	14	531	858	477	171	409		Q8BGA9
ENSMUST00000001002	ENSMUSG00000000976	11	83753696	83783754	1	62	70	135	92	87	32	240	1530	412	61	545		Q6P1G0
ENSMUST00000001008	ENSMUSG00000000982	11	83647844	83649355	-1	7	2	4	7	11	6	27	335	45	198	75	Q5QNW0	P10855
ENSMUST00000001009	ENSMUSG00000000983	11	83709015	83711348	1	0	0	2	5	3	2	43	262	46	120	26		P62810
ENSMUST00000001027	ENSMUSG00000063558	1	58029931	58106413	1	21	17	21	9	15	13	43	26	138	22	35	G3X8P9	
ENSMUST00000001036	ENSMUSG00000032175	9	21104069	21127346	-1	41	20	93	93	54	30	1102	1318	1097	95	849	E9QJS1	
ENSMUST00000001040	ENSMUSG00000001014	9	21029373	21030531	1	6	7	43	75	19	5	7	1	2	0	1	Q14AB0	Q9ERM2
ENSMUST00000001042	ENSMUSG00000001016	3	90476126	90488379	1	8	12	24	19	10	4	115	365	134	194	149		Q9CXY6
ENSMUST00000001043	ENSMUSG00000001017	3	90498956	90509498	-1	0	8	0	0	4	0	183	610	0	0	0		Q9CY57
ENSMUST00000001046	ENSMUSG00000001020	3	90603771	90606045	1	1	2	6	0	0	2	976	2287	411	12030	981	Q545V2	P07091
ENSMUST00000001047	ENSMUSG00000001021	3	90560578	90602702	1	7	6	14	3	11	4	5	9	7	6	1	Q496W1	P62818
ENSMUST00000001049	ENSMUSG00000001023	3	90608523	90611780	1	2	2	2	11	7	0	0	1	0	3	1	Q149U2	P63084
ENSMUST00000001051	ENSMUSG00000001025	3	90612882	90624181	1	21	29	75	296	44	42	62612	124582	57074	186609	22873	Q545I9	P14069
ENSMUST00000001055	ENSMUSG00000001029	11	106377656	106388075	-1	6	4	8	20	9	6	63	132	33	158	181		P35330
ENSMUST00000001059	ENSMUSG00000020715	11	106394650	106487852	-1	29	29	120	17	59	24	700	1130	1028	82	1025		Q9EQY0
ENSMUST00000001063	ENSMUSG00000001036	11	61517249	61579687	-1	0	0	0	0	0	0	0	0	0	0	0		Q8CHU3
ENSMUST00000001079	ENSMUSG00000001052	3	129982759	130061553	-1	21	0	34	39	24	13	696	1279	1126	34	845	Q80ZX0	
ENSMUST00000001080	ENSMUSG00000001053	11	51643063	51650842	-1	10	8	37	174	29	18	17	39	15	7	18		Q8C7U1
ENSMUST00000001081	ENSMUSG00000001054	11	51623671	51635896	-1	15	15	19	113	22	5	763	750	741	166	504		Q91YQ7
ENSMUST00000001083						6	0	2	74	7	2	48	57	36	241	51		
ENSMUST00000001092	ENSMUSG00000001065	8	123254195	123269745	1	19	14	0	90	32	15	373	728	394	61	284		Q8CE64
ENSMUST00000001108	ENSMUSG00000029106	5	34573664	34632308	1	3	8	9	0	0	0	172	131	65	27	122	F8WGR0	
ENSMUST00000001109	ENSMUSG00000001082	5	34633642	34637212	-1	2	0	0	0	0	0	206	332	292	9	247		Q9D2V8
ENSMUST00000001112	ENSMUSG00000052783	5	34660379	34755305	1	0	0	0	0	0	0	8	61	37	16	0		O70291
ENSMUST00000001115	ENSMUSG00000074886	13	55445334	55460925	1	21	13	24	35	46	22	12408	12350	9540	982	6614		O70293
ENSMUST00000001116	ENSMUSG00000001089	4	136469761	136554780	1	54	0	158	0	0	0	31	31	0	20	66		Q8R4U7
ENSMUST00000001122	ENSMUSG00000001095	11	78397087	78422217	-1	26	18	41	28	36	8	0	1	0	0	0		Q9ES88

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000001125	ENSMUSG00000001098	5	114363567	114380508	-1	0	0	0	19	11	0	185	44	301	0	189	F8WGQ9	
ENSMUST00000001126	ENSMUSG00000020829	11	78465697	78472059	1	19	7	52	62	17	9	3	2	2	5	8		Q6PEM8
ENSMUST00000001127	ENSMUSG00000001100	11	78512193	78522736	1	8	7	6	90	8	8	208	306	144	56	139		Q91VA6
ENSMUST00000001130	ENSMUSG00000001103	11	78503447	78505081	1	0	3	14	0	7	6	0	0	0	0	0		P70368
ENSMUST00000001147	ENSMUSG00000001119	10	76708792	76726168	-1	37	26	51	40	35	18	0	0	0	76	447		Q04857
ENSMUST00000001148	ENSMUSG00000001120	10	76761857	76961887	-1	0	3	0	0	0	0	0	0	0	0	13		P57722
ENSMUST00000001155	ENSMUSG00000001127	X	20797814	20860519	1	3	5	8	6	5	2	475	736	450	55	326		P04627
ENSMUST00000001156	ENSMUSG00000001128	X	20925454	20931555	-1	7	10	9	13	13	6	4067	6999	3508	3842	3518	A2AE15	P11680
ENSMUST00000001162						0	0	3	0	0	0	33	114	59	227	42		
ENSMUST00000001166	ENSMUSG00000001138	1	36511867	36528237	1	43	69	97	148	80	0	449	693	540	53	343		Q32NY4
ENSMUST00000001171	ENSMUSG00000001143	1	36419871	36445271	-1	0	0	0	0	0	0	177	384	54	14	0	J3QNZ7	
ENSMUST00000001172	ENSMUSG00000067653	1	36530188	36547201	-1	6	0	15	44	18	4	12	1	9	10	0	Q14A32	Q9D2X0
ENSMUST00000001179	ENSMUSG00000001151	10	76351254	76442912	-1	78	36	115	323	89	48	409	515	1142	58	814	F8VPV0	
ENSMUST00000001181	ENSMUSG00000020241	10	76595762	76623630	-1	17	7	43	269	43	13	0	0	0	20	245		Q02788
ENSMUST00000001183	ENSMUSG00000001155	10	76575648	76590338	1	0	3	23	2	7	3	0	0	0	0	0		Q91XD4
ENSMUST00000001184	ENSMUSG00000001156	6	86647042	86669161	-1	41	39	116	150	67	27	24441	58041	31324	2478	27283	Q8K1Z8	
ENSMUST00000001185	ENSMUSG00000001157	6	86691768	86733383	-1	9	6	5	105	18	12	199	570	335	48	226		Q920G9
ENSMUST00000001186	ENSMUSG00000001158	6	86675151	86684522	-1	4	0	0	6	0	0	173	904	264	891	162		Q8K194
ENSMUST00000001187	ENSMUSG00000029994	6	86736840	86793584	-1	1	0	2	22	3	0	144	179	71	417	139		P97429
ENSMUST00000001202	ENSMUSG00000001173	X	47912387	47965868	1	0	0	7	50	0	2	24	92	169	12	122		Q6NVF0
ENSMUST00000001204	ENSMUSG00000001175	12	100199435	100209806	1	18	7	0	73	11	0	0	31	21	0	63	Q3UKW2	
ENSMUST00000001226	ENSMUSG00000022436	15	78899667	78919517	1	6	7	25	127	29	10	1191	2216	1256	136	1355	A2A5V4	
ENSMUST00000001240	ENSMUSG00000001211	10	78269178	78352489	-1	25	18	53	26	28	13	2	21	33	25	63		Q9D517
ENSMUST00000001242	ENSMUSG00000053329	10	78162067	78169768	-1	12	2	15	69	11	7	252	450	248	111	157		Q9D172
ENSMUST00000001247	ENSMUSG00000029130	5	29195992	29228457	1	0	0	0	0	0	0	0	0	0	0	0		Q9JIT1
ENSMUST00000001253	ENSMUSG00000020651	12	31519827	31559969	-1	14	9	15	82	19	7	0	2	0	0	0		Q9R155
ENSMUST00000001254	ENSMUSG00000001225	12	31390871	31473917	1	8	0	10	8	8	4	0	0	3	0	0		Q9WVC8
ENSMUST00000001256	ENSMUSG00000001227	17	56123085	56140343	-1	21	12	47	540	0	0	19	73	20	0	23	Q3UTK5	O54951
ENSMUST00000001258	ENSMUSG00000001228	17	56303321	56323486	1	26	0	43	42	30	0	65	0	0	0	69		Q8VDF2
ENSMUST00000001279	ENSMUSG00000001247	7	30957770	30973464	-1	10	10	38	58	23	14	19	32	18	0	48		Q99KG5
ENSMUST00000001280	ENSMUSG00000001248	7	31130127	31155896	-1	0	0	0	105	6	0	863	816	635	71	479		Q8VEF1
ENSMUST00000001284	ENSMUSG00000026641	1	171411313	171419142	1	0	0	0	0	0	0	247	117	210	12	133	F8WGH6	
ENSMUST00000001304	ENSMUSG00000001270	12	111669355	111672338	-1	22	17	51	329	26	15	36	57	8	40	163		Q04447
ENSMUST00000001319	ENSMUSG00000001300	8	8617434	8660773	-1	23	14	50	67	28	12	2	11	5	9	78	Q4FJM3	P52800
ENSMUST00000001326	ENSMUSG00000001280	15	102406143	102436404	1	32	36	55	38	36	19	1550	3012	2040	259	1356	G3X8Q0	
ENSMUST00000001327	ENSMUSG00000001281	15	102215995	102231935	-1	26	15	38	131	26	17	872	991	476	106	1220		P26011
ENSMUST00000001331	ENSMUSG00000001285	15	102331709	102338139	1	2	2	0	0	0	0	23	17	80	29	9	F8WGG3	
ENSMUST00000001335	ENSMUSG00000001289	15	102326116	102331873	1	5	0	0	0	0	0	663	1360	553	3826	506	H7BWX1	
ENSMUST00000001339	ENSMUSG00000001305	1	186720978	186749358	-1	0	0	2	3	4	3	11	69	14	273	36		Q9CYX7
ENSMUST00000001347	ENSMUSG00000001313	11	101464999	101471853	1	8	16	0	94	23	0	5	9	2	4	6	A2A4Q3	Q9QYM5
ENSMUST00000001384	ENSMUSG00000001349	9	22099281	22109630	1	18	20	43	38	20	11	0	3	1	0	1	B2RSH3	Q08091
ENSMUST00000001402	ENSMUSG00000001366	9	78081499	78109065	-1	0	4	2	0	0	0	346	670	288	50	205		Q8BK06
ENSMUST00000001412	ENSMUSG00000001376	6	3498382	3603531	1	0	0	1	0	0	1	10	36	37	109	28		Q8CI71
ENSMUST00000001415	ENSMUSG00000006050	18	36666681	36679366	-1	14	11	30	74	19	7	79	288	105	27	164	Q3UR23	Q8R1C9
ENSMUST00000001416	ENSMUSG00000001380	18	36766530	36783205	-1	25	13	112	28	24	11	243	520	331	309	308		Q61035
ENSMUST00000001419	ENSMUSG00000001383	18	36793923	36799660	1	10	18	77	29	22	18	710	4306	1135	3892	1001		Q9CPW7
ENSMUST00000001439	ENSMUSG00000001403	2	164769898	164778822	1	6	11	33	20	16	6	0	0	2	0	0	A2A4Z1	
ENSMUST00000001451	ENSMUSG00000001415	3	88336260	88362338	1	19	6	35	86	32	8	631	742	635	102	559		Q6ZPY2
ENSMUST00000001452	ENSMUSG00000001416	3	88297116	88321767	1	0	0	0	2	0	0	190	590	264	572	450	Q3U4U6	P80318
ENSMUST00000001454	ENSMUSG00000001418	3	88325023	88331313	1	0	0	0	0	0	0	437	439	294	96	115	H9H9R4	
ENSMUST00000001455	ENSMUSG00000001419	3	88142372	88172086	1	19	20	65	45	49	22	918	1675	887	101	1097	Q921S6	
ENSMUST00000001456	ENSMUSG00000001420	3	88328655	88336148	-1	0	3	4	0	3	2	0	0	0	0	0		Q9D709
ENSMUST00000001460	ENSMUSG00000001424	6	28475139	28935162	1	3	7	15	6	9	7	581	630	554	87	610		Q78PY7
ENSMUST00000001479	ENSMUSG00000001440	11	97159714	97187881	-1	31	27	64	95	43	21	988	2500	2070	333	1749		P70168
ENSMUST00000001480	ENSMUSG00000001441	11	97205842	97280638	-1	15	10	9	24	13	6	2333	8109	4396	201	1718		Q11011
ENSMUST00000001484	ENSMUSG00000001444	11	97098071	97115331	-1	20	13	57	342	41	21	6	10	5	0	14	Q3U150	Q9JKD8
ENSMUST00000001485	ENSMUSG00000001445	11	97041560	97049213	1	26	13	49	53	37	15	778	1480	668	214	505		Q3TBW2
ENSMUST00000001497	ENSMUSG00000022219	14	55754045	55758458	-1	2	2	22	0	2	4	0	0	4	8	0		O70303
ENSMUST00000001507	ENSMUSG00000001467	5	4081145	4104746	-1	50	34	45	339	63	35	84	349	210	96	176		Q8K0C4
ENSMUST00000001513	ENSMUSG00000001473	18	67390717	67402748	1	20	9	38	152	28	8	519	387	281	412	580	Q3UMM1	Q922F4
ENSMUST00000001520	ENSMUSG00000031967	8	123477903	123503916	1	33	0	83	55	0	0	564	882	653	101	463		Q920A7
ENSMUST00000001522	ENSMUSG00000001482	8	123442986	123463270	1	15	9	26	0	0	0	44	0	104	0	85		
ENSMUST00000001534	ENSMUSG00000001494	11	101962458	101967015	-1	12	6	25	216	33	6	0	0	0	0	0	B2RQA5	
ENSMUST00000001536	ENSMUSG00000001496	12	56531958	56536908	-1	24	20	39	726	54	24	0	0	0	0	0		P50220
ENSMUST00000001538	ENSMUSG00000001497	12	56691767	56712822	1	26	0	0	0	0	0	0	0	0	0	5	Q3V1K1	P47242
ENSMUST00000001544	ENSMUSG00000023186	9	38718268	38743337	1	0	0	12	15	0	0	101	174	116	259	163		Q99KC8
ENSMUST00000001547	ENSMUSG00000001506	11	94936224	94953042	1	54	41	179	140	88	41	4	3	4	20	167		P11087
ENSMUST00000001548	ENSMUSG00000001507	11	95044474	95076801	-1	14	0	23	214	0	0	0	0	0	79	574		Q62470
ENSMUST00000001559	ENSMUSG00000001518	6	128409444	128424931	-1	6	6	0	19	0	6	29	47	22	13	26		Q91WI7
ENSMUST00000001561	ENSMUSG00000001520	6	128399296	128416427	1	3	1	6	7	3	0	0	0	0	0	0		Q9JHR9
ENSMUST00000001562	ENSMUSG00000001521	6	128321161	128355851	-1	45	25	38	72	37	24	20	24	12	9	57		O88413
ENSMUST00000001565	ENSMUSG00000001524	17	35667730	35673739	-1	17	7	15	40	15	9	48	59	30	19	37	Q542U3	O70422
ENSMUST00000001566	ENSMUSG00000001525	17	35833921	35838306	-1	28	22	66	51	48	18	2740	2495	2070	722	1928		P99024
ENSMUST00000001569	ENSMUSG00000059714	17	35823230	35832791	1	10	3	0	88	8	0	5181	7013	3686	497	2564	Q540I4	O08917
ENSMUST00000001583	ENSMUSG00000001542	13	75707484	75772356	1	34	30	93	174	46	17	142	582	294	104	275		Q3UKU1
ENSMUST00000001592	ENSMUSG00000001552	11	100368958	100397763	-1	15	11	20	0	24	0	909	908	845	31	347		Q02257
ENSMUST00000001595	ENSMUSG00000001555	11	100415697	100424824	1	14	11	24	37	24	7	0	0	0	6	0		Q61576
ENSMUST00000001599	ENSMUSG00000001558	11	100441917	100457022	1	16	10	17	8	16	7	0	0	0	0	0	B2RTD7	Q9D5V2
ENSMUST00000001608	ENSMUSG00000001566	5	29473034	29478470	-1	0	0	0	261	2	0	0	0	0	0	0		Q9QZW9
ENSMUST00000001611	ENSMUSG00000001569	5	29434664	29457843	1	59	55	104	425	96	46	66	232	136	62	151		Q3UFM5
ENSMUST00000001619						3	2	14	9	0	0	36	0	96	19	15		
ENSMUST00000001620	ENSMUSG00000027680	3	34019943	34070322	1	9	16	11	5	0	9	76	289	106	298	117		Q61584
ENSMUST00000001626	ENSMUSG00000001583	11	69851005	69858730	-1	0	0	0	0	21	0	0	0	0	0	0		Q99ML2
ENSMUST00000001631	ENSMUSG00000001588	11	69881567	69895539	-1	14	0	17	14	12	10	2509	3232	2297	222	1876		Q8K2H4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000001652	ENSMUSG00000021070	12	105563172	105593071	1	12	16	12	12	23	10	0	0	1	0	6		P32299
ENSMUST00000001667	ENSMUSG00000001622	5	87925579	87932665	1	21	26	218	27	19	23	1	0	0	27	7		P06796
ENSMUST00000001672	ENSMUSG00000001627	12	40201567	40248504	-1	19	11	45	14	18	13	73	353	161	7	74		P19182
ENSMUST00000001675	ENSMUSG00000001630	6	146724995	146778812	1	7	10	38	20	22	12	14	44	42	12	28		Q7TSE6
ENSMUST00000001699	ENSMUSG00000022484	15	102966796	102971893	1	17	7	57	118	18	3	0	0	0	0	0		P31257
ENSMUST00000001700	ENSMUSG00000001655	15	102921103	102928814	1	11	7	33	166	20	9	0	0	0	0	0		P50207
ENSMUST00000001701	ENSMUSG00000001656	15	102954427	102957708	1	8	6	12	114	21	7	0	0	0	0	0		P31313
ENSMUST00000001703	ENSMUSG00000001657	15	102990607	102994111	1	22	26	172	211	32	21	0	0	1	0	6		P09025
ENSMUST00000001706	ENSMUSG00000036139	15	102976439	102985099	1	189	127	204	6607	416	220	2	15	1	0	7		P09633
ENSMUST00000001709	ENSMUSG00000022485	15	102967443	103017429	1	26	16	35	81	22	4	0	0	0	0	1		P32043
ENSMUST00000001711	ENSMUSG00000001661	15	102998257	103011881	1	7	4	15	60	16	2	0	0	0	0	0	B2RUB8	P10629
ENSMUST00000001712	ENSMUSG00000020196	10	75646110	75764357	-1	72	42	155	191	108	39	834	1023	1021	86	1008	G3X8Q1	
ENSMUST00000001713	ENSMUSG00000001663	10	75783813	75798584	-1	5	1	6	9	0	0	3	2	0	8	0		Q64471
ENSMUST00000001715	ENSMUSG00000001665	10	75774115	75781414	-1	15	9	34	10	28	10	12	20	11	3	23	Q99L20	
ENSMUST00000001716	ENSMUSG00000001666	10	75771230	75773414	-1	4	0	1	20	2	1	95	119	62	117	72	Q3UNI8	O35215
ENSMUST00000001720	ENSMUSG00000001670	8	109990437	109999803	1	16	18	28	12	16	12	0	0	0	10	0		Q8QZR1
ENSMUST00000001722	ENSMUSG00000001672	8	109947914	109962203	-1	7	7	16	120	13	6	0	0	0	0	0	G3X8Q2	
ENSMUST00000001724	ENSMUSG00000001674	1	121553835	121567989	-1	12	10	16	59	9	15	47	209	99	247	147	B2RUM8	Q8K363
ENSMUST00000001757	ENSMUSG00000001707	13	38645698	38659028	-1	4	1	0	76	9	4	14	58	25	134	21		Q9D1M4
ENSMUST00000001780	ENSMUSG00000001729	12	112653821	112674884	-1	14	7	25	24	15	11	5998	9057	5685	904	4232		P31750
ENSMUST00000001790	ENSMUSG00000001739	5	136966616	136975858	1	0	0	0	0	18	9	162	476	115	23	36		Q9Z0S5
ENSMUST00000001792	ENSMUSG00000001741	7	83642848	83745726	-1	4	5	45	22	25	3	22	43	38	11	73		O54824
ENSMUST00000001801	ENSMUSG00000001750	19	3896050	3907133	-1	6	0	0	21	0	0	1178	1106	1130	226	939	Q9JHF5	
ENSMUST00000001802	ENSMUSG00000001751	11	101070012	101077672	1	12	3	27	191	30	14	205	177	147	62	259	O88325	
ENSMUST00000001806	ENSMUSG00000001755	11	101082565	101086619	1	0	1	11	19	12	9	196	311	145	38	98		Q9DBL7
ENSMUST00000001809	ENSMUSG00000022283	15	36595661	36608973	-1	11	8	38	150	29	14	4811	9493	6354	533	4275		P29341
ENSMUST00000001812	ENSMUSG00000001761	6	29735503	29761365	1	39	20	135	616	57	39	24	41	15	16	45	Q4VBD5	P56726
ENSMUST00000001818	ENSMUSG00000001767	2	145917479	145935014	-1	29	19	21	44	25	10	284	1281	701	964	282		P63154
ENSMUST00000001824	ENSMUSG00000001773	7	86719352	86775864	-1	5	0	0	3	3	7	0	0	0	0	0		O35409
ENSMUST00000001825	ENSMUSG00000001774	9	18292267	18314000	1	5	5	21	63	19	2	114	493	198	263	125		Q9D1P4
ENSMUST00000001826	ENSMUSG00000043943	9	18321951	18402995	-1	0	3	0	0	0	0	0	0	0	0	0	G3UWC2	
ENSMUST00000001834	ENSMUSG00000001783	10	85938637	85957823	-1	16	7	28	31	16	4	443	749	465	590	456		Q99LF4
ENSMUST00000001836	ENSMUSG00000001785	10	85871831	85889096	1	8	10	10	27	12	9	139	593	239	292	113		Q99LL5
ENSMUST00000001837	ENSMUSG00000001786	10	86021972	86051873	1	0	1	0	26	0	2	0	29	37	24	19	F8WIP1	
ENSMUST00000001845	ENSMUSG00000001794	7	30186942	30195164	-1	9	0	13	27	5	0	440	435	242	25	182		
ENSMUST00000001854	ENSMUSG00000030495	7	35186385	35201114	1	12	0	14	0	0	0	0	0	0	0	0		P63115
ENSMUST00000001867	ENSMUSG00000001815	2	74652991	74659557	-1	21	12	30	150	24	13	0	0	0	0	0	G5E813	
ENSMUST00000001872	ENSMUSG00000001819	2	74668310	74671599	1	13	7	20	85	9	5	0	0	0	0	0		P70217
ENSMUST00000001878	ENSMUSG00000001823	2	74675013	74677705	1	24	22	53	190	31	11	0	0	0	0	0		P23812
ENSMUST00000001882	ENSMUSG00000001827	7	101858331	101870788	-1	2	0	17	0	0	0	0	0	0	0	0		P35846
ENSMUST00000001884	ENSMUSG00000001829	7	101663633	101790168	1	36	30	76	32	38	19	6	6	11	0	12	Q3URM1	Q60649
ENSMUST00000001900	ENSMUSG00000001844	5	143316489	143329256	-1	0	0	0	28	0	0	237	281	259	15	194		Q9D6H5
ENSMUST00000001920	ENSMUSG00000001864	2	31950139	31973442	1	17	10	42	70	27	7	0	1	1	16	10		Q9EQX4
ENSMUST00000001921	ENSMUSG00000001865	3	20215620	20242181	-1	4	5	5	11	3	1	83	197	94	77	28	Q542E3	P15089
ENSMUST00000001927	ENSMUSG00000001870	17	75005568	75392512	1	17	13	31	186	37	5	0	0	0	0	37		Q8CG19
ENSMUST00000001950	ENSMUSG00000025139	7	141874813	141918507	-1	27	11	62	55	28	9	1314	2332	1536	171	921		Q9QZ06
ENSMUST00000001963	ENSMUSG00000020681	11	105967945	105989964	1	31	12	27	89	31	25	35	56	12	0	53	Q3TU20	P09470
ENSMUST00000001964	ENSMUSG00000020681	11	105967945	105989964	1	8	3	31	7	18	4	4	15	0	1	0		P09470
ENSMUST00000001965	ENSMUSG00000001901	11	106008124	106034549	1	19	17	54	30	41	13	0	0	0	0	0	Q32ME0	
ENSMUST00000001974	ENSMUSG00000001909	8	84686307	84699808	1	8	1	3	3	3	4	0	10	0	0	0		
ENSMUST00000001975	ENSMUSG00000001910	8	84670483	84687862	-1	48	20	139	90	62	36	1326	941	1019	96	893		Q7TSZ8
ENSMUST00000001984	ENSMUSG00000007209	7	16721929	16726132	1	11	9	11	15	17	6	0	0	0	0	0	Q78T27	
ENSMUST00000001989	ENSMUSG00000001924	X	20658326	20683179	1	41	0	42	96	58	22	6132	7034	7047	543	4964	B9EHN0	Q02053
ENSMUST00000001995						0	0	0	28	38	0	55	19	53	0	122		
ENSMUST00000002007	ENSMUSG00000001942	9	37613847	37648318	1	15	22	22	30	19	16	30	91	49	47	97		P70665
ENSMUST00000002008	ENSMUSG00000001943	9	37539255	37544205	1	11	1	24	17	22	9	0	1	0	0	4		Q9Z109
ENSMUST00000002011	ENSMUSG00000001946	9	37528078	37538319	1	17	7	15	72	15	5	7	2	1	8	12	Q3U102	Q925F2
ENSMUST00000002013	ENSMUSG00000001948	9	37603295	37613720	-1	5	8	26	15	3	8	1	14	7	32	4	Q545M2	Q62252
ENSMUST00000002025	ENSMUSG00000025519	8	66511756	66518335	1	12	2	14	4	15	6	0	1	0	0	0		
ENSMUST00000002029	ENSMUSG00000001964	X	74254687	74261548	1	0	3	10	12	4	1	595	886	387	124	253		O08579
ENSMUST00000002043	ENSMUSG00000078622	11	106197408	106216344	-1	34	38	74	74	57	27	262	1051	611	554	410	Q0VBU4	Q9D024
ENSMUST00000002044	ENSMUSG00000020700	11	106084613	106155446	1	15	18	18	91	31	19	4799	6309	6226	610	5649		Q61084
ENSMUST00000002048	ENSMUSG00000001983	11	106066061	106073612	1	12	11	16	184	9	7	59	160	83	56	67		Q8K0Z7
ENSMUST00000002053	ENSMUSG00000001988	7	16455721	16476780	-1	18	17	40	190	33	8	8	4	4	1	1	A2RSH6	P97459
ENSMUST00000002063	ENSMUSG00000001998	2	127008717	127067909	1	39	20	40	19	25	19	47	146	109	5	77		Q80V94
ENSMUST00000002064	ENSMUSG00000001999	2	127070665	127097084	1	3	4	7	2	5	1	61	259	74	683	144		Q9CY64
ENSMUST00000002073	ENSMUSG00000002020	12	84783212	84876532	-1	33	16	0	81	23	25	0	0	0	0	87	E9QNQ3	
ENSMUST00000002079	ENSMUSG00000031385	X	73757090	73772514	1	0	12	0	2	11	14	0	0	0	0	0		Q9QY40
ENSMUST00000002080	ENSMUSG00000002006	X	73793359	73824969	-1	8	9	17	124	19	8	11	11	0	0	23		Q9QY39
ENSMUST00000002081	ENSMUSG00000002007	X	73774405	73778925	1	0	3	10	0	0	0	4	0	0	1	17	Q0VAW8	Q9Z0G2
ENSMUST00000002084	ENSMUSG00000031378	X	73716597	73738534	1	8	7	17	29	13	7	2513	2432	2314	203	1523		P48410
ENSMUST00000002087	ENSMUSG00000002012	X	73655994	73660117	-1	0	3	20	38	5	0	0	0	0	0	0	Q3TYC1	Q9QYK9
ENSMUST00000002090	ENSMUSG00000002014	X	73787028	73790830	1	0	0	2	0	0	1	166	177	122	604	63	Q3TVJ8	Q62186
ENSMUST00000002091	ENSMUSG00000002015	X	73686178	73716175	-1	6	8	16	18	5	4	732	2103	725	1562	614		Q61335
ENSMUST00000002095	ENSMUSG00000002028	9	44803355	44881296	-1	83	48	264	57	0	55	584	814	1503	44	1191		P55200
ENSMUST00000002099	ENSMUSG00000002031	9	44767908	44792714	1	35	36	34	38	30	17	4	2	18	6	14		Q9DB07
ENSMUST00000002100	ENSMUSG00000002032	9	44793776	44799307	-1	0	0	0	42	12	3	1	0	1	0	0		Q9DCF1
ENSMUST00000002101	ENSMUSG00000002033	9	44969572	44980431	-1	5	0	0	11	6	3	52	208	30	302	121	Q3U4Y3	P11942
ENSMUST00000002112	ENSMUSG00000002043	7	19508670	19516145	1	0	0	0	0	0	0	214	291	164	73	85		Q78XR0
ENSMUST00000002121	ENSMUSG00000002052	11	78206746	78245987	-1	25	33	81	163	56	27	1001	1621	2503	161	2067		Q62383
ENSMUST00000002127	ENSMUSG00000002058	11	78343482	78349164	1	0	4	0	60	0	0	2332	3843	2032	1920	939	Q3V299	Q9Z2R6
ENSMUST00000002128	ENSMUSG00000002059	11	78188430	78192193	1	0	4	16	21	0	4	0	0	1	5	13	Q0PD20	
ENSMUST00000002133	ENSMUSG00000002064	11	78245746	78255496	1	8	0	33	6	0	5	219	774	319	965	274		
ENSMUST00000002145	ENSMUSG00000002076	17	31944769	32034508	-1	51	39	341	58	34	23	1	4	4	0	2	Q9D4G2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000002152	ENSMUSG00000002083	7	16309616	16318205	1	8	1	10	358	23	4	198	263	185	42	118	B2RVL4	Q99ML1
ENSMUST00000002171	ENSMUSG00000002102	2	91054009	91066369	1	6	3	0	3	6	4	0	19	5	0	16	B7ZCF1	
ENSMUST00000002172	ENSMUSG00000002103	2	91202885	91214098	1	30	26	37	24	37	16	92	459	169	74	146		P24638
ENSMUST00000002176	ENSMUSG00000002107	2	6539694	7509563	-1	11	0	0	0	0	0	0	0	0	0	0		Q9Z0H4
ENSMUST00000002177	ENSMUSG00000002108	2	91184061	91202834	-1	0	1	4	3	8	0	0	0	0	0	0	Q91X41	Q9Z0Y9
ENSMUST00000002180	ENSMUSG00000002111	2	91082390	91115756	1	14	9	27	169	34	13	11321	16550	8580	1237	5719	Q3U5L4	P17433
ENSMUST00000002198	ENSMUSG00000002129	11	4160350	4182541	1	33	38	93	40	37	15	527	682	496	52	436		Q8K4Z5
ENSMUST00000002259	ENSMUSG00000002190	8	83389867	83428552	1	20	19	32	19	14	10	0	0	0	0	0		P52194
ENSMUST00000002274	ENSMUSG00000002204	7	44572432	44586862	1	21	9	133	51	26	13	4157	4640	2952	638	2154	Q3U7H1	O09043
ENSMUST00000002275	ENSMUSG00000002205	7	44748413	44777515	1	2	0	4	10	0	0	1773	2972	1380	273	997	Q3TAR6	Q8K3G5
ENSMUST00000002280	ENSMUSG00000002210	7	24399619	24422778	1	5	1	5	2	5	0	546	642	409	56	258		Q9DB90
ENSMUST00000002284	ENSMUSG00000046223	7	24462484	24475968	1	22	20	94	41	24	15	3893	6203	3058	700	3181	Q545X5	P35456
ENSMUST00000002289	ENSMUSG00000022111	14	101653967	101696124	1	2	0	2	42	1	0	40	196	52	129	31		Q9JKB1
ENSMUST00000002291	ENSMUSG00000002221	5	27740080	27791691	-1	57	76	210	149	68	38	212	271	305	48	220		Q6NZQ4
ENSMUST00000002292	ENSMUSG00000002222	6	71388634	71440637	-1	8	20	5	87	15	5	554	926	1181	142	760		Q80YQ8
ENSMUST00000002297	ENSMUSG00000002227	3	104794836	104818563	-1	9	15	0	0	0	0	251	825	812	0	276	D3YVL0	
ENSMUST00000002298	ENSMUSG00000002228	3	104781056	104786018	1	17	10	27	153	16	17	82	237	104	8	21		Q149T7
ENSMUST00000002303	ENSMUSG00000002233	3	104788375	104794459	1	0	4	16	6	2	0	316	872	226	461	321		Q62159
ENSMUST00000002305	ENSMUSG00000042599	6	39136623	39206789	-1	45	28	120	137	36	20	4053	10754	6595	615	4937		Q3UWM4
ENSMUST00000002310	ENSMUSG00000002240	5	87825686	87846387	1	7	7	14	17	10	4	0	0	0	0	0	E9Q591	
ENSMUST00000002318	ENSMUSG00000024220	17	28177207	28205886	1	9	0	0	24	6	8	0	0	31	0	17		Q8BMU0
ENSMUST00000002320	ENSMUSG00000002250	17	28232754	28301469	1	22	8	25	59	23	6	1124	1581	1276	86	964	Q546I3	P35396
ENSMUST00000002327	ENSMUSG00000002257	17	28207778	28228608	1	17	13	45	202	40	19	2434	3127	2503	296	1490		
ENSMUST00000002336	ENSMUSG00000002266	7	6671456	6696450	-1	10	10	54	39	25	12	0	0	0	0	0	Q8C393	
ENSMUST00000002344	ENSMUSG00000002274	17	25794571	25797136	-1	1	0	0	88	5	2	28	15	11	42	34	A2RSN4	Q8C1Q4
ENSMUST00000002350	ENSMUSG00000002280	17	25773776	25783332	1	0	2	8	27	0	0	209	338	147	48	149		Q7TMW6
ENSMUST00000002360	ENSMUSG00000002289	17	33773750	33781575	-1	3	18	5	28	13	8	0	0	0	3	0		Q9Z1P8
ENSMUST00000002368	ENSMUSG00000002297	5	8396973	8422716	-1	0	0	0	0	0	0	34	0	27	8	12		Q9QZ41
ENSMUST00000002379	ENSMUSG00000002308	17	33843091	33849774	1	6	9	17	48	31	13	0	0	0	0	3		Q9Z1P5
ENSMUST00000002389	ENSMUSG00000022218	14	55700009	55713492	-1	18	9	61	13	15	0	31	103	0	0	0		
ENSMUST00000002391	ENSMUSG00000002320	14	55635965	55643806	-1	0	0	0	0	8	0	227	430	273	30	273		Q9DBU0
ENSMUST00000002395	ENSMUSG00000002324	14	55618037	55625395	1	16	15	39	24	18	11	1	1	1	0	2		Q8C5S7
ENSMUST00000002397	ENSMUSG00000002326	14	55672235	55678750	1	15	8	10	9	9	4	154	579	206	321	197		Q99L27
ENSMUST00000002398	ENSMUSG00000022220	14	55769058	55784042	-1	26	0	43	0	0	0	20	0	0	8	0		Q91WF3
ENSMUST00000002400	ENSMUSG00000002329	14	55657879	55660508	-1	18	18	56	67	34	12	70	244	84	102	72		Q9D967
ENSMUST00000002403	ENSMUSG00000002332	14	55739020	55745690	-1	0	2	32	12	3	5	1891	2665	1740	545	718		Q99L04
ENSMUST00000002412	ENSMUSG00000002341	8	70093085	70120873	-1	106	89	404	357	140	71	2	3	1	3	6		
ENSMUST00000002413	ENSMUSG00000002342	8	70172356	70183681	1	0	0	6	0	0	0	12	0	0	0	23		Q8VCA6
ENSMUST00000002418	ENSMUSG00000002345	8	70139499	70167488	1	4	9	3	2	9	5	83	109	43	31	12		Q9D6Y4
ENSMUST00000002436	ENSMUSG00000002365	17	5841328	5931033	1	18	15	26	41	29	10	234	678	576	117	474	Q3U1P2	Q91VH2
ENSMUST00000002444	ENSMUSG00000024206	17	56775897	56831008	-1	0	21	44	0	0	24	82	0	48	0	206		P48379
ENSMUST00000002445	ENSMUSG00000002372	17	56673225	56711769	1	25	16	54	62	39	18	745	1077	642	133	684		Q9CT10
ENSMUST00000002452	ENSMUSG00000002379	17	56717762	56724248	1	18	14	42	65	28	14	407	501	318	1271	155	G5E814	
ENSMUST00000002456	ENSMUSG00000020622	12	10369973	10390173	1	15	4	37	0	24	0	0	0	0	0	0		Q91YE9
ENSMUST00000002457	ENSMUSG00000002384	4	123105165	123132099	1	35	18	23	197	37	13	0	1	0	0	1		P55105
ENSMUST00000002466	ENSMUSG00000002393	8	71374123	71381960	-1	0	3	3	358	2	0	91	214	97	68	93		P43136
ENSMUST00000002469	ENSMUSG00000002396	8	71371298	71379361	1	2	0	15	45	0	2	331	680	300	108	231	G5E815	
ENSMUST00000002473	ENSMUSG00000031820	8	71396855	71404772	1	15	10	23	49	19	8	544	632	335	152	250		Q3UI43
ENSMUST00000002487	ENSMUSG00000002413	6	39603237	39725463	-1	31	31	43	41	29	26	964	3311	1986	206	1599		P28028
ENSMUST00000002490						0	0	0	66	2	0	43	104	21	71	17		
ENSMUST00000002495	ENSMUSG00000041420	7	16175090	16186504	1	0	0	0	0	0	0	0	0	0	0	1		P97368
ENSMUST00000002502	ENSMUSG00000002428	3	20057811	20118490	1	0	0	0	0	0	0	114	255	206	117	147		Q6PCN7
ENSMUST00000002518	ENSMUSG00000054452	10	81559494	81566362	1	11	13	14	81	19	2	4594	5433	2744	724	2222	Q3TYD9	P63002
ENSMUST00000002529	ENSMUSG00000002455	2	181591868	181655660	1	3	2	2	12	0	2	54	88	99	25	48		Q91YR7
ENSMUST00000002532	ENSMUSG00000002458	2	181688419	181693977	-1	0	0	0	20	0	0	1586	3345	1340	8	720	Q78NN4	Q9CX84
ENSMUST00000002533	ENSMUSG00000002459	1	4909576	5070285	-1	214	119	316	2957	382	194	1	6	1	0	0		Q9QZB1
ENSMUST00000002549	ENSMUSG00000002475	18	10644411	10706771	-1	0	2	5	0	0	5	4	1	0	0	5		Q91ZH7
ENSMUST00000002551	ENSMUSG00000002477	18	10617796	10628230	1	6	6	11	33	4	2	99	311	92	583	91		P62315
ENSMUST00000002572	ENSMUSG00000002504	17	24639282	24650305	-1	11	5	34	140	14	13	155	164	140	5	68		
ENSMUST00000002588	ENSMUSG00000002489	16	89787111	89980080	-1	0	0	0	19	0	29	1	170	447	0	365	G3UWG2	
ENSMUST00000002599	ENSMUSG00000002524	15	76070184	76080946	-1	0	10	25	23	30	12	894	1311	674	342	533		Q3UEB3
ENSMUST00000002603	ENSMUSG00000022568	15	76047158	76069784	-1	47	28	111	0	35	0	119	0	155	0	68		Q80U72
ENSMUST00000002625	ENSMUSG00000002550	2	32255002	32260159	-1	14	11	12	109	21	4	233	262	157	36	83	A2AN37	
ENSMUST00000002640	ENSMUSG00000002565	12	40059769	40134228	-1	17	21	17	192	26	9	7	9	7	4	0		Q60604
ENSMUST00000002655	ENSMUSG00000002580	11	98437708	98438991	-1	2	5	8	48	11	2	543	1163	291	325	203		Q9CQ86
ENSMUST00000002663	ENSMUSG00000002588	6	5168090	5193946	-1	7	10	4	0	7	6	0	0	0	5	0		P52430
ENSMUST00000002677	ENSMUSG00000002602	7	25757273	25788705	-1	8	7	10	7	16	7	12	26	0	74	279		Q00993
ENSMUST00000002678	ENSMUSG00000002603	7	25687002	25705077	1	12	7	11	351	19	8	1552	2001	1335	122	1460	Q3UNK5	P04202
ENSMUST00000002683	ENSMUSG00000002608	7	25711106	25719088	-1	33	10	35	226	27	22	1623	2154	1272	135	1171		Q9DBT3
ENSMUST00000002699	ENSMUSG00000024045	17	32303676	32321153	-1	51	47	79	50	65	22	273	1810	667	246	896	Q059U9	Q9DBR0
ENSMUST00000002708	ENSMUSG00000002633	5	28456815	28467256	-1	16	7	21	154	24	4	0	2	0	0	2		Q62226
ENSMUST00000002710	ENSMUSG00000002635	7	34184499	34196661	-1	6	8	24	103	14	5	148	408	151	239	120		Q8C5N5
ENSMUST00000002733	ENSMUSG00000002658	17	57003405	57011288	-1	18	12	22	19	27	6	405	905	537	1094	543		Q3THK3
ENSMUST00000002735	ENSMUSG00000002660	17	56990264	56996371	1	9	4	31	113	17	15	114	121	62	89	76		O88696
ENSMUST00000002737	ENSMUSG00000002661	17	56997339	56999322	1	4	0	4	42	11	4	38	64	18	15	24		Q9D6Z0
ENSMUST00000002740	ENSMUSG00000002664	17	56999457	57000018	-1	3	2	7	8	8	0	2	3	0	0	1	A1L3Q1	
ENSMUST00000002756	ENSMUSG00000002679	12	81573557	81595008	-1	0	0	0	0	0	0	46	312	95	84	2		
ENSMUST00000002757	ENSMUSG00000091803	12	81359026	81485127	-1	20	16	34	13	17	4	3	1	0	0	2		Q9CR63
ENSMUST00000002765	ENSMUSG00000002688	12	50341231	50649223	-1	13	12	7	36	22	6	0	0	0	0	0		Q62101
ENSMUST00000002790	ENSMUSG00000002718	2	166906040	166946389	1	0	0	8	59	7	0	18	146	131	195	95		Q9ERK4
ENSMUST00000002805	ENSMUSG00000002728	2	145902099	145916425	1	0	0	0	0	0	0	0	18	23	55	0	Q9DB82	
ENSMUST00000002808	ENSMUSG00000002731	2	76629898	76648015	-1	5	2	4	83	7	4	139	619	207	313	127		Q9WTX2
ENSMUST00000002809	ENSMUSG00000002732	2	76663044	76673116	-1	0	2	2	0	5	0	4	14	2	50	5	Q3UU11	O54998
ENSMUST00000002817	ENSMUSG00000057897	11	5969644	6066362	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SVJ1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000002818	ENSMUSG00000002741	11	5955693	5967780	1	28	14	66	142	38	5	1621	2953	1782	359	1054		Q9CQW1
ENSMUST00000002825	ENSMUSG00000002748	5	135187264	135246129	1	34	28	60	118	46	31	972	2373	2296	212	1829		Q9Z277
ENSMUST00000002837	ENSMUSG00000063406	5	108106366	108132620	-1	0	5	0	30	0	0	231	406	182	163	143	A2RS96	Q9CXE7
ENSMUST00000002839	ENSMUSG00000059409	17	46682991	46705002	-1	28	19	153	87	43	16	560	731	575	71	526	Q91V89	
ENSMUST00000002840	ENSMUSG00000002763	17	46711463	46725541	1	0	0	0	0	0	0	658	499	370	34	266		Q99LC9
ENSMUST00000002844	ENSMUSG00000002767	17	46646229	46650139	1	0	0	0	8	0	0	74	161	117	61	130		Q9D773
ENSMUST00000002845	ENSMUSG00000002768	17	46681137	46683105	1	12	7	25	25	18	6	687	923	445	1067	369		Q64327
ENSMUST00000002846	ENSMUSG00000002769	17	46725664	46729168	-1	5	4	4	83	11	9	11	26	15	30	11		Q9QXF8
ENSMUST00000002848	ENSMUSG00000002771	7	45831883	45870928	-1	34	24	78	444	65	22	8	4	3	5	10		Q03391
ENSMUST00000002850	ENSMUSG00000030834	7	45976380	46030302	-1	42	30	71	47	70	28	0	0	0	2	0		Q9R1S7
ENSMUST00000002855	ENSMUSG00000002778	7	45872772	45883731	1	0	0	3	123	11	1	718	1559	723	158	637		Q99JH8
ENSMUST00000002874						2	1	4	48	1	1	1	67	6	29	2		
ENSMUST00000002880	ENSMUSG00000002803	12	112976482	112978930	1	0	0	0	156	24	0	0	0	0	0	0	G5E817	
ENSMUST00000002881	ENSMUSG00000002804	12	112934733	112942118	-1	5	6	8	31	16	5	70	79	30	31	38		Q9D142
ENSMUST00000002883	ENSMUSG00000021319	13	19623175	19632821	1	11	8	49	98	6	4	0	0	0	0	0		Q9Z1N6
ENSMUST00000002885	ENSMUSG00000002808	13	19591709	19619830	-1	16	10	17	148	21	10	4	6	1	5	3		Q99M71
ENSMUST00000002889	ENSMUSG00000002812	11	60714123	60727263	-1	35	19	26	49	48	17	5388	5769	6040	510	4390		Q9JJ28
ENSMUST00000002891	ENSMUSG00000002814	11	60740058	60777365	-1	27	9	0	23	23	12	74	167	129	13	147	Q5NCT2	O70157
ENSMUST00000002902	ENSMUSG00000002825	9	21411837	21420277	1	5	7	33	169	20	6	33	41	21	46	42		Q9JMA2
ENSMUST00000002908	ENSMUSG00000002831	17	56100591	56109803	-1	32	22	70	0	43	16	15	38	24	1	46		O88492
ENSMUST00000002911	ENSMUSG00000002833	17	56079657	56100596	1	19	13	40	69	40	10	397	817	506	66	491		Q3UMU9
ENSMUST00000002914	ENSMUSG00000002835	17	56040416	56068026	1	17	20	43	33	40	9	154	139	117	12	120		Q9QWF0
ENSMUST00000002923	ENSMUSG00000002844	16	38445399	38452689	-1	11	16	29	143	22	5	2726	3700	1620	207	1246	Q3U5N4	P54923
ENSMUST00000002924	ENSMUSG00000002845	16	38558698	38592162	1	0	8	0	0	0	0	10	33	10	0	0		Q9CYC3
ENSMUST00000002925	ENSMUSG00000002846	16	38498347	38522663	-1	74	117	415	182	95	50	110	315	123	49	101		Q8BUY5
ENSMUST00000002926	ENSMUSG00000002847	16	38396119	38433145	-1	9	12	20	12	9	9	0	0	2	50	32		Q8VI78
ENSMUST00000002964	ENSMUSG00000002885	8	83723251	83741326	-1	0	0	0	11	2	2	2390	3013	1842	185	2253	A0A0D9SEG8	
ENSMUST00000002976	ENSMUSG00000002897	6	120463247	120487559	1	155	87	693	379	120	61	8627	19766	12674	1002	11963		Q60943
ENSMUST00000002979	ENSMUSG00000002900	12	31265234	31329644	1	9	6	60	4	24	2	0	3	0	67	253	E9QN70	
ENSMUST00000002989	ENSMUSG00000002910	8	70835155	70839720	-1	16	17	36	141	14	19	206	513	242	71	238		Q9D668
ENSMUST00000003017	ENSMUSG00000029925	6	38875404	39084585	1	2	0	0	0	3	0	106	148	92	340	291		P36423
ENSMUST00000003027	ENSMUSG00000002948	8	4238740	4251423	1	0	0	0	10	0	0	0	0	0	0	0		Q8CE90
ENSMUST00000003029	ENSMUSG00000002949	8	4259731	4275913	-1	0	6	0	13	0	0	85	265	177	187	172		O35857
ENSMUST00000003035	ENSMUSG00000030768	1	183086266	183221522	-1	41	0	0	0	0	0	44	85	66	0	33		Q3TDN0
ENSMUST00000003038	ENSMUSG00000002957	7	141562173	141633011	1	31	26	83	123	42	29	2473	3361	3586	311	1876		P17427
ENSMUST00000003044	ENSMUSG00000002963	7	44857139	44862992	1	4	0	15	17	0	11	1472	2006	1235	98	612	G5E8N7	
ENSMUST00000003049	ENSMUSG00000002968	7	44879391	44892397	-1	20	8	40	170	27	11	459	640	457	52	452		Q8VCB2
ENSMUST00000003061	ENSMUSG00000002980	7	19756131	19771016	-1	17	15	18	76	20	6	0	0	1	11	37		Q9R069
ENSMUST00000003066	ENSMUSG00000002985	7	19696109	19699166	-1	0	0	0	10	0	0	0	0	0	0	0	Q3TXU4	P08226
ENSMUST00000003071	ENSMUSG00000074336	7	19678094	19681416	-1	2	2	12	5	2	5	0	0	0	34	1		Q61268
ENSMUST00000003074	ENSMUSG00000002992	7	19671579	19681423	-1	2	2	0	4	3	0	461	864	230	1401	178	Q3UJG0	Q05020
ENSMUST00000003079	ENSMUSG00000002997	12	31958476	32061296	-1	1	0	0	150	8	0	105	768	511	68	205		P31324
ENSMUST00000003100	ENSMUSG00000052974	7	27119909	27133660	1	21	7	30	21	22	7	0	0	0	2	0		P33267
ENSMUST00000003115	ENSMUSG00000003031	6	134920401	134925513	1	2	0	8	169	3	3	1379	2320	1570	562	1742		P46414
ENSMUST00000003117	ENSMUSG00000003033	8	72240018	72257385	1	12	10	34	64	28	9	3906	4389	2755	395	2230	Q3UG16	P35585
ENSMUST00000003121	ENSMUSG00000003037	8	72161200	72183904	1	80	72	168	116	76	53	1972	4854	2153	1240	1774	Q0PD50	P55258
ENSMUST00000003123	ENSMUSG00000003039	8	72219730	72223764	1	16	10	56	84	17	11	2875	8702	2976	9139	2759		Q9CR80
ENSMUST00000003135	ENSMUSG00000003051	1	135253575	135258568	-1	23	22	17	13	21	0	0	0	0	0	0		Q3UPW2
ENSMUST00000003137	ENSMUSG00000003053	19	39269405	39330713	1	0	0	0	0	0	0	0	0	0	0	0		Q64458
ENSMUST00000003152	ENSMUSG00000003068	10	80115803	80130682	1	0	0	0	186	0	0	548	520	671	37	233		Q9WTK7
ENSMUST00000003154	ENSMUSG00000003070	10	80179482	80190010	1	12	5	20	138	12	9	0	0	0	1	2		P52801
ENSMUST00000003156	ENSMUSG00000003072	10	80138632	80145818	1	8	10	5	0	13	1	1152	1625	762	187	546	Q4FK74	Q9D3D9
ENSMUST00000003183	ENSMUSG00000003099	7	17004640	17027924	-1	0	2	0	13	6	2	93	124	117	7	128		Q60676
ENSMUST00000003191	ENSMUSG00000024070	17	78949405	79020816	-1	16	23	20	0	28	0	123	639	254	115	211		Q8K1Y2
ENSMUST00000003203	ENSMUSG00000003119	11	98203059	98278504	1	6	6	39	2	0	2	30	0	10	0	77		Q14AX6
ENSMUST00000003207	ENSMUSG00000003123	7	25379527	25398710	-1	22	12	105	143	35	21	617	366	372	28	293		P54310
ENSMUST00000003219	ENSMUSG00000003135	1	39534992	39546889	1	0	16	34	0	1	5	148	392	211	38	219		Q9CWN7
ENSMUST00000003238	ENSMUSG00000003154	6	122819914	122845366	1	24	32	158	216	63	16	332	174	419	24	411		Q9ES18
ENSMUST00000003245						0	0	0	0	0	0	3267	6587	3298	3004	1755		
ENSMUST00000003268	ENSMUSG00000003200	17	56016753	56036637	-1	16	7	16	157	24	14	927	1534	875	114	850	Q3TRJ7	Q62419
ENSMUST00000003274	ENSMUSG00000003206	17	55952623	55957021	1	5	5	41	46	10	6	1092	2435	1029	138	611	Q3U1K3	O35228
ENSMUST00000003284	ENSMUSG00000003184	7	44997648	45002847	1	7	10	14	25	4	1	55	15	7	13	18	Q3U9K6	P70671
ENSMUST00000003290	ENSMUSG00000003190	7	44991225	44997579	-1	3	0	20	45	0	4	31	62	30	4	18	Q9D3J3	
ENSMUST00000003310	ENSMUSG00000003226	10	58446852	58494155	1	30	23	26	59	27	11	619	1953	1635	641	849		Q9ERU9
ENSMUST00000003312	ENSMUSG00000003227	10	58600789	58675654	-1	29	18	28	36	35	21	0	0	0	0	0		Q9R187
ENSMUST00000003313	ENSMUSG00000003228	19	60889749	61092553	1	21	21	20	382	32	7	289	597	471	93	349	Q3TST4	Q8VEB1
ENSMUST00000003318	ENSMUSG00000003233	16	20516982	20532520	1	9	6	9	152	9	6	88	40	144	0	59		Q61062
ENSMUST00000003319	ENSMUSG00000003234	16	20548577	20561379	1	14	8	54	20	21	7	434	624	435	245	395		Q8K268
ENSMUST00000003320	ENSMUSG00000003235	16	20498817	20509955	1	22	15	33	80	26	7	302	476	314	76	262		Q8CHW4
ENSMUST00000003345	ENSMUSG00000021314	13	18948351	19150915	1	29	19	41	60	31	12	0	1	0	0	0		Q7TQF7
ENSMUST00000003351	ENSMUSG00000020734	11	115249169	115267243	-1	2	0	0	127	33	11	1	0	1	0	1	A2A6S2	Q01098
ENSMUST00000003360	ENSMUSG00000003273	7	45699867	45704659	1	7	3	4	150	14	9	0	1	0	0	1	Q541E9	O70354
ENSMUST00000003369	ENSMUSG00000003282	4	3900996	3938423	-1	20	12	20	16	32	12	6	9	18	3	21		Q9QYE0
ENSMUST00000003370	ENSMUSG00000003283	2	153108468	153151441	1	2	1	5	23	4	2	1505	2029	1375	237	630	F6UND7	
ENSMUST00000003386	ENSMUSG00000003299	9	21002737	21008835	1	12	8	14	122	24	17	434	678	379	80	264		Q9DCU6
ENSMUST00000003395	ENSMUSG00000032177	9	21165714	21213248	1	9	8	23	44	9	4	0	0	0	0	8		O89084
ENSMUST00000003397	ENSMUSG00000003309	9	21295457	21312333	-1	13	14	22	29	14	6	34	55	30	11	26		
ENSMUST00000003404	ENSMUSG00000003316	8	111154421	111259216	-1	2	0	0	0	4	0	7	0	337	0	53	F8WHM5	
ENSMUST00000003413	ENSMUSG00000061126	17	32468462	32492479	1	16	13	14	42	20	9	1	0	0	0	0	Q8BGU0	
ENSMUST00000003416	ENSMUSG00000048440	17	32536558	32551798	1	0	11	17	12	18	0	316	741	342	75	151	Q99N17	
ENSMUST00000003433	ENSMUSG00000020190	10	80665327	80678112	-1	24	26	77	151	38	31	8491	7342	5531	796	4318		
ENSMUST00000003434	ENSMUSG00000003344	10	80642617	80657071	-1	8	2	2	92	4	0	10	5	10	0	0	E9PUS2	
ENSMUST00000003436	ENSMUSG00000003346	10	80583654	80590341	-1	2	4	6	114	9	11	653	708	398	78	314		Q99JW1
ENSMUST00000003438	ENSMUSG00000003348	10	80685256	80701820	-1	11	21	41	33	26	9	6693	7076	5248	1155	3248		Q8BSU7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000003442	ENSMUSG00000003352	15	98632220	98644530	1	0	0	8	57	15	0	0	0	0	0	0		P54285
ENSMUST00000003444	ENSMUSG00000003354	15	98708207	98723326	1	13	9	25	12	12	2	0	0	0	1	0		Q8VHI7
ENSMUST00000003445	ENSMUSG00000003355	15	98724373	98728198	-1	4	4	11	34	8	3	9	24	8	40	18		Q9D1M7
ENSMUST00000003450	ENSMUSG00000003360	15	98645134	98662889	-1	18	21	67	90	31	21	671	1202	991	187	759	D3Z0M9	
ENSMUST00000003451	ENSMUSG00000054855	15	98663421	98677461	-1	40	33	160	52	54	34	2057	4954	2444	712	1247		Q8BLR7
ENSMUST00000003459	ENSMUSG00000020437	11	6506548	6520965	-1	0	11	11	18	0	0	2532	2838	2427	276	1420		Q5SUA5
ENSMUST00000003461	ENSMUSG00000020456	11	6291633	6356642	1	0	0	52	9	8	0	1260	1936	1741	136	1389		Q60597
ENSMUST00000003468	ENSMUSG00000003378	7	25009849	25072346	-1	28	22	60	451	51	27	34	97	47	5	86		Q61626
ENSMUST00000003469	ENSMUSG00000003379	7	24897381	24902197	1	20	16	44	13	30	14	194	119	98	131	402		P11911
ENSMUST00000003493	ENSMUSG00000003402	9	22003035	22014219	1	0	11	34	30	0	18	343	437	262	2	306	Q3U518	O08795
ENSMUST00000003501	ENSMUSG00000003410	9	22015005	22052023	-1	89	50	217	610	142	73	0	3	2	1	4		Q60900
ENSMUST00000003502	ENSMUSG00000003411	4	108879063	108943324	1	3	0	0	5	3	0	2	0	0	0	0	Q0PD62	Q9CZT8
ENSMUST00000003509	ENSMUSG00000003418	2	13651021	13794064	-1	22	23	36	213	29	23	4	21	7	4	23	Q148N5	Q8K4T1
ENSMUST00000003512	ENSMUSG00000003420	7	45092993	45103822	-1	16	6	13	16	25	7	209	236	75	676	523		Q61559
ENSMUST00000003513	ENSMUSG00000003421	7	45062429	45078503	1	30	27	54	37	48	22	51	24	11	23	13		Q9D6T0
ENSMUST00000003521	ENSMUSG00000003429	7	45122388	45124389	-1	20	16	46	67	31	9	3334	8625	2844	9350	2439	Q3UC02	P62281
ENSMUST00000003527	ENSMUSG00000003435	7	28314898	28338719	-1	32	26	66	84	55	20	1826	2331	2121	275	1881		O55201
ENSMUST00000003529	ENSMUSG00000003437	7	28392951	28399388	1	4	4	5	22	8	3	315	947	456	80	378		Q8K2T8
ENSMUST00000003536	ENSMUSG00000003444	7	28386146	28392708	-1	21	12	28	87	26	16	110	140	68	152	59		Q9DB91
ENSMUST00000003544	ENSMUSG00000003452	6	149408886	149563329	1	2	0	4	0	0	2	0	0	0	0	0	B2KG46	
ENSMUST00000003550	ENSMUSG00000003458	1	172066013	172082795	-1	0	0	0	0	0	0	2919	4390	3002	254	2151		P57716
ENSMUST00000003554	ENSMUSG00000007122	1	172209894	172219868	-1	4	9	11	11	17	8	0	0	0	0	0		O09165
ENSMUST00000003561	ENSMUSG00000003469	14	70457476	70468832	1	19	13	39	33	29	18	1	1	0	0	3	B9EIC7	Q8K0S0
ENSMUST00000003568	ENSMUSG00000003476	6	55090049	55133016	-1	23	8	34	16	28	6	0	0	0	0	0	Q3UQP0	
ENSMUST00000003569	ENSMUSG00000003477	6	55170626	55175043	-1	10	6	8	6	9	2	0	0	0	5	0		P40936
ENSMUST00000003572	ENSMUSG00000029777	6	55038007	55079500	1	13	13	9	112	15	7	730	1633	1068	262	666		Q9CZD3
ENSMUST00000003574	ENSMUSG00000003484	8	71988482	72009626	-1	7	8	16	9	6	2	4168	6705	4418	2397	4707		Q99N16
ENSMUST00000003575	ENSMUSG00000031799	8	72134975	72153142	1	17	18	47	88	26	11	1862	13322	2980	3638	2671		Q6IRU2
ENSMUST00000003597	ENSMUSG00000003505	7	18345422	18355009	-1	0	3	0	5	3	0	0	0	0	0	0	B2RSG7	
ENSMUST00000003599	ENSMUSG00000103088	18	37742094	37841873	1	9	10	20	142	7	6	5	21	8	2	6	Q91XX4	
ENSMUST00000003612	ENSMUSG00000003518	11	101971143	101987013	-1	0	0	0	44	0	0	294	456	420	122	284		Q9D7X3
ENSMUST00000003620	ENSMUSG00000003526	16	18060357	18090203	-1	9	5	17	200	8	17	10	0	14	0	0		Q9WU79
ENSMUST00000003621	ENSMUSG00000003527	16	17900711	17911348	-1	26	16	53	79	37	18	333	425	325	45	239	Q3UFM6	
ENSMUST00000003622	ENSMUSG00000003528	16	17925211	17928219	-1	5	2	19	27	11	7	286	363	196	43	147		Q8JZU2
ENSMUST00000003628	ENSMUSG00000003534	17	35681567	35704621	-1	0	14	0	0	0	0	0	0	0	0	0		Q03146
ENSMUST00000003635	ENSMUSG00000003541	17	35821684	35822923	1	5	7	27	141	19	7	1214	2142	1069	262	860	Q91VZ5	
ENSMUST00000003640	ENSMUSG00000003545	7	19302721	19310045	-1	22	20	69	203	33	16	21	2443	6	2	48	A2RSD4	P13346
ENSMUST00000003642	ENSMUSG00000003546	17	46630631	46645144	-1	14	23	50	27	35	15	707	1118	613	105	535		Q9DBS5
ENSMUST00000003643	ENSMUSG00000030399	7	19411094	19421583	1	12	7	36	72	26	6	2	0	4	7	1	A2RTA0	P07310
ENSMUST00000003645	ENSMUSG00000003549	7	19344778	19356524	1	17	7	20	116	10	18	22	35	13	25	43		P07903
ENSMUST00000003655	ENSMUSG00000003559	19	46707443	46741095	1	9	6	18	24	8	8	64	146	90	81	87		Q91WU5
ENSMUST00000003659	ENSMUSG00000031849	8	70373548	70382065	1	23	14	45	253	40	14	1	5	0	1	2		Q9R0G6
ENSMUST00000003669	ENSMUSG00000003573	8	70282827	70294361	1	5	0	1	0	0	0	74	161	24	0	68		Q99JP6
ENSMUST00000003677	ENSMUSG00000003581	11	4135202	4141172	1	11	0	17	41	17	7	138	287	145	35	129		Q5SPX3
ENSMUST00000003681	ENSMUSG00000003585	11	4097039	4123415	-1	5	5	20	38	28	5	2	0	0	3	9		Q99J08
ENSMUST00000003687	ENSMUSG00000021253	12	86056744	86079041	-1	38	24	62	31	45	22	0	1	4	8	39	Q91YU7	
ENSMUST00000003705	ENSMUSG00000003604	2	112492964	112634573	1	112	65	67	60	70	31	16	53	17	23	32		Q9D9K3
ENSMUST00000003710	ENSMUSG00000057230	6	86849517	87003223	1	26	18	38	2	8	3	0	0	13	0	24		Q3UHJ0
ENSMUST00000003714	ENSMUSG00000003617	3	19957054	20009145	1	0	0	2	0	3	0	1	12	1	75	27	G3X8Q5	
ENSMUST00000003717	ENSMUSG00000042476	5	8893717	8959231	1	21	16	24	28	37	11	0	1	2	7	4		P21440
ENSMUST00000003720	ENSMUSG00000003623	5	8966033	8997324	-1	7	5	4	62	12	4	259	1433	659	921	392		Q9DC50
ENSMUST00000003726	ENSMUSG00000024002	17	32196274	32284722	-1	0	0	0	98	27	18	260	67	401	0	446	Q3UH70	
ENSMUST00000003741	ENSMUSG00000003644	4	133847290	133887797	-1	0	7	0	8	0	4	56	0	93	0	85		P18653
ENSMUST00000003754	ENSMUSG00000003657	8	110142539	110168206	-1	8	8	19	50	12	8	0	0	0	0	0		Q08331
ENSMUST00000003759	ENSMUSG00000003662	2	127240938	127247816	-1	14	8	3	26	9	5	95	284	125	23	63		Q99KN2
ENSMUST00000003762	ENSMUSG00000003665	17	17843328	17855188	-1	19	8	67	183	23	12	1	8	3	6	24		Q61647
ENSMUST00000003777	ENSMUSG00000003680	19	8772522	8786417	-1	0	0	0	0	0	4	0	80	25	4	19	K3W4L1	
ENSMUST00000003808	ENSMUSG00000038508	8	70629393	70632456	-1	10	4	12	153	4	8	0	9	4	0	33		Q9Z0J7
ENSMUST00000003818	ENSMUSG00000003721	1	121304353	121332589	-1	6	3	33	144	17	8	83	379	122	134	78		Q91WG1
ENSMUST00000003826	ENSMUSG00000032269	9	48899214	48911099	-1	20	13	34	41	27	11	0	0	0	0	0	E9QLC0	
ENSMUST00000003828	ENSMUSG00000003731	4	129643980	129672767	-1	0	3	3	0	4	0	60	0	66	38	0	Q4FJZ2	
ENSMUST00000003843	ENSMUSG00000003746	10	53904788	54075796	-1	7	13	11	66	5	11	169	269	129	100	246	Q544T7	P45700
ENSMUST00000003850	ENSMUSG00000003752	7	27207172	27228661	-1	16	17	59	253	33	22	121	138	73	14	87		Q7TS72
ENSMUST00000003857	ENSMUSG00000089832	7	27342133	27356019	-1	0	0	12	77	0	0	2627	2095	1385	224	1147		Q6P7W2
ENSMUST00000003860	ENSMUSG00000003762	7	27233023	27257950	1	0	6	7	9	22	8	558	416	416	74	296	E9QLB8	
ENSMUST00000003870	ENSMUSG00000025025	19	53310506	53375810	1	5	0	3	130	15	14	687	1406	1689	82	1088	Q3U3X2	
ENSMUST00000003876	ENSMUSG00000003778	18	34598615	34624601	-1	0	0	0	0	10	0	0	0	0	0	85		Q8R3B7
ENSMUST00000003898	ENSMUSG00000022842	16	20611593	20646485	1	0	0	0	42	0	0	0	0	0	0	0	B2RQR8	
ENSMUST00000003906	ENSMUSG00000003808	8	84856989	84869257	1	0	0	0	51	0	0	179	226	138	50	147		Q8C0C7
ENSMUST00000003907	ENSMUSG00000003809	8	84886393	84893921	-1	13	11	16	26	21	0	0	80	28	0	17	A0A0A0MQ68	
ENSMUST00000003908	ENSMUSG00000003810	4	116306762	116464183	-1	31	0	139	0	34	28	110	35	121	15	201	B1AST8	
ENSMUST00000003910	ENSMUSG00000003812	8	84908560	84922915	1	76	54	169	12	55	38	412	576	276	435	286	Q3UM14	P56542
ENSMUST00000003911	ENSMUSG00000003813	8	84834019	84840665	-1	0	2	0	0	0	0	106	108	55	0	55	Q8CAP3	
ENSMUST00000003912	ENSMUSG00000003814	8	84841850	84846934	-1	2	5	11	69	2	4	2026	4176	1980	792	2609	B2MWM9	P14211
ENSMUST00000003922	ENSMUSG00000003824	8	84872111	84888221	1	1	5	0	2	0	0	11	16	1	20	4	F8WHI9	
ENSMUST00000003946	ENSMUSG00000003848	8	107412486	107425051	-1	0	0	0	0	0	0	39	65	35	73	52	Q148S3	Q8BW10
ENSMUST00000003947	ENSMUSG00000003849	8	107388225	107403206	-1	14	9	9	15	13	13	74	363	137	263	77	Q542Y0	Q64669
ENSMUST00000003961	ENSMUSG00000003863	7	45339126	45367019	-1	0	0	0	179	0	18	0	0	0	0	0	B8QI35	P60469
ENSMUST00000003964	ENSMUSG00000003865	7	45434844	45456619	1	17	10	42	40	49	11	1722	1578	1670	64	865		Q9Z1E4
ENSMUST00000003971	ENSMUSG00000003872	7	45367891	45370583	-1	2	1	2	35	6	3	0	0	0	0	0		O88951
ENSMUST00000003981	ENSMUSG00000003882	15	9506161	9529876	-1	45	36	51	180	52	26	101	270	79	241	212		P16872
ENSMUST00000004036	ENSMUSG00000003934	11	69554092	69560205	-1	21	18	58	259	38	19	2	22	4	0	10	Q543Q7	O35393
ENSMUST00000004050	ENSMUSG00000003948	11	90187684	90278589	1	7	1	9	22	11	0	92	198	83	47	177		Q9CQY7
ENSMUST00000004051	ENSMUSG00000003949	11	90336536	90390895	-1	9	17	33	36	26	3	17	24	13	3	12		Q8BW74

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000004054	ENSMUSG00000022905	16	35978750	36037131	1	7	8	1	17	22	13	440	1098	614	235	315		Q60960
ENSMUST00000004055	ENSMUSG00000042156	14	118875520	118925314	-1	25	15	41	195	21	9	0	16	5	22	46		Q8BMD2
ENSMUST00000004057	ENSMUSG00000003955	16	36043844	36071515	-1	2	4	3	32	8	1	195	616	195	1243	193		Q9D6U8
ENSMUST00000004072	ENSMUSG00000003970	15	76904071	76906318	1	18	19	24	190	35	12	5491	6173	4155	2239	3245		P62918
ENSMUST00000004076	ENSMUSG00000003974	5	9485541	9725170	-1	17	20	46	33	21	11	0	2	0	0	0		Q9QYS2
ENSMUST00000004094	ENSMUSG00000003992	13	91460283	91703429	1	13	5	30	22	15	9	2	8	10	2	7	Q540I3	Q9CYZ8
ENSMUST00000004097	ENSMUSG00000029705	5	136248135	136567490	-1	51	46	223	75	44	32	625	1428	1638	72	1317	E9QKE9	
ENSMUST00000004120	ENSMUSG00000004018	11	26386135	26471876	1	5	5	9	29	11	4	4	14	3	31	2		Q9CR14
ENSMUST00000004133	ENSMUSG00000004031	1	158245269	158356326	-1	2	0	0	1	3	3	0	0	0	0	0		Q6DFY8
ENSMUST00000004134	ENSMUSG00000004032	3	107895821	107898686	1	4	0	2	22	4	2	5	10	0	47	5		P48774
ENSMUST00000004136	ENSMUSG00000004038	3	107963696	107969283	-1	19	13	15	22	20	6	0	0	0	0	0		P19639
ENSMUST00000004137	ENSMUSG00000004035	3	107926334	107931817	-1	12	12	9	8	9	5	0	5	0	0	0		Q80W21
ENSMUST00000004140	ENSMUSG00000058135	3	108012255	108017973	-1	7	9	7	18	24	6	360	301	174	93	126		P10649
ENSMUST00000004143	ENSMUSG00000020919	11	100780731	100850724	-1	0	0	0	64	0	0	186	1069	1071	35	964		P42232
ENSMUST00000004145	ENSMUSG00000004043	11	100859351	100885169	1	7	6	7	13	7	0	0	0	0	0	26	Q9JIA0	P42230
ENSMUST00000004156	ENSMUSG00000004054	19	5689131	5702862	1	22	17	86	593	66	29	4224	3340	3050	386	2184		Q80XI6
ENSMUST00000004172	ENSMUSG00000004070	16	4726361	4766742	1	5	1	0	14	8	1	363	1077	432	1093	337	Q544R7	O70252
ENSMUST00000004173	ENSMUSG00000004071	16	4750348	4790292	-1	6	8	52	66	10	8	16	85	15	11	27		Q9DB75
ENSMUST00000004200	ENSMUSG00000004096	9	14500617	14510577	1	6	8	11	9	5	2	651	2263	831	2169	657		Q9JHS9
ENSMUST00000004201	ENSMUSG00000004098	9	20770050	20815067	-1	40	29	118	72	68	36	6	8	5	10	62	Q9JLI2	
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ENSMUST00000004203	ENSMUSG00000004100	9	20888175	20892178	1	0	0	8	25	5	0	46	73	32	5	56		Q91YU8
ENSMUST00000004206	ENSMUSG00000070319	9	20894352	20898600	-1	5	9	48	110	18	3	340	596	294	147	350	Q544H0	Q9Z1D1
ENSMUST00000004208	ENSMUSG00000004105	2	33216069	33247717	1	15	15	35	42	26	13	8	11	7	44	159		Q9R045
ENSMUST00000004214	ENSMUSG00000004110	1	154390731	154884501	-1	0	27	0	0	7	0	5	0	9	1	52	E9QK20	
ENSMUST00000004222	ENSMUSG00000022702	16	18877037	18970309	1	9	8	29	60	27	6	283	407	325	35	219		Q61666
ENSMUST00000004232	ENSMUSG00000074207	3	138260991	138290698	1	0	2	0	0	4	0	0	0	0	4	0	Q3UKA4	P00329
ENSMUST00000004281	ENSMUSG00000028630	10	118859349	118868903	-1	11	10	25	103	13	7	66	106	118	23	104		Q5U4C9
ENSMUST00000004294	ENSMUSG00000004187	15	76660641	76668196	1	36	11	64	179	46	18	19	84	20	3	62	G3X8Q6	
ENSMUST00000004316	ENSMUSG00000004207	10	60277627	60302597	1	0	0	0	10	19	0	0	394	72	0	308	K3W4L3	
ENSMUST00000004326	ENSMUSG00000031398	X	74329066	74344689	1	28	23	31	41	40	7	3	0	2	4	10		P70208
ENSMUST00000004327	ENSMUSG00000031400	X	74409483	74429194	-1	19	19	18	48	13	19	23670	47119	25621	11140	12582	Q790Y8	Q00612
ENSMUST00000004330	ENSMUSG00000004221	X	74393290	74453854	1	0	0	75	30	0	0	0	70	0	26	0	Q7TSS3	
ENSMUST00000004340	ENSMUSG00000004231	19	44756045	44837871	1	5	0	5	4	0	0	0	0	0	0	0	G3X8Q7	
ENSMUST00000004343	ENSMUSG00000004233	3	99141068	99239186	1	76	69	66	107	46	33	16	23	22	10	55		Q9CYK1
ENSMUST00000004375	ENSMUSG00000004264	6	124712336	124716950	1	0	0	0	10	0	1	578	894	592	134	492	Q3V235	O35129
ENSMUST00000004377	ENSMUSG00000004266	6	124720707	124738714	-1	7	5	22	0	18	8	379	1015	398	89	365	Q3UCJ0	P29351
ENSMUST00000004378	ENSMUSG00000004267	6	124760053	124769673	-1	12	11	2	70	11	2	6	0	0	0	7	Q545V3	P17183
ENSMUST00000004379	ENSMUSG00000004268	6	124704085	124712178	-1	0	0	0	17	0	3	200	456	182	693	216	Q542P8	O35130
ENSMUST00000004381	ENSMUSG00000004270	6	124663027	124704418	1	2	2	3	29	0	0	953	1424	773	123	405		Q91V01
ENSMUST00000004389	ENSMUSG00000072772	6	124739183	124741374	-1	7	5	5	61	14	13	141	563	265	674	174		O35127
ENSMUST00000004392	ENSMUSG00000029771	6	29526625	29541871	1	0	0	0	68	0	4	600	996	329	137	521	Q3U169	P56477
ENSMUST00000004396	ENSMUSG00000004285	6	29467718	29470512	1	2	2	6	12	9	3	1181	2317	768	3190	659		Q9D1K2
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ENSMUST00000004430	ENSMUSG00000004319	8	60910389	60983300	-1	0	0	0	0	0	0	21	30	137	0	0	Q3TF45	
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ENSMUST00000004456	ENSMUSG00000004344	13	21286429	21292731	-1	0	0	16	12	0	0	0	0	0	0	0		P21765
ENSMUST00000004470	ENSMUSG00000004356	10	88746607	88826814	-1	48	48	48	99	57	23	30	94	69	27	159	E9QK83	
ENSMUST00000004473	ENSMUSG00000004359	10	88674772	88685015	-1	1190	1260	1098	724	1267	540	28	87	37	40	62		Q6P3D7
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ENSMUST00000004494	ENSMUSG00000031622	8	72723288	72758203	1	23	18	86	126	47	18	248	580	312	31	309		Q62141
ENSMUST00000004497	ENSMUSG00000004383	8	72814599	73353540	-1	0	8	24	1	0	9	16	30	5	1	13	Q059X9	Q9Z1M7
ENSMUST00000004505	ENSMUSG00000020447	11	6211013	6230143	-1	42	28	92	61	71	31	0	2	0	0	2	Z4YJC9	
ENSMUST00000004507	ENSMUSG00000004393	11	6258919	6267772	-1	14	8	20	30	12	8	119	169	94	42	137	Q5SVX3	Q9D0R4
ENSMUST00000004508	ENSMUSG00000004394	11	6270369	6274870	-1	10	10	23	14	8	5	381	898	366	161	279		Q8R1V4
ENSMUST00000004554	ENSMUSG00000012848	7	12922290	12926686	1	3	7	0	5	0	5	5480	4876	3343	17637	2349	Q91V55	
ENSMUST00000004560	ENSMUSG00000004446	6	120891930	120916853	-1	6	7	0	72	13	5	856	2277	1061	689	779		P70444
ENSMUST00000004565	ENSMUSG00000004451	1	119470305	119504794	-1	11	11	19	36	22	5	1571	4176	2171	497	1478		Q9JIW9
ENSMUST00000004574	ENSMUSG00000004460	16	22857845	22879634	1	5	3	5	0	0	0	691	1734	1022	211	797		Q99KV1
ENSMUST00000004576	ENSMUSG00000004462	16	22813215	22857569	-1	10	18	18	10	10	3	44	127	80	46	63		Q640P7
ENSMUST00000004587	ENSMUSG00000004473	7	44302687	44306902	-1	12	15	31	170	29	17	5	4	4	5	2		O88200
ENSMUST00000004614	ENSMUSG00000058638	7	12834761	12850577	1	18	9	37	16	24	6	124	742	267	493	174		
ENSMUST00000004622	ENSMUSG00000004508	7	97081586	97308946	1	46	27	97	95	56	33	1218	2760	2238	257	2213	Q3ZB57	
ENSMUST00000004634	ENSMUSG00000020142	11	20302180	20332713	-1	19	17	0	7	42	0	0	5	1	4	25	Q5SSP3	
ENSMUST00000004646	ENSMUSG00000004530	5	113842436	113908758	-1	6	39	0	10	22	5	2836	2083	3410	409	2114	Q499X7	Q9WUM4
ENSMUST00000004655	ENSMUSG00000004540	7	18813937	18821607	-1	10	13	12	16	20	10	0	0	0	3	3	Q62056	
ENSMUST00000004657	ENSMUSG00000004542	7	18789567	18798520	-1	13	13	65	5	10	16	0	0	0	0	1	Q4KL31	
ENSMUST00000004673	ENSMUSG00000004558	14	51905271	51913488	-1	0	17	96	0	0	0	0	0	11	0	0		Q9QYG0
ENSMUST00000004681	ENSMUSG00000004565	8	3515384	3544266	1	39	21	13	0	42	0	52	247	153	37	182		Q3TRM4
ENSMUST00000004683	ENSMUSG00000004567	8	3500457	3515232	1	4	0	0	13	4	0	182	283	223	29	159		Q99J21
ENSMUST00000004684	ENSMUSG00000004568	8	3393006	3456601	1	0	4	0	0	0	0	1529	1848	2241	105	1658		Q6P9R4
ENSMUST00000004686	ENSMUSG00000069633	8	3457105	3467680	-1	20	17	39	25	26	16	39	62	33	13	41		Q6P6M5
ENSMUST00000004715	ENSMUSG00000061778	X	164936169	164980375	-1	0	0	1	4	0	2	61	210	154	138	91	B1AU74	
ENSMUST00000004728	ENSMUSG00000004609	7	43524216	43544428	-1	0	0	91	31	14	12	2356	8078	5397	1337	6260		Q63994
ENSMUST00000004729	ENSMUSG00000004610	7	43444083	43457800	1	7	5	15	20	8	3	492	774	392	466	305		Q9DCW4
ENSMUST00000004732	ENSMUSG00000004613	7	43430088	43435996	1	3	0	0	0	2	6	0	1	0	0	0		P56563
ENSMUST00000004745	ENSMUSG00000004626	8	3630955	3643644	1	0	0	0	0	0	0	6016	7892	4491	1308	3255	F8WGM5	
ENSMUST00000004749	ENSMUSG00000004630	8	3623371	3625545	-1	0	0	0	1	0	0	0	0	0	0	1		
ENSMUST00000004750	ENSMUSG00000004631	6	4674350	4747207	-1	0	0	0	0	0	4	0	0	0	0	0	F8WGM3	
ENSMUST00000004756	ENSMUSG00000004637	8	114439655	115352708	1	12	3	6	47	11	1	33	74	51	24	40		Q91WL8
ENSMUST00000004761	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7X0	
ENSMUST00000004770	ENSMUSG00000004651	7	87427405	87493411	-1	38	38	33	46	51	41	4	18	4	0	8	Q91XK0	P11344
ENSMUST00000004774	ENSMUSG00000004655	6	55336432	55348555	1	30	13	56	20	43	14	66	10	13	32	80		Q02013
ENSMUST00000004780	ENSMUSG00000004661	9	57790353	57836793	-1	0	0	53	0	0	0	601	926	548	70	521		Q9Z1N7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000004784	ENSMUSG00000004665	10	79988584	79996062	1	23	18	74	86	39	25	9177	19378	9271	1528	6774	Q543F3	Q08093
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ENSMUST00000004827	ENSMUSG00000004707	1	171588624	171607410	-1	0	0	0	6	0	0	2	162	75	132	140	E9PX73	
ENSMUST00000004829	ENSMUSG00000004709	1	171559193	171609746	1	14	13	19	30	0	12	312	2787	781	578	1196		Q07763
ENSMUST00000004850	ENSMUSG00000004730	17	57358686	57483529	1	14	11	0	0	0	9	77	197	260	291	355	Q3U9R0	Q61549
ENSMUST00000004868	ENSMUSG00000004748	11	4091480	4095445	-1	11	8	15	42	25	13	7	14	2	1	3		Q9CRB8
ENSMUST00000004892	ENSMUSG00000004771	9	64715299	64737758	-1	0	0	1	21	0	0	34	323	223	558	173	F8WGS1	
ENSMUST00000004910	ENSMUSG00000004788	12	85219481	85226628	1	4	5	3	36	12	6	600	869	391	92	252		Q99LD9
ENSMUST00000004913	ENSMUSG00000004791	12	85166639	85177296	-1	13	7	37	24	19	11	2	2	0	1	1	Q544A5	P49764
ENSMUST00000004920	ENSMUSG00000004798	11	61775649	61855073	-1	7	9	9	168	15	4	240	645	332	31	172		Q9QY01
ENSMUST00000004936	ENSMUSG00000004814	5	135569937	135573049	-1	16	15	30	32	15	6	69	103	57	2020	311	Q3U0A4	Q9JKC0
ENSMUST00000004943	ENSMUSG00000004821	5	108777235	108795363	-1	3	1	0	1	4	0	0	0	0	0	0	A2RTW8	Q9D2R4
ENSMUST00000004949	ENSMUSG00000027164	2	101678429	101701669	1	36	25	65	78	40	24	341	777	695	76	489		P70196
ENSMUST00000004955	ENSMUSG00000020528	11	61729650	61762088	-1	0	0	0	0	11	0	0	0	0	0	16	Q5SWZ0	Q8R574
ENSMUST00000004959	ENSMUSG00000004837	11	61653265	61672784	1	60	36	53	436	104	73	216	162	205	96	177		Q9CX99
ENSMUST00000004964	ENSMUSG00000004842	16	65520511	65535005	1	23	16	10	129	12	4	0	2	1	1	0	F8WGJ8	
ENSMUST00000004965	ENSMUSG00000004843	16	65539133	65562697	-1	7	5	5	91	7	3	358	1203	566	118	313		Q8BJF9
ENSMUST00000004968	ENSMUSG00000004846	5	136987019	136996648	1	6	8	20	315	24	8	1616	1834	1125	166	1290		Q9R0E1
ENSMUST00000004985	ENSMUSG00000063952	17	28801090	28838546	1	18	7	22	72	35	11	454	345	718	23	738	B2KF05	
ENSMUST00000004986	ENSMUSG00000004864	17	28769307	28778698	1	5	13	5	76	8	0	3775	7007	2964	486	1624	Q3UIB2	Q9Z1B7
ENSMUST00000004987	ENSMUSG00000004865	17	28587648	28622521	-1	0	0	0	0	0	0	35	15	112	39	63	F8WGJ7	
ENSMUST00000004990	ENSMUSG00000053436	17	28691342	28748404	1	3	0	8	35	0	0	601	879	751	199	751	Q5U421	P47811
ENSMUST00000004994	ENSMUSG00000004872	1	78101267	78197134	-1	29	28	12	0	31	25	1	1	0	1	3	Q8BRF1	
ENSMUST00000005003	ENSMUSG00000004880	1	181815335	181843046	-1	11	9	12	29	12	0	6444	14643	9856	2105	6493		Q3U9G9
ENSMUST00000005014	ENSMUSG00000004894	3	88021750	88027583	-1	0	0	0	135	8	4	0	0	0	0	0	B2RRU7	Q9ESM3
ENSMUST00000005015	ENSMUSG00000004895	3	87858903	87885608	-1	21	11	43	151	17	15	505	825	472	64	326	Q9EQC8	
ENSMUST00000005016	ENSMUSG00000004896	3	87922601	87930717	-1	0	0	0	0	0	0	10	0	0	0	12	G3X8Q8	
ENSMUST00000005017	ENSMUSG00000004897	3	87906321	87916132	1	15	5	20	70	15	11	728	1370	745	158	789		P51859
ENSMUST00000005019	ENSMUSG00000004885	3	87948666	87953376	1	3	7	19	28	11	3	0	0	0	14	2		P22935
ENSMUST00000005041	ENSMUSG00000030435	7	5062143	5079945	1	41	20	45	68	57	11	1310	1647	1355	164	1067		P26369
ENSMUST00000005051	ENSMUSG00000063229	7	46841475	46855627	1	18	15	34	5	16	8	27	84	45	0	36	G5E8N5	
ENSMUST00000005053	ENSMUSG00000004945	17	5410870	5440259	-1	3	5	14	7	15	6	107	257	126	335	74		Q8VCR3
ENSMUST00000005057	ENSMUSG00000004929	10	81070035	81082559	1	17	6	42	199	25	21	29	42	26	23	57		
ENSMUST00000005064	ENSMUSG00000004934	10	81153266	81167923	-1	3	0	12	454	10	9	216	651	365	67	275	Q3ULQ6	Q9JM05
ENSMUST00000005066	ENSMUSG00000004936	9	64185770	64253631	-1	9	3	18	202	18	6	1557	3209	1705	413	1115	Q3TMJ8	P31938
ENSMUST00000005067	ENSMUSG00000004937	10	81044075	81060178	-1	9	14	40	51	28	7	1203	1501	905	178	659		Q8BJU0
ENSMUST00000005069	ENSMUSG00000004939	10	81198170	81202037	-1	33	49	147	57	56	24	1	13	6	1	15		Q9D7C9
ENSMUST00000005072	ENSMUSG00000004947	5	135994800	136032872	1	0	0	0	0	0	0	0	16	0	13	0		
ENSMUST00000005073	ENSMUSG00000004948	5	135980099	135988624	1	14	8	13	15	9	7	0	0	0	0	0		P10761
ENSMUST00000005077	ENSMUSG00000004951	5	135887919	135889563	1	5	0	4	173	10	4	0	0	0	17	11	Q545F4	P14602
ENSMUST00000005103	ENSMUSG00000029832	6	51432670	51458768	1	10	7	5	50	17	2	1	9	5	2	4	Q3UZC1	Q9WTM4
ENSMUST00000005108	ENSMUSG00000030180	6	120364124	120444574	1	64	0	0	0	48	0	0	0	0	0	0	E9Q8F1	Q3UXZ9
ENSMUST00000005114	ENSMUSG00000004988	6	117933559	117937692	-1	8	3	6	3	10	5	3	2	2	2	6		Q9D2W0
ENSMUST00000005120	ENSMUSG00000004994	8	84257795	84270380	-1	0	0	0	0	4	0	65	155	76	73	51		Q9D516
ENSMUST00000005122	ENSMUSG00000004996	8	84249906	84257326	-1	0	0	0	0	0	0	8	0	0	8	4	F8WI95	
ENSMUST00000005164	ENSMUSG00000005034	3	146729574	146812990	-1	0	10	7	2	6	3	90	231	178	93	282		P68181
ENSMUST00000005173	ENSMUSG00000005043	11	119343425	119355536	-1	32	0	0	59	63	0	480	161	808	0	596	Q9EQ08	
ENSMUST00000005175	ENSMUSG00000005045	4	152338651	152390194	1	23	16	67	20	41	0	0	0	1	0	0		A2A8L1
ENSMUST00000005185	ENSMUSG00000005054	10	78425670	78427619	1	6	0	5	38	10	5	851	2341	580	4129	429		Q62426
ENSMUST00000005188	ENSMUSG00000005057	5	136218147	136246556	-1	16	11	42	412	34	14	96	107	61	4	98		Q9JID9
ENSMUST00000005218	ENSMUSG00000005087	2	102811141	102901665	-1	24	16	0	13	0	0	176	301	340	71	421	A2APM2	
ENSMUST00000005220	ENSMUSG00000005089	2	102658659	102790784	1	3	4	0	0	9	0	0	0	0	0	0	A2APL7	P43006
ENSMUST00000005233	ENSMUSG00000005102	2	118388618	118475234	1	0	0	0	95	0	0	17	68	51	11	34	A2AUM0	
ENSMUST00000005234	ENSMUSG00000005103	5	38526813	38563221	-1	19	30	36	90	36	14	7680	16201	8947	2117	6100	Q3TJY2	O88342
ENSMUST00000005238	ENSMUSG00000005107	5	38349273	38503143	-1	0	0	0	0	0	6	0	9	0	0	0	Q99JJ2	
ENSMUST00000005255	ENSMUSG00000005124	15	66891320	66923201	1	19	20	24	27	18	15	3	2	1	5	2	Q3UFJ5	O54775
ENSMUST00000005256	ENSMUSG00000005125	15	66929321	66969640	-1	13	21	48	29	25	12	923	1736	716	147	742	Q545R3	Q62433
ENSMUST00000005262	ENSMUSG00000005131	9	53405286	53432803	1	8	8	4	4	2	4	0	1	0	0	0		Q9D4W2
ENSMUST00000005279	ENSMUSG00000005148	14	99298691	99313405	1	20	7	82	261	25	7	226	487	499	37	261		Q9Z0Z7
ENSMUST00000005292	ENSMUSG00000005161	8	84969587	84974834	1	0	0	0	3	0	0	153	110	94	276	128		Q61171
ENSMUST00000005334	ENSMUSG00000005202	11	69614804	69617905	-1	8	7	18	17	8	0	0	0	0	0	0		P97497
ENSMUST00000005336	ENSMUSG00000005204	11	69673115	69682084	-1	7	5	0	115	10	7	597	709	378	73	321		Q9EP97
ENSMUST00000005352	ENSMUSG00000005220	5	72300025	72504473	-1	10	6	35	110	26	14	0	0	0	0	0		Q9Z319
ENSMUST00000005364	ENSMUSG00000005232	2	69211073	69227841	1	13	5	0	0	7	10	0	0	0	0	0		Q9Z186
ENSMUST00000005365	ENSMUSG00000005233	2	69193895	69206194	-1	0	0	6	39	6	1	29	79	29	49	17		Q3UA16
ENSMUST00000005371	ENSMUSG00000059552	11	69580359	69591873	1	5	2	2	0	9	1	95	315	70	12	63		P02340
ENSMUST00000005394	ENSMUSG00000005262	16	18811779	18835261	1	22	29	58	44	33	27	232	1141	318	275	298		P70362
ENSMUST00000005399	ENSMUSG00000005267	11	62700356	62731905	-1	20	7	20	16	12	2	2	0	8	0	9	Q5SVS9	
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ENSMUST00000005406	ENSMUSG00000022892	16	84954440	85173707	-1	16	21	37	61	28	11	6521	12392	11908	1211	9884	Q6GR78	P12023
ENSMUST00000005413	ENSMUSG00000052675	7	24112314	24127952	1	12	18	36	15	11	9	1	0	10	0	18		Q0VAW7
ENSMUST00000005431	ENSMUSG00000005299	5	33739673	33782817	-1	34	29	38	101	41	14	400	519	525	77	350		Q9Z2I0
ENSMUST00000005452	ENSMUSG00000005320	13	55152640	55168759	1	23	21	36	173	37	23	0	1	0	0	0		
ENSMUST00000005470	ENSMUSG00000005338	1	173333258	173367695	-1	0	0	0	0	0	0	1	1	0	0	0	K4DI58	
ENSMUST00000005477	ENSMUSG00000030483	7	25897620	25926624	1	0	0	8	4	14	5	1	0	0	1	4	G3X8Q9	
ENSMUST00000005487	ENSMUSG00000005354	15	77915047	77929006	-1	0	0	3	3	9	0	655	906	324	219	292		P97493
ENSMUST00000005488	ENSMUSG00000005355	10	78711997	78718293	-1	10	11	26	30	12	6	0	0	0	0	0	Q542Q1	O89094
ENSMUST00000005490	ENSMUSG00000005357	10	78780496	78814825	1	22	12	21	59	16	7	0	0	0	0	0	B2RQX4	O35544
ENSMUST00000005493	ENSMUSG00000005360	15	8634124	8710764	-1	13	8	11	10	20	6	0	0	0	0	0	Q543U3	P56564
ENSMUST00000005503	ENSMUSG00000005370	17	87975050	87990883	1	35	21	55	203	32	19	85	313	202	54	198		P54276
ENSMUST00000005504	ENSMUSG00000005371	17	87990859	88065291	-1	0	0	0	36	17	0	44	256	420	30	314		Q7TPD1
ENSMUST00000005507	ENSMUSG00000005373	5	135089890	135138382	1	23	8	24	31	31	13	1	7	4	24	78		Q99MZ3
ENSMUST00000005508	ENSMUSG00000005374	5	135149657	135165760	1	0	0	0	0	0	0	0	0	18	0	3	F8WI46	
ENSMUST00000005509	ENSMUSG00000007207	5	135023482	135051100	1	0	6	0	66	0	0	0	0	0	0	0	Q497P1	O35526

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000005518	ENSMUSG00000045098	19	3767421	3818303	1	0	0	0	0	0	0	0	0	0	0	0		Q3U8K7
ENSMUST00000005532	ENSMUSG00000005397	13	13437602	13512275	1	50	39	80	141	42	21	3	3	4	6	45		P10493
ENSMUST00000005548	ENSMUSG00000005413	8	75093591	75100596	1	11	5	36	47	17	12	2744	5370	2192	1575	2077	Q3U5U6	P14901
ENSMUST00000005578	ENSMUSG00000005442	7	25267704	25294159	1	0	2	0	26	11	0	0	0	0	0	0	E9QP01	
ENSMUST00000005583	ENSMUSG00000005447	7	25295049	25297986	-1	5	0	6	13	5	4	30	30	12	49	27	Q3TJC2	Q61205
ENSMUST00000005592	ENSMUSG00000030468	7	43408204	43418358	1	4	0	2	5	0	0	10	36	16	0	48	Q80ZE3	
ENSMUST00000005597	ENSMUSG00000056592	7	43562256	43575461	1	0	0	0	0	0	0	1	0	41	8	0	Q5PPQ4	
ENSMUST00000005600	ENSMUSG00000031706	8	84066836	84096992	1	35	13	64	199	55	23	633	798	657	51	787		P48377
ENSMUST00000005601	ENSMUSG00000005465	8	84030287	84042575	-1	21	19	25	77	34	17	63	100	39	22	148		O70394
ENSMUST00000005606	ENSMUSG00000005469	8	83972978	83996445	1	17	12	37	47	10	8	757	1002	562	67	455		P05132
ENSMUST00000005607	ENSMUSG00000005470	8	83955507	83970197	1	7	5	3	45	9	6	305	192	202	52	90		Q9DAP7
ENSMUST00000005611	ENSMUSG00000005474	5	136693146	136701094	1	6	4	4	3	11	5	0	0	0	0	0	E9QNY3	
ENSMUST00000005616	ENSMUSG00000057672	8	83669762	83699179	-1	0	0	0	0	0	0	1025	731	1072	48	699		P70268
ENSMUST00000005620	ENSMUSG00000005483	8	83608175	83611902	1	27	24	203	154	40	26	690	1437	634	286	531	Q3TU79	Q9QYJ3
ENSMUST00000005630	ENSMUSG00000005493	3	153857149	153906138	-1	0	1	8	112	9	2	0	0	0	0	0	A6H6D5	Q99MT2
ENSMUST00000005643	ENSMUSG00000005506	2	90940382	91019497	1	0	0	0	0	0	0	0	0	0	0	0		P28659
ENSMUST00000005647	ENSMUSG00000005510	2	90894634	90904827	-1	0	0	15	36	6	0	120	362	120	156	181		Q9DCT2
ENSMUST00000005651	ENSMUSG00000005514	5	135670033	135735326	1	7	0	0	29	0	4	4994	8763	4140	561	4609		P37040
ENSMUST00000005669	ENSMUSG00000040583	7	26061497	26096197	1	14	9	11	23	17	5	0	2	0	3	0	A6H6J2	
ENSMUST00000005671	ENSMUSG00000005533	7	67952859	68226780	1	28	25	64	87	46	20	1722	1830	3041	113	2908	E9QNX9	
ENSMUST00000005678	ENSMUSG00000005540	8	3681737	3694174	-1	50	45	100	42	57	32	11	26	18	9	66		P20693
ENSMUST00000005685	ENSMUSG00000005547	7	26835305	26843548	1	6	7	6	6	16	8	0	0	0	4	0	Q91X75	
ENSMUST00000005692	ENSMUSG00000005553	7	30712209	30725535	1	0	6	33	0	16	0	0	0	0	0	0	E9QNX7	
ENSMUST00000005705	ENSMUSG00000005566	7	13024152	13031035	1	3	5	0	106	14	3	658	761	583	78	630	Q5EBP9	Q62318
ENSMUST00000005711	ENSMUSG00000033916	7	13032006	13034777	-1	5	7	19	72	14	6	1631	5101	1757	6765	1525		Q9DB34
ENSMUST00000005714	ENSMUSG00000005575	7	13035120	13038275	-1	0	0	0	42	3	2	20	45	71	25	81		P61082
ENSMUST00000005719	ENSMUSG00000005580	16	4287529	4420498	-1	47	25	1	0	0	20	27	10	16	2	15		P51830
ENSMUST00000005722	ENSMUSG00000005583	13	83504034	83667080	1	13	25	0	10	7	10	0	0	0	15	11	A0A0H2UKB6	
ENSMUST00000005749	ENSMUSG00000005609	7	111028951	111056377	1	45	30	42	1507	66	38	362	985	747	164	497		Q62018
ENSMUST00000005751	ENSMUSG00000005611	7	110868266	110982461	-1	13	25	40	59	45	9	0	0	0	0	29		Q9WUX5
ENSMUST00000005768	ENSMUSG00000028126	3	95058530	95106930	-1	0	12	0	0	0	0	313	757	333	40	121	F8WI18	
ENSMUST00000005769	ENSMUSG00000005628	3	95124476	95129209	1	0	6	7	2	4	0	0	54	16	0	11	Q3UN19	Q9JLH8
ENSMUST00000005791	ENSMUSG00000005649	7	13398132	13408887	1	42	17	16	211	63	25	0	1	0	0	0	Q543X4	Q9JLK3
ENSMUST00000005798	ENSMUSG00000005656	12	54746349	54795703	-1	5	7	5	19	6	0	667	2643	1129	1762	739		Q6P8X1
ENSMUST00000005810	ENSMUSG00000005667	6	83305691	83325908	-1	8	5	6	121	13	7	152	238	171	28	108		P18155
ENSMUST00000005815	ENSMUSG00000005672	5	75574916	75656722	1	26	18	24	3	34	0	527	2234	1533	0	412		P05532
ENSMUST00000005817	ENSMUSG00000005674	1	171216011	171222514	-1	8	10	20	10	23	2	0	5	0	3	8		Q9CZR3
ENSMUST00000005820	ENSMUSG00000005677	1	171213970	171220701	1	0	0	0	0	0	0	0	0	0	0	0		O35627
ENSMUST00000005824	ENSMUSG00000005681	1	171225054	171226379	1	5	0	0	0	0	0	0	0	0	106	0		P09813
ENSMUST00000005825	ENSMUSG00000005682	10	128303335	128321358	1	30	22	69	50	49	18	286	1120	588	59	612		Q8BGF7
ENSMUST00000005826	ENSMUSG00000005683	10	128337832	128362479	1	16	11	15	71	34	7	1894	3941	2485	375	1883		Q9CZU6
ENSMUST00000005829	ENSMUSG00000005686	7	110768206	110812405	1	4	7	32	14	12	7	2704	6991	1246	87	832		O08739
ENSMUST00000005830	ENSMUSG00000005687	3	103171655	103179166	1	0	0	6	38	9	11	90	107	67	182	105		Q9D287
ENSMUST00000005839	ENSMUSG00000005696	X	42502453	42529330	1	0	2	0	0	0	0	2	25	0	26	10	Q544F1	O88890
ENSMUST00000005841	ENSMUSG00000005698	8	105636568	105682922	1	11	12	10	10	15	6	661	1888	1072	125	719		Q61164
ENSMUST00000005849	ENSMUSG00000005705	8	105566698	105637393	-1	4	1	12	3	10	4	0	0	0	0	0	Q3UU47	P56473
ENSMUST00000005860	ENSMUSG00000005716	15	78191114	78206400	-1	0	0	0	27	0	0	0	0	0	0	0	Q545M7	P32848
ENSMUST00000005862	ENSMUSG00000005718	16	4544661	4559720	-1	13	11	47	101	13	11	21	34	14	1	21	Q9JIZ5	
ENSMUST00000005889	ENSMUSG00000034116	17	57279100	57328031	1	13	0	24	117	32	13	2794	4147	3799	265	2862	Q3U9E2	P27870
ENSMUST00000005891	ENSMUSG00000047884	7	43791891	43796757	1	13	7	27	37	15	7	0	0	0	0	2	Q32M27	
ENSMUST00000005907	ENSMUSG00000005763	1	165788681	165877277	1	14	13	26	7	10	8	58	93	26	56	75		P24161
ENSMUST00000005923	ENSMUSG00000005779	3	94884093	94886961	-1	4	3	10	98	8	1	575	1274	750	903	510		P99026
ENSMUST00000005933	ENSMUSG00000038968	7	44136767	44141610	1	13	7	23	14	10	7	0	0	0	0	0		P04071
ENSMUST00000005950	ENSMUSG00000049723	9	7344381	7369499	1	7	7	9	8	8	5	0	0	0	0	0		P34960
ENSMUST00000005952	ENSMUSG00000005802	2	122681233	122702663	-1	40	46	50	42	44	31	14	43	31	12	26		O35149
ENSMUST00000005953	ENSMUSG00000005803	2	122765237	122809569	1	2	2	0	40	9	0	2935	4690	2738	3513	1381		Q9R112
ENSMUST00000005954	ENSMUSG00000005804	2	122738503	122749475	1	18	20	16	31	32	16	172	854	314	97	234		Q9R0C0
ENSMUST00000005964	ENSMUSG00000028138	3	138443093	138455499	1	11	10	20	37	30	6	281	915	362	1180	289	Q6P5I3	P28474
ENSMUST00000005975	ENSMUSG00000005823	17	57234914	57247641	-1	13	13	55	57	28	16	1037	1383	958	237	690		Q91WD0
ENSMUST00000005976	ENSMUSG00000005824	17	57189492	57194189	-1	22	16	49	68	44	5	2143	6622	2760	1319	2459		Q9QYH9
ENSMUST00000006005	ENSMUSG00000032492	9	110722085	110747145	-1	0	0	28	76	0	0	0	0	0	0	0		P41593
ENSMUST00000006020	ENSMUSG00000005864	X	71991849	72010218	1	4	6	12	3	7	7	0	0	0	0	0		Q62398
ENSMUST00000006027	ENSMUSG00000005873	18	34344889	34373415	-1	15	8	25	38	19	7	1399	2428	1102	818	861	G3X8R0	
ENSMUST00000006029	ENSMUSG00000078954	15	84720052	84772207	1	0	0	0	0	13	0	0	0	0	0	0		Q9CXP4
ENSMUST00000006035	ENSMUSG00000005881	2	156008045	156018279	1	0	0	0	66	9	0	903	944	633	219	524		Q9CQE7
ENSMUST00000006036	ENSMUSG00000005882	2	155846894	155930310	-1	0	0	0	0	0	0	0	0	0	6	0	A6PWX5	
ENSMUST00000006037	ENSMUSG00000005886	1	13139105	13374083	-1	6	0	12	40	9	4	164	36	685	3	485		Q61026
ENSMUST00000006046	ENSMUSG00000005892	6	92242061	92244650	-1	12	11	20	22	20	11	0	0	0	1	0		Q62361
ENSMUST00000006053	ENSMUSG00000005899	16	17619354	17644828	1	0	0	7	14	9	6	17	0	0	0	23		Q6ZPR5
ENSMUST00000006061	ENSMUSG00000005907	5	3596066	3637232	1	18	0	0	0	17	11	14	0	0	0	17		Q5BL07
ENSMUST00000006071	ENSMUSG00000005917	11	21994764	22002897	-1	27	0	0	129	6	29	0	1	0	1	3	Q5SS54	P80205
ENSMUST00000006094	ENSMUSG00000022445	15	82790107	82794245	-1	17	10	22	13	28	12	0	3	0	6	0		
ENSMUST00000006101	ENSMUSG00000005947	11	73090583	73147446	1	27	18	23	21	14	6	12	25	9	9	47		Q60677
ENSMUST00000006103	ENSMUSG00000005949	11	73183596	73199042	-1	0	0	0	0	0	0	448	2247	1013	322	487	Q542U5	P57757
ENSMUST00000006104	ENSMUSG00000005950	11	73160421	73172685	1	16	15	50	124	23	18	0	0	0	1	2	Q3UYI1	
ENSMUST00000006105	ENSMUSG00000005951	11	73199460	73224511	1	0	0	33	102	11	6	47	152	91	26	60		Q9D5J6
ENSMUST00000006106	ENSMUSG00000005952	11	73234292	73261242	1	0	9	5	0	4	1	0	0	1	0	0	Z4YJD4	
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ENSMUST00000006123	ENSMUSG00000005968	3	94612757	94658872	-1	28	9	24	26	23	7	22	31	30	10	74	Q3V1F5	O08970
ENSMUST00000006128	ENSMUSG00000005973	2	105386291	105399319	-1	7	8	4	118	9	8	16	26	33	26	54		Q05186
ENSMUST00000006136	ENSMUSG00000005980	16	4036942	4040024	1	0	0	0	0	0	0	0	0	0	0	0	Q14BW6	P49183
ENSMUST00000006137	ENSMUSG00000005981	16	4039971	4077827	-1	8	22	12	21	20	7	135	295	135	88	231		Q9CQN1
ENSMUST00000006138	ENSMUSG00000005982	16	3872375	3904780	1	15	7	3	0	0	0	1979	2537	2713	329	1730		Q9DBU2
ENSMUST00000006139	ENSMUSG00000005983	16	3895179	3908689	-1	3	0	6	4	0	0	0	18	9	6	12		

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ENSMUST00000006151	ENSMUSG00000005994	4	80834123	80851719	1	0	0	11	3	4	9	0	0	0	0	0	Q3UFS3	P07147
ENSMUST00000006167	ENSMUSG00000006010	1	150361305	150393080	-1	0	2	0	2	0	0	1	0	7	0	0		Q4PJX1
ENSMUST00000006171	ENSMUSG00000006014	1	150449412	150466165	-1	0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000006178	ENSMUSG00000006021	7	16119895	16127516	1	6	7	4	13	15	2	205	263	115	26	80	G3X8R1	
ENSMUST00000006181	ENSMUSG00000006024	7	16098458	16117975	1	15	6	22	102	20	7	943	1983	830	228	740		Q9DB05
ENSMUST00000006205	ENSMUSG00000024483	18	36559987	36665917	1	0	0	0	133	16	0	0	0	0	0	0	E9Q1M6	
ENSMUST00000006209	ENSMUSG00000006050	18	36666681	36679366	-1	0	0	2	0	0	0	137	227	111	515	143	G3X8R2	
ENSMUST00000006217	ENSMUSG00000006058	11	96034885	96047430	1	0	0	0	44	2	0	407	838	353	135	333		Q9CZ28
ENSMUST00000006221	ENSMUSG00000020128	11	21239281	21321136	1	13	10	0	0	0	4	257	519	388	0	304		Q5SPW0
ENSMUST00000006235	ENSMUSG00000021939	14	63122462	63145919	1	40	31	70	104	42	49	11266	26538	10382	8292	12300		P10605
ENSMUST00000006254	ENSMUSG00000006095	7	30224131	30232272	-1	6	6	14	69	17	4	391	403	249	155	148		Q9D1E6
ENSMUST00000006286	ENSMUSG00000006127	11	75630988	75648871	1	0	0	5	11	8	0	2581	2299	2605	983	1756	Q5ND43	Q8C5L6
ENSMUST00000006293	ENSMUSG00000006134	16	17451987	17486255	1	27	21	42	326	38	15	550	1155	985	76	740	A2RS58	P47941
ENSMUST00000006301	ENSMUSG00000029703	5	136122772	136136074	-1	3	0	6	0	3	0	659	601	387	142	269		Q8BUI3
ENSMUST00000006303	ENSMUSG00000006143	5	136054492	136064326	1	0	0	0	0	0	0	0	0	0	0	0	F8WJ60	
ENSMUST00000006311	ENSMUSG00000030353	6	128224288	128300823	-1	14	13	49	60	32	6	18	19	10	2	8		
ENSMUST00000006341	ENSMUSG00000006179	13	22002176	22009742	-1	7	4	15	54	17	6	235	474	272	46	60	Q5SZ30	Q9QXE5
ENSMUST00000006353	ENSMUSG00000006191	13	29191746	29855674	-1	24	31	148	38	22	17	14	60	28	54	27		Q91WE6
ENSMUST00000006362	ENSMUSG00000006200	X	37826910	37829857	1	2	1	1	2	3	1	0	0	0	0	0	O70238	
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ENSMUST00000006377	ENSMUSG00000006215	4	141444654	141467930	1	0	0	0	29	6	0	402	341	242	23	187		Q60821
ENSMUST00000006378	ENSMUSG00000006216	4	141404353	141416014	-1	20	12	0	9	0	0	0	1	0	0	0		Q9WUB6
ENSMUST00000006380	ENSMUSG00000006218	4	141368220	141384175	1	9	6	11	94	14	4	0	0	0	0	0	A2ADB2	
ENSMUST00000006381	ENSMUSG00000006219	4	141576062	141606096	-1	0	20	0	0	0	0	0	0	0	0	0		Q71FD7
ENSMUST00000006391	ENSMUSG00000045827	13	33003250	33017957	1	31	27	16	16	22	0	7	27	10	88	46	O08797	
ENSMUST00000006392	ENSMUSG00000021403	13	33027416	33041884	1	18	15	30	25	30	7	3	34	3	36	21	Q9DAV6	
ENSMUST00000006397	ENSMUSG00000006235	9	21958899	21963576	-1	12	10	20	99	26	12	0	3	0	0	2	Q3UTV9	P14753
ENSMUST00000006403	ENSMUSG00000006241	9	21927471	21935872	1	9	5	0	0	10	0	0	5	5	1	6		Q8C963
ENSMUST00000006415						6	4	51	29	17	0	135	181	183	10	275		
ENSMUST00000006424	ENSMUSG00000006262	5	88720855	88764220	1	0	0	0	0	0	0	57	27	16	0	0	Q3T9U1	Q8BPB0
ENSMUST00000006431	ENSMUSG00000006269	6	83742990	83758855	1	16	7	20	38	17	7	0	0	0	0	0	Q91YH6	
ENSMUST00000006435	ENSMUSG00000006273	8	69088646	69113711	1	5	7	65	44	14	5	5559	15092	6092	1333	3787		P62814
ENSMUST00000006444	ENSMUSG00000006281	14	50824062	50870560	-1	55	46	95	95	74	38	168	267	213	79	357		P97499
ENSMUST00000006451	ENSMUSG00000006288	14	50765415	50785518	-1	26	14	20	14	28	15	290	571	237	253	232		Q99LG4
ENSMUST00000006452	ENSMUSG00000006289	14	50906478	50924893	-1	0	0	0	0	0	0	0	0	0	0	0	E9QMF4	
ENSMUST00000006462	ENSMUSG00000006299	1	74279840	74284738	-1	4	0	0	52	9	0	1220	1423	914	353	639	Q3TJ22	
ENSMUST00000006467	ENSMUSG00000006304	1	74236084	74268209	1	0	0	0	106	8	8	1705	13580	7589	3815	4287		Q9CVB6
ENSMUST00000006470	ENSMUSG00000006307	7	30568858	30588726	-1	10	3	83	213	56	28	1392	708	1401	24	1338	F8WJ40	
ENSMUST00000006476	ENSMUSG00000006313	7	30603092	30612734	-1	8	6	26	11	16	8	2	4	1	0	2	A2RSB9	Q9D132
ENSMUST00000006478	ENSMUSG00000006315	7	30727701	30729534	-1	1	1	10	105	10	4	146	277	111	110	99	B2RVQ1	Q9CQG6
ENSMUST00000006496	ENSMUSG00000006333	7	3703993	3706897	1	27	47	4	95	77	22	21357	30806	18739	11757	14820		Q6ZWN5
ENSMUST00000006508	ENSMUSG00000006345	10	75561604	75586200	1	6	11	0	5	2	3	30	78	153	0	60	Q4FK56	Q60928
ENSMUST00000006523	ENSMUSG00000006360	12	113146316	113153879	1	2	0	13	17	6	5	1284	885	297	8783	963		P63254
ENSMUST00000006525	ENSMUSG00000006362	8	122628739	122699109	-1	10	6	0	6	0	8	7	4	17	0	26		O54972
ENSMUST00000006544	ENSMUSG00000006378	15	79030874	79043558	1	4	10	17	36	12	13	8	22	3	58	66		O88986
ENSMUST00000006556	ENSMUSG00000006389	4	118442415	118457513	-1	0	0	28	36	2	13	3	0	1	0	11	A2A9D4	
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ENSMUST00000006565	ENSMUSG00000006398	4	118432901	118437352	-1	21	5	5	224	18	18	228	178	263	29	192		Q9JJ66
ENSMUST00000006578	ENSMUSG00000006411	1	171370099	171388598	1	42	0	41	127	0	15	0	0	0	0	12		Q8R007
ENSMUST00000006579	ENSMUSG00000006412	1	171345670	171359254	1	0	0	0	3	0	0	43	91	20	133	41	F8WJ30	
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ENSMUST00000006611	ENSMUSG00000006442	4	148591503	148594993	1	19	16	59	68	27	15	44	95	18	37	69	Q543H0	Q64674
ENSMUST00000006614	ENSMUSG00000006445	4	141301240	141329384	1	41	15	66	169	33	20	8	0	5	27	213		Q03145
ENSMUST00000006618	ENSMUSG00000028919	4	141239499	141257564	1	24	14	56	104	28	16	1	0	0	1	3		Q8BWA8
ENSMUST00000006625	ENSMUSG00000006456	19	4800569	4811634	-1	3	3	36	66	6	0	322	301	316	36	205		Q8C2Q3
ENSMUST00000006626	ENSMUSG00000006457	19	4861223	4877909	-1	26	16	37	70	39	17	0	0	0	1	0		O88990
ENSMUST00000006629	ENSMUSG00000020315	11	30099395	30268175	-1	0	0	0	0	2	0	0	0	0	38	27		Q62261
ENSMUST00000006632	ENSMUSG00000006463	19	4878668	4885397	1	9	0	15	116	41	0	122	191	204	0	113		Q6IR37
ENSMUST00000006638	ENSMUSG00000006469	2	25228898	25234364	-1	8	10	16	13	18	1	0	0	0	0	0		Q80SU6
ENSMUST00000006646	ENSMUSG00000006476	2	25054355	25062881	1	0	0	0	0	0	0	42	0	0	0	52		Q99NF2
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ENSMUST00000006660	ENSMUSG00000046899	13	27658956	27668036	-1	2	1	0	0	1	0	0	0	0	0	0		O54831
ENSMUST00000006662	ENSMUSG00000006490	13	27558009	27564604	-1	0	1	0	1	2	0	0	0	0	0	0		Q9CQ58
ENSMUST00000006664	ENSMUSG00000019756	13	27573922	27582171	-1	1	0	0	0	1	0	0	0	0	0	0	Q9DAV8	
ENSMUST00000006667	ENSMUSG00000045868	7	106156556	106215326	-1	0	0	0	0	0	0	0	0	0	0	0	L7N451	
ENSMUST00000006669	ENSMUSG00000006494	2	71873224	71903858	1	34	30	105	100	46	24	42	192	79	17	69		Q8BFP9
ENSMUST00000006679	ENSMUSG00000057729	10	79874476	79883174	1	6	3	17	11	9	3	2297	1215	1274	206	348		
ENSMUST00000006687	ENSMUSG00000028359	4	63356162	63359511	1	5	6	8	13	9	0	4	15	16	9	32	J3JRU4	
ENSMUST00000006692	ENSMUSG00000006517	8	122433596	122443422	-1	9	5	36	44	25	22	543	1087	676	106	732	Q3UYC1	Q99JF5
ENSMUST00000006697	ENSMUSG00000006522	14	30908573	30923760	-1	11	10	16	8	16	11	0	0	0	92	0		Q61704
ENSMUST00000006701	ENSMUSG00000006526	14	30825590	30876986	1	25	19	33	26	28	18	483	863	418	55	510		Q3UF25
ENSMUST00000006703	ENSMUSG00000021922	14	30886476	30901981	1	14	14	17	40	33	0	0	12	0	12	0		A6X935
ENSMUST00000006704	ENSMUSG00000006529	14	30929180	30943289	-1	12	4	25	0	17	8	4	5	6	6	0	F8WJ05	
ENSMUST00000006716	ENSMUSG00000033227	1	74771892	74785322	1	10	4	22	146	16	7	0	0	2	1	2		P22727
ENSMUST00000006718	ENSMUSG00000026167	1	74791516	74804179	1	24	11	29	619	38	24	0	0	0	4	10		P70701
ENSMUST00000006721	ENSMUSG00000006546	1	74889934	74893143	-1	1	1	0	5	2	0	0	0	0	0	0		Q9JJV1
ENSMUST00000006742	ENSMUSG00000006567	8	21992785	22060305	-1	37	24	63	198	63	31	3	0	0	0	0		Q64446
ENSMUST00000006745	ENSMUSG00000006570	8	21839926	21843482	1	1	0	6	0	0	0	0	0	0	0	0	Q32MH3	P82020
ENSMUST00000006749	ENSMUSG00000006574	11	102348824	102366203	-1	37	26	43	62	58	23	63	2	21	46	86	Q53ZN9	P04919
ENSMUST00000006750	ENSMUSG00000006575	11	102393403	102402555	1	0	0	4	93	0	0	0	17	0	0	12		O08576
ENSMUST00000006754	ENSMUSG00000020923	11	102304560	102319742	-1	0	0	0	0	0	0	0	28	0	10	0	A2AWT7	
ENSMUST00000006760	ENSMUSG00000006585	8	122568015	122573128	1	14	10	19	152	25	7	197	255	145	22	133		Q8R4E9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000006761	ENSMUSG00000006586	4	13743436	13893649	1	0	0	31	111	22	4	0	0	0	1	1	Q3UQX8	
ENSMUST00000006762	ENSMUSG00000006587	8	122454206	122460692	-1	13	9	19	56	16	4	1	1	0	0	1		Q9QY31
ENSMUST00000006764	ENSMUSG00000006589	8	122574637	122576907	-1	15	10	22	154	22	10	1630	2059	1005	1206	563		P08030
ENSMUST00000006774	ENSMUSG00000006599	7	46796103	46823800	1	3	3	5	13	7	4	172	910	385	590	255	G3X8R4	
ENSMUST00000006785	ENSMUSG00000021335	13	23867750	23895730	1	0	0	0	12	0	0	0	0	0	0	0		Q61983
ENSMUST00000006786	ENSMUSG00000036110	13	23806993	23825180	1	27	18	40	21	27	17	0	0	0	0	0		Q5SZA1
ENSMUST00000006787	ENSMUSG00000006611	13	23702034	23710854	-1	0	0	11	0	0	2	0	0	0	0	0	Q5SZ91	
ENSMUST00000006792	ENSMUSG00000062524	7	4337724	4345164	1	0	2	4	0	0	3	7	0	8	20	21		
ENSMUST00000006817						0	0	0	0	0	0	2	53	0	7	31		
ENSMUST00000006818	ENSMUSG00000006642	5	30968662	30977018	1	37	29	67	58	35	16	1	3	1	1	6		Q9JLR5
ENSMUST00000006825	ENSMUSG00000006649	7	30458315	30487223	1	61	39	121	189	83	37	0	0	1	0	2		Q9QZS7
ENSMUST00000006828	ENSMUSG00000006651	7	30434981	30445582	-1	16	13	38	100	28	8	29	20	11	6	14		
ENSMUST00000006838	ENSMUSG00000032604	9	108507713	108515941	1	8	8	6	5	9	2	958	338	815	286	377	Q8BML9	
ENSMUST00000006851	ENSMUSG00000006673	9	108516806	108560163	1	4	0	10	12	0	0	201	169	57	0	42	G3X8R5	
ENSMUST00000006853	ENSMUSG00000006675	9	108578862	108597667	-1	8	2	37	222	11	3	5	4	2	1	4	Q2M2M8	Q8BG58
ENSMUST00000006854	ENSMUSG00000006676	9	108490602	108502337	1	0	0	16	140	19	0	220	102	302	9	238		Q3UJD6
ENSMUST00000006856	ENSMUSG00000006678	X	93304767	93632155	-1	6	7	1	13	8	4	26	77	59	79	44		P33609
ENSMUST00000006893	ENSMUSG00000006711	13	24845135	24901270	1	30	0	79	0	46	26	0	0	0	0	0		Q5SZV5
ENSMUST00000006898	ENSMUSG00000006715	13	24751845	24761923	-1	3	0	0	103	11	3	0	0	0	0	0	Q3V295	O88513
ENSMUST00000006900	ENSMUSG00000006717	13	24817948	24831517	-1	2	3	0	13	6	0	78	290	102	541	71	Q4VA32	Q9CQR4
ENSMUST00000006903	ENSMUSG00000006720	13	21945094	21960779	1	0	0	9	0	0	3	1	5	0	0	0		Q7TSH9
ENSMUST00000006911	ENSMUSG00000006728	10	127063534	127067920	1	0	0	0	67	0	0	78	243	79	60	104	Q545C3	P30285
ENSMUST00000006912	ENSMUSG00000026737	2	18842255	18998126	-1	22	13	33	129	28	28	1448	4702	2897	457	2119	Q544E3	O70172
ENSMUST00000006914	ENSMUSG00000006731	10	127165156	127172340	1	19	9	57	355	36	16	4309	3482	3146	366	2523	Q3UN35	Q09200
ENSMUST00000006915	ENSMUSG00000006732	10	127041414	127046365	1	3	4	22	42	12	3	15	49	5	9	26		Q9Z120
ENSMUST00000006948						3	12	28	10	7	1	32	89	18	84	3		
ENSMUST00000006949	ENSMUSG00000006764	10	115078641	115185022	-1	17	14	15	8	16	6	3	16	6	1	5		Q8CGV2
ENSMUST00000006952	ENSMUSG00000040017	7	46728017	46732543	-1	189	125	1064	253	123	68	1	19	8	11	2		P31532
ENSMUST00000006956	ENSMUSG00000040026	7	46711998	46715676	-1	8	12	17	20	25	28	38044	35179	42965	114127	7679		P04918
ENSMUST00000006963	ENSMUSG00000055937	11	99364872	99374903	-1	10	9	24	21	8	11	0	0	0	0	0		A6BLY7
ENSMUST00000006969	ENSMUSG00000006777	11	99477974	99493137	-1	19	8	27	18	21	7	0	1	0	1	0	Q544I8	Q99PS0
ENSMUST00000006973	ENSMUSG00000020918	11	100704746	100712465	-1	0	0	0	45	20	6	52	49	50	26	31	Q6P3Z8	
ENSMUST00000006976	ENSMUSG00000006784	11	100545607	100572568	1	6	7	25	7	14	14	0	2	0	0	0	B8A5X0	
ENSMUST00000006991	ENSMUSG00000021730	13	117602480	117976802	1	24	18	90	112	28	18	0	1	0	0	0		O88704
ENSMUST00000007005	ENSMUSG00000023832	17	12942890	12960747	-1	2	5	17	47	15	8	58	192	68	15	73		Q8CAY6
ENSMUST00000007007	ENSMUSG00000060475	17	12966796	12992546	-1	19	17	19	2	0	6	257	1325	442	596	376	E0CYH0	
ENSMUST00000007012	ENSMUSG00000006818	17	13007839	13018119	1	41	33	66	172	35	23	350	760	385	300	318	Q4FJX9	P09671
ENSMUST00000007042	ENSMUSG00000024474	18	36744656	36757639	1	6	18	15	23	20	8	616	2471	1165	3840	994		Q9Z1M8
ENSMUST00000007046	ENSMUSG00000006850	18	36735068	36742391	1	12	16	20	119	31	7	350	687	251	72	327		Q8BQX5
ENSMUST00000007130	ENSMUSG00000006932	9	120929216	120960507	1	0	0	0	27	0	0	175	542	1089	132	384		Q02248
ENSMUST00000007131	ENSMUSG00000020917	11	100476353	100528000	-1	18	12	35	82	19	13	243	0	488	61	424		Q91V92
ENSMUST00000007139	ENSMUSG00000006941	9	120492606	120495327	1	9	6	2	112	12	4	399	1143	411	243	226		Q9CXU9
ENSMUST00000007156	ENSMUSG00000044485	7	43995877	43999875	1	3	4	18	5	9	9	0	0	0	0	0		P15946
ENSMUST00000007161	ENSMUSG00000006948	7	43881160	43885804	1	13	5	54	29	22	7	0	0	0	2	3	Q9Z0M1	
ENSMUST00000007171	ENSMUSG00000006958	16	20733127	20742384	1	0	0	0	0	5	8	0	0	0	3	0		Q9Z0E2
ENSMUST00000007207	ENSMUSG00000022843	16	20702964	20717746	-1	0	0	0	0	0	0	0	0	5	2	0		Q9R0A1
ENSMUST00000007212	ENSMUSG00000006998	16	20651652	20663414	1	17	12	2	82	25	6	1303	2974	1857	496	1389	Q3TKV1	Q8VDM4
ENSMUST00000007216	ENSMUSG00000022841	16	20535478	20544909	1	92	76	131	125	123	59	172	270	225	70	182	Q5FWI9	P84091
ENSMUST00000007236	ENSMUSG00000007021	17	24685092	24689955	-1	8	13	22	59	14	10	1	0	0	0	0		Q8R191
ENSMUST00000007245	ENSMUSG00000007030	17	35016579	35026741	1	26	7	44	100	45	7	7	16	6	0	19	B2RQ76	Q9JHA8
ENSMUST00000007248	ENSMUSG00000007033	17	34972703	34979285	1	16	7	19	42	17	14	0	15	1	0	5	A1L347	P16627
ENSMUST00000007249	ENSMUSG00000007034	17	34914466	34930436	1	0	0	11	0	0	0	0	0	0	0	0	Q3ULA4	Q91VA1
ENSMUST00000007250	ENSMUSG00000007035	17	35028605	35046745	-1	0	3	0	72	0	3	106	490	150	6	219		
ENSMUST00000007251	ENSMUSG00000007036	17	35089263	35102987	1	0	16	39	22	0	0	799	792	514	74	355		Q9Z1Q2
ENSMUST00000007253	ENSMUSG00000007038	17	34931253	34935953	1	1	0	5	79	12	6	1486	1771	1057	220	848	Q3UL64	O35657
ENSMUST00000007255	ENSMUSG00000007039	17	35059035	35062095	1	8	0	0	62	14	3	24	94	19	24	15		Q99LD8
ENSMUST00000007257	ENSMUSG00000007041	17	35049966	35058749	1	15	7	22	112	15	12	11483	19016	9116	13259	5739	Q542F1	Q9Z1Q5
ENSMUST00000007259	ENSMUSG00000073413	17	35071443	35078065	-1	2	0	0	6	2	2	0	0	0	0	0		Q9Z1Q3
ENSMUST00000007266	ENSMUSG00000007050	17	34981862	34985891	1	3	4	3	36	3	0	5	5	0	9	0	O35901	
ENSMUST00000007272	ENSMUSG00000045545	11	100203162	100207548	-1	26	14	94	39	27	12	0	0	0	6	6		Q61781
ENSMUST00000007275	ENSMUSG00000044041	11	100117327	100121566	-1	12	19	74	26	19	8	0	0	0	10	0		P08730
ENSMUST00000007280	ENSMUSG00000053797	11	100246091	100248902	-1	28	19	123	27	27	19	0	0	0	0	2	Q3SYP5	Q9Z2K1
ENSMUST00000007296	ENSMUSG00000007080	5	110286306	110337474	1	28	13	21	30	38	9	36	28	64	1	82		Q9WVF7
ENSMUST00000007301	ENSMUSG00000020908	11	67078300	67102291	1	30	35	41	0	0	10	0	2	0	1	0		P13541
ENSMUST00000007317	ENSMUSG00000020911	11	100140810	100148665	-1	6	6	14	70	14	8	0	0	0	12	23	B1AQ78	P19001
ENSMUST00000007318	ENSMUSG00000048981	11	100046646	100050551	-1	5	8	3	20	10	10	0	0	0	0	0		Q61765
ENSMUST00000007340	ENSMUSG00000022229	14	56365068	56388551	1	28	16	15	70	30	12	0	0	0	0	0		Q9Z1W8
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ENSMUST00000007433	ENSMUSG00000098306	1	133309827	133329901	1	8	0	3	18	0	0	0	0	0	0	0	I0J0X7	Q6Y4S4
ENSMUST00000007444	ENSMUSG00000069631	11	106163330	106202168	-1	18	8	0	9	28	0	185	410	208	36	181		Q3UUJ4
ENSMUST00000007449	ENSMUSG00000052131	6	34412334	34423142	1	4	6	10	5	6	3	0	0	0	1	0	Q5M9J9	P21300
ENSMUST00000007482	ENSMUSG00000007338	19	6053630	6057751	-1	23	11	33	26	23	7	152	454	177	221	119		Q9CQ40
ENSMUST00000007533	ENSMUSG00000078656	11	101253707	101259549	1	0	0	0	7	1	0	4	22	9	22	4		Q9CQ80
ENSMUST00000007559	ENSMUSG00000007415	5	3632932	3657185	-1	4	8	9	41	11	10	457	1554	483	207	346		Q920S3
ENSMUST00000007584	ENSMUSG00000103255	18	37090013	37187657	1	14	22	41	75	18	20	0	0	0	0	0	Q91Y10	
ENSMUST00000007601	ENSMUSG00000007457	5	87969459	87972870	1	4	8	4	8	4	1	0	0	0	0	0	Q9CV82	
ENSMUST00000007602	ENSMUSG00000007458	6	122308720	122317680	1	0	0	34	19	0	0	811	2790	1196	646	1001	Q3UKQ5	P24668
ENSMUST00000007708	ENSMUSG00000007564	17	20945311	20965916	1	18	16	37	61	36	19	4612	4868	3344	510	2452		Q76MZ3
ENSMUST00000007733	ENSMUSG00000007589	14	55679083	55681817	-1	13	10	11	162	17	6	241	560	266	98	254	Q8K1K3	
ENSMUST00000007735	ENSMUSG00000007591	14	55650182	55652539	1	0	0	18	0	7	0	4	11	5	6	13	A3QQR1	
ENSMUST00000007738	ENSMUSG00000007594	8	70083529	70090862	1	24	26	36	299	45	26	1	2	0	0	3		Q80WM4
ENSMUST00000007747	ENSMUSG00000007603	17	56764751	56770092	1	16	12	72	187	29	12	289	510	223	54	243		
ENSMUST00000007754	ENSMUSG00000007610	8	71488103	71499583	1	15	9	31	78	14	8	22	40	18	3	6	B2RRS4	Q923K4
ENSMUST00000007757	ENSMUSG00000007613	4	47353222	47414931	1	21	7	24	25	14	9	497	1291	667	130	466	Q4FJL1	Q64729

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000007790	ENSMUSG00000007646	11	87376645	87404954	-1	5	0	4	23	1	0	0	0	7	0	0		Q924H5
ENSMUST00000007797	ENSMUSG00000007653	11	42419757	42629028	1	14	15	27	15	12	9	0	0	0	0	0		P63137
ENSMUST00000007799	ENSMUSG00000007655	6	17306335	17341452	1	11	6	3	5	0	0	0	0	1	82	22		P49817
ENSMUST00000007800	ENSMUSG00000007656	9	75037614	75060313	1	0	0	0	14	0	0	9	0	28	0	0		P56212
ENSMUST00000007803	ENSMUSG00000007659	2	152780668	152831728	-1	0	8	0	42	28	18	1072	1009	564	242	530	Q5HZH3	Q64373
ENSMUST00000007814	ENSMUSG00000007670	17	57021058	57031507	-1	45	34	97	208	50	30	987	1551	1380	123	1159		Q3U0V1
ENSMUST00000007865	ENSMUSG00000007721	8	70868227	70873490	-1	4	6	14	113	11	4	728	862	467	319	359		Q9D8X2
ENSMUST00000007884	ENSMUSG00000023882	17	21423227	21435640	1	8	11	0	5	9	0	3	25	6	8	3	E9PW05	
ENSMUST00000007921	ENSMUSG00000007777	11	51685386	51688874	-1	2	3	1	1	3	1	59	158	53	216	36	Q8R3W2	
ENSMUST00000007949	ENSMUSG00000007805	1	91801461	91848028	1	3	5	5	60	8	2	0	0	0	0	0	A5D6P6	
ENSMUST00000007959	ENSMUSG00000007815	9	108306129	108337934	1	22	23	46	41	29	21	8158	20506	7528	4048	5136	Q4VAE6	Q9QUI0
ENSMUST00000007961	ENSMUSG00000007817	14	25459185	25666743	1	21	12	97	43	38	7	133	12	256	0	212		Q6P1E1
ENSMUST00000007977	ENSMUSG00000007833	7	45140684	45154584	-1	0	25	60	41	20	25	330	282	206	75	59		
ENSMUST00000007980	ENSMUSG00000007836	13	58125879	58128556	-1	6	6	9	329	23	5	747	1442	855	201	654		Q9CX86
ENSMUST00000007981	ENSMUSG00000007837	7	45053613	45061652	-1	0	0	9	117	0	0	318	453	139	47	174		Q8R182
ENSMUST00000007993	ENSMUSG00000029701	6	29123576	29165006	-1	474	391	511	418	534	269	135	606	325	77	301		Q8CGC6
ENSMUST00000008004	ENSMUSG00000057788	8	70292866	70302489	-1	0	8	12	46	8	7	249	127	229	147	111		Q4FZF3
ENSMUST00000008016	ENSMUSG00000007872	4	136143497	136145755	1	9	5	9	122	10	6	24	44	11	5	33	Q545W1	P41133
ENSMUST00000008021	ENSMUSG00000007877	11	98383811	98384953	1	11	12	19	84	24	6	1	7	1	0	2	Q545G3	O70548
ENSMUST00000008024	ENSMUSG00000007880	4	133679008	133756769	-1	44	13	49	106	46	17	1130	11	1858	21	1974		A2BH40
ENSMUST00000008032	ENSMUSG00000007888	8	70493158	70504081	1	1	5	11	81	13	3	0	0	0	0	0		Q9JM58
ENSMUST00000008036	ENSMUSG00000007892	9	61913284	61914538	-1	10	17	28	95	20	14	7690	9782	5571	18319	2978	Q58E35	P47955
ENSMUST00000008051	ENSMUSG00000007907	5	87979439	87981544	1	5	5	10	0	4	3	0	0	0	0	0		Q8C633
ENSMUST00000008052	ENSMUSG00000007908	9	76014855	76136350	1	0	0	11	0	11	0	0	0	0	0	0		Q8JZS7
ENSMUST00000008088	ENSMUSG00000007944	7	27653915	27657346	1	6	1	5	139	10	5	0	0	0	0	1		Q9D6E4
ENSMUST00000008090	ENSMUSG00000007946	7	101818313	101822726	1	6	3	21	273	16	10	0	0	0	0	0		Q62066
ENSMUST00000008094	ENSMUSG00000007950	8	71456700	71463657	-1	17	11	47	427	32	23	138	115	67	27	105		Q8R0P8
ENSMUST00000008131	ENSMUSG00000007987	5	136908150	136915404	1	5	6	10	19	6	4	34	60	29	66	30	A0A0H2UKB7	
ENSMUST00000008179	ENSMUSG00000008035	X	10715013	10719690	1	0	3	31	161	16	5	1020	1688	962	128	770	Q4FK31	Q9CQ20
ENSMUST00000008273	ENSMUSG00000030069	6	99711299	99726392	-1	0	0	0	31	0	8	107	448	77	11	62	G3X8R6	
ENSMUST00000008280	ENSMUSG00000008136	1	43123074	43196984	-1	5	0	3	49	6	2	0	8	0	41	25	Q543D7	O70433
ENSMUST00000008284						9	0	0	0	6	0	220	226	148	33	149		
ENSMUST00000008297	ENSMUSG00000008153	6	124430759	124464794	-1	16	17	57	17	31	13	6	0	6	0	3		Q99JH7
ENSMUST00000008350	ENSMUSG00000008206	8	4493026	4531680	1	455	377	714	408	491	237	3	49	23	6	41		Q9D6J1
ENSMUST00000008445	ENSMUSG00000008301	18	56562443	56587712	1	7	7	20	66	6	5	41	119	86	291	69		Q9JJT9
ENSMUST00000008451	ENSMUSG00000008307	5	3571566	3584356	1	3	0	3	4	0	2	1	11	0	0	5	Q9D9C0	
ENSMUST00000008462	ENSMUSG00000008318	7	100845848	100863446	-1	6	3	66	24	28	14	2050	3338	1392	374	1219		Q8BX43
ENSMUST00000008477	ENSMUSG00000008333	2	143063039	143072853	1	0	0	7	21	9	5	76	464	149	611	98		Q9CQI7
ENSMUST00000008517	ENSMUSG00000008373	7	3629985	3642486	1	0	0	0	34	0	0	47	125	64	33	48		Q8CCF0
ENSMUST00000008528	ENSMUSG00000008384	7	27486910	27490316	1	11	9	19	82	24	9	875	1530	564	325	388		Q9JL10
ENSMUST00000008537	ENSMUSG00000008393	16	8658587	8672153	-1	28	16	33	45	37	8	4179	8961	4371	733	2974	Q5M9P7	Q9CR86
ENSMUST00000008542	ENSMUSG00000008398	10	93247414	93311135	-1	18	7	32	25	24	9	144	547	259	50	318		P41971
ENSMUST00000008573	ENSMUSG00000008429	9	25108130	25151781	-1	10	6	15	255	9	8	654	1498	1064	133	716		Q9JJC9
ENSMUST00000008579	ENSMUSG00000008435	7	4424770	4445649	-1	35	30	64	61	41	19	19	27	32	14	42		Q8CEE7
ENSMUST00000008582	ENSMUSG00000008438	12	81558584	81568474	-1	11	8	8	12	14	8	0	3	0	1	0		Q9JI76
ENSMUST00000008594	ENSMUSG00000008450	8	105860634	105880402	1	3	3	17	38	10	12	9	52	12	16	14		P61971
ENSMUST00000008605	ENSMUSG00000008461	7	45617606	45621059	1	71	42	64	321	74	34	0	0	0	0	0	P97327	
ENSMUST00000008626	ENSMUSG00000008482	17	24715839	24718057	-1	4	3	16	25	8	9	2	1	0	0	2		Q9CQ29
ENSMUST00000008633	ENSMUSG00000008489	4	91250763	91400785	-1	0	0	0	0	0	0	0	0	0	0	0	Q564D8	Q60899
ENSMUST00000008684	ENSMUSG00000008540	6	138140316	138156755	1	2	2	5	27	6	2	306	352	161	815	229	Q53ZD4	Q91VS7
ENSMUST00000008733	ENSMUSG00000029131	5	29735688	29818134	1	58	33	204	247	65	44	478	1602	809	212	747		O54946
ENSMUST00000008734	ENSMUSG00000008590	9	48935008	48964990	-1	32	19	29	37	32	19	0	1	1	0	3		Q9JHJ5
ENSMUST00000008745	ENSMUSG00000008601	3	88542029	88548300	-1	6	5	29	13	9	3	0	13	5	0	3	Q0PD30	Q9WTL2
ENSMUST00000008748	ENSMUSG00000008604	3	88553758	88569725	1	11	6	31	43	33	15	319	425	288	48	265		Q99NB8
ENSMUST00000008801	ENSMUSG00000073424	17	32685627	32703352	1	0	0	4	0	16	9	0	0	0	0	0	Q8VCA4	
ENSMUST00000008812	ENSMUSG00000008668	17	33951999	33956001	-1	0	0	0	5	0	0	31	12	39	540	30	Q561N5	P62270
ENSMUST00000008826	ENSMUSG00000008682	X	74270812	74273135	1	0	0	7	27	21	0	26	78	68	88	58		Q6ZWV3
ENSMUST00000008830	ENSMUSG00000094441	17	33241519	33255040	-1	8	7	7	4	5	2	6	25	7	14	8	Q80XR7	
ENSMUST00000008847						7	8	5	3	7	1	35	153	52	6	79		
ENSMUST00000008878	ENSMUSG00000008734	7	118972040	118995211	-1	24	33	78	116	44	18	2	0	2	35	103		Q923Z0
ENSMUST00000008893	ENSMUSG00000024835	19	4148619	4154035	1	6	2	9	11	10	5	4239	3699	2597	991	1669	A2RS22	Q9WUM3
ENSMUST00000008907	ENSMUSG00000008763	3	100562208	100685503	-1	28	24	21	104	33	19	404	1077	799	106	505		P39098
ENSMUST00000008957	ENSMUSG00000008813	14	51918425	51920699	1	5	0	0	4	6	0	0	0	0	0	0		Q0P5Y3
ENSMUST00000008966	ENSMUSG00000008822	12	85272398	85288438	-1	0	0	2	0	0	0	28	110	49	185	53		P56376
ENSMUST00000008987	ENSMUSG00000008843	5	134914249	134915526	-1	11	2	27	8	15	1	1	0	0	0	0	Q547B2	Q9Z0S4
ENSMUST00000008991	ENSMUSG00000067889	19	4711208	4752353	1	84	53	150	239	130	46	3	3	6	3	8	Q68FG2	
ENSMUST00000008995	ENSMUSG00000026313	1	91928779	92180341	-1	0	0	0	14	3	1	107	0	235	0	185		Q6NZM9
ENSMUST00000008999	ENSMUSG00000008855	11	102194432	102230166	-1	4	2	11	23	4	3	80	147	153	0	109	B7ZDF5	
ENSMUST00000009003	ENSMUSG00000008859	13	17880575	17944239	-1	12	10	11	17	13	5	306	1677	627	476	376		P63321
ENSMUST00000009018	ENSMUSG00000008874	8	114418086	114425846	1	10	3	15	6	8	1	0	0	0	0	0	B2RVD1	Q9EPW4
ENSMUST00000009036	ENSMUSG00000008892	8	22577075	22593813	-1	7	6	9	58	4	0	470	1789	687	1130	421	Q3TX38	Q60931
ENSMUST00000009039	ENSMUSG00000058600	15	34440505	34443640	-1	16	8	70	3	27	2	142	382	130	251	64	Q58DZ3	P62889
ENSMUST00000009058	ENSMUSG00000028970	5	8798147	8866315	1	28	25	26	36	24	22	8	54	10	69	77	B2RUR3	P06795
ENSMUST00000009099	ENSMUSG00000021144	12	113098278	113137206	1	0	0	0	0	0	0	0	56	0	0	5	M1VHG1	Q8K4B0
ENSMUST00000009102	ENSMUSG00000008958	3	95111022	95123051	1	23	19	63	62	22	14	260	424	191	49	206		Q62481
ENSMUST00000009120	ENSMUSG00000008976	16	84834925	84863779	1	25	6	21	61	14	5	267	800	402	159	307		Q00422
ENSMUST00000009138	ENSMUSG00000024006	17	28970885	29007945	-1	9	6	22	31	14	0	3060	14353	7278	719	4885		Q91VJ4
ENSMUST00000009143	ENSMUSG00000008999	2	172868012	172940321	-1	118	94	662	351	104	64	5	4	1	5	18		P23359
ENSMUST00000009157	ENSMUSG00000009013	5	115297110	115300999	-1	69	81	194	153	63	33	29	61	33	21	27		P63168
ENSMUST00000009174	ENSMUSG00000009030	2	37350074	37359332	-1	2	0	7	5	5	3	269	576	230	553	143		Q9DBX2
ENSMUST00000009191	ENSMUSG00000009047	16	88777896	88778528	1	1	0	4	2	5	5	0	0	0	0	0	D3Z724	
ENSMUST00000009214	ENSMUSG00000009070	10	74957477	75032586	-1	7	0	0	5	9	7	0	0	0	0	0		Q9D3W1
ENSMUST00000009219	ENSMUSG00000009075	11	4736892	4746778	-1	22	13	52	56	25	16	1	1	0	0	1	Q5NCJ7	Q91ZM8
ENSMUST00000009220	ENSMUSG00000009076	11	4704678	4737669	1	1	0	3	0	0	0	181	130	98	230	62		Q9CQR5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000009234	ENSMUSG00000009090	11	4986824	5042791	1	22	0	35	58	35	11	1082	831	1022	116	962		O35643
ENSMUST00000009236	ENSMUSG00000009092	10	75893398	75895941	1	11	8	25	101	20	4	3	1	2	1	8	Q14C34	Q9D8K3
ENSMUST00000009241	ENSMUSG00000009097	16	18581713	18586969	-1	3	7	8	211	7	3	0	0	0	0	1	B9EII4	
ENSMUST00000009256	ENSMUSG00000009112	6	120836212	120892842	1	51	39	64	162	51	26	549	845	756	106	458		P59017
ENSMUST00000009259	ENSMUSG00000009115	10	76562272	76570201	1	8	5	18	21	22	11	0	0	0	0	0		Q9D9W0
ENSMUST00000009321	ENSMUSG00000022718	16	18253948	18289249	-1	0	0	0	0	0	0	38	72	41	12	65		Q9EQM6
ENSMUST00000009329	ENSMUSG00000009185	11	82115185	82116799	1	4	1	3	6	1	0	1	1	0	295	16	Q149U7	Q9Z121
ENSMUST00000009340	ENSMUSG00000026536	1	173896345	173913046	-1	7	5	6	4	8	2	5	81	16	307	88		Q08619
ENSMUST00000009344	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	0	0	0	0	1861	3874	2162	77	1380		Q924Z6
ENSMUST00000009354	ENSMUSG00000009210	11	106365472	106377558	1	5	2	5	41	7	7	0	0	0	0	0		B1ARI9
ENSMUST00000009356	ENSMUSG00000062345	1	107511423	107535478	1	2	3	6	0	0	3	4	0	10	185	31	Q542A3	P12388
ENSMUST00000009358	ENSMUSG00000009214	2	27061636	27072179	-1	0	6	18	7	21	10	0	0	0	0	0		Q9D1N4
ENSMUST00000009390	ENSMUSG00000009246	7	143069153	143094642	-1	0	0	0	17	0	0	0	0	0	0	0		Q9JJH7
ENSMUST00000009392	ENSMUSG00000009248	7	142966822	142969264	-1	0	0	0	4	0	5	0	0	0	0	0	Q3TJR9	O35885
ENSMUST00000009396	ENSMUSG00000000244	7	143005046	143019644	1	5	0	2	13	5	0	146	159	93	17	51		Q9JHH2
ENSMUST00000009411	ENSMUSG00000052763	6	47920476	47932639	1	18	18	64	194	39	10	376	492	339	65	274	G3X8R7	
ENSMUST00000009420	ENSMUSG00000052751	6	48593883	48599082	1	0	0	0	0	0	7	21	0	23	0	0		Q5U4E2
ENSMUST00000009425	ENSMUSG00000009281	6	48569696	48572789	-1	3	1	3	3	5	2	0	2	1	121	22		Q9DD06
ENSMUST00000009435	ENSMUSG00000009291	10	77581720	77598732	1	9	9	17	36	14	6	1792	3241	1461	571	1285		Q8R143
ENSMUST00000009522	ENSMUSG00000009378	19	34668403	34747289	-1	17	21	38	128	18	6	6	23	11	6	14		Q8BGC3
ENSMUST00000009530	ENSMUSG00000001131	X	20870166	20874735	1	3	4	0	2	0	0	2	2	0	234	53		P12032
ENSMUST00000009538	ENSMUSG00000009394	6	115134902	115282006	1	17	15	25	163	31	14	0	0	0	1	0		Q64332
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ENSMUST00000009617	ENSMUSG00000027895	3	107438303	107459552	-1	20	19	76	271	42	14	0	0	0	0	0		Q8R1C0
ENSMUST00000009667	ENSMUSG00000030838	7	46195350	46238503	-1	26	0	36	30	19	0	0	0	0	0	0	E9QMN1	
ENSMUST00000009679	ENSMUSG00000009535	18	68300355	68324852	1	4	0	0	4	8	5	21	149	37	34	40		Q9D0L8
ENSMUST00000009689	ENSMUSG00000009545	7	143106362	143427042	1	12	19	58	140	40	16	0	0	0	0	2		P97414
ENSMUST00000009693	ENSMUSG00000009549	2	118475850	118479711	-1	0	3	0	40	6	3	649	1645	568	2326	450		P16254
ENSMUST00000009695	ENSMUSG00000009551	2	32732620	32741016	-1	4	4	7	7	11	2	22	56	45	3	38	A2AK85	
ENSMUST00000009699	ENSMUSG00000009555	2	32705784	32713076	-1	0	0	0	0	0	0	1542	1337	1074	107	633		Q99J95
ENSMUST00000009705	ENSMUSG00000026814	2	32646595	32682669	1	4	17	34	0	15	10	17	0	0	0	0		Q63961
ENSMUST00000009707	ENSMUSG00000009563	2	32757234	32762244	1	0	0	0	0	0	0	932	835	666	242	425		Q8R1J9
ENSMUST00000009713	ENSMUSG00000009569	16	13256481	13417529	1	0	0	0	25	0	0	15	3	53	0	0	G3X8R8	
ENSMUST00000009727	ENSMUSG00000022415	15	80091334	80119501	1	27	21	55	44	54	29	12	2	6	0	3		O55100
ENSMUST00000009728	ENSMUSG00000022415	15	80091334	80119501	1	4	0	4	13	0	1	17	14	8	2	6	Q3U6D7	O55100
ENSMUST00000009732	ENSMUSG00000009588	11	116765025	116775507	-1	35	18	103	90	34	29	0	0	0	0	3		Q9QZ39
ENSMUST00000009740	ENSMUSG00000009596	X	134460118	134476490	-1	1	3	4	45	5	2	0	0	0	0	0		Q9D3R9
ENSMUST00000009772	ENSMUSG00000009628	8	33516738	33585582	1	24	14	19	4	10	3	41	83	29	8	26	F8VPN2	
ENSMUST00000009774	ENSMUSG00000009630	8	33599621	33619794	1	4	9	3	37	10	2	1066	2156	1196	315	724		P62715
ENSMUST00000009777	ENSMUSG00000009633	1	193272161	193273217	-1	12	2	26	52	14	3	857	1386	341	1103	503	Q545U0	Q61585
ENSMUST00000009789	ENSMUSG00000019916	10	59323296	59373304	1	23	19	32	109	31	8	57	284	101	70	85		Q60715
ENSMUST00000009790	ENSMUSG00000009646	10	59403660	59421976	1	10	7	13	10	9	5	0	0	0	0	0	Q8VC81	
ENSMUST00000009791	ENSMUSG00000009647	10	59446984	59616692	-1	0	0	0	3	0	0	5	18	5	0	19		Q3UMR5
ENSMUST00000009798	ENSMUSG00000009654	10	59422958	59441778	-1	23	18	42	25	36	10	3	3	8	0	2		Q8R4V5
ENSMUST00000009814	ENSMUSG00000009670	X	100838648	101059667	-1	5	0	3	7	3	0	0	1	0	1	1		Q14AT2
ENSMUST00000009831	ENSMUSG00000009687	7	31032722	31042481	-1	0	0	0	0	0	0	3387	5409	1875	11882	1768	F8WJA1	
ENSMUST00000009875	ENSMUSG00000009731	X	7822289	7838280	1	38	22	131	67	44	14	47	225	58	4	133	A2AEX0	Q03719
ENSMUST00000009877	ENSMUSG00000009733	15	100502799	100552008	-1	22	24	34	79	27	15	39	100	65	6	67		Q9ERA0
ENSMUST00000009885	ENSMUSG00000009741	9	113930934	113977199	1	23	0	40	57	26	11	48	1609	829	97	178		Q811S7
ENSMUST00000009972	ENSMUSG00000009828	9	78109192	78172107	1	6	4	84	30	5	4	1	0	0	0	0	Q9D7Q7	
ENSMUST00000010007	ENSMUSG00000009863	4	140961203	140979193	1	6	1	4	46	7	2	1374	2605	1158	2927	808		Q9CQA3
ENSMUST00000010020	ENSMUSG00000009876	2	152754173	152765037	1	0	2	12	14	7	0	3	3	0	2	4		Q91W29
ENSMUST00000010038	ENSMUSG00000009894	11	59407134	59451186	-1	8	10	19	5	20	6	79	114	53	83	64		Q8R570
ENSMUST00000010044	ENSMUSG00000009900	11	59248033	59290752	-1	21	16	47	122	35	16	0	0	0	0	0		P27467
ENSMUST00000010049	ENSMUSG00000009905	1	106720459	106759727	-1	44	44	153	75	47	27	58	178	74	47	84	Q8CII3	Q6GV12
ENSMUST00000010085	ENSMUSG00000009941	X	134944526	134964754	-1	0	0	0	0	5	0	0	0	0	0	0	Q4ZGD8	
ENSMUST00000010127	ENSMUSG00000031397	X	74177259	74208500	1	2	7	5	1	8	4	0	2	2	1	3		Q99MX0
ENSMUST00000010188	ENSMUSG00000010044	9	107547298	107551319	1	7	6	7	11	7	5	0	5	3	0	3		Q99ML0
ENSMUST00000010189	ENSMUSG00000010045	9	107533945	107538673	1	21	12	50	275	38	11	747	683	554	103	395	Q543Y8	Q9WUH1
ENSMUST00000010191	ENSMUSG00000010047	9	107567945	107572779	1	0	0	0	0	0	0	41	31	10	21	33	Q3UZE4	O35632
ENSMUST00000010192	ENSMUSG00000010048	9	107587642	107593385	1	0	0	5	85	28	0	27	25	21	8	56	Q9D8U0	
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ENSMUST00000010198	ENSMUSG00000010054	9	107563255	107566112	1	9	5	15	54	11	11	368	543	262	89	141	Q542N4	Q9WVF8
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ENSMUST00000010239	ENSMUSG00000010095	19	8706882	8723369	-1	142	64	61	323	92	29	1057	1735	1102	178	868		P10852
ENSMUST00000010241	ENSMUSG00000010097	19	8757073	8772475	1	4	0	0	11	0	0	358	1497	521	218	509		Q99JX7
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ENSMUST00000010249	ENSMUSG00000003680	19	8772522	8786417	-1	3	1	10	29	4	4	637	1521	512	721	316		Q9CY24
ENSMUST00000010250	ENSMUSG00000024650	19	8617996	8628299	1	27	16	49	28	45	25	0	0	0	0	0		Q8VC69
ENSMUST00000010251	ENSMUSG00000063796	19	8591254	8611834	1	57	0	194	55	62	27	0	0	0	0	0		O88909
ENSMUST00000010254	ENSMUSG00000010110	19	8741413	8756069	1	2	0	0	0	0	0	116	115	0	12	43	I1E4X1	
ENSMUST00000010267	ENSMUSG00000010122	11	61343401	61378345	-1	12	9	4	79	27	8	0	0	0	1	0		Q8K0H1
ENSMUST00000010278	ENSMUSG00000000561	3	105959369	105970037	1	0	0	0	8	0	0	551	2008	372	27	219		Q99J09
ENSMUST00000010279	ENSMUSG00000074344	3	105870903	105924042	1	4	3	4	3	6	3	6	35	22	5	27	G3X8R9	
ENSMUST00000010280	ENSMUSG00000010136	3	105996957	106014646	-1	0	4	2	3	6	5	0	0	0	0	0		Q9D9W1
ENSMUST00000010286	ENSMUSG00000010142	11	61126755	61149372	1	5	7	20	34	19	4	700	1928	1090	257	295	A5D8Y6	Q9ET35
ENSMUST00000010298	ENSMUSG00000010154	8	123332713	123369515	1	16	8	23	174	33	7	4	0	2	3	11		Q8K1S6
ENSMUST00000010319	ENSMUSG00000010175	1	190118035	190170714	-1	0	5	50	29	4	0	0	0	0	0	0		P48437
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000010421	ENSMUSG00000010277	11	78261752	78290623	1	35	30	52	48	47	14	1081	1851	2225	349	2245		Q5SYL3
ENSMUST00000010434	ENSMUSG00000010290	1	43098710	43115947	1	25	11	21	55	25	8	82	240	111	57	96		Q922M7
ENSMUST00000010451	ENSMUSG00000010307	7	47050640	47054776	1	15	9	57	73	32	8	559	368	552	97	153		Q9D8N3
ENSMUST00000010502	ENSMUSG00000010358	11	101448407	101458698	1	0	0	0	5	8	0	311	445	172	141	252		Q9D8C4
ENSMUST00000010506	ENSMUSG00000010362	11	101627195	101636100	1	2	0	0	3	0	0	79	100	26	61	44		Q9CQK3
ENSMUST00000010520	ENSMUSG00000010376	14	55662265	55671906	-1	6	0	15	10	6	1	964	2090	757	3509	469	Q3UI46	P29595
ENSMUST00000010536	ENSMUSG00000010392	11	76726602	76763579	-1	24	18	46	28	36	21	389	964	568	269	450		O88630
ENSMUST00000010550	ENSMUSG00000010406	14	54426909	54429756	1	3	0	7	47	3	3	132	590	210	807	144		Q9D0Y8
ENSMUST00000010579	ENSMUSG00000010435	8	12573049	12600738	1	1	2	8	4	8	3	0	0	0	0	0		Q9D2S4
ENSMUST00000010597	ENSMUSG00000010453	1	36335730	36369181	-1	0	0	0	50	0	0	496	190	695	58	732		A2RSY1
ENSMUST00000010673	ENSMUSG00000010529	12	111484611	111485823	-1	3	3	4	205	9	3	1	4	0	0	0	A6H634	
ENSMUST00000010682	ENSMUSG00000010538	3	88282757	88296999	-1	2	0	5	0	0	3	1	0	4	0	0		Q9DA44
ENSMUST00000010698	ENSMUSG00000010554	11	74770830	74828525	1	0	2	0	0	0	0	5	41	17	16	33	Q5SW15	
ENSMUST00000010736	ENSMUSG00000010592	17	50279394	50293599	-1	2	4	2	87	6	2	0	0	0	0	0		Q64368
ENSMUST00000010745	ENSMUSG00000010601	15	77388221	77399110	-1	0	0	0	0	0	0	0	2	1	0	2	B2RT54	
ENSMUST00000010753	ENSMUSG00000010609	1	180227004	180263438	-1	3	0	0	1	0	0	0	0	0	0	0	Q3U4P5	
ENSMUST00000010795	ENSMUSG00000010651	9	119148023	119157093	-1	2	14	23	115	16	4	120	153	70	14	39	Q3UKM0	Q8VCH0
ENSMUST00000010804	ENSMUSG00000010660	9	119071527	119093496	-1	16	17	33	69	34	9	4	6	0	0	4		Q8R3B1
ENSMUST00000010807	ENSMUSG00000010663	19	10182888	10196870	1	24	16	30	182	27	15	76	143	105	26	140		Q920L1
ENSMUST00000010899	ENSMUSG00000010755	7	143557230	143600090	-1	6	13	20	28	14	0	8	25	20	0	16		Q9ER72
ENSMUST00000010904	ENSMUSG00000010760	7	143501545	143502541	-1	3	3	5	118	9	4	0	0	0	1	1		O08969
ENSMUST00000010940	ENSMUSG00000010796	6	18050964	18109061	-1	2	3	4	0	2	0	0	0	0	0	0		Q8VD46
ENSMUST00000010941	ENSMUSG00000010797	6	17988940	18030585	-1	9	0	13	129	18	7	0	0	0	0	0		P21552
ENSMUST00000010969	ENSMUSG00000010825	5	143357338	143392152	1	3	0	14	9	0	0	0	0	0	0	0		Q0QWG9
ENSMUST00000010974	ENSMUSG00000010830	15	79516408	79527739	1	14	1	17	75	23	7	0	4	1	13	28		Q8R1L4
ENSMUST00000010985	ENSMUSG00000010841	11	101984279	101992264	1	2	0	0	0	3	0	0	0	0	0	0		Q9DAN9
ENSMUST00000011029	ENSMUSG00000027679	3	34056020	34081321	-1	1	4	5	5	6	4	5	27	12	8	4	G3X8S1	
ENSMUST00000011055	ENSMUSG00000010911	2	103073675	103092644	1	0	0	0	70	9	0	51	210	57	121	43		Q9WVQ5
ENSMUST00000011058	ENSMUSG00000010914	2	103021075	103073513	-1	6	4	10	18	4	9	89	221	101	97	69		Q8BKZ9
ENSMUST00000011152	ENSMUSG00000011008	3	146149833	146195513	1	8	10	9	88	4	6	10	0	0	19	26		Q8K595
ENSMUST00000011178	ENSMUSG00000011034	5	33104219	33162870	1	25	13	42	123	30	11	1	1	0	0	0	Q9QXI6	
ENSMUST00000011262	ENSMUSG00000011118	9	37659902	37669222	-1	14	8	8	12	10	8	0	0	0	0	0	Q6IMP0	Q8CEG0
ENSMUST00000011285	ENSMUSG00000042826	11	69796068	69801857	-1	21	22	16	0	25	28	0	8	2	0	3	Q6NXW2	
ENSMUST00000011298	ENSMUSG00000011154	7	83774101	83794880	-1	6	4	4	3	4	0	0	0	0	0	0		Q6P8Y0
ENSMUST00000011302	ENSMUSG00000011158	12	112959862	113000621	-1	25	10	39	40	30	14	310	906	527	62	593	G3X8S2	
ENSMUST00000011315	ENSMUSG00000011171	12	116077726	116146261	1	39	21	195	68	46	18	3	5	2	0	0	Q546Q8	P41588
ENSMUST00000011391	ENSMUSG00000047257	9	110834588	110841313	1	14	0	25	0	0	0	0	0	0	0	0		Q8K4I7
ENSMUST00000011398	ENSMUSG00000011254	11	45946843	45955494	-1	12	13	28	25	24	7	24	65	35	128	38		Q9CY52
ENSMUST00000011400	ENSMUSG00000011256	11	46055992	46147343	1	106	68	317	172	102	66	5166	13048	8522	687	9645	Q3UHT3	O35674
ENSMUST00000011407	ENSMUSG00000011263	7	19489056	19496760	1	6	7	15	0	17	0	1	1	0	0	0	E9Q180	
ENSMUST00000011445	ENSMUSG00000031495	8	3871827	3878555	-1	6	4	3	2	5	3	0	0	0	7	4	Q3UW57	Q91ZW8
ENSMUST00000011450	ENSMUSG00000011306	8	70042813	70071953	1	25	15	31	44	29	14	581	966	577	118	526		Q8CH02
ENSMUST00000011492	ENSMUSG00000027710	3	36065979	36092853	1	1820	1671	3419	1504	2280	1165	113	388	193	114	241		Q8JZN5
ENSMUST00000011493	ENSMUSG00000011349	7	24870057	24877651	1	8	6	30	59	18	5	0	0	0	0	0		Q8CGW9
ENSMUST00000011526	ENSMUSG00000011382	7	45472956	45488805	-1	184	160	687	194	146	86	29	73	43	18	42		Q9DBB8
ENSMUST00000011607	ENSMUSG00000011463	3	20248264	20275733	-1	38	34	207	21	34	20	0	0	1	0	0	B2RS76	
ENSMUST00000011623	ENSMUSG00000002668	17	57066056	57078510	-1	21	17	77	31	27	21	1758	4468	2114	192	3053		Q8CFK6
ENSMUST00000011733	ENSMUSG00000011589	17	55986511	55996881	1	13	5	33	64	22	11	0	0	0	0	0		Q7TPM6
ENSMUST00000011776	ENSMUSG00000011632	7	24541658	24546118	-1	2	1	7	5	3	2	0	0	2	0	0	B2RSX2	Q9CQD7
ENSMUST00000011877	ENSMUSG00000020315	11	30099395	30268175	-1	0	0	0	0	15	0	1147	1390	2285	250	2139		Q62261
ENSMUST00000011895	ENSMUSG00000011751	7	27356383	27447686	-1	37	6	0	555	37	6	0	0	1	0	0	E9PX29	
ENSMUST00000011896	ENSMUSG00000011752	19	41911871	41918664	1	30	36	64	198	49	27	6613	12677	5257	753	2792	Q3U7Z6	Q9DBJ1
ENSMUST00000011934	ENSMUSG00000051747	2	76703980	76982547	-1	106	317	387	111	84	0	3	5	0	1	12		A2ASS6
ENSMUST00000011981	ENSMUSG00000011837	8	4253102	4256219	1	21	14	18	48	25	9	176	244	128	21	84		Q91XA5
ENSMUST00000012028	ENSMUSG00000011884	5	114669398	114690984	-1	13	11	21	16	25	20	1784	3345	1705	165	997		Q9JL62
ENSMUST00000012104	ENSMUSG00000011960	15	98538689	98570923	-1	0	0	0	0	6	0	0	0	74	5	93		Q9QWV9
ENSMUST00000012152	ENSMUSG00000003166	16	17839482	17894145	-1	0	0	0	32	0	0	409	325	555	0	376	Q6P5A9	
ENSMUST00000012161	ENSMUSG00000012017	16	17797282	17808287	1	27	11	34	662	36	17	0	1	0	12	31	Q58A84	P59222
ENSMUST00000012186	ENSMUSG00000012042	3	138164078	138193825	-1	11	5	72	12	11	5	0	0	0	0	0	E9Q3L6	
ENSMUST00000012259	ENSMUSG00000012114	16	17651221	17722930	-1	9	7	0	0	28	17	737	507	804	108	661	G3X8S4	
ENSMUST00000012262	ENSMUSG00000012117	4	133969028	134000918	-1	0	0	0	0	0	0	153	330	1	0	177		Q99KU1
ENSMUST00000012279	ENSMUSG00000022738	16	17913107	17915059	-1	8	5	8	173	12	8	0	0	0	0	0	A2RTU1	
ENSMUST00000012281	ENSMUSG00000032179	9	75775364	75900310	1	77	46	344	162	69	35	4	10	1	0	11		P49003
ENSMUST00000012314	ENSMUSG00000021510	13	67617001	67637791	-1	10	12	17	10	9	6	131	467	172	89	105	Q4QQP3	
ENSMUST00000012331	ENSMUSG00000012187	1	78510991	78538173	1	0	1	0	0	1	4	0	0	0	9	0		Q91ZV4
ENSMUST00000012348	ENSMUSG00000040562	3	107981702	107986453	-1	9	8	32	15	17	6	0	0	0	97	20		P15626
ENSMUST00000012355	ENSMUSG00000012211	12	113074502	113088917	1	9	7	23	40	17	5	0	0	0	0	0		Q9D9U4
ENSMUST00000012426	ENSMUSG00000012282	18	34542313	34548273	1	13	8	24	32	16	12	0	0	0	0	0		Q64527
ENSMUST00000012440	ENSMUSG00000012296	17	46257851	46283026	-1	10	6	62	42	19	0	45	78	54	7	76		Q9DCD5
ENSMUST00000012540	ENSMUSG00000012396	6	122707489	122714633	1	20	20	0	20	30	7	0	0	0	0	0	A2RS90	Q80Z64
ENSMUST00000012566	ENSMUSG00000012422	13	90089123	90143907	1	3	5	3	6	2	0	164	498	109	195	49		Q9CR64
ENSMUST00000012580	ENSMUSG00000027615	3	19995945	20035315	-1	68	74	68	64	88	43	0	153	234	106	108		Q91VB4
ENSMUST00000012587	ENSMUSG00000012443	19	37376403	37421859	1	28	31	52	86	31	13	152	291	332	104	87		Q6P9P6
ENSMUST00000012612	ENSMUSG00000041164	11	6389074	6406158	1	0	0	0	0	0	0	0	32	38	0	64		Q8CIE2
ENSMUST00000012627	ENSMUSG00000012483	6	8255936	8259173	-1	0	0	0	38	2	0	63	148	41	141	17		Q9CQ71
ENSMUST00000012664	ENSMUSG00000012520	5	67094399	67099301	-1	13	12	11	80	31	11	0	0	0	0	0		O35690
ENSMUST00000012679	ENSMUSG00000012535	6	29540827	29609887	-1	0	16	30	108	15	5	429	686	982	295	561		Q6P2B1
ENSMUST00000012725	ENSMUSG00000030446	13	67813740	67827002	1	0	0	0	0	0	0	2	1	0	2	2	F6UQD0	
ENSMUST00000012734	ENSMUSG00000029131	5	29735688	29818134	1	3	3	11	11	2	5	4	9	15	26	22	G3X8S5	
ENSMUST00000012759						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000012796	ENSMUSG00000012640	7	43296197	43313294	-1	4	6	0	6	1	1	7	35	15	10	12	Q9D082	
ENSMUST00000012798	ENSMUSG00000039013	7	43351341	43359531	1	0	0	2	0	16	0	160	1038	258	39	214		Q920G3
ENSMUST00000012847	ENSMUSG00000031494	8	3743395	3748984	-1	10	5	13	12	12	1	1	9	0	17	22		Q91ZX1
ENSMUST00000012849	ENSMUSG00000012705	8	3655770	3660110	1	27	32	46	32	38	15	36	108	36	105	45	Q5BMX4	Q99P87

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000012873	ENSMUSG00000058093	13	67589443	67609707	-1	8	6	1	6	7	7	109	481	126	142	73	Q80VN4	
ENSMUST00000012921	ENSMUSG00000012777	7	44252148	44257378	-1	4	0	0	0	6	0	0	0	0	0	0	F6WRF1	
ENSMUST00000013130	ENSMUSG00000020954	12	51608541	51691914	-1	9	0	16	0	0	0	91	301	124	65	148		Q9ERG2
ENSMUST00000013220	ENSMUSG00000013076	9	14541966	14615483	-1	109	86	518	0	106	68	2	9	4	18	152		Q9D4H4
ENSMUST00000013227	ENSMUSG00000013083	7	30699783	30700380	1	3	3	1	1	5	8	3	10	3	16	4	Q9D807	
ENSMUST00000013235	ENSMUSG00000013091	7	4782937	4784341	1	4	5	15	7	5	7	0	0	0	0	0		Q9D2E9
ENSMUST00000013262	ENSMUSG00000020472	11	59485520	59526751	-1	0	0	27	180	0	9	41	41	53	6	124		Q5SXI5
ENSMUST00000013294	ENSMUSG00000013150	8	105713854	105758664	-1	159	128	387	259	159	85	45	88	49	12	56		Q9CYH5
ENSMUST00000013299	ENSMUSG00000013155	8	105703655	105707933	-1	10	8	28	138	22	4	44	89	42	8	29		Q7TSV9
ENSMUST00000013302	ENSMUSG00000013158	8	105708291	105710244	1	5	6	12	14	13	10	0	0	0	0	0		Q9D4A5
ENSMUST00000013304	ENSMUSG00000013160	8	105524465	105566047	-1	12	4	13	62	21	10	4073	7206	3094	604	2099		P51863
ENSMUST00000013338	ENSMUSG00000064145	9	108602942	108649386	-1	0	4	0	0	0	0	461	1837	702	147	705	Q3TK92	Q9Z1K6
ENSMUST00000013455	ENSMUSG00000053054	3	138313286	138331134	1	15	11	53	13	8	16	0	0	0	1	0	E9Q4Y1	
ENSMUST00000013458	ENSMUSG00000037797	3	138415466	138430892	1	6	2	8	8	4	1	0	0	0	0	0		Q9QYY9
ENSMUST00000013497	ENSMUSG00000013353	7	43492044	43505940	-1	74	46	117	384	72	51	6	31	19	2	62	A2RSL7	
ENSMUST00000013559	ENSMUSG00000013415	11	95957163	96005940	-1	57	38	113	282	71	43	0	0	0	2	0		O88477
ENSMUST00000013615	ENSMUSG00000039860	5	135806890	135874772	1	0	0	0	237	0	5	0	0	0	0	0	H7BWX3	
ENSMUST00000013633	ENSMUSG00000008090	5	108692382	108706924	1	21	14	32	183	47	21	0	0	0	5	19		Q91V87
ENSMUST00000013667	ENSMUSG00000013523	2	170346991	170427845	-1	12	0	33	0	5	0	0	0	0	0	0		Q80YN3
ENSMUST00000013693	ENSMUSG00000029213	5	72156575	72168189	-1	56	50	85	45	44	25	337	1331	511	762	349	Q4QQP1	Q9CZG3
ENSMUST00000013706						0	4	0	8	6	0	0	4	6	1	0		
ENSMUST00000013737	ENSMUSG00000013593	1	171234853	171251388	-1	0	0	0	0	12	0	1077	1166	902	274	754		Q91WD5
ENSMUST00000013755	ENSMUSG00000013611	15	36504062	36555573	-1	8	8	0	30	5	14	0	0	0	0	0		Q6P8Y7
ENSMUST00000013759	ENSMUSG00000008200	2	90745370	90781021	1	14	13	33	70	39	13	268	1903	716	146	878		
ENSMUST00000013766	ENSMUSG00000013622	5	31048312	31054623	1	0	0	4	21	3	0	248	590	261	852	170	A8C1S6	Q6PGD0
ENSMUST00000013771	ENSMUSG00000062077	5	31116712	31137630	1	0	9	32	52	23	14	0	0	0	0	0		Q9ERP3
ENSMUST00000013773	ENSMUSG00000013629	5	31054780	31078479	1	22	23	70	212	58	31	166	171	147	15	333		B2RQC6
ENSMUST00000013787	ENSMUSG00000013643	11	58379043	58390728	1	11	5	3	11	4	0	0	0	0	3	0		Q9D7S0
ENSMUST00000013797	ENSMUSG00000013653	11	58421111	58426024	1	7	6	17	7	5	2	0	0	0	0	0	Q5NC41	
ENSMUST00000013807	ENSMUSG00000013663	19	32757497	32826160	1	35	38	127	120	39	32	4007	13623	5963	519	2884		O08586
ENSMUST00000013842	ENSMUSG00000013698	1	172196728	172206804	-1	1	9	21	0	16	8	184	315	116	142	211		Q62048
ENSMUST00000013845	ENSMUSG00000013701	14	32180162	32201898	-1	0	6	0	84	0	0	167	531	330	584	230	Q9CXU4	
ENSMUST00000013851	ENSMUSG00000013707	3	95139521	95142360	-1	18	5	50	33	14	9	3283	4930	2363	3011	1597		Q9D8Y7
ENSMUST00000013882	ENSMUSG00000005362	6	106780201	106800077	-1	3	2	1	0	0	0	25	146	82	188	58		Q8C7D2
ENSMUST00000013886	ENSMUSG00000019254	7	4481520	4501680	-1	0	0	0	12	0	0	0	303	173	38	17		Q3UMT1
ENSMUST00000013910	ENSMUSG00000013766	17	35076902	35078804	1	11	1	24	8	10	5	0	0	0	0	0	Q9D7E5	
ENSMUST00000013931	ENSMUSG00000013787	17	34898469	34914052	1	0	0	0	0	17	0	111	131	221	0	324		Q9Z148
ENSMUST00000013949	ENSMUSG00000032000	9	7848699	7873186	-1	7	0	5	32	9	0	1663	5129	2874	2037	2482	A2CGA5	
ENSMUST00000013966	ENSMUSG00000013822	9	22112989	22117148	-1	6	0	11	18	2	4	362	577	238	406	169	Q545S6	P60003
ENSMUST00000013970	ENSMUSG00000025417	10	127197067	127211622	-1	23	29	66	73	39	17	1120	1960	1225	191	965		Q91XU3
ENSMUST00000013995	ENSMUSG00000028125	3	122044443	122180123	1	19	24	13	44	35	13	0	0	0	2	0		O35600
ENSMUST00000014022	ENSMUSG00000013878	8	26119368	26143871	1	14	16	13	50	25	7	70	410	130	72	146		Q8CBG9
ENSMUST00000014058	ENSMUSG00000030693	7	43781035	43785410	1	18	11	19	40	17	4	0	0	0	0	0	Q99M20	
ENSMUST00000014063	ENSMUSG00000044430	7	43768897	43773585	1	2	5	18	7	12	2	0	0	0	0	0	B2RVZ0	
ENSMUST00000014065	ENSMUSG00000013921	7	30291672	30308367	1	24	16	161	110	38	8	0	1	1	1	5		B9EHT4
ENSMUST00000014072	ENSMUSG00000013928	7	30280094	30290237	1	0	6	0	0	12	5	0	0	0	1	0	E9Q695	
ENSMUST00000014080	ENSMUSG00000013936	5	122100951	122113472	1	0	0	0	0	0	0	0	0	0	5	0		P51667
ENSMUST00000014089	ENSMUSG00000029510	5	138273655	138280005	-1	0	0	0	0	0	0	0	0	0	1	0	F8WHY9	
ENSMUST00000014118	ENSMUSG00000013974	8	3665762	3668905	1	10	8	50	37	15	16	7546	31217	8066	23315	5630		Q9D8U6
ENSMUST00000014174	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	7	8	0	0	0	0	3	5	41		Q02650
ENSMUST00000014218	ENSMUSG00000014074	16	32277459	32301434	1	84	80	139	24	79	53	77	304	157	51	131		Q80XJ2
ENSMUST00000014220	ENSMUSG00000014075	16	32419702	32429099	1	2	0	9	13	5	1	196	923	214	995	198		Q9CQ66
ENSMUST00000014221	ENSMUSG00000014077	2	119547697	119587027	1	18	23	40	138	9	12	5815	14601	7328	937	4005		P61022
ENSMUST00000014248	ENSMUSG00000014104	6	41852989	41864413	1	1	0	1	0	4	2	0	0	0	0	0	Q99N75	
ENSMUST00000014263	ENSMUSG00000054545	1	88134809	88218997	1	2	0	19	0	4	0	0	0	0	98	0		Q64435
ENSMUST00000014290	ENSMUSG00000026786	2	22774094	22875653	1	9	5	21	52	6	0	3246	8331	3480	253	2327	B1AYC9	Q8R5A3
ENSMUST00000014321	ENSMUSG00000014177	11	62879455	62916780	1	5	2	15	17	1	1	49	227	94	164	62		Q9D8T4
ENSMUST00000014339	ENSMUSG00000014195	11	100582818	100620168	-1	9	7	9	73	23	10	287	1539	671	1303	460		Q9QYI3
ENSMUST00000014370	ENSMUSG00000014226	1	160202367	160212875	-1	4	8	1	33	11	6	122	547	158	407	151		Q9CXW3
ENSMUST00000014389	ENSMUSG00000014245	11	62458460	62514417	1	39	32	100	105	48	25	31	114	83	21	80		Q5SX19
ENSMUST00000014421	ENSMUSG00000055204	5	90227166	90366577	-1	27	28	98	0	48	21	202	246	413	0	306		Q99NH0
ENSMUST00000014438	ENSMUSG00000014294	18	36742332	36744557	-1	3	4	6	27	5	1	533	879	400	2634	261		Q9CQ75
ENSMUST00000014445	ENSMUSG00000014301	16	4616464	4624988	-1	4	0	7	49	0	0	14	41	13	139	5		Q9CQV1
ENSMUST00000014447	ENSMUSG00000014303	16	4594713	4624924	1	0	8	0	78	7	14	0	0	0	0	29		Q8VDL9
ENSMUST00000014457	ENSMUSG00000014313	15	35925886	35938246	-1	0	2	10	15	5	3	929	1672	815	4351	391		Q9CPQ1
ENSMUST00000014473	ENSMUSG00000014329	10	70922832	71159700	-1	0	7	21	40	26	0	0	0	0	0	0	G3X8S6	
ENSMUST00000014476	ENSMUSG00000089727	6	130115226	130129898	-1	0	0	0	0	0	0	0	1	0	0	0		Q60682
ENSMUST00000014499	ENSMUSG00000014355	2	128610104	128687391	-1	23	26	36	56	32	12	340	778	621	81	395		P53995
ENSMUST00000014505	ENSMUSG00000014361	2	128698956	128802894	1	27	19	66	78	41	16	25	11	19	14	118		Q60805
ENSMUST00000014545	ENSMUSG00000030851	7	46861203	46878142	1	11	7	19	4	6	4	5	51	9	13	2	Q548Z6	P00342
ENSMUST00000014546	ENSMUSG00000014402	7	46888949	46919969	-1	7	4	9	44	7	2	273	1039	415	346	249	Q3UCW0	Q61187
ENSMUST00000014562	ENSMUSG00000014418	7	46760466	46796064	-1	2	4	6	82	0	0	5	68	78	0	100		P59438
ENSMUST00000014578	ENSMUSG00000059481	17	12378609	12419384	1	15	11	32	18	26	15	0	0	0	55	0		P20918
ENSMUST00000014597	ENSMUSG00000014453	14	63372837	63417187	-1	26	22	55	30	32	9	40	14	23	16	135		P16277
ENSMUST00000014614	ENSMUSG00000014470	8	122466147	122476064	-1	6	1	12	27	10	6	1400	1497	1012	187	566	A2RS02	Q3U9F6
ENSMUST00000014640	ENSMUSG00000014496	14	31700015	31830415	-1	23	21	39	32	17	18	341	1188	748	213	465		Q505D1
ENSMUST00000014642	ENSMUSG00000014498	10	128377115	128408704	1	47	29	107	95	62	23	975	639	1132	35	956		Q8BTI7
ENSMUST00000014647	ENSMUSG00000014503	18	34409423	34442789	1	6	0	7	0	0	9	18	27	8	2	8		Q9JLG4
ENSMUST00000014673	ENSMUSG00000014529	5	3651181	3680325	1	29	21	15	36	42	28	0	2	0	0	1	Q9D592	
ENSMUST00000014683	ENSMUSG00000030173	6	129898996	129917650	-1	2	1	1	6	1	0	1	8	2	0	0	Q548A2	Q60652
ENSMUST00000014684	ENSMUSG00000061613	17	31647082	31658754	-1	7	0	8	10	13	14	364	721	345	1142	278	Q14C24	Q9D883
ENSMUST00000014686	ENSMUSG00000014542	6	83644542	83656187	-1	10	12	46	20	18	7	0	1	0	3	1		
ENSMUST00000014687	ENSMUSG00000014543	6	129831154	129876672	-1	0	0	0	0	0	0	343	2405	342	2063	456	Q9JMA4	
ENSMUST00000014691	ENSMUSG00000014547	14	62837690	62956886	1	5	12	15	160	26	15	285	282	572	45	447		Q8BUB4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000014694	ENSMUSG00000014550	6	92186712	92214925	-1	39	35	76	140	44	17	394	1206	750	83	400		Q80Y56
ENSMUST00000014695						2	4	0	5	4	0	11	36	10	47	21		
ENSMUST00000014698	ENSMUSG00000014554	6	83480217	83506969	-1	0	0	3	0	0	0	79	238	82	75	123		Q9QX60
ENSMUST00000014743	ENSMUSG00000014599	3	107741048	107760469	-1	13	5	73	203	46	20	3263	2841	3040	161	2019		P07141
ENSMUST00000014747	ENSMUSG00000014603	3	107595031	107605776	1	15	13	10	171	22	10	0	0	0	0	0	Q3UQX2	O70137
ENSMUST00000014750	ENSMUSG00000014606	11	70644196	70647479	-1	6	0	7	62	5	2	2131	3723	1473	490	1114	Q5SX53	Q9CR62
ENSMUST00000014753	ENSMUSG00000014609	11	70614883	70619216	-1	0	11	0	0	0	0	0	6	0	0	0	Q5SXG9	
ENSMUST00000014777	ENSMUSG00000052560	15	90487482	90679432	-1	13	0	14	198	6	11	18	17	64	48	29	Q9DB19	
ENSMUST00000014812	ENSMUSG00000014668	5	110135842	110171972	1	0	5	12	57	13	7	123	1107	579	1	350		Q810L3
ENSMUST00000014830	ENSMUSG00000014686	7	19852097	19861299	-1	12	8	20	65	11	3	16	47	45	1	56		E9QA28
ENSMUST00000014848	ENSMUSG00000014704	6	52162417	52164831	-1	13	8	14	51	13	13	0	0	0	2	5		P31245
ENSMUST00000014891	ENSMUSG00000014747	6	83762644	83768326	1	13	6	35	116	25	9	1	7	2	0	5		Q3V0J4
ENSMUST00000014892	ENSMUSG00000014748	6	83768885	83775813	-1	17	7	28	36	20	10	971	886	663	213	494		Q62302
ENSMUST00000014911	ENSMUSG00000014767	17	15499888	15528379	1	0	0	0	0	0	0	0	205	0	38	14	Q6RI65	P29037
ENSMUST00000014913	ENSMUSG00000014769	17	15475721	15498276	-1	4	7	14	46	9	4	1098	3025	1166	4349	829	Q6RI64	O09061
ENSMUST00000014917	ENSMUSG00000014773	17	15367354	15376872	-1	24	15	60	210	18	5	0	0	0	1	6		Q61483
ENSMUST00000014920	ENSMUSG00000014776	8	105276447	105281939	1	168	108	410	4186	246	120	5	29	18	5	19	Q53YU5	Q9D1X0
ENSMUST00000014922	ENSMUSG00000014778	8	105329163	105347953	-1	48	71	418	283	28	1	742	1176	803	39	826		Q6P9Q4
ENSMUST00000014927	ENSMUSG00000014782	8	105373274	105382862	1	0	0	0	0	22	2	0	0	0	0	4	F8VPS6	
ENSMUST00000014957	ENSMUSG00000014813	14	69029289	69041401	1	30	24	95	25	23	14	0	1	1	0	3	Q3UYZ1	O55183
ENSMUST00000014981	ENSMUSG00000014837	8	105280410	105289528	-1	38	51	82	154	89	63	5	22	8	4	5		Q810A5
ENSMUST00000014990	ENSMUSG00000014846	8	105467493	105471526	-1	7	1	12	33	9	7	280	157	82	163	162		Q9CRB6
ENSMUST00000014996	ENSMUSG00000014852	2	26973416	27009628	1	29	10	40	10	28	23	0	1	0	3	1	A2ALB3	
ENSMUST00000015000	ENSMUSG00000014856	8	105326354	105335219	1	0	0	0	4	0	5	173	286	97	344	73		Q9CR96
ENSMUST00000015003	ENSMUSG00000014859	8	105297663	105305369	1	13	10	37	58	15	9	717	936	653	88	550		Q8R0K9
ENSMUST00000015011	ENSMUSG00000014867	2	26920040	26933928	-1	13	7	48	83	20	12	3923	5467	3616	487	2124	Q545Q2	Q64310
ENSMUST00000015017	ENSMUSG00000014873	2	26916367	26920183	1	0	1	2	0	0	0	19	49	16	135	17	Q4VAF7	P09926
ENSMUST00000015049	ENSMUSG00000014905	12	44205897	44210068	-1	8	5	1	63	8	3	230	869	243	73	142		Q9QYI6
ENSMUST00000015100	ENSMUSG00000014956	5	32458843	32517433	1	39	43	73	91	56	33	1835	1796	390	290	460		P62141
ENSMUST00000015107	ENSMUSG00000020694	11	105178807	105283959	1	0	0	0	0	0	0	22	137	163	125	185		O55047
ENSMUST00000015124	ENSMUSG00000014980	1	152370735	152386688	-1	0	3	0	0	9	4	6	28	9	12	9	G3X8S8	
ENSMUST00000015137	ENSMUSG00000029674	5	134656039	134688598	-1	0	8	0	129	0	0	52	13	61	0	31		P53668
ENSMUST00000015138	ENSMUSG00000029675	5	134702593	134747323	-1	21	22	129	130	47	21	0	0	0	3	13		P54320
ENSMUST00000015146	ENSMUSG00000015002	15	65787034	65873816	1	18	8	23	15	19	13	286	749	527	149	383		Q8BG67
ENSMUST00000015157	ENSMUSG00000015013	8	122611626	122615588	1	5	4	16	14	5	1	335	992	191	868	172		Q9JME7
ENSMUST00000015160	ENSMUSG00000015016	8	122775505	122817880	1	25	13	47	42	36	18	34	29	25	8	38		Q3URE1
ENSMUST00000015171	ENSMUSG00000015027	8	122578238	122611487	-1	27	7	47	81	21	11	1273	1475	958	124	599		Q571E4
ENSMUST00000015197	ENSMUSG00000015053	6	88193891	88207032	1	0	0	28	212	36	0	30	59	23	0	89	Q3U320	O09100
ENSMUST00000015227	ENSMUSG00000015083	2	25498651	25501719	-1	2	0	11	11	4	1	9	13	11	7	11	Q9DAC2	
ENSMUST00000015234	ENSMUSG00000015090	2	25466709	25470046	-1	4	3	0	7	0	0	0	0	0	0	0		O09114
ENSMUST00000015236	ENSMUSG00000015092	2	25557847	25562082	1	0	0	0	64	0	0	815	1231	727	632	590		Q9JMG1
ENSMUST00000015239	ENSMUSG00000015095	2	25500750	25505471	1	25	15	94	60	38	17	414	509	305	52	282		Q9QXW2
ENSMUST00000015256	ENSMUSG00000015112	6	6041218	6217173	-1	18	19	11	0	0	0	24	77	47	18	34		Q9QXX4
ENSMUST00000015267	ENSMUSG00000024171	17	25308646	25311876	1	9	7	27	6	15	4	0	5	0	0	1		
ENSMUST00000015271	ENSMUSG00000015127	17	25188397	25234443	1	7	5	0	0	0	0	51	192	20	18	28		Q5FWH2
ENSMUST00000015277	ENSMUSG00000015133	7	66226912	66388350	-1	39	43	86	100	91	34	156	200	237	19	400		Q3UHC2
ENSMUST00000015278	ENSMUSG00000015134	7	66390892	66427517	-1	17	7	16	85	19	12	0	0	0	1	2	Q3UIA4	Q9JHW9
ENSMUST00000015333	ENSMUSG00000015189	6	4600839	4643355	1	9	8	23	73	14	2	265	937	431	161	220		Q7TN73
ENSMUST00000015346	ENSMUSG00000015202	10	7119063	7212237	-1	18	14	42	342	25	19	11	34	23	0	29		Q8BMA3
ENSMUST00000015358	ENSMUSG00000015214	X	71364760	71419196	1	3	4	0	0	0	4	184	286	280	116	190		Q9Z2C4
ENSMUST00000015361	ENSMUSG00000015217	X	71555918	71560676	1	2	3	529	0	30	37	0	29	0	0	4	Q544R9	O54879
ENSMUST00000015368	ENSMUSG00000066097	4	96294508	96348662	-1	7	6	7	5	7	3	0	0	0	0	0	Q3UNV2	
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ENSMUST00000015391	ENSMUSG00000015247	4	53011880	53022060	1	0	0	8	31	0	2	578	1200	537	711	380		Q9CQE1
ENSMUST00000015394	ENSMUSG00000050578	9	7272514	7283333	1	7	8	11	3	9	2	0	2	1	8	3	Q3U9V5	P33435
ENSMUST00000015427	ENSMUSG00000031399	X	74384719	74393272	-1	0	0	0	0	0	0	0	194	0	0	0		Q9D8T0
ENSMUST00000015433	ENSMUSG00000015289	X	74351276	74353618	-1	0	0	0	1	0	0	55	133	59	277	50		Q9CR70
ENSMUST00000015434	ENSMUSG00000015290	X	74365718	74373218	-1	0	0	1	0	0	0	33	16	2	42	28	F8WHM4	
ENSMUST00000015435	ENSMUSG00000015291	X	74304998	74311862	1	37	0	62	55	0	14	857	2552	555	205	599		P50396
ENSMUST00000015449	ENSMUSG00000015305	10	8722219	8886070	-1	45	47	84	218	59	27	2	2	4	15	77	F8VQK5	
ENSMUST00000015456	ENSMUSG00000015312	10	80930091	80932204	1	3	7	15	120	9	3	466	1218	414	166	364		P22339
ENSMUST00000015460	ENSMUSG00000015316	1	171767127	171801184	1	11	12	39	10	19	2	5	19	12	117	46	Q544K1	Q9QUM4
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ENSMUST00000015481	ENSMUSG00000015337	2	30171493	30174069	1	4	5	5	128	6	7	9	20	4	6	16	Q3UN47	O08600
ENSMUST00000015484	ENSMUSG00000015340	X	9435252	9487771	-1	24	17	163	62	29	15	8886	29823	18343	2900	8784	Q3U6G0	Q61093
ENSMUST00000015486	ENSMUSG00000015342	X	9272756	9313250	1	21	30	121	73	28	19	47	109	46	9	35	Q059K7	Q9QXY7
ENSMUST00000015498	ENSMUSG00000015354	9	95637601	95698096	1	35	15	33	89	34	11	0	1	0	12	27		Q8R4W6
ENSMUST00000015499	ENSMUSG00000015355	1	171682009	171705258	1	0	0	1	0	0	2	0	11	0	5	0	F8WHM0	
ENSMUST00000015501	ENSMUSG00000015357	9	65294260	65330658	1	0	0	0	44	0	4	138	359	189	113	155		Q9JHS4
ENSMUST00000015509	ENSMUSG00000015365	15	88982909	89055152	1	21	0	0	0	14	21	0	0	0	0	0	G3X8T0	
ENSMUST00000015511	ENSMUSG00000030123	6	115954811	115995005	-1	64	38	117	806	120	41	402	180	270	20	264		Q3UH93
ENSMUST00000015540	ENSMUSG00000015396	13	43785107	43803130	1	10	12	24	112	10	8	16	8	22	54	73		O88324
ENSMUST00000015545	ENSMUSG00000015401	X	164088830	164118860	1	2	1	0	0	0	0	0	0	0	0	0		Q9ESG4
ENSMUST00000015576	ENSMUSG00000022226	14	56042123	56044634	1	8	7	12	13	4	6	0	0	0	0	0	Q541U2	P15119
ENSMUST00000015578	ENSMUSG00000040284	14	56156582	56159579	-1	7	6	16	16	9	1	0	0	0	9	3	Q4KL28	P13366
ENSMUST00000015581	ENSMUSG00000015437	14	56258856	56262260	-1	9	10	11	10	18	9	11	55	11	65	52	Q3TZH4	P04187
ENSMUST00000015583	ENSMUSG00000040314	14	56099881	56102574	-1	11	5	18	13	13	4	833	767	493	1410	184	Q059V7	P28293
ENSMUST00000015585	ENSMUSG00000079186	14	56231401	56234656	-1	11	4	16	9	5	4	0	1	0	9	2	Q0VB76	P08882
ENSMUST00000015587	ENSMUSG00000015443	14	56165797	56174596	-1	6	9	8	13	8	3	0	0	0	0	0	Q920S1	
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ENSMUST00000015596	ENSMUSG00000015452	17	34597862	34600936	1	0	0	0	0	0	0	11	131	51	0	90	O35444	
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ENSMUST00000015611	ENSMUSG00000015467	17	34613349	34615971	-1	0	0	0	0	0	0	1	0	0	0	0	B9EJ41	Q6GUQ1
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000015620	ENSMUSG00000015476	17	34629533	34633126	1	13	10	28	215	24	13	0	4	0	0	5	A2CG20	O35449
ENSMUST00000015622	ENSMUSG00000015478	17	34601091	34603690	-1	4	0	15	36	6	3	515	878	424	203	354		O35445
ENSMUST00000015628	ENSMUSG00000015484	1	156075966	156205026	-1	26	16	70	93	35	11	1	0	0	0	1	A9ZNB6	Q8CAA5
ENSMUST00000015645	ENSMUSG00000015501	10	13966075	14151374	1	10	9	25	163	23	15	49	41	58	22	53		Q3UHF7
ENSMUST00000015663	ENSMUSG00000015519	10	28972288	28986303	-1	0	0	0	0	1	0	0	0	0	0	0		Q8C6C9
ENSMUST00000015664	ENSMUSG00000028111	3	95499256	95509362	1	6	14	28	9	16	7	3	76	15	72	36	Q545T0	P55097
ENSMUST00000015666	ENSMUSG00000015522	3	95434388	95497240	1	0	0	0	0	0	0	0	0	0	0	0	E9QLT6	
ENSMUST00000015667	ENSMUSG00000038642	3	95526786	95556403	1	4	4	7	0	3	4	107	398	184	1717	259	F6WR04	
ENSMUST00000015680	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	19	206	55	211	27		
ENSMUST00000015712	ENSMUSG00000015568	8	68880491	68907448	1	37	38	71	89	45	34	7	12	13	13	6		P11152
ENSMUST00000015719	ENSMUSG00000015575	17	26676396	26699644	1	2	0	1	75	7	1	4306	4836	1792	5426	1076		Q9CQD8
ENSMUST00000015723	ENSMUSG00000015579	17	26838664	26841565	-1	9	2	25	376	21	9	0	0	0	0	0	Q3UQU2	P42582
ENSMUST00000015725	ENSMUSG00000024191	17	26781079	26792565	1	0	0	4	0	0	0	9	71	51	0	62		Q6QD59
ENSMUST00000015749	ENSMUSG00000015605	17	46546839	46556162	-1	18	15	77	195	43	15	1210	1320	847	115	749		Q9JM73
ENSMUST00000015771	ENSMUSG00000015627	2	180325133	180334699	-1	47	44	103	397	59	32	0	3	5	3	10		P97489
ENSMUST00000015791	ENSMUSG00000015647	2	180176373	180225859	-1	112	69	203	412	181	82	100	39	77	38	887		Q61001
ENSMUST00000015796	ENSMUSG00000015652	5	5736317	5749326	-1	4	2	5	57	7	2	0	0	0	76	13		Q9CWR7
ENSMUST00000015797	ENSMUSG00000015653	5	5664829	5694578	-1	0	0	0	7	0	0	0	0	0	3	3	B2RX33	Q8BWB6
ENSMUST00000015800	ENSMUSG00000015656	9	40800984	40805200	1	0	0	0	79	0	0	0	0	0	0	0		P63017
ENSMUST00000015812	ENSMUSG00000015668	X	100622883	100626568	-1	5	0	15	26	5	1	27	66	32	169	29		Q9CZG9
ENSMUST00000015816	ENSMUSG00000015672	13	14610301	14613037	-1	3	1	4	7	6	4	105	455	168	591	98		Q9DCI9
ENSMUST00000015829	ENSMUSG00000030861	7	131410601	131446211	1	0	7	8	75	3	4	328	1179	579	647	422		Q9DBL1
ENSMUST00000015841	ENSMUSG00000015697	3	95323525	95357202	-1	0	13	0	156	22	7	0	211	142	0	58	D3YYC3	
ENSMUST00000015846	ENSMUSG00000015702	3	95296096	95307176	-1	0	0	19	15	11	0	34	100	74	18	56		Q9JHQ0
ENSMUST00000015855	ENSMUSG00000015711	3	95253674	95282076	-1	24	19	77	75	36	20	749	1370	673	120	492		Q8BIW1
ENSMUST00000015858	ENSMUSG00000015714	3	95314791	95323599	1	3	8	8	116	10	4	2530	7602	2919	589	2067		Q924Z4
ENSMUST00000015866	ENSMUSG00000015721	7	23385889	23441922	1	0	0	0	0	0	0	0	0	0	0	0		Q9R1M5
ENSMUST00000015877	ENSMUSG00000015733	6	17636234	17666972	1	2	1	18	17	5	2	1598	7158	1950	2540	1041	Q5DQJ3	P47754
ENSMUST00000015889	ENSMUSG00000015745	3	95988429	95996001	-1	8	8	0	18	10	8	17	75	32	25	26		Q9JIY0
ENSMUST00000015891	ENSMUSG00000015747	3	95999832	96058466	-1	18	15	47	37	23	16	47	201	77	103	59		P97390
ENSMUST00000015892	ENSMUSG00000015748	3	95830124	95855885	-1	10	11	14	50	11	3	11	65	13	16	93		Q922U1
ENSMUST00000015893	ENSMUSG00000015749	3	95929246	95947390	1	0	0	0	0	0	0	29	16	9	130	42		P97822
ENSMUST00000015894	ENSMUSG00000015750	3	95893969	95898288	1	13	5	24	80	27	11	2112	2770	1388	220	997	Q6GTF1	Q8BVF7
ENSMUST00000015901	ENSMUSG00000015757	10	7792891	7823135	1	11	12	30	10	14	7	223	1232	464	520	370		Q9CXG3
ENSMUST00000015903	ENSMUSG00000015759	14	46775582	46788411	-1	15	6	0	72	10	7	141	333	121	121	81		O35372
ENSMUST00000015920	ENSMUSG00000015776	2	26905262	26910677	-1	0	0	0	0	1	0	6	0	12	0	12		Q62276
ENSMUST00000015934	ENSMUSG00000015790	2	26913381	26916530	-1	5	3	11	60	7	0	39	37	109	36	63		P09925
ENSMUST00000015941	ENSMUSG00000042118	13	93655720	93674302	-1	329	361	286	305	311	149	16	93	42	38	21		Q91WS4
ENSMUST00000015948						0	6	4	0	2	0	180	353	128	261	79		
ENSMUST00000015950	ENSMUSG00000015806	5	45434021	45450236	-1	0	5	13	80	7	3	28	102	12	15	34		Q8BVI4
ENSMUST00000015981	ENSMUSG00000015837	11	50199366	50210827	-1	3	0	36	17	16	0	158	186	174	69	134		Q64337
ENSMUST00000015987	ENSMUSG00000015843	1	167598384	167639623	1	40	24	24	462	85	41	0	3	1	1	6		P28705
ENSMUST00000015994	ENSMUSG00000015850	3	95676201	95687917	-1	0	11	35	0	0	0	1035	496	857	62	489		Q80T21
ENSMUST00000015998	ENSMUSG00000015854	3	87357881	87371073	1	14	11	37	12	28	12	2	0	1	1026	716		Q9QWK4
ENSMUST00000016023	ENSMUSG00000015879	5	45529705	45639614	-1	34	19	60	105	34	13	1	4	2	0	1		Q0KK56
ENSMUST00000016026	ENSMUSG00000015882	5	45697181	45857615	-1	0	0	0	0	0	0	25	0	44	27	24		Q3U285
ENSMUST00000016031	ENSMUSG00000020017	10	93488768	93519304	1	3	0	10	0	0	0	102	39	96	69	212	F8WH73	
ENSMUST00000016033	ENSMUSG00000015889	10	93453396	93484896	1	4	2	22	128	11	6	1889	4983	2326	321	1334		P24527
ENSMUST00000016034	ENSMUSG00000015890	10	93523338	93540033	-1	11	5	15	51	10	9	3	3	1	2	1		Q9DBA8
ENSMUST00000016072	ENSMUSG00000027422	2	143947395	144011263	-1	11	29	53	36	53	22	889	2229	2327	294	2636	A2AVJ7	
ENSMUST00000016081	ENSMUSG00000015937	13	56073619	56136361	-1	0	0	0	102	1	0	1870	4978	2337	487	1464		Q9QZQ8
ENSMUST00000016086	ENSMUSG00000015942	5	134184019	134224355	1	9	9	26	15	18	7	228	556	432	32	308		Q99NI3
ENSMUST00000016087	ENSMUSG00000015943	3	96196588	96219709	-1	0	0	3	120	6	0	33	17	0	70	6		Q9D8S9
ENSMUST00000016088	ENSMUSG00000015944	5	134099711	134144343	1	85	85	387	319	106	62	96	116	97	26	181		Q8CAB8
ENSMUST00000016094	ENSMUSG00000015950	5	134220053	134229625	-1	0	0	0	0	0	0	77	911	841	132	138	F8WH69	
ENSMUST00000016105	ENSMUSG00000015961	1	177762962	177796511	-1	0	5	4	24	9	4	433	2189	659	538	341	B9EIE9	P46664
ENSMUST00000016106	ENSMUSG00000015962	1	177729814	177753324	1	3	5	2	2	2	1	0	0	1	0	0		Q9DAA7
ENSMUST00000016110	ENSMUSG00000015966	14	29996141	30008896	-1	2	0	1	35	4	0	0	0	0	0	3	Q543U7	Q9JIP3
ENSMUST00000016115	ENSMUSG00000015971	14	29978337	29993221	1	17	15	28	169	27	9	145	530	236	113	236		Q8R2S9
ENSMUST00000016124	ENSMUSG00000015980	7	139212988	139242979	1	6	8	23	66	9	0	33	96	54	56	59		Q80YS5
ENSMUST00000016125	ENSMUSG00000015981	7	139103638	139213307	-1	13	0	0	86	7	10	0	0	0	0	0		Q8QZV4
ENSMUST00000016138	ENSMUSG00000015994	8	25998729	26015601	-1	12	13	4	47	16	7	382	1455	621	353	395	Q541Z2	Q61239
ENSMUST00000016143	ENSMUSG00000029636	5	146384985	146473615	1	35	23	36	69	37	20	0	0	0	0	0		Q8VHI6
ENSMUST00000016144	ENSMUSG00000021759	13	112800894	112867881	1	6	3	15	5	7	5	0	6	0	9	16		Q61469
ENSMUST00000016168	ENSMUSG00000016024	2	158306493	158332852	1	20	19	143	34	45	32	2281	3337	2998	367	1558		Q61805
ENSMUST00000016172	ENSMUSG00000016028	15	85898758	86033777	-1	102	64	146	485	161	72	35	15	36	1	76		O35161
ENSMUST00000016231	ENSMUSG00000016087	9	32422204	32542861	-1	39	21	101	550	66	38	624	1431	938	455	604	Q544B3	P26323
ENSMUST00000016279	ENSMUSG00000041132	5	150571644	150597188	-1	6	8	10	107	13	5	443	2077	772	173	574		Q3V2Q8
ENSMUST00000016294	ENSMUSG00000016150	X	42527866	43429126	-1	0	3	24	0	7	0	0	1	0	0	0	A2ANM0	Q9WTS4
ENSMUST00000016309	ENSMUSG00000006301	1	74288247	74305622	-1	0	0	7	43	1	1	105	171	49	43	137	Q3U717	
ENSMUST00000016315	ENSMUSG00000026639	1	193207699	193343878	1	16	16	53	10	0	0	0	0	0	0	1		Q61087
ENSMUST00000016323	ENSMUSG00000016179	1	193346346	193370298	-1	12	15	27	22	24	10	0	0	0	0	0		Q91VB2
ENSMUST00000016338	ENSMUSG00000016194	1	193221634	193264075	-1	3	12	3	0	13	3	90	261	141	282	81	Q4JHD9	P50172
ENSMUST00000016344	ENSMUSG00000016200	1	192891233	193035775	-1	0	0	3	10	0	0	0	0	0	0	0	B7ZP31	
ENSMUST00000016383	ENSMUSG00000016239	X	36328353	36362341	1	5	1	5	4	0	5	24	25	35	8	4		Q9D4H7
ENSMUST00000016396	ENSMUSG00000016252	2	174461072	174464105	-1	0	0	0	10	0	3	967	2052	728	2449	445	Q545F5	P56382
ENSMUST00000016397	ENSMUSG00000016253	2	174415804	174427502	1	2	12	21	5	22	7	0	0	0	107	0	Q3TW27	
ENSMUST00000016399	ENSMUSG00000016255	2	174450695	174457882	1	9	7	12	10	18	3	15	11	39	25	104		A2AQ07
ENSMUST00000016400	ENSMUSG00000016256	2	174427493	174439039	-1	12	9	10	153	25	19	2130	3408	1465	911	1865	Q545I6	Q9WUU7
ENSMUST00000016401	ENSMUSG00000016257	2	174465067	174473081	-1	7	6	14	26	11	1	189	442	305	671	225		Q9CYY7
ENSMUST00000016406	ENSMUSG00000016262	1	192844488	192855756	-1	18	23	53	1	7	5	0	0	0	0	1		A7DTG3
ENSMUST00000016427	ENSMUSG00000016283	17	37480851	37483552	-1	48	27	45	263	44	16	0	29	0	4	4	Q6W9J6	
ENSMUST00000016452	ENSMUSG00000016308	X	36873900	36884222	1	3	0	1	92	5	2	352	1013	384	115	239	Q3UCS1	Q9Z255
ENSMUST00000016463	ENSMUSG00000016319	X	36795651	36798807	1	3	7	2	29	9	8	2295	5864	2416	4302	2117	Q545A2	P51881

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000016471	ENSMUSG00000016327	X	38316184	38336769	1	0	4	1	0	1	0	0	5	0	0	0		Q99ME6
ENSMUST00000016488	ENSMUSG00000016344	2	181187247	181188771	1	5	0	19	127	12	7	20	49	14	11	22		Q9CR37
ENSMUST00000016491	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZBV4	
ENSMUST00000016498	ENSMUSG00000027579	2	181205562	181213185	-1	19	15	37	38	34	11	0	3	0	1	4	Q0VBH4	
ENSMUST00000016511	ENSMUSG00000038751	2	181193721	181202789	-1	66	81	148	66	71	32	13	10	7	1	12	Q05AA8	Q64434
ENSMUST00000016530	ENSMUSG00000016386	2	106693269	106868356	1	0	2	3	0	0	0	0	0	0	0	0	B1APT2	Q9CZJ0
ENSMUST00000016553	ENSMUSG00000016409	X	37126795	37150746	1	33	31	306	189	38	17	102	376	187	35	129		Q9D0F4
ENSMUST00000016569	ENSMUSG00000034021	5	150673739	150810690	1	0	0	0	32	0	0	39	286	145	103	174		Q4VA53
ENSMUST00000016571	ENSMUSG00000016427	X	37187588	37191163	-1	29	28	28	77	24	14	370	1058	442	2246	301	Q545K0	O35683
ENSMUST00000016631	ENSMUSG00000016487	6	146888487	147032025	1	0	0	0	67	10	5	33	0	45	76	150		Q8C8U0
ENSMUST00000016638	ENSMUSG00000016494	1	194938819	194961279	1	0	0	9	52	8	5	101	164	62	42	40	Q543B6	Q64314
ENSMUST00000016639	ENSMUSG00000016495	19	29348599	29367390	-1	0	0	4	0	0	0	0	221	10	0	35		Q9D3P8
ENSMUST00000016640	ENSMUSG00000016496	19	29367455	29388095	1	106	60	280	262	85	45	50	380	77	68	406	Q3U472	Q9EP73
ENSMUST00000016654	ENSMUSG00000016510	5	146951573	146963800	-1	4	5	0	12	5	0	51	154	51	97	65	A4QMQ0	Q9CZD5
ENSMUST00000016664	ENSMUSG00000016520	5	147016655	147076586	-1	25	21	55	183	43	11	101	143	125	25	129		Q91XL2
ENSMUST00000016668	ENSMUSG00000016524	1	130932656	130940115	-1	0	0	0	3	5	0	0	0	0	0	0	Q14BK1	Q8CJ70
ENSMUST00000016670	ENSMUSG00000016526	1	131127455	131138340	-1	21	10	21	50	25	8	60	61	36	11	42		Q922Y0
ENSMUST00000016672	ENSMUSG00000016528	1	131053700	131097826	-1	18	13	60	129	23	9	6297	6887	4545	657	3009	Q3U2P8	P49138
ENSMUST00000016673	ENSMUSG00000016529	1	131019845	131024974	1	12	10	8	9	13	8	1	1	1	3	1		P18893
ENSMUST00000016678	ENSMUSG00000016534	X	38401357	38456454	-1	2	1	0	9	0	0	1227	4937	2577	5219	1508		P17047
ENSMUST00000016680	ENSMUSG00000031446	8	13105621	13147940	1	0	0	0	42	0	3	323	687	670	59	425		Q3TCH7
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ENSMUST00000016696	ENSMUSG00000016552	15	77940522	77956722	-1	0	3	11	79	24	19	22	29	32	0	0		Q3USW5
ENSMUST00000016698						14	13	21	70	31	8	0	0	2	0	0		
ENSMUST00000016703	ENSMUSG00000016559	11	116021912	116027962	-1	0	5	19	0	0	2	2723	8254	1656	1645	1428		P84244
ENSMUST00000016768	ENSMUSG00000016624	15	84785381	84856049	-1	7	0	41	110	13	5	4	6	0	0	9	F8WGM2	
ENSMUST00000016771	ENSMUSG00000022443	15	77760587	77842175	-1	50	43	113	137	95	55	33192	34073	59534	1974	36075		Q8VDD5
ENSMUST00000016781	ENSMUSG00000016637	15	78159465	78174108	-1	13	4	18	20	7	4	79	90	55	32	22		Q9D0P8
ENSMUST00000016897	ENSMUSG00000022442	15	83483772	83510893	-1	41	23	78	49	34	15	95	160	97	29	79		Q91V51
ENSMUST00000016901	ENSMUSG00000016757	15	83575119	83595157	-1	13	4	22	93	31	8	80	84	46	12	98		Q3UDE2
ENSMUST00000016902	ENSMUSG00000016758	15	83526862	83544635	1	5	5	14	51	7	7	1	2	1	3	1		O70337
ENSMUST00000016907	ENSMUSG00000016763	15	83602583	83725021	-1	3	8	18	33	12	0	0	0	0	0	0		Q6NZL8
ENSMUST00000016951	ENSMUSG00000051029	13	33084125	33094380	1	5	0	5	1	5	1	0	1	1	1	0		Q8VHP7
ENSMUST00000016977	ENSMUSG00000016833	5	100798627	100804471	1	0	0	0	33	2	2	233	744	204	608	57		Q8R2L5
ENSMUST00000017065	ENSMUSG00000016921	2	162931528	162937121	1	0	0	6	0	0	0	416	1602	727	176	664	A0A0A6YXX6	
ENSMUST00000017077						3	2	5	6	11	5	15	0	0	0	14		
ENSMUST00000017086	ENSMUSG00000016942	15	78439668	78468634	-1	34	15	76	104	42	21	0	0	0	10	0		Q9DBI0
ENSMUST00000017090	ENSMUSG00000016946	17	24047734	24073485	-1	14	17	12	85	18	11	199	449	215	67	191		
ENSMUST00000017126	ENSMUSG00000016982	13	21981194	21988734	1	28	14	68	34	25	9	2	1	10	0	1		Q5SW25
ENSMUST00000017142	ENSMUSG00000016998	2	164275952	164278459	-1	0	1	0	2	2	3	0	0	0	0	1		P18419
ENSMUST00000017144	ENSMUSG00000017000	2	164316751	164318453	1	2	4	1	3	4	3	0	0	0	0	0	Q9D268	
ENSMUST00000017147	ENSMUSG00000017003	2	164289268	164291500	1	14	12	53	0	7	0	0	0	0	0	0	F2Z472	
ENSMUST00000017148	ENSMUSG00000017004	2	164332740	164334396	1	8	2	5	9	7	2	0	0	0	0	0	Q545K7	P30933
ENSMUST00000017151	ENSMUSG00000017007	2	164403141	164415448	1	15	7	34	62	18	9	0	0	0	0	0	Q3V2I2	O08674
ENSMUST00000017153	ENSMUSG00000017009	2	164424247	164443887	-1	16	7	36	94	21	12	18	5	11	98	265	Q3U5S6	O35988
ENSMUST00000017184	ENSMUSG00000042842	13	32965209	32979067	1	4	0	10	0	0	0	0	0	0	48	17	F7B9A0	
ENSMUST00000017188	ENSMUSG00000060147	13	33917918	34002794	-1	0	1	0	0	5	1	0	0	16	0	0	F8WIV2	
ENSMUST00000017193	ENSMUSG00000017049	8	21969775	21974041	1	10	0	0	9	6	2	0	0	0	0	0		Q9D9B0
ENSMUST00000017208	ENSMUSG00000017064	13	28142484	28151611	1	1	3	0	2	2	5	0	0	0	0	0		Q9JII2
ENSMUST00000017255	ENSMUSG00000020913	11	99279959	99285262	-1	24	8	36	34	24	6	0	0	0	0	0		A1L317
ENSMUST00000017270	ENSMUSG00000053654	11	100262882	100269871	-1	10	2	19	11	9	0	0	0	0	0	0		Q6IFX2
ENSMUST00000017276	ENSMUSG00000017132	11	118132019	118248592	-1	0	0	0	0	20	0	126	344	264	2	384	Q8K3E8	Q9QX11
ENSMUST00000017288	ENSMUSG00000017144	2	51130438	51149111	-1	8	2	13	7	9	3	20	166	29	72	51		P61588
ENSMUST00000017290	ENSMUSG00000017146	11	101488764	101551955	-1	32	33	58	35	29	18	33	83	81	34	68		P48754
ENSMUST00000017309	ENSMUSG00000017165	11	100334407	100336996	1	4	4	9	5	4	2	0	0	0	0	0		P48757
ENSMUST00000017316	ENSMUSG00000019326	11	101330605	101341938	1	14	8	39	17	19	5	0	0	2	0	0	A2A4I8	
ENSMUST00000017332	ENSMUSG00000017188	11	101277968	101279114	-1	4	1	6	10	8	4	338	575	240	146	155		Q9D2R6
ENSMUST00000017339	ENSMUSG00000017195	11	98551097	98558665	1	0	0	0	0	0	0	0	0	0	0	0		Q6X786
ENSMUST00000017348	ENSMUSG00000017204	11	98664351	98677708	1	24	24	45	24	31	10	2	3	2	4	3		Q9EST1
ENSMUST00000017354	ENSMUSG00000017210	11	98704591	98729435	-1	0	2	0	0	0	0	373	391	286	46	257		Q99K74
ENSMUST00000017355	ENSMUSG00000017211	11	98646759	98657964	1	10	6	6	15	16	0	0	4	2	0	3		Q32M21
ENSMUST00000017365	ENSMUSG00000017221	11	98682554	98695979	1	0	0	9	101	6	3	783	1140	858	117	676		P14685
ENSMUST00000017384	ENSMUSG00000078676	11	98804905	98833814	1	0	0	0	97	0	0	18	159	106	18	35		Q8K3W3
ENSMUST00000017408	ENSMUSG00000017264	4	148558429	148582401	1	0	0	0	20	0	0	285	518	384	115	344		P56960
ENSMUST00000017430	ENSMUSG00000017286	11	76120987	76243725	-1	1	4	9	37	2	0	280	931	315	1232	307		Q9CPV4
ENSMUST00000017435	ENSMUSG00000017291	11	77529162	77607815	-1	7	28	54	0	0	16	735	1825	1228	180	1017	B2RX66	Q5F2E8
ENSMUST00000017443	ENSMUSG00000017299	2	164745983	164768607	1	9	3	15	14	12	5	437	877	423	129	290	Q3THA4	Q99LB0
ENSMUST00000017451	ENSMUSG00000017307	2	164792768	164804882	-1	0	0	0	8	0	2	0	0	0	0	0	Q8BZR4	
ENSMUST00000017453	ENSMUSG00000017309	11	102041509	102055620	1	53	43	96	1247	76	47	23	74	25	15	34		Q1ERP8
ENSMUST00000017454	ENSMUSG00000017310	2	164698501	164702453	1	6	3	8	2	4	4	0	0	0	0	0		Q9D263
ENSMUST00000017455	ENSMUSG00000017311	11	102106676	102107832	-1	2	6	1	2	0	0	0	0	0	0	0	Q3V334	Q9EPS2
ENSMUST00000017458	ENSMUSG00000017314	11	102057015	102088515	-1	33	31	32	54	34	13	0	0	0	0	0		Q9WV34
ENSMUST00000017460	ENSMUSG00000017316	11	102099930	102101319	-1	4	0	11	0	6	0	0	0	0	0	0	Q496X5	P10601
ENSMUST00000017488	ENSMUSG00000017344	11	78499091	78502324	1	7	0	8	12	9	8	0	0	0	53	0		P29788
ENSMUST00000017530	ENSMUSG00000017386	11	78158499	78165589	-1	1	0	0	0	0	7	76	33	24	12	68		Q61382
ENSMUST00000017534	ENSMUSG00000017390	11	78322968	78327781	1	11	15	64	17	19	7	20	25	38	4	23		P05063
ENSMUST00000017544	ENSMUSG00000017400	11	98036623	98053462	-1	27	17	53	184	27	16	25	7	4	1	40		Q8R1B0
ENSMUST00000017548	ENSMUSG00000017404	11	98026710	98030492	1	0	17	43	79	28	25	5240	7684	4324	26042	3362	Q5I0T8	P84099
ENSMUST00000017549	ENSMUSG00000017405	11	78166106	78176675	-1	0	4	0	0	0	4	26	52	28	0	18		Q91ZR4
ENSMUST00000017552	ENSMUSG00000020882	11	98001508	98023034	-1	14	7	58	129	24	12	6	3	2	0	0	A2A543	
ENSMUST00000017561	ENSMUSG00000017417	11	97923238	97986444	-1	22	13	37	45	28	22	17	31	6	4	23		Q91ZV7
ENSMUST00000017562	ENSMUSG00000017418	2	15049395	15082456	1	17	36	84	3	33	17	0	0	0	0	0	Q8BLF9	
ENSMUST00000017567	ENSMUSG00000017421	11	80383279	80405733	1	4	3	9	0	6	3	513	1596	737	1166	356		Q9JMD0
ENSMUST00000017572	ENSMUSG00000017428	11	80428615	80473248	1	13	8	17	33	20	5	298	879	350	62	241	Q5BKQ9	Q8BG32

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000017576	ENSMUSG00000025576	11	118489762	118911597	-1	15	5	67	34	32	13	0	0	0	0	0		Q8BIF2
ENSMUST00000017590	ENSMUSG00000017446	11	118428203	118449963	1	0	0	16	0	24	0	0	0	0	0	0		Q9QXP7
ENSMUST00000017597	ENSMUSG00000017453	11	77880615	77894096	-1	20	7	27	14	11	10	0	0	0	4	0	Q3UEJ8	Q9D826
ENSMUST00000017604	ENSMUSG00000006519	8	122424772	122432940	-1	5	15	46	111	17	8	12584	17001	8217	2264	4787	B3VQI8	Q61462
ENSMUST00000017610	ENSMUSG00000017466	11	118301069	118355740	-1	18	15	42	185	35	12	1545	3313	1801	405	1654	Q6PI17	
ENSMUST00000017620	ENSMUSG00000025575	11	118406289	118419086	-1	28	15	41	138	43	24	798	751	854	41	598		Q8VCF1
ENSMUST00000017622	ENSMUSG00000017478	8	122376609	122417360	1	0	0	0	32	0	0	152	187	271	21	80	G3X8T2	
ENSMUST00000017629	ENSMUSG00000017485	14	16365179	16430787	1	11	13	16	188	17	6	511	2122	1329	278	812		Q64511
ENSMUST00000017637	ENSMUSG00000017493	11	99041244	99054392	1	181	155	665	2965	252	127	198	584	169	489	1343		P47879
ENSMUST00000017692	ENSMUSG00000017548	11	79993106	80034123	1	0	0	0	0	19	0	421	442	248	0	153		Q80U70
ENSMUST00000017694	ENSMUSG00000017550	11	80089400	80135794	1	6	8	11	36	8	5	14	0	11	1	8		Q4QY64
ENSMUST00000017732	ENSMUSG00000017588	11	99345565	99351104	-1	15	11	16	62	23	4	0	0	0	0	0		Q9Z320
ENSMUST00000017741	ENSMUSG00000020912	11	99415666	99422259	-1	13	8	56	46	16	14	0	0	0	0	0	Z4YJD9	
ENSMUST00000017743	ENSMUSG00000035775	11	99428403	99438150	-1	17	11	19	16	18	9	0	0	1	0	0		Q9D312
ENSMUST00000017751	ENSMUSG00000017607	11	99065678	99089306	-1	142	126	589	166	130	90	7	59	15	76	516		Q8BZ33
ENSMUST00000017759	ENSMUSG00000017615	11	78522850	78536332	-1	39	20	15	44	30	13	86	536	136	69	148		O70479
ENSMUST00000017783	ENSMUSG00000017639	11	79591212	79698023	1	77	56	131	129	86	41	879	1676	1065	145	1203		Q8BQP8
ENSMUST00000017799	ENSMUSG00000017652	2	165055627	165072948	1	201	173	392	172	211	108	31	110	33	26	82		P27512
ENSMUST00000017808	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	278	793	141	51	162	Q5GMH2	Q8VCX2
ENSMUST00000017821	ENSMUSG00000017677	11	79239372	79254671	-1	11	3	17	21	2	3	550	3547	997	256	554	Q3TFQ2	O54927
ENSMUST00000017831	ENSMUSG00000017686	11	80209019	80267907	1	0	0	0	0	0	0	32	196	156	47	49		Q8BG51
ENSMUST00000017836	ENSMUSG00000017692	11	80300912	80355955	1	57	53	292	192	59	28	0	5	3	1	8		P58873
ENSMUST00000017839	ENSMUSG00000020707	11	80183851	80199757	1	14	8	49	113	39	16	98	285	136	54	103	B2RRA5	Q9CWS1
ENSMUST00000017841	ENSMUSG00000017697	2	163726584	163750239	-1	10	5	34	73	18	11	110	90	86	93	120	Q4FK28	P03958
ENSMUST00000017851	ENSMUSG00000017707	2	163623272	163645131	-1	10	8	37	54	21	15	8743	22476	12476	8126	8080		Q9QZI9
ENSMUST00000017859	ENSMUSG00000017715	11	117986292	118024011	1	0	0	0	1	0	2	1234	2632	1416	158	1372	F8WI04	
ENSMUST00000017864	ENSMUSG00000017720	2	164470301	164473724	-1	3	5	10	6	8	4	2	1	1	0	2	Q9D976	
ENSMUST00000017867	ENSMUSG00000017723	2	164562413	164568510	1	8	3	6	16	5	2	7	0	0	310	125	Q4FZJ6	Q9DAU7
ENSMUST00000017868	ENSMUSG00000017724	11	101769742	101785371	-1	0	0	0	0	0	0	0	0	0	14	28	A2A5C3	
ENSMUST00000017878	ENSMUSG00000017734	2	164486106	164493319	1	9	4	12	6	9	5	14	15	0	0	5	Q330P7	Q9CRD4
ENSMUST00000017881	ENSMUSG00000017737	2	164940780	164955850	1	22	17	59	120	52	29	55655	69048	54345	3135	36297		P41245
ENSMUST00000017891	ENSMUSG00000017747	11	100766032	100770957	-1	59	46	136	212	80	41	180	299	250	50	187		Q99J23
ENSMUST00000017900	ENSMUSG00000017756	13	73763697	73816743	1	41	22	125	130	62	24	206	412	403	37	398	B9EIV8	Q9WVL3
ENSMUST00000017904	ENSMUSG00000017760	2	164832873	164841032	1	0	0	0	60	49	0	0	0	0	0	0	G3X8T3	
ENSMUST00000017908	ENSMUSG00000017764	2	164822686	164826871	1	11	13	27	71	15	6	74	89	54	6	56		Q9CWV7
ENSMUST00000017911	ENSMUSG00000017767	2	164826389	164828537	-1	5	5	32	32	11	7	0	0	0	0	2		Q9DA57
ENSMUST00000017920	ENSMUSG00000017776	11	75679259	75706908	1	0	2	0	21	0	7	497	2433	939	349	656	Q5ND51	Q64010
ENSMUST00000017922						0	0	0	25	3	3	131	277	191	1088	99		
ENSMUST00000017945	ENSMUSG00000017801	11	101087277	101092207	1	5	0	0	0	0	0	161	273	70	0	132	A2BFB0	
ENSMUST00000017946	ENSMUSG00000017802	11	101096322	101119893	-1	16	0	32	16	1	0	2092	3887	1941	354	1599		Q9CQV4
ENSMUST00000017961	ENSMUSG00000017817	2	163336242	163397993	-1	0	21	80	220	55	18	5	0	0	0	0		Q9ET78
ENSMUST00000017974	ENSMUSG00000017830	11	100694884	100704271	-1	12	8	31	21	20	9	362	801	352	80	410		Q99J87
ENSMUST00000017975	ENSMUSG00000017831	17	53479234	53507671	1	8	6	16	156	5	10	524	1722	911	285	474		Q9CQD1
ENSMUST00000017976	ENSMUSG00000017832	11	100713850	100714575	1	0	5	0	0	0	0	0	8	0	1	0		Q9DAM3
ENSMUST00000017981	ENSMUSG00000017837	11	100619244	100627607	1	10	9	36	44	14	5	1475	1594	828	148	586		Q9CR56
ENSMUST00000018002	ENSMUSG00000017858	2	163017354	163046141	1	18	11	8	18	14	1	236	1051	460	180	305		Q62559
ENSMUST00000018005	ENSMUSG00000017861	2	163054687	163084688	1	40	12	93	106	58	28	107	125	96	6	88		P48972
ENSMUST00000018012	ENSMUSG00000017868	2	162987330	163014127	1	6	2	11	4	11	11	0	0	0	1	1		Q9QZS5
ENSMUST00000018050	ENSMUSG00000039671	2	165784152	165899016	-1	0	0	18	10	0	0	0	0	0	4	0	A2A483	
ENSMUST00000018061	ENSMUSG00000021342	13	27057570	27065204	1	1	1	4	0	2	1	0	0	0	0	0	Q9CPQ0	
ENSMUST00000018066	ENSMUSG00000017922	13	27196659	27203749	1	0	0	0	3	0	0	0	0	0	0	0	Q0VBM3	Q9QUN5
ENSMUST00000018087	ENSMUSG00000017943	2	163438476	163455324	1	20	0	21	11	14	0	0	0	0	0	0	Q3USC7	
ENSMUST00000018094	ENSMUSG00000017950	2	163506808	163572910	1	0	16	0	30	34	15	7	5	4	3	0		P49698
ENSMUST00000018113	ENSMUSG00000017969	2	167191805	167240604	-1	14	7	31	98	22	5	0	0	0	27	86		O35074
ENSMUST00000018122	ENSMUSG00000017978	6	23262773	23839421	-1	0	0	0	0	0	0	0	0	0	0	0	A4PI81	Q8BYR5
ENSMUST00000018143	ENSMUSG00000017999	2	167015193	167034947	1	17	4	35	90	15	9	136	287	219	66	217		Q921N6
ENSMUST00000018156	ENSMUSG00000018012	11	120721470	120723969	1	8	0	12	19	0	6	1	0	0	2	4	Q14A12	P60764
ENSMUST00000018184	ENSMUSG00000018040	15	83113433	83122801	-1	25	19	42	59	50	26	535	506	334	66	309		Q9D1C9
ENSMUST00000018186	ENSMUSG00000018042	15	83153494	83172592	-1	52	38	236	499	86	41	282	585	336	148	464		Q9DCN2
ENSMUST00000018212	ENSMUSG00000018068	11	86210681	86257575	-1	6	7	26	6	5	4	36	61	56	14	34		Q80UK8
ENSMUST00000018246	ENSMUSG00000018102	13	23684199	23692488	1	0	0	10	31	5	2	493	1586	325	579	369		Q6ZWY9
ENSMUST00000018274	ENSMUSG00000025162	11	120961749	120991330	-1	0	0	50	203	25	19	132	482	315	42	339		Q9DC28
ENSMUST00000018287	ENSMUSG00000018143	5	139791513	139802653	1	12	3	0	40	11	2	652	1141	637	94	540	Q3UP84	Q61827
ENSMUST00000018295	ENSMUSG00000068206	15	79229173	79256674	1	0	2	0	15	0	0	26	32	28	13	53	E9PUZ5	
ENSMUST00000018304	ENSMUSG00000018160	11	98152154	98193293	-1	4	0	12	109	15	4	0	0	15	0	31		Q925J9
ENSMUST00000018311	ENSMUSG00000018167	11	98358368	98381112	1	15	11	37	54	24	5	1062	1631	915	200	637	Q544C3	Q61542
ENSMUST00000018313	ENSMUSG00000018169	15	78755882	78773475	-1	19	6	43	96	28	12	109	144	66	18	111	Q3UPI0	O09008
ENSMUST00000018315	ENSMUSG00000018171	11	86583865	86683836	-1	8	7	17	30	11	0	321	1013	240	405	265		Q99KU0
ENSMUST00000018333	ENSMUSG00000018189	1	143777272	143807466	1	0	0	0	0	0	0	65	156	45	42	20		Q9WUP7
ENSMUST00000018337	ENSMUSG00000026361	1	143598800	143702893	-1	40	45	94	90	27	22	150	487	282	49	227		Q8JZM7
ENSMUST00000018343						12	14	15	5	18	4	0	5	4	9	7		
ENSMUST00000018353	ENSMUSG00000018209	2	164070322	164155524	1	0	14	30	76	32	5	3009	5400	5590	1599	3686		Q9JI11
ENSMUST00000018355	ENSMUSG00000018211	2	164214454	164221660	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JHY4
ENSMUST00000018361	ENSMUSG00000018217	11	63128982	63159547	1	5	4	9	23	8	0	1	0	0	292	158	Q5SXS3	
ENSMUST00000018382	ENSMUSG00000018238	11	53431023	53437904	1	18	16	44	15	25	17	2	9	0	3	3	Q3UWR9	Q07105
ENSMUST00000018383	ENSMUSG00000018239	11	53324679	53333301	1	3	1	10	11	1	2	19	61	22	82	12		Q9CX48
ENSMUST00000018389	ENSMUSG00000021346	13	27506968	27513215	-1	1	2	2	4	1	0	0	0	0	0	0		Q9DAS4
ENSMUST00000018392	ENSMUSG00000021345	13	27432681	27438688	-1	2	0	1	0	0	1	0	0	0	0	0		Q9DAY2
ENSMUST00000018399	ENSMUSG00000035592	11	100011195	100016212	-1	14	6	17	43	15	5	0	0	0	0	0		Q8K0Y2
ENSMUST00000018403	ENSMUSG00000018259	13	27345683	27354216	1	1	0	0	0	1	0	0	0	0	0	0	O54832	
ENSMUST00000018407	ENSMUSG00000018263	5	119832668	119885219	1	172	93	202	1579	267	147	1	5	6	1	6	Q5CZX7	P70326
ENSMUST00000018429	ENSMUSG00000020828	11	70540064	70558110	1	0	4	4	34	22	3	33	57	0	3	82	Q5SXG5	P97813
ENSMUST00000018430	ENSMUSG00000018286	11	70525367	70527858	1	0	3	0	0	0	0	611	1024	482	1276	343		Q60692
ENSMUST00000018431	ENSMUSG00000018287	11	70663771	70669416	-1	47	28	199	79	35	23	246	758	226	459	249		Q7TNE3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000018437	ENSMUSG00000018293	11	70651850	70654644	-1	6	11	19	60	0	9	29199	40236	18987	4249	12445	Q5SX50	P62962
ENSMUST00000018449	ENSMUSG00000020850	11	75486816	75509449	1	5	0	0	78	60	31	251	537	2723	0	2110		Q99PV0
ENSMUST00000018466	ENSMUSG00000018322	2	164053540	164071169	-1	4	3	0	323	21	8	12	260	193	27	279		Q9CYG7
ENSMUST00000018470	ENSMUSG00000018326	2	163994960	164018588	1	20	14	48	77	14	6	2451	7407	3807	653	2060	A2A5N2	Q9CQV8
ENSMUST00000018476	ENSMUSG00000022329	15	34875496	35155806	-1	6	2	5	115	0	0	45	110	97	71	78		Q9JI10
ENSMUST00000018478	ENSMUSG00000018334	11	79013440	79146407	-1	39	26	64	118	56	27	2297	2003	2559	141	1831		Q61097
ENSMUST00000018482	ENSMUSG00000020400	11	54910785	54962917	-1	0	0	33	0	0	0	0	0	0	16	0	E9QM75	
ENSMUST00000018485	ENSMUSG00000018341	6	67291318	67376188	-1	12	10	18	60	5	5	3	3	0	1	6		P97378
ENSMUST00000018491	ENSMUSG00000018347	11	65807175	65829239	1	14	0	0	3	20	0	0	116	24	0	19		Q810A1
ENSMUST00000018506	ENSMUSG00000018362	11	106988629	106999541	-1	15	0	0	61	0	0	9	14	9	52	20	Q52L97	P52293
ENSMUST00000018516	ENSMUSG00000018372	11	106789252	106819930	1	0	0	0	3	7	0	68	407	188	50	188		Q8BVV7
ENSMUST00000018521	ENSMUSG00000018377	11	88068279	88084729	1	7	3	15	17	15	2	262	421	435	37	330	Q5SXC4	
ENSMUST00000018522	ENSMUSG00000018378	11	88098058	88194140	1	0	0	0	0	0	0	16	36	0	0	0		Q8R3V6
ENSMUST00000018531	ENSMUSG00000018387	11	53457205	53467766	1	0	0	0	110	0	0	0	0	0	3	0		Q5SX79
ENSMUST00000018544	ENSMUSG00000020486	11	87568903	87590539	1	0	0	0	0	0	0	0	0	0	0	0		P28661
ENSMUST00000018547	ENSMUSG00000020530	11	84832361	84870817	-1	4	0	0	0	0	0	38	294	137	0	52		Q5SV77
ENSMUST00000018549	ENSMUSG00000018405	11	84813061	84819515	-1	18	15	35	495	38	15	77	163	67	20	68		Q99J25
ENSMUST00000018556	ENSMUSG00000018412	11	104333229	104468861	-1	10	5	3	72	10	0	117	517	31	37	0		Q80TG1
ENSMUST00000018561	ENSMUSG00000018417	1	51749765	51916071	-1	0	0	0	0	0	0	0	0	0	27	0	Q7TQD7	
ENSMUST00000018568	ENSMUSG00000020537	11	60454591	60468754	1	24	16	52	17	31	13	150	306	159	124	153		Q9QXB9
ENSMUST00000018569	ENSMUSG00000018425	11	86768846	86807746	-1	102	64	241	939	100	64	582	3337	1236	263	798		Q6PE54
ENSMUST00000018571	ENSMUSG00000018427	11	86936425	86993707	-1	19	26	63	100	32	15	23	101	35	16	77	Q0VA86	Q65Z95
ENSMUST00000018572	ENSMUSG00000018428	11	88830792	88864586	-1	0	0	0	89	5	3	0	0	0	0	48		O08715
ENSMUST00000018577	ENSMUSG00000018433	11	107166663	107189381	-1	0	0	0	35	0	0	53	0	73	52	108		Q8BJW5
ENSMUST00000018586	ENSMUSG00000018442	11	71007164	71019841	-1	1	0	6	0	0	0	42	73	52	47	29	J3QMF4	
ENSMUST00000018593	ENSMUSG00000018449	11	70970213	70977833	1	0	3	0	11	5	0	75	158	24	173	19		Q9CWY9
ENSMUST00000018610	ENSMUSG00000020826	11	78920787	78960254	1	26	25	57	33	54	28	6171	4881	5739	317	2813		P29477
ENSMUST00000018614	ENSMUSG00000018470	11	69326258	69333042	1	0	9	5	234	20	13	0	2	0	0	0	Q8VD73	
ENSMUST00000018623	ENSMUSG00000018479	11	85170404	85181145	1	3	3	6	8	9	3	0	0	0	0	0		Q9D979
ENSMUST00000018625	ENSMUSG00000018481	11	85187262	85235130	-1	40	36	47	113	65	29	615	1653	1261	281	670		Q9DAX9
ENSMUST00000018630	ENSMUSG00000018486	11	103727364	103749821	-1	40	21	53	120	59	37	0	0	0	0	0	Q2TBA6	O35468
ENSMUST00000018632	ENSMUSG00000057003	11	67238029	67260446	1	55	35	45	0	44	26	0	0	0	0	0		Q5SX39
ENSMUST00000018637	ENSMUSG00000056328	11	67200052	67224575	1	0	0	0	22	5	21	0	0	0	0	0		Q5SX40
ENSMUST00000018641	ENSMUSG00000033196	11	67171027	67197517	1	42	22	71	27	51	27	0	0	0	0	0	G3UW82	
ENSMUST00000018644	ENSMUSG00000018500	11	62248984	62266453	1	9	9	15	154	17	11	95	129	79	33	63		Q60614
ENSMUST00000018645	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	0	17	0	0	55	0	230	71	381	Q5RIM6	
ENSMUST00000018651	ENSMUSG00000018507	11	62574486	62600515	1	89	107	276	75	80	45	1718	1757	1235	230	992		Q9WTR1
ENSMUST00000018653	ENSMUSG00000018509	11	62524946	62539261	-1	0	0	0	42	6	0	7	0	0	2	0		Q9CXS4
ENSMUST00000018681	ENSMUSG00000018537	11	97688823	97700497	-1	0	7	2	198	19	3	0	0	0	0	5		P23798
ENSMUST00000018685	ENSMUSG00000018541	11	97745481	97766556	-1	42	20	46	85	18	11	380	774	523	68	433		Q9DBF7
ENSMUST00000018691	ENSMUSG00000018547	11	97715157	97744704	-1	44	33	94	127	62	17	631	786	793	67	637	Q3UJ95	Q80XI4
ENSMUST00000018698	ENSMUSG00000018554	11	69935796	69941605	1	0	0	0	70	0	0	0	0	0	0	0	B2RUF0	
ENSMUST00000018699	ENSMUSG00000020884	11	70054085	70057894	1	0	0	0	0	6	0	0	0	0	0	0		P34927
ENSMUST00000018700	ENSMUSG00000020886	11	70017085	70045532	1	0	0	0	0	0	0	54	35	12	4	47		Q62108
ENSMUST00000018710	ENSMUSG00000018566	11	69942539	69948188	-1	0	0	19	0	0	0	0	0	1	0	0		P14142
ENSMUST00000018711	ENSMUSG00000018567	11	69991143	69994951	1	7	7	20	32	5	4	3699	8184	3128	4910	2050		Q9DCD6
ENSMUST00000018713	ENSMUSG00000018569	11	69964779	69967885	1	2	3	7	157	10	3	0	0	0	0	0		Q9Z261
ENSMUST00000018714	ENSMUSG00000018570	11	69897352	69900987	-1	0	0	0	0	0	0	0	18	0	0	0	B1AR42	
ENSMUST00000018716	ENSMUSG00000018572	11	69995777	70000009	1	0	3	0	157	8	0	383	289	336	58	204		Q8BSN5
ENSMUST00000018718	ENSMUSG00000018574	11	70010183	70015411	-1	7	5	0	0	7	4	0	458	0	96	53	B1AR28	
ENSMUST00000018719	ENSMUSG00000033987	11	118021723	118129219	-1	68	39	32	80	55	32	1	2	7	1	10	A2A519	
ENSMUST00000018727	ENSMUSG00000018583	11	55469685	55504838	1	71	56	232	105	62	56	508	951	612	262	723		P97855
ENSMUST00000018737	ENSMUSG00000018593	11	55394500	55420080	-1	9	5	22	12	24	6	0	0	0	33	82	Q5NCU5	P07214
ENSMUST00000018739	ENSMUSG00000018595	X	136757674	136780141	-1	2	0	4	6	0	0	0	0	0	0	1		Q61603
ENSMUST00000018743	ENSMUSG00000018599	11	60728398	60732951	1	25	15	94	221	39	15	399	474	231	38	144		Q5NCS9
ENSMUST00000018744	ENSMUSG00000020534	11	60788104	60811718	-1	4	9	12	80	12	6	32	66	44	7	52		P50431
ENSMUST00000018748	ENSMUSG00000018604	5	119670669	119684724	1	0	0	0	0	0	6	0	0	0	0	0		P70324
ENSMUST00000018755	ENSMUSG00000020388	11	54054928	54069014	-1	0	4	5	37	9	10	16	10	8	6	40		P70271
ENSMUST00000018765	ENSMUSG00000005800	9	7558429	7568486	1	16	17	28	22	28	28	34145	98499	53587	83289	24225		O70138
ENSMUST00000018767	ENSMUSG00000018623	9	7692090	7699585	1	7	9	8	3	7	3	0	0	0	0	0	Q3UN27	
ENSMUST00000018792	ENSMUSG00000018648	11	84048041	84069261	-1	16	10	31	8	10	2	0	0	0	0	0	Q542U4	Q9JLY7
ENSMUST00000018795	ENSMUSG00000018651	11	84078920	84129600	-1	11	15	13	12	8	5	12	24	16	16	23		Q8CHV6
ENSMUST00000018798	ENSMUSG00000018654	11	11685003	11772926	1	9	2	15	0	0	7	274	0	638	11	653	Q5SWU0	
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ENSMUST00000018803	ENSMUSG00000018659	11	96937825	96943986	-1	0	0	17	15	7	3	490	581	280	100	236		Q91XF0
ENSMUST00000018805	ENSMUSG00000018661	11	113649169	113667054	1	24	14	35	27	30	12	562	652	552	76	525		Q9Z160
ENSMUST00000018810	ENSMUSG00000018666	11	96789127	96808640	1	16	17	38	82	27	9	12	20	19	0	46	Q7TPM0	
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ENSMUST00000018821	ENSMUSG00000018677	11	102402985	102407946	-1	0	0	0	3	0	4	989	738	495	65	539	Q14BQ5	Q9D8K8
ENSMUST00000018841	ENSMUSG00000018697	11	84422855	84513522	-1	0	6	0	19	8	3	71	366	115	49	128		Q9JKX4
ENSMUST00000018842	ENSMUSG00000018698	11	84518284	84525535	-1	20	20	77	333	29	19	69	357	68	7	56	Q569N5	P63006
ENSMUST00000018851	ENSMUSG00000018707	12	110601452	110666945	1	93	66	114	305	141	48	2270	2480	5727	172	5017		Q9JHU4
ENSMUST00000018871	ENSMUSG00000018727	11	113698172	113710017	-1	2	1	3	0	5	0	2	0	0	0	0	Q9DBA5	
ENSMUST00000018875	ENSMUSG00000035152	11	83299024	83405035	1	17	26	28	99	37	12	1351	2942	2293	275	1388	Q5SWR1	Q9DBG3
ENSMUST00000018877	ENSMUSG00000018733	11	83294642	83302586	-1	7	0	14	19	2	4	7	0	0	0	0	Q5SWQ8	Q8VC48
ENSMUST00000018880	ENSMUSG00000018736	11	68821434	68871858	-1	4	6	21	97	16	8	1207	4374	1881	719	1290		Q9ERR1
ENSMUST00000018884	ENSMUSG00000018740	11	68968131	68974365	1	20	17	17	52	36	21	0	12	3	1	11	A0A0A0MQ70	
ENSMUST00000018887	ENSMUSG00000020900	11	68691559	68816632	1	14	19	5	0	13	0	10	0	0	18	6	Q5SV64	
ENSMUST00000018896	ENSMUSG00000089669	11	69682846	69685784	-1	5	0	0	0	0	2	64	151	32	170	75	Q5F2A4	
ENSMUST00000018905	ENSMUSG00000018761	11	69656697	69662642	-1	3	1	22	8	9	2	600	887	435	104	266	Q8R0J2	
ENSMUST00000018909	ENSMUSG00000018765	11	69632990	69653297	1	11	7	11	82	14	3	563	1119	642	133	618	Q6P5B5	
ENSMUST00000018914	ENSMUSG00000018770	2	73908447	73911326	-1	1	0	6	44	0	1	653	1683	653	564	374	Q14BC2	P56384
ENSMUST00000018918	ENSMUSG00000018774	11	69664213	69666153	-1	0	0	34	11	13	7	1631	2807	1209	787	1103		P31996
ENSMUST00000018963	ENSMUSG00000018819	7	142460809	142494867	1	0	0	0	7	0	0	0	976	0	0	0		P19973

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000018965	ENSMUSG00000018821	19	42123273	42129059	-1	1	7	20	49	14	3	13	25	12	38	37		Q9D7H4
ENSMUST00000018966	ENSMUSG00000018822	19	42197971	42202252	-1	13	12	19	367	27	16	2	12	3	2	3		
ENSMUST00000018971	ENSMUSG00000053046	7	141949751	142004247	1	0	0	2	0	6	4	0	1	1	0	0		Q69Z98
ENSMUST00000018985	ENSMUSG00000018841	11	82876434	82890614	-1	9	0	45	35	0	8	125	250	182	33	122	Q3UGT8	O55230
ENSMUST00000018988	ENSMUSG00000018844	11	82892124	82900801	1	19	12	56	22	24	14	0	0	1	0	0	B2RQ03	Q9D2H8
ENSMUST00000018989	ENSMUSG00000018845	11	82910550	82943403	1	0	6	3	3	0	0	0	0	0	0	1		Q8CGY6
ENSMUST00000018990	ENSMUSG00000018846	11	35769484	35791285	1	23	21	51	76	36	14	363	547	612	175	343	Q5SXA7	Q8R2W9
ENSMUST00000018992	ENSMUSG00000018848	11	35808381	35834506	-1	10	4	4	33	20	8	255	1213	533	1633	365		Q9D0I9
ENSMUST00000018993	ENSMUSG00000018849	11	35838400	35980527	-1	40	24	59	159	62	20	1	0	0	1	7		Q5SXA9
ENSMUST00000019006	ENSMUSG00000018862	11	115334731	115346927	1	25	0	60	0	0	10	0	0	0	0	0	F8VQ32	
ENSMUST00000019012	ENSMUSG00000018868	15	84112621	84123175	-1	16	9	34	23	25	6	0	0	0	0	0		Q32LZ8
ENSMUST00000019026	ENSMUSG00000018882	11	97315716	97329920	1	45	38	66	88	56	22	303	625	419	290	223		Q9D0Q7
ENSMUST00000019037	ENSMUSG00000018893	15	77015489	77050670	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UVB1	P04247
ENSMUST00000019038	ENSMUSG00000059248	11	117199661	117362325	1	9	4	22	145	9	11	0	0	0	27	67		Q80UG5
ENSMUST00000019043	ENSMUSG00000018899	11	53770014	53778374	1	0	8	37	0	17	5	49	352	61	75	220	Q5SX13	P15314
ENSMUST00000019044	ENSMUSG00000018900	11	53864542	53891660	-1	7	15	36	33	18	5	41	134	51	23	59	Q5SX17	Q9Z0E8
ENSMUST00000019050	ENSMUSG00000018906	11	54100095	54131665	1	0	0	0	0	0	0	0	0	0	0	0	Q5SX75	
ENSMUST00000019051	ENSMUSG00000018907	11	70315610	70322628	-1	13	14	22	26	18	15	3	3	0	1	4	Q5F2E4	P55249
ENSMUST00000019058	ENSMUSG00000018914	11	54265303	54267277	-1	5	5	4	7	6	0	0	0	0	0	0	Q5SX77	P01586
ENSMUST00000019060	ENSMUSG00000018916	11	54247271	54249667	-1	8	6	9	6	7	2	1	3	0	0	2	Q5SX78	P01587
ENSMUST00000019063	ENSMUSG00000018919	11	70505244	70511178	1	5	5	2	7	9	6	0	0	0	0	0	Q91XF2	
ENSMUST00000019064	ENSMUSG00000018920	11	70453983	70459984	-1	5	8	14	34	15	4	2	6	6	18	8		Q8BSU2
ENSMUST00000019065	ENSMUSG00000018921	11	70392883	70410031	-1	19	22	45	52	57	16	213	224	210	20	247		Q9DBD5
ENSMUST00000019067	ENSMUSG00000018923	11	70451919	70453727	1	11	0	12	2	6	4	430	887	304	1146	185		Q9D8C6
ENSMUST00000019068	ENSMUSG00000018924	11	70344152	70352031	-1	24	22	24	22	35	11	59	62	82	275	1955	A2CF88	P39654
ENSMUST00000019069	ENSMUSG00000018925	11	83511736	83522175	-1	12	6	18	14	13	3	0	2	1	0	2		Q5QNV8
ENSMUST00000019071	ENSMUSG00000018927	11	83587882	83593087	-1	10	16	24	19	17	23	4423	12478	5403	52462	7784		P27784
ENSMUST00000019074	ENSMUSG00000018930	11	83662584	83664683	1	2	7	10	5	4	1	54	416	79	210	95	Q5QNV9	P14097
ENSMUST00000019075	ENSMUSG00000018931	11	60902246	60914750	-1	46	18	49	89	37	13	386	390	324	51	176		Q9DBW3
ENSMUST00000019076	ENSMUSG00000018932	11	60932033	60952811	1	0	0	0	40	23	4	2194	4624	2429	123	2137	Q5SWN9	O09110
ENSMUST00000019101	ENSMUSG00000000037	X	161117193	161258213	1	1	0	0	0	0	0	0	0	0	0	0	B1AVB5	
ENSMUST00000019109	ENSMUSG00000018965	5	33018816	33027966	1	14	14	18	76	14	4	1974	6450	2081	723	1307		P68510
ENSMUST00000019117	ENSMUSG00000018973	11	96365752	96368256	1	33	34	335	178	44	20	4	0	3	0	1		P17919
ENSMUST00000019118	ENSMUSG00000018974	5	113742446	113772510	-1	44	25	56	176	46	25	616	928	691	85	592		Q9JLI8
ENSMUST00000019128	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	0	0	0	0	0	4	3	2		Q60668
ENSMUST00000019130	ENSMUSG00000018986	11	83191330	83215154	1	7	6	21	3	14	4	17	51	25	32	41	Q9Z0I5	
ENSMUST00000019133	ENSMUSG00000057897	11	5969644	6066362	-1	4	5	13	26	10	7	0	0	0	0	0	Q5SVJ0	
ENSMUST00000019135	ENSMUSG00000020740	11	115584255	115604051	-1	0	0	0	0	0	0	565	571	555	34	464		Q8BMI3
ENSMUST00000019143	ENSMUSG00000018999	6	34153380	34177111	-1	20	20	65	51	54	18	85	327	137	20	96		Q8CIA5
ENSMUST00000019169	ENSMUSG00000002395	8	71366848	71369732	1	0	0	0	2	1	0	878	1186	723	3396	563		Q9CQ56
ENSMUST00000019183	ENSMUSG00000019039	9	108569886	108572774	1	0	0	3	10	14	0	272	529	297	26	254		Q6PJN8
ENSMUST00000019192	ENSMUSG00000024041	17	31677933	31681722	1	9	6	34	17	30	10	0	0	0	1	4	Q546L9	P24622
ENSMUST00000019198	ENSMUSG00000019054	5	136953275	136966234	1	9	2	14	6	3	0	2946	3861	1695	4253	1200		Q9CQ92
ENSMUST00000019199	ENSMUSG00000019055	4	147909753	147936767	-1	7	0	22	26	22	6	1259	1189	1017	156	853		Q9R0E2
ENSMUST00000019220	ENSMUSG00000030374	7	16815889	16840931	1	0	0	0	57	0	2	10	75	0	7	33		P58404
ENSMUST00000019224	ENSMUSG00000019080	15	76701542	76704239	1	24	8	47	41	17	13	19	30	12	14	17		
ENSMUST00000019226	ENSMUSG00000019082	7	141429744	141437892	-1	14	0	18	8	10	0	0	0	0	0	0		Q9D6M3
ENSMUST00000019229	ENSMUSG00000006392	4	118409337	118415782	1	0	0	0	0	0	0	454	1293	510	507	292		Q9D7W5
ENSMUST00000019231	ENSMUSG00000019087	X	74297097	74304721	1	3	0	8	0	0	0	6619	13605	4932	1288	3513	Q3TWN7	Q9R1Q9
ENSMUST00000019232	ENSMUSG00000019088	X	74273217	74282337	-1	7	0	13	13	4	3	255	824	366	520	226		Q9D7J6
ENSMUST00000019246	ENSMUSG00000019102	11	61207537	61218421	1	0	0	0	0	10	0	0	0	0	0	0		P47739
ENSMUST00000019248	ENSMUSG00000030577	7	30865402	30880342	-1	264	179	287	2668	514	266	22	58	41	21	123	Q3UP36	
ENSMUST00000019257	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0	Q3ZB65	Q9Z0E3
ENSMUST00000019266	ENSMUSG00000019122	11	83572919	83578636	-1	71	70	126	52	75	40	736	2849	451	5219	1447	Q3U9T8	P51670
ENSMUST00000019268	ENSMUSG00000019124	6	54501173	54566489	-1	41	38	66	382	80	33	0	0	10	6	17		Q9CZC8
ENSMUST00000019276	ENSMUSG00000019132	13	24801657	24814013	1	21	18	111	122	29	17	3087	10943	3932	418	2668	Q3TVJ4	Q99LU8
ENSMUST00000019281	ENSMUSG00000027381	2	128126038	128162547	1	0	8	26	0	7	5	8	0	101	0	36	Q3U7X3	O54918
ENSMUST00000019283	ENSMUSG00000019139	8	70594481	70597288	1	11	9	54	267	18	8	222	297	204	75	276		Q9JHU9
ENSMUST00000019287	ENSMUSG00000019143	18	36783008	36792562	1	0	2	0	0	0	4	51	207	154	26	104	G5E823	
ENSMUST00000019290	ENSMUSG00000019146	15	77991748	78120028	-1	70	41	339	426	92	35	0	4	3	0	1	Q3ZB20	O88602
ENSMUST00000019291	ENSMUSG00000030373	7	18422536	18432041	-1	53	49	467	70	47	36	1	2	1	1	2	Q4KL66	
ENSMUST00000019302	ENSMUSG00000019158	7	16452779	16455489	1	3	2	13	75	4	4	210	321	140	282	90		Q9D938
ENSMUST00000019317	ENSMUSG00000019173	11	100715009	100738215	-1	0	0	36	0	5	0	239	729	460	104	442	Q8C266	
ENSMUST00000019323	ENSMUSG00000019179	5	135778480	135790398	1	0	4	0	49	7	0	1178	2220	1258	318	1521		P08249
ENSMUST00000019333	ENSMUSG00000019189	11	44518964	44565520	1	11	13	25	41	22	12	1893	4045	2579	349	2266		Q5SWK7
ENSMUST00000019354	ENSMUSG00000019210	6	120794305	120822793	-1	5	6	14	37	14	4	1068	4031	1444	3049	1039		P50518
ENSMUST00000019362	ENSMUSG00000020888	11	70000595	70012301	1	7	0	0	175	20	0	230	316	144	7	146		Q60838
ENSMUST00000019374	ENSMUSG00000019230	1	138825186	138848577	-1	16	12	16	165	28	22	0	0	0	0	0		Q9WUH2
ENSMUST00000019378	ENSMUSG00000021245	12	85234529	85270591	-1	38	0	129	16	0	14	17	51	0	10	26	Q68FG1	
ENSMUST00000019379	ENSMUSG00000019235	12	85135596	85151264	-1	24	14	56	66	35	18	2	12	8	0	5		Q8R2S1
ENSMUST00000019382	ENSMUSG00000031708	8	83571700	83594491	-1	20	0	33	0	25	21	2204	1137	1280	252	932		Q9CY27
ENSMUST00000019386	ENSMUSG00000005251	16	97741933	97763737	-1	0	4	0	88	21	0	0	0	0	1	2		Q9ERK0
ENSMUST00000019405	ENSMUSG00000019261	8	70905974	70917526	1	24	23	73	1079	53	23	232	320	239	28	257		Q8C052
ENSMUST00000019422	ENSMUSG00000019278	8	123186235	123201810	1	19	10	19	17	20	4	0	0	0	1	0		P31428
ENSMUST00000019426	ENSMUSG00000001804	18	20436175	20471821	1	24	18	40	18	19	13	0	0	0	0	0		Q7TMD7
ENSMUST00000019439	ENSMUSG00000019295	5	33653216	33658416	-1	0	0	0	81	7	0	129	304	166	0	96		Q8K304
ENSMUST00000019441	ENSMUSG00000019297	14	55745693	55755500	1	24	18	84	114	36	17	476	534	378	68	269		Q8BMC4
ENSMUST00000019443	ENSMUSG00000047098	14	55591708	55603693	1	0	0	0	45	0	0	799	850	959	77	1028		Q924T7
ENSMUST00000019445	ENSMUSG00000019301	11	101078411	101080527	1	10	6	23	62	18	6	13	20	10	0	18	Q790P4	P51656
ENSMUST00000019447	ENSMUSG00000019303	11	101091823	101095436	-1	2	0	0	25	4	2	0	18	0	30	0	C4PFH5	O35047
ENSMUST00000019456	ENSMUSG00000019312	11	98446394	98455373	1	5	2	4	4	3	5	0	0	0	0	0		Q03160
ENSMUST00000019464	ENSMUSG00000019320	17	24696234	24700529	1	6	3	13	80	7	7	8	20	5	3	5		Q8VCM2
ENSMUST00000019469	ENSMUSG00000078650	11	101367561	101377903	1	14	17	29	19	21	11	0	0	0	1	0		P35576
ENSMUST00000019470	ENSMUSG00000078652	11	101316213	101323537	1	13	13	30	51	23	15	901	1833	1104	145	769	Q4FK54	P61290

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000019482	ENSMUSG00000019338	3	95006590	95015448	-1	0	0	12	58	0	0	447	601	488	38	547		Q9D2D7
ENSMUST00000019503	ENSMUSG00000019359	X	100729873	100738895	1	0	0	0	0	0	0	0	0	0	0	0		Q9ESM6
ENSMUST00000019506	ENSMUSG00000019362	8	84246237	84249761	-1	9	7	13	67	12	9	809	1615	686	2739	678		Q8R1F0
ENSMUST00000019512	ENSMUSG00000019368	11	4031462	4048024	1	2	0	0	0	1	0	0	0	0	0	0		Q8R0F9
ENSMUST00000019514	ENSMUSG00000019370	7	16915379	16924114	-1	20	3	46	129	14	6	3887	5126	2882	1733	1994		P62204
ENSMUST00000019516	ENSMUSG00000075590	15	76085595	76090013	-1	27	16	67	44	36	19	1	16	6	4	14		
ENSMUST00000019517	ENSMUSG00000019373	11	59817795	59839838	-1	2	0	0	6	0	2	170	940	338	690	166	Q3UQL2	O88543
ENSMUST00000019572	ENSMUSG00000059839	13	67471514	67484225	-1	54	78	179	49	70	32	138	775	237	202	178	Q7M6X2	
ENSMUST00000019576	ENSMUSG00000005481	8	83715177	83726892	1	0	0	0	55	3	0	209	146	147	90	23		Q8VDW0
ENSMUST00000019577	ENSMUSG00000019433	8	83652678	83664788	1	28	22	79	117	50	28	672	657	467	72	272		Q9Z0G0
ENSMUST00000019605	ENSMUSG00000019461	11	69846376	69852058	1	6	0	8	24	5	6	369	430	409	21	218	Q5F283	Q9JIZ9
ENSMUST00000019608	ENSMUSG00000019464	8	83666833	83672753	1	27	13	43	40	19	18	131	525	222	14	489	B2RS62	P35375
ENSMUST00000019611	ENSMUSG00000019467	10	127182521	127190054	-1	8	0	0	50	0	16	0	0	0	0	0	G5E825	
ENSMUST00000019614	ENSMUSG00000019470	8	3608421	3621316	-1	0	0	0	8	0	0	1238	1203	932	184	676		Q9DCD2
ENSMUST00000019615	ENSMUSG00000019471	9	21138541	21149906	-1	27	26	57	102	34	11	1572	2132	1336	740	1076		Q61081
ENSMUST00000019616	ENSMUSG00000032174	9	21032038	21039036	1	21	20	37	482	44	25	0	1	0	0	0		Q60625
ENSMUST00000019625	ENSMUSG00000055775	11	67277124	67308634	1	19	8	49	27	39	15	0	0	0	0	0		P13542
ENSMUST00000019631	ENSMUSG00000019487	17	57249451	57263697	1	22	11	38	90	24	13	45	50	48	16	74		Q8CJ53
ENSMUST00000019633	ENSMUSG00000019489	17	57145997	57149777	-1	5	4	13	35	13	3	0	0	0	0	1	Q05A52	O55237
ENSMUST00000019638	ENSMUSG00000019494	5	138161071	138164646	1	1	2	2	28	9	3	40	50	25	16	5	Q3UIT2	O88545
ENSMUST00000019649	ENSMUSG00000019505	11	62551171	62553213	1	22	11	50	29	34	12	23538	39873	21416	20442	16981	Q78XY9	P0CG49
ENSMUST00000019660	ENSMUSG00000029729	5	138085084	138107822	1	27	0	38	73	35	21	73	225	128	58	127		Q8BGS3
ENSMUST00000019662	ENSMUSG00000019518	5	138172002	138180429	1	0	0	0	0	0	0	47	26	53	26	27		Q9JKC7
ENSMUST00000019677	ENSMUSG00000028708	4	115839198	115879250	1	0	8	0	10	12	8	1553	3609	2271	300	1623	A2A8W8	
ENSMUST00000019679	ENSMUSG00000002343	8	70220172	70234466	-1	0	0	0	4	9	3	147	114	91	26	55		Q8BNU0
ENSMUST00000019683	ENSMUSG00000019539	7	45082914	45092213	-1	0	0	57	0	23	0	0	0	0	0	38		Q8BH97
ENSMUST00000019684	ENSMUSG00000002504	17	24639282	24650305	-1	14	4	13	1	10	0	70	52	20	20	31		
ENSMUST00000019697	ENSMUSG00000078762	7	30653711	30664994	-1	6	5	11	34	16	4	97	97	79	8	59		Q9D786
ENSMUST00000019701	ENSMUSG00000031383	X	73639419	73643514	1	15	18	44	100	20	4	2	4	2	4	23	Q7TNL7	
ENSMUST00000019708	ENSMUSG00000019564	10	79927043	79955018	1	0	5	39	211	26	0	2789	5500	4004	397	3144		Q62431
ENSMUST00000019721	ENSMUSG00000019577	6	5483351	5496309	-1	46	50	100	687	67	39	5	17	3	3	11	Q544J2	O70571
ENSMUST00000019722	ENSMUSG00000019578	17	56067045	56075028	-1	2	7	21	72	16	4	546	712	431	245	208		Q99PL6
ENSMUST00000019723	ENSMUSG00000019579	17	56175744	56183920	-1	126	100	436	290	114	69	325	592	267	646	263		Q9CPT4
ENSMUST00000019726	ENSMUSG00000024197	17	56278962	56290511	-1	58	63	118	79	60	26	2503	2924	2106	269	835		Q9DBG5
ENSMUST00000019734	ENSMUSG00000019590	11	105933702	105953336	-1	13	10	44	18	24	10	6	4	2	6	35		Q60720
ENSMUST00000019749	ENSMUSG00000027102	2	74704615	74707933	1	9	2	31	91	14	0	0	0	0	0	0		P23463
ENSMUST00000019791	ENSMUSG00000019647	18	47235598	47368870	-1	22	3	0	0	0	0	0	0	0	0	0		O35464
ENSMUST00000019803	ENSMUSG00000019659	9	110656503	110711606	1	10	4	24	35	11	10	1480	2378	1142	1517	712		Q8R344
ENSMUST00000019808	ENSMUSG00000011305	17	56111601	56117596	-1	0	4	0	106	11	9	312	264	181	30	73		Q8BVZ1
ENSMUST00000019829						0	0	0	3	0	0	2	45	1	13	3		
ENSMUST00000019833	ENSMUSG00000019689	6	38533502	38539449	1	0	3	0	68	2	1	51	67	35	145	19		Q9CR13
ENSMUST00000019843	ENSMUSG00000019699	1	177020073	177258203	-1	0	0	0	0	1	0	0	0	18	0	0		Q9WUA6
ENSMUST00000019854	ENSMUSG00000019710	3	87919506	87923672	1	2	0	0	0	0	0	76	293	79	268	36		Q9CQ06
ENSMUST00000019859	ENSMUSG00000019715	2	29935426	29960371	1	34	21	72	38	32	16	247	352	248	42	189		Q8R322
ENSMUST00000019861	ENSMUSG00000042197	1	33761545	33814595	-1	0	8	0	0	4	0	59	144	141	52	103		Q8C0P7
ENSMUST00000019862	ENSMUSG00000019718	12	72073428	72085439	-1	0	1	0	24	0	0	0	1	0	3	3		Q9CXA2
ENSMUST00000019876	ENSMUSG00000019732	8	72424176	72443870	-1	6	6	16	9	6	1	0	0	2	3	0		Q9D9Q6
ENSMUST00000019878	ENSMUSG00000078813	7	3660098	3665840	-1	11	13	41	60	20	14	71	245	114	32	126		Q9DB98
ENSMUST00000019882	ENSMUSG00000019738	7	30231948	30233390	1	2	3	0	25	2	0	16	0	16	75	14		P60898
ENSMUST00000019896	ENSMUSG00000019762	10	3540240	3554877	1	7	2	22	4	12	3	0	0	0	0	0		Q9DCX8
ENSMUST00000019901	ENSMUSG00000019767	10	4482502	4562231	1	1	0	1	0	3	0	0	0	0	1	2	F6ST92	
ENSMUST00000019906	ENSMUSG00000019772	10	5639218	5647614	1	6	3	10	5	5	3	0	0	0	0	0		
ENSMUST00000019907	ENSMUSG00000019773	10	5799160	5805600	-1	7	5	8	90	11	6	39	98	78	28	32		Q7TSG3
ENSMUST00000019908	ENSMUSG00000019774	10	5811887	5823910	-1	13	14	23	77	22	6	7	52	18	20	17		Q8BJU9
ENSMUST00000019909	ENSMUSG00000019775	10	5825663	5922400	-1	0	0	0	0	0	0	0	0	0	0	0	F8WH97	
ENSMUST00000019911	ENSMUSG00000019777	10	36974544	37001889	1	4	3	0	105	6	1	75	371	158	161	134		
ENSMUST00000019913	ENSMUSG00000019779	10	34483400	34611226	1	0	12	95	0	37	0	1	4	1	0	16		Q922K9
ENSMUST00000019917	ENSMUSG00000019782	10	33996555	34019624	-1	1	0	4	62	5	3	109	635	220	646	118		Q9CQK7
ENSMUST00000019920	ENSMUSG00000019785	10	33512286	33624769	-1	8	6	3	17	10	6	0	0	0	0	0		Q8BG92
ENSMUST00000019924	ENSMUSG00000019789	10	30832359	30842801	-1	11	7	24	107	21	9	0	0	0	0	0	Q0VGJ1	Q9QUS4
ENSMUST00000019925	ENSMUSG00000019791	10	30608141	30618479	-1	0	2	0	0	0	1	18	34	28	45	13	F8WH96	
ENSMUST00000019927	ENSMUSG00000019792	10	30534225	30600749	-1	4	3	11	41	11	4	11	64	14	59	12	E9QKG3	
ENSMUST00000019929	ENSMUSG00000019794	10	7726000	7763150	1	4	3	8	6	6	2	212	1125	343	304	219	E9QKG2	
ENSMUST00000019931	ENSMUSG00000019796	10	7589800	7625483	1	2	7	0	13	25	9	0	6	0	0	0		Q8CB67
ENSMUST00000019932	ENSMUSG00000019797	10	43525121	43540994	-1	0	0	0	29	0	0	40	155	43	201	46		Q9CQF4
ENSMUST00000019937	ENSMUSG00000019802	10	42761496	42832514	1	58	72	122	2100	68	37	204	1291	557	141	438		Q8VHE0
ENSMUST00000019938	ENSMUSG00000019803	10	42561963	42583632	-1	30	24	35	658	50	23	0	1	1	0	2	Q78ZM1	Q64104
ENSMUST00000019939	ENSMUSG00000019804	10	42502030	42535381	1	4	0	4	22	3	0	705	1644	836	202	679	Q78ZM0	
ENSMUST00000019942	ENSMUSG00000019806	10	13647054	13868980	-1	2	4	2	3	1	1	0	8	0	4	0		Q9D8B1
ENSMUST00000019944	ENSMUSG00000019808	10	13552894	13563376	1	10	10	24	85	17	4	18	35	21	37	23		Q6P6J0
ENSMUST00000019945	ENSMUSG00000019809	10	13523842	13553142	-1	0	0	3	3	8	6	44	195	42	105	22	Q3UIG2	Q9QXY9
ENSMUST00000019950	ENSMUSG00000019814	10	13178640	13193137	-1	10	6	10	39	10	4	76	292	133	297	123		Q6NSQ7
ENSMUST00000019951	ENSMUSG00000019813	10	41718840	41809871	-1	0	0	0	0	0	0	0	0	0	0	0	G5E828	
ENSMUST00000019954	ENSMUSG00000019815	10	13149540	13177991	-1	10	5	11	3	6	2	0	0	0	0	0	B9EHC9	
ENSMUST00000019955	ENSMUSG00000075225	10	41538846	41709300	-1	3	0	0	0	0	0	0	0	2	0	0		Q0VG85
ENSMUST00000019962	ENSMUSG00000019818	10	41519414	41531048	1	6	8	28	38	10	6	2622	4652	2316	720	1460		Q9R0L9
ENSMUST00000019965	ENSMUSG00000019822	10	41485642	41490369	-1	0	0	0	0	0	0	260	308	208	61	178		O70572
ENSMUST00000019967	ENSMUSG00000019823	10	41476314	41487032	1	6	5	16	0	13	0	2259	2130	2083	260	1927		Q8VDP3
ENSMUST00000019974	ENSMUSG00000019832	10	10545011	10558233	-1	12	8	10	89	18	5	1680	6333	1761	492	1253	Q0PD23	Q9CZE3
ENSMUST00000019975	ENSMUSG00000019831	10	40883475	40938570	1	14	9	11	92	25	10	1	1	0	1	10		Q8R5H6
ENSMUST00000019977	ENSMUSG00000063428	10	40630011	40649931	1	36	28	116	35	26	18	0	5	0	0	0		Q922Z0
ENSMUST00000019978	ENSMUSG00000019834	10	40570336	40604132	1	3	13	0	2	17	5	0	0	0	0	0		Q497L8
ENSMUST00000019982	ENSMUSG00000019837	10	40249203	40257665	-1	7	6	7	28	6	3	45	229	91	427	90		Q9D8P7
ENSMUST00000019986	ENSMUSG00000019841	10	39732118	39875211	1	0	27	0	134	32	0	0	0	0	0	0		Q61493

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000019987	ENSMUSG00000019842	10	39612934	39655307	1	20	16	38	54	23	9	10	25	18	3	59	Q8N7N6	
ENSMUST00000019991	ENSMUSG00000019845	10	39134023	39151058	1	14	12	21	64	14	6	38	47	37	13	24		Q9D6T1
ENSMUST00000019992	ENSMUSG00000019846	10	38965515	39110188	1	17	16	14	14	17	16	0	0	0	2	10		P97927
ENSMUST00000019994	ENSMUSG00000019848	10	45178098	45318452	1	11	0	7	38	11	4	0	0	0	0	0		Q9ES81
ENSMUST00000019997	ENSMUSG00000019850	10	19000910	19015657	-1	7	0	0	121	6	0	50	0	93	0	192		Q60769
ENSMUST00000019998	ENSMUSG00000019851	10	18845071	18857073	1	6	7	21	149	16	4	5	1	4	2	1		Q9JK95
ENSMUST00000019999	ENSMUSG00000019852	10	18588011	18743758	-1	56	38	111	144	76	29	2	2	6	0	5		Q3UGY8
ENSMUST00000020000	ENSMUSG00000019853	10	18540123	18546076	-1	8	14	18	92	16	8	0	8	1	18	8		Q9WU63
ENSMUST00000020002	ENSMUSG00000078453	10	18011263	18023252	-1	7	7	10	28	13	10	560	1979	610	1996	353	E9QMV2	
ENSMUST00000020003	ENSMUSG00000019856	10	53633145	53750909	-1	0	0	0	11	0	0	0	0	0	0	0	E9PW83	
ENSMUST00000020004	ENSMUSG00000019857	10	53596961	53609213	1	6	3	2	34	8	2	49	162	71	72	39		Q9CQE6
ENSMUST00000020008	ENSMUSG00000019861	10	52337024	52382124	-1	14	16	25	118	22	7	130	473	286	26	165		Q8BH60
ENSMUST00000020012	ENSMUSG00000019863	10	43874188	43901745	-1	4	4	11	24	9	3	35	75	36	39	27		Q9CZN8
ENSMUST00000020015	ENSMUSG00000019865	10	14705591	14770850	1	0	3	13	0	9	2	0	0	0	0	0	Q0VEH1	O54799
ENSMUST00000020016	ENSMUSG00000019867	10	14715623	14718214	-1	29	38	121	21	43	18	6	7	2	4	7		Q9CX92
ENSMUST00000020017	ENSMUSG00000019866	10	43950307	44148853	-1	35	24	92	598	70	31	159	482	267	61	438	E9PVP1	
ENSMUST00000020018	ENSMUSG00000019868	10	14654755	14705560	-1	5	5	15	1	0	0	181	638	230	366	148	F8WJC2	
ENSMUST00000020022	ENSMUSG00000019872	10	57794335	57811830	1	8	3	6	16	16	7	3920	20418	6725	8074	3033		P70158
ENSMUST00000020023	ENSMUSG00000019873	10	67009189	67096988	-1	112	136	241	147	186	103	1695	3482	2848	850	1856		Q99KK1
ENSMUST00000020024	ENSMUSG00000019874	10	57784881	57788450	1	0	2	6	3	4	4	1	14	6	334	37		P51880
ENSMUST00000020027	ENSMUSG00000019877	10	57515774	57532530	-1	3	2	7	58	5	3	698	2238	1103	1955	866	A9CLV6	Q9QZI8
ENSMUST00000020034	ENSMUSG00000019883	10	29313166	29346661	1	0	8	4	11	0	0	22	23	13	14	28		Q9D9V3
ENSMUST00000020039	ENSMUSG00000019888	10	101681487	102391469	1	2	13	19	14	0	3	0	1	0	0	2		Q9D306
ENSMUST00000020040	ENSMUSG00000019890	10	102481760	102490418	-1	4	5	4	3	8	0	0	0	0	1	0		Q9D3P9
ENSMUST00000020043	ENSMUSG00000019892	10	103063198	103236322	-1	7	2	0	18	1	0	0	0	0	0	0		Q0P5X1
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ENSMUST00000020049	ENSMUSG00000019897	10	105841067	105847833	1	0	0	3	152	10	0	65	368	97	297	41		Q8R2N0
ENSMUST00000020057	ENSMUSG00000019906	10	107271843	107425143	1	14	0	0	0	0	0	0	0	0	0	0		Q8JZS0
ENSMUST00000020062	ENSMUSG00000019905	10	51614823	51631458	-1	8	11	19	8	11	8	0	0	0	0	0		Q8K4Z6
ENSMUST00000020064	ENSMUSG00000019909	10	51585420	51590480	-1	2	1	2	43	2	2	0	0	0	0	0	B2RV81	Q9CX19
ENSMUST00000020071	ENSMUSG00000019913	10	50895651	50989152	1	40	41	210	74	43	11	0	0	0	0	0		Q61045
ENSMUST00000020077	ENSMUSG00000019920	10	58323466	58424691	1	2	0	6	4	0	0	0	0	4	4	0	Q9D7B2	
ENSMUST00000020078	ENSMUSG00000019920	10	58323466	58424691	1	9	10	23	35	9	11	1772	4542	1847	1559	1231		
ENSMUST00000020081	ENSMUSG00000019923	10	72654845	72674964	1	26	16	22	68	16	13	306	802	487	865	242		Q9CQU5
ENSMUST00000020085	ENSMUSG00000019927	10	71254980	71285262	-1	1	3	0	24	7	0	316	1005	360	53	182	Q3UFQ4	P61080
ENSMUST00000020094	ENSMUSG00000019936	10	97644068	97682454	1	2	1	5	0	0	0	0	0	0	0	0		P70186
ENSMUST00000020099	ENSMUSG00000019942	10	69336635	69352938	-1	9	3	17	31	19	8	0	12	10	8	6		P11440
ENSMUST00000020101	ENSMUSG00000019944	10	69151434	69291791	1	33	45	212	124	55	40	4	6	6	1	9		Q9DAK3
ENSMUST00000020102	ENSMUSG00000019935	10	89574020	89621253	-1	97	92	350	1082	121	50	4	43	17	4	11		Q8BFU8
ENSMUST00000020103	ENSMUSG00000019945	10	68430953	68541896	-1	3	5	12	11	6	6	0	4	2	2	0		
ENSMUST00000020106	ENSMUSG00000019947	10	68095593	68278726	-1	34	24	133	46	26	19	356	285	675	28	530		Q8BM75
ENSMUST00000020107	ENSMUSG00000019943	10	98915152	99026143	1	32	23	61	91	33	18	783	1838	1641	416	1609		G5E829
ENSMUST00000020109	ENSMUSG00000019948	10	89711973	89732295	-1	1	6	1	6	5	3	39	201	71	141	29		
ENSMUST00000020112	ENSMUSG00000019951	10	89744991	89819869	1	23	15	38	102	29	13	967	2127	2078	169	1075		A2RSJ4
ENSMUST00000020113	ENSMUSG00000019952	10	99107036	99198074	1	5	0	1	20	0	0	90	213	140	0	35		Q8BHD1
ENSMUST00000020118	ENSMUSG00000019960	10	99263231	99267488	1	15	19	49	227	39	20	146	703	167	100	482		Q9DBB1
ENSMUST00000020123	ENSMUSG00000019961	10	91147571	91171582	-1	8	13	31	75	20	12	578	2354	963	134	576		Q61033
ENSMUST00000020129	ENSMUSG00000019966	10	100015630	100100413	1	1	3	5	0	2	0	0	0	0	0	3		P20826
ENSMUST00000020145	ENSMUSG00000019970	10	21882184	21999903	1	0	0	0	1	0	0	2491	7519	3131	847	1919		Q9WVC6
ENSMUST00000020149	ENSMUSG00000019975	10	91082940	91102607	1	45	66	130	82	46	34	13	69	28	35	43	E9QMH7	
ENSMUST00000020150	ENSMUSG00000019975	10	91082940	91102607	1	4	5	8	17	4	1	16	60	13	70	18		Q9DBZ1
ENSMUST00000020153	ENSMUSG00000019977	10	21295979	21368889	1	15	15	16	56	23	11	175	760	379	94	332		Q69ZS7
ENSMUST00000020157	ENSMUSG00000019979	10	90989311	91082770	-1	19	0	9	3	30	13	343	496	1083	120	565		O88879
ENSMUST00000020158	ENSMUSG00000019982	10	21124936	21160905	-1	0	0	0	0	0	0	33	73	68	6	6		P06876
ENSMUST00000020159	ENSMUSG00000019984	10	24869986	24913681	1	0	0	0	0	0	0	51	51	54	0	0	F8WJB0	
ENSMUST00000020161	ENSMUSG00000019987	10	24915208	24927470	-1	5	6	5	6	11	6	14	1	8	14991	1855		Q61176
ENSMUST00000020163	ENSMUSG00000019988	10	92684746	92722420	-1	14	22	13	64	15	19	42	109	89	119	80		P33215
ENSMUST00000020165	ENSMUSG00000019990	10	20398004	20725078	-1	12	9	11	73	6	3	177	788	426	65	460		Q9QXQ1
ENSMUST00000020169	ENSMUSG00000019989	10	24773814	24836195	-1	13	20	4	16	21	11	0	0	0	2	1		Q6DYE8
ENSMUST00000020171	ENSMUSG00000019997	10	24595442	24598683	1	2	7	21	236	29	5	0	1	0	6	2		P29268
ENSMUST00000020173	ENSMUSG00000019996	10	20148471	20281589	1	15	11	22	81	31	11	0	0	2	0	1	E9QMU3	
ENSMUST00000020174	ENSMUSG00000019998	10	24149317	24188959	1	7	4	21	123	15	8	1140	3065	1494	1115	1230	Q8BH40	
ENSMUST00000020182	ENSMUSG00000020003	10	19859929	19907689	-1	6	0	9	16	4	1	73	450	141	90	75		P97865
ENSMUST00000020185	ENSMUSG00000020007	10	19712587	19760053	1	11	11	25	40	18	3	0	0	0	0	0		Q6PHB0
ENSMUST00000020188	ENSMUSG00000020009	10	19591949	19610229	1	7	8	15	26	10	8	6638	19416	9125	3184	4694		P15261
ENSMUST00000020190	ENSMUSG00000020010	10	23851462	23869843	1	11	5	20	8	18	7	5	32	6	5	9		Q9QZ25
ENSMUST00000020197	ENSMUSG00000028886	4	132638987	132724765	1	0	0	28	43	2	21	0	0	0	0	0		P97480
ENSMUST00000020200	ENSMUSG00000020014	10	92775619	93081618	-1	0	0	0	3	0	1	15	34	8	0	0		
ENSMUST00000020203	ENSMUSG00000020018	10	93583029	93589706	-1	1	0	2	10	0	0	42	149	41	245	52	Q497K3	P62307
ENSMUST00000020204	ENSMUSG00000020019	10	93640681	93747207	1	26	29	43	254	54	29	1	6	0	1	0		Q9JI33
ENSMUST00000020208	ENSMUSG00000020021	10	94036001	94145339	1	48	39	81	208	53	33	112	307	297	9	200		Q69ZL1
ENSMUST00000020209	ENSMUSG00000020022	10	94198955	94221443	1	5	5	4	20	11	1	2	10	4	2	8		Q7TMF3
ENSMUST00000020212	ENSMUSG00000020024	10	94688790	94790336	1	6	6	15	213	13	8	218	1306	844	375	516		Q9D5R3
ENSMUST00000020215	ENSMUSG00000020027	10	95385362	95417180	-1	15	0	10	94	11	0	0	0	5	0	0	Q548Q7	O35717
ENSMUST00000020217	ENSMUSG00000020029	10	95547007	95564167	-1	12	20	24	111	25	10	3602	13825	5403	1101	4130	Q4FJR0	Q8R2U6
ENSMUST00000020220	ENSMUSG00000020032	10	84370905	84440597	-1	69	45	157	234	91	44	6	12	5	4	9		Q641K5
ENSMUST00000020223	ENSMUSG00000020034	10	84576626	84614359	1	6	16	8	160	22	11	4803	8939	6088	982	3375		Q8K1H7
ENSMUST00000020226						6	4	16	11	17	7	0	0	0	0	0		
ENSMUST00000020227	ENSMUSG00000020038	10	85131702	85185054	-1	6	8	21	254	15	7	604	1030	877	111	551		P97784
ENSMUST00000020231	ENSMUSG00000020042	10	85386814	85660292	1	12	11	60	582	31	20	6	3	0	0	0	H7BWX5	
ENSMUST00000020234	ENSMUSG00000020044	10	86300372	86349506	1	64	53	94	543	120	64	2	1	1	23	40	Q54AE5	P39876
ENSMUST00000020238	ENSMUSG00000020048	10	86690209	86705509	-1	6	7	5	105	3	1	682	3866	1689	3778	1748	Q3UAD6	P08113
ENSMUST00000020241	ENSMUSG00000020051	10	87521795	87584136	1	6	6	17	8	17	5	0	0	0	1	0		P16331
ENSMUST00000020243	ENSMUSG00000020052	10	87490819	87493660	-1	11	16	43	280	27	7	0	0	1	0	0		Q02067

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000020248	ENSMUSG00000020056	10	88201093	88246158	1	0	5	0	0	0	5	73	157	129	291	71		Q9CR27
ENSMUST00000020249	ENSMUSG00000020057	10	88322804	88379080	-1	19	0	0	80	16	0	416	1448	633	186	506		Q9DC58
ENSMUST00000020251	ENSMUSG00000035311	10	88379132	88447329	1	0	0	0	100	0	0	166	58	260	0	290		Q69ZN6
ENSMUST00000020252	ENSMUSG00000020059	10	88459569	88473236	1	0	4	7	34	4	0	0	0	0	0	0	A2RSE7	
ENSMUST00000020253	ENSMUSG00000060002	10	88452745	88504073	-1	0	0	0	0	0	0	4	0	4	0	8		Q8C025
ENSMUST00000020255	ENSMUSG00000020062	10	88885992	88929505	1	17	15	30	125	11	12	0	0	0	0	0		Q8BYF6
ENSMUST00000020257	ENSMUSG00000020063	10	63319005	63381704	-1	0	0	0	0	0	0	24	64	62	1	34	Q53Z05	Q923E4
ENSMUST00000020258	ENSMUSG00000020064	10	63243797	63317881	1	17	16	17	129	15	11	1044	5986	2523	959	1856		Q6PAV2
ENSMUST00000020262	ENSMUSG00000020072	10	63024315	63077962	1	21	10	42	15	26	9	0	1	0	2	0		Q9CXN7
ENSMUST00000020263	ENSMUSG00000020069	10	63014664	63024217	-1	0	0	0	0	0	0	0	0	4	14	0	D3Z3N4	
ENSMUST00000020266	ENSMUSG00000020072	10	63024315	63077962	1	31	31	44	39	29	31	0	0	5	0	5	K3W4L7	
ENSMUST00000020268	ENSMUSG00000020074	10	62743928	62792368	-1	4	10	13	41	13	5	286	1681	851	599	653		Q8CH18
ENSMUST00000020270	ENSMUSG00000020076	10	62616023	62651218	-1	7	6	6	60	11	6	252	1381	619	963	383		Q99MJ9
ENSMUST00000020271	ENSMUSG00000020077	10	62493833	62527451	-1	0	0	0	0	0	0	8448	4720	998	7049	2297		P13609
ENSMUST00000020273	ENSMUSG00000020079	10	62429209	62449738	-1	0	0	0	76	0	13	48	32	64	16	60		Q80YD1
ENSMUST00000020277	ENSMUSG00000020080	10	62383137	62422491	-1	29	23	34	30	44	12	0	0	0	0	0		Q91W97
ENSMUST00000020278	ENSMUSG00000020081	10	62252438	62265990	1	20	18	66	17	18	7	0	1	0	0	1	Q3KP20	P30549
ENSMUST00000020283	ENSMUSG00000020086	10	61738665	61784147	-1	11	19	36	145	28	8	8	22	6	4	4		Q8CCK0
ENSMUST00000020284	ENSMUSG00000020087	10	61695514	61702773	1	16	5	49	420	26	17	126	208	113	22	95		Q9DBA6
ENSMUST00000020285	ENSMUSG00000020088	10	61680310	61693295	1	13	6	45	34	11	6	808	2163	1082	791	808	Q99JZ4	
ENSMUST00000020286	ENSMUSG00000020089	10	61648552	61674168	1	5	5	1	96	8	0	21	121	41	94	75	Q4FK49	Q9D819
ENSMUST00000020287	ENSMUSG00000020090	10	61595492	61628565	1	19	2	26	168	20	2	0	0	0	0	0	E9Q468	
ENSMUST00000020288	ENSMUSG00000020091	10	61432497	61452669	-1	13	6	22	38	19	12	2607	2534	2486	172	2056	Q3UFP6	P70445
ENSMUST00000020289	ENSMUSG00000020092	10	61319657	61383523	-1	30	21	104	137	66	22	13	5	10	9	13		
ENSMUST00000020298	ENSMUSG00000020098	10	61089343	61094328	1	8	4	7	24	8	5	1	2	0	2	1		P61458
ENSMUST00000020301	ENSMUSG00000020101	10	60346851	60372684	1	12	11	99	85	24	15	20603	21968	16774	2663	9578		Q9D659
ENSMUST00000020307	ENSMUSG00000020107	10	59987409	60003135	-1	6	0	0	0	0	0	140	386	114	120	64	S4R2B6	
ENSMUST00000020308	ENSMUSG00000020108	10	59949675	59951770	-1	12	9	22	227	23	13	204	237	184	60	445	B7ZNP9	Q9D3F7
ENSMUST00000020309	ENSMUSG00000020109	10	59879556	59899302	1	0	0	26	0	0	0	82	274	158	0	98		Q9QYI4
ENSMUST00000020311	ENSMUSG00000020111	10	59702477	59864132	1	14	0	0	0	0	9	15	0	20	90	321		Q8VCX5
ENSMUST00000020312	ENSMUSG00000009647	10	59446984	59616692	-1	13	14	28	18	16	14	629	1320	863	69	529		Q3UMR5
ENSMUST00000020315	ENSMUSG00000020114	10	119199255	119240055	-1	37	38	38	177	43	32	355	1039	623	114	405		Q6ZQ38
ENSMUST00000020316	ENSMUSG00000020115	10	121546455	121586794	-1	18	14	8	22	22	11	429	2332	1112	384	1049	A1L361	Q9WUN2
ENSMUST00000020317	ENSMUSG00000020116	11	17203198	17211568	-1	2	2	2	43	11	0	24	135	39	208	62		Q9CPS7
ENSMUST00000020321	ENSMUSG00000020120	11	16971206	17052381	-1	0	0	0	0	0	0	1063	2451	85	0	0	Q8CAG6	
ENSMUST00000020322	ENSMUSG00000020121	10	121780991	122047315	-1	0	41	78	0	0	0	18	30	0	11	0		Q91Z69
ENSMUST00000020323	ENSMUSG00000020123	10	122448499	122453453	1	11	8	52	199	27	11	0	0	0	0	0	Q3U1H9	Q6J463
ENSMUST00000020329	ENSMUSG00000020122	11	16752203	16918158	1	132	130	172	202	217	114	4	6	4	13	25		Q01279
ENSMUST00000020334	ENSMUSG00000020124	10	123113244	123196935	-1	16	11	21	34	15	12	516	2636	1313	1768	804		Q8R5H1
ENSMUST00000020339	ENSMUSG00000020130	10	115197877	115251493	-1	7	5	11	26	11	8	1769	5107	2571	4157	1908		Q9CXF4
ENSMUST00000020340	ENSMUSG00000020131	10	80321283	80329498	-1	0	0	0	30	0	0	0	0	0	0	0		P29121
ENSMUST00000020341	ENSMUSG00000020133	10	80318254	80320537	-1	20	10	41	166	17	14	1531	1549	784	330	496		Q9D7E4
ENSMUST00000020343	ENSMUSG00000020132	10	115289863	115315591	-1	7	1	11	57	11	3	1020	2256	1248	169	739	Q0PD35	P35282
ENSMUST00000020346	ENSMUSG00000020137	10	115369966	115384435	-1	17	13	22	55	18	22	23	85	45	16	27		Q9D305
ENSMUST00000020349	ENSMUSG00000020135	10	80295977	80318263	1	1	0	63	524	48	60	3	5	1	0	0	G5E832	
ENSMUST00000020350	ENSMUSG00000020140	10	115450311	115587780	-1	27	27	75	95	26	8	0	9	1	2	3		Q9Z1P4
ENSMUST00000020358	ENSMUSG00000020149	11	20201432	20226856	1	0	0	0	72	0	0	114	3503	1793	498	1041	Q5SW88	
ENSMUST00000020359	ENSMUSG00000020150	10	80258151	80261012	-1	5	0	12	0	3	1	6	0	1	0	6		O35969
ENSMUST00000020361	ENSMUSG00000020153	10	80249121	80256794	1	0	0	0	0	0	0	378	466	263	98	201		Q9DC70
ENSMUST00000020362	ENSMUSG00000020155	11	33963013	33973641	1	142	123	458	365	160	92	1	6	4	0	13	Q5SQK1	
ENSMUST00000020365	ENSMUSG00000020156	10	80226434	80243903	1	0	0	0	91	0	14	55	79	40	26	41		Q6DID5
ENSMUST00000020366	ENSMUSG00000020159	11	33550781	33578959	-1	13	15	17	11	25	9	0	0	0	0	0		Q8QZW7
ENSMUST00000020372	ENSMUSG00000020163	10	80402997	80406830	-1	5	2	0	7	0	0	352	376	183	1187	116		Q9CPX8
ENSMUST00000020374	ENSMUSG00000020166	10	116485161	116581511	-1	0	0	0	0	0	0	0	0	1	0	0	H7BWX6	
ENSMUST00000020375	ENSMUSG00000064181	10	116905784	116950380	-1	18	16	39	25	19	14	52	148	81	21	73		Q68EF0
ENSMUST00000020377	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	1	0	0	0	245	34	56	15	72		
ENSMUST00000020378	ENSMUSG00000020169	10	116986314	117025040	1	18	21	57	86	18	12	0	0	0	0	0		Q6H1V1
ENSMUST00000020379	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	5	126	0	0	62	27	107	21	144		
ENSMUST00000020381	ENSMUSG00000020170	10	117070129	117148474	-1	32	19	66	63	35	18	281	553	490	51	377		Q8C180
ENSMUST00000020382	ENSMUSG00000020171	10	117215142	117224507	-1	5	5	19	59	11	2	269	1250	546	184	301		Q9CR11
ENSMUST00000020383	ENSMUSG00000003341	10	80519585	80539124	-1	38	39	101	81	47	29	0	0	0	0	0		Q6UQ17
ENSMUST00000020391	ENSMUSG00000020175	10	75037058	75054748	1	0	3	0	0	0	3	3	0	0	0	8		Q8CAM5
ENSMUST00000020392	ENSMUSG00000020177	10	117232237	117238703	-1	6	7	13	12	10	2	1	2	0	0	0	Q8BM26	
ENSMUST00000020397	ENSMUSG00000020180	10	75517551	75537373	1	13	21	37	28	23	17	275	789	301	1334	237		P62320
ENSMUST00000020399	ENSMUSG00000020183	10	117629500	117687352	1	34	31	48	52	47	35	0	17	2	2	10		Q80V42
ENSMUST00000020400	ENSMUSG00000060780	6	77242689	77257791	1	14	12	40	99	35	8	0	1	1	0	0		Q8K377
ENSMUST00000020403	ENSMUSG00000020186	10	110920177	110939599	1	5	5	7	30	7	4	83	112	34	174	63		P97314
ENSMUST00000020408	ENSMUSG00000020184	10	117688888	117710758	-1	0	0	0	14	0	0	180	1108	1153	224	1125		P23804
ENSMUST00000020410	ENSMUSG00000020191	11	11462094	11515192	1	0	0	4	0	1	0	1	0	0	0	0	F8WJ82	
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ENSMUST00000020413	ENSMUSG00000020193	11	11279626	11462408	-1	10	3	1	16	7	4	1	4	1	1	1	Q5NC84	
ENSMUST00000020420	ENSMUSG00000020198	10	80706978	80742211	-1	40	16	85	138	71	27	1995	3618	2751	249	2741		O54774
ENSMUST00000020434	ENSMUSG00000020214	10	112083354	112108098	1	0	5	0	2	2	0	0	0	0	0	0		Q9CQ35
ENSMUST00000020435	ENSMUSG00000020216	10	80808496	80813498	-1	0	2	2	106	0	1	1	0	1	1	0		Q3MI48
ENSMUST00000020437	ENSMUSG00000020212	10	118141787	118168997	1	0	0	32	0	0	0	113	265	278	76	167		Q9D067
ENSMUST00000020439	ENSMUSG00000020218	10	121033960	121100650	1	9	0	41	88	26	0	0	0	0	0	0	Q3TYU1	Q9WUA1
ENSMUST00000020440	ENSMUSG00000020219	10	80899450	80900969	-1	10	7	21	248	24	12	356	416	176	205	146		P62075
ENSMUST00000020441	ENSMUSG00000020220	4	144972622	145195005	-1	0	0	186	0	103	0	563	274	1238	0	1146	B1ART1	
ENSMUST00000020444	ENSMUSG00000020224	10	120227070	120232071	1	25	26	63	38	22	7	98	514	178	1067	170		Q9D945
ENSMUST00000020446	ENSMUSG00000020225	10	120201590	120224917	1	0	0	0	27	7	0	579	1320	457	421	235		Q9DA39
ENSMUST00000020448	ENSMUSG00000020227	10	120141648	120202130	-1	0	0	9	42	12	5	34	328	255	57	105	Q0VB14	Q8K4B2
ENSMUST00000020449	ENSMUSG00000020228	10	120083608	120112987	-1	36	36	53	172	49	15	235	843	589	102	580		Q6NVF4
ENSMUST00000020450	ENSMUSG00000020229	10	76147451	76189265	1	10	9	20	12	17	3	0	0	0	0	0	G5E836	
ENSMUST00000020452	ENSMUSG00000020230	10	76207222	76237865	-1	0	0	0	0	0	7	18	8	7	21	39	Q3UKX1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000020454	ENSMUSG00000020232	10	81346048	81350480	-1	0	0	0	54	0	0	0	0	55	12	0	Q3U1L0	Q9Z104
ENSMUST00000020456	ENSMUSG00000020234	10	81363067	81365816	-1	0	0	0	0	0	0	0	0	1	0	0		A6H6Q4
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ENSMUST00000020461	ENSMUSG00000055053	10	81396186	81431005	-1	0	0	23	220	0	0	40	0	258	0	233		P70255
ENSMUST00000020463	ENSMUSG00000020238	10	81486249	81496392	-1	11	11	35	115	41	18	19	436	198	49	132		Q8VCM8
ENSMUST00000020478	ENSMUSG00000020246	10	82696160	82742428	1	163	110	1346	246	110	50	78	330	280	61	105	G5E837	
ENSMUST00000020484	ENSMUSG00000020250	10	82859206	82897724	1	32	20	41	115	36	10	854	1984	1415	110	1061		Q9JMH6
ENSMUST00000020485	ENSMUSG00000020251	10	82650433	82690650	-1	7	10	8	11	3	4	0	0	0	0	0	E9QLV1	
ENSMUST00000020488	ENSMUSG00000020255	10	83360221	83368835	1	23	18	34	95	31	15	94	279	157	38	136		Q9CX66
ENSMUST00000020490	ENSMUSG00000020257	9	106170928	106191136	1	13	21	35	38	23	10	772	2102	1034	292	822	B2RXQ8	Q8BFQ4
ENSMUST00000020493	ENSMUSG00000020260	10	77259300	77269586	1	14	18	36	63	28	11	550	616	430	114	405	B2RV73	Q8VHI3
ENSMUST00000020496	ENSMUSG00000020262	10	77290726	77418270	-1	0	0	20	0	0	0	6	19	12	6	0		Q91ZS8
ENSMUST00000020497	ENSMUSG00000020256	10	83487450	83534140	-1	24	14	51	34	25	9	0	2	0	0	2		Q8K009
ENSMUST00000020499	ENSMUSG00000020261	11	55204350	55236330	1	0	0	0	0	0	0	0	0	20	0	48	Q5F227	Q8K4D3
ENSMUST00000020500	ENSMUSG00000020263	10	83600033	83648738	-1	0	0	3	73	11	0	46	289	188	24	144	Q3TVI6	Q8K3G9
ENSMUST00000020501	ENSMUSG00000020265	10	77606097	77641543	1	8	10	27	12	12	0	7	58	12	9	19		Q9Z172
ENSMUST00000020502	ENSMUSG00000049491	11	55124815	55151708	-1	0	0	0	11	5	6	16	50	27	0	0		Q811P0
ENSMUST00000020504	ENSMUSG00000020267	11	54866383	54870501	1	0	1	0	38	1	3	395	809	310	2284	362		P70349
ENSMUST00000020507	ENSMUSG00000057967	11	33117430	33147400	-1	11	0	33	29	13	4	0	0	0	0	0		O89101
ENSMUST00000020508	ENSMUSG00000020270	11	32818529	32824605	-1	8	2	7	12	0	0	0	0	0	0	0		Q9DAL0
ENSMUST00000020513	ENSMUSG00000020273	11	23862646	23895253	-1	7	6	9	19	13	6	147	437	167	247	153		Q6PCL9
ENSMUST00000020518	ENSMUSG00000020279	11	32187541	32200279	-1	0	2	4	3	9	0	2	0	0	1	4	F8WJ69	
ENSMUST00000020520	ENSMUSG00000020280	11	23665674	23732876	1	0	0	0	0	0	1	0	18	46	26	0		Q9D3U0
ENSMUST00000020522	ENSMUSG00000020277	10	77986947	78010083	-1	33	30	111	158	59	31	1895	1851	1492	242	1555		P12382
ENSMUST00000020523	ENSMUSG00000020283	11	23646479	23665959	-1	48	54	157	104	54	38	72	439	132	149	86		Q9D0K1
ENSMUST00000020524	ENSMUSG00000020282	11	32209585	32222300	-1	0	0	0	21	4	0	2	0	0	8	18		Q6PIX5
ENSMUST00000020527	ENSMUSG00000020286	11	23516203	23521155	-1	6	3	10	5	6	1	0	0	0	0	0		Q810S2
ENSMUST00000020528	ENSMUSG00000020287	11	32226505	32232700	1	0	0	0	0	4	0	41	77	33	22	37		Q04841
ENSMUST00000020529	ENSMUSG00000020288	11	23487882	23498030	-1	0	0	0	14	0	0	0	229	180	200	27		Q8N9S3
ENSMUST00000020530	ENSMUSG00000020289	11	32225628	32267707	-1	0	0	0	12	4	0	0	0	0	6	0		Q8VIJ8
ENSMUST00000020531	ENSMUSG00000055609	11	32276400	32278116	1	1	4	16	10	10	2	0	0	0	0	0	Q78PA4	P06467
ENSMUST00000020535	ENSMUSG00000020295	11	32300069	32300873	1	9	1	20	5	3	7	1	0	0	5	3	Q8BYM1	
ENSMUST00000020537	ENSMUSG00000020297	11	32000463	32059202	1	6	10	18	7	18	7	12	8	8	6	19	Q5SS02	P47759
ENSMUST00000020538	ENSMUSG00000020290	11	23256041	23298249	1	0	8	0	47	0	0	157	444	164	113	216		Q6P5F9
ENSMUST00000020543	ENSMUSG00000020300	11	31872211	31935634	1	5	10	38	8	3	9	66	138	385	6	332		Q7TN98
ENSMUST00000020546	ENSMUSG00000020303	11	31357307	31370074	-1	21	28	70	237	29	3	3	4	2	0	0	Q5SS12	O88452
ENSMUST00000020547	ENSMUSG00000055515	10	79247777	79294535	1	7	11	8	6	5	5	0	0	0	0	0	Q80Z09	
ENSMUST00000020549	ENSMUSG00000054206	10	79689020	79695261	1	4	6	9	5	6	6	20	28	12	5	14	O08643	
ENSMUST00000020550	ENSMUSG00000020307	10	79682195	79688394	1	0	0	0	35	0	0	0	93	0	13	7		Q8CFI2
ENSMUST00000020551	ENSMUSG00000020305	11	30885416	31102704	1	0	4	8	2	0	0	39	225	64	34	13		Q9WV72
ENSMUST00000020552	ENSMUSG00000020308	10	79669410	79676126	1	8	3	9	301	15	11	276	688	260	307	159	B2RRP1	Q99MS8
ENSMUST00000020553	ENSMUSG00000020309	11	30976707	30986350	-1	1	1	8	2	4	1	15	87	9	19	12		Q9CQG1
ENSMUST00000020554	ENSMUSG00000020310	10	79664574	79668536	1	7	4	40	71	17	7	0	0	0	0	0	G5E838	
ENSMUST00000020562	ENSMUSG00000007739	11	22990519	23003780	1	5	0	0	0	0	0	255	1508	447	784	334	G5E839	
ENSMUST00000020564	ENSMUSG00000020312	10	79617940	79637918	-1	0	0	0	63	0	0	0	0	0	1	1	E9QLZ0	
ENSMUST00000020566	ENSMUSG00000020317	10	79576379	79587331	-1	17	6	29	12	18	11	0	0	0	0	1		Q9JMB1
ENSMUST00000020568	ENSMUSG00000020319	11	21572235	21898989	1	5	2	18	33	6	7	0	6	7	32	9	B1ATJ7	Q8C456
ENSMUST00000020573	ENSMUSG00000020323	10	79781474	79790961	-1	0	2	0	5	0	9	145	183	146	48	45		Q14B24
ENSMUST00000020575	ENSMUSG00000020325	10	79777272	79782630	1	6	0	3	34	0	4	4	4	4	2	13	Q542M9	Q9EQC7
ENSMUST00000020576	ENSMUSG00000020326	11	40748552	40755311	-1	12	11	15	112	20	7	469	1839	915	1118	486	Q5NC86	P51945
ENSMUST00000020577	ENSMUSG00000020327	10	79755119	79756961	1	9	4	16	63	5	4	0	0	1	0	0		Q9ESS2
ENSMUST00000020578	ENSMUSG00000020328	11	40733667	40740046	1	0	3	0	16	3	2	26	53	26	53	5		Q9CQ48
ENSMUST00000020579	ENSMUSG00000020330	11	40701395	40733422	-1	487	502	482	384	549	293	89	288	214	183	180		Q00547
ENSMUST00000020580	ENSMUSG00000020329	10	79736123	79746581	-1	0	0	0	0	0	0	55	0	66	0	2	Q3U3J3	Q8BKF1
ENSMUST00000020581	ENSMUSG00000020331	10	79716634	79736108	1	7	8	14	0	24	0	1	0	0	0	1		O88703
ENSMUST00000020586	ENSMUSG00000020334	11	53983123	54028090	-1	19	11	33	70	15	9	16	142	34	18	26		Q9Z306
ENSMUST00000020608	ENSMUSG00000020349	11	52098681	52127778	1	112	99	253	160	99	42	1967	7202	2550	682	1650		P63330
ENSMUST00000020617	ENSMUSG00000020357	11	49609263	49652739	1	39	32	119	107	75	38	0	1	0	2	5	Q5SU94	P35917
ENSMUST00000020624	ENSMUSG00000020362	11	49671503	49712723	-1	0	0	0	58	0	2	132	189	307	0	44		Q8K3P5
ENSMUST00000020625	ENSMUSG00000020359	11	51584757	51604489	1	0	0	0	0	0	0	16	0	19	15	10		Q8R1K4
ENSMUST00000020628	ENSMUSG00000020364	11	51059257	51072799	1	0	0	0	0	2	0	0	0	0	0	0		Q61751
ENSMUST00000020629	ENSMUSG00000020363	11	49794178	49838613	1	36	14	31	22	39	12	0	4	0	5	25		Q9Z2Z9
ENSMUST00000020630	ENSMUSG00000020361	11	53259814	53300457	-1	10	7	14	63	16	5	288	1474	628	263	573	Q3U2G2	
ENSMUST00000020634	ENSMUSG00000020366	11	49846751	49886421	1	0	0	0	0	0	7	98	149	94	58	151	Q5NCK8	Q9WTU6
ENSMUST00000020637	ENSMUSG00000020368	11	50293961	50325673	-1	0	5	8	66	0	1	625	1669	869	641	901	Q5SUC3	P35564
ENSMUST00000020640	ENSMUSG00000020372	11	48800332	48806434	1	0	23	8	37	11	2	7635	6627	4892	10113	3613		P68040
ENSMUST00000020643	ENSMUSG00000020375	11	50389286	50431125	-1	6	7	14	140	26	15	197	879	402	87	337		Q8BIJ7
ENSMUST00000020647	ENSMUSG00000020381	11	50174444	50200115	1	8	4	20	9	8	6	5	9	8	33	9		Q9D1F5
ENSMUST00000020649	ENSMUSG00000020380	11	53649519	53707319	-1	26	18	29	23	22	14	68	251	203	50	135	Q5SV02	
ENSMUST00000020650	ENSMUSG00000020383	11	53631324	53634702	-1	10	6	15	9	13	5	2	1	1	1	1		P20109
ENSMUST00000020653	ENSMUSG00000020386	11	51763687	51791925	1	6	3	5	32	7	7	228	593	191	854	138	Q0VGU0	Q9CQC9
ENSMUST00000020655	ENSMUSG00000020387	11	51813455	51857653	-1	0	0	0	109	0	0	0	107	86	0	135		Q6ZQF7
ENSMUST00000020657	ENSMUSG00000020390	11	51985497	52000762	-1	6	3	9	19	12	2	1231	4428	922	1377	719	A2RSE4	P63147
ENSMUST00000020662	ENSMUSG00000020393	11	5191552	5261558	-1	30	12	93	71	50	30	1103	665	1420	114	852		Q99N43
ENSMUST00000020664	ENSMUSG00000020395	11	46325150	46389515	-1	0	6	26	16	0	3	108	202	90	9	39	Q5STT8	
ENSMUST00000020665	ENSMUSG00000020397	11	46436925	46442721	1	1	0	0	0	0	3	166	799	148	94	138		Q9CZB6
ENSMUST00000020668	ENSMUSG00000020399	11	46454935	46481255	1	0	0	56	0	38	0	14	28	0	56	0		Q8VIM0
ENSMUST00000020672	ENSMUSG00000020405	11	43596049	43601540	-1	3	4	3	6	4	3	0	0	0	0	1		P51162
ENSMUST00000020673	ENSMUSG00000020402	11	52360860	52389397	1	0	0	0	0	0	0	145	0	180	31	127		Q60932
ENSMUST00000020677	ENSMUSG00000020407	11	9118103	9136170	1	8	4	16	4	9	7	10	20	10	29	0	Q5SUC8	P52624
ENSMUST00000020679	ENSMUSG00000020411	11	46148155	46166508	-1	151	125	110	1338	218	126	4	12	7	2	12		Q8BZF2
ENSMUST00000020681	ENSMUSG00000020409	11	43433744	43447981	1	0	0	0	5	0	0	372	1153	821	1911	696		Q8BHJ9
ENSMUST00000020683	ENSMUSG00000020413	11	8993137	9011191	-1	16	0	0	37	0	0	43	65	69	28	32		Q8BQY8
ENSMUST00000020685	ENSMUSG00000020415	11	43420250	43426251	-1	0	0	0	0	0	0	111	62	40	81	39		Q9CQJ7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000020687	ENSMUSG00000020415	11	43420250	43426251	-1	4	0	1	13	0	1	0	80	62	133	0		Q9CQJ7
ENSMUST00000020689	ENSMUSG00000020419	11	4345814	4441105	-1	0	3	2	1	2	0	0	0	0	3	1	H7BWX7	
ENSMUST00000020692	ENSMUSG00000020423	1	134075170	134079120	-1	12	12	56	62	22	16	2139	10396	3317	643	3037	Q3TF68	Q04211
ENSMUST00000020695	ENSMUSG00000020422	11	8431652	8664535	-1	70	55	198	108	91	42	144	270	166	40	346		Q5SSZ5
ENSMUST00000020699	ENSMUSG00000020424	11	4218225	4222409	1	12	8	36	112	27	18	46	39	16	5	50		Q9CWQ8
ENSMUST00000020702	ENSMUSG00000020427	11	7206086	7213923	-1	10	6	2	13	7	2	0	0	0	2	7		P47878
ENSMUST00000020703	ENSMUSG00000020428	11	42306437	42321072	-1	0	3	0	3	2	0	0	0	0	0	0		P16305
ENSMUST00000020704	ENSMUSG00000020429	11	7197782	7202546	1	7	3	18	54	10	3	0	0	0	0	0		P47876
ENSMUST00000020705	ENSMUSG00000020430	11	3963975	3980004	1	22	0	19	40	24	14	300	584	369	473	334		Q9EQ61
ENSMUST00000020706	ENSMUSG00000020431	11	7063489	7178506	1	85	58	110	220	93	36	0	1	0	0	0		O88444
ENSMUST00000020707	ENSMUSG00000010803	11	42130939	42182930	-1	14	8	13	17	6	4	0	0	0	0	0	Q544F7	P62812
ENSMUST00000020710	ENSMUSG00000020432	11	3917192	3932159	-1	0	0	0	0	0	0	1977	2187	370	377	685		O88968
ENSMUST00000020712	ENSMUSG00000020434	11	3886088	3895098	-1	31	36	108	68	33	11	8	7	5	1	8		Q9CR34
ENSMUST00000020717	ENSMUSG00000020440	6	28423560	28426602	1	6	6	119	56	19	3	2324	4673	1690	597	1006		P84084
ENSMUST00000020718	ENSMUSG00000020439	11	3517523	3540612	-1	13	3	29	110	20	10	0	0	0	0	5	D3YVS1	
ENSMUST00000020719	ENSMUSG00000020441	11	59208321	59210738	1	3	4	19	41	23	5	83	244	117	20	80		Q99LX5
ENSMUST00000020721	ENSMUSG00000020439	11	3517523	3540612	-1	0	8	0	103	0	0	30	0	63	0	49		Q921U8
ENSMUST00000020732	ENSMUSG00000061462	11	58994256	59136402	-1	69	88	138	233	187	136	0	0	0	0	0	Z4YJE4	
ENSMUST00000020734	ENSMUSG00000020454	11	3202392	3244588	1	0	0	0	81	18	6	335	1106	224	134	488		Q9EST3
ENSMUST00000020741	ENSMUSG00000020457	11	3187360	3266415	-1	4	0	7	0	4	0	379	1017	402	443	272	Q5NBZ3	P32233
ENSMUST00000020749	ENSMUSG00000020459	11	29526408	29545279	1	110	98	154	8	76	0	26	111	55	93	60		Q91YJ5
ENSMUST00000020753	ENSMUSG00000020461	11	29547950	29578367	1	5	3	1	7	7	2	0	2	0	0	0		Q5M6W3
ENSMUST00000020754	ENSMUSG00000020462	11	29221532	29247409	-1	0	5	4	19	8	2	35	320	149	469	101		Q8C6E0
ENSMUST00000020755	ENSMUSG00000020463	11	29172890	29220797	1	13	12	4	4	7	5	692	2313	1080	575	677		Q922R5
ENSMUST00000020756	ENSMUSG00000020464	11	29130744	29161828	1	0	0	0	0	0	0	18	142	51	32	37		Q8K1R3
ENSMUST00000020759	ENSMUSG00000020467	11	28853204	28926743	1	8	5	0	19	6	6	0	0	0	0	0		Q8BPB5
ENSMUST00000020767	ENSMUSG00000020474	11	5827860	5838016	-1	17	17	38	66	29	0	153	37	76	13	165		Q9JIW4
ENSMUST00000020768	ENSMUSG00000020475	11	5801640	5803733	-1	3	4	2	10	9	2	112	120	194	17	102	Q5NCI4	O70250
ENSMUST00000020769	ENSMUSG00000020476	11	5788488	5800962	1	7	0	8	26	14	0	313	109	265	51	254		Q62418
ENSMUST00000020770						0	0	0	3	0	0	268	448	191	396	140		
ENSMUST00000020775	ENSMUSG00000020483	11	87979525	87987533	-1	0	0	0	114	0	0	0	82	72	10	71		Q9D0M5
ENSMUST00000020776	ENSMUSG00000020482	11	5528887	5542187	-1	13	17	34	103	33	14	417	1141	503	121	358		Q6PB51
ENSMUST00000020779	ENSMUSG00000009350	11	87793581	87804413	1	2	2	3	2	8	7	221	294	240	7	167		P11247
ENSMUST00000020792	ENSMUSG00000020490	11	58917908	58927158	1	0	0	0	0	0	0	0	0	0	0	0		Q9JK39
ENSMUST00000020794	ENSMUSG00000020492	11	87109234	87124635	1	62	64	142	56	67	34	29	81	30	47	35		Q9CR46
ENSMUST00000020801	ENSMUSG00000020495	11	87077732	87086774	-1	23	17	46	132	24	18	352	639	447	59	316		Q8VE18
ENSMUST00000020804	ENSMUSG00000061666	11	87033867	87074062	-1	15	5	7	47	15	3	0	4	0	16	3		Q9CRY7
ENSMUST00000020820	ENSMUSG00000020514	11	58171661	58179565	1	2	0	4	10	3	2	62	140	59	269	55		Q8BU88
ENSMUST00000020821	ENSMUSG00000020513	11	86544991	86567360	1	0	0	0	0	0	0	0	0	0	0	0	Q8CDD3	
ENSMUST00000020822	ENSMUSG00000020515	11	58104153	58118594	1	13	0	0	71	13	4	743	2772	997	544	762		Q9D8X5
ENSMUST00000020824						0	0	9	20	0	0	48	367	173	124	100		
ENSMUST00000020826	ENSMUSG00000020519	11	57801637	57810217	1	3	1	3	74	7	6	355	558	341	229	287		Q5SQF8
ENSMUST00000020827	ENSMUSG00000020521	11	86484657	86499025	1	18	5	9	19	8	7	91	328	107	63	67		Q9DCN7
ENSMUST00000020830	ENSMUSG00000020522	11	57518664	57533815	1	3	2	44	16	37	17	71	118	177	0	116		
ENSMUST00000020831	ENSMUSG00000020523	11	57482993	57518617	-1	12	17	31	56	24	13	260	1253	562	347	445		Q8VE88
ENSMUST00000020835	ENSMUSG00000020525	11	85311244	85347066	1	14	8	24	132	18	11	260	956	512	102	316		Q9QZ67
ENSMUST00000020837	ENSMUSG00000020527	11	84880148	84911226	1	9	9	88	18	23	8	0	2	1	1	5		Q5SV80
ENSMUST00000020843	ENSMUSG00000020532	11	84129672	84401651	1	0	1	0	0	0	0	201	280	540	48	499		Q5SWU9
ENSMUST00000020846	ENSMUSG00000020538	11	60199089	60222581	-1	20	12	0	164	22	20	865	839	906	123	817		Q9WTN3
ENSMUST00000020849	ENSMUSG00000020541	11	90643465	90688366	-1	15	10	12	22	8	4	4	38	10	0	8		Q923U0
ENSMUST00000020851	ENSMUSG00000020544	11	90638173	90644931	1	0	1	1	265	7	0	10	75	23	10	20		Q6P8I6
ENSMUST00000020853	ENSMUSG00000020545	12	36208345	36253398	-1	6	5	2	4	4	0	0	3	0	0	0	Q9D9C3	
ENSMUST00000020855	ENSMUSG00000020548	11	65151910	65159891	-1	4	2	0	2	6	2	0	0	0	0	0	Q9D9E9	
ENSMUST00000020856	ENSMUSG00000020547	12	36091846	36156825	-1	9	9	5	58	14	8	56	281	82	377	155		Q91VK1
ENSMUST00000020858	ENSMUSG00000020546	11	90476492	90638084	-1	5	1	6	19	4	1	0	0	3	0	0		Q9WV89
ENSMUST00000020864	ENSMUSG00000020553	11	89982665	90002894	-1	26	26	80	65	42	14	47	110	63	15	48	Q5SV41	
ENSMUST00000020877	ENSMUSG00000020561	12	33429624	33439380	1	10	4	7	102	17	4	145	858	303	154	153	B2RT77	Q78WZ7
ENSMUST00000020878	ENSMUSG00000020562	12	33394854	33401269	1	6	5	3	2	5	2	0	0	0	0	0		Q9D581
ENSMUST00000020884	ENSMUSG00000020566	12	17284721	17329359	-1	3	0	8	0	6	0	0	0	0	0	0		Q99L60
ENSMUST00000020885	ENSMUSG00000020570	12	32953891	32979050	1	0	0	0	56	1	0	820	1375	558	347	262	Q3TVX7	O09117
ENSMUST00000020886	ENSMUSG00000020572	12	32820335	32853369	1	14	18	21	35	13	2	422	2765	848	1440	758		Q99KQ4
ENSMUST00000020896	ENSMUSG00000020577	12	36014557	36042500	-1	18	19	29	25	24	13	1474	6733	1664	1177	1875		Q9D8C2
ENSMUST00000020898	ENSMUSG00000020581	12	35992907	36004087	1	2	0	0	3	6	1	0	0	0	0	0		O88312
ENSMUST00000020899	ENSMUSG00000020583	12	8947929	8972028	1	15	8	20	79	17	10	1	3	0	0	1		O35701
ENSMUST00000020904	ENSMUSG00000020580	12	16894978	16988274	1	21	25	28	28	21	11	277	1051	776	131	618	F8VPK5	
ENSMUST00000020908	ENSMUSG00000057469	12	16810965	16826743	1	19	17	27	123	11	9	32	100	26	15	45		O54917
ENSMUST00000020909	ENSMUSG00000020585	12	8921664	8938742	1	10	12	7	112	20	8	1998	5458	1564	1416	1116	E9QLR3	
ENSMUST00000020911	ENSMUSG00000020592	12	8771323	8793715	1	11	11	32	52	24	0	4	7	0	59	47	Q3V1F2	P18828
ENSMUST00000020915	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	0	0	0	41	5	44	0	89	Q3TQ29	
ENSMUST00000020920	ENSMUSG00000020599	11	109225355	109298129	-1	0	0	3	107	0	6	0	0	0	0	0		O54828
ENSMUST00000020922	ENSMUSG00000020601	12	15791727	15816877	-1	20	17	32	132	37	19	44	115	55	26	186		Q8K4K3
ENSMUST00000020926	ENSMUSG00000020607	12	14147599	14152038	-1	11	10	48	403	30	17	0	0	0	0	1		
ENSMUST00000020927	ENSMUSG00000020605	12	8313433	8343824	1	20	14	44	67	30	14	376	436	244	35	157		Q3TC93
ENSMUST00000020928	ENSMUSG00000020604	11	109473374	109573330	1	0	7	0	0	0	9	0	32	0	0	6		Q3TYD4
ENSMUST00000020929	ENSMUSG00000020610	11	109425946	109452813	1	3	0	0	0	0	0	40	253	71	30	26	B1AT60	
ENSMUST00000020930	ENSMUSG00000020611	11	109362831	109401369	1	87	50	367	158	74	38	1243	3673	2471	260	1742		P27601
ENSMUST00000020931	ENSMUSG00000020608	12	11265886	11319785	1	39	41	154	116	39	14	293	1044	667	248	475		Q924W5
ENSMUST00000020938	ENSMUSG00000020614	11	109669749	109722279	-1	4	0	15	150	0	0	11	0	0	15	89		Q8CID3
ENSMUST00000020939	ENSMUSG00000020598	12	44328885	44601846	1	59	0	98	72	0	0	0	0	0	0	0		Q810U4
ENSMUST00000020941	ENSMUSG00000020617	11	109787651	109828046	-1	0	0	5	0	0	0	0	0	0	0	0	Q9DAE9	
ENSMUST00000020947	ENSMUSG00000020621	12	10390780	10395562	1	1	3	5	186	12	5	45	143	59	70	53		Q9ERI6
ENSMUST00000020948	ENSMUSG00000020620	11	109932190	109995845	-1	72	70	80	65	87	50	5	8	5	5	6	A2AM56	Q8K440
ENSMUST00000020949	ENSMUSG00000020623	11	110399122	110525522	1	0	0	0	4	11	5	18	31	32	11	26	Q543Z5	P70236
ENSMUST00000020954	ENSMUSG00000020628	12	28690629	28750453	-1	0	7	19	19	16	7	90	65	86	23	90		Q8K2L8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000020957	ENSMUSG00000020629	12	28675231	28682175	1	284	245	279	251	326	171	69	180	70	22	98		Q99JT9
ENSMUST00000020958	ENSMUSG00000020627	12	5077472	5375682	-1	41	31	74	401	54	24	0	0	1	0	1		Q80T74
ENSMUST00000020959	ENSMUSG00000020630	12	28649602	28659591	1	5	4	12	96	13	6	69	219	86	110	105	E9QLN8	
ENSMUST00000020962	ENSMUSG00000020634	12	4879032	4907705	-1	31	33	166	72	34	19	72	401	211	40	166		Q99KJ0
ENSMUST00000020963	ENSMUSG00000020633	12	28437795	28552303	-1	1	1	4	110	8	2	0	0	0	0	0	K3W4L8	
ENSMUST00000020964	ENSMUSG00000020635	12	4833175	4841595	-1	7	5	6	122	12	3	61	179	60	33	35	A9E3L2	Q9Z2I2
ENSMUST00000020965	ENSMUSG00000020636	12	28553755	28582523	-1	12	0	13	18	14	0	0	0	0	0	0		Q9JHX6
ENSMUST00000020967	ENSMUSG00000020639	12	4769295	4778266	1	7	4	23	10	11	1	0	1	0	0	0	Q6JEK6	Q9D6I3
ENSMUST00000020969	ENSMUSG00000020638	12	26469204	26479835	1	15	12	36	353	41	12	69	431	138	17	214		Q3U5Q7
ENSMUST00000020970	ENSMUSG00000020641	12	26442753	26456452	-1	17	14	74	34	10	9	28	199	18	60	154		Q8CBB9
ENSMUST00000020971	ENSMUSG00000020642	12	26306797	26415256	-1	33	0	69	0	19	0	1234	1965	1744	275	1587		Q925F3
ENSMUST00000020974	ENSMUSG00000020644	12	25093801	25096092	-1	2	5	17	48	8	5	1069	5338	2141	3824	1202	Q545T4	P41136
ENSMUST00000020977	ENSMUSG00000020648	12	31640055	31654826	-1	10	5	8	57	11	2	7	37	12	22	8		
ENSMUST00000020979	ENSMUSG00000020650	12	31595354	31634658	-1	0	0	0	14	5	0	0	0	8	0	0	Q542A1	Q61334
ENSMUST00000020980	ENSMUSG00000020649	12	24708241	24714146	1	15	17	15	153	33	12	400	498	448	49	190		P11157
ENSMUST00000020981	ENSMUSG00000020652	12	4196004	4234294	-1	0	0	0	2	0	0	121	304	139	88	78	B8JK52	
ENSMUST00000020982	ENSMUSG00000020653	12	24651371	24662774	1	123	75	686	181	84	32	190	703	259	53	311		Q8K1S5
ENSMUST00000020984	ENSMUSG00000020654	12	4133103	4213525	1	0	0	0	0	0	0	0	8	11	2	8		Q8VHH7
ENSMUST00000020985	ENSMUSG00000020656	12	24572287	24617391	1	1	5	0	0	0	0	0	27	0	0	4	E9QMF0	
ENSMUST00000020986	ENSMUSG00000020657	12	4082574	4110612	1	24	31	64	102	57	34	11	29	21	5	35		Q8CFP6
ENSMUST00000020990	ENSMUSG00000020660	12	3954951	3960618	1	9	5	37	247	24	11	1	4	0	0	1		P01193
ENSMUST00000020991	ENSMUSG00000020661	12	3806007	3914443	1	71	57	122	42	91	41	0	142	0	10	61		O88508
ENSMUST00000020997	ENSMUSG00000020669	12	30911668	30960162	1	2	0	0	55	0	0	21	36	34	8	17		O08641
ENSMUST00000020999	ENSMUSG00000020668	12	3365132	3406494	1	39	35	131	148	75	34	60	57	47	9	94		O35066
ENSMUST00000021001	ENSMUSG00000020671	12	3247430	3309969	-1	8	13	18	217	22	7	771	2371	1197	298	827	Q4FJL0	P61027
ENSMUST00000021004	ENSMUSG00000020672	12	30174482	30373375	-1	13	11	0	47	0	11	0	0	0	0	0		Q925E0
ENSMUST00000021005	ENSMUSG00000020673	12	30054659	30132624	-1	21	10	31	63	21	7	0	0	0	0	0		P35419
ENSMUST00000021009	ENSMUSG00000061911	12	29528384	29923209	1	16	22	15	53	44	20	0	1	0	0	2	E9QLD2	
ENSMUST00000021011	ENSMUSG00000035373	11	82045712	82047525	1	1	3	4	4	3	4	0	0	0	116	9	A9Z1Z1	Q03366
ENSMUST00000021016	ENSMUSG00000020679	11	83850063	83905819	1	0	7	0	22	0	15	0	0	0	0	0		P27889
ENSMUST00000021018	ENSMUSG00000020680	11	83473086	83506743	1	14	8	26	27	16	7	226	1045	551	113	450	Q8BQ46	
ENSMUST00000021020	ENSMUSG00000020682	11	83440768	83463071	-1	0	0	0	13	11	7	0	0	0	0	0	Q8CGV5	
ENSMUST00000021022	ENSMUSG00000020684	11	83409137	83421039	1	6	2	2	55	5	0	0	0	0	0	1		Q5SSG5
ENSMUST00000021028	ENSMUSG00000020689	11	104608000	104670476	1	51	24	96	133	51	52	232	322	255	56	366		O54890
ENSMUST00000021029	ENSMUSG00000020690	11	105063592	105117537	1	6	4	4	8	5	3	0	0	0	0	0		Q80X60
ENSMUST00000021030	ENSMUSG00000020691	11	105126425	105140394	1	0	0	0	6	0	3	3	20	11	0	22		Q8BMK1
ENSMUST00000021033	ENSMUSG00000018841	11	82876434	82890614	-1	6	0	0	0	7	5	29	10	55	0	0	Q9EP85	
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ENSMUST00000021038	ENSMUSG00000020695	11	105292643	105351139	1	6	3	4	1	2	5	3	0	0	0	0	A2AAA9	
ENSMUST00000021039	ENSMUSG00000020697	11	82781108	82804274	1	15	6	4	27	25	0	9	0	0	0	0	K4DI59	
ENSMUST00000021040	ENSMUSG00000020698	11	82719250	82764321	-1	11	10	0	0	0	0	1	8	2	7	7	Q497N0	Q61390
ENSMUST00000021043	ENSMUSG00000020702	11	82176657	82305690	-1	3	0	4	3	3	4	0	0	0	0	0	B1AVL8	
ENSMUST00000021044	ENSMUSG00000020703	11	81860673	81894582	1	10	3	2	4	9	0	0	0	0	0	0	Q9D3H9	
ENSMUST00000021045	ENSMUSG00000020704	11	80880169	81968457	-1	11	18	64	449	33	14	0	0	0	0	0	B2RRQ1	Q925H0
ENSMUST00000021046	ENSMUSG00000020705	11	106216926	106249139	1	18	13	46	112	37	18	388	1582	823	220	708		Q810A7
ENSMUST00000021048	ENSMUSG00000020706	11	106249142	106256079	-1	8	7	22	20	11	6	66	335	155	291	284		Q9DBE9
ENSMUST00000021049	ENSMUSG00000020708	11	106256154	106263120	1	0	8	0	0	0	8	471	975	456	717	395		P62196
ENSMUST00000021050	ENSMUSG00000020709	11	80154105	80178958	1	14	10	23	43	25	9	6	23	11	13	49	Q5SSK2	Q8R2V5
ENSMUST00000021052	ENSMUSG00000078619	11	106263179	106272972	-1	0	2	19	120	2	4	2272	1632	1788	218	1363		Q99JR8
ENSMUST00000021056	ENSMUSG00000001027	11	106318592	106353288	-1	43	39	145	66	72	55	11	6	8	3	22	G3X8T7	
ENSMUST00000021060	ENSMUSG00000020718	11	106768253	106779537	-1	1	0	0	0	0	1	21	157	25	14	20		Q9QZM2
ENSMUST00000021062	ENSMUSG00000020719	11	106780355	106789185	-1	7	5	9	20	13	3	1971	23372	4077	1601	2880	Q8BTS0	
ENSMUST00000021063	ENSMUSG00000020720	11	107479484	107504362	1	9	4	14	175	10	3	108	413	186	256	145		Q9D8W5
ENSMUST00000021065	ENSMUSG00000020722	11	107703218	107716522	-1	11	7	22	44	13	5	0	0	0	0	0	Q4KL26	O70578
ENSMUST00000021066	ENSMUSG00000020723	11	107732357	107794557	-1	52	34	195	257	62	25	1	6	1	0	1	A2AAU2	Q9JJV4
ENSMUST00000021071	ENSMUSG00000051043	11	114851152	114872617	1	3	2	0	261	26	5	0	0	0	0	0	J3JS84	
ENSMUST00000021076	ENSMUSG00000020732	11	115091431	115162236	1	10	9	11	70	14	14	225	559	221	157	239	Q544E8	
ENSMUST00000021077	ENSMUSG00000020733	11	115163341	115181181	1	14	8	65	238	27	14	6755	6956	5125	964	3943	Q3TG37	P70441
ENSMUST00000021078	ENSMUSG00000018861	11	115268024	115277050	-1	5	0	21	37	11	0	116	144	91	24	92		Q61578
ENSMUST00000021079						5	0	0	49	11	0	0	0	0	0	0		
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ENSMUST00000021083	ENSMUSG00000020737	11	115497353	115514387	-1	18	11	37	50	20	12	1105	1504	597	397	672		P97825
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ENSMUST00000021085	ENSMUSG00000020739	11	115564434	115583985	1	0	0	10	124	10	7	71	88	74	16	110		Q8R480
ENSMUST00000021087	ENSMUSG00000020743	11	115607918	115612969	-1	0	0	15	34	0	0	581	829	409	122	329		Q3UBZ5
ENSMUST00000021089	ENSMUSG00000020744	11	115614178	115628295	-1	5	0	18	18	4	7	86	141	57	20	52		Q9DAM5
ENSMUST00000021090	ENSMUSG00000059923	11	115644045	115708597	-1	0	0	0	14	0	0	3155	4295	3867	405	2338	Q3U5I5	Q60631
ENSMUST00000021091	ENSMUSG00000020745	11	74673949	74724670	-1	0	3	0	81	0	0	1192	4386	1992	579	1235	Q5SW18	P63005
ENSMUST00000021097	ENSMUSG00000020752	11	115892595	115933477	-1	0	1	0	6	0	7	299	294	302	34	207		Q8VID5
ENSMUST00000021101						0	0	0	10	0	0	119	124	102	483	97		
ENSMUST00000021107	ENSMUSG00000020758	11	115974709	116008412	1	0	0	0	24	0	0	0	0	0	6	19	A2A864	
ENSMUST00000021114	ENSMUSG00000020766	11	116008457	116012719	-1	9	6	29	98	24	6	69	63	19	55	104		Q9R0N0
ENSMUST00000021116	ENSMUSG00000020770	11	116030322	116061214	1	0	0	0	87	37	0	0	127	66	0	45		Q8BL48
ENSMUST00000021119	ENSMUSG00000020774	11	73304992	73329596	-1	5	0	0	0	2	0	2	0	0	33	9		Q8R3P0
ENSMUST00000021120	ENSMUSG00000020773	11	116105752	116127210	-1	0	0	0	257	4	11	0	0	0	0	29		Q8C0E3
ENSMUST00000021130	ENSMUSG00000020778	11	116198855	116215318	1	2	0	0	3	1	0	204	259	138	148	94		Q9D7K2
ENSMUST00000021133	ENSMUSG00000020780	11	116245166	116274217	-1	0	0	5	19	6	5	301	469	404	76	462		Q8BMA6
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ENSMUST00000021135	ENSMUSG00000020783	11	73047783	73089317	1	20	9	60	78	13	13	316	937	581	235	381		Q8BZR9
ENSMUST00000021141	ENSMUSG00000020787	11	72999103	73015200	1	19	15	12	16	24	5	134	211	125	49	95		P51576
ENSMUST00000021142	ENSMUSG00000020788	11	72961169	72993044	1	0	0	0	39	48	0	1592	1673	1165	161	1403		Q64518
ENSMUST00000021147	ENSMUSG00000020792	11	116288001	116307233	-1	0	0	0	11	0	0	0	0	0	0	0	Q3USE0	O35250
ENSMUST00000021148	ENSMUSG00000020794	11	72607283	72686481	1	9	9	8	32	0	0	300	594	211	10	138	Q5F239	P62254
ENSMUST00000021154	ENSMUSG00000020798	11	72494919	72550506	-1	0	0	0	9	9	0	61	4	0	6	29		Q9D232

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000021155	ENSMUSG00000020799	11	72344722	72362442	-1	0	5	8	0	4	0	0	0	0	0	0	Q5NBU4	Q9DAJ2
ENSMUST00000021157	ENSMUSG00000020801	11	72211724	72215592	-1	3	9	6	183	16	1	171	301	155	540	102		Q9CXU1
ENSMUST00000021158	ENSMUSG00000020803	11	72207547	72210015	1	8	12	18	57	13	8	489	2223	644	2282	444		Q9CQM5
ENSMUST00000021160	ENSMUSG00000020804	11	116586432	116597680	1	0	0	0	0	0	0	0	0	1	0	0	Q9QUP1	
ENSMUST00000021161	ENSMUSG00000020805	11	72241994	72267222	-1	26	15	28	23	26	17	0	0	0	1	0		Q67BT3
ENSMUST00000021164	ENSMUSG00000020808	11	72042032	72047370	1	15	5	23	40	15	7	77	42	59	29	31		Q8BFY7
ENSMUST00000021166	ENSMUSG00000020810	11	116645595	116654313	-1	23	28	31	649	39	25	0	0	0	1	3	Q546K1	Q9CX80
ENSMUST00000021168	ENSMUSG00000020811	11	71749920	71789647	1	17	11	80	59	30	9	0	0	0	0	0		Q80XH4
ENSMUST00000021170	ENSMUSG00000020814	11	116803062	116828046	-1	36	22	173	84	33	17	15	50	16	3	31		Q9CZH7
ENSMUST00000021173	ENSMUSG00000020818	11	116852440	116875635	1	48	54	67	22	64	29	95	356	186	180	214		Q8BJ51
ENSMUST00000021177	ENSMUSG00000020823	11	117115168	117159268	1	0	0	0	0	0	0	153	7	466	24	237	A2A9B9	
ENSMUST00000021179	ENSMUSG00000020830	11	70513516	70514616	-1	6	3	22	3	14	2	0	0	0	0	0		Q5SXG7
ENSMUST00000021180	ENSMUSG00000020831	11	70235206	70237914	-1	0	0	0	0	0	0	10	1	13	0	0	F8WH46	
ENSMUST00000021181	ENSMUSG00000020831	11	70235206	70237914	-1	0	0	0	0	0	0	0	0	18	65	0		Q9DCT6
ENSMUST00000021183	ENSMUSG00000020832	11	78073376	78080383	-1	51	0	150	5	53	11	118	111	88	16	41		Q9CZU4
ENSMUST00000021187	ENSMUSG00000020834	11	78032280	78037866	1	7	4	13	46	13	0	40	112	13	7	18		Q5SS80
ENSMUST00000021190	ENSMUSG00000020836	11	77462411	77470484	1	0	0	0	15	0	1	0	0	0	0	0		Q920M5
ENSMUST00000021195	ENSMUSG00000020838	11	76998603	77032340	1	0	9	47	0	0	4	15	11	8	15	28		Q60857
ENSMUST00000021197	ENSMUSG00000020840	11	76924809	76987379	1	14	8	31	134	13	9	166	527	225	155	163		Q8R016
ENSMUST00000021201	ENSMUSG00000020841	11	76778424	76847018	-1	35	22	61	302	41	28	7516	23307	19403	1683	9047		O89001
ENSMUST00000021203	ENSMUSG00000020843	11	76406952	76416292	1	23	14	27	33	26	19	90	127	49	40	50		Q9CQ85
ENSMUST00000021204	ENSMUSG00000020844	11	76257198	76399140	-1	17	9	22	61	26	11	733	1067	565	94	388		P97346
ENSMUST00000021207	ENSMUSG00000020846	11	76019194	76027782	-1	64	68	324	307	90	44	3940	15444	8986	877	5615		Q5SVD0
ENSMUST00000021208	ENSMUSG00000020847	11	75830999	75938429	-1	20	17	24	6	12	14	1	4	0	0	2		Q768S4
ENSMUST00000021209	ENSMUSG00000020848	11	75768966	75796049	-1	42	17	56	90	40	15	0	0	0	0	0		P70169
ENSMUST00000021217	ENSMUSG00000020857	11	93949814	93956259	-1	19	7	9	222	20	19	248	382	216	1130	213	Q5NC82	Q01768
ENSMUST00000021220	ENSMUSG00000037601	11	93956979	93968521	-1	4	0	3	1	0	1	33	37	31	148	33	Q5NC80	
ENSMUST00000021226	ENSMUSG00000020863	11	94287890	94321988	-1	0	1	5	5	0	4	10	0	6	0	36		Q5SUF2
ENSMUST00000021227	ENSMUSG00000020864	11	94328001	94341841	1	3	1	2	8	6	2	18	31	92	0	38		Q5SUE8
ENSMUST00000021231	ENSMUSG00000020865	11	94343295	94392997	-1	25	0	46	0	30	12	0	0	46	13	143		
ENSMUST00000021234	ENSMUSG00000020866	11	94408391	94474198	-1	0	0	0	239	0	0	0	0	0	0	0	E9PWL1	
ENSMUST00000021239	ENSMUSG00000020869	11	94629767	94645216	1	16	10	31	47	24	10	727	1254	863	214	817		Q922Q8
ENSMUST00000021240	ENSMUSG00000020870	11	94741782	94743033	1	9	1	23	80	9	5	0	0	0	0	0		
ENSMUST00000021241	ENSMUSG00000020871	11	95140447	95146263	-1	10	7	32	104	20	14	0	0	0	0	2		P70436
ENSMUST00000021242	ENSMUSG00000020872	11	95261529	95269265	1	18	13	36	23	16	5	1	1	0	2	1		Q99N14
ENSMUST00000021243	ENSMUSG00000020873	11	95384692	95391776	1	0	0	20	28	12	0	85	142	48	114	118		P97858
ENSMUST00000021246	ENSMUSG00000020876	11	96767555	96777559	-1	15	6	28	9	16	7	201	629	253	23	276		Q91WL6
ENSMUST00000021249	ENSMUSG00000020877	11	97029938	97033958	1	16	9	0	13	8	10	15	22	9	8	13		Q8VCA8
ENSMUST00000021251	ENSMUSG00000020878	11	97034602	97041407	-1	11	7	21	13	18	10	17	56	15	22	13		Q9DAP0
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ENSMUST00000021262	ENSMUSG00000020891	11	69183932	69197843	-1	78	54	100	60	57	43	21	22	14	1	22		O35936
ENSMUST00000021268	ENSMUSG00000020892	11	69125896	69149115	1	17	7	44	25	24	20	38	76	63	8	19		Q9WV07
ENSMUST00000021271	ENSMUSG00000020893	11	69095217	69109960	1	0	0	0	83	0	15	1177	883	1362	0	1905		O35973
ENSMUST00000021273	ENSMUSG00000020894	11	69088490	69092384	1	8	11	20	47	5	14	360	1351	366	56	585	Q8CHR4	P63044
ENSMUST00000021277	ENSMUSG00000020897	11	69045647	69051664	1	0	10	14	0	0	0	137	136	135	12	88		O70126
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ENSMUST00000021282	ENSMUSG00000020899	11	68985697	69008460	-1	19	0	104	47	33	9	95	134	126	3	151		Q5SUR0
ENSMUST00000021283	ENSMUSG00000020901	11	68432121	68497849	1	282	167	1823	423	190	102	2940	7450	4974	438	5031	A1A4T4	Q5SW28
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ENSMUST00000021285	ENSMUSG00000020903	11	67966193	68207148	1	26	20	43	32	34	18	45	126	45	270	44		O88983
ENSMUST00000021286	ENSMUSG00000020903	11	67966193	68207148	1	90	71	223	447	127	50	24	104	47	84	25	Q9D0J1	
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ENSMUST00000021289	ENSMUSG00000049928	11	67661502	67771153	-1	5	6	14	13	17	12	0	0	0	0	1	Q8BM22	
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ENSMUST00000021296	ENSMUSG00000020921	11	102152546	102156404	-1	11	12	22	30	16	7	201	191	112	25	65		Q91VP7
ENSMUST00000021297	ENSMUSG00000020922	11	102162497	102185296	-1	0	0	0	27	0	1	281	798	350	212	196		Q9D0R8
ENSMUST00000021302	ENSMUSG00000020928	11	102835849	102838040	1	4	1	5	5	10	5	0	0	0	0	0		Q99JY6
ENSMUST00000021306	ENSMUSG00000020929	11	102838473	102880985	-1	0	6	13	0	0	4	0	93	145	87	3	A2AH85	
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ENSMUST00000021311	ENSMUSG00000051378	11	102905529	102925124	-1	36	18	79	70	48	14	127	86	127	14	62		Q6PFD6
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ENSMUST00000021314	ENSMUSG00000020936	11	103028190	103068912	1	35	14	52	46	50	22	749	2654	1128	844	924	Q3UJC3	O70310
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ENSMUST00000021324	ENSMUSG00000020941	11	103219762	103267472	-1	30	10	85	78	47	19	864	870	610	63	660	Q544K4	Q9WUL6
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ENSMUST00000021329	ENSMUSG00000020946	11	103676849	103697898	-1	18	19	62	127	35	25	1412	2776	1601	585	965		O35166
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ENSMUST00000021335	ENSMUSG00000020952	12	51377580	51450096	1	11	6	2	4	9	1	95	810	319	751	210		Q8BRF7
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ENSMUST00000021339	ENSMUSG00000020956	12	51988312	52006501	-1	18	19	11	44	17	12	9	23	7	10	7		Q8BHA3
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ENSMUST00000021347	ENSMUSG00000020964	12	91806043	91849157	-1	0	0	0	27	7	0	836	1246	571	83	342		Q9Z2G6
ENSMUST00000021356	ENSMUSG00000020973	12	69189087	69198429	-1	34	21	90	791	40	14	38	147	49	25	65		Q8BPI1
ENSMUST00000021359	ENSMUSG00000020974	12	69201779	69228190	-1	7	3	15	23	3	9	16	70	23	74	31		O54956
ENSMUST00000021362	ENSMUSG00000020978	12	69296681	69310687	1	6	8	8	8	5	4	271	1337	387	154	274		Q4G5Y1
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ENSMUST00000021372	ENSMUSG00000054894	12	69724962	69744658	1	4	4	4	20	6	2	9	24	8	23	10		Q9CRA7

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ENSMUST00000021375	ENSMUSG00000020986	12	58958383	59012017	-1	7	13	19	5	13	3	193	281	155	214	137		Q01405
ENSMUST00000021377	ENSMUSG00000020990	12	69746848	69790707	-1	11	5	12	22	21	2	0	1	1	0	1	Q14BG3	Q8CEQ0
ENSMUST00000021379	ENSMUSG00000060121	12	59013393	59028470	1	14	0	28	29	13	7	16	141	48	68	39		Q9CQQ4
ENSMUST00000021380	ENSMUSG00000020993	12	59043093	59061461	-1	5	3	7	243	9	2	287	1256	426	198	266		Q9D289
ENSMUST00000021381	ENSMUSG00000020994	12	59066919	59074017	1	6	2	15	56	12	13	178	974	469	456	548	Q3TUQ5	
ENSMUST00000021384	ENSMUSG00000035349	12	59095799	59109130	1	5	5	6	14	12	4	12	9	45	10	24		Q91ZV0
ENSMUST00000021390	ENSMUSG00000021003	12	98202304	98259459	-1	17	17	22	70	21	12	511	1544	926	127	672		P54818
ENSMUST00000021399	ENSMUSG00000021012	12	98746968	98787774	1	2	0	0	0	2	0	0	0	0	0	0		Q8BJ05
ENSMUST00000021405	ENSMUSG00000021018	16	20717665	20722267	1	8	6	10	74	11	6	200	564	145	359	90		Q923G2
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ENSMUST00000021407	ENSMUSG00000073079	12	55089202	55112891	1	0	0	0	0	0	0	80	489	181	127	126		P14576
ENSMUST00000021410	ENSMUSG00000021022	12	55280814	55303000	-1	8	9	21	10	8	3	190	1306	395	550	207		Q9JK24
ENSMUST00000021411	ENSMUSG00000021023	12	55299577	55382533	1	0	5	0	0	0	0	18	18	15	11	8		Q8JZY4
ENSMUST00000021412	ENSMUSG00000021024	12	55384222	55418454	1	0	2	0	11	0	0	735	3881	997	2704	633		Q9QUM9
ENSMUST00000021413	ENSMUSG00000021025	12	55489411	55492647	-1	11	11	39	44	17	7	1619	4993	3249	964	2629		Q9Z1E3
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ENSMUST00000021420	ENSMUSG00000021032	12	87097531	87102539	-1	16	0	0	93	1	0	0	0	0	0	0	Q5ZPR7	Q9ER97
ENSMUST00000021423	ENSMUSG00000072919	12	87221255	87233556	-1	8	4	9	9	9	4	117	789	129	170	95		Q9D3S5
ENSMUST00000021424	ENSMUSG00000021036	12	87305058	87388355	-1	18	24	41	54	29	14	691	2998	1311	319	996	Q542D6	P97363
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ENSMUST00000021428	ENSMUSG00000021039	12	87449936	87472299	-1	20	18	10	14	8	7	485	1851	933	2596	681	A0A0B4J1E2	
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ENSMUST00000021443	ENSMUSG00000021048	12	76255232	76319820	1	22	27	46	105	26	20	46	119	55	46	132		Q922D8
ENSMUST00000021447	ENSMUSG00000021051	12	75450883	75596200	-1	20	20	47	242	35	12	324	954	581	71	315		Q61151
ENSMUST00000021450	ENSMUSG00000021054	12	75714248	75735729	-1	12	7	15	110	15	7	401	793	550	197	367	Q3UDY2	Q9JI99
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ENSMUST00000021458	ENSMUSG00000021061	12	76580488	76710547	-1	41	31	71	339	64	35	26	43	64	3	76	Q3UGX2	
ENSMUST00000021459	ENSMUSG00000021062	12	76797960	76822908	-1	25	21	74	39	47	17	14	6	12	0	10	Q3TYH2	
ENSMUST00000021466	ENSMUSG00000021066	12	69893105	69964085	1	12	13	14	46	18	7	2	9	2	2	3		Q8BH66
ENSMUST00000021467	ENSMUSG00000021067	12	69965012	69987002	-1	3	13	6	63	15	2	456	1202	713	93	518		Q8VEB2
ENSMUST00000021468	ENSMUSG00000021068	12	70011435	70111925	-1	0	23	0	76	0	24	452	170	2435	0	1017		Q61043
ENSMUST00000021471	ENSMUSG00000021072	12	70453095	70468040	1	4	8	34	94	12	1	333	862	269	410	340		Q8VBT0
ENSMUST00000021479	ENSMUSG00000021076	12	70937857	70964718	1	48	43	62	61	44	20	719	2399	906	1678	506		Q9QZB7
ENSMUST00000021482	ENSMUSG00000021078	12	71111428	71123222	1	5	4	3	53	6	3	0	0	0	0	0		Q9D4V6
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ENSMUST00000021490	ENSMUSG00000021081	12	103688044	103695529	-1	6	0	0	0	0	0	0	0	0	0	0	G3X9Z5	
ENSMUST00000021494	ENSMUSG00000021086	12	72101292	72185029	-1	11	11	5	7	6	1	0	0	0	0	0		E9PVB3
ENSMUST00000021495	ENSMUSG00000041550	12	104101113	104106137	1	14	13	12	18	15	9	0	1	0	1	0		P70458
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ENSMUST00000021497	ENSMUSG00000021087	12	72211752	72409054	-1	0	0	0	0	0	0	0	0	0	0	0	Q7M6W1	
ENSMUST00000021506	ENSMUSG00000021091	12	104406729	104414329	1	9	16	24	20	15	8	0	1	0	78	17	G3X8T9	
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ENSMUST00000021519	ENSMUSG00000021099	12	72939892	72944899	1	39	31	44	102	26	12	0	2	0	0	3	B2RSE8	Q9QZ28
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ENSMUST00000021548	ENSMUSG00000021123	12	79208914	79222665	1	0	0	0	0	0	0	3631	4823	2896	4020	1602		Q8BYK4
ENSMUST00000021550	ENSMUSG00000021125	12	79130777	79156301	1	5	5	13	9	9	7	2725	12296	3330	6711	2668		O08691
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ENSMUST00000021559	ENSMUSG00000021131	12	80634022	80644341	-1	10	9	8	49	14	11	107	349	88	438	108	Q4FZH7	P84089
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ENSMUST00000021573	ENSMUSG00000021148	13	8941575	8948231	-1	6	0	3	0	2	0	0	0	0	0	0		Q8BFZ6
ENSMUST00000021574	ENSMUSG00000021149	13	8972071	8996017	-1	19	25	62	81	36	14	59	388	173	595	185		Q99ME9
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ENSMUST00000021594	ENSMUSG00000021177	12	99884517	99955219	1	0	0	0	0	0	4	0	0	67	0	0	B8JJC1	
ENSMUST00000021595	ENSMUSG00000021178	12	100110186	100123364	1	15	12	18	13	14	2	487	1736	796	2095	737	Q542I9	P62192
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ENSMUST00000021603	ENSMUSG00000021186	12	101746565	101819055	-1	45	26	72	102	35	13	0	3	0	1	1		Q9WVH9
ENSMUST00000021605	ENSMUSG00000021188	12	101834043	101913267	-1	44	40	49	85	52	33	374	1421	906	118	819	E9Q512	
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ENSMUST00000021609	ENSMUSG00000021192	12	102469134	102497902	1	11	11	20	0	8	3	291	1010	525	230	390		Q9QYE6
ENSMUST00000021610	ENSMUSG00000021194	12	102554969	102565027	1	28	3	61	85	42	14	0	0	0	0	0		P26339
ENSMUST00000021611	ENSMUSG00000021193	13	6548157	6580139	1	23	19	30	35	30	13	36	127	59	85	136		Q8K411
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ENSMUST00000021617	ENSMUSG00000021200	12	103321142	103356001	-1	8	2	15	26	20	9	4	0	0	0	0		Q8K0L0
ENSMUST00000021620	ENSMUSG00000021203	12	103388682	103406350	1	0	0	0	0	0	0	4	0	0	4	0		Q9CQX0
ENSMUST00000021628	ENSMUSG00000021207	13	4574075	4586541	1	1	7	3	2	4	0	0	0	0	0	0		Q91WR5
ENSMUST00000021630	ENSMUSG00000021210	13	4434306	4457530	1	2	0	1	0	2	0	0	0	0	6	0	Q3UEM0	P70694

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
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ENSMUST00000021632	ENSMUSG00000021211	13	4268172	4279433	-1	4	1	7	1	8	5	0	1	0	31	0	Q9JLI0	
ENSMUST00000021634	ENSMUSG00000021213	13	4191184	4205596	1	7	8	1	3	6	2	11	37	6	140	33		Q8VC28
ENSMUST00000021635	ENSMUSG00000021214	13	4132615	4150654	-1	3	0	0	0	6	2	0	0	7	9	0	Q3U538	Q8K023
ENSMUST00000021639	ENSMUSG00000021216	13	3924695	3935276	1	38	29	231	42	41	25	1	5	3	3	1		Q3UX10
ENSMUST00000021641	ENSMUSG00000021217	7	36698118	36773553	1	30	23	120	61	40	17	2	4	2	0	7		
ENSMUST00000021645	ENSMUSG00000021222	12	83520466	83541988	1	25	16	42	29	23	8	7	20	18	17	38	Q99LF7	
ENSMUST00000021646	ENSMUSG00000021223	12	83763634	83792382	1	0	23	1	0	36	26	0	0	3	0	14		Q9EPX2
ENSMUST00000021647	ENSMUSG00000021224	12	83794034	83921934	-1	0	1	23	0	9	0	92	0	305	6	282		Q9QZS3
ENSMUST00000021649	ENSMUSG00000021226	12	83987861	83993873	1	83	46	584	283	68	35	22	121	28	6	46		Q9QYR9
ENSMUST00000021652	ENSMUSG00000052392	12	84038379	84044723	1	16	5	8	135	11	4	0	1	0	0	1	Q14DI6	Q8BWN8
ENSMUST00000021653	ENSMUSG00000021228	12	84052144	84059565	1	19	8	16	104	25	12	0	0	0	0	0	Q53YL1	Q9QYR7
ENSMUST00000021659	ENSMUSG00000021234	12	84345309	84361833	-1	0	0	0	21	0	0	0	0	0	0	0		Q8CB59
ENSMUST00000021661	ENSMUSG00000021235	12	84361657	84373796	1	0	0	0	5	0	0	0	0	0	17	18		Q8R1S0
ENSMUST00000021662	ENSMUSG00000021236	12	84373857	84409029	-1	0	0	0	0	29	11	125	11	4	0	0		Q9WUZ9
ENSMUST00000021665	ENSMUSG00000021239	12	84569762	84595457	1	39	0	69	277	60	38	0	0	0	0	0	Q80WF9	Q61412
ENSMUST00000021666	ENSMUSG00000021240	12	84602531	84617466	-1	57	66	156	127	70	40	67	206	100	20	122		O89016
ENSMUST00000021667	ENSMUSG00000021241	12	84773270	84775089	1	6	2	7	13	8	3	148	335	110	237	100		Q9DCB8
ENSMUST00000021668	ENSMUSG00000021242	12	84754560	84773112	-1	23	16	54	115	35	18	3023	5247	2074	2766	2244		Q9Z0J0
ENSMUST00000021669	ENSMUSG00000021243	12	84970897	84983303	1	11	0	4	4	9	4	123	672	206	1044	147		Q9CTH6
ENSMUST00000021670	ENSMUSG00000021244	12	84996321	85070515	1	36	23	105	46	56	20	150	0	460	0	321	D3YWX2	
ENSMUST00000021674	ENSMUSG00000021250	12	85473890	85477273	1	15	8	36	146	12	10	476	28687	842	128	3536		P01101
ENSMUST00000021676	ENSMUSG00000021252	12	85815448	85824550	-1	2	2	4	0	4	2	88	123	90	169	81		Q9ERY9
ENSMUST00000021680	ENSMUSG00000021255	12	86361117	86521628	1	3	0	0	36	0	2	0	0	0	0	0		Q61539
ENSMUST00000021681	ENSMUSG00000021256	12	86678700	86692091	1	15	17	36	275	36	21	5	1	1	0	2		Q8C1W1
ENSMUST00000021682	ENSMUSG00000021257	12	86700502	86726460	-1	22	30	52	106	41	18	28	14	16	2	22		Q8VCU0
ENSMUST00000021684	ENSMUSG00000021259	12	108334377	108362231	1	24	14	54	144	37	7	0	0	2	2	3	Q3US73	Q9WVK8
ENSMUST00000021685	ENSMUSG00000021260	12	108306270	108328300	1	15	11	26	393	42	21	1	0	2	1	1		Q14DK5
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ENSMUST00000021691	ENSMUSG00000021263	12	108686792	108702306	-1	4	8	7	29	6	10	0	0	0	0	0		Q8R2F2
ENSMUST00000021692	ENSMUSG00000021264	12	108792973	108816632	1	4	5	24	163	11	4	847	1642	905	98	566		Q00899
ENSMUST00000021693	ENSMUSG00000021265	12	108825873	108835883	-1	10	14	26	183	26	6	29	21	14	4	12		Q8BL03
ENSMUST00000021698	ENSMUSG00000021270	12	110690605	110702728	-1	4	0	3	9	0	0	337	2020	672	2235	571	Q80Y52	P07901
ENSMUST00000021701						27	16	34	16	25	8	3	4	3	2	3		
ENSMUST00000021706	ENSMUSG00000021277	12	111166370	111267153	1	37	12	0	0	0	0	409	462	511	0	307		Q60803
ENSMUST00000021707	ENSMUSG00000021278	12	111271111	111276426	1	8	10	23	391	21	6	0	16	2	0	5		Q99JB7
ENSMUST00000021714	ENSMUSG00000021286	12	111814170	111828388	1	13	6	13	152	16	6	25	65	26	32	31		Q8VCM3
ENSMUST00000021715	ENSMUSG00000021287	12	111803192	111813873	-1	43	20	96	0	27	0	28	73	63	14	101		Q9CXE6
ENSMUST00000021719	ENSMUSG00000021290	12	111961376	111966977	-1	1	0	4	15	6	1	387	1507	387	1998	258		P56379
ENSMUST00000021726	ENSMUSG00000011148	12	112620045	112641354	1	5	8	0	0	0	13	1172	1758	1012	224	778	Q3UBP0	P28650
ENSMUST00000021728	ENSMUSG00000064326	12	112644828	112649152	1	0	1	4	0	3	1	181	223	98	129	84		O54926
ENSMUST00000021729	ENSMUSG00000021298	12	112850876	112860916	-1	20	18	45	12	18	8	154	343	121	17	300		Q9Z282
ENSMUST00000021734	ENSMUSG00000021303	13	13784059	13827897	1	20	17	24	131	27	11	5	5	3	2	3		P50153
ENSMUST00000021738	ENSMUSG00000021306	13	13357623	13393624	-1	31	32	36	196	56	14	611	1803	911	232	1065		
ENSMUST00000021750	ENSMUSG00000021313	13	11553103	12106945	-1	120	52	90	455	94	41	1	1	1	0	3		E9Q401
ENSMUST00000021757	ENSMUSG00000021322	13	20794119	21024252	1	36	24	86	23	32	17	52	237	66	32	79		O35298
ENSMUST00000021761	ENSMUSG00000021326	13	21179445	21194724	1	153	137	163	282	110	47	292	839	371	49	259		Q62158
ENSMUST00000021769	ENSMUSG00000021336	13	23897738	23915007	-1	14	0	0	16	0	0	0	0	0	0	0	A0A044PY53	
ENSMUST00000021770	ENSMUSG00000021337	13	23953456	23991214	-1	6	11	15	18	4	6	0	0	0	0	0		Q91WD9
ENSMUST00000021772	ENSMUSG00000021339	13	24992483	25020379	-1	7	6	17	32	8	2	94	129	172	34	149		Q5NCE8
ENSMUST00000021773	ENSMUSG00000021340	13	24943152	24990753	1	32	31	79	25	27	16	411	764	351	166	256	Q8VCU2	
ENSMUST00000021776	ENSMUSG00000021348	13	27709016	27716737	-1	1	0	2	0	2	1	0	0	0	0	0	Q5SVM4	P04769
ENSMUST00000021778	ENSMUSG00000055360	13	13182715	13191923	1	0	0	0	0	0	0	0	0	0	0	0	Q9JLV9	
ENSMUST00000021779	ENSMUSG00000005891	13	28016212	28023548	1	2	4	6	0	1	2	0	0	0	0	0		O35256
ENSMUST00000021784	ENSMUSG00000021356	13	30749226	30766927	1	9	10	12	15	12	5	23	17	17	8	44	Q5SUZ4	Q64287
ENSMUST00000021785	ENSMUSG00000021357	13	30813919	30974047	-1	20	9	0	26	13	11	265	1022	842	158	489		Q9D4H1
ENSMUST00000021787	ENSMUSG00000021359	13	40715675	40733823	-1	21	13	212	431	38	0	0	10	0	0	6	Q8BPN4	
ENSMUST00000021790	ENSMUSG00000021361	13	41016250	41022575	1	5	4	27	75	7	11	2022	3132	1396	854	1026		Q9CQN6
ENSMUST00000021791	ENSMUSG00000021362	13	41101427	41109988	-1	26	20	88	43	28	12	0	0	0	0	2		
ENSMUST00000021792	ENSMUSG00000021363	13	41025120	41079706	-1	14	0	0	0	0	0	22	0	0	0	0		Q04859
ENSMUST00000021793	ENSMUSG00000021364	13	41182495	41220405	-1	23	22	0	2	0	0	1	0	2	3	1	Q543J1	Q9JLJ4
ENSMUST00000021794	ENSMUSG00000021365	13	41309916	41487320	-1	28	23	61	12	22	26	1831	3627	2884	877	2566		O35177
ENSMUST00000021796	ENSMUSG00000021367	13	42301270	42307989	1	12	12	42	60	29	16	0	1	0	0	0	Q544E0	P22387
ENSMUST00000021797	ENSMUSG00000021368	13	43151744	43171501	-1	11	7	0	0	0	3	7	0	6	15	0		Q9D0K0
ENSMUST00000021800	ENSMUSG00000021371	13	43538412	43560191	-1	20	18	41	63	17	14	304	939	525	104	335		Q9CXD6
ENSMUST00000021802	ENSMUSG00000021373	13	46501848	46649642	1	14	6	24	78	28	3	0	0	0	0	0		Q9CYT6
ENSMUST00000021803	ENSMUSG00000021374	13	46679905	46727940	-1	10	11	16	229	42	9	658	1527	1444	271	1044	E9Q3G8	
ENSMUST00000021806	ENSMUSG00000021376	13	47025170	47044737	-1	4	5	5	0	0	0	0	32	0	42	9		
ENSMUST00000021807	ENSMUSG00000021377	13	47084775	47106201	-1	0	0	6	0	0	0	305	1098	309	159	256		Q7TNV0
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ENSMUST00000021813	ENSMUSG00000021381	13	48662998	48666507	1	7	2	10	200	17	9	0	0	0	0	0		Q9ER42
ENSMUST00000021816	ENSMUSG00000021384	13	49230690	49248706	-1	1	4	14	3	5	3	127	0	69	12	7		Q9D176
ENSMUST00000021817	ENSMUSG00000021385	13	49421311	49462990	1	20	11	48	80	26	12	77	213	113	36	86		Q6P1C1
ENSMUST00000021818	ENSMUSG00000021391	13	49464027	49652746	-1	8	1	6	41	6	4	12	36	15	52	9	B2RVI6	Q9CZ92
ENSMUST00000021820	ENSMUSG00000021388	13	49544443	49567557	1	0	0	0	0	0	1	0	0	0	0	0	A6H6K1	Q99MQ4
ENSMUST00000021822	ENSMUSG00000021390	13	49608071	49624500	1	1	4	4	1	2	1	0	0	0	16	0	Q543C5	Q62000
ENSMUST00000021824	ENSMUSG00000021392	13	49653350	49679015	1	15	17	13	27	19	10	23	131	46	113	62	E9QKD1	
ENSMUST00000021828	ENSMUSG00000021396	13	51171025	51175187	1	2	3	19	221	14	6	1	0	0	0	1		Q9D531
ENSMUST00000021832	ENSMUSG00000021400	13	32802038	32822609	1	10	10	35	330	24	8	108	194	163	63	84		Q91XU0
ENSMUST00000021834	ENSMUSG00000079049	13	32881833	32898161	-1	0	3	4	1	5	0	0	2	0	2	0		Q5SV42
ENSMUST00000021837	ENSMUSG00000021404	13	33149275	33159742	-1	9	5	0	0	11	1	0	0	0	0	0	I7HJI5	
ENSMUST00000021843	ENSMUSG00000046949	13	33964659	33988465	1	48	0	96	48	46	0	0	203	64	53	0		Q9JI75
ENSMUST00000021844	ENSMUSG00000021408	13	34002363	34035170	1	0	0	0	41	3	0	351	1825	1011	337	627		Q60855
ENSMUST00000021847	ENSMUSG00000021411	13	34627840	34652681	-1	13	6	19	12	0	16	4	0	0	0	13		Q8JZU6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000021851	ENSMUSG00000021414	13	34909964	34919992	-1	8	10	37	77	22	9	0	0	0	0	1	F8WGE0	
ENSMUST00000021853	ENSMUSG00000021416	13	34946614	34963810	-1	9	10	9	3	0	5	0	0	0	0	0	Q78JN3	
ENSMUST00000021854	ENSMUSG00000021417	13	34977748	35027094	-1	4	3	7	0	0	0	41	274	168	233	87		Q9WUR2
ENSMUST00000021857	ENSMUSG00000021420	13	36117411	36537592	1	13	3	36	7	13	6	75	98	56	50	59		Q99M01
ENSMUST00000021860	ENSMUSG00000021423	13	37345345	37419036	1	11	4	11	19	11	6	52	530	97	1145	267		O88188
ENSMUST00000021864	ENSMUSG00000021427	13	37971401	37994190	-1	79	61	222	140	86	37	729	1873	1049	273	830		Q9CY50
ENSMUST00000021866	ENSMUSG00000021428	13	38036989	38061433	1	12	12	18	125	14	12	122	576	275	270	200		Q922Q2
ENSMUST00000021870	ENSMUSG00000021432	13	38932140	38960875	-1	8	0	20	65	6	1	8	0	37	6	0	F8WGD7	
ENSMUST00000021880	ENSMUSG00000044258	13	60934155	60936625	-1	781	816	3313	777	1091	411	163	652	316	4272	814		P12399
ENSMUST00000021884	ENSMUSG00000074874	13	60895351	60897447	-1	0	3	0	3	0	0	8	23	18	319	33		P12400
ENSMUST00000021885	ENSMUSG00000033834	13	60938692	60941935	-1	6	6	11	2	8	4	0	0	0	0	0	Q9CPR0	
ENSMUST00000021888	ENSMUSG00000021439	13	61035027	61040631	-1	3	2	4	2	1	2	0	0	0	0	0	Q91ZF4	
ENSMUST00000021889	ENSMUSG00000055679	13	61159214	61164256	-1	3	8	2	2	3	1	0	0	0	0	0	Q497X4	Q9JIA9
ENSMUST00000021890	ENSMUSG00000021441	13	61195132	61203410	-1	5	5	5	6	5	1	0	0	0	0	1	Q9ET52	
ENSMUST00000021891	ENSMUSG00000057446	13	61246747	61255348	-1	32	37	200	21	35	9	0	1	0	0	2	Q9JI81	
ENSMUST00000021892	ENSMUSG00000021440	13	61352461	61358170	-1	5	7	4	1	6	1	0	0	0	0	0		Q91ZF2
ENSMUST00000021898	ENSMUSG00000021448	13	51431041	51567084	-1	21	6	11	31	31	14	0	0	0	0	0		Q61120
ENSMUST00000021900	ENSMUSG00000021451	13	51701246	51793747	-1	1	0	0	64	0	0	434	752	576	3	744		O09126
ENSMUST00000021903	ENSMUSG00000021453	13	51846678	51848468	1	5	3	20	62	8	2	461	1300	395	99	222	Q9R0S0	
ENSMUST00000021907	ENSMUSG00000021456	13	62836884	62858400	-1	13	4	5	10	8	5	0	0	0	1	0	Q3TKP4	P70695
ENSMUST00000021911	ENSMUSG00000021458	13	63014934	63326096	1	11	4	11	56	11	4	75	180	85	150	71	F8WGB2	
ENSMUST00000021913	ENSMUSG00000021460	13	52835119	52929681	-1	0	0	0	0	0	0	230	876	291	138	176		
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ENSMUST00000021920	ENSMUSG00000021468	13	53332716	53377365	-1	15	14	24	35	27	11	413	746	448	189	320		O35704
ENSMUST00000021921	ENSMUSG00000021466	13	63508328	63573598	-1	26	26	0	41	17	20	0	0	0	0	43		Q61115
ENSMUST00000021922	ENSMUSG00000021469	13	53466884	53473074	-1	49	39	88	256	76	30	1	1	1	0	3	Q3UZH5	Q03358
ENSMUST00000021925	ENSMUSG00000021470	13	63815240	63900302	1	0	0	0	0	0	0	5	8	3	0	0	G8JL31	
ENSMUST00000021926	ENSMUSG00000021470	13	63815240	63900302	1	6	0	4	47	3	1	0	10	0	0	0		Q9JIM3
ENSMUST00000021929	ENSMUSG00000021476	13	64161866	64186536	1	21	18	25	84	31	10	16	89	55	12	77	E9QKB2	
ENSMUST00000021930	ENSMUSG00000021474	13	54071845	54108346	1	30	23	15	22	33	15	79	200	145	48	167		Q99JR1
ENSMUST00000021932	ENSMUSG00000021478	13	54051186	54055658	-1	35	25	30	53	33	18	0	0	0	0	1		Q61616
ENSMUST00000021933	ENSMUSG00000021477	13	64363214	64370306	-1	11	8	13	57	10	13	773	2840	1095	18858	2344	Q543M3	P06797
ENSMUST00000021937	ENSMUSG00000021481	13	55105311	55134825	1	27	14	69	25	31	12	126	286	167	21	152		Q9R0B7
ENSMUST00000021938	ENSMUSG00000021482	13	64291836	64312710	-1	5	2	2	34	11	2	193	824	365	319	263		Q9D1A0
ENSMUST00000021939	ENSMUSG00000021483	13	64432553	64439720	1	17	8	41	49	25	16	145	216	103	30	70		Q9JHU3
ENSMUST00000021940	ENSMUSG00000021484	13	55343833	55362783	-1	18	28	58	118	37	16	3221	3742	2503	637	1923		Q9DBH5
ENSMUST00000021941	ENSMUSG00000021485	13	55325168	55329758	-1	1	4	0	29	7	3	130	74	48	7	20		Q80US8
ENSMUST00000021942	ENSMUSG00000021486	13	55322055	55325271	1	13	15	38	146	42	17	8447	9992	6104	2970	3865		Q8R107
ENSMUST00000021948	ENSMUSG00000021492	13	55417958	55426793	-1	19	7	47	67	19	16	14	56	16	5	15		Q80YC5
ENSMUST00000021950	ENSMUSG00000034675	13	55473429	55488111	-1	0	0	0	14	19	0	0	0	0	0	0		Q9QXS6
ENSMUST00000021956	ENSMUSG00000021494	13	55530410	55536658	-1	14	6	16	116	18	5	1081	1434	787	420	597		Q91VN6
ENSMUST00000021957	ENSMUSG00000021495	13	55539319	55571120	-1	22	12	83	158	41	20	598	2709	1013	109	1710		Q3U2K0
ENSMUST00000021958	ENSMUSG00000021496	13	55727368	55776830	1	1	0	0	0	0	1	67	142	51	83	42		Q9CZL5
ENSMUST00000021959	ENSMUSG00000021497	13	55714650	55726221	1	7	3	11	101	6	3	171	667	248	137	207		Q6P6J9
ENSMUST00000021961	ENSMUSG00000021499	13	55784568	55808998	1	5	4	27	10	0	7	0	0	0	0	1	E0Z0E0	Q80W99
ENSMUST00000021963	ENSMUSG00000021501	13	55623005	55632411	1	0	0	5	73	12	5	47	216	111	120	77		P49070
ENSMUST00000021968	ENSMUSG00000021506	13	55825051	55836192	-1	8	13	38	736	41	17	0	0	0	5	7	Q3UQH0	P70314
ENSMUST00000021970	ENSMUSG00000021508	13	56288647	56296551	-1	11	10	11	180	19	8	1	2	0	33	24		Q9WUQ5
ENSMUST00000021971	ENSMUSG00000021509	13	56438355	56474239	1	39	32	37	96	60	25	0	1	1	2	14		Q8BW66
ENSMUST00000021990	ENSMUSG00000021518	13	66932830	66998401	1	16	10	44	215	30	18	589	1213	707	212	440		Q99LH2
ENSMUST00000021991	ENSMUSG00000021519	13	66906968	66933088	-1	0	0	0	0	0	0	31	65	24	108	4		Q8R3J4
ENSMUST00000021993	ENSMUSG00000021520	13	66900617	66905378	-1	2	4	1	7	2	0	182	968	262	752	115	Q9CQB4	
ENSMUST00000021997	ENSMUSG00000058900	13	67173207	67183126	1	7	3	3	2	3	0	2	43	4	12	6	Q7M6Y1	
ENSMUST00000022007	ENSMUSG00000021534	13	68597439	68614231	1	2	7	13	15	5	10	0	0	0	0	0		Q9DAR0
ENSMUST00000022009	ENSMUSG00000021537	13	81783292	81797143	1	3	1	1	35	2	0	141	587	231	708	126	Q545L8	O35648
ENSMUST00000022013	ENSMUSG00000021536	13	68620043	68999541	-1	21	25	13	76	22	18	0	0	1	1	1	Q3V1Q3	
ENSMUST00000022019	ENSMUSG00000021538	13	56479277	56482246	-1	3	2	5	4	5	1	0	0	0	0	0		P15247
ENSMUST00000022023	ENSMUSG00000021541	13	56773113	56895789	-1	0	0	101	104	1	0	2	3	0	0	2	Q0VFY2	Q9WVC5
ENSMUST00000022028	ENSMUSG00000021545	17	48089632	48090920	1	8	7	10	16	10	1	0	0	0	0	0	G3X8U2	
ENSMUST00000022030	ENSMUSG00000021548	13	85189408	85223469	1	0	0	0	14	3	4	18	20	0	5	6		Q61458
ENSMUST00000022032	ENSMUSG00000021550	13	58380046	58385225	-1	172	139	243	314	205	88	206	412	187	56	144	G3X8U3	
ENSMUST00000022036	ENSMUSG00000021553	13	58545399	58610877	-1	97	98	112	97	78	43	24	60	56	4	29		Q9ERH8
ENSMUST00000022038	ENSMUSG00000021555	13	59585259	59634798	1	5	0	8	16	7	3	358	1145	578	378	363		Q6PHQ8
ENSMUST00000022039	ENSMUSG00000021556	13	59634996	59675784	-1	27	12	32	31	46	0	316	1221	937	220	483		Q91XA2
ENSMUST00000022040	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	0	0	0	0	147	724	348	97	121		Q641K1
ENSMUST00000022048	ENSMUSG00000021565	13	73679745	73704865	-1	17	6	5	19	12	6	0	0	0	0	0	Q3KN89	Q9D687
ENSMUST00000022051	ENSMUSG00000021567	13	73818534	73847631	-1	40	21	65	93	34	24	0	0	0	0	0		Q8VE28
ENSMUST00000022053	ENSMUSG00000021569	13	73911347	73937767	-1	8	11	16	136	23	11	32	78	35	12	30		Q3UA06
ENSMUST00000022057	ENSMUSG00000021573	13	74009407	74035753	1	35	23	45	38	39	10	29	48	24	12	70	Q3URG1	Q7TQD2
ENSMUST00000022059	ENSMUSG00000021575	13	74211118	74292331	-1	32	20	23	56	39	9	2	11	0	2	4		
ENSMUST00000022060	ENSMUSG00000021576	13	74303121	74317326	-1	9	6	21	66	11	9	974	2830	1283	3001	854		P12815
ENSMUST00000022062	ENSMUSG00000021577	13	74322254	74350280	-1	13	14	20	18	13	0	1006	3224	1848	637	1465		Q8K2B3
ENSMUST00000022063	ENSMUSG00000021578	13	74350309	74365783	1	85	103	149	129	113	51	72	340	123	102	128		Q3TC33
ENSMUST00000022064	ENSMUSG00000021579	13	74359578	74364005	-1	22	7	26	3	10	0	0	0	0	0	0		Q3UJB3
ENSMUST00000022075	ENSMUSG00000021587	13	75089826	75132498	1	15	15	12	9	10	10	0	0	0	0	0	Q32MU0	P63239
ENSMUST00000022078	ENSMUSG00000021589	13	75869537	75943925	-1	14	12	44	16	14	5	5	10	2	3	24		Q9CTN4
ENSMUST00000022081	ENSMUSG00000021590	13	75967739	75998968	1	3	4	4	2	5	0	0	1	0	0	1		Q9D9R3
ENSMUST00000022082	ENSMUSG00000021591	13	75839868	75850151	1	10	14	18	25	12	9	9069	22452	8971	27588	5981	Q3U6L3	Q9QUH0
ENSMUST00000022087	ENSMUSG00000021595	13	69533746	69635780	1	20	18	49	57	30	11	0	6	9	0	15		Q1HFZ0
ENSMUST00000022089	ENSMUSG00000021598	13	69809882	69816094	1	3	4	14	67	9	4	226	581	255	415	191		Q9CXU0
ENSMUST00000022091	ENSMUSG00000021600	13	70882948	70884503	1	3	3	2	3	5	1	0	0	0	0	0	Q9CX45	
ENSMUST00000022095	ENSMUSG00000021604	13	73260479	73269608	1	12	0	37	84	0	0	0	0	0	0	0		Q9QY61
ENSMUST00000022097	ENSMUSG00000021606	13	73319874	73328542	-1	3	1	0	20	1	0	208	354	122	663	82		P52503
ENSMUST00000022098	ENSMUSG00000021607	13	73331009	73332175	1	8	6	9	102	4	5	237	647	212	288	148		Q99N90

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ENSMUST00000022099	ENSMUSG00000021608	13	73467197	73516422	1	0	15	31	53	29	0	351	331	467	25	221		Q3TFD2
ENSMUST00000022100	ENSMUSG00000021609	13	73536747	73578672	1	28	23	70	37	41	14	1	0	1	0	1		Q61327
ENSMUST00000022102	ENSMUSG00000021610	13	73604002	73620639	1	19	6	25	74	13	15	1418	2380	1415	212	951		Q8BXA5
ENSMUST00000022104	ENSMUSG00000021611	13	73627001	73649041	1	25	21	56	103	39	19	4	1	4	1	6		O70372
ENSMUST00000022105	ENSMUSG00000021612	13	73661750	73678023	-1	0	0	0	0	0	0	0	0	0	0	0		O88576
ENSMUST00000022108	ENSMUSG00000021613	13	89540636	89611832	1	38	23	184	34	38	15	0	0	0	0	0		Q9QUP5
ENSMUST00000022115	ENSMUSG00000021615	13	89774027	90089608	-1	0	1	0	3	1	0	42	304	102	333	40		
ENSMUST00000022119	ENSMUSG00000021619	13	90935349	91223987	-1	30	23	54	27	8	13	13	73	22	57	12		
ENSMUST00000022120	ENSMUSG00000021620	13	91741512	91786148	1	8	13	9	32	14	10	0	0	0	0	0	A2RSC2	Q9DBK0
ENSMUST00000022121	ENSMUSG00000021621	13	91796533	91807705	-1	0	0	0	77	0	7	56	298	95	164	77		Q8R1J3
ENSMUST00000022122	ENSMUSG00000021622	13	91853387	91876885	-1	12	2	24	29	13	2	0	0	0	0	0		Q6P8J7
ENSMUST00000022124	ENSMUSG00000021624	13	102693558	102739629	1	12	8	16	14	8	6	45	174	69	47	93		Q62192
ENSMUST00000022135	ENSMUSG00000078941	13	100650979	100666359	1	6	3	5	61	10	0	53	255	80	346	61		Q8VCP8
ENSMUST00000022136	ENSMUSG00000021635	13	100617165	100651059	-1	9	8	0	47	8	0	0	55	20	57	18	Q3UYY2	Q6NXW6
ENSMUST00000022137	ENSMUSG00000021636	13	100595957	100616971	-1	15	13	20	13	31	11	0	7	0	0	9	A1BQX3	Q3UZP0
ENSMUST00000022140	ENSMUSG00000021638	13	100496507	100552718	-1	19	0	5	87	18	6	0	0	0	0	0	B2RS24	Q61146
ENSMUST00000022142	ENSMUSG00000021640	13	100407770	100446406	-1	53	47	57	31	37	29	6	8	10	32	28		Q9QWK5
ENSMUST00000022145	ENSMUSG00000021643	13	100107997	100114571	1	0	0	0	45	0	0	0	13	0	22	0		O88892
ENSMUST00000022147	ENSMUSG00000021645	13	100124852	100137690	1	0	0	0	11	0	1	193	407	193	42	118	Q549F9	P97801
ENSMUST00000022148	ENSMUSG00000021646	13	99948533	100015639	-1	24	13	36	110	19	10	15	22	8	9	15	B2RUK5	Q3ULD5
ENSMUST00000022150	ENSMUSG00000021647	13	99898484	99900683	-1	3	6	6	59	5	3	0	0	0	0	0		P56388
ENSMUST00000022153	ENSMUSG00000021650	13	99319649	99344678	-1	12	11	12	25	21	9	98	286	116	126	101		Q8R3K3
ENSMUST00000022163	ENSMUSG00000021660	13	98309896	98317006	-1	4	0	4	105	21	0	4	30	11	21	18		Q64152
ENSMUST00000022164	ENSMUSG00000021661	13	98263158	98274750	1	0	0	0	0	0	0	67	208	65	55	40		Q99PE2
ENSMUST00000022169	ENSMUSG00000021665	13	97176332	97198357	-1	14	3	8	129	11	7	1093	2760	1477	635	876	Q3TXR9	P20060
ENSMUST00000022170	ENSMUSG00000021666	13	97137937	97181195	1	0	0	0	0	0	0	65	0	0	0	69		Q8R2Q4
ENSMUST00000022172	ENSMUSG00000021668	13	96480689	96542485	-1	26	21	45	46	22	18	161	720	336	224	172		Q9QUG2
ENSMUST00000022176	ENSMUSG00000021670	13	96648967	96670936	-1	15	0	12	27	9	9	316	910	543	134	466		Q01237
ENSMUST00000022182	ENSMUSG00000021675	13	95696853	95702739	1	34	28	47	25	40	23	89	335	88	61	53		O08675
ENSMUST00000022185	ENSMUSG00000021678	13	95511732	95525240	-1	34	21	214	167	36	20	5	18	9	8	24	Q3TU81	P55086
ENSMUST00000022186	ENSMUSG00000021679	13	95477301	95478655	-1	2	0	2	0	3	2	0	0	0	0	0	B9EJL3	
ENSMUST00000022189	ENSMUSG00000021681	13	95350683	95375352	-1	4	11	3	37	21	9	486	1482	968	225	709		Q7TN31
ENSMUST00000022192	ENSMUSG00000021684	13	95024454	95250336	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q8J6	
ENSMUST00000022195	ENSMUSG00000021685	13	94875602	94885130	1	46	24	218	418	37	24	0	0	2	0	1		O09113
ENSMUST00000022196	ENSMUSG00000021686	13	94358960	94566316	1	19	17	33	160	35	14	1084	2973	2493	378	1347		Q9Z1T1
ENSMUST00000022197	ENSMUSG00000021687	13	94201310	94285857	-1	25	24	116	246	25	16	971	2893	1209	480	698	Q3TD71	Q8K021
ENSMUST00000022203	ENSMUSG00000021692	13	106947129	106960224	1	10	9	5	77	10	8	5	36	18	66	22		Q9D0D4
ENSMUST00000022204	ENSMUSG00000021693	13	106958996	107022126	-1	9	11	12	18	19	7	234	1272	232	153	175		P28740
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ENSMUST00000022212	ENSMUSG00000021701	13	110395044	110400844	1	10	10	15	160	13	16	118	514	148	87	278	Q548A9	P53351
ENSMUST00000022213	ENSMUSG00000021702	13	92751590	92794818	-1	23	11	39	83	42	11	6	1	6	0	0	B2RTL6	Q9Z1T2
ENSMUST00000022217	ENSMUSG00000021706	13	92487108	92530868	-1	19	12	8	61	19	14	133	385	292	59	210		Q80U44
ENSMUST00000022218	ENSMUSG00000021707	13	92354783	92389053	1	32	23	97	127	29	28	35	133	56	104	36	Q544T5	P00375
ENSMUST00000022220	ENSMUSG00000014850	13	92211872	92355003	-1	0	8	0	6	0	0	17	95	48	0	0	E9QPY6	
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ENSMUST00000022225	ENSMUSG00000021712	13	104178797	104203372	1	5	0	0	9	0	0	82	218	93	97	61		Q8BGX0
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ENSMUST00000022230	ENSMUSG00000021716	13	104792484	104839274	1	11	0	19	3	14	7	49	216	83	195	71		Q4V9W2
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ENSMUST00000022239	ENSMUSG00000021725	13	116854824	117025516	-1	16	14	28	136	33	13	234	1656	533	248	600	F8WIK2	
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ENSMUST00000022256	ENSMUSG00000021737	14	14112184	14120984	-1	6	3	0	38	4	0	323	1441	606	1507	359		Q99JI4
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ENSMUST00000022269	ENSMUSG00000021749	14	8348948	8378763	-1	37	19	122	44	31	5	0	0	0	0	0		P97805
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ENSMUST00000022281	ENSMUSG00000016018	13	112867780	112927380	-1	13	12	9	7	7	8	126	678	317	509	228		Q9CZU3
ENSMUST00000022282	ENSMUSG00000021760	13	113042763	113046388	-1	3	2	4	5	8	1	2	2	0	180	38		Q9D7B7
ENSMUST00000022286	ENSMUSG00000021764	13	114287795	114388094	-1	9	5	17	20	13	8	193	1023	330	1430	216	E9QPX3	
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ENSMUST00000022292	ENSMUSG00000021770	14	21750531	21798725	1	0	0	0	10	5	2	9	68	19	6	23	Q14AQ4	Q9DA37
ENSMUST00000022293	ENSMUSG00000021771	14	21831269	21845879	1	2	0	2	219	12	9	749	2657	935	1362	526		Q60930
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ENSMUST00000022310	ENSMUSG00000021785	14	16249280	16311926	1	6	4	4	51	6	5	344	1842	706	673	451		Q9JI78
ENSMUST00000022311	ENSMUSG00000021786	14	16238656	16249808	-1	283	287	945	369	433	194	65	445	110	22	86		Q9D404
ENSMUST00000022314	ENSMUSG00000021789	14	41131782	41136452	1	3	0	2	2	0	0	0	0	0	0	0	Q9CQI1	
ENSMUST00000022315	ENSMUSG00000021790	14	41072911	41092197	1	6	0	0	0	11	6	0	0	0	0	0		Q9D9T0
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ENSMUST00000022322	ENSMUSG00000021794	14	34310727	34345144	1	24	16	24	153	29	12	1904	6881	2920	642	2131		P26443
ENSMUST00000022325	ENSMUSG00000021797	14	34511619	34522801	-1	2	2	1	1	4	1	0	0	0	0	0	Q9D260	
ENSMUST00000022327	ENSMUSG00000021798	14	34526699	34588681	-1	17	0	0	80	0	0	0	0	0	0	0		Q9JKS4
ENSMUST00000022328	ENSMUSG00000021798	14	34526699	34588681	-1	1	0	16	0	0	0	0	0	0	0	0		Q9JKS4
ENSMUST00000022330	ENSMUSG00000021798	14	34526699	34588681	-1	10	8	39	22	20	10	0	0	0	0	0		Q9JKS4
ENSMUST00000022331	ENSMUSG00000021799	14	34590618	34600142	-1	12	9	40	9	18	3	0	0	0	0	0		Q9QXZ9
ENSMUST00000022337	ENSMUSG00000021803	14	37077850	37098311	-1	34	21	52	88	30	13	0	0	0	0	0		Q8VHP6
ENSMUST00000022338	ENSMUSG00000021804	14	37037490	37048964	-1	8	5	13	9	8	3	0	0	0	0	0	Q543X1	Q9Z2B3
ENSMUST00000022340	ENSMUSG00000021806	14	19751257	19811787	1	31	21	53	219	59	27	8	7	8	11	38		O88322
ENSMUST00000022341	ENSMUSG00000021807	14	19811402	19823823	-1	6	7	5	32	9	6	243	1389	369	1058	224	Q4VA29	Q9CQE8
ENSMUST00000022343	ENSMUSG00000021809	14	20294690	20317575	1	14	13	19	11	19	10	52	182	68	23	61		Q8JZU0
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ENSMUST00000022358	ENSMUSG00000021819	14	20707552	20723618	1	43	36	103	233	93	32	1441	1724	1490	116	1708		Q3UHH1
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ENSMUST00000022378	ENSMUSG00000021831	14	45283092	45318572	-1	32	12	17	44	27	7	814	1685	965	154	525	Q4FK57	Q8R180
ENSMUST00000022380	ENSMUSG00000021832	14	45329824	45349071	1	0	3	6	7	2	2	259	1547	538	1230	292	Q14AQ1	P62334
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ENSMUST00000022418	ENSMUSG00000021867	14	26203369	26207041	-1	8	1	3	6	3	0	18	53	0	0	15		Q9DCV5
ENSMUST00000022419	ENSMUSG00000021868	14	25694154	25700468	1	0	0	0	74	0	0	64	139	67	22	81		Q99KR7
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ENSMUST00000022429	ENSMUSG00000021877	14	26638074	26665084	1	0	3	0	102	9	3	122	341	139	38	66	Q14BR4	P61750
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ENSMUST00000022459	ENSMUSG00000021902	14	31237696	31251218	-1	16	14	19	58	8	6	56	260	109	45	61	A2RTI5	Q9DAG9
ENSMUST00000022460	ENSMUSG00000021903	14	32028989	32062197	1	48	36	125	67	80	30	0	0	0	3	5		Q9D2N8
ENSMUST00000022461	ENSMUSG00000021905	14	32080566	32085692	-1	0	0	0	5	0	0	6	92	7	23	19		Q8K0W9
ENSMUST00000022462	ENSMUSG00000021906	14	32085374	32103202	1	0	0	0	24	18	0	53	88	46	65	39		Q8VE38
ENSMUST00000022464	ENSMUSG00000021907	14	32142026	32158370	1	0	3	5	4	0	2	0	0	0	0	0		O08540
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ENSMUST00000022480	ENSMUSG00000021913	14	32322019	32347820	1	19	17	45	63	43	14	0	1	1	0	4	E9Q7L0	
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ENSMUST00000022496	ENSMUSG00000021929	14	61365186	61439947	-1	11	10	17	22	7	10	78	340	131	173	102	Q543M7	O35344
ENSMUST00000022497	ENSMUSG00000021930	14	61531993	61556886	-1	25	18	26	62	37	18	5	40	8	5	13		Q3TFQ1
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ENSMUST00000022501	ENSMUSG00000021933	14	62392676	62456289	-1	21	16	22	19	16	0	0	0	0	0	0	Q8BXH3	
ENSMUST00000022504	ENSMUSG00000021936	14	33377898	33447158	-1	0	0	0	0	0	0	21	109	40	69	28	G3X8U9	
ENSMUST00000022507	ENSMUSG00000021938	14	56722441	56778316	-1	2	5	12	103	9	0	101	265	191	79	192		Q8R326
ENSMUST00000022508	ENSMUSG00000021940	14	33589270	33640754	1	7	11	12	2	5	3	0	0	0	0	0		O55082
ENSMUST00000022511	ENSMUSG00000021945	14	56887795	56962579	1	15	20	22	12	21	7	423	1535	747	404	492		Q9CU65
ENSMUST00000022517	ENSMUSG00000021947	14	57275034	57398483	-1	12	7	21	16	13	1	41	96	42	75	130	A7VMV2	Q99KP3
ENSMUST00000022518	ENSMUSG00000021951	14	57549598	57571569	-1	5	4	4	4	4	2	60	134	68	356	43	A0A0D2X7Z2	
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ENSMUST00000022528	ENSMUSG00000021958	14	63860312	63919859	1	10	9	21	25	3	6	8	56	16	127	36		Q9CZX5
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ENSMUST00000022531	ENSMUSG00000021959	14	57642077	57758388	-1	8	10	42	38	22	12	794	1293	1003	82	825		Q7TSJ6
ENSMUST00000022532	ENSMUSG00000021961	14	63971122	63987780	-1	11	5	26	13	9	4	0	0	0	0	0		Q80ZQ3
ENSMUST00000022535	ENSMUSG00000021962	14	30479565	30527056	1	29	25	102	98	42	39	387	543	523	61	373		Q91YD3
ENSMUST00000022536	ENSMUSG00000021965	14	57806561	57826163	-1	28	34	49	89	36	26	27	53	44	19	21		Q8C263
ENSMUST00000022537	ENSMUSG00000021966	14	64104286	64113755	1	8	3	8	6	8	11	0	2	2	0	1		Q9D9M0
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ENSMUST00000022543	ENSMUSG00000021973	14	57916280	57999262	-1	9	12	25	36	16	7	391	2329	742	416	544		Q8CD10
ENSMUST00000022544	ENSMUSG00000021972	14	64811600	64949871	-1	16	9	61	19	19	9	142	419	346	43	266		Q8BJA3
ENSMUST00000022545	ENSMUSG00000021974	14	58070547	58112337	1	4	4	15	32	8	4	0	0	0	0	0		P54130
ENSMUST00000022548	ENSMUSG00000021977	14	59133040	59142893	-1	0	0	0	0	4	0	0	0	0	0	0	Q9CQ77	
ENSMUST00000022550	ENSMUSG00000021978	14	65052060	65098106	-1	51	45	86	177	79	30	309	433	410	46	436	Q6P1H4	
ENSMUST00000022551	ENSMUSG00000035469	14	59201209	59237265	1	0	0	0	0	0	0	0	0	0	26	72		
ENSMUST00000022553	ENSMUSG00000021981	14	59440981	59548903	1	12	12	27	33	29	9	156	598	231	296	155		Q9DB16
ENSMUST00000022555	ENSMUSG00000021982	14	59560896	59597836	-1	0	2	0	52	0	3	0	76	17	0	10		Q8BMD5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000022561	ENSMUSG00000021986	14	60378286	60381003	1	24	11	58	796	37	31	117	243	168	38	136		
ENSMUST00000022563	ENSMUSG00000021987	14	60265205	60302370	1	13	10	34	77	17	11	1132	4154	2445	948	1499		Q8VE11
ENSMUST00000022566	ENSMUSG00000021990	14	60634001	60764556	1	9	0	0	157	38	0	22	14	23	0	33	E9Q3I3	
ENSMUST00000022567	ENSMUSG00000021991	14	28904943	29721864	-1	15	16	35	36	26	12	0	0	0	0	0		Q9Z1L5
ENSMUST00000022573	ENSMUSG00000021996	14	74732297	74750765	1	14	12	12	35	12	8	23	113	23	81	18		Q9R0P3
ENSMUST00000022574	ENSMUSG00000021997	14	75084303	75130881	-1	11	10	21	23	10	8	3	12	17	4	17	G3X8V0	
ENSMUST00000022576	ENSMUSG00000021999	14	75242287	75283551	1	7	10	12	10	9	3	0	0	0	13	0		Q9JHH6
ENSMUST00000022577	ENSMUSG00000022000	14	75284373	75344426	1	23	30	52	126	42	20	304	797	781	106	705	E9Q784	E9Q784
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ENSMUST00000022580	ENSMUSG00000022003	14	75761999	75787037	-1	10	10	7	36	23	7	250	521	464	121	399		Q9CR58
ENSMUST00000022585	ENSMUSG00000022008	14	76086232	76110815	-1	93	89	257	112	109	55	282	998	596	354	477		Q69ZC8
ENSMUST00000022586	ENSMUSG00000022009	14	76110891	76137379	1	66	57	210	188	83	50	29	175	60	40	66		Q9QXX8
ENSMUST00000022587	ENSMUSG00000022010	14	76414961	76507765	1	3	13	4	26	7	3	100	184	101	855	379	Q3UXU0	P62500
ENSMUST00000022589	ENSMUSG00000022012	14	77156763	77721760	1	19	17	27	99	26	16	1	0	0	0	2		Q8BHR2
ENSMUST00000022590	ENSMUSG00000022013	14	77826217	77874917	-1	1	5	4	48	3	0	21	121	38	192	29		Q78YY6
ENSMUST00000022591	ENSMUSG00000022014	14	77904239	78002656	1	3	3	11	16	1	5	16	132	13	99	81		
ENSMUST00000022592	ENSMUSG00000022015	14	78277445	78308043	-1	0	2	5	128	12	5	0	1	0	3	0		O35235
ENSMUST00000022593	ENSMUSG00000022016	14	78492246	78536860	-1	0	0	0	94	1	0	0	0	0	0	154	E9Q774	
ENSMUST00000022595	ENSMUSG00000022018	14	79288756	79301645	-1	5	5	8	72	7	8	47	59	30	46	50		Q9DBX1
ENSMUST00000022597	ENSMUSG00000022020	14	79334204	79390778	-1	5	13	138	51	16	9	35	271	73	45	51		Q9DBB4
ENSMUST00000022599	ENSMUSG00000022021	14	86655367	87141224	-1	35	22	69	194	36	25	15	41	17	9	23	F8WIG5	
ENSMUST00000022600	ENSMUSG00000022022	14	79397772	79423650	1	9	7	3	7	7	5	7	34	12	68	11		Q8K126
ENSMUST00000022601	ENSMUSG00000022023	14	79459937	79481268	-1	27	21	125	124	28	14	147	882	358	250	266		Q61048
ENSMUST00000022603	ENSMUSG00000022025	14	79637690	79662170	-1	0	6	19	25	5	3	0	0	0	0	0		Q9Z1F6
ENSMUST00000022609	ENSMUSG00000022031	14	65530446	65593112	-1	27	12	48	28	25	16	90	242	128	77	145		Q9CZX0
ENSMUST00000022610	ENSMUSG00000022032	14	65666403	65764826	1	15	13	27	60	23	19	0	0	0	35	51		Q8K299
ENSMUST00000022612	ENSMUSG00000022033	14	65805837	65817822	1	10	9	10	40	14	4	55	95	52	44	29		Q9JJ78
ENSMUST00000022613	ENSMUSG00000022034	14	65819038	65833994	-1	3	2	12	24	5	6	43	37	37	25	11		Q8CIB9
ENSMUST00000022614	ENSMUSG00000022035	14	65837302	65866604	1	87	98	665	212	77	51	98	547	170	323	140	A0PK78	Q78PG9
ENSMUST00000022616	ENSMUSG00000022037	14	65968483	65981548	1	11	12	25	42	12	7	40	41	51	200	155	Q549A5	Q06890
ENSMUST00000022618	ENSMUSG00000022039	14	66027329	66077733	-1	12	12	15	20	15	4	0	0	0	0	0		Q60718
ENSMUST00000022620	ENSMUSG00000022041	14	66135039	66152948	1	49	35	56	55	62	36	6	32	17	3	16		Q91X60
ENSMUST00000022622	ENSMUSG00000059456	14	66153257	66281052	-1	0	0	0	0	39	15	27	0	0	0	0	K7QD41	Q9QVP9
ENSMUST00000022623	ENSMUSG00000022043	14	66297031	66311424	1	28	20	62	86	22	12	229	302	223	41	280		
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ENSMUST00000022634	ENSMUSG00000022051	14	66985239	67008877	-1	7	3	19	42	32	8	1470	4779	1834	1820	1148		Q9Z2F7
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ENSMUST00000022638	ENSMUSG00000022054	14	68082590	68124846	-1	22	7	50	38	27	14	0	0	0	0	0		
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ENSMUST00000022640	ENSMUSG00000022056	14	68497336	68533689	-1	12	9	8	15	8	5	0	0	0	0	0		O35227
ENSMUST00000022641	ENSMUSG00000022057	14	68563388	68582086	-1	9	9	12	6	6	9	0	8	2	8	8	Q3U0T4	Q9R0X2
ENSMUST00000022642	ENSMUSG00000014725	14	68606027	68655842	-1	2	2	3	1	7	1	0	0	0	0	0		Q9JLN6
ENSMUST00000022646	ENSMUSG00000022061	14	69190638	69194662	1	22	24	45	165	27	21	0	0	0	0	0	Q3UVH8	P97436
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ENSMUST00000022663	ENSMUSG00000022074	14	69767472	69784403	1	1360	1222	2786	1048	1740	869	157	613	291	52	238		Q9QZM4
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ENSMUST00000022681	ENSMUSG00000022090	14	70164218	70177681	-1	4	3	15	0	0	2	481	941	141	42	104		Q8R1G6
ENSMUST00000022682	ENSMUSG00000022091	14	70180468	70207637	-1	20	15	40	56	35	17	7	11	11	16	82		Q9R1Z8
ENSMUST00000022688	ENSMUSG00000022094	14	70303469	70351425	-1	0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000022691	ENSMUSG00000022096	14	70552212	70573548	1	6	0	0	8	0	0	0	0	0	0	0		Q61645
ENSMUST00000022692	ENSMUSG00000022097	14	70520941	70524081	-1	7	5	23	7	14	6	0	0	1	0	0	Q6P8P8	
ENSMUST00000022693	ENSMUSG00000022098	14	70474557	70520260	-1	19	26	44	124	45	17	2	4	2	22	139		P98063
ENSMUST00000022694	ENSMUSG00000022099	14	70602184	70636048	-1	23	54	28	9	10	0	0	0	0	0	0		Q9WV69
ENSMUST00000022695	ENSMUSG00000022099	14	70602184	70636048	-1	32	0	20	183	39	25	0	2	2	1	8		Q9WV69
ENSMUST00000022696	ENSMUSG00000022100	14	70654246	70766628	-1	305	308	564	361	347	173	338	907	723	45	498		Q9EPK7
ENSMUST00000022697	ENSMUSG00000022101	14	70636205	70642268	-1	7	12	28	96	19	11	0	1	1	0	0	Q0VF19	P63075
ENSMUST00000022698	ENSMUSG00000022102	14	70766036	70778495	1	5	11	47	39	20	14	2232	2123	1061	283	823	Q3TX09	O70469
ENSMUST00000022699	ENSMUSG00000022103	14	70890130	70979838	1	139	79	374	695	149	67	5	7	2	1	10		O08842
ENSMUST00000022701	ENSMUSG00000022105	14	73183673	73325822	-1	5	6	3	17	7	5	302	701	453	44	329		P13405
ENSMUST00000022702	ENSMUSG00000022106	14	73123037	73207843	1	0	4	0	0	2	0	9	19	0	14	26	G1EE51	Q99LJ7
ENSMUST00000022704	ENSMUSG00000022108	14	73362231	73385271	-1	9	11	20	145	18	8	9770	28218	10786	4400	8389		O89051
ENSMUST00000022705	ENSMUSG00000022109	14	73510049	73518545	1	14	9	16	67	10	4	171	747	306	793	247		Q9CQA5
ENSMUST00000022706	ENSMUSG00000022110	14	73525319	73596142	1	0	0	0	7	1	4	92	581	289	681	156		Q9Z2I9
ENSMUST00000022707	ENSMUSG00000022112	14	115092215	116525179	1	3	5	2	0	2	0	0	0	0	0	0		Q8CAL5
ENSMUST00000022708	ENSMUSG00000022113	14	106106198	106135859	1	14	16	40	109	14	8	0	0	0	0	0	Q8CDV4	
ENSMUST00000022709	ENSMUSG00000022114	14	105891949	105896819	-1	20	9	62	29	15	14	130	444	185	36	235	B2RS85	Q9QXV8
ENSMUST00000022715	ENSMUSG00000022119	14	105106751	105177327	-1	0	6	16	122	0	0	1	50	22	0	51		Q6NZN0
ENSMUST00000022716	ENSMUSG00000022120	14	104477534	104522666	-1	54	37	278	120	41	21	17	44	28	37	27	G3X8V5	
ENSMUST00000022718	ENSMUSG00000022122	14	103814625	103844173	-1	28	0	1	116	7	13	46	31	24	97	165		P48302
ENSMUST00000022720	ENSMUSG00000022124	14	103080239	103099566	-1	49	52	74	67	36	17	60	246	186	37	98	Q5PRF6	Q8C4V4
ENSMUST00000022721	ENSMUSG00000022125	14	103070216	103077579	1	8	7	22	61	7	10	960	3839	1293	304	853	B2RUP8	Q3UMW8
ENSMUST00000022722	ENSMUSG00000022126	14	103046977	103056573	1	20	13	28	24	13	16	360	2406	386	409	744		
ENSMUST00000022725	ENSMUSG00000022129	14	118012792	118052246	-1	17	16	28	19	17	7	0	0	0	0	0		P29812
ENSMUST00000022727	ENSMUSG00000022130	14	118111911	118132765	-1	24	18	42	36	28	14	172	863	257	556	232		Q8VDR7
ENSMUST00000022728	ENSMUSG00000022131	14	118137127	118164232	1	428	317	4310	705	201	92	26	73	25	31	65		Q8BPS4
ENSMUST00000022734	ENSMUSG00000022136	14	118937932	118981702	1	14	26	21	51	17	8	418	1283	821	1009	764	Q3UFV9	Q91YW3
ENSMUST00000022744	ENSMUSG00000022144	15	7811011	7837575	1	33	25	20	139	32	18	0	0	0	0	0		P48540
ENSMUST00000022746	ENSMUSG00000022146	15	6813577	6874969	-1	7	18	11	26	11	0	0	0	0	52	22	G3X8V6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000022749	ENSMUSG00000022149	15	6445327	6498751	1	4	5	11	2	6	0	0	0	0	1	0		
ENSMUST00000022751	ENSMUSG00000022151	15	5185525	5218336	1	6	4	6	11	5	4	0	93	21	128	30		Q9D6K7
ENSMUST00000022757	ENSMUSG00000015441	14	56205266	56211407	-1	7	3	13	10	13	4	0	0	0	14	1	Q497Z7	P08883
ENSMUST00000022765	ENSMUSG00000022159	14	52261759	52279545	-1	0	0	0	21	11	0	14	20	0	0	0	Q0PD64	P59279
ENSMUST00000022766	ENSMUSG00000016831	14	52279146	52296391	1	94	88	367	162	112	38	902	2097	1223	230	761		Q8BU11
ENSMUST00000022767	ENSMUSG00000022160	14	52294668	52305128	-1	0	4	6	10	0	0	82	211	89	63	102		
ENSMUST00000022781	ENSMUSG00000022174	14	54235479	54254104	-1	3	1	13	27	7	0	450	449	290	1005	276		P61804
ENSMUST00000022782	ENSMUSG00000022175	14	54464164	54471497	1	33	27	40	258	48	14	7085	7480	5890	546	4786		Q7TQH7
ENSMUST00000022784	ENSMUSG00000022177	14	54541785	54554361	-1	13	4	11	79	8	10	157	170	117	41	97		Q8BFT2
ENSMUST00000022786	ENSMUSG00000022179	14	54583663	54605908	-1	17	4	34	58	20	6	41	62	23	3	24		Q8K2W9
ENSMUST00000022787	ENSMUSG00000022180	14	54722216	54781886	-1	63	33	293	102	68	39	105	96	95	44	250		Q9QXW9
ENSMUST00000022788	ENSMUSG00000022181	15	4727175	4815456	1	0	0	0	0	0	0	0	0	0	4	3	Q91X70	
ENSMUST00000022791	ENSMUSG00000022184	15	3965445	3979573	-1	7	5	4	94	8	1	120	528	158	46	80		Q8CHQ0
ENSMUST00000022793	ENSMUSG00000022185	14	54642161	54686931	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JIX8
ENSMUST00000022794	ENSMUSG00000022185	14	54642161	54686931	-1	0	2	0	0	0	0	98	433	98	0	178	B8JJ92	
ENSMUST00000022803	ENSMUSG00000022193	14	54614120	54617995	-1	7	9	6	196	16	2	821	997	570	679	437		O55234
ENSMUST00000022806	ENSMUSG00000089682	14	54883377	54888234	1	0	0	18	17	0	0	43	76	42	14	34		P70345
ENSMUST00000022808	ENSMUSG00000022194	14	54892500	54898169	1	0	0	0	17	0	0	0	382	204	43	130		Q8CCS6
ENSMUST00000022813	ENSMUSG00000022203	14	54916543	54926788	-1	32	23	65	461	60	23	0	0	0	1	2		Q64355
ENSMUST00000022815	ENSMUSG00000022204	14	55015454	55024135	1	7	4	8	9	10	4	237	657	272	1244	255		Q9DB96
ENSMUST00000022816	ENSMUSG00000022205	15	11981339	11996983	-1	11	6	7	28	16	2	133	190	45	209	65		P11031
ENSMUST00000022819	ENSMUSG00000022208	14	55106830	55116935	-1	19	10	23	18	24	15	0	0	0	0	0		Q80WT0
ENSMUST00000022820	ENSMUSG00000022209	14	55222007	55241435	1	5	4	13	9	11	0	0	0	1	0	0	Q149L0	
ENSMUST00000022821	ENSMUSG00000022210	14	55478758	55490338	1	3	9	11	38	17	4	43	121	52	47	50		Q99LB2
ENSMUST00000022826	ENSMUSG00000022215	14	55575617	55576952	1	10	5	11	56	18	7	0	0	0	1	0		Q91V79
ENSMUST00000022828	ENSMUSG00000022217	14	55581516	55585302	-1	5	5	14	137	4	0	10	30	4	14	12	Q793L1	Q9DB76
ENSMUST00000022830	ENSMUSG00000022221	14	55784996	55788857	-1	0	0	0	4	0	0	279	517	364	82	259		Q9QZL0
ENSMUST00000022831	ENSMUSG00000047153	14	55884969	55896781	1	33	21	83	200	45	33	1673	3025	2567	83	2519		Q80U38
ENSMUST00000022834	ENSMUSG00000022225	14	55941453	55944661	-1	5	8	30	15	17	4	7	19	0	22	15	A4QPC5	
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ENSMUST00000022842	ENSMUSG00000022234	15	31590800	31601847	-1	6	6	1	54	5	5	662	2255	1048	3182	1102		P80316
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ENSMUST00000022861	ENSMUSG00000072664	15	9273319	9315032	1	19	16	15	11	13	7	0	0	0	0	0		Q3UP75
ENSMUST00000022865	ENSMUSG00000022255	15	34082694	34142386	1	2	4	0	9	0	3	228	398	272	40	154		Q80WJ7
ENSMUST00000022867	ENSMUSG00000022257	15	34238026	34284295	1	13	9	18	181	14	7	83	133	67	35	60	B2CZK6	Q91XQ6
ENSMUST00000022871	ENSMUSG00000022261	15	32920723	33034730	1	21	14	32	18	19	6	1	3	3	133	75		P43407
ENSMUST00000022875	ENSMUSG00000022265	15	27466677	27594909	1	18	10	22	112	34	15	71	114	75	78	356	Q3UG85	Q9JHZ2
ENSMUST00000022881	ENSMUSG00000022270	15	25843264	25973687	1	8	6	7	87	13	3	1179	3025	1120	217	776		Q8VE91
ENSMUST00000022882	ENSMUSG00000022272	15	25622525	25813673	1	26	23	89	0	4	25	0	12	14	9	21	E9Q5G1	
ENSMUST00000022890	ENSMUSG00000022280	15	36239934	36283147	-1	19	21	41	97	29	8	407	1256	659	208	521		P50636
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ENSMUST00000022895	ENSMUSG00000022286	15	37233036	37363569	1	0	10	25	39	0	0	0	0	0	0	2		Q8K5C0
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ENSMUST00000022901	ENSMUSG00000022292	15	37923952	37961318	-1	22	22	41	127	37	10	154	459	210	153	234		Q6PEE3
ENSMUST00000022904	ENSMUSG00000022295	15	38661904	38692443	1	9	8	27	41	7	5	446	2118	744	713	392		Q9Z1G3
ENSMUST00000022906	ENSMUSG00000022297	15	39006280	39038186	1	12	8	18	87	39	6	1	2	2	8	12	Q542J1	Q61089
ENSMUST00000022908	ENSMUSG00000022299	15	39094191	39112716	-1	3	4	6	125	14	4	52	169	84	41	75		Q8BMG8
ENSMUST00000022909	ENSMUSG00000022300	15	39112865	39146856	1	9	8	18	10	1	1	146	680	252	971	187		Q6PAC3
ENSMUST00000022913	ENSMUSG00000022303	15	39745932	39760934	1	20	12	32	21	11	5	0	0	1	2	0		Q7TNJ0
ENSMUST00000022915	ENSMUSG00000022304	15	39768485	39857470	-1	4	11	12	19	12	10	0	0	0	0	0		Q9EQF5
ENSMUST00000022916	ENSMUSG00000022305	15	39870603	39943994	-1	24	23	25	0	25	0	118	310	223	54	172		Q8BUJ9
ENSMUST00000022918	ENSMUSG00000022307	15	41447482	41861048	1	10	0	0	0	4	0	30	107	27	0	0		Q4KMM3
ENSMUST00000022921	ENSMUSG00000022309	15	42424727	42676977	-1	19	22	34	8	19	11	4	14	11	42	13		O08538
ENSMUST00000022925	ENSMUSG00000022312	15	51786558	51865481	-1	27	22	31	93	27	12	1545	4222	2009	1478	1326	Q5M9L0	Q91WK2
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ENSMUST00000022947	ENSMUSG00000022324	15	34306680	34436242	1	0	19	35	0	0	12	0	3	3	6	11		O08746
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ENSMUST00000022960	ENSMUSG00000022336	15	43250040	43282736	-1	11	9	5	28	16	11	307	1597	598	1911	335	Q3UIG0	P60229
ENSMUST00000022962	ENSMUSG00000022337	15	43477229	43527777	1	3	1	3	10	3	1	180	1207	414	872	196	Q6A0D1	Q9CRD2
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ENSMUST00000022977	ENSMUSG00000022351	15	59315077	59331192	1	0	0	0	0	0	0	114	212	221	56	167	Q3TQK8	P52019
ENSMUST00000022980	ENSMUSG00000022354	15	58933810	58939489	1	7	6	10	35	6	2	1104	2398	706	3014	683		Q9CQJ8
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ENSMUST00000022986	ENSMUSG00000022358	15	58175879	58214892	-1	74	74	163	376	118	44	22	94	42	18	59		Q9CPU7
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ENSMUST00000022995	ENSMUSG00000022366	15	57243767	57477625	-1	1	0	1	7	0	0	0	0	0	0	0	Q8R0S9	
ENSMUST00000022998	ENSMUSG00000022369	15	55557408	55626423	1	0	0	0	0	0	4	13	30	21	39	51		Q8BJS8
ENSMUST00000023006	ENSMUSG00000022375	15	66379858	66500910	-1	5	7	21	28	14	16	0	1	0	1	1		O88978
ENSMUST00000023007	ENSMUSG00000022376	15	64699042	64922296	-1	37	23	33	314	49	31	0	0	0	0	0		P97490
ENSMUST00000023008	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	76	17	0	0	0	0	0	0	E9QN63	

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ENSMUST00000023015	ENSMUSG00000022382	15	85535439	85581821	-1	0	0	5	113	0	0	1	0	0	23	112		P28047
ENSMUST00000023019	ENSMUSG00000022386	15	85879312	85897394	1	0	0	0	0	0	0	8	55	18	8	0		Q9DAT5
ENSMUST00000023024	ENSMUSG00000022389	15	81802421	81826861	1	0	7	6	88	4	0	51	96	49	0	58		Q9JLC6
ENSMUST00000023029	ENSMUSG00000022394	15	81663889	81688315	1	17	0	28	27	0	0	114	102	100	0	54		P59178
ENSMUST00000023036	ENSMUSG00000022400	15	81466316	81476369	1	31	49	50	78	45	27	561	1286	476	1563	292		P62878
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ENSMUST00000023044	ENSMUSG00000022408	15	80671847	80700420	1	18	12	76	247	36	21	5	11	2	1	3		
ENSMUST00000023048	ENSMUSG00000022412	15	80234080	80253366	1	23	13	62	40	42	18	409	722	461	38	276	B2RPW2	Q8BGV8
ENSMUST00000023050	ENSMUSG00000022414	15	80133154	80161701	1	17	14	41	28	30	16	354	286	237	32	180		Q8CF89
ENSMUST00000023053	ENSMUSG00000022371	15	55307750	55520803	1	4	7	59	6	9	0	0	0	0	1	23		Q80X19
ENSMUST00000023054	ENSMUSG00000009585	15	79891659	79915906	1	1	5	11	4	0	0	0	0	0	0	14	Q3TI69	
ENSMUST00000023055	ENSMUSG00000022420	15	79761453	79777849	-1	16	14	37	22	20	12	353	331	153	28	145		Q9DCM4
ENSMUST00000023056	ENSMUSG00000022419	15	55112317	55259271	1	42	37	219	0	11	0	3	0	0	0	2	B2ZRS7	Q570Y9
ENSMUST00000023057	ENSMUSG00000022421	15	79786352	79804766	-1	0	0	0	89	0	0	0	0	0	0	0	F7BX42	
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ENSMUST00000023060	ENSMUSG00000089837	15	79789675	79834237	-1	0	0	1	0	0	0	0	0	0	0	0	H3BLN6	
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ENSMUST00000023062	ENSMUSG00000022427	15	79670861	79672862	1	6	0	10	74	13	5	1052	2779	935	1053	700		Q9CPQ3
ENSMUST00000023064	ENSMUSG00000022428	15	79659227	79667660	1	9	3	17	16	6	8	232	301	147	154	124		Q9D1C2
ENSMUST00000023065	ENSMUSG00000022429	15	79561500	79605084	-1	4	5	9	38	4	2	4	5	12	3	1	Q14AN8	Q61880
ENSMUST00000023067	ENSMUSG00000022431	15	85132099	85144569	1	11	10	15	50	21	9	0	0	0	1	1	G3X8W0	
ENSMUST00000023068	ENSMUSG00000022432	15	85064691	85131957	-1	6	7	11	57	9	9	0	1	0	1	0	A1L2Z0	Q920F6
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ENSMUST00000023075	ENSMUSG00000022440	15	78523346	78529625	-1	11	0	28	31	25	0	11	34	17	11	55		Q6IR41
ENSMUST00000023076	ENSMUSG00000058099	15	82997721	83033306	-1	0	0	0	6	0	11	68	0	113	0	54		Q8R4V1
ENSMUST00000023083	ENSMUSG00000061740	15	82370528	82380260	-1	20	17	26	30	30	12	11	39	20	5	20	Q9JKY7	
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ENSMUST00000023087	ENSMUSG00000022451	15	94577951	94589889	-1	11	13	18	14	6	5	353	1294	562	262	498		Q91YR1
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ENSMUST00000023095	ENSMUSG00000022456	15	82274935	82294442	1	27	39	79	62	37	18	2	7	2	4	34		Q9Z1S5
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ENSMUST00000023104	ENSMUSG00000022466	15	97675105	97705822	-1	11	15	13	34	21	10	16	63	11	19	34		Q9D706
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ENSMUST00000023110	ENSMUSG00000022472	15	81992523	82033862	-1	2	0	2	19	3	0	4	3	8	0	0	F8WJJ8	
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ENSMUST00000023113	ENSMUSG00000022476	15	81915030	81926213	-1	18	11	37	153	38	14	25	30	18	10	16		Q9D2C6
ENSMUST00000023116	ENSMUSG00000022477	15	81872309	81915133	1	19	19	40	28	32	11	1050	1770	1437	352	1216		Q99KI0
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ENSMUST00000023143	ENSMUSG00000022500	16	10959275	11066157	-1	14	14	51	78	16	15	11497	25006	9265	1269	5908		Q9JLJ0
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ENSMUST00000023146	ENSMUSG00000022503	16	10411948	10424428	1	5	7	0	25	5	0	132	249	105	34	157		Q9R060
ENSMUST00000023147	ENSMUSG00000022504	16	10488178	10527564	1	67	74	412	88	114	46	65	42	53	7	197	Q3U5G4	P79621
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ENSMUST00000023151	ENSMUSG00000022508	16	23965052	23988852	-1	16	12	40	65	15	9	2081	5387	3138	233	2927	Q544F9	P41183
ENSMUST00000023154	ENSMUSG00000022512	16	26356642	26371841	-1	9	7	27	32	17	9	32	50	28	19	24	Q4FJV3	O88551
ENSMUST00000023156	ENSMUSG00000022514	16	26581704	26730117	1	8	10	13	10	21	6	1306	2856	1984	1315	2092		Q61730
ENSMUST00000023157	ENSMUSG00000022515	16	4941415	4964237	-1	32	11	32	74	34	11	432	917	516	100	508		Q9CZK6
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ENSMUST00000023161	ENSMUSG00000022519	16	4480216	4541816	-1	35	37	63	56	59	26	0	0	0	0	0		Q7TQ48
ENSMUST00000023165	ENSMUSG00000022521	16	4081328	4213997	-1	77	54	263	133	84	38	878	1372	2197	69	1867	F8VPR5	
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ENSMUST00000023176	ENSMUSG00000022529	16	3744093	3750790	1	5	2	37	128	17	0	223	752	295	98	325	Q8CF60	
ENSMUST00000023179	ENSMUSG00000033669	15	76879259	76892392	1	16	23	45	37	25	13	38	117	68	30	62	Q3TFZ4	
ENSMUST00000023180	ENSMUSG00000022534	16	3707215	3718124	-1	0	0	23	0	0	0	350	2413	744	233	1032		Q9JJ26
ENSMUST00000023189	ENSMUSG00000022536	16	5013906	5049910	-1	0	16	35	71	32	10	176	1189	1129	208	1113		Q922P9
ENSMUST00000023191	ENSMUSG00000022540	16	5008730	5013553	-1	16	8	14	30	15	14	1624	2624	1139	217	859		Q3TDK6
ENSMUST00000023203	ENSMUSG00000022546	15	76696764	76699674	1	18	10	32	78	15	11	33	56	37	15	30	Q566C3	Q8QZR5
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ENSMUST00000023211	ENSMUSG00000022552	15	76347040	76351111	-1	0	0	0	0	0	4	506	523	469	67	322		Q91WA6
ENSMUST00000023212	ENSMUSG00000022553	15	76351294	76354380	1	0	0	0	0	11	0	1845	2419	1221	270	929		Q9D0U6
ENSMUST00000023213	ENSMUSG00000022554	15	76368898	76371403	1	13	15	26	481	39	9	31	58	21	9	38		Q8C3I8
ENSMUST00000023214	ENSMUSG00000022555	15	76502015	76511951	-1	0	0	17	165	12	1	810	1567	625	131	523	Q54AA6	Q9Z2A7
ENSMUST00000023217	ENSMUSG00000022557	15	76452996	76477269	-1	34	27	44	131	45	16	242	265	197	71	255		P97452

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ENSMUST00000023219	ENSMUSG00000022559	15	76535730	76538746	-1	4	5	22	189	25	10	377	582	300	63	258		Q9QXW0
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ENSMUST00000023225	ENSMUSG00000022564	15	76246807	76249904	1	16	14	34	62	19	16	38289	68129	28540	4118	29082		Q9ESF4
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ENSMUST00000023237	ENSMUSG00000022574	15	75890964	75894481	-1	25	12	65	178	35	9	704	908	368	38	209		Q8CC86
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ENSMUST00000023244	ENSMUSG00000022580	15	75704280	75714410	1	3	7	0	9	0	0	0	0	0	0	0		Q61085
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ENSMUST00000023282	ENSMUSG00000022613	15	89334398	89337015	1	10	0	12	10	4	0	0	0	0	0	0		Q9QXN5
ENSMUST00000023283	ENSMUSG00000022614	15	89351004	89355659	-1	34	18	56	143	44	14	431	367	341	36	285		Q8C3X8
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ENSMUST00000023289	ENSMUSG00000022617	15	89416405	89429908	-1	0	0	0	17	0	0	131	392	313	13	309	Q54AG5	O55229
ENSMUST00000023291	ENSMUSG00000022619	15	89453913	89464468	1	52	26	136	368	69	31	1	0	0	0	1	Q548W8	Q9ERE9
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ENSMUST00000023295	ENSMUSG00000022622	15	89568326	89574585	1	9	9	29	22	16	12	0	0	0	0	0		P23578
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ENSMUST00000023334	ENSMUSG00000022656	16	46387706	46498525	-1	4	7	5	4	4	2	0	0	1	5	1		Q9JLB9
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ENSMUST00000023341	ENSMUSG00000022661	16	45382135	45409053	-1	0	17	27	164	16	16	1	3	0	1	0	E9QMY1	
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ENSMUST00000023348	ENSMUSG00000022668	16	44736768	44746363	-1	0	0	0	0	0	0	13	31	0	14	0		Q9CY28
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ENSMUST00000023352	ENSMUSG00000022672	16	15637866	15842235	1	36	34	39	29	48	17	44	117	87	28	117		P97313
ENSMUST00000023353	ENSMUSG00000022673	16	15623897	15637400	-1	16	12	33	132	29	8	277	819	505	101	394	Q542F4	P49717
ENSMUST00000023356	ENSMUSG00000022676	16	14705852	14709395	1	90	53	448	203	77	35	4	11	4	0	16	Q3UZ96	P97469
ENSMUST00000023357	ENSMUSG00000022677	16	14299244	14317375	-1	9	0	0	2	0	0	236	799	264	670	84		Q9CZS3
ENSMUST00000023359	ENSMUSG00000022678	16	14163275	14192928	1	0	9	0	35	8	2	0	136	78	0	52		Q9CZA6
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ENSMUST00000023361	ENSMUSG00000022680	16	13833148	13903131	-1	40	36	54	54	37	31	36	148	80	42	139		
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ENSMUST00000023363	ENSMUSG00000022682	16	13780699	13814840	1	26	15	29	74	26	8	89	228	129	22	114		B2RS91
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ENSMUST00000023365	ENSMUSG00000022684	16	13671858	13703612	1	6	8	32	86	15	0	120	485	288	93	195		
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ENSMUST00000023390	ENSMUSG00000022705	16	43762221	43822932	1	15	10	21	10	18	10	0	0	1	0	0	Q0VEC4	P30728
ENSMUST00000023391	ENSMUSG00000022706	16	18872018	18876767	-1	19	17	45	92	20	7	54	153	62	165	80	Q3UKS6	Q9Z2Q5
ENSMUST00000023393	ENSMUSG00000022707	16	70313949	70569716	1	0	0	0	0	0	0	7	0	0	0	0	F6ZHD8	
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ENSMUST00000023400	ENSMUSG00000022715	16	8409276	8425136	-1	20	18	41	209	15	12	0	0	0	0	0		Q9D563
ENSMUST00000023405	ENSMUSG00000022722	16	59612949	59639391	-1	4	4	9	0	0	0	0	6	3	17	4	Q3TUM2	O88848
ENSMUST00000023407	ENSMUSG00000022724	16	59471775	59492461	1	0	0	0	55	0	0	30	108	42	54	30		Q8CD15
ENSMUST00000023426	ENSMUSG00000022744	16	58727910	58734251	1	1	5	0	42	7	0	244	717	197	92	146		Q9CQX5
ENSMUST00000023431	ENSMUSG00000022749	16	57168866	57231466	-1	6	7	18	22	10	6	704	2701	1526	1183	1104		Q8K0F1
ENSMUST00000023432	ENSMUSG00000022751	16	57156671	57167332	-1	6	5	14	19	5	6	33	160	31	98	54		Q9JHW2
ENSMUST00000023434	ENSMUSG00000022753	16	57266139	57292865	-1	55	89	16	15	21	14	6	0	10	0	2		Q9D4D7
ENSMUST00000023435	ENSMUSG00000022754	16	56805161	56886166	-1	6	7	7	11	7	9	0	0	0	5	0	Q8BFU6	
ENSMUST00000023437	ENSMUSG00000022755	16	56724609	56795855	-1	9	11	21	2	19	8	2	4	1	0	0		Q8BM96
ENSMUST00000023441	ENSMUSG00000022758	16	17561885	17577800	1	25	16	11	5	17	6	0	0	0	0	0	G3X8W3	
ENSMUST00000023442	ENSMUSG00000022759	16	17544465	17561247	-1	180	120	1556	328	263	104	9	15	13	4	15		Q14BP6
ENSMUST00000023444	ENSMUSG00000022761	16	17508688	17526333	1	0	0	0	0	12	0	423	381	320	63	204		Q9CQ33
ENSMUST00000023448	ENSMUSG00000022763	16	17489611	17507485	1	6	0	18	38	11	4	0	1	0	0	0		Q3TY86
ENSMUST00000023449	ENSMUSG00000022765	16	17406003	17430826	1	14	11	14	81	23	9	1065	4811	2095	623	1275		Q9ERB0
ENSMUST00000023450	ENSMUSG00000022766	16	17331371	17343575	1	0	0	15	20	0	0	0	0	0	0	0		P49182
ENSMUST00000023452	ENSMUSG00000022768	16	17139064	17147229	-1	53	32	117	175	58	48	14	28	13	0	11		Q80X53
ENSMUST00000023453	ENSMUSG00000022769	16	17130138	17132383	-1	9	7	25	195	28	13	118	227	89	45	140		Q9ESP1
ENSMUST00000023454	ENSMUSG00000022770	16	31663443	31873356	1	0	0	0	0	0	0	46	0	168	35	165	H7BWY4	
ENSMUST00000023455	ENSMUSG00000022771	16	17086555	17111257	-1	6	2	7	10	5	0	538	1656	819	290	640		Q9D787

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000023457	ENSMUSG00000022772	16	31962506	32003287	-1	11	17	24	65	29	21	59	152	134	21	126		Q6NXL6
ENSMUST00000023460	ENSMUSG00000022774	16	31948513	31961781	1	6	4	15	55	22	1	67	371	125	148	100		Q9CQ49
ENSMUST00000023462	ENSMUSG00000063358	16	16983382	17047453	1	0	0	3	60	2	7	516	1389	1131	156	600		P63085
ENSMUST00000023464	ENSMUSG00000022780	16	31878810	31899020	1	44	33	47	69	50	21	1	0	0	0	0	Q544J8	Q9R0R1
ENSMUST00000023465	ENSMUSG00000022779	16	16870736	16892990	1	0	0	0	0	0	0	29	13	95	18	25	Q3UJF5	Q9Z321
ENSMUST00000023467	ENSMUSG00000022781	16	32016290	32079342	-1	18	17	29	77	28	9	2941	8599	5773	441	3381		Q8CIN4
ENSMUST00000023468	ENSMUSG00000022783	16	16753016	16829456	-1	0	6	7	1	5	6	3	1	4	1	2	Q497N2	Q9JLI7
ENSMUST00000023469						21	19	62	26	21	7	3	40	11	10	18		
ENSMUST00000023474	ENSMUSG00000022787	16	32247227	32257083	1	11	12	22	5	22	4	24	102	27	44	14		Q9DB94
ENSMUST00000023477	ENSMUSG00000022789	16	16312235	16359030	-1	22	22	53	18	35	0	107	180	85	98	102		Q8K1M6
ENSMUST00000023478	ENSMUSG00000022790	16	38901471	39027159	1	55	27	235	141	58	27	0	4	0	2	0		P0C673
ENSMUST00000023482	ENSMUSG00000022793	16	38742264	38769049	1	0	0	0	15	4	0	0	0	0	0	0		Q9JJ04
ENSMUST00000023486	ENSMUSG00000022797	16	32608920	32632794	1	12	3	23	95	4	4	69	197	94	178	101	Q542D9	Q62351
ENSMUST00000023487	ENSMUSG00000022799	16	38598340	38713274	-1	66	58	289	375	90	42	63	92	118	27	205	B2RSI0	A6X8Z5
ENSMUST00000023489	ENSMUSG00000022800	16	32877500	32908963	1	0	0	0	21	9	1	73	276	56	91	72		Q91Z49
ENSMUST00000023491	ENSMUSG00000022801	16	32914100	33015647	1	17	15	21	97	35	4	476	949	934	74	657		Q8BVU0
ENSMUST00000023494	ENSMUSG00000022803	16	38362209	38378216	1	3	16	36	23	26	14	0	0	0	0	6	Q6P3F7	
ENSMUST00000023497	ENSMUSG00000022802	16	33062521	33127695	1	74	40	82	368	77	37	9	11	17	3	18		Q8BMN4
ENSMUST00000023501	ENSMUSG00000022805	16	38297754	38342143	-1	13	11	14	13	12	3	0	0	0	0	0		Q8BRC6
ENSMUST00000023502	ENSMUSG00000022808	16	33251456	33299562	1	15	14	30	142	21	6	718	2637	1379	2068	864		Q91YJ2
ENSMUST00000023504	ENSMUSG00000022809	16	38248323	38294824	-1	13	17	25	21	28	12	0	0	0	1	0	Q0P525	O54915
ENSMUST00000023507	ENSMUSG00000022812	16	38089001	38246084	1	111	88	382	426	110	66	758	1664	1586	116	1234	Q5KU03	Q9WV60
ENSMUST00000023509	ENSMUSG00000062901	16	20097554	20127744	1	52	44	86	129	52	26	2284	4221	4812	1184	2624		Q8BRG6
ENSMUST00000023510	ENSMUSG00000022814	16	33954782	33967038	-1	17	19	37	70	25	0	137	162	114	122	79	Q544K9	P13439
ENSMUST00000023513	ENSMUSG00000022818	16	20308387	20323065	-1	15	0	10	9	0	0	0	0	0	0	0	E9PZ31	
ENSMUST00000023514	ENSMUSG00000022820	16	37647170	37654453	-1	5	4	7	58	11	3	61	88	58	293	26		Q9CQC7
ENSMUST00000023520	ENSMUSG00000022824	16	33794037	33819934	1	38	42	174	0	53	28	71	176	0	18	27	Q3V1S6	P19467
ENSMUST00000023524	ENSMUSG00000022827	16	37539885	37572385	1	0	0	0	0	0	0	28	184	45	34	21		Q9D4V7
ENSMUST00000023525	ENSMUSG00000022828	16	37509790	37539789	-1	21	15	20	15	19	8	104	258	112	127	94		Q9D0D5
ENSMUST00000023526	ENSMUSG00000022829	16	37114942	37384962	-1	3	4	0	0	0	0	0	0	0	0	0		Q5DQR4
ENSMUST00000023530	ENSMUSG00000022832	16	34649921	34678618	1	3	6	5	0	2	5	0	0	0	0	0		Q9ESG2
ENSMUST00000023531	ENSMUSG00000022831	16	36934983	36963212	1	17	12	22	16	22	18	9265	18524	10252	1054	7757		P49710
ENSMUST00000023532	ENSMUSG00000022833	16	34690616	34725194	1	23	13	23	62	25	7	8	30	21	24	18		Q8K2J4
ENSMUST00000023534	ENSMUSG00000034243	16	36875140	36933085	1	0	0	0	72	4	2	0	0	0	0	0	Q3U286	
ENSMUST00000023535	ENSMUSG00000022837	16	36828385	36872721	1	0	0	7	0	0	4	5	2	2	16	5		Q8BP00
ENSMUST00000023537	ENSMUSG00000022838	16	36792884	36875003	-1	0	0	0	0	0	0	0	0	0	0	0	K4DI60	
ENSMUST00000023538	ENSMUSG00000022836	16	34745210	35002420	1	65	48	125	77	95	44	9	15	16	15	49	B1B1A8	
ENSMUST00000023550	ENSMUSG00000022844	16	35397313	35490873	-1	17	13	27	100	22	6	17	28	16	13	35		Q921X9
ENSMUST00000023554	ENSMUSG00000022848	16	35694062	35769356	-1	71	66	79	183	90	41	91	297	110	33	134		Q8BFQ6
ENSMUST00000023555	ENSMUSG00000022849	16	35770386	35828446	1	53	44	59	146	67	32	163	452	173	77	215		Q8BK58
ENSMUST00000023559	ENSMUSG00000022853	16	21761287	21787844	-1	15	13	30	44	25	6	6	3	10	5	13		Q9DBM2
ENSMUST00000023561	ENSMUSG00000022855	16	22009484	22049269	1	14	18	50	67	28	6	493	2774	1125	164	869		Q91ZX6
ENSMUST00000023562	ENSMUSG00000022856	16	21934327	21947552	-1	10	8	15	70	14	4	7	30	6	10	18		Q9D8U2
ENSMUST00000023564	ENSMUSG00000022858	16	22244549	22266005	-1	6	12	12	0	11	0	198	406	198	329	89	F8WJG3	
ENSMUST00000023566	ENSMUSG00000022857	16	78953008	79091097	-1	0	0	0	0	0	5	0	0	0	0	0		P97435
ENSMUST00000023568	ENSMUSG00000022860	16	78930948	78951733	1	0	2	0	9	4	5	0	0	0	0	0		Q9CXM0
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ENSMUST00000023572	ENSMUSG00000022865	16	78301496	78359785	1	8	14	18	151	36	10	14	43	7	22	60		P97792
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ENSMUST00000023580	ENSMUSG00000022867	16	77014069	77116779	1	14	16	10	4	22	7	1048	2842	2162	321	1653		P57080
ENSMUST00000023583	ENSMUSG00000022868	16	22892042	22899438	1	11	10	18	8	17	7	0	0	0	176	0	Q3UEK9	P29699
ENSMUST00000023587	ENSMUSG00000022871	16	22918382	22939766	1	0	4	3	0	2	0	0	0	0	7	0		Q9QXC1
ENSMUST00000023589	ENSMUSG00000022875	16	23057865	23082068	1	6	4	11	0	10	3	0	0	0	7	0		
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ENSMUST00000023593	ENSMUSG00000022878	16	23146536	23158028	1	4	7	3	6	13	10	0	0	0	0	0		Q60994
ENSMUST00000023598	ENSMUSG00000022881	16	23113943	23127737	-1	0	0	0	7	1	0	31	90	27	53	16		Q99J62
ENSMUST00000023599	ENSMUSG00000022884	16	23107444	23114136	1	5	4	7	26	0	0	0	14	7	0	6	Q52KC1	P10630
ENSMUST00000023600	ENSMUSG00000022883	16	72663149	73046095	1	33	34	97	199	61	38	1	0	0	0	1	G5E843	
ENSMUST00000023601	ENSMUSG00000022885	16	23224740	23360350	1	9	0	16	34	14	26	40	27	106	0	207		Q64685
ENSMUST00000023602	ENSMUSG00000022886	13	27801654	27808729	1	4	3	3	0	3	0	0	0	0	0	0		Q9JHK0
ENSMUST00000023608	ENSMUSG00000022890	16	84827866	84835625	-1	0	0	0	34	0	0	360	1093	515	1820	398		P97450
ENSMUST00000023610	ENSMUSG00000022893	16	85793827	85803113	-1	24	14	40	321	36	10	1	4	0	6	27		P97857
ENSMUST00000023611	ENSMUSG00000022894	16	85858170	85901125	-1	36	27	76	221	29	26	17	91	22	5	31		Q9R001
ENSMUST00000023612	ENSMUSG00000022895	16	95702075	95721051	1	19	12	36	260	42	17	1554	2954	1519	161	2735	Q3UP99	P15037
ENSMUST00000023614	ENSMUSG00000022897	16	94570010	94695517	1	34	20	31	4	41	11	1	631	0	84	178	A9C475	Q61214
ENSMUST00000023615	ENSMUSG00000022898	16	94497783	94526830	-1	12	11	30	98	15	10	761	2194	838	948	623		O35075
ENSMUST00000023616	ENSMUSG00000022899	16	36750178	36784962	-1	9	0	5	12	8	5	2	0	0	0	1	E9QMN8	
ENSMUST00000023617	ENSMUSG00000022900	16	36693978	36726804	1	0	0	0	134	16	0	0	0	0	0	0		Q8CBR1
ENSMUST00000023619	ENSMUSG00000022902	16	36403946	36408363	-1	10	11	25	54	5	25	18613	75192	40499	114376	18184		P35174
ENSMUST00000023622	ENSMUSG00000022906	16	35938470	35972605	1	0	0	0	0	0	0	296	2331	575	1123	639	H7BWY5	
ENSMUST00000023629	ENSMUSG00000022912	16	62854307	62929346	1	10	16	25	57	6	5	92	337	188	94	272	Q3TR66	Q08761
ENSMUST00000023630	ENSMUSG00000022913	16	95979933	95990960	-1	0	3	0	72	0	4	38	93	32	81	38		Q9JK23
ENSMUST00000023631	ENSMUSG00000022914	16	95992092	96082526	-1	0	0	9	16	0	7	96	50	231	21	179		Q921C3
ENSMUST00000023648	ENSMUSG00000022931	16	88820215	88829844	1	1	1	0	0	0	0	0	0	0	0	0	F6Z3P4	
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ENSMUST00000023655	ENSMUSG00000000386	16	97447035	97462907	-1	5	0	17	11	7	3	0	0	0	0	0	E9Q0J3	
ENSMUST00000023660	ENSMUSG00000022941	16	94328420	94336935	1	53	61	70	139	78	28	1	7	1	0	7		Q924S9
ENSMUST00000023666	ENSMUSG00000022945	16	93883901	93906115	1	0	0	41	20	12	3	49	0	0	38	39		Q9D0N7
ENSMUST00000023669	ENSMUSG00000022948	16	93583457	93604063	-1	0	2	0	0	0	4	0	0	0	0	9	G3X9W6	
ENSMUST00000023670	ENSMUSG00000022949	16	92485736	92541243	1	29	19	61	504	46	12	0	0	0	0	0		Q8BHB9
ENSMUST00000023672	ENSMUSG00000022951	16	92391953	92466146	-1	20	9	26	4	13	0	307	726	172	55	132	Q542V6	Q9JHG6
ENSMUST00000023673	ENSMUSG00000022952	16	92601466	92826149	-1	24	15	53	26	39	23	297	542	381	40	238	Q3UM65	
ENSMUST00000023677	ENSMUSG00000022956	16	91684398	91931687	-1	2	0	6	48	4	3	600	1290	624	2869	448		Q9DB20
ENSMUST00000023682	ENSMUSG00000022960	16	91677268	91688765	-1	0	0	0	0	0	0	107	361	97	0	9		Q9QXP4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000023684	ENSMUSG00000022962	16	91621186	91646952	-1	15	3	0	37	24	7	49	41	62	30	84		Q64737
ENSMUST00000023686	ENSMUSG00000022964	16	91574503	91597800	-1	6	6	20	14	9	3	2529	4894	2576	722	1631		Q9D1X9
ENSMUST00000023687	ENSMUSG00000022965	16	91547072	91565169	1	0	16	24	142	0	4	1600	6379	2272	446	1544	Q63953	
ENSMUST00000023689	ENSMUSG00000022967	16	91485238	91507441	1	14	20	7	72	36	13	587	1890	844	151	772		P33896
ENSMUST00000023691	ENSMUSG00000022969	16	91406164	91425834	1	0	0	0	0	1	0	1571	4461	1954	900	1417	Q8VHM7	
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ENSMUST00000023694	ENSMUSG00000022972	16	90925809	90934927	-1	0	3	0	0	0	0	25	36	23	39	34		Q8BL95
ENSMUST00000023698	ENSMUSG00000022974	16	91014037	91044543	-1	0	0	0	0	0	0	135	840	253	42	174	F6YY19	
ENSMUST00000023707	ENSMUSG00000022982	16	90220742	90226322	1	0	5	10	60	6	4	525	1849	485	885	453		P08228
ENSMUST00000023709	ENSMUSG00000061527	15	101707070	101712891	-1	22	11	122	71	32	7	0	0	0	0	0	Q32P04	Q922U2
ENSMUST00000023710	ENSMUSG00000051879	15	101733950	101743109	-1	21	19	33	22	43	16	0	0	0	0	0		Q9R0H5
ENSMUST00000023712	ENSMUSG00000064201	15	101810689	101818169	-1	26	15	71	104	31	25	0	0	0	0	0		Q3TTY5
ENSMUST00000023713	ENSMUSG00000049548	15	101541229	101550659	-1	20	11	46	81	26	17	0	0	0	0	0		Q99M74
ENSMUST00000023714	ENSMUSG00000048699	15	101552356	101562950	-1	24	16	60	36	29	19	0	0	0	0	0	E9Q1Z0	
ENSMUST00000023718	ENSMUSG00000067613	15	101485131	101491512	-1	14	10	13	57	22	6	8	7	0	0	2	E9Q1Y9	
ENSMUST00000023720	ENSMUSG00000044294	15	101525026	101532820	-1	19	18	118	45	55	16	0	0	0	0	0		Q99M73
ENSMUST00000023722	ENSMUSG00000022987	15	98285588	98296130	-1	5	27	23	56	20	0	0	0	0	0	0		Q8BZ34
ENSMUST00000023726	ENSMUSG00000022991	15	98480400	98482683	-1	2	1	3	5	3	3	0	0	0	0	0	A0A077S9Z6	P29752
ENSMUST00000023727	ENSMUSG00000022992	15	98518821	98534244	-1	20	10	13	138	21	14	63	302	120	60	101	F8WJE3	
ENSMUST00000023728	ENSMUSG00000022993	15	98571004	98589588	1	3	4	3	6	9	5	0	1	0	0	0	Q8CDT5	
ENSMUST00000023732	ENSMUSG00000022996	15	98771753	98778150	-1	15	3	12	262	28	7	2	0	0	3	3		P48614
ENSMUST00000023734	ENSMUSG00000022997	15	98789857	98793837	1	13	14	54	384	28	8	0	0	0	0	0	Q3UR96	P04426
ENSMUST00000023736	ENSMUSG00000022999	15	98903921	98918231	-1	0	0	13	70	5	0	1107	1434	894	188	820		Q9D1E5
ENSMUST00000023737	ENSMUSG00000023000	15	98893031	98898540	-1	18	9	27	325	32	7	0	0	0	0	4	Q544P6	Q61488
ENSMUST00000023741	ENSMUSG00000048154	15	98831669	98871204	-1	177	0	176	915	259	127	2105	1134	3848	31	5569	A0A0A0MQ73	
ENSMUST00000023745	ENSMUSG00000023007	15	99295087	99317018	1	0	0	0	0	0	0	0	0	0	0	0	E9QMI6	
ENSMUST00000023747	ENSMUSG00000023009	15	99422035	99457748	-1	43	24	216	629	82	52	34	37	25	1	47		Q6GQX2
ENSMUST00000023749	ENSMUSG00000023010	15	99392882	99410049	1	17	4	38	31	15	20	11540	21832	12070	1382	8576		Q9D2C7
ENSMUST00000023750	ENSMUSG00000023011	15	99497005	99528017	-1	52	28	93	317	83	47	1	1	3	3	4		Q8K097
ENSMUST00000023752	ENSMUSG00000023013	15	99579056	99584545	1	19	9	31	214	26	13	0	0	0	0	1	Q3UQD4	P56402
ENSMUST00000023754	ENSMUSG00000043144	15	99601400	99605477	1	16	20	34	16	29	13	0	0	0	0	0		Q8C4A0
ENSMUST00000023756	ENSMUSG00000023015	15	99620496	99651656	-1	0	0	0	18	0	10	242	383	154	47	132		Q9WVM1
ENSMUST00000023758	ENSMUSG00000023017	15	99670718	99701127	1	39	26	61	159	58	38	47	84	57	5	51		Q6NXK8
ENSMUST00000023759	ENSMUSG00000023018	15	99702287	99713995	1	13	11	35	54	43	15	202	269	212	25	166		Q61466
ENSMUST00000023760	ENSMUSG00000023019	15	99717515	99725005	1	17	18	61	31	34	18	3	6	0	4	6		P13707
ENSMUST00000023761	ENSMUSG00000023020	15	99725618	99728136	1	3	5	4	79	11	1	444	840	309	671	175		Q8BH51
ENSMUST00000023762	ENSMUSG00000023021	15	99734881	99772885	-1	0	0	0	139	8	4	507	1835	594	331	635		Q9D6K9
ENSMUST00000023768	ENSMUSG00000023026	15	100038664	100219473	1	0	0	0	0	0	0	14	0	2	0	124	D3Z5G8	
ENSMUST00000023769	ENSMUSG00000023027	15	100227819	100261244	1	15	8	73	11	14	6	550	2138	714	148	545		P81269
ENSMUST00000023774	ENSMUSG00000023030	15	100387898	100425072	-1	47	47	207	58	56	13	25	30	16	10	38		P49282
ENSMUST00000023775	ENSMUSG00000023031	15	100674425	100687920	-1	3	4	16	7	20	3	78	108	46	111	45		Q91X79
ENSMUST00000023776	ENSMUSG00000023032	15	100761747	100823968	1	74	43	157	217	108	38	3	14	13	1	13		Q8JZR6
ENSMUST00000023779	ENSMUSG00000023034	15	101266846	101274792	1	19	13	24	109	34	15	122	378	74	21	408	Q545Q1	P12813
ENSMUST00000023781	ENSMUSG00000063971	15	101447745	101453909	1	10	8	24	8	6	7	1	1	0	0	1	Q9CPR6	
ENSMUST00000023786	ENSMUSG00000023041	15	101676034	101680289	-1	20	17	57	30	44	16	0	0	0	1	0	Q3UV11	
ENSMUST00000023788	ENSMUSG00000058354	15	101689932	101694307	-1	10	11	51	22	22	11	0	0	0	0	0		P50446
ENSMUST00000023790	ENSMUSG00000046834	15	101845428	101850786	-1	22	15	50	277	29	14	0	0	0	0	1		P04104
ENSMUST00000023797	ENSMUSG00000059668	15	101918536	101924735	-1	16	14	36	87	18	15	0	0	0	0	0		P07744
ENSMUST00000023799	ENSMUSG00000061397	15	101929332	101940324	-1	19	13	49	51	21	11	0	0	0	0	0		Q8VED5
ENSMUST00000023803	ENSMUSG00000023043	15	102028216	102032026	1	18	17	24	107	20	12	6	9	3	305	313		P05784
ENSMUST00000023805	ENSMUSG00000023044	15	102176998	102189043	-1	14	8	58	27	27	6	71	290	113	24	209		Q9DBE0
ENSMUST00000023806	ENSMUSG00000023045	15	102150526	102163474	1	71	64	104	109	89	44	450	2291	890	196	1433		O88908
ENSMUST00000023807	ENSMUSG00000023046	15	102144362	102149511	1	10	3	20	115	13	4	1422	3364	874	2134	673		P47880
ENSMUST00000023809	ENSMUSG00000023047	15	102445367	102454630	1	15	8	25	23	20	9	7	14	13	2	21		Q8K592
ENSMUST00000023810	ENSMUSG00000023048	15	102459028	102462806	1	11	3	0	0	7	10	2221	2851	1252	207	940		Q9CQJ5
ENSMUST00000023812	ENSMUSG00000023050	15	102497649	102517064	-1	16	17	13	2	14	10	0	32	0	0	6		Q60700
ENSMUST00000023813	ENSMUSG00000023051	15	102518192	102523676	1	7	0	0	0	0	0	145	158	78	19	3		P97473
ENSMUST00000023814	ENSMUSG00000023052	15	102523839	102524942	-1	0	0	0	0	1	1	0	6	3	0	0		Q9WVA8
ENSMUST00000023818	ENSMUSG00000023055	15	102706779	102722178	-1	6	3	19	5	13	5	870	916	843	105	624		Q8CGU1
ENSMUST00000023820	ENSMUSG00000023057	3	122895072	122899506	1	5	3	2	0	1	2	0	0	0	0	0	Q53YP5	P55050
ENSMUST00000023826	ENSMUSG00000023064	14	34370274	34374789	-1	7	2	17	11	6	3	0	0	0	97	16	Q5GQ64	Q9Z0F7
ENSMUST00000023828	ENSMUSG00000023066	18	88971790	89131013	1	33	27	23	31	33	14	16	57	43	15	34		Q8R4Y8
ENSMUST00000023829	ENSMUSG00000023067	17	29090979	29100722	1	8	12	41	41	15	5	438	528	292	84	521	Q564P6	P39689
ENSMUST00000023830	ENSMUSG00000023068	10	52417547	52440192	1	52	51	383	254	39	20	198	708	282	135	240		Q99LJ8
ENSMUST00000023832	ENSMUSG00000023070	X	20549787	20562089	1	5	4	8	3	8	1	0	0	0	4	0		Q64374
ENSMUST00000023835	ENSMUSG00000023073	8	5085623	5105232	-1	27	28	150	41	20	14	11	56	5	2	6	Q0VBB8	P70172
ENSMUST00000023836	ENSMUSG00000023074	X	53344598	53370502	-1	7	8	10	0	8	2	0	30	27	52	65		Q8VEL0
ENSMUST00000023840	ENSMUSG00000023078	5	95956951	95961068	1	4	6	7	3	3	1	0	0	0	107	45	Q3U1E8	O55038
ENSMUST00000023845	ENSMUSG00000023083	17	36284227	36286490	-1	9	6	20	16	17	5	0	0	1	0	1	Q85ZW9	
ENSMUST00000023846	ENSMUSG00000023084	3	87736923	87748625	-1	14	13	36	14	11	4	0	14	2	2	0		Q9D3W5
ENSMUST00000023849	ENSMUSG00000023087	3	51224447	51251644	1	6	0	2	188	3	0	0	0	0	0	0	B2RTJ8	O35710
ENSMUST00000023851	ENSMUSG00000023089	6	24518666	24528013	-1	6	1	23	43	5	2	5	20	14	111	9		Q9CPP6
ENSMUST00000023854	ENSMUSG00000023092	X	56731787	56793346	1	0	0	0	5	0	0	0	0	0	32	0		P97447
ENSMUST00000023856	ENSMUSG00000023094	2	19371440	19394976	1	6	6	13	48	0	10	145	611	188	183	80		Q78J03
ENSMUST00000023861	ENSMUSG00000058017	1	107078167	107083506	-1	2	9	1	1	6	3	0	0	0	0	0	Q6UKZ0	
ENSMUST00000023867	ENSMUSG00000023104	5	134581366	134601805	1	12	6	34	40	15	10	1082	1968	915	591	638	Q4KL82	Q9WUK4
ENSMUST00000023869	ENSMUSG00000023106	5	123907175	123928835	1	33	30	44	28	42	22	43	313	99	216	111		Q9CQJ6
ENSMUST00000023873	ENSMUSG00000023110	14	54507187	54517525	-1	13	12	33	24	25	10	76	162	64	37	135		
ENSMUST00000023882	ENSMUSG00000023118	7	19024377	19054618	1	8	0	14	31	10	0	1425	1021	1184	41	889	F8WJD4	
ENSMUST00000023884	ENSMUSG00000023120	4	130209109	130222401	-1	20	11	36	16	24	8	0	0	0	0	0	Q3UNZ2	
ENSMUST00000023886	ENSMUSG00000023122	17	53829637	53846339	-1	7	7	15	8	15	9	0	0	0	0	0		Q9D939
ENSMUST00000023897	ENSMUSG00000023132	13	113093825	113100979	-1	4	5	0	5	2	4	28	472	25	192	81	Q3U0N0	P11032
ENSMUST00000023906	ENSMUSG00000023140	6	78395623	78408106	1	1	1	4	2	2	1	0	0	0	0	0	Q545J0	Q08731
ENSMUST00000023911	ENSMUSG00000023143	16	5195289	5204012	-1	0	7	16	80	12	6	367	332	335	33	206		Q8BJ48

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ENSMUST00000023913	ENSMUSG00000023147	16	96145407	96157852	1	18	12	64	22	23	13	14	64	23	12	16		Q8K0D7
ENSMUST00000023917	ENSMUSG00000023151	4	14623620	14796060	-1	0	4	0	0	0	2	0	0	0	0	0		Q9D9Q0
ENSMUST00000023918	ENSMUSG00000023150	1	151344477	151364422	1	4	0	0	78	12	7	188	941	308	310	297		Q920Q8
ENSMUST00000023920	ENSMUSG00000023153	4	155469114	155470858	1	0	0	0	0	0	0	0	0	0	0	0		Q9D702
ENSMUST00000023924	ENSMUSG00000023156	14	8080367	8091834	1	14	16	11	55	10	15	28	120	41	91	58		Q9CQH8
ENSMUST00000023931	ENSMUSG00000023165	X	8454345	8461726	-1	4	8	3	10	4	0	0	0	0	0	0	Q8C5Z3	
ENSMUST00000023934	ENSMUSG00000052305	7	103826534	103828096	-1	239	70	271	102	1417	174	4424	2162	1601	89540	11830	A8DUK4	
ENSMUST00000023952	ENSMUSG00000049382	15	101996711	102004342	-1	29	22	21	166	40	15	0	0	0	372	599		P11679
ENSMUST00000023953	ENSMUSG00000023185	7	17812633	17815663	1	9	5	2	0	2	2	0	0	0	0	0	Q78Y72	
ENSMUST00000023958	ENSMUSG00000023191	6	124841089	124857752	-1	11	22	53	85	30	11	0	26	4	8	20		Q8CG70
ENSMUST00000023959	ENSMUSG00000023192	9	106643095	106656082	-1	34	18	43	251	55	12	0	0	0	0	0		Q14BI2
ENSMUST00000023965	ENSMUSG00000057037	1	139547053	139560272	-1	9	12	17	9	13	1	4	7	2	6	2	Q61406	
ENSMUST00000023978	ENSMUSG00000023210	2	25823153	25825537	1	10	5	33	12	8	3	0	0	0	0	0		Q9D267
ENSMUST00000023987	ENSMUSG00000023216	2	121017891	121037072	-1	6	13	14	13	9	3	2	0	0	0	0	Q3UV95	
ENSMUST00000023994	ENSMUSG00000023224	2	84765387	84775444	-1	5	3	17	9	12	11	0	0	0	81	50		P97290
ENSMUST00000024004	ENSMUSG00000023235	8	4325210	4360020	1	5	3	13	0	2	3	3	10	0	0	0		O35903
ENSMUST00000024005	ENSMUSG00000023236	2	113776362	113829121	-1	4	4	6	8	4	3	5	10	4	22	10	Q3TT51	P12961
ENSMUST00000024011	ENSMUSG00000023243	14	20140058	20181782	-1	34	28	68	167	46	26	7	11	7	7	50	Q9JK62	
ENSMUST00000024015	ENSMUSG00000023247	4	119637704	119639471	1	5	7	5	6	8	5	0	0	0	0	1		P33680
ENSMUST00000024026	ENSMUSG00000023257	X	16522869	16523689	1	0	0	0	0	0	0	0	0	0	0	0	B1AX51	
ENSMUST00000024031	ENSMUSG00000023262	9	106432981	106438319	-1	0	4	0	3	0	0	28	22	0	32	37		
ENSMUST00000024032	ENSMUSG00000023263	4	122689275	122705129	1	5	4	9	3	4	0	0	0	0	0	0	Q9EPV7	
ENSMUST00000024035	ENSMUSG00000023267	4	33062999	33095865	1	15	7	0	0	8	4	2	9	0	1	2		P56476
ENSMUST00000024042	ENSMUSG00000023272	15	88819646	88826681	1	9	6	9	60	10	2	149	304	163	75	197		Q9CYA0
ENSMUST00000024044	ENSMUSG00000023274	6	124864692	124888221	-1	34	22	121	56	46	12	44	143	60	14	249	Q3TSV7	P06332
ENSMUST00000024047	ENSMUSG00000023277	9	106203108	106215389	1	0	0	0	32	0	0	4065	4660	2963	1360	1715		Q9Z0P5
ENSMUST00000024049	ENSMUSG00000023279	X	6314107	6320721	-1	4	4	9	5	6	4	0	0	0	0	0		Q9Z0L4
ENSMUST00000024056	ENSMUSG00000023286	4	155943831	155959604	1	0	0	61	22	9	0	24	39	36	3	64	B1ASK8	
ENSMUST00000024059	ENSMUSG00000023289	6	42038394	42042851	1	0	0	0	0	0	0	0	0	0	0	0	Q3SXH3	
ENSMUST00000024078	ENSMUSG00000023307	19	37207543	37222139	1	9	3	6	32	2	2	172	541	138	73	135	A2RTC8	Q3KNM2
ENSMUST00000024099	ENSMUSG00000023328	5	137287519	137294466	1	0	0	21	72	15	0	0	0	0	0	0	Q543Z1	P21836
ENSMUST00000024104	ENSMUSG00000023333	9	78051958	78065624	1	77	52	156	937	73	58	1	20	2	4	6	Q3UQD1	P70348
ENSMUST00000024107	ENSMUSG00000023336	8	119666523	119688222	1	13	6	27	47	21	8	0	1	0	1	0	Q3UQ76	Q9ESH5
ENSMUST00000024112	ENSMUSG00000023341	16	97535308	97560900	1	7	1	6	8	4	0	1	0	2	1	0		Q9WVP9
ENSMUST00000024118	ENSMUSG00000023349	6	123229843	123247021	1	0	0	0	0	0	0	45	237	119	451	121	Q3V2N1	Q9JKF4
ENSMUST00000024119	ENSMUSG00000023348	5	137309654	137314404	-1	12	7	52	37	25	11	79	404	86	32	217	B2RS30	Q9Z1Y4
ENSMUST00000024121	ENSMUSG00000023350	17	33064143	33068058	-1	17	15	13	22	20	5	0	1	0	0	0		
ENSMUST00000024123	ENSMUSG00000023353	5	24452177	24502047	1	26	14	93	150	48	12	768	671	533	84	456	F8VQE9	
ENSMUST00000024155	ENSMUSG00000023387	14	20262756	20269162	-1	7	6	17	15	16	4	0	0	0	0	0	G5E845	
ENSMUST00000024159	ENSMUSG00000023391	2	71543408	71546754	-1	8	11	36	601	30	7	0	0	0	0	0	Q52KJ2	P40764
ENSMUST00000024171	ENSMUSG00000023403	6	49395604	49469501	1	0	0	0	0	0	0	0	0	0	0	0		Q99MW1
ENSMUST00000024179	ENSMUSG00000023411	14	55824795	55833943	1	0	0	0	35	0	0	1	0	0	1	0		Q8K120
ENSMUST00000024200	ENSMUSG00000078520	4	137401554	137409791	-1	5	4	33	9	14	7	0	0	0	0	0	A2A9U8	
ENSMUST00000024206	ENSMUSG00000023439	6	124834240	124840275	-1	6	5	5	25	9	6	0	0	0	0	0	Q54AE3	Q61011
ENSMUST00000024233	ENSMUSG00000023467	7	45486262	45523632	1	5	0	0	0	4	7	0	0	0	0	0		P46686
ENSMUST00000024238	ENSMUSG00000023473	9	108826320	108852969	1	72	37	187	423	134	53	1330	1677	1754	98	1560		Q91ZI0
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ENSMUST00000024260	ENSMUSG00000023495	9	106453291	106464012	1	6	6	16	9	7	2	0	2	0	18	11		
ENSMUST00000024270	ENSMUSG00000023505	6	124829547	124833701	1	9	4	12	11	5	5	75	69	53	118	30		Q99M54
ENSMUST00000024338	ENSMUSG00000023571	4	155962318	155966629	1	7	4	19	99	14	4	24	53	35	13	33		Q8R2Z0
ENSMUST00000024470	ENSMUSG00000023707	5	124112297	124115483	1	11	0	0	41	0	0	177	357	64	54	130		Q9CQ04
ENSMUST00000024486	ENSMUSG00000023723	11	88204388	88211507	1	0	3	0	8	3	0	95	211	68	57	48		Q8VE22
ENSMUST00000024492	ENSMUSG00000056938	11	103101682	103112200	1	0	0	0	0	0	0	0	0	0	0	0	E9Q289	
ENSMUST00000024518	ENSMUSG00000023755	15	98877778	98881404	-1	2	0	7	92	5	4	21	39	13	15	11		Q9D8T3
ENSMUST00000024543	ENSMUSG00000023781	11	69120404	69124055	1	204	167	558	1098	231	142	2	4	1	0	3		Q8BKT2
ENSMUST00000024570	ENSMUSG00000015659	17	6042196	6079741	-1	0	0	0	0	0	0	1	0	7	0	0		Q3U213
ENSMUST00000024572	ENSMUSG00000023806	17	6904716	6948356	-1	0	9	13	86	8	0	157	386	222	104	165		Q9DA80
ENSMUST00000024575	ENSMUSG00000023809	17	7170115	7303313	1	87	54	120	130	112	59	1598	1354	1309	81	871		Q9WUT3
ENSMUST00000024594	ENSMUSG00000023827	17	12118704	12219645	1	49	40	247	122	33	35	64	142	54	31	86		Q8K4X7
ENSMUST00000024595	ENSMUSG00000023828	17	12419972	12507704	-1	14	7	41	190	34	11	25	29	16	2	10	Q547K2	Q9WTW5
ENSMUST00000024596	ENSMUSG00000023829	17	12648874	12675838	-1	18	4	73	37	25	16	0	2	0	3	2		O08966
ENSMUST00000024599	ENSMUSG00000023830	17	12682406	12769664	-1	79	75	116	146	111	48	738	1078	1714	76	1242		Q07113
ENSMUST00000024620	ENSMUSG00000023852	17	15704967	17394898	1	30	22	10	285	60	18	42	199	88	264	72		Q9CQS5
ENSMUST00000024627	ENSMUSG00000023852	17	15704967	17394898	1	21	23	30	25	16	9	632	1881	1368	232	971		P40201
ENSMUST00000024636	ENSMUSG00000069135	17	8165501	8196804	1	0	0	0	0	0	0	44	206	80	95	81		Q66JX5
ENSMUST00000024639	ENSMUSG00000015222	1	66175273	66442583	1	0	0	0	0	0	0	0	0	0	0	0	Q80ZL4	
ENSMUST00000024647	ENSMUSG00000023868	17	8525372	8986648	1	0	5	0	0	0	0	0	0	0	0	1	F8WHK3	
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ENSMUST00000024657	ENSMUSG00000023883	17	14945009	14961273	-1	0	0	0	29	6	3	269	1172	602	181	332	K4DI61	
ENSMUST00000024660	ENSMUSG00000023886	17	14279506	14404790	1	24	9	33	87	17	10	0	0	0	2	0		Q8CD91
ENSMUST00000024696	ENSMUSG00000023903	17	23629458	23645269	-1	37	36	90	235	72	27	6497	8373	7546	213	4923		Q3U435
ENSMUST00000024697	ENSMUSG00000023904	17	23673596	23675227	1	0	4	15	82	6	0	217	246	137	59	48		Q9CYQ5
ENSMUST00000024698	ENSMUSG00000023905	17	23675447	23677449	-1	6	6	19	93	5	0	44	72	44	69	90		Q9CR75
ENSMUST00000024699	ENSMUSG00000023906	17	23679365	23682446	1	16	7	28	27	18	4	0	0	0	0	0	Q0GH64	Q9Z262
ENSMUST00000024701	ENSMUSG00000023908	17	23726336	23736729	1	14	10	40	203	42	20	64	97	70	3	60		Q9ESG9
ENSMUST00000024702	ENSMUSG00000023909	17	23736186	23740330	-1	14	14	52	357	39	20	14	12	9	7	19		Q9JJE4
ENSMUST00000024704	ENSMUSG00000023911	17	23776916	23786081	-1	3	2	3	18	5	0	1	0	2	3	2		Q9CQE9
ENSMUST00000024705	ENSMUSG00000023912	17	43641900	43667015	-1	45	42	68	386	57	28	7	131	55	3	81	Q9D6D0	
ENSMUST00000024706	ENSMUSG00000023913	17	43568098	43612201	1	14	12	17	5	19	15	4751	30331	8550	11718	7404		Q60963
ENSMUST00000024707	ENSMUSG00000023914	17	43474324	43502812	-1	0	0	15	20	19	6	0	0	0	0	0		
ENSMUST00000024708	ENSMUSG00000023915	17	43016555	43089188	1	42	21	77	247	53	23	1134	1665	1089	78	784		Q9EPU5
ENSMUST00000024709	ENSMUSG00000061665	17	42792951	42876424	-1	53	46	112	81	42	22	55	266	98	123	219		Q9JLQ0
ENSMUST00000024711	ENSMUSG00000023918	17	42656891	42692284	-1	19	0	35	0	20	10	0	0	0	0	0	A0A0D9SEG9	
ENSMUST00000024717	ENSMUSG00000023923	17	50733127	51179349	-1	34	27	51	180	45	22	214	436	402	64	341		Q80XQ2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000024721	ENSMUSG00000023926	17	40811126	40840754	1	21	17	34	19	31	10	4	6	3	1	2		Q9QUT0
ENSMUST00000024724	ENSMUSG00000023930	17	40764734	40807003	-1	2	2	0	0	1	0	0	1	0	0	0		P16563
ENSMUST00000024725	ENSMUSG00000023931	17	53398889	53463321	-1	17	9	15	16	23	9	0	0	0	1	0		Q8CDU5
ENSMUST00000024727	ENSMUSG00000023932	17	45391892	45433707	-1	140	132	298	244	143	65	530	2298	1134	1605	783	Q3UCF2	Q6A068
ENSMUST00000024731	ENSMUSG00000023935	17	45448937	45474938	-1	14	8	7	8	6	6	0	0	0	0	0		A2RRY8
ENSMUST00000024733	ENSMUSG00000023938	17	45506841	45520842	1	29	12	52	178	58	19	36	41	30	1	42		Q14CH7
ENSMUST00000024734	ENSMUSG00000023939	17	45686322	45698495	1	0	0	0	0	0	2	465	543	223	355	131		Q9D1I6
ENSMUST00000024736	ENSMUSG00000023940	17	53674786	53689333	-1	8	6	17	23	9	2	20	69	59	52	25		Q9CXH7
ENSMUST00000024738	ENSMUSG00000023943	17	53961615	53990674	-1	10	5	12	12	6	4	0	0	0	2	0		Q80VR3
ENSMUST00000024739	ENSMUSG00000023944	17	45567775	45573271	-1	21	22	36	38	25	25	2853	7434	3780	740	4676	Q71LX8	P11499
ENSMUST00000024742	ENSMUSG00000023947	17	45555716	45563169	1	19	6	28	215	15	11	179	354	125	16	169		O54910
ENSMUST00000024747	ENSMUSG00000023951	17	46016993	46032377	-1	18	40	256	32	53	23	44	22	0	8	2		Q00731
ENSMUST00000024748	ENSMUSG00000023952	17	46161032	46169370	1	0	0	26	12	0	0	1153	2195	1220	95	1098		Q3UJK4
ENSMUST00000024749	ENSMUSG00000023953	17	46172004	46202625	-1	13	6	19	23	13	6	81	111	130	18	70		Q9JJN0
ENSMUST00000024755	ENSMUSG00000023959	17	44188572	44280168	1	51	56	258	136	64	48	2	10	7	0	5		Q8BXK9
ENSMUST00000024756	ENSMUSG00000023960	17	44078813	44086567	1	9	6	16	55	8	10	36	126	30	0	16		Q9EQG7
ENSMUST00000024757	ENSMUSG00000023961	17	44096308	44105809	-1	0	0	39	153	43	29	39	39	25	0	0		Q8BTJ4
ENSMUST00000024761	ENSMUSG00000023965	17	63057452	63500017	-1	4	4	0	212	8	2	27	54	39	12	23		Q9QZN1
ENSMUST00000024762	ENSMUSG00000023966	17	46122035	46144216	-1	10	8	28	41	15	4	11	6	5	11	6		Q9D9V4
ENSMUST00000024763	ENSMUSG00000023967	17	46110986	46128910	1	4	0	4	10	7	0	118	234	95	56	58	Q5U5I3	
ENSMUST00000024764	ENSMUSG00000023968	17	46428926	46431776	1	0	3	0	0	0	0	0	0	0	0	0	Q14B40	Q6Q6R3
ENSMUST00000024766	ENSMUSG00000023971	17	46667458	46674255	-1	12	7	21	18	14	11	114	302	128	79	115		
ENSMUST00000024773	ENSMUSG00000023978	17	46910459	46924933	1	29	12	20	19	64	19	0	2	0	0	0	Q3UWK3	P15499
ENSMUST00000024774	ENSMUSG00000023979	17	47385393	47392967	1	13	9	17	13	19	9	0	0	0	0	0		Q8VBV8
ENSMUST00000024778	ENSMUSG00000092558	17	47611582	47624418	1	0	6	28	2	7	0	282	680	296	130	175		Q9R0X0
ENSMUST00000024779	ENSMUSG00000090115	17	47630690	47686738	1	48	36	93	88	73	29	35	132	59	8	74		Q6P9L4
ENSMUST00000024782	ENSMUSG00000023987	17	47726842	47734482	1	11	2	13	14	12	2	0	0	0	0	0		Q9D7R7
ENSMUST00000024783	ENSMUSG00000023988	17	47599331	47611492	-1	33	28	116	165	48	20	208	315	195	21	188		O54825
ENSMUST00000024786	ENSMUSG00000023990	17	47737030	47792419	1	9	0	6	3	6	6	553	0	0	0	0	Q3UKG7	
ENSMUST00000024791	ENSMUSG00000023992	17	48346401	48354147	1	1	0	2	2	0	0	114	91	32	264	62		Q99NH8
ENSMUST00000024792	ENSMUSG00000023993	17	48359916	48367174	1	13	6	45	21	13	8	18	19	22	25	34		Q8K558
ENSMUST00000024794	ENSMUSG00000023995	17	48447956	48451522	-1	4	1	0	0	0	0	4	0	0	2	0		Q9CRZ8
ENSMUST00000024797	ENSMUSG00000064120	17	49428362	49455435	1	0	0	0	0	0	0	544	1126	561	179	474		Q5RKZ7
ENSMUST00000024798						6	0	23	6	15	0	0	0	0	0	0		
ENSMUST00000024802	ENSMUSG00000024007	17	29250803	29264158	-1	5	5	19	20	9	4	74	105	48	51	67	B9EJX8	Q9D0W5
ENSMUST00000024805	ENSMUSG00000024008	17	29156550	29237797	-1	44	13	61	92	33	38	0	0	0	0	6		Q8JZW4
ENSMUST00000024810	ENSMUSG00000024013	17	29360914	29379660	1	0	0	0	1	0	0	90	122	61	7	174		Q8BY35
ENSMUST00000024811	ENSMUSG00000024014	17	29490812	29496111	1	24	29	72	279	43	21	5086	12004	4856	835	4803	Q8CFN8	
ENSMUST00000024816	ENSMUSG00000024019	17	29660595	29705979	1	12	9	40	110	34	25	993	1254	1112	141	915		Q9DBC3
ENSMUST00000024817	ENSMUSG00000090083	17	29614790	29641664	1	5	0	3	35	10	5	132	183	127	131	29		Q8VC56
ENSMUST00000024823	ENSMUSG00000024026	17	30592866	30612659	-1	23	7	16	15	22	2	125	369	82	331	182	A5GZX3	Q9CPU0
ENSMUST00000024826	ENSMUSG00000024028	17	31141049	31144282	-1	10	4	10	6	6	2	0	0	0	0	0	Q9QX97	
ENSMUST00000024827	ENSMUSG00000024029	17	31125306	31129646	-1	4	2	14	6	3	4	0	0	0	0	0		Q62395
ENSMUST00000024829	ENSMUSG00000024030	17	31057698	31115777	1	27	19	24	55	45	12	1154	1410	1121	103	1193	Q0VDW9	Q64343
ENSMUST00000024831	ENSMUSG00000024032	17	31161396	31165053	-1	6	5	1	14	5	5	0	0	0	0	0	Q149Y8	Q08423
ENSMUST00000024832	ENSMUSG00000024033	17	31255019	31277356	-1	10	7	24	29	11	7	25	159	54	84	30	Q3YEA4	Q8VIG3
ENSMUST00000024833	ENSMUSG00000024034	17	31179272	31198975	-1	22	22	82	35	37	20	6	13	8	0	2		Q8K1T0
ENSMUST00000024839	ENSMUSG00000024042	17	31844248	31855792	-1	46	29	193	288	47	32	867	1936	1146	102	2054		Q60670
ENSMUST00000024840	ENSMUSG00000024043	17	67842713	68004120	-1	19	24	52	104	33	10	2	7	1	6	13		Q8BN58
ENSMUST00000024846	ENSMUSG00000024048	17	70993656	71002878	-1	2	0	0	0	0	2	2802	4035	1008	632	585	Q6ZWQ9	
ENSMUST00000024847	ENSMUSG00000024049	17	71019521	71126856	1	0	13	0	0	0	0	0	0	0	0	0	Z4YJF5	
ENSMUST00000024849	ENSMUSG00000024053	17	71252176	71310965	-1	27	18	66	225	41	22	14232	23136	17530	2983	16408	Q3U1J9	Q8K482
ENSMUST00000024851	ENSMUSG00000024056	17	71496100	71526857	-1	14	6	16	25	8	11	33	98	89	148	34		Q9D0F1
ENSMUST00000024854	ENSMUSG00000024059	17	71781947	71858351	1	21	24	33	18	20	10	0	2	1	4	16		Q8CI96
ENSMUST00000024857	ENSMUSG00000024063	17	72918305	72941942	1	45	39	173	325	67	45	688	1254	531	133	747		Q9CX60
ENSMUST00000024858	ENSMUSG00000024064	17	73493228	73710453	-1	99	34	183	413	110	45	0	0	1	1	2	Q08EC9	
ENSMUST00000024860	ENSMUSG00000024065	17	73804841	73832093	1	37	42	155	112	59	19	19	27	20	5	58		Q9QXY6
ENSMUST00000024866	ENSMUSG00000024066	17	73883908	73950182	-1	43	23	67	45	49	30	8316	17466	15730	950	14235		Q00519
ENSMUST00000024869	ENSMUSG00000024068	17	74338987	74391113	1	8	8	24	100	8	21	238	660	419	98	225		Q9QYY8
ENSMUST00000024870	ENSMUSG00000024069	17	74395608	74424229	1	9	7	21	14	13	7	116	291	90	111	81		Q8BJM5
ENSMUST00000024873	ENSMUSG00000024072	17	74489493	74500277	1	4	3	8	123	3	2	396	1036	310	75	196		Q8C407
ENSMUST00000024880	ENSMUSG00000024076	17	78508063	78627409	1	166	90	1089	197	113	46	0	5	5	0	3		Q8VHI5
ENSMUST00000024881	ENSMUSG00000024077	17	78649913	78737196	-1	7	5	13	0	15	4	91	0	470	17	357	F8WH41	
ENSMUST00000024882	ENSMUSG00000024078	17	74717750	74863570	1	15	12	18	15	23	5	8	45	17	45	55		Q8CD92
ENSMUST00000024884	ENSMUSG00000024079	17	78852564	78882573	-1	1124	973	2808	1274	1177	588	69	434	167	206	208		Q03963
ENSMUST00000024885	ENSMUSG00000024081	17	78919006	78937070	-1	18	11	33	27	21	12	127	730	352	609	271		
ENSMUST00000024887	ENSMUSG00000024082	17	78937135	78948052	1	60	55	110	62	57	27	49	268	101	94	92		Q9CWG8
ENSMUST00000024888	ENSMUSG00000024083	17	64281005	64331916	-1	13	0	1	0	0	0	61	341	123	173	95		Q80U04
ENSMUST00000024889	ENSMUSG00000024083	17	64281005	64331916	-1	0	0	0	0	19	2	0	0	0	0	40		Q80U04
ENSMUST00000024894	ENSMUSG00000024087	17	79706953	79715041	-1	34	19	33	206	20	17	0	0	0	5	20		Q64429
ENSMUST00000024896	ENSMUSG00000024088	17	64832523	64836071	-1	2	4	3	1	4	3	0	0	0	0	0	Q9D2E3	
ENSMUST00000024897	ENSMUSG00000024091	17	65580056	65613555	-1	0	7	11	47	7	2	1115	4351	1258	398	832		Q9WV55
ENSMUST00000024905	ENSMUSG00000024096	17	65848433	65885755	-1	0	0	0	133	0	0	1345	3272	3043	258	1885		Q62172
ENSMUST00000024906	ENSMUSG00000024098	17	65923066	65951187	-1	13	13	35	10	9	12	72	131	122	60	195		Q9EP52
ENSMUST00000024909	ENSMUSG00000024099	17	66078795	66101559	-1	0	0	0	10	1	0	326	1290	296	846	160		Q9D6J6
ENSMUST00000024914	ENSMUSG00000024105	17	66555252	66594621	-1	9	6	14	8	11	6	0	0	0	0	0		Q9CU24
ENSMUST00000024916	ENSMUSG00000024107	17	88741549	88791976	-1	22	19	10	41	17	11	0	0	0	0	0		P30730
ENSMUST00000024926	ENSMUSG00000024114	17	23836785	23844172	-1	0	0	0	0	0	0	0	0	0	0	0		Q920S2
ENSMUST00000024928	ENSMUSG00000024116	17	23868056	23873114	1	11	4	8	17	14	10	0	0	0	0	0	Q54AE4	Q9JHJ7
ENSMUST00000024930	ENSMUSG00000024118	17	24215054	24220851	-1	10	5	24	28	19	12	5	28	9	7	0		Q6GQV0
ENSMUST00000024931	ENSMUSG00000036473	17	24175431	24209387	-1	32	20	64	868	72	37	0	2	0	0	1	Q52KG2	Q9R1A3
ENSMUST00000024932	ENSMUSG00000024121	17	24163866	24169702	-1	10	14	16	98	11	9	7771	7920	4355	1545	3230	A3KML5	P63082
ENSMUST00000024936	ENSMUSG00000024124	17	23972126	23975230	-1	71	78	122	90	115	46	4	6	9	3	11		Q9QYZ9
ENSMUST00000024939	ENSMUSG00000024125	17	23953085	23954919	-1	11	5	14	18	11	4	0	0	0	0	0	Q3TUY3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000024940	ENSMUSG00000024128	17	23941672	23945607	1	5	0	2	0	0	0	0	0	0	0	0	Q544L5	P15501
ENSMUST00000024944	ENSMUSG00000024131	17	85028347	85064243	1	16	9	15	6	19	2	3	3	6	6	2		Q91WV7
ENSMUST00000024946	ENSMUSG00000024132	17	24426683	24439316	1	23	8	43	95	16	4	48	113	38	29	64		P42125
ENSMUST00000024947	ENSMUSG00000024134	17	85684277	85688274	-1	0	0	0	0	0	0	0	0	0	1	0		Q62232
ENSMUST00000024954	ENSMUSG00000024140	17	86753907	86833410	1	145	78	668	302	121	58	22	38	45	12	48		P97481
ENSMUST00000024956	ENSMUSG00000024143	17	86963082	87000069	1	15	7	10	54	20	5	120	324	179	58	121		Q8R527
ENSMUST00000024957	ENSMUSG00000024145	17	86997256	87025406	-1	2	1	12	35	3	0	24	90	24	43	13		O09101
ENSMUST00000024958	ENSMUSG00000033597	17	24488783	24508905	1	53	39	164	816	75	28	7	14	1	1	9		Q6P9K8
ENSMUST00000024959	ENSMUSG00000024146	17	87025550	87035810	1	5	5	10	6	6	2	485	1722	376	1101	236		O70333
ENSMUST00000024963	ENSMUSG00000024150	17	87254658	87265935	-1	10	0	11	0	0	5	421	1707	454	305	253	D0EW11	Q8K5B2
ENSMUST00000024967	ENSMUSG00000024151	17	87672330	87723713	1	13	9	23	115	17	8	36	124	47	14	79	Q3TZI5	P43247
ENSMUST00000024970	ENSMUSG00000024154	17	88668660	88715152	1	9	11	11	6	7	4	0	0	0	0	0		Q8R4I4
ENSMUST00000024972	ENSMUSG00000024155	17	24804382	24839787	1	6	8	1	3	1	2	2	7	1	3	0		Q9D513
ENSMUST00000024974	ENSMUSG00000024158	17	24840143	24864450	1	6	0	4	0	3	0	71	141	12	12	88		
ENSMUST00000024976	ENSMUSG00000024160	17	24886643	24892152	1	9	5	29	8	4	3	88	130	65	6	96		Q571F5
ENSMUST00000024978	ENSMUSG00000073435	17	24896500	24897522	1	1	0	4	0	1	0	70	213	84	101	44		Q9WV85
ENSMUST00000024979	ENSMUSG00000020859	11	93996091	94126085	1	0	0	0	0	0	0	0	0	0	0	0	F8WH31	
ENSMUST00000024981	ENSMUSG00000024165	17	24942156	24960636	-1	48	50	141	87	49	23	187	231	193	90	144	Q3TM10	Q6PGH2
ENSMUST00000024983	ENSMUSG00000024169	17	25016091	25099495	1	15	18	27	75	37	4	198	142	295	7	234	E9PY46	
ENSMUST00000024984	ENSMUSG00000024168	17	25057702	25081181	-1	7	3	18	14	13	9	6	2	3	3	0		Q7TQI0
ENSMUST00000024987	ENSMUSG00000024170	17	25099570	25115967	-1	0	0	0	0	0	0	5	18	12	0	53		Q9DC40
ENSMUST00000024988	ENSMUSG00000024164	17	57203970	57228136	-1	44	31	109	94	65	33	14733	15882	19800	1052	10430		P01027
ENSMUST00000024993	ENSMUSG00000034039	17	25318654	25322681	1	10	8	25	7	12	9	0	0	0	0	0	E9QLD5	
ENSMUST00000024999	ENSMUSG00000033200	17	25369273	25374442	1	0	0	12	0	3	0	0	0	0	0	0	E9QLD4	
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ENSMUST00000025002	ENSMUSG00000024175	17	25471590	25476594	1	12	13	32	57	34	10	0	0	0	0	0		
ENSMUST00000025003	ENSMUSG00000024176	17	25565892	25570686	-1	13	7	42	33	28	11	0	0	0	0	1	Q543C3	Q04886
ENSMUST00000025004	ENSMUSG00000032915	17	55749984	55853662	1	11	4	13	4	10	6	7	57	9	68	54		Q91ZE5
ENSMUST00000025007	ENSMUSG00000024177	17	26091734	26095508	-1	5	2	14	40	9	1	14	23	3	25	16		Q9WV84
ENSMUST00000025010	ENSMUSG00000024180	17	26113316	26123254	1	20	13	40	42	44	16	531	724	358	141	471		Q9ESN3
ENSMUST00000025014	ENSMUSG00000024181	17	26123520	26126613	1	6	1	16	62	21	6	256	345	165	80	155		Q9D1B9
ENSMUST00000025019	ENSMUSG00000073433	17	26196226	26207786	-1	2	0	0	4	0	0	0	0	1	0	2	Q3UNB6	Q62160
ENSMUST00000025020	ENSMUSG00000024186	17	26202951	26211324	1	0	0	2	0	0	0	0	0	0	0	0	G3X8W6	
ENSMUST00000025023	ENSMUSG00000024188	17	26252910	26285504	1	0	0	0	26	7	0	26	77	23	14	62		
ENSMUST00000025025	ENSMUSG00000024190	17	26505590	26508519	-1	5	0	11	204	8	5	2896	28366	4665	887	9314	Q3U8K3	P28563
ENSMUST00000025027	ENSMUSG00000024194	17	26937973	26939478	-1	0	0	0	28	8	0	102	265	134	54	111		Q9CQ89
ENSMUST00000025034	ENSMUSG00000057789	17	27019810	27029009	-1	2	0	4	2	0	0	1300	1523	842	157	602	Q91WX5	
ENSMUST00000025036	ENSMUSG00000024201	17	56326062	56402870	1	40	18	73	51	36	18	565	344	519	23	502		Q91VY5
ENSMUST00000025040						8	6	20	25	10	2	2	4	2	17	4		
ENSMUST00000025045	ENSMUSG00000024208	17	27122663	27133916	-1	0	0	4	19	0	3	121	163	61	706	74		Q9CQY6
ENSMUST00000025046	ENSMUSG00000024210	17	27143969	27167764	-1	18	12	28	22	21	12	3	11	2	0	8		Q8BWD2
ENSMUST00000025048	ENSMUSG00000024209	17	56875477	56888904	1	10	15	56	71	30	15	21	28	8	34	8	Q08EE8	
ENSMUST00000025050	ENSMUSG00000024213	17	27579382	27623465	-1	15	12	23	49	14	10	877	1314	905	116	458		Q9JI46
ENSMUST00000025052	ENSMUSG00000052146	17	27630422	27636629	-1	0	0	0	0	0	0	469	1339	151	271	0	Q3UW83	
ENSMUST00000025053	ENSMUSG00000024212	17	56892612	56935388	-1	44	26	93	108	51	36	344	336	268	28	282	Q9ERL0	
ENSMUST00000025054	ENSMUSG00000024215	17	27714352	27728951	-1	16	0	15	30	19	0	0	0	0	0	0		Q9WTP3
ENSMUST00000025057	ENSMUSG00000024218	17	27901122	27909242	-1	5	1	18	0	0	1	132	426	156	224	105		Q99JX1
ENSMUST00000025058	ENSMUSG00000024219	17	27909340	28062600	1	53	0	0	0	72	43	0	0	0	0	0	Q3UHP6	
ENSMUST00000025060	ENSMUSG00000024223	17	28530860	28538954	1	12	5	9	10	10	5	11	33	25	9	25		Q80X86
ENSMUST00000025061	ENSMUSG00000024224	17	28549489	28552618	1	4	1	12	1	2	4	0	0	0	0	0		Q3UW21
ENSMUST00000025062	ENSMUSG00000024225	17	28558210	28560766	-1	5	3	5	3	7	3	0	0	0	0	0		Q9CQC2
ENSMUST00000025064	ENSMUSG00000024227	17	58878808	58991375	-1	16	10	40	10	25	6	0	0	0	0	0	Q8BGR1	
ENSMUST00000025065	ENSMUSG00000024228	17	58999618	59013372	-1	105	59	179	341	143	62	2	2	6	0	7		Q9DCN1
ENSMUST00000025069	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	0		P27699
ENSMUST00000025073	ENSMUSG00000024231	18	3382988	3436377	1	17	12	0	114	24	2	14	0	16	16	13		Q9D4H8
ENSMUST00000025075	ENSMUSG00000024232	18	3507957	3516404	1	30	9	114	143	27	16	23	51	13	20	14		Q9D0L6
ENSMUST00000025076	ENSMUSG00000024233	18	4165832	4182232	1	2	4	12	3	8	6	0	0	0	0	0	A0A077S9Z4	Q9CPX3
ENSMUST00000025077	ENSMUSG00000024234	18	4375592	4397330	1	12	6	18	53	9	6	113	477	189	174	138		Q9D0D3
ENSMUST00000025078	ENSMUSG00000024235	18	4331327	4353015	-1	12	2	13	0	14	5	314	893	655	397	386	Q3UEB8	Q07174
ENSMUST00000025079	ENSMUSG00000024236	18	4920540	5119299	1	0	8	0	0	0	0	0	0	0	0	0		Q8K4L3
ENSMUST00000025081	ENSMUSG00000024238	18	5591860	5775467	1	12	11	43	77	22	9	243	788	413	194	246		Q64318
ENSMUST00000025083	ENSMUSG00000006740	18	6201002	6242174	-1	79	94	153	180	98	48	936	1887	1334	385	1193		Q61768
ENSMUST00000025089	ENSMUSG00000024242	17	80580512	80728093	-1	10	10	19	67	19	5	40	112	112	21	79		Q99JP0
ENSMUST00000025092	ENSMUSG00000024245	17	80944632	81001816	1	9	6	14	119	18	9	2	2	0	1	0		Q9CZ16
ENSMUST00000025093	ENSMUSG00000024246	17	81026327	81065085	-1	9	5	24	53	9	2	4	28	11	23	15		Q9CZB3
ENSMUST00000025095	ENSMUSG00000024248	17	83501919	83514333	-1	11	11	0	88	12	4	2886	5872	2418	4626	1614	Q3UDK5	Q61387
ENSMUST00000025101	ENSMUSG00000024253	17	84626496	84655558	1	9	6	3	25	10	3	112	404	163	387	81		Q8K0T2
ENSMUST00000025106	ENSMUSG00000024258	18	31789159	31796642	1	3	3	1	9	3	3	130	247	120	316	97		Q9D7M8
ENSMUST00000025109	ENSMUSG00000024260	18	31634371	31723061	1	0	30	91	154	25	13	392	816	619	116	547		
ENSMUST00000025110	ENSMUSG00000024261	18	31437808	31447415	-1	10	7	25	22	5	3	0	0	0	0	0		P40749
ENSMUST00000025117	ENSMUSG00000024268	18	25477632	25753983	-1	87	50	248	405	5	34	4	59	0	23	27		Q7TSY6
ENSMUST00000025120	ENSMUSG00000024271	18	24603961	24638830	1	20	17	27	37	26	10	150	499	252	311	276		Q91WG4
ENSMUST00000025127	ENSMUSG00000024277	18	23752333	23893861	1	0	0	6	60	11	0	170	226	205	40	239		Q8R001
ENSMUST00000025137	ENSMUSG00000024287	18	9958180	9995484	1	13	9	16	16	18	11	45	248	81	231	76		Q8R3N6
ENSMUST00000025142	ENSMUSG00000024293	18	10566602	10610352	-1	6	7	10	146	9	7	172	679	351	372	228		Q69Z69
ENSMUST00000025160	ENSMUSG00000024306	18	21810897	22171396	-1	9	12	4	9	5	6	0	0	0	0	0		Q8CDV0
ENSMUST00000025161	ENSMUSG00000024308	17	33915899	33929288	1	43	43	49	154	50	21	3684	6829	3733	627	3825	Q3TCU5	
ENSMUST00000025163	ENSMUSG00000024309	17	33938821	33940343	-1	6	0	22	7	4	0	187	196	143	264	134	Q792E4	Q03958
ENSMUST00000025166	ENSMUSG00000024304	18	16588877	16809246	-1	37	21	101	245	22	13	0	0	1	0	0		P15116
ENSMUST00000025170	ENSMUSG00000024312	17	33940660	33949695	1	18	12	83	50	23	14	193	351	219	45	204		Q9Z0H1
ENSMUST00000025177	ENSMUSG00000033382	18	20817224	20896078	-1	13	15	10	13	17	6	527	1825	1136	132	678	E9PWG2	
ENSMUST00000025178	ENSMUSG00000024319	17	33955812	33966984	1	22	7	75	51	20	4	368	898	409	36	355		Q8C754
ENSMUST00000025181	ENSMUSG00000061232	17	33996017	34000333	-1	0	3	0	0	0	0	4824	6366	2148	1571	4172	Q7JJ15	P01901
ENSMUST00000025183	ENSMUSG00000024325	17	34020792	34024680	-1	0	2	19	90	6	2	129	153	95	17	109		O35730

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ENSMUST00000025186	ENSMUSG00000024327	17	34028267	34031690	-1	0	0	0	0	0	0	712	911	623	70	393	A0A068BIT0	Q31125
ENSMUST00000025192	ENSMUSG00000024334	17	34092340	34095234	1	0	3	6	5	7	0	37	10	13	18	16	Q9QWV1	
ENSMUST00000025193	ENSMUSG00000024335	17	34112023	34122634	-1	0	5	0	0	1	0	520	1476	1060	145	665	B2RS09	Q7JJ13
ENSMUST00000025196	ENSMUSG00000024338	17	34197721	34201454	1	7	7	18	67	15	13	584	821	398	297	535		P28063
ENSMUST00000025197	ENSMUSG00000024339	17	34203527	34216321	1	13	18	98	72	36	28	222	371	265	42	162	Q792S7	P36371
ENSMUST00000025198	ENSMUSG00000024340	17	34354822	34369493	1	22	7	19	18	34	5	3	35	4	4	27		O70355
ENSMUST00000025202	ENSMUSG00000058975	7	46396497	46438375	1	182	116	655	2232	275	131	1	4	6	1	8	Q3UHB6	P15388
ENSMUST00000025204	ENSMUSG00000024346	18	36403679	36454495	-1	3	5	12	10	7	4	175	527	191	1043	127	Q9CQF7	
ENSMUST00000025208	ENSMUSG00000024350	18	35671103	35703144	-1	68	46	236	86	73	32	33	118	85	69	68		Q9CZJ9
ENSMUST00000025209	ENSMUSG00000024352	18	35656690	35662186	-1	4	0	6	32	4	8	5	17	2	23	6		Q6P926
ENSMUST00000025211	ENSMUSG00000024353	18	35647266	35649367	-1	6	12	18	3	15	7	20	6	4	64	54		Q9D8I1
ENSMUST00000025212	ENSMUSG00000024354	18	35614604	35627244	-1	68	64	755	64	60	38	11	26	30	11	44		Q9Z2J0
ENSMUST00000025215	ENSMUSG00000024357	18	35266400	35498925	-1	13	7	23	72	24	8	30	56	24	24	56		Q9EPK6
ENSMUST00000025217	ENSMUSG00000024359	18	34937414	34954357	-1	4	10	15	113	17	11	191	821	405	321	632		P38647
ENSMUST00000025218	ENSMUSG00000024360	18	34902785	34932007	-1	21	12	17	71	27	12	735	2798	1207	1042	788		Q8BWY3
ENSMUST00000025223	ENSMUSG00000024365	17	34801348	34804561	-1	18	19	40	16	26	19	0	0	0	0	0		
ENSMUST00000025224	ENSMUSG00000024366	18	34689903	34720387	-1	10	12	23	72	30	10	0	0	0	0	0		O35118
ENSMUST00000025228	ENSMUSG00000024370	18	34630951	34651735	-1	0	3	5	14	4	4	30	72	84	28	57	G3X8W7	
ENSMUST00000025229	ENSMUSG00000090231	17	34856374	34862518	-1	23	3	5	0	5	1	0	0	0	62	0	B8JJM5	
ENSMUST00000025230	ENSMUSG00000024371	17	34862604	34898265	-1	7	7	19	21	21	5	0	0	0	0	10		P21180
ENSMUST00000025234	ENSMUSG00000024376	18	33796327	34007206	-1	18	14	24	325	43	19	0	0	0	19	11		P52963
ENSMUST00000025236	ENSMUSG00000024378	18	33199355	33213862	-1	15	17	75	43	16	10	112	373	367	75	169	Q80SX0	
ENSMUST00000025237	ENSMUSG00000024379	18	32815383	32819799	1	5	2	6	5	9	4	3	15	1	63	8		Q9JIE6
ENSMUST00000025239	ENSMUSG00000024381	18	32377217	32435736	1	12	13	20	36	16	14	0	6	0	7	11		O08539
ENSMUST00000025241	ENSMUSG00000024382	18	32240300	32270151	1	16	13	37	5	21	3	398	902	650	174	489		P49135
ENSMUST00000025243	ENSMUSG00000024384	18	32067734	32104331	1	131	139	363	195	95	72	203	697	409	110	400		Q8C1D8
ENSMUST00000025246	ENSMUSG00000024387	17	35116196	35122053	-1	4	0	5	88	9	1	1476	2205	991	432	813		P67871
ENSMUST00000025249	ENSMUSG00000024391	17	35128997	35132050	-1	10	9	5	9	7	10	1	4	4	11	1		Q9Z1R3
ENSMUST00000025250	ENSMUSG00000024392	17	35135178	35147322	1	0	0	0	0	1	17	928	1368	951	61	961		Q9Z1R2
ENSMUST00000025253	ENSMUSG00000024393	17	35149076	35164897	-1	10	0	27	151	43	8	4365	2385	4493	85	3811		Q7TSC1
ENSMUST00000025254	ENSMUSG00000024395	18	31931507	31958619	1	19	12	53	49	32	15	0	1	0	1	0		Q91XD2
ENSMUST00000025257	ENSMUSG00000024397	17	35170991	35176068	-1	0	0	0	0	0	0	0	18	13	0	92	Q4FJL9	O70200
ENSMUST00000025262	ENSMUSG00000024399	17	35194439	35196320	1	3	3	20	101	6	0	3123	3427	1961	246	1605		P41155
ENSMUST00000025263	ENSMUSG00000024401	17	35199381	35202007	-1	9	15	18	24	16	7	271	718	226	32	123	Q3U593	P06804
ENSMUST00000025264	ENSMUSG00000024400	18	31804057	31908987	1	38	40	119	78	38	38	488	1061	892	115	760		Q8K4P0
ENSMUST00000025266	ENSMUSG00000024402	17	35203165	35205351	-1	6	2	16	19	6	8	1	12	4	3	10	Q542S2	P09225
ENSMUST00000025270	ENSMUSG00000024404	18	12128850	12157367	1	148	122	368	169	120	42	1715	6987	3684	1318	2229		Q9DBU3
ENSMUST00000025271	ENSMUSG00000024406	17	35506018	35510772	1	12	9	25	43	14	5	0	0	0	0	0		P20263
ENSMUST00000025273	ENSMUSG00000024409	17	35533201	35534647	1	7	4	8	16	15	2	0	0	0	0	1	Q3UUY0	
ENSMUST00000025276	ENSMUSG00000024410	18	12168717	12189997	1	0	0	0	0	0	0	360	1036	449	381	327	Q3U4H5	Q8VC42
ENSMUST00000025278	ENSMUSG00000024414	11	94653767	94660089	1	60	77	101	64	83	59	124	304	104	681	137		Q99N92
ENSMUST00000025279	ENSMUSG00000024413	18	12189693	12236400	-1	101	94	155	188	89	49	904	1800	1795	119	976		O35604
ENSMUST00000025288	ENSMUSG00000024420	18	13687013	13972733	-1	45	46	72	48	54	29	3	5	1	3	3		Q6KAS7
ENSMUST00000025290	ENSMUSG00000024423	18	12972252	12992948	1	11	5	16	13	16	6	40	287	109	167	145		O55091
ENSMUST00000025292	ENSMUSG00000024422	17	35879819	35892670	1	19	15	28	145	0	0	860	776	710	44	668	G3X8X0	
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ENSMUST00000025294	ENSMUSG00000024424	18	12599926	12737050	1	0	0	2	256	12	0	8	23	0	4	15	G3X8X1	
ENSMUST00000025295	ENSMUSG00000024427	18	38586268	38601268	-1	30	34	127	166	46	32	0	3	0	2	13		Q9WTP2
ENSMUST00000025300	ENSMUSG00000024431	18	39410545	39491301	-1	6	0	0	0	0	0	0	0	250	0	0	E9PUR6	
ENSMUST00000025305	ENSMUSG00000024436	17	35910379	35916389	-1	2	3	0	0	0	0	52	77	28	85	56		Q99N84
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ENSMUST00000025312	ENSMUSG00000054128	17	36185572	36190287	-1	22	15	37	6	9	0	0	0	0	0	0	F6TIX5	
ENSMUST00000025314	ENSMUSG00000024442	18	38250249	38262629	1	13	12	29	73	18	12	176	254	171	30	166		Q9DCV6
ENSMUST00000025319	ENSMUSG00000024446	17	36255645	36258069	-1	1	1	2	18	0	1	118	50	50	236	26		Q8R040
ENSMUST00000025322	ENSMUSG00000024448	17	36322858	36326155	-1	6	7	8	6	10	6	0	0	0	0	0	O19443	
ENSMUST00000025329	ENSMUSG00000050747	17	36860691	36867210	-1	13	0	33	8	0	0	0	0	0	0	0	Q8R096	
ENSMUST00000025337	ENSMUSG00000024456	18	37843601	37935476	-1	0	0	0	0	0	0	2518	901	2730	322	1753	E9PV41	
ENSMUST00000025338	ENSMUSG00000024462	17	37045966	37075067	1	28	8	46	116	40	26	6	10	0	0	28		Q9WV18
ENSMUST00000025349	ENSMUSG00000024471	18	44334074	44355724	1	7	4	7	0	5	0	0	0	0	0	0	A0A509	Q9JIF9
ENSMUST00000025350	ENSMUSG00000024472	18	44380502	44424969	1	97	71	139	372	115	68	253	551	554	87	348		Q9CYC6
ENSMUST00000025354	ENSMUSG00000024477	18	46239949	46280850	-1	16	12	18	55	10	10	60	102	97	38	88		Q8BUY9
ENSMUST00000025356	ENSMUSG00000024479	15	54571366	54602846	1	9	4	46	33	5	2	0	0	0	0	0	Q2KHK7	Q8BI08
ENSMUST00000025357	ENSMUSG00000024480	18	46741917	46790826	1	4	13	16	38	8	5	1570	2944	837	609	462	Q3U8S0	Q9DCR2
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ENSMUST00000025363	ENSMUSG00000024486	18	36504929	36515805	-1	17	10	47	195	18	6	2	6	1	11	21	Q5FW64	Q06186
ENSMUST00000025364	ENSMUSG00000024487	18	40204865	40219399	-1	10	7	9	89	20	4	205	682	283	183	212		Q9EQQ2
ENSMUST00000025374	ENSMUSG00000024497	18	42394539	42397249	1	17	15	49	215	21	3	0	0	0	0	0		Q63955
ENSMUST00000025375	ENSMUSG00000024498	18	42511510	42575551	1	18	10	16	92	9	7	98	258	116	36	151	Q3TH57	Q8CGF7
ENSMUST00000025377	ENSMUSG00000024500	18	42637432	43059471	-1	0	0	0	3	5	2	0	0	0	0	0		Q6ZWR4
ENSMUST00000025379	ENSMUSG00000024501	18	43320979	43438286	-1	0	2	2	42	5	0	0	0	0	0	0		Q62188
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ENSMUST00000025383	ENSMUSG00000024505	18	49696145	49755601	-1	0	0	0	0	0	0	2	0	0	0	0	B2RTH8	Q9D0U1
ENSMUST00000025385	ENSMUSG00000024507	18	50128201	50196269	1	13	10	13	68	15	7	371	854	548	134	439		P51660
ENSMUST00000025388	ENSMUSG00000024510	18	52331536	52332986	1	6	2	9	13	10	5	0	0	0	0	0		Q9D5H4
ENSMUST00000025390	ENSMUSG00000024512	18	70240429	70244584	-1	7	6	17	2	4	3	0	0	0	1	0	Q9D7M5	
ENSMUST00000025391	ENSMUSG00000031337	X	71210767	71315691	1	0	0	0	0	0	0	0	0	0	0	0	B1AW21	
ENSMUST00000025393	ENSMUSG00000024515	18	73639009	73703780	-1	3	3	3	27	0	4	939	1970	875	84	703		P97471
ENSMUST00000025394	ENSMUSG00000024516	18	65800549	65817665	1	0	2	0	9	1	2	433	1317	746	2344	424		Q9D8V7
ENSMUST00000025395	ENSMUSG00000024517	18	65872820	65886579	1	0	0	0	0	0	2	0	0	0	0	0		Q8R1I2
ENSMUST00000025396	ENSMUSG00000024518	18	65934639	65939089	-1	13	9	23	364	25	4	0	1	0	0	0		O35602
ENSMUST00000025397	ENSMUSG00000024519	18	65955727	65970178	-1	6	3	8	9	4	13	0	0	0	0	0		Q80WM3
ENSMUST00000025399	ENSMUSG00000024521	18	66458604	66465550	1	15	15	42	84	30	14	129	607	232	87	153		Q9JM54
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ENSMUST00000025403	ENSMUSG00000024525	18	67289253	67319146	1	10	6	17	173	18	5	282	406	273	31	142	Q3U3B7	Q91UZ5
ENSMUST00000025404	ENSMUSG00000024526	18	67343564	67367794	1	6	6	15	131	11	7	1	0	0	0	1		O70302
ENSMUST00000025406	ENSMUSG00000024528	18	52465693	52490738	1	24	15	78	41	38	16	21	100	56	212	45		Q9CZ91
ENSMUST00000025408	ENSMUSG00000024527	18	67404767	67449166	-1	19	11	19	80	21	10	116	261	169	97	234		Q8JZQ2
ENSMUST00000025409	ENSMUSG00000024529	18	52516069	52529867	-1	3	0	20	380	23	7	0	0	0	3	5	Q3TXH3	P28301
ENSMUST00000025411	ENSMUSG00000024530	18	67464849	67480581	1	21	23	85	105	32	17	0	1	0	0	0		Q8VE85
ENSMUST00000025413	ENSMUSG00000024534	18	52767709	52915935	1	5	0	0	33	7	0	0	0	0	0	0	G5E848	
ENSMUST00000025417	ENSMUSG00000024535	18	53245662	53390823	1	4	0	0	9	0	0	0	0	0	0	0		Q9CRB0
ENSMUST00000025418	ENSMUSG00000024537	18	67641599	67654162	1	6	3	7	96	8	4	37	67	28	97	34		Q9EST4
ENSMUST00000025419	ENSMUSG00000024538	18	53406341	53418007	-1	8	4	7	90	9	3	4	20	2	5	8	Q3UC73	P30412
ENSMUST00000025420	ENSMUSG00000024539	18	67665511	67724595	-1	0	0	0	0	0	0	129	878	260	395	182		Q06180
ENSMUST00000025421	ENSMUSG00000079614	18	67774876	67795461	1	10	9	17	36	11	11	124	455	205	139	178		Q8R2U0
ENSMUST00000025425	ENSMUSG00000024542	18	67800107	67885168	1	34	21	43	49	39	21	119	266	259	39	231	E9Q4Y4	
ENSMUST00000025427	ENSMUSG00000009535	18	68300355	68324852	1	0	0	0	0	0	2	47	160	99	323	76		Q9D0L8
ENSMUST00000025428	ENSMUSG00000024546	18	68944633	68950141	-1	1	3	5	4	3	0	0	0	0	0	0	E9Q4Y3	
ENSMUST00000025430	ENSMUSG00000024548	18	78750380	79109391	-1	51	38	40	129	62	43	2	6	6	0	16	F2Z3U2	Q9Z180
ENSMUST00000025434	ENSMUSG00000024552	18	78146940	78209094	-1	38	15	79	26	28	17	0	0	1	0	0	G5E849	
ENSMUST00000025439	ENSMUSG00000024556	18	73770040	73815392	-1	12	10	22	47	9	8	1426	3543	2308	1182	1027		Q99KE1
ENSMUST00000025444	ENSMUSG00000024560	18	74216131	74221491	1	24	17	47	220	42	22	593	1110	638	105	645	Q541B1	Q9CWW7
ENSMUST00000025453	ENSMUSG00000024563	18	76241580	76305731	1	0	5	0	0	0	0	111	859	160	104	105		Q62432
ENSMUST00000025462	ENSMUSG00000024570	18	80192265	80200658	-1	9	4	18	98	11	4	583	965	458	171	366	Q3UKZ0	Q6P3B9
ENSMUST00000025463	ENSMUSG00000024571	18	80206765	80212741	1	0	0	14	0	6	0	857	0	169	0	1	Q9CQX6	
ENSMUST00000025464	ENSMUSG00000057130	18	80206795	80223533	1	0	3	0	124	1	0	0	0	0	0	0	F8WGE7	
ENSMUST00000025468	ENSMUSG00000024575	18	61220482	61289924	1	25	19	32	21	29	13	0	0	1	0	2	Q8K0A8	
ENSMUST00000025471	ENSMUSG00000024578	18	61687935	61692537	1	4	1	3	74	4	1	1	0	0	0	0		Q9QXT6
ENSMUST00000025472	ENSMUSG00000024579	18	61696837	61707635	-1	14	13	210	55	24	14	22	45	21	3	28		Q8C7K6
ENSMUST00000025474	ENSMUSG00000024581	18	62977836	62999450	1	9	10	9	20	16	4	327	1061	475	200	448		Q9CWZ7
ENSMUST00000025476	ENSMUSG00000024583	18	63662801	63692359	-1	4	6	5	147	4	4	238	925	325	275	184		Q8CDN6
ENSMUST00000025477	ENSMUSG00000056812	18	64254359	64276146	1	53	46	149	417	70	37	0	0	0	0	0		Q64689
ENSMUST00000025482	ENSMUSG00000039529	18	64528979	64661000	-1	34	32	59	173	34	15	0	2	2	0	0		Q148W0
ENSMUST00000025483	ENSMUSG00000024587	18	64499665	64516557	-1	10	12	22	37	11	8	815	3174	1549	963	1172		Q8BP47
ENSMUST00000025484	ENSMUSG00000024588	18	64456550	64489066	-1	23	17	30	65	55	19	290	523	319	181	397	Q544X6	
ENSMUST00000025486	ENSMUSG00000024590	18	56707813	56753424	1	13	11	21	345	28	10	3141	8145	3472	5419	3849		P14733
ENSMUST00000025488	ENSMUSG00000024592	18	56955833	56975368	-1	9	2	10	4	8	6	25	136	31	51	21		Q9CWB7
ENSMUST00000025490	ENSMUSG00000024594	18	57354733	57392719	1	37	30	91	132	54	24	241	357	280	30	212		Q3UPH1
ENSMUST00000025497	ENSMUSG00000024598	18	58008623	58209926	-1	87	53	143	164	78	37	0	1	0	0	2		Q61555
ENSMUST00000025500	ENSMUSG00000024600	18	58556257	58612773	1	16	11	14	5	25	6	0	0	0	1	0	E9Q9W4	
ENSMUST00000025503	ENSMUSG00000024601	18	58659482	58679570	1	50	33	35	98	47	29	36	135	45	20	108		Q91V64
ENSMUST00000025505	ENSMUSG00000024603	18	60526221	60558762	1	11	9	23	26	24	7	538	1710	852	523	541	Q3TQY2	Q8CBY8
ENSMUST00000025506	ENSMUSG00000024604	18	60560736	60572810	1	7	4	6	44	6	4	564	1460	650	79	514		Q8BHS3
ENSMUST00000025511	ENSMUSG00000024608	18	60774510	60778546	1	3	6	0	11	14	0	2504	4312	1313	11395	943		P62264
ENSMUST00000025515	ENSMUSG00000024614	18	90510154	90543267	1	4	6	8	48	9	2	539	1500	557	504	366		Q8BXZ1
ENSMUST00000025519	ENSMUSG00000024617	18	60925618	60988152	1	0	0	0	0	0	0	0	0	0	0	0	F8WIS9	
ENSMUST00000025520	ENSMUSG00000052026	18	60995381	61014199	-1	25	13	49	79	38	17	0	0	0	0	0		Q6PGE7
ENSMUST00000025521	ENSMUSG00000024619	18	61018862	61036199	-1	17	9	18	244	12	4	0	0	0	0	0		P18111
ENSMUST00000025522	ENSMUSG00000024620	18	61045150	61085061	1	43	29	17	39	69	36	17	16	14	7	16	E9QPE2	
ENSMUST00000025523	ENSMUSG00000024621	18	61105572	61132149	1	17	0	54	44	28	17	4022	7521	4303	1031	6613	Q0P635	P09581
ENSMUST00000025541	ENSMUSG00000024639	19	16132831	16387463	1	47	43	136	291	86	40	354	1348	874	83	684	Q3UHH5	P21279
ENSMUST00000025542	ENSMUSG00000024640	19	15904678	15947337	-1	19	18	51	85	20	3	102	207	71	79	95	Q543K5	Q99K85
ENSMUST00000025546	ENSMUSG00000024644	18	84667470	84685633	-1	11	15	21	34	0	0	571	1164	544	287	430		Q9D1A2
ENSMUST00000025547	ENSMUSG00000024645	18	84947294	84951524	-1	5	9	5	10	15	3	23	139	53	153	39	Q3THX0	Q8CCM6
ENSMUST00000025549	ENSMUSG00000024646	18	84851338	84880401	1	6	1	0	0	0	0	125	405	151	869	151	G5E850	
ENSMUST00000025554	ENSMUSG00000024653	19	9083636	9087958	-1	2	3	36	9	6	0	0	0	0	0	1	Q3UKV9	Q06318
ENSMUST00000025561	ENSMUSG00000024659	19	20373428	20390944	-1	21	21	40	155	21	46	34696	209987	71601	192889	34478	Q4FJV4	P10107
ENSMUST00000025562	ENSMUSG00000024660	19	9872297	9899533	-1	26	16	77	73	31	12	417	435	510	61	371		Q9WU62
ENSMUST00000025563	ENSMUSG00000024661	19	9982703	9985092	1	26	43	74	332	112	25	22167	76704	24688	9355	21207		P09528
ENSMUST00000025567	ENSMUSG00000024665	19	10064164	10101503	-1	10	15	29	139	26	5	17	22	15	5	27		Q9Z0R9
ENSMUST00000025568	ENSMUSG00000024666	19	10570478	10577362	-1	9	7	12	14	15	8	84	195	77	80	48		Q9D6G5
ENSMUST00000025569	ENSMUSG00000024667	19	10533865	10556238	-1	0	0	0	4	8	5	54	257	109	36	25		Q9CQC4
ENSMUST00000025570	ENSMUSG00000024668	19	10500513	10525209	-1	11	16	31	40	24	17	423	1879	704	1069	552		Q8C6I2
ENSMUST00000025571	ENSMUSG00000024669	19	10718143	10738974	-1	14	8	25	21	30	21	53	57	22	12	97	Q3UP78	P13379
ENSMUST00000025572						3	4	24	0	14	4	5	15	7	14	15		
ENSMUST00000025574	ENSMUSG00000024672	19	11321039	11336146	-1	4	2	4	4	2	2	0	0	0	0	0	E9Q9V5	
ENSMUST00000025580	ENSMUSG00000024677	19	11516512	11531256	1	0	0	0	0	3	0	164	1342	199	553	274		Q99N09
ENSMUST00000025581	ENSMUSG00000024678	19	11536801	11558467	1	1	6	13	18	11	1	0	0	0	0	0		Q99N05
ENSMUST00000025582	ENSMUSG00000024679	19	11586604	11604849	-1	5	2	8	6	4	4	308	2032	303	2815	597	Q2TVW7	
ENSMUST00000025583	ENSMUSG00000024680	19	11615523	11623719	-1	1	0	0	0	0	1	0	0	2	0	0	Q3UNT6	
ENSMUST00000025585	ENSMUSG00000024682	19	11747554	11763447	1	14	9	6	15	10	7	0	0	0	0	0		P52787
ENSMUST00000025590	ENSMUSG00000024687	19	11965844	11994105	1	36	14	40	57	33	16	715	1959	1432	71	1043		Q3B7Z2
ENSMUST00000025595	ENSMUSG00000024691	19	12545740	12589768	1	0	13	0	0	0	0	579	4692	1510	1792	891		Q9D2L9
ENSMUST00000025598	ENSMUSG00000024694	19	12695786	12719902	1	8	6	6	8	8	0	0	0	0	0	0		Q9DCY0
ENSMUST00000025601	ENSMUSG00000024696	19	12798606	12833807	1	3	6	10	8	6	3	83	178	54	367	116		Q99N69
ENSMUST00000025602	ENSMUSG00000024697	19	16435667	16610818	1	29	23	63	152	33	12	0	7	1	0	1		P30677
ENSMUST00000025617	ENSMUSG00000024712	19	17394043	17401349	1	29	26	179	147	31	23	177	883	286	79	282		Q8CFV9
ENSMUST00000025618	ENSMUSG00000024713	19	17432832	17837632	-1	46	25	59	263	74	34	0	2	0	0	2		Q04592
ENSMUST00000025631	ENSMUSG00000024725	19	18579328	18631789	-1	487	383	1358	582	642	301	6104	13099	7159	4226	4487		Q62422
ENSMUST00000025632	ENSMUSG00000024726	19	18670780	18704788	1	2	0	2	62	0	0	14	2	4	6	4		Q80UY1
ENSMUST00000025635	ENSMUSG00000024729	19	11096816	11130876	-1	7	7	2	4	6	1	1	0	1	0	0	G5E851	
ENSMUST00000025636	ENSMUSG00000024730	19	11067471	11081102	-1	4	2	2	8	5	2	97	279	62	1439	364		Q99N10
ENSMUST00000025639	ENSMUSG00000024732	19	10941481	10949266	-1	0	5	27	82	10	0	84	142	89	47	130		Q9JJ89
ENSMUST00000025641	ENSMUSG00000024734	19	10914287	10920632	-1	8	5	30	20	30	12	0	0	0	0	0	Q059L1	Q62005
ENSMUST00000025642	ENSMUSG00000024735	19	10895231	10909559	1	0	0	0	23	0	0	388	463	425	180	419		Q99KP6
ENSMUST00000025645	ENSMUSG00000024736	19	10857822	10869940	-1	0	0	0	233	5	0	0	0	0	7	26		Q922P8
ENSMUST00000025646	ENSMUSG00000024737	19	10839727	10859362	1	3	5	4	19	2	3	2327	3971	2161	739	2243		Q8BPX9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000025647	ENSMUSG00000024738	19	10668957	10678071	-1	22	8	23	10	21	7	0	0	0	0	0	Q9D106	
ENSMUST00000025649	ENSMUSG00000024740	19	10605625	10629813	1	28	25	74	81	46	22	1865	2752	2315	354	1947		Q3U1J4
ENSMUST00000025651	ENSMUSG00000024742	19	10199132	10204169	-1	23	7	26	48	0	0	13	24	117	0	0	Q91Z50	
ENSMUST00000025656	ENSMUSG00000024747	19	20692953	20727562	-1	16	15	8	8	8	6	0	0	0	1	0	B2RTL5	O35945
ENSMUST00000025659	ENSMUSG00000024750	19	21272278	21282289	1	6	6	8	39	9	0	1081	3551	1185	150	432		O88878
ENSMUST00000025663	ENSMUSG00000024754	19	21778342	21858327	1	0	0	0	136	44	23	677	1617	1464	95	809		Q5FWI3
ENSMUST00000025666	ENSMUSG00000024757	19	7673061	7711310	-1	2	2	11	0	6	4	0	0	0	0	0	Q8VCA0	
ENSMUST00000025667	ENSMUSG00000024758	19	7425901	7483289	-1	6	0	1	66	2	0	2416	9796	3175	848	2290		Q9ES97
ENSMUST00000025668	ENSMUSG00000024759	19	7494040	7538608	1	40	19	74	66	36	9	400	718	656	201	474		Q91YH5
ENSMUST00000025669						7	1	11	30	6	1	0	1	0	0	0		
ENSMUST00000025675	ENSMUSG00000024764	19	7225668	7241222	-1	19	22	59	100	38	17	299	334	304	55	243		Q8VE10
ENSMUST00000025679	ENSMUSG00000024767	19	7198202	7206316	-1	11	12	30	31	20	9	1100	1536	783	242	607		Q7TQI3
ENSMUST00000025680	ENSMUSG00000024768	19	33961187	33976810	1	3	5	3	3	7	2	0	0	0	0	0		Q9CPP7
ENSMUST00000025681	ENSMUSG00000024769	19	6306456	6325652	1	43	32	103	399	85	36	208	214	227	16	210		Q80UW5
ENSMUST00000025682	ENSMUSG00000024770	19	34067358	34084918	1	2	4	9	3	2	2	0	5	1	8	0		Q3U4B4
ENSMUST00000025684	ENSMUSG00000024772	19	6276725	6300096	1	21	12	33	56	24	12	6336	5919	3795	523	2900	Q80ZZ0	Q9WVK4
ENSMUST00000025685	ENSMUSG00000056078	19	34100943	34122687	1	10	5	7	8	16	7	12	24	7	4	3		Q8K2A6
ENSMUST00000025686	ENSMUSG00000024774	19	34122549	34166053	-1	1	6	5	1	5	0	873	3454	1405	1921	724		Q9D3J5
ENSMUST00000025691	ENSMUSG00000024778	19	34290659	34327770	1	6	5	12	13	6	1	287	1872	488	1369	463		P25446
ENSMUST00000025694	ENSMUSG00000024766	19	33517740	33761951	-1	0	0	0	0	0	0	0	0	0	9	9	Q3UT41	
ENSMUST00000025695	ENSMUSG00000024777	19	6227765	6235872	-1	18	16	41	97	25	23	321	386	274	30	226	Q6PD28	
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ENSMUST00000025698	ENSMUSG00000024784	19	6226380	6227768	1	0	0	0	11	3	0	0	0	0	0	0	A2RSW3	Q925Q5
ENSMUST00000025699	ENSMUSG00000024786	19	6184388	6224225	1	3	3	0	0	5	0	0	1	0	0	0		Q9D992
ENSMUST00000025702	ENSMUSG00000024787	19	6119399	6128304	-1	7	2	14	66	16	4	112	193	112	18	75		Q91WE1
ENSMUST00000025704	ENSMUSG00000024791	19	6084983	6091777	1	20	14	14	72	8	0	41	14	27	7	40		Q9CPY3
ENSMUST00000025705	ENSMUSG00000024789	19	29251828	29313080	1	17	12	0	0	19	5	315	2822	360	15	0	G5E852	
ENSMUST00000025706	ENSMUSG00000024793	4	152115934	152120119	1	10	5	9	143	23	10	0	0	0	0	0	B1AWN9	
ENSMUST00000025707	ENSMUSG00000024792	19	6080762	6084944	-1	0	0	7	12	0	0	147	212	101	34	126		Q9DB43
ENSMUST00000025711	ENSMUSG00000024797	19	6067842	6080324	-1	0	0	0	0	0	0	549	576	452	48	315		Q3UVL4
ENSMUST00000025713	ENSMUSG00000024799	19	6062821	6068373	-1	2	0	0	0	0	0	24	30	5	0	9		Q71KT5
ENSMUST00000025714	ENSMUSG00000024800	19	36083716	36104772	1	6	3	10	7	6	1	18	74	34	142	35		O88796
ENSMUST00000025718	ENSMUSG00000024803	19	36111965	36119844	-1	11	11	10	8	12	11	0	0	0	54	15		Q9CR42
ENSMUST00000025719	ENSMUSG00000024806	19	29697921	29708448	1	2	1	19	8	10	1	0	0	0	1	0	Q2TA50	
ENSMUST00000025723	ENSMUSG00000024807	19	6046576	6053712	1	0	0	0	0	0	0	317	464	195	49	316	E9QQ99	
ENSMUST00000025724	ENSMUSG00000024810	19	29925114	29960718	1	5	1	0	5	12	1	0	0	0	59	24		Q8BVZ5
ENSMUST00000025727	ENSMUSG00000024815	19	30003790	30006020	1	13	14	15	10	16	6	0	0	0	0	0	Q9CQ14	
ENSMUST00000025728	ENSMUSG00000024816	19	5849702	5875274	-1	38	21	79	73	55	26	2356	2969	1864	246	1298		Q3UFK8
ENSMUST00000025729	ENSMUSG00000024811	19	36834232	36893477	1	14	13	35	41	19	4	968	2904	2140	313	1138		Q3UES3
ENSMUST00000025732	ENSMUSG00000024818	19	5877808	5885766	1	13	14	8	0	2	0	1236	1505	1156	185	1029		Q8CFJ7
ENSMUST00000025739	ENSMUSG00000024817	19	30030513	30093722	1	8	0	7	11	3	0	190	725	375	77	259		Q7TMI3
ENSMUST00000025740	ENSMUSG00000024824	19	4195198	4201603	-1	9	3	13	9	12	4	246	542	201	23	179		Q9Z0F6
ENSMUST00000025743	ENSMUSG00000024829	19	3282901	3292837	1	4	7	14	10	0	3	40	129	46	161	51		Q9D1N9
ENSMUST00000025745	ENSMUSG00000024829	19	3282901	3292837	1	8	6	5	59	3	5	0	2	5	0	5		Q9D1N9
ENSMUST00000025746	ENSMUSG00000024826	19	5896516	5913010	-1	14	0	31	0	22	0	563	748	356	88	364	F8WIP7	
ENSMUST00000025749	ENSMUSG00000024830	19	4156713	4163354	-1	3	0	4	4	0	0	69	45	13	0	38		Q9Z1M4
ENSMUST00000025751	ENSMUSG00000024831	19	3260924	3283017	-1	8	0	53	69	52	14	58	97	29	11	88	A0A0B4J1E3	
ENSMUST00000025752	ENSMUSG00000024833	19	5940543	5964206	-1	9	10	17	32	13	6	77	159	156	36	107		P33611
ENSMUST00000025755	ENSMUSG00000024837	19	25505618	25604329	1	13	0	28	67	7	6	0	0	0	0	0		Q9QZS9
ENSMUST00000025759	ENSMUSG00000024841	19	5366813	5371511	1	59	46	409	237	43	21	241	582	245	147	165		Q3THJ3
ENSMUST00000025760	ENSMUSG00000024843	19	3851773	3894369	1	0	0	0	0	0	0	66	165	61	13	40		O54804
ENSMUST00000025761	ENSMUSG00000024842	19	4135425	4139609	-1	8	9	14	10	8	10	0	3	2	0	2		Q8VHC5
ENSMUST00000025762	ENSMUSG00000024844	19	5364641	5366645	-1	3	0	0	45	12	6	292	396	179	198	188		O54962
ENSMUST00000025764	ENSMUSG00000024846	19	5344705	5349574	-1	87	71	384	150	86	45	0	0	2	8	4	Q9D1B1	
ENSMUST00000025767	ENSMUSG00000024847	19	4114446	4125858	-1	6	0	0	0	4	2	638	743	352	132	325		O08915
ENSMUST00000025773	ENSMUSG00000024854	19	4231899	4233631	1	6	5	15	11	9	2	365	566	212	138	157	Q547B4	Q9CWP8
ENSMUST00000025774	ENSMUSG00000024853	19	5273923	5295455	-1	17	14	42	72	33	24	4158	8741	5867	833	4333	Q3UJB0	
ENSMUST00000025778	ENSMUSG00000024827	19	30098449	30175418	-1	24	29	58	120	34	13	0	0	0	4	2		Q91W43
ENSMUST00000025779	ENSMUSG00000024856	19	4097182	4099019	1	0	0	0	22	3	0	432	1073	711	261	891		Q9CPY4
ENSMUST00000025786	ENSMUSG00000024855	19	5133688	5273119	-1	22	20	61	198	26	12	3280	4261	3515	201	2812		Q8K212
ENSMUST00000025791	ENSMUSG00000024858	19	4286001	4306222	-1	0	0	7	17	6	11	9670	12936	6294	526	5413	Q7TS64	
ENSMUST00000025794	ENSMUSG00000037263	19	3958645	3972103	1	0	0	0	0	2	0	1	7	1	1	0	F6QPV9	
ENSMUST00000025797	ENSMUSG00000024863	19	30232928	30239685	1	14	7	3	3	9	4	0	0	0	4	0	Q3UEK1	P41317
ENSMUST00000025798	ENSMUSG00000024862	19	5107746	5118560	-1	7	0	0	44	0	0	0	0	98	0	78	D3YXZ3	
ENSMUST00000025800	ENSMUSG00000024867	19	24294794	24555872	-1	5	14	0	46	0	0	263	803	487	138	312		P70181
ENSMUST00000025802	ENSMUSG00000024869	19	4000580	4005816	1	0	0	0	74	0	2	96	96	28	73	16		Q9CR24
ENSMUST00000025803	ENSMUSG00000024868	19	30545863	30549665	-1	107	76	303	401	111	66	2	19	12	0	16		O54908
ENSMUST00000025804	ENSMUSG00000024870	19	5099207	5106996	-1	5	9	49	95	37	13	5511	5060	3401	963	2426	Q0PD66	Q9D1G1
ENSMUST00000025805	ENSMUSG00000024873	19	5092871	5098418	-1	7	5	9	46	5	1	1	25	11	2	9	Q3SYI8	O35089
ENSMUST00000025806	ENSMUSG00000024871	19	4003321	4007005	1	0	0	9	0	4	5	0	21	7	1	8		
ENSMUST00000025811	ENSMUSG00000024875	19	5088538	5092879	1	11	6	19	21	17	8	220	217	157	95	116		Q91XB7
ENSMUST00000025815	ENSMUSG00000024878	19	24919916	24961616	-1	3	8	4	9	10	4	17	170	30	91	27		Q8VEH6
ENSMUST00000025818	ENSMUSG00000024883	19	5050808	5057071	1	40	28	66	117	76	29	7	20	10	9	27		Q921Q7
ENSMUST00000025823	ENSMUSG00000024889	19	4622551	4625617	-1	9	7	16	55	8	6	162	225	83	32	77		P57791
ENSMUST00000025826	ENSMUSG00000024891	19	5024006	5031971	1	18	16	49	154	21	16	6	10	3	3	21		Q61672
ENSMUST00000025827	ENSMUSG00000024896	19	32485769	32515370	1	14	11	22	406	25	8	76	204	128	40	117		Q9Z2L6
ENSMUST00000025830	ENSMUSG00000024897	19	23758876	23949597	1	45	31	94	391	60	40	48	60	38	7	74		B2RUJ5
ENSMUST00000025831	ENSMUSG00000052085	19	24999529	25202432	1	72	63	88	107	68	42	4300	6732	7999	373	5359		Q8C147
ENSMUST00000025833	ENSMUSG00000024899	19	32620005	32667187	1	95	76	432	83	73	42	48	137	48	2	57		O88428
ENSMUST00000025834	ENSMUSG00000024901	19	4930651	4943127	-1	0	1	5	266	16	8	0	1	0	0	0		
ENSMUST00000025835	ENSMUSG00000024900	19	3323301	3385732	1	27	18	51	99	41	19	1259	4651	2153	254	2001	Q7TQD5	P97742
ENSMUST00000025836	ENSMUSG00000024902	19	4962306	4966995	1	37	30	75	71	29	23	63	127	43	231	64		Q9CQF0
ENSMUST00000025840	ENSMUSG00000024905	19	3388857	3407823	1	1	0	16	69	3	0	20	13	30	4	6		Q9WTJ6
ENSMUST00000025841	ENSMUSG00000024906	19	5482345	5488402	-1	0	0	0	0	0	0	76	120	116	27	53	F8WIN9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000025842	ENSMUSG00000024907	19	3409919	3414472	-1	7	4	16	90	13	5	0	2	2	3	0	Q3V002	P47212
ENSMUST00000025844	ENSMUSG00000024910	19	5465240	5468498	-1	13	6	18	13	11	4	21	56	21	23	34	Q8C2M0	P56203
ENSMUST00000025846	ENSMUSG00000024908	19	3454933	3575749	-1	19	0	0	113	24	0	49	106	192	0	303		Q922D4
ENSMUST00000025847	ENSMUSG00000024911	19	5460607	5465052	1	14	5	12	34	24	3	456	937	430	365	324	Q8K2D8	
ENSMUST00000025850	ENSMUSG00000024912	19	5447703	5455945	1	8	4	27	239	25	13	7	6	2	15	78	Q3UMK5	P48755
ENSMUST00000025851	ENSMUSG00000063904	19	4907229	4928287	-1	15	12	55	62	55	16	1455	1447	1049	144	727		Q99KK7
ENSMUST00000025853	ENSMUSG00000024914	19	5422805	5424979	-1	1	0	0	26	0	0	261	350	361	88	179	Q4FJW2	Q9D6N5
ENSMUST00000025856	ENSMUSG00000024913	19	3584828	3686564	-1	0	0	0	0	0	0	118	66	74	22	302		Q91VN0
ENSMUST00000025861	ENSMUSG00000024922	19	5549137	5560575	-1	20	19	43	184	35	15	33	134	40	37	47		Q9WTJ2
ENSMUST00000025862	ENSMUSG00000024921	19	26605115	26778321	1	18	14	0	38	26	0	1	0	8	8	37	F2Z4A9	
ENSMUST00000025864	ENSMUSG00000024925	19	5601873	5603439	1	1	3	0	28	4	2	170	533	269	463	121		Q9CQ18
ENSMUST00000025866	ENSMUSG00000024924	19	27216484	27254231	1	0	0	0	0	0	0	1	2	2	1	3	F8WIN7	
ENSMUST00000025867	ENSMUSG00000024927	19	5637483	5648130	1	9	12	34	116	35	14	2546	2964	2245	266	1813	Q548Y4	Q04207
ENSMUST00000025872	ENSMUSG00000064202	19	28893042	28967800	-1	7	0	0	52	5	2	0	0	0	0	0		B2RV46
ENSMUST00000025875	ENSMUSG00000024935	19	28835049	28913960	1	11	13	13	16	22	9	0	2	0	0	0		P51906
ENSMUST00000025885	ENSMUSG00000079478	19	5728088	5731732	-1	0	0	0	0	0	0	32	37	10	28	24	Q545N1	P56873
ENSMUST00000025890	ENSMUSG00000024941	19	5758427	5771401	-1	18	11	50	124	42	10	883	1050	797	140	631		Q9EQC5
ENSMUST00000025891	ENSMUSG00000024942	19	5988546	6015825	-1	27	13	43	63	25	20	8896	8376	7222	556	4727	Q3TI07	O35350
ENSMUST00000025893	ENSMUSG00000024944	19	6134374	6141406	-1	4	0	0	28	3	3	76	68	27	24	35		Q9D0J4
ENSMUST00000025897	ENSMUSG00000024948	19	6341135	6355615	1	0	0	0	6	0	0	1647	1834	581	69	766		Q61161
ENSMUST00000025903	ENSMUSG00000024952	19	6829085	6840601	-1	14	8	30	151	20	6	712	690	487	56	376		Q9Z2B9
ENSMUST00000025904	ENSMUSG00000024953	19	6906697	6910106	-1	5	0	0	151	12	15	5781	5784	3184	3170	1891		P99029
ENSMUST00000025906	ENSMUSG00000024955	19	6910977	6921813	-1	2	4	11	37	15	4	783	1161	556	126	374		O08580
ENSMUST00000025908	ENSMUSG00000024957	19	6925710	6934515	-1	15	16	26	115	26	8	0	0	1	0	0	Q0VD85	O88454
ENSMUST00000025909	ENSMUSG00000024958	19	6938069	6942450	-1	1	2	14	0	24	6	187	52	51	23	68		Q80ZU9
ENSMUST00000025910	ENSMUSG00000024959	19	6941861	6951898	1	6	6	5	155	12	9	146	221	152	40	134		Q61337
ENSMUST00000025912	ENSMUSG00000024960	19	6953714	6969759	-1	41	20	69	112	48	18	662	1100	849	66	656		P51432
ENSMUST00000025914	ENSMUSG00000024962	19	6982473	6987651	-1	7	0	12	57	9	5	12	40	11	8	40		P49766
ENSMUST00000025915	ENSMUSG00000024963	19	6987911	6992503	-1	9	1	16	43	14	8	58	93	49	44	49	Q6GTN1	
ENSMUST00000025918	ENSMUSG00000024966	19	7020696	7040026	-1	13	5	24	36	16	11	312	755	389	210	543		Q60864
ENSMUST00000025921	ENSMUSG00000024969	19	7275396	7341860	-1	4	13	30	57	25	15	1214	904	1488	24	961	Q3T9A3	
ENSMUST00000025924	ENSMUSG00000024970	19	7356464	7383026	-1	20	12	29	110	42	12	113	156	77	16	98		Q05AH6
ENSMUST00000025925	ENSMUSG00000060675	19	7557459	7588545	1	34	25	50	25	34	15	9	25	0	78	21		Q8R3U1
ENSMUST00000025929	ENSMUSG00000024973	19	7612541	7639642	1	0	6	4	4	4	4	0	0	0	0	0		Q9CPX5
ENSMUST00000025930	ENSMUSG00000024974	19	53600398	53645833	1	22	15	33	49	24	15	314	1338	943	403	628	Q1HL32	Q9CW03
ENSMUST00000025931	ENSMUSG00000024975	19	53892231	53929861	1	0	0	0	9	28	0	242	1113	362	92	268		Q61823
ENSMUST00000025932	ENSMUSG00000024976	19	53944306	54033268	1	0	0	0	44	26	0	521	853	1016	1109	748		O88520
ENSMUST00000025936	ENSMUSG00000024979	19	55180733	55196313	1	6	3	26	11	0	0	0	0	0	0	0	Q1HL20	O08524
ENSMUST00000025940	ENSMUSG00000071347	14	60768134	60780869	1	18	11	22	16	15	13	8	31	8	4	21		Q4ZJN1
ENSMUST00000025944	ENSMUSG00000024986	19	37434810	37440731	1	5	5	4	448	19	10	102	689	302	38	240		P43120
ENSMUST00000025946	ENSMUSG00000024987	19	37697808	37701528	1	11	9	15	303	17	9	0	11	1	4	7		
ENSMUST00000025951	ENSMUSG00000024990	19	38116620	38125321	-1	7	4	16	65	13	11	0	0	0	0	0	H7BWY6	
ENSMUST00000025955	ENSMUSG00000024991	19	60761116	60790693	-1	21	17	28	52	24	15	812	2785	2142	879	1649		P23116
ENSMUST00000025956	ENSMUSG00000024992	19	38132781	38183947	1	22	0	0	0	0	0	0	0	0	0	0		Q91ZQ1
ENSMUST00000025957	ENSMUSG00000024993	19	60811585	60836227	1	0	0	0	0	0	0	55	443	32	239	8		Q9D8N2
ENSMUST00000025961	ENSMUSG00000024997	19	60864051	60874556	-1	3	4	7	37	5	2	216	616	215	788	158		P20108
ENSMUST00000025963	ENSMUSG00000024999	19	38788128	38819237	-1	90	82	277	82	105	59	14	64	35	44	55		Q8VI84
ENSMUST00000025965	ENSMUSG00000025001	19	38930915	38971051	1	24	36	27	81	39	19	33	102	44	22	32		Q60848
ENSMUST00000025966	ENSMUSG00000025002	19	39007019	39042693	1	7	5	1	10	6	5	0	0	0	16	4		Q9D816
ENSMUST00000025968	ENSMUSG00000025003	19	39510862	39568529	1	6	5	6	2	8	8	0	0	0	4	0		P56656
ENSMUST00000025979	ENSMUSG00000025007	19	40550257	40588463	-1	0	0	0	50	21	0	0	0	16	0	35		Q9Z110
ENSMUST00000025981	ENSMUSG00000025008	19	40596446	40612233	-1	18	15	5	36	22	12	39	120	59	11	88		Q8R2Q6
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ENSMUST00000025986	ENSMUSG00000025013	19	41083981	41206774	-1	20	30	76	65	9	19	0	0	0	0	0		Q9WVM6
ENSMUST00000025989	ENSMUSG00000025016	19	41210842	41264004	-1	11	15	28	55	15	12	1509	4588	2054	350	1323		Q9ET30
ENSMUST00000025992	ENSMUSG00000036225	18	14968685	15151446	-1	33	9	33	91	42	25	3	18	0	0	8		Q5M956
ENSMUST00000025993	ENSMUSG00000025020	19	41600257	41743665	-1	16	0	36	235	21	16	0	0	0	0	0		Q80TR4
ENSMUST00000025997	ENSMUSG00000025024	19	53379214	53390573	-1	7	2	4	70	9	2	391	1247	500	84	324		Q8BGT7
ENSMUST00000025998	ENSMUSG00000025025	19	53310506	53375810	1	0	0	0	50	3	0	616	907	979	393	481	Q3USD3	P50540
ENSMUST00000025999	ENSMUSG00000025026	19	53140445	53247399	1	0	0	0	0	0	0	1261	2980	1124	515	1005		Q9QYB5
ENSMUST00000026008	ENSMUSG00000025034	19	46501648	46516444	1	19	14	41	475	33	24	687	1528	1055	102	805		Q99PJ2
ENSMUST00000026009	ENSMUSG00000025035	19	46531109	46573085	-1	9	6	6	16	8	4	182	369	131	387	137	Q543P7	Q9WUL7
ENSMUST00000026011	ENSMUSG00000025036	19	46573365	46596898	1	56	79	164	71	61	35	41	165	85	5	93	Q3UC14	Q925N2
ENSMUST00000026012	ENSMUSG00000003555	19	46667165	46672974	-1	12	15	24	14	19	10	1	0	0	0	0	Q53YJ1	P27786
ENSMUST00000026013	ENSMUSG00000025037	X	16619698	16687818	1	1384	1493	1860	1450	1628	794	17	132	32	127	52		Q64133
ENSMUST00000026014	ENSMUSG00000025038	X	17132049	17319368	-1	5	4	8	1	4	1	0	0	0	0	0	Q059K2	Q9D485
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ENSMUST00000026021	ENSMUSG00000025044	8	39581700	39642678	-1	3	0	4	3	0	2	22	203	37	1231	286		P30204
ENSMUST00000026027	ENSMUSG00000025049	19	47067748	47083479	1	9	4	8	226	10	6	85	350	179	26	96	F8VPY2	
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ENSMUST00000026036	ENSMUSG00000025056	X	86191764	86195947	1	5	6	15	137	13	10	0	0	0	0	0	Q53ZY9	Q61066
ENSMUST00000026039	ENSMUSG00000025059	X	85701937	85776819	-1	6	0	0	34	0	4	140	635	307	463	245		Q64516
ENSMUST00000026043	ENSMUSG00000025060	19	47579678	47645246	1	21	24	42	50	36	14	984	4083	1865	629	1658	A2RRK3	O54988
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ENSMUST00000026062	ENSMUSG00000025076	19	56397129	56442344	1	8	6	14	101	14	6	408	693	480	92	302	Q4FJQ4	P97864
ENSMUST00000026068	ENSMUSG00000025082	19	56874249	56912078	1	31	25	79	149	59	43	0	0	0	0	2		Q70UZ7
ENSMUST00000026072	ENSMUSG00000025086	19	57452906	57491005	1	28	17	41	29	26	14	0	17	4	3	15		Q8C0D0
ENSMUST00000026073	ENSMUSG00000025086	19	57452906	57491005	1	71	51	118	90	106	56	7	25	7	4	15		Q8C0D0
ENSMUST00000026076	ENSMUSG00000025089	19	58235604	58455909	-1	9	20	35	38	23	0	0	0	0	0	0		P97785
ENSMUST00000026078	ENSMUSG00000042243	13	60781893	60786364	-1	7	4	6	14	18	3	0	0	0	0	0	E9Q623	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000026081	ENSMUSG00000025091	19	58759723	58777533	1	8	7	11	10	15	5	0	0	0	0	0	Q4VBW7	
ENSMUST00000026084	ENSMUSG00000025094	19	59260878	59296012	1	14	18	25	74	21	8	40	110	36	3	29		Q8BRU6
ENSMUST00000026092	ENSMUSG00000025102	7	81782182	81789478	-1	1	0	1	9	2	3	11	32	18	88	21		Q9CRC3
ENSMUST00000026093	ENSMUSG00000025103	7	81792075	81829431	-1	15	4	15	55	10	1	477	1712	832	273	499		P58544
ENSMUST00000026094	ENSMUSG00000025104	7	81881251	81934473	-1	26	28	126	62	30	13	3	10	7	1	11		Q9JMG7
ENSMUST00000026096	ENSMUSG00000025105	7	81966672	81992299	-1	31	18	60	23	35	17	0	0	0	5	12	F8VPY0	
ENSMUST00000026119	ENSMUSG00000025127	11	120530699	120538986	1	0	0	0	34	3	0	0	0	0	2	0		Q61606
ENSMUST00000026120	ENSMUSG00000025128	3	18054174	18057517	1	10	12	15	419	16	15	0	1	0	0	0		
ENSMUST00000026121	ENSMUSG00000025129	11	120549979	120551132	-1	3	3	5	13	6	5	0	0	0	0	1		Q9D119
ENSMUST00000026122	ENSMUSG00000025130	11	120560298	120573253	-1	15	13	70	134	25	13	3302	5475	3645	978	3597		P09103
ENSMUST00000026125	ENSMUSG00000025134	11	120592121	120598365	-1	18	6	30	19	17	9	50	82	61	20	71		O08583
ENSMUST00000026126	ENSMUSG00000025133	7	97480956	97541395	1	19	20	49	13	23	10	99	325	210	159	182		Q8CIM8
ENSMUST00000026128	ENSMUSG00000025135	11	120598421	120608198	1	30	19	52	30	39	10	23	52	30	8	32		Q9CPX9
ENSMUST00000026129	ENSMUSG00000025137	11	120610087	120617936	-1	9	12	23	25	19	7	245	657	217	60	205	Q3USD5	Q922E4
ENSMUST00000026133	ENSMUSG00000025140	11	120635712	120643769	-1	79	66	57	3822	115	56	6	7	5	1	2	Q3UTR5	Q922W5
ENSMUST00000026134	ENSMUSG00000025141	11	120646031	120648158	-1	7	5	38	43	13	7	2	2	2	1	0		Q08AU7
ENSMUST00000026135	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	0	0	0	4	97	60	0	3		Q8VBT9
ENSMUST00000026137	ENSMUSG00000025144	11	120710942	120713738	-1	0	0	0	19	6	0	0	0	4	0	6		Q8C4X1
ENSMUST00000026139	ENSMUSG00000025145	11	120713925	120721128	1	0	2	0	28	0	13	111	189	149	27	198		Q8CIM1
ENSMUST00000026142	ENSMUSG00000025151	X	94535474	94542143	-1	0	4	0	29	11	7	119	116	73	122	245		Q9QYH6
ENSMUST00000026144	ENSMUSG00000039450	11	120725399	120727281	-1	0	0	0	82	0	0	15	33	13	30	23		Q91X52
ENSMUST00000026148	ENSMUSG00000025150	11	120729489	120732114	-1	0	0	6	0	2	2	7	2	0	539	259	Q542P5	P08074
ENSMUST00000026150	ENSMUSG00000025154	19	41766588	41802084	-1	27	25	0	0	0	0	833	1001	999	89	555		Q8BRH3
ENSMUST00000026151	ENSMUSG00000025155	11	120789201	120796403	-1	0	0	0	0	0	0	0	0	0	0	0	B1ATU5	
ENSMUST00000026154	ENSMUSG00000025157	19	41933472	41944095	1	11	9	24	39	12	9	241	516	280	75	163		Q9ESG8
ENSMUST00000026156	ENSMUSG00000025158	11	120780746	120784207	-1	0	0	14	76	12	0	385	378	251	25	177		O09009
ENSMUST00000026159	ENSMUSG00000025163	11	121036747	121039418	-1	6	2	9	9	7	5	33	67	7	22	33	Q3U4A8	P50283
ENSMUST00000026162	ENSMUSG00000025165	11	121067407	121081220	-1	19	13	35	8	21	5	0	0	0	0	0	A2ABP9	
ENSMUST00000026168	ENSMUSG00000025159	19	41941086	41981157	-1	0	0	0	0	0	0	81	0	107	2	0		Q9D071
ENSMUST00000026169	ENSMUSG00000025169	11	121177591	121204711	-1	6	7	25	31	16	3	42	51	22	15	33		Q9D136
ENSMUST00000026170	ENSMUSG00000025171	19	41981763	42034641	1	9	10	23	157	26	6	1475	1470	914	236	605		Q91WB7
ENSMUST00000026172	ENSMUSG00000025172	19	42036038	42045110	1	10	3	16	6	21	6	0	2	0	1	0		Q9WV06
ENSMUST00000026173	ENSMUSG00000025173	11	121327224	121354445	-1	7	8	11	55	21	3	520	1388	612	482	457		Q9CR39
ENSMUST00000026175	ENSMUSG00000025175	11	121434913	121450491	1	9	10	20	58	18	6	1	0	1	0	0		Q9ER35
ENSMUST00000026188	ENSMUSG00000025184	19	42518759	42592343	1	19	6	28	32	19	14	243	1189	658	539	337		Q8BJM3
ENSMUST00000026190	ENSMUSG00000025185	19	42593982	42612813	-1	32	23	30	43	26	10	1	1	7	10	68		Q924C6
ENSMUST00000026194	ENSMUSG00000025188	19	42755105	42779978	-1	0	0	0	0	0	0	39	251	0	32	33		
ENSMUST00000026196	ENSMUSG00000025190	19	43499752	43524605	-1	7	10	24	40	17	6	706	748	637	170	457		P05201
ENSMUST00000026199	ENSMUSG00000025193	19	43752996	43768638	1	0	0	0	152	0	5	19	72	32	23	10	F8WHX2	
ENSMUST00000026208	ENSMUSG00000025194	19	43782192	43840740	1	74	58	81	276	97	39	0	8	3	3	4		Q8VI47
ENSMUST00000026209	ENSMUSG00000025195	19	43847967	43912392	-1	45	36	117	104	66	43	607	479	876	41	651		
ENSMUST00000026210	ENSMUSG00000025196	19	43956307	43986556	-1	12	7	26	20	22	9	0	1	1	2	0		Q9JJN5
ENSMUST00000026211	ENSMUSG00000025197	19	44005022	44029247	-1	8	17	19	10	25	6	0	1	0	0	1	E9Q5K4	
ENSMUST00000026217	ENSMUSG00000025199	19	44073335	44107480	-1	0	0	0	17	0	0	258	467	244	79	45	E9QNL4	
ENSMUST00000026218	ENSMUSG00000025200	19	44108644	44135876	-1	21	21	19	23	23	19	66	143	70	37	52		Q8CI33
ENSMUST00000026220	ENSMUSG00000025202	19	44203288	44244016	1	188	128	833	318	140	96	7	15	14	8	18		Q99PL7
ENSMUST00000026221	ENSMUSG00000025203	19	44293676	44306864	1	36	23	55	40	29	20	548	787	1224	106	457		P13011
ENSMUST00000026222	ENSMUSG00000025204	19	44548572	44555440	-1	4	0	0	30	0	0	622	1031	560	427	346		Q9D6J5
ENSMUST00000026225	ENSMUSG00000025207	19	44989101	45003397	1	0	0	0	26	0	0	0	0	4	0	0		Q9WUH7
ENSMUST00000026227	ENSMUSG00000025209	19	45006558	45012762	1	71	52	178	173	65	24	93	318	110	39	97		Q8CIW5
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ENSMUST00000026236	ENSMUSG00000025215	19	45150680	45156943	1	10	5	17	219	12	11	0	0	0	0	0	Q9QX99	
ENSMUST00000026239	ENSMUSG00000025218	19	45552275	45560531	-1	17	14	47	24	27	10	440	498	270	59	229		Q9QXE2
ENSMUST00000026240	ENSMUSG00000025219	19	45736798	45742915	-1	0	0	35	102	10	8	0	0	0	0	0	Q80ZL6	
ENSMUST00000026241	ENSMUSG00000025219	19	45736798	45742915	-1	6	0	40	143	5	0	0	0	0	0	0		P37237
ENSMUST00000026243	ENSMUSG00000025220	19	45750261	45783520	-1	24	20	33	300	40	17	1313	5982	2723	441	2371		Q9EQQ9
ENSMUST00000026247	ENSMUSG00000025221	19	45791839	45816061	-1	0	0	0	95	0	0	0	0	0	0	0	E9QNK8	
ENSMUST00000026252	ENSMUSG00000025223	19	46032593	46045214	-1	0	0	14	0	0	1	776	953	693	107	594		P70662
ENSMUST00000026254	ENSMUSG00000025224	19	46152509	46286510	1	0	0	0	29	0	0	465	358	697	20	507	Q6DFZ1	
ENSMUST00000026256	ENSMUSG00000025226	19	46328184	46330446	1	0	0	0	50	18	7	61	101	74	12	64		Q91W61
ENSMUST00000026259	ENSMUSG00000025229	19	46135685	46148326	-1	11	7	12	666	25	14	0	0	0	0	0		O35160
ENSMUST00000026262	ENSMUSG00000025232	9	59539667	59565105	1	18	11	18	202	33	12	3657	5771	2265	393	1843		P29416
ENSMUST00000026264	ENSMUSG00000025234	9	59388258	59486618	-1	0	0	1	100	0	0	0	0	320	25	150	H7BWY7	
ENSMUST00000026265	ENSMUSG00000025235	9	59321966	59353508	-1	14	7	38	18	17	10	29	163	88	143	63	A6H669	Q8C1Z7
ENSMUST00000026266	ENSMUSG00000025236	9	59291572	59316199	1	10	10	21	101	16	15	9527	27380	11016	919	6973		
ENSMUST00000026267	ENSMUSG00000025237	9	59617284	59650290	1	0	0	4	14	9	0	50	76	87	16	56	G5E856	
ENSMUST00000026269	ENSMUSG00000025239	9	123478701	123521548	1	36	18	69	97	49	28	370	620	473	79	439		Q9QXD8
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ENSMUST00000026273	ENSMUSG00000025243	9	123593820	123632565	-1	8	7	0	0	0	0	0	1	2	0	0		O88575
ENSMUST00000026274	ENSMUSG00000025245	9	123694416	123717625	-1	1	0	0	10	0	0	21	62	19	25	22		Q9JHQ5
ENSMUST00000026284	ENSMUSG00000025255	3	5218526	5415857	1	0	11	0	32	0	0	0	0	0	0	0	E9Q5A7	
ENSMUST00000026288	ENSMUSG00000025257	X	152004582	152016295	-1	5	4	6	7	3	3	10	37	10	40	13		Q9D0B8
ENSMUST00000026289	ENSMUSG00000025260	X	152001845	152004442	1	0	0	8	0	9	5	364	633	260	848	187	Q99N15	
ENSMUST00000026292	ENSMUSG00000025261	X	151800807	151935417	1	0	30	0	0	0	0	474	318	1604	0	1728	A2AFQ0	
ENSMUST00000026295	ENSMUSG00000025264	X	151087094	151096543	-1	0	1	1	1	1	0	0	0	0	0	0	H7BWY8	
ENSMUST00000026296	ENSMUSG00000025265	X	151046150	151089521	1	8	0	8	125	5	5	0	0	0	0	0		P52734
ENSMUST00000026297	ENSMUSG00000025266	X	150983141	151017322	-1	72	70	116	89	61	33	1	3	0	0	0		Q6PGG6
ENSMUST00000026302	ENSMUSG00000025268	X	150806370	150814345	-1	0	0	0	4	0	0	0	0	0	0	0	Q9ER67	
ENSMUST00000026303	ENSMUSG00000025269	X	150519519	150589868	-1	0	0	0	0	0	0	45	39	29	0	13	A2AFM3	
ENSMUST00000026313	ENSMUSG00000025277	14	8002902	8056555	1	7	0	21	18	15	8	0	0	3	8	0		Q8R2Y0
ENSMUST00000026315	ENSMUSG00000025279	14	7964533	7994573	-1	65	44	144	82	69	30	2	6	2	3	8		O55070
ENSMUST00000026318	ENSMUSG00000025283	X	155213132	155216449	-1	9	8	11	19	11	0	3655	13280	1984	5696	752		P48026
ENSMUST00000026322	ENSMUSG00000025280	14	24448694	24487046	-1	39	27	60	61	50	16	109	248	226	48	185	B2RXC6	
ENSMUST00000026324	ENSMUSG00000025287	X	155262443	155297654	1	0	5	0	11	5	0	208	1066	303	628	198		Q9R0X4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000026325	ENSMUSG00000025288	X	67919864	67921450	-1	3	5	7	3	0	2	0	0	0	0	0	Q9D3T1	
ENSMUST00000026328	ENSMUSG00000025289	X	155323918	155340754	-1	0	0	0	0	3	1	55	177	49	733	128		O08807
ENSMUST00000026354	ENSMUSG00000025316	8	121949750	122029258	1	0	0	0	0	0	0	43	44	107	45	86		Q8VBU8
ENSMUST00000026357	ENSMUSG00000025318	8	121729623	121794276	1	11	9	31	238	15	16	171	357	278	106	125		Q9ET77
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ENSMUST00000026367	ENSMUSG00000025323	12	118234933	118301440	-1	16	21	73	42	33	15	294	302	349	170	333	K4DI62	
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ENSMUST00000026378	ENSMUSG00000025329	4	140812983	140845778	-1	39	18	63	59	40	16	1	5	0	9	50	Q544I4	Q9Z185
ENSMUST00000026381	ENSMUSG00000025330	4	140745865	140774236	-1	13	11	25	51	23	12	6025	9565	5858	349	4542		Q9Z183
ENSMUST00000026383	ENSMUSG00000025333	X	152781921	152808646	1	0	4	0	0	1	0	0	0	0	0	0	Q549B6	P70259
ENSMUST00000026387	ENSMUSG00000025337	5	130245731	130255530	-1	3	8	7	80	12	6	195	835	343	890	304		P70122
ENSMUST00000026390	ENSMUSG00000025340	5	130171798	130214342	1	2	0	0	0	0	7	0	0	0	0	0		Q9JM13
ENSMUST00000026398	ENSMUSG00000025347	10	128958277	128960988	-1	11	13	22	14	12	6	0	0	0	3	0		Q9DD20
ENSMUST00000026405	ENSMUSG00000090247	10	128917882	128924035	-1	0	0	5	0	3	0	581	1152	410	2998	328		O55102
ENSMUST00000026406	ENSMUSG00000025350	10	128913593	128922888	-1	0	2	7	10	4	8	4	64	24	8	31		O55240
ENSMUST00000026407	ENSMUSG00000025351	10	128908919	128912816	1	13	0	59	79	8	3	1444	2867	1075	1710	798	Q549D0	P41731
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ENSMUST00000026410	ENSMUSG00000025354	10	128805676	128819446	1	26	20	103	50	34	18	2487	4043	2844	740	2264		Q921R4
ENSMUST00000026411	ENSMUSG00000025355	10	128790953	128800824	1	37	40	143	44	48	24	4800	2472	5980	611	1343	Q2KHP2	Q9JHI0
ENSMUST00000026414	ENSMUSG00000025357	10	128720141	128744056	-1	20	16	48	143	30	19	757	2633	1443	496	1703		O88673
ENSMUST00000026415	ENSMUSG00000025358	10	128697939	128705051	-1	14	14	34	100	18	15	370	1017	667	37	225	Q3U6X7	P97377
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ENSMUST00000026420	ENSMUSG00000025362	10	128624530	128626506	-1	7	8	0	28	14	4	1893	2508	1637	11046	1448	Q497N1	P62855
ENSMUST00000026425	ENSMUSG00000025364	10	128557766	128565934	-1	18	15	18	60	17	16	262	788	337	377	400	Q3TGU7	P50580
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ENSMUST00000026434	ENSMUSG00000025371	11	119913441	119919548	1	8	4	24	50	17	3	433	501	289	91	223	B1AZ39	P0C0A3
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ENSMUST00000026439	ENSMUSG00000025374	10	128401395	128411492	-1	0	0	27	61	9	3	194	411	372	57	202		Q8R2Y9
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ENSMUST00000026459	ENSMUSG00000025393	10	128083273	128090391	1	0	4	14	12	4	1	5377	8158	4994	1210	3965		P56480
ENSMUST00000026461	ENSMUSG00000025395	10	128015168	128030037	1	0	0	0	4	0	0	0	71	56	126	31	Q5FW94	P20664
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ENSMUST00000026470	ENSMUSG00000025403	10	127517123	127522444	-1	19	16	27	36	35	6	190	253	107	30	206	Q9CZN7	
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ENSMUST00000026519	ENSMUSG00000062822	13	119462759	119486117	1	9	9	35	6	19	7	332	2611	739	223	723		Q3UJC8
ENSMUST00000026520	ENSMUSG00000025451	13	119428601	119458218	1	5	0	5	20	4	4	50	82	7	13	14		Q8VE62
ENSMUST00000026537	ENSMUSG00000025464	7	140125657	140134334	1	23	3	17	69	28	5	62	82	45	54	68		Q8C0L6
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ENSMUST00000026539	ENSMUSG00000025466	7	140096770	140102441	-1	3	0	2	46	0	0	26	30	9	67	4		Q8R2K1
ENSMUST00000026540	ENSMUSG00000025467	7	140093395	140097200	1	3	2	3	2	4	3	0	0	0	0	0		Q80XD8
ENSMUST00000026541	ENSMUSG00000025468	7	140069880	140082548	-1	13	8	40	143	18	8	0	0	0	0	0		Q9DCA7
ENSMUST00000026546	ENSMUSG00000025473	7	139978932	139992562	-1	0	0	0	0	0	0	6432	10319	6001	723	5572	Q3U7G2	
ENSMUST00000026547	ENSMUSG00000025474	7	139995955	140036350	-1	17	12	39	144	25	15	171	295	231	64	227		Q921G8
ENSMUST00000026548	ENSMUSG00000025475	7	139834174	139878088	1	54	30	174	264	83	28	0	2	2	1	0		Q8C4G9
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ENSMUST00000026554	ENSMUSG00000025481	7	140835018	140837971	1	2	2	0	3	13	0	0	0	0	0	0		Q9CRB3
ENSMUST00000026555	ENSMUSG00000025482	7	140847805	140851018	1	0	0	0	0	3	2	0	0	0	0	0		Q920N1
ENSMUST00000026557	ENSMUSG00000025484	7	140853384	140856383	-1	11	8	15	21	18	3	682	861	476	489	387		O35153
ENSMUST00000026558	ENSMUSG00000025485	7	140856957	140863730	1	2	4	11	36	11	0	742	1174	802	221	557		Q3TIR3
ENSMUST00000026559	ENSMUSG00000025486	7	140863670	140882309	-1	9	0	0	0	11	0	23	29	26	25	0	Q4FJK3	Q8R104
ENSMUST00000026560	ENSMUSG00000025487	7	140881968	140898643	1	2	3	20	47	8	3	628	1088	596	399	355	B2RT97	Q9WVJ2
ENSMUST00000026561	ENSMUSG00000025488	7	140898943	140900446	-1	2	4	11	12	5	4	0	0	0	0	0	Q545U6	P48772
ENSMUST00000026562	ENSMUSG00000025489	7	140948963	140950239	-1	8	7	7	11	6	5	17	55	31	19	49		O88728

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000026564	ENSMUSG00000025491	7	140967221	140969825	1	8	4	60	16	4	8	6104	11306	5812	21192	3236		Q9D103
ENSMUST00000026565	ENSMUSG00000025492	7	141009586	141010770	-1	10	15	35	37	13	7	11835	17753	5979	16803	5017		Q9CQW9
ENSMUST00000026568	ENSMUSG00000025495	7	141122382	141157021	1	18	13	47	72	32	11	64	89	65	13	45		Q9Z1X2
ENSMUST00000026569	ENSMUSG00000025496	7	141292006	141294999	1	9	3	31	403	12	6	0	0	0	0	0		P51436
ENSMUST00000026571	ENSMUSG00000025498	7	141262706	141266481	-1	0	0	3	0	5	13	393	246	379	108	478	Q542T3	P70434
ENSMUST00000026572	ENSMUSG00000025499	7	141189105	141194005	-1	15	16	71	25	36	11	8	2	4	2	7		Q61411
ENSMUST00000026573	ENSMUSG00000025500	7	141210043	141214082	-1	9	0	39	10	28	20	13	48	9	3	23		Q0VET5
ENSMUST00000026576	ENSMUSG00000025503	7	141392199	141402968	1	8	5	13	55	18	11	15642	25793	12754	8005	10204		Q93092
ENSMUST00000026577	ENSMUSG00000025504	7	141338880	141363020	1	7	4	17	106	11	12	0	7	0	2	20		Q99K30
ENSMUST00000026578	ENSMUSG00000025505	7	141327739	141337156	1	0	0	0	0	2	0	30	69	19	0	10		Q9D3H0
ENSMUST00000026580	ENSMUSG00000025507	7	141438113	141444025	-1	0	0	11	13	0	0	0	0	0	0	0		Q9ERV7
ENSMUST00000026583	ENSMUSG00000025509	7	141455198	141460743	1	0	0	0	0	0	0	3932	5085	2610	388	2727	H3BIT5	
ENSMUST00000026585	ENSMUSG00000025511	7	141475240	141493427	1	0	0	0	119	13	4	0	0	8	19	38	Q4FJW7	Q9DCK3
ENSMUST00000026586	ENSMUSG00000025512	7	141493136	141539857	-1	1	16	42	43	0	1	0	0	0	7	0		
ENSMUST00000026590	ENSMUSG00000025515	7	141690340	141754693	1	0	9	0	0	0	0	0	0	1	0	0		
ENSMUST00000026595	ENSMUSG00000025521	8	64947185	64969034	1	6	6	7	16	6	2	281	565	225	83	111		Q9CXT7
ENSMUST00000026599	ENSMUSG00000025525	X	112311334	112372755	1	5	9	8	7	6	11	43	307	82	280	43		Q78IK4
ENSMUST00000026601	ENSMUSG00000025527	X	112384303	112406779	-1	9	7	133	12	6	7	0	0	0	0	0		Q9D5N8
ENSMUST00000026602	ENSMUSG00000025528	X	112495274	112558343	1	4	2	0	1	0	0	0	0	0	0	0	Q9D3Q9	
ENSMUST00000026607	ENSMUSG00000025531	X	113040593	113185517	-1	0	8	0	0	0	0	328	641	420	216	258	A2AD03	
ENSMUST00000026608	ENSMUSG00000025532	5	130029290	130060789	1	7	12	7	22	6	5	152	705	275	870	209		O35427
ENSMUST00000026613	ENSMUSG00000025534	5	129989011	130003049	-1	9	11	21	15	16	9	959	2040	1121	248	924		P12265
ENSMUST00000026617	ENSMUSG00000025537	5	129863421	129898549	-1	27	9	31	13	25	12	0	0	0	0	2		P07934
ENSMUST00000026624	ENSMUSG00000025544	14	122107038	122159604	1	4	0	8	80	11	1	1000	2359	1066	113	511	Q542E4	P58021
ENSMUST00000026625	ENSMUSG00000025545	14	122181694	122402232	1	7	3	21	32	7	5	1	9	2	22	5		Q8R4N0
ENSMUST00000026631	ENSMUSG00000025551	14	123977907	124677127	-1	12	8	13	81	15	2	0	0	0	0	0		
ENSMUST00000026635	ENSMUSG00000025555	14	121035200	121283744	1	22	22	75	64	48	14	61	64	82	14	90		F8VPU2
ENSMUST00000026649	ENSMUSG00000048277	11	117809668	117814283	1	4	0	0	50	0	0	1618	1802	1406	276	1061		O55101
ENSMUST00000026658	ENSMUSG00000025571	11	117654289	117763439	1	5	6	0	232	9	0	193	633	445	30	342	B1ATC3	
ENSMUST00000026659	ENSMUSG00000025572	11	117765988	117782198	-1	0	0	0	2	0	0	1662	1565	1209	157	968	B1ATB3	
ENSMUST00000026661	ENSMUSG00000025574	11	117815526	117826092	-1	4	5	16	11	12	2	116	70	80	78	83		P04184
ENSMUST00000026662	ENSMUSG00000025577	11	119022962	119031270	1	30	16	104	169	57	16	9	33	4	0	19		P30658
ENSMUST00000026663	ENSMUSG00000025578	11	119036305	119040969	-1	17	9	30	289	27	13	113	287	84	46	45		Q9QXV1
ENSMUST00000026665	ENSMUSG00000039989	11	119077573	119086221	-1	52	18	106	169	38	14	364	917	397	67	376		O55187
ENSMUST00000026666	ENSMUSG00000025579	11	119267887	119285454	1	19	0	28	0	0	14	393	470	253	65	483		P70699
ENSMUST00000026667	ENSMUSG00000025580	11	119288363	119300089	-1	7	0	4	45	15	5	679	1169	550	223	512		Q91VC3
ENSMUST00000026670	ENSMUSG00000025582	11	119538719	119547753	-1	43	34	148	421	77	28	0	0	0	3	14	A2ACL9	Q62443
ENSMUST00000026671	ENSMUSG00000025583	11	119602905	119899576	1	0	0	0	40	0	0	143	38	182	29	92	A2ACM0	
ENSMUST00000026672	ENSMUSG00000025584	7	81213596	81334533	1	17	11	11	74	17	5	522	1047	951	55	381		O88502
ENSMUST00000026677	ENSMUSG00000025588	8	67490758	67492104	1	5	5	2	4	2	4	0	0	0	0	0	Q546L3	P50294
ENSMUST00000026681	ENSMUSG00000025591	8	66474330	66486530	-1	0	0	0	0	0	0	0	0	3	57	0		Q9CR02
ENSMUST00000026693	ENSMUSG00000025602	9	40192316	40213604	1	0	0	0	0	0	0	0	0	0	0	0	Q8C879	
ENSMUST00000026698	ENSMUSG00000025608	6	31519488	31563981	-1	51	33	172	114	53	27	2	1	5	2	31	Q791G4	Q9R0M4
ENSMUST00000026699	ENSMUSG00000025609	6	31398735	31516811	1	97	75	150	102	83	46	86	300	169	33	221		O89050
ENSMUST00000026700	ENSMUSG00000025610	16	87553330	87595336	1	13	9	7	7	15	4	4	16	5	0	11	Q544C0	P58500
ENSMUST00000026703	ENSMUSG00000025612	16	87698945	87733346	1	18	21	21	55	29	15	2495	5299	4448	583	2853	Q3URL4	P97302
ENSMUST00000026704	ENSMUSG00000025613	16	87483326	87495873	-1	17	2	12	26	5	0	88	526	177	476	126	Q3UL22	P42932
ENSMUST00000026710	ENSMUSG00000025616	16	87454703	87483517	1	5	4	5	34	6	5	35	70	71	59	1		Q99LG0
ENSMUST00000026723	ENSMUSG00000025630	X	52988137	53021659	1	6	1	4	24	1	3	387	1437	420	961	267		P00493
ENSMUST00000026735	ENSMUSG00000025645	9	109082493	109092489	1	13	8	10	16	9	7	48	45	25	33	21		Q3URS9
ENSMUST00000026737	ENSMUSG00000025647	9	109038565	109057777	1	0	0	41	105	20	0	1910	2844	1945	394	1778		Q9D7I0
ENSMUST00000026740	ENSMUSG00000025650	9	108953586	108984875	1	85	0	181	0	0	0	9	64	27	9	108		Q63870
ENSMUST00000026743	ENSMUSG00000025651	9	108936633	108949623	1	0	5	2	38	0	0	1895	1836	1191	190	922		Q9CZ13
ENSMUST00000026744	ENSMUSG00000025652	9	108914619	108915563	1	0	2	13	0	0	0	0	0	0	0	0		Q9DA04
ENSMUST00000026750	ENSMUSG00000025658	X	157821436	158043294	-1	14	16	72	97	13	14	0	0	2	0	0		Q80YA9
ENSMUST00000026760	ENSMUSG00000025666	X	81070698	81097872	1	5	8	16	10	5	0	0	0	0	0	0		Q9JJG6
ENSMUST00000026795	ENSMUSG00000025701	6	116410077	116461178	-1	7	5	6	123	10	5	5582	8570	6413	595	3259		P48999
ENSMUST00000026816	ENSMUSG00000025722	7	80890723	80901269	-1	0	0	203	38	17	0	64	255	97	81	67		Q9CWR1
ENSMUST00000026817	ENSMUSG00000025723	7	80902227	80905076	-1	4	0	12	15	2	0	32	29	24	33	16		Q9CR53
ENSMUST00000026818	ENSMUSG00000025724	7	80904889	80947780	-1	0	0	0	0	3	0	174	203	135	299	135		Q9R0P6
ENSMUST00000026820	ENSMUSG00000025726	7	81114799	81170416	1	0	18	0	0	40	11	0	2	0	0	0	E9PXX9	
ENSMUST00000026823	ENSMUSG00000025728	17	25926427	25944510	-1	0	4	0	103	52	11	438	498	339	66	210	Q3TF56	Q9QYT7
ENSMUST00000026826	ENSMUSG00000025730	17	25882114	25919727	-1	0	0	0	0	0	0	1	154	159	0	0	Q0PD11	Q8VHQ4
ENSMUST00000026827	ENSMUSG00000025731	17	25875464	25886007	1	0	0	0	0	0	0	51	37	40	31	0		Q9DCS2
ENSMUST00000026828	ENSMUSG00000025732	17	25863698	25868738	-1	5	2	7	86	10	8	2	8	3	4	4		Q9CQB2
ENSMUST00000026831	ENSMUSG00000025735	17	25834465	25837295	-1	0	0	0	51	3	5	0	20	0	0	8	Q3USF1	Q8VC82
ENSMUST00000026832	ENSMUSG00000025736	17	25828867	25831842	1	0	0	0	0	0	0	81	172	49	9	60		
ENSMUST00000026833	ENSMUSG00000025737	17	25823627	25828730	1	7	6	22	13	9	0	298	192	104	36	125		Q8CFJ9
ENSMUST00000026839	ENSMUSG00000025742	X	167346322	167382749	-1	41	26	162	62	38	21	49	157	47	43	83		Q9CS42
ENSMUST00000026841	ENSMUSG00000059447	5	30155248	30184593	1	0	0	0	9	0	0	337	859	297	413	264		Q99JY0
ENSMUST00000026843						11	0	0	0	0	5	623	1561	1127	397	786		
ENSMUST00000026845	ENSMUSG00000025746	5	30013114	30019981	1	4	3	4	4	11	2	2	13	10	37	29	A2RTD1	P08505
ENSMUST00000026846	ENSMUSG00000025747	5	30058202	30073617	-1	1185	1216	6324	1268	1598	820	85	255	150	112	226	Q544L2	P07607
ENSMUST00000026854	ENSMUSG00000025754	7	76229887	77124698	1	44	36	314	38	38	34	0	0	1	2	0		Q09M05
ENSMUST00000026858	ENSMUSG00000025758	3	40800019	40816883	1	0	0	0	46	0	0	28	28	51	8	0		Q64702
ENSMUST00000026859	ENSMUSG00000025759	3	40818103	40846886	-1	13	19	13	81	15	14	41	277	58	12	47		Q8BH31
ENSMUST00000026862	ENSMUSG00000025762	3	40950354	41040234	1	114	62	132	957	183	92	0	0	0	8	0	Q497V3	
ENSMUST00000026865	ENSMUSG00000025764	3	41555731	41616864	1	15	6	27	3	0	0	184	429	205	78	118		Q6ZPI0
ENSMUST00000026866	ENSMUSG00000059834	3	41626720	41742514	-1	0	0	0	19	0	2	4	25	0	0	0		G5E861
ENSMUST00000026867	ENSMUSG00000025766	3	41742611	41803320	1	0	1	0	1	0	0	0	0	0	0	0		Q8BGN2
ENSMUST00000026868	ENSMUSG00000025766	3	41742611	41803320	1	0	0	0	0	0	0	1	0	1	1	0	F8WJL8	
ENSMUST00000026876	ENSMUSG00000025774	1	18115191	18145902	-1	0	0	0	0	0	0	0	0	0	0	0	G5E862	
ENSMUST00000026879	ENSMUSG00000025777	1	17145362	17164271	1	6	6	5	9	7	6	0	0	0	0	0		O88741
ENSMUST00000026881	ENSMUSG00000025779	1	16688051	16709611	1	17	22	111	45	13	14	59	334	59	58	14	Q14AM4	Q9JHF9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000026886	ENSMUSG00000025780	2	10153571	10256529	1	84	74	270	113	86	51	26	72	78	7	55		Q8BJD1
ENSMUST00000026887	ENSMUSG00000025781	2	10056016	10080510	-1	3	7	5	0	9	0	297	845	226	1902	316	A2AKU9	
ENSMUST00000026888	ENSMUSG00000025782	2	9914552	10048596	-1	3	0	0	268	8	11	55	206	133	17	92	A2ASY1	Q5HZG4
ENSMUST00000026889	ENSMUSG00000025783	2	9881252	9883921	1	6	8	20	180	15	12	0	0	0	0	2	Q9D5M9	
ENSMUST00000026890	ENSMUSG00000025784	9	123150946	123157430	1	4	2	12	84	6	3	2	0	3	11	10	Q8CFZ6	
ENSMUST00000026891	ENSMUSG00000025785	9	123113215	123136129	1	2	5	3	15	6	6	69	342	69	199	68		Q9D0M0
ENSMUST00000026892	ENSMUSG00000025786	9	123066160	123113205	-1	0	0	2	0	0	0	1797	3848	1782	272	888	D6RHA3	
ENSMUST00000026893	ENSMUSG00000025787	9	123034739	123067561	1	11	5	40	17	11	4	6	24	16	0	5		
ENSMUST00000026895	ENSMUSG00000078671	7	73426638	73541830	-1	0	0	0	0	0	0	10	0	27	0	15	F7CDZ7	
ENSMUST00000026896	ENSMUSG00000025789	7	73939119	74013690	-1	30	26	69	67	41	25	0	0	0	0	0		O35696
ENSMUST00000026897	ENSMUSG00000025790	7	74275419	74554780	-1	14	12	36	18	17	9	65	350	152	14	201		Q8R3L5
ENSMUST00000026899	ENSMUSG00000025792	11	120491840	120499187	1	14	6	13	78	16	3	117	60	32	22	63		Q9QZD8
ENSMUST00000026900	ENSMUSG00000025793	11	120467635	120483984	1	0	10	66	45	0	0	676	1045	614	56	412	Q3UMA3	
ENSMUST00000026901						4	0	13	17	6	0	148	618	40	0	65		
ENSMUST00000026902	ENSMUSG00000025795	10	121410350	121476250	-1	22	23	41	70	28	16	3428	11389	6198	704	4305		Q99P51
ENSMUST00000026907	ENSMUSG00000079057	8	45269671	45333216	-1	14	8	6	0	10	0	0	0	0	3	1	H9H9R5	
ENSMUST00000026911	ENSMUSG00000025804	9	123962126	123968692	-1	14	8	40	14	20	17	5220	31633	10504	23188	7462		P51675
ENSMUST00000026912	ENSMUSG00000056018	8	129067134	129183732	1	0	0	0	0	0	0	0	0	0	0	0	E9Q9Y3	
ENSMUST00000026917	ENSMUSG00000025810	8	128359073	128505462	1	51	38	134	138	59	36	57	182	96	84	270		P97333
ENSMUST00000026921	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	17	B7ZNY3	
ENSMUST00000026922	ENSMUSG00000025813	7	81600481	81706925	-1	0	26	28	121	0	0	1	2	1	0	1		Q9QWW1
ENSMUST00000026924	ENSMUSG00000025815	2	5896115	5942792	-1	0	0	0	0	0	0	0	0	0	0	0		A2ATU0
ENSMUST00000026926	ENSMUSG00000025816	2	5870987	5895432	-1	0	0	0	0	0	0	2	4	6	0	0	A2ATT9	
ENSMUST00000026927	ENSMUSG00000025817	2	5845019	5871895	1	48	34	108	44	45	26	15	112	38	32	26		Q9JKX6
ENSMUST00000026937	ENSMUSG00000025825	5	113772748	113778288	1	6	0	16	13	0	4	657	2032	585	1157	369		Q9D7P6
ENSMUST00000026956	ENSMUSG00000025838	2	87506565	87510872	1	5	7	5	0	6	5	0	0	0	0	0	Q810Y9	
ENSMUST00000026957	ENSMUSG00000025839	2	87489087	87497093	-1	9	9	5	15	9	9	0	0	0	0	0	Q810Y8	
ENSMUST00000026972	ENSMUSG00000025854	5	138754514	138810077	1	8	8	31	586	43	12	3325	4041	3372	403	1549		Q5MJS3
ENSMUST00000026973	ENSMUSG00000025855	5	139017306	139150001	-1	15	0	0	20	0	0	0	0	0	0	0		P12849
ENSMUST00000026975	ENSMUSG00000025857	5	139150223	139186510	1	30	34	138	127	54	24	135	185	161	16	136		B9EJR8
ENSMUST00000026976	ENSMUSG00000025858	5	139252324	139270051	1	11	10	8	39	4	9	168	320	134	44	70		Q9D1H7
ENSMUST00000026978	ENSMUSG00000025860	X	42059679	42109656	1	0	0	12	0	0	10	44	64	48	0	32		Q60989
ENSMUST00000026985	ENSMUSG00000025867	13	54371349	54383917	1	105	75	288	1274	135	88	1	9	1	3	27		P84086
ENSMUST00000026986	ENSMUSG00000025868	13	54590207	54591158	1	2	2	7	51	8	4	934	1133	605	886	431		Q9CQJ1
ENSMUST00000026987	ENSMUSG00000025869	13	54584185	54590090	-1	33	29	53	28	37	27	46	131	43	27	63		Q9CPT5
ENSMUST00000026988	ENSMUSG00000025870	13	54575015	54581128	1	5	0	2	50	8	2	11	22	12	3	25		Q9QXJ4
ENSMUST00000026989	ENSMUSG00000025871	13	54551218	54565435	-1	0	0	0	43	0	5	235	359	576	68	314		Q9DBN4
ENSMUST00000026990	ENSMUSG00000025872	13	54458837	54468849	-1	18	20	45	48	30	11	176	333	227	71	179		Q8VE80
ENSMUST00000026991	ENSMUSG00000025873	13	54621784	54664068	1	1	0	0	0	0	0	78	200	135	208	80		Q3TDN2
ENSMUST00000026993	ENSMUSG00000025875	13	54789377	54796776	1	2	4	23	86	21	14	86	227	113	14	112	Q3TAQ3	
ENSMUST00000026994	ENSMUSG00000025876	13	54949411	55006018	1	0	0	24	334	24	0	0	0	0	0	0		Q8K1S4
ENSMUST00000026997	ENSMUSG00000025878	13	55027880	55100300	-1	6	0	0	0	5	0	126	479	149	239	243		
ENSMUST00000026999	ENSMUSG00000025880	18	75367529	75395935	1	7	9	107	329	35	4	153	421	211	26	195	B2RPW6	O35253
ENSMUST00000027009	ENSMUSG00000025887	9	5345430	5373032	1	0	2	2	0	0	0	0	0	0	19	0		O08736
ENSMUST00000027012	ENSMUSG00000033538	9	5308828	5336783	1	0	0	0	4	0	0	476	6010	1378	1283	633		P70343
ENSMUST00000027015	ENSMUSG00000025888	9	5298517	5307265	1	8	6	3	2	6	4	218	2936	615	1130	395		P29452
ENSMUST00000027020	ENSMUSG00000025892	9	4417899	4796234	-1	30	0	18	10	13	3	0	0	0	0	0	G5E863	
ENSMUST00000027027	ENSMUSG00000025898	9	3404085	3479236	1	3	10	14	5	10	5	120	476	309	411	223		Q8BG79
ENSMUST00000027032	ENSMUSG00000025900	1	4290846	4409241	-1	17	12	17	13	20	11	0	0	0	0	0		P56716
ENSMUST00000027035	ENSMUSG00000025902	1	4490931	4497354	-1	2	0	2	5	0	0	0	0	0	0	0		Q61473
ENSMUST00000027036	ENSMUSG00000025903	1	4807788	4848410	1	21	15	34	26	19	5	598	558	340	281	275		P97823
ENSMUST00000027038	ENSMUSG00000025905	1	5588466	5606131	1	1	0	0	0	2	1	0	0	0	0	0	Q14AL5	P33534
ENSMUST00000027040	ENSMUSG00000025907	1	6206197	6276648	1	0	4	6	47	14	2	37	63	21	33	55		Q9ESK9
ENSMUST00000027044	ENSMUSG00000025911	1	9547948	9580673	1	0	0	0	0	0	0	11	29	22	19	1	M0QWD9	
ENSMUST00000027049	ENSMUSG00000025916	1	9968624	10009136	-1	0	0	4	4	0	0	0	50	13	0	8		Q8R1Z4
ENSMUST00000027050	ENSMUSG00000025917	1	10024601	10038168	-1	0	0	0	13	0	0	77	242	140	459	79		O35864
ENSMUST00000027052	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	0	0	0	0	0	0	0	4	0		Q8CJ67
ENSMUST00000027053	ENSMUSG00000025921	1	16105774	16133734	1	11	7	54	318	16	12	130	380	213	65	132		Q8VCH7
ENSMUST00000027054						11	8	8	5	12	7	0	1	4	7	0		
ENSMUST00000027056	ENSMUSG00000048960	1	10993465	11303681	1	36	25	93	72	32	20	17	9	1	0	0		Q3LAC4
ENSMUST00000027057	ENSMUSG00000025925	1	15805646	15844052	1	0	0	0	0	0	0	44	278	89	113	63	Q3V252	
ENSMUST00000027059	ENSMUSG00000025927	1	19208914	19238576	1	78	86	529	130	68	52	1	7	3	0	4		Q61313
ENSMUST00000027061	ENSMUSG00000025929	1	20730905	20734496	1	4	2	20	7	1	1	0	0	0	0	0	Q544E6	Q62386
ENSMUST00000027062	ENSMUSG00000025930	1	14753346	14755992	-1	12	2	24	5	0	6	0	0	0	0	0		O88940
ENSMUST00000027064	ENSMUSG00000025933	1	21218575	21230167	1	3	13	10	3	10	0	0	0	0	2	0	D3YV08	
ENSMUST00000027065	ENSMUSG00000025933	1	21218575	21230167	1	4	0	13	13	10	5	1	1	1	3	1		P56983
ENSMUST00000027066	ENSMUSG00000025932	1	14168954	14310235	-1	0	6	18	14	12	9	0	0	0	0	5		P97767
ENSMUST00000027067	ENSMUSG00000025934	1	21240589	21265661	1	3	5	7	0	2	5	0	0	0	11	1		P30115
ENSMUST00000027068	ENSMUSG00000025935	1	13564698	13589910	-1	4	7	48	23	15	8	996	2164	1139	259	653	Q4FK14	Q91V04
ENSMUST00000027071	ENSMUSG00000025937	1	13623330	13660546	-1	249	201	1221	361	298	163	39	156	81	108	89		Q99KR3
ENSMUST00000027082	ENSMUSG00000025945	1	65926520	65928307	1	9	0	10	8	5	0	0	0	0	0	0		Q9CXV3
ENSMUST00000027083	ENSMUSG00000025946	1	65282056	65389244	1	15	8	23	59	19	3	0	0	0	0	0		Q91V95
ENSMUST00000027089	ENSMUSG00000025952	1	65071525	65073689	-1	12	1	8	0	9	2	0	0	0	0	0	A3RLD4	Q61597
ENSMUST00000027090	ENSMUSG00000073658	1	65080219	65082288	-1	2	0	1	5	2	5	0	0	0	0	0		P04344
ENSMUST00000027102	ENSMUSG00000025961	1	63754907	63769267	-1	17	6	18	14	19	4	0	0	0	0	0	Q9D4D3	
ENSMUST00000027103	ENSMUSG00000025962	1	63730614	63754655	1	11	12	7	2	15	6	2	7	2	9	0		Q922E6
ENSMUST00000027108	ENSMUSG00000025967	1	63176825	63180486	1	0	3	0	0	1	0	0	45	0	22	22	M0QWH8	
ENSMUST00000027111	ENSMUSG00000025968	1	63143596	63176833	-1	1	0	5	17	0	0	215	741	366	407	135		Q91VD9
ENSMUST00000027112	ENSMUSG00000025969	1	62703285	62818695	1	0	0	85	0	0	4	4	0	4	0	43		O35375
ENSMUST00000027114	ENSMUSG00000025971	1	57406328	57417953	1	8	7	14	33	22	8	44	190	44	34	31		Q8BHE8
ENSMUST00000027121	ENSMUSG00000025978	1	55170159	55226782	-1	8	12	21	14	33	6	8	19	7	5	13		Q8CHX7
ENSMUST00000027122	ENSMUSG00000025979	1	55131231	55154899	1	0	0	0	0	0	0	75	14	0	45	11	G8JL35	
ENSMUST00000027123	ENSMUSG00000025980	1	55077835	55088243	-1	19	20	10	54	20	11	226	972	396	576	422		P63038
ENSMUST00000027125	ENSMUSG00000025981	1	55052770	55072702	1	2	2	29	11	8	0	64	183	45	54	51		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000027127	ENSMUSG00000025982	1	54985169	55027481	-1	10	15	24	42	26	14	2391	17785	5901	3060	4190	G5E866	
ENSMUST00000027128	ENSMUSG00000025983	1	54250683	54368727	1	0	9	0	0	0	2	0	0	0	0	0		Q8CDI7
ENSMUST00000027131	ENSMUSG00000025986	1	46807544	46892852	-1	18	13	12	59	20	13	36	130	50	101	87		Q6P5F6
ENSMUST00000027137	ENSMUSG00000025993	1	45908068	45926523	-1	11	9	18	18	10	5	5355	25264	8799	1996	5383		Q9JHI9
ENSMUST00000027139	ENSMUSG00000025995	1	45795166	45823619	1	12	5	7	18	3	0	5	34	25	104	39	Q3U821	
ENSMUST00000027144	ENSMUSG00000025991	1	67123026	67231259	1	29	29	23	9	19	18	0	0	0	22	0		Q8C196
ENSMUST00000027146	ENSMUSG00000025997	1	69531214	69687245	-1	38	36	96	52	20	32	19	71	15	6	26		P81183
ENSMUST00000027149	ENSMUSG00000026000	1	67000517	67038872	-1	6	0	0	0	0	0	0	0	3	6	8		O89112
ENSMUST00000027151	ENSMUSG00000061816	1	66924295	66945404	-1	0	0	4	0	9	3	0	0	0	0	0	Q545T7	P05977
ENSMUST00000027153	ENSMUSG00000026003	1	66830839	66863277	-1	17	11	13	40	14	9	1839	7768	3773	1125	998		
ENSMUST00000027157	ENSMUSG00000026005	1	66700831	66719805	1	4	3	0	1	0	5	318	819	336	407	199		Q8VEE0
ENSMUST00000027162	ENSMUSG00000026009	1	60977927	61000320	1	2	0	0	2	2	0	0	0	0	0	0	Q5SUZ8	
ENSMUST00000027164	ENSMUSG00000026011	1	60887000	60915832	1	0	0	4	2	0	3	2	0	0	0	0	Q6GTR6	
ENSMUST00000027165	ENSMUSG00000026012	1	60716800	60773359	1	16	10	30	6	19	5	20	38	9	5	62		P31041
ENSMUST00000027168	ENSMUSG00000026014	1	60482292	60567104	-1	0	2	0	47	0	0	5	0	10	0	14	G5E867	
ENSMUST00000027171	ENSMUSG00000026017	1	60098247	60153953	1	0	0	0	0	0	0	0	1	0	2	0	A8VI08	
ENSMUST00000027172	ENSMUSG00000026018	1	59982490	60043184	-1	0	0	0	17	9	0	0	0	0	0	0		Q3TY65
ENSMUST00000027173	ENSMUSG00000026019	1	60069785	60098645	-1	154	168	465	157	145	85	29	152	53	18	95	Q4V9X1	Q9JJA4
ENSMUST00000027174	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	0	0	0	14	103	16	261	97	A0A0A0MQ76	
ENSMUST00000027178	ENSMUSG00000026024	1	59162926	59237231	-1	4	14	38	3	24	15	107	328	214	38	253		Q920R0
ENSMUST00000027185	ENSMUSG00000026027	1	58973522	58995715	1	7	10	15	11	13	4	19	44	27	5	0		Q8K4T3
ENSMUST00000027186	ENSMUSG00000026028	1	58900449	58973430	-1	20	22	55	44	33	13	2999	5384	5085	411	2327	Q6P9N8	
ENSMUST00000027189	ENSMUSG00000026029	1	58795374	58847503	1	16	23	33	17	17	22	16	42	50	55	87	Q3U607	O89110
ENSMUST00000027193	ENSMUSG00000026032	1	58586384	58595964	1	7	2	9	5	10	9	188	549	224	1199	163		Q9CQZ6
ENSMUST00000027198	ENSMUSG00000026037	1	58462771	58505109	-1	20	22	9	41	10	3	23	117	58	31	43	Q543F8	Q60862
ENSMUST00000027202	ENSMUSG00000026039	1	57995971	58025899	1	11	10	32	105	27	2	33	63	74	36	33		Q7TSY8
ENSMUST00000027213	ENSMUSG00000026047	1	44106546	44118808	-1	0	0	0	0	0	0	0	6	15	0	13		Q9JHP7
ENSMUST00000027214	ENSMUSG00000026048	1	44147744	44181260	1	0	21	4	0	29	0	65	275	122	90	157	E9QM61	
ENSMUST00000027215	ENSMUSG00000026049	1	44086613	44102441	-1	0	0	0	0	0	0	0	0	0	7	0		Q3TUU5
ENSMUST00000027217	ENSMUSG00000026051	1	43730602	43742578	1	4	4	27	36	15	3	0	1	2	4	3		Q99LS0
ENSMUST00000027226	ENSMUSG00000026058	1	32172714	32658568	1	0	2	6	9	4	2	0	1	0	0	0		Q9WU01
ENSMUST00000027230	ENSMUSG00000026063	1	31222838	31224288	1	2	4	0	2	1	0	0	0	0	0	0		Q3KNI6
ENSMUST00000027231	ENSMUSG00000026062	1	40680574	40769273	1	31	16	44	391	45	17	1	1	0	0	0	Q3ZAS0	
ENSMUST00000027232	ENSMUSG00000026064	1	30940302	30949770	-1	9	3	10	37	11	6	408	1485	645	203	443	B9EKL6	Q63739
ENSMUST00000027233	ENSMUSG00000026065	1	40580081	40630725	1	31	16	63	17	21	17	0	2	1	7	2		Q8BUE1
ENSMUST00000027237	ENSMUSG00000026068	1	40515362	40551705	1	18	11	23	24	25	10	2611	12610	6445	3765	5786	Q0VBK3	Q9Z2B1
ENSMUST00000027241	ENSMUSG00000026072	1	40225080	40317257	1	47	25	57	18	57	37	0	6	16	12	41	Q32MH0	P13504
ENSMUST00000027243	ENSMUSG00000026073	1	40074079	40125231	1	0	0	14	16	10	11	9241	18626	14339	53039	10836	Q4FK69	P27931
ENSMUST00000027247	ENSMUSG00000026078	1	38985608	38997238	1	23	9	12	78	24	6	47	105	74	172	63		Q8BVF2
ENSMUST00000027249	ENSMUSG00000026080	1	38863867	38898161	-1	0	0	0	0	0	0	0	6	2	1	5	A2RSS2	
ENSMUST00000027250						5	2	11	0	8	0	0	0	0	0	0		
ENSMUST00000027251	ENSMUSG00000026082	1	38052786	38129801	-1	6	10	14	0	3	0	56	129	129	38	102		Q920Q2
ENSMUST00000027252	ENSMUSG00000026083	1	37998010	38055579	1	21	22	35	99	27	12	42	493	206	239	186		Q05D44
ENSMUST00000027254	ENSMUSG00000026085	1	37946736	37957759	-1	0	0	0	2	0	0	0	0	0	0	0	F8WIW2	
ENSMUST00000027256	ENSMUSG00000026087	1	37890477	37898535	1	3	1	3	8	0	0	27	26	10	84	17		Q9D7N6
ENSMUST00000027257	ENSMUSG00000026088	1	37874801	37890411	-1	4	1	0	15	0	0	31	195	87	232	65		Q8VDV8
ENSMUST00000027263	ENSMUSG00000026094	1	53755506	53785224	-1	9	2	33	66	9	11	4149	23273	6568	14382	7049		Q8BG48
ENSMUST00000027264	ENSMUSG00000026095	1	53344617	53352752	-1	3	9	13	19	5	4	1375	7420	3146	3176	1095		Q8BFS9
ENSMUST00000027265	ENSMUSG00000026096	1	53313624	53326343	1	5	0	0	3	0	0	25	85	37	55	8		Q6PEB4
ENSMUST00000027266	ENSMUSG00000026097	1	53297095	53310309	1	10	11	4	15	11	6	220	740	215	351	102		Q921I0
ENSMUST00000027267	ENSMUSG00000026098	1	53189187	53297018	-1	5	7	7	12	0	5	7	48	14	25	20	Q8K119	
ENSMUST00000027269	ENSMUSG00000026100	1	53061640	53068079	1	7	9	6	0	0	4	0	0	0	0	0	Q540E2	O08689
ENSMUST00000027271	ENSMUSG00000026102	1	52785427	52817688	-1	92	73	229	390	86	44	137	487	236	21	166		P49442
ENSMUST00000027277	ENSMUSG00000062939	1	51987148	52107189	1	7	10	18	6	8	2	9	28	0	18	36	Q3V157	
ENSMUST00000027279	ENSMUSG00000026107	1	51465862	51478425	-1	0	4	0	0	0	6	432	149	60	94	104		Q8BGW5
ENSMUST00000027285	ENSMUSG00000026111	1	37430139	37439124	1	0	0	0	9	0	0	88	277	99	87	79		Q9CQ61
ENSMUST00000027286	ENSMUSG00000026112	1	37417084	37430103	-1	34	25	123	107	38	17	770	1861	1011	342	686		Q99M07
ENSMUST00000027287	ENSMUSG00000026113	1	37299865	37410736	1	41	40	121	36	49	27	983	3086	1787	125	1188	F6V2U0	
ENSMUST00000027288	ENSMUSG00000026114	1	37214434	37263384	1	94	113	322	88	122	70	6	6	1	2	4		Q9JJZ8
ENSMUST00000027289	ENSMUSG00000050122	1	37026596	37187613	1	16	8	28	15	17	9	0	0	0	0	0	J9JI28	
ENSMUST00000027290	ENSMUSG00000026116	1	36792191	36943666	-1	23	0	45	0	37	0	1533	3427	2806	118	1889		O70472
ENSMUST00000027291	ENSMUSG00000026117	1	36761798	36782818	1	6	12	15	34	13	5	36	29	12	2	41		P43404
ENSMUST00000027297	ENSMUSG00000026123	1	34849976	34879580	1	27	12	39	32	23	7	946	1463	682	169	503		Q9QZC7
ENSMUST00000027298	ENSMUSG00000026124	1	34535648	34544313	1	11	4	14	3	10	5	0	0	0	0	0		P97766
ENSMUST00000027299	ENSMUSG00000026125	1	34498410	34503063	1	16	8	22	13	18	7	0	0	0	0	0		O70169
ENSMUST00000027302	ENSMUSG00000026126	1	34459762	34475733	1	13	0	19	8	13	6	357	656	254	407	318		Q61152
ENSMUST00000027303	ENSMUSG00000026127	1	34439851	34449356	1	34	17	78	58	40	21	166	456	156	95	226		Q8VHZ7
ENSMUST00000027312	ENSMUSG00000026134	1	33453810	33669795	-1	9	9	15	39	12	0	82	137	101	164	65		P33610
ENSMUST00000027315	ENSMUSG00000026135	1	74565127	74588246	-1	25	17	40	84	29	21	193	91	139	9	213	G5E869	
ENSMUST00000027322	ENSMUSG00000026142	1	82316452	82445366	1	10	10	18	65	0	0	160	459	340	74	227		Q8BHC7
ENSMUST00000027331	ENSMUSG00000026149	1	82756649	82768461	-1	0	4	9	5	3	3	0	0	0	0	0		Q9CQY8
ENSMUST00000027337	ENSMUSG00000026153	1	24011093	24100341	-1	13	12	15	0	12	10	0	0	0	0	11		Q6NS59
ENSMUST00000027338	ENSMUSG00000026154	1	23995939	24005656	-1	5	3	1	12	3	4	25	82	19	165	26		Q8BTE0
ENSMUST00000027339	ENSMUSG00000026155	1	23844846	23922317	-1	0	0	12	24	8	5	406	1355	390	39	238		Q91VZ6
ENSMUST00000027343	ENSMUSG00000026158	1	23366424	23397772	-1	17	14	30	93	26	7	2181	5614	2737	866	2488		Q8VE52
ENSMUST00000027351	ENSMUSG00000026166	1	83116766	83119167	1	3	1	2	0	4	0	0	0	0	0	0	F8WHA7	
ENSMUST00000027356	ENSMUSG00000026170	1	74713574	74737892	1	18	9	9	43	20	7	11	111	7	15	73		Q9DBG1
ENSMUST00000027357	ENSMUSG00000026171	1	74593748	74601397	-1	0	0	42	0	0	0	457	649	381	160	316		Q9QZR0
ENSMUST00000027358	ENSMUSG00000026172	1	74588289	74592443	1	8	5	8	17	13	7	25	69	36	0	27		Q9CZP5
ENSMUST00000027362	ENSMUSG00000026173	1	74542888	74567794	1	0	0	0	4	0	0	0	0	0	0	0		Q8K3R3
ENSMUST00000027366	ENSMUSG00000026175	1	74409376	74435559	1	28	14	65	28	43	13	1	4	1	0	0		Q62468
ENSMUST00000027367	ENSMUSG00000026176	1	74391509	74397285	1	21	0	64	125	29	40	9154	8841	5766	1216	3995	Q5I0X8	P58466
ENSMUST00000027368	ENSMUSG00000026177	1	74375195	74386062	1	7	3	25	0	11	0	1867	3604	2120	256	2168		P41251
ENSMUST00000027370	ENSMUSG00000026179	1	74284930	74353694	1	0	26	0	0	0	0	19	0	0	0	23		Q69ZP3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000027372	ENSMUSG00000026180	1	74153989	74161246	1	0	0	0	0	1	0	2910	704	3173	43	1566		P35343
ENSMUST00000027373	ENSMUSG00000026181	16	16896469	16927364	1	54	33	82	71	43	21	218	195	158	35	170		Q8CGA0
ENSMUST00000027374	ENSMUSG00000026182	1	73015074	73015909	-1	3	0	5	1	1	2	0	0	0	0	0	Q545L6	P10856
ENSMUST00000027377	ENSMUSG00000026185	1	72857932	72874884	-1	35	31	93	69	55	24	0	0	0	8	64	Q3UQV0	Q07079
ENSMUST00000027379	ENSMUSG00000026187	1	72307421	72394952	1	9	13	24	26	15	10	17	67	27	144	34		P27641
ENSMUST00000027380	ENSMUSG00000026188	1	72284369	72303104	1	14	12	9	18	16	10	0	1	2	0	0		Q8BG50
ENSMUST00000027381	ENSMUSG00000026189	1	72259167	72284314	-1	7	4	6	12	0	0	5	15	0	9	16		Q99MZ7
ENSMUST00000027384	ENSMUSG00000026192	1	71557150	71579631	1	23	24	138	70	32	14	160	242	105	72	251		Q9CWJ9
ENSMUST00000027393	ENSMUSG00000026196	1	71027498	71103146	-1	58	50	86	379	84	43	45	73	85	0	44		O70445
ENSMUST00000027394	ENSMUSG00000026197	1	75168646	75171629	1	0	0	0	0	0	0	106	124	49	18	25		Q91X58
ENSMUST00000027396	ENSMUSG00000026198	1	75171717	75180392	-1	8	8	6	75	1	4	87	49	67	6	50		Q9DC29
ENSMUST00000027401	ENSMUSG00000026201	1	75210838	75215606	1	0	0	0	20	3	0	0	11	14	0	0		O88697
ENSMUST00000027404	ENSMUSG00000026204	1	75247027	75264502	-1	14	17	36	56	48	18	0	2	3	2	9	A6MDD2	
ENSMUST00000027405	ENSMUSG00000026205	1	75125541	75133890	-1	11	5	49	34	18	7	6	36	16	4	15		
ENSMUST00000027409	ENSMUSG00000026208	1	75360329	75368579	1	31	18	47	238	46	15	0	0	0	1	3	Q3V1K9	P31001
ENSMUST00000027414	ENSMUSG00000026213	1	75521529	75537335	1	5	4	19	16	20	8	25	103	26	13	80		Q3TAA7
ENSMUST00000027415	ENSMUSG00000006576	1	75546266	75562172	1	0	0	0	8	0	0	0	3	0	1	6	F8WHM3	
ENSMUST00000027421	ENSMUSG00000026219	1	84721189	84840516	-1	24	0	0	18	0	0	9	69	14	0	0		G5E870
ENSMUST00000027422	ENSMUSG00000026220	1	84905898	84935134	-1	21	29	41	91	28	13	16	42	46	4	38		Q8K1C7
ENSMUST00000027425	ENSMUSG00000026223	1	85894281	85908675	1	17	9	36	100	23	21	1170	1105	501	384	647		Q91VK4
ENSMUST00000027426	ENSMUSG00000026224	1	85928483	85940624	1	5	0	2	3	2	3	0	3	0	0	0	Q9D476	
ENSMUST00000027429	ENSMUSG00000026227	1	86045863	86055456	1	0	0	0	133	1	3	0	0	0	1	0		Q9CYS6
ENSMUST00000027431	ENSMUSG00000026228	1	86099026	86111970	-1	12	8	22	5	9	1	0	0	5	1	0		Q02152
ENSMUST00000027432	ENSMUSG00000026229	1	86064387	86139151	1	11	13	12	13	25	0	318	1236	693	326	625		Q3TXS7
ENSMUST00000027434	ENSMUSG00000062590	1	86154780	86278284	1	312	216	147	1004	525	98	5	27	17	3	40		Q9D2I5
ENSMUST00000027438	ENSMUSG00000026234	1	86344719	86359400	-1	85	84	168	132	107	71	131	603	287	254	224		P09405
ENSMUST00000027440	ENSMUSG00000026237	1	86386242	86388162	-1	8	9	17	13	14	2	0	0	1	1	0	G5E871	
ENSMUST00000027444	ENSMUSG00000026239	1	86542994	86582629	-1	6	5	8	0	5	2	250	612	256	77	142	Q3TDQ8	O55057
ENSMUST00000027446	ENSMUSG00000026240	1	86582904	86609375	1	0	0	0	0	0	0	66	182	119	11	20		Q8BV13
ENSMUST00000027449	ENSMUSG00000026241	1	86666291	86670571	-1	6	5	12	139	10	3	0	0	0	0	0	Q544K5	Q61839
ENSMUST00000027451	ENSMUSG00000026235	1	77367185	77515088	-1	44	6	20	6	5	2	0	0	0	0	0		Q03137
ENSMUST00000027455	ENSMUSG00000026246	1	87086694	87089928	-1	18	17	26	72	23	0	0	0	0	0	0		P24823
ENSMUST00000027463	ENSMUSG00000026247	1	87147655	87156521	-1	24	0	0	0	0	0	0	0	0	0	0		Q9JMI0
ENSMUST00000027464	ENSMUSG00000026248	1	79776018	79781445	1	9	6	31	19	16	7	140	229	115	32	71		Q9CY73
ENSMUST00000027467	ENSMUSG00000026249	1	79794197	79861180	-1	2	2	15	3	7	2	42	29	39	52	105	Q543R5	Q07235
ENSMUST00000027470	ENSMUSG00000026253	1	87204657	87212694	1	15	9	35	25	17	8	0	0	1	0	0	F8VQK4	
ENSMUST00000027472	ENSMUSG00000026255	1	87264363	87310839	1	9	7	0	43	17	9	0	0	2	0	0		Q9D4J1
ENSMUST00000027475	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	20	6	0	173	704	590	57	483		Q6Y7W8
ENSMUST00000027476	ENSMUSG00000026258	1	87470271	87475482	1	3	4	6	15	4	0	0	0	0	1	0	A0A0A7EP66	Q9CXL7
ENSMUST00000027477	ENSMUSG00000026259	1	87476834	87573870	-1	0	0	0	114	9	0	1	5	0	2	1		Q8CHT1
ENSMUST00000027478	ENSMUSG00000026260	1	92439010	92473860	-1	9	8	15	24	11	4	23	199	67	29	37		Q99LC3
ENSMUST00000027487	ENSMUSG00000026269	1	92910783	92924384	1	0	0	0	5	0	0	644	341	456	32	259	G5E872	
ENSMUST00000027488	ENSMUSG00000026270	1	92934376	92947941	1	3	8	27	133	35	12	125	154	109	20	70		Q9ESK3
ENSMUST00000027489	ENSMUSG00000026271	1	92950865	92986391	1	17	27	46	6	32	0	110	900	117	42	179	A0A0A0MQ77	
ENSMUST00000027491	ENSMUSG00000026272	1	93135240	93145421	1	7	7	25	47	9	9	0	0	0	0	0		O35423
ENSMUST00000027492	ENSMUSG00000026273	1	93299211	93305915	-1	7	1	7	48	15	0	87	468	105	295	82		Q8BVN4
ENSMUST00000027493	ENSMUSG00000026274	1	93308770	93343482	-1	40	38	63	161	42	23	30	31	35	2	33		Q8CEE6
ENSMUST00000027494	ENSMUSG00000026275	1	93342854	93373489	1	248	248	395	490	254	138	136	464	219	215	198		Q3UM45
ENSMUST00000027495	ENSMUSG00000026276	1	93478964	93510260	1	13	7	6	33	13	0	21	62	128	51	57		P42208
ENSMUST00000027498	ENSMUSG00000026277	1	93619751	93658659	-1	24	14	50	112	38	10	4	57	32	12	40		Q9Z2W1
ENSMUST00000027499	ENSMUSG00000026278	1	93685660	93695764	1	0	3	8	85	21	0	0	0	2	23	25	Q3TH93	O35425
ENSMUST00000027502	ENSMUSG00000026280	1	93751500	93790610	1	29	14	37	52	28	12	446	586	302	143	204		
ENSMUST00000027503	ENSMUSG00000026281	1	93792576	93801934	-1	5	2	1	33	4	4	66	157	78	209	56		P97930
ENSMUST00000027505	ENSMUSG00000026283	1	93803965	93822101	1	0	0	71	39	29	0	479	1054	926	162	495		Q9D8Y8
ENSMUST00000027507	ENSMUSG00000026285	1	94038305	94052553	-1	21	16	39	20	30	9	7	0	4	19	56	Q544F3	Q02242
ENSMUST00000027512	ENSMUSG00000026289	1	87755870	87792428	1	0	0	0	55	0	0	109	98	124	71	117		Q8C0J2
ENSMUST00000027517	ENSMUSG00000070738	1	87853287	87945180	1	16	35	36	54	58	17	1206	1554	1528	98	1464	E9PUQ8	
ENSMUST00000027518	ENSMUSG00000026295	1	88406961	88426438	1	6	2	0	10	8	2	0	0	0	0	0		Q8K1I3
ENSMUST00000027521	ENSMUSG00000055013	1	89454806	89897617	1	99	74	262	94	114	69	167	116	182	9	202		Q8BXK8
ENSMUST00000027528	ENSMUSG00000026303	1	90915085	90951142	1	138	129	275	3381	265	139	1	23	5	1	5		
ENSMUST00000027529	ENSMUSG00000026304	1	90958133	90969661	-1	14	0	13	21	16	12	0	0	0	0	0	Q0PD39	P35292
ENSMUST00000027532	ENSMUSG00000026307	1	91298338	91321075	1	12	7	34	65	12	9	126	128	81	24	122		
ENSMUST00000027533	ENSMUSG00000026308	1	91351016	91362416	1	25	17	47	79	42	23	1	2	1	1	0		Q8C3F7
ENSMUST00000027534	ENSMUSG00000026309	1	91373861	91398815	-1	0	0	5	0	0	0	319	629	350	129	273		Q8R0F6
ENSMUST00000027538	ENSMUSG00000026311	1	91540544	91559589	1	79	71	172	76	77	36	179	250	172	44	180	A0A0A0MQ78	
ENSMUST00000027542	ENSMUSG00000026312	1	109982431	110140157	1	0	0	0	0	0	0	0	0	0	0	0		Q8BM92
ENSMUST00000027554	ENSMUSG00000026317	8	14881335	14901720	1	122	118	265	200	146	71	113	207	129	54	187	Q542J5	Q9QUK3
ENSMUST00000027559	ENSMUSG00000026321	1	105780718	105847981	1	333	187	1129	441	226	109	24	81	47	14	63		O35305
ENSMUST00000027560	ENSMUSG00000026322	18	62324204	62467802	1	22	20	24	59	24	11	0	0	0	0	1		P97288
ENSMUST00000027564	ENSMUSG00000048775	1	106980984	107001195	1	14	19	79	17	12	9	0	0	0	0	1		Q8CDC0
ENSMUST00000027565	ENSMUSG00000073601	1	107271201	107278371	-1	9	5	7	4	6	10	0	0	0	0	0	A2RSF9	
ENSMUST00000027566	ENSMUSG00000026327	1	107361198	107380475	1	8	4	6	9	7	3	0	0	0	0	0		Q9CQV3
ENSMUST00000027567	ENSMUSG00000044594	1	107045587	107052303	-1	0	0	0	0	0	0	0	0	0	0	0	G3X9V8	
ENSMUST00000027569	ENSMUSG00000026331	1	97059038	97128301	-1	138	204	194	202	168	110	12	84	16	3	13	Q8C0X7	
ENSMUST00000027571	ENSMUSG00000026333	1	97770172	97793709	1	7	5	13	0	6	0	5	0	9	15	0		Q8K259
ENSMUST00000027575	ENSMUSG00000026336	1	98421124	98516991	1	0	0	0	0	0	5	0	0	0	0	0	Q9D5W6	
ENSMUST00000027579	ENSMUSG00000026341	1	125392905	125435727	-1	4	0	8	3	0	0	94	245	0	0	0	Q3ULF7	Q99JY9
ENSMUST00000027580	ENSMUSG00000026342	1	125560595	125595820	1	8	6	13	87	9	8	254	1187	542	146	375		Q8R314
ENSMUST00000027581	ENSMUSG00000026343	1	125676995	125873862	1	18	6	29	24	21	10	0	0	0	12	13	A0A0B4J1E4	
ENSMUST00000027582	ENSMUSG00000026344	1	125867622	125913101	-1	1	0	5	0	1	2	0	0	0	0	0	E0CXP0	
ENSMUST00000027585	ENSMUSG00000026347	1	127486546	127679548	-1	0	0	0	9	0	0	0	0	0	0	0		Q8C996
ENSMUST00000027587	ENSMUSG00000026349	1	127774164	127808061	1	0	0	0	0	8	0	0	91	0	34	0	Q7TQK0	
ENSMUST00000027592	ENSMUSG00000026353	1	128243964	128279378	1	54	56	93	274	58	34	439	2770	1159	440	1011		
ENSMUST00000027601	ENSMUSG00000026355	1	128331590	128359664	-1	2	1	0	89	4	0	220	408	256	98	253	Q542I2	P97311

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000027602	ENSMUSG00000026356	1	128363707	128417368	-1	2	4	1	0	8	3	144	488	194	397	146		Q922B2
ENSMUST00000027603	ENSMUSG00000026357	1	144752683	144775435	-1	4	4	0	2	6	3	351	1540	484	586	225	Q544K2	Q99PG4
ENSMUST00000027606	ENSMUSG00000026360	1	143999338	144004161	-1	4	0	0	20	0	0	537	2647	995	2695	638	A0A087WPY2	
ENSMUST00000027612	ENSMUSG00000070594	1	139697623	139781243	-1	4	0	0	0	5	0	0	0	0	0	0	E9PUM5	
ENSMUST00000027615	ENSMUSG00000026368	1	139501702	139523752	1	6	3	7	2	1	5	0	1	0	1	0		Q07968
ENSMUST00000027623	ENSMUSG00000026374	1	118294778	118311739	-1	58	57	123	67	80	39	86	409	144	79	178	Q545E6	Q62348
ENSMUST00000027626	ENSMUSG00000026377	1	118321839	118333822	1	10	11	15	18	14	5	40	267	57	356	62		Q91VE6
ENSMUST00000027629	ENSMUSG00000026380	1	118627945	118685168	1	111	108	205	106	122	64	2	8	1	0	7		Q3UNW5
ENSMUST00000027632	ENSMUSG00000026383	1	119545037	119649000	-1	0	0	0	0	0	0	0	0	0	1	0		Q8BGS1
ENSMUST00000027634	ENSMUSG00000026385	1	120113280	120121078	-1	0	2	4	8	1	0	1390	1498	1096	4699	525	Q548W7	P31786
ENSMUST00000027637	ENSMUSG00000026388	1	120121187	120188189	1	8	3	6	55	5	1	0	0	0	0	0		Q9CRW3
ENSMUST00000027639	ENSMUSG00000026390	1	120474538	120505024	-1	12	12	35	15	20	4	0	0	0	19	23	A2RT24	Q60754
ENSMUST00000027642	ENSMUSG00000026393	1	138482875	138620141	-1	0	0	119	26	5	2	180	752	447	100	289	Q3TN15	
ENSMUST00000027643	ENSMUSG00000026394	1	138273738	138289462	1	7	2	13	3	5	4	0	1	0	1	0		Q8BMC1
ENSMUST00000027649	ENSMUSG00000026398	1	136842571	136960448	-1	20	13	30	5	21	7	0	0	0	0	0		P45448
ENSMUST00000027650	ENSMUSG00000026399	1	130439027	130462744	-1	21	14	41	113	7	9	118	610	160	127	101		Q61475
ENSMUST00000027655	ENSMUSG00000026404	1	136415271	136440158	1	8	11	26	12	6	4	35	110	74	81	70		Q9DBN9
ENSMUST00000027657	ENSMUSG00000026405	1	130634773	130661632	-1	5	4	4	3	9	3	0	0	0	11	0		P08607
ENSMUST00000027667	ENSMUSG00000026413	1	135871395	135919207	-1	20	31	84	166	56	25	0	0	0	0	0		P97350
ENSMUST00000027670	ENSMUSG00000026415	1	130800902	130814740	1	0	14	35	10	13	12	0	1	0	0	2		Q2TB54
ENSMUST00000027671	ENSMUSG00000026414	1	135836354	135852260	1	0	6	0	0	11	5	0	0	0	0	1		P50752
ENSMUST00000027673	ENSMUSG00000026416	1	130906985	130911451	-1	5	4	37	3	13	0	0	0	0	0	0	Q2NKI0	Q9JKV9
ENSMUST00000027675	ENSMUSG00000026417	1	130826684	130852249	1	51	29	80	187	53	15	1	1	0	3	0		O70570
ENSMUST00000027677	ENSMUSG00000026421	1	135720061	135752232	1	0	2	4	64	16	11	318	255	206	67	219	Q4FJX4	P97315
ENSMUST00000027682	ENSMUSG00000026424	1	135160234	135167681	-1	19	17	74	30	40	17	0	0	0	0	0		Q99JG2
ENSMUST00000027684	ENSMUSG00000026426	1	135146824	135156269	1	3	0	8	71	3	3	780	959	1098	137	673		Q8VEH3
ENSMUST00000027687	ENSMUSG00000026429	1	134962565	134974162	1	5	0	1	32	3	8	21	31	13	24	11		Q9CQ37
ENSMUST00000027688	ENSMUSG00000026430	1	131176410	131245258	-1	0	0	0	0	0	0	5	0	0	0	14		Q5EBH1
ENSMUST00000027690	ENSMUSG00000026432	1	131599239	131612000	1	32	39	61	53	52	34	0	3	0	0	0		Q9WU02
ENSMUST00000027693	ENSMUSG00000026433	1	131867224	131872887	1	0	0	9	0	7	2	169	620	161	306	140	E9QLQ7	
ENSMUST00000027695	ENSMUSG00000026435	1	131962967	131982969	1	20	22	36	8	33	5	0	0	0	0	0		Q8K0H7
ENSMUST00000027696	ENSMUSG00000026436	1	132007607	132032612	1	0	0	3	9	0	0	14	0	0	0	40		P41158
ENSMUST00000027697	ENSMUSG00000026437	1	132112237	132139684	-1	55	28	127	159	74	33	28	36	21	3	21	Q0VDL6	Q04899
ENSMUST00000027700	ENSMUSG00000026439	1	132477365	132505659	1	0	5	0	21	0	0	48	240	170	30	136		Q8BX09
ENSMUST00000027706	ENSMUSG00000026443	1	132880273	132940005	1	20	17	58	112	33	22	1	0	2	0	4	Q6PHP6	
ENSMUST00000027719	ENSMUSG00000020083	10	62107655	62143920	-1	23	9	60	10	23	11	1	0	0	0	2	F8WHN9	
ENSMUST00000027725	ENSMUSG00000026455	1	134455531	134491018	1	0	0	0	0	0	0	51	50	45	18	159		Q8BZM0
ENSMUST00000027726	ENSMUSG00000026456	1	134405559	134411740	1	9	6	87	88	0	6	314	1642	277	25	189		Q9DB73
ENSMUST00000027727	ENSMUSG00000026457	1	134415378	134433351	1	37	41	75	8	37	43	8182	19605	5493	1363	4573	Q53YY4	Q91VH1
ENSMUST00000027730	ENSMUSG00000026459	1	134289989	134292548	1	9	9	41	22	19	9	0	0	0	0	0		P12979
ENSMUST00000027736	ENSMUSG00000102976	1	133619862	133661380	-1	4	10	9	3	10	16	254	1608	1091	347	1087	Q3UL31	Q6NZF1
ENSMUST00000027738	ENSMUSG00000026466	1	156004599	156036480	-1	7	6	0	10	5	0	0	44	0	283	59		Q921T2
ENSMUST00000027740	ENSMUSG00000026468	1	155698031	155751684	-1	60	53	316	67	63	37	0	1	0	0	0		P53776
ENSMUST00000027741	ENSMUSG00000026469	1	155275701	155417415	-1	31	24	83	43	26	22	706	2418	1332	115	938		Q9Z0U0
ENSMUST00000027743	ENSMUSG00000026470	1	155158715	155208256	1	34	16	36	49	32	4	398	925	460	82	345		Q9JKK1
ENSMUST00000027744	ENSMUSG00000026471	1	155127277	155146814	-1	0	0	0	0	0	0	6	16	19	48	13		Q8HWB0
ENSMUST00000027748	ENSMUSG00000026475	1	153740349	153745468	1	17	6	23	60	25	20	0	2	2	4	5	Q542U0	P97428
ENSMUST00000027752	ENSMUSG00000026478	1	153218922	153332786	-1	45	31	50	177	87	34	98	140	246	70	564	F8VQJ3	
ENSMUST00000027753	ENSMUSG00000026479	1	153122756	153186447	-1	0	0	1	52	24	28	0	0	0	0	0	G5E874	
ENSMUST00000027754	ENSMUSG00000026480	1	152800194	152836991	1	0	0	0	25	5	0	14651	34822	18264	11925	12960		O70145
ENSMUST00000027760	ENSMUSG00000026482	1	152516760	152766351	-1	41	26	250	90	46	20	9	20	5	28	102		Q60695
ENSMUST00000027764	ENSMUSG00000043939	17	48151896	48167270	-1	13	25	0	18	58	8	178	735	206	263	174	Q8C239	
ENSMUST00000027766	ENSMUSG00000026489	1	180165238	180199602	-1	0	0	0	36	26	0	0	294	363	0	89		Q60936
ENSMUST00000027768	ENSMUSG00000026491	1	179744894	179803680	-1	26	12	17	26	19	12	515	1134	1480	175	640		Q8CJF7
ENSMUST00000027769	ENSMUSG00000026492	1	179528055	179546267	-1	32	48	36	129	119	49	51	291	135	130	75	B2RSE6	Q3TL26
ENSMUST00000027775	ENSMUSG00000026495	1	178406085	178484513	1	16	10	12	16	14	10	19	75	41	47	43		Q9CQ46
ENSMUST00000027777	ENSMUSG00000026496	1	180568924	180601254	1	30	22	55	28	41	12	179	317	169	59	341	Q921K2	
ENSMUST00000027778	ENSMUSG00000026497	1	180693043	180697034	-1	16	15	43	183	18	12	0	0	0	0	0		Q9WUI0
ENSMUST00000027780	ENSMUSG00000026499	1	180726043	180754204	1	14	9	9	128	9	4	373	1521	780	103	676		
ENSMUST00000027781	ENSMUSG00000026500	1	178319130	178322693	1	0	0	3	8	1	0	42	180	48	95	25		Q9D7J4
ENSMUST00000027783	ENSMUSG00000026502	1	178187417	178257301	1	158	201	645	343	226	143	135	516	200	50	197		Q9D291
ENSMUST00000027785	ENSMUSG00000026504	1	176814660	177020437	1	0	2	0	0	4	0	97	479	251	194	99		Q80UF4
ENSMUST00000027792	ENSMUSG00000026511	1	182124737	182132407	1	0	4	5	13	4	2	233	565	128	344	131	Q5EAT0	P49962
ENSMUST00000027795	ENSMUSG00000026514	1	181352628	181460641	1	46	52	218	223	48	49	0	0	1	0	1		Q6ZWS4
ENSMUST00000027797	ENSMUSG00000026516	1	181087138	181144204	-1	810	785	1590	1020	1013	550	191	611	451	159	404		Q9DBY8
ENSMUST00000027800	ENSMUSG00000026519	1	180942344	180975112	1	24	14	90	9	12	13	522	777	889	68	534		Q91YT8
ENSMUST00000027802	ENSMUSG00000026520	1	180904293	180908088	1	0	2	0	52	3	0	199	213	109	38	124	Q3TMZ1	Q922Q4
ENSMUST00000027809	ENSMUSG00000026525	1	175662421	175692776	-1	3	13	11	215	17	14	4	18	9	6	13		Q9WUK7
ENSMUST00000027810	ENSMUSG00000026526	1	175600374	175625635	-1	160	121	764	230	236	108	88	349	156	541	238		P97807
ENSMUST00000027812	ENSMUSG00000026527	1	175059087	175492500	-1	1	0	6	0	3	0	0	0	0	0	0		O54829
ENSMUST00000027816	ENSMUSG00000026531	1	174330518	174332873	1	3	5	1	0	0	0	0	0	0	0	0		
ENSMUST00000027817	ENSMUSG00000026532	1	174172776	174248450	1	53	29	67	25	66	15	0	2	12	25	35		P08032
ENSMUST00000027824	ENSMUSG00000026542	1	172893961	172895041	-1	3	5	3	3	3	1	0	0	0	45	0	Q4JFI8	P12246
ENSMUST00000027826	ENSMUSG00000026544	1	172630764	172632962	-1	17	13	43	190	19	10	16	21	6	4	18		Q6NT99
ENSMUST00000027830	ENSMUSG00000026548	1	172475358	172478575	1	6	8	8	8	12	10	6	12	1	276	44		
ENSMUST00000027833	ENSMUSG00000026553	1	172082529	172122330	1	9	0	0	0	10	7	2287	4367	2888	521	1953	F8WHL2	
ENSMUST00000027837	ENSMUSG00000026556	1	172000960	172028444	-1	81	55	632	0	52	23	14	25	17	2	32		Q91ZD4
ENSMUST00000027839	ENSMUSG00000026558	1	167222883	167285320	-1	0	0	6	0	2	0	18	0	12	13	63	A0A0B4J1E5	
ENSMUST00000027843	ENSMUSG00000026560	1	166662055	166681845	-1	5	16	3	3	17	0	0	0	0	0	0	Q8C116	
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ENSMUST00000027847						1	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000027849	ENSMUSG00000005763	1	165788681	165877277	1	1	0	0	5	1	0	18	27	15	12	17		P29020
ENSMUST00000027850	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	2	0	2	0	14	0	0	I1E4X2	
ENSMUST00000027852	ENSMUSG00000026567	1	165485183	165576774	1	0	7	3	9	15	6	0	0	0	2	0		Q8C0T9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000027853	ENSMUSG00000026568	1	165460637	165481214	1	3	0	0	73	0	0	105	629	254	276	174		Q9D023
ENSMUST00000027856	ENSMUSG00000026571	1	165328698	165460475	-1	15	11	30	29	19	11	232	764	445	96	252		Q9DC22
ENSMUST00000027859	ENSMUSG00000026572	1	165137855	165160773	-1	25	18	33	22	32	15	0	0	0	0	0		Q99ME7
ENSMUST00000027860	ENSMUSG00000026573	1	164931644	164935527	-1	2	4	2	2	6	3	0	2	0	5	1	Q542T1	P47993
ENSMUST00000027861	ENSMUSG00000026574	1	164796644	164824266	1	7	9	10	8	14	10	0	0	0	1	1		Q9QZZ6
ENSMUST00000027863	ENSMUSG00000026576	1	164437109	164458355	-1	4	4	18	91	10	4	41	60	28	7	65	Q545P0	P14094
ENSMUST00000027866	ENSMUSG00000026577	1	164289800	164307489	-1	13	12	34	6	12	7	12	63	7	25	7		Q8R2X8
ENSMUST00000027867	ENSMUSG00000026578	1	164275585	164287847	1	10	7	30	32	12	6	36	163	67	138	59		Q80ZU5
ENSMUST00000027871	ENSMUSG00000026581	1	164061982	164084181	1	0	0	0	0	0	0	5923	25711	6882	7407	4914	Q3UV83	P18337
ENSMUST00000027874	ENSMUSG00000026582	1	164048234	164057677	1	14	6	21	12	17	9	9	17	17	16	38	Q3U5F6	
ENSMUST00000027876	ENSMUSG00000026584	1	163929100	163955126	1	0	0	11	172	0	0	132	493	237	16	121		Q9DBQ7
ENSMUST00000027877	ENSMUSG00000026585	1	163779583	163917109	1	22	18	13	12	21	0	24	54	18	24	15		P70188
ENSMUST00000027878	ENSMUSG00000026586	1	163245119	163313710	-1	56	35	81	952	102	49	0	0	0	1	6		P63013
ENSMUST00000027881	ENSMUSG00000026589	1	157506728	157568425	1	0	0	0	0	6	0	0	0	0	0	0		Q91XT4
ENSMUST00000027884	ENSMUSG00000026592	1	157099139	157108680	-1	0	0	16	7	0	3	0	0	0	0	0		
ENSMUST00000027885	ENSMUSG00000033544	1	156838562	156861078	1	27	22	34	117	38	12	0	0	0	0	3		Q640P2
ENSMUST00000027886	ENSMUSG00000026594	1	156804166	156939626	-1	0	0	0	1	0	0	2	0	10	0	1		Q9ERD6
ENSMUST00000027888	ENSMUSG00000026596	1	156558786	156649568	1	0	0	21	12	3	0	10	4	36	2	26	F8VQH0	
ENSMUST00000027895						4	4	15	7	5	9	0	3	0	0	0		
ENSMUST00000027896	ENSMUSG00000026602	1	156310727	156328035	1	7	3	23	87	22	3	0	3	0	0	0	C0LL94	Q91X05
ENSMUST00000027897	ENSMUSG00000026603	1	189880492	189922363	-1	0	0	0	21	8	2	19	14	16	49	60		Q8R5A0
ENSMUST00000027898	ENSMUSG00000026604	1	189728268	189876695	1	0	0	0	0	7	0	0	0	0	0	0		
ENSMUST00000027906	ENSMUSG00000026610	1	187608791	188214885	1	16	9	29	4	14	6	0	0	0	0	0		P62509
ENSMUST00000027908	ENSMUSG00000026611	1	187044648	187215465	-1	0	0	0	0	0	0	0	0	0	0	0		Q9D552
ENSMUST00000027916	ENSMUSG00000026617	1	185332149	185357777	1	202	164	410	140	127	41	27	77	15	9	29		Q9Z0S1
ENSMUST00000027921	ENSMUSG00000026618	1	185284726	185329396	-1	8	11	24	16	0	12	169	545	360	111	327		Q8BIJ6
ENSMUST00000027929	ENSMUSG00000026620	1	184896789	184999570	-1	25	20	30	97	34	25	0	0	0	1	0		Q8VHJ5
ENSMUST00000027931	ENSMUSG00000026622	1	191821444	191833050	1	26	20	70	139	27	12	40	85	67	26	107		O35942
ENSMUST00000027933	ENSMUSG00000037474	1	191537356	191575544	-1	77	85	273	154	0	39	47	67	37	19	42		Q3TLR7
ENSMUST00000027940	ENSMUSG00000026627	1	191325912	191350914	1	17	13	30	61	20	14	12	22	16	10	27		Q9D771
ENSMUST00000027941	ENSMUSG00000026628	1	191170296	191218039	-1	4	6	5	100	14	5	75	449	107	0	160	Q4FJW1	Q60765
ENSMUST00000027943	ENSMUSG00000026630	1	191097847	191108945	1	0	1	0	21	0	0	20	12	4	4	16		Q9D275
ENSMUST00000027945	ENSMUSG00000026632	1	191045826	191062932	-1	0	4	0	0	11	0	11	11	20	122	7	D3YXH9	
ENSMUST00000027947	ENSMUSG00000026634	1	190925112	190946962	1	19	29	41	7	28	17	258	812	45	0	48		Q8K1C0
ENSMUST00000027952	ENSMUSG00000026640	1	194618218	194816869	1	76	61	108	81	83	42	0	1	0	0	1		P70207
ENSMUST00000027955	ENSMUSG00000026645	2	3341982	3397210	-1	4	0	16	9	0	4	0	0	0	0	0		Q8R197
ENSMUST00000027956	ENSMUSG00000026646	2	3455815	3475031	-1	23	13	28	24	16	10	9	24	12	2	38		
ENSMUST00000027959	ENSMUSG00000026649	1	171113918	171126967	1	3	4	0	3	0	0	7	9	2	28	8		Q6P8X9
ENSMUST00000027961	ENSMUSG00000051396	2	3488850	3512814	-1	3	0	0	14	4	2	231	812	440	336	301		Q99M31
ENSMUST00000027965	ENSMUSG00000026655	2	3613758	3782142	1	11	22	26	33	23	2	3008	9699	3604	794	2319		Q3TGF2
ENSMUST00000027966	ENSMUSG00000026656	1	170958617	170976547	-1	87	36	198	2698	126	83	215	819	249	156	473	A0A0B4J1E6	
ENSMUST00000027970	ENSMUSG00000026659	1	170873498	170885540	-1	0	0	0	0	0	0	0	0	0	4	0	Q4KL39	Q9D0T2
ENSMUST00000027973	ENSMUSG00000026662	2	4881564	4910557	1	24	26	61	74	31	17	29	170	100	95	106		Q8BH69
ENSMUST00000027974	ENSMUSG00000026663	1	170704674	170867771	-1	34	27	96	77	69	37	514	1591	1194	241	957		F6VAN0
ENSMUST00000027975	ENSMUSG00000026664	2	4919019	4938730	1	12	1	8	34	11	3	885	3346	1287	656	963	Q3TPC7	O35386
ENSMUST00000027978	ENSMUSG00000026668	2	4976122	4985748	1	6	4	0	0	5	4	0	0	0	0	0		Q14BU0
ENSMUST00000027979	ENSMUSG00000026667	1	170193420	170215397	-1	0	0	0	82	0	0	125	0	1119	0	515		P97343
ENSMUST00000027980	ENSMUSG00000026669	2	4989714	5012791	-1	3	0	7	27	6	0	14	51	45	29	62		Q0VBD2
ENSMUST00000027981	ENSMUSG00000026670	1	170141938	170174957	-1	8	2	7	0	7	0	0	0	0	0	0		
ENSMUST00000027985	ENSMUSG00000026674	1	169972307	170110762	-1	0	2	0	0	8	0	0	0	0	0	26		Q62371
ENSMUST00000027986	ENSMUSG00000026672	2	5020642	5064051	-1	0	0	5	0	0	0	158	434	214	26	176		Q8K3K8
ENSMUST00000027988	ENSMUSG00000026676	2	5137776	5230878	1	41	24	192	95	37	27	0	3	2	0	2		Q9D6Y1
ENSMUST00000027989	ENSMUSG00000026675	1	169949535	169969241	-1	27	27	72	27	29	15	75	139	136	18	91		O88736
ENSMUST00000027991	ENSMUSG00000038530	1	169741477	169747642	-1	6	12	0	15	8	8	0	0	0	0	0	Q5D078	
ENSMUST00000027992	ENSMUSG00000026679	2	21180731	21205365	-1	2	5	4	4	0	0	2	12	7	19	9	Q4KL11	Q6SP97
ENSMUST00000027997	ENSMUSG00000026678	1	169655501	169695813	1	19	24	61	29	18	12	0	1	0	1	0		O08850
ENSMUST00000028000	ENSMUSG00000026683	1	169497934	169531464	-1	0	0	0	0	0	0	74	148	96	169	29		Q99P69
ENSMUST00000028003	ENSMUSG00000026686	1	167689237	167848741	1	23	45	23	0	60	31	0	0	0	0	0	Q543W2	Q9JKU8
ENSMUST00000028004	ENSMUSG00000026687	1	167349991	167368532	1	21	19	35	152	37	9	148	459	172	26	219	Q3U367	
ENSMUST00000028005	ENSMUSG00000026688	1	167371966	167393841	-1	7	3	6	12	13	6	51	58	26	184	30		Q9CPU4
ENSMUST00000028010	ENSMUSG00000026691	1	162953800	162984528	-1	0	6	3	0	3	0	0	0	0	1	0	Q3UEN4	P97501
ENSMUST00000028014	ENSMUSG00000026692	1	162793188	162813972	-1	0	2	0	0	0	0	0	0	0	0	0		Q8VHG0
ENSMUST00000028016	ENSMUSG00000040225	1	162670725	162740556	-1	0	0	0	19	0	0	148	0	626	0	854	A0A0A0MQ79	
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ENSMUST00000028020	ENSMUSG00000026697	1	162639155	162649693	1	18	24	26	31	31	15	0	12	1	0	9	Q05AC1	O70624
ENSMUST00000028021	ENSMUSG00000026698	1	161969186	161973435	1	0	0	4	5	5	5	218	1268	312	105	176		Q9CXR4
ENSMUST00000028024	ENSMUSG00000026700	1	161395409	161418410	1	13	7	11	11	9	1	0	0	0	2	3	B6DXE3	P43488
ENSMUST00000028034	ENSMUSG00000026707	2	14995131	15055069	-1	0	0	0	12	16	0	14	60	11	5	21		Q7TS68
ENSMUST00000028035	ENSMUSG00000026708	1	161070713	161086724	1	3	35	110	61	35	9	0	0	0	0	0		Q3U3S3
ENSMUST00000028045	ENSMUSG00000026712	2	14229392	14332057	1	15	19	32	11	15	7	15	16	31	1284	514	Q2HZ94	Q61830
ENSMUST00000028049	ENSMUSG00000026721	1	160219174	160793211	-1	0	4	3	26	6	2	44	134	104	37	86		A6H6A9
ENSMUST00000028050	ENSMUSG00000026718	2	14074098	14149634	1	7	18	6	10	16	6	11	39	31	0	8	Q3UGN9	
ENSMUST00000028052	ENSMUSG00000026721	1	160219174	160793211	-1	16	9	15	14	7	4	79	124	50	56	102		A6H6A9
ENSMUST00000028055						0	3	5	7	3	3	19	149	70	168	21		
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ENSMUST00000028062	ENSMUSG00000026728	2	13573927	13582826	1	16	29	37	101	28	26	7802	25160	9121	1267	5022	Q5FWJ3	P20152
ENSMUST00000028063	ENSMUSG00000026730	2	12924041	13003455	1	0	0	0	0	5	0	2	5	7	33	9		Q60866
ENSMUST00000028068	ENSMUSG00000026735	2	19445663	19447501	1	8	2	7	358	6	4	0	0	0	0	0	A2ATA7	Q9QX98
ENSMUST00000028069	ENSMUSG00000026736	2	18998343	18999801	1	2	3	3	84	8	4	5	33	8	6	12	E9Q0N7	
ENSMUST00000028071	ENSMUSG00000026739	2	18677018	18686629	1	3	0	0	41	0	0	25	22	6	8	18	Q2LC58	P25916
ENSMUST00000028072	ENSMUSG00000026740	2	18195654	18392830	-1	0	0	0	0	0	0	0	0	0	0	0	F8WH68	
ENSMUST00000028076	ENSMUSG00000026743	2	18055237	18212388	1	15	19	46	3	0	0	262	656	252	5	372		O54826
ENSMUST00000028080	ENSMUSG00000053702	2	17343909	17731464	-1	35	61	245	68	52	31	1	11	0	4	4		Q9DC07
ENSMUST00000028081	ENSMUSG00000026748	2	16356304	16755839	1	16	16	30	180	23	18	9	3	6	10	51		Q9DC11

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000028083	ENSMUSG00000026750	2	38588036	38644087	-1	3	2	3	53	11	10	421	2242	537	3034	510		P70195
ENSMUST00000028084	ENSMUSG00000026751	2	38692656	38714542	-1	31	15	13	21	32	11	0	1	0	0	0		P33242
ENSMUST00000028087	ENSMUSG00000026753	2	39194354	39226451	-1	18	11	7	65	21	3	652	1766	577	882	323		Q9CQR6
ENSMUST00000028098	ENSMUSG00000026761	2	48902824	48950277	-1	10	6	4	13	9	1	52	252	61	78	44		O88708
ENSMUST00000028100	ENSMUSG00000024240	18	6435951	6516108	-1	0	0	31	0	16	0	328	1131	703	126	643		Q8C9X6
ENSMUST00000028102	ENSMUSG00000026764	2	49619298	49774778	1	43	27	94	251	39	26	1	7	2	3	2		P28738
ENSMUST00000028103	ENSMUSG00000026765	2	49787688	49948849	1	25	11	21	20	12	15	24	105	23	14	27		Q9D7F2
ENSMUST00000028105	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	0	27	5	0	82	421	18	74	0		Q9CV28
ENSMUST00000028106	ENSMUSG00000026768	2	12106632	12301922	-1	28	13	36	0	13	11	0	0	0	1	0		A2ARA8
ENSMUST00000028110	ENSMUSG00000026771	2	23506220	23572106	-1	0	0	0	18	0	0	12	70	20	13	36	A0A0A6YWE7	
ENSMUST00000028111	ENSMUSG00000026770	2	11642807	11693193	1	102	128	117	134	166	105	6	20	21	5	48	Q544I2	P01590
ENSMUST00000028113	ENSMUSG00000026774	2	23207476	23267129	1	7	6	7	0	9	7	0	0	0	3	2	Q9D4J9	
ENSMUST00000028114	ENSMUSG00000026773	2	11471433	11554077	-1	42	0	50	82	14	0	0	284	0	0	47	Q7TS91	
ENSMUST00000028117	ENSMUSG00000026775	2	23156369	23199260	1	4	6	34	15	7	7	513	2256	732	959	527		O88967
ENSMUST00000028118	ENSMUSG00000026778	2	11172108	11301222	1	7	5	7	25	11	6	31	23	21	3	86	A6H667	Q02111
ENSMUST00000028119	ENSMUSG00000026779	2	23115606	23156024	-1	34	31	51	67	43	20	19	35	29	58	35		Q8C0P0
ENSMUST00000028121	ENSMUSG00000026781	2	23068168	23114510	1	0	0	7	7	0	4	0	125	0	0	150		Q5XG73
ENSMUST00000028123	ENSMUSG00000026787	2	22622205	22693874	1	78	64	207	253	70	38	3	9	4	0	8	Q548L4	P48320
ENSMUST00000028125	ENSMUSG00000026788	2	33450287	33468559	-1	0	0	0	38	30	0	169	8	322	0	70		Q9DAI4
ENSMUST00000028128	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	62	0	3	0	0	0	0	0		A3KGV1
ENSMUST00000028129	ENSMUSG00000026791	2	32972990	32982083	-1	0	0	0	0	0	0	31	27	22	4	35		Q9JIF3
ENSMUST00000028132	ENSMUSG00000026792	2	32925216	32961614	-1	28	27	77	73	40	15	258	0	209	34	171		Q80ZI6
ENSMUST00000028135	ENSMUSG00000026796	2	32876114	32925254	1	27	21	72	185	45	13	741	635	749	91	654		Q8R1F1
ENSMUST00000028137	ENSMUSG00000026798	2	29787493	29797935	1	0	0	0	0	0	0	126	256	91	28	23	B9EID1	Q8BGB8
ENSMUST00000028139	ENSMUSG00000026799	2	29346819	29524793	1	0	0	0	10	0	0	112	126	77	38	45		Q9DB40
ENSMUST00000028148	ENSMUSG00000009566	2	32682609	32704145	-1	0	0	0	98	5	0	48	32	7	0	45		P48760
ENSMUST00000028151	ENSMUSG00000026810	2	32570858	32573579	1	0	1	0	1	0	0	410	585	271	270	146	Q545R7	Q9Z324
ENSMUST00000028155	ENSMUSG00000026812	2	28641228	28691167	1	13	0	0	0	0	0	0	205	347	0	98		Q9EP53
ENSMUST00000028156	ENSMUSG00000026815	2	28609450	28621982	-1	0	6	17	0	0	0	27	26	24	17	14		O70237
ENSMUST00000028157	ENSMUSG00000026816	2	28566311	28583751	-1	2	0	51	60	0	0	100	83	88	21	80	Q3UI98	Q8R2T8
ENSMUST00000028160	ENSMUSG00000026819	2	32414487	32451445	-1	0	0	21	0	17	0	112	26	0	0	0		A2ASZ8
ENSMUST00000028161	ENSMUSG00000026818	2	28555795	28563403	-1	25	14	24	14	28	9	0	0	0	0	0	Q3V2H7	Q64285
ENSMUST00000028162	ENSMUSG00000026820	2	32395896	32405772	1	195	176	559	296	246	108	246	535	186	54	121		Q8BWM0
ENSMUST00000028166	ENSMUSG00000026826	2	57106830	57124003	-1	0	6	0	0	0	0	0	0	0	0	21	Q3TYI4	Q06219
ENSMUST00000028167	ENSMUSG00000026827	2	57237635	57370719	1	0	36	35	0	28	0	800	1633	1353	138	945		Q64521
ENSMUST00000028170	ENSMUSG00000026821	2	28513125	28553081	1	0	0	14	0	16	0	62	22	24	15	62		Q03385
ENSMUST00000028172	ENSMUSG00000026829	2	28496891	28505415	1	7	1	18	0	6	2	0	1	0	0	2		Q8VI38
ENSMUST00000028175	ENSMUSG00000026832	2	58129137	58195532	-1	30	41	76	236	59	37	2388	8771	2919	3948	3406		Q91VY6
ENSMUST00000028177	ENSMUSG00000026833	2	28192992	28230736	1	0	0	0	18	4	9	0	77	0	1	167	Q8R357	
ENSMUST00000028178	ENSMUSG00000026834	2	58267453	58357895	-1	20	20	18	65	33	13	0	2	1	0	2		Q8K348
ENSMUST00000028179	ENSMUSG00000026835	2	28076378	28084885	-1	4	4	22	7	8	0	1039	692	554	254	164		O70497
ENSMUST00000028187	ENSMUSG00000026840	2	31887291	31946539	1	48	28	51	39	64	17	0	0	0	1	11		Q9R0B6
ENSMUST00000028188	ENSMUSG00000026841	2	31813290	31846005	-1	52	29	84	245	68	27	0	0	1	0	2		A2AV25
ENSMUST00000028190	ENSMUSG00000026842	2	31688376	31804227	1	50	32	123	212	70	26	25	86	53	61	170		P00520
ENSMUST00000028199	ENSMUSG00000026848	2	30952959	30959015	1	0	0	0	34	8	0	67	201	231	124	106		Q9ER41
ENSMUST00000028200	ENSMUSG00000026849	2	30960627	30967933	-1	0	0	0	77	3	0	640	1101	474	604	362	Q3TV62	Q9ER39
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ENSMUST00000028207	ENSMUSG00000026853	2	30400471	30415813	-1	0	0	73	70	23	0	522	835	541	84	395		P47934
ENSMUST00000028209	ENSMUSG00000026856	2	30392254	30400529	1	6	0	0	65	4	6	28	50	75	0	24		Q9JMF7
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ENSMUST00000028220	ENSMUSG00000035949	2	34804514	34826311	-1	0	0	0	0	0	0	87	0	0	0	6	Q9QUH1	
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ENSMUST00000028223	ENSMUSG00000026866	2	43555329	43682715	1	31	23	29	452	49	29	15	43	16	15	19	A2ARD6	
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ENSMUST00000028225	ENSMUSG00000026869	2	34849734	34874968	-1	0	0	8	30	2	0	234	822	413	541	271		Q8BJY1
ENSMUST00000028228	ENSMUSG00000026870	2	34874396	34892132	1	3	0	27	4	8	0	0	0	0	0	0		
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ENSMUST00000028232	ENSMUSG00000026873	2	34893757	34914026	-1	0	12	20	18	0	0	99	63	96	9	60		Q9CXG9
ENSMUST00000028233	ENSMUSG00000026874	2	34983331	35061438	-1	36	15	37	38	20	16	43	241	77	62	36		P06684
ENSMUST00000028234	ENSMUSG00000026875	2	34941750	34961772	-1	0	0	0	0	0	0	26	31	32	8	52		P39428
ENSMUST00000028235	ENSMUSG00000057110	2	35109492	35178822	1	0	1	0	42	5	3	5	36	3	0	7		A2AL36
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ENSMUST00000028239	ENSMUSG00000026879	2	35256380	35307892	1	21	15	32	87	23	18	11578	10825	8137	1787	4667		P13020
ENSMUST00000028241	ENSMUSG00000026880	2	35313986	35336976	-1	17	26	45	54	28	15	4384	5661	4705	985	1217		P54116
ENSMUST00000028243	ENSMUSG00000026882	2	35354218	35367729	-1	3	8	3	3	0	0	0	0	0	0	0		A2AUQ7
ENSMUST00000028248	ENSMUSG00000026885	2	35751241	35979913	-1	0	0	9	32	0	0	0	0	0	0	0		A4Q9F4
ENSMUST00000028250	ENSMUSG00000026887	2	36136389	36190647	1	14	12	25	27	29	20	31	83	25	74	41		Q9D6S7
ENSMUST00000028251	ENSMUSG00000026889	2	36116079	36136773	-1	3	5	15	50	6	1	253	933	260	389	211		Q9CR83
ENSMUST00000028252	ENSMUSG00000026888	2	64912476	65024987	-1	2	2	2	104	8	5	0	0	2	0	0	A2ASX2	Q9JLM9
ENSMUST00000028256	ENSMUSG00000026894	2	36049458	36079718	1	9	12	8	9	9	8	0	0	0	2	0		Q9DAI9
ENSMUST00000028257	ENSMUSG00000026893	2	62664285	62694109	1	39	22	138	126	37	14	841	2079	1001	454	513		Q8VC88
ENSMUST00000028259	ENSMUSG00000026896	2	62595798	62646255	-1	4	12	18	14	19	15	42	267	64	11	117	D2CGM4	Q8R5F7
ENSMUST00000028278	ENSMUSG00000026914	2	61711694	61800376	1	3	6	18	15	6	3	222	1129	455	362	308		O35593
ENSMUST00000028279	ENSMUSG00000026915	2	37483228	37703859	-1	163	172	529	139	165	86	31	66	40	4	61		Q91WM1
ENSMUST00000028280	ENSMUSG00000026837	2	27886425	28039514	1	68	49	167	392	109	49	973	794	2175	34	510	B1AWB9	O88207
ENSMUST00000028282	ENSMUSG00000026918	2	27445579	27507662	-1	0	0	0	86	21	0	0	0	28	0	0	Q3TUI3	Q8K2F0
ENSMUST00000028283	ENSMUSG00000026919	2	26667674	26671282	-1	5	3	3	5	8	6	1	3	1	4	2	Q24JQ8	Q62472
ENSMUST00000028286	ENSMUSG00000026922	2	26593057	26604417	-1	0	0	0	19	3	0	707	916	733	405	449	Q059U0	Q8K3K7
ENSMUST00000028288	ENSMUSG00000026923	2	26457903	26516663	-1	72	34	168	225	105	49	4570	4956	5361	203	5070		Q01705
ENSMUST00000028291						32	19	8	37	26	8	122	0	47	0	77		
ENSMUST00000028293	ENSMUSG00000026927	2	26382802	26389316	-1	5	0	0	0	0	0	123	379	155	0	0		A2AIW0
ENSMUST00000028294	ENSMUSG00000026928	2	26352176	26360918	-1	0	0	21	16	19	0	1604	3517	1788	518	1688		A2AIV8
ENSMUST00000028295	ENSMUSG00000075467	2	26348121	26352110	-1	19	0	19	259	19	0	95	182	80	31	78		Q9D113

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000028299	ENSMUSG00000026931	19	58785803	58794461	-1	4	8	9	5	11	10	0	0	0	0	0		
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ENSMUST00000028302	ENSMUSG00000026934	2	26200212	26208289	-1	0	0	0	68	4	2	0	0	0	0	0	A2ALD8	P50481
ENSMUST00000028304	ENSMUSG00000026936	2	25765569	25768099	1	8	6	14	5	13	2	0	0	0	0	0	Q14AJ3	
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ENSMUST00000028307	ENSMUSG00000026938	2	25624666	25628030	-1	10	12	16	5	14	7	1	2	2	1453	718	Q4FJM1	O70165
ENSMUST00000028308	ENSMUSG00000026939	2	25620067	25622005	-1	1	0	0	0	5	2	0	0	18	0	0	F8WGV9	
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ENSMUST00000028311	ENSMUSG00000026942	2	25517982	25546940	-1	8	2	14	25	11	1	135	138	115	36	124	Q3U8L1	P39429
ENSMUST00000028312	ENSMUSG00000026943	2	25490845	25493911	-1	5	0	7	12	2	2	0	0	0	0	0	Q2TA58	Q6JVL5
ENSMUST00000028314	ENSMUSG00000026946	2	51948487	51973494	-1	0	0	0	4	0	0	19	24	0	37	26	Q3UJ82	O35309
ENSMUST00000028320	ENSMUSG00000026950	2	52136647	52338798	-1	33	19	21	22	22	11	0	6	0	1	38	A2AQB2	
ENSMUST00000028328	ENSMUSG00000015085	2	25395874	25401321	1	0	0	23	109	20	3	0	0	0	0	0	Q921R1	O55026
ENSMUST00000028329	ENSMUSG00000026955	2	25372321	25378213	1	19	11	24	37	18	11	8	14	2	4	4		Q9D818
ENSMUST00000028332	ENSMUSG00000026958	2	25352276	25356359	-1	0	3	2	2	0	0	68	79	27	49	63		Q9ET22
ENSMUST00000028335	ENSMUSG00000026959	2	25291181	25319187	-1	0	0	12	84	0	0	0	0	0	0	0		P35438
ENSMUST00000028336	ENSMUSG00000026960	2	53191726	53219220	1	3	5	21	133	2	10	217	372	158	51	131		Q8BH07
ENSMUST00000028337	ENSMUSG00000026961	2	25289915	25291180	1	13	11	28	151	15	4	0	0	0	0	0		Q91W20
ENSMUST00000028340	ENSMUSG00000026963	2	25288145	25289189	1	17	5	43	11	5	8	0	0	0	0	0		Q9D2F0
ENSMUST00000028341	ENSMUSG00000026965	2	25272478	25285915	1	19	15	30	59	25	12	1703	2024	1366	164	1112		Q8BZQ7
ENSMUST00000028342	ENSMUSG00000026966	2	25271039	25272438	-1	0	0	0	0	0	0	562	608	339	849	171		Q9JJ94
ENSMUST00000028346	ENSMUSG00000026969	2	25218745	25222280	1	9	5	35	17	18	0	2	1	2	0	0		Q9D4K5
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ENSMUST00000028348	ENSMUSG00000026971	2	60598292	60722643	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0T9
ENSMUST00000028349	ENSMUSG00000026972	2	24925352	24935252	-1	0	0	0	36	0	8	733	1564	654	127	500		Q99KN1
ENSMUST00000028350	ENSMUSG00000026974	2	24949792	24962075	1	30	29	22	56	32	21	14	52	20	4	29		Q9CQG3
ENSMUST00000028351	ENSMUSG00000026975	2	24962400	24972163	1	13	0	14	0	7	0	0	51	15	29	8		Q9CYU6
ENSMUST00000028355	ENSMUSG00000026976	2	24420560	24475599	-1	5	10	28	33	12	0	9	15	4	1	6		Q00288
ENSMUST00000028356	ENSMUSG00000060703	2	60251993	60284488	-1	0	0	4	64	6	0	0	140	21	84	88		Q9DCG2
ENSMUST00000028360	ENSMUSG00000026983	2	24276954	24283426	1	22	8	10	15	16	8	0	0	0	0	0		Q9QYY1
ENSMUST00000028361	ENSMUSG00000026984	2	24215418	24225702	1	2	0	0	5	0	1	0	0	0	0	0	Q149U6	Q9JLA2
ENSMUST00000028362	ENSMUSG00000026980	2	60292103	60383303	-1	16	0	2	0	0	0	164	104	1028	8	415		Q60767
ENSMUST00000028363	ENSMUSG00000026985	2	24153161	24160519	1	6	8	5	4	3	2	2	14	2	2	0	Q08EA6	Q9D6Z6
ENSMUST00000028368	ENSMUSG00000026988	2	59852364	59882591	-1	19	15	35	19	18	13	37	160	54	22	62		Q9D0I6
ENSMUST00000028369	ENSMUSG00000026989	2	59484653	59505020	1	0	0	15	3	4	2	6	25	3	62	15		Q9D757
ENSMUST00000028377	ENSMUSG00000075318	2	65620771	65767447	1	0	0	0	0	55	0	0	0	0	0	0	B1AWN6	
ENSMUST00000028378	ENSMUSG00000026994	2	66082766	66124994	-1	13	7	3	118	10	5	47	244	85	17	65		P70419
ENSMUST00000028382	ENSMUSG00000026999	2	80617236	80658906	1	0	0	0	14	3	0	32	132	44	113	50		Q8R4R6
ENSMUST00000028384	ENSMUSG00000027001	2	80617045	80632361	1	14	8	29	12	10	2	0	11	0	19	4	Q99N12	
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ENSMUST00000028389	ENSMUSG00000027004	2	80411970	80447625	-1	27	10	20	282	16	15	0	0	0	0	0		P97401
ENSMUST00000028392	ENSMUSG00000027006	2	80315466	80354043	1	14	7	6	13	19	3	614	2283	1163	1412	815		Q9DC23
ENSMUST00000028398	ENSMUSG00000027011	2	78868124	78921293	1	2	9	6	21	3	3	115	155	40	21	30		P52483
ENSMUST00000028403	ENSMUSG00000027015	2	71117923	71142926	1	115	105	98	359	138	69	4	6	4	0	6		Q925G2
ENSMUST00000028406						14	18	12	16	19	7	2	10	4	8	10		
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ENSMUST00000028410	ENSMUSG00000027022	2	67446002	67526614	1	34	39	78	49	41	21	0	0	0	0	0		Q4U4S6
ENSMUST00000028426	ENSMUSG00000027035	2	68861441	69114282	1	58	38	272	91	55	24	2239	7834	4529	500	3433		Q8C172
ENSMUST00000028430	ENSMUSG00000056436	2	76353942	76360450	-1	3	4	3	2	2	2	0	0	0	1	1		P00015
ENSMUST00000028465	ENSMUSG00000027071	2	84998583	85037462	-1	14	0	19	7	11	3	0	0	0	0	0		Q3UR32
ENSMUST00000028466	ENSMUSG00000027072	2	84988215	84993886	1	4	4	8	13	6	6	8	0	5	3	0		Q9JL95
ENSMUST00000028467	ENSMUSG00000027073	2	84980461	84983632	1	11	8	11	13	8	7	119	7	55	52	22	Q545D8	Q61878
ENSMUST00000028469	ENSMUSG00000027075	2	84838850	84863594	1	0	0	0	0	0	0	0	0	0	0	0	G3X8X3	
ENSMUST00000028470	ENSMUSG00000027076	2	84826997	84830213	1	5	2	6	3	7	2	31	16	10	114	5		P62073
ENSMUST00000028471	ENSMUSG00000027077	2	84811176	84822652	-1	12	10	32	19	27	6	0	0	0	0	0		Q99LM3
ENSMUST00000028475	ENSMUSG00000027079	2	84722104	84727350	-1	2	0	15	5	0	2	252	506	297	225	205		Q99LI9
ENSMUST00000028487	ENSMUSG00000027082	2	84432855	84476775	-1	0	0	1	0	0	0	0	0	0	0	0		O54819
ENSMUST00000028494	ENSMUSG00000027088	2	69789623	69800005	1	0	0	0	0	0	0	108	578	201	215	101		Q9D9M5
ENSMUST00000028499	ENSMUSG00000027087	2	83724397	83806916	1	0	0	25	17	18	12	184	158	449	0	416		P43406
ENSMUST00000028509	ENSMUSG00000014959	2	70661576	70712636	1	2	0	0	7	4	0	579	984	513	117	421		Q99JX3
ENSMUST00000028511	ENSMUSG00000027099	2	74825803	74878431	1	30	22	49	61	35	26	42	108	36	84	42		O88441
ENSMUST00000028515	ENSMUSG00000027107	2	73563215	73580338	-1	91	94	306	99	89	48	1	12	3	1	2	Q05A24	P04756
ENSMUST00000028517	ENSMUSG00000027108	2	73092801	73218924	-1	6	5	8	43	5	5	22	143	33	46	46		Q9CZ30
ENSMUST00000028522	ENSMUSG00000027111	2	71745616	71858416	1	0	0	0	0	7	0	0	49	74	22	396	Q8CC06	Q61739
ENSMUST00000028525	ENSMUSG00000049044	2	71981240	72257474	1	25	12	27	28	30	20	0	0	8	0	5	A2ASW8	
ENSMUST00000028527	ENSMUSG00000027115	2	109280738	109341747	1	13	3	8	15	10	0	12	31	21	24	6		Q91WD7
ENSMUST00000028533	ENSMUSG00000027120	2	107056140	107059656	-1	6	10	6	5	9	7	0	0	0	0	0	A0A0F7RQR1	Q60687
ENSMUST00000028536	ENSMUSG00000027122	2	106962527	106974424	-1	8	9	13	19	12	18	91	313	149	119	140		Q8BIX3
ENSMUST00000028549	ENSMUSG00000027130	2	112265825	112363163	1	0	0	0	0	0	0	1523	3658	2828	237	1714		Q924N4
ENSMUST00000028551	ENSMUSG00000027131	2	112363011	112368027	-1	6	3	4	0	2	6	85	272	103	164	96		Q9CZX9
ENSMUST00000028552	ENSMUSG00000027132	2	112379211	112414240	1	5	2	4	42	4	2	35	65	29	46	13		Q9CWJ3
ENSMUST00000028553	ENSMUSG00000027133	2	112261926	112263269	1	11	11	19	6	14	2	117	231	75	619	74		Q9CQS2
ENSMUST00000028554	ENSMUSG00000027134	2	112239468	112247111	1	12	5	27	129	22	6	944	833	841	72	518		Q6NVG1
ENSMUST00000028577	ENSMUSG00000027157	2	111162061	111229602	-1	3	3	2	0	2	2	0	0	0	0	0	Q05AC5	
ENSMUST00000028580	ENSMUSG00000027160	2	110017817	110173360	1	0	4	0	139	16	0	28	52	45	43	23		Q3UI66
ENSMUST00000028583	ENSMUSG00000027162	2	109890853	109901003	1	15	9	12	29	11	7	428	1270	535	949	487		O88952
ENSMUST00000028584	ENSMUSG00000027163	2	101886247	101901646	1	8	7	23	11	21	8	89	131	71	97	37		Q8K2Q0
ENSMUST00000028588	ENSMUSG00000027167	2	105701027	105904564	-1	0	0	0	0	0	0	3	11	5	1	3	A2A414	
ENSMUST00000028592	ENSMUSG00000027170	2	104999656	105017080	-1	7	2	16	32	0	3	239	1046	411	1806	296		Q99JX4
ENSMUST00000028593	ENSMUSG00000027171	2	104830741	104849876	-1	30	25	225	227	32	19	8	2	1	1	8	Q4KL73	Q8BGN6
ENSMUST00000028595	ENSMUSG00000027173	2	104721784	104742878	-1	7	1	3	31	4	5	3	58	6	52	10		Q91WS7
ENSMUST00000028597	ENSMUSG00000027175	2	104657288	104712169	-1	0	0	28	17	2	6	9	0	0	0	0		Q8BTG3
ENSMUST00000028599	ENSMUSG00000027176	2	104590523	104665429	1	1	5	11	30	14	6	135	570	242	74	165		Q99LI7
ENSMUST00000028600	ENSMUSG00000027177	2	104426481	104494446	-1	13	23	20	247	20	18	867	1274	824	113	569		Q9ERH7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000028603	ENSMUSG00000027180	2	104027721	104063240	1	19	14	13	13	19	1	29	692	279	157	170		Q9DC63
ENSMUST00000028607	ENSMUSG00000027184	2	103762941	103797649	-1	9	6	16	65	28	3	17	104	40	7	20		Q60865
ENSMUST00000028608	ENSMUSG00000027185	2	103721256	103761270	-1	0	0	0	0	6	0	51	98	35	13	86		Q8K224
ENSMUST00000028609	ENSMUSG00000027186	2	103411688	103450989	1	9	5	34	8	2	0	0	0	0	0	0	Q3V1F7	Q8VDK3
ENSMUST00000028610	ENSMUSG00000027187	2	103453849	103485160	-1	30	11	51	62	28	7	242	679	313	56	334		P24270
ENSMUST00000028612	ENSMUSG00000027188	2	102550012	102643041	1	11	14	16	30	18	4	0	0	0	0	0		Q8BU25
ENSMUST00000028617	ENSMUSG00000027193	2	94411682	94438136	-1	14	21	16	10	18	8	1148	4696	1941	1062	1108		O35841
ENSMUST00000028619	ENSMUSG00000027195	2	94032689	94157964	-1	0	0	0	28	0	2	78	220	181	181	206	Q0VGQ1	O70503
ENSMUST00000028623	ENSMUSG00000027198	2	93661028	93822568	-1	8	4	6	25	5	8	188	214	172	96	265		P70428
ENSMUST00000028624	ENSMUSG00000027199	2	122594467	122611303	-1	3	4	9	88	17	7	301	789	345	327	411		Q9D964
ENSMUST00000028630	ENSMUSG00000027202	2	125152505	125230002	1	0	0	0	0	7	0	0	0	0	0	0	A2AQ50	
ENSMUST00000028633	ENSMUSG00000027204	2	125300594	125507993	-1	52	7	73	23	26	10	54	111	143	9	41	A2AQ53	
ENSMUST00000028635	ENSMUSG00000027206	2	125830304	125859139	-1	3	1	7	16	8	8	111	611	233	381	100		P61202
ENSMUST00000028636	ENSMUSG00000027207	2	125859109	125984299	1	8	6	17	3	3	0	0	0	0	0	0	Q8BUU7	
ENSMUST00000028639	ENSMUSG00000027210	2	115863064	116065839	-1	0	0	0	0	0	0	0	0	0	0	0		P97367
ENSMUST00000028640	ENSMUSG00000057147	2	114516416	114654964	-1	19	27	17	32	26	0	0	21	14	13	13		Q9CQ28
ENSMUST00000028644	ENSMUSG00000027215	2	93419111	93463140	-1	11	3	13	41	3	0	3383	3296	2236	532	1699	Q3UII2	P40237
ENSMUST00000028646	ENSMUSG00000027217	2	93201760	93334505	-1	0	1	1	1	3	1	0	0	0	0	0		Q80WR1
ENSMUST00000028648	ENSMUSG00000027220	2	92915098	92956058	1	34	35	51	133	42	18	0	1	0	40	197		Q9EQT6
ENSMUST00000028650	ENSMUSG00000027222	2	92374676	92381217	1	3	5	23	51	9	5	300	215	128	65	70		Q91XC9
ENSMUST00000028652	ENSMUSG00000027219	2	122426477	122461137	1	6	4	25	21	25	11	391	437	588	161	399		O88627
ENSMUST00000028653	ENSMUSG00000027224	2	122302191	122313730	-1	0	0	0	0	0	0	0	0	0	0	0		Q8VE49
ENSMUST00000028656	ENSMUSG00000027225	2	122298900	122302885	1	3	5	41	97	14	2	0	0	0	0	0		Q9D311
ENSMUST00000028661	ENSMUSG00000027229	2	122186272	122206397	1	3	6	20	7	9	5	0	0	0	0	0		Q9D494
ENSMUST00000028663	ENSMUSG00000027230	2	91982328	92024502	-1	20	7	60	127	23	11	17	8	8	0	10		
ENSMUST00000028665	ENSMUSG00000027233	2	122120108	122186189	-1	18	16	24	23	23	13	0	0	1	0	1		A2ARM1
ENSMUST00000028667	ENSMUSG00000040479	2	91932824	91975864	-1	0	0	0	34	0	0	49	94	37	0	128		Q80UP3
ENSMUST00000028668	ENSMUSG00000027236	2	122028546	122056598	1	26	21	15	48	40	5	21	104	53	28	71		Q3UGC7
ENSMUST00000028672	ENSMUSG00000027239	2	91929805	91932297	-1	5	4	15	109	11	3	0	29	10	4	11		P12025
ENSMUST00000028676	ENSMUSG00000027242	2	121506723	121544860	1	0	0	0	0	0	0	5	0	0	0	0		A6PWY4
ENSMUST00000028677						0	0	0	0	0	0	0	0	0	14	0		
ENSMUST00000028678	ENSMUSG00000027244	2	91674618	91710576	-1	0	0	14	0	5	0	0	0	0	0	0		Q91YI1
ENSMUST00000028679	ENSMUSG00000027246	2	121439010	121444278	-1	20	11	38	106	25	10	0	4	4	0	15		Q80VR2
ENSMUST00000028681	ENSMUSG00000027249	2	91625320	91636414	-1	0	7	9	0	26	0	0	7	0	0	0	Q3TJ94	P19221
ENSMUST00000028683	ENSMUSG00000027248	2	121413775	121438687	1	10	12	26	46	10	7	918	5850	2124	641	1526		P27773
ENSMUST00000028689	ENSMUSG00000027253	2	91457511	91513779	1	73	61	140	90	126	47	36	28	40	3	37		Q8VI56
ENSMUST00000028691	ENSMUSG00000027255	2	91264974	91276931	1	3	6	71	0	0	1	817	1251	676	172	517		Q99K28
ENSMUST00000028694	ENSMUSG00000027257	2	91255954	91264679	1	0	0	0	0	0	0	0	0	0	0	18	Q543N7	Q99JB8
ENSMUST00000028696	ENSMUSG00000002109	2	91211572	91236982	-1	14	0	22	34	7	6	35	0	29	68	85		Q99J79
ENSMUST00000028702	ENSMUSG00000027259	2	121140428	121156680	1	0	0	0	0	0	0	0	23	33	17	25		Q80SY6
ENSMUST00000028704	ENSMUSG00000027261	2	134497361	134554368	-1	4	8	20	5	9	1	0	8	2	9	0	Q3UEE8	Q9WU19
ENSMUST00000028721	ENSMUSG00000053675	2	121046111	121085841	-1	19	11	39	17	31	11	0	0	0	0	0		Q9D7I9
ENSMUST00000028726	ENSMUSG00000074771	2	136501910	136562091	1	0	0	0	29	0	0	0	0	0	0	0		Q9D2J7
ENSMUST00000028727	ENSMUSG00000027273	2	136713453	136782428	1	0	6	43	16	4	3	0	0	0	0	0		P60879
ENSMUST00000028728	ENSMUSG00000027272	2	120860269	120970715	-1	21	6	18	47	15	20	427	1224	841	76	521		O70481
ENSMUST00000028730	ENSMUSG00000027274	2	136873780	136891389	-1	0	11	3	0	7	1	8	91	17	21	23		Q9JI70
ENSMUST00000028735	ENSMUSG00000027276	2	137081456	137116644	-1	28	29	52	61	34	17	36	109	54	5	86	Q3UVN4	Q9QXX0
ENSMUST00000028737	ENSMUSG00000027281	2	136891218	137071950	1	8	0	0	10	6	0	6	0	15	12	24		Q9D7Y9
ENSMUST00000028740	ENSMUSG00000090100	2	120732816	120850604	-1	86	91	223	117	45	0	166	141	260	0	12	A2AW15	
ENSMUST00000028741	ENSMUSG00000027285	2	120609383	120621560	1	0	0	0	0	0	0	76	34	49	17	23	H7BWZ0	
ENSMUST00000028743	ENSMUSG00000027287	2	120567671	120601255	1	23	77	0	0	48	26	89	2441	342	309	159	A2AKH4	O09044
ENSMUST00000028748	ENSMUSG00000079110	2	120456019	120504913	1	0	0	0	0	0	0	0	0	0	0	0	Q0VGP9	
ENSMUST00000028749	ENSMUSG00000079110	2	120456019	120504913	1	7	0	0	1	8	0	0	0	0	0	7		Q64691
ENSMUST00000028752	ENSMUSG00000027291	2	120316461	120353137	-1	15	0	0	0	0	16	194	819	147	47	388	Q5KU38	Q8R5L3
ENSMUST00000028755	ENSMUSG00000027293	2	120089175	120154606	-1	24	19	47	134	32	17	189	616	255	71	537	Q3TM70	Q9EQP2
ENSMUST00000028758	ENSMUSG00000027296	2	119742337	119751263	1	20	12	26	181	20	7	1	1	0	1	1		Q8R071
ENSMUST00000028759	ENSMUSG00000027297	2	119751320	119760431	-1	7	4	28	155	28	0	0	0	0	0	0		P08923
ENSMUST00000028761	ENSMUSG00000027300	2	130590002	130630038	-1	21	22	35	73	39	18	70	96	46	16	52	Q543N0	Q925F4
ENSMUST00000028763	ENSMUSG00000027298	2	119797733	119818104	1	0	0	0	41	0	0	3	5	0	0	22		P55144
ENSMUST00000028764	ENSMUSG00000027301	2	130576173	130577054	1	12	7	25	87	14	10	2	2	2	0	0	Q545V4	P35454
ENSMUST00000028767	ENSMUSG00000027304	2	119675068	119735407	1	36	32	121	57	51	31	402	1456	1008	162	915		A2AQ19
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ENSMUST00000028769	ENSMUSG00000027303	2	130450278	130554026	1	0	0	0	93	9	17	376	812	832	241	683	Q91V35	
ENSMUST00000028771	ENSMUSG00000027306	2	119618298	119651244	1	14	16	35	19	26	6	9	24	13	34	21		Q9ERH4
ENSMUST00000028780	ENSMUSG00000027313	2	119351229	119354381	1	10	5	40	134	16	9	65	63	58	6	40		Q8R3J5
ENSMUST00000028781	ENSMUSG00000027312	2	130906495	131030333	1	48	51	97	156	84	48	1954	4394	4858	328	3195		Q9WU60
ENSMUST00000028783	ENSMUSG00000027315	2	119237362	119249527	1	0	11	0	92	6	0	118	134	212	25	43		Q9R097
ENSMUST00000028787	ENSMUSG00000027316	2	131039632	131043088	-1	0	0	0	0	0	0	0	0	0	0	0	A2AP45	Q9JJT2
ENSMUST00000028794	ENSMUSG00000027322	2	131069220	131086765	-1	27	11	38	33	12	11	1	3	2	20	134	G3X8X6	
ENSMUST00000028795	ENSMUSG00000027323	2	119112793	119147445	1	0	3	0	11	14	8	0	27	0	10	0		Q08297
ENSMUST00000028796	ENSMUSG00000027324	2	119034790	119039769	1	27	21	71	293	34	18	6	10	6	1	8		Q149F1
ENSMUST00000028799	ENSMUSG00000027326	2	119047119	119105501	1	1	0	5	88	9	0	0	0	18	0	2		Q66JQ7
ENSMUST00000028800	ENSMUSG00000027327	2	131146324	131160081	-1	4	1	0	11	3	3	0	9	0	8	16	F8WIU1	
ENSMUST00000028801	ENSMUSG00000027329	2	131170261	131187282	-1	0	1	6	65	16	4	0	0	0	0	0		Q99JL1
ENSMUST00000028802	ENSMUSG00000027326	2	119047119	119105501	1	38	47	73	33	30	20	63	127	113	19	47	A3KGI3	
ENSMUST00000028803	ENSMUSG00000027331	2	118814003	118853957	1	0	0	8	0	1	1	36	138	55	221	40	A3KGG6	
ENSMUST00000028804	ENSMUSG00000027330	2	131186949	131198497	1	0	0	9	143	25	0	508	568	447	43	253	Q3U535	P30306
ENSMUST00000028806	ENSMUSG00000027333	2	131491496	131525922	1	0	0	5	102	8	2	0	236	46	29	27	Q3UPW5	Q99K82
ENSMUST00000028807	ENSMUSG00000027332	2	118861954	118882909	1	14	7	13	25	22	4	238	715	217	63	152		Q9JHI5
ENSMUST00000028814	ENSMUSG00000027339	2	131989415	132030258	-1	207	120	438	599	213	112	140	786	328	32	293		Q8BMS9
ENSMUST00000028815	ENSMUSG00000027340	2	132052496	132145108	-1	27	30	70	54	25	19	170	265	210	27	263		Q9EPR4
ENSMUST00000028816	ENSMUSG00000027341	2	132239492	132247807	-1	0	0	0	10	15	0	184	354	63	29	79		Q8CIB6
ENSMUST00000028817	ENSMUSG00000027342	2	132249162	132253314	-1	10	5	8	83	12	2	575	1207	515	1470	366	Q542J9	P17918
ENSMUST00000028820	ENSMUSG00000027344	2	118204888	118256966	-1	4	3	0	9	1	2	0	0	0	0	0		Q9D3V5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000028821	ENSMUSG00000027344	2	118204888	118256966	-1	9	4	14	23	9	5	0	0	0	0	0		Q9D3V5
ENSMUST00000028822	ENSMUSG00000027346	2	132529082	132587729	-1	6	8	6	8	10	7	260	1010	424	261	567	B0R058	
ENSMUST00000028825	ENSMUSG00000027349	2	117249739	117271540	1	7	6	5	5	5	6	179	551	294	178	176		Q80VD1
ENSMUST00000028826	ENSMUSG00000027350	2	132781278	132795079	1	21	11	72	130	35	25	0	0	0	1	0	Q3TY66	P16014
ENSMUST00000028829	ENSMUSG00000027351	2	117121374	117182279	1	20	12	32	25	22	6	42	75	38	25	104		Q924S8
ENSMUST00000028831	ENSMUSG00000027353	2	132816141	132844197	1	2	0	0	0	0	0	11	8	0	12	6		Q9CWV1
ENSMUST00000028834	ENSMUSG00000027355	2	116878691	116892494	1	7	0	9	0	9	0	0	0	0	0	0		Q9D9D5
ENSMUST00000028835	ENSMUSG00000027357	2	132846666	132866785	1	0	0	0	22	2	0	34	169	60	36	14		Q80ZM8
ENSMUST00000028836	ENSMUSG00000027358	2	133552159	133562885	1	20	11	20	548	40	10	0	2	0	8	13		P21274
ENSMUST00000028838	ENSMUSG00000027360	2	126593667	126619299	-1	16	16	30	25	29	18	19709	35235	13803	4231	17007		P23738
ENSMUST00000028841	ENSMUSG00000027363	2	126707328	126759297	1	13	16	33	24	16	10	649	1797	1527	313	1079		Q80U87
ENSMUST00000028842	ENSMUSG00000027364	2	126709096	126783458	-1	0	0	2	0	4	4	0	0	0	0	0		Q6P8X6
ENSMUST00000028843	ENSMUSG00000027365	2	126791565	126876230	-1	4	0	0	0	0	7	173	874	79	0	113	A2AI57	
ENSMUST00000028844	ENSMUSG00000027366	2	126890391	126933235	-1	42	36	125	97	69	25	628	2112	1031	778	773		Q9JJF9
ENSMUST00000028846	ENSMUSG00000027368	2	127336159	127338376	1	5	4	18	136	8	3	14	65	15	6	76		Q05922
ENSMUST00000028848	ENSMUSG00000027371	2	127436215	127444565	-1	0	0	0	3	3	0	35	44	22	0	24		
ENSMUST00000028850	ENSMUSG00000079056	2	127456498	127522094	-1	0	28	207	50	0	0	0	2	0	2	3	A2AHT3	
ENSMUST00000028852	ENSMUSG00000027374	2	127587222	127606829	1	62	38	136	128	48	25	13	32	13	19	24		Q99N87
ENSMUST00000028853	ENSMUSG00000027375	2	127633226	127656695	-1	0	0	0	16	0	0	0	0	0	0	0		O09198
ENSMUST00000028854	ENSMUSG00000027375	2	127633226	127656695	-1	14	13	26	73	22	11	0	0	0	0	1		O09198
ENSMUST00000028855	ENSMUSG00000027376	2	127526473	127541467	-1	40	8	90	89	39	24	0	0	0	0	0		Q3UUY6
ENSMUST00000028856	ENSMUSG00000027377	2	127704386	127729932	-1	13	10	18	46	14	10	0	0	0	0	0		Q91X49
ENSMUST00000028857	ENSMUSG00000027378	2	127740732	127788897	-1	13	10	13	0	11	5	3	7	3	11	14	A2APS1	
ENSMUST00000028858	ENSMUSG00000027379	2	127801122	127831865	-1	5	4	13	56	8	8	53	142	86	69	36	A2APR8	
ENSMUST00000028859	ENSMUSG00000027380	2	127838876	128123873	1	13	11	33	15	11	5	0	0	1	0	0		Q9DBS4
ENSMUST00000028864	ENSMUSG00000027386	2	128862981	128897034	1	17	0	38	65	16	6	2	4	2	0	3		Q501P1
ENSMUST00000028866	ENSMUSG00000027387	2	128926268	128944077	-1	4	5	12	52	17	5	5	40	18	29	20		Q9JJ48
ENSMUST00000028874	ENSMUSG00000027395	2	129100995	129126594	1	4	4	22	18	11	2	0	0	0	0	9	A2AP84	
ENSMUST00000028880	ENSMUSG00000027397	2	129198764	129211616	1	7	1	3	52	19	7	152	439	528	94	625		Q61609
ENSMUST00000028881	ENSMUSG00000027398	2	129364570	129371139	-1	10	3	13	33	13	11	1910	42144	3984	24747	12735		P10749
ENSMUST00000028882	ENSMUSG00000027399	2	129299610	129309972	-1	4	5	3	6	5	4	1	7	2	26	7	Q3U0Y6	P01582
ENSMUST00000028883	ENSMUSG00000027400	2	129686565	129699844	-1	14	12	9	12	19	8	0	0	0	0	1	O35852	
ENSMUST00000028888	ENSMUSG00000027403	2	130112416	130154232	1	0	0	79	0	23	0	0	0	0	0	0	Q8BM11	
ENSMUST00000028890	ENSMUSG00000027405	2	130274430	130279313	1	2	0	34	0	0	0	0	47	23	118	8	A2APD7	
ENSMUST00000028892	ENSMUSG00000027406	2	130279309	130284547	-1	7	9	33	46	11	5	308	1011	382	379	403	Q91VA7	
ENSMUST00000028897	ENSMUSG00000027408	2	130390775	130397574	-1	17	14	28	115	35	10	0	2	0	0	1		Q9Z100
ENSMUST00000028898	ENSMUSG00000027409	2	130405259	130406074	1	0	0	0	2	0	0	0	0	0	0	0	Q9DA59	
ENSMUST00000028900	ENSMUSG00000027411	2	130424339	130444269	1	18	14	16	23	14	4	398	627	405	95	324	G3X8X7	
ENSMUST00000028902	ENSMUSG00000027416	2	143078473	143081713	1	6	3	3	2	7	5	0	0	0	0	0	Q548U4	Q9JIE3
ENSMUST00000028905	ENSMUSG00000027419	2	143546156	143816285	1	31	32	189	40	60	21	0	2	0	0	1	Q547J8	P21661
ENSMUST00000028907	ENSMUSG00000027420	2	143826528	143863173	-1	5	19	26	107	19	0	0	0	0	0	0		A2AMT1
ENSMUST00000028909	ENSMUSG00000027423	2	144250123	144270906	-1	9	3	10	21	0	6	288	1641	455	741	466		Q9D8U8
ENSMUST00000028910	ENSMUSG00000027424	2	144270663	144281227	1	33	37	169	45	59	19	5	25	4	3	22		Q9CXC3
ENSMUST00000028911	ENSMUSG00000027425	2	144368983	144407676	1	13	9	27	20	17	10	102	157	156	26	133		Q8CID0
ENSMUST00000028914	ENSMUSG00000027427	2	144527718	144541995	1	75	64	240	120	67	24	117	489	215	108	170		Q921X6
ENSMUST00000028915	ENSMUSG00000027428	2	144542265	144550869	-1	7	8	9	6	7	5	6	72	8	73	28	A2AN96	O88851
ENSMUST00000028916	ENSMUSG00000027429	2	144556229	144590749	1	0	0	0	28	7	0	433	574	535	185	242		Q9D662
ENSMUST00000028917	ENSMUSG00000027430	2	144599897	144768758	1	2	0	13	39	2	3	23	97	21	112	42		Q9DD18
ENSMUST00000028918	ENSMUSG00000027431	2	144823656	144824415	1	7	2	2	6	8	3	0	0	0	0	0		Q9DAH1
ENSMUST00000028921	ENSMUSG00000027433	2	147012996	147078000	1	7	7	9	95	14	3	459	1723	984	377	685		Q9DBR1
ENSMUST00000028926	ENSMUSG00000027438	2	148693985	148732467	-1	0	35	28	114	0	0	0	0	0	0	0		P28663
ENSMUST00000028928	ENSMUSG00000027439	2	148681023	148692949	1	18	22	30	72	30	15	215	996	440	144	316		Q4VBD9
ENSMUST00000028931	ENSMUSG00000027442	2	148798785	148805595	1	2	0	3	0	0	3	0	0	0	0	0		P32766
ENSMUST00000028932	ENSMUSG00000027443	2	148789361	148793546	1	0	2	0	0	7	0	0	0	0	0	0		Q9DAN8
ENSMUST00000028933	ENSMUSG00000027444	2	148782009	148785937	1	2	1	5	3	1	0	0	0	0	0	0		Q8VII3
ENSMUST00000028934	ENSMUSG00000036958	2	148768609	148771497	-1	2	0	2	5	4	4	0	0	0	0	0	Q7M731	Q9D269
ENSMUST00000028935	ENSMUSG00000027445	2	148835147	148838738	1	2	0	3	3	1	1	0	0	0	0	0		Q9Z0H6
ENSMUST00000028937	ENSMUSG00000027446	2	148846711	148865038	-1	2	1	2	2	6	0	1	0	0	1	0	Q9D264	
ENSMUST00000028938	ENSMUSG00000027447	2	148871722	148875692	-1	8	3	5	75	4	6	4728	9648	3488	11545	3397		P21460
ENSMUST00000028944	ENSMUSG00000027452	2	150618105	150668500	-1	70	52	289	150	74	46	41	63	35	10	117	Q569W4	Q99NB1
ENSMUST00000028948	ENSMUSG00000027454	2	150905400	150931280	1	3	6	6	31	5	0	17	56	23	57	19		Q9CZ15
ENSMUST00000028949	ENSMUSG00000027455	2	151494182	151511414	1	0	0	0	0	0	0	197	481	266	333	181		Q9CZ44
ENSMUST00000028950	ENSMUSG00000027456	2	151572622	151590005	1	17	9	15	9	10	6	2	11	3	18	10	Q3UN51	Q99JZ0
ENSMUST00000028951	ENSMUSG00000027457	2	151590549	151632593	-1	3	31	90	0	33	0	0	0	0	0	0		Q80U23
ENSMUST00000028955	ENSMUSG00000027460	2	151911210	151945337	1	19	13	32	47	28	15	1	0	3	0	1	Q3V0P7	Q9WVH6
ENSMUST00000028963	ENSMUSG00000027465	2	152293828	152313996	1	5	15	0	42	3	0	3809	4183	3541	550	2297	Q0P648	Q9D9I4
ENSMUST00000028964	ENSMUSG00000027466	2	152316334	152332653	-1	9	8	29	89	7	3	267	170	81	0	16		Q9WUB0
ENSMUST00000028966	ENSMUSG00000027468	2	152485663	152490138	-1	3	4	17	14	11	2	0	0	0	0	0	Q8BVC1	
ENSMUST00000028969	ENSMUSG00000027469	2	152847964	152895321	1	0	0	0	0	0	0	0	0	55	16	0		A2APB8
ENSMUST00000028970	ENSMUSG00000027470	2	152911352	152923068	1	23	18	146	69	43	17	0	0	2	0	0		Q8VCR8
ENSMUST00000028972	ENSMUSG00000027472	2	153008890	153015427	-1	5	6	0	0	0	2	64	156	66	86	48	Q3UKN2	P59048
ENSMUST00000028977	ENSMUSG00000027475	2	153291413	153333390	1	29	28	54	89	37	27	1199	4434	3237	498	2223	Q3UHC4	Q61771
ENSMUST00000028981	ENSMUSG00000027479	2	153741274	153773310	1	38	54	144	94	77	29	964	2745	1525	1575	1100	Q3U4H0	Q61166
ENSMUST00000028982	ENSMUSG00000027480	2	153856188	153871084	-1	11	7	10	4	11	7	0	0	0	0	0		
ENSMUST00000028983	ENSMUSG00000027481	2	153875045	153895270	1	16	7	32	9	8	12	0	0	0	0	0	Q14AV3	Q8C1E1
ENSMUST00000028984	ENSMUSG00000027482	2	154130336	154138356	1	0	0	0	0	14	0	0	0	0	0	0	Q80X83	
ENSMUST00000028985	ENSMUSG00000027483	2	154142880	154149219	1	4	3	4	11	4	0	0	0	0	0	0		P97361
ENSMUST00000028986	ENSMUSG00000027484	2	154162607	154168450	1	7	8	7	6	6	4	0	0	0	0	0		Q9CQX3
ENSMUST00000028987	ENSMUSG00000027485	2	154190818	154220369	1	3	0	2	0	3	0	0	0	0	0	0		Q61114
ENSMUST00000028990	ENSMUSG00000027487	2	154335380	154373010	-1	0	0	0	0	0	4	27	95	46	24	39		Q8BTW8
ENSMUST00000028991	ENSMUSG00000027488	2	154376313	154408099	-1	19	0	11	0	20	5	0	0	0	0	0		Q61234
ENSMUST00000028995	ENSMUSG00000027495	2	172345565	172355749	1	25	13	48	117	31	21	148	279	183	27	138		Q9D8B6
ENSMUST00000028997	ENSMUSG00000027496	2	172356190	172370535	-1	6	4	10	13	3	3	0	0	8	0	0		P97477
ENSMUST00000028999	ENSMUSG00000027499	3	7366669	7445366	1	13	6	7	7	10	5	0	1	0	1	1		P63248

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ENSMUST00000029002	ENSMUSG00000027500	3	8509360	8561606	1	15	14	9	9	15	6	0	0	0	11	0	Q545S4	P55821
ENSMUST00000029005	ENSMUSG00000027502	2	172440556	172469908	1	0	8	22	73	16	16	3959	7573	3385	1320	3016		Q99K95
ENSMUST00000029007	ENSMUSG00000027505	2	172472520	172474331	1	7	2	14	11	13	5	9	58	12	3	31	A2APA5	
ENSMUST00000029013	ENSMUSG00000027509	2	173000117	173015739	1	7	7	10	107	14	2	310	696	296	78	226		Q8C570
ENSMUST00000029014	ENSMUSG00000027510	2	173020498	173034734	1	0	0	0	0	0	0	1511	1779	1264	157	598		Q62176
ENSMUST00000029017	ENSMUSG00000027513	2	173153048	173159273	1	0	68	336	62	19	0	0	1	1	10	1		Q9Z2V4
ENSMUST00000029018	ENSMUSG00000027514	2	173206612	173218923	-1	5	0	0	6	8	2	92	422	102	114	354	A2APF7	
ENSMUST00000029023	ENSMUSG00000027518	2	173522586	173528501	1	4	2	7	2	6	1	0	0	0	0	0		Q9DA42
ENSMUST00000029024	ENSMUSG00000027519	2	173659760	173707343	1	31	0	0	0	38	0	475	1096	719	111	548	Q0PD34	P35285
ENSMUST00000029025	ENSMUSG00000027520	1	63273265	63314576	1	47	45	41	0	48	0	0	0	0	1	1		Q5SS00
ENSMUST00000029030	ENSMUSG00000027524	2	174760619	174784042	1	7	17	8	91	22	4	0	0	0	0	0	A2APU5	P48299
ENSMUST00000029034	ENSMUSG00000052468	3	10179851	10183929	-1	0	5	0	0	6	2	0	0	0	0	0		P24526
ENSMUST00000029038	ENSMUSG00000027528	3	10193621	10197283	-1	0	0	0	0	0	0	0	0	0	0	0		O08716
ENSMUST00000029041	ENSMUSG00000062515	3	10204088	10208576	-1	0	1	6	0	4	0	2	0	0	41	1	Q542H7	P04117
ENSMUST00000029043	ENSMUSG00000027530	3	10244209	10301183	-1	24	14	61	23	18	12	0	0	0	0	0		Q9DAK4
ENSMUST00000029046	ENSMUSG00000027533	3	10012548	10016607	1	6	3	4	37	5	0	237	868	171	744	147	Q497I3	Q05816
ENSMUST00000029047	ENSMUSG00000027534	3	10417817	10440102	-1	2	0	0	0	0	3	10	8	7	15	4		Q8C080
ENSMUST00000029049	ENSMUSG00000027536	3	10366907	10428856	1	94	93	271	140	98	57	8	13	9	4	9		Q9D7F7
ENSMUST00000029053	ENSMUSG00000027540	2	167932057	167979385	1	7	0	74	18	0	28	9410	12738	9548	1041	7986	Q3TZW9	P35821
ENSMUST00000029057	ENSMUSG00000027544	2	168476410	168601657	-1	1	9	0	0	0	0	0	0	0	0	5	B5B2R5	
ENSMUST00000029060	ENSMUSG00000027546	2	168634438	168742409	-1	0	0	0	0	0	0	0	0	0	0	0		O70228
ENSMUST00000029061	ENSMUSG00000027547	2	168748332	168767943	-1	32	22	101	157	56	9	0	0	0	0	0		Q8BX22
ENSMUST00000029069	ENSMUSG00000027552	3	14578641	14606309	1	0	0	0	87	0	0	0	13	0	0	0		Q61502
ENSMUST00000029071	ENSMUSG00000027555	3	14641727	14663002	1	5	7	5	30	9	6	5	9	4	59	16		Q9D6N1
ENSMUST00000029075	ENSMUSG00000027560	2	170731807	170879769	1	42	22	58	710	80	27	1	1	0	0	1		Q91ZM9
ENSMUST00000029076	ENSMUSG00000027559	3	14863512	14872523	1	7	8	20	4	19	2	0	0	0	0	3		P16015
ENSMUST00000029078	ENSMUSG00000027562	3	14886273	14900770	1	6	5	17	115	17	5	18	6	6	47	30		P00920
ENSMUST00000029080	ENSMUSG00000027564	3	17948410	17948959	1	1	1	9	4	1	1	0	0	0	0	0	Q9DAR6	
ENSMUST00000029082	ENSMUSG00000027566	2	180036373	180042433	-1	0	0	0	12	0	0	1203	2540	1040	3246	756	Q542H2	Q9Z2U0
ENSMUST00000029084	ENSMUSG00000027568	2	180499976	180544980	1	35	29	26	126	41	15	0	0	0	0	0	A2ACT4	O88319
ENSMUST00000029085	ENSMUSG00000027569	2	180581304	180586304	1	0	0	0	0	0	0	47	111	28	50	29		Q9DAT2
ENSMUST00000029087	ENSMUSG00000049401	2	180589245	180595836	1	21	12	78	291	37	24	1493	2253	1106	306	1077		Q99PG2
ENSMUST00000029090	ENSMUSG00000027573	2	180710117	180718733	1	3	0	10	37	2	0	719	1915	908	805	657		Q9D7M1
ENSMUST00000029092	ENSMUSG00000027575	2	180967225	180982526	1	9	5	31	6	0	8	319	442	417	69	380		Q9EPJ9
ENSMUST00000029105	ENSMUSG00000027582	2	181364928	181383628	1	0	1	0	212	2	0	12	0	22	9	20		Q8VDM1
ENSMUST00000029106	ENSMUSG00000027583	2	181387762	181459426	-1	28	19	32	37	31	11	0	4	1	1	13		Q8BID6
ENSMUST00000029116	ENSMUSG00000027589	2	181837854	181857461	1	12	0	9	12	8	3	390	1279	476	198	364		Q8BHD8
ENSMUST00000029120	ENSMUSG00000027593	2	154791096	154867261	1	0	0	0	0	0	5	66	0	0	0	0		Q64012
ENSMUST00000029123	ENSMUSG00000027596	2	154791402	155051012	1	0	0	0	0	2	0	0	0	0	0	0		Q03288
ENSMUST00000029124						16	5	26	6	32	5	0	0	0	0	0		
ENSMUST00000029125	ENSMUSG00000027599	3	19131402	19163065	-1	14	14	36	45	24	5	83	337	183	83	117		Q9D7A8
ENSMUST00000029126	ENSMUSG00000027598	2	155133509	155226855	1	10	0	8	37	0	5	1570	3385	2518	816	1245		Q8C863
ENSMUST00000029128	ENSMUSG00000027602	2	155276297	155278073	1	4	0	4	58	3	4	57	115	55	28	14		Q91VR7
ENSMUST00000029129	ENSMUSG00000027601	3	19187327	19220817	1	0	0	0	0	2	0	46	241	28	18	0	F8WI92	
ENSMUST00000029131	ENSMUSG00000027603	2	155490379	155518237	-1	17	10	26	41	30	19	0	0	0	1	0		Q99JP7
ENSMUST00000029132	ENSMUSG00000027606	3	19508595	19610862	1	0	1	0	0	4	3	0	0	0	0	0		Q9CQ94
ENSMUST00000029135	ENSMUSG00000027605	2	155517948	155585724	1	2	6	17	46	17	8	382	847	478	99	222		Q9QXG4
ENSMUST00000029139	ENSMUSG00000060913	3	19644474	19692421	1	15	8	20	15	15	7	0	0	0	0	0	G3X8Y1	
ENSMUST00000029140	ENSMUSG00000027611	2	155751117	155755471	1	0	0	28	24	8	7	20	48	10	19	29		Q64695
ENSMUST00000029141	ENSMUSG00000027612	2	155775342	155818366	1	45	16	64	74	62	26	149	213	98	34	84		Q9R0S2
ENSMUST00000029142	ENSMUSG00000027613	2	155819832	155826925	-1	7	0	12	149	19	8	909	896	596	170	410	Q545K4	O55135
ENSMUST00000029143	ENSMUSG00000074647	2	155827548	155834854	-1	74	49	335	130	93	54	1	3	2	0	5	A2ARK0	
ENSMUST00000029147	ENSMUSG00000027618	2	156123639	156144186	-1	15	9	10	12	12	3	206	477	285	150	190		Q9Z1J3
ENSMUST00000029149	ENSMUSG00000027620	2	156147239	156180238	-1	0	5	0	0	0	0	98	0	503	577	547	Q3U313	Q8VH51
ENSMUST00000029155	ENSMUSG00000027624	2	156420909	156543214	1	0	30	0	0	0	0	0	0	0	0	0	A2AUK5	
ENSMUST00000029158	ENSMUSG00000027628	2	156547584	156568972	1	30	16	43	18	12	14	51	46	29	10	15		Q9D2V5
ENSMUST00000029164	ENSMUSG00000027636	2	156872457	156887192	-1	0	0	9	33	18	2	8	66	0	14	37		Q8R4L0
ENSMUST00000029165	ENSMUSG00000027637	2	156863128	156873563	1	0	0	0	43	0	2	2193	6050	1779	1427	872		Q9CQT9
ENSMUST00000029170	ENSMUSG00000027641	2	157145893	157204534	-1	7	8	17	8	7	3	134	238	220	19	112		Q64701
ENSMUST00000029171	ENSMUSG00000027642	2	157279017	157326319	1	0	0	0	0	0	0	0	0	0	0	14	A2ACG7	
ENSMUST00000029172	ENSMUSG00000027643	2	157329497	157347506	-1	4	4	0	3	6	0	0	0	0	0	0	Q544X5	P16043
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ENSMUST00000029178	ENSMUSG00000027649	2	157737401	157891614	1	24	18	17	24	24	17	450	568	441	199	312		Q9CWL8
ENSMUST00000029179	ENSMUSG00000027650	2	157981803	158028433	-1	32	0	13	43	33	26	175	292	233	57	383		Q91V83
ENSMUST00000029180	ENSMUSG00000027651	2	158028497	158132297	1	24	0	25	0	29	0	480	463	405	81	250		Q9CSU0
ENSMUST00000029183	ENSMUSG00000027654	2	158768093	158786637	1	8	0	14	201	20	16	23	15	28	5	10		Q9D7I8
ENSMUST00000029186	ENSMUSG00000027655	2	158794807	158858214	1	0	0	22	49	36	0	0	0	21	0	0	Q8K1G9	
ENSMUST00000029188	ENSMUSG00000027656	2	163820861	163833146	1	8	4	27	40	16	2	0	0	0	18	8	A2AHD1	
ENSMUST00000029194	ENSMUSG00000027660	3	31095058	31122577	1	0	14	30	0	17	0	0	59	0	0	0		Q60665
ENSMUST00000029196	ENSMUSG00000027661	2	165503787	165519917	1	38	23	190	120	64	17	4	8	5	0	8	A2A4V1	Q8VHD6
ENSMUST00000029199	ENSMUSG00000027663	3	32334792	32366014	-1	107	75	361	642	121	73	72	114	1	0	77	B9EI21	
ENSMUST00000029201	ENSMUSG00000027665	3	32397671	32468486	1	54	42	113	16	47	25	27	57	92	11	82		P42337
ENSMUST00000029203	ENSMUSG00000027667	3	32510259	32520833	1	4	0	0	0	0	0	28	227	83	98	66		Q99KZ6
ENSMUST00000029208	ENSMUSG00000018459	2	165405028	165473230	-1	23	18	47	27	35	10	10	5	0	0	9	Q3UUJ6	Q91Y63
ENSMUST00000029213	ENSMUSG00000027670	2	165393760	165400405	-1	214	221	415	285	309	145	27	40	20	7	40		Q9D611
ENSMUST00000029214	ENSMUSG00000027671	3	32706298	32726973	1	0	3	0	18	0	2	143	198	108	213	166	Q505L1	Q9Z2N8
ENSMUST00000029217	ENSMUSG00000027673	3	32736990	32751566	1	0	0	0	3	5	0	0	3	0	0	4	F8WI84	
ENSMUST00000029222	ENSMUSG00000027676	3	33812362	33844310	-1	5	12	9	7	16	7	0	6	4	3	0		Q9D5Y1
ENSMUST00000029240	ENSMUSG00000027690	3	28697903	28731359	1	4	5	9	6	0	5	0	0	0	0	0		P14246
ENSMUST00000029252	ENSMUSG00000027702	3	30624267	30647869	-1	6	10	9	7	11	7	0	5	0	2	1	Q14B04	Q9DAM1
ENSMUST00000029256	ENSMUSG00000027706	3	30792875	30821263	1	4	7	17	241	18	7	404	1953	828	1959	732		Q8BU14
ENSMUST00000029257	ENSMUSG00000037400	3	35754106	35856276	1	7	9	21	66	15	5	1918	7460	4413	436	2120	Q6DFW5	
ENSMUST00000029259	ENSMUSG00000027709	3	35959312	36000678	-1	17	12	12	83	20	4	22	68	37	59	41		Q99MR8
ENSMUST00000029266	ENSMUSG00000027712	3	36448923	36475894	-1	13	12	22	164	20	8	1021	2356	952	1336	1081		P48036

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000029268	ENSMUSG00000027713	3	36475937	36482299	1	8	7	11	22	7	5	0	2	0	3	2	G3X8Y2	
ENSMUST00000029269	ENSMUSG00000027714	3	36552606	36565727	1	0	0	0	0	0	0	35	221	61	394	51		Q9JHI7
ENSMUST00000029270	ENSMUSG00000027715	3	36564865	36572150	-1	6	6	2	39	14	0	162	334	155	43	73		P51943
ENSMUST00000029271	ENSMUSG00000027716	3	36620482	36690167	-1	17	13	15	23	23	5	0	0	0	0	0	B1ATV3	
ENSMUST00000029273	ENSMUSG00000027718	3	37222759	37232636	-1	11	10	21	18	14	5	0	0	0	0	0	Q5SUE2	Q9ES17
ENSMUST00000029274	ENSMUSG00000027719	3	37063527	37121930	1	1	0	0	0	0	1	0	0	0	0	0	F8WI80	
ENSMUST00000029275	ENSMUSG00000027720	3	37120523	37125959	-1	4	4	6	2	2	2	1	2	0	0	0		P04351
ENSMUST00000029277	ENSMUSG00000027722	3	37419896	37579096	1	0	0	0	0	0	0	1	78	13	30	43	A0A0A0MQ80	
ENSMUST00000029297	ENSMUSG00000027737	3	49892526	50443614	-1	64	44	231	67	59	21	33	191	48	13	130	Q542C8	Q9WTR6
ENSMUST00000029303	ENSMUSG00000063273	3	51415148	51476507	1	0	0	16	0	0	1	80	369	160	79	140	G3X8Y3	
ENSMUST00000029307	ENSMUSG00000027744	3	53488653	53508502	1	110	74	550	132	62	36	1	3	1	1	3	B2RS16	Q6PE84
ENSMUST00000029309	ENSMUSG00000027746	3	53853376	53863830	-1	0	0	0	0	0	0	0	2	4	0	0	H7BWZ1	
ENSMUST00000029311	ENSMUSG00000027748	3	54156035	54318471	1	14	12	15	39	21	5	0	0	0	1	0	Q0VB97	Q9QUQ5
ENSMUST00000029315	ENSMUSG00000027751	3	54692807	54728766	1	5	9	5	20	17	8	215	866	320	166	441	Z4YJG1	
ENSMUST00000029316	ENSMUSG00000027752	3	54728678	54735393	-1	0	0	0	105	0	0	58	122	28	156	57	Q546F8	Q9D753
ENSMUST00000029325	ENSMUSG00000027761	3	60025717	60040160	1	1	1	1	0	0	0	0	0	0	0	0		Q99PG0
ENSMUST00000029326	ENSMUSG00000027762	3	60081869	60087566	1	9	4	3	4	9	2	1	0	0	0	0		Q99MT6
ENSMUST00000029331	ENSMUSG00000027765	3	61002795	61008982	1	14	14	28	0	14	0	178	691	220	14	99	Q544J5	P49650
ENSMUST00000029336	ENSMUSG00000027770	3	62468013	62507004	-1	8	9	16	52	14	7	146	553	236	80	143		Q8VHK9
ENSMUST00000029344	ENSMUSG00000027775	3	67582741	67604237	1	13	14	19	119	13	9	531	1987	702	293	582		Q9DC37
ENSMUST00000029345	ENSMUSG00000027776	3	68690644	68698547	1	0	0	0	0	3	0	0	0	11	0	7	F8WI71	
ENSMUST00000029346	ENSMUSG00000027777	3	68064802	68626481	1	0	4	0	2	5	7	0	0	0	0	8		Q3TI53
ENSMUST00000029347	ENSMUSG00000027778	3	68892499	69004570	-1	0	0	0	0	0	0	7	152	78	58	63		Q8K057
ENSMUST00000029353	ENSMUSG00000027782	3	69067149	69127113	-1	42	40	52	44	36	14	95	549	160	21	243	A0A0B4J1E7	
ENSMUST00000029355	ENSMUSG00000027784	3	69316861	69560802	1	42	36	50	281	66	24	17	53	67	15	81		Q8BHN0
ENSMUST00000029358	ENSMUSG00000027787	3	69721985	69756373	1	47	44	170	83	45	33	15	78	35	113	23		Q99L48
ENSMUST00000029367	ENSMUSG00000027792	3	73635808	73708415	-1	17	10	6	3	10	5	0	0	0	0	0		Q03311
ENSMUST00000029368	ENSMUSG00000027793	3	55045469	55055501	-1	7	7	11	33	10	2	0	0	0	0	0		Q61456
ENSMUST00000029369	ENSMUSG00000027794	3	55182028	55209957	1	17	15	14	29	11	8	0	0	0	0	0		Q9D489
ENSMUST00000029371	ENSMUSG00000027796	3	54755582	54801257	1	41	47	95	89	76	33	0	0	2	1	0	Q3UVC6	Q9JIW5
ENSMUST00000029374	ENSMUSG00000027799	3	55625195	56183701	-1	48	44	54	140	52	26	0	0	0	3	11		Q9EPN1
ENSMUST00000029376	ENSMUSG00000027800	3	57285611	57301988	-1	7	8	9	7	6	9	0	12	6	651	93		Q64302
ENSMUST00000029377	ENSMUSG00000027801	3	57425314	57441677	1	9	5	12	8	11	2	0	0	0	5	0	Q3TMT3	
ENSMUST00000029380	ENSMUSG00000027803	3	57455649	57575910	-1	20	14	28	173	18	0	22	28	21	28	94		Q9EPK5
ENSMUST00000029382	ENSMUSG00000027804	3	79591342	79603650	1	5	0	5	118	5	2	44	344	58	165	85		Q9CR16
ENSMUST00000029385	ENSMUSG00000027808	3	58519817	58525892	-1	4	9	31	181	7	4	3876	9494	3141	971	1904		Q9Z1W5
ENSMUST00000029386	ENSMUSG00000027809	3	79603788	79629500	-1	0	2	0	0	0	0	107	395	255	461	57		Q921G7
ENSMUST00000029387	ENSMUSG00000027810	3	58525821	58557501	1	0	0	5	23	0	1	10	169	67	255	62		Q8BJW6
ENSMUST00000029388	ENSMUSG00000027811	3	79629079	79632820	1	72	69	146	36	46	46	72	101	54	16	51		Q3UUX7
ENSMUST00000029393	ENSMUSG00000056476	3	59005825	59318682	1	8	0	0	0	0	0	0	0	0	0	0		Q8BQM9
ENSMUST00000029400	ENSMUSG00000027820	3	63241537	63386030	1	3	0	0	59	1	3	0	0	0	1	0		Q61391
ENSMUST00000029402	ENSMUSG00000027822	3	63933507	63964768	-1	0	3	7	25	0	0	106	149	50	24	26		Q99J27
ENSMUST00000029404	ENSMUSG00000053825	10	106470310	106933467	1	12	17	18	16	24	5	0	0	0	0	0	B8QI34	
ENSMUST00000029405	ENSMUSG00000027823	3	63976106	64022579	1	46	29	43	134	34	32	133	596	230	305	157	B2RRH9	Q3THK7
ENSMUST00000029406	ENSMUSG00000027824	3	64081642	64105458	1	6	2	6	8	17	2	0	0	0	1	0	G3X8Y6	
ENSMUST00000029414	ENSMUSG00000027828	3	65379655	65392623	-1	8	12	22	67	17	7	1098	3520	1511	1151	939	Q4FK79	Q9DCF9
ENSMUST00000029416	ENSMUSG00000027829	3	65946151	65958249	-1	2	0	0	53	2	0	10	23	8	21	0		Q52KE7
ENSMUST00000029419	ENSMUSG00000027831	3	66053558	66296837	-1	515	546	614	534	717	327	15	60	21	3	26		A1A535
ENSMUST00000029421	ENSMUSG00000027832	3	66219910	66225805	1	15	7	13	15	13	4	0	0	0	0	1		P48759
ENSMUST00000029422	ENSMUSG00000027833	3	66971727	66981771	-1	2	6	2	136	5	7	0	0	0	0	1		P70390
ENSMUST00000029423	ENSMUSG00000027834	3	75557547	75643495	1	73	54	76	332	126	60	6	21	12	29	21		O35684
ENSMUST00000029424	ENSMUSG00000027835	3	75516490	75556856	-1	0	0	0	0	0	0	289	1569	541	963	231	F8WI55	
ENSMUST00000029429	ENSMUSG00000027840	3	104945272	104961921	-1	21	12	37	111	31	17	3	7	13	2	20		O70283
ENSMUST00000029433	ENSMUSG00000027843	3	103859795	103912247	1	9	11	15	0	13	2	334	510	610	304	374		P29352
ENSMUST00000029435	ENSMUSG00000027845	3	103800605	103809444	-1	21	0	0	75	0	22	217	1015	573	47	268		Q8C7W7
ENSMUST00000029438	ENSMUSG00000008730	3	103739815	103791563	-1	2	0	0	0	15	0	0	0	4702	0	2054		O88904
ENSMUST00000029440	ENSMUSG00000027848	3	103722222	103738001	-1	0	0	57	12	5	5	0	0	0	0	0		
ENSMUST00000029441	ENSMUSG00000063260	15	89782393	89841860	-1	10	8	33	73	19	6	0	0	0	0	0	Q059J3	Q9R0N4
ENSMUST00000029444	ENSMUSG00000033014	3	103279293	103358775	1	0	0	0	0	0	0	262	640	566	0	296	E9QP19	
ENSMUST00000029445	ENSMUSG00000027852	3	103058285	103067914	1	42	49	147	94	45	17	529	2164	887	312	531	Q9D091	
ENSMUST00000029446	ENSMUSG00000068823	3	103020426	103058186	1	24	24	46	69	46	21	970	5065	2273	2053	1261	Q3U1S6	Q91W50
ENSMUST00000029447	ENSMUSG00000027854	3	102995708	103008459	1	26	29	138	67	23	20	160	614	262	60	236		Q9CPR7
ENSMUST00000029448	ENSMUSG00000027855	3	102818499	102936100	-1	6	5	21	82	14	1	7	9	11	2	16		Q62209
ENSMUST00000029450	ENSMUSG00000027857	3	102775465	102782718	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4F3	
ENSMUST00000029451	ENSMUSG00000027858	3	102734529	102801513	1	16	13	14	155	18	10	116	438	97	30	199		Q922J6
ENSMUST00000029453	ENSMUSG00000027860	3	102153583	102204693	-1	0	0	0	3	1	0	0	0	0	0	0	F8WI52	Q80Z96
ENSMUST00000029454	ENSMUSG00000027861	3	102086415	102146514	1	17	11	24	2	0	6	0	0	0	0	0		O09161
ENSMUST00000029456	ENSMUSG00000027863	3	101275899	101287939	-1	10	3	6	9	6	0	112	155	53	309	229	Q549Q4	P08920
ENSMUST00000029459	ENSMUSG00000027865	3	100162381	100206981	1	9	7	9	50	13	3	361	1318	535	388	326		Q9DBL2
ENSMUST00000029462	ENSMUSG00000027868	3	99240381	99354259	1	30	24	167	123	32	13	1	2	1	0	10		O70306
ENSMUST00000029463	ENSMUSG00000027869	3	98805504	98814443	-1	11	15	28	16	14	6	1	1	0	0	1		O35469
ENSMUST00000029464	ENSMUSG00000027870	3	98874521	98893239	-1	3	5	8	10	10	3	0	0	0	0	0		Q9NYQ2
ENSMUST00000029465	ENSMUSG00000027871	3	98852194	98859794	-1	8	6	0	5	10	4	0	0	0	0	0	A2AEP8	P24815
ENSMUST00000029469	ENSMUSG00000027876	3	98222156	98236748	1	9	4	6	2	6	7	0	0	0	0	1		Q9D8G5
ENSMUST00000029476	ENSMUSG00000027879	3	97901190	97923276	1	35	29	38	51	29	29	143	619	176	35	100		O08547
ENSMUST00000029477	ENSMUSG00000040322	3	109123149	109168457	1	22	13	39	40	29	10	1222	3441	2306	322	1130		Q8BMD8
ENSMUST00000029478	ENSMUSG00000027880	3	109080469	109116687	1	7	0	1	18	3	0	0	0	0	0	0	B1AUS6	
ENSMUST00000029480	ENSMUSG00000027881	3	108902805	108911727	-1	0	8	40	77	0	0	257	2011	661	248	684		Q80SY5
ENSMUST00000029482	ENSMUSG00000027883	3	108678638	108722309	-1	13	12	25	68	13	4	81	149	169	49	93	Q3UPG3	Q8VDU0
ENSMUST00000029483	ENSMUSG00000027884	3	108653913	108678840	1	3	5	33	18	7	0	0	35	11	0	9		Q99LI2
ENSMUST00000029485	ENSMUSG00000027886	3	108534150	108544723	1	5	3	5	4	9	4	0	0	0	0	0		Q9DAD0
ENSMUST00000029486						18	15	0	0	16	10	0	0	0	0	2		
ENSMUST00000029489	ENSMUSG00000027890	3	108040408	108044894	-1	18	9	43	37	18	5	14	27	7	7	27	Q8R5I6	
ENSMUST00000029490	ENSMUSG00000027893	3	107663118	107696560	-1	9	6	7	57	8	3	268	504	583	67	326		Q80SW1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000029499	ENSMUSG00000027894	3	107467543	107518018	-1	0	81	578	0	0	0	0	18	2	0	6		
ENSMUST00000029502	ENSMUSG00000027896	3	107291230	107312115	1	6	5	6	0	10	2	4	2	3	3	1		Q8R0M8
ENSMUST00000029504	ENSMUSG00000046213	3	107211293	107221732	-1	6	8	10	10	9	14	0	0	0	1	1	B7ZWD6	
ENSMUST00000029507	ENSMUSG00000027900	3	106547798	106575890	1	0	0	0	0	0	0	89	53	20	77	16	Q9D835	
ENSMUST00000029508	ENSMUSG00000027901	3	106482405	106503030	1	7	3	6	50	14	1	102	676	212	82	126		Q91VV4
ENSMUST00000029510	ENSMUSG00000027902	3	106387384	106406182	-1	7	3	4	7	5	2	0	12	0	0	3	Q80W26	
ENSMUST00000029515	ENSMUSG00000027907	3	93520488	93526287	1	12	10	49	63	25	14	34576	97942	26858	82531	19777		P50543
ENSMUST00000029516	ENSMUSG00000027908	3	93468754	93471980	1	25	16	95	19	21	9	0	0	0	0	0		Q9D3P1
ENSMUST00000029520	ENSMUSG00000027912	3	93017810	93019060	-1	4	6	11	87	8	6	0	0	0	0	0	Q9CR91	
ENSMUST00000029521	ENSMUSG00000027913	3	93014205	93015687	-1	0	2	3	19	3	0	0	0	0	0	0	Q6PAI5	
ENSMUST00000029524	ENSMUSG00000103243	3	92685499	92687210	-1	2	1	18	14	1	3	0	0	0	0	0	Q9D731	
ENSMUST00000029527	ENSMUSG00000027919	3	92750148	92752338	-1	5	2	8	23	6	2	0	0	0	0	0	Q9D195	
ENSMUST00000029530	ENSMUSG00000068890	3	92668613	92670315	-1	2	0	5	12	3	1	0	0	0	0	0	Q9D1K4	
ENSMUST00000029531	ENSMUSG00000027923	3	92655650	92656926	-1	1	1	10	17	8	2	0	0	0	0	0	Q9D149	
ENSMUST00000029533	ENSMUSG00000027925	3	92418082	92419396	1	3	3	27	7	4	2	0	0	0	0	0		O70561
ENSMUST00000029535	ENSMUSG00000027927	3	92134997	92142744	-1	8	11	24	7	9	3	0	0	0	0	0		Q9DAE3
ENSMUST00000029540	ENSMUSG00000027931	3	90450591	90465866	-1	25	8	45	535	43	15	0	0	1	8	12	Q2TAY4	P18293
ENSMUST00000029541	ENSMUSG00000027932	3	90385239	90389938	-1	0	0	0	86	0	0	9	27	11	0	2	G3X8Y7	
ENSMUST00000029542	ENSMUSG00000027933	3	90391388	90433622	-1	0	28	61	78	48	0	732	889	605	38	398		Q7TPD0
ENSMUST00000029545	ENSMUSG00000027936	3	90254163	90264125	1	0	0	12	151	6	0	324	292	412	48	186		Q3U182
ENSMUST00000029546	ENSMUSG00000027937	3	90231597	90235838	1	4	0	0	75	5	0	125	891	282	293	183	Q542D4	O88824
ENSMUST00000029547	ENSMUSG00000027938	3	90237500	90243512	-1	2	10	0	0	0	2	0	10	0	0	0		Q9D2A5
ENSMUST00000029548	ENSMUSG00000027939	3	90104132	90212048	1	38	23	41	35	55	26	10	41	25	0	15		Q9D2F7
ENSMUST00000029549	ENSMUSG00000027940	3	90072649	90100902	1	10	8	27	69	0	0	912	2179	1165	80	723	Q58E70	P21107
ENSMUST00000029551	ENSMUSG00000027942	3	90051636	90068347	1	57	49	84	60	55	31	50	510	107	38	165		
ENSMUST00000029552	ENSMUSG00000027942	3	90051636	90068347	1	1	0	2	2	2	2	5	4	14	0	16		Q8R092
ENSMUST00000029553	ENSMUSG00000042520	3	90000140	90052628	-1	3	3	3	4	5	1	127	151	112	25	111		Q80X50
ENSMUST00000029559	ENSMUSG00000027947	3	89864059	89913196	-1	35	23	142	205	43	21	3120	4964	6712	283	4181		P22272
ENSMUST00000029562	ENSMUSG00000027950	3	89746195	89764632	-1	37	30	110	144	61	23	15	22	25	2	19		Q9ERK7
ENSMUST00000029563	ENSMUSG00000027951	3	89715022	89753446	1	12	0	0	2	0	0	666	0	796	0	593		Q99MU3
ENSMUST00000029564	ENSMUSG00000027952	3	89454541	89469013	1	6	7	68	15	7	0	209	267	168	113	113		Q9D1G2
ENSMUST00000029565	ENSMUSG00000027953	3	89268246	89270570	-1	0	0	7	60	4	2	149	138	85	110	91		Q9CXK4
ENSMUST00000029566	ENSMUSG00000027954	3	89271733	89281142	-1	0	7	0	32	0	2	0	0	0	0	13		P52793
ENSMUST00000029567	ENSMUSG00000027955	3	79884533	79946280	1	53	0	80	58	0	13	1	11	4	6	9		Q3UPI1
ENSMUST00000029568	ENSMUSG00000027956	3	79812564	79852773	-1	0	4	4	4	4	4	0	2	0	5	0		Q8VEH0
ENSMUST00000029569	ENSMUSG00000027957	3	116669470	116712831	-1	19	29	56	45	21	14	231	365	264	70	185		Q8R1T4
ENSMUST00000029570	ENSMUSG00000089911	3	116631164	116662677	-1	5	6	9	44	6	5	757	2638	1285	850	772		P70187
ENSMUST00000029571	ENSMUSG00000027959	3	116594982	116631004	1	58	57	79	49	44	18	108	311	206	60	145		
ENSMUST00000029573	ENSMUSG00000027961	3	116562973	116583134	1	12	14	7	14	26	13	7	28	8	3	9	Q0VDT4	Q8BGI7
ENSMUST00000029574	ENSMUSG00000027962	3	116109949	116129688	-1	12	13	23	14	24	8	0	4	1	158	62	Q3UPN1	
ENSMUST00000029575	ENSMUSG00000027963	3	116007462	116029017	1	7	9	0	24	5	0	0	0	15	20	14		Q9ES89
ENSMUST00000029587	ENSMUSG00000027967	3	127633135	127635631	1	13	7	21	493	29	8	0	0	0	0	0	Q6GTH9	
ENSMUST00000029588	ENSMUSG00000027968	3	127536714	127553349	-1	9	11	17	31	19	6	40	250	108	240	123		Q05CL8
ENSMUST00000029598	ENSMUSG00000027973	3	124400989	124426040	-1	5	7	4	6	9	10	0	0	0	0	0	B9EHI3	
ENSMUST00000029602	ENSMUSG00000027977	3	123526166	123690853	-1	0	0	68	0	6	0	1	0	0	0	3	E9PZJ4	
ENSMUST00000029603	ENSMUSG00000027978	3	123446913	123506597	1	12	16	22	260	16	10	0	1	0	0	0		O08762
ENSMUST00000029610	ENSMUSG00000027984	3	131233419	131272101	-1	11	5	15	27	9	7	85	212	63	63	129		Q61425
ENSMUST00000029611	ENSMUSG00000027985	3	131110471	131224356	1	0	0	0	78	54	0	17	0	19	3	10	Q3TYB0	P27782
ENSMUST00000029623	ENSMUSG00000027995	3	83836272	83841767	-1	22	13	35	137	42	13	2057	7055	3090	671	2193	G3X8Y8	
ENSMUST00000029624	ENSMUSG00000027994	3	129914960	129970206	-1	0	4	6	34	6	0	74	174	87	94	107		Q810S1
ENSMUST00000029625	ENSMUSG00000027996	3	83766321	83774316	1	13	8	12	148	8	7	0	0	0	6	8	Q3UI35	P97299
ENSMUST00000029626	ENSMUSG00000027997	3	129901425	129914103	1	6	4	5	42	5	4	953	1946	1024	1925	225	Q3TPJ9	O08738
ENSMUST00000029628	ENSMUSG00000027998	3	83055522	83072355	1	0	0	0	0	0	0	113	82	0	248	21	F8WI31	
ENSMUST00000029629	ENSMUSG00000027999	3	129878606	129895825	1	3	6	6	45	5	0	22	22	15	22	28		Q9EPR2
ENSMUST00000029630	ENSMUSG00000028001	3	83026076	83033627	1	7	7	7	6	18	0	0	0	0	131	0		E9PV24
ENSMUST00000029632	ENSMUSG00000028003	3	82892579	82903973	-1	38	35	30	49	34	12	0	1	1	1	2	B2RUR5	Q9JI60
ENSMUST00000029633	ENSMUSG00000028004	3	82538383	82548084	-1	0	8	8	6	16	0	0	0	0	0	0		P97295
ENSMUST00000029635	ENSMUSG00000028005	3	82032006	82074689	-1	11	0	13	8	12	0	0	0	3	20	15		O54865
ENSMUST00000029639	ENSMUSG00000028007	3	117781647	117868936	-1	0	0	6	29	7	0	4	0	2	10	11	F8WI30	
ENSMUST00000029641	ENSMUSG00000028008	3	81982290	82021233	1	0	0	0	3	2	3	0	0	0	0	0		Q9R0Y1
ENSMUST00000029643	ENSMUSG00000028010	3	129824912	129831396	-1	0	0	7	96	0	0	18	18	27	0	31		Q9CY66
ENSMUST00000029644	ENSMUSG00000028013	3	133310110	133378235	1	0	0	0	6	0	0	62	264	81	74	60		Q91VM9
ENSMUST00000029645	ENSMUSG00000028011	3	81957090	81976202	-1	6	2	6	0	7	6	3	1	1	0	0	Q8VCW3	P48776
ENSMUST00000029648	ENSMUSG00000028012	3	129804408	129822587	-1	0	0	0	0	0	3	0	0	0	0	0	Q80XL3	
ENSMUST00000029649	ENSMUSG00000028015	3	81932601	81956725	1	14	8	37	19	13	3	68	311	103	81	97		Q8BM88
ENSMUST00000029650	ENSMUSG00000028016	3	133091840	133110988	1	11	6	41	38	12	5	637	3153	1201	2332	629		Q9D168
ENSMUST00000029651	ENSMUSG00000028018	3	132981752	133092033	-1	0	0	3	0	3	0	52	102	44	6	25		Q5RL51
ENSMUST00000029652	ENSMUSG00000028019	3	81036416	81214040	1	4	5	0	340	18	12	0	0	0	0	0		Q8CI19
ENSMUST00000029653	ENSMUSG00000028017	3	129677565	129755316	-1	21	20	46	53	34	20	0	6	0	1	6		P01132
ENSMUST00000029654	ENSMUSG00000028020	3	80843599	80913660	-1	0	0	0	0	0	0	0	0	0	0	0		P48168
ENSMUST00000029657	ENSMUSG00000028023	3	129199878	129219591	1	0	2	4	34	4	1	0	3	1	1	0	G3X8Y9	
ENSMUST00000029658	ENSMUSG00000028024	3	129269175	129332720	-1	4	5	0	8	4	8	0	0	1	4	0	Q52JJ6	P16406
ENSMUST00000029662	ENSMUSG00000028028	3	127670310	127780527	-1	0	0	0	0	0	0	195	485	558	38	591	E9QNX4	
ENSMUST00000029663	ENSMUSG00000028029	3	132660499	132684370	-1	4	9	10	6	7	4	104	656	228	1182	188	Q3UZG4	
ENSMUST00000029664						12	7	5	56	6	15	5	0	5	0	0		
ENSMUST00000029665	ENSMUSG00000028031	3	132085292	132180304	1	40	35	119	159	39	24	2	14	1	0	2		Q9QYZ8
ENSMUST00000029666	ENSMUSG00000028032	3	131564768	131643671	1	25	13	29	60	24	13	181	257	192	64	217	Q3U647	Q60967
ENSMUST00000029667	ENSMUSG00000028033	1	21398403	21961942	-1	10	18	40	0	20	0	2	1	2	0	4		Q9JK45
ENSMUST00000029669	ENSMUSG00000028035	3	152178511	152210302	-1	3	0	2	0	3	0	11	17	12	24	25		Q9D832
ENSMUST00000029670	ENSMUSG00000028036	3	151796502	151837630	-1	16	18	21	132	26	21	0	0	0	0	0	Q60I90	P43117
ENSMUST00000029671	ENSMUSG00000028037	3	151730922	151749960	-1	36	39	203	46	34	21	1	77	3	46	72		Q8BV66
ENSMUST00000029673	ENSMUSG00000028039	3	89313899	89322965	-1	16	13	18	122	15	9	0	0	0	0	0		O08545
ENSMUST00000029674	ENSMUSG00000028040	3	89333390	89338028	-1	10	8	26	90	30	12	1	9	0	3	8	Q3UQB5	O08542
ENSMUST00000029676	ENSMUSG00000028041	3	89338542	89349996	-1	0	0	0	17	0	0	2412	2782	1625	246	1221		O88839

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000029677	ENSMUSG00000028042	3	89377644	89394776	-1	0	0	0	146	22	0	1152	1699	1797	398	1201	Q5BJ24	Q64321
ENSMUST00000029679	ENSMUSG00000028044	3	89415472	89418383	-1	5	9	7	27	14	5	97	121	70	369	89		P61025
ENSMUST00000029682	ENSMUSG00000028047	3	89215180	89226837	1	0	0	0	0	0	0	77	15	92	15	27		Q05895
ENSMUST00000029684	ENSMUSG00000028049	3	89177473	89182765	1	0	0	0	62	0	0	430	553	287	0	283		O35609
ENSMUST00000029686	ENSMUSG00000028051	3	89146074	89160196	-1	25	13	49	225	38	11	1	1	0	0	2	B2RRB5	O88705
ENSMUST00000029692	ENSMUSG00000028057	3	88716838	88731049	1	0	2	0	10	8	0	602	800	463	576	266		P70426
ENSMUST00000029694	ENSMUSG00000028059	3	88607454	88648052	1	11	0	23	219	53	20	1180	3267	2231	179	1863		Q60875
ENSMUST00000029696	ENSMUSG00000028060	3	88685803	88712924	1	9	10	13	91	23	4	448	1553	891	142	901		Q3TCX3
ENSMUST00000029698	ENSMUSG00000028062	3	88549819	88553074	-1	0	0	0	1	3	2	402	555	360	1380	258		Q9JHS3
ENSMUST00000029699	ENSMUSG00000028063	3	88480147	88509956	-1	3	0	20	21	29	14	138	106	82	77	442		P48678
ENSMUST00000029700	ENSMUSG00000028064	3	88435959	88461182	-1	6	0	12	38	7	0	4409	3705	4637	398	4269		Q62178
ENSMUST00000029707	ENSMUSG00000028069	3	88043108	88055993	1	6	6	0	0	0	13	14	46	14	204	48		Q3TFK5
ENSMUST00000029708	ENSMUSG00000028070	3	88056520	88058495	-1	10	3	12	138	11	3	170	368	137	77	132		Q8K4Z3
ENSMUST00000029709	ENSMUSG00000028071	3	87846755	87855722	1	74	44	296	101	60	13	37	118	30	8	79	Q5D0E4	Q9QXK9
ENSMUST00000029711	ENSMUSG00000005640	3	87796951	87816101	1	37	23	69	104	56	22	0	0	0	0	0		Q9WTL4
ENSMUST00000029712	ENSMUSG00000028072	3	87778244	87795162	-1	20	16	32	81	35	6	0	0	0	0	0		Q3UFB7
ENSMUST00000029714	ENSMUSG00000028073	3	87747890	87824306	-1	0	0	0	9	0	0	0	0	3	0	10		Q8VIK5
ENSMUST00000029717	ENSMUSG00000028076	3	86995834	86999441	-1	0	7	0	4	11	0	13	117	29	28	30		
ENSMUST00000029719	ENSMUSG00000028078	3	86786151	86920852	-1	0	0	0	376	9	3	0	0	0	0	0		Q6PGN3
ENSMUST00000029722	ENSMUSG00000028081	3	86137940	86142702	-1	9	7	15	104	21	6	2222	9423	3999	19741	3105	Q564F3	P97351
ENSMUST00000029726						0	0	0	0	0	0	14	12	0	16	28		
ENSMUST00000029727	ENSMUSG00000028086	3	84815268	84979198	1	3	6	17	2	7	3	0	0	0	4	0		Q8VBV4
ENSMUST00000029729	ENSMUSG00000028088	3	97628804	97655282	1	32	5	28	368	19	19	1038	2094	1028	165	510		P97872
ENSMUST00000029730	ENSMUSG00000028089	3	97560742	97610203	-1	22	22	24	53	27	13	90	200	133	22	95		Q9CXF7
ENSMUST00000029738	ENSMUSG00000028096	3	96868281	96905346	-1	20	23	45	22	40	17	1	62	20	35	47		Q8BS95
ENSMUST00000029740	ENSMUSG00000028098	3	96727664	96791638	1	6	4	11	60	13	2	1003	3177	1483	958	853		Q9D0C1
ENSMUST00000029741	ENSMUSG00000028099	3	96711490	96727628	-1	0	0	0	17	24	3	429	933	544	135	396	B2RX77	Q9D483
ENSMUST00000029742	ENSMUSG00000028100	3	96706067	96708562	-1	6	0	24	18	14	15	0	11	0	0	13		Q9CWD3
ENSMUST00000029744	ENSMUSG00000090210	3	96645584	96664519	1	3	18	0	13	25	3	0	0	0	0	1	E9Q6R1	
ENSMUST00000029748	ENSMUSG00000015947	3	96282909	96293969	-1	13	17	35	23	24	16	61	286	67	672	273		P26151
ENSMUST00000029752	ENSMUSG00000028107	3	95739976	95760206	-1	0	0	0	0	0	0	156	240	188	37	264		Q3UQ84
ENSMUST00000029753	ENSMUSG00000028108	3	95734147	95739569	-1	15	0	0	57	0	0	643	480	528	126	598	F8WI14	
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ENSMUST00000029759	ENSMUSG00000028114	3	123368297	123386108	-1	11	10	10	23	19	6	58	257	132	60	113		Q3UIK4
ENSMUST00000029761	ENSMUSG00000028116	3	123006206	123035015	-1	7	3	4	0	6	3	0	0	0	0	0		Q9JJW5
ENSMUST00000029766	ENSMUSG00000028121	3	122294136	122530191	1	29	19	57	209	35	22	33	33	23	8	82		Q9QZK2
ENSMUST00000029769	ENSMUSG00000028124	3	122245557	122270732	1	11	18	26	37	19	6	718	1324	646	108	259	Q4FJZ6	O09172
ENSMUST00000029770	ENSMUSG00000028127	3	121758774	121815302	-1	13	5	11	33	11	2	42	155	72	29	90		P55096
ENSMUST00000029771	ENSMUSG00000028128	3	121723537	121735048	1	10	6	1	149	14	7	4	18	9	6	8		
ENSMUST00000029772	ENSMUSG00000005774	3	94954075	94961561	1	0	16	3	0	17	11	28	0	0	0	25		Q9JL61
ENSMUST00000029773	ENSMUSG00000053931	3	121426497	121458207	1	18	15	36	151	40	13	8	10	7	223	148		Q9DAW9
ENSMUST00000029777	ENSMUSG00000028132	3	121201761	121283098	-1	16	9	10	22	11	2	0	0	0	0	0		Q8CGF5
ENSMUST00000029780	ENSMUSG00000028134	3	119718742	119784466	-1	8	7	12	31	10	2	96	396	186	119	159		Q91Z31
ENSMUST00000029783	ENSMUSG00000028136	3	94497544	94582716	-1	30	25	61	39	43	23	1165	4346	2450	207	1626		Q3UHD6
ENSMUST00000029784	ENSMUSG00000028137	3	94478295	94492198	1	25	17	43	47	25	12	0	3	5	0	7		Q8CIN6
ENSMUST00000029785	ENSMUSG00000028139	3	94464983	94480341	-1	2	0	3	2	0	0	0	4	0	0	1		Q3KNY5
ENSMUST00000029786	ENSMUSG00000028140	3	94443318	94451130	1	22	23	53	169	36	17	175	644	281	183	210	Q14B21	Q99N94
ENSMUST00000029794	ENSMUSG00000028148	3	94342099	94347352	1	19	11	20	8	13	11	0	0	0	0	0		Q9CQJ0
ENSMUST00000029795	ENSMUSG00000028150	3	94372794	94398276	1	17	15	49	50	23	10	0	1	1	5	9		
ENSMUST00000029796	ENSMUSG00000028149	3	138925902	139075201	-1	11	0	0	35	0	0	118	1393	555	0	81	E9Q6Q4	
ENSMUST00000029800	ENSMUSG00000028152	3	138742195	138907905	1	0	0	0	69	0	0	0	497	27	0	2		P62080
ENSMUST00000029803	ENSMUSG00000028156	3	138526179	138559696	1	19	17	19	19	13	15	171	671	208	924	258	Q3TK95	P63073
ENSMUST00000029804	ENSMUSG00000005813	3	138458956	138489515	-1	15	14	26	49	15	5	233	588	322	234	229	Q4VAA9	Q8BP48
ENSMUST00000029805	ENSMUSG00000028158	3	138089854	138144968	-1	18	19	15	16	8	9	22	0	0	15	0		O08601
ENSMUST00000029806	ENSMUSG00000028159	3	137931007	137981545	-1	40	0	69	23	36	36	291	1447	536	549	453	Q3UK44	Q9QXT1
ENSMUST00000029810	ENSMUSG00000053897	3	135825279	135888572	1	0	0	12	126	9	6	0	5	0	0	2		Q91W10
ENSMUST00000029812	ENSMUSG00000028163	3	135584655	135691547	-1	0	15	0	0	0	0	209	183	318	26	168		P25799
ENSMUST00000029814	ENSMUSG00000028164	3	135485611	135571404	1	7	13	10	31	16	7	176	702	290	92	326		
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ENSMUST00000029817	ENSMUSG00000028167	3	135281221	135304426	1	0	0	0	0	0	0	0	0	0	0	0		Q8JZV9
ENSMUST00000029822	ENSMUSG00000028172	3	134829007	134934579	1	21	16	28	171	19	8	0	0	0	0	0		P47937
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ENSMUST00000029825	ENSMUSG00000028175	3	159495433	159529955	1	0	0	0	6	0	6	0	0	8	0	12		Q8CIG0
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ENSMUST00000029833	ENSMUSG00000028182	3	155093434	155194280	1	7	1	0	0	10	2	0	0	0	0	0		Q14DL3
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ENSMUST00000029838	ENSMUSG00000028187	3	146505956	146521429	-1	6	5	4	115	13	5	91	569	220	441	115		Q7TND5
ENSMUST00000029839	ENSMUSG00000028188	3	146457196	146499753	-1	0	1	4	2	3	2	16	67	15	3	5		Q9D5R4
ENSMUST00000029840	ENSMUSG00000028189	3	146449795	146465849	1	4	0	0	30	0	0	0	0	0	0	0		Q8R242
ENSMUST00000029842	ENSMUSG00000028191	3	145922804	145934356	1	7	3	17	40	10	8	1781	4219	2351	636	1705	B7ZWE5	Q9Z0H7
ENSMUST00000029845	ENSMUSG00000028194	3	145758675	145894277	1	23	24	15	154	25	10	0	0	0	0	1		Q9CWS0
ENSMUST00000029846	ENSMUSG00000028195	3	145646976	145649981	-1	14	6	11	165	17	2	0	0	0	17	25	Q3TX21	P18406
ENSMUST00000029848	ENSMUSG00000028197	3	145292472	145552011	1	22	23	42	19	32	11	0	0	0	1	0		Q30D77
ENSMUST00000029850	ENSMUSG00000028199	3	154596711	154623182	1	2	5	8	36	7	3	6	13	9	8	5		P47199
ENSMUST00000029865	ENSMUSG00000028211	4	11156431	11174379	1	0	23	0	56	15	5	2041	2885	3362	2246	1720	Q3UQK9	Q9QXE4
ENSMUST00000029866	ENSMUSG00000028212	4	11191351	11204779	1	10	0	0	13	0	0	0	0	6	7	0	A2API1	
ENSMUST00000029868	ENSMUSG00000028214	4	11704457	11714752	1	0	11	0	3	15	0	3	3	1	5	11	Q3TH76	P55041
ENSMUST00000029871	ENSMUSG00000028217	4	11758147	11817895	1	5	9	8	2	9	4	0	1	0	6	8		Q9R100
ENSMUST00000029875	ENSMUSG00000028221	4	14864076	14915176	1	6	6	6	109	13	3	103	228	80	107	54		Q9CZX7
ENSMUST00000029876	ENSMUSG00000028222	4	15881264	15908064	1	5	1	9	13	6	1	0	0	0	0	0		P12658
ENSMUST00000029877	ENSMUSG00000028223	4	15917240	15945507	-1	26	23	68	90	19	12	21	66	16	116	32	Q4FJK0	Q9CQ62
ENSMUST00000029879	ENSMUSG00000028224	4	15957925	15992589	1	16	8	7	69	18	6	30	154	51	137	38		Q9R207
ENSMUST00000029881	ENSMUSG00000028226	4	17852893	18119145	1	7	4	1	54	3	4	0	0	0	0	0		Q9WTR0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000029885	ENSMUSG00000028228	4	19519254	19570108	-1	86	63	253	363	97	67	2035	3893	3065	602	1637		Q8BT60
ENSMUST00000029888	ENSMUSG00000028229	4	19575162	19606932	1	2	1	6	0	7	3	93	435	135	51	51		Q9DCV4
ENSMUST00000029891	ENSMUSG00000028232	4	3549041	3574853	-1	9	6	2	26	8	3	36	123	29	102	38		Q9D850
ENSMUST00000029900	ENSMUSG00000028238	4	19876841	19922605	-1	21	13	65	20	23	13	2	0	0	4	0		Q80SY3
ENSMUST00000029905	ENSMUSG00000028240	4	6265612	6275633	-1	25	25	28	26	22	17	0	2	2	0	0		Q64505
ENSMUST00000029907	ENSMUSG00000028243	4	6191098	6221688	1	63	67	337	154	63	40	32	157	81	44	70		Q0KL01
ENSMUST00000029908	ENSMUSG00000028246	4	21931329	21996839	1	0	0	5	3	3	0	0	0	0	0	0		Q3UMF9
ENSMUST00000029909	ENSMUSG00000028247	4	21879673	21912162	1	14	9	98	76	24	15	21	105	24	68	30		Q8BMS4
ENSMUST00000029910	ENSMUSG00000028245	4	6396207	6454271	-1	0	0	0	0	0	0	48	189	103	88	183		O35242
ENSMUST00000029911	ENSMUSG00000028248	4	21847583	21876475	1	8	9	14	18	19	12	103	710	203	441	369	A2AJT5	
ENSMUST00000029912	ENSMUSG00000028249	4	6365650	6408423	1	8	8	8	38	4	4	772	2028	633	2821	628		O08992
ENSMUST00000029915	ENSMUSG00000028251	4	21757382	21767212	-1	48	56	96	109	58	19	31	228	53	163	46		Q9D0B5
ENSMUST00000029919	ENSMUSG00000028255	3	145003817	145032776	-1	14	12	16	15	19	10	0	0	0	0	0		Q9D7Z6
ENSMUST00000029920	ENSMUSG00000028256	3	145118588	145153915	1	0	0	2	29	0	3	0	26	4	12	0		Q9D478
ENSMUST00000029922	ENSMUSG00000028259	4	25199908	25242876	-1	2	0	7	3	0	2	0	0	0	0	0		Q9WTX7
ENSMUST00000029923	ENSMUSG00000068547	3	144952480	144975045	-1	5	9	0	6	13	6	0	0	0	0	0	G3X8Z1	
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ENSMUST00000029927	ENSMUSG00000028264	4	34024874	34050191	-1	2	2	0	178	0	4	0	0	0	0	0	B1AWF2	Q9DA48
ENSMUST00000029929	ENSMUSG00000028262	3	144796559	144819494	-1	22	16	34	26	33	20	0	3	1	1	1	Q9EQR4	
ENSMUST00000029932	ENSMUSG00000056025	3	144729677	144760977	-1	14	9	23	0	14	14	0	0	0	0	0	Q91Z28	
ENSMUST00000029935	ENSMUSG00000028268	3	142560026	142573209	1	0	4	0	0	0	0	0	0	0	0	0		Q61107
ENSMUST00000029936	ENSMUSG00000040264	3	142594847	142619179	1	18	13	22	11	19	9	256	2955	616	1766	1354	A4UUI2	
ENSMUST00000029938	ENSMUSG00000028271	3	142765045	142783606	1	4	3	5	20	9	11	374	1884	721	2566	497	Q3ULN2	P62915
ENSMUST00000029941	ENSMUSG00000028273	3	142239590	142395696	-1	29	15	77	28	28	11	779	2188	1401	186	1012		Q8CI51
ENSMUST00000029942	ENSMUSG00000028274	4	33310311	33502614	1	0	0	0	63	5	0	37	157	88	83	33	Q9DCC1	
ENSMUST00000029944	ENSMUSG00000028277	4	33031416	33052363	1	3	0	4	4	2	5	121	151	201	148	132	B1AWT7	
ENSMUST00000029946	ENSMUSG00000028278	4	32983037	33022180	1	66	21	112	0	15	25	0	0	0	0	0	B1AWT3	
ENSMUST00000029947	ENSMUSG00000028280	4	33132521	33163588	1	20	17	18	16	28	12	0	0	0	0	0		P56475
ENSMUST00000029948	ENSMUSG00000052430	3	141837136	142169425	-1	13	18	9	5	15	8	0	0	0	0	0	B2RRZ4	P36898
ENSMUST00000029950	ENSMUSG00000028282	4	32615451	32653265	1	17	0	0	67	29	0	0	28	25	25	0		Q9WUF3
ENSMUST00000029955	ENSMUSG00000028287	4	39450295	39451776	1	8	4	2	6	9	1	0	0	0	0	0	Q14AA6	
ENSMUST00000029964	ENSMUSG00000028289	4	28813131	28967499	1	34	0	228	40	41	27	0	0	0	0	0		Q61772
ENSMUST00000029968	ENSMUSG00000028292	4	34614957	34660167	1	0	0	0	14	0	8	28	210	82	222	77		Q3U186
ENSMUST00000029970	ENSMUSG00000028293	4	34663257	34687438	-1	17	26	36	438	38	14	13	152	49	70	41		Q61420
ENSMUST00000029971	ENSMUSG00000028294	4	34688559	34730206	-1	4	8	24	15	26	10	0	0	0	0	0		Q6PE87
ENSMUST00000029972	ENSMUSG00000028295	4	34768664	34778423	-1	1	0	0	6	0	1	51	176	63	190	19		Q9CQQ0
ENSMUST00000029975	ENSMUSG00000028298	4	34893779	34907370	1	4	0	1	3	4	0	0	0	0	0	0	A0A0F7RQH1	P01216
ENSMUST00000029987	ENSMUSG00000028307	4	49535995	49549546	-1	7	6	22	10	4	3	0	0	2	34	0	Q3UER1	Q91Y97
ENSMUST00000029989	ENSMUSG00000028309	4	49632006	49656887	1	0	13	0	0	0	0	618	2097	1088	345	893		Q5DTM8
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ENSMUST00000029995	ENSMUSG00000028314	4	52596274	52612430	1	0	8	15	9	7	5	0	0	0	0	0	Q9D2F8	
ENSMUST00000029999	ENSMUSG00000028318	4	45018583	45036565	1	4	3	0	3	4	0	19	4	21	55	0		Q8K202
ENSMUST00000030003	ENSMUSG00000028322	4	45316613	45342732	-1	7	1	2	35	0	5	50	154	28	26	52		Q7TQK4
ENSMUST00000030010	ENSMUSG00000015243	4	53030787	53159895	-1	58	37	104	133	78	46	1020	1870	2695	112	1573		P41233
ENSMUST00000030011	ENSMUSG00000028327	4	45848664	45887008	1	0	0	0	6	0	0	0	4	0	2	0	Q9DBN1	
ENSMUST00000030013	ENSMUSG00000028329	4	46155347	46196311	-1	3	0	0	24	0	0	92	485	224	376	88		Q64267
ENSMUST00000030014	ENSMUSG00000028330	4	46138613	46172403	1	13	7	16	36	27	15	748	2004	1125	820	545		Q3UYV9
ENSMUST00000030015	ENSMUSG00000028331	4	46376505	46389437	-1	0	0	0	14	2	0	3	6	11	17	7		Q562D6
ENSMUST00000030018	ENSMUSG00000028334	4	46489248	46503632	1	2	1	8	71	19	8	219	257	162	192	216	Q99J77	
ENSMUST00000030021	ENSMUSG00000028337	4	46536937	46602202	-1	38	29	75	0	38	0	784	1422	168	0	41	B1AVH4	Q8C0P5
ENSMUST00000030025	ENSMUSG00000028341	4	48045153	48086447	1	26	18	9	161	24	17	0	0	0	0	9		Q9QZB6
ENSMUST00000030028	ENSMUSG00000028343	4	48193323	48279558	-1	6	5	8	113	12	5	302	1109	366	160	230		Q9D1Q6
ENSMUST00000030029	ENSMUSG00000028344	4	48279760	48431954	1	53	23	98	67	56	29	43	115	86	16	63	A2AM57	
ENSMUST00000030030	ENSMUSG00000028345	4	48430858	48473459	-1	0	10	0	63	0	0	98	297	153	77	138		Q3URQ0
ENSMUST00000030032	ENSMUSG00000028347	4	48585174	48663131	1	2	2	0	4	3	0	0	2	2	0	2		Q6PFE7
ENSMUST00000030033	ENSMUSG00000028348	4	48663514	48673502	1	9	5	13	11	15	8	0	0	0	0	0		A2AMM0
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ENSMUST00000030039	ENSMUSG00000028354	1	174501825	174822729	1	43	30	63	235	41	28	0	0	0	0	0		Q9JL04
ENSMUST00000030041	ENSMUSG00000028356	4	63143275	63154799	-1	8	5	20	15	11	3	140	757	185	242	178		Q07456
ENSMUST00000030042	ENSMUSG00000028357	4	63165634	63172131	-1	0	0	0	27	4	5	0	0	0	0	0		Q9D2Z8
ENSMUST00000030043	ENSMUSG00000028358	4	62965573	63139708	1	4	4	10	22	7	2	0	0	0	1	0	R4GMK9	
ENSMUST00000030044	ENSMUSG00000039196	4	63344560	63348163	1	5	4	14	10	10	0	635	797	430	872	199		Q60590
ENSMUST00000030047	ENSMUSG00000028362	4	63831308	63861347	-1	6	9	7	15	12	10	19	56	18	34	39	Q544U1	P32972
ENSMUST00000030051	ENSMUSG00000028367	4	57943373	57956411	-1	12	10	23	77	12	9	5225	19902	4768	13205	3595		P10639
ENSMUST00000030056	ENSMUSG00000028364	4	63959785	64047015	-1	0	21	0	0	0	0	0	0	0	3	0		Q80YX1
ENSMUST00000030069	ENSMUSG00000028378	4	58965439	58987119	-1	27	18	23	28	31	14	206	487	212	578	131		Q91YR9
ENSMUST00000030074	ENSMUSG00000028381	4	59189257	59222833	1	14	14	61	34	20	17	707	2879	1087	205	815		O88693
ENSMUST00000030076	ENSMUSG00000028382	4	59471868	59549364	-1	0	0	0	41	0	10	293	0	0	0	309		Q8BHD7
ENSMUST00000030078	ENSMUSG00000028383	4	59581563	59618689	1	4	0	11	34	12	0	106	383	161	311	154		Q2TPA8
ENSMUST00000030080	ENSMUSG00000028385	4	59805840	59904737	1	88	54	185	91	96	44	46	149	83	24	176		Q8CE50
ENSMUST00000030081	ENSMUSG00000028386	4	59905126	59915056	-1	21	15	69	46	35	19	0	0	0	0	0		Q8CA03
ENSMUST00000030087	ENSMUSG00000028391	4	62448653	62470896	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JHB4
ENSMUST00000030088	ENSMUSG00000028392	4	62480053	62497298	1	0	0	0	41	0	0	1	0	0	0	0	B2RT02	Q80YW5
ENSMUST00000030090	ENSMUSG00000028393	4	62509169	62519918	-1	0	0	8	37	4	9	53	39	20	10	46		P10518
ENSMUST00000030091	ENSMUSG00000028394	4	62522649	62525068	-1	18	12	0	0	35	0	51	270	104	275	71		
ENSMUST00000030095	ENSMUSG00000008305	4	72117142	72200919	-1	0	0	0	0	1	0	34	0	36	3	38	Q5SQA3	
ENSMUST00000030101	ENSMUSG00000028396	4	73939371	73950846	-1	3	1	6	3	8	2	0	0	0	0	0	Q14C20	
ENSMUST00000030102	ENSMUSG00000028397	4	74242497	74405860	1	20	3	13	57	18	0	239	925	564	243	422		Q8VCD7
ENSMUST00000030103	ENSMUSG00000028398	4	75277354	75278305	-1	4	1	3	125	8	4	88	263	98	139	71		Q9CQ00
ENSMUST00000030110	ENSMUSG00000028403	4	82798738	82859958	-1	45	33	122	72	54	28	59	180	78	33	133		Q9D270
ENSMUST00000030117	ENSMUSG00000028409	4	40736542	40757923	-1	5	4	37	18	4	3	441	1606	687	1553	373		Q3UKJ7
ENSMUST00000030118	ENSMUSG00000028410	4	40722150	40737149	1	7	0	0	38	6	3	156	891	290	769	200	Q5NTY0	P63037
ENSMUST00000030119	ENSMUSG00000028411	4	40682382	40703194	-1	55	47	251	78	62	31	0	45	0	7	0		Q7TQC5
ENSMUST00000030121	ENSMUSG00000028413	4	40804602	40854005	-1	14	10	35	35	18	23	1699	2593	1945	158	1091	Q3U478	P15535

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000030122	ENSMUSG00000028415	4	40920052	40931395	1	0	3	5	7	2	1	0	0	0	0	1		O35679
ENSMUST00000030124	ENSMUSG00000028417	4	53779705	53788712	1	19	11	24	194	27	11	2	7	0	3	0	Q2TB09	Q62282
ENSMUST00000030125	ENSMUSG00000028416	4	40936398	40948294	-1	12	8	13	0	0	2	488	1614	666	202	485	F6TCF9	
ENSMUST00000030127	ENSMUSG00000028420	4	53826045	53862019	1	79	76	9784	2183	152	141	625	2796	994	348	577		Q9DAV9
ENSMUST00000030128	ENSMUSG00000028419	4	40948407	40965303	1	7	6	9	16	9	5	811	2989	1000	3328	731		Q9D7S9
ENSMUST00000030131	ENSMUSG00000060206	4	54945048	55083563	1	1	12	0	6	0	0	0	0	0	0	5	B1AWL4	
ENSMUST00000030133	ENSMUSG00000028423	4	40970906	41025993	1	16	21	22	20	21	4	16	84	43	5	27		B1AY10
ENSMUST00000030134	ENSMUSG00000028426	4	55350043	55392237	1	17	13	24	35	17	9	418	1135	517	106	361		P54728
ENSMUST00000030136	ENSMUSG00000028427	4	41033074	41048139	-1	33	13	47	20	53	27	0	0	0	0	0	Q5DX24	O54794
ENSMUST00000030138	ENSMUSG00000028430	4	41114427	41124455	-1	31	30	95	73	64	29	183	153	157	28	241		Q8R5K4
ENSMUST00000030140	ENSMUSG00000028431	4	56749680	56802331	-1	44	42	66	97	42	20	115	255	151	98	181		Q7TT37
ENSMUST00000030142	ENSMUSG00000028434	4	56991972	57143437	-1	18	9	2	22	27	12	2	6	3	1	1		Q9JMC8
ENSMUST00000030143	ENSMUSG00000028433	4	41194313	41275144	-1	0	18	0	0	32	0	170	233	281	21	308		Q91VX2
ENSMUST00000030145	ENSMUSG00000028436	4	41291300	41314889	-1	41	24	158	184	51	19	1578	4096	2139	329	1521		Q8BGZ3
ENSMUST00000030148	ENSMUSG00000028438	4	41390745	41464887	-1	0	0	0	3	7	0	14	0	0	0	0		Q6NWW5
ENSMUST00000030152	ENSMUSG00000028441	4	41505009	41517333	-1	2	3	0	0	0	0	0	0	0	0	0		Q2MH31
ENSMUST00000030154	ENSMUSG00000028443	4	41465151	41480926	1	9	1	8	6	2	5	20	63	31	155	16		P56380
ENSMUST00000030158	ENSMUSG00000028447	4	41714798	41723170	-1	0	4	15	16	16	3	623	1062	347	216	238		Q9Z0Y1
ENSMUST00000030163	ENSMUSG00000028451	4	42969604	42983640	1	14	12	98	54	28	10	1	1	1	0	3		Q3V0E1
ENSMUST00000030164	ENSMUSG00000028452	4	42979963	43000507	-1	17	10	28	132	41	10	1819	5909	3349	648	2806		Q01853
ENSMUST00000030165	ENSMUSG00000028453	4	43002343	43010506	-1	0	4	42	44	3	7	138	176	94	4	35		Q9EQR6
ENSMUST00000030169	ENSMUSG00000028455	4	43027690	43031710	-1	12	12	9	31	9	12	4	30	22	0	12		Q99JB2
ENSMUST00000030170	ENSMUSG00000034799	8	71624417	71671757	-1	83	49	180	262	102	46	11	41	7	3	30		Q4KUS2
ENSMUST00000030179	ENSMUSG00000028459	4	43446462	43454628	-1	0	0	3	0	0	0	0	7	0	33	39	Q3UZ35	
ENSMUST00000030180	ENSMUSG00000028460	4	43482081	43483734	-1	8	10	16	9	20	0	9	11	0	7	17		Q8C503
ENSMUST00000030181	ENSMUSG00000028461	4	43492900	43495921	1	2	0	8	32	9	0	22	57	6	21	36		Q9DCC3
ENSMUST00000030183	ENSMUSG00000028463	4	43506966	43513729	1	14	17	17	28	0	0	17	0	0	11	6	Q3UUZ9	Q8VHB5
ENSMUST00000030184	ENSMUSG00000028464	4	43514711	43523765	-1	0	9	47	25	23	0	0	0	0	0	0	A2AIM4	
ENSMUST00000030185	ENSMUSG00000032366	9	67022590	67049406	-1	2	6	0	0	5	2	1	3	2	0	6	Q8BSH3	
ENSMUST00000030187	ENSMUSG00000028465	4	43531519	43562691	-1	52	46	107	129	97	50	32027	24841	41967	1387	31170		P26039
ENSMUST00000030189	ENSMUSG00000028467	4	43566928	43578873	-1	0	0	0	99	26	6	780	677	746	57	446		Q69ZF3
ENSMUST00000030190	ENSMUSG00000028468	4	43578715	43587487	1	5	2	6	0	0	0	12	0	6	0	4		Q8BHT7
ENSMUST00000030191	ENSMUSG00000028469	4	43631935	43651244	1	0	11	35	236	16	12	0	0	0	0	0		Q6VVW5
ENSMUST00000030192	ENSMUSG00000028470	4	43654227	43656466	-1	0	0	0	26	0	0	50	68	29	73	24	Q5M9J2	Q9D0S9
ENSMUST00000030198	ENSMUSG00000028476	4	43875530	43944806	1	29	0	38	0	30	0	495	973	612	174	405		Q9Z0J1
ENSMUST00000030201	ENSMUSG00000028479	4	44034075	44084177	-1	36	26	112	28	53	17	17	35	41	14	16	Q3UW64	
ENSMUST00000030202	ENSMUSG00000028480	4	43957401	43979118	1	9	18	27	178	28	21	8655	7010	8567	2865	5651		Q9CYL5
ENSMUST00000030205	ENSMUSG00000038172	4	83220300	83324255	-1	0	0	0	27	3	3	0	0	0	5	0		Q8BYY4
ENSMUST00000030206	ENSMUSG00000028483	4	83417724	83467676	1	0	0	3	6	4	0	16	117	68	16	16		Q9D2C9
ENSMUST00000030207	ENSMUSG00000028484	4	83455680	83486459	-1	4	2	9	11	9	4	313	1118	532	154	393		Q99JF8
ENSMUST00000030212	ENSMUSG00000028488	4	85205126	85639195	1	37	53	19	89	39	23	12	8	6	0	7		Q62420
ENSMUST00000030216	ENSMUSG00000028492	4	86444641	86558328	-1	9	4	30	13	0	3	0	0	0	0	0	B1AXP3	
ENSMUST00000030221	ENSMUSG00000028497	4	88396144	88438928	-1	0	0	0	4	0	3	150	0	84	117	0		A2AKM2
ENSMUST00000030243	ENSMUSG00000028518	4	105029874	105109890	-1	28	42	48	28	46	15	0	1	0	0	0		Q8BRK8
ENSMUST00000030245	ENSMUSG00000028520	4	103230445	103290863	-1	0	0	0	0	0	0	0	0	0	0	0		Q9D5Q8
ENSMUST00000030247	ENSMUSG00000028522	4	103114390	103165754	1	28	0	0	0	25	4	1053	1366	157	9	0		Q5UAK0
ENSMUST00000030248	ENSMUSG00000028523	4	102986379	103005594	1	4	2	6	0	3	0	5	3	1	0	0	B7ZNE0	Q9D5I4
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ENSMUST00000030257	ENSMUSG00000028532	4	100776675	101029220	1	41	39	96	487	67	18	0	0	0	0	2		Q6PDJ1
ENSMUST00000030261	ENSMUSG00000028536	4	118526999	118530228	1	4	4	11	29	5	1	0	0	0	0	0		Q9CQM1
ENSMUST00000030263	ENSMUSG00000028538	4	117932154	118134914	-1	17	6	26	131	12	7	21	14	19	0	26		P97325
ENSMUST00000030265	ENSMUSG00000028540	4	117888643	117892032	-1	9	7	11	6	14	6	0	0	0	0	12		Q9CR25
ENSMUST00000030266	ENSMUSG00000028541	4	117869260	117883487	-1	0	0	0	42	6	0	0	4	0	4	20	B1ASJ2	Q9Z2Y2
ENSMUST00000030269	ENSMUSG00000028542	4	117834506	117875198	1	1	0	2	43	8	2	0	0	0	0	0		P28571
ENSMUST00000030274	ENSMUSG00000028545	4	111415006	111460298	1	6	4	0	26	10	1	0	2	0	4	0		Q8C6D4
ENSMUST00000030279	ENSMUSG00000028550	4	99193934	99259787	1	28	21	31	191	25	10	8	8	16	0	49		Q811C2
ENSMUST00000030280	ENSMUSG00000028553	4	99030954	99046111	1	3	5	13	0	2	2	0	0	0	9	0	Q3UEF5	Q9R182
ENSMUST00000030281	ENSMUSG00000028552	4	109280268	109387817	1	0	0	0	0	0	0	0	411	128	144	102		
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ENSMUST00000030285	ENSMUSG00000028558	4	109234485	109254571	1	7	0	0	13	9	0	0	0	0	0	0	Q3TQS0	
ENSMUST00000030286	ENSMUSG00000028556	4	98936671	99120915	-1	1	1	1	0	17	0	0	0	1	0	126	A2A9M5	
ENSMUST00000030288	ENSMUSG00000028559	4	109061145	109202272	-1	0	0	0	0	0	0	0	0	0	0	0		A2A8Z1
ENSMUST00000030289	ENSMUSG00000028560	4	98923810	98935543	1	0	10	0	80	11	15	71	132	185	79	135		Q8BJQ2
ENSMUST00000030290	ENSMUSG00000061859	4	98395785	98719603	1	3	4	12	15	5	4	0	4	2	0	10		Q63ZW7
ENSMUST00000030292	ENSMUSG00000028563	4	98355370	98383306	-1	0	0	0	0	0	0	0	0	0	0	0		Q99MB3
ENSMUST00000030296	ENSMUSG00000028567	4	108834601	108862127	1	2	5	9	11	1	6	387	1301	505	853	363		Q9CQU0
ENSMUST00000030299	ENSMUSG00000052520	4	96628773	96664154	-1	23	35	97	36	21	6	0	0	0	4	0	Q3TNC5	O54749
ENSMUST00000030303	ENSMUSG00000052914	4	96516138	96553661	-1	15	20	15	12	24	16	0	0	0	27	7		O54750
ENSMUST00000030305	ENSMUSG00000028571	4	96027534	96077546	-1	209	171	265	117	232	123	5	16	9	6	9	Q3UNV4	
ENSMUST00000030306	ENSMUSG00000028572	4	95967240	96025413	1	0	0	0	49	7	4	69	253	156	29	21		Q8BIL5
ENSMUST00000030309	ENSMUSG00000028575	4	94907267	94928843	-1	2	5	4	2	2	0	0	2	0	0	0		Q9D9V2
ENSMUST00000030311	ENSMUSG00000028576	4	94614491	94693229	1	4	3	3	15	0	5	17	98	36	64	17		Q8BKE9
ENSMUST00000030313	ENSMUSG00000028578	4	94500081	94556796	-1	4	2	0	13	7	0	95	221	120	50	65		Q8VDY9
ENSMUST00000030315	ENSMUSG00000028580	4	130663321	130781564	1	0	23	0	13	0	9	181	418	209	0	247		Q80U78
ENSMUST00000030316	ENSMUSG00000028581	4	130913125	130936141	1	1	0	22	5	0	0	1149	0	993	0	623	F8WH95	
ENSMUST00000030317	ENSMUSG00000028583	4	143267431	143299564	-1	4	2	3	13	3	1	1	4	0	8	10		Q62011
ENSMUST00000030320	ENSMUSG00000028582	4	108619940	108634123	1	0	4	0	46	12	8	357	527	599	34	432		Q8BRN9
ENSMUST00000030323	ENSMUSG00000028589	4	144418189	144438772	-1	8	3	10	9	8	1	0	0	0	0	0		Q4KKZ1
ENSMUST00000030326	ENSMUSG00000028591	4	144391674	144408464	-1	16	9	17	12	15	6	0	0	0	0	0	Q9D2F1	
ENSMUST00000030328	ENSMUSG00000028593	4	144519822	144529353	1	13	2	22	6	15	8	0	0	0	0	0		Q8BM81
ENSMUST00000030332	ENSMUSG00000028597	4	108400390	108406961	-1	5	7	10	78	14	6	0	1	0	11	1	Q3TNK3	Q99LJ6
ENSMUST00000030336	ENSMUSG00000028599	4	145213463	145246870	-1	64	44	393	134	53	40	6610	9818	5468	844	5648	Q545P4	P25119
ENSMUST00000030339	ENSMUSG00000028602	4	145267137	145315164	-1	22	13	58	0	25	11	19	12	10	4	0	A1L3C9	Q60846

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000030340	ENSMUSG00000028603	4	108043839	108144998	-1	7	0	6	8	6	4	1521	4189	1914	2108	1401		P32020
ENSMUST00000030345	ENSMUSG00000028607	4	107903981	107923610	-1	19	4	10	28	20	7	464	736	467	88	234		P52825
ENSMUST00000030346						0	0	5	5	0	0	35	41	23	118	18		
ENSMUST00000030347						0	0	0	0	0	0	16	15	12	80	11		
ENSMUST00000030348	ENSMUSG00000028609	4	107879755	107887424	1	9	8	9	12	9	4	315	1083	293	1150	196		P61327
ENSMUST00000030356	ENSMUSG00000028613	4	107802261	107876840	1	0	0	26	22	16	11	6	36	54	5	21	B1AXJ4	
ENSMUST00000030357	ENSMUSG00000028614	4	107367784	107416346	1	0	0	0	53	0	6	30	33	30	2	20	J3QMD9	
ENSMUST00000030360	ENSMUSG00000028617	4	107233514	107253532	-1	2	4	15	50	8	5	95	162	88	28	86		Q8R2U7
ENSMUST00000030361	ENSMUSG00000028618	4	107178399	107200996	1	7	6	0	69	6	6	0	173	149	381	253		Q9QY73
ENSMUST00000030362	ENSMUSG00000028619	4	107134155	107179116	-1	1	0	0	37	0	0	10	8	12	11	19		Q8R2M0
ENSMUST00000030364	ENSMUSG00000028621	4	107066988	107088268	1	0	0	19	11	0	0	0	7	1	0	2		B1AS42
ENSMUST00000030365	ENSMUSG00000028622	4	107055874	107066868	-1	9	0	0	50	12	6	69	155	47	21	100		Q921S7
ENSMUST00000030367	ENSMUSG00000061887	4	106910701	107049694	1	4	5	31	29	11	5	133	348	328	39	126		Q9D032
ENSMUST00000030372	ENSMUSG00000028626	4	121039385	121055322	1	37	19	54	177	37	20	1	2	6	0	0	I7HJR1	
ENSMUST00000030375	ENSMUSG00000028629	4	120921196	120925017	-1	14	0	0	9	12	0	0	70	0	0	15		Q9CXP9
ENSMUST00000030376	ENSMUSG00000028631	4	120696138	120748612	-1	28	23	76	128	54	24	0	0	0	0	1		Q9JK97
ENSMUST00000030381	ENSMUSG00000028633	4	120539868	120570276	-1	9	9	22	50	24	15	29	56	34	23	61		P70698
ENSMUST00000030384	ENSMUSG00000028635	4	120161206	120167360	1	11	8	28	58	11	7	0	0	0	0	0		P22389
ENSMUST00000030385	ENSMUSG00000028636	4	119418530	119422420	-1	11	0	0	265	13	11	17	37	17	23	15		Q8VDG5
ENSMUST00000030391	ENSMUSG00000028640	2	172549593	172558622	1	3	0	0	105	10	3	0	0	0	0	0	A0A023UF19	Q61312
ENSMUST00000030393	ENSMUSG00000028641	4	119232915	119248975	1	0	9	6	16	20	0	0	0	6	2	0	A6PW84	
ENSMUST00000030394	ENSMUSG00000028642	4	119205107	119218217	-1	13	7	21	11	13	9	0	0	0	0	0	Q9D4Y8	
ENSMUST00000030395	ENSMUSG00000028643	4	119195306	119201298	1	0	0	0	53	0	0	155	345	121	338	97		Q99LQ4
ENSMUST00000030396	ENSMUSG00000028644	4	119175457	119190011	-1	269	216	1130	419	314	199	2	8	14	5	30	E9QKE5	
ENSMUST00000030398	ENSMUSG00000028645	4	119108711	119137983	1	13	9	29	73	24	10	4178	5512	3920	475	3194		P17809
ENSMUST00000030399	ENSMUSG00000028646	4	123917446	123936997	1	0	9	0	15	4	0	676	2180	1023	141	523		Q99K70
ENSMUST00000030400	ENSMUSG00000028647	4	123904832	123912269	1	7	1	10	31	5	0	45	178	51	66	26		Q9EQS3
ENSMUST00000030401	ENSMUSG00000028648	4	123712710	123718202	-1	0	0	0	6	4	2	349	719	323	1371	207		Q99LY9
ENSMUST00000030404	ENSMUSG00000028651	4	123127115	123139951	-1	9	7	5	12	11	9	88	123	63	167	65		Q9QZH3
ENSMUST00000030407	ENSMUSG00000028654	4	122995652	123002485	1	17	17	0	361	40	7	0	6	0	0	0	Q3UIE0	P10166
ENSMUST00000030408	ENSMUSG00000028655	4	122946850	122961188	-1	17	5	22	9	11	0	27	76	28	5	15		Q9DA75
ENSMUST00000030412	ENSMUSG00000028657	4	122836242	122859175	1	0	0	0	29	11	10	2595	10364	2796	1116	2147	Q3U6J9	O88531
ENSMUST00000030417	ENSMUSG00000006699	4	137319696	137357720	-1	2	3	13	10	3	8	26	354	62	54	44		P60766
ENSMUST00000030420	ENSMUSG00000028661	4	136929419	136956816	-1	40	23	91	354	77	28	0	0	0	0	0		O09127
ENSMUST00000030427	ENSMUSG00000028668	4	136003368	136021763	-1	35	29	96	73	27	24	1495	4922	3121	1425	1996		Q8CB77
ENSMUST00000030432	ENSMUSG00000028672	4	135946448	135962617	1	2	0	4	19	0	6	2138	3514	1713	487	1201		P38060
ENSMUST00000030434	ENSMUSG00000028673	4	135920735	135940311	1	99	77	154	315	143	86	1971	3678	2009	762	1629		Q99LJ1
ENSMUST00000030436	ENSMUSG00000028675	4	135870918	135873850	-1	9	4	14	40	5	3	878	5004	1320	2210	838		Q9CR73
ENSMUST00000030438						0	4	0	0	0	0	19	182	0	0	20		
ENSMUST00000030439	ENSMUSG00000028677	4	117271463	117497052	-1	21	13	55	57	16	2	10	17	3	2	8		Q6PDX6
ENSMUST00000030443	ENSMUSG00000028681	4	117096075	117116101	1	34	0	72	204	0	0	0	0	0	0	0		O35595
ENSMUST00000030446	ENSMUSG00000028684	4	116989965	116994413	-1	64	34	213	126	60	32	492	769	343	515	250		P70697
ENSMUST00000030451	ENSMUSG00000028688	4	116794310	116807640	-1	6	6	20	37	8	3	74	179	126	104	97		Q9D2E2
ENSMUST00000030452	ENSMUSG00000028689	4	116708509	116751206	1	3	5	0	8	0	0	0	19	0	0	0	A8Y5M7	
ENSMUST00000030453	ENSMUSG00000028690	4	116702279	116708406	-1	61	55	182	89	63	29	17	36	31	19	45		Q9CZD0
ENSMUST00000030454	ENSMUSG00000028691	4	116685544	116700822	1	0	1	0	0	0	0	35	233	51	0	66	B1AXW6	
ENSMUST00000030455	ENSMUSG00000028692	4	116636510	116651680	-1	1	2	11	44	6	0	2296	4881	1996	1692	1628	Q540D7	Q9JII6
ENSMUST00000030456	ENSMUSG00000028693	4	116601052	116627941	-1	9	6	12	28	9	8	7	13	11	16	30	B1AU75	
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ENSMUST00000030460	ENSMUSG00000034042	4	116557658	116593882	1	32	25	13	72	36	25	919	3639	1212	484	1185		Q6NZP2
ENSMUST00000030461	ENSMUSG00000028696	4	116507549	116538243	1	6	9	13	0	6	4	34	0	11	0	0		P28575
ENSMUST00000030464	ENSMUSG00000028698	4	116221618	116303056	1	26	23	43	20	27	11	0	11	5	3	5	Q3UXE9	Q64143
ENSMUST00000030465	ENSMUSG00000028699	4	116161869	116167601	-1	8	11	20	20	14	9	0	0	0	0	0		Q99J59
ENSMUST00000030469	ENSMUSG00000028701	4	116132406	116151338	-1	50	36	94	230	47	21	2	11	7	2	2	A2A8F6	Q9D6I9
ENSMUST00000030471	ENSMUSG00000028703	4	116075269	116097043	1	13	11	46	25	22	5	525	488	383	120	272		Q8K1C9
ENSMUST00000030474	ENSMUSG00000028706	4	116032842	116053876	-1	8	3	27	3	0	8	0	13	0	0	11	A0A0A0MQ81	
ENSMUST00000030475	ENSMUSG00000028706	4	116032842	116053876	-1	0	0	0	24	14	2	83	146	95	38	78		Q9CZ57
ENSMUST00000030477	ENSMUSG00000028709	4	115828092	115836185	1	141	115	580	173	93	69	126	885	325	58	262	B1ASD4	Q8BJG4
ENSMUST00000030480	ENSMUSG00000028712	4	115563649	115579015	1	28	61	363	283	33	53	3	7	3	1	8	Q91WU1	
ENSMUST00000030486	ENSMUSG00000028712	4	115563649	115579015	1	72	20	22	47	67	9	0	0	0	0	0	F8WGU9	
ENSMUST00000030487	ENSMUSG00000028715	4	115486200	115496142	-1	15	13	42	14	11	6	0	0	0	0	0		O35728
ENSMUST00000030488	ENSMUSG00000028716	4	115088708	115093899	1	7	0	5	0	12	4	0	0	0	0	0		Q9CQH0
ENSMUST00000030489	ENSMUSG00000028717	4	115056426	115071755	1	9	6	19	44	20	9	8	76	33	11	25	Q3TZH7	P22091
ENSMUST00000030490	ENSMUSG00000028718	4	115000159	115043196	1	12	0	0	78	0	0	34	30	64	6	15	A2AD39	
ENSMUST00000030491	ENSMUSG00000028719	4	114959336	114987241	-1	19	19	30	41	21	12	577	1637	478	597	333		
ENSMUST00000030501	ENSMUSG00000028729	4	118620799	118627776	1	104	86	358	129	124	45	94	398	140	367	118		Q9D903
ENSMUST00000030508	ENSMUSG00000028736	4	139737062	139833528	-1	44	32	62	180	49	41	0	0	0	0	0		P47239
ENSMUST00000030510	ENSMUSG00000028738	4	139653538	139670280	1	3	9	23	57	6	0	0	0	0	0	0		Q925I4
ENSMUST00000030513	ENSMUSG00000028741	4	139347435	139352576	-1	0	0	0	0	0	0	95	243	0	0	0	A2AMV1	
ENSMUST00000030518	ENSMUSG00000028745	4	139192899	139291818	1	7	5	19	11	12	1	2225	995	1069	717	904		P47757
ENSMUST00000030524	ENSMUSG00000041193	4	138799244	138863482	-1	0	9	0	0	0	0	0	0	0	0	0	Q6GTW1	
ENSMUST00000030526	ENSMUSG00000028749	4	138750533	138757626	-1	26	10	38	27	27	12	0	0	0	0	0		Q9QZT4
ENSMUST00000030528	ENSMUSG00000041202	4	138775735	138782046	1	45	51	238	73	64	31	0	1	1	0	1	Q3TYT9	Q9WVF6
ENSMUST00000030530	ENSMUSG00000028750	4	138724792	138746132	1	0	0	0	0	0	0	0	0	0	0	0	A2APR1	
ENSMUST00000030531	ENSMUSG00000028751	4	138877942	138882817	1	7	3	19	0	2	0	0	0	0	0	0	Q3UG05	Q9QUL3
ENSMUST00000030533	ENSMUSG00000028753	4	138565360	138635884	-1	83	55	183	299	116	51	0	1	1	0	0	B1AZ81	A9Z1V5
ENSMUST00000030535	ENSMUSG00000028755	4	138338424	138367992	-1	1	2	10	86	13	4	0	1	1	2	5		P56389
ENSMUST00000030536	ENSMUSG00000028756	4	138313409	138326307	-1	9	2	0	80	16	11	1045	1935	1073	422	700		Q99MQ3
ENSMUST00000030538	ENSMUSG00000028757	4	138304730	138312628	1	20	24	47	74	41	9	724	818	560	168	678		O54734
ENSMUST00000030539	ENSMUSG00000028758	4	138250435	138301967	1	0	3	9	58	0	0	0	0	0	0	3		Q99PW8
ENSMUST00000030541	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	0	0	0	907	2484	1473	234	1272		Q3TEA8
ENSMUST00000030547	ENSMUSG00000028763	4	137468769	137570630	1	43	27	90	397	71	36	1	2	0	5	391	B1B0C7	
ENSMUST00000030551	ENSMUSG00000028766	4	137741733	137796384	-1	8	11	29	57	28	16	0	1	1	2	13		P09242
ENSMUST00000030552	ENSMUSG00000064280	5	21292961	21424677	-1	0	0	0	2	0	0	0	31	4	0	3	G3X8Z3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000030555						6	4	15	12	8	1	0	0	0	0	0		
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ENSMUST00000030560	ENSMUSG00000028776	4	130164454	130175122	-1	3	4	11	25	6	7	0	20	5	3	4		Q99JR5
ENSMUST00000030561	ENSMUSG00000028777	5	17962549	18019834	1	1	3	5	8	0	4	0	0	0	0	0	B2RVZ3	Q3V3I2
ENSMUST00000030562	ENSMUSG00000028778	4	130130217	130139359	-1	0	0	0	54	0	0	0	0	0	0	0		P58307
ENSMUST00000030563	ENSMUSG00000028779	4	130102558	130128135	1	7	8	0	0	0	6	2573	2527	1368	739	912		Q8BFY6
ENSMUST00000030568	ENSMUSG00000028780	5	17574281	17730268	1	6	12	0	24	13	0	0	0	0	13	10		Q62181
ENSMUST00000030571	ENSMUSG00000028782	4	129984870	130022633	1	0	0	0	130	52	0	0	0	0	0	0	H7BWZ2	
ENSMUST00000030572	ENSMUSG00000028785	4	129111570	129122036	-1	0	0	0	0	0	0	0	0	2	0	0		P84075
ENSMUST00000030575	ENSMUSG00000028786	4	129105548	129111626	1	9	2	0	4	0	0	0	0	0	0	0	A2A7R1	
ENSMUST00000030577	ENSMUSG00000028786	4	129105548	129111626	1	0	0	21	0	16	4	0	1	0	0	0	A2A7R2	
ENSMUST00000030578	ENSMUSG00000028788	4	129811219	129850003	1	0	0	0	23	0	0	325	520	473	218	258		O70274
ENSMUST00000030581	ENSMUSG00000028789	4	128930233	128962442	-1	0	0	0	0	19	0	19	10	15	0	7	B2RSR5	Q8BVM4
ENSMUST00000030583	ENSMUSG00000028792	4	128991958	129011529	1	2	0	4	80	2	2	181	209	212	166	153		Q9WTP6
ENSMUST00000030584	ENSMUSG00000028793	4	129058271	129085886	1	0	0	0	32	10	0	0	0	18	0	0		A2A7Q9
ENSMUST00000030585	ENSMUSG00000028794	4	128755364	128769298	1	21	19	60	37	27	14	3	1	0	0	11		Q3V1N9
ENSMUST00000030586	ENSMUSG00000028795	4	129619274	129623947	-1	7	0	0	2	6	0	291	382	181	547	104		Q8CEG5
ENSMUST00000030588	ENSMUSG00000028796	4	128654702	128752881	1	24	0	0	25	0	0	0	0	0	0	0		Q9QWH1
ENSMUST00000030606	ENSMUSG00000059713	4	135412308	135433853	-1	51	44	219	105	65	28	105	129	98	8	112		Q9JKK0
ENSMUST00000030610	ENSMUSG00000028807	4	129353628	129378116	-1	60	66	196	104	76	37	15	24	9	4	35		Q9CWH1
ENSMUST00000030613	ENSMUSG00000028809	4	135320484	135353321	-1	0	0	0	0	3	0	0	51	95	0	0	E9QKA4	
ENSMUST00000030614	ENSMUSG00000028813	4	127927592	127970951	-1	47	35	87	579	87	46	2	0	0	1	0	B1AYM9	
ENSMUST00000030622	ENSMUSG00000028821	4	134930898	134937548	1	5	4	8	63	11	4	1680	4320	1829	5760	1396		Q9D198
ENSMUST00000030623	ENSMUSG00000028820	4	127021324	127037013	1	5	2	4	159	11	3	746	1673	1149	137	905		Q8VIJ6
ENSMUST00000030626	ENSMUSG00000028822	4	134897849	134915024	-1	39	22	71	100	40	20	1989	5099	2266	1499	1615	Q52KP1	Q9CXL1
ENSMUST00000030627	ENSMUSG00000028825	4	134864536	134896172	1	11	11	20	13	11	9	4	8	6	2	10		
ENSMUST00000030628	ENSMUSG00000028826	4	134802759	134853345	-1	4	6	10	16	0	0	75	310	211	53	156		Q7TQE6
ENSMUST00000030636	ENSMUSG00000028832	4	134468320	134473843	1	9	9	18	110	7	8	365	740	280	53	151	Q545B6	P54227
ENSMUST00000030637	ENSMUSG00000028833	4	126743750	126753438	-1	29	11	53	145	29	17	248	233	196	27	212		Q9Z0E0
ENSMUST00000030638	ENSMUSG00000028834	4	134315120	134329629	1	13	0	0	9	0	0	0	0	0	0	0	A2A9L4	
ENSMUST00000030642	ENSMUSG00000028837	4	126677630	126709714	1	0	5	8	46	4	0	658	1213	590	2084	414		Q9R1P3
ENSMUST00000030643	ENSMUSG00000028838	4	134356372	134383850	-1	32	23	112	88	51	26	0	1	1	0	3		Q9JKV7
ENSMUST00000030644	ENSMUSG00000028840	4	134243289	134245592	-1	11	6	0	130	0	0	19	34	16	21	20		Q9DB42
ENSMUST00000030645	ENSMUSG00000028841	4	134228041	134238399	-1	20	0	0	52	34	11	0	0	0	0	0	A2A9K7	
ENSMUST00000030651	ENSMUSG00000028843	4	134127406	134128789	-1	0	4	11	42	7	7	8810	9697	4951	4843	3141		Q91VW3
ENSMUST00000030658	ENSMUSG00000028845	4	126322121	126325688	-1	11	9	24	0	0	0	0	0	0	0	0		Q922G7
ENSMUST00000030660	ENSMUSG00000028847	4	126262325	126275883	1	10	4	11	69	21	4	718	1266	614	791	358	Q3U9K9	O55013
ENSMUST00000030661	ENSMUSG00000028848	4	133584362	133591735	1	4	4	6	96	8	11	82	156	72	61	72		Q8VEJ1
ENSMUST00000030662	ENSMUSG00000028850	4	133574745	133584243	1	17	5	22	132	20	7	216	193	133	15	72		Q8BIY1
ENSMUST00000030665	ENSMUSG00000028851	4	133532542	133545996	-1	5	2	16	97	22	7	269	611	325	240	325		O35685
ENSMUST00000030669	ENSMUSG00000028854	4	133369706	133423702	1	29	29	90	181	73	27	1031	1096	1114	53	906	Q3UDC9	Q61165
ENSMUST00000030673	ENSMUSG00000028859	4	126024550	126044440	1	102	152	314	171	100	82	53230	123534	55457	7133	62536		P40223
ENSMUST00000030674	ENSMUSG00000028860	4	133253090	133263113	-1	7	0	24	16	13	4	552	639	318	65	244	A2AE94	
ENSMUST00000030675	ENSMUSG00000028861	4	126046925	126055532	1	4	3	2	76	3	7	69	588	171	146	150		Q9DC71
ENSMUST00000030676	ENSMUSG00000001985	4	125490700	125714173	1	178	174	728	1305	270	130	2	23	9	0	7		B1AS29
ENSMUST00000030677	ENSMUSG00000028862	4	133240818	133252929	1	31	13	60	383	64	22	33	34	22	3	54	A0A0A0MQ82	
ENSMUST00000030683	ENSMUSG00000028864	5	16553495	16620152	1	11	8	6	9	12	8	82	198	187	149	162		Q08048
ENSMUST00000030684	ENSMUSG00000028869	4	125016585	125055380	1	8	10	31	30	8	5	92	426	248	575	198		Q99LH1
ENSMUST00000030687	ENSMUSG00000028871	4	124986430	125009099	1	30	49	287	114	41	16	1	16	2	0	8	B1ASC1	
ENSMUST00000030690	ENSMUSG00000028873	4	124918465	124939311	-1	12	8	5	31	3	7	4	0	0	0	7		Q8BHX3
ENSMUST00000030691	ENSMUSG00000061601	5	14514918	14863459	1	0	0	0	0	0	0	0	0	0	0	0		Q9QYX7
ENSMUST00000030693	ENSMUSG00000028874	4	132974095	133001910	1	13	9	52	30	24	10	8165	25858	10212	1555	8376		P14234
ENSMUST00000030696	ENSMUSG00000028878	4	132899213	132922558	-1	18	20	48	38	28	3	469	1163	580	139	496		Q922G2
ENSMUST00000030698	ENSMUSG00000028879	4	132853501	132884509	-1	6	14	15	101	11	7	298	1059	458	491	386		Q9ER00
ENSMUST00000030702	ENSMUSG00000028882	4	132826929	132843169	-1	7	2	19	26	14	13	177	494	169	103	171		Q8R3G1
ENSMUST00000030709	ENSMUSG00000028885	4	132732966	132757252	-1	10	10	27	72	20	18	18	38	8	21	54	Q3TLX9	P58242
ENSMUST00000030714	ENSMUSG00000028883	5	13125414	13602565	1	13	12	26	9	22	6	0	1	0	3	0		O08665
ENSMUST00000030723	ENSMUSG00000028890	4	124802104	124849800	1	0	0	10	0	0	24	320	925	731	69	444		Q07243
ENSMUST00000030724	ENSMUSG00000028893	4	132492032	132510501	-1	16	23	76	221	40	29	1843	2866	1420	155	1162		P58043
ENSMUST00000030726	ENSMUSG00000028896	4	132331919	132353605	-1	14	0	0	0	24	10	0	25	5	24	106	Q6PFB2	
ENSMUST00000030730	ENSMUSG00000028898	4	132311763	132329538	-1	0	0	0	0	0	0	49	70	21	94	25		Q80VC6
ENSMUST00000030731	ENSMUSG00000028899	4	132274375	132295766	1	154	118	1010	246	119	71	385	1093	321	376	250		Q8VE65
ENSMUST00000030733	ENSMUSG00000028901	4	132221025	132261602	-1	0	0	2	0	0	0	25	58	62	0	41		Q9JL60
ENSMUST00000030734	ENSMUSG00000028902	4	124714776	124732460	1	11	8	11	29	11	6	180	576	252	776	238	Q58E59	Q9D554
ENSMUST00000030738	ENSMUSG00000028907	4	124678160	124693600	-1	22	26	67	115	21	14	84	424	181	548	132		Q9CZJ1
ENSMUST00000030739	ENSMUSG00000028906	4	131923413	132075321	-1	21	8	96	23	27	0	25	31	47	12	77		P48193
ENSMUST00000030741	ENSMUSG00000028909	4	131768457	131838288	-1	0	0	0	0	0	0	0	6	8	0	0		B1AUH1
ENSMUST00000030742	ENSMUSG00000028910	4	131843470	131867786	1	0	1	0	30	3	0	11	19	6	22	13		Q9DCS3
ENSMUST00000030743						22	17	22	16	30	8	39	38	73	0	90		
ENSMUST00000030747	ENSMUSG00000028914	4	141793612	141815976	1	24	13	76	37	24	8	986	1140	762	58	442		Q8C3Q9
ENSMUST00000030751	ENSMUSG00000028917	4	141625734	141664899	-1	17	0	56	0	1	0	15	129	0	0	0	A2ADE0	
ENSMUST00000030757	ENSMUSG00000028920	4	141147913	141204062	1	35	36	55	46	43	14	663	854	837	50	636		Q6PDJ6
ENSMUST00000030760	ENSMUSG00000028923	4	141066512	141078357	-1	13	0	44	56	0	11	1879	2324	1199	225	948		Q9D1J1
ENSMUST00000030763	ENSMUSG00000028926	5	4803391	5420312	-1	0	0	0	13	0	0	7	35	19	0	32		O35495
ENSMUST00000030765	ENSMUSG00000028927	4	140906344	140952586	1	67	54	96	87	78	51	31	50	19	8	72		Q08642
ENSMUST00000030768	ENSMUSG00000028931	4	152390742	152477871	-1	0	8	0	0	0	0	222	171	35	0	23	Q3UPV6	
ENSMUST00000030769	ENSMUSG00000028932	5	21785283	21803787	1	9	11	42	49	16	6	549	1702	764	1923	603	Q8BVQ9	
ENSMUST00000030771	ENSMUSG00000029014	5	21757267	21785251	-1	0	3	0	37	0	3	29	113	125	113	71		P54103
ENSMUST00000030773	ENSMUSG00000028933	5	25689812	25705825	-1	43	34	34	53	43	21	7	25	16	2	23		Q9CX47
ENSMUST00000030775	ENSMUSG00000005045	4	152338651	152390194	1	30	26	9	149	0	0	0	0	0	0	0	E9PYL1	
ENSMUST00000030778	ENSMUSG00000028938	5	25181460	25220297	1	7	0	0	0	3	0	0	0	0	0	0		Q9D4M9
ENSMUST00000030779	ENSMUSG00000028937	4	152178134	152271855	1	0	0	0	0	0	0	43	0	0	0	64		Q91V12
ENSMUST00000030782	ENSMUSG00000028940	4	152158867	152162469	1	22	15	30	47	19	14	0	1	0	0	0		O54792
ENSMUST00000030784	ENSMUSG00000028944	5	24862744	25100642	-1	11	7	27	163	27	4	75	160	110	19	172		Q91WG5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000030785	ENSMUSG00000028943	4	152120331	152152371	-1	6	4	13	5	0	0	2	0	3	0	4		Q9ET47
ENSMUST00000030787	ENSMUSG00000028945	5	24802823	24842624	-1	15	16	9	133	22	9	253	1146	478	641	299	Q540E6	Q921J2
ENSMUST00000030791	ENSMUSG00000028949	5	24590818	24624411	-1	1	1	5	31	0	0	0	0	0	0	9		Q6P9Z1
ENSMUST00000030792	ENSMUSG00000028950	4	152027914	152038568	-1	0	0	2	10	0	0	1	2	0	1	0	Q3U5H1	
ENSMUST00000030795	ENSMUSG00000028953	5	24565345	24577467	-1	32	21	38	43	34	25	463	734	558	356	442		Q99LE6
ENSMUST00000030797	ENSMUSG00000028955	4	151047300	151057963	-1	35	26	83	48	36	11	892	3079	1148	529	820		P63024
ENSMUST00000030799	ENSMUSG00000028958	5	24445458	24447854	-1	4	0	18	62	5	3	456	361	220	48	151		Q9JMG3
ENSMUST00000030800	ENSMUSG00000028959	5	24438440	24445287	-1	0	0	3	42	0	4	193	109	153	44	26	Q8C725	
ENSMUST00000030803	ENSMUSG00000028963	4	150997097	151001810	1	5	1	6	9	5	3	0	0	0	0	1	Q541G7	Q9QZQ3
ENSMUST00000030805	ENSMUSG00000028964	4	150897133	150914437	-1	0	0	0	31	2	0	363	454	246	498	258		Q99LX0
ENSMUST00000030806	ENSMUSG00000063077	4	149176319	149307693	-1	22	27	58	25	21	20	146	292	255	22	201	A2AH75	
ENSMUST00000030808	ENSMUSG00000028965	4	150914562	150946102	1	0	0	0	0	0	0	0	0	0	13	18	Q3U3R1	P20334
ENSMUST00000030811	ENSMUSG00000028967	4	150853919	150868892	1	0	0	5	94	24	1	164	345	291	100	284	Q3TK48	Q99JZ7
ENSMUST00000030813	ENSMUSG00000073705	4	149127121	149137629	-1	6	7	16	22	13	4	12	19	5	31	7		Q9D084
ENSMUST00000030814	ENSMUSG00000028969	5	24418241	24423530	-1	10	8	32	23	25	2	316	737	302	143	244	Q543F6	P49615
ENSMUST00000030815	ENSMUSG00000028971	4	149125034	149126763	-1	7	7	17	19	11	12	0	4	1	0	4		P56469
ENSMUST00000030816	ENSMUSG00000028974	4	149104146	149120647	1	33	33	44	57	38	20	464	624	406	86	276		O54786
ENSMUST00000030817	ENSMUSG00000028972	4	150187015	150201332	-1	8	0	2	5	7	3	0	0	0	0	0		P18761
ENSMUST00000030826	ENSMUSG00000028976	4	150119283	150144169	1	17	18	62	27	27	20	0	0	0	0	0		Q9WV38
ENSMUST00000030830	ENSMUSG00000028980	4	149979475	150009023	-1	0	0	0	68	16	0	131	27	131	27	182	A2A7A7	
ENSMUST00000030834	ENSMUSG00000028978	5	24364810	24384474	1	9	0	27	37	43	0	4	2	2	4	0		P70313
ENSMUST00000030839	ENSMUSG00000028988	4	149518236	149566437	1	17	10	39	34	30	12	873	1577	1102	141	558		Q9JJN6
ENSMUST00000030840	ENSMUSG00000028989	4	148495183	148500460	-1	41	31	52	29	52	28	1	18	9	25	11		Q8R1Q3
ENSMUST00000030841	ENSMUSG00000028986	5	24100605	24160792	1	7	19	18	0	0	0	56	161	87	98	90		Q8BUL5
ENSMUST00000030842	ENSMUSG00000028990	4	149485229	149496668	1	12	9	20	92	20	7	76	188	95	88	65		Q8K3C3
ENSMUST00000030845	ENSMUSG00000028992	4	149467572	149485202	-1	0	0	0	0	0	0	0	5	9	0	0	Q3V449	Q9EPA7
ENSMUST00000030848	ENSMUSG00000028996	4	149449687	149454978	-1	0	0	0	0	1	1	0	0	0	0	0	Q540P4	Q9EPC5
ENSMUST00000030849	ENSMUSG00000028995	5	23915276	24030690	-1	10	20	26	110	28	8	255	523	398	64	245		
ENSMUST00000030851	ENSMUSG00000028998	5	23838944	23844161	-1	7	6	7	30	4	3	642	1879	573	3049	393		Q9D173
ENSMUST00000030852	ENSMUSG00000028999	5	23787711	23820369	1	0	0	50	0	0	13	16	155	59	0	85		Q8BZ36
ENSMUST00000030858	ENSMUSG00000055401	4	148145716	148152140	-1	0	0	0	6	0	0	32	87	18	8	24		Q9QZN4
ENSMUST00000030860	ENSMUSG00000029003	4	148130384	148145699	1	9	12	14	111	9	2	25	16	12	0	14		Q9D752
ENSMUST00000030862	ENSMUSG00000029005	4	148098437	148130698	-1	48	37	200	202	56	17	3	15	19	11	25		Q6PAL1
ENSMUST00000030865	ENSMUSG00000029007	4	148077061	148088031	-1	83	59	208	107	79	45	2016	2912	2326	296	1334		Q9WVK0
ENSMUST00000030868	ENSMUSG00000040254	5	12383385	12588948	1	15	8	16	59	25	10	0	0	0	5	2		Q8BH34
ENSMUST00000030872	ENSMUSG00000029012	5	22486485	22550429	-1	13	0	0	7	12	0	31	150	51	126	35		Q9WUV0
ENSMUST00000030878	ENSMUSG00000029015	5	21810655	21865604	-1	0	0	0	20	4	7	0	0	0	0	0		Q99NH7
ENSMUST00000030879	ENSMUSG00000029016	4	148004259	148038821	-1	0	0	0	0	0	0	0	3	16	0	8	Q3UM91	O35454
ENSMUST00000030882	ENSMUSG00000029017	5	21737141	21757152	1	0	0	0	38	0	3	131	668	199	267	207		Q9CXT8
ENSMUST00000030884	ENSMUSG00000029020	4	147873599	147904704	-1	0	25	35	14	22	0	0	0	24	0	0		Q80U63
ENSMUST00000030886	ENSMUSG00000029022	4	147860778	147868816	-1	0	2	4	20	0	0	161	31	126	9	38	C0KL25	A2A7Y5
ENSMUST00000030893	ENSMUSG00000029027	4	153964449	153975126	-1	23	13	24	45	13	6	127	284	153	41	88		O54788
ENSMUST00000030894	ENSMUSG00000029028	4	154011731	154021513	1	35	31	159	40	42	10	807	909	671	95	534	B1AX98	Q505F5
ENSMUST00000030895	ENSMUSG00000029029	4	154142372	154167420	1	0	2	0	27	0	4	232	168	130	20	85		Q9JM98
ENSMUST00000030896	ENSMUSG00000029030	4	154157485	154160666	-1	5	9	10	19	15	7	3902	5890	2897	1034	2096		Q9DBS2
ENSMUST00000030897	ENSMUSG00000057751	4	154170730	154275713	1	40	18	50	207	52	22	0	0	0	0	6	A0A0A0MQ83	
ENSMUST00000030898	ENSMUSG00000029032	4	154278486	154301676	-1	0	0	0	85	0	2	0	0	0	0	0		Q3U5C8
ENSMUST00000030901	ENSMUSG00000029034	4	155869546	155889103	1	0	0	3	0	9	9	314	524	289	94	149		Q9CWS4
ENSMUST00000030902	ENSMUSG00000039410	4	154316125	154636873	-1	0	0	0	0	0	0	0	0	0	0	0		A2A935
ENSMUST00000030903	ENSMUSG00000029036	4	155740641	155761093	-1	13	14	11	52	32	5	50	36	35	14	97		Q925I1
ENSMUST00000030905	ENSMUSG00000029038	4	155704800	155733879	1	3	0	5	77	3	0	1103	2801	1015	3222	802		Q9CY97
ENSMUST00000030910						1	1	3	1	6	2	0	0	0	0	0		
ENSMUST00000030914	ENSMUSG00000029048	4	155074110	155086382	-1	0	0	0	14	0	0	667	2212	543	521	268		Q9CQU3
ENSMUST00000030915	ENSMUSG00000029049	4	155086577	155145505	1	6	1	8	7	9	2	0	2	4	2	1	A2RTS7	
ENSMUST00000030917	ENSMUSG00000029050	4	155154075	155222592	-1	26	0	0	486	0	0	232	206	618	0	644	B1AUF1	
ENSMUST00000030920	ENSMUSG00000048271	5	28317121	28419239	1	6	3	13	4	7	2	5	52	5	3	5		Q9CXK9
ENSMUST00000030922	ENSMUSG00000029053	4	155260129	155361361	-1	17	15	10	50	3	0	5	7	11	1	25		Q02956
ENSMUST00000030925	ENSMUSG00000029054	4	155384980	155398112	-1	0	0	9	27	0	5	0	0	0	0	0	Q14AH9	P22933
ENSMUST00000030931	ENSMUSG00000029056	4	154964123	154980938	1	0	0	31	64	0	0	124	142	136	14	125		Q80YV4
ENSMUST00000030935	ENSMUSG00000029059	4	154895504	154899135	-1	6	6	12	23	13	6	5	21	4	126	54		Q9DB60
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ENSMUST00000030939	ENSMUSG00000029063	4	155562378	155591001	1	0	23	32	2	0	14	10471	19823	11462	3657	8539		P58058
ENSMUST00000030940	ENSMUSG00000029064	4	155491361	155559269	1	0	0	10	0	0	0	125	1062	0	0	0	Q3TQ70	P62874
ENSMUST00000030942	ENSMUSG00000029066	4	155802878	155809975	1	0	0	0	41	4	7	413	394	236	1297	182		Q9CQL4
ENSMUST00000030944	ENSMUSG00000029068	4	155812489	155824543	1	1	0	18	119	16	0	81	251	371	38	264		Q9JJA7
ENSMUST00000030947	ENSMUSG00000029070	4	155839680	155844088	1	8	2	12	34	0	10	4	4	0	13	15		Q9DBV4
ENSMUST00000030948	ENSMUSG00000029071	4	155847402	155859303	1	0	0	0	0	0	0	64	429	87	37	102		P51141
ENSMUST00000030949	ENSMUSG00000029072	4	155859268	155863362	-1	49	44	289	91	49	26	21	35	29	5	25		Q925D8
ENSMUST00000030950	ENSMUSG00000029073	4	155864723	155869440	-1	0	13	15	27	21	0	36	33	7	0	12		Q8BS40
ENSMUST00000030951						8	4	27	5	10	4	0	0	0	0	0		
ENSMUST00000030952	ENSMUSG00000029075	4	156013843	156016612	1	5	2	14	0	12	3	0	49	0	18	17	B1ASL3	
ENSMUST00000030964	ENSMUSG00000029084	5	43868553	43912375	1	51	66	52	59	70	30	198	413	405	224	311	Q4FJL8	P56528
ENSMUST00000030968	ENSMUSG00000029089	5	48327952	48414294	1	4	3	4	48	6	4	17	80	28	43	19		Q9D3X5
ENSMUST00000030971	ENSMUSG00000029090	5	49959956	50059006	-1	18	21	47	63	32	10	12	15	3	14	44		Q7TT36
ENSMUST00000030973	ENSMUSG00000029086	5	43993620	44102032	-1	0	8	8	0	6	0	0	0	19	0	0		
ENSMUST00000030975						3	0	0	2	2	2	0	0	0	0	0		
ENSMUST00000030980	ENSMUSG00000029097	5	35557313	35575070	-1	13	9	40	43	21	8	82	106	104	13	58		Q9D2Q2
ENSMUST00000030984	ENSMUSG00000029101	5	34949445	35039644	1	7	11	0	22	0	0	4	19	12	0	23		Q8CGE9
ENSMUST00000030985	ENSMUSG00000029102	5	35041509	35048461	1	24	8	57	33	40	24	1	2	0	1	0	Q545J3	Q9R098
ENSMUST00000030986	ENSMUSG00000029103	5	35091501	35105766	-1	10	14	26	50	25	9	218	540	301	266	308	Q52KI7	P55302
ENSMUST00000030991	ENSMUSG00000059866	5	34496087	34513991	-1	0	0	0	0	0	0	15	0	0	0	0	Q80VZ7	
ENSMUST00000030992	ENSMUSG00000029110	5	34336289	34355629	1	0	4	0	0	0	0	190	1202	239	107	269		Q9QZS2
ENSMUST00000030993	ENSMUSG00000029111	5	33897916	33936413	-1	8	12	36	102	22	14	363	510	403	73	306		Q8BG30
ENSMUST00000031002	ENSMUSG00000029119	5	36806921	36830653	-1	24	17	31	53	41	11	1131	986	1018	142	866		O54782

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000031003	ENSMUSG00000029120	5	36868513	36955078	1	32	21	134	66	39	22	0	0	0	0	0		Q8BG02
ENSMUST00000031004	ENSMUSG00000029121	5	37241940	37292133	1	17	18	38	97	16	13	2	5	2	0	5		P97427
ENSMUST00000031005	ENSMUSG00000029122	5	37289098	37336894	-1	11	4	21	73	15	0	0	0	0	2	16		P57680
ENSMUST00000031008	ENSMUSG00000029125	5	38038742	38137765	1	0	0	0	46	1	0	56	273	139	57	162		Q8VDS8
ENSMUST00000031009	ENSMUSG00000029126	5	38137192	38159907	-1	22	11	101	74	30	9	0	2	0	0	5		Q62092
ENSMUST00000031011	ENSMUSG00000029128	5	41624976	41708157	-1	9	8	7	112	7	6	584	1539	732	453	323	Q3TWY9	Q99KL7
ENSMUST00000031017	ENSMUSG00000029135	5	32135801	32157842	1	32	30	93	250	70	28	5684	10769	6767	465	7774		P47930
ENSMUST00000031018	ENSMUSG00000029136	5	31624439	31697627	-1	1	3	3	67	7	2	68	136	64	126	67		Q8R1Q9
ENSMUST00000031020	ENSMUSG00000029138	5	31485740	31488476	1	5	10	20	14	10	16	0	0	0	0	2	Q9D496	
ENSMUST00000031024	ENSMUSG00000106918	5	31596935	31664384	1	2	0	0	52	5	0	1128	5364	1158	5200	772		Q9CQP0
ENSMUST00000031029	ENSMUSG00000029146	5	31193227	31199143	1	0	6	0	0	0	2	1539	1499	1081	170	721		Q8BVL3
ENSMUST00000031032	ENSMUSG00000029147	5	31202664	31220687	-1	13	3	26	106	20	9	818	1628	973	160	779		Q61074
ENSMUST00000031034	ENSMUSG00000029148	5	31240864	31251566	1	3	0	0	44	4	0	1755	3171	2033	694	1356		Q99J45
ENSMUST00000031037	ENSMUSG00000029151	5	31086106	31108237	-1	0	0	0	103	21	13	0	0	0	0	0	Q3TMQ7	P97441
ENSMUST00000031038	ENSMUSG00000029152	5	73292784	73314069	1	4	0	0	14	6	0	535	1650	738	515	583		Q9CRD0
ENSMUST00000031040	ENSMUSG00000029154	5	73406075	73453435	1	9	5	29	73	19	5	0	0	0	0	0		Q91YL7
ENSMUST00000031045	ENSMUSG00000029158	5	69516671	69542648	-1	5	5	2	1	4	4	0	0	0	0	0		Q9JIM5
ENSMUST00000031049						3	0	0	0	26	0	0	0	0	0	0		
ENSMUST00000031051	ENSMUSG00000029161	5	30933143	30945591	-1	10	7	34	52	13	1	5	9	4	0	5	E9QPK1	
ENSMUST00000031053	ENSMUSG00000029162	5	30921431	30931248	1	22	4	23	39	19	16	200	212	77	38	97	E9Q1Q9	
ENSMUST00000031055	ENSMUSG00000029163	5	30913402	30921277	1	17	10	38	62	27	13	943	591	713	83	516		Q99K41
ENSMUST00000031057						0	7	4	36	8	0	0	6	5	5	0		
ENSMUST00000031058	ENSMUSG00000029166	5	30814641	30866106	1	0	2	3	168	0	0	0	0	0	0	12	Q2UZW7	Q6PER3
ENSMUST00000031059	ENSMUSG00000029167	5	51454250	51567726	-1	2	0	40	0	3	4	0	0	0	0	0	Q3LIG2	
ENSMUST00000031061	ENSMUSG00000029169	5	52150203	52190514	-1	11	11	19	44	11	6	499	2024	1075	301	744	Q3UKJ6	O35286
ENSMUST00000031069	ENSMUSG00000029173	5	52640087	52669708	-1	19	18	0	93	0	13	0	0	0	0	67		Q6P6M7
ENSMUST00000031072	ENSMUSG00000029176	5	52834012	52867797	1	5	6	64	72	24	13	7	97	38	38	42	Q3TM92	Q91W96
ENSMUST00000031073	ENSMUSG00000029177	5	30666777	30674830	1	0	0	0	0	1	0	153	125	26	0	32	D6RJ71	
ENSMUST00000031077	ENSMUSG00000029179	5	52775409	52824665	1	52	43	92	55	56	29	6	14	11	6	12		Q8BKW4
ENSMUST00000031078	ENSMUSG00000029182	5	30466047	30484088	1	4	3	0	0	4	0	0	0	0	0	0		Q9DAS2
ENSMUST00000031080	ENSMUSG00000029185	5	64970071	65041886	1	20	19	25	47	12	5	167	810	382	365	482		Q9D281
ENSMUST00000031081	ENSMUSG00000029186	5	52741574	52769340	1	3	3	6	3	9	5	40	185	62	85	124		Q8CBQ5
ENSMUST00000031082	ENSMUSG00000029186	5	52741574	52769340	1	4	5	0	19	4	1	6	0	28	0	0		Q8CBQ5
ENSMUST00000031086	ENSMUSG00000029184	17	37466208	37467152	1	11	1	6	3	6	1	0	0	0	0	0	Q8VG96	
ENSMUST00000031089						0	2	8	0	13	0	0	0	0	0	49		
ENSMUST00000031090	ENSMUSG00000029189	5	53107083	53213927	-1	33	21	37	76	42	16	0	0	0	2	5		Q80TS8
ENSMUST00000031091	ENSMUSG00000029190	5	36600485	36696024	-1	0	13	0	0	0	0	204	140	405	46	375	E9QPJ5	
ENSMUST00000031092						0	19	0	28	25	0	162	464	339	214	206		
ENSMUST00000031093	ENSMUSG00000029193	5	53697776	53707705	-1	54	55	300	92	34	26	0	0	0	0	3		O08786
ENSMUST00000031094	ENSMUSG00000029192	5	36490604	36593276	-1	0	0	0	9	0	0	1009	55	1718	0	582	E9Q8K4	
ENSMUST00000031096	ENSMUSG00000029195	5	65348314	65384007	1	21	11	22	11	26	5	2	3	3	8	4		Q99N32
ENSMUST00000031097	ENSMUSG00000029196	5	36473670	36484285	-1	34	17	62	147	41	26	236	580	431	35	259	D3Z4Z0	
ENSMUST00000031099	ENSMUSG00000029198	5	36464998	36474080	1	13	5	21	41	22	9	343	707	326	769	326		Q99LP6
ENSMUST00000031101	ENSMUSG00000029199	5	65391497	65410693	1	25	11	50	39	24	15	42	223	49	23	26		
ENSMUST00000031103	ENSMUSG00000029201	5	65413221	65435949	-1	0	0	0	112	4	1	446	1229	650	350	582	Q3TS38	O70475
ENSMUST00000031104	ENSMUSG00000029202	5	65605721	65698273	-1	16	9	32	16	27	5	328	857	873	156	508	E9QPI5	
ENSMUST00000031105						0	0	0	208	2	0	146	484	258	556	184		
ENSMUST00000031106	ENSMUSG00000029204	5	65861213	65896700	1	54	44	112	59	54	36	103	161	62	120	118	Q504M6	Q9D3G9
ENSMUST00000031108	ENSMUSG00000029205	5	65934921	65977326	1	12	5	10	11	7	2	3	2	3	0	6	G3X8Z7	
ENSMUST00000031109	ENSMUSG00000029206	5	66259897	66298026	1	0	0	0	3	0	0	0	0	0	0	0	E9QL78	
ENSMUST00000031113	ENSMUSG00000029208	5	69556923	69575973	1	0	0	0	0	0	0	0	26	0	0	0		Q8C3X4
ENSMUST00000031117	ENSMUSG00000029209	5	69573108	69592340	-1	0	2	7	46	1	0	53	180	50	116	8		Q9CRC9
ENSMUST00000031119	ENSMUSG00000001260	5	70751047	70842617	-1	7	7	8	2	10	4	0	0	0	0	0		Q9R0Y8
ENSMUST00000031121	ENSMUSG00000029211	5	71569749	71658308	-1	18	13	16	72	21	7	0	0	0	0	2	Q543Z0	Q9D6F4
ENSMUST00000031122	ENSMUSG00000029212	5	71658113	72149037	1	20	19	30	111	25	14	0	1	2	1	2	Q53WT3	P50571
ENSMUST00000031124	ENSMUSG00000060204	5	72581638	72587551	-1	5	9	38	24	9	10	0	0	0	0	1	Q8BJG1	
ENSMUST00000031127	ENSMUSG00000029219	5	73006883	73012955	1	41	24	75	749	46	24	0	0	0	0	0	A2RTJ6	Q3UEZ8
ENSMUST00000031131	ENSMUSG00000029223	5	66676091	66687234	1	8	0	11	14	8	0	0	0	0	0	0		Q9R0P9
ENSMUST00000031143	ENSMUSG00000029233	5	76140271	76155504	1	0	0	0	162	0	0	272	792	332	21	118		Q9WUP4
ENSMUST00000031144	ENSMUSG00000029234	5	76183880	76209245	1	3	4	4	14	0	2	801	1569	604	211	329		P52875
ENSMUST00000031145	ENSMUSG00000029235	5	76312115	76331156	-1	0	1	0	3	3	2	0	0	0	0	0		Q78Y63
ENSMUST00000031146	ENSMUSG00000029236	5	76333495	76363788	-1	7	3	16	44	7	4	0	0	0	0	0	Q059S5	Q9QXK8
ENSMUST00000031158						0	4	0	0	0	0	14	14	18	36	26		
ENSMUST00000031160	ENSMUSG00000029247	5	76951307	76967509	1	27	8	9	237	27	8	0	71	18	111	47		Q9DCL9
ENSMUST00000031161	ENSMUSG00000029248	5	77016023	77061529	1	13	12	12	0	20	13	0	0	0	0	0		Q9DA15
ENSMUST00000031167	ENSMUSG00000029250	5	77310147	77349324	1	15	9	10	20	20	5	472	1563	1117	1132	627		Q8CFI7
ENSMUST00000031170	ENSMUSG00000029253	5	86012024	86065583	-1	8	8	14	29	9	8	51	132	86	76	48		P49452
ENSMUST00000031171	ENSMUSG00000029254	5	86071746	86106125	1	1	1	0	0	1	0	117	558	144	235	109	A0A0H2UKC0	
ENSMUST00000031172	ENSMUSG00000029255	5	86180754	86197901	-1	0	0	2	0	0	0	0	0	0	0	0		Q01776
ENSMUST00000031175	ENSMUSG00000061259	5	86302217	86373420	-1	0	23	0	0	12	0	0	0	0	0	0		Q8VHK8
ENSMUST00000031181	ENSMUSG00000029260	5	86889767	86906937	-1	7	16	25	7	13	5	0	0	0	0	0	Q8K154	
ENSMUST00000031183	ENSMUSG00000035836	5	86916638	86926530	-1	9	7	9	7	10	3	0	0	0	0	0	Q8R084	
ENSMUST00000031186	ENSMUSG00000035811	5	87000860	87013275	1	13	7	7	2	6	5	0	0	0	0	0	Q8BJL9	
ENSMUST00000031189	ENSMUSG00000029263	5	108312609	108349355	1	13	0	0	260	24	0	8	0	19	0	0	D3Z4I0	
ENSMUST00000031190	ENSMUSG00000029265	5	108268897	108280526	1	9	7	12	241	24	7	473	630	541	99	353		Q91WV0
ENSMUST00000031195	ENSMUSG00000035780	5	87324972	87337195	-1	7	9	6	2	5	5	0	0	0	1	0		Q8BWQ1
ENSMUST00000031198	ENSMUSG00000029270	5	107908053	107987085	-1	0	8	7	8	6	0	115	471	160	180	98		Q9D6I7
ENSMUST00000031199	ENSMUSG00000029269	5	87513339	87538195	-1	4	0	1	4	7	0	0	0	0	0	0		Q9QWG7
ENSMUST00000031201	ENSMUSG00000029272	5	87575969	87591594	-1	1	1	1	0	3	0	0	0	0	0	0	Q9D566	
ENSMUST00000031205	ENSMUSG00000029275	5	107716657	107726036	-1	14	14	22	223	12	10	0	26	13	0	0		
ENSMUST00000031211	ENSMUSG00000029280	5	88002549	88008534	1	0	0	21	3	3	3	0	0	0	0	0		Q61900
ENSMUST00000031215	ENSMUSG00000029279	5	107331159	107387058	1	22	23	33	60	25	11	0	3	0	1	3		Q91Y44
ENSMUST00000031221	ENSMUSG00000029283	5	106964322	106984432	1	0	0	0	24	0	5	15	8	0	26	10		Q9Z0H0
ENSMUST00000031222	ENSMUSG00000029286	5	88487975	88506049	1	30	24	147	35	46	13	0	0	0	0	0	Q548P8	O55196

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000031224	ENSMUSG00000029287	5	107106570	107289629	-1	14	15	47	58	21	14	9	21	9	15	77		
ENSMUST00000031226	ENSMUSG00000029288	5	88455991	88468531	1	8	2	30	4	10	4	0	0	0	0	0		O55189
ENSMUST00000031227	ENSMUSG00000029290	5	105876565	105915818	1	2	0	3	0	3	5	12	17	25	47	36		
ENSMUST00000031229	ENSMUSG00000029291	5	88565040	88651392	1	35	39	299	85	49	22	28	92	69	6	66		Q9D394
ENSMUST00000031235	ENSMUSG00000034438	5	105014150	105139540	-1	11	4	9	7	11	3	2	49	3	20	31	Q2V6D6	
ENSMUST00000031238	ENSMUSG00000029298	5	105077630	105139539	-1	12	23	4	19	15	5	19	135	23	20	99	Q8BTS3	
ENSMUST00000031239	ENSMUSG00000029299	5	104935057	104982718	-1	10	10	10	18	14	10	0	12	4	13	20		Q99P81
ENSMUST00000031243	ENSMUSG00000029304	5	104435118	104441050	1	4	0	0	2	0	4	38	111	71	5140	638	Q547B5	P10923
ENSMUST00000031246	ENSMUSG00000029306	5	104299171	104311469	1	7	15	33	17	10	8	0	0	0	15	1		Q61711
ENSMUST00000031249	ENSMUSG00000029309	5	104079111	104113733	-1	17	11	58	23	16	9	0	0	0	4	0		P70663
ENSMUST00000031250	ENSMUSG00000029310	5	104046306	104065379	1	4	5	3	36	6	7	113	202	111	157	132		Q8BVU5
ENSMUST00000031251	ENSMUSG00000029311	5	103989762	104021919	-1	10	7	7	19	7	2	2484	8594	3432	4353	2146		Q9EQ06
ENSMUST00000031254	ENSMUSG00000029312	5	103861973	103911259	-1	16	9	6	7	21	0	0	11	12	0	16		P59280
ENSMUST00000031255	ENSMUSG00000029314	5	100845713	100899102	1	6	6	6	0	0	0	90	1256	118	0	52		Q8C0N2
ENSMUST00000031256	ENSMUSG00000029313	5	103692374	103855322	1	29	37	146	0	0	0	415	556	298	0	420	E9Q921	
ENSMUST00000031261	ENSMUSG00000029320	5	103648039	103656010	-1	0	0	6	111	0	0	0	0	0	0	0	Q810Q2	
ENSMUST00000031262	ENSMUSG00000029319	5	100654723	100675140	-1	11	8	12	23	14	6	63	257	74	37	80		Q66JT7
ENSMUST00000031263	ENSMUSG00000029321	5	103605711	103629403	-1	21	11	19	11	15	9	0	0	0	2	1		Q9CXB2
ENSMUST00000031264	ENSMUSG00000029322	5	100553725	100572245	-1	0	3	8	0	0	0	5407	14395	4871	17328	3451		Q9JI48
ENSMUST00000031268	ENSMUSG00000029326	5	100039985	100068760	1	0	0	28	91	5	5	12	0	3	8	0		Q8BGB7
ENSMUST00000031273	ENSMUSG00000029330	5	101765130	101823858	1	24	19	28	44	26	17	10	43	13	1	41		P98191
ENSMUST00000031276	ENSMUSG00000029333	5	99217426	99252927	-1	17	12	14	29	7	2	0	5	3	3	0		Q8JZL7
ENSMUST00000031277	ENSMUSG00000029334	5	98929773	99037351	-1	0	0	0	0	0	0	0	0	0	0	0	E9QPH0	
ENSMUST00000031278	ENSMUSG00000029335	5	98854415	98884396	1	18	14	47	217	31	19	1	4	2	0	6	Q149J9	Q8BHE5
ENSMUST00000031280	ENSMUSG00000029337	5	98254184	98277030	1	89	44	452	571	79	68	0	0	1	0	0		P15656
ENSMUST00000031281	ENSMUSG00000029338	5	97882783	98031043	-1	37	29	157	153	35	19	1818	5026	3773	625	2454	Q3TCL6	Q6DFX2
ENSMUST00000031286	ENSMUSG00000029343	5	112255815	112269585	1	0	5	10	53	7	9	0	0	0	0	0		Q9WVJ5
ENSMUST00000031287	ENSMUSG00000029344	5	112276691	112315361	1	6	0	0	0	0	3	606	1182	949	187	648	Q3TQN1	
ENSMUST00000031288	ENSMUSG00000029345	5	112326358	112338073	1	28	12	61	114	45	27	1221	1267	1139	98	934	Q3TTV6	Q9ERA6
ENSMUST00000031289	ENSMUSG00000029346	5	112337392	112343040	-1	0	4	0	6	0	0	8	20	22	0	27		Q8K2M3
ENSMUST00000031291	ENSMUSG00000029348	5	112384354	112394866	-1	18	8	68	82	22	11	0	0	0	0	0		Q80VP9
ENSMUST00000031295	ENSMUSG00000042240	5	113058258	113070117	-1	0	0	0	9	6	3	0	0	0	0	0		P62696
ENSMUST00000031304	ENSMUSG00000029359	5	118027743	118061878	1	2	0	6	38	0	0	0	19	22	0	0	D0EM45	Q9JKL5
ENSMUST00000031305						13	11	8	10	16	7	1	0	1	0	3		
ENSMUST00000031309	ENSMUSG00000029364	5	117357304	117378601	1	27	6	54	20	26	15	647	1192	687	114	513		O54929
ENSMUST00000031311	ENSMUSG00000029366	5	88764996	88783281	1	7	7	40	109	28	14	1527	3953	2077	315	1607	Q545E8	P43346
ENSMUST00000031314	ENSMUSG00000029368	5	90460897	90476602	1	17	14	10	4	10	4	0	0	1	1315	2	Q546G4	P07724
ENSMUST00000031317	ENSMUSG00000029370	5	90603076	90640657	-1	15	7	10	10	16	7	0	6	0	33	4	G3X8Z9	
ENSMUST00000031318	ENSMUSG00000029371	5	90759360	90761624	1	12	7	9	47	12	7	0	0	0	32	6		P50228
ENSMUST00000031319	ENSMUSG00000029372	5	90768518	90770063	1	2	7	8	11	8	5	27	46	24	314	81	Q9EQI5	
ENSMUST00000031320	ENSMUSG00000029373	5	90772435	90773383	1	3	4	17	4	11	3	65	46	75	2815	247	Q3TVN6	Q9Z126
ENSMUST00000031322	ENSMUSG00000029375	5	90794534	90803067	1	157	120	277	110	136	70	1	6	3	2	9		Q9WVL7
ENSMUST00000031324	ENSMUSG00000029377	5	91074622	91093646	1	22	12	72	50	30	14	0	3	0	3	1		Q61521
ENSMUST00000031325	ENSMUSG00000029378	5	91139599	91148432	1	2	6	9	77	8	6	0	4	0	14	24	Q4FJT2	P31955
ENSMUST00000031326	ENSMUSG00000029379	5	90786103	90789600	1	7	8	18	53	8	6	1	2	0	5	8		Q6W5C0
ENSMUST00000031327	ENSMUSG00000029380	5	90891241	90893115	1	2	4	11	27	7	4	0	4	0	39	20	A2RTH0	P12850
ENSMUST00000031330	ENSMUSG00000029384	5	93206518	93213475	1	2	3	1	5	5	0	0	1	0	0	1	Q9D875	
ENSMUST00000031331	ENSMUSG00000029385	5	93267257	93276231	1	3	2	10	81	3	0	32	608	637	212	315	Q5HZK4	O08918
ENSMUST00000031333	ENSMUSG00000029387	5	124579140	124597680	1	14	8	32	24	22	9	53	176	33	5	12	Q3UZB8	Q8VD76
ENSMUST00000031334	ENSMUSG00000029388	5	124570213	124579131	-1	37	19	48	43	32	24	110	318	148	449	105	Q3UZR8	Q99LC8
ENSMUST00000031341	ENSMUSG00000029394	5	124345417	124363082	-1	11	8	0	39	14	8	497	996	372	130	245		O35207
ENSMUST00000031344	ENSMUSG00000038126	5	124250959	124327972	-1	36	26	44	41	42	9	32	57	24	13	57	E9QPF8	
ENSMUST00000031345	ENSMUSG00000029397	5	91948904	91963068	-1	4	0	3	283	12	0	492	1390	787	312	572		Q9CR50
ENSMUST00000031347	ENSMUSG00000029401	5	124463265	124478366	-1	7	6	19	214	15	9	512	674	346	126	228		Q99LE1
ENSMUST00000031349	ENSMUSG00000029402	5	124483134	124491124	1	7	2	13	35	16	12	38	54	47	61	27		Q9D384
ENSMUST00000031351	ENSMUSG00000029404	5	124116089	124118196	1	13	2	7	159	21	0	339	518	340	256	207		Q9JM93
ENSMUST00000031354	ENSMUSG00000029408	5	124061530	124095798	-1	23	18	78	178	34	15	104	91	63	4	39		Q9JJ59
ENSMUST00000031355	ENSMUSG00000029407	5	92137938	92202798	1	14	11	17	111	13	12	417	1427	997	232	663		Q9Z1Z0
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ENSMUST00000031359	ENSMUSG00000029410	5	92226679	92256278	-1	18	11	30	20	19	11	2	39	7	1	16		O35385
ENSMUST00000031364	ENSMUSG00000029415	5	92284010	92310479	-1	28	24	90	170	46	22	139	368	300	160	331		
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ENSMUST00000031367	ENSMUSG00000029416	5	127595664	127632897	-1	18	0	29	0	11	0	203	469	244	32	189		Q91W98
ENSMUST00000031376	ENSMUSG00000029427	5	123698294	123721100	-1	23	21	65	94	29	25	397	1683	847	111	814		Q9CYA6
ENSMUST00000031377	ENSMUSG00000029426	5	92441314	92506833	-1	10	7	43	142	25	4	1413	4613	1627	698	1360		O35114
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ENSMUST00000031382	ENSMUSG00000049550	5	123577795	123684618	-1	0	0	0	0	0	0	535	991	1750	35	1175	F8WIA1	
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ENSMUST00000031384	ENSMUSG00000029431	5	123510460	123511882	1	3	8	11	11	14	3	0	3	0	1	2		Q1RLK6
ENSMUST00000031385	ENSMUSG00000029433	5	123509765	123525488	-1	2	10	4	10	2	5	38	21	22	11	6	D3Z3K5	
ENSMUST00000031388	ENSMUSG00000029434	5	123528659	123573038	-1	23	17	36	74	28	9	539	1129	758	193	489		Q9D2N9
ENSMUST00000031389	ENSMUSG00000029437	5	123480157	123489489	-1	3	1	1	2	3	2	0	0	0	0	0		Q6EAL8
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ENSMUST00000031401	ENSMUSG00000029449	5	123103044	123132692	-1	5	5	7	33	14	0	703	779	694	128	382	Q4VA10	Q8BYP3
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ENSMUST00000031411	ENSMUSG00000029455	5	121566027	121593824	-1	27	28	60	136	49	21	5865	11408	5032	611	2609	Q544B1	P47738
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ENSMUST00000031414	ENSMUSG00000029458	5	121660563	121687256	1	0	0	0	5	0	0	930	805	1067	42	715		Q99MP8
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ENSMUST00000031421	ENSMUSG00000029465	5	122391878	122414184	1	32	42	19	40	60	25	2594	8229	2588	7478	1430	H7BWZ3	
ENSMUST00000031422	ENSMUSG00000029466	5	122421693	122444912	1	0	0	0	0	0	0	361	569	339	93	273		Q9WVM3
ENSMUST00000031423	ENSMUSG00000029467	5	122453513	122502225	-1	9	15	9	19	25	5	445	683	493	105	809		O55143
ENSMUST00000031425	ENSMUSG00000029468	5	122643911	122691432	1	6	0	4	7	0	3	0	0	3	3	1	F8WI93	
ENSMUST00000031426	ENSMUSG00000029469	5	122550204	122614518	-1	7	0	0	19	9	0	2	8	8	42	14		O35594
ENSMUST00000031429	ENSMUSG00000029470	5	122707544	122729738	1	25	26	54	31	38	19	5	54	19	6	22	Q9Z257	
ENSMUST00000031434	ENSMUSG00000029474	5	122850048	122871291	1	12	15	9	63	19	11	806	2220	1001	1453	673		Q99KR6
ENSMUST00000031435	ENSMUSG00000029475	5	122870665	122989823	-1	7	11	0	94	16	8	163	327	146	17	118		Q6P1G2
ENSMUST00000031437	ENSMUSG00000029477	5	123035769	123047016	-1	4	9	0	0	4	0	0	5	0	2	6		Q8C5T4
ENSMUST00000031445	ENSMUSG00000029482	5	125475814	125517410	1	16	14	63	95	41	22	2095	1961	1923	251	1165		Q9D2R0
ENSMUST00000031446	ENSMUSG00000070498	5	125531774	125792583	1	45	36	142	76	54	32	5	26	15	2	7	F7BAB2	
ENSMUST00000031447	ENSMUSG00000029484	5	96793339	96845966	1	7	8	12	45	8	9	2057	7571	3157	5530	1829		O35639
ENSMUST00000031455	ENSMUSG00000029490	5	108441054	108448891	-1	23	13	56	37	22	10	100	269	158	38	143		Q8CE47
ENSMUST00000031456	ENSMUSG00000029491	5	108388391	108432397	1	0	7	14	0	14	0	0	0	1	0	0		P23440
ENSMUST00000031472	ENSMUSG00000029499	5	110274282	110286186	-1	18	3	9	59	10	5	9	3	0	6	2	Q5D073	
ENSMUST00000031474	ENSMUSG00000029501	5	110231004	110256651	1	33	22	57	67	32	22	388	1801	861	142	772		Q6P1H6
ENSMUST00000031477	ENSMUSG00000029502	5	110176701	110226470	1	0	0	0	0	9	8	312	522	752	102	732	E9QP99	
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ENSMUST00000031486	ENSMUSG00000029513	5	116013586	116024508	-1	3	2	3	89	9	6	1993	4000	1901	365	1114	Q542K0	Q9R078
ENSMUST00000031488						22	14	112	29	15	10	0	0	0	0	0		
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ENSMUST00000031490	ENSMUSG00000029512	5	110784488	110810097	-1	47	37	85	110	54	44	3920	5636	4160	294	3808		
ENSMUST00000031492	ENSMUSG00000029518	5	115631908	115647736	1	18	8	33	34	27	10	2078	4492	2302	259	1686	Q3U0T9	Q6PHN9
ENSMUST00000031495	ENSMUSG00000029522	5	115466262	115474722	1	4	0	4	2	3	0	0	0	0	0	0		Q9Z0Y2
ENSMUST00000031501	ENSMUSG00000029526	5	138561840	138564712	-1	8	6	14	11	4	7	0	0	0	0	0	Q9D991	
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ENSMUST00000031513	ENSMUSG00000029538	5	115327177	115333080	1	2	3	8	42	7	1	413	449	425	79	257		Q9D0B0
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ENSMUST00000031521	ENSMUSG00000029541	5	139352617	139357033	1	8	8	31	48	7	7	0	0	1	0	0		E9Q816
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ENSMUST00000031530	ENSMUSG00000029550	5	115011137	115098790	1	5	8	24	14	3	5	907	1226	821	119	568		Q9CUS9
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ENSMUST00000031533	ENSMUSG00000029553	6	16833373	16898441	-1	6	3	4	7	6	8	62	208	103	494	98		Q9WTW4
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ENSMUST00000031535	ENSMUSG00000029556	5	114948980	114971094	-1	3	0	37	66	30	15	0	0	0	1	0		P22361
ENSMUST00000031536	ENSMUSG00000029557	5	140327674	140331898	-1	8	4	8	14	15	9	45	56	23	24	16		Q9CPY0
ENSMUST00000031538	ENSMUSG00000029559	5	114942158	114949783	1	19	10	14	25	18	7	73	167	89	30	78		
ENSMUST00000031539	ENSMUSG00000029560	5	140340299	140389262	-1	26	17	89	51	39	18	172	154	126	45	197		Q8CFD4
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ENSMUST00000031542	ENSMUSG00000029561	5	114896936	114912234	1	19	0	29	22	0	10	18	232	32	36	234		Q9Z2F2
ENSMUST00000031545	ENSMUSG00000029563	6	14901349	15441977	1	0	0	0	0	0	4	1	0	0	0	0		P58463
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ENSMUST00000031574	ENSMUSG00000029586	5	143181017	143205075	1	5	8	11	18	0	5	0	0	0	0	0	Q8CDE8	
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ENSMUST00000031591	ENSMUSG00000029595	5	120431699	120441223	1	43	24	80	894	76	39	0	0	0	0	3	Q543P4	P61375
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ENSMUST00000031617	ENSMUSG00000029614	5	121204481	121209241	1	13	11	60	52	15	17	3853	7789	4798	21854	4047	Q3UCH0	P47911
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ENSMUST00000031632	ENSMUSG00000029627	5	145194946	145201868	-1	15	12	41	34	24	12	272	566	218	155	194		Q9Z1D9
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ENSMUST00000031637	ENSMUSG00000029632	6	11900292	11907497	-1	8	1	12	2	9	8	481	1157	431	2345	282		Q62425
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ENSMUST00000031646	ENSMUSG00000029641	5	146845071	146847726	1	8	5	6	97	14	8	0	1	0	1	0		Q6IMB1
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ENSMUST00000031652						3	3	1	58	2	2	0	0	1	0	0		
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ENSMUST00000031654	ENSMUSG00000029649	5	147860461	147876456	1	8	6	13	49	5	6	965	2273	940	3678	670		Q9CQT5
ENSMUST00000031655	ENSMUSG00000029650	5	147878437	147894815	-1	15	4	17	70	12	15	33	0	32	0	25		Q9DC26
ENSMUST00000031663	ENSMUSG00000029656	4	104766317	104804548	1	5	1	16	8	9	3	0	0	0	0	0		Q8BH35
ENSMUST00000031667	ENSMUSG00000029660	5	149439660	149470979	1	5	10	14	7	11	3	0	0	0	0	1		
ENSMUST00000031668	ENSMUSG00000029661	6	4504814	4541544	1	24	18	31	17	23	11	0	0	0	44	277	Q3TX57	Q01149
ENSMUST00000031670	ENSMUSG00000032766	6	4003904	4008445	1	10	8	4	138	19	9	37	113	57	842	120		P61953
ENSMUST00000031673	ENSMUSG00000029663	6	3993792	3997436	1	29	31	39	57	23	9	3	4	13	1	6		Q61012
ENSMUST00000031674	ENSMUSG00000029664	6	3962595	3988919	-1	9	6	8	9	7	6	0	0	1	0	0	Q3V1S9	O35536
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ENSMUST00000031680	ENSMUSG00000029670	6	21949571	21976038	1	0	5	10	3	8	7	20	108	16	6	0		Q8VEK6
ENSMUST00000031681	ENSMUSG00000029671	6	22288227	22298522	1	8	5	12	15	5	4	0	5	0	0	0		Q9QYS1
ENSMUST00000031689	ENSMUSG00000029678	6	24857997	24891958	1	4	9	0	4	11	4	0	0	0	0	0	Q812F3	
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ENSMUST00000031691	ENSMUSG00000029680	6	24748329	24767662	1	8	5	4	8	11	8	0	0	0	0	0	L0MX76	Q05A56
ENSMUST00000031692	ENSMUSG00000029681	5	135168283	135181855	1	0	0	0	34	0	0	372	521	300	38	219		Q921K9
ENSMUST00000031693	ENSMUSG00000029682	6	24791188	24801048	1	7	7	4	0	8	3	0	0	0	0	0		P48794
ENSMUST00000031694	ENSMUSG00000029683	6	24597762	24605414	1	11	4	9	15	14	2	0	0	1	0	0		Q3UHZ5
ENSMUST00000031695	ENSMUSG00000029684	6	24613805	24665009	-1	6	6	11	35	11	15	103	340	160	29	136	Q3TXX8	Q91YD9
ENSMUST00000031696	ENSMUSG00000029685	6	24528144	24573164	1	0	4	5	4	9	0	0	0	0	0	0		Q8VHS6
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ENSMUST00000031707	ENSMUSG00000029695	6	23072173	23132986	-1	11	14	21	15	12	10	0	0	0	2	1	Q3UEQ9	Q99K67
ENSMUST00000031709	ENSMUSG00000029697	6	23245044	23248362	-1	20	11	32	300	32	11	0	0	0	0	0		Q0VDQ9
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ENSMUST00000031718	ENSMUSG00000029706	6	28442334	28449353	-1	10	6	0	22	0	2	0	0	0	0	0	A2RRY5	P32115
ENSMUST00000031719	ENSMUSG00000029707	6	28427789	28438622	1	13	7	20	15	12	2	0	2	0	0	0		Q9QXW4
ENSMUST00000031723	ENSMUSG00000029711	5	137483020	137533242	-1	7	2	0	0	0	0	0	0	0	0	0	Q0VED9	P07321
ENSMUST00000031725	ENSMUSG00000029712	5	137553517	137569582	1	14	15	19	8	17	0	0	0	0	0	0	F8WI57	
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ENSMUST00000031731	ENSMUSG00000029718	5	137605103	137613784	-1	0	0	12	57	6	8	1	14	12	47	149	Q3UIP2	Q61398
ENSMUST00000031732	ENSMUSG00000089984	5	137612503	137629002	-1	0	9	37	40	19	9	14	70	34	0	53		Q9D417
ENSMUST00000031734	ENSMUSG00000093445	5	137629121	137641099	1	8	0	25	32	14	8	0	16	0	0	9		Q921G6
ENSMUST00000031736	ENSMUSG00000029722	5	137650463	137684726	-1	9	0	0	22	6	0	74	158	80	17	0		Q80WC7
ENSMUST00000031738	ENSMUSG00000029723	5	137745730	137768450	1	2	2	0	0	1	0	1	1	1	0	2	D3Z6V5	
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ENSMUST00000031740	ENSMUSG00000029726	5	137781906	137787655	-1	15	6	43	285	26	12	851	1318	735	120	614		Q8K3A9
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ENSMUST00000031749	ENSMUSG00000029736	6	43303674	43309554	-1	8	4	15	23	12	7	0	0	0	0	0		Q8VIH1
ENSMUST00000031750	ENSMUSG00000033542	6	43265582	43289320	1	25	29	69	66	43	9	3	1	4	3	43	E9Q7D5	
ENSMUST00000031766	ENSMUSG00000029752	6	7675169	7693254	-1	7	3	3	89	12	2	684	1708	939	346	381		Q61024
ENSMUST00000031768	ENSMUSG00000029754	6	6863334	6868568	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000031773	ENSMUSG00000029759	6	5220852	5256286	-1	4	0	3	3	9	0	14	64	9	205	44		Q62087
ENSMUST00000031775	ENSMUSG00000029761	6	34598500	34775473	1	0	0	0	0	4	0	0	0	3	22	56	D3Z6I7	
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ENSMUST00000031779	ENSMUSG00000029767	6	29348069	29377110	1	7	0	31	43	13	9	220	863	401	895	379	Q3TUF3	O35887
ENSMUST00000031787	ENSMUSG00000005503	6	52313498	52318378	1	17	6	29	157	25	15	0	0	0	0	0		P23683
ENSMUST00000031788	ENSMUSG00000029776	6	52546228	52640389	-1	6	4	8	76	8	6	180	716	231	100	134		Q99L13
ENSMUST00000031793	ENSMUSG00000029780	6	56882400	56923932	-1	0	0	0	17	0	0	39	216	117	195	95		Q9D020
ENSMUST00000031795	ENSMUSG00000029781	6	56832059	56879358	1	22	10	36	94	27	7	8	25	9	23	56		Q9Z247
ENSMUST00000031797	ENSMUSG00000029784	6	30509849	30520254	1	3	5	6	4	7	3	0	0	0	0	0	Q9DAA0	
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ENSMUST00000031805	ENSMUSG00000029787	6	56714899	56761912	1	21	17	15	41	17	10	453	971	743	89	516		Q80U56
ENSMUST00000031806	ENSMUSG00000054446	6	30639218	30645363	1	14	7	29	11	18	5	0	0	0	0	0		Q7TPZ8
ENSMUST00000031810	ENSMUSG00000029790	6	30653457	30693749	-1	6	0	16	67	8	0	6	15	3	0	4		Q99NF3
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ENSMUST00000031822	ENSMUSG00000029802	6	58584523	58695676	1	21	11	6	13	18	15	0	109	61	145	16		
ENSMUST00000031823	ENSMUSG00000029804	6	58831465	58920398	1	15	4	7	0	5	7	0	3	0	0	0	G5E876	
ENSMUST00000031835	ENSMUSG00000029811	6	48872896	48909188	1	0	0	16	6	14	11	0	0	0	0	0	E9PYN9	
ENSMUST00000031837	ENSMUSG00000029813	6	48929895	48933687	1	27	17	55	35	32	7	0	0	0	0	0	E9Q745	
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ENSMUST00000031839						0	1	3	102	8	2	122	419	125	261	79		
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ENSMUST00000031845	ENSMUSG00000029821	6	50188888	50263862	-1	7	6	17	16	6	0	0	18	0	0	0		Q9Z2D3
ENSMUST00000031850	ENSMUSG00000029826	6	38305286	38354603	-1	0	0	31	19	19	14	839	1338	1234	125	1369		Q3UPF5
ENSMUST00000031851	ENSMUSG00000029829	6	38109255	38115809	1	11	1	27	13	13	10	0	0	0	0	0		
ENSMUST00000031852	ENSMUSG00000029828	6	50573302	50596632	-1	10	6	15	82	8	6	10	22	10	21	11		Q9D5Y0
ENSMUST00000031853	ENSMUSG00000029831	6	50650672	50654439	-1	5	5	23	6	6	3	0	0	0	0	0	Q3UUP8	Q9ESQ8
ENSMUST00000031859	ENSMUSG00000029833	6	37870811	37966296	1	0	10	0	0	0	0	15	0	0	0	0		Q64127
ENSMUST00000031862	ENSMUSG00000029836	6	51470360	51483704	1	18	29	9	35	0	6	163	292	297	598	260	Q9DCC5	
ENSMUST00000031866	ENSMUSG00000029840	6	35508906	35539888	-1	15	27	83	194	33	26	2048	6757	2923	426	2180		P62774
ENSMUST00000031868	ENSMUSG00000029843	6	35267957	35308131	-1	32	12	41	21	36	20	0	0	0	0	0	Q8BZ82	
ENSMUST00000031876	ENSMUSG00000029848	6	34920163	34939344	1	5	4	20	5	18	0	0	0	0	0	0		P70278
ENSMUST00000031879	ENSMUSG00000029851	6	42623016	42645254	-1	34	15	69	23	36	20	0	2	1	2	5		Q921K8
ENSMUST00000031891	ENSMUSG00000029861	6	42315312	42324643	-1	0	0	0	0	0	0	0	0	0	0	0		Q3TY60
ENSMUST00000031894	ENSMUSG00000029862	6	42286685	42315756	1	22	3	11	8	21	0	0	0	0	0	3		Q64347
ENSMUST00000031895	ENSMUSG00000029863	6	42264985	42282508	1	13	7	40	42	11	7	545	1025	511	99	298		P29594
ENSMUST00000031897	ENSMUSG00000029864	6	42245935	42250447	1	4	4	19	27	10	1	23	39	14	60	16		Q9DCM2
ENSMUST00000031898	ENSMUSG00000029865	6	41951630	41956098	1	3	3	0	1	1	0	0	0	0	0	0	Q9D2X6	
ENSMUST00000031899	ENSMUSG00000029866	6	41686330	41704339	-1	17	12	21	12	22	10	4	0	0	0	0		Q9EQF2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000031900	ENSMUSG00000029867	6	41684431	41685717	1	4	9	24	8	1	4	0	0	0	1	0		Q9D9P8
ENSMUST00000031901	ENSMUSG00000036899	6	41652173	41680769	-1	5	6	13	8	8	5	0	0	3	0	0		P69744
ENSMUST00000031902	ENSMUSG00000029868	6	41620621	41636405	-1	25	16	55	26	21	14	0	0	0	0	4		
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ENSMUST00000031913	ENSMUSG00000054106	6	41302269	41305532	1	2	4	4	1	4	0	0	0	0	0	0	Q9R0T7	
ENSMUST00000031914	ENSMUSG00000029875	15	98167806	98170134	1	15	12	78	298	26	17	0	0	0	1	0		Q8BMK5
ENSMUST00000031931	ENSMUSG00000029882	6	41030268	41035509	-1	25	29	35	18	50	27	1	1	0	0	1	Q9CPN9	
ENSMUST00000031935	ENSMUSG00000029883	6	40920437	40940557	-1	0	0	4	0	0	0	0	0	0	0	0	Q9D9G7	
ENSMUST00000031937	ENSMUSG00000029885	6	40878794	40887494	-1	7	8	14	13	18	10	0	0	0	0	0		Q7TT41
ENSMUST00000031967	ENSMUSG00000029909	6	40514824	40519508	-1	2	1	10	2	4	2	0	0	0	0	0		Q9DAA4
ENSMUST00000031971	ENSMUSG00000029911	6	40471352	40484700	1	7	1	12	1	2	1	13	27	12	103	16		Q9CYR0
ENSMUST00000031973	ENSMUSG00000029913	6	65778988	65937010	1	0	0	0	0	0	0	2	7	0	1	0	E9Q707	
ENSMUST00000031975						4	5	2	2	17	6	338	2714	948	1639	440		
ENSMUST00000031976	ENSMUSG00000029913	6	65778988	65937010	1	10	0	0	38	9	0	0	0	0	0	0		Q9CXE0
ENSMUST00000031977	ENSMUSG00000029916	6	40325172	40396762	1	22	21	58	40	29	15	27	46	25	23	38		Q9ESW4
ENSMUST00000031978	ENSMUSG00000029918	6	39801804	39810988	-1	2	4	1	34	4	1	55	126	61	233	35	Q58DZ5	Q9D2R8
ENSMUST00000031982	ENSMUSG00000029919	6	65117293	65144908	-1	42	54	122	61	46	15	2	12	5	46	13		Q9JHF7
ENSMUST00000031984	ENSMUSG00000029920	6	65042583	65116061	1	16	17	34	44	23	6	73	188	135	41	88		Q04692
ENSMUST00000031985	ENSMUSG00000029922	6	39397804	39420462	-1	0	0	17	82	43	13	1604	4333	1966	479	1711	Q8C5V4	
ENSMUST00000031986	ENSMUSG00000029923	6	39381175	39390380	1	10	11	30	12	14	10	20	71	22	91	35		P35294
ENSMUST00000032057	ENSMUSG00000029992	6	87042846	87092197	1	0	0	0	0	4	0	4	0	55	15	64		P47856
ENSMUST00000032060	ENSMUSG00000029993	6	87009236	87028461	1	0	0	0	0	0	0	0	0	7	3	3		
ENSMUST00000032065	ENSMUSG00000029998	6	86386006	86397154	-1	23	21	54	66	34	12	367	1031	721	158	478		Q9CQF9
ENSMUST00000032066	ENSMUSG00000029999	6	86195223	86275719	1	17	23	54	26	34	17	0	0	1	1	21	Q545E4	P48030
ENSMUST00000032069	ENSMUSG00000030000	6	86028681	86124409	1	17	16	59	45	42	17	0	0	1	0	1		Q9QYB8
ENSMUST00000032070	ENSMUSG00000030001	6	86016171	86020996	1	2	3	4	45	5	3	0	0	0	0	0	H6UWL1	O55208
ENSMUST00000032071	ENSMUSG00000030002	6	85942268	85961667	-1	24	24	35	46	32	13	768	2877	1744	900	1350		Q6NXK5
ENSMUST00000032073	ENSMUSG00000030004	6	85830388	85832082	-1	7	5	20	11	14	8	0	1	0	0	0		Q9JIY7
ENSMUST00000032074	ENSMUSG00000079494	6	85817218	85820972	-1	3	3	7	10	6	2	0	0	0	0	0		Q9QXS8
ENSMUST00000032078	ENSMUSG00000030007	6	85451514	85468475	1	18	14	26	209	30	8	1183	2151	1215	578	1010	Q3TIJ7	P80313
ENSMUST00000032080	ENSMUSG00000030008	6	85446810	85451970	-1	0	0	0	10	0	0	132	256	87	43	46		Q9D9N8
ENSMUST00000032088	ENSMUSG00000030016	6	83867109	83989550	1	20	11	14	95	18	10	367	2539	1077	707	514	E9QML5	
ENSMUST00000032089	ENSMUSG00000030017	6	78466269	78468872	-1	0	3	0	0	0	0	0	0	0	1	0	Q545I1	O09049
ENSMUST00000032093	ENSMUSG00000030020	6	92370908	92706155	-1	13	0	18	19	4	9	0	0	0	0	0	A7YQ68	
ENSMUST00000032094	ENSMUSG00000030019	6	119479668	119482630	1	35	13	82	529	36	29	2064	3507	2269	315	1526		Q8BID8
ENSMUST00000032105	ENSMUSG00000030029	6	94604529	94700158	-1	24	19	43	145	42	15	0	8	0	0	0		P70193
ENSMUST00000032106	ENSMUSG00000030030	6	83156404	83162945	1	15	13	36	320	22	10	7	6	2	1	4		Q9DAQ4
ENSMUST00000032107	ENSMUSG00000030031	6	95117240	95129790	1	9	0	8	68	6	11	0	24	12	16	0		Q3UQV5
ENSMUST00000032108						0	0	0	0	0	0	0	0	1	0	2		
ENSMUST00000032109	ENSMUSG00000030034	6	83121765	83125431	-1	0	0	26	0	0	0	102	203	120	28	90		
ENSMUST00000032111	ENSMUSG00000030035	6	83119044	83121559	-1	0	0	0	0	0	0	272	416	173	92	113		P97764
ENSMUST00000032114	ENSMUSG00000030036	6	83115496	83118898	1	14	12	43	80	19	8	333	506	338	74	328		Q80UM7
ENSMUST00000032122	ENSMUSG00000030043	6	82402334	82560104	1	112	82	290	471	145	103	1	7	4	0	3		P30548
ENSMUST00000032124	ENSMUSG00000030045	6	81957851	81965958	-1	149	122	323	165	124	68	145	384	214	119	131		Q9D338
ENSMUST00000032125	ENSMUSG00000030046	6	87428994	87437677	1	10	11	10	7	17	7	0	0	0	0	0		Q9R229
ENSMUST00000032127	ENSMUSG00000030048	6	87383256	87388935	-1	7	9	22	13	5	6	0	0	0	0	0		Q9D0T7
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ENSMUST00000032129	ENSMUSG00000030050	6	87345650	87350942	-1	3	5	11	13	7	6	0	0	0	0	0	Q53YU8	
ENSMUST00000032130	ENSMUSG00000030051	6	87628424	87672193	-1	87	34	87	209	109	0	0	72	74	26	22		Q9D842
ENSMUST00000032132	ENSMUSG00000068263	6	87730869	87755908	1	21	26	52	74	28	7	0	1	0	0	0	A0A0A0MQ84	
ENSMUST00000032133	ENSMUSG00000030054	6	87778072	87779768	1	5	5	14	15	6	3	28	19	26	243	38		O88186
ENSMUST00000032134	ENSMUSG00000030055	6	87788853	87812164	-1	4	4	23	2	5	6	102	4	76	0	66	Q91Z34	
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ENSMUST00000032138	ENSMUSG00000030057	6	87842615	87851106	-1	4	3	16	0	5	2	45	86	125	339	73	Q5QJQ9	P53996
ENSMUST00000032141	ENSMUSG00000030060	6	87913935	87936629	1	0	0	0	17	0	3	143	299	149	35	109		Q8R1M0
ENSMUST00000032143	ENSMUSG00000030062	6	88084482	88105304	1	23	19	47	116	24	16	1041	1592	942	486	1011		Q91YQ5
ENSMUST00000032146	ENSMUSG00000030064	6	97286867	97617541	-1	0	5	13	34	8	6	6	0	4	0	30		Q920B0
ENSMUST00000032151	ENSMUSG00000093661	6	99625135	99666771	-1	14	16	32	68	23	24	370	1680	584	70	361		Q9DBB5
ENSMUST00000032152	ENSMUSG00000030069	6	99711299	99726392	-1	0	0	0	0	0	0	394	808	301	22	137	Q14AB2	Q9QXU7
ENSMUST00000032157	ENSMUSG00000030074	6	100704734	100810913	1	6	8	3	20	6	6	0	1	0	0	1		Q810K9
ENSMUST00000032159	ENSMUSG00000030075	6	102162655	102573101	-1	98	67	521	129	85	54	0	12	6	0	5		Q07409
ENSMUST00000032165	ENSMUSG00000030079	6	88465409	88497572	1	13	9	19	52	21	11	68	182	88	91	118	Q3U1C2	P60122
ENSMUST00000032168	ENSMUSG00000030082	6	88503579	88518905	-1	17	9	38	36	18	9	2063	2950	2139	457	1583		P61620
ENSMUST00000032169	ENSMUSG00000030083	6	88835914	88841984	-1	17	14	56	120	35	26	10061	9480	5390	1190	4025		
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ENSMUST00000032174	ENSMUSG00000030087	6	90462576	90475238	1	0	0	13	29	0	10	0	0	0	1	0		Q9EPW2
ENSMUST00000032175	ENSMUSG00000030088	6	90486427	90600203	1	0	7	9	7	0	0	10	5	9	12	24		Q8R0Y6
ENSMUST00000032177	ENSMUSG00000030089	6	90604725	90646412	1	23	20	175	20	37	0	36	73	39	13	72		Q921R8
ENSMUST00000032179	ENSMUSG00000030091	6	91013068	91116829	-1	0	46	193	110	78	36	769	340	700	0	718		Q9QY81
ENSMUST00000032180	ENSMUSG00000030093	6	91363981	91411363	-1	20	13	69	112	26	11	0	0	0	0	0		P24383
ENSMUST00000032182	ENSMUSG00000030094	6	91489305	91515888	-1	21	5	47	56	30	5	1694	3288	1471	1064	1342		P51612
ENSMUST00000032183	ENSMUSG00000030095	6	91473703	91488463	1	28	20	83	43	36	15	4480	5704	3905	545	3110		Q9DBS1
ENSMUST00000032185	ENSMUSG00000030096	6	91684053	91759066	1	61	50	378	223	78	43	3604	7270	6761	376	5463	Q3UPI8	O35316
ENSMUST00000032191	ENSMUSG00000030101	6	108107028	108185582	-1	35	44	41	85	44	35	251	632	303	104	263		Q8R0F3
ENSMUST00000032192	ENSMUSG00000030102	6	108213096	108551109	1	54	62	82	100	90	46	119	214	224	26	382		P11881
ENSMUST00000032194	ENSMUSG00000030103	6	108660629	108666925	1	20	16	56	60	18	16	1036	1625	882	117	944	Q542A5	O35185
ENSMUST00000032196	ENSMUSG00000030105	6	108783099	108825278	1	12	6	4	105	15	3	609	2042	757	112	404		Q9CQW2
ENSMUST00000032198	ENSMUSG00000030107	6	121245906	121270917	1	13	10	16	24	17	10	11	217	12	45	77		Q9WTV6
ENSMUST00000032200	ENSMUSG00000030109	6	121343076	121365775	1	16	14	25	15	20	17	2	1	0	0	0	Q8VCS9	
ENSMUST00000032201	ENSMUSG00000030110	6	118151745	118197718	-1	0	0	22	103	29	11	0	0	3	0	3		P35546
ENSMUST00000032203	ENSMUSG00000030111	6	121635376	121679227	1	23	14	16	17	15	17	0	0	0	0	0		Q6GQT1
ENSMUST00000032206	ENSMUSG00000041920	11	109450855	109473598	-1	2	0	1	0	0	0	17	63	38	0	49	H9KUY0	
ENSMUST00000032207	ENSMUSG00000030114	6	122270596	122282882	-1	5	3	29	10	8	2	4	24	3	16	12		O88713
ENSMUST00000032210	ENSMUSG00000030116	6	122505845	122529290	1	0	0	0	0	0	0	1	0	0	0	0	F8WJ99	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000032211	ENSMUSG00000030117	6	122605403	122610087	-1	71	78	89	47	44	22	0	4	4	1	4		Q07104
ENSMUST00000032214	ENSMUSG00000030120	6	124931386	124937238	1	11	0	0	0	0	0	119	92	106	0	56	Q3UNV7	Q99KX1
ENSMUST00000032216	ENSMUSG00000030122	6	124913681	124920103	-1	6	4	9	23	5	6	924	1324	464	151	594		Q9D0J8
ENSMUST00000032217	ENSMUSG00000030124	6	124904361	124911705	-1	99	67	282	349	90	62	26	36	10	2	18		Q61790
ENSMUST00000032218	ENSMUSG00000030125	6	124769863	124779727	-1	5	8	0	0	8	0	0	0	0	0	0		O35125
ENSMUST00000032220	ENSMUSG00000030127	6	124958413	124965538	-1	2	5	0	50	8	0	129	222	104	42	94		Q9CZ04
ENSMUST00000032222	ENSMUSG00000030126	6	116018611	116193486	-1	5	2	0	0	3	0	612	1700	982	492	889	F8WJ98	
ENSMUST00000032228	ENSMUSG00000059908	6	121838541	121889057	1	8	3	28	11	14	8	0	0	0	60	0		P28665
ENSMUST00000032233	ENSMUSG00000030137	6	121210696	121226854	1	12	10	41	60	24	13	45	41	30	11	18		Q9JJZ2
ENSMUST00000032234	ENSMUSG00000008845	6	124304656	124330527	1	21	29	56	39	0	20	7	0	13	219	199		Q2VLH6
ENSMUST00000032237	ENSMUSG00000030138	6	118383381	118419474	-1	19	19	47	73	51	23	258	769	542	84	523	Q6PGF5	
ENSMUST00000032238	ENSMUSG00000096630	6	124024758	124062035	1	9	9	12	7	9	0	1	0	0	6	6		Q6TAC4
ENSMUST00000032239	ENSMUSG00000030142	6	123281789	123289870	-1	0	6	1	0	1	0	901	3934	645	1257	630	Q4FK29	Q9R0Q8
ENSMUST00000032240	ENSMUSG00000030144	6	123262111	123275265	1	6	7	16	23	9	6	3227	18418	4531	16684	3662	Q4KL29	Q9Z2H6
ENSMUST00000032248	ENSMUSG00000030148	6	123106428	123143999	1	0	0	0	0	0	0	201	1354	189	562	139	Q923C7	
ENSMUST00000032252	ENSMUSG00000030149	6	129610323	129623864	-1	0	2	7	0	0	3	0	28	1	10	15	Q4FJM0	O54709
ENSMUST00000032257	ENSMUSG00000030154	6	129045901	129057464	1	8	10	9	4	9	2	13	66	19	14	16	I3QI43	Q8VD98
ENSMUST00000032258	ENSMUSG00000030155	6	129091998	129100913	-1	61	49	31	93	79	43	0	1	0	0	1	H7BWZ4	
ENSMUST00000032259	ENSMUSG00000030156	6	129267325	129275436	-1	10	4	7	3	9	9	14	113	28	92	67	Q3U6A8	P37217
ENSMUST00000032260	ENSMUSG00000030157	6	129180615	129186534	1	8	0	3	7	5	4	414	3093	380	509	133	F5BFH0	Q91V08
ENSMUST00000032261	ENSMUSG00000030158	6	129375515	129385874	-1	3	3	0	7	10	3	8	75	8	7	41		
ENSMUST00000032262	ENSMUSG00000030159	6	129397297	129409335	1	4	0	16	7	2	3	19	80	20	332	60		Q9JL99
ENSMUST00000032263	ENSMUSG00000030160	6	129512555	129519227	1	36	35	192	54	36	18	3	3	3	2	4		Q0VBF2
ENSMUST00000032264	ENSMUSG00000030161	6	129533160	129542346	1	14	12	30	54	15	12	261	442	204	90	178		Q8R3R8
ENSMUST00000032265	ENSMUSG00000030162	6	129485244	129507165	-1	19	36	175	43	23	18	101	124	94	58	74		Q9EQ09
ENSMUST00000032268	ENSMUSG00000030165	6	129591782	129598775	1	2	5	4	0	1	0	4	22	0	1	2	E9Q3T9	
ENSMUST00000032269	ENSMUSG00000030166	6	119902698	119922828	1	0	0	0	10	10	0	0	58	11	17	33	G5E879	
ENSMUST00000032270	ENSMUSG00000030167	6	129666015	129678973	-1	2	0	3	2	0	0	1	7	0	2	2	Q9Z202	
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ENSMUST00000032272	ENSMUSG00000030168	6	119353150	119417704	-1	12	19	31	17	30	17	2681	5814	3273	688	2365	Q53YY3	Q8BQS5
ENSMUST00000032279	ENSMUSG00000030172	6	119570796	119848167	-1	0	27	42	0	24	19	194	340	140	20	233	F8VPM7	
ENSMUST00000032283	ENSMUSG00000030177	6	120324323	120364374	-1	19	0	9	12	0	12	39	222	88	43	38		Q9CZH8
ENSMUST00000032286	ENSMUSG00000067599	6	130218605	130233322	-1	0	1	0	0	3	2	0	3	0	0	0	F8WJ94	
ENSMUST00000032288	ENSMUSG00000079853	6	130363917	130386874	-1	0	0	0	0	0	0	0	0	0	0	0	Q8MHR8	
ENSMUST00000032306	ENSMUSG00000030187	6	131219223	131247362	-1	87	58	476	109	56	28	278	1288	229	390	282	Q9D3R1	
ENSMUST00000032307	ENSMUSG00000030188	6	131284388	131293244	-1	0	0	1	19	2	0	6	16	7	24	11	A0A023T778	
ENSMUST00000032309	ENSMUSG00000030189	6	131364855	131388476	-1	0	7	19	33	18	9	16	66	47	7	78		Q9JKB3
ENSMUST00000032315	ENSMUSG00000030194	6	132855438	132856355	1	5	3	2	4	2	2	0	0	0	0	0		Q7M713
ENSMUST00000032317	ENSMUSG00000030196	6	133036163	133037101	-1	1	1	0	1	0	1	0	0	0	0	0		Q9JKA3
ENSMUST00000032321	ENSMUSG00000030200	6	134396318	134438736	1	3	6	0	0	9	0	0	0	0	0	0		Q9CPT0
ENSMUST00000032322	ENSMUSG00000030201	6	134446476	134566965	-1	38	35	103	45	51	20	117	254	369	39	307		
ENSMUST00000032326	ENSMUSG00000030204	6	135011612	135023776	1	0	0	0	0	0	0	427	958	465	283	334	Q4VBG1	Q9CWX9
ENSMUST00000032327	ENSMUSG00000030205	6	135105991	135118283	-1	6	9	0	0	13	2	0	0	0	0	0	Q3UUY8	Q9JIL6
ENSMUST00000032330	ENSMUSG00000030208	6	135362545	135383173	1	0	0	0	0	0	0	255	422	210	1010	754	Q4FK43	P47801
ENSMUST00000032331	ENSMUSG00000059003	16	9567898	9995560	-1	15	0	115	0	17	18	0	0	0	0	0		P35436
ENSMUST00000032335	ENSMUSG00000030213	6	136506167	136610862	1	50	35	131	92	41	18	1026	2692	2073	113	1386		Q7TT18
ENSMUST00000032336	ENSMUSG00000030214	6	136612070	136661928	-1	9	4	20	151	7	9	2639	12323	4251	1040	3369		
ENSMUST00000032338	ENSMUSG00000042638	6	136697284	136781765	-1	28	22	128	40	35	11	0	0	0	0	0		Q3UWA6
ENSMUST00000032341	ENSMUSG00000030217	6	136848451	136857733	-1	9	8	30	20	17	5	1	5	6	4	3		Q9CRA0
ENSMUST00000032342	ENSMUSG00000030218	6	136872435	136875823	-1	1	2	1	3	7	3	0	0	0	994	91		P19788
ENSMUST00000032343	ENSMUSG00000030219	6	136907311	136922180	-1	4	3	3	7	4	2	5	52	11	9	16		Q9D8U3
ENSMUST00000032344	ENSMUSG00000030220	6	136923655	136941899	-1	10	7	7	77	16	0	4535	8492	5059	10440	3479		Q61599
ENSMUST00000032347	ENSMUSG00000030222	6	137054825	137170497	-1	10	12	0	0	0	0	0	0	0	0	1		Q8R367
ENSMUST00000032353	ENSMUSG00000030228	6	139587221	139969284	1	0	0	0	0	0	0	0	0	0	0	0	Q4FZD4	
ENSMUST00000032356	ENSMUSG00000030230	6	139989673	140041457	-1	0	5	5	0	5	6	0	0	0	0	0		Q8K4D7
ENSMUST00000032359	ENSMUSG00000030232	6	140622663	140678472	1	8	12	24	9	11	11	49	168	51	12	59		Q9Z248
ENSMUST00000032362	ENSMUSG00000030235	6	141524368	141570177	1	6	0	6	0	6	6	0	0	0	0	0		Q9ERB5
ENSMUST00000032364	ENSMUSG00000030237	6	141805440	141856199	-1	0	0	6	0	0	0	0	0	0	0	0		Q9EP96
ENSMUST00000032370	ENSMUSG00000030243	6	142350342	142387087	-1	2	4	0	0	0	0	42	21	42	60	47	Q3UUK0	Q9Z129
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ENSMUST00000032372	ENSMUSG00000030245	6	142387221	142403858	1	18	12	43	13	15	8	61	192	76	54	67		Q9CR60
ENSMUST00000032373	ENSMUSG00000030246	6	142490249	142507957	-1	9	8	14	5	5	6	48	133	52	98	54		P16125
ENSMUST00000032374	ENSMUSG00000030247	6	142564837	142571614	-1	16	5	25	100	19	6	15	111	14	5	19		
ENSMUST00000032376	ENSMUSG00000057604	6	112273758	112330425	1	9	10	27	18	8	6	0	0	0	1	1	Q3TVW6	Q8VEE1
ENSMUST00000032383	ENSMUSG00000030255	6	145931641	145965223	1	14	0	8	54	19	14	0	0	0	0	18	Q3TRE0	
ENSMUST00000032386	ENSMUSG00000030256	6	145858243	145865558	-1	42	50	155	179	51	22	5	11	7	3	38	Q6L8F5	Q99PV5
ENSMUST00000032388	ENSMUSG00000030259	6	145746748	145821079	1	1	3	0	3	1	0	6	2	14	0	27		Q8CJ96
ENSMUST00000032395						18	12	68	8	12	12	0	0	3	3	2		
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ENSMUST00000032398	ENSMUSG00000030264	6	113046225	113068273	1	0	2	2	11	2	1	78	495	175	275	102		P97770
ENSMUST00000032399	ENSMUSG00000030265	6	145216699	145250239	-1	12	11	53	15	14	16	428	1205	550	169	489	Q5J7N1	P32883
ENSMUST00000032402	ENSMUSG00000030268	6	144993835	145076184	-1	54	40	71	151	43	26	0	3	0	0	0	Q8CBC8	
ENSMUST00000032406	ENSMUSG00000030271	6	113326972	113335068	1	0	0	0	23	18	4	42	140	64	17	71	Q3UIL3	O08760
ENSMUST00000032409	ENSMUSG00000030272	6	113334124	113343984	-1	0	0	2	23	0	0	197	563	206	83	229	Q3UY68	Q91YS8
ENSMUST00000032410	ENSMUSG00000048930	6	113366025	113377883	-1	17	9	50	32	15	9	122	97	91	7	48		Q8R0L9
ENSMUST00000032413	ENSMUSG00000030275	6	143167221	143232307	1	21	19	51	83	30	11	603	1412	928	73	784		Q9D4V0
ENSMUST00000032414	ENSMUSG00000030276	6	113389260	113414587	1	0	0	0	217	10	6	0	17	0	0	18		A4Q9E5
ENSMUST00000032416	ENSMUSG00000030278	6	113424634	113435760	-1	14	0	0	24	20	25	0	0	0	0	0		P56198
ENSMUST00000032419	ENSMUSG00000030282	6	142756686	142775714	1	1	5	9	11	9	2	926	3386	1259	298	548		
ENSMUST00000032421	ENSMUSG00000030283	6	142821545	142964452	-1	266	208	1442	1315	239	155	75	156	131	49	98		Q64687
ENSMUST00000032422	ENSMUSG00000030284	6	113483297	113493343	1	9	8	9	0	11	3	46	26	19	10	20	A8C1T7	Q91XD7
ENSMUST00000032425	ENSMUSG00000030286	6	113514874	113531652	-1	17	18	41	59	13	6	457	1289	638	489	478		Q99KI3
ENSMUST00000032427	ENSMUSG00000040250	6	146549632	146577835	-1	15	2	12	79	7	2	103	519	341	161	181		Q8QZV7
ENSMUST00000032429	ENSMUSG00000030291	6	146642547	146650732	1	0	0	0	0	0	0	150	459	135	212	51		Q9CQ39

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000032433	ENSMUSG00000030292	6	146850104	146871406	1	1	5	5	0	0	1	0	0	0	0	0		Q9DA21
ENSMUST00000032440	ENSMUSG00000030298	6	113728062	113740743	-1	9	3	15	12	14	1	510	930	490	630	429		Q9D1M0
ENSMUST00000032441	ENSMUSG00000030301	6	147475828	147632612	1	17	6	7	78	13	12	20	106	73	65	60		Q9D8L5
ENSMUST00000032443	ENSMUSG00000030303	6	148047259	148182758	1	15	10	42	55	14	7	6	12	14	2	9		Q7TNT2
ENSMUST00000032446	ENSMUSG00000030304	6	148179079	148212374	-1	0	0	0	0	0	0	83	421	207	567	151	F8WJ78	
ENSMUST00000032447						4	8	0	15	6	0	6	25	3	0	11		
ENSMUST00000032451	ENSMUSG00000030307	6	114131241	114249952	1	30	17	43	57	28	15	0	0	0	0	0		P31650
ENSMUST00000032454	ENSMUSG00000030310	6	114282635	114317532	1	32	28	70	60	47	26	0	0	0	0	0		P31648
ENSMUST00000032457	ENSMUSG00000030314	6	114643097	114860614	1	0	0	61	48	16	26	1021	2320	1033	190	837		Q9D906
ENSMUST00000032459	ENSMUSG00000030315	6	114860628	114969994	-1	7	4	24	12	9	4	180	309	229	9	205		Q80V24
ENSMUST00000032461	ENSMUSG00000030316	6	115004381	115037876	-1	7	1	2	22	0	0	14	65	19	15	30	G5E881	
ENSMUST00000032462	ENSMUSG00000030317	6	115241892	115252205	-1	5	10	20	32	9	4	0	0	0	0	0	Q3USH7	Q9JHB3
ENSMUST00000032468	ENSMUSG00000030321	6	115810729	115838412	-1	4	2	0	7	5	0	0	0	0	0	1	V9GXH0	
ENSMUST00000032469	ENSMUSG00000030322	6	115840697	115853371	-1	47	9	31	53	19	19	48	150	58	28	46		
ENSMUST00000032471	ENSMUSG00000030324	6	115931748	115940036	1	26	21	37	55	43	20	0	1	0	0	0		P15409
ENSMUST00000032472	ENSMUSG00000079298	6	128813706	128826331	-1	18	8	8	6	7	10	0	0	1	5	5		Q99JB4
ENSMUST00000032473	ENSMUSG00000054072	18	60376029	60392627	1	0	14	21	0	16	0	0	0	0	0	12	J7NNX8	Q9QZ85
ENSMUST00000032476	ENSMUSG00000003153	6	122727809	122801640	-1	0	3	10	10	6	3	10645	20334	10874	1649	7998	Q3TPL8	P32037
ENSMUST00000032477	ENSMUSG00000030327	6	122874474	122888941	1	29	19	47	40	32	17	199	1054	319	88	290	Q0VB06	Q9CR95
ENSMUST00000032479	ENSMUSG00000030329	6	124996694	125003096	1	0	0	11	53	0	0	11	11	11	0	22		Q6P1B3
ENSMUST00000032480	ENSMUSG00000030330	6	125039760	125049265	1	0	0	0	0	0	0	567	2468	319	252	343		Q8C0D7
ENSMUST00000032481	ENSMUSG00000072770	6	125049689	125063267	1	0	0	9	5	6	0	2	0	0	0	5	Q6P8Q6	
ENSMUST00000032485	ENSMUSG00000030335	6	125191801	125196269	1	151	113	305	121	126	74	52	180	87	64	75		Q9CPY1
ENSMUST00000032486	ENSMUSG00000030336	6	125232622	125237010	-1	48	29	245	45	60	22	54	96	32	6	93	Q3U4X0	P41272
ENSMUST00000032487	ENSMUSG00000030337	6	125215551	125245964	1	6	8	21	17	19	0	10	142	13	0	15		Q62442
ENSMUST00000032489	ENSMUSG00000030339	6	125306571	125313885	-1	9	5	42	156	16	11	2532	3352	2028	311	1465	B2RRV3	P50284
ENSMUST00000032491	ENSMUSG00000030341	6	125349362	125362484	1	12	11	26	65	20	13	7629	10701	6383	805	4997	Q3U479	P25118
ENSMUST00000032492	ENSMUSG00000030342	6	125460266	125494791	-1	5	3	9	48	14	1	2416	5255	2234	3550	2293		P40240
ENSMUST00000032495						5	0	0	8	13	1	0	0	1	0	0		
ENSMUST00000032497	ENSMUSG00000030347	6	126939962	126975967	1	10	12	18	20	12	8	96	443	214	452	138		Q91YN0
ENSMUST00000032500	ENSMUSG00000030350	6	127689011	127769472	-1	35	26	195	173	33	17	0	0	0	0	0		Q6PAK3
ENSMUST00000032501	ENSMUSG00000030351	6	127887589	127953977	1	37	17	75	53	56	22	0	0	0	9	8		Q9D1D1
ENSMUST00000032503	ENSMUSG00000030352	6	127961396	128143594	-1	0	0	0	34	0	0	0	0	0	0	0		Q8BJU2
ENSMUST00000032508	ENSMUSG00000030357	6	128429735	128438677	-1	0	0	0	0	0	0	337	381	182	142	258		P30416
ENSMUST00000032510						1	1	2	1	18	1	0	0	0	0	0		
ENSMUST00000032512	ENSMUSG00000030361	6	128609227	128623533	-1	11	9	13	4	4	9	0	0	0	11	3	G5E882	
ENSMUST00000032517						0	2	0	1	2	0	0	0	0	0	0		
ENSMUST00000032518	ENSMUSG00000030364	6	128662385	128677374	1	36	27	34	47	30	17	1	6	0	1	5		Q8C1T8
ENSMUST00000032519	ENSMUSG00000030365	6	128887588	128898167	1	2	0	0	0	0	3	3	15	0	18	8	B2RTA4	Q9WVF9
ENSMUST00000032520	ENSMUSG00000030366	7	18065929	18077986	1	0	0	0	0	1	2	0	0	0	0	0	Q3UKP4	
ENSMUST00000032539	ENSMUSG00000030382	7	12988346	12998192	-1	0	7	25	12	12	3	1	0	0	8	1		Q4LDG0
ENSMUST00000032541	ENSMUSG00000030385	7	12512517	12556323	1	2	1	1	3	2	1	0	0	0	0	0	Q5I0V9	
ENSMUST00000032551	ENSMUSG00000030393	7	10487229	10495394	-1	25	18	27	14	26	9	8	6	4	6	4		Q80YP6
ENSMUST00000032555	ENSMUSG00000002984	7	19701313	19715438	-1	0	0	0	99	0	0	0	0	0	0	0		Q9QYA2
ENSMUST00000032557	ENSMUSG00000024969	19	7275396	7341860	-1	10	6	30	15	23	8	3386	5642	3716	244	2904		
ENSMUST00000032559	ENSMUSG00000030401	7	19282662	19296164	1	14	5	13	158	21	11	3	1	2	0	2	Q6IM75	O70622
ENSMUST00000032560	ENSMUSG00000030402	7	19276805	19280064	-1	11	10	28	462	29	10	0	2	1	1	0		Q8BGL1
ENSMUST00000032561	ENSMUSG00000030403	7	19256929	19271817	-1	23	7	21	263	21	16	20732	26464	15151	1394	9551		P70460
ENSMUST00000032566	ENSMUSG00000030407	7	19139702	19149291	-1	11	11	33	48	18	12	146	249	134	25	139		Q8BH73
ENSMUST00000032568	ENSMUSG00000030409	7	19083849	19093821	1	0	0	12	25	14	0	0	0	0	0	0		P54265
ENSMUST00000032570	ENSMUSG00000030410	7	19076227	19082776	1	0	0	0	120	16	0	0	0	0	0	0		Q08274
ENSMUST00000032571	ENSMUSG00000030411	7	18925888	18965319	1	89	64	186	808	113	58	0	4	1	1	0	D3YVV7	
ENSMUST00000032573	ENSMUSG00000030413	7	18871331	18890459	1	12	5	33	32	16	11	29088	39055	18219	13073	8836	Q4FK86	O88593
ENSMUST00000032585	ENSMUSG00000030423	7	38261996	38271423	-1	6	4	5	4	10	4	95	335	166	439	113		Q9CR08
ENSMUST00000032590	ENSMUSG00000056014	5	138622859	138652414	1	23	21	203	33	23	17	3	4	4	3	1	Q3V2D1	
ENSMUST00000032591	ENSMUSG00000029587	5	143235163	143248834	1	15	30	30	39	11	5	6	5	6	5	18		Q7TSI0
ENSMUST00000032594	ENSMUSG00000030428	7	4119408	4136708	1	0	1	0	0	0	0	0	0	0	0	0	G8JL37	
ENSMUST00000032597	ENSMUSG00000030432	7	4792874	4795066	1	6	3	10	18	1	0	1929	2147	1455	3854	1141	Q5M9J8	P41105
ENSMUST00000032598	ENSMUSG00000030433	7	4956134	4964390	-1	4	3	4	35	8	0	0	0	0	0	0		P0C5K1
ENSMUST00000032622	ENSMUSG00000063535	7	7130678	7136755	-1	114	62	474	99	113	47	0	25	6	13	16	Q9CZ29	
ENSMUST00000032627	ENSMUSG00000033790	7	55794154	55831677	1	8	15	13	22	12	9	45	191	125	186	89		Q8BKN5
ENSMUST00000032629	ENSMUSG00000030447	7	55841745	55932602	1	0	0	4	25	0	4	360	54	84	15	41		Q7TMB8
ENSMUST00000032633	ENSMUSG00000030450	7	56239760	56536518	1	7	0	1	2	0	7	0	0	0	0	0		Q62052
ENSMUST00000032635	ENSMUSG00000030452	7	55931287	55962476	-1	0	0	0	0	0	0	86	380	164	85	200		Q9JJC8
ENSMUST00000032648	ENSMUSG00000030463	7	42445462	42448120	-1	14	12	29	21	12	4	0	1	0	0	0	Q9D420	
ENSMUST00000032658	ENSMUSG00000030470	7	48830398	48848051	-1	3	0	2	7	12	3	4	10	0	3	1	Q545C7	P50462
ENSMUST00000032661	ENSMUSG00000055102	7	43607169	43618285	1	11	3	0	0	0	4	0	0	0	0	0	Q80V81	
ENSMUST00000032663	ENSMUSG00000030472	7	43634707	43649295	1	75	57	345	112	56	40	31	262	95	6	100		Q9D871
ENSMUST00000032667	ENSMUSG00000030474	7	43651070	43660161	-1	34	22	60	29	43	15	7220	12946	7032	824	6283		Q91Y57
ENSMUST00000032673	ENSMUSG00000074282	7	24301704	24316666	-1	0	0	36	25	28	15	5	8	8	1	3	Q61117	
ENSMUST00000032683	ENSMUSG00000030484	7	24349196	24355109	1	4	4	12	35	5	2	0	0	0	0	0		Q9D7Z7
ENSMUST00000032696	ENSMUSG00000055305	7	24270420	24277794	1	18	10	16	12	21	19	1	0	5	3	3		Q61116
ENSMUST00000032701	ENSMUSG00000030491	7	35469098	35537745	-1	0	7	10	10	1	0	0	0	1	0	0		Q9CWU0
ENSMUST00000032703	ENSMUSG00000030492	7	35448796	35466036	1	6	0	0	2	5	2	0	0	0	0	0	Q3UQE3	Q9QXA6
ENSMUST00000032704	ENSMUSG00000030493	7	35392152	35396836	-1	11	7	13	0	21	8	61	84	79	15	54		Q8BHL6
ENSMUST00000032705	ENSMUSG00000030494	7	35334170	35392289	1	38	24	45	114	45	15	0	4	7	2	13		Q8BWR8
ENSMUST00000032709	ENSMUSG00000030499	7	34639014	34656732	-1	0	0	0	54	7	0	0	0	0	0	0		Q8K0E1
ENSMUST00000032710	ENSMUSG00000030500	7	51621830	51671125	1	16	24	24	20	25	10	0	0	0	0	1		
ENSMUST00000032715	ENSMUSG00000030505	7	49778346	49858265	1	7	9	4	5	9	3	31	130	55	67	81		Q922H1
ENSMUST00000032717	ENSMUSG00000030507	7	49631499	49636849	-1	19	10	29	256	29	12	0	0	0	0	0		P52950
ENSMUST00000032719	ENSMUSG00000020181	10	109682660	110456204	-1	42	30	129	42	54	23	0	0	0	0	12	E9QMF5	
ENSMUST00000032723	ENSMUSG00000030512	7	66059003	66074587	1	0	0	0	0	0	1	11	41	27	25	7	G5E883	
ENSMUST00000032726	ENSMUSG00000078681	7	65691169	65701913	1	0	0	11	0	4	0	76	169	87	216	63		Q8BJ83
ENSMUST00000032728	ENSMUSG00000030515	7	65644898	65692091	1	8	8	3	28	8	11	9	20	16	6	24		Q8BLY2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000032729	ENSMUSG00000030516	7	65296165	65527781	-1	21	0	57	0	36	9	1	5	3	0	86	B9EHJ3	
ENSMUST00000032732	ENSMUSG00000030519	7	64501706	64753878	1	11	11	34	165	46	13	0	0	0	0	0		P98084
ENSMUST00000032735	ENSMUSG00000030521	7	64376527	64392268	-1	7	2	5	15	4	2	76	377	196	456	87		Q810V0
ENSMUST00000032736	ENSMUSG00000030522	7	64287653	64340806	1	10	14	13	12	24	9	185	275	266	97	224		Q7TPM9
ENSMUST00000032737						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000032738	ENSMUSG00000030525	7	63098692	63212526	-1	17	9	19	81	20	11	0	0	0	0	0	Q53YJ9	P49582
ENSMUST00000032747	ENSMUSG00000030532	7	80343104	80350547	1	4	4	22	37	7	3	39	96	32	191	26		Q9D114
ENSMUST00000032748	ENSMUSG00000030533	7	80325292	80341005	-1	1	0	0	0	0	0	764	976	721	62	669		Q99KD5
ENSMUST00000032749	ENSMUSG00000030534	7	80269649	80291754	1	7	73	0	376	0	0	62	102	94	12	92		P59016
ENSMUST00000032754	ENSMUSG00000030539	7	80186841	80226527	1	78	40	131	144	74	29	253	298	283	23	299		Q62179
ENSMUST00000032760	ENSMUSG00000030544	7	79792241	79793788	-1	9	10	8	255	18	9	0	0	0	0	0		P97309
ENSMUST00000032761	ENSMUSG00000030545	7	79735957	79743131	-1	10	10	21	10	18	13	6	36	12	12	25		Q9Z211
ENSMUST00000032762	ENSMUSG00000030546	7	79720218	79732903	-1	16	9	32	34	41	0	0	0	0	0	0		Q8CGN5
ENSMUST00000032766	ENSMUSG00000030549	7	79593363	79617657	-1	15	12	32	45	16	9	2	6	3	1	0		Q9QXP0
ENSMUST00000032768	ENSMUSG00000030551	7	70351946	70366735	-1	37	24	74	600	91	41	1	0	0	0	2	Q3UST6	P43135
ENSMUST00000032770	ENSMUSG00000030553	7	68236608	68264233	-1	8	6	25	34	7	6	2	3	2	1	3	E9QM76	
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ENSMUST00000032775	ENSMUSG00000030556	7	67513411	67645268	-1	3	1	14	3	7	0	13	26	4	21	10	Q9D7Y1	
ENSMUST00000032776	ENSMUSG00000030557	7	67231163	67372858	-1	0	5	0	2	3	0	57	20	324	4	122		Q60929
ENSMUST00000032779	ENSMUSG00000030560	7	88278085	88310888	1	5	3	12	44	7	1	1152	5293	1406	1265	1577	Q3UBY5	P97821
ENSMUST00000032781	ENSMUSG00000030562	7	87246096	87398710	1	0	2	1	0	0	0	0	0	0	0	0	B2RSM1	Q9JHI8
ENSMUST00000032796	ENSMUSG00000011427	7	29816072	29832042	1	27	18	41	19	28	0	70	252	165	97	116	Q80ZX2	
ENSMUST00000032797	ENSMUSG00000059975	7	29930815	29954089	-1	0	0	0	0	0	0	7	0	6	3	8		Q80W31
ENSMUST00000032800	ENSMUSG00000030579	7	30413788	30417577	1	17	22	70	67	20	9	18830	33644	12647	54038	9361	Q3U419	O54885
ENSMUST00000032802	ENSMUSG00000046185	7	29768552	29779821	1	36	27	85	33	50	14	178	465	374	313	272	Q9D654	
ENSMUST00000032803	ENSMUSG00000047473	7	29783998	29794702	1	0	0	42	36	0	0	8	28	15	0	11	Q78FW7	
ENSMUST00000032808	ENSMUSG00000030587	7	29246561	29248432	-1	12	18	60	136	11	10	0	0	0	39	3	Q9D809	
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ENSMUST00000032811	ENSMUSG00000030589	7	29134851	29153961	1	7	2	9	37	0	4	3607	8359	4482	450	4340		Q8BTM9
ENSMUST00000032813	ENSMUSG00000030592	7	29003340	29125151	-1	85	0	12	299	1	64	44	88	67	26	43	K3W4M2	
ENSMUST00000032815	ENSMUSG00000030595	7	28758251	28767512	-1	9	9	9	11	17	4	36	57	44	12	35		Q60778
ENSMUST00000032818	ENSMUSG00000030598	7	28716804	28738144	1	26	12	20	212	31	0	6	0	0	5	13	Q3V064	Q9QZM8
ENSMUST00000032820	ENSMUSG00000022228	13	21442175	21453730	-1	34	28	40	38	51	19	55	351	133	28	120	F8WJ31	
ENSMUST00000032823	ENSMUSG00000030602	7	28399549	28598185	-1	73	46	299	227	79	43	81	48	16	2	44		Q8BTW9
ENSMUST00000032824	ENSMUSG00000030603	7	28041707	28050101	-1	2	0	4	4	0	0	637	997	636	429	453		P54775
ENSMUST00000032825	ENSMUSG00000030605	7	79133768	79149060	-1	0	0	8	19	19	0	13	11	20	38	43		P21956
ENSMUST00000032827	ENSMUSG00000030606	7	79115102	79131018	-1	15	6	39	41	20	8	1	0	0	0	1		Q80WM5
ENSMUST00000032835	ENSMUSG00000030607	7	79053483	79115099	1	60	37	161	122	79	42	0	0	0	0	0		Q61282
ENSMUST00000032839	ENSMUSG00000030610	7	78821547	78847263	-1	16	9	9	69	8	9	127	116	145	42	63		Q9D0A0
ENSMUST00000032840	ENSMUSG00000030611	7	78783119	78792989	1	6	0	0	0	0	1	9	54	0	25	0	Q3U8Y1	
ENSMUST00000032841	ENSMUSG00000030612	7	78775236	78783531	-1	7	7	16	23	6	1	59	178	70	280	45		Q9EQI8
ENSMUST00000032842	ENSMUSG00000030613	7	92561149	92582294	1	0	0	5	12	3	0	6	72	27	70	32		Q8C3X2
ENSMUST00000032843	ENSMUSG00000030614	7	90468194	90476001	-1	6	4	10	13	12	0	50	219	77	197	40		Q9D1R1
ENSMUST00000032844	ENSMUSG00000030615	7	90450700	90457229	-1	0	0	3	26	0	0	34	144	28	57	13		Q9D8Y1
ENSMUST00000032853	ENSMUSG00000030621	7	89632392	89854359	1	2	0	4	3	0	0	0	0	0	0	0	E9PZP7	
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ENSMUST00000032865	ENSMUSG00000030630	7	84585159	84606722	-1	3	8	14	30	19	7	876	1294	928	130	287		P35505
ENSMUST00000032872						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000032874	ENSMUSG00000030638	7	82173840	82307419	1	0	0	0	6	0	0	0	0	0	0	0		
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ENSMUST00000032879	ENSMUSG00000030643	7	92741603	92837117	1	3	3	0	8	5	0	0	2	0	0	0	Q0PD24	Q923S9
ENSMUST00000032882	ENSMUSG00000030647	7	97400003	97407802	1	3	3	15	100	19	5	163	91	30	278	39		Q9CQ54
ENSMUST00000032884						0	0	0	0	0	0	30	30	16	50	18		
ENSMUST00000032887	ENSMUSG00000030652	7	118509659	118533356	-1	1	1	6	21	4	0	25	43	19	58	26		P97478
ENSMUST00000032888	ENSMUSG00000030654	7	118118891	118129662	-1	11	8	25	51	18	3	1887	5417	1871	1665	1309	Q80ZW9	Q9JKW0
ENSMUST00000032891	ENSMUSG00000030655	7	118131308	118243637	-1	65	64	98	53	95	46	1325	3242	2073	195	1747		Q8BKX6
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ENSMUST00000032895	ENSMUSG00000030659	7	116504369	116540584	1	9	5	9	16	7	3	206	874	468	1065	349		P81117
ENSMUST00000032898	ENSMUSG00000030662	14	120911194	120948042	1	24	20	33	40	24	12	175	485	274	207	355		Q8BKC5
ENSMUST00000032899	ENSMUSG00000030663	7	116039397	116105210	1	12	8	19	73	26	0	384	802	435	484	351		Q9R0P4
ENSMUST00000032902	ENSMUSG00000030666	7	114718643	114723365	1	0	0	0	0	3	4	0	0	0	0	0	Q3UW96	
ENSMUST00000032906	ENSMUSG00000030669	7	114631478	114636357	-1	6	4	8	0	2	4	0	0	0	0	0		Q99JA0
ENSMUST00000032907	ENSMUSG00000030669	7	114631478	114636357	-1	7	6	13	22	5	4	0	0	0	4	1		P70160
ENSMUST00000032908	ENSMUSG00000030670	7	114550166	114562972	-1	0	0	0	0	0	0	0	0	0	0	0	Q32MW1	Q6VVW9
ENSMUST00000032909	ENSMUSG00000030671	7	114415281	114539251	1	23	29	89	293	35	11	23	67	32	20	73	E9QLQ3	
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ENSMUST00000032912	ENSMUSG00000030674	7	127107114	127122226	-1	56	61	132	87	54	22	9	17	6	6	12		Q91X91
ENSMUST00000032915	ENSMUSG00000030677	7	127027729	127042471	-1	16	12	22	42	14	8	181	178	198	48	131		Q3V300
ENSMUST00000032916	ENSMUSG00000030678	7	127022130	127027037	-1	14	8	34	406	25	8	1562	2557	1199	215	1136	F8VPK3	
ENSMUST00000032918						21	15	81	85	31	20	691	878	498	109	364		
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ENSMUST00000032924	ENSMUSG00000030685	7	126928879	126945631	1	7	7	37	170	16	4	185	397	175	24	187		Q8BGV7
ENSMUST00000032926	ENSMUSG00000060538	7	126886171	126922917	-1	0	0	0	0	0	0	263	259	237	326	124		Q9D123
ENSMUST00000032927	ENSMUSG00000030688	7	101317086	101346626	1	0	2	0	27	0	0	0	0	0	0	0	Q0VG22	Q9JMD3
ENSMUST00000032931	ENSMUSG00000030691	7	101108775	101284405	1	18	0	16	2	22	5	0	0	0	0	0		Q3USJ8
ENSMUST00000032934	ENSMUSG00000030695	7	126795234	126800751	-1	4	7	13	68	14	5	21772	23459	13406	3013	8535	Q5FWB7	P05064
ENSMUST00000032936	ENSMUSG00000030697	7	126785866	126792496	-1	6	9	26	151	16	10	1858	4606	1592	444	1303	Q3UNF2	P97470
ENSMUST00000032944	ENSMUSG00000030703	7	126766334	126775649	1	4	5	17	15	9	5	67	189	54	198	61		Q99LY2
ENSMUST00000032946	ENSMUSG00000030704	7	100607410	100641268	1	5	0	0	0	13	0	453	1723	1220	117	509	Q0PD54	P35279
ENSMUST00000032949	ENSMUSG00000030707	7	126699773	126707787	-1	7	14	7	110	19	9	57192	55667	27908	12731	17927	Q3U1N0	O89053
ENSMUST00000032955	ENSMUSG00000030713	7	43811294	43816359	1	20	16	28	21	20	15	0	0	0	0	0	A0A0B6VPC4	Q91VE3
ENSMUST00000032956	ENSMUSG00000030714	7	126649309	126672925	1	3	0	6	6	10	1	90	75	61	47	59		Q9DA08
ENSMUST00000032958	ENSMUSG00000032942	7	100472990	100486432	1	7	13	12	16	22	9	3	2	0	0	4	B2RTM2	P56501
ENSMUST00000032961	ENSMUSG00000030717	7	126623249	126630861	-1	3	5	20	0	2	0	89	358	122	513	81		Q9WTK0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000032962	ENSMUSG00000030720	7	126571207	126585817	-1	0	0	0	0	0	0	0	0	0	0	0		Q61124
ENSMUST00000032963	ENSMUSG00000030718	7	100326737	100371896	-1	16	12	40	55	25	9	458	557	368	138	345		Q8BVQ5
ENSMUST00000032967	ENSMUSG00000030725	7	100159277	100161365	1	9	9	10	204	12	1	1	15	3	2	0		Q9D009
ENSMUST00000032968	ENSMUSG00000030724	7	126408450	126414889	-1	23	13	50	21	24	12	89	75	52	28	338		P25918
ENSMUST00000032969	ENSMUSG00000030726	7	100082111	100121565	-1	14	4	20	85	12	4	144	531	234	83	186	Q8BH76	
ENSMUST00000032974	ENSMUSG00000030730	7	126445858	126463108	-1	23	15	56	40	32	14	3	27	12	4	18		Q8R429
ENSMUST00000032977	ENSMUSG00000030732	7	100006404	100034728	1	10	0	26	6	12	0	0	0	0	0	0	A0A0B4J1E8	
ENSMUST00000032978	ENSMUSG00000030733	7	126466994	126475424	-1	31	31	56	172	43	28	755	1325	736	59	790		Q91ZM2
ENSMUST00000032981	ENSMUSG00000030735	8	67514000	67515606	-1	10	14	5	3	20	9	0	0	8	0	0	D3YVN7	
ENSMUST00000032985	ENSMUSG00000030737	7	99657804	99711340	-1	9	11	11	3	13	8	0	0	0	0	0		Q8BXB6
ENSMUST00000032988	ENSMUSG00000030800	7	127925716	127930104	-1	13	15	34	25	33	11	4	3	0	2	3	Q99L44	
ENSMUST00000032992	ENSMUSG00000030738	7	126546455	126566411	-1	19	19	22	67	31	8	1132	3116	2166	1331	1538		Q8R1B4
ENSMUST00000032994	ENSMUSG00000030741	7	126370060	126377450	-1	0	0	28	14	8	0	277	157	72	0	177		Q8R0G7
ENSMUST00000032995	ENSMUSG00000018909	7	99535466	99606771	1	0	5	0	0	0	0	0	0	0	0	0		Q8BWG8
ENSMUST00000032997	ENSMUSG00000030742	7	126363824	126369570	-1	16	13	25	100	18	10	105	158	52	48	132	Q546H1	O54957
ENSMUST00000032998	ENSMUSG00000030744	7	99477896	99483738	-1	19	24	48	58	14	14	4671	5709	3160	14121	2322	Q5YLW3	P62908
ENSMUST00000033000	ENSMUSG00000030745	7	125603429	125633570	1	77	76	280	1086	117	71	41	47	25	29	168	Q3TAI3	Q9JHX3
ENSMUST00000033001	ENSMUSG00000030747	7	99153663	99182713	-1	17	16	31	130	31	9	6584	6303	4773	478	3031		Q9DCV3
ENSMUST00000033004	ENSMUSG00000030748	7	125552120	125579474	1	45	24	132	118	62	24	20389	21534	17248	2377	11067	Q3U905	P16382
ENSMUST00000033006	ENSMUSG00000030750	7	125467640	125491596	-1	7	1	25	63	10	4	693	1392	514	1344	308		
ENSMUST00000033008	ENSMUSG00000030751	7	114264606	114276118	-1	1	1	2	24	5	0	589	2583	559	2357	555	Q3TS44	Q9R1P4
ENSMUST00000033009	ENSMUSG00000030753	7	98703103	98718062	1	24	25	46	49	33	20	70	271	113	64	140		Q9CUX1
ENSMUST00000033010	ENSMUSG00000030752	7	125444676	125462269	1	27	16	42	37	42	21	55	93	67	7	56		Q9CXT6
ENSMUST00000033012	ENSMUSG00000030754	7	114215559	114254680	-1	9	9	15	35	9	2	693	3303	1502	1148	798		Q9JIF7
ENSMUST00000033015	ENSMUSG00000074141	7	44816088	44840809	1	7	9	14	0	14	7	29	31	0	3	27		
ENSMUST00000033018	ENSMUSG00000030759	7	113513834	113571511	1	0	0	0	30	0	5	318	1041	244	465	194		Q922J9
ENSMUST00000033020	ENSMUSG00000030760	7	98206389	98321208	-1	16	0	35	35	0	12	160	563	197	206	73		Q9D099
ENSMUST00000033023	ENSMUSG00000030762	7	123462291	123468004	1	9	8	27	10	0	3	0	0	0	0	0		P56404
ENSMUST00000033025	ENSMUSG00000030763	7	123369784	123430358	1	13	6	29	57	20	9	114	313	110	118	84	A2RTH5	
ENSMUST00000033030	ENSMUSG00000030770	7	112427505	112591692	1	13	22	27	78	25	10	0	0	0	23	65		Q9EPC1
ENSMUST00000033033	ENSMUSG00000030771	7	112368308	112413104	1	21	13	52	16	20	9	0	0	0	0	0		Q9D5U9
ENSMUST00000033035	ENSMUSG00000030769	7	123214780	123273253	1	15	10	0	20	10	6	0	0	0	0	0		Q8K0E3
ENSMUST00000033036	ENSMUSG00000030772	7	112116019	112159057	-1	17	21	87	83	40	15	0	0	0	1	5		Q9QUN9
ENSMUST00000033040	ENSMUSG00000030774	7	97788541	97912381	1	8	13	8	26	0	8	176	775	286	146	207	G5E884	
ENSMUST00000033044	ENSMUSG00000030780	7	128271379	128298170	-1	0	14	0	131	16	7	32	39	25	0	35		
ENSMUST00000033045	ENSMUSG00000030781	7	128265657	128272430	1	0	0	0	4	4	0	0	0	0	0	0		
ENSMUST00000033049	ENSMUSG00000030785	7	128205435	128206387	-1	6	1	6	6	1	4	0	3	0	11	0		P43023
ENSMUST00000033050	ENSMUSG00000030787	7	110850607	110862953	-1	18	14	30	26	15	15	4	12	6	184	154		Q8BHC0
ENSMUST00000033051	ENSMUSG00000070369	7	128154376	128223816	1	14	11	0	0	14	6	0	0	0	0	0	E9PXZ7	
ENSMUST00000033053	ENSMUSG00000030789	7	128129547	128150657	1	22	26	82	56	46	23	109	653	165	53	489		Q9QXH4
ENSMUST00000033054	ENSMUSG00000030790	7	110627661	110629820	1	36	27	188	0	33	20	1	2	1	4	5		P97297
ENSMUST00000033056	ENSMUSG00000030793	7	127989708	127993867	-1	14	7	39	32	9	7	677	768	492	2424	327	Q54AA2	Q9EPB4
ENSMUST00000033057	ENSMUSG00000030792	7	45207525	45211883	-1	9	14	34	18	16	12	17	12	8	2	3		Q9QZL9
ENSMUST00000033058	ENSMUSG00000038371	7	110308013	110614922	-1	0	0	0	17	0	10	0	0	0	0	0	E9PXF8	
ENSMUST00000033060	ENSMUSG00000030796	7	45215753	45233635	1	0	0	0	7	7	2	0	0	0	4	6	Q3UPV9	P48301
ENSMUST00000033063	ENSMUSG00000030798	7	45233632	45239115	-1	3	2	12	0	14	2	655	972	750	103	548	Q3U429	
ENSMUST00000033070	ENSMUSG00000030801	7	127912516	127925837	1	8	8	33	74	25	6	150	427	154	179	169		Q9D1P2
ENSMUST00000033074	ENSMUSG00000096145	7	127893063	127895617	-1	4	2	24	32	11	0	35	47	19	52	29		Q9CRC0
ENSMUST00000033075	ENSMUSG00000030805	7	127824294	127849019	1	5	2	9	93	8	1	275	589	346	132	222		P70452
ENSMUST00000033081	ENSMUSG00000030811	7	127744543	127769483	1	0	0	0	90	14	0	0	26	58	0	29		Q6PB97
ENSMUST00000033086	ENSMUSG00000030815	7	127573340	127583307	1	0	0	0	0	0	0	425	476	459	374	351		Q9DB30
ENSMUST00000033087	ENSMUSG00000003868	7	45421852	45438096	-1	8	9	15	40	23	18	29	43	74	0	105	Q3TXT7	Q9WTM5
ENSMUST00000033088	ENSMUSG00000030816	7	127588767	127604799	1	30	15	72	146	44	24	1867	2608	1999	213	1776		Q3U319
ENSMUST00000033093	ENSMUSG00000003873	7	45461695	45466898	-1	8	2	5	22	8	5	549	630	272	336	295	Q544Z6	Q07813
ENSMUST00000033095	ENSMUSG00000030822	7	127459611	127476759	1	5	8	24	101	18	7	482	921	644	90	655		Q7TPN9
ENSMUST00000033096	ENSMUSG00000030824	7	45492874	45510406	-1	22	11	46	16	22	15	1967	1683	1477	221	1169		Q02819
ENSMUST00000033098	ENSMUSG00000030826	7	45570153	45589710	1	0	7	14	58	10	5	148	76	113	35	1	Q3ULU3	O35855
ENSMUST00000033099	ENSMUSG00000030827	7	45613907	45615490	-1	6	7	20	15	7	5	0	0	0	0	0		Q9JJN1
ENSMUST00000033100	ENSMUSG00000064158	7	45621811	45628823	1	6	3	3	2	6	5	0	1	0	1	0		Q9D9J7
ENSMUST00000033121	ENSMUSG00000030835	7	46033698	46084212	1	27	28	66	83	40	17	304	265	324	32	373		Q6GQT9
ENSMUST00000033123	ENSMUSG00000040136	7	46104523	46180033	-1	41	29	107	86	62	36	4	15	12	0	10	B2RUS7	
ENSMUST00000033127	ENSMUSG00000030839	7	46443168	46639807	-1	3	7	16	38	5	8	60	71	39	31	27		Q80YD6
ENSMUST00000033131	ENSMUSG00000030842	7	101905904	101926675	1	9	15	33	52	20	11	2847	3139	1586	812	951		Q9CQ22
ENSMUST00000033133	ENSMUSG00000030844	7	128373621	128418758	-1	1	2	0	23	3	2	77	325	83	392	126	Q32MD7	Q9CQE5
ENSMUST00000033135	ENSMUSG00000030846	7	128439777	128461717	-1	0	0	0	0	0	0	110	728	241	15	113	Q921W2	
ENSMUST00000033136	ENSMUSG00000030847	7	128523616	128546981	1	25	15	76	259	38	18	75	124	56	22	135		Q9JLV1
ENSMUST00000033139	ENSMUSG00000030850	7	130391526	130519961	-1	0	21	43	100	35	23	77	276	69	39	23		Q9Z2A5
ENSMUST00000033141	ENSMUSG00000030852	7	130577484	130764784	1	11	9	0	178	24	11	0	0	0	0	0	E9QL08	
ENSMUST00000033142	ENSMUSG00000030854	7	47077798	47133684	-1	0	7	2	113	0	8	0	0	0	0	0		P54830
ENSMUST00000033146	ENSMUSG00000030858	7	131325944	131329516	-1	3	1	0	3	1	1	0	0	0	0	0		Q9DAL9
ENSMUST00000033149	ENSMUSG00000030862	7	132042816	132154739	-1	29	15	42	64	21	13	0	0	0	0	0		
ENSMUST00000033152	ENSMUSG00000030865	7	122219496	122222824	1	10	1	15	18	10	2	0	0	0	6	5		Q9D869
ENSMUST00000033153	ENSMUSG00000030866	7	122169893	122186207	-1	23	18	58	30	32	8	0	0	0	0	0		Q9Z2E3
ENSMUST00000033154	ENSMUSG00000030867	7	122159439	122169873	1	21	21	63	114	25	15	252	148	265	12	117	Q3TPZ2	Q07832
ENSMUST00000033156	ENSMUSG00000030868	7	122133041	122149044	1	0	12	0	9	8	6	394	1722	500	706	361		Q9QZB9
ENSMUST00000033157	ENSMUSG00000030869	7	122085403	122101886	-1	28	31	61	36	18	10	11	47	14	7	16	Q569N0	Q9CR21
ENSMUST00000033158	ENSMUSG00000030870	7	122067175	122082194	1	27	20	89	85	33	15	79	209	99	22	91		Q78JW9
ENSMUST00000033159	ENSMUSG00000030871	7	122037213	122067263	-1	3	1	2	126	6	0	6	8	0	11	10		Q9CXJ1
ENSMUST00000033160	ENSMUSG00000030872	7	121986722	122021222	-1	85	80	171	137	90	51	15	8	28	7	62		Q6P5E6
ENSMUST00000033161	ENSMUSG00000030873	7	121865038	121918514	1	23	23	86	51	39	17	0	1	0	0	0	A2RS45	Q9WU38
ENSMUST00000033163	ENSMUSG00000030876	7	121034445	121076834	1	7	13	51	120	11	6	2941	14015	3947	5324	1782		Q9EPL4
ENSMUST00000033166	ENSMUSG00000030877	7	120982509	121014787	1	3	11	8	10	13	4	1	3	2	0	0	Q9D3Y2	
ENSMUST00000033169	ENSMUSG00000030878	7	120957036	120982312	-1	6	0	0	70	5	10	31	126	89	0	31		P97817
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000033171	ENSMUSG00000030881	7	105634203	105640416	-1	0	0	0	0	0	4	88	47	15	10	49	H7BWZ6	
ENSMUST00000033173	ENSMUSG00000030880	7	120917744	120947432	1	0	0	0	0	9	0	40	77	39	26	84		Q9CZT4
ENSMUST00000033176	ENSMUSG00000030884	7	120635176	120659478	1	4	0	3	77	8	2	466	2175	837	2577	569		Q9DB77
ENSMUST00000033178	ENSMUSG00000030887	7	120659296	120670343	-1	10	0	0	14	0	4	0	0	0	0	0	B9EJT5	Q9D9M4
ENSMUST00000033179	ENSMUSG00000030888	7	105732207	105737376	-1	7	7	0	114	8	3	31	124	46	17	34		Q9DB85
ENSMUST00000033180	ENSMUSG00000030889	7	120739557	120805742	1	0	0	0	0	0	0	0	0	0	0	0		Q3UVV9
ENSMUST00000033182	ENSMUSG00000030890	7	105736592	105742925	1	0	0	0	0	0	0	2351	2330	1870	371	1256		O55222
ENSMUST00000033184	ENSMUSG00000030894	7	105744847	105752207	-1	22	14	20	32	30	8	695	1708	724	266	790		O89023
ENSMUST00000033185	ENSMUSG00000030895	7	105591613	105600116	-1	9	9	12	10	11	4	3	10	3	244	3		Q91X72
ENSMUST00000033187	ENSMUSG00000030897	7	105404568	105408738	1	18	11	34	15	25	10	19	35	18	25	12		Q3UW12
ENSMUST00000033189	ENSMUSG00000030898	7	105425817	105470898	1	13	13	50	139	27	9	0	0	0	0	0	Q3ZB46	P56481
ENSMUST00000033198	ENSMUSG00000030905	7	120186380	120202111	-1	16	7	9	89	12	3	0	0	0	2	4	Q3UPX0	O54983
ENSMUST00000033201	ENSMUSG00000030909	7	120173858	120183716	1	10	8	8	16	16	7	0	0	0	0	0		Q8K3X6
ENSMUST00000033207	ENSMUSG00000030911	7	120132361	120145290	-1	9	10	14	15	7	4	0	0	0	0	0		P20239
ENSMUST00000033210	ENSMUSG00000030917	7	120102376	120120992	1	4	4	17	28	12	0	46	48	32	14	25		Q922Z1
ENSMUST00000033211	ENSMUSG00000057596	7	104470014	104507849	-1	8	3	3	10	3	5	19	69	58	55	69	E9PWL0	
ENSMUST00000033218	ENSMUSG00000030924	7	119794006	119848943	1	1	2	1	96	4	7	3	0	9	0	0	Q7TSF9	
ENSMUST00000033224	ENSMUSG00000030929	7	119768679	119794058	-1	0	0	0	0	0	0	13	0	7	13	0	F8WH13	
ENSMUST00000033229	ENSMUSG00000052187	7	103851745	103853240	-1	4	2	3	2	5	1	0	0	0	0	0	Q9CR49	
ENSMUST00000033230	ENSMUSG00000017713	11	117867952	117873481	-1	0	0	0	68	9	0	9	60	22	8	19	Q6XPS7	
ENSMUST00000033236	ENSMUSG00000030942	7	119715096	119720765	-1	10	6	47	71	18	3	42	182	50	77	101		Q99J36
ENSMUST00000033241	ENSMUSG00000030946	7	132610638	132706420	1	10	9	60	9	12	1	29	40	18	9	29		Q9D7I5
ENSMUST00000033255	ENSMUSG00000030954	7	119442544	119459272	-1	7	12	16	14	17	10	0	0	0	0	0		
ENSMUST00000033257	ENSMUSG00000030960	7	132827457	132852673	-1	3	0	2	16	3	1	38	120	35	62	14		Q9D853
ENSMUST00000033263	ENSMUSG00000030963	7	119462866	119479255	-1	30	15	44	26	34	8	0	0	0	0	0		Q91X17
ENSMUST00000033264	ENSMUSG00000030966	7	102557922	102565469	-1	0	17	15	0	17	0	79	476	187	210	221	Q3U7K7	
ENSMUST00000033265	ENSMUSG00000030967	7	132931142	132986391	1	3	1	0	0	0	2	47	224	217	132	145		Q7M760
ENSMUST00000033267	ENSMUSG00000030968	7	119486587	119523482	-1	15	13	20	9	22	10	0	0	0	0	0		Q9DAN1
ENSMUST00000033269	ENSMUSG00000030970	7	132987563	133124354	-1	0	0	0	0	0	0	122	184	272	18	141	Q3UGL5	P56546
ENSMUST00000033275	ENSMUSG00000030976	7	133587024	133602115	-1	5	7	5	4	4	6	0	0	0	0	0	Q9D5N9	
ENSMUST00000033276	ENSMUSG00000030979	7	133686243	133710072	-1	9	3	2	29	7	4	0	7	0	8	12	Q3UG55	P51163
ENSMUST00000033277	ENSMUSG00000030980	7	118842222	118856254	-1	7	2	20	105	5	9	5	0	38	110	46	E9QKQ3	
ENSMUST00000033278	ENSMUSG00000030981	7	133674270	133680061	-1	0	0	0	0	0	0	0	0	0	0	0	Q3KP73	Q8K3F2
ENSMUST00000033280	ENSMUSG00000030982	7	118740226	118842966	1	31	28	34	36	30	20	7	24	20	9	58		Q8BWQ6
ENSMUST00000033282	ENSMUSG00000030983	7	133709333	133721145	1	3	1	0	19	0	0	98	200	123	453	114		Q9CWI3
ENSMUST00000033283	ENSMUSG00000030978	7	102441695	102469771	1	15	22	51	39	23	8	221	602	421	457	270		P07742
ENSMUST00000033289	ENSMUSG00000030987	7	102267824	102436848	1	26	15	36	141	28	22	1646	2062	1725	116	1144		P70302
ENSMUST00000033290	ENSMUSG00000030986	7	133720942	133782726	-1	0	0	0	84	8	6	0	11	0	0	0		Q8BZS9
ENSMUST00000033292	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	0	0	0	16	0	0	0	0		Q3TQR0
ENSMUST00000033300	ENSMUSG00000030996	7	102101743	102111148	1	13	6	18	171	16	16	0	0	0	0	0	Q545U9	Q60935
ENSMUST00000033310	ENSMUSG00000031004	7	135689788	135716379	-1	45	36	370	173	86	33	1262	2247	3543	533	1556	E9PVX6	
ENSMUST00000033313	ENSMUSG00000031007	X	12587801	12617049	1	4	6	20	14	4	1	1137	2588	1231	648	694	Q1XID4	Q9CYN9
ENSMUST00000033321	ENSMUSG00000031012	X	13517080	13851367	-1	0	0	0	0	0	0	223	735	397	243	349		O70589
ENSMUST00000033325	ENSMUSG00000031015	7	110221703	110283503	1	28	19	56	130	56	21	958	3265	1398	193	1233		Q6A028
ENSMUST00000033326	ENSMUSG00000031016	7	110122350	110142112	1	4	5	9	163	12	3	21	34	25	4	28		P47810
ENSMUST00000033331	ENSMUSG00000034825	7	109758055	109782025	-1	23	22	0	99	0	7	1	3	0	1	1		Q9JJR9
ENSMUST00000033333	ENSMUSG00000031021	7	109735834	109752875	-1	7	4	0	39	6	0	607	1970	730	524	425		Q9JJR8
ENSMUST00000033334	ENSMUSG00000031022	7	109712181	109723850	-1	6	0	0	0	0	0	0	0	0	1	0	Q3UQ01	Q9JJR6
ENSMUST00000033335	ENSMUSG00000031023	7	109703690	109712189	1	3	4	0	37	6	5	11	34	20	13	19		Q9JJR5
ENSMUST00000033339	ENSMUSG00000031026	7	109449006	109508134	-1	25	0	6	0	0	0	0	0	0	0	0		Q924W6
ENSMUST00000033341	ENSMUSG00000031028	7	109010825	109034460	1	79	48	223	123	83	36	1	2	2	3	5	Q4VA41	P50586
ENSMUST00000033342	ENSMUSG00000031029	7	108934417	108942951	1	12	8	10	75	20	6	1988	3611	1706	284	1368		Q9DCH4
ENSMUST00000033372	ENSMUSG00000060090	X	20364481	20405653	1	16	3	11	25	0	0	359	975	334	238	261		Q9EPK2
ENSMUST00000033378	ENSMUSG00000010476	7	137193673	137314445	-1	78	2	396	0	0	45	0	0	0	0	3		O08791
ENSMUST00000033380	ENSMUSG00000031065	X	20687954	20699880	1	6	2	0	37	0	6	397	1142	527	59	549	Q543G3	Q04735
ENSMUST00000033383	ENSMUSG00000031066	X	20703906	20720539	1	8	9	18	23	15	6	50	71	61	8	48		Q99K46
ENSMUST00000033386	ENSMUSG00000031070	7	145300828	145309557	1	18	0	0	14	6	0	0	0	0	0	13		Q8VCJ6
ENSMUST00000033388	ENSMUSG00000031072	7	144915100	144930748	1	17	14	14	15	23	5	236	569	295	93	231	Q3TF33	
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ENSMUST00000033393	ENSMUSG00000031075	7	144588549	144751974	-1	0	0	0	77	18	0	0	0	0	0	0		Q8BHY3
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ENSMUST00000033407	ENSMUSG00000031078	7	144435733	144471009	-1	0	0	0	0	13	8	11	37	23	39	114	Q921L6	
ENSMUST00000033414	ENSMUSG00000031089	X	21714896	21742355	1	0	3	7	5	8	4	0	0	0	0	0	A1L359	Q9JMA9
ENSMUST00000033415	ENSMUSG00000031090	7	143795584	143822849	-1	0	7	0	12	7	0	22	76	13	0	47		Q711T7
ENSMUST00000033418	ENSMUSG00000017057	X	36112110	36171259	1	9	4	8	62	9	2	2010	12805	3484	2222	2360		O09030
ENSMUST00000033419	ENSMUSG00000031093	X	35888832	36076562	1	9	0	16	55	17	6	637	679	1964	117	954		A2AF47
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ENSMUST00000033429	ENSMUSG00000031103	X	48411046	48463132	-1	17	17	53	0	5	0	2814	3741	3109	134	2244		Q9Z2U4
ENSMUST00000033430	ENSMUSG00000031104	X	48519285	48530232	1	4	5	10	57	15	5	0	0	1	6	2	Q3SXA7	P97950
ENSMUST00000033431	ENSMUSG00000031105	X	48623413	48662294	1	0	2	3	5	6	0	0	0	0	0	0		Q9Z2B2
ENSMUST00000033433	ENSMUSG00000031107	X	48695004	48710723	1	6	6	5	16	7	3	22	75	38	131	35		Q8R0F5
ENSMUST00000033437	ENSMUSG00000031109	X	49009707	49288259	-1	0	0	0	0	0	0	0	36	0	3	0		Q8R0Z2
ENSMUST00000033442	ENSMUSG00000031111	X	49782536	49797749	-1	0	3	0	11	10	5	0	0	0	0	0		Q7TQA1
ENSMUST00000033444	ENSMUSG00000031112	X	50841047	50893097	1	7	2	11	33	11	1	130	579	493	609	277	A2AD85	Q99JT2
ENSMUST00000033449	ENSMUSG00000031118	X	51968695	51972772	-1	0	2	2	0	4	0	0	0	0	0	0	Q9D9G4	
ENSMUST00000033450	ENSMUSG00000031119	X	52053021	52165252	-1	6	3	18	204	8	2	2	4	1	5	13		P51655
ENSMUST00000033458	ENSMUSG00000031125	X	56136572	56153498	1	0	0	2	0	0	0	3	2	3	29	1	Q9D6C3	
ENSMUST00000033463	ENSMUSG00000031129	9	94669909	95230445	1	21	28	56	31	24	18	38	264	84	74	103		Q8BZ00
ENSMUST00000033464	ENSMUSG00000031130	X	57043074	57048758	1	4	4	8	2	10	6	0	0	0	0	0		O54798
ENSMUST00000033465	ENSMUSG00000031131	X	57088106	57106540	1	0	6	0	0	0	0	0	0	0	0	0		Q99NC0
ENSMUST00000033466	ENSMUSG00000031132	X	57212143	57224042	1	5	3	4	2	4	2	3	12	3	3	6	Q0VEI3	P27548
ENSMUST00000033468	ENSMUSG00000031133	X	57231485	57338729	-1	0	0	0	0	0	2	702	1917	1661	413	920	F6WMJ3	
ENSMUST00000033473	ENSMUSG00000031137	X	59062145	59568071	-1	6	0	12	368	18	24	0	0	1	0	0		P70377
ENSMUST00000033477	ENSMUSG00000031138	X	59999464	60030759	1	31	8	29	151	31	27	0	6	4	2	1		P16294

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000033478	ENSMUSG00000031139	X	60055956	60179089	-1	0	0	0	2	2	0	0	0	0	0	0	A2AET8	
ENSMUST00000033480	ENSMUSG00000062949	X	60223290	60592698	-1	0	0	4	32	0	4	85	229	242	51	44	E9QKK8	
ENSMUST00000033483	ENSMUSG00000031143	X	7593809	7605517	-1	8	4	5	10	5	3	294	354	254	79	185		Q9JIG7
ENSMUST00000033485	ENSMUSG00000031145	X	7657260	7668186	1	1	1	9	79	9	0	0	256	391	45	240		Q80VL3
ENSMUST00000033486	ENSMUSG00000031146	X	7667941	7671390	-1	0	26	0	64	19	9	7118	17423	6375	1329	3800	Q0VEW4	Q9R1Q7
ENSMUST00000033489	ENSMUSG00000031149	X	7728439	7731064	1	8	11	31	47	13	4	63	100	45	32	67		Q9JIG8
ENSMUST00000033490	ENSMUSG00000031150	X	7731714	7750905	-1	13	18	30	158	34	5	1	1	0	1	4	A2AEV7	
ENSMUST00000033494	ENSMUSG00000031154	X	7841364	7876626	1	12	1	19	15	16	9	324	1388	568	38	394		Q3U2S4
ENSMUST00000033495	ENSMUSG00000031155	X	7878262	7883432	1	0	0	1	1	1	0	1	1	1	0	0	F6WGR1	
ENSMUST00000033497	ENSMUSG00000031157	X	7894519	7899269	-1	0	0	0	1	0	0	224	419	266	242	183	A2AER7	Q91VJ5
ENSMUST00000033498	ENSMUSG00000031158	X	7899357	7908351	1	183	168	622	212	158	95	144	265	137	44	123	Q545H3	Q9Z0V7
ENSMUST00000033500	ENSMUSG00000031160	X	7924276	7928607	-1	6	2	4	2	8	0	0	0	0	0	0	Q0VEC9	Q7TN89
ENSMUST00000033501	ENSMUSG00000031161	X	7930120	7947889	-1	0	0	0	0	0	0	7	47	99	0	8		Q9Z2V5
ENSMUST00000033502	ENSMUSG00000031162	X	7959260	7978071	-1	5	5	11	2	11	5	33	14	9	6	17		P17679
ENSMUST00000033503	ENSMUSG00000031163	X	8004200	8018492	-1	3	6	2	3	0	2	0	0	1	1	0		Q9D8I3
ENSMUST00000033505	ENSMUSG00000031165	X	8081453	8090498	-1	28	22	109	191	44	20	2600	5426	3209	242	2306	Q53WY0	P70315
ENSMUST00000033506	ENSMUSG00000031166	X	8123301	8132892	-1	6	0	0	0	0	7	0	272	38	31	0	Q32P16	Q91V09
ENSMUST00000033509	ENSMUSG00000031168	X	8185329	8193512	-1	7	3	16	13	8	2	335	511	314	332	255		P70245
ENSMUST00000033512	ENSMUSG00000031170	X	8271133	8280179	1	0	0	0	1	1	0	0	0	0	0	0		Q3U1J0
ENSMUST00000033513	ENSMUSG00000031171	X	8238668	8252406	-1	49	59	170	30	41	20	10	28	7	2	25	Q8CBC7	
ENSMUST00000033519	ENSMUSG00000031176	X	9654267	9663003	-1	8	5	7	3	8	1	120	564	174	278	99	Q542J7	P56387
ENSMUST00000033522	ENSMUSG00000031179	X	64173548	64178778	1	5	1	1	4	7	1	0	0	0	0	0	Q8BQJ2	
ENSMUST00000033524	ENSMUSG00000031181	X	65047644	65049014	1	3	3	5	3	4	0	0	0	0	0	0	Q9D9S4	
ENSMUST00000033525	ENSMUSG00000031182	X	66303361	66304224	-1	0	0	0	0	0	0	0	0	0	0	0	A2AFR2	
ENSMUST00000033532	ENSMUSG00000031189	X	69360294	69868037	1	16	8	48	24	12	3	10	16	20	1	11		O55112
ENSMUST00000033537	ENSMUSG00000031194	X	62467991	62468812	1	1	1	0	0	1	0	0	0	0	0	0	Q9D4M5	
ENSMUST00000033539	ENSMUSG00000031196	X	75172715	75382615	-1	15	16	0	21	23	8	0	0	0	0	0		Q06194
ENSMUST00000033540	ENSMUSG00000031197	X	75514299	75534942	1	2	1	0	3	2	0	279	948	220	356	175		P61759
ENSMUST00000033541	ENSMUSG00000031198	X	75382399	75396459	1	11	18	15	8	20	13	59	202	52	171	56		Q9D6K8
ENSMUST00000033542	ENSMUSG00000031200	X	75410444	75416588	-1	0	0	0	0	3	0	0	13	5	1	4		Q60945
ENSMUST00000033543	ENSMUSG00000090110	X	75404846	75416584	-1	0	1	0	48	0	0	7	18	12	9	10	A3KGA5	Q61908
ENSMUST00000033544	ENSMUSG00000031201	X	75416628	75454001	1	1	2	5	12	0	1	19	45	13	37	14		P46737
ENSMUST00000033545	ENSMUSG00000031202	X	75572046	75578231	-1	8	4	7	34	10	2	2	1	0	1	3	Q0PD14	Q8BHC1
ENSMUST00000033547	ENSMUSG00000016382	X	75785654	75875182	-1	0	0	3	19	0	5	0	0	0	18	0		Q99K51
ENSMUST00000033549	ENSMUSG00000031204	X	95470201	95478129	-1	8	3	8	6	8	2	1	0	0	1	0	Q3KNI9	Q9D738
ENSMUST00000033553	ENSMUSG00000031209	X	96455359	96574485	1	8	5	10	3	5	3	0	0	0	0	0		Q9Z0Z4
ENSMUST00000033554	ENSMUSG00000031210	X	96713441	96719388	1	7	2	2	0	6	2	0	0	0	0	0	Q3V3A3	
ENSMUST00000033556	ENSMUSG00000031212	X	97072596	97082104	1	11	7	4	10	16	4	0	0	0	0	0	Q80T54	
ENSMUST00000033560	ENSMUSG00000031214	X	98554277	98891025	-1	15	5	11	4	16	9	0	2	3	0	10		Q99J31
ENSMUST00000033567	ENSMUSG00000031220	X	100402221	100442717	-1	4	0	1	0	1	0	0	0	0	1	0	A2ADU0	Q6E1M8
ENSMUST00000033570	ENSMUSG00000031221	X	100494291	100516125	1	3	8	6	6	11	2	251	1192	447	2117	366		Q61249
ENSMUST00000033575	ENSMUSG00000031224	X	104854952	104857267	-1	23	17	117	25	22	5	2	0	0	0	2	Q52KG3	
ENSMUST00000033577	ENSMUSG00000031226	X	105079756	105117090	1	9	5	21	1	9	2	55	251	57	347	70		Q9D0B6
ENSMUST00000033578	ENSMUSG00000031227	X	105120378	105123927	1	15	7	42	215	15	12	15	36	12	2	16		Q6PCZ4
ENSMUST00000033581	ENSMUSG00000031230	X	105764279	105774939	1	5	3	7	62	9	2	0	0	0	0	0		Q9ESL8
ENSMUST00000033582	ENSMUSG00000031231	X	106015700	106022450	1	1	1	1	1	2	2	223	664	362	2195	203	Q5FW98	P56393
ENSMUST00000033583	ENSMUSG00000031232	X	105968084	106011906	-1	40	66	76	65	65	49	63	306	70	103	129	A2ADH1	
ENSMUST00000033585	ENSMUSG00000031233	17	40207018	40208609	-1	14	12	5	11	8	5	0	0	0	0	0		P09041
ENSMUST00000033591	ENSMUSG00000031239	X	107397099	107403376	-1	3	0	4	3	2	5	9	21	10	36	16		Q61500
ENSMUST00000033597	ENSMUSG00000031245	X	109004534	109013404	-1	6	3	4	2	3	3	54	258	114	378	69		Q9JL35
ENSMUST00000033598	ENSMUSG00000031246	X	109095365	109197873	1	5	9	9	46	10	1	466	800	245	1137	320		Q9JJU8
ENSMUST00000033602	ENSMUSG00000031250	X	133850980	133865577	1	5	2	3	3	2	1	0	0	0	0	0		Q9EP64
ENSMUST00000033606	ENSMUSG00000031253	X	133908426	133932446	1	0	3	8	11	10	5	0	0	0	0	0		Q8R054
ENSMUST00000033608	ENSMUSG00000031255	X	133936385	133981812	-1	17	0	38	17	8	14	0	8	6	8	9	Q549X6	Q9R0Q1
ENSMUST00000033609	ENSMUSG00000031256	X	134059187	134086819	1	0	0	0	0	0	0	99	222	44	26	35		Q8BIQ5
ENSMUST00000033610	ENSMUSG00000031257	X	134086421	134221956	-1	3	3	0	3	3	0	0	0	1	0	0		Q8CIZ9
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ENSMUST00000033617	ENSMUSG00000031264	X	134542336	134583570	-1	7	4	6	5	0	0	631	3905	1508	879	1167		P35991
ENSMUST00000033621	ENSMUSG00000031266	X	134588149	134601125	-1	23	26	96	38	37	25	183	733	219	320	210	Q8BGZ6	
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ENSMUST00000033626	ENSMUSG00000031271	X	139079257	139085236	-1	0	0	0	3	0	6	0	0	0	0	0	Q3UEL9	
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ENSMUST00000033643	ENSMUSG00000031286	3	85869849	85887516	-1	17	15	19	18	16	10	1	4	0	1	4	Q8BML3	
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ENSMUST00000033650	ENSMUSG00000031293	X	160768013	160799663	1	80	81	418	81	100	42	0	6	3	1	2		Q9Z1L4
ENSMUST00000033652	ENSMUSG00000031295	X	160502166	160598878	1	0	0	0	2	0	0	10	62	74	0	62		Q8BWJ3
ENSMUST00000033662	ENSMUSG00000031299	X	160122209	160138413	-1	8	3	7	39	14	6	775	2649	1405	1001	934	Q3UFJ3	P35486
ENSMUST00000033664	ENSMUSG00000031304	X	101264378	101268255	-1	0	2	8	9	10	5	282	663	218	138	407	Q3UPA9	P34902
ENSMUST00000033665	ENSMUSG00000031303	X	159988433	160123351	1	16	15	23	19	10	3	196	1264	467	74	727		A2AQW0
ENSMUST00000033671	ENSMUSG00000031309	X	159210307	159368244	1	8	7	12	13	11	3	719	1749	901	170	658		P18654
ENSMUST00000033673	ENSMUSG00000031311	X	101429318	101448591	1	19	12	45	36	24	17	1206	3331	1710	2758	1431	Q4FK11	Q99K48
ENSMUST00000033674	ENSMUSG00000031312	X	101449088	101453541	1	2	3	9	1	4	1	0	5	5	0	6		Q9R000
ENSMUST00000033683	ENSMUSG00000031320	X	102184941	102189394	-1	15	24	35	58	39	22	4473	18378	6940	33197	4894	Q545X8	P62702
ENSMUST00000033686	ENSMUSG00000031323	X	102903216	102908687	-1	0	0	0	0	0	0	0	0	0	0	0	B1AX34	Q9D9R7
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ENSMUST00000033689	ENSMUSG00000031326	X	103321398	103330592	1	3	7	13	16	9	5	0	3	0	5	4	Q78Z64	Q07424
ENSMUST00000033691	ENSMUSG00000031329	X	103414467	103424580	1	1	6	4	8	2	2	0	0	0	0	1	Q78Z65	P70675
ENSMUST00000033692	ENSMUSG00000031330	X	103630586	103631670	1	1	0	6	4	2	3	0	0	0	0	0	Q9D548	
ENSMUST00000033695	ENSMUSG00000031333	X	104280657	104413856	-1	13	16	9	20	16	18	126	342	191	115	133		Q61102
ENSMUST00000033699	ENSMUSG00000031328	X	74223461	74249820	-1	0	0	0	8	0	0	5064	0	10094	0	3834		Q8BTM8
ENSMUST00000033700	ENSMUSG00000031337	X	71210767	71315691	1	0	0	0	0	0	0	45	305	100	243	94		Q9Z2C5
ENSMUST00000033711	ENSMUSG00000031344	X	72825178	72842602	1	0	0	5	0	0	1	0	0	0	0	0	Q0VEX8	Q9JLF1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000033713	ENSMUSG00000031347	X	72913532	72918411	-1	0	2	0	0	1	0	25	331	104	174	33	Z4YJH1	
ENSMUST00000033715	ENSMUSG00000031349	X	72918557	72958514	1	12	1	3	6	7	10	96	355	179	155	106	Q3US15	Q9R1J0
ENSMUST00000033717	ENSMUSG00000031352	X	169250193	169320372	-1	0	5	0	0	0	0	79	320	68	25	49		P53702
ENSMUST00000033720	ENSMUSG00000031353	X	162760402	162779092	1	0	0	0	35	0	0	38	36	0	9	24		Q60973
ENSMUST00000033721	ENSMUSG00000031355	X	168795099	169304435	1	9	10	23	108	20	8	0	0	0	0	0		O54834
ENSMUST00000033723	ENSMUSG00000031357	X	162857057	162888447	-1	8	8	9	183	9	12	429	1710	759	539	479		Q9D5V6
ENSMUST00000033725	ENSMUSG00000031358	X	168654117	168673898	-1	0	0	0	0	2	0	17	67	58	0	23		Q9WVG9
ENSMUST00000033727	ENSMUSG00000031360	X	162901238	163032508	1	0	0	0	0	0	0	17	48	37	17	31		P70303
ENSMUST00000033730	ENSMUSG00000031364	X	163513904	163549677	-1	48	32	367	82	31	18	1	0	2	0	2	Q53WV4	P21729
ENSMUST00000033731	ENSMUSG00000031365	X	73342621	73359080	1	14	0	0	0	0	0	189	138	236	0	114	G3X904	
ENSMUST00000033734	ENSMUSG00000031367	X	163909017	163933666	1	0	0	2	0	0	0	492	1685	418	112	214	Q3TIV9	
ENSMUST00000033737	ENSMUSG00000031371	X	73437315	73459044	-1	16	6	18	15	17	15	23	54	35	121	36		Q8BKT8
ENSMUST00000033738	ENSMUSG00000031372	X	73433705	73435344	-1	5	2	5	12	4	4	2	0	1	0	2	Q3SXB3	Q9R1A9
ENSMUST00000033739	ENSMUSG00000031373	X	163976822	164027997	-1	129	132	239	296	106	71	25	95	55	64	47		Q9QZA0
ENSMUST00000033740	ENSMUSG00000031374	X	73411096	73428385	1	334	223	1248	414	172	99	12	31	12	2	26		Q62396
ENSMUST00000033741	ENSMUSG00000031375	X	73483602	73495933	1	23	21	144	29	21	16	0	0	1	4	18	Q3TNY9	P28653
ENSMUST00000033744	ENSMUSG00000031376	X	73503086	73571005	1	1	2	0	0	0	0	0	0	0	0	0	Q8C048	
ENSMUST00000033749	ENSMUSG00000031379	X	164269371	164373011	1	0	1	6	12	3	0	0	24	9	20	2		Q9D711
ENSMUST00000033751	ENSMUSG00000031380	X	164373378	164402650	1	2	3	2	2	1	3	0	1	0	1	2		P97946
ENSMUST00000033752	ENSMUSG00000019558	X	73673150	73682502	1	0	0	27	141	17	8	0	0	0	0	9		Q8VBW1
ENSMUST00000033754	ENSMUSG00000031381	X	164419793	164433916	1	0	0	0	11	0	0	148	283	237	88	93	A2AIH5	Q64323
ENSMUST00000033755	ENSMUSG00000031382	X	164436994	164459170	1	4	3	1	0	0	2	2	0	0	4	0		Q9CQ31
ENSMUST00000033756	ENSMUSG00000031384	X	164506327	164539752	1	2	3	8	5	4	7	0	0	0	0	0		Q91ZT8
ENSMUST00000033761	ENSMUSG00000031386	X	73942792	73966357	-1	10	17	0	27	0	23	519	351	1121	0	709		Q61191
ENSMUST00000033763	ENSMUSG00000031388	X	73916873	73921944	-1	0	0	0	35	0	2	0	0	0	0	30	Q540H0	Q9QY36
ENSMUST00000033765	ENSMUSG00000031390	X	73892102	73895502	1	0	0	0	0	0	0	0	0	0	0	0	Q3SWS1	O88721
ENSMUST00000033769	ENSMUSG00000031392	X	74013914	74023918	-1	7	0	16	0	7	0	66	11	156	0	161	B1AUW6	
ENSMUST00000033770	ENSMUSG00000031393	X	74026592	74135363	-1	3	0	7	39	0	0	81	133	69	53	107		Q9Z2D6
ENSMUST00000033771	ENSMUSG00000031394	X	74127464	74150760	1	4	0	7	6	7	2	0	0	0	0	0		O35599
ENSMUST00000033775	ENSMUSG00000031402	X	75109733	75131016	-1	3	7	8	10	13	0	1676	6318	1523	1141	948	Q542P4	P70290
ENSMUST00000033776	ENSMUSG00000031403	X	75095854	75109777	1	41	51	157	46	55	32	45	262	83	128	101		Q9ESX5
ENSMUST00000033783	ENSMUSG00000031409	X	135208687	135210687	-1	8	1	0	5	7	3	0	0	0	0	0	Q9DB24	
ENSMUST00000033784	ENSMUSG00000031410	X	135579555	135598777	-1	0	0	0	0	0	3	0	0	0	0	0	Q80SZ6	
ENSMUST00000033786	ENSMUSG00000031411	X	135613002	135627705	-1	0	0	0	0	0	0	0	0	0	0	0	Q9D4Z5	
ENSMUST00000033797	ENSMUSG00000031422	X	136732942	136743690	-1	0	7	5	27	4	0	0	0	15	0	0		Q9R0Q4
ENSMUST00000033800	ENSMUSG00000031425	X	136822671	136839733	1	26	21	148	93	33	16	1	2	2	0	9	Q3UYM8	P60202
ENSMUST00000033804	ENSMUSG00000031428	X	136993155	136998472	1	18	7	20	12	17	8	0	0	0	0	2		Q8VD24
ENSMUST00000033805	ENSMUSG00000031429	X	140948429	140956728	-1	1	0	0	0	0	0	209	997	285	985	196		Q9Z2X2
ENSMUST00000033806	ENSMUSG00000031430	X	140907608	140939472	1	0	0	0	7	0	1	0	0	0	0	0	A0A0B4J1E9	
ENSMUST00000033809	ENSMUSG00000031432	X	140456613	140476140	1	5	4	4	4	3	2	143	451	196	247	126		Q9D7G0
ENSMUST00000033810	ENSMUSG00000031433	X	139889511	139998595	-1	10	4	5	19	0	7	0	0	4	0	10		Q8JZV4
ENSMUST00000033811	ENSMUSG00000031434	X	139821632	139871677	-1	3	7	10	2	0	0	0	0	0	0	4		Q8BMD7
ENSMUST00000033818	ENSMUSG00000031441	8	12757014	12868728	1	0	0	0	81	34	0	3955	4363	7259	299	7314	E9Q3G7	
ENSMUST00000033820	ENSMUSG00000031443	8	13026034	13035809	1	18	7	17	23	22	11	32	31	28	47	91	Q542C2	P70375
ENSMUST00000033821	ENSMUSG00000031444	8	13037308	13056676	1	0	1	0	0	0	0	961	692	869	496	422	Q3U3V1	
ENSMUST00000033822	ENSMUSG00000031445	8	13060908	13075006	1	22	12	40	28	32	24	26	80	35	12	51		Q9CQW3
ENSMUST00000033824	ENSMUSG00000031447	8	13159135	13175338	1	12	17	24	33	14	9	4046	8313	4236	1476	3670	Q3TA96	P11438
ENSMUST00000033825	ENSMUSG00000031448	8	13221663	13254162	-1	14	7	17	14	19	7	0	0	0	0	0		Q8BGK2
ENSMUST00000033826	ENSMUSG00000031449	8	13386209	13396778	-1	7	5	44	16	17	1	0	0	0	0	0	Q0VBB6	P50992
ENSMUST00000033827	ENSMUSG00000031450	8	13405081	13421945	1	7390	12219	8999	3272	6548	2670	37	147	73	25	88	G3X905	
ENSMUST00000033828	ENSMUSG00000031451	8	13465374	13494535	-1	17	16	33	186	32	9	1	1	1	37	72		Q61592
ENSMUST00000033830	ENSMUSG00000031452	8	13550733	13562461	-1	0	0	0	0	0	0	0	0	6	0	4	G3X906	
ENSMUST00000033839	ENSMUSG00000031458	8	13884788	13890271	-1	5	5	21	46	9	2	4	17	9	5	10		Q9CQ13
ENSMUST00000033842	ENSMUSG00000031461	8	15057653	15133541	1	30	21	46	50	35	16	0	0	0	0	0	Q14BI5	
ENSMUST00000033846	ENSMUSG00000031465	8	18690263	18741562	-1	61	46	167	78	26	24	1	14	1	44	11	B9EHQ4	O35608
ENSMUST00000033847	ENSMUSG00000031467	8	18846277	18891361	1	0	0	0	22	0	0	67	334	67	151	57	F8WGD9	
ENSMUST00000033852	ENSMUSG00000039775	8	19293360	19295291	1	0	0	0	1	0	0	0	0	0	0	0		Q9WTL0
ENSMUST00000033854	ENSMUSG00000031471	8	19445769	19447606	-1	0	0	0	1	0	0	0	0	0	0	0		
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ENSMUST00000033866	ENSMUSG00000031479	8	22192809	22220843	1	30	25	151	43	40	14	309	1166	571	589	472	Q3TSR1	Q91XD6
ENSMUST00000033871	ENSMUSG00000031482	8	22375554	22398621	-1	21	23	34	50	27	12	19	51	23	11	31	Q543E2	Q9WVD5
ENSMUST00000033873	ENSMUSG00000031483	8	27023799	27039433	1	23	17	37	79	30	13	261	679	378	69	320		Q8BFZ9
ENSMUST00000033875	ENSMUSG00000031485	8	27042555	27056131	1	12	7	27	23	34	20	188	765	332	92	280	Q544R1	Q9Z2Y8
ENSMUST00000033876	ENSMUSG00000031486	8	27085583	27123436	1	32	36	94	97	0	33	0	6	4	0	18		Q91ZV8
ENSMUST00000033877	ENSMUSG00000031487	8	27123832	27128632	-1	11	5	22	75	22	11	96	119	68	11	60		
ENSMUST00000033878	ENSMUSG00000031488	8	27138773	27174646	-1	22	43	69	232	2	46	507	3053	662	170	1139		Q9D620
ENSMUST00000033880	ENSMUSG00000031490	8	27260327	27275656	1	4	6	22	128	17	10	3332	4979	2742	2401	2003		Q60876
ENSMUST00000033882	ENSMUSG00000031491	8	27403214	27413944	-1	15	11	28	19	19	3	0	0	0	0	0		Q9R0W9
ENSMUST00000033886	ENSMUSG00000031493	7	29170220	29173933	1	0	0	0	0	3	0	3	0	0	0	0		Q80WJ1
ENSMUST00000033888	ENSMUSG00000040197	8	3847965	3854309	-1	12	14	6	4	10	1	0	0	0	5	3	Q3KNN8	Q91ZW7
ENSMUST00000033892	ENSMUSG00000031497	8	10006843	10035441	1	14	16	34	28	33	12	38	148	51	76	74	Q3KP92	Q9WU72
ENSMUST00000033898	ENSMUSG00000031502	8	11198423	11312826	-1	55	45	99	216	85	23	6	15	4	31	260		P02463
ENSMUST00000033899	ENSMUSG00000031503	8	11312805	11449287	1	43	29	108	233	55	18	27	54	40	32	208	B2RQQ8	P08122
ENSMUST00000033900	ENSMUSG00000031504	8	11453392	11478638	-1	14	5	13	112	19	3	484	882	338	182	387	Q3TPA7	P35295
ENSMUST00000033901	ENSMUSG00000031505	8	11497506	11514960	1	4	0	0	57	5	7	0	126	10	12	0	K3W4M4	
ENSMUST00000033905	ENSMUSG00000031508	8	11611583	11635754	-1	10	12	23	123	16	3	76	163	79	30	142		Q99LW0
ENSMUST00000033906	ENSMUSG00000031509	8	11654924	11701063	-1	102	106	125	105	147	72	10	43	36	2	75	Q9DAA5	
ENSMUST00000033908	ENSMUSG00000031511	8	11728105	11835219	1	10	8	24	30	17	12	3	3	20	0	8		
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ENSMUST00000033910	ENSMUSG00000031513	8	34135572	34147033	-1	13	14	27	49	19	12	862	1579	816	288	581		Q9CQ74
ENSMUST00000033913	ENSMUSG00000031516	8	34090420	34108796	-1	2	0	10	5	4	0	10	0	0	0	30		Q9WUB4
ENSMUST00000033915	ENSMUSG00000031517	8	54954728	55060877	1	15	8	12	6	8	4	0	0	0	29	2	Q542P2	P35802
ENSMUST00000033917	ENSMUSG00000031518	8	54600781	54610098	1	5	1	9	3	5	3	0	0	0	0	0		Q8K3V1
ENSMUST00000033918	ENSMUSG00000031519	8	54550331	54587836	1	2	8	1	1	0	0	1	4	1	1	0	Q2VPQ8	Q9D1A4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000033919	ENSMUSG00000031520	8	54077532	54186454	1	3	6	5	152	10	2	0	2	0	0	6		P97953
ENSMUST00000033920	ENSMUSG00000031521	8	53511702	53523421	1	5	6	22	56	10	5	23	99	22	54	41	A2RSS6	Q64191
ENSMUST00000033923	ENSMUSG00000031523	8	36567751	36953143	-1	3	47	0	219	71	49	0	0	0	0	14	E9QKB1	
ENSMUST00000033927	ENSMUSG00000031527	8	35465265	35495533	-1	24	15	32	96	17	12	197	545	367	131	164		
ENSMUST00000033929	ENSMUSG00000031529	8	34829179	34965690	-1	25	17	39	72	38	16	300	532	697	44	605		Q6PFX9
ENSMUST00000033930	ENSMUSG00000031530	8	34807297	34819894	1	16	8	36	504	24	9	2	3	6	0	26		Q8BFV3
ENSMUST00000033933	ENSMUSG00000031532	8	34154563	34170845	1	19	5	20	82	17	10	894	1924	898	478	773		
ENSMUST00000033934	ENSMUSG00000031533	8	22411340	22429665	1	10	8	25	16	10	3	21	108	50	176	40		Q61733
ENSMUST00000033935	ENSMUSG00000031534	8	22462615	22476879	-1	2	0	8	21	6	3	206	695	186	83	94		Q80ZU4
ENSMUST00000033936	ENSMUSG00000031535	8	22624043	22627536	1	11	7	20	5	25	8	0	0	1	0	1		Q8VEJ3
ENSMUST00000033938	ENSMUSG00000031536	8	22628119	22653437	-1	8	2	2	34	11	4	80	419	151	402	131		Q8K409
ENSMUST00000033939	ENSMUSG00000031537	8	22659212	22706589	-1	0	0	0	0	0	0	833	1670	1216	162	851	Q5D0E0	
ENSMUST00000033941	ENSMUSG00000031538	8	22757744	22782847	1	20	17	26	19	21	13	3	1	1	9	20		P11214
ENSMUST00000033947	ENSMUSG00000031543	8	22974844	23150497	1	2	6	7	5	3	0	0	2	0	1	0		Q02357
ENSMUST00000033950	ENSMUSG00000031546	8	23226610	23237668	-1	6	7	6	77	11	2	133	500	236	314	178		Q99LZ3
ENSMUST00000033952	ENSMUSG00000031548	8	23411502	23449632	1	29	25	125	175	47	25	0	0	0	12	34		Q8C4U3
ENSMUST00000033956	ENSMUSG00000031551	8	24584136	24597009	-1	3	5	2	5	3	3	0	2	0	0	4		P28776
ENSMUST00000033957	ENSMUSG00000031552	8	24602246	24674755	-1	0	6	0	0	0	0	0	7	0	0	0		Q9R157
ENSMUST00000033958	ENSMUSG00000031553	8	24677225	24725852	-1	20	0	11	7	11	7	11	75	23	78	27	F8VQ03	
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ENSMUST00000033963	ENSMUSG00000031559	8	49370886	49521095	1	3	2	1	0	1	0	0	0	0	0	0	Q9D4V1	
ENSMUST00000033965	ENSMUSG00000031561	8	48227682	48844026	-1	0	0	0	0	0	0	0	0	0	0	0	G3X907	
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ENSMUST00000033967	ENSMUSG00000031558	5	47983138	48307733	1	0	0	0	18	0	0	0	0	0	0	0	G3X909	
ENSMUST00000033973	ENSMUSG00000031568	8	47533664	47552955	1	7	3	6	6	18	7	32	77	26	9	32		Q9CPR1
ENSMUST00000033975	ENSMUSG00000061313	8	25725324	25754280	-1	31	42	72	101	48	21	60	186	99	18	140		Q80Y98
ENSMUST00000033979	ENSMUSG00000031574	8	25808474	25814723	1	17	14	33	24	15	8	10	26	21	7	16		P51557
ENSMUST00000033983	ENSMUSG00000031578	8	31159468	31168724	-1	10	9	5	32	11	1	48	355	128	435	118		Q8BGS0
ENSMUST00000033990	ENSMUSG00000031583	8	33234384	33385527	-1	38	0	139	72	41	0	124	183	228	0	214		O09053
ENSMUST00000033991	ENSMUSG00000031583	8	33234384	33385527	-1	0	28	0	0	0	31	0	220	38	87	0		O09053
ENSMUST00000033992	ENSMUSG00000031584	8	33652523	33698163	1	5	9	19	25	10	7	2043	5186	2484	628	1543		P47791
ENSMUST00000033994	ENSMUSG00000031586	8	33782643	33929863	-1	0	12	0	0	0	0	0	0	0	0	0	T1ECW4	
ENSMUST00000033995	ENSMUSG00000031586	8	33782643	33929863	-1	0	0	3	40	1	0	10	12	0	0	24		Q9WVB0
ENSMUST00000033999	ENSMUSG00000031590	8	41397457	41417118	-1	26	14	36	316	49	8	362	2729	678	2045	484	Q78P92	P97376
ENSMUST00000034000	ENSMUSG00000031591	8	41340197	41374773	-1	7	0	6	4	15	6	518	1210	1232	2028	954	Q78P93	Q9WV54
ENSMUST00000034003	ENSMUSG00000031594	8	41191434	41215156	-1	2	1	3	2	2	1	12	133	25	111	12		
ENSMUST00000034004	ENSMUSG00000031595	8	40926212	40990785	1	1	3	4	7	5	2	2	10	1	12	20		
ENSMUST00000034012	ENSMUSG00000031601	8	40492540	40515847	-1	0	0	0	7	0	0	0	982	152	69	138	Q543X5	Q60809
ENSMUST00000034014	ENSMUSG00000031603	8	40279166	40308331	-1	5	2	7	45	10	3	0	0	0	0	0		Q9ESL9
ENSMUST00000034015	ENSMUSG00000031604	8	64718139	64733792	-1	0	0	0	12	0	0	244	704	262	509	169		Q9CRA4
ENSMUST00000034017	ENSMUSG00000031605	8	64739863	64849818	-1	16	11	32	45	21	12	2396	4649	3205	596	2209		Q8JZP3
ENSMUST00000034021	ENSMUSG00000031608	8	57523828	57653032	-1	0	9	0	14	7	0	209	297	129	60	162		Q80VA0
ENSMUST00000034022	ENSMUSG00000031609	8	57482707	57487860	-1	2	3	4	169	9	6	265	1647	511	393	319		O88574
ENSMUST00000034023	ENSMUSG00000031610	8	57455923	57477585	1	3	3	2	2	3	1	143	432	163	566	102	Q543T5	O88745
ENSMUST00000034026	ENSMUSG00000031613	8	56294552	56321046	1	10	2	6	52	9	5	3	35	6	35	16		Q8VCC1
ENSMUST00000034029	ENSMUSG00000031616	8	77663031	77724464	-1	11	19	57	20	16	7	16	66	16	17	37		Q61614
ENSMUST00000034030	ENSMUSG00000031617	8	77595982	77610698	-1	12	4	15	33	11	7	55	304	100	55	92		Q3TPR7
ENSMUST00000034031	ENSMUSG00000031618	8	76899442	77245012	1	1	0	26	2	0	8	0	0	0	1	0	E9Q8M8	
ENSMUST00000034033	ENSMUSG00000031620	8	75448694	75984503	1	8	4	12	10	4	0	0	0	0	0	0	Q149I8	
ENSMUST00000034034	ENSMUSG00000031621	8	74873173	74893506	1	13	9	7	14	11	5	0	0	0	0	0	B1Q2M1	A1A546
ENSMUST00000034041	ENSMUSG00000031627	8	46739745	46847458	1	6	16	15	21	15	8	1501	4209	2245	217	1738	Q3U2Z2	P23906
ENSMUST00000034045	ENSMUSG00000031629	8	46552055	46580007	1	2	0	0	0	0	0	30	25	3	37	16		Q8C4M7
ENSMUST00000034046	ENSMUSG00000018796	8	46471041	46536051	1	0	0	0	42	14	9	1094	2641	791	114	516		P41216
ENSMUST00000034048	ENSMUSG00000031631	8	46151771	46195590	1	0	0	45	42	0	9	47	93	93	47	183		Q6ZPR1
ENSMUST00000034049	ENSMUSG00000031633	8	46206797	46211284	-1	7	7	8	128	6	5	92	351	75	198	194		P48962
ENSMUST00000034051	ENSMUSG00000031634	8	45975528	45996958	1	0	3	0	5	1	3	203	959	446	1239	288		Q99K23
ENSMUST00000034052	ENSMUSG00000031635	8	62057042	62123118	-1	5	8	3	3	6	3	0	0	0	0	0		Q9QZ10
ENSMUST00000034053	ENSMUSG00000031636	8	45885485	45919546	1	11	10	30	14	12	3	0	0	0	1	0		O70209
ENSMUST00000034054	ENSMUSG00000031635	8	62057042	62123118	-1	0	0	0	2	0	0	0	0	0	0	0	Q9D272	
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ENSMUST00000034060	ENSMUSG00000031642	8	61224171	61396072	1	22	15	59	80	44	28	11	22	18	2	36	E9QQ33	
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ENSMUST00000034065	ENSMUSG00000031644	8	60993195	61131346	1	6	9	7	0	7	9	17	38	37	29	18		P51954
ENSMUST00000034066	ENSMUSG00000031647	8	60632827	60676729	1	0	2	0	12	4	7	0	0	1	7	2		Q9D3X9
ENSMUST00000034074	ENSMUSG00000031652	8	86841139	86885258	-1	90	62	332	240	91	38	1988	5227	4133	312	3269		Q6A037
ENSMUST00000034076	ENSMUSG00000031654	8	87468854	87472592	-1	4	11	4	137	11	10	0	0	0	0	0	Q7TNF5	Q9R171
ENSMUST00000034079	ENSMUSG00000031657	8	88137855	88172027	1	16	11	19	222	36	19	19	78	52	39	88		Q8BQM4
ENSMUST00000034085	ENSMUSG00000031660	8	88331039	88362194	-1	19	19	49	20	20	11	367	1300	665	321	445		O88665
ENSMUST00000034086	ENSMUSG00000031661	8	88521344	88594887	1	44	20	52	165	34	20	0	0	0	0	0		Q99MH6
ENSMUST00000034087	ENSMUSG00000031662	8	88626828	88636128	-1	8	5	17	306	17	9	1888	3719	1634	1026	1316		
ENSMUST00000034090	ENSMUSG00000031665	8	89027248	89044162	-1	49	58	228	109	86	39	2	3	0	2	2	Q6P5E3	
ENSMUST00000034091	ENSMUSG00000031666	8	91070057	91123844	1	15	13	34	11	23	6	774	1996	1651	189	1040		Q64700
ENSMUST00000034093	ENSMUSG00000031668	6	70844515	70905245	1	11	9	21	16	24	21	729	2146	1619	259	1281	E9QQ30	
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ENSMUST00000034109	ENSMUSG00000031682	8	79210430	79248583	-1	10	4	5	10	12	3	0	0	0	0	2		Q9DAF8
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ENSMUST00000034121	ENSMUSG00000005142	8	85083269	85098739	1	26	24	123	74	36	20	10733	20042	14980	1116	13363		O09159
ENSMUST00000034131	ENSMUSG00000031696	8	85260397	85299513	-1	8	9	14	21	8	9	1022	4383	1996	2425	868	Q3TRJ1	Q9EQH3
ENSMUST00000034132	ENSMUSG00000031697	8	85299632	85308278	1	7	8	11	0	0	0	47	149	74	236	60	Q66JV6	

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ENSMUST00000034138	ENSMUSG00000031701	8	85537640	85555271	-1	17	5	26	34	14	10	573	2052	1011	547	656		Q9QYJ0
ENSMUST00000034140	ENSMUSG00000031703	8	85717557	85840949	-1	8	5	5	100	11	6	367	1607	679	438	374		Q99KW9
ENSMUST00000034141	ENSMUSG00000047866	8	86624043	86723873	1	0	0	0	7	0	5	916	2714	1610	402	815		Q9DBN5
ENSMUST00000034145	ENSMUSG00000031709	8	83165352	83272934	1	11	0	18	56	42	9	0	52	53	0	22		Q3UYK3
ENSMUST00000034146	ENSMUSG00000031710	8	83290348	83298456	1	8	17	21	36	18	7	0	0	0	3	1		P12242
ENSMUST00000034147	ENSMUSG00000031711	8	82763621	82774160	-1	9	7	6	55	13	5	134	727	286	614	202		Q922H9
ENSMUST00000034148	ENSMUSG00000031712	8	82331637	82403222	-1	11	10	29	19	21	9	43	382	58	128	153	Q3U1Z6	P48346
ENSMUST00000034150	ENSMUSG00000031714	8	80764434	80880479	-1	27	18	54	561	57	29	190	618	501	50	209	Q505A4	Q9QYY0
ENSMUST00000034159	ENSMUSG00000031723	8	109565892	109574051	1	18	19	37	12	27	13	417	1632	467	250	442		Q8BUH1
ENSMUST00000034162	ENSMUSG00000031727	8	109494027	109542642	1	20	19	62	40	33	23	0	0	0	0	0	B2RR67	Q9WVQ0
ENSMUST00000034163	ENSMUSG00000031728	8	109705549	109724932	1	7	9	23	39	18	8	251	668	280	78	253		Q6PD05
ENSMUST00000034164	ENSMUSG00000031729	8	109671322	109693294	-1	10	14	32	50	15	18	1676	4801	2051	889	1649		Q9CX00
ENSMUST00000034171	ENSMUSG00000031731	8	109778554	109864204	1	1	0	0	0	1	0	610	957	1134	113	672		P22892
ENSMUST00000034172	ENSMUSG00000056973	8	93166068	93197838	-1	7	10	18	3	13	4	0	0	0	1	0		Q8VCT4
ENSMUST00000034173	ENSMUSG00000061959	8	93201218	93229619	-1	15	0	40	0	15	10	0	0	0	1	0	Q3UN14	Q64176
ENSMUST00000034175	ENSMUSG00000031732	8	109868542	109944671	1	23	21	50	6	41	21	24	37	30	4	62		Q8BXA7
ENSMUST00000034178	ENSMUSG00000031725	8	93256236	93279747	-1	10	7	9	6	5	2	0	0	0	0	0	Q91WU0	
ENSMUST00000034184	ENSMUSG00000031737	8	92357796	92361456	1	6	3	21	409	15	13	0	1	0	0	1		Q9JKQ4
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ENSMUST00000034187	ENSMUSG00000031740	8	92827328	92853417	1	25	19	60	147	34	12	17	29	20	27	30	Q3UG07	P33434
ENSMUST00000034189	ENSMUSG00000057400	8	93099015	93131283	-1	5	11	17	0	8	4	0	0	0	19	0		P23953
ENSMUST00000034190	ENSMUSG00000010936	8	110618638	110720396	1	33	20	58	95	40	15	404	512	440	51	360		Q80WQ2
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ENSMUST00000034198	ENSMUSG00000031748	8	93809966	93969388	1	0	0	7	0	12	6	0	4	1	0	7	Q543S2	P18872
ENSMUST00000034203	ENSMUSG00000031753	8	110846600	110882227	1	15	4	12	6	7	3	402	961	580	340	567		Q8R1U1
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ENSMUST00000034207	ENSMUSG00000031757	8	94137204	94139031	1	1	3	0	2	4	1	0	0	0	0	0	Q3V2E2	P47945
ENSMUST00000034211	ENSMUSG00000031760	8	94152607	94154148	1	1	2	3	40	5	2	0	0	0	1	0	Q3USP9	P28184
ENSMUST00000034214	ENSMUSG00000031762	8	94172618	94173567	1	12	7	8	85	12	6	2	0	1	829	80		P02798
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ENSMUST00000034218	ENSMUSG00000031766	8	94329192	94366213	1	25	16	89	28	45	22	5	1	3	2	2	Q543E4	P59158
ENSMUST00000034219	ENSMUSG00000033409	8	113643213	113655533	1	7	10	20	11	11	10	0	5	0	0	0		Q5D525
ENSMUST00000034220	ENSMUSG00000031770	8	94386438	94395377	1	5	0	19	8	0	15	0	291	55	55	141	Q8C4N0	
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ENSMUST00000034226	ENSMUSG00000031774	8	94574943	94601726	-1	14	9	34	37	14	4	556	1621	825	233	558		Q91WE2
ENSMUST00000034227	ENSMUSG00000031775	8	94674895	94696242	-1	8	12	19	64	15	10	1	2	3	1	5		Q9DCU2
ENSMUST00000034228	ENSMUSG00000031776	8	94666755	94674417	1	10	0	13	60	22	17	593	1291	778	92	498		Q9D385
ENSMUST00000034230	ENSMUSG00000031778	8	94772009	94782423	1	21	12	60	69	28	17	1	0	0	1	19		O35188
ENSMUST00000034231	ENSMUSG00000031779	8	94745590	94751699	1	24	19	34	16	24	13	0	1	1	2	13	Q546S6	O88430
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ENSMUST00000034244	ENSMUSG00000031791	8	72572103	72587282	1	11	10	40	65	17	6	107	160	95	21	71		Q3TMP8
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ENSMUST00000034259	ENSMUSG00000056019	8	71882019	71895727	1	0	0	0	0	0	0	0	33	0	0	0	F6R4Z5	
ENSMUST00000034260	ENSMUSG00000031803	8	71691719	71701800	-1	18	6	32	417	24	22	14	12	22	8	34		Q5JCS9
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ENSMUST00000034277	ENSMUSG00000031819	8	120653914	120668573	-1	47	43	147	60	57	30	13	101	25	9	78	Q3TPU5	O70378
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ENSMUST00000034296	ENSMUSG00000031834	8	70768176	70776713	-1	16	5	45	266	19	16	740	675	541	55	506		O08908
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ENSMUST00000034311	ENSMUSG00000031848	8	70673248	70678752	1	2	1	10	56	8	1	219	330	177	59	143	Q9CY46	
ENSMUST00000034313	ENSMUSG00000031851	8	125729963	125748235	1	7	3	7	25	7	0	287	680	346	99	142		Q9CQA9
ENSMUST00000034316	ENSMUSG00000031853	8	125910450	125947439	1	34	25	43	220	59	24	0	0	0	1	0		Q8VDG6
ENSMUST00000034325	ENSMUSG00000031861	8	69822429	69831102	1	34	0	0	4	54	19	23	19	109	12	65	Q6P290	
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ENSMUST00000034328	ENSMUSG00000031864	8	68793929	68829410	1	18	4	144	73	0	11	15	72	47	7	4		Q8K2A7
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ENSMUST00000034344	ENSMUSG00000074127	8	104281042	104293178	-1	3	1	3	10	4	1	5	11	7	3	6		Q9DAR1
ENSMUST00000034346	ENSMUSG00000055730	8	104734003	104741634	1	10	11	17	15	0	0	0	0	0	0	0		Q8QZR3
ENSMUST00000034349	ENSMUSG00000031878	8	104511028	104534637	-1	0	0	0	8	0	1	69	596	129	168	0	Q3UK27	Q8VBW6
ENSMUST00000034351	ENSMUSG00000031880	8	104628066	104631321	-1	16	10	24	196	20	8	8	20	9	9	26	Q6PGA2	
ENSMUST00000034355	ENSMUSG00000031886	8	104926260	104934672	1	12	4	8	8	12	0	0	0	0	0	0		Q8BK48
ENSMUST00000034359	ENSMUSG00000031887	8	105258286	105264609	-1	7	5	36	102	17	9	654	890	481	109	259	B2RRZ7	Q3U0V2
ENSMUST00000034361	ENSMUSG00000031889	8	105225145	105253053	1	0	0	0	95	8	0	631	1362	829	149	537		Q922R1
ENSMUST00000034363	ENSMUSG00000031891	8	105518746	105523984	1	9	9	17	131	16	9	0	1	1	0	4		P51661
ENSMUST00000034365	ENSMUSG00000031893	8	105827744	105844676	1	16	18	14	20	30	14	0	0	1	0	0		Q99P25
ENSMUST00000034368	ENSMUSG00000031896	8	105931994	105933862	-1	14	3	10	11	7	8	1	3	2	1	6	Q9ER05	
ENSMUST00000034369	ENSMUSG00000031897	8	105935728	105938392	-1	16	10	38	75	25	8	460	621	330	576	453		O35955
ENSMUST00000034370	ENSMUSG00000017765	8	105943590	105966115	-1	0	0	0	93	0	21	0	49	26	0	0	F8WIJ0	
ENSMUST00000034371	ENSMUSG00000031898	8	105973520	105979419	-1	13	3	26	70	14	5	30	146	79	19	38		Q9DA79
ENSMUST00000034373	ENSMUSG00000053687	8	105984944	105996423	-1	0	0	7	6	0	0	868	643	823	777	411		Q8C255
ENSMUST00000034375	ENSMUSG00000031901	8	105991337	106053840	1	8	3	8	8	0	0	52	79	90	26	37	Q14A90	Q9D7B1
ENSMUST00000034377	ENSMUSG00000031903	8	106150399	106164713	1	28	22	67	59	30	13	1365	2973	1193	151	686		Q8VEB4
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ENSMUST00000034388	ENSMUSG00000031913	8	107031222	107045755	1	7	9	18	56	20	4	395	1251	551	196	445		Q8VEJ9
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ENSMUST00000034392	ENSMUSG00000031917	8	107056877	107060926	1	83	35	21	36	17	21	166	446	156	525	107		Q9CXK8
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ENSMUST00000034398	ENSMUSG00000031922	9	13807792	13827107	-1	0	5	0	23	0	0	0	0	0	52	0		Q8CEE0
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ENSMUST00000034408	ENSMUSG00000031932	9	14860210	14870789	1	0	0	17	176	44	8	10	0	5	0	2	Q542Q9	P30731
ENSMUST00000034409	ENSMUSG00000031933	9	14885814	14903949	-1	10	0	3	7	13	10	18	16	10	4	21		Q9EQF4
ENSMUST00000034411	ENSMUSG00000031935	9	15260352	15279867	-1	45	32	50	105	57	21	432	1368	743	258	473		Q8VCD5
ENSMUST00000034413	ENSMUSG00000031937	9	15239045	15259393	1	23	8	26	70	36	9	0	0	1	0	0		Q9D806
ENSMUST00000034414	ENSMUSG00000031938	9	15283337	15306448	-1	14	10	33	1	7	2	0	0	0	0	0		Q91V76
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ENSMUST00000034426	ENSMUSG00000031948	8	111993440	112011323	-1	4	12	0	27	18	0	154	467	250	341	279	Q3TIV6	Q99MN1
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ENSMUST00000034428	ENSMUSG00000031950	8	111940703	111953612	1	16	13	28	40	18	7	646	1850	664	930	458		P60521
ENSMUST00000034429	ENSMUSG00000031951	8	111912018	111933791	-1	34	18	73	159	41	14	5	3	5	5	9		Q3U284
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ENSMUST00000034431	ENSMUSG00000031953	8	111864898	111876675	-1	20	22	155	55	21	8	47	126	50	5	34		Q9D342
ENSMUST00000034432	ENSMUSG00000031954	8	111768473	111854310	-1	5	10	3	31	10	3	85	489	134	900	195		O88271
ENSMUST00000034435	ENSMUSG00000031957	8	111686510	111691010	-1	11	7	10	16	22	7	0	0	0	0	0		Q9CR35
ENSMUST00000034437	ENSMUSG00000031959	8	111448784	111522107	-1	119	75	346	265	71	46	18	164	79	0	51	D3Z1F9	
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ENSMUST00000034443	ENSMUSG00000031962	8	122848374	122867397	1	20	20	62	99	33	19	0	1	0	0	1		P33146
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ENSMUST00000034457	ENSMUSG00000031976	8	124021508	124048505	1	0	12	2	2	12	0	75	97	76	0	67	E9Q7L1	
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ENSMUST00000034460	ENSMUSG00000031979	8	124520767	124552008	1	16	6	25	13	17	15	509	729	597	113	408		Q921L5
ENSMUST00000034463	ENSMUSG00000031982	8	124722139	124734123	1	9	9	12	51	7	5	9	25	19	15	25	Q0VBH5	Q9D0U9
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ENSMUST00000034467	ENSMUSG00000031986	8	124897886	124903813	1	9	7	43	215	18	9	238	290	411	38	275		G3X912
ENSMUST00000034469	ENSMUSG00000031987	8	124908596	124949254	-1	29	17	79	345	48	22	734	1308	868	162	653		Q91YE3
ENSMUST00000034470	ENSMUSG00000031988	9	27004503	27030094	-1	45	40	62	338	57	22	1584	3645	2274	179	1468		Q8C0E2
ENSMUST00000034472	ENSMUSG00000031990	9	27097385	27155421	-1	14	6	16	25	17	9	18	110	27	20	17		Q9D8B7
ENSMUST00000034473	ENSMUSG00000031991	9	27396821	27401710	1	5	2	1	6	5	2	0	0	0	0	0	I6ZYN5	Q9DAQ9
ENSMUST00000034478	ENSMUSG00000031995	9	31089402	31131853	-1	20	10	73	112	41	24	17	16	16	6	36	Q543E3	P56677
ENSMUST00000034483	ENSMUSG00000031998	9	8221889	8241987	1	566	418	5096	1173	760	388	2	10	21	3	21	Q9D970	
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ENSMUST00000034488	ENSMUSG00000047562	9	7502352	7510238	1	5	10	1	6	7	0	0	0	0	9	0	A1L3D0	O55123
ENSMUST00000034492	ENSMUSG00000043089	9	7464141	7476869	1	3	4	3	11	6	0	0	0	0	3	0	E9QPT8	
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ENSMUST00000034507	ENSMUSG00000032009	9	14276301	14326138	1	14	14	37	41	17	11	24	57	82	17	118	A2RSF4	Q9CYP7
ENSMUST00000034508	ENSMUSG00000032010	9	44067021	44095627	1	12	5	61	14	7	15	135	564	206	22	120		O88623
ENSMUST00000034510	ENSMUSG00000032012	9	43744576	43807454	1	40	23	149	133	58	34	36	51	25	7	56		Q9JKF6
ENSMUST00000034511	ENSMUSG00000032013	9	43310763	43336125	1	33	14	80	135	47	20	0	1	1	2	1		Q8R2Q0
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ENSMUST00000034519	ENSMUSG00000032021	9	40972753	41004628	-1	0	0	0	0	2	4	6	22	4	0	0	E9QPS7	
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ENSMUST00000034522	ENSMUSG00000032024	9	40685962	40785319	1	30	9	136	47	43	20	35	180	89	70	30		Q8R373
ENSMUST00000034524	ENSMUSG00000032026	9	48468514	48480611	-1	4	4	8	151	9	8	112	365	110	169	155		Q9D8S4
ENSMUST00000034527	ENSMUSG00000032028	9	48318006	48353454	-1	14	17	12	16	25	16	2	0	0	10	0		
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ENSMUST00000034534	ENSMUSG00000032035	9	32636221	32757820	1	9	32	56	62	38	14	647	1398	1054	106	1491	Q540Q5	P27577
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ENSMUST00000034552	ENSMUSG00000032051	9	51943307	51963533	-1	0	2	9	149	4	2	8	40	9	27	16	Q545P3	P46656
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ENSMUST00000034566	ENSMUSG00000032064	9	50662752	50739517	-1	0	10	10	0	0	0	3	16	6	5	5		Q80Y83
ENSMUST00000034567	ENSMUSG00000000168	9	50634633	50659780	-1	9	11	15	286	26	6	110	347	214	28	151		Q8BMF4
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ENSMUST00000034602	ENSMUSG00000032094	9	44981793	44987052	1	96	71	300	289	109	56	446	1036	233	1094	360	Q3U4T1	P04235
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ENSMUST00000034609	ENSMUSG00000032098	9	44673233	44686305	1	0	0	4	0	11	0	0	0	0	0	0		Q9JLT2
ENSMUST00000034610	ENSMUSG00000032099	9	35607093	35611935	-1	5	5	1	1	4	6	0	0	0	0	0		Q09098
ENSMUST00000034611	ENSMUSG00000048537	9	44686304	44735198	-1	18	28	0	212	34	39	0	0	0	0	0		Q6PDH0
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ENSMUST00000034618	ENSMUSG00000032105	9	44247312	44251464	-1	17	16	32	19	30	16	53	349	47	19	126		
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ENSMUST00000034621	ENSMUSG00000032109	9	44252713	44268599	-1	48	16	46	16	30	7	1519	1366	1249	57	802		Q3TL44
ENSMUST00000034623	ENSMUSG00000032112	9	44403761	44407548	-1	8	5	9	49	10	4	656	1536	497	1050	301	Q544R8	Q9ES56
ENSMUST00000034625	ENSMUSG00000032113	9	36708482	36727065	-1	0	27	130	0	3	11	0	0	3	12	0		O35280
ENSMUST00000034629	ENSMUSG00000032119	9	44295673	44305671	-1	8	14	24	32	16	2	90	169	155	23	100		Q8K1K9
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ENSMUST00000034643	ENSMUSG00000032128	9	37415669	37433163	-1	11	0	5	0	0	0	0	0	0	0	0	E9QPQ1	
ENSMUST00000034644	ENSMUSG00000032127	9	44348106	44361670	-1	31	25	60	58	38	18	859	1256	1066	239	802		Q91W86
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ENSMUST00000034653	ENSMUSG00000032134	9	18495455	18512885	-1	7	4	3	2	4	1	0	0	0	2	2	Q9D1H1	
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ENSMUST00000034689	ENSMUSG00000032171	9	20652130	20666584	1	33	25	75	65	32	18	351	378	237	209	202		Q9QUR7
ENSMUST00000034692	ENSMUSG00000032172	9	20667986	20728219	-1	18	6	18	16	20	6	0	0	0	0	1		Q8BM13
ENSMUST00000034697	ENSMUSG00000057193	9	21337828	21355025	1	25	26	53	70	38	28	6236	10016	6112	492	4970		Q8BY89
ENSMUST00000034698	ENSMUSG00000032180	9	21507380	21510186	-1	10	7	15	33	20	3	76	64	58	64	73	B2RRM5	Q3V009
ENSMUST00000034699	ENSMUSG00000032181	9	75643264	75683996	-1	11	9	24	37	12	10	0	0	0	0	0		P47867
ENSMUST00000034700	ENSMUSG00000032182	9	21588709	21592831	-1	15	13	42	19	25	0	44	31	49	0	12		Q99LP8
ENSMUST00000034702	ENSMUSG00000032184	9	75625732	75637773	1	4	1	2	74	3	1	4	6	3	1	9	G3X915	
ENSMUST00000034703	ENSMUSG00000032185	9	21546894	21589487	1	0	0	0	0	0	0	127	0	10	0	0		Q9WVG6
ENSMUST00000034707	ENSMUSG00000032187	9	21616169	21704230	1	49	45	178	153	34	35	0	0	0	20	0		Q3TKT4
ENSMUST00000034709	ENSMUSG00000032191	9	75347758	75351632	1	7	5	14	11	13	7	0	4	0	2	1		Q9Z0F3
ENSMUST00000034713	ENSMUSG00000032193	9	21723576	21749916	1	40	22	139	129	42	26	812	1066	1228	94	822		P35951
ENSMUST00000034717	ENSMUSG00000032194	9	21766773	21798546	-1	65	54	304	550	87	49	8	11	8	11	78		Q8BX02
ENSMUST00000034720	ENSMUSG00000032199	9	71478437	71485935	-1	0	0	7	10	6	3	347	872	433	70	314		Q6P6I6
ENSMUST00000034722	ENSMUSG00000032202	9	73044854	73097629	1	57	63	85	57	68	30	1880	8482	3329	721	1933	Q544U7	Q9ERI2
ENSMUST00000034723	ENSMUSG00000013584	9	71215789	71296243	1	11	13	11	61	13	13	1	0	0	8	20		Q62148
ENSMUST00000034728	ENSMUSG00000032198	9	21800184	21852635	-1	55	47	103	150	90	41	12	23	20	3	55	E9QPN7	
ENSMUST00000034731	ENSMUSG00000032207	9	70798129	70934808	-1	15	13	11	19	13	9	4	6	7	16	6		P27656
ENSMUST00000034734	ENSMUSG00000092192	9	72958785	72973064	1	5	11	22	13	3	0	0	0	3	0	0		Q8R368
ENSMUST00000034737	ENSMUSG00000092622	9	73101836	73104438	1	6	4	9	29	14	10	27	205	70	4	73		Q9CWU5
ENSMUST00000034738	ENSMUSG00000032215	9	73113426	73123333	1	7	7	26	55	13	2	229	927	266	213	147	Q5EBK7	Q99L28
ENSMUST00000034739	ENSMUSG00000032217	9	70425429	70503725	-1	0	0	0	27	0	0	33	32	250	0	125		Q99ML9
ENSMUST00000034740	ENSMUSG00000032216	9	72662346	72749852	1	23	15	16	96	29	7	303	409	439	84	445	B2RSC8	P46935
ENSMUST00000034742	ENSMUSG00000032218	9	70407689	70421554	-1	18	12	25	44	16	7	279	502	430	201	217		P30276
ENSMUST00000034745	ENSMUSG00000032220	9	70207350	70400067	1	50	45	80	150	62	19	63	124	169	24	205		E9Q634
ENSMUST00000034746	ENSMUSG00000032221	9	72438011	72462025	1	7	9	7	11	10	5	3	14	4	20	3		Q61884
ENSMUST00000034749	ENSMUSG00000032224	9	70089310	70142560	-1	46	30	39	332	70	54	1	1	0	0	1		Q3UXZ6
ENSMUST00000034751	ENSMUSG00000032226	9	70031496	70038088	-1	22	20	62	33	31	18	0	0	2	0	2		Q5JCT0
ENSMUST00000034754	ENSMUSG00000011958	9	69989466	70008317	1	5	0	0	42	5	3	188	868	481	273	284		O54940
ENSMUST00000034755	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	0	0	26	0	0	0	0		Q61286
ENSMUST00000034756	ENSMUSG00000032231	9	69453620	69491795	1	0	6	2	66	18	15	24925	46649	22012	46584	16362	Q542G9	P07356
ENSMUST00000034761	ENSMUSG00000032235	9	69397906	69433122	1	4	3	0	20	13	11	12	78	34	48	25		Q3UZ18

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000034763	ENSMUSG00000032239	9	22448311	22468356	-1	7	5	51	67	12	9	738	1703	735	248	563	Q3TH81	P97762
ENSMUST00000034766	ENSMUSG00000032238	9	68653786	69388246	1	74	48	208	67	78	37	11	35	15	8	31		P51448
ENSMUST00000034774	ENSMUSG00000032243	9	62677826	62783982	1	65	43	138	83	97	25	0	1	1	1	2	A0A0B4J1F0	
ENSMUST00000034775	ENSMUSG00000032244	9	62791832	62811648	-1	33	29	48	320	45	14	133	365	279	63	156		Q9Z2G0
ENSMUST00000034776	ENSMUSG00000032245	9	62838785	62852006	1	16	22	79	32	30	8	221	233	136	32	157	Q3U466	
ENSMUST00000034777	ENSMUSG00000032246	9	62858104	62875918	1	0	0	10	4	6	6	0	0	0	155	27		Q91WQ9
ENSMUST00000034783	ENSMUSG00000032251	9	82829540	82847687	1	0	2	1	77	1	1	0	0	0	1	1	G5E885	
ENSMUST00000034785	ENSMUSG00000032252	9	62057248	62122655	-1	0	19	29	11	19	0	56	112	42	29	11		Q9EPS3
ENSMUST00000034787	ENSMUSG00000032253	9	82866159	82975516	-1	3	3	8	29	7	4	384	996	548	200	474	F8VQ93	
ENSMUST00000034791	ENSMUSG00000032258	9	83390293	83441127	-1	13	20	15	10	15	11	0	7	4	4	10	G5E886	
ENSMUST00000034792	ENSMUSG00000032257	9	49415222	49427021	-1	24	14	34	40	31	12	0	0	0	0	0		Q8BZ25
ENSMUST00000034793	ENSMUSG00000032258	9	83390293	83441127	-1	6	0	13	5	1	1	1	0	0	0	0	G5E887	
ENSMUST00000034796	ENSMUSG00000032262	9	83778692	83806277	-1	4	5	11	5	10	9	4	1	3	0	0		Q9EQC4
ENSMUST00000034801	ENSMUSG00000032263	9	83925145	84124240	1	6	3	6	0	12	12	0	9	4	9	16		Q6P3A8
ENSMUST00000034802	ENSMUSG00000032265	9	85320439	85327348	-1	0	26	10	123	4	22	279	878	295	103	303	D3Z5S8	
ENSMUST00000034803	ENSMUSG00000032264	9	49055581	49078772	1	20	14	20	139	21	12	126	382	255	67	151		O54692
ENSMUST00000034808	ENSMUSG00000032271	9	48591877	48605153	-1	3	0	3	5	0	0	0	0	0	15	0		O55239
ENSMUST00000034811	ENSMUSG00000032274	9	54165937	54193442	-1	83	60	542	147	76	34	2	3	2	0	0	Q3ZAT3	P28649
ENSMUST00000034815	ENSMUSG00000032254	9	61917280	61946799	-1	7	6	13	53	18	10	291	1013	559	240	748		E9Q5G3
ENSMUST00000034817	ENSMUSG00000032278	9	61953481	62026856	-1	3	21	33	79	16	10	0	0	0	0	6		Q9DCU0
ENSMUST00000034820	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	0	306	190	52	1	F8WIE2	
ENSMUST00000034822	ENSMUSG00000032281	9	54604877	54661870	-1	24	20	22	39	35	15	13	11	14	4	42		Q99PU5
ENSMUST00000034827	ENSMUSG00000032288	9	56937475	56938398	1	3	0	9	64	3	1	201	362	139	222	117		Q921Y2
ENSMUST00000034829	ENSMUSG00000032289	9	59966931	60522046	-1	8	0	0	4	14	0	0	0	0	0	0		Q3UTY6
ENSMUST00000034830	ENSMUSG00000032291	9	54764748	54773110	1	12	8	27	49	13	9	0	0	0	0	0		P62965
ENSMUST00000034831	ENSMUSG00000032292	9	59942771	59960659	-1	0	3	6	0	0	4	0	0	0	0	0	Q543C7	Q9QXZ7
ENSMUST00000034832	ENSMUSG00000032290	9	56994968	57062805	1	17	20	19	287	26	18	261	620	396	76	320	Q2M4G8	O35239
ENSMUST00000034834	ENSMUSG00000032294	9	59656368	59679375	1	43	52	110	158	78	79	63168	66913	49373	10675	31156		P52480
ENSMUST00000034836	ENSMUSG00000032295	9	57130690	57142722	1	0	0	0	0	0	0	152	105	33	14	96	F8WIE1	
ENSMUST00000034840	ENSMUSG00000032297	9	59577917	59607292	1	0	0	11	0	32	0	0	0	0	0	0		Q7TN33
ENSMUST00000034842	ENSMUSG00000032298	9	57142800	57148305	-1	0	0	0	0	0	0	0	0	0	3	6		Q8K4Q6
ENSMUST00000034843	ENSMUSG00000032293	9	54863755	54912534	1	12	18	21	65	18	5	635	1751	1049	184	491		Q811J3
ENSMUST00000034846	ENSMUSG00000032300	9	57252322	57262599	-1	43	27	93	129	62	26	1367	782	1167	98	690		Q3TEI4
ENSMUST00000034848	ENSMUSG00000032301	9	54950790	54958030	1	4	8	0	9	8	6	367	2024	651	2962	458		Q9R1P0
ENSMUST00000034851	ENSMUSG00000032303	9	55011343	55026559	-1	22	19	18	79	22	8	0	0	0	0	0	Q0VBK4	
ENSMUST00000034854	ENSMUSG00000035200	9	55028156	55048544	-1	64	46	208	75	63	34	4	1	4	3	12	Q3USV2	Q8R493
ENSMUST00000034856	ENSMUSG00000032306	9	57544256	57552763	-1	28	12	39	208	12	10	92	184	71	94	65	Q3V100	Q924M7
ENSMUST00000034859	ENSMUSG00000032309	9	55208925	55224433	1	0	11	0	141	48	10	62	139	171	39	117		Q78JE5
ENSMUST00000034860	ENSMUSG00000032310	9	57676937	57683655	-1	18	10	21	13	19	13	0	0	0	1	0	B6VGH4	P00186
ENSMUST00000034862	ENSMUSG00000032313	9	55326913	55438345	1	0	0	5	0	0	0	0	0	0	0	0		Q8BZB3
ENSMUST00000034863	ENSMUSG00000032312	9	57626647	57645653	-1	16	11	60	177	39	24	6033	6201	4881	585	3550		P41241
ENSMUST00000034865	ENSMUSG00000032315	9	57697613	57703822	1	19	15	15	22	20	11	0	2	0	0	2	Q05A20	P00184
ENSMUST00000034866	ENSMUSG00000032314	9	55454508	55512243	-1	6	1	6	60	7	0	112	526	298	196	116		Q99LC5
ENSMUST00000034868	ENSMUSG00000026034	1	58410189	58424066	-1	0	0	0	0	0	0	211	1685	561	747	386		P22518
ENSMUST00000034869	ENSMUSG00000032318	9	55538672	55546180	1	0	0	0	104	7	0	0	0	0	0	0		Q9CXV0
ENSMUST00000034874	ENSMUSG00000032323	9	58006411	58027023	1	10	6	27	14	24	11	252	168	117	11	110		Q9QZ82
ENSMUST00000034876	ENSMUSG00000032324	9	56135885	56161070	-1	8	7	17	113	12	10	37	98	34	58	93	Q545L1	Q9QY33
ENSMUST00000034878	ENSMUSG00000032328	9	79768943	79793507	-1	0	0	0	0	0	0	1058	2844	888	278	546		Q8VEK0
ENSMUST00000034879	ENSMUSG00000032329	9	56418644	56496884	1	21	18	25	27	26	16	239	633	428	98	402		Q9DC33
ENSMUST00000034880	ENSMUSG00000032327	9	58063788	58153996	1	13	16	38	9	17	8	0	0	0	0	0		
ENSMUST00000034881	ENSMUSG00000032330	9	79755241	79759853	-1	6	1	13	27	6	4	918	1742	707	3539	363		P48771
ENSMUST00000034883	ENSMUSG00000032333	9	58253164	58262523	1	19	8	49	111	40	14	83	80	68	23	92	A0A0B4J1F1	
ENSMUST00000034889	ENSMUSG00000032338	9	58823512	58860955	1	28	30	31	795	55	23	0	1	0	0	0	B2RY58	
ENSMUST00000034896	ENSMUSG00000032342	9	78448208	78475348	1	14	7	18	0	8	9	78	177	93	24	77	G5E889	
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ENSMUST00000034900	ENSMUSG00000032346	9	78376109	78378725	-1	36	31	64	58	47	31	1	8	4	2	8		Q9CWE6
ENSMUST00000034902	ENSMUSG00000057933	9	78331018	78355788	-1	5	0	0	0	0	5	0	0	0	0	0		P10648
ENSMUST00000034903	ENSMUSG00000032348	9	78191966	78209348	1	7	3	9	8	7	2	0	1	1	87	4		P24472
ENSMUST00000034904	ENSMUSG00000032349	9	77917364	77984519	1	9	13	13	23	20	6	535	989	801	202	409		Q8BHI7
ENSMUST00000034905	ENSMUSG00000032350	9	77754535	77794485	1	11	14	38	64	21	9	82	216	112	34	143	Q3TEF1	P97494
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ENSMUST00000034911	ENSMUSG00000032357	9	76951693	77045794	-1	0	10	0	10	0	9	0	0	0	0	0	Q9WUR0	
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ENSMUST00000034913	ENSMUSG00000061111	11	120542888	120549727	-1	8	0	1	6	0	8	880	988	466	149	321		Q3UGS4
ENSMUST00000034915	ENSMUSG00000032359	9	90054152	90076089	1	7	7	14	57	15	7	165	371	92	227	209		P49935
ENSMUST00000034916						7	0	27	9	4	0	5	28	3	24	7		
ENSMUST00000034920	ENSMUSG00000058444	9	63163769	63377902	-1	10	8	23	163	28	12	142	258	160	42	134		Q9WVS7
ENSMUST00000034927	ENSMUSG00000032368	9	91358058	91365810	-1	161	84	231	2961	291	203	10	74	24	2	22		P46684
ENSMUST00000034928	ENSMUSG00000032366	9	67022590	67049406	-1	1	0	0	0	0	0	0	0	0	0	0	F8WID5	
ENSMUST00000034929	ENSMUSG00000032370	9	66955393	66975484	-1	6	5	10	83	7	5	89	403	204	77	127	B2RWI2	Q9EP89
ENSMUST00000034932	ENSMUSG00000032372	9	92275602	92297752	1	4	7	3	5	9	1	17	53	28	45	37		Q9DCW2
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ENSMUST00000034940						5	3	5	3	3	1	21	0	118	164	98		
ENSMUST00000034941	ENSMUSG00000032377	9	92457373	92492456	1	10	11	8	4	2	4	0	6	0	5	8		P58196
ENSMUST00000034944	ENSMUSG00000032380	9	66158223	66272242	1	8	3	7	44	14	4	23	56	29	12	43		Q8VDF3
ENSMUST00000034945	ENSMUSG00000032381	9	66126611	66138955	1	21	15	54	23	32	17	909	3267	1205	1777	625		Q9DCL2
ENSMUST00000034946	ENSMUSG00000032382	9	66088133	66126587	-1	9	8	32	51	15	8	2878	8604	4553	2939	2375	Q6NZD2	
ENSMUST00000034947	ENSMUSG00000032383	9	66060169	66066629	1	3	6	6	120	19	5	1785	3012	1700	3872	1408	Q9DCY1	P24369
ENSMUST00000034949	ENSMUSG00000032384	9	65908924	66045015	1	17	20	15	12	16	9	346	871	846	55	480		Q8BTH8
ENSMUST00000034953	ENSMUSG00000059518	5	136982164	136988021	-1	6	0	0	0	0	0	0	0	0	0	0	G8JL39	
ENSMUST00000034955	ENSMUSG00000032388	9	65460937	65488470	1	16	5	16	101	22	6	1441	2544	1183	590	819	A2RT57	Q9CQC8
ENSMUST00000034960	ENSMUSG00000032393	9	65032458	65082650	1	12	14	19	87	8	5	744	2431	1259	284	855		Q80YA7
ENSMUST00000034961	ENSMUSG00000032394	9	65141154	65185857	1	24	12	44	80	45	13	0	0	0	0	1		Q8BQC3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000034964	ENSMUSG00000032397	9	64281607	64304792	1	3	6	1	9	2	1	50	147	63	199	48		Q91WA1
ENSMUST00000034965	ENSMUSG00000032398	9	64179297	64182684	1	8	7	9	33	8	6	267	1503	457	1751	272	E9QPK5	
ENSMUST00000034966	ENSMUSG00000032399	9	64173387	64178562	1	19	27	46	63	34	18	3659	15167	6314	12440	5361	Q564E8	Q9D8E6
ENSMUST00000034969	ENSMUSG00000032401	9	64117147	64138118	1	0	0	21	5	10	0	0	0	0	0	0		Q8K1F9
ENSMUST00000034973	ENSMUSG00000032402	9	63646767	63757994	-1	43	33	49	236	59	21	345	701	489	61	633		Q8BUN5
ENSMUST00000034980	ENSMUSG00000032409	9	95857597	95951644	1	9	8	4	4	13	5	31	130	78	30	68	E9QPK4	
ENSMUST00000034981	ENSMUSG00000032410	9	95954760	96057803	1	0	2	5	20	4	0	10	3	202	9	11	F8VQ87	
ENSMUST00000034982	ENSMUSG00000032411	9	96196275	96323646	1	41	46	103	67	66	36	22	57	31	9	47	Q8BHD2	
ENSMUST00000034983	ENSMUSG00000032412	9	96332655	96364442	-1	21	7	26	61	17	2	1744	3983	4069	687	1306	Q544Q7	P97370
ENSMUST00000034984	ENSMUSG00000032413	9	96539300	96631617	-1	12	9	31	112	21	15	199	593	272	48	272		P58069
ENSMUST00000034986	ENSMUSG00000032415	9	86307306	86464950	-1	0	5	4	5	13	0	6	7	4	3	9		Q8BX13
ENSMUST00000034987	ENSMUSG00000034973	9	86467154	86555923	1	0	0	0	0	0	0	146	293	540	60	215	H7BWZ9	
ENSMUST00000034988	ENSMUSG00000032417	9	86571991	86574899	1	4	9	13	67	10	2	6	12	4	6	0	Q14BN8	
ENSMUST00000034989	ENSMUSG00000032418	9	86581371	86695953	-1	0	0	0	56	0	0	0	0	1	11	19		P06801
ENSMUST00000034991	ENSMUSG00000032419	9	87702800	87731260	-1	62	46	146	337	52	42	2	5	1	1	4	G3X919	
ENSMUST00000034992	ENSMUSG00000032420	9	88327197	88372092	1	8	9	17	162	18	3	66	268	86	92	135	Q0VEE0	Q61503
ENSMUST00000035007	ENSMUSG00000032434	9	114731203	114749343	1	44	27	397	139	55	23	10151	17905	12945	1424	7157		Q9CZ69
ENSMUST00000035009	ENSMUSG00000032436	9	114756837	114781993	-1	11	8	13	33	11	2	1474	2190	1010	304	656		Q9ESD6
ENSMUST00000035010	ENSMUSG00000032437	9	115242607	115310421	-1	12	13	13	237	18	15	755	2291	1541	262	987		
ENSMUST00000035014	ENSMUSG00000032440	9	116087698	116175363	-1	33	16	48	365	57	13	1150	2161	1748	112	1606		Q62312
ENSMUST00000035020	ENSMUSG00000032446	9	118478212	118486132	1	16	12	0	3	16	10	11	30	5	4	20		O54839
ENSMUST00000035024	ENSMUSG00000032449	9	97074961	97111157	-1	18	1	9	0	0	0	101	519	120	38	79	Q8BZJ4	
ENSMUST00000035026	ENSMUSG00000032451	9	97349562	97369958	-1	16	13	27	34	23	14	0	0	0	0	0		Q9D2H5
ENSMUST00000035027	ENSMUSG00000032452	9	97444395	98033181	-1	2	4	4	41	7	3	0	0	0	0	0		Q9ER65
ENSMUST00000035029	ENSMUSG00000032454	9	98486115	98509781	1	0	0	6	3	0	2	0	0	0	21	0	Q059R7	Q08652
ENSMUST00000035033	ENSMUSG00000032458	9	98563721	98588382	1	9	13	15	12	9	7	940	3060	1933	1862	1257		O55029
ENSMUST00000035034	ENSMUSG00000032459	9	98588730	98601660	-1	0	1	1	40	4	5	19	93	38	169	27		Q9CXW2
ENSMUST00000035037	ENSMUSG00000032462	9	99036654	99140621	-1	20	23	20	39	21	15	133	571	285	16	174		Q8BTI9
ENSMUST00000035038	ENSMUSG00000032463	9	98986373	99002021	1	0	0	3	55	1	0	22	95	46	47	47		Q9WUD8
ENSMUST00000035043	ENSMUSG00000032468	9	99478372	99568899	-1	48	52	187	172	41	24	185	779	309	210	252	G3X920	
ENSMUST00000035045	ENSMUSG00000032470	9	99385420	99437381	-1	30	18	63	273	52	22	4	1	5	3	17	Q3TPX5	O08989
ENSMUST00000035048	ENSMUSG00000032473	9	99689461	99717267	-1	12	16	24	10	21	7	0	0	0	0	0		P56857
ENSMUST00000035053	ENSMUSG00000032478	9	109832749	109843116	1	11	3	22	14	10	9	49	49	38	111	31		O88425
ENSMUST00000035055	ENSMUSG00000032479	9	109931460	110083955	1	0	0	0	74	45	0	888	2195	1550	97	1119	A0A0B4J1F2	P27546
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ENSMUST00000035078	ENSMUSG00000032497	9	111117592	111225668	1	0	0	0	0	0	0	52	159	123	0	20	E9QN52	
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ENSMUST00000035083	ENSMUSG00000032502	9	111561437	111690348	-1	0	11	22	23	26	0	0	0	0	0	0	Q3UPL9	P97306
ENSMUST00000035085	ENSMUSG00000032503	9	112065091	112235938	-1	2	2	3	0	2	0	0	0	0	0	0		Q9DCB4
ENSMUST00000035086	ENSMUSG00000032504	9	113651744	113708259	-1	11	17	21	52	35	17	558	1398	750	46	536		Q9WU78
ENSMUST00000035090	ENSMUSG00000032507	9	113963637	114046191	-1	16	11	8	13	14	10	21	55	16	22	25	Q4VA21	Q8BH16
ENSMUST00000035092	ENSMUSG00000032508	9	119335934	119341411	-1	5	4	18	58	7	13	7952	14486	7325	1239	5218	Q3U7M4	P22366
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ENSMUST00000035105	ENSMUSG00000032518	9	120127766	120132369	1	36	46	73	100	38	30	11015	13366	9179	24129	4721		P14206
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ENSMUST00000035112	ENSMUSG00000032525	9	121719169	121756843	1	35	30	56	34	41	24	390	1837	1095	211	1197		P30415
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ENSMUST00000035115	ENSMUSG00000032528	9	121642716	121672954	1	42	22	84	156	50	17	26	47	20	3	74		P97751
ENSMUST00000035116	ENSMUSG00000032527	9	100982032	101034898	-1	13	3	22	13	11	0	47	82	45	14	29		Q99MN9
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ENSMUST00000035148	ENSMUSG00000032548	9	102988712	103096002	1	135	105	278	250	139	73	1	13	4	65	297	Q3TED0	Q9EPT5
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ENSMUST00000035157	ENSMUSG00000032553	9	103188032	103202137	-1	13	14	7	15	17	11	54	155	22	29	42		P47758
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ENSMUST00000035167	ENSMUSG00000032558	9	104002544	104153483	1	30	10	50	69	57	0	0	12	7	2	0		Q7TNH6
ENSMUST00000035170	ENSMUSG00000032560	9	104151282	104262930	-1	6	17	25	36	34	8	286	1332	1009	129	652	G3X922	
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ENSMUST00000035179	ENSMUSG00000032565	9	105128903	105131805	-1	4	10	25	29	13	6	114	359	130	30	118		Q6P3D0
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ENSMUST00000035196	ENSMUSG00000032579	9	107327084	107338350	-1	29	22	89	39	37	17	90	74	45	0	20		Q921L7
ENSMUST00000035199	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	0	0	0	0	200	480	669	0	396		Q91YE7
ENSMUST00000035201	ENSMUSG00000032582	9	107773559	107873237	-1	5	0	0	6	14	0	36	89	50	37	20	Q3ULB0	
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000035203	ENSMUSG00000032584	9	107906873	107920383	1	24	20	52	65	12	0	2	2	2	0	23		Q62190
ENSMUST00000035208	ENSMUSG00000032589	9	108096022	108190384	-1	149	62	518	1224	213	70	4	2	4	2	18		O88737
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ENSMUST00000035220	ENSMUSG00000032601	9	108689314	108750436	1	23	19	45	82	43	22	79	191	173	43	168	Q8K1M3	
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ENSMUST00000035227	ENSMUSG00000032606	9	108290429	108296498	1	15	12	21	24	22	9	18	33	15	9	23		Q9CQM0
ENSMUST00000035230	ENSMUSG00000032607	9	108296853	108302302	1	29	28	102	22	31	13	9	54	25	3	30	A2RSW6	Q8CFA2
ENSMUST00000035232	ENSMUSG00000032609	9	108447636	108461581	-1	0	0	0	0	0	0	3	0	0	0	0		Q9D2D9
ENSMUST00000035234	ENSMUSG00000032611	9	108392805	108410934	1	5	5	0	3	3	2	2	25	5	1	2		
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ENSMUST00000035240	ENSMUSG00000057219	11	115475667	115490467	1	22	11	39	61	27	14	1718	2935	1433	204	997		Q3UIZ3
ENSMUST00000035242	ENSMUSG00000034789	13	55319223	55321980	-1	10	2	16	130	17	4	1399	5906	1661	306	1475	Q0PD31	P35290
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ENSMUST00000035266	ENSMUSG00000078853	11	58199556	58207591	1	21	15	16	33	27	15	141	970	276	370	370	Q9DCE9	
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ENSMUST00000035273	ENSMUSG00000038891	13	27242430	27249679	1	7	2	8	2	5	1	0	0	0	0	0	Q5SZY3	P09586
ENSMUST00000035275	ENSMUSG00000024793	4	152115934	152120119	1	6	2	40	21	11	0	2	18	1	1	9	Q8VD70	
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ENSMUST00000035278	ENSMUSG00000032656	18	56761716	56925548	-1	3	1	13	2	9	3	12	22	12	6	13	F8WJC4	
ENSMUST00000035279	ENSMUSG00000042328	5	112343083	112378414	1	0	2	17	0	0	0	125	194	124	14	103	Q541V2	Q99KG7
ENSMUST00000035283	ENSMUSG00000040667	11	70943058	70969973	-1	0	0	0	0	0	0	0	0	0	0	0		Q8CEC0
ENSMUST00000035288	ENSMUSG00000035459	10	86841198	87008025	-1	43	28	44	59	52	36	0	0	0	0	0	E5RKF9	Q8R4U0
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ENSMUST00000035300	ENSMUSG00000038801	7	140845547	140846769	1	3	1	7	3	3	1	0	0	0	0	0	G5E8B5	
ENSMUST00000035301	ENSMUSG00000039105	4	63544772	63550750	1	24	11	19	75	17	20	4091	7930	3092	9342	2170	Q5HZY7	Q9CR51
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ENSMUST00000035325	ENSMUSG00000033684	1	155776029	155812889	-1	11	7	0	59	27	0	2885	3252	2275	248	1825		Q8BND5
ENSMUST00000035336	ENSMUSG00000040717	14	27039001	27107286	1	82	69	185	150	89	44	6	10	1	3	7		Q8JZL1
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ENSMUST00000035342	ENSMUSG00000022449	15	94270163	94465418	-1	35	18	59	8	40	18	0	0	0	0	0		P59511
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ENSMUST00000035351	ENSMUSG00000041479	14	34219595	34230421	1	160	125	467	144	158	63	2	6	2	1	4		Q8C6N3
ENSMUST00000035371	ENSMUSG00000038486	3	96181151	96195521	1	22	21	94	116	41	17	4	3	0	1	9		Q9JIS5
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ENSMUST00000035399	ENSMUSG00000036218	15	92396915	92771819	1	8	8	48	2	6	10	0	0	0	0	0	E9Q5P6	
ENSMUST00000035419	ENSMUSG00000037202	10	61297836	61304263	1	27	13	40	28	40	23	19	64	15	8	69	A2RSY7	P10820
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ENSMUST00000035444	ENSMUSG00000032773	19	8663789	8683587	1	0	0	15	0	5	4	0	0	0	0	0		P12657
ENSMUST00000035458	ENSMUSG00000030850	7	130391526	130519961	-1	29	0	0	0	0	0	152	702	360	98	275	Q80YP1	Q9Z2A5
ENSMUST00000035462	ENSMUSG00000038702	1	111858702	111864918	-1	4	14	15	38	20	12	14	19	17	5	16		Q0VBN2
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ENSMUST00000035501	ENSMUSG00000032818	18	77281958	77442341	1	6	11	29	7	11	0	0	0	0	0	0	E9PVB2	
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ENSMUST00000035519	ENSMUSG00000038495	3	96104527	96161129	1	5	25	24	81	0	27	645	895	1189	180	768		B2RUR8
ENSMUST00000035521	ENSMUSG00000040866	7	19054690	19074447	1	0	6	6	179	39	13	0	0	0	0	1	B2RQM5	Q8CDR2
ENSMUST00000035532	ENSMUSG00000041417	13	101680563	101768217	-1	8	3	11	14	11	3	3	0	0	17	34	Q80UI5	
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ENSMUST00000035539	ENSMUSG00000005237	11	69420809	69549110	-1	13	0	1	0	1	75	5	17	41	3	16		P0C6F1
ENSMUST00000035540	ENSMUSG00000038025	13	48801750	48870885	-1	44	36	113	155	61	28	939	885	1108	65	851		Q9WTU0
ENSMUST00000035548	ENSMUSG00000032845	18	65265529	65393888	-1	28	18	140	50	54	29	0	0	0	0	0		Q91ZB0
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ENSMUST00000035560	ENSMUSG00000033701	1	155558120	155691330	1	193	152	299	617	266	122	0	30	16	4	16	Q14BV7	Q9D061
ENSMUST00000035563	ENSMUSG00000034127	10	115817284	115849893	1	0	0	0	0	7	0	0	0	0	0	0		Q8R3G9
ENSMUST00000035565	ENSMUSG00000032855	17	24549950	24596514	1	140	80	264	318	203	77	564	365	558	19	863		O08852
ENSMUST00000035569	ENSMUSG00000073664	1	60180599	60338328	1	0	0	0	0	5	0	0	0	0	0	0	E9PV03	
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ENSMUST00000035577	ENSMUSG00000042501	1	10324720	10719945	-1	0	0	0	0	5	0	0	0	0	0	0		Q5U901
ENSMUST00000035579	ENSMUSG00000032898	5	117976730	118010201	1	32	31	63	144	52	23	23	31	30	11	55		Q8VDH1
ENSMUST00000035597	ENSMUSG00000035206	10	80855275	80868705	1	21	10	64	160	31	11	470	571	384	68	330		Q3TD49
ENSMUST00000035604	ENSMUSG00000037275	11	58120002	58168539	-1	5	6	7	28	5	0	27	63	26	7	46		Q8BX17

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000035606	ENSMUSG00000038774	10	50592669	50851202	1	27	28	14	77	33	10	186	598	445	178	306		E9PZJ8
ENSMUST00000035608	ENSMUSG00000039830	16	91225550	91228677	1	23	7	22	343	23	11	0	0	0	0	0	Q542S0	Q9EQW6
ENSMUST00000035612	ENSMUSG00000033712	14	70138177	70153811	-1	25	21	98	146	54	16	746	915	913	74	783		Q8VDP4
ENSMUST00000035622	ENSMUSG00000039099	7	79743163	79785950	1	22	19	35	27	18	11	0	0	0	0	0		Q402B2
ENSMUST00000035625	ENSMUSG00000039519	3	18071950	18243338	-1	3	13	15	64	18	9	1	8	0	5	6		Q60991
ENSMUST00000035626	ENSMUSG00000035651	X	78369643	78371128	1	4	3	3	2	3	1	0	0	0	0	0	Q0VG34	
ENSMUST00000035635	ENSMUSG00000034663	5	96997689	97091867	1	56	44	169	52	51	48	744	2226	1838	198	1480		Q91Z96
ENSMUST00000035640	ENSMUSG00000032900	18	56588350	56594782	1	5	1	0	0	2	4	1	0	0	0	0	C9W8M4	Q9D9I1
ENSMUST00000035645	ENSMUSG00000035969	4	43381979	43427088	1	0	0	0	436	0	0	0	25	0	0	0	Q3V1Z0	
ENSMUST00000035646	ENSMUSG00000039943	2	135659011	136014593	1	0	0	0	0	0	0	0	0	1	0	33	Q91UZ1	
ENSMUST00000035648	ENSMUSG00000032905	18	46732417	46741579	-1	14	20	57	66	16	13	488	1994	755	634	482		Q9CQY1
ENSMUST00000035651	ENSMUSG00000039883	5	21543559	21575904	1	13	13	29	24	23	20	5	71	7	77	2		Q9CXD9
ENSMUST00000035657	ENSMUSG00000036613	12	28751828	28867491	1	18	8	29	14	21	12	260	356	159	194	167		Q8K0G5
ENSMUST00000035661	ENSMUSG00000032911	9	56865104	56899870	1	84	57	192	258	130	52	0	0	0	0	1		Q8VHY0
ENSMUST00000035667	ENSMUSG00000041000	4	128883580	128911328	1	23	18	44	44	45	23	18	35	39	5	36		Q80V85
ENSMUST00000035672	ENSMUSG00000039457	16	5086291	5132481	-1	60	29	93	152	73	26	3	3	3	17	111	G5E898	
ENSMUST00000035673	ENSMUSG00000033933	6	113623959	113631633	1	8	10	28	141	17	9	496	1194	446	185	253	Q3TTE7	P40338
ENSMUST00000035682	ENSMUSG00000022773	16	17069696	17087045	1	6	6	9	200	13	6	0	9	0	0	0	Q65Z96	Q9ESC7
ENSMUST00000035689	ENSMUSG00000039851	16	91053935	91095122	-1	10	7	9	23	8	5	1	0	0	4	0		Q9D4G1
ENSMUST00000035695	ENSMUSG00000041534	14	33954022	33964216	1	42	23	73	91	59	32	0	0	0	0	0		
ENSMUST00000035700	ENSMUSG00000032936	9	107935674	107949691	1	0	0	0	33	27	18	0	0	0	0	0		Q3UHL1
ENSMUST00000035701	ENSMUSG00000032937	17	88985170	89200612	-1	14	14	9	18	16	10	0	0	0	0	0	B2RQM3	P35378
ENSMUST00000035715	ENSMUSG00000044664	9	110798166	110803754	1	37	26	201	68	28	18	1	1	0	0	2		Q8VIF2
ENSMUST00000035716	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	636	515	445	177	510		Q9QUG9
ENSMUST00000035719	ENSMUSG00000040183	4	32804035	32950841	-1	16	0	10	0	0	0	0	0	0	0	0		Q69ZU8
ENSMUST00000035721	ENSMUSG00000039449	2	4622058	4652113	-1	30	28	48	25	29	12	677	3343	1304	504	1027		Q8BM39
ENSMUST00000035724	ENSMUSG00000039158	4	63367125	63403354	-1	68	53	447	177	118	38	9002	12332	11946	694	10263		Q80VW7
ENSMUST00000035725	ENSMUSG00000033940	6	113604772	113616951	1	11	9	21	64	12	8	2731	5703	2154	1968	1469		Q91VR8
ENSMUST00000035732	ENSMUSG00000042189	11	63061654	63094964	1	9	18	32	23	14	8	0	0	0	0	0	Q5SXS5	Q6X6Z7
ENSMUST00000035735	ENSMUSG00000040280	10	127514939	127517152	1	10	4	19	72	12	7	0	0	0	0	1		Q4FZG9
ENSMUST00000035742	ENSMUSG00000037613	7	143665809	143685872	-1	16	11	60	54	32	14	238	621	207	56	209	F8WH78	
ENSMUST00000035748	ENSMUSG00000033460	X	134717963	134721917	1	0	0	0	0	0	0	0	0	0	0	0		Q9CX83
ENSMUST00000035751	ENSMUSG00000035576	2	162943472	162974522	1	2	0	0	3	5	0	3	0	2	1	0		A2A5N8
ENSMUST00000035757	ENSMUSG00000036749	4	144270633	144280488	-1	0	0	0	0	0	6	0	0	0	0	0	Q7TPY4	
ENSMUST00000035766	ENSMUSG00000036769	X	23693051	23806025	1	5	1	4	18	1	0	75	35	121	0	56		Q6NVE8
ENSMUST00000035771	ENSMUSG00000042502	7	127191660	127196050	-1	4	5	6	4	6	0	332	118	226	51	264		Q9CWK3
ENSMUST00000035773	ENSMUSG00000034801	12	69583762	69681852	-1	0	0	0	0	0	0	796	1078	558	47	36	A0A0A0MQ87	
ENSMUST00000035775	ENSMUSG00000035215	10	80852825	80855209	-1	0	0	0	13	18	0	0	21	0	107	36		Q9CQQ8
ENSMUST00000035776	ENSMUSG00000039756	3	122274388	122285271	1	6	2	9	39	8	4	191	1450	541	1240	334		Q8R2M2
ENSMUST00000035777	ENSMUSG00000078908	8	113635586	113645178	1	0	16	76	99	62	17	536	682	729	26	649		Q8BMQ8
ENSMUST00000035779	ENSMUSG00000032883	1	78657825	78707743	1	8	8	12	69	14	3	0	5	0	0	0		Q9CZW4
ENSMUST00000035780	ENSMUSG00000035069	4	103313812	103371868	1	16	8	17	29	9	1	185	589	270	162	251		Q9D8H7
ENSMUST00000035785	ENSMUSG00000041355	3	88575876	88588419	1	6	0	6	70	9	5	0	0	0	0	0		Q9CPW5
ENSMUST00000035797	ENSMUSG00000079657	17	24527241	24534210	-1	8	0	13	75	9	2	0	0	0	0	0	Q148R0	Q504M8
ENSMUST00000035799	ENSMUSG00000039899	5	21372642	21378374	1	10	13	16	127	27	11	3181	7483	4203	2963	5681	Q544K3	P12804
ENSMUST00000035800	ENSMUSG00000033016	18	80606205	80713071	-1	17	17	26	35	17	10	1249	1588	1523	84	1417	Q9DBQ6	
ENSMUST00000035804	ENSMUSG00000033022	18	46713205	46728342	-1	10	9	13	79	13	9	9	98	25	40	31		P60334
ENSMUST00000035812	ENSMUSG00000027394	2	129065942	129096283	1	23	25	43	53	21	17	29	27	41	10	50		P38585
ENSMUST00000035813	ENSMUSG00000032827	6	4902917	5165661	1	41	19	24	34	32	31	13	37	27	0	31	Q7TN74	
ENSMUST00000035822	ENSMUSG00000033033	19	47105353	47138294	-1	0	3	4	21	9	0	115	133	49	10	69		Q8VEC4
ENSMUST00000035824	ENSMUSG00000038042	13	48577873	48625573	-1	28	21	29	43	33	14	5	15	3	7	32		Q6NZK8
ENSMUST00000035836	ENSMUSG00000032737	7	101822632	101838076	-1	0	0	35	42	32	0	33	26	0	0	29		Q6P549
ENSMUST00000035839	ENSMUSG00000040287	10	127501686	127508823	1	8	0	14	8	0	0	7	14	8	0	13		Q8BZ71
ENSMUST00000035840	ENSMUSG00000034075	2	84687970	84715180	-1	22	18	47	47	29	18	870	1363	1192	120	827		Q8VDZ4
ENSMUST00000035842	ENSMUSG00000042129	6	116633008	116673952	-1	32	33	69	68	57	29	1421	2240	2142	494	1441		Q8CB96
ENSMUST00000035844	ENSMUSG00000038695	7	44467980	44471662	1	5	3	8	27	8	3	47	20	18	17	0		Q9CR30
ENSMUST00000035849	ENSMUSG00000033053	19	23558760	23652812	-1	6	5	3	9	8	2	0	0	0	0	0		Q9CQC3
ENSMUST00000035850	ENSMUSG00000033054	9	53537047	53574342	1	30	17	36	81	23	12	82	141	134	75	93		Q8BMA5
ENSMUST00000035852	ENSMUSG00000037108	5	137787798	137822621	1	13	6	38	17	6	2	14	16	4	7	18		Q6IR42
ENSMUST00000035854	ENSMUSG00000042200	11	62951193	62993095	1	7	4	35	13	6	10	0	0	0	0	0		Q9DA64
ENSMUST00000035861	ENSMUSG00000005069	6	124396816	124415067	-1	0	0	0	4	0	0	175	234	340	0	89		O09012
ENSMUST00000035870	ENSMUSG00000033963	6	113596761	113600715	-1	10	9	23	0	13	0	0	0	0	0	0		
ENSMUST00000035871	ENSMUSG00000034850	2	127247908	127261107	1	29	20	99	94	36	15	2966	5772	3504	479	2411		Q8BGP5
ENSMUST00000035889	ENSMUSG00000033577	9	80165031	80311729	1	0	0	0	19	0	0	0	0	0	0	33	E9Q3L1	
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ENSMUST00000035894	ENSMUSG00000020096	10	61171954	61188841	1	6	0	5	12	0	0	0	0	0	0	0		Q7TSD4
ENSMUST00000035899	ENSMUSG00000038982	13	38602709	38635109	-1	8	9	6	41	12	7	36	102	42	57	31		Q8R015
ENSMUST00000035908	ENSMUSG00000033730	14	70077445	70080157	1	9	8	20	529	18	15	1	3	1	0	10		P43300
ENSMUST00000035911	ENSMUSG00000040423	1	160906418	160974978	1	4	6	8	0	5	0	150	101	490	13	479	H7BX02	
ENSMUST00000035914	ENSMUSG00000033722	1	155212471	155244444	-1	14	11	7	3	11	1	0	0	0	0	0	F6T2X5	
ENSMUST00000035918	ENSMUSG00000056035	5	145854426	145879964	-1	12	7	12	8	11	2	0	0	0	5	1	Q3UEN8	Q64459
ENSMUST00000035925	ENSMUSG00000033106	8	106200438	106210933	-1	6	6	13	149	12	3	99	705	164	72	190		Q7TPE5
ENSMUST00000035929	ENSMUSG00000038704	7	44465391	44467758	1	7	7	0	2	16	0	0	0	0	0	0		Q9DCQ2
ENSMUST00000035930	ENSMUSG00000039841	6	28239927	28398005	-1	13	7	20	67	10	2	0	15	6	0	17	B7ZMR9	Q0VEE6
ENSMUST00000035931	ENSMUSG00000037892	3	49743296	49757325	-1	0	0	46	0	1	0	0	0	0	0	0		Q8VHR0
ENSMUST00000035934	ENSMUSG00000034152	13	74169805	74208700	-1	34	29	39	31	28	15	436	1613	839	439	618	Q8K0E2	Q6KAR6
ENSMUST00000035935	ENSMUSG00000039963	11	119228572	119265236	1	10	23	44	103	21	10	0	0	0	0	0		Q8BI79
ENSMUST00000035938	ENSMUSG00000035042	11	83525778	83530518	-1	7	7	5	7	5	5	53	191	23	151	110	Q5XZF2	P30882
ENSMUST00000035939						6	16	34	38	12	3	0	0	0	0	0		
ENSMUST00000035952	ENSMUSG00000027859	3	102469919	102521013	1	5	5	0	20	7	7	0	0	0	0	1		P01139
ENSMUST00000035960	ENSMUSG00000035439	8	71248561	71272934	-1	0	3	4	118	3	2	24	83	36	19	14		Q99L00
ENSMUST00000035973	ENSMUSG00000036782	X	23219271	23365082	-1	0	0	0	0	0	0	0	0	0	0	1		Q80TF4
ENSMUST00000035977	ENSMUSG00000046591	7	79660196	79698148	1	44	35	180	284	56	32	43	37	76	2	49		Q8BQ33
ENSMUST00000035980	ENSMUSG00000033219	5	14910122	14914899	-1	5	5	7	4	5	0	0	0	0	0	0	Q80ZT2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000035982	ENSMUSG00000041058	4	19608303	19708993	-1	3	13	9	0	18	0	39	108	54	32	58		Q8BZZ3
ENSMUST00000035983	ENSMUSG00000041453	5	146832890	146837032	1	20	8	47	140	37	6	6	17	10	23	12	Q9CQM8	
ENSMUST00000035985	ENSMUSG00000066640	5	142866946	142895421	-1	0	0	0	0	0	0	35	0	0	3	0	F8VQK6	
ENSMUST00000035987	ENSMUSG00000042724	12	81714950	81781170	-1	51	38	140	322	85	45	4525	4393	5628	222	3309		Q3U1V8
ENSMUST00000035988	ENSMUSG00000038991	13	38500273	38528824	-1	0	0	0	74	5	0	340	527	195	203	581	Q3TEE8	Q91W90
ENSMUST00000035991	ENSMUSG00000041684	1	44118957	44144770	1	10	7	0	14	11	0	20	78	22	13	0		Q8CBX9
ENSMUST00000036003	ENSMUSG00000040102	6	147091379	147112778	1	31	19	54	360	32	16	107	170	149	22	96	B2KFS7	Q8BFQ9
ENSMUST00000036004	ENSMUSG00000046434	15	103240432	103244955	1	50	24	127	91	76	16	53	126	59	262	163	Q5EBP8	
ENSMUST00000036016	ENSMUSG00000035262	10	80805248	80807648	1	10	9	11	331	22	8	4	18	4	1	7	Q5EC55	
ENSMUST00000036018	ENSMUSG00000040891	7	19013284	19023538	-1	14	11	72	155	21	16	0	0	0	0	0		P35584
ENSMUST00000036019	ENSMUSG00000034687	5	96373955	96784728	1	85	67	141	310	142	49	0	0	2	1	12		Q80T14
ENSMUST00000036025	ENSMUSG00000026339	1	121431049	121506460	1	55	29	126	83	62	39	186	776	415	57	407		Q7TQK5
ENSMUST00000036030	ENSMUSG00000033184	18	46560235	46597535	-1	0	0	0	0	0	0	21	0	43	2	9	E9Q7G1	
ENSMUST00000036031	ENSMUSG00000039934	5	21186255	21315132	1	20	14	43	188	22	15	427	2554	814	366	852		Q3TCV3
ENSMUST00000036033	ENSMUSG00000020231	10	76259429	76345291	-1	19	0	0	0	0	8	243	160	359	17	289	F8WI56	
ENSMUST00000036041	ENSMUSG00000040701	14	55098578	55106593	-1	0	0	0	0	4	2	79	0	158	0	174		O88512
ENSMUST00000036043	ENSMUSG00000036790	X	66649318	66661393	1	3	3	6	7	2	0	0	0	0	0	0	Q14DT0	Q810C0
ENSMUST00000036044	ENSMUSG00000034163	10	115384959	115432772	1	14	23	65	562	44	18	297	1215	1041	47	848	B2RT41	
ENSMUST00000036045	ENSMUSG00000036216	11	53422181	53423170	-1	1	2	4	2	4	2	0	3	0	6	0		Q91V13
ENSMUST00000036049	ENSMUSG00000034189	8	119561979	119575200	-1	22	18	95	68	27	17	1128	1596	977	131	632		Q8BTX9
ENSMUST00000036060	ENSMUSG00000042258	13	116298281	116309689	-1	12	3	5	55	3	7	0	0	0	0	0	A2RSV5	P61372
ENSMUST00000036068	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	K3W4M8	
ENSMUST00000036069	ENSMUSG00000033207	19	23302609	23448322	-1	16	11	17	42	20	7	1	5	2	0	7		
ENSMUST00000036070	ENSMUSG00000021750	14	8296274	8318023	-1	80	100	628	45	38	51	0	15	17	1	8	Q78TU8	
ENSMUST00000036072	ENSMUSG00000034959	14	75016027	75052532	1	19	13	28	17	23	9	571	930	548	150	332	F8WGX2	
ENSMUST00000036074	ENSMUSG00000036246	8	69808679	69821870	1	30	16	54	51	25	12	2404	5354	3148	257	2851		Q6PGG2
ENSMUST00000036085	ENSMUSG00000090173	11	62847069	62877465	1	26	4	42	0	24	12	0	0	0	0	0		Q5SUS0
ENSMUST00000036088	ENSMUSG00000038811	11	95837216	95845734	1	18	17	54	24	23	11	30	210	31	37	107	A2A614	Q61017
ENSMUST00000036089	ENSMUSG00000033368	2	122160700	122179027	1	11	6	14	3	15	9	1	8	4	3	4		Q80X56
ENSMUST00000036092	ENSMUSG00000038319	5	24319589	24351604	-1	23	12	88	279	38	13	0	0	0	2	1	Q53Z09	
ENSMUST00000036104						11	5	2	1	6	0	0	0	0	0	0		
ENSMUST00000036109	ENSMUSG00000037962	5	125003221	125012547	1	7	5	25	177	11	5	0	0	0	0	0		Q7TS73
ENSMUST00000036111	ENSMUSG00000040112	6	147042764	147073991	1	1	4	0	40	0	0	121	562	158	128	85		
ENSMUST00000036113	ENSMUSG00000039976	11	119143045	119228499	-1	43	29	122	132	85	32	48	28	31	10	75	A2ABG4	
ENSMUST00000036116	ENSMUSG00000042734	12	81631369	81664941	1	24	11	32	122	34	11	0	2	1	6	17		Q3V038
ENSMUST00000036125	ENSMUSG00000040731	5	134619721	134639490	-1	17	16	41	94	27	18	3331	4945	3451	577	2394	Q3TG58	Q9WUK2
ENSMUST00000036126	ENSMUSG00000036023	14	50807946	50821300	1	7	11	9	10	4	3	46	278	94	78	104		O88554
ENSMUST00000036127	ENSMUSG00000033249	8	105269801	105275845	1	0	0	12	21	14	0	0	0	0	0	0	B2RQY2	Q9R0L1
ENSMUST00000036136	ENSMUSG00000036655	12	28594173	28623290	-1	11	6	7	8	17	11	1	2	4	1	0		
ENSMUST00000036153	ENSMUSG00000034432	1	90602981	90613341	1	9	8	25	60	11	6	384	624	358	213	245		Q8VBV7
ENSMUST00000036155	ENSMUSG00000035211	7	99859218	99917824	1	23	19	46	72	38	16	7	2	5	4	14		Q3U3V8
ENSMUST00000036156	ENSMUSG00000033365	4	117894486	117914999	-1	36	17	74	178	42	15	594	564	506	63	423		Q8K0C1
ENSMUST00000036158	ENSMUSG00000033272	18	36679215	36683861	1	19	4	1	0	24	0	647	727	430	97	297		Q9D321
ENSMUST00000036161	ENSMUSG00000041720	16	17280351	17406314	-1	32	36	40	0	39	0	506	1207	958	92	935	E9Q3L2	
ENSMUST00000036172	ENSMUSG00000032908	1	78310345	78420289	1	35	30	62	82	52	23	1	1	1	2	6		Q810K3
ENSMUST00000036174	ENSMUSG00000036292	16	43980350	44027945	-1	13	5	40	0	4	10	0	0	0	0	0		Q8CI52
ENSMUST00000036176	ENSMUSG00000033697	15	76723985	76818170	-1	15	0	9	53	43	0	83	212	94	2	197	G3X932	
ENSMUST00000036177	ENSMUSG00000039095	5	28165694	28172166	1	16	3	26	580	27	12	0	0	0	0	0	Q3TZM2	P09066
ENSMUST00000036181	ENSMUSG00000038526	3	95897768	95904691	-1	7	2	6	15	5	6	0	1	1	1	0		Q9WVT6
ENSMUST00000036187	ENSMUSG00000036327	2	26208637	26237525	-1	2	3	1	190	11	3	11	22	20	2	26		Q3TMX7
ENSMUST00000036188	ENSMUSG00000042677	4	125118423	125127840	-1	20	21	44	72	48	23	582	1072	556	71	592		Q5D1E7
ENSMUST00000036194	ENSMUSG00000040121	6	147032584	147034245	1	3	6	8	8	8	3	0	0	0	0	1		Q9D7T1
ENSMUST00000036195	ENSMUSG00000028521	4	103170649	103215164	-1	3	18	57	17	7	22	46	108	43	13	63	A2AKQ0	
ENSMUST00000036206	ENSMUSG00000037979	5	124834418	124862424	-1	19	0	32	246	20	6	28	39	53	17	18		Q8VDN4
ENSMUST00000036208	ENSMUSG00000036123	13	74121515	74166064	1	31	16	97	79	35	20	0	1	0	0	0		G3X939
ENSMUST00000036210	ENSMUSG00000034064	16	38525137	38550258	-1	0	7	11	48	15	6	63	201	94	144	39		Q8BYB9
ENSMUST00000036211	ENSMUSG00000041468	5	146582398	146585239	-1	14	11	10	35	23	10	0	0	0	0	0		P35412
ENSMUST00000036215	ENSMUSG00000034227	11	116330704	116335399	-1	20	10	71	424	38	15	1	1	1	0	1		Q61660
ENSMUST00000036221	ENSMUSG00000033313	8	105264648	105269326	1	16	9	7	181	18	8	190	227	118	24	87	Q3TD55	Q8CIG9
ENSMUST00000036225	ENSMUSG00000038388	6	50110241	50198939	1	0	0	0	0	1	0	30	101	79	7	42	Q3UN60	Q9JLB0
ENSMUST00000036226	ENSMUSG00000033319	18	46501746	46525971	-1	20	15	13	87	19	9	415	1822	645	105	537	B2RRW5	Q8CEF1
ENSMUST00000036227	ENSMUSG00000039106	5	27842149	27855088	1	45	26	62	92	39	13	0	0	0	0	0		P30966
ENSMUST00000036229	ENSMUSG00000033323	18	80407959	80469695	-1	15	15	38	122	30	14	526	512	690	79	443		Q7TSG2
ENSMUST00000036236	ENSMUSG00000038388	6	50110241	50198939	1	0	0	0	6	0	0	13	39	0	16	34	B9EHZ5	Q9JLB0
ENSMUST00000036247	ENSMUSG00000033707	15	76715276	76723845	-1	10	7	30	233	19	6	105	174	107	14	58		Q8VE95
ENSMUST00000036248	ENSMUSG00000038400	2	173224458	173276533	-1	13	19	67	87	23	10	5	7	2	7	28	A2APF4	
ENSMUST00000036252	ENSMUSG00000028063	3	88480147	88509956	-1	14	0	3	95	10	4	140	6	0	10	130		P48678
ENSMUST00000036253						32	12	57	63	29	44	289	868	475	12	578		
ENSMUST00000036267	ENSMUSG00000033350	9	95399292	95406722	-1	115	96	611	458	112	48	2	7	3	3	24		Q80WV3
ENSMUST00000036273	ENSMUSG00000035356	16	55811375	55838899	-1	0	0	23	0	22	0	0	0	0	0	0		Q9EST8
ENSMUST00000036274	ENSMUSG00000035227	7	99837569	99858883	-1	21	16	27	60	19	16	669	1684	681	1110	491		Q9CYN2
ENSMUST00000036288	ENSMUSG00000056211	1	128103301	128237736	1	0	4	0	0	0	0	167	330	326	30	213	E9Q9Q2	
ENSMUST00000036299	ENSMUSG00000040712	11	70669463	70688105	-1	0	0	0	0	0	0	60	0	0	0	110		Q80Y50
ENSMUST00000036300	ENSMUSG00000045672	4	63214004	63334991	1	12	12	27	19	7	6	0	17	3	4	5		Q5QNQ9
ENSMUST00000036303	ENSMUSG00000041380	X	146962513	147197277	1	0	0	0	0	7	0	0	0	0	0	0		P34968
ENSMUST00000036315	ENSMUSG00000020524	11	57011387	57330244	1	0	7	51	21	0	13	0	0	0	0	0		P23818
ENSMUST00000036320	ENSMUSG00000034175	11	5098926	5106093	1	0	0	0	0	0	0	18	19	15	5	13		Q8BP97
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ENSMUST00000036328	ENSMUSG00000040721	14	55060262	55092324	-1	76	49	199	343	116	48	23	34	26	3	53	Q2MHN3	
ENSMUST00000036329	ENSMUSG00000038733	1	181173228	181211552	-1	0	0	0	0	0	0	1141	404	2648	53	854	F8WH48	
ENSMUST00000036331	ENSMUSG00000035239	7	99811439	99828417	-1	95	99	204	133	101	45	14	24	18	4	35	Q543I9	Q9JMH7
ENSMUST00000036333	ENSMUSG00000035725	X	77761411	77796278	-1	38	45	117	226	49	21	325	1104	596	43	441		Q922R0
ENSMUST00000036340	ENSMUSG00000034023	6	113531682	113597017	1	20	21	36	29	27	6	36	53	57	8	34	B2RSU4	Q80V62
ENSMUST00000036347	ENSMUSG00000033419	9	86765923	86880654	-1	0	0	0	40	0	2	0	0	0	0	0	E9QQ05	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000036350	ENSMUSG00000039496	2	3513030	3526376	1	89	79	487	213	127	77	6	33	21	13	34		Q8CC36
ENSMUST00000036354	ENSMUSG00000034403	X	99465734	99471273	-1	9	8	6	22	13	8	61	88	38	33	114	Q05CG5	O55176
ENSMUST00000036355	ENSMUSG00000033149	16	45746243	45953598	-1	24	35	1	56	14	16	2	0	0	0	0		Q8K1N2
ENSMUST00000036357	ENSMUSG00000034583	7	6487913	6488876	-1	3	15	6	5	8	3	0	0	0	0	0	Q8VF33	
ENSMUST00000036360	ENSMUSG00000038543	3	95883954	95892005	-1	15	0	22	24	0	0	36	235	28	212	46		Q8R2K8
ENSMUST00000036362	ENSMUSG00000040751	5	134600022	134615025	-1	0	7	0	0	0	0	410	780	314	313	206		Q9JHL0
ENSMUST00000036370	ENSMUSG00000033450	17	7926000	7934897	1	22	13	65	31	27	19	355	613	521	158	418		B2RWW0
ENSMUST00000036372	ENSMUSG00000032640	7	66109515	66173798	1	17	18	34	53	27	8	1454	4704	2072	581	2132		Q6ZQ11
ENSMUST00000036374	ENSMUSG00000038845	11	95666957	95680773	1	0	0	13	0	2	1	76	36	30	99	44	Q5SQG5	
ENSMUST00000036376	ENSMUSG00000034757	11	102284931	102289237	1	0	0	0	0	0	0	937	1419	452	100	352		Q3V209
ENSMUST00000036380	ENSMUSG00000033379	4	117884326	117887333	-1	0	0	0	6	3	2	2958	4442	1561	652	1191	Q3U889	Q91V37
ENSMUST00000036381	ENSMUSG00000034190	14	69716979	69732570	-1	21	16	32	265	35	20	603	1284	637	79	450		Q8R1T1
ENSMUST00000036382	ENSMUSG00000020258	9	106152857	106158138	-1	62	36	161	33	60	28	0	0	0	0	0		
ENSMUST00000036383	ENSMUSG00000042707	4	125055338	125065703	-1	14	12	28	13	19	14	1	1	0	2	0	Q0IIN3	Q8BVN8
ENSMUST00000036387	ENSMUSG00000033208	10	76253853	76261159	1	11	5	24	9	10	3	0	0	0	0	0	Q3UY00	P50114
ENSMUST00000036407	ENSMUSG00000033478	19	57361009	57389594	1	23	22	44	52	47	18	1035	1633	1627	161	1233		Q8CDM8
ENSMUST00000036412	ENSMUSG00000064310	16	55225175	55297986	-1	5	7	13	1	7	6	0	0	0	0	0		Q8BGZ8
ENSMUST00000036418	ENSMUSG00000038550	3	95878503	95882251	-1	0	0	0	0	0	0	5	9	0	0	1	A2RTE4	Q3TQ03
ENSMUST00000036423	ENSMUSG00000033728	15	76710623	76717699	1	0	0	3	2	0	0	84	97	0	2	26		Q8VC16
ENSMUST00000036424	ENSMUSG00000032807	11	69156989	69169792	1	27	14	41	57	57	19	0	1	0	0	0	Q2KHL0	O70582
ENSMUST00000036426	ENSMUSG00000033491	9	86743649	86758443	1	209	180	427	272	290	158	5	0	23	2	27		Q8C0F9
ENSMUST00000036437	ENSMUSG00000029486	5	96209493	96266727	1	9	11	0	0	18	6	37	219	57	11	29		Q99N96
ENSMUST00000036439	ENSMUSG00000039385	15	13034200	13173639	-1	14	14	24	23	22	11	0	0	0	0	0		P97326
ENSMUST00000036450	ENSMUSG00000033396	2	122053520	122118386	-1	42	34	53	89	43	25	380	757	759	74	695		Q3UHA3
ENSMUST00000036451	ENSMUSG00000035126	4	103038065	103114555	-1	14	2	10	0	2	3	0	41	17	0	1		E9PYY5
ENSMUST00000036453	ENSMUSG00000040390	7	27656375	27674598	-1	13	12	47	156	13	11	26	54	0	0	13		Q66L42
ENSMUST00000036456	ENSMUSG00000021572	13	74036495	74062285	-1	27	16	23	51	34	18	22	39	39	15	24		Q9D3R3
ENSMUST00000036462	ENSMUSG00000036002	4	43032414	43046220	-1	0	0	0	0	0	0	0	0	3	0	44		Q8BR27
ENSMUST00000036467	ENSMUSG00000034768	11	102268743	102279462	1	26	11	29	126	32	22	1	1	1	1	1		Q8VHS5
ENSMUST00000036470	ENSMUSG00000039983	2	119017779	119029393	-1	11	13	20	22	12	13	112	295	160	136	90	Q3UHY7	
ENSMUST00000036473	ENSMUSG00000039254	2	32236590	32255005	1	0	0	0	7	2	0	108	125	60	0	71		Q8R2R1
ENSMUST00000036476	ENSMUSG00000040606	4	142102390	142239401	-1	0	0	0	81	9	0	0	0	0	0	0		Q69ZS8
ENSMUST00000036489	ENSMUSG00000039968	5	20893028	20956398	-1	15	11	40	216	21	10	428	1176	793	256	620	D3Z0K6	
ENSMUST00000036493	ENSMUSG00000033161	3	101576219	101604684	-1	19	15	47	74	32	13	4171	5219	5044	891	4067		Q8VDN2
ENSMUST00000036497	ENSMUSG00000002997	12	31958476	32061296	-1	0	0	0	0	0	11	0	0	0	25	91		P31324
ENSMUST00000036503	ENSMUSG00000108273	6	116285891	116329484	1	0	0	0	7	0	8	312	1047	809	1061	818	D3Z5M1	
ENSMUST00000036509	ENSMUSG00000036352	2	25998543	26021747	-1	3	10	14	36	0	0	62	217	91	79	90		Q8VDI7
ENSMUST00000036540	ENSMUSG00000041040	1	59913006	59985346	1	21	24	31	226	19	14	836	1707	1208	104	721		Q3U3E2
ENSMUST00000036541	ENSMUSG00000036093	2	52397951	52424901	-1	21	26	21	55	19	12	423	1264	603	134	414	Q498A0	Q80ZU0
ENSMUST00000036554	ENSMUSG00000032849	14	118482692	118706219	-1	25	0	0	0	25	17	251	177	455	0	303	E9Q236	
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ENSMUST00000036557	ENSMUSG00000035126	4	103038065	103114555	-1	0	0	0	0	9	2	0	0	24	0	24		E9PYY5
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ENSMUST00000036564	ENSMUSG00000039760	10	19621998	19634681	1	9	0	7	16	10	3	5	32	6	26	11		Q80XF5
ENSMUST00000036570	ENSMUSG00000040760	14	26918988	26971232	-1	26	17	32	75	35	18	172	594	320	249	236		Q8K3H0
ENSMUST00000036572	ENSMUSG00000040616	4	142030992	142084304	-1	11	7	44	121	25	7	141	143	45	37	157		Q99LG1
ENSMUST00000036575	ENSMUSG00000074369	7	15388721	15398545	1	0	3	8	0	3	0	0	0	0	0	0	E9PXV9	
ENSMUST00000036576	ENSMUSG00000038010	10	58497970	58576242	1	28	47	180	64	20	23	10	28	19	20	8		Q0VF22
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ENSMUST00000036579	ENSMUSG00000020220	4	144972622	145195005	-1	95	73	0	87	0	53	204	153	688	51	430	B1ART2	
ENSMUST00000036584	ENSMUSG00000033610	19	34810894	34879455	-1	7	6	5	255	22	8	8	0	3	3	5		Q8K4K6
ENSMUST00000036592	ENSMUSG00000040163	6	146950329	146954422	-1	23	19	36	14	25	11	0	0	0	0	2		Q80W69
ENSMUST00000036606	ENSMUSG00000031216	X	99003248	99074728	1	21	13	42	45	30	15	266	509	405	31	354		Q8K031
ENSMUST00000036615	ENSMUSG00000033629	9	64986985	65021717	-1	21	15	37	100	25	10	45	215	53	40	123		Q8K2C9
ENSMUST00000036618	ENSMUSG00000042286	14	31139013	31168641	-1	40	30	85	31	54	22	151	107	204	46	683	G3X973	
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ENSMUST00000036643	ENSMUSG00000040485	1	167445669	167466780	-1	13	5	11	8	15	5	0	0	0	0	0		Q5M8M9
ENSMUST00000036646	ENSMUSG00000034724	5	96070333	96164171	-1	0	0	0	0	0	0	94	0	90	0	22	F8WJG1	
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ENSMUST00000036649	ENSMUSG00000033983	11	88970252	88991613	1	0	5	9	11	6	12	13	42	0	13	11		Q5SU73
ENSMUST00000036653	ENSMUSG00000034997	14	74640840	74706859	1	26	15	46	25	28	7	13	4	55	30	22	Q543D4	P35363
ENSMUST00000036665	ENSMUSG00000027742	3	52981875	53017237	-1	2	0	0	13	3	0	189	509	218	125	134		
ENSMUST00000036680	ENSMUSG00000039759	4	151982639	151988997	-1	6	1	8	43	11	4	160	272	64	51	99	Q52KE1	Q8BJ25
ENSMUST00000036682	ENSMUSG00000033885	14	8098213	8165111	1	16	0	18	40	14	13	1062	2845	1756	291	1359		Q8BX57
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ENSMUST00000036701	ENSMUSG00000051435	4	141890438	142015082	-1	3	5	9	11	8	5	0	0	0	0	0		A6PWD2
ENSMUST00000036712						0	0	0	0	0	0	1404	1352	996	200	657		
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ENSMUST00000036719	ENSMUSG00000039621	2	166566342	166713832	-1	18	16	36	61	34	23	8668	6164	9555	279	8357		Q69ZK0
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ENSMUST00000036732	ENSMUSG00000033187	16	45626848	45654118	-1	9	10	26	24	12	7	0	4	4	0	1	E9QP50	
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ENSMUST00000036737	ENSMUSG00000038591	15	54410774	54466358	1	21	15	30	14	20	16	0	0	0	1	0		Q8CF98
ENSMUST00000036742	ENSMUSG00000039208	11	121701544	121716306	1	10	2	9	112	6	0	321	654	322	136	336		Q8VE43
ENSMUST00000036744	ENSMUSG00000033760	19	4756543	4767065	1	0	0	0	0	0	0	28	71	33	13	50		Q8VE92
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ENSMUST00000036759	ENSMUSG00000024104	6	116208038	116262686	1	35	17	39	79	38	27	2118	8423	5309	1087	4370		Q6PGL7
ENSMUST00000036765	ENSMUSG00000090264	18	36664060	36665917	1	3	3	2	13	8	3	0	64	11	29	29		Q80VV3
ENSMUST00000036796	ENSMUSG00000036264	11	52764634	53188538	1	41	25	92	99	33	24	0	0	0	0	0		Q5STE3
ENSMUST00000036805	ENSMUSG00000035278	10	80796100	80798626	-1	3	2	7	178	6	3	713	1108	497	212	382		Q9D240

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000036807	ENSMUSG00000037214	8	26158212	26162940	1	10	7	30	23	12	0	48	133	33	30	43		Q8CHW1
ENSMUST00000036811	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	18		P30999
ENSMUST00000036819	ENSMUSG00000038768	1	181051237	181060667	1	8	8	15	23	18	4	0	0	0	0	0	Q3TS87	
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ENSMUST00000036825	ENSMUSG00000034891	13	54758860	54766595	-1	6	3	13	113	5	9	0	0	0	0	0		Q91ZZ3
ENSMUST00000036852	ENSMUSG00000033762	15	76703553	76710559	-1	28	23	100	203	57	24	17	13	15	2	23		
ENSMUST00000036854	ENSMUSG00000040659	4	141858142	141874920	-1	18	16	37	68	30	10	9102	10039	8649	1519	4693	Q8C845	
ENSMUST00000036858	ENSMUSG00000031382	X	164436994	164459170	1	0	0	0	1	3	0	0	9	4	0	0		Q9CQ31
ENSMUST00000036862	ENSMUSG00000035933	12	31654869	31937630	1	13	17	9	72	13	6	120	237	233	194	177		Q8C0L8
ENSMUST00000036865	ENSMUSG00000039187	7	79391929	79450264	1	0	0	0	0	12	0	10	27	35	5	0		Q8K368
ENSMUST00000036872	ENSMUSG00000029578	5	142627698	142670588	1	22	25	57	67	39	20	625	1708	877	118	820		Q80W47
ENSMUST00000036876	ENSMUSG00000041735	4	144703191	144721404	-1	4	4	16	4	4	2	0	0	0	0	0	B1AVU7	
ENSMUST00000036877	ENSMUSG00000038456	6	39462378	39557867	-1	16	16	31	27	38	15	45	66	68	7	58		Q8C4S8
ENSMUST00000036880	ENSMUSG00000033862	8	123224841	123232250	1	21	10	74	69	29	7	99	247	102	16	117		Q3UMM4
ENSMUST00000036884	ENSMUSG00000033863	19	23141226	23166911	1	16	16	48	309	26	22	155	165	427	44	189	Q8CEC4	
ENSMUST00000036904	ENSMUSG00000037075	15	58889229	58902390	1	13	16	16	63	13	12	387	1745	556	252	271		
ENSMUST00000036917	ENSMUSG00000037335	11	57828705	57832818	-1	0	8	0	45	20	0	0	0	0	0	0	Q5SQG1	Q64279
ENSMUST00000036928	ENSMUSG00000038776	1	180976210	181020904	-1	13	0	0	29	0	0	20	0	15	0	35		Q9D379
ENSMUST00000036932	ENSMUSG00000035910	13	25056004	25210706	1	7	12	9	111	24	6	0	0	0	0	0		Q5DU00
ENSMUST00000036934	ENSMUSG00000026950	2	52136647	52338798	-1	104	78	145	74	91	0	6	0	0	0	91	E9Q1W3	
ENSMUST00000036937	ENSMUSG00000037085	15	58872649	58876781	1	21	16	26	107	30	15	122	358	119	49	122		Q8BG71
ENSMUST00000036938	ENSMUSG00000020600	12	8528483	8599066	-1	13	16	53	21	32	9	0	0	0	0	0	Q8BZV2	
ENSMUST00000036951	ENSMUSG00000032959	5	117282654	117287625	-1	19	11	53	60	22	10	357	437	230	272	355	Q5EBQ2	P70296
ENSMUST00000036952	ENSMUSG00000036275	11	52396428	52408728	1	7	0	8	17	15	7	2595	3975	2247	227	1158	Q3U339	Q8K201
ENSMUST00000036954	ENSMUSG00000034486	1	89927956	89931179	-1	5	2	2	334	11	7	0	0	1	2	3		P48031
ENSMUST00000036972	ENSMUSG00000036242	14	49681560	49783383	-1	0	6	32	29	38	0	0	0	0	0	0		Q8BT18
ENSMUST00000036976						1	2	1	0	6	0	145	531	104	19	83		
ENSMUST00000036977	ENSMUSG00000039018	7	140137564	140150786	1	0	0	4	19	13	0	24	51	15	54	25		Q8R2R6
ENSMUST00000036987	ENSMUSG00000008690	15	89355719	89372826	1	19	0	0	0	22	17	40	77	18	20	47	E9PY48	
ENSMUST00000036991	ENSMUSG00000041548	5	116408491	116422864	-1	13	7	31	33	13	5	0	0	0	52	63		Q9JK92
ENSMUST00000036992	ENSMUSG00000036111	7	109138572	109170308	-1	12	7	16	42	18	5	216	164	146	26	47	Q3UZX1	Q924W9
ENSMUST00000036996	ENSMUSG00000033938	8	83566671	83571626	1	0	0	6	66	9	2	1262	1841	932	2356	529		Q9CR61
ENSMUST00000036999	ENSMUSG00000063146	5	134489383	134552434	-1	55	33	128	375	77	30	191	272	146	26	249		Q9Z0H8
ENSMUST00000037001	ENSMUSG00000037353	15	100469034	100479252	1	19	16	42	93	29	10	112	265	144	23	99		Q924L1
ENSMUST00000037007	ENSMUSG00000034282	11	116220559	116238077	-1	61	36	116	425	103	40	10	3	4	2	13		Q9D952
ENSMUST00000037011	ENSMUSG00000033949	18	46165302	46212607	-1	35	51	96	37	16	11	1	1	2	0	4		Q80WG7
ENSMUST00000037012	ENSMUSG00000042604	2	107290639	107298502	1	21	22	86	79	22	17	0	0	0	0	2		Q61423
ENSMUST00000037014	ENSMUSG00000037594	12	112808975	112816245	1	8	3	13	312	8	5	42	59	31	5	20		Q8BHN9
ENSMUST00000037023	ENSMUSG00000034892	12	69157722	69159186	-1	8	15	16	42	18	5	4545	6223	4028	23169	2680		P62274
ENSMUST00000037025	ENSMUSG00000038080	13	47043499	47084613	1	14	11	17	85	15	8	23	65	95	23	83		Q8CIG3
ENSMUST00000037029	ENSMUSG00000033960	18	4634929	4682868	1	74	28	185	117	79	38	5	4	4	5	46	B7ZN02	Q5DTX6
ENSMUST00000037035	ENSMUSG00000041135	4	16122733	16163647	-1	0	0	7	106	17	4	56	215	71	54	87	Q547H1	P58801
ENSMUST00000037044	ENSMUSG00000038822	10	45577829	45712345	1	5	9	4	124	9	0	53	145	116	34	55		Q3U0D9
ENSMUST00000037048	ENSMUSG00000039533	5	142562358	142608800	-1	60	46	91	199	95	61	0	0	0	0	0	Q3V1Z9	Q8R189
ENSMUST00000037049	ENSMUSG00000036306	8	69132669	69184225	-1	9	0	0	0	12	0	3	0	0	1	0		P60853
ENSMUST00000037055	ENSMUSG00000036622	4	140986873	141007330	1	0	0	0	0	0	0	3768	4254	3009	223	1526		Q9CTG6
ENSMUST00000037056	ENSMUSG00000038690	5	145183698	145192062	-1	5	0	19	9	8	4	259	450	78	1040	74	F8WHP8	
ENSMUST00000037057	ENSMUSG00000002617	17	23173869	23193252	-1	3	5	5	5	6	0	3	45	10	5	10	B1B1D3	
ENSMUST00000037059	ENSMUSG00000062478	4	141814962	141846359	-1	0	0	11	0	0	0	0	0	0	0	0	E9QL79	
ENSMUST00000037064	ENSMUSG00000034248	14	69241848	69285112	-1	0	0	32	73	5	18	257	1967	352	95	223		Q920G8
ENSMUST00000037071	ENSMUSG00000052012	10	129607547	129612095	-1	12	5	15	13	4	6	0	0	0	0	0	Q8VGJ1	
ENSMUST00000037072	ENSMUSG00000024483	18	36559987	36665917	1	9	0	6	0	2	4	32	267	0	8	50	F7DE17	
ENSMUST00000037096	ENSMUSG00000038085	2	156312299	156375638	1	0	0	0	85	0	5	41	328	95	111	84		Q9D5U8
ENSMUST00000037097	ENSMUSG00000034295	18	24709445	25133500	1	40	22	47	102	51	19	0	1	0	3	24		Q76LL6
ENSMUST00000037099	ENSMUSG00000037242	4	135213969	135272814	-1	27	18	79	52	50	20	228	257	213	74	418	Q543N5	Q9QYB1
ENSMUST00000037115	ENSMUSG00000038622	15	52712445	52730431	1	3	2	1	66	0	3	131	701	141	281	151		Q9CQI9
ENSMUST00000037117	ENSMUSG00000035666	2	28822299	28840360	-1	27	34	78	30	45	21	192	411	273	48	200		Q8BMQ2
ENSMUST00000037119	ENSMUSG00000041911	2	71528113	71533981	1	6	1	18	354	23	13	0	0	0	0	0		Q64317
ENSMUST00000037127	ENSMUSG00000033423	4	117550365	117674297	1	0	0	7	180	11	0	79	75	63	7	67		Q8C460
ENSMUST00000037134	ENSMUSG00000040424	7	27523267	27531175	1	21	19	86	81	28	19	0	3	1	0	2		Q3V016
ENSMUST00000037141	ENSMUSG00000037111	3	51515319	51560879	-1	42	23	84	496	91	41	1259	3150	2550	160	2002		Q8VHL1
ENSMUST00000037142	ENSMUSG00000034028	18	89197431	89270201	1	5	3	6	2	3	9	8	14	5	19	21	Q5DW69	Q8K4F0
ENSMUST00000037145	ENSMUSG00000034918	13	54701461	54736662	1	39	31	84	42	47	27	0	0	1	0	0	E9Q7P9	
ENSMUST00000037146	ENSMUSG00000034201	11	5054132	5065327	-1	0	0	0	0	8	6	0	0	1	0	0	Q9D2H3	
ENSMUST00000037154	ENSMUSG00000062609	16	95257558	95300260	1	0	0	0	0	0	0	0	0	0	0	0	Q3TNE6	
ENSMUST00000037165	ENSMUSG00000034041	8	84701457	84704715	1	23	11	50	261	19	4	745	1203	538	60	435		P27792
ENSMUST00000037181	ENSMUSG00000034912	12	66469568	67222549	-1	10	13	0	29	6	2	0	0	0	0	0	B2RQF5	
ENSMUST00000037182	ENSMUSG00000037234	8	26021421	26119224	-1	67	61	239	174	58	20	581	1123	1211	180	862		Q8BUK6
ENSMUST00000037190	ENSMUSG00000038005	8	60890418	60907580	1	0	0	0	0	0	0	70	371	107	89	72		Q8CFE2
ENSMUST00000037198	ENSMUSG00000041153	4	15997121	16013888	-1	0	0	0	27	0	0	19	48	37	18	12	Q3TEE9	
ENSMUST00000037205	ENSMUSG00000033429	7	64392607	64412125	1	6	3	6	47	4	0	150	375	147	429	81		Q9D1I5
ENSMUST00000037206	ENSMUSG00000040812	2	90782727	90834437	1	7	6	13	15	9	0	0	0	0	0	0		Q8CDK2
ENSMUST00000037210	ENSMUSG00000041921	2	71453276	71525194	1	0	0	0	9	0	3	10	22	0	33	0		Q9CPW9
ENSMUST00000037218	ENSMUSG00000034209	11	5058128	5060385	1	5	4	13	254	18	10	2	0	0	0	15		Q8K5A4
ENSMUST00000037219	ENSMUSG00000040812	2	90782727	90834437	1	0	0	0	0	0	0	0	0	0	0	0		Q8CDK2
ENSMUST00000037220	ENSMUSG00000038782	7	44229930	44236122	-1	17	7	30	40	28	7	10	23	4	4	4	Q9D9U7	
ENSMUST00000037232	ENSMUSG00000039087	13	37778400	37952002	1	7	12	0	0	15	0	151	460	471	56	581		Q3UH06
ENSMUST00000037235	ENSMUSG00000042631	2	153031852	153055775	1	17	9	23	220	34	15	0	0	0	0	0		Q5GH64
ENSMUST00000037240	ENSMUSG00000022315	15	52295553	52335798	1	44	40	215	70	34	27	2	1	4	0	0		Q8BGG0
ENSMUST00000037246	ENSMUSG00000034108	19	4825366	4839322	-1	10	5	17	14	14	3	140	168	91	46	94	Q543K2	Q9WU84
ENSMUST00000037248	ENSMUSG00000042606	7	126861972	126865377	1	24	13	8	30	16	7	35	101	55	36	70		Q8BLH7
ENSMUST00000037260	ENSMUSG00000050846	15	75940952	75949377	1	9	17	21	117	17	6	19	83	19	34	31	Q9CY99	
ENSMUST00000037261	ENSMUSG00000034117	19	10937160	10942511	1	15	12	27	202	23	7	0	0	0	0	1		Q9Z2J6
ENSMUST00000037268	ENSMUSG00000034031	11	88294058	88295261	1	6	2	14	19	10	5	0	0	0	0	0		Q9D9C6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000037270	ENSMUSG00000037119	15	58415468	58457801	1	31	28	53	21	20	13	285	781	555	261	546	B6YY24	Q3UVG3
ENSMUST00000037275	ENSMUSG00000034303	9	37275835	37348392	-1	25	17	40	126	26	24	7	17	21	1	24		Q8C9M2
ENSMUST00000037280	ENSMUSG00000034216	2	119288740	119298453	1	25	0	17	16	29	0	373	362	453	29	344		Q8R307
ENSMUST00000037284						55	37	322	91	53	21	0	2	0	0	0		
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ENSMUST00000037286	ENSMUSG00000036907	1	120340582	120343174	1	10	10	28	534	31	14	0	0	0	0	0		Q8CFR0
ENSMUST00000037287	ENSMUSG00000037664	7	143458350	143461050	-1	6	6	0	0	20	5	10	10	6	1	7	Q791X1	P49919
ENSMUST00000037290	ENSMUSG00000040354	10	127296221	127311786	-1	13	10	13	132	6	23	269	394	279	21	174		Q68FL6
ENSMUST00000037294	ENSMUSG00000042596	1	19103022	19166346	1	8	9	21	35	14	4	0	0	0	0	0		Q91ZK0
ENSMUST00000037297	ENSMUSG00000079705	X	8413305	8422157	1	2	3	3	3	6	2	0	0	0	0	0	Q9CPU1	
ENSMUST00000037299	ENSMUSG00000038848	2	180904377	180920949	-1	12	3	17	13	14	7	600	1161	467	110	280		P59326
ENSMUST00000037302	ENSMUSG00000048720	19	38836579	38919923	1	14	11	21	175	10	7	9	9	7	4	17	E9QQ68	
ENSMUST00000037313	ENSMUSG00000037660	12	8297934	8301954	-1	5	4	10	303	6	3	0	0	0	0	0		P43029
ENSMUST00000037315	ENSMUSG00000039202	7	79273199	79365508	1	47	43	120	102	64	26	2256	3394	3960	288	3163		Q9QXM0
ENSMUST00000037321	ENSMUSG00000039710	3	14480697	14505830	1	0	5	0	0	5	0	0	0	0	0	0	Q8VIE6	
ENSMUST00000037324	ENSMUSG00000036309	11	52231995	52246858	1	0	9	0	0	0	0	377	1847	488	729	244	Q5SUR3	Q9WTX5
ENSMUST00000037330	ENSMUSG00000032968	1	75507077	75510366	1	10	10	28	124	17	9	0	0	0	0	0		Q04997
ENSMUST00000037333	ENSMUSG00000034165	17	47505051	47599691	1	0	0	36	0	1	0	5006	2710	1321	809	717	Q3TSW4	P30282
ENSMUST00000037337	ENSMUSG00000039178	5	53809606	53903965	1	13	7	8	76	8	3	4	21	9	21	16	Q8VDV7	
ENSMUST00000037341	ENSMUSG00000039835	10	18390322	18533892	1	32	17	0	34	45	0	0	0	0	0	0		Q8CAF4
ENSMUST00000037349	ENSMUSG00000036932	X	48474944	48513563	-1	7	0	7	76	0	0	121	320	255	187	168		Q9Z0X1
ENSMUST00000037353	ENSMUSG00000034457	X	97333840	97377216	-1	11	4	8	5	6	6	0	0	0	1	0	Q3KP88	Q8BX35
ENSMUST00000037356	ENSMUSG00000046862	4	143412426	143421091	1	0	0	2	0	3	0	125	378	155	14	108	Q8CE24	
ENSMUST00000037359	ENSMUSG00000035298	7	99466004	99474022	1	7	0	10	115	20	6	0	0	0	3	0		Q9CZ49
ENSMUST00000037360	ENSMUSG00000034226	2	119269201	119271272	-1	16	12	25	152	21	14	974	1273	622	93	423		Q8VDU1
ENSMUST00000037361	ENSMUSG00000038793	1	180935022	180938400	1	14	7	23	99	18	10	17	9	18	6	11		Q64280
ENSMUST00000037362	ENSMUSG00000036282	14	49172226	49191031	1	0	4	0	205	0	0	0	0	0	0	0	E9QMB7	
ENSMUST00000037370	ENSMUSG00000029093	5	36017180	36398139	-1	58	30	116	79	70	20	2	0	0	5	44		Q9EPR5
ENSMUST00000037372	ENSMUSG00000032999	13	65177111	65205716	-1	18	22	15	17	9	16	0	0	0	1	1	L7N1W9	
ENSMUST00000037374	ENSMUSG00000032750	X	74966843	75085458	-1	22	27	3	140	16	19	67	275	99	74	65		Q8BSM5
ENSMUST00000037375	ENSMUSG00000040600	3	107877229	107892900	1	23	10	57	31	19	7	2	1	0	0	0		Q91WL0
ENSMUST00000037376	ENSMUSG00000034744	6	83794982	83804018	1	4	0	12	81	11	3	74	132	53	33	65	Q3U2G9	Q9QZ08
ENSMUST00000037378	ENSMUSG00000035085	11	83437677	83441233	1	2	0	9	45	0	2	304	327	153	68	63		Q8C1R3
ENSMUST00000037380	ENSMUSG00000037685	5	67618140	67847434	-1	19	14	22	29	26	20	748	3687	1614	254	1003		P70704
ENSMUST00000037383	ENSMUSG00000037669	12	8208107	8285758	1	14	0	23	31	0	0	243	1004	328	202	161	A0A0F6AIX5	
ENSMUST00000037391	ENSMUSG00000035776	X	71420060	71492849	-1	0	7	0	0	0	0	20	0	0	8	0		Q8BIF0
ENSMUST00000037397	ENSMUSG00000040729	9	8076633	8134294	-1	16	11	23	17	9	10	0	2	1	2	3		Q0VBV7
ENSMUST00000037399	ENSMUSG00000040466	7	27447978	27466144	1	1	3	0	51	3	4	229	271	108	296	122	Q3U6G1	Q923D2
ENSMUST00000037401	ENSMUSG00000038116	2	156196466	156309952	1	0	27	15	43	0	0	191	359	437	116	339		Q8BLG0
ENSMUST00000037408	ENSMUSG00000034007	9	55549883	55919605	-1	9	10	23	17	16	17	133	592	327	149	220	F8VQ70	
ENSMUST00000037409	ENSMUSG00000033233	3	100922202	100936920	1	26	20	26	19	0	16	0	0	5	0	0		Q6PFY8
ENSMUST00000037416	ENSMUSG00000040270	4	32238804	32586108	1	0	0	0	0	0	0	0	0	2	3	2		P97303
ENSMUST00000037418	ENSMUSG00000034111	12	87166242	87200229	-1	33	24	58	124	44	12	781	2207	1666	90	1009		Q3UHI4
ENSMUST00000037419	ENSMUSG00000041805	4	143394428	143400160	1	6	6	10	10	4	2	0	0	0	0	0	Q99MW3	
ENSMUST00000037422	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	8	0	8	0	2675	3734	2887	90	2726		Q3UHJ8
ENSMUST00000037423	ENSMUSG00000037279	2	144305175	144332146	-1	6	0	24	226	11	5	0	1	0	0	0		Q8CIV7
ENSMUST00000037434	ENSMUSG00000041460	6	119236526	119352407	1	23	18	44	29	44	17	1	9	4	0	8	F8VPL1	
ENSMUST00000037448	ENSMUSG00000074283	7	24227572	24237560	-1	22	16	37	17	23	11	2	4	4	0	5	Q9R166	
ENSMUST00000037453	ENSMUSG00000056399	17	25298394	25300161	1	12	5	19	16	21	4	672	537	319	25	98	Q80UR4	
ENSMUST00000037472	ENSMUSG00000035545	7	4137039	4148177	1	0	0	0	0	0	0	785	3615	1349	118	2629		Q8CBY3
ENSMUST00000037473	ENSMUSG00000036291	14	49066495	49087723	1	14	9	15	7	13	2	134	392	211	139	140		
ENSMUST00000037478	ENSMUSG00000036330	8	69037711	69089235	-1	24	10	74	16	28	11	0	9	6	0	1	Q32XG7	Q8R090
ENSMUST00000037480	ENSMUSG00000038013	11	98863638	98905040	1	150	153	456	560	165	101	818	1653	1212	86	906		Q6PEV3
ENSMUST00000037481	ENSMUSG00000033082	6	129424772	129452000	-1	13	13	18	9	17	12	9	46	12	7	44		Q8BWY2
ENSMUST00000037484	ENSMUSG00000034252	9	80066903	80144953	1	4	0	14	15	0	0	7	29	13	5	14		Q6P7W0
ENSMUST00000037488	ENSMUSG00000035954	12	40446053	40846486	1	51	30	51	209	55	19	60	93	110	8	120		P59764
ENSMUST00000037489	ENSMUSG00000034254	17	34604262	34613449	1	1	5	0	39	0	0	311	568	273	108	242		
ENSMUST00000037491	ENSMUSG00000039109	13	36867178	37050244	-1	0	18	21	27	30	0	1226	5540	1920	4083	2218		Q8BH61
ENSMUST00000037499	ENSMUSG00000042670	2	105904638	105965558	1	4	4	3	1	6	2	73	250	40	95	27		Q9CQU8
ENSMUST00000037502	ENSMUSG00000038893	11	95337018	95381872	1	14	8	27	105	26	6	567	651	493	86	399		Q7TNF9
ENSMUST00000037504	ENSMUSG00000034263	9	64960832	64986974	1	17	14	32	116	25	12	11	0	12	12	32		Q8R3P6
ENSMUST00000037520	ENSMUSG00000020609	12	7977648	8016835	1	2	17	0	0	31	0	0	0	0	0	0	E9Q1Y3	
ENSMUST00000037522	ENSMUSG00000040594	11	33211795	33513746	-1	34	36	95	53	50	30	2	4	2	0	6	Q5SSA5	
ENSMUST00000037526	ENSMUSG00000035168	2	59612042	59846149	1	26	21	0	9	25	20	0	10	0	0	0		Q0VGY8
ENSMUST00000037528	ENSMUSG00000035314	7	99381549	99460983	1	33	25	108	372	69	32	15	24	14	5	26		Q640M6
ENSMUST00000037534	ENSMUSG00000040746	11	70647235	70651421	1	2	4	0	6	0	0	2595	4122	1854	347	1667		Q91XF4
ENSMUST00000037539	ENSMUSG00000039903	16	90826719	90905109	1	0	0	0	0	6	0	0	0	0	7	12		P58659
ENSMUST00000037540	ENSMUSG00000032860	7	100996572	101011991	-1	26	7	41	162	31	14	729	1062	759	100	813		
ENSMUST00000037541	ENSMUSG00000067597	X	100524838	100546144	1	0	2	1	1	0	0	0	0	0	0	0		A2ADU8
ENSMUST00000037547	ENSMUSG00000040035	2	118779719	118811293	1	52	30	124	134	72	37	2	0	3	0	5		Q8CIP5
ENSMUST00000037548	ENSMUSG00000038876	10	29344178	29362442	-1	4	0	0	0	15	0	59	312	23	35	37		Q9CZW6
ENSMUST00000037551	ENSMUSG00000033819	15	76671615	76694919	1	0	0	0	120	9	0	390	250	226	20	119		Q923M0
ENSMUST00000037552	ENSMUSG00000057722	4	101717404	101815352	1	8	10	0	13	16	0	0	6	0	0	0		P48356
ENSMUST00000037553	ENSMUSG00000034660	7	6197090	6216137	1	9	8	31	7	12	5	0	0	0	0	0		Q810H5
ENSMUST00000037557	ENSMUSG00000034602	10	122992061	123076505	-1	16	18	18	41	0	11	568	1058	1640	154	985		Q80TL7
ENSMUST00000037565	ENSMUSG00000066000	4	147611937	147642513	-1	0	0	0	0	0	0	0	0	0	0	0	A2A799	
ENSMUST00000037575	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	0	0	0	0	164	263	906	0	44	E9Q9Y2	
ENSMUST00000037580	ENSMUSG00000058740	2	25863734	25918273	1	0	0	0	48	0	0	0	0	0	0	0	A2AHB8	
ENSMUST00000037585	ENSMUSG00000040818	14	26579561	26634322	1	62	62	224	252	91	42	113	233	123	47	162		Q8BH65
ENSMUST00000037593	ENSMUSG00000037907	11	77470485	77489678	-1	20	15	14	0	35	0	9	11	0	0	0		Q5F259
ENSMUST00000037596	ENSMUSG00000036959	X	48341358	48408049	1	14	0	59	30	17	22	168	247	192	12	75		A2AQH4
ENSMUST00000037603	ENSMUSG00000034320	18	61192919	61211612	-1	16	10	107	24	16	7	5	6	0	0	11	F8WI08	
ENSMUST00000037607	ENSMUSG00000028284	4	31964097	32023467	1	0	0	0	176	0	0	197	189	404	94	248	Q923A8	
ENSMUST00000037609	ENSMUSG00000037260	8	25944459	25976744	-1	11	10	59	33	12	3	1732	3423	1736	421	1848		Q3UDW8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000037615	ENSMUSG00000035936	13	24907579	24937661	-1	26	29	75	223	39	28	3	16	5	3	7	B2RS41	Q8BWF0
ENSMUST00000037618	ENSMUSG00000039191	5	53466152	53657362	1	13	8	21	147	17	0	97	146	141	0	315		P31266
ENSMUST00000037620	ENSMUSG00000037221	5	137596645	137601058	-1	3	2	6	26	12	6	42	49	32	4	16	Q05DT5	Q8BGG6
ENSMUST00000037623	ENSMUSG00000039114	13	36725625	36734477	-1	6	8	6	22	6	7	0	1	0	5	0		Q8CFV4
ENSMUST00000037633	ENSMUSG00000037965	16	11136592	11176393	-1	7	3	24	22	5	4	290	1093	650	351	613	E9PWW6	
ENSMUST00000037636	ENSMUSG00000034336	19	47014698	47025327	1	23	10	59	288	30	15	0	0	1	0	0		P46660
ENSMUST00000037640						25	11	14	15	29	20	0	2	0	0	1		
ENSMUST00000037644	ENSMUSG00000034342	9	44142976	44234049	-1	85	65	121	228	84	27	1783	1051	4122	52	2496		P22682
ENSMUST00000037646	ENSMUSG00000035529	10	85891970	85916945	-1	31	14	34	92	23	9	217	676	414	75	264		Q80V63
ENSMUST00000037649	ENSMUSG00000036104	1	127868773	127943868	1	30	25	88	23	32	11	268	704	578	87	333		Q80UJ7
ENSMUST00000037666	ENSMUSG00000070056	8	35587798	35679449	1	40	55	146	455	73	29	38	64	41	16	100		Q3V1N1
ENSMUST00000037678	ENSMUSG00000034371	19	10592200	10604258	-1	21	19	34	22	22	10	146	185	172	15	111		Q8VC30
ENSMUST00000037682	ENSMUSG00000037393	11	56024987	56041010	-1	16	13	24	13	15	14	0	0	0	0	0		Q8BZ39
ENSMUST00000037685	ENSMUSG00000036925	15	103895859	103899309	-1	3	3	20	3	8	6	0	0	0	0	0	Q9DA65	
ENSMUST00000037687	ENSMUSG00000033578	X	134295225	134305969	1	2	5	4	5	9	4	0	0	0	0	0		Q9D328
ENSMUST00000037696	ENSMUSG00000039215	6	48986861	48991722	1	11	16	36	22	26	11	0	0	0	0	0	Q6WIZ7	
ENSMUST00000037698	ENSMUSG00000039599	14	20348162	20383489	1	14	8	16	31	2	3	30	89	38	15	48		Q6NSV7
ENSMUST00000037701	ENSMUSG00000034382	17	47436615	47470638	1	0	2	12	34	5	2	0	2	0	2	0		Q91Z58
ENSMUST00000037708	ENSMUSG00000033007	1	75450436	75474343	1	7	0	4	7	10	15	0	0	0	0	0		Q7TNS7
ENSMUST00000037709	ENSMUSG00000040234	6	146602352	146642824	-1	28	10	42	10	19	10	165	282	176	29	170		
ENSMUST00000037715	ENSMUSG00000042662	2	152940997	152951698	-1	3	8	5	9	4	2	0	0	0	0	0		Q8R4V2
ENSMUST00000037718	ENSMUSG00000034391	18	84935158	84981376	1	8	7	8	10	6	2	0	0	0	1	0	Q3TJW2	
ENSMUST00000037722	ENSMUSG00000037307	2	144033059	144073979	1	8	3	9	3	5	2	0	0	0	0	0		Q8BVR0
ENSMUST00000037726	ENSMUSG00000041594	14	122918971	122984035	-1	5	1	0	22	0	3	0	17	0	0	13		Q8BG19
ENSMUST00000037728	ENSMUSG00000034690	7	6045161	6105149	1	21	15	21	12	17	9	0	0	0	0	0		Q3TKR3
ENSMUST00000037739	ENSMUSG00000042354	14	31012434	31019089	-1	3	5	6	23	8	4	41	207	69	308	101		Q8CI11
ENSMUST00000037746	ENSMUSG00000040610	11	33200752	33203589	-1	7	1	10	408	10	7	0	0	0	0	0		O55144
ENSMUST00000037748	ENSMUSG00000039630	1	178324343	178337797	-1	18	11	15	86	25	11	832	3505	992	258	875		Q8VEK3
ENSMUST00000037762	ENSMUSG00000004328	7	17031507	17062427	-1	16	4	51	84	19	12	0	0	0	0	0		Q0VBL6
ENSMUST00000037763	ENSMUSG00000034653	18	44827746	44889724	1	25	14	16	88	26	14	31	91	94	24	50		B2RR83
ENSMUST00000037764	ENSMUSG00000038914	2	180657964	180709999	-1	67	61	311	76	75	36	0	51	28	4	29		
ENSMUST00000037776	ENSMUSG00000071172	17	29032673	29043366	1	0	0	0	35	0	0	361	1483	536	1195	523	Q3U781	P84104
ENSMUST00000037783	ENSMUSG00000034083	6	91878053	91899843	1	0	0	18	12	3	0	86	648	225	460	174		
ENSMUST00000037785	ENSMUSG00000022762	16	81200697	81624285	1	27	30	153	58	20	16	1	8	1	0	5		O35136
ENSMUST00000037788	ENSMUSG00000034126	12	87106866	87147902	-1	39	26	63	403	56	27	63	116	82	13	80		Q8BGQ4
ENSMUST00000037796	ENSMUSG00000033021	1	75435930	75443179	1	0	0	0	0	3	0	76	164	103	17	128		Q922H4
ENSMUST00000037798	ENSMUSG00000034452	9	64922861	64951607	-1	48	23	233	64	42	29	3	17	10	4	16	Q91WD8	
ENSMUST00000037807	ENSMUSG00000034777	6	83711264	83738313	1	29	8	121	345	26	8	0	2	3	0	4	Q14B19	Q9WTP9
ENSMUST00000037811	ENSMUSG00000020609	12	7977648	8016835	1	63	25	92	35	37	31	0	0	0	2	0		E9Q414
ENSMUST00000037813	ENSMUSG00000040009	10	74967177	75016907	1	0	74	31	80	20	0	0	0	0	0	0	Q542R8	O70443
ENSMUST00000037814	ENSMUSG00000040759	14	54936470	54939256	1	6	3	18	8	9	5	0	0	0	0	0		Q9D6G9
ENSMUST00000037820	ENSMUSG00000038422	4	62499008	62503467	-1	38	26	78	278	77	24	10	9	3	17	5		Q9CYW4
ENSMUST00000037824	ENSMUSG00000033837	15	76668284	76669948	-1	8	9	56	46	20	2	0	0	0	0	0	Q0VEP8	O88621
ENSMUST00000037827	ENSMUSG00000039838	4	150628572	150652174	-1	17	14	36	31	18	9	3	13	14	0	10		Q8BIV7
ENSMUST00000037828	ENSMUSG00000037295	4	134741554	134768024	-1	24	18	83	132	27	23	1088	1296	880	75	691		Q8C142
ENSMUST00000037831	ENSMUSG00000042279	6	115944938	115950236	1	0	0	0	13	0	0	0	0	0	0	0		Q8VIK3
ENSMUST00000037836	ENSMUSG00000040242	6	146577203	146599198	1	0	2	3	1	0	3	70	204	0	0	0	F8WGG1	
ENSMUST00000037839	ENSMUSG00000039795	3	10339953	10351317	-1	0	0	0	0	0	0	19	76	16	80	4		Q8BFR6
ENSMUST00000037840	ENSMUSG00000036962	1	119923341	119997234	-1	19	0	0	0	7	0	0	0	0	0	0		A9Q751
ENSMUST00000037843	ENSMUSG00000039568	16	4874778	4880315	-1	4	3	17	262	12	6	539	794	377	89	383		Q6P3B2
ENSMUST00000037849	ENSMUSG00000034482	17	35108279	35111991	1	6	4	8	6	5	2	0	0	0	0	0		Q8K1T5
ENSMUST00000037850	ENSMUSG00000034484	18	53176365	53220860	1	6	2	7	43	12	4	461	2261	812	2611	698		Q9CWK8
ENSMUST00000037853	ENSMUSG00000034487	9	53384023	53401867	1	126	107	339	131	105	67	10	37	10	14	45	G5E897	
ENSMUST00000037854	ENSMUSG00000034480	X	129749742	130465834	1	0	0	0	0	0	0	86	0	344	0	108	Q6W4W7	
ENSMUST00000037863	ENSMUSG00000040770	14	54932695	54935837	1	10	10	34	25	35	7	0	0	0	0	0	Q8VHH8	
ENSMUST00000037865	ENSMUSG00000038023	5	124628576	124724455	1	13	29	40	112	39	14	456	704	595	60	467		P15920
ENSMUST00000037872	ENSMUSG00000036052	4	42949814	42959425	1	0	0	0	75	0	0	0	0	0	0	0	A2AG30	
ENSMUST00000037875	ENSMUSG00000027422	2	143947395	144011263	-1	25	3	304	70	54	35	35	428	179	21	166		Q99PL5
ENSMUST00000037877	ENSMUSG00000038932	2	180621956	180642708	-1	10	3	5	10	10	2	0	1	0	0	0	Q32NY8	
ENSMUST00000037879	ENSMUSG00000039879	10	17900466	17948067	-1	12	20	42	58	15	12	1620	2184	2387	291	1688	Q3V1N5	
ENSMUST00000037881	ENSMUSG00000039270	4	70427065	70534995	-1	0	0	0	415	0	0	0	1	12	0	12	F8WHT8	
ENSMUST00000037882	ENSMUSG00000034783	6	83671215	83677857	-1	12	10	18	12	15	3	0	2	0	3	0		Q8VBX4
ENSMUST00000037900	ENSMUSG00000034796	8	123117374	123135182	1	0	0	0	28	0	0	0	0	0	0	0		Q0VE82
ENSMUST00000037901	ENSMUSG00000052387	19	22139119	22989884	1	8	4	14	3	11	2	0	0	0	0	0	B2RUS0	
ENSMUST00000037903	ENSMUSG00000026991	2	59160850	59355208	1	0	8	0	5	8	14	0	0	14	11	42	A2AS45	
ENSMUST00000037906	ENSMUSG00000036975	1	119907890	119913208	-1	21	18	52	46	37	16	18	23	8	14	25		Q8BPE4
ENSMUST00000037907	ENSMUSG00000040296	4	40203773	40239828	-1	0	3	0	0	0	1	414	1353	715	243	826		Q6Q899
ENSMUST00000037912	ENSMUSG00000037926	11	77216287	77460220	1	73	56	199	143	66	51	5544	14764	10823	798	8650		Q5SW75
ENSMUST00000037913	ENSMUSG00000037991	16	10835059	10892966	1	224	271	566	359	278	137	16	43	38	5	45		Q3UPE3
ENSMUST00000037915	ENSMUSG00000052915	11	98795516	98807859	1	24	27	199	207	41	32	1293	8562	3021	338	2655		Q6PDM1
ENSMUST00000037918	ENSMUSG00000037720	5	67260565	67291461	1	7	14	25	38	8	11	85	247	124	36	76		Q9CR67
ENSMUST00000037923	ENSMUSG00000038132	13	46418300	46431090	1	9	9	7	133	14	8	0	0	0	0	0		D3Z4I3
ENSMUST00000037928	ENSMUSG00000040749	X	164070705	164076493	-1	0	0	2	14	0	0	0	0	0	0	0	A2AHZ2	
ENSMUST00000037930	ENSMUSG00000052915	11	98795516	98807859	1	3	2	5	1	0	0	444	445	593	40	401		Q6PDM1
ENSMUST00000037941	ENSMUSG00000037706	7	143052739	143067934	1	4	0	22	85	9	5	181	131	94	132	222		P35762
ENSMUST00000037942	ENSMUSG00000036745	3	146852367	146984009	1	7	25	47	17	18	0	0	0	0	0	7	A0A0G2LB90	
ENSMUST00000037947	ENSMUSG00000038612	3	95658788	95663176	1	26	22	44	140	31	24	17857	74060	22466	5179	17843		P97287
ENSMUST00000037955	ENSMUSG00000034308	8	117661399	117673689	-1	7	8	24	0	0	0	0	29	21	0	0		Q9D665
ENSMUST00000037958	ENSMUSG00000039831	3	121952541	122016753	1	23	19	70	45	25	10	6	7	4	19	16		Q8CGF1
ENSMUST00000037960	ENSMUSG00000036985	X	48171969	48208878	-1	19	17	40	547	0	0	931	642	1045	105	917		P59268
ENSMUST00000037964	ENSMUSG00000039891	10	17796226	17845665	1	13	13	50	11	15	8	0	3	0	0	0		Q8VBT1
ENSMUST00000037967	ENSMUSG00000032806	X	74369217	74373349	-1	0	0	8	16	0	0	104	228	107	63	176		P21129
ENSMUST00000037968	ENSMUSG00000035354	7	98886743	99141144	-1	188	156	55	370	157	29	486	1362	1023	147	776		Q8K245
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000037976	ENSMUSG00000037849	1	173468509	173491041	-1	2	2	1	0	0	1	0	2	0	0	0	G3UY50	
ENSMUST00000037977	ENSMUSG00000034563	9	72985429	73016340	1	0	0	24	28	8	0	152	630	319	146	420		Q640L3
ENSMUST00000037983	ENSMUSG00000038619	3	95624993	95632102	1	16	8	31	35	18	0	2133	4487	2046	866	1515		P60840
ENSMUST00000037991	ENSMUSG00000038244	7	112225856	112355194	1	4	4	4	18	11	13	0	0	0	0	0		Q8BML1
ENSMUST00000037992	ENSMUSG00000034616	19	4261668	4269172	-1	28	17	0	80	0	16	599	1163	695	54	646		Q8K330
ENSMUST00000037994	ENSMUSG00000078763	11	83116849	83122670	1	18	14	45	21	16	7	6519	27631	8915	14106	7185	Q9Z0I7	
ENSMUST00000037996	ENSMUSG00000038015	16	10791380	10796134	-1	3	4	15	9	2	3	0	0	0	0	0	Q545M0	P07978
ENSMUST00000037998	ENSMUSG00000041779	1	20996299	21079229	-1	36	17	126	148	59	34	308	607	541	28	450		Q924Z5
ENSMUST00000038004	ENSMUSG00000035831	11	99315516	99322951	-1	25	12	25	18	21	10	0	0	0	0	0		Q8VCW2
ENSMUST00000038006	ENSMUSG00000026348	1	127729413	127767978	1	13	14	8	16	34	13	0	8	8	4	8		Q8R519
ENSMUST00000038007	ENSMUSG00000041476	X	157698910	157752591	1	0	0	2	0	0	4	0	0	0	0	0		Q9DC77
ENSMUST00000038010	ENSMUSG00000036401	2	25793859	25815848	-1	1	3	4	3	7	1	0	0	0	0	0		Q2NKH9
ENSMUST00000038014	ENSMUSG00000040697	4	141760189	141790931	-1	30	29	58	189	49	24	140	237	252	15	168		Q80TN4
ENSMUST00000038027	ENSMUSG00000036427	7	34201330	34230336	-1	31	35	39	103	60	33	36997	36657	32962	4099	18127		P06745
ENSMUST00000038038	ENSMUSG00000072620	11	83065112	83070678	1	44	28	44	69	73	23	8252	35283	13703	31536	9785	Q9Z0I6	
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ENSMUST00000038053	ENSMUSG00000033306	16	24393350	24992576	1	154	0	111	324	45	0	352	789	855	70	573		Q8BFW7
ENSMUST00000038069	ENSMUSG00000054169	7	24777206	24784657	1	1	2	4	6	8	4	1529	4482	1857	3480	688		
ENSMUST00000038073	ENSMUSG00000033486	2	121392631	121413792	-1	4	1	17	110	12	1	1	5	7	3	0	A0A0A0MQ85	
ENSMUST00000038075	ENSMUSG00000041625	14	122816223	122913757	-1	3	3	7	34	8	9	4	14	6	35	20		Q923B0
ENSMUST00000038080	ENSMUSG00000000127	17	63896018	64139494	1	14	10	20	10	18	9	0	14	13	0	4		P70451
ENSMUST00000038090						9	6	2	77	7	6	0	0	0	0	14		
ENSMUST00000038091	ENSMUSG00000038806	1	180851127	180868113	1	25	23	51	81	33	23	477	1157	574	87	463		Q8K1J5
ENSMUST00000038096	ENSMUSG00000039253	11	121421401	121431288	1	77	75	162	67	51	44	14	32	15	10	25		Q8K274
ENSMUST00000038099	ENSMUSG00000038037	16	10783808	10785536	-1	2	2	9	453	12	3	39	60	26	15	53		O35716
ENSMUST00000038101	ENSMUSG00000034987	13	54192129	54222432	1	20	14	75	50	42	7	356	685	596	45	492		P97292
ENSMUST00000038104	ENSMUSG00000049658	13	100017994	100104070	-1	16	12	11	130	16	18	193	288	218	0	121		Q571C7
ENSMUST00000038107	ENSMUSG00000039910	10	17723228	17725673	1	13	11	11	485	22	9	704	2101	899	108	827		O35740
ENSMUST00000038108	ENSMUSG00000037152	3	51404677	51408988	-1	77	66	149	74	72	30	20	45	15	4	25		Q9CQY9
ENSMUST00000038116	ENSMUSG00000034647	17	65967501	66077089	-1	22	23	67	37	27	9	382	1124	854	237	545	G5E893	
ENSMUST00000038118	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	0	17	4	0	434	535	153	18	168		Q80XR2
ENSMUST00000038121	ENSMUSG00000035983	12	40222758	40229184	1	1	1	3	128	7	4	0	10	0	14	9	Q9DC38	
ENSMUST00000038128	ENSMUSG00000034659	19	10870660	10882001	-1	9	8	17	12	14	7	257	331	135	57	204		Q3UBX0
ENSMUST00000038131	ENSMUSG00000033970	5	151642756	151651242	-1	0	0	2	23	6	0	23	75	29	131	25	Q3TKD1	Q8R323
ENSMUST00000038141	ENSMUSG00000035208	11	83002158	83020810	-1	21	32	20	19	26	12	83	649	149	212	410	B1ARD8	
ENSMUST00000038142	ENSMUSG00000039236	7	78913424	78920396	1	2	6	80	11	5	2	102	454	113	503	188	Q4FK39	Q9JL16
ENSMUST00000038144	ENSMUSG00000042379	13	113209659	113218098	1	16	12	78	37	32	11	2	6	11	1	2	B9EJX9	Q9QYY7
ENSMUST00000038145	ENSMUSG00000068663	16	10545339	10744878	1	14	7	13	12	7	5	4	13	4	2	8		Q80U30
ENSMUST00000038149	ENSMUSG00000034673	17	34591266	34597400	1	16	10	38	255	26	10	1205	3983	1298	307	1123	Q4FJL3	O35984
ENSMUST00000038154	ENSMUSG00000037161	3	51388412	51396738	-1	0	10	0	23	0	10	0	0	0	1	1		Q8VI64
ENSMUST00000038160	ENSMUSG00000036446	10	97565501	97572703	1	7	10	13	5	8	3	0	0	0	1	0		P51885
ENSMUST00000038161	ENSMUSG00000040706	4	141746672	141759263	1	13	10	41	145	9	7	0	0	1	1	1		A2AS89
ENSMUST00000038163	ENSMUSG00000041141	7	16959679	16964607	1	18	10	45	21	13	9	0	0	0	0	0		Q80VM8
ENSMUST00000038166	ENSMUSG00000035051	17	80238304	80290476	-1	0	0	0	133	0	0	0	160	55	40	1		Q6P5D3
ENSMUST00000038169	ENSMUSG00000033307	10	75859353	75860250	-1	14	8	17	162	12	8	641	604	306	608	423	Q545F0	P34884
ENSMUST00000038172	ENSMUSG00000039458	15	12205028	12272240	1	0	0	0	57	0	0	198	47	0	0	0		Q80TA6
ENSMUST00000038174	ENSMUSG00000039720	8	27197460	27202547	-1	9	4	7	10	11	8	0	0	2	0	0		Q7TSV6
ENSMUST00000038176	ENSMUSG00000030427	7	3908280	3915503	-1	0	0	3	0	0	7	1539	4107	2305	1445	2092	A0A0B4J1F3	
ENSMUST00000038185	ENSMUSG00000032705	12	80463095	80498135	1	87	49	416	211	47	24	68	201	124	19	84	F8WID1	
ENSMUST00000038188	ENSMUSG00000037736	5	66745827	67057158	1	10	12	0	9	19	11	0	0	0	0	0		Q3UH68
ENSMUST00000038191	ENSMUSG00000042429	1	134199223	134235431	-1	38	37	385	256	55	26	0	0	0	0	1		Q60612
ENSMUST00000038193	ENSMUSG00000031959	8	111448784	111522107	-1	40	0	103	0	34	16	70	103	108	24	75		Q8C0M0
ENSMUST00000038194	ENSMUSG00000022360	15	58094047	58135082	-1	47	27	61	158	45	18	222	438	425	118	396	G3X963	
ENSMUST00000038196	ENSMUSG00000034121	11	87853215	87863803	1	21	12	39	68	29	11	19	41	17	5	29	Q284W0	Q5SW45
ENSMUST00000038197	ENSMUSG00000039956	16	90738324	90749785	1	0	0	10	0	4	3	0	0	0	3	0		Q9D159
ENSMUST00000038207	ENSMUSG00000028528	4	101496648	101642799	1	14	0	33	4	6	12	0	0	0	0	10		Q80TZ3
ENSMUST00000038210	ENSMUSG00000036391	11	51692264	51763634	-1	0	1	0	0	4	0	32	71	166	3	91	A2AA71	
ENSMUST00000038211	ENSMUSG00000069793	11	82979629	82991830	-1	814	814	3994	1397	764	419	51	181	111	42	91	B1ARD6	
ENSMUST00000038212	ENSMUSG00000042385	13	113171608	113225908	-1	3	0	0	0	9	6	0	4	3	7	3		O35205
ENSMUST00000038213	ENSMUSG00000019790	10	9755547	9901079	-1	24	17	39	11	16	8	282	632	401	54	203		Q8K400
ENSMUST00000038214	ENSMUSG00000035849	11	99232761	99244085	-1	5	4	10	3	0	3	0	0	0	1	2		Q8CCX5
ENSMUST00000038217	ENSMUSG00000040415	10	127190378	127195728	-1	0	0	0	0	0	0	97	239	71	16	105		Q80V91
ENSMUST00000038223	ENSMUSG00000034552	2	83915079	83941228	-1	10	5	4	0	2	0	0	0	0	0	0	Q0VB10	Q9D9X6
ENSMUST00000038225	ENSMUSG00000038963	2	180456245	180474867	1	0	12	11	0	0	4	0	0	0	0	0		Q8K078
ENSMUST00000038227	ENSMUSG00000037872	1	173331886	173333750	-1	12	8	17	0	9	0	0	0	0	3	0		
ENSMUST00000038228	ENSMUSG00000034723	2	134594185	134644145	-1	25	21	24	52	25	13	733	1925	1226	202	708	Q0P5W2	Q8C0L0
ENSMUST00000038229	ENSMUSG00000035121	14	63182443	63193541	-1	8	2	21	11	16	12	1	1	0	0	3		Q6R2P8
ENSMUST00000038234	ENSMUSG00000030323	6	115853470	115926699	1	0	16	3	0	0	7	0	8	0	0	0		Q6NWV3
ENSMUST00000038237	ENSMUSG00000034274	11	4895320	4928867	1	0	0	0	3	8	7	167	401	267	202	234		
ENSMUST00000038244	ENSMUSG00000034786	17	34589806	34591754	1	20	11	16	38	23	11	5682	6276	3586	532	2925	Q0VGT5	Q3U1Z5
ENSMUST00000038252	ENSMUSG00000033849	1	143640664	143654614	1	14	17	26	18	14	6	0	1	4	1	4		O54905
ENSMUST00000038257	ENSMUSG00000033318	10	75831845	75834881	-1	20	9	36	20	14	13	21	25	10	26	18		Q61133
ENSMUST00000038259	ENSMUSG00000038963	2	180456245	180474867	1	18	0	0	138	28	13	50	1	114	1	33		Q8K078
ENSMUST00000038275	ENSMUSG00000038175	13	45389742	45412019	1	48	22	44	605	74	44	322	797	515	111	517		Q8BM54
ENSMUST00000038280	ENSMUSG00000027356	2	132904389	132945906	-1	39	33	93	150	65	32	0	0	0	1	2		P59113
ENSMUST00000038281	ENSMUSG00000038055	16	10502531	10543054	-1	0	0	0	80	3	1	43	37	42	9	21		Q9WUQ7
ENSMUST00000038287	ENSMUSG00000034765	19	53529109	53542431	1	9	8	24	92	19	9	388	1176	267	34	311	Q1HL35	
ENSMUST00000038295	ENSMUSG00000041757	1	133181321	133303435	1	16	7	13	7	26	15	0	0	0	0	0		Q7TQG1
ENSMUST00000038304						6	8	16	24	13	0	0	0	0	0	0		
ENSMUST00000038332	ENSMUSG00000038888	7	43672016	43678298	1	13	17	82	484	33	9	51	83	46	5	43		Q99J10
ENSMUST00000038336	ENSMUSG00000038725	15	44457553	44597143	1	19	38	20	12	40	13	1	0	1	4	16	F8WH29	
ENSMUST00000038341	ENSMUSG00000040084	2	118598211	118641591	1	24	23	21	23	27	18	198	330	330	63	170		Q9Z1S0
ENSMUST00000038343	ENSMUSG00000013418	11	95865943	95914891	-1	7	10	11	40	12	8	1	0	1	0	0	A2A615	Q09199
ENSMUST00000038356	ENSMUSG00000042572	3	89773616	89784000	1	22	6	23	83	33	8	1293	4381	1804	351	1478		Q7TSS2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000038359	ENSMUSG00000035401	7	98587137	98656783	-1	18	23	79	51	27	21	192	461	448	195	438		Q8BMB0
ENSMUST00000038361	ENSMUSG00000036155	1	127205015	127488336	1	123	87	212	696	149	80	387	704	548	58	406	Q059T5	Q8R4G6
ENSMUST00000038364	ENSMUSG00000034098	3	76074270	76710019	1	14	9	17	28	16	11	0	0	0	0	0		Q8BFR2
ENSMUST00000038366						24	26	22	22	33	16	0	7	10	2	24		
ENSMUST00000038368	ENSMUSG00000042745	2	152736251	152737410	1	0	0	0	0	0	0	440	915	475	369	493	Q6GTZ3	P20067
ENSMUST00000038369	ENSMUSG00000034157	12	86947043	86965362	1	8	4	16	31	9	6	48	124	59	22	57	Z4YJJ0	
ENSMUST00000038372	ENSMUSG00000038174	1	58522806	58586323	-1	8	0	4	61	2	2	0	0	14	8	3		Q8C729
ENSMUST00000038374	ENSMUSG00000041650	14	122534324	122891100	1	3	5	8	8	9	0	21	90	43	64	36	Q3UGC8	Q91ZA3
ENSMUST00000038377	ENSMUSG00000036478	10	96617001	96622813	1	17	42	75	99	50	28	8610	40138	8960	2131	8804	Q3UEG0	P62325
ENSMUST00000038379	ENSMUSG00000034820	19	10525244	10547735	1	26	15	46	42	43	16	757	2834	1351	180	1307		Q8BTV2
ENSMUST00000038381	ENSMUSG00000021959	14	57642077	57758388	-1	0	5	7	3	5	3	35	36	28	4	22	Q8VHE1	
ENSMUST00000038382	ENSMUSG00000042686	1	16964560	17097889	-1	32	35	124	475	46	19	2	5	1	0	2		Q9ET80
ENSMUST00000038383	ENSMUSG00000061758	6	34384218	34396950	1	0	0	15	0	7	9	0	78	26	67	41	G5E895	
ENSMUST00000038384	ENSMUSG00000035851	5	86804221	86836659	1	0	2	0	0	0	0	212	1217	240	0	35		E9Q5K9
ENSMUST00000038388	ENSMUSG00000034560	10	83543941	83596469	1	31	31	28	45	31	18	502	1628	1100	617	828		Q3UMB9
ENSMUST00000038389	ENSMUSG00000033498	2	121363728	121387168	-1	23	26	62	29	46	21	0	0	0	0	0		Q8VIM6
ENSMUST00000038391						2	3	3	2	7	2	1	0	0	3	0		
ENSMUST00000038398	ENSMUSG00000038507	6	39086410	39118349	-1	13	8	13	112	30	5	177	714	289	46	356		Q8BZ20
ENSMUST00000038403	ENSMUSG00000062995	6	8630527	8778488	-1	0	0	5	61	8	0	0	0	28	13	0		P97411
ENSMUST00000038404	ENSMUSG00000042417	13	112987802	112990778	1	15	12	43	442	43	12	294	716	254	47	438	B2RWG0	P0C242
ENSMUST00000038406	ENSMUSG00000029762	6	34354119	34368463	1	8	10	5	1	14	5	0	2	0	97	30		P45377
ENSMUST00000038407	ENSMUSG00000034839	9	60712989	60738801	1	11	11	41	110	35	10	0	0	0	0	0		Q8BN59
ENSMUST00000038409	ENSMUSG00000033152	6	88842558	88875044	-1	2	0	25	3	13	7	0	0	0	0	0	G3X9D3	
ENSMUST00000038411	ENSMUSG00000035370	10	80602880	80615783	1	0	0	0	319	0	5	8	2	9	2	15		Q6PAT0
ENSMUST00000038421	ENSMUSG00000037296	8	25785591	25803975	1	7	6	13	44	14	3	168	428	196	288	129	Q544C9	Q8VC85
ENSMUST00000038422	ENSMUSG00000034168	12	86880703	86884814	-1	40	18	80	1774	72	34	500	918	880	68	656		Q8K3X4
ENSMUST00000038423	ENSMUSG00000033355	16	23609919	23614222	1	6	6	14	17	15	13	133	1953	103	836	523		Q9ER80
ENSMUST00000038424	ENSMUSG00000022498	16	11074911	11134650	-1	6	3	23	18	14	4	137	277	237	26	157		Q8K2W3
ENSMUST00000038431	ENSMUSG00000038967	11	95026258	95041354	-1	13	16	30	89	33	12	47	57	42	5	47		Q9JK42
ENSMUST00000038432	ENSMUSG00000037924	1	172956382	172957817	1	5	4	12	4	4	2	0	0	0	0	0	Q62007	
ENSMUST00000038434	ENSMUSG00000036114	4	41712033	41713534	-1	7	3	15	54	13	6	182	240	98	158	83		Q99JH1
ENSMUST00000038439	ENSMUSG00000034278	2	119172500	119208795	-1	5	0	0	5	3	3	77	134	82	166	65		Q91WT4
ENSMUST00000038445	ENSMUSG00000042451	1	134193448	134201232	1	14	5	32	0	12	0	0	14	6	0	14		P70402
ENSMUST00000038446	ENSMUSG00000034868	17	70973920	70990787	-1	17	11	34	156	22	8	10120	17690	7743	12344	4760		Q3THE2
ENSMUST00000038447	ENSMUSG00000041809	1	20951626	20990841	1	16	11	14	14	10	6	4	12	2	1	3	B2CKC6	
ENSMUST00000038448	ENSMUSG00000035861	5	86657631	86676362	-1	289	333	463	253	293	166	10	47	10	9	12		Q14C59
ENSMUST00000038450						60	46	92	102	82	25	9	43	34	5	37		
ENSMUST00000038455	ENSMUSG00000070868	4	112232245	112300468	1	6	5	17	5	5	3	0	0	0	0	0		A7TZF0
ENSMUST00000038463	ENSMUSG00000035275	4	101068983	101152370	1	28	6	18	33	18	13	2	12	4	1	4		Q7TPD6
ENSMUST00000038472	ENSMUSG00000034551	X	111569931	111697079	-1	6	14	10	15	13	0	0	0	1	0	1		Q14B70
ENSMUST00000038474	ENSMUSG00000039356	2	31670715	31681349	1	51	54	159	76	53	35	65	180	64	95	87	Q3TKQ3	Q8VBV3
ENSMUST00000038475	ENSMUSG00000033579	8	111345135	111393824	-1	0	0	0	51	15	8	0	0	0	0	0		Q5MPP0
ENSMUST00000038477	ENSMUSG00000036006	13	24582189	24733816	1	0	0	0	0	0	0	0	0	0	0	0		Q80U16
ENSMUST00000038482	ENSMUSG00000036449	2	25653120	25656217	1	10	4	9	4	9	4	0	0	0	0	0		Q924P3
ENSMUST00000038488	ENSMUSG00000034908	9	45937857	45955247	-1	0	0	0	63	40	16	869	1390	887	123	759	Q3U1L8	Q8CIF6
ENSMUST00000038489	ENSMUSG00000034910	9	72925645	72952181	1	57	34	108	224	63	31	0	1	0	1	1	Q1JPR5	Q9D0P5
ENSMUST00000038495	ENSMUSG00000037942	1	172698055	172833031	1	37	48	25	65	36	29	0	0	0	2	2		P14847
ENSMUST00000038498	ENSMUSG00000037316	8	25764538	25785209	-1	5	2	25	122	15	8	91	156	107	21	61	A6H6S8	Q8CI61
ENSMUST00000038507	ENSMUSG00000034923	17	35080480	35085610	-1	10	6	18	10	19	10	0	0	0	0	0	B2RXM6	
ENSMUST00000038514	ENSMUSG00000034826	5	92415540	92435219	-1	9	6	11	69	8	5	93	443	156	132	155		Q8BTS4
ENSMUST00000038521	ENSMUSG00000035585	7	3692863	3701024	1	0	0	0	0	0	0	39	71	70	0	21	H7BX14	
ENSMUST00000038522	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	2	152	0	38	0		Q3URD3
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ENSMUST00000038529	ENSMUSG00000038980	2	180277646	180289879	-1	20	17	77	64	36	9	0	0	0	1	0	A2ABX0	
ENSMUST00000038532	ENSMUSG00000038537	2	172248492	172251114	1	19	20	31	37	44	14	0	0	0	0	1	Q544G7	P33033
ENSMUST00000038537	ENSMUSG00000036459	7	34109543	34133268	-1	10	10	16	75	25	6	0	3	0	5	5		Q7TQJ8
ENSMUST00000038539	ENSMUSG00000040822	14	54686171	54690742	1	16	9	24	200	15	16	454	1249	521	1046	363		Q9JJ93
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ENSMUST00000038552	ENSMUSG00000039637	16	4626133	4679777	-1	29	13	51	26	22	11	1496	1889	1805	119	1045		Q9D2V7
ENSMUST00000038558	ENSMUSG00000035397	10	80567124	80577321	-1	14	5	69	283	13	11	179	219	121	21	116	B2RPU7	P58334
ENSMUST00000038562	ENSMUSG00000039911	4	149896283	149955043	-1	17	9	22	10	20	15	28	44	30	11	50		Q9D5L7
ENSMUST00000038563	ENSMUSG00000034109	3	75875084	75956949	-1	53	52	117	106	92	62	30	110	92	28	55		Q8BXA1
ENSMUST00000038564	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	6	0	0	0	3	0	0	0	A2AL78	
ENSMUST00000038569	ENSMUSG00000037211	3	37639947	37644598	1	0	0	17	32	0	0	0	0	0	0	0	Q53ZU1	Q9QXV9
ENSMUST00000038570	ENSMUSG00000034285	11	4873951	4894200	1	6	3	6	48	10	6	16	42	10	28	30	Q5SVF7	O55125
ENSMUST00000038572	ENSMUSG00000015165	7	28808541	28822266	1	0	0	0	0	0	0	24	942	403	3	140		Q8R081
ENSMUST00000038574	ENSMUSG00000042426	13	112927730	112969431	1	15	14	29	127	29	16	105	257	266	27	156		Q6PGC1
ENSMUST00000038580	ENSMUSG00000016206	17	37270220	37274484	1	13	11	28	8	15	6	40	123	39	66	116	Q31093	
ENSMUST00000038584	ENSMUSG00000041997	2	70712407	70825728	-1	0	0	0	61	9	0	323	1471	881	99	520		Q8C0V0
ENSMUST00000038598	ENSMUSG00000033520	13	8952863	8960945	1	32	23	64	22	31	14	1	0	2	1	1		Q8BFZ6
ENSMUST00000038600	ENSMUSG00000035772	2	28468066	28471178	1	165	132	0	50	118	94	30	104	38	15	66		Q924T2
ENSMUST00000038608	ENSMUSG00000035596	7	3677789	3693523	-1	10	11	3	66	13	0	897	1250	1099	91	871		Q8CHK3
ENSMUST00000038614	ENSMUSG00000042675	7	126776955	126780514	1	0	0	0	15	4	0	529	1605	403	228	291		P61237
ENSMUST00000038618	ENSMUSG00000040488	7	27305136	27337692	-1	12	5	38	271	35	0	0	0	0	0	7		Q8K4G1
ENSMUST00000038626	ENSMUSG00000035559	8	70758649	70760921	-1	4	3	14	89	18	5	182	253	111	53	86		Q8VIK2
ENSMUST00000038627	ENSMUSG00000024695	19	12763660	12796126	-1	10	11	36	20	14	16	444	1475	852	283	647		Q62511
ENSMUST00000038628	ENSMUSG00000037306	4	134561690	134704290	-1	111	80	299	0	43	41	229	514	167	40	98	Q6NXK9	
ENSMUST00000038644	ENSMUSG00000032892	11	68972484	68975185	-1	1	14	0	5	3	0	7	18	10	14	2		Q9JIB0
ENSMUST00000038648	ENSMUSG00000035032	9	105162156	105395524	-1	35	29	27	104	59	24	0	8	0	0	6		Q8C0Q4
ENSMUST00000038650	ENSMUSG00000033904	7	118712552	118737024	1	0	0	0	0	0	2	16	17	35	31	0		Q7TSH4
ENSMUST00000038658	ENSMUSG00000043131	6	83326016	83343776	1	13	2	32	0	15	13	486	4254	1078	276	391		Q921Y0
ENSMUST00000038661	ENSMUSG00000040740	4	141618824	141623821	-1	23	15	46	77	25	14	0	2	2	0	1		A2ADF7
ENSMUST00000038665	ENSMUSG00000041552	X	155573455	155623814	-1	6	3	5	25	4	2	0	2	0	0	0		Q14B62

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000038671	ENSMUSG00000035047	9	21273457	21287969	-1	0	0	0	0	0	3	810	2211	1260	349	1245	F6WIU1	
ENSMUST00000038673	ENSMUSG00000035048	9	102626296	102634425	1	0	0	4	0	0	0	44	185	85	472	43		Q8R034
ENSMUST00000038675	ENSMUSG00000037772	7	142532799	142540747	1	1	2	0	51	3	0	0	6	0	12	0		O35972
ENSMUST00000038676	ENSMUSG00000036596	5	35502218	35525698	-1	20	10	22	151	39	15	0	0	0	1	2		Q8R4V4
ENSMUST00000038677	ENSMUSG00000035049	19	41862852	41896153	-1	61	34	99	255	72	25	87	97	80	12	128	Q3UJA1	Q6P5B0
ENSMUST00000038684	ENSMUSG00000032643	4	124700701	124708611	1	33	30	129	102	40	29	471	849	416	43	256		Q9R059
ENSMUST00000038690	ENSMUSG00000039182	13	14630245	14638202	1	14	9	15	14	0	7	21	0	29	144	29		Q91WD4
ENSMUST00000038692	ENSMUSG00000035057	8	83348471	83382320	1	5	4	5	5	6	4	0	0	0	0	0		Q9D4R2
ENSMUST00000038693	ENSMUSG00000038064	8	47824482	47825475	1	7	9	30	11	25	5	0	0	0	0	0		Q9D7U6
ENSMUST00000038694	ENSMUSG00000035523	7	23658316	23660663	1	0	0	0	3	6	0	0	0	0	0	0	Q9EPS4	
ENSMUST00000038695	ENSMUSG00000040724	3	107101146	107115005	1	34	23	42	42	19	14	1	0	3	0	2		P63141
ENSMUST00000038696	ENSMUSG00000038976	11	94991035	95006899	1	11	17	52	1298	44	17	2353	2584	2977	380	2661		Q6R891
ENSMUST00000038699	ENSMUSG00000039623	5	142463944	142478710	1	37	25	110	107	58	21	408	848	515	38	443		Q3U829
ENSMUST00000038701	ENSMUSG00000004500	7	12965838	12974236	1	0	11	73	68	0	5	8	81	23	3	32	Q78F42	
ENSMUST00000038705	ENSMUSG00000040359	4	25248600	25281821	-1	1	0	0	0	0	0	62	286	143	284	121		Q8CCJ3
ENSMUST00000038709	ENSMUSG00000039294	11	121222588	121229322	-1	0	0	0	15	0	3	1587	1640	1695	640	1659		Q3TYS2
ENSMUST00000038710	ENSMUSG00000044322	18	20084703	20114773	-1	26	13	14	31	12	13	0	1	0	0	0	Q32ME9	
ENSMUST00000038719	ENSMUSG00000038736	15	44375227	44428307	-1	8	8	11	141	17	9	13	60	28	117	39		Q6PIP5
ENSMUST00000038720	ENSMUSG00000040189	7	45924072	45948956	1	17	10	44	69	30	15	24	46	28	6	54		Q3UX62
ENSMUST00000038730	ENSMUSG00000033383	16	23429133	23433960	1	12	14	26	37	23	14	0	0	0	0	0	B2RSL5	Q8C8C1
ENSMUST00000038738	ENSMUSG00000038069	8	47709344	47713931	-1	13	13	20	27	22	12	246	843	471	118	350		Q8BI72
ENSMUST00000038739	ENSMUSG00000033596	8	111270944	111300222	-1	34	43	30	115	40	24	439	1188	944	181	496		Q8CIK8
ENSMUST00000038743	ENSMUSG00000019734	7	3665790	3677553	-1	0	0	0	0	2	0	26	25	3	0	0	F8VQ45	
ENSMUST00000038749	ENSMUSG00000040935	4	140727355	140742643	-1	21	8	29	16	32	5	1	1	0	0	0		Q8K3V4
ENSMUST00000038750	ENSMUSG00000037140	6	40493529	40494541	1	2	1	2	1	3	0	0	0	0	0	0		Q9JKT3
ENSMUST00000038753	ENSMUSG00000040711	11	32347820	32428173	1	63	44	129	61	73	26	79	76	78	31	255		A2AAY5
ENSMUST00000038757	ENSMUSG00000042109	15	81936759	81950941	1	69	38	329	122	57	31	0	2	2	0	4		Q91YQ3
ENSMUST00000038760	ENSMUSG00000041782	1	135818598	135833342	1	25	13	33	151	21	16	0	0	0	0	1		P57016
ENSMUST00000038765	ENSMUSG00000037035	1	119415465	119422248	-1	30	23	41	448	44	20	0	0	1	3	4		Q04999
ENSMUST00000038769	ENSMUSG00000040808	X	162961992	162964599	-1	0	1	1	0	0	0	0	0	0	1	0	Q5VM59	P97816
ENSMUST00000038770	ENSMUSG00000039646	16	4639941	4650802	1	14	15	53	49	36	10	57	15	142	10	234		Q9CZT5
ENSMUST00000038772	ENSMUSG00000034620	10	122078114	122097371	-1	0	0	0	4	0	0	34	154	58	130	50	Q5XK09	
ENSMUST00000038775	ENSMUSG00000033585	7	62348277	62349928	1	8	7	11	90	12	6	0	1	0	2	1		P25233
ENSMUST00000038782	ENSMUSG00000040629	1	166201201	166238747	-1	7	8	2	0	0	2	0	0	0	0	0		Q8BVN9
ENSMUST00000038791	ENSMUSG00000033917	7	118688545	118705778	-1	7	8	40	159	15	6	131	347	199	110	152		Q9JL56
ENSMUST00000038794	ENSMUSG00000001229	17	56186682	56218889	-1	33	32	64	98	37	30	809	913	994	55	668		Q8BVG4
ENSMUST00000038804						1	2	2	2	0	3	0	0	1	0	0		
ENSMUST00000038811	ENSMUSG00000039264	6	48764464	48770851	-1	5	1	13	6	8	2	96	129	77	56	356		Q99MI6
ENSMUST00000038815	ENSMUSG00000041540	6	143828425	144781977	-1	0	0	0	0	0	0	0	0	0	0	0	B2KFM9	
ENSMUST00000038816	ENSMUSG00000034855	5	92346638	92348889	-1	1	1	2	0	1	0	5	8	1	3	9	Q548V9	P17515
ENSMUST00000038824	ENSMUSG00000038567	2	170482708	170497145	-1	17	16	32	99	33	18	0	0	0	0	0	Q3TWW0	Q64441
ENSMUST00000038829	ENSMUSG00000042474	1	130865669	130880791	1	11	10	58	19	6	9	24	38	36	6	86	A0A0G2LB91	
ENSMUST00000038830	ENSMUSG00000035171	19	21581202	21652976	-1	6	0	6	6	8	5	78	499	121	211	43		Q9CQ90
ENSMUST00000038831	ENSMUSG00000039307	11	121204433	121222655	1	0	0	0	65	0	2	0	0	0	0	0		Q3U4H6
ENSMUST00000038835	ENSMUSG00000036521	7	31290508	31304977	1	6	0	1	3	1	2	0	0	0	0	0	G5E8B4	
ENSMUST00000038841	ENSMUSG00000041216	4	9269293	9451691	1	0	16	104	0	4	3	0	0	0	0	0		Q9D4C9
ENSMUST00000038842	ENSMUSG00000035179	19	10474257	10482897	-1	11	6	33	19	16	8	5	55	11	10	26		
ENSMUST00000038844	ENSMUSG00000035186	17	37193892	37196095	1	5	4	7	8	8	2	0	0	0	0	0		P63072
ENSMUST00000038845	ENSMUSG00000040747	3	106759921	106790149	-1	7	6	12	8	8	8	5383	21821	6706	14065	4055	Q3U0W1	Q61451
ENSMUST00000038856	ENSMUSG00000038760	15	44196135	44235912	1	35	31	18	38	27	17	0	0	1	0	0	Q32MS1	P21761
ENSMUST00000038859	ENSMUSG00000039936	4	149649168	149702571	-1	17	0	0	1	16	22	3110	3021	3738	384	4031	Q8CI98	
ENSMUST00000038860	ENSMUSG00000038180	2	156065175	156070617	1	0	0	0	0	0	0	0	0	0	0	0		Q9JJF2
ENSMUST00000038863	ENSMUSG00000035202	9	123366940	123462664	1	8708	12564	41262	90891	38550	6329	7915	70362	22804	27879	9047		Q8VDC0
ENSMUST00000038867	ENSMUSG00000038084	16	29579334	29654884	1	0	0	0	0	0	0	36	186	76	50	30	H7BX01	
ENSMUST00000038868	ENSMUSG00000034401	4	111719984	111829184	1	0	0	0	19	0	0	27	438	193	83	162		Q3U6K5
ENSMUST00000038874	ENSMUSG00000035236	2	39066214	39190734	-1	11	21	15	11	18	8	97	102	92	33	122		Q8C8N2
ENSMUST00000038876	ENSMUSG00000040212	7	45918023	45921426	-1	6	4	8	14	2	4	1289	1364	821	1028	740		O35912
ENSMUST00000038885	ENSMUSG00000037225	3	37348346	37410108	1	0	0	0	59	0	0	0	0	0	0	0	Q925A3	
ENSMUST00000038886	ENSMUSG00000038067	11	98701263	98703629	1	7	4	21	15	10	4	0	0	0	13	17	Q0VB73	P09920
ENSMUST00000038889	ENSMUSG00000030276	6	113389260	113414587	1	3	0	8	24	22	7	34	29	79	0	159	H7BX03	
ENSMUST00000038890	ENSMUSG00000053641	9	64811340	64919667	1	29	25	40	103	33	21	3204	6091	6819	1511	4839	E9Q8V6	
ENSMUST00000038893	ENSMUSG00000040945	4	140700541	140723220	1	13	0	81	58	13	22	703	562	452	70	535		Q8BK67
ENSMUST00000038896	ENSMUSG00000035237	8	105939551	105943382	-1	13	9	45	23	18	10	0	0	0	6	2		P16301
ENSMUST00000038900	ENSMUSG00000034021	5	150673739	150810690	1	18	6	76	0	20	13	53	51	90	39	0	F8WHU5	
ENSMUST00000038901						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000038907	ENSMUSG00000037159	6	40439088	40466813	1	5	6	15	9	14	4	2	15	9	0	5		Q66JT0
ENSMUST00000038913	ENSMUSG00000035632	7	3645268	3661109	1	0	5	0	0	0	0	790	1235	722	12	496		Q8K0V4
ENSMUST00000038920	ENSMUSG00000040372	4	24966407	25009233	1	9	6	23	16	11	8	0	4	5	0	2		Q9EQQ3
ENSMUST00000038926	ENSMUSG00000035021	12	54892989	55014348	-1	32	22	66	27	35	29	45	277	45	25	79		O88379
ENSMUST00000038928	ENSMUSG00000038994	11	94967593	94968456	1	9	7	34	5	14	3	0	0	0	0	0	Q5SWB1	Q9QYL0
ENSMUST00000038932	ENSMUSG00000032921	11	68921835	68927081	-1	0	0	43	12	0	0	0	0	0	0	0		Q8VI88
ENSMUST00000038942	ENSMUSG00000042613	3	89436706	89450952	1	68	37	125	134	100	32	8613	13766	10473	817	8211		Q3TVI8
ENSMUST00000038945	ENSMUSG00000041801	1	135766119	135769136	1	6	2	10	187	13	3	2	1	0	5	2		Q9WV95
ENSMUST00000038946	ENSMUSG00000018819	7	142460809	142494867	1	0	0	0	12	0	0	0	0	0	0	0		P19973
ENSMUST00000038949	ENSMUSG00000035283	19	56722372	56724862	1	8	4	22	259	13	7	3	1	0	0	2		P34971
ENSMUST00000038956	ENSMUSG00000041673	14	32991382	33015292	1	12	14	9	6	4	4	0	1	0	0	2		Q9CQ07
ENSMUST00000038959	ENSMUSG00000030465	8	67689082	68062286	-1	24	12	20	3	32	12	0	2	0	0	2	F6Z9E6	
ENSMUST00000038973	ENSMUSG00000035521	17	25233331	25240124	-1	5	8	1	36	8	3	219	349	233	149	156		
ENSMUST00000038980	ENSMUSG00000045482	5	144767732	144859778	1	0	26	0	0	0	0	428	26	410	1	617	E9PZA7	
ENSMUST00000039007	ENSMUSG00000039725	2	165490110	165493324	-1	19	11	56	150	30	16	51	87	28	10	35	Q5U452	
ENSMUST00000039008	ENSMUSG00000037172	6	40401375	40436135	-1	9	9	45	80	7	5	7	1	19	0	20		Q3UHG7
ENSMUST00000039011	ENSMUSG00000035337	9	64235201	64236362	1	12	5	15	11	9	5	0	3	1	1	1	B2RTM4	P58321
ENSMUST00000039013	ENSMUSG00000024130	17	24351950	24410201	1	0	0	0	0	0	0	717	83	603	67	416		Q8R420
ENSMUST00000039016	ENSMUSG00000035342	19	45015176	45027104	1	19	0	0	392	43	15	0	0	0	0	0		Q91YU6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000039021	ENSMUSG00000036825	3	146404642	146440144	1	0	0	0	0	3	0	0	63	0	14	0		
ENSMUST00000039026	ENSMUSG00000037010	X	48025146	48034853	-1	13	7	36	71	15	12	8	24	24	6	25	Q544B5	Q9R0R4
ENSMUST00000039043	ENSMUSG00000024670	19	10789341	10830058	-1	17	9	5	21	8	0	17	22	0	0	50		Q61003
ENSMUST00000039044	ENSMUSG00000039321	11	121160271	121161973	1	21	6	42	36	27	12	0	0	0	0	0	Q05AD1	Q8VIH9
ENSMUST00000039046	ENSMUSG00000041872	1	20777146	20790617	-1	0	1	2	0	2	0	0	1	0	0	0		Q7TNI7
ENSMUST00000039047	ENSMUSG00000034139	3	75242370	75270078	-1	3	2	3	4	5	8	0	0	0	0	0	Q4G0D3	Q9JK88
ENSMUST00000039048	ENSMUSG00000035372	19	3708333	3717881	1	22	5	166	69	16	13	121	172	108	13	92		Q9D8N1
ENSMUST00000039049	ENSMUSG00000040231	7	45885222	45896714	-1	0	0	26	8	8	6	0	0	0	0	0		
ENSMUST00000039059	ENSMUSG00000035382	9	45906569	45929692	1	33	20	65	241	39	16	975	1560	1174	198	1027		Q61139
ENSMUST00000039061	ENSMUSG00000038102	8	47490115	47533470	-1	0	16	0	0	0	0	398	912	787	151	563		B2RXC1
ENSMUST00000039064	ENSMUSG00000035184	14	62555737	62608486	1	66	54	184	766	89	53	2	11	3	0	3	D3Z5V4	
ENSMUST00000039071	ENSMUSG00000040373	11	107874605	107915055	-1	0	11	0	27	0	19	0	0	0	0	0	Q544Q4	Q8VHW4
ENSMUST00000039074	ENSMUSG00000022623	15	89499623	89560261	1	33	11	56	467	59	25	0	0	0	0	0		Q4ACU6
ENSMUST00000039075	ENSMUSG00000059463	8	19140759	19143010	1	0	0	0	1	0	0	0	0	0	0	0		Q8K4N2
ENSMUST00000039088	ENSMUSG00000039329	11	121146143	121148319	1	18	10	98	38	13	11	0	0	0	1	1		Q99MV2
ENSMUST00000039090	ENSMUSG00000038094	16	29395853	29544864	-1	10	15	4	7	13	0	0	0	0	0	0		
ENSMUST00000039093	ENSMUSG00000040829	11	70459433	70466202	1	0	0	0	4	0	3	0	0	0	0	0		Q8C0R7
ENSMUST00000039101	ENSMUSG00000041079	16	87433407	87440573	-1	22	7	16	14	20	8	46	163	51	30	52		Q99M03
ENSMUST00000039110	ENSMUSG00000042626	3	89418443	89430027	1	38	0	67	25	33	0	338	195	185	67	123		P98083
ENSMUST00000039113	ENSMUSG00000024184	17	26195999	26199087	-1	5	3	13	14	5	0	0	0	0	0	0		D3Z6P0
ENSMUST00000039118	ENSMUSG00000041703	14	122456795	122465677	-1	44	41	136	460	57	20	0	2	1	1	2		
ENSMUST00000039121	ENSMUSG00000035420	18	50278369	50283019	1	5	2	24	12	13	2	0	0	0	0	0		Q66LM6
ENSMUST00000039127	ENSMUSG00000038538	6	38433950	38524825	1	0	0	0	0	0	0	0	0	75	0	87		Q80WC1
ENSMUST00000039132	ENSMUSG00000053600	17	32965814	32979233	1	8	2	5	12	11	9	33	195	53	82	22	B0V2W5	
ENSMUST00000039135	ENSMUSG00000044447	14	67751928	67933572	-1	79	78	106	168	89	51	2022	4328	4349	176	2831		B2RY04
ENSMUST00000039144	ENSMUSG00000039953	4	149586468	149648899	1	0	0	15	27	17	12	0	0	0	0	0		Q9EPL2
ENSMUST00000039146	ENSMUSG00000039337	11	121116215	121118677	-1	33	11	56	81	34	17	0	0	0	0	0	B2RUP5	Q9D5S1
ENSMUST00000039152	ENSMUSG00000034931	11	101732919	101767358	1	46	32	75	57	49	19	981	1617	1215	176	975		A2A4P0
ENSMUST00000039153	ENSMUSG00000040774	3	106502260	106547802	-1	3	5	5	0	7	3	125	1013	217	62	105		Q8BGS7
ENSMUST00000039156	ENSMUSG00000036504	2	25573430	25575224	-1	8	3	15	24	0	2	22	36	8	74	21		Q9DAK9
ENSMUST00000039160	ENSMUSG00000040133	2	118277110	118373419	-1	39	29	47	167	44	23	0	2	1	0	2		Q80WT4
ENSMUST00000039161	ENSMUSG00000035443	9	26999677	27007330	1	4	0	4	2	4	2	21	74	43	311	30		Q91YJ3
ENSMUST00000039164	ENSMUSG00000036832	3	146220963	146286186	1	50	35	86	467	117	55	0	2	0	0	0	Q544B4	Q9EQ31
ENSMUST00000039165	ENSMUSG00000026754	2	39016155	39065541	-1	0	0	37	95	31	7	18	209	28	60	72		Q9CW79
ENSMUST00000039171	ENSMUSG00000035448	9	124021971	124031689	1	4	10	5	9	6	1	7	95	13	31	30		P51678
ENSMUST00000039173	ENSMUSG00000026319	1	105663861	105755191	1	0	0	0	0	0	0	0	0	0	0	0	E9QM90	
ENSMUST00000039174	ENSMUSG00000038151	10	44437177	44528501	-1	20	13	54	149	36	17	6	45	0	6	40		Q60636
ENSMUST00000039177	ENSMUSG00000033308	3	118562129	119432924	1	12	13	26	9	9	4	0	0	0	6	0		Q8CHR6
ENSMUST00000039178	ENSMUSG00000026725	1	160085029	160153580	-1	13	9	35	6	38	16	0	0	0	0	0		Q80Z71
ENSMUST00000039191	ENSMUSG00000041707	14	32785963	32817968	1	17	11	25	16	15	8	33	120	57	133	36	E9PVZ2	
ENSMUST00000039197	ENSMUSG00000039865	3	121459528	121532404	-1	23	12	25	62	30	12	0	0	0	2	2		Q921V7
ENSMUST00000039204	ENSMUSG00000040964	4	140514485	140666012	-1	0	0	0	0	0	0	0	0	0	0	0		A2AWP8
ENSMUST00000039205	ENSMUSG00000035473	17	80127471	80185101	1	19	8	17	27	18	8	136	551	197	161	182		Q8K157
ENSMUST00000039212	ENSMUSG00000068323	6	83219828	83304945	1	0	25	0	10	45	0	0	0	0	0	0	D3YVG0	
ENSMUST00000039213	ENSMUSG00000035941	9	85687360	85749334	-1	8	4	7	0	10	0	530	1481	1111	16	234		Q6ZPR6
ENSMUST00000039229	ENSMUSG00000035498	9	123170824	123216038	-1	37	29	72	79	31	21	2	2	6	6	23		Q5U462
ENSMUST00000039234	ENSMUSG00000040410	4	22357543	22434091	1	0	0	0	1	0	0	0	25	30	81	0		Q8BH70
ENSMUST00000039247	ENSMUSG00000024331	18	20030633	20059554	-1	15	0	0	54	16	5	0	0	0	0	0	Q544V1	P55292
ENSMUST00000039259	ENSMUSG00000025422	10	127078907	127093169	1	35	25	101	850	76	30	758	740	667	55	580		Q3UHD9
ENSMUST00000039267	ENSMUSG00000041235	4	8690406	8867659	1	10	0	145	64	50	0	0	0	984	0	1514		A2AJK6
ENSMUST00000039269	ENSMUSG00000034151	3	75037907	75165034	-1	0	0	8	0	10	2	0	0	0	0	0	F8WIV1	
ENSMUST00000039271	ENSMUSG00000060301	10	79064374	79097600	-1	14	14	24	21	21	12	19	122	32	47	31	G3X964	
ENSMUST00000039280	ENSMUSG00000022983	16	90228957	90284425	-1	24	22	53	374	27	11	160	218	320	19	241	Q6PFF0	
ENSMUST00000039286	ENSMUSG00000038160	10	44268358	44364291	1	5	15	16	52	10	7	326	1551	592	1491	330		Q99J83
ENSMUST00000039303	ENSMUSG00000036437	8	66697422	66706798	1	136	165	339	103	91	69	0	9	5	3	10	Q3V1K5	Q04573
ENSMUST00000039305	ENSMUSG00000020264	11	55158470	55185077	-1	9	7	7	20	17	10	0	0	0	2	0		Q8BHK3
ENSMUST00000039309	ENSMUSG00000039364	11	121053458	121063569	-1	12	10	33	16	17	9	0	1	0	0	0	Q9D966	
ENSMUST00000039317	ENSMUSG00000038540	7	83584927	83625614	1	30	23	51	34	33	17	7	42	11	4	23	F8VQI4	
ENSMUST00000039318	ENSMUSG00000033102	13	64192545	64274973	-1	19	0	0	228	32	26	0	64	0	0	31		Q6PFY9
ENSMUST00000039323	ENSMUSG00000042510	1	130731976	130744622	1	20	19	109	13	26	11	9	42	26	6	18		Q8BI29
ENSMUST00000039324	ENSMUSG00000035435	17	24264259	24351029	-1	0	0	0	0	0	0	0	0	0	0	0	E9PX95	
ENSMUST00000039327	ENSMUSG00000035735	19	10245265	10304877	-1	0	0	111	231	84	52	0	0	0	0	76		Q6WQJ1
ENSMUST00000039331	ENSMUSG00000040972	4	140026846	140246784	-1	11	8	26	215	29	9	0	0	0	0	0		Q7TNR6
ENSMUST00000039333	ENSMUSG00000033624	8	111094630	111137074	1	27	14	34	31	21	14	378	359	835	26	485		Q7TSQ8
ENSMUST00000039338	ENSMUSG00000060459	16	22985854	23029101	-1	0	0	0	0	0	0	0	0	0	0	0	Q6S9I2	
ENSMUST00000039340	ENSMUSG00000041138	13	19645078	19697794	-1	0	0	5	1	0	0	1	0	2	0	0		Q715T0
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ENSMUST00000039366	ENSMUSG00000035580	17	52602709	52979194	1	19	21	32	16	25	12	0	0	0	0	0	F6TUN6	
ENSMUST00000039370	ENSMUSG00000040118	5	15934691	16374511	1	0	0	0	0	0	7	0	0	0	0	0		O08532
ENSMUST00000039373	ENSMUSG00000035898	5	86109287	86172803	-1	3	0	0	35	0	3	46	84	31	68	30		Q8C7R4
ENSMUST00000039374	ENSMUSG00000035967	X	56454857	56507843	1	0	0	0	0	0	0	436	1729	1375	85	371		Q8BND4
ENSMUST00000039375						0	1	2	4	3	1	0	0	0	0	0		
ENSMUST00000039380	ENSMUSG00000040055	14	57123303	57133611	-1	7	3	20	56	12	3	0	0	0	0	0	Q3URC5	P70689
ENSMUST00000039388	ENSMUSG00000034936	11	101665541	101667832	1	17	9	38	111	21	16	7	31	5	7	13		Q99PE9
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ENSMUST00000039408	ENSMUSG00000041957	16	16213318	16272712	1	7	4	12	5	3	5	0	3	1	1	0	Q9CQ73	
ENSMUST00000039412	ENSMUSG00000039842	8	18595131	18803189	1	88	63	370	266	70	32	22	57	32	10	31		Q7TT79
ENSMUST00000039413	ENSMUSG00000032177	9	21165714	21213248	1	13	18	32	162	23	11	14	61	19	7	47	B2RTL2	O89084
ENSMUST00000039419	ENSMUSG00000036334	3	59316735	59344394	-1	30	22	8	15	49	0	3	13	12	0	7		Q3V1M1
ENSMUST00000039424	ENSMUSG00000041633	X	153685154	153696391	-1	0	0	0	0	0	0	2	0	3	10	0	Q8C7J6	
ENSMUST00000039431	ENSMUSG00000059146	7	78175959	78738012	-1	9	0	15	77	6	3	0	0	0	0	0		Q6VNS1
ENSMUST00000039435	ENSMUSG00000001249	7	31098725	31115290	-1	0	2	6	4	8	0	0	0	0	3	2	E9Q5P0	
ENSMUST00000039438	ENSMUSG00000059146	7	78175959	78738012	-1	0	0	0	0	0	0	0	0	0	0	0		Q6VNS1
ENSMUST00000039442	ENSMUSG00000039887	3	121291773	121363094	1	2	7	3	4	5	2	15	79	34	105	28		Q9D081

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ENSMUST00000039443	ENSMUSG00000038127	16	27388869	27452218	1	5	14	19	6	9	7	0	0	2	3	6		Q810U5
ENSMUST00000039447	ENSMUSG00000033737	X	106420041	106485401	-1	5	9	6	14	14	9	0	0	1	1	1		Q6DFV6
ENSMUST00000039449	ENSMUSG00000052299	16	87376651	87432606	-1	30	27	50	86	32	9	364	887	633	161	435		Q6A009
ENSMUST00000039450	ENSMUSG00000036853	3	146117450	146141806	1	15	11	8	12	14	7	1	6	1	1	3	Q3KP78	Q8R4F0
ENSMUST00000039476	ENSMUSG00000041977	3	87617559	87738034	1	0	10	0	13	30	18	297	316	359	38	373	Q68FM7	
ENSMUST00000039480	ENSMUSG00000035671	8	84210942	84237042	-1	28	22	68	95	41	14	1545	1062	1171	129	1022		Q8C7B8
ENSMUST00000039484	ENSMUSG00000039981	10	7832470	7870397	1	111	78	297	288	115	50	828	2765	1407	138	756	E9QNR7	
ENSMUST00000039487	ENSMUSG00000034345	17	6079786	6086517	1	14	12	30	20	11	5	64	142	66	265	47		Q8K2X8
ENSMUST00000039490	ENSMUSG00000035678	17	57105385	57107757	1	9	10	19	156	13	10	4	6	2	1	12	Q3U1Z9	P41274
ENSMUST00000039492	ENSMUSG00000022875	16	23057865	23082068	1	9	3	5	4	4	4	0	0	0	127	0		O08677
ENSMUST00000039500	ENSMUSG00000024749	19	20783458	20954202	-1	17	15	24	16	18	10	0	0	0	1	1		Q8R4P5
ENSMUST00000039506	ENSMUSG00000038034	1	172261641	172319841	1	0	0	0	146	0	0	0	606	490	23	420		
ENSMUST00000039507	ENSMUSG00000054594	7	3609813	3616157	-1	13	0	17	0	0	4	0	0	0	0	0		Q8VBT3
ENSMUST00000039516	ENSMUSG00000035105	12	54178981	54203860	-1	13	8	21	263	22	7	904	1705	780	294	597		
ENSMUST00000039517	ENSMUSG00000036863	3	145987870	146021720	1	37	22	25	105	42	18	1	0	0	1	5	E9PUP1	
ENSMUST00000039522	ENSMUSG00000042759	7	126584942	126589112	1	37	17	55	65	71	35	5357	15201	9387	1373	8062		Q8VBT6
ENSMUST00000039534	ENSMUSG00000033061	1	75272199	75278415	-1	3	2	0	2	6	0	0	0	0	0	0		P47939
ENSMUST00000039535	ENSMUSG00000035295	2	38997476	39006168	1	17	20	2	158	23	21	1	3	2	2	7		Q9D994
ENSMUST00000039537	ENSMUSG00000038712	3	95281345	95296166	1	0	0	0	0	0	0	0	0	0	0	0		Q76LS9
ENSMUST00000039538	ENSMUSG00000039219	13	14063232	14199603	1	0	0	0	0	0	0	0	60	10	0	0		A2CG63
ENSMUST00000039540	ENSMUSG00000036469	8	65617900	66471637	1	15	24	361	0	19	0	114	725	152	392	346		Q6NZQ8
ENSMUST00000039541	ENSMUSG00000027263	2	121170654	121198770	1	2	0	0	0	19	0	88	395	241	31	76	Q543T6	Q9D4F8
ENSMUST00000039545	ENSMUSG00000041649	X	153237466	153396132	1	4	5	18	6	12	4	9	25	21	1	14		Q8BLM0
ENSMUST00000039551	ENSMUSG00000038628	2	181864337	181870830	1	54	59	65	62	61	37	87	233	103	327	87		Q9CQZ7
ENSMUST00000039554	ENSMUSG00000037376	2	132804207	132816055	-1	0	0	0	0	0	3	42	242	104	95	89		Q8CE96
ENSMUST00000039557	ENSMUSG00000039031	10	26753421	26918648	1	0	10	15	8	11	0	104	448	283	697	272		Q8K0Q5
ENSMUST00000039559	ENSMUSG00000040152	2	118111876	118127133	1	65	36	69	48	56	17	22	98	51	208	3341	Q80YQ1	
ENSMUST00000039562	ENSMUSG00000035235	14	61598226	61605946	1	8	0	0	28	5	8	0	89	28	49	37		Q9CYB0
ENSMUST00000039564	ENSMUSG00000033342	3	117574836	117689507	1	0	7	14	0	9	0	0	0	0	0	0		Q8BJ52
ENSMUST00000039568	ENSMUSG00000036422	14	79766775	79771312	-1	0	13	0	433	0	0	0	0	0	0	0		Q7TSK3
ENSMUST00000039571	ENSMUSG00000036873	3	145938014	145944829	1	0	3	3	52	0	3	14	22	62	52	59		Q9CWU4
ENSMUST00000039577	ENSMUSG00000023892	17	21450352	21465591	1	7	9	13	6	7	8	52	359	86	97	50	Q3U4L8	
ENSMUST00000039581	ENSMUSG00000034947	11	101582242	101591788	1	11	0	0	14	0	0	129	338	89	17	197		Q8VC04
ENSMUST00000039597	ENSMUSG00000033633	8	111058920	111092426	-1	0	0	3	0	0	0	0	0	0	0	0		Q7TSQ1
ENSMUST00000039601	ENSMUSG00000040767	11	32205415	32208984	1	0	0	0	14	0	0	79	99	35	163	26		Q8VIK1
ENSMUST00000039605	ENSMUSG00000038246	13	34734850	34747613	1	17	7	20	180	26	15	0	0	0	0	0		Q9WTJ8
ENSMUST00000039608	ENSMUSG00000035765	18	75018772	75286966	1	10	19	24	80	18	22	766	1493	915	97	497		Q8CHY3
ENSMUST00000039610	ENSMUSG00000035769	9	119357381	119393797	1	32	25	53	151	52	23	9	12	6	1	18		Q3TNA1
ENSMUST00000039612	ENSMUSG00000048814	1	38793645	38836711	-1	0	0	17	0	0	0	0	0	0	0	0	B2RT44	
ENSMUST00000039620	ENSMUSG00000022947	16	93683215	93690990	1	7	4	10	227	9	5	540	1120	460	261	361		Q8K354
ENSMUST00000039627	ENSMUSG00000034156	11	87760541	87785928	1	48	34	167	168	68	36	21	33	34	0	45		Q7TNF8
ENSMUST00000039630	ENSMUSG00000035305	4	100095791	100444765	1	38	30	56	177	43	19	0	0	0	2	2		Q9Z139
ENSMUST00000039631	ENSMUSG00000035783	19	34241090	34255336	-1	7	9	23	14	13	9	191	299	89	86	98		P62737
ENSMUST00000039652	ENSMUSG00000035804	19	52264323	52265456	1	8	6	9	13	8	8	0	0	0	0	0	Q545I7	P01325
ENSMUST00000039655	ENSMUSG00000034377	17	6106437	6251128	1	0	0	0	0	0	0	7	9	27	16	91		Q9JIL5
ENSMUST00000039659	ENSMUSG00000051483	16	93607837	93610505	1	9	7	34	106	14	12	25	47	18	54	31	B2RXY7	P48758
ENSMUST00000039662	ENSMUSG00000052698	9	67217087	67559703	-1	17	8	15	0	18	0	12	5	4	0	22	E9PUM4	
ENSMUST00000039665	ENSMUSG00000032783	15	99074973	99083407	1	19	11	43	62	34	11	45	31	35	14	28		B7ZNG4
ENSMUST00000039666	ENSMUSG00000035818	19	56461637	56486729	1	8	6	12	10	10	6	8	58	0	6	5		Q8BW88
ENSMUST00000039672	ENSMUSG00000041945	1	40772038	40790687	-1	0	0	23	0	5	0	111	230	85	36	67		Q8C0T7
ENSMUST00000039674	ENSMUSG00000035934	9	36890982	37147322	-1	0	0	0	0	0	19	51	63	79	0	32		Q8BG99
ENSMUST00000039680	ENSMUSG00000037997	6	127446840	127494261	1	0	0	13	0	0	0	51	79	61	30	85		Q8CFF0
ENSMUST00000039694	ENSMUSG00000003062	13	19357676	19395795	-1	5	4	13	11	6	2	162	468	157	188	120		Q9DCI3
ENSMUST00000039695	ENSMUSG00000042353	8	80611080	80695356	1	48	51	92	73	66	31	0	0	1	0	0	F8WHZ0	
ENSMUST00000039697	ENSMUSG00000033676	7	57419692	57828802	1	0	0	0	0	0	0	0	0	0	0	0		P63080
ENSMUST00000039718	ENSMUSG00000042774	10	78963309	78970612	1	8	8	4	7	5	1	0	0	0	0	0	Q8VGU8	
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ENSMUST00000039721	ENSMUSG00000036083	13	23839434	23860714	1	21	16	0	18	19	0	0	0	0	0	0	G5E894	
ENSMUST00000039725	ENSMUSG00000039748	1	175880581	175913489	1	116	100	168	154	122	56	10	22	30	1	20		Q9QZ11
ENSMUST00000039726	ENSMUSG00000035868	17	21657582	21662540	1	5	6	2	2	8	1	25	169	31	23	13	E9PUT0	
ENSMUST00000039729	ENSMUSG00000040370	6	145211134	145216939	1	0	10	9	18	8	0	0	51	12	15	15		Q91V16
ENSMUST00000039733	ENSMUSG00000022807	16	33185071	33243311	1	15	14	31	270	30	7	520	1350	1284	221	1064	G5E8A0	
ENSMUST00000039734	ENSMUSG00000015127	17	25188397	25234443	1	0	0	0	7	0	0	79	161	247	15	209		Q5FWH2
ENSMUST00000039742	ENSMUSG00000035878	9	54917283	54949924	1	40	41	58	71	51	22	2	6	4	1	13		Q5U5V2
ENSMUST00000039744	ENSMUSG00000029228	5	74592447	74702912	-1	0	0	0	0	0	0	0	0	7	6	0	A4QPD4	O70263
ENSMUST00000039750	ENSMUSG00000039252	5	52533517	52566462	-1	17	7	22	41	20	9	0	0	0	2	0		Q8K4Z0
ENSMUST00000039752	ENSMUSG00000032988	15	79251014	79254761	-1	7	12	51	325	22	11	0	0	3	0	0	Q5UB50	O35308
ENSMUST00000039758	ENSMUSG00000035885	19	7215158	7217616	-1	5	7	14	57	18	9	1557	3211	1328	1591	856		Q64445
ENSMUST00000039761	ENSMUSG00000028133	3	121155398	121171695	-1	0	0	0	0	0	0	0	0	0	27	0	Q3UYX7	
ENSMUST00000039763	ENSMUSG00000040006	10	7767947	7792824	-1	0	0	0	34	0	0	14	45	95	113	0		Q91WR6
ENSMUST00000039769	ENSMUSG00000060429	15	55638843	55906949	-1	16	15	26	233	20	6	5	13	4	1	20		Q99L88
ENSMUST00000039775	ENSMUSG00000036560	7	31059342	31070935	1	28	14	71	140	40	31	0	6	4	0	0		Q8K1S1
ENSMUST00000039782	ENSMUSG00000057133	2	160946978	161109075	-1	43	46	101	49	80	23	117	306	358	55	342		A3KFM7
ENSMUST00000039784	ENSMUSG00000036138	9	119339676	119350299	1	6	0	4	18	9	0	772	1596	758	95	466		Q921H8
ENSMUST00000039788	ENSMUSG00000035914	9	58524300	58555132	-1	23	18	47	0	9	19	9	32	11	9	32	A6MDC5	Q8VE98
ENSMUST00000039796	ENSMUSG00000033416	10	75351111	75517972	-1	20	20	5	108	34	14	40	345	414	64	279		Q8BZI6
ENSMUST00000039798	ENSMUSG00000035919	9	22475715	22888280	1	5	7	21	15	8	3	38	0	41	0	70		Q811G0
ENSMUST00000039803	ENSMUSG00000041765	14	121878606	122021034	1	7	7	29	109	9	11	592	1022	573	99	462		Q8R1K1
ENSMUST00000039810	ENSMUSG00000034667	10	121587380	121626316	-1	39	45	37	163	68	22	108	251	153	30	167		Q9CRT8
ENSMUST00000039812	ENSMUSG00000040123	14	56790585	56811716	-1	48	0	0	120	0	39	0	298	0	0	87		Q3U2E2
ENSMUST00000039818	ENSMUSG00000028737	4	139622866	139649690	1	5	4	6	16	15	5	455	452	282	27	291		Q8CHT0
ENSMUST00000039827	ENSMUSG00000037138	1	38177326	38664955	-1	44	33	4	39	0	0	0	0	23	0	19	F8WJA7	
ENSMUST00000039832	ENSMUSG00000033122	13	64058274	64089201	-1	2	3	0	0	0	4	0	0	0	0	0		P70385
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000039840	ENSMUSG00000038173	8	46986925	47094895	1	0	15	88	0	7	8	2	1	1	0	1		Q8BGN3
ENSMUST00000039846	ENSMUSG00000064308	17	36977701	36981237	-1	5	5	12	0	0	4	0	0	0	0	0	Q9CWF0	
ENSMUST00000039855	ENSMUSG00000034243	16	36875140	36933085	1	1	19	113	0	23	51	241	783	457	226	579	E9PVZ8	
ENSMUST00000039861	ENSMUSG00000004609	7	43524216	43544428	-1	33	26	14	44	26	18	4725	10155	8570	2463	6507		Q63994
ENSMUST00000039862	ENSMUSG00000042554	1	130576713	130629621	-1	9	0	8	12	0	0	0	0	0	0	0	G3X970	
ENSMUST00000039867	ENSMUSG00000033964	1	139422288	139453005	1	21	27	60	31	26	16	145	299	221	115	177		Q811F1
ENSMUST00000039881	ENSMUSG00000038563	7	82648614	82777852	1	8	21	10	22	8	4	0	76	151	38	111		Q8C0D5
ENSMUST00000039882	ENSMUSG00000037370	10	24637914	24712159	-1	6	0	19	154	14	6	2	13	5	126	17	E9QQ26	
ENSMUST00000039887	ENSMUSG00000034607	X	112638431	112698651	-1	2	3	1	5	2	2	0	0	0	0	0		Q8K4L4
ENSMUST00000039892	ENSMUSG00000039201	X	8154472	8176181	-1	0	10	18	79	13	10	0	14	0	0	0		A1A5B6
ENSMUST00000039894	ENSMUSG00000039233	13	13997949	14039638	-1	0	0	2	4	1	1	6	428	84	253	29		Q8CIV8
ENSMUST00000039900	ENSMUSG00000032673	11	29511757	29515033	-1	14	21	22	40	15	17	111	702	146	437	110		Q9D820
ENSMUST00000039904	ENSMUSG00000024617	18	60925618	60988152	1	0	0	0	0	0	0	0	0	0	0	0	F8WHB5	
ENSMUST00000039909	ENSMUSG00000036570	7	31051678	31057199	-1	0	3	5	22	0	0	0	0	0	0	0		Q9Z239
ENSMUST00000039913	ENSMUSG00000038028	6	127085116	127109557	-1	37	19	41	50	33	15	63	93	74	44	36	B2RWB7	Q8BZA9
ENSMUST00000039922	ENSMUSG00000025231	19	46396896	46488804	1	23	17	60	72	34	13	231	207	211	20	204		Q9Z0P7
ENSMUST00000039925	ENSMUSG00000033427	10	75406911	75441679	1	106	84	205	99	111	64	5	8	13	5	13	Q3UEK4	Q8VC97
ENSMUST00000039926	ENSMUSG00000037887	7	142079490	142095843	-1	27	25	117	328	39	22	2	4	0	1	6		O09112
ENSMUST00000039928	ENSMUSG00000060716	12	79029163	79081648	1	50	42	98	131	97	39	0	0	1	0	3		Q80TI1
ENSMUST00000039939						0	7	33	67	18	6	284	216	226	68	125		
ENSMUST00000039949	ENSMUSG00000039055	11	94644996	94653964	-1	19	15	24	41	18	11	15	30	6	20	19		Q8BJW7
ENSMUST00000039956	ENSMUSG00000034591	10	83230848	83337882	-1	63	61	699	135	78	42	10	16	11	25	58	B2RQZ3	Q8BYR8
ENSMUST00000039959	ENSMUSG00000036027	9	51289686	51328917	-1	5	7	9	12	12	3	0	0	0	0	4		Q9D8Q6
ENSMUST00000039961	ENSMUSG00000032680	2	152415587	152444330	1	8	0	23	7	8	7	0	0	0	1	0	Q8BJX2	
ENSMUST00000039978	ENSMUSG00000027361	2	126627442	126676337	-1	2	0	30	7	7	3	12	12	19	3	18	Q3UT69	
ENSMUST00000039987	ENSMUSG00000041272	4	6686353	6991557	-1	9	6	50	35	16	5	4	8	3	1	18		Q66JW3
ENSMUST00000039990	ENSMUSG00000038168	16	25959288	26105784	-1	43	20	236	181	31	24	1	1	0	2	2		Q8CG71
ENSMUST00000039991	ENSMUSG00000037344	5	137314558	137333597	-1	21	13	101	130	35	13	1096	2158	1188	124	1205		Q99MR3
ENSMUST00000039994	ENSMUSG00000038241	2	155956458	155998900	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5A8	
ENSMUST00000039998	ENSMUSG00000037463	7	28692849	28699338	1	0	9	7	42	0	0	3	0	2	2	3		Q6DIA9
ENSMUST00000040001	ENSMUSG00000033316	5	110544355	110621380	1	7	14	21	117	14	8	0	0	0	0	0	G3X942	
ENSMUST00000040002	ENSMUSG00000037086	X	45090904	45092791	1	3	2	6	8	1	2	0	0	0	0	0		A2AFE9
ENSMUST00000040005	ENSMUSG00000040174	2	93980550	94010807	-1	0	0	0	0	0	0	79	155	56	118	76		Q8K1E6
ENSMUST00000040008	ENSMUSG00000036241	4	41135743	41193380	1	21	9	40	119	33	12	500	2521	821	224	545		Q6ZWZ2
ENSMUST00000040010	ENSMUSG00000031167	X	8138975	8145880	-1	11	9	7	0	25	13	23	120	55	0	44	Q8BG13	
ENSMUST00000040017	ENSMUSG00000042447	6	8209222	8236274	1	10	10	8	74	16	5	68	352	139	32	85		Q8VE19
ENSMUST00000040019	ENSMUSG00000033006	15	79154913	79164490	-1	21	21	66	342	63	27	0	1	0	0	0		Q04888
ENSMUST00000040021	ENSMUSG00000036057	9	110385082	110408213	-1	61	30	122	216	77	41	675	735	579	31	784		Q6PB44
ENSMUST00000040023	ENSMUSG00000041025	4	139530548	139620382	1	31	12	169	0	5	0	22	41	0	3	4	B1AZL1	
ENSMUST00000040025	ENSMUSG00000052698	9	67217087	67559703	-1	86	101	169	147	121	63	12	15	33	6	36	E9PUM4	
ENSMUST00000040042	ENSMUSG00000015083	2	25498651	25501719	-1	7	0	9	2	3	1	1	8	0	0	2		Q8VCG4
ENSMUST00000040043	ENSMUSG00000040021	10	7681209	7716458	1	2	0	0	0	0	1	75	0	285	0	208		Q8BYR2
ENSMUST00000040056	ENSMUSG00000036528	7	107595051	107748582	1	9	11	21	89	19	14	4	40	6	6	31	G3X957	
ENSMUST00000040059	ENSMUSG00000036091	9	107580818	107587359	1	93	95	270	87	88	37	6	12	8	1	19		Q8VEI3
ENSMUST00000040065	ENSMUSG00000033777	X	106143204	106160493	1	17	12	36	22	15	6	3423	13565	7091	7418	4043		Q6R5N8
ENSMUST00000040069	ENSMUSG00000036103	18	9707648	9877995	1	368	374	434	363	400	183	97	678	141	221	412		Q8K4Q8
ENSMUST00000040077	ENSMUSG00000033020	15	79141351	79151774	1	8	6	5	32	11	5	184	237	105	447	122		P61219
ENSMUST00000040081	ENSMUSG00000035504	10	80329953	80336441	1	0	12	11	3	0	0	0	0	0	0	0	D3Z6V2	
ENSMUST00000040084	ENSMUSG00000041700	X	145290359	145349089	-1	7	2	8	1	9	2	0	0	0	0	0		Q8QSV1
ENSMUST00000040089	ENSMUSG00000034177	11	87662722	87735539	1	15	0	32	22	0	7	0	10	0	2	3	A3KMI3	Q5NCP0
ENSMUST00000040090	ENSMUSG00000035142	12	52097737	52312744	1	5	13	8	68	10	3	53	340	82	37	43		Q9CWD8
ENSMUST00000040097	ENSMUSG00000033377	3	116918258	116968987	-1	9	7	59	13	12	4	1	9	2	12	4		
ENSMUST00000040104	ENSMUSG00000038193	8	57320983	57324517	1	6	7	20	181	11	6	0	0	0	0	1		Q61039
ENSMUST00000040105	ENSMUSG00000033444	10	75212073	75312399	1	50	44	70	12	63	29	177	317	242	53	233		
ENSMUST00000040106	ENSMUSG00000034334	13	92449622	92484031	-1	8	5	6	6	9	12	30	114	47	117	45	D3YUE4	
ENSMUST00000040110	ENSMUSG00000034612	10	82985498	83195900	1	35	13	58	215	37	19	964	2612	1816	114	1374	B9EHC3	Q9JME2
ENSMUST00000040111	ENSMUSG00000033209	5	110879803	111289780	1	0	0	0	117	37	21	0	0	0	0	0	A0A0A0MQN9	
ENSMUST00000040112	ENSMUSG00000037469	7	28607634	28631332	-1	22	21	26	36	21	8	0	0	0	0	0	B2RRA7	
ENSMUST00000040117	ENSMUSG00000035139	13	51651697	51684044	1	12	7	53	101	22	3	127	423	258	38	273	Q3U1C4	
ENSMUST00000040128	ENSMUSG00000060131	2	126320973	126500674	-1	53	49	495	73	55	28	1158	5301	2689	711	1515	A2ANX3	
ENSMUST00000040131	ENSMUSG00000036461	14	79481194	79582476	1	24	0	12	111	36	12	33	166	105	23	164	Q3V1H4	Q60775
ENSMUST00000040134	ENSMUSG00000040138	X	16885521	16911774	-1	33	23	69	1068	68	28	0	0	0	0	3		P48744
ENSMUST00000040135	ENSMUSG00000040034	10	7667503	7678881	1	3	4	2	8	1	3	9	58	9	129	28		P59235
ENSMUST00000040147	ENSMUSG00000038214	10	43479140	43515396	1	43	45	96	97	85	33	23	12	14	4	34		Q6PAL0
ENSMUST00000040148	ENSMUSG00000037325	3	36573142	36613477	-1	0	7	21	0	0	6	4	11	0	0	8		Q8K2G4
ENSMUST00000040149	ENSMUSG00000060131	2	126320973	126500674	-1	2	0	0	0	0	2	90	42	501	65	187	A2ANX3	
ENSMUST00000040151	ENSMUSG00000036185	17	35025959	35028016	-1	0	0	0	0	0	1	8	16	2	0	7		Q9CY86
ENSMUST00000040153	ENSMUSG00000036192	19	18930605	19111196	-1	71	111	321	0	47	85	7	13	6	0	11		Q8R1B8
ENSMUST00000040154	ENSMUSG00000041697	5	115345642	115348981	-1	6	4	10	65	0	0	1750	2559	1074	656	786	Q9DCW5	
ENSMUST00000040159	ENSMUSG00000042460	6	7844842	7875687	1	2	5	5	45	6	2	247	614	562	80	203		Q9JJ06
ENSMUST00000040161	ENSMUSG00000035148	12	52023003	52028063	-1	10	5	7	8	3	5	0	0	0	0	2	D8VER2	O88416
ENSMUST00000040162	ENSMUSG00000038259	2	155941023	155945367	-1	19	11	25	33	27	7	0	0	0	0	0		P43027
ENSMUST00000040166	ENSMUSG00000038578	4	59314683	59438633	-1	24	21	0	87	20	10	365	607	613	43	292	E9Q3H4	
ENSMUST00000040167	ENSMUSG00000042032	11	40679314	40695203	-1	0	0	0	86	6	0	496	1228	185	137	292		Q99LB6
ENSMUST00000040177	ENSMUSG00000036214	17	36958592	36965622	1	10	8	104	29	18	0	1	16	7	46	12		
ENSMUST00000040179	ENSMUSG00000012609	12	85824659	86061893	1	0	0	0	0	9	0	12	8	27	0	27		Q8CHB8
ENSMUST00000040182	ENSMUSG00000032740	11	29373658	29510808	1	11	11	16	77	19	9	47	115	94	30	143		Q5SNZ0
ENSMUST00000040184	ENSMUSG00000041710	X	144381671	144688180	-1	26	10	45	34	25	23	0	0	0	0	0	Q2KHN9	Q9QX29
ENSMUST00000040188	ENSMUSG00000036223	18	74195299	74207818	-1	0	0	33	57	21	0	32	58	42	8	15		
ENSMUST00000040202	ENSMUSG00000032637	7	126491708	126503437	-1	6	8	0	340	18	9	369	977	1136	82	885		Q7TQH0
ENSMUST00000040210	ENSMUSG00000036251	1	88277661	88389293	1	14	30	39	10	38	15	0	0	0	0	0		Q8R4D5
ENSMUST00000040213	ENSMUSG00000056310	5	130255619	130341563	1	18	8	27	29	17	12	119	114	125	48	102		Q8BJM7
ENSMUST00000040217	ENSMUSG00000036244	9	58359804	58370369	-1	14	7	11	13	16	6	0	0	0	0	0	Q9D9D3	
ENSMUST00000040218	ENSMUSG00000038206	8	56551090	56592393	1	0	6	8	0	10	6	48	181	72	176	31		Q9QZN3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000040219	ENSMUSG00000039089	10	26274468	26375185	-1	12	0	0	0	23	0	237	485	93	0	27		Q8BLB7
ENSMUST00000040222	ENSMUSG00000040860	4	141016637	141060550	-1	11	0	9	168	11	8	0	0	0	2	0		Q8CJ40
ENSMUST00000040227	ENSMUSG00000038973	7	43440782	43443334	1	2	4	18	11	9	5	0	5	0	0	0	A1A539	Q9D9H2
ENSMUST00000040231	ENSMUSG00000022510	16	25683763	25892102	1	1	1	1	0	0	4	0	0	0	0	0		O88898
ENSMUST00000040234	ENSMUSG00000042389	6	115544664	115578628	1	7	7	23	18	29	14	6	21	0	8	19		Q6P7W5
ENSMUST00000040241	ENSMUSG00000033658	8	111003188	111031751	-1	40	32	83	119	40	21	47	158	73	15	97	Q8R3C7	
ENSMUST00000040248	ENSMUSG00000041974	16	15889227	16146851	-1	14	10	16	39	15	10	274	1203	508	346	490		Q8BGX7
ENSMUST00000040250	ENSMUSG00000039783	1	175620381	175662116	1	2	2	6	0	0	1	1	79	6	39	23		Q91WN4
ENSMUST00000040254	ENSMUSG00000036270	8	105880881	105894908	1	27	23	46	129	52	8	541	864	639	78	742	G5E896	
ENSMUST00000040259	ENSMUSG00000038600	6	38048483	38124586	-1	0	4	0	0	0	0	0	0	0	0	0		Q920R6
ENSMUST00000040260	ENSMUSG00000033386	3	116859464	116908177	1	18	18	25	20	24	9	159	419	260	44	172	A0A0G2JFP4	
ENSMUST00000040261	ENSMUSG00000036278	19	7056768	7198061	1	4	6	9	106	16	12	21	23	19	4	20		Q922B1
ENSMUST00000040270	ENSMUSG00000025228	19	46376814	46395735	-1	30	17	57	35	41	18	3004	3777	2766	756	1839		P61164
ENSMUST00000040271	ENSMUSG00000037443	4	134129858	134187112	-1	0	14	0	44	29	13	31	0	0	0	53		Q8BMK0
ENSMUST00000040273	ENSMUSG00000012609	12	85824659	86061893	1	0	0	0	0	0	0	24	0	4	0	0	E9Q425	
ENSMUST00000040274	ENSMUSG00000041954	4	156026164	156028895	1	0	0	0	0	0	0	3	0	7	1	0		O35714
ENSMUST00000040275	ENSMUSG00000038248	10	43002500	43174530	-1	33	21	162	734	50	28	0	0	2	0	3		Q0P5V2
ENSMUST00000040280	ENSMUSG00000046329	17	57043711	57059863	-1	23	25	141	74	34	24	41	48	33	6	48		Q6GQS1
ENSMUST00000040284	ENSMUSG00000036299	18	75005900	75009933	1	7	5	9	115	21	3	683	1797	514	1882	391		Q91WE4
ENSMUST00000040298	ENSMUSG00000040713	1	165763746	165775308	1	1	0	0	0	1	0	159	681	124	126	112	K4DI63	
ENSMUST00000040307	ENSMUSG00000040502	10	127055011	127060184	-1	12	9	29	83	24	5	14	4	5	3	5		Q3TZ87
ENSMUST00000040308	ENSMUSG00000042594	5	121815488	121837646	-1	0	0	0	0	0	0	0	0	0	0	0		O09039
ENSMUST00000040309	ENSMUSG00000035578	16	33015385	33056218	-1	1	1	0	4	3	0	1	0	1	1	0	F8WHQ8	
ENSMUST00000040311	ENSMUSG00000042581	1	129273302	130219278	1	10	13	14	2	5	4	0	0	0	0	0	Q8BHP3	
ENSMUST00000040312	ENSMUSG00000032715	2	152337422	152344032	-1	14	12	16	107	59	18	77	73	53	11	33		Q8K4K2
ENSMUST00000040313	ENSMUSG00000037525	15	99470084	99474730	-1	10	4	28	85	12	5	57	144	71	20	32		Q91YP1
ENSMUST00000040314	ENSMUSG00000037197	2	11585437	11604153	-1	4	6	9	38	14	13	375	1209	577	174	468		Q8JZX4
ENSMUST00000040320	ENSMUSG00000033039	15	79108972	79136897	1	63	41	208	217	95	33	644	961	810	90	884		Q8BGT6
ENSMUST00000040321	ENSMUSG00000004127	3	138143448	138159821	1	51	60	104	31	4	0	10	82	31	31	23		
ENSMUST00000040324	ENSMUSG00000035829	2	28446800	28455508	1	31	19	73	85	36	46	0	1	1	1	4		Q6A025
ENSMUST00000040325	ENSMUSG00000056476	3	59005825	59318682	1	0	0	0	40	0	0	465	1470	939	139	658		Q8BQM9
ENSMUST00000040330	ENSMUSG00000038215	8	56531522	56551047	-1	0	0	2	3	0	0	20	141	2	40	39		Q5HZK1
ENSMUST00000040336	ENSMUSG00000038267	13	34179158	34345182	-1	14	0	0	104	11	5	0	0	2	9	14		Q3UHH2
ENSMUST00000040338						1	0	0	0	2	0	0	0	1	0	1		
ENSMUST00000040340	ENSMUSG00000041685	13	98723407	98815449	-1	5	4	7	5	8	4	856	1489	1236	454	1032		Q3UQN2
ENSMUST00000040344	ENSMUSG00000034707	10	121365090	121397245	1	23	16	38	46	43	27	1692	2634	2033	329	1778		Q8BFR4
ENSMUST00000040357	ENSMUSG00000040723	1	165646516	165709757	-1	2	4	0	25	0	3	6980	12786	8372	1087	6397		Q3UZA1
ENSMUST00000040359	ENSMUSG00000036412	18	60911780	60918561	1	26	18	55	171	45	14	1	2	0	0	2		Q32KI9
ENSMUST00000040361	ENSMUSG00000039347	6	48537615	48541801	1	14	11	24	86	26	3	19	25	9	4	22		Q91XE7
ENSMUST00000040368	ENSMUSG00000036368	17	79614900	79682152	1	3	7	13	24	13	5	9	23	8	7	8		Q8BSE0
ENSMUST00000040372	ENSMUSG00000036372	19	10204014	10207824	1	0	0	0	0	0	0	264	375	130	1283	141	Q60FD1	P61166
ENSMUST00000040374	ENSMUSG00000032671	2	104122769	104124749	1	4	4	4	252	9	7	0	0	0	0	0		Q9D1Z2
ENSMUST00000040380	ENSMUSG00000040430	11	107207892	107470699	-1	0	6	30	1	8	3	17	308	14	12	7	A0A0A0MQ88	
ENSMUST00000040381	ENSMUSG00000039804	2	165000357	165034867	-1	0	0	22	39	0	0	239	241	124	31	44		Q91W39
ENSMUST00000040383	ENSMUSG00000036686	8	84132828	84147936	-1	0	16	51	60	22	6	618	493	515	42	419		Q8K1A6
ENSMUST00000040398	ENSMUSG00000036395	9	26763044	26806468	-1	9	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000040402	ENSMUSG00000036398	17	36948356	36951741	-1	11	5	13	21	15	6	341	476	244	497	140	A5A4Y9	
ENSMUST00000040404	ENSMUSG00000034634	15	74762056	74763620	-1	9	3	9	7	15	3	2	0	0	17	7		P35459
ENSMUST00000040411	ENSMUSG00000089687	4	132302197	132303385	-1	7	5	14	89	14	4	0	0	0	0	0	Q0PD08	
ENSMUST00000040413	ENSMUSG00000030617	7	90223878	90265432	-1	3	6	3	2	7	9	0	0	0	0	0		Q9D4V3
ENSMUST00000040416	ENSMUSG00000015023	8	110974996	110997800	-1	9	15	6	77	18	14	249	588	389	69	297		Q61655
ENSMUST00000040418	ENSMUSG00000039084	11	94565047	94569127	1	15	11	24	16	29	11	1	0	0	0	4	Q3TYW1	O55226
ENSMUST00000040421	ENSMUSG00000041733	5	115279666	115296972	1	12	4	44	124	13	6	50	172	101	41	118		Q9CXI0
ENSMUST00000040423	ENSMUSG00000032679	2	104095801	104115354	1	0	37	52	81	38	20	2	2	2	25	8	A2BI31	O55186
ENSMUST00000040427						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000040428	ENSMUSG00000093989	11	70238124	70239842	-1	3	0	26	23	3	3	1662	1835	995	208	681		Q8K3C0
ENSMUST00000040429	ENSMUSG00000040455	4	21767156	21837872	1	0	2	0	0	1	0	69	127	0	31	95		Q8K387
ENSMUST00000040430	ENSMUSG00000034993	11	101458745	101466230	-1	9	7	32	170	25	11	388	244	196	165	416	Q499X4	Q62465
ENSMUST00000040434	ENSMUSG00000036430	17	46890621	46892463	1	11	5	33	305	24	6	254	432	190	100	138		
ENSMUST00000040437	ENSMUSG00000037167	X	21068406	21077963	1	0	1	4	2	2	1	0	0	0	0	0	A0A077S1H9	A2AE20
ENSMUST00000040440	ENSMUSG00000036438	17	87433412	87446935	-1	0	7	14	86	4	0	2078	7422	1713	4667	1100		P62204
ENSMUST00000040442	ENSMUSG00000038242	1	58210397	58268597	1	34	20	32	9	28	12	0	0	0	1	0		Q3TYQ9
ENSMUST00000040443						4	0	10	0	9	2	2	9	5	3	12		
ENSMUST00000040445	ENSMUSG00000036442	8	105855103	105856950	1	15	5	39	365	16	7	885	1577	724	246	486		Q9JJD0
ENSMUST00000040448	ENSMUSG00000034354	11	4480868	4594863	-1	17	5	0	23	0	0	1190	1115	1208	112	975	B1ATD5	
ENSMUST00000040454	ENSMUSG00000035759	10	111298679	111301736	1	11	15	11	74	20	10	6	24	8	6	10		Q9DBI2
ENSMUST00000040455	ENSMUSG00000036450	19	44562850	44576274	1	44	29	109	64	62	22	1285	1715	1420	111	892		Q8BLR9
ENSMUST00000040461	ENSMUSG00000034258	12	85746539	85813585	1	31	29	65	78	47	17	0	1	0	0	2		
ENSMUST00000040465	ENSMUSG00000036960	3	145070263	145099443	-1	16	12	18	24	14	10	0	0	0	1	0		Q8BG22
ENSMUST00000040467	ENSMUSG00000073402	17	36164443	36168537	-1	15	12	10	31	0	7	0	0	0	0	0	A7VMS6	
ENSMUST00000040468	ENSMUSG00000038225	8	46575579	46617212	-1	9	5	4	15	5	8	101	654	220	118	126		Q6P1E7
ENSMUST00000040474	ENSMUSG00000036473	17	24175431	24209387	-1	0	0	14	0	0	0	90	0	32	0	0		Q3UUG6
ENSMUST00000040477	ENSMUSG00000035946	5	75075601	75077893	1	0	0	0	50	0	0	0	0	0	0	0		P31316
ENSMUST00000040481	ENSMUSG00000036534	8	95835920	95853539	-1	17	9	31	78	27	9	288	287	202	52	133		Q8BWH0
ENSMUST00000040484	ENSMUSG00000034424	8	116981810	116993537	-1	17	16	17	118	32	21	35	103	26	54	55		Q91WK5
ENSMUST00000040486						14	8	49	15	8	11	0	0	0	0	0		
ENSMUST00000040487	ENSMUSG00000039096	11	94539798	94549255	-1	0	60	134	0	107	37	2	10	13	1	11		Q5SUV1
ENSMUST00000040489	ENSMUSG00000024727	19	18749983	18892510	1	45	49	69	51	60	26	3	34	12	17	45		Q8CIR4
ENSMUST00000040496	ENSMUSG00000032726	4	123312645	123343252	-1	15	16	34	413	45	11	4	4	14	0	8	Q80VZ0	P34821
ENSMUST00000040498	ENSMUSG00000036492	17	36942918	36947986	1	9	5	5	294	23	10	0	0	0	0	0	A2RT81	
ENSMUST00000040500	ENSMUSG00000036095	12	37880705	38633410	1	15	13	16	6	18	4	0	0	0	0	0		Q6NS52
ENSMUST00000040504	ENSMUSG00000025597	X	114474333	114560829	1	0	0	0	0	0	0	0	0	0	0	0	B1AZR0	
ENSMUST00000040506	ENSMUSG00000036501	18	34442352	34506823	-1	7	6	11	141	18	5	349	1607	925	115	654		Q8K2H3
ENSMUST00000040514	ENSMUSG00000038894	8	10986980	11008458	-1	39	14	52	843	60	13	275	328	535	29	521		P81122

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000040518	ENSMUSG00000033047	15	79075223	79094400	1	17	13	13	33	20	3	689	1353	778	1549	818		Q8QZY1
ENSMUST00000040519	ENSMUSG00000037787	12	111713261	111754980	1	21	21	28	63	33	27	35	206	91	120	65		Q9CQW7
ENSMUST00000040522	ENSMUSG00000042436	11	61485431	61488900	1	3	0	10	13	8	4	0	0	1	0	0		Q9D1H9
ENSMUST00000040523	ENSMUSG00000036545	11	50602084	50807573	1	211	182	239	490	227	152	18	82	31	15	44		Q8C9W3
ENSMUST00000040531	ENSMUSG00000030602	7	28399549	28598185	-1	28	17	59	94	45	28	869	1275	1096	61	1118	G5E8A7	
ENSMUST00000040532	ENSMUSG00000037822	5	65446844	65537184	-1	0	0	0	0	0	0	272	383	320	402	241	F8WHW8	
ENSMUST00000040536	ENSMUSG00000034266	12	85686669	85709087	1	4	4	26	22	6	9	444	1128	475	1038	385		O35284
ENSMUST00000040538	ENSMUSG00000038936	1	179668210	179687189	1	0	9	0	0	0	1	0	21	0	25	0		Q8R127
ENSMUST00000040548	ENSMUSG00000036634	7	30899176	30914873	-1	6	0	29	9	0	0	43	60	41	14	17		P20917
ENSMUST00000040555	ENSMUSG00000041740	5	115241412	115272898	-1	0	0	0	148	0	4	1185	994	1000	120	973	H7BX06	
ENSMUST00000040560	ENSMUSG00000040521	10	127011572	127030840	-1	0	1	2	52	1	3	20	35	16	11	7		Q9CZR8
ENSMUST00000040561	ENSMUSG00000035007	11	101425085	101435673	1	21	22	23	228	42	21	303	491	352	76	266		Q0VDN7
ENSMUST00000040562	ENSMUSG00000022321	15	18818947	19014236	1	4	3	0	6	4	5	0	0	0	0	0		P70408
ENSMUST00000040572	ENSMUSG00000039810	10	128541963	128547774	-1	30	33	81	157	45	28	414	839	349	70	334		Q8R205
ENSMUST00000040574						0	0	0	0	11	2	0	0	0	0	0		
ENSMUST00000040576	ENSMUSG00000034981	5	91517615	91626894	1	40	30	153	101	50	21	1	0	2	0	2		Q923D3
ENSMUST00000040577	ENSMUSG00000038046	11	76243715	76250619	1	0	3	8	37	5	4	13	12	8	14	13		Q5ND52
ENSMUST00000040580	ENSMUSG00000032714	10	78584503	78591964	-1	31	29	114	167	51	13	5	0	0	5	13	G3X960	
ENSMUST00000040583	ENSMUSG00000035181	12	51875873	51971321	-1	54	43	94	93	39	23	339	475	652	70	463		Q5PRF0
ENSMUST00000040592	ENSMUSG00000033501	16	22805203	22811410	-1	6	4	13	2	13	3	0	0	0	0	0	Q3UPY3	O35486
ENSMUST00000040594	ENSMUSG00000036552	17	14978864	15064232	1	10	5	11	8	7	8	4	30	13	0	36	Q3TVE4	
ENSMUST00000040599	ENSMUSG00000009418	1	135434580	135607295	-1	66	8	240	0	109	4	29	96	19	17	126		Q8CH77
ENSMUST00000040603	ENSMUSG00000033400	3	116739999	116808166	-1	96	95	143	316	138	68	55	193	62	28	90	F8VPN4	
ENSMUST00000040607	ENSMUSG00000034192	6	91515928	91522625	1	4	3	5	13	1	5	118	430	125	613	94		P62311
ENSMUST00000040609	ENSMUSG00000036557	17	87389571	87427741	-1	7	0	13	34	8	3	0	0	0	0	0		Q9DAG5
ENSMUST00000040616	ENSMUSG00000034110	5	130144861	130155806	1	28	19	48	40	23	12	72	103	82	9	36		Q8BJK1
ENSMUST00000040622	ENSMUSG00000036362	3	59207892	59210882	-1	9	5	34	13	24	11	1028	4412	2150	3288	1342		Q9D8I2
ENSMUST00000040624	ENSMUSG00000036568	17	46798116	46831413	-1	37	28	107	114	63	34	565	781	948	57	707	B2RX81	Q8CHH5
ENSMUST00000040628	ENSMUSG00000054737	X	21028939	21062316	-1	3	5	3	4	1	1	15	227	86	34	83	A2AE18	
ENSMUST00000040636	ENSMUSG00000040364	7	45677689	45694402	-1	20	11	42	103	34	10	0	0	0	0	3	Q8CDC9	
ENSMUST00000040638	ENSMUSG00000038718	2	34171457	34373142	-1	8	0	0	8	0	0	13	1	27	30	35		O35317
ENSMUST00000040647	ENSMUSG00000036585	18	38838673	38929404	-1	7	8	22	15	17	3	0	0	1	4	5	Q6ZWS1	P61148
ENSMUST00000040649						4	5	17	6	2	5	0	0	0	0	0		
ENSMUST00000040655	ENSMUSG00000036594	17	34282744	34287827	-1	0	0	0	6	7	5	364	218	182	1640	1070		P14434
ENSMUST00000040656	ENSMUSG00000038286	13	34037641	34074074	1	9	12	4	47	3	3	30	90	30	27	36		Q8R164
ENSMUST00000040667	ENSMUSG00000031079	X	21079174	21089527	-1	605	558	1687	507	817	381	9	17	21	7	23	A2AE21	
ENSMUST00000040668	ENSMUSG00000039050	2	180119306	180162680	1	10	5	15	17	7	9	1970	4367	2913	703	1616		Q8BX94
ENSMUST00000040676	ENSMUSG00000033055	15	79053094	79062893	-1	6	0	7	5	0	0	216	179	136	20	90	A7YB12	Q91WK7
ENSMUST00000040677	ENSMUSG00000036611	9	25481547	25604110	1	20	16	35	133	35	16	536	826	574	112	420		Q3TGW2
ENSMUST00000040687	ENSMUSG00000040158	11	73177083	73183162	1	5	3	2	74	0	4	182	344	230	55	164		Q9DBG9
ENSMUST00000040689	ENSMUSG00000033124	1	75180860	75192196	-1	0	0	0	0	0	0	962	1311	771	111	275	Q3ZAQ4	
ENSMUST00000040692	ENSMUSG00000039110	11	94501347	94521742	-1	0	3	6	5	2	2	0	0	0	0	0		Q5SUV2
ENSMUST00000040695	ENSMUSG00000032719	1	15853862	15892722	-1	11	8	21	64	14	7	4	5	3	0	2		Q3UPR9
ENSMUST00000040700	ENSMUSG00000025558	14	121542039	121797734	-1	28	26	41	10	39	11	415	674	975	70	601	F8VPN7	
ENSMUST00000040703	ENSMUSG00000034427	11	115858406	115892603	1	0	5	30	59	18	7	0	1	0	0	2	F6V1P1	
ENSMUST00000040706	ENSMUSG00000038949	1	179546370	179627478	1	24	28	60	114	32	30	290	743	470	69	454		Q8CBC4
ENSMUST00000040711	ENSMUSG00000049134	19	56320035	56390037	-1	3	0	0	0	0	0	0	0	0	0	0		Q80XB4
ENSMUST00000040715	ENSMUSG00000042485	14	30879257	30881608	1	6	6	21	12	12	9	617	685	516	565	128		Q99JI1
ENSMUST00000040717	ENSMUSG00000036768	9	122951081	123018725	1	31	26	102	70	28	14	97	205	208	67	74		Q6P9L6
ENSMUST00000040718	ENSMUSG00000038280	10	42583822	42702459	1	8	11	16	90	9	3	476	2158	925	504	540		Q8BGT0
ENSMUST00000040721	ENSMUSG00000034118	5	130073326	130135729	1	0	0	0	60	9	10	0	4	0	0	11	Q4FK50	O70281
ENSMUST00000040729	ENSMUSG00000036636	17	25133391	25162104	1	7	0	0	63	32	0	537	642	808	89	478	Q6RUT9	O70496
ENSMUST00000040735	ENSMUSG00000036820	17	24155833	24163766	-1	10	6	13	20	8	0	921	851	462	100	336		Q8JZV7
ENSMUST00000040746	ENSMUSG00000079707	17	15027157	15041559	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000040750	ENSMUSG00000034394	11	4257557	4272514	1	47	33	73	0	3	0	10	18	10	0	59	F8WH42	
ENSMUST00000040751	ENSMUSG00000038077	6	126708329	126740674	-1	44	17	35	0	48	16	0	0	1	0	0		Q61923
ENSMUST00000040766	ENSMUSG00000021248	12	85340614	85374717	-1	20	18	47	149	30	15	2230	5527	2803	625	2009		Q9D1D4
ENSMUST00000040772	ENSMUSG00000024965	19	6998958	7019469	-1	22	13	63	42	30	27	7385	8464	7263	798	4382	Q3TEE6	Q8K1B8
ENSMUST00000040776	ENSMUSG00000036672	8	105844678	105852008	-1	13	2	25	45	17	6	126	189	122	14	96		Q3TJM4
ENSMUST00000040783	ENSMUSG00000005501	1	87945119	88008551	-1	0	0	0	25	0	6	23	164	105	20	63		Q8BWR4
ENSMUST00000040787	ENSMUSG00000039988	3	157947239	158008034	1	8	4	6	6	3	2	163	511	225	40	157		Q3UX43
ENSMUST00000040789	ENSMUSG00000024084	17	79051906	79090243	1	20	15	32	353	26	16	2	8	1	16	1		
ENSMUST00000040790	ENSMUSG00000039738	16	3979105	4003770	-1	0	0	0	0	0	2	32	0	46	0	37		Q6P1D7
ENSMUST00000040791	ENSMUSG00000038879	15	34572799	34678706	-1	20	17	13	40	17	16	0	0	0	0	0		
ENSMUST00000040802	ENSMUSG00000071262	14	79212353	79247369	-1	14	13	10	20	18	11	0	0	0	0	0	Q3UT76	
ENSMUST00000040806	ENSMUSG00000038057	11	76217608	76218666	1	1	1	8	14	3	0	0	1	0	0	0	Q545L5	O09035
ENSMUST00000040820	ENSMUSG00000040147	X	16709282	16817366	-1	5	3	5	6	5	0	2	8	0	0	0		Q8BW75
ENSMUST00000040821	ENSMUSG00000032744	4	123233556	123249875	1	34	33	53	124	41	27	2	2	1	0	0		Q9DBX7
ENSMUST00000040824	ENSMUSG00000042737	3	89259358	89267079	1	0	0	0	6	0	0	136	134	61	213	38		Q9D1Q4
ENSMUST00000040826	ENSMUSG00000042505	6	6956004	7042979	1	12	9	45	52	15	14	2	5	4	22	3	Q0VF92	Q8BQU3
ENSMUST00000040828	ENSMUSG00000073421	17	34263209	34269418	1	7	0	15	91	8	6	308	195	168	182	1141	Q3TD53	P14483
ENSMUST00000040833	ENSMUSG00000038312	2	155701677	155729475	-1	19	11	33	138	19	10	2943	5299	2528	341	1893	Q8BJT9	
ENSMUST00000040835	ENSMUSG00000034203	6	91462172	91473546	-1	8	10	28	35	11	5	50	92	41	91	55		Q8VEA4
ENSMUST00000040844	ENSMUSG00000034867	7	35586244	35639226	1	22	3	33	40	21	0	405	723	536	59	421		Q3UMR0
ENSMUST00000040846	ENSMUSG00000056476	3	59005825	59318682	1	0	0	0	13	5	1	0	0	0	0	0	H7BX07	Q8BQM9
ENSMUST00000040853	ENSMUSG00000036737	9	119238432	119322427	-1	9	6	32	69	18	9	376	1336	810	178	617		Q6P9R2
ENSMUST00000040856	ENSMUSG00000041255	2	113285732	113297190	1	1	3	11	6	7	6	0	0	0	0	0		Q80X59
ENSMUST00000040859	ENSMUSG00000036602	10	103007846	103029054	-1	0	0	8	0	0	0	0	0	0	0	0		Q8C8B0
ENSMUST00000040860	ENSMUSG00000036743	18	14706151	14762299	1	6	1	4	6	9	5	1	3	2	6	0		Q9CWH6
ENSMUST00000040863	ENSMUSG00000034683	2	79707780	79818496	1	0	0	0	0	2	0	0	0	0	0	0		Q8BKK4
ENSMUST00000040865	ENSMUSG00000035413	11	80810175	80822033	1	13	4	9	31	8	6	2	6	1	2	9		Q91X86
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ENSMUST00000040873	ENSMUSG00000037364	5	137295704	137307674	-1	28	21	43	134	43	21	545	1649	872	97	1092		Q99MR6
ENSMUST00000040876	ENSMUSG00000041323	12	105705982	105782447	1	21	12	8	65	22	12	0	7	2	2	3	F8WIC0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000040880	ENSMUSG00000041205	16	20233310	20241358	-1	20	5	34	108	19	10	5	8	9	2	21		Q14BB9
ENSMUST00000040881	ENSMUSG00000014232	16	3908801	3941147	1	8	8	9	68	17	4	90	430	192	152	140		Q8R3P7
ENSMUST00000040888	ENSMUSG00000042747	3	89245966	89249906	1	3	10	11	17	0	10	61	68	0	15	35		Q5RL79
ENSMUST00000040907	ENSMUSG00000036775	17	26081211	26090329	-1	181	195	312	145	191	65	14	61	21	15	43	Q3UVJ7	Q9WV68
ENSMUST00000040912	ENSMUSG00000036777	9	22331214	22389206	-1	21	17	87	71	26	15	109	188	215	268	264		Q8K298
ENSMUST00000040914	ENSMUSG00000036181	13	23738808	23740367	1	21	10	63	159	24	15	2003	5143	953	522	837	Q5SZA3	P15864
ENSMUST00000040915	ENSMUSG00000042133	2	69722545	69754012	1	18	18	0	173	25	13	69	537	213	394	331		A2AR02
ENSMUST00000040917	ENSMUSG00000036781	9	66946086	66949516	1	3	0	0	22	0	0	275	682	236	1416	190		Q6ZWY3
ENSMUST00000040924	ENSMUSG00000037013	18	14624198	14682914	-1	8	10	0	0	0	6	134	530	304	104	252		Q62280
ENSMUST00000040925	ENSMUSG00000028236	4	3995936	4019663	-1	1	2	9	18	1	1	0	0	0	0	0		Q7TQA3
ENSMUST00000040941	ENSMUSG00000037482	2	131853678	131859747	-1	26	14	57	343	29	22	0	1	4	0	0	Q9DAX3	
ENSMUST00000040944	ENSMUSG00000049685	7	26808892	26821205	1	13	12	16	13	10	6	0	0	0	0	0	Q9WV19	
ENSMUST00000040960	ENSMUSG00000036814	9	123636122	123678885	-1	10	10	29	58	16	13	0	0	0	0	1		Q8VDB9
ENSMUST00000040961	ENSMUSG00000034732	X	119927196	119930165	1	0	0	0	0	0	0	0	0	0	0	0	Q8C7D3	
ENSMUST00000040962	ENSMUSG00000034875	7	35547185	35556304	-1	14	4	35	334	28	7	22	59	32	69	27		P11930
ENSMUST00000040964	ENSMUSG00000037013	18	14624198	14682914	-1	3	8	8	7	6	0	0	10	0	3	0	Q8BKL1	
ENSMUST00000040967	ENSMUSG00000066278	5	124004641	124032270	-1	12	8	42	169	38	9	901	1115	737	118	725		Q8R0J7
ENSMUST00000040971	ENSMUSG00000035547	7	98121559	98178274	-1	27	13	58	95	57	22	8	15	7	12	53	Q3TPL4	O08688
ENSMUST00000040972	ENSMUSG00000041747	13	98246845	98262992	-1	32	21	54	49	23	14	52	193	84	49	96		Q8C7V3
ENSMUST00000040980						0	0	0	11	0	0	55	103	38	87	30		
ENSMUST00000040983	ENSMUSG00000036647	7	106955984	106956934	-1	4	9	3	5	8	3	0	0	0	0	0		
ENSMUST00000040986	ENSMUSG00000035629	16	32821703	32877766	-1	0	0	0	0	21	0	192	86	164	1	162		Q80U62
ENSMUST00000040987	ENSMUSG00000038641	6	37530173	37568815	1	17	14	16	23	14	8	1	8	2	1	3		Q8VCX1
ENSMUST00000040990	ENSMUSG00000058997	14	78849178	79202310	1	38	31	60	107	60	29	54	152	139	56	137		Q8CC88
ENSMUST00000040992	ENSMUSG00000034290	12	85299514	85339362	-1	32	29	83	221	61	19	1690	4752	3117	283	2316		Q8K1R7
ENSMUST00000040999	ENSMUSG00000064294	1	58113130	58200698	1	25	20	46	27	43	22	47	19	226	12	11		G3X982
ENSMUST00000041003	ENSMUSG00000036983	17	3519263	3557713	-1	8	7	13	36	3	3	12	36	10	25	14		Q8JZM0
ENSMUST00000041005	ENSMUSG00000059412	9	45403138	45410278	1	9	6	22	13	10	6	0	0	0	0	3	Q6ITT1	Q04646
ENSMUST00000041007	ENSMUSG00000036855	18	9278607	9282809	-1	45	25	46	46	50	38	0	1	0	0	0		Q8BSD4
ENSMUST00000041008	ENSMUSG00000033373	12	76765589	76921412	1	7	8	3	2	16	3	43	67	47	12	71		Q8K2I1
ENSMUST00000041010	ENSMUSG00000041375	7	16274042	16286795	-1	6	3	15	11	6	3	161	484	209	20	135	G3X927	
ENSMUST00000041011	ENSMUSG00000039098	10	26078255	26079447	1	3	4	2	164	7	0	0	0	0	0	0	G3X930	
ENSMUST00000041012	ENSMUSG00000036858	17	46755663	46763712	-1	40	31	67	32	39	20	1	11	6	2	0		
ENSMUST00000041022	ENSMUSG00000042766	3	89234177	89246309	-1	0	0	0	36	0	0	0	8	0	0	22		Q7TNM2
ENSMUST00000041023	ENSMUSG00000041879	1	135382312	135430499	-1	27	17	36	71	43	15	99	635	328	81	242	E9QKZ2	
ENSMUST00000041024	ENSMUSG00000038302	10	42312585	42478565	-1	0	0	4	71	11	6	18	31	10	7	21		Q3V384
ENSMUST00000041029	ENSMUSG00000036867	9	63953076	64022059	-1	16	7	20	772	32	17	5	5	3	1	2		O35182
ENSMUST00000041042	ENSMUSG00000034412	11	4186789	4215505	1	0	0	0	34	0	0	0	0	0	0	0	Q5SPX8	
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ENSMUST00000041047	ENSMUSG00000023845	17	17527723	17624489	-1	15	12	36	63	15	6	1667	1829	3054	255	1930		Q8C129
ENSMUST00000041048	ENSMUSG00000039747	5	136147459	136170713	-1	35	18	108	83	53	15	1982	2433	2191	331	1541	Q14BR6	Q8BH10
ENSMUST00000041052	ENSMUSG00000036211	13	23695814	23696542	1	7	1	13	6	8	3	0	0	0	0	0	I7HFT9	
ENSMUST00000041053	ENSMUSG00000036880	18	74779197	74806207	1	13	14	15	25	13	4	583	1022	570	466	479		Q8BWT1
ENSMUST00000041055	ENSMUSG00000041341	12	105613539	105685241	-1	84	59	254	285	99	51	204	491	555	43	434		Q80XK6
ENSMUST00000041059	ENSMUSG00000038324	2	155634271	155692384	-1	4	5	0	35	12	2	1705	2434	2766	259	1910	Q3TDP6	Q9JLV2
ENSMUST00000041065	ENSMUSG00000035441	11	80482126	80780025	-1	29	17	58	70	55	23	874	882	941	36	579		Q5SYD0
ENSMUST00000041080	ENSMUSG00000036904	18	9212856	9216201	1	16	12	19	465	21	12	2	1	1	0	2		Q61091
ENSMUST00000041093	ENSMUSG00000038648	6	37327255	37442146	-1	84	68	204	434	121	46	103	180	146	13	188		Q8BH52
ENSMUST00000041095	ENSMUSG00000078651	11	101325063	101329702	1	52	35	54	63	53	25	56	167	123	14	171		Q812C9
ENSMUST00000041096	ENSMUSG00000039278	X	7919822	7924410	1	3	1	9	96	7	6	0	0	0	0	0		Q9QXV0
ENSMUST00000041097	ENSMUSG00000041769	7	138846079	138883057	1	0	0	0	6	0	0	0	0	26	26	58		Q925E7
ENSMUST00000041099	ENSMUSG00000034701	2	79452521	79456751	-1	8	8	24	97	12	15	0	0	0	0	0		Q60867
ENSMUST00000041100	ENSMUSG00000039754	5	136136146	136141615	1	0	4	0	0	0	2	205	241	126	37	81		Q9D8F1
ENSMUST00000041105	ENSMUSG00000061186	2	10370510	10595253	1	0	0	0	0	0	25	11	0	16	0	21	Q3UH63	
ENSMUST00000041106	ENSMUSG00000036913	8	124793019	124834713	1	0	0	0	551	0	0	0	0	0	1	0		Q505D9
ENSMUST00000041110	ENSMUSG00000036918	17	87282886	87381769	1	0	0	0	33	0	0	10100	6634	7218	345	5871		Q8BGB2
ENSMUST00000041111	ENSMUSG00000042541	6	6557294	6578663	-1	1	3	6	38	7	6	2574	7593	3311	15945	1869	Q3TV35	P60897
ENSMUST00000041115	ENSMUSG00000070471	3	58616300	58637207	-1	15	14	16	51	20	14	0	0	0	0	0		D3Z6S9
ENSMUST00000041122	ENSMUSG00000042198	4	3938888	3951046	1	2	0	0	0	0	0	13	73	33	0	28		Q8K2Q5
ENSMUST00000041123	ENSMUSG00000035638	16	32777419	32797435	-1	8	6	103	30	18	0	64	51	51	4	20		Q8BUE7
ENSMUST00000041124	ENSMUSG00000040209	3	9427020	9610085	-1	74	71	134	265	96	37	11	30	40	4	50		Q9ERQ3
ENSMUST00000041126	ENSMUSG00000039086	2	180042509	180070201	1	49	40	173	267	56	21	42	183	79	7	82		Q8BW22
ENSMUST00000041133	ENSMUSG00000036136	12	31073968	31079937	1	19	14	27	106	19	9	34	51	72	10	22		Q8VE94
ENSMUST00000041138	ENSMUSG00000036941	18	73735038	73754479	-1	21	12	20	39	26	13	363	2013	900	147	703		Q8VEB6
ENSMUST00000041139	ENSMUSG00000036943	9	66843672	66919705	-1	79	44	252	369	74	50	2990	11585	5275	1744	3421	Q0PD49	P61028
ENSMUST00000041142	ENSMUSG00000042784	3	89229057	89233381	1	34	16	182	61	49	19	94	118	88	15	68		
ENSMUST00000041159						0	0	0	18	2	0	0	0	15	36	13		
ENSMUST00000041160	ENSMUSG00000038607	4	59035088	59041903	1	0	0	0	12	0	0	434	1067	440	1140	336		Q9CXP8
ENSMUST00000041162	ENSMUSG00000056912	10	100590511	100618401	1	5	0	0	0	0	0	0	0	0	0	0	D3YX67	
ENSMUST00000041163	ENSMUSG00000036961	19	44493472	44514273	1	18	14	37	195	32	9	1	0	0	0	1	Q8BQD1	
ENSMUST00000041164	ENSMUSG00000033099	15	78934933	78943634	1	0	0	0	0	0	0	95	126	83	293	68	F8WGP0	
ENSMUST00000041168	ENSMUSG00000039116	10	14402585	14545036	-1	40	29	59	79	35	15	4	7	8	25	79		Q6F3F9
ENSMUST00000041175	ENSMUSG00000040016	3	157566892	157645888	1	7	9	0	288	20	9	9	27	17	6	10	Q6PDF2	
ENSMUST00000041180	ENSMUSG00000037424	10	24108488	24109534	-1	7	7	19	9	9	4	0	0	0	0	0		Q5QD04
ENSMUST00000041183	ENSMUSG00000036144	12	37108540	37179534	1	20	7	40	106	16	1	0	0	2	0	0		P32443
ENSMUST00000041190	ENSMUSG00000037570	15	99242818	99251961	-1	4	0	29	58	24	16	953	624	598	129	533		Q99L90
ENSMUST00000041195	ENSMUSG00000039391	7	89866148	89903629	-1	0	0	0	0	5	9	0	1	0	0	0		Q9D5W4
ENSMUST00000041197	ENSMUSG00000040997	14	54254188	54270637	1	5	7	40	27	21	11	691	1904	689	125	978	Q3U7M5	
ENSMUST00000041203	ENSMUSG00000030270	6	113282307	113305627	1	0	0	0	13	0	0	0	1	0	1	0		
ENSMUST00000041208	ENSMUSG00000036678	15	102338247	102350759	-1	11	7	16	82	27	17	341	396	199	52	244		P58742
ENSMUST00000041213	ENSMUSG00000033159	1	75134554	75142711	-1	0	0	0	0	0	3	813	1823	1120	108	574		Q8K158
ENSMUST00000041218						17	16	24	3	25	11	3	3	0	3	0		
ENSMUST00000041226	ENSMUSG00000037390	5	137134922	137149322	-1	3	0	7	3	3	2	0	0	0	0	0	E9PWP7	
ENSMUST00000041229	ENSMUSG00000041347	12	105603085	105605428	1	7	13	6	0	6	7	0	0	0	0	4	Q0VBD7	Q61125

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000041231	ENSMUSG00000040850	11	30771726	30880361	1	18	17	23	92	18	9	508	2354	1292	154	677		Q5SSW2
ENSMUST00000041240	ENSMUSG00000041889	1	135371057	135375237	-1	7	0	2	103	15	11	0	0	0	0	5		Q8CA71
ENSMUST00000041252	ENSMUSG00000042647	5	121596775	121618938	-1	10	8	25	11	14	7	99	137	52	10	68	D3Z7X0	
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ENSMUST00000041264	ENSMUSG00000062931	10	82224850	82241280	-1	2	0	0	0	3	4	8	17	3	0	3	E9Q9G3	
ENSMUST00000041265	ENSMUSG00000034968	6	83086367	83088243	1	12	10	28	75	15	6	0	3	0	0	0		Q9WUN8
ENSMUST00000041266	ENSMUSG00000038552	5	31292242	31296080	-1	0	6	18	71	4	0	0	0	0	2	3	B9EI95	Q3TR08
ENSMUST00000041272	ENSMUSG00000034247	11	103364275	103412687	-1	84	47	180	300	127	55	2708	2708	2764	147	2054		Q7TSI1
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ENSMUST00000041284	ENSMUSG00000061859	4	98395785	98719603	1	0	0	0	46	0	0	0	0	4	0	11	A2ADL9	Q63ZW7
ENSMUST00000041297	ENSMUSG00000034333	15	88751660	88784516	1	68	68	47	137	91	36	297	856	596	62	326		Q80WQ9
ENSMUST00000041301	ENSMUSG00000038216	11	98386450	98388181	1	12	6	26	26	21	1	0	0	0	0	0	Q0VB50	P40935
ENSMUST00000041314	ENSMUSG00000037058	18	35598617	35617186	1	0	0	0	28	5	0	698	4707	1110	2143	662		Q9D6V8
ENSMUST00000041316	ENSMUSG00000041359	12	105216750	105222793	-1	0	0	0	0	4	6	0	0	0	0	0		P56280
ENSMUST00000041317	ENSMUSG00000042225	X	142851146	142966728	-1	17	9	34	108	22	8	121	240	181	16	94		Q9JHT5
ENSMUST00000041318	ENSMUSG00000036564	8	95676980	95715119	1	0	0	0	147	18	7	0	0	0	0	0		Q8BTG7
ENSMUST00000041331	ENSMUSG00000037071	19	44394451	44407709	-1	35	32	69	73	62	28	73	37	84	67	413	Q547C4	P13516
ENSMUST00000041342	ENSMUSG00000004113	2	24603887	24763152	-1	1	0	0	0	0	0	3	0	1	0	0		O55017
ENSMUST00000041353	ENSMUSG00000037089	17	45563964	45567669	1	11	10	35	426	26	13	508	383	219	127	192	Q3TJQ2	Q91ZN5
ENSMUST00000041357	ENSMUSG00000037095	17	56119680	56121946	-1	10	12	25	447	28	19	25880	52278	28143	2905	18824	Q91XL1	
ENSMUST00000041361	ENSMUSG00000039834	2	164891882	164911757	-1	30	0	56	0	55	0	878	1099	964	0	975		A2A5K6
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ENSMUST00000041366	ENSMUSG00000039771	5	136116631	136122947	1	2	0	0	40	5	0	329	539	281	846	175	Q6PI63	
ENSMUST00000041367	ENSMUSG00000037103	8	84097075	84104773	-1	21	8	59	50	22	15	536	743	436	66	556		Q6PFH3
ENSMUST00000041369	ENSMUSG00000037104	17	87107679	87137583	1	21	19	36	101	34	18	78	203	172	28	93		O54928
ENSMUST00000041370	ENSMUSG00000038344	X	162778919	162829454	-1	0	0	0	0	0	0	13	208	75	92	69		Q8BHN1
ENSMUST00000041374	ENSMUSG00000040520	4	26324506	26346891	-1	27	35	46	29	34	23	102	177	119	70	89		Q6NXH2
ENSMUST00000041375	ENSMUSG00000037112	9	50892801	51009073	-1	0	0	17	19	0	5	0	0	25	15	0	F8VPT7	
ENSMUST00000041377	ENSMUSG00000042228	4	3678115	3813122	1	0	16	25	62	0	11	4174	13678	7297	927	4124	Q3TCS3	P25911
ENSMUST00000041382	ENSMUSG00000033703	8	110882463	110902459	-1	36	22	91	161	60	27	194	277	154	31	135	Q7TMC8	
ENSMUST00000041385	ENSMUSG00000034255	11	103331497	103363692	-1	14	0	36	20	13	8	1500	2045	1668	86	1233		A2AB59
ENSMUST00000041388	ENSMUSG00000037411	5	137061504	137072268	-1	9	9	55	21	18	5	2	0	0	0	27	G5E899	
ENSMUST00000041389	ENSMUSG00000034339	18	42173370	42173663	1	2	0	1	0	0	0	0	0	0	0	0	F6Y2A6	
ENSMUST00000041391	ENSMUSG00000037126	19	46312087	46327156	-1	20	14	0	235	18	0	36	89	51	4	56		Q5DTT2
ENSMUST00000041392	ENSMUSG00000039555	4	51216678	51230272	1	0	0	0	0	0	3	0	0	0	0	0	B1AWN8	
ENSMUST00000041398	ENSMUSG00000037130	17	36812171	36815564	1	13	4	18	3	15	2	0	0	0	0	0	Q85ZW5	
ENSMUST00000041400	ENSMUSG00000037415	8	105768308	105827350	-1	40	24	102	141	56	27	495	988	854	85	700		
ENSMUST00000041401	ENSMUSG00000029804	6	58831465	58920398	1	13	16	49	13	23	9	103	239	167	30	141	A6H6S0	
ENSMUST00000041403	ENSMUSG00000035086	11	101285952	101302286	-1	0	0	0	0	0	0	917	3588	1274	461	980	E9QAM0	
ENSMUST00000041407	ENSMUSG00000036169	12	36314169	36318452	1	14	6	29	40	17	6	0	0	0	0	0		Q9CQN4
ENSMUST00000041413	ENSMUSG00000038925	14	24293214	24309966	1	0	0	0	0	12	9	0	0	0	0	0	Q3UWX6	
ENSMUST00000041415	ENSMUSG00000037579	15	99224976	99242817	1	37	25	82	251	57	27	0	4	0	1	2	B2RU85	
ENSMUST00000041416	ENSMUSG00000037440	10	23894688	23905343	1	15	5	8	5	5	3	0	0	0	1	0		Q9Z0K8
ENSMUST00000041418	ENSMUSG00000037286	9	100597798	100959375	1	0	0	0	0	0	0	139	462	154	61	40	F8WHU7	
ENSMUST00000041422	ENSMUSG00000029155	5	73651379	73679512	1	0	0	27	120	0	0	0	0	0	0	0	E9QAP8	
ENSMUST00000041425	ENSMUSG00000040037	3	156561794	157316445	1	3	7	4	35	10	8	0	0	0	0	0	A0A4W9	
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ENSMUST00000041447	ENSMUSG00000032769	1	14872648	14918862	-1	9	9	11	18	12	10	1	1	0	0	0		Q8BLA8
ENSMUST00000041459	ENSMUSG00000037190	9	107539007	107542193	-1	8	13	4	6	10	5	9	11	2	3	2		Q9WUE3
ENSMUST00000041460	ENSMUSG00000034825	7	109758055	109782025	-1	0	0	33	42	30	0	0	0	0	0	0	Q6GQT2	
ENSMUST00000041463	ENSMUSG00000037196	17	10403012	10840311	-1	7	7	12	33	19	6	1	0	0	5	1	Q0VB91	Q9DAK2
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ENSMUST00000041475	ENSMUSG00000048612	19	37899036	38043577	-1	15	14	21	26	28	18	122	388	203	135	695		Q69ZN7
ENSMUST00000041477	ENSMUSG00000037206	9	58156265	58159221	-1	26	25	13	22	28	8	0	0	0	0	0		Q6GU68
ENSMUST00000041495	ENSMUSG00000036109	X	51117269	51206532	-1	0	0	0	0	0	0	4	6	0	4	0	Q3TJQ3	
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ENSMUST00000041516	ENSMUSG00000035020	5	91027464	91035215	1	6	3	12	8	7	7	3	44	10	10	4	Q0VEB7	Q924X1
ENSMUST00000041524	ENSMUSG00000033439	3	116581093	116614587	-1	14	7	9	209	11	11	0	14	7	6	15		Q8BYH3
ENSMUST00000041531	ENSMUSG00000037246	17	36772910	36776234	1	9	13	23	13	14	9	0	0	0	0	0	Q85ZW7	
ENSMUST00000041537	ENSMUSG00000023093	9	36431884	36434938	1	3	2	1	3	1	2	0	0	0	0	0	D3YX25	
ENSMUST00000041541	ENSMUSG00000053216	13	23477676	23488857	-1	0	0	0	0	0	0	0	0	0	0	0	I7HIQ7	
ENSMUST00000041543	ENSMUSG00000037428	5	137026392	137033351	1	0	0	0	474	16	0	0	0	0	0	0	Q0VGU4	
ENSMUST00000041544	ENSMUSG00000064080	6	91212455	91272540	1	33	9	59	72	26	0	0	0	0	0	0		P37889
ENSMUST00000041550	ENSMUSG00000040950	11	70130329	70137550	1	32	36	36	9	0	14	4	12	5	0	0	Q8JZN1	
ENSMUST00000041551	ENSMUSG00000037257	9	63602655	63641889	1	22	16	28	52	26	14	731	2058	1043	373	789		Q8R2R3
ENSMUST00000041555	ENSMUSG00000038740	2	33729953	33887946	-1	40	26	109	153	55	24	1146	1140	1276	90	724		Q6KAU4
ENSMUST00000041558	ENSMUSG00000029505	5	110664373	110770717	-1	56	42	120	0	19	23	852	1318	493	106	433		Q8CHI8
ENSMUST00000041565	ENSMUSG00000038564	5	31253277	31291116	-1	40	25	47	35	64	23	99	182	199	97	204		Q6VH22
ENSMUST00000041569	ENSMUSG00000036598	8	95534100	95558888	1	6	5	7	15	11	4	0	0	0	0	0		Q8C5T8
ENSMUST00000041577	ENSMUSG00000037922	3	136053363	136326066	-1	12	16	34	9	15	7	14	78	33	135	121		Q80VH0
ENSMUST00000041582	ENSMUSG00000038291	8	46033261	46152159	-1	0	0	0	36	6	3	0	0	0	0	0		Q3ZT31
ENSMUST00000041587	ENSMUSG00000033128	15	78877190	78894585	1	13	8	79	179	32	12	2357	3239	1882	230	1681		Q8R0H9
ENSMUST00000041588	ENSMUSG00000000148	5	140705011	140719379	1	0	0	0	23	0	0	209	600	506	0	184		Q8C3R1
ENSMUST00000041589	ENSMUSG00000037573	11	94211454	94215495	1	13	8	21	86	18	8	626	1673	779	164	652		Q61471
ENSMUST00000041591	ENSMUSG00000022425	15	54838898	54920146	-1	0	0	14	0	0	0	0	0	0	77	15		Q9R1E6
ENSMUST00000041593	ENSMUSG00000040272	2	93833467	93849943	-1	6	0	13	25	2	2	0	0	0	0	4		A2AIG8
ENSMUST00000041606	ENSMUSG00000040536	4	14952245	15149794	-1	14	4	7	84	19	14	0	0	0	0	0		Q8BG18
ENSMUST00000041609	ENSMUSG00000022401	15	81400138	81456807	1	0	0	3	0	0	0	0	0	0	0	0		B7ZMP1
ENSMUST00000041611	ENSMUSG00000033066	11	67455437	67688990	1	0	1	5	0	0	0	156	0	105	1	14	B1ATI9	
ENSMUST00000041614	ENSMUSG00000037300	8	124671335	124721983	-1	0	0	0	0	0	0	48	405	69	0	68	Q3UMK4	
ENSMUST00000041616	ENSMUSG00000032788	10	78436744	78464975	-1	66	57	142	463	103	48	122	191	115	21	210		Q8K183
ENSMUST00000041618	ENSMUSG00000039117	2	179912152	179976646	-1	0	0	0	28	0	0	4	8	40	0	16	E9QAP7	
ENSMUST00000041621	ENSMUSG00000037216	1	37871738	37876228	1	7	8	14	7	14	2	5	26	20	20	14		Q8VCM4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000041623	ENSMUSG00000041773	13	97241105	97253039	1	41	34	29	272	36	26	67	184	94	14	129		O35709
ENSMUST00000041627	ENSMUSG00000041592	11	113776374	114067046	-1	177	139	399	288	215	86	2	11	4	0	11		Q6V4S5
ENSMUST00000041633	ENSMUSG00000037321	17	34187553	34197225	1	0	0	0	0	0	1	496	1293	264	103	339	Q3TBA3	
ENSMUST00000041638	ENSMUSG00000041303	1	54396004	54438971	-1	24	36	108	55	31	15	38	140	68	96	57	Q3TMP1	
ENSMUST00000041639	ENSMUSG00000096054	10	5020203	5550692	-1	26	24	35	89	36	13	379	265	948	72	756		Q6ZWR6
ENSMUST00000041640	ENSMUSG00000036188	12	36157124	36197291	1	7	6	15	39	20	10	19	71	25	71	51		Q3TPE9
ENSMUST00000041641	ENSMUSG00000037326	17	25959556	25985680	-1	25	15	62	224	39	20	180	188	217	9	213		Q9JLG8
ENSMUST00000041643	ENSMUSG00000039849	2	164879304	164894454	1	41	36	88	90	70	27	2779	2583	2204	207	1997	Q542C3	P59114
ENSMUST00000041646	ENSMUSG00000039358	5	38319367	38322518	1	16	11	50	130	25	9	0	0	0	0	0	B2RQS5	Q8BLD9
ENSMUST00000041649	ENSMUSG00000045027	17	23993535	23998100	-1	34	28	309	92	44	29	13	35	17	7	10	Q7TML0	
ENSMUST00000041654	ENSMUSG00000036587	2	25423267	25426374	1	2	6	33	29	11	2	0	23	14	13	1	Q3SWS0	Q11131
ENSMUST00000041656	ENSMUSG00000051786	15	89098357	89123087	-1	0	0	34	0	0	5	27	0	20	0	0	E9Q6P4	
ENSMUST00000041659	ENSMUSG00000039476	2	30834972	30881251	1	1	3	4	80	7	0	0	0	0	0	0	A2APZ7	
ENSMUST00000041662	ENSMUSG00000037334	17	36670008	36672219	-1	8	6	9	4	5	5	0	0	0	0	0	Q31200	
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ENSMUST00000041676	ENSMUSG00000037346	18	13006990	13022882	1	18	9	17	8	8	12	6	1	2	2	7		Q91ZY2
ENSMUST00000041683	ENSMUSG00000042506	11	61151785	61175055	-1	21	12	25	69	27	12	1868	2004	1965	158	1208		Q5DU02
ENSMUST00000041684	ENSMUSG00000034471	11	115799183	115813639	-1	42	20	113	499	55	31	98	79	69	9	57		Q8VHK1
ENSMUST00000041685	ENSMUSG00000038255	11	98325415	98329648	-1	34	25	164	692	39	10	0	0	1	0	1	Q3TYB2	Q62414
ENSMUST00000041686	ENSMUSG00000037349	19	6993018	6996117	-1	0	2	3	0	10	1	240	266	152	40	106		Q9DD16
ENSMUST00000041703	ENSMUSG00000060962	7	30763756	30781063	1	3	3	0	1	4	1	25	26	18	90	6		Q6P253
ENSMUST00000041705	ENSMUSG00000020867	11	94478904	94486179	-1	7	10	32	9	0	7	0	0	0	0	0		Q80YT5
ENSMUST00000041708	ENSMUSG00000040229	X	13632089	13640858	1	2	1	3	0	2	0	0	0	1	13	8	Q3YL73	Q9R1K6
ENSMUST00000041717	ENSMUSG00000024985	19	55741810	55933654	1	0	0	0	0	0	0	22	0	62	6	5	D3YWT3	
ENSMUST00000041723	ENSMUSG00000035798	10	110941782	111010066	-1	7	15	22	20	13	10	105	316	173	95	171		Q80TN5
ENSMUST00000041725	ENSMUSG00000036620	11	50210890	50235103	1	10	3	20	230	29	12	115	173	98	34	200		Q812F8
ENSMUST00000041726	ENSMUSG00000039483	2	30823097	30830333	-1	18	8	31	129	21	6	5	4	6	0	6		Q91ZU1
ENSMUST00000041730	ENSMUSG00000038765	2	33560965	33640511	-1	44	21	85	102	62	21	0	0	0	0	0		
ENSMUST00000041732	ENSMUSG00000041734	3	87078593	87174747	-1	4	9	12	2	12	5	0	0	0	0	0		Q80W68
ENSMUST00000041733	ENSMUSG00000037343	15	55015129	55072152	-1	41	20	50	122	33	18	238	679	491	112	338	B9EJX5	
ENSMUST00000041736	ENSMUSG00000034245	6	91156665	91174692	1	17	9	33	60	19	18	2	3	7	1	2	Q543U1	Q91WA3
ENSMUST00000041737	ENSMUSG00000029684	6	24613805	24665009	-1	1	3	7	19	2	0	5	5	6	0	21	Q9CXQ9	
ENSMUST00000041758	ENSMUSG00000090132	X	105499772	105500639	1	1	0	1	0	3	0	0	0	0	0	0	Q6P924	
ENSMUST00000041759	ENSMUSG00000034518	8	74993356	75031978	1	12	0	13	71	0	0	0	0	0	13	0	Q80Y32	
ENSMUST00000041761	ENSMUSG00000039405	7	89507785	89517586	-1	25	9	32	42	28	10	1	0	0	15	4		Q9D6X6
ENSMUST00000041763	ENSMUSG00000040919	11	30426006	30471827	-1	3	1	7	1	7	0	0	0	0	0	0		Q5SPV6
ENSMUST00000041767	ENSMUSG00000037410	9	90202027	90270804	-1	35	26	88	71	48	24	2691	4124	3639	347	3087		Q3U0J8
ENSMUST00000041768	ENSMUSG00000033715	13	4049011	4090422	1	0	0	1	0	4	3	0	0	0	0	0	Q91WT7	
ENSMUST00000041769	ENSMUSG00000035770	8	104417674	104443047	-1	37	23	74	285	34	34	265	1103	550	170	482		Q6PDL0
ENSMUST00000041772	ENSMUSG00000037416	18	49832670	49965473	1	0	15	13	4	0	0	12	26	0	8	0	F8WGX5	
ENSMUST00000041776	ENSMUSG00000042671	1	153653025	153700323	1	38	27	130	100	51	33	0	0	0	0	0		Q8BXT1
ENSMUST00000041778	ENSMUSG00000054939	16	3847268	3858880	1	42	34	123	62	61	21	19	28	24	6	28	B9EJW5	
ENSMUST00000041779	ENSMUSG00000030148	6	123106428	123143999	1	4	11	19	292	27	30	209	735	141	143	42		Q9QZ15
ENSMUST00000041782	ENSMUSG00000036376	13	23421539	23423866	-1	18	10	29	51	16	9	160	304	96	142	102		Q9QYL7
ENSMUST00000041783	ENSMUSG00000036555	5	140661827	140702378	-1	22	5	51	26	41	23	75	148	150	12	117		Q6PCQ0
ENSMUST00000041804	ENSMUSG00000038970	5	144100436	144188204	1	76	54	171	196	82	41	1832	2174	3214	97	1894		Q3TYD6
ENSMUST00000041806	ENSMUSG00000019969	12	83688203	83735199	1	1	2	2	28	6	9	715	348	961	45	618	Q3UYK2	P49769
ENSMUST00000041815	ENSMUSG00000060771	1	37754776	37866429	-1	6	4	2	4	3	3	6	5	7	9	0		Q6NY15
ENSMUST00000041819	ENSMUSG00000037446	17	28351515	28365182	-1	0	0	0	1	0	0	0	0	0	0	0		Q9Z273
ENSMUST00000041826	ENSMUSG00000036503	3	57736062	57835233	1	6	6	42	49	7	5	1138	4690	1536	2847	1110		O54965
ENSMUST00000041827	ENSMUSG00000037451	19	5970234	5986143	-1	15	6	36	15	16	13	181	316	175	356	106		Q80UJ1
ENSMUST00000041830	ENSMUSG00000026857	2	30807826	30823033	1	5	8	18	78	14	6	8	49	30	7	15		Q8R2U4
ENSMUST00000041838	ENSMUSG00000033569	1	25067476	25829707	-1	0	0	0	0	0	3	0	0	0	0	0		Q80ZF8
ENSMUST00000041840	ENSMUSG00000072663	15	9578193	9748868	-1	9	6	7	6	8	4	3	6	0	2	0		Q8C9J3
ENSMUST00000041845	ENSMUSG00000040614	7	26322473	26403700	-1	13	12	10	10	17	10	0	0	1	0	0		Q66X01
ENSMUST00000041852	ENSMUSG00000041671	6	142345654	142363257	1	8	6	0	28	6	5	38	273	77	216	76		Q3TMV7
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ENSMUST00000041860	ENSMUSG00000035582	7	97919955	98049663	1	21	25	45	26	21	15	0	0	0	0	0		Q3TT99
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ENSMUST00000041866	ENSMUSG00000063663	X	108737016	108834372	-1	0	0	0	0	0	0	41	148	252	0	236	G3UZT0	
ENSMUST00000041871	ENSMUSG00000037477	19	3992752	3999511	1	14	10	39	14	21	13	0	0	0	0	0		Q810F8
ENSMUST00000041874	ENSMUSG00000042684	1	153503015	153550045	-1	7	9	11	30	9	7	27	32	15	187	23		Q9DCJ9
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ENSMUST00000041890	ENSMUSG00000038623	7	81859001	81884434	1	0	0	1	45	0	1	524	879	593	68	172		P58749
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ENSMUST00000041901	ENSMUSG00000037493	9	54544794	54560218	-1	12	8	31	121	12	14	429	1295	586	281	331	Q544Z8	Q9Z309
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ENSMUST00000041913	ENSMUSG00000032657	3	89183143	89189295	1	0	7	0	0	0	0	75	0	54	0	54		Q5HZJ5
ENSMUST00000041920	ENSMUSG00000041750	3	86986551	86989780	1	0	0	3	0	3	0	0	0	2	2	0	E9QLX1	
ENSMUST00000041924	ENSMUSG00000037974	7	141788972	141819231	1	0	0	0	0	3	0	0	1	0	0	0	E9PWB6	
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ENSMUST00000041954	ENSMUSG00000036513	3	57644349	57651715	-1	0	0	0	3	0	1	202	538	151	471	94	G3X955	
ENSMUST00000041956	ENSMUSG00000020859	11	93996091	94126085	1	0	0	0	0	0	0	484	735	980	88	700		Q58A65
ENSMUST00000041962	ENSMUSG00000034813	10	119454034	120087261	1	8	9	16	6	0	0	0	0	0	0	0	H7BX09	
ENSMUST00000041964	ENSMUSG00000037537	17	36547075	36549250	1	9	5	7	3	5	3	0	0	0	0	1	F6U8V3	
ENSMUST00000041965	ENSMUSG00000021279	12	111292972	111377718	-1	78	44	119	210	77	41	182	240	235	28	427		Q7TT50
ENSMUST00000041968	ENSMUSG00000039428	7	89139723	89404222	-1	13	5	11	24	11	7	94	454	128	28	78		Q9CYV5
ENSMUST00000041973	ENSMUSG00000035785	8	104322237	104330756	1	10	3	2	7	4	2	1	6	1	1	1		Q9DAC0
ENSMUST00000041982	ENSMUSG00000037548	17	34143307	34151553	1	218	281	521	190	144	67	144	112	51	45	165	Q31099	
ENSMUST00000041984	ENSMUSG00000039166	10	25169090	25307870	-1	2	0	22	3	6	1	16	81	38	37	54		Q7TN79
ENSMUST00000041987	ENSMUSG00000041415	12	104687742	104751952	-1	66	56	100	298	99	53	263	682	724	70	513	F8VQ54	
ENSMUST00000041993	ENSMUSG00000041681	6	142298423	142303961	1	4	2	2	1	1	1	0	0	0	0	0		P12968
ENSMUST00000042009	ENSMUSG00000021782	14	24133953	24245920	-1	46	9	64	6	0	0	2	0	3	8	66	F6YZU5	
ENSMUST00000042012	ENSMUSG00000033732	8	110810492	110846803	-1	33	25	65	38	40	10	614	1240	828	180	834	B2RSV4	Q921M3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000042021	ENSMUSG00000038984	15	33683876	33687883	-1	18	16	25	178	24	9	0	0	0	0	0		Q69ZB3
ENSMUST00000042025	ENSMUSG00000033420	6	87133853	87335821	-1	28	24	61	181	46	24	0	1	0	20	40		Q9CZ52
ENSMUST00000042026	ENSMUSG00000037578	19	44147637	44192442	-1	11	0	0	0	0	0	0	0	0	0	0		A2A259
ENSMUST00000042035	ENSMUSG00000034730	15	74516195	74589465	1	8	0	0	245	16	0	0	0	0	0	0		Q3UHD1
ENSMUST00000042042	ENSMUSG00000035699	16	32475522	32487879	-1	17	9	11	14	13	11	0	0	0	0	1		Q8R000
ENSMUST00000042046	ENSMUSG00000034463	14	65919395	65953744	-1	19	14	62	119	29	23	0	0	0	18	40		Q8C850
ENSMUST00000042052	ENSMUSG00000035247	12	51743722	51829536	-1	0	42	56	114	0	33	2369	6979	6521	900	4494	F8WIE5	
ENSMUST00000042054	ENSMUSG00000038402	13	31625816	31631403	1	38	30	202	457	44	25	2	20	7	1	11		O54743
ENSMUST00000042055	ENSMUSG00000039515	2	30416039	30447806	1	0	0	0	48	0	6	1884	1315	1011	121	768	Q543N6	P58389
ENSMUST00000042057	ENSMUSG00000035621	10	80148272	80158368	1	14	5	0	0	24	16	2036	1991	2335	197	1604		Q3TPJ7
ENSMUST00000042061	ENSMUSG00000037603	19	33822908	33825071	1	3	2	2	0	4	3	0	0	0	0	0	D3Z175	
ENSMUST00000042065	ENSMUSG00000033618	16	21891969	21931877	1	52	47	118	43	69	27	0	0	3	0	4		Q1HKZ5
ENSMUST00000042070	ENSMUSG00000033906	X	104536969	104671064	-1	8	11	11	65	15	4	3	16	2	2	8		Q8BGJ0
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ENSMUST00000042078	ENSMUSG00000040310	2	93642384	93681339	1	119	77	216	1461	199	102	0	2	2	2	0		O35137
ENSMUST00000042081	ENSMUSG00000040552	6	122847138	122856161	-1	54	43	373	89	55	30	96	76	94	780	293	Q5U7A4	O09047
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ENSMUST00000042090	ENSMUSG00000056910	17	20345425	20375772	1	7	6	2	6	3	3	0	0	0	0	0	E9PZJ7	
ENSMUST00000042092	ENSMUSG00000039155	2	178430531	178487366	1	0	5	0	0	9	8	0	1	1	0	1		P59862
ENSMUST00000042096	ENSMUSG00000078517	4	139352587	139378730	1	32	31	52	115	74	55	193	660	295	19	0		Q8C7X2
ENSMUST00000042097	ENSMUSG00000071562	16	36277148	36285371	1	0	0	0	0	0	0	16	34	22	75	2		P35175
ENSMUST00000042101	ENSMUSG00000036231	12	35925620	35949736	1	2	2	1	0	2	2	0	0	0	0	0		Q8R3W7
ENSMUST00000042103	ENSMUSG00000039057	8	10272572	10634741	1	45	27	125	138	92	36	1	0	0	0	0	F8WGF8	
ENSMUST00000042105	ENSMUSG00000040435	7	45522916	45526268	-1	8	6	0	241	13	0	175	634	132	19	339	B2RRL7	P17564
ENSMUST00000042118	ENSMUSG00000038415	13	31558324	31560976	1	8	1	17	361	20	9	0	0	1	0	1		O70220
ENSMUST00000042119	ENSMUSG00000041698	6	141907282	141946962	-1	0	0	1	2	2	0	0	0	0	0	0	Q53ZW9	Q9QXZ6
ENSMUST00000042121	ENSMUSG00000037649	17	34135182	34139101	1	12	5	10	10	7	9	184	202	65	36	204	Q31621	
ENSMUST00000042122	ENSMUSG00000003992	13	91460283	91703429	1	0	4	0	15	0	0	59	159	78	107	58		Q9CYZ8
ENSMUST00000042125	ENSMUSG00000033257	1	74661745	74703730	1	45	45	198	93	57	31	7	24	38	5	26		Q80UG8
ENSMUST00000042135	ENSMUSG00000004952	5	136083916	136111860	1	7	0	9	71	4	0	39	48	0	27	50		Q6PFQ7
ENSMUST00000042141	ENSMUSG00000042699	1	153455758	153487660	-1	8	6	0	24	18	0	394	578	924	354	653	E9QNN1	
ENSMUST00000042146	ENSMUSG00000029125	5	38038742	38137765	1	1	1	0	0	0	3	166	361	196	81	71		Q8VDS8
ENSMUST00000042147	ENSMUSG00000033294	5	110648418	110653417	-1	15	15	24	47	14	6	140	232	143	39	143		Q8BHY2
ENSMUST00000042148	ENSMUSG00000040269	3	8802146	8923918	-1	7	5	4	63	8	3	39	130	20	215	52		Q9CY16
ENSMUST00000042158	ENSMUSG00000037681	9	99309963	99358557	-1	43	27	116	40	42	31	2	13	1	0	5		Q5DTI8
ENSMUST00000042161	ENSMUSG00000026110	1	37439340	37541016	-1	0	28	26	59	33	0	120	522	117	51	282		Q812G0
ENSMUST00000042163	ENSMUSG00000042719	5	121397936	121444378	1	12	4	7	26	14	12	19	67	49	15	111	B2RQV1	Q8BWZ3
ENSMUST00000042166	ENSMUSG00000038646	7	81762925	81769491	1	11	4	23	64	7	4	444	1421	436	1083	298		Q9CQY2
ENSMUST00000042167	ENSMUSG00000039007	15	33083129	33594552	1	7	5	14	61	6	0	33	61	33	257	61		Q9WVJ3
ENSMUST00000042172	ENSMUSG00000037689	17	86917348	86922374	1	5	3	4	5	9	2	0	0	0	0	0		Q497K7
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ENSMUST00000042190	ENSMUSG00000037705	9	42329619	42399929	-1	44	25	44	50	66	0	0	0	0	0	0		O08523
ENSMUST00000042191	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	0	0	0	74	193	53	198	11		Q9CQE3
ENSMUST00000042194	ENSMUSG00000038260	7	45303155	45333780	-1	35	28	98	176	55	19	502	733	426	150	208		Q7TN37
ENSMUST00000042196	ENSMUSG00000042116	4	155768149	155774698	-1	56	40	126	319	73	18	2	2	0	2	4		Q8R2Z5
ENSMUST00000042203	ENSMUSG00000034379	16	36041190	36042973	1	11	9	14	13	8	10	47	234	65	68	55		Q9D7H2
ENSMUST00000042205	ENSMUSG00000037716	9	58028677	58118823	-1	0	11	0	7	7	0	0	0	0	0	0		
ENSMUST00000042217	ENSMUSG00000032852	2	151842927	151874668	1	12	11	27	40	25	10	0	0	0	0	0	Q0P5Y9	Q8BJ73
ENSMUST00000042219	ENSMUSG00000033765	13	3837757	3838671	1	6	7	7	12	6	6	0	0	0	0	0		Q9JM83
ENSMUST00000042220	ENSMUSG00000078942	13	100281121	100317674	-1	0	0	108	47	50	20	0	0	0	35	0		Q9JIB6
ENSMUST00000042221	ENSMUSG00000040569	4	14502430	14621805	-1	5	0	5	3	12	1	0	0	0	0	0		Q8R2Z3
ENSMUST00000042227	ENSMUSG00000041623	11	113684412	113694647	1	0	0	0	28	0	0	57	182	132	13	124		Q6PIX9
ENSMUST00000042228	ENSMUSG00000039997	1	173920407	173942672	-1	0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000042235	ENSMUSG00000037742	9	78478449	78489151	-1	106	153	175	466	140	54	24821	80478	33552	63725	29189	Q58E64	P10126
ENSMUST00000042246	ENSMUSG00000035109	2	125627447	125724148	-1	56	10	50	341	18	8	0	0	0	0	0		Q6S5L9
ENSMUST00000042251	ENSMUSG00000019763	10	4401915	4432388	-1	78	66	174	72	64	31	38	303	109	80	115		Q8CI78
ENSMUST00000042261	ENSMUSG00000037490	10	22645011	22704285	1	18	17	31	32	19	10	1	0	2	1	0	B2RRB2	Q8BFW9
ENSMUST00000042266	ENSMUSG00000034219	5	129683391	129708512	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DA97
ENSMUST00000042275	ENSMUSG00000026288	1	87620312	87720507	1	0	0	0	0	0	18	1237	821	1142	159	968		Q9ES52
ENSMUST00000042280	ENSMUSG00000063902	7	83755904	83757356	1	0	6	0	0	0	4	0	0	0	0	0	D3Z5X4	
ENSMUST00000042281	ENSMUSG00000042569	11	60830631	60860195	1	0	1	0	1	0	0	75	81	36	89	33	I7DM66	Q99J47
ENSMUST00000042286	ENSMUSG00000055805	11	103171107	103198901	1	8	0	0	215	12	13	12796	15755	15642	594	11179		Q9JL26
ENSMUST00000042288	ENSMUSG00000033781	13	3634032	3651774	1	86	50	135	249	107	62	8	55	14	9	63		Q8VBX0
ENSMUST00000042290	ENSMUSG00000037254	2	10094593	10131396	-1	29	12	21	31	28	16	0	0	0	13	2	G3X977	
ENSMUST00000042296	ENSMUSG00000062078	17	10206471	10319361	-1	40	45	165	291	68	40	427	715	444	50	299		Q9QYS9
ENSMUST00000042299	ENSMUSG00000034402	12	74897217	75177332	-1	12	13	29	173	32	8	0	1	0	2	0		Q920E3
ENSMUST00000042302	ENSMUSG00000038147	1	171839697	171890718	1	0	0	0	0	0	0	202	0	342	191	79		
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ENSMUST00000042318	ENSMUSG00000038663	7	81533308	81566944	-1	26	25	32	60	30	17	0	0	0	0	0		
ENSMUST00000042322	ENSMUSG00000037801	9	63421455	63602493	-1	0	6	7	6	0	0	0	0	0	0	0		Q9D2K4
ENSMUST00000042329	ENSMUSG00000042271	X	142226770	142239692	1	0	0	0	1	0	0	0	47	0	0	0		Q3UNA4
ENSMUST00000042334	ENSMUSG00000037805	17	28328471	28331032	1	0	9	15	64	19	1	577	793	545	3353	253	Q5XJF6	
ENSMUST00000042344	ENSMUSG00000034493	11	3937541	3976778	-1	20	8	17	12	9	4	0	3	0	0	0	Q9D4U7	
ENSMUST00000042345	ENSMUSG00000037815	18	35118888	35254773	1	22	24	22	40	25	19	693	1495	1417	303	924	Q545R0	P26231
ENSMUST00000042352	ENSMUSG00000037492	8	23636019	24156585	1	13	15	13	8	20	7	0	0	0	0	0		Q8BZ94
ENSMUST00000042360	ENSMUSG00000039676	15	9436028	9466035	1	7	5	11	6	6	4	0	1	1	4	0		Q6P8Y1
ENSMUST00000042365	ENSMUSG00000041297	13	17715962	17805097	-1	34	15	94	313	29	21	668	1938	1490	118	995		Q69ZA1
ENSMUST00000042373	ENSMUSG00000042708	1	153425162	153452574	1	6	1	5	115	8	8	0	3	1	3	1		Q3TTP0
ENSMUST00000042390	ENSMUSG00000036646	2	25332338	25352212	1	17	12	53	54	27	19	1062	1867	1240	178	942		A2AJ15
ENSMUST00000042391	ENSMUSG00000037845	9	50768236	50773348	1	351	361	588	349	329	178	40	114	30	29	38		Q3UY23
ENSMUST00000042392	ENSMUSG00000037847	19	18631950	18652194	1	0	0	0	0	0	0	0	9	0	9	1		Q91W63
ENSMUST00000042399						25	22	69	14	23	14	49	185	94	22	70		
ENSMUST00000042402	ENSMUSG00000038902	3	94837567	94882326	1	0	0	0	0	0	0	54	16	24	0	49	Q0VGT3	
ENSMUST00000042405	ENSMUSG00000046865	7	28169748	28179269	1	36	10	78	224	60	18	234	400	147	189	240		P35550

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000042410	ENSMUSG00000040274	5	3341485	3531008	1	0	0	0	0	0	0	0	0	0	0	0	Q0VBK8	Q64261
ENSMUST00000042412	ENSMUSG00000040289	3	8663359	8667256	-1	7	7	10	158	14	3	1	0	1	0	2	Q9QUM5	
ENSMUST00000042438	ENSMUSG00000040624	10	3740364	3967303	1	23	22	33	0	29	22	32	0	0	6	0	Q3UX37	
ENSMUST00000042444	ENSMUSG00000036198	X	49463945	49500244	1	0	4	0	0	0	4	0	0	0	0	0	Z4YJK0	
ENSMUST00000042450	ENSMUSG00000035367	13	58402597	58411149	1	29	23	21	130	24	13	100	392	148	98	85		Q9D4G9
ENSMUST00000042452	ENSMUSG00000032869	2	151715812	151744186	-1	0	11	4	39	17	6	0	36	34	0	28	A2AU35	Q8BHL8
ENSMUST00000042456	ENSMUSG00000034780	2	67565871	68122689	1	9	0	0	2	5	4	0	0	0	0	0	Q505A3	O54904
ENSMUST00000042468	ENSMUSG00000037971	9	50762828	50775520	-1	29	15	158	49	24	7	33	116	33	71	33		Q9D131
ENSMUST00000042470	ENSMUSG00000030757	7	123475384	123500449	-1	28	20	38	39	22	14	0	0	0	0	0	G3X952	
ENSMUST00000042471	ENSMUSG00000033166	14	99076634	99099770	-1	7	6	15	21	19	5	19	85	37	18	62		Q9CSH3
ENSMUST00000042477	ENSMUSG00000078656	11	101253707	101259549	1	0	1	8	0	0	0	940	1727	706	462	566		Q9CQ80
ENSMUST00000042485	ENSMUSG00000038112	9	39587396	39604403	-1	0	14	28	0	11	0	0	0	0	0	0	Q8BGF0	
ENSMUST00000042493	ENSMUSG00000042111	1	34436670	34439672	-1	18	14	43	108	23	11	283	680	380	343	168		Q8VE99
ENSMUST00000042497	ENSMUSG00000037916	19	4007497	4012806	-1	0	0	10	24	0	0	355	163	252	131	193		Q91YT0
ENSMUST00000042498	ENSMUSG00000034088	1	93405940	93478815	-1	0	0	0	20	0	0	729	1608	1915	452	1794	Q3U4Z7	Q8VDJ3
ENSMUST00000042503	ENSMUSG00000039046	2	6322667	6446390	1	6	8	15	4	8	0	26	0	21	4	25		Q80XC3
ENSMUST00000042506	ENSMUSG00000103565	15	81002628	81011736	1	0	9	17	0	0	0	47	0	19	0	0	F8WIA4	
ENSMUST00000042509	ENSMUSG00000040648	1	97706048	97770411	-1	13	0	21	112	14	0	102	92	95	4	115		Q6ZQB6
ENSMUST00000042512	ENSMUSG00000037262	2	10080593	10092806	1	5	4	3	6	8	2	118	771	242	510	183		Q8K339
ENSMUST00000042517	ENSMUSG00000041817	13	97067287	97129521	1	14	0	25	0	0	0	0	0	0	0	0		Q5XG69
ENSMUST00000042529	ENSMUSG00000037940	8	81342556	82125036	1	0	0	0	0	0	0	0	0	0	0	6		Q6P1Y8
ENSMUST00000042530	ENSMUSG00000042282	X	142081160	142196931	-1	22	20	66	13	24	13	0	5	5	0	2		Q5SDA5
ENSMUST00000042534	ENSMUSG00000032878	11	28385685	28584324	-1	0	0	7	49	0	12	0	0	0	0	0		Q5SP85
ENSMUST00000042546	ENSMUSG00000037949	9	122175879	122294374	-1	21	23	41	50	24	13	1634	2749	1569	170	814		Q8BH79
ENSMUST00000042553	ENSMUSG00000037953	9	99612502	99622367	1	7	11	23	16	10	9	0	0	0	0	0	Q14BT6	
ENSMUST00000042556	ENSMUSG00000032834	10	78170910	78185149	-1	29	27	50	44	49	19	79	106	56	19	87	Q2M1K2	Q8BU03
ENSMUST00000042561	ENSMUSG00000038178	11	75531694	75577575	1	95	61	0	228	22	59	224	1046	587	71	675		Q8CGA3
ENSMUST00000042564	ENSMUSG00000041028	14	37120444	37135322	-1	12	0	0	54	8	0	0	29	0	0	56		Q91VC9
ENSMUST00000042575	ENSMUSG00000036822	4	40259601	40269850	-1	20	18	25	157	26	14	210	1243	518	181	398		Q80Z37
ENSMUST00000042576	ENSMUSG00000037971	9	50762828	50775520	-1	0	1	4	2	0	0	4	45	10	9	2		Q9D131
ENSMUST00000042581	ENSMUSG00000037977	9	107340602	107352422	1	12	23	43	69	24	13	1	2	1	0	1	Q14AT3	Q8BGK9
ENSMUST00000042586	ENSMUSG00000034833	10	130322852	130362642	1	9	3	9	12	7	1	4	37	14	40	29		Q3U132
ENSMUST00000042587	ENSMUSG00000028023	3	129199878	129219591	1	3	0	27	110	3	0	0	0	0	0	2	Q6DIA6	P97474
ENSMUST00000042594	ENSMUSG00000035805	15	88955884	88979007	-1	30	14	0	0	23	0	0	0	0	0	0		Q8VHK5
ENSMUST00000042595	ENSMUSG00000032889	11	28339104	28339867	-1	3	4	0	9	6	0	18	22	16	4	6	D3YYP3	
ENSMUST00000042601	ENSMUSG00000037993	8	109548017	109565601	-1	37	15	88	64	54	30	2966	4115	4021	334	3439	Q80X98	
ENSMUST00000042603	ENSMUSG00000041324	13	16011851	16027211	1	19	10	28	132	23	9	0	4	12	4	4	Q3UY39	Q04998
ENSMUST00000042608	ENSMUSG00000038000	8	105698159	105701095	-1	8	11	37	70	30	7	366	650	327	41	224	B2RS36	Q5EE38
ENSMUST00000042610	ENSMUSG00000073490	1	173723430	173741809	-1	0	20	20	10	0	10	47	321	92	402	143	E9Q3L4	
ENSMUST00000042614	ENSMUSG00000042744	5	121220219	121368577	1	54	29	132	123	79	36	212	277	506	16	463	E9Q2E4	
ENSMUST00000042615	ENSMUSG00000038831	2	33133417	33371486	-1	27	0	50	23	32	21	74	177	34	0	73		A2AR50
ENSMUST00000042617	ENSMUSG00000033770	4	141384610	141398724	-1	0	0	0	0	9	7	0	0	0	0	0		Q9WUB7
ENSMUST00000042627	ENSMUSG00000035642	7	97550331	97579497	-1	3	2	0	0	0	0	0	0	0	0	0	D3Z1Q3	
ENSMUST00000042641	ENSMUSG00000037640	7	27731389	27753702	1	0	0	0	0	0	0	1	0	0	0	0	Q8K0D9	
ENSMUST00000042646	ENSMUSG00000037621	6	72206177	72235577	-1	13	9	26	527	46	10	4	1	0	1	0		Q99NA2
ENSMUST00000042647	ENSMUSG00000038167	6	125362660	125380793	-1	25	12	68	149	34	20	71	105	61	4	92		Q8R0J1
ENSMUST00000042657	ENSMUSG00000041654	11	113244853	113650079	-1	0	11	0	4	0	0	0	7	0	0	0		Q8BWY7
ENSMUST00000042658	ENSMUSG00000039063	2	6188465	6213033	-1	7	5	15	44	12	3	64	89	24	11	27		Q9D7J9
ENSMUST00000042661	ENSMUSG00000036565	5	140620578	140649031	-1	44	25	110	240	69	38	9061	7698	7563	708	7443		Q6P5F7
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ENSMUST00000042664	ENSMUSG00000033965	X	103697414	103821983	-1	4	8	14	99	26	14	5	0	2	1	6	Q05BA2	O70324
ENSMUST00000042665	ENSMUSG00000034422	16	35832874	35871544	-1	44	28	102	51	43	17	520	2235	1324	155	1342		Q2EMV9
ENSMUST00000042666	ENSMUSG00000039878	10	128395934	128401224	-1	16	12	0	13	12	6	0	0	0	0	1		Q9D856
ENSMUST00000042675	ENSMUSG00000028745	4	139192899	139291818	1	2	0	7	6	0	11	270	2844	0	0	0	A2AMW0	
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ENSMUST00000042683	ENSMUSG00000038045	17	78883938	78906992	-1	0	0	4	0	0	0	0	0	0	0	0	E9QNJ5	
ENSMUST00000042692	ENSMUSG00000062859	17	28066747	28080639	-1	0	5	0	87	23	14	0	8	36	0	0	B2KF25	
ENSMUST00000042699	ENSMUSG00000037542	10	21377291	21396585	1	30	21	310	66	35	19	0	8	0	3	2		Q8BH00
ENSMUST00000042700	ENSMUSG00000038155	19	4040285	4042236	-1	4	4	3	2	5	1	2	0	0	0	1		P46425
ENSMUST00000042701	ENSMUSG00000037235	5	34173883	34187720	-1	38	31	80	230	54	31	1423	1538	1784	425	1122	Q91VN7	
ENSMUST00000042702	ENSMUSG00000039065	15	31601852	31621227	1	8	0	0	2	2	2	28	58	39	26	27		Q9D1Z3
ENSMUST00000042706	ENSMUSG00000037583	4	133553376	133556536	1	13	5	21	31	17	8	0	1	0	0	0		Q62227
ENSMUST00000042710	ENSMUSG00000038059	18	60474193	60501983	-1	9	12	17	104	25	11	1109	2005	943	653	647	Q3U1M0	Q99PE5
ENSMUST00000042717	ENSMUSG00000045409	17	36258873	36272247	-1	0	0	9	0	0	0	190	937	93	39	188	E9QLN4	
ENSMUST00000042724	ENSMUSG00000038250	8	80980734	81014906	-1	26	13	39	280	27	12	468	1400	849	144	637		Q8BW70
ENSMUST00000042726	ENSMUSG00000036733	7	30640994	30650317	-1	0	0	14	101	13	12	568	634	583	153	460		Q91V81
ENSMUST00000042729	ENSMUSG00000040998	3	132881745	132950291	-1	1	0	0	0	0	0	0	0	0	0	13		Q91V88
ENSMUST00000042732	ENSMUSG00000035764	16	32230112	32247158	-1	19	15	26	71	22	12	141	582	248	30	173		Q8K3B1
ENSMUST00000042734	ENSMUSG00000038323	1	57377620	57385423	1	7	6	4	9	14	3	16	53	14	10	16		Q9D9H8
ENSMUST00000042740	ENSMUSG00000004668	11	9191942	9684259	1	55	45	80	58	63	28	1827	2484	5259	212	1836		Q5SSE9
ENSMUST00000042744	ENSMUSG00000040998	3	132881745	132950291	-1	0	15	0	0	21	0	0	0	0	26	142		Q91V88
ENSMUST00000042747	ENSMUSG00000038071	18	44270127	44277700	1	8	2	11	0	13	10	0	0	0	0	0		Q61212
ENSMUST00000042750	ENSMUSG00000039611	4	49584506	49597876	-1	12	21	18	80	35	12	1	2	1	1	0		Q91YV9
ENSMUST00000042753	ENSMUSG00000040302	5	3583978	3596585	-1	7	4	21	318	16	5	18	113	39	49	41	H9H9R8	
ENSMUST00000042754	ENSMUSG00000038300	7	45180995	45181838	1	0	1	15	114	4	1	0	0	0	0	0		Q91W27
ENSMUST00000042755	ENSMUSG00000054932	5	90490737	90508907	1	8	2	9	6	10	3	2	2	0	26	6		P02772
ENSMUST00000042766	ENSMUSG00000037826	6	57506502	57535468	-1	119	118	385	107	120	92	40	174	104	43	77	B9EHW0	Q8BXN7
ENSMUST00000042767	ENSMUSG00000033214	14	111675115	111683134	1	22	24	61	332	48	21	0	0	0	0	0		Q810B7
ENSMUST00000042771	ENSMUSG00000035673	10	80057416	80102698	-1	38	29	94	148	70	35	17553	18353	13988	1053	13762		Q7TNB8
ENSMUST00000042775	ENSMUSG00000039873	2	164830732	164833456	-1	7	3	15	172	20	4	7	11	4	4	13	A2A5J5	
ENSMUST00000042779	ENSMUSG00000033454	12	76370266	76396950	1	107	88	166	1115	174	102	329	1074	544	150	400	Q5YB37	Q91VL9
ENSMUST00000042780	ENSMUSG00000040548	11	106502147	106613423	-1	26	14	75	79	42	21	202	500	319	33	377		Q6ZPJ0
ENSMUST00000042790	ENSMUSG00000038086	9	50751072	50752354	-1	14	10	28	26	15	6	1	3	0	1	4		Q99PR8
ENSMUST00000042792	ENSMUSG00000034810	2	66673425	66784914	-1	18	25	58	21	31	6	0	0	0	0	1	B1AYL1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000042808	ENSMUSG00000038188	11	75513540	75526582	1	0	8	25	0	29	0	0	0	0	0	35		Q5ND28
ENSMUST00000042812	ENSMUSG00000030236	6	141629518	141686646	1	4	4	11	3	3	3	0	0	0	6	0		Q9JJL3
ENSMUST00000042818	ENSMUSG00000035828	15	88862186	88865718	1	14	9	32	357	19	11	83	137	65	16	107	Q3TX64	P58750
ENSMUST00000042824	ENSMUSG00000038664	9	66350450	66508775	1	44	35	65	25	39	24	893	1915	2655	210	2252	E9PZP8	
ENSMUST00000042834	ENSMUSG00000038462	13	30540308	30545362	-1	4	6	8	132	11	1	471	1324	560	216	344		Q9CR68
ENSMUST00000042842	ENSMUSG00000038119	9	35421128	35507652	1	39	26	8	0	0	23	7	16	14	29	89		Q32MD9
ENSMUST00000042844	ENSMUSG00000041120	4	139082284	139092993	-1	13	7	20	29	24	7	5	8	2	27	48		Q61477
ENSMUST00000042850	ENSMUSG00000028369	4	58042442	58206859	-1	60	47	81	72	104	47	48	32	189	3	29		A2AVA0
ENSMUST00000042852	ENSMUSG00000038121	18	68260187	68300333	-1	53	49	49	100	46	30	41	112	51	51	88		Q8BGY7
ENSMUST00000042857	ENSMUSG00000038331	1	56793981	56978650	-1	26	53	32	364	26	9	0	4	0	0	11		Q8VI24
ENSMUST00000042861	ENSMUSG00000039232	10	12939983	12964259	-1	5	0	9	11	0	0	709	1270	877	195	709	Q3U5V8	
ENSMUST00000042868	ENSMUSG00000038128	18	32939041	33195767	1	113	86	235	305	108	72	19	50	31	10	58	Q8BGR3	
ENSMUST00000042869	ENSMUSG00000035790	16	32099800	32108069	1	5	0	0	0	3	0	0	20	22	0	0		Q9CQA8
ENSMUST00000042889	ENSMUSG00000034269	6	113077365	113153435	1	0	0	0	41	16	0	0	10	0	0	25		Q5XJV7
ENSMUST00000042901	ENSMUSG00000034349	3	69004738	69034623	1	0	0	0	24	8	0	13	205	220	206	198		Q8CG47
ENSMUST00000042917	ENSMUSG00000037386	15	39198332	39681940	1	24	0	18	0	7	0	0	0	0	0	1	D9HP81	
ENSMUST00000042919	ENSMUSG00000037600	4	133518963	133530790	1	0	4	0	7	0	0	0	0	0	0	0		A2A9F4
ENSMUST00000042923	ENSMUSG00000034748	10	81621785	81627797	-1	14	13	45	60	12	5	198	293	123	17	115		P59941
ENSMUST00000042942	ENSMUSG00000055319	7	128744943	128784836	1	27	29	67	147	43	25	447	1415	805	143	576	G3X928	
ENSMUST00000042943	ENSMUSG00000056158	11	93098028	93601749	1	0	0	0	0	0	8	0	0	0	0	0	Q3V1V7	P61215
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ENSMUST00000042953	ENSMUSG00000020576	12	13269127	13583810	1	38	50	49	63	54	25	60	97	144	15	93	E9Q411	
ENSMUST00000042954	ENSMUSG00000045102	5	34007179	34169448	-1	17	14	16	19	22	14	0	6	2	1	1		
ENSMUST00000042957	ENSMUSG00000022986	15	101563345	101573904	-1	19	20	77	40	39	11	7	4	2	0	0		Q8BGZ7
ENSMUST00000042964	ENSMUSG00000039634	4	49521176	49531517	1	0	0	1	0	0	1	9	21	34	0	0	Q8BKP2	
ENSMUST00000042970	ENSMUSG00000041695	11	111066164	111076821	1	86	77	133	500	137	80	655	2570	1092	434	1104	Q543W5	P35561
ENSMUST00000042971	ENSMUSG00000038352	11	97989578	97996181	-1	9	4	20	51	15	6	21	114	4	20	70		Q6P068
ENSMUST00000042972	ENSMUSG00000038195	11	75510094	75513168	1	8	6	17	145	18	0	0	0	0	0	9	Q14AQ2	Q5ND29
ENSMUST00000042974	ENSMUSG00000035104	6	82041043	82093099	1	10	7	7	53	10	4	0	0	0	0	0		Q91WM6
ENSMUST00000042975	ENSMUSG00000034435	12	73543114	73546395	-1	17	12	11	299	17	2	0	0	0	0	0	Q0VEI2	Q8BHG3
ENSMUST00000042985	ENSMUSG00000034957	7	35119293	35121928	1	20	16	65	577	25	9	581	776	255	115	400		P53566
ENSMUST00000042986	ENSMUSG00000038349	1	55405921	55754285	1	35	48	183	321	64	39	3	10	0	1	2		Q3USB7
ENSMUST00000042988	ENSMUSG00000037526	14	47540894	47568434	-1	23	23	68	146	32	12	142	353	313	38	123		Q8CDJ3
ENSMUST00000042990	ENSMUSG00000036371	6	67238176	67297736	1	10	15	47	140	22	8	845	2505	1494	3021	1164		Q9CY58
ENSMUST00000042993	ENSMUSG00000036586	5	140563119	140565071	-1	8	7	20	10	7	6	0	0	0	0	2		Q9D1U0
ENSMUST00000043011	ENSMUSG00000038233	9	121950988	121980208	1	76	61	192	69	67	44	1	5	0	0	1		Q3UY90
ENSMUST00000043042	ENSMUSG00000041143	4	138972888	139059171	1	12	8	37	5	23	4	161	181	125	23	88		Q91WU4
ENSMUST00000043045	ENSMUSG00000039382	X	7721973	7728201	1	0	0	0	0	1	0	341	719	293	219	296		Q91VM3
ENSMUST00000043050	ENSMUSG00000036599	5	140505550	140525724	1	28	8	68	75	33	21	3119	3363	2135	196	1401		Q99LL3
ENSMUST00000043056	ENSMUSG00000039653	4	49489422	49506557	-1	0	3	20	0	3	6	0	0	0	1	1		Q91X34
ENSMUST00000043058	ENSMUSG00000058207	12	104338486	104346144	1	12	5	17	18	12	7	0	0	0	324	0		
ENSMUST00000043059	ENSMUSG00000038264	9	57940113	57962864	1	18	11	97	169	39	15	54	75	61	6	82		Q9QUR8
ENSMUST00000043061	ENSMUSG00000042655	13	104845283	104863893	-1	8	2	7	123	18	7	0	1	1	1	0		Q9D1Y9
ENSMUST00000043062	ENSMUSG00000024207	17	56843103	56874447	-1	92	70	471	121	73	49	4	21	16	3	15		Q2XU92
ENSMUST00000043069	ENSMUSG00000018008	15	78597047	78622019	1	36	33	42	43	45	27	6622	9962	6532	1397	6072	Q3U0C0	Q80YW0
ENSMUST00000043074	ENSMUSG00000038274	19	6057888	6059524	1	0	15	0	30	0	0	282	339	64	401	117	Q642K5	
ENSMUST00000043077	ENSMUSG00000035686	7	97412938	97417730	-1	13	10	9	7	10	7	0	0	0	4	0	Q543J4	Q62264
ENSMUST00000043081	ENSMUSG00000036658	13	21638580	21642262	-1	6	3	14	0	5	10	0	0	0	0	0		Q60890
ENSMUST00000043082	ENSMUSG00000036257	12	44221370	44312343	1	0	0	2	23	4	0	259	1381	639	589	334		Q8K1N1
ENSMUST00000043087	ENSMUSG00000035845	15	88805244	88819318	-1	0	0	31	0	0	0	16	84	12	15	18	Q8VCA2	
ENSMUST00000043089	ENSMUSG00000034161	15	76457438	76459468	1	6	6	13	202	11	3	0	3	0	12	9	Q53ZC3	Q64124
ENSMUST00000043094	ENSMUSG00000038209	1	171518122	171535294	-1	29	18	34	11	28	14	51	521	108	128	196	D9J349	O88310
ENSMUST00000043098	ENSMUSG00000036390	6	67035096	67037457	-1	2	7	5	2	3	0	874	4633	769	261	822	Q3UMH6	P48316
ENSMUST00000043104	ENSMUSG00000026616	1	195136811	195176716	-1	0	2	0	0	2	3	0	2	0	0	0	E9Q3S5	
ENSMUST00000043108	ENSMUSG00000051278	3	127553489	127618023	1	30	35	44	40	31	16	16	29	25	13	43		Q0VGT4
ENSMUST00000043111	ENSMUSG00000034488	13	88821472	89323223	1	1	10	6	0	3	5	0	0	0	2	2	Q8C4U8	
ENSMUST00000043112	ENSMUSG00000037536	14	47472561	47531962	1	0	0	0	26	0	0	0	355	48	0	0	E9QM55	
ENSMUST00000043126	ENSMUSG00000038369	2	155390656	155473894	-1	27	9	117	0	28	23	951	1375	1971	118	1474	Q5XJV5	
ENSMUST00000043138	ENSMUSG00000042105	7	128611328	128696425	1	2	3	0	5	0	0	55	99	107	25	130	B2RQ14	Q8CDA1
ENSMUST00000043141	ENSMUSG00000059854	8	110266977	110610253	1	116	100	242	198	155	62	0	0	0	0	0		Q80W93
ENSMUST00000043148	ENSMUSG00000036402	6	66896397	67021350	1	15	15	4	24	21	7	279	813	372	114	297		Q9DAS9
ENSMUST00000043149	ENSMUSG00000042351	15	80623505	80650559	1	40	38	213	80	57	41	42	57	29	16	175	Q3U0E8	O89100
ENSMUST00000043150	ENSMUSG00000024981	19	55253369	55296627	1	13	27	76	68	25	14	645	3614	1399	420	1167	Q3UC67	Q8JZR0
ENSMUST00000043151	ENSMUSG00000041020	X	159414572	159498757	1	0	0	0	0	1	1	0	1	0	0	0		A2AG50
ENSMUST00000043152	ENSMUSG00000035575	11	79932321	79962390	-1	14	24	25	27	29	16	60	325	171	145	131		Q8VCY6
ENSMUST00000043160	ENSMUSG00000040383	2	114101170	114187024	-1	6	10	14	10	5	9	253	606	521	97	445		Q8CFQ3
ENSMUST00000043161						8	7	11	13	0	0	380	235	366	54	401		
ENSMUST00000043169	ENSMUSG00000042350	12	84918148	84970900	-1	0	9	15	78	19	13	946	1128	1830	118	1301		Q8CHG5
ENSMUST00000043170						11	5	13	23	12	9	5	57	16	15	30		
ENSMUST00000043172	ENSMUSG00000001288	15	102234938	102257517	-1	5	0	0	70	19	0	0	19	0	0	15		P18911
ENSMUST00000043183	ENSMUSG00000031877	8	104961718	104969537	1	46	51	325	78	69	48	74	13	27	7	18	E9PV38	
ENSMUST00000043189	ENSMUSG00000026442	1	132564690	132741797	-1	49	20	0	296	80	20	0	0	0	0	5	E9Q171	
ENSMUST00000043195	ENSMUSG00000035125	6	81923669	81959915	1	0	1	4	31	8	3	0	2	0	0	3		Q8BKT3
ENSMUST00000043200	ENSMUSG00000032870	4	120968317	121017247	-1	16	8	17	238	22	11	3275	9113	4749	500	3666		Q7TN29
ENSMUST00000043204	ENSMUSG00000035329	12	59200655	59219725	-1	13	3	2	203	6	11	269	1012	492	165	208		Q8VE08
ENSMUST00000043208	ENSMUSG00000034460	12	73099609	73113456	-1	43	36	195	327	58	32	4	3	1	0	9		Q61321
ENSMUST00000043209	ENSMUSG00000031884	8	104867488	104874080	1	23	14	48	26	17	7	0	0	0	1	0		
ENSMUST00000043211	ENSMUSG00000039914	10	128363097	128370032	-1	15	13	23	84	14	8	125	338	135	47	109	E9Q3H6	
ENSMUST00000043214	ENSMUSG00000033220	15	78559169	78572783	-1	111	107	480	156	122	92	43541	60822	32499	11695	22929		Q05144
ENSMUST00000043227	ENSMUSG00000035469	14	59201209	59237265	1	17	24	15	29	24	17	20	125	43	0	28		
ENSMUST00000043235	ENSMUSG00000040843	1	165212286	165236996	-1	21	27	46	38	20	11	106	441	207	231	107		Q8BH58
ENSMUST00000043237	ENSMUSG00000038375	2	155381059	155389850	1	15	18	57	115	46	19	2967	4815	2610	111	1380		Q8CFU8
ENSMUST00000043249	ENSMUSG00000061068	14	56059744	56062310	-1	7	6	24	13	15	5	1	0	0	1	1	Q3UN88	
ENSMUST00000043259	ENSMUSG00000041741	6	141249269	141507448	1	68	65	178	564	87	33	0	3	2	1	6	B2RR84	Q9Z0X4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000043266	ENSMUSG00000041068	14	35809488	35811978	-1	9	6	16	16	3	0	0	0	0	0	0	Q3V0H9	
ENSMUST00000043269	ENSMUSG00000021546	13	58391142	58403343	-1	0	0	0	0	0	0	1302	4608	1301	495	876		P61979
ENSMUST00000043273	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	89	43	65	41	28		Q8BGJ9
ENSMUST00000043279	ENSMUSG00000047495	8	14095865	14847680	1	0	0	0	0	0	0	0	0	0	0	0		Q8BJ42
ENSMUST00000043283	ENSMUSG00000041890	5	114727407	114775517	-1	0	0	0	0	0	0	157	318	835	49	713	Q80XR8	
ENSMUST00000043285	ENSMUSG00000040978	11	9048594	9069356	1	19	7	56	52	26	8	5	23	10	15	4	B2RVL0	Q5SS90
ENSMUST00000043286	ENSMUSG00000038425	18	70508680	70530620	-1	0	0	0	0	4	0	0	112	45	15	24		
ENSMUST00000043294	ENSMUSG00000042607	6	5383386	5433022	1	16	11	39	15	28	9	1	20	7	0	2		Q9WV71
ENSMUST00000043296	ENSMUSG00000037544	14	47387779	47418407	-1	11	16	18	9	6	11	72	93	124	123	66		
ENSMUST00000043301	ENSMUSG00000040627	6	122553801	122564180	1	2	6	11	2	7	8	23	21	26	2	29		Q9WVE0
ENSMUST00000043305	ENSMUSG00000037622	4	133292459	133353481	-1	0	0	66	273	52	29	2667	2181	1884	191	1658		Q80ZK9
ENSMUST00000043311	ENSMUSG00000035697	10	80016653	80031472	1	0	12	8	4	9	5	4150	5475	3609	278	3454		Q3TBD2
ENSMUST00000043313	ENSMUSG00000042751	1	152954993	153119261	1	13	0	25	5	10	0	1	3	0	1	0	Q5HZI3	Q8BNJ3
ENSMUST00000043314	ENSMUSG00000040703	7	25802475	25816913	-1	0	0	0	0	0	0	137	48	119	14	98		Q9DBX6
ENSMUST00000043315	ENSMUSG00000041481	12	104236245	104241939	1	10	6	12	13	16	3	203	181	120	107	133	F2Z405	
ENSMUST00000043317	ENSMUSG00000036764	10	63382443	63408840	1	9	8	0	2	0	4	97	65	99	131	14		Q9R022
ENSMUST00000043321	ENSMUSG00000020366	11	49846751	49886421	1	0	2	1	0	0	0	23	17	30	0	39		Q9WTU6
ENSMUST00000043325	ENSMUSG00000040151	3	144429706	144570181	-1	10	10	33	97	27	5	79	164	141	25	114		Q8R3H7
ENSMUST00000043333	ENSMUSG00000048930	6	113366025	113377883	-1	0	0	0	0	0	0	270	348	248	12	132		Q8R0L9
ENSMUST00000043335	ENSMUSG00000028573	4	95557507	95926939	1	2	5	2	1	0	0	0	0	0	0	0		A2AJL3
ENSMUST00000043336	ENSMUSG00000040710	1	95587682	95667571	-1	3	3	5	13	8	1	666	1930	832	704	842	Q53WR7	Q64692
ENSMUST00000043338	ENSMUSG00000040848	1	165174337	165194438	-1	19	17	85	88	28	17	1917	5663	2649	355	2347		Q8VD57
ENSMUST00000043342	ENSMUSG00000033554	3	115887837	115934361	1	51	71	47	23	58	32	5	25	10	22	24		Q9CWQ0
ENSMUST00000043349	ENSMUSG00000041078	14	34819825	35583379	1	148	88	352	431	152	93	0	2	4	1	7		Q61627
ENSMUST00000043352	ENSMUSG00000037913	5	65054346	65091629	-1	9	5	7	4	6	3	203	1760	593	649	438	D3Z447	
ENSMUST00000043356	ENSMUSG00000042208	11	23564961	23633639	-1	10	6	2	4	12	7	10	17	0	26	24		Q68FF0
ENSMUST00000043359	ENSMUSG00000031715	8	80698507	80739497	-1	43	35	28	547	67	22	270	1275	508	116	187		Q91ZW3
ENSMUST00000043368	ENSMUSG00000034610	4	108459426	108559421	1	0	0	13	0	10	0	121	84	450	1	43		B2RX14
ENSMUST00000043374	ENSMUSG00000040653	10	3366150	3464975	1	18	17	29	455	37	19	1	7	2	3	2		Q8R4S0
ENSMUST00000043377	ENSMUSG00000040985	11	9016054	9048991	-1	0	8	0	0	0	5	0	0	0	0	0	E9LV81	Q5SS91
ENSMUST00000043378	ENSMUSG00000039886	5	135735485	135744448	-1	7	0	7	67	8	7	1423	2149	796	309	622		Q8C1E7
ENSMUST00000043379	ENSMUSG00000036731	2	25238818	25242452	-1	3	2	6	3	13	0	0	0	0	0	0		Q9D1E4
ENSMUST00000043380	ENSMUSG00000038498	19	5335741	5344153	1	16	16	62	25	28	14	0	0	0	0	0		Q91ZR5
ENSMUST00000043382	ENSMUSG00000036463	6	65952609	65954014	1	4	7	2	10	10	5	0	0	0	0	0	Q9CR99	
ENSMUST00000043396	ENSMUSG00000037169	12	12936096	12941914	-1	0	0	0	343	15	6	0	0	0	0	0	Q3UII1	P03966
ENSMUST00000043397	ENSMUSG00000035172	11	101162679	101171351	-1	0	0	43	280	26	0	0	0	0	0	0		Q8VCE9
ENSMUST00000043400	ENSMUSG00000033508	6	86628164	86629710	1	12	18	59	30	29	25	50152	37798	31076	17628	14345		Q09PK2
ENSMUST00000043409	ENSMUSG00000039081	14	21983962	21989601	-1	25	30	39	1208	72	30	22	55	25	14	61		Q7TMA2
ENSMUST00000043414	ENSMUSG00000036661	15	73512560	73572242	1	0	0	0	155	14	0	1546	2582	2286	143	1702		A2RT67
ENSMUST00000043415	ENSMUSG00000039179	16	10357948	10395490	-1	5	3	20	114	18	3	0	0	0	0	0	G5E8A8	
ENSMUST00000043419	ENSMUSG00000078812	11	69916714	69921958	-1	0	3	0	91	0	5	10	34	31	12	36		P63242
ENSMUST00000043422	ENSMUSG00000038213	6	125223933	125231860	-1	39	64	92	66	56	43	186	360	167	68	256		Q8VD31
ENSMUST00000043429	ENSMUSG00000032897	4	120757438	120831572	-1	0	0	0	2	0	0	326	901	355	305	394		P70353
ENSMUST00000043437	ENSMUSG00000038524	18	37957431	37969774	-1	9	14	34	22	17	15	311	381	283	34	328		Q6PFY1
ENSMUST00000043440	ENSMUSG00000040498	7	19937305	19950743	-1	29	11	29	23	26	13	10	3	4	3	6	B2RTN2	
ENSMUST00000043441	ENSMUSG00000040363	X	12036740	12160355	-1	37	9	101	21	13	2	219	423	334	29	353		Q8CGN4
ENSMUST00000043447	ENSMUSG00000033857	11	118476829	118489209	1	6	6	8	121	24	10	0	0	0	0	0		Q8BX80
ENSMUST00000043456	ENSMUSG00000038729	4	57717657	57896982	1	0	0	0	0	0	0	0	0	0	0	0		O54931
ENSMUST00000043458	ENSMUSG00000038541	17	74017706	74047916	-1	8	5	22	48	11	4	0	0	0	0	0		Q99N99
ENSMUST00000043459	ENSMUSG00000037904	12	110975353	110979040	-1	1	2	4	85	7	0	36	19	0	0	14		Q8BH83
ENSMUST00000043464	ENSMUSG00000038545	17	46650337	46664364	1	17	0	0	141	43	21	18	0	13	0	17	A9C491	Q8VE73
ENSMUST00000043475	ENSMUSG00000038676	5	31138063	31138829	-1	1	2	1	151	9	3	0	0	0	0	0		P81615
ENSMUST00000043484	ENSMUSG00000038555	18	34840589	34847463	1	20	14	21	86	22	16	3	18	9	0	10		Q8VCD6
ENSMUST00000043493	ENSMUSG00000034525	13	70588689	70637634	-1	45	45	91	69	61	30	985	2515	2301	198	2140		E9Q286
ENSMUST00000043498	ENSMUSG00000024454	18	37935844	37954988	-1	5	3	13	15	14	2	370	761	319	123	341	Q3UM33	
ENSMUST00000043503	ENSMUSG00000038677	17	28142316	28174852	1	50	12	46	89	43	24	0	0	0	0	0		Q66PY1
ENSMUST00000043517	ENSMUSG00000040511	7	19903578	19921160	-1	43	41	294	78	58	31	21	49	16	26	46	Q8K094	
ENSMUST00000043520	ENSMUSG00000038365	8	13907806	13940521	1	14	8	16	35	12	5	60	154	89	105	60		Q9D2Y6
ENSMUST00000043521	ENSMUSG00000034473	16	35311131	35363918	-1	19	19	15	29	21	3	35	153	60	139	36	B2RSR2	Q8BH47
ENSMUST00000043526	ENSMUSG00000036712	8	88697028	88751945	1	62	0	0	90	0	0	142	192	282	0	198	Z4YJJ5	
ENSMUST00000043531	ENSMUSG00000038604	8	105605229	105622194	1	35	30	127	134	59	30	312	300	291	20	295		Q68FE6
ENSMUST00000043550	ENSMUSG00000037318	1	193175453	193201703	-1	5	0	0	0	5	0	401	1421	835	633	577	G3X949	
ENSMUST00000043551	ENSMUSG00000040351	5	3690000	3802925	-1	33	24	35	194	39	17	214	381	401	46	306		Q6ZPS6
ENSMUST00000043552	ENSMUSG00000060147	13	33917918	34002794	-1	7	0	0	21	0	0	0	11	7	1630	127	Q4FJQ6	Q60854
ENSMUST00000043553						5	6	12	8	9	6	0	0	0	0	0		
ENSMUST00000043560	ENSMUSG00000042772	1	152836995	152902646	-1	10	33	31	0	13	5	197	417	422	69	143		Q5RJH6
ENSMUST00000043577	ENSMUSG00000041378	16	18776847	18778260	1	16	6	21	284	18	9	0	0	0	0	0		O54942
ENSMUST00000043578	ENSMUSG00000033740	1	6487231	6860940	1	17	0	0	0	0	7	0	0	0	0	0	Q148A0	Q80TY4
ENSMUST00000043584	ENSMUSG00000036752	2	25222160	25224702	-1	7	6	22	20	9	8	1552	2869	1572	376	1256		P68372
ENSMUST00000043589	ENSMUSG00000038844	2	142617474	142901531	-1	34	29	47	130	43	11	135	242	271	57	196		B1AVY7
ENSMUST00000043596	ENSMUSG00000034055	X	102513975	102644246	-1	0	16	14	15	26	12	0	47	24	4	0	A2AI91	
ENSMUST00000043598	ENSMUSG00000038217	11	75461715	75470899	1	35	45	54	126	41	9	13	17	9	11	24		Q8VC26
ENSMUST00000043599	ENSMUSG00000021180	12	100549778	100725028	-1	15	13	35	114	18	5	60	144	168	47	113		Q8C050
ENSMUST00000043604	ENSMUSG00000034781	10	81528724	81545190	-1	20	19	31	115	33	10	186	218	126	27	172	Q3UPA1	P21278
ENSMUST00000043605	ENSMUSG00000060176	13	58287516	58354862	-1	26	13	31	17	36	12	0	1	0	2	1		Q7M6Z4
ENSMUST00000043610	ENSMUSG00000038658	19	29522282	29606829	1	11	24	74	56	33	7	198	360	270	24	128	E9QPA1	
ENSMUST00000043612	ENSMUSG00000033847	7	13324655	13360672	1	6	12	8	8	14	5	0	1	0	0	0	Q64GA5	
ENSMUST00000043616	ENSMUSG00000034636	4	108229724	108301096	-1	55	34	60	110	65	31	878	2373	2035	186	1026		Q3UFS0
ENSMUST00000043624	ENSMUSG00000034297	11	86267033	86357602	-1	31	20	60	66	43	23	859	1460	1787	119	1274		Q5SWW4
ENSMUST00000043627	ENSMUSG00000039640	11	120484613	120489065	1	13	5	20	80	12	9	140	208	85	130	92		Q9DB15
ENSMUST00000043628	ENSMUSG00000035158	6	97807052	98021349	1	14	7	34	10	0	0	0	0	0	0	1	Q32MU7	Q08874
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ENSMUST00000043637	ENSMUSG00000035158	6	97807052	98021349	1	9	11	8	21	9	11	113	318	113	42	85	Q3U2D2	
ENSMUST00000043650	ENSMUSG00000041930	5	114568016	114613220	1	25	14	37	688	32	17	8	16	9	3	16		Q6PGH4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000043654	ENSMUSG00000045007	11	101155907	101161787	1	16	10	41	97	28	8	0	1	0	1	2	Q6F4J0	Q8VCK3
ENSMUST00000043658						0	0	0	19	0	2	3	0	0	0	0		
ENSMUST00000043674	ENSMUSG00000038838	17	35655634	35667592	-1	7	14	0	36	9	11	36	69	37	7	56		Q3U2A8
ENSMUST00000043675	ENSMUSG00000038717	9	44913250	44920742	-1	9	11	9	85	20	3	1055	1543	764	5017	642		Q9CPQ8
ENSMUST00000043676	ENSMUSG00000029797	6	48448229	48501250	1	27	54	219	0	87	51	2	5	0	0	1		Q8CG65
ENSMUST00000043680	ENSMUSG00000035198	11	101119938	101126419	1	13	4	56	63	19	11	163	146	134	24	131	Q6F4J1	P83887
ENSMUST00000043693	ENSMUSG00000037315	X	20425688	20519939	1	0	0	8	0	0	0	1	0	15	14	14		Q6IE82
ENSMUST00000043696	ENSMUSG00000038224	11	75431732	75439591	-1	0	0	0	0	0	0	0	0	0	0	0	Q5ND36	Q61247
ENSMUST00000043707	ENSMUSG00000039917	5	135632618	135646448	1	57	53	67	81	25	32	112	214	138	46	156		Q8VEK2
ENSMUST00000043709	ENSMUSG00000034792	10	81502306	81524225	-1	19	6	19	139	23	10	341	321	277	13	203		P30678
ENSMUST00000043711	ENSMUSG00000063656	5	72965808	72974702	-1	0	0	3	0	0	0	2	0	5	0	0	F6TEE5	
ENSMUST00000043716	ENSMUSG00000021276	12	110872610	110889145	-1	17	7	22	20	17	8	43	158	57	159	74		Q9D0V8
ENSMUST00000043718	ENSMUSG00000034159	1	93151349	93160948	-1	28	4	30	10	27	8	0	0	0	0	0		Q8CEZ4
ENSMUST00000043722	ENSMUSG00000033880	11	118392751	118402092	-1	15	6	28	22	21	11	93	177	67	146	805		Q07797
ENSMUST00000043725	ENSMUSG00000070695	1	115684756	116587323	1	80	62	179	115	90	45	1	2	1	0	4		Q0V8T9
ENSMUST00000043726	ENSMUSG00000038742	9	20873809	20879727	-1	7	5	18	88	9	7	1	4	0	2	3		Q8R0Z6
ENSMUST00000043734	ENSMUSG00000038750	9	78327589	78329620	1	0	0	0	0	0	0	0	0	0	0	0	D3YX29	
ENSMUST00000043735	ENSMUSG00000040675	10	3973118	4167081	1	0	0	0	0	0	0	0	37	103	0	112		Q3V3R1
ENSMUST00000043739	ENSMUSG00000038754	19	46131897	46135307	1	9	8	18	12	12	1	9	28	10	3	1		O35949
ENSMUST00000043754	ENSMUSG00000056728	13	60798250	60802844	-1	12	7	8	4	9	5	0	0	0	0	0	Q3ULP7	
ENSMUST00000043755						12	12	3	0	15	2	2	0	57	13	24		
ENSMUST00000043757	ENSMUSG00000038762	17	35956819	35969761	-1	21	19	62	20	25	12	477	1088	808	110	686		Q6P542
ENSMUST00000043760	ENSMUSG00000041939	5	114444269	114460591	1	0	0	0	0	0	0	91	71	98	16	46		Q9R008
ENSMUST00000043765	ENSMUSG00000040725	7	25721165	25754757	-1	34	11	80	188	53	22	3251	5349	5411	582	3884		Q8VDM6
ENSMUST00000043767	ENSMUSG00000038398	8	13785615	13798538	1	4	2	2	110	11	9	140	534	314	133	259	Q3ULJ3	
ENSMUST00000043774	ENSMUSG00000036770	2	25212207	25214637	-1	0	0	0	0	0	0	0	0	0	0	0	A2RSX4	
ENSMUST00000043775	ENSMUSG00000038773	18	34777008	34839370	1	39	24	95	99	75	35	1821	3001	3224	212	2909	B9EKS2	
ENSMUST00000043781	ENSMUSG00000040728	4	11331933	11386783	-1	0	0	0	0	0	8	0	0	0	0	0	Z4YJI3	
ENSMUST00000043785	ENSMUSG00000038781	17	55997081	56005570	-1	15	6	39	27	26	12	21	57	27	15	18		Q8R0L1
ENSMUST00000043793	ENSMUSG00000034645	4	108181934	108217922	-1	0	0	0	12	0	0	0	0	0	0	0	F8WHU3	
ENSMUST00000043794	ENSMUSG00000063646	5	37028335	37148001	1	8	2	14	10	9	3	14	22	7	2	40		Q8BVL9
ENSMUST00000043797	ENSMUSG00000041791	6	140041252	140042778	1	4	7	5	6	9	0	0	0	0	0	0		P70190
ENSMUST00000043803	ENSMUSG00000038791	18	43764289	43767399	1	3	2	3	0	0	0	0	0	0	0	0		Q920H1
ENSMUST00000043805	ENSMUSG00000039048	9	35204206	35211055	-1	0	0	0	0	0	0	21	14	0	9	106		Q3TQB2
ENSMUST00000043812	ENSMUSG00000004591	3	142790902	142882004	-1	7	9	12	15	9	11	165	559	196	44	117		Q8BWW9
ENSMUST00000043813	ENSMUSG00000033405	14	73519864	73548242	-1	31	33	67	65	47	21	24	63	37	18	37		Q8BG93
ENSMUST00000043814	ENSMUSG00000038417	10	41188172	41303241	-1	11	5	16	90	21	8	342	917	667	234	472		Q91WF7
ENSMUST00000043815	ENSMUSG00000038759	6	35177421	35247596	1	26	21	30	67	33	17	101	201	239	106	255	B9EJ54	
ENSMUST00000043822	ENSMUSG00000040525	7	19778881	19796809	-1	0	0	0	37	0	0	0	0	0	0	0		Q80XL1
ENSMUST00000043829	ENSMUSG00000042202	4	155601416	155623340	1	0	0	0	54	1	0	0	0	27	0	10		Q8C811
ENSMUST00000043836	ENSMUSG00000068205	2	140395309	142392966	1	2	6	6	1	5	7	0	0	0	0	0	Q9D117	
ENSMUST00000043839	ENSMUSG00000038235	1	171437535	171464603	1	24	16	91	61	30	16	127	275	131	28	116		O88792
ENSMUST00000043843	ENSMUSG00000038366	11	97799000	97838764	1	44	39	114	147	70	44	11499	13716	10456	615	6955	Q543N3	Q61792
ENSMUST00000043845	ENSMUSG00000032841	2	101714285	101883027	-1	0	0	0	0	0	0	227	1220	448	45	570		A2AVJ5
ENSMUST00000043848	ENSMUSG00000038252	6	125168007	125191701	-1	13	5	31	25	10	10	440	276	570	23	294		
ENSMUST00000043850	ENSMUSG00000036826	7	30565427	30567962	1	0	0	0	0	9	0	10	13	0	2	20		Q3U4N7
ENSMUST00000043864	ENSMUSG00000039128	2	5794294	5845164	-1	99	98	119	89	138	67	146	744	245	505	223		Q8CII2
ENSMUST00000043865	ENSMUSG00000071711	15	78406712	78414002	1	8	8	18	28	19	8	24	26	15	10	8	Q3UW66	
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ENSMUST00000043867	ENSMUSG00000039221	3	28805436	28807424	1	3	2	0	8	0	0	0	30	0	140	0	Q0VBA4	Q9D7S7
ENSMUST00000043870	ENSMUSG00000038489	7	141471860	141475132	-1	29	41	77	73	49	40	64	129	47	92	53		P62876
ENSMUST00000043873	ENSMUSG00000064057	11	49663610	49665118	1	1	0	7	0	3	2	3	26	4	5	9	Q5NCL1	Q920D7
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ENSMUST00000043884	ENSMUSG00000036295	12	41451673	41485751	-1	14	14	12	6	14	6	6	5	0	35	16		Q8CBC6
ENSMUST00000043893	ENSMUSG00000029174	5	64156305	64351486	1	33	17	84	657	48	24	28	109	72	24	48		Q60949
ENSMUST00000043896	ENSMUSG00000038872	8	108703100	108961630	1	116	84	423	1150	169	89	620	412	1357	28	809	E9QMD3	
ENSMUST00000043897	ENSMUSG00000025733	17	25838457	25844851	-1	13	17	18	91	32	12	446	682	406	53	321		Q8JZN7
ENSMUST00000043898	ENSMUSG00000036835	7	30561868	30563184	-1	10	9	23	12	17	9	2100	3016	1183	3189	762		Q9CQR7
ENSMUST00000043907	ENSMUSG00000038880	17	24895116	24897502	1	0	4	0	29	0	0	159	199	107	40	85		Q9JIK9
ENSMUST00000043911	ENSMUSG00000038884	9	20868642	20874307	1	12	14	0	860	59	16	0	30	2	10	10		Q8CAK3
ENSMUST00000043914	ENSMUSG00000021975	14	64950045	65039835	1	14	14	24	18	29	11	340	656	367	79	246		
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ENSMUST00000043922	ENSMUSG00000038895	9	22055460	22071345	-1	22	13	41	38	30	16	35	16	0	0	0		Q6YND2
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ENSMUST00000043929	ENSMUSG00000038903	18	69925426	69969484	1	6	1	10	10	6	1	0	0	0	20	4		Q8BVC4
ENSMUST00000043931	ENSMUSG00000034566	11	115415689	115419962	-1	0	0	0	0	0	0	637	1588	567	3059	403		Q9DCX2
ENSMUST00000043937	ENSMUSG00000041084	3	130695912	130709444	-1	6	1	0	17	3	2	345	1381	397	1430	295		Q78XF5
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ENSMUST00000043944	ENSMUSG00000055489	7	51511029	51598709	1	36	28	36	37	36	24	0	0	0	0	0		Q75UR0
ENSMUST00000043951	ENSMUSG00000037351	1	36698114	36714422	-1	17	8	29	53	29	14	732	1318	700	102	730		Q8R5C5
ENSMUST00000043961	ENSMUSG00000018800	11	110269369	110337716	-1	15	18	11	21	22	7	2	9	7	1	0		Q8K448
ENSMUST00000043962	ENSMUSG00000038416	8	13757676	13781938	1	9	2	12	63	8	6	131	510	207	98	123	Q3TI84	Q8R349
ENSMUST00000043964	ENSMUSG00000039474	5	36966104	36989205	-1	13	8	38	171	38	0	0	13	0	0	40	Q3TDI2	P56695
ENSMUST00000043966	ENSMUSG00000037531	3	32725397	32737605	-1	10	12	20	15	15	4	9	72	23	93	9		Q8K2Y7
ENSMUST00000043970	ENSMUSG00000041358	2	112247948	112259291	-1	29	19	35	49	36	15	2	1	4	0	2		Q8BHP2
ENSMUST00000043975	ENSMUSG00000036845	7	30555441	30559838	-1	0	0	4	0	0	0	146	198	106	147	84		Q9D8N6
ENSMUST00000043983	ENSMUSG00000042035	3	101377083	101463059	1	58	63	170	121	99	36	5	0	2	5	24		Q6ZQA6
ENSMUST00000043990	ENSMUSG00000038957	9	57708540	57752499	1	28	21	46	77	44	10	395	1121	638	122	533	A0ELI5	Q8K2D3
ENSMUST00000044000	ENSMUSG00000021098	12	72881109	72940774	-1	1	1	8	72	0	2	0	0	0	0	0		Q9CTN5
ENSMUST00000044002	ENSMUSG00000036687	5	139802485	139819917	-1	5	0	33	61	17	4	0	0	0	0	0	G3X923	
ENSMUST00000044003	ENSMUSG00000044749	11	110176820	110251776	-1	15	19	12	15	20	8	8	25	9	5	28		Q8K441
ENSMUST00000044005	ENSMUSG00000039200	16	10192712	10243051	1	5	10	28	72	10	1	0	0	0	0	0		Q3UL97
ENSMUST00000044007	ENSMUSG00000039670	11	120456606	120458068	-1	3	4	13	52	9	3	28	45	23	21	16	B2RVP3	Q9CR10

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
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ENSMUST00000044011	ENSMUSG00000032966	2	151542483	151561692	1	16	0	0	94	17	12	210	515	136	103	238		P26883
ENSMUST00000044018	ENSMUSG00000036805	2	25085667	25095149	-1	0	0	19	18	11	15	0	0	0	0	0		Q8CJ00
ENSMUST00000044019	ENSMUSG00000030089	6	90604725	90646412	1	19	15	52	96	23	28	417	351	297	33	198	G3X937	
ENSMUST00000044021	ENSMUSG00000040918	1	164249046	164265385	1	17	8	20	76	8	9	52	152	0	17	0	Q9EQN9	
ENSMUST00000044022	ENSMUSG00000028434	4	56991972	57143437	-1	0	0	4	0	4	1	0	0	0	0	0	B1AXV1	
ENSMUST00000044031	ENSMUSG00000032864	2	101624718	101632529	1	42	43	35	38	50	37	0	4	5	0	7	Q542D1	P21784
ENSMUST00000044036	ENSMUSG00000058318	2	92093117	92364666	1	0	14	0	28	28	0	345	1346	29	76	205	D3Z764	
ENSMUST00000044038	ENSMUSG00000039648	2	30185124	30205847	-1	3	0	1	7	4	4	13	28	0	0	19	Q05CI8	Q8BTY1
ENSMUST00000044039	ENSMUSG00000040367	5	3845173	3866596	1	6	9	6	10	12	7	0	3	3	5	1		Q8C0R9
ENSMUST00000044043	ENSMUSG00000079941	13	21501029	21501418	-1	0	0	6	55	4	3	1	126	18	0	11	Q9D881	
ENSMUST00000044048	ENSMUSG00000036854	7	30552178	30555443	1	10	2	40	62	8	2	9	0	0	0	0		Q5EBG6
ENSMUST00000044051	ENSMUSG00000039016	9	50603901	50605320	1	5	1	4	19	0	3	240	548	176	902	127		P62077
ENSMUST00000044053	ENSMUSG00000090112	10	11149427	11217595	1	49	38	62	17	48	26	63	239	87	56	104		Q7TPQ3
ENSMUST00000044058	ENSMUSG00000041241	4	138434671	138442265	1	0	20	12	326	30	25	462	404	290	45	183		Q8VCM5
ENSMUST00000044059	ENSMUSG00000036816	10	63100156	63100605	1	0	0	0	48	3	1	0	0	0	0	0		Q9Z2E5
ENSMUST00000044060	ENSMUSG00000040165	8	3940222	3954746	-1	965	1053	646	842	1145	540	25	147	56	60	67		Q91ZW9
ENSMUST00000044068	ENSMUSG00000039456	16	93832121	93876072	1	6	8	16	39	19	5	591	2077	1162	1256	932	F7BJB9	
ENSMUST00000044078	ENSMUSG00000036813	2	25080304	25085716	1	0	0	0	0	0	4	0	0	0	0	0		Q8K0L2
ENSMUST00000044081	ENSMUSG00000034575	13	69497959	69534617	-1	26	18	73	70	43	15	71	117	76	9	106		Q6PB75
ENSMUST00000044083	ENSMUSG00000021559	13	60601947	60763185	1	24	14	78	98	29	0	5	30	30	3	125		Q80YE7
ENSMUST00000044089	ENSMUSG00000038997	3	153844209	153855082	1	21	14	15	19	14	7	0	4	3	2	1		Q8VHP9
ENSMUST00000044094	ENSMUSG00000038092	3	98618634	98630252	-1	4	4	29	9	12	8	0	0	0	0	0		Q61694
ENSMUST00000044101						64	57	98	361	79	52	8	11	20	2	32		
ENSMUST00000044103	ENSMUSG00000039209	16	10170226	10174911	1	2	2	0	3	0	0	3	0	3	3	0	Q9CQD0	
ENSMUST00000044105	ENSMUSG00000039691	11	120442644	120446950	1	16	7	21	16	19	13	0	0	0	0	0	Q3UGA5	
ENSMUST00000044106	ENSMUSG00000039067	8	107580381	107588482	-1	11	10	30	155	12	3	308	844	345	321	314	A1L3B8	P26516
ENSMUST00000044111	ENSMUSG00000038387	7	45018007	45021644	1	8	3	24	36	4	7	145	221	72	64	105	Q3U1N3	P10833
ENSMUST00000044113	ENSMUSG00000036698	15	73095844	73184840	-1	112	80	257	149	136	62	2192	2683	4437	149	3461		Q8CJG0
ENSMUST00000044115	ENSMUSG00000038797	7	80860920	80876537	1	14	12	32	125	18	8	11	38	14	3	12		Q07230
ENSMUST00000044116	ENSMUSG00000036580	3	55112108	55137322	1	0	15	0	32	0	6	15	66	36	18	37	Q3TVW1	Q8R1X6
ENSMUST00000044123	ENSMUSG00000039079	8	122356967	122360746	-1	13	7	22	24	23	8	0	0	0	0	0	Q9ERT2	
ENSMUST00000044125	ENSMUSG00000035187	5	101658139	101664996	-1	6	2	18	428	10	6	0	0	1	0	0		Q99MA9
ENSMUST00000044138	ENSMUSG00000037347	X	20059560	20097521	1	7	7	9	280	13	2	0	1	0	0	7		Q9EP78
ENSMUST00000044143	ENSMUSG00000039097	19	29331170	29334670	-1	0	4	13	2	4	5	0	0	0	0	0	A2RTV8	
ENSMUST00000044148	ENSMUSG00000039740	4	47465067	47474333	-1	5	11	12	86	13	8	66	157	91	13	70		Q9DBE8
ENSMUST00000044152	ENSMUSG00000034586	11	115347707	115367756	-1	0	14	80	11	46	0	12	16	5	3	31	Q3UU20	Q8R1F6
ENSMUST00000044155	ENSMUSG00000032020	9	41011098	41161697	-1	31	21	34	311	38	20	190	992	440	74	350		Q8BGG7
ENSMUST00000044158	ENSMUSG00000041560	7	15936183	15946074	-1	8	15	22	186	25	17	2331	2957	1584	308	1216	Q8BK35	
ENSMUST00000044159	ENSMUSG00000060807	12	103646630	103657212	-1	15	14	36	8	11	3	0	0	0	0	0		Q06770
ENSMUST00000044163	ENSMUSG00000038784	6	35022065	35133724	-1	18	10	44	11	14	8	38	56	20	38	34		Q8BT14
ENSMUST00000044165	ENSMUSG00000039115	9	118606690	118901003	1	55	28	146	100	51	33	1	1	1	24	52		B8JK39
ENSMUST00000044166	ENSMUSG00000038446	10	40831626	40883143	-1	22	16	247	48	23	13	480	1940	1037	1369	760		Q9DC48
ENSMUST00000044179	ENSMUSG00000042386	X	140808307	140813433	-1	18	22	20	50	26	16	1	1	1	0	5	Q99MW5	
ENSMUST00000044180	ENSMUSG00000033774	1	5913707	5917398	-1	61	50	413	296	67	38	0	6	3	0	1		P49681
ENSMUST00000044188	ENSMUSG00000037358	X	18414881	18461397	-1	7	0	2	0	3	0	0	0	0	0	0		Q8C3I9
ENSMUST00000044189	ENSMUSG00000033075	15	98038744	98093744	-1	27	21	32	124	40	31	189	670	358	48	228		P59110
ENSMUST00000044190	ENSMUSG00000037375	1	192496711	192771223	-1	4	6	31	46	14	9	0	8	1	1	6		Q8BMT9
ENSMUST00000044195	ENSMUSG00000042246	7	118535843	118584736	-1	26	27	63	39	32	22	4	12	4	1	9		Q8C428
ENSMUST00000044200	ENSMUSG00000038279	6	125131909	125144753	1	24	19	53	62	33	14	195	301	165	55	210	E9QN31	
ENSMUST00000044204	ENSMUSG00000056310	5	130255619	130341563	1	24	31	129	51	36	21	3	21	7	0	7		
ENSMUST00000044207	ENSMUSG00000039148	19	5377523	5388703	-1	30	21	102	153	64	20	967	1824	1386	162	1058		Q9Z315
ENSMUST00000044210	ENSMUSG00000035923	10	107492860	107494729	-1	10	4	11	9	7	2	0	0	0	0	0	Q0VEJ7	P15375
ENSMUST00000044216	ENSMUSG00000039154	17	55970467	55976617	1	12	8	28	130	13	8	1	2	0	0	3		O88834
ENSMUST00000044217	ENSMUSG00000063450	12	75818134	76110926	1	63	48	85	91	88	51	49	2	42	0	58		Q6ZWQ0
ENSMUST00000044220	ENSMUSG00000039163	9	118064529	118150196	-1	4	2	0	46	2	2	45	109	54	155	49		Q9CPZ8
ENSMUST00000044224	ENSMUSG00000032623	5	120914536	120921652	1	12	12	29	17	16	11	0	2	0	0	0	Q8VI95	
ENSMUST00000044228	ENSMUSG00000040592	11	106311341	106314762	-1	14	6	19	6	12	12	18	12	6	12	18	B1ARJ9	
ENSMUST00000044231	ENSMUSG00000061947	12	103614786	103631444	-1	479	352	409	19975	1008	443	8	34	12	7	5		Q8R121
ENSMUST00000044234	ENSMUSG00000007613	4	47353222	47414931	1	0	0	0	0	0	0	9	0	178	0	52		Q64729
ENSMUST00000044248	ENSMUSG00000028600	4	108014791	108096445	-1	24	21	179	0	9	17	0	0	0	1	1		Q7TQ62
ENSMUST00000044250	ENSMUSG00000042650	11	60536381	60558512	1	74	66	354	687	83	49	1525	3032	1939	168	1425		Q3TSG4
ENSMUST00000044252	ENSMUSG00000039183	17	24882611	24886350	-1	10	8	27	15	12	7	745	917	410	210	404		Q9R061
ENSMUST00000044255	ENSMUSG00000035778	2	35400179	35463231	-1	0	0	0	0	0	0	0	0	0	0	13	Q9DBU1	
ENSMUST00000044256	ENSMUSG00000054498	7	86320995	86322050	-1	4	1	2	3	1	3	0	0	0	0	0	Q8VFP2	
ENSMUST00000044260	ENSMUSG00000033364	1	74435511	74544284	-1	34	15	62	24	43	30	100	280	152	41	84		Q8C0R0
ENSMUST00000044271	ENSMUSG00000039703	11	120380370	120437708	-1	0	7	0	0	40	0	1148	1657	1344	127	887		P60670
ENSMUST00000044277	ENSMUSG00000038467	2	154651705	154694785	1	4	7	12	45	17	0	3967	7647	4253	1529	2959		Q9D8B3
ENSMUST00000044278	ENSMUSG00000039037	3	152817081	152982246	-1	49	27	194	112	60	28	0	2	1	0	2	Q6GTI0	
ENSMUST00000044286	ENSMUSG00000039199	8	105472481	105484350	-1	15	8	35	54	30	8	16	24	10	6	29		Q8R0N9
ENSMUST00000044297	ENSMUSG00000035551	4	45809468	45826923	-1	19	19	57	81	41	10	0	0	1	0	0		Q80W15
ENSMUST00000044299	ENSMUSG00000035431	12	58211772	58214444	1	15	3	8	38	4	8	0	0	0	0	0	Q543T0	P30873
ENSMUST00000044306	ENSMUSG00000019828	10	10686059	11082356	-1	25	39	75	44	28	24	4	21	5	0	17		P97772
ENSMUST00000044311	ENSMUSG00000032649	1	152399830	152510695	1	32	19	68	38	24	13	0	0	0	0	0		Q6NVG7
ENSMUST00000044324	ENSMUSG00000022237	15	31291479	31367759	-1	0	0	0	112	0	0	0	0	29	0	27	H7BX04	
ENSMUST00000044326	ENSMUSG00000039269	17	35567450	35568952	1	0	0	0	0	10	2	0	0	0	0	1		Q8BM15
ENSMUST00000044331	ENSMUSG00000031540	8	22859535	22943259	1	50	23	117	33	0	34	942	716	2985	102	3039	G3X940	
ENSMUST00000044332	ENSMUSG00000035891	15	86139128	86186141	-1	22	19	35	220	42	12	194	180	180	33	264		Q8K4Q7
ENSMUST00000044338	ENSMUSG00000036882	7	30522226	30534180	-1	43	31	80	133	60	35	13	18	25	0	13		Q80YF9
ENSMUST00000044352	ENSMUSG00000034501	12	72536357	72580213	1	19	20	38	52	48	14	21	41	21	29	33	E9QN69	
ENSMUST00000044355	ENSMUSG00000041571	7	15917208	15922402	-1	6	0	20	23	13	8	160	197	71	139	152		P63300
ENSMUST00000044359	ENSMUSG00000052331	1	54645340	54926387	-1	0	0	0	0	0	0	0	0	0	0	0	E9QNQ2	
ENSMUST00000044369	ENSMUSG00000033793	1	5070018	5162529	1	0	2	2	16	3	0	140	600	229	326	85		Q8BVE3
ENSMUST00000044373	ENSMUSG00000036615	3	54803115	54807791	-1	4	3	1	139	8	5	34	190	60	24	64	F7DBT7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000044380	ENSMUSG00000035451	12	57540631	57546121	-1	27	20	83	485	35	5	0	0	0	1	6		P35582
ENSMUST00000044382	ENSMUSG00000035062	X	95639193	95658509	-1	5	0	0	0	0	1	0	0	0	0	0		Q68FG0
ENSMUST00000044384	ENSMUSG00000035561	4	45799022	45804604	1	20	14	21	71	33	11	47	46	15	15	32		Q9CZS1
ENSMUST00000044385	ENSMUSG00000042743	13	104109741	104141735	1	9	11	23	21	20	3	5	35	7	8	17		Q8VD33
ENSMUST00000044387	ENSMUSG00000029847	6	34945278	34988404	-1	22	27	49	27	33	24	0	10	6	4	9	E9PW54	
ENSMUST00000044392	ENSMUSG00000040213	3	142701051	142746870	1	0	9	4	12	12	6	0	0	0	0	4		Q71RI9
ENSMUST00000044405	ENSMUSG00000033446	14	73237895	73243294	1	47	63	180	55	47	41	24	288	53	148	102		Q8BMC0
ENSMUST00000044415	ENSMUSG00000039263	2	174110349	174123070	1	8	9	29	93	34	21	82	71	60	30	79		Q6NSR8
ENSMUST00000044423	ENSMUSG00000034329	11	86058138	86201193	-1	300	289	249	264	336	140	40	93	65	41	60		Q5SXJ3
ENSMUST00000044426	ENSMUSG00000032978	4	119656607	119658954	-1	4	10	17	4	0	0	0	0	0	0	0	Q9QUQ3	O09051
ENSMUST00000044434	ENSMUSG00000041578	7	15865947	15879968	-1	29	0	100	30	35	19	0	0	0	0	0	Q543C9	O54751
ENSMUST00000044441	ENSMUSG00000034310	5	127781630	128433077	-1	20	12	57	113	23	18	0	0	0	0	3		
ENSMUST00000044442	ENSMUSG00000023972	17	46564451	46629504	-1	29	22	47	132	58	17	11	4	5	17	98		Q8BKG3
ENSMUST00000044443	ENSMUSG00000032826	3	126921612	127499350	-1	0	17	0	0	11	0	0	8	7	3	13		Q8C8R3
ENSMUST00000044451	ENSMUSG00000054999	19	6105782	6115792	1	18	12	19	20	26	12	1	2	1	0	6		Q7M758
ENSMUST00000044454	ENSMUSG00000039285	9	118040499	118069794	1	3	1	3	81	7	5	412	1370	414	144	337		Q9QYP6
ENSMUST00000044455	ENSMUSG00000042197	1	33761545	33814595	-1	96	82	222	93	107	41	59	143	151	23	102	Q8VCL4	
ENSMUST00000044462	ENSMUSG00000020712	11	106276672	106288745	1	18	11	42	17	19	6	0	3	1	2	5	Q99NB3	
ENSMUST00000044466	ENSMUSG00000018995	7	96951505	97064758	1	18	8	8	13	7	4	214	219	266	239	249		Q8BGV0
ENSMUST00000044475	ENSMUSG00000034160	X	101640060	101684351	1	0	8	14	11	0	5	720	5922	842	240	812		Q8CGY8
ENSMUST00000044478	ENSMUSG00000041426	1	52844929	52920986	1	1	0	0	3	5	0	96	592	190	242	77		Q8QZS1
ENSMUST00000044484	ENSMUSG00000037369	X	18162575	18279936	1	1	1	5	40	1	1	302	1510	706	133	298		O70546
ENSMUST00000044491	ENSMUSG00000039313	9	89587216	89623125	-1	75	45	118	790	81	39	0	3	2	1	6	Q14CG5	Q8K3V7
ENSMUST00000044492	ENSMUSG00000040407	5	3928054	4081310	1	54	35	52	47	62	13	149	361	640	167	600	E9QQ10	
ENSMUST00000044503	ENSMUSG00000039316	17	49992257	50190674	-1	24	8	8	89	19	7	8	61	0	0	23		Q6A0D4
ENSMUST00000044505	ENSMUSG00000004347	6	56069804	56569103	-1	4	11	28	23	17	7	0	1	2	0	0		Q64338
ENSMUST00000044507	ENSMUSG00000034570	11	3494375	3504821	-1	9	0	56	163	12	13	284	200	319	0	83		P59644
ENSMUST00000044509	ENSMUSG00000041096	X	152336852	152342425	-1	0	0	14	69	13	0	64	401	53	31	161		Q7TQI8
ENSMUST00000044521	ENSMUSG00000037692	4	133011260	133078110	1	0	0	0	0	0	0	0	0	0	0	0		Q6PAL7
ENSMUST00000044524	ENSMUSG00000039168	15	31224314	31274341	1	15	13	41	86	28	18	2144	4851	2764	435	1474	Q3U706	Q91XC8
ENSMUST00000044527	ENSMUSG00000039330	19	5390049	5394401	-1	5	1	13	15	9	3	1	3	4	1	0	F7A1F0	
ENSMUST00000044530	ENSMUSG00000018809	11	75348433	75405705	1	60	50	124	79	64	28	10	19	8	11	33		Q8BTK5
ENSMUST00000044532	ENSMUSG00000039716	9	106892825	107231909	-1	34	44	52	53	46	21	0	0	1	2	0	F8VPQ1	
ENSMUST00000044533	ENSMUSG00000036480	1	87183313	87188405	1	15	6	40	126	29	12	0	0	0	0	0		F2YMG0
ENSMUST00000044535	ENSMUSG00000035234	5	100805192	100820965	-1	0	23	50	0	0	0	0	0	0	0	0		Q8BPZ8
ENSMUST00000044547	ENSMUSG00000054385	7	25516042	25539857	-1	34	30	82	0	31	9	0	0	0	0	0		Q925P2
ENSMUST00000044551	ENSMUSG00000009828	9	78109192	78172107	1	15	8	14	14	11	13	0	10	0	3	0		Q9JKV2
ENSMUST00000044554	ENSMUSG00000040432	14	55761428	55763229	1	9	6	4	310	21	2	8	2	5	1	7		Q9JJL9
ENSMUST00000044556	ENSMUSG00000039678	2	30133746	30152013	1	78	62	517	144	64	49	720	726	484	188	471	Q3TZ63	Q8R3D1
ENSMUST00000044564	ENSMUSG00000032998	4	119537004	119629119	1	36	0	0	56	0	0	84	118	169	46	139		Q8BUR3
ENSMUST00000044565	ENSMUSG00000040690	4	130047840	130099283	1	0	0	13	53	0	0	0	0	0	0	57		Q8BLX7
ENSMUST00000044567	ENSMUSG00000036632	3	54735539	54751318	1	1	0	0	5	1	1	104	263	114	693	125		Q9DB25
ENSMUST00000044579	ENSMUSG00000033467	5	109554709	109558993	-1	3	2	7	147	3	2	501	1589	800	310	762		
ENSMUST00000044581	ENSMUSG00000032666	1	151852403	152090125	-1	147	79	337	575	198	88	19	79	20	14	76	Q3TJL3	Q8K207
ENSMUST00000044583	ENSMUSG00000066372	7	84940169	84964009	-1	4	4	1	6	4	1	0	0	0	0	0	G3X931	
ENSMUST00000044584	ENSMUSG00000043501	15	78850862	78855529	-1	5	3	11	6	8	2	0	0	0	2	0		Q9CQW5
ENSMUST00000044598	ENSMUSG00000031174	X	10073621	10216920	-1	0	3	0	11	0	0	0	0	0	0	2	A0A067XG46	
ENSMUST00000044602	ENSMUSG00000057074	8	93302369	93337308	-1	31	20	47	47	20	15	1	1	0	2	1	Q3UW56	Q8VCC2
ENSMUST00000044604	ENSMUSG00000022723	16	59490775	59555752	-1	14	11	18	30	19	5	348	988	1077	84	571		Q80W49
ENSMUST00000044608	ENSMUSG00000038518	13	44729474	44921643	1	0	0	21	50	9	0	42	0	43	7	33		Q62315
ENSMUST00000044616	ENSMUSG00000040738	4	11199158	11254258	-1	0	0	0	0	0	0	0	0	0	0	0		Q80V86
ENSMUST00000044620	ENSMUSG00000041147	5	150522630	150570329	1	31	26	80	104	42	25	29	50	45	6	56		P97929
ENSMUST00000044622	ENSMUSG00000039840	18	77938467	78035027	1	84	78	196	139	97	55	373	602	778	51	607		Q80TA9
ENSMUST00000044624	ENSMUSG00000036760	15	72512119	72546279	-1	8	5	8	13	11	5	0	0	0	0	0		Q3LS21
ENSMUST00000044634	ENSMUSG00000035472	12	56712634	57197472	-1	25	25	262	216	45	18	0	2	0	0	1		Q8BZ09
ENSMUST00000044638	ENSMUSG00000027522	2	174076308	174099771	1	1	0	175	61	0	0	37	566	255	70	114	F6X4N5	
ENSMUST00000044642	ENSMUSG00000036718	5	139706696	139736336	-1	8	0	35	204	27	18	46	34	0	0	17		Q3TN34
ENSMUST00000044660	ENSMUSG00000042178	7	128237342	128245100	1	22	10	89	233	30	16	234	283	199	19	173		Q5EBP3
ENSMUST00000044664	ENSMUSG00000033470	14	73029128	73049114	-1	6	0	0	0	0	0	0	0	0	0	0		Q920A1
ENSMUST00000044668	ENSMUSG00000035948	10	106936164	107123668	-1	3	6	0	3	2	3	0	0	0	0	0		Q14DH7
ENSMUST00000044672	ENSMUSG00000038481	10	40349308	40483818	1	29	21	45	44	33	0	837	3172	1750	242	1063	B7ZMT1	Q8BWD8
ENSMUST00000044673	ENSMUSG00000035601	4	45297127	45316131	1	4	6	6	9	5	6	18	85	41	85	18		Q9D075
ENSMUST00000044675	ENSMUSG00000098789	2	120027483	120032594	1	4	7	12	9	7	3	11	20	0	0	3		P0C872
ENSMUST00000044681	ENSMUSG00000035199	6	97210689	97233315	1	8	10	21	80	9	5	1748	3921	1544	1365	1077		Q8R5J9
ENSMUST00000044682	ENSMUSG00000034579	11	3488284	3499350	1	3	6	13	5	2	4	6	12	10	0	8	Q8BV23	
ENSMUST00000044683						3	3	9	15	3	0	0	0	0	0	0		
ENSMUST00000044684	ENSMUSG00000035266	5	100762145	100798598	-1	8	0	2	55	6	0	6	40	29	0	21		Q2VPA6
ENSMUST00000044687	ENSMUSG00000021208	12	103450898	103457223	-1	2	3	18	10	9	6	1	0	0	0	0		Q8VC49
ENSMUST00000044691	ENSMUSG00000042215	1	33745484	33757795	-1	9	5	43	33	8	5	9	28	4	11	15		Q91YN9
ENSMUST00000044694	ENSMUSG00000039438	9	44799400	44802951	-1	1	3	20	121	12	3	0	3	1	3	0		Q8VBW8
ENSMUST00000044702	ENSMUSG00000042425	X	140367494	140394540	1	3	4	20	8	10	7	0	2	1	0	2	Q8BXG0	
ENSMUST00000044705	ENSMUSG00000039257	7	40898328	40930594	1	13	9	14	139	9	7	0	0	0	0	0		Q9JME9
ENSMUST00000044711	ENSMUSG00000039452	9	66065176	66069731	-1	16	12	44	115	25	14	8	26	11	6	16	Q8C084	
ENSMUST00000044721	ENSMUSG00000019302	11	101009452	101063719	1	0	0	0	47	0	0	0	193	84	0	49		Q9Z1G4
ENSMUST00000044725	ENSMUSG00000039461	9	108302958	108306160	-1	9	3	20	12	6	4	508	1274	464	167	297		Q8VEA7
ENSMUST00000044729	ENSMUSG00000037973	6	55836895	55978735	1	18	9	24	14	11	16	0	0	0	0	0		Q14B48
ENSMUST00000044730	ENSMUSG00000038437	11	97663414	97685463	1	0	0	44	151	0	0	0	0	117	0	213	B1AR09	
ENSMUST00000044734	ENSMUSG00000035226	2	163859751	163918683	-1	81	59	159	420	109	64	0	3	0	0	1		P60191
ENSMUST00000044746	ENSMUSG00000040429	5	3890581	3893933	-1	0	0	0	9	0	0	21	197	36	88	40		Q8CHZ9
ENSMUST00000044749	ENSMUSG00000025716	2	22227503	22618252	1	10	9	0	18	7	4	0	0	0	0	0	F6QNG5	
ENSMUST00000044751	ENSMUSG00000039686	2	30097283	30124585	-1	21	6	54	8	36	17	92	588	182	73	196		Q80ZJ6
ENSMUST00000044752	ENSMUSG00000039481	17	56751325	56757530	-1	3	4	10	280	6	2	2	0	0	0	1		P97463
ENSMUST00000044766	ENSMUSG00000027309	2	130706200	130906406	-1	59	61	107	37	57	27	71	272	180	10	167		Q7TT23
ENSMUST00000044767	ENSMUSG00000037984	6	55677822	55681263	-1	64	28	57	483	98	59	1	4	2	0	3	Q5M8T7	P48986

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000044773	ENSMUSG00000035615	4	45184875	45285936	1	15	31	24	31	25	0	1	0	1	1	2		A2AKB4
ENSMUST00000044776	ENSMUSG00000044005	10	128194457	128210004	1	7	0	0	84	0	12	0	0	0	0	0		Q571F8
ENSMUST00000044781	ENSMUSG00000028637	4	119322893	119415521	-1	6	0	0	0	10	6	0	0	0	0	0		Q8BVF4
ENSMUST00000044783	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	17	0	0	0	0	0	0	0		Q6NZJ6
ENSMUST00000044789	ENSMUSG00000090084	X	10037977	10117709	-1	7	0	0	0	2	0	0	0	0	1	0		Q9R0M3
ENSMUST00000044790	ENSMUSG00000042002	5	114254164	114273807	-1	12	10	29	81	26	6	0	0	0	0	0		Q8K3Q3
ENSMUST00000044792	ENSMUSG00000039601	17	43801851	44039516	1	131	68	316	782	150	78	1	7	2	1	2	Q543P2	Q9JHG2
ENSMUST00000044795	ENSMUSG00000039509	8	123897123	123949265	-1	95	82	212	201	107	63	87	197	92	25	129		Q8R0G9
ENSMUST00000044798	ENSMUSG00000035238	2	163853651	163859746	1	7	5	6	262	14	0	0	0	0	0	0	B2RVL1	
ENSMUST00000044804	ENSMUSG00000039518	17	35552128	35557180	1	17	13	46	29	35	19	0	0	0	0	0		Q7TPC1
ENSMUST00000044806	ENSMUSG00000042433	X	140062879	140106797	1	2	2	0	2	3	0	0	0	0	0	0	Q8C6P5	
ENSMUST00000044812	ENSMUSG00000039210	1	187215508	187351704	1	4	5	10	26	3	3	5	49	29	12	32	E9PY25	
ENSMUST00000044819	ENSMUSG00000098781	13	67317942	67360536	-1	0	0	0	0	0	1	0	0	24	5	3	L7N1X0	
ENSMUST00000044823	ENSMUSG00000033948	4	116877376	116989264	1	51	31	60	96	45	20	3	2	3	0	5		Q80TC6
ENSMUST00000044825	ENSMUSG00000027384	2	140170649	140203689	1	5	5	9	77	0	1	17	53	15	41	19		A2APY7
ENSMUST00000044828	ENSMUSG00000042793	1	134983301	135105276	-1	144	132	250	330	189	103	1	8	7	12	102		Q3UVD5
ENSMUST00000044829	ENSMUSG00000039540	18	6603633	6638966	1	12	8	6	4	7	3	0	0	0	0	0	Q9D5T2	
ENSMUST00000044833	ENSMUSG00000032661	5	120753098	120777661	-1	213	168	603	209	260	110	2299	4374	2134	156	3060		Q8VI93
ENSMUST00000044844	ENSMUSG00000034854	10	81357491	81366225	1	24	13	63	326	43	22	214	227	133	35	138		Q3U481
ENSMUST00000044850	ENSMUSG00000041797	11	110100749	110168196	-1	34	20	25	13	31	18	31	126	31	49	220		Q8K449
ENSMUST00000044851	ENSMUSG00000102428	18	37765580	37841873	1	0	0	0	0	2	0	0	0	0	0	0	Q91XY7	
ENSMUST00000044857	ENSMUSG00000040236	8	3676299	3681255	1	20	15	90	148	31	15	558	999	474	113	293		Q9CQA1
ENSMUST00000044858	ENSMUSG00000039656	17	34031812	34038393	1	0	0	0	82	0	0	87	329	188	42	58	Q3TWJ1	
ENSMUST00000044878	ENSMUSG00000036500	1	87124973	87127912	1	12	8	43	171	17	5	0	0	0	0	1	F8VQM0	
ENSMUST00000044895	ENSMUSG00000039601	17	43801851	44039516	1	13	10	8	585	44	27	0	0	0	0	0	Q8VIP4	
ENSMUST00000044901	ENSMUSG00000039607	9	116572746	117629913	-1	0	0	0	0	0	0	0	0	0	0	2		Q8BWL5
ENSMUST00000044911	ENSMUSG00000039615	17	25830636	25833361	-1	8	6	14	126	18	7	519	796	439	86	367		Q9WUD1
ENSMUST00000044922	ENSMUSG00000039628	17	24753003	24758683	1	5	5	11	255	14	5	4	0	1	0	1	A2RTI7	Q5GFD5
ENSMUST00000044923	ENSMUSG00000041645	12	103407976	103425867	-1	5	0	0	8	0	14	687	1448	746	211	831		Q9ESV0
ENSMUST00000044926	ENSMUSG00000039632	9	21989871	22002634	-1	13	8	28	34	21	0	0	0	0	0	0	G3X951	
ENSMUST00000044937	ENSMUSG00000056271	9	57607085	57620774	-1	6	0	19	0	22	5	0	9	9	0	12		Q8VCD3
ENSMUST00000044949	ENSMUSG00000078789	11	75177643	75191241	-1	3	3	10	30	17	2	40	32	21	30	33		Q5NCQ5
ENSMUST00000044953	ENSMUSG00000040132	2	164235929	164238466	-1	8	5	0	0	10	0	0	0	0	0	0	Q8BS30	
ENSMUST00000044954	ENSMUSG00000037434	1	191906767	191913247	1	14	11	54	181	26	11	235	545	252	36	169	Q3UM63	Q60738
ENSMUST00000044970	ENSMUSG00000042428	15	80173721	80215519	1	47	27	76	151	56	37	1	1	3	10	51	Q5RKT9	
ENSMUST00000044972	ENSMUSG00000040013	5	135291704	135350044	-1	23	31	259	126	31	18	1	0	0	0	0		Q91XW8
ENSMUST00000044976	ENSMUSG00000063683	19	12633308	12653911	1	3	8	2	0	0	2	0	1	0	0	0		Q91XE0
ENSMUST00000044977	ENSMUSG00000071253	10	62920633	62946498	1	12	8	22	30	8	7	190	524	218	46	190		Q8C0K5
ENSMUST00000044985	ENSMUSG00000039741	11	120232947	120292296	1	0	0	124	109	35	0	3	0	1	0	2	E9Q7G4	
ENSMUST00000044987	ENSMUSG00000040456	X	9846928	9847508	1	3	1	7	0	3	0	0	0	0	0	0		Q9CR04
ENSMUST00000044989	ENSMUSG00000043549	X	94355053	94366777	-1	6	6	12	13	10	2	0	0	0	0	0	Q9D4F3	
ENSMUST00000044990	ENSMUSG00000037996	4	86983124	87230477	-1	0	0	0	0	2	0	0	0	0	0	0	B1AXF2	
ENSMUST00000045004	ENSMUSG00000022946	16	93711907	93810585	1	38	36	116	162	70	31	1607	2229	2579	134	2527		Q3UHQ6
ENSMUST00000045008	ENSMUSG00000033634	6	85865422	85869158	-1	22	21	61	41	32	6	2	1	1	11	2		Q8CHQ9
ENSMUST00000045011	ENSMUSG00000025646	9	109059747	109074124	-1	0	2	0	110	0	0	0	15	1	2	0		Q8BMG1
ENSMUST00000045016	ENSMUSG00000038044	5	25516067	25518027	1	16	7	38	19	30	15	0	0	0	0	0	Q80YT3	
ENSMUST00000045022	ENSMUSG00000035177	7	5298554	5351035	-1	24	11	16	23	17	10	0	1	1	0	0	Q4PLS0	
ENSMUST00000045026	ENSMUSG00000002055	11	78301529	78322457	1	9	10	20	54	6	11	104	167	171	52	141		Q7TME2
ENSMUST00000045028	ENSMUSG00000067299	1	65061872	65063452	-1	1	4	8	3	3	2	0	0	0	0	0		P04342
ENSMUST00000045029	ENSMUSG00000039047	3	152714100	152980408	1	0	0	0	0	0	0	11	98	38	237	0	Q8BL63	
ENSMUST00000045035	ENSMUSG00000040564	7	19689484	19692658	-1	2	0	4	0	0	4	25	47	19	189	16		P34928
ENSMUST00000045041	ENSMUSG00000039774	4	47091909	47123070	1	21	0	22	97	17	9	12	21	14	5	22	Q60GT3	Q8BGT9
ENSMUST00000045042	ENSMUSG00000039699	19	6140983	6172476	1	2	6	0	0	0	7	0	8	1	5	10		Q8R1H8
ENSMUST00000045054	ENSMUSG00000036667	6	42668002	42710088	-1	18	10	9	8	6	4	0	0	0	3	5		Q8BNE1
ENSMUST00000045066	ENSMUSG00000035626	14	52443050	52451402	1	7	4	6	7	11	5	0	0	0	0	0	Q7TQQ0	
ENSMUST00000045068	ENSMUSG00000039714	9	57600019	57606281	-1	49	17	77	226	48	32	2	3	0	0	2		Q8R1B5
ENSMUST00000045075	ENSMUSG00000034641	11	114982274	114989922	-1	32	32	166	52	48	19	520	4085	1231	987	849		Q8VCH2
ENSMUST00000045078	ENSMUSG00000035637	4	44981395	44990734	1	9	4	7	16	19	6	54	97	82	25	60	Q3T9Z2	Q91Z53
ENSMUST00000045085	ENSMUSG00000035745	10	79970715	79977190	1	13	12	34	289	28	9	6	14	4	0	7		Q91ZU9
ENSMUST00000045091	ENSMUSG00000032036	9	34485894	35036716	1	17	13	58	0	0	5	0	0	0	0	0	G5E8B6	
ENSMUST00000045096	ENSMUSG00000042717	6	14713977	14755274	-1	12	21	15	20	14	7	0	0	0	0	0		Q99MR9
ENSMUST00000045097	ENSMUSG00000040253	3	142530342	142550149	1	0	0	6	0	0	0	0	0	56	0	47	Q91Z40	
ENSMUST00000045102	ENSMUSG00000034872	10	81337762	81343266	-1	9	10	14	140	19	6	0	1	1	0	0		Q8R5M0
ENSMUST00000045105	ENSMUSG00000024533	18	67488209	67552777	-1	20	11	38	17	16	18	0	0	0	0	13	D3YTL8	
ENSMUST00000045108	ENSMUSG00000039224	1	186967416	186970627	1	10	15	23	211	21	11	0	0	0	1	0	B9EIA2	P16381
ENSMUST00000045110	ENSMUSG00000042046	1	132417555	132466958	1	25	31	53	82	43	14	305	1171	599	85	492		Q6XUX1
ENSMUST00000045114	ENSMUSG00000038510	10	40223246	40247036	-1	12	7	18	150	13	8	0	6	2	0	3	G3X926	
ENSMUST00000045116	ENSMUSG00000038523	2	154547085	154550003	1	1	1	5	34	1	1	0	0	0	0	0	Q9DAQ3	
ENSMUST00000045127	ENSMUSG00000040154	2	164176327	164182742	-1	17	14	46	20	15	12	0	0	0	0	0	Q4KXB6	
ENSMUST00000045138	ENSMUSG00000040124	1	163384908	163403669	-1	10	9	13	43	13	11	23	61	15	93	30		Q8BRM2
ENSMUST00000045140	ENSMUSG00000036667	6	42668002	42710088	-1	20	19	263	43	38	22	2	3	2	0	3		Q8BNE1
ENSMUST00000045142	ENSMUSG00000038816	4	56810935	56865188	-1	5	5	7	62	16	8	1	8	4	38	20		O88327
ENSMUST00000045151	ENSMUSG00000034652	11	114890041	114904654	1	55	204	302	463	47	148	327	944	405	131	502		Q6SJQ0
ENSMUST00000045152	ENSMUSG00000069708	10	23949558	23950589	1	4	3	13	5	8	5	0	1	0	0	0	D8KZH8	Q5QD16
ENSMUST00000045153	ENSMUSG00000034614	11	3330401	3342971	1	17	8	12	16	21	12	1097	605	1386	495	661		Q7TMJ8
ENSMUST00000045154	ENSMUSG00000037731	4	132781843	132796387	-1	19	18	35	69	36	18	4340	11299	5279	588	6449		Q91YX0
ENSMUST00000045167	ENSMUSG00000042302	11	22005828	22342292	-1	28	21	0	0	0	0	3	0	5	0	11		Q69ZW3
ENSMUST00000045173	ENSMUSG00000035493	13	56609603	56639339	1	17	13	33	133	40	16	13735	44158	21853	1929	19274	A1L353	P82198
ENSMUST00000045174	ENSMUSG00000039770	17	72836704	72851195	1	12	13	6	42	16	11	1764	7002	2003	3888	1219		P62700
ENSMUST00000045180	ENSMUSG00000041459	4	148612382	148627019	-1	3	0	0	0	0	0	6	0	0	0	0	Q8BLD4	
ENSMUST00000045186	ENSMUSG00000002500	17	24727820	24736143	1	0	5	7	0	9	3	76	233	67	322	21	Q9CQ09	
ENSMUST00000045196	ENSMUSG00000040164	2	164163619	164171113	-1	34	30	41	481	42	28	3	3	1	0	1		O35173
ENSMUST00000045215	ENSMUSG00000035191	7	5109787	5116911	-1	7	0	27	11	10	4	0	0	0	0	0		Q8VH31
ENSMUST00000045218	ENSMUSG00000031592	8	41239759	41334086	1	17	13	22	116	17	10	385	1532	1132	194	578		Q9R0L6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000045224	ENSMUSG00000038007	4	86874396	86934822	1	0	0	0	56	0	0	0	15	11	14	0		Q8VD53
ENSMUST00000045228	ENSMUSG00000063894	13	21513222	21531120	-1	31	22	33	61	47	20	29	39	45	8	51	Q8BSL0	
ENSMUST00000045229	ENSMUSG00000038497	8	13288013	13322924	1	54	48	94	140	74	45	667	734	744	105	738		Q8BH01
ENSMUST00000045235	ENSMUSG00000042742	6	13625673	13677966	-1	61	44	428	355	82	32	264	393	355	90	202		Q8BXK4
ENSMUST00000045243	ENSMUSG00000038170	3	97689824	97888707	-1	16	14	26	107	18	19	51	244	125	19	117		Q80YT7
ENSMUST00000045245	ENSMUSG00000041912	3	94413273	94434668	1	3	3	13	35	24	6	0	0	0	19	2		Q80VL1
ENSMUST00000045246	ENSMUSG00000026785	2	30077684	30091022	1	0	18	34	13	14	19	14	11	0	0	5		Q8K045
ENSMUST00000045247	ENSMUSG00000035754	10	79960152	79969246	1	24	10	43	121	47	9	105	139	70	52	91		Q4VBE8
ENSMUST00000045262	ENSMUSG00000039058	3	152462815	152668360	-1	15	9	29	64	24	12	1	6	5	2	5		Q920P5
ENSMUST00000045270	ENSMUSG00000038533	2	154436481	154539356	1	0	0	0	0	0	0	132	136	208	10	102		O70374
ENSMUST00000045277	ENSMUSG00000035203	7	5080235	5098178	1	0	0	0	0	0	0	1474	2502	1183	241	361		Q80VP1
ENSMUST00000045279	ENSMUSG00000036819	11	59450045	59458567	1	0	62	83	0	0	0	0	94	73	0	0		Q8BFT6
ENSMUST00000045281	ENSMUSG00000038290	11	74925823	75164448	1	46	23	67	76	46	23	236	433	564	30	438		P61406
ENSMUST00000045286	ENSMUSG00000035964	8	70483876	70487358	-1	18	9	83	49	25	11	0	0	0	0	0		Q7TNI2
ENSMUST00000045288	ENSMUSG00000039239	1	186622792	186705989	-1	29	22	94	151	44	28	0	1	0	0	20		P27090
ENSMUST00000045289	ENSMUSG00000041653	15	84167816	84189512	1	52	43	83	130	52	19	2	5	1	1	1	E9QNZ9	
ENSMUST00000045291	ENSMUSG00000038056	5	25271798	25498783	-1	52	41	128	58	70	41	683	469	2252	28	1866	F8WI37	
ENSMUST00000045295	ENSMUSG00000036833	2	24976033	25054057	1	0	0	41	10	0	0	2412	2430	3374	33	2718		A2AJ88
ENSMUST00000045296	ENSMUSG00000036840	8	86723940	86746006	-1	14	14	13	7	11	10	121	533	155	36	149		P61092
ENSMUST00000045301	ENSMUSG00000052565	13	23555087	23555830	1	15	4	44	108	16	10	2	4	1	2	3	Q149Z9	P43277
ENSMUST00000045303	ENSMUSG00000040447	11	72451638	72489904	-1	14	5	26	90	24	12	100	79	86	15	58		Q91VM4
ENSMUST00000045312	ENSMUSG00000041133	X	152016428	152062694	1	9	12	21	6	13	4	717	3314	2150	1703	1411		Q9CU62
ENSMUST00000045319	ENSMUSG00000034677	11	114798924	114806745	1	13	7	9	0	11	5	0	0	0	0	0		Q7TQN9
ENSMUST00000045325	ENSMUSG00000108653	7	44976900	44986318	-1	0	0	0	0	0	0	83	86	0	113	98	F8WH01	
ENSMUST00000045328	ENSMUSG00000050994	10	10335703	10472326	-1	4	4	7	4	8	3	0	0	0	0	0		G3UZ78
ENSMUST00000045329	ENSMUSG00000037339	5	33600347	33629635	-1	5	3	10	217	17	8	13	36	0	0	16	E9PV82	
ENSMUST00000045351	ENSMUSG00000024773	19	6241668	6262335	1	42	27	50	237	50	21	2459	1077	2570	75	2112		Q6P4T0
ENSMUST00000045356	ENSMUSG00000041841	15	5116613	5119140	1	3	6	12	20	8	8	1035	1557	933	6623	860		Q9D823
ENSMUST00000045366	ENSMUSG00000038506	8	13255963	13288131	-1	0	0	0	0	0	0	0	84	69	0	19		Q8BZJ7
ENSMUST00000045368	ENSMUSG00000038827	4	56802345	56809601	1	34	37	103	66	21	34	65	183	95	0	62		Q80ZQ9
ENSMUST00000045372	ENSMUSG00000038871	6	34476207	34505613	1	21	16	30	19	46	15	117	146	102	379	334		P15327
ENSMUST00000045374	ENSMUSG00000041046	11	6658521	6677475	1	9	0	0	0	13	5	4	6	0	7	10		Q9WUP1
ENSMUST00000045376	ENSMUSG00000039197	14	21052574	21448568	1	4	3	4	36	12	3	152	307	188	627	148		P55264
ENSMUST00000045388	ENSMUSG00000039246	1	186087731	186117310	-1	10	8	6	8	6	0	0	7	0	5	4	E9QLB2	
ENSMUST00000045393	ENSMUSG00000013033	8	83900105	83941954	1	0	0	0	0	0	0	0	0	0	0	13	H7BX15	
ENSMUST00000045396	ENSMUSG00000039901	19	45818144	45998488	-1	16	14	24	44	21	8	104	225	178	16	91		Q6PD19
ENSMUST00000045402	ENSMUSG00000061306	11	120103960	120151346	-1	9	22	36	32	52	0	123	186	149	0	124		Q5I012
ENSMUST00000045428	ENSMUSG00000035509	13	56522472	56537898	1	0	3	0	0	0	1	0	0	0	0	0		Q8BFZ4
ENSMUST00000045441	ENSMUSG00000033059	2	150786735	150831758	1	32	26	73	126	62	15	238	282	248	58	284		Q8CI94
ENSMUST00000045450	ENSMUSG00000037461	1	191575636	191623688	1	40	45	111	59	62	39	24	55	43	11	40		
ENSMUST00000045454	ENSMUSG00000032977	10	77486656	77515813	-1	24	14	36	144	37	10	495	640	405	142	285		P58468
ENSMUST00000045466	ENSMUSG00000049606	5	106616739	106697287	-1	0	0	0	0	0	0	80	134	124	47	94	E9Q624	
ENSMUST00000045467	ENSMUSG00000073422	17	34026033	34028060	-1	0	0	0	0	0	0	82	130	52	32	19		P50171
ENSMUST00000045469	ENSMUSG00000034902	10	81292963	81319973	1	39	11	62	31	21	0	58	732	255	46	554	F8WHW6	
ENSMUST00000045473	ENSMUSG00000042066	1	132356315	132391281	-1	8	0	18	245	17	3	0	7	5	0	31		Q80W04
ENSMUST00000045477	ENSMUSG00000039954	18	43207697	43317481	1	21	24	61	101	32	14	0	0	0	0	0		Q8BGW6
ENSMUST00000045487	ENSMUSG00000039960	8	123653929	123663884	1	28	29	161	61	43	15	1058	3048	1686	153	917		Q9EQT3
ENSMUST00000045493	ENSMUSG00000039962	9	38488031	38488966	1	1	0	2	0	0	0	0	0	0	0	0	K7N5P3	
ENSMUST00000045503	ENSMUSG00000037754	2	158665398	158766334	1	0	0	37	263	80	0	0	0	92	0	109	Q544H9	Q8VHQ3
ENSMUST00000045512	ENSMUSG00000038024	4	86748555	86850603	1	21	26	52	200	47	22	0	0	0	0	17	E9Q449	
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ENSMUST00000045517	ENSMUSG00000040097	17	23755423	23771591	-1	14	12	30	11	36	10	0	17	14	0	13		Q8CI03
ENSMUST00000045521	ENSMUSG00000039982	19	12466341	12501996	-1	40	26	87	462	61	34	1045	2901	874	180	568		Q6PDK8
ENSMUST00000045522	ENSMUSG00000039578	6	61180324	62382865	1	0	0	0	0	0	0	0	0	0	0	0		Q8C0C4
ENSMUST00000045524	ENSMUSG00000038528	10	39958061	39986646	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q694	
ENSMUST00000045526	ENSMUSG00000039339	10	39920382	39926923	-1	13	13	35	60	19	8	2	0	0	0	1	G5E8A5	
ENSMUST00000045529	ENSMUSG00000035773	10	79916971	79922273	1	27	15	57	462	36	23	109	216	157	17	98	B2CP06	Q91V45
ENSMUST00000045537	ENSMUSG00000040495	2	91927249	91928688	1	8	6	35	144	26	9	0	3	0	0	3	Q0VBU3	P32211
ENSMUST00000045540	ENSMUSG00000038485	11	97362551	97398542	1	32	37	184	318	46	42	134	279	227	36	193		Q8VHQ2
ENSMUST00000045542	ENSMUSG00000033985	4	116720948	116805956	1	1	0	0	33	17	12	196	516	468	56	206		Q8VCT9
ENSMUST00000045543	ENSMUSG00000035228	7	5056726	5060779	1	2	0	0	0	1	0	0	0	0	0	0		Q3ULM0
ENSMUST00000045546	ENSMUSG00000042402	7	103460277	103461191	-1	1	3	12	2	4	1	0	0	0	0	0	F7AC91	
ENSMUST00000045550	ENSMUSG00000037752	4	132724897	132732546	-1	69	68	191	114	110	42	140	152	111	21	66		Q8C0T0
ENSMUST00000045555	ENSMUSG00000036617	2	19909780	20810713	1	0	0	0	0	0	0	0	0	0	0	0		A2AQ25
ENSMUST00000045557	ENSMUSG00000040010	8	121881150	121907694	-1	12	10	80	258	28	13	1281	1117	1101	55	611		Q9Z127
ENSMUST00000045560	ENSMUSG00000038496	1	83012523	83038448	-1	12	11	10	0	9	1	0	0	0	0	0		Q99PL8
ENSMUST00000045562	ENSMUSG00000040018	19	43733254	43753000	-1	38	31	81	127	48	21	186	548	321	51	210		Q8BJ03
ENSMUST00000045566	ENSMUSG00000039521	X	7579676	7595243	1	0	13	55	24	0	0	20	31	0	5	0	Q53Z59	Q99JB6
ENSMUST00000045583	ENSMUSG00000021680	13	95431371	95444831	-1	10	5	25	39	6	4	0	0	0	2	2	Q3UY07	Q60571
ENSMUST00000045586	ENSMUSG00000015882	5	45697181	45857615	-1	2	1	3	2	2	0	72	122	40	60	43		Q3U285
ENSMUST00000045593	ENSMUSG00000039206	5	143464584	143505942	1	0	22	39	130	43	12	469	550	591	62	350		Q91WC9
ENSMUST00000045602	ENSMUSG00000040048	17	24722060	24724478	-1	0	0	0	42	3	2	338	869	310	1093	248		Q9DCS9
ENSMUST00000045604	ENSMUSG00000036850	2	24974117	24975098	-1	7	2	19	19	8	5	113	337	119	591	87		Q9CQN7
ENSMUST00000045607	ENSMUSG00000035683	4	44300876	44364675	1	7	11	24	35	18	12	53	61	58	42	54		Q61846
ENSMUST00000045617	ENSMUSG00000035273	5	100679484	100719716	-1	17	14	21	51	19	14	230	543	210	70	215		Q6YGZ1
ENSMUST00000045620	ENSMUSG00000058173	9	15505487	15545260	1	22	7	0	0	0	0	7	0	7	0	0		Q9JIS3
ENSMUST00000045621	ENSMUSG00000040054	10	128092783	128129303	1	32	27	110	100	40	20	1521	2531	3602	144	2913	F8VPM0	
ENSMUST00000045628	ENSMUSG00000035781	10	79910053	79917006	-1	32	19	96	30	33	19	21029	20906	12961	1427	9360	B2RRK4	Q4VBF2
ENSMUST00000045633	ENSMUSG00000040463	11	72441355	72451768	1	0	0	74	0	0	0	291	344	256	76	572	Q3U2W2	Q7TPV4
ENSMUST00000045644	ENSMUSG00000037761	2	158624888	158639211	1	3	3	5	29	3	0	175	179	189	35	53	A0A0A0MQ89	
ENSMUST00000045652	ENSMUSG00000041702	12	102784656	102878406	-1	16	7	35	29	13	12	295	518	663	67	450		Q8CFE5
ENSMUST00000045664	ENSMUSG00000052812	12	4917404	5044047	1	17	16	16	161	18	8	209	425	602	41	337	E9Q166	
ENSMUST00000045665	ENSMUSG00000073557	1	134754658	134955942	-1	56	36	71	57	73	26	56	109	99	14	172		Q8BG95
ENSMUST00000045674	ENSMUSG00000040105	19	28963953	28966811	1	9	8	23	187	25	8	178	452	248	29	139		Q9D4F2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000045682	ENSMUSG00000040111	9	40293233	40531383	-1	8	4	7	298	24	7	232	29	437	32	215		Q80TI0
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ENSMUST00000045692	ENSMUSG00000025738	17	25809085	25821244	1	63	42	124	817	95	60	0	2	2	0	1	B2RPY3	A2RT62
ENSMUST00000045693	ENSMUSG00000033706	6	85431989	85446435	1	8	12	21	30	19	10	75	110	67	12	105		Q3TYX3
ENSMUST00000045694	ENSMUSG00000041396	1	163994889	163997243	1	12	8	13	14	12	0	0	11	0	39	0		Q9CZ09
ENSMUST00000045697	ENSMUSG00000036860	11	59202486	59206134	1	2	0	0	0	4	0	18	23	2	0	14		Q9CZ83
ENSMUST00000045699	ENSMUSG00000040506	2	91730134	91918849	1	0	0	0	0	0	0	681	780	315	78	226		A2AH22
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ENSMUST00000045705	ENSMUSG00000040506	2	91730134	91918849	1	0	13	37	0	0	0	273	247	281	0	349		A2AH22
ENSMUST00000045706	ENSMUSG00000041301	6	18170687	18322768	1	11	24	23	21	17	10	0	2	0	0	0		P26361
ENSMUST00000045713	ENSMUSG00000041073	11	6597823	6606053	-1	24	20	142	291	57	24	42	64	43	6	88		Q5SWP3
ENSMUST00000045714	ENSMUSG00000024254	17	84676302	84700333	1	26	8	44	15	30	5	0	0	0	0	1		Q9DBM0
ENSMUST00000045717	ENSMUSG00000040140	17	43615335	43630299	-1	0	24	44	233	54	23	0	1	0	0	1	F2Z429	
ENSMUST00000045720	ENSMUSG00000074165	7	41633203	41651530	1	0	0	0	0	0	0	0	0	0	8	0	E9PZ68	
ENSMUST00000045726	ENSMUSG00000040146	9	21971527	21989453	-1	16	7	44	158	33	13	0	0	1	1	3		Q3UYI5
ENSMUST00000045730	ENSMUSG00000038587	10	4266329	4359468	1	65	36	207	147	70	42	4	16	7	13	29	B2RRE0	Q9WTQ5
ENSMUST00000045736	ENSMUSG00000022155	15	4898737	4962203	1	41	25	35	31	33	25	0	0	0	0	0		Q7M6Y6
ENSMUST00000045737	ENSMUSG00000038072	5	25221904	25265918	1	0	0	0	0	0	0	24	0	36	49	83		Q921L8
ENSMUST00000045738	ENSMUSG00000037771	2	158610767	158615748	1	18	20	39	503	40	10	25	84	34	10	13	Q49S98	O35633
ENSMUST00000045740	ENSMUSG00000034430	6	90369492	90403490	1	0	17	0	15	10	0	17	17	33	0	0		Q8C8V1
ENSMUST00000045743	ENSMUSG00000038205	3	97658193	97673812	1	29	15	18	8	16	13	7	296	76	10	107		Q6PAM0
ENSMUST00000045744	ENSMUSG00000034917	10	81273207	81291267	-1	16	11	61	247	37	17	188	113	141	18	64	Q921G9	
ENSMUST00000045747	ENSMUSG00000036856	4	137277489	137299726	1	208	222	533	341	196	106	8	35	5	6	50	Q3ZB23	P22724
ENSMUST00000045748	ENSMUSG00000035232	X	93764607	93832201	-1	9	1	7	88	8	4	581	1679	715	106	272	Q4FJR4	Q922H2
ENSMUST00000045756	ENSMUSG00000041959	3	93555080	93564643	1	1	1	2	33	7	2	499	1385	351	7724	857	Q3TC45	P08207
ENSMUST00000045761	ENSMUSG00000037703	2	130632839	130642803	-1	22	33	0	174	45	33	0	27	0	0	23		A2AHG0
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ENSMUST00000045771	ENSMUSG00000041165	11	69820876	69822180	-1	8	6	12	8	10	8	0	0	0	0	0		Q5F289
ENSMUST00000045776	ENSMUSG00000035875	2	35084046	35101543	-1	8	3	10	3	7	3	1	31	16	8	10	A2AS37	
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ENSMUST00000045788	ENSMUSG00000015937	13	56073619	56136361	-1	3	1	12	0	10	5	83	320	161	36	236		Q9QZQ8
ENSMUST00000045791	ENSMUSG00000040188	9	57560944	57588797	1	8	13	48	33	27	10	2011	2818	1902	303	1413	Q3TAL2	Q9ERN0
ENSMUST00000045793	ENSMUSG00000035696	4	44126210	44233789	-1	0	0	27	28	0	0	1297	3307	656	186	933	Q3UH35	
ENSMUST00000045802	ENSMUSG00000040204	9	65890237	65903266	1	36	24	172	40	31	24	180	261	85	99	61		Q9CQX4
ENSMUST00000045807	ENSMUSG00000038335	11	74898071	74909342	1	4	0	2	0	3	0	36	104	42	78	107		Q5SWD9
ENSMUST00000045810	ENSMUSG00000033961	7	12977848	12984340	1	0	0	0	0	0	0	1	4	12	0	0	Q8C9M8	
ENSMUST00000045817	ENSMUSG00000036915	7	30447534	30457690	-1	0	4	0	0	0	0	0	0	0	0	0	A0A4X8	Q7TSU7
ENSMUST00000045827	ENSMUSG00000034617	13	68560780	68582121	-1	56	47	163	64	54	29	15	58	31	13	56		
ENSMUST00000045840	ENSMUSG00000040125	7	131966460	131994405	1	363	291	712	619	330	167	4	12	8	2	22	Q0VBG4	Q8BZA7
ENSMUST00000045843	ENSMUSG00000029477	5	123035769	123047016	-1	6	0	13	14	2	0	1	11	7	0	0		Q8C5T4
ENSMUST00000045846	ENSMUSG00000033720	6	85213049	85333422	-1	26	20	65	40	35	11	1726	5273	2166	287	2821		Q925N0
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ENSMUST00000045866	ENSMUSG00000020075	10	62580248	62602298	-1	26	37	99	85	27	16	173	540	278	308	547		Q9JIK5
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ENSMUST00000045884	ENSMUSG00000040263	8	121796313	121829569	-1	0	5	0	49	3	0	598	561	433	95	178	G3X961	
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ENSMUST00000045892	ENSMUSG00000034689	14	95881266	95882775	1	5	3	19	7	7	5	0	0	0	0	0	Q9CQ47	
ENSMUST00000045896	ENSMUSG00000040276	17	27655509	27711106	1	26	15	30	72	35	10	13	8	21	1	18	Q543Y7	Q61644
ENSMUST00000045897	ENSMUSG00000026238	1	86526726	86530712	1	7	8	16	45	10	0	2505	1210	415	2021	830	Q0VGU2	P26350
ENSMUST00000045898	ENSMUSG00000035246	X	93654863	93749951	1	41	34	5	68	0	27	0	0	0	0	0		Q811Q9
ENSMUST00000045902	ENSMUSG00000040170	1	162874317	162898726	-1	0	18	0	4	0	0	0	0	0	0	0		Q8K2I3
ENSMUST00000045903	ENSMUSG00000032536	9	121366958	121474916	1	59	38	109	95	68	39	269	346	393	35	342		Q6PD31
ENSMUST00000045905	ENSMUSG00000037712	14	45458792	45530118	-1	14	15	29	5	19	9	0	0	0	36	42	Q3TLE2	Q8CIB5
ENSMUST00000045907	ENSMUSG00000034601	12	71136848	71243303	1	15	15	18	1	8	11	44	0	64	0	89	E9Q0E2	
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ENSMUST00000045912	ENSMUSG00000041984	3	93393699	93399442	1	29	21	114	56	36	9	0	0	0	0	0		P97347
ENSMUST00000045918	ENSMUSG00000033809	16	20605451	20610768	-1	0	0	0	21	20	0	39	44	10	10	38		Q8K2A8
ENSMUST00000045919	ENSMUSG00000042333	4	154922210	154928563	-1	0	8	0	0	0	0	88	139	115	20	130	Q80WM9	
ENSMUST00000045921	ENSMUSG00000037336	12	4862440	4874359	-1	0	0	0	0	0	0	10	6	0	0	0	B8JK43	
ENSMUST00000045923	ENSMUSG00000040699	11	106156256	106160860	-1	24	19	23	34	23	16	3116	5566	2392	569	1862		Q8BGB5
ENSMUST00000045924						0	0	0	0	11	8	13	14	0	4	10		
ENSMUST00000045931	ENSMUSG00000042472	12	84316859	84343830	1	18	14	39	177	28	8	182	441	220	164	159		Q8BKX7
ENSMUST00000045942	ENSMUSG00000033726	6	85187438	85204462	1	3	0	4	250	12	5	0	0	0	0	0		Q04742
ENSMUST00000045956	ENSMUSG00000040312	17	35517100	35531015	1	0	2	7	4	0	5	29	0	0	0	0		Q8K2I2
ENSMUST00000045959	ENSMUSG00000038572	2	154223742	154240902	1	11	9	45	19	19	12	0	0	0	0	0	Q3UQ05	
ENSMUST00000045969	ENSMUSG00000055480	13	67254918	67269068	-1	4	3	8	2	2	1	21	58	9	4	10		Q6P5C7
ENSMUST00000045970	ENSMUSG00000034220	1	92831645	92860779	1	21	19	45	185	34	16	717	470	477	134	819	Q3U379	Q9QZF2
ENSMUST00000045971	ENSMUSG00000041189	11	69784036	69795943	-1	8	4	13	119	11	2	3	9	2	19	15		P09690
ENSMUST00000045972	ENSMUSG00000041644	2	110597298	110647779	1	102	143	111	78	113	62	7	34	10	16	7		Q49B93
ENSMUST00000045976	ENSMUSG00000071229	14	122034674	122038420	1	9	1	24	20	5	3	0	2	1	0	3		Q4FZG7
ENSMUST00000045986	ENSMUSG00000033735	6	85130176	85137766	-1	11	0	8	42	13	6	87	151	69	24	88	Q91XH5	
ENSMUST00000045993	ENSMUSG00000035297	5	100518309	100547803	1	0	0	3	11	10	7	230	695	296	796	204	Q14AI7	O88544
ENSMUST00000045994	ENSMUSG00000033931	8	126947175	126971079	-1	47	47	63	137	71	44	43	291	102	152	108	B2RUP0	
ENSMUST00000046001	ENSMUSG00000037727	2	130580620	130582554	-1	4	2	4	68	8	0	0	0	0	0	0	Q3UUQ5	P35455
ENSMUST00000046004	ENSMUSG00000036574	1	86426329	86428052	1	14	12	42	77	20	10	0	0	0	0	0		Q9DA60
ENSMUST00000046005	ENSMUSG00000034762	4	107434591	107635061	1	7	0	0	194	25	9	0	0	0	0	0		Q8K1M4
ENSMUST00000046011	ENSMUSG00000061458	12	17348458	17430094	1	129	102	227	132	96	50	62	168	112	25	108	Q3TUB5	Q5RJG1
ENSMUST00000046022	ENSMUSG00000040356	17	34839228	34850210	-1	1	0	0	0	0	0	1280	1719	1623	116	1163	Q6NZR5	
ENSMUST00000046028	ENSMUSG00000039629	6	29917012	29959681	1	0	5	0	18	0	0	12	0	14	0	0	B2RW20	Q8C9H6
ENSMUST00000046030	ENSMUSG00000045624	2	140119883	140170564	-1	14	6	22	7	5	3	18	101	53	130	30	A2APY6	Q3V1V3
ENSMUST00000046038	ENSMUSG00000040414	19	43663822	43674881	-1	5	2	19	42	28	9	421	898	377	80	445		Q8R0Z5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000046045	ENSMUSG00000039103	3	152236982	152266350	-1	8	13	22	20	8	5	1	1	0	4	5		Q7TPW1
ENSMUST00000046049	ENSMUSG00000040181	1	162829561	162866610	-1	11	4	6	9	6	0	0	0	0	0	0		P50285
ENSMUST00000046064	ENSMUSG00000038346	6	125009145	125037870	1	16	0	6	94	16	0	212	32	236	0	242	E9QAR1	
ENSMUST00000046071	ENSMUSG00000042115	1	132298626	132307357	1	35	14	63	400	41	21	0	0	0	1	2		Q91XA8
ENSMUST00000046073	ENSMUSG00000029475	5	122870665	122989823	-1	0	0	0	0	0	0	8	0	60	0	0		Q6P1G2
ENSMUST00000046091	ENSMUSG00000020125	10	79886312	79888216	1	11	2	8	19	5	5	962	454	432	77	204		Q3UP87
ENSMUST00000046093	ENSMUSG00000040148	7	131542867	131544925	1	8	4	14	400	12	2	0	0	0	0	0		P42581
ENSMUST00000046094	ENSMUSG00000040385	19	4192158	4195419	1	4	4	14	29	9	8	6017	8330	4117	607	2669		P62137
ENSMUST00000046095	ENSMUSG00000033080	2	150680702	150689360	-1	35	30	43	218	35	13	1	0	0	1	0	A2AQX5	Q91V10
ENSMUST00000046110	ENSMUSG00000026587	1	158362273	158691781	1	0	0	57	0	47	0	0	0	0	0	0	Q3UHD7	Q61137
ENSMUST00000046114	ENSMUSG00000034932	10	81264713	81266934	-1	2	2	11	29	3	4	142	185	100	165	80		Q9CPW3
ENSMUST00000046121						41	32	85	60	38	23	1	11	5	0	6		
ENSMUST00000046122	ENSMUSG00000039682	5	45493374	45512691	1	15	15	27	84	12	12	28	90	17	150	123		Q9CPY7
ENSMUST00000046128	ENSMUSG00000034456	6	90333284	90364551	1	0	17	0	7	0	22	0	2	1	0	2		Q8VC12
ENSMUST00000046131	ENSMUSG00000092243	17	36109719	36129425	-1	0	0	0	0	0	0	0	0	0	0	0	Q0WXH6	
ENSMUST00000046144	ENSMUSG00000037003	15	102102988	102116401	1	3	3	117	185	19	4	5	0	0	1	46		Q8CGB6
ENSMUST00000046149						1	0	0	170	4	2	191	324	127	95	166		
ENSMUST00000046154	ENSMUSG00000035310	5	100441918	100500639	-1	0	0	0	0	0	0	59	449	76	0	0		Q571G4
ENSMUST00000046156	ENSMUSG00000038580	7	141278331	141279133	-1	3	4	8	38	4	1	0	0	0	0	0	Q80ZS9	
ENSMUST00000046157	ENSMUSG00000039286	3	27416162	27711307	-1	27	0	44	30	0	15	711	878	1670	116	1603		
ENSMUST00000046168	ENSMUSG00000041708	15	83779467	83858494	1	0	0	0	15	0	0	0	0	0	0	0		Q91ZG2
ENSMUST00000046174	ENSMUSG00000037625	3	31149920	31164324	1	13	11	21	88	13	5	0	0	0	0	0		Q60771
ENSMUST00000046177	ENSMUSG00000036931	7	30421732	30428746	1	12	10	6	2	14	2	162	522	100	0	200		Q2TB02
ENSMUST00000046182						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000046186	ENSMUSG00000037379	5	33198184	33218455	-1	28	10	50	21	38	16	0	0	0	6	11		Q8BMS2
ENSMUST00000046188						38	29	41	145	46	26	2	37	14	26	12		
ENSMUST00000046191	ENSMUSG00000037722	14	45376334	45388802	-1	5	13	4	43	10	5	51	81	31	108	36		Q9JK38
ENSMUST00000046206	ENSMUSG00000040446	18	24484962	24530204	-1	28	18	29	149	44	30	74	359	129	64	122		Q8VDS4
ENSMUST00000046207	ENSMUSG00000037361	12	4817608	4827658	1	46	51	90	46	38	30	598	1942	682	2673	394		P59708
ENSMUST00000046212	ENSMUSG00000032902	3	104638668	104658462	1	18	21	33	73	28	8	45	95	44	93	190	Q544N9	P53986
ENSMUST00000046221	ENSMUSG00000038583	10	53337686	53345999	1	0	0	0	0	11	0	0	0	0	0	0		P61014
ENSMUST00000046223	ENSMUSG00000041828	11	110025634	110095978	-1	0	12	0	10	10	0	0	0	1	0	2	F8WGE3	
ENSMUST00000046227	ENSMUSG00000036893	2	24789928	24919614	-1	0	1	2	1	1	0	2	1	31	0	0		Q5DW34
ENSMUST00000046233	ENSMUSG00000041660	2	110262697	110314560	-1	8	4	7	4	9	10	0	0	0	0	0		Q924Y0
ENSMUST00000046234	ENSMUSG00000042031	3	92932979	92934097	1	3	3	3	11	6	1	0	0	0	0	0	Q9CQM7	
ENSMUST00000046244	ENSMUSG00000040482	17	34837019	34839233	1	0	3	7	85	0	7	129	245	121	0	86		
ENSMUST00000046245	ENSMUSG00000070822	7	12768092	12775658	-1	45	20	240	47	49	18	2	5	5	1	5	E9PUD6	
ENSMUST00000046246	ENSMUSG00000021493	13	55495795	55513676	-1	0	0	0	31	0	0	1559	1966	1236	142	770		Q3TJD7
ENSMUST00000046254	ENSMUSG00000040490	17	48932379	49097588	1	26	12	49	125	35	14	0	0	0	0	0		Q80TG9
ENSMUST00000046255	ENSMUSG00000032641	6	134869093	134898578	-1	1	0	7	0	0	0	11	28	0	9	0		Q61121
ENSMUST00000046257	ENSMUSG00000057738	2	29965560	30031451	1	22	24	51	0	0	23	1139	1766	1086	399	1279		P16546
ENSMUST00000046259	ENSMUSG00000042524	15	79724070	79742536	-1	0	9	17	0	21	0	10253	7271	7856	666	5420		Q8BJS4
ENSMUST00000046260						2	0	0	23	0	0	3	3	0	2	2		
ENSMUST00000046266	ENSMUSG00000042507	12	84149176	84218881	-1	0	9	25	65	9	15	1273	1637	1863	87	1547	E9Q2I4	
ENSMUST00000046274	ENSMUSG00000027652	2	158409848	158499253	1	24	0	0	0	0	0	347	433	998	49	828	F8WHN4	
ENSMUST00000046276						0	0	0	0	4	0	3	1	0	2	0		
ENSMUST00000046283	ENSMUSG00000032932	16	75755190	75766821	-1	3	12	26	7	12	3	130	283	72	100	87		Q8BM72
ENSMUST00000046285	ENSMUSG00000036887	4	136895917	136898803	-1	9	3	21	37	21	3	27	2	9	2041	1383		P98086
ENSMUST00000046288	ENSMUSG00000024038	17	31520115	31531326	1	5	10	79	17	20	10	327	371	310	208	217	Q3U422	
ENSMUST00000046290	ENSMUSG00000033192	8	92855350	92919279	1	4	3	9	91	15	2	2675	8810	3404	1066	2793		Q8BYI6
ENSMUST00000046303	ENSMUSG00000032652	6	134830154	134858931	1	9	14	25	63	21	7	398	1324	576	224	593		
ENSMUST00000046305	ENSMUSG00000048118	12	71015990	71098592	1	23	16	34	43	28	26	505	2356	1487	452	1652	F8VPQ2	
ENSMUST00000046306	ENSMUSG00000040167	7	131388652	131410521	-1	16	14	18	35	32	4	208	334	228	223	176		Q8BU00
ENSMUST00000046316	ENSMUSG00000032913	3	104396418	104511918	-1	29	29	44	139	42	22	160	517	296	42	260		Q52KR2
ENSMUST00000046322	ENSMUSG00000038421	1	170917576	170927583	-1	5	5	0	0	10	0	0	6	4	0	10		Q920A9
ENSMUST00000046331	ENSMUSG00000035560	12	65225517	65228454	1	20	18	18	27	22	12	0	0	1	0	0		Q9D5R2
ENSMUST00000046332	ENSMUSG00000036896	4	136889804	136893065	-1	7	12	36	30	27	2	23	0	4	3665	1052		Q02105
ENSMUST00000046333	ENSMUSG00000040541	9	40148122	40150880	1	5	7	6	6	5	2	0	0	0	0	0		Q9D9S2
ENSMUST00000046334						2	6	30	2	2	0	0	0	0	0	0		
ENSMUST00000046340	ENSMUSG00000042523	12	84114366	84147498	1	0	1	0	0	1	0	0	0	1	0	0		Q05A62
ENSMUST00000046349						53	36	68	238	47	22	29	86	26	19	36		
ENSMUST00000046351	ENSMUSG00000036957	7	30355514	30362772	-1	24	13	48	523	33	21	0	0	0	0	2		Q8BLY3
ENSMUST00000046361	ENSMUSG00000037593	11	78290841	78296805	1	3	1	0	3	4	3	1	2	0	0	4		Q5SYL1
ENSMUST00000046371	ENSMUSG00000040563	9	21937033	21948907	1	0	12	4	57	16	0	15	16	0	0	0		Q8VCY8
ENSMUST00000046373	ENSMUSG00000040797	6	121372933	121473678	-1	0	0	0	520	2	5	0	0	0	0	0		Q3TES0
ENSMUST00000046378	ENSMUSG00000032940	16	75592844	75602829	1	0	0	0	48	0	0	3	0	2	11	0		Q80YT9
ENSMUST00000046383	ENSMUSG00000039304	3	27317028	27342427	1	58	49	136	63	63	28	4	31	12	2	33	Q3U5H0	P50592
ENSMUST00000046384	ENSMUSG00000036905	4	136880129	136886187	-1	10	8	23	13	12	7	21	3	8	2309	1029		P14106
ENSMUST00000046386	ENSMUSG00000061410	8	121598703	121652901	-1	34	26	106	416	74	12	11	21	13	5	86	A2RTC2	Q8VIG0
ENSMUST00000046389	ENSMUSG00000042369	2	76369984	76383768	1	13	9	32	172	24	9	219	620	365	92	179		Q8BHN5
ENSMUST00000046390	ENSMUSG00000018417	1	51749765	51916071	-1	0	0	0	27	0	0	0	0	0	0	0		P46735
ENSMUST00000046399	ENSMUSG00000033096	2	150583080	150608567	-1	16	3	40	43	16	10	779	2177	1010	560	565		Q9D7N9
ENSMUST00000046404	ENSMUSG00000041712	12	102757975	102777701	1	16	6	31	17	21	7	274	664	416	155	280	Q52KC0	Q8BU04
ENSMUST00000046418	ENSMUSG00000039244	5	143301195	143315360	-1	0	0	0	13	0	0	373	224	180	33	140		Q8BGA7
ENSMUST00000046422	ENSMUSG00000042540	12	84069325	84076020	1	8	3	0	12	10	8	0	0	0	0	0		Q6Q2Z6
ENSMUST00000046425	ENSMUSG00000053841	4	129626078	129641065	-1	0	0	13	21	14	9	477	720	481	84	274	Q3UD58	Q6PAM1
ENSMUST00000046426	ENSMUSG00000032741	5	120534153	120588673	-1	33	22	84	132	46	29	619	597	604	52	781		Q9EQJ0
ENSMUST00000046433	ENSMUSG00000036537	X	37191245	37192467	1	4	3	8	68	7	2	46	122	61	41	40	Q8R3P8	
ENSMUST00000046461	ENSMUSG00000040631	8	94863828	94876312	-1	13	15	26	45	37	20	23	33	17	9	25		Q99KE3
ENSMUST00000046463	ENSMUSG00000042535	15	79690895	79721478	1	24	22	123	176	46	25	2264	2453	2204	202	1484		O08582
ENSMUST00000046470	ENSMUSG00000039345	16	8470788	8490684	1	15	9	14	5	20	11	3	10	0	9	9		Q8R1C6
ENSMUST00000046476	ENSMUSG00000026659	1	170873498	170885540	-1	0	0	0	0	0	0	0	19	0	16	13	Q924M1	
ENSMUST00000046485	ENSMUSG00000021176	12	99717531	99883442	-1	13	10	20	37	14	4	13	27	21	19	5		Q9D0E5
ENSMUST00000046490	ENSMUSG00000040652	9	65668001	65690300	1	14	0	0	69	31	11	2373	6560	2914	650	682	J3QNN0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000046497	ENSMUSG00000040658	17	46496789	46499618	1	108	68	159	197	132	57	18	38	12	14	16		Q80VJ3
ENSMUST00000046498	ENSMUSG00000042357	4	127354809	127358181	-1	14	13	44	25	21	13	0	0	0	17	2	Q542M8	Q02739
ENSMUST00000046502	ENSMUSG00000040661	9	106688082	106789194	-1	67	67	167	168	99	68	123	187	248	14	209	E9QKL0	
ENSMUST00000046506	ENSMUSG00000040663	19	4214238	4223490	1	2	0	0	18	0	0	3	14	5	5	29		Q9QZM3
ENSMUST00000046513	ENSMUSG00000037747	10	70557682	70655965	-1	0	0	0	3	2	1	0	0	0	0	0		Q8BGT8
ENSMUST00000046514	ENSMUSG00000026615	1	185363044	185428360	1	11	17	14	14	14	8	111	375	282	336	409		Q8CGC7
ENSMUST00000046515	ENSMUSG00000027698	3	27182965	27284608	1	19	20	69	63	28	20	237	748	431	171	343		Q8BLF1
ENSMUST00000046516						3	1	4	389	3	11	1	1	0	0	1		
ENSMUST00000046518	ENSMUSG00000057963	12	102568582	102704930	-1	39	20	223	256	51	22	498	764	498	67	459		Q8BYN3
ENSMUST00000046520	ENSMUSG00000038074	6	54577604	54597308	-1	2	0	20	10	0	0	0	1	0	3	0	Q542Q0	P59024
ENSMUST00000046521	ENSMUSG00000038256	3	97203662	97297917	-1	11	6	65	26	47	12	123	171	100	18	156		Q9D219
ENSMUST00000046522	ENSMUSG00000040283	11	49165585	49187159	-1	115	68	242	238	126	61	8	48	23	4	15		Q8BJE2
ENSMUST00000046525	ENSMUSG00000040680	17	23741200	23745829	-1	62	59	358	319	80	39	0	6	1	1	4		Q8K1S7
ENSMUST00000046532	ENSMUSG00000042367	4	127325235	127330844	-1	0	0	26	86	18	0	0	0	0	0	0		P28231
ENSMUST00000046533	ENSMUSG00000034686	13	55464267	55473155	1	5	2	8	400	12	6	97	316	176	44	174	B2RSG4	Q3V0I2
ENSMUST00000046534						20	5	25	22	4	12	84	57	62	16	80		
ENSMUST00000046542	ENSMUSG00000034544	3	66981390	67358396	1	2	13	13	0	1	0	0	49	0	0	0	Q3TGY1	
ENSMUST00000046548	ENSMUSG00000050199	2	109917647	110014257	1	18	0	0	109	25	0	0	0	6	0	0		A2ARI4
ENSMUST00000046549	ENSMUSG00000040694	17	48419231	48432728	-1	19	11	12	11	16	6	0	2	0	3	10		Q9WV35
ENSMUST00000046557	ENSMUSG00000036551	X	37150698	37168842	-1	1	4	15	14	6	0	0	2	1	1	3	Q3V0I7	
ENSMUST00000046558	ENSMUSG00000063172	4	107253593	107279938	1	0	0	0	0	0	0	13	0	0	36	0		Q9D6H2
ENSMUST00000046565	ENSMUSG00000035277	X	93286445	93298357	1	0	3	16	130	0	0	0	0	0	0	0		O35085
ENSMUST00000046571	ENSMUSG00000026790	2	29889221	29931746	1	7	4	7	0	0	0	0	0	0	16	0		A3KGV1
ENSMUST00000046575	ENSMUSG00000038502	7	44863069	44869788	-1	3	3	0	93	2	3	162	218	184	26	106		Q91VU8
ENSMUST00000046587	ENSMUSG00000040722	9	57441328	57468024	-1	20	7	59	50	24	10	5	2	0	19	33		Q9JKD3
ENSMUST00000046589	ENSMUSG00000036924	2	148820081	148830410	1	7	6	3	0	4	3	0	0	0	0	0		Q80ZN5
ENSMUST00000046603	ENSMUSG00000062234	5	108569411	108629755	-1	0	0	0	60	24	0	1859	2146	2779	114	1892		
ENSMUST00000046611	ENSMUSG00000040205	7	131308554	131322292	-1	6	4	17	7	13	4	0	0	0	0	0	B2RU69	
ENSMUST00000046614	ENSMUSG00000039131	3	152093533	152166230	-1	7	2	0	2	2	0	0	0	0	5	4		Q9Z2H7
ENSMUST00000046624	ENSMUSG00000037652	3	30899371	30969415	-1	0	0	0	0	6	0	0	0	0	0	28	F8WIN6	
ENSMUST00000046627	ENSMUSG00000040875	9	114978569	115232225	1	0	3	0	0	0	0	0	0	0	0	0	Q8R2T7	
ENSMUST00000046633	ENSMUSG00000041935	15	3982036	3995752	-1	8	9	17	41	12	6	371	940	469	134	271		Q8BR90
ENSMUST00000046638	ENSMUSG00000036009	10	105763189	105841380	-1	1	3	10	3	0	3	37	155	44	17	31		
ENSMUST00000046644	ENSMUSG00000042043	13	94788943	94842899	1	4	3	2	26	6	2	418	1532	451	2050	232	Q5I0U7	P48428
ENSMUST00000046647	ENSMUSG00000036921	4	136610437	136613226	1	3	0	10	5	13	1	0	0	0	0	0	Q9CPU3	
ENSMUST00000046651	ENSMUSG00000040771	17	48410014	48417266	1	0	4	0	0	0	4	92	497	113	307	90		Q8R5F3
ENSMUST00000046656	ENSMUSG00000039033	2	139833480	140066805	-1	4	0	36	162	9	5	0	7	0	0	0		Q8R1G1
ENSMUST00000046658	ENSMUSG00000059149	1	132022806	132068062	-1	23	22	43	63	24	13	1	2	3	2	11		Q6PDC8
ENSMUST00000046659	ENSMUSG00000042388	4	127169204	127237022	1	0	0	29	781	24	15	0	0	0	0	2	Q3TY61	Q6PFD5
ENSMUST00000046662	ENSMUSG00000051081	1	166628971	166647693	-1	28	25	309	66	26	9	0	0	0	0	2	G3X946	
ENSMUST00000046663	ENSMUSG00000035107	16	58408443	58469727	1	30	15	14	68	21	3	0	6	6	19	67		Q91ZV3
ENSMUST00000046673	ENSMUSG00000052062	1	61638824	62642284	1	0	0	0	0	0	0	0	0	0	0	0	Q5SV55	
ENSMUST00000046675	ENSMUSG00000040795	4	129615126	129619099	-1	41	39	51	47	28	19	53	160	77	57	67		A2ADZ8
ENSMUST00000046687	ENSMUSG00000038156	7	113765998	114043370	1	40	22	35	140	45	32	3	29	2	7	119		Q8VCC9
ENSMUST00000046689	ENSMUSG00000032712	6	149309414	149335663	1	0	0	0	52	28	0	375	2587	1723	230	1556	B2KFD2	Q5DTW7
ENSMUST00000046704	ENSMUSG00000078920	11	49076587	49096974	1	4	4	0	5	0	3	87	676	126	687	435	Q61635	
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ENSMUST00000046735	ENSMUSG00000040813	9	106658746	106685927	-1	0	0	8	0	0	0	57	33	97	57	86	E9Q137	
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ENSMUST00000046750	ENSMUSG00000001763	6	29694222	29718559	1	0	9	0	65	15	0	0	0	0	0	0		Q8R3S2
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ENSMUST00000046769	ENSMUSG00000040549	2	91526762	91620664	1	0	0	0	0	0	0	0	0	96	0	28		
ENSMUST00000046770	ENSMUSG00000037499	1	191306789	191318194	-1	5	2	15	58	4	1	14	20	9	100	22		Q9CQ45
ENSMUST00000046777	ENSMUSG00000032965	16	49699233	49765126	1	5	3	6	74	7	5	26	74	58	19	41	B2RQZ0	Q8BXG3
ENSMUST00000046792	ENSMUSG00000038463	1	170644532	170682789	1	20	15	52	104	34	8	2436	2332	2534	105	866		Q3V1G4
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ENSMUST00000046833	ENSMUSG00000035852	10	79821021	79830452	1	32	17	61	38	27	19	4	17	0	7	0		Q9D279
ENSMUST00000046835	ENSMUSG00000035992	11	54438199	54518235	1	9	7	26	58	15	4	522	1075	1153	370	671		Q68FD7
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ENSMUST00000046839	ENSMUSG00000040888	17	24693191	24696156	-1	4	10	20	106	17	6	23	56	11	22	27		P56213
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ENSMUST00000046864	ENSMUSG00000033721	3	109340653	109685698	1	6	0	0	16	0	0	517	1224	1306	139	856		Q9R0C8
ENSMUST00000046869	ENSMUSG00000040913	19	45578254	45660312	-1	0	2	3	372	11	12	149	467	361	55	257		Q9JMJ2
ENSMUST00000046870	ENSMUSG00000019230	1	138825186	138848577	-1	102	86	772	279	86	69	1	6	6	0	1		Q9WUH2
ENSMUST00000046875	ENSMUSG00000037470	1	36140027	36244720	-1	18	21	53	50	62	32	165	807	500	62	628		Q6P5E4
ENSMUST00000046890	ENSMUSG00000038618	7	141215860	141218658	1	3	3	28	60	11	2	57	59	47	22	33		Q9DD19
ENSMUST00000046891	ENSMUSG00000037759	14	44988195	45003820	1	24	11	32	49	34	15	278	893	282	74	342	Q543A9	Q62053

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ENSMUST00000046897	ENSMUSG00000039853	4	46493781	46536141	-1	1	0	3	78	3	0	13	33	36	6	41	Q14AR3	Q8BVW3
ENSMUST00000046898	ENSMUSG00000040929	19	27761721	28011166	-1	15	18	267	8	27	0	0	0	7	0	9	G5E890	
ENSMUST00000046901	ENSMUSG00000025856	5	138976014	138997370	-1	5	7	56	22	8	4	0	0	0	12	16	G5E891	
ENSMUST00000046903	ENSMUSG00000040350	11	48826140	48852209	1	0	0	3	87	9	0	0	0	3	0	0	Q5NCB7	
ENSMUST00000046908	ENSMUSG00000035399	2	163405822	163424697	-1	30	20	29	66	31	7	519	2247	624	1026	451		Q9D722
ENSMUST00000046916	ENSMUSG00000037725	8	22168152	22185819	-1	8	2	11	57	16	2	30	70	59	105	32		Q3V1H1
ENSMUST00000046924	ENSMUSG00000040339	3	108970997	109027607	-1	27	22	18	0	23	18	156	530	219	80	362		Q8BQS4
ENSMUST00000046929	ENSMUSG00000063317	7	121642021	121707253	-1	76	66	259	226	73	36	50	67	71	8	81	E9Q6Y8	
ENSMUST00000046937	ENSMUSG00000041566	16	17894223	17897922	1	45	28	66	53	46	13	1	0	0	0	2		Q61241
ENSMUST00000046941	ENSMUSG00000039328	8	31111820	31131482	1	9	10	35	88	18	6	14	22	8	12	23		
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ENSMUST00000046945	ENSMUSG00000035863	10	79793572	79820896	1	18	19	26	0	20	13	2551	2521	1688	213	1306		Q9Z0P4
ENSMUST00000046948	ENSMUSG00000040957	18	11839220	11945627	1	0	0	8	0	0	16	13	0	4	2	0		Q9ESJ1
ENSMUST00000046950	ENSMUSG00000041229	X	151520672	151633859	1	0	0	0	0	0	0	683	964	1255	52	899		Q80TJ7
ENSMUST00000046951	ENSMUSG00000038683	13	41001023	41013019	1	2	0	0	15	0	0	383	1730	691	649	313		Q9DCE5
ENSMUST00000046955	ENSMUSG00000078970	11	17182107	17233796	1	13	8	4	11	9	2	42	286	57	234	51		Q8BGF3
ENSMUST00000046959	ENSMUSG00000040966	17	12584189	12628465	1	19	13	27	25	25	6	0	3	0	0	0		O70577
ENSMUST00000046962	ENSMUSG00000041229	X	151520672	151633859	1	0	0	0	0	0	0	21	11	39	0	74	A2ABV3	Q80TJ7
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ENSMUST00000046972	ENSMUSG00000024491	18	42275353	42341542	1	9	0	0	30	11	0	74	184	215	23	107		Q5SFM8
ENSMUST00000046974	ENSMUSG00000037816	13	50417864	50433780	1	0	0	0	47	0	0	22	27	27	6	26	Q8CFE8	
ENSMUST00000046975	ENSMUSG00000033623	5	108461232	108506976	1	81	55	288	157	79	36	114	193	160	34	161		Q8BTQ0
ENSMUST00000046977	ENSMUSG00000039167	3	151437887	151545086	1	13	11	18	18	14	2	57	163	58	18	17		Q923X1
ENSMUST00000046983	ENSMUSG00000037049	7	105554360	105558388	1	27	13	77	90	34	9	782	648	499	90	348		Q04519
ENSMUST00000046993	ENSMUSG00000052273	7	119922717	120095177	-1	64	59	69	73	84	37	0	6	0	1	0		Q8BW94
ENSMUST00000046999	ENSMUSG00000040532	5	135009152	135012175	1	7	0	9	17	9	2	45	34	24	20	29		Q8K4F5
ENSMUST00000047005	ENSMUSG00000039335	3	26637620	26983212	1	0	11	24	0	15	6	0	0	0	0	0		Q8C636
ENSMUST00000047008	ENSMUSG00000033156	2	149405057	149410293	1	4	2	2	4	8	1	0	0	0	0	0	Q9JM84	
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ENSMUST00000047020	ENSMUSG00000040705	7	19418812	19421417	-1	5	2	7	31	6	1	0	1	0	0	1	E9Q6Z9	
ENSMUST00000047023	ENSMUSG00000038070	4	84884309	85131921	1	0	0	30	56	22	0	0	0	0	0	0		A2AM05
ENSMUST00000047025	ENSMUSG00000034990	7	121083322	121163097	1	15	14	52	27	40	20	6	3	3	0	6		Q8K561
ENSMUST00000047028	ENSMUSG00000042363	11	20823576	20831056	-1	13	8	20	8	13	8	19	27	15	17	26		Q8VED9
ENSMUST00000047034	ENSMUSG00000015599	17	46442448	46487675	-1	55	50	121	603	79	33	2	1	2	0	5		Q6PCN3
ENSMUST00000047036	ENSMUSG00000047649	7	19356849	19359483	-1	16	16	64	55	21	12	39	109	64	34	69		Q76KJ5
ENSMUST00000047037	ENSMUSG00000037475	X	41794991	41920674	-1	1	1	0	5	0	2	302	653	497	208	390		B1AZI6
ENSMUST00000047040	ENSMUSG00000037060	7	105480607	105482197	-1	5	7	9	158	13	4	2	1	1	48	40		Q91VJ2
ENSMUST00000047045	ENSMUSG00000047026	7	119690026	119714567	1	11	9	10	9	12	5	0	0	0	0	0		Q80W40
ENSMUST00000047055	ENSMUSG00000042092	3	92679247	92680918	1	2	1	5	8	8	3	0	0	0	0	0	Q9D1C5	
ENSMUST00000047057	ENSMUSG00000041035	19	45560615	45579763	1	6	7	15	36	10	8	211	583	186	373	138		Q8BPA8
ENSMUST00000047061	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	2	G3X971	
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ENSMUST00000047086	ENSMUSG00000041057	17	71616215	71659031	1	16	10	18	88	27	12	44	216	89	218	183		Q6ZQL4
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ENSMUST00000047093	ENSMUSG00000038637	7	141194157	141210055	1	0	3	22	9	0	6	14	68	0	0	0		Q8K375
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ENSMUST00000047111	ENSMUSG00000041237	3	89136142	89146784	1	21	14	33	12	0	23	0	2	3	0	1	G3X925	
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ENSMUST00000047144	ENSMUSG00000036046	15	84943936	84988551	-1	34	23	30	56	63	29	2887	8430	3882	465	2632		Q3UE31
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ENSMUST00000047170	ENSMUSG00000040714	7	19394437	19404104	-1	0	3	0	11	8	0	0	0	0	0	0		Q91W40
ENSMUST00000047173	ENSMUSG00000041124	9	4383535	4386861	1	16	6	5	15	3	2	116	413	147	382	118		Q91YU3
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ENSMUST00000047194	ENSMUSG00000035004	7	121064067	121074530	-1	20	29	91	41	31	17	1750	14143	4051	5124	3161		P0C6B7
ENSMUST00000047196	ENSMUSG00000040557	5	134932368	134942637	1	24	15	74	9	38	7	0	5	3	0	3	Q8BGM4	
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ENSMUST00000047203	ENSMUSG00000035890	10	79758515	79766952	-1	9	4	15	145	11	9	199	358	214	27	178	Q3U3G2	Q91YL2
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ENSMUST00000047207	ENSMUSG00000039492	4	154026639	154042677	-1	19	13	35	38	26	11	0	0	0	0	0	B1AX94	Q3V036
ENSMUST00000047208	ENSMUSG00000042156	14	118875520	118925314	-1	5	7	29	9	35	3	0	0	0	0	0		Q8BMD2
ENSMUST00000047218	ENSMUSG00000033589	14	70545251	70548933	1	26	7	59	172	28	14	235	456	254	41	196		Q8K072
ENSMUST00000047226	ENSMUSG00000041168	17	56614301	56626903	-1	9	14	22	130	23	8	289	424	325	51	288		Q8CGK3
ENSMUST00000047232	ENSMUSG00000042410	2	75832177	75931350	1	19	19	41	45	19	8	761	2453	1143	251	619	A2AL50	
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ENSMUST00000047257	ENSMUSG00000041298	5	148871584	148929320	-1	16	15	32	12	17	9	2	8	5	0	9		Q8K0T4
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ENSMUST00000047273	ENSMUSG00000041199	17	25727751	25731456	1	22	17	24	11	24	11	66	97	64	13	48		Q8VCZ8
ENSMUST00000047275	ENSMUSG00000040605	16	97356728	97439012	1	25	20	40	102	21	13	1	1	1	0	0		
ENSMUST00000047281	ENSMUSG00000041203	8	85026833	85030285	1	4	5	8	127	9	3	796	2319	739	275	612		Q9D735
ENSMUST00000047282	ENSMUSG00000031816	8	121091628	121108392	-1	0	0	0	32	3	0	6	0	10	0	7		Q3URQ7
ENSMUST00000047285	ENSMUSG00000032952	3	103809520	103822025	1	0	0	0	0	8	0	58	481	518	37	174		Q9WV76
ENSMUST00000047286	ENSMUSG00000037798	14	41105381	41124412	1	17	15	35	32	23	12	0	0	0	82	0		Q91X83
ENSMUST00000047300	ENSMUSG00000042165	3	92428032	92429423	-1	0	0	0	0	0	0	0	0	0	0	0	D3YUD8	
ENSMUST00000047305	ENSMUSG00000040576	5	134901593	134906733	-1	11	7	50	9	11	12	0	0	0	0	0		Q6UJB9
ENSMUST00000047309	ENSMUSG00000035285	7	4922251	4925006	1	23	28	55	519	52	40	3	13	7	0	13		Q8BVG8
ENSMUST00000047311	ENSMUSG00000038732	13	30136498	30246717	1	17	10	42	67	28	13	40	148	68	14	50		Q8BH98
ENSMUST00000047315	ENSMUSG00000037025	2	148042877	148046969	-1	4	6	9	138	11	4	0	0	0	0	0		P35583
ENSMUST00000047321	ENSMUSG00000055116	7	113207465	113314122	1	16	7	20	27	19	5	57	151	113	26	73	Q3UHZ2	Q9WTL8
ENSMUST00000047322	ENSMUSG00000041238	18	11633276	11743207	1	5	0	15	50	10	0	59	113	134	169	102		Q80YR6
ENSMUST00000047328	ENSMUSG00000039323	1	72824503	72852474	1	0	0	4	87	4	7	0	0	0	0	0		P47877
ENSMUST00000047331	ENSMUSG00000033595	14	70530821	70538323	1	29	15	44	163	53	20	0	0	0	0	0		Q8K406
ENSMUST00000047334	ENSMUSG00000041248	9	32372418	32399192	1	19	10	153	30	0	8	0	4	0	1	0		O88335
ENSMUST00000047348	ENSMUSG00000037617	15	36179368	36235610	1	17	7	9	140	27	3	0	17	0	0	0		Q80ZX8
ENSMUST00000047349	ENSMUSG00000032267	9	48985385	49042517	1	20	23	17	82	30	13	88	311	151	42	158		Q5I043
ENSMUST00000047356	ENSMUSG00000038539	7	44812256	44816599	-1	5	0	0	172	12	0	53	166	134	34	45	Q3UJF3	O70191
ENSMUST00000047357	ENSMUSG00000041781	12	101975974	102005993	1	20	15	30	80	23	16	290	1186	790	312	511		O35218
ENSMUST00000047362	ENSMUSG00000038930	7	80293229	80324454	-1	1	0	0	0	0	0	8	15	0	0	0		Q8BTU7
ENSMUST00000047363	ENSMUSG00000037851	13	49682100	49734267	1	0	16	43	0	0	17	36	207	95	14	108		Q8BU30
ENSMUST00000047368	ENSMUSG00000033752	3	84087933	84155786	-1	4	3	5	85	6	6	7	33	20	48	39		Q8K396
ENSMUST00000047370	ENSMUSG00000039092	2	139493913	139637674	1	8	9	0	6	0	12	0	0	0	0	0		Q8BG54
ENSMUST00000047373	ENSMUSG00000041287	11	69655314	69656727	1	8	1	14	19	5	2	0	7	1	2	2	Q5F2B2	P43267
ENSMUST00000047379	ENSMUSG00000039942	15	5206661	5244187	-1	22	14	30	200	21	0	19	143	54	19	41		P32240
ENSMUST00000047383	ENSMUSG00000039672	16	92292389	92298129	1	4	0	2	0	4	3	0	0	0	0	0		
ENSMUST00000047393	ENSMUSG00000042340	7	127712736	127718192	1	10	6	59	90	9	4	2	2	1	3	2	Q541U3	Q60753
ENSMUST00000047399	ENSMUSG00000041293	17	43270329	43324737	1	24	25	40	22	22	12	1	0	0	0	0		Q8VEC3
ENSMUST00000047404	ENSMUSG00000032435	9	114688790	114724302	1	31	33	170	172	37	14	598	2426	1198	132	848	Q3TWG5	Q8R1Q8
ENSMUST00000047405	ENSMUSG00000022488	15	103453825	103498800	1	35	30	58	64	47	23	5853	14007	10381	1874	9860	Q8K1X4	
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ENSMUST00000047409	ENSMUSG00000037568	1	190947646	190979296	-1	0	27	25	192	28	15	0	0	0	0	0		Q8C5G2
ENSMUST00000047412	ENSMUSG00000032727	13	111686178	111718596	1	0	0	0	17	0	0	42	36	0	0	69		Q3UHF3
ENSMUST00000047413	ENSMUSG00000036792	2	48949508	49325405	1	27	0	33	19	29	0	0	0	0	0	0	B1AYB5	
ENSMUST00000047419	ENSMUSG00000041736	15	83563573	83574201	1	8	9	33	34	12	15	13734	19329	8414	6441	4247	Q541E3	P50637
ENSMUST00000047421	ENSMUSG00000033191	4	118471191	118490061	-1	19	11	23	10	25	15	6	9	0	5	0		Q06806
ENSMUST00000047425	ENSMUSG00000041308	8	106935750	107014192	1	22	13	69	226	24	17	716	1528	1319	78	1766	Q542S9	Q61235
ENSMUST00000047429	ENSMUSG00000039680	16	92058270	92112227	1	2	0	2	55	0	3	11	32	5	19	30	Q3TLQ4	P58064
ENSMUST00000047431	ENSMUSG00000028830	4	126753544	126870070	1	6	11	64	47	32	15	1092	1325	1224	91	765		Q8K135
ENSMUST00000047436	ENSMUSG00000041319	17	23668614	23673882	-1	0	0	0	0	0	0	3	0	0	0	0		Q5U4D9
ENSMUST00000047441	ENSMUSG00000061462	11	58994256	59136402	-1	111	26	143	1083	171	11	0	0	0	0	0	H7BX05	
ENSMUST00000047443	ENSMUSG00000032718	6	134609207	134632488	-1	9	12	35	157	20	8	17	17	6	1	19		Q9CR33
ENSMUST00000047446	ENSMUSG00000022696	16	44240180	44333196	-1	33	20	55	193	20	14	0	0	11	3	0	E9Q247	
ENSMUST00000047447	ENSMUSG00000026870	2	34874396	34892132	1	0	0	0	0	0	0	0	0	0	0	0	Q9D1U5	
ENSMUST00000047450	ENSMUSG00000053007	6	53287270	53700376	1	29	10	59	107	19	13	4	10	11	2	15		
ENSMUST00000047463	ENSMUSG00000033389	11	65002039	65162961	-1	0	1	0	186	0	22	0	0	0	0	0		Q5SSM3
ENSMUST00000047477	ENSMUSG00000042212	3	92339140	92340873	1	4	7	17	5	9	3	0	0	0	0	0		O70555
ENSMUST00000047479	ENSMUSG00000102697	18	37143503	37187657	1	16	15	29	253	26	10	0	0	0	0	0	Q91Y09	
ENSMUST00000047480	ENSMUSG00000041482	18	63010213	63387183	-1	35	44	33	63	67	14	0	0	0	1	35	E9QNW4	
ENSMUST00000047485	ENSMUSG00000040570	5	8490334	8622952	-1	6	14	16	0	13	2	2	10	7	3	8		Q6PDC0
ENSMUST00000047486	ENSMUSG00000006423	X	36823737	36874111	-1	0	27	0	27	54	38	0	0	0	0	0		Q8VDP2
ENSMUST00000047488	ENSMUSG00000038807	11	74383356	74590186	-1	38	22	5	82	18	18	2353	1612	2780	85	1929		Q5SVL6
ENSMUST00000047490	ENSMUSG00000039308	14	20723739	20730327	-1	20	12	55	21	38	20	608	723	517	68	540		P52850
ENSMUST00000047497	ENSMUSG00000039523	4	153975194	154008732	1	24	27	62	129	39	14	216	373	339	21	242		Q80V31
ENSMUST00000047498	ENSMUSG00000033213	2	122636986	122641191	1	3	1	4	24	1	4	1125	3966	1003	2072	250	Q3UCF3	Q810Q5
ENSMUST00000047502	ENSMUSG00000037730	3	30602065	30619873	1	0	2	0	0	0	0	117	205	163	222	140		Q99MD8
ENSMUST00000047503	ENSMUSG00000041354	17	33929543	33937687	1	11	22	36	27	24	9	1358	4192	1597	246	1987		Q61193
ENSMUST00000047510	ENSMUSG00000038429	6	124815019	124829484	-1	18	7	55	61	23	12	49	175	53	19	31		P56399
ENSMUST00000047511	ENSMUSG00000041362	19	58973358	59076069	-1	0	26	0	13	7	0	39	271	142	64	208		Q8K2Q9
ENSMUST00000047521	ENSMUSG00000039787	2	29869164	29882840	1	44	50	104	97	72	32	17	25	22	3	28	B2RSF7	A3KGW5
ENSMUST00000047524	ENSMUSG00000024251	17	84190056	84466196	-1	59	40	106	156	79	29	132	215	222	27	146		A8C756
ENSMUST00000047526	ENSMUSG00000036995	4	136206365	136245216	1	40	31	85	319	60	31	3	1	0	2	6		Q5U464
ENSMUST00000047527	ENSMUSG00000070866	2	82053222	82259879	1	9	11	45	41	11	5	0	0	0	0	1		A2AKY4
ENSMUST00000047531	ENSMUSG00000039958	6	149139849	149151171	1	0	0	0	8	1	0	14	30	34	93	53		Q80ZM3
ENSMUST00000047534	ENSMUSG00000037503	1	34813219	34843065	-1	44	15	0	105	56	15	2355	5030	3696	369	2784		Q80XQ8
ENSMUST00000047558	ENSMUSG00000038943	7	80294450	80316259	1	0	0	0	0	0	0	0	0	0	0	0		Q99K43
ENSMUST00000047560	ENSMUSG00000034449	11	84820856	84828994	-1	9	5	13	36	15	11	169	329	108	7	97		Q3U0B3
ENSMUST00000047568	ENSMUSG00000040405	11	46735080	46779578	1	8	0	0	0	9	0	0	2	0	3	1	A0A0A0MQ86	
ENSMUST00000047577	ENSMUSG00000042414	1	13113457	13127163	-1	19	20	34	21	22	18	2	1	0	0	3		E9Q3T6
ENSMUST00000047611	ENSMUSG00000041429	17	24632682	24638838	1	13	8	23	103	13	5	5	13	6	23	8		O35980
ENSMUST00000047614	ENSMUSG00000103310	18	37020149	37187657	1	20	16	39	135	30	7	0	0	0	0	0	Q91Y18	
ENSMUST00000047615	ENSMUSG00000039354	1	72583251	72633134	1	0	0	0	0	0	0	93	250	105	45	77		Q8BJL0
ENSMUST00000047616	ENSMUSG00000056962	11	116837432	116843449	-1	0	0	0	29	0	0	60	191	138	95	65		Q9ERI5
ENSMUST00000047620	ENSMUSG00000034871	4	106733889	106748292	1	11	1	16	11	14	5	0	0	0	0	0		Q8QZW3
ENSMUST00000047621	ENSMUSG00000040734	7	19359749	19378533	1	25	13	41	403	30	18	48	55	44	4	53	Q3TCU2	Q5I1X5
ENSMUST00000047627	ENSMUSG00000032745	13	111425680	111490111	-1	0	9	22	46	9	18	213	910	413	685	428		Q6NXH3
ENSMUST00000047629	ENSMUSG00000041438	8	106893640	106923093	1	15	7	34	30	17	11	214	708	295	171	351		Q8R2N2
ENSMUST00000047630	ENSMUSG00000037737	3	30597073	30599939	-1	18	14	28	88	23	9	0	1	1	0	1		Q8BXF8
ENSMUST00000047632	ENSMUSG00000036160	2	26888628	26902879	-1	15	5	65	44	35	11	96	145	111	28	116	Q3V1X4	P70279
ENSMUST00000047645	ENSMUSG00000024924	19	27216484	27254231	1	0	0	0	0	0	0	0	0	0	0	0	F8WGI9	
ENSMUST00000047652	ENSMUSG00000037824	14	40906445	40966807	-1	18	12	21	43	25	7	3828	4613	3127	780	2038		Q8QZY6
ENSMUST00000047655	ENSMUSG00000037636	X	36743659	36777202	1	1	2	2	22	4	1	3	6	2	1	2		A2A3V2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000047660	ENSMUSG00000042244	3	92014583	92031582	1	10	5	13	8	6	2	0	0	0	8	4		A1A547
ENSMUST00000047664	ENSMUSG00000037509	1	34678188	34813309	1	5	5	10	38	15	7	336	445	356	62	191	Q3TQN9	Q7TNR9
ENSMUST00000047665	ENSMUSG00000034974	10	81183007	81193197	1	11	6	17	126	16	8	0	0	0	23	12	Q05A21	O54784
ENSMUST00000047666	ENSMUSG00000041731	19	24683016	24861855	-1	17	17	19	129	27	17	0	0	0	0	0		Q8BZF8
ENSMUST00000047672	ENSMUSG00000034024	10	117050998	117063814	-1	9	10	7	28	16	9	778	2053	1080	983	1017	Q542X7	P80314
ENSMUST00000047677	ENSMUSG00000056531	5	108132875	108233628	1	8	8	9	23	10	4	7	15	4	4	7		Q640L5
ENSMUST00000047687	ENSMUSG00000041608	9	120539818	120568318	1	16	18	30	59	36	11	1417	2706	2284	444	1967	Q8BFW6	
ENSMUST00000047689	ENSMUSG00000035455	11	11787431	11808962	-1	0	0	0	0	0	0	29	0	0	14	0		Q8BPY9
ENSMUST00000047697	ENSMUSG00000036964	11	58954685	58973098	1	15	6	1	46	46	15	7	11	5	4	4	A2AB81	
ENSMUST00000047698	ENSMUSG00000041488	19	11775119	11819403	-1	9	0	9	51	14	4	0	0	0	0	0	Q8R1B7	
ENSMUST00000047702	ENSMUSG00000038304	3	96798763	96829351	-1	1	4	2	9	11	4	0	0	0	6	4		O88875
ENSMUST00000047704	ENSMUSG00000041491	19	15955774	15984989	-1	15	10	21	159	14	11	32	135	48	25	55		Q6IRU7
ENSMUST00000047706	ENSMUSG00000032633	11	59791408	59810016	-1	0	0	0	76	0	0	1	0	4	2	3	Z4YJH7	
ENSMUST00000047711	ENSMUSG00000036099	10	93939165	94035817	-1	0	0	22	0	13	0	11	46	12	30	20		Q3ZK22
ENSMUST00000047714	ENSMUSG00000042207	1	134560171	134635285	1	46	41	61	75	53	28	347	1923	689	103	609		Q80Y84
ENSMUST00000047715	ENSMUSG00000020814	11	116803062	116828046	-1	0	1	4	0	4	2	0	0	0	0	0	Q9D1T2	
ENSMUST00000047720	ENSMUSG00000041544	4	148240264	148287965	-1	52	21	92	363	65	31	0	0	0	1	2	E9QL24	
ENSMUST00000047721	ENSMUSG00000041506	9	106475963	106485424	1	0	0	0	23	15	2	46	42	20	13	66		Q91WM3
ENSMUST00000047726	ENSMUSG00000072572	14	51892889	51896745	1	8	3	7	3	8	4	0	0	0	0	0	G3X943	
ENSMUST00000047734	ENSMUSG00000041483	1	136624901	136630053	1	9	12	23	34	0	12	415	988	488	112	312		Q99LI5
ENSMUST00000047737	ENSMUSG00000041515	8	120736358	120756694	1	8	10	24	36	20	12	328	584	225	59	507	Q544J7	P23611
ENSMUST00000047740	ENSMUSG00000041523	9	44452716	44454767	-1	9	8	20	12	17	9	0	0	0	0	0	Q3SXK0	
ENSMUST00000047745	ENSMUSG00000042250	3	90726906	90741517	1	7	3	0	2	3	0	0	0	0	0	32		Q0VB07
ENSMUST00000047746	ENSMUSG00000041528	9	108051534	108083346	-1	11	5	15	1	17	3	0	0	0	10	0		Q5XPI3
ENSMUST00000047749	ENSMUSG00000036934	8	85408759	85432841	-1	5	8	6	36	9	8	42	194	64	156	47		Q9CR55
ENSMUST00000047753	ENSMUSG00000040584	5	8660077	8748575	1	16	25	29	14	25	10	5	11	9	12	27		P21447
ENSMUST00000047760	ENSMUSG00000038451	6	124808661	124810619	1	7	3	34	25	0	0	0	0	0	0	0		O88838
ENSMUST00000047761	ENSMUSG00000022132	14	118787908	118875489	1	0	0	0	0	0	0	0	0	0	0	1		Q9Z0S6
ENSMUST00000047762	ENSMUSG00000005836	18	11052510	11085635	1	16	4	12	344	24	7	0	0	0	5	21		Q61169
ENSMUST00000047768	ENSMUSG00000039396	8	53586867	53639065	-1	4	4	1	34	7	1	41	172	79	36	32		Q8K203
ENSMUST00000047783	ENSMUSG00000033282	8	91217030	91313262	-1	7	28	14	19	21	14	21	88	47	4	36		Q8CG73
ENSMUST00000047786	ENSMUSG00000039372	1	72427112	72536930	-1	156	97	546	930	192	100	1	8	2	0	3		Q80TE3
ENSMUST00000047793	ENSMUSG00000042448	2	74762980	74765142	1	13	9	12	276	19	9	0	0	0	0	0		Q01822
ENSMUST00000047799	ENSMUSG00000090150	9	104063377	104127656	1	7	6	16	13	7	0	261	137	387	137	188		
ENSMUST00000047809	ENSMUSG00000034087	7	10687793	10730168	1	0	6	0	8	12	0	0	0	0	0	0		Q8C6J9
ENSMUST00000047812	ENSMUSG00000035000	2	62330073	62412231	-1	15	25	38	28	21	14	10	106	29	116	88		P28843
ENSMUST00000047815	ENSMUSG00000039463	2	167421712	167477000	1	0	0	40	45	12	0	204	289	197	42	115		Q8R4D1
ENSMUST00000047816	ENSMUSG00000042632	15	79286228	79328390	-1	0	0	0	29	0	20	24	14	0	0	0	Q3UN31	P97819
ENSMUST00000047817	ENSMUSG00000041498	1	136466343	136531511	1	28	62	0	82	2	60	0	5	0	0	71	E9Q3T3	
ENSMUST00000047830	ENSMUSG00000079277	2	74711927	74748442	1	0	0	0	14	0	0	0	0	0	0	0	Q3UZR4	P09027
ENSMUST00000047835	ENSMUSG00000033228	15	96411698	96460843	-1	25	28	55	64	41	25	693	2044	1686	209	1136	E9PZM7	
ENSMUST00000047840	ENSMUSG00000037529	1	34543968	34560943	-1	4	0	11	6	11	4	0	0	0	0	0		A6H6T1
ENSMUST00000047846	ENSMUSG00000049676	7	29181321	29214035	-1	0	0	0	0	0	0	0	0	0	0	0		E9Q355
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ENSMUST00000047852	ENSMUSG00000042595	X	137049594	137082503	1	15	8	27	102	23	10	66	86	90	21	71		Q8K2D0
ENSMUST00000047857	ENSMUSG00000039753	5	43744615	43821638	-1	0	0	0	20	0	6	9	1	401	839	396		Q8C2S5
ENSMUST00000047860	ENSMUSG00000036285	5	77294182	77310084	-1	4	3	9	151	3	0	54	193	92	10	75		Q9JJG9
ENSMUST00000047864	ENSMUSG00000034994	10	81176631	81182507	1	217	200	238	268	246	119	30725	18835	19364	2397	15569		P58252
ENSMUST00000047865	ENSMUSG00000041607	18	82475146	82585637	1	0	1	0	54	0	8	0	0	47	0	33		P04370
ENSMUST00000047870	ENSMUSG00000033850	2	85785513	85786451	1	5	3	10	2	2	1	0	0	0	0	0	Q7TR94	
ENSMUST00000047873	ENSMUSG00000040940	7	24902912	24926594	1	0	0	0	0	0	0	1434	4966	4944	376	4238		Q61210
ENSMUST00000047875	ENSMUSG00000035064	7	120842831	120907219	1	69	49	214	294	89	42	43	211	106	11	119		O08796
ENSMUST00000047877	ENSMUSG00000035711	13	55523235	55528538	-1	12	11	42	264	35	13	6143	12501	6078	1015	4625	Q14AA1	Q9QZK7
ENSMUST00000047883	ENSMUSG00000037031	10	62185396	62231218	-1	34	29	58	149	53	23	3	15	7	15	67		F7BWT7
ENSMUST00000047885	ENSMUSG00000039480	10	34288288	34418552	-1	0	0	0	46	10	0	207	367	41	38	0	Q05AG7	Q8C5P5
ENSMUST00000047888	ENSMUSG00000041620	9	7368239	7388047	-1	3	10	6	9	1	3	0	0	0	0	0	G5E8A9	
ENSMUST00000047889	ENSMUSG00000041329	11	69599736	69605942	-1	0	0	22	61	0	0	7	2	1	0	2	Q3UR55	P14231
ENSMUST00000047891	ENSMUSG00000042184	5	113692422	113724772	-1	0	0	6	2	2	0	0	0	0	0	0	Q9D9H5	
ENSMUST00000047898	ENSMUSG00000054611	19	4314419	4398285	-1	26	33	75	331	72	39	21	46	73	17	75	F6YRW4	
ENSMUST00000047899	ENSMUSG00000004561	14	51884842	51893039	1	0	0	0	0	2	0	0	0	0	0	0		Q3U2U7
ENSMUST00000047903	ENSMUSG00000034807	8	71611024	71624909	1	28	13	30	96	26	11	228	476	185	67	368		Q8K297
ENSMUST00000047904	ENSMUSG00000101174	2	74711929	74729160	1	9	0	11	10	11	9	0	2	0	0	0		P10628
ENSMUST00000047906	ENSMUSG00000034640	3	65528410	65555518	1	7	6	7	10	9	5	312	1914	654	207	426		Q8C1B2
ENSMUST00000047910	ENSMUSG00000036112	10	93858489	93897093	-1	18	13	14	8	8	13	19	56	37	32	23	Q58E65	O08663
ENSMUST00000047922	ENSMUSG00000034919	4	106622432	106640189	1	19	6	36	368	39	16	12	10	12	6	4	A2AVQ6	Q8C159
ENSMUST00000047923	ENSMUSG00000039234	3	123267455	123365641	1	23	15	31	44	29	13	93	113	143	35	221	Q6NXL1	
ENSMUST00000047929	ENSMUSG00000033533	7	119607026	119662515	1	14	11	5	5	12	0	0	0	0	3	0		Q91VA0
ENSMUST00000047935	ENSMUSG00000039485	10	34297442	34301320	1	23	24	57	124	24	16	13	42	22	6	40		Q8VD63
ENSMUST00000047936	ENSMUSG00000042190	5	113612354	113650426	-1	28	33	147	59	43	18	116	85	135	47	424	Q497D3	P97468
ENSMUST00000047945	ENSMUSG00000035454	X	86044199	86047313	1	4	0	2	1	3	0	0	0	0	0	0	A2ARK7	
ENSMUST00000047947	ENSMUSG00000070284	9	108049242	108052801	1	0	0	0	0	0	0	128	78	67	22	71		Q8BTZ7
ENSMUST00000047950	ENSMUSG00000039967	4	34803113	34882960	-1	35	0	1	59	30	0	456	221	994	2	734		Q9Z2U2
ENSMUST00000047951	ENSMUSG00000041556	4	148160621	148166424	1	12	10	16	172	22	8	1	0	0	7	4	Q3USR5	Q80UW2
ENSMUST00000047954	ENSMUSG00000024302	18	23415415	23659714	1	2	6	6	0	2	0	0	0	0	2	0	Q8BTD9	Q9D2N4
ENSMUST00000047963	ENSMUSG00000070953	2	34777556	34799912	-1	0	0	0	0	0	0	0	0	17	18	0	G8JL41	
ENSMUST00000047970	ENSMUSG00000032842	17	46303221	46328352	-1	2	3	0	0	2	0	1	19	0	0	32		Q8R4P9
ENSMUST00000047973	ENSMUSG00000034926	4	106561038	106589113	1	36	19	74	186	66	38	671	411	937	100	379		Q8VCH6
ENSMUST00000047978	ENSMUSG00000042229	1	134494648	134508774	1	25	16	50	124	35	16	566	1891	769	339	435		Q91X96
ENSMUST00000047993	ENSMUSG00000038203	6	52257694	52260880	-1	0	0	0	49	0	0	0	0	0	0	0	E9QM91	
ENSMUST00000047997	ENSMUSG00000038560	11	97013394	97024734	1	35	21	91	9	22	18	0	0	0	1	5	A2A708	Q9ESX2
ENSMUST00000048001	ENSMUSG00000042102	13	93674433	93752831	1	18	14	23	26	33	9	0	0	0	3	0		Q9DBT9
ENSMUST00000048002	ENSMUSG00000055629	7	141061274	141072119	1	23	14	44	226	33	15	121	87	126	6	25		Q766D5
ENSMUST00000048010	ENSMUSG00000039497	10	34151394	34207551	-1	23	17	2	155	26	11	64	137	81	93	173		Q8BLI4
ENSMUST00000048012	ENSMUSG00000040412	3	108455694	108536536	-1	2	4	22	15	5	2	0	2	1	0	0		A2AFS3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000048015	ENSMUSG00000012640	7	43296197	43313294	-1	0	0	3	7	5	0	0	497	239	0	139	G3X9T1	
ENSMUST00000048016	ENSMUSG00000039357	14	20694968	20700197	1	9	11	26	298	25	9	61	158	84	41	84	B2RRR9	Q8BHC9
ENSMUST00000048026	ENSMUSG00000038210	6	52242106	52245810	-1	11	9	41	155	12	23	0	0	0	0	0		P31311
ENSMUST00000048028	ENSMUSG00000036928	5	138280240	138312393	1	0	0	0	0	0	0	0	0	7	0	0		O70576
ENSMUST00000048032	ENSMUSG00000032758	6	133849851	133853762	-1	2	1	1	1	1	4	0	0	0	0	0	Q3UQF0	P61110
ENSMUST00000048043	ENSMUSG00000041729	9	62419492	62537044	-1	21	9	34	62	22	15	1	2	0	0	1		Q8BH44
ENSMUST00000048044	ENSMUSG00000039826	2	29761224	29788502	-1	4	2	0	78	0	0	263	725	288	75	147		Q91WG3
ENSMUST00000048050	ENSMUSG00000041737	9	31426199	31464238	-1	33	26	37	45	40	18	0	0	0	0	1		Q8VCZ2
ENSMUST00000048052	ENSMUSG00000039508	10	34038784	34044313	-1	34	26	21	19	21	18	3	4	7	1	4		Q8CE93
ENSMUST00000048054	ENSMUSG00000019214	17	25718926	25727419	-1	0	0	0	16	0	0	58	23	25	0	30		
ENSMUST00000048061	ENSMUSG00000032894	X	102859186	102867971	-1	4	3	10	11	7	6	0	0	0	0	0	B1AX30	
ENSMUST00000048064	ENSMUSG00000036523	12	16670615	16800886	-1	43	42	97	102	0	33	0	0	0	0	0		Q3UHK3
ENSMUST00000048065	ENSMUSG00000041754	17	48247777	48258841	1	2	3	14	14	9	8	1582	5549	1444	2667	1278	Q9JKE1	
ENSMUST00000048067	ENSMUSG00000036699	X	36195904	36199158	1	0	0	0	0	0	0	4	0	0	0	0		Q9CZA5
ENSMUST00000048068	ENSMUSG00000042659	7	68737045	68749241	-1	17	14	10	76	9	14	298	1893	393	82	664	A0A0B4J1F4	
ENSMUST00000048073	ENSMUSG00000041958	11	78328415	78342782	1	21	22	45	139	35	16	1402	1528	1188	106	936	Q3V307	Q6PD26
ENSMUST00000048077	ENSMUSG00000090077	2	181380078	181383628	1	0	0	0	0	0	3	109	231	124	7	144		Q9EQR5
ENSMUST00000048079	ENSMUSG00000044465	7	105371211	105400054	-1	0	0	0	45	0	0	684	255	653	44	449		Q3U2I3
ENSMUST00000048086						30	18	39	146	31	8	0	1	0	0	0		
ENSMUST00000048096	ENSMUSG00000039005	4	66827584	66930284	1	12	13	10	10	8	1	636	2169	965	1639	827	L0CL36	Q9QUK6
ENSMUST00000048099	ENSMUSG00000040195	10	127666901	127701049	1	118	87	117	155	172	55	466	1306	850	92	720		Q6ZQE4
ENSMUST00000048102	ENSMUSG00000108439	7	44606210	44665497	-1	0	9	0	335	0	0	0	0	0	0	0		Q6URW6
ENSMUST00000048103	ENSMUSG00000042459	2	154008265	154016079	1	0	0	0	0	0	0	0	0	0	0	0		P07743
ENSMUST00000048112	ENSMUSG00000042216	5	113243220	113310786	-1	11	0	0	62	41	17	0	6	0	0	0	B2RQR5	
ENSMUST00000048116	ENSMUSG00000041313	5	148327410	148399904	-1	124	89	626	315	168	85	66	87	91	22	208	Q3UGD6	Q09143
ENSMUST00000048118	ENSMUSG00000034528	5	103955440	103977410	-1	74	57	170	63	100	49	0	11	3	7	5		Q8VCR2
ENSMUST00000048121	ENSMUSG00000041794	9	120303936	120474841	1	27	27	65	88	34	21	0	0	0	0	0		Q8K3I4
ENSMUST00000048122	ENSMUSG00000018654	11	11685003	11772926	1	0	0	0	167	0	0	0	0	6	0	6	Q8C9X3	
ENSMUST00000048128	ENSMUSG00000035011	10	81135220	81152995	1	53	40	451	656	63	43	870	1814	1528	132	1089		O88939
ENSMUST00000048129	ENSMUSG00000033644	14	70372480	70429094	-1	28	18	47	49	33	19	112	603	182	44	406		Q8CDG1
ENSMUST00000048134	ENSMUSG00000036834	3	63696234	63899472	-1	0	0	0	0	0	0	0	0	0	0	0	I1E4X4	
ENSMUST00000048138	ENSMUSG00000042312	3	90514435	90524581	1	3	3	18	3	9	8	724	1924	560	2252	261	A0A0A0MQ90	
ENSMUST00000048139	ENSMUSG00000041346	11	69561758	69580255	-1	16	4	20	25	22	15	168	245	162	24	113		Q8VC51
ENSMUST00000048145	ENSMUSG00000033565	15	77078990	77307053	-1	0	6	0	363	0	22	0	0	0	0	0		Q8BP71
ENSMUST00000048147	ENSMUSG00000036977	8	79711820	79777321	1	100	90	132	83	107	46	14	113	18	84	23		Q8K2H6
ENSMUST00000048150	ENSMUSG00000039765	5	43662346	43740972	1	25	18	8	0	18	13	0	0	0	0	10		Q8CFW7
ENSMUST00000048155	ENSMUSG00000010608	12	83631236	83683123	1	0	5	10	5	12	5	338	1625	478	171	378		B2RY56
ENSMUST00000048162	ENSMUSG00000040859	4	129461581	129488498	1	11	9	40	49	20	10	1205	3066	1638	319	1248		Q80Y55
ENSMUST00000048180	ENSMUSG00000040268	7	130865756	130913312	1	4	16	23	0	0	7	84	264	75	22	98		Q8BUL6
ENSMUST00000048183	ENSMUSG00000041559	1	134037254	134048277	1	23	24	73	85	33	20	0	0	0	0	0	Q543D2	P50608
ENSMUST00000048184	ENSMUSG00000041837	9	65346068	65359642	1	8	9	18	353	20	7	228	560	248	81	202	Q3U2X6	
ENSMUST00000048187	ENSMUSG00000037166	7	29289320	29293390	1	0	4	2	118	4	0	0	0	0	3	1		Q91VC7
ENSMUST00000048188	ENSMUSG00000072501	15	66577572	66645255	1	12	22	27	32	31	15	798	2241	1750	389	1290		Q8CCJ9
ENSMUST00000048192	ENSMUSG00000041840	18	77757567	77767780	-1	2	1	10	18	5	4	13	69	18	97	20		Q8BHX1
ENSMUST00000048194	ENSMUSG00000042477	4	126716006	126736240	-1	21	5	18	198	24	10	0	0	0	0	0		Q6VUP9
ENSMUST00000048197	ENSMUSG00000041845	19	4425459	4439432	-1	7	4	4	8	5	4	0	1	1	9	4	Q545H8	P97348
ENSMUST00000048207	ENSMUSG00000040554	11	72027963	72037509	-1	29	19	77	115	55	22	12	9	17	3	12		Q924K1
ENSMUST00000048208	ENSMUSG00000034795	14	77036772	77112257	1	0	0	0	0	0	0	0	0	0	3	0		Q8BVN0
ENSMUST00000048209	ENSMUSG00000063229	7	46841475	46855627	1	5	9	42	62	38	15	17524	27290	15211	11671	9351	Q564E2	P06151
ENSMUST00000048214	ENSMUSG00000041857	19	11667460	11691150	-1	4	8	7	0	2	4	0	2	0	0	0		Q925U0
ENSMUST00000048216	ENSMUSG00000040396	8	9977707	9992155	1	0	0	0	27	0	0	299	1025	438	99	244		Q80UX8
ENSMUST00000048222	ENSMUSG00000039531	10	33926936	33951212	-1	8	6	8	58	5	5	31	493	104	71	71		Q3T9Z9
ENSMUST00000048223	ENSMUSG00000035027	10	81105915	81124697	1	0	0	0	0	0	0	19	31	0	0	0	M0QWN2	
ENSMUST00000048229	ENSMUSG00000034057	10	116776545	116896879	-1	15	19	42	53	31	11	2	2	0	2	2		Q3UN70
ENSMUST00000048243	ENSMUSG00000034829	8	71560556	71566649	-1	0	0	0	82	0	0	0	0	0	0	0		Q8VC33
ENSMUST00000048246	ENSMUSG00000033831	3	83040141	83049863	-1	25	11	12	18	23	23	0	0	0	270	0	Q3TGR2	Q8K0E8
ENSMUST00000048248	ENSMUSG00000035390	7	4690604	4715997	1	0	0	38	94	0	22	0	0	0	0	0		Q5RJI5
ENSMUST00000048249	ENSMUSG00000041881	17	33824591	33838316	1	2	0	3	2	4	0	357	489	254	1472	160		Q9Z1P6
ENSMUST00000048250	ENSMUSG00000035476	X	85574022	85634469	1	13	8	24	20	9	2	155	359	256	47	214	B1ASY9	Q571K4
ENSMUST00000048252	ENSMUSG00000030268	6	144993835	145076184	-1	10	1	12	33	7	0	0	0	0	0	3	E9Q4K3	
ENSMUST00000048260	ENSMUSG00000041891	18	65980754	66022580	-1	13	6	12	92	13	8	98	311	158	75	225		Q9D0F3
ENSMUST00000048263	ENSMUSG00000041408	14	34673928	34747983	1	18	9	35	113	12	12	409	1217	326	142	319		Q65Z40
ENSMUST00000048265	ENSMUSG00000073946	7	103584024	103584980	1	8	3	5	8	2	2	0	0	0	0	0	Q8VGA1	
ENSMUST00000048269						0	4	12	8	6	0	18	97	34	13	37		
ENSMUST00000048274	ENSMUSG00000038172	4	83220300	83324255	-1	4	0	0	0	0	0	26	47	92	50	75		Q8BYY4
ENSMUST00000048289	ENSMUSG00000037868	10	67535475	67542188	1	4	11	0	2	18	0	0	21	0	0	12	Q3U207	P08152
ENSMUST00000048302	ENSMUSG00000038204	5	24532697	24540978	-1	13	4	2	14	13	12	0	0	0	0	0		Q91ZT7
ENSMUST00000048305	ENSMUSG00000041846	12	101039409	101083702	-1	13	15	14	420	0	8	233	1134	506	32	394		Q6P2K6
ENSMUST00000048308	ENSMUSG00000039349	1	184871926	184883218	-1	56	58	157	372	78	36	0	1	2	3	0		Q8BGN9
ENSMUST00000048309	ENSMUSG00000041570	1	136268123	136346104	-1	11	0	51	9	5	0	0	0	22	14	31	H7BX08	
ENSMUST00000048319	ENSMUSG00000042628	12	83546941	83597147	-1	26	16	37	151	38	14	598	1249	929	121	687		Q810J8
ENSMUST00000048359	ENSMUSG00000041949	8	106683068	106851439	1	34	22	139	112	49	25	54	65	73	8	69		Q8C3S2
ENSMUST00000048361						9	3	8	3	1	4	0	1	3	3	1		
ENSMUST00000048363	ENSMUSG00000035505	5	90214724	90224001	-1	0	0	0	64	8	0	28	18	0	0	0		Q8VC74
ENSMUST00000048371	ENSMUSG00000022010	14	76414961	76507765	1	22	9	56	160	54	11	16	24	12	0	47	E9QLZ1	
ENSMUST00000048372	ENSMUSG00000036944	15	66526212	66561046	-1	15	23	24	15	16	11	454	1903	776	881	594		
ENSMUST00000048374	ENSMUSG00000033031	16	48994185	49019709	1	1	2	0	0	0	0	39	122	103	75	30		Q8BWY9
ENSMUST00000048375	ENSMUSG00000039157	2	32535332	32569756	1	0	0	9	44	0	5	1113	1161	671	97	730		Q78T81
ENSMUST00000048377	ENSMUSG00000040297	1	161816114	161876682	-1	10	13	27	65	12	5	373	1569	759	275	485	B2RRF3	Q8C341
ENSMUST00000048382	ENSMUSG00000035491	X	85249679	85270288	1	5	0	0	2	2	0	0	0	0	0	0	Q9DAX0	
ENSMUST00000048391	ENSMUSG00000042489	4	126556935	126593903	1	21	28	66	103	43	19	44	80	81	19	66		Q80YR7
ENSMUST00000048393	ENSMUSG00000037204	15	101284301	101290934	1	3	5	38	50	20	5	1746	1700	909	558	609		Q9D8Z6
ENSMUST00000048400	ENSMUSG00000033955	2	85048022	85073048	1	9	0	10	0	0	0	247	266	141	40	248	Z4YJL4	
ENSMUST00000048402	ENSMUSG00000021007	12	98628157	98669815	1	0	0	0	24	5	0	8	12	0	28	4		Q80VP2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000048409	ENSMUSG00000041986	9	53911460	53975301	-1	7	0	7	44	12	0	0	0	0	0	0		Q3V1U8
ENSMUST00000048417	ENSMUSG00000047193	9	6928503	7184446	-1	0	0	0	0	0	0	0	0	0	0	0		Q45VK7
ENSMUST00000048418	ENSMUSG00000040029	6	148770683	148831467	-1	0	7	10	44	8	0	118	320	296	37	171		Q7TMY7
ENSMUST00000048421	ENSMUSG00000036948	5	138259656	138264033	-1	0	0	0	0	2	0	147	322	457	18	363	E9Q2V5	
ENSMUST00000048427	ENSMUSG00000038354	3	96670131	96691032	1	20	10	75	161	45	13	0	0	0	2	4	E9Q9D8	
ENSMUST00000048430	ENSMUSG00000038192	4	82881751	82885148	-1	50	47	165	101	60	31	2	2	1	0	2	A2ADM9	O55233
ENSMUST00000048431	ENSMUSG00000039164	2	32450457	32456953	1	23	15	69	199	38	25	234	358	194	30	180		Q6PFD7
ENSMUST00000048432	ENSMUSG00000041577	1	133910304	133921414	-1	32	26	78	47	38	24	0	0	0	4	5	Q543S0	Q9JK53
ENSMUST00000048444	ENSMUSG00000074155	7	43841971	43851181	1	8	10	19	6	10	8	0	0	0	0	0	Q9D140	
ENSMUST00000048452	ENSMUSG00000034845	8	71497754	71511769	-1	19	11	43	168	24	9	1	2	1	2	0	G3X924	
ENSMUST00000048453	ENSMUSG00000040298	7	130774069	130825897	1	189	163	526	203	242	123	23	107	75	44	32		E9Q173
ENSMUST00000048455	ENSMUSG00000035513	2	29194541	29253005	-1	0	0	0	0	0	0	269	231	207	12	223		Q8R4F1
ENSMUST00000048459	ENSMUSG00000055594	6	133292216	133295792	1	0	0	7	0	2	3	0	0	0	0	0	Q9D3I0	
ENSMUST00000048462	ENSMUSG00000026621	1	184786767	184811313	-1	8	10	0	8	4	0	0	0	0	0	0		Q9CW42
ENSMUST00000048471	ENSMUSG00000035258	16	56477846	56690128	1	11	0	9	11	0	0	0	0	0	0	0	Q59IW6	
ENSMUST00000048478	ENSMUSG00000035932	14	51070311	51071442	-1	8	4	19	15	4	4	0	0	0	0	0	E9Q0Z1	
ENSMUST00000048479	ENSMUSG00000036172	16	44943678	44981380	1	0	0	0	0	0	0	0	0	0	0	0		Q5UKY4
ENSMUST00000048482	ENSMUSG00000042041	19	4496790	4498583	-1	11	1	13	14	13	3	0	0	0	0	0		Q8VC23
ENSMUST00000048485	ENSMUSG00000042045	9	53850251	53853844	1	2	4	3	4	5	4	0	0	0	0	0		Q9CQD6
ENSMUST00000048486	ENSMUSG00000033860	3	83007724	83015049	1	9	8	18	18	12	4	0	0	0	223	0	Q3UEM7	Q8VCM7
ENSMUST00000048490	ENSMUSG00000025762	3	40950354	41040234	1	3	0	0	9	2	0	105	198	255	32	132	Q8R3F0	
ENSMUST00000048493	ENSMUSG00000034032	2	119763304	119787537	-1	0	0	0	0	0	0	0	0	6	0	67		Q80TE0
ENSMUST00000048502	ENSMUSG00000040811	7	19176421	19206482	1	2	0	35	1	14	0	374	633	467	14	269		Q7TNG5
ENSMUST00000048504						2	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000048514	ENSMUSG00000069830	11	71092236	71144704	-1	24	14	30	35	32	6	0	0	0	0	0	Q67EY4	
ENSMUST00000048518	ENSMUSG00000035365	10	88091432	88146941	-1	4	5	12	76	9	3	31	40	44	21	17		
ENSMUST00000048519	ENSMUSG00000020590	12	35047189	35147469	1	17	11	21	46	16	11	634	2982	1384	246	770	E9QNG6	
ENSMUST00000048527	ENSMUSG00000042073	9	106447788	106452922	1	9	3	15	8	9	5	2	6	0	5	11	E9QN99	
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ENSMUST00000048545	ENSMUSG00000040459	8	8666577	8690537	-1	6	5	27	62	7	4	186	1637	513	100	492		Q3UL36
ENSMUST00000048557	ENSMUSG00000035528	5	89527429	89583740	1	6	2	4	4	6	3	0	0	0	0	0		Q924H0
ENSMUST00000048560	ENSMUSG00000042099	17	33810520	33822918	1	20	7	34	221	17	6	69	61	47	39	74		Q9Z1P7
ENSMUST00000048565	ENSMUSG00000053490	8	64998457	65018688	-1	21	18	62	35	31	9	0	10	0	0	2		Q8VI40
ENSMUST00000048568	ENSMUSG00000042106	9	107984223	107985879	-1	3	3	6	43	10	1	7	9	4	9	11		Q9CX62
ENSMUST00000048572	ENSMUSG00000039377	1	184727140	184732619	-1	15	10	39	582	19	10	599	2157	1328	106	1033	Q549B7	Q61670
ENSMUST00000048578	ENSMUSG00000041278	11	43729512	43748008	-1	0	5	0	0	0	4	121	655	222	621	183		Q91Z38
ENSMUST00000048580	ENSMUSG00000039032	6	30896981	30915573	-1	8	4	3	11	3	2	0	4	1	0	0		Q9DA17
ENSMUST00000048603	ENSMUSG00000019027	14	31260375	31323896	-1	132	89	240	185	156	67	6	1	2	1	2	E9Q8T7	
ENSMUST00000048604	ENSMUSG00000042138	9	37489321	37524148	1	10	9	13	163	17	5	26	122	52	27	65		Q6NZR2
ENSMUST00000048605	ENSMUSG00000036117	11	53720794	53725106	1	8	6	8	8	11	3	0	0	0	0	0	Q5SV01	P04401
ENSMUST00000048606	ENSMUSG00000040467	8	8661801	8664728	1	8	16	12	52	18	6	0	0	0	0	0	Q9D5T6	
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ENSMUST00000048613	ENSMUSG00000057715	1	11414105	11975901	1	0	0	0	0	0	0	0	0	0	0	0		Q8BZJ8
ENSMUST00000048615	ENSMUSG00000021871	14	50944302	50965237	1	5	5	18	21	20	9	236	779	183	133	53	Q543K9	
ENSMUST00000048621	ENSMUSG00000035383	10	88091072	88092375	1	2	3	0	2	0	1	0	0	0	0	0		P56942
ENSMUST00000048630	ENSMUSG00000042401	19	42283037	42431783	-1	21	13	33	38	24	16	10	31	16	7	16		Q8R555
ENSMUST00000048635	ENSMUSG00000033256	2	122348892	122369162	-1	6	4	16	7	0	3	0	0	0	0	6		Q8CG80
ENSMUST00000048642	ENSMUSG00000033918	16	20279820	20302387	-1	3	6	1	65	3	2	198	741	229	135	241		Q5XJY4
ENSMUST00000048644	ENSMUSG00000042179	19	58728887	58744169	1	14	12	19	10	11	5	0	0	0	0	0		Q5BKQ4
ENSMUST00000048646	ENSMUSG00000037646	15	35371546	35931228	1	49	39	49	161	73	40	555	1048	1313	117	1020	E9QKX5	
ENSMUST00000048647	ENSMUSG00000033882	3	82837228	82876483	-1	4	5	1	117	7	2	0	0	0	0	0		P86049
ENSMUST00000048653	ENSMUSG00000034361	8	94532990	94570529	1	0	14	11	39	0	11	2374	2357	1535	191	912		P59108
ENSMUST00000048655	ENSMUSG00000039384	1	184013302	184075636	1	30	7	58	35	28	15	58	116	64	19	105		Q9ESS0
ENSMUST00000048656	ENSMUSG00000042345	17	31207873	31242202	1	9	1	21	11	9	4	135	113	198	14	37		Q3V3E1
ENSMUST00000048657	ENSMUSG00000039367	14	20674321	20694850	1	41	20	88	66	39	25	1604	3175	2265	237	1971	G3X972	
ENSMUST00000048660	ENSMUSG00000042251	1	131797381	131821473	1	0	0	0	0	0	0	0	0	0	0	0		Q8C165
ENSMUST00000048665	ENSMUSG00000056608	8	90828835	91054508	1	35	39	0	1	0	0	87	0	0	41	0		Q8BYH8
ENSMUST00000048670	ENSMUSG00000042195	9	53771535	53818161	1	18	8	47	70	23	14	3	10	3	0	5		Q7TML3
ENSMUST00000048675	ENSMUSG00000033343	X	72222017	72222964	1	3	2	3	1	2	0	0	0	0	0	0	F2Z493	
ENSMUST00000048677	ENSMUSG00000042203	17	29549788	29606895	1	28	11	155	245	69	31	471	428	412	53	219	Q80VE5	
ENSMUST00000048678	ENSMUSG00000033105	10	76531588	76557138	1	0	0	0	0	0	0	51	39	54	2	57		Q8BLN5
ENSMUST00000048680	ENSMUSG00000038227	6	52223100	52231089	-1	28	17	60	205	44	9	3	20	2	0	1		P09631
ENSMUST00000048685	ENSMUSG00000042210	9	106440051	106447678	-1	0	0	5	7	2	4	15	0	5	0	10	E9Q136	
ENSMUST00000048686	ENSMUSG00000107874	6	132311590	132314757	-1	26	25	202	89	25	16	2	0	1	0	0	E9PXN1	
ENSMUST00000048687	ENSMUSG00000042712	X	136245079	136247139	1	3	0	23	0	8	9	97	676	170	1132	187		Q9DD24
ENSMUST00000048688	ENSMUSG00000042211	18	62504069	62548743	-1	18	21	27	59	22	16	814	2207	1632	591	1147		Q8BMI0
ENSMUST00000048691	ENSMUSG00000042256	17	42315947	42507741	1	28	29	67	122	35	12	0	1	0	0	0	E9QMK6	
ENSMUST00000048698	ENSMUSG00000036980	5	138178617	138187451	-1	0	12	0	0	8	7	351	354	287	37	187		Q62311
ENSMUST00000048702	ENSMUSG00000042167	13	93147400	93192283	-1	6	4	3	63	5	2	182	770	343	108	133		Q91YI6
ENSMUST00000048706	ENSMUSG00000040044	4	34570796	34614944	-1	0	0	0	10	0	0	76	322	126	271	44		Q9JK30
ENSMUST00000048715	ENSMUSG00000038236	6	52214491	52221854	-1	7	6	17	135	16	13	0	2	0	0	0		P02830
ENSMUST00000048716	ENSMUSG00000037946	13	49261554	49320311	-1	12	8	43	18	25	21	94	39	63	0	31	Q3TNB8	
ENSMUST00000048718	ENSMUSG00000037022	8	79266424	79294956	-1	19	19	34	13	19	11	30	113	35	66	46		Q8C7H1
ENSMUST00000048731	ENSMUSG00000039043	7	79925361	79935359	-1	17	19	40	81	30	11	3	9	3	17	23		Q9D0A3
ENSMUST00000048762	ENSMUSG00000042254	9	65265180	65280605	1	13	14	51	58	0	0	0	0	0	0	0		
ENSMUST00000048766	ENSMUSG00000028102	3	96635376	96645366	1	0	0	0	0	0	0	24	0	24	23	35		Q9Z210
ENSMUST00000048770	ENSMUSG00000040666	16	96200470	96228933	1	8	0	28	16	15	5	0	0	0	0	0		Q9WUZ7
ENSMUST00000048774	ENSMUSG00000025607	6	30747554	30896794	-1	5	5	7	9	12	3	699	2790	1251	815	603		Q9QXK3
ENSMUST00000048777	ENSMUSG00000042262	9	120092133	120094906	1	6	7	12	8	19	3	0	0	0	0	0	Q3ZB17	P56484
ENSMUST00000048781	ENSMUSG00000040618	14	55540266	55550017	1	29	19	65	178	35	8	134	168	67	21	120		
ENSMUST00000048782	ENSMUSG00000042265	17	48232768	48246924	1	26	18	185	61	28	19	3900	13528	5421	3298	4267		Q9JKE2
ENSMUST00000048786	ENSMUSG00000042269	8	120166397	120177466	-1	6	11	24	11	16	0	1	16	1	1	2		Q3V2J0
ENSMUST00000048788	ENSMUSG00000036208	16	44724301	44737284	1	70	34	45	101	69	29	52	259	121	32	114	Q8R2U2	
ENSMUST00000048790	ENSMUSG00000033361	X	71962624	71972722	1	108	93	379	275	97	70	1	5	6	2	5		Q6PAQ9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000048792	ENSMUSG00000039195	2	32377097	32381938	-1	0	0	0	102	4	1	604	703	398	730	194		P58686
ENSMUST00000048794	ENSMUSG00000038253	6	52201754	52204587	-1	9	9	16	138	12	5	0	6	0	7	27		P09021
ENSMUST00000048801	ENSMUSG00000037145	11	58608204	58616075	-1	1	3	0	2	0	4	0	0	0	0	0	Q6YI28	
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ENSMUST00000048820	ENSMUSG00000073643	1	79702262	79776143	-1	0	0	0	0	0	0	0	13	36	0	21	Q9DAD3	
ENSMUST00000048824	ENSMUSG00000042293	9	48495345	48495964	1	3	1	3	126	8	4	104	190	61	116	47		Q91VN2
ENSMUST00000048854	ENSMUSG00000054967	15	76910851	76918010	-1	19	11	41	31	23	5	2	3	2	0	3		Q7TNU6
ENSMUST00000048860	ENSMUSG00000039395	1	72159442	72212307	-1	19	9	17	31	12	7	35	88	70	10	13		Q6NVG5
ENSMUST00000048880	ENSMUSG00000041886	12	119443410	119466934	1	15	14	17	9	9	7	0	0	0	2	0	E9PXX8	
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ENSMUST00000048890	ENSMUSG00000039431	8	40551095	40634797	-1	7	2	9	0	4	6	4	3	7	4	8	I6L9A6	
ENSMUST00000048892	ENSMUSG00000039662	4	152297227	152307121	1	0	23	63	74	2	17	491	445	591	154	432	Q3U4N2	
ENSMUST00000048893	ENSMUSG00000041399	4	137453284	137455461	1	15	9	69	16	15	7	0	0	0	0	0	Q9DAC6	
ENSMUST00000048896	ENSMUSG00000042423	7	127479592	127491711	1	24	19	89	78	27	17	1462	2983	1802	114	1961		Q8R089
ENSMUST00000048898	ENSMUSG00000039431	8	40551095	40634797	-1	0	0	8	1	0	0	0	0	0	0	0		Q9Z2C9
ENSMUST00000048914	ENSMUSG00000034880	8	71464926	71465752	1	1	3	5	50	9	4	82	209	99	42	61		Q99N91
ENSMUST00000048915	ENSMUSG00000038374	3	96629933	96633791	1	17	18	52	28	28	12	295	1149	403	1548	382	A0A067XG47	Q9CWZ3
ENSMUST00000048923	ENSMUSG00000037239	7	29158829	29169841	-1	34	14	56	258	45	5	3	6	1	3	19		
ENSMUST00000048934	ENSMUSG00000035033	2	61802930	61814114	1	15	15	21	173	25	12	0	1	0	0	0		Q64336
ENSMUST00000048935	ENSMUSG00000042372	19	25610537	25623920	1	9	10	27	281	24	11	48	102	96	12	63		Q80WT2
ENSMUST00000048937	ENSMUSG00000042487	9	75441524	75466432	1	7	5	4	15	17	3	248	652	474	187	227		Q5XJE5
ENSMUST00000048941	ENSMUSG00000038599	1	182565007	182632352	1	19	6	26	0	0	5	0	0	0	0	0		
ENSMUST00000048945	ENSMUSG00000053719	7	44012168	44016968	1	1	6	2	13	10	4	0	0	0	0	0		P36369
ENSMUST00000048946	ENSMUSG00000037960	13	49202951	49216026	-1	3	7	5	11	13	4	1756	2076	1168	1092	775	B2RV71	Q9D1I2
ENSMUST00000048947	ENSMUSG00000035031	4	104815679	104876398	-1	2	0	3	0	0	0	0	0	0	0	0	A2A997	
ENSMUST00000048953	ENSMUSG00000026463	1	133699457	133801041	-1	0	0	1	0	0	0	0	0	0	0	0	F7AAP4	
ENSMUST00000048957	ENSMUSG00000034573	5	103425192	103598303	1	49	33	73	105	67	44	3	4	8	3	23	G5E8B1	
ENSMUST00000048959	ENSMUSG00000067225	19	40037941	40073811	-1	5	5	16	5	7	3	0	0	0	0	0		Q6XVG2
ENSMUST00000048962	ENSMUSG00000034311	X	100625737	100727214	1	10	14	21	22	12	6	57	114	122	45	76		P33174
ENSMUST00000048964	ENSMUSG00000039205	2	32352327	32380970	1	3	0	7	0	0	0	31	0	33	0	100	Q8VEH2	
ENSMUST00000048966	ENSMUSG00000041852	15	82808629	82912134	-1	55	0	100	138	12	34	894	2130	2406	297	1454		Q9EPQ8
ENSMUST00000048967	ENSMUSG00000037852	8	64592558	64693040	-1	16	2	12	77	14	9	0	0	0	42	81	Q543R4	Q00493
ENSMUST00000048976	ENSMUSG00000033910	3	82092427	82145789	-1	0	8	6	0	0	0	0	1	0	3	7		Q9ERL9
ENSMUST00000048977	ENSMUSG00000042942	18	10325177	10562934	1	27	25	27	23	43	20	1	1	6	1	5		B9EJV3
ENSMUST00000048982	ENSMUSG00000036158	15	93499114	93595891	-1	36	15	52	4	0	0	6	9	6	5	31		Q3U5C7
ENSMUST00000048988	ENSMUSG00000039501	2	167035793	167063015	-1	21	0	6	131	14	16	564	564	1202	30	1046		Q8R151
ENSMUST00000048993	ENSMUSG00000035834	13	81673843	81711013	-1	0	7	17	32	14	16	11	60	0	39	0		Q6NXY9
ENSMUST00000048994	ENSMUSG00000042419	17	35220175	35235792	-1	10	3	30	182	12	9	597	902	474	122	278		O88995
ENSMUST00000049004	ENSMUSG00000039062	7	79821803	79861059	-1	0	14	56	27	14	7	2	4	4	19	33		P97449
ENSMUST00000049005	ENSMUSG00000021796	14	34410734	34503341	-1	16	9	34	28	14	8	247	902	305	125	201	Q53Z43	P36895
ENSMUST00000049009	ENSMUSG00000038569	5	122323223	122354233	-1	0	0	20	24	9	3	2	0	8	0	7	Q8VC54	Q6WBX7
ENSMUST00000049016	ENSMUSG00000042439	18	65580230	65689443	1	19	12	35	51	22	16	0	0	0	11	7		Q6NXK2
ENSMUST00000049020	ENSMUSG00000041037	7	24530689	24538600	1	84	53	319	932	131	61	349	445	418	30	280		Q8VIM9
ENSMUST00000049022	ENSMUSG00000037966	13	49187485	49196244	1	0	0	0	32	0	0	298	735	344	586	587	Q3TXT8	O70131
ENSMUST00000049023	ENSMUSG00000040522	X	167242696	167264329	-1	0	3	4	6	7	1	0	35	0	0	0		P58682
ENSMUST00000049027	ENSMUSG00000042268	1	131744022	131771504	1	77	77	259	197	113	50	1	5	4	1	6		
ENSMUST00000049031	ENSMUSG00000042444	9	70599014	70657174	-1	25	14	33	30	20	14	816	1950	1632	190	970		Q6PDI6
ENSMUST00000049032	ENSMUSG00000038705	2	181251449	181288035	-1	24	18	36	51	33	11	770	1508	767	65	727		P58929
ENSMUST00000049038	ENSMUSG00000040489	11	45980310	46017994	1	13	9	34	152	22	13	0	0	0	0	0		Q8CGW4
ENSMUST00000049040	ENSMUSG00000037905	5	125441568	125460370	1	75	82	259	171	105	56	433	621	361	87	271		Q8BXV2
ENSMUST00000049048	ENSMUSG00000040620	11	70984091	71004437	-1	2	0	4	16	4	2	0	0	0	0	0	K3W4M7	
ENSMUST00000049051	ENSMUSG00000036890	2	44564412	44927657	-1	0	0	0	0	0	0	0	0	0	0	0	G8JL42	
ENSMUST00000049052	ENSMUSG00000030823	7	127382260	127387166	-1	17	21	38	141	43	16	18	27	40	4	14	G3X941	
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ENSMUST00000049055	ENSMUSG00000035840	13	81657806	81671888	1	9	9	20	70	4	4	259	386	376	305	218		Q99LE3
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ENSMUST00000049060	ENSMUSG00000036403	5	76588698	76646466	1	4	3	14	0	0	2	89	294	54	56	167		Q6P5D4
ENSMUST00000049064	ENSMUSG00000036894	3	61361638	61368430	1	33	25	41	23	24	16	321	934	433	87	336	Q6ZWR0	P61226
ENSMUST00000049074	ENSMUSG00000033295	4	118208213	118291405	-1	37	40	86	243	80	45	6	13	18	5	53		A2A8L5
ENSMUST00000049079	ENSMUSG00000058119	6	41392356	41397230	1	4	9	27	10	4	3	0	0	0	0	0	Q792Y9	
ENSMUST00000049081	ENSMUSG00000040928	4	129148005	129189727	-1	0	0	5	0	0	0	18	0	0	1	0		Q9D5K4
ENSMUST00000049089	ENSMUSG00000035799	12	33957671	33959817	1	4	8	11	166	12	3	0	0	0	8	36		P26687
ENSMUST00000049091	ENSMUSG00000042148	11	63962627	64079468	-1	33	14	62	44	41	14	24	51	39	12	49	Q3U3N1	Q8CFY5
ENSMUST00000049093	ENSMUSG00000038393	3	96557957	96561883	1	15	0	44	0	0	8	6326	20406	6933	2949	7639		Q8BG60
ENSMUST00000049095	ENSMUSG00000034171	4	115967145	116017926	-1	2	0	0	123	4	3	23	14	14	2	22		O08914
ENSMUST00000049105	ENSMUSG00000042514	18	21550377	21654718	-1	0	0	0	0	14	0	3	0	2	0	4		Q69ZK5
ENSMUST00000049113	ENSMUSG00000035429	7	4548612	4604041	-1	15	0	22	0	12	4	0	3	0	0	0	E9Q0N2	
ENSMUST00000049117						1	2	1	2	0	0	3	0	0	0	0		
ENSMUST00000049122	ENSMUSG00000036167	15	93398350	93491913	1	0	20	25	45	21	10	30	133	149	78	128	G3X959	
ENSMUST00000049124	ENSMUSG00000038527	6	124493113	124510643	1	45	33	96	49	58	24	1031	2071	1391	392	862		Q3UZ09
ENSMUST00000049126	ENSMUSG00000036766	1	84369839	84696221	-1	9	12	17	99	20	12	0	0	0	1	0		Q8JZM4
ENSMUST00000049128	ENSMUSG00000052917	16	56048338	56190012	1	5	1	0	34	4	1	10	42	49	21	53	Q9CQN9	
ENSMUST00000049130	ENSMUSG00000042750	X	136066564	136068236	-1	0	1	5	37	4	4	2	1	0	1	5		Q9WTZ8
ENSMUST00000049138	ENSMUSG00000032840	5	118245227	118266093	1	92	100	701	256	115	52	371	611	437	105	306		Q8BTG6
ENSMUST00000049146	ENSMUSG00000033805	5	107402736	107430035	1	1	4	3	39	2	0	0	0	0	0	0		Q6IE26
ENSMUST00000049149	ENSMUSG00000040249	10	127538161	127621148	-1	98	59	246	278	172	61	3261	2240	7544	211	7428		
ENSMUST00000049150	ENSMUSG00000032899	6	131299142	131353597	-1	22	21	29	23	27	6	5	4	9	0	7		Q6J9G1
ENSMUST00000049151	ENSMUSG00000033356	15	94522688	94543547	-1	20	17	25	27	27	10	33	107	60	18	56		Q8CE46
ENSMUST00000049152	ENSMUSG00000038301	6	51523901	51590679	1	0	0	0	12	0	0	102	307	216	116	211	Q4FJX6	Q9CWT3
ENSMUST00000049156	ENSMUSG00000034105	8	119760587	119778416	-1	18	14	55	63	32	6	228	171	140	19	80		Q8K0P3
ENSMUST00000049166	ENSMUSG00000032757	6	4076899	4086972	-1	3	4	11	3	10	1	57	158	52	125	38		O35623
ENSMUST00000049167	ENSMUSG00000037791	11	77982754	78030539	1	13	9	9	7	27	10	796	1275	1074	83	840	Q3U2C9	Q5SPL2
ENSMUST00000049168	ENSMUSG00000034893	14	75702351	75754493	-1	17	25	31	92	18	10	239	871	503	101	427	E9QL65	
ENSMUST00000049169	ENSMUSG00000042557	9	57072040	57128366	1	32	0	0	0	0	0	326	1830	755	139	767		Q60520

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000049178	ENSMUSG00000042248	19	39992424	40012243	1	5	4	6	4	7	3	0	0	0	1	0		P56654
ENSMUST00000049184	ENSMUSG00000034911	8	71384274	71395801	-1	32	29	76	108	59	21	0	3	2	0	3		Q8R370
ENSMUST00000049185	ENSMUSG00000033126	10	76459569	76469114	-1	381	408	438	580	522	260	42	77	70	15	36		Q8CAV0
ENSMUST00000049197	ENSMUSG00000036151	8	70072924	70080066	1	7	9	0	0	21	4	4	19	0	1	3		
ENSMUST00000049206	ENSMUSG00000021895	14	27238039	27403904	1	14	18	41	23	28	14	2050	5105	4555	1834	2458		Q91X46
ENSMUST00000049207	ENSMUSG00000039427	16	5233621	5244912	1	0	0	0	0	0	2	0	0	0	0	0		Q921Q3
ENSMUST00000049208	ENSMUSG00000038403	3	96525172	96529210	1	9	9	6	85	11	12	0	0	0	1	0		Q7TQ32
ENSMUST00000049209	ENSMUSG00000035540	5	89417522	89457898	-1	3	4	14	11	2	1	0	0	0	123	0		P21614
ENSMUST00000049230	ENSMUSG00000027827	3	65109384	65378223	1	4	0	0	0	0	2	0	0	0	0	0		P63143
ENSMUST00000049239	ENSMUSG00000034761	12	69803750	69893200	-1	9	0	0	0	0	0	0	0	103	0	149	E9PX30	
ENSMUST00000049241	ENSMUSG00000038692	11	96318267	96321638	1	14	7	21	167	30	10	31	192	63	5	31		P10284
ENSMUST00000049242	ENSMUSG00000037151	10	61475833	61582226	1	43	37	55	45	48	32	102	85	87	6	50		Q8CI70
ENSMUST00000049244	ENSMUSG00000039763	16	91614257	91619026	-1	0	0	0	0	0	0	8	15	17	10	33	Q8C4S9	Q8VCE1
ENSMUST00000049245	ENSMUSG00000037070	8	78505271	78508928	-1	19	20	24	61	23	7	163	558	282	327	276		Q91VM5
ENSMUST00000049246	ENSMUSG00000034639	6	108065045	108077122	1	6	2	8	9	9	3	27	125	46	78	30		Q80UJ9
ENSMUST00000049248	ENSMUSG00000032688	18	65430963	65478823	1	63	39	52	292	77	33	346	1515	822	121	647		Q2TBA3
ENSMUST00000049251	ENSMUSG00000039070	6	30568369	30592418	1	13	19	37	25	18	14	0	0	0	0	0		Q6P8K8
ENSMUST00000049255	ENSMUSG00000037683	2	19199302	19310241	1	17	0	15	10	0	11	38	95	70	218	38	A2AU71	
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ENSMUST00000049260	ENSMUSG00000042680	18	21127201	21300138	-1	20	16	41	124	26	19	2	2	6	0	3		Q3UFT3
ENSMUST00000049262	ENSMUSG00000037902	2	129592835	129632228	1	0	16	54	0	0	6	2592	7374	4801	671	3938	E0CYM8	
ENSMUST00000049263	ENSMUSG00000032212	9	70542920	70592237	1	23	9	41	68	7	9	232	1494	685	687	741	B9EI57	Q8CH25
ENSMUST00000049265	ENSMUSG00000037989	13	49036303	49148014	-1	0	0	0	0	0	0	0	0	0	0	0	E9QJQ9	
ENSMUST00000049271	ENSMUSG00000037466	12	113156421	113166048	1	37	33	312	135	59	21	60	42	53	1	57		Q3UK37
ENSMUST00000049272	ENSMUSG00000038700	11	96303336	96306121	1	0	7	0	238	11	0	0	0	0	0	0		P09079
ENSMUST00000049281	ENSMUSG00000034300	18	34758906	34773760	1	45	20	20	20	55	20	18	73	0	0	69		Q8BXQ8
ENSMUST00000049285	ENSMUSG00000034648	6	107529768	107570214	1	20	21	45	188	22	10	0	0	0	0	0		Q61809
ENSMUST00000049289	ENSMUSG00000090171	1	88200601	88218997	1	11	2	28	15	6	3	0	14	18	0	34		P70691
ENSMUST00000049294	ENSMUSG00000040824	7	19149722	19153542	1	18	8	17	8	23	3	278	397	200	1286	109	Q14AF6	P62317
ENSMUST00000049295	ENSMUSG00000024937	19	5707376	5726317	-1	34	31	78	106	67	29	2047	4182	3592	209	3051	E9QP49	
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ENSMUST00000049304	ENSMUSG00000067599	6	130218605	130233322	-1	0	0	2	0	0	0	0	0	0	0	0		Q60654
ENSMUST00000049305	ENSMUSG00000028943	4	152120331	152152371	-1	2	4	12	26	10	7	2	0	0	0	3	Q9DD12	
ENSMUST00000049308	ENSMUSG00000042644	17	27057304	27122223	1	80	53	144	465	113	49	285	380	479	23	608		P70227
ENSMUST00000049312	ENSMUSG00000035953	14	50926070	50930856	-1	0	0	0	5	0	0	225	550	130	59	182	F8WHW3	
ENSMUST00000049323	ENSMUSG00000042660	18	36760239	36763708	1	9	12	38	19	12	3	80	226	116	98	88		Q9CX97
ENSMUST00000049324	ENSMUSG00000042817	5	147330741	147400489	-1	0	0	0	0	0	0	71	69	33	5	65	Q3UEW6	
ENSMUST00000049333	ENSMUSG00000035165	7	100176670	100184869	1	5	2	0	0	0	0	0	3	3	2	0	Q545H9	Q9WTW2
ENSMUST00000049339	ENSMUSG00000037171	10	61417972	61425338	1	12	5	30	83	7	3	0	2	0	0	0		P43021
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ENSMUST00000049344	ENSMUSG00000042042	6	118107452	118139140	-1	0	0	0	7	0	0	771	1384	1055	733	748		Q8C1F4
ENSMUST00000049346	ENSMUSG00000038276	5	24413392	24417835	1	26	13	43	37	28	9	2	3	1	0	2		Q6X1Y6
ENSMUST00000049348	ENSMUSG00000032586	9	107950136	107972270	1	7	6	15	15	13	3	18	25	22	27	8		Q8VIG6
ENSMUST00000049352	ENSMUSG00000038721	11	96286623	96290162	1	4	10	24	147	12	2	0	0	0	0	0		P09024
ENSMUST00000049353	ENSMUSG00000037243	11	58307069	58314627	1	16	9	24	66	0	16	81	252	37	0	106		Q3U381
ENSMUST00000049355	ENSMUSG00000042688	9	75369062	75410005	-1	21	0	0	52	0	0	941	3165	3082	398	1105		Q61532
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ENSMUST00000049378	ENSMUSG00000032735	18	61799395	61911852	-1	14	14	14	182	42	22	0	0	0	0	0		Q69ZX8
ENSMUST00000049382	ENSMUSG00000042390	3	90293178	90363407	1	14	8	18	5	15	8	295	319	640	20	517		Q8VHR5
ENSMUST00000049385	ENSMUSG00000035530	11	100319885	100322096	1	22	27	35	156	18	11	2994	10301	3633	961	2361	Q4V9T8	P48024
ENSMUST00000049388	ENSMUSG00000042705	18	46958862	47087992	1	12	11	35	39	18	13	65	188	75	103	67	Q3TKN7	Q8JZY2
ENSMUST00000049389	ENSMUSG00000039470	8	40423815	40510268	1	9	15	34	28	13	3	10	29	13	11	21		P59267
ENSMUST00000049393	ENSMUSG00000037007	5	138139702	138155744	-1	199	196	652	264	195	106	24	78	51	18	45	Q8C689	
ENSMUST00000049395	ENSMUSG00000037101	8	78213297	78394326	1	8	3	0	0	12	0	0	0	0	0	0	E9QLU4	
ENSMUST00000049400	ENSMUSG00000032702	19	25236975	25434496	1	21	22	27	233	39	18	1	0	0	6	21	E9Q238	
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ENSMUST00000049411	ENSMUSG00000035960	14	50924968	50927139	1	0	0	12	15	4	9	52	123	34	325	99	Q544Z7	P28352
ENSMUST00000049412	ENSMUSG00000039536	2	166947549	166996299	-1	0	0	0	0	0	0	117	104	0	4	57	A2A5R8	
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ENSMUST00000049430	ENSMUSG00000038296	7	111471661	111779977	-1	0	0	0	56	0	0	0	0	0	0	0		Q8K1B9
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ENSMUST00000049454	ENSMUSG00000040841	7	19094594	19098549	1	24	21	36	338	42	19	2	2	5	1	3		P70178
ENSMUST00000049457	ENSMUSG00000042761	9	87144306	87184045	1	44	34	301	179	26	24	1	10	6	4	2		D3Z1Q2
ENSMUST00000049460	ENSMUSG00000034708	11	102430315	102437048	1	0	1	0	4	3	5	10630	11048	8188	790	6467	Q3U9N4	
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ENSMUST00000049463	ENSMUSG00000038883	13	27259436	27276660	1	2	3	3	1	3	0	0	0	0	0	0	Q78Y73	
ENSMUST00000049469	ENSMUSG00000036435	5	76529311	76570294	1	0	4	0	0	0	0	405	1484	901	141	618	Q5PPR2	
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ENSMUST00000049474	ENSMUSG00000032867	5	118064965	118155464	-1	33	30	123	162	65	32	702	510	593	123	385		Q8BIA4
ENSMUST00000049476	ENSMUSG00000036951	3	59925214	59937949	1	10	8	13	10	9	5	1	4	2	0	4	Q8BUY2	
ENSMUST00000049483	ENSMUSG00000036053	2	52857860	53134202	1	6	0	18	10	22	3	0	0	0	0	0	F8VPR2	
ENSMUST00000049484	ENSMUSG00000036197	15	93239742	93275161	-1	90	53	314	147	75	39	345	1158	839	93	677		Q3UHH8
ENSMUST00000049488	ENSMUSG00000021703	13	92611138	92711944	1	37	18	79	132	41	17	504	1476	931	118	891		Q8BHJ6
ENSMUST00000049501	ENSMUSG00000040586	X	166390033	166440704	-1	5	8	4	54	5	1	38	285	117	32	86	A2AEG2	
ENSMUST00000049503	ENSMUSG00000032624	17	83350931	83480361	1	26	23	7	15	34	0	0	110	2	52	173		
ENSMUST00000049506	ENSMUSG00000044068	11	22973215	22976496	1	32	14	44	39	25	18	124	801	297	445	316	Q793C9	Q64707
ENSMUST00000049507	ENSMUSG00000044254	4	106442329	106464329	-1	24	32	80	208	57	21	2	2	0	1	0		Q80W65
ENSMUST00000049509	ENSMUSG00000046844	8	114205612	114374071	1	13	9	8	18	10	8	0	0	0	1	0		Q80TB8
ENSMUST00000049519	ENSMUSG00000046879	11	48861968	48871683	-1	22	18	8	16	14	9	85	1387	251	742	562		Q60766

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000049520						4	4	26	10	9	5	0	0	0	0	0		
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ENSMUST00000049530	ENSMUSG00000047878	15	83226726	83251774	-1	0	16	37	26	11	20	3	0	0	0	6	Q3UF00	Q67BJ4
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ENSMUST00000049537	ENSMUSG00000039361	7	90130232	90209447	1	11	7	35	76	26	7	8342	33867	12916	3803	10204		Q7M6Y3
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ENSMUST00000049545	ENSMUSG00000045318	5	35278319	35281763	1	3	4	21	454	15	2	0	0	0	0	0		Q01337
ENSMUST00000049559	ENSMUSG00000050766	14	51203689	51204156	1	6	0	0	2	4	1	0	0	0	0	0	F6YUX7	
ENSMUST00000049567	ENSMUSG00000003308	9	21229730	21239332	-1	0	0	0	104	0	0	74	64	53	0	27		Q9Z2X8
ENSMUST00000049572	ENSMUSG00000024781	19	34492318	34527474	-1	13	13	46	35	18	2	611	2083	644	307	783		Q9Z0M5
ENSMUST00000049575	ENSMUSG00000047547	13	54592401	54611344	-1	0	0	0	75	0	0	68	42	69	26	44		Q6IRU5
ENSMUST00000049577	ENSMUSG00000048516	8	43568278	43576707	-1	6	11	5	12	3	2	0	0	0	0	0		Q9R158
ENSMUST00000049583	ENSMUSG00000060862	4	136979732	137048801	-1	49	39	93	72	85	39	95	131	94	2	110	Q6PCS8	
ENSMUST00000049584	ENSMUSG00000020657	12	4082574	4110612	1	3	0	0	94	0	0	3	0	1	1	0		Q8CFP6
ENSMUST00000049614	ENSMUSG00000043740	17	48316141	48327024	1	51	35	264	60	43	23	2426	6028	2577	629	2075	Q6QX36	
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ENSMUST00000049620	ENSMUSG00000071084	17	37952051	37953022	-1	10	7	6	8	3	2	0	0	0	0	0	Q7TRJ0	
ENSMUST00000049621	ENSMUSG00000048001	4	154960923	154962371	1	11	2	18	329	11	6	0	0	0	0	4	Q499J8	P70120
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ENSMUST00000049628	ENSMUSG00000050856	5	108433244	108434448	-1	0	2	3	6	4	3	526	868	439	2041	243		Q06185
ENSMUST00000049630	ENSMUSG00000045438	5	139336189	139351418	-1	55	43	333	141	59	26	246	396	153	356	144		Q8K0C8
ENSMUST00000049642	ENSMUSG00000045316	17	24848896	24850302	-1	12	11	20	44	16	4	8	68	10	44	26		Q8R0F8
ENSMUST00000049644	ENSMUSG00000046323	6	122626410	122630272	1	0	4	6	9	2	0	0	0	0	0	0		Q8QZY3
ENSMUST00000049648	ENSMUSG00000025893	9	4309743	4331721	1	7	4	5	8	5	3	12	74	15	35	5		Q8BHI4
ENSMUST00000049655	ENSMUSG00000046593	4	40472180	40477168	1	28	17	19	138	32	23	2	0	0	0	0	B7ZN35	A7E1Z1
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ENSMUST00000049675						0	0	1	0	2	0	48	138	32	59	50		
ENSMUST00000049676	ENSMUSG00000043029	11	73267388	73300363	1	42	34	133	75	57	29	0	0	0	0	0		Q8K424
ENSMUST00000049680	ENSMUSG00000048897	7	80024814	80094173	1	0	10	40	79	36	0	1574	1579	2275	39	1354		Q3U288
ENSMUST00000049681	ENSMUSG00000032925	14	123659971	123975618	1	0	5	4	6	15	6	0	0	0	0	0		Q8VDV0
ENSMUST00000049694	ENSMUSG00000048697	6	58008183	58009202	-1	3	8	1	0	5	2	0	0	0	0	0	Q8R2D7	
ENSMUST00000049697	ENSMUSG00000050520	16	88560828	88563183	-1	5	10	19	9	10	6	0	0	0	0	0	Q3UZK2	Q9Z260
ENSMUST00000049699	ENSMUSG00000048310	8	105900441	105931778	1	19	12	48	56	37	18	494	388	335	71	260		Q91YA2
ENSMUST00000049703	ENSMUSG00000090202	3	146645193	146651317	-1	0	7	2	0	0	1	2	0	0	0	0	Q80ZP0	
ENSMUST00000049705	ENSMUSG00000055341	13	67292450	67306467	-1	581	869	394	568	910	488	5	21	5	1	6	L7N1X4	
ENSMUST00000049706	ENSMUSG00000005339	1	173221284	173227214	-1	4	0	0	0	0	0	32	67	11	37	15		P20489
ENSMUST00000049714	ENSMUSG00000034940	11	83964428	84044578	1	0	0	0	0	0	0	32	37	26	0	22		Q5SV85
ENSMUST00000049719	ENSMUSG00000094426	7	108031397	108032341	-1	1	5	1	2	6	0	0	0	0	0	0		Q8VG04
ENSMUST00000049721	ENSMUSG00000022938	16	97471050	97504936	-1	5	4	6	2	2	2	2	2	0	1	1		Q9D309
ENSMUST00000049724	ENSMUSG00000045030	19	12678166	12683843	1	23	32	86	20	41	18	0	0	0	0	0	Q8VFW8	
ENSMUST00000049729	ENSMUSG00000046210	14	50345376	50348851	-1	5	6	20	3	10	1	0	0	0	0	0	Q7TRM4	
ENSMUST00000049732	ENSMUSG00000058351	14	31088132	31128930	-1	0	0	0	0	0	2	99	163	78	387	33		Q8C1Q6
ENSMUST00000049740	ENSMUSG00000048047	X	38189793	38197046	1	4	8	3	20	2	2	259	352	133	72	128	A2A3Z3	Q8BN78
ENSMUST00000049743	ENSMUSG00000093839	11	87888959	87889894	-1	9	5	14	8	12	5	0	0	0	0	0	Q5SW50	
ENSMUST00000049744	ENSMUSG00000012429	13	17695413	17699105	1	226	199	905	579	328	188	85	253	88	135	75	B2RTG9	Q9D011
ENSMUST00000049768	ENSMUSG00000052234	11	87864000	87875536	-1	18	13	21	27	31	12	42	7	17	6	3		P49290
ENSMUST00000049778	ENSMUSG00000051034	5	129654593	129670099	-1	76	71	176	116	83	52	22	36	31	10	24		P10751
ENSMUST00000049780	ENSMUSG00000037426	5	32863701	32994236	1	2	0	0	1	0	0	0	0	0	0	0	E9QAT3	
ENSMUST00000049784	ENSMUSG00000061911	12	29528384	29923209	1	30	17	62	20	13	13	0	0	0	0	0	D3Z1P7	
ENSMUST00000049787	ENSMUSG00000043110	2	132868305	132880891	-1	27	21	76	218	44	22	3	4	6	5	14		P59383
ENSMUST00000049788	ENSMUSG00000045404	12	99964499	100062682	1	0	0	46	43	27	12	0	0	0	0	0	Q3TYG8	Q8R1P5
ENSMUST00000049789	ENSMUSG00000071203	13	100211739	100246323	-1	51	46	51	50	55	31	74	476	135	50	214	Q8CGT2	
ENSMUST00000049790	ENSMUSG00000014592	4	150917322	151861876	-1	0	0	0	0	7	0	0	0	0	0	0		A2A891
ENSMUST00000049792	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZBV6	
ENSMUST00000049793	ENSMUSG00000048502	14	25978577	25990088	1	18	16	51	66	17	13	0	0	1	0	0	Q7TNE6	
ENSMUST00000049810	ENSMUSG00000048521	9	123806477	123811754	1	8	8	18	2	14	5	1	18	1	12	9		Q9EQ16
ENSMUST00000049811	ENSMUSG00000048799	18	53681724	53744547	-1	37	24	46	36	44	18	490	1377	1024	239	907		Q7TSG1
ENSMUST00000049813	ENSMUSG00000046404	1	130717327	130724358	1	88	92	256	354	110	53	114	389	148	25	110		Q8CB27
ENSMUST00000049819	ENSMUSG00000046924	7	23928386	23929357	1	2	2	1	1	1	2	0	0	0	0	0	Q8R2B4	
ENSMUST00000049821	ENSMUSG00000045699	4	146892406	146909590	-1	7	4	4	6	8	9	1	0	0	0	1	J3KMS0	
ENSMUST00000049822	ENSMUSG00000028145	3	94310089	94332540	1	7	2	6	33	4	4	7	42	9	50	12		Q3UUI3
ENSMUST00000049836	ENSMUSG00000042331	11	61956763	62223013	1	20	16	67	74	33	21	110	475	157	35	115		Q5SXY1
ENSMUST00000049845	ENSMUSG00000030084	6	89316314	89362620	-1	2	15	69	41	0	0	0	0	6	0	31		P70206
ENSMUST00000049849	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	0	0	0	0	0	A2AUP5	
ENSMUST00000049852	ENSMUSG00000070368	3	107232797	107239707	-1	1	2	5	3	4	3	0	0	0	0	0		Q14A28
ENSMUST00000049859	ENSMUSG00000048810	16	59283572	59284495	-1	4	3	1	5	7	3	0	0	0	0	0	Q8VGQ3	
ENSMUST00000049861	ENSMUSG00000061898	5	143172186	143180775	-1	0	0	0	55	0	11	0	0	0	0	24		Q8BQC8
ENSMUST00000049863	ENSMUSG00000046020	2	153241533	153270247	1	81	84	104	100	88	38	223	351	315	23	201		Q91ZW2
ENSMUST00000049872	ENSMUSG00000051212	14	121952331	121965193	-1	23	16	83	17	21	12	52	99	58	162	122		Q3U6B2
ENSMUST00000049874	ENSMUSG00000050103	12	37241641	37582202	1	5	3	1	0	2	1	0	0	0	7	0		Q8BS35
ENSMUST00000049877	ENSMUSG00000047002	12	11208382	11208948	-1	4	3	12	5	6	3	0	0	0	0	1		Q9JK54
ENSMUST00000049887	ENSMUSG00000048439	5	24164963	24184013	1	50	38	31	138	44	22	28	100	42	16	38	E9QL43	
ENSMUST00000049896	ENSMUSG00000031148	X	7697131	7710262	1	20	15	34	37	23	10	539	1534	864	500	822		Q56A08
ENSMUST00000049908	ENSMUSG00000070003	8	70597491	70608314	-1	8	5	25	240	10	7	738	1019	704	167	646	Q3U4B1	
ENSMUST00000049910	ENSMUSG00000031173	X	10252305	10321024	1	3	5	3	3	8	1	0	0	0	3	0	Q543H3	P11725
ENSMUST00000049911	ENSMUSG00000015120	17	25261916	25274622	-1	10	7	4	9	17	5	673	1572	678	342	524		P63280
ENSMUST00000049912	ENSMUSG00000002983	7	19606217	19629438	-1	0	0	0	55	0	0	0	103	0	21	37	Q8K220	
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ENSMUST00000049922						0	7	13	5	0	3	2	0	0	0	0		
ENSMUST00000049926	ENSMUSG00000048031	3	87435773	87500678	1	0	0	0	0	0	0	0	0	0	0	0		Q68SN8
ENSMUST00000049927						8	3	12	268	7	1	18	41	32	11	20		
ENSMUST00000049930	ENSMUSG00000045680	10	22817279	22820128	-1	9	5	8	115	16	7	0	1	2	1	0		O35437
ENSMUST00000049931	ENSMUSG00000051457	7	127132232	127137823	-1	35	26	93	62	58	27	1460	1511	1388	254	1133	Q544C5	P15702

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000049932	ENSMUSG00000025958	1	64532645	64604548	1	0	0	5	0	0	6	173	0	180	39	131	Q547S9	Q01147
ENSMUST00000049937	ENSMUSG00000001017	3	90498956	90509498	-1	12	0	27	31	21	9	254	740	504	235	432		Q9CY57
ENSMUST00000049940	ENSMUSG00000049362	16	58796779	58800254	-1	1	2	0	0	6	2	0	0	1	0	0	E9QAT7	
ENSMUST00000049941	ENSMUSG00000049281	9	40269216	40291618	1	0	0	0	0	0	0	0	0	0	0	0	Q0P666	Q8BHK2
ENSMUST00000049942	ENSMUSG00000063889	18	3266048	3337748	-1	5	6	0	1	2	4	0	0	0	0	4	D3Z6A5	
ENSMUST00000049948	ENSMUSG00000024654	19	9109868	9135636	-1	227	176	1823	269	174	83	66	164	89	33	97		Q8C0M9
ENSMUST00000049956	ENSMUSG00000033707	15	76715276	76723845	-1	10	2	28	224	15	9	0	0	0	0	2		Q8BHA1
ENSMUST00000049966	ENSMUSG00000030058	6	87887814	87913595	1	4	5	3	17	5	0	0	16	5	3	6	Q7TNQ1	
ENSMUST00000049968	ENSMUSG00000047394	15	89377450	89379254	-1	8	4	10	149	22	5	0	1	0	0	1		Q5M8M2
ENSMUST00000049972	ENSMUSG00000050711	1	79434669	79440120	-1	18	10	25	32	19	10	0	0	0	0	0		Q03517
ENSMUST00000049977	ENSMUSG00000030584	7	29303951	29317588	1	0	0	0	0	0	2	0	4	0	1	0	Q6GTK4	Q9QX66
ENSMUST00000049985	ENSMUSG00000044156	6	3457096	3498298	-1	7	6	17	0	10	5	1	0	0	0	0		Q4VAH7
ENSMUST00000049994	ENSMUSG00000048899	4	119465283	119492628	-1	22	14	39	51	32	10	2	2	1	1	3		Q6PFX8
ENSMUST00000049995	ENSMUSG00000078627	11	105360798	105456735	-1	2	10	0	48	19	11	0	0	0	0	0	E9PX79	
ENSMUST00000049997	ENSMUSG00000050558	2	132337733	132385447	-1	0	0	0	0	0	0	0	0	0	0	0		Q8K458
ENSMUST00000049999	ENSMUSG00000046550	X	153832225	153834243	1	2	3	4	2	7	0	1	1	0	1	0		Q6NVE3
ENSMUST00000050000	ENSMUSG00000026797	2	32787602	32847245	-1	21	17	46	60	21	19	0	10	8	0	52		Q08599
ENSMUST00000050003	ENSMUSG00000044320	2	30794769	30803661	-1	12	0	3	267	12	1	0	0	0	0	0	A2APZ1	
ENSMUST00000050004	ENSMUSG00000033107	18	20944625	20983848	1	11	5	11	6	11	5	141	250	245	22	204		Q9D9R0
ENSMUST00000050010	ENSMUSG00000026696	1	162570515	162599084	1	15	23	158	15	0	0	128	315	23	0	0	Q8BSN6	
ENSMUST00000050011	ENSMUSG00000079362	5	105214907	105293695	-1	17	14	17	22	20	16	9	38	7	68	72	L7N1X8	
ENSMUST00000050020	ENSMUSG00000048534	9	45079183	45108530	1	14	9	42	30	11	7	883	7308	1920	2618	2367		Q80UL9
ENSMUST00000050026	ENSMUSG00000047841	2	181220013	181222854	1	5	0	15	16	7	1	0	0	0	0	0		Q80WB0
ENSMUST00000050027	ENSMUSG00000037362	15	54745702	54754039	1	7	9	13	63	24	20	1	0	1	0	4		Q64299
ENSMUST00000050029	ENSMUSG00000051367	12	73040015	73053887	-1	11	13	12	490	17	7	0	0	0	2	3	Q3V2C3	Q62231
ENSMUST00000050034	ENSMUSG00000047033	18	37473540	37476340	1	16	16	39	21	27	9	0	0	0	0	0	Q91Y04	
ENSMUST00000050038	ENSMUSG00000051424	2	88486734	88487669	1	4	5	7	0	3	1	0	0	0	0	0	Q8VG86	
ENSMUST00000050044	ENSMUSG00000048173	X	50425496	50426494	-1	2	0	2	3	2	1	0	0	0	0	0	Q8VEU7	
ENSMUST00000050047	ENSMUSG00000044816	1	65105285	65123214	-1	27	13	148	40	19	5	0	2	0	0	2		Q8C3M9
ENSMUST00000050063	ENSMUSG00000044147	12	69372150	69375979	1	19	23	43	180	30	12	2338	3862	1636	283	1160	Q3U0D7	P62331
ENSMUST00000050067	ENSMUSG00000046861	4	116995317	117005277	1	29	18	48	273	56	21	1301	2045	1347	138	926		Q3U487
ENSMUST00000050069	ENSMUSG00000046667	4	12140264	12146731	1	8	3	0	0	0	0	19	54	14	35	44		Q80YR9
ENSMUST00000050073	ENSMUSG00000028035	3	152178511	152210302	-1	7	8	20	7	7	9	16	123	41	76	35		Q9D832
ENSMUST00000050077	ENSMUSG00000062190	6	57702540	57739439	1	9	3	14	43	4	0	24	54	32	18	27		Q9JJK2
ENSMUST00000050078	ENSMUSG00000029076	4	155992872	156013610	1	47	28	126	157	49	32	278	905	407	96	348		Q61112
ENSMUST00000050083	ENSMUSG00000031095	X	38533274	38576196	-1	0	0	2	0	2	0	89	291	199	148	49		A2A432
ENSMUST00000050092	ENSMUSG00000049164	19	40894705	40917947	1	12	4	13	45	17	5	178	435	208	168	137		B2RRF6
ENSMUST00000050096	ENSMUSG00000025026	19	53140445	53247399	1	5	0	0	114	0	6	714	1502	2095	428	1074	Q3UNK1	Q9QYB5
ENSMUST00000050101	ENSMUSG00000046351	13	23353103	23369208	-1	32	46	66	44	40	19	67	267	118	89	50		Q8BZ89
ENSMUST00000050103	ENSMUSG00000044312	10	62133090	62134763	1	10	6	33	133	15	7	0	0	0	0	0	Q548G3	P70661
ENSMUST00000050104	ENSMUSG00000046733	6	135065651	135084709	1	23	11	15	27	22	14	0	1	0	5	35	G5E8C3	
ENSMUST00000050106	ENSMUSG00000048294	11	99809078	99809892	-1	11	6	20	68	11	4	0	0	0	0	0	Q9D7P3	
ENSMUST00000050120	ENSMUSG00000046523	14	75955003	75965217	1	7	10	9	3	9	5	0	0	1	0	2		Q9D7X1
ENSMUST00000050123						4	3	0	0	8	0	0	0	0	0	0		
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ENSMUST00000050128						11	13	79	18	22	9	0	0	0	0	0		
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ENSMUST00000050131						2	0	0	1	1	0	0	0	0	0	6		
ENSMUST00000050132						4	5	6	10	21	7	0	0	0	0	0		
ENSMUST00000050139						19	14	12	6	16	12	0	1	0	0	0		
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ENSMUST00000050143						0	3	26	0	0	0	0	0	0	0	0		
ENSMUST00000050148	ENSMUSG00000024780	19	28990494	29017569	1	12	19	10	105	23	8	127	471	259	102	224		Q9CZP7
ENSMUST00000050149	ENSMUSG00000038244	7	112225856	112355194	1	36	19	48	62	44	17	12	15	16	3	39		Q8BML1
ENSMUST00000050151						0	0	13	313	4	2	12	7	1	1	7		
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ENSMUST00000050160	ENSMUSG00000051669	16	5211828	5222299	-1	10	13	30	12	14	7	0	0	0	0	2		Q3UST5
ENSMUST00000050166	ENSMUSG00000040537	5	8072352	8368160	-1	16	0	0	0	0	0	10	47	0	2	12		Q9R1V6
ENSMUST00000050171	ENSMUSG00000021918	14	30951486	30987439	1	7	7	25	88	11	10	24	68	74	26	43	Q6GTE9	
ENSMUST00000050178	ENSMUSG00000043913	5	116124641	116288985	-1	47	23	132	61	30	18	1	0	2	1	3		Q8C4J0
ENSMUST00000050183	ENSMUSG00000034485	9	60794548	60880370	1	54	19	85	118	58	22	12	41	35	28	56		
ENSMUST00000050201	ENSMUSG00000063065	7	126759601	126765819	1	0	3	10	41	5	0	0	13	0	0	12	D3Z3G6	
ENSMUST00000050205	ENSMUSG00000036639	5	140321656	140338137	1	0	0	0	0	0	0	30	40	20	78	17		P53368
ENSMUST00000050207	ENSMUSG00000046909	11	80136678	80142175	-1	4	0	6	11	6	6	7	17	0	45	3		Q5SSK3
ENSMUST00000050211	ENSMUSG00000035824	8	104226691	104248558	-1	22	13	36	63	23	12	891	2570	1125	246	1010	Q8BN51	
ENSMUST00000050214	ENSMUSG00000002625	17	32321425	32350581	-1	12	13	29	152	18	20	250	1371	426	90	649	Q5RL57	
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ENSMUST00000050226	ENSMUSG00000045667	11	72389164	72411713	-1	72	62	191	201	51	18	3	20	6	3	10		Q8CI12
ENSMUST00000050227	ENSMUSG00000044106	9	20098626	20101690	1	4	5	5	4	2	0	0	0	0	0	0	Q8VFI8	
ENSMUST00000050228	ENSMUSG00000049411	18	11981303	12121480	-1	9	0	0	16	0	5	39	29	24	22	46	H7BX28	
ENSMUST00000050234	ENSMUSG00000046380	15	74702301	74709535	-1	45	28	169	197	66	32	9	8	6	0	15	Q543Z9	Q60976
ENSMUST00000050236	ENSMUSG00000050612	17	65637505	65642204	-1	5	11	208	28	16	8	1	2	2	1	1	H7BX21	
ENSMUST00000050239	ENSMUSG00000034755	X	120290259	120910619	1	0	0	0	11	0	3	0	0	0	0	0	E9Q622	
ENSMUST00000050248	ENSMUSG00000022601	16	55973883	56008913	1	3	4	8	195	17	7	169	579	426	83	297	G5E8B9	
ENSMUST00000050255	ENSMUSG00000050613	17	37834911	37836028	1	5	3	5	3	3	3	0	0	0	0	0	Q14AJ9	
ENSMUST00000050258	ENSMUSG00000051036	3	88069410	88078304	-1	10	16	21	21	28	8	0	0	0	0	0	B9EJT8	Q8BYG0
ENSMUST00000050273	ENSMUSG00000046516	16	38346991	38352763	1	1	0	0	18	0	0	371	790	322	1573	267	Q54AC6	P56394
ENSMUST00000050276	ENSMUSG00000071452	13	33395761	33405285	1	7	4	1	7	0	6	0	0	0	0	0	F6V5V4	
ENSMUST00000050288	ENSMUSG00000033326	4	118136957	118180043	-1	10	0	10	15	25	0	56	33	94	3	130	A2A8L9	
ENSMUST00000050300	ENSMUSG00000031554	8	24727093	24824369	-1	0	0	0	0	0	0	0	0	0	0	0		Q3TTE0
ENSMUST00000050306	ENSMUSG00000044854	1	184033030	184034301	-1	0	0	0	138	0	6	0	5	0	2	0	F7CNM6	
ENSMUST00000050309	ENSMUSG00000043727	2	129458359	129536602	-1	10	11	24	11	13	5	3	16	5	10	0	Q8BJ95	
ENSMUST00000050312	ENSMUSG00000027223	2	92383676	92401263	-1	21	6	27	121	43	13	2	1	2	8	14		Q9WVI9
ENSMUST00000050323	ENSMUSG00000002104	2	91035620	91045729	1	0	0	17	4	3	0	0	0	0	0	0		P12672

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ENSMUST00000050325	ENSMUSG00000067341	17	34325665	34340229	1	21	20	37	117	31	12	1	1	0	1	5	Q3UUV9	
ENSMUST00000050327	ENSMUSG00000044534	9	121898464	121911064	1	20	16	35	25	36	8	0	1	1	0	10		O08707
ENSMUST00000050328	ENSMUSG00000035150	X	94188707	94212862	-1	29	27	108	40	35	9	462	2894	788	576	526	Q3TML6	Q9Z0N1
ENSMUST00000050331	ENSMUSG00000045427	X	134601179	134607060	1	0	0	0	0	0	0	74	2394	1010	1225	799		P70333
ENSMUST00000050339						0	0	0	0	3	1	0	1	0	0	0		
ENSMUST00000050342	ENSMUSG00000043468	3	98160630	98164169	1	15	12	14	12	24	11	1	11	1	1	4	Q811Q3	
ENSMUST00000050349	ENSMUSG00000049687	15	82338942	82345743	1	1	8	0	65	20	0	19	30	16	0	9		
ENSMUST00000050360	ENSMUSG00000036353	3	59216272	59262871	-1	9	6	3	0	12	2	57	289	148	367	144	Q546L4	Q9CPV9
ENSMUST00000050366	ENSMUSG00000001105	11	78536361	78541737	1	4	0	3	18	0	0	24	41	17	0	11	Z4YJL9	
ENSMUST00000050372	ENSMUSG00000035403	2	37776249	37799103	1	48	30	130	521	73	24	0	0	0	0	8		Q80YA8
ENSMUST00000050373	ENSMUSG00000047654	8	69902184	69903518	1	8	2	10	417	22	1	13	32	16	4	11		Q925K9
ENSMUST00000050374	ENSMUSG00000051225	15	57985419	58011009	1	0	2	0	0	4	3	0	0	0	0	1		Q8K2P2
ENSMUST00000050383	ENSMUSG00000049739	7	127876221	127885996	1	31	27	72	59	64	22	961	1335	1194	97	947	Q6NV66	
ENSMUST00000050385	ENSMUSG00000043932	6	129729041	129740484	-1	15	24	22	24	35	11	0	20	1	7	8	Q5DT36	
ENSMUST00000050389	ENSMUSG00000046082	13	98634978	98637410	-1	23	10	15	21	24	12	0	0	0	0	0		Q9DCX7
ENSMUST00000050391						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000050397	ENSMUSG00000050635	3	92365187	92366442	1	5	5	9	4	6	4	0	0	0	0	0		O70557
ENSMUST00000050398	ENSMUSG00000042642	3	89401004	89411870	-1	0	0	1	3	0	3	25	73	50	8	26		Q8R123
ENSMUST00000050401	ENSMUSG00000046280	3	89831370	89858834	1	44	27	71	151	41	29	1	10	8	2	12		Q8BSD5
ENSMUST00000050406	ENSMUSG00000026409	1	130689182	130729253	-1	1	0	5	1	0	1	0	0	94	5	0	B2Z892	
ENSMUST00000050410	ENSMUSG00000044627	2	32278816	32288075	-1	0	0	8	68	0	0	0	0	0	105	0	A0A0A0MQ99	
ENSMUST00000050412	ENSMUSG00000045479	6	41771258	41775177	-1	7	3	4	7	8	4	0	0	0	0	0	Q924H8	
ENSMUST00000050416	ENSMUSG00000047655	7	11846775	11847689	1	2	2	2	0	1	1	0	0	0	0	0	Q8R290	
ENSMUST00000050433	ENSMUSG00000031997	9	8544196	8680565	1	17	18	6	68	13	7	0	2	0	4	0		Q61143
ENSMUST00000050434	ENSMUSG00000051228	X	13466110	13489313	1	148	128	318	411	200	108	9	24	11	7	16		P83503
ENSMUST00000050442	ENSMUSG00000005883	2	172977700	172993576	1	0	0	0	8	0	4	0	0	0	0	0		Q9WTK8
ENSMUST00000050446	ENSMUSG00000045751	4	24496451	24602950	1	21	10	38	0	7	3	20	18	0	8	35	G8JL47	
ENSMUST00000050451	ENSMUSG00000054036	15	98492402	98498406	1	3	9	29	8	12	6	0	0	0	0	0	Q8VFD8	
ENSMUST00000050455	ENSMUSG00000019900	10	51677756	51730429	1	0	14	0	2	0	0	0	0	0	0	0		Q8C7R7
ENSMUST00000050467	ENSMUSG00000048546	15	81848270	81858326	-1	37	17	140	338	52	21	452	678	657	68	495	Q543X9	Q9JM55
ENSMUST00000050471	ENSMUSG00000047104	6	135309127	135310405	-1	6	2	14	7	10	3	0	0	0	0	1	E9QLE5	
ENSMUST00000050472	ENSMUSG00000041264	5	149184350	149215434	1	0	0	16	0	31	6	77	32	49	7	142	E9QLC6	
ENSMUST00000050476	ENSMUSG00000033272	18	36679215	36683861	1	0	0	18	0	6	8	192	132	155	21	161		Q9D321
ENSMUST00000050480	ENSMUSG00000046753	14	27482412	27508460	-1	14	7	26	11	11	8	10	60	21	47	25		Q6NS45
ENSMUST00000050482	ENSMUSG00000044705	7	104959792	104960730	-1	1	2	4	3	2	1	0	0	0	0	0	Q7TRP3	
ENSMUST00000050483	ENSMUSG00000025237	9	59617284	59650290	1	5	9	0	0	8	15	119	340	135	36	163		
ENSMUST00000050484	ENSMUSG00000049107	6	126101412	126166910	-1	0	0	0	0	9	7	17	125	39	69	8		P20181
ENSMUST00000050487	ENSMUSG00000024610	18	60803848	60812646	1	0	6	4	22	0	0	1289	780	666	745	4533	Q545Y5	P04441
ENSMUST00000050491	ENSMUSG00000018196	1	143716338	143749676	1	0	0	0	0	0	0	0	0	0	2	0	A0A0A0MQ94	
ENSMUST00000050493	ENSMUSG00000049008	8	15041444	15046078	-1	11	17	0	29	2	16	0	0	0	0	0	Q8C5R5	
ENSMUST00000050497	ENSMUSG00000046679	6	86438374	86473500	1	9	0	10	14	0	0	0	56	52	16	34		Q8R3C1
ENSMUST00000050511	ENSMUSG00000026866	2	43555329	43682715	1	25	12	27	145	14	12	0	0	2	0	3	A2ARD7	
ENSMUST00000050516	ENSMUSG00000044475	10	60002805	60099990	1	11	0	0	21	0	0	109	184	84	0	0		Q9D8Z1
ENSMUST00000050519	ENSMUSG00000048988	5	139907943	139974722	1	47	41	278	488	72	28	0	0	0	0	1		Q8C8T7
ENSMUST00000050535	ENSMUSG00000051246	5	34908012	34923839	1	27	14	29	26	30	16	0	0	0	1	0		Q8BIL2
ENSMUST00000050536	ENSMUSG00000046856	1	63182691	63214543	-1	8	2	10	11	15	0	0	0	0	0	0		Q8K087
ENSMUST00000050541	ENSMUSG00000051591	7	106740910	106741956	-1	4	6	10	1	2	8	0	0	0	0	0	Q8VFM4	
ENSMUST00000050542	ENSMUSG00000024240	18	6435951	6516108	-1	0	3	2	105	1	0	6	32	6	8	10	Q6PBH3	
ENSMUST00000050544	ENSMUSG00000022367	15	56665627	56694539	-1	22	20	70	24	35	12	1	4	2	40	23		P70312
ENSMUST00000050551	ENSMUSG00000051159	X	102247381	102252181	-1	10	9	31	22	10	10	0	0	0	0	0	Q3UGA1	P97769
ENSMUST00000050552	ENSMUSG00000051223	1	58392898	58407353	1	26	20	30	115	34	21	728	2389	743	1332	477		Q9CQC6
ENSMUST00000050555	ENSMUSG00000046731	11	69878261	69881406	-1	33	31	171	378	59	38	631	1098	534	73	455		Q8K485
ENSMUST00000050556	ENSMUSG00000061755	5	41787538	41844315	-1	45	36	125	122	48	26	324	941	1064	144	747	E9Q6J5	E9Q6J5
ENSMUST00000050561	ENSMUSG00000031858	8	70016123	70042734	-1	54	0	148	179	0	0	1063	1852	1523	222	1836		Q9D2X5
ENSMUST00000050562	ENSMUSG00000050370	19	34473786	34475135	-1	14	8	18	66	23	3	0	0	1	1	1		Q9Z0F5
ENSMUST00000050567	ENSMUSG00000043629	1	52922324	53020179	-1	2	0	3	59	10	3	0	0	0	0	0		Q9CPS8
ENSMUST00000050571						4	3	10	4	8	3	0	0	0	0	0		
ENSMUST00000050574	ENSMUSG00000044707	11	43528784	43586997	1	16	10	86	55	31	17	85	198	131	25	151		Q5SRT8
ENSMUST00000050575	ENSMUSG00000045691	14	55053884	55098986	1	21	9	42	93	33	26	46	57	40	12	31		Q8JZL3
ENSMUST00000050580	ENSMUSG00000063882	4	116066965	116075071	-1	1	0	0	0	0	1	11	25	7	22	0	Q9D2Q7	
ENSMUST00000050581						16	15	111	19	30	11	22	26	0	4	6		
ENSMUST00000050584	ENSMUSG00000046727	18	36345619	36402980	1	3	1	3	108	11	2	165	202	84	78	46		Q8K353
ENSMUST00000050585	ENSMUSG00000051180	7	140161939	140163014	-1	17	11	16	7	19	4	0	0	0	0	0	Q8VGL1	
ENSMUST00000050586	ENSMUSG00000006204	7	131174402	131250945	1	15	13	22	32	17	5	0	0	0	0	0		Q8BZE1
ENSMUST00000050595	ENSMUSG00000048728	11	50872720	50887651	-1	8	5	10	24	13	0	0	0	0	0	0	Q80Y34	
ENSMUST00000050599	ENSMUSG00000051172	7	104995964	104996902	-1	4	2	0	0	3	0	0	0	0	0	0	Q8VG28	
ENSMUST00000050611	ENSMUSG00000044066	11	20227037	20249429	-1	18	17	39	17	33	16	36	60	54	11	62		Q8C0D9
ENSMUST00000050623	ENSMUSG00000074677	3	15795145	15848528	-1	0	0	0	0	6	0	846	6563	1566	4786	1286	Q1AN90	
ENSMUST00000050625	ENSMUSG00000052133	16	35541145	35664732	1	36	32	199	0	0	26	1	2	4	0	2		Q60519
ENSMUST00000050630	ENSMUSG00000038954	17	44777152	45119290	1	3	0	6	38	4	0	10	48	0	4	9	Q8BVY4	
ENSMUST00000050646	ENSMUSG00000042298	11	62281473	62328451	1	23	15	23	17	14	8	51	227	118	31	102		Q8CC21
ENSMUST00000050649	ENSMUSG00000043398	12	72069618	72070991	-1	8	1	8	372	15	4	0	0	0	0	1	A7E1Z8	Q7TQP2
ENSMUST00000050658	ENSMUSG00000046957	13	92574631	92576232	-1	8	10	23	14	25	11	0	0	0	0	0		Q99MY0
ENSMUST00000050660	ENSMUSG00000047053	1	153891742	153893058	1	10	7	23	20	12	6	0	0	1	0	2	E9QLK8	
ENSMUST00000050668	ENSMUSG00000040321	2	114193461	114201469	-1	15	20	7	15	12	7	10	47	10	12	17		Q8BIQ8
ENSMUST00000050672						0	0	2	6	0	0	0	4	0	0	0		
ENSMUST00000050678	ENSMUSG00000047444	11	74044325	74056551	-1	2	0	15	4	4	1	0	0	0	0	0		Q60891
ENSMUST00000050686	ENSMUSG00000049488	4	12039355	12090020	-1	1	0	5	0	0	1	0	194	22	30	3	E9QNI1	
ENSMUST00000050687	ENSMUSG00000034271	12	85599105	85639878	1	0	0	0	44	0	0	95	381	292	58	207		P97875
ENSMUST00000050702	ENSMUSG00000035916	10	107517049	107720051	-1	28	19	21	15	17	14	0	0	0	1	0		P0C5E4
ENSMUST00000050705	ENSMUSG00000058550	16	48283735	48294292	1	12	16	33	7	14	9	0	0	0	0	0	E9PUG8	
ENSMUST00000050706						6	5	14	5	7	11	0	0	0	0	0		
ENSMUST00000050707	ENSMUSG00000044206	X	96247203	96293438	-1	4	2	1	0	7	2	0	0	0	503	36	Q80WA3	
ENSMUST00000050709	ENSMUSG00000044716	5	35056766	35087839	1	27	17	63	114	31	18	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000050714	ENSMUSG00000046070	17	24878770	24882008	1	32	16	31	22	33	14	1	0	1	0	0		
ENSMUST00000050715	ENSMUSG00000024713	19	17432832	17837632	-1	10	25	23	43	17	4	0	4	0	0	1	Q91VK0	Q04592
ENSMUST00000050717	ENSMUSG00000039684	10	31248140	31251045	1	25	7	24	39	27	9	0	0	1	0	0	J3KMQ2	
ENSMUST00000050719	ENSMUSG00000036053	2	52857860	53134202	1	16	17	11	184	14	6	35	0	95	1	93	E9PXE6	
ENSMUST00000050729	ENSMUSG00000049168	6	42834384	42838888	1	7	6	2	14	7	5	0	0	0	0	0	Q8VGW8	
ENSMUST00000050732	ENSMUSG00000051727	7	97451323	97459557	1	18	21	35	142	33	10	2	20	4	0	4	Q5EER8	
ENSMUST00000050733	ENSMUSG00000049334	9	38448792	38449847	1	1	3	4	3	3	1	0	0	0	0	0	E9Q6Z7	
ENSMUST00000050735	ENSMUSG00000049421	7	30094777	30107622	1	21	8	17	10	14	0	10	0	29	22	0		Q62513
ENSMUST00000050744	ENSMUSG00000051361	X	38772671	38962686	1	5	0	0	5	3	0	0	0	0	0	0	B1AX85	
ENSMUST00000050753	ENSMUSG00000045506	17	63863300	63863791	-1	1	2	1	153	4	5	2	4	6	3	10	Q8C8Y3	
ENSMUST00000050754	ENSMUSG00000047828	12	112413915	112423212	-1	26	13	46	29	37	14	0	0	0	0	0	Q8C987	
ENSMUST00000050756	ENSMUSG00000044071	10	123264076	123741204	1	23	16	61	469	27	22	0	0	0	1	0		
ENSMUST00000050757	ENSMUSG00000028399	4	75941238	78211961	-1	0	0	0	0	0	4	0	0	0	0	0	E9Q7I7	
ENSMUST00000050758	ENSMUSG00000102439	3	93273523	93293686	1	13	8	51	732	23	16	0	0	0	0	0	A0A0A6YY62	
ENSMUST00000050770	ENSMUSG00000049130	7	16246743	16259540	-1	0	13	0	33	0	0	10031	21395	10219	1297	6401		P30993
ENSMUST00000050771	ENSMUSG00000051452	11	84148351	84167476	-1	6	8	22	6	17	4	0	0	0	0	0		Q5QR91
ENSMUST00000050772	ENSMUSG00000022199	14	54906727	54913132	-1	12	14	62	234	45	11	1	4	0	2	7		Q9D9E0
ENSMUST00000050776	ENSMUSG00000026805	2	28907679	28916668	-1	0	0	39	366	32	13	0	0	0	0	0		P63157
ENSMUST00000050780	ENSMUSG00000051262	6	85732513	85765754	-1	13	39	47	48	24	11	0	0	0	0	0		
ENSMUST00000050785	ENSMUSG00000026822	2	32384633	32388252	-1	13	33	11	85	11	54	95589	163144	73248	144810	43340		P11672
ENSMUST00000050797	ENSMUSG00000032035	9	32636221	32757820	1	0	0	2	109	0	1	10	13	0	5	54	E9PWI8	
ENSMUST00000050807	ENSMUSG00000048299	9	39613544	39614560	1	4	3	17	6	3	1	0	0	0	0	0	Q05AA1	Q60887
ENSMUST00000050813	ENSMUSG00000049038	10	85119435	85128027	-1	7	9	4	1	6	4	5	53	11	28	11		Q8BKY8
ENSMUST00000050826	ENSMUSG00000047146	10	62804570	62899118	-1	44	0	1	0	0	16	6	6	5	1	11		Q3URK3
ENSMUST00000050827	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	7	0	0	0	0	47	0	0		A2RTL5
ENSMUST00000050833	ENSMUSG00000030689	7	126850960	126862377	-1	7	13	16	4	11	0	0	0	0	0	0	Q8R359	
ENSMUST00000050850	ENSMUSG00000051675	4	65604986	65616238	1	0	7	8	0	13	4	10	11	11	3	7	Q3TLR3	Q8CH72
ENSMUST00000050859	ENSMUSG00000016756	13	24327420	24477285	1	1	0	0	2	0	0	265	489	1417	10	686		Q61419
ENSMUST00000050864	ENSMUSG00000050058	16	10790505	10790914	-1	2	0	11	16	6	2	0	0	0	0	0		Q62100
ENSMUST00000050867	ENSMUSG00000034889	10	81321103	81326251	1	20	9	52	319	44	11	538	695	504	70	480	A1L013	Q9CS00
ENSMUST00000050872	ENSMUSG00000008575	4	82290173	82705750	-1	45	29	82	0	71	32	0	0	0	11	38		P97863
ENSMUST00000050874	ENSMUSG00000050106	11	117782076	117793110	1	5	0	8	130	15	7	371	356	419	22	208	B1ATC0	Q7TN58
ENSMUST00000050876	ENSMUSG00000026254	1	87213914	87240488	1	5	11	7	9	5	3	12	24	26	3	19	D3YUV9	
ENSMUST00000050880	ENSMUSG00000039908	11	119355557	119381079	1	13	6	49	11	20	13	150	565	209	53	210		Q80ZD3
ENSMUST00000050881	ENSMUSG00000022516	16	4939111	4941020	1	9	6	36	202	20	11	462	526	247	79	187		Q8VHN8
ENSMUST00000050882	ENSMUSG00000050704	16	88707169	88707962	-1	2	4	14	8	3	1	0	0	0	0	0	Q9D6S9	
ENSMUST00000050884	ENSMUSG00000040681	16	96120618	96127729	-1	34	36	107	126	43	17	25	143	46	80	118		P18608
ENSMUST00000050887	ENSMUSG00000049409	6	87578591	87590743	-1	25	22	64	90	52	20	0	1	0	0	1		Q9JKL1
ENSMUST00000050890	ENSMUSG00000034000	1	94020451	94028334	1	22	16	75	20	18	10	0	0	0	1	0		Q8BZL1
ENSMUST00000050897	ENSMUSG00000043065	16	44347121	44388497	1	31	36	50	63	17	14	4	8	5	0	19		Q8C804
ENSMUST00000050899	ENSMUSG00000051703	1	75479532	75485705	1	9	17	56	87	14	4	0	0	0	0	0		Q8BG75
ENSMUST00000050900						102	83	86	48	125	44	0	3	3	0	8		
ENSMUST00000050901	ENSMUSG00000047631	10	128267997	128270151	1	22	20	81	30	25	11	4	7	6	15	7		
ENSMUST00000050905	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	4	3	0	0	0	0	0	0	Q8BP43	
ENSMUST00000050909	ENSMUSG00000050947	3	108186335	108192286	1	0	0	71	9	39	6	8	10	12	3	14		Q80ZD8
ENSMUST00000050914	ENSMUSG00000051638	3	108940053	108940445	-1	0	0	3	130	1	0	0	0	0	0	0	F7CXR1	
ENSMUST00000050915	ENSMUSG00000042801	10	129111428	129112511	-1	7	5	4	2	3	3	0	0	0	0	0	Q8K501	
ENSMUST00000050916	ENSMUSG00000032733	9	56917200	56928371	-1	42	26	81	143	58	23	64	164	100	14	136		Q4VAA7
ENSMUST00000050918	ENSMUSG00000046447	4	138454314	138460123	1	25	15	62	175	44	19	1	2	0	1	4		Q6QWF9
ENSMUST00000050921	ENSMUSG00000020887	8	70863127	70865428	1	11	6	28	171	20	13	0	0	0	0	0	Q8C546	
ENSMUST00000050928	ENSMUSG00000045306	14	50319836	50320868	-1	5	6	9	1	7	4	0	0	0	0	0	Q8VFT4	
ENSMUST00000050933	ENSMUSG00000050810	4	144157557	144162663	-1	10	9	4	5	10	7	0	0	0	0	0	Q3UWY1	
ENSMUST00000050937	ENSMUSG00000046974	11	46571536	46589232	1	18	18	13	29	20	10	0	3	2	0	3	A0A0B4J1F6	
ENSMUST00000050940	ENSMUSG00000044518	4	114925147	114926013	-1	1	2	0	245	7	5	0	0	0	0	0		Q9QY14
ENSMUST00000050942	ENSMUSG00000043267	2	85991819	85992829	1	6	2	0	1	6	1	0	0	0	0	0	Q7TR87	
ENSMUST00000050949	ENSMUSG00000041143	4	138972888	139059171	1	0	0	0	37	0	8	70	34	88	0	61		Q91WU4
ENSMUST00000050952	ENSMUSG00000047963	5	92603041	92606579	1	20	14	28	153	25	10	1	5	0	16	9		Q8C7E7
ENSMUST00000050958	ENSMUSG00000049555	9	110865711	110880113	-1	33	25	63	103	42	25	5	4	1	2	12	B2RSF0	Q8K467
ENSMUST00000050962	ENSMUSG00000047109	16	93919031	94008837	-1	5	4	5	35	4	7	0	0	0	0	0	A2RSP0	Q9Z0S3
ENSMUST00000050963	ENSMUSG00000046108	8	122422020	122423639	1	8	2	15	23	14	6	2	8	3	1	10		
ENSMUST00000050970	ENSMUSG00000029642	5	147077050	147111597	1	18	11	16	37	18	13	289	761	218	868	197	Q545W2	P97304
ENSMUST00000050975	ENSMUSG00000044505	3	94398517	94404501	1	40	35	76	196	54	46	2	6	4	0	5		
ENSMUST00000050983	ENSMUSG00000047490	11	89390223	89418948	-1	16	13	33	33	30	12	0	0	0	0	0	Q8CDJ6	
ENSMUST00000050990	ENSMUSG00000052632	12	21111748	21270171	1	0	0	0	0	0	0	0	0	0	0	0	D3YX85	
ENSMUST00000050993	ENSMUSG00000021282	12	111538101	111546753	1	1	5	8	52	12	0	746	3624	2095	229	914	Q3TQR3	P59325
ENSMUST00000050996	ENSMUSG00000044205	9	40092017	40093558	-1	2	3	5	2	8	4	0	0	0	0	0	Q8VG90	
ENSMUST00000050997	ENSMUSG00000043190	13	76001535	76018712	-1	0	0	0	0	7	6	9	135	12	34	16		Q8K2P6
ENSMUST00000051004	ENSMUSG00000043911	9	38815408	38816539	1	0	3	1	2	2	2	0	0	0	0	0	Q8VG50	
ENSMUST00000051005	ENSMUSG00000049511	9	81628291	81633828	-1	0	0	0	0	0	0	0	0	5	0	3	Q0VES5	P28334
ENSMUST00000051008	ENSMUSG00000047508	9	18443456	18446312	1	7	6	3	3	5	2	0	0	0	0	0	Q3UXB0	
ENSMUST00000051011	ENSMUSG00000047090	10	128800036	128804370	-1	8	4	0	6	3	0	198	511	277	60	210	Q8CFU0	
ENSMUST00000051014	ENSMUSG00000034584	9	53301670	53377514	1	30	36	77	49	63	26	0	0	0	0	0		Q0VAV2
ENSMUST00000051016	ENSMUSG00000049686	5	123015074	123030456	1	0	0	0	0	0	0	2055	1355	1077	271	858	A3KCG1	Q8BWG9
ENSMUST00000051017	ENSMUSG00000044748	8	21776599	21795185	1	2	4	4	4	5	0	0	0	0	0	0	Q3UQE2	P56386
ENSMUST00000051025	ENSMUSG00000089876	11	69803603	69805624	-1	13	9	42	359	42	9	3	2	3	1	6		Q3UPR7
ENSMUST00000051039	ENSMUSG00000051705	9	59734259	59750649	-1	16	17	33	15	16	8	10	38	17	0	9		Q9D2Z4
ENSMUST00000051043	ENSMUSG00000046133	4	101890020	101893789	-1	8	8	0	7	6	4	0	3	6	1	9	Q8C4L8	
ENSMUST00000051053	ENSMUSG00000044949	11	32455370	32516687	1	7	7	2	33	9	1	6	7	5	3	10		Q6PGH0
ENSMUST00000051058	ENSMUSG00000045225	2	87867993	87868925	1	2	1	0	1	3	1	0	0	0	0	0	Q7TR34	
ENSMUST00000051064	ENSMUSG00000043542	3	7503483	7553836	1	6	7	5	29	9	6	0	3	0	23	9		Q8BJH1
ENSMUST00000051065	ENSMUSG00000045441	6	59347226	59426294	-1	15	15	71	47	16	6	2	1	1	0	6	B2RQZ6	Q8BWS5
ENSMUST00000051079	ENSMUSG00000048982	12	75411720	75416781	-1	18	10	33	16	17	17	0	0	1	0	0	B2RTN6	Q812B2
ENSMUST00000051080						1	0	0	131	11	1	0	0	3	0	6		
ENSMUST00000051087	ENSMUSG00000042834	18	33437019	33464029	-1	4	5	4	12	3	3	0	0	0	0	0	Q542Q5	Q07475

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000051089						6	7	22	67	24	8	77	198	68	14	92		
ENSMUST00000051091	ENSMUSG00000047246	13	23583742	23621124	-1	4	0	0	0	9	0	82	208	19	19	39		Q6ZWY9
ENSMUST00000051094	ENSMUSG00000015341	8	23241353	23257074	-1	9	13	19	45	4	0	631	1361	656	665	479		Q91W53
ENSMUST00000051097	ENSMUSG00000048752	9	110857967	110864629	1	6	8	13	128	15	9	0	0	0	0	0		Q8BLH5
ENSMUST00000051100	ENSMUSG00000051412	GL456233.1	10738	39148	-1	2	1	3	0	6	1	131	209	79	179	50		P70280
ENSMUST00000051103	ENSMUSG00000043982	16	88884786	88885089	-1	2	2	8	1	4	1	0	0	0	0	0		Q925H7
ENSMUST00000051111	ENSMUSG00000096794	9	38472745	38473681	1	0	5	1	7	5	1	0	0	0	0	0	L7N1X5	
ENSMUST00000051117	ENSMUSG00000051503	5	112353801	112356033	-1	14	15	102	17	29	15	6	19	9	5	8	E9Q8Z1	
ENSMUST00000051118	ENSMUSG00000050908	16	10420557	10447362	-1	23	20	50	50	38	14	2	9	2	1	8	Q6NVH0	
ENSMUST00000051122	ENSMUSG00000049350	7	127050156	127087328	-1	4	2	2	7	12	2	0	1	0	0	0		Q8K0C5
ENSMUST00000051126	ENSMUSG00000045657	18	37411664	37414514	1	22	18	47	32	37	9	0	0	0	0	0	Q91VE5	
ENSMUST00000051129	ENSMUSG00000046807	10	75550125	75560330	-1	66	54	118	145	82	61	156	200	183	18	133		Q7TPD7
ENSMUST00000051133	ENSMUSG00000096442	10	24076500	24077534	1	4	17	18	6	8	0	0	0	0	0	0		Q5QD07
ENSMUST00000051137	ENSMUSG00000044265	7	104153013	104164831	-1	13	8	3	5	11	11	0	0	0	0	0	Q8BU90	
ENSMUST00000051139	ENSMUSG00000044098	3	103914120	103966636	1	6	4	7	28	23	0	90	230	116	38	109		Q80T69
ENSMUST00000051145	ENSMUSG00000040389	3	108591279	108645719	1	12	8	23	69	26	7	48	216	103	34	97		Q8CGF6
ENSMUST00000051153	ENSMUSG00000063364	2	150310935	150362765	-1	0	6	18	0	13	6	0	3	0	2	0	Q9CXH3	
ENSMUST00000051159	ENSMUSG00000044542	11	50950806	50953765	-1	8	5	5	6	5	5	0	0	0	0	0		P97458
ENSMUST00000051160	ENSMUSG00000050761	16	18620319	18622403	-1	0	0	0	98	10	1	0	2	0	0	0	B2RR03	
ENSMUST00000051163	ENSMUSG00000045876	18	37355121	37358604	1	28	19	55	55	37	10	0	0	0	0	2	Q91XZ2	
ENSMUST00000051169	ENSMUSG00000039990	7	133637543	133672971	1	26	10	32	102	19	5	21	93	88	10	57	E9Q9F9	
ENSMUST00000051171						0	0	0	0	0	0	5	68	59	4	28		
ENSMUST00000051176	ENSMUSG00000047420	6	35312668	35326141	-1	12	10	18	4	20	7	0	1	0	3	0		Q8BR21
ENSMUST00000051179						26	26	35	585	22	16	1	4	3	0	2		
ENSMUST00000051184	ENSMUSG00000046168	14	61607482	61611916	1	3	4	7	5	2	3	6	24	13	3	12		Q2TUM3
ENSMUST00000051186	ENSMUSG00000050697	15	5143861	5181899	1	14	12	20	54	24	8	985	2265	1340	693	762		Q5EG47
ENSMUST00000051201	ENSMUSG00000043925	7	102484114	102488307	-1	11	4	21	6	8	6	0	0	0	0	0	E9PX47	
ENSMUST00000051207	ENSMUSG00000048807	11	3907021	3914664	-1	32	0	49	440	0	0	332	265	162	62	182		
ENSMUST00000051209	ENSMUSG00000002265	7	6703892	6730421	-1	55	44	170	85	68	24	0	0	0	0	3		Q3URU2
ENSMUST00000051212						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000051221	ENSMUSG00000020864	11	94328001	94341841	1	0	0	5	103	0	0	27	62	30	15	0		Q5SUE8
ENSMUST00000051224						48	27	86	35	43	30	0	0	0	0	0		
ENSMUST00000051226	ENSMUSG00000033065	15	98092589	98132447	1	35	0	10	45	40	12	44	0	36	0	54		P47857
ENSMUST00000051234	ENSMUSG00000036748	19	46329812	46338660	-1	0	9	0	12	0	0	668	738	351	224	177		Q9CXX9
ENSMUST00000051236	ENSMUSG00000049866	1	88673125	88702221	-1	6	4	7	53	10	3	0	2	2	1	1		P61208
ENSMUST00000051238	ENSMUSG00000044798	9	38827615	38828682	1	5	2	4	1	2	2	0	0	0	0	0	Q7TRB9	
ENSMUST00000051239	ENSMUSG00000043461	3	69819542	69859940	-1	5	0	3	3	3	0	0	0	0	0	0		Q925E8
ENSMUST00000051241	ENSMUSG00000044786	7	28376784	28379255	-1	20	5	52	215	38	12	6508	39570	5570	539	6455	Q3U3D2	P22893
ENSMUST00000051249	ENSMUSG00000046947	6	39573873	39588769	1	3	1	9	0	0	0	207	321	244	23	167	E9QL72	
ENSMUST00000051253	ENSMUSG00000059857	3	109780040	110144011	-1	4	2	8	32	2	0	0	0	0	0	0	Q8BPN6	
ENSMUST00000051256	ENSMUSG00000033460	X	134717963	134721917	1	0	0	0	0	0	0	0	0	0	0	0		Q9CX83
ENSMUST00000051259	ENSMUSG00000060470	8	95017692	95045247	1	19	10	35	27	28	9	1104	2994	1386	210	1248		Q8R0T6
ENSMUST00000051264	ENSMUSG00000047798	11	115116214	115133992	-1	0	0	12	0	0	0	5017	12179	5018	1119	4707		Q6SJQ7
ENSMUST00000051272	ENSMUSG00000042845	2	164189231	164190608	-1	10	5	58	15	10	5	0	0	0	0	2	Q3V469	Q9JHY3
ENSMUST00000051274	ENSMUSG00000047894	14	51195486	51195923	-1	5	0	6	2	6	2	0	0	0	2	0	W0UV59	Q64438
ENSMUST00000051277	ENSMUSG00000045052	19	60466733	60468304	-1	14	7	27	251	17	8	0	0	0	0	0		Q6VMN6
ENSMUST00000051283	ENSMUSG00000047720	6	129322164	129331796	-1	8	7	5	3	4	3	1	8	2	0	1	Q8C634	
ENSMUST00000051293	ENSMUSG00000044197	5	139377697	139396415	1	24	0	0	49	0	0	2078	3794	1953	329	1357		Q99LE2
ENSMUST00000051297	ENSMUSG00000043050	16	10787936	10788655	-1	6	1	20	64	10	3	0	0	0	0	0	Q91XK4	
ENSMUST00000051301	ENSMUSG00000043991	18	36281097	36301521	1	78	77	286	412	82	43	218	401	260	44	291		P42669
ENSMUST00000051308	ENSMUSG00000030771	7	112368308	112413104	1	9	0	42	18	16	4	0	0	0	0	0		Q9D5U9
ENSMUST00000051309	ENSMUSG00000027965	3	114904078	115125722	1	3	3	0	1	6	5	0	0	0	0	0		P63056
ENSMUST00000051310	ENSMUSG00000037697	14	45593174	45658143	-1	12	12	5	53	19	26	26	177	55	26	105	F8WHP5	
ENSMUST00000051312	ENSMUSG00000050397	9	98955607	98956847	1	1	1	9	285	5	4	0	0	0	0	0	Q2TVT7	O88470
ENSMUST00000051330	ENSMUSG00000043126	10	61475245	61476937	-1	10	4	23	331	17	14	1	2	2	0	0	Q8BG14	
ENSMUST00000051341	ENSMUSG00000045665	15	102279456	102281744	1	16	5	22	96	23	13	1153	1192	701	210	576		Q921Y4
ENSMUST00000051344	ENSMUSG00000026141	1	24261890	24587472	-1	7	4	2	0	4	4	0	0	0	0	0	F8WHV4	
ENSMUST00000051346	ENSMUSG00000047545	7	103740294	103741238	-1	5	1	8	0	2	5	0	0	0	0	0	Q0VBH3	
ENSMUST00000051355	ENSMUSG00000047794	7	105180313	105181400	-1	9	6	9	9	8	0	0	0	0	0	0	Q7TRN7	
ENSMUST00000051356	ENSMUSG00000004056	7	27591552	27640826	1	0	3	53	0	5	6	2868	3023	1667	325	1458	Q3TY95	Q60823
ENSMUST00000051358	ENSMUSG00000048520	5	21483847	21645634	-1	4	10	12	8	14	5	0	0	2	1	2		Q8CDU4
ENSMUST00000051363						23	19	134	69	21	10	118	320	85	10	42		
ENSMUST00000051364	ENSMUSG00000044709	7	19564946	19573823	-1	0	0	0	0	0	0	425	675	283	125	163		Q9CWY4
ENSMUST00000051377	ENSMUSG00000043671	7	35685165	35754454	-1	48	32	51	72	67	33	65	161	95	18	124		Q71B07
ENSMUST00000051379	ENSMUSG00000045636	8	40990914	41133726	-1	10	10	3	25	23	14	6594	29828	18306	5555	11544		
ENSMUST00000051386	ENSMUSG00000038775	9	119052778	119071525	1	0	0	0	0	0	0	0	0	0	0	0	G5E8C6	
ENSMUST00000051389	ENSMUSG00000030554	7	67730161	67759742	-1	0	0	0	354	0	16	11	6	11	2	0		Q70IV5
ENSMUST00000051390	ENSMUSG00000049600	7	13004936	13009822	-1	0	4	0	170	0	0	101	131	57	5	43	Q52KG4	
ENSMUST00000051395	ENSMUSG00000020493	11	87089153	87108708	-1	67	71	73	53	80	26	87	121	147	10	34		Q8BHE0
ENSMUST00000051396	ENSMUSG00000026600	1	156424525	156474331	-1	0	0	0	0	0	0	2161	3612	2118	87	986		Q61263
ENSMUST00000051400	ENSMUSG00000047155	4	115106323	115134281	-1	0	0	0	0	0	0	0	0	0	0	0		Q6A152
ENSMUST00000051401	ENSMUSG00000047501	5	134945119	134946934	-1	14	5	33	45	15	7	0	0	0	0	2	Q3UM35	O35054
ENSMUST00000051408	ENSMUSG00000043850	3	58844028	58885340	-1	0	0	0	0	1	0	0	0	0	0	0	B7ZNE8	Q8K445
ENSMUST00000051414	ENSMUSG00000045330	X	62283499	62292078	1	0	0	0	0	6	0	0	0	0	0	0	Q9D4D2	
ENSMUST00000051416	ENSMUSG00000026986	2	24002910	24049394	-1	0	0	0	0	0	0	0	203	16	64	0	A2AQK4	Q91VF2
ENSMUST00000051419	ENSMUSG00000027200	2	124089969	124667770	1	0	0	0	0	0	0	0	0	0	0	0		Q76KF0
ENSMUST00000051430	ENSMUSG00000001672	8	109947914	109962203	-1	9	19	26	57	28	15	0	0	1	0	0	G3X9A4	
ENSMUST00000051431	ENSMUSG00000047539	1	182313102	182341629	-1	16	18	31	40	27	13	207	909	415	97	251		Q8BIG4
ENSMUST00000051435	ENSMUSG00000034538	7	7171330	7183562	1	14	14	16	31	24	9	0	11	5	5	7	Q8BFS8	
ENSMUST00000051437						2	2	0	2	2	1	0	0	0	0	0		
ENSMUST00000051442	ENSMUSG00000047910	18	37477814	37483038	1	37	34	125	54	44	15	0	0	2	0	1	Q91Y03	
ENSMUST00000051443	ENSMUSG00000050315	3	123076519	123236149	-1	28	26	81	36	55	20	0	0	1	1	2		Q91YE8
ENSMUST00000051446	ENSMUSG00000037876	10	67096125	67256326	1	0	0	0	30	0	0	0	3	0	0	0	A0A0A0MQ98	
ENSMUST00000051453	ENSMUSG00000050431	14	50186262	50187218	-1	2	1	1	1	2	1	0	0	0	0	0	E9Q8M3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000051454	ENSMUSG00000048388	2	83812636	83883486	1	14	14	26	71	14	15	0	0	1	0	3		Q14CH0
ENSMUST00000051477	ENSMUSG00000006699	4	137319696	137357720	-1	16	14	43	46	22	16	7047	32052	9744	8088	5484		P60766
ENSMUST00000051479	ENSMUSG00000040936	9	120960268	121277197	-1	0	0	0	0	0	0	1	0	0	0	0	E9QKJ7	
ENSMUST00000051482	ENSMUSG00000045053	17	83585957	83631895	-1	13	21	20	285	26	19	0	0	0	0	2		P59053
ENSMUST00000051484	ENSMUSG00000047238	X	153036166	153037575	-1	4	1	26	55	13	2	0	1	0	3	0	Q3UKU3	Q9NWG9
ENSMUST00000051490	ENSMUSG00000050002	13	58157649	58164693	1	0	0	64	33	16	0	151	272	108	89	122		Q8R0J8
ENSMUST00000051493						18	6	10	33	22	7	0	1	1	0	3		
ENSMUST00000051504	ENSMUSG00000043631	13	49504810	49532789	1	62	65	111	69	30	34	3	11	5	2	7		Q5FW85
ENSMUST00000051505	ENSMUSG00000043354	7	102973052	102973990	-1	3	3	7	8	4	3	0	0	0	0	0	Q8VH11	
ENSMUST00000051509	ENSMUSG00000029074	4	156034840	156059414	-1	14	6	19	88	3	12	0	0	0	0	0	B1ASM0	
ENSMUST00000051510	ENSMUSG00000039047	3	152714100	152980408	1	0	0	0	0	0	0	31	12	14	0	1	A0A0G2JEE7	
ENSMUST00000051520	ENSMUSG00000049648	4	52855514	52858466	-1	0	0	0	3	0	0	0	0	0	0	0	Q8VG87	
ENSMUST00000051521	ENSMUSG00000049593	3	92763215	92765065	-1	8	1	12	19	4	3	0	0	0	0	0	Q9D6R3	
ENSMUST00000051522	ENSMUSG00000063902	7	83755904	83757356	1	5	0	2	0	10	3	9	5	12	0	0	D3YWG1	
ENSMUST00000051526	ENSMUSG00000045378	17	28934291	28942262	-1	4	4	6	5	7	6	6	11	12	2	2		Q8K459
ENSMUST00000051530	ENSMUSG00000049815	X	127394293	127395898	1	2	1	1	1	2	0	0	0	0	0	0	Q8BVT7	
ENSMUST00000051531						5	6	5	0	8	1	0	0	0	0	0		
ENSMUST00000051532	ENSMUSG00000056379	10	23920356	23921469	1	4	4	3	3	3	3	0	0	0	0	0		Q923Y8
ENSMUST00000051540	ENSMUSG00000045514	6	40571357	40572417	1	14	0	24	11	8	8	0	3	0	0	0	Q8VF31	
ENSMUST00000051552	ENSMUSG00000042371	11	61672781	61720826	-1	0	0	0	0	13	0	0	0	0	0	0		Q5SWY8
ENSMUST00000051558	ENSMUSG00000041235	4	8690406	8867659	1	53	36	13	27	26	33	1311	3121	2650	249	2043		A2AJK6
ENSMUST00000051563	ENSMUSG00000050030	14	50139702	50140637	-1	2	0	4	0	2	2	0	0	0	0	0	Q7TRM6	
ENSMUST00000051565	ENSMUSG00000040936	9	120960268	121277197	-1	25	13	9	25	18	7	0	0	0	0	0	H7BX20	
ENSMUST00000051569	ENSMUSG00000050424	X	73033981	73037103	-1	15	4	12	14	18	4	0	0	0	0	0		Q5DTT8
ENSMUST00000051572	ENSMUSG00000045954	1	51289126	51302960	1	23	10	70	17	20	10	1	3	5	176	65		Q63918
ENSMUST00000051574	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JIM1
ENSMUST00000051589	ENSMUSG00000025894	9	4294793	4309494	-1	57	57	94	146	77	46	44	206	57	120	49		Q9CQF6
ENSMUST00000051594	ENSMUSG00000021697	13	108316332	108407782	1	11	12	46	27	22	9	462	618	436	41	174		Q8BH88
ENSMUST00000051600	ENSMUSG00000051593	4	52910833	52919172	-1	7	2	8	2	0	2	0	0	0	0	0	Q8VGA0	
ENSMUST00000051601	ENSMUSG00000050671	12	87278638	87299705	-1	0	5	8	0	10	0	0	0	0	0	0	F6YQQ5	
ENSMUST00000051605	ENSMUSG00000027203	2	125247190	125258608	1	8	11	18	210	19	6	10	25	2	8	10	Q9CQ43	
ENSMUST00000051614	ENSMUSG00000046723	8	40675094	40682199	1	15	7	35	3	8	1	0	0	0	0	0		Q9R160
ENSMUST00000051620	ENSMUSG00000044795	11	69391925	69395631	-1	0	0	1	0	0	1	13	55	35	4	29		Q5NCY3
ENSMUST00000051629						4	3	0	10	10	2	0	0	0	0	0		
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ENSMUST00000051653	ENSMUSG00000095322	9	39510783	39511718	-1	1	4	8	1	4	2	0	0	0	0	0	Q9EQB7	
ENSMUST00000051665	ENSMUSG00000046658	5	143249697	143270022	-1	2	0	418	677	0	6	0	0	4	1	0	G3XA34	
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ENSMUST00000051672	ENSMUSG00000046718	8	71534264	71537437	-1	4	8	17	90	7	3	71	193	37	243	206		Q8R2Q8
ENSMUST00000051674	ENSMUSG00000050966	4	134003330	134018841	-1	21	16	52	80	33	12	993	3205	1444	90	678		Q8K3Y3
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ENSMUST00000051687	ENSMUSG00000043192	8	5639584	5640996	1	17	5	34	18	21	24	1240	936	1067	107	538	F6SAC3	
ENSMUST00000051691	ENSMUSG00000025060	19	47579678	47645246	1	4	1	0	2	0	13	534	857	2160	159	1195		O54988
ENSMUST00000051698	ENSMUSG00000022587	15	74955051	74959905	1	16	0	25	31	1	0	18	0	9	9	3	Q99JA5	
ENSMUST00000051704	ENSMUSG00000029516	5	115845278	116008947	1	43	27	199	165	53	27	54	43	106	0	32	E9QL53	
ENSMUST00000051705	ENSMUSG00000039639	16	92346001	92359468	-1	11	13	36	43	15	13	0	0	0	0	0	Q545H6	P23299
ENSMUST00000051706	ENSMUSG00000047619	9	6265028	6266547	-1	14	7	20	7	13	6	0	0	0	0	0		Q9DAF3
ENSMUST00000051711	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	0	0	0	18	0	E9QMP6	
ENSMUST00000051714	ENSMUSG00000045587	7	24709242	24714535	1	6	5	11	16	13	13	0	2	1	1	1	Q810N3	
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ENSMUST00000051756	ENSMUSG00000050377	13	112522810	112580662	-1	21	23	33	23	29	8	0	2	1	0	4		Q8K5B1
ENSMUST00000051757	ENSMUSG00000046959	5	108669878	108675569	-1	16	0	49	25	30	10	0	0	3	0	6	Q3UPH6	P58735
ENSMUST00000051758	ENSMUSG00000066735	5	129941970	129986692	1	32	24	17	23	29	5	141	333	240	26	108	Q0VGU5	Q6TEK5
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ENSMUST00000051768	ENSMUSG00000050865	19	13749108	13750055	1	5	6	6	5	1	7	0	0	0	0	0	Q8VGP8	
ENSMUST00000051772	ENSMUSG00000049670	19	42074939	42086370	-1	20	14	24	54	22	22	2	0	0	0	1		Q6PGF2
ENSMUST00000051773	ENSMUSG00000045518	10	80494835	80517276	1	107	78	281	634	104	56	2	12	10	6	12		Q8K557
ENSMUST00000051777	ENSMUSG00000047248	7	100372233	100470152	1	8	10	40	17	27	8	418	482	745	52	493		Q52KB6
ENSMUST00000051784	ENSMUSG00000021532	13	68582248	68592279	1	18	6	15	72	19	9	32	79	45	38	29		Q8BSN9
ENSMUST00000051795	ENSMUSG00000060441	7	104263386	104288094	-1	0	0	0	0	0	0	0	0	0	0	0	D3YYU4	
ENSMUST00000051803	ENSMUSG00000024885	19	3913493	3929761	-1	13	10	22	28	18	11	5675	6288	4120	1510	2608	Q3TX25	Q80VQ0
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ENSMUST00000051809	ENSMUSG00000046916	10	5593728	5606787	1	15	15	12	28	8	4	9	15	5	41	8		Q8R411
ENSMUST00000051810	ENSMUSG00000040428	7	45526330	45554229	1	0	0	0	0	0	5	0	0	4	0	0	D3Z3Y7	
ENSMUST00000051822	ENSMUSG00000061559	9	54714735	54734519	-1	0	0	0	0	0	0	37	276	138	513	92	A0MNP4	Q9ERF3
ENSMUST00000051826						5	12	14	79	16	6	0	0	1	0	0		
ENSMUST00000051831	ENSMUSG00000040812	2	90782727	90834437	1	4	0	10	3	3	0	0	0	0	0	0		Q8CDK2
ENSMUST00000051839	ENSMUSG00000046240	9	37367368	37386572	1	29	14	39	134	32	15	0	0	0	0	4	B2RSY3	Q640R3
ENSMUST00000051846	ENSMUSG00000060613	19	40153353	40187333	-1	8	8	1	6	7	4	0	0	0	9	0		Q91W64
ENSMUST00000051849	ENSMUSG00000037994	3	135307700	135345387	1	5	0	0	0	7	0	0	0	0	0	0		Q5BKR2
ENSMUST00000051857	ENSMUSG00000045440	12	55598917	55602018	1	11	11	21	695	32	12	0	0	0	0	0		Q9JMC2
ENSMUST00000051862	ENSMUSG00000078161	3	154663859	154767790	1	4	3	7	0	7	3	1	0	0	1	0	Q8BVT3	
ENSMUST00000051864	ENSMUSG00000050824	17	25489875	25497288	-1	17	14	18	76	39	0	0	0	0	0	0		O08858
ENSMUST00000051867	ENSMUSG00000031683	8	78804865	78821140	-1	1	1	0	18	1	0	38	130	33	45	39	Q542U7	P62313
ENSMUST00000051869	ENSMUSG00000034035	4	116596654	116600266	1	0	0	0	0	6	2	6	0	0	0	0		Q8CE13
ENSMUST00000051870	ENSMUSG00000047710	8	13869641	13881639	1	26	21	49	29	26	23	90	187	72	27	82		Q8K327
ENSMUST00000051873	ENSMUSG00000025648	9	108991778	109032228	1	24	20	67	29	44	22	7427	11031	7331	1460	6137		Q6DTY7
ENSMUST00000051874	ENSMUSG00000051258	13	21611020	21612004	-1	7	5	4	6	7	6	0	0	0	0	0	Q5SZZ8	
ENSMUST00000051888	ENSMUSG00000045176	11	69059717	69061578	1	8	13	67	402	26	5	1015	1902	832	192	641		Q9D6W8
ENSMUST00000051906	ENSMUSG00000059708	X	36608314	36645395	-1	10	9	9	109	32	12	7	22	7	3	4		A2A3V1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000051907	ENSMUSG00000045004	4	141088333	141112760	1	21	18	42	26	17	15	1	0	0	0	3		Q8BHW6
ENSMUST00000051912	ENSMUSG00000030498	7	51862015	51994975	1	3	3	0	11	3	0	1	29	4	0	0		P11862
ENSMUST00000051915	ENSMUSG00000039599	14	20348162	20383489	1	0	0	2	0	0	0	11	38	0	8	0		Q6NSV7
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ENSMUST00000051929	ENSMUSG00000026739	2	18677018	18686629	1	9	8	19	0	7	1	17	34	27	54	41	Q2LC58	P25916
ENSMUST00000051934	ENSMUSG00000044715	12	105685352	105703047	1	25	18	76	49	22	18	318	1131	377	764	215	Q3TBR1	Q8BGR8
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ENSMUST00000051943	ENSMUSG00000050366	7	140201743	140202800	-1	14	6	11	12	13	7	0	0	0	0	0	Q7TRU0	
ENSMUST00000051947	ENSMUSG00000017837	11	100619244	100627607	1	2	0	0	0	0	0	77	10	69	10	0		Q9CR56
ENSMUST00000051950	ENSMUSG00000042605	5	121711337	121816493	1	3	0	0	18	8	9	28	134	96	7	67	E9QM77	
ENSMUST00000051955	ENSMUSG00000049517	13	90923131	90924942	1	2	0	2	73	0	5	1223	2411	1015	3752	476		P62267
ENSMUST00000051965	ENSMUSG00000045337	8	21905376	21906412	-1	0	0	0	0	1	0	0	0	0	0	0		Q8R2I7
ENSMUST00000051973	ENSMUSG00000044903	7	18718090	18727248	1	2	8	9	7	16	7	0	0	0	0	0	Q810J1	
ENSMUST00000051982	ENSMUSG00000048067	7	6514396	6515449	-1	8	3	27	51	11	7	0	0	0	0	0	Q7TQV1	
ENSMUST00000051985						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000051995	ENSMUSG00000031805	8	71676296	71690575	1	9	7	0	0	0	0	716	716	855	56	551		
ENSMUST00000051996	ENSMUSG00000040022	19	59902884	59943654	-1	5	0	63	95	11	7	15	35	47	0	36		G3XA57
ENSMUST00000051997	ENSMUSG00000050100	7	131548773	131556589	1	0	0	0	288	6	11	0	0	0	0	3		P43687
ENSMUST00000052011	ENSMUSG00000024642	19	14448072	14598051	-1	2	1	3	36	2	9	284	504	341	4	209		Q62441
ENSMUST00000052012	ENSMUSG00000034055	X	102513975	102644246	-1	0	0	0	0	0	0	0	0	0	0	31		P18826
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ENSMUST00000052029	ENSMUSG00000033526	2	121310561	121355396	-1	0	0	0	0	0	0	0	66	0	0	0		A2ARP1
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ENSMUST00000052068	ENSMUSG00000046402	9	98422961	98446575	1	27	15	125	123	27	21	2	7	1	199	43	Q58EU7	Q00915
ENSMUST00000052069	ENSMUSG00000037280	15	100691813	100729376	-1	30	7	9	92	41	5	2298	2583	3566	286	1948		Q8C7U7
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ENSMUST00000052079	ENSMUSG00000032739	17	33638056	33645706	1	8	0	78	0	10	10	6258	10158	7300	467	4927		Q6BCL1
ENSMUST00000052085	ENSMUSG00000049864	9	38367548	38368543	1	4	4	8	1	2	0	0	0	0	0	0	E9PV37	
ENSMUST00000052089	ENSMUSG00000046962	16	97947435	97962621	-1	0	8	222	89	0	17	84	155	113	11	112	G3X9A3	
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ENSMUST00000052104	ENSMUSG00000027318	2	131050591	131063814	-1	5	3	18	111	16	2	0	0	0	0	0	A2AP51	Q923W9
ENSMUST00000052107	ENSMUSG00000045822	2	164805098	164822130	1	18	12	42	40	22	8	131	236	123	19	88		Q8CFL8
ENSMUST00000052113	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	0	0	0	0	0	Q99M95	Q99M96
ENSMUST00000052119	ENSMUSG00000026819	2	32414487	32451445	-1	7	7	0	0	12	7	0	0	0	0	10		A2ASZ8
ENSMUST00000052120	ENSMUSG00000033285	3	100138180	100162407	-1	6	5	9	0	9	5	249	883	519	558	456		Q8BHB4
ENSMUST00000052124	ENSMUSG00000039193	17	74426295	74459108	-1	51	40	63	58	63	24	17	83	53	12	42		Q3UP24
ENSMUST00000052125	ENSMUSG00000044641	2	168081004	168101203	1	43	33	227	235	48	27	1	3	3	0	3		Q9JK83
ENSMUST00000052126	ENSMUSG00000043681	14	34351881	34355433	-1	3	2	3	5	6	1	0	0	0	1	0		Q8CF02
ENSMUST00000052130	ENSMUSG00000047797	X	101376378	101385629	1	0	0	10	0	0	4	0	0	0	0	0		P28230
ENSMUST00000052135	ENSMUSG00000030779	7	122965686	123002557	1	46	24	54	170	63	35	491	1218	1162	241	878		P97868
ENSMUST00000052138	ENSMUSG00000033430	8	112011359	112020528	1	158	141	229	415	224	92	146	685	269	49	253		Q91VL8
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ENSMUST00000052168	ENSMUSG00000043415	2	19657752	19660583	1	9	9	28	182	18	11	51	129	43	10	47		Q9CUB6
ENSMUST00000052172	ENSMUSG00000045382	1	128588199	128592293	-1	1	7	31	8	10	4	1175	3275	897	534	1317		
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ENSMUST00000052176	ENSMUSG00000044092	5	139405280	139415623	1	7	0	8	6	4	0	74	418	51	59	194	Q497Y9	
ENSMUST00000052179	ENSMUSG00000046191	18	37504264	37507822	1	5	12	55	40	17	7	0	0	0	0	1	Q91XZ9	
ENSMUST00000052183	ENSMUSG00000050213	4	125066672	125074042	1	17	9	34	51	28	11	250	768	338	93	244		Q8BIZ6
ENSMUST00000052185	ENSMUSG00000050796	4	155989466	155992649	-1	22	15	46	206	23	11	8	21	9	3	17		Q91Z92
ENSMUST00000052201	ENSMUSG00000047534	12	65132734	65172604	-1	7	0	2	0	0	0	22	61	51	42	6		Q80WQ8
ENSMUST00000052204	ENSMUSG00000047037	7	55977567	56019954	-1	64	43	136	83	75	27	4	12	5	3	18		Q8BHK1
ENSMUST00000052209	ENSMUSG00000031885	8	105170674	105217989	1	0	0	0	46	8	2	0	0	262	1	192		Q08024
ENSMUST00000052211	ENSMUSG00000044526	17	56511248	56512483	-1	7	5	3	430	20	6	1	0	0	0	0	Q9DAH2	
ENSMUST00000052224	ENSMUSG00000043430	5	36204021	36206568	1	26	25	56	38	32	11	0	0	0	0	0		
ENSMUST00000052236	ENSMUSG00000048232	4	45034247	45084604	-1	41	21	64	75	43	10	165	191	195	23	194		Q7TQF2
ENSMUST00000052239	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	1	0	0	0	0	0	0	15	D3Z1W6	
ENSMUST00000052245	ENSMUSG00000044835	1	161142691	161170498	1	0	0	0	0	0	0	0	0	0	0	0	G3X9E0	
ENSMUST00000052248	ENSMUSG00000071644	19	8967041	8978479	1	0	33	14	67	24	15	1867	3127	1404	462	1674	Q4FZK2	Q9D8N0
ENSMUST00000052249	ENSMUSG00000041632	13	99344786	99415561	1	18	6	22	17	17	15	34	65	24	19	39		Q8BK72
ENSMUST00000052250	ENSMUSG00000045333	8	87661810	87959595	-1	35	25	0	7	47	25	0	0	0	0	0		Q80TS5
ENSMUST00000052254	ENSMUSG00000063116	11	74334282	74335229	-1	11	7	7	5	6	6	0	0	0	0	0	Q8VFX7	
ENSMUST00000052258	ENSMUSG00000029596	5	120458186	120472810	-1	5	6	13	33	24	8	7	11	1	2	1		Q8R238
ENSMUST00000052266	ENSMUSG00000029763	6	33249085	33973979	1	24	14	35	28	21	18	138	299	295	71	199		O35382
ENSMUST00000052277	ENSMUSG00000046192	6	24444865	24515067	-1	12	9	14	16	10	8	0	0	0	0	0		Q8CDK3
ENSMUST00000052281	ENSMUSG00000043439	11	97627389	97629702	-1	12	10	20	766	34	3	16	31	10	10	32		Q7TNS8
ENSMUST00000052283	ENSMUSG00000046942	X	79623231	79671435	-1	8	0	12	14	9	9	0	0	0	0	0		Q9CWV4
ENSMUST00000052285	ENSMUSG00000050343	11	50969020	50969967	1	6	6	7	3	13	3	0	0	0	0	0	Q8VGH0	
ENSMUST00000052286	ENSMUSG00000095304	14	25887932	25903100	-1	0	0	0	0	0	0	0	0	0	0	0		Q8K262
ENSMUST00000052290	ENSMUSG00000022325	15	34495304	34530648	1	24	12	0	41	29	0	0	0	0	0	0	Q8K205	
ENSMUST00000052296	ENSMUSG00000048776	6	147252101	147264183	-1	9	6	70	175	25	9	0	0	0	1	6	Q924X4	
ENSMUST00000052300	ENSMUSG00000048197	2	87896177	87897133	1	1	5	3	1	8	4	0	0	0	0	0	A2AVC0	
ENSMUST00000052307	ENSMUSG00000101976	2	85590542	85591486	1	4	1	7	0	2	1	0	0	0	0	0		Q8VF76
ENSMUST00000052315						0	0	0	0	0	0	0	93	39	14	35		
ENSMUST00000052325	ENSMUSG00000005732	16	18239784	18248732	-1	1	3	4	3	0	0	44	138	35	27	60	H7BX22	
ENSMUST00000052332	ENSMUSG00000026782	1	60409619	60481158	1	2	0	10	72	0	0	15	11	3	0	19		P62484
ENSMUST00000052337	ENSMUSG00000045331	16	88626786	88627666	-1	4	1	3	8	10	2	0	0	0	0	0	Q9D6L6	
ENSMUST00000052338						0	2	17	7	0	2	0	0	0	2	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000052342	ENSMUSG00000033767	3	83897655	84040175	-1	0	10	0	0	0	0	359	1580	959	57	470	A0A0B4J1F5	
ENSMUST00000052346	ENSMUSG00000020536	11	60699723	60714186	1	0	0	0	130	0	0	188	184	128	34	183		
ENSMUST00000052347	ENSMUSG00000045569	18	68406907	68429251	-1	8	5	8	7	5	1	0	0	0	0	0	Q544P9	Q64326
ENSMUST00000052348	ENSMUSG00000000154	7	143473721	143499334	1	0	0	4	0	0	0	0	6	3	0	0		
ENSMUST00000052355	ENSMUSG00000035351	10	88146992	88178388	1	0	19	7	30	15	0	26	73	28	108	19		Q9CWU9
ENSMUST00000052366	ENSMUSG00000051663	18	37264938	37267525	1	18	11	34	25	17	4	0	0	0	0	0	Q91Y08	
ENSMUST00000052368	ENSMUSG00000037369	X	18162575	18279936	1	0	0	0	2	0	0	0	147	0	0	0		O70546
ENSMUST00000052374	ENSMUSG00000022391	15	81704248	81729919	-1	27	0	5	0	0	14	423	448	345	47	367		P46061
ENSMUST00000052375	ENSMUSG00000051079	1	144138654	144177372	-1	2	0	2	2	2	4	0	0	0	0	0		Q8K443
ENSMUST00000052380	ENSMUSG00000050957	19	29321344	29325356	-1	4	2	2	6	8	2	2	3	1	81	12	Q545M1	Q9QY05
ENSMUST00000052387	ENSMUSG00000044043	18	37447656	37456350	1	116	105	377	359	160	94	2	2	4	0	4		Q6PB90
ENSMUST00000052396	ENSMUSG00000024317	18	21001341	21028223	1	0	0	0	0	0	0	50	152	33	33	28		Q9CQE0
ENSMUST00000052404	ENSMUSG00000026383	1	119545037	119649000	-1	69	46	226	101	45	34	0	1	2	0	3		Q8BGS1
ENSMUST00000052413	ENSMUSG00000002699	11	34046920	34092295	1	131	97	207	1779	210	115	85	242	156	37	132	B1ATD2	
ENSMUST00000052416	ENSMUSG00000045794	2	181696793	181698442	-1	7	8	18	26	24	3	1	0	0	0	0		Q8BIG2
ENSMUST00000052420	ENSMUSG00000045071	4	59626211	59761439	1	3	0	1	42	10	2	4	15	13	0	15		Q8C4P0
ENSMUST00000052431	ENSMUSG00000050394	X	134748461	134751417	-1	18	0	19	14	0	0	2	5	0	1	2		Q8K3A6
ENSMUST00000052437	ENSMUSG00000049988	8	70616844	70620850	1	17	8	26	40	27	4	3393	3246	1808	341	1567	B9EHD0	Q8K1T1
ENSMUST00000052438	ENSMUSG00000048065	7	107748455	107758032	-1	25	17	20	21	27	9	0	0	0	0	0		Q3KNK3
ENSMUST00000052440						0	1	5	23	3	0	0	6	0	0	6		
ENSMUST00000052441	ENSMUSG00000049624	9	78536488	78588041	-1	27	0	0	52	0	0	125	241	283	51	177		Q8BN82
ENSMUST00000052448	ENSMUSG00000024936	19	5704367	5707101	1	6	4	29	27	20	13	3	26	12	3	26	Q9JJ14	
ENSMUST00000052449	ENSMUSG00000039473	16	5050068	5086285	1	37	27	134	169	47	27	1430	2946	2677	213	2043		Q4G0F8
ENSMUST00000052455	ENSMUSG00000050229	1	172376546	172384099	1	73	83	76	363	76	54	527	1230	637	71	512		Q8C2R7
ENSMUST00000052457	ENSMUSG00000033763	8	110721476	110741400	1	10	17	42	106	19	17	4	3	0	3	25		Q6P9S0
ENSMUST00000052458	ENSMUSG00000028584	4	143349757	143371032	1	6	4	8	101	10	8	0	0	0	0	0		A2VDH3
ENSMUST00000052462	ENSMUSG00000024122	17	24073680	24150924	-1	0	3	5	4	8	0	0	0	33	0	0	F2Z3X6	
ENSMUST00000052472	ENSMUSG00000047454	12	78226655	78684767	1	13	9	14	52	12	7	13	0	0	0	9		Q8BUV3
ENSMUST00000052478	ENSMUSG00000043753	4	89679436	89694772	1	66	54	302	215	46	31	0	16	5	1	11		Q8CFG4
ENSMUST00000052499	ENSMUSG00000051518	15	80260614	80264306	-1	9	4	8	51	6	6	58	117	50	92	50		Q8C6B9
ENSMUST00000052500	ENSMUSG00000043569	X	127721182	127736554	-1	1	0	0	0	1	1	0	0	0	0	0	A2ANA3	
ENSMUST00000052501	ENSMUSG00000047992	18	84720019	84740436	1	19	14	102	43	23	13	0	0	0	1	1		Q8BQT2
ENSMUST00000052502						0	0	1	24	0	0	0	2	0	0	0		
ENSMUST00000052503	ENSMUSG00000043931	6	48718621	48724636	1	10	8	8	7	12	7	15	37	17	85	41	Q8R379	
ENSMUST00000052505	ENSMUSG00000043140	16	8633884	8637712	-1	11	12	42	37	16	12	40	62	44	15	51	Q78HW2	Q9CR76
ENSMUST00000052509	ENSMUSG00000054716	7	127244274	127254803	1	3	2	4	257	14	1	19	64	23	16	21		Q8BJ90
ENSMUST00000052512	ENSMUSG00000050239	16	88610709	88612279	-1	8	4	6	6	8	4	0	0	0	0	0	G3X9A2	
ENSMUST00000052514	ENSMUSG00000047789	13	112660766	112738743	1	41	32	57	40	45	31	92	514	203	97	227		Q8BGD6
ENSMUST00000052515	ENSMUSG00000020836	11	77462411	77470484	1	0	3	3	3	2	0	0	0	0	0	0	B9EIZ7	
ENSMUST00000052516	ENSMUSG00000050158	16	19407039	19423134	-1	2	8	5	1	5	2	0	0	0	0	0	Q8VFA2	
ENSMUST00000052521	ENSMUSG00000020686	11	83421902	83429455	-1	38	23	55	123	38	0	0	0	0	0	0		Q5SSG4
ENSMUST00000052528	ENSMUSG00000050974	12	14494561	14495157	1	0	0	0	15	0	0	0	0	0	0	0	D3Z193	
ENSMUST00000052529	ENSMUSG00000046062	1	133131143	133139783	1	58	29	88	300	57	26	5543	6950	9292	588	5379		Q8BFW3
ENSMUST00000052535	ENSMUSG00000096487	7	106885865	106886815	-1	7	6	6	5	5	1	0	0	0	0	0	Q9EPF8	
ENSMUST00000052539	ENSMUSG00000041263	3	89083981	89093311	-1	4	17	16	0	0	0	51	23	34	0	0		Q8BG26
ENSMUST00000052550	ENSMUSG00000049252	2	40595246	42653624	-1	23	40	37	24	33	13	0	0	0	0	0	A2API5	
ENSMUST00000052556	ENSMUSG00000047368	19	21653309	21685637	1	4	6	1	17	9	5	321	677	342	72	228		Q7M759
ENSMUST00000052558	ENSMUSG00000096436	19	12321887	12322825	-1	4	4	1	1	6	2	0	0	0	0	0	Q7TQR7	
ENSMUST00000052560	ENSMUSG00000044286	14	52034493	52036408	-1	4	8	16	11	7	7	0	1	0	0	0	B2RVX8	
ENSMUST00000052566	ENSMUSG00000051232	11	78507055	78512172	-1	8	2	2	121	15	3	61	180	52	41	41	B2RV69	Q5SYH2
ENSMUST00000052580	ENSMUSG00000050751	8	124369049	124439658	-1	3	2	0	0	0	0	54	40	67	5	35	D3Z077	
ENSMUST00000052588	ENSMUSG00000047141	16	64780351	64786321	-1	7	4	11	8	4	0	204	588	182	56	112		Q9DAU9
ENSMUST00000052590	ENSMUSG00000029616	5	121428590	121452506	-1	0	0	0	30	0	0	943	1852	715	610	712	F8WJI4	
ENSMUST00000052596	ENSMUSG00000050087	11	50354462	50359699	1	2	1	7	177	0	6	0	0	0	0	0	Z4YJN4	
ENSMUST00000052601	ENSMUSG00000046354	8	19194357	19195212	1	1	0	0	1	0	0	0	0	0	0	0		Q7TNV9
ENSMUST00000052602	ENSMUSG00000050390	4	129219578	129261404	-1	0	0	0	298	22	0	0	0	0	0	67		A2A7S8
ENSMUST00000052605	ENSMUSG00000049848	7	19875742	19887965	-1	63	46	240	76	56	33	10	10	2	2	6	Q3TQ88	
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ENSMUST00000052615						15	8	8	40	10	5	0	1418	0	0	0		
ENSMUST00000052622	ENSMUSG00000056313	8	24437180	24438984	-1	10	6	16	13	10	5	0	0	0	141	29		Q9D915
ENSMUST00000052629	ENSMUSG00000037995	1	172481788	172498878	1	0	0	136	0	0	0	0	0	0	0	4		Q05BQ1
ENSMUST00000052631	ENSMUSG00000042821	2	167538195	167542814	1	6	4	10	368	20	9	286	476	239	36	365	Q4FK48	Q02085
ENSMUST00000052645	ENSMUSG00000050174	3	37404910	37420211	-1	0	0	0	28	0	0	0	0	11	0	13	Q3ULU4	
ENSMUST00000052648	ENSMUSG00000059554	10	18213676	18234998	-1	8	7	4	3	7	7	59	234	91	62	105	Q8CEI3	
ENSMUST00000052650	ENSMUSG00000056648	11	96281905	96285315	1	14	12	9	57	14	13	0	0	0	0	0	A2A9Z8	P09632
ENSMUST00000052652	ENSMUSG00000056148	10	127776386	127792697	1	431	341	211	220	536	220	0	66	0	15	36	Q8K5C8	
ENSMUST00000052659	ENSMUSG00000042909	7	104179456	104180406	-1	9	6	3	11	12	1	0	0	0	0	0	Q8VG19	
ENSMUST00000052660	ENSMUSG00000049797	7	104049408	104050352	-1	4	5	10	6	6	6	0	0	0	0	0	Q924X8	
ENSMUST00000052668	ENSMUSG00000048378	11	49160016	49160954	1	6	5	49	14	16	8	0	0	0	0	0	Q8VET2	
ENSMUST00000052670	ENSMUSG00000045174	1	34579657	34590944	1	27	25	86	53	47	18	0	1	0	0	0		Q6NS69
ENSMUST00000052678	ENSMUSG00000025278	14	7817957	7951588	1	81	77	184	104	105	55	234	158	316	81	1006		Q80X90
ENSMUST00000052686	ENSMUSG00000049932	9	44334694	44336077	1	9	8	22	479	32	11	434	499	409	48	219		P27661
ENSMUST00000052690	ENSMUSG00000048400	8	95559133	95575455	-1	13	5	25	8	17	5	0	0	0	0	0	A6H685	
ENSMUST00000052691	ENSMUSG00000050088	17	14943184	14959570	1	0	7	0	33	6	0	120	408	129	205	88		Q9DAY5
ENSMUST00000052699	ENSMUSG00000045098	19	3767421	3818303	1	33	19	56	279	44	24	0	0	0	0	0		Q3U8K7
ENSMUST00000052700	ENSMUSG00000044453	7	30857390	30861564	-1	6	6	28	23	18	8	0	0	2	1	3		Q76JU9
ENSMUST00000052702	ENSMUSG00000047515	6	136827626	136840662	1	8	10	20	3	9	5	0	1	0	3	0		Q810N5
ENSMUST00000052708	ENSMUSG00000048327	2	129268210	129297212	-1	20	17	91	36	22	12	111	185	200	241	109		Q7TS74
ENSMUST00000052712	ENSMUSG00000028233	4	3574875	3616619	1	14	17	71	59	23	16	82	394	168	174	139		Q923W1
ENSMUST00000052715	ENSMUSG00000045268	4	119169513	119174195	-1	28	18	19	28	37	0	30	104	44	4	40	A2A7P4	
ENSMUST00000052716	ENSMUSG00000057396	13	67128228	67141787	1	6	7	12	4	5	2	12	61	18	17	9	Q7M6X3	
ENSMUST00000052718	ENSMUSG00000047959	3	107036169	107038070	1	8	10	30	346	25	10	6	5	13	3	19		P16390
ENSMUST00000052724	ENSMUSG00000049699	9	108986010	108987164	1	6	14	31	10	5	6	0	2	6	0	3		Q99ML8
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000052727	ENSMUSG00000038451	6	124808661	124810619	1	7	8	10	54	10	4	341	531	273	82	147		O88838
ENSMUST00000052730	ENSMUSG00000050425	7	48550965	48558086	-1	4	4	9	2	5	4	0	0	0	0	0	W8W3G3	Q3KNA1
ENSMUST00000052737	ENSMUSG00000051156	19	13704829	13705788	1	3	6	7	7	6	4	0	0	0	0	0	Q8VEZ5	
ENSMUST00000052740	ENSMUSG00000046603	9	122805539	122836334	1	0	0	0	60	0	10	19	86	60	0	22	G3X983	
ENSMUST00000052747	ENSMUSG00000044231	13	47012558	47014850	-1	14	11	15	205	22	7	1	7	0	1	2	Q0VF71	Q8BR37
ENSMUST00000052751	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	0	0	0	0	0	0	0	0		P42866
ENSMUST00000052761	ENSMUSG00000002010	X	73778963	73786897	-1	0	0	0	0	0	0	371	1146	459	1162	419	Q3TGZ3	P70404
ENSMUST00000052774	ENSMUSG00000047583	3	154576431	154597104	-1	0	0	0	35	20	0	25	80	90	39	23		Q8BSA9
ENSMUST00000052776	ENSMUSG00000050799	13	23933773	23934156	-1	5	5	10	53	11	2	0	0	0	0	0		P70696
ENSMUST00000052778	ENSMUSG00000049823	17	34879483	34896867	1	7	2	30	66	7	12	13	16	17	3	20	Q9Z150	
ENSMUST00000052798	ENSMUSG00000071072	10	128058954	128077272	1	13	13	20	125	6	5	72	366	124	33	61		Q9R0Q7
ENSMUST00000052806	ENSMUSG00000042940	10	19644750	19660801	1	12	18	17	8	26	6	1	0	1	0	2	Q8CC72	
ENSMUST00000052825	ENSMUSG00000051502	5	137294629	137295665	1	4	4	18	68	15	10	13	14	8	10	6		Q9CZP0
ENSMUST00000052827	ENSMUSG00000002930	6	56017497	56032689	1	26	25	32	250	59	27	0	1	0	0	2		Q9Z2E4
ENSMUST00000052829	ENSMUSG00000042788	4	43427019	43429134	-1	5	7	17	27	0	13	0	0	0	0	0		A2AIP0
ENSMUST00000052832	ENSMUSG00000049760	17	56607452	56609771	-1	3	6	8	6	9	2	316	396	179	1266	166		Q8R404
ENSMUST00000052835	ENSMUSG00000050493	4	129576815	129578549	-1	9	5	24	21	17	5	0	0	0	0	0		P17257
ENSMUST00000052836	ENSMUSG00000029106	5	34573664	34632308	1	4	0	0	1	0	0	26	0	163	0	82	F8WHZ9	
ENSMUST00000052837	ENSMUSG00000046532	X	98149721	98323215	1	17	19	86	106	30	19	2	8	2	0	4		P19091
ENSMUST00000052838	ENSMUSG00000024294	18	10725548	10818704	1	1336	985	6215	1664	872	397	318	838	530	56	443		Q80SY4
ENSMUST00000052839	ENSMUSG00000031217	X	99136130	99148991	1	5	10	39	401	20	9	60	69	45	5	50	Q544L9	P52795
ENSMUST00000052843	ENSMUSG00000046101	1	9908638	9942085	1	25	24	92	30	32	17	0	12	9	0	9		E9Q956
ENSMUST00000052853	ENSMUSG00000055891	3	107553687	107555073	-1	15	17	21	37	21	12	0	0	0	0	0		Q9CQ84
ENSMUST00000052854	ENSMUSG00000026226	1	86016816	86029958	1	0	11	7	0	8	2	0	0	0	0	0		Q9D9T6
ENSMUST00000052865	ENSMUSG00000050912	9	7764041	7794333	1	14	11	0	68	10	0	321	1531	722	519	561		Q91Z22
ENSMUST00000052867	ENSMUSG00000050299	16	76403209	76403712	-1	2	9	13	0	29	8	11206	14290	6564	23366	4741	Q642K5	
ENSMUST00000052872	ENSMUSG00000061462	11	58994256	59136402	-1	64	20	189	274	35	3	0	0	0	0	0	E9QQ96	
ENSMUST00000052876	ENSMUSG00000050212	4	126147744	126149875	1	7	0	28	170	14	6	0	13	6	0	8		Q8K2Y3
ENSMUST00000052882						2	3	1	0	9	0	530	2305	847	4330	642		
ENSMUST00000052885	ENSMUSG00000013858	10	79974948	79984330	-1	5	3	0	172	0	0	328	1140	393	94	343		Q8CIV2
ENSMUST00000052888						3	0	0	10	4	0	0	0	80	206	67		
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ENSMUST00000052901	ENSMUSG00000094810	9	38498671	38499603	1	1	1	1	3	5	3	0	0	0	0	0	Q7TRC7	
ENSMUST00000052902	ENSMUSG00000045455	10	11609257	11610438	1	16	15	3	0	12	7	15	50	18	61	17		Q9WVA2
ENSMUST00000052904	ENSMUSG00000048655	3	55137339	55172935	1	12	18	18	8	7	0	0	0	0	0	0		Q8BXX9
ENSMUST00000052907	ENSMUSG00000053441	18	58836764	59053678	1	18	15	32	229	32	15	0	0	0	0	0		P59509
ENSMUST00000052910	ENSMUSG00000047565	15	20665219	20666750	-1	11	4	2	4	10	6	0	2	0	0	0		Q32MW3
ENSMUST00000052911	ENSMUSG00000046367	1	134540941	134549682	-1	3	0	11	0	4	6	0	0	0	0	1		A6H684
ENSMUST00000052915	ENSMUSG00000000142	11	108920349	108950783	1	17	4	36	69	14	12	11	3	0	0	19		O88566
ENSMUST00000052919	ENSMUSG00000038150	11	98581256	98587368	-1	28	13	68	91	23	14	279	329	190	104	210		Q9CPZ6
ENSMUST00000052927	ENSMUSG00000037754	2	158665398	158766334	1	0	0	0	0	0	0	39	76	138	21	8	Q544H9	Q8VHQ3
ENSMUST00000052932	ENSMUSG00000043702	14	26659958	26669883	-1	42	55	107	467	64	22	325	773	532	147	292		Q3TIU4
ENSMUST00000052937	ENSMUSG00000046378	7	126945567	126949582	-1	0	0	0	0	0	0	0	0	0	0	0		Q2TA57
ENSMUST00000052939	ENSMUSG00000051146	16	20619215	20621287	-1	5	3	3	132	4	6	23	26	17	6	12	B2RXL5	Q78WH7
ENSMUST00000052946	ENSMUSG00000031965	9	24720812	24774303	-1	101	83	363	162	103	53	1	1	4	0	2		Q9ES03
ENSMUST00000052949	ENSMUSG00000025877	13	55005985	55021385	-1	23	11	55	66	0	17	9540	4670	7026	710	3705		Q3TRM8
ENSMUST00000052965	ENSMUSG00000022141	15	8291225	8444463	-1	25	33	95	150	31	24	1005	2529	2662	336	1798		Q6KCD5
ENSMUST00000052969	ENSMUSG00000020961	12	91638542	91788387	-1	10	19	60	28	32	31	117	105	159	11	113		Q8BZ60
ENSMUST00000052975	ENSMUSG00000045381	1	174041118	174043523	1	7	4	20	7	17	6	0	3	2	0	2	Q7TRV9	
ENSMUST00000052978	ENSMUSG00000043986	13	59725925	59731752	-1	41	24	162	62	51	16	0	0	0	0	0	E9Q5W2	
ENSMUST00000052997	ENSMUSG00000045824	7	102948467	102949507	1	5	8	4	0	7	9	0	0	0	0	0	F8VQ18	
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ENSMUST00000053008	ENSMUSG00000095629	7	13219339	13220289	1	6	6	1	1	4	4	0	0	0	0	0	Q8R256	
ENSMUST00000053013	ENSMUSG00000027788	3	70007613	70028708	1	13	13	29	18	22	15	0	0	0	0	0		Q4ZJM7
ENSMUST00000053015	ENSMUSG00000051695	6	86524492	86526321	-1	18	10	27	300	25	8	2603	3083	2275	463	1627		P60335
ENSMUST00000053016	ENSMUSG00000048349	14	104461676	104467999	-1	18	22	87	185	31	18	0	0	0	0	1		P17208
ENSMUST00000053017	ENSMUSG00000047161	18	15451924	15760157	-1	4	3	0	0	2	0	0	0	0	0	0		Q76EC5
ENSMUST00000053020	ENSMUSG00000034413	17	26414829	26446349	1	75	92	368	206	112	57	10	22	17	5	34		Q0MW30
ENSMUST00000053024	ENSMUSG00000043445	17	24470473	24471591	1	4	0	6	187	6	6	186	324	194	52	106		Q8CHP8
ENSMUST00000053033	ENSMUSG00000044768	1	97606318	97662074	-1	488	428	1315	784	508	280	90	393	260	86	378		Q8VEB3
ENSMUST00000053034	ENSMUSG00000051721	12	4843303	4856925	1	37	36	199	66	52	13	6	33	18	11	15		Q6NV72
ENSMUST00000053035	ENSMUSG00000046589	8	4226827	4237470	1	73	69	102	111	92	54	3	4	4	5	13		Q66JT1
ENSMUST00000053037	ENSMUSG00000045062	18	37341702	37345202	1	15	12	87	34	25	3	0	2	1	0	3	Q8CDY9	
ENSMUST00000053042	ENSMUSG00000048485	4	129425765	129440853	-1	49	0	62	0	0	0	0	1	4	0	5		
ENSMUST00000053043	ENSMUSG00000026069	1	40429570	40465415	1	57	69	104	41	34	33	70	116	84	17	122		P14719
ENSMUST00000053050	ENSMUSG00000044487	2	87191689	87192645	1	7	1	0	2	4	1	0	0	0	0	0	A2ATA0	
ENSMUST00000053063	ENSMUSG00000048878	11	103116231	103119725	1	14	9	51	143	24	14	1334	2931	1715	447	1536		Q8R409
ENSMUST00000053065	ENSMUSG00000045326	3	108853678	108890008	-1	0	0	0	0	50	0	0	0	0	0	0		A2AED3
ENSMUST00000053068	ENSMUSG00000048138	19	25672420	25679010	1	10	13	37	142	26	11	0	0	0	0	0		Q8BG36
ENSMUST00000053073	ENSMUSG00000051486	18	37421418	37425836	1	25	12	45	59	26	16	0	2	0	0	1	Q91UZ8	
ENSMUST00000053075						14	13	20	6	8	6	0	0	0	0	0		
ENSMUST00000053078	ENSMUSG00000050930	8	125669818	125673359	1	20	13	40	136	32	24	60	184	129	12	59		Q8BJS7
ENSMUST00000053079	ENSMUSG00000009073	11	4765845	4849536	-1	0	0	6	0	1	0	0	0	8	3	13		P46662
ENSMUST00000053085	ENSMUSG00000074151	8	94472763	94527272	1	48	21	71	51	53	50	117	255	166	26	591		C3VPR6
ENSMUST00000053086	ENSMUSG00000043945	12	113543908	113546465	1	9	14	22	14	13	8	0	0	0	0	0	B2RSY5	
ENSMUST00000053087	ENSMUSG00000042155	2	69821944	69836651	1	26	19	32	62	29	9	5	23	18	5	5		Q6GQU2
ENSMUST00000053094	ENSMUSG00000038022	6	55203383	55320222	1	42	23	71	45	55	22	5	3	5	2	5		Q3UQI9
ENSMUST00000053098	ENSMUSG00000066798	2	37425500	37443171	-1	140	151	220	0	185	43	231	840	168	294	163		Q8K088
ENSMUST00000053106	ENSMUSG00000048218	15	97244074	97247287	-1	20	15	29	100	22	10	11	15	6	21	50	Q4VBE6	Q80ZD9
ENSMUST00000053107	ENSMUSG00000049128	3	92570902	92573735	-1	16	11	123	15	19	8	0	0	0	2	0	G3X9D9	
ENSMUST00000053109	ENSMUSG00000050428	7	19119859	19140172	1	22	22	54	50	23	13	321	586	296	19	282		Q8BG80
ENSMUST00000053113	ENSMUSG00000045678	19	13633113	13634054	1	5	1	7	3	3	1	0	0	0	0	0	Q8VFQ5	
ENSMUST00000053116	ENSMUSG00000051022	5	39613935	39755475	-1	0	0	2	31	2	0	11	0	4	3	4		O35310
ENSMUST00000053120	ENSMUSG00000044197	5	139377697	139396415	1	0	0	0	0	0	0	0	12	0	0	0	Q8C3F6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000053134	ENSMUSG00000095430	7	11669599	11670519	-1	2	1	0	3	6	2	0	0	0	0	0	Q8K3N7	
ENSMUST00000053144	ENSMUSG00000044055	1	92644218	92648841	-1	3	3	6	1	0	3	1	1	1	2	1	Q497Y7	Q8R448
ENSMUST00000053148	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	0	0	0	0	12		Q99M96
ENSMUST00000053149	ENSMUSG00000050224	16	88750747	88751628	-1	8	5	16	8	7	4	0	0	0	0	0	O88375	
ENSMUST00000053150	ENSMUSG00000050621	9	114982371	114982740	-1	8	10	21	32	9	6	5205	12680	2933	25734	2578		Q6ZWU9
ENSMUST00000053156	ENSMUSG00000051314	7	30818348	30823775	-1	23	25	15	48	32	16	79	260	100	18	50		Q8VCK6
ENSMUST00000053157	ENSMUSG00000059816	4	108367777	108383349	-1	5	3	23	87	11	3	0	0	0	0	0		A2A9G7
ENSMUST00000053168	ENSMUSG00000046196	17	80207460	80217936	1	6	0	6	0	0	0	0	0	0	0	0	Q0VF76	
ENSMUST00000053171	ENSMUSG00000047766	9	60568859	60688158	-1	0	0	0	8	3	3	0	0	0	0	0	D3YUD9	
ENSMUST00000053173						0	0	0	0	0	0	0	0	8	0	9		
ENSMUST00000053175	ENSMUSG00000050666	14	32856756	32939487	1	0	6	6	39	19	6	0	0	0	0	0		T1NXB5
ENSMUST00000053177	ENSMUSG00000043940	5	101832956	102069921	-1	6	18	69	101	104	16	2700	2764	5338	126	3955		Q6VNB8
ENSMUST00000053178	ENSMUSG00000051509	1	174424126	174431552	1	7	3	0	0	3	0	0	1	0	0	0	E9Q5P8	
ENSMUST00000053179	ENSMUSG00000094612	7	108316896	108317828	1	4	4	1	2	1	2	0	0	0	0	0		Q8VG06
ENSMUST00000053180	ENSMUSG00000050645	2	152576086	152580312	-1	4	1	4	3	5	1	0	0	0	0	0		Q8K3I8
ENSMUST00000053183	ENSMUSG00000051853	15	98737621	98763214	-1	391	262	2281	629	217	103	4692	6226	4035	572	3326	Q3U344	P61205
ENSMUST00000053202	ENSMUSG00000043333	4	123787874	123829904	1	19	8	0	0	0	0	0	0	0	0	0		A2AGA4
ENSMUST00000053208	ENSMUSG00000050447	2	50066429	50193569	1	0	0	0	3	0	0	0	0	0	0	0		Q8BPP5
ENSMUST00000053211	ENSMUSG00000048329	11	68556186	68558245	1	15	6	62	76	26	12	13	48	19	8	47		Q8R3N2
ENSMUST00000053215	ENSMUSG00000020573	12	32173473	32208659	-1	3	11	10	10	9	2	854	3037	889	195	505		Q9JHG7
ENSMUST00000053218	ENSMUSG00000048826	17	14195231	14203831	-1	24	16	73	307	51	18	1	0	0	3	8		Q7TN08
ENSMUST00000053225	ENSMUSG00000045591	10	19356560	19358606	1	46	21	37	556	68	32	1	4	3	0	1		Q6PFG8
ENSMUST00000053230	ENSMUSG00000032308	9	57589452	57596233	1	111	76	694	541	105	70	249	557	230	27	270		Q3U3Q1
ENSMUST00000053232	ENSMUSG00000059895	15	73723145	73758766	1	17	19	134	95	48	34	0	41	0	0	0		Q9D658
ENSMUST00000053239	ENSMUSG00000044933	15	78537015	78544345	-1	32	20	89	192	54	26	0	0	1	0	1		P30935
ENSMUST00000053245	ENSMUSG00000013483	11	119307768	119345375	1	0	0	0	2	26	3	0	0	0	0	0		Q99KF0
ENSMUST00000053249	ENSMUSG00000055789	16	58635167	58638739	-1	12	8	0	3	8	6	0	0	0	0	0	Q8BU47	
ENSMUST00000053250	ENSMUSG00000049530	5	45453751	45464149	1	14	7	11	14	9	8	0	0	0	0	0	B2RVW2	
ENSMUST00000053251	ENSMUSG00000031586	8	33782643	33929863	-1	6	0	6	20	0	5	13	32	0	0	0		Q9WVB0
ENSMUST00000053252	ENSMUSG00000048644	8	4257648	4259274	-1	9	5	10	140	7	8	25	51	34	7	24	Q3TYB7	Q8K129
ENSMUST00000053253	ENSMUSG00000091635	5	109156068	109192107	-1	8	3	4	11	0	2	0	0	0	2	0	L7N1X2	
ENSMUST00000053257	ENSMUSG00000048703	5	27495639	27501438	-1	14	10	7	23	15	3	0	0	0	0	0	Q9D9F7	
ENSMUST00000053263	ENSMUSG00000043085	4	141613376	141618633	-1	0	0	0	7	0	0	0	0	0	0	0		Q8R115
ENSMUST00000053265	ENSMUSG00000046573	13	35978797	36117357	-1	11	6	27	26	6	3	16	54	20	29	14		Q8K215
ENSMUST00000053266	ENSMUSG00000041859	1	20802968	20820312	-1	0	14	0	84	0	0	262	312	272	99	294	Q3UI57	P25206
ENSMUST00000053271						55	49	252	0	64	27	2350	4149	3299	342	2341		
ENSMUST00000053273	ENSMUSG00000030287	6	146108299	146502223	-1	0	40	0	0	74	6	224	1816	1032	64	2150		Q9Z329
ENSMUST00000053286	ENSMUSG00000043923	9	44410160	44418003	-1	7	7	8	114	9	3	70	386	123	31	156		Q4VA36
ENSMUST00000053287	ENSMUSG00000051306	5	143710325	143732280	-1	28	13	18	36	10	8	184	213	242	23	145		B2RQC2
ENSMUST00000053288	ENSMUSG00000050910	11	115381916	115396132	1	31	34	170	274	59	34	0	8	1	0	26		A2A6T1
ENSMUST00000053289	ENSMUSG00000095432	13	67538641	67553138	-1	0	0	0	32	0	0	2	3	9	0	0	Q8BTB4	
ENSMUST00000053290	ENSMUSG00000048933	14	49894258	49901941	-1	3	4	5	4	1	1	0	0	0	0	0	Q8VFC8	
ENSMUST00000053293	ENSMUSG00000036721	13	21362827	21369824	1	16	11	16	16	15	7	10	24	10	44	17		Q9Z1D7
ENSMUST00000053298						7	0	0	43	0	0	342	1357	504	3092	370		
ENSMUST00000053304	ENSMUSG00000038330	4	88627320	88634411	-1	11	0	0	0	0	0	0	0	0	0	0	Q3UX49	
ENSMUST00000053306	ENSMUSG00000049112	6	112473683	112489943	-1	99	46	431	397	91	41	1	10	6	0	8		P97926
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ENSMUST00000053318	ENSMUSG00000049349	3	138048761	138067388	-1	8	5	11	5	5	1	0	0	0	0	0	Q8C6Y9	
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ENSMUST00000053355	ENSMUSG00000050967	1	39618406	39651474	-1	107	71	391	406	88	43	9	46	24	5	25		Q8BGC9
ENSMUST00000053361	ENSMUSG00000051043	11	114851152	114872617	1	47	20	142	49	55	19	9	5	2	1	11	I7HPW4	
ENSMUST00000053364	ENSMUSG00000033952	1	139454772	139494091	1	37	39	45	146	50	19	86	113	185	44	128		Q8CJ27
ENSMUST00000053373	ENSMUSG00000044359	X	100590154	100594869	-1	34	38	113	41	48	20	1	4	5	0	4	Q0VBT7	Q9JJS7
ENSMUST00000053375	ENSMUSG00000050921	X	107088492	107104974	1	0	8	1	2	0	0	31	77	35	93	85		Q8BFU7
ENSMUST00000053376	ENSMUSG00000038347	17	13482553	13761825	-1	4	5	13	9	6	4	0	0	0	0	0	Q9DAF6	
ENSMUST00000053386	ENSMUSG00000043162	6	57686576	57692078	-1	36	28	34	155	42	25	24	113	39	63	39		Q9D1C3
ENSMUST00000053389	ENSMUSG00000048480	1	74191785	74194631	-1	3	3	0	0	4	0	1407	2513	909	192	703		Q810W6
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ENSMUST00000053410	ENSMUSG00000045252	7	25072567	25083492	1	0	0	0	334	47	0	188	94	48	42	95		Q8BY46
ENSMUST00000053413	ENSMUSG00000048895	11	80477023	80481184	1	23	15	64	260	35	18	118	308	185	18	94	Q542T9	P61809
ENSMUST00000053414	ENSMUSG00000052407	4	83525545	83864670	1	10	22	12	32	10	13	4	5	0	0	11		E9Q1U1
ENSMUST00000053419	ENSMUSG00000049799	4	94636653	94650144	-1	27	30	25	412	32	15	1	1	0	0	3		Q8BZT5
ENSMUST00000053426	ENSMUSG00000038582	5	122284365	122324281	1	12	4	17	133	22	9	402	1008	546	120	442		Q6NVE9
ENSMUST00000053427	ENSMUSG00000049680	11	5713417	5762376	-1	0	13	0	0	17	11	0	0	0	0	0		Q5NCI0
ENSMUST00000053429	ENSMUSG00000051390	17	33915904	33919324	1	11	9	32	106	35	9	1080	1286	774	181	702	Q3TXW4	Q9Z0G7
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ENSMUST00000053440	ENSMUSG00000039963	11	119228572	119265236	1	20	2	47	5	23	7	1	0	0	0	1		Q8BI79
ENSMUST00000053441	ENSMUSG00000046258	8	55870912	55906948	-1	7	9	4	14	6	4	0	0	0	0	0	G3X9B5	
ENSMUST00000053445	ENSMUSG00000066129	7	139894696	139941537	1	0	0	52	54	0	0	0	0	0	0	0		Q0KK55
ENSMUST00000053451	ENSMUSG00000052673	12	69371835	69372458	-1	0	0	0	172	8	11	0	13	5	1	3	F6RFI0	
ENSMUST00000053456	ENSMUSG00000050379	X	36911326	36991794	-1	12	11	9	7	7	2	198	821	249	128	192		Q9R1T4
ENSMUST00000053458	ENSMUSG00000050545	12	4746216	4769267	-1	14	16	38	97	11	12	0	1	0	0	0		Q497Q6
ENSMUST00000053459	ENSMUSG00000021411	13	34627840	34652681	-1	0	0	0	0	0	0	0	6	1	3	7		Q8JZU6
ENSMUST00000053460	ENSMUSG00000051802	16	88895968	88896450	-1	0	4	1	2	2	3	0	0	0	0	0	F8VQ65	
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ENSMUST00000053464	ENSMUSG00000043073	7	104768160	104777470	-1	10	12	32	30	15	15	0	0	0	0	0		
ENSMUST00000053467	ENSMUSG00000022306	15	40655042	41104592	1	27	21	77	99	32	13	0	0	0	0	1		Q8CCH7
ENSMUST00000053469	ENSMUSG00000025956	1	64606473	64617242	-1	10	4	23	130	25	15	0	29	0	4	4		Q9CQL0
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000053491	ENSMUSG00000090125	4	124656807	124660655	1	8	5	24	608	32	13	0	0	0	0	0		P21952
ENSMUST00000053498	ENSMUSG00000045078	5	142990893	143112994	-1	29	17	53	109	46	23	1215	2469	2405	145	1599		P58283
ENSMUST00000053499	ENSMUSG00000039342	1	72642980	72700564	-1	6	17	9	13	21	7	0	0	0	0	0		A2RT91
ENSMUST00000053506	ENSMUSG00000006464	19	4886898	4906627	-1	107	95	233	147	148	70	23	33	29	9	31	Q3V3N7	
ENSMUST00000053521	ENSMUSG00000062040	7	29893333	29906572	-1	3	0	0	0	0	0	0	0	0	13	0		P10077
ENSMUST00000053536	ENSMUSG00000041598	11	113726850	113751881	-1	0	0	0	115	20	12	820	787	558	113	416		Q9JM96
ENSMUST00000053540	ENSMUSG00000046432	X	136270253	136271978	1	0	0	0	0	0	2	0	0	48	18	2		Q9WTZ9
ENSMUST00000053543	ENSMUSG00000049537	5	83278145	83355195	-1	1	0	3	4	7	0	0	0	0	0	0		Q8BFZ1
ENSMUST00000053558	ENSMUSG00000050914	8	45996902	45999867	-1	0	0	0	32	6	0	117	148	67	230	60		Q569N2
ENSMUST00000053568	ENSMUSG00000049556	9	56618475	56685253	-1	14	13	56	26	35	25	0	0	0	0	0		Q9D1T0
ENSMUST00000053569	ENSMUSG00000043088	6	113458484	113470758	1	0	0	0	16	15	0	0	0	2	0	0		Q8BH06
ENSMUST00000053575	ENSMUSG00000049124	17	26098872	26099257	-1	0	8	12	29	10	2	168	350	135	842	114		P62309
ENSMUST00000053577	ENSMUSG00000045394	17	87635979	87651106	1	10	7	17	50	11	3	5	1	8	7	10		Q99JW5
ENSMUST00000053583	ENSMUSG00000051238	9	21955753	21958270	1	11	16	17	71	24	17	43	63	42	13	33		Q8VCI7
ENSMUST00000053593	ENSMUSG00000050029	X	51003912	51018018	-1	2	1	20	19	5	2	1284	2721	1369	1379	948		Q8BU31
ENSMUST00000053594	ENSMUSG00000045867	10	95174746	95324097	-1	52	42	230	126	33	32	78	236	70	121	60	Q549T4	O88843
ENSMUST00000053597	ENSMUSG00000045045	19	4611785	4615667	-1	15	9	31	215	38	12	0	4	0	0	11		Q80XU8
ENSMUST00000053599	ENSMUSG00000044985	17	37805069	37806190	1	7	5	7	5	3	1	0	0	0	0	0	Q8VGW6	
ENSMUST00000053604	ENSMUSG00000051219	4	124609931	124610803	-1	3	7	15	7	2	1	0	0	0	0	0	Q9CXW6	
ENSMUST00000053611	ENSMUSG00000043319	12	102899306	102900534	1	7	1	7	2	0	4	0	0	0	0	0		A6H666
ENSMUST00000053612	ENSMUSG00000043939	17	48151896	48167270	-1	32	18	34	22	0	10	965	4646	1199	1334	900	Q8BNV8	
ENSMUST00000053635						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000053640	ENSMUSG00000045730	18	62177817	62179959	-1	22	31	160	176	41	18	1374	7634	1934	364	1756		P18762
ENSMUST00000053646	ENSMUSG00000044199	10	81497745	81500132	-1	75	48	250	380	78	36	3675	3398	2380	317	1342		Q9Z0L1
ENSMUST00000053647	ENSMUSG00000095831	6	42744039	42744992	1	3	5	8	6	4	2	0	0	0	0	0	Q7TRV7	
ENSMUST00000053652	ENSMUSG00000051153	6	131686532	131687495	-1	2	2	7	5	1	3	0	0	0	0	0	Q53Z46	
ENSMUST00000053657	ENSMUSG00000044339	5	114123926	114128218	-1	6	0	8	60	11	2	0	3	0	0	6		Q6P6J4
ENSMUST00000053659	ENSMUSG00000047678	X	13661363	13667433	1	2	3	2	3	4	1	6	35	5	20	3		Q8BZR0
ENSMUST00000053661	ENSMUSG00000047867	6	48701582	48708225	-1	3	2	0	0	6	0	55	196	66	508	210		Q8K349
ENSMUST00000053663	ENSMUSG00000038299	18	32837225	32866420	1	9	0	0	10	15	10	29	115	0	19	45	Q3TAQ9	
ENSMUST00000053664	ENSMUSG00000050043	2	84671316	84679140	-1	10	4	0	0	0	0	63	229	55	88	80		Q9D710
ENSMUST00000053666	ENSMUSG00000027130	2	112265825	112363163	1	9	4	0	8	9	8	0	0	57	0	46		Q924N4
ENSMUST00000053668	ENSMUSG00000047415	12	100876682	100908198	-1	50	58	318	0	50	47	0	15	0	0	15		Q8BFQ3
ENSMUST00000053670	ENSMUSG00000048200	7	141461094	141466613	1	0	5	30	115	24	0	16	32	0	0	8		Q80ZJ8
ENSMUST00000053681	ENSMUSG00000045589	4	56957173	56990391	-1	34	39	50	159	58	31	0	6	0	1	4		B1AXV0
ENSMUST00000053683	ENSMUSG00000048731	17	26973217	27036378	1	1	0	0	2	0	0	5	27	1	0	0		Q6K1E7
ENSMUST00000053686	ENSMUSG00000026558	1	167222883	167285320	-1	24	20	53	240	65	20	142	241	172	74	298	Q543C2	Q99PM9
ENSMUST00000053692	ENSMUSG00000061306	11	120103960	120151346	-1	21	9	51	35	13	2	24	11	8	2	18		Q5I012
ENSMUST00000053699	ENSMUSG00000035093	2	125736986	125782870	-1	23	19	44	96	35	14	362	794	841	71	573	A2AQE2	
ENSMUST00000053705	ENSMUSG00000047379	19	5038826	5041134	1	8	13	15	180	25	9	68	117	60	21	43		Q8BWP8
ENSMUST00000053708	ENSMUSG00000050241	6	129577905	129585827	1	99	93	739	150	59	41	0	29	4	5	7	Q8CJC7	
ENSMUST00000053713	ENSMUSG00000044030	7	19004044	19006777	1	8	5	93	630	24	10	543	737	370	64	290		Q8R3Y8
ENSMUST00000053716	ENSMUSG00000050866	7	135511466	135528654	-1	15	12	32	19	11	7	0	3	0	1	0		Q8BHH8
ENSMUST00000053717						2	2	6	9	8	0	0	0	0	0	0		
ENSMUST00000053718	ENSMUSG00000039194	7	79374870	79387048	-1	19	14	29	25	0	0	0	0	0	0	0	Q544Y3	Q9Z275
ENSMUST00000053722	ENSMUSG00000020420	7	27857527	27880825	1	7	10	6	9	6	7	4	19	12	16	19	Q3TQG9	
ENSMUST00000053729	ENSMUSG00000026784	2	22895522	22940266	1	4	4	3	4	2	0	7	35	23	42	24		Q33DR2
ENSMUST00000053733	ENSMUSG00000029245	5	84054761	84417382	-1	2	0	17	5	0	0	0	1	0	0	1		Q60629
ENSMUST00000053734	ENSMUSG00000068452	2	122279247	122298165	-1	57	31	125	132	65	33	0	0	0	0	0	A2AQ99	
ENSMUST00000053737	ENSMUSG00000029439	5	129501221	129571384	1	23	18	49	155	24	8	461	1150	802	76	722		Q3USH5
ENSMUST00000053740	ENSMUSG00000017421	11	80383279	80405733	1	0	0	0	0	0	0	33	190	581	1081	353		Q9JMD0
ENSMUST00000053743	ENSMUSG00000055643	7	104127912	104129826	-1	15	9	25	19	20	9	0	0	0	0	0	Q9D4I8	
ENSMUST00000053744	ENSMUSG00000046791	12	83950608	83952953	1	15	11	65	286	34	12	709	1384	919	150	423		Q9JJF3
ENSMUST00000053748	ENSMUSG00000019978	10	25359798	25523519	1	7	0	0	58	0	0	160	200	439	80	399		O70318
ENSMUST00000053753	ENSMUSG00000050234	4	127311421	127314039	-1	14	12	54	63	39	11	0	0	0	0	0	Q3UPZ2	P28235
ENSMUST00000053760	ENSMUSG00000079470	1	78658038	78671512	1	41	50	137	55	62	26	11	84	46	0	51	E9Q9S3	
ENSMUST00000053764	ENSMUSG00000044167	3	52268336	52353221	1	52	46	127	248	53	40	145	256	186	20	230		Q9R1E0
ENSMUST00000053766	ENSMUSG00000031751	8	93971588	94012663	-1	18	16	48	89	22	17	3466	5309	3385	329	2432	Q3TCI2	Q9R049
ENSMUST00000053768	ENSMUSG00000046314	12	44852488	45074493	-1	60	61	412	468	56	45	10	15	6	8	15	Q3TYA4	
ENSMUST00000053771	ENSMUSG00000036879	8	85840959	86061376	1	17	14	52	10	9	1	123	368	321	87	218		Q7TSH2
ENSMUST00000053772	ENSMUSG00000045883	19	13165016	13165954	1	8	2	1	0	0	1	0	0	0	0	0	Q8VEV7	
ENSMUST00000053785	ENSMUSG00000032839	9	95705082	95750375	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZMP6	
ENSMUST00000053792	ENSMUSG00000045008	10	43174704	43176562	1	18	19	25	126	26	11	0	2	2	1	1	Q8CE20	
ENSMUST00000053811	ENSMUSG00000004789	12	85110833	85134091	1	12	24	40	93	32	9	1462	3350	1962	498	1440		Q9D2G2
ENSMUST00000053819	ENSMUSG00000028911	4	131873617	131901706	1	0	0	34	181	0	0	768	1315	954	121	685	Q542V3	
ENSMUST00000053821	ENSMUSG00000050961	14	51800046	51826359	1	17	13	17	12	10	14	0	0	0	0	0	Q6UY53	
ENSMUST00000053830	ENSMUSG00000048686	4	128260212	128260957	-1	9	3	11	7	5	5	0	0	0	0	0		Q6P8W9
ENSMUST00000053855	ENSMUSG00000046818	3	137621612	137628333	1	31	17	33	132	43	12	1	0	2	0	0	B2RVG4	Q8VHZ5
ENSMUST00000053856	ENSMUSG00000046387	18	37484795	37489454	1	24	9	37	53	24	8	0	0	1	0	4	Q91VD8	
ENSMUST00000053862	ENSMUSG00000028744	4	139294029	139310708	-1	0	0	9	55	0	0	212	140	123	34	79		Q8C4N4
ENSMUST00000053865	ENSMUSG00000046687	10	62071015	62072609	1	16	4	60	4	14	12	0	0	0	0	0	J3QNG0	
ENSMUST00000053871	ENSMUSG00000046841	10	84526305	84534036	-1	19	9	47	0	16	12	6227	11889	7269	419	3537		Q8BMK4
ENSMUST00000053872	ENSMUSG00000046722	3	95228732	95236409	1	26	14	46	61	29	19	7499	12923	6506	1177	4826		Q8BHL7
ENSMUST00000053874	ENSMUSG00000049041	11	73983662	73990290	-1	9	0	8	0	0	2	0	0	0	0	0	Q8VFY0	
ENSMUST00000053876	ENSMUSG00000089992	5	61808816	61811163	1	7	5	8	17	12	2	5	4	6	1	3	G3UWD6	
ENSMUST00000053880	ENSMUSG00000030209	6	135713233	136173511	-1	158	135	544	191	172	116	1	1	1	2	0	G3X9V4	
ENSMUST00000053896	ENSMUSG00000048602	17	33135588	33139683	-1	0	17	33	24	5	7	0	0	0	0	0		Q8C5W4
ENSMUST00000053902	ENSMUSG00000035151	8	83312632	83332486	-1	4	0	15	45	0	0	122	402	164	124	94		Q8BGF6
ENSMUST00000053906	ENSMUSG00000019178	5	135747220	135778385	-1	27	22	16	0	19	13	0	0	0	0	0	Q9DAR2	
ENSMUST00000053909	ENSMUSG00000032690	5	120730333	120749853	-1	32	0	0	0	0	13	434	2416	699	35	1611		E9Q9A9
ENSMUST00000053910	ENSMUSG00000044647	2	65845767	66031546	1	0	0	0	0	0	0	0	0	0	0	0		P59055
ENSMUST00000053913	ENSMUSG00000004815	5	108646693	108669672	-1	0	0	0	0	0	0	52	46	71	11	0		Q6P5E8
ENSMUST00000053917	ENSMUSG00000024286	18	9314044	9450150	-1	12	7	16	122	22	14	477	1136	766	195	405		Q8BGU5
ENSMUST00000053918	ENSMUSG00000022571	15	75916463	75921560	-1	10	11	25	153	15	6	68	68	21	18	42		Q9DCC4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000053919	ENSMUSG00000049028	9	20300129	20301190	1	5	5	12	2	3	0	0	0	0	0	0	Q8VFJ0	
ENSMUST00000053922	ENSMUSG00000045648	1	70725715	70885397	1	12	18	5	7	25	13	0	0	0	0	0		Q505H4
ENSMUST00000053926	ENSMUSG00000068206	15	79229173	79256674	1	3	0	13	66	3	3	0	0	0	0	0	E9QAC6	
ENSMUST00000053927	ENSMUSG00000021709	13	103818787	103920514	-1	0	0	0	0	0	0	1	0	0	0	0		Q80TH2
ENSMUST00000053931	ENSMUSG00000044801	4	43770050	43771009	-1	5	4	13	7	6	3	0	0	0	0	0	Q9QZ19	
ENSMUST00000053932	ENSMUSG00000100642	2	74726728	74747918	1	15	6	17	190	7	3	0	0	0	0	0	A0A0A0MQ91	
ENSMUST00000053941	ENSMUSG00000051528	1	174136746	174137693	1	10	6	13	0	2	1	0	0	0	0	0	E9Q0Q2	
ENSMUST00000053949	ENSMUSG00000044461	14	59625281	59631658	1	20	12	40	178	24	10	1	6	2	1	1		Q8QZV2
ENSMUST00000053950	ENSMUSG00000030556	7	67513411	67645268	-1	0	0	3	16	0	0	54	172	68	29	55		Q3TX51
ENSMUST00000053956	ENSMUSG00000047995	9	24625185	24625827	1	3	1	7	5	6	3	0	0	0	0	0	Q6P925	
ENSMUST00000053958	ENSMUSG00000039608	7	86394496	86395535	-1	4	6	2	4	5	1	0	0	0	0	0	Q8VFP0	
ENSMUST00000053959	ENSMUSG00000035161	14	62676330	62761112	-1	42	48	69	268	44	32	99	452	255	25	144		Q6PCM2
ENSMUST00000053969	ENSMUSG00000042700	12	82170016	82451782	1	15	0	0	6	48	11	657	2235	1675	127	1584		Q8C0T5
ENSMUST00000053970	ENSMUSG00000051209	X	48667979	48674478	-1	9	13	5	3	11	7	0	0	0	0	0		Q7TQP3
ENSMUST00000053974	ENSMUSG00000045417	17	20846551	20847501	1	1	1	0	2	1	0	0	0	0	0	0	Q8R2A2	
ENSMUST00000053981	ENSMUSG00000045237	X	70385877	70389417	1	11	7	8	7	11	6	119	434	150	649	106		Q9D1F3
ENSMUST00000053986	ENSMUSG00000051067	10	80832807	80844039	-1	29	25	67	915	63	30	0	0	0	1	0		Q6GQU6
ENSMUST00000053990	ENSMUSG00000049018	2	37331749	37332732	1	7	6	3	15	14	1	0	0	0	0	0	Q8VF22	
ENSMUST00000054002	ENSMUSG00000053113	11	117966079	117970047	-1	21	15	53	334	34	22	9042	18437	8655	1187	9088		O35718
ENSMUST00000054004	ENSMUSG00000044560	2	111780313	111781260	1	12	1	4	2	3	2	0	0	0	0	0	Q8VGE9	
ENSMUST00000054014	ENSMUSG00000055065	15	79527707	79546741	-1	18	14	49	129	27	16	1900	6042	3595	391	4277	Q3U741	
ENSMUST00000054018	ENSMUSG00000044820	9	54950230	54950998	-1	59	73	333	90	57	18	0	3	2	0	7	Q8R5F9	
ENSMUST00000054022	ENSMUSG00000044361	15	76119517	76126596	-1	7	24	0	33	0	0	2	1	1	0	2	Q8BVJ3	
ENSMUST00000054030	ENSMUSG00000024866	19	3986661	3990007	1	13	6	36	24	11	9	3	3	0	0	4		Q91XE4
ENSMUST00000054034	ENSMUSG00000034206	16	37011786	37095417	1	27	28	42	13	14	4	12	0	37	0	17	Q80XB7	Q8CGS6
ENSMUST00000054048	ENSMUSG00000048965	7	143778365	143784500	-1	1114	545	2757	2028	579	286	13	59	28	5	48	Q4V9R2	Q91ZB7
ENSMUST00000054050	ENSMUSG00000051124	6	48676129	48679114	1	12	4	8	8	17	2	78	476	113	278	128	G3X987	
ENSMUST00000054051	ENSMUSG00000049010	9	40074297	40075262	1	7	1	7	6	13	2	0	0	0	0	0	Q8VGB3	
ENSMUST00000054052	ENSMUSG00000049577	8	122282141	122337251	1	9	8	35	524	17	15	21	12	13	2	44		O35615
ENSMUST00000054055	ENSMUSG00000051527	7	6730583	6967216	1	17	4	59	16	18	12	0	0	0	0	0		Q9ES63
ENSMUST00000054059	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	0	0	0	0	0	0	0	0		Q9CS84
ENSMUST00000054067	ENSMUSG00000043331	9	39949837	39950769	-1	8	6	7	3	3	2	0	0	0	0	0	Q8VG91	
ENSMUST00000054072	ENSMUSG00000003929	17	33329342	33358878	-1	38	31	55	38	36	23	18	42	15	33	21	B8JJZ7	
ENSMUST00000054080	ENSMUSG00000039985	6	148921035	148946467	-1	39	28	90	12	26	14	42	169	49	58	22		Q8C8M1
ENSMUST00000054083	ENSMUSG00000046324	19	29608214	29648415	-1	0	0	0	1	0	0	246	723	444	10	167	G8JL46	
ENSMUST00000054095	ENSMUSG00000037653	5	69109285	69341679	-1	8	9	28	120	17	7	0	0	0	0	0		Q50H33
ENSMUST00000054096	ENSMUSG00000037306	4	134561690	134704290	-1	0	0	0	486	54	0	11	109	185	11	250	Q6NXK9	
ENSMUST00000054098	ENSMUSG00000044026	19	38395980	38405607	1	27	32	60	46	28	13	15	36	11	1	30		Q8BY79
ENSMUST00000054099	ENSMUSG00000026934	2	26200212	26208289	-1	9	6	21	26	5	11	0	0	0	0	0	A2ALD9	P50481
ENSMUST00000054105	ENSMUSG00000040969	3	133112278	133234949	-1	0	6	3	4	0	0	0	0	0	1	0	F6U786	
ENSMUST00000054106	ENSMUSG00000049229	9	19318536	19319465	1	2	3	4	2	2	2	0	0	0	0	0	Q7TRG3	
ENSMUST00000054107	ENSMUSG00000044952	7	97332327	97350213	1	22	14	49	52	24	24	100	174	107	7	48	B2RTJ2	
ENSMUST00000054125	ENSMUSG00000025359	10	128706258	128720238	1	10	12	48	19	20	8	20	73	33	4	45	Q9CZB2	
ENSMUST00000054128	ENSMUSG00000034774	18	20247340	20285031	1	24	16	21	21	23	15	0	0	0	0	0		Q7TSF0
ENSMUST00000054145	ENSMUSG00000049106	12	80335847	80436601	-1	40	21	112	95	57	19	722	1407	1116	100	940	Q3UV57	Q80T85
ENSMUST00000054146	ENSMUSG00000044444	13	55414753	55415166	-1	1	0	3	102	3	1	0	0	0	0	0		Q9DAD6
ENSMUST00000054147	ENSMUSG00000051038	X	38076594	38085141	-1	4	2	1	5	8	1	0	0	0	0	0	Q810N8	
ENSMUST00000054148						2	0	0	0	0	0	55	183	28	202	33		
ENSMUST00000054162	ENSMUSG00000044743	8	21858901	21862011	1	0	0	2	0	0	0	0	0	0	0	0		Q8R2I8
ENSMUST00000054167	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0		G5E8K5
ENSMUST00000054173	ENSMUSG00000050860	11	95824499	95832140	1	0	0	0	70	0	0	8786	9890	6450	761	4541		Q8R2H9
ENSMUST00000054174	ENSMUSG00000024292	17	32905071	32917342	-1	6	0	20	17	15	10	0	0	0	0	0		Q9EP75
ENSMUST00000054175	ENSMUSG00000047980	9	35838329	35844150	-1	1	1	0	0	3	0	0	0	0	0	0	Q9D262	
ENSMUST00000054178	ENSMUSG00000048490	16	76287400	76373827	-1	25	7	58	43	13	16	6	0	18	0	84		Q8CBD1
ENSMUST00000054197	ENSMUSG00000043895	9	20965952	20976793	-1	18	21	52	125	34	27	187	410	281	32	174		P52592
ENSMUST00000054201	ENSMUSG00000043892	2	85822973	85823908	1	1	3	3	2	5	1	0	0	0	0	0	A2ASV3	
ENSMUST00000054202	ENSMUSG00000044248	6	89931649	89940507	-1	19	17	24	17	22	6	0	0	0	0	0		Q8VIC7
ENSMUST00000054212	ENSMUSG00000031488	8	27138773	27174646	-1	46	20	110	95	106	15	2578	3355	4360	243	4008	E9Q8L9	
ENSMUST00000054213	ENSMUSG00000048007	X	134537256	134541865	-1	0	3	12	84	6	0	17	58	17	58	12		Q9WVA2
ENSMUST00000054220	ENSMUSG00000045128	8	70894722	70897443	-1	16	15	79	58	38	15	5320	5229	3141	19706	2407		P62717
ENSMUST00000054223	ENSMUSG00000048830	16	88773179	88774206	-1	0	2	7	13	6	8	0	0	0	0	0	Q9D6T8	
ENSMUST00000054226	ENSMUSG00000045942	11	51253651	51263046	-1	6	0	5	11	3	5	7	9	0	0	1	Q8C601	
ENSMUST00000054230	ENSMUSG00000006527	14	30714849	30822713	1	24	12	21	87	20	16	45	186	119	24	95		Q9JMD1
ENSMUST00000054234	ENSMUSG00000026749	2	38511643	38594606	1	0	12	8	20	12	6	46	116	68	0	23		Q9ES70
ENSMUST00000054237	ENSMUSG00000027797	3	55242364	55539068	1	45	40	79	87	41	19	0	0	0	0	11		Q9JLM8
ENSMUST00000054244	ENSMUSG00000045608	15	95623563	95655960	-1	16	11	28	147	22	8	1	0	0	0	0	F8VQH7	
ENSMUST00000054245	ENSMUSG00000020701	11	82388900	82446332	1	0	15	0	331	15	0	0	0	0	0	0	A0A0A0MQ93	
ENSMUST00000054251	ENSMUSG00000021147	13	8802968	8871909	-1	0	13	0	0	0	0	15	0	0	0	0		Q8CBE3
ENSMUST00000054252	ENSMUSG00000001445	11	97041560	97049213	1	0	0	0	0	0	0	0	6	0	0	0	A2A715	
ENSMUST00000054254	ENSMUSG00000045319	2	6097607	6130211	-1	11	3	11	291	17	9	1	0	0	3	3		Q8C5R2
ENSMUST00000054260	ENSMUSG00000024771	19	34008254	34047903	1	6	6	22	20	14	8	0	0	0	0	0		Q8BM14
ENSMUST00000054266	ENSMUSG00000079020	15	73577424	73645762	-1	0	0	0	0	0	0	0	0	0	0	0		Q0P5V9
ENSMUST00000054274	ENSMUSG00000045312	13	94057796	94195409	1	0	0	0	36	0	0	0	31	31	0	0		Q8BGA2
ENSMUST00000054279	ENSMUSG00000026222	1	85649988	85709998	1	37	55	79	39	37	28	106	429	140	95	177	E9Q4Y0	
ENSMUST00000054280	ENSMUSG00000048029	19	58943425	58971421	1	19	9	20	32	18	13	0	2	0	0	0		Q8C042
ENSMUST00000054287	ENSMUSG00000044617	10	127739538	127747335	1	37	24	88	47	56	24	419	1028	678	34	707	Q6PDK0	
ENSMUST00000054289	ENSMUSG00000044533	17	24718116	24721929	1	0	0	14	110	0	0	13	26	29	0	22	Q58EU3	P25444
ENSMUST00000054294	ENSMUSG00000044674	5	4753839	4758035	-1	27	19	48	640	51	10	1	1	0	7	39		O70421
ENSMUST00000054301	ENSMUSG00000003123	7	25379527	25398710	-1	0	0	0	2	0	0	1076	1571	1100	111	896		P54310
ENSMUST00000054308	ENSMUSG00000035293	12	51348061	51376986	1	12	8	16	234	20	17	59	120	62	48	37		Q5RJY2
ENSMUST00000054310	ENSMUSG00000044881	7	100537100	100540369	1	9	8	4	36	13	6	69	210	42	169	30		Q8BT51
ENSMUST00000054311	ENSMUSG00000047040	11	96928104	96937830	1	0	0	3	0	0	0	0	0	0	0	0		Q8JZM2
ENSMUST00000054316	ENSMUSG00000044916	2	92382538	92385708	1	0	0	0	0	0	0	0	0	0	0	0		Q8CF31
ENSMUST00000054324	ENSMUSG00000055994	8	88647315	88688474	1	0	2	0	19	0	0	0	0	51	0	0		Q8K3Z0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000054327	ENSMUSG00000044056	11	32522751	32532081	-1	4	3	9	0	3	0	0	0	0	1	0		Q9DAM2
ENSMUST00000054343	ENSMUSG00000011096	7	44848991	44855421	1	0	0	18	49	2	0	110	315	160	37	79		Q9D1F4
ENSMUST00000054344	ENSMUSG00000035245	6	97110024	97149182	-1	44	38	131	192	41	19	26	114	35	28	65		Q8BYW9
ENSMUST00000054351	ENSMUSG00000049001	6	65671590	65712326	1	11	15	18	85	25	10	2	3	0	0	4		Q8C119
ENSMUST00000054356	ENSMUSG00000045934	3	96162004	96171718	1	0	3	13	11	1	0	0	0	0	4	23		Q3V1L6
ENSMUST00000054364	ENSMUSG00000044897	10	130030390	130034560	1	0	0	1	0	3	0	0	0	0	0	0	Q8VG45	
ENSMUST00000054368	ENSMUSG00000090019	6	48739054	48743795	1	308	286	320	393	333	136	40	67	42	29	99	Q3TFI6	
ENSMUST00000054380						5	4	4	2	3	2	0	0	0	0	0		
ENSMUST00000054384	ENSMUSG00000043279	5	137105644	137116209	-1	90	70	294	242	113	51	670	2498	1480	121	1716		
ENSMUST00000054385	ENSMUSG00000043357	16	59035780	59039767	-1	4	1	1	1	3	1	0	0	0	0	0	E9QNM5	
ENSMUST00000054387	ENSMUSG00000027739	3	51483920	51496232	1	30	32	27	210	45	10	231	1137	350	117	408	Q0PD21	O35963
ENSMUST00000054395	ENSMUSG00000047061	13	45078692	45081222	1	24	18	21	46	23	9	1	4	3	0	1	Q9D2M0	
ENSMUST00000054399	ENSMUSG00000045969	8	11556066	11563250	1	21	5	46	195	16	8	639	1852	1009	452	899		Q9QXV3
ENSMUST00000054414	ENSMUSG00000047898	9	114490316	114496544	-1	42	18	107	133	41	11	8	6	10	3	28		P51680
ENSMUST00000054415	ENSMUSG00000049728	7	127863047	127876828	-1	12	20	35	59	5	13	66	97	51	0	49		Q8K2R5
ENSMUST00000054418	ENSMUSG00000019864	10	43901807	43947862	1	19	24	54	41	26	8	48	53	26	6	41		
ENSMUST00000054425	ENSMUSG00000045022	13	98984085	98984565	-1	6	0	11	6	2	4	0	0	0	0	0		Q9D9Z7
ENSMUST00000054426	ENSMUSG00000046676	3	92849949	92851286	-1	7	2	22	3	11	1	0	0	0	0	0	Q9D1G7	
ENSMUST00000054427	ENSMUSG00000060962	7	30763756	30781063	1	0	0	0	0	0	0	0	0	0	0	0	E9QQ29	
ENSMUST00000054434	ENSMUSG00000094197	7	107954643	107955575	1	1	1	0	3	4	6	0	0	0	0	0		Q8VFC9
ENSMUST00000054436	ENSMUSG00000030729	7	100227394	100278868	1	7	5	10	3	10	3	7	46	17	14	21		Q8CAA7
ENSMUST00000054440	ENSMUSG00000030922	7	119895861	119916756	1	0	0	0	0	0	0	3	27	18	11	11		Q9CQB7
ENSMUST00000054442	ENSMUSG00000044442	16	87354185	87368742	1	0	0	0	79	22	0	0	23	15	19	16	Q6SKR2	
ENSMUST00000054445	ENSMUSG00000043421	6	29272488	29275446	1	3	4	28	31	6	2	12	62	12	119	29		Q9JLS0
ENSMUST00000054449	ENSMUSG00000022565	15	76170974	76232574	-1	0	0	0	0	0	0	0	0	1	0	0		Q9QXS1
ENSMUST00000054450	ENSMUSG00000014771	17	15519208	15527301	-1	0	1	0	9	0	0	24	125	31	46	30		
ENSMUST00000054459	ENSMUSG00000044700	4	149715375	149738044	-1	59	44	113	49	54	19	5	10	5	0	16		A2A8U2
ENSMUST00000054462	ENSMUSG00000003134	1	39371492	39478755	-1	13	4	17	100	23	14	1103	2696	1666	162	883		Q9Z1A9
ENSMUST00000054470						16	16	39	10	8	4	0	0	1	0	2		
ENSMUST00000054471	ENSMUSG00000046567	10	100572274	100589259	-1	8	12	6	85	12	4	18	37	22	68	17		Q8BHN7
ENSMUST00000054472	ENSMUSG00000025418	4	106483456	106492283	-1	28	12	49	41	46	23	0	0	0	0	0		Q8VIM4
ENSMUST00000054477						0	0	27	0	0	0	102	114	111	0	79		
ENSMUST00000054483	ENSMUSG00000046688	3	127789805	127832164	1	0	30	38	87	20	16	0	81	18	33	27	I3PQW8	Q793I8
ENSMUST00000054484	ENSMUSG00000026904	2	62046462	62326730	1	0	0	5	0	0	3	0	0	0	1	0	B1AWV9	
ENSMUST00000054487	ENSMUSG00000022178	14	54567469	54577661	-1	32	35	99	882	71	33	1	12	2	3	27		Q91XC0
ENSMUST00000054491	ENSMUSG00000046470	2	181669836	181671640	-1	6	7	18	370	17	5	0	1	0	1	0		P43680
ENSMUST00000054500	ENSMUSG00000047990	9	67830532	67832330	-1	6	3	8	207	9	2	0	0	0	0	0	E9Q861	
ENSMUST00000054514	ENSMUSG00000050896	2	84871924	84886710	-1	0	1	4	0	0	0	0	0	0	0	0		Q7M6Z0
ENSMUST00000054523	ENSMUSG00000049287	11	59155369	59163739	-1	39	26	123	127	61	37	73	58	37	6	37		Q8CAK1
ENSMUST00000054530	ENSMUSG00000079679	6	13156299	13224965	-1	16	12	18	7	16	13	0	0	0	0	0		Q6DFV8
ENSMUST00000054532	ENSMUSG00000047253	11	99579976	99581016	-1	6	5	20	25	13	1	0	0	0	0	0	A2A590	
ENSMUST00000054534	ENSMUSG00000051257	X	139333683	139338169	1	2	4	5	23	3	1	0	0	0	0	1	Q3UIV7	P19473
ENSMUST00000054536	ENSMUSG00000045679	12	16988648	17000408	-1	1	0	0	50	2	1	582	2303	751	655	479		Q8C6U2
ENSMUST00000054538	ENSMUSG00000051517	4	43496142	43499695	-1	6	2	0	25	4	2	40	8	18	0	4		Q66JY6
ENSMUST00000054541	ENSMUSG00000051706	X	74594328	74595275	1	0	1	0	0	2	1	0	0	0	0	0	Q8VF43	
ENSMUST00000054544	ENSMUSG00000049751	12	69182731	69184083	-1	0	3	6	14	0	0	468	1415	499	4220	539	Q5M9P1	P83882
ENSMUST00000054547	ENSMUSG00000043733	5	121130533	121191397	-1	3	0	0	6	0	0	340	580	637	96	299		P35235
ENSMUST00000054551	ENSMUSG00000046999	3	68869586	68872163	1	6	3	21	241	15	3	7	2	4	0	2		E9Q0B3
ENSMUST00000054553	ENSMUSG00000038346	6	125009145	125037870	1	6	0	43	12	14	3	98	628	87	74	98	D3YX49	
ENSMUST00000054555	ENSMUSG00000047003	15	75616679	75625300	1	34	24	7	81	13	20	0	0	0	0	0		Q02526
ENSMUST00000054556						1	3	0	108	4	0	0	4	6	20	0		
ENSMUST00000054562	ENSMUSG00000048528	7	132594878	132599637	-1	70	59	408	453	102	35	1	3	1	0	2		P42580
ENSMUST00000054564	ENSMUSG00000029718	5	137605103	137613784	-1	0	1	5	14	2	2	0	0	0	25	0	D3YUE2	
ENSMUST00000054565	ENSMUSG00000007867	12	86082561	86162458	1	2	5	7	23	4	3	4	3	3	40	14		Q9DA69
ENSMUST00000054567	ENSMUSG00000046650	19	12394265	12395212	1	4	3	8	4	6	4	0	0	0	0	0		Q8VFV4
ENSMUST00000054588	ENSMUSG00000026147	1	24177610	24252684	1	13	4	10	12	0	5	0	0	0	0	0	G3X995	
ENSMUST00000054591	ENSMUSG00000048550	2	21205724	21215009	1	18	17	47	25	26	5	22	122	47	50	37	Q149D1	Q8BH55
ENSMUST00000054594	ENSMUSG00000019737	7	30314807	30319046	1	0	0	0	0	0	1	0	0	0	0	0		Q8CII8
ENSMUST00000054598	ENSMUSG00000029095	5	35757880	35884973	1	0	8	18	74	0	21	0	0	0	0	0		Q8BL65
ENSMUST00000054599	ENSMUSG00000050359	3	92483952	92485895	-1	7	2	35	118	11	7	0	0	0	3	1		Q62266
ENSMUST00000054606	ENSMUSG00000045341	16	19514696	19515634	-1	4	5	5	5	8	7	0	0	0	0	0	Q8VGJ5	
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ENSMUST00000054622	ENSMUSG00000038685	2	181319739	181356616	1	0	0	0	0	0	0	29	35	71	0	73		Q0VGM9
ENSMUST00000054629	ENSMUSG00000049674	7	107073830	107074783	1	5	6	3	3	5	2	0	0	0	0	0	Q7TRN0	
ENSMUST00000054635	ENSMUSG00000047094	13	40001882	40288011	-1	12	14	15	2	18	5	1	2	2	5	1	C3S7Q5	
ENSMUST00000054636	ENSMUSG00000049792	12	111709488	111713257	-1	7	0	0	54	6	4	32	120	29	37	63		Q8CI32
ENSMUST00000054650	ENSMUSG00000051456	13	113662896	113663676	-1	9	12	18	7	16	3	0	1	0	0	0		Q9QZ57
ENSMUST00000054651	ENSMUSG00000046971	2	120299957	120314165	-1	22	6	46	29	32	6	0	0	0	0	0		Q50L41
ENSMUST00000054653						6	5	30	6	4	4	0	0	0	0	0		
ENSMUST00000054654	ENSMUSG00000047342	11	62753377	62789462	-1	11	5	22	14	15	9	1	3	1	0	0	Q8C0E6	
ENSMUST00000054661	ENSMUSG00000045875	14	66635251	66733462	1	10	11	13	13	0	0	0	0	0	0	0		P97718
ENSMUST00000054664						24	8	4	5	13	3	3	4	5	0	6		
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ENSMUST00000054666	ENSMUSG00000045193	10	80165985	80172786	1	0	2	0	0	2	0	46	88	62	9	40	K4DI65	
ENSMUST00000054668	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	0	0	0	0	4	5	4	0	1		Q8CJ67
ENSMUST00000054674	ENSMUSG00000044783	1	88262471	88277633	-1	139	144	397	466	219	124	1834	4608	2474	201	1759	E9QKG8	
ENSMUST00000054680	ENSMUSG00000044876	7	6172226	6191349	1	21	24	50	58	35	12	28	65	26	3	28	Q3TDV8	
ENSMUST00000054683	ENSMUSG00000056564	11	58597345	58598466	1	9	7	9	6	6	4	0	0	0	0	0	Q5NCC7	
ENSMUST00000054684	ENSMUSG00000020376	11	50025346	50104758	1	0	7	11	16	5	3	118	444	480	165	382	Q5SVR5	
ENSMUST00000054687	ENSMUSG00000049015	19	13364630	13365556	1	4	3	3	0	2	0	0	0	0	0	0	Q8VFW1	
ENSMUST00000054691	ENSMUSG00000046714	8	121116171	121118895	1	5	8	38	585	27	8	0	0	0	1	10	B9EI61	Q61850
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ENSMUST00000054702	ENSMUSG00000074870	13	61564631	61570127	-1	8	2	3	4	9	1	0	0	0	0	0	Q91ZD5	
ENSMUST00000054708	ENSMUSG00000032123	9	44326845	44333600	1	7	7	52	151	20	19	133	284	133	77	172		P42867

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000054711						8	3	16	9	12	0	0	0	0	1	0		
ENSMUST00000054716	ENSMUSG00000055194	13	111255013	111257749	1	13	7	13	6	13	7	0	0	0	0	0		Q8BFZ3
ENSMUST00000054723	ENSMUSG00000028318	4	45018583	45036565	1	1	1	1	1	2	1	0	38	10	25	10	G8JL51	
ENSMUST00000054730	ENSMUSG00000038212	13	65064663	65112982	-1	14	10	26	46	6	9	2201	4030	2143	814	1614		Q8CIA9
ENSMUST00000054736	ENSMUSG00000057761	2	85868594	85869541	1	3	5	4	0	6	5	0	0	0	0	0	L7MTT3	
ENSMUST00000054737	ENSMUSG00000048456	19	12919363	12920307	-1	2	3	4	0	5	2	0	0	0	0	0	Q8VFX1	
ENSMUST00000054738	ENSMUSG00000042816	18	42578020	42579652	-1	15	9	9	10	13	5	0	1	0	1	2		Q7TSN6
ENSMUST00000054742	ENSMUSG00000042895	15	41865293	41869720	-1	15	5	29	10	14	3	0	1	0	0	0		Q8BUZ1
ENSMUST00000054746	ENSMUSG00000047149	2	86297818	86298756	1	5	3	1	0	1	1	0	0	0	0	0	A2AVX6	
ENSMUST00000054748	ENSMUSG00000045202	17	37795435	37796375	1	6	3	6	2	11	3	0	0	0	0	0	Q8VFQ1	
ENSMUST00000054760	ENSMUSG00000048185	10	63421401	63421739	-1	1	1	0	4	2	0	0	0	0	1	0	D3Z497	
ENSMUST00000054764	ENSMUSG00000049858	10	128669887	128673918	-1	19	14	41	39	20	12	77	90	39	11	38		Q8R086
ENSMUST00000054769	ENSMUSG00000061132	19	40928927	40994535	-1	0	0	0	6	0	0	5	16	0	16	41		Q9QUN3
ENSMUST00000054776	ENSMUSG00000049969	4	10988662	11007927	-1	5	8	10	57	11	3	691	2731	888	149	487		Q91WB4
ENSMUST00000054780	ENSMUSG00000003198	17	55892120	55898928	1	18	36	87	42	35	16	43	386	80	101	48	Q91VM8	
ENSMUST00000054781	ENSMUSG00000045929	7	6410277	6441691	1	78	52	334	107	63	30	0	2	0	0	3	E9Q3L7	
ENSMUST00000054783	ENSMUSG00000050538	11	97840780	97844099	1	5	0	0	0	0	0	0	0	0	0	2	E9Q3Z1	
ENSMUST00000054786	ENSMUSG00000046717	6	138657089	138658544	-1	6	11	16	10	10	1	0	0	0	0	0	A0A0B4J1F7	
ENSMUST00000054791	ENSMUSG00000051076	3	100825459	100896922	1	11	9	17	18	9	5	0	0	0	2	0		Q7TSP5
ENSMUST00000054799	ENSMUSG00000049694	6	90301219	90305449	1	10	4	13	13	9	5	3	2	2	0	2		Q8C5S3
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ENSMUST00000054819	ENSMUSG00000053747	9	99874106	99876170	-1	3	0	10	398	24	8	0	0	0	0	0	Q3UUP3	Q04892
ENSMUST00000054825	ENSMUSG00000049404	3	67478972	67515523	-1	2	7	4	136	11	3	0	0	0	4	1	F6ZIS7	
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ENSMUST00000054835	ENSMUSG00000021694	13	108158731	108195364	1	9	0	8	0	0	0	0	0	6	19	19		Q8CFD5
ENSMUST00000054836	ENSMUSG00000046607	5	118164648	118189478	1	34	39	215	76	60	32	1	2	0	0	4		P62816
ENSMUST00000054845	ENSMUSG00000045150	2	88024724	88025689	1	5	3	2	0	4	2	0	0	0	0	0	Q7TR29	
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ENSMUST00000054860						11	12	9	10	8	13	0	0	1	0	1		
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ENSMUST00000054867	ENSMUSG00000039904	6	25665878	25690729	-1	23	21	31	152	39	15	0	0	1	0	0		Q9QY42
ENSMUST00000054868	ENSMUSG00000050603	2	85689431	85690372	1	2	4	0	2	2	0	0	0	0	0	0	Q8VGC7	
ENSMUST00000054871	ENSMUSG00000079700	17	17887852	17971677	1	7	0	0	0	0	0	0	0	0	0	0		O08790
ENSMUST00000054878	ENSMUSG00000057367	9	7818227	7837064	-1	2	0	1	81	4	1	0	0	7	2	0	F6X8Q0	
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ENSMUST00000054895	ENSMUSG00000029699	5	135960211	135974531	-1	2	1	0	2	10	4	328	369	158	130	111	G3X988	
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ENSMUST00000054910	ENSMUSG00000043795	7	142491074	142506771	-1	10	10	52	19	25	19	345	1052	533	51	916		Q8C494
ENSMUST00000054912						0	0	6	7	0	0	0	23	11	38	0		
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ENSMUST00000054920	ENSMUSG00000046312	4	41495604	41503076	-1	53	51	204	467	82	32	3	10	3	2	14		Q69ZQ1
ENSMUST00000054923	ENSMUSG00000030708	7	100503018	100514960	-1	6	4	9	5	11	4	0	6	10	0	16		Q80Y75
ENSMUST00000054925	ENSMUSG00000047237	9	109139447	109162041	-1	8	12	7	10	10	1	0	0	0	0	0	Q8BI38	
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ENSMUST00000054930	ENSMUSG00000044172	17	25120760	25125268	1	16	13	30	18	12	6	0	0	0	0	0	E9QNW3	
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ENSMUST00000054946	ENSMUSG00000045744	17	24473884	24475469	1	0	0	7	0	0	5	0	0	0	0	0	Q8BV89	
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ENSMUST00000054955	ENSMUSG00000058070	12	108370957	108539617	1	12	0	3	4	3	7	0	0	0	6	22		Q05BC3
ENSMUST00000054956	ENSMUSG00000024776	19	34192229	34240333	1	12	10	9	203	24	14	105	309	215	171	143		Q76N33
ENSMUST00000054960	ENSMUSG00000051495	8	126588296	126593986	-1	37	24	215	331	75	23	830	1795	981	153	1009		E9Q1P8
ENSMUST00000054963	ENSMUSG00000021273	14	63145153	63177793	-1	23	20	40	30	26	10	243	534	269	227	200		P53798
ENSMUST00000054973	ENSMUSG00000043873	3	106016919	106032814	-1	4	0	0	0	0	0	97	660	97	458	106	F7D8T8	
ENSMUST00000054974	ENSMUSG00000043274	2	87418050	87419021	1	0	0	0	4	3	1	0	0	0	0	0	A2AT85	
ENSMUST00000054979	ENSMUSG00000029313	5	103692374	103855322	1	8	0	0	156	52	29	1187	2116	2882	138	2279	A3KMF4	
ENSMUST00000054984	ENSMUSG00000044982	18	31909094	31911903	-1	16	5	16	235	19	14	34	56	44	23	25	E9QJT3	
ENSMUST00000054990	ENSMUSG00000027993	3	84160439	84306877	-1	2	0	5	4	2	1	0	0	0	0	0	E9QKC6	
ENSMUST00000055001	ENSMUSG00000025959	1	64029447	64122282	-1	2	3	3	8	12	3	8	11	18	6	50	Q3UES6	
ENSMUST00000055006	ENSMUSG00000047821	11	62820231	62850808	1	18	25	18	30	41	11	69	105	8	0	38	Q5SVT2	
ENSMUST00000055009	ENSMUSG00000040325	9	106821874	106880992	1	0	0	0	0	6	0	0	102	103	7	41		Q80TR8
ENSMUST00000055012	ENSMUSG00000047989	18	24104757	24121953	-1	11	2	7	0	8	5	44	7	47	79	6	F8WIA0	
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ENSMUST00000055014	ENSMUSG00000049214	4	111972923	111988223	1	7	7	82	40	6	7	0	4	4	0	1		A7XV04
ENSMUST00000055018	ENSMUSG00000038668	4	58435255	58553898	-1	0	0	0	110	3	0	0	0	0	0	0	Q544V2	P61793
ENSMUST00000055022	ENSMUSG00000002871	6	88902251	88912238	1	0	0	3	38	0	5	179	331	246	28	181		Q99MU1
ENSMUST00000055028	ENSMUSG00000049657	4	44991242	45012412	-1	43	19	13	3	16	0	149	222	181	31	146		Q7TQG0
ENSMUST00000055032	ENSMUSG00000056673	Y	897788	956786	1	1605	1549	2836	1606	1509	847	187	488	453	153	403		Q62240
ENSMUST00000055036	ENSMUSG00000045620	9	56848659	56851963	-1	10	13	10	9	11	3	0	0	0	0	0		Q810P2
ENSMUST00000055040	ENSMUSG00000049588	11	55049731	55078131	-1	3	4	26	7	10	2	11	74	29	86	33		Q3TCJ8
ENSMUST00000055052	ENSMUSG00000061825	8	104847068	104854483	1	0	13	14	0	25	9	0	0	0	0	0		Q91WG0
ENSMUST00000055056	ENSMUSG00000017686	11	80209019	80267907	1	20	14	15	29	23	6	4	0	9	0	4		Q8BG51
ENSMUST00000055064	ENSMUSG00000042861	3	107183056	107195721	1	18	8	12	28	14	8	0	0	0	0	0	B2RQA1	
ENSMUST00000055070	ENSMUSG00000051687	7	11756257	11757168	1	2	1	2	2	0	0	0	0	0	0	0	Q8R293	
ENSMUST00000055071	ENSMUSG00000079017	12	103442167	103443680	-1	4	3	5	5	6	4	65	624	31	942	231		Q8R412
ENSMUST00000055077	ENSMUSG00000047986	8	84021471	84030295	1	15	15	52	19	27	15	0	0	0	0	0		A2TJV2
ENSMUST00000055081	ENSMUSG00000027194	2	94300767	94406689	-1	5	10	0	0	17	0	22	408	34	39	49	A2AGG1	
ENSMUST00000055083	ENSMUSG00000045471	11	100761069	100762931	-1	11	5	20	96	13	3	0	0	0	0	0	Q547R2	O55241
ENSMUST00000055085	ENSMUSG00000045282	7	4628040	4631422	-1	11	6	28	22	16	13	53	173	92	8	136		Q497J1
ENSMUST00000055087	ENSMUSG00000021457	13	52583173	52648792	1	8	1	68	0	0	6	7106	17004	6541	766	7614	Q3UPF7	P48025

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000055096	ENSMUSG00000040219	9	49436963	49486225	-1	29	20	46	46	26	14	8	62	17	75	23		Q8BW49
ENSMUST00000055097	ENSMUSG00000046806	6	34871771	34878060	-1	20	0	20	78	22	7	83	247	87	29	82		Q8BHZ5
ENSMUST00000055099	ENSMUSG00000046150	9	38672504	38673481	-1	3	4	10	3	8	0	0	0	0	0	0	E9PVZ7	
ENSMUST00000055100	ENSMUSG00000043004	14	19872559	19977627	-1	0	2	0	0	0	0	149	359	135	468	118		P63213
ENSMUST00000055102	ENSMUSG00000040413	11	46668960	46707061	-1	2	0	0	0	0	3	0	0	0	4	0	A8C1R4	
ENSMUST00000055104	ENSMUSG00000049536	X	136707982	136711478	1	8	9	11	7	12	8	0	1	0	3	1		Q921P9
ENSMUST00000055107	ENSMUSG00000044624	10	18779813	18785011	-1	15	10	28	12	6	8	0	0	0	0	0		Q8C0N0
ENSMUST00000055110	ENSMUSG00000030600	7	28451980	28468242	1	0	0	0	0	0	0	5	2	8	1	0		Q2WF71
ENSMUST00000055115	ENSMUSG00000043789	19	10634233	10665210	1	43	29	97	88	62	32	0	0	0	1	2		Q3U515
ENSMUST00000055117	ENSMUSG00000044857	17	27189601	27204438	-1	15	12	33	82	27	17	920	1149	563	89	475		Q6DVA0
ENSMUST00000055121	ENSMUSG00000045109	11	99643106	99644089	-1	8	10	27	139	13	9	0	0	0	0	0	Q9D732	
ENSMUST00000055125	ENSMUSG00000043670	10	81019589	81025662	-1	24	13	174	169	38	12	0	0	0	0	0		Q91Z61
ENSMUST00000055128	ENSMUSG00000046985	5	44175154	44226626	-1	15	8	27	21	11	9	565	1891	883	196	627		Q4VBD2
ENSMUST00000055129	ENSMUSG00000049843	2	87001971	87002945	1	3	1	5	1	1	3	0	0	0	0	0		Q8VES2
ENSMUST00000055130	ENSMUSG00000050015	2	36850048	36850986	1	2	4	6	1	7	4	0	0	0	0	0	Q8VFP8	
ENSMUST00000055131	ENSMUSG00000043411	4	137593755	137658537	1	0	15	0	0	28	0	60	180	291	52	221		Q3V0C5
ENSMUST00000055144	ENSMUSG00000057147	2	114516416	114654964	-1	0	0	0	0	7	6	0	6	0	0	26		Q9CQ28
ENSMUST00000055146	ENSMUSG00000051200	7	108754858	108755787	1	7	6	4	3	5	3	0	0	0	0	0	Q8VFZ3	
ENSMUST00000055156	ENSMUSG00000047014	12	101404673	101626009	1	11	9	11	5	10	3	0	0	0	0	0		A2RTF1
ENSMUST00000055159	ENSMUSG00000043157	14	61309753	61311936	1	8	4	21	9	16	8	793	1751	820	777	549		Q6P3A9
ENSMUST00000055168	ENSMUSG00000047976	6	126640397	126646384	-1	67	37	163	412	77	51	0	0	0	0	0		P16388
ENSMUST00000055184	ENSMUSG00000050675	11	70639122	70642036	1	12	0	58	18	9	0	5	56	18	12	72	A2CFB8	O35930
ENSMUST00000055190	ENSMUSG00000038859	5	144264526	144358112	-1	13	4	18	145	24	1	3	7	10	17	27		Q9DBJ3
ENSMUST00000055195	ENSMUSG00000010721	5	29229802	29378390	-1	26	0	40	0	0	0	0	9	0	0	17		Q9JIT0
ENSMUST00000055204	ENSMUSG00000043314	11	58454915	58455980	-1	8	6	21	19	17	9	0	0	0	0	0	Q8VGD8	
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ENSMUST00000055220						17	20	24	22	27	14	0	21	7	1	9		
ENSMUST00000055221	ENSMUSG00000050138	17	87745837	87797994	-1	10	1	17	403	11	3	9	4	6	0	4	Q76M80	
ENSMUST00000055223	ENSMUSG00000026203	1	75236406	75245692	1	0	0	2	147	14	3	0	0	0	2	0		Q9QYI5
ENSMUST00000055224	ENSMUSG00000045095	6	93675455	94283917	-1	22	0	0	234	21	18	1	0	1	0	0		
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ENSMUST00000055241	ENSMUSG00000027288	2	120506820	120563843	-1	62	37	199	71	61	30	2048	5918	4740	688	4151	R4GML0	
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ENSMUST00000055244	ENSMUSG00000026843	2	31572651	31617526	1	0	0	0	0	0	0	0	39	25	5	29	Q3TIX6	
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ENSMUST00000055256	ENSMUSG00000029478	5	125017153	125179219	-1	32	0	25	68	0	42	71	30	151	0	10	E9Q701	
ENSMUST00000055257	ENSMUSG00000043068	8	124740257	124751809	-1	8	4	8	102	4	5	6	8	4	1	6		Q14BJ1
ENSMUST00000055261	ENSMUSG00000043131	6	83326016	83343776	1	0	15	3	63	7	0	2506	5781	4363	749	2899		Q921Y0
ENSMUST00000055262	ENSMUSG00000021124	12	79156017	79172667	-1	8	1	0	300	10	11	194	920	315	1062	256	Q91XH6	
ENSMUST00000055273	ENSMUSG00000047969	2	86785732	86786700	1	1	3	7	4	5	3	0	0	0	0	0	Q8VF14	
ENSMUST00000055276	ENSMUSG00000044061	11	59612966	59614225	1	13	4	4	0	7	2	0	0	0	0	0	E9PWF9	
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ENSMUST00000055294	ENSMUSG00000050069	1	174833785	174921819	-1	16	12	18	31	26	9	0	0	0	0	3	Q3TST1	O88273
ENSMUST00000055296	ENSMUSG00000049553	6	71909053	71984935	1	46	31	59	56	61	35	438	694	759	80	720		O35134
ENSMUST00000055298	ENSMUSG00000045474	13	21142018	21145867	-1	6	4	8	1	5	3	0	0	0	0	0	Q8VFG3	
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ENSMUST00000055304	ENSMUSG00000046854	2	32574797	32583782	1	9	0	3	34	10	3	0	0	0	0	1		Q6U7H8
ENSMUST00000055305	ENSMUSG00000046088	17	22689771	22689941	1	0	1	0	0	0	0	0	0	0	0	0	F6YK59	
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ENSMUST00000055314	ENSMUSG00000043282	1	153874345	153876871	1	32	39	44	27	37	10	0	15	6	4	8	Q8CC62	
ENSMUST00000055316	ENSMUSG00000078931	8	107044698	107048614	-1	0	0	0	112	1	0	7	34	5	5	10	S4R2K0	
ENSMUST00000055322	ENSMUSG00000056708	1	155096361	155099636	-1	5	9	45	324	34	15	2662	11593	3544	385	2661	Q3UJ54	O89113
ENSMUST00000055324	ENSMUSG00000043827	17	37196707	37198011	-1	2	3	8	151	6	2	0	0	0	0	0	Q6UAH0	
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ENSMUST00000055334	ENSMUSG00000048763	11	96323326	96347930	1	10	2	31	416	1	5	0	0	0	0	1		P09026
ENSMUST00000055341	ENSMUSG00000051335	13	43195519	43304172	-1	36	25	73	411	69	29	620	1167	1074	71	840		Q3UHD2
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ENSMUST00000055345	ENSMUSG00000049526	9	59518686	59525501	-1	2	3	1	6	8	3	10	91	21	40	11	B9EHM8	Q80W35
ENSMUST00000055349	ENSMUSG00000053347	17	21962552	22071168	1	6	3	3	5	4	3	52	261	55	65	42	Q6NZP4	
ENSMUST00000055352	ENSMUSG00000014763	17	15396246	15433580	1	23	17	55	36	35	18	172	869	366	130	385		Q6RI63
ENSMUST00000055353	ENSMUSG00000025469	7	140046157	140049089	-1	0	11	15	204	23	13	0	0	0	0	0	G3X9C7	
ENSMUST00000055355	ENSMUSG00000044921	10	102512222	102546560	1	9	9	11	13	8	2	0	0	0	0	0		Q8K342
ENSMUST00000055369	ENSMUSG00000045231	16	23220656	23225368	-1	66	59	62	228	86	54	2	9	4	5	19	Q8C9L1	
ENSMUST00000055372	ENSMUSG00000040720	4	11485958	11550684	1	4	0	3	49	6	2	61	25	14	21	50		A2AIV2
ENSMUST00000055374	ENSMUSG00000045521	16	17898637	17900023	1	13	8	16	16	19	7	1	2	2	0	1		O54863
ENSMUST00000055375	ENSMUSG00000045475	3	92944486	92945733	1	7	7	10	12	5	5	0	0	0	0	0	Q91V05	
ENSMUST00000055389	ENSMUSG00000047434	16	30955627	31081432	-1	14	8	22	95	24	10	264	1023	433	85	370		Q3U4G3
ENSMUST00000055390	ENSMUSG00000046768	12	75308322	75401456	1	10	6	6	13	16	8	3	9	4	8	10		Q9ER71
ENSMUST00000055401	ENSMUSG00000046450	4	43705628	43710231	-1	0	8	0	0	0	0	0	0	0	0	0	Q9QZ18	
ENSMUST00000055404	ENSMUSG00000045065	11	109413917	109420405	1	10	10	30	23	18	12	0	0	0	0	1	Q8BG27	
ENSMUST00000055406	ENSMUSG00000049897	2	26934047	26953496	1	15	12	39	19	24	11	4	14	5	5	2		Q80YS9
ENSMUST00000055408	ENSMUSG00000041609	5	115648175	115731621	-1	0	3	10	87	15	0	279	396	307	14	112		A0JNT9
ENSMUST00000055409	ENSMUSG00000048217	11	102145513	102149477	1	0	0	0	0	0	0	0	0	0	0	0		Q8R4H7
ENSMUST00000055413	ENSMUSG00000071632	16	18836578	18840160	1	0	0	17	18	0	0	0	52	14	15	44		Q3U595
ENSMUST00000055421	ENSMUSG00000049692	2	130406478	130407902	1	20	13	267	54	27	12	0	2	0	0	0		Q9DA47
ENSMUST00000055424	ENSMUSG00000025144	11	120710942	120713738	-1	0	0	0	4	0	0	194	249	139	495	69		Q8C4X1
ENSMUST00000055425	ENSMUSG00000058388	3	103968110	104024598	1	0	0	0	0	0	0	0	21	0	0	9	Q8C2F6	
ENSMUST00000055433	ENSMUSG00000046997	9	96943482	97018843	-1	0	0	0	445	16	0	4	4	1	0	6		Q8R5B6
ENSMUST00000055436	ENSMUSG00000043155	4	116819904	116821707	-1	13	10	57	163	32	11	0	2	1	0	1		Q8K248
ENSMUST00000055438	ENSMUSG00000046442	11	87226906	87359023	-1	17	16	28	380	33	17	21	17	19	5	14	B2KGP3	Q80TL0
ENSMUST00000055439						0	6	38	5	27	0	0	0	0	11	20		
ENSMUST00000055444	ENSMUSG00000046438	7	33737190	33739312	-1	1	4	3	11	4	0	0	0	0	0	0	D2XZ39	Q7M747
ENSMUST00000055447	ENSMUSG00000049411	18	11981303	12121480	-1	0	10	12	0	10	0	0	63	47	7	0	Z4YJM6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000055454	ENSMUSG00000038500	17	35972541	35980236	-1	0	0	13	188	20	0	0	17	5	0	0		Q811B5
ENSMUST00000055458	ENSMUSG00000045664	19	5917556	5924816	-1	12	7	37	22	18	14	1209	2343	729	146	481		Q8JZX9
ENSMUST00000055475	ENSMUSG00000050350	14	121911435	121915774	-1	11	6	39	10	13	6	30	102	31	115	91		Q8K1Z6
ENSMUST00000055483	ENSMUSG00000025860	X	42059679	42109656	1	0	0	0	0	0	0	705	690	195	0	192		Q60989
ENSMUST00000055485	ENSMUSG00000039108	2	180024987	180035465	1	0	0	0	44	6	7	162	443	234	28	109		Q8CGC4
ENSMUST00000055490	ENSMUSG00000050201	11	115307163	115332303	1	18	10	37	44	7	0	0	0	0	0	0		Q80SX5
ENSMUST00000055495	ENSMUSG00000043458	18	37435621	37438654	1	23	13	49	19	30	14	0	0	1	0	0	Q91Y07	
ENSMUST00000055497	ENSMUSG00000047242	X	106206883	106221158	-1	0	7	16	89	7	4	0	21	0	0	0		Q6NZA9
ENSMUST00000055502	ENSMUSG00000047564	11	99566027	99566630	-1	6	4	28	71	8	6	0	0	0	0	0		A2A591
ENSMUST00000055503	ENSMUSG00000039814	8	18932729	18950975	-1	0	0	0	139	27	5	0	0	0	1	0	Q8BG78	
ENSMUST00000055506	ENSMUSG00000032777	7	125640954	125707780	-1	53	42	164	247	104	51	916	1063	1229	70	1137		Q8K284
ENSMUST00000055517	ENSMUSG00000043226	2	85721407	85722351	1	3	5	4	7	7	4	0	0	0	0	0	A2ALD4	Q8VFK1
ENSMUST00000055518	ENSMUSG00000041417	13	101680563	101768217	-1	48	36	199	74	39	38	709	2146	1625	125	1107		P26450
ENSMUST00000055528	ENSMUSG00000054715	7	12897815	12909083	1	19	11	25	26	25	6	18	2	0	0	0	Q8BGS5	
ENSMUST00000055535	ENSMUSG00000036030	9	72806874	72917291	1	45	40	100	201	56	29	0	1	0	0	2		Q2EY15
ENSMUST00000055539	ENSMUSG00000039994	10	128232065	128252941	1	0	0	0	18	0	0	0	0	0	2	0		Q9R1X4
ENSMUST00000055545	ENSMUSG00000050215	4	43695000	43700807	-1	19	15	32	22	29	11	0	0	0	0	0	Q80ZX9	
ENSMUST00000055549	ENSMUSG00000051650	11	22834747	22860961	-1	8	4	27	30	27	10	220	354	409	198	249	Q3TVJ9	Q9Z222
ENSMUST00000055557	ENSMUSG00000047854	16	62814676	62824346	1	33	27	21	45	37	16	8	10	6	1	9		Q8R1Q0
ENSMUST00000055558	ENSMUSG00000043505	6	48746197	48754210	1	12	8	11	14	19	10	20	15	12	8	32		Q8BWF2
ENSMUST00000055559	ENSMUSG00000050786	6	49319274	49341582	1	4	7	8	56	10	2	144	505	193	119	104		Q8BIS8
ENSMUST00000055562	ENSMUSG00000050328	15	102936757	102938609	1	6	3	14	228	14	7	0	0	0	0	0		Q8K5B8
ENSMUST00000055567	ENSMUSG00000094182	9	39059729	39060664	-1	2	5	2	2	4	1	0	0	0	0	0	Q9EQB4	
ENSMUST00000055575	ENSMUSG00000050188	4	126096623	126098584	1	12	7	10	65	12	2	380	388	292	335	201	Q3UPL7	Q8QZX5
ENSMUST00000055576	ENSMUSG00000030513	7	65861734	66050386	1	0	0	0	29	0	0	0	0	0	0	0	F6XJP7	
ENSMUST00000055584	ENSMUSG00000047702	11	49443853	49444788	1	6	4	8	3	10	4	0	0	0	0	0	Q8VFA3	
ENSMUST00000055593						2	0	9	8	0	0	0	4	14	0	0		
ENSMUST00000055604	ENSMUSG00000046541	7	25221425	25227507	1	26	14	55	216	36	9	178	140	189	8	150		Q8BI66
ENSMUST00000055607	ENSMUSG00000047117	13	96416134	96471198	-1	9	0	0	10	7	0	0	0	0	0	0		Q14DN9
ENSMUST00000055615	ENSMUSG00000049737	13	21658368	21659321	-1	6	5	8	18	5	5	0	0	0	0	0	Q8VFH0	
ENSMUST00000055619	ENSMUSG00000043099	11	75164565	75169519	-1	24	19	38	1102	57	12	0	4	1	0	5	Z4YJP0	
ENSMUST00000055636	ENSMUSG00000043850	3	58844028	58885340	-1	167	125	193	776	166	77	4	9	5	5	14		Q8K445
ENSMUST00000055647	ENSMUSG00000063077	4	149176319	149307693	-1	0	1	0	0	0	0	0	0	166	0	247		Q60575
ENSMUST00000055655	ENSMUSG00000025153	11	120805846	120824547	-1	96	63	146	167	132	81	346	144	316	13	573		P19096
ENSMUST00000055662	ENSMUSG00000045776	14	29018208	29033642	1	45	27	56	48	42	20	1	0	2	0	3	A6H6T2	Q8BXQ3
ENSMUST00000055671	ENSMUSG00000048806	4	88522025	88522774	-1	6	5	4	12	4	1	0	0	0	0	0	Q0VE17	P01575
ENSMUST00000055672	ENSMUSG00000045395	19	13814607	13815658	-1	8	4	5	2	3	1	0	0	0	0	0	Q8VG65	
ENSMUST00000055673	ENSMUSG00000043673	12	11090202	11150842	-1	4	0	0	39	7	0	0	0	0	0	0		Q8BQZ8
ENSMUST00000055676	ENSMUSG00000045092	3	115710433	115715072	-1	8	15	47	87	34	12	99	207	120	53	298		O08530
ENSMUST00000055688	ENSMUSG00000047777	4	151989633	151996258	-1	17	20	43	118	41	14	217	303	206	18	161	Q3V230	Q8K2W6
ENSMUST00000055690	ENSMUSG00000054054	7	86306185	86313509	-1	2	2	3	1	0	2	0	0	0	0	0	Q7TS01	
ENSMUST00000055693	ENSMUSG00000015224	4	96568429	96591578	-1	10	6	6	5	10	2	0	6	1	2	0	Q924D1	
ENSMUST00000055698	ENSMUSG00000046352	14	57098600	57104702	-1	16	13	18	129	15	13	0	0	0	0	0	Q3UJE9	Q00977
ENSMUST00000055704	ENSMUSG00000032562	9	107614125	107635367	-1	5	9	15	30	22	20	37543	39965	31414	4004	21513		P08752
ENSMUST00000055719	ENSMUSG00000047728	15	75216376	75222661	1	16	6	37	24	12	9	3	6	2	7	7	Q8R155	
ENSMUST00000055721	ENSMUSG00000068083	15	82759835	82764183	-1	7	3	22	20	23	13	0	0	0	0	0	Q6P8N9	
ENSMUST00000055723	ENSMUSG00000045362	7	143607685	143627845	-1	57	47	526	47	68	32	125	370	208	57	135	Q3U3N2	P83626
ENSMUST00000055725	ENSMUSG00000044176	18	62548911	62661366	1	4	8	0	0	0	0	0	0	2	0	0		Q8CAC8
ENSMUST00000055735	ENSMUSG00000046881	8	72107040	72110509	1	7	4	22	8	9	4	1	3	1	0	3	Q7TRY0	
ENSMUST00000055738	ENSMUSG00000031431	X	140539528	140600659	-1	2	0	35	0	26	14	10588	16238	8423	3025	5815		Q9Z2S7
ENSMUST00000055745	ENSMUSG00000049709	7	108921860	108930158	-1	82	76	94	782	182	91	20	25	41	4	12	Q6JGS9	Q8CCN1
ENSMUST00000055754	ENSMUSG00000042804	4	152274232	152285337	1	25	15	0	254	46	17	0	1	1	5	0		Q8K0Z9
ENSMUST00000055758	ENSMUSG00000044308	2	69897246	70024013	1	9	11	13	11	16	7	271	408	675	0	379		Q5U430
ENSMUST00000055763	ENSMUSG00000045708	6	42911525	42912457	1	9	2	7	6	6	3	0	0	0	0	0	Q8VGP6	
ENSMUST00000055770	ENSMUSG00000049539	13	23763717	23764358	1	4	4	20	28	7	3	0	0	0	5	1		P43275
ENSMUST00000055775	ENSMUSG00000038060	9	119102478	119148246	1	0	0	0	0	0	0	0	0	0	0	0	E9QNI0	
ENSMUST00000055776	ENSMUSG00000049744	2	43748824	44395953	1	0	1	11	5	2	1	485	3247	1276	2413	506		Q811M1
ENSMUST00000055787	ENSMUSG00000046396	7	103491917	103492876	-1	6	6	2	6	7	1	0	0	0	0	0	E9Q4X7	
ENSMUST00000055792	ENSMUSG00000047044	19	18713193	18718428	1	9	12	10	0	19	0	1	0	12	0	0	Q3U2A5	
ENSMUST00000055796						0	3	1	2	7	7	0	0	0	0	0		
ENSMUST00000055808	ENSMUSG00000051391	5	135908409	135934616	-1	104	76	187	877	167	138	2318	3143	2234	248	1496	A8IP69	P61982
ENSMUST00000055815	ENSMUSG00000035653	12	61523150	61858342	1	15	0	9	11	3	2	0	0	0	0	0		Q8BXA0
ENSMUST00000055819	ENSMUSG00000025139	7	141874813	141918507	-1	1	2	0	8	2	0	0	0	0	0	0	Q8C5G6	
ENSMUST00000055820						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000055822	ENSMUSG00000050812	4	58798911	58912749	-1	0	1	0	104	6	2	0	0	0	0	0	A2ALW1	
ENSMUST00000055833	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	0	0	21	0	0		P16951
ENSMUST00000055840	ENSMUSG00000046975	2	85849454	85850407	1	6	0	3	1	7	1	0	0	0	0	0	Q0VEQ7	Q8VFK7
ENSMUST00000055843	ENSMUSG00000074102	9	106880918	106887428	-1	45	32	50	187	62	21	487	717	556	72	355		Q6PHZ5
ENSMUST00000055844	ENSMUSG00000032387	9	65629648	65660528	1	0	0	12	98	7	4	0	0	0	0	0		Q8VC52
ENSMUST00000055847	ENSMUSG00000045340	7	10633587	10634483	1	1	4	1	1	7	0	0	0	0	0	0	Q8R254	
ENSMUST00000055858	ENSMUSG00000045411	7	44246722	44252319	1	4	0	0	51	0	0	43	0	17	18	12	Q3TE80	
ENSMUST00000055868	ENSMUSG00000095706	16	59361299	59362216	-1	5	3	4	8	7	2	0	0	0	0	0	L7N1X3	
ENSMUST00000055872	ENSMUSG00000020793	11	116280939	116283938	1	16	7	29	211	14	6	0	3	4	0	4		O88854
ENSMUST00000055873	ENSMUSG00000050134	1	174069300	174070253	1	6	5	2	6	6	7	0	0	0	0	0	E9Q5F1	
ENSMUST00000055875						0	0	0	0	0	0	0	9	5	0	9		
ENSMUST00000055878						1	1	5	3	1	4	0	0	0	1	0		
ENSMUST00000055879	ENSMUSG00000044976	9	74110356	74283308	1	24	14	31	19	22	8	0	0	0	0	0	D3YYM4	
ENSMUST00000055884	ENSMUSG00000050534	1	121509842	121528465	-1	14	8	18	141	13	9	0	0	0	0	2	G3X9C6	
ENSMUST00000055890	ENSMUSG00000051051	7	140176061	140177116	1	11	6	16	13	15	9	0	0	0	0	0	Q8VFE7	
ENSMUST00000055892	ENSMUSG00000048003	4	134211970	134227383	-1	0	8	13	10	23	6	0	0	0	0	0		Q8BVN3
ENSMUST00000055895	ENSMUSG00000048226	2	88958468	88959403	1	1	0	2	1	5	2	0	0	0	0	0	Q7TR08	
ENSMUST00000055911	ENSMUSG00000044390	19	5891139	5894107	-1	43	49	122	97	52	20	17	33	16	4	8		Q7TM95
ENSMUST00000055915	ENSMUSG00000045835	13	26768173	26770119	-1	11	7	31	57	18	14	0	0	0	0	0	Q2VPR5	
ENSMUST00000055918	ENSMUSG00000049103	9	124101950	124113557	1	0	0	0	0	0	0	305	0	582	2199	862	Q543S8	P51683

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000055921	ENSMUSG00000015094	2	25399351	25409494	1	0	0	0	0	0	0	0	0	0	0	0	A2AJ21	
ENSMUST00000055922	ENSMUSG00000048706	4	80910646	80955628	1	7	6	10	134	14	6	0	0	0	2	1		Q8K2P1
ENSMUST00000055923	ENSMUSG00000045581	7	106944067	106948312	-1	7	8	3	2	2	4	0	0	0	0	0	Q9EP55	
ENSMUST00000055930	ENSMUSG00000079324	2	68656486	68748467	1	0	0	0	0	0	0	0	0	0	0	0	Q8CEQ9	
ENSMUST00000055931	ENSMUSG00000047205	11	3895240	3901296	1	47	56	314	61	59	28	121	172	197	14	172		Q8VE01
ENSMUST00000055935	ENSMUSG00000102543	18	37819513	37841873	1	0	0	65	0	0	0	0	0	0	0	9	Q91XW9	
ENSMUST00000055941	ENSMUSG00000033792	X	106027276	106124926	1	0	11	9	0	0	7	270	537	465	77	55	A2AG68	
ENSMUST00000055944	ENSMUSG00000050141	4	42868004	42874234	-1	0	8	0	0	8	0	0	0	0	0	0		Q80YD3
ENSMUST00000055946	ENSMUSG00000045967	2	21367542	21830547	1	34	27	85	46	44	12	0	0	0	0	0		Q8C419
ENSMUST00000055947	ENSMUSG00000047181	11	95009879	95026087	1	29	19	26	138	53	19	28	14	8	21	54		Q8K070
ENSMUST00000055949	ENSMUSG00000048347	18	37489465	37494505	1	18	17	41	54	19	12	0	0	0	0	1		Q91Y02
ENSMUST00000055957						6	9	6	12	15	2	3	2	1	1	0		
ENSMUST00000055964	ENSMUSG00000046716	7	10446789	10447784	1	7	2	1	2	1	1	0	0	0	0	0	G5E8C1	
ENSMUST00000055966	ENSMUSG00000031343	X	72432681	72656848	-1	6	12	18	11	13	8	0	0	0	7	3		P26049
ENSMUST00000055984	ENSMUSG00000048039	3	87930314	87940686	1	40	24	86	54	37	13	229	526	351	55	260		
ENSMUST00000055990	ENSMUSG00000016349	2	181147653	181157014	-1	21	6	25	126	27	12	0	0	0	0	0		P62631
ENSMUST00000055993	ENSMUSG00000048330	7	109034312	109083331	-1	0	0	0	23	0	0	0	0	0	0	0		Q8BPM6
ENSMUST00000056002	ENSMUSG00000044025	10	129500813	129501882	1	3	4	1	2	1	0	0	0	0	0	0	Q7TRI0	
ENSMUST00000056005	ENSMUSG00000049498	19	12934737	12935684	1	8	4	30	2	7	2	0	0	0	0	0	Q8VEV8	
ENSMUST00000056006	ENSMUSG00000043013	9	74861921	74891781	1	23	25	80	477	39	19	0	0	0	0	0		O08755
ENSMUST00000056010						2	4	0	13	0	0	0	10	4	5	3		
ENSMUST00000056014	ENSMUSG00000045364	4	88879538	88880201	-1	6	4	3	4	3	4	0	0	0	0	0		Q80ZF2
ENSMUST00000056023	ENSMUSG00000050190	8	43624951	43627270	-1	8	9	9	11	8	11	0	0	0	0	0	Q7M766	
ENSMUST00000056028	ENSMUSG00000042978	7	126272619	126295016	1	27	16	62	599	57	24	287	280	227	27	278		Q8QZX0
ENSMUST00000056032	ENSMUSG00000024137	17	24443792	24455311	-1	36	27	59	308	62	30	440	851	413	136	517		Q8CCE9
ENSMUST00000056034	ENSMUSG00000024426	17	35897595	35910075	-1	4	0	0	24	8	0	0	37	0	0	0		Q8K341
ENSMUST00000056035	ENSMUSG00000024672	19	11321039	11336146	-1	0	0	0	0	0	0	2	14	4	57	4	Q9D2W6	
ENSMUST00000056038	ENSMUSG00000026388	1	120121187	120188189	1	0	0	0	0	0	0	2	0	4	0	1		Q9CRW3
ENSMUST00000056042	ENSMUSG00000051900	7	120409647	120544813	1	5	3	5	3	3	8	0	0	0	0	0	E9QAF2	
ENSMUST00000056045	ENSMUSG00000047221	5	21424958	21482124	1	13	9	19	59	29	10	13	44	27	11	24		Q7TPD2
ENSMUST00000056046						2	1	1	0	0	2	0	1	4	0	3		
ENSMUST00000056047	ENSMUSG00000049985	13	112288451	112384002	1	8	3	7	0	2	3	0	0	0	0	0	Q8BYH9	
ENSMUST00000056050	ENSMUSG00000049225	4	11958184	11966452	-1	0	10	0	29	6	5	7	0	8	18	4	A8Y5Q1	Q3UV70
ENSMUST00000056051	ENSMUSG00000031883	8	104534700	104550343	1	0	0	0	46	6	0	0	0	0	0	0		Q9ERQ8
ENSMUST00000056053	ENSMUSG00000038384	5	123142193	123168629	1	41	22	101	0	78	15	1073	726	1431	34	991		Q8CFT2
ENSMUST00000056071	ENSMUSG00000043263	1	173630917	173647928	1	39	22	127	38	17	16	17	185	23	52	48		Q8BV49
ENSMUST00000056073	ENSMUSG00000039543	14	20394190	20452226	-1	15	0	0	0	0	0	0	0	2	0	0	D3YVL2	
ENSMUST00000056078	ENSMUSG00000045948	7	28739641	28741820	-1	0	0	7	0	0	0	104	180	69	31	46		O35680
ENSMUST00000056085	ENSMUSG00000046934	10	99757705	99759658	-1	20	9	18	19	16	9	0	0	0	0	0	Q80X68	
ENSMUST00000056086	ENSMUSG00000053603	10	81182605	81183849	-1	7	5	7	99	15	5	4	1	4	0	5	Q9D5G7	
ENSMUST00000056087	ENSMUSG00000048399	16	25286817	25422344	1	8	6	8	0	3	2	0	0	0	0	0		Q8CB49
ENSMUST00000056089	ENSMUSG00000050777	1	120067377	120074074	-1	16	10	28	67	14	5	30	12	5	64	48		Q9JJV3
ENSMUST00000056096	ENSMUSG00000050064	3	98382461	98753812	1	33	0	33	78	0	18	0	0	4	0	0	G5E8C0	
ENSMUST00000056097	ENSMUSG00000049109	10	28668360	28883818	1	11	0	15	7	14	7	0	32	0	25	20		Q8BGW0
ENSMUST00000056102	ENSMUSG00000050272	16	96592079	97170752	-1	60	30	113	61	57	29	0	0	3	0	2		Q9ERC8
ENSMUST00000056103						9	7	7	2	12	1	0	0	0	0	0		
ENSMUST00000056106	ENSMUSG00000041343	7	92581723	92637142	-1	11	0	0	0	3	0	2	4	4	2	9		Q3V096
ENSMUST00000056107	ENSMUSG00000062743	17	21383748	21399265	1	8	6	9	8	7	4	12	42	15	0	0	Q6PEP4	
ENSMUST00000056108	ENSMUSG00000047909	2	11777876	11790329	1	6	0	0	21	0	0	21	34	44	11	45		A2AS55
ENSMUST00000056110	ENSMUSG00000040856	12	109452823	109463336	1	12	0	19	19	20	6	0	0	0	0	0	Q925U3	
ENSMUST00000056113	ENSMUSG00000045019	17	56953490	56982126	-1	196	240	850	329	171	102	7	12	5	1	6		Q8R4X1
ENSMUST00000056117	ENSMUSG00000015533	13	114835916	114932041	-1	20	14	15	20	20	8	8	6	11	2	22		Q62469
ENSMUST00000056118	ENSMUSG00000056706	16	89507704	89508323	-1	7	2	8	3	5	0	0	0	0	0	0		Q9D3I6
ENSMUST00000056120	ENSMUSG00000048620	7	6460511	6461455	1	8	4	10	7	9	6	0	0	0	0	0	Q8VGH5	
ENSMUST00000056124	ENSMUSG00000043323	5	110361754	110448503	-1	0	0	29	361	0	0	7	62	26	7	24	E9PUB6	
ENSMUST00000056129	ENSMUSG00000045903	19	4984355	4989971	-1	20	22	75	189	25	13	0	0	1	0	0		Q8BGD7
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ENSMUST00000056136	ENSMUSG00000044708	1	172341210	172374085	1	154	100	287	1182	201	127	6	16	14	1	26	Q56VN0	Q9JM63
ENSMUST00000056140	ENSMUSG00000055271	12	103406822	103407820	-1	7	4	13	11	11	3	1	3	3	0	1	Q9D253	
ENSMUST00000056144	ENSMUSG00000054938	7	6474088	6475153	1	57	23	137	771	144	69	1	0	0	0	1	Q8VGH6	
ENSMUST00000056146	ENSMUSG00000044145	2	127186355	127208280	-1	7	11	9	15	14	9	1	1	2	5	0	Q8BWE1	
ENSMUST00000056147	ENSMUSG00000062101	17	55938381	55949500	-1	0	0	1	40	0	0	52	275	73	112	25	Q8K0G9	
ENSMUST00000056149	ENSMUSG00000032046	2	150832493	150904741	-1	0	0	0	78	13	0	285	442	299	33	212		Q99LR1
ENSMUST00000056153	ENSMUSG00000044788	11	115279622	115297663	-1	45	37	61	134	42	41	5	20	9	4	14		Q80UG1
ENSMUST00000056157	ENSMUSG00000012519	8	111311797	111338177	-1	18	15	25	0	0	0	0	30	0	13	31		Q9D2Y4
ENSMUST00000056159	ENSMUSG00000025069	19	47865545	47886324	1	0	0	12	15	0	5	0	0	0	0	0		Q8K2Q2
ENSMUST00000056170	ENSMUSG00000046085	2	103966943	104028361	-1	7	3	6	23	3	4	0	0	0	0	0	A2BHN9	
ENSMUST00000056176	ENSMUSG00000009621	2	27262104	27427033	-1	41	13	0	253	53	33	50	53	37	15	133		Q60992
ENSMUST00000056177	ENSMUSG00000016664	15	83375607	83464606	-1	21	24	166	43	11	22	462	872	895	59	634	Q3TDA7	Q9WVE8
ENSMUST00000056181	ENSMUSG00000050373	2	164785823	164793816	1	7	0	0	0	0	0	0	17	16	0	31	Q3UR97	
ENSMUST00000056184	ENSMUSG00000044243	11	76672470	76673676	1	8	5	28	259	14	6	0	2	0	0	1		Q5RJB0
ENSMUST00000056191						4	13	10	46	3	1	0	1	0	0	8		
ENSMUST00000056198	ENSMUSG00000044957	17	53507460	53539451	-1	11	19	25	15	26	11	0	7	2	1	2		Q8BVT6
ENSMUST00000056222	ENSMUSG00000045540	7	103345982	103346926	-1	0	0	3	2	2	3	0	0	0	0	0	E9PUN7	
ENSMUST00000056228	ENSMUSG00000044408	12	54645374	54656572	-1	5	0	8	61	6	3	187	436	158	401	103		Q8R207
ENSMUST00000056232	ENSMUSG00000045598	7	127233061	127238179	1	17	4	100	38	23	19	88	116	54	7	50		Q3US17
ENSMUST00000056234	ENSMUSG00000045946	12	49401277	49401837	1	0	1	0	111	3	1	0	0	0	0	0	F6QM68	
ENSMUST00000056235	ENSMUSG00000045792	7	102984221	102985162	-1	6	3	8	5	9	5	0	0	0	0	0	Q8VH17	
ENSMUST00000056237	ENSMUSG00000037134	8	77549397	77581338	1	0	0	0	13	0	0	87	517	244	168	162	F8WIU7	
ENSMUST00000056241	ENSMUSG00000002059	11	78188430	78192193	1	1	0	0	0	0	0	0	0	0	4	4	B1AQD3	
ENSMUST00000056246	ENSMUSG00000062116	7	7114690	7121445	-1	9	17	36	22	17	6	97	363	130	92	110	Q7TNU5	
ENSMUST00000056256	ENSMUSG00000045877	11	43587040	43589048	1	44	27	144	67	29	11	7	27	13	1	25	Q9D443	
ENSMUST00000056288	ENSMUSG00000045165	7	127091359	127093986	1	15	6	32	44	20	9	4936	5534	2875	936	2116		Q8C708
ENSMUST00000056290	ENSMUSG00000009073	11	4765845	4849536	-1	30	4	15	205	30	15	0	0	17	0	26		P46662

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000056292						6	4	6	0	2	2	104	587	153	290	79		
ENSMUST00000056312	ENSMUSG00000046110	2	121439059	121456781	-1	0	0	0	0	0	0	0	0	0	0	0		Q5XK03
ENSMUST00000056328	ENSMUSG00000053128	9	44066327	44113517	-1	35	20	145	97	71	33	257	161	212	20	131		Q8BUH7
ENSMUST00000056329	ENSMUSG00000044737	7	43690418	43695536	1	22	20	30	191	33	15	1	3	1	0	1	A0A0B6VSR0	Q8CGR5
ENSMUST00000056331	ENSMUSG00000046282	8	40793273	40797303	1	4	11	6	10	9	5	0	0	0	0	0	Q7M763	
ENSMUST00000056336	ENSMUSG00000050511	4	132110726	132144486	-1	32	20	71	297	37	21	0	5	1	0	1	A2AD37	P32300
ENSMUST00000056338	ENSMUSG00000043456	7	37472135	37773641	-1	0	5	31	135	15	0	0	0	0	0	0		Q8K083
ENSMUST00000056339	ENSMUSG00000045575	17	20993727	20994686	-1	0	6	4	0	2	4	0	0	0	0	0	Q8R294	
ENSMUST00000056344	ENSMUSG00000050830	11	11114223	11268931	1	0	2	9	167	6	1	0	0	0	0	1		Q8C8N3
ENSMUST00000056355	ENSMUSG00000048142	5	33995984	34005916	1	51	30	206	595	83	39	140	147	79	11	119		
ENSMUST00000056362	ENSMUSG00000043485	11	100037347	100041554	-1	10	8	10	60	11	2	0	0	0	0	0		Q9D646
ENSMUST00000056364	ENSMUSG00000049098	9	38401720	38403829	1	3	4	1	2	5	7	0	0	0	0	0		Q60886
ENSMUST00000056365	ENSMUSG00000050248	5	37338499	37425055	1	33	8	26	83	38	22	1	0	0	1	12		Q8K1G2
ENSMUST00000056370	ENSMUSG00000028066	3	88394143	88410331	-1	0	0	0	4	3	0	168	169	67	9	52		Q9CPV5
ENSMUST00000056376	ENSMUSG00000026836	2	58388644	58567157	-1	0	0	5	32	0	0	9	0	3	3	17		P37172
ENSMUST00000056385	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	0	0	0	0	0	0	0	0		P42866
ENSMUST00000056391	ENSMUSG00000024947	19	6334979	6340891	1	13	0	15	391	14	15	0	153	213	0	102		O88559
ENSMUST00000056396	ENSMUSG00000051255	19	23675844	23676712	1	0	3	0	0	0	4	0	208	77	105	42	B2RXM7	Q9D1J3
ENSMUST00000056398	ENSMUSG00000044155	6	18848579	18855751	1	4	1	1	47	0	0	165	346	167	617	120		Q6ZWM4
ENSMUST00000056401	ENSMUSG00000051237	15	25137530	25149159	-1	6	5	9	4	9	3	0	0	0	1	1	Q8BHE6	
ENSMUST00000056403	ENSMUSG00000044927	6	87980421	87981637	-1	0	6	12	199	9	2	2	3	1	0	1	Q80ZM5	
ENSMUST00000056406	ENSMUSG00000050592	2	32050055	32084857	-1	25	16	63	148	37	18	127	169	85	24	199	A2ATN4	Q8C552
ENSMUST00000056408	ENSMUSG00000050128	2	85886802	85887737	1	6	3	2	5	3	2	0	0	0	0	0	A2ASU6	
ENSMUST00000056409						0	6	0	3	0	0	0	0	0	0	0		
ENSMUST00000056410	ENSMUSG00000040621	X	166170454	166190512	1	73	84	164	82	82	59	8	25	20	7	21		Q8BHE1
ENSMUST00000056416	ENSMUSG00000008658	16	6809222	7412479	1	14	15	18	15	17	11	0	0	0	0	0		Q9JJ43
ENSMUST00000056427	ENSMUSG00000058672	13	34074301	34078008	-1	30	19	63	146	36	9	102	178	66	288	260		Q7TMM9
ENSMUST00000056433	ENSMUSG00000000194	2	31152316	31218775	1	99	68	179	98	94	41	899	1412	1157	153	883	Q148Z6	Q8BUV8
ENSMUST00000056435	ENSMUSG00000047594	2	87387707	87388687	1	2	1	4	3	2	3	0	0	0	0	0	Q8VGT9	
ENSMUST00000056442	ENSMUSG00000039728	7	49910146	49963856	1	158	99	267	1591	213	125	2	7	3	3	8	B2RQX9	
ENSMUST00000056449	ENSMUSG00000048865	1	171388954	171410298	1	0	0	0	0	0	0	4932	16193	11649	1125	7992	E9QMX7	
ENSMUST00000056458	ENSMUSG00000060288	4	119300010	119320546	-1	0	0	0	0	0	0	17	54	29	40	0		Q9D868
ENSMUST00000056460	ENSMUSG00000048875	18	50567656	50568699	-1	2	4	8	6	7	3	0	0	0	0	0	A0A0C3SFZ4	
ENSMUST00000056467	ENSMUSG00000047036	9	122851914	122862128	-1	11	13	25	20	12	11	189	497	476	64	333		Q8R2V3
ENSMUST00000056470	ENSMUSG00000055560	13	67405722	67421418	-1	280	331	467	174	260	122	7	41	16	15	24	Q8BZ17	
ENSMUST00000056474	ENSMUSG00000043633	4	43659622	43669145	-1	9	7	75	31	20	9	0	0	0	0	0		Q8C627
ENSMUST00000056480	ENSMUSG00000039059	2	180099465	180104488	-1	15	5	20	221	38	6	0	0	0	0	0	Q540P3	P58406
ENSMUST00000056482	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	0	0	0	63	291	172	62	267		Q9Z0R4
ENSMUST00000056484	ENSMUSG00000051790	11	69823122	69837784	-1	10	9	164	19	23	0	13	53	18	0	41		Q69ZK9
ENSMUST00000056495	ENSMUSG00000027478	2	153649450	153687730	1	0	0	28	0	0	0	0	0	2	0	0	Q3KR45	
ENSMUST00000056499	ENSMUSG00000048501	9	39077698	39078816	-1	4	0	0	1	2	1	0	0	0	0	0	Q9EQ93	
ENSMUST00000056502	ENSMUSG00000046449	X	104077434	104201185	-1	3	2	13	69	8	4	0	0	0	0	0	Q003Y7	Q5DTT1
ENSMUST00000056508	ENSMUSG00000004319	8	60910389	60983300	-1	0	0	0	0	0	0	0	0	0	0	0	Q8K4W8	
ENSMUST00000056512	ENSMUSG00000042015	13	94976344	95023314	1	5	6	9	5	24	4	54	194	104	20	72		Q3UDP0
ENSMUST00000056517	ENSMUSG00000051056	4	32600644	32602760	-1	10	8	17	14	12	4	0	0	0	0	0		Q9WUS4
ENSMUST00000056518	ENSMUSG00000050821	16	20693282	20703048	1	8	13	20	26	26	3	13	0	13	0	21		Q8BWU3
ENSMUST00000056521	ENSMUSG00000044117	16	13986604	14101500	1	7	10	19	16	16	10	0	0	0	0	0		Q8R1Y2
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ENSMUST00000056549	ENSMUSG00000047603	7	24134169	24143241	1	19	15	55	42	22	8	13	52	26	8	25	Q499D5	
ENSMUST00000056558	ENSMUSG00000050919	13	99184823	99247037	1	24	18	63	114	30	11	0	1	1	0	5	Q6NS86	
ENSMUST00000056567	ENSMUSG00000039577	4	152476706	152563183	1	0	0	0	0	0	0	0	0	0	0	0		P59240
ENSMUST00000056578	ENSMUSG00000047843	5	144244437	144446757	1	0	2	0	27	1	4	86	195	83	16	42		P28662
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ENSMUST00000056590	ENSMUSG00000046203	3	92373915	92375229	1	0	5	9	6	6	3	0	0	0	0	0		O70558
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ENSMUST00000056614	ENSMUSG00000050232	X	101731535	101734269	-1	9	6	12	9	7	3	37	50	39	13	46		O88410
ENSMUST00000056617	ENSMUSG00000044017	5	129096750	129204599	1	62	28	82	63	69	32	1	2	0	13	52		Q80T32
ENSMUST00000056623	ENSMUSG00000048108	6	116679063	116716913	-1	54	20	499	99	58	19	0	3	2	0	0		Q8C3K5
ENSMUST00000056635	ENSMUSG00000049878	4	121145373	121215084	-1	0	0	33	149	20	21	1070	5930	2948	996	2314	A2A7F4	
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ENSMUST00000056641	ENSMUSG00000026979	2	24367580	24414954	1	0	0	46	8	8	1	2693	3963	2567	473	1842		Q8BLR5
ENSMUST00000056649	ENSMUSG00000034201	11	5054132	5065327	-1	9	4	0	33	0	5	0	0	4	4	75		Q8JZP9
ENSMUST00000056654	ENSMUSG00000044134	5	121848984	121854632	1	12	5	32	316	35	11	126	170	97	12	65		Q8BH49
ENSMUST00000056660	ENSMUSG00000046157	12	78961795	79007627	-1	16	0	0	163	34	15	35	0	37	0	52		Q8BFQ2
ENSMUST00000056665	ENSMUSG00000048732	11	100462614	100472741	-1	11	15	8	269	24	3	56	51	141	11	68	Q14DU1	Q8CE33
ENSMUST00000056674	ENSMUSG00000044348	X	136981116	137038302	-1	3	0	0	0	0	0	0	0	3	0	7	A2AF34	
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ENSMUST00000056677	ENSMUSG00000046010	11	82764345	82765935	1	13	4	33	41	17	8	169	449	227	144	199		Q8R1N0
ENSMUST00000056683	ENSMUSG00000087598	7	24193947	24211443	-1	5	9	15	15	6	0	5	0	0	0	13	Q9R164	
ENSMUST00000056686	ENSMUSG00000074217	8	84010222	84012171	-1	0	0	0	0	0	2	0	0	0	0	0	F6WBA1	
ENSMUST00000056708	ENSMUSG00000047298	19	27322588	27337179	1	34	25	57	124	46	13	0	0	0	0	0		Q8CFS6
ENSMUST00000056710	ENSMUSG00000015750	3	95893969	95898288	1	5	3	6	89	0	1	0	0	122	20	136		Q8BVF7
ENSMUST00000056712	ENSMUSG00000045689	18	37307455	37311172	1	23	16	25	44	25	11	0	0	0	0	0	Q91XZ6	
ENSMUST00000056715	ENSMUSG00000009569	16	13256481	13417529	1	4	1	6	0	0	1	3	4	1	3	5	Q8R2L3	
ENSMUST00000056718	ENSMUSG00000042863	2	85923270	85924193	1	4	5	2	4	6	3	0	0	0	0	0	Q7TR90	
ENSMUST00000056725	ENSMUSG00000051592	X	6979652	7041619	-1	0	0	0	0	0	2	1	0	1	0	0	A2AEP2	
ENSMUST00000056727	ENSMUSG00000050742	16	19285743	19286837	-1	4	1	1	3	7	1	0	0	0	0	0	Q8VF87	
ENSMUST00000056728	ENSMUSG00000038570	7	82632960	82648528	-1	9	9	8	10	16	8	0	0	0	0	0		Q8BQB6
ENSMUST00000056732	ENSMUSG00000048222	2	121460235	121474067	-1	17	7	29	33	22	6	464	1495	735	2013	815		Q9CQU1
ENSMUST00000056736	ENSMUSG00000046041	10	129691113	129692039	-1	0	3	5	0	0	1	0	0	0	0	0	Q8VFI3	
ENSMUST00000056740	ENSMUSG00000046167	9	54286486	54341786	1	26	28	49	109	34	14	0	6	0	0	0		Q8BMF8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000056745	ENSMUSG00000074060	9	109552602	109568262	-1	6	16	10	7	13	6	1	10	3	0	0	L7N1X6	
ENSMUST00000056749	ENSMUSG00000042997	3	53448583	53463332	-1	35	22	46	0	0	0	284	487	401	85	269		Q8CCH2
ENSMUST00000056754	ENSMUSG00000048573	X	153558593	153559429	1	0	3	3	4	0	0	0	0	0	0	0	Q80ZR9	
ENSMUST00000056755	ENSMUSG00000031934	9	15005161	15045478	-1	0	0	2	187	2	0	55	116	41	19	63	B1PL19	
ENSMUST00000056758	ENSMUSG00000028161	3	136670124	136937727	1	15	4	9	0	10	0	441	1472	1360	129	743	B2RRX2	P63328
ENSMUST00000056759	ENSMUSG00000040328	11	48978889	49135387	1	35	17	79	31	46	19	0	15	5	0	0		Q8VGD6
ENSMUST00000056760	ENSMUSG00000051379	2	140650914	140671469	-1	9	8	0	9	14	3	0	0	0	0	0	Q8BGT1	Q8BGT1
ENSMUST00000056767						36	27	102	56	40	14	0	0	0	0	0		
ENSMUST00000056773	ENSMUSG00000026504	1	176814660	177020437	1	40	42	49	153	71	33	6	9	4	4	0	E9Q2E2	
ENSMUST00000056781	ENSMUSG00000048445	11	120826529	120932872	-1	19	14	36	95	35	26	39	169	96	5	107		Q6PHN1
ENSMUST00000056795	ENSMUSG00000045812	9	40100544	40101488	-1	2	2	6	3	2	2	0	0	0	0	0	Q8VFN1	
ENSMUST00000056815	ENSMUSG00000026077	1	39193731	39363236	1	20	15	42	138	38	12	0	0	0	0	1	G3X9B7	
ENSMUST00000056820	ENSMUSG00000003269	7	45806637	45814581	-1	0	0	0	32	0	0	0	0	0	0	0		P63034
ENSMUST00000056822	ENSMUSG00000043487	12	84100654	84111349	1	23	16	97	180	27	15	0	2	0	1	0	B2RTE4	Q32Q92
ENSMUST00000056849	ENSMUSG00000044923	2	85983842	85984798	1	5	2	6	1	4	4	0	0	0	0	0	A0PK66	Q8VFL5
ENSMUST00000056865	ENSMUSG00000049315	2	36784276	36787468	1	5	0	2	3	0	0	0	0	0	0	0	Q8VGK3	
ENSMUST00000056866	ENSMUSG00000043286	17	28858411	28890308	1	77	56	105	82	109	56	150	247	225	16	108	B2KF06	Q3V1D5
ENSMUST00000056882	ENSMUSG00000046160	16	91269772	91271933	1	8	0	7	302	16	6	0	0	0	0	0	Q3UN59	Q9JKN5
ENSMUST00000056888	ENSMUSG00000005986	19	4270180	4283137	-1	0	0	0	0	0	8	126	424	171	0	260		Q6PD24
ENSMUST00000056889	ENSMUSG00000063870	6	125095981	125130591	1	18	0	16	0	0	0	1	0	9	6	6		Q6PDQ2
ENSMUST00000056890	ENSMUSG00000050503	9	66508459	66514593	-1	22	19	29	208	39	23	65	171	102	11	77		Q8C7B6
ENSMUST00000056898	ENSMUSG00000051431	3	59178923	59195104	-1	2	5	0	1	7	0	0	1	1	1	1	Q059H2	
ENSMUST00000056900						30	27	68	25	35	16	0	2	4	0	11		
ENSMUST00000056904	ENSMUSG00000051220	X	102141716	102157091	-1	261	206	175	167	249	104	64	179	122	121	76		Q8BHK9
ENSMUST00000056907	ENSMUSG00000049323	11	60777524	60788287	1	30	34	96	55	51	33	628	1417	1258	110	977		Q3UMB5
ENSMUST00000056914	ENSMUSG00000048186	2	4717831	4802142	1	0	9	0	2	9	0	0	0	0	0	0	Q0VE44	Q8BSV3
ENSMUST00000056915	ENSMUSG00000047307	18	37442500	37446209	1	33	26	129	34	44	14	0	2	4	0	1	Q91Y06	
ENSMUST00000056919	ENSMUSG00000046707	8	95446096	95488820	-1	41	31	59	48	47	19	220	616	319	43	192	Q545V8	O54833
ENSMUST00000056924	ENSMUSG00000051413	2	153227759	153241426	-1	35	23	17	58	49	27	862	1254	1299	79	679	Q925T4	
ENSMUST00000056925	ENSMUSG00000048126	1	90765923	90843971	-1	72	51	182	66	78	37	0	0	0	0	25	E9PWQ3	
ENSMUST00000056931	ENSMUSG00000025223	19	46032593	46045214	-1	7	4	10	110	5	3	18	20	31	15	9		P70662
ENSMUST00000056932	ENSMUSG00000049357	18	34579846	34597468	-1	0	12	0	0	0	8	100	294	46	57	31	G3X9B4	
ENSMUST00000056937	ENSMUSG00000043510	5	110829070	110839777	-1	0	0	2	90	7	2	35	158	77	45	42		
ENSMUST00000056941	ENSMUSG00000044084	11	69816566	69818465	-1	17	9	97	25	17	12	0	0	0	0	0		Q8C5U4
ENSMUST00000056946	ENSMUSG00000047180	1	36264597	36274679	-1	483	393	1592	673	515	272	3861	7152	2636	430	2438		Q8CJC5
ENSMUST00000056948						0	0	0	0	0	0	0	0	72	123	5		
ENSMUST00000056949	ENSMUSG00000046846	9	62270729	62282179	-1	20	12	28	27	25	10	0	0	0	0	0		Q9D5A0
ENSMUST00000056950	ENSMUSG00000044456	12	102283048	102390855	1	0	0	0	163	0	0	141	76	397	0	183		P59729
ENSMUST00000056955	ENSMUSG00000047988	11	97490783	97500340	-1	2	6	19	31	14	8	1	3	3	0	9	Q9D3X4	
ENSMUST00000056961	ENSMUSG00000049217	10	129472694	129473629	1	6	4	5	1	3	0	0	0	0	0	0	Q8VFI0	
ENSMUST00000056962	ENSMUSG00000041617	16	17646470	17650738	1	9	4	11	47	12	2	0	0	0	0	2	E9Q9U8	
ENSMUST00000056965	ENSMUSG00000055401	4	148145716	148152140	-1	3	0	0	35	0	0	208	268	102	153	56		Q9QZN4
ENSMUST00000056972	ENSMUSG00000046441	8	110215665	110224486	1	24	14	20	28	18	9	26	75	38	25	42		Q8BWQ4
ENSMUST00000056974	ENSMUSG00000048756	10	42181841	42276755	-1	0	6	1	10	10	0	0	0	0	0	0		Q9WVH4
ENSMUST00000056977	ENSMUSG00000070691	4	135120652	135177990	1	80	60	429	463	126	78	130	215	122	12	207	Q3U1Q3	
ENSMUST00000056978	ENSMUSG00000021375	13	46749087	46929718	-1	44	24	62	75	58	37	53	90	95	14	192	F8VQ75	
ENSMUST00000056991	ENSMUSG00000042800	1	170308803	170312125	1	8	3	10	4	14	3	4	2	4	0	9		Q4FZF2
ENSMUST00000056994	ENSMUSG00000044544	10	120765774	120778886	1	59	65	183	65	61	32	5	12	5	3	5	Q9D5W2	
ENSMUST00000056997	ENSMUSG00000021982	14	59560896	59597836	-1	5	0	0	0	0	0	116	349	215	341	106		Q8BMD5
ENSMUST00000057000	ENSMUSG00000021012	12	98746968	98787774	1	11	3	0	39	0	0	0	0	24	0	25		Q8BJ05
ENSMUST00000057015	ENSMUSG00000021733	14	14703025	14799943	1	9	13	25	66	14	11	159	291	252	24	210	F8VQC9	
ENSMUST00000057018	ENSMUSG00000038094	16	29395853	29544864	-1	0	0	0	0	0	0	0	0	0	0	0	E9QPP7	
ENSMUST00000057019	ENSMUSG00000044338	2	85136225	85139923	1	38	25	52	26	40	17	18	37	7	0	4		Q9WV08
ENSMUST00000057021	ENSMUSG00000048387	12	9574442	9581499	1	32	25	204	173	37	10	1	1	0	1	9		Q9WVG7
ENSMUST00000057023	ENSMUSG00000051048	7	100285520	100319699	1	0	0	0	0	0	0	0	0	0	0	0	H7BX23	
ENSMUST00000057026	ENSMUSG00000048856	12	108851129	108856814	1	17	10	46	47	28	9	6	18	4	8	16		Q6IS41
ENSMUST00000057028	ENSMUSG00000044433	8	3587450	3609074	1	0	17	0	212	41	16	0	5	0	1	6	U5LK19	Q80VC9
ENSMUST00000057029	ENSMUSG00000062012	17	23575845	23599487	-1	3	8	10	40	15	0	0	0	0	0	0		P10754
ENSMUST00000057037	ENSMUSG00000057335	1	176733653	176814067	-1	0	0	0	0	0	0	90	0	0	0	0	H7BX26	
ENSMUST00000057038						2	0	0	5	4	3	0	0	0	0	0		
ENSMUST00000057043	ENSMUSG00000028619	4	107134155	107179116	-1	152	149	398	225	203	108	162	486	321	135	183		Q8R2M0
ENSMUST00000057054	ENSMUSG00000001493	11	101877510	101894374	-1	19	9	51	33	18	10	0	3	1	1	2		P32442
ENSMUST00000057062	ENSMUSG00000046836	1	183276352	183297269	-1	16	26	0	0	0	0	280	1051	435	236	382		Q8K2Q7
ENSMUST00000057067	ENSMUSG00000043289	9	81863670	82206007	1	72	88	316	242	100	39	0	5	1	1	5		Q8BRM6
ENSMUST00000057070	ENSMUSG00000078995	13	67362113	67375810	-1	19	13	6	10	19	6	6	37	12	5	1	B2RUK9	
ENSMUST00000057071	ENSMUSG00000050504	X	50009306	50010235	-1	4	1	3	0	3	1	0	0	0	0	0	Q8VF35	
ENSMUST00000057072	ENSMUSG00000050114	2	80292472	80295356	1	10	9	9	17	9	6	0	0	0	0	0	Q8BG37	
ENSMUST00000057074	ENSMUSG00000043346	17	91236787	91238116	1	6	0	0	0	0	3	18	39	15	39	17		Q9CPT3
ENSMUST00000057076	ENSMUSG00000047390	8	21881713	21885421	-1	4	0	0	4	0	0	0	0	0	0	0	Q32MD8	Q8R2I6
ENSMUST00000057080	ENSMUSG00000045111	10	23984609	23985646	-1	4	2	14	5	8	5	0	0	0	0	0		Q5QD13
ENSMUST00000057089	ENSMUSG00000020453	11	3288874	3309083	1	0	0	9	0	0	0	119	63	15	0	58	Q9JMG9	
ENSMUST00000057090	ENSMUSG00000039376	14	20658946	20668354	-1	44	19	0	0	50	24	0	0	0	0	0		Q8BWB1
ENSMUST00000057093	ENSMUSG00000044149	X	36887540	36902899	-1	2	8	10	12	7	3	5	33	9	3	11		Q8BY02
ENSMUST00000057101	ENSMUSG00000050089	X	7067519	7078609	1	5	0	0	0	0	0	0	0	0	0	0	A1L3T6	Q60662
ENSMUST00000057104	ENSMUSG00000051340	7	104084131	104085078	-1	7	7	12	2	3	4	0	0	0	0	0	Q7TRQ1	
ENSMUST00000057110	ENSMUSG00000043424	18	43475418	43477796	-1	0	3	1	50	4	3	125	875	239	83	132		Q66JS6
ENSMUST00000057113	ENSMUSG00000048994	X	9849703	9850255	1	1	2	8	3	0	1	0	0	0	0	0	Q9D4U4	
ENSMUST00000057115	ENSMUSG00000044792	13	59755409	59769810	-1	15	11	16	18	39	5	159	430	178	413	220		Q9D924
ENSMUST00000057123	ENSMUSG00000046130	7	26266831	26267775	1	2	3	0	3	4	1	0	0	0	0	0	E9Q2N4	
ENSMUST00000057135	ENSMUSG00000090100	2	120732816	120850604	-1	0	0	0	0	46	48	0	132	0	44	116		Q3UVR3
ENSMUST00000057145	ENSMUSG00000045502	5	123863570	123865499	-1	16	12	24	24	10	4	114	864	120	138	281	Q0VBA6	Q9EP66
ENSMUST00000057150	ENSMUSG00000047757	X	164980592	164997272	1	2	0	4	0	1	0	0	0	0	0	0	B1AW75	
ENSMUST00000057151	ENSMUSG00000043061	12	30584443	30591213	1	7	6	18	28	5	10	132	512	182	113	100		Q3TUD9
ENSMUST00000057161	ENSMUSG00000044292	9	39993812	39994747	1	5	9	6	10	9	7	0	0	0	0	0	E9Q985	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000057167	ENSMUSG00000021490	13	55399648	55414695	1	18	15	75	37	36	10	2	0	0	0	4	Q9D2V6	
ENSMUST00000057169	ENSMUSG00000050700	2	160906437	160912328	-1	0	23	70	233	46	23	0	0	0	0	0		P59900
ENSMUST00000057174	ENSMUSG00000005936	17	28951950	28969549	1	0	0	0	9	0	0	706	159	570	17	584		Q8CDD8
ENSMUST00000057176	ENSMUSG00000043418	14	37068049	37073735	1	35	26	39	19	46	18	0	0	0	0	1		Q6PFC5
ENSMUST00000057177	ENSMUSG00000045996	15	36174010	36177010	1	0	3	0	0	4	0	37	68	24	128	5	Q8BFX0	
ENSMUST00000057178	ENSMUSG00000044220	19	43612325	43615892	1	19	9	35	319	35	11	0	3	0	0	1		P97334
ENSMUST00000057180	ENSMUSG00000044150	X	159526688	159593081	1	0	0	6	0	3	2	5	82	71	14	45		A2AG58
ENSMUST00000057185	ENSMUSG00000051375	18	38185914	38212053	-1	13	4	24	23	13	14	0	0	0	0	0	Q8CFX3	
ENSMUST00000057186	ENSMUSG00000051136	3	27371351	27378010	1	21	14	35	242	31	10	0	0	0	0	1	Q0VBE5	Q99P50
ENSMUST00000057188	ENSMUSG00000044288	4	33924593	33948831	1	0	0	73	0	16	14	0	0	0	0	0		P47746
ENSMUST00000057190	ENSMUSG00000046173	17	9666497	9669704	-1	18	17	25	45	26	7	0	0	0	0	0	Q9D4E6	
ENSMUST00000057194	ENSMUSG00000046417	11	62604884	62648523	-1	10	9	16	63	17	5	18	19	8	3	16		Q7TSF4
ENSMUST00000057195	ENSMUSG00000074141	7	44816088	44840809	1	1	0	1	186	1	0	766	763	563	170	370	Q5FWJ9	Q63850
ENSMUST00000057198	ENSMUSG00000050549	3	127869058	127896324	-1	2	1	1	23	4	0	238	634	212	28	85	A0A0H2UKC2	
ENSMUST00000057207	ENSMUSG00000049336	11	36006656	37235964	-1	0	12	0	28	0	0	0	0	0	0	0	A0A0A0MQ92	
ENSMUST00000057208	ENSMUSG00000060679	1	42851233	42905683	1	7	2	4	26	3	3	96	312	173	253	133		Q9D7N3
ENSMUST00000057209	ENSMUSG00000042216	5	113243220	113310786	-1	9	16	34	0	0	0	0	1	0	3	3		Q8BPQ7
ENSMUST00000057216						0	0	0	0	0	0	57	312	98	206	38		
ENSMUST00000057224	ENSMUSG00000048038	2	26271646	26294557	-1	11	13	48	30	35	15	0	0	0	0	0	Q8C5V8	
ENSMUST00000057228	ENSMUSG00000051242	18	37400855	37403909	1	17	15	29	34	24	11	0	0	0	0	0	E9Q5G2	
ENSMUST00000057229	ENSMUSG00000043308	7	11880343	11881260	1	1	0	6	1	3	1	0	0	0	0	0	Q8R289	
ENSMUST00000057236	ENSMUSG00000047108	15	81406926	81408299	-1	3	1	7	1	5	3	0	1	0	1	0		Q9QYI8
ENSMUST00000057241	ENSMUSG00000069206	13	67424549	67451624	-1	103	105	86	132	132	81	3	26	8	7	14	Q3UWF5	
ENSMUST00000057243	ENSMUSG00000048572	19	24674008	24679661	1	27	21	106	27	18	10	1	0	3	0	1		Q8C353
ENSMUST00000057251	ENSMUSG00000090631	6	42486163	42487214	-1	6	6	27	9	12	4	10	19	20	30	22	B2RT27	
ENSMUST00000057254	ENSMUSG00000051618	7	104140623	104143279	-1	22	8	31	29	21	15	0	0	0	0	0	Q497R3	Q8C5U9
ENSMUST00000057256	ENSMUSG00000022195	15	12808177	12824657	-1	51	59	209	101	71	41	64	303	145	15	171		Q8BGC1
ENSMUST00000057257	ENSMUSG00000005078	12	72085589	72101461	1	6	1	20	244	13	0	29	55	64	95	50		Q8BI36
ENSMUST00000057258	ENSMUSG00000046572	5	38668484	38684826	-1	43	31	77	0	53	16	20	48	52	0	44	J3QPN0	
ENSMUST00000057261	ENSMUSG00000053040	9	66814994	66834726	-1	0	0	20	0	0	0	163	670	193	69	125	Q4R1J7	
ENSMUST00000057262	ENSMUSG00000047330	1	78816758	78820028	1	6	3	34	19	16	0	0	0	0	0	0		Q9WTW3
ENSMUST00000057265	ENSMUSG00000050641	9	108436482	108446086	1	5	5	6	6	9	0	0	0	0	0	0	Q80ZQ7	
ENSMUST00000057270	ENSMUSG00000046008	19	58670365	58681786	1	10	3	11	4	15	8	0	0	0	0	0		Q6P8U6
ENSMUST00000057272	ENSMUSG00000037270	3	36863104	37053033	1	0	0	34	39	54	26	288	324	1946	202	1326		A2AAE1
ENSMUST00000057279	ENSMUSG00000046618	2	38931978	38963753	1	100	75	207	184	121	48	12	32	18	1	22	B2RQD8	Q8BHP7
ENSMUST00000057283	ENSMUSG00000041372	6	120203073	120294559	-1	0	0	0	0	0	0	0	0	0	0	0		Q6L8S8
ENSMUST00000057288	ENSMUSG00000020571	12	17266545	17284770	1	5	1	7	14	7	0	532	1199	727	2163	1174	Q3TML0	
ENSMUST00000057293	ENSMUSG00000046574	7	45027707	45052881	-1	59	37	121	759	78	44	257	221	275	19	270	E9PYL2	
ENSMUST00000057311	ENSMUSG00000047281	4	133600556	133602168	-1	52	28	123	96	79	43	113	224	117	21	115		O70456
ENSMUST00000057314	ENSMUSG00000047182	5	137643031	137645714	-1	32	12	63	202	31	13	2	6	2	1	1	O54718	
ENSMUST00000057320	ENSMUSG00000030650	7	118597297	118675086	1	8	10	17	3	4	6	0	0	0	0	0		Q32NZ6
ENSMUST00000057324	ENSMUSG00000047414	12	95692226	95785215	1	9	11	21	4	29	15	0	0	0	6	9	Q8BLU0	Q8BLU0
ENSMUST00000057325	ENSMUSG00000048924	13	100669481	100697240	1	25	31	38	26	36	0	532	2758	1019	873	735		Q5U465
ENSMUST00000057330	ENSMUSG00000018395	11	53567379	53601967	1	0	0	7	45	0	0	0	31	11	47	36	Q3UI47	
ENSMUST00000057337	ENSMUSG00000047632	19	36917550	36919615	-1	9	7	8	198	12	4	2	3	1	0	4		
ENSMUST00000057341	ENSMUSG00000050844	10	21593145	21622376	1	4	2	8	3	15	3	0	0	0	0	0	Q8CF20	
ENSMUST00000057343	ENSMUSG00000006498	10	79854427	79864771	1	0	0	0	0	0	0	443	47	579	9	382	E9QMW9	
ENSMUST00000057344	ENSMUSG00000048827	8	109614517	109672592	1	0	0	297	56	26	11	20	94	35	14	90	A2A258	Q2EG98
ENSMUST00000057361						4	6	6	10	5	1	0	0	0	0	0		
ENSMUST00000057369	ENSMUSG00000045148	2	89816328	89817260	1	2	1	7	0	3	0	0	0	0	0	0	A2AUA4	
ENSMUST00000057373	ENSMUSG00000077450	17	33742484	33760530	-1	46	38	52	61	37	27	537	1335	783	83	521	Q78ZJ8	P46638
ENSMUST00000057385	ENSMUSG00000051182	7	104596253	104597179	-1	7	2	9	10	10	3	0	0	0	0	0	E9Q252	
ENSMUST00000057386	ENSMUSG00000056184	15	98378096	98379197	-1	10	3	13	9	8	7	0	0	0	0	0	Q8VGU2	
ENSMUST00000057390	ENSMUSG00000048356	19	13780548	13781614	1	4	2	4	2	4	2	0	0	0	0	0	B9EHG2	
ENSMUST00000057394	ENSMUSG00000054940	17	38304521	38305460	-1	3	10	7	8	3	4	0	0	0	0	0	Q8VFC2	
ENSMUST00000057398	ENSMUSG00000046652	6	42400238	42401119	1	6	1	6	10	3	3	2	1	5	1	23		Q7TQB9
ENSMUST00000057405	ENSMUSG00000044375	17	71743557	71752885	-1	32	25	87	57	67	21	0	0	0	0	0		Q6PAC4
ENSMUST00000057407	ENSMUSG00000043102	2	31806166	31810580	-1	22	14	71	67	35	11	4	12	7	1	15		Q8CE23
ENSMUST00000057410	ENSMUSG00000006369	15	85205949	85286535	1	25	21	119	67	40	16	0	0	3	0	7	B2CQD6	Q08879
ENSMUST00000057416	ENSMUSG00000046675	12	102743760	102747561	1	7	12	33	136	17	10	99	501	138	137	96		Q8BH26
ENSMUST00000057421	ENSMUSG00000048668	6	128357000	128362911	-1	0	3	0	110	0	0	28	16	30	0	32	E9Q1D4	
ENSMUST00000057423	ENSMUSG00000051373	2	32095528	32110820	1	7	11	34	130	21	4	2	0	0	0	3		Q91WB2
ENSMUST00000057427						6	13	6	10	8	6	13	51	16	9	6		
ENSMUST00000057428	ENSMUSG00000044951	13	32700827	32783954	-1	173	112	299	2488	263	117	6	56	4	3	9	F8WIP5	
ENSMUST00000057431	ENSMUSG00000078173	3	89400988	89402793	-1	5	4	19	9	13	3	0	0	0	0	0	Q543C4	Q9WVB6
ENSMUST00000057438	ENSMUSG00000045210	1	9718622	9748382	-1	47	27	95	295	74	23	495	1151	868	93	684		
ENSMUST00000057439	ENSMUSG00000050023	2	88339567	88340514	1	1	2	3	1	3	1	0	0	0	0	0	Q8VG40	
ENSMUST00000057442	ENSMUSG00000047842	13	52504375	52530836	-1	112	81	591	463	117	75	8	13	10	2	28	Q3UWU7	Q5PR73
ENSMUST00000057453	ENSMUSG00000046016	13	21573510	21581652	-1	7	3	6	5	11	4	0	0	0	0	0	Q5SZS9	
ENSMUST00000057454	ENSMUSG00000046814	2	119167773	119172390	1	5	1	11	44	5	3	13	23	30	15	11	Q4VAF4	P99025
ENSMUST00000057465	ENSMUSG00000043122	12	112489448	112499927	1	28	16	67	39	48	15	0	1	0	0	0		
ENSMUST00000057477	ENSMUSG00000047626	10	129526229	129527167	1	3	3	2	0	4	0	0	0	0	0	0	Q8VGJ0	
ENSMUST00000057481	ENSMUSG00000051329	2	90677215	90736328	1	22	8	18	154	37	20	111	161	203	29	129		Q9Z0W3
ENSMUST00000057486	ENSMUSG00000048307	15	36477668	36496791	-1	18	13	26	28	17	9	454	1049	506	178	281		Q8BTZ5
ENSMUST00000057488	ENSMUSG00000022667	16	44765736	44794978	1	6	4	15	6	9	6	334	718	307	450	208		Q9ES57
ENSMUST00000057495	ENSMUSG00000035762	13	84222314	84295870	1	8	7	16	13	8	3	32	271	79	95	49		Q8C2L6
ENSMUST00000057497	ENSMUSG00000004415	5	136741759	136883209	-1	0	0	14	0	14	11	0	0	0	0	0		Q91VF6
ENSMUST00000057500	ENSMUSG00000051234	9	96470937	96478675	-1	16	13	19	52	15	6	218	640	205	484	135		Q9WTZ1
ENSMUST00000057501	ENSMUSG00000024298	17	32771236	32788287	-1	6	7	9	6	3	4	30	34	83	13	53	Q80XN4	
ENSMUST00000057502	ENSMUSG00000048231	17	36458917	36462334	-1	13	0	0	3	10	0	0	0	0	0	0	Q85ZW8	
ENSMUST00000057503	ENSMUSG00000027270	2	136052239	136069917	1	5	7	7	7	4	3	0	0	0	0	0		Q9D387
ENSMUST00000057516	ENSMUSG00000046932	13	22218861	22219820	-1	2	8	5	0	2	2	0	0	0	0	0	Q8R258	
ENSMUST00000057521						20	11	71	53	25	18	0	0	0	0	5		
ENSMUST00000057525	ENSMUSG00000036989	7	105604463	105633571	-1	0	1	0	14	0	7	34	34	0	0	15		Q9R1R2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000057528	ENSMUSG00000043948	7	105336746	105337714	-1	3	9	11	9	8	5	1	1	3	0	0	Q8VGW5	
ENSMUST00000057540	ENSMUSG00000059878	6	116624016	116628999	-1	0	1	1	62	0	0	95	169	43	49	58		Q9ERU3
ENSMUST00000057548	ENSMUSG00000046643	1	173203358	173204299	1	4	4	3	5	4	5	0	0	0	0	0	E9PWV2	
ENSMUST00000057551	ENSMUSG00000004642	5	33634952	33652574	-1	2	0	0	65	4	5	116	37	0	0	16	Q3U4T7	P97440
ENSMUST00000057557	ENSMUSG00000048170	7	128696441	128740495	-1	23	9	29	14	22	8	673	1758	962	146	621		Q8R3C0
ENSMUST00000057561	ENSMUSG00000031563	8	47826083	47990543	-1	34	27	55	167	49	19	42	77	106	19	108		Q6NXJ0
ENSMUST00000057567	ENSMUSG00000044103	2	24186476	24193568	1	586	645	535	465	614	278	3510	20324	4898	5355	3126	Q3U0P4	
ENSMUST00000057569	ENSMUSG00000046908	14	55765962	55768494	1	25	12	35	145	31	9	4916	9508	4800	315	2616	A7VJD3	O88855
ENSMUST00000057576	ENSMUSG00000034951	7	121879363	121981711	-1	158	104	319	653	167	73	133	268	209	25	156		
ENSMUST00000057578	ENSMUSG00000013736	6	106769120	106782474	1	3	4	5	24	9	0	133	679	90	145	51		Q8K1J6
ENSMUST00000057580	ENSMUSG00000028991	4	148448611	148557683	1	0	0	0	7	0	0	30	33	21	48	4		Q9JLN9
ENSMUST00000057596	ENSMUSG00000051118	9	19917229	19922510	1	7	3	4	0	3	0	0	0	0	0	0	Q8VEY9	
ENSMUST00000057598	ENSMUSG00000051098	13	81711417	81753275	1	15	10	20	191	22	9	19	68	31	8	20		Q8BL86
ENSMUST00000057608	ENSMUSG00000051652	10	77897575	77902536	-1	196	165	984	174	146	90	1	15	1	2	2	Q543Z4	P59034
ENSMUST00000057610	ENSMUSG00000040260	17	49456022	49564337	-1	54	42	114	95	69	29	26	58	46	2	44		Q80U19
ENSMUST00000057611	ENSMUSG00000047370	7	60155538	60156170	1	1	0	0	22	1	1	0	64	79	0	0	D3YZA3	
ENSMUST00000057612	ENSMUSG00000035279	7	4925844	4944821	1	55	27	217	299	76	33	4	2	0	0	1		Q8BV57
ENSMUST00000057613	ENSMUSG00000051279	4	9844372	9862345	1	15	16	40	247	18	9	0	0	0	0	1	A2AII0	P43028
ENSMUST00000057623	ENSMUSG00000062075	10	80901203	80918245	-1	21	8	45	120	27	19	0	23	0	0	0		
ENSMUST00000057625	ENSMUSG00000048355	X	136033367	136034946	1	3	9	4	76	7	0	0	0	0	0	0		Q9D365
ENSMUST00000057627	ENSMUSG00000047030	2	167481133	167492887	-1	39	27	88	46	62	34	807	1002	792	65	563	Q8K004	
ENSMUST00000057631	ENSMUSG00000038351	11	74849261	74897060	-1	33	0	71	70	18	0	26	30	25	8	54		Q80U12
ENSMUST00000057632	ENSMUSG00000023025	15	99970074	100016351	1	0	0	14	0	8	4	0	0	0	0	21	E9Q066	
ENSMUST00000057633	ENSMUSG00000045267	15	32177289	32178294	1	5	4	7	7	7	0	0	0	0	0	0	G3X986	
ENSMUST00000057634	ENSMUSG00000066392	12	88722876	90334935	1	3	0	0	0	0	0	0	0	0	0	0		Q6P9K9
ENSMUST00000057645	ENSMUSG00000036357	X	57496668	57503757	-1	15	12	10	28	14	4	0	0	0	0	0	Q1WKE2	Q80T62
ENSMUST00000057649	ENSMUSG00000045886	10	43524102	43524617	1	0	3	2	0	10	0	46	97	35	36	33		Q9CQV1
ENSMUST00000057650						6	1	41	16	11	7	0	0	0	0	0		
ENSMUST00000057652	ENSMUSG00000058402	7	29859979	29877292	1	0	0	0	0	0	0	7	13	0	0	11	Q7TMN8	
ENSMUST00000057653	ENSMUSG00000025317	8	121916126	121944904	-1	41	50	109	43	39	23	3	4	3	2	4		P23589
ENSMUST00000057659	ENSMUSG00000038039	10	58255497	58305599	1	0	0	15	46	8	0	205	347	581	167	281	B2RSU7	
ENSMUST00000057669	ENSMUSG00000063065	7	126759601	126765819	1	0	0	0	35	6	0	7542	4794	4142	629	2294		Q63844
ENSMUST00000057676	ENSMUSG00000050628	11	116434094	116439077	1	2	6	11	27	5	2	3041	3946	1949	663	1244		Q8BQH4
ENSMUST00000057679	ENSMUSG00000046491	11	43474276	43491525	1	0	0	0	0	5	9	0	0	0	0	0		Q9D8U4
ENSMUST00000057685	ENSMUSG00000046811	11	70519196	70520736	1	8	0	10	126	16	6	0	0	0	0	0		Q8K0R6
ENSMUST00000057686	ENSMUSG00000047102	6	42140936	42141895	1	4	3	1	2	1	0	0	0	0	0	0		Q7TQA5
ENSMUST00000057692	ENSMUSG00000029823	6	38551334	38609470	1	0	0	0	93	0	0	49	0	222	18	391		Q7TNC4
ENSMUST00000057716	ENSMUSG00000050623	19	6922426	6925380	-1	3	8	3	3	6	1	2	0	0	0	0		Q9CQP8
ENSMUST00000057717	ENSMUSG00000046556	8	95326137	95331950	-1	30	18	58	496	50	15	455	518	536	36	436		Q9ERR8
ENSMUST00000057718	ENSMUSG00000042888	14	101197690	101200330	-1	3	9	6	20	7	13	0	0	0	1	0		Q9D9B7
ENSMUST00000057722	ENSMUSG00000049427	11	53469749	53470479	-1	6	9	21	18	9	3	0	0	0	0	0	Q8C607	
ENSMUST00000057725	ENSMUSG00000027639	2	157097533	157135265	-1	28	30	52	332	56	42	3881	11092	5182	532	4777	F8WJE0	
ENSMUST00000057734	ENSMUSG00000020168	7	86465413	86466405	1	1	1	0	3	2	3	0	0	0	0	0	Q7TS05	
ENSMUST00000057740						15	20	45	26	56	18	5081	8302	4712	10749	2414		
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ENSMUST00000057752						4	2	6	2	3	1	0	0	0	0	0		
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ENSMUST00000057773	ENSMUSG00000049285	5	138194314	138195621	1	10	4	30	337	13	7	13	34	14	5	7		Q8BWY4
ENSMUST00000057775	ENSMUSG00000049052	10	129842020	129845997	-1	5	0	6	1	2	1	0	0	0	0	0	Q8VG64	
ENSMUST00000057781	ENSMUSG00000044938	9	77636500	77660127	1	49	37	62	234	53	26	1	5	7	1	4	G3X9D8	
ENSMUST00000057783	ENSMUSG00000044067	12	31706867	31713947	-1	8	5	3	5	15	2	0	0	0	0	0	G3X9C3	
ENSMUST00000057784	ENSMUSG00000031596	8	40862396	40922308	1	70	55	332	153	77	39	0	11	0	30	68		P18581
ENSMUST00000057792	ENSMUSG00000032667	6	5264147	5298455	-1	36	27	362	76	37	20	416	1666	723	447	447		Q62086
ENSMUST00000057793	ENSMUSG00000051149	2	168180986	168207112	-1	0	13	50	0	0	7	27	85	125	0	185	A2BDX0	Q9Z103
ENSMUST00000057795	ENSMUSG00000029422	5	123728426	123749414	-1	2	0	0	0	0	0	65	342	6	80	44		A2RTL5
ENSMUST00000057798	ENSMUSG00000004931	10	81268172	81273246	1	15	10	56	205	20	8	572	562	421	70	272		O88888
ENSMUST00000057799	ENSMUSG00000054519	11	59461197	59472474	-1	15	17	20	51	19	13	14	41	19	72	9	E9Q2M4	
ENSMUST00000057801	ENSMUSG00000044216	15	79483718	79505241	-1	15	10	26	70	23	12	0	0	0	0	0	Q8R435	
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ENSMUST00000057816	ENSMUSG00000089917	2	181569149	181584892	-1	0	0	0	31	0	0	0	441	223	92	127		Q91YL3
ENSMUST00000057817	ENSMUSG00000051680	7	106677534	106678485	-1	4	3	6	4	2	2	0	0	0	0	0	Q8VF89	
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ENSMUST00000057843	ENSMUSG00000051355	11	22896136	22982382	-1	4	2	12	2	5	3	6	48	12	20	7	Q8VI86	
ENSMUST00000057844	ENSMUSG00000045767	13	55693124	55703499	1	29	42	116	59	28	26	566	1033	852	98	556		Q80X32
ENSMUST00000057846	ENSMUSG00000049690	1	125913620	126830799	-1	14	20	81	0	0	15	0	0	0	0	0	Q29SA9	
ENSMUST00000057849	ENSMUSG00000045532	11	102939264	102946688	-1	4	6	17	107	12	5	0	0	0	0	0		O88992
ENSMUST00000057855	ENSMUSG00000043251	8	105289924	105296098	-1	14	12	60	202	33	18	11	18	6	1	7		Q8BI71
ENSMUST00000057859	ENSMUSG00000048285	12	70825514	70902232	1	37	30	47	122	47	19	135	212	154	46	186		Q8C0V9
ENSMUST00000057860	ENSMUSG00000047674	3	141210004	141212355	-1	7	9	5	8	16	3	0	0	0	0	0		P35487
ENSMUST00000057866	ENSMUSG00000048978	13	25252040	25270502	-1	17	7	0	28	3	6	0	0	0	0	0		P97799
ENSMUST00000057870	ENSMUSG00000046215	11	103649570	103650579	1	5	9	9	316	10	7	0	0	0	0	0	B2RV63	Q3URD2
ENSMUST00000057884	ENSMUSG00000023170	11	69913888	69916591	1	7	5	23	71	8	0	148	489	337	0	205	Q921N8	
ENSMUST00000057885	ENSMUSG00000047215	5	65388364	65391444	-1	17	21	39	73	28	7	3875	12752	3940	18894	2873	Q5EBQ6	P51410
ENSMUST00000057886	ENSMUSG00000048101	16	16672876	16676405	-1	3	7	4	0	4	1	0	0	0	0	1	A2RSZ3	Q9JHB2
ENSMUST00000057889						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000057892	ENSMUSG00000040481	11	107033081	107132127	-1	29	23	63	54	87	45	651	1548	2042	59	1554	E9Q6A7	
ENSMUST00000057893	ENSMUSG00000050288	11	102604396	102608058	1	20	9	58	323	29	18	0	0	0	7	7		Q9JIP6
ENSMUST00000057896	ENSMUSG00000036197	15	93239742	93275161	-1	3	0	3	31	0	0	25	34	109	0	32	D3Z6W7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000057897	ENSMUSG00000044477	17	30005087	30210019	1	22	13	35	51	17	19	2400	3678	2394	394	1547		Q497H0
ENSMUST00000057907	ENSMUSG00000029001	4	148152800	148160482	-1	7	2	7	105	16	9	0	0	0	0	0	A2A7H5	
ENSMUST00000057910	ENSMUSG00000047417	10	80540922	80561560	-1	32	22	103	354	56	23	704	586	680	23	719		Q7TT28
ENSMUST00000057911	ENSMUSG00000042874	13	32802457	32802849	-1	0	0	0	122	0	2	0	0	0	0	0	Q9D2K6	
ENSMUST00000057920	ENSMUSG00000050901	9	15824528	15874556	-1	3	1	0	2	0	5	0	0	0	0	0	Q3SXF8	
ENSMUST00000057921	ENSMUSG00000062421	11	103966739	103985337	1	8	3	35	50	6	0	601	1097	876	743	438		Q8BSL7
ENSMUST00000057924	ENSMUSG00000044441	19	12674179	12675243	1	5	2	2	0	2	2	0	0	0	0	0	Q0VEV7	
ENSMUST00000057927	ENSMUSG00000044562	7	45627488	45639093	1	15	10	21	381	24	7	15	21	5	1	18		Q3U0S6
ENSMUST00000057932	ENSMUSG00000075605	15	74742764	74746693	-1	6	2	13	3	4	2	0	0	0	0	0		Q9WVC2
ENSMUST00000057934	ENSMUSG00000001472	8	123373824	123404173	1	7	15	12	104	16	7	1700	1882	1991	372	2224		Q8R3L2
ENSMUST00000057935	ENSMUSG00000050144	3	88410498	88425139	-1	25	0	22	44	11	0	722	0	478	20	547	Q3TMC4	
ENSMUST00000057942	ENSMUSG00000047259	18	66857715	66860472	-1	16	17	34	16	16	6	0	0	0	0	0		P56450
ENSMUST00000057944	ENSMUSG00000032854	3	125865271	125938619	-1	8	4	11	35	13	4	259	776	283	55	161		Q64676
ENSMUST00000057950	ENSMUSG00000024565	18	80966376	80986578	-1	55	40	127	353	83	33	0	0	0	0	0		Q62255
ENSMUST00000057974	ENSMUSG00000047586	7	28543596	28547254	-1	10	8	13	109	21	6	28	39	22	1	10	A0A0A0MQ97	
ENSMUST00000057975	ENSMUSG00000051444	3	37312554	37321453	1	0	9	0	0	0	9	5	22	8	0	10		Q5SUD9
ENSMUST00000057977	ENSMUSG00000048636	6	92816478	92847174	1	15	2	9	11	10	8	0	0	0	0	0	Q8C940	
ENSMUST00000057979	ENSMUSG00000022383	15	85734983	85802819	1	0	0	1	5	0	0	0	0	0	0	0	Q542P9	P23204
ENSMUST00000058004	ENSMUSG00000006378	15	79030874	79043558	1	1	2	11	184	7	4	0	0	1	0	1		O88853
ENSMUST00000058007	ENSMUSG00000060735	15	11033717	11037991	-1	26	27	58	172	41	33	0	0	0	0	0	Q5Y988	Q8BGE9
ENSMUST00000058009	ENSMUSG00000036006	13	24582189	24733816	1	7	1	11	11	14	4	5	32	20	0	38		Q80U16
ENSMUST00000058011	ENSMUSG00000002870	6	88883474	88898780	-1	36	18	48	53	30	21	302	221	224	50	213		P97310
ENSMUST00000058016	ENSMUSG00000029503	5	110339812	110343212	-1	19	7	21	9	22	0	0	0	0	0	0		Q8K3P1
ENSMUST00000058022	ENSMUSG00000048677	7	145253923	145283927	-1	22	13	86	33	26	20	1000	2331	1203	237	1222		Q8BWC0
ENSMUST00000058030	ENSMUSG00000062937	4	89137122	89181081	1	21	20	50	98	21	15	19	98	20	181	218		Q9CQ65
ENSMUST00000058033	ENSMUSG00000049076	16	31092413	31201238	-1	28	16	63	137	38	18	1849	3887	3943	241	2643		Q6ZQK5
ENSMUST00000058038	ENSMUSG00000045639	7	127607031	127615797	-1	60	33	130	73	78	16	0	11	0	0	0		Q6A085
ENSMUST00000058039	ENSMUSG00000047203	6	90269106	90270053	1	4	4	5	4	4	1	0	0	0	0	0		Q9EPB8
ENSMUST00000058040	ENSMUSG00000074491	8	3707064	3720651	-1	6	4	0	0	6	4	0	0	0	0	0	Q9D4Q9	
ENSMUST00000058041						0	0	0	0	0	0	0	65	0	11	0		
ENSMUST00000058045	ENSMUSG00000044576	5	30105161	30118378	1	33	19	45	354	40	27	0	0	1	0	1		Q6PAJ3
ENSMUST00000058046	ENSMUSG00000092077	17	37299446	37300484	-1	4	5	2	3	9	4	1	0	0	0	0	Q920Z0	
ENSMUST00000058056	ENSMUSG00000046845	2	24291196	24293820	1	7	3	3	5	8	6	0	0	0	0	0	Q3KNF2	Q8R459
ENSMUST00000058060	ENSMUSG00000044502	11	31665181	31671885	-1	10	20	39	50	17	9	28	76	32	20	59		Q5SQY2
ENSMUST00000058077	ENSMUSG00000043164	3	27866066	27896368	-1	1	2	8	6	3	3	0	0	0	0	0		Q8C6V3
ENSMUST00000058086	ENSMUSG00000044863	2	152604327	152612729	1	2	1	1	6	3	4	0	0	0	0	0		Q8K3U4
ENSMUST00000058089	ENSMUSG00000027593	2	154791096	154867261	1	0	3	14	0	0	0	1108	3415	1308	386	1140	Q3U3F6	Q64012
ENSMUST00000058092	ENSMUSG00000050276	7	143763711	143766993	-1	13	16	34	23	46	18	0	0	0	0	0		Q91ZB5
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ENSMUST00000058096	ENSMUSG00000057406	5	33820725	33897975	1	11	10	0	0	3	2	131	250	226	14	148		Q8BVE8
ENSMUST00000058098	ENSMUSG00000046873	X	157535371	157598715	-1	44	49	855	129	61	15	70	179	92	34	56		Q8CHX6
ENSMUST00000058099	ENSMUSG00000050147	8	72761880	72763874	1	16	10	55	93	24	10	9	10	5	2	5		O88634
ENSMUST00000058103						12	8	10	1	7	4	0	1	0	4	1		
ENSMUST00000058104	ENSMUSG00000030469	7	43579610	43593235	1	13	12	24	14	22	11	84	397	197	261	160	Q8BIV1	
ENSMUST00000058109	ENSMUSG00000046756	11	115603925	115608036	1	22	10	11	111	33	8	102	255	104	117	119		Q80X85
ENSMUST00000058118	ENSMUSG00000048693	6	43201646	43202587	1	3	4	10	4	6	3	0	0	0	0	0	Q8VFS3	
ENSMUST00000058119	ENSMUSG00000048040	X	135993824	135995355	1	7	0	5	37	0	5	0	1	2	3	2		Q9D365
ENSMUST00000058123	ENSMUSG00000045559	10	130210092	130211149	-1	3	7	3	1	5	3	0	0	0	0	0	Q8VEV5	
ENSMUST00000058125	ENSMUSG00000050071	X	136213972	136215513	-1	0	0	3	48	5	3	0	0	0	0	0		Q9R224
ENSMUST00000058126	ENSMUSG00000047638	10	89454234	89533585	-1	0	6	0	0	0	3	0	0	6	20	1	Q3V1T8	Q60641
ENSMUST00000058133	ENSMUSG00000028760	4	137993022	138208508	1	4	4	21	36	5	5	3	13	18	1	13	Q8BQR8	
ENSMUST00000058135	ENSMUSG00000047227	12	64917911	64924591	1	8	2	7	2	5	0	13	58	12	2	7		Q4KL13
ENSMUST00000058136	ENSMUSG00000047123	17	56269319	56276786	-1	25	15	53	52	36	20	334	392	370	34	218		Q80UF7
ENSMUST00000058137	ENSMUSG00000015087	2	25583018	25608521	-1	6	4	25	63	14	9	180	430	256	70	261		Q5U3K5
ENSMUST00000058139	ENSMUSG00000044712	12	73286779	73354049	1	19	6	0	63	0	6	0	29	22	564	0	Q3USV8	
ENSMUST00000058142	ENSMUSG00000045539	3	92456502	92458720	-1	14	7	49	4	6	3	0	0	0	0	0		O09116
ENSMUST00000058150	ENSMUSG00000043165	3	92080271	92083142	-1	9	4	18	1092	25	15	0	0	0	0	0		P18165
ENSMUST00000058153	ENSMUSG00000094380	9	38464043	38464975	1	2	3	3	0	2	2	0	0	0	0	0	Q7TRC9	
ENSMUST00000058154	ENSMUSG00000036676	10	100443902	100487350	-1	13	20	31	38	20	2	19	27	20	36	57	G5E8C4	
ENSMUST00000058159	ENSMUSG00000044629	11	17051586	17079371	1	9	6	15	99	12	7	0	4	1	2	1		Q5M8N0
ENSMUST00000058162	ENSMUSG00000051510	11	120625117	120633600	-1	40	35	264	78	70	34	1539	3037	1862	261	1410		O54790
ENSMUST00000058163	ENSMUSG00000020280	11	23665674	23732876	1	12	6	11	23	7	11	45	39	71	86	73		Q9D3U0
ENSMUST00000058167	ENSMUSG00000048174	1	132506230	132508639	1	12	0	29	11	14	4	21	32	39	12	44		Q9D5K1
ENSMUST00000058168	ENSMUSG00000042869	13	21072349	21073299	-1	0	4	4	5	11	3	0	0	1	0	0	Q8VFG4	
ENSMUST00000058173	ENSMUSG00000047804	11	61871307	61930252	-1	0	0	0	0	3	0	8	0	13	0	0		O88845
ENSMUST00000058176	ENSMUSG00000049758	2	112155953	112156915	1	2	4	4	6	8	4	0	0	0	0	0	Q7TQW6	
ENSMUST00000058178	ENSMUSG00000051397	6	67534062	67535796	-1	31	20	40	270	36	22	854	3024	914	607	884		Q8BGV3
ENSMUST00000058183	ENSMUSG00000050323	4	11051045	11076205	-1	0	0	0	3	0	0	0	0	0	0	7		A2AIL4
ENSMUST00000058196	ENSMUSG00000021384	13	49230690	49248706	-1	2	2	14	39	2	3	326	705	346	133	168		Q9D176
ENSMUST00000058210	ENSMUSG00000015766	6	137477245	137654876	-1	12	4	34	15	7	4	8	197	34	23	40		Q08509
ENSMUST00000058213	ENSMUSG00000044819	14	120019585	120042435	-1	26	15	34	24	35	10	0	0	1	0	1		Q6IYF8
ENSMUST00000058229	ENSMUSG00000046049	14	63992431	64033504	1	64	52	127	89	86	43	0	0	0	0	1	A1L340	Q8CGM2
ENSMUST00000058230	ENSMUSG00000038619	3	95624993	95632102	1	5	5	20	8	8	5	231	839	354	517	245		P60840
ENSMUST00000058232	ENSMUSG00000028329	4	46155347	46196311	-1	4	1	4	7	1	2	0	20	0	11	6	Q8K2X7	
ENSMUST00000058237	ENSMUSG00000090124	1	88095062	88220002	1	24	41	39	26	41	11	2790	10430	3525	750	2136		Q6ZQM8
ENSMUST00000058240	ENSMUSG00000044551	14	70154405	70159502	-1	2	1	1	13	3	1	0	221	22	14	111		Q66JV7
ENSMUST00000058245	ENSMUSG00000040242	6	146577203	146599198	1	0	0	0	30	0	0	40	0	254	134	226	F8WGG1	
ENSMUST00000058265	ENSMUSG00000048970	X	38630785	38635087	-1	1	0	3	10	3	0	126	738	193	365	106		Q9JMG2
ENSMUST00000058266	ENSMUSG00000045467	7	80246376	80260821	1	3	10	27	72	24	3	9	34	19	5	14		A4Q9F6
ENSMUST00000058269	ENSMUSG00000049811	11	23007531	23030788	1	0	4	18	3	16	0	1	1	0	0	0	B1AVK0	
ENSMUST00000058274	ENSMUSG00000009739	15	100575318	100599984	-1	0	19	0	0	0	0	0	2	0	1	0	Q6X2R9	
ENSMUST00000058280	ENSMUSG00000036892	7	30493622	30513402	1	1	5	16	6	10	3	0	0	0	2	0		Q8VCZ9
ENSMUST00000058286	ENSMUSG00000020516	11	86498871	86544805	-1	7	4	12	8	11	10	7	9	3	0	8	Q8C3J7	
ENSMUST00000058292	ENSMUSG00000043003	4	73714579	73790709	-1	13	4	8	14	5	0	0	0	0	0	0		Q5RI75

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000058295	ENSMUSG00000062312	11	98412470	98437716	1	21	25	110	72	61	19	1	0	0	0	0		P70424
ENSMUST00000058296	ENSMUSG00000051160	9	19537011	19537928	-1	2	3	1	2	3	4	0	0	0	0	0	Q8VGG6	
ENSMUST00000058300	ENSMUSG00000030281	6	113471427	113483140	1	0	0	13	116	18	11	0	0	0	5	0		Q8K4C2
ENSMUST00000058307	ENSMUSG00000026113	1	37299865	37410736	1	0	0	15	0	0	2	52	120	34	2	93		
ENSMUST00000058326	ENSMUSG00000049532	14	52311172	52328762	-1	25	23	52	5	25	11	0	0	0	0	0		Q9QX96
ENSMUST00000058333	ENSMUSG00000089847	7	105640056	105655748	1	0	0	0	0	0	0	252	840	243	220	180		Q9WV96
ENSMUST00000058347	ENSMUSG00000049641	10	52022502	52028471	1	0	0	7	43	18	5	0	0	0	0	0		
ENSMUST00000058351	ENSMUSG00000025791	4	99929414	99987294	1	8	0	0	52	0	0	959	1501	961	240	521		Q9D0F9
ENSMUST00000058352	ENSMUSG00000046080	6	129408862	129424763	1	0	0	0	0	0	0	0	0	11	9	43		Q8BRU4
ENSMUST00000058358	ENSMUSG00000043432	7	4147915	4150374	-1	25	13	24	197	49	27	99	215	97	15	83		Q8BTN6
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ENSMUST00000058370	ENSMUSG00000049957	11	120458115	120464358	1	21	13	18	53	30	12	54	169	64	23	98		Q8R0K4
ENSMUST00000058383	ENSMUSG00000045896	6	83805401	83831741	-1	33	32	82	62	47	19	44	135	58	37	71		Q91W45
ENSMUST00000058393	ENSMUSG00000047613	4	153957237	153961925	1	0	0	3	15	0	0	44	155	92	170	59		Q80WR5
ENSMUST00000058404	ENSMUSG00000044597	X	5466898	5469265	-1	9	3	12	88	3	4	0	0	0	0	0		Q9Z304
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ENSMUST00000058411	ENSMUSG00000051414	9	18856627	18857592	1	1	3	2	1	0	0	0	0	0	0	0	Q8VGX1	
ENSMUST00000058418	ENSMUSG00000050822	5	142692512	142722490	1	36	20	58	212	44	27	13	13	10	0	11		Q8R139
ENSMUST00000058429	ENSMUSG00000044701	7	126589010	126594941	-1	6	6	21	23	16	6	161	506	142	16	94		Q8K3I6
ENSMUST00000058437	ENSMUSG00000043716	1	16101295	16104662	-1	15	25	45	58	34	13	1742	10453	3227	16811	2373	Q5M9N8	P14148
ENSMUST00000058438	ENSMUSG00000049354	11	106036872	106059324	1	34	25	114	72	54	21	1692	2094	2003	197	1395		P61963
ENSMUST00000058440	ENSMUSG00000038011	5	124725085	124834308	1	110	37	165	150	110	55	0	0	0	0	0	D3YYQ8	
ENSMUST00000058444	ENSMUSG00000051403	7	19530967	19562398	-1	26	17	61	206	30	17	574	756	387	64	478		Q8BKR5
ENSMUST00000058464	ENSMUSG00000058260	12	103994743	104013755	-1	145	91	81	2077	233	85	5	3	6	3	6		Q9D7D2
ENSMUST00000058470	ENSMUSG00000005198	11	69733997	69758637	-1	30	7	96	104	64	19	2613	5213	3555	148	3703		P08775
ENSMUST00000058472	ENSMUSG00000042078	5	114026910	114091570	-1	16	11	38	121	28	27	0	0	0	0	0		Q8BFT9
ENSMUST00000058475	ENSMUSG00000048904	13	56250505	56252163	-1	6	9	15	376	14	7	0	0	0	0	0		P70660
ENSMUST00000058476	ENSMUSG00000033510	7	63444751	63759028	1	7	0	2	83	7	5	0	0	0	0	0		Q8R554
ENSMUST00000058479	ENSMUSG00000031786	8	95055103	95078141	1	20	12	57	31	28	12	3	6	1	0	0		Q6V3W6
ENSMUST00000058488	ENSMUSG00000032353	9	89699205	89705068	-1	7	8	28	110	20	11	475	846	357	465	324		Q78IS1
ENSMUST00000058491	ENSMUSG00000049036	12	113185930	113189523	1	3	2	20	199	10	3	0	0	0	3	2		Q80XA0
ENSMUST00000058496	ENSMUSG00000017291	11	77529162	77607815	-1	21	0	0	150	40	0	21	125	581	21	353	B2RX66	Q5F2E8
ENSMUST00000058524	ENSMUSG00000047749	6	38287396	38299259	-1	58	37	266	164	53	51	28	60	47	2	51	B9EHM1	Q8BFR1
ENSMUST00000058534	ENSMUSG00000045248	8	72494558	72548310	-1	22	11	51	448	33	12	183	263	180	28	154		Q7TN02
ENSMUST00000058535	ENSMUSG00000043441	3	62529077	62605140	-1	45	27	66	551	81	37	0	0	0	0	0		Q3UVY1
ENSMUST00000058538	ENSMUSG00000030259	6	145746748	145821079	1	0	0	6	5	0	2	5	16	1	4	0	F7BB71	
ENSMUST00000058548	ENSMUSG00000043088	6	113458484	113470758	1	19	15	31	34	36	17	1	1	0	2	1		Q8BH06
ENSMUST00000058550	ENSMUSG00000063015	5	93181933	93206495	-1	34	31	67	240	58	20	4329	7986	4609	710	3224		Q9Z2V9
ENSMUST00000058564	ENSMUSG00000044029	16	58889259	58892058	-1	2	0	6	3	7	2	0	0	0	0	0	E9Q9T3	
ENSMUST00000058577	ENSMUSG00000049504	3	53463666	53481755	1	24	21	60	289	46	17	275	516	375	24	349		Q5PRE5
ENSMUST00000058578	ENSMUSG00000049940	3	41066326	41083046	-1	9	5	9	175	17	9	160	583	243	40	186		Q80UU9
ENSMUST00000058579	ENSMUSG00000045538	8	106009621	106011882	-1	15	15	53	297	31	14	574	1144	647	176	335		Q9CWT6
ENSMUST00000058585	ENSMUSG00000028619	4	107134155	107179116	-1	0	0	0	0	0	0	73	263	155	9	60		Q8R2M0
ENSMUST00000058593	ENSMUSG00000042961	15	7206120	7398395	-1	12	23	50	0	14	6	0	0	0	0	0		Q4VBE4
ENSMUST00000058595	ENSMUSG00000042993	4	35152056	35154005	1	5	4	4	7	5	1	1	0	0	0	0	Q4FZL7	Q7TSL0
ENSMUST00000058600	ENSMUSG00000051490	19	24898965	24901309	-1	22	7	31	688	28	13	0	1	1	0	1		Q60688
ENSMUST00000058605	ENSMUSG00000049972	4	112385969	112433985	-1	0	0	0	0	0	0	0	0	0	0	0		A7TZG3
ENSMUST00000058609	ENSMUSG00000047286	8	83541093	83542188	1	10	2	14	3	6	4	0	0	0	0	0	E9Q848	
ENSMUST00000058610	ENSMUSG00000044988	13	3940688	3945349	-1	14	4	43	24	17	6	0	0	0	0	0	Q3UFJ9	Q924A4
ENSMUST00000058615	ENSMUSG00000041777	2	73283105	73312701	-1	39	28	96	204	55	24	272	1646	698	1371	463		Q9DA19
ENSMUST00000058626	ENSMUSG00000028273	3	142239590	142395696	-1	0	0	0	31	0	0	0	0	10	0	33	F8WJI6	
ENSMUST00000058633	ENSMUSG00000050875	18	59062248	59076962	1	0	0	0	13	3	1	0	0	0	0	0		
ENSMUST00000058635	ENSMUSG00000050304	18	37637377	37638745	-1	5	11	13	15	8	2	0	3	0	0	0	Q99ML6	
ENSMUST00000058636	ENSMUSG00000047171	8	46292050	46294671	-1	23	9	25	219	20	6	0	0	0	0	0		Q7TS99
ENSMUST00000058639	ENSMUSG00000049882	12	69577628	69583028	-1	5	5	3	190	11	2	21	43	15	36	20		Q8C436
ENSMUST00000058643	ENSMUSG00000048230	15	36150060	36164884	-1	60	56	84	117	72	41	3	12	5	0	4	G3X9B2	
ENSMUST00000058644	ENSMUSG00000048004	12	119945957	120019211	1	8	6	9	9	10	7	0	0	0	0	0	D3YWQ9	
ENSMUST00000058651	ENSMUSG00000024903	4	118961578	118968912	1	15	6	40	14	17	9	0	0	0	0	0	B1ARV3	
ENSMUST00000058652	ENSMUSG00000047759	11	64435332	64522841	1	12	12	18	267	33	5	0	0	0	0	0	Q52KJ0	Q8BKN6
ENSMUST00000058659	ENSMUSG00000044986	15	78399556	78405859	-1	6	9	18	45	12	5	370	309	141	77	65	Q545S0	P52196
ENSMUST00000058661	ENSMUSG00000011486	17	57032773	57041654	-1	4	0	6	13	0	0	0	0	0	0	0	B8ZHC8	Q8BVN7
ENSMUST00000058667	ENSMUSG00000047085	7	44429018	44463351	1	16	11	56	445	17	10	0	0	1	0	0		P0C192
ENSMUST00000058668	ENSMUSG00000043119	6	42896453	42897385	1	7	1	9	4	4	1	0	0	0	0	0	Q8VES9	
ENSMUST00000058669	ENSMUSG00000009108	3	108092789	108101432	1	14	4	0	6	13	0	3	7	5	0	10	A2AE33	P50149
ENSMUST00000058678	ENSMUSG00000049999	2	178411206	178414472	-1	24	15	55	434	35	18	2745	7356	3620	542	2397	A2AJW4	
ENSMUST00000058679	ENSMUSG00000035078	14	63523616	63543953	-1	12	11	24	107	17	12	287	392	393	37	200		Q9Z2D0
ENSMUST00000058682	ENSMUSG00000034107	1	93373930	93404303	1	10	14	42	79	20	7	0	0	0	1	0		Q14AT5
ENSMUST00000058688	ENSMUSG00000047496	1	105276914	105356710	-1	84	90	458	355	117	85	0	0	0	0	0		Q8BG47
ENSMUST00000058692	ENSMUSG00000032006	9	6168612	6378843	1	2	4	3	5	3	0	0	0	0	2	0		Q925I7
ENSMUST00000058702	ENSMUSG00000054499	7	25199915	25220615	-1	11	2	29	258	23	9	3169	4134	2184	412	1909		Q8QZV0
ENSMUST00000058704	ENSMUSG00000069874	11	58199618	58222779	1	26	2	30	30	29	1	378	2271	671	211	893	Q9Z1M2	
ENSMUST00000058710						2	3	6	3	8	0	0	0	0	0	0		
ENSMUST00000058713	ENSMUSG00000045291	6	136400317	136415569	-1	1	5	5	15	7	3	0	0	0	0	0	Q8BW45	
ENSMUST00000058714	ENSMUSG00000047139	10	43579169	43584262	1	20	34	52	120	36	15	6866	26697	8661	16277	4482	Q3THW4	P24807
ENSMUST00000058716	ENSMUSG00000036817	5	139200637	139249840	1	0	13	7	45	14	0	223	182	357	46	156		Q9D666
ENSMUST00000058720	ENSMUSG00000042790	9	45863425	45906894	-1	0	0	0	48	0	0	0	31	22	0	12		Q8BFU3
ENSMUST00000058725	ENSMUSG00000047441	14	34053470	34075999	1	15	11	44	22	19	13	0	0	0	0	0		Q8BVM2
ENSMUST00000058728	ENSMUSG00000095388	3	98552542	98588807	-1	0	10	0	10	10	0	0	0	0	0	0		Q61767
ENSMUST00000058733	ENSMUSG00000044600	8	72565188	72571088	-1	0	2	2	2	0	0	157	283	124	183	78	F8WIU9	
ENSMUST00000058735	ENSMUSG00000005312	13	58176156	58215653	-1	0	0	0	0	17	0	459	1005	992	119	615		Q8R317
ENSMUST00000058737	ENSMUSG00000070853	2	87357446	87358390	1	3	7	1	1	3	2	0	0	0	0	0	Q8VGT7	
ENSMUST00000058738	ENSMUSG00000044499	10	36506814	36834397	1	0	5	0	0	0	3	0	0	0	0	0	B2RXW6	Q8BSL4
ENSMUST00000058744	ENSMUSG00000050085	7	103639185	103640138	-1	3	2	4	3	0	0	0	0	0	0	0	Q8VGY7	
ENSMUST00000058745	ENSMUSG00000046179	7	48866429	48881596	-1	44	15	55	146	46	26	135	165	129	0	94		Q58FA4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000058746	ENSMUSG00000025510	7	141467362	141471479	1	4	11	7	2	0	3	22	44	13	35	41		O35566
ENSMUST00000058747	ENSMUSG00000045555	10	40683282	40811083	1	6	6	17	107	9	6	1	0	2	5	3		Q8CCB5
ENSMUST00000058748	ENSMUSG00000043230	1	80198706	80218473	-1	27	22	89	19	21	14	1	2	2	0	4		Q8BLQ0
ENSMUST00000058750	ENSMUSG00000044824	7	102493823	102494773	-1	4	5	10	5	17	0	0	0	0	0	2	Q9WU94	
ENSMUST00000058754	ENSMUSG00000043207	4	121059237	121098241	-1	25	20	26	25	20	16	667	1468	1057	1060	671	B9EHY2	Q80W54
ENSMUST00000058755	ENSMUSG00000049791	7	89404366	89410110	1	22	17	60	188	40	14	13	11	12	2	22	Q3V1B2	Q61088
ENSMUST00000058761	ENSMUSG00000051481	11	99936291	99937225	1	7	1	5	6	7	0	0	0	0	0	0	Q8CAY5	
ENSMUST00000058762	ENSMUSG00000026335	1	97795114	98095646	-1	15	13	44	0	7	7	32	0	3	64	0		P97467
ENSMUST00000058764	ENSMUSG00000039108	2	180024987	180035465	1	13	7	15	6	19	0	30	95	12	0	74	Q8BM41	
ENSMUST00000058771	ENSMUSG00000043831	7	67222544	67228468	1	9	14	7	19	12	0	27	74	46	21	32		Q8CC84
ENSMUST00000058772	ENSMUSG00000045713	7	11930311	11931285	-1	3	3	4	0	5	0	0	0	0	0	0	F8VQ63	
ENSMUST00000058777	ENSMUSG00000047822	9	21835510	21837346	1	10	4	25	10	10	6	2	1	0	2	1	A0A0A0R784	Q8R1L8
ENSMUST00000058785	ENSMUSG00000066072	4	115518264	115533649	1	14	9	16	0	21	3	0	0	0	0	0		O88833
ENSMUST00000058787	ENSMUSG00000018589	X	165129017	165327393	-1	5	13	32	12	18	5	0	2	1	0	0	Q3UTL8	Q7TNC8
ENSMUST00000058789	ENSMUSG00000063221	9	38930173	38931099	1	4	2	4	1	3	3	0	0	0	0	0	Q9EQ99	
ENSMUST00000058790	ENSMUSG00000048058	2	101950203	102186385	-1	0	0	0	49	0	0	0	0	18	0	31	B2RR20	A2AR95
ENSMUST00000058791	ENSMUSG00000034359	4	112557194	112652248	1	1	0	0	0	0	0	0	0	0	0	0	M9MMJ5	
ENSMUST00000058793	ENSMUSG00000041815	15	83125978	83149384	-1	0	0	0	52	0	0	2005	1820	1377	192	1394		Q8BG81
ENSMUST00000058796	ENSMUSG00000053914	9	14462548	14500482	-1	15	14	32	27	30	13	0	0	0	0	0		Q3U2K5
ENSMUST00000058801	ENSMUSG00000056116	17	36037128	36042747	-1	2	0	0	0	0	0	0	0	0	0	0	Q9BCZ1	
ENSMUST00000058804	ENSMUSG00000044676	8	110079764	110090181	1	17	12	41	82	25	10	0	1	0	0	2	G5E8C8	
ENSMUST00000058806	ENSMUSG00000046006	13	110352615	110357172	-1	16	12	32	12	7	4	482	1348	527	127	425		Q8CB93
ENSMUST00000058814	ENSMUSG00000043463	X	136858147	136868755	-1	118	99	820	141	98	51	0	2	1	0	1	Q3KNA5	Q8BHH2
ENSMUST00000058825	ENSMUSG00000050625	1	181509633	181511451	-1	13	6	22	14	15	9	0	0	0	0	0	E9Q6D3	
ENSMUST00000058826	ENSMUSG00000049618	17	37336289	37339678	-1	4	0	1	4	4	4	0	0	0	0	0	Q920Y8	
ENSMUST00000058829	ENSMUSG00000050321	18	86394952	86501897	1	10	9	25	96	27	5	0	0	0	0	0		Q8R4I7
ENSMUST00000058839	ENSMUSG00000043008	16	19946499	19983037	-1	12	5	13	17	16	8	2902	3487	4305	4643	1937		Q6V595
ENSMUST00000058844	ENSMUSG00000051499	6	47819266	47830867	-1	24	13	41	93	30	7	1	0	0	0	0	B2RSK4	Q8BV42
ENSMUST00000058845	ENSMUSG00000045763	15	25363285	25413764	-1	2	2	8	213	7	4	106	901	143	78	149		Q91XV3
ENSMUST00000058846	ENSMUSG00000047897	9	87015537	87019917	1	0	0	0	37	0	2	0	0	0	0	0		Q2WG76
ENSMUST00000058856	ENSMUSG00000050195	19	44333092	44346743	1	70	64	182	95	90	50	2	11	4	2	4		Q6T707
ENSMUST00000058860	ENSMUSG00000058239	7	30945248	30956803	-1	0	0	0	16	0	0	1321	1894	1055	199	650		Q64705
ENSMUST00000058865	ENSMUSG00000038298	3	96829284	96870926	1	4	0	0	5	0	0	0	0	0	0	4		
ENSMUST00000058866	ENSMUSG00000046719	11	95509845	95514570	-1	10	4	25	229	20	15	0	0	0	0	0	Q544G3	Q91VX5
ENSMUST00000058868	ENSMUSG00000036411	9	22411577	22444677	1	12	12	17	41	5	6	31	154	38	43	63		Q7TQE7
ENSMUST00000058879	ENSMUSG00000074121	7	45413695	45417178	1	14	25	31	261	18	14	1	4	0	0	2		Q80VU4
ENSMUST00000058880	ENSMUSG00000006335	7	3620324	3629929	-1	0	0	3	0	0	0	0	0	0	0	0	F8WIZ9	
ENSMUST00000058881						5	4	7	10	0	1	0	0	0	0	1		
ENSMUST00000058884	ENSMUSG00000022685	16	13537964	13668170	-1	98	76	319	140	73	19	30	115	55	33	55		
ENSMUST00000058889	ENSMUSG00000055884	12	65075606	65132058	1	53	45	46	205	67	29	21	48	44	5	37		Q8BGE5
ENSMUST00000058897	ENSMUSG00000046245	5	137821952	137836281	-1	15	13	62	19	26	6	1459	7221	2417	1768	1956		Q2YFS3
ENSMUST00000058899	ENSMUSG00000048938	3	102939658	102964133	-1	24	34	35	42	44	30	2	3	2	0	2	E9Q5A6	
ENSMUST00000058902	ENSMUSG00000044072	11	29743048	30026033	-1	33	28	48	179	40	16	0	0	0	0	2		Q5SQM0
ENSMUST00000058905	ENSMUSG00000043572	4	106651069	106655282	1	0	4	40	0	4	6	26	11	14	8	10		Q8CFI5
ENSMUST00000058906	ENSMUSG00000049422	10	75935573	75937725	1	8	3	12	75	8	2	27	19	20	11	16	Q7TNL9	
ENSMUST00000058907	ENSMUSG00000049806	13	65152226	65153152	1	4	3	6	0	5	2	0	0	0	0	0	E9Q2B9	
ENSMUST00000058912	ENSMUSG00000047356	2	25682726	25686081	1	11	12	16	8	11	3	0	0	0	0	0	Q0VBF7	Q810Z1
ENSMUST00000058914	ENSMUSG00000043091	15	99029891	99038105	1	13	9	61	304	52	24	2450	2944	1999	565	1264	Q52L87	P68373
ENSMUST00000058918	ENSMUSG00000048484	8	4677539	4678365	-1	4	2	6	127	5	5	0	0	0	0	0	Q8C5X8	
ENSMUST00000058921	ENSMUSG00000089798	5	107534709	107551542	1	2	2	1	8	2	1	0	0	0	0	0	G3X9D1	
ENSMUST00000058942	ENSMUSG00000047692	10	70868669	70934324	1	7	5	13	7	12	4	0	0	0	2	0	E9PXV0	
ENSMUST00000058943	ENSMUSG00000049097	3	96596636	96599775	1	15	8	35	396	22	13	0	0	0	0	1	B2RW11	
ENSMUST00000058951						4	2	7	72	7	0	0	0	0	0	0		
ENSMUST00000058955	ENSMUSG00000079842	8	19157886	19159578	1	2	2	1	0	1	3	0	0	0	0	0	Q0VB31	Q8K4N2
ENSMUST00000058960	ENSMUSG00000043036	5	122108040	122140823	-1	13	2	21	14	20	9	9	43	34	51	26		
ENSMUST00000058965	ENSMUSG00000047716	14	50392758	50393696	1	5	2	6	3	1	5	0	0	0	0	0	Q8VFT6	
ENSMUST00000058972	ENSMUSG00000094692	14	50413546	50414481	1	2	7	8	7	6	3	0	0	0	0	0	L7N1X7	
ENSMUST00000058978	ENSMUSG00000046949	13	33964659	33988465	1	21	52	145	20	0	34	138	335	75	275	119		Q9JI75
ENSMUST00000058981	ENSMUSG00000047557	3	67457998	67463926	-1	3	3	14	139	8	4	158	364	129	348	98	Q14BZ3	P70202
ENSMUST00000058987	ENSMUSG00000044649	11	99634111	99635084	-1	9	6	6	109	8	5	0	0	0	0	0	B1AQ85	
ENSMUST00000058991	ENSMUSG00000046493	10	78981050	78984721	1	5	5	6	4	3	1	0	0	0	0	0	Q8VGX5	
ENSMUST00000058994	ENSMUSG00000044528	3	124320855	124324743	1	37	22	105	98	25	6	7	23	13	2	28		Q8QZR0
ENSMUST00000058997	ENSMUSG00000044646	18	75820178	76148561	1	22	22	65	67	39	24	0	0	0	0	2		Q8VCZ7
ENSMUST00000058999						2	4	9	7	3	2	0	0	0	0	0		
ENSMUST00000059003	ENSMUSG00000045802	X	96306178	96456294	-1	0	0	0	0	0	0	0	0	0	0	0	E9QNK9	
ENSMUST00000059018	ENSMUSG00000052934	8	121549440	121578806	-1	22	15	109	145	55	20	2382	1881	1678	191	1365		Q3TQF0
ENSMUST00000059021	ENSMUSG00000040374	3	5560188	5576239	-1	0	0	0	48	2	2	114	314	116	228	65	Q91YZ5	
ENSMUST00000059026	ENSMUSG00000018381	11	95830074	95842476	-1	11	12	42	208	26	6	422	1543	570	77	809		Q8BYZ1
ENSMUST00000059033	ENSMUSG00000050815	19	12422265	12423352	1	3	6	56	14	10	4	0	0	0	0	0	Q8VFV3	
ENSMUST00000059034	ENSMUSG00000033720	6	85213049	85333422	-1	1	3	5	6	2	3	0	2	12	8	9	Q8BRQ9	
ENSMUST00000059037	ENSMUSG00000057143	7	104338754	104353362	-1	876	673	483	29571	1382	484	713	4775	1489	1448	1505	E9Q987	
ENSMUST00000059038	ENSMUSG00000050478	10	129754489	129755485	-1	2	3	2	4	1	1	0	0	0	0	0	Q8VGI9	
ENSMUST00000059042	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	10	16	16	0	20	0	0	0	0		Q9ESZ8
ENSMUST00000059045	ENSMUSG00000034259	15	76327397	76330677	1	20	18	68	80	25	5	362	630	291	55	253	Q542B0	Q92II9
ENSMUST00000059049	ENSMUSG00000050587	2	96318169	97631666	1	6	10	15	9	12	4	0	1	0	0	0		Q8C031
ENSMUST00000059052	ENSMUSG00000044763	16	56032609	56037819	-1	12	8	11	99	16	6	22	229	70	145	57		Q3UFY8
ENSMUST00000059053	ENSMUSG00000043472	3	92957390	92958505	1	5	0	3	0	7	2	0	0	0	0	0	E9Q8V1	
ENSMUST00000059056	ENSMUSG00000035506	16	33517328	33664135	1	16	30	62	0	54	11	0	0	0	0	0		Q8VI23
ENSMUST00000059057	ENSMUSG00000050471	9	35216965	35267805	-1	0	0	0	10	6	0	85	396	105	350	112		Q8C569
ENSMUST00000059065						3	0	4	2	1	3	0	0	0	0	0		
ENSMUST00000059072	ENSMUSG00000052819	8	85007202	85014408	-1	19	8	32	158	29	16	0	0	1	1	0		
ENSMUST00000059078	ENSMUSG00000046546	16	30599723	30602797	1	32	25	46	843	62	36	248	407	175	34	225		Q8BUP8
ENSMUST00000059080	ENSMUSG00000039001	2	180257377	180258445	1	1	4	7	23	14	5	3116	3363	1874	11680	1309		Q9CQR2
ENSMUST00000059081	ENSMUSG00000039217	9	50575273	50581837	1	2	1	0	3	2	0	0	0	0	0	0	K3W4N2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000059082	ENSMUSG00000040554	11	72027963	72037509	-1	18	8	14	35	17	2	0	6	0	0	0	I6L993	
ENSMUST00000059091	ENSMUSG00000056025	3	144729677	144760977	-1	29	21	16	33	36	18	7	20	7	4	14	Q9QX15	
ENSMUST00000059093	ENSMUSG00000051671	8	126422501	126425434	1	3	1	2	99	3	3	50	163	45	265	26		Q8BGD8
ENSMUST00000059099	ENSMUSG00000015668	X	100622883	100626568	-1	0	1	0	0	0	1	123	388	145	381	101		Q9CZG9
ENSMUST00000059102	ENSMUSG00000026839	2	58567298	58792971	1	11	12	12	8	10	7	0	0	0	1	0	Q8R093	
ENSMUST00000059110						1	3	16	0	7	2	5	6	4	15	4		
ENSMUST00000059112	ENSMUSG00000048175	15	98134637	98165625	-1	0	0	0	0	0	0	43	11	38	28	25		
ENSMUST00000059115	ENSMUSG00000045636	8	40990914	41133726	-1	0	0	0	32	0	0	0	0	0	0	53		
ENSMUST00000059118						27	16	37	206	37	25	0	1	1	0	0		
ENSMUST00000059121	ENSMUSG00000051437	7	104148259	104150556	-1	22	17	44	23	16	13	0	0	0	0	0		Q14DL0
ENSMUST00000059138	ENSMUSG00000045725	6	54325835	54330201	1	13	13	58	43	15	9	0	6	0	5	2	A2RT92	Q9D1T5
ENSMUST00000059145	ENSMUSG00000030852	7	130577484	130764784	1	0	0	3	0	0	0	31	32	59	11	58	E9Q9Z4	
ENSMUST00000059155	ENSMUSG00000045294	5	28071363	28078662	1	23	20	21	149	34	17	167	553	359	159	311		Q8BGI3
ENSMUST00000059190						6	8	21	15	23	15	0	3	1	0	2		
ENSMUST00000059193	ENSMUSG00000048376	13	95601804	95618459	-1	27	29	56	101	41	13	46	99	53	18	102		P30558
ENSMUST00000059199	ENSMUSG00000045757	7	127403668	127406822	-1	24	16	71	84	37	0	23	0	23	0	24	E9QAP1	
ENSMUST00000059204	ENSMUSG00000043556	15	26543084	26895049	-1	16	13	15	24	18	9	0	0	0	0	0		Q5BJ29
ENSMUST00000059206	ENSMUSG00000032322	9	56089962	56128888	1	0	0	10	96	18	23	4717	6905	3865	1584	2533		
ENSMUST00000059216	ENSMUSG00000045508	13	21346910	21347964	1	3	7	21	6	6	2	0	0	0	0	0	Q8VFG2	
ENSMUST00000059223	ENSMUSG00000045777	7	142325837	142373753	-1	0	0	6	66	2	0	0	0	0	0	1		Q8BR26
ENSMUST00000059226	ENSMUSG00000054203	1	174011998	174031810	-1	0	0	1	0	4	4	2	27	3	61	21		Q8CGE8
ENSMUST00000059229	ENSMUSG00000029500	5	110259130	110269913	-1	0	13	7	117	12	2	90	64	47	6	0		Q8BX10
ENSMUST00000059231	ENSMUSG00000047604	19	41845978	41848132	-1	83	57	827	417	78	42	343	724	264	129	246		Q8K025
ENSMUST00000059235						3	0	8	45	7	0	0	0	0	0	1		
ENSMUST00000059241	ENSMUSG00000045733	7	140150628	140154877	-1	16	13	29	80	25	13	0	0	0	0	0		Q8BWU1
ENSMUST00000059244	ENSMUSG00000048745	10	130017301	130018361	1	1	2	1	1	2	0	0	0	0	0	0	Q8VFU5	
ENSMUST00000059250	ENSMUSG00000012076	12	55836366	55869735	1	10	10	15	138	15	7	22	132	51	44	73		Q3U1T3
ENSMUST00000059256	ENSMUSG00000041353	X	150397773	150459154	-1	7	5	8	0	0	0	0	0	0	0	0	A2ANF5	
ENSMUST00000059270	ENSMUSG00000050244	13	12395398	12438677	1	43	39	77	55	53	14	146	426	349	118	390	G3X9B1	
ENSMUST00000059271	ENSMUSG00000045576	3	104864005	104930064	1	0	0	0	0	0	1	0	471	265	60	0		Q8K4P7
ENSMUST00000059272	ENSMUSG00000043342	2	74697727	74700208	1	19	19	301	296	22	23	0	1	0	1	0		P28357
ENSMUST00000059279	ENSMUSG00000034239	11	103534577	103621140	-1	38	44	91	44	51	21	0	0	0	0	0	A2A9H6	
ENSMUST00000059286	ENSMUSG00000060477	6	113638467	113695026	1	77	15	15	67	15	0	398	475	456	46	310		Q8CFA1
ENSMUST00000059287	ENSMUSG00000028664	4	136647539	136835988	-1	42	23	54	361	52	47	0	5	0	0	2	A3KG02	
ENSMUST00000059295	ENSMUSG00000049303	19	4445908	4477447	-1	162	155	304	196	136	91	1	10	7	0	8	Q14AG7	
ENSMUST00000059297	ENSMUSG00000045427	X	134601179	134607060	1	0	0	0	0	2	0	383	0	0	0	0		P70333
ENSMUST00000059305	ENSMUSG00000102252	7	59982495	60140219	-1	0	8	20	11	0	6	1	2	1	1	4	Q3UN87	P63163
ENSMUST00000059315	ENSMUSG00000045204	9	19035125	19036060	1	1	1	0	2	4	0	0	0	0	0	0	Q7TRG7	
ENSMUST00000059318	ENSMUSG00000034063	6	91902809	91950725	1	17	13	46	20	33	18	1	4	0	0	2		Q8CDN1
ENSMUST00000059319	ENSMUSG00000049904	11	22512088	22519234	1	11	10	16	134	20	5	0	3	0	4	4		Q8K0U3
ENSMUST00000059320	ENSMUSG00000083695	X	163760139	163761329	-1	5	1	2	35	6	2	1	3	0	1	2	Q9D9M9	
ENSMUST00000059329	ENSMUSG00000094740	13	66851847	66852017	-1	0	0	0	0	0	0	0	0	0	0	0	L7N1Y9	
ENSMUST00000059331	ENSMUSG00000048481	7	18991245	19001766	1	1	3	2	78	16	2	3	6	23	0	8		Q8R4U1
ENSMUST00000059339	ENSMUSG00000045731	14	65400673	65425472	-1	22	22	56	102	43	29	0	2	1	3	2	Q543U6	Q64387
ENSMUST00000059341	ENSMUSG00000045064	12	85288591	85299358	1	28	26	56	37	46	20	2	38	5	1	8		Q8CCG1
ENSMUST00000059343	ENSMUSG00000028876	4	124880899	124917800	1	44	48	207	384	73	19	0	0	0	0	0		Q8BYG9
ENSMUST00000059348	ENSMUSG00000023982	17	47394560	47400584	-1	6	1	8	42	11	3	39	69	24	85	10		P43081
ENSMUST00000059349	ENSMUSG00000044827	5	64924679	64933563	-1	7	14	26	23	23	15	1415	11402	2897	2489	2346	B9EJ46	Q9EPQ1
ENSMUST00000059351	ENSMUSG00000048544	8	33428709	33429548	1	3	0	0	0	3	1	0	1	0	0	0	Q8C4Y4	
ENSMUST00000059352	ENSMUSG00000048096	1	135324807	135368065	1	39	34	97	38	38	21	0	0	0	0	0	F8VPR1	
ENSMUST00000059354	ENSMUSG00000036078	4	41738493	41756157	-1	5	0	0	37	0	0	183	237	72	49	194		O55242
ENSMUST00000059362	ENSMUSG00000047977	14	69289344	69294299	-1	75	100	178	126	78	33	5	44	16	22	18	Q8BI41	
ENSMUST00000059372	ENSMUSG00000048911	2	131298064	131352892	-1	0	0	0	36	0	0	0	33	64	0	102	Q4VA59	Q8BGI1
ENSMUST00000059374	ENSMUSG00000030465	8	67689082	68062286	-1	14	11	11	10	17	9	0	0	0	0	0	Q8C0E9	
ENSMUST00000059379	ENSMUSG00000050763	11	49142907	49149212	1	9	2	14	8	9	5	0	0	0	0	0	Q8VGD7	
ENSMUST00000059383	ENSMUSG00000050035	10	85097019	85102495	-1	8	11	27	38	10	3	0	1	2	2	1	Q8CDC8	
ENSMUST00000059390	ENSMUSG00000030982	7	118740226	118842966	1	54	46	178	66	46	24	39	129	40	14	28	I1E4X5	
ENSMUST00000059401	ENSMUSG00000038295	5	24384181	24392143	-1	12	7	28	165	31	4	3	3	7	0	4		Q6EBV9
ENSMUST00000059407	ENSMUSG00000048304	3	73047265	73057803	-1	0	9	15	75	17	4	0	0	0	0	0		Q810B9
ENSMUST00000059410						7	5	63	5	0	9	21	50	29	11	26		
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ENSMUST00000059428	ENSMUSG00000045790	5	52374651	52471521	-1	22	14	34	114	30	12	2	2	2	1	12	F6V035	
ENSMUST00000059433	ENSMUSG00000044250	15	97247107	97385689	1	27	15	44	16	31	11	201	390	245	28	168		Q8BGX1
ENSMUST00000059438	ENSMUSG00000040177	7	131342718	131362698	-1	15	11	29	90	14	9	26	57	32	13	15		Q9D2Q3
ENSMUST00000059440	ENSMUSG00000043692	11	74053776	74054778	-1	4	8	6	15	6	3	0	0	0	0	0	Q7TRX3	
ENSMUST00000059448	ENSMUSG00000049506	11	104186327	104191163	1	8	7	8	11	15	6	0	0	0	0	1		A2A6C4
ENSMUST00000059449	ENSMUSG00000050097	8	104831572	104840093	1	1528	1803	2003	1273	1701	836	22	90	47	8	83	Q6PDB7	
ENSMUST00000059452	ENSMUSG00000050600	2	174643534	174710832	1	82	44	151	170	104	48	243	477	395	45	538	A2ADM8	
ENSMUST00000059458	ENSMUSG00000050567	11	50255634	50292311	-1	0	0	0	244	9	0	180	191	351	18	352		Q6T264
ENSMUST00000059462	ENSMUSG00000053119	6	71543797	71582609	1	13	16	31	35	21	6	532	2409	701	1089	492		Q9CQ10
ENSMUST00000059466	ENSMUSG00000046615	X	46329007	46330345	1	2	0	1	5	2	3	0	0	0	0	0		Q9D9J3
ENSMUST00000059468	ENSMUSG00000049489	11	78750506	78751729	-1	16	11	28	83	25	11	32	81	34	18	35		Q8QZR8
ENSMUST00000059472	ENSMUSG00000053907	6	72432799	72439558	-1	13	13	17	39	12	14	156	518	201	114	210	Q99J57	Q3THS6
ENSMUST00000059474						1	3	14	293	7	1	5	9	4	2	12		
ENSMUST00000059482	ENSMUSG00000050762	17	24038144	24045954	1	8	4	29	19	19	7	0	3	2	1	0		Q8BJR6
ENSMUST00000059486	ENSMUSG00000043529	3	106821556	106822582	-1	10	0	9	4	10	1	0	0	0	0	0	Q8VFC3	
ENSMUST00000059498	ENSMUSG00000043019	1	151755371	151822051	1	22	15	25	21	21	16	332	591	585	115	367		Q2HXL6
ENSMUST00000059509	ENSMUSG00000050435	X	114905012	114905941	1	3	2	0	11	2	2	0	0	0	0	0	A2AFH1	
ENSMUST00000059512	ENSMUSG00000043605	6	43173952	43175005	1	5	13	6	1	11	2	0	0	0	0	0	Q0VAZ7	P34984
ENSMUST00000059515	ENSMUSG00000021218	13	3538075	3566261	1	9	16	30	68	20	12	2154	10091	3834	1195	2045		Q61598
ENSMUST00000059524	ENSMUSG00000048087	16	46152997	46155077	-1	22	30	34	16	25	23	405	519	246	208	292	Q3TF14	P50247
ENSMUST00000059534	ENSMUSG00000048284	6	42434535	42435464	1	5	8	31	21	9	7	1	0	0	0	3		P59532
ENSMUST00000059539	ENSMUSG00000055430	6	58905233	58907076	-1	2	2	14	137	16	5	0	1	0	1	1		Q9JJF0
ENSMUST00000059546						2	7	16	5	7	0	6	12	8	15	6		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000059551	ENSMUSG00000046822	10	81028538	81037426	-1	0	0	1	0	15	0	269	178	146	37	126		Q99K24
ENSMUST00000059555	ENSMUSG00000032307	9	55148854	55207529	1	6	6	0	177	13	4	131	361	87	48	73		Q8K2Z8
ENSMUST00000059560	ENSMUSG00000043312	17	38081970	38088693	-1	8	0	8	4	3	1	0	0	0	0	0	Q8VGC8	
ENSMUST00000059562	ENSMUSG00000048332	3	53041528	53261679	1	5	0	0	82	20	0	0	0	0	12	24		Q8BM86
ENSMUST00000059565	ENSMUSG00000048080	14	50237903	50238883	-1	1	2	4	3	7	2	0	0	0	0	0	F8VQB9	
ENSMUST00000059566	ENSMUSG00000027257	2	91255954	91264679	1	0	0	0	0	0	7	0	0	0	0	0	Q543N7	Q99JB8
ENSMUST00000059571	ENSMUSG00000043313	18	37496991	37504128	1	35	22	42	87	28	22	1	3	0	5	3	Q91Y01	
ENSMUST00000059579	ENSMUSG00000037808	9	13827716	13846541	1	5	2	5	7	8	2	179	595	341	113	241		Q80XP8
ENSMUST00000059580	ENSMUSG00000049327	5	124439930	124462308	1	33	23	40	105	47	16	523	1537	739	74	515	E9QNB8	
ENSMUST00000059582	ENSMUSG00000024667	19	10533865	10556238	-1	0	2	0	8	0	0	15	37	43	53	15		Q9CQC4
ENSMUST00000059588	ENSMUSG00000048371	8	104591468	104596836	1	39	36	179	97	40	17	12	28	17	7	26	Q504M2	
ENSMUST00000059589	ENSMUSG00000043811	16	18127642	18152408	1	21	12	34	130	21	11	5	0	2	0	2		Q99PI8
ENSMUST00000059595	ENSMUSG00000050965	11	107933387	108343928	-1	56	46	145	106	59	36	23	46	23	17	88	Q4VA93	
ENSMUST00000059596	ENSMUSG00000046058	7	28267881	28269272	1	3	2	2	64	7	5	8	12	4	1	6		Q6X7S9
ENSMUST00000059598	ENSMUSG00000042857	13	94355839	94358818	-1	279	216	344	279	266	153	14	64	22	4	38	Q8BRW6	
ENSMUST00000059599	ENSMUSG00000022313	15	51877429	51884614	1	0	0	0	5	0	0	25	0	2	121	6	G3X989	
ENSMUST00000059607	ENSMUSG00000045968	1	153849542	153900228	-1	29	30	141	3	36	11	0	1	0	0	0	Q208S0	
ENSMUST00000059608	ENSMUSG00000043385	4	58784779	58785720	-1	4	5	4	17	5	1	0	0	0	0	0	A2AM35	
ENSMUST00000059617	ENSMUSG00000046431	7	108880603	108881604	-1	4	4	19	4	3	6	0	0	0	0	0	Q8VEW1	
ENSMUST00000059619	ENSMUSG00000049521	15	78842647	78850902	1	11	9	35	70	28	16	0	0	1	33	134		
ENSMUST00000059637	ENSMUSG00000047889	13	33661405	33671581	1	9	11	5	2	10	4	0	0	0	0	0	Q3UWK8	
ENSMUST00000059642	ENSMUSG00000030591	7	29174188	29180701	-1	0	0	0	74	0	4	0	0	30	0	30		Q9CX56
ENSMUST00000059644	ENSMUSG00000048271	5	28317121	28419239	1	0	0	31	84	54	32	615	927	849	141	994		Q9CXK9
ENSMUST00000059647	ENSMUSG00000089824	2	156091958	156111978	-1	0	0	0	0	0	0	131	386	189	0	146		Q8R4X3
ENSMUST00000059650	ENSMUSG00000043659	9	24097996	24316398	1	5	11	6	6	10	7	0	0	0	0	0	A1KXK3	Q8BZP8
ENSMUST00000059657	ENSMUSG00000050553	5	97455142	97457021	-1	5	11	11	8	10	4	0	0	0	0	0		Q9WU65
ENSMUST00000059662	ENSMUSG00000046034	15	27605919	27630693	-1	5	4	9	15	11	5	309	927	381	195	300		Q3UCV8
ENSMUST00000059666	ENSMUSG00000045107	14	20075646	20083172	-1	33	20	99	101	46	25	27	57	19	44	18		Q8K190
ENSMUST00000059667	ENSMUSG00000046093	4	123183227	123194701	1	29	18	78	29	36	24	0	0	0	0	0	B2RRY8	Q8BGZ1
ENSMUST00000059672	ENSMUSG00000025017	19	41274218	41385070	-1	33	22	23	64	49	20	888	1158	1611	104	1356		Q9EQ32
ENSMUST00000059675	ENSMUSG00000046272	19	12861742	12862771	1	3	4	3	3	4	4	0	1	0	0	0	Q0VEZ4	Q8VFX2
ENSMUST00000059676	ENSMUSG00000045091	1	93006334	93012269	1	9	4	21	36	10	5	1	0	0	0	0		Q8CHJ2
ENSMUST00000059680	ENSMUSG00000022200	15	12321496	12351265	1	7	6	21	13	10	2	1096	2328	1319	430	847		Q9CRA5
ENSMUST00000059692	ENSMUSG00000031651	8	43129807	43141486	-1	11	4	13	9	16	7	0	0	0	0	0		Q8BVP1
ENSMUST00000059693	ENSMUSG00000045684	2	25676786	25681608	1	12	6	26	7	17	10	0	0	0	0	0	A2AJC0	
ENSMUST00000059696						0	0	0	0	0	0	0	19	0	0	0		
ENSMUST00000059699	ENSMUSG00000045912	10	79606857	79614025	-1	0	0	0	371	0	0	0	0	0	0	0		Q5HZI2
ENSMUST00000059704						17	9	41	173	29	11	9	19	11	4	12		
ENSMUST00000059707	ENSMUSG00000051617	11	100186781	100193246	-1	21	16	83	40	27	10	0	0	0	0	0		Q6RHW0
ENSMUST00000059718	ENSMUSG00000047492	10	127349402	127351772	-1	14	18	22	19	26	7	0	0	0	1	0		O08717
ENSMUST00000059737						5	6	12	10	6	2	0	0	0	0	0		
ENSMUST00000059740	ENSMUSG00000050705	17	35892677	35897431	-1	0	1	0	0	0	3	27	56	28	1	16	F6X1P1	
ENSMUST00000059743	ENSMUSG00000034343	1	91250304	91290337	1	0	0	0	12	10	0	19	64	16	95	27		Q9CY34
ENSMUST00000059754	ENSMUSG00000049605	1	173270147	173271137	1	9	10	20	5	13	3	0	0	0	0	0		
ENSMUST00000059768	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	295	0	0	0	0	0	0	0	Q3USK5	
ENSMUST00000059775	ENSMUSG00000047407	17	70844205	70853546	-1	0	0	5	10	4	3	59	99	44	7	54		P70284
ENSMUST00000059787	ENSMUSG00000044393	18	20558074	20604521	1	47	36	60	334	62	27	1	0	1	3	5		O55111
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ENSMUST00000059794	ENSMUSG00000051251	1	172052292	172057573	-1	13	9	35	74	27	12	0	0	0	1	0		Q02576
ENSMUST00000059802	ENSMUSG00000048758	9	106429454	106431568	1	4	5	0	79	0	0	5	15	4	4	13	Q5M8M8	P47915
ENSMUST00000059805	ENSMUSG00000050473	10	19847917	19851459	-1	8	7	28	338	20	9	2	6	3	0	3	B9EI54	Q8BGF8
ENSMUST00000059808	ENSMUSG00000048155	X	136927325	136928376	1	9	3	23	8	10	1	0	0	0	0	0	Q9DAB5	
ENSMUST00000059817	ENSMUSG00000044934	13	64133022	64153202	-1	9	6	15	27	14	0	36	31	25	15	15		Q0VDT2
ENSMUST00000059824	ENSMUSG00000073457	17	13230257	13237184	1	0	0	0	0	0	0	0	0	0	0	0		Q9QYZ3
ENSMUST00000059825	ENSMUSG00000063681	1	139197056	139377100	-1	39	40	59	13	45	18	0	0	0	1	0		Q8VHS2
ENSMUST00000059826	ENSMUSG00000050556	2	167103378	167190155	-1	27	12	47	151	40	19	0	2	1	0	1		Q03717
ENSMUST00000059833	ENSMUSG00000043060	12	64471333	64474898	-1	16	20	85	31	16	11	0	0	0	0	0	E9QJV1	
ENSMUST00000059836	ENSMUSG00000050382	7	79698098	79715720	-1	0	0	35	0	0	0	2	3	2	0	7	E9QMU1	
ENSMUST00000059839	ENSMUSG00000050468	2	127338639	127357651	1	31	15	12	12	35	17	0	0	0	0	0		Q6HA09
ENSMUST00000059844	ENSMUSG00000023973	17	46735705	46752214	-1	19	12	37	23	41	11	1262	1323	796	161	803		Q9DAU1
ENSMUST00000059845	ENSMUSG00000046259	3	92385685	92387324	1	6	2	20	11	6	4	0	0	0	0	0		O70559
ENSMUST00000059849	ENSMUSG00000013465	2	25199712	25211489	-1	4	8	7	132	6	0	1530	2112	1406	148	989		Q8C4Y3
ENSMUST00000059851	ENSMUSG00000048787	7	119853163	119896291	-1	11	4	20	59	19	4	101	412	197	15	92		Q8K0V2
ENSMUST00000059857	ENSMUSG00000051735	7	28788969	28798963	1	19	16	70	100	37	19	2168	4196	2040	278	1553		Q80UW3
ENSMUST00000059859	ENSMUSG00000046678	9	40022352	40023348	1	6	2	6	11	13	0	0	0	0	0	0	Q8VEU2	
ENSMUST00000059873	ENSMUSG00000051682	17	48264295	48275360	1	13	9	41	16	14	0	47	627	131	61	303		Q3LRV9
ENSMUST00000059880	ENSMUSG00000043715	X	74570639	74571574	-1	2	2	1	3	4	1	0	0	0	0	0		
ENSMUST00000059882	ENSMUSG00000054672	7	140247301	140299791	1	10	10	53	32	27	9	0	0	0	1	6	Q8C9T4	
ENSMUST00000059886	ENSMUSG00000078776	7	28129466	28164811	1	2	2	3	2	4	2	0	0	0	0	0	E9PVG8	
ENSMUST00000059888	ENSMUSG00000026971	2	60598292	60722643	-1	51	42	120	120	44	26	1	4	3	0	0		Q9Z0T9
ENSMUST00000059889	ENSMUSG00000044405	2	158502612	158508198	1	6	8	19	8	7	0	0	0	2	0	2		Q8R400
ENSMUST00000059891	ENSMUSG00000050251	10	129774717	129776926	1	9	1	5	2	2	0	0	0	0	0	0	Q7TRH6	
ENSMUST00000059893	ENSMUSG00000062064	4	150148972	150168482	1	14	5	23	17	27	10	0	0	0	0	0	B1ARZ3	
ENSMUST00000059899	ENSMUSG00000061273	X	56585512	56598069	-1	24	16	39	55	19	12	341	1139	407	111	297		Q8K273
ENSMUST00000059906	ENSMUSG00000049620	17	23833360	23836056	-1	11	6	22	18	17	4	0	0	0	0	0		Q80WM7
ENSMUST00000059914	ENSMUSG00000040720	4	11485958	11550684	1	25	9	33	22	12	0	543	1470	1269	170	795		A2AIV2
ENSMUST00000059930	ENSMUSG00000048852	11	48904656	48992226	-1	50	0	1	1	111	55	6	51	14	11	43	Q5NCB2	
ENSMUST00000059937	ENSMUSG00000048411	1	28776117	28780252	-1	13	13	33	31	19	13	0	0	0	0	0	E9Q8J5	
ENSMUST00000059946	ENSMUSG00000045662	3	108939873	108960774	1	0	10	12	0	9	0	0	0	0	0	0		Q8CAE2
ENSMUST00000059954	ENSMUSG00000017754	2	164839518	164857711	-1	0	0	0	29	3	0	134	22	33	103	596	Q3UFS5	P55065
ENSMUST00000059955	ENSMUSG00000022792	16	16302965	16309640	1	0	0	0	0	0	2	6	49	0	17	0		Q8BYL4
ENSMUST00000059957	ENSMUSG00000044293	10	129567662	129571619	1	1	1	1	0	1	0	0	0	0	0	0	Q8VF26	
ENSMUST00000059967	ENSMUSG00000045797	X	9104562	9106342	1	1	4	17	5	7	1	0	0	0	0	0	B1AW18	
ENSMUST00000059970	ENSMUSG00000034450	14	65986787	66009210	-1	17	10	49	21	34	10	0	0	0	4	0		P58710

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000059973	ENSMUSG00000036834	3	63696234	63899472	-1	0	0	0	0	0	0	0	0	0	0	0	I1E4X6	
ENSMUST00000059975	ENSMUSG00000051185	1	95313623	95335284	1	0	0	0	246	6	9	627	1044	455	522	278		Q9D3L0
ENSMUST00000059980	ENSMUSG00000046330	1	72711260	72713809	1	8	14	18	35	8	8	2649	3343	2179	11173	1412	Q4VAF2	P61514
ENSMUST00000059983	ENSMUSG00000050732	6	72385223	72390703	-1	3	2	1	8	6	2	1445	2641	840	4383	550		
ENSMUST00000059986	ENSMUSG00000044164	13	43615710	43670945	1	14	8	54	125	24	15	0	0	0	0	0		Q8C432
ENSMUST00000059996	ENSMUSG00000048153	14	54281895	54282925	-1	7	5	8	7	4	3	0	0	0	0	0		Q9Z1V0
ENSMUST00000059997	ENSMUSG00000045838	2	118754158	118762661	-1	47	30	83	80	47	14	0	1	1	3	21		A3KGF9
ENSMUST00000060004	ENSMUSG00000029452	5	121451893	121524183	1	0	0	0	0	2	0	6	0	0	1	0	Q8VCT8	
ENSMUST00000060005	ENSMUSG00000022951	16	92391953	92466146	-1	0	0	0	99	4	4	96	98	117	22	111	Q7TNY3	
ENSMUST00000060009	ENSMUSG00000048647	2	119516505	119547627	-1	8	32	168	210	48	16	16	32	18	0	32		Q8CDF7
ENSMUST00000060010	ENSMUSG00000044367	11	70216789	70221064	-1	21	20	65	33	47	12	22	35	6	8	28		Q8CE94
ENSMUST00000060013	ENSMUSG00000048621	X	109196756	109200439	1	1	0	4	0	1	2	3	3	0	5	2	Q8BHV4	
ENSMUST00000060041	ENSMUSG00000043429	1	182747126	182749180	-1	15	16	23	138	30	10	0	0	0	0	0	Q3V118	
ENSMUST00000060043	ENSMUSG00000045962	6	119923969	120038672	-1	15	0	15	95	10	0	730	696	2386	32	1558		P83741
ENSMUST00000060049	ENSMUSG00000079555	5	34153880	34169527	-1	3	5	4	8	3	2	35	207	37	59	41		Q8QZX2
ENSMUST00000060050	ENSMUSG00000050105	4	134251110	134254106	-1	8	0	4	330	23	6	0	0	0	0	0		Q80X91
ENSMUST00000060057	ENSMUSG00000044400	X	37048845	37050418	1	4	5	23	221	7	6	0	0	0	0	1		Q8BY98
ENSMUST00000060061	ENSMUSG00000047824	3	89430214	89435128	1	0	0	37	150	23	25	149	554	664	66	583	Q80V76	
ENSMUST00000060062	ENSMUSG00000051276	4	154666433	154667867	-1	14	11	15	10	28	3	0	0	0	0	0		Q9D9L5
ENSMUST00000060063	ENSMUSG00000058192	9	20581325	20595194	1	0	0	0	0	0	0	6	18	13	6	4	G3X996	
ENSMUST00000060066						1	1	1	8	1	0	0	0	0	0	0		
ENSMUST00000060067	ENSMUSG00000004069	16	4639989	4707695	1	12	0	0	24	11	0	24	24	15	17	27		Q99M87
ENSMUST00000060072	ENSMUSG00000003279	17	69969073	70821413	1	0	0	0	0	0	0	0	0	0	0	0	Q3UHD8	Q9D415
ENSMUST00000060077	ENSMUSG00000022742	16	58670208	58680391	1	95	73	107	299	130	53	47	96	65	7	58		P36552
ENSMUST00000060092	ENSMUSG00000043241	2	5951469	6056703	1	22	15	15	67	18	11	391	940	1017	528	704	A2AT37	
ENSMUST00000060095	ENSMUSG00000030306	6	148232430	148444389	-1	40	0	73	0	0	0	0	0	0	0	0		Q3UV71
ENSMUST00000060098	ENSMUSG00000050776	2	112141947	112142897	1	5	4	5	6	5	2	0	0	0	0	0	Q8VF84	
ENSMUST00000060100	ENSMUSG00000050677	5	36484588	36488172	1	34	24	97	167	46	30	4	16	9	1	20		Q9CR92
ENSMUST00000060101	ENSMUSG00000051579	X	136168984	136172342	-1	0	0	0	0	5	1	20	46	18	178	21		Q9CZY2
ENSMUST00000060108	ENSMUSG00000044148	X	12654879	12673668	-1	191	182	214	222	226	113	182	762	349	120	310	A2BDN9	Q8C5K5
ENSMUST00000060125	ENSMUSG00000046480	9	45138437	45154152	1	23	26	69	264	59	21	1	5	1	0	2	Q1MXF9	Q7M729
ENSMUST00000060128	ENSMUSG00000055976	8	35824709	35826559	-1	21	10	56	592	37	16	2	9	2	0	0		Q9D7D7
ENSMUST00000060133	ENSMUSG00000048478	8	123212858	123222045	1	2	0	5	40	1	1	0	0	0	1	2		Q8C624
ENSMUST00000060147						5	4	13	5	5	4	0	0	0	0	0		
ENSMUST00000060148	ENSMUSG00000021366	13	42052021	42185026	1	70	54	229	372	96	54	844	909	1845	53	1349	F8VPM9	
ENSMUST00000060167	ENSMUSG00000044287	8	105893567	105895023	1	0	0	3	0	2	0	0	0	4	0	0		Q8C4W3
ENSMUST00000060173	ENSMUSG00000038605	2	181595218	181599212	-1	8	0	31	197	18	0	35	0	24	18	109	Q3TBN2	Q7TST3
ENSMUST00000060174	ENSMUSG00000048779	7	100937638	100964391	-1	15	10	48	35	29	11	311	529	289	82	292	Q3UQ86	Q9ERK9
ENSMUST00000060175	ENSMUSG00000046096	7	120677620	120734854	1	20	22	41	59	27	16	68	170	102	24	82		Q8C784
ENSMUST00000060185	ENSMUSG00000048721	11	46235531	46239872	1	12	12	17	23	16	13	64	175	119	8	104		Q8BJN4
ENSMUST00000060187	ENSMUSG00000043366	7	102740721	102759471	-1	8	15	8	0	12	0	0	0	0	0	0		Q8VBV9
ENSMUST00000060188	ENSMUSG00000047714	16	31251537	31275277	-1	24	23	48	584	65	23	1032	2063	788	128	564		Q9DCL8
ENSMUST00000060196	ENSMUSG00000044364	2	151702008	151712157	1	14	2	14	75	4	7	0	0	0	0	0	A2AU34	
ENSMUST00000060204	ENSMUSG00000051046	6	116554316	116557412	1	13	2	11	5	9	4	0	0	0	0	0	Q8VG27	
ENSMUST00000060208	ENSMUSG00000042064	2	70039126	70429198	1	0	0	0	46	0	0	0	0	0	0	0	F8VQ79	
ENSMUST00000060210	ENSMUSG00000031342	X	166238911	166388988	1	0	0	0	0	0	0	0	2	0	0	11		P35803
ENSMUST00000060212	ENSMUSG00000019810	10	13499540	13519035	1	0	0	0	0	0	0	735	2761	1101	621	915	Q505Q3	Q99KR8
ENSMUST00000060214	ENSMUSG00000050854	4	118540941	118544044	-1	10	7	10	70	10	2	0	1	0	1	0		Q8CHQ6
ENSMUST00000060215						30	15	139	2	19	12	0	0	4	0	4		
ENSMUST00000060223	ENSMUSG00000049090	18	84088158	84097514	1	17	16	29	70	32	4	76	283	123	36	168	Q14AZ9	Q8BGC4
ENSMUST00000060225	ENSMUSG00000044317	7	19212538	19224174	1	13	17	31	109	26	17	5	7	2	0	7		Q8BUD0
ENSMUST00000060226	ENSMUSG00000029390	5	124540695	124550506	1	0	0	28	121	25	0	0	561	385	94	191	A2RS53	Q9R0Q3
ENSMUST00000060232	ENSMUSG00000047187	4	8535644	8607778	1	16	12	8	28	20	7	1071	4347	1500	1214	1000	Q0PD65	P53994
ENSMUST00000060241	ENSMUSG00000051582	X	100429013	100429885	1	4	4	1	6	4	2	0	0	0	0	1		Q6IE21
ENSMUST00000060242	ENSMUSG00000046460	9	54538984	54545020	1	8	8	37	12	28	4	3	1	0	0	0		Q8BI17
ENSMUST00000060243	ENSMUSG00000071481	6	43163359	43168027	1	12	8	9	2	7	1	0	0	0	0	0	Q8VEV1	
ENSMUST00000060251	ENSMUSG00000038412	9	121848560	121858000	-1	12	8	36	170	19	7	164	619	184	839	127	Q1XG81	Q9JLR9
ENSMUST00000060253	ENSMUSG00000043683	17	56256793	56263608	1	39	28	92	413	77	22	710	756	640	117	558		Q9Z2G1
ENSMUST00000060255	ENSMUSG00000010086	11	61448442	61454131	-1	20	17	24	42	26	22	0	0	0	0	0		Q96DY5
ENSMUST00000060265	ENSMUSG00000046000	5	97382198	97392379	-1	19	10	26	73	19	8	0	0	0	0	0	A8W660	Q3UX61
ENSMUST00000060270	ENSMUSG00000048012	7	44731481	44751050	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BI67
ENSMUST00000060271	ENSMUSG00000047861	11	34204338	34208089	-1	23	14	59	76	23	12	0	0	0	0	0		Q922I5
ENSMUST00000060274	ENSMUSG00000021277	12	111166370	111267153	1	0	16	111	0	75	31	0	92	135	44	299	Q3UHJ1	
ENSMUST00000060298						1	8	9	8	6	5	0	3	0	0	3		
ENSMUST00000060301	ENSMUSG00000044678	15	74796874	74799986	-1	5	0	12	10	11	0	0	0	0	0	0		Q9CWP4
ENSMUST00000060303	ENSMUSG00000046982	18	84011627	84086404	-1	0	5	15	151	40	10	15	10	5	5	20		Q5DTH5
ENSMUST00000060309	ENSMUSG00000051323	X	133582860	133688987	-1	6	5	0	0	0	0	0	0	1	0	0	A2AGW4	
ENSMUST00000060311	ENSMUSG00000039959	5	135406531	135545120	-1	55	34	107	119	100	39	1143	2329	2311	181	2701		Q8VD75
ENSMUST00000060315	ENSMUSG00000056144	7	104244457	104340693	1	0	2	0	1	0	0	17	67	13	12	35	E9PYZ4	
ENSMUST00000060323	ENSMUSG00000046519	3	95588934	95619247	1	13	15	0	0	11	0	0	0	0	0	0	K3W4N3	
ENSMUST00000060327	ENSMUSG00000048766	4	112711147	112774866	-1	1	0	5	0	3	5	0	0	0	0	0		A7TZG1
ENSMUST00000060328	ENSMUSG00000051050	18	44027869	44032208	1	0	0	0	0	0	0	0	0	0	0	0	B9EJP9	
ENSMUST00000060330	ENSMUSG00000031927	9	14756587	14771030	-1	4	0	2	54	0	6	0	0	0	4	0	Q9DAE7	
ENSMUST00000060336	ENSMUSG00000050917	7	144861386	144865243	1	17	17	24	147	21	13	0	0	0	0	0		P11403
ENSMUST00000060345	ENSMUSG00000049073	9	40126924	40128039	-1	11	9	28	1	6	6	0	0	0	0	0	Q8VGB4	
ENSMUST00000060348	ENSMUSG00000049740	7	107623971	107625161	-1	10	8	6	9	10	3	0	0	0	0	0	Q9D3P2	
ENSMUST00000060356	ENSMUSG00000048377	7	135410367	135413615	1	11	12	24	168	23	7	0	0	0	0	0	A2RTG9	
ENSMUST00000060357	ENSMUSG00000046408	8	84001502	84004770	1	0	0	1	109	0	0	0	0	0	0	0		Q8CF25
ENSMUST00000060360	ENSMUSG00000090107	11	87566653	87569250	1	16	16	127	23	27	12	0	0	0	0	0		Q5ND19
ENSMUST00000060366	ENSMUSG00000045817	17	84183931	84187947	-1	14	11	16	430	18	14	3511	20667	6919	651	6925		P23949
ENSMUST00000060369	ENSMUSG00000046178	6	8948431	9249032	1	16	13	20	72	7	6	0	0	0	0	0		Q61200
ENSMUST00000060374	ENSMUSG00000043066	7	10273828	10275351	-1	3	3	4	9	1	1	0	0	0	0	0	Q8K4I0	
ENSMUST00000060389	ENSMUSG00000050079	8	94601955	94660275	1	14	6	24	99	18	7	403	1124	722	339	433		Q8BVR6
ENSMUST00000060396	ENSMUSG00000024259	18	31580168	31609902	-1	171	137	201	218	215	130	154	643	239	72	147		Q9CQS4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000060397	ENSMUSG00000020037	10	84756062	84906538	1	12	5	40	25	11	11	0	0	0	0	0		Q7TNK1
ENSMUST00000060398	ENSMUSG00000107444	11	49112777	49113757	-1	0	5	27	13	2	5	0	0	1	0	2	Q8VEY7	
ENSMUST00000060402	ENSMUSG00000022857	16	78953008	79091097	-1	6	8	14	6	15	0	0	0	0	0	0	E9Q6Y6	
ENSMUST00000060404	ENSMUSG00000050565	1	156035403	156068861	1	50	46	77	0	29	21	131	653	132	29	167		Q8BYU6
ENSMUST00000060409	ENSMUSG00000049109	10	28668360	28883818	1	0	4	0	1	1	0	0	0	7	0	8		Q8BGW0
ENSMUST00000060415						22	24	48	76	23	17	12	1	22	4	13		
ENSMUST00000060416	ENSMUSG00000051504	7	55768178	55778925	1	0	0	0	0	0	0	1	0	0	0	5	Q4QQK7	
ENSMUST00000060417	ENSMUSG00000044328	11	77508099	77515980	-1	3	2	14	156	19	11	32	99	27	8	30	B2RVS3	Q5F267
ENSMUST00000060418	ENSMUSG00000046287	X	73064787	73068191	1	13	17	66	20	19	9	0	0	0	0	0		Q8JZW8
ENSMUST00000060419	ENSMUSG00000046623	4	127351086	127354081	-1	0	10	0	0	0	9	0	0	0	10	6		Q02738
ENSMUST00000060427	ENSMUSG00000053560	8	84661331	84662852	-1	15	10	16	364	27	10	2220	11057	1725	324	1705		P17950
ENSMUST00000060433	ENSMUSG00000045752	7	143069249	143071093	1	0	6	0	11	4	0	82	106	0	6	67		Q9JHE7
ENSMUST00000060434	ENSMUSG00000044170	11	49513618	49514651	1	6	3	7	5	8	6	0	0	0	0	0	Q8VFA8	
ENSMUST00000060435	ENSMUSG00000050989	4	134537892	134552166	-1	21	25	41	34	38	24	1834	2574	1461	213	1850	D3Z2R5	
ENSMUST00000060440	ENSMUSG00000044899	7	104189266	104195960	-1	5	0	0	0	0	0	0	0	0	0	0	Q8VGW1	
ENSMUST00000060441	ENSMUSG00000046207	11	68503019	68552698	1	1	0	77	0	0	1	189	681	242	0	8		Q3U6Q4
ENSMUST00000060442	ENSMUSG00000048216	6	13834458	13839942	-1	5	0	9	2	11	0	0	0	0	0	0	Q6ZWR2	P60894
ENSMUST00000060444	ENSMUSG00000043602	11	70764209	70772928	1	11	11	16	268	19	8	8	27	12	10	14		Q8BLB0
ENSMUST00000060447	ENSMUSG00000051730	2	69871198	69885615	-1	0	0	0	32	0	0	17	94	8	0	0		Q8K1A0
ENSMUST00000060455	ENSMUSG00000023572	2	121008403	121016904	1	0	1	0	26	5	8	1168	3355	1042	1168	605		Q3TVC7
ENSMUST00000060468	ENSMUSG00000050702	9	55962589	55980914	-1	3	0	0	1	2	0	0	0	0	0	0	E9QAA9	
ENSMUST00000060474	ENSMUSG00000050379	X	36911326	36991794	-1	5	1	21	19	9	6	8	45	8	15	6		Q9R1T4
ENSMUST00000060477						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000060479	ENSMUSG00000026609	1	188262023	188965041	1	83	60	185	104	106	62	0	0	0	0	0		Q2QI47
ENSMUST00000060481	ENSMUSG00000045284	X	44786570	44790197	-1	0	0	0	97	0	0	0	0	0	0	0		Q8CBW4
ENSMUST00000060484	ENSMUSG00000049037	6	122921848	122934619	1	6	7	21	5	9	9	295	1060	187	183	207	Q80UI7	
ENSMUST00000060490	ENSMUSG00000007617	13	93303757	93404129	1	0	0	0	0	0	3	11	37	7	4	46		Q9Z2Y3
ENSMUST00000060494	ENSMUSG00000056350	16	88728862	88729609	1	4	5	9	7	6	3	0	0	0	0	0	Q8K198	
ENSMUST00000060500	ENSMUSG00000050192	3	28781276	28798846	1	24	16	33	26	26	7	14	27	16	35	28		Q8BGY2
ENSMUST00000060501	ENSMUSG00000044303	4	89274471	89294653	-1	1	3	5	24	3	4	0	0	0	4	0		P51480
ENSMUST00000060513	ENSMUSG00000031969	9	26974135	26999566	-1	0	0	5	0	8	6	93	299	139	57	63		
ENSMUST00000060516	ENSMUSG00000005087	2	102811141	102901665	-1	0	1	0	0	0	0	6	0	6	0	0	Q80X37	
ENSMUST00000060522	ENSMUSG00000015001	15	65876053	65912397	-1	8	0	0	6	6	0	0	0	0	0	0		Q9Z0L3
ENSMUST00000060524	ENSMUSG00000073400	17	36869574	36877833	1	21	18	71	49	28	23	16	2	5	1	16		Q9WUH5
ENSMUST00000060531	ENSMUSG00000046079	5	105699969	105832436	1	22	0	0	62	13	22	42	552	198	1	238		Q8BGR2
ENSMUST00000060537	ENSMUSG00000063077	4	149176319	149307693	-1	19	16	84	48	41	17	599	1533	1186	110	897		Q60575
ENSMUST00000060539	ENSMUSG00000044122	11	78193392	78205763	1	2	0	2	9	5	0	9	47	16	26	4	F6V8V6	
ENSMUST00000060551	ENSMUSG00000050982	15	77477047	77491069	1	30	16	35	29	25	17	1	0	0	0	0	Q8CCA5	
ENSMUST00000060553	ENSMUSG00000044060	5	107497378	107512556	1	0	0	0	0	0	0	3	0	0	0	0	Q3TEG0	
ENSMUST00000060561	ENSMUSG00000047115	6	49367739	49390539	1	12	8	3	52	8	1	0	0	3	0	0		Q8C790
ENSMUST00000060562	ENSMUSG00000043383	4	118689476	118690450	-1	7	5	11	8	7	2	0	1	0	0	0	Q8VFY3	
ENSMUST00000060574	ENSMUSG00000047228	6	128539821	128581608	-1	35	32	39	66	39	14	0	0	0	0	0		Q3UU35
ENSMUST00000060576	ENSMUSG00000049929	X	106920625	106933900	1	10	11	89	17	13	11	0	0	0	0	1		Q8BLG2
ENSMUST00000060579	ENSMUSG00000043998	12	69184157	69186770	1	8	5	14	228	6	6	394	1108	635	230	471		Q921V5
ENSMUST00000060581	ENSMUSG00000049154	11	58792797	58801960	-1	3	6	4	2	5	1	0	0	0	0	0		
ENSMUST00000060587	ENSMUSG00000044222	8	21946762	21948850	1	1	2	2	3	4	0	0	0	0	0	0		Q8R2I4
ENSMUST00000060598	ENSMUSG00000044249	2	152538714	152540098	-1	3	2	1	5	6	1	0	0	0	0	0	A3KGR0	Q8BGW9
ENSMUST00000060601	ENSMUSG00000095957	9	18944650	18945588	1	3	1	1	0	0	0	0	0	0	0	0	Q7TRG9	
ENSMUST00000060603	ENSMUSG00000050102	17	21260427	21262863	1	10	10	10	7	10	2	0	0	0	0	0	Q8R297	
ENSMUST00000060608	ENSMUSG00000049439	1	60343323	60388060	1	0	0	52	13	0	0	13	26	26	26	105		Q8BKE6
ENSMUST00000060609	ENSMUSG00000058246	13	67833235	67843113	1	0	1	0	0	2	1	0	0	0	0	0	E9PX85	
ENSMUST00000060618	ENSMUSG00000026646	2	3455815	3475031	-1	0	0	0	0	0	0	0	0	0	0	0	Q8K085	
ENSMUST00000060632	ENSMUSG00000033009	8	94037198	94067921	1	0	0	0	0	0	13	0	216	0	37	0	D3YTU2	
ENSMUST00000060634	ENSMUSG00000051169	6	113415319	113419340	-1	0	3	4	0	6	1	0	0	0	0	0	B7ZMQ0	
ENSMUST00000060636	ENSMUSG00000049894	10	129765483	129768436	1	2	3	1	2	2	2	0	0	0	0	0	Q8VGI8	
ENSMUST00000060640						3	1	3	0	0	0	4	10	0	29	8		
ENSMUST00000060642	ENSMUSG00000036273	15	91673175	91816120	1	37	21	32	102	52	14	1895	4766	4753	583	2865		Q5S006
ENSMUST00000060645	ENSMUSG00000078923	2	167607638	167632095	-1	60	29	51	0	50	25	716	1130	405	133	384		Q9CZY3
ENSMUST00000060650	ENSMUSG00000036131	X	50895180	50942710	-1	0	0	0	10	0	8	0	4	0	0	0		A2AD83
ENSMUST00000060651	ENSMUSG00000018569	11	69964779	69967885	1	6	1	7	64	10	6	0	0	0	0	0	B1AR46	
ENSMUST00000060652	ENSMUSG00000022338	15	44428111	44437685	1	8	9	15	3	13	9	59	213	62	458	80		Q9JIX0
ENSMUST00000060655	ENSMUSG00000038058	6	54923949	54972612	-1	10	0	12	287	28	18	171	116	205	17	222	Q540J8	Q8BHB0
ENSMUST00000060673	ENSMUSG00000044626	16	21953826	21995542	-1	0	18	0	42	17	0	0	0	0	0	0		Q8CIV3
ENSMUST00000060680						2	0	3	59	6	2	0	0	0	0	0		
ENSMUST00000060693	ENSMUSG00000049528	1	174084331	174089980	1	7	6	6	10	1	2	0	0	0	0	0	Q7TRW1	
ENSMUST00000060700	ENSMUSG00000047606	9	89725239	89738475	-1	0	5	10	10	0	0	0	0	0	0	0	B2RPW9	Q8BLB8
ENSMUST00000060703	ENSMUSG00000047025	10	97693059	97694926	1	15	8	19	74	17	9	0	0	0	0	0		Q9CQL2
ENSMUST00000060705	ENSMUSG00000050765	13	60211933	60212934	1	18	23	9	19	23	13	0	0	0	0	0	Q8CAZ1	
ENSMUST00000060710	ENSMUSG00000044201	18	34732997	34751533	-1	11	6	19	23	19	11	16	41	31	48	37	Q3UR74	P48967
ENSMUST00000060711	ENSMUSG00000046785	9	111271929	111279093	1	28	26	26	40	48	23	133	288	148	32	165		Q8VEH5
ENSMUST00000060714	ENSMUSG00000050148	X	153498227	153501570	1	7	6	17	74	17	3	291	316	335	17	308		Q9QZM0
ENSMUST00000060716	ENSMUSG00000051354	10	26229707	26272172	1	8	12	9	6	9	4	0	10	1	4	4	E9Q3G4	
ENSMUST00000060719	ENSMUSG00000044583	X	167304929	167330558	-1	0	2	0	0	0	0	267	688	417	400	204	Q548J0	P58681
ENSMUST00000060722	ENSMUSG00000046668	18	35829818	35861687	1	13	11	41	180	15	12	23	18	17	2	36		Q91WA4
ENSMUST00000060728	ENSMUSG00000049561	17	37210894	37211867	-1	8	7	18	46	13	2	0	0	0	0	0	Q8VFE2	
ENSMUST00000060738	ENSMUSG00000044080	3	90511034	90514392	-1	4	0	10	5	5	5	416	604	255	1429	146	Q91V77	
ENSMUST00000060747	ENSMUSG00000052271	5	144190286	144194441	1	80	39	114	510	110	39	3	16	4	1	13		Q9QYC3
ENSMUST00000060752	ENSMUSG00000034729	17	47368887	47381417	1	0	1	0	0	0	3	0	0	0	0	0	E9QJS0	
ENSMUST00000060761	ENSMUSG00000055108	10	99125167	99126325	-1	19	13	41	18	16	10	0	5	2	0	3		P15972
ENSMUST00000060762	ENSMUSG00000024276	18	23954688	23964671	1	45	41	63	91	40	16	159	450	283	86	244	Q7TNK4	
ENSMUST00000060766	ENSMUSG00000047126	11	86694351	86757565	-1	12	14	33	0	0	0	2047	5553	4877	466	2555	Q5SXR6	
ENSMUST00000060780	ENSMUSG00000044454	9	20054466	20055461	-1	2	0	5	2	2	0	0	0	0	0	0		Q7TRF3
ENSMUST00000060782	ENSMUSG00000051716	10	128254131	128255901	1	11	6	25	17	21	8	1	7	3	4	3	G3X9D6	
ENSMUST00000060783	ENSMUSG00000047371	7	127342795	127345589	-1	18	14	41	112	19	16	337	425	265	35	175		Q8R0T2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000060792	ENSMUSG00000004044	11	100956733	100970887	-1	17	14	67	534	38	16	7	11	5	129	403		O54724
ENSMUST00000060795	ENSMUSG00000049057	2	89878444	89881809	1	8	0	3	0	8	0	0	0	0	0	0	Q8VGP0	
ENSMUST00000060797	ENSMUSG00000043541	6	145174834	145211005	-1	0	0	0	0	0	0	1	11	0	0	5		
ENSMUST00000060798	ENSMUSG00000046562	5	115122550	115134975	-1	40	19	101	74	51	16	1127	1189	998	160	674		Q8C4B4
ENSMUST00000060805	ENSMUSG00000038014	13	48879219	48968017	-1	37	18	68	248	40	20	1128	1575	1774	158	1404		Q6A0A9
ENSMUST00000060807	ENSMUSG00000046761	15	76001093	76014336	-1	32	0	83	0	0	14	3	1	0	7	25		Q148V8
ENSMUST00000060808	ENSMUSG00000036606	15	89155549	89171120	-1	0	0	5	108	0	2	0	0	0	3	195		B2RXS4
ENSMUST00000060818	ENSMUSG00000044628	2	25242255	25244262	1	10	2	0	0	7	0	0	1	1	0	1		Q8K0W3
ENSMUST00000060820	ENSMUSG00000049691	5	41761483	41764501	-1	7	9	10	527	19	6	0	0	0	0	0		P97503
ENSMUST00000060824	ENSMUSG00000031271	X	139079257	139085236	-1	1	0	0	0	2	0	0	0	0	0	0	Q8BII9	
ENSMUST00000060833	ENSMUSG00000000544	1	166130238	166166510	1	12	11	23	24	22	12	0	0	0	0	69		
ENSMUST00000060834	ENSMUSG00000042831	7	30308717	30314304	1	2	0	0	0	0	3	47	37	24	27	0		Q8K2U2
ENSMUST00000060835	ENSMUSG00000010342	11	87405065	87555823	1	18	20	26	28	22	8	0	17	8	12	8		Q7M6U3
ENSMUST00000060837	ENSMUSG00000051343	6	85334962	85374634	-1	32	31	74	247	63	31	490	758	434	105	747		Q8R361
ENSMUST00000060839	ENSMUSG00000039419	6	45060061	47304213	1	0	3	6	0	3	1	1	0	0	0	0		Q9CPW0
ENSMUST00000060847	ENSMUSG00000034387	6	112359324	112388023	-1	10	7	13	7	13	6	0	0	0	0	0		Q8C3L1
ENSMUST00000060855	ENSMUSG00000048077	15	98255982	98257307	-1	10	11	44	35	23	11	0	0	0	0	0		Q8CJI4
ENSMUST00000060864	ENSMUSG00000028458	4	43441939	43448064	1	17	9	20	334	27	14	34	34	25	0	32		O70146
ENSMUST00000060871						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000060879	ENSMUSG00000095373	7	106873293	106874243	-1	8	6	4	5	6	3	0	0	0	0	0	Q9EPF7	
ENSMUST00000060893	ENSMUSG00000047225	7	105156742	105157680	-1	2	3	5	2	4	0	0	0	0	0	0	Q7TRN8	
ENSMUST00000060894	ENSMUSG00000044726	15	34453312	34473892	1	41	41	152	73	36	24	1	10	8	2	11		Q8K0S2
ENSMUST00000060895	ENSMUSG00000001891	11	21321138	21371201	-1	0	0	0	61	0	3	727	3697	1327	405	581	Q3U548	Q91ZJ5
ENSMUST00000060896	ENSMUSG00000043719	9	105687809	105828160	-1	10	3	0	3	0	0	0	0	0	0	0		Q8C6K9
ENSMUST00000060899	ENSMUSG00000044968	5	21662901	21701396	-1	99	2	222	67	0	14	9	16	20	3	0		Q8BH82
ENSMUST00000060901	ENSMUSG00000028965	4	150914562	150946102	1	3	0	0	2	2	1	0	0	0	8	4	Q8R037	
ENSMUST00000060904	ENSMUSG00000044550	X	136590842	136668378	1	0	4	7	18	0	0	0	0	0	0	0		Q8R0A5
ENSMUST00000060912	ENSMUSG00000051392	3	97410217	97411179	-1	8	5	24	12	5	2	0	0	0	0	0	Q8VET1	
ENSMUST00000060913	ENSMUSG00000047067	1	92906981	92908435	1	4	2	8	213	14	1	53	70	43	49	36		Q8BTR5
ENSMUST00000060917	ENSMUSG00000032204	9	71110659	71168682	-1	33	25	120	44	50	37	10	130	12	0	89	D3YYD6	
ENSMUST00000060918	ENSMUSG00000050022	5	140724127	140761439	1	0	0	0	0	0	7	200	127	96	19	131	A1L312	Q8BVF9
ENSMUST00000060930	ENSMUSG00000050050	5	92607954	92675271	-1	14	12	21	39	26	12	0	1	0	0	2		Q8CDI6
ENSMUST00000060943	ENSMUSG00000031492	8	27368711	27399729	1	0	0	0	33	0	0	0	0	0	0	0		Q8BMN3
ENSMUST00000060945	ENSMUSG00000049470	11	53350833	53421830	1	28	19	104	58	27	14	623	1605	1414	194	1199		Q9ESC8
ENSMUST00000060947	ENSMUSG00000046798	5	5489537	5514958	-1	0	0	5	13	6	0	44	0	36	0	0		Q9ET43
ENSMUST00000060955	ENSMUSG00000027346	2	132529082	132587729	-1	0	0	0	0	0	0	3199	5879	4942	4329	4448		Q8C0L9
ENSMUST00000060956	ENSMUSG00000049299	11	69323980	69325793	1	0	0	6	0	0	0	0	0	0	17	0	B1ASW6	
ENSMUST00000060972	ENSMUSG00000045534	6	126532551	126535412	-1	22	10	32	113	34	15	0	0	0	0	0		Q61762
ENSMUST00000060987	ENSMUSG00000035242	10	80826656	80829290	1	7	0	0	45	7	0	53	0	0	0	0	F8WI29	
ENSMUST00000060989	ENSMUSG00000049313	9	41964720	42124297	-1	77	49	105	209	82	59	19516	37504	41516	1501	35348		O88307
ENSMUST00000060991	ENSMUSG00000006736	10	127067317	127070261	-1	32	16	77	40	47	19	512	957	461	142	290		Q9CQ88
ENSMUST00000060992	ENSMUSG00000020458	11	29692947	29744331	1	0	3	0	2	2	4	507	1513	21	0	0	Q78NS1	Q99P72
ENSMUST00000060994						2	8	8	7	3	0	2	2	0	4	0		
ENSMUST00000060997						9	5	17	42	10	2	5	0	0	15	0		
ENSMUST00000061008	ENSMUSG00000040473	5	5579278	5664239	-1	0	0	1	58	1	0	0	0	0	0	0	G3X999	
ENSMUST00000061013	ENSMUSG00000079429	1	88226986	88262289	1	347	88	320	3	175	189	1	1	0	0	0		D3Z750
ENSMUST00000061019	ENSMUSG00000046755	11	91575315	91577558	-1	12	12	29	14	23	12	0	0	0	0	0	A2RSC8	Q8C0N1
ENSMUST00000061020	ENSMUSG00000049011	14	50147901	50148872	-1	2	0	2	0	1	0	0	0	0	0	0	Q8VET4	
ENSMUST00000061030	ENSMUSG00000047531	16	23925548	23930787	-1	11	9	22	14	9	8	0	0	0	0	0		Q80ZI2
ENSMUST00000061035	ENSMUSG00000046518	12	33928425	33929310	1	11	8	11	13	6	8	0	0	0	0	0		Q923Z4
ENSMUST00000061038	ENSMUSG00000050092	3	92316620	92318085	1	8	11	15	6	14	5	0	0	0	0	0	A9JTY7	
ENSMUST00000061045	ENSMUSG00000044772	14	13670876	13683148	1	4	5	3	6	4	3	0	0	0	0	0		Q8C9X1
ENSMUST00000061046						24	24	179	95	23	9	1	3	0	0	7		
ENSMUST00000061047	ENSMUSG00000044340	1	106171752	106394250	1	25	33	81	672	77	25	56	96	86	13	111		Q8CHE4
ENSMUST00000061050	ENSMUSG00000022665	16	45093402	45127924	1	0	17	129	38	0	8	0	15	6	0	0		Q8R2G6
ENSMUST00000061052	ENSMUSG00000024426	17	35897595	35910075	-1	0	0	0	12	3	0	0	0	0	0	0		Q8K341
ENSMUST00000061055	ENSMUSG00000051362	7	103154792	103155745	-1	3	5	4	1	7	3	0	0	0	0	0	Q8VGV8	
ENSMUST00000061070	ENSMUSG00000044950	11	43681998	43721491	1	0	6	0	26	0	8	0	0	0	0	0		Q69Z61
ENSMUST00000061071	ENSMUSG00000044667	3	117319139	117360876	-1	46	23	70	257	46	25	1	0	0	0	9		Q7TME0
ENSMUST00000061073						0	0	0	0	0	0	3	0	0	17	0		
ENSMUST00000061074	ENSMUSG00000096861	7	85221518	85237704	-1	9	6	8	3	5	1	0	0	0	0	0	L7N2B3	
ENSMUST00000061081	ENSMUSG00000047039	2	87857177	87858103	1	2	3	1	1	5	2	0	0	0	0	0	Q8VFQ8	
ENSMUST00000061086	ENSMUSG00000045826	19	4154606	4156751	1	2	2	8	68	6	3	64	80	32	37	50	Q542J3	Q64697
ENSMUST00000061088	ENSMUSG00000027684	3	29951296	30548008	-1	0	0	0	0	0	0	0	0	0	0	0	F6SZX1	
ENSMUST00000061091	ENSMUSG00000023805	17	5941280	6044290	1	2	4	0	0	3	4	0	0	0	0	0		Q9D2G5
ENSMUST00000061093	ENSMUSG00000026614	1	185454848	185468762	1	58	54	112	262	55	30	0	0	0	0	0		Q3UVU3
ENSMUST00000061096	ENSMUSG00000048469	7	102803480	102804430	1	12	10	13	12	15	10	0	0	0	0	0	E9PWA8	
ENSMUST00000061099	ENSMUSG00000048655	3	55137339	55172935	1	3	7	20	17	3	2	1	1	0	0	1		Q8BXX9
ENSMUST00000061101	ENSMUSG00000032440	9	116087698	116175363	-1	0	0	0	0	0	0	723	540	1037	203	742	Q543C0	Q62312
ENSMUST00000061103	ENSMUSG00000046318	18	66045302	66302739	-1	23	18	68	30	30	20	0	0	0	4	14		Q3MI99
ENSMUST00000061111	ENSMUSG00000044345	19	42147400	42151703	1	17	4	39	602	37	13	376	534	422	25	168		Q7TQJ1
ENSMUST00000061118	ENSMUSG00000045100	6	94500331	94604672	1	10	9	17	54	22	6	18	20	16	8	12		Q5U680
ENSMUST00000061135	ENSMUSG00000039693	4	48539935	48561919	1	3	3	21	21	0	0	23	67	66	13	0		Q9CR78
ENSMUST00000061143	ENSMUSG00000028849	4	126232167	126256343	-1	0	0	0	215	24	0	0	0	1	0	0		A2AJI0
ENSMUST00000061155	ENSMUSG00000032489	9	110476958	110525179	1	9	12	3	14	32	3	24	120	40	43	68	Q8C0X6	
ENSMUST00000061156	ENSMUSG00000035376	16	35022421	35109175	1	15	18	17	107	27	11	275	1150	395	146	231		Q9D3B1
ENSMUST00000061158	ENSMUSG00000051154	2	18672384	18676231	1	1	2	7	15	0	2	101	423	157	733	96		Q63829
ENSMUST00000061165	ENSMUSG00000027999	3	129878606	129895825	1	2	0	2	3	8	4	4	0	4	10	0		Q9EPR2
ENSMUST00000061169	ENSMUSG00000047658	19	5298331	5308738	1	99	78	203	967	120	74	3	22	4	1	18		P61315
ENSMUST00000061174	ENSMUSG00000050132	11	78472330	78497754	-1	13	10	26	215	34	6	0	0	0	0	0		Q6PDS3
ENSMUST00000061179	ENSMUSG00000035437	2	37443279	37566454	1	10	20	19	18	27	5	151	194	483	41	588	B2RRC5	A2AWA9
ENSMUST00000061185	ENSMUSG00000067615	15	101459061	101463765	-1	11	11	25	67	27	10	2	0	0	2	2		Q9ERE2
ENSMUST00000061187	ENSMUSG00000047143	4	109978053	109983687	1	2	6	3	546	20	5	0	0	0	5	8		A2A9A2
ENSMUST00000061190	ENSMUSG00000047953	16	30307686	30310779	-1	20	12	50	355	30	18	8	17	16	12	26	Q9QZU3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000061193	ENSMUSG00000049123	7	29697219	29727015	-1	13	10	21	29	28	11	0	0	1	1	6		C6KI89
ENSMUST00000061201						7	5	15	9	9	3	0	1	0	0	0		
ENSMUST00000061203	ENSMUSG00000063406	5	108106366	108132620	-1	142	103	168	208	173	123	21	111	56	29	46	E9Q2J2	
ENSMUST00000061209	ENSMUSG00000049305	9	108460527	108465938	1	17	0	0	6	7	0	191	398	337	118	201		Q8VEG0
ENSMUST00000061213						0	0	20	46	0	0	0	7	8	0	1		
ENSMUST00000061215	ENSMUSG00000046790	4	118709409	118710347	1	11	6	7	5	5	3	0	0	0	0	0	Q7TQV4	
ENSMUST00000061222	ENSMUSG00000043881	14	79426511	79431039	1	8	11	23	146	32	13	566	1023	778	71	397	G5E8C2	
ENSMUST00000061226						3	1	1	9	3	1	0	0	0	0	0		
ENSMUST00000061234	ENSMUSG00000050890	4	134275002	134287895	-1	9	6	0	78	0	0	0	0	31	20	0		Q8QZR7
ENSMUST00000061235	ENSMUSG00000048292	19	11828077	11829024	-1	21	10	34	13	22	8	0	0	0	1	0	Q8VGJ6	
ENSMUST00000061239	ENSMUSG00000022436	15	78899667	78919517	1	0	0	0	0	0	0	35	22	0	5	0	A2A5V3	
ENSMUST00000061241	ENSMUSG00000049233	13	107413865	107414767	-1	4	4	0	0	0	0	4	15	0	36	0		Q9DCZ4
ENSMUST00000061242	ENSMUSG00000048076	11	59211412	59228270	-1	19	17	40	13	20	4	7119	11637	6787	3924	4864		P84078
ENSMUST00000061244	ENSMUSG00000029710	5	137350109	137378669	1	0	0	0	271	26	7	0	0	0	0	31		P54761
ENSMUST00000061251	ENSMUSG00000072694	5	114808196	114813976	-1	10	14	10	65	10	9	115	299	142	572	48	Q3TTH7	
ENSMUST00000061260	ENSMUSG00000046743	3	38886940	39011985	1	117	70	237	327	145	69	0	0	0	0	3		Q2PZL6
ENSMUST00000061262	ENSMUSG00000033152	6	88842558	88875044	-1	8	0	23	137	0	16	0	0	0	0	0	G3X9D3	
ENSMUST00000061273	ENSMUSG00000044548	12	71309884	71320107	1	11	9	18	85	6	3	1	6	0	0	0		Q8R4A3
ENSMUST00000061274	ENSMUSG00000046961	16	37916496	38007527	1	38	24	72	63	46	21	1	1	1	0	2		
ENSMUST00000061277	ENSMUSG00000047799	4	143437164	143450324	-1	5	0	0	0	4	2	0	0	0	0	0	Q8BHX9	
ENSMUST00000061278	ENSMUSG00000050933	17	20889716	20890651	-1	7	1	3	1	7	2	0	0	0	0	0	Q8R2A3	
ENSMUST00000061279	ENSMUSG00000102742	18	37755731	37841873	1	21	17	23	23	15	8	2	2	13	2	5	Q91XY8	
ENSMUST00000061280	ENSMUSG00000051285	1	7088920	7173628	1	13	10	0	16	15	0	158	663	253	247	298	Q3TGS5	P59913
ENSMUST00000061283	ENSMUSG00000017561	11	80046493	80080991	-1	11	7	19	27	14	0	771	2398	999	310	782		Q9Z2L7
ENSMUST00000061284	ENSMUSG00000044120	7	105143350	105144309	-1	10	1	14	0	3	8	0	0	0	0	0	Q8VGV1	
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ENSMUST00000061289	ENSMUSG00000051190	10	78846951	78852166	-1	3	3	3	5	4	2	0	0	0	0	0	Q7TQU8	
ENSMUST00000061293	ENSMUSG00000048919	11	59589067	59590177	-1	7	4	8	5	5	3	0	0	0	0	0	Q8VF69	
ENSMUST00000061294	ENSMUSG00000049796	3	19693401	19695396	-1	3	0	7	185	7	3	0	0	0	0	0		Q8CIT0
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ENSMUST00000061299	ENSMUSG00000048373	5	43978858	43981779	-1	12	12	43	9	19	6	0	0	0	22	7		O70514
ENSMUST00000061309	ENSMUSG00000044034	11	120608477	120609093	1	0	0	0	0	0	2	0	0	0	0	0	A2ABY2	
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ENSMUST00000061322	ENSMUSG00000048416	3	67374097	67400003	1	0	0	0	0	0	0	0	2	1	5	0	Q8JZS2	
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ENSMUST00000061334	ENSMUSG00000046994	1	55237177	55248470	1	59	38	131	204	46	38	32	53	45	11	35	A2RT28	Q499X9
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ENSMUST00000061360	ENSMUSG00000046804	2	118772769	118778165	1	1	0	8	10	10	0	0	0	0	1	0	K3W4T6	
ENSMUST00000061365	ENSMUSG00000048391	9	19248357	19249463	-1	2	1	2	2	0	4	0	0	0	0	0	Q7TRG4	
ENSMUST00000061372	ENSMUSG00000047514	10	34282190	34285275	1	37	55	81	449	59	19	1007	2681	1321	147	925		O88852
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ENSMUST00000061391	ENSMUSG00000044362	7	90426312	90428660	1	17	11	23	13	23	12	1	0	0	2	0		Q9DA73
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ENSMUST00000061421	ENSMUSG00000047343	1	44009408	44020034	-1	4	4	4	1	3	5	0	0	0	0	1	B2RVS5	Q8BLU2
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ENSMUST00000061427	ENSMUSG00000043635	5	89677087	89883334	-1	50	24	27	90	32	0	2	11	1	0	6	G3X9D2	
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ENSMUST00000061446	ENSMUSG00000043388	5	144735915	144761818	-1	47	26	70	447	80	26	4	0	4	0	7		Q6NXM3
ENSMUST00000061450	ENSMUSG00000045980	11	115187487	115247023	1	12	5	13	60	15	7	649	604	400	86	407		Q3TB48
ENSMUST00000061455	ENSMUSG00000044468	3	100451628	100489324	-1	81	35	138	170	118	39	714	1630	1207	217	789		Q5SSF7
ENSMUST00000061456	ENSMUSG00000049314	9	109179227	109195975	-1	10	7	3	4	10	3	0	1	0	2	1	Q8BI57	
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ENSMUST00000061458	ENSMUSG00000044937	10	86705811	86776843	1	3	3	4	0	4	3	0	3	0	0	0	A0A0G2LB92	
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ENSMUST00000061469	ENSMUSG00000044177	11	94235956	94246005	-1	37	29	74	44	63	24	42	98	68	6	32		Q7TQN3
ENSMUST00000061481	ENSMUSG00000049291	11	59372669	59375657	-1	8	6	17	18	15	4	0	0	0	0	0		Q3UKY7
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ENSMUST00000061483	ENSMUSG00000049086	2	25706739	25707721	1	7	4	10	216	8	4	10	39	3	7	24	A0PJL6	Q6P8Z1
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ENSMUST00000061496	ENSMUSG00000024985	19	55741810	55933654	1	8	0	0	19	0	12	0	59	0	0	0	Q80WT9	
ENSMUST00000061497	ENSMUSG00000044429	1	65100389	65103373	-1	2	3	9	5	0	2	0	0	0	0	0		P04345
ENSMUST00000061498	ENSMUSG00000049307	9	14748459	14752122	-1	25	20	90	583	44	15	143	335	196	26	194	Q544B8	Q11127
ENSMUST00000061506	ENSMUSG00000036019	10	105187663	105574451	-1	17	5	14	7	15	9	0	0	0	0	5		Q56A06
ENSMUST00000061507						1	1	0	156	7	1	0	0	0	0	0		
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ENSMUST00000061514	ENSMUSG00000043518	X	161717069	161779496	1	4	7	16	49	5	0	0	0	0	0	0		Q9QVY8
ENSMUST00000061516	ENSMUSG00000045551	17	17876471	17883940	-1	12	6	16	6	6	8	2820	14870	5085	9539	2962		P33766
ENSMUST00000061522	ENSMUSG00000044595	18	36763671	36766214	-1	8	5	4	15	11	5	0	7	4	0	2		Q6VY05
ENSMUST00000061537						13	2	13	99	11	7	33	88	12	220	46		
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ENSMUST00000061544	ENSMUSG00000026854	2	30982279	31023586	1	4	7	10	3	4	3	0	1	3	0	0	Q8C9A6	
ENSMUST00000061545	ENSMUSG00000049630	2	13003457	13011806	-1	12	6	24	261	20	6	0	1	0	0	0		Q9ESN4
ENSMUST00000061552	ENSMUSG00000074305	9	56201126	56418067	-1	40	26	172	110	64	24	86	37	207	11	396		Q69Z38

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000061568	ENSMUSG00000043885	9	15709738	15742384	1	68	64	100	47	92	43	374	1021	688	66	378		
ENSMUST00000061571	ENSMUSG00000048015	10	130268153	130280240	-1	7	12	16	12	11	6	0	0	0	1	1	Q545C0	O09105
ENSMUST00000061578	ENSMUSG00000043535	2	29124181	29182471	1	55	51	56	251	59	28	868	2211	2387	179	1509		A2AKX3
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ENSMUST00000061587	ENSMUSG00000043964	7	127769815	127775150	1	0	21	41	17	24	19	1040	1536	670	112	458	A3KCG3	Q6P8G8
ENSMUST00000061590	ENSMUSG00000060798	3	40531286	40704774	1	10	11	20	238	20	10	0	0	1	1	3		Q059U7
ENSMUST00000061593						0	0	0	0	1	0	0	0	0	0	0		
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ENSMUST00000061597	ENSMUSG00000049902	13	59687402	59694101	-1	10	16	15	14	20	6	0	0	0	1	1	Q8CET0	
ENSMUST00000061601	ENSMUSG00000047712	10	8204753	8518825	-1	19	13	35	293	35	20	8	8	5	5	26		Q8BUB6
ENSMUST00000061611	ENSMUSG00000089872	1	190700202	190911770	-1	0	15	20	39	0	0	349	436	662	69	420	E9QMX4	
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ENSMUST00000061617	ENSMUSG00000049764	10	76032654	76043234	1	48	46	87	79	61	31	57	99	55	5	61	Q505F4	
ENSMUST00000061618	ENSMUSG00000046139	19	11912399	11945096	1	17	12	32	38	28	13	440	1113	758	68	633		Q3TC46
ENSMUST00000061620	ENSMUSG00000055567	1	66468367	66699866	1	126	107	320	177	166	89	4	5	6	0	11	B8XCJ6	
ENSMUST00000061628	ENSMUSG00000050505	14	88464743	88471396	-1	13	7	6	2	5	2	0	0	0	0	0		Q8BIZ0
ENSMUST00000061632	ENSMUSG00000050663	10	114398823	114802307	-1	10	12	31	11	10	15	0	0	0	0	0		Q8K093
ENSMUST00000061637	ENSMUSG00000058728	11	114956116	114969157	-1	0	0	0	5	5	1	0	3	2	0	0	F7C5I0	
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ENSMUST00000061653	ENSMUSG00000061780	10	79890853	79892656	1	5	1	7	16	9	4	0	0	0	0	1	Q3UP47	P03953
ENSMUST00000061656	ENSMUSG00000050310	15	6708381	6800398	1	77	70	263	104	67	34	331	893	746	164	768		Q6QI06
ENSMUST00000061660	ENSMUSG00000043537	17	20502299	20503195	1	5	0	0	0	2	0	0	0	0	0	0	Q8R2A5	
ENSMUST00000061669	ENSMUSG00000047207	19	13768307	13769395	1	4	6	1	18	6	6	0	0	0	0	0	Q8VEZ4	
ENSMUST00000061673	ENSMUSG00000042284	13	114958079	115101964	-1	24	19	33	106	41	20	27	74	57	7	45		Q3V3R4
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ENSMUST00000061690	ENSMUSG00000049280	7	108645584	108646658	-1	10	12	6	2	8	1	0	0	0	0	0	Q8VF20	
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ENSMUST00000061695	ENSMUSG00000045989	7	126830468	126831639	-1	5	5	20	5	8	5	0	0	0	0	0	E9Q9R3	
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ENSMUST00000061701	ENSMUSG00000051313	2	90000145	90003322	1	3	0	0	9	0	0	0	0	0	0	0	Q8VGN2	
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ENSMUST00000061706	ENSMUSG00000048581	3	63914684	63929472	-1	27	29	53	98	35	21	6	47	12	18	40		Q8BN57
ENSMUST00000061717	ENSMUSG00000051678	18	37333921	37337674	1	15	16	45	28	23	6	0	0	0	0	1	Q91XZ4	
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ENSMUST00000061721	ENSMUSG00000018983	4	136172394	136196057	1	21	19	86	144	44	21	3892	3948	3185	229	1600		P56931
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ENSMUST00000061723	ENSMUSG00000050654	6	116581938	116583031	-1	8	6	2	4	10	7	0	0	0	0	0	Q8VF82	
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ENSMUST00000061738	ENSMUSG00000043310	7	102908869	102909837	-1	5	3	14	5	8	2	0	0	0	0	0	E9Q407	
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ENSMUST00000061756	ENSMUSG00000042848	17	20687508	20688404	1	3	2	0	1	2	0	0	0	0	0	0	Q8R2A8	
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ENSMUST00000061796	ENSMUSG00000046922	10	41069989	41072285	-1	7	4	31	162	21	2	0	0	0	0	0		Q6YNI2
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ENSMUST00000061829	ENSMUSG00000051439	18	36725074	36726736	-1	25	10	27	93	18	14	3729	6356	3488	2647	3815	Q4FJP7	P10810
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ENSMUST00000061833	ENSMUSG00000048503	9	43108653	43116570	-1	73	57	168	1649	115	46	1	12	6	0	11		Q3TYE7
ENSMUST00000061835	ENSMUSG00000049598	1	172555938	172563717	1	6	0	12	34	14	4	0	6	7	0	6		Q6P3A4
ENSMUST00000061837	ENSMUSG00000047284	11	69901072	69913820	1	25	5	29	27	5	0	296	609	351	17	311		Q5NCX5
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ENSMUST00000061852	ENSMUSG00000026648	2	3424131	3464130	1	75	65	77	63	63	33	77	306	127	28	175		Q8K4J0
ENSMUST00000061856	ENSMUSG00000024978	19	55069734	55099451	-1	27	24	45	51	31	18	9	14	17	1	35		Q61586
ENSMUST00000061859	ENSMUSG00000043311	17	35126373	35128855	1	85	99	224	82	56	30	498	942	437	51	252	B2RS43	Q9Z1R4
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ENSMUST00000061875	ENSMUSG00000052253	15	25984366	25998482	1	24	22	65	362	45	14	323	814	338	134	294		Q91VY9
ENSMUST00000061878	ENSMUSG00000045259	1	171358446	171360798	-1	7	6	35	108	13	4	4	3	3	1	1		Q3USL1
ENSMUST00000061882	ENSMUSG00000048755	15	83546797	83555711	-1	22	10	47	130	29	14	191	276	140	68	105		Q8R3F5
ENSMUST00000061885	ENSMUSG00000047150	17	47412734	47437376	-1	10	7	23	19	13	4	1	4	1	1	1	Q8K168	
ENSMUST00000061890	ENSMUSG00000025821	6	47877204	47908485	1	34	32	51	467	49	19	112	130	87	19	107	E9PVC2	
ENSMUST00000061891	ENSMUSG00000044991	2	132686931	132751055	1	3	0	9	12	4	1	142	229	53	241	45	B2RR16	Q9D112
ENSMUST00000061895	ENSMUSG00000023452	5	32736301	32785646	-1	0	5	0	44	0	0	55	134	108	54	40	Q505E1	Q8BSF4
ENSMUST00000061905						1	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000061920	ENSMUSG00000050266	7	105329217	105330278	-1	4	2	7	13	9	0	1	0	0	0	1	Q8VH18	
ENSMUST00000061923	ENSMUSG00000045232	8	84042929	84045000	-1	7	1	14	80	13	4	2	1	0	0	0		Q8CHK2
ENSMUST00000061925	ENSMUSG00000049148	15	4375491	4575553	1	3	3	0	2	2	2	0	0	0	0	0	G3X9A7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000061934						0	0	1	74	0	2	4	10	2	1	1		
ENSMUST00000061936	ENSMUSG00000047222	14	51255266	51256112	-1	9	3	4	6	5	5	14	15	9	115	7	Q8K196	
ENSMUST00000061937	ENSMUSG00000028189	3	146449795	146465849	1	11	10	4	108	15	4	242	791	441	237	250	Q102J0	Q8R242
ENSMUST00000061938	ENSMUSG00000057534	11	88964658	88966931	-1	5	7	30	7	10	11	0	0	0	0	0	A6PWE0	
ENSMUST00000061947						39	29	33	29	36	18	0	9	5	0	1		
ENSMUST00000061970	ENSMUSG00000031337	X	71210767	71315691	1	0	0	0	0	0	0	39	0	0	0	0		Q9Z2C5
ENSMUST00000061973	ENSMUSG00000049734	9	109057933	109059734	-1	2	0	34	3	1	0	104	11	55	0	0		Q91XB0
ENSMUST00000061986	ENSMUSG00000044813	4	45423278	45532470	-1	7	2	0	144	6	5	13	3	6	3	26		Q6PD21
ENSMUST00000061990	ENSMUSG00000050788	1	174249889	174250976	-1	9	6	20	8	3	4	0	0	0	0	0	E9Q0Y7	
ENSMUST00000061993	ENSMUSG00000044040	19	13794665	13795609	-1	3	0	5	6	5	3	0	0	0	0	0	Q8VG11	
ENSMUST00000061995	ENSMUSG00000051346	10	128209908	128211794	-1	12	7	6	12	26	8	28	47	10	13	16		Q91WK1
ENSMUST00000062000	ENSMUSG00000042903	X	101254528	101260873	1	7	7	12	30	9	0	619	938	679	153	500	B1AUT3	Q9WVH3
ENSMUST00000062002	ENSMUSG00000047591	15	75746843	75747922	-1	3	1	6	339	7	1	0	2	2	0	3		Q8CF90
ENSMUST00000062005	ENSMUSG00000048643	16	88924050	88924217	-1	0	2	5	0	2	1	0	0	0	0	0	F8WH65	
ENSMUST00000062009	ENSMUSG00000037174	3	51252720	51340663	-1	0	0	0	0	0	0	98	148	96	15	158	Q3TVH6	Q9JHC9
ENSMUST00000062010	ENSMUSG00000047686	X	106837082	106840644	-1	15	4	60	16	20	7	0	0	0	0	0	Q6P1Y1	
ENSMUST00000062015	ENSMUSG00000016128	5	151037510	151233836	-1	0	21	0	31	0	0	0	0	0	5	0	F8WIY7	
ENSMUST00000062024	ENSMUSG00000046275	11	76679808	76698664	1	26	26	54	34	47	24	2	0	0	1	0		Q8C838
ENSMUST00000062028	ENSMUSG00000046793	3	108148321	108154882	-1	15	11	8	39	12	16	0	7	3	0	9		Q8C010
ENSMUST00000062037	ENSMUSG00000074491	8	3707064	3720651	-1	12	1	18	13	10	7	3	1	2	17	0		Q8BNX1
ENSMUST00000062041	ENSMUSG00000043153	12	36381519	36689444	1	9	13	6	5	8	4	0	4	2	9	7		Q5RJG7
ENSMUST00000062045	ENSMUSG00000051627	13	23621755	23622502	-1	12	8	100	171	10	8	14	55	13	17	16		P43274
ENSMUST00000062047	ENSMUSG00000027459	2	151969398	151980219	-1	8	5	11	210	19	8	318	347	189	19	77		Q8R184
ENSMUST00000062058	ENSMUSG00000049288	3	96601149	96626171	1	8	11	20	43	25	13	4	5	7	7	32	G3X9C8	
ENSMUST00000062060	ENSMUSG00000026734	2	19462837	19553914	-1	6	8	1	4	9	0	0	0	0	0	0	Q8CET2	
ENSMUST00000062067	ENSMUSG00000050552	5	138255482	138259398	1	5	0	4	4	4	3	1369	2233	1036	2911	479		Q8CF66
ENSMUST00000062069	ENSMUSG00000047250	2	36230426	36252272	1	15	15	69	95	27	16	685	930	1006	243	750	Q543T1	P22437
ENSMUST00000062085	ENSMUSG00000045336	1	56636044	56637435	-1	5	12	4	0	8	2	0	0	0	0	0	Q80Y37	
ENSMUST00000062092	ENSMUSG00000047832	12	112820237	112829389	-1	13	8	18	202	21	10	384	477	371	147	258		Q9CWM2
ENSMUST00000062108	ENSMUSG00000042349	1	131254343	131279606	-1	11	10	40	24	22	14	410	370	566	75	359		Q9R0T8
ENSMUST00000062113	ENSMUSG00000043787	8	19111931	19114839	-1	0	5	2	3	3	2	0	0	0	0	0		
ENSMUST00000062117	ENSMUSG00000051615	14	120478461	120507194	1	7	7	14	112	14	0	399	449	585	43	449		Q80ZJ1
ENSMUST00000062118	ENSMUSG00000043257	4	133660387	133672647	-1	70	66	144	109	80	60	415	811	429	51	283		Q7TPN3
ENSMUST00000062122	ENSMUSG00000047419	13	93040713	93144724	-1	75	69	153	304	106	45	2	1	0	1	4	E9QLJ0	
ENSMUST00000062124	ENSMUSG00000049926	9	38773088	38776354	1	3	1	1	1	3	2	0	0	0	0	0	Q7TRC0	
ENSMUST00000062125	ENSMUSG00000048429	9	21592722	21595970	1	28	30	56	222	33	15	219	595	258	52	177		Q8BGX2
ENSMUST00000062127						9	9	7	9	11	6	0	0	0	0	0		
ENSMUST00000062129	ENSMUSG00000045566	3	92500263	92500493	-1	4	3	4	1	3	1	0	0	0	0	0		Q8CGN8
ENSMUST00000062144	ENSMUSG00000045780	7	103670103	103671029	-1	6	5	12	2	5	0	0	0	0	0	0	F8VQI7	
ENSMUST00000062145	ENSMUSG00000058046	4	62525369	62547993	1	7	12	21	7	7	9	0	0	1	0	1	Q8BHW4	
ENSMUST00000062147	ENSMUSG00000062825	11	120345690	120348542	-1	0	1	1	19	0	0	56	5822	10	0	9	B1ATY1	
ENSMUST00000062148	ENSMUSG00000042814	2	152687035	152687951	1	13	5	4	8	11	5	8	41	21	16	21		Q9CQ21
ENSMUST00000062149	ENSMUSG00000020642	12	26306797	26415256	-1	0	24	41	186	26	21	1413	4196	1735	70	1333		Q925F3
ENSMUST00000062153	ENSMUSG00000029392	5	124493080	124531391	-1	15	11	17	274	32	14	5	13	6	9	16		Q9JJC6
ENSMUST00000062156						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000062160	ENSMUSG00000048455	3	92436809	92438789	-1	4	2	10	29	3	0	0	0	0	0	0		Q62267
ENSMUST00000062161	ENSMUSG00000045036	17	65256005	65540782	-1	0	10	6	0	9	0	0	0	0	0	0		Q5K6N0
ENSMUST00000062163	ENSMUSG00000051207	7	145314835	145324059	1	18	23	40	28	31	15	0	0	0	0	0	Q5UCB4	Q91ZB8
ENSMUST00000062166	ENSMUSG00000042796	2	86007778	86008710	1	6	10	2	0	2	3	0	0	0	0	0	A2ATE3	
ENSMUST00000062172	ENSMUSG00000047040	11	96928104	96937830	1	0	0	0	0	0	0	0	0	0	0	0		Q8JZM2
ENSMUST00000062181	ENSMUSG00000037029	7	30161274	30169727	-1	16	5	12	32	22	10	34	143	56	226	95		Q8BQN6
ENSMUST00000062182	ENSMUSG00000072974	12	81376991	81379464	-1	13	6	16	8	14	7	0	3	1	1	0	B2RUD9	
ENSMUST00000062193						0	0	0	0	6	3	0	0	0	0	0		
ENSMUST00000062202	ENSMUSG00000047793	1	93235841	93301065	1	43	33	186	151	85	17	66	179	133	13	327		
ENSMUST00000062206	ENSMUSG00000047671	4	117126794	117128738	1	5	2	12	15	2	0	7	6	0	2	5		Q8CDY7
ENSMUST00000062211	ENSMUSG00000046338	2	127425199	127436092	1	27	20	53	27	35	17	0	0	0	1	2		Q14DK4
ENSMUST00000062213	ENSMUSG00000025212	19	45047576	45056383	1	0	0	58	0	0	0	365	296	386	113	361		Q91V61
ENSMUST00000062215	ENSMUSG00000047880	9	44511788	44556391	-1	0	0	9	10	6	12	128	181	125	83	161		Q04683
ENSMUST00000062216	ENSMUSG00000043969	19	59458372	59465357	1	14	7	22	262	22	15	0	0	0	0	0		Q04744
ENSMUST00000062226						1	0	4	4	3	2	0	0	0	0	0		
ENSMUST00000062229	ENSMUSG00000051095	9	40187079	40188094	1	2	3	3	4	3	2	0	0	0	0	0	Q8VFN6	
ENSMUST00000062232	ENSMUSG00000040632	14	55518978	55524981	-1	19	0	0	0	12	8	0	0	0	0	0	Q543Y0	P54846
ENSMUST00000062241	ENSMUSG00000045322	9	106222598	106226883	1	27	27	48	169	41	18	32	20	46	3	95		Q9EQU3
ENSMUST00000062242						1	3	1	0	2	1	0	0	17	17	21		
ENSMUST00000062246	ENSMUSG00000050395	4	63727084	63745113	-1	32	29	59	217	40	21	6	9	4	0	4	F6VXB8	
ENSMUST00000062248	ENSMUSG00000050803	9	20026959	20028035	-1	1	3	0	1	2	0	0	0	0	0	0	Q8VFI7	
ENSMUST00000062254	ENSMUSG00000045930	12	58264720	58269258	-1	36	16	33	43	34	21	0	0	0	0	0		Q8VCP9
ENSMUST00000062264	ENSMUSG00000026434	1	131910534	131936321	1	24	18	78	34	39	25	214	554	219	67	201		Q80XU3
ENSMUST00000062289	ENSMUSG00000042182	1	33852052	33907816	-1	0	0	0	0	0	0	0	7	0	0	4		Q6PFX2
ENSMUST00000062292	ENSMUSG00000050295	13	31806691	31810643	1	11	7	48	512	15	4	0	2	1	3	16		Q61572
ENSMUST00000062304	ENSMUSG00000049939	6	28661831	28831747	-1	21	16	98	30	43	23	0	0	0	0	1		Q99PH1
ENSMUST00000062306	ENSMUSG00000047940	3	139205694	139710299	1	4	0	3	2	1	2	0	0	0	0	0		Q8C8J0
ENSMUST00000062307	ENSMUSG00000044703	14	59276913	59297522	-1	9	4	9	7	8	7	4	16	4	110	38		Q8BVM9
ENSMUST00000062314	ENSMUSG00000047868	10	129132831	129138794	-1	3	5	1	2	1	4	0	0	0	0	0	Q8VGC2	
ENSMUST00000062315	ENSMUSG00000051498	5	64952031	64960097	-1	24	19	12	12	18	20	845	4774	1754	1339	1543	Q3UV88	
ENSMUST00000062317	ENSMUSG00000045180	X	152609509	152769465	-1	0	0	11	56	0	4	0	0	0	0	9		A2ALU4
ENSMUST00000062322	ENSMUSG00000055491	19	46044886	46072915	1	11	0	0	0	38	0	38	47	0	10	116		Q6NZN1
ENSMUST00000062350	ENSMUSG00000037017	5	138116903	138134265	1	0	4	0	5	5	0	0	0	0	0	16		Q07231
ENSMUST00000062353	ENSMUSG00000042849	1	92511048	92518515	-1	9	0	0	0	8	0	0	0	0	0	0	Q8VGU5	
ENSMUST00000062355	ENSMUSG00000043583	2	170579418	170602017	-1	13	4	12	6	18	2	0	0	1	0	0	Q9D542	
ENSMUST00000062356	ENSMUSG00000047945	4	129513581	129515985	1	13	15	61	143	32	18	2024	3402	1294	264	900		P28667
ENSMUST00000062357	ENSMUSG00000048905	17	28896397	28915324	-1	244	206	462	274	328	169	26	65	24	6	39		Q8CC96
ENSMUST00000062368	ENSMUSG00000032480	9	110084320	110117830	-1	9	0	18	88	30	7	9	27	10	0	54		Q99PU8
ENSMUST00000062369	ENSMUSG00000049672	17	69383050	69390750	1	0	0	52	3	0	0	110	229	0	0	22	Q544H8	Q08376

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000062370	ENSMUSG00000045690	12	75630596	75669537	-1	85	60	366	149	81	59	14	40	5	6	18		Q9D0R9
ENSMUST00000062372	ENSMUSG00000042453	5	21884454	22344702	-1	33	2	0	0	16	29	0	0	1	0	11		Q60841
ENSMUST00000062380	ENSMUSG00000047960	16	59026923	59030278	-1	1	3	0	7	5	1	0	0	0	0	0		Q8VEX5
ENSMUST00000062387	ENSMUSG00000038026	1	172320501	172329318	-1	19	20	31	60	29	7	1	10	0	0	5	Q544N3	P48543
ENSMUST00000062389	ENSMUSG00000024805	19	36379067	36456192	1	6	0	11	16	0	0	0	44	44	22	99		Q3UK78
ENSMUST00000062397	ENSMUSG00000024213	17	27579382	27623465	-1	0	0	0	0	0	0	5	0	0	0	0	I1E4X7	
ENSMUST00000062405	ENSMUSG00000049892	11	59963181	59964944	-1	14	18	24	47	27	12	10	4	10	0	2	Q5SWR8	O35626
ENSMUST00000062407	ENSMUSG00000050781	2	111379002	111379937	1	4	5	5	2	5	1	0	0	0	0	0	Q8VF29	
ENSMUST00000062428	ENSMUSG00000043290	7	5034439	5038446	-1	8	3	9	37	15	8	65	168	76	7	63	B2RVK6	Q8BI69
ENSMUST00000062429						7	3	8	9	8	0	0	0	0	0	0		
ENSMUST00000062437	ENSMUSG00000044186	14	69171802	69175518	1	12	4	10	204	17	9	0	0	0	0	0		P43688
ENSMUST00000062439	ENSMUSG00000050685	16	50589859	50591154	-1	7	4	9	7	5	1	0	1	0	0	0		Q9DAL3
ENSMUST00000062446	ENSMUSG00000041607	18	82475146	82585637	1	0	4	0	0	0	0	55	1	0	0	0		P04370
ENSMUST00000062451	ENSMUSG00000048191	7	141633456	141655319	-1	103	0	225	0	204	24	0	0	7	4	15	F8WIM6	
ENSMUST00000062454						1	2	2	144	6	3	0	0	0	0	0		
ENSMUST00000062458	ENSMUSG00000044847	11	45928269	45944935	-1	0	0	0	112	0	0	25	16	8	1	1	Q5SUH5	Q8BUV6
ENSMUST00000062463	ENSMUSG00000043865	6	23969161	23970060	-1	7	4	2	2	4	1	0	0	0	0	0		P59529
ENSMUST00000062474	ENSMUSG00000050445	9	121914356	121916305	-1	19	10	28	24	28	8	0	0	0	5	0		
ENSMUST00000062483	ENSMUSG00000048402	1	118834132	119053619	-1	46	20	117	271	72	26	0	0	0	0	0		Q0VGT2
ENSMUST00000062492	ENSMUSG00000001289	15	102326116	102331873	1	0	1	0	9	4	2	275	818	349	1816	252	E9PVG3	
ENSMUST00000062494	ENSMUSG00000050772	2	87434489	87435445	1	1	0	4	0	1	0	0	0	0	0	0	A2AT86	
ENSMUST00000062495	ENSMUSG00000047636	4	107096891	107107748	1	30	18	55	70	38	13	0	0	0	0	0		Q8BQH6
ENSMUST00000062519	ENSMUSG00000048249	17	26715650	26776635	1	24	29	95	34	17	11	1095	3010	1520	1246	1112		Q8CDG5
ENSMUST00000062524	ENSMUSG00000044227	16	89157952	89158348	1	3	6	12	6	6	4	0	0	0	0	0	Q8BIG3	
ENSMUST00000062525	ENSMUSG00000048234	1	39551296	39577405	-1	5	8	15	86	6	8	2510	9486	3154	846	3321		Q3U2C5
ENSMUST00000062528	ENSMUSG00000050840	1	104768529	104995481	1	51	37	318	226	48	24	0	1	0	0	2		Q9Z0M3
ENSMUST00000062530	ENSMUSG00000043372	11	103132429	103139876	1	18	11	52	25	22	5	4	14	5	5	5		Q3TVI4
ENSMUST00000062534	ENSMUSG00000050028	14	50642195	50643369	1	6	5	10	9	2	6	0	0	0	0	0	Q7TRL9	
ENSMUST00000062535	ENSMUSG00000045528	9	38179871	38180821	-1	1	3	1	1	3	0	0	0	0	0	0	E9Q843	
ENSMUST00000062542	ENSMUSG00000046180	X	58909360	58920304	1	0	4	0	0	0	0	3	12	16	34	5	Q99PA7	
ENSMUST00000062545	ENSMUSG00000050853	9	39549928	39550869	-1	6	5	6	3	6	2	0	0	0	0	0		Q8VEY3
ENSMUST00000062555	ENSMUSG00000070852	2	87371534	87372478	1	6	6	1	0	7	1	0	0	0	0	0	L7MTT1	
ENSMUST00000062560	ENSMUSG00000050217	1	31176401	31204725	1	5	12	16	10	14	8	0	0	1	0	0		Q8CIX8
ENSMUST00000062562	ENSMUSG00000044309	15	77524867	77533315	-1	20	13	36	10	20	8	19	80	23	0	0	Q8C6E1	
ENSMUST00000062572	ENSMUSG00000049551	5	135248938	135251230	-1	19	8	28	336	29	8	0	0	0	0	2		Q9R216
ENSMUST00000062574	ENSMUSG00000050357	8	105690906	105698178	1	15	18	25	162	32	23	79	155	66	4	129		Q3V3V9
ENSMUST00000062580	ENSMUSG00000020640	12	4593008	4713950	1	31	33	43	128	44	17	1212	3203	3197	246	2445	E9QNG1	
ENSMUST00000062584	ENSMUSG00000041225	18	6024427	6136098	-1	0	0	0	0	0	0	0	0	69	1	13	A0A0A0MQ95	
ENSMUST00000062586	ENSMUSG00000048500	8	21929799	21932710	-1	2	2	2	1	1	0	0	0	0	0	0		Q8R2I5
ENSMUST00000062591						2	1	1	0	1	1	0	3	0	1	0		
ENSMUST00000062600	ENSMUSG00000020070	10	62980223	63017210	1	0	0	7	1	0	0	0	1	0	0	4	D6RET4	
ENSMUST00000062601	ENSMUSG00000062006	3	130726831	130730398	-1	0	2	4	66	5	0	37	90	69	101	39		Q9D1R9
ENSMUST00000062606	ENSMUSG00000042985	5	136038496	136046487	1	20	14	32	32	35	10	0	0	0	13	36		
ENSMUST00000062609	ENSMUSG00000054931	13	21478907	21485507	1	17	9	18	18	14	10	2	8	1	7	1	Q5SZT6	
ENSMUST00000062613	ENSMUSG00000050052	8	13952009	13975032	-1	10	14	13	28	23	5	11	25	4	4	19		Q8C5P7
ENSMUST00000062620	ENSMUSG00000050440	7	30942368	30944032	-1	4	1	3	0	4	0	0	4	1	3	3		Q9EQ21
ENSMUST00000062623	ENSMUSG00000047819	3	84593574	84597032	1	84	81	159	137	110	90	1	10	4	4	12		Q8BUZ3
ENSMUST00000062626	ENSMUSG00000049232	6	59208870	59212033	1	10	9	12	91	19	3	73	303	167	56	81		Q0VBL1
ENSMUST00000062629	ENSMUSG00000047911	14	70647302	70653084	-1	6	13	17	10	11	7	0	3	0	1	0		Q80W85
ENSMUST00000062631	ENSMUSG00000045350	15	99918348	99967075	-1	2	4	11	4	9	1	0	0	0	0	0		Q9D9R9
ENSMUST00000062638	ENSMUSG00000051728	16	92318763	92321441	-1	24	21	24	15	27	13	0	0	0	0	0		Q8CDS7
ENSMUST00000062642						4	4	7	5	3	1	0	0	0	0	1		
ENSMUST00000062652	ENSMUSG00000018678	11	96953340	96982959	-1	10	3	50	19	12	12	32	0	44	6	0	Q8BNQ4	
ENSMUST00000062654	ENSMUSG00000046605	11	121616197	121673153	-1	10	9	25	47	13	3	8	12	20	0	49		Q3U129
ENSMUST00000062657	ENSMUSG00000043807	17	35113948	35115428	-1	0	0	0	0	0	3	42	87	13	4	27	N0E6I7	Q8K1T4
ENSMUST00000062658	ENSMUSG00000021156	13	9684836	9765321	-1	2	0	0	0	4	5	0	0	0	0	0	Q8BJZ0	
ENSMUST00000062665	ENSMUSG00000047048	1	174050375	174051313	1	1	2	7	7	10	1	0	0	0	1	0	E9Q8M2	
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ENSMUST00000062677	ENSMUSG00000043284	11	60864452	60879272	-1	0	8	13	168	19	7	84	157	96	40	66		Q8BK08
ENSMUST00000062678	ENSMUSG00000061032	10	78400362	78413043	-1	18	9	34	90	32	8	694	1404	972	325	862		P56183
ENSMUST00000062683	ENSMUSG00000049809	11	99597347	99598105	-1	11	4	11	60	4	5	0	0	0	0	0		Q3V2C1
ENSMUST00000062684	ENSMUSG00000043252	4	15265831	15286753	1	7	21	49	258	22	10	49	112	53	30	98		Q3U145
ENSMUST00000062686	ENSMUSG00000002948	8	4238740	4251423	1	14	0	38	0	21	0	284	415	228	0	173		Q8CE90
ENSMUST00000062694	ENSMUSG00000053436	17	28691342	28748404	1	0	0	0	32	0	0	0	41	2	0	17		P47811
ENSMUST00000062695	ENSMUSG00000047079	X	114907582	114908510	1	1	2	5	0	2	2	0	0	0	0	0	A2AFH2	
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ENSMUST00000062709	ENSMUSG00000049604	11	96194316	96197447	1	17	18	27	28	22	9	0	0	0	0	0		P70321
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ENSMUST00000062721	ENSMUSG00000032948	16	75540514	75586061	-1	0	1	0	0	3	1	0	0	0	0	0	F6YQT7	
ENSMUST00000062723	ENSMUSG00000032561	9	104288316	104337728	-1	12	10	20	17	21	13	526	1601	986	173	590		Q8CE08
ENSMUST00000062740	ENSMUSG00000044573	12	30893326	30911612	-1	47	31	35	0	0	11	43	339	136	332	63	Q4VAI2	Q9D358
ENSMUST00000062747	ENSMUSG00000048626	4	117757836	117765648	-1	25	28	61	40	34	16	0	0	0	0	0		Q8CFA7
ENSMUST00000062750	ENSMUSG00000048794	6	90403479	90428797	-1	3	7	4	7	0	0	4	0	2	0	1		Q80VN0
ENSMUST00000062753	ENSMUSG00000047044	19	18713193	18718428	1	0	0	0	195	0	8	35	136	18	22	25	Q3UMB2	Q8VCE4
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ENSMUST00000062758	ENSMUSG00000029788	6	30611010	30631745	1	0	2	4	0	8	5	0	0	0	0	0	B2RQW9	Q8R4H4
ENSMUST00000062759	ENSMUSG00000044052	11	101172997	101175443	-1	17	13	38	227	41	9	2	5	3	0	2		Q9JL21
ENSMUST00000062765	ENSMUSG00000030443	7	6315660	6331285	-1	5	6	1	60	8	5	1	9	0	3	0		Q3V080
ENSMUST00000062769	ENSMUSG00000050996	18	9615524	9619478	-1	10	6	5	8	12	6	0	0	0	0	0		P41209
ENSMUST00000062784	ENSMUSG00000046031	10	34126069	34127972	-1	5	6	8	136	13	8	3	22	6	2	9		Q8C9E8
ENSMUST00000062787	ENSMUSG00000048498	11	115051917	115062177	-1	7	9	14	14	10	9	13	38	31	21	18		Q8K249
ENSMUST00000062789	ENSMUSG00000044350	14	77024200	77036904	-1	13	15	15	5	11	2	2	15	15	6	37		Q8BZT9
ENSMUST00000062801	ENSMUSG00000052373	11	101999652	102028461	-1	0	0	0	1	0	0	0	0	0	0	0	Q6XE40	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000062802	ENSMUSG00000045854	4	32800253	32801559	1	1	0	0	25	3	2	87	434	134	384	99		Q8R033
ENSMUST00000062804	ENSMUSG00000021065	12	77238104	77476338	1	0	4	8	63	0	0	0	0	15	7	50		Q9WTS2
ENSMUST00000062806	ENSMUSG00000021539	13	56542460	56548538	-1	5	5	14	9	11	7	0	0	0	7	0		
ENSMUST00000062811	ENSMUSG00000096735	7	12176193	12177113	1	0	5	4	11	7	7	0	0	0	0	0	Q8R285	
ENSMUST00000062821	ENSMUSG00000034164	11	5106265	5152257	-1	16	0	8	30	16	4	0	0	0	0	11	Q5SUT2	Q91VF5
ENSMUST00000062824	ENSMUSG00000048772	4	117251951	117268582	1	0	0	0	0	0	0	0	14	12	0	0		Q9D0Z3
ENSMUST00000062829	ENSMUSG00000043219	6	52206288	52208722	-1	6	3	5	26	7	3	0	0	0	0	3	Q0VEU7	P09092
ENSMUST00000062831	ENSMUSG00000030400	7	19382010	19395694	1	24	14	0	59	0	16	197	121	145	0	197		O08811
ENSMUST00000062833	ENSMUSG00000051493	9	39942215	39943294	1	3	3	4	3	6	1	0	0	0	0	0	Q8VH09	
ENSMUST00000062844	ENSMUSG00000051650	11	22834747	22860961	-1	6	0	7	122	4	2	62	236	125	49	134	Q3TVJ9	Q9Z222
ENSMUST00000062855	ENSMUSG00000042570	10	79540245	79555199	-1	13	14	22	0	31	12	27	32	0	4	0		Q3U3N0
ENSMUST00000062860	ENSMUSG00000048497	11	62648664	62666354	1	0	0	0	15	1	0	0	0	0	2	4		
ENSMUST00000062861	ENSMUSG00000040472	14	55715873	55722257	-1	18	24	41	33	0	17	128	498	140	24	158		Q9JHK4
ENSMUST00000062862	ENSMUSG00000020053	10	87858265	87937042	1	16	6	39	48	11	11	0	0	0	0	0	Q8CAR0	
ENSMUST00000062869	ENSMUSG00000050818	11	58528929	58534836	-1	12	3	7	18	11	7	0	0	0	0	0	Q8VGD9	
ENSMUST00000062879	ENSMUSG00000064232	15	101624028	101628188	-1	16	14	60	20	21	11	0	0	0	0	0	Q6IFZ8	
ENSMUST00000062883	ENSMUSG00000043259	10	70440668	70558731	1	0	9	0	0	0	0	0	0	0	0	0		Q9DBR2
ENSMUST00000062893	ENSMUSG00000045328	3	135215537	135273611	1	34	23	85	57	32	15	79	258	284	226	157	E9QKK1	
ENSMUST00000062902						74	72	247	190	100	42	0	8	6	0	7		
ENSMUST00000062904	ENSMUSG00000039768	4	151933691	151982137	1	5	6	1	21	13	6	140	160	128	52	132		Q5U458
ENSMUST00000062915	ENSMUSG00000050973	7	80232865	80242061	1	48	55	267	113	92	29	77	120	69	18	60		Q3TLS3
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ENSMUST00000062931	ENSMUSG00000047197	11	98982180	98983016	-1	4	0	6	250	3	2	0	0	0	0	0		Q91YD1
ENSMUST00000062934	ENSMUSG00000050530	2	3114224	3227806	1	16	5	0	256	5	16	0	21	15	5	0	A2ATL0	
ENSMUST00000062944	ENSMUSG00000049908	3	96913566	96926020	-1	13	9	30	17	16	5	0	0	0	0	0	Q548M7	P28236
ENSMUST00000062945	ENSMUSG00000044165	3	103832601	103854618	1	1	3	0	1	1	0	50	22	108	530	31		Q08ED0
ENSMUST00000062946	ENSMUSG00000048696	10	80380355	80387659	-1	12	8	36	785	36	15	91	85	77	7	67	E9PUA0	
ENSMUST00000062957	ENSMUSG00000033530	12	100300771	100520822	-1	25	19	33	86	38	8	528	925	715	65	491	E9Q6P5	
ENSMUST00000062962	ENSMUSG00000029175	5	30647933	30659729	1	28	19	111	56	35	16	314	876	248	143	271		Q8VE96
ENSMUST00000062964	ENSMUSG00000046300	1	92588207	92589297	1	13	3	14	6	11	5	0	0	0	0	0	Q8VET3	
ENSMUST00000062967	ENSMUSG00000043782	17	23660523	23668610	1	13	5	26	79	27	13	11	14	5	1	11		Q8CHW5
ENSMUST00000062978	ENSMUSG00000049946	8	58911755	58914298	1	5	4	7	13	10	1	0	0	0	0	0	Q8K0R8	
ENSMUST00000062990	ENSMUSG00000047518	4	120532231	120536661	1	16	13	48	36	36	18	1	2	1	1	1		Q8BHW9
ENSMUST00000062991	ENSMUSG00000024580	18	61712440	61726331	-1	17	16	31	47	27	21	49	189	89	65	69	Q0VB85	O88396
ENSMUST00000063004	ENSMUSG00000049721	11	3983636	3999326	1	14	8	7	13	3	0	0	0	0	0	0		Q9JHE4
ENSMUST00000063006	ENSMUSG00000045915	11	68587021	68597966	1	4	4	12	7	7	7	0	0	0	0	0	Q5SV65	
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ENSMUST00000063029	ENSMUSG00000031283	X	143285674	143394262	-1	0	0	0	0	0	3	0	0	0	0	0		Q920C1
ENSMUST00000063030	ENSMUSG00000046486	1	174117091	174118014	-1	4	4	7	4	3	0	0	0	0	0	0	E9Q0M4	
ENSMUST00000063031	ENSMUSG00000050198	10	129093034	129093972	-1	6	6	4	3	3	2	0	0	0	0	0	Q8VGC4	
ENSMUST00000063036	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	0	0	0	0	3	0	0	0		P42866
ENSMUST00000063040						0	0	3	0	0	0	142	630	69	418	88		
ENSMUST00000063042	ENSMUSG00000045594	9	114401076	114474376	1	10	10	28	48	16	8	242	320	209	93	219	Q3TAW7	P23780
ENSMUST00000063059						5	1	0	1	1	1	0	2	0	0	5		
ENSMUST00000063062	ENSMUSG00000040809	3	106147554	106167564	-1	10	5	17	9	15	18	14461	19382	16725	28579	6728		O35744
ENSMUST00000063063	ENSMUSG00000044770	10	42860370	42960780	1	73	53	269	80	63	23	17	72	44	1	94		Q80VG1
ENSMUST00000063071	ENSMUSG00000051648	8	105382807	105413502	-1	0	27	0	14	0	0	0	0	0	0	0		Q562E2
ENSMUST00000063076	ENSMUSG00000050783	16	64924729	65105784	-1	6	6	3	24	3	5	0	0	0	0	0	Q543V2	Q02284
ENSMUST00000063084	ENSMUSG00000020484	11	5520659	5525893	1	7	4	18	137	9	0	3064	6119	3160	1103	2059		O35426
ENSMUST00000063089	ENSMUSG00000050312	16	62732444	62786818	-1	0	30	39	0	30	0	82	226	23	94	83		Q8CCT7
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ENSMUST00000063093	ENSMUSG00000046159	13	9875486	10360844	-1	11	4	6	18	16	13	26	18	55	16	131	Q542R4	Q9ERZ3
ENSMUST00000063103	ENSMUSG00000043773	9	121938135	121947014	1	151	154	238	135	197	90	7	11	14	8	23	F6VFT9	
ENSMUST00000063109	ENSMUSG00000045584	7	103505997	103506944	-1	2	1	2	5	7	2	0	0	0	0	0	E9Q598	
ENSMUST00000063112	ENSMUSG00000050756	8	19225478	19228209	1	2	3	4	5	0	2	0	0	0	0	0	Q0VDZ1	Q91VD6
ENSMUST00000063116	ENSMUSG00000048450	5	37820485	37824583	-1	5	10	13	153	12	8	0	0	0	0	0		P13297
ENSMUST00000063117	ENSMUSG00000021033	12	87147707	87164721	1	25	19	40	59	44	11	38	75	57	67	77		Q9WVL0
ENSMUST00000063119	ENSMUSG00000049741	3	88651898	88653142	-1	12	5	27	13	14	5	0	0	0	0	1	Q5Y985	Q7TQP4
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ENSMUST00000063138	ENSMUSG00000047669	10	56106917	56116880	1	11	5	18	382	29	5	5	14	4	0	3	G3X992	
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ENSMUST00000063191	ENSMUSG00000045827	13	33003250	33017957	1	0	0	0	0	0	12	0	0	0	0	0	O08797	
ENSMUST00000063192	ENSMUSG00000050640	5	100077872	100159808	-1	21	9	30	50	28	8	1	0	0	0	0		Q8C8S3
ENSMUST00000063197						4	1	0	4	2	3	0	0	0	1	0		
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ENSMUST00000063204	ENSMUSG00000051736	10	39118804	39133914	-1	0	0	0	0	1	0	0	0	0	0	0	B2RVF6	Q8CF36
ENSMUST00000063216	ENSMUSG00000073197	12	18514738	18534191	1	23	21	26	3	0	0	2	32	7	1	4	Q3UT17	
ENSMUST00000063219	ENSMUSG00000051732	18	39773497	39776082	1	14	8	24	42	17	5	0	0	0	0	0	Q62029	
ENSMUST00000063220						0	1	0	0	0	3	0	0	0	0	0		
ENSMUST00000063232	ENSMUSG00000009079	11	5069689	5099266	-1	9	6	12	9	6	5	0	1	0	0	0	Q8BQU4	
ENSMUST00000063249	ENSMUSG00000051768	7	24546289	24573440	1	21	14	52	62	30	8	235	244	202	29	195		Q60596
ENSMUST00000063251	ENSMUSG00000051769	2	164198863	164200130	-1	2	2	1	1	10	4	0	0	0	0	1		Q8BH89
ENSMUST00000063262	ENSMUSG00000058291	5	138603652	138619761	-1	3	6	7	24	2	6	74	379	156	168	111	Q9Z116	
ENSMUST00000063263	ENSMUSG00000051777	3	67892220	68056593	1	7	15	45	7	13	3	0	0	0	0	0		Q8BPW0
ENSMUST00000063272	ENSMUSG00000013495	5	108629770	108648782	1	0	0	0	0	0	0	69	152	57	8	23		Q9CXY1
ENSMUST00000063278	ENSMUSG00000031980	8	124556534	124569706	-1	12	10	23	23	17	8	0	0	0	5	0	Q3UTR7	

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ENSMUST00000063289	ENSMUSG00000051793	15	98340022	98340987	-1	7	5	20	7	12	5	0	0	0	0	0	Q8VET7	
ENSMUST00000063292	ENSMUSG00000063661	15	101793308	101802343	-1	21	12	23	24	35	13	0	0	0	0	0		Q6NXH9
ENSMUST00000063303	ENSMUSG00000020389	11	52004221	52089784	1	0	0	0	0	0	0	0	0	0	0	0		Q8BLF2
ENSMUST00000063307	ENSMUSG00000033871	18	61298136	61400431	-1	19	8	0	73	28	6	1	0	23	2	1		Q8VHJ7
ENSMUST00000063314	ENSMUSG00000020962	12	91555916	91590487	-1	0	2	0	19	3	0	27	0	122	2	57	Q149E9	
ENSMUST00000063317	ENSMUSG00000051804	12	113489511	113492057	1	9	11	11	8	6	4	0	1	0	0	1	Q6IMH7	
ENSMUST00000063318	ENSMUSG00000020102	10	125226464	125328963	-1	14	16	19	7	11	11	10	7	7	2	5	Q149G3	O70451
ENSMUST00000063321	ENSMUSG00000020389	11	52004221	52089784	1	1	0	0	0	0	1	3	0	9	7	0		Q8BLF2
ENSMUST00000063324	ENSMUSG00000051811	7	4751792	4753094	-1	4	0	6	0	3	0	25	0	0	5	0	Q059Q8	Q80ZN9
ENSMUST00000063332	ENSMUSG00000051817	2	152393611	152398063	-1	0	0	0	0	0	0	0	0	0	0	0		Q04890
ENSMUST00000063339	ENSMUSG00000001288	15	102234938	102257517	-1	17	7	45	108	28	6	204	219	139	38	256		P18911
ENSMUST00000063340	ENSMUSG00000051827	X	37244976	37249686	1	14	3	6	7	1	0	0	0	0	0	0	Q9D4Y3	
ENSMUST00000063344	ENSMUSG00000002279	17	25579174	25662826	1	4	5	1	19	0	5	3	0	0	1	0	Z4YJR1	
ENSMUST00000063347	ENSMUSG00000062421	11	103966739	103985337	1	6	13	6	197	17	5	0	28	15	0	16		Q8BSL7
ENSMUST00000063359	ENSMUSG00000051839	8	80494045	80510785	1	6	7	7	10	4	9	2	0	1	6	5	Q3TZH8	P14220
ENSMUST00000063380	ENSMUSG00000026159	1	82839483	82901182	1	0	0	0	0	0	0	87	59	20	0	11		Q8K2K6
ENSMUST00000063384	ENSMUSG00000051851	X	53608032	53608432	1	2	0	3	3	4	0	2	4	2	6	6	Q9D6I0	
ENSMUST00000063396	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	122	0	0	0	0	0	0	9		Q8CI15
ENSMUST00000063401	ENSMUSG00000031537	8	22659212	22706589	-1	10	7	9	20	22	9	17	146	159	4	245		
ENSMUST00000063414	ENSMUSG00000051864	15	86214459	86498503	1	28	20	54	198	41	22	827	1192	864	135	603		Q8R5A6
ENSMUST00000063417	ENSMUSG00000024097	17	80200089	80207305	-1	5	2	4	46	5	5	295	1265	277	900	437	Q3THA6	Q8BL97
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ENSMUST00000063444	ENSMUSG00000020374	11	49901835	49980994	1	26	16	53	81	46	12	0	0	0	0	0		Q9D300
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ENSMUST00000063446	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	6	0	0	0	0	0	0	0		Q8CI15
ENSMUST00000063456	ENSMUSG00000051896	6	70913087	70918927	-1	3	4	11	7	5	3	0	0	0	0	0		Q9DAG4
ENSMUST00000063463	ENSMUSG00000074735	2	150254518	150255591	-1	3	4	4	3	0	1	1	11	10	1	1	F6T2D2	
ENSMUST00000063465	ENSMUSG00000021994	14	28504750	28527447	1	157	101	790	580	132	68	2	7	0	0	10		P22725
ENSMUST00000063470	ENSMUSG00000020151	10	116018213	116274932	1	5	0	2	4	9	0	0	0	0	0	0	Q5U1U6	Q62132
ENSMUST00000063481	ENSMUSG00000073386	17	48125605	48146307	-1	45	42	64	51	52	29	463	2503	834	767	634	D3Z5D6	
ENSMUST00000063489	ENSMUSG00000051917	6	42215328	42216287	1	5	2	3	5	4	3	0	0	0	0	0		Q7TQB8
ENSMUST00000063492	ENSMUSG00000051920	15	43020811	43170818	-1	21	7	26	147	21	8	0	0	0	0	0		Q8BFU0
ENSMUST00000063496	ENSMUSG00000027506	3	8925593	9004723	-1	0	0	0	1	0	0	784	50	1442	2155	1382	E9PUA7	
ENSMUST00000063502	ENSMUSG00000027845	3	103800605	103809444	-1	1	26	33	0	36	0	0	110	0	56	0		Q8C7W7
ENSMUST00000063507	ENSMUSG00000031139	X	60055956	60179089	-1	7	0	8	36	5	5	0	0	0	0	0	A2AEU1	
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ENSMUST00000063509	ENSMUSG00000030378	7	14410686	14446769	-1	0	0	0	0	4	0	0	0	0	0	0	Q8BGL3	
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ENSMUST00000063531	ENSMUSG00000028551	4	109660876	109667189	-1	0	1	0	0	4	4	41	61	7	110	39		Q60772
ENSMUST00000063539	ENSMUSG00000095620	16	36221468	36257444	1	0	0	0	0	0	0	0	0	0	0	0	Q9D8D6	
ENSMUST00000063542	ENSMUSG00000022698	16	44139830	44163366	1	0	0	0	0	0	0	72	122	108	23	50		Q6PGB6
ENSMUST00000063544	ENSMUSG00000022756	16	17572018	17576998	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BLQ7
ENSMUST00000063548	ENSMUSG00000051956	6	23648869	23650305	-1	0	0	0	3	4	0	0	0	0	0	0		Q14B02
ENSMUST00000063551	ENSMUSG00000021719	13	104947153	105054930	-1	33	27	37	374	50	16	1	4	4	1	3		Q8BQP9
ENSMUST00000063562	ENSMUSG00000021993	14	60784566	60903610	1	11	10	25	122	16	10	67	188	111	29	61		A6H611
ENSMUST00000063563	ENSMUSG00000051965	7	18987400	18988962	1	10	9	48	19	26	15	0	0	0	0	0	I6ZHM2	P60322
ENSMUST00000063570	ENSMUSG00000051969	14	50357914	50363663	1	6	9	23	0	20	4	1	2	0	2	5		Q6R5P0
ENSMUST00000063574	ENSMUSG00000015126	17	25240170	25242798	1	8	14	18	91	19	5	117	223	76	45	74		Q5HZH2
ENSMUST00000063577	ENSMUSG00000031310	X	101404384	101420849	-1	0	0	0	40	0	9	0	15	0	0	0	B1AXS5	Q9JLM4
ENSMUST00000063578	ENSMUSG00000004654	6	55376295	55388530	1	12	15	29	10	20	6	0	0	0	0	0		P32082
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ENSMUST00000063588	ENSMUSG00000030337	6	125215551	125245964	1	0	0	0	0	0	0	0	0	9	1	0	D3YTU0	
ENSMUST00000063594	ENSMUSG00000025969	1	62703285	62818695	1	102	64	725	0	6	26	41	148	20	19	141	Q8QZY7	O35375
ENSMUST00000063597	ENSMUSG00000051980	16	36493696	36562141	-1	0	0	0	0	12	19	0	0	0	0	0		Q9QY96
ENSMUST00000063605	ENSMUSG00000046962	16	97947435	97962621	-1	55	38	84	115	60	13	54	146	18	19	0	E9Q3R9	
ENSMUST00000063607	ENSMUSG00000030980	7	118842222	118856254	-1	0	0	0	47	0	0	0	22	0	0	18	K4DI66	
ENSMUST00000063632	ENSMUSG00000051984	19	44516957	44545864	-1	20	0	54	88	49	20	10	44	10	0	40		Q3TZ89
ENSMUST00000063635	ENSMUSG00000029576	5	142484839	142551098	-1	0	0	0	48	8	0	0	0	0	0	1		Q69Z89
ENSMUST00000063641	ENSMUSG00000051989	16	92301286	92313041	1	5	2	2	2	1	1	89	254	74	375	61		Q99J19
ENSMUST00000063642	ENSMUSG00000028637	4	119322893	119415521	-1	15	3	22	164	24	6	0	0	0	0	0		Q8BVF4
ENSMUST00000063645	ENSMUSG00000059474	11	93885852	93946985	1	7	13	18	6	12	11	3	0	15	3	16	A2ABG6	
ENSMUST00000063650	ENSMUSG00000039137	4	63414910	63495991	-1	0	0	0	0	0	0	2	2	1	0	2		Q80VW5
ENSMUST00000063654	ENSMUSG00000052013	16	45224315	45252895	1	0	0	0	3	14	5	0	71	0	21	34	E9QNY6	
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ENSMUST00000063661	ENSMUSG00000052459	16	44085402	44139705	-1	0	0	15	0	0	0	1380	5057	4143	1402	1598		P50516
ENSMUST00000063663	ENSMUSG00000026156	1	23761753	23849158	1	17	12	22	26	11	16	16	65	23	13	46		P59270
ENSMUST00000063669	ENSMUSG00000030986	7	133720942	133782726	-1	5	0	10	0	5	4	50	15	34	9	64		Q8BZS9
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ENSMUST00000063683	ENSMUSG00000052031	17	6954965	6961156	-1	8	5	44	27	7	9	50	212	79	36	93		P0CAX8
ENSMUST00000063690	ENSMUSG00000027068	2	69380445	69404533	1	32	23	63	54	28	16	4236	8674	9643	4262	4897	Q148Q4	Q58NB6
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ENSMUST00000063704	ENSMUSG00000078496	4	147492417	147513486	1	0	0	0	0	0	0	1	2	0	0	0	A2A8Q4	
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ENSMUST00000063710	ENSMUSG00000052056	2	170108643	170148103	-1	0	0	0	36	0	0	1151	1391	2981	0	2329	Q3U0X6	
ENSMUST00000063716	ENSMUSG00000052058	9	38430284	38431219	1	3	6	18	1	0	1	0	0	0	0	0	Q7TRD1	
ENSMUST00000063717	ENSMUSG00000058388	3	103968110	104024598	1	0	0	0	57	4	2	0	0	19	0	0	Q5IBN5	Q9QZ09
ENSMUST00000063718	ENSMUSG00000059474	11	93885852	93946985	1	0	0	0	0	0	0	11	19	36	0	39		Q6P5G3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000063719	ENSMUSG00000026411	1	136008150	136035342	1	13	5	11	22	6	7	24	21	0	14	14		Q9CR23
ENSMUST00000063726	ENSMUSG00000094861	X	91392500	91393534	1	2	0	10	8	4	1	0	0	0	0	0	A2AHM1	
ENSMUST00000063747	ENSMUSG00000022568	15	76047158	76069784	-1	0	0	1	0	40	23	843	511	726	39	572		Q80U72
ENSMUST00000063750	ENSMUSG00000017491	14	16430842	16575472	-1	13	15	19	103	15	15	3	16	5	13	14	Q6DFX0	P22605
ENSMUST00000063761	ENSMUSG00000007783	7	44959373	44974851	-1	21	16	29	84	36	30	0	0	0	2	5		Q8BGD5
ENSMUST00000063770	ENSMUSG00000030935	7	119760923	119787513	1	0	5	0	0	2	2	0	0	0	0	0		Q3UNX5
ENSMUST00000063771	ENSMUSG00000052087	13	55369732	55384687	1	11	5	39	36	14	0	2771	3045	2109	282	1934		P97492
ENSMUST00000063775	ENSMUSG00000024544	18	67933257	68255549	1	15	8	28	70	28	11	7	9	7	3	14	Q4VAH9	Q8BWJ4
ENSMUST00000063776	ENSMUSG00000018661	11	113649169	113667054	1	0	4	0	71	0	0	6	24	0	0	8	Q810S7	
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ENSMUST00000063785	ENSMUSG00000052099	14	64086234	64097670	1	8	0	7	8	0	0	0	0	0	0	0	Q9DAL4	
ENSMUST00000063788	ENSMUSG00000002346	8	70184340	70212305	-1	10	15	5	46	19	14	0	0	7	0	4		Q8R0Y8
ENSMUST00000063813	ENSMUSG00000052139	5	31697684	32084962	1	0	0	0	0	0	0	0	0	0	0	0		Q8K3W0
ENSMUST00000063814	ENSMUSG00000052102	18	38327558	38339003	-1	20	7	22	45	21	10	1872	3619	1486	415	1094		O88958
ENSMUST00000063816	ENSMUSG00000052117	4	57908483	57916297	-1	25	14	76	39	33	14	4	3	2	0	1	Q8K0M7	
ENSMUST00000063817	ENSMUSG00000062691	17	78916500	78920306	1	0	3	1	98	4	2	8	18	24	23	8		Q8BTE5
ENSMUST00000063820	ENSMUSG00000031444	8	13037308	13056676	1	72	64	201	140	95	39	124	487	287	140	174	Q3TBR2	O88947
ENSMUST00000063824	ENSMUSG00000052142	17	32390659	32403583	-1	0	0	0	22	0	0	85	137	104	0	1		Q8C2K5
ENSMUST00000063838	ENSMUSG00000022378	15	63929097	64060448	-1	7	7	13	29	9	4	41	376	179	93	177		Q921M7
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ENSMUST00000063854	ENSMUSG00000052144	6	100833622	100869934	1	20	25	28	76	28	10	666	2289	1007	295	603		
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ENSMUST00000063858	ENSMUSG00000052143	9	60821855	60838200	-1	0	2	11	2	7	3	3	0	0	0	0	F6YGD6	
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ENSMUST00000063882	ENSMUSG00000051674	5	73481000	73560794	1	0	10	26	25	27	10	27	82	35	16	0		Q8CCA0
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ENSMUST00000063888	ENSMUSG00000052160	12	112760655	112768986	1	19	8	48	27	28	11	884	1855	476	201	1046		Q8BG07
ENSMUST00000063902	ENSMUSG00000030929	7	119768679	119794058	-1	4	0	2	2	3	3	0	0	0	0	0	Q9D405	
ENSMUST00000063905	ENSMUSG00000049550	5	123577795	123684618	-1	0	0	0	0	0	0	0	0	15	0	75	D3Z3M7	
ENSMUST00000063918	ENSMUSG00000048562	12	118846329	118852578	1	14	17	21	401	22	17	0	0	2	0	0	Q5QR90	Q8BMJ8
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ENSMUST00000063923	ENSMUSG00000052182	9	19440915	19441853	1	1	3	4	2	1	3	0	0	0	0	0	Q8VFF6	
ENSMUST00000063956	ENSMUSG00000052212	7	24743983	24760311	-1	37	25	43	38	51	47	65439	75269	66550	6033	28512		Q8R2S8
ENSMUST00000063957	ENSMUSG00000052217	7	103841636	103843164	-1	1	1	6	3	3	1	0	0	0	0	0	Q5EBL1	P04444
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ENSMUST00000063977	ENSMUSG00000052221	12	76417599	76439473	1	15	8	15	28	11	5	0	0	0	0	0		D3Z0R2
ENSMUST00000063980	ENSMUSG00000063488	9	122888471	122896124	1	14	10	14	12	18	3	2	13	13	4	10	E9PVW1	
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ENSMUST00000063988	ENSMUSG00000027630	3	22076652	22216594	1	2	81	115	1	73	46	1014	3881	1419	82	1118		Q8BHJ5
ENSMUST00000063989	ENSMUSG00000050945	18	5210031	5334439	-1	17	15	73	38	27	11	18	40	17	16	21	Q8BFX2	
ENSMUST00000064002						1	0	1	1	3	1	0	0	0	0	0		
ENSMUST00000064013						2	1	7	112	1	0	2	0	4	0	0		
ENSMUST00000064016	ENSMUSG00000052229	18	31942997	31949636	-1	41	23	96	50	60	27	0	0	0	0	0		Q6NS65
ENSMUST00000064019	ENSMUSG00000000538	11	60226714	60352905	-1	3	5	24	21	13	3	22	24	35	11	47		Q5SRX1
ENSMUST00000064032	ENSMUSG00000058351	14	31088132	31128930	-1	3	3	3	3	3	4	9	3	0	13	3		Q8C1Q6
ENSMUST00000064035	ENSMUSG00000033855	17	88597684	88662586	1	0	2	14	0	0	5	0	0	0	0	0		Q8CDJ8
ENSMUST00000064050	ENSMUSG00000020083	10	62107655	62143920	-1	0	0	0	0	0	1	0	0	0	0	0		Q9D882
ENSMUST00000064054	ENSMUSG00000035864	10	108497650	109010982	-1	0	14	31	60	20	7	0	0	0	0	0	H6RXZ1	P46096
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ENSMUST00000064067	ENSMUSG00000036061	15	103153307	103158002	-1	23	27	56	91	42	20	50	92	47	14	38		Q6P5C5
ENSMUST00000064068	ENSMUSG00000052270	17	17887824	17893952	1	15	16	38	22	7	6	5488	18350	6514	10752	2611		O88536
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ENSMUST00000064091	ENSMUSG00000026384	1	119652467	119837613	-1	11	18	15	238	24	9	59	56	41	14	35		Q9WU22
ENSMUST00000064098	ENSMUSG00000021798	14	34526699	34588681	-1	0	0	87	0	0	26	0	0	0	0	0	E9PYJ9	
ENSMUST00000064099	ENSMUSG00000052296	7	4631495	4659019	-1	33	24	52	196	50	33	6625	5271	5808	774	4559		Q7TSI3
ENSMUST00000064101						14	0	9	333	14	1	20	88	33	10	24		
ENSMUST00000064102	ENSMUSG00000096365	19	13234252	13235184	1	3	2	2	3	5	0	0	0	0	0	0	Q7TQR3	
ENSMUST00000064104	ENSMUSG00000052298	11	54717456	54787675	-1	15	10	30	34	14	17	1219	2241	1388	348	1053		Q8BGH7
ENSMUST00000064107	ENSMUSG00000052302	10	121263824	121311189	-1	36	31	178	296	55	32	7	10	1	1	9		Q69ZT9
ENSMUST00000064110	ENSMUSG00000052301	7	126847416	126852705	1	8	0	9	182	22	13	0	0	0	0	0		Q7TNF0
ENSMUST00000064129	ENSMUSG00000028555	4	109406623	109444745	1	0	0	34	13	27	2	2	7	3	3	6		A2ACP1
ENSMUST00000064139	ENSMUSG00000028517	4	105157347	105232764	1	16	19	43	236	20	9	0	0	1	3	10		Q99JY8
ENSMUST00000064141	ENSMUSG00000041966	2	71055328	71099142	1	2	1	1	0	6	0	0	21	4	0	9		Q3TUL7
ENSMUST00000064151	ENSMUSG00000025509	7	141455198	141460743	1	0	0	0	59	0	0	796	1299	796	155	432		Q8BJ56
ENSMUST00000064162	ENSMUSG00000052334	14	41943995	42003821	1	127	113	181	88	144	68	0	0	0	0	0	E9Q6D7	
ENSMUST00000064165	ENSMUSG00000052336	9	119901616	120068283	-1	77	48	80	915	75	43	49	248	20	20	76	Q543X3	Q9Z0D9
ENSMUST00000064166	ENSMUSG00000045281	15	73694604	73707505	-1	27	14	67	148	40	15	0	0	0	0	0		Q8BYC4
ENSMUST00000064167	ENSMUSG00000028557	4	109451098	109484728	-1	0	0	0	0	0	0	1123	3373	824	150	496		Q9QYK7
ENSMUST00000064174	ENSMUSG00000052353	7	83932857	84086502	-1	19	19	39	53	53	19	0	0	1	3	14		Q8BI06
ENSMUST00000064187	ENSMUSG00000058756	11	98740638	98769006	1	10	4	23	90	22	12	31	49	36	9	46		P63058
ENSMUST00000064190	ENSMUSG00000062115	11	60105013	60199197	1	0	0	0	0	0	0	0	0	102	0	0		Q61818
ENSMUST00000064192	ENSMUSG00000052363	16	32496265	32561966	1	14	11	20	20	26	5	0	0	0	0	0		Q810M5
ENSMUST00000064196	ENSMUSG00000052364	X	8892382	8894964	1	7	4	14	197	5	5	1	11	3	0	3	Q7TNS5	
ENSMUST00000064200	ENSMUSG00000052369	15	97964229	97970286	1	12	6	28	71	22	5	47	69	25	28	31		Q80VP8
ENSMUST00000064204	ENSMUSG00000052374	13	12269426	12340760	-1	19	33	76	34	59	17	2	2	2	5	4		Q9JI91
ENSMUST00000064214	ENSMUSG00000052382	14	51038459	51041869	-1	10	7	14	4	5	4	0	0	0	0	0	Q5QJV3	P60154
ENSMUST00000064225	ENSMUSG00000019775	10	5825663	5922400	-1	0	0	0	42	0	0	0	0	0	0	0	G5E8E0	
ENSMUST00000064230	ENSMUSG00000052395	14	30654360	30691317	1	0	0	0	59	0	15	71	100	61	35	0		Q8C3B8
ENSMUST00000064231	ENSMUSG00000052396	7	99219084	99238619	-1	13	4	15	35	12	7	16	7	9	0	6		Q80W94

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000064234	ENSMUSG00000052397	17	6738041	6782784	-1	26	19	44	195	44	23	5626	3959	5785	1119	4351	Q4KML7	P26040
ENSMUST00000064240	ENSMUSG00000020659	12	31484829	31499616	-1	0	0	0	0	0	0	0	0	0	0	3		Q9JIY2
ENSMUST00000064244	ENSMUSG00000052406	2	26953563	26964386	-1	4	3	4	6	3	2	18	44	39	16	21	A2ALB2	
ENSMUST00000064257	ENSMUSG00000052415	3	93442330	93449077	1	58	36	182	1215	99	44	14	52	34	12	43	A0A0B4J1F9	
ENSMUST00000064265	ENSMUSG00000034579	11	3488284	3499350	1	6	0	47	11	12	6	0	0	3	2	0	Q8BZT7	
ENSMUST00000064271						92	60	426	190	75	52	3	7	14	3	36		
ENSMUST00000064272	ENSMUSG00000052423	1	171270328	171276896	1	0	0	0	42	2	3	990	1154	1063	140	1099	Q3U260	Q91YY2
ENSMUST00000064285	ENSMUSG00000029638	6	8509600	8597548	1	0	14	7	77	17	6	0	0	7	0	0	E9QKK4	
ENSMUST00000064290	ENSMUSG00000052435	14	54710363	54712174	-1	11	5	30	200	24	8	1026	1241	877	174	297		Q6PZD9
ENSMUST00000064297	ENSMUSG00000036391	11	51692264	51763634	-1	2	0	0	0	0	0	0	0	0	0	0		Q3U2P1
ENSMUST00000064305						79	85	423	48	57	43	15	18	8	3	21		
ENSMUST00000064307	ENSMUSG00000025375	11	120007313	120047167	-1	5	0	0	0	0	0	0	0	0	0	0	B1AZF3	
ENSMUST00000064309	ENSMUSG00000026356	1	128363707	128417368	-1	3	4	5	88	3	3	0	1	0	15	0	Q8BJY7	
ENSMUST00000064314	ENSMUSG00000052456	8	85017934	85025278	-1	8	8	22	15	16	7	1068	1154	739	686	489		O54984
ENSMUST00000064324	ENSMUSG00000036938	6	41311233	41316841	-1	0	2	1	2	2	3	0	0	0	0	0	Q9QUK9	
ENSMUST00000064330	ENSMUSG00000029782	6	30479053	30509783	-1	0	0	0	0	0	0	0	2	0	0	0		Q8BRG8
ENSMUST00000064334	ENSMUSG00000030706	7	100545751	100608297	-1	0	0	0	0	0	0	0	0	0	0	0	Q8C3P2	
ENSMUST00000064341	ENSMUSG00000052477	1	84992690	85270566	-1	40	13	113	24	59	45	2	53	20	29	34	Q3KNJ6	
ENSMUST00000064347	ENSMUSG00000052485	13	98686235	98694834	-1	7	7	15	14	10	5	0	4	0	3	0		Q4KL18
ENSMUST00000064349						6	5	8	13	11	1	0	0	0	0	0		
ENSMUST00000064353						3	3	7	3	14	1	6	3	8	7	4		
ENSMUST00000064364	ENSMUSG00000020448	11	3415982	3452363	-1	0	7	11	24	22	0	30	19	0	0	33		Q91YT2
ENSMUST00000064370	ENSMUSG00000052496	15	85814676	85821733	-1	52	35	44	74	55	33	0	0	0	0	0	F8VQF3	
ENSMUST00000064371	ENSMUSG00000052539	3	104013259	104220374	-1	0	0	0	52	27	0	69	80	17	18	62		Q9EQJ9
ENSMUST00000064376	ENSMUSG00000031389	X	73891442	73921870	-1	0	0	0	0	0	0	528	997	1265	29	544	Q80Z68	
ENSMUST00000064377	ENSMUSG00000029708	6	28416091	28428390	-1	13	14	42	11	22	15	110	0	135	0	185		Q9D4H2
ENSMUST00000064383						15	8	59	26	19	10	0	0	0	0	0		
ENSMUST00000064391	ENSMUSG00000052560	15	90487482	90679432	-1	9	0	0	40	18	0	70	252	462	89	49		Q9DC53
ENSMUST00000064392	ENSMUSG00000052508	7	140500856	140507318	-1	140	131	249	148	176	65	1	8	7	2	9	Q8VFE9	
ENSMUST00000064393	ENSMUSG00000024785	19	29101375	29143843	1	6	7	18	78	17	7	31	71	28	31	76		Q9JJT0
ENSMUST00000064395	ENSMUSG00000052512	7	48908716	49610090	1	69	69	69	625	97	52	0	0	0	0	17	E9Q842	
ENSMUST00000064404	ENSMUSG00000031068	7	137437648	137468594	1	5	7	6	48	6	0	110	465	153	723	143		Q9CQM9
ENSMUST00000064405	ENSMUSG00000052504	16	63543538	63864158	-1	17	15	8	26	15	11	0	0	0	1	0	Q8BRB1	
ENSMUST00000064407	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	0	0	223	1144	466	136	280	Q8VC91	
ENSMUST00000064420	ENSMUSG00000052525	17	71552061	71589533	1	3	2	0	0	0	0	1	8	1	2	4	B8JJB9	
ENSMUST00000064433	ENSMUSG00000032186	9	75565621	75611325	-1	1	0	132	128	30	0	4	6	1	1	4		Q9JKK7
ENSMUST00000064438	ENSMUSG00000052534	1	168119364	168432270	-1	0	0	0	0	2	0	0	0	0	0	0	D9J2V6	
ENSMUST00000064443	ENSMUSG00000028444	4	41657498	41697089	-1	0	0	0	45	0	0	0	5	0	0	5	Q9D586	
ENSMUST00000064444	ENSMUSG00000042763	4	124855239	124862171	-1	17	12	29	84	17	12	1	3	1	0	2		Q6P1J0
ENSMUST00000064445						21	16	36	33	16	11	2	0	0	0	0		
ENSMUST00000064447	ENSMUSG00000052533	2	30286397	30344266	1	32	29	66	58	32	21	248	212	278	22	311		Q6ZQH8
ENSMUST00000064452	ENSMUSG00000052537	16	59201466	59202519	-1	5	5	4	9	5	2	0	0	0	0	0	Q7TS40	
ENSMUST00000064454	ENSMUSG00000041638	5	115565254	115622654	1	12	0	0	48	37	0	844	287	1017	11	872	E9PVA8	
ENSMUST00000064460	ENSMUSG00000052544	3	153198266	153725174	-1	4	2	4	5	3	1	0	0	2	0	1	A0A0H2UKC4	
ENSMUST00000064462	ENSMUSG00000001076	15	99084686	99087817	-1	5	1	8	217	9	2	0	0	0	0	0		Q4ZJM9
ENSMUST00000064473	ENSMUSG00000052551	13	8202866	8768747	1	19	10	32	22	25	19	0	0	0	0	0		Q9JI20
ENSMUST00000064475	ENSMUSG00000052554	8	19123752	19126540	1	1	1	0	1	1	2	0	0	0	0	0		Q7TNV8
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ENSMUST00000064477	ENSMUSG00000022770	16	31663443	31873356	1	0	0	0	0	2	0	254	431	539	89	296		Q811D0
ENSMUST00000064480	ENSMUSG00000026271	1	92950865	92986391	1	6	0	0	8	0	6	0	0	60	0	45	Q3TBY9	Q9ES90
ENSMUST00000064481	ENSMUSG00000043924	4	135369576	135398227	-1	7	10	10	8	13	1	0	0	2	0	3		Q99JS0
ENSMUST00000064488	ENSMUSG00000052557	8	117158135	117215997	1	11	0	34	40	20	4	0	0	30	7	84		Q8CA72
ENSMUST00000064493	ENSMUSG00000052563	11	51650954	51657681	1	0	0	1	0	0	12	0	0	6	0	0	A2AA67	
ENSMUST00000064495	ENSMUSG00000052566	8	84990595	85003364	1	13	10	30	54	24	11	45	129	66	13	76		Q7TMK6
ENSMUST00000064503	ENSMUSG00000009207	2	74520291	74579435	-1	0	0	0	18	0	0	68	32	0	6	19		Q7TQ95
ENSMUST00000064507	ENSMUSG00000052562	19	8335371	8405111	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVA5	
ENSMUST00000064513	ENSMUSG00000039850	11	119491347	119511437	1	7	7	14	4	11	6	2	20	9	2	9	F8WJ25	
ENSMUST00000064517	ENSMUSG00000052584	14	76532814	76556687	-1	6	2	6	80	6	5	1	2	0	4	4		Q6TAW2
ENSMUST00000064536	ENSMUSG00000052593	12	21323509	21373632	-1	0	0	85	63	22	6	938	3793	2304	3	1166		Q9Z0F8
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ENSMUST00000064547	ENSMUSG00000052605	7	4844960	4866179	-1	5	5	7	9	7	6	31	41	9	30	0		Q9DCC7
ENSMUST00000064550	ENSMUSG00000051036	3	88069410	88078304	-1	5	0	12	2	1	2	0	0	0	0	0		Q8BYG0
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ENSMUST00000064576	ENSMUSG00000052616	8	104446719	104509910	-1	3	1	4	37	3	3	0	0	0	0	0		Q8C0V1
ENSMUST00000064580	ENSMUSG00000030108	6	121300227	121337733	1	9	17	23	21	44	13	12	23	9	35	6		P31649
ENSMUST00000064582	ENSMUSG00000052625	9	19496750	19497688	1	1	0	2	0	1	0	0	0	0	0	0	Q7TRG0	
ENSMUST00000064594	ENSMUSG00000079055	12	81197915	81333180	-1	0	0	0	0	0	0	0	0	0	0	0	E9PX50	
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ENSMUST00000064606	ENSMUSG00000052316	16	30269302	30283256	-1	39	44	112	71	62	34	3	0	3	0	7		Q80X72
ENSMUST00000064614	ENSMUSG00000052642	11	58446149	58452923	-1	5	1	7	4	1	0	0	0	0	0	0	Q8C5Z9	
ENSMUST00000064635	ENSMUSG00000022544	16	5244152	5255983	-1	14	19	47	42	24	19	35	131	84	25	77		Q3UZW7
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ENSMUST00000064639	ENSMUSG00000042520	3	90000140	90052628	-1	115	93	736	164	91	57	660	1381	941	105	975		Q80X50
ENSMUST00000064642	ENSMUSG00000025512	7	141493136	141539857	-1	1	2	15	6	8	0	9	0	0	18	0	G8JL55	
ENSMUST00000064646	ENSMUSG00000052658	9	120577346	120578072	1	6	6	18	124	11	2	4	14	6	10	2		
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ENSMUST00000064656	ENSMUSG00000037855	10	67886103	67912662	-1	8	36	45	90	26	11	0	0	0	0	0		Q8BG89
ENSMUST00000064659	ENSMUSG00000052676	X	134971372	135009209	-1	8	0	0	52	13	0	28	225	82	35	68	G5E8E4	
ENSMUST00000064664	ENSMUSG00000052688	1	131688695	131715439	1	7	0	0	3	7	4	9	24	31	43	34	J9UUF7	Q8VEA8
ENSMUST00000064667	ENSMUSG00000052681	10	117814471	117845935	-1	3	6	33	45	13	5	5864	18046	6728	2942	3683	Q52L50	Q99JI6
ENSMUST00000064674	ENSMUSG00000006362	8	122628739	122699109	-1	0	0	0	192	0	0	2	0	0	0	0	E9QM80	
ENSMUST00000064679	ENSMUSG00000052688	1	131688695	131715439	1	24	26	75	21	30	24	35	113	33	32	44		Q8VEA8
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000064690	ENSMUSG00000020333	11	54303798	54364756	1	12	7	7	2	5	9	0	0	0	0	0	Q8C028	
ENSMUST00000064694	ENSMUSG00000024050	17	32354055	32389401	-1	0	0	11	0	0	0	0	0	0	0	9		O88286
ENSMUST00000064701	ENSMUSG00000021504	13	55599896	55610443	1	22	56	85	11	32	26	264	419	241	34	148	Q3TAW1	Q8R087
ENSMUST00000064703	ENSMUSG00000035268	2	163658386	163726158	1	0	0	0	0	7	0	132	131	38	1	48	Q3TP50	O70139
ENSMUST00000064709	ENSMUSG00000052712	17	29268788	29302881	1	22	15	37	49	30	7	111	117	155	90	107		Q99KU6
ENSMUST00000064718	ENSMUSG00000037652	3	30899371	30969415	-1	0	0	0	0	0	0	0	0	44	0	0	B7ZNA5	
ENSMUST00000064725	ENSMUSG00000026715	1	160978585	161005863	1	6	4	1	1	4	3	0	139	25	33	29	Q543J5	P32261
ENSMUST00000064740	ENSMUSG00000052738	6	73248382	73276911	1	5	2	14	28	11	4	450	1087	617	1160	373		Q9WUM5
ENSMUST00000064744	ENSMUSG00000052730	6	48589445	48590584	1	2	0	0	1	1	1	0	0	2	0	0	Q8C9M4	
ENSMUST00000064759	ENSMUSG00000014601	3	107612532	107631694	-1	32	25	38	142	38	16	853	1232	994	107	700		Q8C079
ENSMUST00000064762	ENSMUSG00000052727	13	99421464	99516602	-1	63	48	301	271	101	44	51	148	60	13	156		P14873
ENSMUST00000064763	ENSMUSG00000052713	18	54888045	54990180	-1	30	24	151	236	54	28	564	1655	1338	108	1431	B9EKR3	Q56A10
ENSMUST00000064765	ENSMUSG00000061455	4	48124915	48186507	1	0	0	0	0	0	0	67	183	250	180	268		Q9D0I4
ENSMUST00000064770	ENSMUSG00000008575	4	82290173	82705750	-1	0	0	0	0	0	0	2	1	0	0	0	Q6GSP7	P97863
ENSMUST00000064771	ENSMUSG00000052748	1	151367699	151428455	-1	6	4	10	4	6	3	137	687	182	255	187		Q9DBQ9
ENSMUST00000064775	ENSMUSG00000024256	17	93199422	93205485	1	8	4	19	34	11	8	0	0	0	0	0	Q3UYH8	O70176
ENSMUST00000064780	ENSMUSG00000031340	X	72255999	72274803	-1	56	41	225	49	41	13	0	5	3	1	0	A2AMW3	
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ENSMUST00000064786	ENSMUSG00000049755	11	58315114	58330339	-1	10	0	28	25	3	2	0	86	0	4	0		Q99LH4
ENSMUST00000064788	ENSMUSG00000052760	1	85717083	85778643	-1	3	0	5	1	0	0	20	186	39	126	34	Q3UTB2	
ENSMUST00000064793	ENSMUSG00000025404	10	127380327	127499384	1	18	9	57	20	0	22	0	0	0	0	0		Q80TM6
ENSMUST00000064794	ENSMUSG00000027208	2	126034658	126091185	1	7	7	0	12	12	7	0	0	0	3	0	Q544I6	P36363
ENSMUST00000064795	ENSMUSG00000038418	18	34859823	34864984	1	25	15	49	346	21	15	0	101	0	0	6	Q544D6	P08046
ENSMUST00000064797	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0N0	
ENSMUST00000064798	ENSMUSG00000024038	17	31520115	31531326	1	0	0	3	23	1	0	478	734	304	1747	168		Q8BK30
ENSMUST00000064806	ENSMUSG00000028707	4	115915119	115939926	-1	65	35	116	66	82	45	1	0	0	0	3		Q91ZK4
ENSMUST00000064807	ENSMUSG00000039693	4	48539935	48561919	1	14	11	21	67	7	4	17	0	0	18	15		Q9CR78
ENSMUST00000064809						5	5	13	61	8	9	1	3	0	0	1		
ENSMUST00000064814	ENSMUSG00000028358	4	62965573	63139708	1	4	3	1	2	4	1	2	0	0	0	0	F8WIU3	
ENSMUST00000064821	ENSMUSG00000030786	7	128062640	128118491	1	0	0	51	24	0	0	9511	20347	19185	2455	12404	G5E8F1	
ENSMUST00000064826						2	0	0	66	2	1	0	0	0	0	0		
ENSMUST00000064830						2	2	2	4	7	0	0	0	0	0	0		
ENSMUST00000064831	ENSMUSG00000095463	14	69337174	69367270	1	1	2	0	0	4	6	19	28	48	0	23		Q9DBT4
ENSMUST00000064846	ENSMUSG00000022066	14	69555424	69585520	1	53	40	339	73	54	26	2	12	5	0	3	Q80WR8	
ENSMUST00000064848	ENSMUSG00000052798	10	117750624	117792705	-1	22	8	25	82	23	12	117	258	210	202	189		Q8BH74
ENSMUST00000064853	ENSMUSG00000052794	8	72443880	72461001	1	0	0	11	13	15	0	43	75	38	4	17		Q922C1
ENSMUST00000064856	ENSMUSG00000023176	16	30256378	30267532	-1	54	38	85	72	67	30	2	0	1	4	2		Q9DBB9
ENSMUST00000064862	ENSMUSG00000054385	7	25516042	25539857	-1	0	0	5	47	0	3	0	5	3	0	0		Q925P2
ENSMUST00000064872	ENSMUSG00000029772	6	29768011	29912310	1	0	0	0	0	0	0	0	0	0	0	10	F8WI65	
ENSMUST00000064873	ENSMUSG00000035031	4	104815679	104876398	-1	0	34	40	57	0	0	0	0	0	0	0		Q8K182
ENSMUST00000064883	ENSMUSG00000031557	8	25039144	25102194	-1	16	24	52	185	52	21	120	514	299	37	181		Q9ERS5
ENSMUST00000064889	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	7	19	0	0	59	53	24	55	73	Q3TCZ2	Q9JIM1
ENSMUST00000064892	ENSMUSG00000052821	X	106574346	106603679	-1	0	0	0	0	0	0	3	14	0	0	0		Q99JA4
ENSMUST00000064893	ENSMUSG00000052818	10	129856520	129857452	1	2	2	0	3	4	2	0	0	0	0	0	Q7TRH5	
ENSMUST00000064900	ENSMUSG00000028101	3	96696384	96706070	1	0	0	0	5	0	0	34	57	48	0	45		O54714
ENSMUST00000064910	ENSMUSG00000030224	6	137735078	137751932	1	5	7	11	83	11	0	536	1844	766	529	550	B2RUC7	Q9Z1Z2
ENSMUST00000064911	ENSMUSG00000031060	X	20617503	20650901	1	0	0	0	0	0	0	0	0	0	0	0		Q99KG3
ENSMUST00000064916	ENSMUSG00000062345	1	107511423	107535478	1	0	0	0	0	0	0	0	4	0	68	52	Q542A3	P12388
ENSMUST00000064921	ENSMUSG00000052889	7	122288751	122634402	1	0	0	0	0	0	0	524	1489	932	68	615		P68404
ENSMUST00000064922	ENSMUSG00000052837	8	84976909	84978748	-1	14	9	17	618	24	10	6030	23954	6239	1449	6985	Q569U6	P09450
ENSMUST00000064924	ENSMUSG00000058290	15	102296293	102324356	1	36	21	78	84	79	28	156	98	162	22	176		P60330
ENSMUST00000064930						14	21	53	29	27	14	0	0	0	0	0		
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ENSMUST00000064941	ENSMUSG00000020889	11	98767932	98775333	-1	24	18	65	62	33	11	0	4	3	1	15		Q3UV55
ENSMUST00000064948	ENSMUSG00000052861	6	73017606	73221651	-1	0	0	43	42	32	23	0	0	0	0	0	E9Q0B6	
ENSMUST00000064950	ENSMUSG00000013973	1	171329145	171342331	1	0	0	0	0	0	0	349	707	359	94	247	Q3U001	Q9Z1L3
ENSMUST00000064953	ENSMUSG00000015474	17	34616662	34628510	-1	0	0	0	0	0	2	0	0	34	0	28		O35448
ENSMUST00000064976	ENSMUSG00000025927	1	19208914	19238576	1	2	2	5	9	7	6	0	0	0	0	0	E9Q5N4	
ENSMUST00000064989	ENSMUSG00000052889	7	122288751	122634402	1	4	3	3	13	6	0	696	538	1788	35	1086		P68404
ENSMUST00000064991	ENSMUSG00000000085	4	120405281	120530186	1	0	7	0	0	0	0	6	18	0	8	31		Q8K214
ENSMUST00000064993	ENSMUSG00000064177	6	113716119	113719880	-1	5	4	4	6	3	3	3	4	3	0	11	A2RSS9	Q9EQX0
ENSMUST00000065001	ENSMUSG00000026883	2	35558266	35730994	1	5	4	39	4	10	4	0	0	18	0	0	A2AUX5	
ENSMUST00000065005	ENSMUSG00000002820	9	21265299	21274368	1	28	14	58	207	35	20	887	1215	538	110	517		Q8BGV9
ENSMUST00000065014	ENSMUSG00000052911	9	108479736	108490530	1	42	41	79	105	77	36	0	4	1	6	41		Q61292
ENSMUST00000065024	ENSMUSG00000096714	7	106790049	106790999	-1	3	4	5	4	8	2	0	0	0	0	0	Q7TRN3	
ENSMUST00000065028	ENSMUSG00000017631	11	76416734	76622314	-1	0	0	11	6	14	12	0	3821	158	203	389		Q5SSL4
ENSMUST00000065039	ENSMUSG00000052922	2	158258094	158284531	1	13	13	0	0	17	22	0	0	0	0	0		Q67E05
ENSMUST00000065040	ENSMUSG00000052921	11	68943155	68957480	-1	68	9	0	220	32	60	4	7	5	2	16		Q5FWH6
ENSMUST00000065047	ENSMUSG00000034544	3	66981390	67358396	1	20	14	60	25	20	7	0	1	1	0	1	Q8BR75	
ENSMUST00000065049	ENSMUSG00000052926	8	84956610	84969767	-1	0	0	0	0	0	0	92	100	52	74	15	Q05C51	
ENSMUST00000065060	ENSMUSG00000020023	10	94311949	94590956	1	24	12	24	64	18	11	7	9	14	17	49		Q8R310
ENSMUST00000065067	ENSMUSG00000052920	19	30567551	31765033	-1	15	4	9	12	4	3	0	0	0	0	3	Q8BND1	P0C605
ENSMUST00000065072	ENSMUSG00000029656	4	104766317	104804548	1	1	3	1	8	6	6	0	0	0	1	0		Q8BH35
ENSMUST00000065074	ENSMUSG00000034544	3	66981390	67358396	1	11	0	0	0	13	8	26	43	38	127	52		Q9DBU6
ENSMUST00000065079	ENSMUSG00000049723	9	7344381	7369499	1	1	0	2	1	3	0	0	0	0	3	0	Q8BJC0	
ENSMUST00000065080	ENSMUSG00000032120	9	44309237	44320282	-1	33	16	55	449	70	23	878	1244	586	68	629		Q80X80
ENSMUST00000065086	ENSMUSG00000052957	13	60174405	60177365	-1	9	2	13	348	20	8	0	0	0	4	7		
ENSMUST00000065090	ENSMUSG00000068699	6	29433256	29461883	1	0	1	59	0	126	0	0	0	0	0	103	D3Z576	Q8VHX6
ENSMUST00000065103	ENSMUSG00000052962	6	71812997	71826969	-1	174	178	630	143	150	62	48	148	58	256	65		Q9CQL6
ENSMUST00000065111	ENSMUSG00000040455	4	21767156	21837872	1	17	0	0	0	0	0	117	349	250	33	73		Q8K387
ENSMUST00000065112	ENSMUSG00000033453	9	30899155	30922452	-1	43	22	63	274	68	23	0	0	0	1	5		P59384
ENSMUST00000065113	ENSMUSG00000052942	19	28258851	28680077	-1	0	0	0	0	0	0	9	0	0	0	11	E0CYJ3	
ENSMUST00000065118	ENSMUSG00000052981	13	69702835	69739897	-1	11	10	21	232	13	9	0	0	0	0	1	E9QMD2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000065119	ENSMUSG00000037339	5	33600347	33629635	-1	0	0	0	9	0	0	91	96	66	14	60	E9PV82	
ENSMUST00000065124	ENSMUSG00000040006	10	7767947	7792824	-1	0	0	0	3	0	0	2	0	1	0	0	F7AHX3	
ENSMUST00000065125	ENSMUSG00000022759	16	17544465	17561247	-1	12	6	3	9	11	4	0	0	0	0	0		Q14BP6
ENSMUST00000065134	ENSMUSG00000089762	2	30471537	30474219	-1	11	4	9	455	19	15	1	17	0	21	37		Q99J55
ENSMUST00000065135	ENSMUSG00000031851	8	125729963	125748235	1	6	6	35	11	10	2	133	183	133	21	61	Q8C373	
ENSMUST00000065143	ENSMUSG00000040363	X	12036740	12160355	-1	0	0	0	0	0	19	13	0	72	0	0		Q8CGN4
ENSMUST00000065162	ENSMUSG00000037339	5	33600347	33629635	-1	63	44	312	78	71	41	17	32	19	5	37	E9PV65	
ENSMUST00000065163	ENSMUSG00000030538	7	80227147	80232813	-1	0	0	0	47	0	0	683	727	529	552	393		Q9Z0F4
ENSMUST00000065167	ENSMUSG00000042249	5	112910482	113015791	-1	50	47	229	95	90	31	30	143	33	4	103		Q3UYH7
ENSMUST00000065169	ENSMUSG00000036180	8	69907069	69996379	-1	0	0	71	29	60	0	696	570	633	0	413	E9QMN5	
ENSMUST00000065173	ENSMUSG00000045083	4	35706647	36951747	-1	12	5	0	18	5	0	0	0	0	0	0	B2RQD4	Q3URE9
ENSMUST00000065181	ENSMUSG00000030584	7	29303951	29317588	1	0	0	0	0	0	0	0	0	0	0	0		Q9QX66
ENSMUST00000065196	ENSMUSG00000032511	9	119483408	119579016	-1	69	0	139	58	67	11	0	0	0	0	50	K3W4N7	
ENSMUST00000065204	ENSMUSG00000040901	19	59219648	59237370	1	21	24	48	31	25	22	0	0	0	0	0		Q6VV64
ENSMUST00000065210	ENSMUSG00000064030	10	128747879	128766568	1	0	0	19	17	5	10	0	31	13	17	0		Q8CHP5
ENSMUST00000065211	ENSMUSG00000001323	11	74906359	74925948	-1	0	0	4	0	0	0	0	0	33	0	0		Q9QZX7
ENSMUST00000065213	ENSMUSG00000046490	11	68888553	68895777	1	31	24	38	108	36	16	0	1	0	0	0		Q8CEF8
ENSMUST00000065216	ENSMUSG00000053030	5	77205107	77211471	-1	0	0	0	4	0	0	14	36	3	37	7		Q8BMY7
ENSMUST00000065220	ENSMUSG00000036381	3	59113855	59153618	-1	0	11	0	5	10	1	18	5	9	32	10	Q544F4	Q9ESG6
ENSMUST00000065224	ENSMUSG00000024553	18	82392496	82406777	-1	34	15	53	209	38	16	0	0	0	0	0		P56479
ENSMUST00000065243						0	0	0	0	0	0	17	22	22	12	20		
ENSMUST00000065248	ENSMUSG00000053044	6	71322788	71337494	1	45	46	110	14	36	18	76	70	33	101	69	Q3TEK8	P10300
ENSMUST00000065253	ENSMUSG00000034853	4	106744555	106804998	-1	0	2	0	16	0	0	37	6	84	0	23	A2AVR6	
ENSMUST00000065263	ENSMUSG00000038095	5	124368702	124426001	-1	49	48	100	51	57	25	703	2256	1448	218	1128	B2RRI2	
ENSMUST00000065286	ENSMUSG00000057858	19	60198586	60226697	-1	6	3	14	130	12	2	62	287	172	124	110		Q8C6C7
ENSMUST00000065289	ENSMUSG00000053063	6	129342691	129365303	1	2	2	1	1	3	2	822	7036	1335	2999	705		
ENSMUST00000065291	ENSMUSG00000053070	9	8021672	8042823	-1	13	8	9	61	10	7	0	3	1	2	3	Q8CC70	
ENSMUST00000065297	ENSMUSG00000039633	8	36216064	36249516	-1	275	175	1404	487	156	67	325	1310	691	82	734	D3YY23	
ENSMUST00000065302	ENSMUSG00000064128	14	56526761	56571846	-1	19	20	35	68	23	7	61	305	170	122	118		Q569L8
ENSMUST00000065304	ENSMUSG00000024758	19	7425901	7483289	-1	0	0	0	41	0	0	0	0	0	0	0		Q9ES97
ENSMUST00000065308	ENSMUSG00000037458	15	38487430	38519266	-1	5	8	26	32	22	5	86	162	29	14	13		O35484
ENSMUST00000065323	ENSMUSG00000053091	7	66689889	66717256	1	0	0	0	0	0	0	167	914	421	163	248	D6RFA2	
ENSMUST00000065329	ENSMUSG00000053094	5	130217081	130243765	1	18	25	83	11	30	16	585	706	592	27	305		Q3TBN1
ENSMUST00000065330	ENSMUSG00000032316	9	57750711	57765860	-1	16	12	28	454	35	18	829	2298	1124	308	925		O35492
ENSMUST00000065334	ENSMUSG00000002578	10	128630843	128645991	-1	0	0	0	0	0	0	0	0	0	0	0		Q8C208
ENSMUST00000065335	ENSMUSG00000053101	13	19749682	19824257	-1	8	7	16	10	5	10	1061	1792	1376	1842	680		Q7TQP0
ENSMUST00000065353	ENSMUSG00000053110	9	7931999	8004596	-1	0	18	0	30	20	0	0	0	0	0	0		P46938
ENSMUST00000065358	ENSMUSG00000032299	9	57155041	57158299	-1	6	6	22	18	10	4	196	345	140	366	129		Q9CQ02
ENSMUST00000065359	ENSMUSG00000053111	7	133776861	133881532	1	15	8	14	36	10	5	0	0	0	0	0		Q9DAM9
ENSMUST00000065360	ENSMUSG00000032368	9	91358058	91365810	-1	0	0	0	0	0	0	0	0	0	0	0		P46684
ENSMUST00000065364	ENSMUSG00000053119	6	71543797	71582609	1	3	0	0	12	6	0	242	508	391	1669	354		Q9CQ10
ENSMUST00000065371	ENSMUSG00000030956	7	132712082	132813886	-1	0	0	0	0	0	0	478	437	393	56	486		Q8BGR5
ENSMUST00000065372	ENSMUSG00000053121	5	29735637	29735936	-1	3	0	3	10	2	3	0	0	0	1	0	F6YHA9	
ENSMUST00000065373	ENSMUSG00000025940	1	16665207	16678275	1	23	23	0	4	0	23	29	121	45	49	59		Q921N7
ENSMUST00000065379	ENSMUSG00000053128	9	44066327	44113517	-1	6	0	16	17	2	0	0	0	0	0	0		Q8BUH7
ENSMUST00000065380	ENSMUSG00000027993	3	84160439	84306877	-1	6	3	8	0	5	0	0	0	0	0	0		Q9ESN6
ENSMUST00000065382	ENSMUSG00000053129	5	147188696	147190947	1	8	6	9	228	17	8	0	0	0	0	0	B2RQ55	P31315
ENSMUST00000065388	ENSMUSG00000053134	5	31514564	31527807	-1	42	76	57	19	103	3	91	270	111	19	110		Q9CZV5
ENSMUST00000065398	ENSMUSG00000001855	2	31974436	32053975	1	34	20	26	50	74	21	494	386	697	36	522		Q80U93
ENSMUST00000065403	ENSMUSG00000053161	1	83159752	83210574	1	0	0	0	0	0	0	0	0	0	0	0	D3Z7A5	
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ENSMUST00000065411						17	13	55	25	16	13	1	3	3	1	8		
ENSMUST00000065416	ENSMUSG00000053146	2	36869568	36870515	1	5	3	4	1	5	6	0	0	0	0	0	Q8VGJ9	
ENSMUST00000065417	ENSMUSG00000022577	15	75551268	75567255	-1	0	0	0	15	0	0	0	0	0	0	0	Q544M1	Q9WUC3
ENSMUST00000065418	ENSMUSG00000027935	3	90213695	90226385	1	5	0	0	67	5	4	8	20	6	31	20		Q9DD03
ENSMUST00000065420	ENSMUSG00000044783	1	88262471	88277633	-1	14	0	71	0	4	0	165	25	280	0	101	E9Q4T0	
ENSMUST00000065422	ENSMUSG00000033773	5	107597373	107661838	1	0	5	0	0	4	1	6	60	17	67	24		Q8VC34
ENSMUST00000065425	ENSMUSG00000053153	1	69826970	70725132	1	0	2	0	0	0	0	0	0	0	0	0		Q8K450
ENSMUST00000065433	ENSMUSG00000018654	11	11685003	11772926	1	13	5	4	125	0	0	1707	1853	2974	138	1444	Q5SWT9	
ENSMUST00000065436	ENSMUSG00000053161	1	83159752	83210574	1	4	0	2	2	5	2	0	0	0	0	0	A6H6T7	
ENSMUST00000065438	ENSMUSG00000053166	2	165111507	165234853	-1	15	6	47	505	30	20	0	0	0	0	0		Q9WTP5
ENSMUST00000065441	ENSMUSG00000053164	2	37516332	37520603	1	10	7	11	10	13	10	0	0	6	0	3		Q8BX79
ENSMUST00000065461	ENSMUSG00000032010	9	44067021	44095627	1	0	1	4	10	7	6	52	88	70	11	45		O88623
ENSMUST00000065465	ENSMUSG00000053181	13	48513570	48514859	1	3	2	6	0	1	0	1	1	0	3	1	Q8BRT5	
ENSMUST00000065478	ENSMUSG00000029275	5	107716657	107726036	-1	3	5	11	196	10	4	46	37	26	5	38	H3BJM0	
ENSMUST00000065482	ENSMUSG00000053192	3	95219135	95232171	-1	10	6	32	47	16	13	32	173	48	23	51	Q543U0	P97783
ENSMUST00000065486	ENSMUSG00000053194	5	30485583	30545836	-1	12	7	9	8	11	7	0	0	0	0	0		Q9D9N5
ENSMUST00000065487	ENSMUSG00000053198	7	27499324	27520214	1	0	0	0	94	0	0	48	9	30	0	16	Q6NVF7	
ENSMUST00000065494	ENSMUSG00000048368	13	49582766	49592609	1	2	3	1	4	0	0	0	0	0	0	0		O35103
ENSMUST00000065496	ENSMUSG00000053199	9	51765337	51853856	1	24	29	96	25	45	25	0	2	1	0	4		Q6IFT4
ENSMUST00000065499	ENSMUSG00000036106	15	84669620	84703673	1	0	0	0	209	16	16	0	16	4	0	0		Q812A5
ENSMUST00000065504	ENSMUSG00000021814	14	20455261	20480133	-1	0	0	0	0	14	7	2213	5922	3136	704	1654		Q07076
ENSMUST00000065509	ENSMUSG00000053470	6	71588972	71632990	-1	0	21	36	32	17	0	374	1891	903	356	624		Q6PCM1
ENSMUST00000065512	ENSMUSG00000034930	6	83135463	83152579	1	2	0	18	72	7	0	18	20	7	7	17		Q8C6B2
ENSMUST00000065515	ENSMUSG00000022757	16	56690332	56717450	-1	4	3	11	56	6	1	247	562	234	177	251	Q9Z1A1	
ENSMUST00000065519						4	1	7	3	7	2	0	0	0	0	0		
ENSMUST00000065523	ENSMUSG00000022510	16	25683763	25892102	1	10	0	0	7	13	0	0	0	0	0	0		O88898
ENSMUST00000065527	ENSMUSG00000053219	10	22158569	22374139	1	0	2	0	0	0	3	109	352	151	329	49	D7F2B6	Q9CZQ6
ENSMUST00000065530						14	7	23	110	27	13	0	0	0	0	0		
ENSMUST00000065532	ENSMUSG00000053217	6	132777179	132778162	-1	2	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000065533	ENSMUSG00000049755	11	58315114	58330339	-1	0	0	12	0	0	0	0	0	0	0	2	Q3USW9	
ENSMUST00000065534	ENSMUSG00000001482	8	123442986	123463270	1	0	0	0	8	31	0	574	883	307	94	74		Q99J78
ENSMUST00000065536	ENSMUSG00000021234	12	84345309	84361833	-1	21	25	60	3	18	18	4	27	10	0	9		Q8CB59
ENSMUST00000065537	ENSMUSG00000021690	13	93430097	93499808	-1	38	25	40	558	76	26	200	421	363	41	219		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000065539	ENSMUSG00000053226	8	84815405	84822823	-1	13	9	60	36	18	9	39	103	42	11	15		Q76LW6
ENSMUST00000065540						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000065543	ENSMUSG00000029154	5	73406075	73453435	1	4	0	0	5	0	0	0	0	0	0	0		Q91YL7
ENSMUST00000065545	ENSMUSG00000053211	Y	725128	797409	-1	0	2	2	0	0	1	0	0	0	0	0		P10925
ENSMUST00000065562	ENSMUSG00000048379	14	47276931	47296098	1	29	30	44	215	25	19	458	702	532	132	407		Q91ZA6
ENSMUST00000065567						333	326	567	269	263	126	5	16	12	0	15		
ENSMUST00000065573	ENSMUSG00000039210	1	187215508	187351704	1	0	0	0	6	0	0	57	67	67	5	86		Q7TQC7
ENSMUST00000065574	ENSMUSG00000078681	7	65691169	65701913	1	9	9	5	82	10	6	0	0	0	0	3		Q8BJ83
ENSMUST00000065587	ENSMUSG00000044337	1	90203980	90216751	1	53	33	220	83	37	17	0	1	0	204	89		P56485
ENSMUST00000065588	ENSMUSG00000105096	5	105215699	105239533	-1	18	8	32	13	6	5	2	4	0	28	21	Q000W5	
ENSMUST00000065600	ENSMUSG00000053684	10	121739937	121752878	1	20	40	59	60	99	20	60	20	67	0	77		Q6P1I3
ENSMUST00000065601	ENSMUSG00000025217	19	45363734	45533341	1	106	0	58	0	58	0	76	203	114	0	58		Q3ULA2
ENSMUST00000065603	ENSMUSG00000047766	9	60568859	60688158	-1	2	2	1	4	10	5	0	0	32	0	0	E9QM16	
ENSMUST00000065625	ENSMUSG00000053286	1	151428542	151458161	1	7	7	15	10	0	0	43	336	248	26	193		
ENSMUST00000065626	ENSMUSG00000053287	2	85769803	85770720	1	6	0	2	7	2	0	0	0	0	0	0		Q7TR96
ENSMUST00000065629	ENSMUSG00000021585	13	74694286	74807921	-1	20	15	38	21	21	14	1112	3933	2583	2168	1836	Q8CE80	
ENSMUST00000065630	ENSMUSG00000053289	9	53098454	53248112	-1	17	11	18	151	13	10	35	151	49	128	85		Q80Y44
ENSMUST00000065634	ENSMUSG00000053303	19	7781041	7802667	-1	1	8	12	7	3	0	0	0	0	0	0	Q91WJ2	
ENSMUST00000065638						58	42	5	0	0	32	0	21	19	34	1		
ENSMUST00000065648	ENSMUSG00000050565	1	156035403	156068861	1	0	0	0	0	0	0	33	0	45	52	33		Q9ER81
ENSMUST00000065651	ENSMUSG00000063590	19	8062209	8131982	-1	2	5	1	0	7	2	0	0	0	0	0	B2RT89	
ENSMUST00000065664	ENSMUSG00000048796	3	108195687	108201212	-1	10	0	0	0	0	0	288	1024	433	27	141	Q3TPE5	
ENSMUST00000065666	ENSMUSG00000022651	16	48872608	48874498	1	23	39	105	247	51	67	73977	243233	63820	332049	38632	Q8K426	
ENSMUST00000065668	ENSMUSG00000053310	9	37544492	37552904	-1	14	7	30	153	18	9	63	108	70	205	287		P60761
ENSMUST00000065678	ENSMUSG00000053317	4	47474658	47483242	1	1	3	4	13	1	0	715	1812	691	1926	420		Q9CQS8
ENSMUST00000065679	ENSMUSG00000053318	1	172581758	172590568	-1	9	9	16	14	22	8	3	9	2	2	8	Q3UQA2	
ENSMUST00000065692	ENSMUSG00000035152	11	83299024	83405035	1	0	0	0	0	0	0	220	44	440	4	271		Q9DBG3
ENSMUST00000065694	ENSMUSG00000053333	1	86703808	87050095	1	0	4	19	0	0	0	52	102	82	29	72		Q8CI75
ENSMUST00000065698	ENSMUSG00000053334	5	113735803	113740600	1	20	11	50	85	30	16	126	167	104	13	98		Q8BIX9
ENSMUST00000065703	ENSMUSG00000053338	7	3486500	3502624	-1	6	7	9	13	9	4	2023	4735	1627	1983	1258		B6A8R8
ENSMUST00000065716	ENSMUSG00000051166	12	98786604	98901484	-1	28	23	23	173	34	13	16	40	29	13	78		Q8BQM8
ENSMUST00000065740	ENSMUSG00000053358	7	121033252	121035096	-1	2	1	6	68	8	11	32	163	92	9	133	E9PXZ0	
ENSMUST00000065745	ENSMUSG00000053368	5	150018675	150082184	1	0	0	0	0	17	0	0	0	0	0	0		Q91ZZ5
ENSMUST00000065753	ENSMUSG00000042854	2	166792531	166799505	1	10	5	7	229	15	10	0	3	0	0	0	A2A5R0	
ENSMUST00000065758	ENSMUSG00000053375	17	86944109	86947887	-1	5	4	5	14	7	1	0	0	0	0	0		Q9D593
ENSMUST00000065766	ENSMUSG00000046169	13	104287873	104494763	1	14	6	11	14	12	11	5	15	4	3	20	D3Z1A5	
ENSMUST00000065767	ENSMUSG00000026047	1	44106546	44118808	-1	3	0	7	10	5	5	0	27	0	5	0		Q9JHP7
ENSMUST00000065778	ENSMUSG00000032571	9	105642978	105687657	1	0	14	0	6	3	0	223	619	440	69	272		Q8VD65
ENSMUST00000065781	ENSMUSG00000053389	6	131659118	131660149	-1	1	1	1	3	2	0	0	0	0	0	0		Q7M725
ENSMUST00000065784	ENSMUSG00000033658	8	111003188	111031751	-1	0	0	0	32	0	3	40	0	43	5	44	Q8BZY3	
ENSMUST00000065785	ENSMUSG00000053388	5	135353295	135368005	1	17	24	63	42	58	35	1	0	0	0	0		Q810I2
ENSMUST00000065786	ENSMUSG00000053391	6	116489101	116494540	1	5	8	4	7	5	6	0	0	0	0	0	Q8VGH2	
ENSMUST00000065788	ENSMUSG00000063142	14	23289431	24004859	-1	47	0	631	77	0	17	0	1	1	0	1	F6ZSN2	
ENSMUST00000065793	ENSMUSG00000053398	3	98313170	98339990	-1	48	21	53	53	51	21	129	126	53	68	143		Q61753
ENSMUST00000065796	ENSMUSG00000024789	19	29251828	29313080	1	0	0	34	52	0	0	601	750	2170	561	1797	G5E852	
ENSMUST00000065797	ENSMUSG00000027221	2	92599707	92615250	1	61	34	97	521	95	39	22	29	13	3	9	Q3UY35	Q9EQC0
ENSMUST00000065806	ENSMUSG00000091736	X	157566119	157568985	-1	5	5	0	7	2	1	15	29	6	1	7		Q3TTC2
ENSMUST00000065815	ENSMUSG00000020251	10	82650433	82690650	-1	4	3	1	7	9	6	0	3	1	0	0	E9PWN8	
ENSMUST00000065826	ENSMUSG00000053420	10	94293665	94298703	-1	3	1	1	7	7	1	0	0	0	0	0	Q569Q2	
ENSMUST00000065841	ENSMUSG00000058435	17	34469042	34475937	-1	22	11	52	23	21	16	0	0	0	0	0	A2CG29	
ENSMUST00000065842						1	3	2	1	2	0	0	0	0	0	0		
ENSMUST00000065856	ENSMUSG00000053414	16	90386397	90499553	1	34	20	85	115	41	18	13	67	15	3	34		O88866
ENSMUST00000065857						0	0	3	0	0	2	0	0	27	5	21		
ENSMUST00000065858	ENSMUSG00000031302	X	101299168	101325963	1	0	0	0	31	53	58	0	0	7	0	11		Q8BYM5
ENSMUST00000065865	ENSMUSG00000053453	14	13949014	13961225	-1	1	2	1	2	6	1	114	835	212	697	185		Q7TMY4
ENSMUST00000065870	ENSMUSG00000059810	4	62559847	62704001	1	13	7	30	9	18	2	0	0	0	0	0	Z4YJQ4	
ENSMUST00000065871	ENSMUSG00000061544	17	21730795	21769342	1	33	32	148	46	7	10	0	0	0	3	0	E9PWT2	
ENSMUST00000065878						4	7	5	68	4	3	4	8	14	6	4		
ENSMUST00000065887	ENSMUSG00000036955	10	62538626	62578457	-1	0	0	3	24	0	0	152	209	255	10	116		Q6ZPU9
ENSMUST00000065889	ENSMUSG00000027014	2	77881159	77946375	-1	0	0	0	0	10	0	0	0	0	0	0		Q8C5N3
ENSMUST00000065894	ENSMUSG00000053862	9	65412753	65422773	-1	1	2	16	2	4	0	0	0	0	0	0		Q80WK2
ENSMUST00000065896	ENSMUSG00000028678	4	117159639	117182639	-1	4	5	29	15	0	7	87	143	121	96	77		Q922S8
ENSMUST00000065900	ENSMUSG00000053461	1	183418215	183436808	1	17	4	0	26	23	13	0	0	0	0	0		Q9D2G9
ENSMUST00000065904	ENSMUSG00000053465	14	119138415	119869594	1	4	6	20	337	20	11	0	0	0	0	0		Q9QYK4
ENSMUST00000065906	ENSMUSG00000053460	6	72414308	72430712	1	17	18	42	42	21	11	16	35	19	3	27	B2RS80	Q9QYC7
ENSMUST00000065913	ENSMUSG00000008822	12	85272398	85288438	-1	2	0	9	21	3	1	7	6	7	20	7	Q8BMV3	
ENSMUST00000065916	ENSMUSG00000053469	15	66670753	66850721	1	43	24	52	61	45	33	236	34	301	16	146		O08710
ENSMUST00000065917	ENSMUSG00000058799	10	111473192	111498142	1	1	0	0	52	1	1	291	1598	624	379	575		P28656
ENSMUST00000065927	ENSMUSG00000053475	2	52038009	52056686	1	16	18	27	17	18	7	45	97	42	20	52	Q3USX6	O08859
ENSMUST00000065928	ENSMUSG00000028252	4	21727701	21759922	1	9	0	5	28	0	0	31	181	94	142	59	Q8CAS3	
ENSMUST00000065932	ENSMUSG00000031153	X	7789765	7820567	1	0	0	0	5	5	0	443	151	137	58	276		Q8VD04
ENSMUST00000065938	ENSMUSG00000027531	3	10311956	10331439	-1	14	17	28	12	11	13	8	23	45	4	39	Q924B0	
ENSMUST00000065941	ENSMUSG00000053483	1	171281945	171287991	-1	0	7	25	157	16	12	552	706	427	50	334	E9PUE2	
ENSMUST00000065950	ENSMUSG00000045942	11	51253651	51263046	-1	10	6	10	18	7	0	0	0	4	6	0	Q8C601	
ENSMUST00000065956	ENSMUSG00000053499	13	4771649	4836485	1	14	12	37	15	20	10	0	0	1	0	0	Q8CDE5	
ENSMUST00000065957	ENSMUSG00000004961	7	4539765	4547541	-1	15	9	25	51	22	5	0	0	1	0	0		Q9R0N5
ENSMUST00000065967	ENSMUSG00000055214	1	175962306	176275312	-1	0	0	13	0	0	0	0	0	0	0	0		Q3UNN8
ENSMUST00000065970	ENSMUSG00000053519	11	33629339	33993152	-1	0	0	0	0	0	11	0	0	0	1	0	Q3YAB6	Q9JJ57
ENSMUST00000065973	ENSMUSG00000027605	2	155517948	155585724	1	6	8	11	13	5	4	0	7	4	0	7	A2AQN5	
ENSMUST00000065976	ENSMUSG00000025665	X	111388192	111537959	-1	3	0	0	0	0	0	0	0	0	0	0	A2CEE6	
ENSMUST00000065977	ENSMUSG00000053510	4	109000655	109061777	1	0	0	0	0	25	0	270	901	638	41	546		Q8BHG1
ENSMUST00000065978	ENSMUSG00000053508	15	103438965	103448459	-1	3	4	0	1	1	1	0	0	0	0	0	Q80Y74	
ENSMUST00000065987	ENSMUSG00000057880	16	8513429	8621568	1	19	25	27	72	58	12	0	0	0	0	1		P61922
ENSMUST00000065997	ENSMUSG00000030051	6	87628424	87672193	-1	86	165	119	10	123	101	42	98	0	30	85		Q9D842

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000066003	ENSMUSG00000027109	2	72936427	72980446	-1	11	12	10	0	9	3	1089	2598	1665	739	800		O70494
ENSMUST00000066005	ENSMUSG00000053528	7	83148644	83155922	1	2	2	0	0	2	0	0	0	0	0	0	Q8BS29	
ENSMUST00000066026	ENSMUSG00000040327	17	46500572	46546388	-1	0	0	0	0	0	0	50	0	20	4	0	E9QP09	
ENSMUST00000066027	ENSMUSG00000003531	16	18052860	18071632	1	0	0	0	1	0	0	42	1	0	11	14	E9QP31	
ENSMUST00000066028	ENSMUSG00000019876	10	57631981	57741112	1	0	11	30	0	6	0	46	317	44	118	27	Q3TZU5	
ENSMUST00000066037	ENSMUSG00000022641	16	50191844	50432390	-1	12	14	0	17	0	0	26	48	49	0	24		Q8VBW5
ENSMUST00000066039	ENSMUSG00000053536	19	31082841	31086590	1	18	19	37	44	28	12	319	728	410	141	336		Q8C7E9
ENSMUST00000066041	ENSMUSG00000053550	7	4825552	4844696	-1	0	0	0	159	0	0	0	0	0	0	0		Q8C3Q5
ENSMUST00000066049	ENSMUSG00000049420	10	25991186	26079052	-1	15	16	35	96	28	10	0	0	0	0	0	B2RUN2	Q8C817
ENSMUST00000066052	ENSMUSG00000053553	5	139359739	139460527	-1	50	35	245	123	64	22	288	674	311	177	296		Q9CXL3
ENSMUST00000066055	ENSMUSG00000035437	2	37443279	37566454	1	2	0	1	1	5	3	5	2	8	2	11		A2AWA9
ENSMUST00000066058	ENSMUSG00000033902	2	119972699	120027408	1	86	53	185	75	95	54	47	135	83	8	122	A0A0A0MQA2	
ENSMUST00000066060	ENSMUSG00000048251	12	107910403	108003602	-1	53	34	146	451	62	29	29	49	34	4	59		Q99PV8
ENSMUST00000066068	ENSMUSG00000053559	15	100621342	100636865	-1	0	0	12	37	0	0	0	0	5	6	4		Q99KC7
ENSMUST00000066070	ENSMUSG00000053565	7	28971373	28981814	-1	4	9	12	18	6	5	1773	2563	1362	4318	886		Q9DBZ5
ENSMUST00000066078	ENSMUSG00000038517	11	97136171	97151495	-1	26	3	46	5	17	4	173	318	372	21	222		A2A9T0
ENSMUST00000066081	ENSMUSG00000031681	8	79338395	79399518	-1	3	4	2	91	3	0	0	7	2	0	0	Q8CC31	
ENSMUST00000066091	ENSMUSG00000031681	8	79338395	79399518	-1	12	3	19	15	7	1	220	497	368	54	173		P70340
ENSMUST00000066106	ENSMUSG00000053588	14	55559942	55560406	-1	13	1	14	22	9	6	0	6	3	1	12	Q8BGD2	
ENSMUST00000066107	ENSMUSG00000032641	6	134869093	134898578	-1	8	4	0	16	0	8	2	0	0	0	0		Q61121
ENSMUST00000066112	ENSMUSG00000031354	X	169176114	169187200	-1	0	4	0	0	0	0	0	0	0	0	0	Q6PCW7	
ENSMUST00000066116	ENSMUSG00000053593	X	71972986	71989046	1	2	1	5	0	2	0	0	0	0	0	0		Q8CEK7
ENSMUST00000066121	ENSMUSG00000079557	17	33685692	33718670	-1	0	0	0	17	20	7	7	45	28	12	26	Q8CA25	
ENSMUST00000066127	ENSMUSG00000003166	16	17839482	17894145	-1	0	1	12	0	0	0	0	35	0	16	0	Q8C2R4	
ENSMUST00000066133	ENSMUSG00000005871	18	34220924	34322189	1	1	0	0	0	0	1	0	3	2	0	0	Q8C493	
ENSMUST00000066134	ENSMUSG00000053604	6	70765720	70792232	-1	4	4	27	40	5	4	322	586	330	70	217		P47968
ENSMUST00000066140	ENSMUSG00000023036	18	37815079	37841873	1	7	13	21	33	19	0	0	0	2	0	3	Q91XX0	
ENSMUST00000066148	ENSMUSG00000037287	9	42412316	42507809	-1	0	0	0	18	0	0	0	33	0	0	33		Q8C5W3
ENSMUST00000066149	ENSMUSG00000103897	18	37725706	37841873	1	22	19	47	44	34	15	0	0	0	0	0	Q91XY0	
ENSMUST00000066155	ENSMUSG00000027259	2	121140428	121156680	1	0	0	0	0	5	0	15	108	45	43	0		Q80SY6
ENSMUST00000066157	ENSMUSG00000053615	2	125505089	125507881	1	13	4	15	331	25	3	0	0	0	0	0	Q8BQQ2	
ENSMUST00000066160	ENSMUSG00000029521	5	110839979	110874145	1	24	37	103	31	23	19	31	69	36	15	27	Q543W6	Q9Z265
ENSMUST00000066163	ENSMUSG00000054057	2	18025193	18037737	-1	19	16	87	461	45	23	1	2	1	2	10	Q8C8W7	
ENSMUST00000066166	ENSMUSG00000053626	8	64014770	64205993	-1	167	121	649	224	98	53	1	11	9	2	18	G3X9F5	
ENSMUST00000066173	ENSMUSG00000046152	8	31187331	31261738	1	11	0	14	12	7	3	0	11	13	0	21		Q5F2L2
ENSMUST00000066175	ENSMUSG00000040505	17	84658234	84683011	-1	23	11	19	15	19	13	0	0	0	0	0	Q540E8	Q99PE8
ENSMUST00000066177	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	45	152	62	41	96		P30999
ENSMUST00000066179	ENSMUSG00000037287	9	42412316	42507809	-1	5	6	23	5	2	2	0	0	0	0	0		Q8C5W3
ENSMUST00000066187	ENSMUSG00000048540	3	102010076	102015492	1	23	21	36	240	40	22	0	1	0	0	0		Q64221
ENSMUST00000066193	ENSMUSG00000053624	18	52693679	52695668	1	4	3	2	12	7	5	0	0	0	0	0	Q8C635	
ENSMUST00000066197	ENSMUSG00000020704	11	80880169	81968457	-1	32	10	62	9	26	13	0	0	0	0	0	Q3UYD3	Q925H0
ENSMUST00000066207	ENSMUSG00000053863	5	104325329	104338611	1	5	8	60	11	34	19	0	0	0	0	0	Q8K4L6	
ENSMUST00000066208	ENSMUSG00000053644	18	56509687	56572951	-1	0	6	6	15	0	0	0	0	0	0	27		Q9DBF1
ENSMUST00000066211	ENSMUSG00000053647	5	139423151	139427800	1	15	8	31	34	29	11	1	7	0	2	10		Q8BMP4
ENSMUST00000066237	ENSMUSG00000020182	11	11814101	11898144	-1	6	0	0	0	0	0	0	1	0	0	0	Q5SUV8	O88533
ENSMUST00000066241						5	1	12	1	5	3	0	1	0	0	1		
ENSMUST00000066257	ENSMUSG00000028790	4	129703164	129742303	-1	11	9	21	11	12	11	625	1722	493	42	257		Q60749
ENSMUST00000066258	ENSMUSG00000053678	8	18974940	18978256	-1	1	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000066264	ENSMUSG00000053898	7	28825217	28832247	1	0	0	0	0	0	0	1555	1884	926	2322	663		O35459
ENSMUST00000066272	ENSMUSG00000051316	18	37640491	37644204	-1	8	3	15	34	10	6	77	552	141	320	105		Q9R1C0
ENSMUST00000066277	ENSMUSG00000010025	11	61223417	61267464	-1	17	7	8	3	12	13	4	2	0	0	4	B1ATI0	
ENSMUST00000066279	ENSMUSG00000036206	1	89070415	89155068	1	48	30	57	93	55	34	16	23	19	16	68		Q921I6
ENSMUST00000066282	ENSMUSG00000053695	8	18986233	18991055	-1	1	0	1	0	1	1	0	0	0	0	0		Q7TMD2
ENSMUST00000066283	ENSMUSG00000034394	11	4257557	4272514	1	0	0	17	63	70	32	17	0	0	6	0		P09056
ENSMUST00000066285	ENSMUSG00000025092	19	58795751	58860984	-1	34	28	70	97	62	27	1	4	1	1	14		Q8K0U4
ENSMUST00000066295	ENSMUSG00000049265	5	30588170	30625271	1	57	40	141	799	104	48	2	6	0	0	3		O35111
ENSMUST00000066296	ENSMUSG00000035614	12	64965742	65022573	1	29	18	46	440	52	12	104	225	228	31	186		Q6A070
ENSMUST00000066298	ENSMUSG00000053706	3	61362250	61365951	-1	11	4	0	424	34	17	0	0	0	3	2	Q8BQQ8	
ENSMUST00000066308	ENSMUSG00000046585	19	47937712	48035379	1	25	17	26	46	26	12	0	0	0	0	0		B2RW38
ENSMUST00000066316						4	2	3	0	5	0	3	1	1	0	2		
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ENSMUST00000066319	ENSMUSG00000010136	3	105996957	106014646	-1	4	2	2	4	2	0	1	2	0	1	0		Q9D9W1
ENSMUST00000066328	ENSMUSG00000053729	18	44166358	44175073	-1	0	2	0	1	0	0	0	0	0	0	0		Q8CEK3
ENSMUST00000066330	ENSMUSG00000005417	11	59661305	59780860	1	26	20	120	66	58	15	61	105	136	6	219	Q5SWZ5	
ENSMUST00000066337	ENSMUSG00000025270	X	150547375	150570638	1	27	5	0	9	135	0	297	69	135	415	604	A2AFM0	P08680
ENSMUST00000066345	ENSMUSG00000068663	16	10545339	10744878	1	0	0	29	34	0	0	0	0	0	0	0		Q80U30
ENSMUST00000066352	ENSMUSG00000053746	2	32775786	32777597	1	4	0	0	24	2	0	6	0	0	6	16		Q8BW00
ENSMUST00000066368	ENSMUSG00000032717	17	47815328	47834691	-1	10	6	19	236	13	6	0	0	0	0	0		P70331
ENSMUST00000066374	ENSMUSG00000079550	1	59120935	59163389	-1	0	0	0	1	1	0	0	0	1	0	0	K3W4N9	
ENSMUST00000066378						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000066379	ENSMUSG00000053768	6	32790976	33060260	-1	4	0	0	31	7	0	114	386	166	491	116		Q9CRB9
ENSMUST00000066384	ENSMUSG00000036972	9	91362413	91389348	1	15	12	13	3	15	9	0	1	0	0	1		Q61467
ENSMUST00000066386	ENSMUSG00000053769	3	95134088	95139518	1	22	9	37	0	28	13	130	340	154	26	153	A6H624	Q9D0E3
ENSMUST00000066387	ENSMUSG00000053773	9	20818504	20826163	1	20	14	26	22	22	3	0	0	0	0	0	D3Z6W3	
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ENSMUST00000066401	ENSMUSG00000007891	7	142371148	142388038	-1	6	0	0	4	4	10	35292	62108	20973	7777	13936	F8WIR1	
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ENSMUST00000066412	ENSMUSG00000049115	13	30336441	30382867	1	9	8	9	6	5	8	0	0	0	1	0		P29754
ENSMUST00000066416	ENSMUSG00000053790	8	19023407	19026566	-1	1	0	1	0	0	0	0	0	0	0	0	Q05A65	Q7TNV7
ENSMUST00000066420	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	1	64	0	0	0	0	0	0	0	A6PWP8	
ENSMUST00000066427	ENSMUSG00000026222	1	85649988	85709998	1	72	40	86	1167	192	86	904	5043	1497	393	1412	Q8C405	
ENSMUST00000066431	ENSMUSG00000057897	11	5969644	6066362	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SVI9	
ENSMUST00000066432	ENSMUSG00000057182	2	65457118	65567627	-1	20	26	37	22	16	19	0	1	0	0	1	A2ASI5	
ENSMUST00000066437	ENSMUSG00000045655	14	78081021	78089007	-1	3	17	13	5	10	5	0	0	0	0	0		Q8CC14

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000066439	ENSMUSG00000053799	19	37550418	37683245	1	12	12	7	34	13	8	465	2036	954	1158	571	Q3U9D6	
ENSMUST00000066451	ENSMUSG00000031637	8	45999303	46029477	1	0	0	7	11	4	0	1	0	1	0	5	G5E8E5	
ENSMUST00000066452	ENSMUSG00000053819	3	126596302	126846326	1	1	0	0	0	0	0	29	14	96	0	63	E9PXV3	
ENSMUST00000066457	ENSMUSG00000053815	14	50618161	50619265	1	7	3	11	2	5	2	0	0	0	0	0	Q7TRM0	
ENSMUST00000066460	ENSMUSG00000053820	9	114330135	114330578	1	0	0	0	0	2	2	0	0	0	1	0	Q0P538	
ENSMUST00000066461	ENSMUSG00000053821	14	101729380	101729814	-1	3	0	3	93	12	4	0	0	0	0	0	Q8C3P1	
ENSMUST00000066465	ENSMUSG00000030972	7	119526304	119543793	1	25	18	34	28	21	20	0	0	0	1	0		Q8BGA8
ENSMUST00000066466	ENSMUSG00000053819	3	126596302	126846326	1	0	16	17	0	0	3	428	1370	570	123	193		Q6PHZ2
ENSMUST00000066469	ENSMUSG00000055681	8	70302518	70312993	1	4	2	7	9	3	0	599	635	478	252	258		O89079
ENSMUST00000066473	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	0	0	0	0	0	0	0	0	0	E9QN47	
ENSMUST00000066475	ENSMUSG00000030510	7	66743504	66823692	1	15	12	34	50	21	16	6	25	12	1	3		Q1A3B0
ENSMUST00000066478	ENSMUSG00000039021	2	32757026	32775633	-1	9	0	0	24	11	6	0	0	0	0	0	Q3V0B6	
ENSMUST00000066489	ENSMUSG00000006931	11	100408456	100414836	-1	13	13	22	246	33	7	0	0	0	5	5		Q8K2B0
ENSMUST00000066496	ENSMUSG00000053838	11	6105691	6200415	-1	6	19	130	154	45	15	359	331	480	67	433	B0FTY3	Q8R1N4
ENSMUST00000066497	ENSMUSG00000051469	18	24009702	24020810	-1	16	14	22	36	23	13	120	529	145	158	130		Q91VN1
ENSMUST00000066498	ENSMUSG00000036502	X	38196573	38252439	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BHW5
ENSMUST00000066503	ENSMUSG00000054385	7	25516042	25539857	-1	0	0	12	0	0	7	4	0	2	0	1		Q925P2
ENSMUST00000066504	ENSMUSG00000020847	11	75830999	75938429	-1	8	0	8	1	5	0	5	3	0	0	11		Q768S4
ENSMUST00000066509	ENSMUSG00000036617	2	19909780	20810713	1	3	0	0	0	0	0	0	0	0	0	0		A2AQ25
ENSMUST00000066510	ENSMUSG00000050876	13	59700083	59706197	-1	64	25	165	74	61	42	0	1	0	0	0	E9QA35	
ENSMUST00000066514	ENSMUSG00000031767	8	114133557	114154739	1	0	0	0	0	0	0	23	130	14	46	13		Q99P30
ENSMUST00000066529	ENSMUSG00000022206	15	11839896	11905674	-1	53	44	145	175	54	23	1	2	3	3	4		P70180
ENSMUST00000066530	ENSMUSG00000040562	3	107981702	107986453	-1	0	0	10	0	0	0	0	0	0	0	2	D3YX76	
ENSMUST00000066531	ENSMUSG00000040283	11	49165585	49187159	-1	5	2	4	13	3	1	0	0	0	0	0		Q8BJE2
ENSMUST00000066532	ENSMUSG00000053846	18	74939322	74961263	-1	27	29	76	72	50	20	6150	14059	11629	959	4142	C0LQ91	Q9WVG5
ENSMUST00000066537	ENSMUSG00000043873	3	106016919	106032814	-1	0	7	4	1	5	5	16	163	32	19	21	F7AQE8	
ENSMUST00000066540	ENSMUSG00000029597	5	120476526	120483932	1	2	5	11	41	6	6	0	0	0	0	0	Q3UEN6	Q8VBT2
ENSMUST00000066544	ENSMUSG00000053856	5	31106285	31112526	1	7	5	0	3	6	2	0	0	0	0	0	Q8C632	
ENSMUST00000066545	ENSMUSG00000022623	15	89499623	89560261	1	15	11	30	10	13	21	1	1	0	2	2		Q4ACU6
ENSMUST00000066554	ENSMUSG00000054134	17	30954679	31010708	1	23	26	119	45	61	27	0	0	0	0	0		Q5DID3
ENSMUST00000066558	ENSMUSG00000053868	14	59158503	59178749	-1	1	2	3	24	3	1	0	0	0	0	0	Q8C5X9	
ENSMUST00000066559	ENSMUSG00000027353	2	132816141	132844197	1	23	18	32	50	17	15	0	5	8	0	7		Q9CWV1
ENSMUST00000066560	ENSMUSG00000036395	9	26763044	26806468	-1	9	16	69	42	29	10	0	3	1	3	8	E0CYE1	
ENSMUST00000066568	ENSMUSG00000053870	3	155084918	155093403	-1	3	10	13	19	8	7	14	75	28	66	25	G5E8F4	
ENSMUST00000066573	ENSMUSG00000053873	5	113357294	113357821	1	3	3	11	8	7	1	0	0	0	0	0	E9Q2J1	
ENSMUST00000066576	ENSMUSG00000031391	X	73853778	73896105	-1	0	0	0	0	0	0	257	19	267	5	396	A2AFG7	
ENSMUST00000066582	ENSMUSG00000053877	7	127511983	127561219	1	4	0	4	3	2	1	0	0	4	0	8	E9Q9V7	
ENSMUST00000066583	ENSMUSG00000053861	18	74065102	74065584	1	0	1	16	87	7	6	0	0	0	0	0	F6T2U3	
ENSMUST00000066587	ENSMUSG00000020777	11	116171888	116199045	-1	6	0	0	47	21	12	450	268	608	75	321		Q9R0H0
ENSMUST00000066594	ENSMUSG00000053886	8	68276567	68347694	1	155	128	1317	350	259	122	1	16	6	1	10		Q9D7V1
ENSMUST00000066597	ENSMUSG00000055707	8	70450228	70476943	-1	17	16	33	63	51	12	99	90	147	17	34		Q8BGY4
ENSMUST00000066601	ENSMUSG00000032115	9	44379490	44392369	1	19	9	11	15	8	0	372	475	642	5	274		Q9JKR6
ENSMUST00000066610	ENSMUSG00000048458	3	105704599	105720842	1	49	47	110	242	60	33	5	12	19	0	12		Q80VY2
ENSMUST00000066617	ENSMUSG00000029729	5	138085084	138107822	1	0	21	20	3	0	0	0	35	0	0	0		Q8BGS3
ENSMUST00000066632	ENSMUSG00000026634	1	190925112	190946962	1	0	0	0	0	0	0	78	467	536	158	480		Q8K1C0
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ENSMUST00000066646	ENSMUSG00000024968	19	7267325	7275225	1	0	0	0	336	13	0	0	0	0	0	0		Q8C796
ENSMUST00000066650	ENSMUSG00000032469	9	99575799	99584501	1	2	3	2	84	3	7	41	246	103	30	77		Q923B1
ENSMUST00000066652	ENSMUSG00000036333	12	24974932	25059697	1	23	20	69	92	56	21	840	2393	2077	289	1521	E9Q9B7	
ENSMUST00000066658						271	503	311	292	248	155	1	16	15	141	10		
ENSMUST00000066668	ENSMUSG00000026209	1	75307896	75317990	-1	0	0	5	0	0	0	0	24	14	0	7		Q9Z2W0
ENSMUST00000066674	ENSMUSG00000041261	4	8143362	8239041	-1	32	35	74	75	37	8	12	61	15	21	25		P28651
ENSMUST00000066675	ENSMUSG00000016510	5	146951573	146963800	-1	35	20	82	51	46	25	7	13	7	2	7	A4QMQ0	Q9CZD5
ENSMUST00000066677	ENSMUSG00000053929	15	76643395	76660117	-1	8	9	0	0	0	0	20	0	0	15	0		Q9QXA1
ENSMUST00000066679	ENSMUSG00000053930	11	66211725	66525964	-1	5	0	0	64	8	2	0	0	0	0	0		Q3UH99
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ENSMUST00000066715	ENSMUSG00000028952	4	152019774	152027671	-1	1	0	0	0	29	0	34	85	35	1	52		Q1H9T6
ENSMUST00000066717	ENSMUSG00000053477	18	69343356	69689079	1	3	1	10	72	9	5	0	0	0	0	0	E9Q8G4	
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ENSMUST00000066728	ENSMUSG00000053965	3	122728947	122859374	1	86	92	392	168	99	61	12	61	37	11	76		Q8CG03
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ENSMUST00000066747	ENSMUSG00000053977	6	71373427	71379173	1	0	0	127	89	126	0	24	76	0	13	79		P01731
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ENSMUST00000066774	ENSMUSG00000054000	4	93334138	93335511	-1	2	4	3	162	6	1	125	225	91	28	47		Q673H1
ENSMUST00000066778	ENSMUSG00000025178	19	42090435	42122218	1	26	22	37	95	40	9	1302	1863	1604	178	1068		Q2TBE6
ENSMUST00000066780	ENSMUSG00000054005	7	18245347	18266092	1	25	16	99	31	17	11	0	1	1	0	0	Q8HWE7	
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ENSMUST00000066794						23	9	32	34	21	5	1	0	0	0	0		
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ENSMUST00000066807	ENSMUSG00000054051	14	32513521	32580989	1	56	74	141	65	92	41	84	235	243	20	207	F8VPZ5	
ENSMUST00000066814	ENSMUSG00000054033	8	40823009	40826861	1	10	3	4	12	10	0	0	0	0	0	0	Q7M762	
ENSMUST00000066819	ENSMUSG00000054034	X	136200948	136203876	-1	0	2	16	4	5	0	0	0	0	0	0	Q14C38	Q8CCT4
ENSMUST00000066824	ENSMUSG00000028524	4	102741297	102973628	1	4	2	16	47	8	3	0	0	0	0	0		Q8VD37
ENSMUST00000066834	ENSMUSG00000054046	7	43712567	43727534	1	2	5	10	8	3	5	0	0	0	0	0	Q8CGR6	
ENSMUST00000066849	ENSMUSG00000027985	3	131110471	131224356	1	0	0	0	13	0	30	0	16	0	0	21	D3Z654	
ENSMUST00000066852	ENSMUSG00000052276	16	27307489	27351212	1	22	18	16	199	37	28	0	4	1	1	0		P61364
ENSMUST00000066854	ENSMUSG00000057406	5	33820725	33897975	1	15	3	53	0	1	0	22	0	0	0	0		Q8BVE8
ENSMUST00000066859	ENSMUSG00000026365	1	140084708	140183764	-1	0	0	0	0	4	0	17	656	61	714	419		P06909

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
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ENSMUST00000066873	ENSMUSG00000054065	7	141078218	141090510	1	0	6	6	34	10	0	0	2	0	9	27		Q9QY23
ENSMUST00000066875	ENSMUSG00000054069	8	106500522	106507342	1	2	3	4	5	8	2	0	0	0	0	0	Q8CD33	
ENSMUST00000066880	ENSMUSG00000054083	7	28881656	28893585	1	25	12	63	102	49	17	1	3	0	0	0	E9QL26	
ENSMUST00000066882	ENSMUSG00000027805	3	57841895	57848079	-1	4	2	11	9	0	2	0	3	5	0	5		Q9JJV2
ENSMUST00000066885	ENSMUSG00000054074	2	18040676	18049051	-1	15	9	22	165	19	11	1	1	1	1	0		Q80YR3
ENSMUST00000066888	ENSMUSG00000054079	11	93859243	93885766	-1	0	0	0	128	4	0	72	331	136	85	68	Q3U3Q3	Q5SSI6
ENSMUST00000066889	ENSMUSG00000026930	2	26315515	26348237	1	25	21	33	2	0	13	0	0	0	0	0		Q6IR34
ENSMUST00000066890	ENSMUSG00000054477	18	45268860	45686024	1	0	0	0	14	0	0	0	0	0	0	0		P58390
ENSMUST00000066905	ENSMUSG00000030077	6	103510586	103750211	1	49	35	40	32	34	17	1	3	1	6	2		P70232
ENSMUST00000066912	ENSMUSG00000054072	18	60376029	60392627	1	14	0	0	9	0	4	2	7	3	105	39	J7NNX8	Q9QZ85
ENSMUST00000066921	ENSMUSG00000054099	5	8422850	8454797	1	3	5	9	55	12	4	0	65	13	11	0		Q8BGP6
ENSMUST00000066928	ENSMUSG00000054728	13	42680623	43138526	1	0	1	0	10	0	0	0	0	0	0	0		Q2M3X8
ENSMUST00000066936	ENSMUSG00000026930	2	26315515	26348237	1	0	0	0	81	27	0	26	5	0	0	64		Q6IR34
ENSMUST00000066940	ENSMUSG00000021639	13	100460218	100492579	-1	0	0	3	26	0	0	0	4	0	0	0	Q8C5I2	
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ENSMUST00000066958	ENSMUSG00000027316	2	131039632	131043088	-1	0	0	0	0	0	2	0	0	0	0	0		Q9JJT2
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ENSMUST00000066983	ENSMUSG00000033157	16	45729725	45742955	-1	7	3	22	17	10	4	24	71	29	6	14		Q6PE15
ENSMUST00000066984	ENSMUSG00000021639	13	100460218	100492579	-1	1	4	24	9	7	3	2	20	2	0	0		Q9JIB4
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ENSMUST00000066987	ENSMUSG00000020520	11	57645442	57787514	1	37	23	54	46	63	37	565	611	296	30	310	Q5SQF9	Q6P9S7
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ENSMUST00000066994	ENSMUSG00000034522	14	65358676	65398930	1	62	32	103	255	81	40	332	352	449	38	374	E9Q5N9	
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ENSMUST00000066998	ENSMUSG00000054142	17	21286533	21287653	1	4	4	6	1	6	1	0	0	0	0	0	Q05A06	
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ENSMUST00000067007	ENSMUSG00000054156	9	49268572	49278783	1	1	1	1	3	2	0	0	0	0	0	0	Q8CA09	
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ENSMUST00000067033	ENSMUSG00000022329	15	34875496	35155806	-1	1	0	0	0	8	4	15	204	64	86	5		Q9JI10
ENSMUST00000067036	ENSMUSG00000023175	10	79704491	79711969	1	3	7	37	62	16	8	507	523	360	123	430		P18572
ENSMUST00000067043	ENSMUSG00000050714	2	37432168	37443135	-1	7	12	19	12	11	7	27	58	15	10	31	Q6P9Q3	
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ENSMUST00000067058	ENSMUSG00000045140	11	84876315	84880285	-1	9	10	13	230	19	8	0	6	2	11	11	B7ZN11	Q8C398
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ENSMUST00000067082	ENSMUSG00000021684	13	95024454	95250336	-1	0	0	0	26	0	0	0	0	0	0	0		E9Q4S1
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ENSMUST00000067087	ENSMUSG00000054204	12	30884322	30893854	1	4	6	3	163	16	7	0	0	0	0	0		Q80UG6
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ENSMUST00000067102	ENSMUSG00000054215	3	92432582	92433925	1	3	0	2	3	2	0	0	0	0	0	0	G5E8D1	
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ENSMUST00000067120	ENSMUSG00000027577	2	181018380	181043546	-1	43	36	108	61	69	23	0	0	0	0	0	Q53YK0	O70174
ENSMUST00000067124	ENSMUSG00000020593	12	16535669	16589770	-1	19	22	10	45	31	0	0	7	23	0	16		
ENSMUST00000067137	ENSMUSG00000054226	6	85911865	85930284	1	159	178	309	77	195	77	44	347	123	93	100		Q8QZZ7
ENSMUST00000067143	ENSMUSG00000054236	7	108080796	108081734	1	13	3	8	3	6	0	0	0	0	0	0		Q8VGI5
ENSMUST00000067145	ENSMUSG00000083012	5	143548706	143564531	1	29	33	0	35	0	20	16	614	234	80	188		Q3ZN08
ENSMUST00000067150	ENSMUSG00000054252	5	33721674	33737068	1	0	0	0	0	0	0	0	0	0	0	0	Q7TSI8	
ENSMUST00000067161						3	0	4	61	4	1	0	0	0	0	0		
ENSMUST00000067167	ENSMUSG00000054237	19	38188481	38224138	-1	3	4	6	109	10	2	8	50	17	37	23		Q8BP78
ENSMUST00000067168	ENSMUSG00000054256	5	115429599	115455698	1	3	0	1	72	2	5	0	0	0	0	0	F8WJA5	
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ENSMUST00000067176	ENSMUSG00000054258	13	41655697	41656524	1	9	6	15	10	9	11	0	0	0	0	0	B2RV89	
ENSMUST00000067178	ENSMUSG00000050122	1	37026596	37187613	1	5	0	21	12	14	0	0	0	0	0	0	Q8BH17	
ENSMUST00000067186						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000067190	ENSMUSG00000054263	15	7129559	7197489	1	0	0	0	36	0	0	4	0	50	0	67		P42703
ENSMUST00000067198	ENSMUSG00000054266	13	33192959	33203129	1	2	2	1	4	5	1	0	0	0	0	0	Q8BMT0	
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ENSMUST00000067210	ENSMUSG00000090714	7	11161374	11166182	-1	2	8	9	6	9	1	0	0	0	0	0		A7KBS4
ENSMUST00000067215	ENSMUSG00000054277	15	83299740	83350247	-1	18	10	45	54	33	11	304	420	373	57	255		
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ENSMUST00000067219	ENSMUSG00000025592	X	113297510	113836386	1	0	0	0	0	0	0	0	0	0	0	0		Q925Q8
ENSMUST00000067230	ENSMUSG00000076431	13	28948919	28953713	-1	37	35	177	569	49	22	25	42	24	15	72		Q06831
ENSMUST00000067232	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0		P30999
ENSMUST00000067240	ENSMUSG00000000409	4	129548344	129573641	-1	8	10	26	17	12	0	0	0	0	0	24		P06240
ENSMUST00000067246	ENSMUSG00000021629	13	100802649	100833427	-1	13	9	17	76	20	5	180	787	333	128	301		Q8R4H9
ENSMUST00000067249	ENSMUSG00000054293	X	107148927	107173661	1	1	1	4	2	14	1	18	37	0	1	0	Q8BY68	
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ENSMUST00000067258	ENSMUSG00000050541	11	43774606	43901210	-1	35	28	0	8	35	25	0	0	0	0	0	Q9DBL0	
ENSMUST00000067268	ENSMUSG00000029528	5	115506676	115555987	1	0	0	6	0	0	5	14082	18135	11416	1063	8895		Q8VI36
ENSMUST00000067272	ENSMUSG00000054302	12	54670340	54695897	-1	0	0	0	32	0	0	16	4	10	60	0	F8WGY8	
ENSMUST00000067277						31	18	53	58	24	13	1	5	7	1	5		
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ENSMUST00000067288	ENSMUSG00000054310	7	15388948	15556866	1	24	10	0	15	9	15	0	0	0	0	0	Q9D350	
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ENSMUST00000067305	ENSMUSG00000054320	8	105413571	105464086	1	13	12	14	10	26	9	1	0	0	0	0		Q3V0M2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000067307	ENSMUSG00000039578	6	61180324	62382865	1	0	0	1	0	0	1	0	0	0	0	0	A0A0H2UKC3	
ENSMUST00000067318	ENSMUSG00000054325	3	92925287	92926230	-1	3	4	6	8	2	0	0	0	0	0	0	Q497I5	
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ENSMUST00000067384	ENSMUSG00000054364	12	8497763	8499985	-1	7	5	28	397	26	5	2060	3659	1468	202	1345	Q4FJM5	P62746
ENSMUST00000067386	ENSMUSG00000049643	7	27553233	27582099	1	21	13	0	84	26	11	286	249	174	22	154	G5E8E3	
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ENSMUST00000067404	ENSMUSG00000040242	6	146577203	146599198	1	18	12	0	15	0	9	362	1271	1000	161	560		Q9CRA9
ENSMUST00000067410	ENSMUSG00000062393	X	6779306	6948363	1	22	13	31	33	16	0	0	0	0	0	0	E9Q7N4	
ENSMUST00000067414	ENSMUSG00000009418	1	135434580	135607295	-1	37	74	0	240	0	73	0	0	0	0	0		Q8CH77
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ENSMUST00000067425	ENSMUSG00000054381	7	127372537	127376050	-1	26	17	71	124	37	9	89	331	176	46	134	Q8BHM7	
ENSMUST00000067426	ENSMUSG00000037628	14	46760541	46771525	1	2	1	8	53	11	6	73	181	126	267	51		Q810P3
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ENSMUST00000067437						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000067444	ENSMUSG00000020932	11	102887336	102900912	-1	13	9	31	52	25	16	0	0	0	0	0		P03995
ENSMUST00000067458	ENSMUSG00000022231	15	32244813	32696341	1	88	77	236	248	73	38	1	0	0	2	28	Q3UPZ0	
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ENSMUST00000067496	ENSMUSG00000054428	4	132530555	132533659	-1	2	0	0	23	4	0	354	840	367	2574	254		O35143
ENSMUST00000067503	ENSMUSG00000054431	6	42817473	42818405	1	2	4	21	5	3	2	0	0	0	0	0	Q8VF81	
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ENSMUST00000067506	ENSMUSG00000054435	6	48684549	48692060	1	0	3	4	0	0	0	0	0	0	0	0		Q99JY3
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ENSMUST00000067530	ENSMUSG00000054455	2	173737511	173784336	1	38	40	62	83	51	21	571	1624	853	232	646	Q8BH80	
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ENSMUST00000067543	ENSMUSG00000032501	15	59648350	59656550	1	26	15	39	323	32	16	695	2752	716	67	1127		Q8K4K4
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ENSMUST00000067584	ENSMUSG00000039501	2	167035793	167063015	-1	25	25	65	7	47	9	630	932	603	63	561	A2A5R6	
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ENSMUST00000067620	ENSMUSG00000015970	14	30009023	30040466	1	34	18	70	142	57	23	39	40	60	7	33		Q8BJ64
ENSMUST00000067621	ENSMUSG00000079741	9	124348831	124354028	1	3	3	1	4	7	2	0	0	0	0	0	F8VQK0	
ENSMUST00000067625	ENSMUSG00000062310	1	88499871	88510066	-1	44	19	88	182	36	16	2	5	1	33	10	E9Q9S8	
ENSMUST00000067630	ENSMUSG00000027900	3	106547798	106575890	1	38	29	99	28	42	33	26	68	11	31	50		Q9CR48
ENSMUST00000067631	ENSMUSG00000049922	2	92452764	92460538	-1	23	3	35	188	29	21	508	372	320	46	338		Q8BLX4
ENSMUST00000067632	ENSMUSG00000054517	11	116121846	116131128	-1	0	0	75	0	10	0	18	34	21	7	47		Q8BFW4
ENSMUST00000067638	ENSMUSG00000054520	5	34525838	34563641	1	11	14	7	0	0	0	1038	2079	1202	111	649	Q5U3L0	
ENSMUST00000067646	ENSMUSG00000032178	9	21368019	21405361	1	26	25	68	37	43	14	113	160	154	24	151		Q9Z1X4
ENSMUST00000067663	ENSMUSG00000002102	2	91054009	91066369	1	0	3	0	41	5	2	616	911	582	821	510		O88685
ENSMUST00000067664	ENSMUSG00000020849	11	75732869	75765845	1	8	11	25	56	10	8	2108	7885	2634	876	1608	Q5SS40	P62259
ENSMUST00000067670	ENSMUSG00000054526	19	13827435	13828459	-1	9	5	14	7	8	4	0	0	0	0	0	Q7TQQ3	
ENSMUST00000067673	ENSMUSG00000054523	19	11273238	11283873	-1	0	1	0	0	7	0	0	0	0	0	0	Q810P8	
ENSMUST00000067680	ENSMUSG00000054555	7	133883199	134232146	-1	79	48	140	96	49	17	0	0	2	1	2		Q61824
ENSMUST00000067689	ENSMUSG00000047888	15	80711319	80941086	1	209	145	688	425	241	114	1226	2663	3298	162	3294		Q8BKI2
ENSMUST00000067692	ENSMUSG00000007646	11	87376645	87404954	-1	121	100	1417	228	115	43	10	59	13	0	38		Q924H5
ENSMUST00000067695	ENSMUSG00000054568	7	104857009	104862667	1	310	300	476	10428	442	259	8	48	11	0	19		Q61068
ENSMUST00000067700	ENSMUSG00000058690	14	36874936	36968777	-1	5	1	0	0	0	0	261	561	391	48	264		Q3UHI0
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ENSMUST00000067708						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000067737						2	5	4	4	5	1	2	27	6	4	14		
ENSMUST00000067741	ENSMUSG00000004633	6	54039554	54301810	1	19	14	60	23	28	9	0	10	0	2	5		Q80XD1
ENSMUST00000067743	ENSMUSG00000054589	18	62180126	62184405	1	6	12	31	29	13	3	45	111	71	129	50	Q8C9F4	
ENSMUST00000067744	ENSMUSG00000054604	16	64851996	64859507	1	9	10	25	52	12	9	1153	3045	962	137	701		Q8BHG9
ENSMUST00000067752	ENSMUSG00000054619	15	100304817	100314348	1	12	10	38	93	35	13	375	1096	511	82	347	Q8C6B0	
ENSMUST00000067754	ENSMUSG00000020732	11	115091431	115162236	1	0	0	0	0	0	0	0	8	8	0	5	Q8BQX0	
ENSMUST00000067757	ENSMUSG00000027695	3	27938695	28133362	1	25	20	0	0	11	9	0	372	0	0	0	Q6NVF2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000067760	ENSMUSG00000022253	15	9071260	9110487	1	3	0	0	0	0	0	22	18	11	0	61		Q8C5H8
ENSMUST00000067763	ENSMUSG00000054626	X	53777118	53797706	-1	0	1	1	0	0	0	18	5	9	12	0	Q544L6	P05531
ENSMUST00000067778	ENSMUSG00000021360	13	40859768	40960891	1	13	19	91	97	31	23	3911	18940	7389	1611	7209	Q7TPQ8	
ENSMUST00000067780	ENSMUSG00000027201	2	125084628	125123661	-1	0	0	0	0	0	0	0	43	0	0	0		Q8C854
ENSMUST00000067782	ENSMUSG00000054626	X	53777118	53797706	-1	40	24	58	38	42	24	2	3	4	3	4	Q8BS74	
ENSMUST00000067784	ENSMUSG00000059674	14	54631992	54641364	-1	23	7	34	237	28	18	4	19	15	4	22		Q6PFX6
ENSMUST00000067786	ENSMUSG00000037656	8	22476700	22569607	1	21	16	48	40	42	14	63	106	61	35	133		Q80UP8
ENSMUST00000067790	ENSMUSG00000054630	5	87124960	87140318	-1	9	8	4	3	13	0	0	0	0	10	0	Q8K169	
ENSMUST00000067795	ENSMUSG00000025019	19	41482645	41562246	1	11	7	57	38	18	7	84	99	191	19	124	A4FTY7	Q6ZPI3
ENSMUST00000067801	ENSMUSG00000024039	17	31612623	31637199	-1	19	18	34	69	39	8	0	0	0	0	0		Q91WT9
ENSMUST00000067821	ENSMUSG00000021470	13	63815240	63900302	1	0	0	0	0	0	0	0	0	0	0	0		Q9JIM3
ENSMUST00000067826	ENSMUSG00000055817	17	83706163	83821516	1	31	31	151	51	21	18	193	826	506	101	399		Q924K8
ENSMUST00000067836	ENSMUSG00000054662	7	141101219	141117806	-1	20	27	46	25	38	10	0	0	0	2	4		P86044
ENSMUST00000067837	ENSMUSG00000029634	5	146209192	146221555	-1	5	0	0	0	12	2	88	12	478	222	390		Q9DBU5
ENSMUST00000067840	ENSMUSG00000054666	17	33268722	33269676	1	10	5	7	5	5	1	0	0	0	0	0	A0PK62	Q8VBW9
ENSMUST00000067841	ENSMUSG00000054667	X	141710998	141725263	-1	16	10	41	153	29	11	0	0	0	0	0		Q9Z0Y7
ENSMUST00000067843	ENSMUSG00000021972	14	64811600	64949871	-1	12	0	0	0	15	11	39	117	125	9	116		Q8BJA3
ENSMUST00000067853	ENSMUSG00000054675	5	113793729	113800516	-1	11	7	30	50	23	8	9	17	3	24	24		Q8R138
ENSMUST00000067854	ENSMUSG00000054676	7	38183217	38197568	1	31	3	0	0	0	9	2218	3120	1701	319	1392		Q8WUR0
ENSMUST00000067857	ENSMUSG00000020085	10	61715263	61739260	1	0	0	0	0	0	3	72	72	47	13	67		Q8BUE4
ENSMUST00000067864	ENSMUSG00000054679	4	33208991	33233340	1	24	12	97	60	25	20	0	1	0	0	3		Q8C8K3
ENSMUST00000067872	ENSMUSG00000005107	5	38349273	38503143	-1	0	0	0	18	0	0	0	40	0	0	0	B9EHN5	
ENSMUST00000067880	ENSMUSG00000054693	9	70678997	70780229	1	7	11	19	2	10	7	1506	3172	1250	263	873		O35598
ENSMUST00000067886	ENSMUSG00000005107	5	38349273	38503143	-1	18	0	26	0	19	14	44	36	67	15	55	Q3T9X0	
ENSMUST00000067888	ENSMUSG00000029735	6	43345001	43666278	-1	0	0	0	51	0	1	3	20	13	10	0		Q9R0M5
ENSMUST00000067896	ENSMUSG00000006390	4	118428093	118432953	1	4	2	5	4	2	3	128	271	50	0	173	Q548M4	Q9JLJ5
ENSMUST00000067902	ENSMUSG00000043257	4	133660387	133672647	-1	0	0	0	0	0	0	57	89	99	24	85		Q7TPN3
ENSMUST00000067908	ENSMUSG00000019944	10	69151434	69291791	1	0	0	0	0	0	0	0	0	0	0	0		Q9DAK3
ENSMUST00000067912	ENSMUSG00000055148	8	72319033	72321656	1	6	5	15	224	15	12	3563	11906	3387	707	3638		Q60843
ENSMUST00000067916	ENSMUSG00000026173	1	74542888	74567794	1	0	10	0	25	30	4	0	0	0	0	0		Q8K3R3
ENSMUST00000067917						0	0	0	50	0	0	0	0	0	0	0		
ENSMUST00000067918	ENSMUSG00000034613	10	122678762	122945795	1	30	26	71	45	51	17	234	613	317	23	280		Q3UYC0
ENSMUST00000067924	ENSMUSG00000054720	5	105519388	105613018	1	56	45	77	143	67	33	70	140	81	27	197		Q8R502
ENSMUST00000067925	ENSMUSG00000054717	8	57511843	57515999	1	31	34	43	169	57	21	5588	18730	7670	27425	5207		P30681
ENSMUST00000067927	ENSMUSG00000054733	14	64122623	64455903	-1	20	11	39	161	36	22	2422	5727	2301	1551	1242		Q9D6Y7
ENSMUST00000067929	ENSMUSG00000030759	7	113513834	113571511	1	7	5	23	0	12	5	36	0	13	27	43		Q922J9
ENSMUST00000067931	ENSMUSG00000054723	17	56713932	56717699	-1	0	0	0	93	0	9	0	0	0	0	23		Q8BP01
ENSMUST00000067935	ENSMUSG00000043614	5	135072900	135078266	-1	8	5	19	61	15	10	1	4	0	2	0		Q810I0
ENSMUST00000067936	ENSMUSG00000025132	11	120578104	120581624	-1	6	6	17	55	22	0	73	129	142	13	97		Q99PT1
ENSMUST00000067940	ENSMUSG00000054727	X	53742901	53757831	-1	2	2	8	3	6	1	0	0	0	0	0	Q9DAC5	
ENSMUST00000067947	ENSMUSG00000024290	18	10064401	10181792	-1	15	7	18	181	22	12	867	2619	1992	173	865		P70335
ENSMUST00000067955	ENSMUSG00000021905	14	32080566	32085692	-1	0	10	26	8	11	9	109	297	177	76	103		Q8K0W9
ENSMUST00000067972	ENSMUSG00000054758	10	56745134	56748254	1	14	10	37	8	10	9	0	0	0	0	0	Q8C3H7	
ENSMUST00000067975	ENSMUSG00000078945	13	100144063	100202092	-1	10	0	23	7	15	8	209	1462	84	209	170		Q9QUK4
ENSMUST00000067976	ENSMUSG00000026626	1	191351975	191403272	-1	56	35	66	564	65	35	4312	13979	6645	965	3676		Q6PD03
ENSMUST00000067978	ENSMUSG00000054759	7	142174535	142176005	-1	0	3	0	0	2	0	0	0	0	0	0	E9QML2	
ENSMUST00000067980	ENSMUSG00000074264	3	113555710	113606699	-1	0	0	0	0	0	0	0	0	0	0	0		P00687
ENSMUST00000067984	ENSMUSG00000054764	8	45069137	45088356	1	11	5	12	42	8	7	0	0	0	0	0	Q14AC3	Q61184
ENSMUST00000067987	ENSMUSG00000054745	18	24709040	24709348	-1	1	1	0	16	3	0	0	0	0	0	0	Q8CEJ8	
ENSMUST00000067990	ENSMUSG00000054763	14	63046991	63058149	1	4	0	0	0	2	0	0	0	0	0	0	Q8BVB5	Q8BVB5
ENSMUST00000067996	ENSMUSG00000054766	2	30057378	30072577	1	0	0	0	39	8	0	233	1051	327	218	309		Q9EQU5
ENSMUST00000067997						0	0	0	0	0	0	1	1	2	2	0		
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ENSMUST00000068004	ENSMUSG00000024892	19	4510472	4621752	1	0	0	0	77	16	0	37	0	0	0	0	E9QPD7	
ENSMUST00000068006	ENSMUSG00000039616	18	24653691	24701556	1	11	10	45	142	22	18	2705	3131	2083	347	1271		Q14CH1
ENSMUST00000068021	ENSMUSG00000020717	11	106654217	106750628	-1	13	15	32	29	20	7	44	61	82	10	82	B1ARB3	
ENSMUST00000068023	ENSMUSG00000054793	7	24482023	24504539	1	20	8	13	79	23	8	0	1	1	4	11		Q8R464
ENSMUST00000068025	ENSMUSG00000054792	9	110425926	110476694	-1	31	25	90	114	50	20	1435	2401	1870	156	1283	E9Q4F2	
ENSMUST00000068031	ENSMUSG00000020914	11	98992943	99024189	-1	15	11	14	26	9	4	459	716	978	906	555		Q01320
ENSMUST00000068036	ENSMUSG00000028747	4	139061108	139075570	-1	0	0	0	83	6	15	0	0	0	0	0	Q14AW8	Q9R1C8
ENSMUST00000068044	ENSMUSG00000022094	14	70303469	70351425	-1	31	20	81	40	46	26	60	148	66	32	236		Q75N73
ENSMUST00000068045	ENSMUSG00000054808	7	28893248	28962340	-1	0	0	16	102	18	20	1064	2033	1799	222	1677	Q3ULT2	P57780
ENSMUST00000068054	ENSMUSG00000006906	6	83543211	83572729	-1	22	22	141	42	29	11	136	464	173	149	121		Q9CQ26
ENSMUST00000068056	ENSMUSG00000019432	17	35241746	35253707	1	0	0	0	26	10	9	1044	1811	1009	231	982		Q9Z1N5
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ENSMUST00000068063	ENSMUSG00000078922	11	48985327	48994172	-1	0	0	0	29	16	0	15	81	34	82	48	Q62293	
ENSMUST00000068071	ENSMUSG00000054836	9	110305173	110322102	1	21	16	59	22	29	10	16	36	15	13	15	A0A0H2UH13	
ENSMUST00000068079	ENSMUSG00000045519	9	20345136	20385177	-1	70	48	117	187	105	86	10	35	17	8	17	Q3URI6	
ENSMUST00000068088	ENSMUSG00000054863	15	87625230	87759336	1	11	10	17	151	29	9	0	0	0	2	1		Q91WE9
ENSMUST00000068094	ENSMUSG00000054827	19	40089688	40113950	1	4	4	0	3	6	4	0	0	0	6	0		Q91X77
ENSMUST00000068106	ENSMUSG00000054850	X	56374586	56377799	1	23	9	39	157	44	8	0	1	0	0	3	A0A0B4J1F8	
ENSMUST00000068110	ENSMUSG00000029108	5	57717967	58133230	1	9	5	0	460	17	5	3	8	0	0	0	A2RS43	
ENSMUST00000068116	ENSMUSG00000026305	1	90998737	91128944	1	0	6	6	0	6	10	75	899	207	137	312	G5E8E1	
ENSMUST00000068125	ENSMUSG00000028411	4	40682382	40703194	-1	0	0	0	0	0	0	28	69	48	17	52		Q7TQC5
ENSMUST00000068133	ENSMUSG00000037992	11	98927818	98974942	1	0	0	0	4	0	0	49	185	90	0	55	Q3U3R3	P11416
ENSMUST00000068135	ENSMUSG00000031994	9	30942562	30963838	1	9	3	9	204	25	5	0	0	0	0	1	F8VQ15	
ENSMUST00000068137	ENSMUSG00000013523	2	170346991	170427845	-1	0	15	21	31	0	13	0	0	0	0	0	A2AVX1	
ENSMUST00000068140	ENSMUSG00000054871	9	123259058	123260789	-1	3	5	11	234	7	3	1	7	3	4	2	B2RTM1	
ENSMUST00000068143						1	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000068150	ENSMUSG00000020926	11	102761439	102780262	1	32	11	84	1144	74	11	2	0	0	0	11	Q7TQG7	
ENSMUST00000068156	ENSMUSG00000046230	19	16616763	16780822	-1	27	19	17	25	19	15	105	203	205	55	166		Q5H8C4
ENSMUST00000068158	ENSMUSG00000054885	4	42735545	42846248	1	0	5	0	3	0	0	0	1	9	0	3	Q9D4Q4	
ENSMUST00000068163	ENSMUSG00000054890	13	21555040	21556020	-1	5	2	1	5	5	3	0	0	0	0	0	Q7TQU0	
ENSMUST00000068167	ENSMUSG00000026305	1	90998737	91128944	1	0	0	21	35	6	0	20	37	93	9	49	E9Q9T1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000068168	ENSMUSG00000026004	1	66719248	66817562	-1	7	0	4	9	4	0	90	406	90	41	97		Q5DTI6
ENSMUST00000068169	ENSMUSG00000054874	19	5664635	5688908	-1	11	0	57	0	0	0	394	476	391	0	241		Q8VI59
ENSMUST00000068175	ENSMUSG00000054901	17	80307407	80388688	1	18	12	9	159	27	9	0	1	0	0	0		Q8BW86
ENSMUST00000068182	ENSMUSG00000054905	16	36450537	36455392	-1	8	1	14	26	6	13	12911	40932	23292	87496	10753		P35173
ENSMUST00000068214	ENSMUSG00000028373	4	65380803	66404611	-1	15	35	52	191	52	0	13	7	0	0	0		Q80Z10
ENSMUST00000068225	ENSMUSG00000027306	2	119618298	119651244	1	3	6	0	9	0	0	134	212	203	293	100		Q9ERH4
ENSMUST00000068233	ENSMUSG00000054934	10	116417861	116473878	-1	1	1	6	84	7	2	0	0	0	0	0		Q9JIN6
ENSMUST00000068235	ENSMUSG00000059395	13	21467047	21468509	-1	16	10	11	78	8	8	1	1	4	7	1	Q5SZT7	
ENSMUST00000068237	ENSMUSG00000038342	5	123394798	123457932	1	0	0	0	57	0	25	1887	993	2706	49	2530	G5E8D8	
ENSMUST00000068240	ENSMUSG00000029775	6	30401868	30455179	1	0	5	10	19	0	0	0	0	127	0	32		Q6PAR0
ENSMUST00000068242	ENSMUSG00000040649	6	122447296	122498761	-1	12	13	39	42	18	10	0	0	0	0	0		Q80WS1
ENSMUST00000068243	ENSMUSG00000054942	3	152273849	152340407	-1	0	0	0	0	6	0	0	41	0	0	0		Q4QQM5
ENSMUST00000068250	ENSMUSG00000054945	5	90367204	90368487	1	3	3	3	12	6	2	2	16	4	0	3	Q8C9U4	
ENSMUST00000068258	ENSMUSG00000054951	17	40875482	40880558	-1	12	15	67	109	19	5	3	5	6	4	3	Q9D2Z6	
ENSMUST00000068259	ENSMUSG00000029775	6	30401868	30455179	1	33	21	108	48	49	15	404	800	594	81	403		Q6PAR0
ENSMUST00000068261	ENSMUSG00000024403	17	35233660	35238767	1	5	0	4	3	6	3	29	166	42	0	33	Q54A87	Q9WTT4
ENSMUST00000068262	ENSMUSG00000054958	4	123201504	123216275	1	11	8	19	58	15	4	0	0	0	0	0		A3KFX0
ENSMUST00000068264	ENSMUSG00000020160	11	18879817	19018985	-1	0	0	0	0	0	0	13	25	5	4	13		Q60954
ENSMUST00000068271	ENSMUSG00000026817	2	32621758	32635058	1	0	0	15	6	3	0	2	1	0	15	0		Q9R0Y5
ENSMUST00000068275	ENSMUSG00000054976	1	81076950	81341764	1	9	9	15	9	3	13	0	0	0	0	0		
ENSMUST00000068277						3	0	1	7	4	1	0	0	0	0	0		
ENSMUST00000068282	ENSMUSG00000059811	17	79848392	79896123	-1	0	0	46	75	0	0	125	460	212	244	147		Q6PA06
ENSMUST00000068286	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	14	0	0	0	0	Q540G0	Q62406
ENSMUST00000068291	ENSMUSG00000067235	17	35470089	35474563	1	1	3	6	40	0	0	226	248	152	38	73		P01898
ENSMUST00000068293	ENSMUSG00000043298	6	136829927	136835452	-1	14	5	3	2	5	2	0	0	0	0	0		Q8BQM7
ENSMUST00000068296	ENSMUSG00000060510	9	20495068	20521417	-1	3	0	0	0	0	0	13	13	26	8	12	E9Q2S7	
ENSMUST00000068301	ENSMUSG00000040774	3	106502260	106547802	-1	0	0	0	4	0	0	66	402	44	76	13		Q8BGS7
ENSMUST00000068302	ENSMUSG00000058349	6	132802818	132803975	1	1	0	1	1	1	0	0	0	0	0	0		Q7M715
ENSMUST00000068304	ENSMUSG00000005886	1	13139105	13374083	-1	0	0	0	0	0	0	611	1162	1131	104	944	E9PV80	
ENSMUST00000068307	ENSMUSG00000054978	9	65388684	65391652	-1	20	14	30	176	22	14	1	1	1	0	0		Q8C828
ENSMUST00000068316	ENSMUSG00000054988	3	20314473	20367177	-1	16	23	63	15	18	13	0	0	0	0	1		P29755
ENSMUST00000068317	ENSMUSG00000029630	5	145977194	146009618	-1	6	2	0	0	3	2	0	0	0	0	0		O09158
ENSMUST00000068322	ENSMUSG00000054986	11	4064841	4077736	1	24	20	25	41	34	21	0	2	1	0	1	Q5SQ27	
ENSMUST00000068326	ENSMUSG00000032754	5	120511168	120534024	1	15	46	23	140	68	0	694	691	595	169	380		Q925Q3
ENSMUST00000068333	ENSMUSG00000026245	1	78417975	78488897	-1	8	11	16	34	16	0	37	72	54	130	0		Q9WUA2
ENSMUST00000068340	ENSMUSG00000054994	X	135494588	135504594	1	0	15	0	3	0	0	0	0	0	0	0	A2AWL3	
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ENSMUST00000068355	ENSMUSG00000043972	17	42556783	42611313	-1	10	7	22	6	10	2	0	0	0	0	0		Q6VZZ7
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ENSMUST00000068367	ENSMUSG00000032396	9	64306756	64341288	-1	0	0	0	41	33	0	0	0	0	0	0		Q8C0S1
ENSMUST00000068378	ENSMUSG00000055022	15	92051165	92341967	1	11	8	0	5	0	5	0	0	0	0	0		P12960
ENSMUST00000068387	ENSMUSG00000055024	15	81585351	81652077	1	35	33	95	71	46	25	2970	3601	6583	211	4730		B2RWS6
ENSMUST00000068388	ENSMUSG00000031921	8	107069400	107096547	-1	7	0	7	14	0	0	0	10	17	0	15	E9QM06	
ENSMUST00000068394	ENSMUSG00000055026	7	56716465	57387188	-1	4	4	13	4	5	5	0	0	0	0	0	Q8BQW9	
ENSMUST00000068397	ENSMUSG00000055015	16	11901363	11930600	1	3	2	8	6	5	4	0	0	0	0	0	Q8BNV2	
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ENSMUST00000068403	ENSMUSG00000055033	1	174158722	174159767	1	10	3	11	4	9	2	0	0	0	0	0	E9Q4G0	
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ENSMUST00000068411	ENSMUSG00000021182	12	100912700	101028983	-1	47	33	3	210	99	0	2199	2409	4536	145	3173		Q6VGS5
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ENSMUST00000068421	ENSMUSG00000031921	8	107069400	107096547	-1	0	0	0	5	0	0	13	199	49	25	111		O35144
ENSMUST00000068423	ENSMUSG00000024647	18	86711110	86718283	1	0	0	0	4	0	0	0	0	0	0	0		Q8BGU2
ENSMUST00000068437						8	0	0	0	8	3	0	0	0	0	13		
ENSMUST00000068439	ENSMUSG00000055044	19	40221173	40271842	-1	9	14	18	40	34	5	40	49	18	21	16		O70400
ENSMUST00000068448	ENSMUSG00000055072	11	79296179	79296906	-1	415	386	299	102	202	80	0	5	10	5	7	E9Q9S5	
ENSMUST00000068449	ENSMUSG00000055069	9	53684110	53706232	-1	6	5	15	93	14	12	17	44	29	20	24	Q0PD15	Q8BHD0
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ENSMUST00000068452	ENSMUSG00000036550	8	95719451	95807462	-1	43	34	51	47	59	25	90	327	552	239	642	B7ZWL1	
ENSMUST00000068456	ENSMUSG00000055078	7	57407672	57510059	-1	19	11	32	51	21	7	0	0	0	0	0		Q8BHJ7
ENSMUST00000068457	ENSMUSG00000036167	15	93398350	93491913	1	44	0	0	0	0	0	244	603	344	80	260	Q3UBL8	
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ENSMUST00000068505	ENSMUSG00000026509	1	182467260	182517608	-1	11	8	25	34	18	6	280	755	479	151	668		O08529
ENSMUST00000068508	ENSMUSG00000024160	17	24886643	24892152	1	0	0	0	0	1	0	0	0	2	0	0		Q571F5
ENSMUST00000068513	ENSMUSG00000040272	2	93833467	93849943	-1	2	0	0	0	0	0	13	0	2	4	6		A2AIG8
ENSMUST00000068515	ENSMUSG00000055114	15	58341874	58364148	-1	4	8	10	6	5	5	0	0	0	0	0	F6ZSM3	
ENSMUST00000068519	ENSMUSG00000021133	12	80790532	80880832	1	20	15	72	142	32	26	2331	4719	3866	287	2490		Q8BGE4
ENSMUST00000068526						12	6	14	0	14	5	0	0	0	0	0		
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ENSMUST00000068532	ENSMUSG00000055128	14	46832134	46854193	1	7	5	8	50	10	3	121	384	152	232	104		Q8BMJ7
ENSMUST00000068545	ENSMUSG00000055137	13	16857855	17694732	-1	1	4	2	41	5	2	1	3	2	4	3		Q7TNE1
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ENSMUST00000068551	ENSMUSG00000031362	X	73233688	73243130	-1	15	5	23	13	17	5	0	4	3	2	2	Q3TKR2	
ENSMUST00000068563	ENSMUSG00000029098	5	35583040	35615352	1	12	10	22	20	15	5	203	346	378	12	429	Q8C178	
ENSMUST00000068564	ENSMUSG00000026430	1	131176410	131245258	-1	24	11	75	73	36	14	7049	15122	9430	1775	7481		Q5EBH1
ENSMUST00000068567	ENSMUSG00000039697	10	30645584	30803107	-1	24	15	30	75	23	9	25	67	45	22	60		Q6DFV7
ENSMUST00000068569	ENSMUSG00000089929	9	89199209	89207827	1	7	3	2	0	0	3	11	40	5	453	71	Q497M6	
ENSMUST00000068580	ENSMUSG00000096445	17	23880876	23882853	1	6	7	4	1	10	6	0	0	0	0	0	L7N1X9	
ENSMUST00000068581	ENSMUSG00000050953	10	56377300	56390419	1	24	19	43	17	36	11	5	7	5	316	274		P23242
ENSMUST00000068583	ENSMUSG00000030232	6	140622663	140678472	1	0	0	0	0	0	0	27	43	144	6	75		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000068584	ENSMUSG00000015355	1	171682009	171705258	1	6	5	4	3	4	0	91	838	164	745	215		P18181
ENSMUST00000068586	ENSMUSG00000040434	2	92365046	92374869	-1	0	0	0	20	0	2	0	0	0	0	0		Q5XPT3
ENSMUST00000068592	ENSMUSG00000055170	10	118441047	118445892	1	4	2	6	3	3	4	0	1	0	4	0		P01580
ENSMUST00000068593	ENSMUSG00000055172	6	124512405	124523443	1	41	29	49	38	40	22	32	117	56	69	233		Q8CG16
ENSMUST00000068595	ENSMUSG00000060988	2	54436317	55118309	1	0	0	0	0	0	0	0	0	0	0	0	A2RRI8	Q8CF93
ENSMUST00000068603	ENSMUSG00000021676	13	95627177	95891922	-1	40	22	54	159	34	15	851	2501	2834	502	1769		Q3UQ44
ENSMUST00000068613	ENSMUSG00000055184	1	131527903	131539872	1	13	11	9	165	15	8	9	28	11	4	7		Q8BFZ8
ENSMUST00000068617	ENSMUSG00000040557	5	134932368	134942637	1	0	0	16	0	0	5	0	0	0	0	0	Q8BY07	
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ENSMUST00000068641	ENSMUSG00000055200	7	27473768	27477364	1	15	10	66	41	20	5	732	1161	564	129	362	Q3UYB0	Q9ERC3
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ENSMUST00000068663						37	46	69	44	41	22	10	58	21	3	41		
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ENSMUST00000068681	ENSMUSG00000026259	1	87476834	87573870	-1	22	16	38	11	42	14	0	0	0	0	0	E9QK62	
ENSMUST00000068686	ENSMUSG00000006056	11	96099326	96111964	-1	10	10	24	12	5	0	0	0	0	0	0		A2A6M5
ENSMUST00000068690	ENSMUSG00000057337	10	60181532	60219260	-1	97	93	434	7	79	52	18	18	0	24	91		O88199
ENSMUST00000068693	ENSMUSG00000055235	5	24711738	24730727	-1	10	10	17	125	16	7	3	0	0	3	2	D3Z757	
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ENSMUST00000068700	ENSMUSG00000066357	9	108572311	108578739	-1	39	32	110	139	63	29	68	93	66	14	159		Q99ME2
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ENSMUST00000068705	ENSMUSG00000026566	1	165592240	165634538	-1	0	9	7	12	10	0	24	33	13	15	0		
ENSMUST00000068714	ENSMUSG00000024241	17	80393752	80480453	-1	25	25	70	131	32	17	182	409	306	19	235		Q62245
ENSMUST00000068725	ENSMUSG00000073481	1	184813068	184846451	-1	0	5	1	24	3	0	0	0	0	0	0		Q922Q1
ENSMUST00000068726	ENSMUSG00000005506	2	90940382	91019497	1	27	0	0	0	49	0	0	109	96	31	319		
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ENSMUST00000068767	ENSMUSG00000040601	7	26435113	26476142	1	21	21	62	25	13	14	0	0	0	0	1	B2RUQ7	Q8BU40
ENSMUST00000068783	ENSMUSG00000052471	16	91168197	91171401	-1	27	38	87	72	36	25	0	3	0	0	5	Q8BR56	
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ENSMUST00000068792	ENSMUSG00000055296	4	56866923	56947437	-1	970	998	1746	1310	1091	499	120	310	253	77	304		B1AZA5
ENSMUST00000068795	ENSMUSG00000055302	5	36794867	36796772	-1	26	22	35	337	33	13	1155	5113	1360	654	973		Q9CQL7
ENSMUST00000068797	ENSMUSG00000079343	6	124624625	124636085	-1	22	3	22	23	28	8	0	0	0	14	2	W4VSN5	Q8CFG8
ENSMUST00000068798	ENSMUSG00000027942	3	90051636	90068347	1	0	0	0	0	0	0	78	471	126	262	132	H7BX33	
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ENSMUST00000068813	ENSMUSG00000055312	2	105224320	105379796	1	4	3	9	19	7	5	1	1	0	0	0	Q9DCP4	
ENSMUST00000068822	ENSMUSG00000028389	4	62189540	62208446	-1	284	186	1477	373	165	62	3	30	11	2	22		P17141
ENSMUST00000068825	ENSMUSG00000028954	5	24685532	24710378	1	14	23	39	37	31	14	1113	3315	1948	1454	1582	Q3UYM1	P54729
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ENSMUST00000068830	ENSMUSG00000062585	4	135895394	135920207	1	13	0	11	0	0	0	0	2952	0	0	29		P47936
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ENSMUST00000068851	ENSMUSG00000048766	4	112711147	112774866	-1	1	0	1	0	1	2	0	0	0	0	0	Q8CA07	
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ENSMUST00000068856	ENSMUSG00000055334	9	56950878	56983206	1	9	11	34	14	10	4	14	44	10	54	11		Q80W37
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ENSMUST00000068865	ENSMUSG00000055541	7	4003402	4063204	-1	12	12	37	2	7	0	50	360	129	227	108		Q8BG84
ENSMUST00000068874	ENSMUSG00000055357	X	169776257	169779635	-1	5	0	0	0	2	0	0	0	0	0	0	Q9CR52	
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ENSMUST00000068877	ENSMUSG00000055546	11	46810800	46844332	1	20	18	47	18	17	4	0	1	0	111	75		Q6U7R4
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ENSMUST00000068879	ENSMUSG00000044098	3	103914120	103966636	1	0	0	0	1	0	0	0	0	0	0	0		Q80T69
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ENSMUST00000068891	ENSMUSG00000038068	13	47122720	47247991	1	26	0	10	54	22	16	0	0	0	0	0		Q8BKD6
ENSMUST00000068892	ENSMUSG00000031575	8	25816191	25847694	-1	34	41	117	135	31	18	29	83	53	0	60		Q91X20
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ENSMUST00000068904	ENSMUSG00000023039	15	101411043	101430313	1	70	74	417	282	116	58	5	77	20	0	55		Q9DCV7
ENSMUST00000068911	ENSMUSG00000055026	7	56716465	57387188	-1	65	56	228	127	59	31	0	1	4	0	4		P27681
ENSMUST00000068916	ENSMUSG00000031570	8	25720061	25724887	1	0	0	0	0	0	0	0	0	13	17	13		Q3UMZ3
ENSMUST00000068933	ENSMUSG00000034520	11	102799579	102819700	-1	0	0	0	5	0	0	0	0	0	0	0		P28229
ENSMUST00000068938	ENSMUSG00000041730	14	32599407	32649246	1	6	7	15	36	0	4	0	0	0	0	0		Q8BYH0
ENSMUST00000068944	ENSMUSG00000050721	9	65554386	65580040	-1	19	8	75	49	41	22	5731	6273	4896	562	4255		Q8K124
ENSMUST00000068946	ENSMUSG00000055385	5	108729308	108774953	-1	2	0	3	0	1	1	0	0	0	0	0	Z4YJP7	
ENSMUST00000068947	ENSMUSG00000029098	5	35583040	35615352	1	9	7	18	37	20	13	2063	4921	2745	270	2056		Q9EPL9
ENSMUST00000068952	ENSMUSG00000028173	3	159839672	159938664	1	15	14	14	22	19	3	284	1437	497	267	425		Q6DID7
ENSMUST00000068958	ENSMUSG00000036533	17	79334025	79355091	-1	12	7	30	57	17	12	903	3894	1677	194	988		Q9CQC5
ENSMUST00000068962	ENSMUSG00000039607	9	116572746	117629913	-1	2	0	28	2	0	0	0	0	0	0	0		Q8BWL5
ENSMUST00000068967	ENSMUSG00000036466	9	64385626	64709205	1	25	27	42	9	23	17	1	4	7	0	12		Q80T91
ENSMUST00000068968						10	0	12	0	1	2	0	0	0	0	0		
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ENSMUST00000068975	ENSMUSG00000057101	7	24081924	24107713	1	69	46	168	111	60	30	139	578	312	155	245	Q6NZI9	
ENSMUST00000068980	ENSMUSG00000030509	7	66644565	66689596	-1	13	10	20	24	20	13	108	294	139	19	114	Q8BQC5	
ENSMUST00000068981	ENSMUSG00000020758	11	115974709	116008412	1	0	0	0	0	0	0	0	8	1	11	273		A2A863
ENSMUST00000068987	ENSMUSG00000055416	15	31276491	31276907	1	2	2	2	3	2	2	1	3	1	0	0		
ENSMUST00000068992	ENSMUSG00000055421	14	93013410	93890679	-1	4	7	36	0	2	14	0	0	0	0	0	F8VPK8	
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ENSMUST00000068996	ENSMUSG00000040139	7	137375574	137410762	-1	0	0	0	6	0	0	42	96	36	46	38	Q9CX25	
ENSMUST00000068997	ENSMUSG00000055424	5	31240675	31241232	-1	0	0	1	82	0	0	0	1	0	0	1	F6ZED4	
ENSMUST00000068999	ENSMUSG00000039478	8	40307458	40386308	1	3	3	2	227	15	5	1	2	0	3	1		Q9CTY5
ENSMUST00000069000	ENSMUSG00000032392	9	65214690	65239219	1	12	8	27	149	20	10	46	95	48	7	39		Q7TMM8
ENSMUST00000069004	ENSMUSG00000019891	10	52233619	52321378	1	0	0	0	42	0	0	0	16	14	0	6		Q9D4J3
ENSMUST00000069005	ENSMUSG00000020589	12	12262139	12376359	1	29	23	15	0	0	12	21	476	161	109	181		Q8BHZ0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000069009	ENSMUSG00000055435	8	115682942	115707794	-1	8	10	6	24	15	4	11	10	21	37	55		P54843
ENSMUST00000069011	ENSMUSG00000072115	14	51091077	51102007	1	0	0	4	5	5	1	3	0	0	0	2	Q3TBG7	P21570
ENSMUST00000069023	ENSMUSG00000018656	6	42584866	42597692	-1	16	18	27	23	25	8	1	4	9	0	9		Q6QR59
ENSMUST00000069025	ENSMUSG00000055436	3	158010473	158036639	-1	0	10	5	0	2	0	55	783	355	65	247	F6RDI8	
ENSMUST00000069035						6	5	7	10	2	3	0	0	0	0	0		
ENSMUST00000069036	ENSMUSG00000032575	9	106838312	106891979	-1	1	0	3	1	0	0	277	781	290	653	317	Q80ZP8	
ENSMUST00000069041	ENSMUSG00000031367	X	163909017	163933666	1	0	0	0	40	4	4	36	98	17	15	21		Q9DB50
ENSMUST00000069044						8	13	33	14	28	9	0	0	0	0	0		
ENSMUST00000069051	ENSMUSG00000055456	11	43035746	43037278	1	5	11	2	6	2	4	0	0	0	0	0	E9Q053	
ENSMUST00000069057	ENSMUSG00000017774	11	75650504	75673910	1	0	0	0	36	9	0	1136	1325	1189	137	1171		Q9WTI7
ENSMUST00000069058	ENSMUSG00000031730	8	109591343	109608673	-1	0	0	0	0	8	0	0	0	0	0	0		O35435
ENSMUST00000069063	ENSMUSG00000044537	10	129311165	129312108	1	0	0	1	4	5	1	0	0	0	0	0	E9PUS9	
ENSMUST00000069064	ENSMUSG00000041774	16	17144621	17160701	1	0	0	0	0	0	2	30	30	23	4	17		Q14BV6
ENSMUST00000069066	ENSMUSG00000020589	12	12262139	12376359	1	0	0	0	36	26	0	66	0	0	0	32		Q8BHZ0
ENSMUST00000069074	ENSMUSG00000017978	6	23262773	23839421	-1	0	0	0	0	0	5	0	0	0	0	0		
ENSMUST00000069077	ENSMUSG00000067768	X	73214333	73222453	1	0	0	0	0	0	0	17	10	3	5	0	Q9JJQ7	
ENSMUST00000069095						8	2	7	6	9	4	0	0	0	0	0		
ENSMUST00000069097	ENSMUSG00000028842	4	126331704	126429556	-1	46	40	70	61	71	23	65	133	145	28	175		Q8CJF9
ENSMUST00000069098	ENSMUSG00000055485	2	157015799	157079254	-1	45	40	117	481	78	35	14	7	4	9	117	A2ACV6	
ENSMUST00000069103	ENSMUSG00000067768	X	73214333	73222453	1	7	10	12	11	8	6	0	12	24	18	8	Q9JJQ7	
ENSMUST00000069106	ENSMUSG00000055493	10	11343404	11459644	1	18	14	25	140	26	15	9	29	19	11	13		Q9WUA5
ENSMUST00000069107	ENSMUSG00000063358	16	16983382	17047453	1	15	18	13	32	10	7	687	1665	748	140	519		P63085
ENSMUST00000069125	ENSMUSG00000049872	10	34091352	34096519	-1	10	10	24	5	11	7	0	2	0	0	0		Q8R100
ENSMUST00000069128	ENSMUSG00000046667	4	12140264	12146731	1	0	0	0	2	13	3	0	16	22	0	0		Q80YR9
ENSMUST00000069142	ENSMUSG00000025955	1	65012689	65032759	-1	0	0	0	0	0	3	0	0	0	0	0	Q3UXL1	
ENSMUST00000069148	ENSMUSG00000022860	16	78930948	78951733	1	5	8	14	10	5	3	0	0	0	0	0	Q8BVU2	
ENSMUST00000069168	ENSMUSG00000055531	10	117344673	117380015	-1	7	11	6	4	9	6	134	127	50	28	109		Q6NVF9
ENSMUST00000069169						7	10	17	3	0	0	214	957	75	26	81		
ENSMUST00000069174	ENSMUSG00000021712	13	104178797	104203372	1	8	7	15	24	7	4	0	0	0	0	0		Q8BGX0
ENSMUST00000069180	ENSMUSG00000055538	14	25711642	25769039	-1	7	14	29	123	14	7	36	29	36	29	100		B2RVL6
ENSMUST00000069183	ENSMUSG00000055523	19	55198297	55241236	-1	38	22	44	27	37	15	1	1	0	0	0		Q6TL19
ENSMUST00000069184	ENSMUSG00000036062	4	42916660	42944752	1	0	0	0	0	0	0	0	0	0	0	0		Q80TL4
ENSMUST00000069187	ENSMUSG00000021712	13	104178797	104203372	1	0	0	0	0	0	1	7	0	0	5	7		Q8BGX0
ENSMUST00000069188						0	0	7	1	0	8	10	10	0	13	69		
ENSMUST00000069195	ENSMUSG00000051351	4	136284683	136293942	1	82	52	363	373	73	37	195	319	257	28	175		Q8BPP0
ENSMUST00000069209	ENSMUSG00000055555	X	53724826	53738441	1	2	6	22	7	6	2	0	0	0	0	0	Q14BQ3	
ENSMUST00000069215	ENSMUSG00000041923	18	22693181	23041653	-1	0	0	0	0	3	0	0	0	0	0	0	F7BIN0	
ENSMUST00000069218	ENSMUSG00000038691	9	18478379	18485292	1	6	3	13	6	3	2	0	0	0	0	0	Q0P5Y0	Q9D9H3
ENSMUST00000069221	ENSMUSG00000032423	9	88447009	88482574	-1	9	10	13	13	14	16	64	52	12	33	43		Q7TMK9
ENSMUST00000069226	ENSMUSG00000022032	14	65666403	65764826	1	0	0	0	0	0	0	0	0	0	0	0		Q8K299
ENSMUST00000069236	ENSMUSG00000055571	7	86363376	86364335	-1	4	2	7	1	1	4	0	0	0	0	0	Q7TS02	
ENSMUST00000069245	ENSMUSG00000055561	18	43963235	44022501	1	15	13	13	8	16	5	0	0	0	0	0	Q148R4	
ENSMUST00000069250	ENSMUSG00000036036	17	37001163	37010635	1	0	0	0	0	5	0	0	0	0	0	0		Q8C6P8
ENSMUST00000069256	ENSMUSG00000055320	7	112679318	112906807	1	107	76	137	7	134	45	2	2	3	8	77	Q6PAQ8	
ENSMUST00000069259	ENSMUSG00000029601	5	120589016	120607118	1	0	9	73	0	0	0	3	4	1	6	2		Q9D3V1
ENSMUST00000069268	ENSMUSG00000056901	6	132762131	132763174	1	4	5	2	3	4	2	0	0	0	0	0	F8VPL4	
ENSMUST00000069271	ENSMUSG00000028610	4	107676290	107684230	-1	7	8	20	234	12	9	0	0	0	0	0		A2A9I7
ENSMUST00000069279	ENSMUSG00000055610	7	86335406	86336417	-1	5	3	4	1	2	2	0	0	0	0	0	Q8VFN8	
ENSMUST00000069281	ENSMUSG00000022684	16	13671858	13703612	1	6	0	0	0	0	5	0	202	0	41	28		Q8R079
ENSMUST00000069284	ENSMUSG00000022788	16	16416917	16600549	-1	0	0	0	0	0	0	250	569	819	226	331	F8WGX0	
ENSMUST00000069285	ENSMUSG00000041488	19	11775119	11819403	-1	2	10	42	53	15	13	80	361	106	92	123	Q3TBP0	Q64704
ENSMUST00000069289	ENSMUSG00000030380	7	13042303	13054764	-1	14	12	8	0	20	0	0	14	8	0	16	F6VC78	
ENSMUST00000069292	ENSMUSG00000030145	6	118427319	118455528	-1	65	43	118	453	86	65	1	12	3	6	3	Q640N4	
ENSMUST00000069293	ENSMUSG00000041144	1	46066315	46373546	1	30	44	13	22	39	34	0	0	0	0	0	L7N1Y0	
ENSMUST00000069298	ENSMUSG00000025188	19	42755105	42779978	-1	13	5	12	8	9	6	26	69	14	0	55	E9Q045	
ENSMUST00000069304	ENSMUSG00000007850	11	50376990	50386528	1	0	0	8	22	0	0	86	84	17	0	55	Q811L7	O35737
ENSMUST00000069309	ENSMUSG00000068457	Y	1096861	1245759	-1	0	0	0	0	0	0	18	0	0	23	0	G3X9F2	
ENSMUST00000069311	ENSMUSG00000029442	5	123252102	123327484	1	0	0	0	0	0	0	0	0	0	0	0	G3X9E9	
ENSMUST00000069324	ENSMUSG00000055633	7	5051532	5053722	1	3	5	10	204	8	6	5	13	3	1	3		Q9DB38
ENSMUST00000069325	ENSMUSG00000034706	11	114727408	114757889	1	5	4	0	19	6	3	0	0	0	0	0		A2AC93
ENSMUST00000069330	ENSMUSG00000001348	9	22126731	22135746	-1	12	3	0	70	11	6	43	77	54	55	115		Q05117
ENSMUST00000069333	ENSMUSG00000026031	1	58711508	58758884	1	0	0	0	0	0	0	35	0	316	0	99	Q812G4	
ENSMUST00000069334	ENSMUSG00000055639	14	97786853	98169765	-1	0	0	0	6	5	10	296	641	721	37	236		Q9QYB2
ENSMUST00000069342	ENSMUSG00000095839	9	39719229	39720167	1	4	7	2	4	6	3	0	0	0	0	0	Q7TRA7	
ENSMUST00000069343	ENSMUSG00000025576	11	118489762	118911597	-1	2	0	26	7	3	0	0	0	0	0	0		Q8BIF2
ENSMUST00000069345	ENSMUSG00000022817	16	33829665	33949153	1	0	13	0	0	0	18	0	24	0	0	0	G5E8F8	
ENSMUST00000069360	ENSMUSG00000055653	X	52272426	52613950	-1	2	5	7	3	4	0	498	499	455	130	100	Q3TWB2	Q8CFZ4
ENSMUST00000069372	ENSMUSG00000097327	10	22113050	22149270	-1	22	19	0	0	26	0	0	39	29	5	30	F6UW72	
ENSMUST00000069385	ENSMUSG00000017734	2	164486106	164493319	1	0	0	0	0	0	0	0	0	0	0	0	Q330P7	Q9CRD4
ENSMUST00000069395	ENSMUSG00000055670	11	72796226	72927120	1	54	4	86	0	13	1	48	0	0	42	20		Q5SSH7
ENSMUST00000069399	ENSMUSG00000055675	8	15011025	15033333	1	43	30	287	547	43	26	65	152	81	16	175		Q8BNW9
ENSMUST00000069408	ENSMUSG00000031933	9	14885814	14903949	-1	5	2	6	7	1	2	0	0	1	9	0	Q8BY83	
ENSMUST00000069417	ENSMUSG00000055691	X	160902116	160907052	-1	4	3	2	6	2	1	0	1	2	1	0		Q6S5G4
ENSMUST00000069419	ENSMUSG00000025090	19	58512002	58553085	1	5	3	4	18	6	2	0	0	0	0	0		Q810N9
ENSMUST00000069420	ENSMUSG00000055692	16	17276300	17283229	1	6	0	4	47	10	0	4	0	0	0	11		Q9JJB1
ENSMUST00000069423	ENSMUSG00000027239	2	91929805	91932297	-1	0	4	0	12	0	2	0	0	0	0	0		P12025
ENSMUST00000069430	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	0	0	0	2	0	E9Q3S2	
ENSMUST00000069431	ENSMUSG00000055704	10	78484570	78487842	-1	111	102	117	147	134	64	21	84	38	7	26	Q8C4R4	
ENSMUST00000069443	ENSMUSG00000055717	14	103650228	103704907	1	0	0	0	184	5	0	0	0	0	0	18		Q68FF7
ENSMUST00000069449	ENSMUSG00000055723	7	114046785	114117781	-1	12	12	20	91	11	8	47	115	68	90	76		P62071
ENSMUST00000069451	ENSMUSG00000055737	15	3317760	3583492	-1	6	6	3	8	3	8	3	3	1	3	20	Q3UP14	
ENSMUST00000069453	ENSMUSG00000055725	5	97082329	97111596	-1	4	3	9	1	6	3	6	22	12	0	14	Q0VAZ2	Q6TCG8
ENSMUST00000069456	ENSMUSG00000018501	11	62316426	62458541	-1	49	39	56	24	51	18	49	78	61	9	70	Q8BK32	
ENSMUST00000069457	ENSMUSG00000055732	13	40704005	40707949	1	33	25	109	73	36	21	0	2	0	0	1	G5E8F2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000069476	ENSMUSG00000055745	15	84553398	84557823	-1	46	21	71	253	54	25	45	26	34	6	43		Q505G4
ENSMUST00000069477	ENSMUSG00000055746	X	155027201	155093666	-1	9	6	0	4	0	7	0	0	0	0	0	Q9R2A2	
ENSMUST00000069483	ENSMUSG00000043323	5	110361754	110448503	-1	24	14	35	280	58	17	216	272	282	24	313	E9Q9T0	
ENSMUST00000069486	ENSMUSG00000055760	17	80224441	80228497	1	2	1	9	1	8	4	6	21	3	76	14		Q9CX53
ENSMUST00000069489						1	0	3	6	0	0	6	0	0	0	0		
ENSMUST00000069503	ENSMUSG00000020513	11	86544991	86567360	1	13	0	5	0	0	0	22	76	31	47	17	Q5SWF8	Q9R1K7
ENSMUST00000069507	ENSMUSG00000073418	17	34728380	34743882	-1	91	57	138	113	106	43	27	100	42	246	3040		P01029
ENSMUST00000069509	ENSMUSG00000055780	X	51753959	51801233	-1	7	7	19	3	15	1	0	0	0	0	0		Q99MX1
ENSMUST00000069511	ENSMUSG00000055782	15	91145884	91191807	-1	46	57	81	34	56	36	1019	3632	2136	1846	1316		
ENSMUST00000069520	ENSMUSG00000031144	X	7638471	7653256	1	7	7	9	47	16	6	67	206	72	34	63		Q62277
ENSMUST00000069529						1	1	3	1	1	1	0	4	1	4	0		
ENSMUST00000069530	ENSMUSG00000022471	15	81987835	82040085	1	0	0	0	0	0	0	33	106	53	142	63		
ENSMUST00000069533	ENSMUSG00000028656	4	122859047	122886056	-1	7	25	28	29	28	0	18865	52969	25575	6654	15162		P40124
ENSMUST00000069536	ENSMUSG00000055799	6	72626378	72789254	-1	15	8	7	268	23	18	0	0	0	2	5	A1A550	
ENSMUST00000069537	ENSMUSG00000030629	7	84615054	84679361	-1	8	0	0	0	5	0	10	80	80	34	17		Q9DCH6
ENSMUST00000069538	ENSMUSG00000056004	5	9266118	9481825	1	0	2	0	0	0	5	2	0	0	0	0	B9EHI9	Q3UZV7
ENSMUST00000069548	ENSMUSG00000040345	10	127323727	127329943	1	13	8	20	85	28	15	7526	12070	6168	1324	4573	Q8QZW8	
ENSMUST00000069549	ENSMUSG00000055811	16	88505807	88506978	-1	10	4	8	3	9	0	0	0	0	0	0		Q8BXA6
ENSMUST00000069552	ENSMUSG00000055795	18	14424868	14425311	1	4	0	1	1	4	1	0	0	0	16	3	F8VPN3	
ENSMUST00000069553						7	3	6	13	8	9	2	1	1	1	3		
ENSMUST00000069556	ENSMUSG00000079349	X	155053061	155063145	-1	6	0	16	0	10	0	0	0	0	0	0	O89009	
ENSMUST00000069557	ENSMUSG00000021540	13	56703010	56742377	1	18	12	31	14	30	15	102	274	176	59	218		P97454
ENSMUST00000069561	ENSMUSG00000055820	9	39750388	39751320	1	4	1	0	2	4	0	0	0	0	0	0	Q7TRA6	
ENSMUST00000069562	ENSMUSG00000055826	7	24333082	24333936	-1	9	7	13	90	13	6	0	0	0	0	0	Q9DAJ7	
ENSMUST00000069568	ENSMUSG00000026502	1	178187417	178257301	1	0	0	0	0	0	0	0	0	0	0	0	Q8C5I4	
ENSMUST00000069578	ENSMUSG00000055838	2	36996812	36997738	1	4	8	4	2	5	0	0	0	0	0	0	Q8VFP4	
ENSMUST00000069579	ENSMUSG00000055839	17	23824740	23829109	-1	3	8	22	23	12	12	1813	1888	945	4828	751		P62869
ENSMUST00000069580	ENSMUSG00000055850	6	72359714	72366956	-1	0	3	6	21	0	4	534	613	428	299	320		Q9CY62
ENSMUST00000069595	ENSMUSG00000055850	6	72359714	72366956	-1	0	1	1	0	0	0	0	637	0	0	0		Q9CY62
ENSMUST00000069597	ENSMUSG00000073563	18	53862113	53955684	1	13	7	9	39	18	5	168	706	349	96	227		Q8C4X2
ENSMUST00000069600	ENSMUSG00000027634	2	156927345	156992056	-1	16	0	0	0	0	13	0	0	0	0	20	Q8VCV2	
ENSMUST00000069604	ENSMUSG00000029009	4	148039077	148059551	1	35	25	80	32	41	19	279	303	288	11	286	A2A7F7	
ENSMUST00000069609	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	0	0	0		P25425
ENSMUST00000069614	ENSMUSG00000035910	13	25056004	25210706	1	58	47	277	86	65	29	1	14	8	2	8	R4GML1	
ENSMUST00000069616	ENSMUSG00000033825	17	25366550	25368094	1	5	5	19	10	12	8	0	0	0	5	4	E9QJW9	
ENSMUST00000069619	ENSMUSG00000025862	X	42149317	42277185	1	0	1	2	19	0	0	1335	2806	2265	1458	1108		O35638
ENSMUST00000069620	ENSMUSG00000055866	1	91415982	91459324	-1	43	31	105	190	52	29	754	554	785	77	1083		
ENSMUST00000069623	ENSMUSG00000040964	4	140514485	140666012	-1	5	8	33	40	23	6	0	0	0	0	28		A2AWP8
ENSMUST00000069626						1	2	3	0	0	0	0	0	0	0	0		
ENSMUST00000069631	ENSMUSG00000049287	11	59155369	59163739	-1	6	4	8	6	8	2	0	0	0	0	0	J3JS81	
ENSMUST00000069634	ENSMUSG00000055874	6	70956531	70961066	1	7	5	28	0	0	8	0	0	0	0	0	D3Z120	
ENSMUST00000069637	ENSMUSG00000055917	12	40315046	40445790	-1	0	0	3	6	0	0	6	33	19	91	4	Q3U0V6	
ENSMUST00000069648	ENSMUSG00000021767	14	21481434	21672478	1	0	0	36	81	12	0	0	84	0	0	0		Q8BRB7
ENSMUST00000069649	ENSMUSG00000055882	2	181493206	181494980	1	11	4	10	27	17	7	0	0	2	0	1		Q80YU0
ENSMUST00000069651	ENSMUSG00000056880	9	115909455	116076176	1	90	60	237	1316	138	87	5	17	3	3	3	E9QP13	
ENSMUST00000069652	ENSMUSG00000039318	1	185204117	185286759	1	7	11	0	0	15	0	78	158	105	16	103	E9QKE4	
ENSMUST00000069660	ENSMUSG00000032743	7	125707888	125874793	1	27	20	93	34	0	15	286	310	503	26	479		Q8C753
ENSMUST00000069673						30	13	88	9	43	6	234	152	470	17	482		
ENSMUST00000069674	ENSMUSG00000055900	4	116551633	116555936	-1	0	0	0	0	0	0	8	0	0	0	0		Q3KQJ0
ENSMUST00000069686	ENSMUSG00000021720	13	105149352	105271039	-1	14	11	32	8	16	9	7	11	9	4	14		Q3U827
ENSMUST00000069690	ENSMUSG00000021144	12	113098278	113137206	1	0	0	37	0	0	0	110	135	225	0	126	F8WHY8	
ENSMUST00000069692	ENSMUSG00000055917	12	40315046	40445790	-1	2130	3031	3538	1604	2041	977	113	650	245	268	156	E9Q6D6	
ENSMUST00000069695	ENSMUSG00000055912	6	72355447	72359762	1	0	0	9	11	4	0	0	11	8	0	6		Q91WN2
ENSMUST00000069705	ENSMUSG00000029165	5	30888694	30906965	1	5	7	15	48	7	2	0	7	3	0	12		Q09M02
ENSMUST00000069709	ENSMUSG00000055923	5	76873659	76905514	-1	9	7	0	0	0	0	0	0	2	0	16		Q80WC9
ENSMUST00000069711	ENSMUSG00000055926	2	119174509	119177575	1	75	47	359	177	79	34	12	37	31	14	57	B2RX56	
ENSMUST00000069712	ENSMUSG00000000827	2	181497142	181517966	1	0	0	0	0	0	0	174	184	183	311	143	Q8BKP1	
ENSMUST00000069718	ENSMUSG00000055932	8	91313532	91668439	1	15	11	11	39	27	9	141	204	142	31	151		Q8BGW1
ENSMUST00000069722	ENSMUSG00000009995	X	74281912	74290151	1	0	0	5	0	0	0	189	294	188	0	0	Q91WF0	
ENSMUST00000069731	ENSMUSG00000062170	X	68761839	68804567	1	0	0	0	0	0	0	0	0	0	0	0		Q80ZA7
ENSMUST00000069740	ENSMUSG00000055942	7	14659496	14665996	1	2	0	7	4	0	2	0	0	0	0	0	Q4KL20	
ENSMUST00000069742	ENSMUSG00000055945	17	8340406	8344112	1	24	0	70	259	19	8	13	0	0	0	15		Q6PAN7
ENSMUST00000069747	ENSMUSG00000055943	2	112454997	112472162	1	42	40	47	87	34	26	286	868	328	344	239	Q14C26	Q9EP72
ENSMUST00000069749	ENSMUSG00000024511	18	69979131	70141605	-1	6	4	9	73	0	4	3	7	1	24	17	Q549X4	Q99P58
ENSMUST00000069756	ENSMUSG00000021638	13	100496507	100552718	-1	5	2	18	55	5	4	0	0	0	0	0	B2RS24	Q61146
ENSMUST00000069760	ENSMUSG00000055933	19	11697055	11711874	1	0	2	3	0	0	0	0	0	0	0	0	G5E8D7	
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ENSMUST00000069763	ENSMUSG00000047344	X	9199902	9268085	1	6	8	8	253	24	5	0	0	0	0	0		Q8CD19
ENSMUST00000069768						8	2	6	170	4	2	0	0	0	0	0		
ENSMUST00000069769	ENSMUSG00000055960	4	112072016	112168076	1	0	0	0	0	0	0	0	0	0	0	0		A7TZF3
ENSMUST00000069772	ENSMUSG00000002781	7	45896941	45917413	1	0	0	8	9	0	0	15	37	25	0	50	G3X9F4	
ENSMUST00000069773						8	15	72	16	10	5	0	0	0	0	0		
ENSMUST00000069778						14	6	8	10	11	7	1	2	0	0	1		
ENSMUST00000069782	ENSMUSG00000021185	12	100779057	100896981	1	11	0	18	0	14	14	0	36	0	0	0		Q8BH86
ENSMUST00000069786						1	3	0	164	9	7	0	0	0	0	0		
ENSMUST00000069789	ENSMUSG00000059201	6	29060220	29073877	1	17	8	40	33	11	9	0	0	0	0	0	Q544U0	P41160
ENSMUST00000069790	ENSMUSG00000055971	11	73425037	73428477	-1	8	0	0	0	0	0	0	0	0	0	0	Q8VGT2	
ENSMUST00000069792	ENSMUSG00000002881	1	52457294	52500679	-1	16	0	0	46	0	0	246	231	214	0	227		Q61122
ENSMUST00000069794	ENSMUSG00000036202	2	52072837	52122383	1	10	16	10	10	12	9	37	43	51	5	39		Q6PR54
ENSMUST00000069799	ENSMUSG00000055980	1	82233101	82291416	-1	48	26	131	354	72	40	0	0	0	1	20	Q543V3	
ENSMUST00000069800	ENSMUSG00000055978	7	45648595	45666308	-1	20	16	43	18	27	6	0	1	0	0	7	A6H6C9	Q9JL27
ENSMUST00000069803	ENSMUSG00000089996	X	136955265	136958025	-1	1	0	0	0	3	0	3	0	1	0	0	A2AF31	
ENSMUST00000069805	ENSMUSG00000060671	3	89939481	89963508	-1	0	0	0	89	21	4	0	0	89	0	0		P98199
ENSMUST00000069808	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	0	50	99	0	49	39	Q99K73	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000069816	ENSMUSG00000049491	11	55124815	55151708	-1	2	2	5	7	8	2	0	1	0	0	0	Q810P4	
ENSMUST00000069817	ENSMUSG00000039262	2	32151082	32234537	1	89	41	238	300	96	59	666	493	1164	17	1341	F8WHT3	
ENSMUST00000069828	ENSMUSG00000031480	8	22227313	22261334	1	37	14	114	55	34	21	0	28	9	0	0		
ENSMUST00000069831	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	0	0	0	12	0	17	Q3UXF4	
ENSMUST00000069837	ENSMUSG00000056427	11	35121224	35708507	1	36	23	62	102	57	21	0	2	0	7	40		Q9WVB4
ENSMUST00000069852	ENSMUSG00000056008	11	94694498	94704499	-1	8	3	12	13	9	7	0	0	0	0	0	Q8C4D8	
ENSMUST00000069861	ENSMUSG00000049676	7	29181321	29214035	-1	21	11	28	13	25	14	0	14	0	0	6		E9Q355
ENSMUST00000069862	ENSMUSG00000056014	5	138622859	138652414	1	152	115	192	206	219	48	14	39	22	17	24	E9Q8G5	
ENSMUST00000069870	ENSMUSG00000017418	2	15049395	15082456	1	32	0	0	32	0	0	141	362	202	21	148	Q6NXZ5	
ENSMUST00000069877	ENSMUSG00000022420	15	79761453	79777849	-1	1	0	0	0	0	0	36	52	50	11	0	Q8CDT8	
ENSMUST00000069902	ENSMUSG00000025453	13	119335448	119408997	-1	0	8	13	0	0	0	47	184	98	28	26	Q8C9V5	
ENSMUST00000069912	ENSMUSG00000056043	7	35578993	35585582	-1	69	53	334	500	89	37	2	9	13	1	18		Q148R9
ENSMUST00000069922	ENSMUSG00000056050	1	183326725	183369553	-1	6	10	22	0	3	3	114	731	308	52	350	J3KMG3	
ENSMUST00000069926	ENSMUSG00000046699	X	64264885	64276996	-1	68	66	400	289	64	38	2	6	4	1	3	Q149A4	Q810B8
ENSMUST00000069927	ENSMUSG00000056054	3	90668978	90670035	1	59	98	507	1111	128	199	511436	1554660	325453	840251	66780	Q53X15	P27005
ENSMUST00000069929	ENSMUSG00000021493	13	55495795	55513676	-1	0	0	0	0	0	1	44	104	62	0	81		Q3TJD7
ENSMUST00000069936	ENSMUSG00000035270	16	56204313	56273756	1	98	92	387	94	88	50	12	90	24	12	38		Q80XH2
ENSMUST00000069937	ENSMUSG00000029403	5	92006074	92043883	-1	15	0	8	7	0	6	13	33	34	0	0		Q9QUK0
ENSMUST00000069941	ENSMUSG00000020490	11	58917908	58927158	1	201	172	1178	283	194	102	3	10	2	0	9		Q9JK39
ENSMUST00000069949	ENSMUSG00000004980	6	51460932	51469894	-1	0	4	0	155	9	3	682	3198	1916	1650	1498		O88569
ENSMUST00000069958	ENSMUSG00000021360	13	40859768	40960891	1	33	25	89	33	48	24	590	1615	1323	213	805		P97402
ENSMUST00000069960	ENSMUSG00000056071	3	90692632	90695721	-1	75	123	395	1153	224	426	380560	2169820	671897	3034730	352895	Q3UP42	P31725
ENSMUST00000069965	ENSMUSG00000020015	10	93160876	93241342	1	36	26	94	80	33	10	261	1341	445	85	427		Q8K0D0
ENSMUST00000069968	ENSMUSG00000021493	13	55495795	55513676	-1	0	0	0	0	0	0	255	156	122	30	0	Q8BVJ7	
ENSMUST00000069992	ENSMUSG00000056089	15	25414192	25414844	1	4	2	13	23	5	5	0	0	0	0	0	Q8C3D3	
ENSMUST00000069994	ENSMUSG00000056091	6	72097592	72154571	1	45	25	174	7	33	17	712	1565	732	306	677		O88829
ENSMUST00000070000	ENSMUSG00000057315	5	102481391	102897937	1	20	17	56	12	19	19	3	0	3	0	0	D3Z5T4	
ENSMUST00000070004	ENSMUSG00000031958	8	111623785	111630374	-1	8	9	29	38	0	0	4	27	4	4	2		Q7TNG8
ENSMUST00000070018	ENSMUSG00000028943	4	152120331	152152371	-1	0	0	0	0	0	0	0	0	0	0	0		Q9ET47
ENSMUST00000070021						129	160	843	91	101	69	2	19	7	7	4		
ENSMUST00000070028	ENSMUSG00000056115	2	51627511	51628408	1	6	5	2	7	4	3	0	0	0	0	0		Q7TQB0
ENSMUST00000070039	ENSMUSG00000056121	17	78377885	78418131	-1	16	0	0	105	17	8	108	324	167	60	153	Q3U049	Q6TYB5
ENSMUST00000070059	ENSMUSG00000056133	17	7363712	7385305	-1	15	3	15	2	13	11	0	0	0	0	0	B2RWK3	
ENSMUST00000070064	ENSMUSG00000056131	9	86554377	86571842	-1	0	1	0	0	0	0	0	0	0	0	0		Q9CYR6
ENSMUST00000070070	ENSMUSG00000032285	9	54698873	54716315	1	0	8	7	55	0	0	7	9	5	9	20		Q9JMC3
ENSMUST00000070080	ENSMUSG00000056124	18	20684599	20746404	-1	67	60	197	333	70	56	456	1690	791	67	500	Q3UUA9	Q9WVK5
ENSMUST00000070084	ENSMUSG00000056130	18	46559155	46574533	-1	12	19	40	23	28	18	47	227	104	21	91		Q8BJQ4
ENSMUST00000070102	ENSMUSG00000056155	8	84173733	84176552	-1	7	3	8	6	10	7	0	1	0	0	1		P60324
ENSMUST00000070112	ENSMUSG00000026895	2	36036326	36049406	-1	6	2	13	88	14	7	905	1454	888	524	596		Q9DCJ5
ENSMUST00000070116	ENSMUSG00000056153	18	88665224	88927481	-1	36	34	219	35	38	33	27	119	57	6	49		Q9JLY0
ENSMUST00000070117	ENSMUSG00000056167	9	114585878	114640200	-1	25	11	31	59	19	15	195	689	392	254	397		Q8BH15
ENSMUST00000070118	ENSMUSG00000024909	19	5473973	5481853	1	0	0	7	2	15	5	7	47	23	0	0	G5E8D6	
ENSMUST00000070124	ENSMUSG00000071516	13	21716422	21716814	1	3	2	2	202	30	9	0	7	0	0	0	B2RVF0	P22752
ENSMUST00000070125	ENSMUSG00000021919	14	32408203	32465909	-1	37	21	57	86	50	20	0	0	0	0	1	Q8BQV2	
ENSMUST00000070132	ENSMUSG00000056174	4	126286793	126314330	1	36	20	115	321	58	23	2	2	0	1	3		P25318
ENSMUST00000070135	ENSMUSG00000034006	18	80253292	80292725	1	0	0	0	0	0	0	868	812	412	118	240		Q80XM9
ENSMUST00000070139	ENSMUSG00000056162	18	84610509	84650084	-1	17	10	6	11	19	7	0	0	0	0	0		
ENSMUST00000070141	ENSMUSG00000079350	X	154985775	154995850	-1	2	9	0	5	4	3	0	0	0	0	0	O89012	
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ENSMUST00000070150	ENSMUSG00000045071	4	59626211	59761439	1	100	83	319	161	87	69	7	33	23	3	26	Q0P6E2	Q8C4P0
ENSMUST00000070152	ENSMUSG00000041920	11	109450855	109473598	-1	4	6	18	87	21	11	465	2036	583	155	795		B1AT66
ENSMUST00000070163	ENSMUSG00000056197	6	73468573	73469667	-1	3	4	1	7	2	2	0	0	0	0	0	Q9CR05	
ENSMUST00000070165	ENSMUSG00000063550	7	102134204	102210120	-1	11	19	20	33	29	14	411	722	973	31	693		
ENSMUST00000070166	ENSMUSG00000001700	18	56432132	56503792	1	11	12	19	118	21	16	39	160	37	84	143	Q9D2W5	
ENSMUST00000070172	ENSMUSG00000056185	19	5495278	5510489	-1	10	11	9	14	17	7	63	115	52	12	56		Q80ZJ7
ENSMUST00000070173	ENSMUSG00000056204	8	70646436	70659738	-1	42	22	137	130	76	32	76	60	34	18	40		Q9ESW8
ENSMUST00000070174	ENSMUSG00000046157	12	78961795	79007627	-1	0	0	48	0	12	0	0	0	38	0	54		Q8BFQ2
ENSMUST00000070178	ENSMUSG00000056203	6	42405434	42406526	1	12	1	5	6	4	4	2	8	5	0	21	B9EII2	
ENSMUST00000070181	ENSMUSG00000038855	1	180330485	180424802	1	36	28	138	403	94	26	1773	1826	1641	120	1796	B2RXC2	
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ENSMUST00000070200	ENSMUSG00000056220	1	149829618	149961290	-1	12	8	13	4	3	8	81	466	168	282	121	Q3UMQ1	P47713
ENSMUST00000070203	ENSMUSG00000036553	5	35697180	35739987	-1	12	4	60	62	18	0	370	89	309	28	300	G3X9F6	
ENSMUST00000070210	ENSMUSG00000013662	19	32672563	32712298	-1	5	8	14	21	5	5	238	1069	484	1037	284		Q9D5T0
ENSMUST00000070215	ENSMUSG00000056209	19	45747734	45749591	-1	6	4	8	37	0	3	93	278	70	112	131		Q9CPP0
ENSMUST00000070216	ENSMUSG00000056223	13	64917406	64923184	1	16	11	60	22	12	12	0	0	0	0	0		E9QAF0
ENSMUST00000070218	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	3	0	0	0	0	0	0		Q9DCB4
ENSMUST00000070219	ENSMUSG00000056214	18	80046895	80119640	1	21	12	49	91	29	11	2	4	6	1	9		Q9JK84
ENSMUST00000070223	ENSMUSG00000041722	1	21368331	21370845	1	6	7	0	0	13	5	2	0	0	1	0		Q4KL78
ENSMUST00000070246	ENSMUSG00000012126	4	134102570	134127593	1	16	5	68	21	23	13	0	7	2	0	0	I7HIQ5	
ENSMUST00000070256	ENSMUSG00000056258	15	65986387	66286224	-1	486	431	1318	688	636	351	10	22	15	7	22		Q8K3F6
ENSMUST00000070257	ENSMUSG00000020412	11	4637747	4685699	1	0	0	11	27	13	0	142	127	204	24	121		Q91WR3
ENSMUST00000070258	ENSMUSG00000056257	13	30974204	30975976	1	2	6	5	14	11	5	0	0	0	1	0	Q8BPB2	
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ENSMUST00000070300	ENSMUSG00000047648	10	11281330	11298052	1	0	2	0	21	0	0	80	425	241	29	84		Q8BJL1
ENSMUST00000070304	ENSMUSG00000056281	X	49885469	49886401	-1	1	1	0	0	8	1	0	0	0	0	0	Q7TQW3	
ENSMUST00000070313	ENSMUSG00000039410	4	154316125	154636873	-1	0	43	0	0	45	0	1	1	0	0	2		A2A935
ENSMUST00000070316	ENSMUSG00000056679	X	152343598	152368704	-1	72	29	94	202	66	31	0	0	0	0	0		Q6PI62
ENSMUST00000070323	ENSMUSG00000056296	14	13284780	13615459	1	8	0	15	27	7	4	0	0	0	1	0		Q8BGN8
ENSMUST00000070326	ENSMUSG00000038379	9	83834689	83872389	1	0	0	0	0	0	0	26	61	45	44	0		P35761
ENSMUST00000070328	ENSMUSG00000037833	14	40813789	40893266	-1	5	10	22	3	10	6	4	14	8	2	3		A6X942
ENSMUST00000070330	ENSMUSG00000040265	1	161982453	162478034	-1	0	6	14	86	20	0	0	0	0	0	0		Q8BZ98

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000070334	ENSMUSG00000034793	11	102189620	102194081	1	3	0	12	0	0	0	66	88	34	15	34		Q6NSQ9
ENSMUST00000070340	ENSMUSG00000049184	8	33386325	33417468	1	5	4	34	95	12	9	5	6	20	0	27		Q8R4E6
ENSMUST00000070342	ENSMUSG00000056306	3	54897068	54915887	-1	0	7	7	41	12	6	0	0	0	0	0		Q8CD78
ENSMUST00000070345	ENSMUSG00000056305	6	72318678	72345184	-1	3	7	11	53	10	4	195	555	283	109	170		Q3TIX9
ENSMUST00000070353	ENSMUSG00000035183	2	125068124	125088677	1	4	3	2	2	7	2	0	2	2	0	0	A2ATP8	Q8C261
ENSMUST00000070359	ENSMUSG00000056316	10	29143282	29144194	-1	10	3	5	7	11	0	0	0	0	0	0	Q8CDX6	
ENSMUST00000070368	ENSMUSG00000036432	3	58674938	58692400	-1	7	9	18	243	14	8	46	134	52	11	53	Q3UEV2	Q06986
ENSMUST00000070375	ENSMUSG00000045573	4	4133531	4138819	-1	11	12	28	23	18	8	8	8	2	3	4		P22005
ENSMUST00000070380	ENSMUSG00000057163	6	41521787	41525079	1	5	4	3	0	7	4	0	4	0	3	0	Q792Y6	P07146
ENSMUST00000070390	ENSMUSG00000032268	9	49081260	49117587	1	0	8	6	0	0	4	0	0	0	0	0	A2RSL0	Q9ER04
ENSMUST00000070395	ENSMUSG00000075528	11	101406839	101417615	-1	6	2	17	39	17	4	56	111	54	20	76		Q3THG9
ENSMUST00000070418	ENSMUSG00000027797	3	55242364	55539068	1	34	5	36	9	37	9	0	1	1	9	0	H7BX36	
ENSMUST00000070420	ENSMUSG00000033705	2	120629126	120731895	1	0	11	0	0	0	0	13	63	22	0	14	A2AKI0	
ENSMUST00000070425	ENSMUSG00000056359	12	73364075	73371445	-1	1	1	1	2	1	0	0	0	0	0	0	E9Q3E7	
ENSMUST00000070435	ENSMUSG00000056366	10	86731754	86732409	-1	2	0	0	1	10	2	0	1	0	0	2		
ENSMUST00000070437	ENSMUSG00000056370	6	72304610	72314371	1	0	0	0	0	0	0	0	0	0	3	0	F8WGK6	
ENSMUST00000070449	ENSMUSG00000056380	X	71663667	71669257	1	8	9	21	12	10	6	0	0	0	0	0		O88495
ENSMUST00000070453						23	21	65	362	29	23	1	0	1	0	0		
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ENSMUST00000070463	ENSMUSG00000031870	9	8899833	8968611	1	2	2	11	178	0	1	0	0	0	0	0	A6H6A5	
ENSMUST00000070478	ENSMUSG00000025743	4	130792537	130826319	1	38	35	150	66	58	16	99	97	41	448	2837		Q64519
ENSMUST00000070481	ENSMUSG00000046794	8	35375741	35388124	1	40	41	173	58	43	22	1368	4180	1781	247	1816		Q8C767
ENSMUST00000070487	ENSMUSG00000029625	5	145167213	145182041	1	0	0	0	0	0	0	0	152	0	0	0		Q8BQZ5
ENSMUST00000070508	ENSMUSG00000041679	8	105312341	105326276	-1	20	10	22	36	24	5	82	105	86	26	62	F6SF53	
ENSMUST00000070513	ENSMUSG00000034401	4	111719984	111829184	1	0	0	0	127	3	1	0	0	0	0	1	A2AED9	
ENSMUST00000070514	ENSMUSG00000056426	8	67523854	67548627	1	3	3	1	4	4	4	0	0	0	0	0	Q546K5	P50296
ENSMUST00000070515	ENSMUSG00000022040	14	66084377	66124500	-1	15	13	32	39	12	9	1	1	0	4	2		P34914
ENSMUST00000070518	ENSMUSG00000004612	7	43437073	43438249	1	10	9	44	15	11	5	169	158	81	27	79	Q9CY55	
ENSMUST00000070522	ENSMUSG00000032374	9	92542223	92608428	1	0	12	14	161	8	14	0	1	2	0	0		Q9R0B9
ENSMUST00000070524	ENSMUSG00000056429	6	72608432	72617000	-1	26	22	98	88	34	9	1286	3718	2096	1374	1407	Q4FJY3	Q62313
ENSMUST00000070531	ENSMUSG00000056423	16	27353322	27370239	-1	5	5	0	0	6	0	0	0	0	0	0	Q3V249	Q765I1
ENSMUST00000070532	ENSMUSG00000028773	4	130308595	130315463	1	12	5	8	88	12	4	1	0	0	35	3	Q5EBJ0	P11404
ENSMUST00000070533	ENSMUSG00000051951	1	3205901	3671498	-1	11	13	21	150	16	10	0	0	0	0	0		Q5GH67
ENSMUST00000070538	ENSMUSG00000023460	17	66494512	66519717	-1	0	0	0	16	8	0	0	0	0	0	0	A2CG35	
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ENSMUST00000070565	ENSMUSG00000056458	12	110807798	110840939	-1	3	3	2	15	4	1	2	8	1	5	6		Q9WVS4
ENSMUST00000070575	ENSMUSG00000025162	11	120961749	120991330	-1	30	17	76	0	22	0	1855	2343	1953	236	1376	Q3UBT6	Q9DC28
ENSMUST00000070577	ENSMUSG00000031847	8	116969599	116978943	-1	18	14	80	78	30	14	37	36	50	8	22	B9EHE0	Q8BHB7
ENSMUST00000070579	ENSMUSG00000056486	2	73610660	73775346	-1	6	0	3	0	7	2	0	0	0	0	0	A7VK14	Q91V57
ENSMUST00000070584	ENSMUSG00000051788	3	105066844	105078806	1	8	3	8	7	6	0	0	0	0	0	0	Q9D4S4	
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ENSMUST00000070597	ENSMUSG00000056666	6	72598475	72608425	1	17	12	21	31	19	6	48	42	17	4	33		Q64FW2
ENSMUST00000070607	ENSMUSG00000038047	4	86578855	86612055	-1	26	24	18	19	22	10	40	137	83	18	48	Q6NV99	
ENSMUST00000070610	ENSMUSG00000028683	4	117019402	117087306	1	3	0	0	0	0	0	0	0	0	0	0	B1AUN3	
ENSMUST00000070617	ENSMUSG00000034115	9	119753763	119825456	-1	39	33	66	51	38	24	2	3	1	2	0		Q9R053
ENSMUST00000070630	ENSMUSG00000056481	19	5068078	5070637	1	41	24	81	340	53	17	0	0	0	4	8		Q91V98
ENSMUST00000070631	ENSMUSG00000037921	8	61928087	62037701	1	2	5	8	2	6	2	32	769	157	178	313	G3X9F7	
ENSMUST00000070635	ENSMUSG00000029860	6	42349630	42360213	1	12	16	23	215	27	24	49820	47244	35309	3108	28800	Q7TQE2	Q62523
ENSMUST00000070639	ENSMUSG00000074417	7	3884242	3898120	-1	9	7	18	8	11	4	5379	10438	10019	3427	6355	E9Q1Z6	
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ENSMUST00000070649	ENSMUSG00000017049	8	21969775	21974041	1	0	5	3	0	0	0	0	0	0	0	0		Q9D9B0
ENSMUST00000070653	ENSMUSG00000025161	11	120948480	120960868	1	0	2	3	12	13	3	9466	12738	5544	824	4605	Q3UDP9	P57787
ENSMUST00000070656	ENSMUSG00000030782	7	128246812	128255699	1	17	8	9	29	11	6	5	0	0	0	0		Q62219
ENSMUST00000070658	ENSMUSG00000022517	16	4886100	4938296	1	13	14	36	60	33	12	1235	1968	1342	157	1225		Q9D074
ENSMUST00000070659	ENSMUSG00000056508	12	110667689	110682619	-1	7	6	20	5	7	3	3	0	2	0	4	Q80ZT1	
ENSMUST00000070663	ENSMUSG00000019907	10	108162400	108277575	1	8	13	17	65	18	11	1075	3931	3327	394	2192		Q9DBR7
ENSMUST00000070673	ENSMUSG00000056515	17	65651726	65772752	-1	22	15	31	127	32	13	4689	10472	6136	1214	3667	Q3TXV4	
ENSMUST00000070681	ENSMUSG00000018415	11	60417145	60450927	1	34	40	89	43	35	10	47	184	116	24	92		Q9CPY6
ENSMUST00000070690	ENSMUSG00000056529	4	132564067	132582683	1	45	44	96	54	46	14	2127	5537	2745	603	2506		Q62035
ENSMUST00000070699	ENSMUSG00000056536	1	105518422	105663677	-1	17	10	41	10	16	5	0	371	1	0	46	G3X9F1	
ENSMUST00000070705	ENSMUSG00000056537	X	103957163	103981284	-1	14	10	26	0	10	9	601	1497	606	212	495		Q9WTV7
ENSMUST00000070709	ENSMUSG00000044024	18	37955079	37959179	1	0	0	0	0	0	0	0	4	0	0	0		Q8BRJ3
ENSMUST00000070713	ENSMUSG00000031864	8	68793929	68829410	1	17	25	0	0	0	0	0	0	0	0	35		
ENSMUST00000070720	ENSMUSG00000029093	5	36017180	36398139	-1	5	5	13	163	12	5	0	0	0	0	2	Q8BI74	
ENSMUST00000070722	ENSMUSG00000056544	2	152572744	152574944	1	3	0	1	3	1	2	0	0	0	0	0	Q8C5Z4	
ENSMUST00000070724	ENSMUSG00000051177	2	134786067	135475258	1	0	8	9	3	8	2	9	0	13	0	63		Q9Z1B3
ENSMUST00000070725	ENSMUSG00000020436	11	41910203	42000857	-1	2	9	0	7	9	4	0	0	0	0	0		P22723
ENSMUST00000070726	ENSMUSG00000024270	18	24579881	24603817	-1	10	8	20	132	12	20	72	187	112	25	106		Q8C145
ENSMUST00000070731	ENSMUSG00000021756	13	112464070	112510086	1	0	0	0	0	0	0	215	107	459	14	389		Q00560
ENSMUST00000070733	ENSMUSG00000056553	12	116485720	117276849	1	17	12	3	11	6	9	0	0	0	0	0		P80560
ENSMUST00000070735	ENSMUSG00000020436	11	41910203	42000857	-1	3	0	3	2	2	0	0	0	0	0	0		P22723
ENSMUST00000070736	ENSMUSG00000029778	6	55451978	55501451	1	0	0	0	25	0	0	0	0	0	0	0		P70205
ENSMUST00000070741						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000070742	ENSMUSG00000032344	9	78430526	78443237	-1	29	35	117	83	47	22	18	123	41	4	41		Q8C6L5
ENSMUST00000070748	ENSMUSG00000039706	5	44472132	44799680	-1	13	11	35	9	7	7	0	0	0	0	0		Q55203
ENSMUST00000070755	ENSMUSG00000078773	4	11558922	11615805	1	15	8	7	6	12	9	4	16	15	4	10		Q6PFE3
ENSMUST00000070756	ENSMUSG00000029778	6	55451978	55501451	1	86	55	285	96	62	37	0	4	3	2	13	Q6NXJ9	
ENSMUST00000070758	ENSMUSG00000056569	1	171150711	171161130	1	11	7	5	14	8	3	0	2	0	0	0	E9QK82	
ENSMUST00000070761	ENSMUSG00000021714	13	104228955	104249615	1	1	2	2	1	1	1	2	12	0	5	2		Q9ESN5
ENSMUST00000070774						0	0	0	0	0	0	0	0	0	5	9		
ENSMUST00000070777	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	0	107	0	0	0	Q8C2K8	
ENSMUST00000070782	ENSMUSG00000061689	2	156613705	156764363	1	0	0	27	246	8	15	0	0	0	0	0		B1AZP2
ENSMUST00000070785	ENSMUSG00000021327	13	21387013	21402755	-1	6	9	11	0	0	6	115	695	244	65	104		
ENSMUST00000070797	ENSMUSG00000103442	18	36930184	37187661	1	0	0	0	0	0	0	0	0	0	0	0	Q91Y21	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000070801	ENSMUSG00000041718	X	144317804	144374450	1	1	1	1	22	3	6	9	22	2	22	5		Q9D8C3
ENSMUST00000070804	ENSMUSG00000043880	11	58625073	58626044	-1	8	1	8	10	7	1	0	0	0	0	0	Q5NCD0	
ENSMUST00000070805	ENSMUSG00000056598	11	60353329	60394341	1	63	44	48	42	55	27	2	16	11	0	19	Q5SX99	
ENSMUST00000070808	ENSMUSG00000056600	17	37085191	37086236	-1	16	3	5	7	17	4	0	0	0	0	0	Q0VEL5	
ENSMUST00000070810	ENSMUSG00000044014	8	66679965	66688094	-1	12	3	26	43	16	11	0	0	0	0	0	Q543U8	O70342
ENSMUST00000070814	ENSMUSG00000056606	12	104474488	104477489	1	27	11	23	33	32	14	0	0	0	0	0	Q8BR97	
ENSMUST00000070816	ENSMUSG00000028539	4	117926162	117929763	-1	17	10	20	239	25	8	0	0	0	2	5		Q9Z0L2
ENSMUST00000070820	ENSMUSG00000042672	3	89350219	89365253	-1	17	6	15	106	14	5	5	5	5	4	5		Q059Y8
ENSMUST00000070832	ENSMUSG00000051748	11	83746940	83752642	1	8	7	59	89	6	19	18601	48479	15822	72911	7379	Q8BTE6	
ENSMUST00000070849	ENSMUSG00000051952	8	85230497	85231435	1	4	2	5	7	8	2	0	0	0	0	0	Q8VGB8	
ENSMUST00000070850	ENSMUSG00000056612	19	6975048	6977324	1	6	6	24	85	16	11	115	133	43	170	170		Q62084
ENSMUST00000070864	ENSMUSG00000004113	2	24603887	24763152	-1	47	67	520	502	42	95	0	3	0	9	14	A2AIS0	
ENSMUST00000070872	ENSMUSG00000041920	11	109450855	109473598	-1	14	4	27	16	8	2	245	181	717	61	669		B1AT66
ENSMUST00000070875	ENSMUSG00000047034	15	101115755	101120022	1	8	8	33	22	13	2	0	1	0	0	3		Q8BXP5
ENSMUST00000070877	ENSMUSG00000022244	15	10981756	10996624	1	11	7	15	158	13	17	30	83	28	13	26		O09174
ENSMUST00000070878	ENSMUSG00000056629	19	6977741	6980461	-1	0	0	0	0	0	0	32	88	29	33	37	Q3TND1	P45878
ENSMUST00000070886	ENSMUSG00000021621	13	91796533	91807705	-1	31	23	249	0	21	9	0	42	0	7	3	F7A6K2	
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ENSMUST00000070892	ENSMUSG00000056632	18	20510304	20541310	1	41	35	314	35	27	22	0	0	0	0	0	Q3UFC6	
ENSMUST00000070898	ENSMUSG00000079434	1	87509889	87597845	1	0	0	0	0	0	0	0	0	0	0	0	Q0VGI4	Q9JMH3
ENSMUST00000070911	ENSMUSG00000056656	15	77747799	77755229	-1	17	7	8	19	11	0	1	0	1	5	3	A2VDH7	
ENSMUST00000070918	ENSMUSG00000022235	15	31568791	31590119	1	6	2	9	11	0	2	0	0	0	28	4		Q8R1G2
ENSMUST00000070923	ENSMUSG00000056665	15	74721204	74724639	1	8	2	19	196	20	11	36	37	20	12	30		Q80ZW2
ENSMUST00000070932	ENSMUSG00000063245	4	146610961	146658160	1	0	0	0	0	0	0	1	3	2	0	0	E9Q4Q0	
ENSMUST00000070943	ENSMUSG00000066258	7	104299894	104315466	-1	2	0	0	2	1	1	4	19	13	7	19		Q99PQ1
ENSMUST00000070949	ENSMUSG00000056671	18	41875696	41951194	-1	5	9	8	18	10	4	13	66	20	81	17		Q0VBB0
ENSMUST00000070951	ENSMUSG00000021759	13	112800894	112867881	1	6	0	0	124	7	0	1	0	3	10	6		Q61469
ENSMUST00000070953	ENSMUSG00000029056	4	154964123	154980938	1	12	7	0	0	23	0	0	24	0	17	0		Q80YV4
ENSMUST00000070968	ENSMUSG00000026104	1	52119440	52161865	1	7	0	0	32	18	6	31	0	64	2	178	Q8C3V4	
ENSMUST00000070980	ENSMUSG00000013668	7	131137713	131146314	-1	12	11	42	21	22	8	0	2	1	0	0	Q8CDT9	
ENSMUST00000070985	ENSMUSG00000056696	7	6569993	6570919	1	8	1	12	13	6	4	0	0	0	0	0	Q8VF34	
ENSMUST00000070989	ENSMUSG00000064302	1	118389058	118612678	1	0	3	0	0	0	0	0	0	0	0	0	E9QNY9	
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ENSMUST00000070991	ENSMUSG00000063762	6	132951102	132952066	1	0	3	1	0	1	0	0	0	0	0	0		Q7M709
ENSMUST00000070996	ENSMUSG00000078812	11	69916714	69921958	-1	0	0	12	8	0	0	21	161	47	35	50		P63242
ENSMUST00000070997	ENSMUSG00000035441	11	80482126	80780025	-1	0	3	5	28	3	0	0	27	23	0	18		Q5SYD0
ENSMUST00000071005	ENSMUSG00000073830	4	61300023	61304000	-1	3	0	0	0	0	0	0	0	0	0	0	A2CEK7	
ENSMUST00000071006	ENSMUSG00000024217	17	27839974	27851968	1	4	3	5	74	7	4	428	1047	297	102	217	Q569X3	Q62241
ENSMUST00000071016	ENSMUSG00000056718	2	5862080	5862934	-1	0	3	0	0	0	0	0	1	0	1	0	Q8C8E0	
ENSMUST00000071023	ENSMUSG00000036022	X	53243415	53269805	-1	7	0	0	3	5	0	0	24	14	0	26		Q6NZE7
ENSMUST00000071024	ENSMUSG00000030047	6	87458545	87533259	-1	6	0	3	0	0	0	30	352	168	44	60		Q8BYW1
ENSMUST00000071026	ENSMUSG00000078812	11	69916714	69921958	-1	13	6	10	0	14	0	0	96	0	13	0		P63242
ENSMUST00000071044	ENSMUSG00000056737	6	72544391	72562983	1	3	3	4	9	7	0	2865	4638	1905	697	1135	Q99LB4	
ENSMUST00000071056	ENSMUSG00000030802	7	127904082	127910221	1	35	48	81	110	57	18	368	411	250	58	173	Q3UCB5	O55028
ENSMUST00000071057	ENSMUSG00000029389	5	124552864	124569660	1	0	0	0	44	40	17	52	184	85	21	69		Q6ZPL9
ENSMUST00000071062						1	0	5	138	3	1	0	0	0	0	0		
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ENSMUST00000071065	ENSMUSG00000056749	13	52967209	52981073	-1	16	15	10	26	25	17	4112	8658	3512	468	3511		O08750
ENSMUST00000071067	ENSMUSG00000056753	8	84065236	84067287	-1	10	8	28	16	8	8	8	23	19	4	9	Q8C7V4	
ENSMUST00000071068	ENSMUSG00000051355	11	22896136	22982382	-1	2	0	6	23	2	0	112	238	97	412	56	G8JL54	
ENSMUST00000071069	ENSMUSG00000057596	7	104470014	104507849	-1	7	4	9	8	13	7	0	9	0	12	6	Q3TNW3	
ENSMUST00000071076	ENSMUSG00000056755	6	110645581	111567230	1	0	0	21	133	5	15	0	0	0	0	0	G5E8D5	
ENSMUST00000071077	ENSMUSG00000029155	5	73651379	73679512	1	0	0	0	8	21	0	0	0	0	0	0		Q0P557
ENSMUST00000071081	ENSMUSG00000029152	5	73292784	73314069	1	0	2	0	58	3	1	2	0	8	5	0		Q9CRD0
ENSMUST00000071083						3	0	0	15	2	0	270	622	592	54	369		
ENSMUST00000071087	ENSMUSG00000056763	1	10037987	10136768	1	3	3	0	0	0	0	119	687	236	94	157		B2RX88
ENSMUST00000071093	ENSMUSG00000032890	4	120854816	120896579	1	0	0	0	69	0	31	0	0	53	0	0	Q14BY7	Q80U57
ENSMUST00000071095	ENSMUSG00000056770	12	108106431	108179314	-1	7	13	33	14	12	3	538	1487	782	210	418		Q91WC0
ENSMUST00000071096	ENSMUSG00000028332	4	46393989	46413506	-1	0	19	6	45	25	0	2	9	5	3	1		Q9ERZ0
ENSMUST00000071101						37	25	31	132	30	9	0	0	0	0	0		
ENSMUST00000071103	ENSMUSG00000037149	12	13219308	13249213	-1	13	6	6	53	14	4	56	277	80	231	182		Q91VR5
ENSMUST00000071104	ENSMUSG00000056605	15	101776172	101786458	-1	21	11	23	152	25	3	0	0	0	0	0		Q6IME9
ENSMUST00000071106	ENSMUSG00000021254	12	86241890	86291414	1	21	19	41	48	29	21	707	1217	1067	147	800		Q6PE65
ENSMUST00000071108	ENSMUSG00000028799	4	128773088	128806045	-1	0	0	0	79	0	9	18	83	23	12	37	B1ASA5	
ENSMUST00000071112	ENSMUSG00000057067	7	86526759	86527691	1	4	2	5	3	6	1	0	0	0	0	0	Q7TS07	
ENSMUST00000071115						10	3	5	92	14	3	0	4	3	2	0		
ENSMUST00000071118	ENSMUSG00000057762	13	97098237	97099296	-1	12	0	23	12	15	9	7	0	0	0	7	Q0VEW4	Q9R1Q7
ENSMUST00000071119	ENSMUSG00000060794	15	76371958	76374938	-1	8	5	13	8	16	4	0	0	0	0	0		Q8C1R0
ENSMUST00000071120						0	0	1	1	2	0	0	0	0	0	1		
ENSMUST00000071126	ENSMUSG00000094734	10	129647130	129648065	1	3	1	5	0	1	0	0	0	0	0	0	Q8VGI7	
ENSMUST00000071130	ENSMUSG00000060063	5	149264767	149288153	1	35	74	44	176	50	37	49648	86392	39944	55198	23866		P30355
ENSMUST00000071132	ENSMUSG00000095774	9	39819641	39820576	1	2	3	4	2	1	0	0	0	0	0	0	Q8VFN3	
ENSMUST00000071134	ENSMUSG00000062380	8	123411424	123422015	1	41	27	65	134	56	29	4	1	1	0	1		Q9ERD7
ENSMUST00000071135	ENSMUSG00000062591	17	57080066	57087782	-1	26	17	75	95	42	25	3	4	9	7	17		Q9D6F9
ENSMUST00000071149	ENSMUSG00000033027	6	129639064	129643337	-1	3	0	5	1	2	0	1	4	1	4	4	Q9QXN7	
ENSMUST00000071152	ENSMUSG00000020696	11	82802449	82871210	-1	0	0	0	93	0	3	232	318	414	48	225	Q3UCG9	
ENSMUST00000071168	ENSMUSG00000006386	4	94739289	94874976	1	2	0	0	4	28	0	1	0	0	2	0		Q02858
ENSMUST00000071169	ENSMUSG00000040945	4	140700541	140723220	1	17	31	0	18	46	0	0	17	17	0	51		Q8BK67
ENSMUST00000071172						2	0	10	2	0	0	0	5	4	7	0		
ENSMUST00000071182	ENSMUSG00000072813	5	95775990	95804708	1	30	22	28	36	33	21	0	0	0	0	0	Q3UL33	
ENSMUST00000071184						3	6	16	7	5	5	0	0	0	0	0		
ENSMUST00000071189	ENSMUSG00000060701	17	20623846	20624877	-1	7	5	15	7	6	1	0	0	0	0	0		O88537
ENSMUST00000071199	ENSMUSG00000063820	5	77004055	77010606	1	1	3	0	0	3	5	0	0	0	1	2	Q6IMB2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000071201	ENSMUSG00000035513	2	29194541	29253005	-1	14	5	39	53	12	7	321	264	302	7	346	A2AKX2	
ENSMUST00000071204	ENSMUSG00000062168	X	160623094	160735765	-1	4	4	3	0	1	2	0	0	0	0	0		O35655
ENSMUST00000071207	ENSMUSG00000011658	7	44896079	44900623	1	0	2	0	12	0	0	0	0	0	3	0	E9QL29	
ENSMUST00000071208	ENSMUSG00000091873	14	50281228	50282271	-1	6	2	7	4	6	0	0	0	0	0	0	Q8VFT5	
ENSMUST00000071213	ENSMUSG00000005198	11	69733997	69758637	-1	32	27	54	0	1	5	1558	0	1693	0	1440		
ENSMUST00000071215	ENSMUSG00000063787	14	20703027	20704417	1	8	4	8	28	11	6	104	292	86	607	65		Q9CQA6
ENSMUST00000071219	ENSMUSG00000032098	9	44673233	44686305	1	21	13	43	0	0	14	0	0	0	0	0	E9PYP7	
ENSMUST00000071221	ENSMUSG00000094140	14	52372110	52373051	-1	9	6	16	6	14	3	0	0	0	0	0	Q8VF72	
ENSMUST00000071230	ENSMUSG00000021116	12	78861819	78887010	1	21	6	20	64	19	9	119	702	241	935	241		Q6ZWX6
ENSMUST00000071233	ENSMUSG00000058881	18	82910879	83005314	1	41	34	146	129	0	0	850	1197	303	0	129		Q7TSH3
ENSMUST00000071235						1	1	15	4	3	1	0	0	0	0	1		
ENSMUST00000071237						4	4	21	3	12	0	0	2	0	10	0		
ENSMUST00000071242	ENSMUSG00000059768	7	105126372	105128405	-1	3	2	4	0	5	2	0	0	0	0	0		
ENSMUST00000071243	ENSMUSG00000064006	16	59074155	59077835	-1	0	0	4	1	2	0	0	0	0	0	0	K7N5T5	
ENSMUST00000071248	ENSMUSG00000041936	4	156165290	156197488	-1	10	3	17	0	0	0	0	0	0	1	0	Z4YJS5	
ENSMUST00000071250	ENSMUSG00000021069	12	70190811	70231488	-1	18	11	37	88	16	19	17985	59443	36387	12605	20959		Q9ET01
ENSMUST00000071254	ENSMUSG00000031802	9	13431361	13432736	1	37	26	32	35	49	25	1	1	3	1	4	Q3KNH0	P15974
ENSMUST00000071259	ENSMUSG00000061614	9	19338459	19339400	1	7	3	1	2	3	1	0	0	0	0	0	Q7TRG2	
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ENSMUST00000071267	ENSMUSG00000024805	19	36379067	36456192	1	0	10	0	1	4	3	112	372	142	30	0		Q3UK78
ENSMUST00000071268	ENSMUSG00000059981	7	126865678	126884703	-1	21	12	31	152	33	15	505	956	651	89	698		Q6ZQ29
ENSMUST00000071277	ENSMUSG00000096730	JH584292.1	3536	11935	1	0	0	0	0	0	0	0	0	0	0	0	D3YWX8	
ENSMUST00000071280	ENSMUSG00000040374	3	5560188	5576239	-1	0	0	9	0	1	0	0	111	45	0	21	Q91YZ5	
ENSMUST00000071281	ENSMUSG00000059246	9	69757710	69760940	-1	33	43	194	485	25	23	0	0	0	0	0		Q64732
ENSMUST00000071282						4	8	1	4	13	2	30	27	27	40	28		
ENSMUST00000071294	ENSMUSG00000094285	14	50533414	50534349	1	2	2	0	0	0	3	0	0	0	0	0	L7N1Y2	
ENSMUST00000071296	ENSMUSG00000045411	7	44246722	44252319	1	14	11	14	11	22	18	5	64	12	2	53	Q3TE80	
ENSMUST00000071300	ENSMUSG00000074829	9	124291804	124312696	-1	0	0	0	0	0	0	0	7	0	3	0	J3KMG5	
ENSMUST00000071301	ENSMUSG00000051234	9	96470937	96478675	-1	4	1	6	8	1	1	0	0	28	68	9	D3Z392	
ENSMUST00000071302	ENSMUSG00000063058	9	98856494	98857374	1	3	4	13	117	7	1	0	0	0	0	0	D3YWX5	
ENSMUST00000071304	ENSMUSG00000058731	6	57258149	57259048	1	2	3	0	4	0	1	0	0	0	0	0	Q14C10	
ENSMUST00000071308	ENSMUSG00000057116	8	13835233	13838089	-1	40	37	229	47	37	28	0	1	2	0	1	G3X9P9	
ENSMUST00000071320	ENSMUSG00000074830	13	66670769	66673330	-1	4	3	4	0	0	5	0	0	0	0	0	L7N452	
ENSMUST00000071325	ENSMUSG00000020716	11	79339693	79581612	1	24	28	37	32	37	12	162	442	318	26	334		Q04690
ENSMUST00000071329	ENSMUSG00000060376	7	25629946	25658981	-1	11	10	42	16	20	7	1239	1140	778	288	473	Q3U3J1	
ENSMUST00000071355	ENSMUSG00000058194	2	87457167	87458111	1	7	1	5	3	3	2	0	0	0	0	0	Q7TR49	
ENSMUST00000071361	ENSMUSG00000064264	7	24507006	24515682	1	0	0	0	102	0	0	0	0	0	0	0		Q8C1M2
ENSMUST00000071362	ENSMUSG00000056782	7	104916314	104917294	-1	4	3	3	1	6	0	0	0	0	0	0	Q7TRP4	
ENSMUST00000071370	ENSMUSG00000035566	14	84443563	84537060	1	76	49	372	323	106	49	1	9	5	0	3	E9PXF0	
ENSMUST00000071378	ENSMUSG00000100079	4	88690302	88691359	-1	9	3	19	4	8	0	0	0	0	0	0	L7MTU6	
ENSMUST00000071393	ENSMUSG00000060888	7	102856321	102857271	-1	2	4	0	0	4	0	0	0	0	0	0	Q7TRS5	
ENSMUST00000071399	ENSMUSG00000066760	7	17074040	17133450	1	2706	2551	3958	2435	2984	1502	263	1468	729	767	724	Q8K0U8	
ENSMUST00000071400	ENSMUSG00000045031	3	37307749	37312708	-1	6	3	6	0	5	5	0	0	0	0	0		Q8K4K1
ENSMUST00000071402	ENSMUSG00000041220	3	129532355	129638495	1	71	50	331	99	84	37	15	84	33	17	63		Q920L5
ENSMUST00000071404	ENSMUSG00000064039	9	123976949	123978408	-1	7	2	14	18	12	2	0	0	2	0	1		P51676
ENSMUST00000071410	ENSMUSG00000062434	7	108845064	108846008	-1	15	5	5	4	9	5	0	0	0	0	0	Q8VFZ5	
ENSMUST00000071414	ENSMUSG00000060699	6	66678794	66679684	-1	4	3	5	2	0	2	0	0	0	0	0	Q8R2E2	
ENSMUST00000071419	ENSMUSG00000072487	15	73761410	73839699	-1	14	12	8	24	23	7	0	0	0	0	0	Q3TY91	
ENSMUST00000071421	ENSMUSG00000061707	5	145029600	145032754	-1	11	8	2	0	7	0	0	0	0	0	0	D3Z0W7	
ENSMUST00000071423	ENSMUSG00000025078	19	56548261	56598846	1	27	10	13	173	28	10	227	355	353	49	285	B2RR26	Q8BZW8
ENSMUST00000071425	ENSMUSG00000056961	9	38697429	38698376	-1	2	5	0	3	6	7	0	0	0	0	0	Q8VF78	
ENSMUST00000071430	ENSMUSG00000062619	17	46772635	46773407	1	16	8	3	244	17	11	22	64	29	55	26		Q9D727
ENSMUST00000071437	ENSMUSG00000094464	2	36421400	36422329	1	9	7	1	4	4	2	0	0	0	0	0	Q8VGK8	
ENSMUST00000071442	ENSMUSG00000015094	2	25399351	25409494	1	3	2	0	103	4	0	0	0	0	8	0		Q64322
ENSMUST00000071449	ENSMUSG00000058270	9	38329492	38330559	1	0	4	2	0	4	2	0	0	0	0	0	Q7TRD6	
ENSMUST00000071452	ENSMUSG00000034206	16	37011786	37095417	1	0	4	0	26	17	0	0	20	0	3	2		Q8CGS6
ENSMUST00000071453	ENSMUSG00000059327	X	99975606	100400762	1	0	0	0	0	0	2	0	0	0	0	0	Q1L2D9	
ENSMUST00000071455	ENSMUSG00000029344	5	112276691	112315361	1	2	1	10	14	1	2	846	512	172	5	201	Q3TQN1	
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ENSMUST00000071458						13	11	13	57	20	12	1	1	1	0	2		
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ENSMUST00000071465	ENSMUSG00000018347	11	65807175	65829239	1	0	14	36	15	0	8	393	844	424	181	386		Q810A1
ENSMUST00000071478	ENSMUSG00000056921	11	73887438	73888370	-1	5	2	0	1	5	2	0	0	0	0	0	Q8VGR5	
ENSMUST00000071484	ENSMUSG00000060303	19	12900759	12901861	-1	2	6	3	3	4	0	0	0	0	0	0	Q8VFX3	
ENSMUST00000071487	ENSMUSG00000037331	11	58009064	58062034	1	52	29	189	35	104	31	0	0	0	0	0	Z4YJT3	
ENSMUST00000071488	ENSMUSG00000027933	3	90391388	90433622	-1	40	0	0	0	0	32	0	127	218	0	234		Q7TPD0
ENSMUST00000071492	ENSMUSG00000057497	6	86365646	86370058	1	19	19	19	119	14	9	22	73	18	92	36		Q9CR98
ENSMUST00000071500	ENSMUSG00000061576	5	26817203	27727505	1	0	0	0	0	0	0	0	0	0	0	0		Q9Z218
ENSMUST00000071505	ENSMUSG00000094104	7	108395122	108396114	1	7	4	2	6	2	3	0	0	0	0	0		Q8VF12
ENSMUST00000071510	ENSMUSG00000057058	11	96464593	96759130	1	0	0	2	0	0	0	55	67	15	0	29		Q3UUV5
ENSMUST00000071515						1	1	0	0	6	0	0	1	0	0	0		
ENSMUST00000071521	ENSMUSG00000057464	1	92490818	92496101	-1	16	5	9	5	13	1	0	0	0	0	0	Q7TQS4	
ENSMUST00000071522	ENSMUSG00000057913	14	66784529	66793758	1	103	82	184	70	122	66	2	7	7	4	12	Q8BS28	
ENSMUST00000071523						0	9	0	0	0	0	825	5951	1651	6106	1426		
ENSMUST00000071526	ENSMUSG00000055298	13	61000278	61005916	-1	6	10	4	1	2	4	0	0	0	0	0		
ENSMUST00000071531	ENSMUSG00000052139	5	31697684	32084962	1	0	0	0	0	0	0	0	0	0	0	0		Q8K3W0
ENSMUST00000071533	ENSMUSG00000055639	14	97786853	98169765	-1	15	8	28	0	0	0	613	359	763	19	269		Q9QYB2
ENSMUST00000071535	ENSMUSG00000068587	6	40628831	40769123	1	44	42	105	52	57	32	2053	6847	6571	288	3618	B5THE2	
ENSMUST00000071536						2	0	2	1	1	2	0	1	0	0	0		
ENSMUST00000071537	ENSMUSG00000017119	11	101552149	101581951	1	0	0	0	0	0	0	51	0	386	0	304	K3W4P1	
ENSMUST00000071539	ENSMUSG00000041654	11	113244853	113650079	-1	22	8	0	0	0	15	373	389	241	60	210		Q8BWY7
ENSMUST00000071543	ENSMUSG00000026839	2	58567298	58792971	1	7	4	3	13	13	7	0	0	0	0	0	A2APN2	
ENSMUST00000071544	ENSMUSG00000028483	4	83417724	83467676	1	5	4	10	116	9	0	0	0	16	9	26	Q9CQB0	
ENSMUST00000071546	ENSMUSG00000022132	14	118787908	118875489	1	8	3	7	1	6	4	0	0	0	0	0		Q9Z0S6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000071553	ENSMUSG00000095095	11	73588798	73589736	-1	6	3	8	0	2	2	0	0	0	0	0	Q8VGT1	
ENSMUST00000071554	ENSMUSG00000033024	6	130178675	130193112	-1	3	1	0	0	0	0	0	6	0	1	1	Q2TJJ8	
ENSMUST00000071555	ENSMUSG00000062825	11	120345690	120348542	-1	0	14	0	176	25	12	21597	15104	13596	2640	7708	Q4KL81	P63260
ENSMUST00000071557	ENSMUSG00000061961	10	129901776	129902726	-1	1	2	0	0	1	0	0	0	0	0	0	Q8VFU0	
ENSMUST00000071559	ENSMUSG00000056853	10	129046132	129047061	-1	5	2	5	5	1	1	0	0	0	0	0	Q7TRI6	
ENSMUST00000071561	ENSMUSG00000036078	4	41738493	41756157	-1	0	4	13	0	5	7	0	98	15	4	0	A2AMS0	O55242
ENSMUST00000071562	ENSMUSG00000038268	11	75175942	75178835	-1	12	10	16	22	11	11	105	208	72	16	34		Q9D7E3
ENSMUST00000071563	ENSMUSG00000061414	6	127561338	127630033	1	6	5	14	13	5	2	38	38	50	2	52		Q3UP38
ENSMUST00000071564	ENSMUSG00000058594	2	11742573	11777582	-1	0	3	6	19	6	8	710	1890	1332	444	905		Q8K2I9
ENSMUST00000071565	ENSMUSG00000062874	9	69450232	69451035	-1	7	9	28	15	6	3	0	0	0	0	0	F6VBB8	
ENSMUST00000071573						7	4	16	5	0	8	2	2	0	4	0		
ENSMUST00000071580	ENSMUSG00000066027	12	88175589	88181894	-1	13	6	5	8	6	11	0	0	0	0	0	L7N1Y3	
ENSMUST00000071585	ENSMUSG00000027584	2	181715016	181720985	1	8	4	0	0	10	9	0	0	0	0	0	Q542U1	P35377
ENSMUST00000071588	ENSMUSG00000063672	8	23153269	23158948	1	21	9	27	90	22	11	0	0	0	0	0	B2RU70	Q3UHX8
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ENSMUST00000071591						6	1	10	13	6	0	0	1	0	0	0		
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ENSMUST00000071605	ENSMUSG00000063715	10	129911338	129912276	-1	6	2	0	0	1	1	0	0	0	0	0	Q8VFU2	
ENSMUST00000071617	ENSMUSG00000094970	9	39166310	39185124	1	3	4	3	1	4	0	0	0	0	0	0	Q9EQ92	
ENSMUST00000071625	ENSMUSG00000094805	11	58841116	58842042	1	3	1	0	9	4	2	0	0	0	0	0	Q5NC59	
ENSMUST00000071632						4	1	1	3	3	0	0	0	0	2	0		
ENSMUST00000071641						0	13	17	78	19	16	1090	4118	1580	10175	1447		
ENSMUST00000071642	ENSMUSG00000058006	4	32657119	32775217	1	2	66	0	125	106	46	130	337	237	13	443	A2ANY6	
ENSMUST00000071646	ENSMUSG00000069456	10	127801152	127846565	1	23	17	63	37	24	0	0	3	0	1	0	O54909	
ENSMUST00000071648	ENSMUSG00000023951	17	46016993	46032377	-1	0	3	0	0	10	8	189	598	223	10	162	F8WH10	
ENSMUST00000071650	ENSMUSG00000033540	5	108660331	108684557	1	0	22	69	160	47	13	0	0	0	0	0	Q8BMG0	
ENSMUST00000071652	ENSMUSG00000029376	5	90931117	91021368	1	5	8	5	22	7	6	2	22	3	8	12		D3YZG8
ENSMUST00000071658	ENSMUSG00000063120	7	108065768	108066796	-1	3	4	5	2	5	0	0	0	0	0	0		
ENSMUST00000071664	ENSMUSG00000005625	3	95032694	95042614	-1	0	0	0	0	0	0	493	1123	521	274	428	Q3ULG4	O35226
ENSMUST00000071667	ENSMUSG00000040749	X	164070705	164076493	-1	0	4	0	6	4	0	12	36	8	0	15	A2AHZ2	
ENSMUST00000071677	ENSMUSG00000005378	5	135052957	135064959	-1	0	0	0	0	0	0	154	100	109	27	52	Q9DCT4	
ENSMUST00000071681	ENSMUSG00000060114	9	38580244	38582211	1	5	2	0	0	3	1	0	0	0	0	0	F8VQ31	
ENSMUST00000071691	ENSMUSG00000100950	10	24049510	24050586	1	11	4	15	6	5	5	0	0	0	0	0		Q5QD08
ENSMUST00000071696	ENSMUSG00000057381	6	132847142	132848143	1	2	1	0	2	0	3	0	0	0	0	0		P59528
ENSMUST00000071697	ENSMUSG00000036570	7	31051678	31057199	-1	3	0	0	0	6	1	0	0	0	0	0		Q9Z239
ENSMUST00000071698	ENSMUSG00000025198	19	44034944	44069785	-1	3	14	0	0	0	0	0	97	118	55	116		
ENSMUST00000071699	ENSMUSG00000017670	2	165288031	165326479	-1	31	0	0	13	33	16	0	0	0	0	0		Q8BHL5
ENSMUST00000071703	ENSMUSG00000035248	13	59771879	59823147	-1	31	10	49	38	43	31	1765	7357	5141	922	3972	E9PUA2	
ENSMUST00000071704	ENSMUSG00000060073	12	70974621	70996347	1	0	0	0	0	0	0	130	651	100	309	71	F8WH02	
ENSMUST00000071707	ENSMUSG00000059382	6	132656953	132657844	1	0	0	0	0	0	0	0	0	0	0	0		Q7M721
ENSMUST00000071708	ENSMUSG00000059049	4	82897920	83052339	-1	0	0	1	0	20	15	0	0	0	0	1		Q684R7
ENSMUST00000071711	ENSMUSG00000059334	X	53774048	53776394	-1	10	7	24	106	16	7	0	0	1	0	0		Q5ISE2
ENSMUST00000071718	ENSMUSG00000026701	1	161240112	161251219	-1	11	5	26	15	15	0	260	209	166	48	143	Q6GT24	
ENSMUST00000071725	ENSMUSG00000059623	9	20282351	20286648	1	7	2	6	1	1	0	0	0	0	0	0	E9PVX1	
ENSMUST00000071728	ENSMUSG00000029822	6	50293330	50456201	-1	0	0	0	0	0	0	1	0	16	0	35	F8WH20	
ENSMUST00000071732	ENSMUSG00000092086	8	112013433	112015036	-1	28	25	101	42	45	6	7	23	9	3	3	B2RXM2	
ENSMUST00000071737	ENSMUSG00000063180	13	73988963	73989148	-1	5	2	0	4	2	2	0	0	0	0	0	D3YYL7	
ENSMUST00000071739	ENSMUSG00000057177	7	25228258	25237851	-1	0	9	0	0	21	3	2757	3430	2143	286	1691		Q2NL51
ENSMUST00000071745						8	6	12	129	9	4	16	8	16	5	5		
ENSMUST00000071750	ENSMUSG00000032332	9	79598991	79718831	-1	35	57	41	23	58	3	0	0	1	0	0		Q60847
ENSMUST00000071755	ENSMUSG00000056883	7	140466158	140467209	1	6	4	12	7	8	1	0	0	0	0	0	Q7TRT7	
ENSMUST00000071760	ENSMUSG00000098505	2	181991226	182001766	1	3	9	0	0	0	3	0	0	0	0	0	K7N5U4	
ENSMUST00000071770						0	0	18	2	0	1	0	0	0	0	1		
ENSMUST00000071780	ENSMUSG00000054102	7	26535023	26575615	1	0	0	0	5	0	5	0	0	0	0	0	E9QKM4	
ENSMUST00000071782	ENSMUSG00000059991	5	144545902	144557478	1	21	9	41	202	30	14	1	0	0	0	0		O70340
ENSMUST00000071792	ENSMUSG00000063236	15	76948539	76950729	1	13	3	47	181	29	8	148	212	115	42	87		Q3U6N9
ENSMUST00000071798	ENSMUSG00000064179	7	4504570	4516382	-1	3	0	0	0	0	5	0	14	14	0	7	Q3TVB8	O88346
ENSMUST00000071804	ENSMUSG00000056383	7	41372923	41393379	-1	6	0	2	10	12	2	94	509	163	203	72	Q7TPX5	
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ENSMUST00000071807	ENSMUSG00000059729	11	49494535	49495464	1	9	3	6	4	2	0	0	0	0	0	0	Q7TQT1	
ENSMUST00000071812	ENSMUSG00000028068	3	88081971	88121048	1	0	0	0	47	0	0	131	12	133	0	88	F8VQ29	
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ENSMUST00000071816	ENSMUSG00000021820	14	20734875	20794088	-1	0	5	0	0	0	0	0	0	0	0	54		Q923T9
ENSMUST00000071825	ENSMUSG00000059301	12	36090379	36091829	1	13	10	9	9	10	2	0	0	0	0	0		Q3UWQ3
ENSMUST00000071826	ENSMUSG00000044279	17	57059105	57065918	1	6	1	0	17	10	4	0	0	0	0	3		Q8QZT4
ENSMUST00000071829	ENSMUSG00000023452	5	32736301	32785646	-1	0	0	29	0	8	0	77	217	59	22	63	D3YY63	
ENSMUST00000071841	ENSMUSG00000063576	17	46674550	46680930	-1	14	13	6	12	0	0	1083	1299	1025	181	821		
ENSMUST00000071842						12	10	106	31	19	16	37	44	41	7	32		
ENSMUST00000071844	ENSMUSG00000059874	7	103383062	103384000	-1	8	2	3	5	4	0	0	0	0	0	0	L7N1Y4	
ENSMUST00000071847						17	5	18	23	4	7	0	0	0	0	2		
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ENSMUST00000071852	ENSMUSG00000056941	2	153616933	153632781	-1	57	49	71	87	82	30	121	454	195	51	130	Q56A13	Q8BG94
ENSMUST00000071857	ENSMUSG00000056917	19	5651185	5663707	-1	0	0	15	0	15	0	237	440	437	40	329	E9Q0Y4	
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ENSMUST00000071865	ENSMUSG00000095932	6	90072086	90078498	-1	6	6	1	3	14	0	0	0	0	0	0		Q9WUF1
ENSMUST00000071866	ENSMUSG00000062083	19	50030124	50030735	-1	8	2	10	4	9	2	0	3	0	8	1		
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ENSMUST00000071871	ENSMUSG00000057443	17	38261067	38275711	1	2	0	3	3	0	2	0	0	0	0	0	Q7TRI7	
ENSMUST00000071873	ENSMUSG00000062342	13	33249612	33260846	1	7	5	10	3	7	2	0	0	0	0	0	O08806	
ENSMUST00000071874	ENSMUSG00000064210	15	95790843	95975464	1	37	29	85	68	50	31	550	1283	1199	154	1169		Q6P9J9
ENSMUST00000071876	ENSMUSG00000064284	15	85806972	85811697	-1	7	2	4	15	2	9	21	16	17	22	22		Q8R3A2
ENSMUST00000071878	ENSMUSG00000029651	5	147957320	148316065	1	2	0	0	0	15	0	0	0	0	0	0	D3YY58	
ENSMUST00000071880	ENSMUSG00000042678	11	60469339	60528369	1	2	0	191	208	152	1	0	0	0	0	0		Q9QZZ4
ENSMUST00000071881	ENSMUSG00000036639	5	140321656	140338137	1	7	2	4	31	6	4	0	19	7	0	8		P53368

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000071885	ENSMUSG00000064137	X	37874778	37878944	-1	20	17	46	361	20	13	0	11	0	0	1	Q6VSS7	
ENSMUST00000071886	ENSMUSG00000058618	8	21702519	21703645	-1	6	3	6	4	3	1	0	0	0	0	0	Q9D848	
ENSMUST00000071889	ENSMUSG00000032373	9	66713686	66766845	1	10	9	28	33	21	8	0	0	0	0	0		
ENSMUST00000071891	ENSMUSG00000020549	11	64979038	65002069	1	0	1	0	72	0	0	2	44	25	0	0	Q3U0M8	Q80Y81
ENSMUST00000071898	ENSMUSG00000034022	15	76595809	76607591	-1	37	19	72	132	45	24	447	608	472	47	477		Q9EPU4
ENSMUST00000071902	ENSMUSG00000058620	2	127363208	127367221	1	79	79	548	0	28	9	1	13	0	0	6	F8VQ23	
ENSMUST00000071905	ENSMUSG00000108167	11	49465090	49471181	1	3	5	7	6	4	2	0	0	0	0	0	Q7TQT0	
ENSMUST00000071917	ENSMUSG00000059547	9	109717566	109746089	-1	15	10	14	7	17	1	0	0	1	0	0	Q8BI58	
ENSMUST00000071920	ENSMUSG00000052736	6	129647496	129660689	-1	0	3	4	1	0	2	0	2	0	2	5	D3YXP2	
ENSMUST00000071921	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	10	0	0	117	290	0	149	145		Q8CE22
ENSMUST00000071926	ENSMUSG00000063200	13	43398376	43402858	1	0	1	3	88	8	1	97	573	208	189	172	A1L3B6	Q9D7Z3
ENSMUST00000071932	ENSMUSG00000095765	14	50472947	50486395	1	1	4	2	2	6	1	0	0	0	0	0	L7N1Y5	
ENSMUST00000071935	ENSMUSG00000004677	8	71272714	71360712	1	0	0	0	0	0	37	2485	3102	3125	265	2556	E9QKV6	
ENSMUST00000071937	ENSMUSG00000058743	7	45816461	45824756	-1	20	15	68	170	27	9	1	9	2	0	2		Q8JZN3
ENSMUST00000071943	ENSMUSG00000059610	11	59570695	59571813	-1	9	3	23	7	21	8	0	0	0	0	0	Q7TS30	
ENSMUST00000071944	ENSMUSG00000029217	5	72755716	72868483	-1	0	0	0	0	0	0	133	0	141	0	27	Q3U436	
ENSMUST00000071949	ENSMUSG00000060708	5	36747378	36748650	-1	4	1	3	202	14	4	92	273	86	43	74		Q8VED2
ENSMUST00000071951	ENSMUSG00000060550	17	35439155	35443773	1	0	0	0	0	0	0	51	33	25	0	88		P14429
ENSMUST00000071968	ENSMUSG00000014158	5	114622152	114658421	-1	0	1	13	46	3	2	0	0	1	2	72		Q9EPK8
ENSMUST00000071972	ENSMUSG00000028730	4	118554551	118620777	-1	15	11	29	44	27	0	0	15	5	7	0		Q9D180
ENSMUST00000071973	ENSMUSG00000057069	13	12565883	12609526	1	31	27	76	116	38	13	199	608	321	80	317		Q8R2E9
ENSMUST00000071975						3	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000071977	ENSMUSG00000060572	4	141010418	141015984	1	0	0	9	0	11	5	0	10	0	3	4	Q99PM0	
ENSMUST00000071979	ENSMUSG00000096705	4	118916524	118917465	-1	8	5	21	14	7	4	0	0	0	0	0	L7MTV4	
ENSMUST00000071982	ENSMUSG00000031963	9	23223076	23485202	1	21	14	26	174	35	17	0	0	0	2	4		Q8CJ69
ENSMUST00000071985	ENSMUSG00000040693	1	96816270	96872171	-1	12	11	26	47	23	9	599	1272	1025	181	527		Q8BGD4
ENSMUST00000071986	ENSMUSG00000089661	7	27179742	27181157	-1	0	2	0	0	0	0	0	0	0	0	0		Q61865
ENSMUST00000071991	ENSMUSG00000060461	9	78367052	78368177	-1	11	6	12	14	11	5	0	0	0	0	1		Q9CQS7
ENSMUST00000071993	ENSMUSG00000039458	15	12205028	12272240	1	23	4	62	14	5	0	0	468	0	34	0		Q80TA6
ENSMUST00000072008	ENSMUSG00000057719	18	42053667	42158960	1	37	31	39	35	39	24	0	0	0	0	0		Q8BZT2
ENSMUST00000072012	ENSMUSG00000058022	13	41763148	41847684	-1	11	28	9	12	28	23	18	81	23	14	23		
ENSMUST00000072014	ENSMUSG00000071362	12	23778912	23780265	-1	55	53	72	65	56	39	1	3	0	0	0	Q8BKS1	
ENSMUST00000072018	ENSMUSG00000063810	6	85587531	85702753	1	39	51	49	293	49	20	12	24	28	9	33		Q8K4E0
ENSMUST00000072020	ENSMUSG00000034758	10	81590904	81601073	-1	0	0	0	45	0	0	0	0	0	0	3		Q9WVB3
ENSMUST00000072030	ENSMUSG00000063549	11	58665561	58666544	1	20	9	37	32	11	12	0	0	0	0	0	Q5NCC8	
ENSMUST00000072031	ENSMUSG00000005417	11	59661305	59780860	1	0	85	245	68	84	42	25	54	38	4	80		P97434
ENSMUST00000072035	ENSMUSG00000096068	7	108171798	108172742	-1	3	2	5	3	4	2	0	0	0	0	0		Q8VFD0
ENSMUST00000072037	ENSMUSG00000031111	X	49782536	49797749	-1	9	0	5	2	6	0	0	0	0	0	0		Q7TQA1
ENSMUST00000072040	ENSMUSG00000021115	12	106010263	106077410	1	0	0	10	53	0	0	432	1748	749	1577	499		Q80X41
ENSMUST00000072044	ENSMUSG00000061296	13	22827194	22828114	-1	4	5	0	3	4	3	0	0	0	0	0	Q8R274	
ENSMUST00000072050						2	1	3	0	8	2	0	1	1	1	1		
ENSMUST00000072055	ENSMUSG00000024843	19	3851773	3894369	1	0	0	0	0	0	0	0	15	0	0	0		O54804
ENSMUST00000072057	ENSMUSG00000064084	2	88817173	88818102	1	4	13	6	5	5	2	0	0	0	0	0	Q8VF98	
ENSMUST00000072061	ENSMUSG00000021236	12	84373857	84409029	-1	22	24	34	25	0	0	4	12	0	0	0	Q3TQC7	
ENSMUST00000072063	ENSMUSG00000058513	10	129669561	129673865	-1	4	5	2	0	5	2	0	0	0	0	0	Q8VEU1	
ENSMUST00000072079	ENSMUSG00000061024	1	9545408	9547455	1	38	21	68	379	54	21	53	79	44	19	69		Q9CYH6
ENSMUST00000072080	ENSMUSG00000063052	3	158036662	158068487	1	6	7	12	49	13	5	20	17	13	40	3		
ENSMUST00000072093	ENSMUSG00000053646	9	109095389	109119917	1	94	53	155	113	118	47	1	0	1	4	29		Q8CJH3
ENSMUST00000072097	ENSMUSG00000062007	8	72189668	72200995	1	0	0	26	10	20	6	46	74	78	17	132		Q6VYH9
ENSMUST00000072100	ENSMUSG00000029878	12	74297474	74300468	1	45	32	288	56	37	23	1	0	1	0	0	Q8IWX3	
ENSMUST00000072103	ENSMUSG00000071521	6	41354105	41357914	1	2	4	9	2	1	4	0	0	0	0	0	Q792Z1	
ENSMUST00000072111	ENSMUSG00000026811	2	32599709	32620806	1	0	0	0	0	0	0	123	156	33	27	19		Q9JM95
ENSMUST00000072113	ENSMUSG00000062373	15	58782269	58823530	-1	14	18	75	54	11	14	91	366	121	41	116		Q4VAE3
ENSMUST00000072114	ENSMUSG00000094949	2	36793238	36794176	1	3	4	3	3	3	0	0	0	0	0	0		Q8VGK5
ENSMUST00000072119	ENSMUSG00000041431	13	100778650	100786570	-1	18	15	14	58	21	15	71	79	128	174	24	Q3TQW9	P24860
ENSMUST00000072123						9	3	9	22	6	1	0	1	0	0	0		
ENSMUST00000072125	ENSMUSG00000057439	X	136448107	136544056	-1	4	0	0	0	0	0	0	0	0	0	0	Q673W2	
ENSMUST00000072133	ENSMUSG00000067929	17	21691860	21692114	1	0	0	0	0	0	0	2	34	1	3	1	O88253	
ENSMUST00000072141	ENSMUSG00000025047	19	47090766	47131143	1	56	49	107	159	82	33	58	116	132	30	218		Q6NS46
ENSMUST00000072152	ENSMUSG00000059397	11	51027004	51027945	1	5	1	10	3	14	4	0	0	0	0	0	Q8VFE6	
ENSMUST00000072154	ENSMUSG00000021120	12	79080673	79089670	-1	23	10	50	110	29	18	17	64	23	20	25		Q5M9N4
ENSMUST00000072155	ENSMUSG00000057176	7	127582383	127588595	-1	16	14	17	15	28	13	148	279	151	118	135		Q6NZQ0
ENSMUST00000072156	ENSMUSG00000023800	17	3326573	3519397	1	0	0	62	0	34	19	364	1277	578	706	500		Q6ZPF3
ENSMUST00000072166						0	0	2	3	3	1	0	0	0	0	0		
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ENSMUST00000072177	ENSMUSG00000009772	1	132316126	132333488	1	22	0	56	181	21	15	767	1090	532	129	695		Q8BZN4
ENSMUST00000072178	ENSMUSG00000020333	11	54303798	54364756	1	0	0	5	3	5	2	0	0	1	0	0	Q5ICG4	Q91WC3
ENSMUST00000072182	ENSMUSG00000062713	16	94085260	94127032	1	23	25	63	354	24	14	2	2	1	0	2		Q61079
ENSMUST00000072186	ENSMUSG00000026915	2	37483228	37703859	-1	0	0	0	0	0	0	56	204	87	104	79		Q91WM1
ENSMUST00000072187	ENSMUSG00000020821	11	70700548	70731964	1	17	16	8	5	32	0	52	553	75	1	115	E9Q9B0	
ENSMUST00000072204	ENSMUSG00000063089	7	43950664	43954941	1	7	6	9	7	4	1	0	0	0	0	0		P07628
ENSMUST00000072206	ENSMUSG00000023345	9	106281061	106350521	1	6	0	4	17	0	0	55	23	44	0	1		Q8JZX3
ENSMUST00000072217	ENSMUSG00000006344	10	75589340	75617200	1	33	23	45	40	24	10	2080	3562	1748	348	1450		Q9Z2A9
ENSMUST00000072219	ENSMUSG00000095484	19	13529675	13530622	1	5	3	3	1	2	4	0	0	0	0	0	Q7TQQ6	
ENSMUST00000072222	ENSMUSG00000057894	7	12804977	12818858	-1	104	88	334	117	59	44	45	99	51	30	62	B2RSV9	Q6GQR8
ENSMUST00000072228	ENSMUSG00000059434	5	31297443	31327314	1	17	7	35	16	23	7	0	0	0	1	0		Q91X44
ENSMUST00000072232	ENSMUSG00000058587	9	75497796	75559657	-1	23	23	32	174	31	13	1086	2466	1971	2275	1221		Q9JHJ0
ENSMUST00000072235	ENSMUSG00000060715	1	53158577	53187636	-1	0	4	0	0	0	0	0	0	0	0	0	Q9DA74	
ENSMUST00000072237	ENSMUSG00000020827	11	70562881	70614483	1	0	0	0	147	0	0	0	0	45	0	0	G3X9G2	
ENSMUST00000072239	ENSMUSG00000019961	10	91147571	91171582	-1	11	2	9	16	10	0	1518	5689	2730	500	1690		Q61029
ENSMUST00000072249	ENSMUSG00000032803	9	103353094	103365840	-1	0	35	69	0	0	0	244	724	465	83	294		Q4VAA2
ENSMUST00000072256	ENSMUSG00000022935	16	87896196	88056176	-1	0	0	0	0	0	0	0	0	0	0	0	F6QF13	
ENSMUST00000072265	ENSMUSG00000061336	17	37623668	37624633	-1	2	7	8	3	5	4	0	0	0	0	0	Q923Q6	
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ENSMUST00000072271	ENSMUSG00000019232	3	130617448	130637521	1	11	9	5	11	24	2	0	0	0	1	0		Q8BWU8
ENSMUST00000072280	ENSMUSG00000059632	16	89487374	89487952	-1	4	6	3	3	4	4	0	0	0	0	0		O08633
ENSMUST00000072286	ENSMUSG00000067700	5	26017278	26022916	-1	26	14	12	20	18	12	0	1	1	0	3	K7N5V5	
ENSMUST00000072287	ENSMUSG00000038861	3	94974731	95006843	1	12	0	27	49	39	22	181	260	324	24	338		Q8BKC8
ENSMUST00000072289	ENSMUSG00000061981	11	78037931	78060434	1	12	9	0	23	15	0	7926	9800	7694	699	3904		Q60634
ENSMUST00000072290	ENSMUSG00000096356	9	38115692	38116727	1	3	3	10	8	4	3	0	0	0	0	0	L7N1Y6	
ENSMUST00000072292	ENSMUSG00000036916	X	48541625	48594504	-1	0	0	0	0	5	0	0	0	42	39	0		Q6P3Y5
ENSMUST00000072298	ENSMUSG00000027634	2	156927345	156992056	-1	0	16	36	12	14	0	253	662	289	86	229	Q5441I	Q9QYF9
ENSMUST00000072299	ENSMUSG00000054459	12	11325247	11436649	-1	22	15	113	46	29	6	0	2	1	0	1	Q4W4C9	P62761
ENSMUST00000072306	ENSMUSG00000057674	11	99602646	99603308	-1	14	9	38	159	15	8	0	0	0	0	0	Q9D3H4	
ENSMUST00000072311	ENSMUSG00000014932	5	32611171	32687057	1	12	6	25	345	6	13	19	90	31	10	24	Q3TJI7	Q04736
ENSMUST00000072312	ENSMUSG00000056900	3	32817546	32938071	1	50	31	95	78	50	23	0	1	0	0	0		Q5BKP2
ENSMUST00000072316	ENSMUSG00000094133	19	12209568	12210506	1	0	0	0	0	1	0	0	0	0	0	0	Q8VF59	
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ENSMUST00000072329	ENSMUSG00000057531	13	44922079	45002096	-1	0	0	0	0	0	0	276	418	254	116	200		Q91WZ8
ENSMUST00000072331	ENSMUSG00000057092	7	31068172	31076704	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000072334	ENSMUSG00000000826	2	181520485	181555133	1	53	43	117	113	44	34	982	4910	1456	245	1053		P60904
ENSMUST00000072357	ENSMUSG00000037012	10	62268855	62379908	-1	9	0	0	0	0	0	1310	2114	1327	70	899		P17710
ENSMUST00000072359	ENSMUSG00000058126	14	113314608	113316713	1	17	14	19	15	26	11	7968	20474	11216	2385	7321	D3Z2H9	
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ENSMUST00000072363	ENSMUSG00000059832	3	92823074	92827247	-1	23	16	33	112	35	12	0	0	0	0	0		B2RUR4
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ENSMUST00000072381						5	10	8	13	10	0	0	0	0	0	0		
ENSMUST00000072383	ENSMUSG00000024101	17	66111546	66120503	1	1	1	32	138	36	0	372	642	304	120	313		Q8VDD8
ENSMUST00000072385	ENSMUSG00000096099	13	23183628	23184524	-1	3	3	4	1	2	4	0	0	0	0	0	Q8R272	
ENSMUST00000072386	ENSMUSG00000040987	7	18839966	18863113	1	0	5	0	0	0	0	0	0	0	0	0	Q8HWE5	
ENSMUST00000072391	ENSMUSG00000060081	13	23934462	23934851	1	5	6	8	64	9	4	10	42	3	7	4	Q8CGP4	
ENSMUST00000072393	ENSMUSG00000031174	X	10073621	10216920	-1	0	0	0	6	0	0	0	0	11	13	0	A2ADP5	
ENSMUST00000072395	ENSMUSG00000058981	1	173183442	173190635	-1	5	6	4	7	5	4	0	0	0	0	0	E9Q8X1	
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ENSMUST00000072404	ENSMUSG00000061977	6	131684836	131685744	-1	1	3	0	3	2	0	0	0	0	0	0		Q7M723
ENSMUST00000072406	ENSMUSG00000024127	17	85063477	85090267	-1	21	0	0	8	0	16	22	32	53	80	46		Q8C167
ENSMUST00000072410	ENSMUSG00000060245	17	20776059	20777501	-1	2	2	0	0	2	0	0	0	0	0	0	Q8R2A7	
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ENSMUST00000072431	ENSMUSG00000040928	4	129148005	129189727	-1	0	16	0	0	1	8	4	231	0	0	26		Q9D5K4
ENSMUST00000072437	ENSMUSG00000062282	13	46175428	46191048	-1	21	20	22	103	23	14	0	0	0	0	0	Q8CE57	
ENSMUST00000072438	ENSMUSG00000030483	7	25897620	25926624	1	14	6	7	0	0	0	0	0	0	0	0	Q9WUD0	
ENSMUST00000072451	ENSMUSG00000037341	X	20105755	20291807	-1	2	1	3	0	3	0	6	6	6	0	11		Q8BLV3
ENSMUST00000072452	ENSMUSG00000045503	2	164456964	164479638	1	7	0	0	8	3	1	968	1474	680	336	507		Q78S06
ENSMUST00000072453	ENSMUSG00000100916	7	45420820	45421861	1	4	3	16	43	4	4	0	0	0	0	0	G3X9G6	
ENSMUST00000072460	ENSMUSG00000030557	7	67231163	67372858	-1	0	0	0	13	0	0	18	6	42	0	14	S4R2H4	
ENSMUST00000072465	ENSMUSG00000057982	9	22225714	22243197	1	5	2	6	98	6	8	38	229	96	60	78		G3X9G7
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ENSMUST00000072476	ENSMUSG00000001168	5	120861421	120873506	1	14	20	13	13	19	10	0	2	0	0	0	Q8VI97	
ENSMUST00000072477	ENSMUSG00000044501	17	22361453	22377281	1	0	0	0	0	9	4	14	29	18	16	16	E9Q8W2	
ENSMUST00000072480	ENSMUSG00000059994	3	87376387	87402934	1	0	0	0	0	0	0	94	29	9	0	0		
ENSMUST00000072481	ENSMUSG00000028524	4	102741297	102973628	1	0	0	0	0	0	0	2	10	4	8	0		Q8VD37
ENSMUST00000072482	ENSMUSG00000036469	8	65617900	66471637	1	2	0	0	0	8	0	202	1199	367	721	296		Q6NZQ8
ENSMUST00000072503	ENSMUSG00000059070	7	45715457	45720835	1	8	4	0	0	0	6	4154	4047	2349	9663	1705	Q58EW0	P35980
ENSMUST00000072505	ENSMUSG00000042540	12	84069325	84076020	1	0	3	13	124	0	3	0	1	0	0	0	Q91YQ6	
ENSMUST00000072513	ENSMUSG00000061626	7	103777396	103778343	-1	8	7	5	2	12	8	0	0	0	0	0	E9PYY2	
ENSMUST00000072514	ENSMUSG00000009471	7	46376474	46379092	1	14	5	17	154	29	18	0	0	0	0	0		P10085
ENSMUST00000072517	ENSMUSG00000095928	16	59314488	59315405	-1	4	0	5	1	1	1	0	0	0	0	0	E9Q8M0	
ENSMUST00000072518	ENSMUSG00000100194	X	118427227	118428256	1	4	1	2	2	1	3	0	0	0	0	0	Q8K5B9	
ENSMUST00000072519	ENSMUSG00000041112	13	20090596	20606528	1	39	19	28	289	46	24	1284	2929	2119	151	1464		Q8BPU7
ENSMUST00000072521	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0		Q80TS3
ENSMUST00000072530	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	637	1375	582	176	459		Q91VU6
ENSMUST00000072532						7	2	2	3	3	0	0	0	0	2	0		
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ENSMUST00000072551	ENSMUSG00000043850	3	58844028	58885340	-1	0	0	0	0	0	0	0	0	0	0	0	Q8K444	
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ENSMUST00000072566	ENSMUSG00000020857	11	93949814	93956259	-1	9	4	12	106	13	0	104	547	97	667	235	Q5NC82	Q01768
ENSMUST00000072570						11	9	45	10	22	6	1	1	0	1	0		
ENSMUST00000072572	ENSMUSG00000063362	8	22060721	22071627	1	37	0	77	0	39	33	34	113	51	62	51	A0A077K846	Q3TZM9
ENSMUST00000072576	ENSMUSG00000014504	18	34330847	34336599	1	0	0	0	0	0	0	50	278	117	312	75	Q9D104	
ENSMUST00000072578	ENSMUSG00000063447	5	107830099	107831776	1	7	7	13	27	16	6	0	0	0	0	0		Q6ZWY6
ENSMUST00000072580	ENSMUSG00000062044	7	45783738	45804144	1	0	0	42	21	0	0	0	2	0	0	0		
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ENSMUST00000072582						4	2	2	0	1	1	0	0	0	0	1		
ENSMUST00000072585	ENSMUSG00000056131	9	86554377	86571842	-1	0	2	2	0	0	2	3	38	25	28	41	Q8BWW3	
ENSMUST00000072587	ENSMUSG00000054312	3	95862634	95871519	-1	0	1	0	0	0	0	162	82	5	345	58	Q059G7	P58059
ENSMUST00000072593	ENSMUSG00000062814	X	21115820	21121192	1	0	0	0	0	0	0	0	0	0	0	0	B1AUS7	
ENSMUST00000072596	ENSMUSG00000059857	3	109780040	110144011	-1	0	3	3	2	0	0	0	0	0	0	0		Q8R4G0
ENSMUST00000072600	ENSMUSG00000057123	3	96904693	97077416	1	68	36	376	129	63	27	58	133	58	3	29		Q01231
ENSMUST00000072602	ENSMUSG00000064267	5	122206804	122242297	1	5	11	0	19	36	14	558	595	621	153	626		Q3U2S8
ENSMUST00000072607	ENSMUSG00000029547	5	139751282	139775674	-1	88	43	180	436	145	45	557	490	634	35	615	K3W4P2	
ENSMUST00000072608	ENSMUSG00000063020	16	59119148	59120068	-1	0	2	1	1	0	0	0	0	0	0	0	L7N1Y8	
ENSMUST00000072612	ENSMUSG00000064299	9	114276683	114317028	-1	73	60	96	44	50	34	0	1	0	0	3	Q9D5S6	
ENSMUST00000072621	ENSMUSG00000038909	11	95274259	95310246	-1	0	0	13	0	16	0	98	1	34	21	67		Q5SVQ0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000072631	ENSMUSG00000058669	12	56611389	56613284	-1	87	63	664	382	67	34	0	3	0	0	2		O70584
ENSMUST00000072632	ENSMUSG00000099787	13	22187146	22188048	-1	1	2	3	2	5	0	0	0	0	0	0	Q8K4C9	
ENSMUST00000072633	ENSMUSG00000020839	11	76902159	76916587	1	0	0	0	2	1	4	0	4	0	3	0		Q9D7L8
ENSMUST00000072634	ENSMUSG00000031996	9	31149557	31211815	-1	31	16	39	99	0	0	1189	2309	1700	276	1593	Q60709	
ENSMUST00000072639	ENSMUSG00000047821	11	62820231	62850808	1	3	0	9	0	0	1	39	0	52	0	37	Q5SVT1	
ENSMUST00000072646	ENSMUSG00000021280	12	111417430	111431182	1	31	18	55	107	56	20	7	16	4	41	16		
ENSMUST00000072655	ENSMUSG00000093942	7	140610168	140611124	1	2	4	9	11	8	4	0	0	0	0	0	Q8VGJ4	
ENSMUST00000072662	ENSMUSG00000058028	7	6222278	6239423	1	29	20	87	45	40	16	1	2	3	0	3	B2RTN3	
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ENSMUST00000072671	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	0	0	0	0	0	0	0	0		Q9CS84
ENSMUST00000072678	ENSMUSG00000089873	4	61224307	61228286	-1	0	0	0	3	0	0	0	0	0	0	0	A2CEK6	
ENSMUST00000072685	ENSMUSG00000043531	19	50143301	50678646	-1	10	11	26	107	12	19	0	2	1	0	2	E9QQ02	
ENSMUST00000072692	ENSMUSG00000022565	15	76170974	76232574	-1	0	17	24	835	40	35	2039	935	3003	72	2213		Q9QXS1
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ENSMUST00000072697	ENSMUSG00000062908	3	153922357	153944632	-1	16	13	15	93	15	13	169	812	345	559	268		P45952
ENSMUST00000072699	ENSMUSG00000015217	X	71555918	71560676	1	53	54	0	33	0	0	73	160	86	149	56	Q544R9	O54879
ENSMUST00000072713	ENSMUSG00000030486	7	24254794	24262445	1	16	17	41	19	21	9	0	1	0	1	1	E9Q8I5	
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ENSMUST00000072726	ENSMUSG00000040560	18	63708695	63989760	1	29	58	50	89	37	21	406	732	791	38	403		Q920I9
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ENSMUST00000072731	ENSMUSG00000096757	9	38377883	38378833	1	3	0	3	0	0	3	0	0	0	0	0	E9Q891	
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ENSMUST00000072739	ENSMUSG00000064317	10	78393309	78393756	1	2	7	22	0	0	8	50	97	42	237	0		Q9CQQ8
ENSMUST00000072740	ENSMUSG00000017631	11	76416734	76622314	-1	12	16	31	165	17	13	0	0	0	0	0		Q5SSL4
ENSMUST00000072744	ENSMUSG00000021038	12	87238875	87266286	-1	0	0	0	0	0	0	803	2774	1269	448	857		Q8BGQ1
ENSMUST00000072748	ENSMUSG00000024731	19	10962293	10974670	-1	7	3	7	3	13	6	0	0	0	0	0	B2RWS0	Q99N03
ENSMUST00000072750	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	125	2	5	49	157	155	46	248	G5E8G0	
ENSMUST00000072751	ENSMUSG00000078440	10	81384428	81391560	1	2	4	25	154	11	7	165	232	103	162	93		Q99LN9
ENSMUST00000072753	ENSMUSG00000061887	4	106910701	107049694	1	0	0	0	0	0	0	66	60	166	0	112		Q9D032
ENSMUST00000072755	ENSMUSG00000001435	10	77052178	77166548	-1	16	20	105	0	3	13	0	0	0	0	0	E9QPX1	
ENSMUST00000072767	ENSMUSG00000059495	9	42963842	43105718	-1	67	58	91	0	56	26	23	30	59	27	145		Q8R4H2
ENSMUST00000072776	ENSMUSG00000094806	15	82402846	82407194	-1	19	4	21	10	21	8	0	0	0	10	0		P24456
ENSMUST00000072777	ENSMUSG00000056758	10	120361275	120476469	-1	0	0	8	169	19	14	11	40	29	28	87		P52927
ENSMUST00000072779						1	0	3	0	0	0	0	4	1	5	1		
ENSMUST00000072784	ENSMUSG00000060878	19	11895999	11897050	1	7	4	13	6	7	5	0	0	0	0	2	Q8VF55	
ENSMUST00000072787	ENSMUSG00000066828	7	9205546	9223653	-1	0	3	3	0	3	0	0	0	0	0	0	F8VQD3	
ENSMUST00000072796						13	11	12	64	10	22	40	0	136	129	32		
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ENSMUST00000072801	ENSMUSG00000058132	7	12304802	12305719	1	7	2	4	4	8	1	0	0	0	0	0	Q8R283	
ENSMUST00000072804	ENSMUSG00000051910	7	115470872	116038796	-1	0	0	0	0	0	16	0	0	0	0	0	Q3V1J7	P40645
ENSMUST00000072818	ENSMUSG00000061906	5	87409942	87424203	-1	2	4	0	0	4	4	0	0	0	0	0	Q91WH2	
ENSMUST00000072829	ENSMUSG00000064194	7	43114229	43192109	1	1	5	6	2	3	2	0	0	0	0	0	F6QN44	
ENSMUST00000072835	ENSMUSG00000071855	18	46282151	46311928	-1	4	2	1	46	5	2	1	6	2	6	5	D3Z1J2	
ENSMUST00000072836	ENSMUSG00000057342	7	45709467	45718002	-1	9	12	53	183	29	12	328	242	178	7	171	Q58E38	Q9JIA7
ENSMUST00000072837	ENSMUSG00000056493	5	142401497	142462011	1	98	89	408	291	105	55	1543	1433	2018	90	1586		P42128
ENSMUST00000072838	ENSMUSG00000022556	15	76477445	76500972	1	12	13	26	129	24	11	167	246	142	25	191	A0A075F882	P38532
ENSMUST00000072841	ENSMUSG00000060600	11	70657202	70662513	1	3	3	10	12	5	5	34	34	36	71	78		P21550
ENSMUST00000072847	ENSMUSG00000024317	18	21001341	21028223	1	4	3	4	274	7	7	27	112	17	0	16		Q9CQE0
ENSMUST00000072853	ENSMUSG00000063137	16	58872219	58873977	-1	3	2	3	4	3	2	0	0	0	0	0	E9Q7W1	
ENSMUST00000072854	ENSMUSG00000094266	2	36452587	36453525	1	1	6	5	1	6	3	0	0	0	0	0	Q8VGL0	
ENSMUST00000072857	ENSMUSG00000062110	5	74204816	74531759	-1	30	26	71	495	42	20	9	95	17	6	24		Q8BTY8
ENSMUST00000072859	ENSMUSG00000062818	6	90122643	90130990	1	9	4	4	0	5	1	0	0	0	0	0		
ENSMUST00000072863	ENSMUSG00000052534	1	168119364	168432270	-1	0	0	0	0	0	0	102	38	152	19	119	Q71VB4	P41778
ENSMUST00000072866	ENSMUSG00000028437	4	41348996	41390525	1	20	14	53	47	31	8	130	497	172	23	157		Q8BH48
ENSMUST00000072868	ENSMUSG00000050963	15	34837381	34842337	1	27	18	20	170	31	14	0	0	0	0	0		O35174
ENSMUST00000072873	ENSMUSG00000020827	11	70562881	70614483	1	0	0	4	19	0	0	12	0	54	20	33	Q5SXG3	
ENSMUST00000072875	ENSMUSG00000055436	3	158010473	158036639	-1	0	2	3	108	4	2	321	531	298	112	401	Q3UIX4	
ENSMUST00000072876	ENSMUSG00000066366	12	103853589	103863562	-1	8	3	21	21	11	14	0	0	0	7	0	A0A0A0MQA3	
ENSMUST00000072886	ENSMUSG00000026387	1	120006894	120063536	1	4	7	26	32	12	6	0	0	0	0	0	H7BX37	
ENSMUST00000072887						4	2	3	5	7	3	0	0	0	0	0		
ENSMUST00000072889	ENSMUSG00000021338	13	24012344	24280795	-1	2	0	0	34	11	0	0	0	3	9	10		Q6EDY6
ENSMUST00000072895	ENSMUSG00000078905	2	175061549	175067781	-1	1	0	2	1	0	0	0	0	0	0	0	A2ARW5	
ENSMUST00000072896	ENSMUSG00000038525	5	21645813	21662694	1	18	4	32	72	24	8	76	277	110	36	105		Q9D0L7
ENSMUST00000072899	ENSMUSG00000032232	9	71626509	71771602	-1	40	18	23	0	31	16	0	0	63	28	483	B2RSU6	
ENSMUST00000072904						10	0	0	0	0	4	0	66	0	0	0		
ENSMUST00000072910	ENSMUSG00000063765	15	81678296	81697287	-1	2	6	15	602	16	12	0	0	0	0	0		E9Q7T7
ENSMUST00000072914	ENSMUSG00000063764	7	108629994	108630926	1	6	1	12	1	3	1	0	0	0	0	0		Q8VG42
ENSMUST00000072915	ENSMUSG00000056829	19	16872316	16873830	-1	5	4	14	479	19	10	0	0	0	0	0	B9EII5	Q64733
ENSMUST00000072916	ENSMUSG00000014243	11	62267224	62281375	-1	2	1	6	38	4	4	46	108	39	213	26		Q9CWQ2
ENSMUST00000072933	ENSMUSG00000059900	6	115729131	115762410	-1	0	0	0	0	0	0	1722	2554	1149	761	544		Q4FJU9
ENSMUST00000072939	ENSMUSG00000055368	8	92960079	93001667	1	59	48	151	109	80	45	4	3	12	7	17		O55192
ENSMUST00000072940						6	2	8	1	3	1	3	7	0	0	1		
ENSMUST00000072943	ENSMUSG00000060738	13	27773495	27780803	-1	10	12	8	1	19	8	0	0	0	0	0		Q9CRB5
ENSMUST00000072948	ENSMUSG00000020777	11	116171888	116199045	-1	0	0	14	0	0	0	24	456	198	0	99		Q9R0H0
ENSMUST00000072954	ENSMUSG00000062190	6	57702540	57739439	1	8	4	0	210	7	24	0	6	0	0	4		Q9JJK2
ENSMUST00000072955	ENSMUSG00000050530	2	3114224	3227806	1	38	27	77	0	66	12	0	0	0	2	0	A2ATL1	
ENSMUST00000072961	ENSMUSG00000041236	13	18717292	18866809	1	19	17	21	17	16	11	159	891	457	827	291		Q5KU39
ENSMUST00000072965	ENSMUSG00000015149	7	28766735	28788665	1	0	0	0	0	0	0	711	784	969	193	498		Q8VDQ8
ENSMUST00000072968	ENSMUSG00000096465	7	108255192	108256136	-1	4	2	5	1	5	1	0	0	0	0	0		Q8VG02
ENSMUST00000072971	ENSMUSG00000037685	5	67618140	67847434	-1	0	0	1	4	0	0	219	41	541	0	254		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000072972	ENSMUSG00000099917	13	23075792	23076694	1	1	2	1	5	6	1	0	0	0	0	0	Q8R264	
ENSMUST00000072974	ENSMUSG00000094461	9	38025808	38026737	1	2	4	1	1	7	1	0	0	0	0	0	Q8VF64	
ENSMUST00000072976	ENSMUSG00000096000	10	129186484	129187419	-1	4	3	5	5	4	5	0	0	0	0	0	F6VS78	
ENSMUST00000072977	ENSMUSG00000062103	9	38848116	38849042	1	0	1	3	3	4	1	0	0	0	0	0	Q7TRB8	
ENSMUST00000072982						13	12	3	6	17	3	0	3	0	1	0		
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ENSMUST00000072993	ENSMUSG00000060335	11	73602582	73603520	1	1	3	2	0	5	2	0	0	0	0	0	Q7TRX8	
ENSMUST00000072997	ENSMUSG00000027478	2	153649450	153687730	1	0	0	0	0	0	0	0	0	0	0	0		O88509
ENSMUST00000072999	ENSMUSG00000026288	1	87620312	87720507	1	0	0	0	0	0	0	0	4	0	0	0		Q9ES52
ENSMUST00000073001	ENSMUSG00000001123	11	78962974	78984946	-1	0	0	0	4	0	0	273	279	239	68	318	B1AQR8	
ENSMUST00000073012	ENSMUSG00000027750	3	54361109	54391037	1	0	0	0	3	0	0	0	0	0	0	0		Q62009
ENSMUST00000073014						0	10	32	0	7	4	0	0	0	4	0		
ENSMUST00000073025	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	0	0	0	0	165	0	0	0		Q6PCP5
ENSMUST00000073029	ENSMUSG00000021461	13	63304709	63497278	-1	11	9	19	17	14	4	4	5	3	5	7	Q8CBR3	
ENSMUST00000073043	ENSMUSG00000061353	6	117168535	117181367	1	49	38	111	52	62	33	0	0	0	0	0	H7BX38	
ENSMUST00000073049	ENSMUSG00000089960	1	88211959	88218997	1	76	49	85	77	56	28	12	157	43	13	125		Q63886
ENSMUST00000073054	ENSMUSG00000062526	18	67225530	67245830	-1	14	11	18	178	22	7	542	1325	753	137	667		Q80XL7
ENSMUST00000073056						1	4	3	2	0	0	0	0	0	0	0		
ENSMUST00000073059	ENSMUSG00000059227	7	108367490	108368436	1	3	1	12	1	4	5	0	0	0	0	0		Q8VG07
ENSMUST00000073062	ENSMUSG00000056824	2	165351297	165368729	-1	53	52	309	19	40	19	0	1	0	0	0	Q6NXM6	
ENSMUST00000073067	ENSMUSG00000032806	X	74369217	74373349	-1	0	2	5	10	4	0	191	357	0	122	65		P21129
ENSMUST00000073076	ENSMUSG00000028973	5	24393663	24410054	1	0	2	10	0	0	0	79	57	84	0	72		Q9CXJ4
ENSMUST00000073080	ENSMUSG00000058927	19	24875686	24876634	1	6	0	0	0	1	0	215	543	170	794	119	Q56A15	P62897
ENSMUST00000073081	ENSMUSG00000057047	2	173719415	173722089	1	14	9	30	15	18	8	1	1	0	0	0	Q9DAI7	
ENSMUST00000073088	ENSMUSG00000057160	12	24493207	24493656	-1	2	2	1	68	2	0	2	30	7	7	6	E9Q2K4	
ENSMUST00000073089	ENSMUSG00000054942	3	152273849	152340407	-1	20	13	40	66	28	26	27	28	43	20	66	B2RRB9	Q4QQM5
ENSMUST00000073094	ENSMUSG00000040990	X	159627272	159978069	1	0	0	0	0	0	0	152	156	582	83	424		Q8R550
ENSMUST00000073102	ENSMUSG00000096773	7	105024025	105024966	-1	2	3	1	0	1	2	0	0	0	0	0	Q7TRP1	
ENSMUST00000073104	ENSMUSG00000061950	17	65782573	65841926	1	0	0	0	0	0	0	495	61	519	169	275	E9QPR5	
ENSMUST00000073109	ENSMUSG00000047409	9	118926453	119043998	1	24	23	67	43	41	20	214	490	387	29	202		P58465
ENSMUST00000073111	ENSMUSG00000059113	16	89151086	89151550	1	2	0	13	1	4	1	0	0	0	0	0	D3Z714	
ENSMUST00000073115	ENSMUSG00000063689	3	96219865	96220308	1	3	4	5	81	5	5	0	0	0	0	0		Q64522
ENSMUST00000073116	ENSMUSG00000025225	19	46304737	46312090	1	19	8	19	104	18	12	1169	1399	1104	113	1013	Q3UG25	Q9WTK5
ENSMUST00000073120	ENSMUSG00000062729	1	171275990	171281186	-1	0	0	1	0	0	0	216	173	165	39	83		P51175
ENSMUST00000073122	ENSMUSG00000061457	9	20212207	20213353	1	1	3	2	4	4	0	0	0	0	0	0	Q7TRF0	
ENSMUST00000073124	ENSMUSG00000057691	6	48062395	48086593	-1	22	14	31	280	41	16	343	717	412	65	336		Q3U133
ENSMUST00000073126	ENSMUSG00000078130	11	99649599	99650236	-1	0	0	8	64	0	3	0	0	0	0	0	E9PUW3	
ENSMUST00000073127	ENSMUSG00000035024	9	27030175	27095311	1	33	24	35	41	27	20	209	390	465	111	265	K4DI67	
ENSMUST00000073128	ENSMUSG00000013646	11	58330724	58347728	1	0	0	0	0	0	0	1044	1108	864	67	465		Q99LH9
ENSMUST00000073139	ENSMUSG00000036564	8	95676980	95715119	1	7	10	31	21	8	4	0	0	0	0	6		Q8BTG7
ENSMUST00000073143	ENSMUSG00000047150	17	47412734	47437376	-1	4	5	19	3	3	1	0	0	0	0	0	E9Q6U5	
ENSMUST00000073149	ENSMUSG00000014786	8	105348258	105369881	1	49	33	83	206	73	33	5	9	9	1	24	B2RXE2	
ENSMUST00000073150	ENSMUSG00000021846	14	48120869	48260883	1	28	24	101	139	34	12	1132	1507	1436	183	765	E9QPQ6	
ENSMUST00000073151	ENSMUSG00000060508	7	20008023	20073306	1	13	14	4	16	15	12	0	0	0	0	0		Q66X22
ENSMUST00000073152	ENSMUSG00000027086	2	69686815	69713516	-1	24	16	20	15	15	12	16	41	19	11	22		Q6DI86
ENSMUST00000073156						0	0	0	387	0	0	0	1	0	0	2		
ENSMUST00000073157	ENSMUSG00000071281	13	67705306	67729119	-1	1386	1587	1893	1195	1673	692	16	262	57	101	87	Q91W94	
ENSMUST00000073161	ENSMUSG00000023079	5	134357656	134456716	-1	0	0	0	0	0	0	0	0	0	0	19		Q9JI57
ENSMUST00000073173	ENSMUSG00000030249	6	142587862	142702315	-1	0	0	119	72	0	0	0	0	0	0	0		P70170
ENSMUST00000073179	ENSMUSG00000073730	1	23100473	23102253	-1	9	7	11	52	17	3	0	0	0	0	0	Q14BX6	
ENSMUST00000073192	ENSMUSG00000020311	11	30930774	30954335	-1	2	1	3	3	3	0	68	344	81	26	53		Q8VEH8
ENSMUST00000073196						0	6	3	4	0	2	0	0	0	1	0		
ENSMUST00000073201	ENSMUSG00000058748	8	4613167	4629549	1	3	3	2	3	6	4	21	129	25	56	18	F6R9A8	
ENSMUST00000073208	ENSMUSG00000079507	17	35320405	35325099	1	0	0	0	0	0	0	0	0	0	0	0	O19441	
ENSMUST00000073211	ENSMUSG00000024049	17	71019521	71126856	1	37	9	69	26	52	24	0	0	0	0	0		Q62234
ENSMUST00000073214	ENSMUSG00000057444	9	38537882	38539829	1	3	0	1	5	5	3	0	0	0	0	0	Q8VG76	
ENSMUST00000073226	ENSMUSG00000063823	7	140418842	140419771	-1	7	2	13	9	8	7	0	0	0	0	0	Q8VGT4	
ENSMUST00000073228	ENSMUSG00000027463	2	151996511	152009258	1	0	6	0	0	25	13	156	0	180	34	89		Q9D6X5
ENSMUST00000073234	ENSMUSG00000059995	11	102289300	102296631	-1	0	0	0	23	0	13	0	254	203	0	323		A2AWT3
ENSMUST00000073238	ENSMUSG00000060143	14	105681828	105682211	1	13	7	10	8	27	19	34	232	20	86	0		P62947
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ENSMUST00000073251	ENSMUSG00000062961	12	80754046	80760541	-1	48	26	69	698	52	24	0	0	0	0	0		Q3UHB8
ENSMUST00000073252	ENSMUSG00000026251	1	87190607	87200070	1	1	29	5	43	22	7	1	1	2	0	0	Q80VZ5	P02716
ENSMUST00000073261	ENSMUSG00000061991	13	23533906	23534304	1	3	3	2	198	11	0	2	8	0	6	0		Q8CGP5
ENSMUST00000073277	ENSMUSG00000059562	17	25162461	25171913	1	6	0	12	13	0	3	0	0	0	0	2		Q6RUT8
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ENSMUST00000073295	ENSMUSG00000064224	11	98626360	98638226	1	0	0	0	0	10	0	0	0	0	0	0		Q5Y4Y6
ENSMUST00000073302	ENSMUSG00000057315	5	102481391	102897937	1	0	0	0	128	9	0	7	0	0	12	12		Q8C4V1
ENSMUST00000073308	ENSMUSG00000009079	11	5069689	5099266	-1	0	0	23	0	6	0	674	1483	536	239	589	Q5SUT0	
ENSMUST00000073309	ENSMUSG00000021879	14	26693274	26891703	1	2	1	3	1	0	0	0	0	0	0	0	F7D0D4	
ENSMUST00000073312	ENSMUSG00000067928	17	21707741	21725636	1	14	15	18	6	11	9	35	131	56	13	47	E9QAF5	
ENSMUST00000073316	ENSMUSG00000001517	6	128362967	128376146	1	26	15	95	50	49	16	198	154	219	19	112	Q6P1H7	
ENSMUST00000073317						0	3	0	0	2	0	0	0	0	3	0		
ENSMUST00000073320	ENSMUSG00000062105	16	58995385	59000616	1	3	1	0	2	2	0	0	0	0	0	0	E9QKE8	
ENSMUST00000073322	ENSMUSG00000063844	2	111257117	111258055	1	3	5	4	1	9	0	0	0	0	0	0	Q8VF40	
ENSMUST00000073325	ENSMUSG00000074277	7	24610763	24629297	1	15	17	59	201	29	14	130	125	98	16	86	E9QAF4	
ENSMUST00000073337	ENSMUSG00000038002	17	24961228	25015230	-1	82	49	241	285	80	42	460	1050	870	54	816		Q6PG95
ENSMUST00000073339	ENSMUSG00000006373	X	36598206	36606079	1	4	3	3	106	3	4	116	563	189	63	143	Q3TXU8	O55022
ENSMUST00000073347						2	5	9	323	10	4	0	0	0	0	0		
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ENSMUST00000073352	ENSMUSG00000062175	2	156840007	156855570	1	11	19	40	0	0	36	87	210	0	34	5	Q3TZS1	
ENSMUST00000073363	ENSMUSG00000029282	5	88376108	88385916	1	5	3	9	5	9	2	0	0	0	0	0		Q9D3J8
ENSMUST00000073364	ENSMUSG00000025262	X	151344175	151471842	1	14	0	0	218	22	12	5	10	12	3	23		Q8C3F2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000073371	ENSMUSG00000065979	16	11803721	11909445	-1	28	14	60	50	23	11	5	24	2	4	7		Q8BFS6
ENSMUST00000073379	ENSMUSG00000060534	18	71258738	72351069	-1	0	0	2	22	15	0	0	0	0	0	0		P70211
ENSMUST00000073380	ENSMUSG00000057240	19	11169418	11196737	-1	0	0	0	3	0	0	0	0	0	0	0		Q5FWC3
ENSMUST00000073384	ENSMUSG00000057981	6	57158920	57159854	1	1	5	3	0	2	2	0	0	0	0	0	G5E8G1	
ENSMUST00000073387	ENSMUSG00000029859	6	42358487	42373268	-1	15	20	47	63	25	14	282	288	260	54	352		Q60750
ENSMUST00000073388	ENSMUSG00000017718	11	117825924	117839908	1	0	6	0	0	0	0	61	55	60	32	21		Q8K4H1
ENSMUST00000073391	ENSMUSG00000062432	19	37685581	37693398	1	7	4	19	190	23	7	1	3	3	1	4	B2RXA7	
ENSMUST00000073392	ENSMUSG00000031174	X	10073621	10216920	-1	0	0	0	0	0	0	0	40	0	0	0	A2ADP2	
ENSMUST00000073394	ENSMUSG00000057321	7	103249737	103252505	-1	15	5	63	10	10	0	0	0	0	0	0	G5E8G2	
ENSMUST00000073406	ENSMUSG00000061877	7	81494275	81498281	-1	2	2	3	1	0	0	0	0	0	0	0	Q6XL63	
ENSMUST00000073410	ENSMUSG00000090744	7	41545674	41573662	-1	8	2	26	11	0	5	2	15	3	1	4	L7N1Z0	
ENSMUST00000073415	ENSMUSG00000057592	6	90035933	90036841	-1	4	0	2	29	19	7	1	0	0	0	0		Q9EQ52
ENSMUST00000073418	ENSMUSG00000022565	15	76170974	76232574	-1	0	11	1	0	26	0	0	0	4	10	0		Q9QXS1
ENSMUST00000073428	ENSMUSG00000063354	15	76612385	76616852	-1	15	14	44	86	23	10	28	69	18	17	29		Q78IQ7
ENSMUST00000073430	ENSMUSG00000010110	19	8741413	8756069	1	0	0	0	0	0	0	459	806	613	115	536		Q8K1E0
ENSMUST00000073433	ENSMUSG00000064110	9	39669059	39669994	1	7	3	2	3	5	5	0	0	0	0	0	Q7TRA9	
ENSMUST00000073441	ENSMUSG00000042772	1	152836995	152902646	-1	31	0	106	59	27	14	359	1309	794	81	747		Q5RJH6
ENSMUST00000073447	ENSMUSG00000104346	18	37674307	37841873	1	15	12	46	32	23	6	0	0	2	0	2	Q91XY5	
ENSMUST00000073448	ENSMUSG00000057969	9	107597674	107609229	-1	0	0	0	0	0	0	0	0	0	0	0	M9MMK0	
ENSMUST00000073456	ENSMUSG00000060739	13	97129427	97137926	-1	36	32	46	65	44	17	416	2850	829	4230	690		Q9CR47
ENSMUST00000073458	ENSMUSG00000059023	2	88794384	88795307	1	1	1	3	0	6	1	0	0	0	0	0	Q8VGF5	
ENSMUST00000073459	ENSMUSG00000062542	7	107370728	107548656	1	8	7	27	27	18	0	0	0	0	0	0		Q9R0N9
ENSMUST00000073466	ENSMUSG00000058240	16	91689322	91728975	-1	1	0	5	0	0	6	19	26	70	18	27		Q921W4
ENSMUST00000073468	ENSMUSG00000070459	7	84915781	84916728	1	6	5	16	3	5	0	0	0	0	0	0	Q7TS13	
ENSMUST00000073471	ENSMUSG00000060938	11	68901583	68906989	1	8	9	9	29	4	1	823	2500	818	5418	572	Q4FZH2	P61255
ENSMUST00000073488	ENSMUSG00000060601	7	44549616	44553951	-1	0	0	0	18	0	0	566	2	673	178	262		Q60644
ENSMUST00000073490	ENSMUSG00000026354	1	128284756	128328318	-1	44	28	67	53	68	26	5	7	5	0	1	F8VPT3	
ENSMUST00000073507	ENSMUSG00000060049	19	12268163	12269241	1	6	1	2	1	0	1	0	0	0	0	0	E9Q9Z6	
ENSMUST00000073521	ENSMUSG00000031767	8	114133557	114154739	1	21	14	38	26	22	8	9	76	12	11	13		Q99P30
ENSMUST00000073527	ENSMUSG00000042581	1	129273302	130219278	1	2	0	0	0	19	0	0	0	0	0	0		Q6P4U0
ENSMUST00000073528	ENSMUSG00000063935	5	72576806	72581254	-1	3	5	6	226	14	4	0	0	0	0	0		Q80SU3
ENSMUST00000073532	ENSMUSG00000070617	4	143696500	143702711	-1	3	3	3	1	5	4	0	0	0	0	0	A2AGW7	
ENSMUST00000073534	ENSMUSG00000024220	17	28177207	28205886	1	0	1	20	55	2	0	247	138	205	18	124		Q8BMU0
ENSMUST00000073536	ENSMUSG00000049134	19	56320035	56390037	-1	0	16	56	0	3	13	0	10	0	0	0		Q80XB4
ENSMUST00000073543	ENSMUSG00000057890	11	51048109	51049050	1	7	7	10	7	12	7	0	0	0	0	0		
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ENSMUST00000073551	ENSMUSG00000042063	12	116047724	116063360	1	1	2	9	12	1	1	32	119	44	51	20	Q3TN43	
ENSMUST00000073554	ENSMUSG00000062329	5	37735519	37739820	1	8	8	8	3	11	2	0	0	0	0	0	A1E5L0	
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ENSMUST00000073560						0	0	29	2	3	1	0	0	0	0	0		
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ENSMUST00000073570	ENSMUSG00000073423	17	33629090	33631779	1	2	2	6	0	6	1	27	0	49	1	0	Q14A93	Q9DCK4
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ENSMUST00000073572	ENSMUSG00000064068	3	89209081	89227088	-1	0	0	0	190	12	0	16	32	22	4	45	F7C846	
ENSMUST00000073575	ENSMUSG00000002105	2	91061791	91070417	-1	0	0	0	106	14	8	32	100	91	18	138	B2RQ45	Q8BZH0
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ENSMUST00000073601	ENSMUSG00000062201	13	27156790	27162590	1	0	2	3	0	0	5	0	0	0	0	0	Q8CGZ7	
ENSMUST00000073605	ENSMUSG00000057666	6	125161715	125166467	-1	0	0	0	0	0	0	3643	5750	7353	4852	3750	D2KHZ9	P16858
ENSMUST00000073612						4	8	5	11	7	3	0	0	0	0	0		
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ENSMUST00000073618	ENSMUSG00000038528	10	39958061	39986646	-1	15	9	9	107	13	4	4	8	7	2	3	Q3TN71	
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ENSMUST00000073636	ENSMUSG00000095286	17	37659378	37660331	-1	1	0	3	10	5	0	0	0	0	0	0	L7N1Z1	
ENSMUST00000073639	ENSMUSG00000089789	10	127759721	127768297	1	837	705	4875	1106	1060	479	16	63	28	8	61	Q8CGV4	
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ENSMUST00000073660	ENSMUSG00000061981	11	78037931	78060434	1	4	0	42	11	20	0	348	924	383	5	372	Q5SS83	
ENSMUST00000073663	ENSMUSG00000062527	1	173130200	173137334	-1	5	4	10	12	2	1	0	0	0	0	0	Q8VG32	
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ENSMUST00000073674	ENSMUSG00000060726	X	135718667	135725261	-1	0	0	5	0	0	0	0	0	0	0	0	Q9D2R9	
ENSMUST00000073675	ENSMUSG00000070379	11	74155115	74156126	1	7	3	4	1	2	1	0	0	0	0	0	Q8VFX8	
ENSMUST00000073687	ENSMUSG00000021782	14	24133953	24245920	-1	13	41	0	157	0	2	0	0	0	0	62	E9Q9I2	
ENSMUST00000073691	ENSMUSG00000023022	15	99778470	99875428	-1	0	0	0	54	15	0	0	0	0	0	0		Q9ERG0
ENSMUST00000073704	ENSMUSG00000095483	10	129260963	129261901	1	1	6	0	0	4	3	0	0	0	0	0	Q7TRI3	
ENSMUST00000073705	ENSMUSG00000037750	11	78094660	78156700	1	0	0	18	72	15	0	449	1045	458	49	135		Q6P539
ENSMUST00000073707	ENSMUSG00000017652	2	165055627	165072948	1	0	0	0	0	0	0	0	0	0	19	0		P27512
ENSMUST00000073713	ENSMUSG00000063713	7	44188236	44192455	1	3	9	4	7	7	3	0	0	0	1	0		Q61754
ENSMUST00000073721	ENSMUSG00000095040	5	146182441	146185304	-1	0	3	3	2	3	0	0	4	0	0	2	Q80ZR8	
ENSMUST00000073722	ENSMUSG00000060019	8	106572966	106573461	-1	8	2	4	21	4	0	10	17	2	32	6	E9Q3T0	
ENSMUST00000073724	ENSMUSG00000024193	17	26933127	26937890	1	18	5	36	303	48	15	1209	3716	1168	189	1706		Q9Z1B8
ENSMUST00000073728	ENSMUSG00000063998	13	22851554	22852543	-1	5	1	9	3	7	1	0	0	0	0	0	Q8R266	
ENSMUST00000073732	ENSMUSG00000094986	19	13063413	13064336	1	3	2	0	4	2	1	0	0	0	0	0	Q8VFW2	
ENSMUST00000073748	ENSMUSG00000063583	1	92607839	92608847	1	5	5	13	5	19	4	0	0	0	0	0	Q8VFC5	
ENSMUST00000073764						0	0	0	0	0	0	21	18	6	42	13		
ENSMUST00000073765	ENSMUSG00000063842	9	19883309	19884343	-1	1	2	4	1	5	0	0	0	0	0	0	Q8VFJ1	
ENSMUST00000073772	ENSMUSG00000090175	1	88070800	88218997	1	1	4	8	3	4	1	0	0	0	0	0		Q62452
ENSMUST00000073781	ENSMUSG00000020185	10	110745439	110787384	1	25	14	29	37	43	16	23	39	44	0	21		Q6S7F2
ENSMUST00000073782	ENSMUSG00000060336	2	150218073	150240725	1	275	219	218	188	347	129	5	10	14	12	11	A2ANU7	
ENSMUST00000073783	ENSMUSG00000060002	10	88452745	88504073	-1	60	64	106	88	53	48	7	20	8	9	21		Q8C025
ENSMUST00000073787	ENSMUSG00000028743	4	139310744	139318426	1	9	5	11	116	19	7	66	82	31	14	55		Q8CG76

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000073790						11	0	0	0	0	0	0	0	5	0	0		
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ENSMUST00000073792	ENSMUSG00000034602	10	122992061	123076505	-1	2	0	2	4	0	1	299	907	539	115	301		Q80TL7
ENSMUST00000073793	ENSMUSG00000052303	7	47185707	47204920	-1	0	2	11	1	4	6	2	1	0	0	0		Q91ZC6
ENSMUST00000073822	ENSMUSG00000062257	9	27790775	28925410	1	47	32	199	51	24	17	1	4	2	0	1	G5E8G3	
ENSMUST00000073824	ENSMUSG00000063386	11	49459681	49460616	1	4	4	2	7	8	1	0	0	0	0	0	Q8VFA9	
ENSMUST00000073833	ENSMUSG00000087598	7	24193947	24211443	-1	11	0	19	13	9	9	0	0	3	7	0	Q99K53	
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ENSMUST00000073837	ENSMUSG00000009739	15	100575318	100599984	-1	0	0	0	71	0	0	7	0	88	0	43	Q5U4D4	
ENSMUST00000073840	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	1034	779	1024	0	810	E9Q9E1	
ENSMUST00000073843	ENSMUSG00000029217	5	72755716	72868483	-1	0	1	5	0	0	0	1	134	89	27	0	Q8CFK4	
ENSMUST00000073853	ENSMUSG00000062278	11	99619619	99620435	-1	11	9	13	70	11	9	0	0	0	0	0	A0PK51	
ENSMUST00000073857	ENSMUSG00000100133	X	118479708	118480737	-1	4	1	2	0	1	0	0	0	0	0	0	Q8K5B9	
ENSMUST00000073860	ENSMUSG00000060615	14	51763878	51773590	-1	4	4	3	4	7	4	0	0	0	0	0	W0UUX7	Q3TMQ6
ENSMUST00000073868	ENSMUSG00000061315	10	128035346	128048637	1	2	1	0	53	1	0	746	3668	1066	5796	889		Q60817
ENSMUST00000073870	ENSMUSG00000063821	14	21676582	21714576	-1	7	6	13	65	11	12	0	0	0	0	0		Q8BK84
ENSMUST00000073873	ENSMUSG00000039463	2	167421712	167477000	1	0	0	0	0	0	0	18	41	0	0	0		Q8R4D1
ENSMUST00000073878	ENSMUSG00000058454	7	143823145	143848410	1	0	0	0	0	0	0	0	21	0	0	0		O88455
ENSMUST00000073879	ENSMUSG00000075415	2	31026206	31142008	-1	100	55	174	106	87	54	813	2413	1702	152	1458	A2AQ43	
ENSMUST00000073881	ENSMUSG00000006392	4	118409337	118415782	1	0	0	0	0	0	0	0	0	0	0	0	A2A9C8	
ENSMUST00000073884	ENSMUSG00000062991	8	31818028	31918203	-1	8	12	46	26	20	8	38	103	50	24	36	Q6DR99	
ENSMUST00000073889	ENSMUSG00000039176	7	79446231	79466362	-1	9	9	19	144	24	0	171	464	172	11	102	Q75WC0	
ENSMUST00000073890	ENSMUSG00000057723	11	100023634	100029868	-1	6	4	15	43	22	4	0	0	0	4	0		Q61897
ENSMUST00000073892	ENSMUSG00000036578	7	31042513	31051467	-1	7	1	10	27	2	2	2	6	3	3	10		P59648
ENSMUST00000073895	ENSMUSG00000058856	9	39426093	39427148	-1	3	0	0	0	0	0	0	0	0	0	0	Q8VFD7	
ENSMUST00000073899	ENSMUSG00000024743	19	10389090	10453181	1	0	70	444	0	24	2	0	1	0	1	0		Q9R0N7
ENSMUST00000073909	ENSMUSG00000041477	6	119175253	119221616	1	0	0	0	89	9	0	27	27	20	3	17		Q3U564
ENSMUST00000073924	ENSMUSG00000020491	11	58867216	58883288	1	26	22	29	56	26	16	41	307	93	53	102	Q8BIB6	
ENSMUST00000073926	ENSMUSG00000061983	10	23785211	23787195	-1	0	0	23	0	0	0	3880	7105	5426	24047	1896	Q6ZWZ6	
ENSMUST00000073927	ENSMUSG00000031297	X	101079210	101086020	-1	0	0	0	0	0	0	0	9	0	0	4		P70423
ENSMUST00000073932	ENSMUSG00000060254	9	40006015	40006947	-1	4	0	13	6	12	1	0	1	0	0	0	Q8VH08	
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ENSMUST00000073935	ENSMUSG00000046182	7	125878420	126082411	-1	177	169	549	343	185	92	8	79	23	1	45		D3Z7H4
ENSMUST00000073939	ENSMUSG00000006386	4	94739289	94874976	1	0	19	43	12	0	21	0	5	2	0	1	Q80YS4	
ENSMUST00000073942	ENSMUSG00000038085	2	156312299	156375638	1	59	46	101	150	79	24	374	1179	638	124	479	A2AV95	
ENSMUST00000073945	ENSMUSG00000066735	5	129941970	129986692	1	3	0	0	63	5	4	29	54	31	18	36		
ENSMUST00000073946	ENSMUSG00000063176	9	39469780	39470724	-1	3	3	0	2	3	4	0	0	0	0	0	Q9EQ97	
ENSMUST00000073948	ENSMUSG00000091260	6	123308333	123336537	1	13	9	17	10	10	3	0	0	0	0	0	G5E8G4	
ENSMUST00000073949	ENSMUSG00000100200	X	9283764	9284298	1	2	5	9	9	8	0	0	10	3	0	0	Q9DAD9	
ENSMUST00000073957	ENSMUSG00000063531	5	14025276	14256689	1	53	40	121	91	48	27	1	9	3	0	21		P70275
ENSMUST00000073961	ENSMUSG00000041836	7	135537824	135686294	1	62	49	203	175	56	33	1028	3105	2262	214	2291		P49446
ENSMUST00000073962	ENSMUSG00000062275	9	109601116	109626057	-1	9	7	15	11	10	5	0	8	9	2	5	E9PXM9	
ENSMUST00000073966	ENSMUSG00000057270	19	13838224	13839171	-1	4	2	3	7	2	3	0	0	0	0	0	Q8VFQ3	
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ENSMUST00000074015	ENSMUSG00000040037	3	156561794	157316445	1	11	12	13	26	12	6	0	0	0	0	0		Q80Z24
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ENSMUST00000074038	ENSMUSG00000044573	12	30893326	30911612	-1	1	10	36	49	45	11	59	115	76	426	118	Q561M1	
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ENSMUST00000074043	ENSMUSG00000037465	15	38294413	38300707	-1	9	7	26	61	24	6	553	1315	511	195	555		O89091
ENSMUST00000074046	ENSMUSG00000017670	2	165288031	165326479	-1	0	0	0	0	14	0	0	0	38	0	24		Q8BHL5
ENSMUST00000074051	ENSMUSG00000079015	12	103894926	103904887	-1	7	5	38	22	22	2	0	0	0	233	0		
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ENSMUST00000074056	ENSMUSG00000061769	6	130013033	130026954	-1	0	0	0	0	0	0	0	1	0	0	0		Q60653
ENSMUST00000074058	ENSMUSG00000024513	18	70568189	70626131	1	0	2	0	71	5	2	1820	9304	3746	1787	2378		Q9Z2E1
ENSMUST00000074064	ENSMUSG00000095559	7	104058656	104059600	-1	3	2	9	6	2	2	0	0	0	0	0	Q8VGY1	
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ENSMUST00000074072	ENSMUSG00000069117	13	97760130	97760588	-1	7	12	10	9	10	0	2469	3139	1858	9444	1243	F6YVP7	
ENSMUST00000074077	ENSMUSG00000021835	14	46383520	46390669	-1	21	24	118	120	44	30	0	0	0	0	0	Q3ULR1	P21275
ENSMUST00000074082	ENSMUSG00000032786	9	106233455	106248126	-1	0	0	0	0	0	0	1060	1348	1189	147	629		
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ENSMUST00000074103	ENSMUSG00000021699	13	108449948	109953461	1	0	0	0	0	0	0	7	0	1	0	10		Q01063
ENSMUST00000074107						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000074113	ENSMUSG00000029086	5	43993620	44102032	-1	0	0	0	0	0	0	41	0	48	0	41	G5E8G5	
ENSMUST00000074114	ENSMUSG00000023079	5	134357656	134456716	-1	26	9	24	37	32	13	3	0	16	0	10		Q9JI57
ENSMUST00000074116						2	2	0	2	5	2	0	0	0	0	0		
ENSMUST00000074125	ENSMUSG00000094422	16	59328590	59329507	-1	2	2	2	2	2	5	0	0	0	0	0	Q7TS37	
ENSMUST00000074127	ENSMUSG00000010025	11	61223417	61267464	-1	11	11	9	26	16	15	1039	3280	1800	484	1227		P47740
ENSMUST00000074132	ENSMUSG00000074401	7	5453400	5454838	-1	4	7	14	3	18	6	0	0	0	0	0	Q8R2B9	
ENSMUST00000074133	ENSMUSG00000039488	9	9660891	10904775	-1	0	0	0	0	0	0	0	0	0	0	0		P68500
ENSMUST00000074141	ENSMUSG00000002661	17	56997339	56999322	1	0	2	0	47	0	0	0	0	0	2	0		Q9D6Z0
ENSMUST00000074142	ENSMUSG00000057609	3	92646535	92648307	-1	6	3	8	26	16	7	0	0	0	0	0	Q9CQH5	
ENSMUST00000074144	ENSMUSG00000026554	1	172148084	172197005	1	18	26	52	163	32	12	132	870	219	79	339		Q8N7N5
ENSMUST00000074148	ENSMUSG00000059645	5	26257691	26264308	1	26	25	36	27	25	24	0	0	0	0	0	D3Z6R1	
ENSMUST00000074156	ENSMUSG00000026807	2	28700164	28813165	1	8	5	24	13	16	4	3	7	6	6	13		Q32M07
ENSMUST00000074157	ENSMUSG00000025885	18	74440936	74771493	1	10	8	0	71	24	0	0	0	0	0	0	G5E8G6	
ENSMUST00000074161	ENSMUSG00000095804	10	130126108	130127055	-1	2	4	3	0	4	1	0	0	0	0	0	Q8VFU4	
ENSMUST00000074163	ENSMUSG00000062563	12	24665838	24681813	-1	0	8	0	37	0	0	0	0	0	0	0		
ENSMUST00000074168	ENSMUSG00000059429	2	37201243	37202181	1	2	4	4	1	4	0	0	0	0	0	0	Q8VFT2	
ENSMUST00000074171	ENSMUSG00000062372	5	30367062	30461932	-1	40	21	68	52	0	0	0	0	0	0	0	E9PYR6	
ENSMUST00000074173	ENSMUSG00000049653	15	76268089	76292572	1	6	7	26	22	24	11	686	1278	532	508	594		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000074177	ENSMUSG00000060974	7	140372587	140373666	-1	6	1	12	8	8	3	0	0	0	0	0	Q8VFE8	
ENSMUST00000074180	ENSMUSG00000096289	19	13585306	13586253	1	5	6	0	1	6	3	0	0	0	0	0	Q8VEU6	
ENSMUST00000074187	ENSMUSG00000061723	7	142498836	142516009	1	0	0	4	9	0	0	0	18	3	0	0		
ENSMUST00000074192	ENSMUSG00000061305	2	36527414	36528352	1	6	2	6	5	7	2	0	0	0	0	0	Q8VGK7	
ENSMUST00000074204	ENSMUSG00000019894	10	103367808	103419378	1	27	0	0	0	0	8	0	0	0	0	0		Q8BG16
ENSMUST00000074205						3	7	9	10	7	2	0	2	1	182	26		
ENSMUST00000074208	ENSMUSG00000070283	9	108565537	108567434	-1	5	2	8	217	9	5	42	82	32	68	23		Q9JKL4
ENSMUST00000074211	ENSMUSG00000057424	9	38982110	38983042	-1	3	1	3	3	5	4	0	0	0	0	0	Q9EQ87	
ENSMUST00000074216	ENSMUSG00000008305	4	72117142	72200919	-1	3	5	2	65	3	0	6	6	0	0	6	E9Q2Q6	
ENSMUST00000074221	ENSMUSG00000056858	19	13861795	13862745	1	5	1	3	2	4	0	0	0	0	0	0	Q8VG66	
ENSMUST00000074225	ENSMUSG00000022212	14	55510445	55517431	1	0	0	0	0	0	0	0	0	0	0	0		Q9Z140
ENSMUST00000074230	ENSMUSG00000044626	16	21953826	21995542	-1	31	30	49	8	28	27	0	3	4	0	5		Q8CIV3
ENSMUST00000074231	ENSMUSG00000073002	6	72368794	72380468	-1	27	6	32	108	34	13	10	9	5	8	4	Q791P0	Q9Z2P8
ENSMUST00000074232	ENSMUSG00000060967	X	53434918	53443576	1	1	0	0	0	2	1	0	0	0	0	0	Q80SW5	
ENSMUST00000074233	ENSMUSG00000030554	7	67730161	67759742	-1	53	50	115	121	78	9	0	0	0	0	5		Q70IV5
ENSMUST00000074240	ENSMUSG00000036186	2	26628457	26636497	1	10	4	29	23	12	9	17	10	3	3	6		Q99ML4
ENSMUST00000074241	ENSMUSG00000054474	6	71128166	71144439	-1	2	0	1	5	5	0	3	0	0	7	0		Q80W22
ENSMUST00000074245						17	14	21	43	24	10	1209	4632	1442	9123	1300		
ENSMUST00000074246	ENSMUSG00000057367	9	7818227	7837064	-1	0	15	16	15	3	8	66	1086	145	237	302		Q62210
ENSMUST00000074248	ENSMUSG00000059013	2	32721055	32755512	1	22	10	55	33	42	21	3773	6985	4034	340	5022		Q9QZS8
ENSMUST00000074249	ENSMUSG00000078580	7	127389673	127393629	-1	0	0	2	3	0	0	47	17	12	4	0	D3Z6C2	
ENSMUST00000074252	ENSMUSG00000061829	13	23034338	23035441	1	0	2	2	4	5	4	0	0	0	0	0	Q8R279	
ENSMUST00000074253	ENSMUSG00000059169	11	99537485	99543158	-1	0	0	0	4	9	4	0	0	0	0	0		Q6IFX3
ENSMUST00000074259	ENSMUSG00000059791	17	35861318	35865402	1	19	7	13	21	24	5	411	595	392	59	296		Q8VC65
ENSMUST00000074262	ENSMUSG00000059588	2	84330626	84425411	-1	188	106	161	2669	355	177	24	31	23	39	28	A2AR99	Q9R1W5
ENSMUST00000074267	ENSMUSG00000061477	12	28630847	28635953	-1	24	6	4	78	13	15	1152	1379	1085	7442	917	Q4FZE6	P62082
ENSMUST00000074272	ENSMUSG00000057461	7	103172691	103173635	-1	5	1	2	6	3	3	0	0	0	0	0	Q7TRR7	
ENSMUST00000074273	ENSMUSG00000052572	7	91090706	92447003	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2L2	
ENSMUST00000074285	ENSMUSG00000027210	2	115863064	116065839	-1	48	18	203	0	13	29	0	2	4	3	7	Q3TYM2	
ENSMUST00000074295	ENSMUSG00000071267	17	21926960	21962464	-1	0	0	6	0	0	0	7	22	0	0	0	B8JJA7	
ENSMUST00000074298	ENSMUSG00000024485	18	36528157	36541293	1	0	0	5	11	11	12	0	0	0	0	0	Q8BUG8	
ENSMUST00000074300						2	2	12	8	0	4	32	0	175	3	196		
ENSMUST00000074301	ENSMUSG00000055027	6	71213940	71322233	-1	22	9	64	0	28	6	0	0	0	0	0		P97443
ENSMUST00000074308	ENSMUSG00000058071	10	129945104	129949100	-1	3	8	3	0	2	4	0	0	0	0	0	Q8VG46	
ENSMUST00000074309						7	5	14	6	16	8	0	0	0	0	0		
ENSMUST00000074322	ENSMUSG00000074221	7	29983955	30028282	1	0	0	7	0	0	0	0	0	1	0	0	E9PYI1	
ENSMUST00000074324	ENSMUSG00000101073	13	22395029	22395967	1	1	0	6	0	5	2	0	0	0	0	0	Q8R281	
ENSMUST00000074339	ENSMUSG00000028107	3	95739976	95760206	-1	0	3	0	0	0	0	0	0	0	0	0	Q922A3	
ENSMUST00000074343	ENSMUSG00000060070	8	21618183	21618972	1	0	0	0	2	0	0	0	0	0	0	0		Q3L180
ENSMUST00000074346	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	0	0	0	0		P58462
ENSMUST00000074352	ENSMUSG00000044252	18	12755314	12941841	-1	0	2	0	0	0	0	14	0	21	0	28		Q91XL9
ENSMUST00000074353						5	1	5	37	3	2	2	0	2	3	0		
ENSMUST00000074357	ENSMUSG00000041926	1	135262712	135284084	-1	2	13	12	271	15	19	585	1916	701	143	371	E9PYF1	
ENSMUST00000074359	ENSMUSG00000066512	7	44215945	44220703	1	11	5	20	15	7	5	0	0	1	0	0		P15945
ENSMUST00000074366	ENSMUSG00000010461	10	23104168	23349895	-1	8	10	3	0	14	0	0	0	0	1	0		Q9Z191
ENSMUST00000074368	ENSMUSG00000021852	14	49298519	49526046	-1	0	0	0	23	0	3	0	0	0	0	0	B2RSS2	Q8BZK4
ENSMUST00000074369	ENSMUSG00000069208	13	74480054	74493970	-1	5	0	6	7	1	1	41	207	48	46	25	K7N5X2	
ENSMUST00000074370	ENSMUSG00000024182	17	26138688	26195811	1	21	8	65	65	37	15	388	675	452	69	433	E9QMJ8	
ENSMUST00000074371	ENSMUSG00000024975	19	53892231	53929861	1	21	21	54	13	0	8	0	0	0	0	0		Q61823
ENSMUST00000074372	ENSMUSG00000001504	13	72628820	72634198	1	7	2	26	262	10	6	0	0	0	7	25		P81066
ENSMUST00000074380	ENSMUSG00000062154	15	78378400	78395912	-1	10	7	17	7	0	0	0	0	0	0	0	Q3KNN2	Q9D9J2
ENSMUST00000074381	ENSMUSG00000091012	6	66636823	66637752	-1	1	3	0	0	3	2	0	0	0	0	0	G3XA52	
ENSMUST00000074387	ENSMUSG00000073888	4	41769467	41774247	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000074403	ENSMUSG00000062181	8	105083753	105093929	1	17	3	14	10	13	10	0	0	0	0	0		Q8VCU1
ENSMUST00000074408	ENSMUSG00000062157	4	135686287	135708181	1	61	49	294	212	82	35	745	2002	1080	85	799	Q3URN4	Q8CGK5
ENSMUST00000074412						1	0	4	5	6	2	0	0	0	0	0		
ENSMUST00000074416	ENSMUSG00000041669	12	103196908	103242150	-1	7	4	22	73	14	6	0	0	0	0	0	F8VQJ2	
ENSMUST00000074422	ENSMUSG00000006476	2	25054355	25062881	1	0	0	11	0	0	0	0	98	0	6	0	A2AJ92	
ENSMUST00000074425	ENSMUSG00000034210	4	115737744	115777327	1	19	22	95	51	23	16	428	1694	706	103	391	Q6PCQ6	
ENSMUST00000074449	ENSMUSG00000078664	3	92215799	92221911	1	0	3	0	13	0	5	0	0	0	0	0		Q4KL71
ENSMUST00000074455	ENSMUSG00000066838	7	7202122	7209998	-1	95	87	232	83	98	43	12	67	33	10	29	Q3UQL6	
ENSMUST00000074465	ENSMUSG00000032204	9	71110659	71168682	-1	0	0	0	0	3	0	83	290	149	34	114	Q4FK77	Q9JJJ3
ENSMUST00000074466	ENSMUSG00000060559	8	47413129	47415359	1	42	30	43	521	60	52	1	2	0	0	3	F6WB82	
ENSMUST00000074468	ENSMUSG00000033419	9	86765923	86880654	-1	0	0	0	0	0	0	0	0	0	0	0	E9QLK9	
ENSMUST00000074477	ENSMUSG00000062148	14	51853699	51854643	1	2	0	0	2	0	0	31	0	20	26	12	Q923L7	
ENSMUST00000074499	ENSMUSG00000095236	6	42762054	42763007	1	4	5	13	10	5	0	0	0	0	0	0	Q8VGP4	
ENSMUST00000074501	ENSMUSG00000033419	9	86765923	86880654	-1	0	0	1	0	3	0	0	0	0	0	0	Q3TWS4	
ENSMUST00000074510	ENSMUSG00000042496	9	31280538	31378543	1	26	16	64	17	30	14	43	53	126	6	109	D3YYD1	
ENSMUST00000074512						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000074515	ENSMUSG00000020696	11	82802449	82871210	-1	10	12	0	0	0	2	11	372	38	47	38	Q3UD78	Q6ZQM0
ENSMUST00000074519	ENSMUSG00000038393	3	96557957	96561883	1	0	6	0	11	31	8	6800	15374	7449	3774	8754		Q8BG60
ENSMUST00000074523	ENSMUSG00000022044	14	66344296	66361680	1	0	0	0	6	0	0	0	0	0	0	0		P63042
ENSMUST00000074525	ENSMUSG00000056870	1	44551511	44796838	1	5	0	7	61	14	1	0	0	0	0	0		Q8K2A1
ENSMUST00000074540	ENSMUSG00000061561	8	72099762	72100706	1	9	7	19	9	3	0	0	0	1	0	0	E9Q4J3	
ENSMUST00000074541	ENSMUSG00000063568	6	52768797	53068631	-1	4	9	0	38	9	0	11	29	0	0	9		Q80ZQ5
ENSMUST00000074543	ENSMUSG00000063827	11	49535187	49536122	1	9	5	3	14	12	8	0	0	0	0	1	Q7TQT3	
ENSMUST00000074546	ENSMUSG00000039683	5	141241490	142215586	1	32	2	12	12	18	6	0	0	0	0	0		Q3UH53
ENSMUST00000074550	ENSMUSG00000093808	7	108286180	108287124	-1	1	6	1	5	5	0	0	0	0	0	0		Q8VFD2
ENSMUST00000074552	ENSMUSG00000008690	15	89355719	89372826	1	0	12	24	9	0	0	921	683	603	126	437		Q8BSP2
ENSMUST00000074555	ENSMUSG00000060017	17	37748866	37753009	1	11	5	8	6	5	5	0	0	0	0	0	Q5CZY0	
ENSMUST00000074556	ENSMUSG00000060032	6	136808244	136810074	1	19	15	55	366	33	17	479	2038	743	630	479		Q8R1M2
ENSMUST00000074557	ENSMUSG00000060586	17	34305877	34316199	1	11	5	13	22	11	2	363	182	185	406	1448	O78196	
ENSMUST00000074562	ENSMUSG00000043051	8	125054195	125261858	1	0	0	0	0	0	0	2	0	0	0	0	D3YYC9	
ENSMUST00000074566	ENSMUSG00000094254	9	39795377	39796312	1	0	3	0	1	2	0	0	0	0	0	0	Q8VG89	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000074570	ENSMUSG00000061577	8	94923694	94943290	1	0	0	0	25	0	0	0	0	0	0	0		Q3V3Z3
ENSMUST00000074572	ENSMUSG00000057135	11	70790932	70812586	-1	0	0	3	0	0	2	0	7	3	0	8	F8WHN0	
ENSMUST00000074574	ENSMUSG00000043592	17	48454901	48539714	1	21	17	63	46	26	6	15	8	2	2	8	E9QLC2	
ENSMUST00000074575	ENSMUSG00000063511	7	45376453	45395742	-1	15	5	24	348	28	18	938	4697	1717	312	2680	A2RS68	Q62376
ENSMUST00000074582	ENSMUSG00000028041	3	89338542	89349996	-1	0	0	0	0	0	0	1	0	374	6	46		O88839
ENSMUST00000074606	ENSMUSG00000060703	2	60251993	60284488	-1	8	7	0	14	0	7	89	536	186	281	86		Q9DCG2
ENSMUST00000074608	ENSMUSG00000061633	15	81980540	81981563	1	16	7	4	43	15	7	0	0	0	1	1	Q9CQ68	
ENSMUST00000074611	ENSMUSG00000060583	9	37992492	37993439	1	6	5	4	4	4	2	0	0	0	0	0	Q8VF63	
ENSMUST00000074613	ENSMUSG00000060923	11	30505991	30649587	-1	2	2	1	37	6	5	3	10	6	45	4		P56375
ENSMUST00000074615	ENSMUSG00000096486	10	96136603	96136914	1	1	2	1	0	2	0	1	0	0	1	0	J3QNM7	
ENSMUST00000074616	ENSMUSG00000032621	13	103741615	103764504	-1	31	38	198	27	26	20	83	380	220	98	160		Q8BZX4
ENSMUST00000074618	ENSMUSG00000027544	2	168476410	168601657	-1	0	0	11	0	6	0	68	51	83	0	13		Q60591
ENSMUST00000074619	ENSMUSG00000057836	X	73086293	73097095	-1	1	0	0	0	2	0	0	0	0	0	0	Q99L59	
ENSMUST00000074622	ENSMUSG00000035131	1	146494760	146902472	1	9	12	6	10	18	4	0	0	0	0	0		Q499E0
ENSMUST00000074628	ENSMUSG00000034341	11	116078573	116086995	-1	8	6	12	24	15	10	2688	3856	1985	212	1555	Q544A1	P97765
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ENSMUST00000074642						4	4	5	5	2	2	2	9	4	2	0		
ENSMUST00000074651	ENSMUSG00000052783	5	34660379	34755305	1	3030	2922	11386	3393	3198	1437	56	234	89	17	108	Q8BP13	
ENSMUST00000074653	ENSMUSG00000047466	18	77633281	77714010	-1	18	16	34	53	27	9	232	543	434	89	316	Q0VAW6	
ENSMUST00000074654	ENSMUSG00000021974	14	58070547	58112337	1	0	0	6	100	3	3	1	0	0	1	0	E9Q2N2	
ENSMUST00000074660	ENSMUSG00000031283	X	143285674	143394262	-1	0	6	2	0	9	3	0	0	0	0	2	Q3TP73	Q920C1
ENSMUST00000074662	ENSMUSG00000052581	6	80018877	80810143	1	32	4	114	26	21	0	1	2	2	1	1		Q80XG9
ENSMUST00000074667	ENSMUSG00000062327	17	8434423	8442496	1	12	12	3	125	18	14	0	0	0	0	1	Q78ZW9	P20293
ENSMUST00000074669	ENSMUSG00000020358	11	51600100	51606847	-1	5	10	27	36	25	13	317	1106	420	123	418	Q544Z3	Q99020
ENSMUST00000074671	ENSMUSG00000056978	7	30922389	30924681	-1	0	0	9	4	2	0	0	0	0	0	0	Q5M9M1	
ENSMUST00000074674	ENSMUSG00000059069	14	50736219	50744319	-1	5	3	2	7	5	5	0	0	0	0	0	E9Q438	
ENSMUST00000074679	ENSMUSG00000057719	18	42053667	42158960	1	0	0	16	0	3	0	0	0	0	1	0		Q8BZT2
ENSMUST00000074680						2	6	18	0	12	2	3	3	5	14	0		
ENSMUST00000074681	ENSMUSG00000096167	9	38084838	38085767	1	3	1	1	2	6	1	1	0	0	0	0	Q9EQA6	
ENSMUST00000074686	ENSMUSG00000044465	7	105371211	105400054	-1	0	0	0	0	23	0	47	193	199	0	352	F8WHJ1	
ENSMUST00000074690	ENSMUSG00000012126	4	134102570	134127593	1	0	0	0	5	0	0	50	197	89	7	58		Q9D572
ENSMUST00000074693	ENSMUSG00000063232	12	103980243	103989957	-1	0	4	0	9	15	0	0	14	0	17	18	E9QLL8	
ENSMUST00000074694	ENSMUSG00000057614	5	18265135	18360355	-1	13	12	11	65	13	4	0	0	0	1	1		B2RSH2
ENSMUST00000074698	ENSMUSG00000023443	X	137115397	137122083	-1	0	6	9	166	12	4	0	0	0	0	0	O88933	
ENSMUST00000074700	ENSMUSG00000078688	4	60135932	60154289	-1	0	0	0	0	0	0	0	0	0	0	0	A2AKN9	
ENSMUST00000074713	ENSMUSG00000093866	10	129681799	129686098	-1	9	4	5	4	9	4	0	0	0	0	0	Q8VGJ2	
ENSMUST00000074721	ENSMUSG00000027102	2	74704615	74707933	1	0	0	0	0	0	0	0	0	0	0	0	A2ASN1	
ENSMUST00000074729	ENSMUSG00000034731	14	78569609	78725089	-1	20	17	39	100	27	19	150	224	257	12	187	D3YXJ0	
ENSMUST00000074730	ENSMUSG00000056946	7	108713320	108714375	1	4	4	8	3	4	1	0	0	0	0	0	Q8VFZ4	
ENSMUST00000074733	ENSMUSG00000058013	5	93093437	93176447	1	40	30	73	116	54	36	96	203	177	55	286		Q8C1B7
ENSMUST00000074734	ENSMUSG00000038775	9	119052778	119071525	1	3	4	3	0	5	0	2	0	0	0	0	G5E8H0	
ENSMUST00000074739	ENSMUSG00000056822	16	19486793	19487832	1	10	7	9	3	4	1	0	0	0	0	0	Q8VGX2	
ENSMUST00000074740	ENSMUSG00000061039	9	38752796	38756863	1	4	9	5	0	5	5	0	5	4	2	2	E9Q413	
ENSMUST00000074752	ENSMUSG00000063021	13	21753435	21753827	-1	6	4	4	112	11	0	0	0	0	3	0		Q8CGP7
ENSMUST00000074758	ENSMUSG00000061099	7	30729775	30743681	-1	0	8	11	15	5	7	1	16	10	0	9		
ENSMUST00000074761	ENSMUSG00000063611	2	28506095	28506475	1	106	104	300	126	93	50	0	6	5	2	13	F6ZQC6	
ENSMUST00000074770	ENSMUSG00000052387	19	22139119	22989884	1	13	0	0	112	15	0	0	0	0	0	1	Q5F4S8	
ENSMUST00000074783	ENSMUSG00000066842	1	150562524	150993435	-1	26	53	40	51	66	18	0	0	0	0	0	D3YXG0	
ENSMUST00000074787	ENSMUSG00000096679	7	108465326	108466318	1	8	9	4	2	4	3	0	0	0	0	0		
ENSMUST00000074792	ENSMUSG00000059183	9	65435782	65453054	1	48	58	79	99	50	26	22	106	57	30	43		Q9D799
ENSMUST00000074801						4	1	10	1	1	1	0	0	0	0	0		
ENSMUST00000074802	ENSMUSG00000000037	X	161117193	161258213	1	1	4	2	26	14	6	0	0	0	0	2	B1AVB4	
ENSMUST00000074805	ENSMUSG00000056888	10	111985448	112002631	-1	0	0	0	3	6	1	998	7666	1630	4807	1301	Q4QQK5	Q9CWG1
ENSMUST00000074806	ENSMUSG00000091705	17	35342242	35346762	1	3	0	12	56	8	4	1213	1665	914	239	1141	Q4KN81	
ENSMUST00000074807	ENSMUSG00000020105	10	125966219	126015359	1	27	21	26	195	41	11	1	3	0	2	4		Q6P1C6
ENSMUST00000074813	ENSMUSG00000069476	11	74069955	74087292	1	9	11	0	4	3	3	0	0	0	0	0	A7DTG8	
ENSMUST00000074828						6	4	24	3	2	0	3	0	2	4	2		
ENSMUST00000074829	ENSMUSG00000062545	4	128615443	128618619	-1	38	16	70	35	40	32	6	6	4	2	5	A2RRZ9	Q6QNU9
ENSMUST00000074834	ENSMUSG00000022565	15	76170974	76232574	-1	8	0	0	297	12	22	15	200	253	0	8		Q9QXS1
ENSMUST00000074839	ENSMUSG00000072596	14	44102654	44103534	1	10	4	5	7	3	0	36	104	28	131	47	W0UVF7	P97425
ENSMUST00000074840	ENSMUSG00000045302	5	30950853	30960361	-1	0	13	0	63	0	0	726	1997	780	174	1216	Q3UAP1	Q9WUQ2
ENSMUST00000074846	ENSMUSG00000029657	5	149614287	149636376	-1	7	0	7	15	14	10	30	155	39	0	34		Q61699
ENSMUST00000074849	ENSMUSG00000037313	5	33658128	33678995	1	14	0	0	21	0	0	0	17	0	9	5	Q99LH8	
ENSMUST00000074854	ENSMUSG00000063275	2	13850282	14056135	-1	0	0	5	7	0	0	0	0	0	0	0	B9EHK9	
ENSMUST00000074856	ENSMUSG00000031511	8	11728105	11835219	1	0	0	0	55	35	6	620	900	914	92	684		
ENSMUST00000074859	ENSMUSG00000058904	1	92573125	92574206	1	12	3	7	6	8	5	0	0	0	0	0	Q8VGU3	
ENSMUST00000074861	ENSMUSG00000061082	X	53069995	53240111	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JI83
ENSMUST00000074863						0	0	0	5	2	2	0	0	24	170	88		
ENSMUST00000074874	ENSMUSG00000060787	11	87913920	87916685	-1	9	10	7	8	11	2	0	0	0	0	0	Q5SW48	
ENSMUST00000074875	ENSMUSG00000059439	11	85353167	85826058	1	0	0	0	0	0	5	0	0	0	0	0		Q8CCN5
ENSMUST00000074876	ENSMUSG00000058402	7	29859979	29877292	1	0	13	0	10	14	0	0	26	11	22	0	Q7TMN8	
ENSMUST00000074880	ENSMUSG00000059383	9	76164102	76213657	-1	3	5	0	0	5	0	0	0	0	0	0		Q6SJE0
ENSMUST00000074881	ENSMUSG00000060724	6	90021888	90022820	1	0	9	3	2	0	4	0	0	0	0	0		
ENSMUST00000074883	ENSMUSG00000096009	17	38175086	38176024	1	3	3	4	3	3	1	3	9	4	0	0	Q8VG95	
ENSMUST00000074894	ENSMUSG00000056815	X	68892375	68893053	-1	2	1	6	2	2	2	0	0	0	0	0	B1AXU1	
ENSMUST00000074897	ENSMUSG00000063230	7	140492617	140493607	1	5	5	7	6	8	1	0	0	0	0	0	Q8VGL3	
ENSMUST00000074898	ENSMUSG00000031722	8	109575130	109579172	-1	25	14	41	65	28	29	66537	83580	45379	45101	30590	Q3UBS3	Q61646
ENSMUST00000074912	ENSMUSG00000062376	19	46689906	46703382	1	51	47	119	427	66	42	41	168	76	122	47		Q9CRC6
ENSMUST00000074913	ENSMUSG00000016534	X	38401357	38456454	-1	0	4	0	7	3	3	5	45	7	13	3	Q8C5K0	P17047
ENSMUST00000074919	ENSMUSG00000024283	18	7868832	7973547	1	5	0	4	0	20	0	516	2653	1035	212	497		Q924H7
ENSMUST00000074926	ENSMUSG00000060756	11	99614019	99614846	-1	0	0	7	119	6	2	0	0	0	0	0	Q9D3H4	
ENSMUST00000074936	ENSMUSG00000059883	15	94543643	94581815	1	21	10	28	33	16	15	1057	3528	1793	214	1364		Q8R4K2
ENSMUST00000074941	ENSMUSG00000063281	18	23989632	24005376	1	21	15	29	34	23	14	96	647	196	482	108	Q3V142	P15620
ENSMUST00000074943	ENSMUSG00000094606	7	10037235	10053178	-1	0	0	0	0	0	0	0	0	0	0	0	E9PW61	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000074945	ENSMUSG00000055013	1	89454806	89897617	1	0	0	0	633	55	15	188	648	571	46	466	E9Q3K3	
ENSMUST00000074948	ENSMUSG00000072889	5	72513301	72559684	-1	0	2	9	293	11	2	0	0	3	1	0	E9Q3K1	
ENSMUST00000074949	ENSMUSG00000057137	6	34863146	34874946	1	6	11	33	14	13	16	345	1475	311	190	451		Q8BGY5
ENSMUST00000074950	ENSMUSG00000045427	X	134601179	134607060	1	0	0	0	0	0	6	388	726	456	594	404		P70333
ENSMUST00000074957	ENSMUSG00000032077	9	46283008	46298783	1	0	0	0	0	0	0	220	374	220	21	204		Q8R149
ENSMUST00000074963	ENSMUSG00000063145	2	69647171	69667571	1	0	0	0	0	0	0	0	0	0	0	0		Q9CZQ9
ENSMUST00000074969	ENSMUSG00000044566	13	38006052	38037069	-1	3	3	0	0	0	0	5	10	2	10	4		Q5IR70
ENSMUST00000074970	ENSMUSG00000063445	16	4710059	4719356	-1	0	0	0	5	0	2	11	7	0	0	3		Q8K2T1
ENSMUST00000074976	ENSMUSG00000063954	3	96239749	96240276	-1	5	0	17	0	18	13	488	1075	228	109	159	B2RWH3	Q6GSS7
ENSMUST00000074981	ENSMUSG00000059087	7	106752451	106753386	-1	6	3	10	3	8	2	0	0	0	0	0	Q7TRN4	
ENSMUST00000074982	ENSMUSG00000060427	8	69610857	69625548	-1	1	1	0	0	1	0	0	0	0	0	0	Q3UTQ6	
ENSMUST00000074983	ENSMUSG00000063142	14	23289431	24004859	-1	0	0	0	0	0	0	0	0	0	0	0	F6XW53	
ENSMUST00000074986	ENSMUSG00000059303	9	19120957	19121911	1	4	1	1	1	1	2	0	0	0	0	0	Q8VFJ3	
ENSMUST00000074987	ENSMUSG00000062621	9	38523730	38524669	1	2	3	2	5	1	0	0	0	0	0	0		
ENSMUST00000074989	ENSMUSG00000063382	9	44499136	44510388	1	35	22	138	360	64	31	285	299	291	12	498		Q67FY2
ENSMUST00000074991	ENSMUSG00000009035	15	79360684	79403303	-1	0	0	0	20	0	0	217	1444	2115	144	1861		Q8BG09
ENSMUST00000074992	ENSMUSG00000060490	13	23136485	23137381	1	6	4	0	4	3	1	0	0	0	0	0	Q8R261	
ENSMUST00000075010	ENSMUSG00000062797	7	89917529	89941199	-1	3	2	0	0	0	0	9	94	29	44	23		Q9DD02
ENSMUST00000075012	ENSMUSG00000020721	11	107547930	107693826	1	0	0	0	81	0	0	240	207	550	11	371		
ENSMUST00000075017	ENSMUSG00000059305	16	16868402	16870843	-1	7	5	17	2	9	5	0	0	0	0	0	Q545E0	P13372
ENSMUST00000075018	ENSMUSG00000040775	17	22006510	22007301	-1	0	0	0	0	1	0	0	0	0	0	0	F6XPD8	
ENSMUST00000075020	ENSMUSG00000094113	6	131486400	131553763	1	0	0	0	0	0	0	0	0	0	0	0	E9Q328	
ENSMUST00000075025	ENSMUSG00000057735	2	88525585	88526496	1	2	2	0	0	1	0	0	0	0	0	0	Q7TR16	
ENSMUST00000075030	ENSMUSG00000096254	14	49960091	49961096	-1	2	2	3	3	2	2	0	0	0	0	0	K7N5X7	
ENSMUST00000075036	ENSMUSG00000057948	11	116062095	116077961	-1	0	8	0	0	0	0	0	292	0	0	142		B2RUP2
ENSMUST00000075040	ENSMUSG00000021768	14	21733394	21751181	-1	0	0	0	0	0	0	0	0	0	0	0		Q6B8I0
ENSMUST00000075044	ENSMUSG00000027547	2	168748332	168767943	-1	0	2	0	0	0	0	0	0	0	0	0		Q8BX22
ENSMUST00000075045	ENSMUSG00000059218	4	143809245	143816093	-1	5	5	9	9	0	0	0	0	0	0	0	A2A8N0	
ENSMUST00000075052	ENSMUSG00000059742	2	62693414	63184287	-1	118	124	224	319	126	90	101	378	168	94	180		Q9ER47
ENSMUST00000075053	ENSMUSG00000057161	7	12192965	12193891	1	4	3	2	2	1	0	0	0	0	0	0	L7N1Z3	
ENSMUST00000075054	ENSMUSG00000063887	3	25426215	26332460	-1	0	2	0	0	0	0	0	0	0	0	0		Q99K10
ENSMUST00000075062	ENSMUSG00000064109	7	30417717	30419854	-1	5	5	7	7	9	4	998	1133	480	2561	374		Q9QUJ0
ENSMUST00000075068	ENSMUSG00000063931	7	34912379	35044708	1	5	3	11	31	13	9	101	157	65	164	191	A2RS23	Q11136
ENSMUST00000075069	ENSMUSG00000059974	9	28994750	29963141	-1	19	10	19	98	15	14	0	0	0	0	0	Q8BG33	
ENSMUST00000075072	ENSMUSG00000021886	12	98268635	98276624	1	12	8	7	7	13	6	306	2208	674	1518	638		
ENSMUST00000075076	ENSMUSG00000056692	17	27751232	27820558	-1	8	2	19	38	13	6	21	14	8	0	13	B2KF52	
ENSMUST00000075077						1	1	17	3	0	1	2	21	2	3	9		
ENSMUST00000075080	ENSMUSG00000059187	6	96113154	96657198	1	33	34	305	82	34	13	0	3	2	0	2		Q7TPG8
ENSMUST00000075081						1	4	16	6	5	2	0	0	1	1	0		
ENSMUST00000075082						0	0	0	0	0	0	213	824	130	0	0		
ENSMUST00000075084	ENSMUSG00000037124	11	58640465	58652404	1	16	11	17	477	32	11	2	4	0	0	3		Q5NCC9
ENSMUST00000075085	ENSMUSG00000058631	7	5802345	5805445	-1	38	36	218	42	20	16	0	6	1	0	3	Q9EPT1	
ENSMUST00000075087	ENSMUSG00000052033	2	170496428	170519123	1	1	2	4	9	3	0	0	0	0	0	0	Q6P0X1	
ENSMUST00000075092	ENSMUSG00000059734	19	3908870	3912717	-1	17	5	16	120	15	6	460	597	326	1413	246	Q5M9P5	Q8K3J1
ENSMUST00000075095	ENSMUSG00000072780	6	123778971	123816280	1	8	14	11	8	12	5	0	0	0	0	0	D3YUI0	
ENSMUST00000075099	ENSMUSG00000060843	10	63430098	65003667	1	0	0	0	0	0	0	0	0	0	0	0		Q65CL1
ENSMUST00000075108	ENSMUSG00000096373	7	7383985	7399627	-1	4	12	5	0	12	4	0	0	0	0	0	L7N1Z4	
ENSMUST00000075109	ENSMUSG00000061490	15	58846590	58847321	-1	1	3	4	4	3	2	0	0	0	0	0	D3YUH6	
ENSMUST00000075117	ENSMUSG00000034430	6	90369492	90403490	1	45	27	185	226	51	30	513	806	491	36	409		Q8C8V1
ENSMUST00000075118	ENSMUSG00000020439	11	3517523	3540612	-1	27	11	43	0	6	0	76	24	15	13	65		Q921U8
ENSMUST00000075132	ENSMUSG00000040452	15	21111452	21589533	1	12	20	55	20	15	3	0	0	0	0	1		Q5RJH3
ENSMUST00000075141	ENSMUSG00000036964	11	58954685	58973098	1	14	13	36	22	0	0	0	0	3	0	0		Q7TPM3
ENSMUST00000075144	ENSMUSG00000025969	1	62703285	62818695	1	5	1	0	38	17	8	0	3	9	0	5		O35375
ENSMUST00000075147						9	7	34	13	20	2	108	0	26	0	42		
ENSMUST00000075152						10	3	39	12	13	4	1	2	0	2	0		
ENSMUST00000075158	ENSMUSG00000096051	6	89714203	89715135	1	12	4	2	0	8	3	0	0	0	0	0		Q9EQ46
ENSMUST00000075159	ENSMUSG00000029238	5	76209868	76304792	-1	33	17	63	40	23	12	162	341	337	150	196		O08785
ENSMUST00000075161	ENSMUSG00000059430	6	83512905	83536265	-1	4	0	10	0	5	4	0	0	0	0	0	Q3UJ36	P63268
ENSMUST00000075162	ENSMUSG00000063903	7	44225360	44229618	1	13	13	29	10	11	6	1	4	0	55	17	A0A0B6VSQ6	P15947
ENSMUST00000075164	ENSMUSG00000041642	1	136131389	136177998	1	46	0	71	206	37	44	4670	4550	6528	185	5253	F8VQE2	
ENSMUST00000075170	ENSMUSG00000061637	19	13094693	13095646	-1	4	4	1	1	0	0	0	0	0	0	0	Q8VFK3	
ENSMUST00000075172	ENSMUSG00000000244	7	143005046	143019644	1	3	4	3	4	0	2	0	0	0	0	0	Q3U3L6	
ENSMUST00000075175	ENSMUSG00000058833	8	70504292	70506752	-1	0	0	2	12	0	0	115	146	68	147	78		Q9CYZ6
ENSMUST00000075177	ENSMUSG00000061952	11	50981967	50985720	1	6	5	12	4	9	5	0	0	0	0	0	Q8VGH1	
ENSMUST00000075178	ENSMUSG00000059070	7	45715457	45720835	1	25	19	60	55	31	12	145	578	279	204	154	Q58EW0	P35980
ENSMUST00000075180	ENSMUSG00000025372	11	119942763	120006782	1	0	0	0	8	0	0	35	6	31	0	1	Q3UKP6	Q8BKX1
ENSMUST00000075181	ENSMUSG00000040268	7	130865756	130913312	1	0	0	0	0	0	0	4	0	37	0	44		Q8BUL6
ENSMUST00000075190	ENSMUSG00000031673	8	102632995	102785111	-1	17	14	9	33	15	11	1	1	1	7	13		P55288
ENSMUST00000075192	ENSMUSG00000058794	15	103248212	103258403	-1	2	3	14	144	13	11	5749	9031	4831	822	2857		
ENSMUST00000075206	ENSMUSG00000073830	4	61300023	61304000	-1	0	0	0	1	0	0	0	0	0	0	0	A2CEK7	
ENSMUST00000075214	ENSMUSG00000024331	18	20030633	20059554	-1	0	0	0	0	0	0	0	0	0	0	0		P55292
ENSMUST00000075220	ENSMUSG00000059288	13	35659862	35874064	1	15	14	48	2	28	13	214	280	288	26	208		Q9WTK2
ENSMUST00000075221	ENSMUSG00000058755	11	4236420	4241026	1	18	10	77	101	37	18	782	3954	790	249	1242		P53347
ENSMUST00000075226	ENSMUSG00000062226	X	111168340	111168693	1	1	3	3	0	0	0	0	0	0	0	0	D3YWP5	
ENSMUST00000075228	ENSMUSG00000095527	9	38108688	38109632	1	6	4	9	0	6	5	0	0	0	0	0	Q9EQA5	
ENSMUST00000075242	ENSMUSG00000073676	1	55088132	55091307	1	6	3	3	71	5	1	92	281	52	617	106	Q4KL76	Q64433
ENSMUST00000075243						7	3	6	21	5	4	0	0	0	0	0		
ENSMUST00000075245	ENSMUSG00000062151	9	73479422	73968966	-1	18	21	35	15	4	5	0	0	0	0	0		Q8K0T7
ENSMUST00000075249	ENSMUSG00000052609	12	76533560	76579039	1	164	115	917	319	155	79	1768	2717	2210	120	1998		Q4VAC9
ENSMUST00000075251						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000075253	ENSMUSG00000024055	17	32924688	32947402	-1	6	7	11	25	8	0	176	254	229	23	185	Q99N19	
ENSMUST00000075255	ENSMUSG00000069206	13	67424549	67451624	-1	0	4	2	2	0	0	35	207	63	90	26	Q8BX23	
ENSMUST00000075258	ENSMUSG00000040543	11	72047528	72135778	-1	0	0	28	0	11	29	0	0	0	0	0		Q3UHE1
ENSMUST00000075261	ENSMUSG00000057903	14	50424521	50425450	1	2	2	8	2	2	1	0	0	0	0	0	E9Q1P0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000075263						0	0	20	0	0	0	0	41	50	73	56		
ENSMUST00000075268	ENSMUSG00000063206	8	21665797	21666732	1	4	1	4	2	0	1	0	0	0	0	0	D3Z0J0	
ENSMUST00000075269	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	190	0	0	27	33	0	0	0	0	A2AGQ2	
ENSMUST00000075275	ENSMUSG00000022454	15	95219451	95528706	-1	2	0	0	5	12	11	0	0	0	0	0		Q61220
ENSMUST00000075280	ENSMUSG00000034321	19	41922980	41933314	-1	19	0	13	0	13	13	38	73	44	111	41		Q9DAA6
ENSMUST00000075281	ENSMUSG00000007411	12	111574510	111656227	1	7	12	24	139	23	11	418	897	643	181	482		Q03141
ENSMUST00000075282	ENSMUSG00000059921	3	141465216	141834924	1	0	0	0	0	0	0	0	0	0	0	0	Q3UQ08	O08747
ENSMUST00000075284	ENSMUSG00000060469	16	88877513	88878038	-1	1	3	3	0	2	3	0	0	0	0	0		Q925H6
ENSMUST00000075290	ENSMUSG00000025425	18	77185853	77255450	1	0	0	18	4	18	3	0	0	0	0	0		P70126
ENSMUST00000075293						2	0	2	5	6	5	1	2	0	4	3		
ENSMUST00000075296	ENSMUSG00000059408	17	12876034	12877842	1	11	13	7	13	15	6	0	0	0	0	0	W8W3M0	Q99MT8
ENSMUST00000075299	ENSMUSG00000033871	18	61298136	61400431	-1	29	14	108	56	19	11	11	17	0	0	22		Q8VHJ7
ENSMUST00000075301	ENSMUSG00000026950	2	52136647	52338798	-1	30	0	60	0	45	50	5	0	25	6	0	A2AQA9	
ENSMUST00000075303	ENSMUSG00000058979	6	120509494	120531319	-1	9	12	36	65	21	8	48	83	36	4	66		Q91WM2
ENSMUST00000075304	ENSMUSG00000041488	19	11775119	11819403	-1	6	12	8	6	0	0	4	16	3	11	9		Q64704
ENSMUST00000075305	ENSMUSG00000058537	10	58222972	58224930	-1	6	2	10	6	2	7	0	0	0	0	0	F6WF45	
ENSMUST00000075312	ENSMUSG00000061808	18	20665250	20674324	1	5	2	9	7	12	2	0	0	0	259	2	Q5M9K1	P07309
ENSMUST00000075316	ENSMUSG00000033981	3	80681450	80802835	-1	10	21	7	16	20	8	0	0	0	0	0	G5E8H1	
ENSMUST00000075317	ENSMUSG00000022197	15	12359711	12739924	-1	83	54	245	107	119	50	7	33	25	6	23	E9Q1M1	
ENSMUST00000075321	ENSMUSG00000056797	8	34327910	34328353	1	1	2	14	4	1	0	0	0	0	0	0	F6VZG1	
ENSMUST00000075326	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	0	0	0	0	20	0	160	0	170	A2AQ42	
ENSMUST00000075329	ENSMUSG00000059503	1	174391046	174392055	1	2	5	1	7	6	5	0	0	0	0	0	E9Q1L6	
ENSMUST00000075340	ENSMUSG00000063063	6	76881637	77979699	-1	0	0	0	0	0	0	0	0	0	0	0		Q61301
ENSMUST00000075341	ENSMUSG00000061540	4	63362449	63365878	1	9	5	12	4	4	7	13	25	23	31	34		P07361
ENSMUST00000075351	ENSMUSG00000058499	6	41847535	41852065	1	2	1	1	0	1	1	0	0	0	0	0	Q3UU48	P02816
ENSMUST00000075361	ENSMUSG00000090951	16	58925557	58928644	-1	4	1	3	0	3	0	0	0	0	0	0		Q8VGQ7
ENSMUST00000075363	ENSMUSG00000028937	4	152178134	152271855	1	4	2	0	143	7	2	155	186	111	44	75		Q91V12
ENSMUST00000075371	ENSMUSG00000059280	16	17980565	17981080	1	1	3	7	4	5	2	2	0	0	0	0		P13373
ENSMUST00000075372	ENSMUSG00000041607	18	82475146	82585637	1	0	0	0	0	0	0	1	0	8	0	0		P04370
ENSMUST00000075374	ENSMUSG00000052062	1	61638824	62642284	1	35	58	0	121	39	0	0	0	0	0	0		Q9CSB4
ENSMUST00000075377						1	2	3	5	4	1	0	0	0	1	0		
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ENSMUST00000075382						1	3	7	3	1	0	1	0	0	7	0		
ENSMUST00000075387	ENSMUSG00000058153	5	112419151	112577185	-1	33	15	50	165	33	24	0	0	0	0	1		
ENSMUST00000075388	ENSMUSG00000096457	X	28584992	28607842	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
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ENSMUST00000075406	ENSMUSG00000033253	4	118362743	118409273	-1	68	46	172	228	149	59	1127	539	1548	18	1362		A2A9C3
ENSMUST00000075410	ENSMUSG00000062098	2	138256565	138589292	1	44	30	35	0	21	0	0	0	0	0	10		P58545
ENSMUST00000075414	ENSMUSG00000036744	7	106814144	106820709	1	19	16	27	24	27	15	0	0	0	0	1	Q9D3U9	
ENSMUST00000075418	ENSMUSG00000046027	7	83631959	83653127	1	49	28	81	146	48	28	842	1532	564	277	436		Q9EPQ7
ENSMUST00000075420	ENSMUSG00000058057	15	100334929	100340341	1	21	19	44	31	23	15	0	8	3	3	3	G3X9G9	
ENSMUST00000075421	ENSMUSG00000094012	10	77711457	77712009	1	5	2	11	1	6	1	0	0	0	0	0	A0A0A0MQA4	
ENSMUST00000075422	ENSMUSG00000056947	3	55782510	55785001	1	22	16	47	27	26	10	0	0	0	0	0		O70299
ENSMUST00000075433	ENSMUSG00000058427	5	90903871	90905938	1	3	6	17	14	10	6	15	1350	28	82	221	Q3U1J5	P10889
ENSMUST00000075444	ENSMUSG00000059213	15	98803782	98807925	-1	21	18	65	673	51	16	1	2	0	0	4		Q80TS7
ENSMUST00000075447	ENSMUSG00000062300	7	19716644	19749573	-1	5	9	19	64	25	9	239	385	322	27	81		P32507
ENSMUST00000075448	ENSMUSG00000028565	4	97772734	98118874	1	0	1	0	0	15	0	0	0	0	0	0		Q02780
ENSMUST00000075451	ENSMUSG00000016481	1	195097382	195131586	-1	0	0	2	0	2	0	440	1563	505	639	474		Q64735
ENSMUST00000075452	ENSMUSG00000029229	5	74997988	75044774	-1	34	49	48	80	40	21	472	1541	512	160	302		Q9D9G3
ENSMUST00000075453	ENSMUSG00000041453	5	146832890	146837032	1	0	2	9	20	16	2	54	129	77	388	67	Q9CQM8	
ENSMUST00000075467	ENSMUSG00000093934	9	39839436	39840359	1	2	0	4	3	2	0	0	0	0	0	0	Q9EQ96	
ENSMUST00000075468	ENSMUSG00000094192	6	42790041	42790994	1	6	4	17	4	5	5	0	0	0	0	0	Q7TRV8	
ENSMUST00000075469	ENSMUSG00000005677	1	171213970	171220701	1	0	1	1	0	0	1	0	1	0	1	0		O35627
ENSMUST00000075470	ENSMUSG00000060112	7	140345052	140345987	-1	6	3	5	14	8	3	0	0	0	0	0	Q8VGL4	
ENSMUST00000075471	ENSMUSG00000059203	X	137570608	138846946	1	0	0	9	0	2	1	0	0	0	0	0	Q0VBP3	Q9ERS6
ENSMUST00000075474	ENSMUSG00000096822	2	36568600	36569529	1	3	4	3	6	4	0	0	0	0	0	0	Q8VFP9	
ENSMUST00000075477	ENSMUSG00000062694	6	112459505	112472872	1	9	7	26	20	21	5	0	0	0	0	0		P51637
ENSMUST00000075483	ENSMUSG00000092618	17	34507804	34517352	-1	3	2	0	5	1	1	0	0	0	0	0	A2CG22	
ENSMUST00000075491	ENSMUSG00000019428	8	70527724	70535328	1	0	0	0	0	0	0	3106	2667	1625	969	1086		O35465
ENSMUST00000075496						14	12	24	7	7	0	0	0	0	0	0		
ENSMUST00000075504	ENSMUSG00000061847	8	19052826	19064810	-1	2	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000075510	ENSMUSG00000042625	17	56560965	56584585	-1	0	0	0	23	0	0	557	1836	1017	98	1300		Q80YR5
ENSMUST00000075515	ENSMUSG00000038327	13	33324077	33335370	1	3	8	0	0	7	3	0	0	0	0	0	Q80UK5	
ENSMUST00000075518						1	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000075523	ENSMUSG00000074489	3	88368616	88372743	-1	11	15	55	15	7	0	0	0	0	0	0		P54615
ENSMUST00000075528	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	0	0	0	0	0	0	0	0		Q69Z98
ENSMUST00000075532	ENSMUSG00000072709	11	73453275	73457458	-1	7	4	6	0	1	0	0	0	0	0	0	Q8VGT3	
ENSMUST00000075537	ENSMUSG00000045031	3	37307749	37312708	-1	0	0	0	0	0	0	1	1	0	0	0		Q8K4K1
ENSMUST00000075540	ENSMUSG00000058298	10	53536329	53630439	-1	22	19	112	80	31	17	101	323	174	32	170		Q2KHI9
ENSMUST00000075549						8	0	8	7	8	3	0	0	0	26	0		
ENSMUST00000075550	ENSMUSG00000045273	13	100759674	100775899	-1	6	8	7	73	7	3	24	54	36	47	18		Q9QYM8
ENSMUST00000075552	ENSMUSG00000060407	7	27029081	27037375	1	7	8	36	13	9	11	0	0	0	4	0		P56593
ENSMUST00000075558	ENSMUSG00000100210	13	23544465	23545312	1	1	7	3	70	5	1	2	12	0	6	2	B9EI85	P84228
ENSMUST00000075571	ENSMUSG00000003271	7	45729983	45759612	-1	0	0	0	79	14	5	0	0	0	0	7		O35400
ENSMUST00000075573	ENSMUSG00000095891	9	3025417	3033289	1	16099	16835	17604	14904	19547	13825	4	3	0	0	0	D3Z1I8	
ENSMUST00000075578	ENSMUSG00000031974	8	123952459	123983122	-1	16	17	50	243	43	11	62	90	60	14	62		Q9JI39
ENSMUST00000075585						7	4	8	0	7	5	8	8	0	18	3		
ENSMUST00000075588	ENSMUSG00000010751	7	143634806	143649661	-1	0	25	36	0	0	24	22	37	32	12	40		Q9ER62
ENSMUST00000075591	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0		Q01815
ENSMUST00000075595	ENSMUSG00000060105	7	108564837	108565793	-1	0	4	3	0	4	4	0	0	0	0	0	Q7TRU7	
ENSMUST00000075602	ENSMUSG00000070713	8	72304118	72305276	-1	9	5	5	2	0	0	19	26	37	8	8	Q5BL14	P09602
ENSMUST00000075603	ENSMUSG00000000263	11	55514238	55608198	-1	0	0	0	0	7	0	0	0	0	0	0		Q64018
ENSMUST00000075606	ENSMUSG00000024937	19	5707376	5726317	-1	21	22	66	324	24	24	1840	3613	1500	269	1022	G5E8Y6	
ENSMUST00000075607	ENSMUSG00000060030	11	58732096	58733223	-1	6	0	4	7	22	5	0	0	1	0	0	Q5NCD6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000075609						7	4	6	5	3	3	0	3	3	1	1		
ENSMUST00000075610	ENSMUSG00000063179	7	131371141	131387839	1	0	0	0	12	0	0	10	35	1	0	0		Q8BP74
ENSMUST00000075611						0	0	0	0	0	0	34	0	0	28	0		
ENSMUST00000075613	ENSMUSG00000095138	10	129328965	129333818	1	2	2	1	1	3	0	0	0	0	0	0	Q8VFZ8	
ENSMUST00000075619	ENSMUSG00000067656	19	7864388	7966027	-1	0	0	0	0	3	0	0	0	0	0	0	Q76M72	
ENSMUST00000075630	ENSMUSG00000062683	15	102662864	102672352	-1	0	0	1	0	0	1	53	26	30	163	34		P56383
ENSMUST00000075632	ENSMUSG00000044937	10	86705811	86776843	1	24	21	33	41	40	19	2	3	2	1	1	F8VPV8	
ENSMUST00000075637	ENSMUSG00000038764	4	57190841	57301837	-1	23	26	57	56	31	17	107	170	217	18	88		A2ALK8
ENSMUST00000075639	ENSMUSG00000063458	14	22019712	23056085	1	2	0	0	66	4	0	26	40	14	68	0		Q9D9B4
ENSMUST00000075640	ENSMUSG00000056995	2	88391249	88392220	1	6	1	9	2	7	2	0	0	0	0	0	Q7TR20	
ENSMUST00000075641	ENSMUSG00000057113	11	33152287	33163206	-1	0	5	3	48	3	0	0	13	0	19	5	Q5SQB7	Q61937
ENSMUST00000075644	ENSMUSG00000023964	6	3685680	3764714	-1	0	0	0	0	3	0	0	0	0	0	0		Q60755
ENSMUST00000075648	ENSMUSG00000059606	14	51162260	51163018	1	5	5	18	6	5	2	0	0	0	1	0	W0UVC5	O35292
ENSMUST00000075650						3	1	6	3	2	0	42	27	45	317	72		
ENSMUST00000075654	ENSMUSG00000059690	X	69945300	69945978	1	0	1	6	2	2	2	0	0	0	0	0	L7MTX3	
ENSMUST00000075657	ENSMUSG00000063801	7	79875325	79920649	-1	107	73	133	876	157	99	262	442	249	91	190		Q8BSZ2
ENSMUST00000075666	ENSMUSG00000058301	8	70331522	70353273	-1	40	43	171	275	74	29	1388	1777	1761	72	1398		Q9EPU0
ENSMUST00000075667	ENSMUSG00000041775	7	138835823	138846273	-1	0	2	0	0	0	0	23	327	104	37	0		Q9D7G9
ENSMUST00000075670	ENSMUSG00000004642	5	33634952	33652574	-1	22	34	90	59	37	43	43	280	217	333	207	Q3V2L1	
ENSMUST00000075671	ENSMUSG00000030722	7	126382854	126396737	-1	37	41	323	174	49	30	122	251	128	22	106		O09130
ENSMUST00000075675	ENSMUSG00000093789	15	100353149	100383964	1	2	1	0	12	6	0	0	0	0	0	0	Q76I26	
ENSMUST00000075680	ENSMUSG00000058515	9	38975651	38976653	1	3	3	3	4	3	5	0	0	0	0	0	Q9EQA0	
ENSMUST00000075686	ENSMUSG00000057134	10	67544512	67548955	-1	19	32	101	405	45	29	79	150	72	20	74		Q6PDY2
ENSMUST00000075689	ENSMUSG00000063268	15	76231174	76243441	-1	4	0	22	10	0	0	1081	1647	745	71	949	Q8CIE4	
ENSMUST00000075693	ENSMUSG00000057375	4	107314363	107359823	1	0	0	0	0	2	0	601	1210	535	716	383		Q91VU1
ENSMUST00000075695	ENSMUSG00000020859	11	93996091	94126085	1	0	0	9	0	13	0	0	0	0	0	0		Q58A65
ENSMUST00000075704	ENSMUSG00000095910	7	107822523	107823467	-1	5	13	6	2	4	0	0	0	0	0	0		Q8VF66
ENSMUST00000075717	ENSMUSG00000058491	9	20129101	20138089	1	4	5	3	2	2	2	0	0	0	0	0	E9PX82	
ENSMUST00000075723						11	0	9	0	0	0	2570	4200	2830	18087	2004		
ENSMUST00000075724	ENSMUSG00000036120	8	70130812	70139197	-1	60	71	217	113	95	35	269	528	206	242	176	Q53X17	Q9Z205
ENSMUST00000075730	ENSMUSG00000043051	8	125054195	125261858	1	0	0	0	0	0	0	0	0	0	0	0		Q811T9
ENSMUST00000075734	ENSMUSG00000056328	11	67200052	67224575	1	0	27	0	0	0	0	0	0	0	0	0		Q5SX40
ENSMUST00000075738	ENSMUSG00000036751	7	30616974	30626151	-1	2	5	16	19	10	2	1339	2852	1081	6265	826		P56391
ENSMUST00000075748	ENSMUSG00000021758	13	112598333	112652310	-1	0	0	4	25	8	0	0	0	0	1	0		Q61496
ENSMUST00000075756	ENSMUSG00000053251	6	116506516	116517965	1	15	15	31	17	16	6	1	2	0	0	0	Q7TS33	
ENSMUST00000075759	ENSMUSG00000026842	2	31688376	31804227	1	0	0	0	0	0	0	721	677	889	18	619	Q3SYK5	P00520
ENSMUST00000075764	ENSMUSG00000032259	9	49340662	49407214	1	10	11	40	21	9	5	2	14	5	0	9		P61168
ENSMUST00000075767	ENSMUSG00000026657	2	4017717	4614043	1	21	15	44	242	39	20	0	0	0	0	0		Q8BIE6
ENSMUST00000075770	ENSMUSG00000024593	18	57133090	57297467	1	23	27	40	101	29	13	0	0	0	0	0		Q6DIB5
ENSMUST00000075774	ENSMUSG00000045136	13	34127008	34130354	-1	28	16	55	81	32	11	3	4	1	26	27	B2RSN3	Q9CWF2
ENSMUST00000075775	ENSMUSG00000067919	4	147021850	147060794	1	14	12	32	27	0	0	0	0	0	0	0	A2AWF2	
ENSMUST00000075789	ENSMUSG00000000248	6	128934381	128984707	1	0	0	0	0	0	0	0	1	0	0	0	F5CSM6	Q9D676
ENSMUST00000075792	ENSMUSG00000060685	X	8975710	8976559	-1	0	7	12	8	2	3	0	0	0	0	0	A2AHC6	
ENSMUST00000075797	ENSMUSG00000061653	6	89969304	89977127	1	3	1	4	2	7	2	0	0	0	0	0		Q9EQ45
ENSMUST00000075798						2	4	1	0	1	3	0	0	0	0	0		
ENSMUST00000075805	ENSMUSG00000026586	1	163245119	163313710	-1	0	0	0	1	0	0	0	0	0	0	0		P63013
ENSMUST00000075806	ENSMUSG00000048939	16	29231851	29378732	-1	21	0	15	0	0	6	0	0	0	0	0		Q3TYU2
ENSMUST00000075809						9	11	14	37	23	8	0	0	0	0	0		
ENSMUST00000075812	ENSMUSG00000057406	5	33820725	33897975	1	0	0	0	41	0	19	7	59	102	0	22		Q8BVE8
ENSMUST00000075821	ENSMUSG00000019088	X	74273217	74282337	-1	0	0	0	0	0	4	0	229	0	0	0		Q9D7J6
ENSMUST00000075827	ENSMUSG00000002799	12	112908590	112929495	-1	34	15	82	398	66	30	6	6	7	3	13		Q9QYE5
ENSMUST00000075829	ENSMUSG00000062981	10	95480806	95501927	-1	3	4	20	15	4	4	43	216	82	666	83		Q9CPV3
ENSMUST00000075832						4	1	2	3	0	0	0	0	0	0	0		
ENSMUST00000075836	ENSMUSG00000028556	4	98936671	99120915	-1	18	21	22	23	0	16	22	40	49	23	0	E9PX48	
ENSMUST00000075837	ENSMUSG00000075552	5	145558664	145584730	-1	10	0	13	0	6	4	0	0	0	0	0		Q9JMA7
ENSMUST00000075838	ENSMUSG00000052595	19	31868761	31949406	1	20	14	37	12	15	9	0	1	0	0	0		Q5YD48
ENSMUST00000075843	ENSMUSG00000002885	8	83723251	83741326	-1	0	0	24	3	6	0	6342	5089	8127	790	7377	E9QJS7	
ENSMUST00000075844	ENSMUSG00000060170	11	52213052	52213987	-1	9	3	19	9	0	10	0	0	0	0	0	Q7TQT7	
ENSMUST00000075845	ENSMUSG00000058230	7	16493719	16614993	-1	66	57	101	154	87	35	9	34	19	18	88	B2RTN5	Q91YM2
ENSMUST00000075848	ENSMUSG00000062110	5	74204816	74531759	-1	4	4	0	8	5	2	0	0	0	0	14	Q3TR67	Q8BTY8
ENSMUST00000075851	ENSMUSG00000063780	15	98431674	98438397	1	16	10	14	8	12	5	0	0	0	0	0	A1L1B4	
ENSMUST00000075853	ENSMUSG00000062248	13	51645232	51650660	1	11	10	14	104	9	4	260	420	149	406	139	Q545R9	P56390
ENSMUST00000075856	ENSMUSG00000054611	19	4314419	4398285	-1	0	0	0	0	0	0	1718	4173	3585	216	3014	F6YRW4	
ENSMUST00000075858	ENSMUSG00000057425	5	87240493	87254804	-1	7	2	5	4	8	0	0	0	0	0	0	Q8VCN3	
ENSMUST00000075859	ENSMUSG00000094673	10	78913171	78917936	1	7	2	2	3	4	1	0	0	0	0	0	E9Q5G9	
ENSMUST00000075868	ENSMUSG00000096485	19	13341760	13342692	1	1	4	1	0	5	0	0	0	0	0	0	Q8VFW4	
ENSMUST00000075869	ENSMUSG00000047746	16	36963460	36990467	-1	35	16	35	26	33	14	0	7	2	1	9	Q3KN92	P62932
ENSMUST00000075872	ENSMUSG00000062627	4	94942040	94979100	-1	5	6	0	34	18	5	330	973	636	282	638		Q69Z66
ENSMUST00000075884	ENSMUSG00000063011	17	25748614	25754327	-1	25	17	33	25	36	27	0	0	0	99	125		Q61468
ENSMUST00000075888	ENSMUSG00000061524	14	122475435	122479852	1	11	3	24	315	23	10	0	0	0	0	0	F8VPV3	
ENSMUST00000075895	ENSMUSG00000003464	1	172126755	172136493	1	7	0	7	0	8	1	733	986	634	263	525		Q8VCI5
ENSMUST00000075896	ENSMUSG00000056820	8	125012997	125034192	1	25	25	39	145	21	16	115	261	193	59	169		Q9QZE7
ENSMUST00000075898						8	8	16	71	5	6	0	3	1	0	1		
ENSMUST00000075909	ENSMUSG00000062224	10	51756173	51757194	-1	2	2	0	1	2	2	0	0	0	0	0	Q9D466	
ENSMUST00000075916	ENSMUSG00000029587	5	143235163	143248834	1	58	17	53	5	51	0	23	0	28	0	63	M0QWS1	
ENSMUST00000075922	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	0	0	0	0	0	19	12	0		Q9WV30
ENSMUST00000075924						2	1	0	0	1	1	67	808	234	607	130		
ENSMUST00000075928	ENSMUSG00000095903	9	39771772	39772798	-1	3	2	1	0	3	3	0	0	0	0	0	Q8VFN4	
ENSMUST00000075934	ENSMUSG00000023159	7	17203477	17215760	1	103	118	87	97	97	46	3	10	8	8	19	Q3URN6	
ENSMUST00000075941	ENSMUSG00000043154	9	101105084	101251795	-1	6	20	22	56	30	10	9	3	17	4	20	B2RXC8	
ENSMUST00000075946	ENSMUSG00000022838	16	36792884	36875003	-1	295	252	314	270	344	189	13	39	22	14	28		Q91ZD6
ENSMUST00000075953	ENSMUSG00000060256	3	93796398	93797510	1	6	1	12	6	10	7	0	0	0	0	0		Q6YCH2
ENSMUST00000075954	ENSMUSG00000059669	12	24498581	24558571	1	20	12	17	16	12	5	68	529	155	365	113		P97358
ENSMUST00000075962						4	9	10	3	17	4	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000075968						27	21	54	36	18	11	38	189	140	160	90		
ENSMUST00000075973	ENSMUSG00000041333	4	59956804	59960710	-1	4	5	4	1	2	4	0	0	0	0	0	A2ANT5	P11590
ENSMUST00000075980	ENSMUSG00000020895	11	69070806	69073293	1	0	1	0	38	0	0	0	9	3	1	2		Q9CPV0
ENSMUST00000075982	ENSMUSG00000057465	7	46751833	46754314	1	3	0	8	6	9	3	8	12	13	88	0		P05367
ENSMUST00000075983	ENSMUSG00000057615	X	61709497	61710955	1	2	4	7	14	8	2	0	0	0	0	0		Q7TPY9
ENSMUST00000075992	ENSMUSG00000019876	10	57631981	57741112	1	64	59	199	46	50	29	3	28	19	5	21	Q3TZU5	
ENSMUST00000075994	ENSMUSG00000035357	6	101149609	101377897	-1	35	18	146	180	49	19	0	0	1	3	25		Q69ZS0
ENSMUST00000075995	ENSMUSG00000030319	6	115774538	115805557	1	60	27	137	474	75	32	5	5	8	3	35		Q6ZQ73
ENSMUST00000075999	ENSMUSG00000037028	4	101909121	101911908	1	4	7	2	4	4	7	0	0	0	0	0	B1AUV4	
ENSMUST00000076006	ENSMUSG00000064057	11	49663610	49665118	1	0	7	5	5	0	0	0	32	3	6	8	Q8CJC6	
ENSMUST00000076016	ENSMUSG00000064127	X	12675369	12762073	-1	1	3	1	29	1	3	15	12	29	9	30	A2BDN7	
ENSMUST00000076019	ENSMUSG00000073770	4	118829485	118836273	-1	5	0	21	8	1	3	0	0	0	0	0	Q7TQV7	
ENSMUST00000076022	ENSMUSG00000017264	4	148558429	148582401	1	5	16	3	0	21	0	0	0	0	0	43	Q8K366	
ENSMUST00000076034	ENSMUSG00000059479	7	25626654	25635100	1	10	8	39	32	29	11	88	115	52	6	38		Q8R3I9
ENSMUST00000076037						0	0	0	0	0	3	4	0	1	52	11		
ENSMUST00000076038	ENSMUSG00000038048	17	57769570	58410342	1	13	11	16	11	22	8	0	0	0	0	0		Q0V8T7
ENSMUST00000076043	ENSMUSG00000019647	18	47235598	47368870	-1	191	100	1319	280	123	58	3	7	3	3	12		O35464
ENSMUST00000076046	ENSMUSG00000059326	19	61224402	61228418	-1	58	57	626	619	64	43	1851	8062	3000	395	3793		Q00941
ENSMUST00000076048	ENSMUSG00000074483	3	88383501	88384464	-1	0	1	0	1	4	3	0	0	0	1	0		P86546
ENSMUST00000076051	ENSMUSG00000032754	5	120511168	120534024	1	31	39	41	0	10	26	805	795	521	13	425		Q925Q3
ENSMUST00000076052	ENSMUSG00000061119	7	92875253	92934573	1	21	18	57	50	35	13	160	432	140	152	213		Q7TMR0
ENSMUST00000076060	ENSMUSG00000016763	15	83602583	83725021	-1	0	0	0	0	0	0	0	0	1	0	0	A2A442	
ENSMUST00000076061	ENSMUSG00000058295	6	132595913	132601236	1	0	0	0	0	0	0	0	0	0	0	0	F8VPU9	
ENSMUST00000076069	ENSMUSG00000029352	5	113075839	113081584	-1	3	0	0	44	0	6	0	0	0	0	0		Q9JJU9
ENSMUST00000076070	ENSMUSG00000022635	15	93386097	93398334	-1	0	0	0	12	0	0	78	446	148	249	91		Q9CZ96
ENSMUST00000076084	ENSMUSG00000027317	2	119218119	119229906	-1	2	1	9	11	7	0	0	3	0	0	0		Q7TT52
ENSMUST00000076085	ENSMUSG00000035173	19	56787481	56822190	-1	0	0	0	0	0	0	49	0	230	0	138		Q8C9S4
ENSMUST00000076086	ENSMUSG00000057697	6	90223317	90224438	-1	6	7	2	5	7	2	0	0	0	0	0	A2RS76	
ENSMUST00000076091	ENSMUSG00000060034	7	127718106	127732166	-1	107	110	152	74	102	45	7	54	10	6	5	Q0VB69	P83714
ENSMUST00000076095	ENSMUSG00000025856	5	138976014	138997370	-1	0	0	7	90	6	3	0	0	0	0	12	Q99L56	
ENSMUST00000076099	ENSMUSG00000058643	5	17476098	17480936	1	6	11	9	15	14	5	0	0	0	0	0	Q9D5Q6	
ENSMUST00000076106	ENSMUSG00000059648	14	51049451	51050163	-1	0	2	5	7	5	3	0	0	0	0	0	W0UVF9	Q5GAM9
ENSMUST00000076110	ENSMUSG00000026484	1	151458004	151500955	-1	0	0	0	93	0	0	214	605	216	282	270		Q9CQJ4
ENSMUST00000076119	ENSMUSG00000059410	6	132909651	132910587	1	4	1	2	0	3	1	0	0	0	0	0		Q7M710
ENSMUST00000076123	ENSMUSG00000071291	13	67490167	67500555	-1	6	3	21	0	0	1	0	0	35	11	0		P16372
ENSMUST00000076124	ENSMUSG00000063919	5	116439275	116591817	-1	41	8	112	215	52	26	0	0	0	0	0	J9QHX6	Q8BKA3
ENSMUST00000076133	ENSMUSG00000058317	14	18573575	18894267	-1	0	0	0	0	0	0	1	0	0	3	0		Q91W82
ENSMUST00000076136	ENSMUSG00000061175	3	79455974	79567796	-1	0	0	0	0	0	3	123	25	576	0	200		Q80TD3
ENSMUST00000076140	ENSMUSG00000033577	9	80165031	80311729	1	1	0	0	0	1	0	0	0	0	0	0	E9PVU0	
ENSMUST00000076147	ENSMUSG00000079355	9	104084157	104126933	-1	11	26	50	21	16	20	0	0	0	1	2		Q924I3
ENSMUST00000076150	ENSMUSG00000060412	6	132754730	132755659	1	2	1	2	1	1	0	0	0	0	0	0		Q7M718
ENSMUST00000076155	ENSMUSG00000059040	18	48045335	48048378	1	39	34	61	20	50	34	10958	14910	9089	4337	6383	Q5FW97	P17182
ENSMUST00000076166						3	0	0	3	4	2	0	0	0	8	0		
ENSMUST00000076169	ENSMUSG00000021704	13	92844787	92858230	1	41	27	217	84	46	22	3	34	9	9	43	D3YTP3	
ENSMUST00000076180	ENSMUSG00000061376	13	23162643	23163581	1	1	9	5	3	2	3	0	0	0	0	0	Q8R271	
ENSMUST00000076183	ENSMUSG00000058498	4	152307019	152318993	-1	8	9	19	21	10	2	2	0	0	0	1		Q3V3A7
ENSMUST00000076186	ENSMUSG00000057650	16	88873665	88874269	-1	3	0	20	6	5	4	0	0	0	0	0		Q925I0
ENSMUST00000076194	ENSMUSG00000060201	18	62592413	62596264	-1	0	3	2	0	1	0	0	0	0	0	0	F8WGH2	
ENSMUST00000076195	ENSMUSG00000055228	13	62454323	62466709	-1	5	3	3	9	7	2	49	150	75	36	27	Q14DI0	
ENSMUST00000076203	ENSMUSG00000043614	5	135072900	135078266	-1	0	0	0	241	8	0	0	0	1	0	0		Q810I0
ENSMUST00000076206	ENSMUSG00000040478	4	21677480	21685963	-1	0	0	0	0	0	0	0	2	0	0	0		E9PZZ1
ENSMUST00000076212	ENSMUSG00000032724	2	103566310	103718423	1	30	17	50	682	63	21	1613	2020	1931	126	1583	Q3T9J9	Q7TQI7
ENSMUST00000076219	ENSMUSG00000041360	19	27388702	27429820	-1	45	28	57	33	35	16	62	266	148	435	164		
ENSMUST00000076224	ENSMUSG00000079020	15	73577424	73645762	-1	0	0	0	0	0	0	584	530	530	0	457		Q0P5V9
ENSMUST00000076226	ENSMUSG00000030451	7	56050196	56231800	1	76	1	33	66	0	41	188	376	980	61	484		Q4U2R1
ENSMUST00000076228	ENSMUSG00000061979	5	134148054	134176774	-1	15	4	18	85	19	6	25	37	11	9	34	Q548B0	Q9CYF5
ENSMUST00000076236	ENSMUSG00000022211	14	55491093	55508246	1	43	30	91	85	69	24	0	3	0	0	1		Q3UFQ8
ENSMUST00000076238	ENSMUSG00000059459	13	21479097	21479441	-1	0	0	0	10	0	0	0	0	0	0	0	F6TJM2	
ENSMUST00000076245	ENSMUSG00000057801	17	38208169	38209247	1	6	2	1	3	7	3	0	0	0	0	0	Q8VEY4	
ENSMUST00000076249	ENSMUSG00000062488	19	34607970	34613401	1	48	22	90	39	27	22	6	78	2	22	21	E9PV48	
ENSMUST00000076250	ENSMUSG00000059379	2	85776586	85777503	1	6	5	8	0	4	5	0	0	0	0	0	Q7TR95	
ENSMUST00000076251	ENSMUSG00000074405	7	5020376	5033223	1	8	3	14	1272	27	19	133	419	295	29	205		Q3U3I9
ENSMUST00000076256	ENSMUSG00000060550	17	35439155	35443773	1	0	0	0	0	0	0	0	0	0	0	0	E9QJR9	
ENSMUST00000076258	ENSMUSG00000020253	9	106194172	106199746	-1	19	20	45	13	27	13	496	925	570	48	276	F8WGF9	
ENSMUST00000076260	ENSMUSG00000062352	12	21240825	21286237	-1	0	0	0	12	0	0	0	211	52	197	100		O35671
ENSMUST00000076262	ENSMUSG00000060057	16	59109625	59110631	-1	0	3	0	0	0	0	0	0	0	0	0	Q7TS43	
ENSMUST00000076263	ENSMUSG00000060742	2	86508461	86509402	1	1	2	0	2	4	0	0	0	0	0	0	A2AK60	
ENSMUST00000076264	ENSMUSG00000062761	5	31452431	31481754	1	25	18	62	43	33	9	57	220	142	29	159		Q69Z99
ENSMUST00000076265	ENSMUSG00000036572	X	37091678	37110322	-1	2	1	5	5	3	1	35	235	101	101	83	Q3ULL6	
ENSMUST00000076270	ENSMUSG00000020817	11	70844778	70943105	1	9	10	11	7	12	2	68	426	138	57	99		O35551
ENSMUST00000076272	ENSMUSG00000054746	7	120328684	120407687	1	9	5	7	12	9	6	0	0	0	0	0	Q6XBG2	
ENSMUST00000076275	ENSMUSG00000063972	2	38723370	38927688	-1	0	0	0	0	0	0	0	116	67	0	44		Q64249
ENSMUST00000076276	ENSMUSG00000063651	7	25367620	25369724	-1	0	0	9	63	2	0	0	0	0	0	0		Q6PCW6
ENSMUST00000076281	ENSMUSG00000096718	10	81905073	81910899	-1	2	0	0	0	7	0	6	0	0	0	8	Q0P5U5	
ENSMUST00000076289	ENSMUSG00000096209	7	108667418	108668362	1	6	2	12	2	4	0	0	0	0	0	0		Q8VEW6
ENSMUST00000076306	ENSMUSG00000028944	5	24862744	25100642	-1	9	10	9	9	17	11	7	0	0	0	0	Q8BIQ9	
ENSMUST00000076313	ENSMUSG00000061136	2	53134704	53191284	-1	13	15	16	5	11	8	404	1115	666	472	349		Q9R1C7
ENSMUST00000076314						6	2	8	8	4	1	0	1	0	5	0		
ENSMUST00000076316	ENSMUSG00000037148	8	77250366	77517907	-1	17	27	52	60	26	11	55	124	83	34	117		Q6Y5D8
ENSMUST00000076317						0	2	4	7	2	0	13	17	9	21	15		
ENSMUST00000076321	ENSMUSG00000070686	5	93634993	93671551	-1	0	0	0	0	0	0	0	0	0	0	0	K7N5Y9	
ENSMUST00000076325	ENSMUSG00000030557	7	67231163	67372858	-1	0	0	0	0	0	0	46	53	0	0	19		Q60929
ENSMUST00000076326	ENSMUSG00000057191	9	21526176	21545333	1	5	21	0	15	8	0	278	349	252	28	238	G8JL59	
ENSMUST00000076331	ENSMUSG00000058114	17	37903522	37904616	1	9	5	11	1	10	3	0	0	0	0	0	Q8VF25	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000076333	ENSMUSG00000033149	16	45746243	45953598	-1	0	0	46	0	4	0	0	10	0	0	0		Q8K1N2
ENSMUST00000076335	ENSMUSG00000027200	2	124089969	124667770	1	0	0	0	536	0	0	0	0	0	0	0		Q76KF0
ENSMUST00000076349	ENSMUSG00000001986	X	41400854	41678601	1	0	1	1	12	19	0	0	30	7	0	11		Q9Z2W9
ENSMUST00000076352	ENSMUSG00000044734	13	32842092	32851185	-1	11	0	0	10	13	0	4744	20065	7833	14694	3157		Q9D154
ENSMUST00000076354	ENSMUSG00000058254	X	10485158	10596605	1	0	0	0	0	0	0	0	0	0	0	0		Q62283
ENSMUST00000076359						3	0	0	5	1	2	0	0	0	0	0		
ENSMUST00000076362	ENSMUSG00000026254	1	87213914	87240488	1	81	10	1278	141	53	99	167	688	319	38	217	G3X9H1	
ENSMUST00000076364	ENSMUSG00000058443	9	50344240	50344981	-1	37	27	0	28	0	15	3180	9862	3202	13454	2678		Q6ZWV3
ENSMUST00000076372	ENSMUSG00000068856	3	96172332	96177564	1	8	3	20	93	30	9	604	755	485	79	421		Q8QZY9
ENSMUST00000076373	ENSMUSG00000063696	8	102864779	102865853	-1	18	38	34	43	38	13	7474	7982	5940	6324	3139	E9Q070	
ENSMUST00000076379	ENSMUSG00000061937	5	87774567	87788797	1	0	1	0	0	1	0	0	0	0	0	0	Q547D1	Q02862
ENSMUST00000076383	ENSMUSG00000020271	11	32642724	32746816	1	18	20	13	3	34	18	66	0	61	0	30		Q5SRY7
ENSMUST00000076384	ENSMUSG00000062826	8	104947356	104955962	1	16	9	31	17	21	4	0	0	0	0	0	Q08ED5	
ENSMUST00000076393	ENSMUSG00000059504	11	58782961	58787269	1	8	11	26	9	13	4	0	0	0	0	0	Q7TRZ7	
ENSMUST00000076406	ENSMUSG00000095239	7	108422573	108423517	1	4	6	3	1	5	2	0	0	0	0	0		Q8VG08
ENSMUST00000076410						3	9	10	12	9	2	0	0	0	3	0		
ENSMUST00000076421	ENSMUSG00000057093	7	27689340	27706484	1	0	0	0	0	0	0	1	0	2	0	0	G3X9H3	
ENSMUST00000076422	ENSMUSG00000022847	16	20725158	20734511	-1	3	0	7	0	6	0	0	1	0	1	0	Q543R9	P40226
ENSMUST00000076431	ENSMUSG00000026926	2	26389339	26397122	1	12	12	6	29	10	4	537	930	573	147	450		Q9DC61
ENSMUST00000076435	ENSMUSG00000026707	2	14995131	15055069	-1	0	0	0	0	0	0	0	0	0	0	0		Q7TS68
ENSMUST00000076437	ENSMUSG00000063173	10	129801564	129802523	-1	4	0	0	3	2	1	0	0	0	0	0	Q8VFI1	
ENSMUST00000076438	ENSMUSG00000057447	2	88831119	88832042	1	2	1	3	1	6	0	0	0	0	0	0	A2ATJ7	
ENSMUST00000076442	ENSMUSG00000022565	15	76170974	76232574	-1	38	0	2	847	40	0	197	0	187	33	218		Q9QXS1
ENSMUST00000076443	ENSMUSG00000040471	11	72435526	72438400	1	12	4	17	8	23	0	0	0	0	0	0		Q6PDE7
ENSMUST00000076451	ENSMUSG00000058216	19	4057477	4059446	-1	2	2	4	2	2	2	4	7	4	0	0	F6RWR5	
ENSMUST00000076454	ENSMUSG00000005312	13	58176156	58215653	-1	9	4	19	47	0	6	205	578	151	0	177		Q8R317
ENSMUST00000076463	ENSMUSG00000041762	2	73341506	73386572	-1	22	15	11	90	17	0	0	24	12	4	6	A2AWR3	
ENSMUST00000076465						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000076467	ENSMUSG00000029283	5	106964322	106984432	1	2	3	0	0	0	0	0	22	0	0	8	Q66JY4	
ENSMUST00000076470	ENSMUSG00000045693	7	23301275	23362270	1	24	20	36	11	21	10	0	0	0	0	0		Q66X19
ENSMUST00000076478	ENSMUSG00000058725	11	99609794	99610189	-1	0	5	0	51	4	0	0	0	0	0	0	Q9D3H4	
ENSMUST00000076493	ENSMUSG00000063652	11	53949965	53980332	-1	23	7	29	351	31	12	5	10	7	2	14	A2RSK7	Q9WTN6
ENSMUST00000076500	ENSMUSG00000063163	16	69856874	69863744	-1	9	7	5	5	11	3	0	0	0	0	0	E9Q9U2	
ENSMUST00000076501	ENSMUSG00000062369	7	104840257	104842603	-1	0	6	20	9	14	0	0	0	0	0	0	E9Q9U0	
ENSMUST00000076504	ENSMUSG00000094588	9	38349085	38350035	1	8	7	4	1	10	2	0	0	0	0	0	L7N1Z5	
ENSMUST00000076505	ENSMUSG00000060224	19	42725858	42752775	-1	20	20	52	47	24	16	30	121	42	10	93		Q3U4I7
ENSMUST00000076508	ENSMUSG00000095696	10	129427424	129437752	1	3	6	11	2	2	1	0	0	0	0	0	Q8VFH8	
ENSMUST00000076514	ENSMUSG00000060918	11	51006974	51007897	1	11	6	9	5	6	8	0	0	0	0	0	Q8VGG9	
ENSMUST00000076516	ENSMUSG00000057349	9	39318647	39319612	-1	2	2	0	3	3	3	0	0	0	0	0	Q9EQ95	
ENSMUST00000076521	ENSMUSG00000026638	1	193153111	193172023	1	13	13	13	77	23	10	0	2	2	2	4		P97431
ENSMUST00000076532	ENSMUSG00000060147	13	33917918	34002794	-1	0	1	4	0	0	1	97	562	149	233	148	Q4FJQ6	Q60854
ENSMUST00000076538						14	2	29	96	18	5	0	0	0	0	0		
ENSMUST00000076541	ENSMUSG00000039298	4	70216856	70410443	-1	0	0	0	57	2	0	47	100	121	17	94	H7BX43	
ENSMUST00000076542	ENSMUSG00000063225	9	38664913	38665842	-1	2	7	3	0	2	0	0	0	0	0	0	Q7TRC3	
ENSMUST00000076548	ENSMUSG00000059106	9	39646724	39647672	1	4	2	2	2	2	3	0	0	0	0	0	Q9EQ84	
ENSMUST00000076565	ENSMUSG00000058250	6	40612315	40613310	-1	9	4	5	10	5	4	0	0	0	0	1		Q7TQA6
ENSMUST00000076575	ENSMUSG00000094496	10	129540539	129541474	1	1	2	1	0	4	2	0	0	0	0	0	Q7TRH9	
ENSMUST00000076576	ENSMUSG00000070810	7	14222403	14254870	-1	5	0	0	2	0	0	0	0	0	0	0	B2RVI8	
ENSMUST00000076585						11	14	15	7	8	7	0	6	0	0	4		
ENSMUST00000076587	ENSMUSG00000026064	1	30940302	30949770	-1	13	34	5	24	15	13	1969	3016	1550	204	1014	B9EKL6	Q63739
ENSMUST00000076592	ENSMUSG00000047220	9	108403611	108428484	-1	55	38	153	46	71	41	1	21	13	5	17		Q6PDM4
ENSMUST00000076599	ENSMUSG00000032952	3	103809520	103822025	1	0	6	2	31	0	0	287	672	87	101	105		Q9WV76
ENSMUST00000076605	ENSMUSG00000024524	18	67088336	67226792	1	43	34	97	44	22	12	185	764	195	46	159		Q8CGK7
ENSMUST00000076614						5	1	3	0	5	0	1	0	0	0	0		
ENSMUST00000076615	ENSMUSG00000003575	8	70382355	70439579	-1	4	3	10	189	0	11	124	110	110	6	108		Q68ED7
ENSMUST00000076617	ENSMUSG00000074061	9	109476654	109495875	-1	7	10	21	11	4	3	0	0	0	0	0	Q8C2W8	
ENSMUST00000076622	ENSMUSG00000063529	13	46273721	46300115	1	3	4	21	0	10	4	0	0	0	0	0		Q6P3A1
ENSMUST00000076623	ENSMUSG00000037999	5	62602445	62766159	-1	16	26	22	64	26	10	16	41	37	33	72	E9QP44	
ENSMUST00000076633						7	12	15	0	18	6	0	5	0	2	0		
ENSMUST00000076634	ENSMUSG00000021055	12	76120419	76177259	-1	0	0	83	29	0	0	0	0	0	0	0		
ENSMUST00000076635	ENSMUSG00000036916	X	48541625	48594504	-1	6	0	0	0	0	0	0	0	0	0	10		Q6P3Y5
ENSMUST00000076638	ENSMUSG00000094808	6	40964754	40968435	1	0	3	0	2	0	0	0	0	0	0	0	Q9CPN7	
ENSMUST00000076639	ENSMUSG00000001017	3	90498956	90509498	-1	0	7	0	0	0	0	60	322	0	0	1		Q9CY57
ENSMUST00000076648	ENSMUSG00000047730	7	28071236	28120862	1	27	9	40	32	40	17	0	0	0	0	0	E9Q9C6	
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ENSMUST00000076661	ENSMUSG00000016984	11	17938756	17953875	-1	7	11	10	67	12	2	43	246	71	46	49		Q5SVT3
ENSMUST00000076664	ENSMUSG00000057409	17	21491256	21509764	1	12	6	8	5	6	0	61	363	61	44	44	Q9Z117	
ENSMUST00000076670	ENSMUSG00000063446	4	49059273	49340259	1	31	20	25	127	30	21	0	0	0	0	0		Q8BFZ2
ENSMUST00000076671	ENSMUSG00000057402	X	155124917	155128412	-1	1	3	1	2	0	1	0	0	0	0	0	Q9D9N2	
ENSMUST00000076674	ENSMUSG00000039579	4	49661611	49845744	-1	0	30	53	39	0	13	12	33	0	4	0	A2AIR4	
ENSMUST00000076675	ENSMUSG00000070378	11	74186249	74196446	1	15	8	13	9	4	5	0	0	0	0	0	Q7TRX2	
ENSMUST00000076677	ENSMUSG00000063305	7	18674107	18686185	-1	9	2	0	3	8	0	0	0	0	0	0	E9Q9B4	
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ENSMUST00000076694	ENSMUSG00000061904	10	91116574	91124059	-1	0	0	12	14	7	0	243	46	279	146	0		Q8VEM8
ENSMUST00000076697	ENSMUSG00000061306	11	120103960	120151346	-1	4	2	3	20	7	2	66	36	11	2	21		Q5I012
ENSMUST00000076698	ENSMUSG00000020570	12	32953891	32979050	1	27	26	42	108	33	21	133	379	183	52	114		O09117
ENSMUST00000076700	ENSMUSG00000018654	11	11685003	11772926	1	12	14	40	20	51	13	1682	5211	2045	164	1172	G5E8H3	
ENSMUST00000076702	ENSMUSG00000064215	12	103434211	103440239	1	3	0	1	0	14	0	0	0	0	33	0	Q70LN0	
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ENSMUST00000076710						0	0	0	0	0	0	2	5	4	5	4		
ENSMUST00000076713	ENSMUSG00000062074	10	39150971	39163794	-1	6	9	11	12	13	6	3	7	5	2	4		D3Z5L9
ENSMUST00000076715	ENSMUSG00000001911	8	84699876	84800344	-1	0	0	0	18	0	0	4	0	5	2	26		P70257
ENSMUST00000076729	ENSMUSG00000062844	19	13102379	13103284	-1	3	2	2	10	4	2	0	0	0	0	0	E9Q6S2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000076730	ENSMUSG00000044860	9	99006790	99035715	-1	7	7	8	51	13	3	1	5	2	0	0	Q1RME4	
ENSMUST00000076734	ENSMUSG00000046201	17	3114972	3198855	1	21	27	40	53	34	17	481	1452	950	109	823		Q6DID3
ENSMUST00000076737	ENSMUSG00000061928	18	20376729	20410196	1	37	37	84	51	39	31	0	1	0	0	1	B2RQH0	Q7TSF1
ENSMUST00000076752	ENSMUSG00000059411	6	43213065	43217938	1	8	2	6	10	9	1	0	0	0	0	0	Q8VF17	
ENSMUST00000076754	ENSMUSG00000074447	8	21025545	21026516	1	2	2	1	3	1	1	0	0	0	0	0		Q8C1P2
ENSMUST00000076756	ENSMUSG00000057754	6	131677960	131678886	-1	3	4	0	1	2	0	0	0	0	0	0		Q7M724
ENSMUST00000076757	ENSMUSG00000003531	16	18052860	18071632	1	0	0	12	0	5	0	65	55	56	28	12	Q3TV71	
ENSMUST00000076759	ENSMUSG00000061150	17	20814495	20815415	1	2	1	0	0	2	0	0	0	0	0	0	Q8R2A9	
ENSMUST00000076786	ENSMUSG00000058052	8	21938352	21940878	1	1	2	27	5	4	1	0	0	0	0	0		Q8R2I3
ENSMUST00000076788	ENSMUSG00000064215	12	103434211	103440239	1	0	1	1	0	0	0	0	22	12	38	0	Q70LM9	
ENSMUST00000076791	ENSMUSG00000063757	7	5034118	5035246	1	50	39	127	51	32	18	4	60	8	5	20	Q9D656	
ENSMUST00000076802	ENSMUSG00000095390	9	39909805	39910728	1	3	5	2	2	5	0	0	0	0	0	0	Q8VFN5	
ENSMUST00000076803	ENSMUSG00000027244	2	91674618	91710576	-1	14	14	0	74	17	13	965	1280	1015	144	728		Q91YI1
ENSMUST00000076807	ENSMUSG00000102918	18	37806364	37841873	1	0	0	0	0	0	0	4	0	9	4	59	Q91XX1	
ENSMUST00000076810	ENSMUSG00000061751	16	33974258	34573532	-1	0	0	0	4	0	0	0	0	0	0	0		A2CG49
ENSMUST00000076813	ENSMUSG00000062054	12	21316392	21323605	1	0	7	4	59	10	8	123	257	90	107	106		Q9DB29
ENSMUST00000076814	ENSMUSG00000058084	10	130162264	130163422	-1	6	10	7	0	4	0	0	0	0	0	0	Q8VFU7	
ENSMUST00000076817	ENSMUSG00000019820	10	12382188	12861735	-1	66	55	65	50	78	43	307	566	871	53	963	E9Q6R7	
ENSMUST00000076828						3	0	0	2	1	0	0	7	2	0	2		
ENSMUST00000076831	ENSMUSG00000063838	7	4151260	4164860	-1	7	1	16	156	11	3	2	3	5	8	19		Q9Z0X0
ENSMUST00000076832	ENSMUSG00000094721	19	13190669	13191592	1	4	3	3	1	0	1	0	0	0	0	0	Q8VFW3	
ENSMUST00000076836	ENSMUSG00000026872	2	44983632	45117395	-1	0	10	0	0	0	0	0	42	0	0	0	H9H9S3	
ENSMUST00000076840	ENSMUSG00000048915	17	62604184	62881317	-1	19	9	67	95	16	18	1	1	0	5	25		O08543
ENSMUST00000076842						0	1	0	0	0	1	3369	3950	1855	489	1820		
ENSMUST00000076846	ENSMUSG00000031750	8	110741829	110805924	-1	13	0	4	2	0	7	0	0	0	0	6		Q8R1R4
ENSMUST00000076850	ENSMUSG00000059251	2	36640041	36640976	1	4	2	1	0	12	1	0	0	0	0	0	Q8VGK4	
ENSMUST00000076856	ENSMUSG00000094846	19	13619164	13620111	1	3	0	5	1	3	0	0	0	0	0	0	Q8VFQ6	
ENSMUST00000076859	ENSMUSG00000028680	4	117128655	117133963	-1	0	8	0	93	0	0	76	0	63	11	79	Q6P571	
ENSMUST00000076887	ENSMUSG00000040866	7	19054690	19074447	1	13	12	29	0	0	2	0	0	0	0	0	Q99MM9	
ENSMUST00000076889	ENSMUSG00000032192	9	75311395	75344964	1	6	10	30	71	11	7	201	296	243	68	131		P62881
ENSMUST00000076891	ENSMUSG00000024982	19	55298301	55316032	-1	20	19	21	74	23	6	274	874	394	195	235		Q9CPV7
ENSMUST00000076894	ENSMUSG00000040782	1	159232320	159347640	1	13	4	5	6	14	6	166	1035	331	129	244		Q9R1A8
ENSMUST00000076896	ENSMUSG00000062687	8	85171322	85173622	1	23	29	48	27	35	21	0	6	0	0	2	Q3UNC9	
ENSMUST00000076897	ENSMUSG00000060024	13	23011249	23012403	1	4	2	0	1	9	2	0	0	0	0	0	Q8R278	
ENSMUST00000076903	ENSMUSG00000063380	9	39257720	39258682	-1	3	2	3	4	7	0	0	0	0	0	0	Q9EQB5	
ENSMUST00000076906	ENSMUSG00000058172	16	89031699	89032292	1	0	2	7	3	3	0	0	0	0	0	0	O09048	
ENSMUST00000076914	ENSMUSG00000062629	17	37589382	37590381	-1	7	1	5	1	6	0	0	0	0	0	0	Q923Q8	
ENSMUST00000076921	ENSMUSG00000057594	11	120464866	120467607	-1	0	0	0	0	0	0	15	0	6	8	0	B1ATY8	
ENSMUST00000076922	ENSMUSG00000030921	7	104409025	104465193	-1	10	16	13	14	13	11	1518	7915	2662	2774	2826		P15533
ENSMUST00000076936	ENSMUSG00000061777	17	37850594	37851553	1	0	2	12	2	9	3	0	0	0	0	0	Q8VGF0	
ENSMUST00000076939	ENSMUSG00000061535	5	43515538	43618803	1	26	32	106	26	27	17	0	0	0	0	1	E9PVG1	
ENSMUST00000076941	ENSMUSG00000033222	3	100938860	100969663	-1	22	8	3	26	23	0	17	112	67	9	80		Q5NC05
ENSMUST00000076942	ENSMUSG00000022237	15	31291479	31367759	-1	6	7	5	225	9	6	142	457	213	84	236		Q3U0L2
ENSMUST00000076946	ENSMUSG00000036912	9	14696230	14740733	-1	10	8	3	6	8	4	0	0	0	0	0		
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ENSMUST00000076949	ENSMUSG00000064037	5	31494741	31512904	1	37	53	131	61	38	31	33	96	43	51	58	Q4VAB2	Q8VCE2
ENSMUST00000076951	ENSMUSG00000061654	GL456233.1	101352	106395	-1	7	6	8	10	8	6	0	0	0	0	0	Q3UUD2	
ENSMUST00000076952	ENSMUSG00000062510	1	191063012	191086474	1	1	0	0	38	4	0	0	0	2	2	1	D3Z4S2	
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ENSMUST00000076961	ENSMUSG00000003380	7	24969752	24972754	-1	7	5	27	131	28	14	3240	3126	1479	2111	1046		Q9Z0S9
ENSMUST00000076965	ENSMUSG00000064044	11	58701703	58702623	1	5	6	23	11	12	1	0	0	0	0	0	L7MTY4	
ENSMUST00000076968	ENSMUSG00000024743	19	10389090	10453181	1	86	0	0	6	0	0	0	0	0	0	0	Q8CF96	
ENSMUST00000076982	ENSMUSG00000072968	17	9422060	9422458	1	5	0	2	0	0	0	0	0	0	0	0	E9Q5K2	
ENSMUST00000076986	ENSMUSG00000063728	X	154924012	154935987	-1	0	3	7	4	3	3	0	0	0	0	0	O89010	
ENSMUST00000076989	ENSMUSG00000059625	2	25842995	25847248	-1	9	2	37	19	16	6	0	0	0	2	0		Q6IUP1
ENSMUST00000076991	ENSMUSG00000059920	16	64751751	64771161	-1	67	72	91	292	69	50	177	430	256	219	165		Q3TTL0
ENSMUST00000076997	ENSMUSG00000057363	1	43746966	43827800	-1	0	0	9	3	0	0	106	350	182	268	143	G5E8H4	
ENSMUST00000077001	ENSMUSG00000062165	17	20913205	20914363	-1	1	2	1	1	3	6	0	0	0	0	0	A2RTT5	
ENSMUST00000077004	ENSMUSG00000063522	15	74876987	74897021	-1	1	0	3	1	2	1	0	0	0	0	0	Q9CQ11	
ENSMUST00000077008	ENSMUSG00000063188	17	37405477	37406509	1	8	3	8	5	8	1	0	1	0	0	0	Q7TRK4	
ENSMUST00000077016						0	0	0	0	0	0	17	14	21	56	12		
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ENSMUST00000077024	ENSMUSG00000095075	10	129350565	129351509	1	7	3	3	0	5	0	0	0	0	0	0	Q7TRI2	
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ENSMUST00000077046	ENSMUSG00000025404	10	127380327	127499384	1	0	0	0	0	0	0	26	0	0	0	0		Q80TM6
ENSMUST00000077055	ENSMUSG00000058884	2	85917927	85918865	1	0	0	0	5	0	0	0	0	0	0	0		
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ENSMUST00000077075	ENSMUSG00000100631	2	85579241	85580185	1	2	2	4	1	3	3	0	0	0	0	0	Q7TRA0	
ENSMUST00000077078	ENSMUSG00000020448	11	3415982	3452363	-1	11	10	0	74	0	8	527	1515	736	187	506		Q91YT2
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ENSMUST00000077083						45	36	44	60	46	29	94	256	133	69	136		
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ENSMUST00000077093	ENSMUSG00000042810	6	48395586	48419781	1	36	44	49	26	43	30	2	0	5	0	20	D3Z4B8	
ENSMUST00000077110						0	1	1	3	0	0	0	0	0	0	0		
ENSMUST00000077111						3	3	0	0	3	0	1	0	0	3	1		
ENSMUST00000077115	ENSMUSG00000030223	6	137252319	137463233	1	0	0	0	0	0	29	0	0	0	0	0		E9Q612
ENSMUST00000077116	ENSMUSG00000061022	13	23232115	23233041	-1	6	0	2	3	1	2	0	0	0	0	0	Q8R269	
ENSMUST00000077119	ENSMUSG00000056966	5	137953461	137963098	-1	670	674	2170	586	725	323	5	56	28	5	39		Q921C1
ENSMUST00000077123	ENSMUSG00000089859	2	90322222	90325208	1	0	3	3	0	0	0	0	0	0	0	0	A2ATW2	
ENSMUST00000077127						0	0	0	0	0	0	3	0	0	0	0		
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000077133	ENSMUSG00000041505	5	146514123	146516902	1	0	0	0	0	0	0	0	0	0	0	0	L7N1Z6	
ENSMUST00000077136	ENSMUSG00000021795	14	41172212	41185198	-1	8	6	13	4	7	0	0	1	0	0	0		P50404
ENSMUST00000077142	ENSMUSG00000063623	7	29953621	29955992	1	40	25	146	178	50	27	0	10	4	2	8	F7D818	
ENSMUST00000077143	ENSMUSG00000107417	11	49519866	49524660	1	4	2	19	8	11	1	0	0	0	0	0	Q7TQT2	
ENSMUST00000077146	ENSMUSG00000069441	18	20310811	20343350	1	26	18	41	18	20	15	0	0	0	0	0		Q61495
ENSMUST00000077159	ENSMUSG00000051586	6	120931707	121130999	-1	27	14	53	34	41	19	20	6	17	1	22		Q8CJ19
ENSMUST00000077160	ENSMUSG00000041540	6	143828425	144781977	-1	0	17	11	0	0	9	0	0	0	0	0	Q2TBA9	
ENSMUST00000077163						2	0	0	0	0	0	92	3	158	2146	267		
ENSMUST00000077173	ENSMUSG00000064010	11	46607772	46629261	-1	16	8	11	6	19	8	0	1	0	0	0	Q810Y7	
ENSMUST00000077175	ENSMUSG00000034453	10	84622437	84727177	1	25	24	35	39	38	24	151	420	288	36	198		P59470
ENSMUST00000077178	ENSMUSG00000036172	16	44943678	44981380	1	0	0	0	0	0	0	0	0	12	0	3		Q5UKY4
ENSMUST00000077182	ENSMUSG00000033768	19	6418731	6544169	1	1	12	60	0	0	0	0	0	0	0	0	E9Q5N7	
ENSMUST00000077190	ENSMUSG00000032564	9	104547286	105034544	1	0	6	6	0	11	4	1	8	0	4	1	Q9D6C8	
ENSMUST00000077191	ENSMUSG00000064254	7	24587543	24608925	1	12	7	18	76	13	3	1268	1388	692	192	418		Q9DCM0
ENSMUST00000077194	ENSMUSG00000031481	8	22283441	22371418	1	7	6	7	13	9	2	0	0	0	0	0	G5E8H5	
ENSMUST00000077196	ENSMUSG00000037185	15	101349571	101370125	-1	17	13	81	51	26	12	303	733	385	41	377		Q0VBK2
ENSMUST00000077200	ENSMUSG00000039913	2	136081104	136387967	-1	13	7	44	24	17	6	0	0	0	0	0		Q8C015
ENSMUST00000077203	ENSMUSG00000096840	17	38335159	38336097	1	1	2	0	1	3	2	0	0	0	0	0	Q8VG72	
ENSMUST00000077208	ENSMUSG00000059775	8	107439176	107439585	-1	5	5	3	0	7	6	6	4	0	27	6	Q497N1	P62855
ENSMUST00000077210	ENSMUSG00000062426	7	86385657	86386658	-1	4	0	21	4	6	0	0	0	0	0	0	Q7TS03	
ENSMUST00000077220	ENSMUSG00000033434	5	110103975	110108197	-1	0	0	0	44	0	0	41	207	148	23	43		
ENSMUST00000077221	ENSMUSG00000020354	11	46896253	47988969	-1	14	8	5	37	17	6	0	0	0	0	0	Q544D4	P82347
ENSMUST00000077225	ENSMUSG00000063659	1	177442351	177450764	1	15	17	39	39	21	16	75	123	68	9	51		Q9WUK6
ENSMUST00000077228	ENSMUSG00000030147	6	123049962	123071555	1	2	0	10	0	1	5	1	6	0	7	4	Q9D8Q7	
ENSMUST00000077233						205	128	452	4256	274	121	10	41	4	3	16		
ENSMUST00000077235	ENSMUSG00000063897	GL456216.1	15881	36183	1	14	10	78	1108	18	9	212	494	248	71	216		
ENSMUST00000077243	ENSMUSG00000031371	X	73437315	73459044	-1	0	0	0	16	0	0	0	0	0	0	0		Q8BKT8
ENSMUST00000077247	ENSMUSG00000061075	4	118781636	118782583	-1	9	7	22	6	6	3	0	0	0	0	0	A2ACY8	
ENSMUST00000077249	ENSMUSG00000095301	7	107967399	107968331	1	6	3	6	3	5	2	0	0	0	0	0		Q8VGI4
ENSMUST00000077257	ENSMUSG00000015846	2	27676440	27762957	1	38	17	63	45	23	20	412	434	395	67	458	A2AJP1	P28700
ENSMUST00000077271	ENSMUSG00000027774	3	67430096	67476529	1	9	6	14	22	18	5	20	148	69	34	86		Q8K0D5
ENSMUST00000077273	ENSMUSG00000061731	15	53064038	53346159	-1	37	17	48	52	34	11	20	74	23	29	93	Q3V1P4	P97464
ENSMUST00000077278						5	4	4	9	6	0	0	0	0	0	0		
ENSMUST00000077282	ENSMUSG00000054843	19	57611034	58133338	1	28	27	60	263	43	23	870	2451	2407	174	1386		Q6A051
ENSMUST00000077290	ENSMUSG00000025823	6	47796141	47813430	-1	13	12	19	99	15	14	253	435	331	471	487		
ENSMUST00000077301	ENSMUSG00000058030	17	21313963	21314912	1	6	2	2	2	11	8	0	0	0	0	0	Q8R296	
ENSMUST00000077302	ENSMUSG00000062757	2	88864607	88865530	1	2	2	1	0	1	0	0	0	0	0	0	A2ATJ9	
ENSMUST00000077303	ENSMUSG00000027303	2	130450278	130554026	1	15	13	23	1	16	0	264	682	184	0	1		P18052
ENSMUST00000077309						9	4	23	9	7	8	0	0	0	0	0		
ENSMUST00000077312	ENSMUSG00000095401	10	129704880	129705824	1	10	3	0	0	4	0	0	0	0	0	0	Q7TRH7	
ENSMUST00000077320	ENSMUSG00000034173	5	129895723	129903623	1	3	2	3	35	3	0	0	0	0	0	0	D3Z5B1	
ENSMUST00000077337	ENSMUSG00000060969	13	71957921	71963723	-1	11	5	37	336	17	10	0	0	0	1	5		P81068
ENSMUST00000077338	ENSMUSG00000057229	7	25619414	25625551	1	0	4	0	5	1	0	53	92	61	20	32		Q9D7K5
ENSMUST00000077340	ENSMUSG00000041926	1	135262712	135284084	-1	3	0	8	35	9	0	2745	4744	3042	211	2021		Q8VCT3
ENSMUST00000077343	ENSMUSG00000058244	7	108612280	108613287	1	2	2	0	1	2	1	0	0	0	0	0	Q7TRU6	
ENSMUST00000077347	ENSMUSG00000094535	9	19477301	19478248	-1	2	5	5	1	3	3	0	0	0	0	0	Q8VFF2	
ENSMUST00000077353	ENSMUSG00000032126	9	44336350	44344228	-1	0	0	0	54	21	10	54	188	125	72	80		P22907
ENSMUST00000077354	ENSMUSG00000066513	7	44207435	44211754	1	8	8	17	18	10	4	0	0	0	0	0		P00757
ENSMUST00000077355	ENSMUSG00000015222	1	66175273	66442583	1	7	2	0	0	3	1	0	0	0	0	0	Q80ZL4	
ENSMUST00000077356	ENSMUSG00000040650	7	26665227	26686437	-1	13	17	57	30	21	6	0	0	0	0	0	E9Q593	
ENSMUST00000077367	ENSMUSG00000028048	3	89202928	89208966	1	0	8	0	6	0	0	792	1514	819	453	723		P17439
ENSMUST00000077375	ENSMUSG00000000037	X	161117193	161258213	1	5	0	1	1	0	3	0	0	0	0	0	B1AVB3	
ENSMUST00000077376	ENSMUSG00000047635	5	124328089	124341844	1	85	74	114	42	59	29	24	111	44	35	32		Q80VP5
ENSMUST00000077385	ENSMUSG00000061374	7	5007057	5014697	-1	9	0	0	0	33	12	106	500	192	51	90	Q3TRV0	Q9WTJ4
ENSMUST00000077389						2	2	7	0	0	1	1678	6703	2092	13557	1709		
ENSMUST00000077407	ENSMUSG00000031865	6	83165920	83200117	1	0	0	0	13	7	0	2923	2910	3137	173	2261	E9Q586	
ENSMUST00000077408	ENSMUSG00000057667	7	19505814	19508331	-1	51	81	225	303	83	34	656	1416	508	124	287		Q5U5M8
ENSMUST00000077417	ENSMUSG00000094302	7	104068085	104069029	-1	13	7	21	2	4	2	0	0	0	0	0	Q8VH21	
ENSMUST00000077420						13	11	40	8	14	1	0	0	0	6	2		
ENSMUST00000077422	ENSMUSG00000034800	2	127574662	127587094	-1	0	0	14	0	4	4	4	3	5	0	2		Q8BIQ3
ENSMUST00000077433	ENSMUSG00000020317	10	79576379	79587331	-1	2	0	8	0	0	0	0	0	0	0	0		Q9JMB1
ENSMUST00000077435						11	11	15	12	17	17	2	0	2	2	0		
ENSMUST00000077440	ENSMUSG00000003847	8	107293470	107379517	1	140	128	452	0	164	74	512	2197	829	97	1066		Q9WV30
ENSMUST00000077447						1	0	0	5	0	6	0	0	0	0	0		
ENSMUST00000077451	ENSMUSG00000017686	11	80209019	80267907	1	0	0	0	66	0	0	33	33	0	9	0		Q8BG51
ENSMUST00000077452	ENSMUSG00000061958	8	21095074	21096050	-1	1	3	3	0	2	0	0	0	0	0	0	Q5ERJ0	
ENSMUST00000077453	ENSMUSG00000021559	13	60601947	60763185	1	20	20	0	97	25	28	10	20	10	30	60		Q80YE7
ENSMUST00000077456	ENSMUSG00000020564	12	33147693	33375659	1	11	9	11	15	1	0	103	242	83	31	82		Q9CZ05
ENSMUST00000077458	ENSMUSG00000026797	2	32787602	32847245	-1	12	6	26	15	24	0	14	0	0	3	12		O08599
ENSMUST00000077460	ENSMUSG00000063374	10	129011222	129012265	1	17	7	24	7	16	0	0	0	0	0	0	Q8VGC1	
ENSMUST00000077462	ENSMUSG00000021040	12	87443896	87452206	1	0	0	0	0	0	0	28	58	23	123	18	F8WHU8	
ENSMUST00000077471	ENSMUSG00000061520	2	87532035	87532958	1	1	5	0	0	1	1	0	0	0	0	0	Q7TR48	
ENSMUST00000077472	ENSMUSG00000030930	7	132235780	132317228	-1	87	22	93	423	77	57	39	0	51	37	104		Q91XQ5
ENSMUST00000077477	ENSMUSG00000061207	17	34823993	34836945	-1	0	2	2	16	3	0	139	183	86	44	78	Q3TG64	Q9JHN8
ENSMUST00000077478	ENSMUSG00000070458	7	85857547	85875938	-1	14	5	0	5	8	2	0	0	0	0	0	D3Z7M3	
ENSMUST00000077482	ENSMUSG00000057612	6	66731392	66732300	1	0	5	3	4	4	2	0	0	0	0	0	Q8R2E4	
ENSMUST00000077485	ENSMUSG00000029587	5	143235163	143248834	1	0	0	0	76	0	28	0	91	31	20	0		Q7TSI0
ENSMUST00000077489	ENSMUSG00000064329	2	66270778	66440840	-1	0	0	0	4	0	0	0	0	0	0	0	A2APX6	
ENSMUST00000077493						9	10	91	8	14	7	0	5	2	11	1		
ENSMUST00000077494	ENSMUSG00000024426	17	35897595	35910075	-1	0	0	0	0	0	0	0	0	0	3	0		Q8K341
ENSMUST00000077495						2	0	3	3	0	0	0	3	1	1	1		
ENSMUST00000077498	ENSMUSG00000063994	17	37725999	37726991	1	6	2	7	9	5	5	0	0	0	0	0	Q8VFQ2	
ENSMUST00000077500	ENSMUSG00000060268	4	117213333	117252125	-1	5	0	11	4	0	9	0	0	0	0	0	Q3V0P4	
ENSMUST00000077501	ENSMUSG00000095189	19	13453571	13454515	-1	0	3	5	3	3	2	0	0	0	0	0	Q7TQQ9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000077502	ENSMUSG00000009145	6	83057844	83067318	1	87	54	149	63	79	47	28	168	35	4	94		Q924H9
ENSMUST00000077517	ENSMUSG00000061531	2	14174523	14221993	1	31	22	101	18	21	14	7	14	10	0	9		A2ARJ3
ENSMUST00000077523	ENSMUSG00000037411	5	137061504	137072268	-1	11	2	6	0	15	0	0	0	0	14	5	G5E899	
ENSMUST00000077524	ENSMUSG00000057777	3	86545581	86548629	-1	0	0	0	8	0	0	0	0	0	0	0		Q8BPP1
ENSMUST00000077528	ENSMUSG00000060177	7	44112673	44116922	1	9	4	22	6	6	5	0	0	0	0	0	Q540N3	P15948
ENSMUST00000077530	ENSMUSG00000054052	10	127849928	127861176	1	82	47	51	670	101	47	0	0	0	0	0	G5E8H9	
ENSMUST00000077535	ENSMUSG00000024446	17	36255645	36258069	-1	0	0	0	3	0	1	5	25	15	64	9	Q80XY2	
ENSMUST00000077538	ENSMUSG00000063777	19	13410571	13411500	1	2	1	2	2	0	2	0	0	0	0	0	Q8VFW5	
ENSMUST00000077548	ENSMUSG00000062127	3	105001915	105053146	-1	0	0	88	85	35	19	0	0	0	0	0		Q99LJ0
ENSMUST00000077549	ENSMUSG00000058398	9	110826690	110831839	1	18	14	59	32	16	8	1	0	0	0	0	Q76HL1	
ENSMUST00000077551						1	2	4	4	1	2	0	0	0	0	0		
ENSMUST00000077569	ENSMUSG00000031099	X	47809368	47892974	-1	0	0	0	0	0	0	0	0	0	0	0		Q6PGB8
ENSMUST00000077577	ENSMUSG00000023004	15	98931425	98934565	-1	25	36	56	57	50	33	5343	4483	3123	1359	2897		P05213
ENSMUST00000077580	ENSMUSG00000061875	2	87833041	87833985	1	1	1	0	0	2	0	0	0	0	0	0	Q7TR35	
ENSMUST00000077582	ENSMUSG00000058908	4	138831857	138835186	1	0	6	0	7	0	4	0	0	0	0	0	S4R1F8	
ENSMUST00000077585	ENSMUSG00000061972	17	37279501	37280418	-1	6	7	2	1	3	1	0	2	0	2	3	Q8VFE4	
ENSMUST00000077595	ENSMUSG00000031169	X	8193848	8206525	-1	0	0	0	0	0	0	0	0	0	0	3		Q9JJJ7
ENSMUST00000077605	ENSMUSG00000022884	16	23107444	23114136	1	15	5	0	5	6	3	258	3408	473	712	564	Q8BTU6	
ENSMUST00000077609	ENSMUSG00000030795	7	127967457	127985701	1	0	0	0	0	0	0	629	2151	1135	233	954	Q8CFQ9	
ENSMUST00000077610	ENSMUSG00000006342	10	75636619	75644008	-1	0	0	17	62	0	0	2	7	0	0	5		Q9DBX3
ENSMUST00000077626	ENSMUSG00000038383	2	155278243	155357430	-1	0	8	8	17	14	0	161	237	104	0	71	Q3TAA8	
ENSMUST00000077630						2	1	0	1	2	1	0	0	0	0	0		
ENSMUST00000077636	ENSMUSG00000040751	5	134600022	134615025	-1	12	0	62	35	20	9	288	766	241	275	126		Q9JHL0
ENSMUST00000077639	ENSMUSG00000062464	17	32621319	32636184	1	18	8	32	43	17	8	0	2	1	0	0	Q3V1F1	
ENSMUST00000077642	ENSMUSG00000026585	1	163779583	163917109	1	0	0	0	60	0	17	0	0	0	0	48		P70188
ENSMUST00000077659	ENSMUSG00000055415	11	43149877	43262285	1	47	46	72	39	77	34	0	2	2	0	2	B1AWN4	
ENSMUST00000077666	ENSMUSG00000064105	19	46761596	46878795	1	20	12	0	427	37	15	539	1408	1099	65	419		Q3TWN3
ENSMUST00000077667	ENSMUSG00000062061	2	25700043	25703326	1	3	4	14	9	8	2	0	0	0	0	0		Q8K1H9
ENSMUST00000077672	ENSMUSG00000021669	13	96542618	96640167	1	0	12	16	0	11	0	386	537	451	57	116		Q9EQG9
ENSMUST00000077680	ENSMUSG00000000134	X	7762560	7775202	1	0	0	0	22	0	0	260	345	939	61	595	A2AEW1	
ENSMUST00000077687	ENSMUSG00000036641	2	58821697	59160683	-1	12	18	50	43	27	13	1	0	0	0	1		Q6P5U8
ENSMUST00000077689	ENSMUSG00000042121	5	113937094	113993894	-1	0	9	7	35	7	0	142	0	160	39	144	F8WHT2	
ENSMUST00000077693	ENSMUSG00000029145	5	31187558	31193430	-1	3	0	0	0	0	2	70	30	72	50	76		Q61749
ENSMUST00000077696	ENSMUSG00000032816	9	65101486	65137940	1	41	44	117	8	68	27	0	0	0	0	0	E9QAQ0	
ENSMUST00000077698	ENSMUSG00000063130	13	3802893	3804318	-1	10	11	24	16	15	6	0	0	0	0	0		Q9D6P8
ENSMUST00000077705	ENSMUSG00000063415	6	84571414	84593908	-1	25	0	43	267	35	34	0	0	1	0	0		Q811W2
ENSMUST00000077706	ENSMUSG00000032530	9	121577843	121642096	-1	2	3	1	2	14	6	0	0	0	4	0	Q78ID0	Q9D925
ENSMUST00000077709	ENSMUSG00000045917	4	63558781	63586357	1	0	0	0	64	0	19	441	461	395	35	585		Q8R239
ENSMUST00000077715	ENSMUSG00000057174	16	88931804	88932264	-1	2	1	8	0	1	0	0	0	0	0	0		Q99NG9
ENSMUST00000077719	ENSMUSG00000066153	4	62147932	62150863	-1	1	4	2	1	3	0	0	0	0	0	0	Q80YX8	
ENSMUST00000077730	ENSMUSG00000026447	1	133045667	133108687	1	144	76	356	820	135	67	191	683	255	32	169	E9QAN8	
ENSMUST00000077732	ENSMUSG00000095893	9	38046581	38048153	1	0	3	5	0	0	0	0	0	0	0	0	Q7TRE1	
ENSMUST00000077735	ENSMUSG00000021262	12	108554720	108688513	1	0	0	0	25	0	0	0	0	0	0	0		P70429
ENSMUST00000077737	ENSMUSG00000026918	2	27445579	27507662	-1	28	32	145	20	8	18	470	1094	621	73	594	Q3TUI3	Q8K2F0
ENSMUST00000077741	ENSMUSG00000060681	X	56609757	56664230	1	10	6	0	20	8	0	98	223	40	32	35	A1L3P4	
ENSMUST00000077747						5	9	0	14	6	0	1	4	3	9	2		
ENSMUST00000077755	ENSMUSG00000008475	1	152766542	152775597	1	11	13	0	21	0	11	7099	32881	9832	5048	6389		Q9CPW4
ENSMUST00000077757	ENSMUSG00000062649	9	39484204	39493988	-1	5	2	3	1	2	0	0	0	0	0	0	Q9EQB8	
ENSMUST00000077766						2	5	10	1	2	0	0	21	0	9	0		
ENSMUST00000077772	ENSMUSG00000056055	1	87803680	87845158	1	1	0	2	2	0	0	4	12	3	3	0	Q3UPX6	P20443
ENSMUST00000077773	ENSMUSG00000040732	16	95359169	95586593	-1	0	2	4	3	0	3	10	10	0	4	0	B7ZND4	P81270
ENSMUST00000077775	ENSMUSG00000037005	X	48108725	48136981	1	4	4	24	12	6	9	0	0	0	0	0	B1AVD1	
ENSMUST00000077776						4	8	12	5	6	0	3	10	10	363	67		
ENSMUST00000077780	ENSMUSG00000050605	7	24291039	24301232	-1	8	5	24	24	20	10	0	20	0	0	0	Q923D1	
ENSMUST00000077783	ENSMUSG00000058706	6	72347317	72353148	1	56	42	76	1596	81	41	545	1500	962	68	617		Q149G0
ENSMUST00000077785	ENSMUSG00000061295	2	89991238	89994315	1	4	1	9	7	6	4	0	0	0	0	0	Q8VFB0	
ENSMUST00000077787	ENSMUSG00000053985	7	30038053	30044734	-1	11	6	9	6	16	6	1	1	0	4	1		P10755
ENSMUST00000077788	ENSMUSG00000044469	17	56162477	56173955	1	19	16	30	89	32	12	58	38	36	12	23		Q8K288
ENSMUST00000077791	ENSMUSG00000055835	8	111643443	111671008	1	18	10	26	49	29	15	27	102	49	81	76	Q3UI68	
ENSMUST00000077794	ENSMUSG00000058275	11	74364671	74365665	1	2	5	3	10	11	3	0	0	0	0	0	Q7TRW7	
ENSMUST00000077798	ENSMUSG00000027067	2	85037234	85047109	1	0	0	0	21	17	0	342	714	655	252	526		Q08943
ENSMUST00000077800	ENSMUSG00000062878	7	86488551	86489549	-1	1	4	12	0	6	3	0	0	0	0	0	Q7TS06	
ENSMUST00000077816	ENSMUSG00000058019	8	93499213	93535707	-1	8	4	13	6	7	4	0	0	0	0	0		Q6AW46
ENSMUST00000077817	ENSMUSG00000007850	11	50376990	50386528	1	0	0	0	0	0	0	0	190	44	65	70	Q8C2Q7	
ENSMUST00000077820	ENSMUSG00000060183	5	92359544	92365485	-1	6	9	4	2	4	0	0	1	0	2	4	M0QWR7	
ENSMUST00000077821	ENSMUSG00000033697	15	76723985	76818170	-1	0	18	37	82	0	14	28	0	32	8	37	H7BX46	
ENSMUST00000077836	ENSMUSG00000096497	10	129462678	129463616	1	0	2	4	4	0	1	0	0	0	0	0	Q7TRI1	
ENSMUST00000077839	ENSMUSG00000075000	10	67266689	67285305	-1	8	4	4	68	4	0	272	1007	372	95	276		Q8VCQ3
ENSMUST00000077843	ENSMUSG00000108674	13	21698471	21703965	1	0	11	17	6	12	4	0	0	0	0	0	Q5SZZ5	
ENSMUST00000077846						2	0	18	0	1	1	0	0	0	0	2		
ENSMUST00000077847	ENSMUSG00000027200	2	124089969	124667770	1	0	0	0	0	0	0	0	0	0	0	0		Q76KF0
ENSMUST00000077851	ENSMUSG00000028397	4	74242497	74405860	1	0	15	14	0	0	12	0	0	0	0	0		Q8VCD7
ENSMUST00000077853	ENSMUSG00000021413	13	34875494	34902877	1	13	9	45	110	23	10	235	633	610	306	597		Q61136
ENSMUST00000077855	ENSMUSG00000066704	7	26757142	26772630	1	17	13	39	9	23	9	0	0	0	0	0		O55071
ENSMUST00000077856	ENSMUSG00000063316	11	101442298	101445529	1	0	6	9	28	8	5	22	37	25	122	8	Q5BLJ9	P61358
ENSMUST00000077867	ENSMUSG00000022822	16	20331303	20426394	-1	4	0	3	21	15	2	25	23	40	0	38	F8WJ10	
ENSMUST00000077868						37	32	82	340	38	27	1	43	16	0	17		
ENSMUST00000077871	ENSMUSG00000034813	10	119454034	120087261	1	1	0	0	0	0	0	0	0	0	0	0		Q925T6
ENSMUST00000077876	ENSMUSG00000046032	X	101097786	101222563	-1	0	0	0	21	0	1	48	56	24	41	14	Q3TGS7	
ENSMUST00000077879	ENSMUSG00000035284	9	67840396	67995634	1	51	40	43	69	69	31	674	1028	1846	88	1415	A1ILG8	Q8BX70
ENSMUST00000077886	ENSMUSG00000094973	6	136327539	136329983	1	29	27	36	138	50	30	0	0	0	0	0	E9PV04	
ENSMUST00000077889	ENSMUSG00000057072	1	191036639	191042942	1	4	1	2	2	2	4	0	0	0	0	0		Q9CVW4
ENSMUST00000077890	ENSMUSG00000036555	5	140661827	140702378	-1	0	0	0	0	0	0	55	22	81	7	73		Q6PCQ0
ENSMUST00000077902	ENSMUSG00000020932	11	102887336	102900912	-1	15	3	46	30	12	3	0	0	0	0	0		P03995

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000077909	ENSMUSG00000031024	7	109523911	109617147	-1	20	7	46	36	32	20	0	0	0	0	0		Q924W7
ENSMUST00000077915	ENSMUSG00000057322	11	114668524	114672331	1	0	0	15	11	0	0	244	455	215	1489	165	Q52KP0	Q9JJI8
ENSMUST00000077916	ENSMUSG00000048416	3	67374097	67400003	1	0	0	0	14	4	2	0	1	0	2	0	Q3V042	Q9QWV4
ENSMUST00000077918	ENSMUSG00000058952	3	129835884	129875332	1	18	18	10	7	9	9	0	0	0	11	0		Q61129
ENSMUST00000077925	ENSMUSG00000020099	10	60762610	60831581	-1	71	35	227	301	116	29	1	0	0	3	34		Q8K1S3
ENSMUST00000077930	ENSMUSG00000071454	12	3572381	3781796	1	5	4	4	15	7	0	49	0	0	0	0	Q8K0N0	
ENSMUST00000077935	ENSMUSG00000038679	15	50654752	50890463	-1	8	6	45	28	18	10	61	68	264	7	234	G3UW90	
ENSMUST00000077938	ENSMUSG00000061046	17	25779843	25785673	-1	4	9	3	22	4	0	116	99	110	23	36		Q9DB32
ENSMUST00000077941	ENSMUSG00000040687	2	91137360	91183837	-1	0	2	0	0	9	0	0	0	0	0	0	A2AGQ4	
ENSMUST00000077946	ENSMUSG00000038608	1	80501073	80758527	-1	0	0	0	4	10	0	264	152	143	62	171	E9QM99	
ENSMUST00000077954	ENSMUSG00000035296	14	61221059	61258490	-1	6	6	17	4	6	4	0	0	0	0	0	Q9EQ83	P82348
ENSMUST00000077955	ENSMUSG00000063605	8	94902869	94918098	-1	14	13	34	293	26	7	37	86	15	4	43	B2RTE5	Q3TMW1
ENSMUST00000077958	ENSMUSG00000043897	3	64116432	64140543	-1	9	6	0	3	0	2	0	0	0	1	0	L7N1Z7	
ENSMUST00000077960	ENSMUSG00000056116	17	36037128	36042747	-1	0	6	9	0	0	0	347	609	259	167	426	Q31615	
ENSMUST00000077962	ENSMUSG00000059852	18	80294546	80364254	-1	13	13	28	202	19	6	0	1	0	0	1	F7A6P6	
ENSMUST00000077967	ENSMUSG00000053091	7	66689889	66717256	1	0	0	0	0	0	0	154	473	186	115	276		Q3U1D0
ENSMUST00000077968	ENSMUSG00000056987	12	78691535	78734513	1	7	5	16	8	8	1	0	0	1	0	0	D3YV92	
ENSMUST00000077972	ENSMUSG00000042359	2	76406508	76600647	1	0	0	41	0	0	0	0	0	0	0	0	F8WIZ7	
ENSMUST00000077976						1	0	2	2	2	0	0	4	1	1	0		
ENSMUST00000077977	ENSMUSG00000026858	2	30364233	30385521	1	5	0	0	2	21	0	24	32	17	3	35		Q8BK03
ENSMUST00000077981	ENSMUSG00000021959	14	57642077	57758388	-1	1	2	0	4	4	0	5	8	9	3	7	Q8VHE2	
ENSMUST00000077983	ENSMUSG00000026927	2	26382802	26389316	-1	0	1	0	0	0	0	158	852	348	65	269		A2AIW0
ENSMUST00000077985	ENSMUSG00000064272	1	74278550	74279624	1	5	7	24	29	12	6	0	1	1	0	1	Q14AA9	Q80SS6
ENSMUST00000077988	ENSMUSG00000060332	2	130195194	130264445	1	59	51	165	51	44	25	0	4	0	0	1		Q8R4P4
ENSMUST00000077990						17	10	18	22	26	14	0	9	0	3	19		
ENSMUST00000077991						7	11	33	16	20	6	4	7	4	0	4		
ENSMUST00000077997	ENSMUSG00000059830	9	53884082	53884561	1	6	3	15	7	3	2	0	0	0	0	0	E9PZU9	
ENSMUST00000078001	ENSMUSG00000062773	7	24668007	24676675	-1	8	3	9	17	11	1	1	0	0	0	0		Q9JMI7
ENSMUST00000078012						0	0	9	50	2	6	0	0	0	0	2		
ENSMUST00000078019	ENSMUSG00000022150	15	6299788	6440712	1	0	2	0	0	0	4	0	0	0	0	0	Q3TRE6	
ENSMUST00000078021	ENSMUSG00000029276	5	107548967	107597888	-1	0	0	0	0	0	2	0	0	0	29	0		Q8BZM1
ENSMUST00000078027	ENSMUSG00000068205	2	140395309	142392966	1	0	0	1	0	3	0	0	0	0	0	1		Q3UYG8
ENSMUST00000078030						2	4	1	2	3	1	0	0	0	0	0		
ENSMUST00000078034	ENSMUSG00000062456	19	32465885	32466575	-1	7	6	0	0	0	0	0	30	0	0	0		
ENSMUST00000078039	ENSMUSG00000061602	7	12152464	12153405	1	1	1	2	1	2	1	0	0	0	0	0	K7N608	
ENSMUST00000078049	ENSMUSG00000033016	18	80606205	80713071	-1	3	0	0	9	27	13	255	421	460	26	226	Q6P7T9	
ENSMUST00000078050	ENSMUSG00000006418	2	167492645	167516173	1	5	0	44	116	21	5	835	983	763	166	717		Q9ET26
ENSMUST00000078052						3	3	6	7	1	0	0	0	1	0	0		
ENSMUST00000078053	ENSMUSG00000034327	14	67715937	67742310	1	12	9	7	46	6	3	0	28	59	8	32		Q80UN1
ENSMUST00000078057	ENSMUSG00000061210	6	43235578	43236636	1	3	11	5	4	2	5	0	0	0	0	0	Q8VF18	
ENSMUST00000078058	ENSMUSG00000049184	8	33386325	33417468	1	9	2	0	3	9	2	22	87	9	5	14		Q8R4E6
ENSMUST00000078060	ENSMUSG00000062564	X	74150944	74167838	-1	4	3	11	3	3	2	0	0	0	0	0	B1AYN9	
ENSMUST00000078061	ENSMUSG00000013787	17	34898469	34914052	1	30	7	1	0	25	1	179	220	82	0	318		Q9Z148
ENSMUST00000078070	ENSMUSG00000064065	10	6885796	7052478	-1	0	0	0	0	0	0	36	17	108	0	29		Q5DU31
ENSMUST00000078074	ENSMUSG00000064289	2	61578585	61654171	1	0	0	0	0	0	0	0	68	0	30	0		P70347
ENSMUST00000078075	ENSMUSG00000057179	14	50680691	50692543	-1	8	9	6	3	0	2	0	0	0	0	0	E9PXH6	
ENSMUST00000078079	ENSMUSG00000057561	18	46597704	46610225	1	9	8	8	15	13	3	80	689	194	785	171	Q4FJR7	Q60872
ENSMUST00000078084	ENSMUSG00000037266	4	134923592	134927671	1	0	1	0	146	7	0	621	2954	1361	40	574		Q3UC65
ENSMUST00000078090	ENSMUSG00000028496	4	87769925	88033364	-1	8	9	14	49	11	15	2	26	8	10	26		A2AM29
ENSMUST00000078094						6	10	17	13	7	5	1	8	2	1	6		
ENSMUST00000078095	ENSMUSG00000042638	6	136697284	136781765	-1	0	0	0	0	0	0	0	2	1	0	2		Q3UWA6
ENSMUST00000078099	ENSMUSG00000044122	11	78193392	78205763	1	5	4	25	10	8	4	0	0	0	0	0	B0QZF6	
ENSMUST00000078103	ENSMUSG00000061489	7	140322602	140323651	1	11	6	1	13	12	6	1	0	0	0	0	Q8VGL5	
ENSMUST00000078108	ENSMUSG00000096584	7	103517411	103518382	-1	2	6	4	0	2	0	0	0	0	0	0	K7N609	
ENSMUST00000078111	ENSMUSG00000032086	9	45838580	45864399	1	0	0	0	260	8	11	11	0	6	1	37	Q8C4F4	
ENSMUST00000078112	ENSMUSG00000059022	6	29473162	29507952	-1	0	1	2	265	1	0	0	0	0	0	0		Q3U492
ENSMUST00000078121	ENSMUSG00000061845	8	21065038	21065996	1	0	1	3	9	2	0	0	0	0	0	0	E9QLQ1	
ENSMUST00000078124	ENSMUSG00000062929	12	54858817	54862877	-1	5	3	2	27	11	2	63	188	66	74	77	Q3UHW9	P45591
ENSMUST00000078137	ENSMUSG00000024947	19	6334979	6340891	1	0	4	15	0	21	0	35	0	0	0	46		O88559
ENSMUST00000078139	ENSMUSG00000028207	4	9448069	9669344	-1	13	0	2	0	24	0	31	70	0	11	63		Q8BSY0
ENSMUST00000078149						3	0	8	5	2	0	0	0	0	0	5		
ENSMUST00000078155	ENSMUSG00000003500	6	29200434	29216364	-1	0	6	0	50	0	5	174	52	53	0	66		P50096
ENSMUST00000078156	ENSMUSG00000064168	13	23542970	23543357	-1	6	3	7	55	8	0	0	0	0	0	2		Q64478
ENSMUST00000078162	ENSMUSG00000060759	7	108544527	108545498	1	4	1	1	0	2	3	0	0	0	0	0	Q7TRU8	
ENSMUST00000078163	ENSMUSG00000021763	13	113317084	113379711	1	0	0	21	0	0	0	0	0	0	0	0	F6ZML1	
ENSMUST00000078170	ENSMUSG00000034467	8	116505015	116515896	1	1	5	10	4	11	3	0	0	0	0	0		Q9DAJ5
ENSMUST00000078171	ENSMUSG00000063867	14	52389815	52390771	-1	7	0	13	4	9	1	0	0	0	0	0	E9PWU0	
ENSMUST00000078172	ENSMUSG00000070460	7	84853573	84857318	1	0	2	5	5	6	3	0	0	0	0	0	Q8VF60	
ENSMUST00000078182	ENSMUSG00000063594	7	16891786	16895436	1	1	6	19	23	18	10	0	2	0	0	0	Q3UMY0	P63078
ENSMUST00000078185	ENSMUSG00000055053	10	81396186	81431005	-1	5	0	0	92	8	0	185	114	72	17	6		P70255
ENSMUST00000078186	ENSMUSG00000061208	6	57035913	57037125	1	2	3	4	5	5	3	0	0	0	0	0	Q8R2C2	
ENSMUST00000078191	ENSMUSG00000062142	7	102887207	102888151	-1	4	2	8	7	5	3	0	0	0	0	0	Q8VGZ2	
ENSMUST00000078193	ENSMUSG00000096644	X	155088686	155089793	-1	2	0	10	2	7	0	0	0	0	0	0	O89006	
ENSMUST00000078200	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	21	0	0	0	0	0	0	0		Q69Z98
ENSMUST00000078205	ENSMUSG00000060550	17	35439155	35443773	1	0	0	0	0	0	0	0	0	0	17	0	E9PWT4	
ENSMUST00000078207	ENSMUSG00000059687	17	37445480	37446517	1	3	3	14	5	2	1	0	0	1	0	0	Q8VFA1	
ENSMUST00000078209	ENSMUSG00000064121	17	37225091	37226141	1	7	6	34	11	18	8	0	0	0	0	0	Q8VFE3	
ENSMUST00000078214	ENSMUSG00000059182	6	51857422	52012549	-1	5	10	10	31	2	6	3461	14766	5485	9597	3999		Q3UND0
ENSMUST00000078217	ENSMUSG00000096806	11	58831156	58832082	1	10	7	16	9	10	2	0	0	0	0	0	Q7TRZ9	
ENSMUST00000078218	ENSMUSG00000058586	15	83089506	83116674	1	0	0	0	16	1	2	203	187	103	81	29	Q80XK9	Q9EPB5
ENSMUST00000078222	ENSMUSG00000000308	2	121357714	121363737	1	0	8	5	0	0	0	0	0	1	1	0	Q545N7	P30275
ENSMUST00000078223	ENSMUSG00000064262	6	48647234	48660875	1	62	71	65	70	85	55	32	142	53	83	205		Q75N62
ENSMUST00000078226	ENSMUSG00000027674	3	32949408	33143247	-1	8	0	0	0	0	0	0	0	0	0	0	F8SLQ3	
ENSMUST00000078229	ENSMUSG00000056854	X	110814280	110817207	1	39	43	198	214	39	12	0	0	0	0	0	A6H6L6	P62515

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000078239	ENSMUSG00000054757	13	4486972	4523344	-1	4	2	3	3	6	0	0	0	0	0	0	Q9CZU0	
ENSMUST00000078246						0	6	0	2	3	1	48	217	104	562	85		
ENSMUST00000078252						1	2	2	0	1	0	0	0	0	0	0		
ENSMUST00000078257	ENSMUSG00000079038	8	69300776	69303162	1	3	3	2	0	2	0	0	2	1	2	0	Q8BII3	
ENSMUST00000078259	ENSMUSG00000062510	1	191063012	191086474	1	167	174	703	169	144	85	29	45	42	7	20	E9QME3	
ENSMUST00000078264	ENSMUSG00000062204	11	52144593	52145528	-1	16	7	18	12	13	0	0	2	1	0	1	Q7TQT6	
ENSMUST00000078267	ENSMUSG00000056895	11	58948920	58949533	1	5	6	26	75	7	4	0	0	0	3	1		Q9D2U9
ENSMUST00000078271	ENSMUSG00000063687	18	37320381	37323915	1	148	109	1454	220	225	63	5	27	7	3	23	Q91XZ5	
ENSMUST00000078272	ENSMUSG00000040118	5	15934691	16374511	1	8	0	8	18	16	0	0	0	0	0	1		O08532
ENSMUST00000078282	ENSMUSG00000059105	19	13887221	13888305	-1	3	4	5	5	13	1	0	0	0	0	0	Q8VFQ4	
ENSMUST00000078284	ENSMUSG00000025075	19	56287137	56320822	1	0	0	4	9	0	3	0	0	0	2	0	E9QM92	
ENSMUST00000078286	ENSMUSG00000063888	17	46773907	46782656	-1	54	55	94	54	63	29	716	1914	1026	1006	671		Q9D8M4
ENSMUST00000078289	ENSMUSG00000064333	9	38877126	38878176	1	2	3	2	0	3	1	0	0	0	0	0	Q9EQ98	
ENSMUST00000078299	ENSMUSG00000057503	19	13145643	13146743	-1	3	5	7	0	6	5	0	0	0	0	0	Q8VFV9	
ENSMUST00000078307	ENSMUSG00000061584	1	37905923	37916493	-1	21	15	9	8	29	11	0	0	0	0	0		Q3V1I0
ENSMUST00000078308	ENSMUSG00000070565	1	157135182	157412595	-1	72	50	167	82	65	36	12	29	14	9	31	E9PW37	
ENSMUST00000078312						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000078314	ENSMUSG00000019834	10	40570336	40604132	1	13	0	35	56	11	5	0	0	0	0	0	B2RRB7	Q497L8
ENSMUST00000078320	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0		Q01815
ENSMUST00000078322	ENSMUSG00000059862	10	130179937	130184173	-1	7	2	2	4	4	3	0	0	1	0	0	Q8VFU6	
ENSMUST00000078323	ENSMUSG00000013495	5	108629770	108648782	1	0	7	0	16	10	0	0	222	96	65	30		Q9CXY1
ENSMUST00000078324	ENSMUSG00000017412	2	52428320	52676831	-1	41	27	79	115	19	25	0	0	0	0	0	A2ATZ8	Q8R0S4
ENSMUST00000078326						3	0	11	1	2	1	0	1	0	0	1		
ENSMUST00000078332	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	39	0	0	0	66	41	116	59		Q6PCP5
ENSMUST00000078350	ENSMUSG00000036356	8	68356781	68735146	-1	16	6	36	63	3	3	4	17	3	8	13		Q8BJQ9
ENSMUST00000078352	ENSMUSG00000026825	2	32308471	32353338	-1	12	0	13	3	0	0	0	0	3	0	0		P39053
ENSMUST00000078357	ENSMUSG00000022505	16	10281749	10313968	-1	34	20	61	108	63	35	0	0	0	25	67	Q548I4	O88662
ENSMUST00000078358	ENSMUSG00000072708	11	73485887	73491477	-1	0	10	3	10	0	2	0	0	0	0	0	Q5SSP0	
ENSMUST00000078362	ENSMUSG00000064090	11	26471322	26593999	-1	0	0	0	0	3	0	14	21	30	96	43		Q8BN21
ENSMUST00000078364	ENSMUSG00000060747	7	28522836	28524322	1	9	3	4	6	10	4	0	0	0	0	0		Q8CGK6
ENSMUST00000078367	ENSMUSG00000037784	9	99629496	99669256	1	0	0	0	0	0	0	0	0	0	0	0	B2RR42	Q499E4
ENSMUST00000078369	ENSMUSG00000061615	13	23751126	23751598	1	2	2	2	23	6	2	0	0	0	7	3	B2RVF0	P22752
ENSMUST00000078371	ENSMUSG00000062546	6	90202793	90203682	1	0	3	1	2	2	2	0	0	0	0	0		Q9EQ48
ENSMUST00000078374	ENSMUSG00000032407	9	95456898	95511996	-1	4	8	10	33	5	0	77	178	71	95	40		Q6NV83
ENSMUST00000078386	ENSMUSG00000045871	14	110748578	110755149	-1	14	17	15	14	19	12	0	0	0	0	0	A6H6M2	Q8C110
ENSMUST00000078393						4	0	3	0	3	0	0	1	0	1	1		
ENSMUST00000078404	ENSMUSG00000056851	15	102470632	102500059	1	11	0	0	29	0	0	307	528	184	28	113		Q61990
ENSMUST00000078409	ENSMUSG00000079042	8	65012976	65037336	-1	21	14	14	14	12	11	0	0	0	0	0	Q8JZK6	
ENSMUST00000078414	ENSMUSG00000062873	10	78875549	78880106	1	4	2	13	2	5	4	0	0	0	0	0	Q7TQU9	
ENSMUST00000078419						4	6	0	6	4	0	9	6	3	8	10		
ENSMUST00000078422	ENSMUSG00000058368	16	89403027	89403774	-1	3	1	34	4	3	2	0	0	0	0	0	B9EK12	
ENSMUST00000078431						11	4	2	5	8	7	0	0	0	0	0		
ENSMUST00000078432	ENSMUSG00000030432	7	4792874	4795066	1	8	8	19	136	14	6	33	42	17	2	42	Q5M9J8	P41105
ENSMUST00000078434	ENSMUSG00000022092	14	70217898	70289449	-1	7	6	20	64	11	10	47	113	96	50	65	Q3V074	P48455
ENSMUST00000078438	ENSMUSG00000058063	17	36898118	36910214	1	8	11	18	27	24	7	0	0	0	0	0		Q8R0K2
ENSMUST00000078442	ENSMUSG00000059845	11	99879187	99880229	1	0	4	23	38	13	5	0	0	0	0	0	Q9D141	
ENSMUST00000078447	ENSMUSG00000059319	7	86583903	86586206	1	2	5	0	2	5	0	0	0	0	0	0	Q7TS08	
ENSMUST00000078448	ENSMUSG00000064307	7	101912984	101933895	-1	0	0	0	0	0	0	0	0	0	0	0	G5E8I1	
ENSMUST00000078451	ENSMUSG00000058818	7	3711409	3720391	-1	93	81	190	65	56	40	784	4465	1472	279	1351		P97484
ENSMUST00000078458	ENSMUSG00000062483	7	23631988	23633568	1	11	9	3	4	7	0	0	0	0	0	0	Q9EPS6	
ENSMUST00000078459	ENSMUSG00000058704	17	74200706	74294883	-1	6	1	8	47	9	2	83	167	73	107	72		Q91VH6
ENSMUST00000078469	ENSMUSG00000064129	X	91632194	91635671	1	2	0	10	2	2	0	0	0	0	0	0	A2A9Q9	
ENSMUST00000078470	ENSMUSG00000058248	1	192190774	192510159	1	30	28	57	0	58	21	0	0	0	0	0	Q3USQ9	Q60603
ENSMUST00000078471	ENSMUSG00000064063	13	67863326	67863923	1	5	3	3	3	5	3	0	0	0	0	0	Q80ZS7	
ENSMUST00000078475	ENSMUSG00000058399	7	5883580	5884542	-1	4	3	7	3	4	2	0	0	0	0	0	Q8R2B8	
ENSMUST00000078478	ENSMUSG00000043587	9	96823336	96892669	-1	0	0	0	0	0	0	142	250	119	20	144		Q8BHA9
ENSMUST00000078481	ENSMUSG00000002565	12	40059769	40134228	-1	33	32	19	0	28	24	0	6	0	0	19		Q60604
ENSMUST00000078482	ENSMUSG00000036862	7	105752989	105787654	-1	74	58	146	0	130	0	0	0	0	0	0		E9PVD3
ENSMUST00000078486	ENSMUSG00000053477	18	69343356	69689079	1	20	19	47	45	40	52	51	242	62	35	58		Q60722
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ENSMUST00000078494	ENSMUSG00000061311	2	101638282	101649501	-1	32	29	45	29	31	17	0	3	1	1	1		P15919
ENSMUST00000078496	ENSMUSG00000024112	17	25374285	25433783	-1	46	0	80	326	29	22	0	0	0	0	0	E9Q6P9	
ENSMUST00000078497	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	Z4YJU0	
ENSMUST00000078505	ENSMUSG00000021087	12	72211752	72409054	-1	19	18	73	425	38	22	0	1	0	0	1	Q4FJL2	Q8K0T0
ENSMUST00000078508	ENSMUSG00000060284	15	102356609	102366325	-1	34	22	85	296	46	19	0	0	0	0	0	Q2KHK9	Q8VI67
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ENSMUST00000078515						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000078517	ENSMUSG00000094539	16	59085552	59089797	-1	3	2	1	3	2	1	0	0	0	0	0	L7N1Z8	
ENSMUST00000078521	ENSMUSG00000030345	6	126876020	126921839	-1	6	11	43	7	0	0	0	0	0	0	0		Q8BI55
ENSMUST00000078525	ENSMUSG00000047747	8	82863356	83091271	1	90	74	367	564	117	49	41	154	104	11	140		Q5DTZ6
ENSMUST00000078527	ENSMUSG00000034009	3	79641611	79737880	-1	65	53	347	70	54	35	3	4	4	0	12		Q6R6I7
ENSMUST00000078528	ENSMUSG00000018446	11	70977836	70983026	-1	0	1	5	27	4	2	57	162	52	28	111	Q8R5L1	
ENSMUST00000078531	ENSMUSG00000094269	9	39393793	39394737	1	2	4	0	6	2	0	0	0	0	0	0	Q9EQ94	
ENSMUST00000078532	ENSMUSG00000095647	10	23992405	23993481	-1	11	9	10	7	2	6	0	0	0	0	0		Q5QD12
ENSMUST00000078547	ENSMUSG00000061536	9	121680047	121705490	-1	87	70	208	621	140	76	329	415	419	24	227		Q8BXT9
ENSMUST00000078554	ENSMUSG00000061361	16	19529980	19530918	-1	7	2	6	6	2	1	0	0	0	0	0	Q8VF05	
ENSMUST00000078557	ENSMUSG00000094353	9	39736817	39737755	1	0	2	6	4	2	1	0	0	0	0	0		Q60895
ENSMUST00000078559	ENSMUSG00000030147	6	123049962	123071555	1	0	3	0	3	0	0	0	8	3	13	0	Q7TS58	
ENSMUST00000078568	ENSMUSG00000050150	3	135348029	135397827	1	2	2	0	0	0	0	0	0	0	0	0	G5E8I2	
ENSMUST00000078572	ENSMUSG00000032182	9	21588709	21592831	-1	0	0	0	0	0	9	53	152	52	38	39		Q99LP8
ENSMUST00000078573	ENSMUSG00000061474	13	100735955	100744659	-1	4	0	0	21	0	5	11	41	30	68	13	Q9D6T9	
ENSMUST00000078574	ENSMUSG00000058328	X	73107635	73292976	-1	0	4	0	1	0	0	0	0	0	0	0	A2BI45	
ENSMUST00000078588	ENSMUSG00000062042	7	86615636	86616643	-1	6	6	3	7	5	0	0	0	0	0	0	F7CWV4	
ENSMUST00000078589	ENSMUSG00000014633	8	116888685	116921455	-1	0	0	0	0	0	0	7	10	23	61	7	F8WHQ0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000078593	ENSMUSG00000062598	7	23893529	23894443	1	2	6	0	4	1	2	0	0	0	0	0	Q8R2B6	
ENSMUST00000078603	ENSMUSG00000062245	16	19605696	19606703	-1	9	6	1	6	6	1	0	0	0	0	0	Q8VGL6	
ENSMUST00000078605	ENSMUSG00000058252	X	135654698	135693790	-1	1	4	8	2	1	2	7	14	9	8	4	A2AEI7	
ENSMUST00000078615	ENSMUSG00000057246	17	34398820	34460734	1	0	8	56	3	12	7	0	0	0	0	0	A2CG24	
ENSMUST00000078616	ENSMUSG00000026930	2	26315515	26348237	1	0	0	0	0	0	0	39	23	38	0	14		Q6IR34
ENSMUST00000078617	ENSMUSG00000059343	4	72850583	72852634	-1	3	1	9	6	5	2	0	0	0	0	0	A6ZI46	
ENSMUST00000078621	ENSMUSG00000027200	2	124089969	124667770	1	0	18	130	0	73	36	0	0	0	0	0		Q76KF0
ENSMUST00000078623	ENSMUSG00000000724	11	77718615	77725283	-1	3	0	4	7	2	3	0	0	0	0	0	Q9QXC6	
ENSMUST00000078626	ENSMUSG00000062296	9	111311739	111395775	1	91	66	151	214	109	55	0	2	0	0	2		Q8BV79
ENSMUST00000078631	ENSMUSG00000061798	2	88851952	88852881	1	3	0	6	0	2	2	0	0	0	0	0	Q7TR10	
ENSMUST00000078634	ENSMUSG00000000766	10	6758506	7038198	1	2	0	5	2	2	1	0	0	0	1	0		
ENSMUST00000078642	ENSMUSG00000094379	13	22501337	22502245	-1	7	2	2	3	1	0	0	0	0	0	0	Q8R259	
ENSMUST00000078647	ENSMUSG00000030055	6	87788853	87812164	-1	28	18	56	66	48	28	3599	3065	2870	403	2130	Q0PD10	Q8CG50
ENSMUST00000078665	ENSMUSG00000060038	8	85071757	85075162	1	0	0	0	46	6	0	147	159	80	62	88		Q3TXU5
ENSMUST00000078673	ENSMUSG00000058656	15	53461621	53902537	-1	4	3	0	8	7	3	0	0	0	1	1		Q0VE29
ENSMUST00000078676	ENSMUSG00000063882	4	116066965	116075071	-1	5	10	7	7	3	3	1380	4154	1081	6337	821		P99028
ENSMUST00000078680	ENSMUSG00000030838	7	46195350	46238503	-1	0	0	0	0	0	3	20	80	13	72	17		
ENSMUST00000078686	ENSMUSG00000060402	7	34674468	34812711	-1	12	9	29	18	23	8	0	0	0	0	0		Q8BQ86
ENSMUST00000078687	ENSMUSG00000027573	2	180710117	180718733	1	15	14	25	9	20	10	5	9	4	0	8		Q9D7M1
ENSMUST00000078690	ENSMUSG00000036817	5	139200637	139249840	1	0	0	0	0	1	6	0	0	0	0	30		Q9D666
ENSMUST00000078691	ENSMUSG00000057789	17	27019810	27029009	-1	18	9	23	21	18	12	786	510	460	63	316		O08734
ENSMUST00000078694	ENSMUSG00000061718	11	98348404	98357796	1	2	2	11	298	7	7	0	0	0	0	0		Q60829
ENSMUST00000078695	ENSMUSG00000046435	4	143719455	143729158	1	11	12	11	10	20	6	0	0	0	0	0	A2AGW8	
ENSMUST00000078710	ENSMUSG00000094531	7	104975042	104975983	-1	3	2	1	2	6	1	0	0	0	0	0	Q7TRP2	
ENSMUST00000078717	ENSMUSG00000034158	16	37868389	37888858	1	57	70	120	247	65	34	295	466	411	42	262		Q3UGP9
ENSMUST00000078719	ENSMUSG00000022995	1	181896384	182019990	-1	0	0	0	0	0	0	5	0	0	0	0	E9QLZ9	
ENSMUST00000078723	ENSMUSG00000025081	19	56826209	56870012	1	16	0	0	0	0	0	0	3	2	0	1		Q99MV1
ENSMUST00000078729						7	10	55	0	9	0	5	2	4	20	0		
ENSMUST00000078734	ENSMUSG00000011257	4	123262351	123298925	1	0	0	0	0	0	0	36	55	163	12	158	Q91YZ8	
ENSMUST00000078739						16	3	93	0	18	0	0	0	5	0	0		
ENSMUST00000078748	ENSMUSG00000058921	3	10331734	10335656	-1	28	26	76	23	25	14	0	9	0	2	4		Q5PT54
ENSMUST00000078752	ENSMUSG00000060227	2	121866970	121936220	1	0	0	46	0	0	0	0	0	0	6	29		Q6P2L7
ENSMUST00000078756	ENSMUSG00000064220	3	96245497	96246082	1	0	16	0	412	19	0	19	321	283	189	255	B2RWH3	Q6GSS7
ENSMUST00000078757	ENSMUSG00000049721	11	3983636	3999326	1	0	0	23	57	4	5	0	0	0	0	0		Q9JHE4
ENSMUST00000078761	ENSMUSG00000057351	2	36734323	36735261	1	3	4	5	2	3	2	0	0	0	0	0	Q8VGK2	
ENSMUST00000078764	ENSMUSG00000017778	13	86044816	86046904	-1	1	5	7	74	18	5	2	6	9	19	10	B8JJB0	
ENSMUST00000078766						6	0	0	0	0	4	552	53	686	9512	1005		
ENSMUST00000078768						2	2	0	0	1	4	5	89	8	6	21		
ENSMUST00000078770	ENSMUSG00000024728	19	11139664	11165320	-1	3	1	0	0	2	0	0	0	0	0	0	Q9D9Y7	
ENSMUST00000078774	ENSMUSG00000058692	9	19360415	19361356	-1	2	1	2	0	1	1	0	0	0	0	0	Q8VET8	
ENSMUST00000078775	ENSMUSG00000079845	X	73074345	73082478	-1	0	4	0	0	0	0	0	5	0	0	0	A2BI40	
ENSMUST00000078778	ENSMUSG00000062593	10	51480640	51496613	1	0	0	6	30	14	15	448	27459	0	1	0		Q64281
ENSMUST00000078800	ENSMUSG00000023994	17	48386885	48409906	-1	2	2	6	3	32	1	226	446	317	4	59		P23708
ENSMUST00000078803	ENSMUSG00000059323	15	76622088	76639958	-1	4	5	15	18	17	6	1607	3028	1328	3218	1007		Q9D1C8
ENSMUST00000078804	ENSMUSG00000060636	16	33056453	33060189	1	21	17	0	16	14	6	1132	2892	1056	5368	727	Q6ZWX1	O55142
ENSMUST00000078816	ENSMUSG00000062944	7	128234458	128238031	-1	14	8	12	34	21	10	67	217	124	20	70	Q8BG98	
ENSMUST00000078825	ENSMUSG00000059089	1	171018920	171029761	1	19	24	75	25	23	14	3253	10871	3604	12222	2887	A0A0B4J1G0	
ENSMUST00000078827	ENSMUSG00000062783	GL456221.1	111572	163011	-1	185	156	290	271	238	114	99	633	165	102	166	Q8BYZ8	
ENSMUST00000078830	ENSMUSG00000020458	11	29692947	29744331	1	2	0	0	0	0	1	0	0	3	3	14	Q8BH78	
ENSMUST00000078832	ENSMUSG00000057805	X	91575210	91575911	-1	0	0	0	1	1	0	0	0	0	0	0	B1AT01	
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ENSMUST00000078835	ENSMUSG00000063133	7	43966751	43971318	1	13	4	16	12	11	5	0	0	0	0	0		P00755
ENSMUST00000078839	ENSMUSG00000048915	17	62604184	62881317	-1	1	0	0	19	0	1	0	0	0	0	0		O08543
ENSMUST00000078842						1	1	3	0	1	1	0	0	0	0	0		
ENSMUST00000078845	ENSMUSG00000060791	7	28437447	28448233	1	3	4	0	0	4	5	3107	10770	3448	18770	2591	A7VJA4	Q9ERL7
ENSMUST00000078847	ENSMUSG00000042870	8	75033686	75070121	1	28	15	32	32	0	23	27	161	39	0	52	Q3UDC3	
ENSMUST00000078849	ENSMUSG00000058571	14	116925297	117979529	1	87	74	195	1135	105	51	1	18	0	2	6	Q3V1C9	Q9R087
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ENSMUST00000078856	ENSMUSG00000058488	5	150952607	150993817	1	33	48	169	250	51	33	0	1	1	0	0		O35082
ENSMUST00000078861	ENSMUSG00000062868	9	18875329	18876276	1	0	2	0	3	4	0	0	0	0	0	0	Q8VFJ5	
ENSMUST00000078869	ENSMUSG00000071177	12	103763594	103773592	-1	2	0	13	11	7	1	0	0	0	29	0		Q00897
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ENSMUST00000078874	ENSMUSG00000079550	1	59120935	59163389	-1	0	0	0	1	1	0	0	0	1	0	0		Q6P7F1
ENSMUST00000078875	ENSMUSG00000052372	X	86740870	88115645	-1	4	1	0	0	3	0	0	0	0	0	0	B1ASU0	
ENSMUST00000078876	ENSMUSG00000096858	10	129722583	129727172	-1	2	5	0	0	4	0	0	0	0	2	2	Q8VFI4	
ENSMUST00000078878	ENSMUSG00000058267	1	160195215	160202170	1	0	0	0	0	0	0	175	402	200	900	123	M0QWY3	
ENSMUST00000078879	ENSMUSG00000058568	8	21823539	21831296	1	1	0	0	3	2	0	0	0	0	0	0		Q6TU36
ENSMUST00000078880	ENSMUSG00000063434	19	48206025	48805505	1	26	37	31	213	33	15	0	0	0	0	0	Q1HL22	Q8VI51
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ENSMUST00000078886	ENSMUSG00000040761	4	141467890	141538597	-1	77	48	326	446	28	52	1187	1506	2857	76	2436	A2ADB1	
ENSMUST00000078890	ENSMUSG00000095670	6	58434842	58435894	-1	4	3	0	2	1	2	0	0	0	0	0	Q8R2D2	
ENSMUST00000078897						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000078902	ENSMUSG00000020646	12	24831599	24960301	1	12	15	0	0	15	8	1	5	0	1	0		Q8R3I2
ENSMUST00000078908	ENSMUSG00000060621	7	19518731	19525050	1	10	7	25	822	30	9	0	1	2	2	0	H7BX48	
ENSMUST00000078912	ENSMUSG00000027889	3	108074062	108086651	-1	33	3	26	12	6	4	693	817	707	45	428	A2AE27	
ENSMUST00000078914	ENSMUSG00000061367	10	129160029	129160982	-1	6	3	2	1	3	1	0	0	0	0	0	Q8VFH6	
ENSMUST00000078918	ENSMUSG00000062797	7	89917529	89941199	-1	0	0	0	19	4	0	39	79	37	32	22	G5E8I4	
ENSMUST00000078932	ENSMUSG00000059864	11	49280150	49281085	1	3	7	8	7	5	1	0	2	2	0	1	Q8VFA7	
ENSMUST00000078933	ENSMUSG00000058014	7	108522909	108523967	-1	7	9	8	2	10	5	0	0	0	0	0		Q8VG09
ENSMUST00000078936	ENSMUSG00000070377	11	74206198	74211379	-1	6	6	5	11	9	0	0	0	0	0	0	Q7TRX1	
ENSMUST00000078939						470	367	5274	1311	533	260	6	31	16	3	16		
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ENSMUST00000078945	ENSMUSG00000044221	5	88659448	88676171	-1	5	0	0	93	7	5	40	174	96	30	119		Q8C5Q4
ENSMUST00000078947	ENSMUSG00000035299	X	169685199	170005736	1	0	5	41	5	0	0	14	0	5	0	10	B1AV01	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000078952	ENSMUSG00000063881	11	73371246	73375704	1	4	2	4	2	4	0	0	0	0	0	0	E9Q4M1	
ENSMUST00000078953	ENSMUSG00000015377	15	89182217	89196474	-1	44	24	61	222	42	27	12	69	15	4	44		Q9D9V7
ENSMUST00000078961	ENSMUSG00000024301	17	26917091	26932579	1	24	12	20	173	29	14	76	71	66	15	69	E9PUA5	
ENSMUST00000078967	ENSMUSG00000059136	7	140667289	140668248	1	7	7	5	2	12	1	0	0	0	0	0	Q8VGL9	
ENSMUST00000078975	ENSMUSG00000034793	11	102189620	102194081	1	6	8	9	15	4	0	11	36	0	0	27		Q6NSQ9
ENSMUST00000078976	ENSMUSG00000062397	15	36997031	37007402	-1	176	182	286	174	124	45	499	1569	537	187	417	B2RVQ7	Q9D115
ENSMUST00000078977	ENSMUSG00000058835	2	22940073	23040241	-1	0	8	0	0	0	0	0	823	0	0	0	B7ZCU3	
ENSMUST00000078988	ENSMUSG00000033306	16	24393350	24992576	1	92	23	62	6	31	53	0	0	0	0	67		Q8BFW7
ENSMUST00000079009	ENSMUSG00000054003	12	111971559	112068854	1	21	22	30	51	25	20	0	0	0	0	0		Q14BI7
ENSMUST00000079012	ENSMUSG00000025702	6	116338024	116409540	1	19	0	3	0	0	0	184	461	215	79	162		Q9DBD2
ENSMUST00000079020	ENSMUSG00000041771	12	102128733	102267091	1	4	0	12	0	5	2	1	0	0	0	0		
ENSMUST00000079024	ENSMUSG00000050619	2	121158273	121171125	-1	0	0	0	0	0	0	0	0	0	0	0	A2ARU6	
ENSMUST00000079028	ENSMUSG00000022325	15	34495304	34530648	1	0	0	22	0	0	7	5	20	18	14	27	Q9D4G5	
ENSMUST00000079031	ENSMUSG00000029033	4	155891822	155907251	1	0	6	10	0	18	0	0	0	0	0	0	A2ADA6	
ENSMUST00000079033	ENSMUSG00000057506	19	44139266	44146446	-1	10	13	13	48	18	7	199	1676	386	1035	325		Q9CWG9
ENSMUST00000079035	ENSMUSG00000056926	6	132893011	132893940	1	2	0	1	0	1	0	0	0	0	0	0		Q7M711
ENSMUST00000079038	ENSMUSG00000064325	8	79966115	80058006	-1	22	17	30	86	26	14	1	0	0	3	12		Q7TN16
ENSMUST00000079041	ENSMUSG00000060181	10	117733679	117746358	-1	37	28	58	155	53	17	97	214	116	8	142		Q6PGC7
ENSMUST00000079042	ENSMUSG00000057551	9	19641224	19648048	1	16	4	13	16	7	6	16	76	58	58	64	Q8C0Q5	
ENSMUST00000079045	ENSMUSG00000030795	7	127967457	127985701	1	30	29	25	20	30	17	20	46	18	2	26	Q8BNR3	
ENSMUST00000079050	ENSMUSG00000060404	13	21115694	21116647	1	0	3	6	4	2	0	0	0	0	0	0		
ENSMUST00000079056	ENSMUSG00000060216	11	70432635	70440828	1	3	0	5	22	0	0	0	27	0	0	13	J3JS97	Q91YI4
ENSMUST00000079057						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000079063	ENSMUSG00000063632	12	27334264	27342574	-1	32	30	79	512	30	30	1	1	0	0	1		Q7M6Y2
ENSMUST00000079077	ENSMUSG00000050270	11	67025154	67035312	1	0	0	0	0	0	0	0	0	0	0	0		Q8BP07
ENSMUST00000079080	ENSMUSG00000001034	11	61488812	61494406	-1	0	0	0	54	4	13	680	549	474	59	281		Q9WVS8
ENSMUST00000079081	ENSMUSG00000024411	18	15389394	15403684	-1	25	20	12	24	22	8	0	0	0	0	0		
ENSMUST00000079083	ENSMUSG00000028073	3	87747890	87824306	-1	0	0	0	0	0	0	23	0	0	0	0		Q8VIK5
ENSMUST00000079085	ENSMUSG00000062006	3	130726831	130730398	-1	15	11	9	20	11	0	3534	5089	2525	14690	1620		Q9D1R9
ENSMUST00000079086	ENSMUSG00000007617	13	93303757	93404129	1	0	5	4	5	9	0	21	35	15	5	5		Q9Z2Y3
ENSMUST00000079090						2	1	6	0	3	0	0	0	0	0	0		
ENSMUST00000079099	ENSMUSG00000096152	7	20121656	20122579	-1	0	2	0	1	1	0	0	0	0	0	0	D3YZG3	
ENSMUST00000079113	ENSMUSG00000059206	7	10747502	10749538	-1	3	4	0	1	5	2	0	0	0	0	0	Q8VIC0	
ENSMUST00000079114						3	5	1	3	1	0	0	0	0	1	0		
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ENSMUST00000079121	ENSMUSG00000057388	17	12911349	12916345	-1	4	9	6	54	2	3	222	691	317	484	179		Q9CQL5
ENSMUST00000079125	ENSMUSG00000046229	2	156311847	156312704	-1	1	2	0	134	5	4	73	1123	415	1051	290	Q2M4I6	
ENSMUST00000079130	ENSMUSG00000063445	16	4710059	4719356	-1	4	4	5	8	8	6	3	0	0	0	0		Q8K2T1
ENSMUST00000079132	ENSMUSG00000062778	3	106113229	106132120	1	3	12	12	14	8	5	0	0	0	0	0		Q91XA9
ENSMUST00000079134	ENSMUSG00000059763	10	23938572	23941583	1	3	1	11	3	2	5	0	0	0	0	0		Q5QD17
ENSMUST00000079135	ENSMUSG00000108534	13	21674001	21674992	-1	15	0	12	6	6	4	0	0	0	0	0	Q7TQU5	
ENSMUST00000079142	ENSMUSG00000059488	14	50126553	50127587	1	2	4	4	2	3	5	0	0	0	0	0	A2RTN7	
ENSMUST00000079146	ENSMUSG00000021013	12	98920574	98983238	1	0	5	0	0	0	0	1	1	0	0	0		Q8VD72
ENSMUST00000079151	ENSMUSG00000057855	16	89084015	89084534	1	3	4	0	0	4	0	0	0	0	0	0	F6T6A9	
ENSMUST00000079153						8	1	17	1	7	1	0	5	0	6	0		
ENSMUST00000079157	ENSMUSG00000028886	4	132638987	132724765	1	21	0	25	0	0	0	82	0	0	0	0		P97480
ENSMUST00000079158	ENSMUSG00000022822	16	20331303	20426394	-1	0	21	93	72	30	13	99	339	439	66	345		Q9R1X5
ENSMUST00000079160	ENSMUSG00000037363	8	25578492	25597487	-1	17	8	70	54	18	14	54	282	83	86	131		Q7TNU7
ENSMUST00000079163	ENSMUSG00000067010	5	108993412	109006471	-1	6	5	0	9	12	5	0	0	0	0	0	K7N621	
ENSMUST00000079169	ENSMUSG00000040896	3	105452330	105674002	1	0	0	5	0	0	0	0	0	0	0	0	B2RUE0	Q9Z0V1
ENSMUST00000079176	ENSMUSG00000030701	7	100642892	100662414	-1	4	0	3	15	0	0	0	0	0	0	0		Q9QYE9
ENSMUST00000079178	ENSMUSG00000059366	9	39572260	39573314	-1	3	4	6	4	8	4	0	0	0	0	0	Q9EQ86	
ENSMUST00000079184	ENSMUSG00000059657	16	36156811	36161948	1	6	13	41	47	18	17	14823	53118	26955	79063	14502	Q8BWM3	
ENSMUST00000079186						32	26	43	40	59	25	0	0	1	0	0		
ENSMUST00000079195	ENSMUSG00000038143	8	47180048	47352348	-1	18	16	8	446	31	28	0	0	0	0	9		Q499E5
ENSMUST00000079204	ENSMUSG00000029608	5	120940499	121010092	-1	73	57	223	188	91	58	40	56	53	1	25		P47708
ENSMUST00000079205	ENSMUSG00000032997	1	75474569	75479307	-1	0	0	0	21	5	10	33	30	10	7	67		Q6IQX7
ENSMUST00000079206	ENSMUSG00000079698	17	18298281	18326441	1	5	4	8	2	5	1	0	0	0	0	0	L7N1Z9	
ENSMUST00000079213	ENSMUSG00000063800	4	108563172	108579336	-1	8	3	3	8	8	9	195	683	240	825	184	B2RTE3	Q4FK66
ENSMUST00000079223	ENSMUSG00000028573	4	95557507	95926939	1	0	0	0	0	0	1	10	0	16	42	17		A2AJL3
ENSMUST00000079228	ENSMUSG00000062551	13	27849344	27857793	1	2	0	0	0	0	0	0	0	0	0	0	Q5SVM1	
ENSMUST00000079229	ENSMUSG00000071295	13	66852174	66854872	-1	6	9	4	8	11	0	0	0	0	0	0	E9Q1C9	
ENSMUST00000079234	ENSMUSG00000059101	4	43835532	43836488	-1	8	4	18	10	13	13	0	0	0	0	0	Q9QZ20	
ENSMUST00000079235	ENSMUSG00000020096	10	61171954	61188841	1	8	0	2	0	16	0	0	0	0	0	0	G5E8I6	
ENSMUST00000079237	ENSMUSG00000069755	12	20899822	20900867	-1	17	8	15	12	9	4	4	13	3	1	1	F6SU29	
ENSMUST00000079242	ENSMUSG00000051341	17	21555046	21562066	1	6	5	9	4	8	2	32	217	49	53	21	Q8BJ45	
ENSMUST00000079244	ENSMUSG00000020827	11	70562881	70614483	1	16	0	0	0	0	0	81	224	0	7	105	Q5SXG1	
ENSMUST00000079247	ENSMUSG00000019188	2	152669461	152708670	1	2	0	0	0	0	3	0	41	0	0	12	A3KGR9	
ENSMUST00000079251	ENSMUSG00000058385	13	23571408	23571884	1	7	4	12	66	9	8	4	66	8	24	10		Q6ZWY9
ENSMUST00000079252	ENSMUSG00000060733	10	71347763	71433327	1	24	17	43	36	41	14	920	3374	1558	158	892		Q7TT16
ENSMUST00000079258	ENSMUSG00000063160	7	27258433	27282144	1	0	0	0	136	0	0	20	16	6	2	12		O08919
ENSMUST00000079261						10	15	9	145	8	0	0	0	0	0	3		
ENSMUST00000079268	ENSMUSG00000070419	5	145345279	145390926	1	10	0	0	7	0	0	0	0	0	0	0	D3YYZ0	
ENSMUST00000079269	ENSMUSG00000058183	4	154869585	154895528	1	5	0	14	4	1	4	0	0	0	0	0	B1AS15	
ENSMUST00000079272	ENSMUSG00000071302	8	129216354	129234406	-1	0	0	0	0	0	0	0	1	0	0	0	E9Q1C8	
ENSMUST00000079278	ENSMUSG00000059361	2	152368755	152376638	-1	11	8	13	22	9	4	0	0	0	0	0		Q5HZK2
ENSMUST00000079279	ENSMUSG00000062561	10	63924866	63927434	-1	6	11	28	8	7	0	0	0	0	0	0	Q8C8J5	
ENSMUST00000079282	ENSMUSG00000031024	7	109523911	109617147	-1	8	4	31	9	10	4	0	0	0	3	7		Q924W7
ENSMUST00000079286	ENSMUSG00000063767	3	90654302	90658669	1	5	6	15	12	11	3	23	59	22	23	18		Q6S5I3
ENSMUST00000079287	ENSMUSG00000035984	18	34562634	34579115	-1	2	0	2	0	3	0	1	7	0	2	0	Q3V2L8	Q99MH5
ENSMUST00000079294	ENSMUSG00000064215	12	103434211	103440239	1	0	6	0	0	0	0	0	0	0	0	0	E9Q1C5	
ENSMUST00000079298	ENSMUSG00000102091	2	86046484	86047416	1	2	8	5	3	6	2	0	0	0	0	0	A2ATE5	
ENSMUST00000079300	ENSMUSG00000036885	3	62338344	62462221	1	14	23	24	156	21	8	6	17	10	3	14	D3YYY8	
ENSMUST00000079306	ENSMUSG00000062732	7	24864620	24869941	-1	6	7	11	57	13	0	0	0	0	0	0		Q8BVP6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000079312	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	0	0	159	0	415	11	415	B7ZCP4	
ENSMUST00000079314	ENSMUSG00000062014	14	46808149	46822242	-1	13	8	21	36	16	10	155	103	131	80	0		Q9CQI3
ENSMUST00000079322	ENSMUSG00000031209	X	96455359	96574485	1	0	2	0	0	7	0	0	0	0	0	0	A2AI62	
ENSMUST00000079323	ENSMUSG00000032776	7	72077830	72306608	-1	23	17	21	50	19	19	820	2582	1856	410	1101		Q5RJH2
ENSMUST00000079324	ENSMUSG00000001687	5	148504635	148552789	-1	8	4	4	222	8	8	1261	3000	743	154	588		Q9Z2M6
ENSMUST00000079327	ENSMUSG00000024947	19	6334979	6340891	1	0	0	0	11	0	0	141	30	54	0	207		O88559
ENSMUST00000079348	ENSMUSG00000058976	7	103415072	103419880	1	0	0	0	0	0	0	0	0	0	0	0	G5E8I7	
ENSMUST00000079360	ENSMUSG00000025085	19	57032733	57314919	-1	13	6	9	6	29	22	0	0	0	0	0	E9QK41	
ENSMUST00000079362	ENSMUSG00000005871	18	34220924	34322189	1	23	6	120	50	43	28	218	455	853	102	708	B2RUG9	
ENSMUST00000079363	ENSMUSG00000061062	17	78491565	78493541	1	30	29	44	23	55	0	226	679	368	184	167	D3YYI8	
ENSMUST00000079368	ENSMUSG00000062438	5	121500098	121503435	-1	24	14	56	77	41	16	0	1	0	0	0		Q8R534
ENSMUST00000079379	ENSMUSG00000059639	6	122990367	123024105	1	3	5	12	5	7	0	1	35	1	8	6	Q5YIR8	
ENSMUST00000079389						2009	1906	3403	6350	2072	734	14	19	50	8	61		
ENSMUST00000079390	ENSMUSG00000063804	10	45376620	45470201	-1	51	30	122	31	38	16	0	1	1	0	0		Q45KJ6
ENSMUST00000079391	ENSMUSG00000029761	6	34598500	34775473	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0M9	
ENSMUST00000079400	ENSMUSG00000037686	12	112106683	112127573	1	17	20	60	56	35	21	0	0	0	5	0		A0JNU3
ENSMUST00000079403	ENSMUSG00000062031	7	140941391	140947664	1	0	0	14	0	0	0	736	543	479	89	293		Q8BP56
ENSMUST00000079405	ENSMUSG00000042097	6	117862100	117873291	1	5	8	29	0	8	14	0	0	0	0	0		P24399
ENSMUST00000079413	ENSMUSG00000024222	17	28399095	28517524	-1	10	1	7	25	10	6	2682	3698	3809	385	2595	Q4FJN2	Q64378
ENSMUST00000079414	ENSMUSG00000023072	7	35397035	35438689	1	0	4	0	0	0	0	17	20	52	43	26		Q9CZX2
ENSMUST00000079415	ENSMUSG00000030428	7	4119408	4136708	1	0	0	0	0	0	0	0	0	0	0	0		Q9D3A9
ENSMUST00000079416	ENSMUSG00000064293	6	105677660	106699310	1	6	6	3	1	10	3	0	0	0	0	0	F8WH58	
ENSMUST00000079419	ENSMUSG00000012405	14	18267823	18271391	-1	0	15	11	60	18	0	118	88	73	265	86	Q5M8Q0	Q9CZM2
ENSMUST00000079420	ENSMUSG00000063851	4	62427540	62435252	-1	0	0	0	7	0	4	0	1	0	1	0		Q8QZS5
ENSMUST00000079421	ENSMUSG00000002307	17	33909414	33915589	1	7	2	4	49	6	0	277	407	190	74	212	Q3UKR0	
ENSMUST00000079423	ENSMUSG00000058966	7	126797668	126830219	1	6	3	5	86	17	5	0	0	0	0	0		Q7TNV1
ENSMUST00000079424	ENSMUSG00000035778	2	35400179	35463231	-1	0	0	0	0	0	0	57	232	0	49	0	Q91W00	
ENSMUST00000079431	ENSMUSG00000025221	19	45791839	45816061	-1	0	0	0	0	0	0	0	0	1	0	0	Q3YAB2	
ENSMUST00000079439	ENSMUSG00000061702	7	25669139	25675166	-1	4	2	8	57	2	1	7	2	6	0	5		Q8C581
ENSMUST00000079441	ENSMUSG00000022708	16	42875881	43642602	1	0	0	0	0	0	0	0	0	0	0	0		Q8K0L9
ENSMUST00000079443	ENSMUSG00000035299	X	169685199	170005736	1	6025	2710	143815	12330	6214	3234	0	30	7	0	37	Q6PD02	
ENSMUST00000079447	ENSMUSG00000073119	5	26032846	26039558	-1	44	34	57	40	51	27	0	0	0	0	0	F8VPX6	
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ENSMUST00000079459	ENSMUSG00000063106	14	52409914	52414373	-1	6	7	6	7	12	1	0	0	0	0	0	E9PZZ6	
ENSMUST00000079461	ENSMUSG00000073434	17	25844771	25861501	-1	0	0	0	0	0	0	0	83	0	0	0	H7BX49	
ENSMUST00000079463	ENSMUSG00000031492	8	27368711	27399729	1	22	22	77	0	32	22	0	0	0	1	0		Q8BMN3
ENSMUST00000079464	ENSMUSG00000026202	1	75214228	75219865	-1	0	1	0	24	0	0	634	887	538	157	360	A0A0A0MQA5	
ENSMUST00000079465	ENSMUSG00000059448	4	43820403	43821359	-1	14	5	14	9	14	6	0	0	0	0	0	Q8VGA9	
ENSMUST00000079469	ENSMUSG00000061356	14	65598546	65648531	1	0	6	6	0	14	5	0	0	0	0	0	D3YY21	
ENSMUST00000079472	ENSMUSG00000057228	8	60506124	60545677	1	3	5	12	12	5	5	0	0	0	1	0		Q9WVM8
ENSMUST00000079476	ENSMUSG00000032691	11	59541568	59566956	1	0	17	22	24	40	16	814	1842	1152	128	1626		Q8R4B8
ENSMUST00000079490	ENSMUSG00000055733	X	122394565	122397401	-1	2	6	7	74	13	4	1	1	1	2	1		Q794H2
ENSMUST00000079491	ENSMUSG00000058153	5	112419151	112577185	-1	20	9	30	100	21	16	0	0	0	0	0		Q6P1D5
ENSMUST00000079496	ENSMUSG00000060860	7	4794546	4812590	-1	10	10	30	193	20	9	792	892	428	190	345		Q921J4
ENSMUST00000079510	ENSMUSG00000052488	8	72460489	72475233	-1	29	24	78	221	33	25	763	933	907	68	705	G5E8I8	
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ENSMUST00000079528	ENSMUSG00000060208	8	21655780	21656735	1	1	1	2	0	2	1	0	0	0	0	0		P28310
ENSMUST00000079533	ENSMUSG00000059060	12	79297351	79508656	1	5	3	2	7	11	2	0	0	0	0	2		O35719
ENSMUST00000079534	ENSMUSG00000037313	5	33658128	33678995	1	1	19	25	37	17	13	0	5	0	0	0	Q6NV52	
ENSMUST00000079542	ENSMUSG00000000134	X	7762560	7775202	1	0	0	0	5	0	0	0	0	0	0	0	A2AEW0	
ENSMUST00000079545	ENSMUSG00000057286	11	116675303	116694868	-1	18	8	7	104	3	7	0	0	0	4	11		P70277
ENSMUST00000079548	ENSMUSG00000061701	9	109217432	109234754	-1	16	10	6	8	10	5	0	0	0	0	0	Q5U467	
ENSMUST00000079560	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	0	0	0	0	2	0	0	0	11	Q7TT35	
ENSMUST00000079568						4512	6948	3425	3099	4237	1811	24	155	69	22	122		
ENSMUST00000079573	ENSMUSG00000030287	6	146108299	146502223	-1	51	6	64	67	0	30	368	253	786	110	8		Q9Z329
ENSMUST00000079582	ENSMUSG00000030172	6	119570796	119848167	-1	108	87	462	174	66	36	16	19	8	5	19		Q99MI1
ENSMUST00000079584	ENSMUSG00000062905	6	66552183	66559708	-1	7	3	4	3	10	3	0	0	0	0	0	Q8R2D9	
ENSMUST00000079589	ENSMUSG00000020923	11	102304560	102319742	-1	0	0	0	0	0	0	115	16	0	0	1	A2AWT5	
ENSMUST00000079590	ENSMUSG00000025401	10	127705170	127720887	1	18	21	64	25	48	21	5	57	19	1	35		O88329
ENSMUST00000079594	ENSMUSG00000024130	17	24351950	24410201	1	2	17	25	23	12	5	144	546	472	31	642		Q8R420
ENSMUST00000079597	ENSMUSG00000064225	9	95559657	95568023	1	27	35	77	236	48	17	4	0	3	5	9		Q6TCG2
ENSMUST00000079599	ENSMUSG00000061342	2	88184879	88185817	1	1	7	4	3	7	4	0	0	0	0	0	Q7TR25	
ENSMUST00000079600	ENSMUSG00000022842	16	20611593	20646485	1	0	0	0	0	0	0	0	0	0	1	0	E9QKA6	
ENSMUST00000079601	ENSMUSG00000013089	16	22381309	22439719	-1	0	0	93	69	0	9	72	0	0	18	19		Q9CXC9
ENSMUST00000079605	ENSMUSG00000060206	4	54945048	55083563	1	23	1	13	0	27	20	0	0	0	0	0	B1AWL5	
ENSMUST00000079611	ENSMUSG00000087385	4	119530308	119539529	-1	30	18	77	13	23	7	19	62	28	5	22	Q6P3A2	
ENSMUST00000079618	ENSMUSG00000025425	18	77185853	77255450	1	15	9	16	52	0	0	0	0	0	0	0	Q3TRR3	P70126
ENSMUST00000079620	ENSMUSG00000059821	9	19374941	19375879	-1	2	4	0	0	1	0	0	0	0	0	0	Q8VFF4	
ENSMUST00000079624	ENSMUSG00000029607	5	143890741	143897685	-1	5	10	85	22	8	4	2	0	7	1	12		Q9CQM6
ENSMUST00000079625	ENSMUSG00000060519	1	156653617	156674356	-1	0	0	0	47	4	14	105	438	105	44	109		Q9ER38
ENSMUST00000079633	ENSMUSG00000057203	17	21228826	21229815	1	4	3	6	1	6	8	0	0	0	0	0	Q8R298	
ENSMUST00000079634	ENSMUSG00000061286	7	25659164	25671368	1	3	8	15	56	12	5	359	475	195	34	173		Q9CRA8
ENSMUST00000079639	ENSMUSG00000061974	8	47822143	47822805	1	12	5	66	28	14	8	1	0	1	0	0	D3YXJ9	
ENSMUST00000079642	ENSMUSG00000057835	17	55864892	55878930	-1	5	6	2	96	4	3	35	103	42	53	21	Q9JIC0	
ENSMUST00000079644	ENSMUSG00000028639	4	119277981	119294604	-1	0	13	12	82	29	21	808	3033	2026	657	1683	Q3UBT1	P62960
ENSMUST00000079648	ENSMUSG00000063320	10	82619851	82623228	-1	7	0	2	82	16	2	5	18	7	9	0		Q8BTC1
ENSMUST00000079650	ENSMUSG00000096555	9	39217359	39218294	1	6	5	0	3	2	4	0	0	0	0	0	Q9EQ91	
ENSMUST00000079652	ENSMUSG00000063060	14	63943674	63950732	1	50	42	265	141	51	24	0	3	1	1	3	Q3U1W5	P40646
ENSMUST00000079659	ENSMUSG00000032407	9	95456898	95511996	-1	15	9	13	6	10	8	46	145	27	47	55		Q6NV83
ENSMUST00000079660	ENSMUSG00000058659	9	19780283	19784064	1	5	5	0	0	4	1	0	0	0	0	0	Q7TRF6	
ENSMUST00000079663	ENSMUSG00000058932	X	56447965	56448366	1	0	3	0	0	0	3	3	0	0	8	0	F6ZVF2	
ENSMUST00000079669	ENSMUSG00000058923	6	57002300	57003363	1	1	2	1	1	6	1	0	0	0	0	0	Q8R2D4	
ENSMUST00000079678	ENSMUSG00000059375	6	66611582	66612617	-1	0	0	0	0	0	1	0	0	0	0	0	Q8R2E0	
ENSMUST00000079681	ENSMUSG00000057778	11	72777232	72796142	-1	45	0	82	101	61	0	4	28	17	5	26		Q5SSH8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000079684	ENSMUSG00000050490	10	85313488	85314439	1	9	3	2	3	0	2	0	0	0	0	0	D3YX79	
ENSMUST00000079690						4	1	6	4	6	5	0	0	0	0	0		
ENSMUST00000079691	ENSMUSG00000027610	2	155563181	155592810	-1	0	8	0	37	10	0	15	41	11	33	44	Q541E2	P51855
ENSMUST00000079692	ENSMUSG00000058396	10	127747276	127751732	-1	90	60	596	115	69	50	20	83	31	4	85	G3X9R9	
ENSMUST00000079693	ENSMUSG00000063808	7	35276536	35318440	-1	0	6	0	8	6	0	30	109	23	0	50		Q9DBM1
ENSMUST00000079697	ENSMUSG00000073842	4	60066469	60070475	-1	0	0	0	0	0	0	0	0	0	0	0	Q58EV3	
ENSMUST00000079698	ENSMUSG00000062866	10	13207717	13474396	-1	2	0	0	27	5	3	0	0	0	4	22	B1AVN9	
ENSMUST00000079702	ENSMUSG00000018666	11	96789127	96808640	1	0	0	0	0	0	4	51	27	54	17	22	Q9CYJ8	
ENSMUST00000079703	ENSMUSG00000059586	15	59374198	59601683	1	8	5	10	30	11	5	108	417	145	420	87		Q91VT1
ENSMUST00000079706						0	0	0	14	0	2	0	0	0	2	0		
ENSMUST00000079711	ENSMUSG00000059205	2	87607390	87608334	1	3	2	0	0	3	1	0	0	0	0	0	A2AV42	
ENSMUST00000079716	ENSMUSG00000062328	18	75000477	75003381	1	0	16	31	68	30	25	2553	12650	3726	26179	3318	Q6ZWZ7	
ENSMUST00000079719	ENSMUSG00000018604	5	119670669	119684724	1	22	0	22	356	49	26	0	0	0	0	0	Q4VA43	P70324
ENSMUST00000079721	ENSMUSG00000058665	1	120602418	120607992	1	14	9	27	148	15	8	0	0	0	0	0		P09065
ENSMUST00000079724	ENSMUSG00000027944	3	89995446	89998780	-1	12	10	113	25	19	9	393	992	324	449	296	B9EJR4	O35387
ENSMUST00000079733	ENSMUSG00000058064	18	15832794	15833330	1	5	6	1	2	7	0	8	50	15	199	19	E9PYL9	
ENSMUST00000079735	ENSMUSG00000058600	15	34440505	34443640	-1	3	8	7	200	28	17	21	36	30	44	21	Q58DZ3	P62889
ENSMUST00000079736	ENSMUSG00000062037	15	98312589	98313548	-1	3	6	3	9	6	1	0	0	0	0	0	Q7TS17	
ENSMUST00000079738	ENSMUSG00000058925	18	57533780	57731065	1	7	0	5	0	0	0	0	0	0	0	0	E9PYL8	
ENSMUST00000079746	ENSMUSG00000037373	5	33247723	33274994	-1	18	4	23	34	33	6	2556	2809	2066	270	1353		O88712
ENSMUST00000079749	ENSMUSG00000059878	6	116624016	116628999	-1	49	65	260	51	56	18	0	37	12	19	27		Q9ERU3
ENSMUST00000079751	ENSMUSG00000056073	10	49099460	49788766	-1	3	0	0	0	0	0	0	0	0	0	0		P39087
ENSMUST00000079754	ENSMUSG00000039652	19	37021291	37208601	-1	0	5	0	3	0	0	16	0	0	0	0		
ENSMUST00000079755	ENSMUSG00000058174	3	37714190	37724490	-1	4	0	7	0	0	0	0	0	2	0	0	Q8BGG2	
ENSMUST00000079758	ENSMUSG00000031996	9	31149557	31211815	-1	0	0	0	0	27	18	57	253	43	0	90		Q06335
ENSMUST00000079759	ENSMUSG00000060565	7	38518139	38528193	-1	7	6	54	20	12	8	0	0	0	0	0	Q8CDK1	
ENSMUST00000079761						12	6	15	0	12	6	0	5	0	0	0		
ENSMUST00000079764	ENSMUSG00000059355	8	85080740	85082339	1	1	0	0	5	0	2	62	117	42	49	53	Q3UI07	Q6ZWX0
ENSMUST00000079767	ENSMUSG00000094449	9	39873277	39874221	1	2	4	8	3	5	1	0	0	0	0	0	Q9EQA2	
ENSMUST00000079770	ENSMUSG00000020836	11	77462411	77470484	1	0	0	0	0	0	0	0	0	0	0	0		Q920M5
ENSMUST00000079772	ENSMUSG00000063727	15	54250619	54278484	-1	11	8	34	14	14	1	0	0	0	13	0	Q3UK97	O08712
ENSMUST00000079773	ENSMUSG00000003345	10	80622780	80640771	1	14	13	35	174	11	5	191	263	186	11	165	Q99K78	
ENSMUST00000079776	ENSMUSG00000015001	15	65876053	65912397	-1	8	0	22	0	0	0	0	0	0	0	0	Q80ZM2	
ENSMUST00000079777	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000079780	ENSMUSG00000022686	16	19760208	19772753	1	0	0	0	0	0	0	0	6	0	0	0		Q8BGY6
ENSMUST00000079784	ENSMUSG00000059741	9	110741861	110769798	1	5	0	9	6	4	5	0	0	0	0	0		P09542
ENSMUST00000079788	ENSMUSG00000061013	18	6910459	7004780	-1	15	4	29	9	13	1	0	0	0	1	2	B2RQ30	
ENSMUST00000079790	ENSMUSG00000063583	1	92607839	92608847	1	5	5	13	5	0	4	0	0	0	0	0	E9PYK6	
ENSMUST00000079791	ENSMUSG00000005615	16	32430921	32475070	1	0	0	0	8	22	3	913	2402	2041	161	1158		P49586
ENSMUST00000079793	ENSMUSG00000059077	7	113385576	113388573	-1	4	2	6	1	4	1	0	0	0	0	0	Q9Z0L6	
ENSMUST00000079794						3	1	18	10	5	2	0	0	0	0	0		
ENSMUST00000079797	ENSMUSG00000095293	X	27924017	27946885	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000079804	ENSMUSG00000096409	9	38143137	38144081	1	1	3	4	1	4	2	0	0	0	0	0	Q7TRD9	
ENSMUST00000079810	ENSMUSG00000095002	10	129625124	129627886	-1	3	2	3	3	4	1	0	0	0	0	0	Q7TRH8	
ENSMUST00000079811	ENSMUSG00000029268	5	87459490	87482260	-1	3	3	2	3	4	2	0	0	0	0	0		Q6PDD0
ENSMUST00000079812	ENSMUSG00000027878	3	98013527	98150361	1	65	45	146	192	95	56	7750	10093	13179	550	12295	G5E8J0	
ENSMUST00000079817	ENSMUSG00000063410	14	121286343	121379334	-1	7	10	14	122	17	12	4078	8419	5450	520	3604	Q3U335	Q99KH8
ENSMUST00000079818	ENSMUSG00000064081	15	99006056	99006370	1	6	10	4	30	8	3	0	0	0	0	1	D3YX71	
ENSMUST00000079824	ENSMUSG00000063234	15	103308236	103310438	-1	20	9	70	57	44	13	961	963	704	55	294		
ENSMUST00000079827	ENSMUSG00000070380	11	74121291	74122238	1	9	3	7	3	8	1	0	0	0	0	0	Q8VFX6	
ENSMUST00000079828	ENSMUSG00000055254	13	58806596	59133970	1	36	42	45	81	59	30	0	3	1	0	2		P15209
ENSMUST00000079832	ENSMUSG00000060816	6	90178716	90179645	1	5	0	0	0	2	0	0	0	0	0	0		Q9EP79
ENSMUST00000079833	ENSMUSG00000019878	10	57486385	57513133	1	16	8	20	36	13	11	27	102	41	28	29		P38533
ENSMUST00000079838	ENSMUSG00000022475	15	97792664	97844502	-1	0	0	0	0	0	0	0	1	17	0	0		Q8C2B3
ENSMUST00000079841						0	2	0	0	2	0	0	0	0	0	1		
ENSMUST00000079847	ENSMUSG00000061838	6	95473009	95718800	-1	11	11	18	18	13	6	40	150	90	39	113		Q9Z2I8
ENSMUST00000079855	ENSMUSG00000058470	19	11485938	11512577	1	9	0	0	0	0	0	0	0	0	0	5	E9PZI3	
ENSMUST00000079857	ENSMUSG00000027330	2	131186949	131198497	1	14	12	58	26	33	10	1259	1856	972	102	580	Q9DBN8	
ENSMUST00000079859	ENSMUSG00000063177	7	44052290	44056712	1	6	5	8	8	11	2	0	1	1	13	3		Q9JM71
ENSMUST00000079865						6	2	6	3	2	0	0	0	0	0	0		
ENSMUST00000079866	ENSMUSG00000018379	11	88047373	88053755	1	0	3	4	5	2	0	282	657	214	43	179		Q6PDM2
ENSMUST00000079867	ENSMUSG00000094196	X	154948543	154949505	-1	0	2	0	5	0	2	0	0	0	0	0	Q6T340	
ENSMUST00000079869	ENSMUSG00000058446	6	54816916	54893500	1	52	42	192	63	39	24	430	1196	665	128	460		Q71FD5
ENSMUST00000079875	ENSMUSG00000060556	19	11854930	11856001	-1	2	9	17	5	14	4	0	0	0	0	0	Q7TQS3	
ENSMUST00000079881	ENSMUSG00000062519	6	47835661	47873537	1	4	3	6	0	7	4	11	24	25	0	13	Q8BV16	
ENSMUST00000079883	ENSMUSG00000078441	10	80602882	80615783	1	0	7	0	25	0	7	257	177	128	35	188	Q3TGX0	Q9JKV5
ENSMUST00000079884						5	2	3	5	3	0	1	1	0	0	1		
ENSMUST00000079891	ENSMUSG00000060480	16	19624157	19629916	-1	10	7	4	2	6	4	0	0	0	0	0	G5E8J1	
ENSMUST00000079896	ENSMUSG00000025521	8	64947185	64969034	1	0	0	0	19	0	0	9	39	7	8	5		Q9CXT7
ENSMUST00000079902	ENSMUSG00000024972	19	7596660	7607193	-1	0	0	0	35	10	0	0	0	0	0	0		Q91VD1
ENSMUST00000079915	ENSMUSG00000057977	4	114163384	114245028	1	0	1	2	0	0	0	0	0	0	0	0	A2A9I2	
ENSMUST00000079924	ENSMUSG00000062202	17	30215524	30576287	-1	29	0	0	22	0	0	7	164	0	14	112		Q8C726
ENSMUST00000079926	ENSMUSG00000059654	6	78422711	78428667	1	2	1	2	5	4	0	0	0	0	0	0	Q3TV26	P43137
ENSMUST00000079934	ENSMUSG00000033943	2	119897228	119969581	1	2	0	20	71	0	0	3	300	0	30	101	H7BX50	
ENSMUST00000079936	ENSMUSG00000094493	7	106805510	106806460	-1	6	8	6	0	9	1	0	0	0	1	0	Q8VFM5	
ENSMUST00000079945	ENSMUSG00000057457	X	157162075	157415312	-1	12	12	12	5	23	7	0	0	0	2	0	Q3TYM9	P70669
ENSMUST00000079949	ENSMUSG00000009079	11	5069689	5099266	-1	0	5	0	70	0	1	18	86	101	0	53		Q61545
ENSMUST00000079952	ENSMUSG00000061065	X	9571901	9572409	-1	2	1	10	1	3	0	0	0	0	0	0	L7MU04	
ENSMUST00000079955	ENSMUSG00000060663	16	58823781	58826782	-1	3	5	2	0	2	2	0	0	0	0	0		
ENSMUST00000079957	ENSMUSG00000058715	1	171229572	171234365	-1	0	6	23	50	11	6	8942	23001	6529	22446	5124		P20491
ENSMUST00000079960	ENSMUSG00000059835	14	58893506	58894129	1	4	6	20	61	9	1	0	2	2	2	0		
ENSMUST00000079961	ENSMUSG00000032939	8	94214597	94315066	1	0	0	0	15	0	0	73	28	51	46	143		Q8BJ71
ENSMUST00000079966	ENSMUSG00000070857	2	87212894	87213874	1	11	3	7	0	2	0	0	0	0	0	0	Q7TR54	
ENSMUST00000079970	ENSMUSG00000063802	7	4660521	4685068	-1	11	8	25	31	18	5	121	115	50	69	100		Q99P31

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000079975	ENSMUSG00000021699	13	108449948	109953461	1	3	0	7	3	0	1	0	0	0	0	0	B1PSD9	
ENSMUST00000079976	ENSMUSG00000002105	2	91061791	91070417	-1	7	3	34	3	2	0	54	106	0	11	0		Q8BZH0
ENSMUST00000079978	ENSMUSG00000028456	4	43058953	43264871	1	25	28	51	40	33	20	0	10	5	3	12		Q9Z1N9
ENSMUST00000079987	ENSMUSG00000057421	X	95935335	95956962	-1	18	7	26	63	20	8	57	358	117	144	157		A2BE28
ENSMUST00000079996	ENSMUSG00000053581	5	139471211	139484549	-1	34	0	0	63	0	27	90	248	66	0	124		Q9JII7
ENSMUST00000079998	ENSMUSG00000048495	1	57388237	57407101	-1	0	0	0	0	0	0	3	19	0	0	0		A2RSX7
ENSMUST00000080001	ENSMUSG00000062963	1	171288563	171295024	-1	0	0	0	0	0	0	345	1122	311	427	250		Q9CR09
ENSMUST00000080008	ENSMUSG00000027255	2	91264974	91276931	1	16	11	0	138	24	11	456	276	372	55	219		Q99K28
ENSMUST00000080014	ENSMUSG00000061000	7	108621814	108622764	1	4	4	4	1	6	1	0	0	0	0	0		Q8VG13
ENSMUST00000080015	ENSMUSG00000056116	17	36037128	36042747	-1	0	0	0	17	0	3	0	0	0	0	0	Q31615	
ENSMUST00000080030	ENSMUSG00000062203	16	11219292	11254270	-1	0	0	0	131	0	4	160	731	330	71	232		Q8R050
ENSMUST00000080031						2	0	0	2	3	1	0	0	0	0	0		
ENSMUST00000080033	ENSMUSG00000024456	18	37843601	37935476	-1	0	0	27	0	0	0	0	0	2	0	0	E9PXV7	
ENSMUST00000080035	ENSMUSG00000035776	X	71420060	71492849	-1	0	0	6	0	0	0	0	51	11	33	53		Q8BIF0
ENSMUST00000080036	ENSMUSG00000029104	5	34761740	34912534	1	72	68	127	98	108	38	386	413	749	33	659	G3X9H5	
ENSMUST00000080042	ENSMUSG00000028943	4	152120331	152152371	-1	0	0	0	0	0	0	0	0	0	0	0		Q9ET47
ENSMUST00000080050	ENSMUSG00000038903	18	69925426	69969484	1	0	0	0	0	0	0	0	0	0	0	0		Q8BVC4
ENSMUST00000080058	ENSMUSG00000058709	7	27158658	27166802	-1	12	3	46	42	21	8	1509	1546	978	266	725	Q80X29	Q91YE2
ENSMUST00000080061						3	1	2	4	3	0	1	0	0	2	1		
ENSMUST00000080062	ENSMUSG00000091732	12	4689402	4689926	-1	5	7	17	6	12	3	2	0	2	16	1	F6YJW4	
ENSMUST00000080065	ENSMUSG00000059316	2	29802634	29817522	1	24	14	86	163	55	18	5704	5387	3427	297	2454		Q91VE0
ENSMUST00000080066						1	1	0	2	0	1	0	0	0	0	0		
ENSMUST00000080067	ENSMUSG00000028962	5	24423837	24440950	1	0	0	7	8	0	0	802	382	748	0	473		
ENSMUST00000080083	ENSMUSG00000060673	X	81419575	81458121	-1	1	2	5	0	2	1	0	0	0	0	0	A2RRY9	
ENSMUST00000080085	ENSMUSG00000000600	5	3803184	3845564	1	0	0	0	85	27	0	170	712	270	71	196	B2RUA8	Q6S5J6
ENSMUST00000080089	ENSMUSG00000024231	18	3382988	3436377	1	4	0	8	69	8	0	57	164	86	31	66	H7BX52	
ENSMUST00000080094	ENSMUSG00000057149	2	111754251	111755189	1	4	1	7	2	2	0	0	0	0	0	0	Q8VGE7	
ENSMUST00000080097						4	3	6	6	3	1	4	3	5	15	0		
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ENSMUST00000080106	ENSMUSG00000093980	7	108346035	108346979	-1	11	7	4	2	7	6	0	0	0	0	0		Q8VEW5
ENSMUST00000080115	ENSMUSG00000036872	8	86482260	86580686	-1	0	0	0	0	0	0	0	0	0	0	0		Q80WJ6
ENSMUST00000080123	ENSMUSG00000063129	12	55565239	55566896	1	16	13	20	10	27	15	2	0	0	0	1	A6ZI47	
ENSMUST00000080126	ENSMUSG00000035896	14	51145002	51146767	-1	3	7	19	10	10	7	0	2	0	0	0	Q8C6G3	
ENSMUST00000080127	ENSMUSG00000007617	13	93303757	93404129	1	5	1	2	0	0	0	22	15	34	0	23		Q9Z2Y3
ENSMUST00000080132	ENSMUSG00000061525	2	151470542	151476153	-1	35	14	125	43	23	13	0	0	0	0	0		Q8C0X8
ENSMUST00000080135	ENSMUSG00000063900	8	43519864	43528137	-1	14	8	3	1	10	5	0	0	0	0	0	Q6IMH6	
ENSMUST00000080138	ENSMUSG00000033701	1	155558120	155691330	1	2	0	0	146	0	2	69	158	74	37	76		Q9D061
ENSMUST00000080141	ENSMUSG00000063296	15	94629185	95096097	1	18	10	6	6	5	9	0	0	0	1	0		Q8BH18
ENSMUST00000080142	ENSMUSG00000062199	19	13313360	13314283	-1	6	4	10	4	3	1	0	0	0	0	0	Q7TQR2	
ENSMUST00000080145	ENSMUSG00000049538	13	70727802	70841811	-1	20	0	22	49	23	27	0	0	0	2	0		Q69Z28
ENSMUST00000080149	ENSMUSG00000063524	4	150236721	150248879	1	5	4	14	2	3	0	44	396	47	25	72	Q6PHC1	
ENSMUST00000080152						0	0	0	0	0	6	103	406	114	385	71		
ENSMUST00000080153	ENSMUSG00000062712	7	140400130	140401044	-1	8	5	5	6	6	3	0	0	0	0	0	Q8VGL2	
ENSMUST00000080160	ENSMUSG00000056899	12	41024090	41955588	1	0	0	0	0	0	0	0	0	0	6	1	K3W4P5	
ENSMUST00000080162	ENSMUSG00000061387	19	13654446	13655396	1	5	1	12	6	4	0	0	0	0	0	0	Q7TQQ5	
ENSMUST00000080164	ENSMUSG00000029227	5	74535449	74598800	1	11	8	4	22	13	6	112	505	180	29	139		Q9D824
ENSMUST00000080165	ENSMUSG00000060688	7	86688340	86695384	1	0	2	1	4	2	1	0	0	0	0	0	F8VQ84	
ENSMUST00000080167	ENSMUSG00000061815	1	74125541	74148223	1	21	14	35	36	27	8	684	2367	930	327	1039		Q3TYX8
ENSMUST00000080171	ENSMUSG00000054827	19	40089688	40113950	1	0	0	0	0	0	0	0	0	0	0	0		Q91X77
ENSMUST00000080175	ENSMUSG00000030604	7	27807196	27822916	1	7	3	3	1	3	2	11	16	20	5	10	E9QA60	
ENSMUST00000080178	ENSMUSG00000011257	4	123262351	123298925	1	0	4	0	85	0	9	22	127	59	0	50	Q6PHQ9	
ENSMUST00000080190	ENSMUSG00000062753	17	27563575	27565749	-1	0	0	0	0	0	1	61	29	49	173	5	D6RHA8	
ENSMUST00000080202	ENSMUSG00000025138	11	120618372	120625240	-1	0	0	0	0	0	0	1687	2858	1476	420	985		Q8BKJ9
ENSMUST00000080204	ENSMUSG00000070031	1	85600378	85645037	1	27	24	113	89	42	26	1432	9347	3378	3637	1623	Q6NSQ5	
ENSMUST00000080208	ENSMUSG00000024044	17	69156810	69289985	1	38	16	39	40	34	0	0	1	0	3	6		Q9WV92
ENSMUST00000080210	ENSMUSG00000005089	2	102658659	102790784	1	146	110	543	544	131	118	0	9	0	1	9	Q3UYK6	P43006
ENSMUST00000080211	ENSMUSG00000067616	7	43774604	43779263	1	0	6	15	9	8	7	0	0	0	0	0	A0A0B6VLT0	Q9QYN3
ENSMUST00000080215	ENSMUSG00000030930	7	132235780	132317228	-1	4	37	117	420	49	0	983	2330	1397	105	1337		Q91XQ5
ENSMUST00000080217	ENSMUSG00000061130	17	84956741	85023991	1	3	2	0	34	8	2	104	99	100	30	109	Q99NF7	
ENSMUST00000080223						3	5	27	4	7	1	0	4	0	12	3		
ENSMUST00000080231	ENSMUSG00000059030	17	37923516	37924555	1	8	3	11	3	4	5	0	0	0	0	0	Q7TRJ1	
ENSMUST00000080233	ENSMUSG00000059891	7	44943240	44958033	1	0	0	0	87	10	2	0	0	1	0	0	Q147V4	
ENSMUST00000080234						3	2	2	1	0	1	0	0	0	2	0		
ENSMUST00000080237	ENSMUSG00000072714	14	11227552	11227992	1	1	3	16	0	2	4	0	0	0	0	0		
ENSMUST00000080249	ENSMUSG00000063383	17	22144359	22166190	-1	20	7	9	7	15	8	3	16	4	23	4	Q8BIQ6	
ENSMUST00000080251						4	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000080253	ENSMUSG00000057799	13	23099149	23100045	1	4	1	2	0	4	2	0	0	0	0	0	Q8R257	
ENSMUST00000080254	ENSMUSG00000062638	17	34377132	34385776	1	7	9	30	18	9	10	0	0	0	0	0		Q7TST0
ENSMUST00000080271						0	2	4	4	0	1	0	0	0	0	0		
ENSMUST00000080279						0	2	11	5	4	6	1	3	0	8	0		
ENSMUST00000080281	ENSMUSG00000012405	14	18267823	18271391	-1	14	6	9	17	18	3	233	331	224	938	170	Q5M8Q0	Q9CZM2
ENSMUST00000080283	ENSMUSG00000023805	17	5941280	6044290	1	0	0	0	0	0	0	0	23	0	0	0		Q9D2G5
ENSMUST00000080288	ENSMUSG00000058741	7	25301411	25304132	1	11	8	21	11	18	8	0	0	2	0	0	B2RW88	
ENSMUST00000080292	ENSMUSG00000024670	19	10789341	10830058	-1	0	7	25	0	33	7	55	66	42	0	95		Q61003
ENSMUST00000080299	ENSMUSG00000022634	15	93284278	93336935	-1	2	1	0	0	4	2	154	305	150	97	93		Q99LW6
ENSMUST00000080300	ENSMUSG00000009927	9	44407714	44410405	1	13	18	21	90	18	19	4223	12451	5084	29574	3237	Q58EA6	P62852
ENSMUST00000080311	ENSMUSG00000059910	2	90036921	90037850	1	1	4	9	6	3	5	0	0	0	0	0	Q8VEZ3	
ENSMUST00000080313	ENSMUSG00000062914	10	129268386	129270550	-1	6	4	2	1	5	0	0	0	0	0	0	Q8VFH3	
ENSMUST00000080316	ENSMUSG00000014075	16	32419702	32429099	1	0	0	0	0	0	0	33	126	19	45	7	Q9CQJ9	
ENSMUST00000080322	ENSMUSG00000052776	5	120896256	120907521	-1	15	12	27	10	15	17	716	2223	407	163	695		P11928
ENSMUST00000080324	ENSMUSG00000071745	X	73137232	73149450	-1	25	14	26	0	0	25	0	0	0	0	0	Q52KH6	
ENSMUST00000080329	ENSMUSG00000094745	9	39461433	39462377	1	2	3	6	0	4	4	0	0	0	0	0	Q9EQB6	
ENSMUST00000080330						0	1	6	0	0	1	0	0	3	3	2		
ENSMUST00000080333	ENSMUSG00000057816	5	98329304	98802047	1	5	2	2	36	1	0	0	0	0	0	0		Q810M1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000080335	ENSMUSG00000058897	3	130131501	130599877	1	0	0	0	48	0	0	0	0	0	0	0		Q99MQ5
ENSMUST00000080336	ENSMUSG00000045917	4	63558781	63586357	1	12	25	62	0	40	0	2276	4809	2102	491	1849		Q8R239
ENSMUST00000080348	ENSMUSG00000034071	7	12415153	12422751	-1	26	12	68	7	19	9	0	1	0	2	3		B2RUI1
ENSMUST00000080353	ENSMUSG00000063049	8	47667178	47675556	-1	0	3	8	139	0	8	37	269	103	14	71		Q9ESK4
ENSMUST00000080356	ENSMUSG00000061479	7	27187005	27196271	-1	10	0	0	94	0	0	130	99	94	52	52		Q62189
ENSMUST00000080359	ENSMUSG00000029249	5	77265491	77286432	1	0	22	87	178	27	0	376	540	640	74	676		Q8VIG1
ENSMUST00000080361	ENSMUSG00000054757	13	4486972	4523344	-1	0	2	3	0	4	0	0	0	0	0	0	Q8VC77	
ENSMUST00000080365	ENSMUSG00000054406	11	74346624	74352621	-1	6	3	7	7	5	3	0	0	0	0	0	Q7TRW8	
ENSMUST00000080368	ENSMUSG00000021983	14	59647531	60197179	-1	19	12	41	22	35	23	6	9	5	2	5		P98200
ENSMUST00000080371	ENSMUSG00000022353	15	58941244	59082026	-1	32	21	76	220	47	11	47	68	74	64	395	G3X9H7	
ENSMUST00000080379	ENSMUSG00000060904	10	88730858	88744094	1	5	8	51	24	11	5	21	89	48	0	0	F8WIB1	
ENSMUST00000080386	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	0	0	0	23	0	66	1	0		Q8R1D1
ENSMUST00000080391	ENSMUSG00000058019	8	93499213	93535707	-1	1960	1896	27590	5132	2293	1101	0	27	22	0	16	Q9D998	
ENSMUST00000080394	ENSMUSG00000040990	X	159627272	159978069	1	0	0	0	0	0	0	806	2045	1172	277	592		Q8R550
ENSMUST00000080403	ENSMUSG00000056972	7	62376979	62381640	1	44	25	134	675	74	31	0	0	1	0	0		Q9QZ04
ENSMUST00000080405	ENSMUSG00000066030	4	144190719	144196934	1	12	12	5	4	18	15	0	0	0	0	0	Q7TPX8	
ENSMUST00000080406	ENSMUSG00000022526	15	76852148	76871435	-1	24	20	51	346	51	32	15	52	36	5	33	Q6PCX8	
ENSMUST00000080407	ENSMUSG00000060630	11	73688778	73713798	1	3	2	9	5	5	4	0	0	0	0	0	B1ARH2	
ENSMUST00000080411	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	0	0	258	970	246	921	224		Q9R0Q4
ENSMUST00000080415	ENSMUSG00000024430	18	12741324	12755146	1	0	0	1	0	0	0	0	0	0	0	0		Q9D424
ENSMUST00000080418	ENSMUSG00000024589	18	64887756	65217826	1	61	68	399	44	107	58	0	55	17	0	0	G3X9H8	
ENSMUST00000080428	ENSMUSG00000058831	6	29376671	29388468	-1	13	6	29	16	21	7	0	0	0	0	0		P51491
ENSMUST00000080431	ENSMUSG00000006641	5	31036036	31048924	-1	0	16	59	51	10	0	23	7	29	0	0		Q5U4D8
ENSMUST00000080435	ENSMUSG00000039952	9	108204634	108263958	-1	0	0	0	7	0	0	0	0	0	12	144	Q544G5	Q62165
ENSMUST00000080437	ENSMUSG00000035901	7	109893780	109960470	-1	0	0	0	30	0	9	3987	3531	5919	175	4816		Q6PAL8
ENSMUST00000080440	ENSMUSG00000021820	14	20734875	20794088	-1	0	5	0	0	45	0	544	1384	1188	53	734		Q923T9
ENSMUST00000080443	ENSMUSG00000057657	8	107262817	107263248	-1	0	10	0	0	12	8	735	804	438	2379	142		
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ENSMUST00000080453	ENSMUSG00000061809	2	24071721	24096595	-1	0	0	0	0	5	0	0	0	2	0	0		Q6SJ95
ENSMUST00000080460	ENSMUSG00000058251	10	130074409	130075350	1	2	2	1	7	2	0	0	0	0	0	0	Q8VFU1	
ENSMUST00000080461	ENSMUSG00000020697	11	82781108	82804274	1	3	5	8	5	10	0	0	9	0	0	0	B1AT03	
ENSMUST00000080469	ENSMUSG00000009376	6	17463800	17573980	1	0	0	0	0	0	0	0	0	13	0	37	F8VQL0	
ENSMUST00000080474	ENSMUSG00000100208	7	103358248	103359192	-1	10	6	14	4	7	3	0	0	0	0	0	A2RS33	
ENSMUST00000080483	ENSMUSG00000059964	17	37696664	37701818	1	11	5	9	1	3	0	0	0	0	0	0	Q7TRJ5	
ENSMUST00000080492	ENSMUSG00000057863	17	56613395	56614243	1	3	11	24	269	28	13	1305	1921	940	6220	623	Q6ZWZ4	
ENSMUST00000080493	ENSMUSG00000027523	2	174284320	174346744	1	1	1	18	175	0	5	0	0	0	0	1		Q6R0H7
ENSMUST00000080505	ENSMUSG00000078537	13	119949357	119950806	-1	0	0	0	0	1	0	0	0	0	0	0	Q3UT11	
ENSMUST00000080511	ENSMUSG00000058773	13	21779883	21780625	-1	6	7	27	17	15	3	0	0	2	3	1		P43276
ENSMUST00000080514	ENSMUSG00000062309	9	57504102	57505447	1	7	5	6	200	22	4	0	0	0	2	1		Q91WE3
ENSMUST00000080517	ENSMUSG00000059482	4	10874498	10899425	1	10	0	13	29	10	4	29	33	36	74	18		Q3UJP5
ENSMUST00000080518	ENSMUSG00000046056	7	30734739	30756134	1	18	18	29	15	24	12	1	5	3	0	13	E9QPB2	
ENSMUST00000080527	ENSMUSG00000037801	9	63421455	63602493	-1	0	4	0	0	0	1	0	0	0	1	1		Q9D2K4
ENSMUST00000080530	ENSMUSG00000040187	6	146796055	146833529	1	0	0	0	0	0	0	0	0	0	0	0		Q2VPD4
ENSMUST00000080533	ENSMUSG00000064213	8	21734494	21735471	1	0	3	0	2	1	0	0	0	0	0	0		Q5G865
ENSMUST00000080536	ENSMUSG00000058355	8	79683442	79711740	-1	9	14	15	22	10	7	94	420	178	436	195	Q3UHY8	P61222
ENSMUST00000080537	ENSMUSG00000001847	5	143503634	143528036	-1	21	20	27	61	27	7	4916	12255	4951	717	3037	K7Q7T7	P63001
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ENSMUST00000080557	ENSMUSG00000005069	6	124396816	124415067	-1	0	0	0	8	0	0	561	1227	662	70	561		O09012
ENSMUST00000080559	ENSMUSG00000058183	4	154869585	154895528	1	28	22	101	38	9	5	0	0	0	0	0	E9QPA9	
ENSMUST00000080560	ENSMUSG00000034684	9	107681500	107710475	-1	11	16	38	67	22	5	0	0	1	15	25		O88632
ENSMUST00000080572	ENSMUSG00000002249	17	28331671	28350805	-1	0	0	0	0	2	2	0	0	0	0	0	B8JJC8	
ENSMUST00000080583	ENSMUSG00000028018	3	132981752	133092033	-1	3	6	0	63	14	11	38	75	99	16	69		Q5RL51
ENSMUST00000080594	ENSMUSG00000062028	7	24431922	24452297	-1	12	13	27	460	21	13	0	0	0	0	0	D3Z720	
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ENSMUST00000080598						3	6	5	95	5	3	343	570	278	358	251		
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ENSMUST00000080616	ENSMUSG00000058188	14	50653239	50654183	1	0	4	6	0	8	1	0	0	0	0	0	E9Q840	
ENSMUST00000080619	ENSMUSG00000063478	6	131689134	131690063	-1	0	0	1	0	3	1	0	0	0	0	0		Q7M722
ENSMUST00000080622	ENSMUSG00000063480	15	82041319	82047598	-1	8	21	32	59	22	0	218	491	176	726	153		Q9D0T1
ENSMUST00000080626	ENSMUSG00000070324	9	109378400	109404296	-1	9	8	13	12	7	2	0	0	0	0	0	Q5XG67	
ENSMUST00000080630	ENSMUSG00000034127	10	115817284	115849893	1	0	0	0	0	0	0	0	0	0	16	0		Q8R3G9
ENSMUST00000080634	ENSMUSG00000058628	9	37772637	37773640	1	1	1	7	5	5	2	0	0	0	0	0	Q7TRE5	
ENSMUST00000080635	ENSMUSG00000062556	7	31290519	31291821	-1	4	3	2	5	2	1	0	0	0	0	0	O35176	
ENSMUST00000080647	ENSMUSG00000073458	17	13221188	13227658	1	8	10	5	5	14	4	0	0	0	0	0	G5E8M0	
ENSMUST00000080651	ENSMUSG00000060314	7	140807449	140822178	-1	7	2	13	11	6	0	0	0	0	0	0	Q3URY5	
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ENSMUST00000080658	ENSMUSG00000041607	18	82475146	82585637	1	0	0	0	0	0	0	0	0	0	0	0	Q542T4	P04370
ENSMUST00000080660	ENSMUSG00000099743	7	103442177	103443121	-1	4	6	12	2	5	1	0	0	0	0	0	E9Q838	
ENSMUST00000080664	ENSMUSG00000025932	1	14168954	14310235	-1	36	23	107	113	25	15	1	17	3	0	9	Q8C9D0	
ENSMUST00000080665	ENSMUSG00000056752	11	65831282	66168551	-1	89	63	81	77	107	36	0	5	0	0	0	B1AR51	
ENSMUST00000080666	ENSMUSG00000036564	8	95676980	95715119	1	0	0	0	0	0	9	0	0	3	0	0		Q8BTG7
ENSMUST00000080669	ENSMUSG00000056885	7	142273764	142274363	-1	6	3	9	17	7	7	0	0	0	0	0	A4IF42	
ENSMUST00000080671						0	1	4	0	1	0	1	3	2	0	0		
ENSMUST00000080673	ENSMUSG00000057378	2	112631355	113217096	-1	12	0	87	0	0	0	0	0	0	0	0		A2AGL3
ENSMUST00000080681	ENSMUSG00000057997	7	140704165	140705267	1	6	4	11	0	4	2	0	0	0	0	0	Q8VGM0	
ENSMUST00000080694	ENSMUSG00000058176	16	49296648	49297394	-1	4	4	5	5	5	1	0	0	0	0	0	E9Q7Q1	
ENSMUST00000080698	ENSMUSG00000057207	2	85951065	85952039	1	0	0	3	0	7	2	0	0	0	0	0	Q7TR89	
ENSMUST00000080713	ENSMUSG00000063785	X	48256862	48282453	1	3	9	11	11	4	5	389	2580	834	3091	695		Q640M1
ENSMUST00000080718	ENSMUSG00000057454	7	24636550	24641118	1	17	10	87	95	45	7	0	0	0	9	20		Q91YK8
ENSMUST00000080721	ENSMUSG00000058152	18	59175401	59410446	1	15	17	34	343	23	8	0	0	0	0	0		Q5DTK1
ENSMUST00000080723	ENSMUSG00000004535	6	52713729	52766780	1	11	9	11	17	5	3	1547	8799	4164	5164	2611		Q3UKC1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000080726						11736	12506	3380	4999	6533	2575	275	644	812	126	856		
ENSMUST00000080728	ENSMUSG00000028524	4	102741297	102973628	1	9	9	4	14	6	4	0	0	0	0	3		Q8VD37
ENSMUST00000080730	ENSMUSG00000063216	10	79012513	79018283	1	2	6	8	4	2	2	0	0	0	0	0	Q8VGU6	
ENSMUST00000080732	ENSMUSG00000037017	5	138116903	138134265	1	0	0	0	0	0	0	1	92	48	62	0		Q07231
ENSMUST00000080742	ENSMUSG00000062833	6	41968140	41973090	1	3	1	2	0	3	1	0	0	0	0	0	Q76I99	
ENSMUST00000080744	ENSMUSG00000061298	4	110397661	111664324	1	0	0	0	0	0	0	0	0	0	0	0		Q09LZ8
ENSMUST00000080748	ENSMUSG00000059595	9	38994507	38995433	-1	5	2	2	1	0	0	0	0	0	0	0	Q8VG16	
ENSMUST00000080751	ENSMUSG00000062760	15	84379203	84447097	-1	37	22	151	62	66	19	0	4	1	0	0	H7BX53	
ENSMUST00000080754	ENSMUSG00000035934	9	36890982	37147322	-1	0	0	0	35	0	0	0	0	0	0	5		Q8BG99
ENSMUST00000080755	ENSMUSG00000062737	13	27121701	27127546	1	3	0	0	0	5	0	0	0	0	0	0	Q5SZY7	
ENSMUST00000080759	ENSMUSG00000063660	17	37262711	37263749	-1	8	9	23	11	10	4	0	0	0	0	3	Q8VFD9	
ENSMUST00000080762	ENSMUSG00000021345	13	27432681	27438688	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DAY2
ENSMUST00000080766	ENSMUSG00000062705	13	60901297	60904847	-1	3	3	5	1	1	2	0	0	0	0	0	Q9CQC0	
ENSMUST00000080771	ENSMUSG00000019826	10	41450396	41465571	1	11	14	29	47	12	12	256	681	346	101	315		Q80X44
ENSMUST00000080780	ENSMUSG00000062252	17	28575718	28583593	1	7	6	6	58	13	2	0	0	0	0	0		Q4KL25
ENSMUST00000080797	ENSMUSG00000061048	8	106510913	106556908	1	31	32	49	65	47	29	0	0	0	1	5		P10287
ENSMUST00000080801	ENSMUSG00000096708	19	13479252	13480196	-1	10	3	5	4	3	5	0	0	0	0	0	Q8VEV6	
ENSMUST00000080806	ENSMUSG00000063698	19	60837277	60861479	-1	53	48	65	419	63	37	6	31	7	8	12	F8WI63	
ENSMUST00000080812	ENSMUSG00000039130	6	30366380	30391028	-1	0	6	7	7	0	0	116	145	81	47	73		Q80YV2
ENSMUST00000080813	ENSMUSG00000061787	7	81342732	81345254	-1	0	13	0	11	12	8	2456	4447	2609	15139	2026	Q5M9L7	P63276
ENSMUST00000080817	ENSMUSG00000058761	7	99920257	99980458	-1	43	29	91	147	48	17	927	2302	2131	182	1212		E9Q7F2
ENSMUST00000080824	ENSMUSG00000056917	19	5651185	5663707	-1	18	5	0	14	0	0	445	232	137	1	256	E9Q0Y4	
ENSMUST00000080831	ENSMUSG00000059371	1	174099460	174100407	1	5	6	0	4	5	3	0	0	0	0	0	E9Q7E7	
ENSMUST00000080834	ENSMUSG00000098022	7	30054489	30072900	-1	0	0	0	60	5	0	0	0	0	0	0		Q6P9Y7
ENSMUST00000080835	ENSMUSG00000059473	9	40000206	40001250	-1	7	7	18	5	4	4	0	0	0	0	0	Q8VH10	
ENSMUST00000080839	ENSMUSG00000058147	X	73254540	73265390	-1	3	3	4	7	4	3	0	0	0	0	0	B1B0S0	
ENSMUST00000080849	ENSMUSG00000030143	6	132361041	132364134	-1	9	6	119	67	9	1	0	0	0	0	0	E9Q7E4	
ENSMUST00000080853	ENSMUSG00000020717	11	106654217	106750628	-1	0	0	0	3	19	0	55	199	31	35	0		Q08481
ENSMUST00000080856	ENSMUSG00000042590	13	106794439	106936958	-1	0	0	0	26	0	0	18	45	30	24	37		Q8K2V6
ENSMUST00000080857	ENSMUSG00000022565	15	76170974	76232574	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q3W4	
ENSMUST00000080859	ENSMUSG00000099517	13	23535434	23535860	1	6	4	9	107	7	4	0	4	0	2	0		P68433
ENSMUST00000080860	ENSMUSG00000059554	10	18213676	18234998	-1	1	0	0	0	0	0	111	237	139	229	95	Q3UFK1	
ENSMUST00000080861	ENSMUSG00000062997	2	39001580	39005624	-1	3	0	26	10	2	0	16	23	26	277	27		Q6ZWV7
ENSMUST00000080866						0	0	2	0	4	1	1	4	2	2	0		
ENSMUST00000080872						4	4	5	3	2	2	4	18	12	10	3		
ENSMUST00000080880	ENSMUSG00000022150	15	6299788	6440712	1	12	22	11	48	42	14	0	1	8	0	81		
ENSMUST00000080882	ENSMUSG00000040907	7	24978167	25005958	-1	0	0	0	40	0	0	3385	4253	3066	202	3538		Q6PIC6
ENSMUST00000080884	ENSMUSG00000025271	X	150588229	150643878	1	0	1	0	0	0	0	7	27	17	12	13	A2AFM9	P70266
ENSMUST00000080885	ENSMUSG00000059824	7	45705088	45710155	1	7	8	10	196	18	16	1	9	4	4	8		Q60925
ENSMUST00000080891						3	1	3	2	1	3	0	1	0	0	0		
ENSMUST00000080893	ENSMUSG00000035557	11	100256217	100261029	-1	19	14	30	16	21	14	0	0	0	1	0		Q9QWL7
ENSMUST00000080898	ENSMUSG00000063953	10	35708691	35711891	-1	25	26	22	5	38	35	29	174	65	53	43		D3Z6H8
ENSMUST00000080899	ENSMUSG00000056863	7	106823489	106826743	-1	5	7	11	4	10	1	0	0	0	1	0	Q920Z2	
ENSMUST00000080905	ENSMUSG00000055202	17	32795676	32809853	-1	9	2	6	3	9	2	1	4	0	1	0	F7CTH4	
ENSMUST00000080917	ENSMUSG00000059043	16	3838975	3839913	1	8	4	24	5	9	3	0	0	0	0	0		P23275
ENSMUST00000080919	ENSMUSG00000043962	4	126164082	126202760	-1	8	8	11	63	7	16	948	2124	2090	230	1420		Q569Z6
ENSMUST00000080925	ENSMUSG00000057832	7	106713732	106716345	-1	4	4	17	4	6	4	0	0	0	0	0	Q8VFM3	
ENSMUST00000080926	ENSMUSG00000063524	4	150236721	150248879	1	6	7	8	129	9	5	11271	11450	9106	4395	6309	Q5FW97	P17182
ENSMUST00000080929	ENSMUSG00000057000	X	136072099	136085255	-1	4	11	0	8	8	4	0	0	0	0	0	Q4ZGD9	
ENSMUST00000080932	ENSMUSG00000053158	7	80377756	80387946	-1	21	14	51	59	45	26	8824	13413	8382	882	7749		P16879
ENSMUST00000080933	ENSMUSG00000028284	4	31964097	32023467	1	66	22	36	0	22	0	132	885	284	26	156	Q543B5	Q62073
ENSMUST00000080934	ENSMUSG00000028289	4	28813131	28967499	1	3	0	5	3	6	3	0	0	0	0	0	Q8CC52	Q61772
ENSMUST00000080936	ENSMUSG00000012114	16	17651221	17722930	-1	14	8	90	144	4	0	157	808	375	2	386	E9Q7C1	
ENSMUST00000080945						7	7	41	6	3	9	0	0	0	1	0		
ENSMUST00000080949	ENSMUSG00000053012	6	71271677	71285319	1	3	0	10	0	5	0	417	2247	831	456	415		Q99JT5
ENSMUST00000080953	ENSMUSG00000027070	2	69424340	69586065	-1	75	68	80	87	93	53	1	0	1	2	14		A2ARV4
ENSMUST00000080975	ENSMUSG00000040462	10	127094259	127121160	-1	21	0	52	33	0	19	1118	2209	1502	205	1181		Q8K2C7
ENSMUST00000080982						3	1	2	4	9	0	1	1	3	4	1		
ENSMUST00000080987	ENSMUSG00000054648	8	69706332	69710724	-1	7	10	6	3	8	3	88	489	201	165	149	Q9DC47	
ENSMUST00000080995	ENSMUSG00000060044	10	68723746	68782654	1	18	27	29	63	30	18	2	0	0	0	0		Q3UP23
ENSMUST00000081007	ENSMUSG00000063251	11	99627224	99628238	-1	6	2	9	144	12	7	0	0	0	0	0	Q3UUY3	
ENSMUST00000081017	ENSMUSG00000059230	8	19198706	19201545	1	2	3	10	2	2	1	0	0	0	0	0	Q499H9	P82019
ENSMUST00000081022	ENSMUSG00000062861	7	6383318	6396633	1	35	30	60	165	47	17	17	92	35	12	22		P10078
ENSMUST00000081026	ENSMUSG00000060743	1	180800832	180813943	-1	19	9	26	49	28	14	11485	31268	6608	14595	4111	F8WI35	
ENSMUST00000081028	ENSMUSG00000030199	6	134035700	134270158	1	6	0	0	0	9	24	286	908	687	78	355		P97360
ENSMUST00000081029						20	22	217	36	27	17	8	8	0	4	6		
ENSMUST00000081033	ENSMUSG00000017195	11	98551097	98558665	1	3	0	6	30	4	0	0	0	0	1	0	Q5FWC7	Q6X786
ENSMUST00000081034	ENSMUSG00000062272	2	87575086	87576030	1	7	5	0	0	1	3	0	0	0	0	0	A2AV41	
ENSMUST00000081035	ENSMUSG00000046805	19	12460779	12465284	1	30	25	60	35	29	14	2707	19261	5493	3162	6179	E9QN37	
ENSMUST00000081042	ENSMUSG00000042828	7	128003949	128011033	1	9	0	64	173	29	6	0	191	15	0	85		Q1XH17
ENSMUST00000081044	ENSMUSG00000062987	7	107105912	107106859	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q725	
ENSMUST00000081064	ENSMUSG00000031262	X	134308084	134362639	1	0	0	0	10	0	0	0	7	0	0	0		Q8K1K4
ENSMUST00000081074	ENSMUSG00000058670	X	126812462	126815868	-1	25	30	298	204	23	17	0	3	0	0	1	Q8C0S0	
ENSMUST00000081079	ENSMUSG00000025192	19	43689672	43733697	1	31	18	89	110	47	17	257	499	361	24	203		Q3TCT4
ENSMUST00000081093	ENSMUSG00000000159	16	96361668	96525580	1	0	2	0	2	4	0	0	0	0	0	0		
ENSMUST00000081094	ENSMUSG00000028836	4	134343181	134354484	1	13	3	9	10	7	3	0	0	2	0	0	D3Z5N1	
ENSMUST00000081095	ENSMUSG00000059189	9	38592803	38595161	1	1	2	2	1	2	0	0	0	0	0	0	E9Q716	
ENSMUST00000081102	ENSMUSG00000059279	11	58566399	58567343	-1	0	0	0	0	0	0	0	0	0	0	0	M9MMK4	
ENSMUST00000081103	ENSMUSG00000026656	1	170958617	170976547	-1	0	0	0	0	0	0	648	2540	767	2943	629	A0A0B4J1G1	
ENSMUST00000081104	ENSMUSG00000062580	1	135295213	135313778	-1	128	126	231	173	155	65	35	80	47	141	59	Q545U2	Q9Z0V8
ENSMUST00000081111	ENSMUSG00000062867	9	108560286	108565584	1	7	6	22	83	6	2	309	517	263	24	350	Q3UAT9	P24547
ENSMUST00000081116	ENSMUSG00000063582	7	104892670	104893626	-1	9	4	7	4	6	3	0	0	0	0	0	Q8VH00	
ENSMUST00000081121	ENSMUSG00000063873	2	145167754	145642166	1	0	0	0	0	0	0	4	1	2	0	0	Q8VD29	
ENSMUST00000081125	ENSMUSG00000010505	2	181763332	181827797	1	15	0	68	25	33	9	0	0	0	0	0	B0R0C1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000081132	ENSMUSG00000063166	13	53525703	53526059	1	3	6	13	5	5	12	1	0	0	2	0	D3Z5N9	
ENSMUST00000081133	ENSMUSG00000064016	X	56543874	56549606	-1	1	4	2	5	4	0	1	2	1	0	0	Q3UJ22	
ENSMUST00000081134	ENSMUSG00000060445	2	178345293	178407685	-1	6	4	9	45	2	2	50	632	133	71	203		Q9CUU3
ENSMUST00000081154	ENSMUSG00000025949	1	65186683	65278695	1	363	313	281	861	375	281	252	722	399	131	384	D3Z5N5	
ENSMUST00000081162	ENSMUSG00000057156	14	54852736	54870961	-1	41	50	25	5	33	27	12	33	0	0	0		
ENSMUST00000081165	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	0	0	0	5	0	0	0	0	0		Q9QXJ1
ENSMUST00000081170	ENSMUSG00000029156	5	73632749	73647790	-1	11	13	16	15	18	10	15	49	12	28	35		P82349
ENSMUST00000081180	ENSMUSG00000061518	1	36691484	36693681	1	0	0	4	0	4	0	0	38	0	0	27	F7C106	
ENSMUST00000081182	ENSMUSG00000028693	4	116601052	116627941	-1	0	0	0	0	0	0	94	241	127	573	103		Q99MD9
ENSMUST00000081184	ENSMUSG00000059031	7	108094597	108095568	-1	1	7	6	1	7	6	0	0	0	0	0		Q8VG03
ENSMUST00000081186	ENSMUSG00000058588	6	57843464	57850354	-1	2	0	2	2	3	4	0	0	0	0	0	Q8R2C6	
ENSMUST00000081193						22	15	75	20	30	16	0	2	0	0	0		
ENSMUST00000081196	ENSMUSG00000094701	9	38657458	38658390	-1	0	3	2	0	0	0	0	0	0	0	0	Q8VG53	
ENSMUST00000081202	ENSMUSG00000063019	2	157367594	157396763	1	7	7	27	23	28	13	370	447	251	89	216	A2BGN7	
ENSMUST00000081204	ENSMUSG00000062093	14	89896223	89898466	-1	5	0	2	1	3	0	0	0	0	14	7	D3Z5M2	
ENSMUST00000081214	ENSMUSG00000058486	6	34880426	34910876	-1	34	0	40	78	37	10	183	140	171	9	245		Q7TMQ7
ENSMUST00000081216	ENSMUSG00000039997	1	173920407	173942672	-1	84	84	56	110	121	70	31	267	18	31	68	E9PUG6	
ENSMUST00000081219	ENSMUSG00000029913	6	65778988	65937010	1	0	2	0	24	0	0	0	0	0	0	2	Q9D1T8	
ENSMUST00000081224	ENSMUSG00000023008	15	99317225	99370482	-1	3	0	7	0	8	9	543	634	513	5	329		Q6ZPF4
ENSMUST00000081232	ENSMUSG00000034330	8	117498291	117635140	1	36	21	59	108	51	32	3528	5597	4897	326	3444		Q8CIH5
ENSMUST00000081236	ENSMUSG00000057817	19	12889615	12890658	-1	3	8	2	0	0	1	0	0	0	0	0	Q8VFX4	
ENSMUST00000081241						0	1	4	3	1	0	161	204	118	303	138		
ENSMUST00000081260	ENSMUSG00000034813	10	119454034	120087261	1	7	4	2	1	4	4	0	2	0	0	1	Q6X4T6	
ENSMUST00000081265	ENSMUSG00000057098	11	44617317	45008091	1	27	36	80	29	43	13	5	11	9	8	34	Q5SWK5	Q07802
ENSMUST00000081271	ENSMUSG00000061144	18	44104407	44108543	1	3	2	4	3	2	2	0	0	0	0	0		
ENSMUST00000081274	ENSMUSG00000061616	1	92619881	92620936	1	14	13	19	6	11	9	0	0	0	0	0	Q0VBN7	Q60894
ENSMUST00000081275	ENSMUSG00000061802	18	7088233	7297901	-1	17	9	8	1	21	7	0	0	0	0	0		B2RY50
ENSMUST00000081277	ENSMUSG00000059956	1	106934449	106957080	1	0	0	2	0	0	0	1	0	0	0	0		Q9D7P9
ENSMUST00000081285	ENSMUSG00000067629	17	26941253	26972434	1	17	14	38	103	15	11	0	0	0	0	0		
ENSMUST00000081288	ENSMUSG00000029672	6	22306520	22356243	-1	0	0	0	17	0	0	52	127	43	31	27	G3X9I1	
ENSMUST00000081291	ENSMUSG00000053929	15	76643395	76660117	-1	28	12	70	28	36	10	730	932	602	156	469		Q9QXA1
ENSMUST00000081309	ENSMUSG00000032590	9	108085413	108094606	-1	0	0	0	0	0	0	274	234	81	9	189		
ENSMUST00000081310	ENSMUSG00000017652	2	165055627	165072948	1	1	0	0	2	0	0	3	0	0	18	0		P27512
ENSMUST00000081314	ENSMUSG00000030528	7	80454733	80535119	-1	0	0	0	19	0	0	31	85	63	42	35		O88700
ENSMUST00000081318	ENSMUSG00000023764	11	3131850	3193463	-1	0	0	0	0	0	0	88	32	49	0	5		Q3UZY0
ENSMUST00000081321	ENSMUSG00000063932	8	27447670	27495172	1	10	1	5	8	10	4	0	0	0	0	0	A5H0M4	
ENSMUST00000081326	ENSMUSG00000071551	13	4228700	4248681	1	2	0	5	0	0	0	0	0	0	0	0	G3X9Y6	
ENSMUST00000081327	ENSMUSG00000059626	X	37542019	37551082	1	0	0	0	0	0	0	0	0	0	0	0	Q4TU90	
ENSMUST00000081333	ENSMUSG00000059363	19	24261453	24280605	-1	367	288	122	117	174	64	33	50	26	6	29	Q3TV21	O35943
ENSMUST00000081334	ENSMUSG00000060691	16	88868918	88869410	-1	0	0	7	0	3	2	0	0	0	0	0	G3XA43	
ENSMUST00000081335	ENSMUSG00000062175	2	156840007	156855570	1	21	0	19	244	57	0	27	77	110	0	150	A2AVY9	Q8C0Y1
ENSMUST00000081336						5	7	1	12	5	2	0	0	0	7	0		
ENSMUST00000081339	ENSMUSG00000058392	17	32036100	32062865	1	18	12	29	149	23	22	49	177	69	12	59		Q91YK2
ENSMUST00000081342	ENSMUSG00000094777	13	21833026	21833507	-1	8	6	0	227	11	5	0	8	4	20	0	B2RVF0	P22752
ENSMUST00000081349	ENSMUSG00000044042	2	113327736	113716767	1	12	7	24	21	10	0	0	5	0	0	0		Q05860
ENSMUST00000081361						11	8	5	11	7	6	0	1	0	0	0		
ENSMUST00000081362	ENSMUSG00000020817	11	70844778	70943105	1	0	0	0	3	0	0	0	0	55	0	0		O35551
ENSMUST00000081367	ENSMUSG00000059134	10	129873823	129874755	-1	0	3	4	0	0	3	0	0	0	0	0	Q7TRH4	
ENSMUST00000081374	ENSMUSG00000059455	18	42178675	42196709	-1	6	5	9	6	9	1	0	0	0	0	0		Q08EJ0
ENSMUST00000081379	ENSMUSG00000060863	12	105146014	105155225	1	0	0	0	0	0	0	0	0	0	0	0	Q4FZI4	P56841
ENSMUST00000081380	ENSMUSG00000063975	6	142234227	142322981	-1	0	0	2	5	8	0	0	0	0	0	0		
ENSMUST00000081381	ENSMUSG00000031835	8	119508156	119558761	-1	30	15	37	35	5	12	530	779	838	93	616		Q9WTZ2
ENSMUST00000081387	ENSMUSG00000017716	11	117849251	117855743	1	2	0	0	44	0	0	143	306	183	281	115	Q549P2	O70201
ENSMUST00000081393	ENSMUSG00000039577	4	152476706	152563183	1	25	27	53	207	50	39	0	0	0	0	0		P59240
ENSMUST00000081399	ENSMUSG00000059042	7	43976061	43980376	1	13	6	25	9	13	3	0	0	0	0	0		P15949
ENSMUST00000081417	ENSMUSG00000093920	11	87892987	87893922	-1	5	7	16	15	11	1	0	0	0	0	0	Q5SW49	
ENSMUST00000081423	ENSMUSG00000041923	18	22693181	23041653	-1	3	0	3	1	0	0	0	0	0	0	0		P60954
ENSMUST00000081435	ENSMUSG00000035929	17	35379617	35385290	1	1130	1337	4408	1073	2293	1143	1098	2467	1097	428	1887	Q8HWB2	
ENSMUST00000081438	ENSMUSG00000031489	8	27225776	27229588	-1	31	10	47	88	22	17	0	0	0	0	0	Q3UP63	P25962
ENSMUST00000081440	ENSMUSG00000030340	6	125320659	125344943	1	20	13	48	47	33	19	342	328	122	4	200	Q3USG4	
ENSMUST00000081455						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000081457	ENSMUSG00000053522	7	28863853	28866284	1	8	3	7	16	8	4	0	0	0	88	8	Q9CRB1	
ENSMUST00000081469	ENSMUSG00000096747	10	130111841	130112788	-1	5	4	3	0	7	1	0	0	0	0	0	Q7TRH2	
ENSMUST00000081471	ENSMUSG00000063905	13	65512678	65512848	1	6	5	0	13	5	4	0	1	0	0	0	O88245	
ENSMUST00000081474	ENSMUSG00000063394	7	86663664	86664674	1	2	1	4	1	4	1	0	0	0	0	0	Q7TS10	
ENSMUST00000081488						0	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000081491	ENSMUSG00000032690	5	120730333	120749853	-1	0	25	38	34	38	0	50	1448	304	56	542		E9Q9A9
ENSMUST00000081496	ENSMUSG00000024940	19	5740904	5758532	1	34	17	72	576	72	27	20	19	4	40	238	F8VQ06	
ENSMUST00000081497	ENSMUSG00000060152	5	115235836	115245351	1	3	3	10	11	6	2	3	3	0	10	0		Q9DB28
ENSMUST00000081499	ENSMUSG00000039364	11	121053458	121063569	-1	4	0	0	3	0	0	0	0	0	0	0	Q9D966	
ENSMUST00000081503	ENSMUSG00000031860	8	69832491	69872292	1	6	7	5	40	22	7	0	0	0	0	0		Q99NE9
ENSMUST00000081506	ENSMUSG00000063253	8	83434493	83458391	-1	7	6	6	0	8	7	33	2	0	0	0		Q78YZ6
ENSMUST00000081510	ENSMUSG00000054612	7	136894611	137128187	1	4	5	14	12	7	6	3	8	3	17	8		P26187
ENSMUST00000081520	ENSMUSG00000062314	19	13918942	13920044	1	3	5	2	0	2	2	0	0	0	0	0	Q7TQQ2	
ENSMUST00000081525	ENSMUSG00000037348	4	134496697	134510235	1	3	5	14	35	3	3	474	384	289	50	98		Q80ZE4
ENSMUST00000081527	ENSMUSG00000060244	1	171503478	171504750	1	5	7	22	85	9	6	49	135	75	87	46	G3X9I4	
ENSMUST00000081528	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZBV5	
ENSMUST00000081529	ENSMUSG00000074529	2	177903340	177925613	-1	0	0	0	0	0	0	0	0	0	0	0	A2AW65	
ENSMUST00000081533	ENSMUSG00000056959	11	58773388	58779086	1	6	2	10	4	12	4	0	0	0	0	0	Q8VFG7	
ENSMUST00000081541	ENSMUSG00000060317	4	49379840	49408151	-1	12	7	9	6	15	8	0	0	0	0	0		Q8BGG9
ENSMUST00000081542	ENSMUSG00000060882	6	21215503	21729805	1	19	17	21	124	36	15	0	0	0	0	1		Q9Z0V2
ENSMUST00000081544	ENSMUSG00000041670	1	22286251	22805724	-1	11	0	0	7	0	0	0	0	0	0	0	F6TZK4	
ENSMUST00000081551	ENSMUSG00000033813	1	4857814	4897909	1	8	28	23	79	14	7	273	1094	408	488	265	Q3UWX7	P10711
ENSMUST00000081553	ENSMUSG00000063507	2	148990343	149003251	-1	1	0	0	2	0	0	0	0	0	0	0	Q6IE35	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000081554	ENSMUSG00000029470	5	122707544	122729738	1	0	0	0	13	0	0	124	318	161	142	189	Q9Z256	
ENSMUST00000081558	ENSMUSG00000094796	13	120308146	120308649	1	8	7	10	6	5	5	1	44	3	17	9	Q3V185	
ENSMUST00000081560	ENSMUSG00000058076	1	171127165	171150603	-1	0	0	0	0	0	0	384	510	326	109	230	F8WGB3	
ENSMUST00000081564	ENSMUSG00000027750	3	54361109	54391037	1	0	7	1	0	0	0	0	0	0	0	3		Q62009
ENSMUST00000081567	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	3	0	0	81	17	4	17	32		Q02395
ENSMUST00000081569	ENSMUSG00000059493	X	161833296	162159730	-1	0	0	19	0	0	0	0	0	0	0	4	B9EJX2	
ENSMUST00000081571	ENSMUSG00000094080	10	78950662	78956139	1	0	4	0	0	6	0	0	0	0	0	0		Q60892
ENSMUST00000081574	ENSMUSG00000058420	7	118380717	118448190	-1	8	11	34	14	20	6	0	0	0	0	0		Q920M7
ENSMUST00000081580	ENSMUSG00000064052	14	122434854	122451115	-1	12	14	9	16	20	16	0	0	0	0	1	A1L3C8	
ENSMUST00000081582	ENSMUSG00000098905	13	67339307	67360605	-1	65	67	43	81	61	60	64	275	106	59	54	Q3UPV7	
ENSMUST00000081591	ENSMUSG00000027091	2	83644435	83664622	1	0	0	0	29	12	6	160	1185	476	245	230		Q3TIV5
ENSMUST00000081593	ENSMUSG00000062070	X	106187100	106203699	1	29	0	19	95	0	0	4569	13598	5721	4284	3083		P09411
ENSMUST00000081606	ENSMUSG00000028641	4	119232915	119248975	1	0	0	0	0	0	0	8	30	0	0	0		Q3V1T4
ENSMUST00000081618	ENSMUSG00000063047	7	27959135	27979171	-1	16	20	59	19	19	12	31	92	62	60	36	E9Q2S6	
ENSMUST00000081619	ENSMUSG00000053617	19	47260174	47464411	-1	0	84	336	362	158	61	15	0	0	0	140		O89032
ENSMUST00000081628	ENSMUSG00000027478	2	153649450	153687730	1	18	0	0	0	0	19	0	0	0	0	0		O88509
ENSMUST00000081631	ENSMUSG00000057234	2	109092297	109280748	-1	13	0	23	4	4	8	12	28	14	28	7		Q9DCL4
ENSMUST00000081635	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	0	0	0	0	0		Q99M96
ENSMUST00000081636	ENSMUSG00000006542	1	74738922	74749221	-1	12	7	7	28	6	0	0	0	0	0	0		Q8BGM7
ENSMUST00000081640	ENSMUSG00000022151	15	5185525	5218336	1	4	0	0	2	0	0	20	61	28	224	88		Q9D6K7
ENSMUST00000081645	ENSMUSG00000078512	4	143894237	143900380	-1	9	1	10	11	11	2	0	0	0	0	0	E9Q2S4	
ENSMUST00000081649	ENSMUSG00000060591	7	140954839	140955961	-1	19	20	26	30	31	16	31620	40907	18397	22938	11583		Q99J93
ENSMUST00000081650	ENSMUSG00000060036	15	80077794	80091868	-1	0	0	0	11	8	11	455	2841	767	2324	691		P27659
ENSMUST00000081654	ENSMUSG00000001435	10	77052178	77166548	-1	29	18	0	100	53	23	0	4	4	32	193		P39061
ENSMUST00000081657	ENSMUSG00000058717	7	24715023	24726908	-1	4	1	11	7	4	5	0	0	0	0	0	Q8CFJ5	
ENSMUST00000081668						1	7	11	0	2	0	0	0	2	2	0		
ENSMUST00000081670	ENSMUSG00000002546	2	32287384	32307921	1	0	0	0	0	0	0	576	992	973	147	1099	Z4YJU8	
ENSMUST00000081677	ENSMUSG00000026035	1	58430994	58445486	-1	3	0	0	0	0	0	0	96	0	72	0		Q9D6L8
ENSMUST00000081679						1	5	2	3	4	2	0	0	0	0	0		
ENSMUST00000081684	ENSMUSG00000059128	7	28508836	28510455	-1	10	10	20	20	21	9	0	0	0	0	0		Q4VK74
ENSMUST00000081688	ENSMUSG00000020121	10	121780991	122047315	-1	54	0	0	58	56	25	30	93	112	0	41	D3YZW1	
ENSMUST00000081695	ENSMUSG00000054199	3	88835231	88910103	1	40	0	3	0	0	0	245	696	407	44	111	E9Q507	
ENSMUST00000081697	ENSMUSG00000060827	2	88677857	88678813	1	9	4	4	3	4	3	0	0	0	0	0	A2AV13	
ENSMUST00000081702	ENSMUSG00000015363	15	89075124	89087077	1	0	3	0	8	0	0	353	564	306	115	241		Q99JY4
ENSMUST00000081703	ENSMUSG00000057195	7	18009889	18019221	1	0	4	1	6	9	3	0	0	0	0	0	Q9DAT7	
ENSMUST00000081706	ENSMUSG00000094553	6	90101556	90108207	1	6	4	3	2	4	3	0	0	0	0	0		Q9EP51
ENSMUST00000081710	ENSMUSG00000027012	2	71211706	71263303	1	1	0	0	81	4	3	64	19	44	33	17	A2BFF7	O88487
ENSMUST00000081713	ENSMUSG00000005886	1	13139105	13374083	-1	26	14	52	11	36	15	42	0	17	0	0	E9PV80	
ENSMUST00000081714	ENSMUSG00000025176	19	42045610	42070953	1	29	29	58	42	40	12	1	2	7	1	6		Q9DCU9
ENSMUST00000081721	ENSMUSG00000029687	6	47530139	47595341	-1	0	0	0	0	0	0	0	0	60	36	3		Q61188
ENSMUST00000081726	ENSMUSG00000028886	4	132638987	132724765	1	0	0	0	0	2	0	366	1128	639	109	568	Q6P4T3	
ENSMUST00000081728	ENSMUSG00000022240	15	30172593	31029311	1	41	19	56	300	45	27	1	2	1	0	4	E9QKH8	
ENSMUST00000081735	ENSMUSG00000069355	5	10242041	10246526	-1	0	0	18	7	9	2	0	0	0	0	0	L7N200	
ENSMUST00000081742	ENSMUSG00000065999	4	147553277	147585198	1	7	7	8	5	6	4	0	0	0	0	0	A2A7A5	
ENSMUST00000081743	ENSMUSG00000058807	11	58501598	58502572	-1	0	0	0	2	0	4	0	0	0	0	0	Q5NC44	
ENSMUST00000081746	ENSMUSG00000034858	9	74953053	75032468	1	22	18	30	1	22	23	0	0	0	0	17		Q69ZK7
ENSMUST00000081747	ENSMUSG00000060512	5	63812363	63899625	1	15	7	25	40	16	8	478	1462	645	143	448		Q99K99
ENSMUST00000081748	ENSMUSG00000063615	7	103892810	103893733	-1	4	3	5	0	8	0	0	0	0	0	0	F8VPZ8	
ENSMUST00000081752	ENSMUSG00000027965	3	114904078	115125722	1	10	3	11	53	8	0	0	0	0	0	0	Q3UVC5	P63056
ENSMUST00000081769	ENSMUSG00000034488	13	88821472	89323223	1	0	0	0	2	0	0	0	0	0	0	0		O35474
ENSMUST00000081775	ENSMUSG00000038615	11	96817414	96829968	-1	31	0	0	95	0	0	246	499	588	106	589	Q6GTN8	Q61985
ENSMUST00000081776	ENSMUSG00000057346	15	77403789	77411080	-1	5	0	30	12	13	15	2	1	0	2	13	Q8VDU3	
ENSMUST00000081777	ENSMUSG00000030131	6	122006761	122085965	1	26	17	22	15	22	9	0	0	0	1	0		P28666
ENSMUST00000081780	ENSMUSG00000058005	3	93826020	93827117	1	4	6	0	15	5	6	0	0	0	0	0		Q717B4
ENSMUST00000081790	ENSMUSG00000033417	19	60524696	60581023	-1	38	0	0	25	46	0	558	1539	832	0	246		Q8R0X2
ENSMUST00000081794	ENSMUSG00000020346	11	49244191	49263030	1	0	10	0	0	17	2	625	393	204	147	603	Q544F0	P27808
ENSMUST00000081799	ENSMUSG00000038351	11	74849261	74897060	-1	0	19	0	74	37	18	0	0	0	0	0		Q80U12
ENSMUST00000081809						6	2	0	1	1	1	0	0	0	1	3		
ENSMUST00000081816	ENSMUSG00000027485	2	154190818	154220369	1	2	2	2	4	16	2	0	0	0	0	0		Q61114
ENSMUST00000081819	ENSMUSG00000040405	11	46735080	46779578	1	0	0	0	0	11	0	0	0	0	0	0	Q3V033	
ENSMUST00000081823	ENSMUSG00000042678	11	60469339	60528369	1	0	0	3	0	8	0	0	1	0	0	0		Q9QZZ4
ENSMUST00000081827	ENSMUSG00000067768	X	73214333	73222453	1	0	0	0	0	0	0	1	65	0	0	0	Q9JJQ7	
ENSMUST00000081828	ENSMUSG00000057265	12	84409071	84433780	1	9	7	27	20	9	4	3	6	2	3	2		Q3V079
ENSMUST00000081834	ENSMUSG00000049047	X	134756595	134761455	1	21	15	4	6	8	15	35	205	25	33	36		Q8BHS6
ENSMUST00000081838	ENSMUSG00000015335	2	30090944	30093648	-1	0	0	0	18	0	2	12	56	8	14	42		Q8VC90
ENSMUST00000081840	ENSMUSG00000057841	6	115805505	115808747	-1	19	16	26	26	35	15	2864	5481	2947	15143	2124		P62911
ENSMUST00000081848	ENSMUSG00000059743	3	89093588	89101959	-1	20	7	26	34	25	9	1282	1465	1383	736	469	Q4FJN9	Q920E5
ENSMUST00000081849	ENSMUSG00000040669	6	122317731	122340561	-1	6	0	17	0	0	0	25	185	4	0	114	Q3V116	
ENSMUST00000081851	ENSMUSG00000026109	1	50900647	51187270	1	8	11	36	140	14	5	0	0	0	0	0		Q9QYM9
ENSMUST00000081857	ENSMUSG00000040752	14	54941981	54966927	-1	64	31	90	103	61	28	0	0	0	0	0	B2RQQ1	Q02566
ENSMUST00000081864	ENSMUSG00000062742	18	35536583	35536951	1	1	4	7	1	3	0	10	5	10	60	5	D3YYZ2	
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ENSMUST00000081872	ENSMUSG00000055409	7	49974864	50865255	1	21	6	44	4	15	5	0	0	0	0	0		Q2VWQ2
ENSMUST00000081879	ENSMUSG00000026811	2	32599709	32620806	1	0	3	11	5	9	2	0	0	0	0	0		Q9JM95
ENSMUST00000081880	ENSMUSG00000041247	16	19653381	19706365	-1	9	6	9	9	8	7	0	0	0	2	0		Q7TST5
ENSMUST00000081891						6	0	27	12	19	4	4	23	13	4	2		
ENSMUST00000081893	ENSMUSG00000037217	X	20860511	20921004	-1	6	5	0	0	15	7	61	92	80	1	68		O88935
ENSMUST00000081894	ENSMUSG00000020456	11	6291633	6356642	1	14	0	0	2	19	6	554	149	509	0	388	Z4YJV4	
ENSMUST00000081896	ENSMUSG00000062511	11	11589223	11627835	-1	58	77	2173	388	17	110	7	12	0	0	15	Q5SQK8	
ENSMUST00000081904	ENSMUSG00000033788	6	84008590	84211060	1	2	7	3	0	0	16	0	0	0	0	0		Q9ESD7
ENSMUST00000081907	ENSMUSG00000008789	7	17713238	17761132	1	16	21	11	20	10	16	0	0	0	0	0		Q3UKK2
ENSMUST00000081908	ENSMUSG00000060499	12	66283379	66284401	-1	9	3	14	51	10	1	0	0	0	0	0		P86048
ENSMUST00000081911	ENSMUSG00000060180	11	67321658	67371586	1	13	2	33	0	0	0	0	0	0	0	1	B1AR69	
ENSMUST00000081914	ENSMUSG00000055204	5	90227166	90366577	-1	3	0	0	56	0	0	188	918	825	100	683	E9QKG6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000081918	ENSMUSG00000057540	7	86268730	86269811	-1	3	2	2	4	3	0	0	0	0	0	0	B2RVZ1	
ENSMUST00000081919	ENSMUSG00000057280	4	58285960	58374303	1	0	0	27	0	0	0	0	0	0	0	0	K3W4P7	
ENSMUST00000081921	ENSMUSG00000028730	4	118554551	118620777	-1	13	0	17	6	0	16	2	18	0	0	11		Q9D180
ENSMUST00000081924	ENSMUSG00000059108	7	141015812	141016892	-1	9	12	17	27	15	21	46795	110367	38896	103113	14937	Q3SXF0	
ENSMUST00000081926	ENSMUSG00000059842	2	154613297	154646821	1	0	0	24	48	22	12	68	0	24	0	0	Q6PGC9	
ENSMUST00000081927	ENSMUSG00000057726	13	33484790	33495998	1	7	7	4	2	7	0	0	0	0	0	0	Q8VHQ1	
ENSMUST00000081929						440	444	6023	455	329	252	3	13	8	0	4		
ENSMUST00000081932	ENSMUSG00000026643	2	3284212	3328877	1	11	27	21	23	24	5	26	125	49	41	42	Q3THR4	O70311
ENSMUST00000081933	ENSMUSG00000049502	16	35926511	35939151	-1	83	98	269	72	67	36	603	2336	1222	146	1137		Q3UIR3
ENSMUST00000081940	ENSMUSG00000090137	8	70508263	70510801	-1	0	0	3	0	0	0	681	717	620	3174	367	Q66JP1	P62984
ENSMUST00000081945	ENSMUSG00000047641	15	101431490	101438804	-1	19	8	48	134	28	18	1	1	1	0	4		Q6IMF0
ENSMUST00000081946	ENSMUSG00000003438	7	28305516	28312072	-1	12	5	16	18	8	6	169	153	90	62	78		Q9D880
ENSMUST00000081956	ENSMUSG00000039985	6	148921035	148946467	-1	0	0	0	80	22	0	0	0	0	0	27		Q8C8M1
ENSMUST00000081960	ENSMUSG00000096368	4	118933899	118934840	-1	8	2	22	6	8	6	0	0	0	0	0	B1ARV2	
ENSMUST00000081964	ENSMUSG00000059325	5	77086988	77115121	-1	6	7	0	3	9	2	0	0	0	0	0		Q8R1H0
ENSMUST00000081966	ENSMUSG00000061923	15	38219203	38226735	1	16	6	6	51	15	12	0	0	0	0	0	A6H656	
ENSMUST00000081978	ENSMUSG00000053897	3	135825279	135888572	1	6	8	25	33	9	0	0	0	0	0	0		Q91W10
ENSMUST00000081980	ENSMUSG00000061650	11	59948206	59962205	1	23	18	73	99	33	7	126	126	100	33	59		Q8VCS6
ENSMUST00000081982	ENSMUSG00000037259	2	144470557	144527414	-1	14	8	332	110	10	8	0	1	1	0	1		Q8C008
ENSMUST00000081985	ENSMUSG00000096424	9	38061322	38062251	1	3	3	2	3	3	1	0	0	0	0	0	Q7TRE0	
ENSMUST00000081986	ENSMUSG00000070856	2	87251939	87252919	1	6	1	0	5	1	0	0	0	0	1	0	Q7TR53	
ENSMUST00000081987						3	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000081989	ENSMUSG00000063760	10	31493193	31609184	-1	19	27	30	259	35	15	13	80	30	13	35		D3YYI7
ENSMUST00000081993	ENSMUSG00000057262	15	52477614	52478228	-1	4	6	14	0	0	0	13	31	10	56	8	E9QAZ2	
ENSMUST00000081996	ENSMUSG00000095929	7	108211583	108212527	-1	1	9	4	0	2	1	0	0	0	0	0	Q7TRU9	
ENSMUST00000081998	ENSMUSG00000053687	8	105984944	105996423	-1	21	1	22	9	26	12	33	49	53	8	18		Q8C255
ENSMUST00000082002	ENSMUSG00000091460	9	19927896	19928282	-1	0	0	0	1	2	0	0	4	5	11	4	J3QK04	
ENSMUST00000082006	ENSMUSG00000062892	19	12953591	12954568	1	5	5	7	1	4	2	0	0	0	0	0	Q8VF19	
ENSMUST00000082008	ENSMUSG00000000244	7	143005046	143019644	1	0	0	0	0	0	0	7	0	0	0	0	Q7TNQ7	
ENSMUST00000082014	ENSMUSG00000062952	6	132868008	132869009	1	6	1	3	0	3	2	0	0	0	0	0		Q7M712
ENSMUST00000082024	ENSMUSG00000021112	12	78748947	78840711	1	16	23	34	77	23	6	270	1028	539	591	465	B2RRY4	Q9JLB2
ENSMUST00000082026	ENSMUSG00000038024	4	86748555	86850603	1	13	8	0	3	16	4	172	400	179	54	237		A6H8H2
ENSMUST00000082027	ENSMUSG00000062121	9	39701793	39702822	-1	9	3	7	1	10	2	0	0	0	0	0		Q60888
ENSMUST00000082032						4	2	6	0	0	0	0	0	0	0	0		
ENSMUST00000082034	ENSMUSG00000025665	X	111388192	111537959	-1	0	0	0	0	0	0	0	0	0	0	0	E9QK39	
ENSMUST00000082048	ENSMUSG00000061392	X	91779544	91783018	-1	0	7	0	0	0	0	0	0	0	0	0	Q14AN0	
ENSMUST00000082054	ENSMUSG00000037386	15	39198332	39681940	1	0	24	11	110	20	16	0	0	0	0	0		Q9EQZ7
ENSMUST00000082057	ENSMUSG00000060261	5	134237834	134314760	-1	0	9	0	0	0	9	0	0	0	0	0		Q9ESZ8
ENSMUST00000082059	ENSMUSG00000018166	10	128567523	128589652	-1	33	32	41	101	68	32	28	79	51	7	49		Q61526
ENSMUST00000082060	ENSMUSG00000064246	1	134182176	134190181	1	5	14	22	4	17	0	17730	24114	12977	16087	10197		Q61362
ENSMUST00000082064						5	1	4	6	11	2	16	12	22	21	8		
ENSMUST00000082065	ENSMUSG00000062433	16	89419326	89420111	-1	8	9	23	8	8	4	0	0	0	0	0	A0A087WP75	
ENSMUST00000082070	ENSMUSG00000057455	18	30973489	31317290	-1	2	3	4	0	0	3	0	0	0	0	0	F8WGU6	
ENSMUST00000082079	ENSMUSG00000057170	13	27094212	27100255	1	4	3	3	0	3	2	0	0	0	0	0	Q5SY42	
ENSMUST00000082085	ENSMUSG00000057699	6	132956884	132957919	-1	0	1	3	0	4	1	0	0	0	0	0	Q7M708	
ENSMUST00000082088	ENSMUSG00000059401	X	71050256	71156056	1	10	10	16	16	13	8	0	0	0	2	4		P0C6A2
ENSMUST00000082089	ENSMUSG00000031060	X	20617503	20650901	1	0	0	0	0	0	0	79	0	0	0	146		Q99KG3
ENSMUST00000082090	ENSMUSG00000062444	7	81460399	81493925	-1	14	6	18	90	18	7	0	0	0	0	0		Q9JME5
ENSMUST00000082091	ENSMUSG00000064223	7	106688782	106689729	-1	7	4	0	8	3	5	0	0	0	0	0	K7N641	
ENSMUST00000082092	ENSMUSG00000057322	11	114668524	114672331	1	0	0	0	0	0	0	11	14	11	81	0	Q52KP0	Q9JJI8
ENSMUST00000082093	ENSMUSG00000059256	14	56129556	56132608	-1	10	10	16	8	16	6	0	0	0	16	1		P11033
ENSMUST00000082094	ENSMUSG00000063884	6	71880638	71908750	-1	10	16	9	11	14	5	61	359	119	225	130		Q14C51
ENSMUST00000082104	ENSMUSG00000060924	8	15892537	17535586	-1	49	40	85	48	94	22	0	0	0	0	0		Q923L3
ENSMUST00000082108	ENSMUSG00000028649	4	123349633	123684360	-1	0	0	18	0	0	0	0	0	0	0	0	A0A0A0MQA6	
ENSMUST00000082120	ENSMUSG00000051176	8	43295068	43307009	-1	19	12	25	14	27	19	0	0	0	0	0	E9QK22	
ENSMUST00000082121	ENSMUSG00000029276	5	107548967	107597888	-1	7	4	4	6	0	0	0	16	0	0	0		Q8BZM1
ENSMUST00000082122	ENSMUSG00000027203	2	125247190	125258608	1	1	0	6	45	2	2	85	213	64	80	64	Q8VCG1	
ENSMUST00000082125	ENSMUSG00000009772	1	132316126	132333488	1	0	12	18	0	18	0	395	823	592	36	395		Q8BZN4
ENSMUST00000082130	ENSMUSG00000027297	2	119751320	119760431	-1	0	0	0	0	0	2	0	0	0	0	0		P08923
ENSMUST00000082131	ENSMUSG00000059762	10	129078972	129080057	-1	1	4	6	7	7	4	0	0	0	0	0	Q8VG33	
ENSMUST00000082134	ENSMUSG00000037563	7	28350652	28352696	1	0	9	4	73	0	0	3439	5604	3032	15443	1988	A4FUS1	P14131
ENSMUST00000082136	ENSMUSG00000059436	12	76937269	76962248	-1	0	0	73	310	46	14	2694	7325	3136	1495	2360	Q8C4Y1	
ENSMUST00000082141	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	0		P27699
ENSMUST00000082150						0	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000082152	ENSMUSG00000020802	11	116537740	116581447	-1	15	30	70	198	38	21	200	142	176	12	298		Q6ZPJ3
ENSMUST00000082158	ENSMUSG00000026203	1	75236406	75245692	1	0	0	0	0	0	0	5	0	0	0	0		Q9QYI5
ENSMUST00000082167	ENSMUSG00000099887	2	111368634	111369551	1	3	2	5	1	2	1	0	0	0	0	0	Q7TQY4	
ENSMUST00000082170	ENSMUSG00000074505	9	15910205	16378231	-1	96	81	201	111	94	73	0	3	0	0	0	E9QK16	
ENSMUST00000082175	ENSMUSG00000073968	7	102677580	102687326	-1	21	4	17	57	14	17	15	70	31	21	36	G3X9I6	
ENSMUST00000082177	ENSMUSG00000025332	X	152233020	152274535	1	0	0	7	1	0	4	722	1327	1104	68	691		P41230
ENSMUST00000082183	ENSMUSG00000035045	X	95711678	95932637	1	0	0	0	0	0	2	0	0	0	0	0	G3X9I7	
ENSMUST00000082191	ENSMUSG00000059873	2	85975245	85976219	1	7	3	0	2	3	2	0	0	0	0	0	A2ATE0	
ENSMUST00000082197	ENSMUSG00000062906	15	89123307	89128700	-1	0	0	31	0	14	8	53	60	51	0	46		Q6P3E7
ENSMUST00000082203	ENSMUSG00000074865	13	62517500	62520544	-1	0	0	2	0	0	0	1	0	0	0	0	L7N201	
ENSMUST00000082209	ENSMUSG00000023033	15	100869858	101045938	1	27	0	132	42	113	22	0	0	0	0	0	F6U329	
ENSMUST00000082214	ENSMUSG00000040660	7	26173411	26210661	1	13	6	10	13	11	3	0	16	3	5	8		P12790
ENSMUST00000082219	ENSMUSG00000063779	3	106201490	106219507	-1	4	8	5	1	8	1	3	2	1	11	6		Q91Z98
ENSMUST00000082220	ENSMUSG00000070438	11	58816928	58818001	1	0	1	4	6	4	4	0	0	0	0	0	Q5NC55	
ENSMUST00000082223	ENSMUSG00000058558	5	107900502	107909005	1	0	0	0	29	10	0	0	8	12	90	4	Q58EU6	P47962
ENSMUST00000082225						2	0	14	0	0	0	0	0	0	0	1		
ENSMUST00000082235	ENSMUSG00000024313	18	21072344	21100199	1	19	10	11	5	13	11	0	0	0	0	0		Q61847
ENSMUST00000082237	ENSMUSG00000057706	7	82867333	82871563	1	18	12	47	404	25	16	8	11	9	3	9	F8WJD6	
ENSMUST00000082243	ENSMUSG00000024533	18	67488209	67552777	-1	11	11	0	0	9	0	0	0	0	0	18		Q52KF3
ENSMUST00000082244	ENSMUSG00000060205	10	79034723	79035802	1	5	7	4	6	8	1	0	0	0	0	0	Q8VGU7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000082254	ENSMUSG00000024502	18	43531408	43687773	-1	21	19	46	20	27	13	0	0	0	0	0	D3YXK0	
ENSMUST00000082262	ENSMUSG00000078517	4	139352587	139378730	1	20	20	32	0	0	0	0	0	0	11	0	Z4YJW0	
ENSMUST00000082269	ENSMUSG00000060375	12	107488632	107489636	1	7	5	14	10	3	7	0	0	0	0	0	Q9CXS0	
ENSMUST00000082283						1	0	6	3	4	2	11	0	22	138	0		
ENSMUST00000082287	ENSMUSG00000058523	4	61831319	61835233	-1	3	0	3	4	2	0	0	0	0	0	0	B5TE77	
ENSMUST00000082290	ENSMUSG00000036949	2	14388316	14494977	1	0	0	0	0	0	0	0	0	0	0	0		Q5FWH7
ENSMUST00000082300						0	8	23	45	31	16	37	40	43	6	45		
ENSMUST00000082303	ENSMUSG00000028339	4	47208161	47313167	1	27	0	57	140	21	19	0	0	0	0	0	A2AJY2	
ENSMUST00000082306	ENSMUSG00000060491	4	109505337	109531297	-1	7	0	2	3	1	3	0	0	0	0	0		Q9CPZ3
ENSMUST00000082319	ENSMUSG00000024400	18	31804057	31908987	1	11	18	85	82	26	12	33	85	79	113	45	D3YX80	
ENSMUST00000082320	ENSMUSG00000031169	X	8193848	8206525	-1	7	0	0	44	0	0	0	0	0	0	0		Q9JJJ7
ENSMUST00000082321	ENSMUSG00000026616	1	195136811	195176716	-1	21	0	31	0	0	13	1	5	8	3	16	Q9DC83	
ENSMUST00000082337	ENSMUSG00000061607	17	35841515	35859670	1	153	125	339	141	148	73	262	558	461	64	518	E9QK89	
ENSMUST00000082339	ENSMUSG00000057534	11	88964658	88966931	-1	0	0	0	0	0	0	0	0	0	0	0	F8VPW8	
ENSMUST00000082342	ENSMUSG00000094347	10	129387635	129388594	1	7	4	1	3	3	3	0	0	0	0	0	Q8VFZ9	
ENSMUST00000082357	ENSMUSG00000059663	X	154339225	154343392	-1	1	0	4	1	6	1	0	0	0	0	0	Q9D519	
ENSMUST00000082365	ENSMUSG00000018865	15	84076097	84105754	-1	23	5	52	67	27	9	3	3	2	0	1		P63046
ENSMUST00000082367	ENSMUSG00000002944	5	17781690	17888801	-1	8	0	0	0	2	0	0	0	0	61	0	Q3UAI3	Q08857
ENSMUST00000082370	ENSMUSG00000063157	5	87692624	87699630	-1	8	7	8	6	9	3	0	0	0	0	0	Q8BGL0	
ENSMUST00000082373	ENSMUSG00000063297	7	54835498	55268885	1	1	3	6	9	7	1	0	0	0	0	0		Q8BGY3
ENSMUST00000082382	ENSMUSG00000057068	5	92555069	92591279	1	0	0	0	0	0	0	0	0	0	0	0	E9PYM1	
ENSMUST00000082392	ENSMUSG00000064341	MT	2751	3707	1	2	6	8	14	24	32	1752	7135	1458	12756	2191	Q4JFN6	P03888
ENSMUST00000082396	ENSMUSG00000064345	MT	3914	4951	1	1	5	33	7	10	16	1120	2366	528	2263	934	Q9MD59	P03893
ENSMUST00000082402	ENSMUSG00000064351	MT	5328	6872	1	41	54	136	52	156	139	34052	138597	48693	118499	22932	Q9MD68	P00397
ENSMUST00000082405	ENSMUSG00000064354	MT	7013	7696	1	28	28	28	0	1	1	3944	41481	1522	9897	225	Q7JCZ1	P00405
ENSMUST00000082407	ENSMUSG00000064356	MT	7766	7969	1	1	1	3	3	4	3	1543	2376	739	3774	920	Q7JCZ0	P03930
ENSMUST00000082408	ENSMUSG00000064357	MT	7927	8607	1	0	0	0	0	0	1	3694	13581	1110	7917	2296	Q7JCY9	P00848
ENSMUST00000082409	ENSMUSG00000064358	MT	8607	9390	1	4	24	36	4	8	5	11749	36591	1750	18752	1378	Q7JCX7	P00416
ENSMUST00000082411	ENSMUSG00000064360	MT	9459	9806	1	0	0	0	5	0	0	156	211	16	358	155	Q7GIP5	P03899
ENSMUST00000082414	ENSMUSG00000064363	MT	10167	11544	1	12	18	31	38	24	24	2442	11513	2560	8315	2800	Q7JCY6	P03911
ENSMUST00000082418	ENSMUSG00000064367	MT	11742	13565	1	28	32	78	70	41	56	2402	9722	3172	3973	2566	Q9MD82	P03921
ENSMUST00000082419	ENSMUSG00000064368	MT	13552	14070	-1	1	7	76	20	13	4	794	4425	431	1573	541	Q7JCY4	P03925
ENSMUST00000082421	ENSMUSG00000064370	MT	14145	15288	1	9	16	30	25	50	56	2868	25986	3878	15108	3491	Q7JCZ3	P00158
ENSMUST00000082424	ENSMUSG00000064373	15	3268547	3280508	1	0	9	11	14	26	9	518	1827	768	2901	1285		P70274
ENSMUST00000082426	ENSMUSG00000034785	4	107291465	107307169	-1	11	9	16	5	4	2	0	0	0	0	0		
ENSMUST00000082428	ENSMUSG00000049091	7	127271879	127274055	-1	7	5	16	112	15	3	1834	4553	2390	350	1614		P97364
ENSMUST00000082429	ENSMUSG00000063856	9	108338903	108340343	1	8	4	27	17	8	7	3409	5301	1915	1589	1162		P11352
ENSMUST00000082430	ENSMUSG00000018339	11	54902453	54910377	1	7	5	18	35	9	5	281	259	161	115	100		P46412
ENSMUST00000082431	ENSMUSG00000042808	12	76792335	76795554	-1	17	11	26	14	24	17	0	0	0	0	0		
ENSMUST00000082432	ENSMUSG00000007682	12	90724554	90738438	-1	31	29	37	11	30	8	11	26	14	43	51		Q9Z1Y9
ENSMUST00000082437	ENSMUSG00000037072	3	144570304	144597680	1	6	5	3	53	9	6	18	258	163	917	165		
ENSMUST00000082439	ENSMUSG00000035757	15	89089084	89100340	1	0	0	1	123	4	0	275	466	270	103	202		Q9DBC0
ENSMUST00000084013	ENSMUSG00000065947	MT	9877	10173	1	0	0	5	2	0	2	344	1410	653	1141	586	Q9MD77	P03903
ENSMUST00000084017						0	0	0	0	2	0	0	11	0	0	3		
ENSMUST00000084026	ENSMUSG00000054823	8	25601601	25719667	1	58	27	130	5	0	21	504	2507	0	0	261	D3Z357	
ENSMUST00000084027	ENSMUSG00000031565	8	25513654	25575714	1	9	2	0	0	13	0	0	0	0	13	20		P16092
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ENSMUST00000084031	ENSMUSG00000037406	8	25025451	25038962	-1	9	3	16	90	19	4	0	0	4	2	3		A2RT60
ENSMUST00000084032	ENSMUSG00000031555	8	24949611	25016922	-1	11	13	30	0	0	8	734	1965	1502	230	1028	E9Q638	
ENSMUST00000084035	ENSMUSG00000031555	8	24949611	25016922	-1	0	0	0	76	25	0	0	111	134	15	18		Q61072
ENSMUST00000084038	ENSMUSG00000031543	8	22974844	23150497	1	0	0	0	0	0	0	0	0	0	0	0	G5E8J2	
ENSMUST00000084040	ENSMUSG00000065956	8	21565386	21566349	1	0	0	0	0	0	0	0	0	0	0	0	K9J724	
ENSMUST00000084041	ENSMUSG00000094818	8	21529032	21530012	1	0	0	0	0	0	0	0	0	0	0	0		Q45VN2
ENSMUST00000084042	ENSMUSG00000095066	8	21509258	21510237	1	0	0	0	0	0	0	0	0	0	0	0		Q45VN2
ENSMUST00000084046	ENSMUSG00000074449	8	20337664	20363210	-1	275	254	158	106	248	104	1	0	1	0	0	E9Q637	
ENSMUST00000084055	ENSMUSG00000068631	8	13895816	13896613	1	5	3	4	2	4	1	6	14	11	34	1	D3YX42	
ENSMUST00000084086	ENSMUSG00000065987	8	3917655	3926844	-1	21	18	8	11	7	12	0	0	0	0	0	Q3UTX5	Q8CJ91
ENSMUST00000084097	ENSMUSG00000065990	4	155831272	155833130	1	9	3	2	55	0	4	113	141	88	155	27		Q9DCJ7
ENSMUST00000084103	ENSMUSG00000029050	4	155154075	155222592	-1	7	14	63	0	78	37	613	330	730	47	522	B1AUF2	
ENSMUST00000084105	ENSMUSG00000036834	3	63696234	63899472	-1	0	0	0	0	0	0	0	0	0	0	0		Q4KWH5
ENSMUST00000084114	ENSMUSG00000028943	4	152120331	152152371	-1	0	0	0	0	0	0	0	0	0	0	0		Q9ET47
ENSMUST00000084115	ENSMUSG00000039713	4	152072498	152115400	1	16	16	25	30	20	9	0	0	0	0	0		Q66T02
ENSMUST00000084116	ENSMUSG00000028948	4	152039321	152061494	1	9	0	0	69	12	0	132	162	27	0	95		Q3TZX8
ENSMUST00000084117	ENSMUSG00000028980	4	149979475	150009023	-1	34	18	99	12	33	27	904	946	914	45	689		Q8CFX1
ENSMUST00000084123						2	4	0	8	0	1	0	0	60	0	0		
ENSMUST00000084124	ENSMUSG00000028961	4	149149991	149166771	-1	16	10	22	49	24	13	26580	35362	21660	3451	11363		Q9DCD0
ENSMUST00000084125	ENSMUSG00000041459	4	148612382	148627019	-1	0	16	9	25	30	11	194	330	131	101	573	Q544R5	Q921F2
ENSMUST00000084129	ENSMUSG00000029003	4	148130384	148145699	1	9	2	14	12	6	3	2	27	15	21	0		Q9D752
ENSMUST00000084141	ENSMUSG00000069743	17	21816876	21845759	-1	7	5	2	19	6	2	3	5	2	1	1	E9Q5G8	
ENSMUST00000084149	ENSMUSG00000067916	4	147132038	147180579	1	2	11	4	11	4	7	46	96	44	87	37	Q8R1N3	
ENSMUST00000084170	ENSMUSG00000066043	4	132355923	132422489	-1	23	16	14	0	20	9	174	215	218	36	105		Q501J7
ENSMUST00000084171						3	3	0	6	2	10	0	4	5	15	5		
ENSMUST00000084184	ENSMUSG00000066026	4	144892827	144928209	1	0	0	3	38	0	5	114	265	89	26	137	H7BX54	
ENSMUST00000084191	ENSMUSG00000073724	4	144059126	144069327	1	0	13	0	0	9	6	0	0	0	0	0	Q810Z0	
ENSMUST00000084199						5	3	8	20	10	3	0	0	1	0	0		
ENSMUST00000084203	ENSMUSG00000028917	4	141625734	141664899	-1	0	15	0	116	58	18	546	487	427	47	446	Z4YJW6	
ENSMUST00000084207	ENSMUSG00000071176	8	14911663	15001085	1	47	0	0	72	67	18	0	0	0	0	0		Q8C033
ENSMUST00000084214	ENSMUSG00000028760	4	137993022	138208508	1	0	0	7	0	0	4	696	1345	1392	2	945		
ENSMUST00000084215	ENSMUSG00000028760	4	137993022	138208508	1	0	15	47	0	65	4	220	236	417	0	322	A2AMI2	
ENSMUST00000084219	ENSMUSG00000066037	4	136310942	136359447	1	0	0	0	0	0	0	0	0	0	3	0	F7B5B5	
ENSMUST00000084238	ENSMUSG00000037553	4	133605299	133650154	-1	33	21	70	72	58	24	5230	6365	4078	390	3222		Q5Y5T2
ENSMUST00000084241	ENSMUSG00000028868	4	133130505	133199756	1	23	26	62	89	55	22	4718	5722	6098	459	4660		Q8BH43
ENSMUST00000084249	ENSMUSG00000066043	4	132355923	132422489	-1	0	5	0	0	0	0	0	0	0	0	0		Q501J7
ENSMUST00000084250	ENSMUSG00000028896	4	132331919	132353605	-1	1	0	0	39	0	1	94	149	67	0	1		Q8VE37

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000084253	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	0	0	0	0	0	26	0	0		P48193
ENSMUST00000084263	ENSMUSG00000028784	4	129947547	129957115	1	21	11	35	16	25	5	0	4	0	0	2	B1ASB6	
ENSMUST00000084264	ENSMUSG00000053841	4	129626078	129641065	-1	0	4	0	0	0	0	258	113	272	45	203	Q3UD58	Q6PAM1
ENSMUST00000084275	ENSMUSG00000038346	6	125009145	125037870	1	0	0	0	0	0	0	444	541	402	65	106	E9Q1A5	
ENSMUST00000084276						8	6	53	8	0	0	5	16	2	4	7		
ENSMUST00000084281						3	2	0	0	1	1	0	0	0	2	0		
ENSMUST00000084289	ENSMUSG00000042500	4	126489541	126533472	-1	41	30	43	98	36	19	94	486	232	37	280		Q8CJF8
ENSMUST00000084296	ENSMUSG00000028873	4	124918465	124939311	-1	9	4	18	13	15	4	226	208	202	38	95		Q8BHX3
ENSMUST00000084299	ENSMUSG00000028291	4	34550937	34566908	1	3	5	8	9	15	2	392	1025	326	47	121		B1AXD8
ENSMUST00000084301	ENSMUSG00000028649	4	123349633	123684360	-1	0	0	9	0	0	13	1	0	0	0	173	E9QA63	
ENSMUST00000084306	ENSMUSG00000028634	4	119733784	120138045	1	17	21	17	235	31	14	0	0	0	0	0	F7D7H6	
ENSMUST00000084307	ENSMUSG00000028637	4	119322893	119415521	-1	0	0	0	8	0	0	0	0	0	0	0	A8WHU1	
ENSMUST00000084309	ENSMUSG00000066058	4	119255414	119262438	1	2	0	8	5	0	0	0	0	0	0	0		Q9ET38
ENSMUST00000084313	ENSMUSG00000066061	4	118808797	118809944	-1	4	5	0	5	7	6	0	0	0	0	0	B2RVY8	
ENSMUST00000084315	ENSMUSG00000095218	4	118753595	118754536	-1	4	6	17	6	10	3	0	0	0	0	0	A2ACY7	
ENSMUST00000084319	ENSMUSG00000006392	4	118409337	118415782	1	0	0	0	0	0	0	33	108	80	56	48	Q9CY05	
ENSMUST00000084325	ENSMUSG00000028541	4	117869260	117883487	-1	24	15	52	37	24	11	0	0	0	0	0	B1ASJ2	Q9Z2Y2
ENSMUST00000084338	ENSMUSG00000028707	4	115915119	115939926	-1	1	17	58	202	3	2	0	0	0	0	0		Q91ZK4
ENSMUST00000084342	ENSMUSG00000063929	4	115600969	115621602	1	6	2	10	2	5	5	0	0	0	0	0	A2A8T1	
ENSMUST00000084343	ENSMUSG00000066071	4	115299046	115332815	1	15	11	7	19	8	3	0	0	0	1	0		Q91WL5
ENSMUST00000084345						25	26	221	42	18	18	2	5	4	0	2		
ENSMUST00000084354	ENSMUSG00000034401	4	111719984	111829184	1	0	7	3	0	0	2	121	95	59	0	0	A2AED8	
ENSMUST00000084366	ENSMUSG00000028559	4	109061145	109202272	-1	0	6	0	0	0	0	0	0	0	105	0		A2A8Z1
ENSMUST00000084368	ENSMUSG00000010021	11	114765388	114790739	1	20	5	30	0	20	21	0	8	3	0	0	A9XMT8	Q99PT9
ENSMUST00000084382	ENSMUSG00000066090	4	103017872	103026842	-1	3	4	13	3	3	0	0	0	0	0	0		Q9WUG6
ENSMUST00000084383	ENSMUSG00000031060	X	20617503	20650901	1	0	0	0	0	0	0	265	805	433	100	349		Q99KG3
ENSMUST00000084386	ENSMUSG00000035201	4	101834969	101844023	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UTC0	
ENSMUST00000084396	ENSMUSG00000010751	7	143634806	143649661	-1	0	1	0	0	0	1	0	0	3	7	8		Q9ER62
ENSMUST00000084412	ENSMUSG00000045777	7	142325837	142373753	-1	6	6	16	66	10	9	19	36	10	5	19		Q8BR26
ENSMUST00000084413	ENSMUSG00000066100	7	142296334	142297118	-1	3	0	4	0	0	0	0	0	0	0	0	J3QK63	
ENSMUST00000084414	ENSMUSG00000046248	7	142201364	142203015	1	0	0	0	0	0	3	0	0	0	0	0	E9QPH6	
ENSMUST00000084415	ENSMUSG00000066101	7	142189473	142190389	-1	12	9	87	104	11	1	0	0	0	0	0	D3Z4H5	
ENSMUST00000084418	ENSMUSG00000025147	7	142008553	142061034	-1	11	7	33	26	11	9	560	758	500	327	315		Q8VI63
ENSMUST00000084433	ENSMUSG00000038007	4	86874396	86934822	1	28	20	105	3	35	10	15	0	0	0	20		Q8VD53
ENSMUST00000084434	ENSMUSG00000025508	7	141447370	141451585	1	12	8	7	86	21	5	370	1850	951	264	616		P99027
ENSMUST00000084436	ENSMUSG00000060240	7	141426446	141429491	-1	0	0	0	0	12	3	0	2	0	0	0		Q9JKC6
ENSMUST00000084445						0	0	0	0	0	0	0	0	0	5	0		
ENSMUST00000084446	ENSMUSG00000038637	7	141194157	141210055	1	27	12	14	20	18	0	25	76	17	23	15	Q8BMW2	
ENSMUST00000084451						46	35	27	26	50	19	1	4	2	0	2		
ENSMUST00000084454	ENSMUSG00000066122	7	140690884	140691918	1	1	7	7	9	6	1	0	0	0	0	0	Q8VGM1	
ENSMUST00000084455	ENSMUSG00000096069	7	140637703	140638638	1	7	7	10	9	15	11	0	0	0	0	0	Q8VGM2	
ENSMUST00000084456	ENSMUSG00000094819	7	140646452	140652919	1	4	1	6	6	2	1	0	0	0	0	0	Q8VGL8	
ENSMUST00000084457	ENSMUSG00000095901	7	140574155	140575087	1	5	9	4	9	6	0	0	0	0	0	0	Q7TRT5	
ENSMUST00000084460	ENSMUSG00000025461	7	140218267	140231145	1	31	24	118	76	35	16	0	2	1	4	15	Q8CGY7	
ENSMUST00000084467						1	2	4	0	1	0	0	0	0	0	0		
ENSMUST00000084474	ENSMUSG00000049122	4	74013442	74202214	1	35	21	27	211	40	29	0	3	0	0	1		Q8BHD4
ENSMUST00000084475	ENSMUSG00000095341	4	73683516	73687558	1	0	3	0	7	27	0	0	0	0	0	0	Q3UTE2	
ENSMUST00000084479	ENSMUSG00000095935	4	73607881	73657291	1	0	2	0	19	28	0	0	0	0	0	0	F2Z478	
ENSMUST00000084480	ENSMUSG00000066137	4	73401032	73405072	-1	6	6	7	8	13	5	0	0	0	0	0	Q5RIS0	
ENSMUST00000084488	ENSMUSG00000058325	7	134670687	135173639	1	41	33	79	53	71	35	54	119	109	14	155		Q8BUR4
ENSMUST00000084489	ENSMUSG00000066141	4	71755643	71757965	-1	13	6	28	18	20	11	0	0	0	0	0	Q5SPI8	
ENSMUST00000084493	ENSMUSG00000025212	19	45047576	45056383	1	0	33	29	366	69	49	0	28	0	0	0	Q3U4F0	
ENSMUST00000084496	ENSMUSG00000028373	4	65380803	66404611	-1	97	39	179	1680	113	98	0	12	9	0	13	E9Q8T4	
ENSMUST00000084497	ENSMUSG00000030965	7	132859225	132885111	1	0	0	0	42	0	0	381	1264	707	522	275	Z4YJY0	
ENSMUST00000084500	ENSMUSG00000030934	7	132557475	132576398	-1	10	0	24	47	16	8	1364	2640	1549	3633	1242	Q3TG75	P29758
ENSMUST00000084501	ENSMUSG00000028370	4	65124174	65357509	1	75	57	68	117	60	42	0	0	0	1	5		Q8R4K8
ENSMUST00000084502	ENSMUSG00000066979	7	131560391	131571898	1	16	15	40	40	24	12	915	1404	748	687	462		Q9WVA3
ENSMUST00000084505	ENSMUSG00000030859	7	131334622	131336716	1	4	1	3	1	1	1	0	0	0	0	0		Q8CF27
ENSMUST00000084509	ENSMUSG00000047517	7	131032076	131121626	1	60	45	77	64	65	24	0	1	0	0	1	E9QPG8	
ENSMUST00000084510	ENSMUSG00000039137	4	63414910	63495991	-1	0	0	0	0	0	0	0	0	0	0	0		Q80VW5
ENSMUST00000084512	ENSMUSG00000065954	8	25154552	25201449	-1	0	0	11	90	14	0	532	1993	728	150	836		Q6Y685
ENSMUST00000084513	ENSMUSG00000030852	7	130577484	130764784	1	82	66	375	99	96	54	12	5	7	10	5	E9Q8T1	
ENSMUST00000084519	ENSMUSG00000042055	7	129591863	129635738	1	5	2	0	53	11	2	109	190	144	8	166	G5E8J3	
ENSMUST00000084521	ENSMUSG00000059810	4	62559847	62704001	1	0	0	18	30	26	7	0	0	3	0	0		Q9DC04
ENSMUST00000084524	ENSMUSG00000066148	4	62408797	62426990	1	54	36	106	72	60	28	136	334	172	51	167	Q059T9	Q9DAW6
ENSMUST00000084525	ENSMUSG00000066149	4	62383654	62408642	-1	0	0	0	0	0	0	320	940	304	940	159		Q99JP4
ENSMUST00000084526	ENSMUSG00000066150	4	62360727	62391769	1	26	19	18	35	18	4	679	1960	978	486	455		Q8K211
ENSMUST00000084527	ENSMUSG00000066151	4	62300342	62360548	-1	0	0	0	28	0	8	1260	1412	2361	259	1550		Q6P9Q6
ENSMUST00000084528	ENSMUSG00000066151	4	62300342	62360548	-1	20	16	57	18	18	3	29	55	67	7	83	Q80YW9	
ENSMUST00000084530	ENSMUSG00000066152	4	62262562	62298411	1	39	33	332	98	34	25	789	3466	1541	597	989	Q4KL43	Q9CPU9
ENSMUST00000084531	ENSMUSG00000066154	4	62083476	62087342	-1	5	2	4	2	0	2	0	0	0	11	0	Q3KQQ2	
ENSMUST00000084535	ENSMUSG00000050332	X	95420318	95444872	-1	57	48	109	394	63	24	19	63	40	9	37		Q7TS75
ENSMUST00000084544	ENSMUSG00000073834	4	60658466	60662411	-1	0	0	0	0	0	0	0	0	0	0	0	A2BIN0	
ENSMUST00000084548	ENSMUSG00000078683	4	60498012	60501960	-1	1	0	0	0	0	0	0	0	0	0	0	A2CEL0	
ENSMUST00000084563	ENSMUSG00000106715	7	127561390	127566940	1	4	0	25	0	0	0	151	639	160	57	223	E9Q8G3	
ENSMUST00000084564	ENSMUSG00000045639	7	127607031	127615797	-1	0	6	28	0	10	34	24	42	43	9	21		Q6A085
ENSMUST00000084578	ENSMUSG00000057280	4	58285960	58374303	1	0	0	0	0	0	0	0	0	0	0	0	Q32S50	Q61006
ENSMUST00000084586						3	2	15	5	8	1	20	84	19	0	21		
ENSMUST00000084589	ENSMUSG00000030720	7	126571207	126585817	-1	33	24	132	39	31	10	409	1039	533	22	407		Q61124
ENSMUST00000084593	ENSMUSG00000066178	4	136462250	136463977	1	38	22	223	281	42	25	0	1	1	0	1	E9Q8F9	
ENSMUST00000084598						3	0	16	3	4	0	2	9	2	16	2		
ENSMUST00000084599						78	51	273	57	59	32	46	195	96	8	151		
ENSMUST00000084614						2	0	0	0	0	0	1534	3743	1299	9098	1092		
ENSMUST00000084615	ENSMUSG00000066189	7	122670492	122769393	1	39	33	81	103	35	15	0	1	0	0	0		Q9JJV5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000084616	ENSMUSG00000066191	4	47015669	47057306	-1	0	0	0	63	11	11	7	19	14	2	0	E9PUD3	
ENSMUST00000084621	ENSMUSG00000039813	4	46604390	46650209	-1	24	15	67	235	40	17	1599	1352	1511	123	738		B1AVH7
ENSMUST00000084628	ENSMUSG00000046321	7	121391859	121501770	1	13	9	16	309	27	11	0	0	0	0	0		Q673U1
ENSMUST00000084640	ENSMUSG00000062017	7	120203961	120325352	1	6	11	17	14	12	2	0	0	0	0	0	E9Q8F8	
ENSMUST00000084644	ENSMUSG00000030924	7	119794006	119848943	1	0	0	0	0	0	0	0	8	0	4	5	D3Z3J7	
ENSMUST00000084646	ENSMUSG00000066196	4	43651335	43653594	-1	0	6	4	15	0	0	0	0	0	0	0	Q3V0Q6	
ENSMUST00000084647	ENSMUSG00000030945	7	119554469	119600694	1	0	2	1	1	0	1	0	0	0	0	0		Q8K0L3
ENSMUST00000084650	ENSMUSG00000066197	7	119144323	119184374	-1	8	5	7	16	10	2	0	0	0	0	0		Q80UC8
ENSMUST00000084653	ENSMUSG00000072963	11	53454804	53457110	-1	101	75	468	192	93	45	1	16	2	0	11	Q3UQ92	
ENSMUST00000084662	ENSMUSG00000036052	4	42949814	42959425	1	10	16	41	0	0	0	0	0	15	0	0	Q3TY13	O89114
ENSMUST00000084664	ENSMUSG00000045659	7	116123485	116308376	-1	0	0	9	2	0	1	0	0	0	1	14		Q3UIL6
ENSMUST00000084677	ENSMUSG00000096256	4	42033017	42034726	-1	0	0	4	0	0	2	0	0	0	0	0	Q6GQS8	
ENSMUST00000084695	ENSMUSG00000036073	4	41755228	41758695	1	0	1	0	0	0	0	147	138	64	27	34	A2AMS3	
ENSMUST00000084696	ENSMUSG00000038156	7	113765998	114043370	1	13	11	18	85	14	8	0	1	0	0	1	Q3UYD7	
ENSMUST00000084698	ENSMUSG00000066224	4	41723836	41731142	-1	0	0	0	11	0	0	0	0	0	0	0		A6PWV5
ENSMUST00000084701	ENSMUSG00000028444	4	41657498	41697089	-1	5	1	20	5	10	5	0	0	0	0	0	Q9D586	
ENSMUST00000084705	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	9	0	0	0	0	0	0	0	Q6PAQ8	
ENSMUST00000084715	ENSMUSG00000025241	9	123789510	123851899	-1	1261	910	4397	1056	518	320	0	0	0	0	0		Q8VDC1
ENSMUST00000084721	ENSMUSG00000078941	13	100650979	100666359	1	0	0	0	0	0	0	0	0	0	637	6		Q8VI33
ENSMUST00000084724	ENSMUSG00000028300	4	35191285	35226175	-1	7	13	0	3	9	11	18	60	10	12	22		Q6DFW0
ENSMUST00000084727	ENSMUSG00000061079	7	110061702	110095392	1	0	17	20	30	13	0	218	791	467	525	355		O70230
ENSMUST00000084731	ENSMUSG00000066232	7	110018425	110055114	1	7	4	5	38	9	1	193	1006	490	383	327		Q9EPL8
ENSMUST00000084733	ENSMUSG00000066233	9	123021326	123023490	1	9	10	17	41	10	9	62	326	52	45	32		Q9CR22
ENSMUST00000084734	ENSMUSG00000028264	4	34024874	34050191	-1	2	0	4	0	5	0	0	0	0	0	1	B1AWF1	
ENSMUST00000084736	ENSMUSG00000044288	4	33924593	33948831	1	31	29	0	20	19	15	0	0	0	0	1		P47746
ENSMUST00000084738	ENSMUSG00000031024	7	109523911	109617147	-1	3	12	0	8	15	4	0	0	0	0	0		Q924W7
ENSMUST00000084743	ENSMUSG00000066235	9	121981606	121996026	-1	24	17	54	165	32	13	10	8	6	5	5		Q8BW41
ENSMUST00000084747	ENSMUSG00000028278	4	32983037	33022180	1	0	0	0	28	0	0	0	0	0	0	0	B1AWT4	
ENSMUST00000084748	ENSMUSG00000040183	4	32804035	32950841	-1	8	0	0	44	12	0	0	5	2	0	2		Q69ZU8
ENSMUST00000084749	ENSMUSG00000040183	4	32804035	32950841	-1	0	25	13	0	11	21	0	0	0	0	0		Q69ZU8
ENSMUST00000084750	ENSMUSG00000040183	4	32804035	32950841	-1	0	0	0	0	0	0	0	0	0	0	0		Q69ZU8
ENSMUST00000084752	ENSMUSG00000066239	7	108893461	108894420	-1	6	7	5	15	7	3	0	0	0	0	0	K7N645	
ENSMUST00000084753	ENSMUSG00000066240	7	108868121	108869175	-1	4	7	38	5	6	4	0	0	0	0	0	Q7TRU4	
ENSMUST00000084754	ENSMUSG00000066241	7	108825065	108825997	-1	5	12	31	16	8	4	0	0	0	0	0	Q8VFZ6	
ENSMUST00000084756	ENSMUSG00000066242	7	107814580	107815506	1	10	8	21	5	7	4	0	0	0	0	0	L7N455	
ENSMUST00000084757	ENSMUSG00000094289	7	107844787	107845731	-1	7	4	7	10	3	2	0	0	0	0	0		Q8VF65
ENSMUST00000084760	ENSMUSG00000073893	7	107902627	107903709	1	10	6	15	0	4	1	0	0	0	0	0	A6H654	Q8VG43
ENSMUST00000084761	ENSMUSG00000095212	7	107933522	107934454	1	4	9	6	0	9	1	0	0	0	0	0		Q8VG44
ENSMUST00000084763	ENSMUSG00000016626	7	107166990	107198102	1	14	8	7	8	10	2	0	0	0	0	0		Q6B966
ENSMUST00000084770	ENSMUSG00000055373	4	25609332	25800244	-1	23	10	34	11	16	10	0	0	0	0	0	Q14AE3	O88819
ENSMUST00000084771	ENSMUSG00000071072	10	128058954	128077272	1	0	0	0	71	6	0	290	967	204	61	146	D3Z7C6	
ENSMUST00000084781	ENSMUSG00000040387	4	24612554	24851124	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7Q2	
ENSMUST00000084782	ENSMUSG00000030881	7	105634203	105640416	-1	0	0	0	0	0	0	163	161	126	54	117		Q8K221
ENSMUST00000084787	ENSMUSG00000034533	9	119608456	119719032	-1	47	61	108	63	79	35	0	0	0	0	0	K3W4P8	
ENSMUST00000084791	ENSMUSG00000066257	16	59344722	59345726	-1	3	5	0	0	3	0	0	0	0	0	0	Q8VGP9	
ENSMUST00000084797	ENSMUSG00000074028	9	119193002	119209105	-1	16	13	26	28	32	10	4	10	4	4	6		Q6A4L0
ENSMUST00000084799	ENSMUSG00000066262	7	104021372	104022316	-1	2	2	2	4	4	2	0	0	0	0	0	E9Q7P5	
ENSMUST00000084803	ENSMUSG00000033987	11	118021723	118129219	-1	77	43	5	9	0	0	47	125	1	14	9	E9Q7P0	
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ENSMUST00000084811	ENSMUSG00000066268	7	103121829	103122782	-1	5	8	7	6	8	2	0	0	0	0	0	Q8VH13	
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ENSMUST00000084816	ENSMUSG00000066272	7	102723489	102724510	-1	2	3	16	7	9	2	0	0	0	0	0	Q8VH14	
ENSMUST00000084817	ENSMUSG00000066273	7	102713455	102714411	-1	6	6	8	7	6	3	0	0	0	0	0	Q8VGX7	
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ENSMUST00000084824						5	11	7	13	11	4	0	0	0	0	0		
ENSMUST00000084828	ENSMUSG00000042029	12	116405402	116463531	1	21	23	45	73	30	10	80	117	168	74	98		Q6DFV1
ENSMUST00000084830	ENSMUSG00000066279	7	102111266	102116713	-1	22	13	47	182	47	21	0	1	0	0	1	B2RX82	
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ENSMUST00000084843	ENSMUSG00000070425	7	102065713	102096864	1	0	0	1	0	0	0	0	0	5	0	0	F8VQM8	
ENSMUST00000084846	ENSMUSG00000028809	4	135320484	135353321	-1	6	0	0	0	23	12	518	629	492	69	286	A2A8V9	
ENSMUST00000084852	ENSMUSG00000066306	7	101969843	102014959	1	54	37	125	115	86	30	1558	1297	2648	134	2577	E9Q7G0	
ENSMUST00000084853	ENSMUSG00000050627	9	114899341	114933987	-1	2	4	7	76	3	1	0	0	57	31	92		Q3ULJ0
ENSMUST00000084867	ENSMUSG00000032436	9	114756837	114781993	-1	0	0	0	202	6	0	88	266	24	22	60		Q9ESD6
ENSMUST00000084881	ENSMUSG00000032431	9	114375134	114390675	-1	11	0	8	198	14	5	35	37	20	45	110		Q9CYD3
ENSMUST00000084882	ENSMUSG00000006356	12	113140236	113145506	1	8	9	15	140	20	14	29	5	3	8	25	Q4FJU3	Q9DCT8
ENSMUST00000084885	ENSMUSG00000009741	9	113930934	113977199	1	0	15	0	0	0	0	886	3007	1469	103	1626		Q811S7
ENSMUST00000084891	ENSMUSG00000021143	12	113014508	113074401	1	85	61	194	104	87	47	685	856	734	85	753	E9Q7E9	
ENSMUST00000084892	ENSMUSG00000045205	4	11261315	11322137	-1	0	0	0	43	24	6	69	126	123	24	93		A2AJQ3
ENSMUST00000084894	ENSMUSG00000030653	7	101421691	101512829	1	26	14	84	0	0	0	5715	7216	4417	434	3305	Q5PR72	
ENSMUST00000084895	ENSMUSG00000032812	7	101348067	101412586	1	12	0	37	0	19	8	157	340	583	49	810		Q4LDD4
ENSMUST00000084896	ENSMUSG00000032812	7	101348067	101412586	1	17	9	5	15	26	13	3408	3715	3076	174	2217		Q4LDD4
ENSMUST00000084912	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	103	1	1	0	0	0	0	0	A2AL83	
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ENSMUST00000084926	ENSMUSG00000044037	9	110879870	110900530	1	0	0	60	71	1	0	0	0	0	0	0		
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ENSMUST00000084937	ENSMUSG00000045411	7	44246722	44252319	1	1	0	0	0	0	0	34	107	0	12	28	Q3TE80	
ENSMUST00000084941	ENSMUSG00000021288	12	111758849	111807844	1	0	0	0	57	3	4	41	191	141	33	227	Q8CD76	
ENSMUST00000084947	ENSMUSG00000060950	12	111678105	111683902	1	42	30	333	204	50	16	24	8	16	0	32		Q80XC2
ENSMUST00000084949	ENSMUSG00000066324	4	4762484	4793355	-1	5	10	38	331	18	8	332	693	516	115	255		Q80V26
ENSMUST00000084952	ENSMUSG00000032489	9	110476958	110525179	1	14	8	40	11	8	4	37	81	117	95	82		Q9WV04
ENSMUST00000084953	ENSMUSG00000007411	12	111574510	111656227	1	0	0	0	0	0	0	108	520	148	54	219		Q03141
ENSMUST00000084954	ENSMUSG00000060216	11	70432635	70440828	1	0	0	0	0	8	4	0	0	0	0	0	Q5F2D9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000084966	ENSMUSG00000067049	17	13108617	13131791	-1	119	121	722	151	105	73	3	11	5	0	8		Q710D3
ENSMUST00000084968	ENSMUSG00000037896	12	111039351	111115901	1	27	15	52	100	29	10	503	817	739	48	451	K3W4P9	
ENSMUST00000084974	ENSMUSG00000056458	12	110807798	110840939	-1	0	4	0	21	1	0	0	0	0	0	0	Q5M8P5	
ENSMUST00000084979	ENSMUSG00000030761	7	98051060	98119524	-1	3	0	7	21	30	35	0	34	54	0	93		
ENSMUST00000084984	ENSMUSG00000074062	9	109432316	109449140	-1	6	8	5	5	13	7	0	0	0	0	0	Q497Z0	
ENSMUST00000084985	ENSMUSG00000017843	12	110485739	110583061	1	29	24	0	0	27	0	595	565	1396	44	803		Q60996
ENSMUST00000084986	ENSMUSG00000042797	7	97724006	97738289	-1	8	16	15	176	15	9	1	6	0	8	2		Q8BHH1
ENSMUST00000085017	ENSMUSG00000030613	7	92561149	92582294	1	0	5	0	0	0	3	0	0	3	0	0		Q8C3X2
ENSMUST00000085018	ENSMUSG00000032599	9	108783796	108806337	1	12	7	0	0	0	0	0	91	0	0	0		Q80V72
ENSMUST00000085026	ENSMUSG00000021115	12	106010263	106077410	1	13	13	0	0	0	12	124	235	172	397	159	Q3UWH3	Q80X41
ENSMUST00000085027	ENSMUSG00000090113	17	25942233	25944961	-1	31	21	159	47	35	13	0	1	2	0	2		Q3UP44
ENSMUST00000085040	ENSMUSG00000050075	3	59096448	59101821	-1	9	4	8	3	4	3	9	66	11	54	43		Q8BG55
ENSMUST00000085043	ENSMUSG00000066359	12	105159690	105166622	1	6	7	24	17	6	7	0	0	0	0	0	Q3UWQ4	P56840
ENSMUST00000085044	ENSMUSG00000006676	9	108490602	108502337	1	0	0	0	0	0	0	9	17	116	0	42		Q3UJD6
ENSMUST00000085050	ENSMUSG00000066361	12	104146382	104153870	-1	12	9	42	25	27	5	0	0	0	27	1		P29621
ENSMUST00000085052	ENSMUSG00000066364	12	104127996	104139545	1	9	6	11	9	13	7	0	0	0	0	0	Q05A44	Q8BYY9
ENSMUST00000085054	ENSMUSG00000072849	12	103946931	103958975	-1	0	0	0	0	0	0	0	0	0	2	0		Q00898
ENSMUST00000085056	ENSMUSG00000066366	12	103853589	103863562	-1	0	0	0	0	0	0	0	0	0	151	0		P07758
ENSMUST00000085060	ENSMUSG00000032593	9	108053159	108055701	1	20	11	44	47	20	10	38	52	20	0	31		Q8C2S7
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ENSMUST00000085073	ENSMUSG00000066368	9	107928469	107932461	1	52	24	121	40	42	33	0	0	0	0	0	Q9D5V1	
ENSMUST00000085077	ENSMUSG00000015709	7	84246281	84409959	-1	57	44	96	48	66	28	0	0	3	0	5		Q61324
ENSMUST00000085079	ENSMUSG00000021198	12	102948859	103184065	1	0	13	10	0	0	0	1	0	0	0	0	G8JL63	
ENSMUST00000085086						3	2	9	153	8	1	1	1	0	0	2		
ENSMUST00000085092	ENSMUSG00000010066	9	107399612	107529343	1	2	61	217	0	44	7	0	0	0	0	0		Q6PHS9
ENSMUST00000085094	ENSMUSG00000066378	7	81855533	81855794	-1	24	38	223	63	24	10	3	3	5	0	2	F6Y577	
ENSMUST00000085096	ENSMUSG00000021182	12	100912700	101028983	-1	2	2	156	7	0	28	0	0	62	0	0		Q6VGS5
ENSMUST00000085102	ENSMUSG00000032578	9	107296026	107302784	1	14	4	5	78	11	13	101	91	75	1	24		Q62225
ENSMUST00000085108	ENSMUSG00000033713	12	99194980	99450111	-1	11	11	0	0	4	1	13	41	207	11	224		Q499D0
ENSMUST00000085109	ENSMUSG00000021013	12	98920574	98983238	1	9	2	0	63	8	0	0	0	4	37	8		Q8VD72
ENSMUST00000085111	ENSMUSG00000041009	9	106568319	106570996	-1	0	2	4	5	1	0	0	0	0	0	0	Q6P8Y2	
ENSMUST00000085113	ENSMUSG00000066382	9	106514573	106516010	1	4	2	4	3	7	2	0	0	0	0	1		Q9DAL7
ENSMUST00000085114	ENSMUSG00000066383	9	106499967	106502249	1	9	1	0	7	6	1	0	0	0	0	0		Q9D9K8
ENSMUST00000085116	ENSMUSG00000021009	12	98676741	98737405	-1	40	21	22	77	58	0	9	0	0	0	0	G5E8J4	
ENSMUST00000085128						2	2	8	5	5	5	0	1	1	5	0		
ENSMUST00000085133	ENSMUSG00000032570	9	105403539	105527319	-1	0	2	7	0	0	5	132	303	41	74	16	Q3UZR5	
ENSMUST00000085144	ENSMUSG00000066031	4	143789352	143795575	1	0	0	7	13	7	0	1	0	1	0	0	A2A8N2	
ENSMUST00000085163	ENSMUSG00000066407	13	73317844	73318143	1	0	3	0	0	0	2	0	0	5	0	0	J3QNN8	
ENSMUST00000085164	ENSMUSG00000053025	7	75114894	75309262	-1	37	18	24	3	11	0	0	0	0	0	2		Q8BG39
ENSMUST00000085169	ENSMUSG00000032537	9	101922128	102354693	-1	3	0	0	0	0	6	0	0	0	0	1		Q8CBF3
ENSMUST00000085177	ENSMUSG00000066415	9	101074101	101104800	1	34	17	33	16	22	10	987	4170	1358	137	810		Q69ZF8
ENSMUST00000085181	ENSMUSG00000040025	4	132184912	132212303	-1	0	7	17	3	2	2	43	71	16	13	14	E9PW90	
ENSMUST00000085192	ENSMUSG00000021238	12	84430723	84450950	-1	9	5	11	46	21	10	37	98	61	27	74		Q9EQ20
ENSMUST00000085206	ENSMUSG00000032449	9	97074961	97111157	-1	4	19	18	145	17	14	49	120	97	42	104		Q922G0
ENSMUST00000085215	ENSMUSG00000021224	12	83794034	83921934	-1	0	0	0	0	0	0	0	187	0	0	0	Q05BE7	
ENSMUST00000085217	ENSMUSG00000041440	9	96119362	96184608	1	9	10	6	84	16	9	46	26	92	6	45		Q8BX05
ENSMUST00000085222	ENSMUSG00000030523	7	64153835	64269775	1	6	0	22	0	17	14	0	0	0	0	0		Q2TV84
ENSMUST00000085228						0	1	0	2	4	1	0	0	0	0	0		
ENSMUST00000085238	ENSMUSG00000079055	12	81197915	81333180	-1	55	44	270	154	50	29	0	0	0	0	0	Q7TS90	
ENSMUST00000085240	ENSMUSG00000033676	7	57419692	57828802	1	27	22	67	51	33	8	0	1	0	0	0	F6ZYH6	
ENSMUST00000085242						2	2	0	13	4	2	0	0	0	0	0		
ENSMUST00000085245	ENSMUSG00000048833	12	80644215	80683341	1	46	49	54	41	60	32	350	574	451	81	396		Q8BFU1
ENSMUST00000085248	ENSMUSG00000062270	9	90091665	90114774	-1	0	0	0	0	3	0	70	345	61	133	29		P60762
ENSMUST00000085254	ENSMUSG00000066441	12	79174337	79192293	-1	5	0	13	1	3	6	37	116	83	74	46	Q9R1R8	
ENSMUST00000085255	ENSMUSG00000030447	7	55841745	55932602	1	0	0	0	0	0	0	54	401	685	159	602		
ENSMUST00000085256	ENSMUSG00000066442	9	89210676	89377713	1	0	0	0	7	0	0	118	495	157	448	171		Q9D110
ENSMUST00000085272	ENSMUSG00000039745	7	49759106	49773999	1	8	7	14	83	13	6	394	893	372	341	279		Q9Z2G9
ENSMUST00000085280	ENSMUSG00000063450	12	75818134	76110926	1	30	13	11	0	4	0	95	276	447	0	273	Q6DFZ2	
ENSMUST00000085289	ENSMUSG00000032343	9	80313330	80465481	-1	35	34	25	270	52	36	0	0	0	0	1		Q8R1W8
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ENSMUST00000085308	ENSMUSG00000066463	9	78311972	78314797	-1	0	0	5	0	0	2	0	0	0	0	0	F6ZJR3	
ENSMUST00000085311	ENSMUSG00000001366	9	78081499	78109065	-1	5	0	0	118	10	0	50	234	207	35	107		Q8BK06
ENSMUST00000085314	ENSMUSG00000021068	12	70011435	70111925	-1	21	14	71	28	37	9	1654	3352	3801	490	2314	E9Q4S3	
ENSMUST00000085319	ENSMUSG00000072972	12	81419443	81421946	-1	9	21	7	9	11	6	1	9	4	0	2	Q8CGQ2	
ENSMUST00000085330	ENSMUSG00000073291	X	7907693	7907835	-1	6	0	22	16	7	0	0	0	0	0	0	D3YU47	
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ENSMUST00000085340						0	4	22	5	6	5	0	3	0	9	3		
ENSMUST00000085350	ENSMUSG00000034563	9	72985429	73016340	1	0	0	0	0	0	0	2342	11734	5404	1652	4045		Q640L3
ENSMUST00000085351	ENSMUSG00000038239	7	45335269	45338968	1	46	29	109	818	59	30	0	1	3	0	0	G5E8J6	
ENSMUST00000085358	ENSMUSG00000090626	9	72450394	72492212	-1	33	53	80	34	44	12	4	16	8	5	17	Z4YJY6	
ENSMUST00000085364	ENSMUSG00000070568	7	45277513	45288998	1	0	4	0	0	4	0	0	0	0	0	0	Q3V0K1	
ENSMUST00000085365						5	3	45	4	7	3	4	22	0	11	7		
ENSMUST00000085368	ENSMUSG00000066487	12	59081019	59081900	1	6	6	17	95	18	7	6	2	2	0	0	J3QMG5	
ENSMUST00000085374	ENSMUSG00000070570	7	45163921	45176138	1	20	20	51	141	40	17	9	11	5	0	4		Q3TXX4
ENSMUST00000085375	ENSMUSG00000003423	7	45154398	45160064	1	0	0	0	9	0	0	376	452	294	99	215		Q9CQJ2
ENSMUST00000085377						2	0	3	26	1	0	16	121	11	15	50		
ENSMUST00000085379						7	1	5	4	1	0	0	0	0	0	0		
ENSMUST00000085383	ENSMUSG00000038406	7	45002948	45016363	-1	3	0	0	619	6	7	73	53	156	0	131		Q5U4C3
ENSMUST00000085385	ENSMUSG00000021027	12	55602929	55821167	-1	0	7	15	12	13	0	314	1254	782	193	725		Q6GYP7
ENSMUST00000085387						0	0	0	0	0	0	65	64	40	60	26		
ENSMUST00000085393	ENSMUSG00000011958	9	69989466	70008317	1	0	7	28	0	6	0	540	2636	1048	443	794	Q91VL0	
ENSMUST00000085399	ENSMUSG00000060279	7	44900374	44929490	-1	17	7	21	0	27	0	0	0	0	0	26		P17426
ENSMUST00000085404	ENSMUSG00000020956	12	51988312	52006501	-1	4	5	2	10	6	0	12	37	22	18	13		Q8BHA3

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ENSMUST00000085412	ENSMUSG00000020953	12	51593341	51605773	1	0	7	14	0	0	0	0	0	0	0	0		Q62507
ENSMUST00000085420	ENSMUSG00000032373	9	66713686	66766845	1	0	0	0	0	0	0	4	15	4	11	23	Q8K2J1	
ENSMUST00000085422	ENSMUSG00000066500	7	44708743	44719842	1	8	3	4	19	6	5	0	0	0	0	0		Q9DA16
ENSMUST00000085425	ENSMUSG00000035692	4	156199424	156200818	-1	24	26	23	41	31	36	70	518	94	401	271	Q4FJR9	Q64339
ENSMUST00000085427	ENSMUSG00000108632	7	5029018	5032771	1	7	7	25	0	15	0	185	115	135	31	142	H9KUY5	
ENSMUST00000085435	ENSMUSG00000003345	10	80622780	80640771	1	13	0	9	78	25	13	2659	2856	1959	305	1684		Q8BVP5
ENSMUST00000085450	ENSMUSG00000066515	7	44198191	44202352	1	9	7	17	9	14	4	0	0	0	0	0		P00756
ENSMUST00000085453	ENSMUSG00000041696	9	65398488	65414853	1	16	7	17	19	19	12	1	4	1	0	1		Q08AT1
ENSMUST00000085455	ENSMUSG00000066516	7	44102328	44106583	1	8	7	14	3	8	12	0	0	0	0	0	Q3UNG6	Q61759
ENSMUST00000085461	ENSMUSG00000064023	7	43797577	43803826	1	12	11	33	51	15	10	30	33	13	70	32	A0A0B6VRH9	Q61955
ENSMUST00000085469	ENSMUSG00000020573	12	32173473	32208659	-1	4	14	36	0	6	18	383	116	1225	112	821		Q9JHG7
ENSMUST00000085487	ENSMUSG00000020659	12	31484829	31499616	-1	0	0	22	34	1	0	22	106	55	4	38	E9QM14	
ENSMUST00000085513	ENSMUSG00000030421	7	37959992	38023551	-1	6	8	21	85	19	8	52	138	89	45	113		Q3TLD5
ENSMUST00000085519	ENSMUSG00000032249	9	62341293	62378812	1	6	6	17	25	3	7	663	2539	1124	2245	912		O35381
ENSMUST00000085546	ENSMUSG00000066551	5	149046702	149184489	-1	91	78	52	39	82	53	486	1144	374	491	175	Q58EV5	P63158
ENSMUST00000085548	ENSMUSG00000051611	17	37563228	37567094	-1	3	9	7	0	2	4	0	0	0	0	0	Q8C0S2	
ENSMUST00000085553	ENSMUSG00000020656	12	24572287	24617391	1	26	9	52	34	27	12	8	0	1	2	9		Q921D9
ENSMUST00000085554	ENSMUSG00000029651	5	147957320	148316065	1	0	0	2	0	0	0	2	19	0	14	0		Q3UHD3
ENSMUST00000085555	ENSMUSG00000016181	1	193091104	193130272	-1	53	45	90	567	67	0	16	23	0	0	50		
ENSMUST00000085556	ENSMUSG00000030494	7	35334170	35392289	1	0	0	0	0	0	0	0	0	0	0	0		Q8BWR8
ENSMUST00000085558	ENSMUSG00000029651	5	147957320	148316065	1	42	28	130	220	56	36	7	39	6	6	1		Q3UHD3
ENSMUST00000085573	ENSMUSG00000026637	1	191997205	192092559	-1	14	4	23	121	24	12	35	86	48	8	39	E9QMA6	
ENSMUST00000085585	ENSMUSG00000066568	7	34344646	34393315	-1	9	4	34	55	8	9	869	3185	1646	310	971		Q8K2F8
ENSMUST00000085589						1	1	8	2	1	1	0	2	2	7	0		
ENSMUST00000085591	ENSMUSG00000029644	5	147269959	147275848	1	27	18	77	340	38	23	0	2	0	0	0		P52946
ENSMUST00000085592	ENSMUSG00000066571	7	34236707	34313551	-1	29	19	50	0	0	26	56	86	150	22	237	Q8C5X1	
ENSMUST00000085614	ENSMUSG00000029640	5	146734809	146795006	-1	0	26	0	24	15	13	322	750	587	104	449		Q9D9M2
ENSMUST00000085618	ENSMUSG00000066583	7	34021483	34022881	1	4	3	8	2	1	0	0	0	0	0	0	Q91WB5	
ENSMUST00000085620	ENSMUSG00000066584	7	34011921	34013942	-1	0	3	8	2	0	0	0	0	0	0	0	Q8R1E9	
ENSMUST00000085623	ENSMUSG00000066586	7	33943002	33945040	-1	2	3	6	4	1	0	0	0	0	0	0	Q8JZX1	
ENSMUST00000085631						5	3	2	0	3	2	6	3	1	10	0		
ENSMUST00000085632						3	2	10	4	4	0	0	1	0	7	1		
ENSMUST00000085633	ENSMUSG00000026632	1	191045826	191062932	-1	3	0	0	0	0	0	3	20	0	0	0		Q3U1C6
ENSMUST00000085635	ENSMUSG00000066595	1	191005847	191026158	-1	0	0	0	71	0	0	214	328	457	52	324		B2RXV4
ENSMUST00000085636	ENSMUSG00000001248	7	31130127	31155896	-1	1	0	16	0	0	0	0	0	0	0	0	F8WJ74	
ENSMUST00000085651	ENSMUSG00000032336	9	58582240	58657955	1	0	0	0	0	0	0	445	1451	404	625	275		P97300
ENSMUST00000085658	ENSMUSG00000066607	9	58488603	58499742	1	13	17	28	324	36	17	0	0	0	0	2		Q8CD60
ENSMUST00000085661	ENSMUSG00000007812	5	145231715	145247302	1	6	0	2	23	3	4	56	91	67	62	60	F7AFH2	
ENSMUST00000085664	ENSMUSG00000096795	10	81704825	81726686	1	8	5	5	4	5	3	18	98	23	27	10	F7AFE4	
ENSMUST00000085668	ENSMUSG00000066647	7	30169875	30180209	1	163	89	1298	198	174	80	16	85	21	7	49	Q3UGK8	
ENSMUST00000085671	ENSMUSG00000055991	5	145204562	145221750	1	24	21	31	22	42	6	59	150	104	22	102		Q9Z1D8
ENSMUST00000085673	ENSMUSG00000036986	9	58218076	58249786	-1	0	0	0	31	0	0	3	0	134	0	222	A0A068EW80	Q60953
ENSMUST00000085677	ENSMUSG00000032327	9	58063788	58153996	1	0	0	0	12	0	0	0	0	0	0	23		
ENSMUST00000085678	ENSMUSG00000026608	1	188971095	189007841	-1	0	0	23	29	13	0	32	92	35	0	37		Q8BFX3
ENSMUST00000085679	ENSMUSG00000029622	5	145114215	145130705	1	54	72	207	147	61	31	6065	17252	6964	1595	4766		Q9WV32
ENSMUST00000085684	ENSMUSG00000038780	5	144876495	144965847	-1	0	22	35	51	45	0	407	576	539	62	375		Q9CUN6
ENSMUST00000085688	ENSMUSG00000060962	7	30763756	30781063	1	14	8	0	0	0	0	0	0	0	0	0	E9QLW8	
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ENSMUST00000085701	ENSMUSG00000066621	5	144194442	144223615	-1	34	34	135	65	65	42	481	572	444	29	420		Q80VP0
ENSMUST00000085702						10	3	6	4	5	3	1	0	0	1	1		
ENSMUST00000085704	ENSMUSG00000029618	5	144019804	144026670	-1	1	0	0	0	0	0	0	0	0	0	0		P51879
ENSMUST00000085708	ENSMUSG00000040033	10	128270576	128292849	1	21	14	75	70	19	11	653	2125	1072	152	1378	Q9QXJ2	
ENSMUST00000085709	ENSMUSG00000063849	9	57412668	57440114	-1	16	7	24	36	13	11	205	825	344	123	423		Q8BZB2
ENSMUST00000085711						4	0	6	4	4	0	1	1	0	3	0		
ENSMUST00000085715	ENSMUSG00000030397	7	19426075	19458494	-1	18	11	35	320	26	11	519	543	540	19	442		Q8CIP4
ENSMUST00000085720	ENSMUSG00000066629	12	12911986	12912369	1	2	5	8	25	6	0	3	3	0	7	1		
ENSMUST00000085724	ENSMUSG00000038576	1	182763860	182896591	1	18	11	28	47	22	5	0	0	0	0	0		Q8BH32
ENSMUST00000085733	ENSMUSG00000039296	5	143216316	143226890	-1	13	6	20	18	12	9	0	0	0	0	0		Q5IBH6
ENSMUST00000085735	ENSMUSG00000066632	12	10898566	10900296	-1	0	0	6	0	2	28	89	0	2	0	0		P09411
ENSMUST00000085741	ENSMUSG00000066637	12	9029997	9036394	1	3	3	4	40	4	7	65	216	80	155	31		Q9DAC7
ENSMUST00000085745	ENSMUSG00000066643	12	8973892	9028847	1	24	0	21	35	19	7	0	0	0	0	0		Q8BND3
ENSMUST00000085754	ENSMUSG00000032313	9	55326913	55438345	1	40	46	107	123	41	27	0	2	3	0	2		Q8BZB3
ENSMUST00000085758	ENSMUSG00000029576	5	142484839	142551098	-1	13	4	58	5	0	5	0	0	0	0	0		Q69Z89
ENSMUST00000085774	ENSMUSG00000039683	5	141241490	142215586	1	59	45	109	166	77	43	2	5	0	0	3		Q3UH53
ENSMUST00000085786	ENSMUSG00000036526	5	140872990	141000582	-1	37	25	86	91	59	24	43	57	37	9	135		Q8CIS0
ENSMUST00000085790	ENSMUSG00000037336	12	4862440	4874359	-1	4	16	0	8	0	0	18	38	13	10	33		Q3T9M1
ENSMUST00000085792	ENSMUSG00000050855	7	29833620	29853669	-1	0	8	18	0	3	6	1	10	0	6	1	Q8R2Q3	
ENSMUST00000085793	ENSMUSG00000051721	12	4843303	4856925	1	4	7	3	3	7	0	11	16	11	3	19		Q6NV72
ENSMUST00000085797	ENSMUSG00000066652	1	180893108	180899103	1	34	38	55	87	49	24	6	5	6	0	4		P57785
ENSMUST00000085803						0	0	5	46	0	0	21	0	0	65	0		
ENSMUST00000085804						7	5	28	3	6	3	0	3	0	0	0		
ENSMUST00000085809	ENSMUSG00000030583	7	29320372	29518641	-1	16	5	43	44	27	12	725	345	884	18	743	G3X9J0	
ENSMUST00000085814	ENSMUSG00000020647	12	4247363	4477182	-1	31	26	83	70	56	21	711	1519	1891	97	1414		P70365
ENSMUST00000085818	ENSMUSG00000046410	7	29221928	29232522	-1	128	106	181	384	162	127	270	800	609	50	423	Q3TBV4	
ENSMUST00000085819						0	0	17	0	0	0	0	0	0	0	0		
ENSMUST00000085826						15	20	29	62	33	16	2	2	10	0	12		
ENSMUST00000085835	ENSMUSG00000037337	7	28982854	29003279	1	18	12	31	81	34	9	561	1119	623	97	467		P70218
ENSMUST00000085840	ENSMUSG00000090100	2	120732816	120850604	-1	0	0	0	0	0	0	0	0	1	0	127		Q3UVR3
ENSMUST00000085851	ENSMUSG00000030595	7	28758251	28767512	-1	0	3	13	74	0	9	473	663	419	85	265		Q60778
ENSMUST00000085852	ENSMUSG00000058291	5	138603652	138619761	-1	0	6	0	0	0	0	13	29	47	56	0	Q8BLK6	
ENSMUST00000085856	ENSMUSG00000036898	5	138441468	138460694	1	39	30	183	44	44	17	24	157	22	63	33	Q6PCM4	
ENSMUST00000085861	ENSMUSG00000066671	1	174442159	174449602	1	3	0	1	0	5	5	0	0	0	0	0	E9Q050	
ENSMUST00000085862	ENSMUSG00000066672	1	174368919	174369848	1	4	2	0	2	2	3	0	0	0	0	0	F8VQB1	
ENSMUST00000085876	ENSMUSG00000066677	1	173673675	173698392	1	144	112	308	151	119	63	3	21	8	13	24		Q3V3Q4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000085885						1	4	0	2	1	4	0	0	0	0	0		
ENSMUST00000085886	ENSMUSG00000075599	5	138021261	138034664	1	53	23	194	62	58	34	0	0	0	0	0		Q9QYZ5
ENSMUST00000085894	ENSMUSG00000026546	1	172520801	172545870	1	11	8	9	19	19	7	12	17	20	14	13	Q9D9U9	
ENSMUST00000085901	ENSMUSG00000002409	7	28179469	28187294	1	0	0	0	141	0	0	267	323	229	0	160		Q9Z188
ENSMUST00000085909	ENSMUSG00000032076	9	47530173	47857637	1	0	0	0	0	0	3	0	0	0	0	1		Q8R5M8
ENSMUST00000085912	ENSMUSG00000038034	1	172261641	172319841	1	2	0	29	0	20	5	893	359	162	79	277		
ENSMUST00000085913	ENSMUSG00000007097	1	172271709	172298064	-1	60	40	87	96	39	33	1	0	3	0	6	Q3UHK5	Q6PIE5
ENSMUST00000085917	ENSMUSG00000004056	7	27591552	27640826	1	0	0	0	0	0	0	199	0	0	0	38	F8WHG5	
ENSMUST00000085919						4	5	0	2	3	1	0	0	0	0	0		
ENSMUST00000085929						84	60	181	1575	142	66	0	7	0	0	3		
ENSMUST00000085934	ENSMUSG00000023328	5	137287519	137294466	1	9	4	0	0	0	7	5	5	4	4	12	Q543Z1	P21836
ENSMUST00000085939	ENSMUSG00000066705	9	45370185	45396158	1	12	9	36	103	20	4	0	0	0	1	1		Q9D164
ENSMUST00000085941	ENSMUSG00000059518	5	136982164	136988021	-1	2	1	5	0	0	0	419	686	218	342	133		Q8R331
ENSMUST00000085944	ENSMUSG00000040614	7	26322473	26403700	-1	7	4	0	0	0	0	0	0	0	0	0		Q66X01
ENSMUST00000085948	ENSMUSG00000002602	7	25757273	25788705	-1	6	0	8	41	9	1	9	0	29	0	0	Q6PE80	
ENSMUST00000085949	ENSMUSG00000090889	14	54976933	54977025	1	1	0	0	0	1	0	0	0	0	0	0	F6XET4	
ENSMUST00000085953	ENSMUSG00000057229	7	25619414	25625551	1	13	5	32	50	16	8	72	268	92	20	148	Q8CA44	
ENSMUST00000085979						3	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000085984	ENSMUSG00000005378	5	135052957	135064959	-1	0	0	0	11	0	0	64	121	74	21	0	Q148S9	Q9CY21
ENSMUST00000085989	ENSMUSG00000066720	17	23682584	23684018	-1	17	10	32	76	30	10	0	0	0	0	0		Q9Z0S7
ENSMUST00000085992	ENSMUSG00000026564	1	166098148	166127922	-1	49	21	75	49	0	32	0	0	0	8	38		Q148W8
ENSMUST00000086002	ENSMUSG00000005763	1	165788681	165877277	1	0	1	1	3	0	4	0	0	0	0	0		P29020
ENSMUST00000086006	ENSMUSG00000087598	7	24193947	24211443	-1	24	35	67	27	33	11	0	10	2	0	5	Q99K53	
ENSMUST00000086010	ENSMUSG00000068962	7	24175060	24183188	1	9	11	41	15	7	7	0	0	2	0	0	Q3UTF4	
ENSMUST00000086012	ENSMUSG00000066723	7	24054774	24055691	1	2	2	0	0	4	3	0	0	0	0	0	Q8K3N5	
ENSMUST00000086013	ENSMUSG00000066724	7	23946649	23947237	-1	0	0	15	0	0	0	309	332	132	217	85		P56383
ENSMUST00000086023	ENSMUSG00000034040	5	130872082	131308497	-1	113	91	360	237	101	58	4	8	3	0	2	Q59J92	Q7TT15
ENSMUST00000086028	ENSMUSG00000026575	1	164304121	164437725	1	0	0	0	0	0	0	0	0	17	4	1	Q8BUH2	
ENSMUST00000086029	ENSMUSG00000060371	5	130369455	130847412	1	11	8	13	2	8	7	0	0	0	0	0	F8WHE1	
ENSMUST00000086032	ENSMUSG00000026577	1	164289800	164307489	-1	6	0	0	0	0	0	15	72	57	118	21		Q8R2X8
ENSMUST00000086040	ENSMUSG00000026579	1	164151838	164220277	1	34	20	81	56	41	24	1313	3288	3681	352	2823		O88783
ENSMUST00000086041	ENSMUSG00000061028	7	19581044	19604468	-1	17	10	26	327	25	11	204	632	297	43	356		Q8CFC7
ENSMUST00000086046	ENSMUSG00000029432	5	129725063	129758327	1	4	3	5	25	9	2	267	773	462	61	308	Q7TMG8	
ENSMUST00000086050	ENSMUSG00000095718	5	94314435	94317255	1	8	0	0	0	0	0	0	0	0	0	0	L7N456	
ENSMUST00000086056	ENSMUSG00000029423	5	128702524	128755474	1	91	46	114	476	135	49	1	0	3	0	1		Q9JMB7
ENSMUST00000086058	ENSMUSG00000071657	19	8837467	8848683	1	0	0	0	0	0	0	469	621	291	106	234		Q9Z2E9
ENSMUST00000086061	ENSMUSG00000066747	9	37918548	37919612	1	4	0	1	3	1	1	0	0	0	0	0	Q9EQA9	
ENSMUST00000086062	ENSMUSG00000066748	9	37897325	37898375	1	5	3	5	5	3	0	0	0	0	0	0	B2RQ58	Q60882
ENSMUST00000086063	ENSMUSG00000066749	9	37854820	37855755	1	2	6	8	3	3	2	0	0	0	0	0	Q8VF62	
ENSMUST00000086064	ENSMUSG00000066750	9	37803889	37804936	1	3	0	10	1	7	1	0	0	0	0	0	Q7TRE4	
ENSMUST00000086074	ENSMUSG00000040265	1	161982453	162478034	-1	33	13	10	20	8	12	0	0	0	0	1	E9QLL2	
ENSMUST00000086075	ENSMUSG00000037936	5	125277087	125341094	-1	0	0	29	207	20	13	928	1610	739	74	544	Q4FK30	Q61009
ENSMUST00000086083	ENSMUSG00000029478	5	125017153	125179219	-1	0	25	0	0	59	11	79	110	273	4	410	E9PY55	
ENSMUST00000086084	ENSMUSG00000066755	1	161494655	161505290	1	7	7	8	4	11	4	0	0	1	0	0		Q7TS55
ENSMUST00000086101	ENSMUSG00000043017	7	16906490	16910905	1	8	0	0	2	0	3	104	455	196	21	92	E9PY53	
ENSMUST00000086104	ENSMUSG00000041187	7	16842902	16870464	1	23	20	39	142	39	14	613	392	759	22	463		Q8BZ03
ENSMUST00000086112	ENSMUSG00000008036	7	16738410	16749294	1	5	3	8	48	9	2	2294	3659	1444	1045	771	Q3UJ76	P62743
ENSMUST00000086122	ENSMUSG00000066772	7	15479825	15639902	-1	16	9	76	44	41	21	0	1	0	0	0	Q3UT54	
ENSMUST00000086123	ENSMUSG00000029406	5	124118690	124249760	-1	32	36	31	84	11	15	28	36	18	5	35		Q6ZPQ6
ENSMUST00000086130	ENSMUSG00000026589	1	157506728	157568425	1	9	15	19	23	5	9	0	0	0	0	0		Q91XT4
ENSMUST00000086145	ENSMUSG00000074646	2	155973279	156007977	-1	0	0	0	11	0	3	0	0	0	0	0	B7ZCN5	
ENSMUST00000086148	ENSMUSG00000070811	7	13733505	13779636	1	8	4	0	2	1	0	0	0	0	0	0	Q3UEP5	
ENSMUST00000086153	ENSMUSG00000033557	1	156678532	156719086	-1	22	18	37	20	23	17	49	608	434	0	246		Q8VCS3
ENSMUST00000086165	ENSMUSG00000054453	X	9885622	9994543	1	0	7	2	0	2	0	0	0	0	0	0		Q80T23
ENSMUST00000086167	ENSMUSG00000042185	9	31386192	31421333	1	0	0	0	34	0	0	110	253	238	35	140		Q6PIJ4
ENSMUST00000086195	ENSMUSG00000066797	1	154201187	154205689	1	20	13	35	281	26	10	0	0	0	0	0	D3Z0W3	
ENSMUST00000086198	ENSMUSG00000035024	9	27030175	27095311	1	0	0	0	0	13	2	0	0	0	0	0	Q80W41	
ENSMUST00000086199	ENSMUSG00000026473	1	153899944	153909723	1	23	10	60	28	42	22	3126	5025	3616	739	2851		P15105
ENSMUST00000086200	ENSMUSG00000029475	5	122870665	122989823	-1	7	0	0	0	0	0	0	0	0	0	45	E9QL25	
ENSMUST00000086209	ENSMUSG00000066800	1	153749426	153764221	1	10	13	13	5	14	9	0	81	445	0	437	B2RQP1	Q05921
ENSMUST00000086210	ENSMUSG00000096593	7	12615233	12636134	-1	14	6	26	8	18	2	0	0	0	0	0	K7N649	
ENSMUST00000086216	ENSMUSG00000029472	5	122787459	122821339	-1	36	23	36	154	40	19	1152	2365	1718	388	1190		Q8BTZ4
ENSMUST00000086228	ENSMUSG00000066803	7	12361808	12362764	-1	3	4	4	4	0	1	0	0	0	0	0	Q8R284	
ENSMUST00000086229	ENSMUSG00000066804	7	12321180	12322175	-1	2	3	2	0	1	2	0	0	0	0	0	Q8R287	
ENSMUST00000086232	ENSMUSG00000094078	7	12259759	12260679	-1	0	0	0	1	0	0	0	0	0	0	0	Q8R286	
ENSMUST00000086233						3	1	0	1	3	0	0	0	0	0	0		
ENSMUST00000086236						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000086238	ENSMUSG00000066810	9	25089422	25089490	1	298	140	265	9822	574	354	0	0	0	0	0	F6VC88	
ENSMUST00000086247	ENSMUSG00000029468	5	122643911	122691432	1	3	3	8	4	6	3	0	7	2	27	7	Q6P5P0	
ENSMUST00000086248	ENSMUSG00000070837	7	6995443	7002945	1	8	7	19	16	29	0	0	0	0	0	0	E9QL04	
ENSMUST00000086267						15	13	30	30	10	14	477	0	644	177	739		
ENSMUST00000086274	ENSMUSG00000073290	X	7909542	7909927	1	12	13	9	12	9	1	1	6	9	0	9	F6VBM2	
ENSMUST00000086278	ENSMUSG00000066829	9	22276748	22307638	-1	16	10	21	76	15	8	46	208	92	84	62	Q99K45	
ENSMUST00000086281	ENSMUSG00000062794	9	22247430	22259895	-1	34	25	50	79	33	15	4	16	8	3	6	E9PWP1	
ENSMUST00000086282	ENSMUSG00000070844	7	8183265	8200320	-1	29	23	67	41	50	34	0	0	0	0	0	O35192	
ENSMUST00000086294	ENSMUSG00000004455	5	122158278	122175273	1	0	0	0	16	0	0	0	0	131	0	0		P63087
ENSMUST00000086297	ENSMUSG00000066820	7	5480641	5493851	-1	9	10	5	8	17	5	0	0	0	0	0	L7N203	
ENSMUST00000086298	ENSMUSG00000094606	7	10037235	10053178	-1	11	9	0	7	11	0	0	0	0	0	0	K7N652	
ENSMUST00000086310	ENSMUSG00000042594	5	121815488	121837646	-1	0	14	22	89	12	0	932	710	1247	83	877		O09039
ENSMUST00000086317	ENSMUSG00000042589	5	121856366	122050102	-1	6	11	0	0	0	0	0	0	0	0	0		P70298
ENSMUST00000086318	ENSMUSG00000096228	7	6480216	6486813	-1	5	4	11	6	8	2	0	0	0	0	0		Q60889
ENSMUST00000086319	ENSMUSG00000093877	7	6501286	6502325	-1	16	3	0	11	8	5	0	0	0	0	0	F6VB59	
ENSMUST00000086323	ENSMUSG00000055150	7	6371364	6379491	1	3	0	15	0	0	3	6	0	0	0	7	Q8BJ21	
ENSMUST00000086325	ENSMUSG00000040097	17	23755423	23771591	-1	0	0	0	146	9	4	97	53	62	8	76		Q8CI03

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000086327	ENSMUSG00000054893	7	6286579	6307883	1	12	0	4	23	0	11	7	0	0	0	7		Q2TL60
ENSMUST00000086338	ENSMUSG00000066850	7	6007750	6011010	-1	366	353	393	359	486	255	6	31	22	13	40	Q9EPS7	
ENSMUST00000086341	ENSMUSG00000015721	7	23385889	23441922	1	0	0	35	0	10	7	0	0	0	0	0		Q9R1M5
ENSMUST00000086349	ENSMUSG00000051184	7	5015501	5018486	1	6	3	8	28	17	4	438	482	282	85	171		Q9D0B1
ENSMUST00000086353	ENSMUSG00000040528	11	106751226	106768794	1	0	0	0	0	9	0	183	1730	402	797	207		Q3TB92
ENSMUST00000086361	ENSMUSG00000057191	9	21526176	21545333	1	5	0	31	34	16	9	8286	14998	6618	2392	5053	A0A0B4J1G2	
ENSMUST00000086363	ENSMUSG00000046456	7	4706832	4725249	-1	4	3	14	9	2	3	14	19	8	4	17		Q8R218
ENSMUST00000086364	ENSMUSG00000046456	7	4706832	4725249	-1	10	19	46	92	21	10	6	15	3	0	9		Q8R218
ENSMUST00000086368	ENSMUSG00000066861	5	120876142	120887613	-1	13	8	14	9	20	5	25	74	10	6	12	Q8K469	
ENSMUST00000086370	ENSMUSG00000026831	2	28462001	28466332	-1	0	2	11	12	13	1	0	0	0	0	0		Q5BN45
ENSMUST00000086372	ENSMUSG00000006154	7	4460674	4480487	1	0	0	0	0	0	0	0	0	0	0	0		Q8R5F8
ENSMUST00000086374	ENSMUSG00000096472	9	21288463	21291209	-1	10	11	39	89	10	11	5407	8426	3485	1769	2350		Q60773
ENSMUST00000086377	ENSMUSG00000029605	5	120812635	120824163	1	177	27	65	256	110	158	0	0	0	0	0	V5IRT6	
ENSMUST00000086395	ENSMUSG00000052759	1	136259797	136260873	-1	1	0	1	254	12	3	0	0	0	0	1		P0C5I1
ENSMUST00000086399	ENSMUSG00000037405	9	21015960	21028797	1	18	13	41	64	40	16	285	477	290	40	341	Q3U8M7	P13597
ENSMUST00000086400	ENSMUSG00000055541	7	4003402	4063204	-1	0	0	0	1	0	4	0	164	0	0	0	G8JL64	
ENSMUST00000086401	ENSMUSG00000055541	7	4003402	4063204	-1	0	0	0	8	0	4	14	213	114	93	28		Q8BG84
ENSMUST00000086421	ENSMUSG00000066877	1	43444579	43570515	1	23	11	56	82	33	8	16	38	12	7	84		O55033
ENSMUST00000086423	ENSMUSG00000066878	17	89908511	89910449	-1	17	41	23	30	54	11	444	696	595	1378	422	Q52L97	P52293
ENSMUST00000086430	ENSMUSG00000026042	1	45374321	45503282	-1	18	12	11	7	18	7	0	0	0	21	50		Q3U962
ENSMUST00000086444	ENSMUSG00000073557	1	134754658	134955942	-1	0	0	14	6	8	0	0	0	0	0	0	A6H644	
ENSMUST00000086451	ENSMUSG00000029361	5	117781032	117958840	1	6	13	7	5	18	13	0	0	0	0	0	S4R255	
ENSMUST00000086458	ENSMUSG00000066892	9	20618118	20644767	-1	0	0	0	0	0	0	129	299	115	47	72		
ENSMUST00000086459	ENSMUSG00000066892	9	20618118	20644767	-1	0	0	0	1	1	0	105	304	83	16	216		Q9EPX5
ENSMUST00000086461	ENSMUSG00000029363	5	117378103	117389047	-1	25	16	42	28	20	8	134	210	171	42	127	Q5HZI8	Q9D0F6
ENSMUST00000086464	ENSMUSG00000066894	5	117319083	117355005	1	0	0	0	0	0	0	9	0	0	0	25	E9PVW4	
ENSMUST00000086465	ENSMUSG00000042429	1	134199223	134235431	-1	32	28	145	36	53	9	0	13	5	0	6		Q60612
ENSMUST00000086470	ENSMUSG00000031374	X	73411096	73428385	1	7	3	3	2	1	2	0	0	0	0	0	Q4VAD4	
ENSMUST00000086471	ENSMUSG00000066900	5	117091680	117116113	-1	13	0	28	53	26	17	1605	2442	1131	342	1185		Q8BR65
ENSMUST00000086473	ENSMUSG00000066896	9	20313892	20336094	-1	7	3	8	3	5	2	0	0	0	0	0		Q0VAX9
ENSMUST00000086474	ENSMUSG00000066897	9	20237162	20260913	1	0	1	1	2	1	0	0	0	0	0	0	E9PVW2	
ENSMUST00000086475	ENSMUSG00000026450	1	134111242	134151540	1	0	0	7	0	4	0	30	13	9	4	2	B2RS82	Q9D7Q1
ENSMUST00000086476	ENSMUSG00000066899	9	20170634	20171569	-1	1	5	2	1	0	5	0	0	0	0	0	Q8VGG4	
ENSMUST00000086479	ENSMUSG00000065952	8	3567990	3584939	1	12	2	61	7	12	9	0	0	0	0	0	Q8C7T0	
ENSMUST00000086480	ENSMUSG00000095448	9	19808320	19809249	1	0	0	4	9	1	0	0	0	0	0	0	Q7TRF5	
ENSMUST00000086482	ENSMUSG00000066905	9	19845623	19849747	-1	5	0	2	0	2	3	0	0	0	0	0	Q8VFF7	
ENSMUST00000086483	ENSMUSG00000043913	5	116124641	116288985	-1	246	192	217	189	346	165	8	7	12	2	27		
ENSMUST00000086492	ENSMUSG00000095525	9	18987990	18988928	1	0	0	3	0	1	3	0	0	0	0	0	Q7TRG8	
ENSMUST00000086493						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000086496	ENSMUSG00000066914	9	18932467	18945092	-1	0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000086502						46	23	265	108	43	9	6	9	5	5	2		
ENSMUST00000086508						6	0	35	6	11	7	0	0	0	1	0		
ENSMUST00000086519	ENSMUSG00000067274	5	115559467	115563727	1	6	14	31	98	25	5	7936	10681	7733	7734	4339	Q5M8R8	P14869
ENSMUST00000086521	ENSMUSG00000053024	1	132509427	132543256	-1	0	0	0	121	0	0	0	1	0	0	1		Q61330
ENSMUST00000086523	ENSMUSG00000029528	5	115506676	115555987	1	0	0	8	44	8	0	1117	298	1445	50	855	F8VQ28	
ENSMUST00000086535	ENSMUSG00000073702	1	39367842	39371911	1	3	9	5	50	5	3	78	401	60	156	26	Q5M9K9	P62900
ENSMUST00000086538	ENSMUSG00000054640	17	81388691	81649607	-1	0	0	0	0	0	0	0	0	0	0	0	G3X9J1	
ENSMUST00000086544	ENSMUSG00000066936	1	132229048	132229767	-1	4	4	10	2	5	4	0	0	0	0	0	Q3V432	
ENSMUST00000086545	ENSMUSG00000033966	17	80523550	80563834	-1	6	15	15	16	11	11	9	43	23	10	11		Q3TZA2
ENSMUST00000086549	ENSMUSG00000066938	17	80373218	80373541	-1	0	0	0	68	0	0	0	0	0	0	0	Q8BSD7	
ENSMUST00000086555	ENSMUSG00000035051	17	80238304	80290476	-1	28	24	41	0	33	17	88	159	164	0	212		Q6P5D3
ENSMUST00000086556	ENSMUSG00000026436	1	132007607	132032612	1	26	16	88	60	22	14	291	362	846	47	615		P41158
ENSMUST00000086559	ENSMUSG00000013275	1	131827493	131848865	1	32	39	88	207	60	30	447	910	671	94	705		Q8BJA2
ENSMUST00000086563	ENSMUSG00000028331	4	46376505	46389437	-1	0	0	0	0	0	0	0	0	0	0	0		Q562D6
ENSMUST00000086564	ENSMUSG00000041890	5	114727407	114775517	-1	0	0	0	0	0	0	586	436	610	145	583	E9PVA6	
ENSMUST00000086570	ENSMUSG00000066944	17	79626677	79628681	1	7	5	3	7	3	5	0	0	3	0	0	G3X9J2	
ENSMUST00000086580	ENSMUSG00000053110	9	7931999	8004596	-1	18	0	22	0	0	8	0	1	0	17	39		P46938
ENSMUST00000086596						14	2	9	0	4	5	0	11	0	9	0		
ENSMUST00000086599	ENSMUSG00000042096	5	114003703	114025682	1	8	5	0	0	0	0	0	0	0	2	0	Q91WH3	
ENSMUST00000086601						0	0	6	3	4	0	0	0	0	0	0		
ENSMUST00000086606						0	0	2	2	1	0	0	5	0	0	0		
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ENSMUST00000086615	ENSMUSG00000066964	5	113226909	113239263	1	29	12	61	11	33	6	0	0	0	0	1		Q3UUA0
ENSMUST00000086617	ENSMUSG00000072720	5	112688876	112896362	-1	31	26	110	183	76	29	0	0	0	0	0	E9PV66	
ENSMUST00000086629	ENSMUSG00000066975	5	112246493	112252518	-1	5	2	7	0	8	1	6	13	0	8	5	Q3V1A0	Q9JJV0
ENSMUST00000086635	ENSMUSG00000050017	5	111330763	111388359	1	18	19	34	79	16	12	426	1312	653	136	484		P53811
ENSMUST00000086639	ENSMUSG00000055471	17	71869442	72603709	-1	38	28	39	369	72	31	0	0	0	0	0		P97793
ENSMUST00000086643	ENSMUSG00000029507	5	110773667	110780659	-1	0	0	0	0	0	0	0	0	0	0	0	H7BX59	
ENSMUST00000086672	ENSMUSG00000066990	4	97182840	97183166	-1	61	62	198	43	66	25	0	5	1	0	1	Q3V0S1	
ENSMUST00000086674	ENSMUSG00000029501	5	110231004	110256651	1	0	7	0	155	0	2	0	0	0	0	0		Q6P1H6
ENSMUST00000086675	ENSMUSG00000073388	17	46889216	46890405	-1	9	4	13	220	22	6	1	1	6	0	2	Q8CA87	
ENSMUST00000086686	ENSMUSG00000023284	5	110110092	110129794	1	0	0	0	0	0	0	0	0	0	9	0	E9QAH2	
ENSMUST00000086687	ENSMUSG00000064247	5	110099969	110105953	1	0	0	0	2	9	0	0	0	0	0	0	G3X9J3	
ENSMUST00000086690	ENSMUSG00000067001	1	107399655	107452689	1	3	4	8	3	7	1	0	0	0	1	0		Q9D695
ENSMUST00000086693	ENSMUSG00000052105	17	66336982	66449750	-1	12	3	0	483	40	4	0	0	0	0	8		Q3UHU5
ENSMUST00000086694	ENSMUSG00000073602	1	107153940	107278361	-1	0	0	0	0	0	0	0	0	0	0	0	Q9D1Q5	
ENSMUST00000086701	ENSMUSG00000067006	1	106861173	106883348	1	0	0	1	0	5	0	0	0	0	0	0		P70124
ENSMUST00000086721	ENSMUSG00000026319	1	105663861	105755191	1	0	0	0	0	0	0	127	430	273	85	259	G3X9J4	
ENSMUST00000086722	ENSMUSG00000045036	17	65256005	65540782	-1	10	0	0	8	0	6	0	0	0	0	0		Q5K6N0
ENSMUST00000086723	ENSMUSG00000024085	17	64600736	64755110	1	27	22	32	629	42	22	2348	5317	5933	364	3153		P27046
ENSMUST00000086725						22	0	0	0	4	0	105	212	19	59	62		
ENSMUST00000086738	ENSMUSG00000067028	1	99772765	100485942	1	16	11	9	7	12	9	0	0	0	0	0		Q0V8T8
ENSMUST00000086739						0	0	2	2	2	0	6	2	6	2	2		
ENSMUST00000086763	ENSMUSG00000004730	17	57358686	57483529	1	0	0	26	19	14	0	207	629	121	397	371	Q3U9R0	Q61549

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000086764	ENSMUSG00000067038	19	59322290	59322783	1	14	21	0	60	19	9	1770	4373	1921	8847	1087	Q6ZWZ6	
ENSMUST00000086787	ENSMUSG00000055602	17	13061104	13082481	1	12	0	20	2	7	4	0	0	0	2	0	E9PYJ0	
ENSMUST00000086795	ENSMUSG00000034384	5	106452523	106458166	-1	21	30	241	380	27	27	0	1	2	0	0		Q8VIB5
ENSMUST00000086801	ENSMUSG00000024206	17	56775897	56831008	-1	26	0	39	63	35	0	968	491	733	78	727		P48379
ENSMUST00000086819	ENSMUSG00000014602	1	93015464	93101951	-1	0	0	0	0	0	0	2	0	0	0	2	Q6TA13	
ENSMUST00000086828	ENSMUSG00000013236	17	56412431	56476483	-1	65	35	118	83	66	22	33	50	29	17	148		B0V2N1
ENSMUST00000086829	ENSMUSG00000003452	6	149408886	149563329	1	9	11	14	27	18	12	0	3	1	0	0		Q8BR07
ENSMUST00000086830						3	7	7	6	4	1	0	0	0	0	0		
ENSMUST00000086831	ENSMUSG00000034462	5	104459450	104505819	1	34	26	45	94	28	8	11	50	24	12	75		O35245
ENSMUST00000086833	ENSMUSG00000029304	5	104435118	104441050	1	2	0	0	1	0	2	0	41	0	0	0	F8WIP8	
ENSMUST00000086835	ENSMUSG00000024201	17	56326062	56402870	1	0	0	0	0	0	0	49	0	10	0	0	B0V2M9	
ENSMUST00000086837	ENSMUSG00000067064	1	92479681	92485113	-1	9	7	9	7	12	9	0	0	0	0	0	Q8VGU4	
ENSMUST00000086843	ENSMUSG00000026311	1	91540544	91559589	1	0	1	19	70	2	5	36	19	31	0	7	Q3U5A0	Q9WV74
ENSMUST00000086844	ENSMUSG00000000782	11	52252371	52283014	-1	17	14	25	4	5	14	229	305	119	33	398	Q80UF1	Q00417
ENSMUST00000086851	ENSMUSG00000067071	1	91411483	91414038	-1	0	8	1	0	0	0	345	380	217	80	173		Q9JHE6
ENSMUST00000086854	ENSMUSG00000046709	5	102907948	103211334	-1	0	2	12	7	0	0	0	0	0	0	0	Q80W80	
ENSMUST00000086861	ENSMUSG00000047443	1	91366430	91374217	1	19	19	59	226	17	11	0	1	0	0	2		Q6PGN1
ENSMUST00000086869	ENSMUSG00000003208	17	55959187	55967949	1	16	11	39	22	29	5	113	204	109	54	85		Q9D6J3
ENSMUST00000086876	ENSMUSG00000024174	17	55652025	55712628	-1	851	722	2029	902	1171	597	33	168	67	56	93	H7BX60	
ENSMUST00000086878	ENSMUSG00000024172	17	55445382	55514581	1	4	3	3	5	4	1	0	0	0	0	0	B2RQY9	Q76K27
ENSMUST00000086880	ENSMUSG00000049047	X	134756595	134761455	1	17	9	48	23	28	8	65	200	76	110	58		Q8BHS6
ENSMUST00000086882	ENSMUSG00000067081	1	89950220	90014666	-1	617	630	774	860	803	408	155	559	165	41	236		Q8VHA6
ENSMUST00000086884	ENSMUSG00000049047	X	134756595	134761455	1	0	0	10	19	14	0	0	11	21	0	28		Q8BHS6
ENSMUST00000086887	ENSMUSG00000067085	19	53371566	53371766	-1	0	1	0	0	1	0	74	65	129	34	91	F6QEY5	
ENSMUST00000086896	ENSMUSG00000064065	10	6885796	7052478	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UX69	
ENSMUST00000086900	ENSMUSG00000029328	5	100033577	100039664	-1	0	0	0	198	10	6	0	0	6	28	13	D3YTQ3	
ENSMUST00000086909	ENSMUSG00000036377	5	76656512	76873554	1	26	44	291	150	34	16	5	3	9	2	8	Q3UP88	
ENSMUST00000086918						3	2	5	5	3	2	0	3	2	2	0		
ENSMUST00000086923	ENSMUSG00000025064	19	47646344	47692094	-1	1	31	0	0	8	20	1	7	2	0	2		Q07563
ENSMUST00000086932	ENSMUSG00000023990	17	47737030	47792419	1	0	0	3	149	8	3	584	1009	608	80	549		Q9R210
ENSMUST00000086950	ENSMUSG00000094043	5	95590599	95594875	-1	0	0	0	0	0	0	0	0	0	0	0	L7N204	
ENSMUST00000086958						11	6	8	10	13	7	0	2	0	2	0		
ENSMUST00000086960	ENSMUSG00000067122	13	111592785	111592856	1	0	1	3	9	0	1	0	0	0	0	0	F6QE68	
ENSMUST00000086961	ENSMUSG00000025041	19	46886831	47015153	-1	17	12	24	0	28	14	0	0	0	0	0	G3X9J6	
ENSMUST00000086969	ENSMUSG00000025227	19	46341121	46375252	1	0	0	0	68	6	3	278	59	229	23	30		Q6PDE8
ENSMUST00000086975	ENSMUSG00000049608	1	85938318	85961007	-1	17	23	44	53	52	23	138	377	284	94	120		Q3UJF0
ENSMUST00000086978	ENSMUSG00000029403	5	92006074	92043883	-1	0	11	0	44	7	0	0	56	0	23	42	Q149A0	Q9QUK0
ENSMUST00000086993	ENSMUSG00000025221	19	45791839	45816061	-1	1	4	3	3	0	0	0	1	0	0	0	Q3YAA4	Q9JJ69
ENSMUST00000087012	ENSMUSG00000067144	17	46432185	46438477	-1	11	7	51	41	27	9	0	0	0	2	0		
ENSMUST00000087016	ENSMUSG00000031355	X	168795099	169304435	1	0	0	0	0	2	0	0	0	0	2	0	A2ALX6	
ENSMUST00000087026	ENSMUSG00000067148	17	46243920	46248054	-1	11	4	16	37	7	3	161	172	129	199	121		P52432
ENSMUST00000087031	ENSMUSG00000067150	17	46202855	46242299	1	34	23	64	63	31	16	186	337	321	51	255		Q924C1
ENSMUST00000087033	ENSMUSG00000067149	5	88519809	88527891	-1	4	6	0	1	3	1	7	7	5	340	240		P01592
ENSMUST00000087043	ENSMUSG00000029281	5	88086556	88109053	1	2	0	0	0	1	0	0	0	0	0	0		O35985
ENSMUST00000087050	ENSMUSG00000067158	1	82448423	82586849	-1	44	31	53	281	88	44	0	4	3	0	5		Q9QZR9
ENSMUST00000087052	ENSMUSG00000028218	4	12153409	12172015	-1	2	0	0	0	0	0	2	10	0	0	0	Z4YJZ2	
ENSMUST00000087085	ENSMUSG00000059493	X	161833296	162159730	-1	52	29	25	270	60	23	0	2	0	0	5	B1AV60	
ENSMUST00000087086	ENSMUSG00000004872	1	78101267	78197134	-1	16	0	54	312	48	0	0	0	0	0	0		P24610
ENSMUST00000087090	ENSMUSG00000000037	X	161117193	161258213	1	3	4	8	8	8	3	0	0	0	0	0	B1AVB2	
ENSMUST00000087092	ENSMUSG00000067173	7	47980837	47982095	-1	8	5	12	14	5	1	0	0	0	0	0	W8W3F5	Q91WW2
ENSMUST00000087104	ENSMUSG00000031292	X	160771923	160994704	-1	11	3	56	17	7	5	1	4	4	0	4		Q3UTQ8
ENSMUST00000087114	ENSMUSG00000023919	17	40923051	40935047	-1	3	5	6	11	12	7	52	300	116	187	58		Q9CPQ5
ENSMUST00000087122	ENSMUSG00000026207	1	75375297	75432320	1	85	57	200	1409	153	64	0	0	0	0	0	E9QQ25	
ENSMUST00000087123	ENSMUSG00000042532	19	42247574	42270348	1	0	0	43	160	45	0	0	1	1	0	0		Q9D428
ENSMUST00000087128	ENSMUSG00000067186	17	38130249	38131190	-1	3	5	9	2	4	0	0	0	0	0	0	Q7TRI8	
ENSMUST00000087129	ENSMUSG00000094878	17	38067173	38068126	1	5	5	0	1	5	4	0	0	0	0	0	Q8VFC1	
ENSMUST00000087133	ENSMUSG00000036435	5	76529311	76570294	1	7	0	3	12	0	0	16	128	169	32	121		Q8R3S6
ENSMUST00000087143	ENSMUSG00000067194	X	159372178	159389928	1	13	19	57	11	13	8	175	693	212	309	113		Q8BMJ3
ENSMUST00000087144	ENSMUSG00000095377	17	37092934	37093872	-1	5	6	19	5	2	3	0	0	0	0	0	Q7TRL3	
ENSMUST00000087155						2	2	0	161	7	0	16	71	23	9	23		
ENSMUST00000087157	ENSMUSG00000047485	X	157818435	157820369	1	10	6	23	20	18	6	0	0	0	0	0	A2AI76	
ENSMUST00000087158	ENSMUSG00000073399	17	36881598	36890123	-1	0	8	7	9	18	7	0	0	0	0	0		Q3UWA4
ENSMUST00000087161	ENSMUSG00000029228	5	74592447	74702912	-1	0	0	0	0	0	0	8	19	0	2	0		O70263
ENSMUST00000087164	ENSMUSG00000015882	5	45697181	45857615	-1	9	1	4	11	15	4	0	47	0	0	0		Q3U285
ENSMUST00000087165	ENSMUSG00000067201	17	36639285	36642666	-1	1	0	1	1	6	3	0	0	0	0	0	Q8HWA1	
ENSMUST00000087167	ENSMUSG00000067201	17	36639285	36642666	-1	4	5	2	2	2	4	0	0	0	0	0	O19442	
ENSMUST00000087169	ENSMUSG00000040621	X	166170454	166190512	1	0	0	0	0	0	0	0	0	0	9	0		Q8BHE1
ENSMUST00000087176	ENSMUSG00000050121	19	41062474	41077113	-1	11	12	16	14	17	10	0	0	0	0	0	Q3USW3	Q7M750
ENSMUST00000087177	ENSMUSG00000067206	5	73606642	73632526	-1	21	13	48	15	36	9	0	0	0	1	0		Q8K0B3
ENSMUST00000087181	ENSMUSG00000051674	5	73481000	73560794	1	6	3	0	0	0	0	0	0	5	1	0	Q8C5X2	
ENSMUST00000087183	ENSMUSG00000033276	1	74601445	74636894	1	17	1	0	0	0	20	37	73	49	3	6		Q69ZM6
ENSMUST00000087186	ENSMUSG00000033276	1	74601445	74636894	1	6	9	22	16	30	6	14	0	14	0	21		Q69ZM6
ENSMUST00000087189	ENSMUSG00000061232	17	33996017	34000333	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0B4J1G3	
ENSMUST00000087195	ENSMUSG00000029153	5	73322199	73341028	-1	51	39	93	42	46	18	11	31	8	49	28		Q9D8W7
ENSMUST00000087200	ENSMUSG00000024429	17	35979851	35989462	1	17	6	33	36	30	10	458	644	293	56	303		P36916
ENSMUST00000087204	ENSMUSG00000056602	5	150118645	150497753	1	63	54	110	160	114	59	945	1205	2406	120	1193		E9Q8I9
ENSMUST00000087205						3	0	20	13	4	4	3	13	5	2	4		
ENSMUST00000087210	ENSMUSG00000039220	17	35916434	35932283	1	0	33	142	107	25	24	1016	1905	1134	88	949		Q80W00
ENSMUST00000087211	ENSMUSG00000039220	17	35916434	35932283	1	50	0	0	0	38	0	0	0	0	0	0		Q80W00
ENSMUST00000087212	ENSMUSG00000067219	5	72647795	72671078	1	14	33	108	66	37	12	1	14	2	6	12		Q8BMW7
ENSMUST00000087213	ENSMUSG00000067220	5	72603696	72644275	-1	7	6	6	8	11	2	0	7	0	0	0		P29974
ENSMUST00000087215	ENSMUSG00000026174	1	74506058	74530842	1	19	17	32	112	25	9	320	635	362	111	227		Q9JKY0
ENSMUST00000087216	ENSMUSG00000072889	5	72513301	72559684	-1	0	0	0	20	0	5	72	136	144	68	135	E9Q8I7	
ENSMUST00000087222						12	7	13	20	17	5	26	21	13	13	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000087225	ENSMUSG00000026179	1	74284930	74353694	1	37	0	58	95	43	1	0	0	0	0	0		Q69ZP3
ENSMUST00000087226	ENSMUSG00000026179	1	74284930	74353694	1	0	0	0	0	0	13	0	27	23	2	0		Q69ZP3
ENSMUST00000087228	ENSMUSG00000029208	5	69556923	69575973	1	4	1	5	21	8	0	7	10	26	15	7		Q8C3X4
ENSMUST00000087231	ENSMUSG00000037653	5	69109285	69341679	-1	0	3	0	190	4	0	0	0	0	0	0		Q50H33
ENSMUST00000087234	ENSMUSG00000067229	19	39113898	39187072	1	5	3	3	7	6	1	0	0	0	0	0	Q5GLZ0	
ENSMUST00000087236	ENSMUSG00000067231	19	39061015	39093944	1	5	11	3	2	6	6	0	0	0	0	0	Q148B1	
ENSMUST00000087241	ENSMUSG00000050010	5	67607882	67623552	1	65	35	162	507	83	60	0	2	2	0	3		Q3UPR0
ENSMUST00000087252	ENSMUSG00000067242	19	38264536	38312214	1	16	22	36	17	29	18	0	1	0	0	0	A0A0G2JEY8	
ENSMUST00000087253	ENSMUSG00000025272	X	150645304	150657583	-1	0	1	0	1	0	0	0	0	0	0	0	E9Q886	
ENSMUST00000087256	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	0	0	0	0	0	0	0	0	E9QPX0	
ENSMUST00000087258	ENSMUSG00000025272	X	150645304	150657583	-1	0	12	29	0	25	0	0	0	0	0	2	Q6DIC6	
ENSMUST00000087264	ENSMUSG00000037795	5	65763521	65830108	1	0	0	0	0	0	0	43	0	243	0	153	F8VQG7	
ENSMUST00000087268	ENSMUSG00000050296	1	71242276	71414910	-1	91	56	82	360	113	70	0	1	5	0	5	E9Q876	
ENSMUST00000087285	ENSMUSG00000067261	4	99656299	99658622	1	5	5	18	413	17	5	0	0	0	0	0	A2BDY3	
ENSMUST00000087313	ENSMUSG00000031285	X	143855842	143933311	-1	12	11	87	0	0	0	0	1	2	0	4		O88809
ENSMUST00000087315	ENSMUSG00000007029	17	35000987	35016322	1	0	0	0	167	0	0	34	376	150	38	390	Q790I0	Q9Z1Q9
ENSMUST00000087316	ENSMUSG00000067276	X	143802231	143827414	-1	7	9	3	1	14	1	0	0	0	3	0		O35646
ENSMUST00000087320	ENSMUSG00000037697	14	45593174	45658143	-1	0	0	0	0	0	0	0	18	0	0	0	F8WIJ5	
ENSMUST00000087321	ENSMUSG00000067279	19	36731737	36736653	-1	13	15	48	44	23	14	0	0	0	0	0		Q7TMB3
ENSMUST00000087324	ENSMUSG00000029171	5	64092950	64128351	1	4	7	9	63	16	13	995	2599	1618	446	879		Q7TSV4
ENSMUST00000087327	ENSMUSG00000047881	5	63908897	63968897	-1	2	10	16	3	4	5	190	445	641	70	235	H7BX61	
ENSMUST00000087328	ENSMUSG00000091971	17	34969190	34972156	-1	18	21	74	1140	29	25	34	126	46	7	68	Q3TU85	Q61696
ENSMUST00000087332	ENSMUSG00000067285	5	42067960	42216798	1	388	224	353	389	505	230	0	0	1	0	4	Q8CBM3	
ENSMUST00000087333	ENSMUSG00000047045	X	142681406	142843494	1	14	15	119	0	29	16	1365	1100	1826	88	1510		Q6PHN7
ENSMUST00000087341	ENSMUSG00000024795	19	34922358	34975731	1	15	11	16	37	14	7	29	89	96	110	42		Q80WE4
ENSMUST00000087342	ENSMUSG00000067288	17	33819027	33824562	-1	0	9	0	3	8	9	310	411	252	1164	229	Q059I1	P62858
ENSMUST00000087348	ENSMUSG00000067292	6	149130170	149130710	1	177	53	260	5352	409	325	0	2	1	1	3	F6QJ09	
ENSMUST00000087351	ENSMUSG00000046434	15	103240432	103244955	1	30	33	0	0	3	25	425	1542	439	2001	660		P49312
ENSMUST00000087357	ENSMUSG00000067297	19	34617049	34640743	-1	0	45	67	0	38	0	0	202	22	45	90	Q3U687	
ENSMUST00000087359	ENSMUSG00000070870	1	65048554	65051149	-1	0	2	7	3	9	0	0	0	0	0	0		Q03740
ENSMUST00000087360	ENSMUSG00000039191	5	53466152	53657362	1	20	21	0	3	20	28	1	140	0	2	61	E9Q7W0	
ENSMUST00000087366	ENSMUSG00000025958	1	64532645	64604548	1	20	24	22	23	20	10	318	1407	499	157	346	Q543W0	Q01147
ENSMUST00000087374	ENSMUSG00000025964	1	63445891	63596276	1	0	0	0	20	0	0	0	0	0	0	0		Q9R1V7
ENSMUST00000087395	ENSMUSG00000029088	5	48389502	49524907	-1	1	1	4	24	6	0	0	0	0	0	0	Q3YAA8	Q6PHZ8
ENSMUST00000087399	ENSMUSG00000033327	17	34670535	34719815	1	89	85	237	169	158	62	0	3	5	4	26	O35452	
ENSMUST00000087400	ENSMUSG00000031433	X	139889511	139998595	-1	2	1	2	1	1	0	4	0	0	0	0		Q8JZV4
ENSMUST00000087401	ENSMUSG00000031434	X	139821632	139871677	-1	0	0	0	14	0	0	0	0	0	2	0		Q8BMD7
ENSMUST00000087409	ENSMUSG00000027583	2	181387762	181459426	-1	13	10	13	7	10	10	0	1	4	1	0		Q8BID6
ENSMUST00000087431						7	13	8	12	9	3	0	0	0	0	0		
ENSMUST00000087435	ENSMUSG00000067336	1	59763400	59879014	1	42	37	92	234	46	25	654	1000	1142	75	821		O35607
ENSMUST00000087441	ENSMUSG00000029086	5	43993620	44102032	-1	0	0	0	0	0	10	46	139	47	25	0	G3X9J8	
ENSMUST00000087442	ENSMUSG00000029086	5	43993620	44102032	-1	1	0	0	4	0	0	0	0	17	0	0		
ENSMUST00000087445	ENSMUSG00000067338	6	145615757	145621479	1	9	12	56	20	43	14	0	0	0	0	1	Q5FW91	P05214
ENSMUST00000087465	ENSMUSG00000039753	5	43744615	43821638	-1	10	14	53	19	13	2	141	693	187	94	397		Q8C2S5
ENSMUST00000087467	ENSMUSG00000003573	8	70282827	70294361	1	0	0	4	67	0	0	6	10	2	4	11	Q501M9	
ENSMUST00000087473						0	0	0	1	4	2	0	0	1	1	0		
ENSMUST00000087475	ENSMUSG00000038079	1	59100590	59120408	-1	5	0	24	10	12	3	6	6	3	28	0		Q3V0J1
ENSMUST00000087485	ENSMUSG00000030279	6	143010920	143100141	-1	10	5	8	144	11	14	0	43	24	0	29		Q7TPS5
ENSMUST00000087486						0	1	44	60	4	2	0	0	0	0	0		
ENSMUST00000087497	ENSMUSG00000024330	17	34039437	34066685	1	36	7	47	43	30	7	103	374	110	14	215	I7HJS8	Q64739
ENSMUST00000087511	ENSMUSG00000067365	5	38260185	38269634	1	3	2	1	25	2	4	106	330	114	192	61		Q9CZB9
ENSMUST00000087514	ENSMUSG00000067367	5	38220470	38234306	1	0	0	0	20	11	0	0	77	43	150	70		Q08288
ENSMUST00000087517	ENSMUSG00000038914	2	180657964	180709999	-1	28	19	95	244	57	14	563	958	1189	89	926		Q8C9B9
ENSMUST00000087521	ENSMUSG00000026036	1	58445151	58481816	1	31	39	107	56	50	31	18	47	7	13	26		Q9EQ80
ENSMUST00000087525	ENSMUSG00000024837	19	25505618	25604329	1	2	2	0	175	0	2	0	0	0	0	0		Q9QZ59
ENSMUST00000087527	ENSMUSG00000030249	6	142587862	142702315	-1	73	0	0	0	1	0	0	0	0	0	0		P70170
ENSMUST00000087540	ENSMUSG00000067369	X	134222339	134276984	-1	4	2	29	8	2	6	15	40	24	32	23	Q8C8J3	
ENSMUST00000087541	ENSMUSG00000067369	X	134222339	134276984	-1	0	0	0	0	0	0	23	23	82	27	0		Q8BQJ6
ENSMUST00000087543	ENSMUSG00000067370	17	33949909	33951477	-1	10	11	16	189	17	10	360	469	277	68	146	A0A068BIS6	Q9Z0F0
ENSMUST00000087556	ENSMUSG00000024943	19	23206441	23273897	-1	35	32	128	150	31	17	101	403	239	99	174		Q8CG46
ENSMUST00000087557	ENSMUSG00000067377	X	133891068	133898429	-1	1	3	2	2	4	0	0	4	2	2	0	Q99L96	
ENSMUST00000087559	ENSMUSG00000002308	17	33843091	33849774	1	4	0	9	11	3	3	17	31	6	29	5		Q9Z1P5
ENSMUST00000087562						36	37	60	18	31	12	0	4	4	0	2		
ENSMUST00000087563	ENSMUSG00000039069	2	180070588	180085902	1	3	1	0	9	0	0	21	96	8	4	15	A2AFK4	
ENSMUST00000087566	ENSMUSG00000030695	7	126795234	126800751	-1	0	0	0	0	0	3	888	768	565	72	366	A6ZI44	
ENSMUST00000087576	ENSMUSG00000052387	19	22139119	22989884	1	0	0	0	1	0	0	0	0	0	0	0	Q5F4S9	
ENSMUST00000087582	ENSMUSG00000059208	17	33646233	33686860	-1	0	1	1	56	0	8	775	3064	1821	395	1275	Q3THB3	Q9D0E1
ENSMUST00000087585	ENSMUSG00000025977	1	55248658	55363469	-1	0	0	0	0	0	0	0	0	0	0	0	E9QPQ9	
ENSMUST00000087600	ENSMUSG00000058624	19	21391307	21473445	-1	57	57	99	557	104	46	10417	43375	15838	5204	10098	Q548F2	Q9R111
ENSMUST00000087605	ENSMUSG00000024300	17	33555719	33607764	1	25	11	44	31	29	22	14312	20252	16746	947	11924	Q8CG29	
ENSMUST00000087614	ENSMUSG00000030232	6	140622663	140678472	1	0	0	0	123	2	0	7	51	62	13	83		Q9Z248
ENSMUST00000087617	ENSMUSG00000025981	1	55052770	55072702	1	4	3	0	23	4	1	8	130	20	0	12	G5E8J7	
ENSMUST00000087622	ENSMUSG00000030231	6	140424054	140597110	1	28	28	47	76	38	25	11	28	22	4	54	E9Q6H8	
ENSMUST00000087623	ENSMUSG00000024299	17	33524204	33553782	1	0	0	0	0	0	0	63	172	8	0	0		P58459
ENSMUST00000087629	ENSMUSG00000029096	5	35652023	35679782	-1	13	9	27	180	23	7	0	0	2	2	9		Q9D236
ENSMUST00000087638	ENSMUSG00000053279	19	20601961	20643462	1	11	10	10	2	17	11	9	4	9	128	40		P24549
ENSMUST00000087654	ENSMUSG00000067430	17	33016863	33033402	-1	11	12	31	11	10	7	3	19	2	9	4	Q8BIC7	
ENSMUST00000087655						37	25	48	135	38	22	10	59	30	2	23		
ENSMUST00000087656	ENSMUSG00000079495	6	85808024	85820954	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JIY8
ENSMUST00000087657	ENSMUSG00000030228	6	139587221	139969284	1	0	0	0	0	0	0	0	0	1	0	0	D3Z6L6	
ENSMUST00000087659	ENSMUSG00000042807	1	53806876	54195168	-1	29	40	64	0	55	0	11	82	36	24	27		Q6I6G8
ENSMUST00000087666	ENSMUSG00000053390	17	32993129	33005457	1	10	10	19	0	0	7	0	107	59	77	43	B0V2W4	
ENSMUST00000087674	ENSMUSG00000067438	5	35389108	35399730	1	2	4	9	183	15	3	0	0	0	0	0		O70218
ENSMUST00000087675	ENSMUSG00000030225	6	137754546	137857340	1	9	9	17	35	13	7	168	408	276	271	129		Q91YP3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000087684	ENSMUSG00000029101	5	34949445	35039644	1	21	0	0	6	0	9	0	0	0	0	7	E9Q652	
ENSMUST00000087689	ENSMUSG00000039126	19	16956118	17223932	1	116	84	245	156	122	52	18	48	44	22	81		Q52KR3
ENSMUST00000087694						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000087699						303	271	193	255	382	158	70	172	190	60	210		
ENSMUST00000087701	ENSMUSG00000041439	1	52656286	52727462	-1	4	4	0	0	3	2	0	2	22	0	54		Q8CBH5
ENSMUST00000087703	ENSMUSG00000024050	17	32354055	32389401	-1	0	0	44	19	16	11	13	55	30	0	0	G5E8J8	
ENSMUST00000087714	ENSMUSG00000067455	13	21735064	21735837	1	6	7	4	75	16	1	1	3	1	0	2	B2RTM0	P62806
ENSMUST00000087721	ENSMUSG00000037577	17	32183770	32189549	-1	153	127	866	427	115	81	3	10	2	0	6		
ENSMUST00000087723	ENSMUSG00000038146	17	32120820	32166880	-1	65	59	180	419	114	38	3	0	2	0	28		Q61982
ENSMUST00000087729	ENSMUSG00000030206	6	135237326	135254351	-1	8	2	2	0	11	5	0	0	0	0	0		Q8R1W2
ENSMUST00000087737	ENSMUSG00000059866	5	34496087	34513991	-1	0	1	9	104	19	6	160	607	302	62	361		Q99JG7
ENSMUST00000087769						0	3	4	1	3	3	0	0	0	0	0		
ENSMUST00000087773	ENSMUSG00000094755	19	13027404	13028327	-1	2	3	0	3	2	0	0	0	0	0	0	Q8VFX0	
ENSMUST00000087812	ENSMUSG00000067513	19	12298183	12299130	-1	3	2	0	2	4	0	0	0	0	0	0	A0PK57	
ENSMUST00000087814	ENSMUSG00000095640	19	12279854	12283988	1	2	4	1	1	4	3	0	0	0	0	0	Q7TQR9	
ENSMUST00000087818	ENSMUSG00000067519	19	12240721	12241659	-1	1	0	5	1	6	0	0	0	0	0	0	Q8VFV8	
ENSMUST00000087820	ENSMUSG00000054252	5	33721674	33737068	1	4	3	0	0	3	0	0	0	0	0	1	Q61563	
ENSMUST00000087822	ENSMUSG00000067522	19	12119653	12120700	-1	7	8	6	8	11	4	0	0	0	0	0	Q8VFV2	
ENSMUST00000087824	ENSMUSG00000067524	19	12108600	12109544	-1	4	4	13	7	9	6	0	0	0	0	0	Q0VDY1	
ENSMUST00000087825	ENSMUSG00000067525	19	12098702	12099639	-1	6	2	6	1	7	7	0	0	0	0	0	Q8VFU9	
ENSMUST00000087828	ENSMUSG00000067526	19	12073695	12074633	-1	16	4	34	3	7	5	0	0	0	0	0	K7N659	
ENSMUST00000087830	ENSMUSG00000067528	19	12058809	12059750	-1	6	6	15	4	6	3	0	0	0	0	0	Q8VFV1	
ENSMUST00000087831	ENSMUSG00000067529	19	12035808	12036740	-1	5	6	6	8	10	3	0	0	1	0	0	Q8VFV0	
ENSMUST00000087853	ENSMUSG00000067543	6	132206795	132210521	-1	17	9	206	240	26	14	0	0	0	0	0	Q91X93	
ENSMUST00000087857	ENSMUSG00000067545	19	11870146	11871305	-1	8	4	19	6	11	2	0	0	0	0	0	Q7TQS2	
ENSMUST00000087864	ENSMUSG00000037355	5	33378549	33419754	1	0	0	53	53	0	0	115	0	187	28	182		Q9D479
ENSMUST00000087865	ENSMUSG00000030189	6	131364855	131388476	-1	4	0	3	0	6	2	155	228	92	45	164		Q9JKB3
ENSMUST00000087867	ENSMUSG00000073016	X	104482818	104507490	1	46	46	195	41	39	30	12	20	16	1	24		B1AVZ0
ENSMUST00000087871	ENSMUSG00000027523	2	174284320	174346744	1	11	14	71	359	35	12	4	11	11	0	11		P63094
ENSMUST00000087876	ENSMUSG00000027523	2	174284320	174346744	1	7	0	0	53	0	0	0	0	0	0	0		Q6R0H7
ENSMUST00000087877	ENSMUSG00000027523	2	174284320	174346744	1	7	9	18	451	29	7	0	0	0	0	0		Q6R0H7
ENSMUST00000087879	ENSMUSG00000046449	X	104077434	104201185	-1	10	19	8	0	0	6	0	0	0	0	0		Q5DTT1
ENSMUST00000087883	ENSMUSG00000026043	1	45311538	45349706	1	10	10	13	2	12	7	0	0	0	133	436	Q3TVI5	P08121
ENSMUST00000087884						2	2	14	1	0	1	0	0	0	0	0		
ENSMUST00000087896	ENSMUSG00000067561	X	102847639	102854616	-1	6	0	0	0	0	6	0	0	0	0	0	Q14AJ8	
ENSMUST00000087897	ENSMUSG00000037426	5	32863701	32994236	1	68	42	127	106	81	46	37	159	84	13	82	Q6GQV2	
ENSMUST00000087899	ENSMUSG00000067561	X	102847639	102854616	-1	4	1	0	0	0	6	0	0	0	0	0	Q9D410	
ENSMUST00000087908	ENSMUSG00000027522	2	174076308	174099771	1	55	51	29	0	56	35	171	626	111	0	372		Q8BVI5
ENSMUST00000087916	ENSMUSG00000067567	X	102284639	102505359	-1	5	0	4	1	8	0	30	117	73	58	26		Q8VH37
ENSMUST00000087923	ENSMUSG00000067571	19	10978307	10993250	-1	10	5	44	23	24	15	1	2	0	0	3		Q3UPL6
ENSMUST00000087927	ENSMUSG00000071064	8	79028437	79193766	1	56	49	99	58	55	19	2	3	5	2	18		Q505G8
ENSMUST00000087933	ENSMUSG00000041763	1	43933647	44003000	1	0	0	0	22	0	0	309	857	446	358	379		Q64514
ENSMUST00000087938	ENSMUSG00000034930	6	83135463	83152579	1	20	15	15	135	12	8	0	0	0	0	0		Q8C6B2
ENSMUST00000087942	ENSMUSG00000064147	17	29135056	29148980	1	31	18	67	43	39	31	1822	2259	1748	123	2653		Q8CB87
ENSMUST00000087947						0	0	0	0	0	0	0	6	0	2	1		
ENSMUST00000087948	ENSMUSG00000079487	X	101274030	101297465	1	0	15	35	0	0	0	437	346	631	23	726		A2AGH6
ENSMUST00000087950	ENSMUSG00000067578	2	172036233	172043466	-1	22	13	43	317	30	10	0	0	0	0	0		Q8BME9
ENSMUST00000087951	ENSMUSG00000048832	19	10688815	10714419	1	16	13	37	127	31	12	811	1251	762	74	645		Q8R105
ENSMUST00000087956	ENSMUSG00000079487	X	101274030	101297465	1	23	0	0	0	0	18	100	292	73	0	120		A2AGH6
ENSMUST00000087965	ENSMUSG00000054934	10	116417861	116473878	-1	14	15	40	6	14	8	0	5	2	0	0	F7C7W9	
ENSMUST00000087971	ENSMUSG00000027551	2	168893331	168955587	-1	13	13	70	168	30	8	43	52	28	17	53	A2AQR4	
ENSMUST00000087978	ENSMUSG00000067586	13	51408618	51422797	1	49	29	183	219	59	32	2	7	1	0	9		Q9Z0U9
ENSMUST00000087983	ENSMUSG00000026070	1	40465552	40500854	1	0	0	0	0	0	0	0	0	0	0	0		Q61098
ENSMUST00000087984	ENSMUSG00000000881	X	100767722	100818410	1	0	0	0	0	1	8	0	0	0	0	0		P70175
ENSMUST00000087996	ENSMUSG00000067594	15	101858732	101869705	-1	39	24	81	109	39	16	0	0	0	0	0	Q08EK5	Q6IFZ6
ENSMUST00000088001	ENSMUSG00000051149	2	168180986	168207112	-1	26	0	0	90	30	0	18	9	122	0	97	A2BDX0	Q9Z103
ENSMUST00000088007	ENSMUSG00000007570	17	28313530	28326568	1	4	0	7	0	5	2	55	71	25	9	53	B8JJD6	
ENSMUST00000088010	ENSMUSG00000106864	5	31156005	31180144	-1	0	0	0	49	0	0	120	505	204	0	1		Q8BL74
ENSMUST00000088011	ENSMUSG00000067599	6	130218605	130233322	-1	0	0	0	0	0	0	1	4	0	0	2		Q60654
ENSMUST00000088013	ENSMUSG00000036098	19	10208272	10240748	-1	13	16	27	37	34	4	12	3	6	5	30		Q3UR85
ENSMUST00000088017	ENSMUSG00000067591	6	130323289	130337574	-1	0	0	2	0	0	0	0	8	0	7	0		Q64329
ENSMUST00000088018	ENSMUSG00000067596	15	101754259	101763504	-1	8	4	14	9	20	6	0	0	0	0	0		Q6IFZ9
ENSMUST00000088027	ENSMUSG00000024219	17	27909340	28062600	1	0	31	94	112	0	0	460	346	370	32	348		P59672
ENSMUST00000088029	ENSMUSG00000067604	1	38939149	38950276	1	1	2	2	2	2	2	0	0	0	0	0		Q5H8A1
ENSMUST00000088040	ENSMUSG00000067608	19	9283238	9284494	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000088041	ENSMUSG00000017969	2	167191805	167240604	-1	7	5	3	20	13	4	0	0	0	0	0	Q8BXC0	
ENSMUST00000088046	ENSMUSG00000067610	6	129697218	129717132	-1	3	6	4	4	6	1	0	3	0	3	3	B2KG20	
ENSMUST00000088049	ENSMUSG00000067614	15	101473478	101479983	1	16	7	39	75	21	17	36	157	45	13	77	B2RTB6	P97861
ENSMUST00000088063						5	0	0	3	6	3	1431	3805	1656	271	1743		
ENSMUST00000088072	ENSMUSG00000060771	1	37754776	37866429	-1	13	7	27	57	15	14	0	8	3	8	0		Q6NY15
ENSMUST00000088075	ENSMUSG00000046080	6	129408862	129424763	1	2	1	0	0	0	0	0	1	1	3	0		Q8BRU4
ENSMUST00000088080	ENSMUSG00000067627	8	9864251	9870315	1	259	208	1791	344	159	89	3	6	1	0	4	F7BLD2	
ENSMUST00000088081	ENSMUSG00000029168	5	30711564	30799375	1	29	20	0	61	20	14	0	0	0	0	2		Q9EQF6
ENSMUST00000088086	ENSMUSG00000006800	2	166073089	166155663	-1	14	0	22	79	19	0	40	62	44	16	162		Q8CFG0
ENSMUST00000088092	ENSMUSG00000071660	19	8809075	8819333	-1	1	1	0	3	1	7	24	53	74	68	48		Q810A3
ENSMUST00000088095	ENSMUSG00000027678	2	165992636	166073242	1	30	27	80	28	74	26	841	3083	1603	148	1352	Q05BA5	
ENSMUST00000088102	ENSMUSG00000079509	X	94074631	94123702	-1	0	0	0	0	0	0	0	56	213	203	50	B1ASD1	P17012
ENSMUST00000088113	ENSMUSG00000039671	2	165784152	165899016	-1	4	0	0	0	5	4	43	0	0	0	52	A2A485	
ENSMUST00000088117	ENSMUSG00000067642	5	30193431	30205722	-1	2	2	4	2	5	2	0	0	7	0	19		Q58Y75
ENSMUST00000088132	ENSMUSG00000017897	2	165595032	165771727	1	0	0	0	26	0	10	0	5	1	0	0		O08575
ENSMUST00000088133						4	1	15	6	2	2	0	0	0	0	0		
ENSMUST00000088134						4	1	0	0	2	2	0	0	0	0	0		
ENSMUST00000088137	ENSMUSG00000067649	X	92118879	92599572	-1	4	0	0	0	1	0	0	0	0	0	0	Q8BQR7	
ENSMUST00000088142	ENSMUSG00000056487	15	100353200	100361840	1	0	7	0	0	5	2	0	0	0	0	0	Q510W6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000088146	ENSMUSG00000035387	X	89930098	89932852	-1	0	2	3	1	1	0	0	0	0	0	0		Q3V0Y1
ENSMUST00000088169	ENSMUSG00000024758	19	7425901	7483289	-1	0	0	3	68	4	6	971	489	764	0	68		Q9ES97
ENSMUST00000088171	ENSMUSG00000024758	19	7425901	7483289	-1	16	26	37	0	14	14	14	25	81	2	79		Q9ES97
ENSMUST00000088172	ENSMUSG00000062184	X	51387212	51681856	-1	8	5	14	53	0	2	1	0	1	0	0		Q80UW0
ENSMUST00000088174	ENSMUSG00000045216	1	36068400	36106446	1	16	15	37	203	34	10	78	149	64	13	129		Q9QYK5
ENSMUST00000088194	ENSMUSG00000000399	6	126821721	126849136	-1	7	4	33	2	10	1	283	663	253	650	205		Q9DC69
ENSMUST00000088198	ENSMUSG00000067679	X	78186777	78192292	1	1	2	0	0	0	0	0	0	0	0	0	A2AEP0	
ENSMUST00000088200	ENSMUSG00000044217	15	99590849	99594829	1	13	2	0	29	18	2	0	0	0	3	0		Q9WTY4
ENSMUST00000088201	ENSMUSG00000067684	X	78085505	78091374	-1	1	0	0	0	0	0	0	0	0	0	0	Q9D3H2	
ENSMUST00000088217	ENSMUSG00000025246	X	77511013	77662983	1	5	11	18	76	12	6	459	1016	829	58	476		Q9QXE7
ENSMUST00000088223	ENSMUSG00000047656	19	6996131	6999044	1	5	3	11	61	8	6	6	15	12	1	12		Q8K3A2
ENSMUST00000088233	ENSMUSG00000023008	15	99317225	99370482	-1	21	0	22	153	18	6	127	129	141	31	159		Q6ZPF4
ENSMUST00000088236	ENSMUSG00000067698	5	26114764	26121421	-1	6	3	0	0	8	4	0	0	0	0	0	K7N660	
ENSMUST00000088237	ENSMUSG00000072437	19	60755987	60759913	1	15	8	27	360	23	9	28	103	67	9	32		Q80WY3
ENSMUST00000088244	ENSMUSG00000056367	5	25759997	25850688	1	13	16	0	6	0	0	0	0	0	0	0		Q641P0
ENSMUST00000088246	ENSMUSG00000067702	6	125278274	125286042	-1	17	9	14	36	14	4	1	0	0	0	3	Q5FW91	P05214
ENSMUST00000088248	ENSMUSG00000001403	2	164769898	164778822	1	27	28	98	95	40	21	239	343	205	52	140	A2A4Z0	Q9D1C1
ENSMUST00000088257	ENSMUSG00000038812	19	6909698	6911049	1	2	8	0	0	0	0	262	195	6	28	80		Q9DCG9
ENSMUST00000088260	ENSMUSG00000067704	2	164685107	164687706	1	20	18	40	94	35	15	0	0	1	0	1		Q5DQQ6
ENSMUST00000088263						0	3	19	0	11	0	0	0	0	0	0		
ENSMUST00000088276						0	0	0	151	0	0	0	0	0	7	0		
ENSMUST00000088287	ENSMUSG00000004768	1	33719887	33742564	1	0	0	0	0	0	0	84	283	72	29	61	Q9D4I9	
ENSMUST00000088291	ENSMUSG00000018209	2	164070322	164155524	1	22	10	0	0	0	12	19	1560	0	0	0	Q8CDG4	
ENSMUST00000088292	ENSMUSG00000067714	6	125067920	125082472	1	4	0	4	79	8	7	18	0	0	2	20	G3X9K0	
ENSMUST00000088294	ENSMUSG00000072770	6	125049689	125063267	1	8	1	8	6	7	4	28	122	51	15	61		Q3V140
ENSMUST00000088295	ENSMUSG00000038181	5	24586741	24594556	1	36	0	80	44	72	19	20	97	50	16	61	Q3UU43	
ENSMUST00000088296	ENSMUSG00000067716	16	48073444	48074187	1	4	5	5	1	6	2	0	0	0	0	0	E9Q1B3	
ENSMUST00000088299						0	0	0	0	0	0	874	2829	490	850	115		
ENSMUST00000088302	ENSMUSG00000038199	5	24543432	24556809	-1	28	24	44	35	34	8	0	0	0	0	1		A6H690
ENSMUST00000088307	ENSMUSG00000067722	17	25184561	25187661	1	38	25	36	331	51	30	57	200	62	67	48		Q6RUT7
ENSMUST00000088308	ENSMUSG00000038346	6	125009145	125037870	1	0	0	0	0	0	0	0	0	0	0	0	E9Q1A5	
ENSMUST00000088310	ENSMUSG00000048874	1	30802339	30873921	-1	12	14	15	14	16	8	697	1392	1609	149	1067	B2RQG2	
ENSMUST00000088311	ENSMUSG00000067724	5	24502757	24527202	-1	21	13	30	149	24	10	0	1	0	0	1		P82976
ENSMUST00000088313	ENSMUSG00000001964	X	74254687	74261548	1	0	1	0	8	0	1	26	89	53	6	24	Q3THM8	
ENSMUST00000088336						2	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000088345	ENSMUSG00000024163	17	24892153	24936977	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UHB5	Q9ESN9
ENSMUST00000088349	ENSMUSG00000026147	1	24177610	24252684	1	13	5	31	14	18	9	0	0	0	0	0	Q9D0D2	
ENSMUST00000088355	ENSMUSG00000022483	15	97975602	98004695	-1	42	22	86	22	39	2	1	0	0	1	0		P28481
ENSMUST00000088356	ENSMUSG00000068284	16	44173246	44227465	1	0	1	5	0	1	2	0	5	2	0	2	F8WJI0	
ENSMUST00000088357	ENSMUSG00000004263	6	124742544	124756524	-1	33	6	90	141	44	0	442	790	466	10	455		O35126
ENSMUST00000088373	ENSMUSG00000030257	6	112717971	112947266	-1	107	100	223	651	136	69	7	15	4	0	27	F8VPQ4	
ENSMUST00000088386	ENSMUSG00000025557	14	121459621	121505254	-1	75	75	307	136	92	50	7	12	5	1	10		Q9JIP7
ENSMUST00000088392	ENSMUSG00000062604	5	23503264	23684617	-1	21	29	36	22	27	15	589	2065	1121	490	786		
ENSMUST00000088402	ENSMUSG00000022475	15	97792664	97844502	-1	0	0	0	120	6	0	0	0	7	0	0		Q8C2B3
ENSMUST00000088407	ENSMUSG00000067750	1	21349641	21352200	1	8	0	28	11	3	3	0	0	0	0	0		Q3UWR2
ENSMUST00000088419	ENSMUSG00000022139	14	120275669	120431697	1	0	13	0	0	0	0	84	230	270	204	362		Q8C181
ENSMUST00000088429	ENSMUSG00000031376	X	73503086	73571005	1	44	40	301	14	0	0	1	0	0	1	1	Q0VF55	
ENSMUST00000088448	ENSMUSG00000043760	1	20057779	20618064	-1	67	60	73	50	63	31	0	0	0	0	0	E9PZ36	
ENSMUST00000088450	ENSMUSG00000067764	X	73282896	73292976	-1	2	4	0	0	0	0	0	0	2	0	0	Q9JJR2	
ENSMUST00000088452	ENSMUSG00000023169	15	96571418	96642913	-1	14	0	0	213	19	20	30	0	306	0	177		Q8K2P7
ENSMUST00000088454	ENSMUSG00000023169	15	96571418	96642913	-1	5	10	15	85	15	12	215	480	165	51	244		Q8K2P7
ENSMUST00000088455	ENSMUSG00000067767	6	123172893	123204671	1	6	3	7	3	5	1	5	4	2	0	4	Q67DU8	
ENSMUST00000088459	ENSMUSG00000067771	X	73117047	73129262	1	0	7	53	44	52	25	0	0	0	0	0	Q52KH6	
ENSMUST00000088463	ENSMUSG00000067773	1	18250980	18265138	-1	0	0	1	1	5	0	0	0	0	0	0		
ENSMUST00000088464	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	833	991	867	85	631	F8WJF7	
ENSMUST00000088468	ENSMUSG00000043832	6	122952515	122969875	1	3	0	12	2	8	0	75	1019	119	406	207	Q8JZX6	
ENSMUST00000088476	ENSMUSG00000067780	1	17601901	17630939	1	1170	933	6504	1456	1304	569	12	54	28	11	52		
ENSMUST00000088480						0	0	0	0	3	0	2262	2373	1276	4448	949		
ENSMUST00000088481	ENSMUSG00000043453	X	72381870	72386858	-1	8	2	1	2	3	7	0	0	0	0	0	A2AMW4	
ENSMUST00000088483	ENSMUSG00000058571	14	116925297	117979529	1	0	0	0	0	0	0	0	0	0	0	0	Q3V1C9	Q9R087
ENSMUST00000088484	ENSMUSG00000067786	2	157560078	157562522	1	0	0	0	0	2	0	0	0	0	0	0	G3X9K1	
ENSMUST00000088494	ENSMUSG00000067787	2	157556362	157571274	-1	0	0	0	57	0	6	26	0	47	18	22		P62951
ENSMUST00000088506	ENSMUSG00000024136	17	24440081	24443105	-1	0	0	0	0	2	0	0	0	8	0	0		Q9D1G0
ENSMUST00000088512	ENSMUSG00000034681	17	24414675	24425895	1	6	0	3	0	7	0	39	0	82	29	23		Q99M28
ENSMUST00000088516	ENSMUSG00000040003	5	19227036	20704792	1	14	17	86	99	24	17	0	0	0	0	0		Q9WVQ1
ENSMUST00000088523	ENSMUSG00000027639	2	157097533	157135265	-1	0	0	0	0	0	0	0	0	955	287	0	E9Q0K6	
ENSMUST00000088538	ENSMUSG00000079056	2	127456498	127522094	-1	10	0	46	148	9	5	0	0	0	0	0	Q3YAA9	
ENSMUST00000088542	ENSMUSG00000067813	1	13668771	13701723	1	2	3	5	2	8	2	0	0	0	0	0		Q5GH62
ENSMUST00000088546	ENSMUSG00000000838	X	68678541	68717963	1	1	0	0	3	0	0	0	34	174	0	65	Q6AXB7	
ENSMUST00000088552	ENSMUSG00000067818	2	156775420	156781658	1	8	4	22	14	14	3	31	19	38	325	86		Q9CQ19
ENSMUST00000088555	ENSMUSG00000047295	15	91838265	91861438	1	0	0	0	0	0	0	0	0	0	0	0		Q6JHY2
ENSMUST00000088561	ENSMUSG00000067825	6	121183667	121198837	1	33	17	9	0	33	20	15	0	0	0	7		Q8BGI5
ENSMUST00000088585	ENSMUSG00000016918	1	12692277	12861192	1	0	0	7	0	0	0	0	0	0	5	0		Q8K007
ENSMUST00000088592	ENSMUSG00000043460	15	78670022	78718113	-1	54	28	95	450	66	24	0	0	0	0	0		Q68FM6
ENSMUST00000088598	ENSMUSG00000096278	17	23880880	23900787	1	0	3	0	0	0	4	0	0	0	0	0	E9PYC2	
ENSMUST00000088610	ENSMUSG00000067847	2	156144039	156145797	1	0	0	1	131	4	0	55	182	90	536	57		P60603
ENSMUST00000088614	ENSMUSG00000022629	15	90933276	91049948	-1	10	0	21	0	0	0	0	0	0	0	0		Q9QXL2
ENSMUST00000088615	ENSMUSG00000067851	1	10137571	10232670	-1	21	13	22	17	26	12	1349	3270	2865	218	1341		G3X9K3
ENSMUST00000088616	ENSMUSG00000091903	5	11594913	11599784	1	0	0	9	8	0	0	0	0	0	0	0	F6YJZ8	
ENSMUST00000088621	ENSMUSG00000039218	17	23790662	23824741	1	45	37	191	51	59	2	2050	6402	4468	121	4160		Q8BTI8
ENSMUST00000088625	ENSMUSG00000069355	5	10242041	10246526	-1	9	2	17	8	4	0	0	0	0	0	0	G3XA03	
ENSMUST00000088627	ENSMUSG00000067860	X	58022700	58041736	1	15	4	17	46	16	0	0	0	0	0	0		Q62521
ENSMUST00000088629	ENSMUSG00000067860	X	58022700	58041736	1	4	0	0	137	0	2	0	0	0	0	0		Q62521
ENSMUST00000088631	ENSMUSG00000067860	X	58022700	58041736	1	0	8	3	0	0	1	0	0	0	0	0	A2AWK6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000088644	ENSMUSG00000045962	6	119923969	120038672	-1	48	0	0	23	15	0	0	28	13	0	93		P83741
ENSMUST00000088646	ENSMUSG00000045962	6	119923969	120038672	-1	0	15	0	0	0	0	1420	1165	2941	47	2044		P83741
ENSMUST00000088648						3	0	4	0	0	1	0	0	0	0	0		
ENSMUST00000088649	ENSMUSG00000052560	15	90487482	90679432	-1	0	13	23	0	0	10	118	277	85	0	38	Q9CYR4	
ENSMUST00000088650	ENSMUSG00000005881	2	156008045	156018279	1	1	0	4	3	0	2	0	0	0	0	11		Q9CQE7
ENSMUST00000088652	ENSMUSG00000067873	X	57053583	57067183	1	8	4	3	8	4	1	55	266	147	141	116		Q8BGC0
ENSMUST00000088653	ENSMUSG00000067872	19	4839366	4842528	1	26	14	56	70	35	9	0	0	0	0	0		Q8CDL9
ENSMUST00000088658	ENSMUSG00000025912	1	9667415	9700209	-1	10	2	2	52	7	8	2	9	0	0	12		
ENSMUST00000088666	ENSMUSG00000067879	1	9601199	9627143	1	21	15	35	46	18	13	0	0	0	0	2		Q8BG31
ENSMUST00000088673	ENSMUSG00000067882	17	23550965	23553566	-1	0	0	2	4	5	1	0	0	0	0	0	I6L890	
ENSMUST00000088677	ENSMUSG00000070687	4	136423524	136444398	1	9	16	8	10	10	5	0	0	0	0	0		Q61224
ENSMUST00000088687	ENSMUSG00000069390	7	106891184	106892107	-1	4	3	6	19	17	0	0	0	0	0	0	K7N662	
ENSMUST00000088696	ENSMUSG00000059142	17	22846697	22867134	-1	0	0	0	0	0	0	0	0	9	8	0	Q66L36	
ENSMUST00000088716	ENSMUSG00000032481	9	110117708	110240178	1	49	34	63	150	52	26	113	287	262	43	264		P97496
ENSMUST00000088717	ENSMUSG00000008690	15	89355719	89372826	1	0	5	9	4	0	0	140	172	129	49	34		Q8BSP2
ENSMUST00000088735	ENSMUSG00000022026	14	80000302	80021930	1	8	4	6	11	14	10	2496	9792	6113	5609	4070	D3YYD0	
ENSMUST00000088737	ENSMUSG00000024858	19	4286001	4306222	-1	0	0	0	1	6	0	3985	4095	5758	595	3790	Q3U1V3	Q99MK8
ENSMUST00000088740	ENSMUSG00000067909	X	55226876	55243723	1	8	5	7	8	3	1	0	0	0	0	0	Q9D515	
ENSMUST00000088744	ENSMUSG00000040537	5	8072352	8368160	-1	33	16	0	0	0	0	0	0	0	0	0		Q9R1V6
ENSMUST00000088761	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	34	10	0	0	0	0	0	D6QSS8	Q9R1V6
ENSMUST00000088763	ENSMUSG00000071266	17	22424222	22456689	1	0	5	0	0	0	0	0	0	0	0	0	Q8K3B4	
ENSMUST00000088765	ENSMUSG00000044501	17	22361453	22377281	1	0	0	0	0	0	0	0	51	3	24	11	E9Q462	
ENSMUST00000088778	ENSMUSG00000067924	X	53669177	53670408	-1	0	4	20	67	4	0	38	38	18	4	32	Q9D1F0	
ENSMUST00000088779	ENSMUSG00000067925	X	53642488	53643682	-1	14	2	9	0	16	13	27	34	8	19	28	Q9D1F0	
ENSMUST00000088784						0	0	6	0	1	0	0	4	2	7	2		
ENSMUST00000088785	ENSMUSG00000078768	7	30077337	30090527	-1	10	10	11	10	9	1	9	39	14	19	16	Q8VCI1	
ENSMUST00000088786	ENSMUSG00000003161	5	8046078	8069379	1	29	10	0	0	6	12	110	757	21	20	16		Q6P069
ENSMUST00000088787	ENSMUSG00000067931	17	21567046	21588697	1	4	4	11	45	7	2	6	58	12	17	12	Q6DFU8	
ENSMUST00000088788	ENSMUSG00000036561	15	89253035	89286261	1	25	20	38	24	28	15	327	432	382	53	376	G3X9K4	
ENSMUST00000088790	ENSMUSG00000030110	6	118151745	118197718	-1	63	38	51	103	34	23	3	5	0	0	0		P35546
ENSMUST00000088796	ENSMUSG00000040514	5	7304119	7311491	1	2	0	0	2	0	2	0	0	0	0	0		Q9D5W8
ENSMUST00000088809	ENSMUSG00000067941	17	13948373	13950678	1	24	17	57	15	30	7	0	0	0	0	0		
ENSMUST00000088811	ENSMUSG00000067942	17	21008941	21028852	1	4	10	5	8	7	3	58	224	76	61	56	E9Q459	
ENSMUST00000088823	ENSMUSG00000053137	15	89142486	89149606	-1	43	34	219	139	65	28	19	47	11	8	64		Q9WUI1
ENSMUST00000088827	ENSMUSG00000022610	15	89130585	89140703	-1	11	5	30	194	16	9	1	5	3	15	20		O08911
ENSMUST00000088842	ENSMUSG00000040464	5	5537454	5559538	-1	2	1	0	1	0	0	1	11	7	0	0	F8WHJ2	
ENSMUST00000088867	ENSMUSG00000030187	6	131219223	131247362	-1	0	0	0	0	0	0	73	924	364	480	180	E9Q433	
ENSMUST00000088874	ENSMUSG00000015217	X	71555918	71560676	1	9	0	9	64	35	0	15	0	18	0	0	Q544R9	O54879
ENSMUST00000088876	ENSMUSG00000067971	X	49726973	49727932	-1	1	2	0	0	2	1	0	0	0	0	0	Q7TQW4	
ENSMUST00000088880						6	2	13	10	8	5	0	0	0	0	0		
ENSMUST00000088896	ENSMUSG00000030126	6	116018611	116193486	-1	24	18	80	61	40	11	612	2943	1139	260	871		Q69ZZ6
ENSMUST00000088898	ENSMUSG00000036916	X	48541625	48594504	-1	0	0	0	4	0	0	36	122	13	0	37		Q6P3Y5
ENSMUST00000088904	ENSMUSG00000049515	1	91322075	91348306	1	51	37	109	108	81	31	1	13	2	3	5		Q3UYR4
ENSMUST00000088911	ENSMUSG00000022387	15	88687300	88734233	-1	66	57	209	126	95	37	28	30	46	4	79	E9Q412	
ENSMUST00000088921	ENSMUSG00000067996	2	154307227	154320646	1	19	16	21	16	23	10	0	0	0	0	0	A2AJD1	
ENSMUST00000088922	ENSMUSG00000067995	14	75896937	76010865	-1	12	2	10	77	10	6	73	299	125	622	100	Q3UMJ4	Q8R0A0
ENSMUST00000088924	ENSMUSG00000067998	2	154257854	154271245	1	11	0	20	0	0	0	0	0	0	0	0		Q80XI7
ENSMUST00000088931	ENSMUSG00000035900	15	86057695	86137634	1	20	11	13	8	0	3	232	245	265	9	296		Q8CB44
ENSMUST00000088935	ENSMUSG00000036985	X	48171969	48208878	-1	21	20	0	1385	48	29	821	2790	765	43	423		P59268
ENSMUST00000088940	ENSMUSG00000038141	17	6270470	6308314	1	15	9	20	353	48	18	94	263	169	64	187	Q3U3W2	
ENSMUST00000088950	ENSMUSG00000068008	2	153918230	153932996	1	11	12	18	26	20	8	0	0	0	0	0		Q80ZU7
ENSMUST00000088955	ENSMUSG00000068009	2	153900388	153912795	1	6	8	20	14	14	6	0	0	0	0	0		Q8BU51
ENSMUST00000088962	ENSMUSG00000068011	6	115583544	115592576	-1	42	25	121	50	55	20	1	1	6	0	4	D3YX48	
ENSMUST00000088970	ENSMUSG00000068015	14	74754674	74947877	-1	19	22	28	395	42	23	194	493	385	40	328		P62046
ENSMUST00000088973	ENSMUSG00000031099	X	47809368	47892974	-1	2	0	0	5	0	0	0	0	0	0	0		Q6PGB8
ENSMUST00000088976	ENSMUSG00000027478	2	153649450	153687730	1	0	0	0	0	0	0	0	0	0	0	0	Q541E5	O88509
ENSMUST00000088987	ENSMUSG00000053004	6	114397936	114483296	1	30	13	23	57	28	2	3	7	4	0	1	B3Y5T0	P70174
ENSMUST00000089003	ENSMUSG00000030302	6	113743831	114042613	-1	0	0	0	140	0	0	0	0	0	0	0	Q3UHJ3	Q9R0K7
ENSMUST00000089011	ENSMUSG00000037972	16	11066298	11074983	1	23	11	23	65	24	11	54	59	51	51	180	Q5M8P0	P61807
ENSMUST00000089015	ENSMUSG00000068037	17	12841079	12868143	-1	7	8	16	11	27	6	0	0	0	0	0	Q0VB49	P30554
ENSMUST00000089017	ENSMUSG00000033487	14	72537946	72710003	-1	33	33	109	50	29	18	483	825	497	90	351		Q8BX90
ENSMUST00000089018	ENSMUSG00000056952	6	113697050	113711069	1	0	8	8	160	20	4	53	80	166	27	129	F8VQE6	
ENSMUST00000089022	ENSMUSG00000060477	6	113638467	113695026	1	29	81	113	0	87	38	35	707	87	23	79		Q8CFA1
ENSMUST00000089023	ENSMUSG00000060477	6	113638467	113695026	1	0	0	0	3	0	0	0	0	3	0	0		Q8CFA1
ENSMUST00000089024	ENSMUSG00000068039	17	12915701	12925067	1	2	0	0	64	2	0	117	960	283	842	283		P11983
ENSMUST00000089027	ENSMUSG00000068040	2	153161303	153210466	1	10	10	24	0	14	9	580	919	706	99	521		Q8BH24
ENSMUST00000089042	ENSMUSG00000022971	16	91372783	91405589	1	6	0	7	0	20	5	500	854	891	197	917	Q923Z6	O35664
ENSMUST00000089049	ENSMUSG00000045211	14	70577847	70582571	1	34	24	199	130	36	23	652	935	478	130	376		Q3U2V3
ENSMUST00000089052	ENSMUSG00000070426	7	102019137	102065469	-1	0	9	45	17	8	0	0	0	0	0	0	K4DI70	
ENSMUST00000089054	ENSMUSG00000036502	X	38196573	38252439	-1	0	6	2	16	0	0	1	0	0	5	3		Q8BHW5
ENSMUST00000089056	ENSMUSG00000036502	X	38196573	38252439	-1	0	1	0	1	0	0	0	0	0	0	0		Q8BHW5
ENSMUST00000089058	ENSMUSG00000014426	17	12227621	12318660	-1	34	28	74	136	78	32	78	200	183	23	175		O08648
ENSMUST00000089059	ENSMUSG00000019188	2	152669461	152708670	1	0	0	2	37	5	0	2985	4047	2170	665	1601		Q9D8V0
ENSMUST00000089060	ENSMUSG00000098348	X	38038199	38043114	-1	3	2	8	3	5	3	0	0	0	0	0	Q3V0X0	
ENSMUST00000089062	ENSMUSG00000068048	X	37899097	37901770	-1	1	0	0	0	1	1	0	0	0	0	0	Q9EQM5	
ENSMUST00000089075	ENSMUSG00000071770	X	37557412	37562283	1	2	0	0	0	8	0	0	0	0	2	0	Q504P9	
ENSMUST00000089084						0	3	0	15	0	4	11	0	14	0	55		
ENSMUST00000089085	ENSMUSG00000023868	17	8525372	8986648	1	0	0	0	0	45	0	0	0	0	0	0		Q8CA95
ENSMUST00000089097	ENSMUSG00000068067	16	89174735	89175199	1	0	0	5	0	0	0	0	0	0	0	0	Q3V4B6	
ENSMUST00000089098	ENSMUSG00000068068	16	89169490	89169648	1	4	2	11	0	2	3	0	0	0	0	0	D3YX18	
ENSMUST00000089101	ENSMUSG00000068071	16	89140851	89141339	1	1	0	7	2	1	2	0	0	0	0	0	D3YWL8	
ENSMUST00000089104	ENSMUSG00000068073	16	89063412	89064002	-1	3	0	22	5	7	6	0	0	0	0	0	O09048	
ENSMUST00000089105	ENSMUSG00000068074	16	89040921	89041452	-1	7	2	7	2	6	0	0	0	0	0	0	O09048	
ENSMUST00000089106	ENSMUSG00000068075	16	89015277	89015846	1	5	3	0	5	2	2	0	0	0	0	0	O08631	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000089111	ENSMUSG00000068078	16	88758847	88759792	1	8	4	12	11	15	10	0	0	0	0	0	Q9D746	
ENSMUST00000089112	ENSMUSG00000068079	2	152143561	152149097	1	4	6	32	64	11	1	0	0	0	0	0		Q60756
ENSMUST00000089119	ENSMUSG00000094724	17	6978860	7011299	1	0	0	0	0	0	0	1281	4262	1345	928	1268	Q5FWA0	Q9CQ01
ENSMUST00000089120	ENSMUSG00000095720	17	7025837	7087467	1	0	0	0	0	0	1	27	34	36	26	10	Q3TRG0	
ENSMUST00000089129	ENSMUSG00000068086	15	82452377	82456827	1	21	22	24	29	18	8	0	0	0	5	0		P11714
ENSMUST00000089140	ENSMUSG00000027455	2	151494182	151511414	1	2	0	8	227	0	1	13	14	0	33	38	Q3UVN5	Q9CZ44
ENSMUST00000089155	ENSMUSG00000068101	15	82233779	82244747	-1	10	4	0	0	8	0	0	0	0	14	0		Q9CQA0
ENSMUST00000089157	ENSMUSG00000068101	15	82233779	82244747	-1	0	3	22	64	5	11	20	29	13	0	15		Q9CQA0
ENSMUST00000089161	ENSMUSG00000068105	15	82221744	82224339	-1	55	77	854	0	40	12	6	18	12	12	19	Q3SXS6	Q9D8D0
ENSMUST00000089162	ENSMUSG00000030104	6	108828641	108859356	1	26	27	92	235	40	18	2431	5771	4093	351	2397		Q925U4
ENSMUST00000089165	ENSMUSG00000079655	X	26028214	26051041	-1	0	0	0	0	0	0	0	0	0	0	0	Q4KL04	
ENSMUST00000089174	ENSMUSG00000068114	15	82127922	82142200	1	16	12	14	39	31	11	69	141	89	13	83		Q8C7V8
ENSMUST00000089178	ENSMUSG00000068117	15	82069997	82126811	1	16	20	21	94	38	8	0	0	0	0	0	F8WHB9	
ENSMUST00000089184	ENSMUSG00000042529	11	61022564	61071131	1	0	0	0	53	11	0	0	0	0	0	0		P52187
ENSMUST00000089185	ENSMUSG00000034265	17	5492600	5753891	1	16	4	38	391	32	23	25	23	24	4	27		Q8BQQ1
ENSMUST00000089187	ENSMUSG00000022472	15	81992523	82033862	-1	0	0	0	12	0	0	20	0	10	1	14	E9Q2Y9	
ENSMUST00000089188	ENSMUSG00000068122	X	21484544	21489164	1	2	1	9	8	5	7	0	0	0	0	0		P35374
ENSMUST00000089200	ENSMUSG00000068129	2	150570415	150578944	1	7	7	16	8	11	4	93	134	53	69	30		O89098
ENSMUST00000089207	ENSMUSG00000068134	2	150114406	150136708	-1	0	0	0	5	14	0	130	375	211	65	98		Q8BZW4
ENSMUST00000089208	ENSMUSG00000064293	6	105677660	106699310	1	8	7	0	3	6	5	0	0	0	0	0		Q69Z26
ENSMUST00000089215	ENSMUSG00000030092	6	104492790	104863406	1	0	0	0	0	0	0	0	0	0	0	0		Q9JMB8
ENSMUST00000089217	ENSMUSG00000001924	X	20658326	20683179	1	0	26	46	0	0	12	27	0	28	0	27	B9EHN0	Q02053
ENSMUST00000089221						15	6	19	19	9	0	0	0	0	0	0		
ENSMUST00000089230	ENSMUSG00000022052	14	67014057	67072471	-1	17	13	22	209	31	14	210	941	422	73	266	Q3TT94	Q6P1F6
ENSMUST00000089236	ENSMUSG00000046204	14	66911170	66920054	1	23	19	41	72	37	9	0	0	0	0	0		Q8BHK0
ENSMUST00000089245	ENSMUSG00000035378	6	100568256	100671157	-1	6	0	18	0	10	7	4	0	0	5	8		Q7TMX5
ENSMUST00000089246	ENSMUSG00000068149	X	19479420	19481319	-1	5	5	7	3	2	1	0	14	3	0	0	Q810P0	
ENSMUST00000089250	ENSMUSG00000059456	14	66153257	66281052	-1	0	0	0	69	0	0	2255	3211	3304	141	2270	E9Q2A6	
ENSMUST00000089257	ENSMUSG00000068154	2	146221921	146225020	1	24	7	40	707	52	19	0	1	0	0	0	Q05BD7	Q63ZV0
ENSMUST00000089275						0	0	0	30	0	0	0	0	5	0	0		
ENSMUST00000089279	ENSMUSG00000068167	16	64477813	64479148	-1	12	10	14	3	9	7	0	0	0	0	0	Q8CH19	
ENSMUST00000089286						3	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000089287	ENSMUSG00000030061	6	97183670	97205647	-1	2	2	7	21	5	5	142	858	267	366	162		Q8C878
ENSMUST00000089289	ENSMUSG00000022911	16	62793685	62847040	-1	9	10	6	9	14	3	172	360	342	79	268		Q640N2
ENSMUST00000089293	ENSMUSG00000053411	15	79915807	79971119	-1	0	2	0	0	0	0	22	31	0	10	0	F8WHN2	
ENSMUST00000089295	ENSMUSG00000046500	6	96831203	97060413	-1	7	8	22	25	21	4	0	0	2	1	0		Q7TPG5
ENSMUST00000089296	ENSMUSG00000070421	7	104642880	104647305	-1	11	13	30	21	17	11	0	0	0	0	1	Q8VGV5	
ENSMUST00000089299	ENSMUSG00000089837	15	79789675	79834237	-1	0	0	0	0	0	0	0	0	0	0	0	F8VQB8	
ENSMUST00000089302	ENSMUSG00000031010	X	13071498	13173328	1	20	27	21	9	29	22	877	1876	1876	184	956	Q4FE56	
ENSMUST00000089304	ENSMUSG00000068181	6	95322112	95322210	1	0	0	0	0	0	0	0	0	0	0	0	F6WLJ2	
ENSMUST00000089305	ENSMUSG00000068182	16	59303152	59304075	1	2	4	3	5	8	4	0	0	0	0	0	L7N205	
ENSMUST00000089311	ENSMUSG00000042524	15	79724070	79742536	-1	0	0	0	49	0	9	929	3087	728	0	508		Q8BJS4
ENSMUST00000089317	ENSMUSG00000045095	6	93675455	94283917	-1	0	0	72	25	12	8	0	0	0	0	22		Q6RHR9
ENSMUST00000089318	ENSMUSG00000047293	16	58717435	58718724	-1	4	1	11	10	9	3	83	407	291	255	70		Q0VDU3
ENSMUST00000089332	ENSMUSG00000068196	16	57624258	57754737	-1	55	50	151	86	57	36	0	1	1	5	26		Q00780
ENSMUST00000089334	ENSMUSG00000034037	6	91978878	92076004	1	37	0	89	78	51	13	0	0	0	0	0	E9QKY4	
ENSMUST00000089338	ENSMUSG00000034623	14	64075438	64090162	-1	4	0	16	6	6	3	0	0	0	0	0	G3X9K6	
ENSMUST00000089360	ENSMUSG00000052917	16	56048338	56190012	1	0	9	5	12	7	3	153	129	278	12	292	E9Q1L5	
ENSMUST00000089362	ENSMUSG00000052917	16	56048338	56190012	1	12	0	0	0	0	0	88	582	214	248	51		Q8BUH8
ENSMUST00000089370	ENSMUSG00000071816	X	8803691	8809386	1	3	5	0	0	0	0	0	0	0	0	0	Q6XAS2	
ENSMUST00000089374	ENSMUSG00000079701	X	8583404	8591816	-1	7	3	0	0	2	0	0	0	0	0	0	Q6XAS4	
ENSMUST00000089377	ENSMUSG00000068220	15	78926725	78930465	1	8	3	17	19	22	10	931	1297	412	26951	2068		P16045
ENSMUST00000089378	ENSMUSG00000022436	15	78899667	78919517	1	13	16	18	96	32	15	15	76	20	3	38		P60487
ENSMUST00000089379	ENSMUSG00000079701	X	8583404	8591816	-1	0	0	0	0	0	0	0	0	0	0	0	Q6XAS4	
ENSMUST00000089394	ENSMUSG00000048279	14	61138457	61240695	1	0	3	0	41	0	0	0	0	0	0	0		
ENSMUST00000089398	ENSMUSG00000068227	15	78480553	78495066	-1	13	15	68	28	17	17	188	130	93	27	270		P16297
ENSMUST00000089399	ENSMUSG00000022641	16	50191844	50432390	-1	0	0	0	0	0	0	0	0	51	0	0		Q8VBW5
ENSMUST00000089402	ENSMUSG00000031169	X	8193848	8206525	-1	0	0	6	0	5	0	6	3	0	2	0		Q9JJJ7
ENSMUST00000089403	ENSMUSG00000031169	X	8193848	8206525	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JJJ7
ENSMUST00000089404	ENSMUSG00000022641	16	50191844	50432390	-1	27	0	25	390	42	21	0	3	0	0	0		Q8VBW5
ENSMUST00000089414	ENSMUSG00000033287	15	78428564	78438909	1	5	0	0	0	6	0	51	17	8	4	26	E0CYQ0	
ENSMUST00000089417	ENSMUSG00000094553	6	90101556	90108207	1	6	2	0	0	4	1	0	0	0	0	0		
ENSMUST00000089418	ENSMUSG00000068231	6	89869461	89870529	-1	10	4	8	6	10	3	0	0	0	0	0		Q8VIC9
ENSMUST00000089419	ENSMUSG00000068232	6	89844518	89845615	-1	6	8	10	5	8	2	0	0	0	0	0	Q05A83	Q8VBS7
ENSMUST00000089420	ENSMUSG00000068234	6	89883622	89894284	1	6	8	4	2	5	6	0	0	0	0	0		Q9EQ47
ENSMUST00000089430	ENSMUSG00000068240	4	3973092	3973595	-1	8	0	42	0	15	4	6399	7322	4484	27507	2898	Q66JP1	P62984
ENSMUST00000089449	ENSMUSG00000033174	6	88724412	88828360	1	0	0	0	0	0	0	29	0	93	0	78		O35678
ENSMUST00000089450	ENSMUSG00000056656	15	77747799	77755229	-1	4	13	7	9	15	11	0	9	0	0	2	F6VS49	
ENSMUST00000089452	ENSMUSG00000057346	15	77403789	77411080	-1	0	11	0	9	0	0	0	0	0	7	9	Q8VDU3	
ENSMUST00000089461	ENSMUSG00000058793	2	132263148	132312050	1	158	106	574	0	102	78	9183	10829	8350	676	6903	A2AMQ5	
ENSMUST00000089465	ENSMUSG00000050014	15	77584158	77596125	-1	12	8	20	12	12	11	0	2	0	16	7	G3X9K7	
ENSMUST00000089469	ENSMUSG00000068252	15	77422210	77447492	-1	105	45	214	66	111	94	5	0	0	1	0	B1AQP7	
ENSMUST00000089473	ENSMUSG00000021969	14	57832702	57890262	-1	72	80	157	189	69	39	338	1331	612	330	552		Q5Y5T1
ENSMUST00000089482	ENSMUSG00000021952	14	57581002	57665430	-1	2	0	0	0	0	3	0	0	13	12	0		Q9ESJ0
ENSMUST00000089485	ENSMUSG00000053580	11	105589986	105929304	1	0	4	0	70	14	5	0	0	0	0	0	F6VCI2	
ENSMUST00000089490	ENSMUSG00000068259	6	40544036	40544977	-1	5	8	6	3	7	1	0	0	0	0	0	Q8VF30	
ENSMUST00000089494	ENSMUSG00000050222	14	57524829	57543165	1	2	3	1	136	6	7	0	0	0	0	0	A0A0B4J1G4	
ENSMUST00000089497	ENSMUSG00000030056	6	87814269	87838798	-1	11	11	16	30	8	3	268	772	382	257	325		Q69ZQ2
ENSMUST00000089501						5	11	13	12	7	4	0	0	2	1	2		
ENSMUST00000089506	ENSMUSG00000068264	2	131207078	131213514	1	7	0	13	0	0	4	35	0	0	0	0	Q80V29	
ENSMUST00000089510	ENSMUSG00000068267	2	131175182	131180067	-1	37	34	83	523	63	31	5263	4355	3218	804	1969		P27790
ENSMUST00000089519	ENSMUSG00000057230	6	86849517	87003223	1	19	13	52	76	31	18	104	49	245	14	168		Q3UHJ0
ENSMUST00000089520	ENSMUSG00000068270	X	6399854	6637448	1	80	45	84	342	122	53	0	1	1	2	6		Q1W617
ENSMUST00000089534	ENSMUSG00000078308	9	51621425	51624874	1	34	33	82	29	47	23	1672	1412	1558	1256	939	D3YYI5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000089549	ENSMUSG00000022156	14	56117619	56120625	-1	17	7	22	14	12	11	0	0	0	5	0		P08884
ENSMUST00000089555	ENSMUSG00000068289	14	55971428	55973995	1	4	8	9	5	8	4	0	0	0	0	0	Q91VB1	
ENSMUST00000089558	ENSMUSG00000057278	6	86371304	86379328	1	8	0	4	1	0	2	115	314	71	682	94		P62309
ENSMUST00000089559	ENSMUSG00000068290	2	130653960	130664659	-1	3	4	5	64	6	3	248	375	232	87	234		Q80WW9
ENSMUST00000089561	ENSMUSG00000037703	2	130632839	130642803	-1	0	0	48	0	0	0	0	0	0	0	0		A2AHG0
ENSMUST00000089565	ENSMUSG00000030551	7	70351946	70366735	-1	3	4	20	3	10	0	0	0	0	0	0	D3YYP4	
ENSMUST00000089570	ENSMUSG00000054226	6	85911865	85930284	1	4	4	0	2	1	1	5	9	1	5	4	G3X9K8	
ENSMUST00000089578	ENSMUSG00000068302	6	85423886	85428877	1	17	11	9	59	13	5	1	1	0	0	2		Q5TIS6
ENSMUST00000089581	ENSMUSG00000037773	2	130417247	130424701	-1	0	5	0	7	0	0	20	4	0	0	15		Q6P1Z5
ENSMUST00000089584						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000089593						17	5	68	24	10	5	0	0	0	0	0		
ENSMUST00000089595	ENSMUSG00000033788	6	84008590	84211060	1	10	0	26	0	0	0	0	0	0	0	0	E9PXU9	
ENSMUST00000089610	ENSMUSG00000022565	15	76170974	76232574	-1	0	0	0	0	0	0	897	188	1753	64	400		Q9QXS1
ENSMUST00000089614	ENSMUSG00000068314	11	26593241	26593862	1	4	2	5	295	14	7	0	3	0	0	1	Q3USS0	
ENSMUST00000089616	ENSMUSG00000062825	11	120345690	120348542	-1	0	0	0	0	0	0	0	0	0	0	3	F8WGM8	
ENSMUST00000089618	ENSMUSG00000022900	16	36693978	36726804	1	5	6	23	0	0	10	0	1	2	0	1		Q8CBR1
ENSMUST00000089619	ENSMUSG00000022216	14	55578123	55581529	1	0	0	0	0	0	0	0	237	0	269	1	G3X9K9	
ENSMUST00000089620	ENSMUSG00000022901	16	36603869	36666081	-1	4	7	13	6	21	1	74	541	163	449	113	Q549Q9	P42082
ENSMUST00000089622	ENSMUSG00000034832	6	83362373	83459084	-1	80	45	171	158	107	48	591	936	1122	59	1145		Q8BG87
ENSMUST00000089628	ENSMUSG00000094733	16	36210403	36217788	1	0	3	1	5	0	1	163	516	235	886	304	Q6IE28	
ENSMUST00000089634	ENSMUSG00000027381	2	128126038	128162547	1	13	7	6	16	7	6	26	138	22	6	29	Q6PEB3	
ENSMUST00000089635						0	2	0	4	0	3	0	2	0	14	0		
ENSMUST00000089641	ENSMUSG00000068327	6	83068324	83070293	-1	1	1	0	26	9	1	0	0	0	0	0		Q61663
ENSMUST00000089645	ENSMUSG00000068329	6	83051266	83055273	-1	0	0	0	0	0	0	188	350	158	18	101		Q9JIY5
ENSMUST00000089651	ENSMUSG00000068335	6	83030934	83033471	-1	0	5	0	18	5	0	426	571	324	57	197		P97465
ENSMUST00000089654	ENSMUSG00000044361	15	76119517	76126596	-1	0	0	0	0	23	26	0	0	0	0	0	E9PXU3	
ENSMUST00000089655	ENSMUSG00000061751	16	33974258	34573532	-1	19	0	0	17	15	14	0	0	0	0	0		A2CG49
ENSMUST00000089667	ENSMUSG00000068341	6	78375874	78378865	-1	3	0	5	3	5	0	0	0	0	0	0	Q9QUS9	
ENSMUST00000089669	ENSMUSG00000063704	15	75993769	75999152	1	3	9	29	59	10	2	0	0	0	0	0		Q80Y86
ENSMUST00000089673	ENSMUSG00000050468	2	127338639	127357651	1	0	0	65	24	8	0	0	0	0	0	0		Q6HA09
ENSMUST00000089677	ENSMUSG00000022811	16	33380775	33503903	1	8	0	9	22	13	2	302	697	547	215	343	Q548L0	Q61624
ENSMUST00000089680	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	1	0	0	0	0	0	0	0	Q91VK2	
ENSMUST00000089681	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	34	0	0	0	8	0	0	0		
ENSMUST00000089684	ENSMUSG00000035629	16	32821703	32877766	-1	12	14	35	4	0	8	0	0	51	0	0		Q80U62
ENSMUST00000089687	ENSMUSG00000052631	6	72513644	72521634	-1	0	4	1	0	0	0	0	0	0	0	2	E9QJU1	
ENSMUST00000089688	ENSMUSG00000000957	14	54431612	54441265	1	18	22	42	86	35	23	8	4	16	54	307		P53690
ENSMUST00000089689						3	0	9	1	4	3	0	0	0	0	0		
ENSMUST00000089726	ENSMUSG00000068373	2	104143073	104410334	-1	0	43	127	945	110	79	0	10	0	1	3	D3YZ21	
ENSMUST00000089739	ENSMUSG00000095030	14	52349103	52350044	-1	6	2	7	6	7	5	0	0	0	0	0	L7N457	
ENSMUST00000089745	ENSMUSG00000027361	2	126627442	126676337	-1	9	9	7	89	4	1	15	7	9	4	19		Q00420
ENSMUST00000089752	ENSMUSG00000053754	14	52198151	52257723	-1	7	10	59	36	29	10	581	888	1343	119	1386		Q09XV5
ENSMUST00000089759	ENSMUSG00000046598	16	31422280	31458901	1	2	2	6	3	6	1	6	0	0	0	0		Q80XN0
ENSMUST00000089765	ENSMUSG00000068391	15	73090392	73097554	1	0	0	0	0	0	0	208	385	179	893	133		Q9JKP8
ENSMUST00000089770	ENSMUSG00000047921	15	72589621	73061204	-1	1	0	0	77	4	15	708	588	882	52	648		Q3U0M1
ENSMUST00000089771	ENSMUSG00000068392	14	51922160	51922773	-1	7	7	25	6	10	2	0	0	0	0	0		Q5GAM7
ENSMUST00000089775	ENSMUSG00000022537	16	30511855	30550842	-1	0	0	0	66	20	13	0	2	1	2	7	F6SF18	
ENSMUST00000089776	ENSMUSG00000068394	2	125563088	125625113	-1	35	33	57	136	40	18	79	216	230	35	176		A2AUM9
ENSMUST00000089785						0	0	0	0	0	0	122	13	129	650	106		
ENSMUST00000089788						0	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000089789	ENSMUSG00000094157	14	42310210	42325394	1	0	0	0	3	0	1	0	0	0	0	0	K7N665	
ENSMUST00000089798	ENSMUSG00000068407	14	51056698	51057242	-1	6	7	10	7	9	4	0	0	1	0	0	W0UUY1	Q5GAM8
ENSMUST00000089824	ENSMUSG00000022525	16	29209695	29230531	1	16	7	8	14	8	11	0	0	0	0	0		
ENSMUST00000089825	ENSMUSG00000027201	2	125084628	125123661	-1	1	0	0	0	0	0	13	16	28	58	45	G8JL68	
ENSMUST00000089830	ENSMUSG00000068426	6	57404366	57405483	1	10	6	4	2	4	1	0	0	0	0	0	Q8R2C7	
ENSMUST00000089832	ENSMUSG00000068428	16	26957236	26989974	-1	6	4	12	10	15	2	0	0	0	0	0		Q3URY2
ENSMUST00000089836	ENSMUSG00000068431	14	50515121	50516240	1	11	4	8	5	5	2	0	0	0	0	0	A2RTP5	
ENSMUST00000089838	ENSMUSG00000095917	14	50453054	50453989	1	9	1	3	6	5	2	0	0	0	0	0	E9PV79	
ENSMUST00000089840	ENSMUSG00000044566	13	38006052	38037069	-1	42	41	95	37	36	21	8	31	13	3	12		Q5IR70
ENSMUST00000089844	ENSMUSG00000068437	14	50034391	50040092	-1	6	2	1	0	2	1	0	0	0	0	0	Q05A45	
ENSMUST00000089860	ENSMUSG00000037709	6	58932090	59024549	-1	23	20	16	27	22	9	0	0	0	2	2		Q8BGI4
ENSMUST00000089874	ENSMUSG00000071856	18	44425060	44812182	-1	68	62	122	139	101	25	0	0	0	0	0	E9PWI3	
ENSMUST00000089883	ENSMUSG00000022887	16	23451785	23520590	-1	17	15	48	31	33	9	0	0	0	5	4		P98064
ENSMUST00000089894	ENSMUSG00000055827	15	63857724	63878558	-1	0	0	0	0	0	0	0	0	0	0	0		Q8CB12
ENSMUST00000089900	ENSMUSG00000056293	15	63824346	63845177	-1	0	0	2	0	0	4	0	0	0	0	1		Q2KHK6
ENSMUST00000089902	ENSMUSG00000022875	16	23057865	23082068	1	0	0	0	5	0	0	0	0	0	5	0	D3YTY9	
ENSMUST00000089906	ENSMUSG00000072774	5	104813169	104860070	-1	4	0	2	0	2	1	0	15	21	8	22	F8VPV1	
ENSMUST00000089912	ENSMUSG00000060227	2	121866970	121936220	1	0	0	0	0	0	0	0	0	0	0	0		Q6P2L7
ENSMUST00000089915	ENSMUSG00000060227	2	121866970	121936220	1	5	5	0	0	0	0	0	0	0	0	0		Q6P2L7
ENSMUST00000089918	ENSMUSG00000093755	6	66804212	66805443	-1	6	3	7	0	5	1	0	0	0	0	0	G3UWE6	
ENSMUST00000089922						3	3	9	59	3	0	46	164	44	7	61		
ENSMUST00000089925	ENSMUSG00000022861	16	22468461	22657221	-1	22	0	98	28	17	8	332	998	792	83	687		Q91WG7
ENSMUST00000089926	ENSMUSG00000068479	2	121491911	121506665	-1	69	63	142	77	72	37	661	3701	1576	1327	1123		Q9CQU1
ENSMUST00000089948	ENSMUSG00000028360	3	153973436	154271722	1	9	5	13	98	12	2	0	1	0	0	0		Q5RJI2
ENSMUST00000089950	ENSMUSG00000038975	3	153907287	153913009	-1	0	8	22	10	12	0	57	256	49	292	106	Q3TVF4	
ENSMUST00000089959	ENSMUSG00000037580	14	47153895	47189413	-1	12	11	25	176	20	15	366	1019	438	90	277	Q3U7P6	Q05915
ENSMUST00000089968	ENSMUSG00000036036	17	37001163	37010635	1	7	3	13	11	8	6	0	0	0	0	0		Q8C6P8
ENSMUST00000089982	ENSMUSG00000039068	3	152395473	152462826	1	0	0	0	0	0	0	157	534	490	427	388	D3YTT9	
ENSMUST00000090002	ENSMUSG00000004980	6	51460932	51469894	-1	19	0	26	9	8	9	1093	5472	2056	1090	2007		O88569
ENSMUST00000090006	ENSMUSG00000025809	8	128685654	128733200	1	13	0	7	140	14	13	461	2289	586	947	1001		P09055
ENSMUST00000090019	ENSMUSG00000029822	6	50293330	50456201	-1	0	10	0	10	7	0	0	0	0	0	0	D3YTT6	
ENSMUST00000090020	ENSMUSG00000038534	11	97050628	97068904	1	33	12	52	91	28	18	347	269	253	0	190	A2A716	
ENSMUST00000090023	ENSMUSG00000022841	16	20535478	20544909	1	0	0	0	24	12	0	3578	4690	3148	1327	2582	Q3TWV4	
ENSMUST00000090024	ENSMUSG00000058690	14	36874936	36968777	-1	22	18	32	56	38	8	0	0	0	0	33		Q3UHI0
ENSMUST00000090025	ENSMUSG00000068522	15	52040107	52045722	1	2	3	16	39	16	3	0	0	0	0	0		Q811W1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000090027	ENSMUSG00000041408	14	34673928	34747983	1	0	0	0	0	0	0	254	325	396	28	207	B7ZP47	
ENSMUST00000090028	ENSMUSG00000079110	2	120456019	120504913	1	0	0	17	0	0	0	0	0	0	6	0	A2AVV5	
ENSMUST00000090031	ENSMUSG00000068523	3	146499807	146505572	1	10	13	15	47	9	4	2334	3077	1183	3506	853	Q3UKC8	Q80SZ7
ENSMUST00000090040	ENSMUSG00000021798	14	34526699	34588681	-1	11	31	0	34	51	0	0	0	0	0	0		Q9JKS4
ENSMUST00000090042	ENSMUSG00000033808	2	120355312	120404113	-1	0	0	100	31	21	19	176	1288	360	573	322	A2AQJ5	
ENSMUST00000090043						10733	10984	4488	4776	7036	2651	900	1083	2107	519	2059		
ENSMUST00000090046	ENSMUSG00000033808	2	120355312	120404113	-1	0	24	0	0	10	0	128	292	180	136	140	A2AQJ6	
ENSMUST00000090052	ENSMUSG00000041215	16	20141063	20232573	1	4	58	87	23	24	0	8	200	31	44	0		Q3TUF7
ENSMUST00000090057	ENSMUSG00000022340	15	44671859	44788063	-1	14	0	0	137	0	0	0	0	0	0	0		Q8BHS8
ENSMUST00000090061	ENSMUSG00000072878	6	96164497	96166243	-1	9	3	22	54	20	9	0	0	0	0	0	Q3V2K7	
ENSMUST00000090062	ENSMUSG00000068535	16	19565940	19566881	-1	3	4	9	1	8	8	0	0	0	0	0	Q7TS53	
ENSMUST00000090063	ENSMUSG00000068536	6	48974963	48978746	1	29	14	78	0	43	23	0	0	0	0	0	F6TPL1	
ENSMUST00000090064						1	1	7	6	0	1	0	0	0	0	0		
ENSMUST00000090070	ENSMUSG00000054435	6	48684549	48692060	1	9	0	0	4	13	0	60	285	60	266	268	D3YTN4	
ENSMUST00000090071	ENSMUSG00000050211	2	120166412	120245335	-1	23	13	48	40	0	0	0	0	0	0	0		Q50L42
ENSMUST00000090086	ENSMUSG00000000884	16	18498768	18566679	1	0	0	0	0	0	0	2	0	0	0	0		Q9EQ15
ENSMUST00000090095	ENSMUSG00000022307	15	41447482	41861048	1	0	9	0	8	0	5	280	643	95	17	39		Q4KMM3
ENSMUST00000090096	ENSMUSG00000022307	15	41447482	41861048	1	0	0	0	12	0	0	0	0	0	0	0		Q4KMM3
ENSMUST00000090103	ENSMUSG00000000325	16	18348182	18407076	1	0	0	0	0	0	0	0	0	0	0	0		P98203
ENSMUST00000090127	ENSMUSG00000105504	3	142493978	142522344	1	87	91	49	1979	120	45	27	180	43	68	196		Q8CFB4
ENSMUST00000090134	ENSMUSG00000028273	3	142239590	142395696	-1	0	21	0	0	0	0	0	0	0	0	0	Q9CRA2	
ENSMUST00000090147	ENSMUSG00000021900	14	31641028	31668579	1	13	5	31	24	25	11	242	241	157	66	115		
ENSMUST00000090150	ENSMUSG00000051359	15	37366175	37792570	-1	15	0	3	28	0	0	0	0	0	0	0		Q91X97
ENSMUST00000090156	ENSMUSG00000068574	6	42460076	42461017	-1	10	6	5	12	9	2	0	1	0	0	3	Q8VF80	
ENSMUST00000090159	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	0	0	0	0	0		Q6ZPR5
ENSMUST00000090165	ENSMUSG00000022756	16	17572018	17576998	-1	0	0	0	0	0	0	0	0	0	0	8	Q91WD3	
ENSMUST00000090166						36	25	167	49	31	16	0	3	1	0	0		
ENSMUST00000090170	ENSMUSG00000068579	15	36308144	36308956	-1	10	0	46	0	15	6	2	0	2	0	0		
ENSMUST00000090171	ENSMUSG00000055301	3	138217760	138233382	1	17	15	17	11	13	11	0	1	0	0	0	Q9D748	Q64437
ENSMUST00000090174	ENSMUSG00000068580	2	119208617	119217049	1	0	0	0	27	10	0	123	48	56	38	43		Q9DAZ9
ENSMUST00000090178	ENSMUSG00000074212	3	137867675	137916557	1	262	293	973	299	319	155	224	649	353	112	282		Q149L6
ENSMUST00000090180	ENSMUSG00000021904	14	31217860	31230350	1	31	23	93	84	60	29	1	0	0	0	3		Q4LFA9
ENSMUST00000090190	ENSMUSG00000050240	16	17233572	17263430	1	121	106	442	210	140	39	5	15	7	4	32		Q9JLZ6
ENSMUST00000090192	ENSMUSG00000038965	16	17152013	17202649	-1	8	11	0	0	10	8	1394	3144	1355	1953	945	Q561N4	P68037
ENSMUST00000090195	ENSMUSG00000078984	12	116275386	116275612	1	153	88	130	1212	227	118	2	7	3	1	2	G8JL69	
ENSMUST00000090199	ENSMUSG00000022773	16	17069696	17087045	1	0	0	0	0	1	0	2	11	0	1	3	D3YU87	
ENSMUST00000090205	ENSMUSG00000058351	14	31088132	31128930	-1	0	0	10	19	5	0	75	124	72	280	37		Q8C1Q6
ENSMUST00000090212	ENSMUSG00000071547	14	31134853	31139121	1	11	11	16	11	15	10	175	173	91	36	111	Q91X76	
ENSMUST00000090214	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	0	0	24	0	0	0	0	E9Q4Y5	
ENSMUST00000090219	ENSMUSG00000040093	2	118528757	118549687	-1	12	10	21	15	20	16	188	261	147	24	107	A2AV75	
ENSMUST00000090227	ENSMUSG00000039100	15	31455899	31531037	-1	20	17	48	43	31	13	1924	2925	2827	180	1482		Q6ZQ89
ENSMUST00000090237						11	9	12	59	24	13	0	12	10	2	3		
ENSMUST00000090243	ENSMUSG00000029924	6	39334773	39377675	-1	26	18	64	53	36	23	517	1756	937	175	593		
ENSMUST00000090246	ENSMUSG00000050931	3	131318985	131491411	-1	54	70	275	93	93	28	1860	2994	2724	328	2021		Q9D4B1
ENSMUST00000090247	ENSMUSG00000022263	15	27730652	28025848	-1	86	54	133	263	117	48	152	214	326	27	438		Q0KL02
ENSMUST00000090257	ENSMUSG00000068604	17	26542760	26543715	1	11	11	19	54	13	8	0	4	0	1	0	D3Z536	
ENSMUST00000090260	ENSMUSG00000068606	18	60268301	60273267	-1	343	252	1508	709	388	235	5	33	12	4	19	E9QAA8	
ENSMUST00000090269	ENSMUSG00000068614	2	114047282	114053548	-1	11	6	35	28	20	6	0	0	0	0	0	Q497E4	P68033
ENSMUST00000090275	ENSMUSG00000068615	2	114009601	114013619	-1	14	14	7	80	15	6	0	0	0	0	0		O54851
ENSMUST00000090277	ENSMUSG00000068617	16	14906637	14925879	1	9	3	33	13	8	7	0	0	0	1	0		Q9D3N2
ENSMUST00000090287	ENSMUSG00000018830	16	14194527	14291408	-1	76	47	103	70	76	44	0	2	3	3	4	E9QPE7	
ENSMUST00000090292	ENSMUSG00000022191	15	12824815	12935290	1	0	0	0	0	15	0	83	146	183	23	175		Q5HZJ0
ENSMUST00000090293	ENSMUSG00000026014	1	60482292	60567104	-1	0	0	1	28	2	4	0	0	0	4	10	F2Z4B7	
ENSMUST00000090300	ENSMUSG00000060657	16	14109166	14159274	-1	56	60	249	98	53	41	1161	2960	2143	121	1504		Q8BJ34
ENSMUST00000090302	ENSMUSG00000040640	14	27622442	28478537	1	28	25	21	44	35	24	1	2	2	2	9		Q6PH08
ENSMUST00000090313	ENSMUSG00000069085	1	63622851	63686927	-1	12	14	22	7	8	3	0	0	0	0	0		A2CI98
ENSMUST00000090314	ENSMUSG00000038665	6	36846022	37300184	-1	0	0	0	170	0	0	0	0	0	0	0	D3Z2W1	
ENSMUST00000090318						0	2	0	0	2	0	9	13	15	0	9		
ENSMUST00000090322	ENSMUSG00000096853	2	111645057	111645995	-1	5	2	1	1	2	1	0	0	0	0	0	Q8VGE6	
ENSMUST00000090326	ENSMUSG00000095156	2	111328421	111329338	1	5	1	5	1	3	6	0	0	0	0	0	Q7TQY6	
ENSMUST00000090328	ENSMUSG00000101946	2	111315481	111316398	1	6	5	0	3	6	2	0	0	0	0	0	Q8VGG8	
ENSMUST00000090329	ENSMUSG00000068646	2	111306201	111307142	1	3	7	13	6	1	1	0	0	0	0	0	Q8VF38	
ENSMUST00000090330	ENSMUSG00000068647	2	111292270	111293211	1	5	4	4	4	2	1	0	0	0	0	0	Q8VF39	
ENSMUST00000090332	ENSMUSG00000050808	2	110721340	110739527	1	0	0	0	0	0	0	0	0	0	0	0	Q0VEM9	Q8C6Z1
ENSMUST00000090337	ENSMUSG00000021898	14	26894557	26915258	1	7	0	0	0	14	0	0	3	0	0	0	E9QPD0	
ENSMUST00000090339	ENSMUSG00000022246	15	10568979	10714631	-1	28	23	34	8	14	0	0	0	0	0	0		Q9EP71
ENSMUST00000090355	ENSMUSG00000048271	5	28317121	28419239	1	0	0	0	31	0	2	10	0	33	9	0	D3YV48	
ENSMUST00000090359	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	6	0	27	0	0	H7BX64	
ENSMUST00000090371	ENSMUSG00000028114	3	123368297	123386108	-1	17	13	127	66	7	10	0	10	10	2	4	E9QPC5	
ENSMUST00000090379	ENSMUSG00000039701	3	122931493	122984510	-1	21	12	41	68	23	11	161	360	293	140	289		P15975
ENSMUST00000090380	ENSMUSG00000039704	15	9140621	9198318	1	17	14	22	79	11	6	44	49	92	12	77		Q8C561
ENSMUST00000090381	ENSMUSG00000029763	6	33249085	33973979	1	4	3	8	6	7	5	11	22	14	19	12	Q9CXE1	
ENSMUST00000090391	ENSMUSG00000027168	2	105668900	105697364	1	5	4	6	216	13	7	0	0	0	0	0		P63015
ENSMUST00000090395						3	2	4	5	3	3	2	5	1	18	0		
ENSMUST00000090397	ENSMUSG00000027168	2	105668900	105697364	1	2	3	2	4	2	0	0	0	0	0	0		P63015
ENSMUST00000090398	ENSMUSG00000021782	14	24133953	24245920	-1	0	0	45	0	79	25	0	0	0	0	0	E9Q9R9	
ENSMUST00000090406	ENSMUSG00000070501	1	173519717	173535957	-1	0	10	27	0	0	6	0	36	4	14	11	E9PVL3	
ENSMUST00000090413	ENSMUSG00000070697	5	88554462	88556090	1	10	6	5	120	14	11	174	1066	457	375	358		Q9JI13
ENSMUST00000090414	ENSMUSG00000031027	7	109279223	109439081	-1	0	0	0	0	0	0	0	0	0	0	0		Q924X7
ENSMUST00000090429	ENSMUSG00000068686	2	104069849	104091187	1	1	2	1	4	3	0	0	0	0	0	0		P58019
ENSMUST00000090433	ENSMUSG00000020823	11	117115168	117159268	1	22	17	87	69	22	15	4152	7165	5080	438	4240	A8Y5H7	
ENSMUST00000090443	ENSMUSG00000057897	11	5969644	6066362	-1	0	6	0	27	18	12	0	0	0	0	0	Q68EG2	
ENSMUST00000090447						5	4	2	0	0	1	0	2	1	0	4		
ENSMUST00000090453	ENSMUSG00000022540	16	5008730	5013553	-1	0	0	5	11	2	0	312	234	234	38	183		Q3TDK6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000090457	ENSMUSG00000022543	16	4968936	4978962	1	17	10	50	30	34	15	43	89	47	14	43	Q8C5G4	
ENSMUST00000090461	ENSMUSG00000022148	15	6579871	6663313	1	9	12	39	15	17	5	1918	6973	4254	2620	3893	B2RUR0	O35601
ENSMUST00000090464	ENSMUSG00000033502	3	116272553	116424032	-1	9	0	0	42	26	15	406	1392	958	46	566		Q6GQT0
ENSMUST00000090469	ENSMUSG00000068697	14	20649102	20656540	-1	2	4	12	7	7	6	3	10	7	7	2		Q9JK37
ENSMUST00000090473	ENSMUSG00000068696	3	116249654	116253503	-1	22	10	25	327	18	11	0	0	0	0	0	B2RXU4	Q9EPB7
ENSMUST00000090474						0	59	141	189	27	69	0	0	0	0	0		
ENSMUST00000090475	ENSMUSG00000012350	2	103263433	103303278	-1	26	0	6	17	23	6	0	0	0	0	0		O70273
ENSMUST00000090476	ENSMUSG00000038543	3	95883954	95892005	-1	0	21	0	0	40	19	4	0	8	5	7		Q8R2K8
ENSMUST00000090480	ENSMUSG00000039637	16	4626133	4679777	-1	2	1	1	14	0	0	8	5	63	0	72	G3X9L5	
ENSMUST00000090481	ENSMUSG00000029767	6	29348069	29377110	1	12	7	0	0	0	0	41	162	102	103	79	Q6XLQ8	
ENSMUST00000090487	ENSMUSG00000039742	6	29319140	29336019	1	0	8	22	7	7	0	0	0	0	0	0		Q3UZD7
ENSMUST00000090488	ENSMUSG00000068706	15	5120602	5121172	-1	0	1	8	3	4	6	0	0	3	0	0	G3X9L6	
ENSMUST00000090499	ENSMUSG00000039599	14	20348162	20383489	1	0	0	0	0	0	0	41	160	110	45	103		Q6NSV7
ENSMUST00000090500	ENSMUSG00000022519	16	4480216	4541816	-1	0	0	0	0	5	0	2	12	19	2	8		Q7TQ48
ENSMUST00000090503	ENSMUSG00000039599	14	20348162	20383489	1	14	12	9	52	16	8	12	0	24	8	0		Q6NSV7
ENSMUST00000090511	ENSMUSG00000029708	6	28416091	28428390	-1	18	15	37	100	35	17	546	991	648	127	368		Q9D4H2
ENSMUST00000090512	ENSMUSG00000024211	6	27275119	28135178	-1	0	3	0	0	0	2	0	0	0	0	0	B7ZMR4	P47743
ENSMUST00000090513	ENSMUSG00000027165	2	101560781	101649532	-1	1	0	2	0	0	0	0	0	0	0	0		Q9CQI4
ENSMUST00000090522	ENSMUSG00000039789	16	3858321	3884561	-1	13	12	24	65	24	9	260	660	361	176	291	E9Q6S0	
ENSMUST00000090527						1	1	0	0	5	2	0	0	0	0	0		
ENSMUST00000090541	ENSMUSG00000006057	11	96068852	96075670	-1	0	0	84	0	0	0	33	74	49	59	56		Q9CR84
ENSMUST00000090543	ENSMUSG00000021775	14	18204054	18239127	-1	23	20	18	91	22	8	14	62	18	19	54	Q4VAB7	Q60674
ENSMUST00000090546	ENSMUSG00000068732	3	108556425	108562466	-1	13	0	23	54	0	0	473	1116	548	378	480		Q80X45
ENSMUST00000090553	ENSMUSG00000068739	3	108424865	108445209	-1	17	20	56	30	28	7	44	132	46	17	48		P26638
ENSMUST00000090554	ENSMUSG00000068735	2	93187548	93201759	1	21	14	0	0	0	0	0	23	20	0	163		Q4QQM4
ENSMUST00000090558	ENSMUSG00000068740	3	108390851	108415552	-1	76	43	190	310	121	59	3	8	8	1	11	A2AEE7	
ENSMUST00000090559	ENSMUSG00000068742	2	92403646	92434043	-1	79	73	469	267	77	49	88	165	116	15	129		Q9R194
ENSMUST00000090561	ENSMUSG00000068744	3	108383839	108388231	1	6	3	2	10	0	1	10	6	5	6	3		Q9D0P7
ENSMUST00000090563	ENSMUSG00000068745	3	108364911	108380057	1	14	8	34	22	15	9	0	0	0	0	1		Q5FW53
ENSMUST00000090568	ENSMUSG00000068748	6	22875502	23052916	1	38	33	60	207	56	35	0	0	1	0	1		B9EKR1
ENSMUST00000090569	ENSMUSG00000068749	3	108256926	108279974	1	10	4	19	86	15	2	348	1258	477	2084	391	Q3UPK6	Q9Z2U1
ENSMUST00000090582	ENSMUSG00000040434	2	92365046	92374869	-1	0	0	0	0	0	0	0	0	0	0	5		Q5XPT3
ENSMUST00000090586	ENSMUSG00000058318	2	92093117	92364666	1	15	0	5	40	0	0	10	3	629	0	660	A2AHG2	
ENSMUST00000090591	ENSMUSG00000068758	14	14346495	14355490	1	3	4	11	114	4	9	96	131	93	11	54		P26952
ENSMUST00000090597	ENSMUSG00000020564	12	33147693	33375659	1	3	0	21	16	0	0	325	598	505	35	344	B2RW07	
ENSMUST00000090601	ENSMUSG00000000416	6	18366478	18514843	-1	10	0	0	70	21	6	0	0	0	0	0		B9EJA2
ENSMUST00000090602	ENSMUSG00000027239	2	91929805	91932297	-1	8	4	10	77	3	4	2	0	3	0	0		P12025
ENSMUST00000090608	ENSMUSG00000027243	2	91710852	91721545	1	17	13	13	16	16	7	42	154	45	65	41		Q8BR93
ENSMUST00000090614	ENSMUSG00000027247	2	91649860	91672326	1	0	0	0	0	0	0	1676	2614	1853	266	1105		Q5FWK3
ENSMUST00000090632	ENSMUSG00000029629	6	11907809	12081205	1	8	6	0	0	6	0	12	48	27	17	12		Q9D4H9
ENSMUST00000090663	ENSMUSG00000090363	14	7153511	7174533	-1	0	0	0	0	0	0	0	0	0	0	0	L7N206	
ENSMUST00000090678	ENSMUSG00000068798	3	105727267	105801336	-1	9	2	7	33	9	0	882	3349	1246	1950	715		P62835
ENSMUST00000090679	ENSMUSG00000061762	6	7554879	7565834	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQA8	
ENSMUST00000090680	ENSMUSG00000027905	3	105678270	105687574	-1	14	7	68	65	10	3	69	284	124	57	74		Q9JJY4
ENSMUST00000090682	ENSMUSG00000005505	2	90904740	90911626	1	14	0	3	0	0	9	59	299	161	26	111		Q8R179
ENSMUST00000090685	ENSMUSG00000058388	3	103968110	104024598	1	0	0	0	0	0	0	6	44	0	10	29	Q80YS3	
ENSMUST00000090686	ENSMUSG00000004631	6	4674350	4747207	-1	0	0	4	0	0	0	0	0	0	0	0	D3Z572	
ENSMUST00000090689	ENSMUSG00000030427	7	3908280	3915503	-1	0	1	0	0	0	0	0	0	0	123	0	E9Q6M9	
ENSMUST00000090695	ENSMUSG00000068806	2	89943184	89944113	-1	3	2	6	1	2	1	0	0	0	0	0	Q8VEZ1	
ENSMUST00000090697	ENSMUSG00000027849	3	103575231	103645569	1	21	14	27	0	17	0	0	0	0	0	0		Q9R0N8
ENSMUST00000090700	ENSMUSG00000068808	2	88591806	88592726	1	2	5	4	1	6	2	0	0	0	0	0	A2AV11	
ENSMUST00000090701	ENSMUSG00000068809	2	88559471	88560409	1	6	2	5	3	4	1	0	0	0	0	0	A2AV10	
ENSMUST00000090702	ENSMUSG00000068810	2	88540124	88540510	-1	0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000090704						10	12	8	24	17	7	0	1	0	0	1		
ENSMUST00000090707	ENSMUSG00000068814	2	87809822	87810799	1	5	0	7	2	2	0	0	0	0	0	0	A2AVC7	
ENSMUST00000090708	ENSMUSG00000068815	2	87802391	87803335	1	4	0	3	2	5	3	0	0	0	0	0	Q8VEU8	
ENSMUST00000090709	ENSMUSG00000068816	2	87782536	87783486	1	0	0	0	0	0	0	0	0	0	0	0	G3X9L8	
ENSMUST00000090711	ENSMUSG00000068818	2	87634819	87635745	-1	2	11	9	4	4	3	0	0	0	0	0	Q8VG97	
ENSMUST00000090712	ENSMUSG00000068819	2	87628465	87629394	1	3	1	4	0	1	0	0	0	0	0	0	Q7TR45	
ENSMUST00000090715	ENSMUSG00000070385	3	103074014	103099720	1	5	0	10	0	5	1	1	3	3	3	1		Q3V1D3
ENSMUST00000090717	ENSMUSG00000089732	2	87308791	87309714	1	1	2	1	0	0	0	0	0	0	0	0	E9PXB8	
ENSMUST00000090726	ENSMUSG00000027074	2	84936579	84958509	1	24	14	55	18	28	7	60	114	72	11	41		A2AVZ9
ENSMUST00000090729	ENSMUSG00000034059	2	84734058	84738655	1	0	3	3	12	0	0	0	0	0	0	0	Q0VEE5	Q65Z93
ENSMUST00000090731						3	2	2	2	5	0	0	0	0	0	0		
ENSMUST00000090732	ENSMUSG00000027082	2	84432855	84476775	-1	14	14	0	0	0	0	0	0	0	0	0	Q8BSB7	
ENSMUST00000090743	ENSMUSG00000062410	3	98741523	98763127	-1	0	0	0	0	2	0	0	0	0	0	0		P26150
ENSMUST00000090746	ENSMUSG00000027875	3	98280435	98310738	1	32	22	40	25	26	13	0	0	0	16	0		P54869
ENSMUST00000090749						8	29	0	0	23	20	3101	7820	3224	19496	2285		
ENSMUST00000090750	ENSMUSG00000038170	3	97689824	97888707	-1	26	50	31	74	76	0	0	0	0	0	0	G3X9L9	
ENSMUST00000090756	ENSMUSG00000059173	2	79834453	80129458	-1	0	0	0	0	2	0	0	0	0	0	0	A2ASF9	
ENSMUST00000090759	ENSMUSG00000028093	3	97158777	97177299	1	6	7	27	56	12	7	32	67	20	16	44		Q8BP40
ENSMUST00000090760	ENSMUSG00000034683	2	79707780	79818496	1	30	27	81	19	17	12	0	1	0	0	1		Q8BKK4
ENSMUST00000090766	ENSMUSG00000027016	2	77410634	77819639	-1	0	6	20	6	0	0	0	0	0	0	0	A2AS57	Q8BXJ8
ENSMUST00000090776	ENSMUSG00000071478	13	23574470	23574932	1	0	0	0	19	0	0	0	14	0	0	5	B2RVF0	P22752
ENSMUST00000090781	ENSMUSG00000068854	3	96221119	96223738	1	42	25	78	36	54	22	25	71	32	7	27		Q64524
ENSMUST00000090782	ENSMUSG00000068855	3	96220361	96220880	-1	2	8	5	126	13	6	1	0	0	0	0	Q149V4	Q64523
ENSMUST00000090785	ENSMUSG00000038495	3	96104527	96161129	1	0	0	129	0	0	0	93	120	135	0	111		B2RUR8
ENSMUST00000090791	ENSMUSG00000028106	3	95760341	95818863	-1	54	32	143	157	61	29	433	1008	915	55	704		Q6NXI6
ENSMUST00000090792	ENSMUSG00000059005	2	75659261	75669407	1	0	0	0	0	0	0	0	42	34	0	0	Q5FB19	Q8BG05
ENSMUST00000090797	ENSMUSG00000028109	3	95559677	95587671	1	0	0	6	4	6	1	0	0	0	0	0		Q9D5T7
ENSMUST00000090802	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	84	0	48	0	0	Q543G2	P16951
ENSMUST00000090804	ENSMUSG00000015522	3	95434388	95497240	1	0	0	128	110	27	0	739	2293	1154	176	809	Q3ULM2	
ENSMUST00000090806	ENSMUSG00000062115	11	60105013	60199197	1	40	24	123	145	70	52	39	44	39	0	54		Q61818
ENSMUST00000090811	ENSMUSG00000008226	2	73312601	73337818	1	17	21	22	37	21	11	30	119	50	52	44		Q3TMH2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000090813	ENSMUSG00000068859	2	73271925	73284706	1	36	28	190	832	67	35	0	0	0	1	1		Q64HY3
ENSMUST00000090815	ENSMUSG00000068860	3	95236920	95241598	-1	8	6	11	23	14	3	2	9	7	2	21	G9MDF2	Q569E4
ENSMUST00000090821	ENSMUSG00000038777	3	95160457	95174024	1	0	2	7	80	0	0	0	3	0	0	0		Q9WTM3
ENSMUST00000090823	ENSMUSG00000038777	3	95160457	95174024	1	0	0	0	0	0	0	0	0	0	0	0	E9Q613	
ENSMUST00000090824	ENSMUSG00000004085	2	72285637	72442610	1	12	4	17	61	16	7	10	22	23	12	27		Q9ESL4
ENSMUST00000090826	ENSMUSG00000049044	2	71981240	72257474	1	0	0	0	4	0	0	0	17	0	0	0	A2ASW4	Q9EQZ6
ENSMUST00000090827	ENSMUSG00000038208	11	98388677	98400490	-1	0	0	0	37	5	0	24	24	14	0	22		A2A559
ENSMUST00000090834	ENSMUSG00000052632	12	21111748	21270171	1	0	0	34	324	39	0	16	90	27	23	67		Q7SIG6
ENSMUST00000090839	ENSMUSG00000068874	3	94933056	94944758	1	0	0	6	0	0	10	152	120	66	72	75		P17563
ENSMUST00000090840	ENSMUSG00000031370	X	163935443	163958661	-1	3	5	46	32	11	6	35	165	62	16	80	B1B0E9	
ENSMUST00000090848	ENSMUSG00000068877	3	94693556	94704413	1	21	11	16	6	10	8	0	0	0	13	0		
ENSMUST00000090849	ENSMUSG00000041975	2	70964561	71055583	-1	70	54	197	308	43	38	3	5	2	0	10	Q8CA70	
ENSMUST00000090852	ENSMUSG00000068882	2	69861562	69871846	1	0	2	0	0	2	2	143	439	113	403	69	Q564E6	P32067
ENSMUST00000090853	ENSMUSG00000068879	3	93773000	93774142	1	7	4	11	12	8	0	0	0	0	0	0		Q717B2
ENSMUST00000090856	ENSMUSG00000041991	3	93319749	93333570	1	102	52	119	122	89	39	0	0	0	0	0	E9QNP3	
ENSMUST00000090858	ENSMUSG00000042133	2	69722545	69754012	1	0	0	38	0	0	0	140	1172	376	305	103		A2AR02
ENSMUST00000090860	ENSMUSG00000062382	13	74406396	74407317	1	71	36	89	98	104	43	141	44	13	0	14	Q9CPX4	
ENSMUST00000090863	ENSMUSG00000068885	3	92992226	92993426	1	2	0	7	10	2	5	0	0	0	0	0	Q6PAI4	
ENSMUST00000090866	ENSMUSG00000068888	3	92777210	92778899	-1	2	0	19	23	7	4	0	0	0	0	0	Q9D6P5	
ENSMUST00000090867	ENSMUSG00000068889	3	92707401	92709074	-1	3	4	10	11	7	1	0	0	0	0	0	Q9D139	
ENSMUST00000090871	ENSMUSG00000068893	3	92215920	92256724	1	6	1	3	0	5	2	0	0	0	0	0		Q4KL71
ENSMUST00000090872	ENSMUSG00000074445	3	92285417	92291405	1	0	0	12	11	9	0	0	0	0	0	0		Q9CQK8
ENSMUST00000090896	ENSMUSG00000034903	2	65088339	65239403	-1	24	0	4	0	8	22	33	14	28	11	50		Q3UMF0
ENSMUST00000090908	ENSMUSG00000042520	3	90000140	90052628	-1	2	1	8	1	2	7	456	900	903	37	641	A0A0H2UH17	
ENSMUST00000090924	ENSMUSG00000042766	3	89234177	89246309	-1	0	0	0	3	0	0	39	23	23	3	3	Q3TC52	
ENSMUST00000090925	ENSMUSG00000026987	2	59899363	60209839	-1	7	36	65	0	46	0	483	2326	1951	25	1619	A2AUY4	
ENSMUST00000090927	ENSMUSG00000068917	3	89164795	89176921	1	0	0	0	0	0	0	132	119	46	2	70	F8WHX0	
ENSMUST00000090929	ENSMUSG00000041263	3	89083981	89093311	-1	13	0	23	486	57	32	25	0	51	0	4		Q8BG26
ENSMUST00000090933	ENSMUSG00000028053	3	88950622	89079375	1	0	1	1	0	0	30	391	1036	1321	89	1032		Q99MY8
ENSMUST00000090935	ENSMUSG00000026836	2	58388644	58567157	-1	17	11	32	7	13	0	0	0	0	0	25		P37172
ENSMUST00000090938	ENSMUSG00000068921	3	88920803	88951181	-1	80	51	163	271	72	28	34	145	89	17	100	G3X9M0	
ENSMUST00000090940	ENSMUSG00000026830	2	58045113	58052864	-1	30	22	31	57	23	18	0	2	0	0	3		Q5EBJ4
ENSMUST00000090942	ENSMUSG00000054199	3	88835231	88910103	1	0	0	0	0	17	0	198	102	500	28	595	K4DI71	
ENSMUST00000090945	ENSMUSG00000068923	3	88744700	88775164	-1	67	17	96	0	29	32	555	841	749	111	1409		Q9R0N3
ENSMUST00000090952	ENSMUSG00000036053	2	52857860	53134202	1	0	0	0	3	0	0	42	12	41	13	48		A2APV2
ENSMUST00000090971	ENSMUSG00000004892	3	87987531	88000230	-1	32	14	62	86	28	18	0	0	0	0	0		Q61361
ENSMUST00000090973	ENSMUSG00000004891	3	87971078	87980451	1	0	0	0	0	0	0	0	0	0	0	0		Q6P5H2
ENSMUST00000090976	ENSMUSG00000026761	2	48902824	48950277	-1	2	0	1	0	1	0	1	29	0	5	0	Q9CZF7	
ENSMUST00000090981	ENSMUSG00000028073	3	87747890	87824306	-1	9	0	18	8	11	11	0	0	0	0	0		Q8VIK5
ENSMUST00000090986	ENSMUSG00000015852	3	87250758	87263738	-1	23	10	24	13	30	5	0	0	0	33	10	Q9EQY5	
ENSMUST00000090990	ENSMUSG00000068940	12	105191043	105195610	1	6	4	19	5	8	4	0	0	0	0	0	Q0VBM6	P56842
ENSMUST00000090993	ENSMUSG00000026755	2	39005348	39015877	1	0	0	0	0	0	0	232	775	262	180	175		Q9D898
ENSMUST00000091001	ENSMUSG00000068947	2	37219491	37220420	1	2	5	7	2	4	1	0	0	0	0	0	Q7TRY4	
ENSMUST00000091002	ENSMUSG00000041842	3	84442198	84480429	-1	15	1	16	166	22	4	20	35	22	5	38		Q3ULZ2
ENSMUST00000091006	ENSMUSG00000068950	2	36376778	36377698	1	5	3	9	0	3	3	0	0	0	0	0	Q8VGK6	
ENSMUST00000091010	ENSMUSG00000026883	2	35558266	35730994	1	0	0	0	0	0	0	0	0	0	0	0		Q3UHC7
ENSMUST00000091014	ENSMUSG00000033900	3	82358044	82395268	1	30	20	37	0	0	6	0	0	0	0	0		Q3TRR0
ENSMUST00000091020	ENSMUSG00000035949	2	34804514	34826311	-1	0	0	0	6	0	2	1	377	122	9	57	A2AUF9	
ENSMUST00000091031						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000091037	ENSMUSG00000068966	2	33406108	33431324	-1	150	91	553	580	186	91	323	754	503	0	393	A2ATY4	
ENSMUST00000091039	ENSMUSG00000038831	2	33133417	33371486	-1	0	0	0	2	0	0	19	0	37	1	44		A2AR50
ENSMUST00000091052						4	3	4	8	7	0	1	1	3	8	1		
ENSMUST00000091059	ENSMUSG00000039021	2	32757026	32775633	-1	0	0	2	65	2	0	0	0	2	0	0	Q3TV33	
ENSMUST00000091064	ENSMUSG00000070934	4	86575668	86577285	1	9	3	11	111	19	8	296	1123	410	125	337		Q80X95
ENSMUST00000091087	ENSMUSG00000033335	9	21424908	21507759	1	12	0	47	0	36	5	614	3503	2102	305	2469		P39054
ENSMUST00000091089	ENSMUSG00000026825	2	32308471	32353338	-1	0	4	0	0	0	0	0	0	0	0	14		P39053
ENSMUST00000091090						6	8	9	94	8	6	1	4	5	5	2		
ENSMUST00000091097						0	1	3	2	2	1	1	0	0	2	0		
ENSMUST00000091112	ENSMUSG00000036381	3	59113855	59153618	-1	9	0	24	0	0	0	0	28	14	42	14	Q544F4	Q9ESG6
ENSMUST00000091117						0	30	75	0	6	0	1480	5658	1392	2325	695		
ENSMUST00000091130						41	21	0	0	42	56	513	3308	1365	4550	1385		
ENSMUST00000091132	ENSMUSG00000079484	2	30266203	30282149	1	0	3	0	0	3	0	0	0	0	12	0		
ENSMUST00000091137	ENSMUSG00000037016	3	53513938	53657355	-1	98	77	154	252	126	50	0	0	0	0	0		Q6NVD0
ENSMUST00000091142	ENSMUSG00000069020	2	29820075	29845002	1	9	11	21	27	16	5	118	138	49	55	32		Q9D2P4
ENSMUST00000091144	ENSMUSG00000037174	3	51252720	51340663	-1	2	0	0	0	0	0	77	155	0	62	0	A0A0B4J1G5	
ENSMUST00000091146	ENSMUSG00000039844	2	29619720	29740978	1	19	0	0	12	8	14	52	64	84	0	66	Q3UGX8	
ENSMUST00000091153	ENSMUSG00000035513	2	29194541	29253005	-1	0	0	0	0	0	0	0	0	0	0	0		Q8R4F1
ENSMUST00000091178	ENSMUSG00000069036	Y	2662471	2663658	-1	12	14	79	16	14	2	0	1	0	1	4	Q53WV7	Q05738
ENSMUST00000091180	ENSMUSG00000069038	X	11327822	11328151	1	2	0	3	2	3	2	0	0	0	0	0	A2BFR3	
ENSMUST00000091184	ENSMUSG00000069041	3	40708855	40726096	1	3	0	27	70	6	1	0	4	1	1	1	B2RTC8	Q3V132
ENSMUST00000091186	ENSMUSG00000060798	3	40531286	40704774	1	750	841	580	449	590	228	29	99	63	25	76		Q059U7
ENSMUST00000091188	ENSMUSG00000069044	Y	1298961	1459782	-1	12	6	5	5	7	3	0	0	0	0	0	F8VPU6	
ENSMUST00000091190	ENSMUSG00000069045	Y	1260771	1286629	-1	7	3	15	4	2	0	227	0	84	227	179		Q62095
ENSMUST00000091197	ENSMUSG00000069049	Y	1010543	1028847	1	2	0	0	0	1	0	129	0	350	552	244		Q9Z0N2
ENSMUST00000091201	ENSMUSG00000042348	13	113794505	114157461	1	17	12	15	26	12	5	82	242	143	93	99		Q8BGR6
ENSMUST00000091203	ENSMUSG00000037225	3	37348346	37410108	1	1	0	1	0	0	0	0	0	0	0	0	Q925A2	
ENSMUST00000091224						8	0	12	9	11	0	0	0	0	1	5		
ENSMUST00000091227	ENSMUSG00000058400	3	36179424	36222313	-1	4	9	23	57	11	2	0	0	0	0	0	Q4VA00	P83861
ENSMUST00000091233	ENSMUSG00000036040	2	27079379	27108981	1	18	17	37	32	35	12	1	0	0	0	0	A1A5B7	Q7TSK7
ENSMUST00000091236	ENSMUSG00000032745	13	111425680	111490111	-1	20	11	0	48	18	0	174	0	0	0	9		Q6NXH3
ENSMUST00000091237	ENSMUSG00000031441	8	12757014	12868728	1	22	1	70	0	0	21	274	500	1541	0	365		P98197
ENSMUST00000091246	ENSMUSG00000032633	11	59791408	59810016	-1	0	0	1	0	0	0	851	1703	710	106	535		Q8QZS3
ENSMUST00000091252	ENSMUSG00000026924	2	26409431	26445216	-1	42	38	0	70	0	35	1190	533	2180	63	1575	E9QAT4	
ENSMUST00000091257	ENSMUSG00000027668	3	32529465	32579239	1	18	12	49	53	19	5	48	185	100	9	78		Q811U4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000091259	ENSMUSG00000069072	3	31202858	31310378	-1	275	257	262	202	313	137	6	17	15	15	19		Q8BXR1
ENSMUST00000091263	ENSMUSG00000036327	2	26208637	26237525	-1	39	38	99	22	39	19	32	76	33	16	53		Q3TMX7
ENSMUST00000091268	ENSMUSG00000026933	2	25926838	25983282	-1	47	46	191	2	74	0	0	0	13	6	0		A2AHC3
ENSMUST00000091269	ENSMUSG00000021709	13	103818787	103920514	-1	0	0	25	0	0	5	569	1913	652	345	708		Q80TH2
ENSMUST00000091278	ENSMUSG00000069080	2	25777017	25780279	1	4	8	8	4	5	4	0	0	0	0	0	A2BHR2	
ENSMUST00000091282	ENSMUSG00000073012	X	106235246	106255376	-1	5	8	31	10	5	3	1	1	1	0	1	A2AP83	
ENSMUST00000091284	ENSMUSG00000027698	3	27182965	27284608	1	0	2	1	0	0	0	0	0	0	0	0	Q8BYQ0	
ENSMUST00000091288	ENSMUSG00000079037	2	131909928	131938429	1	7	4	42	64	18	19	4042	2307	5511	967	1860	Q4FJQ7	P04925
ENSMUST00000091289						0	0	6	0	9	7	0	457	133	113	22		
ENSMUST00000091291	ENSMUSG00000005534	8	3150922	3279617	-1	70	69	193	215	67	48	933	1926	1926	95	1328		P15208
ENSMUST00000091295	ENSMUSG00000041431	13	100778650	100786570	-1	0	0	0	0	0	0	49	40	0	60	15	Q68EM3	
ENSMUST00000091299	ENSMUSG00000069089	13	100697027	100730942	-1	141	145	276	183	136	74	206	763	309	241	248	Q3THG5	Q03147
ENSMUST00000091309	ENSMUSG00000003617	3	19957054	20009145	1	16	20	17	32	21	16	0	0	0	396	37		Q61147
ENSMUST00000091314	ENSMUSG00000069094	3	19223108	19311322	-1	0	3	13	0	6	4	65	174	92	14	70		P70453
ENSMUST00000091318	ENSMUSG00000089953	2	25234476	25236787	-1	15	10	16	18	38	6	0	0	0	0	0		Q3UIW8
ENSMUST00000091319	ENSMUSG00000095028	3	15495751	15575065	-1	0	0	0	0	0	0	281	2246	290	1103	286	Q3U390	
ENSMUST00000091321	ENSMUSG00000021645	13	100124852	100137690	1	0	0	2	18	0	1	0	0	0	0	3	Q5PXT4	
ENSMUST00000091325	ENSMUSG00000027550	3	14533788	14572658	1	0	0	0	0	0	0	0	22	16	12	9	E9QNC6	
ENSMUST00000091328	ENSMUSG00000063065	7	126759601	126765819	1	20	16	30	10	34	23	970	4099	1145	95	1140	D3Z6D8	
ENSMUST00000091348	ENSMUSG00000036893	2	24789928	24919614	-1	0	0	0	0	0	0	53	95	181	0	287	Z4YJZ7	
ENSMUST00000091354	ENSMUSG00000027506	3	8925593	9004723	-1	0	0	9	0	0	0	4308	16134	4534	2465	3108		Q62393
ENSMUST00000091355	ENSMUSG00000027506	3	8925593	9004723	-1	3	0	0	0	0	0	713	3590	959	831	587		Q62393
ENSMUST00000091356	ENSMUSG00000021661	13	98263158	98274750	1	10	12	6	2	11	0	0	0	0	0	0	Q8C4M9	
ENSMUST00000091358	ENSMUSG00000028560	4	98923810	98935543	1	11	0	11	0	6	0	321	996	527	87	191		Q8BJQ2
ENSMUST00000091364	ENSMUSG00000069118	3	6615418	6620443	-1	2	3	3	2	7	3	0	0	0	0	0	Q9DAJ8	
ENSMUST00000091374	ENSMUSG00000026021	1	59586558	59670834	-1	12	15	3	25	9	2	561	2712	728	1247	278		P63166
ENSMUST00000091375						1	2	0	1	3	1	2	3	3	14	1		
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ENSMUST00000091387	ENSMUSG00000021668	13	96480689	96542485	-1	0	0	0	0	0	0	44	0	147	15	0	Q5Q9H7	
ENSMUST00000091391	ENSMUSG00000059022	6	29473162	29507952	-1	5	18	72	3	21	22	0	0	0	0	0	E9QNB3	
ENSMUST00000091394	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	0	0	0	0	6	0	0	0	B7ZCU0	
ENSMUST00000091396						0	1	0	81	1	2	1	2	0	2	4		
ENSMUST00000091403	ENSMUSG00000042082	13	93771679	93943016	1	67	57	103	772	77	29	955	1873	1590	169	856		
ENSMUST00000091418	ENSMUSG00000026740	2	18195654	18392830	-1	50	42	96	427	79	36	31	66	65	10	102		Q61712
ENSMUST00000091420	ENSMUSG00000054074	2	18040676	18049051	-1	11	3	32	169	12	8	0	0	0	0	1	G3X9M2	
ENSMUST00000091429	ENSMUSG00000063275	2	13850282	14056135	-1	0	0	0	0	0	0	17	0	0	31	5	A2AQ81	
ENSMUST00000091436	ENSMUSG00000026726	2	13276338	13491813	-1	56	55	105	45	49	31	8	15	11	14	14		Q9JLB4
ENSMUST00000091440	ENSMUSG00000070828	7	11397915	11402741	1	4	10	6	12	9	4	0	0	0	0	0		Q3URS2
ENSMUST00000091456						6	0	9	2	0	0	0	0	3	0	0		
ENSMUST00000091458	ENSMUSG00000069171	13	78188973	78199757	-1	3	3	7	135	9	6	0	0	0	3	10	Q32NY6	
ENSMUST00000091459	ENSMUSG00000064138	13	77708690	78166238	1	10	12	8	0	0	0	161	431	285	57	116	E9QMA2	
ENSMUST00000091466	ENSMUSG00000033991	13	76098734	76187983	1	18	14	26	16	14	12	21	82	74	50	74	F8VPK0	
ENSMUST00000091471	ENSMUSG00000021779	14	17660960	18038088	1	0	0	0	0	11	0	0	0	0	0	0		P37242
ENSMUST00000091477	ENSMUSG00000054934	10	116417861	116473878	-1	158	170	84	60	97	29	3	3	2	0	12	F6TD25	
ENSMUST00000091481	ENSMUSG00000069184	13	74371426	74376566	-1	5	6	5	3	1	3	0	3	1	2	0	Q0VFY0	
ENSMUST00000091493	ENSMUSG00000069189	13	73963851	73992989	1	11	11	17	7	14	6	0	0	0	0	0		Q14AK4
ENSMUST00000091497	ENSMUSG00000026657	2	4017717	4614043	1	0	0	0	0	0	0	0	85	17	11	82		Q8BIE6
ENSMUST00000091504	ENSMUSG00000026643	2	3284212	3328877	1	0	0	0	0	0	4	2	0	18	24	17	Q8CFK1	
ENSMUST00000091505	ENSMUSG00000050530	2	3114224	3227806	1	0	0	0	150	0	0	8	0	0	0	14	A2ATK8	
ENSMUST00000091506						0	2	7	6	1	0	0	0	0	1	0		
ENSMUST00000091508	ENSMUSG00000074472	9	22188168	22202123	1	0	0	0	0	0	0	0	0	0	0	0	F7APL9	
ENSMUST00000091514	ENSMUSG00000021594	13	69573449	69611442	-1	16	9	18	65	15	18	2	10	5	1	4		
ENSMUST00000091520	ENSMUSG00000058331	13	67747800	67755228	-1	0	3	0	0	0	0	14	75	23	28	11	Q7TMC9	
ENSMUST00000091523	ENSMUSG00000071291	13	67490167	67500555	-1	1	0	1	5	0	1	0	0	3	0	0	E9PY65	
ENSMUST00000091526	ENSMUSG00000074824	13	67096613	67116263	-1	21	17	93	31	22	14	0	5	3	3	6	Q7M6X5	
ENSMUST00000091531						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000091539						0	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000091541	ENSMUSG00000074832	13	66418114	66441118	-1	0	0	0	0	0	0	0	0	0	0	1	Q8C1L2	
ENSMUST00000091545						5	9	6	3	9	1	0	0	0	0	0		
ENSMUST00000091554	ENSMUSG00000033063	13	64737591	64903888	-1	14	16	33	20	19	19	0	1	0	0	0	E9PY62	
ENSMUST00000091556	ENSMUSG00000062098	2	138256565	138589292	1	0	0	40	68	12	19	1	8	5	1	0	Q3TSN9	
ENSMUST00000091560	ENSMUSG00000021458	13	63014934	63326096	1	9	13	22	23	26	10	22	39	49	23	30	Q3UQZ7	
ENSMUST00000091563	ENSMUSG00000072066	13	62603013	62624182	-1	0	0	2	2	3	3	0	6	6	3	0	F7A5Y7	
ENSMUST00000091565	ENSMUSG00000075595	11	95712673	95835115	1	0	3	15	88	2	6	272	307	506	41	354		Q5DU09
ENSMUST00000091569	ENSMUSG00000050345	13	60842621	60864416	-1	4	3	11	6	3	4	0	5	1	34	6		Q80UB0
ENSMUST00000091579	ENSMUSG00000021552	13	58233351	58274188	-1	5	4	6	10	9	4	5	19	9	30	24		Q9JMB0
ENSMUST00000091583	ENSMUSG00000014164	13	58004221	58113592	-1	3	0	5	10	2	0	0	0	1	0	0		E0CZ16
ENSMUST00000091605	ENSMUSG00000096151	7	107990367	107991299	1	2	5	3	1	8	0	0	0	0	0	0		Q8VGI6
ENSMUST00000091609	ENSMUSG00000047547	13	54592401	54611344	-1	22	24	70	92	43	28	33	148	62	24	72	Q3TWZ9	Q6IRU5
ENSMUST00000091614	ENSMUSG00000028423	4	40970906	41025993	1	2	8	18	9	11	0	55	234	143	51	127		B1AY10
ENSMUST00000091623	ENSMUSG00000037989	13	49036303	49148014	-1	27	0	79	155	0	6	0	0	0	0	0	E9QM73	
ENSMUST00000091628	ENSMUSG00000046876	13	45549758	45964991	-1	0	0	0	75	0	0	326	1073	805	70	206		P54254
ENSMUST00000091636	ENSMUSG00000071862	18	35209011	35215024	-1	24	21	19	10	20	8	0	0	0	1	1		Q8BGA3
ENSMUST00000091641	ENSMUSG00000021431	13	38204939	38227663	1	0	5	2	9	4	0	33	171	58	97	46		Q9D361
ENSMUST00000091648	ENSMUSG00000071311	17	13051321	13052280	-1	37	21	80	57	47	25	0	0	1	0	1		F8VQN3
ENSMUST00000091668	ENSMUSG00000044734	13	32842092	32851185	-1	0	9	17	0	0	10	0	19	8	0	0	Z4YK03	
ENSMUST00000091672	ENSMUSG00000069255	13	30659999	30711231	1	2	5	0	4	0	0	50	115	42	44	16		Q99N11
ENSMUST00000091674	ENSMUSG00000006191	13	29191746	29855674	-1	12	12	45	14	16	9	0	2	0	0	0		Q91WE6
ENSMUST00000091676	ENSMUSG00000073724	4	144059126	144069327	1	0	0	36	12	0	0	0	0	0	0	0	Q3ULC4	
ENSMUST00000091678	ENSMUSG00000069258	13	27383339	27390846	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SXK2	
ENSMUST00000091679	ENSMUSG00000069259	13	27312627	27319252	1	0	0	2	0	2	0	0	0	0	0	0	Q5SXJ8	
ENSMUST00000091680	ENSMUSG00000069259	13	27312627	27319252	1	2	1	0	0	1	1	0	0	0	0	0		O35257
ENSMUST00000091692	ENSMUSG00000095251	3	94071622	94072644	-1	4	6	11	6	4	0	0	0	0	0	0	E0CYU8	
ENSMUST00000091694	ENSMUSG00000036006	13	24582189	24733816	1	18	2	0	10	10	0	1682	3188	2061	351	2070		Q80U16

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000091698	ENSMUSG00000036083	13	23839434	23860714	1	0	0	0	0	4	0	0	0	0	0	0	Q5SZ93	
ENSMUST00000091701	ENSMUSG00000069265	13	23761853	23762386	-1	3	5	7	53	3	0	1	0	0	7	1		P68433
ENSMUST00000091703	ENSMUSG00000069267	13	23752267	23752886	1	3	2	9	99	14	4	0	0	0	0	0	B9EI85	P84228
ENSMUST00000091704	ENSMUSG00000047246	13	23583742	23621124	-1	13	3	31	40	10	16	2	113	23	95	65		Q6ZWY9
ENSMUST00000091706	ENSMUSG00000006611	13	23702034	23710854	-1	13	6	23	31	11	13	113	171	63	53	85		P70387
ENSMUST00000091707	ENSMUSG00000006611	13	23702034	23710854	-1	4	2	0	0	4	0	8	0	0	20	23	Q5SZ87	
ENSMUST00000091708	ENSMUSG00000091383	13	51202688	51203065	-1	4	4	1	203	7	1	30	618	245	115	187	F8WIX8	
ENSMUST00000091709	ENSMUSG00000095217	13	21754123	21754503	1	12	0	6	50	4	3	0	0	0	1	6		P10853
ENSMUST00000091710						0	0	0	62	0	0	0	0	0	4	0		
ENSMUST00000091715	ENSMUSG00000069276	12	88329254	88329682	1	2	1	0	2	1	1	0	0	0	0	0	J3QPQ5	
ENSMUST00000091719	ENSMUSG00000069280	13	23249238	23250323	1	6	7	0	0	2	0	0	0	0	0	0	Q5SSA0	
ENSMUST00000091721	ENSMUSG00000094600	13	23113834	23114730	-1	1	0	11	4	5	0	0	0	0	0	0	Q8R270	
ENSMUST00000091728	ENSMUSG00000094637	13	22556201	22557109	1	2	4	3	1	1	2	0	0	0	0	0	I7HIK1	
ENSMUST00000091729	ENSMUSG00000069289	13	22524051	22524986	1	3	2	6	0	8	2	0	0	0	0	0	Q8R273	
ENSMUST00000091730	ENSMUSG00000094898	13	22474618	22475520	1	5	9	3	7	4	1	0	0	0	0	0	Q8R262	
ENSMUST00000091732	ENSMUSG00000069292	13	22382538	22383641	1	6	1	6	2	5	1	0	0	0	0	0	Q8R280	
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ENSMUST00000091734	ENSMUSG00000069294	13	22327911	22328807	1	5	3	9	0	3	2	0	0	0	0	0	Q8R265	
ENSMUST00000091735	ENSMUSG00000069295	13	22293193	22294098	1	3	2	3	5	7	1	0	0	0	0	0	Q5SVD5	
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ENSMUST00000091737	ENSMUSG00000069297	13	22244215	22245105	1	4	1	2	1	4	2	0	0	0	0	0	J3JS27	
ENSMUST00000091739	ENSMUSG00000069299	13	22087878	22088804	1	0	0	0	0	0	0	0	0	0	0	0	Q8K3N2	
ENSMUST00000091741	ENSMUSG00000069301	13	22042460	22042944	-1	4	2	30	124	7	0	2	3	0	4	0	B2RVF0	P22752
ENSMUST00000091742	ENSMUSG00000069302	13	22035164	22035568	-1	10	0	2	106	7	2	0	0	0	11	0	A3KPD0	Q8CGP6
ENSMUST00000091745	ENSMUSG00000094248	13	21810465	21810944	1	8	4	27	21	12	0	2	17	0	0	0	B2RVF0	P22752
ENSMUST00000091749	ENSMUSG00000069307	13	21806412	21810199	-1	0	9	0	30	16	13	13	3	0	0	0	Q8CBB6	
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ENSMUST00000091752	ENSMUSG00000069310	13	23745013	23745501	-1	1	6	4	90	10	0	0	4	2	9	1	B9EI85	P84228
ENSMUST00000091756	ENSMUSG00000094338	13	21715763	21716143	-1	10	6	6	121	14	0	0	15	45	120	15		P10853
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ENSMUST00000091762						3	4	7	29	2	2	0	7	21	7	0		
ENSMUST00000091763	ENSMUSG00000041138	13	19645078	19697794	-1	10	5	0	5	3	1	0	0	0	0	0		Q715T0
ENSMUST00000091776	ENSMUSG00000069324	18	87756286	87758143	1	8	8	9	10	20	0	0	0	0	0	0		O35490
ENSMUST00000091789	ENSMUSG00000041607	18	82475146	82585637	1	37	29	126	97	52	16	1682	2166	1821	178	1593	Q5D096	P04370
ENSMUST00000091790	ENSMUSG00000024566	18	80734143	80934058	-1	30	34	42	96	39	17	380	1018	666	102	631	D3YV00	
ENSMUST00000091791	ENSMUSG00000067541	6	132625111	132651526	-1	4	0	24	0	1	0	0	0	0	0	0	E9PWS6	
ENSMUST00000091798	ENSMUSG00000034006	18	80253292	80292725	1	0	0	8	6	0	0	26	0	0	0	28		Q80XM9
ENSMUST00000091813	ENSMUSG00000059336	18	78100091	78142119	-1	16	11	78	34	8	8	7	10	0	5	9		Q8VHL0
ENSMUST00000091818	ENSMUSG00000057378	2	112631355	113217096	-1	5	17	34	54	68	23	0	0	0	0	0	E9PW34	
ENSMUST00000091829	ENSMUSG00000033499	13	9093881	9174451	1	20	20	38	37	32	13	1060	3345	2116	389	1215		Q6A0A2
ENSMUST00000091831	ENSMUSG00000024563	18	76241580	76305731	1	0	0	0	0	0	0	40	129	190	198	189		Q62432
ENSMUST00000091848	ENSMUSG00000045410	13	4590757	4609174	-1	0	0	0	0	0	0	0	12	0	68	3		Q9DCT1
ENSMUST00000091851	ENSMUSG00000024558	18	73928486	74065359	-1	0	20	0	9	5	0	38	56	38	5	32		Q6P5G0
ENSMUST00000091852	ENSMUSG00000037253	18	73573044	73592575	1	11	10	1	169	17	13	263	715	444	128	253		Q05A36
ENSMUST00000091853	ENSMUSG00000021215	13	3882565	3918220	-1	0	0	0	125	41	13	9	46	55	9	45		Q9Z206
ENSMUST00000091878	ENSMUSG00000066009	4	146097298	146126621	1	0	7	2	0	3	0	1	0	0	0	0	Q32P14	
ENSMUST00000091879	ENSMUSG00000071267	17	21926960	21962464	-1	4	3	5	2	9	0	58	200	70	105	49	B8JJA7	
ENSMUST00000091884	ENSMUSG00000024622	18	61131279	61177050	-1	35	31	76	313	57	21	246	217	271	25	215	G3X9M3	
ENSMUST00000091892	ENSMUSG00000069372	18	57468486	57478134	1	6	9	4	4	13	1	0	0	0	0	0		Q8BXZ0
ENSMUST00000091897						12	4	4	7	9	5	13	5	1	7	4		
ENSMUST00000091900	ENSMUSG00000069378	18	53464546	53575907	1	0	0	0	202	7	7	0	0	0	0	0		Q3UZD5
ENSMUST00000091903	ENSMUSG00000021892	14	31359880	31436078	-1	0	0	17	17	0	0	1096	2344	1756	147	982		Q9Z131
ENSMUST00000091904	ENSMUSG00000024532	18	52646209	52663733	1	3	1	2	0	0	2	0	0	0	0	0	Q9D2T6	
ENSMUST00000091905	ENSMUSG00000069379	18	51865264	51865881	-1	2	3	0	1	9	0	0	0	0	0	0	D3YUM8	
ENSMUST00000091916	ENSMUSG00000069385	18	44156395	44159873	-1	0	0	0	1	0	0	0	0	0	0	0	Q6IE31	
ENSMUST00000091920	ENSMUSG00000024491	18	42275353	42341542	1	8	13	21	94	19	13	243	796	553	55	347		Q5SFM8
ENSMUST00000091924	ENSMUSG00000028104	3	96577872	96594181	-1	33	27	44	66	36	17	131	251	82	42	113		Q8R0C0
ENSMUST00000091925						2	0	4	2	0	0	0	0	0	2	2		
ENSMUST00000091927	ENSMUSG00000051401	18	40258361	40531168	1	9	6	13	10	9	6	0	0	0	0	0		Q5DTY9
ENSMUST00000091932	ENSMUSG00000044024	18	37955079	37959179	1	0	0	0	0	0	0	0	0	0	0	0	Q8CFT0	
ENSMUST00000091935	ENSMUSG00000102440	18	37736936	37841870	1	0	0	0	3	11	0	0	0	0	0	0	Q91XX9	
ENSMUST00000091967	ENSMUSG00000024381	18	32377217	32435736	1	14	0	23	142	16	5	45	96	31	117	181	Q6P1B9	
ENSMUST00000091978	ENSMUSG00000033628	18	30272747	30348126	1	10	6	0	3	8	5	0	0	39	0	20	E9QLS6	
ENSMUST00000091986	ENSMUSG00000069421	10	129790609	129791614	-1	4	3	0	0	3	3	0	0	0	0	0	Q8VFH9	
ENSMUST00000091996	ENSMUSG00000069430	10	128989849	128990900	1	6	5	22	7	12	9	0	0	0	0	0	Q14A42	Q60885
ENSMUST00000092003	ENSMUSG00000037486	12	3426857	3506852	1	172	172	406	213	167	54	16	75	27	10	75	D3Z112	
ENSMUST00000092011	ENSMUSG00000066983	17	70929058	70929546	1	3	2	3	6	3	1	1	0	0	0	0	F8VQK7	
ENSMUST00000092015	ENSMUSG00000041923	18	22693181	23041653	-1	11	20	80	18	12	5	1	5	0	0	0	F6XSA1	
ENSMUST00000092020	ENSMUSG00000069439	15	81843343	81843699	-1	0	0	7	2	0	0	0	1	0	3	0	F6XS56	
ENSMUST00000092033	ENSMUSG00000040043	10	128129470	128180297	-1	27	17	28	30	43	11	300	517	340	85	317		Q8VC70
ENSMUST00000092041	ENSMUSG00000037013	18	14624198	14682914	-1	6	0	42	66	19	7	265	902	483	304	387	Q8BJJ6	
ENSMUST00000092048	ENSMUSG00000061315	10	128035346	128048637	1	51	49	700	154	100	73	3	11	19	2	30		P70670
ENSMUST00000092058	ENSMUSG00000074639	10	127866474	127877317	1	8	9	28	78	20	15	0	0	0	1	0	Q8K3M1	
ENSMUST00000092070	ENSMUSG00000024421	18	12338819	12583013	1	67	63	118	132	91	35	0	0	0	0	0		Q61789
ENSMUST00000092073	ENSMUSG00000055652	7	75848310	75874131	1	2	1	1	66	3	12	99	263	41	0	147		Q8R2P1
ENSMUST00000092074	ENSMUSG00000002147	10	127642986	127660957	1	29	22	80	52	27	20	5964	10035	7448	956	5869		P52633
ENSMUST00000092075	ENSMUSG00000049411	18	11981303	12121480	-1	13	10	8	61	15	6	6	11	9	5	10		Q3UME2
ENSMUST00000092089	ENSMUSG00000074651	13	112993868	113000394	1	39	37	238	321	63	25	1	2	4	1	6		Q3UZ45
ENSMUST00000092094	ENSMUSG00000069475	19	61183890	61183955	1	0	0	0	0	0	0	0	0	0	0	0	O88222	
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ENSMUST00000092112	ENSMUSG00000024283	18	7868832	7973547	1	0	0	0	2	0	10	105	542	28	9	15		Q924H7
ENSMUST00000092123	ENSMUSG00000069495	2	49451486	49551948	1	19	16	16	91	20	10	205	880	556	201	536		Q8C0I4
ENSMUST00000092138						542	528	824	6508	749	359	29	30	52	22	46		
ENSMUST00000092143	ENSMUSG00000051236	10	120781096	120899101	-1	19	17	70	126	25	13	4	15	7	5	29		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000092154	ENSMUSG00000027981	3	113605067	113630149	-1	0	0	0	3	0	3	16	0	0	0	7		Q3UZ01
ENSMUST00000092155	ENSMUSG00000027966	3	114030540	114220718	1	11	10	12	7	14	10	0	0	0	0	0		Q61245
ENSMUST00000092162	ENSMUSG00000069515	10	117287796	117292868	-1	5	8	5	5	11	4	23	86	23	208	46	A0A077S9N1	P17897
ENSMUST00000092163	ENSMUSG00000069516	10	117277334	117282274	-1	19	19	57	92	32	35	55849	168169	37528	165548	38248	A0A077S2U6	P08905
ENSMUST00000092165	ENSMUSG00000069518	10	116956824	116972609	-1	5	0	1	3	3	7	0	0	0	0	0	F6WY25	
ENSMUST00000092167	ENSMUSG00000020154	10	116301374	116389538	1	108	106	356	186	122	51	1	13	1	1	6		B2RU80
ENSMUST00000092170	ENSMUSG00000069520	10	115340739	115362262	-1	10	9	43	18	15	16	476	1270	654	100	394		Q91W52
ENSMUST00000092175	ENSMUSG00000035681	10	112271123	112466304	1	25	21	38	173	31	18	0	0	0	0	0	E9QLW0	
ENSMUST00000092176	ENSMUSG00000035694	10	112163621	112216555	1	0	1	9	2	0	0	0	0	0	0	0		Q8BUG5
ENSMUST00000092213	ENSMUSG00000005897	10	94148023	94197211	1	0	7	3	11	7	0	11	12	25	3	28		Q505F1
ENSMUST00000092215	ENSMUSG00000036168	10	93540632	93584327	1	0	11	4	30	10	2	0	1	1	0	2		Q8CDN8
ENSMUST00000092219	ENSMUSG00000019961	10	91147571	91171582	-1	0	6	8	0	0	0	63	478	117	0	116	Q3TNH0	Q61029
ENSMUST00000092227	ENSMUSG00000069539	10	89638721	89686285	-1	0	0	0	0	2	0	197	743	737	33	354	G5E8J9	
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ENSMUST00000092266	ENSMUSG00000034674	10	82629828	82650799	1	0	14	18	49	12	0	248	618	378	27	214		P56581
ENSMUST00000092279	ENSMUSG00000072825	12	112722174	112746591	1	45	32	164	0	27	20	2	9	17	6	0		Q80U49
ENSMUST00000092285	ENSMUSG00000048240	10	80948624	81014945	-1	0	0	0	0	0	17	7	7	6	1	4	G3X9Q2	
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ENSMUST00000092298	ENSMUSG00000039238	11	121510978	121519333	-1	23	17	173	29	29	26	4	23	6	1	2		Q8BH05
ENSMUST00000092302	ENSMUSG00000025175	11	121434913	121450491	1	0	0	10	6	0	0	0	1	0	0	0	Q6P264	
ENSMUST00000092305	ENSMUSG00000069565	10	80261486	80288408	1	6	8	16	0	12	15	319	404	376	36	313		Q9JII5
ENSMUST00000092325	ENSMUSG00000035835	10	79860475	79874634	-1	0	12	0	205	29	16	14	69	26	0	59		
ENSMUST00000092351	ENSMUSG00000053395	7	3390683	3415648	1	0	0	5	94	0	0	2	4	1	0	1	F7CZ64	
ENSMUST00000092366	ENSMUSG00000069581	10	77829467	77887021	1	7	5	14	6	11	9	0	0	0	0	0		J3S6Y1
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ENSMUST00000092370	ENSMUSG00000069583	10	77720586	77721256	1	8	5	22	12	17	9	0	0	0	0	0		Q9Z287
ENSMUST00000092371	ENSMUSG00000069584	10	77706626	77706958	1	5	2	6	2	11	1	0	0	0	0	0	F7CZ33	
ENSMUST00000092373	ENSMUSG00000046697	11	118988188	118992841	1	6	9	35	13	25	12	0	0	0	0	0	D3Z6V6	
ENSMUST00000092378	ENSMUSG00000025575	11	118406289	118419086	-1	0	0	0	0	0	0	251	376	180	77	181		Q8VCF1
ENSMUST00000092382	ENSMUSG00000033909	11	118259651	118290244	-1	19	0	0	59	0	16	93	91	1	3	0		B1AQJ2
ENSMUST00000092393	ENSMUSG00000001120	10	76761857	76961887	-1	4	2	0	0	3	0	0	2	0	0	0	E9Q7D8	
ENSMUST00000092394	ENSMUSG00000069588	11	117484368	117489014	1	17	5	13	13	17	7	0	0	0	0	0	Q8BQP1	
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ENSMUST00000092405	ENSMUSG00000073141	X	70393901	70394740	-1	0	0	2	1	1	1	0	0	0	0	0	Q3V0K5	
ENSMUST00000092406	ENSMUSG00000009114	10	76449081	76461110	1	13	4	19	10	12	4	0	0	0	0	0	G5E8K1	
ENSMUST00000092415	ENSMUSG00000042331	11	61956763	62223013	1	61	0	83	127	0	15	0	0	0	6	0		Q5SXY1
ENSMUST00000092420	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000092425	ENSMUSG00000017404	11	98026710	98030492	1	28	15	0	0	0	0	41	61	34	157	32	A2A547	
ENSMUST00000092426	ENSMUSG00000070306	9	44240677	44247306	1	10	15	22	17	18	7	1	2	1	3	5		P0C7Q1
ENSMUST00000092430	ENSMUSG00000003923	10	71225464	71238280	-1	18	18	69	186	24	7	46	164	90	48	68		P40630
ENSMUST00000092431	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	G5E8K2	
ENSMUST00000092432	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	G5E8K3	
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ENSMUST00000092459	ENSMUSG00000069607	11	115042131	115048409	-1	12	11	35	20	23	0	98	624	264	59	435		Q6SJQ5
ENSMUST00000092462	ENSMUSG00000036875	10	62947026	62974185	1	0	0	0	0	0	0	0	67	249	0	82		Q6ZQJ5
ENSMUST00000092463	ENSMUSG00000089753	11	115010335	115016193	-1	0	0	0	0	0	0	0	0	0	0	0	L7N207	
ENSMUST00000092464	ENSMUSG00000044811	11	114996721	115001880	-1	8	0	0	13	0	9	864	2065	613	2379	624		Q7TSN2
ENSMUST00000092466	ENSMUSG00000058728	11	114956116	114969157	-1	0	0	0	2	0	0	0	0	0	0	0		D3Z6G7
ENSMUST00000092469	ENSMUSG00000034706	11	114727408	114757889	1	12	4	8	0	15	6	0	0	0	0	0		A2AC93
ENSMUST00000092473	ENSMUSG00000020078	10	62454843	62486805	-1	0	0	0	30	12	0	0	0	0	0	0		P40336
ENSMUST00000092486	ENSMUSG00000059901	10	61197112	61273438	-1	71	44	260	272	105	44	5	32	5	5	84	B2RXX5	
ENSMUST00000092491	ENSMUSG00000095093	17	22547941	22573273	-1	20	17	6	4	11	10	0	0	0	0	0	K7N674	
ENSMUST00000092498	ENSMUSG00000020097	10	61098642	61147703	-1	8	13	30	5	0	0	1098	2373	1146	146	664		Q8R0X7
ENSMUST00000092500	ENSMUSG00000020610	11	109425946	109452813	1	10	12	13	25	15	5	39	120	40	13	20	B1AT59	
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ENSMUST00000092511	ENSMUSG00000069622	10	59395632	59396757	1	26	11	8	0	46	20	25	461	0	0	0	Q9CXU4	
ENSMUST00000092512	ENSMUSG00000019916	10	59323296	59373304	1	0	0	0	0	0	0	120	670	145	169	198	E9Q7B0	
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ENSMUST00000092532	ENSMUSG00000028565	4	97772734	98118874	1	0	76	20	201	33	65	0	0	0	0	0		Q02780
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ENSMUST00000092551	ENSMUSG00000027070	2	69424340	69586065	-1	16	19	47	88	30	15	1	3	2	0	6	Q3V346	
ENSMUST00000092557	ENSMUSG00000034255	11	103331497	103363692	-1	6	4	0	373	11	8	3	8	8	0	1	A2AKN5	
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ENSMUST00000092567	ENSMUSG00000034520	11	102799579	102819700	-1	3	2	18	37	16	0	0	0	0	2	4		P28229
ENSMUST00000092569	ENSMUSG00000020925	11	102684686	102697782	-1	0	0	0	12	11	0	21	119	0	34	47		Q9CR29
ENSMUST00000092576	ENSMUSG00000027646	2	157418444	157471862	1	0	0	60	0	0	14	0	0	0	0	0		P05480
ENSMUST00000092584	ENSMUSG00000069662	10	37133375	37138920	-1	7	5	30	93	11	14	2219	9320	2547	451	2556		P26645
ENSMUST00000092595	ENSMUSG00000022558	15	76380261	76453038	1	47	54	187	57	53	45	70	97	89	4	199	D3Z624	
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ENSMUST00000092602	ENSMUSG00000069670	10	31689310	32890462	-1	0	0	16	35	2	2	0	0	0	0	0	F7C7C4	
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ENSMUST00000092610	ENSMUSG00000039697	10	30645584	30803107	-1	5	7	12	4	5	0	0	9	0	1	3	A9Q6S9	Q6DFV7
ENSMUST00000092614	ENSMUSG00000069678	6	83077869	83080855	1	0	0	0	0	0	0	20	40	0	90	0		
ENSMUST00000092618	ENSMUSG00000068328	6	83054521	83057808	1	13	11	28	53	24	7	1802	2767	1192	249	1180	Q3U3K9	
ENSMUST00000092620						10	1	12	50	22	1	2613	3474	2246	14083	1952		
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ENSMUST00000092623	ENSMUSG00000019880	10	29453109	29535867	-1	6	10	14	102	14	8	0	0	0	0	0		Q2TJ95
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000092629	ENSMUSG00000038916	10	29143996	29199630	1	25	20	61	321	38	8	0	0	0	0	0		Q6NZL0
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ENSMUST00000092640	ENSMUSG00000013846	15	67102875	67113992	-1	85	98	87	89	133	72	1580	2298	1904	239	2223	Q544T4	P54751
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ENSMUST00000092646	ENSMUSG00000019984	10	24869986	24913681	1	8	4	8	33	11	3	25	0	12	10	16	E9QNV2	
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ENSMUST00000092654	ENSMUSG00000100186	10	24091260	24092294	-1	7	7	19	3	10	0	0	0	0	0	0		Q5QD06
ENSMUST00000092656	ENSMUSG00000100689	10	24037614	24038690	1	8	9	10	2	4	3	0	0	0	0	0	A6H6B4	Q5QD09
ENSMUST00000092657	ENSMUSG00000095569	10	24027222	24028298	1	11	10	21	4	11	2	0	0	0	0	0		Q5QD10
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ENSMUST00000092659	ENSMUSG00000069706	10	23970706	23971719	1	6	7	10	10	10	5	0	0	0	0	0	B2RTA0	Q5QD14
ENSMUST00000092660	ENSMUSG00000069707	10	23960494	23961537	1	6	4	6	8	6	0	0	0	0	0	0		Q5QD15
ENSMUST00000092663	ENSMUSG00000019302	11	101009452	101063719	1	26	19	79	0	29	15	3118	6208	3629	137	3183		Q9Z1G4
ENSMUST00000092665	ENSMUSG00000010461	10	23104168	23349895	-1	3	3	7	10	4	13	0	0	0	0	0	Q8BY78	
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ENSMUST00000092672	ENSMUSG00000069712	10	22066307	22068079	-1	11	13	21	16	6	1	0	1	1	0	1	D3Z741	
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ENSMUST00000092674	ENSMUSG00000019977	10	21295979	21368889	1	0	0	0	47	26	14	46	191	32	44	35	L7N209	
ENSMUST00000092678	ENSMUSG00000037608	10	20312469	20344613	1	8	10	0	8	0	0	150	459	80	211	0	F8WI22	
ENSMUST00000092680	ENSMUSG00000069713	10	20310506	20312294	-1	5	3	15	102	17	5	1	8	5	4	4	Q9D488	
ENSMUST00000092684	ENSMUSG00000006784	11	100545607	100572568	1	3	1	7	11	2	4	2	2	2	3	1		Q9D4B2
ENSMUST00000092688	ENSMUSG00000017176	11	100422321	100441808	-1	0	0	0	0	0	0	0	0	41	27	0		Q3UFY7
ENSMUST00000092689	ENSMUSG00000017176	11	100422321	100441808	-1	2	2	7	23	0	7	0	0	0	0	31		
ENSMUST00000092694	ENSMUSG00000090225	11	99864476	99865571	1	22	17	25	57	21	6	0	0	0	0	0	Q9D3H7	
ENSMUST00000092695	ENSMUSG00000069718	11	99657949	99658960	-1	1	5	21	75	6	8	0	0	0	0	0	B1AQ90	
ENSMUST00000092696	ENSMUSG00000069720	5	15652286	15657059	-1	6	4	4	6	6	3	0	0	0	0	0	Q8C5Y0	
ENSMUST00000092699	ENSMUSG00000069721	11	99555823	99556853	-1	4	8	2	40	16	15	0	0	0	0	0		Q9D638
ENSMUST00000092700	ENSMUSG00000069722	11	99550130	99550865	-1	12	2	27	76	6	2	0	0	0	0	0		Q9D638
ENSMUST00000092706	ENSMUSG00000017499	11	98907801	98923940	1	23	10	63	58	42	13	10	7	22	4	0		O89033
ENSMUST00000092720	ENSMUSG00000072763	5	109674545	109691041	-1	94	67	255	77	60	42	14	55	31	23	27	D3Z5L4	
ENSMUST00000092723	ENSMUSG00000069729	17	4994332	5347656	1	46	1	29	1931	59	38	401	419	780	46	651	E9Q6R4	
ENSMUST00000092729	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	0	0	0	0	0	0	0	0		P42866
ENSMUST00000092730	ENSMUSG00000069733	4	100478849	100550147	1	13	0	21	64	8	0	0	0	0	0	0	Q3V081	
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ENSMUST00000092734	ENSMUSG00000000766	10	6758506	7038198	1	3	3	0	0	2	1	0	0	0	0	0		P42866
ENSMUST00000092735	ENSMUSG00000018160	11	98152154	98193293	-1	0	2	0	0	0	0	15	122	9	4	0	B1AQH6	
ENSMUST00000092736	ENSMUSG00000020882	11	98001508	98023034	-1	0	0	0	0	0	3	0	0	0	0	0	A2A545	
ENSMUST00000092750	ENSMUSG00000066007	4	146156824	146198755	1	21	19	28	0	21	20	0	0	0	0	0	A2A7V0	
ENSMUST00000092766	ENSMUSG00000038909	11	95274259	95310246	-1	0	0	0	0	0	13	513	845	76	96	219		Q5SVQ0
ENSMUST00000092768	ENSMUSG00000001510	11	95120119	95125296	1	17	12	62	192	37	11	0	0	1	0	4	Q78ZZ8	Q64205
ENSMUST00000092777	ENSMUSG00000020859	11	93996091	94126085	1	0	0	6	0	9	0	0	0	0	0	0	E9PUD1	
ENSMUST00000092780	ENSMUSG00000056158	11	93098028	93601749	1	2	3	1	55	0	0	0	0	0	0	0	Q78UF4	
ENSMUST00000092788	ENSMUSG00000069763	11	90030348	90036508	1	11	6	8	3	10	8	0	0	0	0	0		Q9CQG9
ENSMUST00000092794	ENSMUSG00000069769	11	88339382	88718513	-1	5	4	0	36	2	5	20	41	34	3	14	Q3TE41	Q920Q6
ENSMUST00000092800	ENSMUSG00000034177	11	87662722	87735539	1	0	0	3	28	13	6	0	0	0	0	0		Q5NCP0
ENSMUST00000092802	ENSMUSG00000018401	11	87592162	87616302	1	14	0	65	0	0	0	58	265	108	0	0		Q91XS1
ENSMUST00000092821	ENSMUSG00000059439	11	85353167	85826058	1	0	0	0	0	0	0	70	19	259	14	82	Q0VF62	
ENSMUST00000092822	ENSMUSG00000059439	11	85353167	85826058	1	0	0	15	0	8	4	18	141	64	18	38	B1AR76	
ENSMUST00000092827	ENSMUSG00000018698	11	84518284	84525535	-1	0	0	0	2	1	0	5	10	10	2	9	A0A0A0MQA9	
ENSMUST00000092834	ENSMUSG00000034940	11	83964428	84044578	1	137	129	600	254	119	73	266	927	637	42	486		Q5SV85
ENSMUST00000092836	ENSMUSG00000069792	11	83703991	83706268	1	6	15	65	85	11	14	39736	194180	31838	102594	10156	Q5SSJ1	
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ENSMUST00000092840	ENSMUSG00000069793	11	82979629	82991830	-1	0	0	5	0	0	0	0	0	0	0	0	B1ARD6	
ENSMUST00000092844	ENSMUSG00000018841	11	82876434	82890614	-1	0	0	0	24	4	0	48	0	16	14	43	B1ARD4	
ENSMUST00000092849	ENSMUSG00000020697	11	82781108	82804274	1	0	0	12	17	0	0	9	0	67	26	143	Q80ZH7	
ENSMUST00000092852	ENSMUSG00000020701	11	82388900	82446332	1	25	4	40	0	33	24	0	0	0	0	0		Q6IEE6
ENSMUST00000092857	ENSMUSG00000017686	11	80209019	80267907	1	0	0	0	0	2	0	5	17	15	13	30		Q8BG51
ENSMUST00000092858						0	4	1	0	0	0	22	17	40	0	51		
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ENSMUST00000092880	ENSMUSG00000019437	11	78176711	78181909	1	6	8	10	54	18	21	19	67	38	12	35		Q99JT6
ENSMUST00000092881	ENSMUSG00000020834	11	78032280	78037866	1	0	0	0	15	0	2	0	0	0	0	2	Q5SS84	
ENSMUST00000092883	ENSMUSG00000069804	11	77785453	77787747	-1	49	51	115	51	63	33	0	0	4	0	7	Q6R5C6	
ENSMUST00000092884	ENSMUSG00000000631	11	77763246	77865980	1	0	1	0	0	0	0	90	0	204	0	76		Q9JMH9
ENSMUST00000092887	ENSMUSG00000000631	11	77763246	77865980	1	0	0	0	0	0	0	173	34	154	0	102		Q9JMH9
ENSMUST00000092888	ENSMUSG00000069805	13	62864753	62888282	-1	11	7	22	10	13	6	88	151	96	33	42		Q9QXD6
ENSMUST00000092889	ENSMUSG00000061288	5	117120129	117275219	1	42	25	0	20	43	20	73	419	25	0	121		Q8BYC6
ENSMUST00000092891	ENSMUSG00000069806	7	3332955	3368221	1	4	4	11	36	10	7	0	0	0	0	0	B9EJ14	P62956
ENSMUST00000092892	ENSMUSG00000037907	11	77470485	77489678	-1	14	0	7	61	0	7	0	0	9	0	15		Q5F259
ENSMUST00000092907	ENSMUSG00000000751	11	75298166	75348324	-1	32	24	46	53	57	25	3	9	0	0	11		Q8VEE4
ENSMUST00000092912	ENSMUSG00000010554	11	74770830	74828525	1	5	0	8	0	4	4	4	0	0	0	10	F8WHZ7	
ENSMUST00000092915	ENSMUSG00000020741	11	74649495	74670847	1	10	0	11	19	17	0	180	157	87	24	207		
ENSMUST00000092917	ENSMUSG00000069816	11	73940205	73941254	1	4	0	0	0	0	0	0	0	0	0	0	Q7TRX4	
ENSMUST00000092919	ENSMUSG00000069818	11	73782966	73787875	1	3	0	0	0	0	0	0	0	0	0	0	Q8VEZ7	
ENSMUST00000092921	ENSMUSG00000095312	11	73516259	73517197	-1	4	3	9	2	4	1	0	0	0	0	0	Q8VF79	
ENSMUST00000092926	ENSMUSG00000069825	11	73329741	73355913	1	4	4	0	0	0	0	0	0	0	0	0	B2KFD7	Q5SV06
ENSMUST00000092931	ENSMUSG00000071633	19	12599974	12628251	1	8	6	9	4	9	6	0	0	0	0	0		Q5FW57
ENSMUST00000092937	ENSMUSG00000020785	11	73019008	73042073	1	5	10	0	0	30	0	92	158	81	24	102		Q8VBY2
ENSMUST00000092938	ENSMUSG00000020787	11	72999103	73015200	1	0	0	12	8	7	2	0	6	2	0	13	B1AUD1	
ENSMUST00000092940	ENSMUSG00000020798	11	72494919	72550506	-1	13	7	40	7	22	10	22	37	36	7	0		Q9D232
ENSMUST00000092955	ENSMUSG00000069833	19	8989284	9076919	1	7	2	4	45	4	4	38	34	40	143	38	G5E8K8	
ENSMUST00000092956	ENSMUSG00000069833	19	8989284	9076919	1	155	117	262	199	228	133	3980	2638	8888	829	9326	E9Q616	
ENSMUST00000092958	ENSMUSG00000040829	11	70459433	70466202	1	0	0	0	0	4	0	0	0	0	4	0	Q5F2D4	
ENSMUST00000092959	ENSMUSG00000020884	11	70054085	70057894	1	0	3	10	8	0	0	0	0	0	0	0		P34927
ENSMUST00000092966	ENSMUSG00000000579	17	6601671	6609774	1	45	8	30	0	66	15	0	0	0	0	0		P51807

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000092969	ENSMUSG00000069835	11	69622024	69623870	1	0	0	7	3	0	0	0	0	0	6	0		Q6P8J2
ENSMUST00000092971	ENSMUSG00000018474	11	69343273	69369406	-1	0	0	0	71	0	0	0	0	0	0	0	E9Q614	
ENSMUST00000092973	ENSMUSG00000032782	11	69299487	69323775	-1	23	0	17	28	0	14	50	45	75	0	45		Q8CB62
ENSMUST00000092984	ENSMUSG00000020900	11	68691559	68816632	1	27	16	41	48	34	20	0	0	0	0	153	Q3UH59	
ENSMUST00000092990	ENSMUSG00000029314	5	100845713	100899102	1	19	0	24	82	15	8	598	639	712	161	518		Q8C0N2
ENSMUST00000092995	ENSMUSG00000074652	2	155611212	155634307	1	48	24	98	405	94	41	1	6	2	0	3		A2AQP0
ENSMUST00000092996	ENSMUSG00000069844	11	67052670	67067070	1	0	0	0	6	16	0	1	0	0	0	1		Q5SUC9
ENSMUST00000093001	ENSMUSG00000033389	11	65002039	65162961	-1	11	3	12	42	15	4	0	0	0	0	0		Q5SSM3
ENSMUST00000093002	ENSMUSG00000033389	11	65002039	65162961	-1	0	19	34	46	40	0	0	0	0	0	3		Q5SSM3
ENSMUST00000093007	ENSMUSG00000041565	17	68273797	68777961	1	3	9	11	8	0	0	0	0	0	0	0	D3YW39	
ENSMUST00000093019	ENSMUSG00000042377	11	61684091	61709951	1	53	21	153	240	65	37	7	0	2	0	10		Q5SWY7
ENSMUST00000093029	ENSMUSG00000069855	11	61301631	61342860	-1	5	8	45	43	13	8	0	0	0	0	0		Q3V050
ENSMUST00000093033	ENSMUSG00000031981	8	124576111	124618731	1	23	15	31	15	26	13	0	0	0	0	0		Q9D805
ENSMUST00000093039	ENSMUSG00000038697	8	123996318	124021309	-1	0	0	0	28	27	0	0	0	31	0	31		Q91WQ5
ENSMUST00000093040	ENSMUSG00000053291	7	27168424	27178896	-1	0	0	3	22	7	0	1454	2470	1345	255	733	Q4V9W8	Q91ZR1
ENSMUST00000093043	ENSMUSG00000040220	8	123518835	123536649	1	16	10	19	19	30	9	26	48	41	12	33	Q49MD7	Q60779
ENSMUST00000093046	ENSMUSG00000000538	11	60226714	60352905	-1	8	0	0	56	0	1	0	0	164	0	0	Q5SXA5	
ENSMUST00000093048	ENSMUSG00000000538	11	60226714	60352905	-1	0	0	0	2	24	0	5	0	1	0	0	Q5SXA4	
ENSMUST00000093049	ENSMUSG00000001482	8	123442986	123463270	1	40	24	31	47	40	7	8	23	44	4	40		Q99J78
ENSMUST00000093059	ENSMUSG00000069867	8	122619471	122622739	-1	9	5	30	12	12	9	0	0	0	1	1		Q5XFR0
ENSMUST00000093061	ENSMUSG00000020455	11	58978093	58991458	1	0	0	0	157	1	4	580	1627	673	104	460		Q99PQ2
ENSMUST00000093073	ENSMUSG00000017478	8	122376609	122417360	1	10	0	0	0	26	8	287	693	634	48	604		Q0P678
ENSMUST00000093078	ENSMUSG00000025316	8	121949750	122029258	1	0	0	10	26	0	0	98	251	68	12	75		Q8VBU8
ENSMUST00000093099	ENSMUSG00000031832	8	119597975	119605222	-1	0	0	0	0	0	0	230	309	141	42	2		Q6PDZ2
ENSMUST00000093100	ENSMUSG00000031831	8	119575235	119598454	1	25	19	36	92	31	18	0	1	0	0	2		Q9D2H9
ENSMUST00000093106	ENSMUSG00000020333	11	54303798	54364756	1	13	8	4	24	12	10	0	1	0	0	0	Q5ICG4	Q91WC3
ENSMUST00000093107	ENSMUSG00000018906	11	54100095	54131665	1	0	0	0	22	0	0	0	0	0	0	6	Q5SX74	Q60716
ENSMUST00000093109	ENSMUSG00000020388	11	54054928	54069014	-1	7	3	2	0	8	0	1	6	2	9	0	Q5SWV3	
ENSMUST00000093110	ENSMUSG00000029659	5	149411749	149431723	1	7	4	0	26	29	12	0	0	2	0	0		Q14BA6
ENSMUST00000093113	ENSMUSG00000053399	8	113697126	113848615	-1	33	30	46	83	43	20	0	0	0	0	0		Q4VC17
ENSMUST00000093114	ENSMUSG00000018387	11	53457205	53467766	1	0	0	14	0	0	0	0	0	0	0	0	D3Z3D5	
ENSMUST00000093115	ENSMUSG00000017776	11	75679259	75706908	1	0	0	0	56	0	0	21	95	44	32	29	Q5ND50	
ENSMUST00000093120	ENSMUSG00000031948	8	111993440	112011323	-1	28	9	59	16	22	19	102	52	123	78	120	Q8R2P8	
ENSMUST00000093121						0	2	0	4	0	0	0	2	0	0	0		
ENSMUST00000093126	ENSMUSG00000046317	3	96433788	96452306	-1	12	8	74	48	25	0	0	0	0	0	0	E9Q5A2	
ENSMUST00000093132	ENSMUSG00000020385	11	51261730	51281766	1	0	0	3	19	0	0	161	1129	249	801	402	Q4FJV9	O35493
ENSMUST00000093138	ENSMUSG00000036644	11	50131396	50172785	1	19	0	39	23	28	5	1053	544	1232	86	810		Q5SVR0
ENSMUST00000093140	ENSMUSG00000025135	11	120598421	120608198	1	2	2	2	58	11	6	384	424	210	80	156		Q9CPX9
ENSMUST00000093141	ENSMUSG00000020374	11	49901835	49980994	1	0	0	10	7	0	2	0	0	0	0	0	B1ATE5	
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ENSMUST00000093146						93	71	630	143	81	58	1	4	2	0	2		
ENSMUST00000093152	ENSMUSG00000069892	11	49015874	49051242	-1	0	6	0	20	17	9	32	121	55	6	13	Q8CB10	
ENSMUST00000093153	ENSMUSG00000069893	11	48946150	48979398	-1	18	6	86	0	0	9	0	0	0	6	13	Q8CB10	
ENSMUST00000093157	ENSMUSG00000031731	8	109778554	109864204	1	16	23	64	206	41	16	884	2879	1304	265	862	Q8CBB7	
ENSMUST00000093162	ENSMUSG00000069895	8	109726451	109737739	-1	40	37	121	145	69	42	782	1205	1321	108	921		P0C7T6
ENSMUST00000093165	ENSMUSG00000020340	11	46193850	46312859	-1	39	42	83	26	49	26	0	0	0	0	0		Q5SQX6
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ENSMUST00000093169	ENSMUSG00000069899	11	46051354	46052321	-1	0	0	0	0	0	0	134	0	11	0	32		Q5SSN7
ENSMUST00000093171	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	0	0	0	327	436	540	249	372	B7ZCU4	
ENSMUST00000093183	ENSMUSG00000046345	16	32271468	32274779	1	132	139	248	86	118	50	3	11	8	4	23		Q8CEZ1
ENSMUST00000093191	ENSMUSG00000069910	11	34809190	34833641	-1	8	4	9	11	5	6	13	27	31	89	21		Q923A2
ENSMUST00000093192	ENSMUSG00000069911	11	34314822	34422640	1	0	0	0	30	3	25	3	2	0	0	22		Q6GQV1
ENSMUST00000093193	ENSMUSG00000020143	11	34226815	34783892	-1	20	22	78	67	40	32	3617	9259	8205	1141	6821		Q8C3J5
ENSMUST00000093195	ENSMUSG00000005699	8	105701154	105703493	1	0	3	0	13	5	0	0	0	0	0	8		Q9Z101
ENSMUST00000093196	ENSMUSG00000066551	5	149046702	149184489	-1	2	0	0	193	5	0	4	53	19	177	46	Q58EV5	P63158
ENSMUST00000093201	ENSMUSG00000057113	11	33152287	33163206	-1	0	0	0	0	0	0	223	1230	241	938	239	Q5SQB0	
ENSMUST00000093205	ENSMUSG00000020271	11	32642724	32746816	1	0	0	0	3	0	0	205	219	0	33	3		Q5SRY7
ENSMUST00000093207	ENSMUSG00000069917	11	32296489	32297298	1	325	79	435	331	2476	220	11747	3733	2435	47598	17869	Q91VB8	
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ENSMUST00000093217	ENSMUSG00000069920	8	105252638	105255153	-1	12	0	0	0	0	0	0	0	13	3	15		Q8VI16
ENSMUST00000093219	ENSMUSG00000020297	11	32000463	32059202	1	4	8	19	5	3	7	1	0	0	0	0	Q5SS03	
ENSMUST00000093221	ENSMUSG00000062181	8	105083753	105093929	1	0	4	0	17	0	6	0	0	0	5	0		Q8VCU1
ENSMUST00000093222	ENSMUSG00000069922	8	105048599	105058414	1	0	7	14	14	18	0	0	0	0	3	0		Q63880
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ENSMUST00000093229						41	36	104	276	55	38	0	2	1	0	3		
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ENSMUST00000093239	ENSMUSG00000020459	11	29526408	29545279	1	8	7	2	81	29	54	2	104	22	6	26		Q91YJ5
ENSMUST00000093245	ENSMUSG00000031872	8	104170513	104219092	1	0	0	0	0	17	0	0	3	0	1	1		Q9EQG5
ENSMUST00000093249	ENSMUSG00000036510	8	99024471	99416471	-1	2	0	1	0	0	0	0	0	0	0	0	Q8C449	
ENSMUST00000093253	ENSMUSG00000032878	11	28385685	28584324	-1	0	8	0	4	0	0	0	0	0	0	0		Q5SP85
ENSMUST00000093267	ENSMUSG00000042208	11	23564961	23633639	-1	3	3	0	0	2	0	0	47	27	31	22		Q68FF0
ENSMUST00000093268	ENSMUSG00000031789	8	95239045	95306585	-1	26	6	141	0	0	0	0	0	0	0	1	Q91WA8	
ENSMUST00000093270	ENSMUSG00000051355	11	22896136	22982382	-1	0	1	0	0	1	0	68	111	87	517	45	F7BZY0	
ENSMUST00000093271	ENSMUSG00000031785	8	94977109	95014208	1	17	0	63	10	22	22	131	86	39	10	82		Q8K209
ENSMUST00000093290	ENSMUSG00000020134	11	21091291	21150323	1	0	0	9	10	8	0	344	1489	729	116	627	Q5SRW7	Q8C669
ENSMUST00000093292	ENSMUSG00000049800	11	20543253	20653021	1	0	19	0	0	13	19	89	92	99	0	81	Q3UGZ1	Q9JJG5
ENSMUST00000093298	ENSMUSG00000045671	11	19924375	20024026	1	0	8	0	290	23	8	17	2	12	0	21		Q924S7
ENSMUST00000093299	ENSMUSG00000045671	11	19924375	20024026	1	40	15	44	61	26	6	44	89	54	15	78	Q5SRF8	
ENSMUST00000093301	ENSMUSG00000033009	8	94037198	94067921	1	31	31	0	29	36	0	0	1	0	0	1		Q3U0K8
ENSMUST00000093312	ENSMUSG00000031734	8	91798525	91801916	-1	0	8	15	404	6	0	0	0	0	0	0		P81067
ENSMUST00000093321	ENSMUSG00000020176	11	11930508	12038683	-1	7	0	32	82	32	12	7	14	0	5	0		Q60760
ENSMUST00000093326						0	0	0	1	4	0	0	0	1	1	0		
ENSMUST00000093336	ENSMUSG00000049916	16	17113399	17125106	-1	5	4	15	24	9	6	5	11	2	5	4	Q80VT5	
ENSMUST00000093342	ENSMUSG00000069971	8	87563853	87589424	1	8	8	20	6	14	11	0	0	0	0	0	Q8BHX0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000093346	ENSMUSG00000041126	11	6427229	6444443	-1	0	0	5	4	0	0	179	276	156	53	70	Q8R029	
ENSMUST00000093350	ENSMUSG00000020456	11	6291633	6356642	1	15	19	8	0	0	0	51	384	152	0	64		Q60597
ENSMUST00000093355	ENSMUSG00000057897	11	5969644	6066362	-1	10	0	18	0	4	0	0	0	0	0	0	Q5SVI1	
ENSMUST00000093357	ENSMUSG00000005150	8	85075035	85081306	-1	0	0	0	7	0	0	45	86	86	38	49		Q9DAJ4
ENSMUST00000093360	ENSMUSG00000031691	8	85036915	85057583	1	28	19	61	50	25	17	453	732	598	58	526	E9PV58	
ENSMUST00000093362	ENSMUSG00000049680	11	5713417	5762376	-1	11	11	13	23	0	0	41	128	62	4	53		Q5NCI0
ENSMUST00000093365	ENSMUSG00000009079	11	5069689	5099266	-1	4	10	80	0	7	15	81	194	151	16	165	Q5SUS8	
ENSMUST00000093369	ENSMUSG00000020396	11	4938754	4948064	-1	39	21	245	204	47	26	2	11	4	0	4		P19246
ENSMUST00000093374	ENSMUSG00000009073	11	4765845	4849536	-1	1	1	0	2	4	1	9	8	37	0	24	F8WJ43	
ENSMUST00000093375	ENSMUSG00000008129	8	84148025	84172590	1	2	13	6	0	0	0	0	3	3	0	6		
ENSMUST00000093380	ENSMUSG00000012889	8	84125989	84132527	1	3	4	14	109	17	8	7	4	0	3	19		
ENSMUST00000093381	ENSMUSG00000051427	11	4141123	4160293	-1	0	0	57	35	6	0	50	68	64	0	90		Q5SPX1
ENSMUST00000093389	ENSMUSG00000034543	11	3649494	3690477	1	42	24	101	75	53	19	86	119	175	21	166		Q69ZX6
ENSMUST00000093393	ENSMUSG00000031709	8	83165352	83272934	1	30	18	31	19	15	18	120	194	219	13	138		Q3UYK3
ENSMUST00000093399	ENSMUSG00000034614	11	3330401	3342971	1	0	0	0	0	0	0	0	0	0	0	0		Q7TMJ8
ENSMUST00000093402	ENSMUSG00000020453	11	3288874	3309083	1	0	0	0	0	0	14	3	0	103	17	70	Q5NBZ1	
ENSMUST00000093411						0	2	23	4	5	0	0	0	0	7	0		
ENSMUST00000093427	ENSMUSG00000048148	8	72646711	72714746	1	52	38	192	85	26	0	0	0	0	0	0		A6H603
ENSMUST00000093430						0	1	23	3	5	0	165	797	411	450	250		
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ENSMUST00000093444	ENSMUSG00000070000	8	71708387	71725716	-1	4	0	7	0	18	10	135	114	140	15	63		Q8K285
ENSMUST00000093450	ENSMUSG00000034863	8	71476023	71486067	-1	22	17	56	560	34	22	32	62	32	13	70		Q6PB70
ENSMUST00000093454	ENSMUSG00000070002	8	70539675	70592858	1	27	22	70	93	41	15	1347	1700	1091	167	1336		O08856
ENSMUST00000093456	ENSMUSG00000055553	8	70508272	70527956	-1	5	5	8	8	0	0	283	841	295	378	211		Q80XH1
ENSMUST00000093458	ENSMUSG00000036054	8	70234226	70279915	1	6	0	0	53	8	9	37	56	78	0	78		Q8CH09
ENSMUST00000093468	ENSMUSG00000030465	8	67689082	68062286	-1	0	1	3	0	0	1	0	0	1	1	1		Q2PFD7
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ENSMUST00000093470	ENSMUSG00000051147	8	67494867	67502580	1	2	2	0	0	0	2	58	286	91	272	32	Q78ZC4	P50295
ENSMUST00000093480	ENSMUSG00000054162	8	62951009	63357103	1	0	0	0	0	0	1	0	0	0	0	0		Q8BKV0
ENSMUST00000093485	ENSMUSG00000037921	8	61928087	62037701	1	3	7	13	3	9	3	58	0	0	0	0	E9PZQ1	
ENSMUST00000093486	ENSMUSG00000019230	1	138825186	138848577	-1	0	0	0	0	0	0	0	0	0	0	0		Q9WUH2
ENSMUST00000093490	ENSMUSG00000004319	8	60910389	60983300	-1	5	0	0	54	2	0	87	243	51	39	109	Q790S0	P51791
ENSMUST00000093494	ENSMUSG00000070023	8	60430024	60503198	-1	8	2	17	2	1	2	0	0	0	0	0	Q8C3L5	
ENSMUST00000093506	ENSMUSG00000052477	1	84992690	85270566	-1	95	81	64	129	106	43	27	69	82	38	56	Q8C898	
ENSMUST00000093508	ENSMUSG00000070034	1	85576899	85598817	-1	19	17	34	6	21	32	686	2845	1039	346	760		Q8BVK9
ENSMUST00000093517	ENSMUSG00000031628	8	46617449	46638706	1	8	6	3	30	5	1	390	1274	812	1110	591		P70677
ENSMUST00000093518	ENSMUSG00000031629	8	46552055	46580007	1	1	4	0	1	0	1	0	13	4	0	0		Q8C4M7
ENSMUST00000093526	ENSMUSG00000070044	8	45336717	45382291	-1	24	17	57	101	27	14	0	0	0	0	0		Q8CFV2
ENSMUST00000093527	ENSMUSG00000074029	9	119159161	119161669	1	34	33	204	113	59	32	0	0	1	0	0	E9PZ13	
ENSMUST00000093534	ENSMUSG00000045636	8	40990914	41133726	-1	0	6	0	0	0	0	1882	10318	1654	139	1166		
ENSMUST00000093546						4	4	1	7	0	2	0	0	0	0	0		
ENSMUST00000093552	ENSMUSG00000002984	7	19701313	19715438	-1	9	8	17	18	10	4	151	197	145	50	156		Q9QYA2
ENSMUST00000093603						78	59	148	80	71	43	0	5	4	3	12		
ENSMUST00000093768	ENSMUSG00000072915	11	58847158	58861956	1	0	0	0	0	0	0	0	4	0	0	0	Q3UFF8	
ENSMUST00000093769	ENSMUSG00000045095	6	93675455	94283917	-1	29	32	77	6	23	14	0	0	0	7	0	E9PZ12	
ENSMUST00000093772	ENSMUSG00000013419	9	121760033	121771742	1	54	30	101	240	89	28	6	20	4	5	24	E9PZ11	
ENSMUST00000093773	ENSMUSG00000032517	9	120149742	120181484	1	32	0	4	0	63	53	0	0	0	0	0		Q9D2P8
ENSMUST00000093774	ENSMUSG00000041991	3	93319749	93333570	1	0	0	0	0	0	0	0	0	0	0	0	F8WJ23	
ENSMUST00000093775	ENSMUSG00000070280	9	119169455	119365553	-1	7	13	47	17	14	6	0	0	0	0	0	Q497L9	
ENSMUST00000093785	ENSMUSG00000079334	9	107578887	107584050	1	8	3	12	14	28	7	124	181	125	26	77	Q3UVC9	Q9R123
ENSMUST00000093786	ENSMUSG00000010067	9	107551555	107562267	1	0	0	0	15	0	0	39	0	4	0	12	A9YZW8	Q99MK9
ENSMUST00000093791	ENSMUSG00000032534	9	102584598	102626534	-1	4	3	1	36	3	1	14	109	48	22	69	F8VPJ7	
ENSMUST00000093792	ENSMUSG00000070287	9	100552188	100571090	-1	3	4	0	36	3	1	10	19	17	2	0		D3YVE8
ENSMUST00000093795	ENSMUSG00000056267	9	99243367	99300404	1	7	9	0	8	3	5	16	117	26	19	16		Q6IQY5
ENSMUST00000093798	ENSMUSG00000040433	9	96682770	96752831	-1	0	0	47	0	10	0	14	0	47	0	70	Q3LR78	
ENSMUST00000093800	ENSMUSG00000049493	9	95752642	95845311	-1	7	8	13	5	9	11	1	1	0	8	3		Q3V0K9
ENSMUST00000093801	ENSMUSG00000032369	9	92249750	92272278	1	2	6	22	43	0	15	867	1194	1253	1072	661		Q9JJ00
ENSMUST00000093802	ENSMUSG00000056919	9	87189577	87255536	-1	249	185	352	210	257	121	34	181	125	56	97		Q6ZQ06
ENSMUST00000093811	ENSMUSG00000034898	9	79815051	79977804	-1	21	13	52	14	17	14	0	0	0	0	0	Q059P4	
ENSMUST00000093812	ENSMUSG00000046186	9	78615546	78716253	1	20	22	27	58	23	24	2	22	7	8	6	A6MDD3	Q8R422
ENSMUST00000093813	ENSMUSG00000004562	14	51984719	52006251	1	14	8	10	26	15	5	0	0	0	0	0		Q3UPH7
ENSMUST00000093819	ENSMUSG00000079469	9	73007419	73040378	-1	0	0	10	0	0	0	197	1289	343	8	333	Q8BSC4	
ENSMUST00000093820	ENSMUSG00000037674	9	72532240	72622937	1	0	0	0	0	0	0	0	0	0	0	0	F8VPJ6	
ENSMUST00000093823	ENSMUSG00000041361	9	71504347	71592360	-1	0	0	0	0	0	0	0	1	0	0	0		Q3ULJ9
ENSMUST00000093829	ENSMUSG00000036466	9	64385626	64709205	1	3	6	18	59	11	4	2	0	1	0	5		Q80T91
ENSMUST00000093832	ENSMUSG00000056271	9	57607085	57620774	-1	8	6	0	22	0	7	14	45	14	2	26		Q8VCD3
ENSMUST00000093833	ENSMUSG00000032305	9	57537528	57543187	1	0	0	0	202	44	0	43	159	0	25	61		Q14DQ1
ENSMUST00000093837	ENSMUSG00000070298	9	57236556	57249863	1	15	19	40	23	24	12	1	2	1	0	6	F8VPJ5	
ENSMUST00000093844	ENSMUSG00000035594	9	54980880	55007779	1	28	22	35	24	33	18	0	1	4	1	3		Q2MKA5
ENSMUST00000093852	ENSMUSG00000066687	9	48654311	48835945	-1	50	33	122	202	58	32	41	50	70	11	180	Q3UQ17	
ENSMUST00000093853	ENSMUSG00000044229	9	48362041	48400025	1	18	14	52	26	24	7	2	2	2	4	3		Q52KP5
ENSMUST00000093855	ENSMUSG00000070304	9	45117876	45130070	1	22	37	86	61	26	19	6	38	0	0	15	Q1MXF8	Q56A07
ENSMUST00000093856						10	13	67	16	5	2	16	0	88	10	41		
ENSMUST00000093859	ENSMUSG00000039579	4	49661611	49845744	-1	32	0	0	0	29	0	0	0	32	0	52	A2AIR5	
ENSMUST00000093864	ENSMUSG00000096427	9	38268515	38269465	1	2	1	2	5	2	0	0	0	0	0	0	L7N210	
ENSMUST00000093865	ENSMUSG00000094778	9	38253419	38254360	1	3	2	2	0	1	2	0	0	0	0	0	F8VQN7	
ENSMUST00000093866	ENSMUSG00000070311	9	38218818	38219766	1	1	4	0	1	4	0	0	0	0	0	0	Q9EQB2	
ENSMUST00000093867	ENSMUSG00000093901	9	38209052	38209993	1	7	1	3	3	4	2	0	0	0	0	0	K7N678	
ENSMUST00000093868	ENSMUSG00000070313	9	36635754	36643376	-1	0	0	0	0	0	0	0	0	0	0	0		Q3UN54
ENSMUST00000093883	ENSMUSG00000027122	2	106962527	106974424	-1	2	0	0	3	0	0	28	89	55	27	18		Q8BIX3
ENSMUST00000093893	ENSMUSG00000050730	9	8994329	9239101	-1	34	38	160	62	33	18	1	15	1	7	10		B2RQE8
ENSMUST00000093896						2	0	2	1	1	0	0	0	4	1	1		
ENSMUST00000093901	ENSMUSG00000025377	11	120090531	120098731	-1	0	0	0	0	27	0	321	494	343	5	237	B2RPS6	Q3U3N6
ENSMUST00000093902	ENSMUSG00000070327	11	119393100	119487418	1	0	105	212	85	80	68	711	962	2015	19	2676	F7A6H4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000093905	ENSMUSG00000070330	11	117860752	117865543	1	12	11	33	133	29	8	0	0	0	0	0		B1AQL3
ENSMUST00000093906	ENSMUSG00000017716	11	117849251	117855743	1	114	115	359	152	128	80	15	41	24	7	18		O70201
ENSMUST00000093907	ENSMUSG00000059248	11	117199661	117362325	1	5	9	7	56	11	0	47	44	23	0	51		Q80UG5
ENSMUST00000093909	ENSMUSG00000070331	11	116441325	116455237	-1	8	0	13	12	18	0	2	9	0	0	8	Q3V2A7	
ENSMUST00000093911	ENSMUSG00000034427	11	115858406	115892603	1	59	36	72	93	64	27	0	0	0	0	0	I7HPW8	
ENSMUST00000093912	ENSMUSG00000020747	11	115765433	115799366	1	17	23	0	83	45	20	472	579	221	72	515		Q7TSH8
ENSMUST00000093914	ENSMUSG00000070332	11	115440545	115448270	1	23	5	22	60	26	10	0	0	0	0	0	Q3V061	
ENSMUST00000093923	ENSMUSG00000020687	11	104502745	104550620	-1	7	7	23	6	0	0	202	759	267	250	199		A2A6Q5
ENSMUST00000093925	ENSMUSG00000018634	11	104132855	104175523	1	23	15	37	127	32	8	0	0	0	0	0	Q3ZAT0	P35347
ENSMUST00000093933	ENSMUSG00000097487	11	101418812	101425333	-1	60	55	167	57	69	18	2	20	6	5	19		Q9D9A7
ENSMUST00000093935	ENSMUSG00000070334	11	99907920	99908892	1	8	3	7	6	6	0	0	0	0	0	0	Q9D644	
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ENSMUST00000093937	ENSMUSG00000017499	11	98907801	98923940	1	0	3	0	13	0	3	57	131	36	35	54		
ENSMUST00000093938	ENSMUSG00000017211	11	98646759	98657964	1	0	5	20	0	0	11	0	0	0	0	0		Q32M21
ENSMUST00000093939	ENSMUSG00000070336	11	97853826	97884154	-1	2	8	0	0	9	1	4	8	1	4	5		A2A6H3
ENSMUST00000093940	ENSMUSG00000049807	11	97415533	97502402	1	0	0	0	186	0	0	0	283	0	18	0		Q69ZH9
ENSMUST00000093942	ENSMUSG00000070337	11	97332109	97352077	-1	84	41	202	234	146	68	1	0	2	1	6	E9PY61	
ENSMUST00000093943	ENSMUSG00000018666	11	96789127	96808640	1	0	0	1	6	0	0	26	239	84	82	97		P83917
ENSMUST00000093944	ENSMUSG00000048763	11	96323326	96347930	1	6	10	10	21	17	7	5	12	4	1	4		P09026
ENSMUST00000093945	ENSMUSG00000039110	11	94501347	94521742	-1	26	0	0	0	0	0	0	0	0	0	1		Q5SUV2
ENSMUST00000093951	ENSMUSG00000028188	3	146457196	146499753	-1	79	68	117	460	119	77	11	25	23	2	18		Q9D5R4
ENSMUST00000093955	ENSMUSG00000020485	11	87737552	87743623	1	0	0	0	16	0	4	1134	3275	914	3347	625		P63271
ENSMUST00000093956	ENSMUSG00000070345	11	87617164	87659542	1	17	11	26	153	20	10	2	0	0	1	0		Q5ND04
ENSMUST00000093962	ENSMUSG00000070348	7	144929931	144939869	-1	25	16	88	134	25	23	12	32	16	151	571	Q790L7	P25322
ENSMUST00000093964						0	0	0	4	0	0	10	12	24	60	10		
ENSMUST00000093969	ENSMUSG00000020527	11	84880148	84911226	1	0	8	7	117	3	0	7	0	8	0	0		Q5SV80
ENSMUST00000093971	ENSMUSG00000040998	3	132881745	132950291	-1	0	0	0	0	11	0	0	0	0	0	19		Q91V88
ENSMUST00000093975	ENSMUSG00000020696	11	82802449	82871210	-1	9	5	19	7	20	2	85	155	87	14	105		Q6ZQM0
ENSMUST00000093976	ENSMUSG00000046561	3	126363684	126440375	1	16	13	29	43	22	12	0	0	0	0	1	Q32KI8	Q8BM89
ENSMUST00000093983	ENSMUSG00000070354	11	79513385	79530589	-1	15	11	20	40	27	8	149	760	181	197	219	L7N211	
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ENSMUST00000093991	ENSMUSG00000049571	7	139600951	139683817	-1	7	5	7	13	14	0	0	0	0	0	0	Q14AD7	
ENSMUST00000093993	ENSMUSG00000060260	7	139248482	139267253	1	20	0	25	77	0	4	48	20	35	12	20	Q3TYY8	
ENSMUST00000093995	ENSMUSG00000000632	11	77930800	77979048	1	0	0	17	49	0	0	0	0	0	0	0		Q7TSK2
ENSMUST00000094002	ENSMUSG00000030994	7	134265779	134385661	-1	16	11	13	11	17	0	0	0	0	1	0		D2J0Y4
ENSMUST00000094004	ENSMUSG00000000686	11	77515121	77538607	1	19	8	34	460	41	14	53	145	66	12	77	B6DQM2	Q5F2F2
ENSMUST00000094012	ENSMUSG00000017631	11	76416734	76622314	-1	14	6	10	36	5	0	0	27	19	0	0		Q5SSL4
ENSMUST00000094014	ENSMUSG00000069808	11	76179671	76214827	1	0	9	0	21	7	0	1	0	0	0	6	Q3TVE0	Q5ND56
ENSMUST00000094015	ENSMUSG00000017288	11	76046226	76179647	-1	6	6	2	0	0	0	0	95	0	54	35	E9PXG9	
ENSMUST00000094017	ENSMUSG00000030850	7	130391526	130519961	-1	0	1	0	17	0	0	38	41	127	85	58	Q4FCQ7	
ENSMUST00000094018	ENSMUSG00000070366	7	129257031	129391412	1	6	7	15	13	4	1	0	0	0	0	0		Q0VBU9
ENSMUST00000094026	ENSMUSG00000070371	7	127932638	127946725	-1	0	0	0	0	0	0	0	0	0	0	0	D3YV46	
ENSMUST00000094028	ENSMUSG00000070372	3	104822779	104864505	-1	11	26	50	109	35	22	5860	26395	10508	12489	5689	Q5RKN9	
ENSMUST00000094037	ENSMUSG00000030699	7	126781483	126785560	1	9	0	17	9	23	3	45	232	65	11	172		P70327
ENSMUST00000094041	ENSMUSG00000040483	11	72301629	72313733	1	0	0	0	0	0	1	1	30	5	11	15	F6ZMN8	
ENSMUST00000094046	ENSMUSG00000070390	11	71153102	71230733	-1	0	0	0	0	1	0	0	0	0	0	0	Q2LKV8	
ENSMUST00000094048	ENSMUSG00000033233	3	100922202	100936920	1	1	0	14	10	0	0	0	1	0	3	0	A2ACL2	
ENSMUST00000094050	ENSMUSG00000062410	3	98741523	98763127	-1	10	5	25	14	3	7	0	0	0	0	0	E9PXG7	
ENSMUST00000094051						5	5	6	0	24	12	0	0	21	0	17		
ENSMUST00000094053	ENSMUSG00000052707	7	123123885	123195296	1	51	43	101	220	78	49	674	2440	1942	200	2034	F6ZMJ4	
ENSMUST00000094055	ENSMUSG00000040938	11	70212752	70216417	1	3	0	9	75	8	0	0	0	0	0	0		Q5NC32
ENSMUST00000094056	ENSMUSG00000022621	15	89582533	89591923	-1	7	1	7	0	6	3	0	28	0	0	3		E9Q9D5
ENSMUST00000094065	ENSMUSG00000070394	11	69838514	69839618	1	0	0	0	14	0	0	506	1229	344	1052	131		Q5F285
ENSMUST00000094077	ENSMUSG00000018476	11	69398508	69413675	-1	40	31	133	607	79	32	5361	6438	6382	236	6861		Q5NCY0
ENSMUST00000094078	ENSMUSG00000020891	11	69183932	69197843	-1	0	0	0	0	0	0	0	0	0	0	0	B1ASX6	
ENSMUST00000094081	ENSMUSG00000020895	11	69070806	69073293	1	2	3	0	8	0	0	0	0	2	3	3		Q9CPV0
ENSMUST00000094097	ENSMUSG00000047554	7	109972187	109986929	-1	9	13	23	59	23	8	22	51	11	17	29		Q8K1A5
ENSMUST00000094103	ENSMUSG00000070407	11	63885792	63922290	-1	21	21	53	548	36	23	11	29	7	6	30		Q9QZS6
ENSMUST00000094105						4	3	5	1	8	3	0	0	0	0	0		
ENSMUST00000094109	ENSMUSG00000070417	7	107000875	107002605	-1	10	6	20	17	5	2	0	0	0	0	0	Q9QWU6	
ENSMUST00000094111	ENSMUSG00000075551	5	145694049	145720136	-1	17	38	63	18	20	8	0	0	0	0	0		Q9JMA7
ENSMUST00000094116	ENSMUSG00000070420	5	145280500	145291278	1	19	10	28	39	30	11	217	261	235	30	185	B2RX31	
ENSMUST00000094120	ENSMUSG00000045482	5	144767732	144859778	1	32	0	13	8	31	0	0	79	0	0	0	E9PWT1	
ENSMUST00000094124	ENSMUSG00000070423	7	102702331	102712054	1	8	13	15	9	12	5	0	0	0	0	0	Q8VGZ7	
ENSMUST00000094128	ENSMUSG00000070424	7	102096879	102102845	-1	7	0	46	5	24	0	0	1	0	0	0		P70352
ENSMUST00000094129	ENSMUSG00000070425	7	102065713	102096864	1	0	0	0	0	0	0	0	0	0	0	0	F8VQM8	
ENSMUST00000094130	ENSMUSG00000099481	7	102065511	102083765	1	0	4	0	0	0	0	17	0	3	2	1	E9PVR2	
ENSMUST00000094134	ENSMUSG00000070427	7	102015079	102018155	-1	8	6	15	11	10	10	418	1082	425	694	458		Q9Z0M9
ENSMUST00000094135	ENSMUSG00000042678	11	60469339	60528369	1	126	71	66	261	13	75	0	0	0	0	0		Q9QZZ4
ENSMUST00000094140	ENSMUSG00000056598	11	60353329	60394341	1	8	6	43	10	20	14	2	4	1	2	1	Q8BWX4	
ENSMUST00000094141	ENSMUSG00000032725	7	101839990	101845331	-1	13	9	17	7	14	10	1	1	0	1024	164		Q05685
ENSMUST00000094148	ENSMUSG00000051000	3	85660061	85817291	-1	0	12	0	5	9	29	4	8	16	0	20		Q505K2
ENSMUST00000094151	ENSMUSG00000020496	11	58932288	58938916	-1	10	9	30	69	21	2	704	998	484	113	435		
ENSMUST00000094154	ENSMUSG00000070436	7	99345375	99353230	-1	10	1	0	0	18	6	1	2	1	105	192		P19324
ENSMUST00000094156	ENSMUSG00000049154	11	58792797	58801960	-1	0	0	0	0	0	0	0	0	0	0	0	D2D553	
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ENSMUST00000094169	ENSMUSG00000078853	11	58199556	58207591	1	0	0	19	0	0	0	91	336	135	558	396	E9PW35	
ENSMUST00000094175						2	0	0	3	8	3	9	4	0	17	6		
ENSMUST00000094179	ENSMUSG00000020524	11	57011387	57330244	1	19	0	0	0	19	0	0	0	0	0	0	Q7TNB5	
ENSMUST00000094190	ENSMUSG00000027790	3	72888557	72967863	-1	5	10	3	0	0	5	0	0	0	0	0	F8VQM5	
ENSMUST00000094193	ENSMUSG00000020332	11	54370652	54426790	1	0	7	0	0	0	3	1	0	0	0	0		Q5F2C3
ENSMUST00000094194	ENSMUSG00000020333	11	54303798	54364756	1	0	0	4	0	4	0	0	0	0	0	0	Q5ICG4	Q91WC3
ENSMUST00000094203	ENSMUSG00000027580	2	181227615	181242027	-1	49	0	0	0	0	10	0	0	0	0	0	A2AS03	
ENSMUST00000094215	ENSMUSG00000038503	7	83884466	83901532	1	18	12	69	131	31	9	97	234	76	50	105		Q9ERE7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000094216	ENSMUSG00000070462	7	83879873	83884305	-1	17	10	28	940	43	26	373	450	356	57	182		Q9ERE8
ENSMUST00000094218	ENSMUSG00000023393	2	180725263	180742280	1	5	9	45	22	18	4	621	960	580	56	328		Q8VCL5
ENSMUST00000094226	ENSMUSG00000070464	5	135560448	135563569	-1	3	1	2	1	5	2	0	0	0	0	0	F8VQM2	
ENSMUST00000094227						5	9	42	9	9	6	1	5	1	0	2		
ENSMUST00000094228						14	10	26	23	20	5	0	0	1	0	4		
ENSMUST00000094245	ENSMUSG00000070473	5	134986214	134987472	1	7	4	13	383	11	2	0	0	0	3	3	Q545A5	Q9Z0G9
ENSMUST00000094251	ENSMUSG00000070476	2	178414524	178424428	1	27	25	94	39	25	9	1417	4113	2256	199	1415	A2AJW5	
ENSMUST00000094273	ENSMUSG00000091476	1	177983423	178172704	1	25	13	63	13	26	11	0	0	0	0	0	B2RW93	
ENSMUST00000094276	ENSMUSG00000063659	1	177442351	177450764	1	9	8	4	6	14	0	11	100	135	0	27	H7BX69	
ENSMUST00000094280	ENSMUSG00000070493	5	129881156	129887470	-1	12	11	26	113	16	11	2035	3110	1349	1594	830		Q9D1L0
ENSMUST00000094287	ENSMUSG00000070495	2	173093609	173119525	-1	134	119	167	44	102	67	3	18	0	0	5		A2APF3
ENSMUST00000094288	ENSMUSG00000026523	1	175698593	175815734	1	0	2	0	0	8	0	0	0	0	0	0	E9QM22	
ENSMUST00000094291						0	0	4	22	4	1	3	18	7	3	6		
ENSMUST00000094294	ENSMUSG00000044950	11	43681998	43721491	1	2	0	25	66	8	7	14	34	75	0	39		Q69Z61
ENSMUST00000094300	ENSMUSG00000044864	3	38449259	38484844	-1	6	0	12	3	14	2	41	32	26	16	32	A6H6J9	
ENSMUST00000094303	ENSMUSG00000070504	1	172596642	172602551	-1	11	13	12	21	9	5	0	2	0	4	0		A1YIY0
ENSMUST00000094307						4	0	2	0	0	0	676	452	1882	0	1441		
ENSMUST00000094312	ENSMUSG00000070509	7	73375509	73419899	1	0	0	0	344	0	17	0	0	0	0	0		Q6PCX7
ENSMUST00000094315	ENSMUSG00000070511	7	71348961	71351485	-1	44	41	163	91	44	27	1	0	2	0	1	Q8CCF3	
ENSMUST00000094320	ENSMUSG00000061882	5	123930679	123969895	1	0	2	0	0	0	0	0	12	13	1	3		E9PVD1
ENSMUST00000094324	ENSMUSG00000032477	9	109875579	109893895	1	20	23	49	207	27	10	170	322	286	18	122		P48964
ENSMUST00000094325	ENSMUSG00000006411	1	171370099	171388598	1	0	14	142	0	12	0	0	25	17	5	0		Q8R007
ENSMUST00000094327	ENSMUSG00000063409	5	123489305	123508205	1	32	18	0	36	20	10	0	0	0	0	0		Q3V0L5
ENSMUST00000094329	ENSMUSG00000017670	2	165288031	165326479	-1	0	0	0	0	0	0	770	573	740	73	613		Q8BHL5
ENSMUST00000094331	ENSMUSG00000070520	7	64867052	64872997	-1	43	31	61	159	29	19	123	298	144	42	113		Q9CPR8
ENSMUST00000094335						6	7	3	17	8	3	3	0	8	31	4		
ENSMUST00000094337	ENSMUSG00000070524	1	170907273	170912941	-1	13	5	27	361	24	8	2	1	1	0	3		Q5DRQ8
ENSMUST00000094339	ENSMUSG00000070526	7	62461871	62464510	-1	19	16	68	213	34	14	49	114	35	8	44	Q9WVA7	
ENSMUST00000094340	ENSMUSG00000070527	7	62417593	62420139	-1	9	8	26	111	17	3	0	0	0	0	0		Q60764
ENSMUST00000094344	ENSMUSG00000070529	2	164656046	164657368	1	4	3	6	2	7	3	0	0	0	0	0	Q3V2J9	
ENSMUST00000094346	ENSMUSG00000070531	2	164613522	164618212	1	9	2	11	8	12	8	0	0	0	0	0		F6ULY1
ENSMUST00000094348	ENSMUSG00000070532	1	169928648	169934653	1	6	3	8	3	6	4	0	0	0	0	0		Q3URK1
ENSMUST00000094351	ENSMUSG00000070533	2	164596458	164613626	-1	2	3	0	0	4	0	0	0	0	0	0	Q4KXB5	
ENSMUST00000094357	ENSMUSG00000029452	5	121451893	121524183	1	0	0	0	0	0	0	0	0	0	0	0	G3X9M9	
ENSMUST00000094360	ENSMUSG00000051504	7	55768178	55778925	1	36	12	18	31	27	0	1	22	0	0	9	G3X9N0	
ENSMUST00000094361	ENSMUSG00000021270	12	110690605	110702728	-1	9	17	15	24	26	5	72	275	197	1097	295	Q80Y52	P07901
ENSMUST00000094363	ENSMUSG00000049811	11	23007531	23030788	1	13	17	21	17	17	5	0	1	4	0	2	F6XT74	
ENSMUST00000094365	ENSMUSG00000027556	3	14766216	14808368	-1	5	3	8	1	3	1	8	0	3	0	1		P13634
ENSMUST00000094378	ENSMUSG00000042626	3	89418443	89430027	1	0	0	0	69	12	9	127	10	130	3	64		P98083
ENSMUST00000094381	ENSMUSG00000027506	3	8925593	9004723	-1	1	3	0	23	11	0	6	7	36	0	10	F8WHQ1	
ENSMUST00000094383	ENSMUSG00000070546	7	48642803	48643811	-1	5	2	5	4	3	1	0	0	0	0	0		Q91ZC1
ENSMUST00000094384	ENSMUSG00000070547	7	48444113	48456342	-1	14	25	68	29	27	7	1	3	1	0	0		Q3UG61
ENSMUST00000094388	ENSMUSG00000070550	7	48198070	48199288	-1	4	4	21	2	4	1	0	0	0	0	0		Q91ZC0
ENSMUST00000094389	ENSMUSG00000070551	7	48167983	48169019	-1	5	2	9	6	2	1	0	0	0	0	0	W8W3Q3	Q91ZB9
ENSMUST00000094390	ENSMUSG00000070552	7	48020971	48027597	-1	10	11	28	8	4	6	0	0	0	0	0		Q8CIP3
ENSMUST00000094391	ENSMUSG00000029601	5	120589016	120607118	1	20	0	18	28	28	15	0	0	0	0	0	B2RPX1	Q9D3V1
ENSMUST00000094398	ENSMUSG00000043262	7	46923216	46958518	-1	0	0	0	20	0	0	54	165	79	63	66		Q3U1V6
ENSMUST00000094408						5	4	6	1	6	3	0	0	0	0	0		
ENSMUST00000094413	ENSMUSG00000094084	3	93669333	93676310	-1	0	0	13	0	9	5	0	0	0	0	0		P0DMR5
ENSMUST00000094421	ENSMUSG00000038241	2	155956458	155998900	1	0	0	0	0	25	0	192	1	298	25	0		Q60952
ENSMUST00000094424	ENSMUSG00000070563	7	45725107	45725813	-1	7	10	30	22	10	6	0	0	0	0	0		Q80ZQ0
ENSMUST00000094427						16	9	37	39	19	11	125	434	99	38	62		
ENSMUST00000094434	ENSMUSG00000050708	7	45457944	45459884	-1	62	122	84	132	138	29	52786	61485	32078	17085	24358	Q9CPX4	
ENSMUST00000094438	ENSMUSG00000028946	4	152285972	152291662	-1	11	8	29	302	26	15	0	0	0	1	1		Q61657
ENSMUST00000094441	ENSMUSG00000002486	5	114707760	114722327	1	6	0	0	31	5	0	3	24	27	0	17		Q3TVW5
ENSMUST00000094451	ENSMUSG00000047875	4	150087365	150105927	1	174	160	374	1037	248	129	52	105	69	5	99	Q148S2	Q8C206
ENSMUST00000094452	ENSMUSG00000063430	5	113490333	113589725	1	20	11	34	155	34	16	2	0	0	0	6		D4PHA7
ENSMUST00000094456	ENSMUSG00000027457	2	151590549	151632593	-1	0	0	0	0	0	0	0	0	0	0	2		Q80U23
ENSMUST00000094460	ENSMUSG00000070574	7	44676965	44678235	1	8	9	19	16	26	3	0	0	1	0	0	Q9D7B4	
ENSMUST00000094463	ENSMUSG00000070576	5	111417362	111457033	1	51	30	168	1540	89	29	1	0	1	1	2	D3YWE6	
ENSMUST00000094464	ENSMUSG00000028977	4	148804429	148954889	1	22	15	29	22	28	11	75	53	30	8	24		Q9CWL2
ENSMUST00000094467	ENSMUSG00000033068	2	150749042	150771675	1	16	13	27	41	33	9	63	140	67	9	75	Q3U0P5	
ENSMUST00000094469	ENSMUSG00000075702	11	3514684	3517351	1	4	2	0	122	11	6	57	41	24	75	26		Q8VHC3
ENSMUST00000094471	ENSMUSG00000020453	11	3288874	3309083	1	19	20	21	404	36	16	72	83	67	4	60	Q5NBZ2	
ENSMUST00000094476	ENSMUSG00000048852	11	48904656	48992226	-1	41	88	129	78	0	0	0	0	0	0	0	Q5NCB2	
ENSMUST00000094477	ENSMUSG00000006010	1	150361305	150393080	-1	4	0	0	0	0	0	0	0	1	0	0	A0A0A0MQB0	
ENSMUST00000094480	ENSMUSG00000001768	2	145784734	145887616	1	0	0	25	0	0	0	173	875	360	94	129	F8WGD2	
ENSMUST00000094481	ENSMUSG00000070583	4	147868979	147870358	1	16	17	26	12	22	15	8	23	21	6	15		P70213
ENSMUST00000094489	ENSMUSG00000033898	1	139804167	139858702	-1	0	0	0	0	0	0	0	0	0	0	0	Q4LDF6	
ENSMUST00000094491	ENSMUSG00000072049	X	124127339	124135910	-1	5	2	4	5	2	1	0	0	0	0	0	A2BE32	
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ENSMUST00000094499	ENSMUSG00000020821	11	70700548	70731964	1	8	6	0	142	6	0	2294	1318	2192	223	1450		O35071
ENSMUST00000094502	ENSMUSG00000070601	10	130385316	130394241	-1	10	8	6	7	16	2	0	5	0	0	0	D3YWE3	
ENSMUST00000094505	ENSMUSG00000056268	1	138963435	139178960	1	33	28	49	25	32	13	64	442	406	29	11		Q3U1T9
ENSMUST00000094510	ENSMUSG00000070609	4	144613707	144623398	1	3	8	12	12	10	6	0	0	0	0	0	B1AVU5	
ENSMUST00000094520	ENSMUSG00000073724	4	144059126	144069327	1	0	0	0	0	0	0	0	0	0	0	0	Q3ULC4	
ENSMUST00000094521	ENSMUSG00000070616	4	143535954	143542471	1	0	0	7	9	3	0	0	0	0	0	0	Q4FZF9	
ENSMUST00000094522	ENSMUSG00000029451	4	143846497	143853637	1	0	6	0	0	3	5	0	0	0	0	0	Q4VAD2	
ENSMUST00000094526	ENSMUSG00000070619	4	144357942	144364419	1	9	4	7	7	6	0	0	0	0	0	0	B1ARV5	
ENSMUST00000094532	ENSMUSG00000092592	7	41399378	41499417	-1	331	328	739	325	320	162	16	46	30	8	51	E9Q3U2	
ENSMUST00000094536	ENSMUSG00000037533	11	54522847	54699285	1	4	2	11	7	2	0	26	7	20	0	59	Q5NCJ4	
ENSMUST00000094538	ENSMUSG00000068134	2	150114406	150136708	-1	0	0	0	0	0	0	0	0	0	0	0	L7N212	
ENSMUST00000094541	ENSMUSG00000070632	5	107437997	107491628	1	1	3	2	59	2	1	3	0	3	0	3		D3YUB6
ENSMUST00000094543	ENSMUSG00000039159	6	30211289	30304539	-1	0	0	0	0	0	0	7	9	3	0	11	E9Q3U1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000094544	ENSMUSG00000070637	4	141432672	141436105	-1	1	1	4	5	7	3	0	0	0	0	0	Q3ULG3	
ENSMUST00000094549						0	3	12	0	0	3	1177	922	563	228	362		
ENSMUST00000094550						6	3	5	5	11	2	0	0	0	0	0		
ENSMUST00000094551	ENSMUSG00000070643	1	133382303	133424377	-1	5	2	5	0	3	0	3	0	0	0	0		Q04891
ENSMUST00000094556	ENSMUSG00000070645	1	133350510	133360325	1	26	33	71	45	49	22	0	0	1	0	0		P06281
ENSMUST00000094557	ENSMUSG00000103421	1	133309800	133323026	1	13	2	25	11	15	9	0	0	0	0	0		Q9DCQ3
ENSMUST00000094559	ENSMUSG00000057315	5	102481391	102897937	1	0	0	0	0	0	0	236	715	725	222	442	G3X9N1	
ENSMUST00000094569	ENSMUSG00000026442	1	132564690	132741797	-1	99	76	363	221	124	93	2	4	1	0	7		Q810U3
ENSMUST00000094578	ENSMUSG00000035325	5	100361649	100416234	-1	16	3	0	86	17	9	402	477	543	42	529		Q3UPL0
ENSMUST00000094583	ENSMUSG00000019429	7	30854330	30856178	-1	6	5	20	7	18	4	0	2	0	0	0	Q08AU6	Q3UFD7
ENSMUST00000094587	ENSMUSG00000072822	5	94066151	94070545	-1	16	21	29	13	11	6	0	0	0	0	0	Q6P8K3	
ENSMUST00000094593	ENSMUSG00000070677	5	95456806	95485587	1	9	15	5	10	13	2	0	0	0	0	0	Q499F0	
ENSMUST00000094604	ENSMUSG00000027207	2	125859109	125984299	1	5	6	0	5	5	6	73	185	94	261	102	Q3U3H5	Q68FH4
ENSMUST00000094609	ENSMUSG00000049690	1	125913620	126830799	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q3G9	
ENSMUST00000094610	ENSMUSG00000049690	1	125913620	126830799	-1	3	0	0	0	3	0	0	0	0	0	0	E2QRQ1	
ENSMUST00000094615	ENSMUSG00000070690	5	90561107	90597871	1	12	14	29	10	18	13	0	0	0	0	0	F8VQ07	
ENSMUST00000094617	ENSMUSG00000030589	7	29134851	29153961	1	16	3	22	0	24	8	46	4639	1104	0	1200	E9QKB7	
ENSMUST00000094623	ENSMUSG00000029836	6	51470360	51483704	1	0	0	14	21	0	0	0	0	0	0	0	Q9DCC5	
ENSMUST00000094626	ENSMUSG00000047216	1	110888326	110977584	-1	6	7	6	3	5	3	0	0	0	0	0	E9Q3A7	
ENSMUST00000094632	ENSMUSG00000070699	7	28741968	28753879	1	11	7	27	88	21	11	43	63	32	8	46		Q9JJL8
ENSMUST00000094639	ENSMUSG00000027254	2	121289600	121310832	1	80	47	308	169	130	88	0	5	2	1	20	A2ARP8	
ENSMUST00000094641	ENSMUSG00000070702	5	87666208	87682578	1	2	0	1	0	0	1	0	0	0	0	0		P19228
ENSMUST00000094644	ENSMUSG00000037552	7	28359604	28372599	-1	0	0	0	3	0	0	268	59	159	27	174	E9QKB6	
ENSMUST00000094646	ENSMUSG00000009907	1	106764071	106796728	-1	18	13	23	106	25	6	898	3323	1645	723	1062	Q3TN07	P46467
ENSMUST00000094649	ENSMUSG00000070704	5	87065927	87092555	-1	5	4	7	0	1	2	0	0	0	5	0	Q3UEP4	
ENSMUST00000094651	ENSMUSG00000070705	7	28277706	28280129	1	26	25	71	248	30	16	38	199	86	12	51	E9Q2Y0	
ENSMUST00000094653	ENSMUSG00000070708	2	163087034	163087855	-1	9	10	28	8	14	4	0	0	0	0	0		Q9CWD0
ENSMUST00000094654	ENSMUSG00000029255	5	86180754	86197901	-1	17	9	13	5	21	6	0	0	0	0	0	Q6P8H4	
ENSMUST00000094657	ENSMUSG00000054405	4	132535550	132553742	1	4	0	15	8	0	4	328	1753	597	1785	459	A2ALF2	Q6NZB0
ENSMUST00000094662	ENSMUSG00000070717	4	132074697	132076992	1	5	8	25	374	21	11	3	6	3	1	4	Q8C8P7	
ENSMUST00000094663	ENSMUSG00000094651	1	93861306	93876494	1	12	17	21	18	35	0	0	0	0	0	0	A2RTS9	
ENSMUST00000094665	ENSMUSG00000070719	2	120265595	120289197	-1	28	18	51	36	33	14	0	0	0	0	0		Q50L43
ENSMUST00000094666	ENSMUSG00000070720	4	131921771	131923140	1	6	6	20	197	18	6	0	0	0	0	1	D3Z0P8	
ENSMUST00000094681	ENSMUSG00000075284	2	73429610	73529734	-1	4	12	0	237	13	17	990	2635	280	31	259		Q8K1I7
ENSMUST00000094693	ENSMUSG00000021134	12	80945504	80950507	1	3	0	13	13	0	0	515	1369	855	1236	876		O35326
ENSMUST00000094695	ENSMUSG00000070730	2	119137001	119157034	-1	18	10	17	40	21	3	48	96	65	14	83		Q3UJU9
ENSMUST00000094698	ENSMUSG00000070732	1	91145089	91170795	1	23	14	9	3	19	2	0	2	1	0	2		Q3V089
ENSMUST00000094700	ENSMUSG00000070733	5	73019987	73256619	-1	15	19	36	0	0	0	38	0	100	0	51	F8VQ05	
ENSMUST00000094705	ENSMUSG00000066721	7	24583838	24587641	-1	94	73	147	601	84	31	3	3	5	3	1	B2RX29	Q3TXZ1
ENSMUST00000094712	ENSMUSG00000070737	4	127123691	127129644	1	6	2	23	59	12	3	107	196	72	49	53		Q3U0Y2
ENSMUST00000094713	ENSMUSG00000042408	4	127077383	127124372	1	0	2	0	0	0	5	0	60	0	0	0	A2A7U2	
ENSMUST00000094715	ENSMUSG00000068082	5	68031835	68166398	1	5	4	6	7	6	0	0	0	0	0	0	G3X9N2	
ENSMUST00000094753	ENSMUSG00000070777	7	19965412	19991113	1	40	33	55	310	56	25	0	3	3	0	2	Q9D2Z1	
ENSMUST00000094754	ENSMUSG00000070778	7	19953783	19954583	1	5	8	38	11	9	5	2	0	2	3	0		
ENSMUST00000094756	ENSMUSG00000070780	5	66016549	66173118	-1	0	0	0	0	0	0	128	0	364	7	244	D3YXZ5	
ENSMUST00000094757	ENSMUSG00000070780	5	66016549	66173118	-1	4	0	1	80	3	0	0	0	0	5	0		Q91WT8
ENSMUST00000094760	ENSMUSG00000073758	4	126150602	126163491	-1	0	0	0	0	0	0	1	0	0	0	6		Q7TSG5
ENSMUST00000094761	ENSMUSG00000042608	4	126103957	126141029	1	0	18	61	42	12	23	1422	2320	1498	174	1466		Q7TNL3
ENSMUST00000094762	ENSMUSG00000002983	7	19606217	19629438	-1	0	0	0	0	0	0	237	7	8	0	3		Q04863
ENSMUST00000094774						15	22	20	37	22	9	0	65	0	10	39		
ENSMUST00000094782	ENSMUSG00000028894	4	124741850	124801511	1	0	11	0	0	4	12	595	1411	1060	258	614		Q8K337
ENSMUST00000094783	ENSMUSG00000029108	5	57717967	58133230	1	12	8	47	130	26	12	0	0	2	0	8	E9Q2S0	
ENSMUST00000094787	ENSMUSG00000029188	5	53038081	53071664	1	25	11	29	28	20	17	0	0	0	0	0		Q9DBP0
ENSMUST00000094790	ENSMUSG00000030406	7	19156061	19166127	-1	18	6	37	79	31	14	0	0	0	1	1		Q0P543
ENSMUST00000094793	ENSMUSG00000070796	7	18646736	18656725	-1	5	0	3	7	6	0	0	0	0	0	0	Q9DAV5	
ENSMUST00000094794	ENSMUSG00000070797	7	18556515	18567305	-1	13	8	12	13	7	9	0	0	0	0	0	Q497W2	
ENSMUST00000094795	ENSMUSG00000070798	7	18519702	18532269	-1	51	45	123	54	50	24	2	0	1	0	0	Q497W1	
ENSMUST00000094798	ENSMUSG00000070799	7	18474583	18484149	-1	7	8	18	9	17	4	0	0	0	0	0	Q4KL65	
ENSMUST00000094799	ENSMUSG00000030368	7	17972124	17978556	1	4	4	5	3	8	3	0	0	0	0	0	Q9D0Z8	
ENSMUST00000094801	ENSMUSG00000027194	2	94300767	94406689	-1	3	2	3	58	14	5	156	633	261	91	236	A2AFY7	
ENSMUST00000094805	ENSMUSG00000041117	7	16992708	16997516	1	106	95	364	161	121	56	10	25	14	2	20		D3YZV8
ENSMUST00000094807	ENSMUSG00000070802	7	16944682	16948828	1	31	27	71	276	42	16	0	1	0	1	0	G3X9N3	
ENSMUST00000094814	ENSMUSG00000070803	4	120666572	120667820	1	6	9	9	382	23	9	1	4	0	0	1	A2A7E7	Q9WUL8
ENSMUST00000094815	ENSMUSG00000052833	7	16327053	16387797	-1	19	12	17	91	25	13	271	555	359	103	284		Q9R1T2
ENSMUST00000094816	ENSMUSG00000006019	7	16197147	16222037	-1	25	0	0	54	12	0	0	0	11	0	27		
ENSMUST00000094818	ENSMUSG00000032997	1	75474569	75479307	-1	0	0	0	262	17	0	0	0	17	0	0		Q6IQX7
ENSMUST00000094819	ENSMUSG00000070806	4	119422814	119467444	1	5	8	5	21	7	4	0	0	0	0	0	A2BGJ5	
ENSMUST00000094821	ENSMUSG00000070808	7	15971262	15999495	-1	37	35	150	982	64	27	1050	978	1144	53	1235	F8VPZ9	
ENSMUST00000094823	ENSMUSG00000066058	4	119255414	119262438	1	37	22	74	45	54	19	0	0	0	0	0	Q3UNX6	Q9ET38
ENSMUST00000094827	ENSMUSG00000070815	7	13131471	13132358	-1	2	1	3	1	4	0	0	0	0	0	0	Q8R255	
ENSMUST00000094828	ENSMUSG00000070816	7	13101997	13102947	-1	6	1	1	0	8	4	0	0	0	0	0	L7N213	
ENSMUST00000094829	ENSMUSG00000070817	7	13084289	13085215	-1	10	7	11	3	8	6	0	0	0	0	0	Q8VIB8	
ENSMUST00000094830	ENSMUSG00000073768	4	118893085	118894032	1	7	9	11	6	11	1	0	0	0	0	0	Q8VEY6	
ENSMUST00000094831	ENSMUSG00000073769	4	118864658	118869736	1	7	5	23	9	0	4	0	0	0	0	0	K7N684	
ENSMUST00000094832	ENSMUSG00000070820	4	118734531	118735478	1	10	9	26	9	8	5	0	0	0	0	0	Q8VGB1	
ENSMUST00000094833	ENSMUSG00000029127	5	38189735	38220457	-1	12	9	14	62	28	7	0	11	0	0	41		Q8BXX2
ENSMUST00000094834	ENSMUSG00000070821	4	118726249	118727196	1	5	7	3	4	4	3	0	0	0	0	0	Q3KPC7	
ENSMUST00000094835	ENSMUSG00000040591	2	91275068	91444704	-1	0	0	3	0	0	0	8	14	0	0	8	A2AII6	
ENSMUST00000094836	ENSMUSG00000029123	5	37446825	37717171	-1	18	24	48	77	27	8	0	0	0	2	1		Q9JJX8
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ENSMUST00000094844	ENSMUSG00000047021	1	74902071	74935599	-1	32	19	66	43	46	23	0	0	1	0	0		Q3V0B4
ENSMUST00000094850	ENSMUSG00000090714	7	11161374	11166182	-1	0	0	0	3	0	0	0	0	0	0	0	L7N214	
ENSMUST00000094853	ENSMUSG00000028677	4	117271463	117497052	-1	0	0	4	1	3	5	0	8	28	0	52	Q9D4L6	
ENSMUST00000094863	ENSMUSG00000058685	7	10087198	10105659	-1	5	3	4	0	4	3	0	0	0	0	0	L7N215	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000094866	ENSMUSG00000096743	7	7463969	7479973	-1	10	0	0	0	0	5	0	0	0	0	0	K7N686	
ENSMUST00000094867	ENSMUSG00000037210	5	34369933	34486456	1	4	11	56	7	5	0	120	244	356	7	228		Q8CGI1
ENSMUST00000094868	ENSMUSG00000037224	5	34194893	34288449	-1	19	19	49	43	31	20	1	1	1	0	8		Q6ZPK7
ENSMUST00000094869	ENSMUSG00000070858	5	33983433	33985013	1	0	0	6	0	2	0	0	9	7	0	0		
ENSMUST00000094870	ENSMUSG00000046792	7	6131489	6155971	-1	6	8	21	519	20	8	250	384	226	149	152		Q8BIF9
ENSMUST00000094886	ENSMUSG00000066072	4	115518264	115533649	1	0	0	0	24	0	0	0	0	0	0	0	A2A977	
ENSMUST00000094887	ENSMUSG00000078597	4	115411624	115439034	1	12	12	21	7	14	9	0	0	0	0	0	A2A974	
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ENSMUST00000094894	ENSMUSG00000070867	4	114406724	114615098	1	67	41	149	167	69	40	2	0	2	1	8		B1ATG9
ENSMUST00000094897	ENSMUSG00000055809	7	4522933	4532453	-1	17	10	60	47	27	20	31	51	41	1	12		Q3UYV8
ENSMUST00000094898	ENSMUSG00000070871	1	64690455	64725644	1	11	13	0	0	0	1	48	201	113	0	80	E9Q226	
ENSMUST00000094906	ENSMUSG00000052062	1	61638824	62642284	1	46	32	570	0	24	55	6	2	6	3	18	Q5SV54	
ENSMUST00000094911	ENSMUSG00000074419	7	3816781	3825687	-1	1	0	0	0	0	0	0	3	3	0	0	D3YYZ3	
ENSMUST00000094913	ENSMUSG00000070875	2	86977829	86978794	-1	2	1	1	0	1	0	0	0	0	0	0	Q8VFM1	
ENSMUST00000094916	ENSMUSG00000070877	4	107209180	107218060	1	17	4	14	33	11	13	0	1	2	2	10	D3YYZ1	
ENSMUST00000094917	ENSMUSG00000038079	1	59100590	59120408	-1	4	0	2	27	0	0	0	5	1	0	17		Q3V0J1
ENSMUST00000094933	ENSMUSG00000028514	4	106316213	106441322	1	37	0	0	1	49	16	521	969	1771	73	893		B1AY13
ENSMUST00000094934	ENSMUSG00000070880	2	70553072	70602014	1	0	0	0	7	0	0	0	0	0	0	0	Q548L6	P48318
ENSMUST00000094942	ENSMUSG00000070883	2	69758033	69789575	-1	4	1	9	9	3	2	3	40	13	12	13		A0JLY1
ENSMUST00000094946	ENSMUSG00000073116	5	26082574	26089291	-1	25	18	24	16	22	4	0	0	0	0	0	E9Q1C7	
ENSMUST00000094947						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000094951	ENSMUSG00000064329	2	66270778	66440840	-1	0	0	0	0	0	0	0	0	0	0	0	A2APX7	
ENSMUST00000094953	ENSMUSG00000028528	4	101496648	101642799	1	0	15	34	60	16	0	0	0	0	0	0		Q80TZ3
ENSMUST00000094955	ENSMUSG00000070891	4	99295900	99297258	1	9	5	7	5	17	7	3	93	9	8	20	Q8BQU9	
ENSMUST00000094962	ENSMUSG00000029004	5	23434441	23504235	1	0	26	0	30	0	0	1458	2605	3014	164	2056		Q3UG20
ENSMUST00000094964	ENSMUSG00000096141	1	53397006	53706784	-1	52	43	35	21	39	20	0	5	2	1	6	E9Q0T8	
ENSMUST00000094969	ENSMUSG00000070900	4	94556546	94557078	1	0	0	0	27	2	0	0	0	0	0	0	Q9CUK2	
ENSMUST00000094972	ENSMUSG00000095498	4	88850087	88850656	1	2	0	6	5	5	2	0	0	0	0	0		P01572
ENSMUST00000094973	ENSMUSG00000070904	4	88841861	88842421	1	0	2	11	6	4	1	0	0	0	0	0	Q540C2	P07351
ENSMUST00000094977	ENSMUSG00000070908	4	88805531	88808380	1	48	29	169	70	64	35	5	6	2	1	14	Q8CD73	
ENSMUST00000094992	ENSMUSG00000094618	4	88754868	88755416	1	0	1	3	2	3	0	0	0	0	0	0	B1AYH9	
ENSMUST00000094993	ENSMUSG00000070923	4	88718292	88722465	-1	22	14	12	21	7	6	410	1555	624	232	333		Q6ZPT1
ENSMUST00000095004	ENSMUSG00000073117	5	26051883	26058581	-1	29	26	47	28	41	21	0	0	0	0	0	D3YYI9	
ENSMUST00000095005	ENSMUSG00000073208	5	15709501	15714271	-1	10	5	4	5	4	0	0	0	0	0	1	G3UXD1	
ENSMUST00000095006	ENSMUSG00000070933	5	15619064	15623864	1	0	3	8	2	2	0	0	0	0	1	0	L7N216	
ENSMUST00000095012	ENSMUSG00000028883	5	13125414	13602565	1	6	8	0	9	0	4	0	0	0	4	1		O08665
ENSMUST00000095014	ENSMUSG00000070939	1	43047200	43098637	-1	43	35	66	0	23	22	23	110	40	0	60		Q3UR70
ENSMUST00000095015						9	4	5	6	0	10	0	0	0	0	0		
ENSMUST00000095017	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	0	0	0	95	572	271	110	95		Q8CE22
ENSMUST00000095020	ENSMUSG00000070942	1	40324610	40367562	1	3	0	0	0	0	0	3	13	20	4	8	Q149G7	Q9ERS7
ENSMUST00000095021	ENSMUSG00000070943	2	36937121	36938068	1	3	1	8	2	2	4	0	0	0	0	0	Q8VFP5	
ENSMUST00000095023	ENSMUSG00000028396	4	73939371	73950846	-1	3	4	0	3	2	0	0	0	0	0	0	Q9D7L5	
ENSMUST00000095027	ENSMUSG00000037138	1	38177326	38664955	-1	0	0	54	257	53	27	29	34	0	7	73	D3YYI6	
ENSMUST00000095035	ENSMUSG00000026788	2	33450287	33468559	-1	29	19	64	0	0	14	50	559	52	53	201	G3X9N4	
ENSMUST00000095037	ENSMUSG00000039137	4	63414910	63495991	-1	0	0	0	119	0	0	0	0	0	2	6		Q80VW5
ENSMUST00000095038	ENSMUSG00000039137	4	63414910	63495991	-1	0	0	0	0	0	0	0	0	0	0	0		Q80VW5
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ENSMUST00000095045	ENSMUSG00000026811	2	32599709	32620806	1	13	5	50	21	11	7	0	0	0	0	0	E9PUI0	
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ENSMUST00000095049	ENSMUSG00000096674	4	61435790	61439743	-1	0	8	0	0	0	0	0	0	0	0	0	A9R9W0	
ENSMUST00000095050						0	4	5	3	13	7	0	0	0	0	0		
ENSMUST00000095051	ENSMUSG00000078675	4	61515592	61519531	-1	0	0	0	0	0	0	0	0	0	0	0	A2CGB6	P02762
ENSMUST00000095058	ENSMUSG00000078687	4	60218621	60222599	-1	0	0	0	0	0	0	0	0	0	0	0	A2AKN8	
ENSMUST00000095062	ENSMUSG00000073725	1	24678630	24766301	1	61	51	165	46	44	23	153	1075	393	257	296		Q8K0B2
ENSMUST00000095063	ENSMUSG00000038544	4	59769637	59801589	-1	38	32	50	40	33	17	87	468	173	37	161		Q3TXT3
ENSMUST00000095070	ENSMUSG00000070972	4	58995062	59025573	1	55	55	144	99	59	31	30	184	38	11	52		A2ALW5
ENSMUST00000095071	ENSMUSG00000090802	9	78321299	78322357	-1	5	1	0	3	4	0	0	0	0	0	0	F6SC55	
ENSMUST00000095074	ENSMUSG00000037348	4	134496697	134510235	1	218	169	873	433	275	163	58	209	89	14	102		Q80ZE4
ENSMUST00000095075	ENSMUSG00000025776	1	17727045	17766344	1	26	13	27	53	43	26	0	0	0	0	0		Q8CGD2
ENSMUST00000095076	ENSMUSG00000028434	4	56991972	57143437	-1	23	34	29	46	30	16	0	1	0	0	0	A2ALK6	
ENSMUST00000095078	ENSMUSG00000007476	2	30237715	30263790	1	0	0	32	3	25	0	119	234	263	0	207		Q80WG5
ENSMUST00000095079	ENSMUSG00000070979	4	56743413	56744925	1	13	6	23	23	16	12	4	0	5	0	10		Q9QY84
ENSMUST00000095080	ENSMUSG00000070980	4	56740005	56741443	-1	11	0	0	11	31	0	2	10	0	0	11		Q9QY83
ENSMUST00000095083	ENSMUSG00000057738	2	29965560	30031451	1	0	0	0	4	18	0	1670	2224	5235	135	3622		P16546
ENSMUST00000095084	ENSMUSG00000070983	4	52970623	52971567	1	0	0	0	0	0	0	0	0	0	0	0	Q7TS19	
ENSMUST00000095085	ENSMUSG00000089717	4	52825399	52826358	1	4	2	3	0	4	4	0	0	0	0	0	Q7TS18	
ENSMUST00000095086	ENSMUSG00000070985	4	49447105	49473912	-1	0	12	45	11	11	9	0	0	0	0	0		A2AKK5
ENSMUST00000095087	ENSMUSG00000039844	2	29619720	29740978	1	0	0	5	18	0	0	0	0	0	11	1	Q3UHC1	
ENSMUST00000095097	ENSMUSG00000070990	4	46343609	46346412	1	15	7	6	593	23	11	0	0	0	0	0		Q8R2I0
ENSMUST00000095107	ENSMUSG00000070999	4	43983483	43985423	1	14	6	20	13	28	13	24	20	18	2	32	B2RX51	Q8CDE2
ENSMUST00000095108	ENSMUSG00000071000	4	43851565	43855463	1	2	4	0	2	0	0	0	0	0	0	0	Q9QZ22	
ENSMUST00000095109	ENSMUSG00000071001	4	43727188	43728639	1	11	14	35	22	24	7	0	0	0	0	0		Q9D6B9
ENSMUST00000095114	ENSMUSG00000094686	4	42772860	42773993	-1	15	8	36	14	30	2	0	0	0	0	0		P84444
ENSMUST00000095117	ENSMUSG00000026941	2	25563115	25574845	-1	26	17	1	40	52	18	0	7	0	0	13	D3YY20	
ENSMUST00000095126	ENSMUSG00000028441	4	41505009	41517333	-1	0	0	10	0	11	0	0	0	0	0	0	A2ANN9	
ENSMUST00000095128	ENSMUSG00000071014	4	40270591	40279421	-1	0	0	3	62	14	14	242	406	128	326	56	A2AP31	Q3UIU2
ENSMUST00000095129	ENSMUSG00000071015	4	34743784	34756263	-1	9	4	19	12	11	7	0	0	0	0	0	A2AT48	Q3V037
ENSMUST00000095132	ENSMUSG00000037708	2	18694032	18750413	1	12	4	6	17	16	8	0	0	0	0	0	Q3V0U9	
ENSMUST00000095141	ENSMUSG00000040478	4	21677480	21685963	-1	12	4	13	375	0	5	0	0	0	0	0		E9PZZ1
ENSMUST00000095143	ENSMUSG00000052137	4	12089439	12096243	1	9	4	18	0	18	12	6	418	140	119	68		Q66JV4
ENSMUST00000095144	ENSMUSG00000049225	4	11958184	11966452	-1	0	0	0	0	0	0	8	4	3	14	0	A2AJP9	
ENSMUST00000095145	ENSMUSG00000078773	4	11558922	11615805	1	4	5	19	7	0	0	3	0	4	1	0	A0A0A0MQB1	
ENSMUST00000095147	ENSMUSG00000025815	2	5896115	5942792	-1	99	113	215	170	129	54	6	20	15	2	25		A2ATU0
ENSMUST00000095151	ENSMUSG00000071019	4	4055929	4077522	-1	4	0	2	0	2	2	0	0	0	0	0		Q05A13

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000095157	ENSMUSG00000068245	14	59347407	59365470	-1	24	20	26	31	35	19	0	0	0	9	8		A6H5X4
ENSMUST00000095158	ENSMUSG00000025808	8	128980019	129065517	-1	0	0	0	1	2	0	0	0	0	0	0		Q9D541
ENSMUST00000095171	ENSMUSG00000034112	8	119700009	119757718	1	27	26	63	117	45	16	4	7	1	2	25		A7L9Z8
ENSMUST00000095172	ENSMUSG00000034390	8	117257019	117461503	1	9	14	18	0	21	17	868	6799	391	4	817		Q9D486
ENSMUST00000095173	ENSMUSG00000033409	8	113643213	113655533	1	0	0	0	0	0	0	0	0	1	1	2		Q5D525
ENSMUST00000095176	ENSMUSG00000033545	8	111536097	111626030	1	3	5	0	43	0	5	855	2452	948	115	857		Q91V17
ENSMUST00000095183	ENSMUSG00000071033	17	91088493	91089391	1	0	0	0	0	0	2	0	0	0	0	0	Q9CVR5	
ENSMUST00000095186	ENSMUSG00000071036	17	86497732	86505232	-1	16	12	37	20	20	8	0	1	1	0	3	Q8C648	
ENSMUST00000095187	ENSMUSG00000024135	17	85984665	86145175	-1	21	15	21	23	10	11	60	181	125	29	82	F8WGW3	
ENSMUST00000095188	ENSMUSG00000071037	17	85090726	85458139	1	7	3	3	51	5	0	9	19	10	3	13	B9EHP1	Q3U2J5
ENSMUST00000095195						0	0	4	3	1	6	0	0	0	0	0		
ENSMUST00000095204	ENSMUSG00000071042	17	75435905	75529043	1	13	29	24	19	13	19	4	9	16	21	36	Q6NZH9	
ENSMUST00000095208	ENSMUSG00000043705	17	73306464	73399296	-1	20	10	27	23	20	6	1	0	0	1	0		Q3UW68
ENSMUST00000095211	ENSMUSG00000071047	8	93020214	93048192	-1	14	10	29	11	24	6	0	0	0	0	0	E9PYP1	
ENSMUST00000095214	ENSMUSG00000036810	8	88118769	88135110	1	0	0	2	3	5	0	90	250	99	187	22		Q3UJ81
ENSMUST00000095217	ENSMUSG00000066772	7	15479825	15639902	-1	17	16	0	6	18	11	0	0	0	0	0	Q3UT54	
ENSMUST00000095218	ENSMUSG00000071052	17	57838427	57839233	-1	12	4	23	7	13	0	0	2	0	7	4		
ENSMUST00000095220	ENSMUSG00000008167	8	85060055	85067124	1	0	8	0	86	0	25	61	45	41	0	40	F8VPX2	
ENSMUST00000095224	ENSMUSG00000071054	17	56584825	56606294	1	0	0	0	0	0	0	755	1554	576	87	846		D3YXK2
ENSMUST00000095227	ENSMUSG00000075225	10	41538846	41709300	-1	6	3	5	0	10	4	0	0	0	0	1	G8JL71	
ENSMUST00000095228	ENSMUSG00000079003	8	83997672	84000386	1	8	4	22	105	4	5	178	207	110	21	111		D3YXK1
ENSMUST00000095239	ENSMUSG00000094632	10	129983480	129984442	-1	5	8	15	8	7	0	0	0	0	0	0	E9PVJ7	
ENSMUST00000095245	ENSMUSG00000071065	10	129737974	129741902	-1	4	0	1	1	3	2	0	0	0	0	0	Q8VFI2	
ENSMUST00000095254	ENSMUSG00000000538	11	60226714	60352905	-1	0	0	0	0	0	16	41	119	0	0	4		Q5SRX1
ENSMUST00000095259	ENSMUSG00000007610	8	71488103	71499583	1	0	0	0	12	0	0	127	134	92	12	63		Q923K4
ENSMUST00000095261	ENSMUSG00000032842	17	46303221	46328352	-1	57	30	86	44	73	26	16	54	15	8	47		Q8R4P9
ENSMUST00000095262	ENSMUSG00000071073	17	46254165	46257316	1	10	7	25	193	20	6	4	10	1	1	5	B2RWC4	
ENSMUST00000095263	ENSMUSG00000071074	17	46248080	46252537	1	4	4	9	89	12	7	284	689	325	40	179		Q3UDR8
ENSMUST00000095266	ENSMUSG00000040258	10	127525473	127534559	-1	14	6	13	253	17	7	0	0	0	0	0	G3X9N5	
ENSMUST00000095267	ENSMUSG00000071076	8	70697739	70700616	1	17	12	55	438	29	7	2255	8008	2383	1173	2826		P15066
ENSMUST00000095268						0	2	12	3	1	1	0	0	0	0	0		
ENSMUST00000095270	ENSMUSG00000040441	10	127172426	127180645	-1	9	14	36	98	29	13	13	21	16	0	10	F8WGV3	
ENSMUST00000095273	ENSMUSG00000071078	8	70131333	70133739	1	2	3	4	4	5	2	73	85	40	33	49		Q3TV70
ENSMUST00000095282	ENSMUSG00000071083	8	69373528	69373914	-1	0	0	1	0	1	0	0	1	1	0	0	F6TSM8	
ENSMUST00000095295	ENSMUSG00000071089	8	64981651	64987646	-1	18	15	20	20	18	11	14	63	18	6	16	B2RTB3	Q3UWZ0
ENSMUST00000095300	ENSMUSG00000054128	17	36185572	36190287	-1	0	0	0	3	1	0	0	0	0	0	0	S4R2B8	
ENSMUST00000095310	ENSMUSG00000020189	10	111164802	111297247	1	0	45	54	198	64	0	897	1391	1200	174	740	G3X9N6	
ENSMUST00000095313	ENSMUSG00000035873	10	108332189	108414391	1	9	4	6	86	13	1	0	0	0	9	9		Q925B0
ENSMUST00000095319	ENSMUSG00000068250	6	149157147	149188712	-1	0	2	0	0	0	0	5	120	41	22	28	B8JKU8	
ENSMUST00000095320						8	5	8	10	7	2	3	2	4	0	4		
ENSMUST00000095323	ENSMUSG00000071103	8	45953606	45975252	-1	16	19	26	185	32	13	0	5	2	0	13		Q3U1D9
ENSMUST00000095326	ENSMUSG00000071104	8	45934619	45944145	1	17	9	105	21	21	7	0	0	0	0	0		Q3V125
ENSMUST00000095328	ENSMUSG00000079057	8	45269671	45333216	-1	12	10	35	56	27	9	39	177	53	45	64	B2RSR0	Q9DBW0
ENSMUST00000095333	ENSMUSG00000020020	10	93831555	93848524	1	38	22	74	30	31	23	1	0	7	0	3	A0A0A0MQB2	
ENSMUST00000095342	ENSMUSG00000041538	17	34238903	34245907	1	9	10	19	12	5	0	27	42	16	13	59	O35424	
ENSMUST00000095345	ENSMUSG00000071113	8	34115030	34125185	1	25	24	97	133	51	20	5	1	3	0	5		P0C7A3
ENSMUST00000095347	ENSMUSG00000024335	17	34112023	34122634	-1	0	1	15	18	10	12	2345	4529	2254	403	1617	U3KLT0	
ENSMUST00000095349	ENSMUSG00000052906	8	33619586	33641976	-1	12	14	45	81	21	12	100	356	184	57	134	Q3TTF2	
ENSMUST00000095350	ENSMUSG00000030232	6	140622663	140678472	1	4	6	12	10	11	5	5	20	4	0	17	F8WGQ1	
ENSMUST00000095360	ENSMUSG00000020053	10	87858265	87937042	1	54	33	292	59	61	25	3	0	0	16	3	Q4VJC0	P05017
ENSMUST00000095364	ENSMUSG00000090765	12	114630680	114630973	1	1	2	2	0	0	0	0	0	0	0	0	A0A075B5I0	
ENSMUST00000095375	ENSMUSG00000071138	8	27344394	27349188	1	17	23	31	23	31	13	0	1	0	0	0	Q5DP50	
ENSMUST00000095383	ENSMUSG00000060935	10	85102627	85117747	1	36	65	154	151	39	23	70	137	75	15	63		Q9DAM7
ENSMUST00000095385	ENSMUSG00000035620	10	84917616	85016446	1	22	12	0	0	0	2	47	163	62	29	67		Q80XE1
ENSMUST00000095388	ENSMUSG00000020037	10	84756062	84906538	1	17	7	0	0	0	6	0	0	0	0	0		Q7TNK1
ENSMUST00000095391	ENSMUSG00000071147	6	133054817	133055816	-1	2	3	3	3	3	0	0	0	0	0	0		Q7TQA4
ENSMUST00000095394	ENSMUSG00000071149	6	132737003	132738035	-1	0	1	1	2	1	2	0	0	0	0	0	Q7M719	
ENSMUST00000095395	ENSMUSG00000071150	6	132700090	132701007	-1	2	2	2	0	2	2	0	0	0	0	0		Q7M720
ENSMUST00000095396	ENSMUSG00000071151	10	82954344	82955000	1	1	1	0	73	3	0	0	5	0	0	0	D3Z694	
ENSMUST00000095409	ENSMUSG00000071158	6	129766568	129784270	-1	0	0	0	0	0	0	0	0	0	0	0	Q58A37	
ENSMUST00000095410	ENSMUSG00000037957	12	110737944	110804238	1	9	9	39	20	23	12	105	331	174	110	149	Q3UWE6	
ENSMUST00000095412	ENSMUSG00000030149	6	129610323	129623864	-1	17	16	24	18	8	1	0	25	3	38	15		O54709
ENSMUST00000095424	ENSMUSG00000094662	8	21427456	21428298	1	0	0	0	0	0	0	0	0	0	0	0	K9J724	
ENSMUST00000095425	ENSMUSG00000094687	8	21084442	21085285	1	0	0	1	3	0	1	0	0	0	0	0		Q5G864
ENSMUST00000095426	ENSMUSG00000055862	10	80702693	80705382	1	4	4	6	40	8	4	59	146	46	39	80		D3Z690
ENSMUST00000095427	ENSMUSG00000024012	17	29332072	29347904	-1	6	0	15	0	0	0	886	648	453	132	332		Q791T5
ENSMUST00000095430	ENSMUSG00000071165	8	20916490	20922071	-1	0	3	0	2	2	4	0	0	0	0	0	Q4QY32	
ENSMUST00000095436	ENSMUSG00000071169	8	19239916	19242143	1	5	2	5	0	0	0	0	0	0	0	0	Q4QY34	
ENSMUST00000095438	ENSMUSG00000039814	8	18932729	18950975	-1	0	0	3	9	0	3	0	16	0	0	10		Q5GH66
ENSMUST00000095439	ENSMUSG00000054150	12	104929949	105009809	-1	38	0	59	24	23	27	228	61	471	15	304		Q4FZC9
ENSMUST00000095440	ENSMUSG00000030344	6	126853098	126874308	1	25	17	32	39	34	17	0	0	0	0	0		O88987
ENSMUST00000095446	ENSMUSG00000043822	10	80339110	80348412	-1	0	0	0	0	0	0	0	0	0	1	2	D3Z689	
ENSMUST00000095450	ENSMUSG00000071178	12	103728156	103830373	-1	0	0	3	0	0	0	0	0	0	162	0		P22599
ENSMUST00000095451	ENSMUSG00000071179	12	103668808	103676139	-1	5	2	0	2	5	0	0	0	0	0	0	D3Z660	
ENSMUST00000095456	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	0	0	0	0	7	0	0	E9QPM7	
ENSMUST00000095457	ENSMUSG00000006498	10	79854427	79864771	1	0	0	0	0	0	0	880	1095	823	269	614	Q8CB58	
ENSMUST00000095458	ENSMUSG00000071180	13	108046424	108049146	1	7	9	26	12	9	7	328	1266	459	1240	352		Q3UTD9
ENSMUST00000095459	ENSMUSG00000071181	13	107031963	107033673	1	4	2	16	8	5	4	0	13	2	1	3	Q8C743	
ENSMUST00000095464	ENSMUSG00000035963	10	79639526	79645738	-1	18	6	39	34	25	9	0	0	0	0	0		Q3TZ65
ENSMUST00000095467	ENSMUSG00000073408	17	35635752	35643695	-1	55	24	231	482	65	23	0	0	0	0	0		Q3TNW5
ENSMUST00000095471	ENSMUSG00000095427	14	76236688	76237353	-1	27	10	25	0	19	11	0	0	4	3	0		
ENSMUST00000095473	ENSMUSG00000071185	10	78611669	78618074	-1	5	1	8	10	4	2	0	0	0	0	0	Q7TQU7	
ENSMUST00000095476	ENSMUSG00000049717	8	9970020	9977686	-1	8	21	24	81	21	0	41	143	29	8	12		Q8BTF7
ENSMUST00000095487	ENSMUSG00000071192	17	25877630	25880305	-1	18	9	36	64	27	11	12	35	8	1	20		Q8R0S6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000095491	ENSMUSG00000094913	10	77810967	77811845	-1	11	11	63	45	30	15	0	0	0	0	0	D3Z5T3	
ENSMUST00000095495	ENSMUSG00000038525	5	21645813	21662694	1	8	11	6	11	13	7	5	43	13	4	4	D3Z5T2	
ENSMUST00000095500	ENSMUSG00000071202	17	25786580	25790513	1	44	43	162	56	56	28	1	43	9	1	9		D3Z5T1
ENSMUST00000095509	ENSMUSG00000096576	12	87602688	87608845	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5G7	
ENSMUST00000095517	ENSMUSG00000031916	8	107046289	107056689	-1	28	40	80	430	51	28	59	155	79	35	50		Q9JJA2
ENSMUST00000095521	ENSMUSG00000048483	12	86983381	86988676	-1	4	5	10	11	19	7	0	0	0	0	0		A0PK84
ENSMUST00000095527	ENSMUSG00000059114	12	86734383	86763795	1	20	13	31	16	22	22	0	0	0	0	1	F6QBN8	
ENSMUST00000095529	ENSMUSG00000025551	14	123977907	124677127	-1	9	0	21	6	3	0	0	0	0	0	0	O89096	
ENSMUST00000095536	ENSMUSG00000012609	12	85824659	86061893	1	14	16	45	76	15	6	1	4	6	0	5	Q8C125	
ENSMUST00000095541	ENSMUSG00000006342	10	75636619	75644008	-1	41	17	33	36	51	14	0	0	1	0	3		Q9DBX3
ENSMUST00000095544	ENSMUSG00000071230	17	24657330	24658457	-1	1	3	7	84	9	3	0	1	0	0	0	F7B5D6	
ENSMUST00000095550	ENSMUSG00000071234	12	84677278	84698807	-1	19	14	34	105	25	12	0	8	2	2	4	B2RRM8	Q3USQ7
ENSMUST00000095551	ENSMUSG00000071235	12	84641019	84651455	1	0	0	39	0	30	7	0	0	0	0	1		Q3SYK4
ENSMUST00000095572	ENSMUSG00000021135	12	80953185	80968079	-1	10	5	11	10	9	6	11	34	38	5	28		O08705
ENSMUST00000095576	ENSMUSG00000022123	14	103513341	103613346	1	18	14	8	11	14	7	1	9	4	6	3	Q14DU0	Q9EQG3
ENSMUST00000095579	ENSMUSG00000041319	17	23668614	23673882	-1	0	0	0	0	0	0	209	231	126	9	96		Q5U4D9
ENSMUST00000095580	ENSMUSG00000020067	10	63115795	63203952	-1	36	29	120	39	44	33	0	1	1	0	1		Q5DTJ9
ENSMUST00000095585	ENSMUSG00000069170	13	81095068	81633154	-1	63	36	53	97	72	34	0	0	0	0	0	B8JJE0	
ENSMUST00000095595	ENSMUSG00000023902	17	23600856	23611019	1	3	0	43	0	0	13	0	0	0	0	0		Q3URR7
ENSMUST00000095606	ENSMUSG00000071256	17	23556769	23564226	-1	20	12	45	211	37	10	48	61	38	15	42	E9QAW0	
ENSMUST00000095610	ENSMUSG00000021057	12	76324891	76334153	1	37	39	192	78	48	24	5	17	13	3	9	H3BIV5	
ENSMUST00000095615						5	2	0	0	0	1	14	1	0	0	0		
ENSMUST00000095625	ENSMUSG00000034795	14	77036772	77112257	1	3	3	2	37	3	1	0	0	0	0	2	Q4VA24	
ENSMUST00000095633	ENSMUSG00000071273	17	20570362	20571198	1	5	1	20	21	14	5	0	0	0	0	0	F8VQ88	
ENSMUST00000095636	ENSMUSG00000071275	17	20182078	20183097	-1	0	1	2	0	3	0	0	0	0	0	0		Q3SXG2
ENSMUST00000095637	ENSMUSG00000071276	17	20113210	20114226	-1	3	5	0	1	6	6	0	0	0	0	0		Q71MR7
ENSMUST00000095646	ENSMUSG00000071280	10	59616063	59616398	1	3	0	7	106	4	0	0	0	1	0	0	F7D7I4	
ENSMUST00000095651	ENSMUSG00000048062	17	18021733	18022704	1	9	4	20	3	3	0	0	0	0	0	0		A4FUQ5
ENSMUST00000095655	ENSMUSG00000044086	6	97238534	97252759	-1	9	15	47	17	32	16	0	0	0	0	0	E9QA62	
ENSMUST00000095664	ENSMUSG00000030059	6	97152997	97179122	-1	18	13	12	61	25	0	344	989	838	156	487		B9EKI3
ENSMUST00000095666	ENSMUSG00000021068	12	70011435	70111925	-1	31	0	34	3	24	0	375	443	631	146	1387		Q61043
ENSMUST00000095668	ENSMUSG00000019876	10	57631981	57741112	1	0	0	44	70	4	5	32	162	36	85	31	F7D7A9	
ENSMUST00000095691	ENSMUSG00000038594	10	53278081	53379851	-1	7	8	9	194	17	9	102	142	314	19	175	E9QA61	
ENSMUST00000095712	ENSMUSG00000023945	17	54273594	54299034	-1	15	14	23	37	26	11	0	0	0	0	0		Q8BGY9
ENSMUST00000095715	ENSMUSG00000071317	10	45335762	45369708	1	7	3	13	7	10	9	0	0	0	0	0		Q9ES83
ENSMUST00000095717						1	2	9	7	9	5	4	0	0	3	0		
ENSMUST00000095719	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	66	0	0	11	Q6VYI4	
ENSMUST00000095724	ENSMUSG00000021470	13	63815240	63900302	1	12	2	5	124	8	5	0	14	26	11	24	E9QPI9	
ENSMUST00000095725	ENSMUSG00000038240	10	43221486	43464882	1	6	0	4	4	3	2	34	37	41	10	16		Q33DR3
ENSMUST00000095726	ENSMUSG00000071322	17	7324646	7345974	1	0	2	20	4	3	0	0	0	0	0	0	Q80W76	
ENSMUST00000095729	ENSMUSG00000071324	10	41914990	42018442	-1	0	47	375	346	73	0	0	0	0	0	0		Q3URY6
ENSMUST00000095737	ENSMUSG00000061603	12	52699383	53151015	1	62	45	94	63	76	40	1	2	1	0	0	E9Q9K8	
ENSMUST00000095739	ENSMUSG00000021556	13	59634996	59675784	-1	0	0	13	15	0	10	50	49	20	91	77		Q91XA2
ENSMUST00000095743	ENSMUSG00000038481	10	40349308	40483818	1	0	0	0	185	0	20	0	0	0	68	37	G5E8L1	
ENSMUST00000095749	ENSMUSG00000071335	10	39946907	39960153	-1	6	6	18	25	18	2	51	98	33	6	35		Q3UN21
ENSMUST00000095752	ENSMUSG00000071337	6	86404219	86433405	1	0	0	0	0	0	0	39	207	122	80	73	G5E8L2	
ENSMUST00000095753	ENSMUSG00000071337	6	86404219	86433405	1	0	10	16	11	12	10	73	68	50	23	25	Q564E7	P52912
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ENSMUST00000095755	ENSMUSG00000067215	X	153006469	153009416	1	6	5	7	82	12	0	0	0	0	0	0	B1AY15	
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ENSMUST00000095758	ENSMUSG00000071340	10	34037597	34109813	1	4	7	2	6	5	7	0	0	0	0	0		Q4KL14
ENSMUST00000095759	ENSMUSG00000071341	6	85511121	85513589	-1	10	3	2	849	23	6	0	0	0	0	0	Q3URA9	Q9WUF2
ENSMUST00000095760	ENSMUSG00000071342	12	40176386	40199315	-1	3	7	19	10	5	7	0	0	0	0	2	B2RVW5	Q3UQS2
ENSMUST00000095762	ENSMUSG00000019787	10	33083483	33476709	1	9	10	9	4	4	2	0	0	0	0	0		E9Q9K5
ENSMUST00000095767	ENSMUSG00000004151	12	38779380	38868215	1	3	4	15	13	7	5	15	0	0	0	23	Q549J8	P41164
ENSMUST00000095774	ENSMUSG00000035860	12	33033796	33092875	-1	20	18	23	20	14	9	0	0	0	0	0		Q8BL00
ENSMUST00000095775	ENSMUSG00000071350	14	59402009	59440884	-1	0	0	0	25	0	0	0	0	0	0	0		Q8C267
ENSMUST00000095778						2	7	0	2	5	0	2	1	0	0	2		
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ENSMUST00000095784	ENSMUSG00000020000	10	24223517	24302790	1	16	12	15	34	21	10	0	1	0	1	0		Q9CXI3
ENSMUST00000095786	ENSMUSG00000030042	6	82618992	82705365	-1	0	2	9	37	8	0	36	105	15	4	10		Q9CQ36
ENSMUST00000095793	ENSMUSG00000000365	14	56402697	56525032	1	3	9	15	28	10	8	0	0	0	1	0		Q99MV7
ENSMUST00000095794	ENSMUSG00000071359	10	22703879	22731938	-1	0	2	2	43	6	1	194	650	192	93	51		P62340
ENSMUST00000095795	ENSMUSG00000078452	10	22360552	22374139	1	9	0	0	0	10	0	97	285	135	255	40		Q9JI58
ENSMUST00000095797	ENSMUSG00000021395	13	51100880	51152546	1	28	34	68	44	31	18	741	1543	1078	149	610		Q61142
ENSMUST00000095798	ENSMUSG00000071361	14	56026864	56030495	-1	18	16	21	15	11	6	0	0	0	0	0		O35164
ENSMUST00000095806	ENSMUSG00000071369	10	19934472	20142753	1	3	9	12	79	4	9	718	3112	998	112	811		O35099
ENSMUST00000095807	ENSMUSG00000028785	4	129111570	129122036	-1	13	5	45	4	15	8	0	0	0	0	0		P84075
ENSMUST00000095817	ENSMUSG00000071392	10	18129022	18210890	-1	19	14	21	17	24	11	0	2	0	0	1	F7CKP4	
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ENSMUST00000095823	ENSMUSG00000071398	12	17003319	17011727	-1	383	296	1505	790	551	296	16	27	31	13	54	D3Z430	
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ENSMUST00000095862	ENSMUSG00000071428	6	58215106	58216017	-1	1	0	2	0	2	0	0	0	0	0	0	K7N688	
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ENSMUST00000095873	ENSMUSG00000043301	16	94749266	94997696	-1	9	6	13	75	7	7	0	0	0	0	0	Q8C4T8	
ENSMUST00000095874	ENSMUSG00000071434	10	3119841	3129546	1	26	19	86	33	39	17	4	14	5	0	1	Q3UW27	
ENSMUST00000095893	ENSMUSG00000061759	10	4432467	4455141	1	0	0	0	20	0	0	125	415	143	53	47		A6H630
ENSMUST00000095898	ENSMUSG00000003476	6	55090049	55133016	-1	3	3	9	154	12	0	0	0	0	0	0	Q5ERJ2	
ENSMUST00000095899	ENSMUSG00000096054	10	5020203	5550692	-1	270	313	977	308	312	134	1628	7017	5312	431	3802	Q0VGB8	Q6ZWR6
ENSMUST00000095903						11	7	0	5	12	4	13	7	61	8	27		
ENSMUST00000095909	ENSMUSG00000022957	16	91729281	91920597	1	107	85	357	179	82	47	16	46	23	6	50	Q6NZJ5	
ENSMUST00000095914	ENSMUSG00000069255	13	30659999	30711231	1	2	0	18	2	7	4	3	22	44	17	29		Q99N11
ENSMUST00000095916	ENSMUSG00000068506	14	51711643	51717183	-1	3	1	2	2	1	2	0	0	0	0	0	Q497L3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000095920	ENSMUSG00000071466	13	27956155	27956415	1	6	4	5	6	8	5	0	0	0	0	0	Q5SW62	
ENSMUST00000095922	ENSMUSG00000090688	5	109085849	109097864	-1	9	9	8	6	9	5	0	0	0	0	0	L7N217	
ENSMUST00000095923	ENSMUSG00000021880	14	51129068	51131122	1	4	1	3	4	11	5	40	345	85	383	105	Q3V3L3	
ENSMUST00000095924	ENSMUSG00000006488	13	27633380	27642474	-1	1	1	2	0	0	1	0	0	0	0	0		O54830
ENSMUST00000095925	ENSMUSG00000068417	14	50955992	50964749	1	4	2	3	3	2	1	41	93	49	95	34	Q9D8C9	
ENSMUST00000095926	ENSMUSG00000019756	13	27573922	27582171	-1	2052	1943	7016	2016	2566	1066	49	351	151	218	237	J3JS25	
ENSMUST00000095932	ENSMUSG00000071470	14	50789249	50795728	-1	9	7	20	6	8	4	3	6	2	0	3		D3Z3K2
ENSMUST00000095934	ENSMUSG00000071471	16	88646824	88647796	-1	6	2	4	4	4	1	0	0	0	0	0		Q9D7N2
ENSMUST00000095940						1	0	13	7	2	3	0	0	0	4	0		
ENSMUST00000095941	ENSMUSG00000037536	14	47472561	47531962	1	0	0	14	30	22	17	78	61	171	0	84		Q80XI1
ENSMUST00000095944	ENSMUSG00000071477	6	48024188	48048911	-1	0	0	0	287	31	20	0	0	0	0	0	G5E8L5	
ENSMUST00000095946						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000095947	ENSMUSG00000049134	19	56320035	56390037	-1	7	0	0	12	40	10	11	20	16	0	0		Q80XB4
ENSMUST00000095948	ENSMUSG00000025075	19	56287137	56320822	1	10	12	25	24	17	2	0	1	0	0	0	Q3V1J8	
ENSMUST00000095950	ENSMUSG00000024983	19	55316351	55626561	1	17	17	47	102	31	12	256	855	522	152	326		O89116
ENSMUST00000095953	ENSMUSG00000094200	6	43153262	43154261	1	6	9	13	7	6	0	0	0	0	0	0		
ENSMUST00000095954	ENSMUSG00000094669	6	43106390	43116676	1	4	5	3	2	6	2	0	0	0	0	0	Q8VFS5	
ENSMUST00000095955	ENSMUSG00000073110	6	42955459	42956508	1	9	7	13	4	12	7	0	0	0	0	0	Q8VFS6	
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ENSMUST00000095974	ENSMUSG00000029861	6	42315312	42324643	-1	33	14	48	0	46	8	0	7	3	2	7		Q3TY60
ENSMUST00000095978	ENSMUSG00000071497	19	53588204	53589067	-1	12	11	8	0	11	0	121	254	96	351	123		P61971
ENSMUST00000095981	ENSMUSG00000093968	14	43671962	43677199	-1	11	0	0	6	3	7	0	0	0	0	0	L7N218	
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ENSMUST00000095987	ENSMUSG00000071506	6	42261970	42264555	1	9	2	19	19	8	10	0	0	0	1	0	E9PX92	
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ENSMUST00000095998	ENSMUSG00000044948	19	47737561	47919299	-1	14	20	44	117	44	19	4880	4807	4123	391	3147		Q3TNL8
ENSMUST00000095999	ENSMUSG00000071517	6	41442216	41446145	-1	2	6	3	3	8	0	0	0	0	0	0	Q792Y8	
ENSMUST00000096000	ENSMUSG00000037833	14	40813789	40893266	-1	14	7	19	13	21	6	11	42	21	9	33		A6X942
ENSMUST00000096003	ENSMUSG00000071519	6	41373814	41377678	-1	8	1	4	4	6	1	0	0	0	0	0	Q792Z0	
ENSMUST00000096006	ENSMUSG00000071522	13	21132698	21133784	1	10	5	14	3	15	6	0	0	0	0	0	Q7TQT8	
ENSMUST00000096012	ENSMUSG00000035258	16	56477846	56690128	1	0	10	0	0	0	0	0	0	0	0	1	Q59IW9	
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ENSMUST00000096014	ENSMUSG00000071528	19	47083471	47090625	-1	0	3	2	30	0	5	388	1112	249	962	107		Q78IK2
ENSMUST00000096019	ENSMUSG00000071531	14	34194441	34201633	-1	22	9	25	79	38	7	0	0	0	0	0	D3Z1D7	
ENSMUST00000096020						0	2	13	0	6	0	0	0	0	49	0		
ENSMUST00000096021	ENSMUSG00000071533	16	56007245	56029739	-1	0	0	0	0	0	0	29	119	73	219	84	F8WI88	
ENSMUST00000096026	ENSMUSG00000035356	16	55811375	55838899	-1	0	0	0	0	0	0	0	0	0	0	0		Q9EST8
ENSMUST00000096029	ENSMUSG00000037126	19	46312087	46327156	-1	10	7	103	107	37	20	15	30	21	1	19		Q5DTT2
ENSMUST00000096030	ENSMUSG00000071537	6	38625693	38637242	-1	8	7	31	369	33	13	3	11	5	5	16	G5E8L6	
ENSMUST00000096038	ENSMUSG00000071540	14	32659119	32685272	-1	54	29	205	111	68	31	1	0	0	0	2	D3Z1D3	
ENSMUST00000096040	ENSMUSG00000029830	6	37983739	38046996	-1	31	34	79	37	33	13	0	5	0	0	3		Q6PDF3
ENSMUST00000096045	ENSMUSG00000058550	16	48283735	48294292	1	0	0	0	0	0	0	0	0	0	0	0		Q8CCG4
ENSMUST00000096052	ENSMUSG00000022656	16	46387706	46498525	-1	0	5	4	0	4	1	0	0	0	0	0		Q9JLB9
ENSMUST00000096053	ENSMUSG00000036097	19	44931119	44983787	1	74	57	244	285	68	47	165	635	428	48	387	E9Q839	
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ENSMUST00000096065	ENSMUSG00000071552	16	43648861	43664184	-1	134	103	405	427	188	97	15	48	24	14	61	A0A0B4J1G6	
ENSMUST00000096066	ENSMUSG00000071553	6	30541582	30564476	1	5	8	3	3	7	7	0	0	0	0	0		Q504N0
ENSMUST00000096069	ENSMUSG00000033799	13	3566036	3611108	-1	23	27	40	210	42	27	54	141	113	33	101		Q5DTT3
ENSMUST00000096084	ENSMUSG00000029769	6	29396309	29426994	1	23	7	23	0	0	0	0	0	0	0	0	E9QP94	
ENSMUST00000096089	ENSMUSG00000071561	16	36359382	36367748	-1	7	9	55	63	11	26	36464	105285	57636	132210	21266	Q497J0	
ENSMUST00000096090	ENSMUSG00000034362	16	36119946	36131241	-1	10	13	3	19	21	10	5	22	9	36	7	B2RT71	P56567
ENSMUST00000096092						11	18	20	22	15	11	0	0	0	0	0		
ENSMUST00000096093						10	0	0	28	17	0	0	0	0	0	0		
ENSMUST00000096096	ENSMUSG00000024989	19	38055025	38074425	1	0	0	0	0	0	0	30	63	0	23	17		Q8BT07
ENSMUST00000096101						1	3	0	29	0	2	0	0	0	0	0		
ENSMUST00000096106	ENSMUSG00000079620	16	32735886	32782391	1	48	36	37	95	0	24	0	0	0	0	0	E9Q7Q0	
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ENSMUST00000096114	ENSMUSG00000071573	19	33137747	33392295	-1	7	8	3	5	4	0	0	9	0	7	9		
ENSMUST00000096119	ENSMUSG00000024887	19	31984654	32061469	-1	25	22	83	15	25	13	2	21	10	4	30	B9EHG7	Q9JHE3
ENSMUST00000096121	ENSMUSG00000095024	14	19594139	19602581	-1	0	0	0	0	0	3	0	0	0	0	0	L7N219	
ENSMUST00000096127	ENSMUSG00000038127	16	27388869	27452218	1	0	0	0	0	0	0	5	0	20	31	19	Q3TNK7	Q810U5
ENSMUST00000096129	ENSMUSG00000022514	16	26581704	26730117	1	14	12	26	68	18	7	4	18	25	7	49	Q3UVZ1	
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ENSMUST00000096151	ENSMUSG00000071591	14	7374667	7412375	-1	0	0	0	0	0	0	0	0	2	0	0	Q9D9B9	
ENSMUST00000096155						4	2	1	4	4	0	0	0	0	0	0		
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ENSMUST00000096168	ENSMUSG00000072739	14	3449379	3459287	1	46	12	31	54	8	6	0	0	0	0	0	K7N693	
ENSMUST00000096170	ENSMUSG00000079244	14	51552790	51662953	1	6	0	6	7	10	5	0	0	0	0	0	Q810Q0	
ENSMUST00000096171	ENSMUSG00000096629	14	5607620	5807982	-1	22	26	16	23	25	17	0	0	0	0	0	E9Q7N2	
ENSMUST00000096173						0	2	9	2	3	0	0	2	0	0	0		
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ENSMUST00000096191	ENSMUSG00000033653	16	21423118	21644680	1	39	28	50	77	60	33	6	10	25	7	6		Q0P5W1
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ENSMUST00000096194	ENSMUSG00000024754	19	21778342	21858327	1	44	32	94	81	17	0	153	141	209	0	125		Q5FWI3
ENSMUST00000096197	ENSMUSG00000046613	16	20589471	20605377	1	0	0	0	0	0	0	0	0	0	0	0		Q3UR50
ENSMUST00000096198	ENSMUSG00000023033	15	100869858	101045938	1	18	21	71	38	18	4	0	5	2	1	1	Q4KL32	
ENSMUST00000096199	ENSMUSG00000022822	16	20331303	20426394	-1	0	0	0	50	0	0	1	0	0	7	5	Q6P8Q2	
ENSMUST00000096200	ENSMUSG00000045631	15	100280837	100293053	1	6	7	6	43	9	5	0	0	0	0	0		Q3V0Q7
ENSMUST00000096201	ENSMUSG00000071629	19	13500546	13503292	1	3	4	7	1	4	5	0	0	0	0	0	Q7TQQ7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000096202	ENSMUSG00000096273	19	13470972	13471916	1	1	2	4	1	1	2	0	0	0	0	0	Q7TQQ8	
ENSMUST00000096203	ENSMUSG00000096320	19	13445014	13445958	1	5	7	3	2	4	0	0	0	0	0	0	F6QVZ8	
ENSMUST00000096222						16	8	8	20	12	5	0	0	3	0	1		
ENSMUST00000096224	ENSMUSG00000022994	15	98589994	98607633	-1	66	67	265	247	86	39	12	21	22	3	64	F8VQ52	
ENSMUST00000096229	ENSMUSG00000022789	16	16312235	16359030	-1	0	0	0	99	0	20	0	48	30	0	26	E9PUD2	
ENSMUST00000096232						1	3	3	391	16	11	1931	6614	2598	1705	2144		
ENSMUST00000096234	ENSMUSG00000022674	16	15552677	15594524	-1	0	3	0	1	0	0	0	0	4	0	0	A6X925	
ENSMUST00000096239	ENSMUSG00000071645	19	8953850	8966207	1	14	11	71	46	32	16	235	312	213	36	213		Q8R3F9
ENSMUST00000096240	ENSMUSG00000071646	19	8941875	8952303	1	14	8	36	218	27	18	2138	4254	2849	304	1942		Q9R190
ENSMUST00000096241	ENSMUSG00000071647	19	8929694	8941563	1	19	8	51	146	30	20	916	2009	1012	105	1099		Q8VC03
ENSMUST00000096242	ENSMUSG00000071648	19	8927382	8929356	-1	7	11	27	91	14	10	159	119	75	14	46		P32958
ENSMUST00000096243	ENSMUSG00000071649	19	8920374	8927234	1	9	3	38	33	27	6	809	986	548	173	406		P58158
ENSMUST00000096246	ENSMUSG00000071650	19	8898090	8916663	1	18	21	60	69	26	21	1461	2883	1745	260	1540	A1A4T2	Q8BHN3
ENSMUST00000096249	ENSMUSG00000071652	19	8888926	8897890	1	14	13	54	92	44	11	415	359	316	29	266		Q8CHT3
ENSMUST00000096250	ENSMUSG00000033237	15	96287518	96404992	1	38	31	69	52	48	23	609	937	1293	71	845	E9Q7E2	
ENSMUST00000096251	ENSMUSG00000071653	19	8888853	8890881	1	2	0	4	2	3	0	131	389	109	755	92		Q9D937
ENSMUST00000096252	ENSMUSG00000040621	X	166170454	166190512	1	0	0	0	0	0	0	0	0	0	9	0	B1AVP5	
ENSMUST00000096253	ENSMUSG00000071654	19	8880016	8880933	-1	9	3	23	19	9	7	189	306	138	383	114	Q3V2E3	Q8K2T4
ENSMUST00000096255	ENSMUSG00000071655	19	8871559	8875663	1	0	0	0	80	0	0	92	951	305	179	480		Q922Y1
ENSMUST00000096257	ENSMUSG00000071656	19	8850785	8853909	1	191	195	608	118	157	57	1	12	9	14	24		Q3TYX2
ENSMUST00000096259	ENSMUSG00000071658	19	8836929	8839246	-1	7	9	42	133	24	10	2	2	5	0	14		P63216
ENSMUST00000096261	ENSMUSG00000071662	19	8793129	8798557	-1	4	7	9	5	6	4	322	868	237	874	164		P62488
ENSMUST00000096265	ENSMUSG00000071665	X	153118786	153132861	1	7	0	14	7	0	0	0	0	0	0	0		Q3UM89
ENSMUST00000096269	ENSMUSG00000052562	19	8335371	8405111	-1	4	0	0	1	0	0	0	0	0	0	0	Q96LX3	
ENSMUST00000096272	ENSMUSG00000065979	16	11803721	11909445	-1	0	0	0	0	0	0	0	70	45	0	43		Q8BFS6
ENSMUST00000096273	ENSMUSG00000071669	16	11322908	11755472	1	14	9	19	2	8	7	11	0	0	0	0		Q9D3S3
ENSMUST00000096275	ENSMUSG00000041115	X	152144268	152225236	1	2	0	24	0	0	0	35	48	31	3	54	D3Z6V7	
ENSMUST00000096279						5	2	2	3	3	4	1	1	0	4	0		
ENSMUST00000096285	ENSMUSG00000041245	X	151198078	151320152	1	12	12	0	3	7	1	0	2	0	0	0	V9GWU7	
ENSMUST00000096299	ENSMUSG00000041380	X	146962513	147197277	1	0	9	0	0	0	0	0	0	0	0	0		P34968
ENSMUST00000096301	ENSMUSG00000071679	X	144688907	145122411	1	15	14	42	8	13	12	0	1	1	0	1		Q3URY0
ENSMUST00000096308						0	0	79	10	1	10	4	2	4	0	0		
ENSMUST00000096313	ENSMUSG00000042473	X	139684996	139753405	1	48	55	135	43	99	38	51	94	91	55	71		A3KGB4
ENSMUST00000096314	ENSMUSG00000071686	X	138208165	138209580	-1	8	2	8	5	3	5	0	0	0	0	0	A2AFS9	
ENSMUST00000096316	ENSMUSG00000031388	X	73916873	73921944	-1	1	0	7	1	2	0	7	49	12	2	7	B1AUZ1	
ENSMUST00000096318	ENSMUSG00000049562	19	5568074	5571261	1	30	14	42	303	58	23	1442	986	1104	77	649		Q3TAP4
ENSMUST00000096321	ENSMUSG00000072969	X	135742733	135747322	1	4	2	3	21	4	0	46	198	99	54	83		Q3UZB0
ENSMUST00000096325	ENSMUSG00000071691	19	4625841	4698668	-1	22	12	16	11	14	7	0	0	0	0	0	Q3UY62	
ENSMUST00000096332	ENSMUSG00000062791	X	127039972	127063986	1	7	5	6	1	5	3	0	0	0	0	0	B1AXN3	
ENSMUST00000096338	ENSMUSG00000044724	19	4139799	4145738	1	16	9	42	21	21	14	0	0	3	0	2		Q8BXS7
ENSMUST00000096347	ENSMUSG00000050439	15	80452240	80560470	-1	14	15	61	16	23	7	0	2	0	0	0	E9Q1Z2	
ENSMUST00000096348	ENSMUSG00000025665	X	111388192	111537959	-1	0	0	0	0	0	0	0	0	0	0	0	A2CEE7	
ENSMUST00000096350	ENSMUSG00000042622	15	79347541	79359072	1	0	0	0	168	10	0	0	0	0	0	37	Q3U0G5	O54791
ENSMUST00000096355	ENSMUSG00000071713	15	78325990	78351000	1	61	51	147	99	72	44	22434	37354	25671	2005	19627		P26955
ENSMUST00000096356	ENSMUSG00000071714	15	78282517	78305603	-1	111	73	309	424	137	93	4216	8985	5941	334	3896		P26954
ENSMUST00000096357	ENSMUSG00000071715	15	78244801	78262580	1	9	9	13	16	13	10	15125	18240	11975	2353	7629		P97369
ENSMUST00000096358	ENSMUSG00000071716	15	77698889	77719288	1	51	83	103	79	78	20	0	25	9	0	8	Q3UZ24	
ENSMUST00000096361	ENSMUSG00000015665	X	100572251	100578205	1	5	2	5	6	7	0	0	2	0	0	0		A2ADU9
ENSMUST00000096363	ENSMUSG00000071719	X	99821021	99848790	1	12	11	36	105	22	11	0	0	0	0	0		A2BDP1
ENSMUST00000096365	ENSMUSG00000048385	15	76516203	76522129	-1	12	13	28	648	37	7	0	1	0	0	0		Q99M85
ENSMUST00000096366						0	0	2	1	2	1	0	0	0	0	0		
ENSMUST00000096367	ENSMUSG00000071722	X	95022510	95026682	-1	8	9	9	20	9	4	0	0	1	2	1		Q8K1L2
ENSMUST00000096368	ENSMUSG00000071723	X	94636069	94643244	1	5	6	1	43	12	7	41	355	98	10	102		Q149F3
ENSMUST00000096369	ENSMUSG00000043929	X	94234599	94277724	1	0	4	2	4	1	2	3	3	4	0	3	Q3TEP6	
ENSMUST00000096370						2	1	0	0	2	0	169	620	160	50	131		
ENSMUST00000096371	ENSMUSG00000071726	X	92489949	92490681	1	6	4	11	0	0	3	0	0	0	0	0	Q497P9	
ENSMUST00000096378	ENSMUSG00000035427	X	86250254	86305093	-1	3	3	12	3	5	2	0	0	0	0	0	A2A9R3	
ENSMUST00000096385	ENSMUSG00000022558	15	76380261	76453038	1	0	0	0	0	0	0	1409	1329	1590	148	1535	E0CZ22	
ENSMUST00000096386	ENSMUSG00000025373	10	128411616	128441438	1	37	8	49	49	29	16	760	979	777	128	510		Q8BH75
ENSMUST00000096389	ENSMUSG00000071738	X	76264304	76267738	1	2	0	1	0	2	0	0	0	0	0	0	Q80ZS5	
ENSMUST00000096397						2	8	7	11	6	6	2	3	6	5	0		
ENSMUST00000096399	ENSMUSG00000068600	15	74819071	74834871	1	5	0	3	0	3	2	0	0	0	0	0	G5E8L7	
ENSMUST00000096400	ENSMUSG00000068349	15	74813452	74818815	-1	8	0	7	8	6	0	0	0	0	0	0	E9PX31	
ENSMUST00000096411						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000096418	ENSMUSG00000022347	15	60917589	60921270	-1	20	14	19	15	12	6	0	0	0	0	0		Q19LI2
ENSMUST00000096420	ENSMUSG00000071748	X	68821093	68825318	1	6	6	10	1	5	5	66	71	34	13	57		Q60969
ENSMUST00000096421	ENSMUSG00000071749	15	60014866	60016618	-1	13	6	48	20	18	10	0	0	0	0	0		Q9D454
ENSMUST00000096424	ENSMUSG00000001964	X	74254687	74261548	1	2	0	0	0	0	0	0	0	0	15	0	I7HJS1	
ENSMUST00000096427						4	3	21	5	8	3	3	2	2	0	5		
ENSMUST00000096430	ENSMUSG00000071757	15	57694665	57839832	1	56	39	130	72	73	28	41	83	59	3	59		Q8C0C0
ENSMUST00000096431	ENSMUSG00000053852	X	56870163	57001558	1	25	32	154	25	39	13	0	10	4	1	5	Q3UNS7	
ENSMUST00000096433	ENSMUSG00000022419	15	55112317	55259271	1	132	89	397	226	140	65	48	131	111	40	163	B2ZRS3	Q570Y9
ENSMUST00000096439	ENSMUSG00000074704	2	151645404	151668533	-1	4	6	4	0	6	0	0	0	0	0	0	R4GML2	
ENSMUST00000096441	ENSMUSG00000034543	11	3649494	3690477	1	0	10	0	2	0	0	17	220	48	5	79		Q69ZX6
ENSMUST00000096447	ENSMUSG00000023074	X	53344598	53370502	-1	0	0	0	8	0	0	84	710	247	329	57		Q8VEL0
ENSMUST00000096449	ENSMUSG00000071764	X	49683504	49684463	1	2	1	7	3	3	4	0	0	0	0	0	A2AHM8	
ENSMUST00000096452	ENSMUSG00000079065	5	104508352	104522611	1	15	19	13	29	11	5	11	15	18	5	17	E9Q5E2	
ENSMUST00000096453	ENSMUSG00000071766	X	38104077	38110907	-1	3	4	5	0	7	4	0	0	0	0	0	Q4TU81	
ENSMUST00000096454	ENSMUSG00000071767	X	37831686	37841275	1	1	1	3	7	5	2	0	0	0	0	0	A2A4F1	
ENSMUST00000096457	ENSMUSG00000071769	X	37657688	37668764	-1	0	0	0	0	0	0	0	0	0	0	0	L7MU37	
ENSMUST00000096458	ENSMUSG00000071771	X	37432494	37437279	1	2	0	0	0	0	2	0	0	0	0	0	Q9JI43	
ENSMUST00000096459	ENSMUSG00000095601	X	37380028	37384493	1	0	0	0	0	0	0	0	0	0	0	0	Q4TU90	
ENSMUST00000096469	ENSMUSG00000096620	X	25277605	25301455	-1	0	0	0	0	0	0	0	0	0	0	0	Q5M8P2	
ENSMUST00000096482	ENSMUSG00000054115	15	9111985	9155425	-1	0	0	0	0	0	1	13	33	22	15	33	Q569Z9	Q9Z0Z3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000096485						17	21	5	7	26	7	26	91	72	45	109		
ENSMUST00000096492	ENSMUSG00000040229	X	13632089	13640858	1	0	0	0	1	0	1	7	12	0	0	0	Q3YL73	Q9R1K6
ENSMUST00000096494	ENSMUSG00000042961	15	7206120	7398395	-1	7	0	0	0	0	0	0	0	0	0	0		Q4VBE4
ENSMUST00000096495	ENSMUSG00000064127	X	12675369	12762073	-1	5	0	6	5	0	0	321	361	262	75	152		A2ABV5
ENSMUST00000096509	ENSMUSG00000071815	X	9033493	9034333	1	6	7	4	0	0	0	0	0	0	0	0		Q99MX2
ENSMUST00000096511	ENSMUSG00000095316	X	21174439	21175653	-1	0	1	0	0	0	1	0	0	0	0	0	F6XK35	
ENSMUST00000096514	ENSMUSG00000031156	X	7884041	7894492	1	0	5	11	4	0	4	205	482	241	34	182	A2AER3	
ENSMUST00000096547	ENSMUSG00000032818	18	77281958	77442341	1	27	23	14	67	38	16	0	0	0	0	0		C8YR32
ENSMUST00000096554	ENSMUSG00000071847	18	62922327	62953195	1	12	3	33	83	21	3	0	2	5	3	36		Q3U128
ENSMUST00000096570	ENSMUSG00000071858	18	43777196	43792878	-1	1	1	0	0	3	2	0	0	0	0	0	B2RV94	Q3V2D2
ENSMUST00000096572	ENSMUSG00000071860	18	40256962	40257684	1	1	2	6	29	3	3	0	0	0	0	0	Q9D6G3	
ENSMUST00000096573	ENSMUSG00000024352	18	35656690	35662186	-1	0	3	11	39	7	0	2	3	5	25	0		Q6P926
ENSMUST00000096575	ENSMUSG00000024383	18	32163089	32236751	1	14	25	58	217	31	21	590	1063	937	96	730	G5E8L8	
ENSMUST00000096579						3	0	1	0	6	5	0	0	0	0	0		
ENSMUST00000096608	ENSMUSG00000071890	1	163024302	163085670	-1	3	13	9	7	15	7	0	0	0	0	0	G5E8L9	
ENSMUST00000096612	ENSMUSG00000071893	6	56924015	56958100	1	2	0	0	0	1	1	0	0	0	0	0	Q8R2D3	
ENSMUST00000096633	ENSMUSG00000071909	13	50467307	50475355	1	21	9	62	24	28	19	0	0	0	0	0		Q3V0C3
ENSMUST00000096639	ENSMUSG00000070426	7	102019137	102065469	-1	21	13	0	19	17	11	211	424	220	151	212		Q8R1Z9
ENSMUST00000096663	ENSMUSG00000071937	8	40752208	40756175	1	7	10	9	6	5	4	0	0	0	0	0		
ENSMUST00000096691	ENSMUSG00000074695	10	118204942	118210047	1	2	4	4	4	6	2	0	0	0	0	0		Q9JJY9
ENSMUST00000096744	ENSMUSG00000068566	7	3289080	3300442	1	4	4	72	0	7	22	9501	17860	9161	696	6552	Q0VE46	O35682
ENSMUST00000096751	ENSMUSG00000071660	19	8809075	8819333	-1	47	51	86	55	51	23	120	533	265	120	132		Q810A3
ENSMUST00000096753	ENSMUSG00000071659	19	8819401	8834142	1	21	17	57	453	29	22	1678	6596	3901	505	3077		Q00PI9
ENSMUST00000096766	ENSMUSG00000032624	17	83350931	83480361	1	0	0	32	32	0	5	108	354	209	16	161	F8WJ93	
ENSMUST00000096791	ENSMUSG00000096730	JH584292.1	3536	11935	1	0	0	4	0	0	0	0	0	0	0	0	O35190	
ENSMUST00000096792						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000096794	ENSMUSG00000096042	4	156349921	156354578	1	1	0	2	0	0	4	0	0	0	0	0	D3Z3M1	
ENSMUST00000096813						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000096852	ENSMUSG00000072100	X	154886805	154890267	-1	2	1	1	2	6	1	0	0	0	0	0	B1AZQ8	
ENSMUST00000096862	ENSMUSG00000079800	GL456210.1	9124	58882	-1	83	49	96	147	63	41	22	126	32	53	44	Q3TR44	
ENSMUST00000096869	ENSMUSG00000072598	14	44001664	44006418	-1	0	0	0	0	2	0	0	0	0	0	0	Q5GAN0	
ENSMUST00000096899	ENSMUSG00000072145	14	44500122	44506345	1	0	4	5	1	5	2	0	0	0	0	0	Q6P8I2	
ENSMUST00000096904	ENSMUSG00000071356	6	78370657	78373466	1	1	3	0	3	2	1	0	0	0	0	0		P35230
ENSMUST00000096913	ENSMUSG00000095063	X	26522656	26545565	-1	7	0	3	3	1	1	0	0	0	0	0	D3Z347	
ENSMUST00000096953	ENSMUSG00000072188	5	14974113	14978935	-1	15	20	38	13	25	7	0	0	0	0	0	K7N6A0	
ENSMUST00000096981						11	15	15	4	20	18	0	0	0	0	0		
ENSMUST00000096987	ENSMUSG00000072214	16	18621811	18629938	-1	15	13	25	61	28	13	2068	2068	1412	94	803		Q9Z2Q6
ENSMUST00000096990	ENSMUSG00000000028	16	18780447	18811987	-1	6	0	5	6	16	5	73	113	144	102	81	F8WJ72	
ENSMUST00000097014	ENSMUSG00000072235	15	98949841	98953551	-1	14	13	12	33	24	22	3360	5245	2194	1330	2190		P68369
ENSMUST00000097023	ENSMUSG00000072244	7	104218793	104235152	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2I6	
ENSMUST00000097029	ENSMUSG00000072249	X	9063015	9063861	1	7	2	5	3	8	1	0	0	0	0	0	Q3SXD2	
ENSMUST00000097040						3	4	9	2	0	2	0	0	1	9	1		
ENSMUST00000097043	ENSMUSG00000072258	1	183388981	183410198	1	0	6	2	6	2	7	0	27	13	6	14	J3KMG9	
ENSMUST00000097044	ENSMUSG00000072259	7	41153841	41290183	1	61	33	519	86	68	18	0	0	0	0	0		Q3V0A6
ENSMUST00000097079	ENSMUSG00000072294	14	99874486	100149764	-1	14	17	35	7	13	10	2	0	0	0	2		O35738
ENSMUST00000097080	ENSMUSG00000072295	1	59050506	59094900	-1	13	2	17	13	16	7	0	0	0	0	0	E9Q152	
ENSMUST00000097103						0	4	2	4	5	0	0	0	0	0	0		
ENSMUST00000097132						4	0	2	2	4	2	0	0	0	0	0		
ENSMUST00000097146						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000097152						7	13	29	6	5	12	3	4	18	0	0		
ENSMUST00000097162	ENSMUSG00000006056	11	96099326	96111964	-1	18	7	23	31	24	16	0	1	1	0	0	G8JL78	
ENSMUST00000097163	ENSMUSG00000096220	10	129250536	129251474	1	5	3	2	0	0	1	0	0	0	0	0	Q7TRI4	
ENSMUST00000097164	ENSMUSG00000096229	10	129236287	129239089	1	1	0	0	1	1	2	0	0	0	0	0	Q7TRI5	
ENSMUST00000097166						3	5	37	1	5	1	0	0	0	0	0		
ENSMUST00000097175	ENSMUSG00000072419	16	48310477	48319723	1	14	27	53	17	24	6	0	1	0	0	0	B2RQ54	Q9CWH0
ENSMUST00000097177	ENSMUSG00000072423	14	54625310	54629556	1	247	225	2118	307	258	129	7	36	5	3	13		Q8BG41
ENSMUST00000097193	ENSMUSG00000058267	1	160195215	160202170	1	1	0	1	8	1	0	0	0	13	12	12	D3Z2K2	
ENSMUST00000097216	ENSMUSG00000030796	7	45215753	45233635	1	0	0	0	0	0	0	17	62	29	0	34	Q80UL2	
ENSMUST00000097218	ENSMUSG00000072476	6	76495432	76497784	-1	5	10	44	6	23	6	0	1	0	0	0	E9PVG0	
ENSMUST00000097219						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000097221	ENSMUSG00000072479	X	73148796	73158872	1	3	0	14	0	6	0	0	0	1	0	0	A2BI50	
ENSMUST00000097227	ENSMUSG00000075706	10	80047166	80056439	1	9	0	0	76	4	3	15	57	0	0	14	Q76LV0	
ENSMUST00000097228	ENSMUSG00000075707	12	110279068	110281097	1	0	0	8	0	11	0	0	0	0	0	0	K3W4Q2	
ENSMUST00000097270						8	1	8	71	0	5	0	0	0	0	0		
ENSMUST00000097271	ENSMUSG00000046879	11	48861968	48871683	-1	0	0	10	2	5	0	48	207	131	543	161	Q5NCB5	
ENSMUST00000097274	ENSMUSG00000045038	17	86167785	86657919	1	0	0	12	5	20	0	0	0	21	0	17		P16054
ENSMUST00000097275	ENSMUSG00000045038	17	86167785	86657919	1	43	40	66	92	56	32	74	121	97	9	142		P16054
ENSMUST00000097278	ENSMUSG00000073371	17	82539258	82539545	1	0	3	26	4	4	4	211	417	302	301	154	J3QM43	
ENSMUST00000097281	ENSMUSG00000039414	17	78752906	78835381	-1	35	23	29	25	36	20	261	510	628	66	514		Q8C547
ENSMUST00000097284	ENSMUSG00000045761	17	71673261	71729669	1	0	0	0	0	0	0	0	0	0	0	0		Q3TYG6
ENSMUST00000097288	ENSMUSG00000003279	17	69969073	70821413	1	4	4	8	7	3	4	0	0	2	0	0	Q3UVU8	
ENSMUST00000097290	ENSMUSG00000073375	17	67630965	67632723	-1	25	7	20	17	22	8	0	0	0	0	0	B2RVX0	
ENSMUST00000097291	ENSMUSG00000052105	17	66336982	66449750	-1	0	8	19	0	0	0	0	0	0	0	0		Q3UHU5
ENSMUST00000097293						3	0	15	9	1	11	0	1280	76	105	46		
ENSMUST00000097295						1	2	3	7	5	2	0	0	0	0	0		
ENSMUST00000097296						0	2	3	5	2	1	0	1	0	1	0		
ENSMUST00000097299	ENSMUSG00000044279	17	57059105	57065918	1	0	0	14	20	0	0	0	4	3	0	0		Q8QZT4
ENSMUST00000097303	ENSMUSG00000073380	17	56294113	56300286	-1	15	3	8	11	19	4	0	0	0	0	0		Q497K5
ENSMUST00000097311	ENSMUSG00000023991	17	47867133	47924645	-1	0	0	0	70	12	9	0	0	23	0	86		
ENSMUST00000097317	ENSMUSG00000023942	17	45585200	45599606	-1	0	3	0	0	0	1	0	15	0	24	29		Q9JIM1
ENSMUST00000097324	ENSMUSG00000092043	17	40561507	40565622	1	22	32	36	30	32	27	0	0	0	0	5	A8R0U0	
ENSMUST00000097325	ENSMUSG00000090675	17	37529957	37530997	1	9	3	3	3	8	0	0	0	0	0	0	Q7TRK1	
ENSMUST00000097329	ENSMUSG00000054128	17	36185572	36190287	-1	1	0	0	0	1	0	0	0	0	0	0	S4R1D6	
ENSMUST00000097331	ENSMUSG00000073407	17	36042961	36058645	1	8	5	20	20	10	1	1	1	3	6	4	E9Q101	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000097333	ENSMUSG00000003534	17	35681567	35704621	-1	12	0	0	0	0	0	6	0	0	5	36	Q544T2	Q03146
ENSMUST00000097335	ENSMUSG00000073402	17	36164443	36168537	-1	0	0	1	280	0	0	17	58	38	6	37	E9Q0G4	
ENSMUST00000097336	ENSMUSG00000073412	17	35185095	35188439	-1	2	0	13	10	5	3	1735	4052	972	5127	1114	B8JJ61	
ENSMUST00000097337	ENSMUSG00000073414	17	35062693	35066184	-1	15	13	36	29	18	19	7	5	5	13	16	D3YVS6	
ENSMUST00000097338	ENSMUSG00000007035	17	35028605	35046745	-1	0	0	0	0	0	0	0	80	0	10	43		
ENSMUST00000097342	ENSMUSG00000013787	17	34898469	34914052	1	0	0	0	343	0	21	0	0	0	0	0	A2CG76	
ENSMUST00000097343	ENSMUSG00000024369	17	34850391	34856372	1	0	0	0	8	9	0	0	20	21	0	0	Q3ULA1	P19426
ENSMUST00000097345	ENSMUSG00000015467	17	34613349	34615971	-1	2	0	0	0	0	3	0	0	0	0	0		Q6GUQ1
ENSMUST00000097346						13	13	41	17	12	4	0	0	0	0	0		
ENSMUST00000097348	ENSMUSG00000057246	17	34398820	34460734	1	13	0	0	0	0	0	1	0	2	0	0	Q3V0M8	
ENSMUST00000097352	ENSMUSG00000006705	17	31564749	31607684	1	0	0	39	2	0	11	209	679	273	55	380		O70477
ENSMUST00000097360	ENSMUSG00000040276	17	27655509	27711106	1	0	4	10	20	0	0	0	0	0	0	0	Q543Y7	Q61644
ENSMUST00000097368	ENSMUSG00000025728	17	25926427	25944510	-1	23	0	35	0	7	6	28	38	15	0	83	Q3TD14	
ENSMUST00000097373	ENSMUSG00000002496	17	24595937	24632629	-1	60	27	87	74	72	23	637	792	777	62	593	Q7TT21	
ENSMUST00000097376	ENSMUSG00000036473	17	24175431	24209387	-1	62	12	41	64	8	8	22	27	0	0	0		Q3UUG6
ENSMUST00000097381	ENSMUSG00000094921	17	22601148	22619133	1	16	19	9	12	17	2	0	0	0	0	0	L7N221	
ENSMUST00000097384	ENSMUSG00000073448	17	21690766	21691024	1	1	0	0	0	0	0	2	12	3	0	1	O88255	
ENSMUST00000097393	ENSMUSG00000036552	17	14978864	15064232	1	0	0	0	0	0	0	103	508	167	82	147	E9Q048	
ENSMUST00000097395	ENSMUSG00000036552	17	14978864	15064232	1	0	0	0	0	0	0	12	0	0	12	0	F6UWZ4	
ENSMUST00000097398	ENSMUSG00000079707	17	15027157	15041559	-1	0	11	3	115	12	7	2	1	0	0	2		P11985
ENSMUST00000097399	ENSMUSG00000079710	17	14964189	15041537	-1	0	0	0	35	9	2	0	0	0	2	0		P11985
ENSMUST00000097400	ENSMUSG00000079710	17	14964189	15041537	-1	11	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000097403	ENSMUSG00000052469	17	13354572	13377223	1	35	24	72	25	17	17	0	0	0	0	0	E9Q046	
ENSMUST00000097413						55	32	79	59	33	12	0	3	2	0	5		
ENSMUST00000097414	ENSMUSG00000062078	17	10206471	10319361	-1	11	7	16	5	10	2	889	1513	1293	178	917		Q9QYS9
ENSMUST00000097418	ENSMUSG00000040899	17	8236043	8257127	1	6	3	7	4	3	0	0	0	0	0	3	Q542B6	O54689
ENSMUST00000097419	ENSMUSG00000069135	17	8165501	8196804	1	10	6	22	13	11	6	5	7	0	0	5		Q66JX5
ENSMUST00000097420	ENSMUSG00000095687	17	8128610	8148097	-1	11	11	47	744	29	15	129	603	233	149	164	Q5FWA0	Q9CQ01
ENSMUST00000097422	ENSMUSG00000094083	17	8038510	8101228	-1	13	7	25	15	14	7	35	52	10	16	16	Q3TRG0	
ENSMUST00000097423	ENSMUSG00000073471	17	7945653	7979824	1	27	8	9	378	30	16	210	521	434	145	175		Q3UFY4
ENSMUST00000097424						2	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000097425	ENSMUSG00000071984	17	7738569	7827302	-1	37	36	151	69	65	34	0	0	0	14	86	E9Q043	
ENSMUST00000097430	ENSMUSG00000041831	17	6673458	6738042	1	0	0	8	0	0	0	16	13	0	0	1		Q99N48
ENSMUST00000097432	ENSMUSG00000015659	17	6042196	6079741	-1	65	41	234	98	67	30	31	136	93	9	108		Q3U213
ENSMUST00000097437	ENSMUSG00000029322	5	100553725	100572245	-1	2	0	2	15	2	0	67	263	95	281	21		Q9JI48
ENSMUST00000097442	ENSMUSG00000026604	1	189728268	189876695	1	90	63	256	102	101	54	8	3	6	7	77		Q62130
ENSMUST00000097443						3	10	7	38	12	4	23	47	35	10	23		
ENSMUST00000097446						1	2	0	3	0	5	0	0	0	0	0		
ENSMUST00000097450	ENSMUSG00000026490	1	179960472	180165603	1	0	0	0	0	0	0	0	0	0	0	22		Q3UU96
ENSMUST00000097453	ENSMUSG00000026490	1	179960472	180165603	1	13	6	11	51	13	0	0	6	2	0	10	D3YYN8	
ENSMUST00000097454	ENSMUSG00000073486	1	179803376	179804676	1	8	2	5	158	6	6	2	0	1	0	5	F6UQQ9	
ENSMUST00000097458	ENSMUSG00000039783	1	175620381	175662116	1	33	40	28	18	34	14	5	20	6	5	28		Q91WN4
ENSMUST00000097462	ENSMUSG00000073491	1	173566284	173599274	-1	24	25	104	27	19	10	1	0	1	1	2	Q3UPZ5	
ENSMUST00000097463	ENSMUSG00000070501	1	173519717	173535957	-1	4	0	0	1	0	0	6	6	0	0	0	E9QL87	
ENSMUST00000097464	ENSMUSG00000007097	1	172271709	172298064	-1	0	0	6	0	7	0	0	0	0	1	0	D3YYN7	
ENSMUST00000097466	ENSMUSG00000073492	1	171895664	171898237	1	162	142	517	691	253	121	147	614	388	29	712	E9PZK0	
ENSMUST00000097467	ENSMUSG00000013973	1	171329145	171342331	1	0	3	8	5	7	0	0	1	30	0	31	Q3U001	Q9Z1L3
ENSMUST00000097470	ENSMUSG00000073494	1	170232749	170253608	1	0	0	1	0	0	0	0	3	9	13	3	M0QWP8	
ENSMUST00000097471						2	2	0	0	0	0	30	106	0	3	41		
ENSMUST00000097473	ENSMUSG00000052428	1	167308378	167333978	1	264	209	1629	392	148	95	4	64	6	2	18		Q921L3
ENSMUST00000097474	ENSMUSG00000040723	1	165646516	165709757	-1	76	70	189	91	91	53	60	149	84	9	82		Q3UZA1
ENSMUST00000097477	ENSMUSG00000073497	5	94339749	94385079	1	14	9	7	4	16	14	0	0	0	0	0	Q8C6S1	
ENSMUST00000097478	ENSMUSG00000095718	5	94314435	94317255	1	12	4	0	0	11	0	0	0	0	0	0	L7N458	
ENSMUST00000097479	ENSMUSG00000094560	5	94302519	94306796	-1	51	18	55	38	51	24	0	0	0	0	0	Q8C9W1	
ENSMUST00000097488						0	0	0	3	0	5	0	0	0	0	0		
ENSMUST00000097490	ENSMUSG00000094836	JH584299.1	4975	7356	1	0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000097491	ENSMUSG00000026581	1	164061982	164084181	1	6	9	12	15	5	3	719	352	3666	9783	5505	B1B507	
ENSMUST00000097493	ENSMUSG00000041406	1	163945993	163994796	-1	8	4	15	23	9	4	0	30	39	0	13		Q3TQQ9
ENSMUST00000097494	ENSMUSG00000069893	11	48946150	48979398	-1	113	99	613	131	203	92	130	160	550	41	532	Q5SVP0	
ENSMUST00000097495	ENSMUSG00000073514	18	89301082	89769528	-1	3	2	6	133	8	3	1	0	0	0	0		Q2MHE5
ENSMUST00000097496	ENSMUSG00000034028	18	89197431	89270201	1	1	0	6	3	3	0	1	7	0	25	13	Q8K4E3	
ENSMUST00000097513	ENSMUSG00000090394	1	160044382	160080208	1	0	0	10	4	0	0	17	5	25	8	26	E9Q2T4	
ENSMUST00000097520	ENSMUSG00000073532	18	77185006	77186257	-1	3	1	4	234	9	2	0	0	0	0	0	Q3TYW4	
ENSMUST00000097521	ENSMUSG00000025421	18	76930126	76972902	1	0	0	0	13	0	0	0	0	0	0	0		Q3UGR5
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ENSMUST00000097526	ENSMUSG00000050565	1	156035403	156068861	1	0	0	0	0	0	0	13	20	0	44	11		Q9ER81
ENSMUST00000097527	ENSMUSG00000026466	1	156004599	156036480	-1	12	2	8	11	11	3	0	0	50	0	0		Q921T2
ENSMUST00000097529	ENSMUSG00000033701	1	155558120	155691330	1	4	4	15	7	8	5	6	54	15	6	14		Q9D061
ENSMUST00000097530	ENSMUSG00000024561	18	74268272	74282685	1	22	9	49	53	34	11	306	622	433	64	291		
ENSMUST00000097536	ENSMUSG00000008475	1	152766542	152775597	1	1	5	17	138	23	0	84	710	71	20	66	Q3UA72	
ENSMUST00000097541	ENSMUSG00000026483	1	151571186	151721939	1	0	12	16	0	15	10	644	29	1702	0	1072	E9PYV4	
ENSMUST00000097542	ENSMUSG00000073542	18	67617397	67641336	-1	24	23	47	120	25	6	31	74	65	15	37		Q0VEJ0
ENSMUST00000097543	ENSMUSG00000023150	1	151344477	151364422	1	0	6	4	0	0	0	0	341	40	0	18		Q920Q8
ENSMUST00000097546	ENSMUSG00000006010	1	150361305	150393080	-1	0	14	20	51	13	15	0	0	2	0	0		Q4PJX1
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ENSMUST00000097557	ENSMUSG00000073551	18	62607539	62741387	-1	4	5	5	1	6	0	0	0	0	0	0		Q3UTS8
ENSMUST00000097558	ENSMUSG00000032126	9	44336350	44344228	-1	5	2	15	0	0	0	83	73	0	0	37	Q3UPG1	P22907
ENSMUST00000097561	ENSMUSG00000026421	1	135720061	135752232	1	21	9	15	7	10	0	0	0	0	0	4	Q4FJX4	P97315
ENSMUST00000097563	ENSMUSG00000024610	18	60803848	60812646	1	13	0	14	0	23	11	163	151	106	44	734	Q3U4Q8	P04441
ENSMUST00000097566	ENSMUSG00000043079	18	60593973	60660142	-1	19	0	0	219	11	0	0	0	0	0	0	Q3U336	Q8CC35
ENSMUST00000097570						1	2	5	0	3	0	1	4	2	0	0		
ENSMUST00000097580	ENSMUSG00000073568	18	46925982	46934222	1	50	37	86	387	44	26	4	20	8	1	1		Q3UKZ7
ENSMUST00000097581						0	2	1	2	0	0	0	0	0	0	0		
ENSMUST00000097586	ENSMUSG00000073572	18	44201264	44206018	1	0	0	0	1	0	0	0	0	0	0	0	F6XDR3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000097587	ENSMUSG00000073573	18	44190045	44196177	-1	0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000097588	ENSMUSG00000026425	1	131285251	131527352	-1	46	48	146	93	66	40	145	637	304	30	355		Q91Z67
ENSMUST00000097590	ENSMUSG00000024493	18	42202350	42262122	-1	29	18	48	22	34	10	188	861	456	502	411	Q7TSZ3	Q8BMJ2
ENSMUST00000097591	ENSMUSG00000073574	18	41986201	41999049	-1	3	9	7	9	7	4	0	0	0	0	0		Q3TYR5
ENSMUST00000097592	ENSMUSG00000024431	18	39410545	39491301	-1	6	0	17	0	0	0	22	0	375	0	213	E9PYV1	
ENSMUST00000097593	ENSMUSG00000036452	18	38601534	39376284	1	37	16	36	65	40	12	101	639	1267	87	875		Q6ZQ82
ENSMUST00000097597						4	0	0	0	1	0	0	0	1	0	0		
ENSMUST00000097609	ENSMUSG00000073591	18	37517871	37524479	1	0	0	0	0	0	0	0	0	0	0	0	Q52KQ3	
ENSMUST00000097617	ENSMUSG00000073598	18	35703225	35730869	1	40	21	73	78	28	13	1	2	1	0	0	Q3TS39	
ENSMUST00000097618	ENSMUSG00000073599	18	35713086	35722356	-1	7	1	26	11	3	4	0	0	0	0	0		Q3TZW0
ENSMUST00000097619	ENSMUSG00000073600	18	35650351	35655238	-1	0	0	0	906	7	3	0	0	0	0	0	Q3UKG2	
ENSMUST00000097622	ENSMUSG00000034300	18	34758906	34773760	1	0	1	113	277	0	3	1501	2699	1763	194	1044		Q8BXQ8
ENSMUST00000097625	ENSMUSG00000026335	1	97795114	98095646	-1	3	3	7	41	2	2	37	293	314	21	249	F8VQA4	
ENSMUST00000097626	ENSMUSG00000003778	18	34598615	34624601	-1	0	0	0	0	0	0	185	778	398	74	307		Q8R3B7
ENSMUST00000097631						37	32	204	66	67	20	1	3	2	0	1		
ENSMUST00000097632	ENSMUSG00000073608	1	93990509	94017147	1	146	142	318	188	155	74	1	22	17	1	16	Q3ULK5	
ENSMUST00000097633	ENSMUSG00000073609	1	93824909	93852348	1	16	10	14	14	34	14	282	525	237	35	247		Q8CIM3
ENSMUST00000097634	ENSMUSG00000073610	18	33464163	33472448	1	1	2	3	47	1	3	0	0	0	0	0	Q3URY4	
ENSMUST00000097642	ENSMUSG00000073616	1	92637145	92641985	-1	0	0	0	0	0	0	380	1084	246	1453	128	B2RVT1	Q3U898
ENSMUST00000097643	ENSMUSG00000033632	18	25168999	25467321	1	11	8	0	15	0	0	10	0	29	0	18		Q6NZK5
ENSMUST00000097644	ENSMUSG00000026313	1	91928779	92180341	-1	26	33	88	61	71	32	2480	3821	3764	225	3474		Q6NZM9
ENSMUST00000097646	ENSMUSG00000024273	18	24470861	24477765	1	12	7	22	22	9	6	21	85	22	70	21		Q5XFZ0
ENSMUST00000097648	ENSMUSG00000034353	1	91179822	91225196	1	10	16	21	26	10	5	80	129	31	38	38	Q3TNJ3	Q9WTJ5
ENSMUST00000097649	ENSMUSG00000026305	1	90998737	91128944	1	0	0	2	2	2	0	2400	3125	5273	2286	3787		Q3UZ39
ENSMUST00000097650	ENSMUSG00000026305	1	90998737	91128944	1	4	5	0	0	0	0	0	0	0	0	0		Q3UZ39
ENSMUST00000097651	ENSMUSG00000041923	18	22693181	23041653	-1	12	16	7	162	24	9	0	0	0	0	0		P60954
ENSMUST00000097652						0	4	8	0	0	0	0	0	0	0	0		
ENSMUST00000097653	ENSMUSG00000048126	1	90765923	90843971	-1	30	0	0	14	11	0	0	0	0	2	30	J3QQ16	
ENSMUST00000097655	ENSMUSG00000045215	18	22344883	22530227	1	62	35	0	0	0	0	0	0	0	0	0		Q8C4A5
ENSMUST00000097656	ENSMUSG00000067081	1	89950220	90014666	-1	1	1	0	0	2	2	0	0	0	0	0	H7BX71	
ENSMUST00000097658	ENSMUSG00000033382	18	20817224	20896078	-1	3	0	2	12	4	1	10	14	6	0	0	E9PY51	
ENSMUST00000097659	ENSMUSG00000089943	1	88166012	88218997	1	7	5	14	8	7	2	4	0	7	15	23	B2RT14	
ENSMUST00000097666	ENSMUSG00000036707	1	85793441	85851576	1	5	0	20	0	11	0	259	33	509	73	444		Q06138
ENSMUST00000097669	ENSMUSG00000073631	1	85100164	85100535	1	1	0	7	9	4	4	1	0	2	0	0	J3QPF1	
ENSMUST00000097670	ENSMUSG00000024293	18	10566602	10610352	-1	0	0	0	7	8	0	0	349	55	33	0	Q3UKT9	
ENSMUST00000097671						23	9	9	25	12	4	21	58	34	11	26		
ENSMUST00000097672	ENSMUSG00000073633	1	84839841	84900487	1	4	1	11	18	5	0	9	21	6	66	0		Q9CQ24
ENSMUST00000097680	ENSMUSG00000073639	18	6765205	6790231	1	2	4	19	52	13	5	384	1076	409	414	301	Q0PD38	P35293
ENSMUST00000097682	ENSMUSG00000073640	18	6332590	6333064	1	3	0	9	0	2	6	2180	2577	1466	10034	1121	Q5BLJ9	P61358
ENSMUST00000097690						5	7	1	1	6	0	76	129	166	114	195		
ENSMUST00000097694	ENSMUSG00000049339	1	75142778	75147913	1	0	0	9	66	0	0	547	683	665	125	601		Q6NS82
ENSMUST00000097697	ENSMUSG00000073650	1	74362108	74369321	1	0	5	18	9	5	6	0	0	0	4	0		B9EKE5
ENSMUST00000097698	ENSMUSG00000026189	1	72259167	72284314	-1	0	0	0	5	5	3	0	0	0	0	0	Q3UXD9	
ENSMUST00000097707	ENSMUSG00000025949	1	65186683	65278695	1	0	0	0	0	0	0	47	0	255	0	105		Q9Z1T6
ENSMUST00000097709	ENSMUSG00000025950	1	65158616	65186500	-1	8	6	11	50	14	6	801	3065	1300	2821	855		O88844
ENSMUST00000097713	ENSMUSG00000051344	1	64785983	64956824	-1	35	26	55	47	49	29	387	1157	796	125	921		Q8BM47
ENSMUST00000097715	ENSMUSG00000025208	19	45005014	45006442	-1	14	9	24	298	14	11	610	1360	562	178	380	Q5RL20	
ENSMUST00000097717						23	19	36	3	20	12	0	0	0	0	6		
ENSMUST00000097718	ENSMUSG00000040865	1	62958418	63114667	-1	102	75	138	235	129	56	258	575	234	62	92	B1AT32	
ENSMUST00000097720	ENSMUSG00000026011	1	60887000	60915832	1	0	0	1	0	0	0	1	0	2	9	1	Q5SSM0	
ENSMUST00000097722	ENSMUSG00000026031	1	58711508	58758884	1	0	0	0	0	0	1	17	0	13	0	11		O35732
ENSMUST00000097723						0	0	0	0	0	0	31	106	43	34	17		
ENSMUST00000097724	ENSMUSG00000038174	1	58522806	58586323	-1	0	0	0	0	0	0	0	0	27	0	12		Q8C729
ENSMUST00000097731						5	7	14	4	11	3	0	0	0	0	0		
ENSMUST00000097732						1	0	0	0	0	0	0	4	0	0	2		
ENSMUST00000097734	ENSMUSG00000029076	4	155992872	156013610	1	1	0	5	15	2	2	16	0	9	0	25		Q61112
ENSMUST00000097737	ENSMUSG00000051557	4	155887879	155891781	-1	4	0	10	24	7	0	8	58	6	0	26		A2ADA5
ENSMUST00000097739	ENSMUSG00000073678	1	54472994	54557684	-1	42	39	81	20	44	21	37	35	28	23	55		Q3UUQ7
ENSMUST00000097741	ENSMUSG00000042807	1	53806876	54195168	-1	3	2	2	3	2	0	0	0	0	0	0	A3KPB7	Q6I6G8
ENSMUST00000097742	ENSMUSG00000073680	4	155781591	155785874	-1	58	65	158	217	80	36	7	23	15	1	9		Q3TYP4
ENSMUST00000097747	ENSMUSG00000073684	4	155249802	155256687	1	7	7	12	141	15	13	60	158	60	12	56		Q3UN58
ENSMUST00000097759	ENSMUSG00000039410	4	154316125	154636873	-1	0	0	113	0	0	0	0	0	0	0	0	A2A930	
ENSMUST00000097762	ENSMUSG00000029026	4	154056253	154140208	-1	1	0	0	10	0	0	0	0	0	0	0		Q9JJP2
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ENSMUST00000097772	ENSMUSG00000026069	1	40429570	40465415	1	0	0	0	21	21	0	0	0	0	0	0		P14719
ENSMUST00000097773	ENSMUSG00000073700	4	152008803	152017680	1	79	46	484	351	77	51	132	216	101	25	103		Q3U410
ENSMUST00000097774	ENSMUSG00000014592	4	150917322	151861876	-1	0	0	0	15	0	0	0	0	0	0	0		A2A891
ENSMUST00000097776	ENSMUSG00000001138	1	36511867	36528237	1	27	0	106	53	0	46	0	44	0	0	0		Q32NY4
ENSMUST00000097778	ENSMUSG00000037447	1	36307733	36324029	1	0	0	0	0	0	0	86	646	85	36	70	D3Z0W0	
ENSMUST00000097781	ENSMUSG00000017264	4	148558429	148582401	1	9	0	41	12	0	10	21	33	30	0	31	F6VYQ6	
ENSMUST00000097785	ENSMUSG00000026131	1	33908225	34308661	1	50	0	144	122	106	0	0	0	0	0	0		Q91ZU6
ENSMUST00000097786	ENSMUSG00000026131	1	33908225	34308661	1	0	0	0	6	0	0	2	0	0	11	51		Q91ZU6
ENSMUST00000097788	ENSMUSG00000029009	4	148039077	148059551	1	2	11	9	26	0	8	0	0	13	1	0		Q9WU20
ENSMUST00000097794	ENSMUSG00000078502	4	145585166	145625345	1	0	0	0	1	0	3	13	23	3	0	4	E9PWQ2	
ENSMUST00000097799	ENSMUSG00000073723	4	144106474	144110101	1	0	21	0	14	8	0	0	0	0	0	0	A2ASJ3	
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ENSMUST00000097801	ENSMUSG00000073722	1	26681814	26687460	-1	34	46	128	65	59	27	2	8	3	3	3	E9PWP9	
ENSMUST00000097805	ENSMUSG00000028914	4	141793612	141815976	1	0	0	0	13	0	0	228	0	144	39	104	A2AS93	
ENSMUST00000097808	ENSMUSG00000041670	1	22286251	22805724	-1	7	3	11	181	14	6	0	0	0	0	0	E9PWP6	
ENSMUST00000097809	ENSMUSG00000041670	1	22286251	22805724	-1	0	0	0	0	0	0	0	0	0	0	0	F6VBV0	
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ENSMUST00000097811	ENSMUSG00000041670	1	22286251	22805724	-1	6	0	29	0	0	0	0	0	0	0	0	F6VBR4	
ENSMUST00000097813	ENSMUSG00000073733	4	141213956	141226756	1	5	4	25	17	2	4	2	0	5	2	1	B2RWG6	A2A825
ENSMUST00000097816	ENSMUSG00000040860	4	141016637	141060550	-1	0	0	0	0	0	0	25	0	25	0	0		Q8CJ40

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000097817	ENSMUSG00000067773	1	18250980	18265138	-1	2	1	0	0	0	0	0	0	0	0	0		Q30KP6
ENSMUST00000097818	ENSMUSG00000073735	1	18236473	18237443	-1	0	0	0	0	0	1	0	0	0	0	0		Q30KP5
ENSMUST00000097820	ENSMUSG00000040964	4	140514485	140666012	-1	0	0	0	7	7	0	8	7	0	0	0		A2AWP8
ENSMUST00000097822	ENSMUSG00000066036	4	139352609	139489588	1	113	77	88	109	148	69	4997	5016	10460	122	6558		A2AN08
ENSMUST00000097824	ENSMUSG00000099032	1	9960163	9967932	-1	0	0	3	0	0	0	0	32	2	2	4	Q3UV43	
ENSMUST00000097826	ENSMUSG00000025915	1	9798107	9900845	1	0	4	0	74	7	6	375	1053	552	487	242		Q9ERE3
ENSMUST00000097830	ENSMUSG00000041161	4	138895379	138913945	-1	8	8	18	72	22	7	276	341	422	37	333		B1AZ99
ENSMUST00000097836	ENSMUSG00000028759	4	138216296	138244683	1	0	0	18	0	0	3	0	413	53	96	256		Q3TEA8
ENSMUST00000097837	ENSMUSG00000041351	4	137664726	137729861	1	0	0	20	11	20	0	0	0	0	0	11		A2ALS5
ENSMUST00000097843	ENSMUSG00000062585	4	135895394	135920207	1	39	33	52	59	71	27	2510	2078	2819	281	2034		P47936
ENSMUST00000097844	ENSMUSG00000028676	4	135855747	135869908	1	12	3	4	8	4	3	0	205	0	79	0		Q9R0U0
ENSMUST00000097849	ENSMUSG00000073747	4	134190804	134203004	-1	33	20	297	34	39	17	0	0	0	0	0	Q3UU21	
ENSMUST00000097855						40	54	65	30	63	53	5	19	11	2	22		
ENSMUST00000097856	ENSMUSG00000028878	4	132899213	132922558	-1	8	0	0	30	7	7	103	81	221	38	112		Q922G2
ENSMUST00000097860	ENSMUSG00000028909	4	131768457	131838288	-1	0	8	6	7	16	0	0	0	0	0	0	Q3V360	
ENSMUST00000097862	ENSMUSG00000028580	4	130663321	130781564	1	28	3	0	0	0	12	71	0	56	0	146	Q3TQ21	Q80U78
ENSMUST00000097864	ENSMUSG00000028580	4	130663321	130781564	1	0	0	54	35	12	1	11	0	330	0	183		Q80U78
ENSMUST00000097865	ENSMUSG00000073752	4	130308162	130308674	-1	6	4	9	87	5	4	0	1	2	0	0	F6VB42	
ENSMUST00000097867						18	17	17	13	13	0	0	0	0	0	15		
ENSMUST00000097868	ENSMUSG00000028782	4	129984870	130022633	1	0	10	46	0	0	0	0	0	0	0	0	H7BX74	
ENSMUST00000097869						10	5	17	12	12	10	0	0	1	0	1		
ENSMUST00000097873	ENSMUSG00000050390	4	129219578	129261404	-1	0	0	5	196	0	17	11	10	2	10	49		A2A7S8
ENSMUST00000097874	ENSMUSG00000028793	4	129058271	129085886	1	5	0	14	0	0	9	1676	2249	1393	183	1068	B2KG08	
ENSMUST00000097877	ENSMUSG00000061894	4	128583539	128610098	-1	31	22	32	108	39	10	31	23	34	2	37		B2KFW1
ENSMUST00000097886	ENSMUSG00000073755	4	126609818	126614371	1	0	0	0	1199	0	85	0	0	0	0	0		Q8BP99
ENSMUST00000097888	ENSMUSG00000041530	4	126435012	126468583	-1	37	21	62	102	44	20	229	445	379	34	356		Q8CJG1
ENSMUST00000097891	ENSMUSG00000073758	4	126150602	126163491	-1	7	3	12	161	35	19	0	0	0	3	0	Z4YK11	
ENSMUST00000097896	ENSMUSG00000073761	4	123859679	123863165	1	441	554	252	464	453	211	8	28	40	12	32	Q3V053	
ENSMUST00000097897	ENSMUSG00000028649	4	123349633	123684360	-1	1	1	0	0	0	0	50	0	35	0	9	E9PVY8	
ENSMUST00000097902	ENSMUSG00000028657	4	122836242	122859175	1	5	0	13	3	6	2	27	57	66	5	90	B1B0P9	
ENSMUST00000097905	ENSMUSG00000073764	4	121316316	121324917	-1	7	3	12	4	9	8	0	0	0	0	0	Q3UW77	
ENSMUST00000097906	ENSMUSG00000032897	4	120757438	120831572	-1	0	0	0	0	0	0	12	0	74	0	9		P70353
ENSMUST00000097908	ENSMUSG00000028643	4	119195306	119201298	1	6	3	6	56	9	3	13	30	3	6	0	A2A7P9	
ENSMUST00000097911	ENSMUSG00000033326	4	118136957	118180043	-1	12	0	51	26	0	17	780	1330	1148	146	1083		Q8BW72
ENSMUST00000097912	ENSMUSG00000028538	4	117932154	118134914	-1	0	7	22	0	8	0	22	0	0	0	0	Q9CZ48	
ENSMUST00000097913	ENSMUSG00000028539	4	117926162	117929763	-1	0	0	0	0	2	0	0	0	0	0	7		Q9Z0L2
ENSMUST00000097915						0	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000097918	ENSMUSG00000073774	4	115884400	115889526	1	3	2	21	11	10	2	0	0	2	0	0		Q307W7
ENSMUST00000097920	ENSMUSG00000061298	4	110397661	111664324	1	0	0	0	0	0	0	0	0	0	0	0		Q09LZ8
ENSMUST00000097921	ENSMUSG00000028551	4	109660876	109667189	-1	5	3	12	447	25	6	101	89	137	26	83		Q60772
ENSMUST00000097925	ENSMUSG00000034610	4	108459426	108559421	1	12	4	0	15	0	0	115	504	0	27	244	A2A8R7	
ENSMUST00000097929	ENSMUSG00000037541	7	144001928	144424494	1	12	11	0	367	21	13	0	0	0	0	0		Q80Z38
ENSMUST00000097934	ENSMUSG00000061887	4	106910701	107049694	1	0	0	0	0	0	0	0	0	0	7	0	B1AS37	
ENSMUST00000097935	ENSMUSG00000073781	7	142831227	142852266	1	11	12	17	3	12	8	0	0	0	0	0	Q3UTU4	
ENSMUST00000097936	ENSMUSG00000048583	7	142650766	142666816	-1	0	0	0	2	0	0	0	0	0	0	0		P09535
ENSMUST00000097939	ENSMUSG00000031098	7	142434850	142440396	1	0	0	0	0	0	0	0	0	0	0	0	F2Z3W8	
ENSMUST00000097942	ENSMUSG00000073785	7	142228795	142229971	-1	18	10	81	39	18	15	0	0	0	0	0		Q2TA51
ENSMUST00000097943						17	13	89	84	23	10	0	0	0	0	0		
ENSMUST00000097944	ENSMUSG00000028520	4	103230445	103290863	-1	2	5	3	4	1	2	0	0	0	0	0		Q9D5Q8
ENSMUST00000097945	ENSMUSG00000028522	4	103114390	103165754	1	0	23	0	0	0	10	0	2	0	0	0		Q5UAK0
ENSMUST00000097948						1	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000097949	ENSMUSG00000028525	4	102087543	102607259	1	0	0	9	0	7	0	0	4	0	0	0	Q6IQY6	
ENSMUST00000097950	ENSMUSG00000028525	4	102087543	102607259	1	9	10	44	18	9	7	68	48	134	50	318	B1AWD0	
ENSMUST00000097952	ENSMUSG00000025498	7	141262706	141266481	-1	0	0	0	3	0	0	101	682	87	0	304	Q3TW14	
ENSMUST00000097954	ENSMUSG00000073789	4	101020298	101020696	-1	3	1	4	5	6	1	0	0	0	0	0	Q3UDV9	
ENSMUST00000097955	ENSMUSG00000028532	4	100776675	101029220	1	5	4	0	0	3	10	0	0	0	0	0	Z4YK18	
ENSMUST00000097957	ENSMUSG00000025499	7	141189105	141194005	-1	0	0	0	0	0	0	253	333	148	61	123		Q61411
ENSMUST00000097958	ENSMUSG00000025494	7	141091175	141100546	-1	14	10	39	65	21	4	86	101	69	24	78	Q3UKS3	Q9JLZ8
ENSMUST00000097959	ENSMUSG00000073791	4	99829198	99912788	1	8	5	7	4	8	3	3	15	4	15	2	F6XAI7	
ENSMUST00000097961	ENSMUSG00000073792	4	99715664	99763460	1	19	21	16	5	7	8	7	34	6	15	15		Q3TAE8
ENSMUST00000097964	ENSMUSG00000073794	4	98818475	98823840	-1	56	53	128	50	34	20	1	7	3	0	4	A6PWL3	
ENSMUST00000097967	ENSMUSG00000025464	7	140125657	140134334	1	2	9	85	42	12	1	0	26	0	6	9	Q3TXR6	
ENSMUST00000097970	ENSMUSG00000073795	7	139972303	139978755	-1	7	7	3	16	3	0	0	17	10	16	11	Q3V2J1	
ENSMUST00000097972	ENSMUSG00000081225	4	96099318	96141152	-1	0	0	0	0	0	2	0	0	0	0	0	G3UXT0	
ENSMUST00000097973	ENSMUSG00000028571	4	96027534	96077546	-1	0	0	0	0	0	0	0	0	0	0	0	B1AWM5	
ENSMUST00000097974	ENSMUSG00000041309	7	139579376	139582797	-1	14	10	29	375	14	8	1	0	0	0	1	D3Z4R4	
ENSMUST00000097975	ENSMUSG00000025477	7	139389109	139579652	1	4	4	35	12	10	6	326	363	514	46	241	Q3TZT4	
ENSMUST00000097981	ENSMUSG00000073802	4	89306289	89311032	-1	6	4	15	159	10	3	6	39	9	3	5	Q549R4	P55271
ENSMUST00000097982	ENSMUSG00000073803	7	135396342	135399544	1	28	28	58	28	38	18	0	0	1	0	0	Q3V0D6	
ENSMUST00000097983	ENSMUSG00000073804	7	135268639	135272942	1	6	4	7	7	3	5	0	0	0	0	0		P0C0P8
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ENSMUST00000097992	ENSMUSG00000038368	4	88094629	88411011	1	16	17	22	8	17	6	0	0	20	15	17		A2AKG8
ENSMUST00000097998	ENSMUSG00000030956	7	132712082	132813886	-1	10	10	71	23	0	15	158	249	179	20	0	Q3TNT2	
ENSMUST00000097999	ENSMUSG00000030956	7	132712082	132813886	-1	10	0	19	306	41	24	23	27	103	0	92		Q8BGR5
ENSMUST00000098005	ENSMUSG00000028399	4	75941238	78211961	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVW8	
ENSMUST00000098006	ENSMUSG00000049122	4	74013442	74202214	1	0	4	4	25	2	0	0	0	0	0	0		Q8BHD4
ENSMUST00000098007						38	35	75	869	44	21	8	29	6	0	11		
ENSMUST00000098015	ENSMUSG00000108596	7	128062683	128128160	1	6	4	15	9	5	7	530	829	767	111	654	Q3U1U4	
ENSMUST00000098025	ENSMUSG00000053877	7	127511983	127561219	1	0	0	0	0	0	0	0	0	0	4	0	Q8BQA6	
ENSMUST00000098031	ENSMUSG00000059810	4	62559847	62704001	1	6	3	4	38	9	1	0	0	0	0	6	I7HPB2	
ENSMUST00000098032	ENSMUSG00000058966	7	126797668	126830219	1	15	15	52	51	20	12	1	0	0	0	0		Q7TNV1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000098033	ENSMUSG00000066151	4	62300342	62360548	-1	0	4	0	0	2	1	33	136	56	4	5	Q80YW7	
ENSMUST00000098035	ENSMUSG00000094948	4	60838256	60839649	1	0	0	0	0	0	0	0	0	0	0	0	J3QPA3	
ENSMUST00000098036	ENSMUSG00000030720	7	126571207	126585817	-1	0	0	0	0	0	0	840	1365	755	110	558	Q6PAH4	
ENSMUST00000098040	ENSMUSG00000078674	4	61670177	61674136	-1	0	0	0	0	0	0	0	0	0	0	0	A2BIM8	
ENSMUST00000098042	ENSMUSG00000089873	4	61224307	61228286	-1	0	0	14	0	10	6	0	0	0	0	0	L7N222	
ENSMUST00000098046	ENSMUSG00000073834	4	60658466	60662411	-1	0	0	0	0	0	0	0	0	0	0	0	A2BIM8	
ENSMUST00000098047	ENSMUSG00000078680	4	60578260	60582199	-1	2	0	2	0	0	0	0	0	0	0	0	A2BIN1	
ENSMUST00000098048	ENSMUSG00000073838	7	126487361	126490731	1	0	2	5	81	9	0	334	398	260	82	230		Q8BFR5
ENSMUST00000098056	ENSMUSG00000030762	7	123462291	123468004	1	4	0	11	2	11	0	0	0	0	1	0	Q3UJ16	
ENSMUST00000098057	ENSMUSG00000057280	4	58285960	58374303	1	0	9	0	0	25	0	0	0	0	0	0	E9PVV8	
ENSMUST00000098059	ENSMUSG00000057280	4	58285960	58374303	1	27	11	0	0	0	0	0	0	0	0	0	F6WVU1	
ENSMUST00000098060	ENSMUSG00000030766	7	123279218	123369915	-1	0	0	0	0	1	0	165	851	252	57	286		Q3UIA2
ENSMUST00000098062	ENSMUSG00000030779	7	122965686	123002557	1	4	2	12	1	4	5	27	36	6	1	11		
ENSMUST00000098064	ENSMUSG00000038729	4	57717657	57896982	1	0	18	66	95	49	0	0	0	0	0	0		O54931
ENSMUST00000098065						2	1	11	3	4	5	0	0	0	0	0		
ENSMUST00000098066	ENSMUSG00000089945	4	57568179	57896984	1	0	0	0	0	0	0	0	0	0	0	0	G3X9P1	
ENSMUST00000098068	ENSMUSG00000044702	7	122107262	122132985	-1	13	8	42	21	0	0	12	24	0	0	23		Q3U0P1
ENSMUST00000098070	ENSMUSG00000060206	4	54945048	55083563	1	60	45	219	91	91	40	0	0	0	4	22	B1AWL2	
ENSMUST00000098080	ENSMUSG00000048787	7	119853163	119896291	-1	6	5	0	11	3	7	71	181	47	5	62		Q8K0V2
ENSMUST00000098084	ENSMUSG00000030945	7	119554469	119600694	1	102	39	234	224	17	0	0	2	2	0	3		Q8K0L3
ENSMUST00000098087	ENSMUSG00000073856	7	118855760	118972652	1	4	3	11	28	3	0	2	0	0	1	3	D3YYL3	
ENSMUST00000098088	ENSMUSG00000030650	7	118597297	118675086	1	0	0	12	12	0	0	0	0	0	0	0		Q32NZ6
ENSMUST00000098090	ENSMUSG00000030652	7	118509659	118533356	-1	6	6	4	4	7	0	0	0	0	0	0	Q3TYT1	
ENSMUST00000098098	ENSMUSG00000035696	4	44126210	44233789	-1	20	12	195	24	0	0	407	261	609	0	302		Q8BI21
ENSMUST00000098100	ENSMUSG00000073862	7	113707715	113708200	-1	3	1	1	6	2	0	0	0	0	0	0	Q8BS55	
ENSMUST00000098104	ENSMUSG00000028459	4	43446462	43454628	-1	4	0	9	6	24	6	0	41	0	10	8	Q3UB58	
ENSMUST00000098105	ENSMUSG00000028459	4	43446462	43454628	-1	0	2	0	0	0	0	0	0	0	20	0	Q3UNJ0	
ENSMUST00000098106	ENSMUSG00000035969	4	43381979	43427088	1	0	13	29	9	25	16	0	0	0	0	0	Q3V1Z0	
ENSMUST00000098109	ENSMUSG00000028454	4	43017635	43025819	-1	17	16	71	97	39	6	56	90	83	9	42	Q562G0	
ENSMUST00000098110	ENSMUSG00000073867	7	110057987	110061325	-1	1272	1670	604	6571	6161	1208	1876	6166	4006	5549	1381	Q3V1U0	
ENSMUST00000098112	ENSMUSG00000036052	4	42949814	42959425	1	0	0	0	0	19	3	8	8	32	0	19	Q3TY13	O89114
ENSMUST00000098119						20	16	25	38	35	13	21	52	47	9	25		
ENSMUST00000098121	ENSMUSG00000073876	4	42158842	42168603	-1	2	3	8	9	6	3	0	0	0	0	0		P70225
ENSMUST00000098122	ENSMUSG00000073877	4	42153436	42158839	1	0	0	0	0	0	0	0	0	0	0	0		Q9Z1X0
ENSMUST00000098123	ENSMUSG00000073878	4	42114817	42115917	1	9	0	0	0	0	0	0	0	2	0	0		P86793
ENSMUST00000098128	ENSMUSG00000094065	4	41903610	41904743	1	0	0	31	7	1	0	0	0	0	0	0		P86793
ENSMUST00000098132	ENSMUSG00000073889	4	41699989	41769474	1	7	5	14	31	4	2	6	17	23	0	33		Q64385
ENSMUST00000098134	ENSMUSG00000036528	7	107595051	107748582	1	28	17	36	17	27	8	0	0	0	0	0		O35711
ENSMUST00000098135	ENSMUSG00000073894	7	107209445	107210916	1	4	4	14	439	9	5	0	0	0	0	0	Q9DAE2	
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ENSMUST00000098138	ENSMUSG00000073897	7	107097467	107098414	1	4	5	10	3	4	3	0	0	0	0	0	Q7TRM9	
ENSMUST00000098139	ENSMUSG00000073898	7	107036136	107037110	1	4	1	4	1	4	2	0	0	0	0	0	Q920G5	
ENSMUST00000098140	ENSMUSG00000073899	7	106914200	106915123	1	0	3	6	0	0	12	0	0	0	0	0		
ENSMUST00000098141	ENSMUSG00000073900	7	106864982	106865929	1	2	4	2	5	3	6	0	0	0	0	0	Q9EPF6	
ENSMUST00000098142	ENSMUSG00000073901	7	106844613	106845572	1	10	7	13	5	5	8	0	0	0	0	0	Q9EPF5	
ENSMUST00000098143	ENSMUSG00000028423	4	40970906	41025993	1	22	7	29	39	14	12	193	631	390	74	337		B1AY10
ENSMUST00000098148	ENSMUSG00000030888	7	105732207	105737376	-1	12	6	72	10	10	12	51	144	58	12	86	E9PVA2	
ENSMUST00000098151	ENSMUSG00000045083	4	35706647	36951747	-1	0	0	5	0	0	0	0	0	0	0	0	B2RQD4	Q3URE9
ENSMUST00000098152	ENSMUSG00000073906	7	105368230	105369355	1	4	8	12	7	6	1	3	0	3	0	2	Q8VF03	
ENSMUST00000098153	ENSMUSG00000073907	7	105313982	105315057	1	2	2	2	0	4	2	0	0	0	0	0	Q8VG18	
ENSMUST00000098154	ENSMUSG00000073908	7	105275517	105276431	1	0	3	0	5	0	3	0	0	0	0	0	F6WFG0	
ENSMUST00000098155	ENSMUSG00000073909	7	105288095	105289060	1	11	9	11	4	4	0	0	0	0	0	0		Q6W049
ENSMUST00000098157	ENSMUSG00000095248	7	105121459	105122406	1	4	0	0	7	0	2	0	0	0	0	0	Q3SXH8	
ENSMUST00000098158	ENSMUSG00000096029	7	105085714	105086665	1	0	8	7	0	8	0	0	0	0	0	0	Q8VGV0	
ENSMUST00000098160	ENSMUSG00000073913	7	105069469	105070410	1	5	4	2	2	4	1	0	0	0	0	0	Q8VG26	
ENSMUST00000098161	ENSMUSG00000073914	7	105056248	105057186	1	3	10	1	1	1	6	0	0	0	0	0	Q8VF06	
ENSMUST00000098162	ENSMUSG00000073915	7	105035200	105036153	1	12	5	5	4	2	3	0	0	0	0	0	Q8VGZ9	
ENSMUST00000098163	ENSMUSG00000039967	4	34803113	34882960	-1	0	19	64	0	0	21	15	1064	67	326	2		Q9Z2U2
ENSMUST00000098164	ENSMUSG00000073916	7	104938528	104939481	1	4	6	2	1	7	3	0	0	0	0	0	Q8VGU9	
ENSMUST00000098165	ENSMUSG00000073917	7	104880709	104881659	1	4	4	1	4	2	4	0	0	0	0	0	Q8VG79	
ENSMUST00000098167						2	3	0	0	7	3	0	0	0	0	0		
ENSMUST00000098168	ENSMUSG00000073920	7	104688013	104688976	1	2	2	1	0	1	3	0	0	0	0	0	Q99NH4	
ENSMUST00000098170	ENSMUSG00000073922	7	104670704	104671672	1	0	4	0	1	2	2	0	0	0	0	0	Q8VGV6	
ENSMUST00000098171	ENSMUSG00000073923	7	104635676	104636636	1	7	2	3	3	5	1	0	0	0	0	0	Q7TRP7	
ENSMUST00000098172	ENSMUSG00000073924	7	104617657	104618647	1	4	6	9	3	5	0	0	0	0	0	0	Q8VGX9	
ENSMUST00000098173	ENSMUSG00000073925	7	104587755	104588780	1	4	7	12	4	5	1	0	0	0	0	0	Q8VF27	
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ENSMUST00000098175	ENSMUSG00000073927	7	104564152	104565212	1	7	0	6	0	9	0	0	0	0	0	0	B9EHE6	
ENSMUST00000098176	ENSMUSG00000073928	7	104552921	104553862	1	7	4	11	6	3	4	0	0	0	0	1	Q8VG78	
ENSMUST00000098179	ENSMUSG00000060441	7	104263386	104288094	-1	0	0	55	0	0	0	18	0	27	28	46	E9PV98	
ENSMUST00000098180	ENSMUSG00000072244	7	104218793	104235152	1	39	39	307	45	32	10	19	175	58	13	66		Q8BGE7
ENSMUST00000098181	ENSMUSG00000054659	4	33174230	33189737	-1	3	3	9	2	4	2	0	0	0	0	0		A3KG59
ENSMUST00000098182	ENSMUSG00000073931	7	104106281	104107219	1	12	8	15	13	17	4	0	0	0	1	0	Q8VGW2	
ENSMUST00000098183	ENSMUSG00000073932	7	104039798	104040736	1	8	4	10	5	6	3	0	0	0	0	0	Q8VGX6	
ENSMUST00000098184	ENSMUSG00000094063	7	104003259	104004224	1	4	5	14	1	7	2	0	0	0	0	0	Q8VH20	
ENSMUST00000098185	ENSMUSG00000094520	7	103979176	103980141	1	14	8	17	4	7	4	0	0	0	0	0	K7N6B1	
ENSMUST00000098188	ENSMUSG00000073937	7	103946568	103947506	1	4	2	10	20	3	3	0	0	0	0	0	Q8VF02	
ENSMUST00000098189	ENSMUSG00000073938	7	103937382	103938335	1	2	8	11	3	12	5	0	0	0	0	0	Q9EPN9	
ENSMUST00000098190	ENSMUSG00000028278	4	32983037	33022180	1	0	26	57	407	51	0	13	34	13	4	15	B1AWT2	
ENSMUST00000098192	ENSMUSG00000073940	7	103812524	103813996	-1	44	7	98	46	195	12	2187	382	327	13887	2476	A8DUK4	
ENSMUST00000098193	ENSMUSG00000096516	7	103731928	103732878	1	4	4	3	0	0	0	0	0	0	0	0	K7N6B2	
ENSMUST00000098194	ENSMUSG00000094822	7	103716596	103717546	1	0	0	1	0	3	2	0	0	0	0	0	E9PV96	
ENSMUST00000098195	ENSMUSG00000073943	7	103682720	103683685	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000098196	ENSMUSG00000073944	7	103603656	103604618	1	3	2	3	2	5	0	0	0	0	0	0	E9PV95	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000098197	ENSMUSG00000073945	7	103597318	103598274	1	1	3	3	2	0	2	0	0	0	0	0	K7N6B3	
ENSMUST00000098198	ENSMUSG00000073947	7	103560479	103561420	1	3	5	2	6	4	4	0	0	0	0	0	Q8VGY4	
ENSMUST00000098199	ENSMUSG00000073948	7	103470041	103470991	1	0	1	3	1	2	1	0	0	0	0	0	E9Q564	
ENSMUST00000098200	ENSMUSG00000073949	7	103451339	103452298	1	2	3	2	5	7	4	0	0	0	0	0	Q8VGZ8	
ENSMUST00000098201	ENSMUSG00000073950	7	103338056	103339003	1	6	3	10	3	1	0	0	0	0	0	0	Q8VG01	
ENSMUST00000098202	ENSMUSG00000073951	7	103328488	103329447	1	8	4	8	3	7	5	0	0	0	0	0	Q7TRR2	
ENSMUST00000098203	ENSMUSG00000073952	7	103320401	103321360	1	4	5	0	0	4	0	0	0	0	0	0	L7N224	
ENSMUST00000098205	ENSMUSG00000073954	7	103219720	103220655	1	4	3	5	2	4	4	0	0	0	0	0	Q7TRR4	
ENSMUST00000098206	ENSMUSG00000073955	7	103211862	103212845	1	0	7	3	1	7	1	0	0	0	0	0	Q8VF28	
ENSMUST00000098207	ENSMUSG00000073956	7	103184803	103187541	1	0	0	0	0	2	0	0	0	0	0	0	E9PYB3	
ENSMUST00000098210	ENSMUSG00000073959	7	103085520	103086479	1	5	5	11	2	7	6	0	0	0	0	0	Q8VGW0	
ENSMUST00000098211	ENSMUSG00000073960	7	103051300	103052259	1	4	7	4	1	9	2	0	0	0	0	0	Q8VG25	
ENSMUST00000098212	ENSMUSG00000073961	7	103041481	103042440	1	10	3	13	8	5	2	0	0	0	0	0	Q8VGV9	
ENSMUST00000098213	ENSMUSG00000073962	7	102965102	102975160	1	2	3	3	2	4	2	0	0	0	0	0	A0A0G2JFH3	
ENSMUST00000098214	ENSMUSG00000073963	7	102927630	102928586	1	4	2	1	2	2	5	0	0	0	0	0	Q8VGZ3	
ENSMUST00000098215	ENSMUSG00000073964	7	102900342	102901386	1	4	2	7	0	9	3	0	0	0	0	0	Q8VH12	
ENSMUST00000098216	ENSMUSG00000073965	7	102877122	102878063	1	3	2	12	1	3	5	0	0	0	0	0	E9Q554	
ENSMUST00000098217	ENSMUSG00000073966	7	102774495	102775565	1	3	2	1	5	1	2	0	0	0	0	0	Q8VGZ6	
ENSMUST00000098218	ENSMUSG00000073967	7	102698216	102699272	1	3	4	5	3	6	3	1	0	0	0	0	E9Q550	
ENSMUST00000098219	ENSMUSG00000073969	7	102669901	102670923	1	4	7	15	6	0	4	0	0	0	0	0	E9Q549	
ENSMUST00000098220	ENSMUSG00000073970	7	102658823	102659770	1	2	3	11	6	4	7	0	0	0	0	0	E9Q547	
ENSMUST00000098221	ENSMUSG00000073971	7	102640248	102641201	1	8	8	23	5	7	2	0	0	0	0	0	E9Q546	
ENSMUST00000098222	ENSMUSG00000073972	7	102614007	102614987	-1	3	12	11	6	5	2	0	0	0	0	0	Q7TRS6	
ENSMUST00000098223	ENSMUSG00000073973	7	102604356	102605309	1	1	1	2	9	5	3	0	0	0	0	0	E9Q545	
ENSMUST00000098224	ENSMUSG00000073974	7	102587741	102588819	-1	10	4	11	7	13	3	0	0	0	0	0	Q8VG23	
ENSMUST00000098225	ENSMUSG00000073975	7	102578469	102579506	1	5	5	8	10	14	4	0	0	0	0	0	E9Q544	
ENSMUST00000098227	ENSMUSG00000073977	7	102554286	102555236	1	16	6	13	9	17	7	0	0	0	0	0	E9Q542	
ENSMUST00000098228						10	4	5	6	22	5	0	0	0	0	0		
ENSMUST00000098229	ENSMUSG00000073979	7	102534749	102535688	1	1	6	6	5	14	3	0	0	0	0	0	E9PXN3	
ENSMUST00000098230	ENSMUSG00000073982	7	102239123	102250123	-1	0	0	17	47	15	0	14433	16858	7625	1346	6023	Q3UDZ1	P84096
ENSMUST00000098236	ENSMUSG00000064307	7	101912984	101933895	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DAK8
ENSMUST00000098237	ENSMUSG00000030649	7	101881325	101901845	1	9	4	1	9	0	0	9	17	3	9	4	G5E8M3	
ENSMUST00000098238	ENSMUSG00000028248	4	21847583	21876475	1	3	0	5	4	0	0	213	2001	633	597	1037		A2AJT4
ENSMUST00000098239						1	0	10	216	6	8	1	2	9	1	10		
ENSMUST00000098242	ENSMUSG00000073987	4	20042052	20066750	1	5	4	6	29	7	4	142	540	116	211	73		Q9Z0L8
ENSMUST00000098243	ENSMUSG00000032812	7	101348067	101412586	1	10	16	6	0	14	8	338	1012	258	112	67	E9PUB0	
ENSMUST00000098244	ENSMUSG00000073988	4	20007938	20030785	1	0	0	1	0	0	7	0	0	0	2	0	Q499J3	Q8BWP5
ENSMUST00000098250	ENSMUSG00000030691	7	101108775	101284405	1	0	13	0	40	9	6	49	137	75	14	94		Q3USJ8
ENSMUST00000098252	ENSMUSG00000030704	7	100607410	100641268	1	0	0	0	0	0	0	0	0	673	33	642	Q3U4W5	P35279
ENSMUST00000098256	ENSMUSG00000006586	4	13743436	13893649	1	39	14	241	73	21	10	1	0	0	0	0	B1AXH9	Q61909
ENSMUST00000098257	ENSMUSG00000006586	4	13743436	13893649	1	0	0	0	0	0	0	0	0	0	0	0	B1AXH8	
ENSMUST00000098258	ENSMUSG00000025245	9	123694416	123717625	-1	0	3	3	0	0	3	0	0	0	0	0	F6VG18	
ENSMUST00000098259	ENSMUSG00000047248	7	100372233	100470152	1	0	0	0	8	0	0	0	0	0	0	0	E9Q526	
ENSMUST00000098260	ENSMUSG00000073995	4	11979560	11981265	-1	16	15	96	24	22	13	1	2	0	0	2	Q3V0X7	
ENSMUST00000098263	ENSMUSG00000073997	7	99767164	99768130	1	8	5	7	5	7	2	0	0	0	0	0	E9Q519	
ENSMUST00000098264	ENSMUSG00000073998	7	99735145	99736095	1	6	1	12	8	10	0	0	0	0	0	0	E9Q518	
ENSMUST00000098266	ENSMUSG00000018909	7	99535466	99606771	1	34	17	41	3	35	16	1171	1274	1470	79	1513		Q8BWG8
ENSMUST00000098272	ENSMUSG00000074001	9	121777607	121783819	1	15	10	34	182	43	6	0	0	0	0	2		
ENSMUST00000098273	ENSMUSG00000048458	3	105704599	105720842	1	101	42	613	180	58	21	0	7	3	0	1		Q80VY2
ENSMUST00000098274	ENSMUSG00000074003	7	98440416	98477479	1	26	17	43	38	41	23	0	0	0	0	0	F6VFS9	
ENSMUST00000098275	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	3	3	0	0	0	0	0	2	A2AL79	
ENSMUST00000098278	ENSMUSG00000074004	7	98192417	98199481	-1	20	17	61	458	31	16	2	4	2	0	2		Q3USF0
ENSMUST00000098281	ENSMUSG00000074006	7	98143359	98145502	-1	21	9	80	58	30	11	0	0	0	0	1	A2RT14	Q64288
ENSMUST00000098286	ENSMUSG00000094195	5	94623979	94626848	1	10	4	6	0	0	0	0	0	0	0	0	L7N460	
ENSMUST00000098289	ENSMUSG00000074011	5	94445784	94448653	1	0	2	0	3	5	2	0	0	0	0	0	D3YX91	
ENSMUST00000098300	ENSMUSG00000035704	7	97371606	97392185	1	9	5	14	12	11	1	10	33	7	13	27		Q6P8H8
ENSMUST00000098307						0	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000098308	ENSMUSG00000052572	7	91090706	92447003	1	3	0	0	7	16	0	0	0	0	0	0	D3YWU0	
ENSMUST00000098310						0	14	0	4	0	0	0	5	0	0	0		
ENSMUST00000098311	ENSMUSG00000043051	8	125054195	125261858	1	0	0	0	0	0	0	2	0	0	0	0		Q811T9
ENSMUST00000098312	ENSMUSG00000074030	8	124890300	124897705	-1	104	77	221	416	129	51	606	1051	780	59	447		Q6PGF7
ENSMUST00000098320	ENSMUSG00000031967	8	123477903	123503916	1	0	31	0	0	41	15	0	23	0	0	0		Q920A7
ENSMUST00000098324	ENSMUSG00000074037	8	123407107	123410744	1	103	103	295	104	101	64	2	6	1	0	5	A0A0B6VTJ4	Q01727
ENSMUST00000098326	ENSMUSG00000025813	7	81600481	81706925	-1	130	106	539	67	137	82	4	15	6	1	11	E9Q4F9	
ENSMUST00000098327	ENSMUSG00000033594	8	123232255	123236209	-1	10	0	14	30	18	3	103	146	50	12	53	B2RTE8	Q8BNN1
ENSMUST00000098331	ENSMUSG00000025586	7	81347026	81455465	-1	0	0	22	12	0	4	0	0	0	0	0		P70166
ENSMUST00000098333	ENSMUSG00000035569	8	122883337	122974793	-1	12	0	75	76	0	22	40	46	253	0	301	E9Q4F8	
ENSMUST00000098334	ENSMUSG00000035569	8	122883337	122974793	-1	15	42	0	46	68	43	1405	3244	3406	216	3431	E9Q4F7	
ENSMUST00000098340	ENSMUSG00000032497	9	111117592	111225668	1	6	13	11	89	15	8	405	1912	875	466	682		
ENSMUST00000098345	ENSMUSG00000032493	9	110813994	110824523	1	20	16	27	14	26	4	0	0	0	0	0		Q402U7
ENSMUST00000098346	ENSMUSG00000038886	7	80349097	80371375	-1	140	118	490	284	138	83	1259	2074	1874	105	1419	Q197W7	Q8BRK9
ENSMUST00000098350	ENSMUSG00000032485	9	110333288	110384950	1	37	14	85	305	62	27	819	717	803	62	610		Q6GQT6
ENSMUST00000098355	ENSMUSG00000032481	9	110117708	110240178	1	7	12	24	64	23	11	2	8	5	2	6	F6SKR9	
ENSMUST00000098359	ENSMUSG00000074059	9	109676734	109702700	-1	8	11	7	8	11	9	0	0	0	0	0	Q3TSA9	
ENSMUST00000098361	ENSMUSG00000024266	8	119612747	119616926	1	13	8	42	236	34	7	0	0	0	0	0	B2RQL4	
ENSMUST00000098362	ENSMUSG00000031835	8	119508156	119558761	-1	0	0	29	0	29	0	25	168	40	29	137		Q9WTZ2
ENSMUST00000098363	ENSMUSG00000031837	8	119446719	119472640	1	3	0	3	91	15	3	0	0	0	0	0		Q91ZP9
ENSMUST00000098365	ENSMUSG00000074063	8	119434124	119446256	1	0	0	0	0	0	0	0	347	176	61	38	D3YWF1	
ENSMUST00000098367	ENSMUSG00000074064	8	119394878	119411102	1	8	0	0	54	9	0	296	360	219	70	124		Q99J39
ENSMUST00000098368						4	7	14	48	11	4	0	1	0	0	0		
ENSMUST00000098371	ENSMUSG00000025790	7	74275419	74554780	-1	6	8	34	34	8	7	41	160	96	17	155		Q8R3L5
ENSMUST00000098374	ENSMUSG00000020262	10	77290726	77418270	-1	0	40	0	0	80	0	0	0	0	0	51		Q91ZS8
ENSMUST00000098375	ENSMUSG00000034416	8	116995679	117082449	-1	43	35	104	32	62	29	50	19	33	5	25	E9Q4D4	
ENSMUST00000098376	ENSMUSG00000023259	9	108853283	108913049	1	3	7	0	1	5	1	0	0	0	0	0	A0A0A0MQB3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000098379						4	8	7	12	10	4	0	0	0	0	0		
ENSMUST00000098382	ENSMUSG00000058145	7	66839735	67152625	1	21	39	154	507	175	67	2	0	0	0	0	E9Q4D1	
ENSMUST00000098391	ENSMUSG00000030513	7	65861734	66050386	1	22	0	26	3	33	0	0	0	0	0	3	E9Q4D0	
ENSMUST00000098402	ENSMUSG00000102252	7	59982495	60140219	-1	12	0	43	0	17	0	0	0	0	0	0	Q3UN87	P63163
ENSMUST00000098407	ENSMUSG00000053062	16	84774123	84825928	1	385	274	2828	501	442	205	16	28	19	16	18	Q9CWD9	
ENSMUST00000098414	ENSMUSG00000074093	7	51997165	52006018	-1	7	2	3	56	11	1	226	1022	272	451	196		Q3UZP4
ENSMUST00000098432						1	4	0	4	7	3	0	14	3	1	7		
ENSMUST00000098433	ENSMUSG00000074109	7	48478619	48499321	-1	8	9	49	7	11	2	0	0	0	0	0		Q3UG50
ENSMUST00000098436	ENSMUSG00000074111	7	47234861	47252848	-1	11	0	0	8	4	1	0	2	0	0	0	L7N225	
ENSMUST00000098438	ENSMUSG00000050650	7	47334875	47354240	-1	1	4	6	11	5	3	1	3	3	0	1	G3UW97	
ENSMUST00000098441	ENSMUSG00000043719	9	105687809	105828160	-1	83	63	215	139	98	40	0	1	2	2	30		Q8C6K9
ENSMUST00000098443	ENSMUSG00000032564	9	104547286	105034544	1	14	5	5	9	10	1	0	0	0	0	0	Q8CEQ2	
ENSMUST00000098444	ENSMUSG00000005699	8	105701154	105703493	1	16	0	14	11	9	3	71	93	41	21	14	D3Z2R1	
ENSMUST00000098453	ENSMUSG00000014856	8	105326354	105335219	1	1	3	11	5	5	5	12	47	17	5	24		Q9CR96
ENSMUST00000098455						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000098457						40	20	74	44	65	31	16	32	30	4	51		
ENSMUST00000098458	ENSMUSG00000044244	9	100457719	100486788	-1	9	12	15	0	11	2	3	38	7	13	23	E9Q9A6	
ENSMUST00000098460	ENSMUSG00000074123	9	98903119	98904622	1	8	8	35	15	12	4	0	0	0	0	0	Q3UX66	
ENSMUST00000098461	ENSMUSG00000030798	7	45233632	45239115	-1	0	2	0	0	0	0	5916	6306	3274	563	1986	Q4FK35	Q61470
ENSMUST00000098464	ENSMUSG00000054400	8	104250903	104264936	1	18	16	90	31	35	17	23	87	74	14	71		Q9DAS1
ENSMUST00000098470	ENSMUSG00000031134	X	57383530	57393036	-1	4	3	71	6	5	11	21	78	45	3	34	A2AFI3	
ENSMUST00000098473	ENSMUSG00000036550	8	95719451	95807462	-1	0	1	2	79	0	0	1247	2508	2703	65	1546		Q6ZQ08
ENSMUST00000098477	ENSMUSG00000074139	9	92309377	92357876	1	0	0	0	0	0	0	0	0	0	0	0	Q3V0U0	
ENSMUST00000098478	ENSMUSG00000002963	7	44857139	44862992	1	0	0	0	0	0	0	2218	2042	1349	285	590	E9Q9A5	
ENSMUST00000098480	ENSMUSG00000090206	8	95310566	95326323	1	4	1	14	10	5	0	0	0	0	0	0		Q6IMH0
ENSMUST00000098483	ENSMUSG00000008193	7	44525993	44532071	-1	0	0	0	0	75	39	0	0	10	0	61		O35906
ENSMUST00000098485	ENSMUSG00000102037	9	88956900	88962419	1	0	2	2	5	2	3	6	31	20	58	20		Q07440
ENSMUST00000098486	ENSMUSG00000099974	9	88723285	88731914	-1	9	5	13	0	11	4	10	17	6	140	26	O55179	
ENSMUST00000098489	ENSMUSG00000074151	8	94472763	94527272	1	7	3	0	12	0	1	0	63	0	47	0	Q3U1H4	
ENSMUST00000098495	ENSMUSG00000033419	9	86765923	86880654	-1	7	3	0	8	0	2	0	0	0	0	0	E9Q9A3	
ENSMUST00000098496	ENSMUSG00000078161	3	154663859	154767790	1	45	34	86	88	61	21	0	0	0	0	1	F6QRE9	
ENSMUST00000098500	ENSMUSG00000035274	9	85842380	85847040	1	0	0	0	318	0	9	2	0	2	7	19		Q9Z0L0
ENSMUST00000098503	ENSMUSG00000074158	7	42609526	42642588	-1	0	0	0	0	1	0	0	0	0	0	0	E9Q981	
ENSMUST00000098508	ENSMUSG00000074165	7	41633203	41651530	1	26	14	189	39	24	18	0	13	0	4	10	E9Q980	
ENSMUST00000098509	ENSMUSG00000074166	7	41478874	41499890	-1	9	17	20	10	24	10	17	104	26	44	19	Q3TPQ7	
ENSMUST00000098513	ENSMUSG00000074170	7	38216972	38228016	-1	32	18	49	113	26	18	53	77	57	10	62		Q3TB82
ENSMUST00000098517	ENSMUSG00000074171	8	90907939	90908415	-1	3	0	1	81	2	0	0	0	0	0	0	Q3UQR9	
ENSMUST00000098518						15	8	40	228	14	4	0	0	2	0	2		
ENSMUST00000098519	ENSMUSG00000036712	8	88697028	88751945	1	0	19	24	0	24	13	0	43	0	0	0		Q80TQ2
ENSMUST00000098521	ENSMUSG00000031659	8	88272403	88329962	1	29	15	15	0	0	0	590	738	1153	112	986		P51829
ENSMUST00000098524	ENSMUSG00000011008	3	146149833	146195513	1	4	5	7	52	13	3	0	8	5	25	0		Q8K595
ENSMUST00000098532	ENSMUSG00000074178	8	86745699	86746603	1	6	0	13	134	5	9	1	5	2	2	2	F6QEG2	
ENSMUST00000098534	ENSMUSG00000074182	3	145576205	145604795	1	37	34	80	67	54	19	3	47	9	55	25		Q3UFB2
ENSMUST00000098537	ENSMUSG00000074183	9	78230656	78242684	1	14	0	2	3	16	4	0	0	0	0	0		P13745
ENSMUST00000098538	ENSMUSG00000028256	3	145118588	145153915	1	0	3	0	9	5	0	0	5	16	9	0		Q9D478
ENSMUST00000098539	ENSMUSG00000028256	3	145118588	145153915	1	3	5	9	0	2	0	5	0	0	0	23		Q9D478
ENSMUST00000098545	ENSMUSG00000019437	11	78176711	78181909	1	20	14	26	270	34	14	16	98	17	3	41		Q99JT6
ENSMUST00000098546	ENSMUSG00000032358	9	76490054	76567116	-1	16	25	54	0	15	0	0	0	0	0	0		Q0VBM2
ENSMUST00000098548	ENSMUSG00000019194	7	31116525	31126945	-1	0	0	0	33	0	0	8	0	0	0	10		P97952
ENSMUST00000098549	ENSMUSG00000074195	3	144910921	144932529	-1	14	10	23	8	13	8	0	0	0	0	0	Q3UW98	
ENSMUST00000098550	ENSMUSG00000074194	8	85109647	85119637	-1	9	7	20	10	14	5	0	2	1	33	10	Q497V9	
ENSMUST00000098551						21	12	17	24	31	14	0	0	1	0	1		
ENSMUST00000098552	ENSMUSG00000032186	9	75565621	75611325	-1	95	97	71	0	69	72	0	0	0	0	0		Q9JKK7
ENSMUST00000098553	ENSMUSG00000001247	7	30957770	30973464	-1	0	2	0	0	0	0	0	60	0	14	0		Q99KG5
ENSMUST00000098559	ENSMUSG00000074199	7	30787896	30791097	1	0	0	0	0	0	0	0	0	0	0	0		Q3V2T4
ENSMUST00000098564						32	18	101	45	18	10	6	49	7	3	6		
ENSMUST00000098566	ENSMUSG00000079469	9	73007419	73040378	-1	0	0	0	60	0	0	0	0	0	0	0		Q9JJQ0
ENSMUST00000098567	ENSMUSG00000092192	9	72958785	72973064	1	0	0	0	57	13	9	4	27	0	8	4	E9Q973	
ENSMUST00000098568	ENSMUSG00000052430	3	141837136	142169425	-1	0	0	0	0	0	3	0	0	0	0	0	B2RRZ4	P36898
ENSMUST00000098571	ENSMUSG00000074203	8	84723007	84726844	1	10	4	18	13	8	2	13	31	10	59	15	E9Q913	
ENSMUST00000098574	ENSMUSG00000028149	3	138925902	139075201	-1	0	8	13	0	18	10	862	1208	1235	133	886	E9Q912	
ENSMUST00000098576	ENSMUSG00000038535	9	72274860	72363777	1	0	0	0	0	0	0	0	24	0	19	0		Q68FE8
ENSMUST00000098578	ENSMUSG00000004994	8	84257795	84270380	-1	17	10	26	38	14	7	8	41	13	10	7		Q9D516
ENSMUST00000098580	ENSMUSG00000028158	3	138089854	138144968	-1	13	16	4	0	31	6	0	64	40	14	26		O08601
ENSMUST00000098585	ENSMUSG00000074210	7	30321740	30323472	1	0	0	0	64	0	0	0	0	0	0	0	Q3UPV3	
ENSMUST00000098586	ENSMUSG00000074211	7	30321406	30323895	-1	32	18	46	50	25	18	58	150	48	60	59		Q3U276
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ENSMUST00000098592	ENSMUSG00000074215	8	84063561	84065137	-1	10	10	42	12	15	13	8	22	14	1	10	Q3URG9	
ENSMUST00000098594	ENSMUSG00000074218	7	30184171	30186028	1	4	4	9	3	6	2	9	11	6	20	8	Q792A4	P56392
ENSMUST00000098595	ENSMUSG00000074219	8	83932329	83955205	-1	25	24	62	33	31	13	2	2	1	1	0	Q3TZG3	
ENSMUST00000098596	ENSMUSG00000074220	7	30121942	30134665	1	6	7	29	27	20	8	11	21	21	10	23		B2RXC5
ENSMUST00000098602	ENSMUSG00000074224	7	29519205	29538057	1	0	0	0	0	0	0	0	0	0	0	0	Q3V0H8	
ENSMUST00000098603	ENSMUSG00000040943	3	133463679	133545139	-1	53	51	271	92	89	34	681	1910	1828	210	1935		Q4JK59
ENSMUST00000098604	ENSMUSG00000074227	7	29256331	29281977	-1	8	9	8	0	8	0	27	38	5	0	0		Q9WU03
ENSMUST00000098605	ENSMUSG00000074228	8	83165081	83166170	-1	6	9	3	205	6	4	1	0	4	0	0	Q3UPY1	
ENSMUST00000098609	ENSMUSG00000031493	7	29170220	29173933	1	28	16	111	1368	58	31	6	5	3	0	4	G5E8M4	
ENSMUST00000098611	ENSMUSG00000027985	3	131110471	131224356	1	0	0	0	0	0	0	57	89	26	13	75	Q8C402	
ENSMUST00000098612	ENSMUSG00000074232	9	66797039	66799074	1	27	29	28	20	26	13	2	7	1	1	2	E9Q8X0	
ENSMUST00000098613	ENSMUSG00000032376	9	66514637	66593142	-1	0	0	0	0	0	0	55	26	2	20	0	E9Q8W9	
ENSMUST00000098614	ENSMUSG00000071064	8	79028437	79193766	1	20	29	50	27	40	27	0	0	0	0	13		Q505G8
ENSMUST00000098624						14	4	24	8	11	7	0	0	0	0	0		
ENSMUST00000098625						6	8	19	50	15	7	0	0	0	0	0		
ENSMUST00000098630	ENSMUSG00000074240	8	72204335	72212837	-1	8	6	10	2	11	1	0	2	0	1	15		Q0P523
ENSMUST00000098634	ENSMUSG00000078384	7	28099660	28102487	-1	23	27	92	106	60	22	0	0	1	0	0	E9Q8W4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000098639	ENSMUSG00000070709	7	27907392	27929460	-1	23	13	11	12	12	9	7	12	6	6	10	Q3UVF6	
ENSMUST00000098644	ENSMUSG00000053198	7	27499324	27520214	1	0	0	33	0	0	18	0	14	8	0	4	E9QQ57	
ENSMUST00000098645						2	0	0	18	0	0	21	10	37	0	27		
ENSMUST00000098646	ENSMUSG00000074248	3	121670762	121682982	1	1	1	5	3	2	1	0	0	0	0	0	Q3V0W9	
ENSMUST00000098650						11	11	15	9	15	7	0	0	0	2	0		
ENSMUST00000098651	ENSMUSG00000032405	9	62880077	62980879	-1	19	11	50	35	18	8	437	1444	671	842	588	Q2M4G9	O88907
ENSMUST00000098653	ENSMUSG00000074252	8	70931405	70933037	1	13	14	37	15	30	7	1	0	1	0	1	Q3USN8	
ENSMUST00000098657	ENSMUSG00000074254	7	26307169	26315088	1	8	5	18	10	10	5	0	0	0	0	0		P15392
ENSMUST00000098660	ENSMUSG00000032289	9	59966931	60522046	-1	89	32	160	123	118	32	0	0	0	0	0		Q3UTY6
ENSMUST00000098661	ENSMUSG00000074259	9	59680144	59718874	1	11	5	3	3	4	4	10	4	0	8	6		Q3V3G7
ENSMUST00000098663	ENSMUSG00000074261	7	25614620	25615892	-1	4	5	11	12	8	6	1	0	1	0	0	G5E8M5	
ENSMUST00000098666	ENSMUSG00000074272	7	25461707	25477603	-1	50	8	0	41	26	0	2289	4881	3198	312	1911		P31809
ENSMUST00000098667	ENSMUSG00000096569	3	113345055	113356658	-1	3	6	4	1	2	2	0	0	0	0	0		P00688
ENSMUST00000098668	ENSMUSG00000074272	7	25461707	25477603	-1	43	58	544	20	27	12	887	3835	1457	405	663	Q3LFS9	
ENSMUST00000098669	ENSMUSG00000074272	7	25461707	25477603	-1	0	5	83	61	38	37	33	0	73	0	383	Q925P3	
ENSMUST00000098673	ENSMUSG00000074268	3	113247178	113258837	-1	3	6	4	1	2	2	0	0	0	0	0		P00688
ENSMUST00000098674	ENSMUSG00000074269	9	58652850	58743964	-1	3	0	15	11	10	1	0	0	0	0	0		Q9CWH4
ENSMUST00000098679	ENSMUSG00000008496	7	25087344	25159922	-1	0	0	3	20	15	5	0	4	2	0	10		Q00196
ENSMUST00000098680	ENSMUSG00000045662	3	108939873	108960774	1	4	0	0	11	0	0	0	0	2	0	0	A2AED5	
ENSMUST00000098681	ENSMUSG00000037716	9	58028677	58118823	-1	5	0	6	7	9	2	0	0	0	0	0		Q3ULW6
ENSMUST00000098682	ENSMUSG00000037716	9	58028677	58118823	-1	17	14	30	16	30	0	0	0	0	0	0	E9QQ55	
ENSMUST00000098683	ENSMUSG00000040940	7	24902912	24926594	1	0	0	0	0	0	0	2839	4091	4197	301	1931		Q61210
ENSMUST00000098686	ENSMUSG00000004661	9	57790353	57836793	-1	0	0	0	30	6	0	73	25	95	5	45	F8WIN2	
ENSMUST00000098689						6	4	1	10	2	2	139	543	94	393	87		
ENSMUST00000098696	ENSMUSG00000030465	8	67689082	68062286	-1	31	16	26	4	41	16	0	3	0	0	3		Q2PFD7
ENSMUST00000098704	ENSMUSG00000074291	7	23540720	23541649	1	0	1	0	4	1	0	0	0	0	0	0	K7N6B6	
ENSMUST00000098708	ENSMUSG00000036469	8	65617900	66471637	1	0	0	0	0	0	0	0	0	0	0	0		Q6NZQ8
ENSMUST00000098716	ENSMUSG00000074302	8	65075033	65077480	1	0	0	0	0	0	0	0	0	0	0	0	F6RZ85	
ENSMUST00000098720	ENSMUSG00000096871	7	22463110	22464075	-1	1	0	0	0	0	0	0	0	0	0	0	K7N6B7	
ENSMUST00000098722	ENSMUSG00000096348	7	22133776	22134741	-1	0	0	0	2	1	0	0	0	0	0	0	K7N6B8	
ENSMUST00000098736	ENSMUSG00000074322	7	21614092	21614985	1	0	0	0	0	0	0	0	0	0	0	0	E9Q8L6	
ENSMUST00000098737	ENSMUSG00000094085	7	20811221	20812186	-1	0	0	0	2	1	0	0	0	0	0	0	L7N226	
ENSMUST00000098739	ENSMUSG00000095309	7	21272179	21273102	1	0	0	0	0	0	0	0	0	0	0	0	L7N227	
ENSMUST00000098744	ENSMUSG00000094762	7	20473960	20474925	-1	1	0	0	0	0	0	0	0	0	0	0	K7N6B7	
ENSMUST00000098747	ENSMUSG00000096164	7	20138123	20139088	-1	0	0	0	2	1	0	0	0	0	0	0	K7N6B8	
ENSMUST00000098750	ENSMUSG00000056260	3	106684987	106736577	1	0	0	0	0	0	0	82	383	98	65	48		Q8CDD9
ENSMUST00000098751	ENSMUSG00000056260	3	106684987	106736577	1	2	1	0	0	8	1	0	33	17	0	0	G3X9P5	
ENSMUST00000098754	ENSMUSG00000002983	7	19606217	19629438	-1	0	0	0	0	0	0	24	335	183	4	150		Q04863
ENSMUST00000098757	ENSMUSG00000096914	8	57774052	58912640	-1	11	16	13	7	18	7	0	0	0	0	1	F6RYQ3	
ENSMUST00000098758	ENSMUSG00000074342	3	105924358	105932664	-1	4	7	20	3	13	4	474	2121	817	751	667		Q3U7U4
ENSMUST00000098760	ENSMUSG00000074345	9	54025606	54068411	-1	9	10	10	65	11	3	2	1	0	0	0		Q3TBL6
ENSMUST00000098761	ENSMUSG00000040896	3	105452330	105674002	1	25	28	34	60	52	23	0	0	0	0	0	Q3UH54	Q9Z0V1
ENSMUST00000098763	ENSMUSG00000062127	3	105001915	105053146	-1	24	22	0	28	11	7	24	115	41	22	129		Q99LJ0
ENSMUST00000098768	ENSMUSG00000078307	9	52673044	52679429	-1	23	21	52	69	27	12	0	1	0	0	0		Q32M26
ENSMUST00000098773						0	3	1	68	19	2	0	0	1	6	0		
ENSMUST00000098778						13	13	26	141	18	11	9	34	16	2	17		
ENSMUST00000098780	ENSMUSG00000074358	7	18890883	18910415	-1	8	0	18	193	25	0	54	88	70	15	90		Q3UJV1
ENSMUST00000098781	ENSMUSG00000074357	8	47675391	47677055	1	23	21	149	193	39	22	4	7	6	1	7	F6RUV8	
ENSMUST00000098782	ENSMUSG00000060594	9	51056780	51077094	-1	12	10	16	114	15	10	6	11	5	8	15		Q8C351
ENSMUST00000098783	ENSMUSG00000003505	7	18345422	18355009	-1	13	12	16	11	14	7	0	0	0	0	0	E9Q8L0	
ENSMUST00000098786	ENSMUSG00000071103	8	45953606	45975252	-1	0	1	0	0	0	0	0	2	0	3	2		Q3U1D9
ENSMUST00000098789	ENSMUSG00000059273	7	16401196	16437694	1	34	35	118	271	76	19	1354	1651	2009	84	1378	E9Q8K8	
ENSMUST00000098792	ENSMUSG00000074361	7	16234585	16244154	-1	111	82	649	127	58	14	288	1330	612	40	328	E9QQ21	
ENSMUST00000098796	ENSMUSG00000070047	8	44935447	45052257	1	5	6	38	0	72	64	0	0	0	3	113	F2Z4A3	
ENSMUST00000098799	ENSMUSG00000074364	7	15946977	15967567	-1	48	38	82	161	52	28	11	16	6	66	250		Q8BH64
ENSMUST00000098801	ENSMUSG00000074365	7	15882617	15904020	1	15	25	6	5	25	14	0	0	1	0	0	Q3UL53	
ENSMUST00000098802	ENSMUSG00000074366	7	15750131	15759800	1	9	4	10	5	12	12	0	0	0	0	0	G3X9P6	
ENSMUST00000098809	ENSMUSG00000074375	7	14067452	14123044	-1	1	1	2	2	3	0	0	0	0	0	0	D3Z1W5	
ENSMUST00000098811	ENSMUSG00000074378	7	13450841	13473449	1	2	1	0	6	0	2	0	0	0	0	0		Q3UW26
ENSMUST00000098814	ENSMUSG00000056394	7	13277283	13311433	1	0	0	4	14	0	0	262	216	285	0	159	Q3U4X8	
ENSMUST00000098816	ENSMUSG00000031596	8	40862396	40922308	1	0	0	0	7	0	0	0	0	0	0	1		P18581
ENSMUST00000098817	ENSMUSG00000031600	8	40511783	40551134	1	94	62	413	374	63	27	179	781	324	77	277		Q8CHS8
ENSMUST00000098822	ENSMUSG00000030386	7	12478293	12496235	1	11	9	10	42	17	7	0	7	0	13	0	Q7TSV0	
ENSMUST00000098825	ENSMUSG00000074384	8	36993575	36995531	1	9	12	39	18	19	13	8	74	23	79	25		Q3TTJ4
ENSMUST00000098826	ENSMUSG00000031523	8	36567751	36953143	-1	67	0	117	303	55	0	0	0	0	0	0		
ENSMUST00000098827	ENSMUSG00000074385	9	45107176	45135606	-1	12	2	26	20	19	6	1	36	3	0	11	Q3V379	
ENSMUST00000098837	ENSMUSG00000074397	9	44434234	44440868	-1	47	28	56	64	29	19	4	11	3	3	12		Q3UTB7
ENSMUST00000098841	ENSMUSG00000046317	3	96433788	96452306	-1	1	6	0	11	0	6	2	5	1	0	2	Q3KNB6	
ENSMUST00000098842	ENSMUSG00000031577	8	31150316	31164702	1	56	54	114	130	55	15	118	381	158	43	143		Q8BGV4
ENSMUST00000098843	ENSMUSG00000074403	3	96268654	96269141	1	6	3	3	299	15	4	0	0	0	5	0	B9EI85	P84228
ENSMUST00000098844	ENSMUSG00000074402	7	5146218	5147501	-1	12	3	14	3	6	5	0	0	0	0	0	E9Q8I6	
ENSMUST00000098845	ENSMUSG00000035203	7	5080235	5098178	1	20	11	29	58	31	3	2854	2373	2180	230	2383		Q80VP1
ENSMUST00000098849	ENSMUSG00000038495	3	96104527	96161129	1	53	17	0	0	83	27	0	243	44	0	0		B2RUR8
ENSMUST00000098851	ENSMUSG00000031485	8	27042555	27056131	1	11	8	9	172	11	2	3	28	35	3	21	Q80ZV3	
ENSMUST00000098852	ENSMUSG00000032135	9	44134469	44142727	1	19	8	36	26	30	15	414	460	378	90	206		Q8R2Y2
ENSMUST00000098853	ENSMUSG00000059851	7	4740115	4747514	1	5	0	0	38	3	0	36	0	0	0	38		Q6Q783
ENSMUST00000098857	ENSMUSG00000028107	3	95739976	95760206	-1	28	20	53	45	40	11	13	26	22	4	38	Q3TP97	
ENSMUST00000098858	ENSMUSG00000031576	8	25849623	25937933	1	20	17	18	12	18	12	0	0	0	0	1	G3X9P7	
ENSMUST00000098859	ENSMUSG00000035458	7	4518305	4524229	-1	7	0	9	5	0	1	0	7	3	0	0	Q497F1	P48787
ENSMUST00000098861	ENSMUSG00000046519	3	95588934	95619247	1	0	0	0	0	1	0	0	0	0	0	0	K3W4Q3	
ENSMUST00000098862	ENSMUSG00000024121	17	24163866	24169702	-1	0	0	0	0	2	3	11	17	12	34	8	A3KML5	P63082
ENSMUST00000098864						1	3	2	3	3	0	2	0	3	14	1		
ENSMUST00000098866	ENSMUSG00000031557	8	25039144	25102194	-1	0	2	4	21	5	3	12	10	36	3	78	F8WIK5	
ENSMUST00000098871	ENSMUSG00000028115	3	95241271	95251193	-1	1	3	0	0	3	0	0	2	2	2	0	E9Q8I3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000098873	ENSMUSG00000038766	3	95181766	95217916	-1	46	45	95	0	56	16	0	907	15	0	398		P81069
ENSMUST00000098874	ENSMUSG00000096463	14	73661225	73662721	1	5119	5039	62996	7581	4125	1990	51	166	107	28	78	L7N228	
ENSMUST00000098878	ENSMUSG00000089696	3	94264036	94266784	1	0	0	0	1	3	0	0	0	0	0	0	L7N229	
ENSMUST00000098879	ENSMUSG00000094163	3	93960292	93961314	-1	4	6	11	6	4	0	0	0	0	0	0	E0CYU8	
ENSMUST00000098884	ENSMUSG00000049133	3	93197278	93221391	1	119	73	155	152	147	70	0	0	0	1	0	E9QPZ3	
ENSMUST00000098886	ENSMUSG00000074433	3	92967061	92968281	1	2	5	3	0	2	2	0	0	0	0	0	F8VQJ0	
ENSMUST00000098887	ENSMUSG00000074434	8	21583027	21583961	1	0	0	0	0	0	0	0	0	0	0	0	D3Z1V9	
ENSMUST00000098888	ENSMUSG00000074435	3	92583867	92588997	-1	0	5	0	0	0	2	0	0	0	0	0		P15265
ENSMUST00000098889						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000098890	ENSMUSG00000074437	8	21325887	21327020	-1	6	4	14	8	3	4	0	0	0	0	0	Q9D815	
ENSMUST00000098892	ENSMUSG00000074439	8	21297439	21298375	1	0	0	1	0	2	0	0	0	0	0	0	L7N230	
ENSMUST00000098893	ENSMUSG00000074440	8	21287409	21288377	1	0	0	0	2	0	0	0	0	0	0	0		P28310
ENSMUST00000098895	ENSMUSG00000074441	8	21249754	21250556	1	9	0	0	0	4	1	0	0	0	0	0	L7N231	
ENSMUST00000098896	ENSMUSG00000074442	8	21191614	21192549	1	1	1	3	0	0	0	0	0	0	0	0		Q5G866
ENSMUST00000098897	ENSMUSG00000074443	8	21162277	21163249	1	0	0	0	0	0	0	0	0	0	0	0	W4VSN6	
ENSMUST00000098898	ENSMUSG00000074444	8	21134642	21135598	1	0	0	8	7	2	4	0	0	0	0	0	E9QPZ2	
ENSMUST00000098899	ENSMUSG00000074446	8	21055047	21056016	1	0	0	0	0	0	0	0	0	0	0	0		Q5G866
ENSMUST00000098900	ENSMUSG00000074448	9	36532397	36541963	-1	108	81	542	148	64	32	5	18	5	0	4	Q3UW02	
ENSMUST00000098906	ENSMUSG00000074452	9	35570284	35690318	1	4	4	1	72	10	2	0	2	0	1	0	D3Z1P9	
ENSMUST00000098908	ENSMUSG00000074454	8	20892669	20897723	1	5	0	2	1	4	3	0	0	0	0	0		Q30KN3
ENSMUST00000098909	ENSMUSG00000096265	8	19729746	19752236	1	17	50	109	27	91	54	0	0	0	0	0	D3Z1P8	
ENSMUST00000098910	ENSMUSG00000074457	3	90537254	90543151	1	0	0	23	2	9	5	0	0	0	0	0	Q9D708	
ENSMUST00000098911	ENSMUSG00000074457	3	90537254	90543151	1	6	0	17	25	0	0	0	0	0	28	11	Q9D708	
ENSMUST00000098914	ENSMUSG00000042404	3	90265185	90280669	1	33	20	54	5	28	12	1507	2049	1474	85	1412		
ENSMUST00000098916	ENSMUSG00000074461	8	14090461	14092590	1	179	163	388	145	201	74	8	14	18	10	27	Q3UYL4	
ENSMUST00000098924	ENSMUSG00000027951	3	89715022	89753446	1	31	0	24	89	57	0	0	0	0	0	0		Q99MU3
ENSMUST00000098927	ENSMUSG00000031442	8	12873806	13020905	1	0	0	5	12	5	0	0	0	0	0	0	E9Q863	
ENSMUST00000098929						4	2	10	18	9	6	2	6	4	0	3		
ENSMUST00000098935	ENSMUSG00000074473	8	12278819	12280657	1	8	11	26	17	16	13	0	0	0	0	0	Q3UUJ8	
ENSMUST00000098937	ENSMUSG00000066839	9	22072246	22085438	-1	7	0	11	0	13	0	0	35	9	4	41		
ENSMUST00000098938	ENSMUSG00000031511	8	11728105	11835219	1	0	0	0	19	0	0	0	0	6	0	0		Q9ES28
ENSMUST00000098941	ENSMUSG00000028049	3	89177473	89182765	1	7	0	0	0	2	0	0	0	0	0	28	E9Q855	
ENSMUST00000098942	ENSMUSG00000074476	9	21755442	21760286	-1	282	265	286	249	188	84	73	106	88	27	51		Q9D083
ENSMUST00000098948	ENSMUSG00000032187	9	21616169	21704230	1	2	2	5	0	30	2	100	230	138	0	143		
ENSMUST00000098949	ENSMUSG00000023235	8	4325210	4360020	1	14	4	21	7	9	5	0	0	0	4	3	Q3U4J3	
ENSMUST00000098950	ENSMUSG00000040028	8	4284782	4325100	-1	24	27	50	35	18	12	499	1007	551	112	441		P70372
ENSMUST00000098952						2	6	3	1	6	1	0	0	0	0	0		
ENSMUST00000098956	ENSMUSG00000074486	3	88377736	88378699	-1	4	0	7	0	0	0	0	0	0	0	0		P86547
ENSMUST00000098958						2	4	18	3	5	3	0	0	0	0	0		
ENSMUST00000098966	ENSMUSG00000074497	8	3353415	3390295	1	600	574	418	212	434	163	572	559	824	59	695	E9Q7Y4	
ENSMUST00000098970						1	0	6	34	0	0	36	46	75	67	44		
ENSMUST00000098971	ENSMUSG00000038685	2	181319739	181356616	1	0	0	0	0	21	0	24	21	51	0	32		Q0VGM9
ENSMUST00000098973	ENSMUSG00000074502	9	18404418	18411502	1	0	0	0	0	0	0	0	0	0	0	0		Q3USZ2
ENSMUST00000098979	ENSMUSG00000046111	9	15316915	15357788	-1	20	21	0	50	26	16	0	0	8	33	75	E9QPW4	
ENSMUST00000098980						0	0	0	0	0	8	196	874	322	767	79		
ENSMUST00000098986	ENSMUSG00000031870	9	8899833	8968611	1	2	2	11	178	0	1	0	0	0	0	0	E9QPW3	
ENSMUST00000098990	ENSMUSG00000074513	3	84496093	84582625	-1	4	3	24	4	9	6	526	2064	551	517	432	A2RSX9	
ENSMUST00000098994	ENSMUSG00000074516	9	7751672	7752325	1	46	28	401	25	86	34	197	300	100	269	132	D3Z1N9	
ENSMUST00000098996	ENSMUSG00000000305	2	179442431	179899373	1	0	0	1	0	0	0	0	0	0	0	0	F6QV10	
ENSMUST00000098997	ENSMUSG00000028004	3	82538383	82548084	-1	10	0	0	0	0	2	0	0	0	0	0		P97295
ENSMUST00000098998	ENSMUSG00000078901	2	175275125	175286805	1	0	0	0	0	0	0	0	0	0	0	0	F7CJN1	
ENSMUST00000099001	ENSMUSG00000074521	2	177897096	177905784	1	0	0	0	0	0	0	0	0	0	0	0	F6QUW6	
ENSMUST00000099002	ENSMUSG00000078866	2	177464733	177478129	1	327	321	726	398	428	233	89	284	182	116	162	B1AYE1	
ENSMUST00000099007	ENSMUSG00000074527	2	176892509	176927809	-1	168	144	244	139	194	119	22	84	58	48	48	A2ARL4	
ENSMUST00000099009	ENSMUSG00000078894	2	176226569	176240328	1	168	144	244	139	194	119	22	84	58	48	48	A2ARL4	
ENSMUST00000099028	ENSMUSG00000078903	2	175191065	175206917	-1	7	3	9	0	9	6	0	4	3	16	6	A2ARX2	
ENSMUST00000099029	ENSMUSG00000090093	2	175129493	175142012	-1	0	0	0	0	0	0	0	5	0	8	0	F6QHQ5	
ENSMUST00000099042	ENSMUSG00000095891	9	3025417	3033289	1	2111	2248	3474	2622	2320	1703	0	2	2	0	0	F6QHK0	
ENSMUST00000099046	ENSMUSG00000095186	9	3023547	3025218	1	156004	202643	110327	75338	151624	97237	30	22	10	29	25	D3Z1I7	
ENSMUST00000099047	ENSMUSG00000095547	9	3017408	3021593	1	73026	66836	87388	68889	80669	52863	0	46	21	16	6	E9Q7T3	
ENSMUST00000099049	ENSMUSG00000095547	9	3017408	3021593	1	46446	45398	71642	39087	43842	28048	11	11	2	4	3	D3Z1I6	
ENSMUST00000099050	ENSMUSG00000074564	9	3015654	3017210	1	4276	5085	4449	3603	5459	4173	0	8	0	0	0	D3Z1I5	
ENSMUST00000099051	ENSMUSG00000095891	9	3025417	3033289	1	909	807	846	792	1008	757	0	0	0	0	0	F6QDW5	
ENSMUST00000099056	ENSMUSG00000095891	9	3025417	3033289	1	4537	4932	6139	4389	5044	3443	0	0	4	0	1	D3Z1I4	
ENSMUST00000099058	ENSMUSG00000028640	2	172549593	172558622	1	15	11	13	193	25	7	0	0	0	0	0	A2APA8	
ENSMUST00000099060	ENSMUSG00000074569	2	172450313	172458596	-1	45	27	46	38	51	26	14	4	25	0	29	F8WK01	Q3V3K7
ENSMUST00000099061	ENSMUSG00000074570	2	172393794	172433757	1	52	54	94	61	82	43	4	14	5	3	26		Q08EC4
ENSMUST00000099067						9	0	29	0	0	7	0	0	2	0	0		
ENSMUST00000099069	ENSMUSG00000074575	2	168260117	168281736	-1	10	7	35	64	6	9	0	0	0	0	2	B2RVK9	A2BDX4
ENSMUST00000099070	ENSMUSG00000001911	8	84699876	84800344	-1	0	0	0	0	0	0	0	0	0	0	0		P70257
ENSMUST00000099071	ENSMUSG00000074576	2	168230622	168232594	1	3	2	14	312	12	6	70	147	51	24	45		A2BDX3
ENSMUST00000099072	ENSMUSG00000078919	2	168209048	168230591	-1	0	0	0	0	0	0	9	159	14	105	7	F8WII3	
ENSMUST00000099073	ENSMUSG00000074577	2	167980164	168010618	-1	0	0	99	0	0	18	0	0	0	0	0		A1L3T7
ENSMUST00000099075	ENSMUSG00000074579	3	65666228	65831159	1	3	3	5	10	3	2	2	9	2	8	4	B2RVN1	
ENSMUST00000099076						0	0	0	329	0	0	10	40	12	0	10		
ENSMUST00000099078	ENSMUSG00000074582	2	166805588	166898052	1	46	52	72	86	58	23	734	1061	1473	95	895		A2A5R2
ENSMUST00000099080	ENSMUSG00000039621	2	166566342	166713832	-1	22	11	63	39	33	17	549	0	280	0	2	I7HPV9	
ENSMUST00000099084	ENSMUSG00000039671	2	165784152	165899016	-1	14	16	10	72	29	0	54	117	89	0	142	A2A482	
ENSMUST00000099086						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000099087	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	29	0	0	269	597	533	411	597	G3X9Q0	
ENSMUST00000099090	ENSMUSG00000027806	3	58414715	58466783	1	29	22	61	1004	65	30	193	528	366	47	297	E9Q7M2	
ENSMUST00000099091	ENSMUSG00000074591	3	57657393	57692799	-1	56	40	319	62	44	14	3	11	2	4	4		Q3UUE9
ENSMUST00000099092	ENSMUSG00000017740	2	164960802	164999731	1	37	26	83	343	92	43	78	195	164	14	218	A0A076FSX1	Q91V14
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ENSMUST00000099095	ENSMUSG00000074594	2	164649631	164656583	-1	0	0	0	3	0	0	0	0	0	0	0		Q3UW41
ENSMUST00000099096	ENSMUSG00000074595	2	164579519	164585447	-1	5	0	10	7	0	4	0	0	0	0	0		Q3UW55
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ENSMUST00000099105	ENSMUSG00000035268	2	163658386	163726158	1	0	0	3	0	0	4	0	9	14	22	23	Q3TP50	O70139
ENSMUST00000099106	ENSMUSG00000074604	3	51660360	51682677	1	0	0	0	0	0	0	266	951	192	627	97	A2RST1	
ENSMUST00000099110	ENSMUSG00000074607	2	163203125	163324170	1	0	3	6	18	6	7	0	1	0	0	0	A2A472	
ENSMUST00000099111	ENSMUSG00000096916	7	27984854	28014115	-1	0	0	11	1	0	1	0	0	0	0	1	Q05CJ1	
ENSMUST00000099112	ENSMUSG00000025348	10	128933813	128958277	1	47	22	98	72	62	31	8	6	3	9	16	G3X9Q1	
ENSMUST00000099113	ENSMUSG00000037902	2	129592835	129632228	1	0	0	0	152	0	0	0	1741	30	36	31	E9QPT7	
ENSMUST00000099118	ENSMUSG00000048930	6	113366025	113377883	-1	0	2	0	0	0	1	39	17	0	2	8		
ENSMUST00000099121	ENSMUSG00000025762	3	40950354	41040234	1	0	0	0	0	0	0	0	0	0	0	3	Q9D423	
ENSMUST00000099123	ENSMUSG00000074619	3	40900196	40902543	-1	19	18	44	28	27	7	1	2	1	0	1	Q9D9Q3	
ENSMUST00000099126	ENSMUSG00000074622	2	160363703	160367065	-1	46	37	338	647	69	26	76	205	89	57	424		P54841
ENSMUST00000099127	ENSMUSG00000074623	2	160311393	160334162	-1	7	1	4	9	6	9	0	0	0	0	0	Q3UQ74	
ENSMUST00000099128	ENSMUSG00000058174	3	37714190	37724490	-1	15	8	74	25	14	0	0	0	0	3	0	Q8BGG2	
ENSMUST00000099130	ENSMUSG00000050174	3	37404910	37420211	-1	0	1	0	0	6	5	4	5	0	8	12		
ENSMUST00000099131	ENSMUSG00000025369	10	128459236	128490173	1	7	0	40	0	25	17	50	246	29	17	280	Q3UID0	
ENSMUST00000099133	ENSMUSG00000074625	2	158512796	158550762	1	16	15	36	36	31	0	0	0	0	0	0	A0A0A0MQB4	
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ENSMUST00000099145	ENSMUSG00000061689	2	156613705	156764363	1	8	12	51	56	22	23	329	759	416	37	374		B1AZP2
ENSMUST00000099147	ENSMUSG00000074634	13	119487941	119610458	1	11	7	5	0	0	6	2	5	0	0	0	H3BJ86	
ENSMUST00000099148	ENSMUSG00000074635	13	119487261	119488383	-1	516	228	8672	1231	583	327	16	10	15	7	4	Q9DAQ7	
ENSMUST00000099149	ENSMUSG00000025453	13	119335448	119408997	-1	17	0	4	8	10	19	260	451	330	38	354	Q8BGK0	
ENSMUST00000099151	ENSMUSG00000074637	3	34650405	34652461	1	8	3	15	267	15	6	0	0	0	0	0	Q60I23	
ENSMUST00000099153	ENSMUSG00000027677	3	33799832	33814860	1	28	19	13	20	7	10	194	432	233	155	303	A6H6N9	
ENSMUST00000099157	ENSMUSG00000025402	10	127660918	127668568	-1	22	33	201	0	17	18	38	13	4	23	30	Q3TYF1	
ENSMUST00000099162	ENSMUSG00000074650	13	113039301	113042243	-1	19	24	25	9	16	12	0	0	0	0	0	Q3US96	
ENSMUST00000099163	ENSMUSG00000037652	3	30899371	30969415	-1	14	18	32	17	10	5	0	0	0	0	5	E9QPT4	
ENSMUST00000099166	ENSMUSG00000021758	13	112598333	112652310	-1	9	9	0	0	0	5	0	0	0	0	0	Q3V086	
ENSMUST00000099170	ENSMUSG00000074655	3	28892617	28926724	1	3	2	4	2	3	0	0	0	0	0	0	Q3V0P3	
ENSMUST00000099172	ENSMUSG00000074657	10	127225696	127263363	-1	42	27	124	149	65	30	1	6	2	1	9		P33175
ENSMUST00000099173	ENSMUSG00000074656	2	154871410	154892935	-1	0	0	15	23	19	5	62	201	271	1305	171	Q3ULL5	Q99L45
ENSMUST00000099178	ENSMUSG00000038533	2	154436481	154539356	1	29	19	24	16	32	12	2	30	17	4	15	Q3UGB2	
ENSMUST00000099181	ENSMUSG00000074665	2	153938212	153964101	1	0	0	23	12	0	0	0	0	0	0	0		A2BGH0
ENSMUST00000099191	ENSMUSG00000046020	2	153241533	153270247	1	0	0	0	13	0	0	0	0	0	4	0	E9Q7A1	
ENSMUST00000099192	ENSMUSG00000046020	2	153241533	153270247	1	0	1	4	2	2	2	0	2	0	0	0	Q3UXG7	
ENSMUST00000099194	ENSMUSG00000074671	2	153222370	153225441	-1	35	23	63	164	49	21	87	87	54	15	61	Q3UYP3	
ENSMUST00000099195	ENSMUSG00000069094	3	19223108	19311322	-1	42	25	62	44	42	12	58	84	102	27	197	Q3U3Y7	P70453
ENSMUST00000099197	ENSMUSG00000074673	2	152962485	153008482	1	0	0	0	0	6	0	0	0	0	0	0		A2APC3
ENSMUST00000099200	ENSMUSG00000074676	2	152931898	152933208	-1	12	7	55	54	24	10	0	0	0	0	0	Q4VA05	Q61574
ENSMUST00000099201	ENSMUSG00000095788	3	15371653	15426520	-1	0	0	0	0	0	2	0	541	57	0	0	A0A0A6YYP6	
ENSMUST00000099202	ENSMUSG00000034751	13	102732486	103334497	-1	14	22	35	30	57	36	0	0	0	0	0	E9QPR4	
ENSMUST00000099203	ENSMUSG00000074678	2	152622356	152623053	-1	1	2	23	0	4	0	0	0	0	0	0		Q30KN8
ENSMUST00000099205	ENSMUSG00000074680	2	152507798	152511692	-1	7	3	15	4	4	1	0	0	0	0	0	Q30KN7	
ENSMUST00000099206	ENSMUSG00000074681	2	152459055	152464620	-1	2	3	16	11	1	3	0	0	0	0	0	Q30KP0	
ENSMUST00000099207	ENSMUSG00000074682	2	152411955	152415027	-1	35	17	90	653	53	30	8	20	11	4	11	Q8BPK2	
ENSMUST00000099223	ENSMUSG00000027534	3	10417817	10440102	-1	0	4	0	3	9	0	0	0	2	0	0	Q3TLM7	
ENSMUST00000099224	ENSMUSG00000074698	2	152226839	152281852	1	21	14	24	79	21	12	683	2235	1235	388	834		Q60737
ENSMUST00000099241	ENSMUSG00000074715	13	119623819	119654354	1	105	68	176	253	149	70	1	6	3	1	2		Q9JIL2
ENSMUST00000099245	ENSMUSG00000074720	GL456354.1	25923	27230	-1	19	18	35	23	8	10	0	0	0	0	0		
ENSMUST00000099261	ENSMUSG00000074734	10	116111664	116113917	-1	9	9	17	10	8	10	0	0	0	0	0	Q3V063	
ENSMUST00000099262	ENSMUSG00000049658	13	100017994	100104070	-1	0	7	14	0	0	0	21	258	63	85	66	F8VQC2	
ENSMUST00000099264	ENSMUSG00000074737	2	149830524	149831213	-1	1	2	3	227	9	2	0	0	0	0	0	F6RGA8	
ENSMUST00000099265	ENSMUSG00000074738	4	155694342	155696481	1	12	9	16	260	19	6	4	12	1	6	9		A2A9Q0
ENSMUST00000099266	ENSMUSG00000074739	2	149015732	149017237	-1	59	50	59	59	74	22	0	7	8	2	16	Q3V0I0	
ENSMUST00000099269	ENSMUSG00000027435	2	148436640	148443563	-1	94	71	163	216	117	59	441	949	474	148	833		O89103
ENSMUST00000099270	ENSMUSG00000074743	2	148404466	148408188	-1	33	16	41	167	47	21	83	213	71	22	215	Q543W3	P15306
ENSMUST00000099272	ENSMUSG00000041453	5	146832890	146837032	1	14	1	0	76	0	0	22	30	21	40	22	Q9CQM8	
ENSMUST00000099274	ENSMUSG00000074746	19	59296084	59345780	-1	21	23	90	404	45	17	1174	3070	2601	198	1251	B9EJ80	
ENSMUST00000099276	ENSMUSG00000074748	10	112925430	112929001	-1	19	16	40	71	38	23	1162	4527	1863	181	1216		Q3UD01
ENSMUST00000099277	ENSMUSG00000041685	13	98723407	98815449	-1	3	3	4	3	4	3	0	0	0	0	0	F6RG68	
ENSMUST00000099278	ENSMUSG00000074749	2	146855864	146970097	1	7	5	8	54	10	6	156	1010	536	706	331		Q3UXL4
ENSMUST00000099285	ENSMUSG00000035798	10	110941782	111010066	-1	6	0	0	4	4	0	0	4	4	0	5	Q3TRB3	
ENSMUST00000099294	ENSMUSG00000025085	19	57032733	57314919	-1	26	13	35	61	12	0	0	0	0	17	0		Q8K4G5
ENSMUST00000099295	ENSMUSG00000021671	13	96388294	96415587	1	20	12	9	44	21	9	51	228	111	30	118		Q9DBS8
ENSMUST00000099296	ENSMUSG00000027420	2	143826528	143863173	-1	8	0	0	0	8	14	1	3	1	3	3		A2AMT1
ENSMUST00000099304	ENSMUSG00000039033	2	139833480	140066805	-1	6	7	0	0	0	0	7	0	2	23	16	Q3UJT0	
ENSMUST00000099307	ENSMUSG00000074766	2	139678178	139758581	1	4	5	20	0	16	5	0	0	0	0	0		A2ATD1
ENSMUST00000099309	ENSMUSG00000074768	13	93616891	93637961	-1	21	10	34	14	14	17	2	0	3	30	5		O35490
ENSMUST00000099311	ENSMUSG00000027281	2	136891218	137071950	1	11	10	2	0	0	0	28	110	29	14	27		Q9D7Y9
ENSMUST00000099318	ENSMUSG00000036676	10	100443902	100487350	-1	3	0	0	0	2	4	0	0	4	0	0		
ENSMUST00000099324	ENSMUSG00000074776	10	97682102	97682416	-1	0	0	1	0	0	1	0	0	0	0	0	Q3UY85	
ENSMUST00000099326	ENSMUSG00000021708	13	91880400	92131656	-1	13	6	9	9	7	2	1	2	1	0	0	D3Z6K8	
ENSMUST00000099328	ENSMUSG00000074780	10	95672991	95673451	-1	4	3	2	3	2	1	0	0	1	0	0		
ENSMUST00000099329	ENSMUSG00000074781	10	95515162	95545658	1	25	32	33	92	29	24	683	2539	775	1315	497	A2RTT4	P61089
ENSMUST00000099337	ENSMUSG00000074785	10	94790866	94944578	-1	24	16	41	557	58	13	1072	2902	2528	224	1356		Q9QZC2
ENSMUST00000099343	ENSMUSG00000005897	10	94148023	94197211	1	11	7	3	8	11	5	0	0	0	0	0		Q505F1
ENSMUST00000099349	ENSMUSG00000074793	2	131127280	131146321	1	17	12	22	137	29	24	17	16	9	0	9		Q9CZJ2
ENSMUST00000099353	ENSMUSG00000025066	19	47731756	47735588	1	8	2	17	17	7	10	482	1372	763	1925	463		Q8BP27
ENSMUST00000099355	ENSMUSG00000019961	10	91147571	91171582	-1	0	0	0	14	0	0	102	229	98	9	20		Q61029
ENSMUST00000099356	ENSMUSG00000074794	13	80883384	80896035	1	17	9	15	5	0	12	1005	5220	1399	1354	1966		Q7TPQ9
ENSMUST00000099358	ENSMUSG00000064138	13	77708690	78166238	1	0	0	0	174	11	2	0	0	0	0	0		Q3TNH5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000099362	ENSMUSG00000074796	2	130684113	130697519	-1	0	3	11	67	7	0	0	0	0	0	8		A2AJN7
ENSMUST00000099364	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0	E9QPP6	
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ENSMUST00000099371						6	5	2	11	7	0	352	768	469	2444	168		
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ENSMUST00000099374	ENSMUSG00000074802	10	89408823	89443967	-1	21	17	0	29	19	18	15	19	26	6	23		
ENSMUST00000099376	ENSMUSG00000047731	19	46599084	46657389	1	27	0	114	0	15	0	3580	4253	3254	0	2672		Q8BGW2
ENSMUST00000099384	ENSMUSG00000057649	13	73937838	73960894	1	11	10	71	75	22	8	263	1107	503	468	462		
ENSMUST00000099385	ENSMUSG00000074807	2	128966593	128967725	-1	4	2	8	107	8	7	8	24	7	8	8	Q9CZN6	
ENSMUST00000099390						2	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000099392	ENSMUSG00000055491	19	46044886	46072915	1	16	8	3	0	8	24	7	0	5	0	7		Q6NZN1
ENSMUST00000099393	ENSMUSG00000074811	19	46003478	46006173	1	30	19	72	507	51	21	299	264	214	27	140		Q8BLY7
ENSMUST00000099396	ENSMUSG00000054027	10	86779005	86838389	1	67	50	180	79	52	30	163	229	228	12	206		Q3UHB1
ENSMUST00000099400	ENSMUSG00000074817	5	142525838	142530076	-1	13	13	23	115	13	11	0	0	0	0	0	A1L349	
ENSMUST00000099401	ENSMUSG00000025216	19	45232684	45235812	-1	11	7	14	384	17	6	0	0	0	0	0		P52955
ENSMUST00000099412	ENSMUSG00000074826	13	66904914	66909236	1	6	8	2	0	6	0	0	5	1	0	2	Q3TQP0	
ENSMUST00000099413	ENSMUSG00000025194	19	43782192	43840740	1	0	0	0	0	0	0	0	0	1	1	3	Q3UNY3	
ENSMUST00000099414	ENSMUSG00000096910	17	33289649	33303196	1	6	4	0	0	10	4	2	33	11	12	12	L7N232	
ENSMUST00000099416	ENSMUSG00000094499	13	66352469	66355385	-1	14	15	9	3	12	6	0	0	0	0	0		
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ENSMUST00000099421						0	0	0	3	0	1	0	0	0	0	0		
ENSMUST00000099422	ENSMUSG00000096730	JH584292.1	3536	11935	1	5	5	10	7	3	1	0	0	1	0	0	Q8CFT4	
ENSMUST00000099423	ENSMUSG00000027364	2	126709096	126783458	-1	1	0	0	3	0	0	137	194	62	312	51	E9Q3B5	
ENSMUST00000099425	ENSMUSG00000074847	13	65259539	65260826	1	171	133	167	241	193	125	3	45	18	1	13	Q3V290	
ENSMUST00000099427	ENSMUSG00000074849	13	65033058	65038004	1	14	22	62	14	19	12	0	0	0	0	0	E9QAF1	
ENSMUST00000099428	ENSMUSG00000074852	19	42788947	43388311	-1	13	6	7	21	17	9	0	0	0	0	0		B2RY83
ENSMUST00000099431						0	0	0	0	0	0	0	23	0	95	0		
ENSMUST00000099439	ENSMUSG00000094076	10	81812186	81826490	1	0	0	0	0	0	0	5	9	1	0	0	F8VPU7	
ENSMUST00000099441	ENSMUSG00000033114	13	64096310	64129330	-1	25	9	31	41	19	16	345	1925	455	564	346		
ENSMUST00000099442	ENSMUSG00000074862	10	81606270	81620703	1	82	112	362	95	84	37	3	37	17	4	31	Q3US60	
ENSMUST00000099443	ENSMUSG00000018820	19	42163951	42194590	1	3	0	0	0	3	0	1444	969	972	120	753		Q3TXX3
ENSMUST00000099444	ENSMUSG00000021461	13	63304709	63497278	-1	0	0	0	0	0	6	0	0	0	0	6	E9QAE8	
ENSMUST00000099449	ENSMUSG00000074867	13	62129916	62173419	1	13	10	16	17	14	1	8	26	8	5	11	B8JJZ4	
ENSMUST00000099450						1	1	4	0	1	0	0	0	0	0	0		
ENSMUST00000099451	ENSMUSG00000074871	13	61536444	61541839	-1	1	5	0	3	8	4	0	0	0	0	0		
ENSMUST00000099452	ENSMUSG00000074872	2	125136692	125147839	1	2	7	3	4	4	0	0	0	0	0	0		
ENSMUST00000099454	ENSMUSG00000074873	19	41593363	41596158	1	5	10	23	18	14	10	39	165	65	7	72	Q8C7B9	
ENSMUST00000099457	ENSMUSG00000005802	2	122681233	122702663	-1	0	0	123	92	0	0	2	0	0	0	16	A2AK40	
ENSMUST00000099459						1792	1712	42091	6912	3128	2026	17	55	84	7	103		
ENSMUST00000099461	ENSMUSG00000033268	2	122315672	122347972	1	55	38	96	107	70	26	0	1	0	0	0	A2AQ92	
ENSMUST00000099462	ENSMUSG00000048240	10	80948624	81014945	-1	0	12	0	8	27	0	0	0	0	0	0	G3X9Q2	
ENSMUST00000099466	ENSMUSG00000025006	19	40295049	40402267	-1	2	0	0	5	5	0	385	792	794	28	363	E9QNA7	
ENSMUST00000099467	ENSMUSG00000025006	19	40295049	40402267	-1	16	6	25	75	16	19	69	62	170	6	123	D3Z5J3	
ENSMUST00000099471	ENSMUSG00000062162	X	92015191	92016333	-1	0	6	7	0	5	5	0	0	0	0	0	Q4U221	
ENSMUST00000099472	ENSMUSG00000074882	19	39688834	39741054	-1	2	6	2	9	2	4	0	0	0	0	0	K7N6C2	
ENSMUST00000099473	ENSMUSG00000027242	2	121506723	121544860	1	0	1	0	0	0	0	0	0	0	0	0	Z4YK23	
ENSMUST00000099475	ENSMUSG00000074884	2	121449195	121458313	1	0	0	9	35	1	2	2493	3108	962	1754	595	A2ARQ4	
ENSMUST00000099476	ENSMUSG00000074885	13	56362901	56365769	1	2	1	5	2	1	3	0	0	0	0	0	Q8CDW6	
ENSMUST00000099479	ENSMUSG00000021500	13	55635027	55681256	1	22	18	0	95	37	17	82	222	82	0	143	F8WHR6	
ENSMUST00000099482	ENSMUSG00000074886	13	55445334	55460925	1	12	4	20	30	6	0	603	273	500	17	627	Q9EP84	
ENSMUST00000099484	ENSMUSG00000066613	5	109996521	110010411	1	7	0	35	14	10	2	0	0	0	38	1	Q8BJ78	
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ENSMUST00000099488	ENSMUSG00000023572	2	121008403	121016904	1	0	0	0	1	0	0	8	16	0	0	13		
ENSMUST00000099489	ENSMUSG00000023572	2	121008403	121016904	1	8	3	12	4	13	0	49	249	102	51	226		Q3TVC7
ENSMUST00000099490	ENSMUSG00000021488	13	55209782	55318325	1	71	58	228	110	105	42	1127	2995	3031	291	2369	E9QAE4	
ENSMUST00000099492	ENSMUSG00000035621	10	80148272	80158368	1	0	9	39	104	0	0	3627	7741	3292	256	3494		Q3TPJ7
ENSMUST00000099494	ENSMUSG00000040565	19	36926079	37012752	1	19	15	22	42	25	9	252	667	658	115	433	E9QAE3	
ENSMUST00000099496	ENSMUSG00000025878	13	55027880	55100300	-1	0	7	0	24	1	1	65	570	233	246	120		
ENSMUST00000099497	ENSMUSG00000074892	16	96235801	96319859	1	10	7	13	91	47	18	0	2	0	0	2		Q9JI67
ENSMUST00000099498	ENSMUSG00000022665	16	45093402	45127924	1	24	0	0	0	31	0	15	55	27	95	113		Q8R2G6
ENSMUST00000099501	ENSMUSG00000035697	10	80016653	80031472	1	12	9	77	122	40	0	10851	9384	9773	716	8715	G3X9Q3	
ENSMUST00000099502	ENSMUSG00000022914	16	95992092	96082526	-1	20	10	0	0	23	0	0	201	0	0	0		Q921C3
ENSMUST00000099503	ENSMUSG00000025875	13	54789377	54796776	1	1	0	0	0	0	0	34	0	0	0	11	E9QN85	
ENSMUST00000099505	ENSMUSG00000024798	19	35958734	36057507	-1	11	4	13	61	9	1	0	0	0	0	4	B6VJS3	
ENSMUST00000099506	ENSMUSG00000069227	13	54736671	54749874	-1	17	28	78	26	42	14	0	0	0	0	0		Q3UNH4
ENSMUST00000099508	ENSMUSG00000043301	16	94749266	94997696	-1	9	12	5	32	12	5	0	0	0	0	0	Q0VB45	
ENSMUST00000099512	ENSMUSG00000040820	16	94129195	94313563	-1	68	62	186	100	77	45	20	59	33	20	41	Q3TZ03	Q920N2
ENSMUST00000099513	ENSMUSG00000020331	10	79716634	79736108	1	0	0	0	696	0	18	0	0	0	0	0		O88703
ENSMUST00000099514	ENSMUSG00000040451	19	32122727	32389714	-1	0	0	0	61	0	0	469	1623	406	241	341		Q8VCQ6
ENSMUST00000099518	ENSMUSG00000094918	13	50698312	50703435	1	63	25	176	69	69	30	0	0	0	0	0	B7ZWJ3	
ENSMUST00000099519	ENSMUSG00000096641	13	50643228	50650271	1	4	0	0	3	0	2	0	0	0	0	0	Q3V2L5	
ENSMUST00000099521	ENSMUSG00000095300	13	50245181	50250308	-1	35	38	166	71	48	20	0	0	0	0	0	Q3V0M1	
ENSMUST00000099525	ENSMUSG00000074909	19	29808400	29812974	-1	13	18	44	32	14	10	126	657	232	132	168	A3KMD2	Q8BIV3
ENSMUST00000099529	ENSMUSG00000034032	2	119763304	119787537	-1	0	0	0	0	0	0	83	0	0	0	12		Q80TE0
ENSMUST00000099536	ENSMUSG00000074913	19	26885925	26888639	1	4	2	0	1	3	1	0	0	0	0	0	Q3UWS2	
ENSMUST00000099537	ENSMUSG00000024921	19	26605115	26778321	1	0	0	0	251	10	12	26	109	60	19	187	E9QAB8	
ENSMUST00000099538	ENSMUSG00000020265	10	77606097	77641543	1	8	0	18	64	10	14	448	903	231	174	196		Q9Z172
ENSMUST00000099542	ENSMUSG00000027326	2	119047119	119105501	1	0	0	0	0	0	0	0	0	0	0	0	A3KGI3	
ENSMUST00000099543	ENSMUSG00000039903	16	90826719	90905109	1	0	0	0	9	0	0	0	0	0	0	3		P58659
ENSMUST00000099546	ENSMUSG00000074916	2	118926496	118928585	1	13	0	0	280	20	10	70	65	69	0	21		Q80V53
ENSMUST00000099547	ENSMUSG00000069237	13	46669522	46678056	1	13	4	13	115	10	8	281	1060	357	77	285	Q3URQ4	
ENSMUST00000099548	ENSMUSG00000039903	16	90826719	90905109	1	7	8	1	2	0	0	0	0	0	0	0		P58659
ENSMUST00000099552	ENSMUSG00000074919	10	77011995	77022214	1	16	3	20	21	15	3	0	0	0	0	0	E9QAB7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000099554	ENSMUSG00000022978	16	90719312	90727404	-1	3	0	0	2	0	0	217	344	197	333	96		Q9CZJ6
ENSMUST00000099556	ENSMUSG00000074922	19	24476502	24477356	-1	10	2	23	98	11	8	327	1220	564	92	577		Q9DB52
ENSMUST00000099557	ENSMUSG00000074923	2	118663303	118698020	1	52	34	34	233	32	5	0	0	0	0	0		Q3ULB5
ENSMUST00000099558	ENSMUSG00000024812	19	24094523	24225026	-1	27	24	49	148	50	23	6	10	9	3	41		Q9Z0U1
ENSMUST00000099560	ENSMUSG00000074925	19	23687400	23721129	1	4	7	10	27	9	4	22	25	19	7	24	E9QAB6	
ENSMUST00000099562	ENSMUSG00000074928	16	88818667	88826145	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNN7	
ENSMUST00000099564	ENSMUSG00000052387	19	22139119	22989884	1	3	5	0	1	0	3	0	0	0	2	0	E9PUC8	
ENSMUST00000099566	ENSMUSG00000052387	19	22139119	22989884	1	3	3	6	0	2	4	0	0	0	0	0	D3Z539	
ENSMUST00000099569	ENSMUSG00000052387	19	22139119	22989884	1	17	29	102	1	29	22	0	0	0	0	0	Q5F4T0	
ENSMUST00000099571	ENSMUSG00000020230	10	76207222	76237865	-1	4	0	0	6	5	0	0	0	0	0	0	Q3UKX1	
ENSMUST00000099572	ENSMUSG00000020230	10	76207222	76237865	-1	10	5	16	2	13	0	0	25	0	0	0	Q3UID4	
ENSMUST00000099575	ENSMUSG00000074934	2	113746164	113758646	-1	198	159	115	9367	371	162	0	5	0	0	7	Q3TNY7	O70326
ENSMUST00000099576	ENSMUSG00000044042	2	113327736	113716767	1	53	28	189	57	51	33	17	34	35	13	35		Q05860
ENSMUST00000099577	ENSMUSG00000033255	10	75954514	76009591	1	17	8	40	29	34	11	0	2	0	0	0	E9QAB5	
ENSMUST00000099582	ENSMUSG00000021420	13	36117411	36537592	1	1	6	1	148	10	0	0	0	13	0	0	G3X9Q4	
ENSMUST00000099588	ENSMUSG00000003604	2	112492964	112634573	1	4	3	0	4	0	1	0	14	10	14	3	A2AGL5	
ENSMUST00000099589	ENSMUSG00000074939	2	112479171	112480769	-1	10	6	35	20	18	4	0	0	0	0	0		Q920H4
ENSMUST00000099596	ENSMUSG00000074943	2	112129871	112130815	-1	10	8	4	8	4	4	0	0	0	0	0	Q8VG12	
ENSMUST00000099598	ENSMUSG00000074945	2	112091761	112092699	-1	4	3	1	4	4	1	0	0	0	0	0	A2AVL6	
ENSMUST00000099599	ENSMUSG00000074946	2	112071646	112072581	-1	6	6	8	0	3	1	0	0	0	0	0	Q7TQW8	
ENSMUST00000099600	ENSMUSG00000074947	2	112042077	112043030	-1	3	2	12	1	3	1	0	0	0	0	0	Q8VF10	
ENSMUST00000099601	ENSMUSG00000099763	2	112020914	112021852	-1	6	6	8	4	4	3	0	0	0	0	0	Q8VET0	
ENSMUST00000099602	ENSMUSG00000100748	2	112008246	112009184	-1	4	0	10	0	1	3	0	0	0	0	0	Q8VF85	
ENSMUST00000099604	ENSMUSG00000074951	2	111983134	111984096	-1	7	8	7	2	6	1	0	0	0	0	0	Q8VF83	
ENSMUST00000099605	ENSMUSG00000074952	2	111960109	111961071	-1	3	4	1	2	5	2	0	0	0	0	0	Q7TQX0	
ENSMUST00000099606	ENSMUSG00000094747	2	111944516	111945454	-1	8	8	10	2	2	3	0	0	0	0	0	Q7TQX1	
ENSMUST00000099607	ENSMUSG00000096566	2	111911990	111912928	-1	0	0	1	4	3	1	0	0	0	0	0	A2BFL7	
ENSMUST00000099608	ENSMUSG00000074955	2	111872915	111873853	-1	5	3	6	3	2	0	0	0	0	0	0	A2AVW3	
ENSMUST00000099609	ENSMUSG00000093804	2	111813786	111814724	-1	14	9	19	8	10	2	0	0	0	0	0	A2AVW1	
ENSMUST00000099610	ENSMUSG00000074957	2	111664228	111665166	1	5	3	3	5	9	1	0	0	0	0	0	Q7TQX5	
ENSMUST00000099612	ENSMUSG00000094858	2	111621134	111622072	-1	3	5	6	1	2	3	0	0	0	0	0	Q8VGE8	
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ENSMUST00000099616	ENSMUSG00000095809	2	111489218	111490156	-1	3	3	1	4	7	3	0	0	0	0	0	Q7TQX8	
ENSMUST00000099617	ENSMUSG00000096703	2	111420032	111420949	-1	5	4	7	2	2	2	0	0	0	0	0	Q7TQY2	
ENSMUST00000099618	ENSMUSG00000096554	2	111335159	111336076	-1	1	4	3	4	4	2	0	0	0	0	0	Q7TQY5	
ENSMUST00000099619	ENSMUSG00000074965	2	111269454	111270365	-1	3	4	10	1	9	2	0	0	0	0	0	Q8VF41	
ENSMUST00000099620	ENSMUSG00000074966	2	111230853	111231791	-1	3	3	1	6	2	3	0	0	0	0	0	Q7TQY8	
ENSMUST00000099623	ENSMUSG00000074968	2	110655201	110950923	-1	19	20	18	11	21	16	0	0	0	0	0		A2AHL1
ENSMUST00000099624						1	0	0	4	1	0	0	0	0	0	0		
ENSMUST00000099626	ENSMUSG00000074971	2	110360917	110363183	-1	10	6	16	10	25	14	0	0	0	0	0		Q9CQS3
ENSMUST00000099628						1	0	0	38	0	0	0	0	0	0	2		
ENSMUST00000099636						14	13	14	19	5	10	17	30	19	5	9		
ENSMUST00000099644						3	2	4	5	3	2	0	0	0	0	0		
ENSMUST00000099646	ENSMUSG00000022722	16	59612949	59639391	-1	7	0	2	71	5	5	0	0	0	0	0		O88848
ENSMUST00000099656	ENSMUSG00000074995	16	59268739	59269665	-1	4	1	5	2	6	0	0	0	0	0	0	Q7TS38	
ENSMUST00000099657	ENSMUSG00000074996	16	59215685	59216615	-1	4	1	3	1	3	5	0	0	0	0	0	F6ZUS0	
ENSMUST00000099658	ENSMUSG00000062551	13	27849344	27857793	1	0	0	0	0	5	0	0	0	0	0	1	Q5SVL8	
ENSMUST00000099659	ENSMUSG00000074997	2	104713926	104716379	-1	16	12	23	21	13	5	4	12	6	6	6	Q3ULQ2	
ENSMUST00000099661	ENSMUSG00000074999	10	67572042	67574263	1	62	45	449	63	50	28	2	8	0	0	0	Q3V073	
ENSMUST00000099663	ENSMUSG00000075002	16	58613686	58616978	-1	2	2	2	0	3	2	0	0	0	0	0	Q3UWK9	
ENSMUST00000099666	ENSMUSG00000075006	2	104068047	104068550	-1	5	1	3	1	2	1	0	0	0	0	0	F7C7U2	
ENSMUST00000099667	ENSMUSG00000043336	16	57353093	57573126	1	6	7	1	7	0	3	0	0	0	0	0		Q6P6L0
ENSMUST00000099673	ENSMUSG00000005087	2	102811141	102901665	-1	12	7	53	9	14	17	7115	12716	9886	4030	8493	Q3U8S1	
ENSMUST00000099676						2	5	16	6	6	2	81	290	56	195	50		
ENSMUST00000099678	ENSMUSG00000075012	2	102449366	102452499	-1	11	15	13	565	29	9	0	0	0	0	0		Q8BQB4
ENSMUST00000099682	ENSMUSG00000027165	2	101560781	101649532	-1	0	0	2	0	5	0	10	8	10	55	0	Z4YK27	
ENSMUST00000099683	ENSMUSG00000075014	2	98666547	98667301	-1	1887690	2125140	1357820	941324	1456660	963839	245	258	160	219	153	D3Z496	
ENSMUST00000099684	ENSMUSG00000075015	2	98662237	98664083	1	237629	273978	240817	145550	208135	120944	32	39	36	30	20	F7C7Q0	
ENSMUST00000099689	ENSMUSG00000087006	2	93955810	93957201	-1	0	0	0	404	15	0	0	0	0	0	0	A0A087WRN5	
ENSMUST00000099690	ENSMUSG00000075023	2	93855361	93869157	-1	18	0	11	7	16	12	0	0	0	0	0		Q3UX83
ENSMUST00000099691	ENSMUSG00000037012	10	62268855	62379908	-1	16	20	29	270	10	15	950	882	1050	114	556	Q6GQU1	P17710
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ENSMUST00000099696	ENSMUSG00000027215	2	93419111	93463140	-1	8	10	0	7	0	5	619	929	388	78	572	Q3UII2	P40237
ENSMUST00000099697	ENSMUSG00000036110	13	23806993	23825180	1	0	0	0	0	0	0	0	0	0	2	0		Q5SZA1
ENSMUST00000099703	ENSMUSG00000075031	13	23746790	23747241	1	4	2	13	27	2	3	1	26	0	8	10		Q64475
ENSMUST00000099705	ENSMUSG00000075033	16	55839953	55895279	-1	49	17	58	164	44	31	110	283	133	26	174	B9EKK6	
ENSMUST00000099706	ENSMUSG00000020085	10	61715263	61739260	1	19	11	24	14	19	7	232	446	221	75	168		Q8BUE4
ENSMUST00000099709	ENSMUSG00000040479	2	91932824	91975864	-1	0	4	6	132	5	14	154	426	0	117	1	A2AHJ7	
ENSMUST00000099710						1	2	12	4	3	1	0	0	0	0	0		
ENSMUST00000099712	ENSMUSG00000040506	2	91730134	91918849	1	30	6	27	172	57	11	253	508	728	0	579		A2AH22
ENSMUST00000099714	ENSMUSG00000075040	2	91643669	91649791	-1	28	5	85	0	16	0	99	483	241	29	139	H7BX78	
ENSMUST00000099716	ENSMUSG00000040549	2	91526762	91620664	1	0	0	0	0	0	0	40	305	136	164	0	K3W4R5	
ENSMUST00000099719	ENSMUSG00000055313	13	21421275	21441058	-1	0	0	0	23	0	0	0	0	0	0	0	E9Q492	
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ENSMUST00000099723	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	0	0	0	0	0	0	0	0	0	A2AGR0	
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ENSMUST00000099726	ENSMUSG00000075045	10	58234848	58236701	-1	69	57	662	121	110	55	0	0	0	0	0	Q3ULJ8	
ENSMUST00000099729	ENSMUSG00000024972	19	7596660	7607193	-1	16	31	47	0	33	16	0	0	0	0	0		Q91VD1
ENSMUST00000099735	ENSMUSG00000075054	13	17986640	17993351	-1	13	9	26	54	22	16	5	37	11	62	18	Q9DAY6	
ENSMUST00000099736	ENSMUSG00000075053	13	18030324	18031629	-1	0	8	3	1	6	9	0	0	0	0	0		
ENSMUST00000099739	ENSMUSG00000038122	10	56014298	56228689	-1	20	21	28	52	35	15	10	33	22	34	26		Q3URV1
ENSMUST00000099742	ENSMUSG00000071550	16	44394796	44482428	1	7	0	0	0	0	0	0	0	0	0	0	E9Q5M6	
ENSMUST00000099747	ENSMUSG00000039242	13	13954674	13999068	1	20	14	6	162	15	9	126	592	291	33	195		Q8BG28
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000099751	ENSMUSG00000075062	2	90265511	90266428	-1	11	2	0	1	4	5	0	0	0	0	0	Q8VG62	
ENSMUST00000099752	ENSMUSG00000075063	2	90252069	90252986	-1	8	3	7	5	5	2	0	0	0	0	0		Q60881
ENSMUST00000099754	ENSMUSG00000075065	2	90149090	90150004	-1	3	6	25	6	8	3	0	0	0	0	0	Q8VGP3	
ENSMUST00000099755	ENSMUSG00000075066	2	90138211	90139137	-1	6	8	10	3	3	1	0	0	0	0	0	Q7TQZ0	
ENSMUST00000099756	ENSMUSG00000075067	2	90118667	90119596	-1	1	4	11	5	4	3	0	0	0	0	0	Q8VEZ2	
ENSMUST00000099757	ENSMUSG00000075068	2	90051414	90063594	-1	1	0	14	0	1	5	0	0	0	0	0		Q60878
ENSMUST00000099758	ENSMUSG00000075069	2	90021138	90022064	-1	7	5	17	7	11	3	0	0	0	0	0	Q9R0K2	
ENSMUST00000099761	ENSMUSG00000061080	16	39984361	42181679	1	45	19	25	31	39	18	0	0	0	0	0	Q3TYE5	
ENSMUST00000099762	ENSMUSG00000075072	2	89844066	89844971	-1	2	5	20	2	9	3	0	0	0	0	0	Q8VGN4	
ENSMUST00000099763	ENSMUSG00000075073	2	89835023	89841133	-1	4	6	5	0	5	2	1	0	0	0	0	Q8VGP1	
ENSMUST00000099764	ENSMUSG00000075074	2	89788406	89793170	-1	4	4	5	1	1	2	0	0	0	0	0	Q8VFB1	
ENSMUST00000099765	ENSMUSG00000075075	2	89751870	89752826	-1	1	2	8	0	0	1	0	0	0	0	0	A2AUA2	
ENSMUST00000099766	ENSMUSG00000100601	2	89574801	89575724	-1	3	5	3	1	1	1	0	0	0	0	0	F7BRC1	
ENSMUST00000099768	ENSMUSG00000075078	2	89656395	89661216	-1	0	2	33	6	2	1	0	0	0	0	0	Q8VGM3	
ENSMUST00000099769	ENSMUSG00000075079	2	89629940	89630896	-1	0	4	5	3	0	1	0	0	0	0	0	L7MU51	
ENSMUST00000099771	ENSMUSG00000075081	2	89609156	89614022	-1	0	0	11	1	3	1	0	0	0	0	0	A2AT78	
ENSMUST00000099774	ENSMUSG00000024958	19	6938069	6942450	-1	5	0	8	105	8	5	349	604	259	99	227	Q3TD99	
ENSMUST00000099775	ENSMUSG00000075084	2	89527491	89531095	-1	4	4	7	4	2	0	0	0	0	0	0	Q8VGM7	
ENSMUST00000099776	ENSMUSG00000024958	19	6938069	6942450	-1	0	0	2	14	0	3	128	239	98	39	127	E9Q9I0	
ENSMUST00000099777	ENSMUSG00000075085	2	89493294	89498213	-1	0	3	2	0	0	0	0	0	0	0	0	Q8VGM6	
ENSMUST00000099778	ENSMUSG00000075086	2	89482189	89483133	-1	1	4	5	1	3	1	0	0	0	0	0	Q8VF91	
ENSMUST00000099780	ENSMUSG00000075088	2	89417494	89418411	-1	2	0	1	0	1	2	0	0	0	0	0	Q8VGM8	
ENSMUST00000099781	ENSMUSG00000075089	2	89406130	89407077	-1	5	4	17	3	8	1	0	0	0	0	0	Q8VG59	
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ENSMUST00000099783	ENSMUSG00000075090	2	89362483	89364865	-1	5	8	4	0	2	0	0	0	0	0	0	A2AVK5	
ENSMUST00000099784	ENSMUSG00000075091	2	89339383	89340300	-1	1	4	5	4	5	1	0	0	0	0	0	Q8VGN0	
ENSMUST00000099785	ENSMUSG00000075092	2	89325243	89326178	-1	1	3	4	1	6	0	0	0	0	0	0	Q8VEX7	
ENSMUST00000099786	ENSMUSG00000075093	2	89302649	89303590	-1	7	4	5	6	10	5	0	0	0	0	0	Q7TQZ8	
ENSMUST00000099787	ENSMUSG00000075094	2	89296351	89297268	-1	7	8	6	6	9	3	0	0	0	0	0	Q8VG58	
ENSMUST00000099788	ENSMUSG00000075095	2	89282139	89287954	-1	3	0	2	0	0	0	0	0	0	0	0	Q7TQZ9	
ENSMUST00000099789	ENSMUSG00000101480	2	89096990	89097925	-1	0	1	2	1	0	1	0	0	0	0	0	F7BL62	
ENSMUST00000099790	ENSMUSG00000075097	2	89193100	89194032	-1	1	3	8	0	3	3	0	0	0	0	0	Q8VGM5	
ENSMUST00000099792	ENSMUSG00000075099	2	89156238	89157173	-1	3	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000099793	ENSMUSG00000075100	2	89144086	89145021	-1	4	6	2	2	3	0	0	0	0	0	0	A3KGY4	
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ENSMUST00000099795	ENSMUSG00000075102	2	89111575	89112510	-1	3	4	12	2	5	3	0	0	0	0	0	L7MU53	
ENSMUST00000099797	ENSMUSG00000075104	2	89074154	89075089	-1	2	4	8	1	0	0	0	0	0	0	0	Q7TR04	
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ENSMUST00000099800	ENSMUSG00000075107	2	89013127	89014062	-1	5	1	0	0	3	1	0	0	0	0	0	Q7TR05	
ENSMUST00000099804	ENSMUSG00000075110	2	88987265	88988200	-1	1	0	3	2	4	0	0	0	0	0	0	A2ATG3	
ENSMUST00000099805	ENSMUSG00000056457	13	12790822	12800078	-1	2	0	6	1	4	3	0	0	0	103	20		P04768
ENSMUST00000099806	ENSMUSG00000089751	2	88972954	88973889	-1	2	2	10	3	0	0	0	0	0	0	0	A2ATG2	
ENSMUST00000099808	ENSMUSG00000075112	2	88929378	88930313	-1	0	4	6	3	2	2	0	0	0	0	0	Q7TR09	
ENSMUST00000099809	ENSMUSG00000075113	2	88909459	88910391	-1	5	3	10	7	3	2	0	0	0	0	0	Q3SXJ3	
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ENSMUST00000099813	ENSMUSG00000089892	2	88755741	88756673	-1	3	3	12	0	3	4	0	0	0	0	0	Q8VF94	
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ENSMUST00000099818	ENSMUSG00000075121	2	88682804	88683730	-1	4	3	2	0	4	5	0	0	0	0	0	Q8VG21	
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ENSMUST00000099821	ENSMUSG00000057554	13	12439415	12464944	-1	0	0	0	0	0	0	0	0	0	0	7	Q542M5	Q9JL15
ENSMUST00000099823	ENSMUSG00000075125	2	88423088	88424023	-1	0	4	0	0	4	2	0	0	0	0	0	Q7TR18	
ENSMUST00000099824	ENSMUSG00000075126	2	88411727	88412656	-1	2	0	2	0	1	2	0	0	0	0	0	Q0VB29	
ENSMUST00000099825	ENSMUSG00000075127	2	88402009	88402932	-1	2	1	1	3	4	8	0	0	0	0	0	A2AUS6	
ENSMUST00000099830	ENSMUSG00000075132	2	88274109	88275047	-1	4	1	6	0	0	0	0	0	0	0	0	Q7TR24	
ENSMUST00000099831	ENSMUSG00000075133	2	88224080	88225030	-1	3	9	6	0	4	0	0	0	0	0	0	Q8VFG1	
ENSMUST00000099832	ENSMUSG00000100899	2	88149067	88150017	-1	2	0	3	2	1	0	0	0	0	0	0	Q7TR26	
ENSMUST00000099833	ENSMUSG00000101078	2	88124033	88124983	-1	8	0	0	4	5	0	0	0	0	0	0	Q7TR27	
ENSMUST00000099834	ENSMUSG00000075136	2	88092954	88093934	-1	3	2	4	3	6	0	0	0	0	0	0	A2AVT5	
ENSMUST00000099835	ENSMUSG00000075137	2	88070430	88071380	-1	4	7	10	4	2	2	0	0	0	0	0	Q8VFR4	
ENSMUST00000099837	ENSMUSG00000075139	2	88049678	88051112	-1	5	1	0	2	3	3	0	0	0	0	0	Q7TR28	
ENSMUST00000099838	ENSMUSG00000075140	2	88034196	88035137	-1	2	2	11	0	0	1	0	0	0	0	0	Q920P2	
ENSMUST00000099839	ENSMUSG00000075141	2	88005817	88006776	-1	3	0	5	0	2	0	0	0	0	0	0	A2AVT0	
ENSMUST00000099840	ENSMUSG00000075142	2	87973707	87974663	-1	0	0	1	1	3	1	0	0	0	0	0	A2BHP6	
ENSMUST00000099841	ENSMUSG00000075143	2	87961952	87962890	-1	7	4	5	3	5	3	0	0	0	0	0	A2AVC4	
ENSMUST00000099842	ENSMUSG00000075144	2	87949260	87950231	-1	2	1	6	3	0	2	0	0	0	0	0	A2AVC3	
ENSMUST00000099843	ENSMUSG00000075145	2	87942682	87943626	-1	3	2	5	2	5	2	0	0	0	0	0	Q8VFR3	
ENSMUST00000099844	ENSMUSG00000075146	2	87902742	87903674	-1	6	6	3	0	5	3	0	0	0	0	0	L7MU57	
ENSMUST00000099846	ENSMUSG00000075148	2	87753056	87753991	-1	5	5	2	0	5	1	0	0	0	0	0	Q8VFQ7	
ENSMUST00000099848	ENSMUSG00000075149	2	87737387	87738322	-1	1	4	3	1	2	1	0	0	0	0	0	Q8VFQ9	
ENSMUST00000099850	ENSMUSG00000075150	2	87710972	87711904	-1	5	4	0	0	1	4	0	0	0	0	0	Q7TR40	
ENSMUST00000099852	ENSMUSG00000075151	2	87692948	87693880	-1	4	1	3	2	2	0	0	0	0	0	0	Q0VBI4	
ENSMUST00000099853	ENSMUSG00000075153	2	87671433	87672365	-1	4	2	4	1	4	0	0	0	0	0	0	Q7TR42	
ENSMUST00000099854	ENSMUSG00000075154	2	87655981	87656919	-1	0	0	0	0	0	0	0	0	0	0	0	Q7TR43	
ENSMUST00000099855	ENSMUSG00000075155	2	87645180	87646121	-1	4	3	1	0	5	2	0	0	0	0	0	Q7TR44	
ENSMUST00000099856	ENSMUSG00000021311	13	12186542	12258113	-1	28	27	74	120	41	29	84	193	227	32	207		A6H5Y3
ENSMUST00000099857	ENSMUSG00000090018	2	87655925	87658457	-1	2	4	0	0	6	0	0	0	0	0	0	Q7TR43	
ENSMUST00000099858	ENSMUSG00000019849	10	45067206	45158997	1	19	14	26	118	26	20	159	255	201	57	253	Q543B9	Q9QUR6
ENSMUST00000099860	ENSMUSG00000075158	2	87149721	87150659	-1	6	2	4	2	2	1	0	0	0	0	0	Q7TR55	
ENSMUST00000099861	ENSMUSG00000075159	2	87135381	87136319	-1	1	3	5	3	1	1	0	0	0	0	0	Q8VG38	
ENSMUST00000099862	ENSMUSG00000075160	2	87107447	87108385	-1	1	2	1	1	1	0	0	0	0	0	0	Q7TS20	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000099863	ENSMUSG00000075161	2	87092457	87093395	-1	2	7	1	1	4	1	0	0	0	0	0	A2AT96	
ENSMUST00000099864						0	0	0	108	4	1	0	0	0	0	0		
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ENSMUST00000099867	ENSMUSG00000075164	2	87048296	87049234	-1	3	4	0	0	5	2	0	0	0	0	0	Q7TR57	
ENSMUST00000099868	ENSMUSG00000075165	2	87033281	87034219	-1	4	2	7	0	3	0	0	0	0	0	0	Q7TR58	
ENSMUST00000099869	ENSMUSG00000075166	2	87021610	87022542	-1	3	3	5	3	3	1	0	0	0	0	0	A2AVB5	
ENSMUST00000099870	ENSMUSG00000075167	2	86988242	86989174	-1	3	3	1	1	4	3	0	0	0	0	0	Q7TR59	
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ENSMUST00000099874	ENSMUSG00000075171	2	86850770	86851696	-1	3	0	3	0	4	2	0	0	0	0	0	A3KPP5	
ENSMUST00000099875	ENSMUSG00000075172	2	86753795	86754736	-1	0	2	2	1	1	1	0	0	0	0	0	Q8VGA6	
ENSMUST00000099876	ENSMUSG00000075173	2	86732675	86733610	-1	2	2	0	3	2	0	0	0	0	0	0	A2BDZ7	
ENSMUST00000099877	ENSMUSG00000075174	2	86690032	86690973	-1	1	3	1	1	2	2	0	0	0	0	0	Q7TR63	
ENSMUST00000099878	ENSMUSG00000075175	2	86676399	86677331	-1	5	4	0	4	2	1	0	0	0	0	0		Q8VFL9
ENSMUST00000099879	ENSMUSG00000075176	2	86657515	86658456	-1	3	0	0	1	3	1	0	0	0	0	0	Q7TR64	
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ENSMUST00000099881	ENSMUSG00000075178	2	86553181	86554122	-1	5	3	1	0	3	1	0	0	0	0	0	Q7TR67	
ENSMUST00000099882	ENSMUSG00000075179	2	86537966	86542480	-1	1	0	0	1	1	0	0	0	0	0	0	Q8VF52	
ENSMUST00000099883	ENSMUSG00000075180	2	86482799	86483767	-1	0	0	3	3	3	0	0	0	0	0	0	A2AK61	
ENSMUST00000099885	ENSMUSG00000075181	2	86455328	86456269	-1	0	0	1	0	0	0	0	0	0	0	0	A2AK62	
ENSMUST00000099886	ENSMUSG00000075182	2	86445039	86445980	-1	5	0	0	0	5	1	0	0	0	0	0	Q7TR70	
ENSMUST00000099888	ENSMUSG00000075184	10	43593427	43630916	1	11	13	9	14	4	8	4	7	3	2	2	Q3TZ88	
ENSMUST00000099889	ENSMUSG00000075185	2	86413109	86414050	-1	3	2	1	0	5	2	0	0	0	0	0	Q7TR72	
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ENSMUST00000099895	ENSMUSG00000075190	2	86332416	86333354	-1	0	4	2	1	0	0	0	0	0	0	0	Q8VGS7	
ENSMUST00000099897	ENSMUSG00000075192	2	86314343	86315284	-1	2	2	1	0	3	0	0	0	0	0	0	L7MU59	
ENSMUST00000099898	ENSMUSG00000075193	2	86275559	86276485	-1	2	0	0	0	0	1	0	0	0	0	0	Q7TR76	
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ENSMUST00000099900	ENSMUSG00000075195	2	86235871	86236833	-1	0	2	1	3	4	2	0	0	0	0	0	Q8VGS2	
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ENSMUST00000099902	ENSMUSG00000075197	2	86216758	86217708	-1	4	3	0	1	7	1	1	0	0	0	0	Q7TR79	
ENSMUST00000099904	ENSMUSG00000075198	2	86197803	86198750	-1	2	9	12	6	7	1	0	0	0	0	0	Q7TR80	
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ENSMUST00000099906	ENSMUSG00000075200	2	86170871	86171815	-1	7	5	1	6	2	1	0	0	0	0	0		Q8VGR9
ENSMUST00000099907	ENSMUSG00000075201	2	86162003	86162947	-1	5	3	3	0	4	1	0	0	0	0	0	Q8VFK4	
ENSMUST00000099908	ENSMUSG00000075202	2	86159427	86160368	-1	7	5	3	1	12	1	0	0	0	0	0	Q7TR81	
ENSMUST00000099909	ENSMUSG00000075203	2	86145791	86146732	-1	0	1	0	0	2	1	0	0	0	0	0	A2ARY1	
ENSMUST00000099910	ENSMUSG00000075204	2	86130702	86131661	-1	1	3	2	0	3	0	0	0	0	0	0	A2ARY0	
ENSMUST00000099911	ENSMUSG00000075205	2	86084810	86085775	-1	2	2	7	2	0	0	0	0	0	0	0	Q7TR84	
ENSMUST00000099912	ENSMUSG00000075206	2	85904069	85905052	-1	0	2	4	0	2	4	0	0	0	0	0	A2ASU7	
ENSMUST00000099915	ENSMUSG00000075209	2	85799339	85800268	-1	3	4	2	2	4	1	0	0	0	0	0	A2ASV2	
ENSMUST00000099916	ENSMUSG00000075210	2	85759439	85760374	-1	2	5	1	2	2	1	0	0	0	0	0	Q8VFJ7	
ENSMUST00000099917	ENSMUSG00000075211	2	85674211	85678741	-1	2	1	4	1	3	3	0	0	0	0	0	A2ALD2	
ENSMUST00000099918	ENSMUSG00000075212	2	85663476	85664432	-1	2	6	6	2	4	2	0	0	0	0	0		Q9QY00
ENSMUST00000099919	ENSMUSG00000075211	2	85674211	85678741	-1	0	0	0	0	0	0	0	0	0	0	0	E9PXR8	
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ENSMUST00000099921	ENSMUSG00000075215	2	85607964	85608908	-1	3	3	4	3	3	2	0	0	0	0	0	Q7TR99	
ENSMUST00000099923	ENSMUSG00000075217	2	85483594	85519024	-1	8	7	4	9	11	7	0	0	0	0	0		Q0VAX3
ENSMUST00000099924	ENSMUSG00000075218	2	85438125	85439237	-1	3	4	1	0	5	3	0	0	0	0	0	Q8VF74	
ENSMUST00000099925	ENSMUSG00000075219	2	85429883	85430827	-1	5	0	6	1	2	2	0	0	0	0	0	Q8VF73	
ENSMUST00000099926	ENSMUSG00000075220	2	85413933	85414877	-1	6	5	0	4	2	6	0	0	0	0	0	Q8VF75	
ENSMUST00000099927	ENSMUSG00000075221	2	85399602	85400531	-1	1	3	7	2	2	1	0	0	0	0	0	Q8VGC6	
ENSMUST00000099928	ENSMUSG00000075222	2	85352925	85363058	-1	1	2	0	0	2	3	0	0	0	0	0	Q7TRA1	
ENSMUST00000099929	ENSMUSG00000075223	2	85330897	85339295	-1	0	0	0	4	0	0	0	0	0	0	0	Q7TRA2	
ENSMUST00000099930	ENSMUSG00000075224	2	85162334	85196699	-1	16	7	10	14	13	5	0	0	0	0	0		Q3UY51
ENSMUST00000099931	ENSMUSG00000038332	10	41810574	41908424	1	16	16	11	23	17	0	66	57	51	5	59	E9PXR3	
ENSMUST00000099932	ENSMUSG00000075225	10	41538846	41709300	-1	3	0	0	0	0	0	0	0	0	0	0	H7BX79	
ENSMUST00000099934	ENSMUSG00000019823	10	41476314	41487032	1	0	0	0	0	0	0	385	1612	477	84	417		Q8VDP3
ENSMUST00000099936						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000099937	ENSMUSG00000075229	16	36071660	36092118	1	0	3	3	1	2	0	0	19	0	21	0	F8WJI3	
ENSMUST00000099941	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	25	D3Z7H6	
ENSMUST00000099944	ENSMUSG00000059588	2	84330626	84425411	-1	2	2	2	17	2	0	0	0	0	0	0	A2AR99	Q9R1W5
ENSMUST00000099945	ENSMUSG00000075232	10	40287458	40302188	-1	24	25	25	54	28	0	328	1618	336	791	293		P0DMN7
ENSMUST00000099946	ENSMUSG00000021215	13	3882565	3918220	-1	52	50	203	63	29	25	67	116	75	53	120	Q3USZ7	Q9Z206
ENSMUST00000099947	ENSMUSG00000079247	2	83990553	83993045	1	7	7	16	6	9	4	0	0	0	0	0	A2AK42	
ENSMUST00000099948	ENSMUSG00000095824	2	83984743	83987235	1	7	7	16	6	9	4	0	0	0	0	0	A2AK42	
ENSMUST00000099951	ENSMUSG00000096729	2	83967313	83969805	1	0	0	0	0	0	0	0	0	0	0	0	A2AK44	
ENSMUST00000099955	ENSMUSG00000024939	19	5728087	5729653	-1	0	0	0	33	0	0	926	1463	815	164	446		Q9QUI1
ENSMUST00000099956						4	7	5	7	9	3	12	3	9	2	5		
ENSMUST00000099958						0	0	0	0	0	0	25	22	27	0	26		
ENSMUST00000099960	ENSMUSG00000020544	11	90638173	90644931	1	2	2	1	2	4	3	7	32	0	0	6	Q5SRC5	
ENSMUST00000099961						5	0	2	4	0	2	1	0	2	8	5		
ENSMUST00000099967	ENSMUSG00000019843	10	39368855	39565381	1	9	0	0	4	0	0	0	29	28	4	39		P39688
ENSMUST00000099972	ENSMUSG00000027009	2	79255426	79333123	1	600	538	913	760	713	426	2347	5506	4391	446	4598	Q792F9	
ENSMUST00000099973	ENSMUSG00000039480	10	34288288	34418552	-1	4	0	0	23	8	3	5	18	52	39	60	E9QN01	
ENSMUST00000099974						93	98	23	128	100	55	0	75	0	3	0		
ENSMUST00000099980	ENSMUSG00000051747	2	76703980	76982547	-1	50	47	75	50	70	40	0	0	0	0	1		A2ASS6
ENSMUST00000099981	ENSMUSG00000051747	2	76703980	76982547	-1	281	22	251	403	518	231	0	0	0	0	0		A2ASS6
ENSMUST00000099985	ENSMUSG00000075266	10	30196011	30200540	-1	3	4	1	62	4	0	16	39	12	69	12	B2RVH1	Q3URR0
ENSMUST00000099986	ENSMUSG00000075267	2	76648476	76658556	1	4	4	9	5	6	5	0	2	0	1	3		Q0ZLH2
ENSMUST00000099988						0	0	1	12	3	1	0	0	0	0	0		
ENSMUST00000099990	ENSMUSG00000075269	16	32186186	32186949	1	4	4	5	15	13	5	1	11	4	2	1		Q3TZW7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000099991	ENSMUSG00000052384	16	32142785	32165594	-1	0	0	0	0	0	0	1845	2131	1562	404	1622		Q8BMT4
ENSMUST00000099992	ENSMUSG00000075270	2	75989141	76338774	-1	15	17	24	91	26	12	0	0	0	0	0		P0C1Q2
ENSMUST00000099994	ENSMUSG00000075271	2	75978247	75981967	-1	21	10	25	27	17	8	117	275	155	92	98		Q99J38
ENSMUST00000099995	ENSMUSG00000075272	2	75975740	75978170	-1	3	9	22	16	15	8	22	107	48	47	36	B2RXQ0	A2AKQ8
ENSMUST00000099996	ENSMUSG00000075273	2	75935849	75938585	-1	19	10	32	40	12	13	49	142	72	47	53	B2RXA2	Q9CY00
ENSMUST00000100001	ENSMUSG00000022770	16	31663443	31873356	1	0	0	0	0	0	0	0	0	0	0	0		Q811D0
ENSMUST00000100009	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	0	282	0	0	0		P16951
ENSMUST00000100012	ENSMUSG00000039166	10	25169090	25307870	-1	0	5	21	34	14	9	0	0	19	33	47		O55074
ENSMUST00000100013	ENSMUSG00000022533	16	30312423	30388837	-1	0	12	0	7	0	0	206	151	224	54	286		Q5XF89
ENSMUST00000100015	ENSMUSG00000027108	2	73092801	73218924	-1	3	2	2	0	0	5	13	28	26	39	22		Q9CZ30
ENSMUST00000100016	ENSMUSG00000075286	16	29958493	29962307	-1	28	26	30	13	27	14	1	3	5	4	3	Q3T9I3	
ENSMUST00000100019						1	0	3	4	0	0	0	0	0	0	0		
ENSMUST00000100022	ENSMUSG00000024851	19	4099998	4113965	1	3	5	14	109	8	1	35	220	118	5	283		O35954
ENSMUST00000100023	ENSMUSG00000051065	16	28826176	28929698	-1	19	18	26	63	32	16	1	4	2	3	6	D3Z742	
ENSMUST00000100024	ENSMUSG00000022523	16	28160120	28445227	-1	10	4	8	43	11	1	0	1	0	0	0		P61329
ENSMUST00000100026	ENSMUSG00000038127	16	27388869	27452218	1	121	84	294	567	142	83	82	278	125	113	207	A6H6M8	Q810U5
ENSMUST00000100028	ENSMUSG00000027012	2	71211706	71263303	1	0	0	0	0	0	0	125	468	488	636	243	Q3TPJ8	
ENSMUST00000100036	ENSMUSG00000019970	10	21882184	21999903	1	0	0	1	0	0	0	68	173	54	71	2	E9Q1B0	
ENSMUST00000100037	ENSMUSG00000041975	2	70964561	71055583	-1	6	12	0	3	9	0	0	0	19	0	29	B0R0U1	
ENSMUST00000100041	ENSMUSG00000075302	2	70508819	70540884	1	6	2	12	38	16	2	0	0	0	0	0	E9Q1A6	
ENSMUST00000100043	ENSMUSG00000075304	2	70474923	70477729	1	8	6	23	491	24	6	0	0	0	0	0		Q9JHX2
ENSMUST00000100046	ENSMUSG00000060459	16	22985854	23029101	-1	12	0	7	20	5	1	0	0	0	0	0	Q6S9I3	
ENSMUST00000100050	ENSMUSG00000075307	2	69670120	69684230	1	392	380	468	48	197	75	11	32	9	3	10		A2AUC9
ENSMUST00000100051	ENSMUSG00000027070	2	69424340	69586065	-1	4	0	0	2	0	0	0	0	0	0	0	A2ARV5	
ENSMUST00000100052	ENSMUSG00000033581	16	22059009	22163299	-1	11	20	82	30	20	8	3	0	0	13	36		Q5SF07
ENSMUST00000100054	ENSMUSG00000039835	10	18390322	18533892	1	0	26	124	28	18	26	0	5	1	5	33		Q8CAF4
ENSMUST00000100063	ENSMUSG00000075316	2	66480080	66634962	-1	11	7	0	13	10	0	0	0	0	0	0	F8VPQ7	
ENSMUST00000100064	ENSMUSG00000075316	2	66480080	66634962	-1	1	0	16	1	0	16	0	0	0	0	0		Q62205
ENSMUST00000100067	ENSMUSG00000075318	2	65620771	65767447	1	70	51	44	249	20	36	0	0	1	0	2	B1AWN6	
ENSMUST00000100069	ENSMUSG00000057182	2	65457118	65567627	-1	27	16	34	9	31	14	0	3	0	1	0	A2ASI5	
ENSMUST00000100070	ENSMUSG00000060487	10	9627259	9675208	-1	9	11	10	164	14	5	0	0	0	0	0		
ENSMUST00000100074	ENSMUSG00000046613	16	20589471	20605377	1	0	5	0	31	8	0	0	0	0	0	0		Q3UR50
ENSMUST00000100077	ENSMUSG00000075327	10	4367074	4388108	-1	9	7	28	40	0	8	100	14	121	14	116	Q3V3W4	
ENSMUST00000100078	ENSMUSG00000075327	10	4367074	4388108	-1	6	12	0	90	24	0	98	579	177	58	138	Q3V3W4	
ENSMUST00000100083	ENSMUSG00000075330	16	19876570	19883897	-1	1	1	2	3	5	0	0	0	0	1	1	Q3U552	
ENSMUST00000100085	ENSMUSG00000026834	2	58267453	58357895	-1	0	0	0	0	0	0	0	0	0	0	0	Q3V348	
ENSMUST00000100089	ENSMUSG00000075334	2	54084093	54085552	-1	12	9	37	215	21	4	0	0	0	0	0		Q9JJ72
ENSMUST00000100099	ENSMUSG00000022721	16	18248679	18254772	1	0	0	0	0	0	0	14	38	39	0	24	E9PUQ7	
ENSMUST00000100105	ENSMUSG00000095520	Y	17093873	17095892	1	2	0	0	0	6	0	0	0	0	0	0	J3QPZ4	
ENSMUST00000100115						2	0	4	0	0	0	33	194	75	6	35		
ENSMUST00000100123	ENSMUSG00000022759	16	17544465	17561247	-1	5	28	0	1	0	0	0	0	0	0	0		Q14BP6
ENSMUST00000100125	ENSMUSG00000022760	16	17527982	17531136	-1	8	1	11	15	8	0	113	127	67	18	60		Q8VCZ3
ENSMUST00000100126	ENSMUSG00000025165	11	121067407	121081220	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TBH1	
ENSMUST00000100127	ENSMUSG00000036890	2	44564412	44927657	-1	51	52	100	68	52	24	4	38	14	9	23		Q8BW56
ENSMUST00000100130	ENSMUSG00000025161	11	120948480	120960868	1	0	0	0	0	2	0	420	948	286	4	149	Q3UDP9	P57787
ENSMUST00000100131	ENSMUSG00000033632	18	25168999	25467321	1	14	9	12	4	14	3	0	0	0	0	0	E0CZ24	
ENSMUST00000100134	ENSMUSG00000025156	11	120784272	120789102	1	22	11	14	4	32	4	31	127	69	86	104	B1ATU4	
ENSMUST00000100136	ENSMUSG00000075370	16	16860671	16863985	-1	0	2	2	0	6	0	0	0	0	0	0		P20764
ENSMUST00000100143	ENSMUSG00000075376	2	37370069	37422903	-1	27	21	41	0	19	16	324	751	259	87	250		P0C090
ENSMUST00000100144	ENSMUSG00000075377	2	37104695	37105648	-1	10	9	28	5	10	6	0	0	0	0	0	Q8VGV7	
ENSMUST00000100145	ENSMUSG00000075378	2	37084778	37085746	-1	4	2	11	8	6	2	0	0	0	0	0	Q8VF16	
ENSMUST00000100146	ENSMUSG00000075379	2	37004620	37005612	-1	10	6	20	3	5	4	0	0	0	0	0	Q7TRY5	
ENSMUST00000100147	ENSMUSG00000075380	2	36927180	36928112	-1	3	1	5	1	4	1	0	0	0	0	0	Q8VFP6	
ENSMUST00000100149	ENSMUSG00000075382	2	36889911	36890846	-1	7	6	11	4	7	3	0	0	0	0	0	Q8VGK0	
ENSMUST00000100150	ENSMUSG00000075383	2	36859414	36860346	-1	6	6	7	5	2	0	0	0	0	0	0	Q8VGK1	
ENSMUST00000100151	ENSMUSG00000075384	2	36812149	36813090	-1	8	10	6	3	4	3	0	0	0	0	0		Q60879
ENSMUST00000100154	ENSMUSG00000075387	2	36479187	36480128	-1	5	2	2	1	9	0	0	0	0	0	0	Q8VGK9	
ENSMUST00000100162	ENSMUSG00000060992	15	103272911	103299862	1	19	17	25	29	21	9	2759	5652	2134	1844	1624	Q542M2	P61924
ENSMUST00000100164	ENSMUSG00000075394	15	103018934	103036852	1	9	8	0	107	8	6	0	0	0	0	1		Q08624
ENSMUST00000100165	ENSMUSG00000075395	16	14562316	14621300	1	0	0	0	0	0	0	0	0	0	0	0	E9PZ45	
ENSMUST00000100167	ENSMUSG00000023088	16	14361558	14475737	1	30	25	25	24	16	24	33	121	36	37	174	A5D6P3	O35379
ENSMUST00000100168	ENSMUSG00000023051	15	102518192	102523676	1	3	0	15	0	14	0	13	0	0	0	37	Q3UNH9	
ENSMUST00000100171	ENSMUSG00000026864	2	34771970	34777547	1	0	0	0	76	0	7	1190	7516	3201	3215	3458		P20029
ENSMUST00000100172	ENSMUSG00000005043	11	119343425	119355536	-1	9	0	181	9	4	0	84	597	0	78	0	B1ATE0	
ENSMUST00000100179	ENSMUSG00000075402	15	101884351	101892920	-1	22	15	61	37	43	16	0	0	0	3	1		Q3UV17
ENSMUST00000100181	ENSMUSG00000017132	11	118132019	118248592	-1	0	0	7	3	7	2	7	30	6	12	13	A2A517	
ENSMUST00000100184	ENSMUSG00000095241	15	101643024	101647380	-1	27	15	63	34	25	13	0	0	0	0	0	D3Z6R0	
ENSMUST00000100185	ENSMUSG00000017715	11	117986292	118024011	1	4	1	31	2	7	0	0	0	0	140	20	F2Z427	
ENSMUST00000100188	ENSMUSG00000046854	2	32574797	32583782	1	8	7	29	25	5	4	0	1	0	0	0		Q6U7H8
ENSMUST00000100190	ENSMUSG00000075405	2	32574184	32575684	-1	8	8	11	14	9	1	0	2	1	0	1	Q8BS47	
ENSMUST00000100191	ENSMUSG00000039200	16	10192712	10243051	1	5	4	0	7	2	0	0	0	0	0	0		Q3UL97
ENSMUST00000100193	ENSMUSG00000059248	11	117199661	117362325	1	2	3	4	1	2	6	130	793	321	91	243		Q80UG5
ENSMUST00000100194	ENSMUSG00000002546	2	32287384	32307921	1	0	1	0	0	0	0	447	467	644	37	523	E9PUQ5	
ENSMUST00000100196	ENSMUSG00000039427	16	5233621	5244912	1	3	0	0	45	6	0	261	286	171	70	124		Q921Q3
ENSMUST00000100201	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	0	4	0	1	0	0	0	9		Q8CI15
ENSMUST00000100202	ENSMUSG00000052949	11	116336353	116413032	-1	39	0	0	0	0	0	10	0	0	0	6	A2AAN9	
ENSMUST00000100203	ENSMUSG00000023026	15	100038664	100219473	1	23	48	30	151	31	23	464	319	885	56	796		Q3UH60
ENSMUST00000100206	ENSMUSG00000023025	15	99970074	100016351	1	17	11	28	162	20	18	263	563	426	271	316	G3X9Q6	
ENSMUST00000100207	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	0	0	0	0	231	0	285	0	0	A2AQ44	
ENSMUST00000100208	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	0	0	0	0	10	0	55	12	54	A2AQ41	
ENSMUST00000100209	ENSMUSG00000045350	15	99918348	99967075	-1	103	82	576	588	129	67	0	0	0	0	0	K3W4Q5	
ENSMUST00000100211	ENSMUSG00000022518	16	4835416	4867691	1	0	0	0	0	0	0	0	0	0	0	0		E9QMW4
ENSMUST00000100214	ENSMUSG00000026858	2	30364233	30385521	1	19	6	31	63	0	11	0	0	0	0	0		Q8BK03
ENSMUST00000100215	ENSMUSG00000026860	2	30344809	30359337	-1	0	0	0	0	6	0	52	2	41	9	88		Q8R3V5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000100219	ENSMUSG00000075419	2	30284231	30286334	-1	16	7	72	246	16	7	106	93	69	20	68		Q8R2Y3
ENSMUST00000100220	ENSMUSG00000039660	2	30173453	30178459	-1	0	0	0	0	0	0	65	57	58	12	67		Q3UHX9
ENSMUST00000100222	ENSMUSG00000022534	16	3707215	3718124	-1	21	13	52	27	27	25	302	2508	660	307	1108	Q32MT0	
ENSMUST00000100225	ENSMUSG00000057738	2	29965560	30031451	1	0	0	0	0	0	0	166	330	468	0	740	A3KGU7	
ENSMUST00000100235	ENSMUSG00000045980	11	115187487	115247023	1	22	8	26	0	27	12	0	0	68	0	0	A2A6S1	
ENSMUST00000100237	ENSMUSG00000026803	2	29060262	29087656	1	30	0	25	52	16	18	234	850	546	139	362		Q62187
ENSMUST00000100239	ENSMUSG00000089722	11	115031486	115037769	-1	1	1	5	20	7	14	4	74	0	0	46	A2A7W1	
ENSMUST00000100240	ENSMUSG00000069609	11	115020728	115027012	-1	1	1	5	0	0	0	0	0	0	0	0	A2A7W1	
ENSMUST00000100241	ENSMUSG00000026821	2	28513125	28553081	1	0	0	0	0	6	0	0	0	0	0	0	Q3TWC1	
ENSMUST00000100244	ENSMUSG00000026833	2	28192992	28230736	1	15	0	0	0	11	0	435	598	427	67	148	G3X9Q7	
ENSMUST00000100248	ENSMUSG00000018727	11	113698172	113710017	-1	3	3	12	7	4	4	2	0	4	0	6	E9Q2N0	
ENSMUST00000100249	ENSMUSG00000022468	15	97711019	97731405	-1	12	7	41	12	25	8	0	0	0	0	0		Q3V188
ENSMUST00000100251	ENSMUSG00000015846	2	27676440	27762957	1	8	0	19	32	7	7	0	0	0	0	0	Q6LC96	
ENSMUST00000100260	ENSMUSG00000020623	11	110399122	110525522	1	7	13	9	9	4	3	0	0	0	0	0	A2AGS2	
ENSMUST00000100262	ENSMUSG00000023169	15	96571418	96642913	-1	31	27	86	358	63	18	64	136	107	0	69		Q8K2P7
ENSMUST00000100275	ENSMUSG00000074165	7	41633203	41651530	1	1	0	0	0	0	0	10	0	13	16	8	Q8BUQ3	
ENSMUST00000100287	ENSMUSG00000041828	11	110025634	110095978	-1	15	0	15	0	5	0	0	0	0	0	1		Q8K442
ENSMUST00000100290	ENSMUSG00000026921	2	26580014	26593120	1	3	2	5	2	2	5	0	0	0	0	0		
ENSMUST00000100293	ENSMUSG00000047295	15	91838265	91861438	1	0	0	0	0	0	0	0	0	0	0	0		Q6JHY2
ENSMUST00000100294	ENSMUSG00000075465	14	122490586	122492121	1	7	4	7	68	11	2	0	0	0	0	0	Q3UTT8	
ENSMUST00000100299	ENSMUSG00000025558	14	121542039	121797734	-1	9	10	9	49	9	12	313	478	709	0	250	E9QMR2	
ENSMUST00000100301	ENSMUSG00000078816	7	3289179	3331099	1	34	24	162	106	45	18	40	146	79	8	145	Q3UN66	P63318
ENSMUST00000100302	ENSMUSG00000050965	11	107933387	108343928	-1	3	0	0	0	0	2	0	0	0	0	3	Q3TQ39	
ENSMUST00000100303	ENSMUSG00000026928	2	26352176	26360918	-1	14	11	8	10	17	8	399	1118	638	40	910		A2AIV8
ENSMUST00000100304	ENSMUSG00000022629	15	90933276	91049948	-1	10	0	21	0	0	0	0	0	0	0	0	E9Q0J5	
ENSMUST00000100305	ENSMUSG00000020721	11	107547930	107693826	1	0	10	10	0	0	7	0	0	0	0	0	A2AAU3	
ENSMUST00000100308						79	69	12	34	54	28	0	4	0	0	0		
ENSMUST00000100309	ENSMUSG00000075470	15	90224311	90230554	1	14	12	43	44	17	8	132	156	196	14	118		Q3UGP8
ENSMUST00000100312	ENSMUSG00000026937	2	25657952	25661977	1	0	0	0	6	0	6	0	0	0	0	0		A2AJB7
ENSMUST00000100313	ENSMUSG00000026937	2	25657952	25661977	1	6	7	27	6	5	0	0	0	0	0	0		A2AJB7
ENSMUST00000100314	ENSMUSG00000022132	14	118787908	118875489	1	10	12	8	168	24	3	0	0	0	16	2		Q9Z0S6
ENSMUST00000100320	ENSMUSG00000036587	2	25423267	25426374	1	9	5	3	15	14	14	167	117	50	8	41	E2D0W5	Q11131
ENSMUST00000100322	ENSMUSG00000075478	14	108909991	108914239	-1	28	15	69	54	32	11	0	0	0	0	0	B2RXM1	Q810C1
ENSMUST00000100323	ENSMUSG00000026955	2	25372321	25378213	1	0	0	0	52	6	4	0	0	0	0	0		Q9D818
ENSMUST00000100326	ENSMUSG00000075480	11	106160850	106161158	1	3	1	11	2	4	6	0	0	1	0	1	Q3V2K9	
ENSMUST00000100327	ENSMUSG00000022119	14	105106751	105177327	-1	0	0	5	0	0	0	55	118	91	9	99	E9PUF4	
ENSMUST00000100329	ENSMUSG00000006471	2	25244821	25256022	-1	28	10	78	38	18	21	172	437	279	42	307		A2AI05
ENSMUST00000100330	ENSMUSG00000053580	11	105589986	105929304	1	83	64	447	86	95	44	3	7	7	13	59		A2A690
ENSMUST00000100332	ENSMUSG00000078627	11	105360798	105456735	-1	5	0	14	65	0	7	0	0	0	0	1	Q497L7	
ENSMUST00000100334	ENSMUSG00000006476	2	25054355	25062881	1	0	7	0	58	0	15	34	0	85	0	55		Q99NF2
ENSMUST00000100335	ENSMUSG00000020695	11	105292643	105351139	1	72	30	107	404	113	55	2	8	3	6	29		Q64449
ENSMUST00000100337	ENSMUSG00000033060	14	101729957	101934710	1	13	4	16	30	23	0	0	0	0	0	3	E9PYF4	
ENSMUST00000100338	ENSMUSG00000075485	11	105146893	105147261	1	14	8	12	17	14	13	0	0	0	1	4	Q3U587	
ENSMUST00000100339	ENSMUSG00000075486	14	101633766	101640686	-1	1	2	7	0	4	3	83	220	69	426	84	B7ZNP2	Q3V4B5
ENSMUST00000100340	ENSMUSG00000033083	14	101442360	101609191	-1	0	8	6	558	38	13	0	0	0	0	0	H7BX82	
ENSMUST00000100347	ENSMUSG00000018411	11	104231390	104332090	1	0	0	0	0	0	0	0	0	0	0	0		P10637
ENSMUST00000100348	ENSMUSG00000004113	2	24603887	24763152	-1	0	2	0	13	4	0	0	0	0	0	0	A2AIR7	
ENSMUST00000100359	ENSMUSG00000075502	14	79451835	79454816	1	31	18	17	490	26	12	13	36	27	4	15	E9PYD7	
ENSMUST00000100360	ENSMUSG00000094658	Y	2830680	2841854	1	0	0	0	25	3	0	0	0	0	0	0		O35698
ENSMUST00000100369	ENSMUSG00000075510	11	102885169	102886731	1	17	7	10	16	22	9	0	0	0	0	0		Q9D3R5
ENSMUST00000100372	ENSMUSG00000075512	14	77794823	77798864	-1	2	1	1	4	1	0	0	0	0	0	0	Q3UT80	
ENSMUST00000100375	ENSMUSG00000041815	15	83125978	83149384	-1	27	16	66	0	30	15	491	1241	776	124	347	Q3UDD3	
ENSMUST00000100377	ENSMUSG00000058099	15	82997721	83033306	-1	9	14	26	72	6	0	13944	18337	14815	1079	12994		Q8R4V1
ENSMUST00000100378	ENSMUSG00000051455	11	102663716	102682237	1	8	10	5	112	17	6	0	0	3	0	0		A2AG06
ENSMUST00000100380	ENSMUSG00000075517	15	82689134	82690499	-1	7	4	6	4	4	1	0	0	0	0	0		
ENSMUST00000100387	ENSMUSG00000034757	11	102284931	102289237	1	0	9	0	0	3	0	371	462	411	104	316	G8JL73	
ENSMUST00000100392	ENSMUSG00000034773	11	102248882	102265187	1	0	0	0	14	0	0	8	0	2	2	9		Q32P12
ENSMUST00000100396	ENSMUSG00000075524	15	82059151	82066538	1	38	19	136	61	51	24	0	0	0	0	0	D3Z5T8	
ENSMUST00000100397						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000100398	ENSMUSG00000017314	11	102057015	102088515	-1	0	0	44	59	17	6	1	2	1	0	0		Q9WV34
ENSMUST00000100399	ENSMUSG00000022471	15	81987835	82040085	1	21	11	24	289	28	12	0	0	0	0	3		
ENSMUST00000100400	ENSMUSG00000052373	11	101999652	102028461	-1	3	2	3	5	5	4	0	0	0	0	0	Q6XE40	
ENSMUST00000100403	ENSMUSG00000034947	11	101582242	101591788	1	0	1	4	6	7	4	0	132	55	51	91		Q8VC04
ENSMUST00000100404	ENSMUSG00000051950	5	149678230	149762599	1	9	9	20	40	25	8	28	65	56	37	54		Q8BHT6
ENSMUST00000100407						18	19	101	24	24	16	2	15	6	0	5		
ENSMUST00000100410	ENSMUSG00000041264	5	149184350	149215434	1	0	0	0	0	0	0	0	0	0	0	0		Q3ULM6
ENSMUST00000100411	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	13	0	0	0	0	A2AUP3	
ENSMUST00000100414	ENSMUSG00000078656	11	101253707	101259549	1	3	3	5	6	9	2	21	67	14	0	31	A2A4K0	
ENSMUST00000100417	ENSMUSG00000006920	11	101191115	101226463	-1	18	10	10	32	18	17	33	43	52	2	76		P70351
ENSMUST00000100420	ENSMUSG00000034205	14	69609068	69695834	1	4	0	8	46	3	0	0	0	0	0	0		P58022
ENSMUST00000100429	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	0	0	0	32	0		Q9Z0H4
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ENSMUST00000100439	ENSMUSG00000042524	15	79724070	79742536	-1	0	0	0	0	0	0	8675	8916	7497	470	4028		Q8BJS4
ENSMUST00000100443						54	59	141	97	73	47	3	11	2	0	12		
ENSMUST00000100448						8	7	21	21	15	7	0	0	0	0	0		
ENSMUST00000100453	ENSMUSG00000075553	14	66868850	66871005	1	28	24	49	177	24	12	0	4	6	0	1	Q3UY29	
ENSMUST00000100458	ENSMUSG00000026646	2	3455815	3475031	-1	4	0	0	15	0	1	13	23	7	0	10	F6WB49	
ENSMUST00000100461	ENSMUSG00000038780	5	144876495	144965847	-1	5	4	0	22	0	5	53	14	120	0	50	E9Q4K9	
ENSMUST00000100463	ENSMUSG00000026648	2	3424131	3464130	1	0	0	0	0	0	0	0	0	0	0	0	Q32MX8	
ENSMUST00000100464						73	82	134	43	118	45	0	4	5	0	6		
ENSMUST00000100467	ENSMUSG00000045482	5	144767732	144859778	1	30	0	25	82	38	0	1325	644	2742	22	1078	E9QLK7	
ENSMUST00000100472	ENSMUSG00000003038	4	133964738	133968650	-1	0	0	0	0	0	0	11	123	580	669	27	Q5XK38	
ENSMUST00000100473	ENSMUSG00000060012	14	64652531	64806296	1	34	34	58	95	52	31	238	229	444	31	369	E9Q4K7	
ENSMUST00000100476	ENSMUSG00000075566	11	99665043	99665960	-1	1	3	12	81	8	0	0	0	0	0	0	Q3V4B7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000100479	ENSMUSG00000075567	11	99583062	99583654	-1	6	7	18	98	10	3	0	0	0	0	0	Q3V2D6	
ENSMUST00000100482	ENSMUSG00000075570	11	99328550	99337966	-1	0	0	2	1	2	0	0	0	0	0	0		Q3TRJ4
ENSMUST00000100483	ENSMUSG00000029610	5	143902704	143909847	-1	0	0	0	0	0	1	0	16	0	18	13	Q8R3V2	
ENSMUST00000100484	ENSMUSG00000016554	15	77958998	77970824	-1	13	13	26	38	29	17	953	1269	849	224	744		O70194
ENSMUST00000100486	ENSMUSG00000005354	15	77915047	77929006	-1	33	55	35	37	43	22	3	15	9	14	30	Q3TUS3	
ENSMUST00000100487	ENSMUSG00000029613	5	143817788	143904251	1	20	20	37	97	25	6	1038	3213	1653	278	1062		Q9Z2R9
ENSMUST00000100489	ENSMUSG00000001847	5	143503634	143528036	-1	0	0	0	16	0	7	40	140	144	41	90	Q3TLP8	
ENSMUST00000100490	ENSMUSG00000075571	14	63034087	63049960	-1	1	6	0	2	3	1	0	0	0	0	0		Q30KN4
ENSMUST00000100491	ENSMUSG00000075572	14	63011771	63018088	1	1	0	2	3	2	0	0	0	0	0	0		Q30KM9
ENSMUST00000100492	ENSMUSG00000075573	14	62998102	63001066	1	1	0	2	1	1	0	0	1	0	0	0	Q30KN1	
ENSMUST00000100493	ENSMUSG00000075574	14	62977524	62984510	-1	4	3	7	3	3	0	0	0	0	0	0	Q3UW22	
ENSMUST00000100496	ENSMUSG00000021930	14	61531993	61556886	-1	0	0	0	74	0	0	15	50	10	32	13	Q3UBW1	
ENSMUST00000100497	ENSMUSG00000029580	5	142903115	142906754	-1	33	65	151	242	104	76	124119	263982	117700	14560	71792	B2RRX1	P60710
ENSMUST00000100500	ENSMUSG00000017210	11	98704591	98729435	-1	0	0	0	0	0	0	63	0	66	0	0	A6PW47	
ENSMUST00000100505	ENSMUSG00000000148	5	140705011	140719379	1	0	10	22	71	7	0	208	173	93	61	162	E9QLK3	
ENSMUST00000100507	ENSMUSG00000056076	5	140419328	140443360	1	12	11	32	251	39	8	653	923	661	137	749		Q8JZQ9
ENSMUST00000100510						10	3	9	8	8	12	2	4	3	16	0		
ENSMUST00000100514	ENSMUSG00000044197	5	139377697	139396415	1	0	28	80	9	35	21	158	178	173	32	431		Q99LE2
ENSMUST00000100517	ENSMUSG00000036817	5	139200637	139249840	1	0	0	0	0	0	5	4	0	0	1	0	Q3TSM1	
ENSMUST00000100519	ENSMUSG00000057058	11	96464593	96759130	1	0	0	0	0	0	0	0	2	1	1	4	Q3U5H2	
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ENSMUST00000100523	ENSMUSG00000075588	11	96350525	96354012	1	0	2	0	185	0	2	0	0	0	0	0		P0C1T1
ENSMUST00000100524	ENSMUSG00000036898	5	138441468	138460694	1	0	0	0	0	0	0	0	0	6	0	7	D3YYT4	
ENSMUST00000100526						7	14	2	5	12	2	2	3	0	0	0		
ENSMUST00000100527	ENSMUSG00000002524	15	76070184	76080946	-1	14	0	0	14	0	0	225	278	237	68	304		Q3UEB3
ENSMUST00000100528	ENSMUSG00000014349	11	96047432	96065388	-1	21	15	62	78	25	13	1328	2468	1545	219	1055		Q3UE37
ENSMUST00000100529	ENSMUSG00000075592	14	55854036	55874735	1	0	14	172	191	55	21	6	0	8	1	20		Q5DTZ0
ENSMUST00000100530	ENSMUSG00000075593	5	138264921	138272840	-1	0	4	0	0	0	0	0	0	0	0	0	Q3V1B8	
ENSMUST00000100532	ENSMUSG00000038811	11	95837216	95845734	1	0	0	0	2	0	0	0	18	0	55	10	A2A614	Q61017
ENSMUST00000100534	ENSMUSG00000075596	11	95723587	95726710	1	10	6	21	14	17	13	0	1	4	3	9	Q8BRH6	
ENSMUST00000100537	ENSMUSG00000079156	5	138021429	138050636	1	0	0	0	0	0	0	0	0	0	0	0		Q9QYZ5
ENSMUST00000100538	ENSMUSG00000075600	15	75754432	75841915	-1	44	0	39	109	34	16	927	988	798	51	724	Q3UUL4	Q8CHP0
ENSMUST00000100539	ENSMUSG00000029723	5	137745730	137768450	1	68	61	346	241	52	40	1784	2636	1498	215	1256		Q9EQN3
ENSMUST00000100540	ENSMUSG00000029723	5	137745730	137768450	1	7	3	1	207	10	12	1976	1450	1608	78	825	Q3U1U6	
ENSMUST00000100542	ENSMUSG00000022584	15	75108158	75111970	-1	0	0	0	0	0	0	1063	2933	476	2194	682		P0CW03
ENSMUST00000100544	ENSMUSG00000029722	5	137650463	137684726	-1	0	0	11	0	0	0	45	0	56	0	79	Q3U2K8	
ENSMUST00000100551	ENSMUSG00000001508	11	94962791	94976327	-1	10	0	0	0	0	5	0	0	0	0	0		P82350
ENSMUST00000100554	ENSMUSG00000075610	11	94777217	94782703	-1	52	25	77	50	72	27	9	27	3	5	3		B7ZWI3
ENSMUST00000100555						14	4	33	152	11	7	8	0	0	0	0		
ENSMUST00000100561	ENSMUSG00000020866	11	94408391	94474198	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SUG4	
ENSMUST00000100564						8	5	19	7	8	0	0	2	0	0	0		
ENSMUST00000100568	ENSMUSG00000039754	5	136136146	136141615	1	11	0	22	49	17	0	0	14	0	0	6		Q9D8F1
ENSMUST00000100570	ENSMUSG00000004952	5	136083916	136111860	1	0	3	0	12	0	0	0	21	15	0	7		Q6PFQ7
ENSMUST00000100572	ENSMUSG00000022372	15	66780819	66831829	-1	0	0	0	21	0	4	3611	17823	5795	2328	3161	Q4FJX0	Q60898
ENSMUST00000100584	ENSMUSG00000072511	15	65922443	65976804	-1	12	11	28	5	15	1	0	0	0	0	0		Q3TYV2
ENSMUST00000100598						0	1	0	0	0	1	1	0	0	2	0		
ENSMUST00000100608						1	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000100614						0	0	0	0	0	0	2	1	0	2	0		
ENSMUST00000100617						0	1	0	0	0	1	1	0	0	2	0		
ENSMUST00000100619	ENSMUSG00000072553	11	89073841	89093040	1	4	2	6	6	7	2	0	0	0	0	0		Q3V3I5
ENSMUST00000100627	ENSMUSG00000000275	11	88999376	89020293	1	22	23	194	267	11	20	22	25	85	0	133	Q5SU72	
ENSMUST00000100631	ENSMUSG00000022159	14	52261759	52279545	-1	30	24	67	10	0	9	0	101	22	8	23	Q3TEG7	
ENSMUST00000100635	ENSMUSG00000072568	15	60818994	60853778	-1	24	23	57	507	70	20	114	312	181	20	124	D3YXJ5	
ENSMUST00000100638	ENSMUSG00000072571	14	52016865	52019787	1	8	9	22	20	11	5	0	0	2	1	1		Q3UNB8
ENSMUST00000100639	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	0	0	0	0	55		Q3UPH7
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ENSMUST00000100641						5	6	6	18	9	4	0	0	0	25	6		
ENSMUST00000100643	ENSMUSG00000091698	14	43747866	43755948	1	3	1	0	7	5	0	0	0	0	0	0	G3X9Q9	
ENSMUST00000100644	ENSMUSG00000034156	11	87760541	87785928	1	0	0	25	167	0	0	0	2	15	4	0	Q5NCP6	
ENSMUST00000100645	ENSMUSG00000072575	14	51114565	51117791	1	6	4	8	7	9	5	0	0	0	0	0	Q8K0E4	
ENSMUST00000100647	ENSMUSG00000063146	5	134489383	134552434	-1	0	0	0	47	0	0	0	0	0	0	27		Q9Z0H8
ENSMUST00000100650	ENSMUSG00000023079	5	134357656	134456716	-1	0	11	0	0	0	0	8	0	8	0	0		Q9JI57
ENSMUST00000100652	ENSMUSG00000023079	5	134357656	134456716	-1	0	0	11	0	0	0	0	24	0	0	5		Q9JI57
ENSMUST00000100654	ENSMUSG00000023079	5	134357656	134456716	-1	0	0	0	0	0	0	4	0	0	0	0		Q9JI57
ENSMUST00000100655	ENSMUSG00000101892	15	58022259	58034325	-1	0	0	0	2	0	6	94	162	66	122	108		Q9D2X8
ENSMUST00000100657	ENSMUSG00000010342	11	87405065	87555823	1	0	0	0	0	0	0	0	10	0	0	2	Q5ND20	
ENSMUST00000100659	ENSMUSG00000053749	15	55099917	55113677	-1	0	4	15	45	9	0	0	0	0	0	2	D3YXJ2	
ENSMUST00000100660	ENSMUSG00000022419	15	55112317	55259271	1	2	0	0	0	0	0	0	0	0	0	0	B2ZRS5	
ENSMUST00000100662	ENSMUSG00000056310	5	130255619	130341563	1	5	3	6	8	4	5	0	16	3	0	4		Q8BJM7
ENSMUST00000100666	ENSMUSG00000072584	15	53884906	53886597	1	7	5	10	5	4	3	0	0	0	0	0	Q3UT34	
ENSMUST00000100670	ENSMUSG00000022311	15	47580637	48792063	-1	0	0	0	0	0	0	0	0	0	0	0		Q80T79
ENSMUST00000100672	ENSMUSG00000021838	14	46882854	47105817	1	0	0	0	0	0	0	0	0	1	2	7		Q8CBY1
ENSMUST00000100676	ENSMUSG00000021835	14	46383520	46390669	-1	24	12	50	36	0	0	0	1	1	0	5	Q3ULR1	P21275
ENSMUST00000100680	ENSMUSG00000029428	5	128984557	129008574	-1	3	11	0	50	0	21	15	368	129	49	1	Q3TJ55	
ENSMUST00000100681	ENSMUSG00000018479	11	85170404	85181145	1	3	0	0	0	0	1	2	8	0	1	2		Q9D979
ENSMUST00000100686	ENSMUSG00000020530	11	84832361	84870817	-1	0	0	0	0	0	0	0	0	93	0	0	H7BX83	
ENSMUST00000100687						5	5	20	4	3	2	0	0	0	3	0		
ENSMUST00000100688	ENSMUSG00000072595	14	44163169	44171371	-1	3	3	3	1	2	2	0	0	0	0	0	Q9D583	
ENSMUST00000100689						5	4	5	1	1	1	0	0	0	0	0		
ENSMUST00000100691	ENSMUSG00000072601	14	43818765	43875517	-1	0	12	12	3	2	3	10	0	11	66	11	Q53ZF0	P97426
ENSMUST00000100692	ENSMUSG00000095528	14	43602627	43608065	-1	0	0	0	0	0	0	0	0	0	0	0	Q5EBJ2	
ENSMUST00000100694	ENSMUSG00000072605	14	43010188	43015628	-1	19	9	14	38	10	11	0	0	0	0	0	D3YXI9	
ENSMUST00000100695	ENSMUSG00000095226	14	42792568	42797987	-1	0	11	0	0	10	0	0	0	0	0	0	D3YXI8	
ENSMUST00000100696	ENSMUSG00000093948	14	42655938	42663605	1	0	0	0	0	0	0	0	0	0	0	0	F6S966	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000100697	ENSMUSG00000095113	14	42636467	42641917	-1	7	0	12	2	0	0	0	0	0	0	0	L7N233	
ENSMUST00000100698	ENSMUSG00000095371	14	42291907	42297358	-1	0	0	0	0	1	2	0	0	0	0	0	L7N234	
ENSMUST00000100700	ENSMUSG00000072612	5	125389322	125390554	1	3	2	2	260	9	5	0	17	4	0	7	Q3V0T5	
ENSMUST00000100701	ENSMUSG00000072613	14	41570696	41576319	1	31	21	8	36	13	8	0	0	0	0	0	E9Q430	
ENSMUST00000100705	ENSMUSG00000018648	11	84048041	84069261	-1	0	0	0	8	0	0	0	0	0	8	3	Q542U4	Q9JLY7
ENSMUST00000100708						2	2	0	10	3	3	0	0	0	0	0		
ENSMUST00000100709	ENSMUSG00000049327	5	124439930	124462308	1	0	0	0	3	3	0	10	101	95	0	72	D3YXI6	
ENSMUST00000100713	ENSMUSG00000072618	15	36870501	36879816	-1	11	12	41	20	11	12	9	21	15	24	15	Q3UQ87	
ENSMUST00000100716						22	11	66	20	27	9	8	34	45	0	66		
ENSMUST00000100718	ENSMUSG00000018841	11	82876434	82890614	-1	0	0	0	9	0	0	52	0	3	8	51	E9Q428	
ENSMUST00000100719	ENSMUSG00000072624	14	34041078	34046981	1	31	24	26	26	27	18	0	3	2	0	0	Q3UQ97	
ENSMUST00000100720	ENSMUSG00000072625	14	33941039	33947198	1	19	7	44	26	32	13	0	0	0	1	0		Q9WV56
ENSMUST00000100721	ENSMUSG00000050666	14	32856756	32939487	1	12	3	8	0	0	7	0	0	0	0	0	D3YXI4	
ENSMUST00000100722	ENSMUSG00000020698	11	82719250	82764321	-1	0	0	12	79	25	9	0	0	0	0	0	B1AT05	
ENSMUST00000100723	ENSMUSG00000072473	14	32376502	32388373	-1	0	3	7	9	2	3	0	0	0	0	0		Q3KNL4
ENSMUST00000100729	ENSMUSG00000029440	5	123169413	123250131	1	45	21	89	61	52	25	273	319	240	66	143		Q9CR00
ENSMUST00000100730	ENSMUSG00000021892	14	31359880	31436078	-1	12	12	14	7	24	6	22	0	0	0	11		Q9Z131
ENSMUST00000100731						16	11	41	86	25	27	2	2	11	0	0		
ENSMUST00000100737	ENSMUSG00000029468	5	122643911	122691432	1	47	25	80	36	49	10	52	118	51	21	166	Q8CHP4	Q9Z1M0
ENSMUST00000100739	ENSMUSG00000056069	15	27655071	27681542	-1	11	10	14	104	14	8	198	1330	317	114	281		Q3TVP5
ENSMUST00000100747	ENSMUSG00000064267	5	122206804	122242297	1	24	7	83	13	4	13	118	141	0	0	0		Q3U2S8
ENSMUST00000100748						3	2	0	0	0	0	0	0	0	2	0		
ENSMUST00000100750	ENSMUSG00000031393	X	74026592	74135363	-1	0	0	0	34	0	0	0	0	0	0	0		Q9Z2D6
ENSMUST00000100754						0	0	0	0	0	0	12	0	6	16	6		
ENSMUST00000100755	ENSMUSG00000002058	11	78343482	78349164	1	0	0	5	1	4	2	1769	2193	1034	1385	659	B1AQD7	
ENSMUST00000100757	ENSMUSG00000072647	5	121518576	121522071	-1	27	14	38	79	27	13	17	100	54	6	55	Q3V0H1	Q60813
ENSMUST00000100763	ENSMUSG00000074793	2	131127280	131146321	1	10	14	31	26	24	5	0	3	0	0	0	H7BX84	
ENSMUST00000100764	ENSMUSG00000021504	13	55599896	55610443	1	54	0	33	103	22	0	0	0	0	0	9		Q8R087
ENSMUST00000100765	ENSMUSG00000032712	6	149309414	149335663	1	0	0	0	0	0	0	100	0	0	0	17	B2KFD2	Q5DTW7
ENSMUST00000100769	ENSMUSG00000042744	5	121220219	121368577	1	8	18	21	15	16	3	7	6	5	0	0	Q6GQX8	
ENSMUST00000100770	ENSMUSG00000043733	5	121130533	121191397	-1	0	0	0	46	0	0	503	872	837	118	862		P35235
ENSMUST00000100772	ENSMUSG00000030306	6	148232430	148444389	-1	0	42	26	106	45	33	2	8	7	2	14		Q3UV71
ENSMUST00000100775	ENSMUSG00000022248	15	10486018	10499063	1	652	663	660	722	833	406	87	290	193	42	217		Q9QWZ1
ENSMUST00000100780	ENSMUSG00000072662	6	147075060	147087032	-1	5	6	32	43	11	8	0	1	1	0	1		Q3UU94
ENSMUST00000100782	ENSMUSG00000037750	11	78094660	78156700	1	6	9	50	0	0	5	218	21	220	9	265	E9PXL0	
ENSMUST00000100784	ENSMUSG00000061981	11	78037931	78060434	1	0	0	0	22	0	0	0	0	0	0	0		Q60634
ENSMUST00000100785	ENSMUSG00000066867	5	120786226	120795530	-1	11	10	15	9	9	4	0	1	0	1	1	Q8C2W3	
ENSMUST00000100789	ENSMUSG00000022253	15	9071260	9110487	1	0	1	9	0	3	1	0	0	0	0	0	Z4YK42	
ENSMUST00000100790	ENSMUSG00000022253	15	9071260	9110487	1	0	0	0	82	0	0	46	96	74	30	38		Q8C5H8
ENSMUST00000100794	ENSMUSG00000000631	11	77763246	77865980	1	15	9	0	0	21	6	330	46	287	10	428	E9Q405	
ENSMUST00000100795						153	113	676	280	138	74	3	16	7	3	10		
ENSMUST00000100799	ENSMUSG00000012405	14	18267823	18271391	-1	15	0	0	0	0	17	712	463	355	1818	435	Q5M8Q0	Q9CZM2
ENSMUST00000100802	ENSMUSG00000037857	11	77686155	77741921	1	66	51	378	160	65	38	657	2117	627	233	601		Q5F2E7
ENSMUST00000100804	ENSMUSG00000072672	14	26257962	26269436	1	0	0	0	0	7	0	0	0	0	0	0	Q7TNE6	
ENSMUST00000100806	ENSMUSG00000021867	14	26203369	26207041	-1	16	0	60	50	19	0	0	0	0	0	0	Q9D890	
ENSMUST00000100807	ENSMUSG00000072673	11	77516660	77519198	-1	7	4	17	14	8	4	5	74	7	8	12	Q3V3I3	
ENSMUST00000100809	ENSMUSG00000072674	14	26167405	26182480	-1	0	0	0	2	3	0	0	0	0	11	0	V9GXX6	
ENSMUST00000100810	ENSMUSG00000072675	14	26118349	26129763	1	5	5	19	25	0	7	0	0	0	1	0	Q7TNE6	
ENSMUST00000100811	ENSMUSG00000072676	14	25924000	25927672	-1	16	0	60	50	19	0	0	0	0	0	0	Q9D890	
ENSMUST00000100812	ENSMUSG00000011877	11	77493562	77507786	1	21	20	68	0	14	16	555	442	403	51	480	Q5F258	
ENSMUST00000100813	ENSMUSG00000072676	14	25924000	25927672	-1	1	1	0	32	0	0	0	1	3	0	0	V9GX22	
ENSMUST00000100816	ENSMUSG00000018076	5	118560679	118765438	1	52	48	203	121	76	48	1587	2099	3436	123	2897	E9QLJ3	
ENSMUST00000100818	ENSMUSG00000072680	14	26063919	26067355	-1	0	20	0	0	0	19	0	0	0	4	0	Q9D890	
ENSMUST00000100819	ENSMUSG00000072680	14	26063919	26067355	-1	1	7	10	0	20	14	60	49	46	16	19		Q9DCV5
ENSMUST00000100827	ENSMUSG00000030249	6	142587862	142702315	-1	0	66	0	0	0	42	3	10	2	0	7		P70170
ENSMUST00000100831	ENSMUSG00000063142	14	23289431	24004859	-1	2	4	0	0	4	0	0	0	0	0	0	F6V0P5	
ENSMUST00000100832	ENSMUSG00000030243	6	142350342	142387087	-1	0	0	0	0	9	0	0	26	6	5	0	E9Q3N0	
ENSMUST00000100834						1	1	20	210	3	1	1	3	2	1	1		
ENSMUST00000100837	ENSMUSG00000021820	14	20734875	20794088	-1	26	7	74	80	0	8	234	1275	450	109	582	Q6ZWS7	Q923T9
ENSMUST00000100841	ENSMUSG00000015766	6	137477245	137654876	-1	6	7	10	10	20	9	434	937	488	155	221		Q08509
ENSMUST00000100844	ENSMUSG00000021814	14	20455261	20480133	-1	17	10	26	98	0	0	265	556	409	92	148		Q07076
ENSMUST00000100847						36	32	89	37	31	11	14	28	13	11	13		
ENSMUST00000100848	ENSMUSG00000072693	5	115097689	115098295	-1	0	0	0	0	0	0	0	99	0	0	0	E9Q3K6	
ENSMUST00000100850	ENSMUSG00000092486	5	114821935	114823468	-1	259	231	313	325	261	169	43	207	41	61	43	Q9CZU9	
ENSMUST00000100857	ENSMUSG00000030203	6	134715468	134792625	-1	20	13	54	70	28	14	542	2423	1327	204	1627	Q6PCP3	
ENSMUST00000100864	ENSMUSG00000072704	6	133104909	133110899	1	2	2	9	69	4	5	83	259	113	25	81	E9Q3K4	
ENSMUST00000100866	ENSMUSG00000069814	11	74619605	74641516	1	30	11	71	296	48	31	0	1	0	2	1	Q5SUE3	
ENSMUST00000100870						9	4	72	56	12	4	0	0	0	0	0		
ENSMUST00000100872	ENSMUSG00000072707	14	14322910	14329066	1	6	8	17	3	7	8	0	0	0	0	0	E9Q3K2	
ENSMUST00000100874	ENSMUSG00000048163	5	113818536	113832644	-1	23	31	141	68	56	24	33025	35592	20393	7636	20213	Q3TA56	
ENSMUST00000100882	ENSMUSG00000072722	5	112449426	112451738	1	20	14	40	46	24	16	0	0	0	0	0	E9Q3K0	
ENSMUST00000100886	ENSMUSG00000072726	14	7323988	7332395	-1	0	0	0	0	0	0	0	0	0	0	0	Q5BKP9	
ENSMUST00000100888	ENSMUSG00000095015	14	7185927	7194540	-1	3	0	11	3	12	4	0	0	0	0	0	K7N6G4	
ENSMUST00000100893	ENSMUSG00000095681	14	5071040	5093318	1	0	0	0	0	0	0	0	0	0	0	0	L7N235	
ENSMUST00000100895	ENSMUSG00000093985	14	7006115	7027449	-1	0	0	0	0	0	0	0	0	0	0	0	A6NAS4	
ENSMUST00000100900	ENSMUSG00000072738	14	6380721	6390319	-1	2	2	0	1	1	0	0	0	0	0	0	K7N6G6	
ENSMUST00000100903	ENSMUSG00000040471	11	72435526	72438400	1	4	0	7	8	0	5	0	0	0	0	0		Q6PDE7
ENSMUST00000100904	ENSMUSG00000091754	14	6735685	6742332	-1	0	0	0	2	1	0	0	0	0	0	0	A6NAV4	
ENSMUST00000100920	ENSMUSG00000079409	14	3188255	3196681	1	0	0	0	0	4	0	0	0	0	0	0	Q497R9	
ENSMUST00000100924	ENSMUSG00000072754	5	110344730	110356094	1	3	3	3	7	10	6	0	0	0	0	0		Q3URS3
ENSMUST00000100926	ENSMUSG00000079304	6	128375456	128385144	1	10	3	35	8	5	3	0	0	0	0	0		Q3TTI8
ENSMUST00000100928	ENSMUSG00000020817	11	70844778	70943105	1	1	0	0	3	7	0	0	71	24	12	46		O35551
ENSMUST00000100933	ENSMUSG00000040712	11	70669463	70688105	-1	0	0	0	0	0	6	0	199	0	14	0		Q80Y50
ENSMUST00000100937	ENSMUSG00000072762	5	109735990	109751886	-1	3	2	9	7	12	6	7	18	21	21	11	Q8C1G8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000100941	ENSMUSG00000001930	6	125546774	125686679	1	3	6	0	6	4	10	0	0	0	2	0	Q3TD35	
ENSMUST00000100942	ENSMUSG00000030337	6	125215551	125245964	1	17	16	56	17	11	19	45	214	67	16	136		Q62442
ENSMUST00000100943						0	0	0	165	7	0	0	0	0	0	0		
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ENSMUST00000100949	ENSMUSG00000029276	5	107548967	107597888	-1	0	0	0	0	0	0	0	0	2	0	0	Q3T9A5	
ENSMUST00000100950	ENSMUSG00000020831	11	70235206	70237914	-1	1	0	0	16	1	0	26	36	17	0	23	F6XN97	
ENSMUST00000100951	ENSMUSG00000044060	5	107497378	107512556	1	0	6	19	0	0	2	0	3	7	4	2	E9QLA8	
ENSMUST00000100955	ENSMUSG00000034345	17	6079786	6086517	1	7	3	6	47	6	3	204	425	187	972	116		Q8K2X8
ENSMUST00000100960	ENSMUSG00000092021	5	105323042	105346472	-1	0	2	13	10	4	0	8	32	10	22	10		
ENSMUST00000100961	ENSMUSG00000029298	5	105077630	105139539	-1	13	2	10	0	14	14	7	121	39	62	187	Q8BTS3	
ENSMUST00000100962	ENSMUSG00000079363	5	105115767	105139586	-1	22	15	19	12	18	11	24	115	37	133	201	A4UUI3	
ENSMUST00000100968	ENSMUSG00000072778	6	124191596	124231784	-1	17	13	14	14	8	7	0	0	0	0	0	D3YUK6	
ENSMUST00000100969	ENSMUSG00000018570	11	69897352	69900987	-1	0	0	16	6	0	4	0	0	0	0	7	B1AR39	
ENSMUST00000100982						5	8	3	5	9	0	0	0	0	0	2		
ENSMUST00000100986	ENSMUSG00000021171	12	116281222	116373096	1	11	12	35	209	22	18	608	1227	1043	162	822		Q3TZZ7
ENSMUST00000100988						0	0	0	27	0	0	0	0	0	0	0		
ENSMUST00000100993	ENSMUSG00000071226	6	120666369	120771190	1	4	5	10	7	6	0	1	2	0	0	3	E9Q2Z1	
ENSMUST00000100996						9	59	101	83	7	48	514	1256	1160	246	785		
ENSMUST00000101004	ENSMUSG00000020893	11	69095217	69109960	1	9	14	30	13	22	13	54	136	102	0	173	Q8C4K7	
ENSMUST00000101010	ENSMUSG00000072812	12	112772194	112802657	-1	0	0	0	0	0	0	1	0	0	3	0	Q3URZ6	
ENSMUST00000101011	ENSMUSG00000072814	5	95742014	95746617	1	0	0	0	0	0	0	0	0	0	0	0	L7MU65	
ENSMUST00000101014	ENSMUSG00000060938	11	68901583	68906989	1	0	0	5	71	0	3	0	0	6	21	0	B1ARA5	
ENSMUST00000101015	ENSMUSG00000079424	5	95305911	95343917	1	13	11	27	18	10	5	0	0	0	0	0	D3YUK0	
ENSMUST00000101017	ENSMUSG00000018736	11	68821434	68871858	-1	9	8	16	11	9	0	124	317	274	93	283		Q9ERR1
ENSMUST00000101018	ENSMUSG00000072825	12	112722174	112746591	1	0	51	175	88	0	0	0	0	0	0	0		Q80U49
ENSMUST00000101021	ENSMUSG00000072821	5	94076385	94080997	1	0	0	0	0	0	0	0	0	0	0	0	L7MU65	
ENSMUST00000101023	ENSMUSG00000095996	5	95182624	95195342	1	60	64	34	61	52	20	0	1	0	0	0	D3YUJ6	
ENSMUST00000101024						8	0	7	0	8	0	0	0	0	0	0		
ENSMUST00000101029	ENSMUSG00000037679	12	112588784	112615556	1	29	17	89	157	61	28	287	329	193	29	403	E9QLA5	
ENSMUST00000101032	ENSMUSG00000025702	6	116338024	116409540	1	0	10	56	95	38	14	57	57	85	0	57		Q9DBD2
ENSMUST00000101042	ENSMUSG00000020542	11	65176561	65269989	-1	0	5	0	0	11	3	0	0	0	0	0		Q8VIM5
ENSMUST00000101044	ENSMUSG00000030302	6	113743831	114042613	-1	16	4	2	29	21	0	0	0	1	0	0	F8WHB1	
ENSMUST00000101045	ENSMUSG00000030302	6	113743831	114042613	-1	3	1	185	0	52	27	0	0	0	0	0	Q3UHJ3	Q9R0K7
ENSMUST00000101049	ENSMUSG00000020549	11	64979038	65002069	1	0	0	18	0	5	0	75	90	69	14	130		Q80Y81
ENSMUST00000101051						12	6	2	16	0	6	0	2	0	0	0		
ENSMUST00000101055	ENSMUSG00000021258	12	108179738	108203359	1	17	8	86	47	12	11	562	992	578	55	472	Q3U3M5	
ENSMUST00000101056	ENSMUSG00000002240	5	87825686	87846387	1	0	0	0	0	0	0	0	0	0	0	0	Q3SYJ2	
ENSMUST00000101057	ENSMUSG00000061388	5	87808082	87824426	1	8	5	94	12	8	7	0	0	1	0	0	Q8CEJ6	
ENSMUST00000101059	ENSMUSG00000045009	6	113493639	113501931	-1	18	14	87	527	31	18	0	2	2	1	1		Q6PE13
ENSMUST00000101065	ENSMUSG00000043088	6	113458484	113470758	1	5	4	38	154	0	3	0	0	0	0	0		Q8BH06
ENSMUST00000101066	ENSMUSG00000018501	11	62316426	62458541	-1	8	6	34	0	21	0	796	1723	1370	14	648	Q5RIM6	
ENSMUST00000101067	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	0	0	0	0	392	107	1493	0	739	E9Q2B2	
ENSMUST00000101068						0	2	0	0	0	0	0	4	0	0	39		
ENSMUST00000101070	ENSMUSG00000051256	6	113442569	113448229	1	8	2	7	130	12	4	65	166	53	44	63		Q5XKN4
ENSMUST00000101071	ENSMUSG00000041359	12	105216750	105222793	-1	10	6	20	14	6	0	0	0	0	0	0	Q3UES7	
ENSMUST00000101073	ENSMUSG00000072845	5	86410410	86468990	-1	5	12	5	7	13	4	0	0	0	0	0		Q3UQ41
ENSMUST00000101075	ENSMUSG00000042298	11	62281473	62328451	1	0	0	0	0	0	0	1	1	1	0	1		Q8CC21
ENSMUST00000101078	ENSMUSG00000079012	12	104338486	104394257	1	0	6	12	7	7	4	0	0	0	29	1		Q03734
ENSMUST00000101080	ENSMUSG00000066363	12	104214544	104221129	1	9	4	15	9	9	0	0	0	0	0	0		Q80X76
ENSMUST00000101082	ENSMUSG00000047757	X	164980592	164997272	1	0	0	0	0	5	0	0	0	0	0	0	B1AW74	
ENSMUST00000101085	ENSMUSG00000001034	11	61488812	61494406	-1	0	0	0	0	0	0	28	0	41	0	0	Q5NCN8	
ENSMUST00000101087	ENSMUSG00000036323	5	76974683	76999937	1	0	0	4	12	0	0	387	1747	665	587	307	F8VQC1	
ENSMUST00000101094	ENSMUSG00000021203	12	103388682	103406350	1	9	9	18	125	19	0	0	0	0	0	0	D3Z0Y8	
ENSMUST00000101095	ENSMUSG00000031360	X	162901238	163032508	1	0	0	0	0	0	0	279	874	422	208	225		P70303
ENSMUST00000101099	ENSMUSG00000021198	12	102948859	103184065	1	27	14	76	232	50	19	0	0	0	0	0		Q0KK59
ENSMUST00000101102	ENSMUSG00000040855	X	162411954	162643649	-1	16	0	0	0	16	7	0	0	3	0	0	B9EI38	
ENSMUST00000101103	ENSMUSG00000010142	11	61126755	61149372	1	0	0	0	0	0	1	0	0	0	0	0	A5D8Y6	Q9ET35
ENSMUST00000101113	ENSMUSG00000000037	X	161117193	161258213	1	0	6	12	1	4	1	0	4	0	1	0	B1AVB1	
ENSMUST00000101114	ENSMUSG00000044456	12	102283048	102390855	1	10	4	25	15	16	7	171	381	306	108	139	Q3UZ87	
ENSMUST00000101118	ENSMUSG00000072872	6	100228565	100287485	-1	20	19	38	24	17	15	611	2298	1097	123	834		Q8CCI5
ENSMUST00000101120	ENSMUSG00000030069	6	99711299	99726392	-1	3	8	17	27	12	0	5870	13924	3844	460	1733		Q9QXU7
ENSMUST00000101122	ENSMUSG00000072875	6	99692679	99695066	1	3	1	11	206	8	4	53	93	62	14	53		O54897
ENSMUST00000101123	ENSMUSG00000035158	6	97807052	98021349	1	0	2	8	0	5	2	0	0	15	0	15	E9QL92	
ENSMUST00000101126	ENSMUSG00000030029	6	94604529	94700158	-1	0	0	0	0	0	0	8	0	6	22	143		P70193
ENSMUST00000101127	ENSMUSG00000070733	5	73019987	73256619	-1	47	32	9	60	85	27	562	831	1426	63	1109	F8VQ05	
ENSMUST00000101137	ENSMUSG00000072888	X	154575228	154579360	-1	4	0	0	0	2	2	0	0	0	0	0	Q497M0	
ENSMUST00000101141	ENSMUSG00000045180	X	152609509	152769465	-1	23	12	0	0	17	0	0	0	0	0	0	A7TU71	
ENSMUST00000101144	ENSMUSG00000021007	12	98628157	98669815	1	0	0	0	0	0	0	0	15	0	0	1	Q3U5D0	
ENSMUST00000101146	ENSMUSG00000021007	12	98628157	98669815	1	11	6	27	0	0	5	0	0	13	0	0	Q3TTL3	
ENSMUST00000101148	ENSMUSG00000032691	11	59541568	59566956	1	27	0	0	8	0	0	221	718	303	90	360		Q8R4B8
ENSMUST00000101150	ENSMUSG00000020472	11	59485520	59526751	-1	42	25	25	0	39	14	54	61	15	0	8		Q5SXI5
ENSMUST00000101151	ENSMUSG00000034312	6	90656088	90810123	-1	28	31	107	140	62	26	7058	9088	9192	356	6845	E9PUA3	
ENSMUST00000101153	ENSMUSG00000034312	6	90656088	90810123	-1	15	0	29	0	5	1	176	14	366	0	498		Q8R0S2
ENSMUST00000101158						4	0	0	139	0	1	0	0	0	0	0		
ENSMUST00000101164	ENSMUSG00000037736	5	66745827	67057158	1	0	0	0	0	0	0	0	0	0	0	0		Q3UH68
ENSMUST00000101165	ENSMUSG00000021044	12	88360554	88461719	1	15	0	6	23	10	6	24	76	45	28	39		Q9D0L4
ENSMUST00000101168	ENSMUSG00000079029	12	88270640	88274500	-1	4	7	5	12	7	0	0	0	0	0	0	Q8BX20	
ENSMUST00000101171	ENSMUSG00000000811	6	89643988	89675529	1	0	0	12	253	16	4	0	5	0	0	0	D3Z0H7	
ENSMUST00000101180	ENSMUSG00000094378	X	149784473	149826694	1	0	0	0	0	0	0	0	0	0	0	0	L7MU67	
ENSMUST00000101181	ENSMUSG00000072923	X	149594570	149636764	1	2	3	11	0	0	0	0	0	0	0	0	A2AJU2	
ENSMUST00000101185	ENSMUSG00000079387	X	148857640	148924139	1	0	0	0	8	0	0	0	0	0	0	0	B1AV09	
ENSMUST00000101186	ENSMUSG00000096834	X	148663598	148703849	1	5	0	39	9	0	0	0	0	0	0	0	B1AVZ5	
ENSMUST00000101190	ENSMUSG00000096834	X	148663598	148703849	1	0	0	0	0	17	9	0	0	0	0	0	L7N236	
ENSMUST00000101191	ENSMUSG00000054920	5	65107539	65168188	1	9	10	0	14	0	13	3	23	275	28	98	Q6PFE1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000101192						0	1	0	34	0	0	489	1066	701	134	566		
ENSMUST00000101195	ENSMUSG00000029174	5	64156305	64351486	1	0	0	0	0	0	0	6	273	599	0	202	Q3U3T9	Q60949
ENSMUST00000101197	ENSMUSG00000030047	6	87458545	87533259	-1	0	0	0	8	0	3	1894	4864	2394	374	1922		Q8BYW1
ENSMUST00000101198	ENSMUSG00000047045	X	142681406	142843494	1	0	10	0	55	2	0	718	1432	1134	114	369	A2AH99	
ENSMUST00000101199						0	0	0	0	0	0	0	7	0	0	0		
ENSMUST00000101202	ENSMUSG00000021244	12	84996321	85070515	1	0	1	0	0	0	0	0	16	21	19	0		Q9R0I7
ENSMUST00000101205	ENSMUSG00000031273	X	141165403	141474076	-1	23	8	32	10	23	11	0	0	0	0	1	B1AVK5	
ENSMUST00000101206	ENSMUSG00000037533	11	54522847	54699285	1	0	12	0	0	0	0	0	0	191	0	236	Q5NCJ1	
ENSMUST00000101208	ENSMUSG00000072941	5	52363791	52371418	1	37	28	51	257	36	12	0	0	1	5	12	Q542X9	O09164
ENSMUST00000101211	ENSMUSG00000020333	11	54303798	54364756	1	0	2	5	3	15	0	0	0	0	0	0	Q5ICG5	
ENSMUST00000101212	ENSMUSG00000072944	X	140006805	140062712	-1	2	0	0	25	4	0	0	0	0	0	0	A2AG10	
ENSMUST00000101213	ENSMUSG00000020333	11	54303798	54364756	1	0	0	0	0	0	0	0	0	0	0	0	Q5ICG5	
ENSMUST00000101214						5	4	16	2	10	3	0	0	0	0	0		
ENSMUST00000101215						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000101217	ENSMUSG00000072945	X	139779549	139782353	-1	3	5	7	61	9	5	0	2	1	1	0		Q2WG77
ENSMUST00000101225	ENSMUSG00000019969	12	83688203	83735199	1	15	15	33	67	25	4	1815	3962	2054	275	1365	Q3UYK2	P49769
ENSMUST00000101227	ENSMUSG00000031428	X	136993155	136998472	1	0	2	7	0	0	0	0	8	4	5	5		Q8VD24
ENSMUST00000101234	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	0	0	0	0	0	0	0	F6WDS8	
ENSMUST00000101237	ENSMUSG00000029082	5	43818885	43843986	1	2	3	0	6	8	8	2321	8418	2847	1394	2073		
ENSMUST00000101245	ENSMUSG00000043131	6	83326016	83343776	1	0	2	6	0	6	4	1	0	496	106	276		Q921Y0
ENSMUST00000101249	ENSMUSG00000020358	11	51600100	51606847	-1	11	6	9	16	10	0	0	41	12	0	27	Q80XR6	
ENSMUST00000101250	ENSMUSG00000020359	11	51584757	51604489	1	3	0	7	7	3	0	10	48	20	0	1	F8WHK6	
ENSMUST00000101251	ENSMUSG00000031262	X	134308084	134362639	1	0	0	0	0	0	0	15	0	17	16	12		Q8K1K4
ENSMUST00000101253	ENSMUSG00000079511	6	83101617	83109939	1	17	19	53	257	29	27	53	140	71	15	85		Q8CAI1
ENSMUST00000101254	ENSMUSG00000107499	6	83101601	83108394	1	9	0	0	282	22	0	0	0	0	0	0		Q8CAI1
ENSMUST00000101257	ENSMUSG00000000693	6	83034173	83052562	1	0	18	31	0	0	13	1	6	4	10	3	E9Q0X7	
ENSMUST00000101258						4	8	29	24	12	3	0	0	0	0	0		
ENSMUST00000101265	ENSMUSG00000020377	11	50236469	50238616	-1	0	0	0	22	0	0	0	0	0	14	13	Q8K355	
ENSMUST00000101269	ENSMUSG00000072995	X	116448944	116478783	1	0	0	3	0	1	1	0	0	0	0	0		Q3V0P1
ENSMUST00000101270	ENSMUSG00000036644	11	50131396	50172785	1	26	23	26	45	32	13	277	804	369	40	296		Q5SVR0
ENSMUST00000101272	ENSMUSG00000079516	6	78380709	78383827	1	8	2	8	7	6	0	0	0	0	0	0	Q794C6	O09037
ENSMUST00000101278						3	4	10	4	6	1	0	0	0	0	1		
ENSMUST00000101280	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	11	9	0	0	0	0	0	0	E9Q0W6	
ENSMUST00000101281	ENSMUSG00000073000	12	76444560	76451336	1	65	51	69	43	49	26	4	69	17	13	21	Q3UW49	
ENSMUST00000101282	ENSMUSG00000073001	X	111110458	111123874	1	2	3	3	4	0	3	0	0	0	0	0	G3X9R0	
ENSMUST00000101283	ENSMUSG00000063663	X	108737016	108834372	-1	1	3	3	5	2	0	0	1	14	1	0		A2AHJ4
ENSMUST00000101285	ENSMUSG00000073002	6	72368794	72380468	-1	0	15	22	15	0	7	209	284	125	137	110	Q791P0	Q9Z2P8
ENSMUST00000101290	ENSMUSG00000073006	X	107945735	107948465	-1	3	1	5	3	2	0	0	0	0	0	0	Q3V0P9	
ENSMUST00000101291	ENSMUSG00000021055	12	76120419	76177259	-1	0	17	0	0	34	28	0	0	0	0	0		
ENSMUST00000101292	ENSMUSG00000073007	X	107792590	107872909	1	0	1	1	2	3	0	0	0	0	0	0	B1ATX6	
ENSMUST00000101293	ENSMUSG00000020346	11	49244191	49263030	1	0	0	8	48	0	3	1271	1174	841	64	761	Q544F0	P27808
ENSMUST00000101294	ENSMUSG00000073008	X	107255878	107296769	1	108	46	119	2007	253	118	9	22	8	7	14		Q3U507
ENSMUST00000101295	ENSMUSG00000069892	11	49015874	49051242	-1	4607	4306	26270	8658	4592	1979	705	2777	1957	517	1618	Q5SVP2	
ENSMUST00000101296	ENSMUSG00000073010	X	106583186	106710557	1	6	0	2	1	1	1	0	4	0	0	0	Q3UQH6	
ENSMUST00000101297	ENSMUSG00000073010	X	106583186	106710557	1	1	0	0	0	0	0	0	0	3	4	3	Q3UQH6	
ENSMUST00000101298	ENSMUSG00000044716	5	35056766	35087839	1	0	0	0	176	4	0	0	0	0	0	0		Q18PE0
ENSMUST00000101301	ENSMUSG00000052337	6	71831331	71877388	1	0	0	0	0	0	0	0	0	64	59	127		Q8CAQ8
ENSMUST00000101305	ENSMUSG00000031229	X	105797615	105929403	-1	6	2	2	4	2	1	1	0	7	3	8	Q3TA30	
ENSMUST00000101306	ENSMUSG00000020395	11	46325150	46389515	-1	3	6	7	15	10	6	4	1	0	5	4	Q5STT7	
ENSMUST00000101313	ENSMUSG00000044712	12	73286779	73354049	1	138	116	3796	3081	1486	941	0	5917	232	2122	656	F2Z3Y3	
ENSMUST00000101316	ENSMUSG00000054520	5	34525838	34563641	1	0	0	0	0	0	0	640	874	585	55	562	Q3UD40	
ENSMUST00000101324	ENSMUSG00000073027	X	102707865	102715209	1	3	0	1	0	0	0	0	0	0	0	0	A2AI93	
ENSMUST00000101325	ENSMUSG00000073028	6	69243158	69243688	-1	4	2	1	0	1	1	0	0	0	5	0	L7N239	
ENSMUST00000101326	ENSMUSG00000057098	11	44617317	45008091	1	0	0	0	20	0	0	2	0	1	0	8	Q5SWK4	
ENSMUST00000101327	ENSMUSG00000019189	11	44518964	44565520	1	17	10	60	23	21	13	28	51	53	6	114	Q8BU61	
ENSMUST00000101336	ENSMUSG00000051159	X	102247381	102252181	-1	0	0	0	34	0	0	0	0	0	0	0	Q3UGA1	P97769
ENSMUST00000101339	ENSMUSG00000079481	X	101849385	102092055	1	0	0	29	160	24	15	283	0	879	0	382	E9Q0V6	
ENSMUST00000101340	ENSMUSG00000020415	11	43420250	43426251	-1	0	0	0	0	0	0	44	0	0	16	0		Q9CQJ7
ENSMUST00000101341	ENSMUSG00000031314	X	101532734	101601789	1	60	49	240	77	73	30	0	152	53	7	72	D3YZK4	
ENSMUST00000101343	ENSMUSG00000029910	6	66535390	66547220	1	13	10	14	2	15	8	43	87	38	40	11	Q5HZH8	Q9Z1B5
ENSMUST00000101347	ENSMUSG00000042032	11	40679314	40695203	-1	3	4	6	4	5	1	279	627	561	517	189		Q99LB6
ENSMUST00000101351	ENSMUSG00000073043	6	64729125	64731245	1	8	1	30	276	20	7	0	0	0	0	0		P48985
ENSMUST00000101354	ENSMUSG00000004642	5	33634952	33652574	-1	0	4	4	0	0	0	197	699	145	162	36	Q8K2W7	
ENSMUST00000101358	ENSMUSG00000090141	X	101261376	101263992	-1	0	0	0	1	0	2	0	11	3	0	11		Q3V2K1
ENSMUST00000101362	ENSMUSG00000031297	X	101079210	101086020	-1	0	1	8	5	5	0	0	0	0	0	0		P70423
ENSMUST00000101364	ENSMUSG00000020143	11	34226815	34783892	-1	5	1	4	3	1	6	2	1	3	0	0	Q3TMS1	
ENSMUST00000101365	ENSMUSG00000020143	11	34226815	34783892	-1	9	0	14	0	7	6	0	3	0	0	10	Q5SRI3	
ENSMUST00000101367	ENSMUSG00000029780	6	56882400	56923932	-1	0	5	0	0	4	7	835	4923	1240	1389	364		Q9D020
ENSMUST00000101368	ENSMUSG00000053519	11	33629339	33993152	-1	9	5	23	11	22	0	0	0	0	0	0		Q9JJ57
ENSMUST00000101371	ENSMUSG00000073052	11	33599302	33625618	1	44	32	17	40	41	26	1	11	2	0	2	Q3UW13	
ENSMUST00000101375	ENSMUSG00000057113	11	33152287	33163206	-1	0	0	9	0	0	3	150	757	466	2893	691	Q5SQB5	
ENSMUST00000101376	ENSMUSG00000029134	5	32232708	32366520	1	15	14	31	8	24	11	0	0	0	0	0		Q3TTY0
ENSMUST00000101377						0	0	0	24	0	0	0	0	0	0	0		
ENSMUST00000101379	ENSMUSG00000034912	12	66469568	67222549	-1	1	0	11	0	0	0	0	0	0	0	0	F6UYI7	
ENSMUST00000101382						14	20	55	15	30	12	0	0	0	0	0		
ENSMUST00000101385	ENSMUSG00000005225	6	54595111	54645839	1	2	0	0	3	2	0	2	25	10	2	9		Q80W71
ENSMUST00000101387	ENSMUSG00000073063	11	32286965	32287784	1	5	5	0	7	10	0	2	0	1	9	0	Q3U0A6	
ENSMUST00000101388	ENSMUSG00000073062	X	94724569	94730187	1	4	4	26	22	6	2	87	125	48	9	47		A2CE44
ENSMUST00000101394	ENSMUSG00000020309	11	30976707	30986350	-1	0	4	0	3	0	0	50	46	56	57	24		Q9CQG1
ENSMUST00000101395	ENSMUSG00000000942	6	52189671	52191753	-1	4	10	18	35	5	1	0	3	1	1	1		
ENSMUST00000101396	ENSMUSG00000096072	X	91480126	91481160	1	2	0	10	8	4	1	0	0	0	0	0	A2AHM1	
ENSMUST00000101397	ENSMUSG00000073069	X	91331690	91333360	1	5	0	0	4	0	0	0	0	0	0	0	A2AHM0	
ENSMUST00000101398	ENSMUSG00000046782	12	57564113	57737928	1	7	2	7	147	8	3	0	0	0	0	0	Q497K6	
ENSMUST00000101402						0	2	6	1	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000101405	ENSMUSG00000029821	6	50188888	50263862	-1	9	7	14	4	15	9	14	48	11	4	24	D3YYP5	
ENSMUST00000101410	ENSMUSG00000073077	X	79266559	79517285	-1	2	1	2	1	4	3	0	0	0	0	0	B1AY26	
ENSMUST00000101411	ENSMUSG00000101678	5	31144739	31179911	-1	0	2	0	10	0	9	29	11	55	0	86	Q3UU56	
ENSMUST00000101419	ENSMUSG00000073085	X	76393350	76397979	1	2	2	0	0	0	0	0	0	0	0	0	Q3V0X2	
ENSMUST00000101425						3	1	3	11	7	0	2	0	0	0	0		
ENSMUST00000101426	ENSMUSG00000023367	6	48840919	48847071	1	5	3	6	13	14	5	99	333	81	191	238		Q9DCS1
ENSMUST00000101429	ENSMUSG00000029810	6	48833818	48841496	-1	1	11	0	6	2	0	251	740	133	378	334		Q9R1Q6
ENSMUST00000101432	ENSMUSG00000021010	12	53248677	54072175	1	34	29	158	427	53	21	0	1	0	0	1	F8VQB2	
ENSMUST00000101433	ENSMUSG00000073094	X	75146056	75163770	-1	0	0	0	0	0	0	0	0	0	0	0		Q3V0X1
ENSMUST00000101434	ENSMUSG00000083012	5	143548706	143564531	1	0	0	36	0	8	4	48	0	47	0	63	Q91X57	
ENSMUST00000101436	ENSMUSG00000073096	6	48554796	48570722	1	160	114	478	1428	291	116	610	1127	515	92	439		
ENSMUST00000101442	ENSMUSG00000029168	5	30711564	30799375	1	4	11	9	8	17	4	0	0	0	0	0	Q3SYJ1	
ENSMUST00000101443	ENSMUSG00000068551	6	48427697	48445825	-1	0	0	0	0	0	4	0	25	0	2	1	Q3USQ2	
ENSMUST00000101445	ENSMUSG00000045466	6	47953390	47965300	1	33	1	53	33	9	11	0	0	6	10	12	Q3UZY6	
ENSMUST00000101448	ENSMUSG00000073102	5	30281388	30366695	1	20	15	29	50	34	16	1	5	1	8	2		Q3USS3
ENSMUST00000101453	ENSMUSG00000043943	9	18321951	18402995	-1	0	10	0	0	0	4	0	0	0	0	0	E9Q049	
ENSMUST00000101454	ENSMUSG00000031328	X	74223461	74249820	-1	0	45	0	0	62	0	40901	26494	62905	2123	40043	B7FAU9	
ENSMUST00000101457	ENSMUSG00000031394	X	74127464	74150760	1	0	0	0	0	0	0	0	0	0	0	0	B1AYN7	
ENSMUST00000101458	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	0	0	0	0	0	B1AUW9	
ENSMUST00000101461	ENSMUSG00000073111	6	42927233	42928159	1	6	1	12	10	5	1	0	0	0	0	0	Q8VEV0	
ENSMUST00000101463						1071	1062	3596	1198	1238	641	15	138	46	11	51		
ENSMUST00000101470	ENSMUSG00000031390	X	73892102	73895502	1	0	1	6	7	7	0	32	168	73	5	77	Q3SWS4	
ENSMUST00000101471	ENSMUSG00000061576	5	26817203	27727505	1	0	0	0	0	8	0	0	0	0	0	0	Q80VM5	
ENSMUST00000101472	ENSMUSG00000047446	12	40005447	40038025	-1	1	5	1	14	5	3	26	149	46	73	18		P61213
ENSMUST00000101477	ENSMUSG00000020134	11	21091291	21150323	1	10	10	0	6	0	10	12	0	0	16	0	Q5SRW7	Q8C669
ENSMUST00000101486	ENSMUSG00000073125	X	73192207	73202930	1	0	0	0	0	0	0	0	0	2	0	0		Q6P205
ENSMUST00000101491	ENSMUSG00000029915	6	40574894	40585821	-1	11	10	15	19	9	3	205	890	281	295	162		Q9R007
ENSMUST00000101492	ENSMUSG00000037172	6	40401375	40436135	-1	36	27	38	95	30	16	604	1642	1574	120	792		Q3UHG7
ENSMUST00000101495	ENSMUSG00000073130	X	71928816	71940870	1	5	7	1	6	4	3	0	2	0	0	0	B9EJU1	
ENSMUST00000101497	ENSMUSG00000002413	6	39603237	39725463	-1	0	0	0	3	8	0	84	64	311	0	235	F6SZ47	
ENSMUST00000101499	ENSMUSG00000020659	12	31484829	31499616	-1	16	13	51	20	14	13	153	233	78	17	69		Q9JIY2
ENSMUST00000101501	ENSMUSG00000031337	X	71210767	71315691	1	3	2	0	2	2	1	0	0	0	0	3	Q3UDN6	
ENSMUST00000101504	ENSMUSG00000059482	4	10874498	10899425	1	0	8	0	0	0	0	0	68	0	0	0	B1AV75	
ENSMUST00000101506	ENSMUSG00000073139	X	70459753	70477180	-1	7	6	17	9	10	4	110	253	130	73	108	Q3TYW3	
ENSMUST00000101509	ENSMUSG00000035847	X	70343069	70365084	-1	31	32	91	63	19	7	358	483	370	57	397		Q08890
ENSMUST00000101513	ENSMUSG00000028995	5	23915276	24030690	-1	0	0	0	28	3	4	0	0	0	0	0	Q3TTP7	
ENSMUST00000101525	ENSMUSG00000020407	11	9118103	9136170	1	0	0	0	0	0	0	1123	3984	670	745	384	Q5SUC8	P52624
ENSMUST00000101526	ENSMUSG00000018572	11	69995777	70000009	1	0	5	10	0	0	1	552	913	416	71	158		Q8BSN5
ENSMUST00000101527	ENSMUSG00000062949	X	60223290	60592698	-1	0	1	0	0	0	0	37	202	69	0	114		Q9QZW0
ENSMUST00000101531	ENSMUSG00000031139	X	60055956	60179089	-1	0	6	3	0	0	0	0	0	0	0	0	Q8C067	
ENSMUST00000101532	ENSMUSG00000038665	6	36846022	37300184	-1	12	9	27	5	10	12	0	0	0	0	0	D3YWQ0	
ENSMUST00000101534	ENSMUSG00000029838	6	36714929	36810220	-1	36	31	160	44	33	21	1	0	0	0	1		P63089
ENSMUST00000101538	ENSMUSG00000073158	12	24044701	24096968	-1	9	7	3	135	8	6	2	2	2	0	0	Q9D308	
ENSMUST00000101544						0	0	0	369	0	0	1	3	0	0	0		
ENSMUST00000101547	ENSMUSG00000074865	13	62517500	62520544	-1	0	2	0	3	3	0	7	13	6	6	7	K7N6H3	
ENSMUST00000101551	ENSMUSG00000052593	12	21323509	21373632	-1	19	0	0	0	0	0	0	5	0	0	116	E9PXU2	
ENSMUST00000101552	ENSMUSG00000073173	X	56524742	56525432	1	0	0	1	0	0	0	2	1	0	0	0	F6SW83	
ENSMUST00000101553	ENSMUSG00000035967	X	56454857	56507843	1	0	6	9	10	10	1	13	113	65	0	45	E9PXU1	
ENSMUST00000101554	ENSMUSG00000020456	11	6291633	6356642	1	0	0	0	52	17	25	0	0	0	0	0		Q60597
ENSMUST00000101558	ENSMUSG00000040003	5	19227036	20704792	1	39	30	49	507	64	40	0	9	2	0	2		Q9WVQ1
ENSMUST00000101560	ENSMUSG00000073176	X	56346400	56365674	1	124	76	893	202	90	42	7	14	7	4	9	Q8CB76	
ENSMUST00000101561	ENSMUSG00000073177	X	56189827	56212881	-1	0	2	0	0	0	0	0	0	0	0	0	Q3TML4	
ENSMUST00000101562	ENSMUSG00000052632	12	21111748	21270171	1	0	36	0	0	0	47	0	0	12	0	2		Q7SIG6
ENSMUST00000101564	ENSMUSG00000056215	6	34029448	34134034	1	7	14	8	6	7	6	0	0	0	0	0	Q8BR18	
ENSMUST00000101568	ENSMUSG00000073184	12	20415938	20433699	1	2	0	0	53	0	0	0	0	0	0	0	K7N6H4	
ENSMUST00000101577						0	5	11	11	5	3	0	0	0	0	0		
ENSMUST00000101581	ENSMUSG00000040118	5	15934691	16374511	1	1	0	0	1	1	0	0	0	0	0	0		O08532
ENSMUST00000101582	ENSMUSG00000094947	12	18853872	18854207	1	12	4	10	1024	20	17	2	0	0	0	0	L7N237	
ENSMUST00000101585	ENSMUSG00000057897	11	5969644	6066362	-1	3	0	0	31	0	0	0	0	0	0	0	Q5SVI3	
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ENSMUST00000101587	ENSMUSG00000025626	X	52912266	52956943	1	72	83	234	87	122	44	2	0	0	0	9	E9QAG2	
ENSMUST00000101588	ENSMUSG00000073207	X	52791200	52799468	1	3	7	12	11	6	1	0	0	0	0	0		Q3UYG1
ENSMUST00000101589	ENSMUSG00000073209	6	30956023	30959078	-1	38	16	43	322	31	11	0	0	0	0	0		Q19A41
ENSMUST00000101610	ENSMUSG00000034175	11	5098926	5106093	1	0	0	0	212	2	5	7	0	0	0	0	B7ZNJ8	Q8BP97
ENSMUST00000101613	ENSMUSG00000009090	11	4986824	5042791	1	0	15	1	0	0	0	0	410	2	53	0	Q5SVG4	
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ENSMUST00000101615	ENSMUSG00000034274	11	4895320	4928867	1	8	9	10	14	12	0	0	22	19	0	0	Q5SVF9	
ENSMUST00000101616	ENSMUSG00000031099	X	47809368	47892974	-1	0	2	3	4	4	0	0	0	0	0	0		Q6PGB8
ENSMUST00000101617	ENSMUSG00000068699	6	29433256	29461883	1	103	0	0	0	0	0	1	0	0	6	0	D3YW87	Q8VHX6
ENSMUST00000101618	ENSMUSG00000022010	14	76414961	76507765	1	5	2	0	6	5	0	0	0	0	0	0	D3YW86	
ENSMUST00000101619						0	3	2	0	0	1	0	0	0	0	0		
ENSMUST00000101625						3	7	21	6	6	0	0	0	0	0	0		
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ENSMUST00000101627						5	4	2	1	5	3	0	0	0	2	0		
ENSMUST00000101632	ENSMUSG00000020435	11	3703731	3863903	-1	0	17	15	38	19	0	0	0	0	0	0	Q5QNQ4	
ENSMUST00000101636	ENSMUSG00000073243	X	37209348	37211041	-1	4	4	12	3	9	1	0	1	0	0	0	Q3UKW5	
ENSMUST00000101637	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	0	13	0	0		O70585
ENSMUST00000101638	ENSMUSG00000020451	11	3344256	3409189	-1	15	0	23	6	0	6	800	561	699	60	436		O54785
ENSMUST00000101640	ENSMUSG00000020451	11	3344256	3409189	-1	0	0	0	0	0	0	0	0	0	0	0	Q5NC03	
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ENSMUST00000101644						0	8	18	0	0	0	12	49	20	0	0		
ENSMUST00000101645	ENSMUSG00000073245	X	35404183	35427093	1	3	0	3	0	5	0	0	0	0	0	0	Q62478	
ENSMUST00000101647	ENSMUSG00000073247	X	35067384	35090316	1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000101654	ENSMUSG00000073255	X	30329772	30352645	1	0	0	0	0	0	0	0	0	0	0	0	Q62478	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000101655	ENSMUSG00000023764	11	3131850	3193463	-1	0	0	0	0	0	0	0	0	0	0	99	E9QJT8	
ENSMUST00000101657	ENSMUSG00000073257	X	29976314	29999162	1	0	0	0	0	0	0	0	0	0	0	0	Q4KL05	
ENSMUST00000101663	ENSMUSG00000041390	6	15720661	15802169	1	3	2	1	28	4	0	9	18	6	11	21		Q8BX65
ENSMUST00000101667	ENSMUSG00000093923	X	24753162	24775164	-1	0	0	1	0	0	0	0	0	0	0	0	Q497S0	
ENSMUST00000101670	ENSMUSG00000036769	X	23693051	23806025	1	0	0	0	0	0	0	56	332	97	13	38		Q6NVE8
ENSMUST00000101677	ENSMUSG00000004631	6	4674350	4747207	-1	0	0	0	0	0	0	0	0	0	0	0	E9PX46	
ENSMUST00000101690	ENSMUSG00000079703	X	8684887	8690844	-1	0	0	0	0	0	0	0	0	0	0	0	B1AY40	
ENSMUST00000101694	ENSMUSG00000031153	X	7789765	7820567	1	0	7	0	0	0	0	0	132	0	4	0	A2AEW9	
ENSMUST00000101695	ENSMUSG00000000134	X	7762560	7775202	1	0	3	1	0	10	0	0	260	62	0	0		Q64092
ENSMUST00000101698	ENSMUSG00000073294	X	6081219	6083419	-1	1	2	0	0	2	3	0	0	0	0	0	Q3UWZ4	
ENSMUST00000101800	ENSMUSG00000075705	17	24736642	24742778	1	17	16	18	7	19	9	6301	9806	4507	4640	3128		Q9JLC3
ENSMUST00000101801	ENSMUSG00000075701	7	66079649	66089405	1	4	2	9	40	9	2	209	645	294	469	213		Q9BCZ4
ENSMUST00000102476	ENSMUSG00000060802	2	122147686	122153083	1	7	3	13	12	17	12	7524	26294	6220	36078	8527		P01887
ENSMUST00000102478	ENSMUSG00000017390	11	78322968	78327781	1	0	1	0	6	0	0	55	70	33	0	20		P05063
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ENSMUST00000102482						0	1	0	0	0	4	2360	2986	1129	2558	813		
ENSMUST00000102483	ENSMUSG00000058546	11	78180932	78183584	-1	17	17	16	30	11	15	4916	8425	4760	24542	2998	Q5M9M5	P62751
ENSMUST00000102484	ENSMUSG00000078515	4	141677549	141723419	-1	36	25	97	87	78	38	3517	10816	8758	573	5289		A2ADY9
ENSMUST00000102486	ENSMUSG00000006221	4	141420779	141425311	1	47	45	214	97	65	31	0	1	1	0	2		P35385
ENSMUST00000102487	ENSMUSG00000040842	4	141113001	141139775	-1	0	0	0	0	0	6	584	887	615	102	489		Q6NXN1
ENSMUST00000102488	ENSMUSG00000000631	11	77763246	77865980	1	0	0	6	0	0	0	0	0	0	0	0		Q9JMH9
ENSMUST00000102490	ENSMUSG00000023216	2	121017891	121037072	-1	55	48	68	51	50	20	0	0	0	3	7		P49222
ENSMUST00000102491	ENSMUSG00000040860	4	141016637	141060550	-1	39	0	59	362	50	20	13	29	36	0	35		Q8CJ40
ENSMUST00000102493	ENSMUSG00000020836	11	77462411	77470484	1	43	43	259	312	59	32	5	25	0	2	14		Q920M5
ENSMUST00000102494	ENSMUSG00000037958	11	77044292	77078435	-1	29	19	137	55	27	14	133	1011	366	1110	367		Q5NCR9
ENSMUST00000102495	ENSMUSG00000020839	11	76902159	76916587	1	2	1	1	0	0	0	2	0	0	0	0		Q9D7L8
ENSMUST00000102496	ENSMUSG00000027286	2	120604238	120609520	-1	0	0	0	0	0	0	56	720	88	0	54	Q8JZX5	
ENSMUST00000102497	ENSMUSG00000027286	2	120604238	120609520	-1	3	4	3	12	8	6	109	176	122	157	78	Q8JZX5	
ENSMUST00000102498	ENSMUSG00000027286	2	120604238	120609520	-1	0	0	0	0	0	0	0	0	0	0	0	Q8JZX5	
ENSMUST00000102499	ENSMUSG00000027286	2	120604238	120609520	-1	0	0	0	0	0	0	27	20	54	60	28	Q8JZX5	
ENSMUST00000102500	ENSMUSG00000049396	11	76210571	76217664	-1	18	16	40	71	21	14	0	0	0	0	0	Q6P6L6	
ENSMUST00000102501	ENSMUSG00000027291	2	120316461	120353137	-1	0	18	57	44	16	0	67	202	90	96	89	Q3USV9	Q8R5L3
ENSMUST00000102503	ENSMUSG00000028741	4	139347435	139352576	-1	9	0	4	61	12	14	70	353	124	99	141	A2AMU9	Q9D0I8
ENSMUST00000102504	ENSMUSG00000017774	11	75650504	75673910	1	11	10	20	10	4	0	0	74	28	0	77		Q9WTI7
ENSMUST00000102505	ENSMUSG00000017774	11	75650504	75673910	1	5	0	15	5	12	11	118	0	0	0	80		Q9WTI7
ENSMUST00000102507	ENSMUSG00000028745	4	139192899	139291818	1	0	0	0	15	0	0	60	318	210	93	266		P47757
ENSMUST00000102508	ENSMUSG00000028745	4	139192899	139291818	1	0	0	6	18	0	0	4356	14831	6467	1898	4170	Q923G3	P47757
ENSMUST00000102509	ENSMUSG00000017781	11	75588097	75628804	1	7	0	6	7	0	0	383	183	665	137	310	F8WGG5	
ENSMUST00000102510	ENSMUSG00000020850	11	75486816	75509449	1	35	32	82	0	0	0	1915	2297	1226	226	950		Q99PV0
ENSMUST00000102511	ENSMUSG00000041193	4	138799244	138863482	-1	2	0	0	0	0	5	0	0	0	0	1	Q6GTW1	
ENSMUST00000102512	ENSMUSG00000041193	4	138799244	138863482	-1	0	0	2	11	0	0	2	0	2	5	0	Q6GTW1	
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ENSMUST00000102514	ENSMUSG00000045287	11	75193783	75267769	1	29	20	76	301	51	14	4	7	4	8	30		Q8K0S5
ENSMUST00000102515	ENSMUSG00000005034	3	146729574	146812990	-1	12	8	0	61	13	7	210	467	300	23	176		P68181
ENSMUST00000102517	ENSMUSG00000027314	2	119325784	119335962	1	32	20	81	303	53	28	1	1	0	0	5		Q9JI71
ENSMUST00000102518	ENSMUSG00000057530	4	137862237	137965229	1	82	47	306	183	80	37	91	162	76	36	304		Q4PZA2
ENSMUST00000102519	ENSMUSG00000068580	2	119208617	119217049	1	0	0	0	5	0	0	102	166	95	78	53	Q4KL52	
ENSMUST00000102520	ENSMUSG00000020745	11	74673949	74724670	-1	5	3	13	150	9	7	125	728	269	78	98	Q5SW18	P63005
ENSMUST00000102521	ENSMUSG00000038807	11	74383356	74590186	-1	0	0	81	42	0	0	0	42	0	42	0		Q5SVL6
ENSMUST00000102522	ENSMUSG00000023433	4	137420999	137430540	-1	7	1	10	12	12	11	1	0	0	0	1		Q9CQ52
ENSMUST00000102523	ENSMUSG00000094488	11	73847185	73848123	-1	4	3	2	0	4	0	0	0	0	0	0	Q8VGR6	
ENSMUST00000102524	ENSMUSG00000040061	2	118707517	118728438	-1	32	19	38	27	32	24	1325	2541	1812	90	1538		A3KGF7
ENSMUST00000102525	ENSMUSG00000029465	5	122391878	122414184	1	1	0	0	14	0	0	5898	10314	5929	21692	3564		Q9JM76
ENSMUST00000102526	ENSMUSG00000005952	11	73234292	73261242	1	19	7	11	20	15	16	0	0	0	0	0		Q704Y3
ENSMUST00000102527	ENSMUSG00000005102	2	118388618	118475234	1	4	0	0	4	0	2	14	46	20	0	38		Q9QZ05
ENSMUST00000102528	ENSMUSG00000004455	5	122158278	122175273	1	24	24	0	77	11	0	1611	4032	1405	330	594	Q6ZWM8	P63087
ENSMUST00000102529	ENSMUSG00000057969	9	107597674	107609229	-1	0	4	26	53	9	6	1	0	0	1	0	M9MMK0	
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ENSMUST00000102534	ENSMUSG00000027347	2	117279993	117343001	-1	37	25	2	95	43	26	0	0	0	0	0		Q9Z1S3
ENSMUST00000102536	ENSMUSG00000059291	4	136028265	136053428	-1	6	13	18	9	10	0	317	404	430	2951	258		Q9CXW4
ENSMUST00000102537	ENSMUSG00000005947	11	73090583	73147446	1	14	15	32	16	32	24	2	27	22	5	30	Q8BS01	
ENSMUST00000102538	ENSMUSG00000027210	2	115863064	116065839	-1	1	0	0	0	0	0	0	0	0	0	0	Q6GU28	P97367
ENSMUST00000102540	ENSMUSG00000028671	4	135963727	135968178	1	6	3	0	0	6	0	20	60	8	0	52		Q8R059
ENSMUST00000102541	ENSMUSG00000028671	4	135963727	135968178	1	0	0	12	23	0	1	326	249	121	31	68		Q8R059
ENSMUST00000102542	ENSMUSG00000057147	2	114516416	114654964	-1	0	6	0	0	0	9	6	20	0	0	0		Q9CQ28
ENSMUST00000102543	ENSMUSG00000040383	2	114101170	114187024	-1	10	0	4	0	10	0	0	9	0	0	0	A2AQA7	
ENSMUST00000102544	ENSMUSG00000028676	4	135855747	135869908	1	0	0	0	97	10	1	42	73	92	62	59	Q3TFP0	
ENSMUST00000102545	ENSMUSG00000041219	2	113831492	113848661	-1	0	0	0	0	0	0	121	224	151	0	0		Q80Y19
ENSMUST00000102546	ENSMUSG00000037157	4	135728172	135752140	1	38	16	91	47	43	13	0	0	0	0	2		Q80XZ4
ENSMUST00000102547	ENSMUSG00000044042	2	113327736	113716767	1	49	41	23	32	42	18	0	13	0	2	8		Q05860
ENSMUST00000102548						0	0	0	0	0	0	71	0	415	0	176		
ENSMUST00000102549	ENSMUSG00000028803	4	135445420	135495038	-1	15	22	44	34	45	11	574	833	539	77	499		Q8BGN5
ENSMUST00000102550	ENSMUSG00000046671	4	134525550	134535387	-1	0	0	13	36	6	7	38	165	61	38	106		Q9CWE0
ENSMUST00000102551	ENSMUSG00000061195	2	111483432	111484328	1	2	6	1	0	3	3	0	0	0	0	0	Q8VF49	
ENSMUST00000102552	ENSMUSG00000003038	4	133964738	133968650	-1	0	0	0	62	0	3	0	23	266	1665	629	Q5BL14	P09602
ENSMUST00000102553	ENSMUSG00000003038	4	133964738	133968650	-1	16	11	1	68	23	4	3801	8788	3634	1294	1361	Q5BL14	P09602
ENSMUST00000102554	ENSMUSG00000020821	11	70700548	70731964	1	0	0	0	0	0	0	0	68	1	0	109		O35071
ENSMUST00000102555	ENSMUSG00000027166	2	105966709	106003549	-1	2	2	6	28	5	4	16	79	32	112	19	A2A4A1	
ENSMUST00000102556	ENSMUSG00000014609	11	70614883	70619216	-1	16	0	23	13	13	9	3	0	0	0	1		P20782
ENSMUST00000102557	ENSMUSG00000029361	5	117781032	117958840	1	0	2	2	1	0	0	0	0	0	0	0	F8WGF2	
ENSMUST00000102558	ENSMUSG00000020827	11	70562881	70614483	1	9	0	0	0	3	0	124	0	135	2	102		Q9JM52

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
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ENSMUST00000102560	ENSMUSG00000029516	5	115845278	116008947	1	0	0	0	0	0	0	18	0	31	0	1	D3YU89	
ENSMUST00000102561	ENSMUSG00000028884	4	132768332	132778752	1	10	10	41	15	18	10	115	185	96	94	108	Q3TE40	
ENSMUST00000102563	ENSMUSG00000060216	11	70432635	70440828	1	0	0	0	0	0	0	1363	559	407	114	235		Q91YI4
ENSMUST00000102564	ENSMUSG00000060216	11	70432635	70440828	1	4	0	0	32	0	0	3744	6317	3150	493	1546		Q91YI4
ENSMUST00000102565	ENSMUSG00000027180	2	104027721	104063240	1	4	0	11	0	13	6	122	346	167	117	161		Q9DC63
ENSMUST00000102567	ENSMUSG00000066042	4	132458731	132463921	-1	54	48	321	91	44	25	43	98	42	8	26		Q9CZ82
ENSMUST00000102568	ENSMUSG00000066043	4	132355923	132422489	-1	0	2	10	53	0	0	263	422	346	0	276		Q501J7
ENSMUST00000102569	ENSMUSG00000020831	11	70235206	70237914	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DCT6
ENSMUST00000102570						3	3	5	179	7	2	84	491	293	77	237		
ENSMUST00000102571	ENSMUSG00000000318	11	70156197	70170834	1	0	0	0	0	0	0	45	24	6	63	46		P49300
ENSMUST00000102572	ENSMUSG00000040963	11	70092644	70106187	1	4	4	3	9	5	4	0	0	0	0	2		P24721
ENSMUST00000102573	ENSMUSG00000027189	2	102300119	102407828	-1	38	45	135	138	59	32	55	171	105	35	194	Q4KMS1	
ENSMUST00000102574	ENSMUSG00000018574	11	70010183	70015411	-1	0	0	2	2	0	0	631	692	659	244	570		P50544
ENSMUST00000102575	ENSMUSG00000020888	11	70000595	70012301	1	12	5	22	28	22	16	9	45	29	6	25		Q60838
ENSMUST00000102576	ENSMUSG00000040533	4	130944385	130955475	1	15	9	46	56	30	14	0	0	0	0	0		P51942
ENSMUST00000102578	ENSMUSG00000041870	5	114774677	114806200	1	13	22	4	313	34	23	5089	5711	6879	812	5476		Q80UP5
ENSMUST00000102580	ENSMUSG00000018570	11	69897352	69900987	-1	0	0	0	0	0	0	0	0	4	0	7	Q6NSU2	
ENSMUST00000102581	ENSMUSG00000001098	5	114363567	114380508	-1	6	0	6	53	7	6	4707	5885	4250	540	2530		Q922M3
ENSMUST00000102582	ENSMUSG00000042010	5	114146535	114250761	1	29	29	115	79	112	48	0	0	0	0	0		E9Q4Z2
ENSMUST00000102584	ENSMUSG00000029591	5	114130386	114139323	1	5	0	5	211	13	29	0	10	0	0	0	Q791V7	P97931
ENSMUST00000102585	ENSMUSG00000042826	11	69796068	69801857	-1	18	6	101	388	30	12	3	0	0	0	0		P70378
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ENSMUST00000102589	ENSMUSG00000059796	11	69666936	69672423	-1	3	0	0	16	0	3	0	3	0	6	0	K3W4Q6	
ENSMUST00000102590	ENSMUSG00000003731	4	129643980	129672767	-1	32	13	66	65	26	21	345	1097	578	119	541	Q8BH30	O35345
ENSMUST00000102591	ENSMUSG00000028797	4	129600668	129624059	1	113	85	248	120	104	73	329	1397	632	310	576		Q8R1E7
ENSMUST00000102592	ENSMUSG00000030516	7	65296165	65527781	-1	6	26	19	95	10	6	0	0	0	5	27		P39447
ENSMUST00000102593	ENSMUSG00000028798	4	129591960	129600648	-1	0	3	7	13	16	5	538	685	403	1726	357		Q9QZD9
ENSMUST00000102594	ENSMUSG00000040591	2	91275068	91444704	-1	13	8	8	17	15	5	3	0	15	6	11		Q8BHR8
ENSMUST00000102596	ENSMUSG00000000409	4	129548344	129573641	-1	5	0	3	5	0	0	172	182	56	0	178		P06240
ENSMUST00000102597	ENSMUSG00000028800	4	129516104	129542713	-1	20	0	16	82	22	26	461	1577	694	571	519	Q58E49	O09106
ENSMUST00000102598	ENSMUSG00000057236	4	129307100	129335370	-1	30	19	45	41	22	18	1213	3390	1315	695	851		Q60972
ENSMUST00000102599	ENSMUSG00000001333	4	129287617	129308559	1	0	0	0	8	0	0	0	1	1	0	2	C0LQ89	Q9EPM5
ENSMUST00000102600	ENSMUSG00000001334	4	129136999	129144593	1	27	32	70	46	53	24	0	11	0	1	2		Q8K4Z2
ENSMUST00000102601	ENSMUSG00000049299	11	69323980	69325793	1	0	6	0	0	6	12	159	369	165	422	103	Q14BF8	Q5NCF2
ENSMUST00000102602	ENSMUSG00000049299	11	69323980	69325793	1	5	0	23	10	0	0	496	1163	263	1486	205	Q14BF8	Q5NCF2
ENSMUST00000102604	ENSMUSG00000028792	4	128991958	129011529	1	20	8	21	15	18	8	1682	2791	1964	533	896		Q9WTP6
ENSMUST00000102605	ENSMUSG00000020893	11	69095217	69109960	1	20	6	0	0	24	0	0	326	0	26	52	Q8CHR1	
ENSMUST00000102606	ENSMUSG00000018740	11	68968131	68974365	1	10	0	14	9	8	4	10	19	3	0	6		Q5SWT3
ENSMUST00000102607	ENSMUSG00000028830	4	126753544	126870070	1	0	0	0	7	6	0	0	0	0	0	0	Z4YK56	
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ENSMUST00000102609	ENSMUSG00000049149	2	89927319	89930746	1	3	0	9	0	0	0	0	0	0	0	0	Q8VGN6	
ENSMUST00000102611	ENSMUSG00000020900	11	68691559	68816632	1	15	0	10	76	13	10	0	31	21	0	0		Q61879
ENSMUST00000102612	ENSMUSG00000045915	11	68587021	68597966	1	6	3	0	0	4	2	0	0	0	0	0		Q5SV66
ENSMUST00000102613	ENSMUSG00000046207	11	68503019	68552698	1	23	0	0	0	1	15	317	160	78	34	385		Q3U6Q4
ENSMUST00000102616	ENSMUSG00000028845	4	126322121	126325688	-1	0	0	0	20	11	14	0	0	0	0	0		Q922G7
ENSMUST00000102617	ENSMUSG00000042558	4	126316047	126321703	-1	0	2	0	110	15	5	164	152	105	41	73		Q8CG72
ENSMUST00000102618	ENSMUSG00000049372	2	88461342	88462253	1	0	0	2	0	3	0	0	0	0	0	0	Q8VFF8	
ENSMUST00000102619	ENSMUSG00000075124	2	88446019	88446936	-1	2	2	6	2	0	0	0	0	0	0	0	Q7TR17	
ENSMUST00000102620	ENSMUSG00000045326	3	108853678	108890008	-1	2	0	21	34	0	0	0	0	0	0	0		A2AED3
ENSMUST00000102621	ENSMUSG00000027882	3	108793176	108840526	-1	2	7	5	9	2	0	229	1014	385	983	369		Q60770
ENSMUST00000102622	ENSMUSG00000062793	2	87990113	87991054	1	5	3	2	3	3	2	0	0	0	0	0	A2BHP7	
ENSMUST00000102624	ENSMUSG00000075156	2	87544607	87545542	-1	2	4	1	5	2	2	0	0	0	0	0	Q7TR47	
ENSMUST00000102625	ENSMUSG00000068739	3	108424865	108445209	-1	10	0	1	6	6	0	619	1020	593	302	613	Q8C483	
ENSMUST00000102626	ENSMUSG00000030854	7	47077798	47133684	-1	7	5	3	2	9	6	5	5	4	0	2		P54830
ENSMUST00000102628	ENSMUSG00000028889	4	124850679	124855242	1	6	0	0	6	6	1	51	204	66	19	68		Q3U5F4
ENSMUST00000102629	ENSMUSG00000068744	3	108383839	108388231	1	0	3	1	0	6	1	0	0	2	3	1		Q9D0P7
ENSMUST00000102631	ENSMUSG00000075186	2	86385466	86386416	-1	2	1	0	0	0	0	0	0	0	0	0	Q7TR74	
ENSMUST00000102632	ENSMUSG00000068747	3	108284082	108361511	1	33	30	70	92	47	29	3797	6250	6397	332	4248		Q6PHU5
ENSMUST00000102633	ENSMUSG00000048997	3	108202222	108210934	-1	5	14	32	18	7	16	0	18	0	0	8	Q8C8K6	
ENSMUST00000102634	ENSMUSG00000075208	2	85840857	85841789	-1	5	4	11	0	3	2	0	0	0	0	0	Q149M3	Q8VGS3
ENSMUST00000102635	ENSMUSG00000020542	11	65176561	65269989	-1	14	0	13	0	0	0	0	0	0	0	0		Q8VIM5
ENSMUST00000102636	ENSMUSG00000023075	4	123734559	123750345	-1	35	23	54	94	44	10	919	3448	1312	480	858		Q99LF1
ENSMUST00000102637	ENSMUSG00000027889	3	108074062	108086651	-1	0	0	1	55	27	3	154	108	104	0	142		Q9DBT5
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ENSMUST00000102640	ENSMUSG00000076436	4	123321875	123323634	-1	18	8	42	381	15	12	2	4	7	0	8		Q9JJN4
ENSMUST00000102641	ENSMUSG00000032726	4	123312645	123343252	-1	5	0	15	0	0	0	44	72	91	3	103		P34821
ENSMUST00000102642	ENSMUSG00000027078	2	84798828	84810335	1	292	252	523	365	430	234	552	722	223	794	315		Q9QZU9
ENSMUST00000102643	ENSMUSG00000018507	11	62574486	62600515	1	1	1	36	4	7	3	651	1244	605	157	225		Q9WTR1
ENSMUST00000102645	ENSMUSG00000027080	2	84678402	84688215	1	7	7	4	89	13	5	56	163	78	31	63		Q8C1S0
ENSMUST00000102646	ENSMUSG00000076437	2	84669215	84670770	-1	2	1	5	4	3	0	3	27	0	4	0		Q3UQA7
ENSMUST00000102647	ENSMUSG00000076437	2	84669215	84670770	-1	0	0	0	0	0	0	17	14	22	57	47		Q3UQA7
ENSMUST00000102648	ENSMUSG00000076438	4	123116266	123118000	1	30	10	37	278	22	8	0	0	2	1	0		
ENSMUST00000102649	ENSMUSG00000028653	4	123016597	123054949	1	13	0	0	0	19	0	22	51	0	35	25		Q80UN9
ENSMUST00000102650	ENSMUSG00000047804	11	61871307	61930252	-1	3	2	13	66	6	0	283	871	594	65	378		O88845
ENSMUST00000102651	ENSMUSG00000059173	2	79834453	80129458	-1	0	0	0	0	0	0	0	0	0	0	0	Q5I7S8	
ENSMUST00000102652	ENSMUSG00000059173	2	79834453	80129458	-1	0	0	0	2	0	0	0	1	0	0	0	Q9JLL9	
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ENSMUST00000102656	ENSMUSG00000052135	4	120267079	120287349	-1	10	4	34	471	20	13	0	0	0	0	0		Q70KY4
ENSMUST00000102657	ENSMUSG00000001039	11	61505144	61512931	1	8	2	0	16	7	0	0	0	0	20	6		Q9R1S0
ENSMUST00000102659	ENSMUSG00000042272	2	77180340	77280592	-1	12	11	10	0	11	10	20	53	33	26	87		Q80UK0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000102660	ENSMUSG00000042272	2	77180340	77280592	-1	42	31	51	19	50	20	3	51	18	20	51		Q80UK0
ENSMUST00000102661	ENSMUSG00000010086	11	61448442	61454131	-1	0	0	0	0	15	0	0	0	0	0	0		Q96DY5
ENSMUST00000102662	ENSMUSG00000028641	4	119232915	119248975	1	0	0	0	0	0	0	0	0	0	0	0	A2A7Q5	
ENSMUST00000102665	ENSMUSG00000076439	17	37010743	37023398	-1	8	5	22	20	17	5	0	0	0	0	0	Q3UY21	
ENSMUST00000102666	ENSMUSG00000043698	4	118665519	118666466	1	5	3	11	12	7	3	0	0	0	0	0	L7MU75	
ENSMUST00000102667	ENSMUSG00000049323	11	60777524	60788287	1	20	17	15	11	19	6	20	0	0	2	0		Q3UMB5
ENSMUST00000102668	ENSMUSG00000002814	11	60740058	60777365	-1	4	13	50	20	16	4	5	0	0	0	4	Q3V3P1	
ENSMUST00000102669						7	0	4	0	4	2	3288	3846	1829	8124	1362		
ENSMUST00000102671	ENSMUSG00000006389	4	118442415	118457513	-1	27	20	22	32	28	0	3	3	7	0	6		Q08351
ENSMUST00000102672	ENSMUSG00000015839	2	75675513	75704641	-1	13	6	51	87	20	15	1767	7307	3198	3936	2353		Q60795
ENSMUST00000102673	ENSMUSG00000006390	4	118428093	118432953	1	0	0	10	3	0	0	734	1313	598	289	382	Q4V9V3	
ENSMUST00000102675	ENSMUSG00000054128	17	36185572	36190287	-1	0	3	0	7	0	5	0	0	0	0	0	Q05A75	
ENSMUST00000102676	ENSMUSG00000009207	2	74520291	74579435	-1	0	0	0	0	0	0	23	185	120	63	74	A2ASL8	
ENSMUST00000102677	ENSMUSG00000056486	2	73610660	73775346	-1	15	15	13	9	20	10	0	0	0	0	0		Q91V57
ENSMUST00000102678	ENSMUSG00000067212	17	36029773	36032855	-1	25	28	19	11	21	18	2523	6255	1941	581	2348	Q3V014	P06339
ENSMUST00000102679	ENSMUSG00000075284	2	73429610	73529734	-1	4	5	9	219	10	8	68	43	123	4	157		Q8K1I7
ENSMUST00000102680	ENSMUSG00000075284	2	73429610	73529734	-1	14	0	20	5	5	0	3309	6149	5553	551	3710		Q8K1I7
ENSMUST00000102682	ENSMUSG00000000538	11	60226714	60352905	-1	3	7	11	17	17	5	15	12	27	0	32		Q5SRX1
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ENSMUST00000102687	ENSMUSG00000009640	4	117674681	117682273	-1	6	8	12	13	4	14	99	171	111	48	61		Q9JI44
ENSMUST00000102688	ENSMUSG00000062115	11	60105013	60199197	1	52	28	181	257	62	31	7	91	107	18	251		Q61818
ENSMUST00000102689	ENSMUSG00000027109	2	72936427	72980446	-1	0	0	11	71	0	0	165	169	138	158	103		O70494
ENSMUST00000102690	ENSMUSG00000028677	4	117271463	117497052	-1	9	0	0	0	2	3	604	779	518	95	336		Q6PDX6
ENSMUST00000102691	ENSMUSG00000055612	2	72476159	72486893	1	7	11	57	71	25	18	201	341	142	21	109		Q9D0M2
ENSMUST00000102692	ENSMUSG00000000301	11	59970614	60046489	-1	7	0	30	3	0	0	0	0	0	0	0		Q61907
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ENSMUST00000102694	ENSMUSG00000027864	3	101040232	101110278	-1	35	29	54	114	48	21	48	106	47	24	253		Q9WV91
ENSMUST00000102695	ENSMUSG00000032615	11	59839447	59880968	1	0	0	0	9	0	0	0	0	8	0	7		Q8VCE6
ENSMUST00000102696	ENSMUSG00000047675	4	117153827	117156243	-1	0	17	16	93	21	5	2300	4818	3237	16230	2351	Q497E9	P62242
ENSMUST00000102697	ENSMUSG00000032633	11	59791408	59810016	-1	74	60	100	101	77	32	178	180	146	10	163		Q8QZS3
ENSMUST00000102698	ENSMUSG00000049044	2	71981240	72257474	1	0	0	0	0	0	0	3	0	0	0	19		Q9EQZ6
ENSMUST00000102699	ENSMUSG00000028687	4	116807723	116819440	1	0	0	0	8	0	0	7	23	0	0	4		Q99P21
ENSMUST00000102701	ENSMUSG00000041966	2	71055328	71099142	1	1	0	0	15	0	0	15	0	0	0	0	Z4YK64	
ENSMUST00000102703	ENSMUSG00000037001	11	58888153	58904225	-1	63	33	256	116	45	33	9	52	33	16	29		Q02525
ENSMUST00000102704	ENSMUSG00000028702	4	116094264	116123690	-1	15	10	24	12	25	18	0	14	11	0	8		P70270
ENSMUST00000102705	ENSMUSG00000028702	4	116094264	116123690	-1	0	0	0	0	0	0	35	30	34	1	20		P70270
ENSMUST00000102706	ENSMUSG00000027086	2	69686815	69713516	-1	0	0	0	0	0	0	1	10	0	0	0		Q6DI86
ENSMUST00000102707	ENSMUSG00000028713	4	115624725	115647723	-1	12	0	27	16	21	10	0	0	0	0	0	Q3TNA0	Q64462
ENSMUST00000102708						0	8	2	24	5	0	4787	8178	2678	552	1743		
ENSMUST00000102709	ENSMUSG00000027048	2	69238282	69342616	-1	0	0	0	0	0	0	0	0	0	0	0		Q9QY30
ENSMUST00000102710	ENSMUSG00000027048	2	69238282	69342616	-1	18	14	27	0	18	6	1	3	4	7	4		Q9QY30
ENSMUST00000102711	ENSMUSG00000037275	11	58120002	58168539	-1	9	10	14	51	8	0	56	0	51	14	61	A2AFQ9	
ENSMUST00000102713	ENSMUSG00000053896	2	68582413	68616387	1	5	1	0	0	2	0	0	0	0	0	0	Q8C5U0	
ENSMUST00000102715	ENSMUSG00000027030	2	68210445	68472268	-1	4	0	3	65	5	0	1	0	0	0	43	A2AQL0	Q9Z1W9
ENSMUST00000102716	ENSMUSG00000000263	11	55514238	55608198	-1	4	12	19	78	17	8	0	0	0	0	0	Q5NCT9	Q64018
ENSMUST00000102718	ENSMUSG00000034848	2	66184327	66256617	-1	16	16	18	57	18	0	8	19	8	25	22		Q0HA38
ENSMUST00000102719	ENSMUSG00000028544	4	111875375	111902918	-1	0	7	0	5	0	15	0	0	0	0	1		Q8VDT1
ENSMUST00000102720	ENSMUSG00000028544	4	111875375	111902918	-1	0	0	0	4	35	11	0	0	0	0	0		Q8VDT1
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ENSMUST00000102722	ENSMUSG00000028546	4	110203722	110351909	-1	0	0	42	10	9	0	0	0	0	0	0	A2A9R6	
ENSMUST00000102723	ENSMUSG00000028546	4	110203722	110351909	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BVA9	
ENSMUST00000102724	ENSMUSG00000010517	4	109676588	109963960	1	18	21	73	85	31	14	215	729	373	153	203		P54731
ENSMUST00000102725	ENSMUSG00000060491	4	109505337	109531297	-1	0	4	0	0	0	0	0	0	0	0	0		Q9CPZ3
ENSMUST00000102726	ENSMUSG00000034903	2	65088339	65239403	-1	0	0	0	0	0	0	0	0	0	0	0	B1AZ15	
ENSMUST00000102727	ENSMUSG00000018340	11	54979108	55033445	-1	18	19	30	50	21	6	487	377	299	209	534	F8WIT2	
ENSMUST00000102728	ENSMUSG00000075324	2	63971507	64098038	-1	0	0	0	5	2	0	0	0	0	0	0	E0CYB7	
ENSMUST00000102729	ENSMUSG00000028552	4	109280268	109387817	1	9	10	27	35	11	10	533	1622	390	273	323	Q80ZL3	P42567
ENSMUST00000102730	ENSMUSG00000020400	11	54910785	54962917	-1	19	14	0	0	0	0	515	510	292	0	285	D3Z2W0	
ENSMUST00000102731	ENSMUSG00000020400	11	54910785	54962917	-1	0	0	0	55	0	0	22	0	0	0	0	E9QM75	
ENSMUST00000102732	ENSMUSG00000000392	2	62500943	62574075	-1	2	0	2	2	4	0	0	19	0	0	9		P97321
ENSMUST00000102733	ENSMUSG00000000394	2	62474530	62483650	-1	5	1	2	2	0	1	0	6	0	2	0		P55095
ENSMUST00000102735	ENSMUSG00000026904	2	62046462	62326730	1	14	0	0	9	19	0	0	0	0	0	0		Q5DTL9
ENSMUST00000102736	ENSMUSG00000053510	4	109000655	109061777	1	4	10	58	168	18	7	0	0	0	68	1	A6PWC3	
ENSMUST00000102737	ENSMUSG00000035033	2	61802930	61814114	1	0	0	0	36	0	0	0	0	0	0	0	A2AR81	
ENSMUST00000102738	ENSMUSG00000073775	4	108847785	108849413	1	4	5	18	127	9	7	25	121	45	14	44		Q9D1R2
ENSMUST00000102739	ENSMUSG00000028568	4	108814295	108833614	-1	2	0	0	0	0	2	0	10	11	10	4	A2A7Z4	Q9CQH7
ENSMUST00000102740	ENSMUSG00000028568	4	108814295	108833614	-1	0	2	0	0	0	0	78	407	152	342	58	A2A7Z4	Q9CQH7
ENSMUST00000102741	ENSMUSG00000028568	4	108814295	108833614	-1	0	0	3	57	9	3	8	23	15	11	15	A2A7Z4	Q9CQH7
ENSMUST00000102742	ENSMUSG00000028568	4	108814295	108833614	-1	15	21	31	27	13	9	92	311	81	196	84	A2A7Z4	Q9CQH7
ENSMUST00000102743	ENSMUSG00000037533	11	54522847	54699285	1	27	7	39	41	41	14	1042	2648	2214	333	1634	Q5NCJ0	
ENSMUST00000102744	ENSMUSG00000028587	4	108579423	108614833	1	9	8	27	20	18	9	7	21	24	8	19		Q9Z1N2
ENSMUST00000102745	ENSMUSG00000021281	12	111442469	111455018	1	11	13	20	90	24	7	7243	12409	6613	717	6675		Q61333
ENSMUST00000102746	ENSMUSG00000052997	7	34140688	34169599	-1	5	4	3	110	12	5	487	1374	733	348	528		Q9Z1F9
ENSMUST00000102747	ENSMUSG00000026977	2	60209887	60250676	1	0	0	0	0	0	0	80	207	293	0	83		Q9WV66
ENSMUST00000102748	ENSMUSG00000026977	2	60209887	60250676	1	0	0	0	41	0	0	1279	1383	188	645	642		Q9WV66
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ENSMUST00000102751	ENSMUSG00000026988	2	59852364	59882591	-1	0	0	0	0	0	0	0	0	0	0	0	A2AUX8	
ENSMUST00000102752	ENSMUSG00000007617	13	93303757	93404129	1	23	23	47	26	8	7	31	30	38	6	38	Q5D052	Q9Z2Y3
ENSMUST00000102754	ENSMUSG00000026991	2	59160850	59355208	1	0	0	0	26	9	0	0	0	0	0	0		Q68FH0
ENSMUST00000102755	ENSMUSG00000026839	2	58567298	58792971	1	0	0	0	0	0	0	0	0	0	0	0	Q3UEN1	Q8CGR7
ENSMUST00000102758	ENSMUSG00000020402	11	52360860	52389397	1	21	25	33	100	25	17	581	1723	679	344	539		Q60932
ENSMUST00000102759	ENSMUSG00000055371	2	52691664	52742281	-1	8	12	30	26	21	5	283	1056	362	275	313	Q3TGH8	O88811
ENSMUST00000102760	ENSMUSG00000017412	2	52428320	52676831	-1	0	11	0	0	0	0	5	15	4	4	9		Q8R0S4
ENSMUST00000102761	ENSMUSG00000017412	2	52428320	52676831	-1	3	0	9	0	17	3	0	0	0	0	0		Q8R0S4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000102762	ENSMUSG00000034853	4	106744555	106804998	-1	125	73	325	128	73	37	97	190	121	13	55	Q543P6	Q8VHQ9
ENSMUST00000102763	ENSMUSG00000020392	11	51967661	51977334	1	9	13	12	111	13	2	436	835	453	322	326		Q9D211
ENSMUST00000102765	ENSMUSG00000063564	11	51289920	51583918	1	42	34	80	92	48	17	0	1	1	1	5		Q8K4G2
ENSMUST00000102766	ENSMUSG00000020364	11	51059257	51072799	1	0	0	3	20	0	0	0	0	0	0	0		Q61751
ENSMUST00000102767	ENSMUSG00000036249	2	51924448	51935163	-1	4	4	2	77	5	0	137	622	389	374	275		Q99J64
ENSMUST00000102768	ENSMUSG00000036249	2	51924448	51935163	-1	11	0	19	29	16	8	21	69	31	9	19		Q99J64
ENSMUST00000102769	ENSMUSG00000026766	2	50279881	50296801	-1	0	1	3	4	3	1	397	1862	634	576	319		Q99LS1
ENSMUST00000102772	ENSMUSG00000020377	11	50236469	50238616	-1	0	6	2	69	7	0	11	14	10	94	155		Q60860
ENSMUST00000102774	ENSMUSG00000015837	11	50199366	50210827	-1	4	8	0	68	13	7	3257	3946	3469	967	2477		Q64337
ENSMUST00000102776	ENSMUSG00000020376	11	50025346	50104758	1	3	0	0	17	0	0	1874	9195	2826	737	1491		Q8VEM1
ENSMUST00000102777	ENSMUSG00000057722	4	101717404	101815352	1	2	0	5	41	6	0	2	8	8	3	0	Q3UNU8	P48356
ENSMUST00000102778	ENSMUSG00000020366	11	49846751	49886421	1	20	17	0	0	31	9	0	226	46	0	20		Q9WTU6
ENSMUST00000102780	ENSMUSG00000028527	4	101419277	101466995	1	0	0	4	37	18	8	0	0	0	0	0	Q3U489	Q9WUR9
ENSMUST00000102781	ENSMUSG00000028530	4	101152367	101265282	-1	16	24	46	44	34	19	4094	11940	8197	1252	6807	B1ASP2	
ENSMUST00000102782	ENSMUSG00000078193	1	156366040	156366484	1	1	0	0	0	0	1	1151	1737	1275	7371	821		Q6ZWV7
ENSMUST00000102783	ENSMUSG00000025791	4	99929414	99987294	1	8	14	25	1	23	12	0	0	0	0	0	A2CEK3	
ENSMUST00000102785	ENSMUSG00000040328	11	48978889	49135387	1	0	0	0	0	0	0	4	0	0	37	22		Q8VGD6
ENSMUST00000102786						0	0	0	0	0	0	1	7	2	14	0		
ENSMUST00000102787	ENSMUSG00000035392	2	37798991	38287390	-1	37	13	83	178	45	28	152	205	184	16	211		Q8K382
ENSMUST00000102789	ENSMUSG00000050714	2	37432168	37443135	-1	7	0	5	0	7	0	1	12	21	0	7	Q8C8S0	
ENSMUST00000102790	ENSMUSG00000035407	4	98754898	98817537	-1	28	22	39	57	55	19	0	0	0	2	1		Q6P9J5
ENSMUST00000102792	ENSMUSG00000061859	4	98395785	98719603	1	14	16	13	4	21	7	0	4	0	0	0		Q63ZW7
ENSMUST00000102793	ENSMUSG00000028563	4	98355370	98383306	-1	0	0	0	85	2	0	62	222	47	27	19		Q99MB3
ENSMUST00000102794	ENSMUSG00000035778	2	35400179	35463231	-1	0	8	21	0	21	16	78	22	37	50	49	Q9DBU1	
ENSMUST00000102795	ENSMUSG00000041231	11	44454571	44470498	-1	7	0	15	36	6	9	197	1124	609	899	398		Q8BGR9
ENSMUST00000102796	ENSMUSG00000004296	11	44400063	44414033	1	12	4	9	10	7	0	0	0	1	4	1	Q3ZAX5	P43432
ENSMUST00000102798	ENSMUSG00000006386	4	94739289	94874976	1	10	0	0	0	0	0	0	0	0	0	0	B1AWS8	
ENSMUST00000102799	ENSMUSG00000008489	4	91250763	91400785	-1	0	0	0	0	0	0	0	0	0	0	0	Q80Y51	
ENSMUST00000102800	ENSMUSG00000026867	2	34674594	34755232	-1	16	16	28	205	15	16	164	710	125	23	0		Q6PAR5
ENSMUST00000102801	ENSMUSG00000049336	11	36006656	37235964	-1	53	28	96	42	48	45	0	0	0	0	0	A0A0A0MQB7	
ENSMUST00000102802	ENSMUSG00000052013	16	45224315	45252895	1	8	10	8	7	0	0	20	0	40	75	30		
ENSMUST00000102803	ENSMUSG00000053093	14	54970688	54994634	-1	0	28	13	76	20	18	0	0	0	0	0	B2RXX9	Q91Z83
ENSMUST00000102804	ENSMUSG00000096682	4	88835525	88836094	1	2	5	15	4	3	0	0	0	0	0	0	Q810G2	
ENSMUST00000102805	ENSMUSG00000090176	16	44867097	44915840	1	239	226	1777	286	328	144	3	8	8	5	18		Q6XJV6
ENSMUST00000102806	ENSMUSG00000073811	4	88602580	88603376	-1	4	5	14	9	7	5	0	0	0	0	0		Q80SS5
ENSMUST00000102807	ENSMUSG00000095270	4	88591813	88592385	-1	9	6	6	9	11	2	0	0	0	0	0		P09235
ENSMUST00000102808	ENSMUSG00000095896	4	88571229	88571798	-1	6	3	18	1	5	4	0	0	0	0	0	Q810G3	
ENSMUST00000102809	ENSMUSG00000096011	4	88557673	88558245	-1	3	2	11	8	4	0	0	0	0	0	0	Q61718	
ENSMUST00000102810	ENSMUSG00000038860	2	32986224	33131654	-1	8	0	0	1	5	0	0	0	0	29	40		Q3V0G7
ENSMUST00000102811	ENSMUSG00000038900	2	32961559	32965345	1	0	0	0	0	6	0	0	42	15	21	6	A0A0A6YVW4	
ENSMUST00000102812	ENSMUSG00000041607	18	82475146	82585637	1	16	0	0	0	0	0	6	0	0	0	0		P04370
ENSMUST00000102813	ENSMUSG00000038987	2	32777381	32784428	-1	11	15	30	12	20	9	1	0	1	0	2		Q0VFX2
ENSMUST00000102814	ENSMUSG00000028495	4	86854660	86857412	-1	35	59	46	86	59	18	1966	5642	3644	12880	2505	Q5BLK1	P62754
ENSMUST00000102815	ENSMUSG00000040594	11	33211795	33513746	-1	14	17	18	52	29	11	0	0	0	0	1		Q99NF8
ENSMUST00000102817	ENSMUSG00000047261	16	42248442	42340651	-1	2	7	7	21	13	3	0	0	0	0	0		P06837
ENSMUST00000102818	ENSMUSG00000079442	2	32587095	32599698	1	22	9	15	70	29	5	170	367	110	47	188	Q8C3J2	
ENSMUST00000102819	ENSMUSG00000038070	4	84884309	85131921	1	1	3	4	98	2	0	0	0	1	0	0		A2AM05
ENSMUST00000102820	ENSMUSG00000028487	4	84275095	84675275	-1	9	0	86	0	14	0	0	0	0	0	0		Q8BMQ3
ENSMUST00000102821	ENSMUSG00000020272	11	32533305	32624587	1	63	36	290	155	72	40	4004	6040	6432	360	4856		O55098
ENSMUST00000102822	ENSMUSG00000025969	1	62703285	62818695	1	41	9	1	367	131	61	0	77	109	10	123		O35375
ENSMUST00000102823	ENSMUSG00000038172	4	83220300	83324255	-1	57	65	80	533	63	31	170	1018	425	78	702		Q8BYY4
ENSMUST00000102824	ENSMUSG00000034459	19	34640871	34650009	1	23	18	59	60	19	23	11	307	21	106	122		Q64282
ENSMUST00000102825	ENSMUSG00000074896	19	34583531	34588731	1	17	6	7	12	13	7	0	92	6	59	48	Q5FW82	Q64345
ENSMUST00000102826	ENSMUSG00000045932	19	34550694	34576419	1	22	13	13	14	8	5	30	155	57	65	78	Q6GTM0	
ENSMUST00000102827	ENSMUSG00000026009	1	60977927	61000320	1	16	15	11	8	22	15	9	26	9	18	32	Q5SUZ7	Q9WVS0
ENSMUST00000102829	ENSMUSG00000020299	11	31965592	31979651	1	7	10	5	164	9	4	0	0	0	0	0		Q24JP4
ENSMUST00000102830	ENSMUSG00000028402	4	81278500	81442815	-1	13	6	21	16	20	11	0	0	0	0	14		Q8VBX6
ENSMUST00000102831	ENSMUSG00000005994	4	80834123	80851719	1	12	7	0	0	0	0	0	0	0	0	0	Q3UFS3	P07147
ENSMUST00000102832	ENSMUSG00000032093	9	44998743	45009590	-1	11	2	14	13	14	6	90	100	40	15	115	A6H6M1	P22646
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ENSMUST00000102837	ENSMUSG00000043003	4	73714579	73790709	-1	6	9	6	36	21	7	0	1	1	0	0		Q5RI75
ENSMUST00000102838	ENSMUSG00000020315	11	30099395	30268175	-1	42	37	64	44	36	16	121	60	412	28	385		Q62261
ENSMUST00000102840	ENSMUSG00000076441	2	31470207	31520672	1	15	14	18	51	12	6	154	264	100	27	165	Q3UJ34	P16460
ENSMUST00000102841	ENSMUSG00000020458	11	29692947	29744331	1	8	4	15	77	4	3	168	382	0	0	0		Q99P72
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ENSMUST00000102844	ENSMUSG00000020460	11	29545846	29548109	-1	9	10	42	84	22	10	3300	8060	1787	4114	635	Q642L7	P62983
ENSMUST00000102845	ENSMUSG00000020460	11	29545846	29548109	-1	5	13	3	70	15	2	1340	3081	1477	9929	1048	Q642L7	P62983
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ENSMUST00000102849	ENSMUSG00000026854	2	30982279	31023586	1	34	0	43	52	0	34	43	43	33	0	0		Q8C6M1
ENSMUST00000102852	ENSMUSG00000050737	2	30889471	30929863	-1	53	60	155	99	61	39	38	113	51	27	70		Q9JM51
ENSMUST00000102853	ENSMUSG00000047363	2	30595040	30608943	1	13	4	23	12	2	3	0	0	0	0	0	Q9D245	
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ENSMUST00000102856	ENSMUSG00000020463	11	29172890	29220797	1	4	0	9	162	12	8	0	0	0	0	27		Q922R5
ENSMUST00000102858	ENSMUSG00000040907	7	24978167	25005958	-1	18	8	57	22	40	23	21	123	12	0	23	Q8VCE0	
ENSMUST00000102861	ENSMUSG00000058935	4	63607089	63622428	-1	0	0	0	0	0	0	0	0	0	0	0	Q9DA81	
ENSMUST00000102862	ENSMUSG00000058935	4	63607089	63622428	-1	8	3	5	3	4	2	0	2	2	0	10	Q9DA81	
ENSMUST00000102863	ENSMUSG00000020273	11	23862646	23895253	-1	1	0	4	20	0	0	0	0	0	0	6	Q8BY05	
ENSMUST00000102864	ENSMUSG00000020275	11	23736847	23770970	-1	8	12	20	110	16	11	165	272	281	26	252	A4QPD3	
ENSMUST00000102865	ENSMUSG00000015335	2	30090944	30093648	-1	0	0	0	18	4	0	63	48	69	11	10		Q8VC90
ENSMUST00000102866	ENSMUSG00000054766	2	30057378	30072577	1	51	48	135	225	47	38	0	117	51	60	104	Q3T9S3	Q9EQU5
ENSMUST00000102867	ENSMUSG00000039137	4	63414910	63495991	-1	0	0	0	0	0	0	4	5	3	0	6		Q80VW5
ENSMUST00000102869	ENSMUSG00000020290	11	23256041	23298249	1	11	8	37	15	26	12	19	93	0	61	0		Q6P5F9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
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ENSMUST00000102871	ENSMUSG00000031391	X	73853778	73896105	-1	18	12	73	60	31	0	0	0	116	0	80	Q6PGJ3	
ENSMUST00000102872	ENSMUSG00000039844	2	29619720	29740978	1	46	49	135	67	77	23	1024	687	1076	27	955	Q91ZZ2	
ENSMUST00000102873	ENSMUSG00000035513	2	29194541	29253005	-1	8	0	0	0	0	0	6	0	6	0	0	A2AKW8	Q8R4F1
ENSMUST00000102874	ENSMUSG00000020321	11	21556787	21572367	-1	11	4	42	4	18	7	503	1151	624	3010	464		P14152
ENSMUST00000102875	ENSMUSG00000001891	11	21321138	21371201	-1	8	8	10	10	7	7	188	890	169	182	111		Q91ZJ5
ENSMUST00000102877	ENSMUSG00000026809	2	28692080	28699727	-1	0	5	0	0	5	0	28	0	7	36	10		Q7TPM5
ENSMUST00000102878	ENSMUSG00000020160	11	18879817	19018985	-1	0	2	0	0	0	11	0	0	0	0	0	A0A0A0MQB8	
ENSMUST00000102879	ENSMUSG00000026833	2	28192992	28230736	1	6	0	0	57	7	0	31	78	28	11	14		O88998
ENSMUST00000102880	ENSMUSG00000033953	11	17159263	17200375	1	3	5	9	124	10	5	1308	3245	1388	209	628		Q63810
ENSMUST00000102881	ENSMUSG00000020120	11	16971206	17052381	-1	34	27	155	77	41	21	3091	14644	7943	12106	6606	Q5F271	Q9JHK5
ENSMUST00000102883	ENSMUSG00000028382	4	59471868	59549364	-1	0	0	0	0	0	2	129	0	0	112	229	G8JL74	
ENSMUST00000102884	ENSMUSG00000020122	11	16752203	16918158	1	1	6	3	25	7	5	0	0	0	0	0	Q9WVF5	
ENSMUST00000102886	ENSMUSG00000009614	2	27188393	27248337	-1	19	31	63	38	39	23	0	0	0	0	0	Q3TWI2	Q99LB7
ENSMUST00000102888	ENSMUSG00000024617	18	60925618	60988152	1	134	55	241	659	162	74	8	10	6	0	14		P11798
ENSMUST00000102889	ENSMUSG00000050812	4	58798911	58912749	-1	4	3	14	4	9	9	376	2039	1069	252	659		Q6PDI5
ENSMUST00000102890	ENSMUSG00000036067	2	27021363	27027998	-1	2	0	14	0	2	0	77	415	0	130	146	A2AR26	
ENSMUST00000102891	ENSMUSG00000014852	2	26973416	27009628	1	9	19	59	47	25	7	0	0	0	1	0		Q769J6
ENSMUST00000102893	ENSMUSG00000057280	4	58285960	58374303	1	0	0	0	18	0	17	2	1	2	0	3	Q32S49	Q61006
ENSMUST00000102894	ENSMUSG00000089672	10	51480632	51486316	1	6	11	33	16	13	2	1651	19733	4275	10882	6556	Q549E3	Q61450
ENSMUST00000102895	ENSMUSG00000032125	9	37401897	37414023	1	0	0	0	0	0	0	1	0	0	2	1		
ENSMUST00000102897	ENSMUSG00000038709	4	57984027	58009124	-1	3	1	8	0	6	2	0	0	0	0	0	Q14AP0	Q69AB2
ENSMUST00000102898	ENSMUSG00000062647	2	26910764	26913318	1	26	47	98	71	50	20	3583	5849	3450	12138	2848	Q58ET1	P12970
ENSMUST00000102899	ENSMUSG00000015776	2	26905262	26910677	-1	22	16	34	69	27	13	905	958	680	116	386		Q62276
ENSMUST00000102900	ENSMUSG00000015787	2	26842503	26864979	-1	3	4	8	7	3	0	0	0	0	0	0		P38649
ENSMUST00000102902	ENSMUSG00000038729	4	57717657	57896982	1	116	67	491	10	96	55	0	6	5	8	0		O54931
ENSMUST00000102903	ENSMUSG00000038729	4	57717657	57896982	1	0	0	0	2	2	2	0	0	0	0	60		O54931
ENSMUST00000102904	ENSMUSG00000090053	4	57434247	57712016	1	55	53	375	44	39	29	0	1	0	0	3		Q8BR92
ENSMUST00000102905	ENSMUSG00000090053	4	57434247	57712016	1	0	0	0	119	17	0	0	0	0	0	0		Q8BR92
ENSMUST00000102907	ENSMUSG00000026921	2	26580014	26593120	1	0	0	0	0	0	0	0	0	0	0	0	Q3UTJ7	
ENSMUST00000102909	ENSMUSG00000040985	11	9016054	9048991	-1	2	0	2	4	12	0	0	0	0	0	1		Q5SS91
ENSMUST00000102910	ENSMUSG00000000381	11	6635482	6638637	-1	2	2	1	3	4	0	0	0	0	0	1	Q7M748	
ENSMUST00000102911	ENSMUSG00000028412	4	53440413	53622478	1	4	9	0	15	5	3	41	142	61	51	90		Q6X893
ENSMUST00000102912	ENSMUSG00000032656	18	56761716	56925548	-1	16	11	36	175	21	12	3	1	2	3	9		Q8BRX9
ENSMUST00000102914	ENSMUSG00000041164	11	6389074	6406158	1	0	14	3	0	0	0	204	298	55	0	137		Q8CIE2
ENSMUST00000102915	ENSMUSG00000028312	4	52439243	52488260	1	5	0	0	34	25	12	71	71	283	150	87		Q8CG48
ENSMUST00000102917	ENSMUSG00000028339	4	47208161	47313167	1	0	24	0	0	33	0	0	0	0	0	6		O35206
ENSMUST00000102918	ENSMUSG00000015093	2	25456838	25458776	1	0	0	0	0	0	0	0	0	0	0	0	A2AJ28	
ENSMUST00000102919	ENSMUSG00000026944	2	25428703	25448540	1	76	45	151	129	111	43	365	336	395	32	525	A2AJ26	
ENSMUST00000102920	ENSMUSG00000041798	11	5900820	5950081	-1	36	20	70	47	29	19	0	0	0	0	0	Q5SVI5	P52792
ENSMUST00000102921	ENSMUSG00000020469	11	5896637	5898782	-1	11	6	14	44	4	4	0	0	0	0	0	Q5SVI8	Q9QVP4
ENSMUST00000102922	ENSMUSG00000020471	11	5872180	5878292	-1	7	10	10	36	7	10	53	43	27	28	72		O35654
ENSMUST00000102923	ENSMUSG00000020473	11	5861947	5872088	1	27	14	196	230	50	21	0	0	0	3	35		Q640N1
ENSMUST00000102924	ENSMUSG00000039853	4	46493781	46536141	-1	111	54	62	988	153	98	3	61	13	6	44		Q8BVW3
ENSMUST00000102925	ENSMUSG00000026956	2	25359889	25365682	-1	16	15	39	39	21	8	272	298	181	91	141		Q3TW96
ENSMUST00000102926	ENSMUSG00000028333	4	46450902	46472657	1	18	11	26	174	27	7	922	3174	1246	293	978		Q9EST5
ENSMUST00000102927	ENSMUSG00000024122	17	24073680	24150924	-1	17	14	24	50	7	8	705	1586	942	139	524		Q9Z2A0
ENSMUST00000102928	ENSMUSG00000020476	11	5788488	5800962	1	16	8	12	13	14	14	3168	6174	2716	429	1763		Q62418
ENSMUST00000102929	ENSMUSG00000035517	4	45965334	46034761	1	0	0	20	37	24	0	181	723	482	181	543		Q8K1H1
ENSMUST00000102930	ENSMUSG00000009079	11	5069689	5099266	-1	15	0	12	0	25	2	645	1457	1421	411	1113	Q5SUS9	
ENSMUST00000102931	ENSMUSG00000006476	2	25054355	25062881	1	0	0	1	0	0	0	0	0	0	1	0		Q99NF2
ENSMUST00000102932	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	0	0	0	A2AKM6	
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ENSMUST00000102935	ENSMUSG00000026972	2	24925352	24935252	-1	6	3	7	0	13	0	397	2	113	0	141		Q99KN1
ENSMUST00000102936	ENSMUSG00000028479	4	44034075	44084177	-1	0	0	2	120	32	15	29	38	53	0	56	Q3TCI8	Q91WG8
ENSMUST00000102938	ENSMUSG00000036893	2	24789928	24919614	-1	24	0	12	0	21	0	1	0	56	0	57	Z4YJZ7	
ENSMUST00000102939	ENSMUSG00000004113	2	24603887	24763152	-1	76	0	0	15	110	0	11	66	78	0	0	A2AIR9	
ENSMUST00000102942	ENSMUSG00000026979	2	24367580	24414954	1	114	56	247	125	102	61	289	879	422	34	422		Q8BLR5
ENSMUST00000102943	ENSMUSG00000076430	13	30946573	30947759	-1	5	9	7	4	12	3	0	1	0	2	0	Q059L7	Q8K572
ENSMUST00000102944	ENSMUSG00000028466	4	43562332	43567060	1	5	7	13	7	7	2	471	710	435	699	220	Q3UNH6	
ENSMUST00000102945	ENSMUSG00000069132	2	23321246	23401973	1	6	6	4	8	3	5	0	0	0	0	0	Q3KP70	Q61199
ENSMUST00000102946	ENSMUSG00000021357	13	30813919	30974047	-1	0	0	32	2	10	0	117	106	18	17	30		Q9D4H1
ENSMUST00000102948	ENSMUSG00000016477	13	29906575	29985668	-1	29	24	61	223	30	14	87	208	105	16	108	Q3UZJ0	O35261
ENSMUST00000102950	ENSMUSG00000020435	11	3703731	3863903	-1	30	0	22	32	17	11	0	0	0	0	0	Q8K0C7	
ENSMUST00000102951	ENSMUSG00000048550	2	21205724	21215009	1	0	0	0	0	0	0	0	4	0	0	0	A2AUG7	
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ENSMUST00000102953	ENSMUSG00000028457	4	43267159	43373833	1	10	19	89	32	27	18	3	10	2	2	3		A3FIN4
ENSMUST00000102954	ENSMUSG00000069258	13	27383339	27390846	-1	2	2	2	2	2	0	0	0	0	0	0	B9EHM9	Q9DAZ2
ENSMUST00000102955	ENSMUSG00000045031	3	37307749	37312708	-1	0	0	0	5	0	0	0	0	0	3	0		Q8K4K1
ENSMUST00000102956	ENSMUSG00000021870	14	26413168	26534931	-1	8	13	17	65	15	8	253	390	396	0	301		Q3URD3
ENSMUST00000102957	ENSMUSG00000071005	4	42754525	42756577	-1	0	0	0	0	0	0	0	0	0	0	0	Q548P0	O70460
ENSMUST00000102960	ENSMUSG00000026718	2	14074098	14149634	1	17	24	48	39	22	9	30	64	30	12	44	Q3TQ49	P70297
ENSMUST00000102961	ENSMUSG00000028444	4	41657498	41697089	-1	0	0	0	54	0	0	0	0	0	0	0		O88507
ENSMUST00000102962	ENSMUSG00000028444	4	41657498	41697089	-1	8	8	15	0	18	5	0	0	0	0	0		O88507
ENSMUST00000102963	ENSMUSG00000061322	4	41569775	41638158	1	15	12	15	38	18	6	0	2	1	1	0	A2ANP4	Q8C0M8
ENSMUST00000102964	ENSMUSG00000060093	13	23760692	23761230	-1	13	2	11	108	10	1	0	0	2	4	0	B2RTM0	P62806
ENSMUST00000102965	ENSMUSG00000069266	13	23757013	23757409	1	3	4	2	47	14	0	0	0	4	5	0	B2RTM0	P62806
ENSMUST00000102967	ENSMUSG00000060678	13	23698060	23698454	-1	2	6	2	30	5	0	3	3	0	2	0	B2RTM0	P62806
ENSMUST00000102968	ENSMUSG00000061482	13	23581598	23581990	1	4	0	1	74	2	2	1	1	1	7	3	B2RTM0	P62806
ENSMUST00000102969	ENSMUSG00000069272	13	23570662	23571121	-1	3	0	2	92	7	0	3	20	14	14	14	B2RVF0	P22752
ENSMUST00000102970	ENSMUSG00000026778	2	11172108	11301222	1	0	0	0	0	0	0	0	0	0	0	0	F8WGT6	
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ENSMUST00000102972	ENSMUSG00000060981	13	23531050	23531522	1	5	5	2	57	5	8	7	24	14	29	11	B2RTM0	P62806
ENSMUST00000102973	ENSMUSG00000028405	4	40143081	40198338	1	29	19	33	100	42	10	188	284	305	85	239		P28271

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000102975	ENSMUSG00000073910	4	34949074	35157484	-1	130	93	211	671	169	84	50	129	42	6	48		Q8VE04
ENSMUST00000102976	ENSMUSG00000015619	2	9857078	9890034	-1	37	26	98	90	36	20	7	15	8	3	49	Q3U0R5	P23772
ENSMUST00000102977	ENSMUSG00000060639	13	22040636	22041362	-1	5	11	9	95	3	2	308	724	174	323	172	B2RTM0	P62806
ENSMUST00000102978	ENSMUSG00000006720	13	21945094	21960779	1	13	8	16	103	13	0	0	0	0	0	0		Q7TSH9
ENSMUST00000102979	ENSMUSG00000069305	13	21831767	21832196	-1	19	16	10	366	38	17	8	50	12	0	20	B2RTM0	P62806
ENSMUST00000102980	ENSMUSG00000001642	6	34302434	34317478	-1	0	11	8	52	0	1	323	632	251	851	311	Q3UDY1	P45376
ENSMUST00000102981	ENSMUSG00000025816	2	5870987	5895432	-1	0	0	3	42	5	0	0	29	0	0	7		Q9JLR1
ENSMUST00000102982	ENSMUSG00000069308	13	21787461	21789213	1	4	12	2	87	20	1	1	2	5	5	0		Q8CGP2
ENSMUST00000102983	ENSMUSG00000064288	13	21750194	21750505	-1	0	3	0	41	4	7	2	0	3	2	5	B2RTM0	P62806
ENSMUST00000102985	ENSMUSG00000026669	2	4989714	5012791	-1	28	23	44	29	30	8	20	21	14	3	11		Q0VBD2
ENSMUST00000102988	ENSMUSG00000026648	2	3424131	3464130	1	6	7	79	6	12	10	81	514	232	142	341		Q8K4J0
ENSMUST00000102989	ENSMUSG00000026643	2	3284212	3328877	1	0	0	0	8	0	0	5	0	0	0	11	A2AJH3	
ENSMUST00000102991	ENSMUSG00000029782	6	30479053	30509783	-1	0	0	0	0	0	0	0	0	6	0	0	F8WGT2	
ENSMUST00000102992	ENSMUSG00000039130	6	30366380	30391028	-1	0	0	0	0	0	0	0	0	0	0	0		Q80YV2
ENSMUST00000102993	ENSMUSG00000039159	6	30211289	30304539	-1	35	32	101	73	55	36	4886	18818	9660	1056	8125	Q3V2N4	P62257
ENSMUST00000102994	ENSMUSG00000040359	4	25248600	25281821	-1	0	2	0	71	6	6	7	97	44	69	12		Q8CCJ3
ENSMUST00000102995	ENSMUSG00000029772	6	29768011	29912310	1	0	0	3	48	0	0	138	112	0	12	300	F8WGT1	
ENSMUST00000102996	ENSMUSG00000021747	14	8431192	8666240	-1	11	9	27	110	10	11	0	1	0	0	0		Q6P2K3
ENSMUST00000102997	ENSMUSG00000028252	4	21727701	21759922	1	0	1	0	0	6	7	80	173	20	0	0		Q62447
ENSMUST00000102998	ENSMUSG00000055761	4	20118874	20778866	-1	269	301	434	515	430	276	2	3	1	0	8		Q3URJ8
ENSMUST00000102999	ENSMUSG00000056494	4	19280850	19510623	1	15	17	23	6	11	7	0	1	1	0	0		Q9JJZ9
ENSMUST00000103000	ENSMUSG00000023165	X	8454345	8461726	-1	0	0	4	0	0	0	0	0	0	0	0	Q80ZT4	
ENSMUST00000103001	ENSMUSG00000035371	X	8748432	8754587	1	0	1	0	0	2	2	0	0	0	0	0	Q6XAS3	
ENSMUST00000103002	ENSMUSG00000076432	12	21390071	21417637	-1	6	0	0	104	26	24	0	352	42	24	19	A3KML3	P68254
ENSMUST00000103003	ENSMUSG00000068219	X	8327424	8336237	1	2	0	3	0	8	1	0	0	0	0	0	Q6XAR7	
ENSMUST00000103004	ENSMUSG00000028207	4	9448069	9669344	-1	8	10	20	3	7	3	0	0	0	0	0	Q9CR06	
ENSMUST00000103005	ENSMUSG00000068270	X	6399854	6637448	1	2	0	36	87	4	2	0	0	0	0	2		Q1W617
ENSMUST00000103006	ENSMUSG00000073293	X	6168696	6173015	-1	2	5	2	235	6	4	0	0	0	0	1		P0C028
ENSMUST00000103007	ENSMUSG00000073295	X	6047453	6055110	1	5	6	15	50	6	5	0	0	0	0	0		P0C028
ENSMUST00000103008	ENSMUSG00000028249	4	6365650	6408423	1	0	2	15	0	11	0	5663	14181	6343	10222	3261	Q3TMX0	
ENSMUST00000103009						0	4	7	79	18	0	2701	5131	2546	10943	1548		
ENSMUST00000103010	ENSMUSG00000042228	4	3678115	3813122	1	6	0	0	0	18	0	1767	7651	3430	2676	4099	Q3U6Q5	P25911
ENSMUST00000103012	ENSMUSG00000078683	4	60498012	60501960	-1	0	1	0	0	0	0	0	0	0	0	0	A2CEL1	
ENSMUST00000103013	ENSMUSG00000039230	11	121451949	121617164	1	20	15	58	152	35	7	232	339	367	46	288		Q8BYA0
ENSMUST00000103014	ENSMUSG00000025175	11	121434913	121450491	1	12	18	24	17	27	8	0	2	1	0	2	Q7TQJ3	
ENSMUST00000103015	ENSMUSG00000000056	11	121237253	121255856	1	27	27	52	68	60	25	1389	3622	2084	585	1501		Q9CYQ7
ENSMUST00000103016	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	4	0	0	23	45	0	0	0		Q8VBT9
ENSMUST00000103017	ENSMUSG00000039703	11	120380370	120437708	-1	32	9	52	44	1	19	0	0	0	16	0		P60670
ENSMUST00000103018	ENSMUSG00000061306	11	120103960	120151346	-1	0	0	0	0	0	12	0	23	14	0	0		Q5I012
ENSMUST00000103019	ENSMUSG00000025375	11	120007313	120047167	-1	0	0	6	4	7	0	2168	2089	2017	120	1693	B1AZF9	
ENSMUST00000103020	ENSMUSG00000025375	11	120007313	120047167	-1	0	0	0	393	0	0	0	0	0	0	0	B1AZF9	
ENSMUST00000103021	ENSMUSG00000025372	11	119942763	120006782	1	0	0	0	0	0	0	0	24	0	30	96		Q8BKX1
ENSMUST00000103023	ENSMUSG00000025576	11	118489762	118911597	-1	5	8	43	0	0	0	0	0	0	0	0		Q8BIF2
ENSMUST00000103024	ENSMUSG00000076433	11	118332360	118342500	-1	11	6	17	17	6	11	0	0	11	0	0		Q497N6
ENSMUST00000103025	ENSMUSG00000025572	11	117765988	117782198	-1	4	7	15	4	4	0	6	25	51	4	45		Q7TN60
ENSMUST00000103026	ENSMUSG00000020823	11	117115168	117159268	1	0	0	0	0	0	0	489	9	347	9	233	Q99J07	
ENSMUST00000103027	ENSMUSG00000043857	11	116918863	116986948	1	22	10	42	65	26	24	0	0	0	0	0		Q765H6
ENSMUST00000103028	ENSMUSG00000020806	11	116598165	116627019	-1	26	11	30	29	44	12	13	27	26	47	0		Q80WQ6
ENSMUST00000103029	ENSMUSG00000020806	11	116598165	116627019	-1	7	4	0	18	0	0	2530	3148	2264	168	1972		Q80WQ6
ENSMUST00000103031	ENSMUSG00000020776	11	116142285	116168166	-1	6	0	0	0	0	7	72	0	14	0	0		A2A870
ENSMUST00000103032	ENSMUSG00000020782	11	115824049	115855780	1	29	0	0	233	29	29	139	117	117	9	105		Q3TJ91
ENSMUST00000103033	ENSMUSG00000020747	11	115765433	115799366	1	25	0	98	30	29	19	1088	733	1102	0	626		Q7TSH8
ENSMUST00000103034	ENSMUSG00000020747	11	115765433	115799366	1	0	1	6	29	0	0	3	0	0	0	0	B1AT98	
ENSMUST00000103035	ENSMUSG00000016940	11	115420128	115431274	1	7	0	6	5	10	1	232	510	176	44	111	Q4VBE7	
ENSMUST00000103036	ENSMUSG00000018858	11	115403752	115412674	1	2	0	0	0	1	0	38	71	48	111	57		Q8R035
ENSMUST00000103037	ENSMUSG00000045288	11	115315192	115322041	-1	26	25	75	548	64	23	0	1	0	0	0	Q0VBT9	Q80T11
ENSMUST00000103038	ENSMUSG00000015542	11	115182832	115187859	-1	4	3	10	0	15	2	67	204	106	54	118		Q3UG98
ENSMUST00000103039	ENSMUSG00000015542	11	115182832	115187859	-1	0	0	0	0	0	0	23	0	0	0	0		Q3UG98
ENSMUST00000103040	ENSMUSG00000015542	11	115182832	115187859	-1	2	0	6	39	9	2	304	363	153	101	98		Q3UG98
ENSMUST00000103041	ENSMUSG00000015542	11	115182832	115187859	-1	0	0	0	0	0	0	0	90	0	10	0		Q3UG98
ENSMUST00000103042	ENSMUSG00000059540	2	181680310	181688071	1	0	0	0	0	0	0	0	39	7	7	8	Q810R3	Q9QVN7
ENSMUST00000103045	ENSMUSG00000027581	2	181306459	181314500	-1	4	6	9	24	2	3	0	0	2	0	0	Q545T6	O70166
ENSMUST00000103047	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	4	0	0	0	0	0	0	B7ZBV8	
ENSMUST00000103048	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZBV7	
ENSMUST00000103049	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	6	0	0	0	0	0	0	0	F6UC55	
ENSMUST00000103050	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	0	0	2	0	0	0	0	B7ZBW2	
ENSMUST00000103051	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZBW1	
ENSMUST00000103053	ENSMUSG00000027574	2	180934772	180954699	-1	3	0	0	11	0	4	0	0	0	26	5		Q9JMG4
ENSMUST00000103054						0	0	0	1	0	0	16	0	0	0	38		
ENSMUST00000103055	ENSMUSG00000038914	2	180657964	180709999	-1	0	11	33	30	10	6	79	343	147	36	223		Q8C9B9
ENSMUST00000103056	ENSMUSG00000038914	2	180657964	180709999	-1	0	0	0	0	0	0	0	0	0	0	0		Q8C9B9
ENSMUST00000103057	ENSMUSG00000038914	2	180657964	180709999	-1	1	0	0	0	0	0	32	0	73	0	53		Q8C9B9
ENSMUST00000103059	ENSMUSG00000027570	2	180597790	180622189	1	0	0	0	0	2	9	5	17	9	1	18	A2ACT7	
ENSMUST00000103060	ENSMUSG00000041895	11	109573331	109611967	-1	11	12	36	22	14	15	514	972	801	110	452		Q8R3E3
ENSMUST00000103061	ENSMUSG00000020610	11	109425946	109452813	1	2	0	9	41	14	2	88	187	104	92	88	B1AT59	
ENSMUST00000103062	ENSMUSG00000020599	11	109225355	109298129	-1	11	8	23	9	11	0	0	0	0	0	0	A2A6V6	
ENSMUST00000103064	ENSMUSG00000040430	11	107207892	107470699	-1	47	33	78	393	55	32	393	960	866	81	630		Q8K4R4
ENSMUST00000103065	ENSMUSG00000027525	2	178118975	178338492	1	2	0	1	1	2	0	0	0	0	1	0	Q6KCA9	Q8BYK5
ENSMUST00000103066	ENSMUSG00000027525	2	178118975	178338492	1	12	4	0	83	13	4	0	0	0	0	0		Q8BYK5
ENSMUST00000103067	ENSMUSG00000018363	11	106820066	106920715	-1	11	9	16	82	14	7	290	959	498	214	427		A2A5Z6
ENSMUST00000103068	ENSMUSG00000018372	11	106789252	106819930	1	12	5	9	29	10	6	29	139	45	46	45	Q14B65	
ENSMUST00000103069	ENSMUSG00000020717	11	106654217	106750628	-1	7	6	0	0	0	0	73	136	83	46	111		Q08481
ENSMUST00000103070	ENSMUSG00000040548	11	106502147	106613423	-1	15	6	24	0	19	0	0	0	43	0	5	B1ATR2	
ENSMUST00000103071	ENSMUSG00000020713	11	106300271	106301865	-1	12	4	4	3	15	6	0	2	0	0	2		P06880

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000103072	ENSMUSG00000069631	11	106163330	106202168	-1	0	0	0	14	0	0	83	48	90	0	73		Q3UUJ4
ENSMUST00000103073	ENSMUSG00000074570	2	172393794	172433757	1	28	21	47	23	35	26	162	172	130	41	192		
ENSMUST00000103074	ENSMUSG00000027547	2	168748332	168767943	-1	0	0	0	0	0	5	0	0	0	0	0		Q8BX22
ENSMUST00000103075	ENSMUSG00000034187	11	103821782	103954056	-1	17	15	30	23	23	5	989	1455	1671	214	814		P46460
ENSMUST00000103076	ENSMUSG00000044787	11	103208127	103218432	-1	11	10	48	36	19	11	2	0	0	0	1		Q8C5V0
ENSMUST00000103077	ENSMUSG00000020937	11	103070304	103101658	-1	11	6	13	209	30	16	0	1	0	0	25		Q8K2J0
ENSMUST00000103079	ENSMUSG00000031078	7	144435733	144471009	-1	41	32	101	139	32	17	0	0	0	9	50		Q60598
ENSMUST00000103081	ENSMUSG00000020926	11	102761439	102780262	1	57	44	65	0	126	81	0	10	2	1	1		Q9R1V4
ENSMUST00000103084	ENSMUSG00000017667	2	165374264	165388259	-1	67	47	127	156	84	34	0	0	2	1	12	A2A4U6	
ENSMUST00000103085	ENSMUSG00000056824	2	165351297	165368729	-1	12	0	116	58	23	12	0	0	0	0	0	Q6NXM6	
ENSMUST00000103086	ENSMUSG00000034664	11	102453297	102470122	-1	2	7	21	43	9	20	252	187	211	93	435		Q9QUM0
ENSMUST00000103088	ENSMUSG00000017670	2	165288031	165326479	-1	0	29	56	29	0	7	84	186	91	9	176		Q8BHL5
ENSMUST00000103091	ENSMUSG00000017670	2	165288031	165326479	-1	20	5	24	26	6	6	37	117	26	11	51		Q8BHL5
ENSMUST00000103092	ENSMUSG00000017760	2	164832873	164841032	1	58	56	122	0	27	32	82	479	180	34	181	Q544R6	P16675
ENSMUST00000103093	ENSMUSG00000017760	2	164832873	164841032	1	0	0	0	0	0	0	5637	11082	5072	1843	4732	Q544R6	P16675
ENSMUST00000103094	ENSMUSG00000017307	2	164792768	164804882	-1	4	0	7	0	0	0	299	381	200	56	105	Q3U965	P58137
ENSMUST00000103095	ENSMUSG00000017300	2	164777161	164779967	-1	0	2	0	1	4	3	0	1	1	0	0		P20801
ENSMUST00000103096	ENSMUSG00000076434	2	164731180	164745931	-1	10	0	9	3	6	6	0	0	0	0	0		Q14AE4
ENSMUST00000103097	ENSMUSG00000074593	2	164715305	164718068	1	0	0	3	0	0	2	0	0	0	0	0	Q32ZM2	
ENSMUST00000103098	ENSMUSG00000017119	11	101552149	101581951	1	0	0	13	7	0	6	0	0	0	0	0	A1L329	P97432
ENSMUST00000103099	ENSMUSG00000017119	11	101552149	101581951	1	0	0	0	0	8	0	0	0	13	0	12	A1L329	P97432
ENSMUST00000103100	ENSMUSG00000017733	2	164588343	164593594	-1	10	6	10	2	10	5	0	0	0	0	0		Q9DA01
ENSMUST00000103101	ENSMUSG00000017721	2	164497520	164508301	1	12	0	0	236	17	13	1125	1199	829	113	727		Q8BXQ2
ENSMUST00000103102	ENSMUSG00000097487	11	101418812	101425333	-1	2	0	2	214	6	0	0	8	5	0	1		Q9D9A7
ENSMUST00000103103	ENSMUSG00000016995	2	164389393	164405160	-1	0	0	0	31	0	0	0	0	0	0	0	F2Z3U4	
ENSMUST00000103104	ENSMUSG00000016995	2	164389393	164405160	-1	0	16	33	0	25	10	0	0	0	0	2	F2Z3U4	
ENSMUST00000103105	ENSMUSG00000019326	11	101330605	101341938	1	30	19	50	34	32	19	6	13	9	0	20		O70423
ENSMUST00000103107	ENSMUSG00000078653	11	101279012	101296317	1	5	8	106	5	3	2	2	0	0	0	0		Q9D995
ENSMUST00000103108	ENSMUSG00000035112	11	101260567	101277409	1	15	0	28	72	54	0	0	0	0	0	12		Q80UE6
ENSMUST00000103109	ENSMUSG00000017167	11	101170523	101190724	1	47	36	78	272	85	49	8	8	8	1	17		O54991
ENSMUST00000103110	ENSMUSG00000019302	11	101009452	101063719	1	0	0	0	0	0	0	484	11	854	10	294		Q9Z1G4
ENSMUST00000103111	ENSMUSG00000035877	2	160748708	160872998	-1	49	39	76	157	21	45	0	0	0	0	21	Q3UPQ8	Q8C0Q2
ENSMUST00000103112	ENSMUSG00000035877	2	160748708	160872998	-1	0	24	67	0	50	0	59	138	151	10	70	Q3UPQ8	Q8C0Q2
ENSMUST00000103114	ENSMUSG00000004040	11	100885098	100939540	-1	37	26	89	71	59	28	90	155	203	6	202	Q6GU23	P42227
ENSMUST00000103115	ENSMUSG00000016933	2	160731300	160775760	1	6	11	57	12	7	2	0	0	0	0	0		Q62077
ENSMUST00000103116	ENSMUSG00000037754	2	158665398	158766334	1	17	0	50	0	0	19	140	190	176	18	302	Q544H9	Q8VHQ3
ENSMUST00000103118	ENSMUSG00000020918	11	100704746	100712465	-1	0	0	0	60	0	2	25	65	16	0	99		Q9JHD2
ENSMUST00000103119	ENSMUSG00000014198	11	100627543	100692455	-1	78	71	73	61	82	29	9	7	13	0	17		A2A5E6
ENSMUST00000103120	ENSMUSG00000006782	11	100574904	100591729	1	11	13	0	62	25	7	523	413	253	107	424	Q3TYV5	P16330
ENSMUST00000103121	ENSMUSG00000037813	2	158182533	158229222	-1	40	44	70	53	52	24	14	53	13	2	17	A2AC60	
ENSMUST00000103122	ENSMUSG00000037820	2	158116402	158146436	-1	28	17	51	55	35	16	107	124	106	204	768		P21981
ENSMUST00000103123	ENSMUSG00000027651	2	158028497	158132297	1	0	0	17	81	29	21	41	0	111	0	90		
ENSMUST00000103124	ENSMUSG00000006930	11	100347327	100356128	-1	14	6	5	79	7	0	0	0	0	0	2		O35668
ENSMUST00000103127	ENSMUSG00000048013	11	100092193	100096241	-1	0	1	1	1	3	0	0	0	0	0	0		Q497I4
ENSMUST00000103129	ENSMUSG00000027635	2	156995265	157007154	-1	2	9	3	0	0	1	30	94	65	43	37		Q9CYC5
ENSMUST00000103130	ENSMUSG00000027635	2	156995265	157007154	-1	7	0	9	54	14	0	22	28	10	0	1		Q9CYC5
ENSMUST00000103131	ENSMUSG00000019761	11	99385254	99389364	-1	11	7	44	122	17	6	1	1	0	5	1	A2A513	
ENSMUST00000103132	ENSMUSG00000035849	11	99232761	99244085	-1	14	17	10	10	13	11	3	4	9	0	9		Q8CCX5
ENSMUST00000103133	ENSMUSG00000037935	11	99209047	99231017	-1	13	6	12	155	22	2	298	1265	502	1259	412		O54941
ENSMUST00000103134	ENSMUSG00000037944	11	99144196	99155077	-1	22	20	42	16	20	9	193	197	63	54	340		P47774
ENSMUST00000103135	ENSMUSG00000027624	2	156420909	156543214	1	18	0	6	20	31	0	0	0	0	0	0	A2AUK5	
ENSMUST00000103136	ENSMUSG00000027624	2	156420909	156543214	1	0	0	0	0	0	0	0	0	0	0	0	A2AUK5	
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ENSMUST00000103139	ENSMUSG00000058756	11	98740638	98769006	1	7	0	27	7	13	2	43	34	37	5	63		P63058
ENSMUST00000103140	ENSMUSG00000038324	2	155634271	155692384	-1	0	0	4	0	0	0	1232	2741	1022	168	649		Q9JLV2
ENSMUST00000103141	ENSMUSG00000018168	11	98464902	98546031	-1	15	12	13	10	24	7	81	107	72	7	198		O08900
ENSMUST00000103142	ENSMUSG00000027605	2	155517948	155585724	1	0	0	0	0	0	0	85	26	74	15	74	A2AQN4	
ENSMUST00000103143	ENSMUSG00000020883	11	98082556	98150403	-1	50	25	95	115	58	24	980	3186	2197	229	2335		Q9CZV8
ENSMUST00000103144	ENSMUSG00000020882	11	98001508	98023034	-1	5	4	3	129	4	0	0	0	0	2	6		
ENSMUST00000103145	ENSMUSG00000027490	2	154559407	154569892	-1	0	33	220	21	74	28	85	91	16	0	18	Q547J6	Q61501
ENSMUST00000103146	ENSMUSG00000071415	11	97777527	97782437	-1	78	70	82	86	87	33	1020	2449	1418	8744	1084		P62830
ENSMUST00000103147	ENSMUSG00000069744	11	97703399	97713500	1	14	11	4	0	8	13	1344	1638	821	3948	583	Q545G0	Q9R1P1
ENSMUST00000103148	ENSMUSG00000018537	11	97688823	97700497	-1	0	0	0	0	0	0	5	3	6	0	9		P23798
ENSMUST00000103149	ENSMUSG00000018537	11	97688823	97700497	-1	0	0	0	0	0	0	0	0	0	0	2	B1AR14	
ENSMUST00000103150	ENSMUSG00000027478	2	153649450	153687730	1	0	0	20	20	12	0	0	35	10	0	0		O88509
ENSMUST00000103151	ENSMUSG00000027478	2	153649450	153687730	1	0	0	0	46	0	0	11	7	0	2	12		O88509
ENSMUST00000103152	ENSMUSG00000018669	11	96907426	96916496	-1	0	0	0	0	4	0	442	579	365	199	258		Q99LM2
ENSMUST00000103154	ENSMUSG00000057058	11	96464593	96759130	1	0	0	0	9	0	0	19	4	16	27	38		Q3UUV5
ENSMUST00000103155	ENSMUSG00000074673	2	152962485	153008482	1	10	0	5	0	1	5	0	0	0	0	0		A2APC3
ENSMUST00000103156	ENSMUSG00000014351	11	96024545	96030831	1	4	4	15	6	5	3	0	0	0	0	0		P48756
ENSMUST00000103157	ENSMUSG00000014351	11	96024545	96030831	1	0	0	0	0	0	0	0	0	0	0	0		P48756
ENSMUST00000103159	ENSMUSG00000038909	11	95274259	95310246	-1	0	5	0	0	0	0	0	533	0	0	0		Q5SVQ0
ENSMUST00000103160	ENSMUSG00000027455	2	151494182	151511414	1	0	0	5	2	2	1	0	0	0	0	14	A2AT02	
ENSMUST00000103162	ENSMUSG00000001508	11	94962791	94976327	-1	0	11	32	34	10	0	0	0	0	0	0		P82350
ENSMUST00000103164	ENSMUSG00000076435	11	94557102	94601871	-1	28	29	112	137	45	23	38	56	20	9	86		Q8VCW8
ENSMUST00000103166	ENSMUSG00000020866	11	94408391	94474198	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SUF6	
ENSMUST00000103168	ENSMUSG00000020859	11	93996091	94126085	1	0	0	0	0	0	14	0	208	0	83	0		
ENSMUST00000103171	ENSMUSG00000037279	2	144305175	144332146	-1	4	11	5	224	11	7	0	0	0	0	0		Q8CIV7
ENSMUST00000103172	ENSMUSG00000015932	2	143915320	143943324	1	12	26	43	111	25	12	5011	18759	7354	12587	3461	Q4FK36	Q9R0P5
ENSMUST00000103173	ENSMUSG00000041954	4	156026164	156028895	1	8	3	13	7	5	4	54	36	18	25	31	Q540M6	O35714
ENSMUST00000103175	ENSMUSG00000023286	4	155943831	155959604	1	0	0	0	0	0	0	20	142	69	32	37		Q6P073
ENSMUST00000103176	ENSMUSG00000029060	4	155654677	155669198	-1	3	0	21	254	14	4	276	266	185	0	96		Q8R516
ENSMUST00000103177	ENSMUSG00000009356	11	87806428	87828289	-1	22	18	37	35	37	14	0	0	0	0	1	Q5SW46	
ENSMUST00000103178	ENSMUSG00000029053	4	155260129	155361361	-1	22	3	13	33	30	16	0	0	4	0	5	Q3V341	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000103179	ENSMUSG00000018401	11	87592162	87616302	1	0	16	0	65	37	16	269	401	195	54	138		Q91XS1
ENSMUST00000103180	ENSMUSG00000029047	4	155067016	155072433	1	9	0	22	9	5	0	51	63	32	9	28		B1AUE5
ENSMUST00000103181	ENSMUSG00000058793	2	132263148	132312050	1	0	15	0	230	52	0	599	2137	4455	365	3389		Q99L43
ENSMUST00000103182	ENSMUSG00000027339	2	131989415	132030258	-1	0	9	272	0	0	0	2982	8102	5463	613	3832		Q8BMS9
ENSMUST00000103184	ENSMUSG00000027335	2	131545850	131562283	-1	7	10	32	483	23	10	0	0	0	0	0	A2ANQ2	
ENSMUST00000103186	ENSMUSG00000047126	11	86694351	86757565	-1	0	0	0	90	38	11	582	983	1474	73	582		Q68FD5
ENSMUST00000103188	ENSMUSG00000027327	2	131146324	131160081	-1	0	0	5	0	0	0	714	969	365	112	279		Q9D1K7
ENSMUST00000103191	ENSMUSG00000028936	4	152325742	152334071	1	0	0	0	0	0	0	963	2290	1017	5739	666	Q4VAG4	P67984
ENSMUST00000103193	ENSMUSG00000074797	2	130667610	130681614	1	19	7	15	38	16	9	151	592	182	313	142	Q60I30	Q9D892
ENSMUST00000103194	ENSMUSG00000000805	11	84957786	84966044	1	6	0	3	0	0	6	17	55	19	15	6		Q64444
ENSMUST00000103195	ENSMUSG00000020526	11	84910950	84916366	-1	4	4	0	2	2	0	22	41	33	147	22		Q9CQK1
ENSMUST00000103196	ENSMUSG00000028943	4	152120331	152152371	-1	0	0	0	0	0	0	0	0	0	0	0	B1AWP9	
ENSMUST00000103197	ENSMUSG00000028948	4	152039321	152061494	1	1	2	15	29	3	0	0	3	5	0	0		Q3TZX8
ENSMUST00000103198	ENSMUSG00000027405	2	130274430	130279313	1	0	5	0	24	5	6	57	216	110	389	236		Q9D6Z1
ENSMUST00000103199	ENSMUSG00000027404	2	130171414	130179403	-1	4	0	0	60	0	0	1459	1986	1137	336	837		P27048
ENSMUST00000103201	ENSMUSG00000020532	11	84129672	84401651	1	41	40	110	65	70	22	0	19	0	0	0		Q5SWU9
ENSMUST00000103202	ENSMUSG00000037902	2	129592835	129632228	1	0	0	0	38	22	0	113	0	1540	0	1029	Q6P6I8	
ENSMUST00000103203	ENSMUSG00000037902	2	129592835	129632228	1	0	0	0	0	0	0	8607	16617	7968	611	4715	Q6P6I8	
ENSMUST00000103204	ENSMUSG00000028957	4	151003652	151044665	-1	0	8	0	22	15	0	0	0	2	0	5		O70361
ENSMUST00000103205	ENSMUSG00000027395	2	129100995	129126594	1	64	57	58	182	69	23	31	59	45	5	67		P70700
ENSMUST00000103208	ENSMUSG00000044700	4	149715375	149738044	-1	0	0	0	0	0	0	3	0	6	0	2		A2A8U2
ENSMUST00000103209	ENSMUSG00000020682	11	83440768	83463071	-1	18	12	22	46	20	12	12	17	2	0	18	Q8BG29	
ENSMUST00000103210	ENSMUSG00000027381	2	128126038	128162547	1	83	59	591	148	78	48	172	0	105	2	233		O54918
ENSMUST00000103211	ENSMUSG00000027381	2	128126038	128162547	1	0	0	0	71	0	0	14	2	2	0	0	Q3U7X3	O54918
ENSMUST00000103212	ENSMUSG00000028960	4	149328416	149426749	-1	12	16	65	104	43	12	452	1392	718	61	593		Q9ES00
ENSMUST00000103213	ENSMUSG00000020692	11	82900768	82908411	-1	0	6	4	26	0	3	23	0	17	7	22		Q8VEJ4
ENSMUST00000103214	ENSMUSG00000027376	2	127526473	127541467	-1	0	11	0	0	14	3	0	0	0	0	0		Q3UUY6
ENSMUST00000103215	ENSMUSG00000079056	2	127456498	127522094	-1	53	7	44	11	68	26	0	0	0	0	0	Q3YAB0	Q9QXT8
ENSMUST00000103216	ENSMUSG00000028974	4	149104146	149120647	1	128	139	161	94	100	33	74	131	179	28	172	Q8C535	O54786
ENSMUST00000103217	ENSMUSG00000028975	4	148960535	149099876	-1	15	9	24	130	17	9	374	409	300	41	272		Q9R0A0
ENSMUST00000103218	ENSMUSG00000020696	11	82802449	82871210	-1	2	0	0	0	8	1	5	6	5	0	0		Q6ZQM0
ENSMUST00000103220	ENSMUSG00000003660	2	127208386	127240451	1	34	23	44	27	36	20	1363	2183	2622	342	2178		Q6P4T2
ENSMUST00000103221	ENSMUSG00000028991	4	148448611	148557683	1	64	40	92	74	93	39	441	567	768	60	640		Q9JLN9
ENSMUST00000103222	ENSMUSG00000053184	11	80858365	80867814	1	5	6	0	0	8	5	0	0	0	0	0	A0A077S9M6	Q9D9X8
ENSMUST00000103223	ENSMUSG00000053184	11	80858365	80867814	1	0	2	3	4	0	0	0	0	0	0	0	A0A077S9M6	Q9D9X8
ENSMUST00000103224	ENSMUSG00000027365	2	126791565	126876230	-1	0	2	14	17	11	0	392	666	991	121	572		Q923J1
ENSMUST00000103225	ENSMUSG00000057181	11	80360492	80378034	-1	2	2	2	73	59	1	107	299	2	67	0		Q9CYI0
ENSMUST00000103226	ENSMUSG00000027361	2	126627442	126676337	-1	0	0	0	12	3	0	14	86	59	12	78		Q00420
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ENSMUST00000103230	ENSMUSG00000041616	4	148000722	148002079	1	6	4	12	13	8	3	0	5	2	0	2		P05125
ENSMUST00000103231	ENSMUSG00000029019	4	147985788	147987205	1	9	10	12	6	9	2	0	0	0	4	1	Q54AE9	P40753
ENSMUST00000103232	ENSMUSG00000044496	4	147940895	147947314	1	25	19	54	215	32	18	3032	2570	1900	339	1379		Q91X21
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ENSMUST00000103238	ENSMUSG00000027200	2	124089969	124667770	1	0	0	0	0	0	0	0	0	0	0	10		Q76KF0
ENSMUST00000103239	ENSMUSG00000027200	2	124089969	124667770	1	0	0	66	0	0	0	0	0	0	0	6		Q76KF0
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ENSMUST00000103262	ENSMUSG00000076461	6	40891229	40891885	1	10	3	6	5	8	4	9	14	10	18	17	A0A0B4J1G7	
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ENSMUST00000103273	ENSMUSG00000076472	6	41141188	41141658	1	0	2	1	1	2	0	0	2	0	3	1	A0A0A6YYE3	
ENSMUST00000103274	ENSMUSG00000076473	6	41151740	41152230	1	2	4	2	0	5	0	1	4	0	5	1	A0A0B4J1H3	
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ENSMUST00000103278	ENSMUSG00000076477	6	41202550	41203044	1	0	1	0	0	0	0	0	0	0	0	0	A0A075B5I8	
ENSMUST00000103279	ENSMUSG00000076478	6	41216073	41216526	1	2	3	3	0	5	2	0	0	0	0	0	A0A075B5I9	
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ENSMUST00000103281	ENSMUSG00000076480	6	41271394	41271881	1	3	3	1	2	3	1	3	7	2	23	1	A0A0A6YYE4	
ENSMUST00000103282	ENSMUSG00000076481	6	41281376	41281990	1	0	0	4	0	0	4	0	0	0	1	0	A0A075B5J2	
ENSMUST00000103284	ENSMUSG00000076483	6	41533864	41533911	1	0	0	0	0	0	1	1	8	0	2	3	A0A0A6YVY0	
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ENSMUST00000103297	ENSMUSG00000076496	6	41543453	41543501	1	0	0	3	4	0	0	0	2	1	8	4	A0A0B4J1P2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000103298	ENSMUSG00000076497	6	41543810	41543856	1	1	0	2	0	2	0	5	9	2	12	0	A0A0A6YXH6	
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ENSMUST00000103300	ENSMUSG00000076499	6	41557691	41558452	-1	0	0	5	0	0	0	0	0	2	8	0	A0A075B5J5	
ENSMUST00000103301	ENSMUSG00000076500	6	43081518	43082097	-1	1	1	1	5	2	2	0	0	0	0	0	A0A075B5J6	
ENSMUST00000103302	ENSMUSG00000076501	6	67555497	67556216	1	0	3	3	1	0	3	1	8	4	31	15	A0A0B4J1H6	
ENSMUST00000103303	ENSMUSG00000096336	6	67609713	67610508	1	3	2	5	2	6	0	9	5	1	83	49	A0A0B4J1H7	
ENSMUST00000103304	ENSMUSG00000094491	6	67724902	67725661	1	0	2	3	2	2	1	0	0	0	1	0	A0A0B4J1H8	
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ENSMUST00000103308	ENSMUSG00000093906	6	67839793	67840266	1	1	4	4	0	4	0	0	0	0	7	2	A0A075B5J8	
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ENSMUST00000103310	ENSMUSG00000094345	6	67896172	67896642	1	5	0	0	0	1	0	0	2	3	60	6	A0A075B5K0	
ENSMUST00000103311	ENSMUSG00000095737	6	67913573	67914052	1	8	2	1	1	2	1	1	0	2	6	0	A0A075B5K1	
ENSMUST00000103312	ENSMUSG00000096632	6	67942074	67942540	-1	0	0	0	1	5	0	0	0	0	8	0	A0A075B5K2	
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ENSMUST00000103317	ENSMUSG00000094335	6	68121046	68121827	1	7	0	0	0	6	1	2	9	7	93	77		
ENSMUST00000103318	ENSMUSG00000076518	6	68219981	68220706	1	1	1	3	0	3	1	0	0	0	0	0	A0A075B5K4	P01627
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ENSMUST00000103320	ENSMUSG00000095771	6	68256389	68256869	1	1	0	4	0	0	0	0	0	1	22	24		
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ENSMUST00000103322	ENSMUSG00000105606	6	68302427	68303158	1	5	3	0	0	1	0	0	0	1	9	11	A0A075B5K6	
ENSMUST00000103323	ENSMUSG00000076522	6	68425575	68426072	1	3	0	0	3	1	0	2	2	1	10	24	A0A0B4J1I1	
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ENSMUST00000103326	ENSMUSG00000076525	6	68541644	68542422	1	0	1	2	2	1	0	1	0	0	1	1	A0A075B5K8	
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ENSMUST00000103328	ENSMUSG00000094420	6	68631963	68632442	-1	4	4	0	0	1	0	4	7	1	44	46		
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ENSMUST00000103330	ENSMUSG00000096490	6	68704508	68704978	-1	1	0	5	0	2	2	4	0	0	26	37	A0A075B5L1	
ENSMUST00000103331						1	0	0	0	0	0	0	0	4	0	0		
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ENSMUST00000103333	ENSMUSG00000076532	6	68768555	68769103	-1	1	2	2	2	1	2	2	0	0	8	7	A0A075B5L2	
ENSMUST00000103334	ENSMUSG00000076533	6	68807179	68807708	-1	2	1	0	1	2	1	0	0	1	0	2	A0A075B5L3	
ENSMUST00000103335	ENSMUSG00000076534	6	68834846	68835307	-1	4	3	0	2	0	1	0	1	0	1	0	A0A075B5L4	
ENSMUST00000103336	ENSMUSG00000076535	6	68862265	68863031	-1	1	2	3	1	2	2	1	0	1	8	8		
ENSMUST00000103337	ENSMUSG00000076536	6	68910411	68910973	-1	3	1	3	0	2	0	0	0	1	12	5	A0A075B5L5	
ENSMUST00000103339	ENSMUSG00000076538	6	68939602	68940067	1	4	1	0	0	3	2	0	4	1	2	7		
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ENSMUST00000103341	ENSMUSG00000076540	6	69016558	69017080	-1	0	5	0	2	2	2	3	1	0	5	1	A0A075B5L7	
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ENSMUST00000103349	ENSMUSG00000076548	6	69283794	69284319	-1	0	0	0	3	1	2	0	0	2	4	0	A0A0B4J1I6	
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ENSMUST00000103351	ENSMUSG00000076550	6	69377944	69378472	-1	4	0	2	0	4	0	0	0	0	3	6	A0A075B5M1	
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ENSMUST00000103356	ENSMUSG00000076555	6	69544359	69544907	-1	0	3	7	2	1	0	1	3	0	5	4	A0A075B5M4	
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ENSMUST00000103363	ENSMUSG00000076562	6	69700767	69701287	-1	0	2	6	0	1	1	0	0	0	6	2	A0A0B4J1J0	
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ENSMUST00000103370	ENSMUSG00000076569	6	69900424	69900977	-1	0	0	0	0	0	0	4	0	2	29	28	A0A075B5M7	
ENSMUST00000103371	ENSMUSG00000076570	6	69943186	69943648	-1	3	1	2	0	1	0	0	0	1	0	0	A0A075B5M8	
ENSMUST00000103372	ENSMUSG00000076571	6	69963312	69963873	-1	1	1	2	0	0	0	1	0	0	0	0		
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ENSMUST00000103374	ENSMUSG00000076573	6	70010949	70011673	-1	0	1	4	3	3	1	0	0	0	0	0	A0A075B5N0	
ENSMUST00000103376	ENSMUSG00000076575	6	70058632	70059199	-1	2	0	1	0	1	0	0	0	0	0	4	A0A075B5N1	
ENSMUST00000103377	ENSMUSG00000076576	6	70074024	70074603	-1	2	3	0	0	1	0	3	5	3	59	28		
ENSMUST00000103378	ENSMUSG00000076577	6	70117061	70117620	-1	2	0	0	0	2	0	4	0	4	28	31		
ENSMUST00000103379	ENSMUSG00000076578	6	70138462	70139110	-1	0	0	0	0	0	0	0	1	0	0	0	A0A075B5N2	
ENSMUST00000103380	ENSMUSG00000094356	6	70143593	70144166	-1	3	1	3	0	1	1	0	1	0	4	14	A0A075B5N3	
ENSMUST00000103381	ENSMUSG00000076580	6	70171809	70172270	-1	0	2	0	1	2	0	4	0	1	18	12	A0A075B5N4	
ENSMUST00000103382	ENSMUSG00000076581	6	70193228	70193797	1	4	3	0	0	3	2	0	0	0	0	0	A0A075B5N5	
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ENSMUST00000103384	ENSMUSG00000076583	6	70216858	70217421	-1	1	1	0	0	4	0	3	1	1	12	36		
ENSMUST00000103386	ENSMUSG00000095630	6	70260409	70260955	-1	2	1	0	0	0	2	2	4	1	34	14		
ENSMUST00000103387	ENSMUSG00000076586	6	70314895	70315472	-1	2	4	6	3	7	1	2	1	2	20	9		
ENSMUST00000103388	ENSMUSG00000076587	6	70335841	70336507	-1	6	4	5	4	6	3	0	0	0	9	6		
ENSMUST00000103389	ENSMUSG00000096594	6	70340876	70341453	-1	2	1	2	0	3	0	0	0	2	11	11		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000103390	ENSMUSG00000076589	6	70355852	70356445	1	2	1	1	0	2	1	0	0	0	3	0	A0A0B4J1J3	
ENSMUST00000103391	ENSMUSG00000095794	6	70371439	70371993	1	2	2	0	1	0	1	5	7	3	34	46		
ENSMUST00000103392	ENSMUSG00000076591	6	70386672	70387252	-1	0	4	1	3	5	3	0	3	1	28	1	A0A075B5N6	
ENSMUST00000103393	ENSMUSG00000094797	6	70406469	70406992	-1	0	2	2	3	0	1	2	2	3	54	61		
ENSMUST00000103394	ENSMUSG00000096844	6	70434952	70435476	-1	0	4	0	0	0	0	0	0	2	2	5		
ENSMUST00000103395	ENSMUSG00000076594	6	70457501	70458036	-1	3	0	3	0	2	0	2	0	1	5	15	A0A075B5N7	
ENSMUST00000103396	ENSMUSG00000094117	6	70518250	70518849	1	0	4	2	0	0	0	1	1	5	42	17		
ENSMUST00000103397	ENSMUSG00000076596	6	70572633	70573230	1	2	0	5	5	2	3	0	0	3	21	14	A0A075B5N8	
ENSMUST00000103398	ENSMUSG00000095338	6	70588189	70588777	1	3	1	2	1	3	0	0	0	0	4	2		
ENSMUST00000103399	ENSMUSG00000076598	6	70607437	70608036	1	1	1	3	0	0	0	3	2	0	28	14	A0A075B5N9	
ENSMUST00000103400	ENSMUSG00000095335	6	70663275	70663895	1	2	0	2	0	0	0	5	1	2	21	13		
ENSMUST00000103401	ENSMUSG00000096715	6	70671788	70672377	1	2	1	1	0	3	1	3	3	1	52	57		
ENSMUST00000103402	ENSMUSG00000094478	6	70686946	70687534	1	0	3	2	0	2	0	0	0	0	3	0		
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ENSMUST00000103404	ENSMUSG00000095682	6	70703578	70704177	1	4	0	1	2	3	0	2	0	1	12	14	A0A075B5P1	
ENSMUST00000103405	ENSMUSG00000076604	6	70722562	70722599	1	0	0	0	0	0	0	6	3	3	37	33	A0A0G2JEZ6	
ENSMUST00000103406						0	0	1	0	0	1	6	4	3	44	28		
ENSMUST00000103407						0	0	0	0	0	0	0	0	1	0	0		
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ENSMUST00000103409						0	0	1	0	0	0	4	5	2	25	26		
ENSMUST00000103410	ENSMUSG00000076609	6	70726435	70726966	1	2	2	8	3	9	1	147	136	85	1886	1230	A0A075B5P2	
ENSMUST00000103416	ENSMUSG00000076612	12	113285325	113288932	-1	0	0	0	0	0	1	0	0	0	0	0	F6TQW2	
ENSMUST00000103418	ENSMUSG00000076613	12	113302965	113307933	-1	4	8	15	8	9	3	1	2	4	34	107	A0A075B5P3	
ENSMUST00000103420	ENSMUSG00000076614	12	113325240	113330523	-1	1	14	0	3	6	3	4	4	13	36	156	A0A075B5P4	
ENSMUST00000103423	ENSMUSG00000076615	12	113359575	113361232	-1	11	8	23	12	12	12	3	11	4	7	36	A0A075B5P5	
ENSMUST00000103426	ENSMUSG00000076617	12	113418558	113422730	-1	0	7	41	0	6	0	45	53	54	343	496	A0A075B5P6	
ENSMUST00000103427	ENSMUSG00000076618	12	113428514	113428567	-1	1	0	0	0	0	0	0	3	1	4	33	A0A0A6YXC7	
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ENSMUST00000103429						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000103430	ENSMUSG00000076621	12	113429781	113429833	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVQ4	
ENSMUST00000103439	ENSMUSG00000076630	12	113482170	113482192	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDD8	
ENSMUST00000103441	ENSMUSG00000076632	12	113528032	113528054	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000103442	ENSMUSG00000076633	12	113578504	113578990	-1	3	1	1	5	2	3	1	0	0	1	1	A0A075B5P7	
ENSMUST00000103443	ENSMUSG00000096464	12	113588267	113588702	-1	3	6	5	2	7	5	0	2	5	3	22	A0A075B5P8	
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ENSMUST00000103446	ENSMUSG00000094951	12	113625506	113625956	-1	4	2	19	1	10	1	2	0	4	2	4	A0A075B5Q0	
ENSMUST00000103447	ENSMUSG00000095866	12	113653291	113653724	-1	2	0	0	1	4	2	1	0	0	0	0	A0A075B5Q1	
ENSMUST00000103448	ENSMUSG00000095285	12	113661769	113662293	-1	7	7	25	10	8	3	0	0	0	0	5	A0A075B5Q2	
ENSMUST00000103449	ENSMUSG00000096498	12	113685482	113686045	-1	0	0	0	0	0	0	1	0	0	1	6	A0A075B5Q3	
ENSMUST00000103450	ENSMUSG00000095429	12	113702124	113702578	-1	4	4	17	8	6	3	2	0	1	0	5	A0A075B5Q4	
ENSMUST00000103451	ENSMUSG00000096638	12	113879096	113879541	-1	0	1	8	1	4	1	3	0	2	4	32	A0A075B5Q5	
ENSMUST00000103452	ENSMUSG00000095210	12	113736111	113736630	-1	0	1	3	0	5	1	0	0	1	0	4	A0A075B5Q6	
ENSMUST00000103455	ENSMUSG00000076646	12	113796138	113796567	-1	4	0	0	0	3	0	0	0	0	0	0	A0A075B5Q7	
ENSMUST00000103456	ENSMUSG00000096824	12	113807314	113807752	-1	3	0	0	2	2	1	0	0	0	0	0	A0A075B5Q8	
ENSMUST00000103457	ENSMUSG00000094134	12	113826646	113827129	-1	2	0	0	0	3	3	1	0	0	1	7	A0A075B5Q9	
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ENSMUST00000103459	ENSMUSG00000095571	12	113859149	113859670	-1	0	0	2	5	3	0	0	0	1	4	38	A0A075B5R1	
ENSMUST00000103461	ENSMUSG00000076652	12	114153180	114153644	-1	2	0	11	2	2	1	1	0	0	0	5	A0A075B5R2	
ENSMUST00000103462	ENSMUSG00000076653	12	113912025	113912483	-1	0	0	0	0	0	0	0	1	0	0	0	A0A075B5R3	
ENSMUST00000103463	ENSMUSG00000094509	12	113931953	113932382	-1	1	3	3	0	1	4	0	0	0	0	6	A0A075B5R4	
ENSMUST00000103464	ENSMUSG00000076655	12	113948282	113948796	-1	2	4	2	2	0	0	1	0	0	0	3	A0A075B5R5	
ENSMUST00000103466	ENSMUSG00000094533	12	113981879	113982341	-1	0	0	0	0	0	5	0	1	0	1	1	A0A075B5R6	
ENSMUST00000103467	ENSMUSG00000095583	12	113994469	113994898	-1	3	0	6	0	5	1	2	0	0	4	14	A0A075B5R7	
ENSMUST00000103468	ENSMUSG00000096108	12	114048241	114048812	-1	4	0	18	6	3	2	1	0	0	0	2	A0A075B5R8	
ENSMUST00000103469	ENSMUSG00000095642	12	114059845	114060321	-1	1	0	0	1	1	0	0	0	0	2	12	A0A075B5R9	
ENSMUST00000103470	ENSMUSG00000076661	12	114068828	114069281	-1	0	0	0	0	0	0	0	0	0	0	0	A0A075B5S0	
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ENSMUST00000103472	ENSMUSG00000094102	12	114109001	114109430	-1	0	0	0	0	1	0	0	0	0	0	5	A0A0B4J1J4	
ENSMUST00000103473	ENSMUSG00000096459	12	114140692	114141122	-1	10	14	10	2	6	3	7	3	2	3	47	A0A0B4J1J5	
ENSMUST00000103474	ENSMUSG00000076665	12	113896408	113896946	-1	5	0	2	0	0	1	0	0	0	1	4	A0A075B5S2	
ENSMUST00000103475	ENSMUSG00000076666	12	114176438	114176867	-1	0	0	0	0	0	0	0	0	0	1	0	A0A075B5S3	
ENSMUST00000103476	ENSMUSG00000094029	12	114196439	114196875	-1	0	1	0	0	2	0	0	0	0	0	0	A0A075B5S4	
ENSMUST00000103477	ENSMUSG00000076668	12	114222788	114223328	-1	2	0	0	1	3	0	0	0	0	0	0	A0A075B5S5	
ENSMUST00000103478	ENSMUSG00000093838	12	113964388	113964818	-1	0	0	0	0	0	0	0	0	1	2	0	A0A075B5S6	
ENSMUST00000103479	ENSMUSG00000076670	12	114262652	114263087	-1	0	0	0	0	0	0	0	0	0	0	3	A0A0A0MQC1	
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ENSMUST00000103481	ENSMUSG00000076672	12	114288152	114288582	-1	0	0	0	0	0	2	0	1	2	3	0	A0A075B5S8	
ENSMUST00000103482	ENSMUSG00000094322	12	114299961	114300389	-1	0	0	0	0	0	0	0	0	1	0	0	A0A075B5S9	
ENSMUST00000103483	ENSMUSG00000076674	12	114322327	114322801	-1	2	0	0	0	1	0	2	0	0	2	14	A0A075B5T0	
ENSMUST00000103485	ENSMUSG00000076676	12	114366521	114366954	-1	0	0	10	1	1	0	0	0	0	0	2	A0A075B5T1	
ENSMUST00000103486	ENSMUSG00000076677	12	114391712	114392169	-1	9	3	46	13	4	3	1	0	0	2	2	A0A075B5T2	
ENSMUST00000103489	ENSMUSG00000076680	12	114434788	114435244	-1	1	1	5	0	6	2	2	0	1	2	1	A0A075B5T3	
ENSMUST00000103492	ENSMUSG00000095981	12	114479005	114479451	-1	2	1	13	1	3	2	1	1	0	2	7	A0A0B4J1J6	
ENSMUST00000103493	ENSMUSG00000095442	12	114487136	114487569	-1	5	10	7	3	14	7	1	0	2	3	19	A0A075B5T4	
ENSMUST00000103494	ENSMUSG00000096499	12	114513330	114513807	-1	0	0	1	0	0	2	0	0	0	2	0	A0A075B5T5	
ENSMUST00000103495	ENSMUSG00000095700	12	114523441	114523905	-1	1	0	3	0	2	1	0	0	1	0	0	A0A075B5T6	
ENSMUST00000103496	ENSMUSG00000095200	12	114538495	114538965	-1	0	3	0	3	0	0	1	0	0	1	8	A0A075B5T7	
ENSMUST00000103497	ENSMUSG00000076688	12	114564578	114565012	-1	2	2	3	0	0	1	0	0	0	0	0	A0A075B5T8	
ENSMUST00000103498	ENSMUSG00000094694	12	114583569	114584002	-1	0	0	0	0	0	0	2	0	3	3	0	A0A075B5T9	
ENSMUST00000103500	ENSMUSG00000095416	12	114615850	114616318	-1	1	0	0	2	0	0	0	0	0	0	0	A0A075B5U0	
ENSMUST00000103501	ENSMUSG00000095554	12	114665872	114666165	-1	0	1	0	1	2	2	0	0	0	0	0	A0A075B5U1	
ENSMUST00000103503	ENSMUSG00000102313	12	115386697	115387128	-1	1	1	2	0	0	0	0	0	0	0	0	A0A075B5U3	
ENSMUST00000103504	ENSMUSG00000076695	12	114682632	114683065	-1	0	0	0	0	3	0	1	0	0	0	0	A0A075B5U4	
ENSMUST00000103505	ENSMUSG00000096410	12	114708648	114709135	-1	0	0	0	0	0	0	0	11	4	0	0	A0A075B5U5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000103506	ENSMUSG00000095761	12	114723772	114724205	-1	8	0	0	0	1	3	0	0	2	1	2	A0A075B5U6	
ENSMUST00000103507	ENSMUSG00000094561	12	114746273	114746706	-1	0	2	3	3	2	3	0	0	0	2	2	A0A075B5U7	
ENSMUST00000103509	ENSMUSG00000094241	12	114772928	114773361	-1	0	1	0	1	0	2	0	0	0	0	0	A0A075B5U9	
ENSMUST00000103510	ENSMUSG00000094546	12	114788372	114788805	-1	3	4	4	0	2	2	0	0	0	2	4	A0A075B5V0	
ENSMUST00000103511	ENSMUSG00000096649	12	114829264	114829697	-1	2	3	0	0	0	1	0	0	0	0	0	A0A075B5V1	
ENSMUST00000103512	ENSMUSG00000093955	12	114851190	114851660	-1	0	4	9	6	4	3	0	0	0	0	6	A0A075B5V2	
ENSMUST00000103513	ENSMUSG00000094051	12	114879888	114880321	-1	0	0	0	0	0	0	1	0	0	0	0	A0A075B5V3	
ENSMUST00000103514	ENSMUSG00000095923	12	114896238	114896671	-1	0	1	2	0	3	0	0	0	0	0	3	A0A075B5V4	
ENSMUST00000103515	ENSMUSG00000095130	12	114914599	114915032	-1	1	3	0	3	1	0	0	0	0	3	4	A0A075B5V5	
ENSMUST00000103516	ENSMUSG00000094652	12	114937113	114937544	-1	0	0	0	0	0	0	0	0	0	0	0	A0A075B5V6	
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ENSMUST00000103518	ENSMUSG00000076709	12	114991108	114991580	-1	0	0	0	0	0	2	0	0	0	0	0	A0A075B5V8	
ENSMUST00000103519	ENSMUSG00000076710	12	115055223	115055656	-1	0	0	0	0	0	0	0	0	0	0	0	A0A075B5V9	
ENSMUST00000103521	ENSMUSG00000094198	12	115119748	115120219	-1	19	10	7	0	17	0	0	0	0	3	10	A0A075B5W1	
ENSMUST00000103522	ENSMUSG00000095204	12	115145487	115145919	-1	0	0	0	0	0	4	0	0	0	0	0	A0A075B5W2	
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ENSMUST00000103525	ENSMUSG00000094787	12	115193675	115194134	-1	19	12	16	3	13	8	1	1	1	3	3	A0A075B5W5	
ENSMUST00000103526	ENSMUSG00000095589	12	115208095	115208591	-1	15	5	12	8	10	4	0	2	1	3	14	A0A075B5W6	
ENSMUST00000103527	ENSMUSG00000094862	12	115242802	115243235	-1	1	1	3	4	1	1	0	0	0	0	3	A0A075B5W7	
ENSMUST00000103529	ENSMUSG00000095889	12	115312166	115312599	-1	4	0	0	0	0	0	0	0	0	0	0	A0A075B5W9	
ENSMUST00000103530	ENSMUSG00000095197	12	115335082	115335514	-1	0	0	0	0	0	0	0	0	0	0	0	A0A075B5X0	
ENSMUST00000103531	ENSMUSG00000094087	12	115359140	115359572	-1	0	0	0	0	0	0	0	0	0	4	0		P01749
ENSMUST00000103532	ENSMUSG00000096767	12	115460999	115461485	-1	0	0	0	0	0	0	0	0	0	0	0		P01754
ENSMUST00000103533	ENSMUSG00000095117	12	115468332	115468780	-1	0	0	0	0	0	0	0	0	0	0	0	A0A075B5X1	
ENSMUST00000103534	ENSMUSG00000096672	12	115495625	115496058	-1	11	7	10	5	9	1	1	1	1	2	2	A0A075B5X2	
ENSMUST00000103535	ENSMUSG00000094088	12	115507545	115508031	-1	3	13	24	16	8	3	0	3	1	2	15	A0A075B5X3	
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ENSMUST00000103537	ENSMUSG00000095519	12	115593110	115593591	-1	15	3	6	4	8	4	0	0	0	0	7	A0A075B5X5	
ENSMUST00000103538	ENSMUSG00000095863	12	115603940	115604376	-1	5	9	3	10	13	2	1	0	0	3	4	A0A075B5X6	
ENSMUST00000103539	ENSMUSG00000094502	12	115623161	115623595	-1	0	7	0	0	11	2	2	5	2	2	8	A0A075B5X7	
ENSMUST00000103540	ENSMUSG00000076731	12	115647945	115648387	-1	3	2	14	7	2	0	1	2	0	0	8	A0A075B5X8	
ENSMUST00000103541	ENSMUSG00000096074	12	115757984	115758461	-1	4	3	3	0	6	4	1	3	0	3	0	A0A075B5X9	
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ENSMUST00000103547	ENSMUSG00000094075	12	115912344	115912776	-1	6	7	5	2	4	0	0	0	0	1	7	A0A075B5Y3	
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ENSMUST00000103553	ENSMUSG00000076744	13	19178024	19178492	1	2	1	4	1	1	1	0	0	0	0	0	A0A0A6YYE8	
ENSMUST00000103554	ENSMUSG00000076745	13	19184974	19185506	1	3	2	5	3	2	1	1	1	0	1	4	A0A0B4J1J8	
ENSMUST00000103555	ENSMUSG00000076746	13	19190356	19190929	1	1	1	3	1	5	1	0	0	0	0	0	A0A075B5Y8	
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ENSMUST00000103566						0	0	0	1	0	0	0	0	0	0	0		
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ENSMUST00000103570	ENSMUSG00000076761	14	52622566	52623082	1	0	2	1	2	6	1	0	4	0	1	1	A0A075B5Z7	
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ENSMUST00000103588	ENSMUSG00000076778	14	52851290	52851866	1	2	3	2	0	9	6	0	0	0	0	2	A0A075B606	
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ENSMUST00000103596	ENSMUSG00000094758	14	52942764	52943289	1	1	0	0	4	0	0	0	0	1	1	1	A0A075B627	
ENSMUST00000103597	ENSMUSG00000095560	14	52948568	52949169	1	0	0	1	0	0	0	0	0	0	0	0	A0A075B612	
ENSMUST00000103598						1	0	0	1	2	1	0	0	0	0	0		
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ENSMUST00000103605	ENSMUSG00000076795	14	53042428	53042891	1	5	3	1	0	5	2	0	1	0	1	3	A0A075B616	
ENSMUST00000103606	ENSMUSG00000076796	14	53047287	53047821	1	5	4	7	4	0	0	0	0	0	1	2	A0A075B617	
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ENSMUST00000103608	ENSMUSG00000094619	14	53078452	53079045	1	1	0	0	3	7	2	0	0	1	5	2	A0A075B619	
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ENSMUST00000103611	ENSMUSG00000076800	14	53104871	53105344	1	1	0	0	0	0	2	2	0	0	0	0	A0A075B621	
ENSMUST00000103612	ENSMUSG00000095646	14	53122114	53122610	1	2	3	1	1	0	0	0	3	0	1	1	A0A075B622	
ENSMUST00000103613	ENSMUSG00000076802	14	53132679	53133137	1	3	0	0	4	1	0	1	0	0	1	1	A0A075B623	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000103616	ENSMUSG00000096653	14	52863299	52863936	1	0	0	19	6	0	0	0	0	0	1	0	A0A075B624	
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ENSMUST00000103622	ENSMUSG00000094779	14	53253792	53254317	1	1	0	0	4	0	0	0	0	1	1	1	A0A075B627	
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ENSMUST00000103636	ENSMUSG00000096417	14	53390635	53391142	1	5	2	9	4	8	2	1	0	0	3	1	Q5R1I3	
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ENSMUST00000103655	ENSMUSG00000093966	14	53598828	53599410	1	1	0	0	1	1	5	0	0	0	0	0	A0A0B4J1K1	
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ENSMUST00000103662	ENSMUSG00000096678	14	53676141	53676630	1	8	9	8	0	8	1	0	0	0	0	0	A0A0B4J1K2	
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ENSMUST00000103671	ENSMUSG00000087666	14	53795357	53795963	1	0	0	2	5	0	2	0	0	1	0	0	A0A0B4J1K3	
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ENSMUST00000103674	ENSMUSG00000076862	14	53845234	53845827	1	1	7	0	1	5	1	1	0	0	1	1	A0A0B4J1K4	
ENSMUST00000103676	ENSMUSG00000076864	14	53881612	53882217	1	0	2	0	3	6	4	0	0	0	0	1	A0A075B657	
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ENSMUST00000103679	ENSMUSG00000076867	14	54074905	54075515	1	1	1	1	0	1	1	0	0	0	0	0	Q5R1A3	
ENSMUST00000103682	ENSMUSG00000076870	14	54123138	54123188	1	0	1	0	0	0	0	0	0	0	5	3	A0A0G2JG53	
ENSMUST00000103683	ENSMUSG00000076871	14	54136779	54136837	1	0	0	0	0	0	0	0	0	0	0	1	A0A0G2JFW2	
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ENSMUST00000103694						0	0	0	0	0	0	1	0	0	1	0		
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ENSMUST00000103722	ENSMUSG00000076910	14	54200386	54200446	1	0	1	0	2	0	0	0	0	0	0	0	A0A0G2JDX6	
ENSMUST00000103723	ENSMUSG00000076911	14	54200777	54200842	1	0	0	0	1	0	0	1	0	0	1	1	A0A0G2JG46	
ENSMUST00000103724	ENSMUSG00000076912	14	54201775	54201837	1	0	0	0	0	1	0	0	1	0	1	0	A0A0G2JEC1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000103725	ENSMUSG00000076913	14	54203134	54203194	1	0	0	0	1	0	0	0	0	0	0	0	A0A0G2JEK3	
ENSMUST00000103726	ENSMUSG00000076914	14	54204422	54204481	1	1	0	0	0	1	0	0	0	0	0	0	A0A0G2JG86	
ENSMUST00000103727						0	1	0	0	0	0	0	0	0	0	1		
ENSMUST00000103728	ENSMUSG00000076916	14	54205741	54205797	1	2	0	0	0	2	0	0	2	0	0	0	A0A0G2JER2	
ENSMUST00000103729	ENSMUSG00000076917	14	54206553	54206610	1	1	2	3	1	1	0	0	0	0	0	0	A0A0G2JDG3	
ENSMUST00000103730	ENSMUSG00000076918	14	54207139	54207197	1	0	0	0	0	0	0	0	0	0	0	1	A0A0G2JE76	
ENSMUST00000103731	ENSMUSG00000076919	14	54209393	54209450	1	0	0	0	1	0	0	2	0	0	0	0	A0A0G2JEW3	
ENSMUST00000103732						2	1	6	1	1	1	0	0	0	0	0		
ENSMUST00000103733	ENSMUSG00000076921	14	54211470	54211528	1	0	1	1	3	1	0	1	0	0	0	0	A0A0G2JFF4	
ENSMUST00000103734	ENSMUSG00000076922	14	54212688	54212749	1	1	1	0	0	2	0	0	0	0	0	0	A0A0G2JEB4	
ENSMUST00000103735	ENSMUSG00000076923	14	54213777	54213838	1	0	1	0	0	0	0	0	0	0	0	0	A0A0G2JFC2	
ENSMUST00000103736	ENSMUSG00000076924	14	54216291	54216353	1	0	0	1	0	1	0	0	1	0	0	0	A0A0G2JF02	
ENSMUST00000103737	ENSMUSG00000076925	14	54217292	54217357	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JFD7	
ENSMUST00000103738	ENSMUSG00000076926	14	54217836	54217901	1	2	0	0	1	0	0	0	0	0	0	0	A0A0G2JDE4	
ENSMUST00000103739						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000103740	ENSMUSG00000076928	14	54220521	54224206	1	2	1	4	1	2	2	48	63	22	155	108	A0A075B662	
ENSMUST00000103746	ENSMUSG00000076934	16	19085017	19085500	-1	0	1	2	0	1	0	3	6	3	96	56	A0A075B663	
ENSMUST00000103749	ENSMUSG00000076937	16	19198396	19200351	-1	4	4	12	3	8	0	23	53	24	297	96		P01844
ENSMUST00000103751	ENSMUSG00000076939	16	19241207	19241690	-1	4	5	6	3	2	2	0	4	4	19	11	A0A0B4J1K5	
ENSMUST00000103752	ENSMUSG00000076940	16	19260401	19260859	-1	2	3	0	1	4	1	6	2	3	18	17	A0A075B664	
ENSMUST00000104874	ENSMUSG00000047667	9	38855060	38855990	1	4	3	7	5	2	0	0	0	0	0	0	Q7TRB7	
ENSMUST00000104875	ENSMUSG00000061165	9	37711348	37712277	-1	17	10	26	7	14	15	0	0	0	0	0	Q8VGE3	
ENSMUST00000104877	ENSMUSG00000073927	7	104564152	104565212	1	0	2	0	3	0	3	0	0	0	0	0	F6VL06	
ENSMUST00000104879	ENSMUSG00000094119	7	103538261	103539232	-1	4	4	4	8	6	2	0	0	0	0	0	L7N462	
ENSMUST00000104880	ENSMUSG00000073953	7	103309723	103310661	1	2	2	2	2	2	5	0	0	0	0	0	F8VQ26	
ENSMUST00000104881	ENSMUSG00000078080	7	103097743	103098699	1	9	3	1	2	2	3	0	0	0	0	0	E9PXW4	
ENSMUST00000104889	ENSMUSG00000044039	2	111478786	111479724	1	0	0	1	0	3	2	0	0	0	0	0	Q7TQY0	
ENSMUST00000104891	ENSMUSG00000078091	2	104065826	104067486	1	333	271	1595	411	369	179	13	75	28	64	44	Q3UXH0	
ENSMUST00000104892	ENSMUSG00000075120	2	88700383	88701327	-1	1	2	0	0	0	1	0	0	0	0	0	Q7TR14	
ENSMUST00000104893	ENSMUSG00000005615	16	32430921	32475070	1	12	9	37	0	3	11	86	0	97	22	63		P49586
ENSMUST00000104902	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	15	6	0	0	0	0	0	0	0	E9Q030	
ENSMUST00000104903	ENSMUSG00000108114	10	129659808	129660743	1	3	2	0	1	2	2	0	0	0	0	0	Q8VFH7	
ENSMUST00000104914	ENSMUSG00000078116	9	18815354	18816292	-1	1	0	0	0	1	0	0	0	0	0	0	Q8VFM8	
ENSMUST00000104915	ENSMUSG00000078117	9	8971791	8975773	1	46	34	228	47	30	24	1	3	3	0	1	Q8C4B7	
ENSMUST00000104916	ENSMUSG00000044424	19	23619742	23620320	1	0	3	3	0	0	0	0	0	3	9	6	F6SVV1	
ENSMUST00000104917	ENSMUSG00000078118	7	108103279	108104343	1	4	3	14	3	9	6	0	0	0	0	0	Q14AB1	Q8VG05
ENSMUST00000104922						2	11	0	0	11	1	0	0	0	0	0		
ENSMUST00000104925	ENSMUSG00000078126	14	34170655	34171168	1	0	3	4	6	0	0	0	1937	0	0	0		
ENSMUST00000104926	ENSMUSG00000078127	14	32833962	32836789	1	18	19	32	48	32	11	0	3	1	1	0	E9PXT9	
ENSMUST00000104927	ENSMUSG00000078128	14	26514554	26514910	1	2	1	1	0	7	1	0	0	0	0	0	D3YWC0	
ENSMUST00000104928	ENSMUSG00000078129	2	154551776	154553276	1	18	15	45	191	29	18	0	0	0	0	0		A2AKE7
ENSMUST00000104929	ENSMUSG00000078130	11	99649599	99650236	-1	3	4	8	29	12	0	0	0	0	0	0	B1AQ89	
ENSMUST00000104930	ENSMUSG00000078131	11	99590461	99591339	-1	5	3	15	77	1	4	0	0	0	0	0	A2A588	
ENSMUST00000104931	ENSMUSG00000078132	11	99559167	99559466	-1	3	1	1	2	4	3	0	0	0	0	0	A2A592	
ENSMUST00000104933	ENSMUSG00000078134	11	98624351	98625661	-1	5	5	5	10	8	1	0	0	2	0	0	A2A4X6	
ENSMUST00000104934	ENSMUSG00000058620	2	127363208	127367221	1	0	0	0	237	51	50	0	0	0	0	0	Q925K6	
ENSMUST00000104936	ENSMUSG00000074881	2	121953752	121956092	-1	4	2	10	66	16	3	0	0	0	0	1	Q9D2H4	
ENSMUST00000104937	ENSMUSG00000078137	2	118699103	118703963	-1	36	22	69	962	59	29	0	4	3	0	0		A2ARS0
ENSMUST00000104941	ENSMUSG00000069306	13	21811746	21812147	1	0	0	0	0	0	0	0	0	0	9	0	B2RTM0	P62806
ENSMUST00000104942	ENSMUSG00000078139	13	21495223	21497146	1	10	16	17	33	15	8	25	108	46	55	43	I3ITR1	
ENSMUST00000104944	ENSMUSG00000078141	13	12702362	12702589	1	0	3	15	115	1	4	0	0	0	0	0	F6SV87	
ENSMUST00000104947	ENSMUSG00000078144	8	92901407	92902407	1	2	5	5	4	8	4	16	56	61	6	105		Q9D7J7
ENSMUST00000104954	ENSMUSG00000035399	2	163405822	163424697	-1	0	0	0	0	0	0	0	0	0	0	0		Q9D722
ENSMUST00000104955	ENSMUSG00000044352	11	53476573	53480274	-1	32	17	55	832	46	25	0	0	0	0	1		Q8BLS7
ENSMUST00000104958	ENSMUSG00000078153	11	48945354	48946190	-1	4	0	11	9	5	4	69	134	241	39	284	Q5SVP3	P97372
ENSMUST00000104959	ENSMUSG00000078154	11	48825346	48826655	-1	0	0	8	28	0	0	0	0	0	0	0		O35207
ENSMUST00000104962	ENSMUSG00000078157	11	29822395	29825668	-1	18	27	46	329	58	15	0	1	2	1	5	Z4YK74	Q8C0T1
ENSMUST00000104964	ENSMUSG00000078160	4	147540218	147543500	1	121	122	105	113	150	65	0	0	8	0	2	Q8C6M9	
ENSMUST00000104965						24	26	39	206	30	14	0	1	4	1	2		
ENSMUST00000104970						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000104977						10	9	59	14	21	5	0	1	0	0	2		
ENSMUST00000104979	ENSMUSG00000078179	6	23653898	23655136	-1	5	7	11	6	8	3	0	0	0	0	0		G3X9R7
ENSMUST00000104983	ENSMUSG00000078184	1	175977777	175979114	-1	15	15	14	29	21	11	1	6	1	1	4		
ENSMUST00000104984	ENSMUSG00000078185	1	175682237	175688353	-1	42	37	55	42	36	20	30	66	68	16	51		
ENSMUST00000104985						4	3	15	11	11	5	0	1	0	0	0		
ENSMUST00000104986						1	0	0	2	0	1	0	0	0	0	0		
ENSMUST00000104990						0	0	3	16	1	0	2	1	1	2	0		
ENSMUST00000104994	ENSMUSG00000078197	2	140152043	140153532	1	27	34	71	23	31	10	6	3	10	0	8	F6SNQ2	
ENSMUST00000104995	ENSMUSG00000078198	2	37146214	37147137	1	5	5	5	2	4	1	0	0	0	0	0		
ENSMUST00000104998	ENSMUSG00000078201	2	25255439	25256292	1	8	2	18	123	9	1	187	269	124	72	103		Q8R235
ENSMUST00000104999	ENSMUSG00000078202	2	25180758	25183339	1	8	8	13	446	20	11	4	8	2	5	11		Q91ZA8
ENSMUST00000105001	ENSMUSG00000062651	2	17996417	17996958	-1	6	4	9	7	8	1	0	0	0	0	0		Q9CQ70
ENSMUST00000105004	ENSMUSG00000078206	X	8985900	8986755	-1	1	0	15	0	8	2	0	0	0	0	0	Q3SXD1	
ENSMUST00000105006	ENSMUSG00000078208	X	8962134	8962975	-1	5	0	6	6	0	4	0	0	0	0	0	A2AHC5	
ENSMUST00000105007	ENSMUSG00000095814	X	5669067	5671026	1	0	8	0	0	0	7	0	0	0	0	0	A2BHG6	
ENSMUST00000105011	ENSMUSG00000078213	X	4800496	4801986	1	0	8	0	0	0	0	0	0	0	0	0	A2CGC2	
ENSMUST00000105014	ENSMUSG00000094273	X	4370636	4372595	1	0	0	0	0	8	0	0	0	0	0	0	L7MU81	
ENSMUST00000105015	ENSMUSG00000094307	X	4196576	4198535	1	0	16	33	13	0	11	0	0	0	0	0	A2CFD5	
ENSMUST00000105016						7	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000105017	ENSMUSG00000099711	X	32726109	32728051	1	0	3	0	13	29	0	0	0	0	0	0		
ENSMUST00000105019	ENSMUSG00000094876	X	3700233	3702192	1	0	0	0	0	16	14	0	0	0	0	0	L7MU83	
ENSMUST00000105020	ENSMUSG00000094558	X	3441731	3443690	-1	57	23	14	36	3	7	0	0	0	0	0	A2BFZ7	
ENSMUST00000105031	ENSMUSG00000078234	4	139960220	139968026	-1	185	206	139	224	183	102	2	18	9	4	9		A2APT9
ENSMUST00000105032	ENSMUSG00000078235	4	138394092	138396528	-1	12	6	22	418	17	2	0	0	0	0	0	A2AM80	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000105035	ENSMUSG00000066061	4	118808797	118809944	-1	0	0	10	0	0	0	0	0	0	0	0	B1ARU7	
ENSMUST00000105038	ENSMUSG00000078240	18	34736359	34738014	1	134	89	236	431	136	101	24	28	28	84	27	W4VSN7	
ENSMUST00000105041	ENSMUSG00000079507	17	35320405	35325099	1	0	0	0	0	0	0	0	0	0	0	0	E9PX63	
ENSMUST00000105046	ENSMUSG00000078249	11	120762794	120764419	1	17	9	34	80	41	9	321	319	205	185	504	Q566K0	P17095
ENSMUST00000105048						70	46	138	171	80	28	0	3	1	0	0		
ENSMUST00000105049	ENSMUSG00000078252	11	99993234	99993994	-1	4	4	2	145	15	5	0	0	0	0	0	A2A5X6	
ENSMUST00000105050	ENSMUSG00000078253	11	99984710	99986597	-1	21	10	61	25	24	9	0	0	0	0	0		A2A5X5
ENSMUST00000105051	ENSMUSG00000078254	11	99978025	99979053	-1	10	5	7	6	12	6	0	0	0	0	0		A2A5X4
ENSMUST00000105052	ENSMUSG00000078255	11	99948475	99949551	1	6	9	28	11	9	6	0	0	0	0	0	A2A5X3	
ENSMUST00000105053	ENSMUSG00000078256	11	99914751	99915671	1	7	4	7	6	8	2	0	0	0	0	0	A2A4M7	
ENSMUST00000105054	ENSMUSG00000078257	11	99836802	99838066	-1	9	3	18	22	11	3	0	0	0	0	0	A2A4M0	
ENSMUST00000105055	ENSMUSG00000078258	11	99814976	99815666	-1	10	5	20	40	15	4	0	0	0	0	0	A2A4L9	
ENSMUST00000105056	ENSMUSG00000078259	11	99803557	99804446	-1	4	0	4	62	0	0	0	0	0	0	0	B1AQB2	
ENSMUST00000105057	ENSMUSG00000078260	11	99798064	99798932	-1	0	2	24	61	12	0	0	0	0	0	0	B1AQB1	
ENSMUST00000105058	ENSMUSG00000078261	11	99792389	99793467	-1	6	3	21	44	10	0	0	0	0	0	0	B1AQB0	
ENSMUST00000105059	ENSMUSG00000078262	11	99785200	99786258	1	8	4	8	92	5	1	0	0	0	0	0	B1AQA9	
ENSMUST00000105060						1	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000105066	ENSMUSG00000078269	11	99734213	99734290	-1	5	0	10	7	3	2	0	0	0	0	0	B1AQA0	
ENSMUST00000105067						7	5	22	65	15	4	0	0	0	0	0		
ENSMUST00000105073	ENSMUSG00000078276	11	99690588	99690740	-1	1	2	2	10	3	1	0	0	0	0	0	B1AQ87	
ENSMUST00000105077	ENSMUSG00000078280	6	132710999	132711928	-1	3	0	1	0	1	0	0	0	0	0	0	D3YU55	
ENSMUST00000105082	ENSMUSG00000041757	1	133181321	133303435	1	14	15	64	33	25	0	22	70	35	5	27	E9PX43	
ENSMUST00000105085						5	2	13	6	4	2	0	3	2	4	0		
ENSMUST00000105087						0	8	16	12	2	10	1	3	2	2	2		
ENSMUST00000105097	ENSMUSG00000032846	13	107724618	107890064	-1	13	20	31	55	34	14	322	645	677	70	599		Q80TB7
ENSMUST00000105098	ENSMUSG00000078302	13	98354242	98356703	1	8	5	11	345	7	9	0	0	0	0	0		Q61345
ENSMUST00000105105	ENSMUSG00000099583	13	23575763	23576322	1	4	8	4	134	7	4	0	15	7	5	5	B9EI85	P84228
ENSMUST00000105106	ENSMUSG00000069268	13	23573736	23574196	-1	2	6	20	39	5	0	0	8	0	4	3		P10853
ENSMUST00000105107	ENSMUSG00000069273	13	23561534	23562369	-1	7	5	5	105	14	3	2	0	2	4	0	B9EI85	P84228
ENSMUST00000105110	ENSMUSG00000078315	X	78737763	78739401	1	3	4	0	5	4	2	0	0	0	0	0	Q14BE7	
ENSMUST00000105111	ENSMUSG00000078317	X	73228291	73230795	1	6	7	17	241	13	5	129	207	119	24	75	Q9JJQ6	
ENSMUST00000105113	ENSMUSG00000078320	X	43591160	43593532	1	9	9	29	12	2	4	0	0	0	0	0	D3YU32	
ENSMUST00000105117	ENSMUSG00000078324	X	33700649	33702349	-1	0	19	0	0	0	4	0	0	0	0	0	Q1LZI5	
ENSMUST00000105124	ENSMUSG00000095770	X	31962044	31962821	1	2	0	3	0	3	0	0	0	0	0	0	E9PWJ8	
ENSMUST00000105137	ENSMUSG00000078346	X	14211148	14211661	1	4	0	4	6	2	0	0	0	0	0	0	Q497L1	
ENSMUST00000105139	ENSMUSG00000078348	10	13005343	13009183	1	56	64	221	217	71	37	390	625	299	391	248		Q923D4
ENSMUST00000105140	ENSMUSG00000078349	4	156203304	156205151	1	33	41	282	322	52	23	36	229	34	7	171	F6S7Q2	
ENSMUST00000105143	ENSMUSG00000100713	4	88816228	88816800	1	0	0	0	0	2	0	0	0	0	0	0	Q810G6	
ENSMUST00000105144	ENSMUSG00000096854	4	88782131	88783592	1	26	6	23	44	6	6	0	0	0	0	0	Q8BQT1	
ENSMUST00000105146	ENSMUSG00000101252	4	88827416	88827985	1	0	0	3	0	0	0	0	0	0	0	0	Q810G5	
ENSMUST00000105147	ENSMUSG00000078354	4	88682881	88683912	-1	5	4	3	11	13	3	0	0	0	0	0	B1AYH7	
ENSMUST00000105148	ENSMUSG00000078355	4	88675915	88676924	-1	10	9	15	8	3	3	1	0	0	0	0	Q810G1	
ENSMUST00000105149	ENSMUSG00000063376	4	88643641	88644459	-1	0	1	9	3	0	0	0	0	0	0	0	B1AYH5	Q80SU4
ENSMUST00000105158	ENSMUSG00000078365	4	3870657	3872105	-1	8	10	22	23	27	11	0	0	0	0	0	A6H643	
ENSMUST00000105159	ENSMUSG00000095982	4	3184382	3185305	-1	14	11	14	0	15	4	0	0	0	0	0	A2AMT7	
ENSMUST00000105160	ENSMUSG00000094798	4	3172083	3173006	1	18	8	0	4	5	5	0	0	0	0	0	A2AMT6	
ENSMUST00000105167	ENSMUSG00000095254	12	19606929	19607264	1	0	0	0	38	0	1	0	0	0	0	0	L7N241	
ENSMUST00000105169						0	0	0	0	3	0	0	0	149	92	0		
ENSMUST00000105172	ENSMUSG00000078380	7	34251038	34251493	1	4	2	48	13	5	5	0	1	0	0	0	D3YTY6	
ENSMUST00000105177	ENSMUSG00000003123	7	25379527	25398710	-1	9	14	155	41	12	2	0	0	0	0	0	Q9D4C4	
ENSMUST00000105187	ENSMUSG00000093917	7	22370122	22371039	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6J2	
ENSMUST00000105195	ENSMUSG00000095191	7	21843344	21844267	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7F4	
ENSMUST00000105196	ENSMUSG00000096760	7	21795811	21796728	-1	0	0	0	0	0	0	0	0	0	0	0	D3YTX5	
ENSMUST00000105197	ENSMUSG00000094680	7	21097569	21098513	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6J4	
ENSMUST00000105199	ENSMUSG00000093890	7	21318944	21319861	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6J5	
ENSMUST00000105200	ENSMUSG00000094221	7	21259694	21260617	-1	0	0	0	0	0	0	0	0	0	0	0	D3YTX4	
ENSMUST00000105202	ENSMUSG00000093986	7	21052867	21053784	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6J6	
ENSMUST00000105209	ENSMUSG00000095806	7	20374493	20375410	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6J2	
ENSMUST00000105210	ENSMUSG00000068816	2	87782536	87783486	1	2	5	0	3	3	1	0	0	0	0	0	Q7TR38	
ENSMUST00000105211	ENSMUSG00000044213	2	86828754	86829746	1	4	0	3	1	0	1	0	0	0	0	0	Q0VAY0	Q8VF13
ENSMUST00000105212	ENSMUSG00000078420	2	86806088	86806997	-1	6	3	0	0	5	0	0	0	0	0	0	A3KPP7	
ENSMUST00000105213	ENSMUSG00000090059	2	86422727	86423674	-1	7	1	19	0	4	4	0	0	0	0	0	Q7TR71	
ENSMUST00000105222						4	2	2	3	8	3	31	9	23	18	13		
ENSMUST00000105229	ENSMUSG00000025351	10	128908919	128912816	1	0	15	0	3	14	3	73	219	78	39	29	Q549D0	P41731
ENSMUST00000105230	ENSMUSG00000078427	10	128821771	128877638	1	9	0	11	58	7	3	165	832	270	1113	180	B2RXM7	Q9D1J3
ENSMUST00000105233	ENSMUSG00000002578	10	128630843	128645991	-1	0	0	1	0	0	0	0	0	0	1	0	G3X9R8	
ENSMUST00000105235	ENSMUSG00000025369	10	128459236	128490173	1	33	0	57	136	31	22	1045	1689	1474	94	1446		Q6PDG5
ENSMUST00000105238	ENSMUSG00000040033	10	128270576	128292849	1	11	7	36	35	10	6	0	2	159	0	115	E9QJX9	
ENSMUST00000105240						9	5	7	2	0	8	126	589	212	26	102		
ENSMUST00000105242	ENSMUSG00000039994	10	128232065	128252941	1	10	0	0	0	49	0	0	0	0	0	0		Q9R1X4
ENSMUST00000105243	ENSMUSG00000039994	10	128232065	128252941	1	0	0	0	3	0	6	12	0	0	0	0	H7BX89	
ENSMUST00000105244	ENSMUSG00000039994	10	128232065	128252941	1	0	0	0	0	0	0	19	58	54	0	62	Q3U574	Q9R1X4
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ENSMUST00000105249	ENSMUSG00000025404	10	127380327	127499384	1	7	0	0	4	0	0	290	1273	476	20	631		Q80TM6
ENSMUST00000105250	ENSMUSG00000025404	10	127380327	127499384	1	0	0	0	0	0	0	769	978	1003	49	571		Q80TM6
ENSMUST00000105251	ENSMUSG00000025404	10	127380327	127499384	1	0	0	0	0	0	0	0	0	0	1	0		Q80TM6
ENSMUST00000105255	ENSMUSG00000078429	10	126978717	126999975	1	6	20	62	5	16	24	1782	3997	1488	243	1340	Q8R3B3	
ENSMUST00000105256	ENSMUSG00000078429	10	126978717	126999975	1	40	9	23	295	23	11	5520	3448	6818	467	4559		Q8BX07
ENSMUST00000105257	ENSMUSG00000020102	10	125226464	125328963	-1	3	0	4	5	5	0	8	18	7	10	19	Q149G3	O70451
ENSMUST00000105261	ENSMUSG00000034813	10	119454034	120087261	1	0	0	9	0	0	1	0	0	0	0	0		Q925T6
ENSMUST00000105262	ENSMUSG00000034813	10	119454034	120087261	1	0	0	0	0	0	0	0	0	0	0	0	H7BX90	
ENSMUST00000105263	ENSMUSG00000020184	10	117688888	117710758	-1	17	0	0	66	0	0	0	362	0	22	0		P23804
ENSMUST00000105264	ENSMUSG00000078430	10	117248024	117250265	1	1	0	1	0	1	1	0	0	0	0	0	D3YTV0	
ENSMUST00000105265	ENSMUSG00000020166	10	116485161	116581511	-1	8	0	0	0	0	0	0	0	56	5	0		Q8C5L3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000105267	ENSMUSG00000020166	10	116485161	116581511	-1	0	0	0	1	0	0	167	557	52	484	177		Q8C5L3
ENSMUST00000105271	ENSMUSG00000020151	10	116018213	116274932	1	0	3	0	2	5	3	0	0	0	0	0		Q62132
ENSMUST00000105272						22	14	7	7	22	8	0	0	0	0	0		
ENSMUST00000105275	ENSMUSG00000020189	10	111164802	111297247	1	58	36	173	1	1	35	123	405	384	0	90	B9EJ86	B9EJ86
ENSMUST00000105276	ENSMUSG00000035864	10	108497650	109010982	-1	15	0	0	0	0	4	0	0	0	0	0	H6RXZ1	P46096
ENSMUST00000105280	ENSMUSG00000019906	10	107271843	107425143	1	16	23	67	30	33	23	0	1	0	0	0	Q3TUM0	
ENSMUST00000105283	ENSMUSG00000019966	10	100015630	100100413	1	9	8	3	41	4	4	0	0	0	12	17		P20826
ENSMUST00000105285	ENSMUSG00000019936	10	97644068	97682454	1	6	3	0	0	6	2	0	0	0	0	0		P70186
ENSMUST00000105286	ENSMUSG00000019932	10	97607205	97613688	1	10	5	12	2	7	8	0	0	0	0	0	A4FUJ3	O35367
ENSMUST00000105287	ENSMUSG00000019929	10	97479500	97518162	1	3	6	0	0	3	4	0	0	0	443	81	Q3UKR1	P28654
ENSMUST00000105290	ENSMUSG00000005897	10	94148023	94197211	1	8	2	3	42	12	11	22	76	8	7	5		Q505F1
ENSMUST00000105293	ENSMUSG00000019961	10	91147571	91171582	-1	0	0	5	30	6	5	44	182	32	26	47		Q61029
ENSMUST00000105294						3	0	0	0	0	1	100	469	28	79	101		
ENSMUST00000105295	ENSMUSG00000019935	10	89574020	89621253	-1	2	1	6	0	2	1	0	0	0	0	0	D3YTT3	
ENSMUST00000105296	ENSMUSG00000047638	10	89454234	89533585	-1	5	0	0	10	0	0	0	0	0	0	0		Q60641
ENSMUST00000105297	ENSMUSG00000047638	10	89454234	89533585	-1	4	5	7	0	7	3	0	29	49	40	0	D3YTT2	
ENSMUST00000105298	ENSMUSG00000074802	10	89408823	89443967	-1	31	26	155	45	29	28	26	35	42	11	44		
ENSMUST00000105300	ENSMUSG00000020053	10	87858265	87937042	1	0	0	0	0	0	0	0	0	0	0	1	Q4VJB9	
ENSMUST00000105304	ENSMUSG00000050108	10	85959340	86011895	-1	0	1	3	2	0	0	0	0	0	0	0	D3YTT0	
ENSMUST00000105306	ENSMUSG00000020042	10	85386814	85660292	1	4	5	0	8	5	0	6	0	1	0	0	E9QJW1	
ENSMUST00000105307	ENSMUSG00000020042	10	85386814	85660292	1	0	0	0	20	0	0	0	0	9	0	12		Q6GQW0
ENSMUST00000105313	ENSMUSG00000061371	10	82058417	82061329	1	4	6	7	6	5	2	5	37	8	22	6	E9PU88	
ENSMUST00000105314	ENSMUSG00000078435	10	82128013	82153065	1	0	2	0	2	0	1	2	15	7	6	5	F8VPU8	
ENSMUST00000105315	ENSMUSG00000096856	10	81649059	81667361	1	0	0	0	0	0	0	5	9	1	0	0	F8VPU7	
ENSMUST00000105316	ENSMUSG00000094622	10	81745983	81747503	-1	0	3	3	2	0	0	0	9	6	5	0	F6TW77	
ENSMUST00000105321	ENSMUSG00000055053	10	81396186	81431005	-1	32	26	101	113	49	22	1022	1094	1104	77	970	Q3UHA6	P70255
ENSMUST00000105322	ENSMUSG00000078439	10	81393051	81395392	1	0	3	22	4	0	2	0	0	8	11	0		Q0VG18
ENSMUST00000105323	ENSMUSG00000020232	10	81346048	81350480	-1	0	0	0	21	0	0	97	333	61	16	60	Q3U1L0	Q9Z104
ENSMUST00000105324	ENSMUSG00000020232	10	81346048	81350480	-1	0	0	0	20	0	0	0	91	16	0	64	Q3U1L0	Q9Z104
ENSMUST00000105325	ENSMUSG00000034881	10	81328732	81335171	1	21	12	46	495	36	5	17	13	6	5	12	Q5FW61	P30987
ENSMUST00000105327	ENSMUSG00000034902	10	81292963	81319973	1	0	0	0	30	0	0	0	0	0	0	0		O70161
ENSMUST00000105328	ENSMUSG00000004933	10	81252935	81263365	1	0	0	0	38	0	0	21	2	0	0	5		
ENSMUST00000105331	ENSMUSG00000035027	10	81105915	81124697	1	0	1	2	40	2	0	1015	1258	807	137	695	Q91YS7	
ENSMUST00000105332	ENSMUSG00000062075	10	80901203	80918245	-1	16	4	11	23	16	7	0	2	0	0	5	Q3V159	P21619
ENSMUST00000105333	ENSMUSG00000059406	10	80879720	80899441	1	39	27	75	446	46	28	0	1	0	0	0	D3YTR8	
ENSMUST00000105336	ENSMUSG00000061589	10	80755206	80795461	1	33	30	94	121	61	37	443	398	401	43	395	Q6XZL8	
ENSMUST00000105339	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	0	0	0	0	0	0	0	0	22	E9PWE5	
ENSMUST00000105340	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	0	0	0	0	0	36	0	0	0	E9PWE4	
ENSMUST00000105341	ENSMUSG00000020167	10	80409514	80433647	-1	11	3	20	0	1	0	375	460	262	36	289	E9PWE3	
ENSMUST00000105342	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	0	0	0	0	5	155	0	12	0	E9PWE2	
ENSMUST00000105343	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVV2	
ENSMUST00000105344	ENSMUSG00000020167	10	80409514	80433647	-1	0	9	0	25	23	6	40	0	0	0	0	E9PVV1	
ENSMUST00000105345	ENSMUSG00000020167	10	80409514	80433647	-1	0	3	0	0	7	0	0	0	0	0	0		P15806
ENSMUST00000105346	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	2	0	0	0	0	76	152	20	2		P15806
ENSMUST00000105347	ENSMUSG00000035478	10	80392539	80399550	-1	2	0	0	0	3	5	62	50	23	0	49	D3YTR5	
ENSMUST00000105348	ENSMUSG00000035478	10	80392539	80399550	-1	2	0	5	6	0	0	23	39	25	0	32	D3YTR4	
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ENSMUST00000105350	ENSMUSG00000048696	10	80380355	80387659	-1	1	1	1	34	2	1	2	1	2	0	1	D3YTR3	
ENSMUST00000105351	ENSMUSG00000035486	10	80356459	80365489	1	12	5	0	64	16	8	0	0	0	0	0		Q4FZD7
ENSMUST00000105352	ENSMUSG00000043822	10	80339110	80348412	-1	0	0	0	0	0	0	1	0	1	2	3	Q9CRC7	
ENSMUST00000105354	ENSMUSG00000035504	10	80329953	80336441	1	0	0	0	4	13	6	0	0	0	0	0		Q9JM62
ENSMUST00000105355	ENSMUSG00000035504	10	80329953	80336441	1	10	0	56	182	8	0	2	0	0	0	0		Q9JM62
ENSMUST00000105357	ENSMUSG00000035504	10	80329953	80336441	1	10	0	56	182	8	0	2	0	0	0	0	D3YTR2	
ENSMUST00000105358	ENSMUSG00000035504	10	80329953	80336441	1	0	0	0	4	13	6	0	0	0	0	0	D3YTR1	
ENSMUST00000105359	ENSMUSG00000020135	10	80295977	80318263	1	74	47	182	829	91	0	0	0	0	0	14	D3YTR0	
ENSMUST00000105361	ENSMUSG00000069565	10	80261486	80288408	1	0	0	2	62	4	0	62	170	190	83	181	Q3UGB5	
ENSMUST00000105362	ENSMUSG00000069565	10	80261486	80288408	1	0	0	0	110	0	0	0	433	0	50	0		Q9JII5
ENSMUST00000105363	ENSMUSG00000020150	10	80258151	80261012	-1	0	0	0	64	3	0	0	13	0	3	6		O35969
ENSMUST00000105364	ENSMUSG00000020153	10	80249121	80256794	1	4	6	5	46	8	3	105	65	42	13	34		Q9DC70
ENSMUST00000105365	ENSMUSG00000045193	10	80165985	80172786	1	1	2	25	57	2	4	816	1521	678	344	694		P60824
ENSMUST00000105366	ENSMUSG00000003072	10	80138632	80145818	1	0	0	0	119	0	0	0	26	17	0	0	D3Z7S4	
ENSMUST00000105367	ENSMUSG00000003072	10	80138632	80145818	1	0	0	0	93	14	8	3	3	0	0	0	Q4FK74	Q9D3D9
ENSMUST00000105369	ENSMUSG00000035640	10	80130451	80140835	-1	0	7	0	315	0	17	0	0	0	0	8	E9QP85	
ENSMUST00000105370	ENSMUSG00000003068	10	80115803	80130682	1	4	0	0	0	0	0	370	815	257	96	394	E9Q811	
ENSMUST00000105371	ENSMUSG00000003068	10	80115803	80130682	1	0	2	0	0	0	2	747	490	529	74	329	D6RGT4	
ENSMUST00000105372	ENSMUSG00000075706	10	80047166	80056439	1	0	0	15	68	19	0	1434	1880	895	2980	615		O70325
ENSMUST00000105373	ENSMUSG00000035697	10	80016653	80031472	1	14	0	26	41	14	29	2006	1557	1488	53	1501	D3Z7R7	
ENSMUST00000105374	ENSMUSG00000004665	10	79988584	79996062	1	0	0	0	37	0	3	2155	925	2736	218	1932	D3Z7R6	
ENSMUST00000105376	ENSMUSG00000019564	10	79927043	79955018	1	20	9	0	49	0	16	388	304	2058	60	830		Q62431
ENSMUST00000105377	ENSMUSG00000019564	10	79927043	79955018	1	0	0	34	0	30	0	0	0	0	0	0		
ENSMUST00000105378	ENSMUSG00000013833	10	79894708	79908923	-1	99	82	202	146	108	41	322	643	229	60	180	E9QP84	
ENSMUST00000105379	ENSMUSG00000035863	10	79793572	79820896	1	0	0	38	286	18	0	849	1047	739	38	447	Q542N8	Q9Z0P4
ENSMUST00000105381	ENSMUSG00000023175	10	79704491	79711969	1	0	0	9	2	0	6	707	667	171	3	184	K3W4Q8	
ENSMUST00000105383	ENSMUSG00000078442	10	78746924	78753067	-1	13	10	36	131	21	8	0	0	0	0	0		Q9D4K7
ENSMUST00000105384	ENSMUSG00000032763	10	78574500	78584498	1	29	13	45	39	26	14	183	243	127	54	162		Q8BU33
ENSMUST00000105385	ENSMUSG00000032788	10	78436744	78464975	-1	0	0	0	0	0	0	3	3	0	5	0	D3Z7R1	
ENSMUST00000105387	ENSMUSG00000001211	10	78269178	78352489	-1	0	2	3	1	3	0	18	18	14	30	50		Q9D517
ENSMUST00000105388	ENSMUSG00000001211	10	78269178	78352489	-1	0	0	0	113	11	0	0	0	0	0	0		Q9D517
ENSMUST00000105389	ENSMUSG00000001211	10	78269178	78352489	-1	12	12	19	6	20	13	39	46	10	14	59		Q9D517
ENSMUST00000105390	ENSMUSG00000001211	10	78269178	78352489	-1	0	8	4	12	0	3	0	0	0	0	0		Q9D517
ENSMUST00000105393	ENSMUSG00000000732	10	78069360	78079525	1	22	9	37	194	25	13	640	1459	717	83	708	Q544C7	Q9JHJ8
ENSMUST00000105395	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000105396	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000105397	ENSMUSG00000020284	10	77978524	77986905	1	0	2	0	28	3	2	185	368	158	49	115		Q8C6G1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000105398	ENSMUSG00000020284	10	77978524	77986905	1	6	9	7	9	15	4	20	13	23	0	14	Q3U699	
ENSMUST00000105399	ENSMUSG00000009292	10	77907722	77970563	-1	3	4	5	2	2	1	26	57	33	48	63	D3Z7Q7	
ENSMUST00000105400						3	0	13	8	14	0	319	1425	583	59	2050		
ENSMUST00000105401	ENSMUSG00000009292	10	77907722	77970563	-1	33	25	111	241	49	24	41	516	57	61	290	Q5KTC0	
ENSMUST00000105404	ENSMUSG00000020262	10	77290726	77418270	-1	23	0	6	0	0	0	1	3	3	1	0	D6RGS1	
ENSMUST00000105406	ENSMUSG00000020262	10	77290726	77418270	-1	40	0	60	60	0	45	0	0	0	0	0		Q91ZS8
ENSMUST00000105408	ENSMUSG00000078444	10	77257776	77259223	-1	21	8	23	111	19	22	5	6	5	3	5	Q3TNV0	
ENSMUST00000105409	ENSMUSG00000001435	10	77052178	77166548	-1	0	0	0	0	0	0	5	0	0	0	22		P39061
ENSMUST00000105410	ENSMUSG00000001436	10	77032241	77061002	1	0	5	0	8	17	12	21	36	0	0	0	Q542F3	P41438
ENSMUST00000105411	ENSMUSG00000001120	10	76761857	76961887	-1	11	16	31	49	6	10	0	0	0	0	7		P57722
ENSMUST00000105413	ENSMUSG00000020241	10	76595762	76623630	-1	17	18	54	163	40	23	0	1	1	2	6	D3Z7D5	
ENSMUST00000105414	ENSMUSG00000009115	10	76562272	76570201	1	5	8	12	2	0	0	0	0	0	0	0	D3Z7D4	
ENSMUST00000105415	ENSMUSG00000009114	10	76449081	76461110	1	0	0	0	21	4	0	0	0	0	0	0	E9Q7R5	
ENSMUST00000105417	ENSMUSG00000020231	10	76259429	76345291	-1	0	0	23	67	20	0	0	0	0	0	0	D3Z7D3	
ENSMUST00000105420	ENSMUSG00000020178	10	75316943	75334788	1	22	8	39	132	25	16	27	24	13	4	28		Q60613
ENSMUST00000105421	ENSMUSG00000033444	10	75212073	75312399	1	0	0	0	39	0	0	0	45	91	0	91		Q2KN98
ENSMUST00000105424	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000105426	ENSMUSG00000052613	10	73099342	74649737	1	0	1	0	0	0	0	0	0	0	0	0		Q99PJ1
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ENSMUST00000105431	ENSMUSG00000019923	10	72654845	72674964	1	8	1	4	7	5	3	19	53	45	60	22		Q9CQU5
ENSMUST00000105432	ENSMUSG00000003923	10	71225464	71238280	-1	0	0	0	0	0	0	18	73	26	1	0		P40630
ENSMUST00000105436	ENSMUSG00000043259	10	70440668	70558731	1	12	0	25	60	6	8	0	0	0	0	0	G3X9S1	
ENSMUST00000105437	ENSMUSG00000037846	10	67979570	68059740	1	19	0	4	0	0	6	0	0	3	0	0	E9QP76	
ENSMUST00000105438	ENSMUSG00000037868	10	67535475	67542188	1	0	0	0	0	0	0	8	78	0	1	0		P08152
ENSMUST00000105439	ENSMUSG00000042846	10	63928472	64090277	-1	3	6	0	4	0	0	0	0	0	0	0		Q8BZ81
ENSMUST00000105440	ENSMUSG00000060843	10	63430098	65003667	1	15	22	30	7	18	10	1	0	0	0	0		Q65CL1
ENSMUST00000105441	ENSMUSG00000060843	10	63430098	65003667	1	6	0	0	11	0	0	0	0	0	0	0		Q65CL1
ENSMUST00000105442	ENSMUSG00000020063	10	63319005	63381704	-1	0	0	0	18	0	0	0	47	25	4	0	Q3UNI1	
ENSMUST00000105447	ENSMUSG00000020078	10	62454843	62486805	-1	8	5	19	1	0	4	561	2136	1007	781	580		P40336
ENSMUST00000105451						4	10	63	4	10	6	0	0	0	0	0		
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ENSMUST00000105453	ENSMUSG00000058806	10	61838236	61979108	-1	0	4	0	0	6	0	0	1	0	0	0	D3Z7B8	
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ENSMUST00000105455	ENSMUSG00000020085	10	61715263	61739260	1	3	0	2	27	0	0	112	35	84	51	0		Q8BUE4
ENSMUST00000105459	ENSMUSG00000020101	10	60346851	60372684	1	0	1	3	0	0	2	11175	10903	6984	1047	3716	D3Z7B7	
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ENSMUST00000105462	ENSMUSG00000012819	10	60302748	60696490	-1	16	0	50	192	57	30	0	140	10	0	31	E9Q7M6	
ENSMUST00000105463	ENSMUSG00000012819	10	60302748	60696490	-1	42	0	0	0	34	14	0	0	0	0	0		Q99PF4
ENSMUST00000105464	ENSMUSG00000012819	10	60302748	60696490	-1	0	25	0	0	0	0	18	0	88	0	56	K4DI74	
ENSMUST00000105465	ENSMUSG00000004207	10	60277627	60302597	1	0	0	0	59	0	0	14488	11250	6179	503	3840	Q8BFQ1	
ENSMUST00000105466	ENSMUSG00000019916	10	59323296	59373304	1	0	0	0	0	0	0	233	419	334	188	351		Q60715
ENSMUST00000105468	ENSMUSG00000019920	10	58323466	58424691	1	0	2	0	0	0	0	11	0	435	207	273	E9QP62	
ENSMUST00000105469	ENSMUSG00000003746	10	53904788	54075796	-1	9	6	7	320	7	5	0	0	0	0	0	D3Z799	
ENSMUST00000105470	ENSMUSG00000003746	10	53904788	54075796	-1	3	4	5	139	10	3	104	66	169	30	260	Q544T7	P45700
ENSMUST00000105472						3	5	10	2	0	0	12	22	12	0	34		
ENSMUST00000105473	ENSMUSG00000038602	10	52690533	53111622	1	31	26	60	277	28	14	0	2	0	0	0		Q8BGK5
ENSMUST00000105475	ENSMUSG00000019861	10	52337024	52382124	-1	0	0	0	0	0	0	0	0	20	0	0	K3W4Q9	
ENSMUST00000105476	ENSMUSG00000019891	10	52233619	52321378	1	13	12	23	0	28	9	7	0	0	0	0		Q9D4J3
ENSMUST00000105481	ENSMUSG00000062593	10	51480640	51496613	1	14	0	70	0	0	0	3654	18984	10595	25492	13365		Q64281
ENSMUST00000105482	ENSMUSG00000062593	10	51480640	51496613	1	4	7	3	0	5	0	41	581	61	488	399		Q64281
ENSMUST00000105483	ENSMUSG00000056073	10	49099460	49788766	-1	74	64	138	74	88	47	0	0	1	0	1	Q6PAQ0	
ENSMUST00000105484	ENSMUSG00000056073	10	49099460	49788766	-1	0	0	0	0	0	0	0	0	0	0	0		P39087
ENSMUST00000105485	ENSMUSG00000056073	10	49099460	49788766	-1	0	0	0	0	1	0	0	0	0	0	0		P39087
ENSMUST00000105486	ENSMUSG00000056073	10	49099460	49788766	-1	0	4	0	0	0	0	0	0	0	0	0	D3Z797	
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ENSMUST00000105490	ENSMUSG00000038151	10	44437177	44528501	-1	4	6	0	0	0	0	0	0	8	0	18		Q60636
ENSMUST00000105492	ENSMUSG00000019864	10	43901807	43947862	1	0	0	0	2	3	7	15	219	52	34	39	D3Z792	
ENSMUST00000105494	ENSMUSG00000044770	10	42860370	42960780	1	0	0	0	0	0	0	21	0	0	3	0		Q80VG1
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ENSMUST00000105496						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000105497	ENSMUSG00000038280	10	42583822	42702459	1	0	0	0	0	0	0	0	0	0	0	0	D3Z790	
ENSMUST00000105498	ENSMUSG00000019803	10	42561963	42583632	-1	0	0	7	4	4	0	0	0	0	0	0	Q3UXE8	
ENSMUST00000105499	ENSMUSG00000019804	10	42502030	42535381	1	6	10	2	26	6	2	566	1447	427	138	321	D3Z789	
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ENSMUST00000105501	ENSMUSG00000048756	10	42181841	42276755	-1	2	4	6	257	10	4	19	20	20	4	14	H9KUZ0	
ENSMUST00000105502	ENSMUSG00000048756	10	42181841	42276755	-1	35	19	62	70	55	28	2004	4334	3268	209	2853		Q9WVH4
ENSMUST00000105503						90	84	308	98	132	83	0	3	0	0	0		
ENSMUST00000105505	ENSMUSG00000019813	10	41718840	41809871	-1	0	0	0	0	0	0	0	0	7	0	13	B2RR53	
ENSMUST00000105507	ENSMUSG00000078451	10	41490439	41514284	1	5	8	13	76	1	5	6	14	2	7	8	B2RWF7	
ENSMUST00000105509	ENSMUSG00000019831	10	40883475	40938570	1	6	0	4	31	5	0	0	0	0	0	0		Q8R5H6
ENSMUST00000105510	ENSMUSG00000019777	10	36974544	37001889	1	6	7	25	18	8	0	3	6	8	0	5	Q8BQ10	
ENSMUST00000105511	ENSMUSG00000039462	10	34389981	34397085	1	16	10	35	25	27	18	0	3	3	0	4		Q05306
ENSMUST00000105512	ENSMUSG00000039480	10	34288288	34418552	-1	0	0	0	0	0	0	0	110	63	54	64		Q8C5P5
ENSMUST00000105516	ENSMUSG00000049109	10	28668360	28883818	1	16	6	13	9	5	6	0	0	0	0	0		Q8BGW0
ENSMUST00000105519	ENSMUSG00000039089	10	26274468	26375185	-1	0	17	19	126	0	10	0	290	247	60	200		Q8BLB7
ENSMUST00000105520	ENSMUSG00000037370	10	24637914	24712159	-1	27	16	29	24	32	19	0	0	2	0	10	G3X9S2	
ENSMUST00000105522	ENSMUSG00000075297	10	22158586	22288849	1	0	7	6	0	0	0	14	96	31	4	27	B1B212	
ENSMUST00000105525	ENSMUSG00000019986	10	20952547	21080428	1	24	22	57	58	14	14	53	180	112	24	117	E9QP54	
ENSMUST00000105527	ENSMUSG00000019850	10	19000910	19015657	-1	8	15	26	0	20	4	99	361	54	37	306		Q60769
ENSMUST00000105534	ENSMUSG00000019806	10	13647054	13868980	-1	1	0	0	0	0	0	0	0	0	5	0	H7BX91	
ENSMUST00000105539	ENSMUSG00000019809	10	13523842	13553142	-1	13	9	0	0	0	0	0	26	0	24	0	D3Z6X4	
ENSMUST00000105541	ENSMUSG00000019809	10	13523842	13553142	-1	0	0	0	0	0	0	2	19	16	0	11	D3Z6X3	
ENSMUST00000105543	ENSMUSG00000062866	10	13207717	13474396	-1	0	0	0	1	0	0	15	39	139	0	37	A3KGD2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000105545	ENSMUSG00000062866	10	13207717	13474396	-1	80	64	226	355	74	48	140	523	257	25	211	Q3UQ19	
ENSMUST00000105546	ENSMUSG00000062866	10	13207717	13474396	-1	2	0	23	1	0	0	0	0	13	0	14	B1AVP0	
ENSMUST00000105547	ENSMUSG00000062866	10	13207717	13474396	-1	2	2	0	240	8	5	35	0	0	0	59	B1AVN8	
ENSMUST00000105560	ENSMUSG00000019828	10	10686059	11082356	-1	13	0	8	8	0	0	0	0	0	0	0		P97772
ENSMUST00000105561	ENSMUSG00000019828	10	10686059	11082356	-1	17	11	9	175	37	11	2	0	0	2	0		P97772
ENSMUST00000105564	ENSMUSG00000078481	10	10681348	10681858	1	0	0	0	0	0	0	0	0	0	0	0	F7D3Z4	
ENSMUST00000105566	ENSMUSG00000006586	4	13743436	13893649	1	9	26	9	0	16	11	0	0	0	0	0	B1AXH8	
ENSMUST00000105569	ENSMUSG00000078484	4	156229044	156234857	-1	13	9	33	142	27	8	104	299	113	20	137	B2RTE7	Q6TDP3
ENSMUST00000105571	ENSMUSG00000078485	4	156221456	156228542	-1	17	7	47	41	21	14	175	699	234	12	235	E9QP36	
ENSMUST00000105572	ENSMUSG00000078486	4	156215868	156221307	1	35	34	59	60	40	18	24	202	43	8	70		Q149B8
ENSMUST00000105574	ENSMUSG00000041936	4	156165290	156197488	-1	0	0	0	0	0	0	122	205	133	3	161	Z4YK85	
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ENSMUST00000105576	ENSMUSG00000059939	4	156109982	156127265	1	0	0	0	0	0	0	0	0	5	0	0	Q8BSD8	
ENSMUST00000105578	ENSMUSG00000029076	4	155992872	156013610	1	3	0	8	35	4	0	253	550	148	218	227		Q61112
ENSMUST00000105579	ENSMUSG00000029076	4	155992872	156013610	1	0	0	0	46	0	0	2361	4419	2202	1769	1885		Q61112
ENSMUST00000105581	ENSMUSG00000023286	4	155943831	155959604	1	3	2	6	44	2	0	154	344	0	0	0		Q6P073
ENSMUST00000105582	ENSMUSG00000023286	4	155943831	155959604	1	0	0	1	5	0	0	11	16	0	0	0	B1ASK8	
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ENSMUST00000105584	ENSMUSG00000029033	4	155891822	155907251	1	4	0	0	152	22	13	205	264	280	30	200	Q6NXL5	
ENSMUST00000105586						10	1	1	0	0	5	127	239	154	21	66		
ENSMUST00000105588	ENSMUSG00000019768	10	4611593	5005614	1	11	11	9	34	4	3	0	0	0	0	0	D3Z6V3	
ENSMUST00000105589	ENSMUSG00000019768	10	4611593	5005614	1	0	0	1	0	0	0	0	0	0	0	0	E7FJU2	P19785
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ENSMUST00000105591	ENSMUSG00000065990	4	155831272	155833130	1	0	0	0	0	0	0	722	1001	395	827	305		Q9DCJ7
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ENSMUST00000105593	ENSMUSG00000078487	4	155790439	155799503	1	7	3	3	17	9	0	0	0	0	0	0	A2AD93	
ENSMUST00000105595	ENSMUSG00000029038	4	155704800	155733879	1	2	1	0	71	3	1	344	2146	496	1208	285		Q9CY97
ENSMUST00000105596	ENSMUSG00000078488	10	6740629	6761761	-1	1	0	8	1	2	0	0	1	0	0	0	F7CYK6	
ENSMUST00000105597	ENSMUSG00000000766	10	6758506	7038198	1	2	0	2	1	0	1	0	0	0	0	0	Q4U2P0	
ENSMUST00000105598	ENSMUSG00000029062	4	155624854	155649938	1	0	0	0	4	0	10	310	1996	204	0	246	A2A9P6	
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ENSMUST00000105601	ENSMUSG00000000766	10	6758506	7038198	1	0	0	6	0	0	0	0	0	0	0	0	A1KZZ4	
ENSMUST00000105602	ENSMUSG00000000766	10	6758506	7038198	1	1	0	0	0	0	1	0	0	0	0	0		P42866
ENSMUST00000105603	ENSMUSG00000000766	10	6758506	7038198	1	4	4	4	0	9	1	0	0	0	0	0	E9Q7D4	
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ENSMUST00000105607	ENSMUSG00000000766	10	6758506	7038198	1	8	10	1	8	8	2	0	0	0	0	0		P42866
ENSMUST00000105608	ENSMUSG00000042202	4	155601416	155623340	1	159	180	418	182	151	89	138	355	197	43	155		Q8C811
ENSMUST00000105611	ENSMUSG00000000766	10	6758506	7038198	1	7	15	20	9	3	2	0	2	3	1	3		P42866
ENSMUST00000105612	ENSMUSG00000029063	4	155562378	155591001	1	12	0	19	0	24	0	72	778	97	13	237	A2A9P2	
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ENSMUST00000105615	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	0	0	0	0	0	0	0	0		P42866
ENSMUST00000105616	ENSMUSG00000029064	4	155491361	155559269	1	12	0	0	0	0	0	266	611	316	74	193	Q3TQ70	P62874
ENSMUST00000105617	ENSMUSG00000064065	10	6885796	7052478	-1	20	30	56	63	36	15	1250	6476	3120	730	2146		Q5DU31
ENSMUST00000105619	ENSMUSG00000078490	4	155409190	155466823	1	2	0	5	0	3	0	0	0	0	0	0	A0A0B4J1K6	
ENSMUST00000105624	ENSMUSG00000029053	4	155260129	155361361	-1	2	0	8	130	6	5	0	0	0	1	0	A2AD75	
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ENSMUST00000105631	ENSMUSG00000029055	4	154983115	155056784	-1	12	0	4	0	24	0	0	0	0	0	4		A2AP18
ENSMUST00000105632						2	2	5	2	0	2	6	70	3	15	33		
ENSMUST00000105634	ENSMUSG00000058183	4	154869585	154895528	1	39	26	63	88	64	34	1	11	4	0	6	B1AS17	
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ENSMUST00000105643	ENSMUSG00000029026	4	154056253	154140208	-1	0	0	17	84	12	0	0	0	0	0	0		Q9JJP2
ENSMUST00000105644	ENSMUSG00000029026	4	154056253	154140208	-1	0	18	14	164	6	0	0	0	0	0	0	Z4YK94	
ENSMUST00000105645	ENSMUSG00000047613	4	153957237	153961925	1	0	0	0	0	0	2	0	17	0	9	0	E9PUH0	
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ENSMUST00000105648	ENSMUSG00000028931	4	152390742	152477871	-1	0	0	3	1	0	0	12	0	34	0	0		P62482
ENSMUST00000105650	ENSMUSG00000042804	4	152274232	152285337	1	0	0	38	59	0	0	0	0	0	0	16	A2A8K5	
ENSMUST00000105651	ENSMUSG00000042804	4	152274232	152285337	1	0	0	0	1	0	0	0	0	0	0	0		Q8K0Z9
ENSMUST00000105652	ENSMUSG00000028937	4	152178134	152271855	1	0	2	6	1	0	3	71	222	86	98	31		Q91V12
ENSMUST00000105653	ENSMUSG00000028943	4	152120331	152152371	-1	0	0	0	0	0	0	0	0	0	0	0		Q9ET47
ENSMUST00000105654	ENSMUSG00000028943	4	152120331	152152371	-1	0	0	0	0	0	0	0	0	0	0	0	B1AWQ0	
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ENSMUST00000105656	ENSMUSG00000028943	4	152120331	152152371	-1	0	0	0	0	0	0	0	0	0	0	0	B1AWP8	
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ENSMUST00000105659	ENSMUSG00000028943	4	152120331	152152371	-1	5	0	5	434	29	17	0	0	0	0	0	B1AWQ4	
ENSMUST00000105661	ENSMUSG00000039713	4	152072498	152115400	1	0	0	0	152	0	0	0	0	10	0	0		Q66T02
ENSMUST00000105662	ENSMUSG00000039713	4	152072498	152115400	1	12	0	27	5	11	10	0	0	0	0	0	A0A0A0MQC2	
ENSMUST00000105663						1	4	0	45	0	1	0	3	0	0	0		
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ENSMUST00000105667	ENSMUSG00000078491	4	151089570	151091449	1	5	4	7	4	8	2	0	0	0	0	0	A2A899	
ENSMUST00000105668	ENSMUSG00000014592	4	150917322	151861876	-1	15	5	0	24	6	6	0	1	0	0	0		A2A891
ENSMUST00000105670	ENSMUSG00000014592	4	150917322	151861876	-1	0	0	0	82	10	6	0	1	0	0	0		A2A891
ENSMUST00000105671	ENSMUSG00000028965	4	150914562	150946102	1	3	0	8	0	0	3	2	0	0	0	7	Q3U3R1	P20334
ENSMUST00000105672	ENSMUSG00000028965	4	150914562	150946102	1	16	14	67	0	5	0	0	11	8	1	0	Q8R037	
ENSMUST00000105673	ENSMUSG00000028964	4	150897133	150914437	-1	2	4	0	55	3	8	0	0	0	12	4		Q99LX0
ENSMUST00000105674	ENSMUSG00000028964	4	150897133	150914437	-1	0	0	0	0	0	0	13	0	6	0	0		Q99LX0
ENSMUST00000105675	ENSMUSG00000028964	4	150897133	150914437	-1	2	2	7	43	12	1	87	103	46	79	39		Q99LX0
ENSMUST00000105676	ENSMUSG00000028964	4	150897133	150914437	-1	0	0	0	0	0	0	4	132	47	16	18	A2A813	
ENSMUST00000105680	ENSMUSG00000039852	4	150281646	150621966	1	37	28	190	11	0	0	1899	3025	2424	127	2260	A2A7T3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000105682	ENSMUSG00000039852	4	150281646	150621966	1	24	18	43	237	69	32	93	63	68	0	146		Q80TZ9
ENSMUST00000105683	ENSMUSG00000028972	4	150187015	150201332	-1	0	8	5	6	3	3	0	0	0	14	2	B1ARR4	
ENSMUST00000105684	ENSMUSG00000039911	4	149896283	149955043	-1	1	1	0	1	0	0	5	0	0	0	0		Q9D5L7
ENSMUST00000105685	ENSMUSG00000039911	4	149896283	149955043	-1	8	3	6	43	7	1	0	0	0	0	0		Q9D5L7
ENSMUST00000105686	ENSMUSG00000028982	4	149744036	149774277	-1	10	6	6	38	5	8	31	130	23	8	40		Q3TZX3
ENSMUST00000105687	ENSMUSG00000044700	4	149715375	149738044	-1	17	21	183	115	19	15	15	8	9	4	31		A2A8U2
ENSMUST00000105688	ENSMUSG00000039936	4	149649168	149702571	-1	3	0	0	0	0	0	564	0	656	0	678	Q3UDT3	
ENSMUST00000105689	ENSMUSG00000039936	4	149649168	149702571	-1	17	3	27	0	0	0	229	0	207	0	0		O35904
ENSMUST00000105690	ENSMUSG00000039936	4	149649168	149702571	-1	0	0	50	137	1	1	1	0	565	301	239	Q3T9Y0	
ENSMUST00000105691	ENSMUSG00000039953	4	149586468	149648899	1	38	27	45	50	35	12	39	78	48	17	161		Q9EPL2
ENSMUST00000105692	ENSMUSG00000028988	4	149518236	149566437	1	6	3	4	2	0	0	335	383	267	71	168		Q9JJN6
ENSMUST00000105693	ENSMUSG00000028992	4	149467572	149485202	-1	0	1	1	32	5	1	0	0	0	0	3	Q3V449	Q9EPA7
ENSMUST00000105695	ENSMUSG00000073705	4	149127121	149137629	-1	2	2	30	2	5	1	0	0	0	1	2		Q9D084
ENSMUST00000105696	ENSMUSG00000073705	4	149127121	149137629	-1	0	4	2	0	3	3	0	2	0	0	2	A6PWQ2	
ENSMUST00000105697						15	15	97	26	30	15	1	22	4	0	14		
ENSMUST00000105698	ENSMUSG00000070577	4	148643317	148671572	1	6	6	15	5	8	10	0	0	0	1	2	B1ARY8	
ENSMUST00000105699	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	20	0	0	0	167	490	344	365	206	Q8R0B4	
ENSMUST00000105700	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	240	106	0	35	Q6VYI5	
ENSMUST00000105701	ENSMUSG00000028979	4	148602554	148615499	1	0	0	0	0	0	0	0	1	0	5	2		Q91WP0
ENSMUST00000105702	ENSMUSG00000041459	4	148612382	148627019	-1	11	0	0	31	0	0	0	1	280	0	1	Q6VYI5	
ENSMUST00000105705	ENSMUSG00000029001	4	148152800	148160482	-1	0	0	0	11	1	3	1	0	0	0	0	A2A7H6	
ENSMUST00000105706	ENSMUSG00000055401	4	148145716	148152140	-1	3	8	25	128	23	5	7	20	19	8	14		Q9QZN4
ENSMUST00000105707	ENSMUSG00000029003	4	148130384	148145699	1	0	0	0	0	0	0	29	32	0	0	33	A2A7G7	
ENSMUST00000105708						5	2	1	2	7	5	4	6	4	0	5		
ENSMUST00000105711	ENSMUSG00000029016	4	148004259	148038821	-1	0	0	0	0	0	0	0	2	0	0	8	E9Q741	
ENSMUST00000105712	ENSMUSG00000019055	4	147909753	147936767	-1	1	4	6	3	5	3	24	33	18	12	20	A8Y5E6	
ENSMUST00000105714	ENSMUSG00000029020	4	147873599	147904704	-1	5	3	8	2	2	3	5	0	18	0	10		Q80U63
ENSMUST00000105715	ENSMUSG00000029020	4	147873599	147904704	-1	0	0	26	40	15	14	0	0	0	0	0		Q80U63
ENSMUST00000105716	ENSMUSG00000029020	4	147873599	147904704	-1	24	0	0	0	0	5	1076	1343	1100	97	710		Q80U63
ENSMUST00000105718	ENSMUSG00000059423	4	147822986	147848366	-1	81	86	274	85	101	60	32	60	38	26	27	Q6PEE4	
ENSMUST00000105720	ENSMUSG00000066000	4	147611937	147642513	-1	0	3	9	3	5	0	0	0	0	4	1	A2A799	
ENSMUST00000105721	ENSMUSG00000078496	4	147492417	147513486	1	13	7	20	6	14	6	0	0	0	1	0	A2A8Q4	
ENSMUST00000105727						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000105730	ENSMUSG00000066009	4	146097298	146126621	1	0	0	0	0	0	0	1	0	0	0	0	B2KG43	
ENSMUST00000105733	ENSMUSG00000070605	4	146449023	146470292	1	219	183	142	166	232	88	66	158	65	100	64	B1ASD8	
ENSMUST00000105734	ENSMUSG00000078495	4	147753974	147809788	-1	21	16	25	9	24	6	99	366	140	165	116	A2A7A2	
ENSMUST00000105735	ENSMUSG00000056300	4	146502027	146539395	1	0	13	17	6	9	6	0	0	0	0	0	A2A8V7	
ENSMUST00000105738	ENSMUSG00000058186	4	145670685	145704441	1	19	21	27	33	26	10	0	0	0	0	0	A2A9J5	
ENSMUST00000105739	ENSMUSG00000078502	4	145585166	145625345	1	0	3	0	0	0	0	0	0	0	0	0	B1ASQ7	
ENSMUST00000105741	ENSMUSG00000078503	4	145510759	145539188	1	3	7	0	4	4	4	0	0	0	0	0	B1AVN5	
ENSMUST00000105742	ENSMUSG00000078503	4	145510759	145539188	1	9	4	12	0	10	0	0	1	0	0	0	B1AVN5	
ENSMUST00000105744	ENSMUSG00000066026	4	144892827	144928209	1	6	4	9	57	11	6	34	128	0	0	0		O88876
ENSMUST00000105746	ENSMUSG00000078504	4	144777204	144786583	-1	3	2	7	11	6	3	0	0	0	0	0	B1ASB3	
ENSMUST00000105747	ENSMUSG00000078505	4	144669937	144686368	-1	11	8	19	5	17	5	0	0	0	0	0	B1AVU6	
ENSMUST00000105748	ENSMUSG00000078506	4	144555000	144565134	-1	5	11	2	3	7	5	0	0	0	0	0	A2A752	
ENSMUST00000105749	ENSMUSG00000078507	4	144453771	144463756	-1	16	15	24	14	23	9	0	0	0	0	0		A2A7Z8
ENSMUST00000105751	ENSMUSG00000078508	4	144330249	144333465	1	10	14	3	0	7	2	0	0	0	0	0	L7MU96	
ENSMUST00000105752	ENSMUSG00000036749	4	144270633	144280488	-1	18	8	8	21	11	0	0	0	0	0	0	Q7TPY4	
ENSMUST00000105753	ENSMUSG00000046262	4	144206775	144213318	-1	7	7	7	2	7	6	0	0	0	0	0	A6PWB6	
ENSMUST00000105754	ENSMUSG00000046262	4	144206775	144213318	-1	6	0	0	0	2	0	0	0	0	0	0	A6PWB4	
ENSMUST00000105755	ENSMUSG00000046262	4	144206775	144213318	-1	0	0	0	0	0	0	0	0	0	0	0	A6PWB1	
ENSMUST00000105757	ENSMUSG00000046262	4	144206775	144213318	-1	0	0	0	0	2	0	0	0	0	0	0	A2A958	
ENSMUST00000105761	ENSMUSG00000073723	4	144106474	144110101	1	26	0	0	0	0	13	0	0	0	0	0	Q3ULC4	
ENSMUST00000105762	ENSMUSG00000078509	4	143991119	143994369	-1	9	3	0	9	3	4	0	0	0	0	0	A2ASJ1	
ENSMUST00000105763	ENSMUSG00000078510	4	143964518	143966950	-1	8	7	6	12	3	6	0	0	0	0	0	A2ASJ0	
ENSMUST00000105765	ENSMUSG00000070618	4	143551700	143573798	1	0	0	2	0	6	3	0	0	0	0	0	Q66JY9	
ENSMUST00000105766	ENSMUSG00000078511	4	143948580	143951016	-1	13	4	5	9	3	3	0	0	0	0	0	A2ASI9	
ENSMUST00000105767	ENSMUSG00000078512	4	143894237	143900380	-1	5	9	0	2	7	4	0	0	0	0	0	A2A8M8	
ENSMUST00000105768	ENSMUSG00000029451	4	143846497	143853637	1	10	1	2	6	0	2	0	0	0	0	0	A6PWA2	
ENSMUST00000105769	ENSMUSG00000059218	4	143809245	143816093	-1	0	3	0	1	9	3	0	0	0	0	0	A6PWA3	
ENSMUST00000105770	ENSMUSG00000066031	4	143789352	143795575	1	0	0	0	0	0	2	0	0	0	0	0	A6PWA5	
ENSMUST00000105771	ENSMUSG00000078513	4	143653760	143657246	-1	6	0	4	3	7	5	0	0	0	0	0	A2AGW6	
ENSMUST00000105773	ENSMUSG00000066688	4	143615003	143618595	1	49	33	40	34	57	27	0	1	2	0	1	A2AGW5	
ENSMUST00000105774	ENSMUSG00000070618	4	143551700	143573798	1	4	5	0	6	0	0	0	0	0	0	0	Q66JY9	
ENSMUST00000105776	ENSMUSG00000096154	4	143551709	143558234	1	0	0	0	6	0	0	0	0	0	0	0	A2A8C4	
ENSMUST00000105778	ENSMUSG00000057637	4	143107391	143212995	-1	76	44	87	346	65	47	1274	2707	2363	165	2079	A2A7B5	
ENSMUST00000105779	ENSMUSG00000051435	4	141890438	142015082	-1	35	10	102	0	16	15	0	0	0	0	0		A6PWD2
ENSMUST00000105780	ENSMUSG00000051435	4	141890438	142015082	-1	0	9	0	52	17	0	0	0	0	0	0		A6PWD2
ENSMUST00000105781	ENSMUSG00000062478	4	141814962	141846359	-1	6	4	10	10	18	3	0	0	0	0	0	A2AAC0	
ENSMUST00000105782	ENSMUSG00000040715	4	141683851	141685599	-1	0	1	0	0	6	0	466	1225	1193	179	797		Q9ER99
ENSMUST00000105784	ENSMUSG00000006219	4	141576062	141606096	-1	23	0	0	40	2	0	0	2	0	7	33		Q71FD7
ENSMUST00000105785	ENSMUSG00000006219	4	141576062	141606096	-1	0	0	50	0	26	9	0	0	0	0	0		Q71FD7
ENSMUST00000105786	ENSMUSG00000040761	4	141467890	141538597	-1	0	0	0	169	112	0	706	218	931	0	669	A2ADB0	
ENSMUST00000105788	ENSMUSG00000006216	4	141404353	141416014	-1	0	0	47	20	39	16	0	0	0	0	0		Q9WUB6
ENSMUST00000105790	ENSMUSG00000033770	4	141384610	141398724	-1	19	11	43	16	7	0	0	0	0	0	0		Q9WUB7
ENSMUST00000105797	ENSMUSG00000040964	4	140514485	140666012	-1	10	0	7	62	0	0	83	112	112	26	101		A2AWP8
ENSMUST00000105798	ENSMUSG00000040964	4	140514485	140666012	-1	7	0	3	0	8	8	60	0	13	0	36	A2AWP6	
ENSMUST00000105799	ENSMUSG00000040964	4	140514485	140666012	-1	0	0	0	0	0	0	0	0	0	0	0		A2AWP8
ENSMUST00000105801	ENSMUSG00000028744	4	139294029	139310708	-1	9	11	29	26	20	6	40	108	18	0	47	A6PWV7	
ENSMUST00000105802	ENSMUSG00000028747	4	139061108	139075570	-1	22	13	58	407	26	2	0	0	0	0	0	Q14AW8	Q9R1C8
ENSMUST00000105803	ENSMUSG00000028751	4	138877942	138882817	1	5	1	0	1	0	2	0	0	0	0	0	A2APQ4	
ENSMUST00000105804	ENSMUSG00000028751	4	138877942	138882817	1	0	0	0	17	9	1	0	0	0	0	0	Q3UG05	Q9QUL3
ENSMUST00000105805	ENSMUSG00000078518	4	138870992	138873964	-1	7	1	8	3	5	0	0	0	0	0	0	A2APQ6	
ENSMUST00000105806	ENSMUSG00000041202	4	138775735	138782046	1	1	0	0	0	2	0	0	0	0	1	0		Q9WVF6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000105808	ENSMUSG00000028750	4	138724792	138746132	1	26	20	35	51	29	15	0	1	0	0	0	A2APR1	
ENSMUST00000105809	ENSMUSG00000043621	4	138709837	138737167	-1	7	13	5	2	11	6	0	0	0	0	0		Q8BG34
ENSMUST00000105810	ENSMUSG00000043621	4	138709837	138737167	-1	4	0	0	0	18	7	0	0	0	0	0		Q8BG34
ENSMUST00000105811	ENSMUSG00000043621	4	138709837	138737167	-1	5	5	29	30	0	0	0	0	0	0	0		Q8BG34
ENSMUST00000105812	ENSMUSG00000028753	4	138565360	138635884	-1	7	0	0	1	7	0	0	0	0	0	0	E9Q709	
ENSMUST00000105813	ENSMUSG00000041241	4	138434671	138442265	1	35	0	56	36	20	0	51	67	34	14	41		Q8VCM5
ENSMUST00000105815	ENSMUSG00000041241	4	138434671	138442265	1	0	0	1	0	5	0	15	6	20	8	13		Q8VCM5
ENSMUST00000105816	ENSMUSG00000028756	4	138313409	138326307	-1	5	3	8	1	4	0	0	191	0	0	0	A2AM76	
ENSMUST00000105817	ENSMUSG00000028756	4	138313409	138326307	-1	3	2	11	15	2	1	515	0	339	44	297	A2AM78	
ENSMUST00000105818	ENSMUSG00000028758	4	138250435	138301967	1	22	16	52	19	40	20	7	21	9	2	0	A2AM74	
ENSMUST00000105820						14	9	23	32	15	6	0	5	6	0	6		
ENSMUST00000105821	ENSMUSG00000028758	4	138250435	138301967	1	0	0	0	0	0	0	12	5	5	0	5	A2AM72	
ENSMUST00000105823	ENSMUSG00000045349	4	138250403	138261332	1	0	0	0	0	0	0	232	492	277	0	131	A2AM67	
ENSMUST00000105824	ENSMUSG00000045349	4	138250403	138261332	1	19	20	52	55	40	14	0	0	0	16	1	A2AM67	
ENSMUST00000105825	ENSMUSG00000028759	4	138216296	138244683	1	32	28	58	0	15	19	17	113	45	33	31	Z4YKA3	
ENSMUST00000105826	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	9	3	0	29	0	43	30	24	Z4YKB8	
ENSMUST00000105827	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	76	10	0	35	15	15	0	30	Z4YKB8	
ENSMUST00000105830	ENSMUSG00000028760	4	137993022	138208508	1	12	3	0	38	6	3	17	25	30	1	21	A2AMI6	
ENSMUST00000105831	ENSMUSG00000028760	4	137993022	138208508	1	0	0	0	0	0	0	832	1680	1929	223	1982	Z4YKC4	
ENSMUST00000105835	ENSMUSG00000041351	4	137664726	137729861	1	0	1	0	0	1	0	0	0	0	0	0	A2ALS4	
ENSMUST00000105837	ENSMUSG00000043411	4	137593755	137658537	1	14	10	4	7	18	8	50	131	88	1	125	A2ALS8	
ENSMUST00000105838	ENSMUSG00000043411	4	137593755	137658537	1	0	0	0	4	0	0	0	0	0	0	0	A2ALS9	
ENSMUST00000105839	ENSMUSG00000043411	4	137593755	137658537	1	7	2	1	15	0	1	34	0	179	3	164	A2ALR8	
ENSMUST00000105840	ENSMUSG00000043411	4	137593755	137658537	1	0	1	18	85	0	0	249	953	455	51	552	A2ALR9	
ENSMUST00000105845	ENSMUSG00000028664	4	136647539	136835988	-1	134	76	390	183	163	58	0	9	3	0	4	A3KG01	P54763
ENSMUST00000105846	ENSMUSG00000028664	4	136647539	136835988	-1	0	0	0	0	0	0	3	1	1	1	0	A3KG00	
ENSMUST00000105847	ENSMUSG00000036940	4	136550540	136602723	-1	0	0	18	0	0	0	246	872	464	76	291	A3KG93	
ENSMUST00000105849	ENSMUSG00000001089	4	136469761	136554780	1	0	0	0	70	0	0	0	39	44	0	39		Q8R4U7
ENSMUST00000105850	ENSMUSG00000066037	4	136310942	136359447	1	0	0	0	0	0	0	49	77	73	26	55	Q8VHM5	
ENSMUST00000105851	ENSMUSG00000028669	4	135975460	135987264	-1	2	6	6	17	3	0	649	1965	562	139	469		Q8BWR2
ENSMUST00000105852	ENSMUSG00000028670	4	135968224	135972626	-1	0	10	36	0	0	0	0	67	60	0	0		Q9WTL7
ENSMUST00000105853	ENSMUSG00000028676	4	135855747	135869908	1	5	1	2	3	2	1	162	440	193	0	154		Q9R0U0
ENSMUST00000105854	ENSMUSG00000037139	4	135759715	135815564	1	50	21	59	73	61	25	0	0	0	0	0		A2ABU4
ENSMUST00000105855	ENSMUSG00000037188	4	135541888	135573630	-1	20	17	99	42	38	15	0	0	0	2	0		Q5FWH3
ENSMUST00000105856	ENSMUSG00000028803	4	135445420	135495038	-1	123	134	241	171	153	70	10	26	16	10	23	A2A987	
ENSMUST00000105857	ENSMUSG00000043924	4	135369576	135398227	-1	0	0	0	0	0	0	0	0	0	0	1		Q99JS0
ENSMUST00000105858	ENSMUSG00000043924	4	135369576	135398227	-1	0	9	0	0	6	0	0	5	0	0	0		Q99JS0
ENSMUST00000105859	ENSMUSG00000043924	4	135369576	135398227	-1	0	0	0	0	0	0	0	0	0	0	0		Q99JS0
ENSMUST00000105860	ENSMUSG00000043924	4	135369576	135398227	-1	8	4	31	9	15	9	0	0	0	0	0	A2A992	
ENSMUST00000105861	ENSMUSG00000028809	4	135320484	135353321	-1	0	6	58	52	0	0	341	1142	263	34	448	A2A8V8	
ENSMUST00000105863	ENSMUSG00000028822	4	134897849	134915024	-1	1	0	2	16	1	0	202	219	227	89	208	Q52KP1	Q9CXL1
ENSMUST00000105866	ENSMUSG00000078521	4	134510999	134523927	1	4	2	9	69	12	2	11	19	9	11	8		E9Q6Z5
ENSMUST00000105867	ENSMUSG00000028832	4	134468320	134473843	1	4	3	13	0	25	1	158	157	102	54	72	D3Z5N2	
ENSMUST00000105868	ENSMUSG00000028832	4	134468320	134473843	1	2	2	0	2	0	3	0	0	0	0	5	Q545B6	P54227
ENSMUST00000105869	ENSMUSG00000037366	4	134396320	134427413	1	5	4	0	4	6	0	33	0	46	0	0		Q8VDG7
ENSMUST00000105870	ENSMUSG00000037366	4	134396320	134427413	1	11	5	37	20	17	15	204	180	125	11	73	E9QNW6	
ENSMUST00000105872	ENSMUSG00000028836	4	134343181	134354484	1	0	10	36	33	29	25	3	0	0	1	2	D3Z5N1	
ENSMUST00000105873	ENSMUSG00000028836	4	134343181	134354484	1	0	0	13	111	3	0	1	0	2	0	0	D3Z5N0	
ENSMUST00000105874	ENSMUSG00000028836	4	134343181	134354484	1	18	0	0	0	0	0	0	0	0	0	0		Q2HJ10
ENSMUST00000105875	ENSMUSG00000028834	4	134315120	134329629	1	0	0	14	0	15	14	0	0	0	0	0	F8VPZ1	
ENSMUST00000105876	ENSMUSG00000050890	4	134275002	134287895	-1	0	0	0	5	0	0	86	87	6	56	52		Q8QZR7
ENSMUST00000105877	ENSMUSG00000050890	4	134275002	134287895	-1	13	13	19	18	23	9	0	56	49	0	0	A2A9L3	
ENSMUST00000105878	ENSMUSG00000048003	4	134211970	134227383	-1	10	15	85	13	24	10	0	1	1	0	2	Z4YKD2	
ENSMUST00000105879	ENSMUSG00000028843	4	134127406	134128789	-1	2	0	0	25	5	0	42	72	35	38	13	I7HPY0	
ENSMUST00000105884	ENSMUSG00000049410	4	134053838	134058996	1	13	9	24	22	18	4	0	0	0	0	1	I7HJS4	
ENSMUST00000105885	ENSMUSG00000012117	4	133969028	134000918	-1	0	0	0	0	0	0	0	0	121	21	89	A3KGL0	
ENSMUST00000105886	ENSMUSG00000012117	4	133969028	134000918	-1	0	0	1	0	0	0	120	0	0	28	0	A3KGL2	
ENSMUST00000105887	ENSMUSG00000012117	4	133969028	134000918	-1	0	0	0	5	0	9	171	56	14	11	34		Q99KU1
ENSMUST00000105889	ENSMUSG00000012117	4	133969028	134000918	-1	0	0	0	2	0	0	34	42	50	0	23	A3KGL3	
ENSMUST00000105893	ENSMUSG00000003038	4	133964738	133968650	-1	0	0	0	0	0	0	0	766	27	31	9	A3KGL9	
ENSMUST00000105894	ENSMUSG00000003644	4	133847290	133887797	-1	0	0	0	17	0	0	36	88	57	15	7	Q505N6	
ENSMUST00000105895	ENSMUSG00000031072	7	144915100	144930748	1	2	6	38	0	0	0	9	4	17	15	8	D3Z5L0	
ENSMUST00000105897	ENSMUSG00000007880	4	133679008	133756769	-1	0	10	0	311	0	24	110	254	201	101	255		A2BH40
ENSMUST00000105898	ENSMUSG00000031074	7	144838083	144844436	1	20	19	72	44	36	11	0	1	2	0	2	Q0VG15	
ENSMUST00000105899	ENSMUSG00000028848	4	133584362	133591735	1	1	1	0	0	0	0	83	81	28	10	14	A2A9F7	
ENSMUST00000105900	ENSMUSG00000037541	7	144001928	144424494	1	23	0	225	257	19	17	0	0	0	0	0	D3Z5K9	
ENSMUST00000105901	ENSMUSG00000037600	4	133518963	133530790	1	1	0	10	33	0	3	0	0	0	0	4		A2A9F4
ENSMUST00000105902	ENSMUSG00000037541	7	144001928	144424494	1	52	31	86	23	69	36	0	0	0	0	0	D3Z5K8	
ENSMUST00000105906	ENSMUSG00000037622	4	133292459	133353481	-1	24	21	0	0	0	0	0	3	0	0	0	A2AE98	
ENSMUST00000105907	ENSMUSG00000028857	4	133266045	133277792	-1	9	10	13	29	15	11	598	736	359	211	267		Q8BVA2
ENSMUST00000105908	ENSMUSG00000028860	4	133253090	133263113	-1	0	3	0	0	1	0	0	0	2	0	0	A2AE95	
ENSMUST00000105909	ENSMUSG00000010755	7	143557230	143600090	-1	19	0	19	64	4	10	218	577	293	77	289	Q3U716	Q9ER72
ENSMUST00000105910	ENSMUSG00000028865	4	133212131	133224555	1	5	4	12	60	10	2	0	2	1	0	0		Q9D6W7
ENSMUST00000105911	ENSMUSG00000049649	4	133209340	133212536	-1	14	18	49	30	30	22	0	3	1	0	4		P35413
ENSMUST00000105912	ENSMUSG00000028868	4	133130505	133199756	1	4	2	0	0	0	7	257	0	365	0	156		Q8BH43
ENSMUST00000105914	ENSMUSG00000037692	4	133011260	133078110	1	2	0	8	752	11	3	0	0	0	0	31		Q6PAL7
ENSMUST00000105915	ENSMUSG00000037692	4	133011260	133078110	1	83	56	369	246	104	14	80	83	78	9	77		Q6PAL7
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ENSMUST00000105917	ENSMUSG00000000154	7	143473721	143499334	1	0	3	33	14	6	14	0	0	0	0	0		
ENSMUST00000105919	ENSMUSG00000028882	4	132826929	132843169	-1	0	0	0	0	0	1	32	0	49	34	40	A2ADR8	
ENSMUST00000105920	ENSMUSG00000045752	7	143069249	143071093	1	0	0	7	9	0	0	9	0	8	10	0	Q9JHE9	Q9JHE7
ENSMUST00000105923	ENSMUSG00000000244	7	143005046	143019644	1	0	0	14	0	0	0	18	54	13	0	0	G3X9S3	
ENSMUST00000105924	ENSMUSG00000000244	7	143005046	143019644	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5A0	
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000105929	ENSMUSG00000000214	7	142892752	142931128	-1	13	11	0	0	9	11	0	0	0	0	0	Q3UTB3	
ENSMUST00000105930	ENSMUSG00000000215	7	142678656	142699510	-1	3	4	22	2	6	6	0	0	0	0	0	D3Z596	
ENSMUST00000105931	ENSMUSG00000000215	7	142678656	142699510	-1	0	0	0	0	0	4	0	0	0	0	0	D3Z595	
ENSMUST00000105932	ENSMUSG00000000215	7	142678656	142699510	-1	0	0	0	0	0	0	0	0	0	0	0	Q5EEX1	P01326
ENSMUST00000105933	ENSMUSG00000000215	7	142678656	142699510	-1	7	0	7	6	5	2	0	0	0	0	0	Q5EEX1	P01326
ENSMUST00000105934	ENSMUSG00000000215	7	142678656	142699510	-1	0	3	0	0	2	0	0	0	0	0	0	Q5EEX1	P01326
ENSMUST00000105935	ENSMUSG00000048583	7	142650766	142666816	-1	0	0	4	2	7	0	0	0	0	0	0		P09535
ENSMUST00000105936	ENSMUSG00000048583	7	142650766	142666816	-1	6	0	56	35	3	6	0	0	0	0	0		P09535
ENSMUST00000105937						2	1	10	2	4	0	0	13	5	0	14		
ENSMUST00000105938						2	0	0	0	0	1	0	0	0	0	2		
ENSMUST00000105939	ENSMUSG00000054405	4	132535550	132553742	1	2	0	0	0	0	0	179	919	455	1389	440	A2ALF0	
ENSMUST00000105940	ENSMUSG00000054405	4	132535550	132553742	1	0	0	0	3	0	0	0	0	16	15	34	A2ALF3	
ENSMUST00000105941	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	6	0	0	0	A2A6I3	
ENSMUST00000105942	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	A2A6I8	
ENSMUST00000105943	ENSMUSG00000061723	7	142498836	142516009	1	3	4	0	0	0	0	0	0	4	0	0	A2A6I5	
ENSMUST00000105944	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	A2A6J1	
ENSMUST00000105945	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	8	0	0	25		
ENSMUST00000105946	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	9		
ENSMUST00000105947	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	Z4YKD9	
ENSMUST00000105948	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	A2A6I0	
ENSMUST00000105949	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	6	0	10	0	A2A6J0	
ENSMUST00000105950	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	Z4YKE7	
ENSMUST00000105951	ENSMUSG00000028896	4	132331919	132353605	-1	0	14	41	0	0	0	37	0	18	0	0		Q8VE37
ENSMUST00000105952	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	Z4YKF8	
ENSMUST00000105953	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	Z4YKG3	
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ENSMUST00000105955	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	A2A6H6	
ENSMUST00000105957	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	Z4YKH8	
ENSMUST00000105958	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000105960	ENSMUSG00000028898	4	132311763	132329538	-1	0	0	0	74	0	0	2	2	2	0	1	A2CEQ9	
ENSMUST00000105962	ENSMUSG00000028898	4	132311763	132329538	-1	0	0	0	0	0	0	0	0	0	23	0	A2CEQ6	
ENSMUST00000105963	ENSMUSG00000028899	4	132274375	132295766	1	2	1	0	0	1	1	189	482	253	548	201	E9QNT5	
ENSMUST00000105964	ENSMUSG00000028901	4	132221025	132261602	-1	0	0	0	0	0	0	77	93	98	21	106		Q9JL60
ENSMUST00000105965	ENSMUSG00000028901	4	132221025	132261602	-1	0	0	146	0	0	0	64	310	148	0	114		Q9JL60
ENSMUST00000105966	ENSMUSG00000018819	7	142460809	142494867	1	0	0	0	0	0	1	0	0	0	0	0	A2A6J4	
ENSMUST00000105967	ENSMUSG00000018819	7	142460809	142494867	1	0	0	2	4	4	0	16655	26907	13931	22027	11400	A2A6J7	
ENSMUST00000105968	ENSMUSG00000018819	7	142460809	142494867	1	5	10	24	0	16	5	1157	2730	843	990	655		P19973
ENSMUST00000105970	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	13	0	0	7	0	0	61	0	22	A2A839	
ENSMUST00000105971	ENSMUSG00000031097	7	142441808	142444410	1	0	0	0	0	1	0	26	88	0	104	23		P13412
ENSMUST00000105972	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	0	16	0	24	0	281	0	121		P48193
ENSMUST00000105973	ENSMUSG00000031097	7	142441808	142444410	1	0	0	0	2	0	0	0	33	5	8	0	A2A6J8	
ENSMUST00000105974	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	0	0	0	0	0	0	0	0	A2A842	
ENSMUST00000105975	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	0	16	0	0	0	0	0	0	A2A841	
ENSMUST00000105976	ENSMUSG00000031098	7	142434850	142440396	1	0	0	0	0	0	0	0	0	0	0	0	F2Z3W8	
ENSMUST00000105977	ENSMUSG00000031098	7	142434850	142440396	1	1	1	2	0	0	0	2	0	0	1	3	E9Q6P7	
ENSMUST00000105981	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	0	0	0	0	0	0	0	0		P48193
ENSMUST00000105987	ENSMUSG00000028909	4	131768457	131838288	-1	17	14	63	133	37	8	4	0	0	0	5		B1AUH1
ENSMUST00000105988	ENSMUSG00000045777	7	142325837	142373753	-1	4	0	5	7	7	3	0	0	4	0	4		Q8BR26
ENSMUST00000105989	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	0	0	0	0	0	0	0	0		Q69Z98
ENSMUST00000105991	ENSMUSG00000028580	4	130663321	130781564	1	4	0	0	0	4	0	135	159	0	48	0	E9Q6M7	
ENSMUST00000105992	ENSMUSG00000028580	4	130663321	130781564	1	0	0	2	0	18	0	32	90	110	0	84	Q3TTW5	
ENSMUST00000105993	ENSMUSG00000078532	4	130531602	130574173	-1	0	0	0	16	0	0	0	0	0	0	0		Q9D035
ENSMUST00000105994	ENSMUSG00000074088	4	130360132	130390026	1	10	8	13	52	17	8	256	452	226	137	223		Q6PE01
ENSMUST00000105996	ENSMUSG00000023232	4	130253495	130279205	-1	0	0	0	19	7	0	0	0	0	6	41		Q8K0E7
ENSMUST00000105998	ENSMUSG00000028776	4	130164454	130175122	-1	4	0	9	34	0	4	0	0	0	0	0		Q99JR5
ENSMUST00000105999	ENSMUSG00000028776	4	130164454	130175122	-1	0	0	0	0	0	0	319	374	239	36	214		Q99JR5
ENSMUST00000106000	ENSMUSG00000025510	7	141467362	141471479	1	12	0	37	39	12	7	208	262	113	55	132		O35566
ENSMUST00000106001						0	9	8	5	11	0	0	2	0	0	0		
ENSMUST00000106003	ENSMUSG00000025508	7	141447370	141451585	1	0	0	8	8	2	2	176	498	117	88	73		P99027
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ENSMUST00000106006	ENSMUSG00000019082	7	141429744	141437892	-1	3	0	11	11	0	2	1	30	0	4	0	E9Q6M6	
ENSMUST00000106007	ENSMUSG00000019082	7	141429744	141437892	-1	0	0	0	0	0	0	24	36	26	9	52		Q9D6M3
ENSMUST00000106008	ENSMUSG00000051007	7	141408135	141414136	-1	1	5	5	23	0	4	623	717	372	111	214		Q8BFQ8
ENSMUST00000106012						1	2	2	2	9	0	0	0	0	0	1		
ENSMUST00000106015	ENSMUSG00000028782	4	129984870	130022633	1	6	0	0	104	1	0	0	0	0	0	0		Q8CGM1
ENSMUST00000106017	ENSMUSG00000028782	4	129984870	130022633	1	11	6	31	317	0	16	0	1	0	0	4		Q8CGM1
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ENSMUST00000106023	ENSMUSG00000025498	7	141262706	141266481	-1	8	0	25	8	5	2	0	7	0	0	0	D3Z4U9	
ENSMUST00000106026	ENSMUSG00000078546	17	21879570	21909926	-1	0	0	6	0	0	0	4	20	1	0	0	E9Q6M3	
ENSMUST00000106027	ENSMUSG00000038611	7	141228784	141262750	1	0	24	18	14	0	27	916	479	782	47	695		A6H619
ENSMUST00000106033	ENSMUSG00000038650	7	141160328	141172851	-1	9	17	3	57	22	11	1540	1392	1243	194	719		Q91VI7
ENSMUST00000106035	ENSMUSG00000028795	4	129619274	129623947	-1	0	0	9	10	0	1	9	79	33	18	19	Q9D1N8	
ENSMUST00000106037	ENSMUSG00000078552	4	129608331	129614257	-1	3	0	0	0	7	2	0	10	0	0	0	F7BCK0	
ENSMUST00000106038						5	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000106039	ENSMUSG00000054065	7	141078218	141090510	1	14	0	37	39	10	19	0	0	0	0	0		Q9QY23
ENSMUST00000106040	ENSMUSG00000025491	7	140967221	140969825	1	8	18	0	38	16	11	38900	87474	29604	121703	14216		Q9D103
ENSMUST00000106041	ENSMUSG00000028175	3	159495433	159529955	1	0	0	0	2	0	0	28	27	16	34	5		Q8CIG0
ENSMUST00000106042	ENSMUSG00000025491	7	140967221	140969825	1	3	3	13	5	8	3	603	5204	948	326	2492		Q9D103
ENSMUST00000106043	ENSMUSG00000078554	4	129491190	129491956	1	4	0	2	83	5	0	0	6	2	0	1		B2KGE5
ENSMUST00000106044	ENSMUSG00000028176	3	158082891	158562221	-1	19	17	46	184	32	12	0	0	0	0	0	E9Q6L9	
ENSMUST00000106045	ENSMUSG00000038745	7	140920902	140929192	1	6	4	4	5	9	2	0	3	0	0	0	E9QNS0	
ENSMUST00000106046	ENSMUSG00000048485	4	129425765	129440853	-1	0	24	0	40	46	20	0	0	0	0	0	I7HLR7	
ENSMUST00000106047	ENSMUSG00000057572	4	129335695	129354547	1	0	0	0	2	0	0	81	218	60	241	40	F7BCB7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000106048	ENSMUSG00000025486	7	140863670	140882309	-1	0	6	27	11	0	6	101	179	92	20	146	Q4FJK3	Q8R104
ENSMUST00000106049	ENSMUSG00000025482	7	140847805	140851018	1	8	0	9	2	6	4	0	1	0	0	2	E9QNR9	
ENSMUST00000106050	ENSMUSG00000025481	7	140835018	140837971	1	5	4	11	4	0	5	0	0	0	0	2	A0A0A0MQC3	
ENSMUST00000106051	ENSMUSG00000050390	4	129219578	129261404	-1	44	42	113	60	46	16	0	0	0	0	1		A2A7S8
ENSMUST00000106052	ENSMUSG00000060314	7	140807449	140822178	-1	21	32	48	48	28	14	2	2	3	2	10	Q6NV92	
ENSMUST00000106054	ENSMUSG00000028811	4	129189760	129219607	1	7	8	13	34	20	6	95	292	146	8	132	A2A7S7	
ENSMUST00000106057	ENSMUSG00000028180	3	157534160	157548410	1	2	0	2	0	0	0	0	65	8	31	29	D3Z4U0	
ENSMUST00000106058	ENSMUSG00000028180	3	157534160	157548410	1	2	0	7	175	18	13	0	45	50	43	56	B2RRT9	Q9R020
ENSMUST00000106059	ENSMUSG00000040928	4	129148005	129189727	-1	0	0	0	17	0	0	33	175	73	29	66		Q9D5K4
ENSMUST00000106061	ENSMUSG00000040928	4	129148005	129189727	-1	21	0	32	24	18	2	82	174	129	8	117		Q9D5K4
ENSMUST00000106063	ENSMUSG00000028180	3	157534160	157548410	1	0	1	0	0	0	0	69	267	121	277	117	A0A0H2UH20	
ENSMUST00000106064	ENSMUSG00000028786	4	129105548	129111626	1	0	0	0	104	0	0	0	0	0	0	0		Q9D7S1
ENSMUST00000106065	ENSMUSG00000040037	3	156561794	157316445	1	5	5	6	15	3	2	0	0	0	0	0	D3Z4T6	
ENSMUST00000106068	ENSMUSG00000028789	4	128930233	128962442	-1	4	3	14	30	1	2	5	0	0	6	0	B2RSR5	Q8BVM4
ENSMUST00000106069	ENSMUSG00000025473	7	139978932	139992562	-1	10	0	0	5	0	0	1952	3161	2708	182	2433	Q3U1J7	Q05910
ENSMUST00000106072	ENSMUSG00000028799	4	128773088	128806045	-1	20	6	64	0	18	0	80	40	80	0	80	B1ASA5	
ENSMUST00000106074						12	4	71	12	12	4	0	0	0	0	0		
ENSMUST00000106077	ENSMUSG00000028794	4	128755364	128769298	1	1	3	8	87	9	10	1	0	1	0	0		Q3V1N9
ENSMUST00000106079	ENSMUSG00000028796	4	128654702	128752881	1	0	0	0	16	13	2	1230	980	879	144	715		Q9QWH1
ENSMUST00000106080	ENSMUSG00000028796	4	128654702	128752881	1	0	0	74	0	33	18	0	6	0	0	10		Q9QWH1
ENSMUST00000106089	ENSMUSG00000039208	11	121701544	121716306	1	3	2	2	1	3	4	853	1150	302	152	367		Q8VE43
ENSMUST00000106090	ENSMUSG00000046623	4	127351086	127354081	-1	18	5	26	16	22	5	0	0	0	5	2		Q02738
ENSMUST00000106091	ENSMUSG00000042367	4	127325235	127330844	-1	11	6	0	4	7	7	0	0	0	3	4		P28231
ENSMUST00000106092	ENSMUSG00000042388	4	127169204	127237022	1	16	18	73	0	0	0	1	0	0	0	0	B1AS06	
ENSMUST00000106093	ENSMUSG00000039230	11	121451949	121617164	1	0	0	4	1	2	4	0	0	0	0	0	B1ATU0	
ENSMUST00000106094	ENSMUSG00000042388	4	127169204	127237022	1	16	19	21	62	21	14	0	0	0	0	0	Q3TY61	Q6PFD5
ENSMUST00000106095	ENSMUSG00000041309	7	139579376	139582797	-1	0	0	0	194	12	1	0	0	2	0	0	D3Z4R4	
ENSMUST00000106097	ENSMUSG00000070737	4	127123691	127129644	1	5	7	0	1	0	0	0	26	6	16	0	A2A7U3	
ENSMUST00000106098	ENSMUSG00000025477	7	139389109	139579652	1	9	0	5	47	5	0	662	1762	722	170	554	Q7TNC9	
ENSMUST00000106099	ENSMUSG00000043872	4	127047094	127061152	-1	6	0	0	0	8	0	1	42	22	0	7	A2A7T8	
ENSMUST00000106100	ENSMUSG00000039068	3	152395473	152462826	1	0	0	0	61	0	0	0	145	43	54	0		Q6KAQ7
ENSMUST00000106101	ENSMUSG00000039068	3	152395473	152462826	1	42	31	181	0	59	14	71	413	101	0	239		Q6KAQ7
ENSMUST00000106102	ENSMUSG00000043872	4	127047094	127061152	-1	9	11	21	33	6	8	4	45	16	40	22	Q3TJB1	
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ENSMUST00000106107	ENSMUSG00000025170	11	121356125	121388251	-1	3	9	7	27	7	5	1	0	1	1	0	B1ATT4	
ENSMUST00000106108	ENSMUSG00000042446	4	126861939	126968135	-1	0	7	11	49	16	0	41	59	53	0	18		A2A791
ENSMUST00000106110	ENSMUSG00000025173	11	121327224	121354445	-1	0	3	8	0	4	3	0	0	11	0	7	F7AZP7	
ENSMUST00000106111	ENSMUSG00000056856	7	138940730	139083976	1	8	2	0	36	15	7	0	0	0	1	0		Q5DTN8
ENSMUST00000106112	ENSMUSG00000078566	7	138890836	138909519	-1	14	7	7	12	7	4	608	1623	479	1084	327		O55003
ENSMUST00000106113	ENSMUSG00000039275	11	121259990	121309896	1	27	17	58	83	50	25	273	483	356	44	317		Q3UCQ1
ENSMUST00000106115	ENSMUSG00000039294	11	121222588	121229322	-1	12	13	19	0	12	0	588	3690	445	208	3		Q3TYS2
ENSMUST00000106116	ENSMUSG00000028833	4	126743750	126753438	-1	0	4	4	0	7	0	54	0	0	0	0		Q9Z0E0
ENSMUST00000106117	ENSMUSG00000039307	11	121204433	121222655	1	0	2	0	0	2	0	11	10	7	6	19		Q3U4H6
ENSMUST00000106118	ENSMUSG00000010476	7	137193673	137314445	-1	0	0	0	0	0	0	0	0	0	0	0		O08791
ENSMUST00000106119	ENSMUSG00000025165	11	121067407	121081220	-1	0	0	0	2	4	0	0	0	0	1	0	A2ABP8	
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ENSMUST00000106121	ENSMUSG00000028034	3	152210422	152236826	1	0	0	0	0	0	0	54	173	163	70	189	Q3TUE1	
ENSMUST00000106126	ENSMUSG00000028036	3	151796502	151837630	-1	2	0	0	0	4	0	0	1	0	0	0	Q60I90	P43117
ENSMUST00000106128	ENSMUSG00000028184	3	148815583	148990555	-1	25	30	37	24	44	17	3	3	3	9	86		Q8JZZ7
ENSMUST00000106129	ENSMUSG00000030994	7	134265779	134385661	-1	0	2	0	5	0	5	0	0	0	0	0	Q9D4E0	
ENSMUST00000106132	ENSMUSG00000028849	4	126232167	126256343	-1	17	0	34	79	0	9	573	1061	1026	73	785	A2AJI1	
ENSMUST00000106133	ENSMUSG00000025155	11	120789201	120796403	-1	0	0	0	0	0	0	0	7	0	22	0	B1ATU5	
ENSMUST00000106134	ENSMUSG00000036745	3	146852367	146984009	1	0	0	0	0	0	0	0	0	2	1	1	E9Q6C6	
ENSMUST00000106135	ENSMUSG00000025155	11	120789201	120796403	-1	0	0	0	45	11	5	67	39	10	0	39	B1ATU5	
ENSMUST00000106137	ENSMUSG00000005034	3	146729574	146812990	-1	3	0	3	1	9	5	0	0	0	0	0		P68181
ENSMUST00000106138	ENSMUSG00000005034	3	146729574	146812990	-1	8	0	10	0	0	0	0	0	0	0	0		P68181
ENSMUST00000106139	ENSMUSG00000030986	7	133720942	133782726	-1	0	0	6	0	0	0	0	53	25	16	0	D3Z4E3	
ENSMUST00000106141	ENSMUSG00000043962	4	126164082	126202760	-1	0	0	1	14	0	0	0	3	3	0	0	E9Q6C5	
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ENSMUST00000106144	ENSMUSG00000030979	7	133686243	133710072	-1	4	11	7	7	15	1	5	8	4	16	0	Q3TPL3	
ENSMUST00000106145	ENSMUSG00000030979	7	133686243	133710072	-1	6	2	13	54	8	2	0	26	20	0	0	Q3UG55	P51163
ENSMUST00000106146	ENSMUSG00000030979	7	133686243	133710072	-1	0	0	0	0	0	0	0	111	0	24	6	Q3UG55	P51163
ENSMUST00000106148	ENSMUSG00000039450	11	120725399	120727281	-1	0	0	3	0	0	2	26	33	9	11	9	A2AC16	
ENSMUST00000106149	ENSMUSG00000036825	3	146404642	146440144	1	12	7	13	2	12	5	0	0	19	2	12		
ENSMUST00000106150	ENSMUSG00000050212	4	126147744	126149875	1	5	2	11	326	8	5	4	20	21	4	11		Q8K2Y3
ENSMUST00000106151	ENSMUSG00000036825	3	146404642	146440144	1	3	5	4	88	3	7	0	0	6	0	0		
ENSMUST00000106152	ENSMUSG00000050212	4	126147744	126149875	1	2	4	0	6	3	0	18	25	0	6	14		Q8K2Y3
ENSMUST00000106153	ENSMUSG00000036825	3	146404642	146440144	1	0	0	0	3	0	0	37	0	35	0	37		Q8VC66
ENSMUST00000106154	ENSMUSG00000025144	11	120710942	120713738	-1	6	0	10	7	6	2	8	27	5	8	9	A2AC07	
ENSMUST00000106155	ENSMUSG00000025144	11	120710942	120713738	-1	0	0	0	0	0	0	0	0	1	0	0	A2AC10	
ENSMUST00000106157	ENSMUSG00000030967	7	132931142	132986391	1	18	32	76	119	30	7	242	1312	387	265	291		Q7M760
ENSMUST00000106158	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	0	0	0	290	210	224	24	77		Q8VBT9
ENSMUST00000106159	ENSMUSG00000025142	11	120672973	120709447	1	0	0	25	0	6	0	617	550	328	129	350		Q8VBT9
ENSMUST00000106160	ENSMUSG00000025142	11	120672973	120709447	1	5	0	0	0	0	2	0	0	0	21	0		Q8VBT9
ENSMUST00000106161	ENSMUSG00000030965	7	132859225	132885111	1	13	4	43	50	21	15	3	7	18	2	9	D3Z4D8	
ENSMUST00000106162	ENSMUSG00000028859	4	126024550	126044440	1	9	10	86	47	71	11	8153	10742	8343	552	10958		P40223
ENSMUST00000106165	ENSMUSG00000030956	7	132712082	132813886	-1	0	0	0	0	0	0	8	0	0	0	0	Q3U0R8	
ENSMUST00000106166	ENSMUSG00000030956	7	132712082	132813886	-1	6	7	34	18	9	0	0	0	0	0	0	Q3U0R8	
ENSMUST00000106168	ENSMUSG00000030956	7	132712082	132813886	-1	18	11	21	3	10	0	109	0	64	0	0		Q8BGR5
ENSMUST00000106169	ENSMUSG00000030956	7	132712082	132813886	-1	0	0	9	0	0	0	0	0	0	0	34		Q8BGR5
ENSMUST00000106170						0	0	3	0	2	0	0	0	0	2	0		
ENSMUST00000106171	ENSMUSG00000028863	4	125085134	125113238	1	0	0	0	0	0	0	0	0	0	0	0	B1ASC8	
ENSMUST00000106176	ENSMUSG00000028869	4	125016585	125055380	1	3	2	6	15	5	4	0	0	0	0	0	B1ASC2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000106177	ENSMUSG00000042988	11	120653788	120661175	-1	0	0	0	147	0	0	0	0	0	0	22		Q8R116
ENSMUST00000106178	ENSMUSG00000042988	11	120653788	120661175	-1	11	0	11	9	0	8	2	0	0	14	21		Q8R116
ENSMUST00000106180	ENSMUSG00000051510	11	120625117	120633600	-1	2	3	1	45	5	0	125	108	130	33	22		O54790
ENSMUST00000106181	ENSMUSG00000051510	11	120625117	120633600	-1	6	0	0	45	7	2	0	8	0	0	0		O54790
ENSMUST00000106182	ENSMUSG00000051510	11	120625117	120633600	-1	8	3	14	24	7	5	271	219	206	41	176		O54790
ENSMUST00000106183	ENSMUSG00000025138	11	120618372	120625240	-1	0	0	0	112	0	0	5	15	18	0	18	A2ABY8	
ENSMUST00000106187						0	0	8	7	0	0	6	26	43	0	13		
ENSMUST00000106188	ENSMUSG00000025137	11	120610087	120617936	-1	0	0	0	0	0	0	63	27	55	0	54	A2ABY3	
ENSMUST00000106190	ENSMUSG00000078570	4	124849080	124851196	-1	0	0	0	48	0	0	0	0	0	0	0		B1ARW8
ENSMUST00000106192	ENSMUSG00000028256	3	145118588	145153915	1	0	0	0	0	0	0	0	0	3	0	0		Q9D478
ENSMUST00000106193	ENSMUSG00000028890	4	124802104	124849800	1	37	28	111	181	51	0	0	0	0	0	122		Q07243
ENSMUST00000106194	ENSMUSG00000044034	11	120608477	120609093	1	0	1	0	0	9	0	4	3	0	0	4	A2ABY0	
ENSMUST00000106195	ENSMUSG00000044034	11	120608477	120609093	1	0	0	4	114	0	0	0	0	0	0	0	Q3UR83	Q8K4P1
ENSMUST00000106197	ENSMUSG00000025132	11	120578104	120581624	-1	20	5	23	3	9	18	10029	9543	6896	953	5202		Q99PT1
ENSMUST00000106199	ENSMUSG00000032643	4	124700701	124708611	1	1	0	0	69	0	0	8	9	15	0	0	F2Z455	
ENSMUST00000106202	ENSMUSG00000028647	4	123904832	123912269	1	3	3	1	4	3	1	1	1	0	6	2	A2A7K5	
ENSMUST00000106203	ENSMUSG00000025793	11	120467635	120483984	1	2	0	0	0	44	3	0	0	0	0	0	B1ATZ1	
ENSMUST00000106204	ENSMUSG00000043333	4	123787874	123829904	1	18	34	101	44	50	19	1	8	9	5	18		A2AGA4
ENSMUST00000106205	ENSMUSG00000025793	11	120467635	120483984	1	6	0	0	0	0	8	435	390	403	29	421	B1ATZ0	
ENSMUST00000106206	ENSMUSG00000028648	4	123712710	123718202	-1	2	4	6	14	4	3	0	0	3	0	7		Q99LY9
ENSMUST00000106207	ENSMUSG00000028648	4	123712710	123718202	-1	9	1	3	2	1	1	3	3	0	5	8		Q99LY9
ENSMUST00000106211	ENSMUSG00000037072	3	144570304	144597680	1	0	0	0	0	0	0	598	1604	640	1913	394	D3Z3Y8	
ENSMUST00000106213	ENSMUSG00000028649	4	123349633	123684360	-1	59	62	92	84	96	36	356	498	1514	79	1724	B1ARU1	
ENSMUST00000106215	ENSMUSG00000062825	11	120345690	120348542	-1	101	83	151	27	100	50	34802	85129	30658	5372	27647	Q4KL81	P63260
ENSMUST00000106216	ENSMUSG00000029580	5	142903115	142906754	-1	0	0	0	10	5	0	0	46	122	0	71	E9Q606	
ENSMUST00000106218	ENSMUSG00000040213	3	142701051	142746870	1	13	0	6	8	2	5	16	60	14	45	14		Q71RI9
ENSMUST00000106220	ENSMUSG00000028649	4	123349633	123684360	-1	0	0	0	0	17	0	7	0	0	0	0	E9QNP1	
ENSMUST00000106221	ENSMUSG00000028268	3	142560026	142573209	1	8	7	9	0	18	0	0	299	60	410	144		Q61107
ENSMUST00000106222	ENSMUSG00000028268	3	142560026	142573209	1	0	4	0	11	0	8	24	64	0	82	137		Q61107
ENSMUST00000106223	ENSMUSG00000078572	11	120098928	120100705	1	12	8	17	28	14	8	25	36	28	16	11		A2AMZ4
ENSMUST00000106224	ENSMUSG00000028649	4	123349633	123684360	-1	48	23	8	0	0	11	149	0	54	0	14	B1ARU4	
ENSMUST00000106225	ENSMUSG00000025377	11	120090531	120098731	-1	20	0	31	97	0	11	20	51	0	27	0	B1AXJ2	
ENSMUST00000106226	ENSMUSG00000030846	7	128439777	128461717	-1	13	11	82	11	12	5	21	192	34	9	6	Q545C1	P70318
ENSMUST00000106227	ENSMUSG00000039781	11	120064430	120086827	-1	0	3	19	0	0	0	58	0	20	5	33	B1AXI9	
ENSMUST00000106228	ENSMUSG00000030846	7	128439777	128461717	-1	0	0	0	0	0	0	10	20	14	2	7	D3Z3Y4	
ENSMUST00000106229	ENSMUSG00000039781	11	120064430	120086827	-1	17	2	8	86	45	13	0	65	8	2	10		Q62036
ENSMUST00000106230	ENSMUSG00000052430	3	141837136	142169425	-1	4	0	3	103	10	0	0	0	0	0	0	B2RRZ4	P36898
ENSMUST00000106231	ENSMUSG00000025372	11	119942763	120006782	1	17	19	47	160	28	17	0	20	8	0	39		Q8BKX1
ENSMUST00000106232	ENSMUSG00000052430	3	141837136	142169425	-1	1	2	9	4	4	0	0	0	0	0	0	B2RRZ4	P36898
ENSMUST00000106233	ENSMUSG00000025372	11	119942763	120006782	1	5	3	0	9	5	5	66	41	0	47	151	B1AZ46	
ENSMUST00000106236	ENSMUSG00000059921	3	141465216	141834924	1	117	83	315	163	74	40	6	77	7	0	10		O08747
ENSMUST00000106237	ENSMUSG00000070369	7	128154376	128223816	1	23	24	16	12	35	11	0	0	0	0	0		Q3V0T4
ENSMUST00000106239	ENSMUSG00000047940	3	139205694	139710299	1	7	2	0	55	9	2	0	0	0	0	0		Q8C8J0
ENSMUST00000106240	ENSMUSG00000030786	7	128062640	128118491	1	0	0	0	0	0	0	4561	44	14426	454	8684		
ENSMUST00000106241	ENSMUSG00000011257	4	123262351	123298925	1	0	0	0	56	9	0	0	41	0	0	0	A3KFU8	
ENSMUST00000106242	ENSMUSG00000030786	7	128062640	128118491	1	12	0	0	45	44	69	370	1	2024	5	689	E9Q604	
ENSMUST00000106243	ENSMUSG00000011257	4	123262351	123298925	1	0	0	50	18	3	0	39	98	13	15	0	A3KFU5	
ENSMUST00000106244	ENSMUSG00000039850	11	119491347	119511437	1	21	57	12	75	0	0	59	9	14	0	65		Q8C9A2
ENSMUST00000106245	ENSMUSG00000039850	11	119491347	119511437	1	51	0	143	43	73	46	0	110	44	12	28		Q8C9A2
ENSMUST00000106246	ENSMUSG00000046093	4	123183227	123194701	1	0	5	0	80	6	0	0	0	0	0	0	B2RRY8	Q8BGZ1
ENSMUST00000106247	ENSMUSG00000053054	3	138313286	138331134	1	9	0	5	4	5	6	0	0	0	0	0	E9Q5Z6	
ENSMUST00000106248	ENSMUSG00000042828	7	128003949	128011033	1	10	15	0	82	0	7	39	0	31	9	40		Q1XH17
ENSMUST00000106250	ENSMUSG00000013483	11	119307768	119345375	1	32	14	12	34	0	17	0	0	0	0	0		Q99KF0
ENSMUST00000106251	ENSMUSG00000030795	7	127967457	127985701	1	20	8	26	48	25	11	41	80	52	17	93	Q564D0	P56959
ENSMUST00000106252	ENSMUSG00000028654	4	122995652	123002485	1	6	9	43	26	0	4	1	0	3	0	7	Q3UIE0	P10166
ENSMUST00000106253	ENSMUSG00000025580	11	119288363	119300089	-1	9	5	10	19	1	0	41	0	56	31	44	A2AFK7	
ENSMUST00000106255	ENSMUSG00000028656	4	122859047	122886056	-1	17	0	0	0	0	24	1885	1533	2747	444	2175		P40124
ENSMUST00000106257	ENSMUSG00000028656	4	122859047	122886056	-1	0	0	0	58	0	0	3992	6371	5422	1118	3508		P40124
ENSMUST00000106258	ENSMUSG00000025579	11	119267887	119285454	1	31	14	46	42	38	15	0	4	0	0	7	A2AFL3	
ENSMUST00000106259	ENSMUSG00000025579	11	119267887	119285454	1	0	10	0	57	30	0	61	137	128	0	101		P70699
ENSMUST00000106261	ENSMUSG00000049728	7	127863047	127876828	-1	0	3	11	3	5	2	54	45	15	10	0		Q8K2R5
ENSMUST00000106262	ENSMUSG00000049728	7	127863047	127876828	-1	4	0	0	366	19	8	0	21	28	0	26		Q8K2R5
ENSMUST00000106263	ENSMUSG00000049728	7	127863047	127876828	-1	8	0	21	0	20	0	34	0	47	13	31		Q8K2R5
ENSMUST00000106265	ENSMUSG00000078575	4	121614271	121622103	-1	2	3	9	2	4	1	0	0	0	0	0	B1AVM1	
ENSMUST00000106266	ENSMUSG00000078576	4	121414735	121423099	-1	16	18	28	15	20	14	0	1	0	0	0	B1AZM5	
ENSMUST00000106267	ENSMUSG00000030806	7	127803900	127824549	-1	291	205	1392	477	204	111	3	12	8	0	31		P61264
ENSMUST00000106268	ENSMUSG00000078577	4	121105651	121109226	-1	4	4	6	1	7	2	0	0	0	0	0	J3JS82	
ENSMUST00000106271	ENSMUSG00000042289	7	127800604	127803802	1	0	0	14	13	0	2	0	24	0	0	11	D3Z3X2	
ENSMUST00000106272	ENSMUSG00000042289	7	127800604	127803802	1	0	0	0	0	0	0	0	0	0	11	0	D3Z3X1	
ENSMUST00000106273	ENSMUSG00000046697	11	118988188	118992841	1	5	0	18	0	0	0	0	0	0	0	0	A2A5N7	
ENSMUST00000106278	ENSMUSG00000025576	11	118489762	118911597	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BIF2
ENSMUST00000106280	ENSMUSG00000064141	4	120930137	120951699	-1	4	16	19	99	16	8	0	74	8	4	62	A2A761	
ENSMUST00000106281	ENSMUSG00000064141	4	120930137	120951699	-1	9	1	25	0	3	5	14	62	18	16	25	A2A761	
ENSMUST00000106282	ENSMUSG00000030814	7	127661456	127708933	-1	69	62	215	244	76	48	20	79	31	6	31	D3Z3W8	
ENSMUST00000106283	ENSMUSG00000032890	4	120854816	120896579	1	54	32	112	0	88	6	26	187	0	8	76	Q14BY7	Q80U57
ENSMUST00000106286	ENSMUSG00000017446	11	118428203	118449963	1	11	9	17	17	0	15	1	0	0	7	17		Q9QXP7
ENSMUST00000106287	ENSMUSG00000025575	11	118406289	118419086	-1	0	0	0	0	0	0	0	6	0	0	0		Q8VCF1
ENSMUST00000106288	ENSMUSG00000025575	11	118406289	118419086	-1	0	0	0	0	0	0	469	610	152	28	283		Q8VCF1
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ENSMUST00000106290	ENSMUSG00000033880	11	118392751	118402092	-1	12	0	5	0	5	5	0	0	5	0	0	E9Q5X5	
ENSMUST00000106291	ENSMUSG00000078578	3	135438149	135468198	1	14	17	5	48	35	17	3621	11945	3675	1710	2253	Q4QQL2	P61079
ENSMUST00000106292	ENSMUSG00000030822	7	127459611	127476759	1	0	0	0	3	0	2	949	1792	803	179	715		Q7TPN9
ENSMUST00000106296	ENSMUSG00000033909	11	118259651	118290244	-1	0	0	56	46	0	0	0	0	71	0	157		B1AQJ2
ENSMUST00000106298	ENSMUSG00000000085	4	120405281	120530186	1	7	0	0	0	16	2	0	35	55	0	55		Q8K214

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ENSMUST00000106299	ENSMUSG00000048921	7	127442136	127449158	-1	0	0	7	36	0	5	0	0	0	0	0	D3Z3V5	
ENSMUST00000106300	ENSMUSG00000045251	7	127418967	127422068	-1	0	0	0	14	0	0	44	37	9	0	20	E9Q5M9	
ENSMUST00000106301	ENSMUSG00000000085	4	120405281	120530186	1	0	0	0	0	0	0	58	0	0	0	0		Q8K214
ENSMUST00000106302	ENSMUSG00000017132	11	118132019	118248592	-1	23	10	54	0	7	14	1121	1450	1410	274	1040	Q3TZ02	
ENSMUST00000106303	ENSMUSG00000078580	7	127389673	127393629	-1	0	0	0	0	0	0	0	0	0	1	0	D3Z3V4	
ENSMUST00000106305	ENSMUSG00000017132	11	118132019	118248592	-1	0	0	0	71	0	0	211	223	0	31	33		Q9QX11
ENSMUST00000106306	ENSMUSG00000030830	7	127296260	127335138	1	0	0	36	0	6	0	5057	8739	7544	528	6852	E9Q5M7	
ENSMUST00000106307	ENSMUSG00000028634	4	119733784	120138045	1	73	42	137	87	92	40	0	12	3	1	42		A2A884
ENSMUST00000106308	ENSMUSG00000033987	11	118021723	118129219	-1	0	0	127	136	134	41	0	0	108	0	148	K3W4R0	
ENSMUST00000106309	ENSMUSG00000032978	4	119656607	119658954	-1	9	4	0	1	6	2	0	0	0	0	0	A2AA35	
ENSMUST00000106310	ENSMUSG00000032998	4	119537004	119629119	1	2	32	161	0	32	21	94	322	150	0	111		Q8BUR3
ENSMUST00000106312	ENSMUSG00000045598	7	127233061	127238179	1	35	33	8	413	31	22	20	10	33	4	9		Q3US17
ENSMUST00000106313	ENSMUSG00000000486	7	127214447	127233130	-1	0	4	6	0	4	0	324	223	296	52	117	D3Z3V3	
ENSMUST00000106314	ENSMUSG00000000486	7	127214447	127233130	-1	0	3	2	9	10	4	709	643	442	216	322		P42209
ENSMUST00000106315	ENSMUSG00000028013	3	133310110	133378235	1	0	0	2	1	2	0	0	15	0	0	0	G8JL76	
ENSMUST00000106316	ENSMUSG00000028636	4	119418530	119422420	-1	0	0	2	0	0	2	11	46	15	0	3		Q8VDG5
ENSMUST00000106317	ENSMUSG00000060288	4	119300010	119320546	-1	5	0	0	0	2	0	0	0	0	0	0		Q9D868
ENSMUST00000106318	ENSMUSG00000060288	4	119300010	119320546	-1	15	10	11	35	23	7	42	135	23	147	57		Q9D868
ENSMUST00000106319	ENSMUSG00000060288	4	119300010	119320546	-1	0	0	1	0	0	3	0	0	0	21	0	A2BGI9	
ENSMUST00000106321	ENSMUSG00000060288	4	119300010	119320546	-1	21	12	35	16	18	10	24	89	35	87	15		Q9D868
ENSMUST00000106331	ENSMUSG00000025573	11	117797660	117807301	1	9	10	22	20	26	7	0	0	2	0	0		Q9CX63
ENSMUST00000106332	ENSMUSG00000030683	7	126950563	126970606	1	0	0	0	0	17	3	0	32	19	2	30		Q4V9Z5
ENSMUST00000106333	ENSMUSG00000030683	7	126950563	126970606	1	3	0	2	0	10	0	38	18	22	0	17		Q4V9Z5
ENSMUST00000106334	ENSMUSG00000050106	11	117782076	117793110	1	0	0	0	0	0	0	293	171	161	0	74	B0QZP6	Q7TN58
ENSMUST00000106335	ENSMUSG00000030683	7	126950563	126970606	1	27	15	53	38	27	21	0	0	0	0	1		Q4V9Z5
ENSMUST00000106337	ENSMUSG00000027983	3	131288441	131303227	-1	17	22	98	168	44	15	1	6	4	1	4		Q9CX98
ENSMUST00000106339	ENSMUSG00000046378	7	126945567	126949582	-1	0	0	0	0	0	0	0	0	0	0	0		Q2TA57
ENSMUST00000106340	ENSMUSG00000046378	7	126945567	126949582	-1	34	44	62	61	44	16	5	13	6	3	15		Q2TA57
ENSMUST00000106341	ENSMUSG00000027985	3	131110471	131224356	1	45	52	384	399	0	0	0	0	0	0	0	Q8BGZ9	
ENSMUST00000106342	ENSMUSG00000030689	7	126850960	126862377	-1	0	0	0	0	0	4	22	31	0	0	0	D3Z3H2	
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ENSMUST00000106344	ENSMUSG00000025571	11	117654289	117763439	1	0	3	25	15	4	0	72	143	185	0	72	B1ATC3	
ENSMUST00000106345	ENSMUSG00000028643	4	119195306	119201298	1	0	1	11	0	5	1	0	25	0	10	0	A2A7Q0	
ENSMUST00000106348	ENSMUSG00000030695	7	126795234	126800751	-1	8	0	32	0	9	6	221	216	65	44	141	Q5FWB7	P05064
ENSMUST00000106349	ENSMUSG00000059248	11	117199661	117362325	1	0	0	11	69	2	6	2335	3524	1902	305	1613		Q80UG5
ENSMUST00000106353	ENSMUSG00000058897	3	130131501	130599877	1	16	13	22	0	22	16	0	0	0	0	0	E9Q5L6	
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ENSMUST00000106355	ENSMUSG00000045268	4	119169513	119174195	-1	27	6	168	49	1	0	99	167	119	22	100	A2A7P4	
ENSMUST00000106356	ENSMUSG00000042675	7	126776955	126780514	1	1	0	0	0	0	5	2314	2997	1262	292	1023		P61237
ENSMUST00000106357	ENSMUSG00000042675	7	126776955	126780514	1	3	3	17	27	9	0	323	2453	603	50	1263		P61237
ENSMUST00000106359	ENSMUSG00000042675	7	126776955	126780514	1	0	0	0	0	0	0	12	113	64	25	61	D3Z3G7	
ENSMUST00000106360	ENSMUSG00000073769	4	118864658	118869736	1	3	3	0	0	8	2	0	0	0	0	0	L7MU98	
ENSMUST00000106361	ENSMUSG00000073770	4	118829485	118836273	-1	0	9	11	0	5	0	0	0	0	0	0	B1ARU8	
ENSMUST00000106363	ENSMUSG00000020818	11	116852440	116875635	1	0	1	0	0	0	0	6	35	68	0	10	I1E4X9	
ENSMUST00000106364	ENSMUSG00000030707	7	126699773	126707787	-1	7	0	13	6	9	8	1246	1849	1062	209	984	Q3U1N0	O89053
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ENSMUST00000106367	ENSMUSG00000028536	4	118526999	118530228	1	5	1	9	13	8	5	0	0	0	0	0		Q9CQM1
ENSMUST00000106369	ENSMUSG00000047721	7	126695401	126699798	1	6	2	13	142	16	4	77	95	39	309	41		Q8BGS2
ENSMUST00000106370	ENSMUSG00000090266	11	116843278	116854263	1	0	0	4	96	3	1	20	110	28	43	12		A2AA28
ENSMUST00000106371	ENSMUSG00000030711	7	126672865	126676432	-1	3	3	12	6	4	1	0	0	0	0	0	D3Z3G5	
ENSMUST00000106372	ENSMUSG00000030711	7	126672865	126676432	-1	5	6	25	12	8	1	0	0	0	0	0	Q91W19	
ENSMUST00000106373	ENSMUSG00000030711	7	126672865	126676432	-1	4	0	5	2	4	2	1	2	0	151	37	E9QNL5	
ENSMUST00000106375	ENSMUSG00000006389	4	118442415	118457513	-1	0	0	0	41	0	0	0	0	4	3	0	Q925F5	
ENSMUST00000106377						0	0	0	0	0	0	0	1	0	0	0		
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ENSMUST00000106381	ENSMUSG00000075410	11	116653534	116668389	1	3	0	1	0	6	2	0	0	0	0	0	A2A7X9	
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ENSMUST00000106384	ENSMUSG00000006392	4	118409337	118415782	1	4	1	8	12	7	2	2	0	2	0	2	Q9DAY7	
ENSMUST00000106386	ENSMUSG00000061878	11	116530925	116536674	1	2	0	1	2	5	0	0	0	0	11	2		Q8CI15
ENSMUST00000106387	ENSMUSG00000061878	11	116530925	116536674	1	5	3	11	30	0	5	0	0	0	0	0		Q8CI15
ENSMUST00000106388	ENSMUSG00000061878	11	116530925	116536674	1	4	1	5	5	7	2	0	0	0	0	9		Q8CI15
ENSMUST00000106391	ENSMUSG00000015869	11	116470845	116494202	-1	0	0	0	21	5	0	293	464	269	43	215	B1AT82	
ENSMUST00000106392	ENSMUSG00000073838	7	126487361	126490731	1	23	9	20	32	12	7	27	59	0	0	10		Q8BFR5
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ENSMUST00000106398	ENSMUSG00000052949	11	116336353	116413032	-1	0	19	10	62	31	0	0	0	11	0	0	A2AAP0	
ENSMUST00000106399	ENSMUSG00000053819	3	126596302	126846326	1	0	0	0	0	0	0	0	27	47	32	20	E9Q1W0	
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ENSMUST00000106402	ENSMUSG00000053819	3	126596302	126846326	1	3	0	0	142	17	0	0	25	17	7	11		Q6PHZ2
ENSMUST00000106403	ENSMUSG00000033326	4	118136957	118180043	-1	0	7	60	0	0	0	5	297	58	1	17		Q8BW72
ENSMUST00000106405	ENSMUSG00000030727	7	126428759	126449245	1	0	2	0	0	0	0	0	1	0	0	0		Q91WG2
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ENSMUST00000106410	ENSMUSG00000028538	4	117932154	118134914	-1	0	0	4	40	0	5	35	65	30	12	37		P97325
ENSMUST00000106411	ENSMUSG00000020792	11	116288001	116307233	-1	0	0	0	1	0	12	533	679	429	111	427	Q542L0	O35250
ENSMUST00000106413	ENSMUSG00000020792	11	116288001	116307233	-1	0	0	0	0	0	0	0	0	0	11	0	A2AAN0	
ENSMUST00000106421	ENSMUSG00000028541	4	117869260	117883487	-1	5	5	20	3	9	3	3	1	0	1	0	B1ASJ2	Q9Z2Y2
ENSMUST00000106422	ENSMUSG00000078588	4	117866524	117872557	-1	0	0	0	0	0	0	0	0	0	0	0	Q3V0I8	
ENSMUST00000106425	ENSMUSG00000020780	11	116245166	116274217	-1	4	0	0	0	11	0	0	168	90	80	0	A2AAN2	
ENSMUST00000106426	ENSMUSG00000050315	3	123076519	123236149	-1	1	1	0	13	42	7	0	0	0	0	0	E9Q1U2	
ENSMUST00000106427	ENSMUSG00000050315	3	123076519	123236149	-1	22	6	40	11	0	14	0	0	0	0	0	D3YVV9	
ENSMUST00000106429	ENSMUSG00000054091	3	122924203	122926184	1	10	13	11	41	9	9	805	1552	605	2191	383		Q99M08
ENSMUST00000106431	ENSMUSG00000078590	3	122913070	122919360	-1	0	0	0	0	0	0	0	0	0	0	0	F7AG78	
ENSMUST00000106433	ENSMUSG00000048772	4	117251951	117268582	1	0	3	0	1	0	0	26	0	0	7	6		Q9D0Z3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000106434	ENSMUSG00000048772	4	117251951	117268582	1	4	0	0	37	0	0	0	13	0	0	0		Q9D0Z3
ENSMUST00000106435	ENSMUSG00000020776	11	116142285	116168166	-1	37	0	94	30	9	0	11	38	50	0	90		A2A870
ENSMUST00000106436	ENSMUSG00000028678	4	117159639	117182639	-1	6	15	16	10	26	5	0	0	0	11	0	Q3TTL2	
ENSMUST00000106437	ENSMUSG00000078591	7	123982869	124398989	1	59	48	194	1467	124	53	2	4	1	0	3	D3YVV6	
ENSMUST00000106439	ENSMUSG00000020775	11	116131817	116138868	-1	4	0	0	3	0	0	54	89	36	40	85		Q8K2M0
ENSMUST00000106440	ENSMUSG00000054517	11	116121846	116131128	-1	297	336	253	402	336	168	25	72	27	9	63		Q8BFW4
ENSMUST00000106441	ENSMUSG00000020773	11	116105752	116127210	-1	2	4	0	0	0	0	0	1	2	6	24		Q8C0E3
ENSMUST00000106442	ENSMUSG00000030766	7	123279218	123369915	-1	24	14	66	167	19	11	157	545	348	0	267		Q3UIA2
ENSMUST00000106443						0	0	0	0	14	0	13	0	0	9	6		
ENSMUST00000106444	ENSMUSG00000034341	11	116078573	116086995	-1	0	0	4	0	0	0	16	0	13	0	25	A2A860	
ENSMUST00000106447	ENSMUSG00000028683	4	117019402	117087306	1	15	21	16	31	17	8	2	4	2	0	6	Q3UKV0	
ENSMUST00000106448	ENSMUSG00000028683	4	117019402	117087306	1	2	0	0	34	0	0	11	46	20	165	29	B1AUN2	
ENSMUST00000106450	ENSMUSG00000057948	11	116062095	116077961	-1	0	0	40	68	24	0	165	220	220	110	212		B2RUP2
ENSMUST00000106451	ENSMUSG00000057948	11	116062095	116077961	-1	9	2	0	0	0	0	1720	2259	1615	29	1066		B2RUP2
ENSMUST00000106452	ENSMUSG00000020770	11	116030322	116061214	1	8	5	0	30	0	25	0	75	60	5	135	Q3UYU7	Q8BL48
ENSMUST00000106454	ENSMUSG00000016559	11	116021912	116027962	-1	19	5	10	34	13	5	0	14	5	14	14		P84244
ENSMUST00000106455	ENSMUSG00000028688	4	116794310	116807640	-1	0	0	4	4	2	0	0	14	0	3	0		Q9D2E2
ENSMUST00000106456	ENSMUSG00000033985	4	116720948	116805956	1	7	10	21	0	5	0	182	465	94	0	90	A2AGD9	
ENSMUST00000106458	ENSMUSG00000020758	11	115974709	116008412	1	9	0	0	0	0	20	0	0	0	0	0		A2A863
ENSMUST00000106459	ENSMUSG00000033985	4	116720948	116805956	1	7	8	10	72	10	0	0	9	3	3	15	A2AGE0	
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ENSMUST00000106467	ENSMUSG00000028133	3	121155398	121171695	-1	6	0	5	57	0	0	0	0	0	0	0	E9Q1R6	
ENSMUST00000106468	ENSMUSG00000044702	7	122107262	122132985	-1	0	0	0	7	0	0	0	9	0	0	0	D3YVU6	
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ENSMUST00000106471	ENSMUSG00000030869	7	122085403	122101886	-1	1	0	0	3	0	0	27	19	20	1	17	F8WJ64	
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ENSMUST00000106475	ENSMUSG00000034042	4	116557658	116593882	1	0	0	28	17	0	0	168	354	574	38	328		Q6NZP2
ENSMUST00000106478	ENSMUSG00000055900	4	116551633	116555936	-1	160	147	177	99	186	77	63	325	97	59	79		Q3KQJ0
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ENSMUST00000106483	ENSMUSG00000030880	7	120917744	120947432	1	31	16	50	34	30	10	0	0	0	0	0		Q9CZT4
ENSMUST00000106484	ENSMUSG00000003810	4	116306762	116464183	-1	0	21	8	0	0	0	94	114	90	0	1	B1AST7	
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ENSMUST00000106489	ENSMUSG00000035064	7	120842831	120907219	1	0	0	9	16	4	0	205	315	108	11	147		O08796
ENSMUST00000106490	ENSMUSG00000028698	4	116221618	116303056	1	4	2	5	3	0	6	1	0	0	0	0	B1AUG0	
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ENSMUST00000106492	ENSMUSG00000078593	4	116173372	116174290	1	1	0	3	6	1	1	0	0	0	0	0	B1AUF7	
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ENSMUST00000106495	ENSMUSG00000059923	11	115644045	115708597	-1	0	4	0	5	5	0	689	2335	855	16	699	B1AT92	
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ENSMUST00000106497	ENSMUSG00000059923	11	115644045	115708597	-1	16	4	36	6	13	21	2	389	35	110	490	Q3U5I5	Q60631
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ENSMUST00000106501	ENSMUSG00000027963	3	116007462	116029017	1	0	0	5	0	0	6	53	59	18	0	8	Q3TSR0	
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ENSMUST00000106503	ENSMUSG00000020744	11	115614178	115628295	-1	0	1	0	3	0	0	52	88	58	6	37	A2A9V5	
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ENSMUST00000106506	ENSMUSG00000020743	11	115607918	115612969	-1	0	0	2	0	0	0	138	36	109	19	51	A2A9W3	
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ENSMUST00000106516	ENSMUSG00000030922	7	119895861	119916756	1	0	0	0	0	0	0	10	29	0	0	0		Q9CQB7
ENSMUST00000106517	ENSMUSG00000030922	7	119895861	119916756	1	5	5	16	59	9	6	7	35	6	38	0		Q9CQB7
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ENSMUST00000106519	ENSMUSG00000048787	7	119853163	119896291	-1	4	7	7	59	7	4	42	14	94	17	58		Q8K0V2
ENSMUST00000106520	ENSMUSG00000030924	7	119794006	119848943	1	1	0	1	0	9	2	3	31	8	2	7	D3YW29	
ENSMUST00000106521	ENSMUSG00000044556	4	115779834	115781018	-1	10	8	13	7	15	4	0	2	0	0	0	D2D552	A2A8T7
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ENSMUST00000106526	ENSMUSG00000030935	7	119760923	119787513	1	4	0	0	0	3	2	0	0	0	0	0		Q3UNX5
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ENSMUST00000106530	ENSMUSG00000020736	11	115490420	115491862	-1	0	0	4	0	0	5	0	0	0	0	0	A2A9X5	
ENSMUST00000106532	ENSMUSG00000045775	11	115462474	115474398	1	10	10	15	19	7	5	4	3	0	0	0	A0A0A0MQC4	
ENSMUST00000106533	ENSMUSG00000016940	11	115420128	115431274	1	15	11	35	14	13	9	69	179	124	25	177	A2A9V9	
ENSMUST00000106535	ENSMUSG00000027981	3	113605067	113630149	-1	2	3	0	0	3	2	3	35	10	10	18		Q3UZ01
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ENSMUST00000106537	ENSMUSG00000034566	11	115415689	115419962	-1	16	13	47	194	33	7	5	53	5	11	8		Q9DCX2
ENSMUST00000106539	ENSMUSG00000018858	11	115403752	115412674	1	9	20	14	0	6	11	0	0	0	3	0	A2A6T4	
ENSMUST00000106540	ENSMUSG00000074264	3	113555710	113606699	-1	0	0	0	3	1	0	0	6	4	5	6		P00687
ENSMUST00000106542	ENSMUSG00000034586	11	115347707	115367756	-1	29	0	0	59	0	25	0	0	0	0	0		Q8R1F6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000106543	ENSMUSG00000018862	11	115334731	115346927	1	0	16	0	79	25	6	0	1	0	0	0		Q80UF9
ENSMUST00000106544	ENSMUSG00000050201	11	115307163	115332303	1	0	0	0	26	15	7	0	0	0	0	0		Q80SX5
ENSMUST00000106545	ENSMUSG00000047155	4	115106323	115134281	-1	2082	2362	2505	1244	2350	1110	18	136	55	26	83	A2A9Y7	
ENSMUST00000106547	ENSMUSG00000073856	7	118855760	118972652	1	0	0	0	0	0	2	0	1	2	0	0	E9PUC1	
ENSMUST00000106548	ENSMUSG00000028716	4	115088708	115093899	1	0	0	10	0	0	0	0	0	0	0	0		Q9CQH0
ENSMUST00000106549	ENSMUSG00000030980	7	118842222	118856254	-1	2	1	7	80	9	5	0	3	0	16	0		Q9Z2Q2
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ENSMUST00000106552	ENSMUSG00000030982	7	118740226	118842966	1	0	0	0	0	0	0	150	262	221	34	211	D3YW20	
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ENSMUST00000106554	ENSMUSG00000020734	11	115249169	115267243	-1	39	22	122	521	30	14	0	0	0	0	0	A2A6S2	Q01098
ENSMUST00000106557	ENSMUSG00000033904	7	118712552	118737024	1	14	17	11	56	25	0	28	42	56	28	73		Q7TSH4
ENSMUST00000106559						1	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000106561	ENSMUSG00000047798	11	115116214	115133992	-1	0	19	0	0	0	0	5354	15367	5457	1925	5949		Q6SJQ7
ENSMUST00000106562	ENSMUSG00000047798	11	115116214	115133992	-1	96	56	209	1172	198	118	384	2528	1108	201	1207	A2A6Z2	
ENSMUST00000106564	ENSMUSG00000055960	4	112072016	112168076	1	121	143	264	114	106	68	0	6	3	0	8		A7TZF3
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ENSMUST00000106568	ENSMUSG00000049214	4	111972923	111988223	1	0	1	0	0	0	1	0	0	0	0	0	A0A0B4J1K7	
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ENSMUST00000106575	ENSMUSG00000059857	3	109780040	110144011	-1	0	3	3	2	0	0	0	0	0	0	0	F8WJ48	
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ENSMUST00000106578	ENSMUSG00000089753	11	115010335	115016193	-1	5	1	7	18	3	0	3	52	20	4	21	A2A7W0	
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ENSMUST00000106581	ENSMUSG00000063193	11	114922781	114934386	-1	0	0	0	0	0	0	2321	3260	1647	962	1267	F8WJE9	Q3U497
ENSMUST00000106582	ENSMUSG00000034652	11	114890041	114904654	1	253	19	170	33	243	14	1265	4425	1139	364	1598		Q6SJQ0
ENSMUST00000106584	ENSMUSG00000034677	11	114798924	114806745	1	0	0	0	12	0	0	0	0	0	0	0	Q1XA02	
ENSMUST00000106586	ENSMUSG00000045662	3	108939873	108960774	1	6	0	0	6	9	9	1	0	0	0	0		Q8CAE2
ENSMUST00000106587	ENSMUSG00000061298	4	110397661	111664324	1	3	4	5	0	3	1	0	0	0	0	0	A2A9S6	
ENSMUST00000106588	ENSMUSG00000008683	7	118104372	118116188	-1	0	3	1	14	3	3	1695	5109	1435	6792	829	Q5M9M4	P62245
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ENSMUST00000106597	ENSMUSG00000028546	4	110203722	110351909	-1	2	0	0	0	0	4	0	0	0	0	0		Q61701
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ENSMUST00000106599	ENSMUSG00000057322	11	114668524	114672331	1	0	0	0	112	5	0	0	0	0	11	3	Q52KP0	Q9JJI8
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ENSMUST00000106612	ENSMUSG00000051910	7	115470872	116038796	-1	23	15	0	31	25	0	0	0	0	0	0	Q8BSS6	
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ENSMUST00000106616	ENSMUSG00000041598	11	113726850	113751881	-1	25	14	55	228	33	11	16	23	33	7	46		Q9JM96
ENSMUST00000106617	ENSMUSG00000018727	11	113698172	113710017	-1	10	1	8	3	7	1	0	10	0	0	5	A2A6P9	
ENSMUST00000106618	ENSMUSG00000028555	4	109406623	109444745	1	12	8	0	14	0	3	0	0	0	0	6		A2ACP1
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ENSMUST00000106625	ENSMUSG00000040412	3	108455694	108536536	-1	23	22	35	27	34	16	1	0	0	0	0	A0A0A0MQC6	
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ENSMUST00000106630	ENSMUSG00000047904	11	113619342	113626028	1	4	1	0	0	2	0	0	0	0	0	0		P30875
ENSMUST00000106631	ENSMUSG00000028558	4	109234485	109254571	1	2	0	7	3	4	2	0	4	0	4	0	A2A8Z3	
ENSMUST00000106633	ENSMUSG00000041654	11	113244853	113650079	-1	0	0	33	18	31	0	20	38	18	0	0		Q8BWY7
ENSMUST00000106635	ENSMUSG00000051497	11	110968033	111027968	1	50	0	0	71	47	0	0	0	0	0	0		Q9Z307
ENSMUST00000106636	ENSMUSG00000051497	11	110968033	111027968	1	0	0	297	7	0	48	1	8	0	1	5		Q9Z307
ENSMUST00000106638	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	0	0	0	0	0	0	0	0	Q3UFP5	
ENSMUST00000106640	ENSMUSG00000030770	7	112427505	112591692	1	3	0	16	6	12	6	0	0	0	0	22	Q3UF75	
ENSMUST00000106643	ENSMUSG00000030770	7	112427505	112591692	1	0	4	0	0	0	0	0	0	0	0	0		Q9EPC1
ENSMUST00000106644	ENSMUSG00000053510	4	109000655	109061777	1	0	1	0	0	0	0	921	3472	2098	189	1571	A2A9Q2	
ENSMUST00000106645	ENSMUSG00000030771	7	112368308	112413104	1	0	7	0	0	0	10	0	0	0	0	0		Q9D5U9
ENSMUST00000106647	ENSMUSG00000038244	7	112225856	112355194	1	2	4	3	1	6	2	0	0	0	2	0	D3YVQ9	
ENSMUST00000106648	ENSMUSG00000038244	7	112225856	112355194	1	108	82	195	629	105	49	5	28	8	2	25		Q8BML1
ENSMUST00000106650	ENSMUSG00000003411	4	108879063	108943324	1	14	19	24	41	23	11	0	0	0	0	0	Q0PD62	Q9CZT8
ENSMUST00000106651	ENSMUSG00000003411	4	108879063	108943324	1	0	0	1	0	0	0	0	0	0	0	0	A2A7Z6	
ENSMUST00000106653	ENSMUSG00000059263	7	112023506	112111386	1	29	20	31	123	34	20	834	3579	2167	937	1366		Q8BY87
ENSMUST00000106654	ENSMUSG00000048796	3	108195687	108201212	-1	11	6	33	83	10	2	85	91	92	7	83	Q3TPE5	
ENSMUST00000106655	ENSMUSG00000048796	3	108195687	108201212	-1	0	7	0	17	6	11	374	264	300	66	471		A2AE42
ENSMUST00000106656	ENSMUSG00000050947	3	108186335	108192286	1	27	23	10	48	0	8	0	12	0	0	8		Q80ZD8
ENSMUST00000106657	ENSMUSG00000034557	4	108637466	108780798	-1	20	0	41	27	0	0	0	55	28	0	45	A2A8R0	
ENSMUST00000106658	ENSMUSG00000034557	4	108637466	108780798	-1	11	26	0	0	47	22	31	121	16	9	28	A8Y5G5	
ENSMUST00000106659	ENSMUSG00000050947	3	108186335	108192286	1	0	0	0	58	0	3	0	0	4	0	0		Q80ZD8
ENSMUST00000106661	ENSMUSG00000050947	3	108186335	108192286	1	4	0	0	1	18	6	0	0	0	0	2	A2AE38	
ENSMUST00000106662	ENSMUSG00000041828	11	110025634	110095978	-1	1	0	0	0	0	1	0	0	0	0	0	A2A6R7	
ENSMUST00000106663	ENSMUSG00000038296	7	111471661	111779977	-1	28	16	38	95	27	7	0	0	0	1	1	Q59J91	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000106664	ENSMUSG00000041828	11	110025634	110095978	-1	0	0	0	0	6	8	0	0	1	0	1		Q8K442
ENSMUST00000106665						9	6	22	8	11	2	5	156	20	0	71		
ENSMUST00000106667						0	3	4	1	3	2	8	43	5	6	8		
ENSMUST00000106669	ENSMUSG00000020620	11	109932190	109995845	-1	0	0	0	0	0	0	0	0	0	0	0		Q8K440
ENSMUST00000106670	ENSMUSG00000027890	3	108040408	108044894	-1	0	2	0	0	0	2	0	5	0	0	0	A2AE91	
ENSMUST00000106673	ENSMUSG00000034610	4	108459426	108559421	1	0	0	0	56	6	1	0	0	0	1	0	A2A9H0	
ENSMUST00000106674	ENSMUSG00000020617	11	109787651	109828046	-1	18	15	13	10	14	2	0	0	0	0	0	Q3V0S8	
ENSMUST00000106676	ENSMUSG00000020612	11	109649405	109669656	1	6	0	10	3	4	0	49	27	47	0	33	A2AI69	
ENSMUST00000106677	ENSMUSG00000020612	11	109649405	109669656	1	19	19	45	11	24	14	42	37	57	72	76		Q9DBC7
ENSMUST00000106680						20	10	36	18	28	9	0	0	0	0	0		
ENSMUST00000106681	ENSMUSG00000068762	3	107938847	107943749	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVP9	
ENSMUST00000106682	ENSMUSG00000030788	7	110800432	110844457	-1	1	4	2	51	1	0	8	10	13	53	40		Q99MB7
ENSMUST00000106683	ENSMUSG00000068762	3	107938847	107943749	-1	0	3	0	4	3	4	0	0	0	2	0	D3YVP8	
ENSMUST00000106684	ENSMUSG00000068762	3	107938847	107943749	-1	0	0	0	0	0	0	0	0	0	0	0	G5E8M7	
ENSMUST00000106685	ENSMUSG00000068762	3	107938847	107943749	-1	8	4	8	5	2	0	0	0	0	0	0		O35660
ENSMUST00000106686						10	5	21	10	10	0	18	30	28	4	69		
ENSMUST00000106687	ENSMUSG00000004035	3	107926334	107931817	-1	0	0	1	4	3	0	2	0	0	0	1	D3YVP6	
ENSMUST00000106688	ENSMUSG00000004035	3	107926334	107931817	-1	1	0	3	0	3	0	0	0	0	0	0	D3YVP5	
ENSMUST00000106689	ENSMUSG00000041895	11	109573331	109611967	-1	8	7	2	15	2	0	8	33	35	0	51	B1AT64	
ENSMUST00000106690	ENSMUSG00000034645	4	108181934	108217922	-1	11	11	10	13	13	9	1	0	0	0	0		A2BFL2
ENSMUST00000106691	ENSMUSG00000028601	4	108165437	108179308	1	0	0	0	0	0	0	0	0	0	2	0	F6Z5N5	
ENSMUST00000106696	ENSMUSG00000020604	11	109473374	109573330	1	8	6	15	10	8	11	0	14	7	33	13		Q3TYD4
ENSMUST00000106697	ENSMUSG00000020604	11	109473374	109573330	1	6	0	27	17	25	0	589	1961	1190	472	914		Q3TYD4
ENSMUST00000106701	ENSMUSG00000028603	4	108043839	108144998	-1	9	6	3	9	1	0	756	2941	1203	3377	888		P32020
ENSMUST00000106702	ENSMUSG00000020611	11	109362831	109401369	1	1	0	1	125	6	1	159	220	124	69	68	Q9D034	
ENSMUST00000106703	ENSMUSG00000078604	3	107631322	107633090	1	1	2	6	27	1	1	0	0	0	0	0	F6Z5I4	
ENSMUST00000106704	ENSMUSG00000020599	11	109225355	109298129	-1	102	107	288	100	72	43	2	5	2	0	6	A2A6V9	
ENSMUST00000106706	ENSMUSG00000020599	11	109225355	109298129	-1	3	6	11	2	6	6	1	0	0	0	0	Q3UUR0	O54828
ENSMUST00000106708	ENSMUSG00000028600	4	108014791	108096445	-1	16	0	0	4	0	0	0	0	0	0	0		Q7TQ62
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ENSMUST00000106710	ENSMUSG00000078605	11	109139291	109144369	-1	4	11	7	16	8	1	0	0	0	0	0	A2A6V5	
ENSMUST00000106711	ENSMUSG00000000142	11	108920349	108950783	1	3	4	12	0	15	2	6	4	9	0	7	A2ABR0	
ENSMUST00000106713	ENSMUSG00000008932	4	107968332	108013532	1	37	35	38	18	52	20	0	0	0	0	0	Z4YKJ7	
ENSMUST00000106715	ENSMUSG00000020728	11	108425192	108860615	1	5	0	2	0	0	3	0	0	0	0	0		Q5PR68
ENSMUST00000106718	ENSMUSG00000020728	11	108425192	108860615	1	0	4	0	0	0	0	0	0	0	0	0	Z4YKK6	
ENSMUST00000106719	ENSMUSG00000028607	4	107903981	107923610	-1	0	0	0	0	0	0	0	11	0	0	0	A2A8E8	
ENSMUST00000106720	ENSMUSG00000028607	4	107903981	107923610	-1	4	0	4	0	11	0	0	42	0	2	26	A2A8E7	
ENSMUST00000106722	ENSMUSG00000035901	7	109893780	109960470	-1	17	10	20	0	10	0	636	4310	916	382	1095		
ENSMUST00000106723	ENSMUSG00000027896	3	107291230	107312115	1	2	2	0	0	0	0	0	0	2	0	0		Q8R0M8
ENSMUST00000106724	ENSMUSG00000020728	11	108425192	108860615	1	1	0	13	2	0	0	0	0	0	0	0	Q9DAQ8	
ENSMUST00000106726	ENSMUSG00000028608	4	107889813	107899384	1	0	0	0	5	0	0	36	16	19	121	13	A2A8E2	
ENSMUST00000106727	ENSMUSG00000028608	4	107889813	107899384	1	0	0	0	0	0	2	2	15	7	18	14		Q8BHG2
ENSMUST00000106728	ENSMUSG00000007279	7	109798676	109865679	-1	12	4	0	29	0	10	0	1	0	0	0	D3YVN5	
ENSMUST00000106729	ENSMUSG00000007279	7	109798676	109865679	-1	9	10	13	16	5	0	0	0	0	0	0	D3YVM9	
ENSMUST00000106731	ENSMUSG00000028613	4	107802261	107876840	1	36	26	49	20	27	9	18	70	27	3	43	F6YZZ8	
ENSMUST00000106732	ENSMUSG00000028613	4	107802261	107876840	1	4	0	0	0	0	0	0	0	0	0	0	B1AXJ3	
ENSMUST00000106733	ENSMUSG00000028613	4	107802261	107876840	1	0	0	0	122	0	0	0	0	13	0	0	B1AXJ5	
ENSMUST00000106735	ENSMUSG00000031022	7	109712181	109723850	-1	13	10	22	15	18	5	0	0	0	0	0	Q3UQ01	Q9JJR6
ENSMUST00000106736	ENSMUSG00000056260	3	106684987	106736577	1	0	0	0	0	0	0	39	92	19	107	55	G5E8M8	
ENSMUST00000106737						0	0	0	0	0	0	0	0	0	9	0		
ENSMUST00000106738	ENSMUSG00000034762	4	107434591	107635061	1	17	13	32	14	10	4	1	0	4	0	0	B1ASP5	
ENSMUST00000106739	ENSMUSG00000031026	7	109449006	109508134	-1	52	44	156	68	79	16	1	3	3	1	0	E9PZP2	
ENSMUST00000106741	ENSMUSG00000031026	7	109449006	109508134	-1	0	12	0	26	30	19	0	0	0	0	0	E9QLR8	
ENSMUST00000106742	ENSMUSG00000040373	11	107874605	107915055	-1	22	12	15	2	35	0	0	0	0	0	0	Q544Q4	Q8VHW4
ENSMUST00000106745	ENSMUSG00000031027	7	109279223	109439081	-1	0	9	0	0	0	0	0	0	0	0	0		Q924X7
ENSMUST00000106746	ENSMUSG00000020721	11	107547930	107693826	1	65	34	108	89	81	44	133	388	330	16	262		Q6DFV5
ENSMUST00000106748	ENSMUSG00000034785	4	107291465	107307169	-1	0	0	0	0	0	0	0	0	0	0	1	D3YVM7	
ENSMUST00000106749	ENSMUSG00000063172	4	107253593	107279938	1	0	1	3	0	0	0	0	54	13	37	0		Q9D6H2
ENSMUST00000106750	ENSMUSG00000020720	11	107479484	107504362	1	0	0	0	0	0	0	98	692	228	307	163	B1AT36	
ENSMUST00000106752	ENSMUSG00000020720	11	107479484	107504362	1	4	5	7	12	8	6	3	5	0	6	0	Q3TRH2	
ENSMUST00000106753	ENSMUSG00000028618	4	107178399	107200996	1	0	0	0	22	6	0	0	35	10	0	0	D3YVM2	
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ENSMUST00000106756	ENSMUSG00000028621	4	107066988	107088268	1	0	0	0	0	0	0	2	3	0	6	5		B1AS42
ENSMUST00000106757	ENSMUSG00000018433	11	107166663	107189381	-1	26	22	35	0	35	23	0	184	0	57	0		Q8BJW5
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ENSMUST00000106760	ENSMUSG00000028621	4	107066988	107088268	1	0	0	0	0	0	0	0	0	0	0	2	B1AS43	
ENSMUST00000106762	ENSMUSG00000040481	11	107033081	107132127	-1	0	0	0	91	0	0	0	0	0	0	0	A2A655	
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ENSMUST00000106766	ENSMUSG00000078606	7	105895139	105953967	-1	0	0	0	0	0	0	509	1324	942	968	1057		Q80SU7
ENSMUST00000106768	ENSMUSG00000018362	11	106988629	106999541	-1	2	2	0	2	0	2	0	0	0	0	0	A2A602	
ENSMUST00000106769	ENSMUSG00000045576	3	104864005	104930064	1	10	9	31	230	20	8	132	16	7	0	143		Q8K4P7
ENSMUST00000106770	ENSMUSG00000047502	4	106680417	106730925	-1	25	17	54	36	34	16	0	0	0	0	0		A2AVR2
ENSMUST00000106772	ENSMUSG00000025413	4	106662256	106678944	-1	0	0	0	0	3	1	0	0	0	4	0	A2AVQ9	
ENSMUST00000106774	ENSMUSG00000002227	3	104794836	104818563	-1	25	0	27	80	0	27	18	125	38	0	40	D3YVL0	
ENSMUST00000106775	ENSMUSG00000002227	3	104794836	104818563	-1	0	0	10	0	0	1	0	0	0	0	0	D3YVL0	
ENSMUST00000106776	ENSMUSG00000030882	7	105640562	105721799	1	1	0	0	3	3	2	2	30	8	5	2	Q9CX41	
ENSMUST00000106778						1	0	0	0	0	0	17	243	38	0	71		
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ENSMUST00000106780	ENSMUSG00000089847	7	105640056	105655748	1	0	0	0	0	0	0	14	69	13	7	10		Q9WV96
ENSMUST00000106781	ENSMUSG00000043572	4	106651069	106655282	1	26	10	6	24	35	9	0	4	0	0	7	A8Y5T6	
ENSMUST00000106782	ENSMUSG00000043572	4	106651069	106655282	1	1	5	3	14	3	1	0	0	0	0	0	A2AVQ7	
ENSMUST00000106783	ENSMUSG00000089847	7	105640056	105655748	1	33	29	100	194	56	38	40	238	65	8	57		Q9WV96
ENSMUST00000106784	ENSMUSG00000089847	7	105640056	105655748	1	0	0	0	0	0	0	0	0	3	0	0	D3YVK6	
ENSMUST00000106785	ENSMUSG00000089847	7	105640056	105655748	1	0	0	0	0	0	0	32	0	21	39	40	D3YVK5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000106786	ENSMUSG00000089847	7	105640056	105655748	1	2	0	2	1	2	1	9	0	4	2	6	D3YVK4	
ENSMUST00000106787	ENSMUSG00000002233	3	104788375	104794459	1	7	0	0	15	7	0	28	21	0	0	0		Q62159
ENSMUST00000106788	ENSMUSG00000054362	4	106590909	106617241	-1	12	8	19	29	17	10	0	0	0	0	0	A0A0F6T326	A2AVQ5
ENSMUST00000106789	ENSMUSG00000036989	7	105604463	105633571	-1	3	0	6	0	7	0	149	211	173	20	128		Q9R1R2
ENSMUST00000106791	ENSMUSG00000036989	7	105604463	105633571	-1	88	36	85	664	124	80	18	43	22	8	60	Q3TDT0	
ENSMUST00000106794	ENSMUSG00000040528	11	106751226	106768794	1	27	27	36	25	34	20	56	294	69	42	30		
ENSMUST00000106796	ENSMUSG00000020717	11	106654217	106750628	-1	3	5	23	0	0	12	0	0	39	0	13		Q08481
ENSMUST00000106798						6	7	6	32	4	2	1	0	0	0	0		
ENSMUST00000106799	ENSMUSG00000020715	11	106394650	106487852	-1	0	2	0	0	0	0	0	0	0	0	3	B1ATQ7	
ENSMUST00000106800	ENSMUSG00000020715	11	106394650	106487852	-1	1	2	0	41	2	1	0	0	2	0	0	B1ARJ5	
ENSMUST00000106801	ENSMUSG00000020715	11	106394650	106487852	-1	11	3	8	29	2	4	3	7	5	2	27	Q3TBZ5	Q9EQY0
ENSMUST00000106803	ENSMUSG00000078612	4	104913456	105016863	1	0	0	0	68	33	0	0	0	0	0	0	E9PZ08	
ENSMUST00000106804	ENSMUSG00000078612	4	104913456	105016863	1	13	16	40	0	0	11	0	1	0	1	0		A2A995
ENSMUST00000106805	ENSMUSG00000078611	7	105375098	105378287	1	8	0	4	7	6	0	4	0	4	0	25	D3YVJ1	
ENSMUST00000106806						0	0	0	6	0	0	82	80	8	14	36		
ENSMUST00000106808	ENSMUSG00000035031	4	104815679	104876398	-1	39	0	11	0	53	23	1	4	2	9	4	A2A998	
ENSMUST00000106809						8	4	8	6	2	0	10	20	3	2	13		
ENSMUST00000106813	ENSMUSG00000001029	11	106377656	106388075	-1	0	0	0	0	0	0	13	14	17	5	53	G5E8M9	
ENSMUST00000106814	ENSMUSG00000062369	7	104840257	104842603	-1	15	4	5	0	0	2	0	0	0	0	0	E9QMF1	
ENSMUST00000106816	ENSMUSG00000009210	11	106365472	106377558	1	0	0	0	2	0	4	0	0	0	0	0		B1ARI9
ENSMUST00000106822	ENSMUSG00000044165	3	103832601	103854618	1	17	10	50	21	13	10	17	6	28	54	28	B0V3P6	
ENSMUST00000106823	ENSMUSG00000032952	3	103809520	103822025	1	9	0	0	0	0	8	0	0	0	0	0	B0V3P4	
ENSMUST00000106824	ENSMUSG00000032952	3	103809520	103822025	1	5	10	15	56	13	0	84	110	88	118	216	B0V3P3	
ENSMUST00000106826	ENSMUSG00000028519	4	103619359	104744844	1	0	2	0	5	3	0	0	0	0	0	0		P97318
ENSMUST00000106827	ENSMUSG00000028519	4	103619359	104744844	1	0	0	0	0	1	0	0	0	0	0	0		P97318
ENSMUST00000106828	ENSMUSG00000078616	7	104382065	104390586	-1	9	7	4	2	7	8	4	9	3	11	37	D3YVI9	
ENSMUST00000106830	ENSMUSG00000028519	4	103619359	104744844	1	18	13	96	18	31	14	0	0	0	0	0	B2RRQ8	P97318
ENSMUST00000106831	ENSMUSG00000052749	7	104355382	104369884	-1	1	0	0	0	0	0	192	2581	687	619	1311	D3YVI7	
ENSMUST00000106832	ENSMUSG00000027845	3	103800605	103809444	-1	48	47	78	73	53	45	1	0	5	0	40		Q8C7W7
ENSMUST00000106834	ENSMUSG00000027845	3	103800605	103809444	-1	0	0	0	0	0	0	201	0	311	51	241		Q8C7W7
ENSMUST00000106837	ENSMUSG00000066258	7	104299894	104315466	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVI1	
ENSMUST00000106839	ENSMUSG00000066258	7	104299894	104315466	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000106841						4	3	0	2	8	1	0	146	10	0	17		
ENSMUST00000106843	ENSMUSG00000078619	11	106263179	106272972	-1	4	0	29	5	18	2	952	2136	646	97	432		Q99JR8
ENSMUST00000106845	ENSMUSG00000008730	3	103739815	103791563	-1	3	0	0	0	7	0	1232	0	52	0	0		O88904
ENSMUST00000106847	ENSMUSG00000090215	7	104300230	104336909	1	0	2	4	0	0	0	43	304	82	30	103	K7N6K2	
ENSMUST00000106848	ENSMUSG00000056144	7	104244457	104340693	1	3	0	0	0	0	0	0	10	0	0	0	E9PYZ4	
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ENSMUST00000106855	ENSMUSG00000028522	4	103114390	103165754	1	0	0	0	0	0	0	49	158	468	117	183		Q5UAK0
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ENSMUST00000106860	ENSMUSG00000033014	3	103279293	103358775	1	34	39	51	161	43	18	80	185	83	95	128	E9QME5	
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ENSMUST00000106863	ENSMUSG00000042219	7	103928825	103929784	1	1	4	11	8	2	4	0	0	0	0	0	F8VPJ9	
ENSMUST00000106864	ENSMUSG00000101488	7	103906441	103907388	1	4	2	2	2	2	3	0	0	0	0	0	E9PYY9	
ENSMUST00000106865	ENSMUSG00000078622	11	106197408	106216344	-1	0	0	0	0	0	0	34	244	125	203	70		Q9D024
ENSMUST00000106866	ENSMUSG00000078621	7	103839145	103840427	-1	2	3	3	1	1	0	0	0	0	0	0	B2RVB7	
ENSMUST00000106867	ENSMUSG00000069631	11	106163330	106202168	-1	57	41	183	93	76	27	15	12	25	3	23	B1AR89	
ENSMUST00000106868	ENSMUSG00000035126	4	103038065	103114555	-1	0	0	11	140	0	3	0	0	0	0	6		E9PYY5
ENSMUST00000106869	ENSMUSG00000066090	4	103017872	103026842	-1	1	0	1	0	0	1	0	0	0	0	1	A2AIY3	
ENSMUST00000106875	ENSMUSG00000040699	11	106156256	106160860	-1	6	7	16	169	15	5	24	24	29	4	11		Q8BGB5
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ENSMUST00000106880	ENSMUSG00000050281	7	103754587	103755652	-1	2	4	4	3	11	5	0	0	0	0	0	Q9EQQ7	
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ENSMUST00000106886	ENSMUSG00000047544	7	103564324	103565277	-1	1	6	5	0	7	4	0	0	0	0	1	Q3KPB0	
ENSMUST00000106888	ENSMUSG00000078624	7	103550368	103555504	1	8784	12558	17477	7090	9200	4010	67	516	177	51	186	E9PYB4	
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ENSMUST00000106893	ENSMUSG00000073956	7	103184803	103187541	1	4	9	14	7	0	2	0	0	0	0	0	E9PYB3	
ENSMUST00000106899	ENSMUSG00000026180	1	74153989	74161246	1	921	842	3633	1244	1168	666	15466	104043	33430	11078	29890		P35343
ENSMUST00000106901	ENSMUSG00000028525	4	102087543	102607259	1	6	8	7	8	3	2	0	15	2	6	13	B1AWD1	
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ENSMUST00000106904	ENSMUSG00000028525	4	102087543	102607259	1	0	0	0	0	0	1	0	0	0	0	0	B1AWC8	
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ENSMUST00000106913	ENSMUSG00000030966	7	102557922	102565469	-1	18	0	0	33	0	10	39	101	0	91	0	Q3U7K7	
ENSMUST00000106914	ENSMUSG00000078625	4	101986626	101990053	1	83	67	73	161	92	57	7	41	15	3	9	B1AUV7	
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ENSMUST00000106921	ENSMUSG00000057722	4	101717404	101815352	1	20	18	20	27	18	18	0	11	0	20	16	Q3US58	P48356
ENSMUST00000106923	ENSMUSG00000073982	7	102239123	102250123	-1	21	8	10	4	6	22	200	127	49	21	76	Q3UDZ1	P84096
ENSMUST00000106925	ENSMUSG00000027859	3	102469919	102521013	1	0	0	20	0	0	0	0	0	0	3	0	Q6LDU8	
ENSMUST00000106927	ENSMUSG00000035212	4	101647718	101659364	1	17	12	30	0	0	12	0	402	12	0	15		O89013
ENSMUST00000106928	ENSMUSG00000033147	3	101855776	101924453	-1	3	1	17	5	0	1	327	220	455	6	221		Q504N2
ENSMUST00000106929	ENSMUSG00000028528	4	101496648	101642799	1	0	0	0	0	0	0	0	7	7	0	0		Q80TZ3
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ENSMUST00000106934	ENSMUSG00000070424	7	102096879	102102845	-1	2	3	0	3	2	0	0	0	0	0	0		P70352
ENSMUST00000106935	ENSMUSG00000070424	7	102096879	102102845	-1	0	2	0	0	0	1	0	0	0	0	0	B7ZMV7	P70352

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000106937	ENSMUSG00000070424	7	102096879	102102845	-1	13	9	24	18	4	8	0	0	0	0	0		P70352
ENSMUST00000106939	ENSMUSG00000020694	11	105178807	105283959	1	29	27	36	32	36	22	12	73	35	5	9		O55047
ENSMUST00000106941	ENSMUSG00000020694	11	105178807	105283959	1	8	6	15	967	38	16	0	0	0	21	0	B1ASU9	
ENSMUST00000106945	ENSMUSG00000028527	4	101419277	101466995	1	17	0	56	0	0	0	3	16	10	1	4	Q3U489	Q9WUR9
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ENSMUST00000106950	ENSMUSG00000099481	7	102065511	102083765	1	0	1	0	0	0	1	0	0	25	0	9	E9PVR2	
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ENSMUST00000106955	ENSMUSG00000035275	4	101068983	101152370	1	11	13	7	29	19	9	0	2	0	0	1	B1ASP0	
ENSMUST00000106956	ENSMUSG00000061086	11	104550663	104595753	1	2	5	17	6	7	0	0	0	0	0	0	Q9CZ19	
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ENSMUST00000106961	ENSMUSG00000020687	11	104502745	104550620	-1	10	13	32	40	10	7	2	8	19	0	44	Q8R568	
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ENSMUST00000106963	ENSMUSG00000064307	7	101912984	101933895	-1	4	0	0	8	4	4	0	0	3	0	0		Q9DAK8
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ENSMUST00000106969	ENSMUSG00000078630	7	101898373	101906359	-1	19	7	28	6	5	3	0	6	5	0	0		A1Y9I9
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ENSMUST00000106971	ENSMUSG00000018412	11	104333229	104468861	-1	34	20	63	62	25	13	561	881	1090	70	620	A2A5Y4	
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ENSMUST00000106980	ENSMUSG00000033233	3	100922202	100936920	1	20	7	40	14	11	7	4	23	0	0	0		Q6PFY8
ENSMUST00000106981	ENSMUSG00000001827	7	101858331	101870788	-1	1	7	0	4	7	2	0	0	0	1	1		P35846
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ENSMUST00000107004	ENSMUSG00000073792	4	99715664	99763460	1	0	0	0	0	0	0	2	0	0	0	0	A2BDY0	
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ENSMUST00000107010	ENSMUSG00000032812	7	101348067	101412586	1	0	0	40	229	0	0	3034	1341	2759	85	1909		Q4LDD4
ENSMUST00000107013	ENSMUSG00000020946	11	103676849	103697898	-1	0	0	4	0	2	0	46	6	94	158	46	A2A9I0	
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ENSMUST00000107021	ENSMUSG00000063730	3	98709255	98724543	-1	0	0	0	0	0	0	0	0	0	0	0		P26149
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ENSMUST00000107023	ENSMUSG00000034255	11	103331497	103363692	-1	0	1	0	15	0	1	0	0	0	0	0	A2AB70	
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ENSMUST00000107027	ENSMUSG00000055805	11	103171107	103198901	1	6	10	31	0	36	7	4429	2476	2516	137	2375	A2AB60	
ENSMUST00000107029	ENSMUSG00000061859	4	98395785	98719603	1	3	5	0	0	23	0	15	13	4	0	15		Q63ZW7
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ENSMUST00000107033	ENSMUSG00000061859	4	98395785	98719603	1	7	4	5	2	3	1	0	3	0	0	0	A2ADS8	
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ENSMUST00000107037	ENSMUSG00000043372	11	103132429	103139876	1	0	0	2	8	14	3	8	20	8	6	10		Q3TVI4
ENSMUST00000107038	ENSMUSG00000038170	3	97689824	97888707	-1	0	0	0	96	2	0	0	0	0	0	0	Q3UR03	
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ENSMUST00000107045	ENSMUSG00000030701	7	100642892	100662414	-1	0	0	0	3	0	2	0	1	0	0	0		Q9QYE9
ENSMUST00000107046	ENSMUSG00000030701	7	100642892	100662414	-1	15	3	47	12	6	5	0	0	3	0	2	Q3TP62	Q9QYE9
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ENSMUST00000107048	ENSMUSG00000030704	7	100607410	100641268	1	0	5	5	29	0	10	1115	3058	477	68	38	D3YV69	
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ENSMUST00000107051	ENSMUSG00000028563	4	98355370	98383306	-1	3	2	8	32	3	5	14	42	6	0	8	A0A0A0MQC8	
ENSMUST00000107053						1	4	1	0	2	0	72	247	74	339	64		
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ENSMUST00000107059	ENSMUSG00000032942	7	100472990	100486432	1	2	0	0	0	0	0	0	1	0	1	0	B2RTM2	P56501
ENSMUST00000107060	ENSMUSG00000020929	11	102838473	102880985	-1	0	0	0	33	0	0	493	432	478	0	434	Q543F1	O08810
ENSMUST00000107062	ENSMUSG00000028565	4	97772734	98118874	1	0	0	0	0	0	0	29	76	12	0	20	B1AUC0	
ENSMUST00000107067	ENSMUSG00000048747	4	97568133	97778078	-1	0	0	0	0	0	0	0	0	0	0	0	A2AK50	
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ENSMUST00000107069	ENSMUSG00000038298	3	96829284	96870926	1	0	0	2	12	7	0	1	0	1	0	0		
ENSMUST00000107070	ENSMUSG00000038298	3	96829284	96870926	1	14	0	0	0	0	11	0	0	0	0	0		
ENSMUST00000107071	ENSMUSG00000078639	4	96723647	96785186	-1	8	5	12	11	6	7	0	0	0	0	0		A2AGB2
ENSMUST00000107072	ENSMUSG00000020928	11	102835849	102838040	1	0	0	0	0	0	0	0	0	0	0	0		Q99JY6
ENSMUST00000107073	ENSMUSG00000020928	11	102835849	102838040	1	5	1	5	4	1	2	0	0	0	0	0		Q99JY6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107074	ENSMUSG00000038304	3	96798763	96829351	-1	12	5	0	0	7	0	0	0	0	0	0		O88875
ENSMUST00000107075	ENSMUSG00000034520	11	102799579	102819700	-1	13	12	20	0	21	11	1	0	3	4	10		P28229
ENSMUST00000107076	ENSMUSG00000028101	3	96696384	96706070	1	0	1	0	31	10	0	187	181	186	0	5		O54714
ENSMUST00000107077	ENSMUSG00000028101	3	96696384	96706070	1	13	3	34	0	0	9	293	739	260	46	345		O54714
ENSMUST00000107078	ENSMUSG00000028571	4	96027534	96077546	-1	0	1	0	0	0	0	0	0	0	0	0	B1AWM4	
ENSMUST00000107080	ENSMUSG00000078640	11	102576398	102579461	-1	5	5	0	2	6	1	0	0	0	0	0	A6PWP4	
ENSMUST00000107081	ENSMUSG00000078640	11	102576398	102579461	-1	2	0	0	0	0	1	0	0	0	0	0	A6PWP4	
ENSMUST00000107083	ENSMUSG00000028572	4	95967240	96025413	1	2	6	0	48	3	1	0	0	0	0	0	Q8BJ23	
ENSMUST00000107084	ENSMUSG00000030732	7	100006404	100034728	1	3	8	11	9	6	8	0	0	0	0	0	D3YV59	
ENSMUST00000107086	ENSMUSG00000030737	7	99657804	99711340	-1	19	10	30	17	25	4	0	0	1	7	3		Q8BXB6
ENSMUST00000107088	ENSMUSG00000030737	7	99657804	99711340	-1	4	4	11	22	7	13	0	0	0	0	0	Q3V1K7	
ENSMUST00000107091	ENSMUSG00000028573	4	95557507	95926939	1	0	0	0	0	0	0	0	0	0	15	9	A2AJL4	
ENSMUST00000107094	ENSMUSG00000052684	4	95049034	95052222	-1	19	15	26	785	46	17	1886	6325	3962	389	1701	Q52L79	P05627
ENSMUST00000107096	ENSMUSG00000030744	7	99477896	99483738	-1	0	0	0	28	7	2	5279	8193	3463	14300	2155	D3YV43	
ENSMUST00000107097	ENSMUSG00000028575	4	94907267	94928843	-1	3	4	0	0	0	0	0	0	0	0	0		Q9D9V2
ENSMUST00000107098	ENSMUSG00000018677	11	102402985	102407946	-1	0	0	0	0	6	0	0	0	0	0	0	A2A697	
ENSMUST00000107099	ENSMUSG00000015943	3	96196588	96219709	-1	9	6	4	4	0	0	0	0	0	0	0		Q9D8S9
ENSMUST00000107100	ENSMUSG00000055407	7	99267447	99337137	1	0	0	48	67	13	0	10	16	9	4	19		Q7TSJ2
ENSMUST00000107101	ENSMUSG00000049799	4	94636653	94650144	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BZT5
ENSMUST00000107102	ENSMUSG00000006575	11	102393403	102402555	1	0	0	0	0	0	0	0	1	0	0	0		O08576
ENSMUST00000107103	ENSMUSG00000006575	11	102393403	102402555	1	2	0	6	0	0	4	0	0	0	0	0		O08576
ENSMUST00000107104	ENSMUSG00000028576	4	94614491	94693229	1	2	4	4	17	6	1	0	0	0	0	0	B1AWG1	
ENSMUST00000107105	ENSMUSG00000006575	11	102393403	102402555	1	2	7	0	37	5	0	0	0	0	0	0		O08576
ENSMUST00000107107	ENSMUSG00000028577	4	94567514	94603244	-1	10	0	8	76	8	3	200	1238	529	148	280		P27612
ENSMUST00000107108	ENSMUSG00000028533	4	92144329	92147234	-1	4	0	0	0	0	2	0	0	0	0	0		A6PWV3
ENSMUST00000107109	ENSMUSG00000008489	4	91250763	91400785	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UR02	
ENSMUST00000107110	ENSMUSG00000008489	4	91250763	91400785	-1	0	0	0	0	0	4	0	0	0	0	0	Q80UJ0	
ENSMUST00000107111	ENSMUSG00000008489	4	91250763	91400785	-1	1	2	0	0	4	2	0	0	0	0	0	B1AXZ0	
ENSMUST00000107112	ENSMUSG00000035547	7	98121559	98178274	-1	9	5	29	0	9	2	9	0	0	0	5	Q3TPL4	O08688
ENSMUST00000107115	ENSMUSG00000020923	11	102304560	102319742	-1	0	0	0	0	0	0	0	0	0	0	16	A2AWT6	
ENSMUST00000107116	ENSMUSG00000008489	4	91250763	91400785	-1	0	4	3	0	2	0	0	0	0	0	0	B1AXZ5	
ENSMUST00000107117	ENSMUSG00000020923	11	102304560	102319742	-1	0	0	0	21	0	0	0	49	41	0	45	A2AWT6	
ENSMUST00000107118	ENSMUSG00000008489	4	91250763	91400785	-1	2	2	12	19	6	0	0	0	0	0	0	B1AXZ6	
ENSMUST00000107119	ENSMUSG00000020923	11	102304560	102319742	-1	0	0	0	5	1	0	355	726	455	175	362	A2AWT6	
ENSMUST00000107120	ENSMUSG00000008489	4	91250763	91400785	-1	0	0	0	0	0	0	0	0	0	0	0	B1AXZ4	
ENSMUST00000107122	ENSMUSG00000030761	7	98051060	98119524	-1	0	0	0	1	4	3	0	1	3	0	2	Q5MJ56	
ENSMUST00000107123	ENSMUSG00000020923	11	102304560	102319742	-1	0	0	0	0	0	0	410	735	615	83	583	A2AWT5	
ENSMUST00000107124	ENSMUSG00000008489	4	91250763	91400785	-1	3	2	3	7	7	0	0	0	0	0	0	Q3UR02	
ENSMUST00000107127	ENSMUSG00000030761	7	98051060	98119524	-1	12	0	0	0	0	0	0	0	0	0	0		P97479
ENSMUST00000107128	ENSMUSG00000030761	7	98051060	98119524	-1	43	49	114	75	86	0	34	0	0	6	37		P97479
ENSMUST00000107129	ENSMUSG00000070902	4	90218820	90225702	1	4	0	7	7	4	2	0	0	0	0	0	A2AML7	
ENSMUST00000107130						4	5	14	5	5	2	0	0	0	0	0		
ENSMUST00000107131	ENSMUSG00000044303	4	89274471	89294653	-1	4	0	2	114	7	2	0	0	0	0	4		Q64364
ENSMUST00000107132	ENSMUSG00000059995	11	102289300	102296631	-1	0	0	0	0	0	0	0	0	0	0	0		A2AWT3
ENSMUST00000107134	ENSMUSG00000059995	11	102289300	102296631	-1	31	16	75	7	17	0	1446	836	841	90	508		A2AWT3
ENSMUST00000107142	ENSMUSG00000038330	4	88627320	88634411	-1	0	0	3	0	0	0	0	0	0	0	0	B1AWZ0	
ENSMUST00000107143	ENSMUSG00000038330	4	88627320	88634411	-1	0	5	0	6	10	3	0	0	0	0	0	B1AWY9	
ENSMUST00000107147	ENSMUSG00000038368	4	88094629	88411011	1	6	1	10	4	3	1	12	54	25	20	51		A2AKG8
ENSMUST00000107148						48	44	222	59	41	16	0	6	0	0	3		
ENSMUST00000107150	ENSMUSG00000008855	11	102194432	102230166	-1	0	0	0	0	0	0	1163	714	783	2	295	B7ZDF7	
ENSMUST00000107151	ENSMUSG00000008855	11	102194432	102230166	-1	15	8	38	32	18	4	7	57	14	3	21	A2AWS5	
ENSMUST00000107152	ENSMUSG00000008855	11	102194432	102230166	-1	0	0	0	0	0	0	1308	1599	1163	177	735	Q3UJF1	
ENSMUST00000107153	ENSMUSG00000035623	7	97579889	97692778	1	37	33	110	22	35	21	84	345	155	38	132	E9Q4Y2	
ENSMUST00000107154	ENSMUSG00000028109	3	95559677	95587671	1	0	0	0	0	0	0	0	0	0	0	0		Q9D5T7
ENSMUST00000107155	ENSMUSG00000037996	4	86983124	87230477	-1	2	0	4	0	0	1	0	0	0	0	0	B1AXF3	
ENSMUST00000107156	ENSMUSG00000020922	11	102162497	102185296	-1	21	14	59	0	14	6	0	0	0	0	0	A0A0A0MQC9	
ENSMUST00000107157	ENSMUSG00000037996	4	86983124	87230477	-1	2	2	57	52	12	1	0	0	0	0	0	Q8BUN9	
ENSMUST00000107158	ENSMUSG00000037996	4	86983124	87230477	-1	36	35	0	0	41	14	0	0	0	0	0	Q14BI1	
ENSMUST00000107159	ENSMUSG00000018995	7	96951505	97064758	1	4	0	2	91	9	9	51	85	191	84	95	D3YV21	
ENSMUST00000107160	ENSMUSG00000015522	3	95434388	95497240	1	0	0	1	26	3	0	8	0	2	0	1	D3YV20	
ENSMUST00000107161	ENSMUSG00000015522	3	95434388	95497240	1	46	46	83	0	0	37	0	296	155	0	83	Q8CEC2	
ENSMUST00000107162	ENSMUSG00000048078	7	96171246	96911093	1	19	34	24	11	41	0	0	0	0	0	0		Q3UHK6
ENSMUST00000107163	ENSMUSG00000017309	11	102041509	102055620	1	11	10	22	51	31	0	29	41	0	0	20		Q1ERP8
ENSMUST00000107164	ENSMUSG00000017309	11	102041509	102055620	1	20	0	41	0	0	0	0	0	0	0	0		Q1ERP8
ENSMUST00000107165	ENSMUSG00000048078	7	96171246	96911093	1	38	14	214	23	69	41	0	0	0	0	0		Q3UHK6
ENSMUST00000107166	ENSMUSG00000048078	7	96171246	96911093	1	62	44	36	219	54	26	3	4	7	5	34		Q3UHK6
ENSMUST00000107167	ENSMUSG00000052373	11	101999652	102028461	-1	48	34	74	237	81	48	0	3	2	2	4	B1AQF7	
ENSMUST00000107168	ENSMUSG00000052373	11	101999652	102028461	-1	35	28	23	23	44	9	0	1	0	0	0	Q6XE40	
ENSMUST00000107170	ENSMUSG00000015697	3	95323525	95357202	-1	13	0	12	13	0	0	274	593	457	0	452	D3YYC3	
ENSMUST00000107171	ENSMUSG00000015697	3	95323525	95357202	-1	0	0	0	0	0	0	0	140	60	112	40	G5E8N3	
ENSMUST00000107172	ENSMUSG00000003518	11	101971143	101987013	-1	12	23	52	0	16	0	0	0	0	0	0		Q9D7X3
ENSMUST00000107173	ENSMUSG00000003518	11	101971143	101987013	-1	0	0	0	4	0	0	0	0	0	0	0	B1AQF4	
ENSMUST00000107176	ENSMUSG00000017724	11	101769742	101785371	-1	5	9	0	52	6	0	0	0	0	0	0	A2A5C2	
ENSMUST00000107177						43	0	65	57	54	22	1	0	2	1	5		
ENSMUST00000107178	ENSMUSG00000066113	4	86053915	86428385	1	0	33	0	0	0	0	0	0	0	0	0	E9PWW5	
ENSMUST00000107179	ENSMUSG00000030643	7	92741603	92837117	1	2	3	4	0	2	3	1	0	4	0	0	D3YV16	
ENSMUST00000107180	ENSMUSG00000030643	7	92741603	92837117	1	0	0	3	0	0	0	0	0	0	9	9	Q0PD24	Q923S9
ENSMUST00000107183	ENSMUSG00000015702	3	95296096	95307176	-1	7	5	2	0	0	10	0	0	0	0	0		Q9JHQ0
ENSMUST00000107184	ENSMUSG00000028488	4	85205126	85639195	1	0	1	2	0	0	0	0	0	0	0	0	A2ALV1	
ENSMUST00000107187	ENSMUSG00000038712	3	95281345	95296166	1	0	7	5	19	22	8	1413	2482	1362	312	1136	B7ZMR0	Q76LS9
ENSMUST00000107188	ENSMUSG00000028488	4	85205126	85639195	1	9	1	6	71	12	6	0	0	0	0	0	A2ALV3	
ENSMUST00000107189	ENSMUSG00000028488	4	85205126	85639195	1	62	71	268	106	73	45	0	3	0	0	4	Q8BXU5	
ENSMUST00000107190	ENSMUSG00000038070	4	84884309	85131921	1	0	0	0	0	0	1	2	2	0	0	0		A2AM05
ENSMUST00000107193	ENSMUSG00000052572	7	91090706	92447003	1	4	15	3	0	8	5	0	0	0	0	0	D3YUZ8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107194	ENSMUSG00000034947	11	101582242	101591788	1	0	0	0	0	0	0	0	0	3	0	0	A2A4N0	
ENSMUST00000107195	ENSMUSG00000028115	3	95241271	95251193	-1	5	1	17	4	8	8	4	13	4	0	13	E9QME1	
ENSMUST00000107196	ENSMUSG00000052572	7	91090706	92447003	1	0	0	0	0	0	0	0	0	0	0	0		Q91XM9
ENSMUST00000107197	ENSMUSG00000068860	3	95236920	95241598	-1	0	0	3	93	0	0	0	4	0	0	0	D3YUZ7	
ENSMUST00000107198	ENSMUSG00000028487	4	84275095	84675275	-1	0	13	0	0	0	8	0	0	0	0	1	H3BIU2	
ENSMUST00000107199	ENSMUSG00000046722	3	95228732	95236409	1	0	0	0	0	0	0	278	813	58	77	125	D3YUZ5	
ENSMUST00000107200	ENSMUSG00000046722	3	95228732	95236409	1	0	0	4	1	2	5	0	78	19	0	15	D3YUZ5	
ENSMUST00000107201	ENSMUSG00000046722	3	95228732	95236409	1	0	0	0	23	2	0	2066	215	1706	519	1197		Q8BHL7
ENSMUST00000107202						234	144	257	166	313	105	9	35	5	3	9		
ENSMUST00000107204	ENSMUSG00000038766	3	95181766	95217916	-1	2	3	3	0	1	4	0	0	3	0	2	Q8C2T8	
ENSMUST00000107205	ENSMUSG00000051451	7	90442729	90447717	1	3	0	0	180	11	4	5	12	39	9	22	D3YUZ4	
ENSMUST00000107206	ENSMUSG00000051451	7	90442729	90447717	1	3	0	6	6	5	0	166	355	60	9	59		Q91ZR3
ENSMUST00000107207						3	9	42	5	10	4	0	0	0	0	0		
ENSMUST00000107208	ENSMUSG00000017119	11	101552149	101581951	1	0	0	0	0	0	0	46	419	191	99	52	A2A4N5	
ENSMUST00000107209	ENSMUSG00000038766	3	95181766	95217916	-1	0	0	0	0	0	0	297	447	842	0	375		P81069
ENSMUST00000107210	ENSMUSG00000030616	7	90348699	90410439	1	0	0	0	0	18	6	0	0	4	3	10		Q99N50
ENSMUST00000107211	ENSMUSG00000030616	7	90348699	90410439	1	21	10	0	10	0	0	0	0	0	0	0		Q99N50
ENSMUST00000107212	ENSMUSG00000017119	11	101552149	101581951	1	14	0	0	0	0	0	0	134	0	0	0	A2A4N7	
ENSMUST00000107213	ENSMUSG00000017119	11	101552149	101581951	1	0	0	0	0	0	0	413	1395	1203	300	976	A2A4N8	
ENSMUST00000107214	ENSMUSG00000028484	4	83455680	83486459	-1	0	0	0	0	0	0	67	122	0	0	53	A2BI12	
ENSMUST00000107215	ENSMUSG00000028484	4	83455680	83486459	-1	3	4	1	2	0	3	0	205	120	22	130		Q99JF8
ENSMUST00000107217	ENSMUSG00000038777	3	95160457	95174024	1	2	0	7	902	4	0	3	0	0	0	0	G5E8N4	
ENSMUST00000107218	ENSMUSG00000017119	11	101552149	101581951	1	5	2	0	0	9	0	0	0	1	0	0	A1L329	P97432
ENSMUST00000107220	ENSMUSG00000030617	7	90223878	90265432	-1	1	3	16	10	4	3	0	0	0	0	0	D3YUZ1	
ENSMUST00000107221	ENSMUSG00000030617	7	90223878	90265432	-1	3	1	6	10	4	0	0	0	0	0	0	D3YUZ0	
ENSMUST00000107227	ENSMUSG00000005628	3	95124476	95129209	1	0	0	0	4	0	0	12	39	0	0	19	Q3UN19	Q9JLH8
ENSMUST00000107229						0	0	2	87	3	4	9	21	13	4	7		
ENSMUST00000107230	ENSMUSG00000059049	4	82897920	83052339	-1	24	4	43	27	13	9	0	0	0	0	0	A2ADN1	Q684R7
ENSMUST00000107231						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000107232	ENSMUSG00000028126	3	95058530	95106930	-1	0	0	0	0	0	18	0	0	0	0	0	D3YUY3	
ENSMUST00000107233	ENSMUSG00000028126	3	95058530	95106930	-1	0	0	45	36	0	0	70	118	184	40	87		P70182
ENSMUST00000107234	ENSMUSG00000030619	7	89954656	89980983	-1	3	8	20	46	8	8	448	2284	723	334	415		Q921E6
ENSMUST00000107236	ENSMUSG00000028126	3	95058530	95106930	-1	20	0	0	0	23	0	121	133	96	0	266		P70182
ENSMUST00000107237	ENSMUSG00000005625	3	95032694	95042614	-1	5	0	3	27	3	0	695	1119	724	430	474		O35226
ENSMUST00000107239	ENSMUSG00000028403	4	82798738	82859958	-1	0	0	1	2	0	0	0	0	5	0	0		Q9D270
ENSMUST00000107245	ENSMUSG00000008575	4	82290173	82705750	-1	0	10	106	50	0	0	0	0	0	0	0	I7HIP8	
ENSMUST00000107246	ENSMUSG00000008575	4	82290173	82705750	-1	0	0	0	0	0	0	0	0	0	0	0	A2BG76	
ENSMUST00000107247	ENSMUSG00000008575	4	82290173	82705750	-1	0	0	0	0	0	0	0	0	0	0	0	A2BG75	
ENSMUST00000107248	ENSMUSG00000008575	4	82290173	82705750	-1	0	0	0	0	0	0	0	0	0	4	8	A2BG77	
ENSMUST00000107249	ENSMUSG00000063316	11	101442298	101445529	1	7	7	9	178	12	13	58	74	58	184	67	Q5BLJ9	P61358
ENSMUST00000107251	ENSMUSG00000038861	3	94974731	95006843	1	6	0	4	6	0	3	0	0	0	0	0		Q8BKC8
ENSMUST00000107252	ENSMUSG00000097487	11	101418812	101425333	-1	1	1	0	0	0	3	2	6	0	0	0	A2A4P5	
ENSMUST00000107253	ENSMUSG00000005774	3	94954075	94961561	1	0	3	6	0	0	0	0	0	0	0	0	Q6DI69	
ENSMUST00000107254	ENSMUSG00000005774	3	94954075	94961561	1	6	0	0	33	5	0	0	0	0	0	0	Q6DI69	
ENSMUST00000107255	ENSMUSG00000005774	3	94954075	94961561	1	7	0	0	0	0	0	0	0	22	0	24		Q9JL61
ENSMUST00000107256	ENSMUSG00000030559	7	88430273	88491466	1	9	8	39	82	14	7	17	56	13	0	5	Q5FW76	Q8QZZ8
ENSMUST00000107257	ENSMUSG00000097239	11	101406664	101424796	-1	3	2	16	1	5	0	0	9	0	0	0	A2A4P3	
ENSMUST00000107258	ENSMUSG00000028402	4	81278500	81442815	-1	0	0	0	0	7	0	0	0	0	0	3	A3KG81	
ENSMUST00000107259	ENSMUSG00000097239	11	101406664	101424796	-1	0	0	0	0	0	0	0	1	0	0	6	A2A4P4	
ENSMUST00000107260	ENSMUSG00000005774	3	94954075	94961561	1	0	3	0	52	3	0	0	2	0	0	0		Q9JL61
ENSMUST00000107262	ENSMUSG00000028402	4	81278500	81442815	-1	6	3	9	7	9	5	0	0	0	0	4	D3YUX2	
ENSMUST00000107263	ENSMUSG00000049583	7	87602544	88134907	1	0	0	10	57	0	0	1	0	0	0	0	E9QMC2	
ENSMUST00000107264	ENSMUSG00000078651	11	101325063	101329702	1	0	0	0	0	0	0	0	0	0	0	0	A2A4I9	
ENSMUST00000107265						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000107266	ENSMUSG00000038902	3	94837567	94882326	1	0	0	5	0	14	0	62	0	107	0	109	D3YUX1	
ENSMUST00000107269	ENSMUSG00000038902	3	94837567	94882326	1	13	25	15	0	0	0	43	297	0	32	1	D3YUW8	
ENSMUST00000107270	ENSMUSG00000038902	3	94837567	94882326	1	18	0	33	52	20	11	0	30	142	0	112	B9EIG6	Q8BZH4
ENSMUST00000107271	ENSMUSG00000001773	7	86719352	86775864	-1	0	4	10	0	0	0	0	0	0	1	1	Q0VDM6	
ENSMUST00000107272	ENSMUSG00000068876	3	94760069	94786492	-1	0	26	81	0	0	24	0	0	4	1	13	D3YUW7	
ENSMUST00000107273	ENSMUSG00000068876	3	94760069	94786492	-1	54	0	13	98	65	0	0	0	0	0	0	E9QMC1	
ENSMUST00000107276	ENSMUSG00000078655	3	94643112	94643600	1	1	0	0	0	0	0	0	0	0	0	0	F6YWI4	
ENSMUST00000107280	ENSMUSG00000078656	11	101253707	101259549	1	0	0	0	4	0	0	0	70	21	0	0	A2A4J8	
ENSMUST00000107282	ENSMUSG00000001240	11	101246028	101259546	1	0	0	0	0	0	0	0	0	0	0	0	F6YPZ1	
ENSMUST00000107283	ENSMUSG00000028136	3	94497544	94582716	-1	0	0	0	116	0	0	35	39	71	2	48		Q3UHD6
ENSMUST00000107284	ENSMUSG00000006920	11	101191115	101226463	-1	1	1	1	57	1	1	13	299	25	4	294		P70351
ENSMUST00000107285	ENSMUSG00000006920	11	101191115	101226463	-1	27	18	38	0	25	11	684	1555	1035	177	692		
ENSMUST00000107287						2	1	11	1	1	1	0	0	0	0	0		
ENSMUST00000107289	ENSMUSG00000028399	4	75941238	78211961	-1	0	12	13	87	12	19	0	0	0	0	0		Q64487
ENSMUST00000107295	ENSMUSG00000017802	11	101096322	101119893	-1	0	19	19	10	20	7	18	79	0	25	0		Q9CQV4
ENSMUST00000107300	ENSMUSG00000078657	3	93144787	93149819	1	15	14	104	10	7	4	0	0	0	0	0	D3YUU6	
ENSMUST00000107301	ENSMUSG00000027913	3	93014205	93015687	-1	0	0	0	19	0	0	0	0	0	0	0	Q6PAI5	
ENSMUST00000107302	ENSMUSG00000017801	11	101087277	101092207	1	0	0	0	22	16	12	250	846	343	86	79	A2BFB1	
ENSMUST00000107303	ENSMUSG00000017801	11	101087277	101092207	1	0	4	11	0	0	0	92	338	76	143	67	A2BFB2	
ENSMUST00000107304	ENSMUSG00000068887	3	92788840	92790514	-1	6	6	14	13	5	0	0	0	0	0	0	D3YUU5	
ENSMUST00000107305	ENSMUSG00000025104	7	81881251	81934473	-1	10	7	6	33	14	9	72	142	90	6	110		Q9JMG7
ENSMUST00000107308	ENSMUSG00000001755	11	101082565	101086619	1	29	9	62	158	27	12	109	61	110	16	73		Q9DBL7
ENSMUST00000107310	ENSMUSG00000093962	4	73916728	73920760	-1	4	2	0	0	4	1	0	1	0	0	0	A2BEJ1	
ENSMUST00000107312	ENSMUSG00000093962	4	73916728	73920760	-1	7	5	0	0	1	6	0	0	0	0	0	A2BEJ2	
ENSMUST00000107318	ENSMUSG00000096333	4	73901907	73905953	-1	4	10	7	7	3	4	0	0	0	0	0	A2BEI5	
ENSMUST00000107319	ENSMUSG00000096333	4	73901907	73905953	-1	3	4	6	24	7	1	0	0	0	0	0	A2BEI6	
ENSMUST00000107320	ENSMUSG00000096750	4	73887066	73891112	-1	4	0	7	0	3	4	0	0	0	0	0	A2BEI7	
ENSMUST00000107321	ENSMUSG00000096750	4	73887066	73891112	-1	3	0	6	0	7	1	0	0	0	0	0	A2BEI8	
ENSMUST00000107322						2	0	3	2	3	0	0	0	0	0	0		
ENSMUST00000107326	ENSMUSG00000096530	4	73872219	73876266	-1	4	10	7	7	3	4	0	0	0	0	0	A2BEI5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107327	ENSMUSG00000096530	4	73872219	73876266	-1	1	2	3	11	4	0	0	0	0	0	0	A2BEI6	
ENSMUST00000107329	ENSMUSG00000001023	3	90608523	90611780	1	0	0	0	0	0	0	0	0	0	0	0	Q149U2	P63084
ENSMUST00000107330	ENSMUSG00000105518	3	90601904	90605885	1	1	4	6	0	3	0	0	0	0	23	4	D3YUT9	
ENSMUST00000107331	ENSMUSG00000074457	3	90537254	90543151	1	0	0	0	0	0	0	0	0	0	0	2	Q9D708	
ENSMUST00000107333	ENSMUSG00000074457	3	90537254	90543151	1	0	0	0	0	3	0	0	0	0	0	0	Q9D708	
ENSMUST00000107334	ENSMUSG00000074457	3	90537254	90543151	1	0	0	0	3	0	0	0	0	0	0	0	Q9D708	
ENSMUST00000107335	ENSMUSG00000074457	3	90537254	90543151	1	0	0	0	0	0	0	0	0	0	0	0	Q9D708	
ENSMUST00000107337	ENSMUSG00000008305	4	72117142	72200919	-1	0	6	1	266	6	0	17	33	11	0	23		Q62440
ENSMUST00000107340	ENSMUSG00000044080	3	90511034	90514392	-1	0	1	0	0	0	0	14	30	17	38	15	D3YUT6	
ENSMUST00000107342	ENSMUSG00000001017	3	90498956	90509498	-1	4	0	7	12	1	6	96	0	200	67	192		Q9CY57
ENSMUST00000107343	ENSMUSG00000001017	3	90498956	90509498	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZMS6	Q9CY57
ENSMUST00000107344	ENSMUSG00000001017	3	90498956	90509498	-1	0	0	0	0	0	0	129	102	0	0	0		Q9CY57
ENSMUST00000107346	ENSMUSG00000001017	3	90498956	90509498	-1	0	0	0	0	0	4	0	0	0	10	0	E9PW20	
ENSMUST00000107348	ENSMUSG00000038763	7	81057600	81105612	1	67	49	212	171	82	43	4	7	18	5	12	D3YUT2	
ENSMUST00000107351						0	0	5	12	2	3	9	34	18	12	23		
ENSMUST00000107352						0	0	0	1	8	0	0	63	14	0	7		
ENSMUST00000107353	ENSMUSG00000005621	7	80993681	81045164	1	51	28	76	78	49	35	823	1292	1282	87	1171		Q8BHZ4
ENSMUST00000107356	ENSMUSG00000004043	11	100859351	100885169	1	10	4	32	17	14	0	302	468	194	0	281	Q9JIA0	P42230
ENSMUST00000107357	ENSMUSG00000004043	11	100859351	100885169	1	0	4	0	11	0	4	136	117	186	39	107	B2C3G8	
ENSMUST00000107358	ENSMUSG00000020919	11	100780731	100850724	-1	29	22	82	16	46	11	3416	4091	2925	439	3025		P42232
ENSMUST00000107359	ENSMUSG00000039270	4	70427065	70534995	-1	283	234	1650	334	253	106	1125	3320	2069	132	1097	Q0VGR4	Q8BH27
ENSMUST00000107360	ENSMUSG00000045471	11	100761069	100762931	-1	0	2	2	0	1	0	0	0	0	0	0	A2A5D9	
ENSMUST00000107361	ENSMUSG00000035355	11	100740376	100759942	-1	0	2	9	0	5	20	0	1	1	0	1	A2A5F7	
ENSMUST00000107362	ENSMUSG00000030530	7	80388585	80405436	-1	0	0	0	0	0	0	9866	6906	4855	481	4320		P23188
ENSMUST00000107363	ENSMUSG00000035355	11	100740376	100759942	-1	24	20	59	137	39	0	0	0	0	0	0	A2A5F7	
ENSMUST00000107364	ENSMUSG00000019173	11	100715009	100738215	-1	11	13	0	50	18	18	6970	7191	5206	1915	3525	Q3TJ39	P35278
ENSMUST00000107365	ENSMUSG00000039005	4	66827584	66930284	1	20	16	14	24	18	5	5	16	12	14	22	A2BHU8	
ENSMUST00000107366	ENSMUSG00000051675	4	65604986	65616238	1	30	17	20	65	30	10	29	42	33	8	25	Q3TLR3	Q8CH72
ENSMUST00000107368	ENSMUSG00000030533	7	80325292	80341005	-1	10	8	25	123	24	8	58	86	38	0	96		Q99KD5
ENSMUST00000107369	ENSMUSG00000027938	3	90237500	90243512	-1	3	0	34	11	11	2	2	7	5	5	9		Q9D2A5
ENSMUST00000107371	ENSMUSG00000028364	4	63959785	64047015	-1	3	0	10	35	13	7	0	0	0	0	0	Q80YX0	
ENSMUST00000107372	ENSMUSG00000028364	4	63959785	64047015	-1	17	0	52	6	46	17	0	0	0	0	0		Q80YX1
ENSMUST00000107373	ENSMUSG00000027935	3	90213695	90226385	1	11	7	7	3	14	8	0	0	0	2	2	D3YUS4	
ENSMUST00000107376	ENSMUSG00000017837	11	100619244	100627607	1	18	2	19	165	19	1	17	12	15	3	20		Q9CR56
ENSMUST00000107377	ENSMUSG00000028364	4	63959785	64047015	-1	35	26	53	48	28	8	0	0	0	0	0		Q80YX1
ENSMUST00000107381						14	5	3	3	15	6	0	3	7	0	11		
ENSMUST00000107383						7	10	44	94	17	9	3	7	8	0	4		
ENSMUST00000107384	ENSMUSG00000030541	7	80094846	80115392	-1	5	0	0	161	17	3	174	284	111	84	194		P54071
ENSMUST00000107385	ENSMUSG00000020917	11	100476353	100528000	-1	5	6	30	13	14	7	30	6	224	0	170	Q3TS02	
ENSMUST00000107389	ENSMUSG00000020917	11	100476353	100528000	-1	0	0	0	0	0	0	1400	1186	2588	262	1939	Q3V117	
ENSMUST00000107392	ENSMUSG00000039062	7	79821803	79861059	-1	36	10	23	13	40	10	20	0	10	0	50		P97449
ENSMUST00000107393	ENSMUSG00000039137	4	63414910	63495991	-1	0	0	0	2	0	0	0	0	0	0	0		Q80VW5
ENSMUST00000107394	ENSMUSG00000030543	7	79810727	79813439	1	26	19	41	160	30	16	0	0	0	0	0	A6H5V4	
ENSMUST00000107395	ENSMUSG00000001558	11	100441917	100457022	1	6	2	0	5	3	0	0	0	0	0	1	Q6P3C9	
ENSMUST00000107396	ENSMUSG00000060671	3	89939481	89963508	-1	18	6	0	29	17	0	145	106	0	0	282	D3YXQ5	
ENSMUST00000107397	ENSMUSG00000017176	11	100422321	100441808	-1	0	0	0	0	7	0	29	67	0	72	39		Q3UFY7
ENSMUST00000107398	ENSMUSG00000017176	11	100422321	100441808	-1	0	7	8	29	17	0	0	4	0	0	0		Q3UFY7
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ENSMUST00000107400	ENSMUSG00000001555	11	100415697	100424824	1	5	0	0	0	0	0	0	0	0	0	9	A2A4H9	
ENSMUST00000107403	ENSMUSG00000001552	11	100368958	100397763	-1	0	0	9	77	8	10	44	0	51	2	35		Q02257
ENSMUST00000107405	ENSMUSG00000027951	3	89715022	89753446	1	0	35	57	0	22	23	1013	2776	1087	137	1329		Q99MU3
ENSMUST00000107406						10	0	11	3	16	2	0	0	0	0	0		
ENSMUST00000107409	ENSMUSG00000030605	7	79133768	79149060	-1	17	10	44	62	19	14	36	27	19	9	98		P21956
ENSMUST00000107410	ENSMUSG00000027952	3	89454541	89469013	1	7	0	0	4	2	3	0	0	19	9	10	D3YXP6	
ENSMUST00000107411	ENSMUSG00000054146	11	100131758	100135928	-1	20	15	34	21	18	5	0	0	0	3	6	B1AQ77	
ENSMUST00000107413	ENSMUSG00000047824	3	89430214	89435128	1	22	17	3	18	10	0	1861	2239	910	111	587	Q3V113	
ENSMUST00000107415	ENSMUSG00000028358	4	62965573	63139708	1	143	92	664	218	158	84	3	36	23	0	21		Q80YY7
ENSMUST00000107416	ENSMUSG00000020916	11	100102007	100105626	-1	16	10	28	21	26	7	0	0	0	0	0		B1AQ75
ENSMUST00000107417	ENSMUSG00000042626	3	89418443	89430027	1	0	0	0	0	0	12	1612	2113	1262	178	614		P98083
ENSMUST00000107419	ENSMUSG00000046095	11	100080848	100088226	-1	5	4	15	17	15	7	0	0	0	0	0	B1ATJ5	
ENSMUST00000107420	ENSMUSG00000059810	4	62559847	62704001	1	16	16	13	54	8	12	4455	5440	4486	630	2688		Q9DC04
ENSMUST00000107421	ENSMUSG00000030609	7	78895854	78911209	1	0	6	59	0	0	12	68	79	42	21	57		Q9CZI9
ENSMUST00000107422	ENSMUSG00000028044	3	89415472	89418383	-1	5	11	3	8	4	3	5	0	0	0	0	D3YXP1	
ENSMUST00000107423	ENSMUSG00000030609	7	78895854	78911209	1	9	0	19	74	13	0	15	17	0	0	13		Q9CZI9
ENSMUST00000107424	ENSMUSG00000059810	4	62559847	62704001	1	12	0	17	17	0	3	0	0	4	0	0		Q9DC04
ENSMUST00000107425	ENSMUSG00000030609	7	78895854	78911209	1	6	14	0	0	7	0	2	0	21	0	0		Q9CZI9
ENSMUST00000107426	ENSMUSG00000042642	3	89401004	89411870	-1	7	0	22	9	28	9	265	255	186	42	175		Q8R123
ENSMUST00000107429	ENSMUSG00000042642	3	89401004	89411870	-1	2	1	5	6	2	1	14	5	9	0	4	F8WGX4	
ENSMUST00000107431	ENSMUSG00000030610	7	78821547	78847263	-1	1	0	7	0	6	0	0	3	2	0	2	D3YXC0	
ENSMUST00000107432	ENSMUSG00000028042	3	89377644	89394776	-1	0	0	0	73	0	0	477	714	107	0	195	Q5BJ24	Q64321
ENSMUST00000107433	ENSMUSG00000028042	3	89377644	89394776	-1	9	6	63	12	0	0	3687	3601	2404	188	1585	Q5BJ24	Q64321
ENSMUST00000107434	ENSMUSG00000069717	11	99857917	99859061	1	10	2	18	29	2	0	0	0	0	0	0	A2A4M2	
ENSMUST00000107435	ENSMUSG00000028042	3	89377644	89394776	-1	24	34	65	125	45	29	312	221	205	12	202	Q5BJ24	Q64321
ENSMUST00000107437	ENSMUSG00000046474	11	99850655	99851608	-1	5	4	4	215	10	3	0	0	0	0	0	Q91W93	
ENSMUST00000107439	ENSMUSG00000089724	11	99779722	99780704	-1	4	6	20	103	6	8	0	0	0	0	0	B1AQA8	
ENSMUST00000107440	ENSMUSG00000078668	11	99771714	99772913	-1	8	5	39	119	21	4	0	0	0	0	0	B1AQA7	
ENSMUST00000107442	ENSMUSG00000025754	7	76229887	77124698	1	1	3	1	0	2	0	1	0	0	0	0		Q09M05
ENSMUST00000107443	ENSMUSG00000059169	11	99537485	99543158	-1	7	2	5	0	5	0	0	2	0	0	0	E9PV64	
ENSMUST00000107444	ENSMUSG00000028393	4	62509169	62519918	-1	5	7	0	156	35	8	0	0	0	0	0		P10518
ENSMUST00000107445	ENSMUSG00000064165	11	99514114	99521338	-1	8	5	14	8	14	5	0	0	0	0	0		Q6IFX4
ENSMUST00000107446	ENSMUSG00000028041	3	89338542	89349996	-1	0	0	0	0	0	0	0	0	0	0	0		O88839
ENSMUST00000107448	ENSMUSG00000028041	3	89338542	89349996	-1	0	0	0	7	0	0	749	967	645	37	975		O88839
ENSMUST00000107449	ENSMUSG00000028392	4	62480053	62497298	1	46	26	38	36	69	24	0	1	2	0	10		Q80YW5
ENSMUST00000107452	ENSMUSG00000028391	4	62448653	62470896	-1	0	0	3	0	0	1	0	0	0	0	0		Q9JHB4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107453	ENSMUSG00000025790	7	74275419	74554780	-1	11	15	30	155	33	12	4	1	7	0	20	D3YXA8	
ENSMUST00000107454	ENSMUSG00000063851	4	62427540	62435252	-1	13	4	22	0	13	2	0	0	0	2	3		Q8QZS5
ENSMUST00000107455	ENSMUSG00000063851	4	62427540	62435252	-1	0	3	10	18	8	0	0	0	0	0	0		Q8QZS5
ENSMUST00000107456	ENSMUSG00000078670	7	73740302	73776919	1	19	12	44	64	39	13	26	62	31	4	40		Q8K064
ENSMUST00000107459	ENSMUSG00000066149	4	62383654	62408642	-1	0	0	0	2	0	0	0	40	0	0	0		Q99JP4
ENSMUST00000107460	ENSMUSG00000027953	3	89268246	89270570	-1	2	3	3	0	2	4	16	41	7	2	0	D3YXA7	
ENSMUST00000107461	ENSMUSG00000066151	4	62300342	62360548	-1	4	2	0	21	5	0	58	156	103	29	78	Q80YW6	
ENSMUST00000107462	ENSMUSG00000042737	3	89259358	89267079	1	6	6	13	15	9	5	0	0	0	0	2		Q9D1Q4
ENSMUST00000107464	ENSMUSG00000042766	3	89234177	89246309	-1	24	8	19	6	11	6	0	0	0	0	0	D3YXA6	
ENSMUST00000107465						1	1	0	0	5	3	0	0	0	1	11		
ENSMUST00000107467	ENSMUSG00000066152	4	62262562	62298411	1	0	0	4	1	5	0	221	53	204	166	74	Q9D524	
ENSMUST00000107468	ENSMUSG00000066152	4	62262562	62298411	1	1	0	4	1	0	2	0	0	0	6	0	Q9D524	
ENSMUST00000107470	ENSMUSG00000030555	7	67647410	67726576	1	2	0	3	9	7	4	0	0	0	0	0	E9QKU9	
ENSMUST00000107471	ENSMUSG00000030555	7	67647410	67726576	1	0	0	0	0	0	0	0	11	0	7	0	E9QKU9	
ENSMUST00000107472	ENSMUSG00000066154	4	62083476	62087342	-1	0	0	0	0	2	0	0	0	0	6	0	Q3KQQ2	
ENSMUST00000107473	ENSMUSG00000037992	11	98927818	98974942	1	33	34	37	555	71	30	2414	3570	2519	229	2628		P11416
ENSMUST00000107474	ENSMUSG00000037992	11	98927818	98974942	1	5	0	5	2	7	0	2521	171	1245	145	1130	Q3U3R3	P11416
ENSMUST00000107475	ENSMUSG00000037992	11	98927818	98974942	1	0	0	0	106	0	0	679	1086	1223	69	1308	Q3U3R3	P11416
ENSMUST00000107476	ENSMUSG00000030557	7	67231163	67372858	-1	21	7	2	11	4	0	156	80	483	41	358		Q60929
ENSMUST00000107477	ENSMUSG00000078673	4	61778324	61782269	-1	0	1	3	1	0	0	0	0	0	0	0	A9C497	
ENSMUST00000107478	ENSMUSG00000058145	7	66839735	67152625	1	100	31	75	0	0	26	0	6	5	0	2	D3YX90	
ENSMUST00000107479	ENSMUSG00000038020	11	98836785	98853697	1	133	88	364	574	112	34	2	1	2	0	2		Q68EF8
ENSMUST00000107482	ENSMUSG00000041237	3	89136142	89146784	1	0	0	0	17	37	0	0	0	0	1	0	E9Q509	
ENSMUST00000107483	ENSMUSG00000078675	4	61515592	61519531	-1	0	0	0	2	0	0	0	0	0	0	0	A2CGB6	P02762
ENSMUST00000107484	ENSMUSG00000096688	4	61591929	61595871	-1	0	0	0	0	0	0	0	0	0	0	0		B5X0G2
ENSMUST00000107485	ENSMUSG00000052915	11	98795516	98807859	1	7	5	20	209	5	10	971	3028	1320	203	773		Q6PDM1
ENSMUST00000107486	ENSMUSG00000078677	7	66365905	66386309	1	34	33	144	92	44	29	1	5	3	0	4	D3YX89	
ENSMUST00000107487	ENSMUSG00000052915	11	98795516	98807859	1	0	0	0	0	0	0	0	0	0	0	54		Q6PDM1
ENSMUST00000107488	ENSMUSG00000066154	4	62083476	62087342	-1	2	0	0	0	2	0	0	0	0	0	0	Q3KQQ2	
ENSMUST00000107490	ENSMUSG00000078688	4	60135932	60154289	-1	0	0	0	0	0	0	0	0	0	0	0	A2AKN9	
ENSMUST00000107491	ENSMUSG00000068921	3	88920803	88951181	-1	0	1	0	0	0	0	149	473	196	264	172		
ENSMUST00000107494	ENSMUSG00000068922	3	88905107	88913999	-1	4	0	5	7	3	4	10	19	0	0	14	D3YX87	
ENSMUST00000107495	ENSMUSG00000078681	7	65691169	65701913	1	0	0	0	0	0	0	33	72	0	65	23		Q8BJ83
ENSMUST00000107498	ENSMUSG00000054199	3	88835231	88910103	1	0	27	70	133	57	27	36	76	1	0	239	E9Q507	
ENSMUST00000107499	ENSMUSG00000078683	4	60498012	60501960	-1	0	0	0	0	0	0	0	0	0	0	0	A2CEL1	
ENSMUST00000107503	ENSMUSG00000068923	3	88744700	88775164	-1	119	153	398	107	114	73	0	867	60	56	23	D3YWW9	
ENSMUST00000107505	ENSMUSG00000068923	3	88744700	88775164	-1	0	11	22	30	23	0	11	22	0	11	0		Q9R0N3
ENSMUST00000107506	ENSMUSG00000078686	4	60418046	60421952	-1	0	0	0	0	0	0	0	0	0	0	0	A2CGB6	P02762
ENSMUST00000107507						27	14	86	0	5	13	0	0	0	0	0		
ENSMUST00000107508	ENSMUSG00000064224	11	98626360	98638226	1	9	8	10	13	0	7	0	0	0	1	0	Z4YKL5	
ENSMUST00000107509	ENSMUSG00000017195	11	98551097	98558665	1	5	9	0	49	5	1	0	0	0	0	0		Q6X786
ENSMUST00000107510	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	242	0	0	0	0	0	0	44		Q60875
ENSMUST00000107511	ENSMUSG00000017195	11	98551097	98558665	1	0	0	0	0	0	0	0	0	0	0	0		Q6X786
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ENSMUST00000107514						6	7	3	5	7	0	0	14	0	0	10		
ENSMUST00000107515						62	114	436	78	76	35	0	13	3	0	5		
ENSMUST00000107516						0	0	0	0	8	7	0	1	0	0	0		
ENSMUST00000107517	ENSMUSG00000078689	4	59964294	60007274	1	3	0	5	0	2	2	0	0	0	0	0	A2AV72	
ENSMUST00000107519						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000107520	ENSMUSG00000078689	4	59964294	60007274	1	0	0	0	1	1	0	0	0	0	0	0	A2AV72	
ENSMUST00000107521	ENSMUSG00000078689	4	59964294	60007274	1	5	3	0	0	4	2	0	4	3	1	11	A2ANT6	
ENSMUST00000107525						0	3	0	0	7	0	0	0	0	0	0		
ENSMUST00000107526	ENSMUSG00000038544	4	59769637	59801589	-1	0	0	1	17	1	1	65	157	57	9	0		Q3TXT3
ENSMUST00000107527						5	5	21	48	9	0	0	0	1	0	0		
ENSMUST00000107528	ENSMUSG00000028383	4	59581563	59618689	1	9	5	0	6	6	8	0	0	0	27	0	B1AX78	
ENSMUST00000107531	ENSMUSG00000028064	3	88435959	88461182	-1	6	2	0	0	0	9	18	142	78	0	22	D3YWV5	
ENSMUST00000107537	ENSMUSG00000025326	7	59228750	59311536	1	41	33	312	260	44	18	223	393	365	82	158		O08759
ENSMUST00000107538	ENSMUSG00000003119	11	98203059	98278504	1	19	0	0	7	7	0	306	411	867	38	622		Q14AX6
ENSMUST00000107539	ENSMUSG00000003119	11	98203059	98278504	1	8	20	65	204	36	18	140	389	264	26	133		Q14AX6
ENSMUST00000107540						0	0	2	4	0	3	0	0	0	0	0		
ENSMUST00000107542	ENSMUSG00000074489	3	88368616	88372743	-1	201	208	440	212	234	122	32	159	45	4	31		P54615
ENSMUST00000107543	ENSMUSG00000074489	3	88368616	88372743	-1	2	0	1	1	3	0	0	0	0	2	0		P54615
ENSMUST00000107544	ENSMUSG00000038578	4	59314683	59438633	-1	0	0	29	136	0	0	0	0	0	27	0	A2AN91	
ENSMUST00000107545	ENSMUSG00000018160	11	98152154	98193293	-1	39	32	121	38	56	25	350	880	751	81	548		Q925J9
ENSMUST00000107547	ENSMUSG00000038598	4	59043753	59138983	-1	20	9	15	20	25	9	0	0	1	0	2	A2ALV5	
ENSMUST00000107552	ENSMUSG00000001420	3	88328655	88336148	-1	5	0	18	43	6	5	0	0	0	0	0		Q9D709
ENSMUST00000107553	ENSMUSG00000001420	3	88328655	88336148	-1	0	6	0	46	6	0	2	0	0	2	11		Q9D709
ENSMUST00000107554	ENSMUSG00000038630	4	58943628	58958355	1	24	10	22	23	24	15	0	0	0	0	1	A2ALW2	
ENSMUST00000107556	ENSMUSG00000010538	3	88282757	88296999	-1	0	7	8	6	8	2	5	5	0	21	0		Q9DA44
ENSMUST00000107557	ENSMUSG00000050812	4	58798911	58912749	-1	19	25	33	33	30	18	4	7	6	0	39	A2ALV6	
ENSMUST00000107558	ENSMUSG00000001419	3	88142372	88172086	1	9	6	16	17	8	6	19	13	7	0	35	E9QKT0	
ENSMUST00000107559	ENSMUSG00000001419	3	88142372	88172086	1	0	0	7	4	0	0	57	0	38	0	17		Q63943
ENSMUST00000107561	ENSMUSG00000020882	11	98001508	98023034	-1	4	3	41	12	6	5	0	0	0	0	0	A2A542	
ENSMUST00000107562	ENSMUSG00000020882	11	98001508	98023034	-1	0	0	0	19	0	0	0	0	2	0	0		Q8R3Z5
ENSMUST00000107563	ENSMUSG00000038352	11	97989578	97996181	-1	50	51	53	45	42	14	20	87	25	14	64	A2A541	
ENSMUST00000107564	ENSMUSG00000017417	11	97923238	97986444	-1	1	1	2	29	1	3	0	0	0	0	0	A2A539	
ENSMUST00000107565	ENSMUSG00000017417	11	97923238	97986444	-1	0	0	0	0	9	0	0	0	0	0	0		Q91ZV7
ENSMUST00000107568						2	8	4	3	2	1	3	8	8	2	4		
ENSMUST00000107569						3	2	9	15	4	3	0	0	0	0	5		
ENSMUST00000107570	ENSMUSG00000038668	4	58435255	58553898	-1	0	0	0	0	3	3	0	1	0	6	0		P61793
ENSMUST00000107571	ENSMUSG00000038668	4	58435255	58553898	-1	4	7	3	5	0	9	0	0	0	0	0	Q544V2	P61793
ENSMUST00000107574	ENSMUSG00000038668	4	58435255	58553898	-1	10	7	35	67	11	0	0	0	0	0	0	Q544V2	P61793
ENSMUST00000107575	ENSMUSG00000038668	4	58435255	58553898	-1	5	0	7	65	0	0	0	0	0	0	19	Q544V2	P61793
ENSMUST00000107576	ENSMUSG00000018543	11	97771481	97775918	-1	3	4	9	2	9	5	0	1	0	1	1		Q9DAQ5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107579	ENSMUSG00000018541	11	97745481	97766556	-1	10	11	15	10	7	4	2	2	3	2	3	A2A6F5	
ENSMUST00000107581	ENSMUSG00000028071	3	87846755	87855722	1	3	3	16	7	6	2	34	0	0	1	20		Q9QXK9
ENSMUST00000107582	ENSMUSG00000005640	3	87796951	87816101	1	0	0	0	0	5	0	0	0	0	0	0		Q9WTL4
ENSMUST00000107583	ENSMUSG00000078695	11	97685826	97688621	1	8	3	25	16	7	6	28	26	4	46	11		B1AR13
ENSMUST00000107584	ENSMUSG00000078695	11	97685826	97688621	1	0	0	0	4	0	0	0	0	3	73	12	Z4YKM2	
ENSMUST00000107585	ENSMUSG00000078695	11	97685826	97688621	1	0	0	0	3	10	0	0	0	0	0	0	B2RWE3	
ENSMUST00000107586	ENSMUSG00000038437	11	97663414	97685463	1	81	47	192	0	97	53	131	176	0	26	186	B1AR10	
ENSMUST00000107589	ENSMUSG00000030498	7	51862015	51994975	1	1	6	4	2	6	0	1	0	0	0	0	D3YWD9	
ENSMUST00000107590	ENSMUSG00000038453	11	97509340	97575226	-1	18	14	32	79	22	11	0	0	0	0	0	B1AQX7	
ENSMUST00000107591	ENSMUSG00000030498	7	51862015	51994975	1	16	16	29	54	24	8	0	0	0	10	12		P11862
ENSMUST00000107593	ENSMUSG00000038453	11	97509340	97575226	-1	2	0	2	364	6	0	0	0	0	0	0	B1AQX6	
ENSMUST00000107596	ENSMUSG00000038453	11	97509340	97575226	-1	37	44	190	63	74	37	0	5	2	0	5	B1AQX9	
ENSMUST00000107598	ENSMUSG00000089945	4	57568179	57896984	1	0	0	7	0	0	0	0	0	0	0	0		O54931
ENSMUST00000107600	ENSMUSG00000038729	4	57717657	57896982	1	4	7	33	0	7	11	3	0	0	0	0	A2API8	
ENSMUST00000107601	ENSMUSG00000049807	11	97415533	97502402	1	18	14	46	144	68	9	261	60	287	30	33	F8VQ11	
ENSMUST00000107603	ENSMUSG00000055409	7	49974864	50865255	1	6	10	9	8	6	6	0	0	0	0	0	D3YWD8	
ENSMUST00000107605	ENSMUSG00000039728	7	49910146	49963856	1	0	0	0	0	0	0	0	0	0	0	0	B2RQX9	
ENSMUST00000107608						0	0	0	0	4	0	17	96	22	9	39		
ENSMUST00000107609	ENSMUSG00000055296	4	56866923	56947437	-1	0	0	0	0	0	0	0	0	0	0	0	D3YWD3	
ENSMUST00000107612	ENSMUSG00000038816	4	56810935	56865188	-1	3	1	4	106	6	4	0	0	0	0	0	B1AZA7	
ENSMUST00000107613	ENSMUSG00000038517	11	97136171	97151495	-1	8	6	12	78	6	9	31	26	49	3	43	G3X9S9	
ENSMUST00000107614	ENSMUSG00000038517	11	97136171	97151495	-1	0	0	0	170	0	0	0	0	26	0	0		A2A9T0
ENSMUST00000107615	ENSMUSG00000038517	11	97136171	97151495	-1	0	11	0	23	0	14	0	0	0	0	0	Z4YKN2	
ENSMUST00000107617						0	4	6	2	7	0	0	0	0	0	0		
ENSMUST00000107618	ENSMUSG00000041734	3	87078593	87174747	-1	52	0	76	122	62	0	0	0	0	0	0		Q80W68
ENSMUST00000107619	ENSMUSG00000003032	4	55527143	55532466	-1	29	19	71	397	45	19	151	498	224	45	312	F2YID5	Q60793
ENSMUST00000107620						27	19	63	33	26	0	8	93	2	4	21		
ENSMUST00000107622	ENSMUSG00000038560	11	97013394	97024734	1	0	0	0	818	45	8	0	0	0	0	0	A2A708	Q9ESX2
ENSMUST00000107623	ENSMUSG00000018678	11	96953340	96982959	-1	0	0	27	5	12	0	43	297	198	30	363	Q8BNQ4	
ENSMUST00000107624	ENSMUSG00000018678	11	96953340	96982959	-1	0	0	0	46	0	0	0	0	0	0	0	Q8BNQ4	
ENSMUST00000107626	ENSMUSG00000018678	11	96953340	96982959	-1	8	4	0	0	15	9	592	428	309	0	89	Q8C5J0	
ENSMUST00000107629	ENSMUSG00000018659	11	96937825	96943986	-1	2	0	20	28	8	1	0	6	0	0	0	A2A6E7	
ENSMUST00000107633	ENSMUSG00000047040	11	96928104	96937830	1	7	6	33	203	20	4	0	8	3	1	8		Q8JZM2
ENSMUST00000107635	ENSMUSG00000028080	3	86224680	86782692	1	0	0	0	9	0	0	63	88	167	10	139	E9Q3Y4	
ENSMUST00000107636	ENSMUSG00000047040	11	96928104	96937830	1	28	40	98	65	30	29	2	1	1	0	2		Q8JZM2
ENSMUST00000107638	ENSMUSG00000028414	4	53713998	53765785	1	6	3	8	2	6	1	3	0	4	0	3	Q8K4R2	
ENSMUST00000107643						7	10	12	23	10	8	0	1	0	0	0		
ENSMUST00000107644	ENSMUSG00000006599	7	46796103	46823800	1	4	2	6	0	0	0	0	12	38	22	31	E9QKD9	
ENSMUST00000107645	ENSMUSG00000028412	4	53440413	53622478	1	3	6	12	3	8	0	0	0	0	0	0	A2AMH8	
ENSMUST00000107646	ENSMUSG00000028412	4	53440413	53622478	1	0	2	0	0	3	2	5	11	0	3	12	A2AMH3	
ENSMUST00000107647	ENSMUSG00000028412	4	53440413	53622478	1	10	2	11	3	11	3	0	3	165	0	164	A2AMH4	
ENSMUST00000107651	ENSMUSG00000028412	4	53440413	53622478	1	15	6	17	9	9	1	378	1862	496	158	516	A2AMH5	
ENSMUST00000107653	ENSMUSG00000014418	7	46760466	46796064	-1	0	0	0	0	0	0	44	55	78	24	89	E9Q3X4	
ENSMUST00000107654	ENSMUSG00000014418	7	46760466	46796064	-1	0	0	0	0	0	0	59	412	88	39	0		P59438
ENSMUST00000107657	ENSMUSG00000038615	11	96817414	96829968	-1	0	0	0	0	0	0	112	0	142	0	263	Q6GTN8	Q61985
ENSMUST00000107658	ENSMUSG00000038615	11	96817414	96829968	-1	0	7	0	0	3	19	25	0	117	50	140	Q6GTN8	Q61985
ENSMUST00000107659	ENSMUSG00000038615	11	96817414	96829968	-1	3	11	184	0	15	17	5	7	23	0	66	A2A6D2	
ENSMUST00000107660						39	32	161	30	29	21	0	10	4	2	10		
ENSMUST00000107661	ENSMUSG00000020876	11	96767555	96777559	-1	0	0	17	64	1	2	435	544	308	57	272		Q91WL6
ENSMUST00000107662	ENSMUSG00000057058	11	96464593	96759130	1	8	5	1	3	6	0	0	0	0	0	2	B1AQX1	
ENSMUST00000107663	ENSMUSG00000057058	11	96464593	96759130	1	10	4	15	9	5	4	4	0	2	0	5	B1AQX5	
ENSMUST00000107664	ENSMUSG00000028082	3	85971109	86130526	1	9	6	0	24	0	0	0	12	5	5	2		Q91X43
ENSMUST00000107665	ENSMUSG00000015247	4	53011880	53022060	1	4	9	0	0	3	0	157	524	274	347	198	B1AWZ5	
ENSMUST00000107666	ENSMUSG00000015242	4	52989272	53001162	1	4	2	0	0	1	0	0	0	0	0	0	B1AWZ3	
ENSMUST00000107667	ENSMUSG00000051593	4	52910833	52919172	-1	0	0	4	0	4	0	0	0	0	0	0	B1AWZ7	
ENSMUST00000107669	ENSMUSG00000040046	7	46647130	46672537	-1	0	3	0	5	0	4	0	0	0	1	0	Q3UK52	P17532
ENSMUST00000107670	ENSMUSG00000049648	4	52855514	52858466	-1	6	4	4	3	5	5	0	0	0	0	0	Q8VG87	
ENSMUST00000107671	ENSMUSG00000028314	4	52596274	52612430	1	16	0	0	0	0	0	0	0	0	0	0	Q9D2F8	
ENSMUST00000107672	ENSMUSG00000028085	3	85574119	85655622	1	2	1	1	1	4	2	3	0	2	0	0	Q3TLZ6	
ENSMUST00000107674	ENSMUSG00000028085	3	85574119	85655622	1	6	0	5	2	4	3	10	0	12	9	0	Q8BW84	
ENSMUST00000107675	ENSMUSG00000028086	3	84815268	84979198	1	5	0	0	4	3	6	0	194	0	0	0	D3YUA8	
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ENSMUST00000107679	ENSMUSG00000028086	3	84815268	84979198	1	3	0	18	267	27	17	173	316	380	68	290	D3YUA5	
ENSMUST00000107680	ENSMUSG00000038756	11	96133786	96165451	1	7	15	8	2	24	5	0	0	0	0	0		A4Q9E8
ENSMUST00000107682	ENSMUSG00000056498	3	84666192	84704575	1	10	8	15	26	9	7	2822	11777	4867	3541	3212		Q8C4Q9
ENSMUST00000107684	ENSMUSG00000006057	11	96068852	96075670	-1	1	0	2	3	0	0	63	80	37	107	51		Q9CR84
ENSMUST00000107686	ENSMUSG00000006057	11	96068852	96075670	-1	1	1	3	8	2	4	0	0	0	0	0		Q9CR84
ENSMUST00000107687	ENSMUSG00000074513	3	84496093	84582625	-1	0	1	0	0	0	0	6	30	52	80	66	E9Q3G5	
ENSMUST00000107689	ENSMUSG00000041842	3	84442198	84480429	-1	33	23	100	65	44	26	0	20	7	0	3		Q3ULZ2
ENSMUST00000107691	ENSMUSG00000027993	3	84160439	84306877	-1	26	20	31	303	36	17	0	0	0	0	16		Q9ESN6
ENSMUST00000107692	ENSMUSG00000027993	3	84160439	84306877	-1	0	20	24	26	5	12	0	5	0	0	0		Q9ESN6
ENSMUST00000107693	ENSMUSG00000027993	3	84160439	84306877	-1	4	0	20	0	0	0	2	5	2	3	0		Q9ESN6
ENSMUST00000107695	ENSMUSG00000027993	3	84160439	84306877	-1	6	0	0	0	0	0	0	0	0	0	0	Q3UHH4	
ENSMUST00000107696	ENSMUSG00000039634	4	49521176	49531517	1	16	7	4	19	9	6	23	90	27	79	26	Q8BKP2	
ENSMUST00000107697	ENSMUSG00000070985	4	49447105	49473912	-1	13	0	0	89	8	0	0	0	0	3	2		A2AKK5
ENSMUST00000107698	ENSMUSG00000060317	4	49379840	49408151	-1	0	1	0	0	0	0	0	0	0	0	0		Q8BGG9
ENSMUST00000107700	ENSMUSG00000006058	11	96034885	96047430	1	8	3	0	0	3	0	95	107	76	23	50	A2A6M1	
ENSMUST00000107704	ENSMUSG00000039693	4	48539935	48561919	1	0	0	0	1	0	0	0	0	0	0	19		Q9CR78
ENSMUST00000107708	ENSMUSG00000038811	11	95837216	95845734	1	0	0	0	0	0	0	12	155	10	231	49	A2A614	Q61017
ENSMUST00000107709	ENSMUSG00000038811	11	95837216	95845734	1	0	0	0	0	0	0	44	343	34	310	30	A2A614	Q61017
ENSMUST00000107711	ENSMUSG00000038811	11	95837216	95845734	1	0	0	0	0	0	0	101	387	52	346	65	A2A614	Q61017
ENSMUST00000107712	ENSMUSG00000038811	11	95837216	95845734	1	0	0	0	0	1	0	0	46	9	0	22	A2A614	Q61017
ENSMUST00000107714	ENSMUSG00000038811	11	95837216	95845734	1	2	0	0	0	0	0	0	91	29	209	21	A2A614	Q61017
ENSMUST00000107716	ENSMUSG00000002781	7	45896941	45917413	1	16	10	17	17	12	8	8	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107717	ENSMUSG00000075595	11	95712673	95835115	1	54	41	177	89	63	29	835	1618	1628	95	1285		Q5DU09
ENSMUST00000107718	ENSMUSG00000002778	7	45872772	45883731	1	6	0	1	19	4	6	354	270	141	56	52	D3YUA0	
ENSMUST00000107719	ENSMUSG00000002778	7	45872772	45883731	1	0	3	0	0	0	4	0	0	0	53	0	D3YU99	
ENSMUST00000107720	ENSMUSG00000061455	4	48124915	48186507	1	52	32	60	32	37	31	350	1630	703	169	728		Q9D0I4
ENSMUST00000107721	ENSMUSG00000061455	4	48124915	48186507	1	0	2	19	10	1	0	12	195	45	48	72	Q9D614	
ENSMUST00000107722	ENSMUSG00000057522	11	95414080	95493406	1	449	251	867	509	217	98	612	3365	1743	466	1597		Q6ZWS8
ENSMUST00000107723	ENSMUSG00000053801	7	45825227	45830944	-1	22	0	0	32	7	0	38	28	26	0	42		Q810D6
ENSMUST00000107724	ENSMUSG00000057522	11	95414080	95493406	1	0	0	0	0	0	0	383	1881	540	313	351		Q6ZWS8
ENSMUST00000107725	ENSMUSG00000007613	4	47353222	47414931	1	212	207	1217	439	231	103	10	20	89	1	68	Q9D5H8	
ENSMUST00000107726	ENSMUSG00000003269	7	45806637	45814581	-1	3	4	3	26	4	0	197	492	204	15	289	D3YU96	
ENSMUST00000107728	ENSMUSG00000003269	7	45806637	45814581	-1	0	0	0	0	0	3	422	518	301	0	253	D3YU95	
ENSMUST00000107729	ENSMUSG00000003269	7	45806637	45814581	-1	13	5	21	0	16	2	47	30	18	11	21	Q99KH2	
ENSMUST00000107730	ENSMUSG00000028339	4	47208161	47313167	1	1	0	0	0	2	1	5	6	1	2	1	A2AJY7	
ENSMUST00000107731	ENSMUSG00000028339	4	47208161	47313167	1	7	7	9	2	10	7	0	2	0	0	0	A2AJY5	
ENSMUST00000107733	ENSMUSG00000038909	11	95274259	95310246	-1	11	0	0	33	10	0	29	0	314	0	94	Q3TD41	Q5SVQ0
ENSMUST00000107734	ENSMUSG00000038909	11	95274259	95310246	-1	0	0	0	0	0	0	154	0	632	0	293	Q1AJD0	Q5SVQ0
ENSMUST00000107735	ENSMUSG00000003271	7	45729983	45759612	-1	7	4	13	3	8	4	0	0	0	0	0	E9QKC1	
ENSMUST00000107736	ENSMUSG00000028008	3	81982290	82021233	1	9	5	11	0	8	2	0	0	0	0	0	D3Z0S5	
ENSMUST00000107737	ENSMUSG00000057342	7	45709467	45718002	-1	4	5	20	11	7	6	310	269	256	51	168	Q58E38	Q9JIA7
ENSMUST00000107738	ENSMUSG00000057342	7	45709467	45718002	-1	10	0	6	0	0	0	1251	1250	749	82	443	Q58E38	Q9JIA7
ENSMUST00000107739	ENSMUSG00000001507	11	95044474	95076801	-1	33	0	32	5	31	22	2	0	0	8	0		Q62470
ENSMUST00000107740	ENSMUSG00000059824	7	45705088	45710155	1	0	0	2	0	0	0	0	0	0	0	0	E9Q3E6	
ENSMUST00000107741	ENSMUSG00000059824	7	45705088	45710155	1	0	0	0	0	0	0	0	0	0	6	0	E9Q3E4	
ENSMUST00000107742	ENSMUSG00000070564	7	45684022	45694556	1	0	2	8	275	1	7	0	0	0	0	0		Q3UQ22
ENSMUST00000107743	ENSMUSG00000028020	3	80843599	80913660	-1	0	0	0	0	2	0	0	0	0	0	0	E9Q3E3	
ENSMUST00000107744	ENSMUSG00000039774	4	47091909	47123070	1	2	5	0	0	0	0	0	3	0	0	0	A2ANU2	
ENSMUST00000107745	ENSMUSG00000033981	3	80681450	80802835	-1	81	60	440	66	47	18	0	10	5	0	0	E9QKC0	
ENSMUST00000107747	ENSMUSG00000066191	4	47015669	47057306	-1	27	18	64	78	37	9	0	0	0	0	17	A2ANT9	
ENSMUST00000107748	ENSMUSG00000038976	11	94991035	95006899	1	25	7	34	13	32	3	1946	1848	770	90	632		Q6R891
ENSMUST00000107749	ENSMUSG00000039809	4	46662305	46991873	-1	55	51	270	266	65	27	0	2	6	1	2		Q80T41
ENSMUST00000107750	ENSMUSG00000039813	4	46604390	46650209	-1	50	29	73	75	73	40	5	9	7	1	10		B1AVH7
ENSMUST00000107752	ENSMUSG00000030825	7	45554893	45567752	1	9	5	16	11	2	2	0	0	0	0	0	E9Q3D4	
ENSMUST00000107756	ENSMUSG00000028337	4	46536937	46602202	-1	0	0	0	303	45	16	624	1718	2292	136	1089	B1AVH4	Q8C0P5
ENSMUST00000107757	ENSMUSG00000028337	4	46536937	46602202	-1	2	2	4	45	0	18	24	341	6	0	245	B1AVH5	
ENSMUST00000107758	ENSMUSG00000023467	7	45486262	45523632	1	0	0	0	0	3	3	0	0	0	0	0	D3Z0R4	
ENSMUST00000107759	ENSMUSG00000023467	7	45486262	45523632	1	0	0	14	0	0	0	0	0	0	0	0		P46686
ENSMUST00000107760	ENSMUSG00000023467	7	45486262	45523632	1	4	7	4	5	4	4	0	0	0	0	0	D3Z0R3	
ENSMUST00000107761	ENSMUSG00000023467	7	45486262	45523632	1	3	0	10	6	5	0	1	21	2	1	6		P46686
ENSMUST00000107762	ENSMUSG00000023467	7	45486262	45523632	1	0	0	0	4	0	0	0	0	0	0	0		P46686
ENSMUST00000107764	ENSMUSG00000028332	4	46393989	46413506	-1	59	29	255	32	18	28	0	0	0	0	0		Q9ERZ0
ENSMUST00000107766	ENSMUSG00000003865	7	45434844	45456619	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0Q6	
ENSMUST00000107770	ENSMUSG00000035495	4	46114746	46138694	-1	0	0	0	0	0	0	0	16	12	0	12		Q3U269
ENSMUST00000107771	ENSMUSG00000003868	7	45421852	45438096	-1	3	5	13	3	4	0	475	446	246	77	217	Q3TXT7	Q9WTM5
ENSMUST00000107772	ENSMUSG00000035495	4	46114746	46138694	-1	46	30	56	28	21	22	300	901	423	38	268		Q3U269
ENSMUST00000107773	ENSMUSG00000028328	4	46038935	46116032	1	19	59	32	122	45	21	2	0	2	2	5		P49813
ENSMUST00000107774	ENSMUSG00000038201	7	45405960	45411382	1	27	13	83	161	32	17	0	0	0	0	2		Q17ST2
ENSMUST00000107775	ENSMUSG00000034151	3	75037907	75165034	-1	2	0	0	1	0	0	0	0	0	0	0	D3Z0P7	
ENSMUST00000107776	ENSMUSG00000034151	3	75037907	75165034	-1	0	0	0	0	2	0	0	0	0	0	0	D3Z0P6	
ENSMUST00000107777	ENSMUSG00000035517	4	45965334	46034761	1	18	21	0	1	8	7	292	1189	489	59	368	A0A0A0MQD1	
ENSMUST00000107778	ENSMUSG00000034151	3	75037907	75165034	-1	7	4	0	5	0	0	0	0	0	0	0		Q0P5X5
ENSMUST00000107779	ENSMUSG00000003863	7	45339126	45367019	-1	37	21	9	40	21	0	0	0	0	0	0	B8QI35	P60469
ENSMUST00000107782	ENSMUSG00000028327	4	45848664	45887008	1	14	12	29	0	21	6	0	0	0	0	0	B1AWX8	
ENSMUST00000107783	ENSMUSG00000028327	4	45848664	45887008	1	0	0	0	0	0	0	0	0	0	0	0	Q9DBN1	
ENSMUST00000107785	ENSMUSG00000020866	11	94408391	94474198	-1	0	0	0	0	44	0	0	0	0	0	0	Q5SUG2	
ENSMUST00000107786	ENSMUSG00000020866	11	94408391	94474198	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SUG1	
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ENSMUST00000107789	ENSMUSG00000020866	11	94408391	94474198	-1	22	32	89	304	23	19	0	0	0	0	0	Q5SUF7	
ENSMUST00000107790	ENSMUSG00000020866	11	94408391	94474198	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SUF9	
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ENSMUST00000107796	ENSMUSG00000045973	4	45395923	45408766	-1	112	108	202	0	104	38	201	512	245	81	263	A2AKW0	
ENSMUST00000107797	ENSMUSG00000030798	7	45233632	45239115	-1	0	0	13	20	6	0	138	519	488	72	345	E9Q2X8	
ENSMUST00000107798						0	0	0	0	0	0	62	85	70	8	30		
ENSMUST00000107800	ENSMUSG00000035601	4	45297127	45316131	1	0	0	0	4	0	0	0	38	2	94	28	Z4YKN9	
ENSMUST00000107801	ENSMUSG00000030796	7	45215753	45233635	1	21	14	59	260	15	9	0	0	0	0	3	Q3UPV9	P48301
ENSMUST00000107802	ENSMUSG00000034317	3	69035288	69044755	-1	0	4	1	7	8	2	50	123	41	12	38		Q922Y2
ENSMUST00000107803	ENSMUSG00000034349	3	69004738	69034623	1	5	0	0	0	0	0	382	809	260	9	0	E9Q2X6	
ENSMUST00000107804	ENSMUSG00000035615	4	45184875	45285936	1	21	9	97	53	39	36	0	0	0	0	0		A2AKB4
ENSMUST00000107807	ENSMUSG00000078713	4	45105208	45108114	-1	0	0	0	5	0	0	0	0	6	17	0		B1AXP6
ENSMUST00000107808	ENSMUSG00000078713	4	45105208	45108114	-1	2	1	10	0	5	3	11	25	5	54	9		B1AXP6
ENSMUST00000107809	ENSMUSG00000078713	4	45105208	45108114	-1	3	4	1	0	5	0	0	0	0	5	5		B1AXP6
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ENSMUST00000107811	ENSMUSG00000003423	7	45154398	45160064	1	0	0	0	0	0	0	54	225	44	0	60		Q9CQJ2
ENSMUST00000107812	ENSMUSG00000027778	3	68892499	69004570	-1	0	0	0	0	0	0	0	0	0	21	0		Q8K057
ENSMUST00000107813						7	0	5	12	0	0	281	247	77	90	96		
ENSMUST00000107814	ENSMUSG00000028318	4	45018583	45036565	1	10	6	27	13	11	4	15	5	0	12	22		Q8K202
ENSMUST00000107815	ENSMUSG00000007833	7	45140684	45154584	-1	16	14	50	31	18	8	1222	1117	868	169	622	D3Z0B9	
ENSMUST00000107816	ENSMUSG00000027776	3	68690644	68698547	1	6	1	9	2	3	4	39	184	48	81	27	Q549G3	P43431
ENSMUST00000107817	ENSMUSG00000049657	4	44991242	45012412	-1	11	10	18	182	10	3	16	21	24	2	20		Q7TQG0
ENSMUST00000107818	ENSMUSG00000020864	11	94328001	94341841	1	14	13	15	26	17	12	257	655	302	48	240		Q5SUE8
ENSMUST00000107820	ENSMUSG00000020863	11	94287890	94321988	-1	0	0	0	0	7	0	103	605	141	117	134		Q5SUF2
ENSMUST00000107821	ENSMUSG00000020863	11	94287890	94321988	-1	0	0	0	139	0	0	61	389	158	192	60		Q5SUF2
ENSMUST00000107822	ENSMUSG00000020863	11	94287890	94321988	-1	3	0	0	0	0	0	13	260	325	350	258	F8WGA8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107823						0	0	0	0	0	0	0	20	0	24	16		
ENSMUST00000107824	ENSMUSG00000035649	4	44755877	44932215	1	2	0	1	43	10	3	42	387	149	168	166		B1AX39
ENSMUST00000107825	ENSMUSG00000014030	4	44524757	44710487	-1	0	4	0	0	0	0	0	0	0	0	0	A2AKM5	
ENSMUST00000107826	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	6	10	14	2	0	0	0	0	0	A2AKM8	
ENSMUST00000107827	ENSMUSG00000014030	4	44524757	44710487	-1	0	1	0	0	0	0	0	0	0	0	0	A2AKM7	
ENSMUST00000107829	ENSMUSG00000003421	7	45062429	45078503	1	0	0	0	0	0	0	538	884	381	178	292		Q9D6T0
ENSMUST00000107830						0	0	0	0	0	0	150	19	147	290	64		
ENSMUST00000107831						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000107832						0	0	0	14	0	0	7	26	11	4	12		
ENSMUST00000107833						9	5	10	0	3	8	0	11	16	0	69		
ENSMUST00000107834	ENSMUSG00000003184	7	44997648	45002847	1	0	0	0	0	0	0	107	247	9	25	57	Q3U9K6	P70671
ENSMUST00000107835						0	3	0	0	0	0	140	259	108	37	85		
ENSMUST00000107836	ENSMUSG00000035696	4	44126210	44233789	-1	1	0	0	2	0	2	0	0	110	0	0	Q3UH35	
ENSMUST00000107837						2	0	8	3	1	0	0	0	0	0	0		
ENSMUST00000107840						0	0	0	0	0	0	114	156	95	136	60		
ENSMUST00000107842						85	74	292	122	74	26	39	101	95	18	75		
ENSMUST00000107843	ENSMUSG00000052429	7	44976756	44986420	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JIF0
ENSMUST00000107844	ENSMUSG00000037601	11	93956979	93968521	-1	0	4	6	8	3	2	0	0	0	0	2	Q5NC79	
ENSMUST00000107845	ENSMUSG00000028478	4	44004452	44032846	1	0	0	0	5	0	0	791	1113	208	57	180	B1AWE0	
ENSMUST00000107846	ENSMUSG00000028478	4	44004452	44032846	1	4	14	16	114	21	5	0	3	0	5	0	Q6PFA2	
ENSMUST00000107847	ENSMUSG00000028478	4	44004452	44032846	1	4	0	0	0	2	0	12	29	10	0	0	B1AWE1	
ENSMUST00000107848						2	0	2	3	0	0	3	3	5	4	3		
ENSMUST00000107849	ENSMUSG00000028478	4	44004452	44032846	1	0	0	0	0	2	0	0	33	0	0	14	B1AWD8	
ENSMUST00000107850	ENSMUSG00000059474	11	93885852	93946985	1	3	0	0	80	3	1	3	4	6	0	15	Q5NC76	
ENSMUST00000107851	ENSMUSG00000028478	4	44004452	44032846	1	0	0	0	0	0	0	0	0	10	0	10	B1AWD9	
ENSMUST00000107852	ENSMUSG00000059474	11	93885852	93946985	1	0	0	0	0	0	0	0	0	0	3	0	Q5NC75	
ENSMUST00000107853	ENSMUSG00000059474	11	93885852	93946985	1	15	14	0	29	15	0	158	455	282	143	184		Q6P5G3
ENSMUST00000107854	ENSMUSG00000059474	11	93885852	93946985	1	0	0	11	0	0	18	14	21	0	44	0		Q6P5G3
ENSMUST00000107855	ENSMUSG00000028480	4	43957401	43979118	1	9	2	11	8	5	0	4367	14204	2484	0	820	B1AWD6	
ENSMUST00000107857	ENSMUSG00000060279	7	44900374	44929490	-1	8	2	13	0	0	9	1573	859	1214	67	626		P17426
ENSMUST00000107858	ENSMUSG00000056158	11	93098028	93601749	1	22	11	221	0	0	9	0	0	2	0	2	E9Q2V1	
ENSMUST00000107859	ENSMUSG00000056158	11	93098028	93601749	1	1	1	2	0	4	2	0	0	0	0	0	Q9CZQ3	
ENSMUST00000107860	ENSMUSG00000071000	4	43851565	43855463	1	8	2	13	7	9	5	0	0	0	0	0	Q9QZ22	
ENSMUST00000107861	ENSMUSG00000056158	11	93098028	93601749	1	11	10	6	42	17	13	1	3	0	0	0	Q3TRQ4	
ENSMUST00000107862	ENSMUSG00000046450	4	43705628	43710231	-1	19	8	27	10	18	8	0	0	0	0	0	Q9QZ18	
ENSMUST00000107863	ENSMUSG00000056158	11	93098028	93601749	1	33	29	87	179	65	0	0	0	0	0	0	Q3V1V7	P61215
ENSMUST00000107864	ENSMUSG00000078716	4	43668971	43692668	1	0	0	0	176	0	0	0	0	0	0	10		B1AWJ5
ENSMUST00000107865	ENSMUSG00000078716	4	43668971	43692668	1	5	0	37	0	30	0	0	0	0	0	0		B1AWJ5
ENSMUST00000107866	ENSMUSG00000078716	4	43668971	43692668	1	63	11	131	75	15	25	0	0	0	0	0	B1AWJ4	
ENSMUST00000107867	ENSMUSG00000020541	11	90643465	90688366	-1	0	0	0	0	0	0	0	0	0	0	0		Q923U0
ENSMUST00000107868	ENSMUSG00000020541	11	90643465	90688366	-1	6	1	0	4	0	0	2	0	0	10	6	Q8BZR6	
ENSMUST00000107869	ENSMUSG00000020541	11	90643465	90688366	-1	0	0	0	0	0	1	0	0	0	23	0		Q923U0
ENSMUST00000107870	ENSMUSG00000066196	4	43651335	43653594	-1	5	0	17	0	16	3	1	0	0	0	1	Q5UAV3	
ENSMUST00000107872	ENSMUSG00000020546	11	90476492	90638084	-1	4	3	5	11	2	6	0	0	0	0	0		Q9WV89
ENSMUST00000107874	ENSMUSG00000028469	4	43631935	43651244	1	12	0	0	3	0	0	0	0	0	0	0	B1AWI7	
ENSMUST00000107875	ENSMUSG00000020546	11	90476492	90638084	-1	7	5	4	2	8	10	0	0	0	0	0		Q9WV89
ENSMUST00000107876	ENSMUSG00000002963	7	44857139	44862992	1	0	0	0	0	0	0	319	0	9	21	0	G5E8N7	
ENSMUST00000107880	ENSMUSG00000011096	7	44848991	44855421	1	0	3	0	190	10	8	48	51	23	0	43		Q9D1F4
ENSMUST00000107881						6	2	5	4	7	3	1	15	8	0	0		
ENSMUST00000107882	ENSMUSG00000011096	7	44848991	44855421	1	0	0	0	9	0	0	0	0	0	0	0	E9QKI5	
ENSMUST00000107884	ENSMUSG00000078719	4	43583216	43584494	-1	2	3	0	0	0	0	0	0	0	0	2		B1AWI6
ENSMUST00000107885	ENSMUSG00000011096	7	44848991	44855421	1	0	3	0	0	8	0	24	24	16	16	24	E9QKI4	
ENSMUST00000107886	ENSMUSG00000028468	4	43578715	43587487	1	34	21	98	89	50	22	1525	1866	1736	126	1200		Q8BHT7
ENSMUST00000107887	ENSMUSG00000003948	11	90187684	90278589	1	4	6	8	78	9	2	0	0	0	0	0	Z4YKP7	
ENSMUST00000107891						34	19	57	0	31	19	0	0	0	9	0		
ENSMUST00000107893	ENSMUSG00000038539	7	44812256	44816599	-1	16	7	26	3	14	11	118	96	14	12	48	Q3UJF3	O70191
ENSMUST00000107894	ENSMUSG00000000276	11	89035179	89066850	-1	127	138	288	356	158	71	9	89	30	0	78		Q9R1C6
ENSMUST00000107896	ENSMUSG00000000275	11	88999376	89020293	1	1	1	1	1	1	0	3034	9773	4843	344	4049		Q61510
ENSMUST00000107898	ENSMUSG00000033983	11	88970252	88991613	1	0	2	8	0	7	0	0	0	5	0	11	E9Q284	
ENSMUST00000107899	ENSMUSG00000030739	7	44605819	44665503	-1	0	0	50	0	43	0	0	0	0	1	1		Q6URW6
ENSMUST00000107900	ENSMUSG00000030739	7	44605819	44665503	-1	0	28	24	0	0	33	0	0	0	0	0	K3W4R2	
ENSMUST00000107903	ENSMUSG00000018428	11	88830792	88864586	-1	2	0	42	0	0	0	0	0	18	14	0		O08715
ENSMUST00000107904	ENSMUSG00000018428	11	88830792	88864586	-1	13	8	30	9	17	6	0	0	0	0	19		O08715
ENSMUST00000107905						4	0	0	0	9	2	0	0	1	0	0		
ENSMUST00000107906	ENSMUSG00000062785	7	44590886	44604750	1	0	2	71	0	0	0	4	15	6	1	34	E9QKI2	
ENSMUST00000107907	ENSMUSG00000062785	7	44590886	44604750	1	23	24	21	203	32	22	0	0	0	0	0	D3YZV2	
ENSMUST00000107908	ENSMUSG00000069769	11	88339382	88718513	-1	7	2	1	0	2	1	3	0	0	0	0	B1AT13	
ENSMUST00000107909	ENSMUSG00000069769	11	88339382	88718513	-1	13	15	28	14	22	6	45	130	61	21	107	Q2M2Q8	Q920Q6
ENSMUST00000107910	ENSMUSG00000060601	7	44549616	44553951	-1	0	0	1	0	0	0	298	27	789	178	112	Q8BP65	
ENSMUST00000107911	ENSMUSG00000060601	7	44549616	44553951	-1	0	0	0	0	0	0	1010	1164	97	130	361	Q8BP65	
ENSMUST00000107912	ENSMUSG00000060601	7	44549616	44553951	-1	2	2	16	0	18	3	774	1132	300	5	442		Q60644
ENSMUST00000107913	ENSMUSG00000028464	4	43514711	43523765	-1	15	0	0	0	0	12	0	0	0	0	0		P58774
ENSMUST00000107914	ENSMUSG00000028464	4	43514711	43523765	-1	2	0	3	128	5	0	0	0	0	11	15	Q6PJ18	P58774
ENSMUST00000107915	ENSMUSG00000023723	11	88204388	88211507	1	0	0	0	0	0	0	17	31	27	31	16	Q5SXC9	
ENSMUST00000107920	ENSMUSG00000018379	11	88047373	88053755	1	0	1	0	0	0	0	19	79	128	11	63	H7BX95	
ENSMUST00000107922	ENSMUSG00000028461	4	43492900	43495921	1	0	0	0	0	0	0	0	2	0	0	7		Q9DCC3
ENSMUST00000107923	ENSMUSG00000020483	11	87979525	87987533	-1	9	0	47	2	20	6	0	0	9	0	9		Q9D0M5
ENSMUST00000107924	ENSMUSG00000075700	3	58576636	58593133	1	38	26	127	110	26	15	981	3076	1143	952	862		P62342
ENSMUST00000107925	ENSMUSG00000028459	4	43446462	43454628	-1	0	0	0	0	0	0	0	0	0	0	0	A2AIN5	
ENSMUST00000107926	ENSMUSG00000028459	4	43446462	43454628	-1	0	0	0	0	0	0	12	28	13	23	24		P21855
ENSMUST00000107927	ENSMUSG00000051113	7	44496581	44501486	1	9	4	11	204	12	7	2	6	2	9	2		A1L3C1
ENSMUST00000107928	ENSMUSG00000042788	4	43427019	43429134	-1	0	0	0	0	3	0	0	0	0	0	0		A2AIP0
ENSMUST00000107929	ENSMUSG00000042788	4	43427019	43429134	-1	2	0	0	11	0	0	0	0	0	0	0		A2AIP0
ENSMUST00000107930	ENSMUSG00000009350	11	87793581	87804413	1	3	1	0	0	0	0	0	0	0	0	0	F8WGZ9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000107933	ENSMUSG00000008028	7	44360043	44385820	-1	7	4	9	84	8	0	0	2	1	0	0		D3Z070
ENSMUST00000107934	ENSMUSG00000038738	7	44310253	44360572	1	0	0	0	1219	0	0	0	0	0	0	6	D3YZU5	
ENSMUST00000107935	ENSMUSG00000038738	7	44310253	44360572	1	0	0	0	0	0	0	0	0	0	0	0	D3YZU4	
ENSMUST00000107937	ENSMUSG00000028457	4	43267159	43373833	1	26	20	46	14	0	16	0	0	0	0	1	D6RG77	
ENSMUST00000107938	ENSMUSG00000038738	7	44310253	44360572	1	40	29	163	471	103	55	2	2	4	0	0		D3YZU1
ENSMUST00000107942	ENSMUSG00000028457	4	43267159	43373833	1	0	0	0	8	33	0	3	5	5	0	0		A3FIN4
ENSMUST00000107945	ENSMUSG00000012777	7	44252148	44257378	-1	3	9	54	3	16	0	0	0	0	0	0	D3YZU0	
ENSMUST00000107948	ENSMUSG00000045411	7	44246722	44252319	1	0	0	0	0	0	0	1	0	0	0	0	Q3TE80	
ENSMUST00000107949	ENSMUSG00000045411	7	44246722	44252319	1	0	0	17	0	0	0	0	0	5	0	0	Q3TE80	
ENSMUST00000107950	ENSMUSG00000045411	7	44246722	44252319	1	0	0	0	0	0	0	8	28	0	0	68	Q3TE80	
ENSMUST00000107952	ENSMUSG00000028456	4	43058953	43264871	1	0	0	0	0	2	0	0	0	0	0	0		Q9Z1N9
ENSMUST00000107953	ENSMUSG00000028456	4	43058953	43264871	1	4	0	0	0	5	0	0	0	0	0	0	E9Q263	
ENSMUST00000107956	ENSMUSG00000036002	4	43032414	43046220	-1	33	21	89	0	0	4	1615	2906	1562	186	1100		Q8BR27
ENSMUST00000107957	ENSMUSG00000036002	4	43032414	43046220	-1	0	0	42	23	7	3	77	419	128	0	192		Q8BR27
ENSMUST00000107958	ENSMUSG00000036002	4	43032414	43046220	-1	12	0	23	160	9	16	12	42	50	12	47		Q8BR27
ENSMUST00000107959	ENSMUSG00000036002	4	43032414	43046220	-1	0	26	92	0	0	0	50	337	87	0	0		Q8BR27
ENSMUST00000107960	ENSMUSG00000020486	11	87568903	87590539	1	0	0	0	0	0	0	0	0	0	0	0		P28661
ENSMUST00000107961	ENSMUSG00000020486	11	87568903	87590539	1	0	2	6	0	2	2	0	0	0	2	0	Q5ND13	
ENSMUST00000107962	ENSMUSG00000020486	11	87568903	87590539	1	0	0	0	13	0	0	0	0	0	0	0		P28661
ENSMUST00000107966	ENSMUSG00000050063	7	43824499	43832030	1	6	2	0	3	0	2	0	0	0	0	0	Q91Y82	
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ENSMUST00000107968	ENSMUSG00000050063	7	43824499	43832030	1	0	0	12	14	4	5	0	0	0	0	0	Q91Y82	
ENSMUST00000107970	ENSMUSG00000044430	7	43768897	43773585	1	6	0	14	10	0	3	0	0	0	0	0	B2RVZ0	
ENSMUST00000107971	ENSMUSG00000036580	3	55112108	55137322	1	0	0	17	0	5	0	3	0	0	6	33		Q8R1X6
ENSMUST00000107972	ENSMUSG00000056592	7	43562256	43575461	1	33	28	60	33	40	14	25	111	34	37	91	Q5PPQ4	
ENSMUST00000107973	ENSMUSG00000036052	4	42949814	42959425	1	0	0	0	0	0	0	167	213	97	35	93	Q3TY13	
ENSMUST00000107974	ENSMUSG00000013367	7	43472904	43490075	-1	78	29	359	138	44	29	10	23	16	2	9		O89114
ENSMUST00000107975	ENSMUSG00000036062	4	42916660	42944752	1	46	44	38	14	52	21	0	0	0	0	0		Q8HW98
ENSMUST00000107976	ENSMUSG00000036062	4	42916660	42944752	1	0	0	67	61	0	0	0	0	0	0	0		Q80TL4
ENSMUST00000107977	ENSMUSG00000070604	7	43463151	43472019	1	35	15	117	246	58	34	826	1486	614	73	630		Q80TL4
ENSMUST00000107978	ENSMUSG00000050141	4	42868004	42874234	-1	7	1	21	22	0	3	0	0	0	0	0		D3YZF7
ENSMUST00000107979	ENSMUSG00000078721	4	42848071	42853888	-1	24	17	50	36	35	4	0	0	0	0	0	D3YZF6	Q80YD3
ENSMUST00000107981	ENSMUSG00000078722	4	42781928	42856771	-1	22	9	46	18	25	8	13	30	16	0	13	A2AKP6	
ENSMUST00000107984	ENSMUSG00000054885	4	42735545	42846248	1	4	4	10	5	4	2	0	0	0	0	0	Q9D4Q4	
ENSMUST00000107985	ENSMUSG00000027750	3	54361109	54391037	1	0	0	0	0	0	0	0	0	0	0	0		Q62009
ENSMUST00000107986	ENSMUSG00000012640	7	43296197	43313294	-1	0	0	0	1	0	0	308	1079	330	441	215	G3X9T1	
ENSMUST00000107987	ENSMUSG00000093828	JH584294.1	2012	3786	1	2	0	0	0	4	3	0	0	2	0	0		
ENSMUST00000107988	ENSMUSG00000095234	4	42439378	42439966	1	0	0	0	0	0	0	0	0	0	0	0	A2APU9	
ENSMUST00000107989	ENSMUSG00000094942	13	62368328	62383177	-1	0	0	0	0	0	0	0	0	0	0	0	D3YUB7	
ENSMUST00000107992	ENSMUSG00000069727	7	42660105	42692742	-1	34	27	34	25	41	13	5	35	12	5	8	Q6NVD6	
ENSMUST00000107994						145	112	864	160	139	76	4	21	3	9	16		
ENSMUST00000108002	ENSMUSG00000094695	4	42294267	42294855	1	0	0	0	0	0	0	0	0	0	0	0	A2APU9	
ENSMUST00000108006	ENSMUSG00000078735	4	42656355	42661893	-1	0	0	0	0	0	0	0	0	0	0	0		P70225
ENSMUST00000108007	ENSMUSG00000095193	17	94873986	94877497	1	5	5	2	1	7	1	7	27	9	11	7	L7N243	
ENSMUST00000108009						48	28	226	70	59	27	0	0	0	0	2		
ENSMUST00000108014	ENSMUSG00000078742	3	53845086	53845278	1	34	23	32	167	34	18	0	8	2	2	0	F6T1P1	
ENSMUST00000108015	ENSMUSG00000068959	7	39517766	39540420	1	59	42	123	89	77	26	50	172	100	79	99	G3X9T2	
ENSMUST00000108017	ENSMUSG00000053742	7	39407294	39413160	-1	10	13	68	14	18	14	0	0	0	0	0	W4VSN8	
ENSMUST00000108018	ENSMUSG00000073877	4	42153436	42158839	1	0	1	10	19	3	0	0	3	0	0	0		Q9Z1X0
ENSMUST00000108021	ENSMUSG00000072582	11	86683985	86692457	1	23	21	57	22	26	19	7	16	11	8	0		Q8R2Y8
ENSMUST00000108022	ENSMUSG00000072582	11	86683985	86692457	1	0	0	8	0	0	0	39	127	33	156	60		Q8R2Y8
ENSMUST00000108023	ENSMUSG00000002068	7	38097984	38107534	-1	6	10	6	10	9	4	63	117	52	15	39		Q61457
ENSMUST00000108026	ENSMUSG00000078746	4	41966058	41971856	1	4	0	1	0	0	0	0	0	0	0	4		A2APU8
ENSMUST00000108027						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000108028	ENSMUSG00000078747	4	41941572	41943124	1	0	0	0	0	0	0	0	0	0	0	0	L7N244	
ENSMUST00000108030	ENSMUSG00000020513	11	86544991	86567360	1	0	0	0	8	0	0	0	0	0	0	9	Q8CDD3	
ENSMUST00000108032	ENSMUSG00000073888	4	41769467	41774247	-1	0	0	0	0	0	0	0	0	0	0	0	A2AMS8	
ENSMUST00000108033	ENSMUSG00000073888	4	41769467	41774247	-1	0	0	0	0	0	0	0	0	0	0	0	A2AMS5	
ENSMUST00000108035	ENSMUSG00000073888	4	41769467	41774247	-1	3	3	17	0	4	3	2	0	0	0	0	A2AMS6	
ENSMUST00000108036	ENSMUSG00000073888	4	41769467	41774247	-1	0	0	0	0	0	0	0	0	0	0	0	A2AMS7	
ENSMUST00000108037	ENSMUSG00000073888	4	41769467	41774247	-1	0	0	0	0	0	0	0	0	0	0	0	A2AMS7	
ENSMUST00000108038	ENSMUSG00000036073	4	41755228	41758695	1	11	7	15	16	7	2	0	47	23	0	36	A2AMS2	
ENSMUST00000108039	ENSMUSG00000018068	11	86210681	86257575	-1	11	0	2	1	3	3	0	24	0	3	18		Q80UK8
ENSMUST00000108040	ENSMUSG00000073889	4	41699989	41769474	1	7	4	2	42	10	6	0	29	0	0	0		Q64385
ENSMUST00000108041	ENSMUSG00000073889	4	41699989	41769474	1	8	0	12	5	3	0	0	0	0	0	0		Q64385
ENSMUST00000108042	ENSMUSG00000073889	4	41699989	41769474	1	3	2	2	1	0	0	25	0	0	37	20		Q64385
ENSMUST00000108044	ENSMUSG00000026070	1	40465552	40500854	1	120	99	720	136	116	53	196	993	452	131	327		Q61098
ENSMUST00000108045	ENSMUSG00000000094	11	85886422	85916097	1	22	0	35	3	0	11	0	0	1	0	1	Q8BSY3	
ENSMUST00000108046	ENSMUSG00000037161	3	51388412	51396738	-1	6	2	0	0	7	0	0	0	0	0	0	G3X9T4	
ENSMUST00000108047	ENSMUSG00000000094	11	85886422	85916097	1	19	0	17	139	22	7	0	0	0	0	0		P70325
ENSMUST00000108049	ENSMUSG00000028439	4	41517691	41569538	-1	56	40	145	0	54	26	16	214	42	0	0		Q9D772
ENSMUST00000108050	ENSMUSG00000028439	4	41517691	41569538	-1	0	0	98	0	0	0	23	81	85	0	0	A2ANP2	
ENSMUST00000108051	ENSMUSG00000037174	3	51252720	51340663	-1	3	0	0	0	3	11	61	358	196	50	163		Q9JHC9
ENSMUST00000108052	ENSMUSG00000028439	4	41517691	41569538	-1	0	0	0	130	0	0	248	139	158	38	267	A2ANP1	
ENSMUST00000108053	ENSMUSG00000037174	3	51252720	51340663	-1	0	0	0	63	0	0	0	0	0	0	0		Q9JHC9
ENSMUST00000108055	ENSMUSG00000028438	4	41390745	41464887	-1	49	63	152	69	49	30	19	30	40	1	40		Q6NWW5
ENSMUST00000108056	ENSMUSG00000059439	11	85353167	85826058	1	8	4	28	5	9	4	2	3	0	2	7		Q8CCN5
ENSMUST00000108060	ENSMUSG00000028437	4	41348996	41390525	1	0	0	0	57	0	0	419	1636	729	118	656		Q8BH48
ENSMUST00000108061	ENSMUSG00000059439	11	85353167	85826058	1	0	0	0	0	0	0	15	54	50	0	16	B1AR74	
ENSMUST00000108062	ENSMUSG00000059439	11	85353167	85826058	1	0	16	0	4	6	2	172	316	179	79	161	B1AR74	
ENSMUST00000108065	ENSMUSG00000025766	3	41742611	41803320	1	0	0	0	0	0	0	0	22	0	14	5		Q8BGN2
ENSMUST00000108068	ENSMUSG00000028433	4	41194313	41275144	-1	25	1	39	44	3	23	7	5	13	1	6	A2AMY5	
ENSMUST00000108069	ENSMUSG00000030499	7	34639014	34656732	-1	0	0	0	10	2	0	0	0	0	4	11		Q8K0E1
ENSMUST00000108070	ENSMUSG00000030499	7	34639014	34656732	-1	12	11	41	58	22	7	0	0	0	1	3		Q8K0E1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108074	ENSMUSG00000066571	7	34236707	34313551	-1	0	0	29	79	25	0	116	232	125	15	2	Q8C5X1	
ENSMUST00000108075	ENSMUSG00000000804	11	84984442	85140161	-1	9	28	40	18	18	14	1362	4369	2941	365	2222	F8VPZ3	
ENSMUST00000108076	ENSMUSG00000000805	11	84957786	84966044	1	2	3	22	7	6	1	5	5	0	0	0	F6ST32	
ENSMUST00000108077	ENSMUSG00000037818	3	40846970	40938138	1	0	0	0	0	0	0	0	0	0	0	0		Q8C1A9
ENSMUST00000108078	ENSMUSG00000037818	3	40846970	40938138	1	0	0	0	0	0	0	16	0	0	18	0		Q8C1A9
ENSMUST00000108080	ENSMUSG00000045140	11	84876315	84880285	-1	3	0	0	0	0	0	8	10	8	1	1	B7ZN11	Q8C398
ENSMUST00000108081	ENSMUSG00000020530	11	84832361	84870817	-1	0	0	10	0	0	0	36	459	495	226	279		Q5SV77
ENSMUST00000108083	ENSMUSG00000078752	7	34095431	34100837	1	6	4	4	7	7	4	0	0	0	0	0	A2BH64	
ENSMUST00000108086	ENSMUSG00000025757	3	40744495	40796103	1	5	5	4	36	3	5	71	200	127	40	33		P48722
ENSMUST00000108087	ENSMUSG00000078753	7	33743799	33744982	1	1	2	1	2	2	1	0	0	0	0	0	B1B0N6	
ENSMUST00000108089	ENSMUSG00000028416	4	40936398	40948294	-1	0	0	0	0	13	0	0	95	32	32	32		Q60739
ENSMUST00000108090	ENSMUSG00000078754	7	31359038	31362072	-1	4	2	1	5	1	2	0	0	0	0	0	D2XZ38	
ENSMUST00000108094	ENSMUSG00000078757	7	32441541	32442722	1	0	0	0	0	0	0	0	0	0	0	0	D2XZ31	
ENSMUST00000108096	ENSMUSG00000028413	4	40804602	40854005	-1	1	2	0	189	14	1	0	5	0	0	23	B1AXY5	
ENSMUST00000108097	ENSMUSG00000078759	7	31712665	31713978	1	0	5	3	3	5	2	0	0	0	0	0	D2XZ31	
ENSMUST00000108101	ENSMUSG00000018648	11	84048041	84069261	-1	2	3	0	0	10	3	0	0	0	9	19	Q542U4	Q9JLY7
ENSMUST00000108102	ENSMUSG00000001249	7	31098725	31115290	-1	0	0	0	32	0	0	10	9	6	0	0		O35453
ENSMUST00000108103	ENSMUSG00000028411	4	40682382	40703194	-1	0	0	0	6	0	0	12	10	5	30	5		Q7TQC5
ENSMUST00000108105	ENSMUSG00000058174	3	37714190	37724490	-1	0	15	0	7	13	6	0	0	0	0	0	Q8BGG2	
ENSMUST00000108107	ENSMUSG00000037211	3	37639947	37644598	1	8	8	13	206	20	8	0	0	0	0	0	Q53ZU1	Q9QXV9
ENSMUST00000108108	ENSMUSG00000071014	4	40270591	40279421	-1	6	8	7	169	8	0	10	22	0	48	22	A2AP32	
ENSMUST00000108109	ENSMUSG00000037211	3	37639947	37644598	1	4	4	0	18	7	2	0	5	1	7	33	Q53ZU1	Q9QXV9
ENSMUST00000108110	ENSMUSG00000036570	7	31051678	31057199	-1	3	0	3	3	0	0	0	0	0	10	0		Q9Z239
ENSMUST00000108112	ENSMUSG00000027722	3	37419896	37579096	1	7	3	12	56	17	7	0	0	0	0	0		Q3UMC0
ENSMUST00000108113	ENSMUSG00000020679	11	83850063	83905819	1	0	3	0	40	8	0	0	0	0	0	0		P27889
ENSMUST00000108114	ENSMUSG00000020679	11	83850063	83905819	1	16	0	30	0	24	0	0	0	0	0	0		P27889
ENSMUST00000108116	ENSMUSG00000001247	7	30957770	30973464	-1	0	0	0	0	0	0	68	31	39	0	92		Q99KG5
ENSMUST00000108117	ENSMUSG00000050174	3	37404910	37420211	-1	0	0	0	0	0	0	0	0	0	0	0	A2ACU1	
ENSMUST00000108118	ENSMUSG00000050174	3	37404910	37420211	-1	0	0	0	8	0	0	0	0	0	0	0	A2ACU7	
ENSMUST00000108119	ENSMUSG00000058239	7	30945248	30956803	-1	0	0	0	0	0	0	14	40	66	10	28		Q64705
ENSMUST00000108120	ENSMUSG00000037225	3	37348346	37410108	1	0	0	0	2	1	3	0	0	0	0	0	Q925A1	
ENSMUST00000108121	ENSMUSG00000051444	3	37312554	37321453	1	12	0	8	6	10	0	0	0	0	8	0	Z4YKQ3	
ENSMUST00000108122	ENSMUSG00000045083	4	35706647	36951747	-1	0	0	0	0	0	0	0	0	0	0	0	B2RQD4	Q3URE9
ENSMUST00000108124	ENSMUSG00000045083	4	35706647	36951747	-1	6	7	7	0	19	9	0	0	0	0	0	B2RQD4	Q3URE9
ENSMUST00000108125	ENSMUSG00000030577	7	30865402	30880342	-1	0	0	3	0	0	0	21	0	0	0	108	Q3UP36	
ENSMUST00000108126	ENSMUSG00000028300	4	35191285	35226175	-1	3	0	15	14	1	0	0	585	0	24	0	A2ANZ2	
ENSMUST00000108127	ENSMUSG00000028300	4	35191285	35226175	-1	0	0	0	7	0	0	266	630	393	340	224	Q3U3D8	
ENSMUST00000108130	ENSMUSG00000028298	4	34893779	34907370	1	0	0	0	0	0	0	0	1	0	0	0	A0A0F7RQH1	P01216
ENSMUST00000108131	ENSMUSG00000028295	4	34768664	34778423	-1	0	0	0	0	0	0	0	42	13	30	6		Q9CQQ0
ENSMUST00000108132	ENSMUSG00000028295	4	34768664	34778423	-1	0	0	4	0	0	0	0	16	0	27	0		Q9CQQ0
ENSMUST00000108133	ENSMUSG00000028295	4	34768664	34778423	-1	0	0	0	0	0	0	6	10	0	0	6		Q9CQQ0
ENSMUST00000108134	ENSMUSG00000028295	4	34768664	34778423	-1	0	3	0	4	0	0	2	33	11	36	13		Q9CQQ0
ENSMUST00000108136	ENSMUSG00000028294	4	34688559	34730206	-1	4	4	20	0	0	1	0	0	0	0	0		Q6PE87
ENSMUST00000108137	ENSMUSG00000020682	11	83440768	83463071	-1	0	0	10	46	0	0	0	0	0	0	4	Q8CGV8	
ENSMUST00000108140	ENSMUSG00000020684	11	83409137	83421039	1	0	0	0	0	0	2	1	1	0	2	0		Q5SSG5
ENSMUST00000108141	ENSMUSG00000036733	7	30640994	30650317	-1	8	9	0	0	2	3	797	1445	760	160	555	D3YYW8	
ENSMUST00000108142	ENSMUSG00000040044	4	34570796	34614944	-1	0	0	1	0	0	1	0	198	2	32	71		Q9JK30
ENSMUST00000108145						0	1	1	1	2	2	0	0	0	0	0		
ENSMUST00000108146	ENSMUSG00000018733	11	83294642	83302586	-1	0	5	0	56	15	5	40	32	74	37	0	Q5SWQ8	Q8VC48
ENSMUST00000108147	ENSMUSG00000006311	7	30633616	30635852	-1	13	7	8	111	14	7	0	0	0	0	0		P41163
ENSMUST00000108148	ENSMUSG00000028264	4	34024874	34050191	-1	0	2	0	0	2	1	0	0	0	0	0	B1AWF0	
ENSMUST00000108150	ENSMUSG00000006310	7	30589681	30598909	-1	0	0	0	5	0	0	0	0	0	0	0		Q9JKD9
ENSMUST00000108151	ENSMUSG00000006310	7	30589681	30598909	-1	15	9	42	24	14	10	47	44	20	15	78	B2RQ06	
ENSMUST00000108152	ENSMUSG00000035208	11	83002158	83020810	-1	110	62	836	169	88	69	0	118	27	0	0	E9Q0R4	
ENSMUST00000108153	ENSMUSG00000028274	4	33310311	33502614	1	20	24	35	58	19	10	42	132	72	30	56	Q3UA94	O55236
ENSMUST00000108154	ENSMUSG00000006307	7	30568858	30588726	-1	54	17	1	81	0	0	0	0	0	0	0		O08550
ENSMUST00000108155	ENSMUSG00000037325	3	36573142	36613477	-1	0	8	3	2	3	3	0	0	5	0	0	E9Q0R0	
ENSMUST00000108156	ENSMUSG00000037325	3	36573142	36613477	-1	9	0	0	54	16	0	0	0	0	21	0		Q8K2G4
ENSMUST00000108157	ENSMUSG00000054404	11	82951349	82962941	1	0	1	0	0	0	0	0	0	11	0	16		Q8CBA2
ENSMUST00000108158	ENSMUSG00000054404	11	82951349	82962941	1	0	0	0	1	0	0	0	0	4	0	3	Q3TAE9	
ENSMUST00000108159	ENSMUSG00000054679	4	33208991	33233340	1	1	1	0	13	0	0	0	0	0	0	0	A3KG57	
ENSMUST00000108160	ENSMUSG00000018845	11	82910550	82943403	1	24	18	40	18	23	20	0	0	0	0	0		Q8CGY6
ENSMUST00000108161	ENSMUSG00000078765	7	30563301	30567960	1	0	11	27	0	0	0	16	0	78	0	25	F8WH71	
ENSMUST00000108162	ENSMUSG00000023267	4	33062999	33095865	1	0	0	17	11	0	0	0	0	0	0	0		P56476
ENSMUST00000108164	ENSMUSG00000036845	7	30555441	30559838	-1	2	4	4	8	10	0	9	27	20	7	17	E9Q0Q9	
ENSMUST00000108165	ENSMUSG00000036864	7	30539134	30552296	-1	47	30	235	54	36	20	9	61	20	0	17		Q7TSA6
ENSMUST00000108166	ENSMUSG00000040183	4	32804035	32950841	-1	0	0	30	2	4	0	0	0	3	1	2	A2ANY8	
ENSMUST00000108173	ENSMUSG00000020696	11	82802449	82871210	-1	0	0	0	0	0	0	610	1558	879	43	413	Q3UD78	Q6ZQM0
ENSMUST00000108175	ENSMUSG00000036931	7	30421732	30428746	1	0	0	20	4	0	0	0	1	78	122	64		Q2TB02
ENSMUST00000108176	ENSMUSG00000036931	7	30421732	30428746	1	0	0	3	71	8	2	81	658	103	0	53		Q2TB02
ENSMUST00000108178	ENSMUSG00000028282	4	32615451	32653265	1	1	0	0	0	1	0	0	4	0	0	0	B1AX75	
ENSMUST00000108180	ENSMUSG00000040270	4	32238804	32586108	1	0	0	0	149	0	42	0	0	16	0	35		P97303
ENSMUST00000108182	ENSMUSG00000027708	3	35892105	35937445	-1	6	8	0	0	0	5	0	212	120	31	75	A0A0B4J1K8	Q9QZ73
ENSMUST00000108183	ENSMUSG00000028284	4	31964097	32023467	1	23	80	400	5	66	57	0	1	0	0	5	A2AP93	
ENSMUST00000108184	ENSMUSG00000028284	4	31964097	32023467	1	0	0	43	0	0	0	0	197	1	41	96	A2AP92	
ENSMUST00000108187	ENSMUSG00000013928	7	30280094	30290237	1	9	1	17	139	2	1	0	0	0	0	0	D3YYI4	
ENSMUST00000108189	ENSMUSG00000020702	11	82176657	82305690	-1	0	1	0	0	0	0	0	0	0	1	0	Q0VB35	P10146
ENSMUST00000108190	ENSMUSG00000037020	7	30240138	30280419	-1	34	36	0	41	0	18	40	72	63	0	50	E9QK36	
ENSMUST00000108191	ENSMUSG00000028289	4	28813131	28967499	1	0	49	7	0	0	0	0	1	2	0	1	A2BDQ4	
ENSMUST00000108192	ENSMUSG00000019738	7	30231948	30233390	1	0	0	0	0	0	0	36	50	37	91	20	D3YYI3	
ENSMUST00000108193	ENSMUSG00000019738	7	30231948	30233390	1	0	0	0	0	0	0	33	50	4	166	18	D3YYI2	
ENSMUST00000108194	ENSMUSG00000028289	4	28813131	28967499	1	0	0	0	10	0	0	0	0	0	0	0		Q61772
ENSMUST00000108195	ENSMUSG00000027679	3	34056020	34081321	-1	2	0	0	21	1	0	16	46	50	346	40		Q9CQV7
ENSMUST00000108196	ENSMUSG00000001794	7	30186942	30195164	-1	0	5	3	0	10	0	4061	4614	2915	877	1715		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108199	ENSMUSG00000055373	4	25609332	25800244	-1	8	2	13	89	15	1	0	0	0	0	0	Q14AE3	O88819
ENSMUST00000108200	ENSMUSG00000049421	7	30094777	30107622	1	0	0	0	5	0	3	63	309	76	153	77		Q62513
ENSMUST00000108204	ENSMUSG00000028259	4	25199908	25242876	-1	0	2	0	0	6	0	0	0	0	0	0		Q9WTX7
ENSMUST00000108205	ENSMUSG00000059975	7	29930815	29954089	-1	33	33	172	52	27	21	4	58	10	17	21		Q80W31
ENSMUST00000108210	ENSMUSG00000027677	3	33799832	33814860	1	11	13	1	64	13	3	65	626	287	164	186	G3X9T5	
ENSMUST00000108211	ENSMUSG00000059975	7	29930815	29954089	-1	1	0	0	0	0	0	0	0	0	0	0	Q8BIJ3	
ENSMUST00000108212	ENSMUSG00000059975	7	29930815	29954089	-1	6	14	18	10	5	13	1	2	4	0	4	Q8BIJ3	
ENSMUST00000108213						2	0	0	0	0	9	0	0	0	0	0		
ENSMUST00000108214	ENSMUSG00000040387	4	24612554	24851124	-1	104	86	583	0	40	52	11	40	14	1	21	A2AJX1	
ENSMUST00000108216	ENSMUSG00000017421	11	80383279	80405733	1	24	15	51	26	14	3	23	21	22	9	25	Q8CCB2	
ENSMUST00000108218	ENSMUSG00000040387	4	24612554	24851124	-1	52	10	46	325	91	12	0	0	0	0	0	A2AJX0	
ENSMUST00000108219						12	14	52	20	11	8	0	0	0	0	0		
ENSMUST00000108221	ENSMUSG00000027674	3	32949408	33143247	-1	2	1	0	0	2	0	0	0	0	1	1	F8SLQ6	Q8C437
ENSMUST00000108222	ENSMUSG00000045751	4	24496451	24602950	1	0	0	0	73	20	0	0	79	49	0	0		B1AUR6
ENSMUST00000108223	ENSMUSG00000050855	7	29833620	29853669	-1	107	82	122	158	134	62	3	19	20	3	16	Q3UVK2	
ENSMUST00000108224	ENSMUSG00000027674	3	32949408	33143247	-1	0	0	0	0	0	0	0	0	0	0	0	D3YYH0	
ENSMUST00000108225	ENSMUSG00000027674	3	32949408	33143247	-1	0	0	0	0	0	0	0	0	0	0	0	F8SLQ3	
ENSMUST00000108226	ENSMUSG00000027674	3	32949408	33143247	-1	0	0	0	0	0	0	0	0	0	0	0	F8SLP9	
ENSMUST00000108228	ENSMUSG00000056900	3	32817546	32938071	1	1	2	3	117	11	0	0	0	0	0	0	J3QSN2	
ENSMUST00000108229	ENSMUSG00000028248	4	21847583	21876475	1	1	0	3	3	11	2	82	132	60	67	190	A2AJT3	
ENSMUST00000108230	ENSMUSG00000030584	7	29303951	29317588	1	2	0	3	110	5	0	0	0	0	0	3	D3YYG6	
ENSMUST00000108231	ENSMUSG00000030584	7	29303951	29317588	1	0	3	0	23	0	0	0	0	0	0	0	D3YY44	
ENSMUST00000108232	ENSMUSG00000040455	4	21767156	21837872	1	6	10	5	3	2	0	24	0	83	6	35		Q8K387
ENSMUST00000108234	ENSMUSG00000027669	3	32580332	32616585	-1	41	21	47	279	64	27	0	5	4	11	9		P29387
ENSMUST00000108236	ENSMUSG00000074227	7	29256331	29281977	-1	5	0	3	222	5	15	402	556	247	69	263		Q9WU03
ENSMUST00000108237	ENSMUSG00000030588	7	29238329	29247593	1	0	0	0	57	12	0	21	3	4	4	7	D3YY42	
ENSMUST00000108238	ENSMUSG00000030588	7	29238329	29247593	1	0	0	0	21	0	0	42	102	27	18	40		Q9CX30
ENSMUST00000108239	ENSMUSG00000017550	11	80089400	80135794	1	13	18	26	83	17	11	15	28	29	4	27	Z4YKQ9	
ENSMUST00000108240	ENSMUSG00000028252	4	21727701	21759922	1	0	0	0	0	0	0	49	93	29	91	25	Q8CAS3	
ENSMUST00000108241	ENSMUSG00000035575	11	79932321	79962390	-1	6	6	15	7	5	0	0	0	23	100	41		Q8VCY6
ENSMUST00000108242	ENSMUSG00000027665	3	32397671	32468486	1	0	0	0	0	0	0	0	896	157	166	44	D3YY41	
ENSMUST00000108243	ENSMUSG00000027665	3	32397671	32468486	1	5	2	5	53	6	2	492	1140	1130	85	790		P42337
ENSMUST00000108245	ENSMUSG00000069072	3	31202858	31310378	-1	6	3	17	4	8	0	0	0	0	0	0	D3YY38	
ENSMUST00000108246	ENSMUSG00000041058	4	19608303	19708993	-1	12	0	20	48	0	11	60	239	163	48	135		Q8BZZ3
ENSMUST00000108249	ENSMUSG00000037643	3	30995747	31052959	1	33	29	46	67	43	24	143	371	258	30	194		Q62074
ENSMUST00000108250	ENSMUSG00000078772	4	19605451	19651130	1	1	1	7	1	1	0	3	7	3	0	0	A2AGJ4	
ENSMUST00000108251	ENSMUSG00000020716	11	79339693	79581612	1	8	0	8	8	0	0	8	0	0	0	0		Q04690
ENSMUST00000108253	ENSMUSG00000028229	4	19575162	19606932	1	38	41	79	74	54	18	29	117	79	187	88	A2AGJ2	
ENSMUST00000108254						5	1	1	7	1	0	2	0	7	2	8		
ENSMUST00000108255	ENSMUSG00000037652	3	30899371	30969415	-1	0	0	0	0	0	0	0	0	0	0	0	D3YY34	
ENSMUST00000108257						16	20	22	6	24	10	0	0	0	0	0		
ENSMUST00000108258	ENSMUSG00000037661	3	30855950	30897192	1	2	0	0	0	0	6	1	21	0	0	29		Q3U3F9
ENSMUST00000108259	ENSMUSG00000037661	3	30855950	30897192	1	8	0	7	0	0	0	0	19	0	46	0		Q3U3F9
ENSMUST00000108261	ENSMUSG00000037661	3	30855950	30897192	1	0	0	0	138	21	0	11	0	58	0	30		Q3U3F9
ENSMUST00000108262	ENSMUSG00000051860	3	30746293	30767174	1	0	0	0	36	0	0	0	0	0	0	0	F8WHA0	
ENSMUST00000108263	ENSMUSG00000074653	3	30679058	30699843	-1	19	15	48	20	25	11	0	0	0	0	2	D3YY33	
ENSMUST00000108264	ENSMUSG00000018334	11	79013440	79146407	-1	8	0	16	178	11	11	3	15	19	0	31	Q5SXE4	
ENSMUST00000108265	ENSMUSG00000027703	3	30644507	30672431	1	14	0	15	7	7	6	0	0	0	0	0		A6H6A4
ENSMUST00000108267	ENSMUSG00000027703	3	30644507	30672431	1	6	12	10	6	12	8	0	0	0	0	0		A6H6A4
ENSMUST00000108268	ENSMUSG00000001123	11	78962974	78984946	-1	11	12	45	27	27	7	3013	5911	2485	2466	2040		O08573
ENSMUST00000108269	ENSMUSG00000001123	11	78962974	78984946	-1	0	0	1	0	0	0	40	149	86	46	75	G3X9T7	
ENSMUST00000108270	ENSMUSG00000027684	3	29951296	30548008	-1	7	0	22	28	6	0	0	0	0	0	0	H9T841	P14404
ENSMUST00000108271	ENSMUSG00000027684	3	29951296	30548008	-1	0	4	8	0	5	0	0	1	0	0	0	Q8CCA6	
ENSMUST00000108273	ENSMUSG00000040536	4	14952245	15149794	-1	33	21	12	4	36	11	3	4	4	1	5		Q8BG18
ENSMUST00000108275	ENSMUSG00000001105	11	78536361	78541737	1	0	0	0	0	0	0	45	100	63	230	57		Q61025
ENSMUST00000108276	ENSMUSG00000023151	4	14623620	14796060	-1	4	0	1	0	2	0	0	2	0	0	0		Q9D9Q0
ENSMUST00000108277	ENSMUSG00000017615	11	78522850	78536332	-1	0	0	12	15	0	0	124	0	110	0	115		O70479
ENSMUST00000108278	ENSMUSG00000030598	7	28716804	28738144	1	0	0	17	0	0	19	10	36	7	0	3	Q3V064	Q9QZM8
ENSMUST00000108279	ENSMUSG00000030598	7	28716804	28738144	1	0	16	11	0	8	0	0	5	10	3	13		Q9QZM8
ENSMUST00000108280	ENSMUSG00000037463	7	28692849	28699338	1	24	0	16	10	6	6	0	12	0	0	0	Q3TEI7	
ENSMUST00000108281	ENSMUSG00000037463	7	28692849	28699338	1	0	3	7	122	19	6	1	0	0	0	1		Q6DIA9
ENSMUST00000108283	ENSMUSG00000030602	7	28399549	28598185	-1	0	0	20	67	0	0	43	99	89	10	76		Q8BTW9
ENSMUST00000108285	ENSMUSG00000028218	4	12153409	12172015	-1	0	0	0	5	3	0	5	0	5	12	0		Q8BP22
ENSMUST00000108287	ENSMUSG00000050132	11	78472330	78497754	-1	17	20	44	93	28	26	0	5	0	0	0		Q6PDS3
ENSMUST00000108288	ENSMUSG00000030600	7	28451980	28468242	1	14	8	50	829	45	9	7	27	8	2	20		Q2WF71
ENSMUST00000108289	ENSMUSG00000060791	7	28437447	28448233	1	3	4	4	0	3	0	91	100	26	172	34	D3YY16	
ENSMUST00000108292	ENSMUSG00000060791	7	28437447	28448233	1	3	0	9	0	2	2	85	237	49	289	48	A7VJA4	Q9ERL7
ENSMUST00000108293	ENSMUSG00000049488	4	12039355	12090020	-1	21	19	24	694	36	30	37	25	62	11	59	A2AJP5	
ENSMUST00000108294	ENSMUSG00000002057	11	78357577	78386558	-1	55	27	238	124	51	31	1	1	0	1	1	Q5SYK1	Q61575
ENSMUST00000108295	ENSMUSG00000002058	11	78343482	78349164	1	4	0	5	4	9	0	0	0	0	0	0	B1AQD9	
ENSMUST00000108296						7	0	0	0	2	1	0	36	32	8	32		
ENSMUST00000108297	ENSMUSG00000049225	4	11958184	11966452	-1	7	0	8	18	2	2	0	10	0	2	3	A8Y5Q1	Q3UV70
ENSMUST00000108298	ENSMUSG00000027699	3	27097222	27153878	-1	0	0	4	0	2	0	0	35	17	0	0		Q07139
ENSMUST00000108299	ENSMUSG00000049225	4	11958184	11966452	-1	0	0	0	0	0	0	0	25	0	0	0	A2AJP9	
ENSMUST00000108300	ENSMUSG00000027699	3	27097222	27153878	-1	0	0	0	0	0	0	0	0	0	0	0		Q07139
ENSMUST00000108301	ENSMUSG00000049225	4	11958184	11966452	-1	10	7	19	49	8	7	0	0	0	0	0	A2AJQ0	
ENSMUST00000108302	ENSMUSG00000049225	4	11958184	11966452	-1	0	0	6	56	4	0	0	0	0	0	11	A8Y5Q0	
ENSMUST00000108303	ENSMUSG00000028217	4	11758147	11817895	1	129	110	618	142	141	63	1	7	4	7	12	A2AKS7	
ENSMUST00000108304	ENSMUSG00000028214	4	11704457	11714752	1	12	0	10	27	0	15	0	0	0	0	0	Q3TH76	P55041
ENSMUST00000108305	ENSMUSG00000039335	3	26637620	26983212	1	10	0	0	1	0	5	0	0	0	0	0		Q8C636
ENSMUST00000108306	ENSMUSG00000078773	4	11558922	11615805	1	0	2	0	1	4	0	1	0	0	0	2	A2AIU9	
ENSMUST00000108307	ENSMUSG00000040720	4	11485958	11550684	1	0	8	0	0	14	14	0	0	0	0	0	E9PZY8	
ENSMUST00000108308	ENSMUSG00000063887	3	25426215	26332460	-1	0	0	50	0	0	5	0	1	1	0	0	E9QK34	
ENSMUST00000108310	ENSMUSG00000040728	4	11331933	11386783	-1	2	0	0	0	0	0	0	0	0	0	0		Q3US41

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108311	ENSMUSG00000040728	4	11331933	11386783	-1	0	15	24	0	8	0	0	0	0	0	0	F8WGU3	
ENSMUST00000108313	ENSMUSG00000040728	4	11331933	11386783	-1	16	0	12	88	11	0	0	0	0	0	0		Q3US41
ENSMUST00000108314						25	18	57	20	41	14	26	567	32	51	53		
ENSMUST00000108315	ENSMUSG00000003436	7	28293553	28302238	-1	35	19	46	148	31	19	3	13	4	2	5	Q3UND5	O88516
ENSMUST00000108316	ENSMUSG00000046750	7	28284652	28291186	-1	9	7	13	0	12	6	0	1	0	0	0	Q5FWB9	
ENSMUST00000108317	ENSMUSG00000044122	11	78193392	78205763	1	0	1	11	4	10	3	5	48	7	21	13		B0QZF7
ENSMUST00000108318	ENSMUSG00000040738	4	11199158	11254258	-1	7	11	10	182	10	9	0	0	0	30	1	A2API3	
ENSMUST00000108319	ENSMUSG00000040738	4	11199158	11254258	-1	0	0	0	0	0	0	143	493	323	62	206		Q80V86
ENSMUST00000108321	ENSMUSG00000027615	3	19995945	20035315	-1	0	0	0	0	0	0	159	414	167	110	229	E9PZY1	
ENSMUST00000108322	ENSMUSG00000002059	11	78188430	78192193	1	0	0	0	306	17	7	0	0	0	0	0	Q0PD20	
ENSMUST00000108324	ENSMUSG00000028212	4	11191351	11204779	1	0	0	6	0	14	0	31	64	13	16	15	Q544H6	Q9Z238
ENSMUST00000108325	ENSMUSG00000003617	3	19957054	20009145	1	0	0	0	0	0	0	0	0	0	0	45	G3X9T8	
ENSMUST00000108328	ENSMUSG00000003617	3	19957054	20009145	1	8	5	75	3	1	4	1	1	1	97	3	G3X8Q5	
ENSMUST00000108329	ENSMUSG00000003617	3	19957054	20009145	1	0	0	0	0	0	0	0	0	0	0	35	E9PZD8	
ENSMUST00000108331	ENSMUSG00000078779	7	27838607	27856438	1	8	16	6	7	8	6	1	6	5	4	3	F8VPX4	
ENSMUST00000108332						31	25	26	51	28	9	0	19	7	12	3		
ENSMUST00000108333	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	0	0	0	0	0	0	0	0	A2AL76	
ENSMUST00000108334	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	0	0	0	0	5	0	0	0	A2AL75	
ENSMUST00000108335	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	2	0	1	0	2	0	0	5	0	A2AL74	
ENSMUST00000108336	ENSMUSG00000037640	7	27731389	27753702	1	128	109	517	197	108	73	27	194	69	55	27	Q8K0D9	
ENSMUST00000108337	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	0	0	0	0	0	3	0	1	Q3TU40	
ENSMUST00000108338	ENSMUSG00000019437	11	78176711	78181909	1	1	1	1	16	7	1	0	0	0	0	0		Q99JT6
ENSMUST00000108339	ENSMUSG00000028207	4	9448069	9669344	-1	39	28	48	56	18	0	0	0	7	0	0	Q8CBM2	
ENSMUST00000108340	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	0	0	28	0	0	26	0	23	A2AL85	
ENSMUST00000108341	ENSMUSG00000040390	7	27656375	27674598	-1	9	0	0	559	24	0	43	0	58	8	36	D3YXM8	
ENSMUST00000108342	ENSMUSG00000004056	7	27591552	27640826	1	6	3	65	9	6	8	6	4	3	2	8	D3YXM7	
ENSMUST00000108343	ENSMUSG00000004056	7	27591552	27640826	1	0	0	15	7	31	0	15	15	61	0	21	Q3TY95	Q60823
ENSMUST00000108344	ENSMUSG00000004056	7	27591552	27640826	1	33	33	51	106	28	25	116	329	148	13	121	Q3TY95	Q60823
ENSMUST00000108345	ENSMUSG00000047213	3	16183212	16217037	1	16	9	0	39	7	0	362	162	56	147	66		Q8BYK6
ENSMUST00000108346	ENSMUSG00000047213	3	16183212	16217037	1	0	0	13	0	0	2	513	1868	630	115	555		Q8BYK6
ENSMUST00000108347	ENSMUSG00000078780	3	15946870	16006437	-1	0	1	0	2	0	5	0	0	138	935	292	Q1AN92	
ENSMUST00000108348	ENSMUSG00000041216	4	9269293	9451691	1	29	6	0	26	5	0	0	0	0	0	0		Q9D4C9
ENSMUST00000108349	ENSMUSG00000074677	3	15795145	15848528	-1	3	0	4	3	2	1	41	525	70	206	50	E9PZD0	
ENSMUST00000108350	ENSMUSG00000074677	3	15795145	15848528	-1	0	3	0	0	0	0	0	22	0	0	0	E9PZC9	
ENSMUST00000108352	ENSMUSG00000074677	3	15795145	15848528	-1	0	3	1	4	0	0	48	70	0	44	0	K7N6K7	
ENSMUST00000108353	ENSMUSG00000040424	7	27523267	27531175	1	8	12	26	45	25	8	4	0	2	0	2		Q3V016
ENSMUST00000108354	ENSMUSG00000074677	3	15795145	15848528	-1	1	0	0	0	0	0	103	1676	293	1277	280	D3YXM0	
ENSMUST00000108355	ENSMUSG00000053198	7	27499324	27520214	1	26	29	64	123	62	0	4	0	9	0	13		O55103
ENSMUST00000108357	ENSMUSG00000040466	7	27447978	27466144	1	1	1	0	0	0	0	7	17	16	10	0	E9PZC4	
ENSMUST00000108358	ENSMUSG00000040466	7	27447978	27466144	1	1	0	3	30	3	2	25	31	33	0	10	E9PZC3	
ENSMUST00000108360	ENSMUSG00000037791	11	77982754	78030539	1	5	6	45	253	4	2	0	72	96	0	210		Q5SPL2
ENSMUST00000108361	ENSMUSG00000078783	3	15296551	15332302	-1	8	3	16	5	6	3	99	777	119	399	144	Q1AN91	
ENSMUST00000108362	ENSMUSG00000011751	7	27356383	27447686	-1	20	10	27	27	40	17	0	0	0	0	0	E9PZC2	
ENSMUST00000108363	ENSMUSG00000011751	7	27356383	27447686	-1	0	0	0	0	0	0	22	26	9	6	11	E9PZC2	
ENSMUST00000108364	ENSMUSG00000011751	7	27356383	27447686	-1	16	0	34	56	13	0	0	0	0	0	0	E9PZC2	
ENSMUST00000108365	ENSMUSG00000078784	3	14606284	14611285	-1	6	0	9	59	5	2	0	2	0	5	4		Q0VG62
ENSMUST00000108369	ENSMUSG00000040488	7	27305136	27337692	-1	0	0	0	0	0	27	0	0	0	0	0	E9QPS5	
ENSMUST00000108370	ENSMUSG00000027550	3	14533788	14572658	1	0	4	0	56	5	2	5	8	0	0	5	B9EI20	
ENSMUST00000108371						0	2	0	1	1	0	0	0	0	0	4		
ENSMUST00000108372	ENSMUSG00000039717	3	13946393	14182287	1	8	0	0	3	0	1	0	0	0	0	0		Q8BTF8
ENSMUST00000108373						0	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000108374	ENSMUSG00000028249	4	6365650	6408423	1	6	8	2	6	11	4	9	61	9	34	45	A2AKJ9	
ENSMUST00000108375	ENSMUSG00000000631	11	77763246	77865980	1	0	0	0	8	0	0	0	15	57	0	194		Q9JMH9
ENSMUST00000108376	ENSMUSG00000000631	11	77763246	77865980	1	0	0	12	120	13	11	0	0	0	0	37		Q9JMH9
ENSMUST00000108377	ENSMUSG00000039795	3	10339953	10351317	-1	0	0	0	0	0	0	1	0	10	0	0	D3Z7G5	
ENSMUST00000108378	ENSMUSG00000003762	7	27233023	27257950	1	0	0	9	12	0	0	0	0	0	0	0	E9QLB8	
ENSMUST00000108379	ENSMUSG00000078786	7	27195781	27210186	1	61	66	322	189	76	44	17	45	21	1	20	D3Z7G4	
ENSMUST00000108380	ENSMUSG00000049119	4	5644090	6108223	1	2	11	23	0	0	7	1	0	0	0	1		Q8C739
ENSMUST00000108382	ENSMUSG00000058709	7	27158658	27166802	-1	3	4	11	241	3	4	0	17	0	0	28	Q80X29	Q91YE2
ENSMUST00000108383	ENSMUSG00000071019	4	4055929	4077522	-1	0	5	0	5	0	0	0	0	0	0	0		Q05A13
ENSMUST00000108384	ENSMUSG00000027508	3	9687479	9833679	-1	0	0	0	0	0	0	229	23	1358	5	1062	A6H659	Q3U1F9
ENSMUST00000108385	ENSMUSG00000078787	7	27153714	27158668	1	0	0	40	18	13	0	0	9	0	0	11	D3Z7F6	
ENSMUST00000108386	ENSMUSG00000042198	4	3938888	3951046	1	0	0	0	4	0	0	18	16	0	22	5		Q8K2Q5
ENSMUST00000108387	ENSMUSG00000054102	7	26535023	26575615	1	8	0	0	4	7	0	0	0	0	0	0	D3Z7F5	
ENSMUST00000108391	ENSMUSG00000020836	11	77462411	77470484	1	0	0	0	0	0	0	0	0	0	0	0		Q920M5
ENSMUST00000108393	ENSMUSG00000017688	3	3508030	3658052	1	0	2	23	23	7	4	0	0	0	0	0	Q059V1	
ENSMUST00000108394	ENSMUSG00000017688	3	3508030	3658052	1	10	5	0	1	2	0	0	0	0	0	0	E9QPS1	
ENSMUST00000108395	ENSMUSG00000040703	7	25802475	25816913	-1	17	21	68	131	27	15	0	0	14	0	7	D3Z7F1	
ENSMUST00000108400	ENSMUSG00000050944	11	77089915	77188968	-1	11	24	16	23	15	0	6	26	16	6	14		A0JP43
ENSMUST00000108401	ENSMUSG00000040725	7	25721165	25754757	-1	2	3	4	40	0	0	0	10	27	0	13		Q8VDM6
ENSMUST00000108402	ENSMUSG00000020838	11	76998603	77032340	1	17	7	0	22	25	0	0	0	0	0	0		Q60857
ENSMUST00000108403	ENSMUSG00000063439	7	25680780	25686558	1	8	7	20	33	12	4	538	876	347	326	347		Q3UK10
ENSMUST00000108404	ENSMUSG00000061702	7	25669139	25675166	-1	0	0	0	0	0	0	0	0	0	2	0	D3Z7E8	
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ENSMUST00000108407	ENSMUSG00000017631	11	76416734	76622314	-1	0	0	0	0	0	0	3142	3010	4331	153	4207	E9PUE7	
ENSMUST00000108408	ENSMUSG00000017631	11	76416734	76622314	-1	3	2	24	96	16	0	271	263	609	74	581		Q5SSL4
ENSMUST00000108409	ENSMUSG00000043843	7	25306106	25316195	1	9	0	9	373	19	10	0	0	0	0	0	E9PUE6	
ENSMUST00000108410	ENSMUSG00000005447	7	25295049	25297986	-1	0	3	3	12	4	0	11	10	3	9	28	D3Z7E6	
ENSMUST00000108411	ENSMUSG00000057177	7	25228258	25237851	-1	15	0	33	105	0	0	0	0	0	0	0	D3Z7E5	
ENSMUST00000108413	ENSMUSG00000008496	7	25087344	25159922	-1	0	0	0	0	0	0	5	0	0	0	0		Q00196
ENSMUST00000108415	ENSMUSG00000008496	7	25087344	25159922	-1	116	83	496	984	131	84	0	71	0	0	84		Q00196
ENSMUST00000108416	ENSMUSG00000008496	7	25087344	25159922	-1	0	0	0	0	0	0	0	0	0	0	0		Q00196
ENSMUST00000108417	ENSMUSG00000008496	7	25087344	25159922	-1	0	0	0	0	0	0	7	0	0	0	1		Q00196
ENSMUST00000108418	ENSMUSG00000008496	7	25087344	25159922	-1	0	0	0	0	0	0	0	0	0	0	0		Q00196

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108419	ENSMUSG00000017288	11	76046226	76179647	-1	0	0	0	0	0	4	0	0	0	9	6		Q8CCB4
ENSMUST00000108420	ENSMUSG00000020847	11	75830999	75938429	-1	0	2	5	5	6	0	0	0	0	0	0		Q768S4
ENSMUST00000108425	ENSMUSG00000017776	11	75679259	75706908	1	12	10	10	19	19	0	73	266	121	65	145	Q8JZR2	
ENSMUST00000108426	ENSMUSG00000017776	11	75679259	75706908	1	1	0	0	60	0	0	0	0	0	0	0	Q3TQV3	
ENSMUST00000108428	ENSMUSG00000040952	7	24884371	24889806	1	7	5	23	18	11	7	2	18	4	1	11	D3Z722	
ENSMUST00000108429	ENSMUSG00000040952	7	24884371	24889806	1	0	0	0	35	9	0	23	19	12	127	20		Q9CZX8
ENSMUST00000108430	ENSMUSG00000040952	7	24884371	24889806	1	4	13	7	31	0	3	34	33	42	163	77		Q9CZX8
ENSMUST00000108431	ENSMUSG00000017774	11	75650504	75673910	1	0	0	0	103	4	0	0	106	159	15	61		Q9WTI7
ENSMUST00000108433	ENSMUSG00000038178	11	75531694	75577575	1	0	0	0	0	0	0	195	16	139	3	74		Q8CGA3
ENSMUST00000108434	ENSMUSG00000002210	7	24399619	24422778	1	0	0	0	5	0	0	8	2	0	0	0	D3Z719	
ENSMUST00000108435	ENSMUSG00000038217	11	75461715	75470899	1	6	5	0	0	0	11	36	174	42	27	34		Q8VC26
ENSMUST00000108436	ENSMUSG00000074282	7	24301704	24316666	-1	14	19	0	0	0	0	0	0	0	0	4	E9Q6Y4	
ENSMUST00000108437	ENSMUSG00000038224	11	75431732	75439591	-1	16	17	53	13	30	21	0	13	1	16	1	Q5ND36	Q61247
ENSMUST00000108438	ENSMUSG00000055305	7	24270420	24277794	1	4	8	64	19	8	6	0	6	0	0	0		Q61116
ENSMUST00000108441	ENSMUSG00000015721	7	23385889	23441922	1	24	3	3	6	0	0	0	0	0	0	0		Q9R1M5
ENSMUST00000108447	ENSMUSG00000001323	11	74906359	74925948	-1	0	0	0	0	0	0	0	0	21	12	0		Q9QZX7
ENSMUST00000108448	ENSMUSG00000001323	11	74906359	74925948	-1	0	0	0	0	0	0	25	42	3	25	0		Q9QZX7
ENSMUST00000108449	ENSMUSG00000040525	7	19778881	19796809	-1	0	2	9	0	0	0	0	0	0	0	0	G3X9U0	
ENSMUST00000108450	ENSMUSG00000062300	7	19716644	19749573	-1	13	8	20	151	28	6	305	522	413	54	144		P32507
ENSMUST00000108451	ENSMUSG00000040564	7	19689484	19692658	-1	0	4	0	5	8	5	0	10	0	0	0		P34928
ENSMUST00000108453	ENSMUSG00000011267	7	19577287	19580656	1	21	8	28	230	30	16	60	71	57	16	45	E9Q6W4	
ENSMUST00000108455	ENSMUSG00000002043	7	19508670	19516145	1	0	0	0	0	0	0	0	0	0	0	0		Q78XR0
ENSMUST00000108457	ENSMUSG00000040714	7	19394437	19404104	-1	5	0	0	0	19	2	0	0	1	0	0	D3Z710	
ENSMUST00000108458	ENSMUSG00000040714	7	19394437	19404104	-1	0	0	0	98	0	5	4	3	0	1	8		Q91W40
ENSMUST00000108459	ENSMUSG00000040714	7	19394437	19404104	-1	0	3	40	42	0	0	0	0	0	0	0		Q91W40
ENSMUST00000108460	ENSMUSG00000030400	7	19382010	19395694	1	0	0	55	9	9	1	0	42	0	15	0	E9Q6K1	
ENSMUST00000108461	ENSMUSG00000030400	7	19382010	19395694	1	0	4	0	0	33	0	30	58	0	17	0	D3Z700	
ENSMUST00000108463	ENSMUSG00000069476	11	74069955	74087292	1	1	1	0	0	1	0	0	0	0	0	0	Q5SVV3	
ENSMUST00000108465	ENSMUSG00000062128	11	73350839	73354795	1	7	8	7	8	5	3	0	0	0	0	0	Q8VEZ6	
ENSMUST00000108468	ENSMUSG00000030401	7	19282662	19296164	1	2	0	7	1	0	4	0	0	0	0	3	Q6IM74	O70622
ENSMUST00000108470	ENSMUSG00000005952	11	73234292	73261242	1	8	4	65	0	25	4	0	0	0	0	0	Z4YKR8	
ENSMUST00000108473	ENSMUSG00000030409	7	19083849	19093821	1	5	15	14	30	8	0	0	0	0	7	8		P54265
ENSMUST00000108474	ENSMUSG00000030409	7	19083849	19093821	1	2	0	0	0	0	0	0	0	0	2	0	E9Q6J9	
ENSMUST00000108476	ENSMUSG00000005949	11	73183596	73199042	-1	10	8	33	29	16	7	475	495	428	3	264	Q542U5	P57757
ENSMUST00000108477	ENSMUSG00000040158	11	73177083	73183162	1	0	0	0	0	0	0	518	1220	347	125	234	B1AUD9	
ENSMUST00000108479	ENSMUSG00000030410	7	19076227	19082776	1	0	0	0	0	0	0	0	0	0	6	8	E9Q6J8	
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ENSMUST00000108481	ENSMUSG00000044903	7	18718090	18727248	1	1	3	3	2	6	2	0	0	0	0	0	E9Q6J7	
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ENSMUST00000108483	ENSMUSG00000030366	7	18065929	18077986	1	3	3	6	3	7	3	0	0	0	0	0	Q9DAS5	
ENSMUST00000108484	ENSMUSG00000020788	11	72961169	72993044	1	0	24	0	16	0	0	0	80	0	0	0	B1ATS4	
ENSMUST00000108485	ENSMUSG00000020788	11	72961169	72993044	1	34	0	0	8	0	0	2944	1617	2875	0	1622	Q8R0X5	Q64518
ENSMUST00000108486	ENSMUSG00000020788	11	72961169	72993044	1	0	0	70	84	15	0	0	87	0	0	0	B1ATS5	
ENSMUST00000108487	ENSMUSG00000030366	7	18065929	18077986	1	18	23	14	17	25	7	0	16	4	1	1	Q3V2Q3	
ENSMUST00000108488	ENSMUSG00000057195	7	18009889	18019221	1	7	0	0	0	0	0	0	0	0	0	0	Q9DAY4	
ENSMUST00000108491	ENSMUSG00000053228	7	17150282	17164253	1	80	60	176	1726	222	96	0	7	0	1	5	E9Q6J4	
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ENSMUST00000108493	ENSMUSG00000078794	7	16875317	16887462	1	11	7	17	341	20	11	1	0	1	0	0		Q0PHV7
ENSMUST00000108495	ENSMUSG00000030374	7	16815889	16840931	1	0	0	2	0	0	0	1050	1166	962	105	819		P58404
ENSMUST00000108496	ENSMUSG00000001918	7	16781340	16798274	1	24	9	14	239	39	0	346	393	356	65	359	Q9ESU7	
ENSMUST00000108498	ENSMUSG00000078795	7	16671331	16675705	-1	10	7	11	8	10	1	0	0	0	0	0	A0A0B4J1L0	
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ENSMUST00000108500	ENSMUSG00000045667	11	72389164	72411713	-1	19	11	82	25	30	19	0	0	0	0	0	Q5F247	
ENSMUST00000108502	ENSMUSG00000020799	11	72344722	72362442	-1	7	2	22	12	10	8	0	0	0	0	0	Q5NBU4	Q9DAJ2
ENSMUST00000108503	ENSMUSG00000020799	11	72344722	72362442	-1	13	5	0	0	5	4	0	0	0	0	0	Q5NBU4	Q9DAJ2
ENSMUST00000108504	ENSMUSG00000070388	11	72314444	72319416	1	12	5	15	42	23	8	0	1	0	0	0		Q5NBU5
ENSMUST00000108505	ENSMUSG00000020807	11	72153929	72207459	-1	1	0	3	31	9	0	0	0	0	0	0	A6QRF1	
ENSMUST00000108506	ENSMUSG00000020807	11	72153929	72207459	-1	24	10	59	12	38	18	0	0	0	0	0		
ENSMUST00000108508	ENSMUSG00000040543	11	72047528	72135778	-1	37	27	155	163	63	0	0	1	0	0	0		Q3UHE1
ENSMUST00000108509	ENSMUSG00000078796	7	16071942	16096328	1	25	18	106	53	46	24	7	39	12	2	22		Q0GGX2
ENSMUST00000108510	ENSMUSG00000020811	11	71749920	71789647	1	0	4	0	0	5	0	0	0	0	0	0		Q80XH4
ENSMUST00000108511	ENSMUSG00000020811	11	71749920	71789647	1	0	0	0	44	7	0	0	0	0	0	0		Q80XH4
ENSMUST00000108513	ENSMUSG00000041583	7	15833241	15839678	-1	3	5	14	8	10	3	0	0	0	0	0	G3X9U1	
ENSMUST00000108514	ENSMUSG00000070390	11	71153102	71230733	-1	0	0	0	7	0	2	0	4	0	0	15	A1Z198	
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ENSMUST00000108518	ENSMUSG00000069830	11	71092236	71144704	-1	11	4	6	0	8	0	10	20	24	2	21	Q2LKU9	
ENSMUST00000108520	ENSMUSG00000074377	7	13909677	13989607	-1	0	0	0	4	2	0	0	0	0	0	0	L7N245	
ENSMUST00000108522	ENSMUSG00000078798	7	13796246	13837409	-1	1	0	1	4	0	3	0	0	0	0	0		P52843
ENSMUST00000108523	ENSMUSG00000018442	11	71007164	71019841	-1	0	2	0	1	0	0	0	13	0	0	4		Q8BNI4
ENSMUST00000108524	ENSMUSG00000094156	7	14465159	14492926	-1	6	2	4	2	7	1	0	0	0	0	0	K7N6K8	
ENSMUST00000108525	ENSMUSG00000078799	7	13623967	13670807	1	1	3	1	3	6	0	0	0	0	0	0	K7N6K9	
ENSMUST00000108526	ENSMUSG00000078800	7	13554864	13571067	-1	1	1	0	3	2	0	0	0	0	0	0	Q0Q236	
ENSMUST00000108527	ENSMUSG00000040620	11	70984091	71004437	-1	19	11	38	36	29	11	40	199	65	14	100		Q80VY9
ENSMUST00000108528	ENSMUSG00000033847	7	13324655	13360672	1	0	0	0	0	0	0	0	0	0	0	0	Q08EC7	
ENSMUST00000108529	ENSMUSG00000018449	11	70970213	70977833	1	0	0	0	0	1	0	0	3	0	17	0	Q0PL78	
ENSMUST00000108530	ENSMUSG00000040667	11	70943058	70969973	-1	0	0	0	0	0	0	170	652	309	134	150	Q5QNU0	Q8CEC0
ENSMUST00000108531	ENSMUSG00000040667	11	70943058	70969973	-1	0	0	0	33	0	0	46	148	142	84	141		Q8CEC0
ENSMUST00000108532	ENSMUSG00000070814	7	13258967	13278721	-1	0	9	17	116	25	10	14	13	26	0	0		
ENSMUST00000108533	ENSMUSG00000020817	11	70844778	70943105	1	0	0	0	0	0	0	0	0	0	0	0		O35551
ENSMUST00000108534	ENSMUSG00000057135	11	70790932	70812586	-1	13	7	13	11	14	0	21	272	58	81	83		Q3UU41
ENSMUST00000108535	ENSMUSG00000033961	7	12977848	12984340	1	0	14	45	19	32	16	0	4	8	2	13	E9Q6F9	
ENSMUST00000108536	ENSMUSG00000033961	7	12977848	12984340	1	16	39	46	3	3	11	7	15	0	0	4	G3X9U2	
ENSMUST00000108537	ENSMUSG00000033961	7	12977848	12984340	1	46	10	46	96	20	3	2	0	0	0	9	Q149D4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108539	ENSMUSG00000012848	7	12922290	12926686	1	2	0	0	23	15	0	131	81	94	513	26	Q91V55	
ENSMUST00000108541	ENSMUSG00000057054	11	70688361	70700155	-1	0	0	0	0	0	0	0	0	0	0	0		Q6PKN7
ENSMUST00000108542	ENSMUSG00000057054	11	70688361	70700155	-1	0	0	0	0	0	0	1	0	3	6	3		Q6PKN7
ENSMUST00000108543	ENSMUSG00000057054	11	70688361	70700155	-1	0	2	0	7	1	1	0	0	0	0	0		Q6PKN7
ENSMUST00000108544	ENSMUSG00000040712	11	70669463	70688105	-1	13	10	29	204	25	16	114	22	91	0	168		Q80Y50
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ENSMUST00000108546	ENSMUSG00000057894	7	12804977	12818858	-1	0	0	0	20	3	4	0	0	0	0	0	D3Z6L7	
ENSMUST00000108548	ENSMUSG00000060600	11	70657202	70662513	1	5	0	0	0	0	0	0	0	0	0	0		P21550
ENSMUST00000108549	ENSMUSG00000018293	11	70651850	70654644	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SX49	
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ENSMUST00000108551	ENSMUSG00000050675	11	70639122	70642036	1	35	31	21	35	31	12	16	0	32	0	37	A2CFB8	O35930
ENSMUST00000108554	ENSMUSG00000095773	7	9074796	9097881	-1	8	0	16	6	19	3	0	0	0	0	0	G3UYA8	
ENSMUST00000108556	ENSMUSG00000020828	11	70540064	70558110	1	54	49	233	110	62	32	1	6	7	0	12	Q80ZW1	
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ENSMUST00000108559	ENSMUSG00000055150	7	6371364	6379491	1	0	6	0	9	11	0	10	80	27	30	15	Q5U406	
ENSMUST00000108560	ENSMUSG00000030443	7	6315660	6331285	-1	6	7	20	6	8	5	0	0	2	0	0		Q3V080
ENSMUST00000108562	ENSMUSG00000054893	7	6286579	6307883	1	5	13	10	0	0	0	0	23	1	13	0		Q2TL60
ENSMUST00000108563	ENSMUSG00000040829	11	70459433	70466202	1	9	0	7	46	15	5	0	0	0	0	3		Q8C0R7
ENSMUST00000108565	ENSMUSG00000044876	7	6172226	6191349	1	0	0	0	98	0	0	0	0	0	0	0	D3Z688	
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ENSMUST00000108568	ENSMUSG00000060216	11	70432635	70440828	1	0	0	23	0	0	0	4070	8771	4143	1115	3297	J3JS97	Q91YI4
ENSMUST00000108569	ENSMUSG00000078808	7	5408887	5413145	-1	4895	5548	6758	3896	5647	2483	38	217	78	18	130	G3X9U3	
ENSMUST00000108571	ENSMUSG00000108789	7	5056185	5060523	1	0	0	0	0	5	0	7	0	6	3	1	E9QPN6	
ENSMUST00000108572	ENSMUSG00000051550	7	4983483	4996158	-1	0	0	0	397	13	0	0	1	0	3	0		Q80VM4
ENSMUST00000108574	ENSMUSG00000000320	11	70241457	70255353	-1	22	17	29	330	51	35	0	5	5	5	0	Q8C587	
ENSMUST00000108575	ENSMUSG00000020831	11	70235206	70237914	-1	1	1	1	0	0	0	68	49	18	24	19	A2CF83	
ENSMUST00000108576	ENSMUSG00000020831	11	70235206	70237914	-1	0	0	0	0	0	0	4	0	0	11	0	D3Z687	
ENSMUST00000108577	ENSMUSG00000020831	11	70235206	70237914	-1	0	0	0	13	0	0	9	31	28	8	22	A2CF80	
ENSMUST00000108578	ENSMUSG00000020831	11	70235206	70237914	-1	0	0	0	0	0	0	85	69	48	0	39		Q9DCT6
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ENSMUST00000108580						24	8	0	27	0	16	1	0	0	0	0		
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ENSMUST00000108584	ENSMUSG00000040950	11	70130329	70137550	1	0	0	0	0	0	0	0	0	0	2	14	F6QSC4	
ENSMUST00000108585	ENSMUSG00000020884	11	70054085	70057894	1	10	7	9	14	0	8	0	0	0	0	1	B1AR34	
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ENSMUST00000108588	ENSMUSG00000020886	11	70017085	70045532	1	0	0	8	104	11	0	23	0	9	0	0		Q62108
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ENSMUST00000108590	ENSMUSG00000078810	7	4363965	4397744	-1	8	11	12	4	7	14	2	2	4	29	4		P0C191
ENSMUST00000108592	ENSMUSG00000018567	11	69991143	69994951	1	0	0	0	21	7	0	5088	11796	2755	6604	1847	B1AR50	
ENSMUST00000108593	ENSMUSG00000018559	11	69981156	69990601	1	7	6	16	73	8	4	539	1007	610	85	467		Q3TP92
ENSMUST00000108594	ENSMUSG00000018565	11	69968222	69982517	-1	0	0	0	0	0	0	176	177	85	23	73		Q99L85
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ENSMUST00000108600	ENSMUSG00000055541	7	4003402	4063204	-1	0	0	0	0	3	1	6	17	13	10	0		Q8BG84
ENSMUST00000108601	ENSMUSG00000018554	11	69935796	69941605	1	0	0	0	44	3	11	0	0	0	0	0	A0A0A0MQD2	
ENSMUST00000108607	ENSMUSG00000078812	11	69916714	69921958	-1	0	0	0	0	0	0	0	0	0	0	0		P63242
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ENSMUST00000108609	ENSMUSG00000078812	11	69916714	69921958	-1	0	0	0	0	0	0	0	4	0	0	92		P63242
ENSMUST00000108610	ENSMUSG00000078812	11	69916714	69921958	-1	0	0	11	52	20	5	9	40	42	8	30		P63242
ENSMUST00000108611	ENSMUSG00000078812	11	69916714	69921958	-1	0	0	0	14	0	0	0	18	0	0	21		P63242
ENSMUST00000108612	ENSMUSG00000078812	11	69916714	69921958	-1	0	0	0	0	4	0	21	545	20	0	0		P63242
ENSMUST00000108613	ENSMUSG00000078812	11	69916714	69921958	-1	0	4	0	0	0	0	3475	4889	2684	1187	1963		P63242
ENSMUST00000108615	ENSMUSG00000089942	7	3836812	3845051	-1	9	6	43	17	22	10	4217	15148	8168	4065	5321	F8VQ94	
ENSMUST00000108617	ENSMUSG00000047284	11	69901072	69913820	1	0	0	12	8	2	11	0	0	0	2	0		Q5NCX5
ENSMUST00000108619	ENSMUSG00000074419	7	3816781	3825687	-1	0	0	0	0	0	0	14	59	12	39	0	D3Z678	
ENSMUST00000108620	ENSMUSG00000074419	7	3816781	3825687	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z674	
ENSMUST00000108621	ENSMUSG00000018570	11	69897352	69900987	-1	4	0	8	0	3	0	3	0	0	0	4	B1AR44	
ENSMUST00000108622	ENSMUSG00000001588	11	69881567	69895539	-1	0	3	0	14	0	0	198	1479	113	14	0	Q8CI47	
ENSMUST00000108623	ENSMUSG00000006333	7	3703993	3706897	1	3	2	9	8	3	0	216	1360	337	129	361	Q9CXW7	
ENSMUST00000108624	ENSMUSG00000006333	7	3703993	3706897	1	0	0	0	0	0	0	5	11	0	0	8	D3Z673	
ENSMUST00000108625	ENSMUSG00000006333	7	3703993	3706897	1	6	10	60	0	0	0	0	108	85	95	79		Q6ZWN5
ENSMUST00000108626	ENSMUSG00000001583	11	69851005	69858730	-1	15	23	64	36	33	18	0	6	1	0	6		Q99ML2
ENSMUST00000108627	ENSMUSG00000035585	7	3692863	3701024	1	0	0	23	0	0	0	389	325	105	69	89		Q8BMZ5
ENSMUST00000108628	ENSMUSG00000001583	11	69851005	69858730	-1	6	4	32	19	0	3	0	2	0	0	10	Q5F2B4	
ENSMUST00000108629	ENSMUSG00000035585	7	3692863	3701024	1	0	0	16	0	0	0	13	0	6	0	0		Q8BMZ5
ENSMUST00000108630	ENSMUSG00000035585	7	3692863	3701024	1	0	4	11	5	9	6	34	83	37	0	67		Q8BMZ5
ENSMUST00000108632	ENSMUSG00000019461	11	69846376	69852058	1	9	4	3	115	15	7	593	1154	388	65	182	Q5F283	Q9JIZ9
ENSMUST00000108633	ENSMUSG00000019461	11	69846376	69852058	1	8	12	16	17	21	3	21	119	47	13	29	Q5F283	Q9JIZ9
ENSMUST00000108634	ENSMUSG00000051790	11	69823122	69837784	-1	26	15	56	554	35	31	10	8	10	12	14		Q69ZK9
ENSMUST00000108636	ENSMUSG00000008373	7	3629985	3642486	1	1	0	0	0	0	0	135	206	153	148	141		Q8CCF0
ENSMUST00000108638	ENSMUSG00000018750	11	69765912	69784023	1	0	0	25	0	0	0	0	0	2	0	0	Q14DI5	
ENSMUST00000108639	ENSMUSG00000018750	11	69765912	69784023	1	43	46	61	45	55	23	47	91	71	12	92	Q5F293	Q5F293
ENSMUST00000108640	ENSMUSG00000018750	11	69765912	69784023	1	8	0	43	146	22	17	13	1	19	13	64	Q5F293	Q5F293
ENSMUST00000108641	ENSMUSG00000006335	7	3620324	3629929	-1	7	0	0	15	6	0	54	175	0	30	50		Q3U1J1
ENSMUST00000108642	ENSMUSG00000018750	11	69765912	69784023	1	0	0	0	0	0	2	4	0	0	0	0	B0QZJ3	
ENSMUST00000108644	ENSMUSG00000035674	7	3617373	3620327	1	2	0	0	0	0	0	17	28	12	20	0	D3Z670	
ENSMUST00000108645	ENSMUSG00000054594	7	3609813	3616157	-1	0	0	0	0	0	0	0	0	0	0	0		Q8VBT3
ENSMUST00000108647	ENSMUSG00000078815	7	3424195	3435667	1	0	0	4	3	2	0	0	0	0	0	0	A0A0A0MQD3	
ENSMUST00000108648	ENSMUSG00000089669	11	69682846	69685784	-1	4	6	32	20	13	4	6	14	0	0	11	Q5F2A3	
ENSMUST00000108649	ENSMUSG00000018752	11	69682577	69696098	-1	0	0	0	0	0	0	0	0	0	0	0	B0QZJ0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108653	ENSMUSG00000078817	7	3218784	3249740	-1	13	13	26	18	19	9	1024	4116	1946	480	2569		E9Q5R7
ENSMUST00000108654	ENSMUSG00000018774	11	69664213	69666153	-1	15	4	45	21	0	0	0	121	95	0	98		
ENSMUST00000108656	ENSMUSG00000069835	11	69622024	69623870	1	3	3	0	0	4	1	0	0	0	0	0		Q6P8J2
ENSMUST00000108657	ENSMUSG00000059552	11	69580359	69591873	1	0	5	17	0	0	6	41	57	14	0	0	I7HIK9	
ENSMUST00000108658	ENSMUSG00000059552	11	69580359	69591873	1	9	3	4	0	16	1	189	9	134	23	142	Q549C9	
ENSMUST00000108659	ENSMUSG00000005237	11	69420809	69549110	-1	93	74	165	159	159	0	0	0	0	0	0	D3Z667	
ENSMUST00000108660	ENSMUSG00000044795	11	69391925	69395631	-1	8	5	24	16	11	2	49	103	81	15	54		Q5NCY3
ENSMUST00000108661	ENSMUSG00000018474	11	69343273	69369406	-1	19	0	0	13	0	0	70	127	70	0	305	B1AR17	
ENSMUST00000108662	ENSMUSG00000049299	11	69323980	69325793	1	0	0	0	0	5	0	9	9	0	0	0	B1ASW5	
ENSMUST00000108664	ENSMUSG00000020890	11	69218117	69237036	-1	0	0	0	0	12	0	0	0	0	0	0		P52785
ENSMUST00000108665	ENSMUSG00000020890	11	69218117	69237036	-1	0	0	16	88	10	0	0	0	0	0	0		P52785
ENSMUST00000108666	ENSMUSG00000020897	11	69045647	69051664	1	2	0	0	63	15	2	23	47	0	5	0		O70126
ENSMUST00000108670						81	99	144	111	87	44	11	34	24	3	29		
ENSMUST00000108671	ENSMUSG00000052921	11	68943155	68957480	-1	35	35	166	104	52	0	0	0	0	0	0		Q5FWH6
ENSMUST00000108672	ENSMUSG00000018736	11	68821434	68871858	-1	0	0	0	4	0	7	0	0	0	0	0		Q9ERR1
ENSMUST00000108673	ENSMUSG00000020900	11	68691559	68816632	1	4	2	8	3	4	1	0	0	0	0	0	Q8BXF2	
ENSMUST00000108674	ENSMUSG00000020902	11	68209364	68400823	-1	31	30	84	363	37	24	0	0	0	0	0		O09118
ENSMUST00000108675	ENSMUSG00000020903	11	67966193	68207148	1	0	5	13	4	2	2	15	27	26	25	12	Q8BS59	
ENSMUST00000108677	ENSMUSG00000020905	11	67854523	67922153	-1	18	12	30	190	31	16	0	0	0	2	0	A6PWR8	
ENSMUST00000108680	ENSMUSG00000033066	11	67455437	67688990	1	0	0	0	0	0	0	97	0	179	11	149	B1ATI9	
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ENSMUST00000108682	ENSMUSG00000033066	11	67455437	67688990	1	41	35	125	67	62	35	1063	1701	1897	234	1054	Q3U432	
ENSMUST00000108684	ENSMUSG00000060180	11	67321658	67371586	1	25	0	25	0	48	31	0	0	0	0	0	B1AR69	
ENSMUST00000108685	ENSMUSG00000055775	11	67277124	67308634	1	7	8	18	12	8	7	0	0	0	0	0	Q8BGE8	
ENSMUST00000108686						4	4	5	5	1	2	0	0	0	0	0		
ENSMUST00000108688						1	0	0	6	4	0	0	0	0	0	0		
ENSMUST00000108689	ENSMUSG00000020908	11	67078300	67102291	1	0	0	0	93	0	0	0	0	0	0	0		P13541
ENSMUST00000108690	ENSMUSG00000069844	11	67052670	67067070	1	58	53	100	160	49	27	27	83	46	15	53	Q5SUD5	
ENSMUST00000108691	ENSMUSG00000056752	11	65831282	66168551	-1	2	0	5	4	0	3	0	0	0	0	0	Q5SX07	
ENSMUST00000108695	ENSMUSG00000020542	11	65176561	65269989	-1	19	20	85	136	21	25	0	0	0	0	0		Q8VIM5
ENSMUST00000108696	ENSMUSG00000020548	11	65151910	65159891	-1	4	2	0	2	6	2	0	0	0	0	0	Q9D9E9	
ENSMUST00000108697	ENSMUSG00000020549	11	64979038	65002069	1	0	0	0	0	0	3	0	0	0	0	0	B1ATP7	
ENSMUST00000108700	ENSMUSG00000018217	11	63128982	63159547	1	0	0	0	25	0	0	0	0	0	28	6	Q5SXS3	
ENSMUST00000108701	ENSMUSG00000018217	11	63128982	63159547	1	0	0	0	36	3	3	0	0	0	0	0	Q5SXS3	
ENSMUST00000108702	ENSMUSG00000018217	11	63128982	63159547	1	0	0	31	0	0	0	0	0	0	0	0	Q5SXS3	
ENSMUST00000108703	ENSMUSG00000047821	11	62820231	62850808	1	0	0	0	0	0	0	112	439	167	12	34		Q99PP9
ENSMUST00000108705	ENSMUSG00000047342	11	62753377	62789462	-1	0	0	0	0	4	0	0	8	0	1	0	Q5SVS7	
ENSMUST00000108707	ENSMUSG00000008348	5	125385965	125390202	-1	39	42	95	68	43	28	8323	16222	16403	486	12886	E9Q5F6	
ENSMUST00000108709	ENSMUSG00000042331	11	61956763	62223013	1	7	44	99	0	69	14	154	297	259	45	232		Q5SXY1
ENSMUST00000108710	ENSMUSG00000047804	11	61871307	61930252	-1	37	23	35	61	37	20	12	30	24	4	41		O88845
ENSMUST00000108711	ENSMUSG00000001036	11	61517249	61579687	-1	0	0	4	0	0	0	0	0	0	0	0	Q5NCM6	
ENSMUST00000108712	ENSMUSG00000001036	11	61517249	61579687	-1	0	0	51	59	0	1	0	0	0	0	0	Q5NCM5	
ENSMUST00000108713	ENSMUSG00000001036	11	61517249	61579687	-1	0	0	0	0	0	11	0	6	7	35	177	Q5NCM7	Q8CHU3
ENSMUST00000108714	ENSMUSG00000001034	11	61488812	61494406	-1	0	0	0	10	0	0	193	282	134	0	0		Q9WVS8
ENSMUST00000108715	ENSMUSG00000010025	11	61223417	61267464	-1	4	9	32	15	8	3	51	154	136	28	107	B1AV77	
ENSMUST00000108716	ENSMUSG00000019102	11	61207537	61218421	1	19	9	17	21	11	11	0	0	1	6	0		P47739
ENSMUST00000108717	ENSMUSG00000042529	11	61022564	61071131	1	4	3	59	3	6	3	0	0	0	0	0		P52187
ENSMUST00000108718	ENSMUSG00000042569	11	60830631	60860195	1	121	107	205	648	165	93	15	78	30	4	39	Z4YKT6	
ENSMUST00000108719	ENSMUSG00000020536	11	60699723	60714186	1	41	30	86	33	59	24	709	566	517	47	363		Q80Y17
ENSMUST00000108721	ENSMUSG00000042709	11	60400626	60418457	-1	23	17	30	35	13	21	99	187	89	35	66		
ENSMUST00000108722	ENSMUSG00000056598	11	60353329	60394341	1	4	5	15	16	8	5	0	0	1	0	0	F6Q537	
ENSMUST00000108723	ENSMUSG00000056598	11	60353329	60394341	1	1	0	0	0	0	0	0	0	0	3	0		Q9D5E4
ENSMUST00000108740						2	4	0	0	4	0	0	0	0	0	0		
ENSMUST00000108743	ENSMUSG00000078840	8	129129097	129131661	-1	1	2	12	8	2	0	0	0	0	0	0	F6Q4M4	
ENSMUST00000108744						67	53	2020	373	113	62	0	4	6	1	4		
ENSMUST00000108745	ENSMUSG00000056018	8	129067134	129183732	1	0	0	8	0	1	0	0	0	0	0	0	B9EJU4	
ENSMUST00000108747	ENSMUSG00000025808	8	128980019	129065517	-1	10	11	25	21	9	8	0	0	0	0	1	G3X9U4	
ENSMUST00000108751	ENSMUSG00000005417	11	59661305	59780860	1	0	0	0	0	0	0	134	97	122	24	141		P97434
ENSMUST00000108752	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	2	0		Q99NH2
ENSMUST00000108754	ENSMUSG00000027589	2	181837854	181857461	1	0	1	0	0	0	0	132	0	136	35	34	B0R0C7	
ENSMUST00000108756	ENSMUSG00000010505	2	181763332	181827797	1	0	0	0	0	0	0	0	0	0	0	0		Q8CFC2
ENSMUST00000108757	ENSMUSG00000010505	2	181763332	181827797	1	0	8	0	6	0	0	0	0	3	0	6		Q8CFC2
ENSMUST00000108759	ENSMUSG00000057060	8	126298558	126395482	1	26	28	61	178	23	20	0	4	4	1	1		Q1LZI2
ENSMUST00000108763	ENSMUSG00000027584	2	181715016	181720985	1	0	4	3	4	11	0	0	0	0	0	0	B0R0C0	
ENSMUST00000108766	ENSMUSG00000027584	2	181715016	181720985	1	5	0	2	8	11	0	0	0	4	0	1		P35377
ENSMUST00000108767	ENSMUSG00000027584	2	181715016	181720985	1	5	6	42	2	0	1	0	0	0	0	0	Q542U1	P35377
ENSMUST00000108768	ENSMUSG00000027584	2	181715016	181720985	1	16	0	75	23	4	5	0	0	0	0	0	Q542U1	P35377
ENSMUST00000108769	ENSMUSG00000002458	2	181688419	181693977	-1	0	0	0	2	0	0	252	993	376	123	537	B7ZCT0	
ENSMUST00000108771	ENSMUSG00000002458	2	181688419	181693977	-1	0	6	3	153	0	0	0	0	0	0	0	Q8BFU4	
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ENSMUST00000108774						2	2	25	3	2	1	0	0	0	0	0		
ENSMUST00000108775	ENSMUSG00000001995	8	125418063	125492710	-1	55	35	61	86	54	34	1877	2224	2810	148	1921		Q80TE4
ENSMUST00000108776	ENSMUSG00000002458	2	181688419	181693977	-1	6	0	14	0	10	3	598	396	620	8	390	Q78NN4	Q9CX84
ENSMUST00000108777	ENSMUSG00000036819	11	59450045	59458567	1	39	0	0	186	0	25	18	0	0	16	78		Q8BFT6
ENSMUST00000108778	ENSMUSG00000002458	2	181688419	181693977	-1	4	2	5	1	3	2	669	1676	785	171	342	B7ZCT1	
ENSMUST00000108779	ENSMUSG00000002458	2	181688419	181693977	-1	0	0	0	0	0	0	0	8	0	0	0	B7ZCS8	
ENSMUST00000108782						0	0	1	6	1	0	0	0	0	0	0		
ENSMUST00000108783	ENSMUSG00000000126	11	59306928	59333552	1	17	18	75	0	20	0	0	1	0	2	2		Q8R5M2
ENSMUST00000108784	ENSMUSG00000036860	11	59202486	59206134	1	8	0	8	36	4	3	12	16	13	7	0		Q9CZ83
ENSMUST00000108785	ENSMUSG00000036860	11	59202486	59206134	1	0	0	0	3	0	2	20	48	17	24	0		Q9CZ83
ENSMUST00000108786	ENSMUSG00000036860	11	59202486	59206134	1	0	0	0	0	0	0	0	6	0	0	0		Q9CZ83
ENSMUST00000108787	ENSMUSG00000036860	11	59202486	59206134	1	0	1	0	0	0	0	14	3	13	56	15		Q9CZ83
ENSMUST00000108789	ENSMUSG00000000823	2	181582103	181592803	-1	0	19	13	38	0	0	48	30	0	17	0	B7ZCR6	
ENSMUST00000108790	ENSMUSG00000043448	11	59175568	59183213	-1	15	4	13	74	12	12	0	0	1	0	1		Q8BQU6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108793	ENSMUSG00000043448	11	59175568	59183213	-1	0	0	12	232	22	0	0	0	0	0	0		Q8BQU6
ENSMUST00000108796	ENSMUSG00000000826	2	181520485	181555133	1	0	0	5	8	0	0	186	0	91	117	137		P60904
ENSMUST00000108797	ENSMUSG00000000826	2	181520485	181555133	1	0	0	10	56	10	0	561	939	1133	160	809		P60904
ENSMUST00000108799	ENSMUSG00000000827	2	181497142	181517966	1	0	0	1	0	0	0	357	581	347	1007	237	A2AUD5	
ENSMUST00000108800	ENSMUSG00000000827	2	181497142	181517966	1	11	13	11	10	11	0	16	56	33	17	0	Q3TUJ9	
ENSMUST00000108803						7	2	4	4	16	0	0	12	9	0	8		
ENSMUST00000108804	ENSMUSG00000090077	2	181380078	181383628	1	0	0	0	0	0	1	0	15	0	5	0	A2AU24	
ENSMUST00000108807	ENSMUSG00000027582	2	181364928	181383628	1	6	0	0	172	10	8	176	0	52	0	38		Q8VDM1
ENSMUST00000108808	ENSMUSG00000038671	2	181357690	181365404	-1	0	0	0	0	0	0	130	175	98	51	79		Q8BXL7
ENSMUST00000108809	ENSMUSG00000020455	11	58978093	58991458	1	32	25	41	106	44	18	1128	3268	1720	174	2003	A2AB83	
ENSMUST00000108810	ENSMUSG00000020455	11	58978093	58991458	1	0	0	0	28	0	0	208	456	256	23	305		Q99PQ2
ENSMUST00000108813	ENSMUSG00000009575	15	103191544	103239816	-1	0	0	0	0	1	0	0	0	0	5	0		Q61686
ENSMUST00000108814	ENSMUSG00000038685	2	181319739	181356616	1	0	0	0	0	0	0	64	0	55	0	0		Q0VGM9
ENSMUST00000108815	ENSMUSG00000038685	2	181319739	181356616	1	2	0	0	0	0	0	0	0	0	0	0		Q0VGM9
ENSMUST00000108817	ENSMUSG00000078851	11	58954685	58956830	1	10	12	61	59	12	3	68	77	40	47	40	A2AB79	Q8BFU2
ENSMUST00000108818	ENSMUSG00000020490	11	58917908	58927158	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000108821	ENSMUSG00000037145	11	58608204	58616075	-1	0	0	0	0	5	0	0	0	0	0	0	Q6YI28	
ENSMUST00000108822	ENSMUSG00000064252	11	58542447	58544938	-1	13	0	6	0	5	0	0	0	0	0	0	M9MMK4	
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ENSMUST00000108824	ENSMUSG00000057654	11	58551305	58555636	-1	0	4	0	5	9	7	0	0	0	0	0	Q5NCD3	
ENSMUST00000108825	ENSMUSG00000058287	11	58432559	58441622	1	10	14	36	20	14	6	2	6	5	0	2	Q5NC48	
ENSMUST00000108826	ENSMUSG00000013643	11	58379043	58390728	1	2	0	40	5	9	7	0	0	0	0	0		Q9D7S0
ENSMUST00000108828	ENSMUSG00000099083	15	102525946	102625464	-1	12	8	9	10	9	2	0	0	2	0	5	Q3U2X8	Q8R0S1
ENSMUST00000108829	ENSMUSG00000049755	11	58315114	58330339	-1	5	8	0	188	19	9	25	57	23	8	35		Q99LH4
ENSMUST00000108830	ENSMUSG00000001482	8	123442986	123463270	1	0	9	24	20	0	12	417	195	211	0	246		Q99J78
ENSMUST00000108831	ENSMUSG00000027580	2	181227615	181242027	-1	0	0	0	0	0	0	1388	893	1457	27	1728		E9QAM5
ENSMUST00000108832	ENSMUSG00000001482	8	123442986	123463270	1	0	0	0	0	0	0	76	51	0	0	0	G3X9U5	
ENSMUST00000108834	ENSMUSG00000069873	11	58274799	58294289	1	12	8	14	19	20	5	1994	4067	2335	774	1056	Q5SPH3	
ENSMUST00000108835	ENSMUSG00000047841	2	181220013	181222854	1	3	4	0	0	0	1	1	0	0	0	0	A2AS00	
ENSMUST00000108836	ENSMUSG00000069874	11	58199618	58222779	1	0	28	0	0	0	13	0	0	0	0	0	Q9Z1M2	
ENSMUST00000108838	ENSMUSG00000056851	15	102470632	102500059	1	0	0	0	0	0	7	1232	2490	1036	404	893		Q61990
ENSMUST00000108840	ENSMUSG00000001472	8	123373824	123404173	1	24	16	48	81	20	17	1220	2938	1387	268	1441		Q8R3L2
ENSMUST00000108841	ENSMUSG00000016344	2	181187247	181188771	1	0	0	0	0	0	0	94	132	54	74	51		Q9CR37
ENSMUST00000108843	ENSMUSG00000020515	11	58104153	58118594	1	11	12	39	80	24	9	0	21	60	14	13		Q9D8X5
ENSMUST00000108845	ENSMUSG00000037335	11	57828705	57832818	-1	1	2	8	21	3	0	0	0	0	0	0	Q5SQG0	
ENSMUST00000108846	ENSMUSG00000020520	11	57645442	57787514	1	9	2	12	50	8	4	9	44	17	3	19	Q5ST18	
ENSMUST00000108848	ENSMUSG00000020522	11	57518664	57533815	1	0	1	3	2	1	2	5	0	0	0	9	D3Z5B4	
ENSMUST00000108849	ENSMUSG00000020522	11	57518664	57533815	1	28	15	0	17	0	0	336	990	510	214	288		
ENSMUST00000108850	ENSMUSG00000020523	11	57482993	57518617	-1	0	0	0	1	0	0	14	0	47	15	68		Q8VE88
ENSMUST00000108851	ENSMUSG00000027577	2	181018380	181043546	-1	0	4	0	0	6	0	0	1	0	0	0	B7ZBU7	
ENSMUST00000108853	ENSMUSG00000000263	11	55514238	55608198	-1	9	3	19	4	3	0	0	3	0	5	3	Q5NCU0	
ENSMUST00000108856	ENSMUSG00000016356	2	180986535	181017540	1	0	0	52	54	39	24	13	187	100	11	148		Q923P0
ENSMUST00000108857	ENSMUSG00000018585	11	55446641	55461239	-1	2	4	8	16	7	0	1012	1500	683	3355	514		O08997
ENSMUST00000108858	ENSMUSG00000018593	11	55394500	55420080	-1	0	0	0	8	3	0	0	0	0	117	240	Q5NCU4	
ENSMUST00000108859	ENSMUSG00000027575	2	180967225	180982526	1	0	4	22	307	25	13	0	8	0	0	12		Q9EPJ9
ENSMUST00000108860	ENSMUSG00000027575	2	180967225	180982526	1	0	0	0	0	0	0	0	0	0	0	0		Q9EPJ9
ENSMUST00000108861	ENSMUSG00000027575	2	180967225	180982526	1	0	0	0	0	0	0	73	62	61	13	66	Q3TGS9	
ENSMUST00000108862	ENSMUSG00000027575	2	180967225	180982526	1	0	0	0	51	9	0	0	0	0	0	0	Q3TGS9	
ENSMUST00000108864	ENSMUSG00000055333	11	55250609	55336564	-1	0	80	74	0	0	0	0	0	1	1	13		Q5F226
ENSMUST00000108867	ENSMUSG00000020261	11	55204350	55236330	1	2	0	3	4	2	0	0	0	9	0	0	Q5F227	Q8K4D3
ENSMUST00000108868	ENSMUSG00000000738	8	123062942	123097760	1	0	0	0	0	0	6	40	120	41	0	90		Q3ULF4
ENSMUST00000108872	ENSMUSG00000020261	11	55204350	55236330	1	72	59	446	139	90	49	564	959	667	65	779	Q5F227	Q8K4D3
ENSMUST00000108873	ENSMUSG00000027574	2	180934772	180954699	-1	0	3	6	10	0	0	0	0	0	0	0		Q9JMG4
ENSMUST00000108875	ENSMUSG00000038840	2	180929023	180934010	1	0	0	13	0	4	1	0	0	0	0	0		A2AWP0
ENSMUST00000108876	ENSMUSG00000038848	2	180904377	180920949	-1	0	7	13	31	5	0	20	0	265	6	219	A2AWN8	
ENSMUST00000108878	ENSMUSG00000045493	2	180774381	180776900	-1	14	9	17	244	23	13	0	0	0	0	0	Q0VEJ8	Q8BGW3
ENSMUST00000108880	ENSMUSG00000049588	11	55049731	55078131	-1	6	2	8	55	5	6	1	7	4	11	5		Q3TCJ8
ENSMUST00000108883	ENSMUSG00000018340	11	54979108	55033445	-1	0	0	0	0	0	0	705	909	667	260	928		P14824
ENSMUST00000108885	ENSMUSG00000020400	11	54910785	54962917	-1	0	0	0	0	0	8	0	0	0	0	0		Q9WUU8
ENSMUST00000108886	ENSMUSG00000020400	11	54910785	54962917	-1	3	0	14	0	30	0	393	699	322	47	193		Q9WUU8
ENSMUST00000108889	ENSMUSG00000020400	11	54910785	54962917	-1	0	0	0	0	0	0	221	271	374	0	279	E9QM75	
ENSMUST00000108891	ENSMUSG00000038990	2	180258540	180273496	-1	9	7	34	14	4	4	329	860	432	45	310		Q8K3M5
ENSMUST00000108894	ENSMUSG00000037533	11	54522847	54699285	1	0	0	0	0	0	0	0	0	0	0	17	Q5NCJ5	
ENSMUST00000108895	ENSMUSG00000037533	11	54522847	54699285	1	2	0	0	0	2	0	0	23	0	0	6	Q5NCJ2	
ENSMUST00000108899	ENSMUSG00000020333	11	54303798	54364756	1	0	3	7	2	5	0	1	0	0	0	0	Q8BYJ0	
ENSMUST00000108901	ENSMUSG00000039069	2	180070588	180085902	1	0	0	0	0	0	0	0	0	0	34	0	A2AFK4	
ENSMUST00000108904	ENSMUSG00000020333	11	54303798	54364756	1	0	0	1	64	0	0	0	0	0	0	0	Q8R1X1	
ENSMUST00000108905	ENSMUSG00000020333	11	54303798	54364756	1	8	5	15	0	8	5	0	1	0	0	0	Q5F2D0	Q91WC3
ENSMUST00000108908	ENSMUSG00000023033	15	100869858	101045938	1	9	1	77	0	0	0	0	2	4	0	0	F7D6K4	
ENSMUST00000108909	ENSMUSG00000023033	15	100869858	101045938	1	45	68	0	129	0	26	0	0	0	23	16	F7D6J5	
ENSMUST00000108910	ENSMUSG00000023033	15	100869858	101045938	1	0	0	0	0	0	0	0	0	0	0	0	F7D6H8	
ENSMUST00000108911	ENSMUSG00000000305	2	179442431	179899373	1	5	10	10	5	8	0	0	0	0	0	0	Q80ZV4	
ENSMUST00000108912	ENSMUSG00000039155	2	178430531	178487366	1	19	13	36	28	26	6	0	0	0	0	0	Q3V1P3	
ENSMUST00000108915	ENSMUSG00000027525	2	178118975	178338492	1	0	1	0	2	6	0	0	0	0	0	0		Q8BYK5
ENSMUST00000108916	ENSMUSG00000027525	2	178118975	178338492	1	0	0	0	0	0	0	0	0	0	0	0		Q8BYK5
ENSMUST00000108917	ENSMUSG00000027525	2	178118975	178338492	1	44	53	337	131	38	29	1	10	3	0	0	A2AHM4	
ENSMUST00000108920	ENSMUSG00000018899	11	53770014	53778374	1	4	0	0	63	0	0	2562	6177	2890	1508	2707	Q5SX13	P15314
ENSMUST00000108922	ENSMUSG00000018899	11	53770014	53778374	1	16	7	55	30	21	7	0	13	4	1	5	Q3U5M1	
ENSMUST00000108923	ENSMUSG00000078861	2	178067695	178078476	-1	1	0	14	7	0	1	3	1	3	5	0	A2AHM3	
ENSMUST00000108924	ENSMUSG00000078861	2	178067695	178078476	-1	0	3	3	3	0	0	0	5	0	1	0	A2AHM2	
ENSMUST00000108925	ENSMUSG00000074519	2	178023284	178034022	1	0	0	0	0	1	1	45	41	27	44	36	Q3V498	
ENSMUST00000108926	ENSMUSG00000074519	2	178023284	178034022	1	2	0	6	11	3	0	151	378	479	40	131	A2BFG8	
ENSMUST00000108928	ENSMUSG00000078862	2	177935993	177957297	-1	4	5	0	5	6	0	11	12	6	33	0	Q8CFP2	
ENSMUST00000108929	ENSMUSG00000090093	2	175129493	175142012	-1	0	4	0	1	0	0	0	0	0	0	0	E9QA51	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000108930	ENSMUSG00000078862	2	177935993	177957297	-1	0	0	6	17	0	0	23	45	53	35	11	A2BFG5	
ENSMUST00000108931	ENSMUSG00000074527	2	176892509	176927809	-1	0	0	0	0	0	0	0	0	0	0	0	F7ACM4	
ENSMUST00000108932	ENSMUSG00000078862	2	177935993	177957297	-1	0	0	0	5	0	8	2	27	8	40	6	A2BFG4	
ENSMUST00000108934	ENSMUSG00000074529	2	177903340	177925613	-1	138	66	1816	217	153	98	0	7	9	2	9	A2AW64	
ENSMUST00000108935	ENSMUSG00000074521	2	177897096	177905784	1	3	0	0	0	0	0	0	0	0	2	0	Q3V498	
ENSMUST00000108939	ENSMUSG00000095362	2	177831791	177840336	-1	0	0	0	0	0	0	0	26	10	2	0	A2AW67	
ENSMUST00000108940	ENSMUSG00000094786	2	177498215	177509763	1	1	0	1	2	0	1	2	7	4	2	3	Q4V784	
ENSMUST00000108942	ENSMUSG00000078864	2	177759288	177770472	1	3	3	8	3	4	0	0	0	0	0	0	L7N246	
ENSMUST00000108943	ENSMUSG00000078865	2	177569204	177578210	-1	2	0	0	4	3	2	0	0	0	0	0	A2ARW4	
ENSMUST00000108945	ENSMUSG00000078865	2	177569204	177578210	-1	4	2	13	9	0	0	0	0	0	0	0	A2BFU6	
ENSMUST00000108947	ENSMUSG00000094786	2	177498215	177509763	1	0	0	0	0	0	0	0	2	1	0	0	A2BFU4	
ENSMUST00000108948	ENSMUSG00000031824	8	120114152	120165306	1	4	2	6	22	11	5	76	36	79	16	82	Q8BQB5	
ENSMUST00000108949	ENSMUSG00000089756	2	175918881	175931100	-1	4	2	0	6	0	0	25	20	4	0	15	A2ART2	
ENSMUST00000108950	ENSMUSG00000031824	8	120114152	120165306	1	3	4	28	10	6	5	1794	0	417	0	493		Q8R0A7
ENSMUST00000108951	ENSMUSG00000031824	8	120114152	120165306	1	48	35	17	73	50	26	11133	13882	12774	898	6484	Q3TA40	
ENSMUST00000108952	ENSMUSG00000078866	2	177464733	177478129	1	2	2	4	0	1	0	1	1	0	0	2	Q08BU3	
ENSMUST00000108955	ENSMUSG00000078867	2	177387124	177398320	-1	5	0	7	0	4	2	0	8	0	3	0	A2ARR5	
ENSMUST00000108959	ENSMUSG00000078868	2	177314520	177324307	-1	5	3	24	20	5	0	0	0	0	0	0	A2ARR7	
ENSMUST00000108961	ENSMUSG00000078895	2	176317638	176319494	-1	0	0	0	0	0	0	0	0	0	0	0	F7CWA7	
ENSMUST00000108963	ENSMUSG00000078869	2	177264654	177267036	-1	3	3	0	0	0	0	6	17	20	0	0	A2ARR8	
ENSMUST00000108964	ENSMUSG00000078870	2	177183453	177206421	-1	0	1	2	0	0	0	3	10	0	5	7	Q8BHI0	
ENSMUST00000108968	ENSMUSG00000078872	2	177074320	177087347	1	1	0	0	0	0	0	0	0	0	0	0	A2ARV8	
ENSMUST00000108969						0	2	0	0	0	0	6	2	0	2	0		
ENSMUST00000108970	ENSMUSG00000078872	2	177074320	177087347	1	0	0	2	4	3	0	0	0	0	0	0	A2ARV7	
ENSMUST00000108971	ENSMUSG00000023026	15	100038664	100219473	1	97	56	661	57	113	44	107	805	397	24	130	B2RQC7	
ENSMUST00000108972	ENSMUSG00000031825	8	119992438	120052793	1	0	0	90	0	0	0	0	0	0	0	36		Q8BZQ2
ENSMUST00000108975	ENSMUSG00000078875	2	177000956	177012787	1	2	0	0	1	0	0	5	0	0	0	2	E9Q9K2	
ENSMUST00000108980	ENSMUSG00000078878	2	176708328	176721813	1	3	3	0	0	0	0	0	0	0	12	6	Q8BHI0	
ENSMUST00000108981	ENSMUSG00000078878	2	176708328	176721813	1	0	0	5	0	0	0	0	3	4	2	2	A2BE23	
ENSMUST00000108982	ENSMUSG00000031826	8	119910360	119957560	1	0	0	0	0	0	0	0	0	0	0	0	G3X9U6	
ENSMUST00000108983	ENSMUSG00000078878	2	176708328	176721813	1	0	0	0	3	0	0	0	0	0	0	0	A2BE23	
ENSMUST00000108985	ENSMUSG00000078879	2	176670522	176719085	1	0	0	0	0	0	0	0	2	0	0	1	A2BE20	
ENSMUST00000108986	ENSMUSG00000074529	2	177903340	177925613	-1	0	0	0	0	0	0	0	0	0	0	0	L7N247	
ENSMUST00000108987	ENSMUSG00000018398	11	53519257	53549565	1	0	16	7	48	0	0	0	20	16	16	98		Q8CHH9
ENSMUST00000108988	ENSMUSG00000031826	8	119910360	119957560	1	12	0	30	5	22	5	35	69	39	4	107		P52479
ENSMUST00000108990	ENSMUSG00000078880	2	176613364	176636344	-1	0	0	0	0	0	0	0	0	0	0	0	A2ART4	
ENSMUST00000108995	ENSMUSG00000089951	2	176423594	176435761	1	3	4	3	4	6	0	12	33	20	6	15	A2CF17	
ENSMUST00000108997	ENSMUSG00000095199	2	176521056	176532479	1	0	1	2	1	0	0	0	0	0	0	0	A2ART1	
ENSMUST00000109002	ENSMUSG00000078896	2	175469985	175482171	1	0	0	0	2	0	0	0	0	0	0	0	A2BE20	
ENSMUST00000109007	ENSMUSG00000078886	2	175965331	175980303	1	0	0	0	6	5	0	0	0	0	7	0	Q8BHI0	
ENSMUST00000109008	ENSMUSG00000078886	2	175965331	175980303	1	0	0	0	0	0	0	0	0	0	0	0	A2ART4	
ENSMUST00000109010						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000109011	ENSMUSG00000078887	2	175869219	175881248	1	2	2	3	0	0	0	0	7	0	3	0	Q8C1K5	
ENSMUST00000109012	ENSMUSG00000078887	2	175869219	175881248	1	1	0	0	0	2	0	0	0	0	0	0	A2ART0	
ENSMUST00000109013	ENSMUSG00000018387	11	53457205	53467766	1	0	6	0	130	10	3	0	2	0	0	0		Q5SX79
ENSMUST00000109018	ENSMUSG00000089756	2	175918881	175931100	-1	2	0	5	0	3	1	2	0	0	2	0	A2ART1	
ENSMUST00000109019	ENSMUSG00000044894	11	53427922	53430831	-1	3	0	18	3	2	1	1	40	4	1	1	I7HPX6	
ENSMUST00000109020	ENSMUSG00000078889	2	175789357	175801093	-1	0	0	0	5	7	0	0	0	0	0	19	A2BDM8	
ENSMUST00000109021	ENSMUSG00000044894	11	53427922	53430831	-1	0	0	2	35	0	0	183	641	270	817	128		Q9CQ69
ENSMUST00000109024	ENSMUSG00000023022	15	99778470	99875428	-1	26	23	58	11	35	18	9	33	10	37	81	Q8CD09	Q9ERG0
ENSMUST00000109027	ENSMUSG00000095545	2	175692223	175703646	-1	0	1	2	1	0	0	0	0	0	0	0	A2ART1	
ENSMUST00000109035	ENSMUSG00000023021	15	99734881	99772885	-1	11	12	18	10	11	5	14	52	14	0	27		Q9D6K9
ENSMUST00000109042	ENSMUSG00000078896	2	175469985	175482171	1	1	0	0	2	1	0	8	3	1	4	2	A2BE19	
ENSMUST00000109043	ENSMUSG00000078896	2	175469985	175482171	1	0	1	2	1	0	0	1	1	0	3	1	A2BE21	
ENSMUST00000109045	ENSMUSG00000078897	2	175422300	175435807	-1	0	0	0	0	0	0	0	0	0	0	0	A2ART4	
ENSMUST00000109046	ENSMUSG00000078897	2	175422300	175435807	-1	0	0	0	0	0	0	0	0	0	0	0	A2ART4	
ENSMUST00000109047	ENSMUSG00000078898	2	175372436	175384201	1	0	0	0	0	0	0	0	5	0	0	0	A2ART2	
ENSMUST00000109048	ENSMUSG00000078898	2	175372436	175384201	1	2	0	5	0	3	1	2	0	0	2	0	A2ART1	
ENSMUST00000109049	ENSMUSG00000095648	2	176141591	176149825	-1	0	0	0	0	1	0	0	0	0	1	0	A2ARL5	
ENSMUST00000109050	ENSMUSG00000078899	2	175321955	175338197	-1	0	0	0	0	0	0	0	0	0	0	0	F7CEW8	
ENSMUST00000109051	ENSMUSG00000078901	2	175275125	175286805	1	0	5	0	0	0	3	32	28	14	8	0	A2BDM8	
ENSMUST00000109054	ENSMUSG00000078902	2	175166255	175175871	-1	405	329	666	455	439	203	28	135	61	56	81	A2ARX0	
ENSMUST00000109055	ENSMUSG00000078903	2	175191065	175206917	-1	0	0	0	0	0	2	0	0	0	1	0	Q8C1K5	
ENSMUST00000109056	ENSMUSG00000078903	2	175191065	175206917	-1	0	0	0	0	0	0	0	0	0	0	0	A2ARX1	
ENSMUST00000109057	ENSMUSG00000036275	11	52396428	52408728	1	1	10	1	2	2	1	230	2406	543	22	486	A0A0A0MQD4	
ENSMUST00000109058	ENSMUSG00000078903	2	175191065	175206917	-1	0	0	7	2	0	0	0	0	0	3	4	A2ART0	
ENSMUST00000109059	ENSMUSG00000090093	2	175129493	175142012	-1	1	3	0	0	1	0	0	0	0	1	0	Q8CFP2	
ENSMUST00000109060	ENSMUSG00000090093	2	175129493	175142012	-1	0	0	12	0	0	0	0	0	3	0	0	A2ARW8	
ENSMUST00000109062	ENSMUSG00000090093	2	175129493	175142012	-1	0	1	2	0	1	0	0	2	0	1	1	A2ARW7	
ENSMUST00000109066	ENSMUSG00000078905	2	175061549	175067781	-1	0	0	0	1	0	1	0	0	0	0	0	A2ARV8	
ENSMUST00000109069	ENSMUSG00000078906	2	175010241	175019248	1	2	5	5	3	3	0	0	2	0	0	0	A2ARW4	
ENSMUST00000109070	ENSMUSG00000078906	2	175010241	175019248	1	0	0	0	0	0	0	0	0	0	4	0	A2ARW3	
ENSMUST00000109071	ENSMUSG00000000782	11	52252371	52283014	-1	6	0	92	89	28	0	27	15	44	2	98	Q80UF1	Q00417
ENSMUST00000109072	ENSMUSG00000036309	11	52231995	52246858	1	13	0	26	112	14	4	8	13	4	4	0	Q5SUR3	Q9WTX5
ENSMUST00000109075	ENSMUSG00000016253	2	174415804	174427502	1	2	0	22	16	0	0	593	758	565	0	349		Q922L6
ENSMUST00000109076	ENSMUSG00000020389	11	52004221	52089784	1	0	0	0	0	0	0	0	0	0	0	0		Q8BLF2
ENSMUST00000109077	ENSMUSG00000020389	11	52004221	52089784	1	2	0	5	23	3	6	0	0	0	3	0		Q8BLF2
ENSMUST00000109078	ENSMUSG00000020389	11	52004221	52089784	1	35	27	115	101	30	16	10	38	25	12	31		Q8BLF2
ENSMUST00000109079	ENSMUSG00000020389	11	52004221	52089784	1	0	0	0	44	0	0	0	0	0	0	0		Q8BLF2
ENSMUST00000109080	ENSMUSG00000020389	11	52004221	52089784	1	7	1	0	0	0	0	2	11	0	0	0	B1AU43	
ENSMUST00000109081	ENSMUSG00000020389	11	52004221	52089784	1	0	0	0	0	0	0	0	0	0	11	0		Q8BLF2
ENSMUST00000109083	ENSMUSG00000027523	2	174284320	174346744	1	0	3	0	0	0	0	0	0	0	0	4	A2A610	
ENSMUST00000109084	ENSMUSG00000027523	2	174284320	174346744	1	0	0	0	0	0	0	1086	1488	1036	90	844	Z4YKV1	
ENSMUST00000109085	ENSMUSG00000027523	2	174284320	174346744	1	0	0	0	0	0	0	960	948	778	109	544		P63094

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000109086	ENSMUSG00000020390	11	51985497	52000762	-1	0	0	0	3	0	2	294	1932	771	1451	435	A2RSE4	P63147
ENSMUST00000109087	ENSMUSG00000027523	2	174284320	174346744	1	0	0	0	0	0	0	1283	1653	1929	261	923		P63094
ENSMUST00000109088	ENSMUSG00000027523	2	174284320	174346744	1	1	1	18	175	0	5	0	0	0	0	1		Q6R0H6
ENSMUST00000109090	ENSMUSG00000020387	11	51813455	51857653	-1	9	0	47	11	38	0	0	0	0	0	0	A2AA59	
ENSMUST00000109091	ENSMUSG00000020387	11	51813455	51857653	-1	31	16	33	15	17	18	365	313	428	69	573		Q6ZQF7
ENSMUST00000109092	ENSMUSG00000036391	11	51692264	51763634	-1	0	1	0	0	4	0	0	0	0	0	0	A2AA72	
ENSMUST00000109093	ENSMUSG00000034416	8	116995679	117082449	-1	30	0	0	32	43	20	31	11	21	3	14	E9QPG2	
ENSMUST00000109095	ENSMUSG00000027523	2	174284320	174346744	1	10	9	36	27	10	7	0	0	0	0	0		Q9Z0F1
ENSMUST00000109096	ENSMUSG00000027523	2	174284320	174346744	1	0	0	0	0	5	0	0	0	0	3	0		Q9Z0F1
ENSMUST00000109097	ENSMUSG00000036391	11	51692264	51763634	-1	9	7	17	14	15	7	86	124	62	16	48		Q3U2P1
ENSMUST00000109098	ENSMUSG00000007777	11	51685386	51688874	-1	2	0	1	18	2	0	0	0	0	3	0	Q8R3W2	
ENSMUST00000109099	ENSMUSG00000047388	8	116943393	116960445	1	35	23	52	99	41	21	342	520	543	76	347		Q6P9S1
ENSMUST00000109100	ENSMUSG00000078907	15	99271018	99287180	-1	27	18	140	88	49	22	0	1	0	0	2	D3Z420	
ENSMUST00000109102	ENSMUSG00000031758	8	116568724	116732991	-1	50	47	114	262	77	48	171	245	277	27	138		Q9D5D8
ENSMUST00000109103	ENSMUSG00000020358	11	51600100	51606847	-1	0	0	0	72	0	0	421	1101	663	202	623	Q20BD0	
ENSMUST00000109104	ENSMUSG00000055435	8	115682942	115707794	-1	89	66	673	537	88	68	42	84	65	33	150		P54843
ENSMUST00000109105						8	11	21	13	10	5	0	5	5	2	8		
ENSMUST00000109107	ENSMUSG00000004637	8	114439655	115352708	1	16	6	15	11	15	5	1	0	0	0	3		Q91WL8
ENSMUST00000109108	ENSMUSG00000004637	8	114439655	115352708	1	4	10	10	12	6	0	14	9	19	0	10		Q91WL8
ENSMUST00000109109	ENSMUSG00000031767	8	114133557	114154739	1	86	53	329	77	61	34	7	13	7	0	5		Q99P30
ENSMUST00000109110	ENSMUSG00000027519	2	173659760	173707343	1	4	2	1	37	0	1	54	35	72	18	28	A2ARZ7	
ENSMUST00000109111	ENSMUSG00000020385	11	51261730	51281766	1	0	0	0	0	0	0	42	211	63	0	0		O35493
ENSMUST00000109112	ENSMUSG00000027517	2	173568666	173578365	-1	7	2	4	0	9	3	0	0	0	0	0	A6PWV4	
ENSMUST00000109113	ENSMUSG00000020385	11	51261730	51281766	1	1	0	0	0	0	0	0	1063	103	230	110		O35493
ENSMUST00000109116	ENSMUSG00000027514	2	173206612	173218923	-1	3	3	0	5	0	6	81	287	71	767	136		Q9QY24
ENSMUST00000109119	ENSMUSG00000020364	11	51059257	51072799	1	2	0	0	4	0	0	0	0	0	0	0	B1ATG3	
ENSMUST00000109122	ENSMUSG00000020364	11	51059257	51072799	1	31	32	81	34	32	18	2	8	6	0	7	Q5PPR4	
ENSMUST00000109123	ENSMUSG00000072983	11	50940711	50943765	-1	13	11	12	14	20	9	0	0	0	0	0	Q9D4D5	
ENSMUST00000109124	ENSMUSG00000020335	11	50921823	50931633	-1	4	4	10	31	11	3	0	0	0	0	0		Q9QXT9
ENSMUST00000109125	ENSMUSG00000005883	2	172977700	172993576	1	1	4	2	47	9	0	0	0	0	0	0		Q9WTK8
ENSMUST00000109126	ENSMUSG00000005883	2	172977700	172993576	1	0	0	0	0	0	0	0	0	0	0	0		Q9WTK8
ENSMUST00000109127	ENSMUSG00000022999	15	98903921	98918231	-1	20	17	13	18	16	13	278	912	329	23	523		Q9D1E5
ENSMUST00000109128	ENSMUSG00000049321	11	50898712	50916165	-1	0	0	0	25	2	0	1	4	1	0	0		P08043
ENSMUST00000109129	ENSMUSG00000049321	11	50898712	50916165	-1	9	9	10	7	11	0	0	0	0	1	0		P08043
ENSMUST00000109131	ENSMUSG00000048728	11	50872720	50887651	-1	0	0	0	0	0	5	0	0	0	0	0	Q5NCH7	
ENSMUST00000109132						10	11	29	38	22	10	487	73	496	534	425		
ENSMUST00000109133	ENSMUSG00000044296	11	50832031	50841552	-1	16	0	9	0	0	7	0	0	0	0	0	Q147Z4	
ENSMUST00000109134	ENSMUSG00000044296	11	50832031	50841552	-1	0	1	2	0	2	1	0	0	0	0	0		Q8BI99
ENSMUST00000109135	ENSMUSG00000044807	11	50811086	50827724	-1	19	7	10	6	12	10	0	6	3	2	3		Q571J5
ENSMUST00000109136	ENSMUSG00000074570	2	172393794	172433757	1	0	0	0	0	3	3	52	19	65	0	113		Q08EC4
ENSMUST00000109139	ENSMUSG00000027496	2	172356190	172370535	-1	6	4	10	13	3	3	0	0	8	0	0	Q3TEY6	P97477
ENSMUST00000109140	ENSMUSG00000027496	2	172356190	172370535	-1	0	0	10	0	7	0	159	171	158	39	80	Q3TEY6	P97477
ENSMUST00000109142	ENSMUSG00000007850	11	50376990	50386528	1	6	2	13	52	16	8	0	0	0	0	7	Q811L7	O35737
ENSMUST00000109147	ENSMUSG00000052033	2	170496428	170519123	1	3	5	1	2	4	0	5	11	22	34	3	E9Q8R1	
ENSMUST00000109148	ENSMUSG00000052033	2	170496428	170519123	1	0	0	0	4	0	0	19	24	7	72	12	Q6P0X1	
ENSMUST00000109149	ENSMUSG00000054855	15	98663421	98677461	-1	1	0	2	5	0	2	49	119	48	31	33		Q8BLR7
ENSMUST00000109150	ENSMUSG00000003352	15	98632220	98644530	1	24	9	42	137	31	16	23	15	22	5	37	D3Z3Z3	
ENSMUST00000109152	ENSMUSG00000013523	2	170346991	170427845	-1	0	0	0	0	6	0	0	0	0	0	0	E9Q8Q5	
ENSMUST00000109155	ENSMUSG00000052056	2	170108643	170148103	-1	40	29	146	22	70	25	1153	4854	1653	287	530	Q3U0X6	
ENSMUST00000109157	ENSMUSG00000047907	2	169633013	170071816	1	15	9	19	13	19	6	0	0	0	0	3		Q68FE9
ENSMUST00000109158	ENSMUSG00000056050	1	183326725	183369553	-1	3	0	0	58	6	6	378	859	669	54	390	J3KMH5	
ENSMUST00000109159	ENSMUSG00000047907	2	169633013	170071816	1	31	25	185	390	58	28	0	1	0	0	2		Q68FE9
ENSMUST00000109160	ENSMUSG00000078912	2	169582845	169587745	-1	5	10	7	6	4	6	0	0	0	0	0	D3Z3L9	
ENSMUST00000109161	ENSMUSG00000027551	2	168893331	168955587	-1	2	0	0	2	0	0	0	2	2	7	2		Q99KE8
ENSMUST00000109162	ENSMUSG00000027551	2	168893331	168955587	-1	18	9	53	202	30	9	11	5	2	3	12	A2AQR3	
ENSMUST00000109163	ENSMUSG00000032987	15	98456285	98457342	1	8	2	8	5	15	7	0	0	0	0	0	Q8VET6	
ENSMUST00000109166	ENSMUSG00000042901	1	183296590	183325476	1	54	42	120	56	64	35	38	199	81	24	100		Q8C4Q6
ENSMUST00000109172						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000109175	ENSMUSG00000027546	2	168634438	168742409	-1	25	23	77	33	54	21	0	0	0	0	14	Q8C288	
ENSMUST00000109176	ENSMUSG00000027546	2	168634438	168742409	-1	0	0	0	0	0	0	0	0	0	0	0	A2AQC3	
ENSMUST00000109177	ENSMUSG00000027546	2	168634438	168742409	-1	0	0	0	33	0	0	10	5	3	20	96	Q8C4G3	
ENSMUST00000109178	ENSMUSG00000020366	11	49846751	49886421	1	0	0	0	0	0	0	9	119	82	22	7		Q9WTU6
ENSMUST00000109179	ENSMUSG00000020366	11	49846751	49886421	1	0	0	5	9	0	2	0	0	0	0	0		Q9WTU6
ENSMUST00000109183						0	2	0	0	12	0	29	262	171	29	111		
ENSMUST00000109184	ENSMUSG00000027544	2	168476410	168601657	-1	0	0	0	242	1	11	0	0	93	0	83	B5B2P7	Q60591
ENSMUST00000109187						0	0	10	12	0	0	0	1	0	1	0		
ENSMUST00000109191	ENSMUSG00000074575	2	168260117	168281736	-1	34	11	48	178	48	8	0	0	0	0	0	B2RVK9	A2BDX4
ENSMUST00000109193	ENSMUSG00000078919	2	168209048	168230591	-1	2	4	4	32	9	5	15	12	9	13	0	A2BDX2	
ENSMUST00000109194	ENSMUSG00000020346	11	49244191	49263030	1	0	7	62	0	15	2	266	805	164	24	0	Q544F0	P27808
ENSMUST00000109197	ENSMUSG00000046311	11	49203292	49218816	1	0	0	0	0	0	0	43	0	0	13	0		Q8C827
ENSMUST00000109198	ENSMUSG00000046311	11	49203292	49218816	1	10	0	17	18	10	3	0	396	211	173	155		Q8C827
ENSMUST00000109201	ENSMUSG00000047511	11	49112777	49114874	-1	4	0	12	0	6	0	0	0	0	0	0	Q7TQS8	
ENSMUST00000109202	ENSMUSG00000078920	11	49076587	49096974	1	0	0	4	0	8	0	23	91	45	199	0	Q61635	
ENSMUST00000109203	ENSMUSG00000025451	13	119428601	119458218	1	2	9	2	17	4	5	197	856	121	65	93	D3Z3J6	
ENSMUST00000109204	ENSMUSG00000025453	13	119335448	119408997	-1	3	2	4	23	11	0	0	0	25	0	23	E9Q8F4	
ENSMUST00000109207	ENSMUSG00000078923	2	167607638	167632095	-1	5	0	21	88	32	19	322	567	472	45	294	Q569Y6	Q9CZY3
ENSMUST00000109209	ENSMUSG00000058163	11	48887422	48902152	-1	0	0	0	0	0	0	0	0	0	0	0	A6PWD6	
ENSMUST00000109210	ENSMUSG00000058163	11	48887422	48902152	-1	114	93	91	93	124	70	15	70	19	66	37	A6PWD6	
ENSMUST00000109211	ENSMUSG00000047030	2	167481133	167492887	-1	0	0	0	15	0	0	2	0	0	0	8	Q3UML2	
ENSMUST00000109212	ENSMUSG00000058163	11	48887422	48902152	-1	1	1	9	7	5	0	3	14	4	7	26	Q5NCB3	
ENSMUST00000109213	ENSMUSG00000040350	11	48826140	48852209	1	5	0	2	13	0	0	0	10	0	0	15		Q923T7
ENSMUST00000109214	ENSMUSG00000006418	2	167492645	167516173	1	3	6	29	169	19	6	0	18	19	6	31		Q9ET26
ENSMUST00000109218	ENSMUSG00000039463	2	167421712	167477000	1	0	0	3	12	0	1	0	0	0	0	0	A2A464	
ENSMUST00000109220	ENSMUSG00000020354	11	46896253	47988969	-1	10	8	34	17	15	6	0	0	0	0	1	A2ACH6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000109221	ENSMUSG00000017929	2	167298444	167349183	-1	32	29	252	70	48	29	1973	2984	2229	173	1482		Q9JMK0
ENSMUST00000109222	ENSMUSG00000035930	8	110029075	110039334	-1	12	5	15	12	16	6	0	0	0	1	0		
ENSMUST00000109223	ENSMUSG00000040405	11	46735080	46779578	1	6	7	36	11	4	2	0	0	0	0	0	Q3V033	
ENSMUST00000109224	ENSMUSG00000040405	11	46735080	46779578	1	1	2	39	4	2	0	0	0	0	2	0	E9QPA7	
ENSMUST00000109225	ENSMUSG00000040413	11	46668960	46707061	-1	2	0	0	3	3	3	0	0	0	0	0	A8C1R4	
ENSMUST00000109226	ENSMUSG00000042275	13	115088357	115090188	-1	14	11	26	229	31	10	66	104	43	8	37		Q80X73
ENSMUST00000109227	ENSMUSG00000064010	11	46607772	46629261	-1	2	0	0	2	0	0	0	0	1	0	0	Q810Y7	
ENSMUST00000109228	ENSMUSG00000078924	11	46524212	46538156	1	5	1	7	5	10	3	0	0	0	0	0	F2Z474	
ENSMUST00000109229	ENSMUSG00000020399	11	46454935	46481255	1	37	24	82	31	0	13	8	24	43	11	55	D3Z3I4	
ENSMUST00000109231	ENSMUSG00000020397	11	46436925	46442721	1	0	0	0	0	0	0	0	37	23	16	33	F2Z473	
ENSMUST00000109232	ENSMUSG00000020397	11	46436925	46442721	1	7	0	0	0	0	0	0	35	7	0	12		Q9CZB6
ENSMUST00000109235	ENSMUSG00000039536	2	166947549	166996299	-1	5	0	8	0	5	2	37	230	36	24	65	Q9DBE7	
ENSMUST00000109236	ENSMUSG00000039536	2	166947549	166996299	-1	10	6	0	99	1	4	19	98	188	0	153		Q9Z108
ENSMUST00000109237	ENSMUSG00000020395	11	46325150	46389515	-1	21	15	26	0	26	7	0	2	0	26	174		Q03526
ENSMUST00000109238	ENSMUSG00000039536	2	166947549	166996299	-1	0	0	0	0	0	0	117	270	271	54	185	A2A5S3	
ENSMUST00000109241	ENSMUSG00000042364	13	113592180	113618564	-1	16	12	57	313	28	6	2598	5309	3653	394	2922	Q8C788	
ENSMUST00000109242	ENSMUSG00000048827	8	109614517	109672592	1	59	46	0	0	45	28	0	0	0	0	0		Q2EG98
ENSMUST00000109244	ENSMUSG00000078926	13	113035111	113091195	1	0	0	0	13	0	0	0	0	0	0	0	D3Z3I0	
ENSMUST00000109246	ENSMUSG00000039621	2	166566342	166713832	-1	0	3	7	3	12	0	159	1090	82	96	138		Q69ZK0
ENSMUST00000109248	ENSMUSG00000059883	15	94543643	94581815	1	11	9	14	17	24	7	31	133	84	11	162	Q3USX5	
ENSMUST00000109249	ENSMUSG00000006800	2	166073089	166155663	-1	15	9	42	29	25	6	0	9	7	0	25		Q8CFG0
ENSMUST00000109252	ENSMUSG00000027678	2	165992636	166073242	1	8	0	29	76	0	0	945	152	1898	20	1443	A2A468	
ENSMUST00000109254	ENSMUSG00000011254	11	45946843	45955494	-1	0	0	0	15	0	0	0	0	0	0	0	Q9CQT0	
ENSMUST00000109255	ENSMUSG00000036158	15	93499114	93595891	-1	0	0	0	130	49	26	0	0	0	0	0		Q3U5C7
ENSMUST00000109256	ENSMUSG00000036167	15	93398350	93491913	1	0	0	0	83	0	0	30	98	67	0	28	G3UWD4	
ENSMUST00000109260	ENSMUSG00000006169	11	45852051	45910625	1	0	0	0	0	0	0	1456	2491	2593	268	1518	Q5SUH7	
ENSMUST00000109261	ENSMUSG00000006169	11	45852051	45910625	1	1	0	12	18	0	4	161	493	431	0	224	Q5SUH6	
ENSMUST00000109262	ENSMUSG00000039671	2	165784152	165899016	-1	18	45	0	52	0	0	0	1	18	50	0	A2A481	
ENSMUST00000109266	ENSMUSG00000039671	2	165784152	165899016	-1	9	2	32	0	9	0	51	309	125	63	162	E9Q8D1	
ENSMUST00000109267	ENSMUSG00000021754	13	111746428	111808993	-1	76	72	384	92	98	52	697	1591	1331	78	1067	F8VQ72	
ENSMUST00000109268	ENSMUSG00000057098	11	44617317	45008091	1	3	0	25	4	0	9	0	0	4	0	9	Q5SWK8	
ENSMUST00000109269	ENSMUSG00000039671	2	165784152	165899016	-1	20	18	65	30	46	12	3	0	15	0	15	A2A484	
ENSMUST00000109271	ENSMUSG00000032727	13	111686178	111718596	1	0	12	6	0	14	14	9	306	332	17	272	F7BFR0	
ENSMUST00000109272	ENSMUSG00000032727	13	111686178	111718596	1	0	0	0	21	0	0	120	351	125	25	267		Q3UHF3
ENSMUST00000109273						0	0	0	0	0	0	1	0	0	0	1		
ENSMUST00000109275	ENSMUSG00000001225	12	31390871	31473917	1	189	157	1260	253	130	65	6	66	12	2	19	F7BFQ2	
ENSMUST00000109276	ENSMUSG00000047295	15	91838265	91861438	1	0	0	2	0	0	0	0	0	0	0	0	D3Z1E5	
ENSMUST00000109277	ENSMUSG00000047295	15	91838265	91861438	1	3	3	4	0	1	0	0	0	0	0	0		Q6JHY2
ENSMUST00000109278	ENSMUSG00000041278	11	43729512	43748008	-1	7	3	21	24	7	0	27	138	34	43	31	A2AJK8	
ENSMUST00000109279	ENSMUSG00000018459	2	165405028	165473230	-1	0	7	0	46	0	0	0	0	5	4	1	A2A4U9	
ENSMUST00000109280	ENSMUSG00000044950	11	43681998	43721491	1	6	3	6	0	13	0	41	184	50	19	82	Z4YKW0	
ENSMUST00000109282						8	8	21	100	7	7	0	0	0	0	0		
ENSMUST00000109283	ENSMUSG00000036298	15	91267696	91573261	-1	24	22	22	83	30	15	0	0	0	0	3		Q3UHK1
ENSMUST00000109284	ENSMUSG00000078932	15	91199494	91260894	1	0	5	0	0	0	0	0	3	1	0	0	F8VQ66	
ENSMUST00000109286	ENSMUSG00000020428	11	42306437	42321072	-1	8	1	2	0	9	4	0	0	0	0	0		P16305
ENSMUST00000109287	ENSMUSG00000022629	15	90933276	91049948	-1	5	0	0	0	0	0	0	1	0	8	8		Q9QXL2
ENSMUST00000109288	ENSMUSG00000022629	15	90933276	91049948	-1	0	31	4	71	0	0	0	0	0	0	0		Q9QXL2
ENSMUST00000109290	ENSMUSG00000020436	11	41910203	42000857	-1	6	4	5	10	5	3	0	0	0	0	0	Q8C7N0	
ENSMUST00000109294						2	1	7	0	0	0	0	0	1	0	1		
ENSMUST00000109296	ENSMUSG00000060098	8	106210936	106252794	1	4	1	3	82	7	1	3	0	0	0	4	D3Z1D0	
ENSMUST00000109297	ENSMUSG00000060098	8	106210936	106252794	1	2	4	1	2	2	2	0	0	0	0	4	D3Z1C9	
ENSMUST00000109298	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	212	498	187	0	0	Q5GMH2	Q8VCX2
ENSMUST00000109299	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	81	0	0	0	0	Q5GMH2	Q8VCX2
ENSMUST00000109300	ENSMUSG00000017664	2	165276554	165287869	-1	0	4	0	28	0	0	1293	108	816	268	402	Q5GMH2	Q8VCX2
ENSMUST00000109304	ENSMUSG00000078935	2	165078693	165090750	-1	7	4	6	11	14	11	0	0	0	0	0	A2A580	
ENSMUST00000109307						11	9	42	12	15	8	17	71	22	4	47		
ENSMUST00000109308	ENSMUSG00000031902	8	106059603	106130537	1	18	17	29	134	34	20	985	2067	1739	206	935	Q3UZ64	
ENSMUST00000109309	ENSMUSG00000022623	15	89499623	89560261	1	0	0	31	501	0	0	0	0	0	0	0	A0A0A0MQD5	
ENSMUST00000109313	ENSMUSG00000078937	15	89416405	89425863	-1	17	8	49	25	25	11	21	61	15	0	56		Q924X2
ENSMUST00000109314	ENSMUSG00000078938	15	89390174	89410503	-1	3	1	0	7	7	1	0	0	0	0	0	E7D6R1	B5KM66
ENSMUST00000109315	ENSMUSG00000021710	13	104023439	104109614	-1	20	19	23	44	22	7	112	356	249	83	173		Q91YP2
ENSMUST00000109316	ENSMUSG00000017754	2	164839518	164857711	-1	0	8	17	0	18	3	20	5	16	4	26	Q3UFS5	P55065
ENSMUST00000109317	ENSMUSG00000017754	2	164839518	164857711	-1	11	0	2	2	0	0	20	29	1	8	148	A2A5K2	
ENSMUST00000109326	ENSMUSG00000017299	2	164745983	164768607	1	1	0	0	3	1	0	0	2	2	0	2	A2A4Y7	
ENSMUST00000109327	ENSMUSG00000017299	2	164745983	164768607	1	0	3	0	10	0	3	18	0	0	0	13	F7B2G8	
ENSMUST00000109328	ENSMUSG00000076434	2	164731180	164745931	-1	0	7	3	18	3	1	0	0	0	0	1	A2A4Y5	
ENSMUST00000109329	ENSMUSG00000002699	11	34046920	34092295	1	6	2	9	8	5	3	632	1719	1364	928	1516	B1ATD1	
ENSMUST00000109331	ENSMUSG00000036606	15	89155549	89171120	-1	41	31	87	0	69	21	849	804	552	67	1252		B2RXS4
ENSMUST00000109332	ENSMUSG00000078940	2	164662894	164674087	-1	2	1	1	1	7	2	0	0	0	0	0		A2A5H7
ENSMUST00000109333	ENSMUSG00000061474	13	100735955	100744659	-1	10	12	6	40	12	2	37	75	22	61	28		Q9CQX8
ENSMUST00000109335	ENSMUSG00000074594	2	164649631	164656583	-1	3	4	11	2	5	1	0	0	0	0	0		Q3UW41
ENSMUST00000109336	ENSMUSG00000070530	2	164634707	164638796	-1	2	2	5	8	4	3	0	0	0	0	0	A2A5H4	
ENSMUST00000109338	ENSMUSG00000070533	2	164596458	164613626	-1	0	0	5	6	0	4	0	0	0	0	0		Q4KUS1
ENSMUST00000109339	ENSMUSG00000070533	2	164596458	164613626	-1	24	21	50	24	32	15	0	0	0	0	0	A2A5H1	
ENSMUST00000109340	ENSMUSG00000053519	11	33629339	33993152	-1	0	1	0	30	0	0	0	0	0	0	0		Q9JJ57
ENSMUST00000109342	ENSMUSG00000074595	2	164579519	164585447	-1	0	5	0	5	4	0	0	0	0	0	0		Q3UW55
ENSMUST00000109344	ENSMUSG00000017723	2	164562413	164568510	1	0	0	0	0	3	0	0	1	0	45	0	A2A5G4	
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ENSMUST00000109347	ENSMUSG00000062906	15	89123307	89128700	-1	3	0	6	14	3	0	0	0	3	7	0	D3Z7T4	
ENSMUST00000109349	ENSMUSG00000017734	2	164486106	164493319	1	18	19	16	36	21	6	1	4	1	6	4	Q330P7	Q9CRD4
ENSMUST00000109350	ENSMUSG00000017734	2	164486106	164493319	1	2	1	3	35	2	2	16	36	21	0	43	Q330P7	Q9CRD4
ENSMUST00000109352	ENSMUSG00000045503	2	164456964	164479638	1	0	0	12	0	0	0	25	58	25	5	30		Q78S06
ENSMUST00000109353	ENSMUSG00000051786	15	89098357	89123087	-1	46	42	99	117	67	24	256	291	419	21	375	G5E8P0	
ENSMUST00000109354	ENSMUSG00000057113	11	33152287	33163206	-1	21	9	12	30	28	12	78	846	174	440	58	Q9DAY9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000109355	ENSMUSG00000054320	8	105413571	105464086	1	1	0	1	0	0	0	0	0	0	0	0	F8WI85	
ENSMUST00000109356						1	2	0	3	9	0	0	0	0	0	2		
ENSMUST00000109358	ENSMUSG00000016995	2	164389393	164405160	-1	11	0	0	219	0	0	0	1	4	0	0	F2Z469	
ENSMUST00000109359	ENSMUSG00000016995	2	164389393	164405160	-1	0	0	0	0	0	0	0	0	0	0	0	F2Z468	
ENSMUST00000109363	ENSMUSG00000057967	11	33117430	33147400	-1	1	4	9	16	0	5	1	0	0	0	0	Q5SQB3	
ENSMUST00000109365	ENSMUSG00000020270	11	32818529	32824605	-1	1	1	2	0	8	2	0	0	0	0	0	A6PWJ8	
ENSMUST00000109366	ENSMUSG00000020271	11	32642724	32746816	1	0	1	38	39	0	0	509	1018	910	55	606		Q5SRY7
ENSMUST00000109367	ENSMUSG00000017002	2	164354070	164389095	-1	11	6	11	6	5	4	6370	11580	4362	4922	4918	Q548X8	P97430
ENSMUST00000109368	ENSMUSG00000035805	15	88955884	88979007	-1	0	0	58	29	0	21	0	0	0	0	0	E9QP87	
ENSMUST00000109370	ENSMUSG00000017003	2	164289268	164291500	1	0	1	0	12	12	6	0	0	0	0	0	F2Z467	
ENSMUST00000109371	ENSMUSG00000022388	15	88890633	88954418	-1	22	20	6	10	26	0	0	0	0	0	0		A4Q9F1
ENSMUST00000109372	ENSMUSG00000014856	8	105326354	105335219	1	4	1	0	0	0	0	17	14	3	16	11	D3Z7S5	
ENSMUST00000109374	ENSMUSG00000040132	2	164235929	164238466	-1	3	0	9	7	0	2	0	0	0	0	0	Q8BS30	
ENSMUST00000109375	ENSMUSG00000014791	8	105305601	105310623	1	20	16	44	70	31	11	27	113	29	16	55		Q8BYZ7
ENSMUST00000109376	ENSMUSG00000018211	2	164214454	164221660	-1	4	3	0	0	0	0	0	0	0	0	0		Q9JHY4
ENSMUST00000109377	ENSMUSG00000044056	11	32522751	32532081	-1	6	2	2	3	3	5	0	1	0	0	0	B1ATW6	
ENSMUST00000109379	ENSMUSG00000049658	13	100017994	100104070	-1	9	7	18	0	12	0	31	23	418	70	285		Q571C7
ENSMUST00000109380	ENSMUSG00000022387	15	88687300	88734233	-1	7	2	0	0	5	0	157	7	391	0	213	G5E8P1	
ENSMUST00000109381	ENSMUSG00000022387	15	88687300	88734233	-1	3	3	36	13	12	7	726	1389	1074	142	1033	E9PZ26	
ENSMUST00000109384	ENSMUSG00000018322	2	164053540	164071169	-1	0	0	10	26	0	0	263	779	187	45	207		Q9CYG7
ENSMUST00000109389	ENSMUSG00000020289	11	32225628	32267707	-1	0	0	0	4	0	0	20	17	18	0	33	A7M7S2	
ENSMUST00000109390						17	9	12	15	15	9	0	0	9	0	3		
ENSMUST00000109392	ENSMUSG00000031885	8	105170674	105217989	1	0	7	0	0	0	0	591	932	531	128	359		Q08024
ENSMUST00000109394	ENSMUSG00000031885	8	105170674	105217989	1	9	0	0	10	0	0	213	470	0	74	0		Q08024
ENSMUST00000109395	ENSMUSG00000031885	8	105170674	105217989	1	2	0	9	13	0	0	0	23	10	4	9		Q08024
ENSMUST00000109396	ENSMUSG00000035238	2	163853651	163859746	1	5	3	5	32	4	5	0	0	0	0	0	A2AHD2	
ENSMUST00000109399	ENSMUSG00000009470	13	98839019	98926384	-1	0	0	0	9	9	15	0	25	31	0	54		Q8BFY9
ENSMUST00000109400	ENSMUSG00000035268	2	163658386	163726158	1	11	7	10	13	7	0	0	0	14	0	0	Q3TP50	O70139
ENSMUST00000109401	ENSMUSG00000009470	13	98839019	98926384	-1	20	14	24	78	35	6	910	1883	1140	321	682		Q8BFY9
ENSMUST00000109403	ENSMUSG00000041685	13	98723407	98815449	-1	0	4	5	13	0	0	0	81	28	0	0		Q3UQN2
ENSMUST00000109405	ENSMUSG00000017679	2	163602314	163619013	1	13	1	24	0	31	7	65	413	187	35	157		Q9D3D0
ENSMUST00000109408	ENSMUSG00000017679	2	163602314	163619013	1	0	0	0	6	0	0	9	0	14	0	10		Q9D3D0
ENSMUST00000109409	ENSMUSG00000020297	11	32000463	32059202	1	7	4	7	7	3	4	0	0	0	0	0	Q5SS04	
ENSMUST00000109410	ENSMUSG00000031886	8	104926260	104934672	1	5	7	27	6	15	8	6	9	4	2	1		Q8BK48
ENSMUST00000109411	ENSMUSG00000017950	2	163506808	163572910	1	34	4	54	7	10	4	1	1	1	1	0	Z4YKX0	
ENSMUST00000109412	ENSMUSG00000020300	11	31872211	31935634	1	6	10	55	14	20	9	194	172	57	52	155	Q5SU48	
ENSMUST00000109415	ENSMUSG00000044502	11	31665181	31671885	-1	6	2	5	40	6	1	0	0	2	0	6		Q5SQY2
ENSMUST00000109416	ENSMUSG00000078949	2	163492318	163502612	1	6	6	15	38	12	8	0	0	0	0	0		A2A5I3
ENSMUST00000109418	ENSMUSG00000048486	2	163466379	163472629	-1	78	62	211	214	97	35	28	38	27	6	34		P59266
ENSMUST00000109420	ENSMUSG00000017943	2	163438476	163455324	1	8	10	7	15	14	7	0	0	0	0	0	Q3USC7	
ENSMUST00000109421	ENSMUSG00000017943	2	163438476	163455324	1	0	5	0	42	0	0	0	0	0	0	0		Q8VE33
ENSMUST00000109422	ENSMUSG00000022383	15	85734983	85802819	1	27	32	121	189	42	18	2	0	0	0	0	Q542P9	P23204
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ENSMUST00000109424	ENSMUSG00000022382	15	85535439	85581821	-1	12	3	35	307	14	0	0	0	0	0	0	Q6NZR1	
ENSMUST00000109425	ENSMUSG00000017817	2	163336242	163397993	-1	23	0	0	215	0	0	0	1	3	0	1		Q9ET78
ENSMUST00000109426	ENSMUSG00000021662	13	97898595	98206165	-1	40	29	116	96	49	22	0	3	0	2	14	G5E8P2	
ENSMUST00000109428	ENSMUSG00000074607	2	163203125	163324170	1	6	2	15	158	11	3	0	0	0	0	2	A2A473	
ENSMUST00000109430	ENSMUSG00000043999	11	30885358	30893729	1	32	33	73	78	36	14	0	3	0	0	1	Q059L0	Q6X632
ENSMUST00000109432	ENSMUSG00000006369	15	85205949	85286535	1	5	8	7	26	9	0	0	3	1	3	3		Q08879
ENSMUST00000109441	ENSMUSG00000053141	2	161521990	162661147	-1	0	0	6	0	5	0	0	0	0	0	0		Q99M80
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ENSMUST00000109444	ENSMUSG00000021669	13	96542618	96640167	1	9	0	0	213	0	12	1550	4068	1954	332	1124		Q9EQG9
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ENSMUST00000109447	ENSMUSG00000078953	8	104321567	104321787	1	2	0	2	1	2	1	0	2	1	0	0	F6ZGD5	
ENSMUST00000109452	ENSMUSG00000044072	11	29743048	30026033	-1	3	0	0	1	0	0	0	0	0	3	0	F6ZBI5	
ENSMUST00000109454	ENSMUSG00000050700	2	160906437	160912328	-1	28	1	23	0	15	0	0	0	0	0	0	A2A4B4	
ENSMUST00000109455	ENSMUSG00000027412	2	160880670	160906002	1	0	24	39	33	7	24	0	0	0	0	0	A2A4B3	
ENSMUST00000109456	ENSMUSG00000027412	2	160880670	160906002	1	45	0	13	0	39	0	0	0	0	0	0	Q149B0	Q99PI4
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ENSMUST00000109460	ENSMUSG00000035877	2	160748708	160872998	-1	6	0	107	0	32	1	16	0	33	3	0	Q3UPQ8	Q8C0Q2
ENSMUST00000109462	ENSMUSG00000016933	2	160731300	160775760	1	10	14	15	16	12	16	120	172	173	32	295	A2A4A6	
ENSMUST00000109467						9	13	37	2	15	8	45	456	43	73	44		
ENSMUST00000109468	ENSMUSG00000070544	2	160645888	160722764	1	19	13	10	59	17	13	609	2198	1285	215	705		Q04750
ENSMUST00000109469	ENSMUSG00000041708	15	83779467	83858494	1	0	1	6	51	5	8	0	0	0	0	0	B1APX5	
ENSMUST00000109470	ENSMUSG00000041708	15	83779467	83858494	1	7	0	31	7	21	16	0	0	0	0	0		Q91ZG2
ENSMUST00000109473	ENSMUSG00000078956	2	160568379	160619971	-1	0	1	4	0	2	0	0	0	0	0	0	A2A5U3	
ENSMUST00000109475	ENSMUSG00000074623	2	160311393	160334162	-1	8	5	7	5	5	3	0	0	0	0	0	A2A5Q3	
ENSMUST00000109477	ENSMUSG00000032740	11	29373658	29510808	1	4	2	5	160	9	2	0	0	0	0	0	Z4YKY0	
ENSMUST00000109478	ENSMUSG00000027655	2	158794807	158858214	1	13	7	0	0	0	0	67	94	4	18	0	A2ACQ1	
ENSMUST00000109479	ENSMUSG00000022442	15	83483772	83510893	-1	11	19	71	42	31	28	0	0	0	0	3	Q8BJG7	
ENSMUST00000109480	ENSMUSG00000022442	15	83483772	83510893	-1	0	3	12	0	2	4	0	0	0	0	0		Q91V51
ENSMUST00000109484	ENSMUSG00000044405	2	158502612	158508198	1	0	0	0	0	0	0	1	3	0	0	0	A2ACC4	
ENSMUST00000109485	ENSMUSG00000027652	2	158409848	158499253	1	0	4	0	0	0	0	154	0	112	0	0	E9Q0J2	
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ENSMUST00000109488	ENSMUSG00000044349	2	158375638	158386145	1	129	111	250	710	159	93	10	27	30	4	49	Q4G0K9	
ENSMUST00000109491	ENSMUSG00000016024	2	158306493	158332852	1	2	5	12	9	7	1	98	130	110	42	55	A2AC65	
ENSMUST00000109492	ENSMUSG00000007617	13	93303757	93404129	1	1	4	2	0	1	0	4	0	1	0	0		Q9Z2Y3
ENSMUST00000109493	ENSMUSG00000007617	13	93303757	93404129	1	1	3	0	3	4	0	14	71	52	11	32	D3Z6A9	
ENSMUST00000109494	ENSMUSG00000007617	13	93303757	93404129	1	1	0	2	159	7	0	3	0	6	0	0	Q3UVL6	
ENSMUST00000109495	ENSMUSG00000007617	13	93303757	93404129	1	0	0	0	0	0	0	0	0	4	2	8	D3Z6A8	
ENSMUST00000109496	ENSMUSG00000007617	13	93303757	93404129	1	2	0	3	1	0	0	2	0	0	1	0	D3Z6A7	
ENSMUST00000109497	ENSMUSG00000007617	13	93303757	93404129	1	2	1	1	0	2	1	2	7	20	8	9	E9Q0I8	
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000109499	ENSMUSG00000052922	2	158258094	158284531	1	1	2	19	0	0	0	0	1	2	0	1		Q67E05
ENSMUST00000109500	ENSMUSG00000052922	2	158258094	158284531	1	0	0	14	30	9	0	0	0	0	0	0		Q67E05
ENSMUST00000109501						31	20	98	251	36	12	0	0	0	1	2		
ENSMUST00000109502	ENSMUSG00000032878	11	28385685	28584324	-1	0	0	0	0	11	0	0	0	0	0	0		Q5SP85
ENSMUST00000109503	ENSMUSG00000058099	15	82997721	83033306	-1	7	10	21	8	26	10	1275	2725	2156	67	1363		Q8R4V1
ENSMUST00000109504	ENSMUSG00000064090	11	26471322	26593999	-1	4	0	6	0	0	2	118	690	196	129	128		Q8BN21
ENSMUST00000109509	ENSMUSG00000004018	11	26386135	26471876	1	2	0	2	0	0	0	18	75	27	73	25		Q9CR14
ENSMUST00000109510	ENSMUSG00000041852	15	82808629	82912134	-1	0	33	37	0	59	0	117	206	275	27	593		Q9EPQ8
ENSMUST00000109511	ENSMUSG00000032985	11	25602763	26210763	-1	0	0	0	0	2	2	0	0	0	0	0	Q5SP45	
ENSMUST00000109514	ENSMUSG00000000861	11	24078056	24174123	1	46	32	85	420	63	35	9	31	10	0	24	Q5STS9	
ENSMUST00000109515	ENSMUSG00000094559	15	82615965	82620907	-1	5	9	22	11	23	5	0	0	0	0	0	L7N463	
ENSMUST00000109516	ENSMUSG00000000861	11	24078056	24174123	1	0	0	0	3	3	0	0	0	0	0	0		Q9QYE3
ENSMUST00000109518	ENSMUSG00000027651	2	158028497	158132297	1	8	34	0	0	0	16	0	196	0	0	0		Q9CSU0
ENSMUST00000109519						10	12	15	177	7	0	0	1	0	0	0		
ENSMUST00000109521	ENSMUSG00000031783	8	94857450	94864242	1	14	17	49	74	40	14	586	691	353	108	278	Q99M46	
ENSMUST00000109522	ENSMUSG00000027650	2	157981803	158028433	-1	0	26	43	0	0	0	138	438	285	7	0		Q91V83
ENSMUST00000109523	ENSMUSG00000037843	2	157914653	157944719	1	6	5	4	177	9	7	0	0	0	0	0	A2ACD2	
ENSMUST00000109525	ENSMUSG00000020280	11	23665674	23732876	1	0	2	0	52	2	0	0	156	0	18	0		Q9D3U0
ENSMUST00000109526	ENSMUSG00000067786	2	157560078	157562522	1	0	0	0	0	0	0	0	8	37	0	15		Q61979
ENSMUST00000109527	ENSMUSG00000031776	8	94666755	94674417	1	0	14	23	0	0	0	1388	2827	1126	181	606		Q9D385
ENSMUST00000109528	ENSMUSG00000067787	2	157556362	157571274	-1	18	10	61	2	10	0	697	1613	673	100	462		P62951
ENSMUST00000109529	ENSMUSG00000027646	2	157418444	157471862	1	10	2	3	30	27	2	0	0	0	0	7		P05480
ENSMUST00000109531	ENSMUSG00000027646	2	157418444	157471862	1	0	0	2	23	0	0	5	0	0	11	0	Q80XU2	
ENSMUST00000109532	ENSMUSG00000042208	11	23564961	23633639	-1	0	0	0	23	0	0	0	0	0	0	0		Q68FF0
ENSMUST00000109533	ENSMUSG00000027646	2	157418444	157471862	1	18	13	0	0	48	11	0	5	0	0	78	Q80XU2	
ENSMUST00000109535	ENSMUSG00000068105	15	82221744	82224339	-1	70	25	50	266	47	50	0	0	0	0	22	Q3U106	
ENSMUST00000109536	ENSMUSG00000027643	2	157329497	157347506	-1	0	0	0	0	5	0	0	0	0	0	0	Q544X5	P16043
ENSMUST00000109537	ENSMUSG00000034361	8	94532990	94570529	1	8	0	1	0	7	0	2485	2313	2195	119	1563		
ENSMUST00000109539	ENSMUSG00000020288	11	23487882	23498030	-1	5	2	5	9	9	2	16	146	24	51	63		Q8N9S3
ENSMUST00000109541	ENSMUSG00000078958	13	90883433	90905355	-1	6	0	0	0	0	0	0	0	0	0	0	D3Z5W0	
ENSMUST00000109542						14737	12319	122345	48396	13650	6164	194	455	374	27	350		
ENSMUST00000109543	ENSMUSG00000021614	13	89655312	89742509	-1	0	0	0	0	0	0	25	33	19	75	100	E9QMK3	
ENSMUST00000109544	ENSMUSG00000021614	13	89655312	89742509	-1	7	0	6	0	12	0	0	0	0	0	15	E9QMK2	
ENSMUST00000109546	ENSMUSG00000021614	13	89655312	89742509	-1	39	30	56	55	26	28	223	832	243	39	167	E9PYH0	
ENSMUST00000109547	ENSMUSG00000032939	8	94214597	94315066	1	53	48	307	73	52	46	0	91	27	0	12		Q8BJ71
ENSMUST00000109549	ENSMUSG00000027639	2	157097533	157135265	-1	57	49	146	97	78	41	83	547	140	89	297	E9PYG9	
ENSMUST00000109551	ENSMUSG00000020290	11	23256041	23298249	1	1	0	0	0	0	0	1	0	0	0	0		Q6P5F9
ENSMUST00000109552	ENSMUSG00000021549	13	85214780	85289029	-1	3	3	6	180	7	9	149	474	295	29	186	E9PYG6	
ENSMUST00000109553	ENSMUSG00000022389	15	81802421	81826861	1	22	14	90	98	33	13	0	24	14	14	22		Q9JLC6
ENSMUST00000109554	ENSMUSG00000022390	15	81744848	81796269	1	43	35	85	126	80	40	85	79	83	15	154	F8VPP8	
ENSMUST00000109556	ENSMUSG00000033009	8	94037198	94067921	1	0	0	48	0	1	0	110	84	167	0	150		Q3U0K8
ENSMUST00000109557	ENSMUSG00000049811	11	23007531	23030788	1	0	0	11	0	0	0	0	0	0	0	0	B1AVK0	
ENSMUST00000109558	ENSMUSG00000027634	2	156927345	156992056	-1	101	96	94	384	118	84	6	60	23	26	42	Q8CBD0	
ENSMUST00000109561	ENSMUSG00000027636	2	156872457	156887192	-1	16	14	29	0	12	10	22	0	5	8	6		Q8R4L0
ENSMUST00000109563	ENSMUSG00000042302	11	22005828	22342292	-1	0	0	12	0	0	0	0	7	0	0	0		Q69ZW3
ENSMUST00000109565	ENSMUSG00000069170	13	81095068	81633154	-1	0	5	13	4	5	0	0	0	0	0	0	G5E8P3	
ENSMUST00000109566	ENSMUSG00000061689	2	156613705	156764363	1	0	0	0	0	0	0	209	552	314	11	159	E9PUF2	
ENSMUST00000109567	ENSMUSG00000061689	2	156613705	156764363	1	0	0	0	120	0	0	0	0	0	0	0		B1AZP2
ENSMUST00000109568	ENSMUSG00000061689	2	156613705	156764363	1	0	0	53	14	15	0	0	0	0	0	0	B7ZNS2	
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ENSMUST00000109572	ENSMUSG00000027624	2	156420909	156543214	1	9	0	6	0	0	20	0	9	11	0	0	A2AUK6	
ENSMUST00000109574	ENSMUSG00000027624	2	156420909	156543214	1	0	0	0	0	0	17	8	0	0	17	120	A2AUK7	
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ENSMUST00000109578	ENSMUSG00000020128	11	21239281	21321136	1	0	0	14	22	6	0	203	745	351	73	71		Q5SPW0
ENSMUST00000109579	ENSMUSG00000042292	15	81012281	81190757	-1	18	14	50	0	16	0	3290	4357	2772	239	2303		Q8K4J6
ENSMUST00000109580	ENSMUSG00000038085	2	156312299	156375638	1	7	5	2	0	5	0	7	29	0	48	15	A2AV96	
ENSMUST00000109581	ENSMUSG00000023015	15	99620496	99651656	-1	0	0	0	10	4	0	0	0	0	0	0	E9Q1Y6	
ENSMUST00000109582	ENSMUSG00000078964	8	93056727	93080017	-1	9	5	17	14	8	2	0	0	0	23	0	D3Z5G7	
ENSMUST00000109583	ENSMUSG00000021596	13	76384535	77031810	1	0	3	0	0	0	1	113	659	430	335	230	E9PW38	
ENSMUST00000109584	ENSMUSG00000027620	2	156147239	156180238	-1	4	1	5	200	0	0	4	0	5	0	0	B7ZD64	
ENSMUST00000109585	ENSMUSG00000049800	11	20543253	20653021	1	4	11	8	3	2	2	0	0	40	0	30	Q3UGZ1	Q9JJG5
ENSMUST00000109586	ENSMUSG00000049800	11	20543253	20653021	1	16	0	55	125	29	0	225	650	359	68	360	Q3UGZ1	Q9JJG5
ENSMUST00000109587	ENSMUSG00000027620	2	156147239	156180238	-1	8	0	0	0	1	0	34	19	0	0	0		Q8VH51
ENSMUST00000109589	ENSMUSG00000021596	13	76384535	77031810	1	5	1	7	1	4	4	8	29	13	20	16	E9Q1Y4	
ENSMUST00000109594	ENSMUSG00000020142	11	20302180	20332713	-1	0	0	36	256	0	21	0	0	0	0	0	Q3UTP8	O35874
ENSMUST00000109596	ENSMUSG00000044066	11	20227037	20249429	-1	0	0	0	0	0	0	1	0	0	2	16		Q8C0D9
ENSMUST00000109597	ENSMUSG00000067847	2	156144039	156145797	1	4	0	3	179	9	8	0	0	0	0	0		P60603
ENSMUST00000109598	ENSMUSG00000067847	2	156144039	156145797	1	0	2	4	0	0	0	44	52	5	78	13		P60603
ENSMUST00000109600	ENSMUSG00000027618	2	156123639	156144186	-1	0	3	4	37	7	2	4	15	2	0	2	A6QRH3	
ENSMUST00000109601	ENSMUSG00000020149	11	20201432	20226856	1	0	0	0	0	0	0	483	214	358	528	255	Q5SW86	
ENSMUST00000109602	ENSMUSG00000020149	11	20201432	20226856	1	32	22	51	3	47	23	0	0	0	0	0	Q5SW87	
ENSMUST00000109604	ENSMUSG00000089824	2	156091958	156111978	-1	20	21	64	75	27	9	0	3	26	10	0		Q8R4X3
ENSMUST00000109605	ENSMUSG00000042406	15	80255184	80257540	1	6	13	20	155	17	7	930	3488	1246	621	1012		Q06507
ENSMUST00000109606	ENSMUSG00000021589	13	75869537	75943925	-1	1	0	0	124	4	0	0	0	0	0	0	Q8BV11	
ENSMUST00000109607	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	12	0	0	0	1400	3436	1324	75	933		Q8C166
ENSMUST00000109608	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	16	4	0	306	428	628	91	395		Q8C166
ENSMUST00000109609	ENSMUSG00000031667	8	91112041	91134465	-1	0	0	0	0	0	0	0	52	23	37	41		Q64362
ENSMUST00000109611	ENSMUSG00000013338	2	156019139	156052947	-1	37	30	89	119	72	23	0	0	0	0	0	Z4YL23	
ENSMUST00000109614	ENSMUSG00000056608	8	90828835	91054508	1	30	1	87	125	72	38	0	164	197	0	251		Q8BYH8
ENSMUST00000109615	ENSMUSG00000053411	15	79915807	79971119	-1	0	0	0	0	0	0	5	0	9	0	15		Q8VDS3
ENSMUST00000109616	ENSMUSG00000053411	15	79915807	79971119	-1	0	1	0	0	11	0	59	260	61	10	144		Q8VDS3
ENSMUST00000109617	ENSMUSG00000074646	2	155973279	156007977	-1	4	10	37	8	6	0	0	0	0	0	0	E9Q1X6	
ENSMUST00000109618	ENSMUSG00000038241	2	155956458	155998900	1	4	4	8	0	7	0	0	0	0	0	0	Q8BZX9	
ENSMUST00000109619	ENSMUSG00000038241	2	155956458	155998900	1	0	0	0	0	0	0	0	182	0	0	430	A3KGJ7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000109620	ENSMUSG00000009585	15	79891659	79915906	1	0	0	8	7	0	0	32	164	62	5	88	E9QMH1	
ENSMUST00000109621	ENSMUSG00000043668	8	90247040	90348343	-1	14	6	47	31	19	5	0	0	0	0	0		Q80W03
ENSMUST00000109623	ENSMUSG00000089715	15	79823896	79834688	-1	0	0	0	118	0	2	0	0	0	0	0	D3Z5F6	
ENSMUST00000109625	ENSMUSG00000089715	15	79823896	79834688	-1	17	0	10	158	17	0	0	0	3	0	0	Q3UK98	
ENSMUST00000109626	ENSMUSG00000036712	8	88697028	88751945	1	0	52	79	0	66	36	588	2101	1200	397	826		Q80TQ2
ENSMUST00000109627	ENSMUSG00000089715	15	79823896	79834688	-1	31	32	174	147	52	31	36	70	23	10	103		Q9DBY5
ENSMUST00000109629	ENSMUSG00000078972	2	155940728	155942750	1	7	10	38	55	11	3	0	0	0	0	0	A6PWY0	
ENSMUST00000109631	ENSMUSG00000005882	2	155846894	155930310	-1	8	8	11	82	0	1	0	0	0	0	0	A6PWX7	
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ENSMUST00000109634	ENSMUSG00000055994	8	88647315	88688474	1	64	64	238	110	131	48	227	543	330	46	482		Q8K3Z0
ENSMUST00000109635	ENSMUSG00000044966	11	16951375	16954772	1	2	1	1	2	1	1	4	24	0	2	3		Q8CAT8
ENSMUST00000109636	ENSMUSG00000005882	2	155846894	155930310	-1	2	0	6	28	29	0	0	9	0	0	0		Q9CWU6
ENSMUST00000109638	ENSMUSG00000027613	2	155819832	155826925	-1	15	14	37	100	17	6	25	48	28	7	44	B1AZQ4	
ENSMUST00000109640	ENSMUSG00000021575	13	74211118	74292331	-1	0	0	0	0	0	0	1	0	1	0	2		
ENSMUST00000109641	ENSMUSG00000078974	11	16500530	16508484	-1	6	5	5	19	10	2	4	0	0	0	0	Q5SWJ8	P60060
ENSMUST00000109642	ENSMUSG00000078974	11	16500530	16508484	-1	0	0	0	0	0	0	2	16	2	49	6	Q5SWJ8	P60060
ENSMUST00000109643	ENSMUSG00000078974	11	16500530	16508484	-1	7	0	5	5	5	0	2	7	3	9	2	Q5SWJ8	P60060
ENSMUST00000109645	ENSMUSG00000048834	11	16257724	16427310	1	7	9	21	60	6	4	0	0	0	0	0		Q8R0A6
ENSMUST00000109646	ENSMUSG00000042564	15	79609576	79658956	-1	0	1	0	0	6	0	0	9	12	8	28	Q08EB1	
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ENSMUST00000109648	ENSMUSG00000042564	15	79609576	79658956	-1	117	124	145	111	137	71	28	171	51	17	101	Q9D3V8	
ENSMUST00000109650	ENSMUSG00000020173	11	12236608	12464960	-1	0	0	0	0	30	0	0	0	0	0	0		Q5NBX1
ENSMUST00000109651	ENSMUSG00000020173	11	12236608	12464960	-1	0	0	0	49	0	0	0	0	0	0	0	G5E8P4	
ENSMUST00000109653	ENSMUSG00000020176	11	11930508	12038683	-1	7	3	1	0	10	1	1	0	3	0	0	Q5SUW3	
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ENSMUST00000109655	ENSMUSG00000045333	8	87661810	87959595	-1	0	0	0	149	0	0	0	0	0	0	0		Q80TS5
ENSMUST00000109659	ENSMUSG00000020182	11	11814101	11898144	-1	0	8	0	3	0	0	0	0	0	0	0	Q5SUV8	O88533
ENSMUST00000109664	ENSMUSG00000035455	11	11787431	11808962	-1	0	9	13	0	0	5	0	23	47	52	35		Q8BPY9
ENSMUST00000109669	ENSMUSG00000038369	2	155390656	155473894	-1	7	0	6	0	0	3	3	0	3	0	3	A2AQN0	
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ENSMUST00000109678	ENSMUSG00000020191	11	11462094	11515192	1	3	2	0	2	2	0	0	1	0	0	0		Q5NC83
ENSMUST00000109679	ENSMUSG00000021612	13	73661750	73678023	-1	343	184	128	259	221	162	15	26	11	1	13		O88576
ENSMUST00000109680	ENSMUSG00000021612	13	73661750	73678023	-1	0	233	110	74	170	85	0	0	0	0	0		O88576
ENSMUST00000109681	ENSMUSG00000050830	11	11114223	11268931	1	5	3	0	79	7	13	0	0	0	0	0		Q8C8N3
ENSMUST00000109682	ENSMUSG00000047459	2	155236533	155250277	1	3	0	0	34	5	3	410	1187	375	2034	353		P62627
ENSMUST00000109685	ENSMUSG00000027598	2	155133509	155226855	1	8	9	0	0	14	0	199	309	636	88	388		Q8C863
ENSMUST00000109686	ENSMUSG00000036902	8	85636588	85690973	-1	18	11	46	11	16	5	9	16	6	1	3		Q8BNJ6
ENSMUST00000109687	ENSMUSG00000033088	15	78947724	79005867	1	0	0	0	142	0	0	1	0	2	0	293		Q99KW3
ENSMUST00000109688	ENSMUSG00000033088	15	78947724	79005867	1	25	6	35	0	26	4	3305	4428	3247	328	1906	E9QMQ3	
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ENSMUST00000109690	ENSMUSG00000033088	15	78947724	79005867	1	1	38	384	186	88	47	1	0	0	0	0		Q99KW3
ENSMUST00000109691	ENSMUSG00000041992	12	117516479	117756978	1	32	15	35	17	21	17	24	21	64	8	19		Q8C0Q9
ENSMUST00000109694	ENSMUSG00000049538	13	70727802	70841811	-1	0	0	0	0	4	0	0	0	0	0	1		Q69Z28
ENSMUST00000109697	ENSMUSG00000027596	2	154791402	155051012	1	0	0	0	2	0	3	0	0	0	0	0		Q03288
ENSMUST00000109698	ENSMUSG00000022436	15	78899667	78919517	1	0	0	0	0	0	0	35	28	72	0	40	A2A5V2	
ENSMUST00000109699	ENSMUSG00000021595	13	69533746	69635780	1	0	0	0	67	3	0	112	450	263	105	252		Q1HFZ0
ENSMUST00000109701	ENSMUSG00000027593	2	154791096	154867261	1	3	0	0	48	0	0	154	0	40	123	80	Q3U3F6	Q64012
ENSMUST00000109702	ENSMUSG00000059842	2	154613297	154646821	1	18	0	16	2	0	0	8	28	58	0	64	A2AVM0	
ENSMUST00000109703	ENSMUSG00000000876	2	154585758	154603708	-1	14	24	37	31	26	12	23	28	8	25	17	A2AKD6	
ENSMUST00000109709	ENSMUSG00000038523	2	154547085	154550003	1	0	3	0	102	1	1	0	0	0	0	0	A2AKE5	
ENSMUST00000109711	ENSMUSG00000095416	12	114615850	114616318	-1	0	0	0	0	0	0	0	1	0	1	1	A0A075B665	
ENSMUST00000109716	ENSMUSG00000027489	2	154544399	154558890	-1	10	0	17	0	18	9	0	1	0	0	0		Q9D6J4
ENSMUST00000109721	ENSMUSG00000000378	11	6546887	6596744	1	0	0	4	0	0	0	1237	1425	629	369	516	F7AVU1	
ENSMUST00000109722	ENSMUSG00000000378	11	6546887	6596744	1	0	3	0	0	8	7	39	152	63	38	98	F7AVU1	
ENSMUST00000109723	ENSMUSG00000021144	12	113098278	113137206	1	7	3	0	22	37	2	16	0	0	0	0	E9PX23	
ENSMUST00000109724	ENSMUSG00000038533	2	154436481	154539356	1	0	0	0	0	0	0	0	0	0	0	15	A2AKD9	
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ENSMUST00000109726	ENSMUSG00000021144	12	113098278	113137206	1	0	0	0	0	0	0	19	85	0	26	65	F8WHY8	
ENSMUST00000109727	ENSMUSG00000021144	12	113098278	113137206	1	10	5	0	32	0	2	0	0	0	0	0	E9PX23	
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ENSMUST00000109729	ENSMUSG00000012211	12	113074502	113088917	1	0	4	0	26	3	0	0	0	0	0	0		Q9D9U4
ENSMUST00000109730	ENSMUSG00000027487	2	154335380	154373010	-1	9	11	71	8	10	2	0	1	0	0	0	Q3UW67	
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ENSMUST00000109732	ENSMUSG00000078994	13	67389309	67399767	-1	30	24	44	12	25	14	21	161	44	62	22	Q7M6Y0	
ENSMUST00000109733	ENSMUSG00000005161	8	84969587	84974834	1	0	6	0	26	11	3	4	0	0	0	4		Q61171
ENSMUST00000109734	ENSMUSG00000005161	8	84969587	84974834	1	4	0	2	0	0	0	0	18	9	19	32		Q61171
ENSMUST00000109735	ENSMUSG00000057842	13	67312998	67332560	-1	7	6	4	6	6	1	38	144	33	39	43	Q8BIN6	
ENSMUST00000109736	ENSMUSG00000052926	8	84956610	84969767	-1	18	0	6	169	20	0	0	15	8	0	0		Q9CWY8
ENSMUST00000109737	ENSMUSG00000041126	11	6427229	6444443	-1	6	3	3	7	9	3	146	260	118	50	79	B2RVP5	Q3THW5
ENSMUST00000109738	ENSMUSG00000052926	8	84956610	84969767	-1	36	49	265	0	33	17	5	19	5	2	14		Q9CWY8
ENSMUST00000109740	ENSMUSG00000048617	8	84946991	84956603	1	0	0	0	0	0	0	0	0	0	0	0		Q8QZY4
ENSMUST00000109741	ENSMUSG00000053693	8	84911903	84937359	-1	0	0	0	24	0	0	0	0	0	0	0		Q9R1L5
ENSMUST00000109742	ENSMUSG00000058883	13	67069398	67081545	-1	0	0	0	0	0	0	0	0	0	0	2	F2Z422	
ENSMUST00000109743	ENSMUSG00000100235	13	67069399	67108604	-1	0	0	0	0	0	0	0	14	0	0	0	F8VPP0	
ENSMUST00000109744	ENSMUSG00000003812	8	84908560	84922915	1	0	0	7	28	0	0	0	23	0	0	0	D3Z512	
ENSMUST00000109745	ENSMUSG00000003809	8	84886393	84893921	-1	0	0	0	0	0	8	16	11	0	16	28		Q60759
ENSMUST00000109746	ENSMUSG00000027482	2	154130336	154138356	1	2	6	29	16	0	5	0	0	0	0	0		Q9D9J8
ENSMUST00000109747	ENSMUSG00000005354	15	77915047	77929006	-1	16	6	41	28	13	7	8	18	5	1	9	A2A439	
ENSMUST00000109748	ENSMUSG00000005354	15	77915047	77929006	-1	7	4	6	93	9	5	4	17	2	0	5		P97493
ENSMUST00000109753	ENSMUSG00000078998	2	153974945	154000495	1	16	9	8	15	8	3	0	0	0	0	0	Q0VGU8	
ENSMUST00000109754	ENSMUSG00000003808	8	84856989	84869257	1	0	0	0	0	0	0	0	0	31	0	0	E9PWY9	
ENSMUST00000109755	ENSMUSG00000064326	12	112644828	112649152	1	3	0	13	39	10	0	0	7	3	0	0		O54926
ENSMUST00000109757	ENSMUSG00000074665	2	153938212	153964101	1	14	0	0	0	8	0	0	0	0	0	0		A2BGH0
ENSMUST00000109759	ENSMUSG00000074665	2	153938212	153964101	1	0	11	0	0	1	12	0	0	0	0	0		A2BGH0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000109760	ENSMUSG00000068008	2	153918230	153932996	1	0	0	15	6	0	0	0	0	0	0	0		Q80ZU7
ENSMUST00000109761	ENSMUSG00000003813	8	84834019	84840665	-1	3	0	0	0	2	0	105	258	125	27	153		P54726
ENSMUST00000109762	ENSMUSG00000001911	8	84699876	84800344	-1	36	22	12	141	25	14	0	1	0	0	4	Q3TYK3	
ENSMUST00000109764	ENSMUSG00000001911	8	84699876	84800344	-1	28	27	122	780	60	26	52	125	43	20	223	E9PUH7	
ENSMUST00000109767	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	12	0	16	0	0		
ENSMUST00000109768	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	64	37	28	7	57	E9PWD4	
ENSMUST00000109769	ENSMUSG00000033102	13	64192545	64274973	-1	150	157	168	26	130	58	47	165	127	24	103		Q6PFY9
ENSMUST00000109770	ENSMUSG00000033102	13	64192545	64274973	-1	1	4	0	0	1	0	5	5	6	5	13		Q6PFY9
ENSMUST00000109771	ENSMUSG00000027478	2	153649450	153687730	1	0	20	0	0	15	0	0	0	13	0	15	Q3KR45	
ENSMUST00000109772	ENSMUSG00000027478	2	153649450	153687730	1	0	0	0	0	0	0	0	0	0	0	0	Q541E5	O88509
ENSMUST00000109773	ENSMUSG00000027478	2	153649450	153687730	1	0	0	0	0	0	0	0	0	0	0	0		O88509
ENSMUST00000109774	ENSMUSG00000027478	2	153649450	153687730	1	0	0	0	0	0	0	0	0	0	0	0		O88509
ENSMUST00000109775	ENSMUSG00000068246	15	77729121	77736381	1	15	15	44	28	24	5	0	0	0	22	20	Q8C7I4	
ENSMUST00000109776						30	29	331	32	25	11	5	7	7	11	5		
ENSMUST00000109782	ENSMUSG00000056941	2	153616933	153632781	-1	0	0	5	24	2	0	262	574	296	98	164	A2AU52	
ENSMUST00000109783	ENSMUSG00000079001	2	153492790	153493841	1	2	3	4	13	1	1	0	0	0	0	0	A2APL1	
ENSMUST00000109784	ENSMUSG00000061411	2	153407462	153529971	-1	39	30	85	69	38	27	14	34	22	7	76	Q3TZG8	
ENSMUST00000109785	ENSMUSG00000041164	11	6389074	6406158	1	15	5	0	6	0	6	60	74	136	25	100		Q8CIE2
ENSMUST00000109786	ENSMUSG00000041164	11	6389074	6406158	1	8	0	75	18	57	17	36	68	0	0	85		Q8CIE2
ENSMUST00000109787	ENSMUSG00000041164	11	6389074	6406158	1	0	0	0	49	0	0	368	84	304	14	257		Q8CIE2
ENSMUST00000109790	ENSMUSG00000042548	2	153345845	153404007	1	43	27	76	130	55	24	3545	9029	6733	695	5959	Q24JP2	P59598
ENSMUST00000109792	ENSMUSG00000021281	12	111442469	111455018	1	0	0	0	129	0	0	2	41	206	0	106	D3Z4L9	
ENSMUST00000109793	ENSMUSG00000055041	15	76899910	76901305	1	9	3	18	15	4	2	96	140	89	83	30		
ENSMUST00000109794	ENSMUSG00000046020	2	153241533	153270247	1	0	0	0	0	0	0	2	0	0	0	0	A2AMC3	
ENSMUST00000109795	ENSMUSG00000051413	2	153227759	153241426	-1	0	0	64	0	0	0	0	0	0	0	0	Q925T4	
ENSMUST00000109799	ENSMUSG00000003283	2	153108468	153151441	1	2	1	5	23	4	2	1505	2029	1375	237	630		P08103
ENSMUST00000109800	ENSMUSG00000027474	2	153065955	153081735	1	13	0	2	4	0	4	27	168	68	6	18		Q8VCC6
ENSMUST00000109801	ENSMUSG00000074673	2	152962485	153008482	1	11	7	0	0	0	0	0	0	0	0	0	E9PUG4	
ENSMUST00000109802	ENSMUSG00000002885	8	83723251	83741326	-1	8	11	12	0	0	0	11278	8996	10085	1690	10103	E9QMJ5	
ENSMUST00000109805						28	5	13	4	0	12	183	704	73	75	59		
ENSMUST00000109810	ENSMUSG00000005481	8	83715177	83726892	1	3	2	18	100	11	1	0	9	0	0	7		Q8VDW0
ENSMUST00000109811	ENSMUSG00000042662	2	152940997	152951698	-1	0	0	3	94	3	0	0	0	0	0	0	A0A0A0MQD6	
ENSMUST00000109812	ENSMUSG00000057897	11	5969644	6066362	-1	3	0	10	0	5	0	0	0	0	0	0	Q5SVI2	
ENSMUST00000109813	ENSMUSG00000057897	11	5969644	6066362	-1	0	0	0	0	0	0	0	0	0	0	0		P28652
ENSMUST00000109815	ENSMUSG00000057897	11	5969644	6066362	-1	0	0	0	0	0	0	0	0	0	0	0		P28652
ENSMUST00000109816	ENSMUSG00000027469	2	152847964	152895321	1	0	0	0	0	0	0	131	172	199	238	77		A2APB8
ENSMUST00000109820	ENSMUSG00000007659	2	152780668	152831728	-1	14	0	24	0	0	0	871	790	430	53	338	Q5HZH3	Q64373
ENSMUST00000109821	ENSMUSG00000009876	2	152754173	152765037	1	6	0	0	0	0	2	0	0	5	0	0		Q91W29
ENSMUST00000109822	ENSMUSG00000041798	11	5900820	5950081	-1	0	0	4	57	7	0	0	1	1	0	0	Q5SVI6	P52792
ENSMUST00000109823	ENSMUSG00000041798	11	5900820	5950081	-1	8	0	0	0	0	0	0	0	0	0	0	Q5SVI6	P52792
ENSMUST00000109824	ENSMUSG00000042745	2	152736251	152737410	1	8	10	11	100	14	9	24	145	46	36	149	A2AHY3	
ENSMUST00000109825	ENSMUSG00000019188	2	152669461	152708670	1	0	1	0	15	5	1	1	13	16	1	12	Q6PGJ8	
ENSMUST00000109829	ENSMUSG00000020473	11	5861947	5872088	1	12	13	2	2	12	0	0	0	1	3	2		Q640N1
ENSMUST00000109830	ENSMUSG00000021557	13	59449537	59585227	-1	2	1	0	0	0	0	35	10	23	0	0		Q641K1
ENSMUST00000109831	ENSMUSG00000002190	8	83389867	83428552	1	2	2	11	33	12	0	0	0	0	1	0		P52194
ENSMUST00000109832	ENSMUSG00000017843	12	110485739	110583061	1	0	0	38	35	0	12	805	3631	1240	898	840		Q60996
ENSMUST00000109834	ENSMUSG00000062124	2	152593191	152599399	-1	5	2	8	3	8	1	0	0	0	0	0	Q3V490	
ENSMUST00000109836	ENSMUSG00000049560	2	152477063	152479934	1	3	4	4	5	3	2	0	0	0	0	0		Q30KP3
ENSMUST00000109837	ENSMUSG00000020474	11	5827860	5838016	-1	0	0	3	2	0	11	164	479	237	39	134	Q5NCI3	
ENSMUST00000109838	ENSMUSG00000055254	13	58806596	59133970	1	92	96	89	325	115	80	7	20	12	14	12	Q3UHE3	P15209
ENSMUST00000109841	ENSMUSG00000040856	12	109452823	109463336	1	0	0	0	0	0	0	0	2	0	0	0	E9PVN3	
ENSMUST00000109842	ENSMUSG00000040856	12	109452823	109463336	1	0	0	0	0	0	0	0	0	0	0	0	B4YB46	
ENSMUST00000109843	ENSMUSG00000040856	12	109452823	109463336	1	0	0	0	0	0	0	1	0	0	0	0	Q9DAU5	
ENSMUST00000109844	ENSMUSG00000040856	12	109452823	109463336	1	0	0	0	88	4	0	0	0	0	0	0	Q925U3	
ENSMUST00000109845	ENSMUSG00000020476	11	5788488	5800962	1	0	2	2	50	3	0	2893	2844	2864	198	1581		Q62418
ENSMUST00000109846	ENSMUSG00000040856	12	109452823	109463336	1	0	0	0	0	0	0	0	0	0	0	0	B4YB48	
ENSMUST00000109847	ENSMUSG00000027466	2	152316334	152332653	-1	0	0	0	21	13	7	1187	1309	952	185	944		Q9WUB0
ENSMUST00000109848	ENSMUSG00000021266	12	108860030	108894174	-1	0	0	19	62	23	0	167	373	223	42	156	Q3U6U7	P32921
ENSMUST00000109851	ENSMUSG00000037940	8	81342556	82125036	1	5	6	9	2	9	0	0	0	0	0	0	F8WJC1	
ENSMUST00000109852	ENSMUSG00000037940	8	81342556	82125036	1	4	0	1	0	0	5	0	0	0	0	0	E9PVM3	
ENSMUST00000109854	ENSMUSG00000021262	12	108554720	108688513	1	9	7	8	8	13	0	13	84	21	1	56	F8WJB9	
ENSMUST00000109855	ENSMUSG00000020481	11	5569684	5689337	1	6	6	18	7	10	7	0	0	0	0	0	Q9EQ29	
ENSMUST00000109856	ENSMUSG00000020481	11	5569684	5689337	1	22	23	23	17	21	6	0	0	0	0	0	D3Z4K0	
ENSMUST00000109857	ENSMUSG00000058070	12	108370957	108539617	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4J9	
ENSMUST00000109858	ENSMUSG00000027463	2	151996511	152009258	1	0	0	15	0	0	0	44	73	0	0	0		Q9D6X5
ENSMUST00000109859	ENSMUSG00000027463	2	151996511	152009258	1	15	0	0	6	7	0	48	0	16	6	28		Q9D6X5
ENSMUST00000109860	ENSMUSG00000058070	12	108370957	108539617	1	0	0	0	38	6	0	0	0	0	0	15		Q05BC3
ENSMUST00000109861	ENSMUSG00000027463	2	151996511	152009258	1	3	6	37	41	9	0	0	79	0	0	0		Q9D6X5
ENSMUST00000109863	ENSMUSG00000027459	2	151969398	151980219	-1	4	1	4	5	0	0	0	0	0	0	0		Q8R184
ENSMUST00000109864	ENSMUSG00000027459	2	151969398	151980219	-1	0	3	5	37	0	0	0	0	0	0	30		Q8R184
ENSMUST00000109865	ENSMUSG00000027459	2	151969398	151980219	-1	10	2	52	114	13	7	23	7	0	0	5		Q8R184
ENSMUST00000109867	ENSMUSG00000041961	11	5276324	5444847	-1	37	37	233	50	38	26	12	22	9	4	43		Q5SSZ7
ENSMUST00000109868	ENSMUSG00000050002	13	58157649	58164693	1	28	33	1	15	31	21	104	199	118	156	114	D3Z4J6	
ENSMUST00000109869	ENSMUSG00000032869	2	151715812	151744186	-1	1	0	4	0	2	0	192	180	131	33	95	A2AU35	Q8BHL8
ENSMUST00000109871	ENSMUSG00000021541	13	56773113	56895789	-1	0	0	5	0	23	0	0	0	0	0	0	E9PVJ9	
ENSMUST00000109872	ENSMUSG00000044364	2	151702008	151712157	1	2	8	5	8	19	11	0	0	0	0	0	A2AU34	
ENSMUST00000109874	ENSMUSG00000021540	13	56703010	56742377	1	14	18	58	68	19	10	1	0	2	0	0		P97454
ENSMUST00000109875	ENSMUSG00000027457	2	151590549	151632593	-1	21	0	0	118	15	19	0	0	0	0	0		Q80U23
ENSMUST00000109876	ENSMUSG00000021540	13	56703010	56742377	1	0	0	0	47	0	3	0	0	0	0	0		P97454
ENSMUST00000109877	ENSMUSG00000027457	2	151590549	151632593	-1	13	3	0	59	12	9	0	0	0	0	0		Q80U23
ENSMUST00000109878	ENSMUSG00000034175	11	5098926	5106093	1	3	3	0	2	13	2	0	44	8	7	30	B7ZNJ8	Q8BP97
ENSMUST00000109879	ENSMUSG00000056770	12	108106431	108179314	-1	5	0	7	0	10	0	11	14	23	0	10	F2Z420	
ENSMUST00000109885	ENSMUSG00000031681	8	79338395	79399518	-1	14	13	43	32	27	14	5	24	14	2	20	Q8C3Y6	
ENSMUST00000109887	ENSMUSG00000048251	12	107910403	108003602	-1	0	0	0	785	11	0	0	0	4	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000109888	ENSMUSG00000079005	2	151098245	151103818	1	29	29	140	95	2	10	0	0	0	0	0	A2AQX6	
ENSMUST00000109890	ENSMUSG00000079006	2	151086786	151092350	-1	0	0	28	5	46	2	0	0	0	0	0	A2AQX6	
ENSMUST00000109891	ENSMUSG00000048251	12	107910403	108003602	-1	0	0	3	0	0	0	0	0	0	0	39		Q99PV8
ENSMUST00000109895	ENSMUSG00000034201	11	5054132	5065327	-1	0	0	0	0	0	0	238	196	201	45	179		Q8JZP9
ENSMUST00000109896	ENSMUSG00000068115	2	150934519	151039382	-1	39	22	83	54	39	22	0	2	1	5	13		Q6ZQ12
ENSMUST00000109897	ENSMUSG00000009090	11	4986824	5042791	1	0	0	0	0	0	0	0	21	139	0	0	Q5SVG5	
ENSMUST00000109898	ENSMUSG00000021499	13	55784568	55808998	1	11	0	0	0	6	0	0	4	0	1	0		Q80W99
ENSMUST00000109901	ENSMUSG00000021111	12	105784694	105838944	1	3	10	0	29	23	9	449	1678	868	308	553		Q61183
ENSMUST00000109902	ENSMUSG00000037101	8	78213297	78394326	1	0	4	10	5	8	3	0	0	0	0	0	E9QLU4	
ENSMUST00000109905	ENSMUSG00000058569	13	55593135	55597663	1	10	8	33	79	8	6	809	1318	803	576	705	Q6PDC2	Q99KF1
ENSMUST00000109908						0	1	0	0	7	1	0	7	32	0	6		
ENSMUST00000109910	ENSMUSG00000009073	11	4765845	4849536	-1	45	22	45	277	47	23	375	720	629	85	490		P46662
ENSMUST00000109911	ENSMUSG00000031618	8	76899442	77245012	1	0	7	0	0	0	0	0	0	0	0	0	D3Z473	
ENSMUST00000109912	ENSMUSG00000031618	8	76899442	77245012	1	0	0	0	0	0	0	0	0	0	0	0	A3KN90	
ENSMUST00000109913	ENSMUSG00000031618	8	76899442	77245012	1	42	11	27	161	39	13	0	0	0	0	0	A3KN90	
ENSMUST00000109914	ENSMUSG00000074731	2	150470991	150485091	-1	62	45	158	47	42	27	7	27	10	7	18	A2AQA1	
ENSMUST00000109916	ENSMUSG00000068130	2	150407141	150451486	-1	3	3	2	1	4	0	1	6	6	0	2	A2AQA0	
ENSMUST00000109921	ENSMUSG00000034675	13	55473429	55488111	-1	0	2	34	19	0	0	1	5	0	0	13		
ENSMUST00000109922	ENSMUSG00000079008	2	150257517	150270300	1	2	3	2	4	2	0	0	1	0	0	2	A2AU83	
ENSMUST00000109923	ENSMUSG00000034675	13	55473429	55488111	-1	21	10	5	0	3	4	0	0	2	13	21	Q3TRK3	Q9QXS6
ENSMUST00000109926	ENSMUSG00000079009	2	150181755	150193279	1	5	0	2	3	4	2	0	0	0	0	0	A2ANU6	
ENSMUST00000109927	ENSMUSG00000054150	12	104929949	105009809	-1	0	29	1	0	0	0	0	0	0	0	0		Q4FZC9
ENSMUST00000109929	ENSMUSG00000079009	2	150181755	150193279	1	0	0	0	0	0	0	0	0	0	0	0	F6ZS36	
ENSMUST00000109930	ENSMUSG00000020412	11	4637747	4685699	1	43	32	77	71	43	35	128	262	133	10	168		Q91WR3
ENSMUST00000109931	ENSMUSG00000068134	2	150114406	150136708	-1	9	10	16	0	0	8	36	131	0	234	0	A2ANU5	
ENSMUST00000109934	ENSMUSG00000074736	2	149829211	150004392	1	18	0	18	0	0	0	0	0	0	0	0		A2ANU3
ENSMUST00000109935	ENSMUSG00000074736	2	149829211	150004392	1	0	8	0	20	21	3	0	0	0	0	0		A2ANU3
ENSMUST00000109936	ENSMUSG00000021097	12	104763114	104865076	-1	176	142	502	139	113	75	0	107	297	26	275		Q8C5W0
ENSMUST00000109937	ENSMUSG00000021097	12	104763114	104865076	-1	0	0	0	91	79	0	184	140	56	0	0		Q8C5W0
ENSMUST00000109938	ENSMUSG00000033156	2	149405057	149410293	1	2	0	0	0	3	1	0	0	0	0	0	Q9JM84	
ENSMUST00000109939	ENSMUSG00000033156	2	149405057	149410293	1	0	0	0	0	0	0	0	0	0	0	0	A2ART7	
ENSMUST00000109940	ENSMUSG00000034518	8	74993356	75031978	1	6	3	6	0	2	9	0	153	0	0	0	Q8BTT5	
ENSMUST00000109941	ENSMUSG00000079010	11	4620067	4621698	1	65	54	189	77	47	18	1	6	1	3	4	F6ZRP0	
ENSMUST00000109942	ENSMUSG00000063507	2	148990343	149003251	-1	0	0	0	2	0	0	0	0	0	0	0	D3Z460	
ENSMUST00000109943	ENSMUSG00000034354	11	4480868	4594863	-1	0	0	0	13	0	0	458	473	793	0	438	B1ATD5	
ENSMUST00000109946	ENSMUSG00000022568	15	76047158	76069784	-1	0	0	0	183	0	0	0	140	0	0	58		Q80U72
ENSMUST00000109947	ENSMUSG00000027442	2	148798785	148805595	1	0	4	3	7	5	0	0	0	0	0	0		P32766
ENSMUST00000109948	ENSMUSG00000020419	11	4345814	4441105	-1	14	6	0	7	10	8	0	0	0	0	0		Q5SQP1
ENSMUST00000109949	ENSMUSG00000020419	11	4345814	4441105	-1	0	0	6	0	0	0	1	0	0	0	0		Q5SQP1
ENSMUST00000109950	ENSMUSG00000031622	8	72723288	72758203	1	6	3	8	67	9	2	1117	1614	866	1594	733	Q3TN09	Q62141
ENSMUST00000109952	ENSMUSG00000055177	2	148750358	148755433	1	2	2	0	6	0	0	0	0	0	0	0	Q80Y72	
ENSMUST00000109954	ENSMUSG00000055177	2	148750358	148755433	1	0	0	0	0	0	0	0	0	0	0	0	Q64FK4	
ENSMUST00000109955	ENSMUSG00000055177	2	148750358	148755433	1	4	1	0	0	7	2	0	0	0	0	0	Q80Y72	
ENSMUST00000109957	ENSMUSG00000079013	12	104314553	104320725	1	9	7	23	13	12	6	0	0	0	0	0	D3Z451	
ENSMUST00000109958	ENSMUSG00000079014	12	104263122	104269372	1	16	11	35	13	19	3	0	0	0	2	0	D3Z450	
ENSMUST00000109960						5	2	8	2	6	5	6	6	4	3	10		
ENSMUST00000109961	ENSMUSG00000036992	2	148672601	148676027	1	0	0	0	41	0	0	21	74	37	33	18		Q9QZV9
ENSMUST00000109962	ENSMUSG00000037014	2	148395344	148396767	1	9	11	25	317	21	8	1	1	5	0	8		
ENSMUST00000109964	ENSMUSG00000037025	2	148042877	148046969	-1	0	0	5	13	15	4	0	0	0	0	0	G5E8P5	
ENSMUST00000109965	ENSMUSG00000041536	12	104112724	104121896	1	12	11	12	9	22	9	0	0	0	1	0		Q6P4P1
ENSMUST00000109966	ENSMUSG00000034429	15	75969123	75975868	1	0	0	7	172	6	8	8	55	1	7	25	D3Z445	
ENSMUST00000109967	ENSMUSG00000034429	15	75969123	75975868	1	0	0	0	0	0	0	55	7	38	0	20	Q8R0U9	
ENSMUST00000109968	ENSMUSG00000037034	2	147361925	147393295	1	77	35	81	676	101	62	0	1	0	0	1		P09084
ENSMUST00000109969						0	0	0	17	2	0	0	0	0	0	0		
ENSMUST00000109970	ENSMUSG00000027434	2	147177546	147194243	-1	0	4	4	37	5	3	0	0	0	0	0	Q8BRS9	
ENSMUST00000109972	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000109974	ENSMUSG00000019732	8	72424176	72443870	-1	3	4	9	0	2	4	0	1	0	12	4	Q8BL82	
ENSMUST00000109975	ENSMUSG00000055762	15	75894796	75909556	-1	10	10	23	43	16	10	0	0	0	0	0		
ENSMUST00000109981	ENSMUSG00000049721	11	3983636	3999326	1	6	7	5	163	19	9	0	1	0	0	0		Q9JHE4
ENSMUST00000109982						2	6	2	0	5	1	2	3	0	0	0		
ENSMUST00000109985	ENSMUSG00000020430	11	3963975	3980004	1	0	16	28	1	0	0	0	0	0	0	0	Q5SQ20	
ENSMUST00000109986	ENSMUSG00000037110	2	146239879	146512026	-1	99	95	382	128	128	57	214	671	494	38	310	A0A0A0MQD7	
ENSMUST00000109987	ENSMUSG00000079016	8	72213494	72213636	-1	0	1	8	23	0	0	0	0	0	0	0	F6ZE74	
ENSMUST00000109988	ENSMUSG00000020432	11	3917192	3932159	-1	4	0	0	17	0	4	86	116	120	0	47		O88968
ENSMUST00000109989	ENSMUSG00000020432	11	3917192	3932159	-1	5	0	0	0	0	0	2688	2393	2494	309	2201		O88968
ENSMUST00000109990	ENSMUSG00000020432	11	3917192	3932159	-1	0	0	0	3	0	0	0	0	0	0	49		O88968
ENSMUST00000109991	ENSMUSG00000020432	11	3917192	3932159	-1	0	0	0	0	0	0	290	394	264	0	173		O88968
ENSMUST00000109992	ENSMUSG00000020432	11	3917192	3932159	-1	0	6	62	0	11	4	188	181	176	33	83		O88968
ENSMUST00000109993	ENSMUSG00000020432	11	3917192	3932159	-1	8	5	0	8	9	4	1269	1019	1012	114	679		O88968
ENSMUST00000109994	ENSMUSG00000025876	13	54949411	55006018	1	17	18	60	0	14	17	9	18	24	1	27		Q8K1S4
ENSMUST00000109995	ENSMUSG00000048807	11	3907021	3914664	-1	9	21	12	116	65	24	0	0	0	0	0		Q8K3D6
ENSMUST00000109996	ENSMUSG00000047205	11	3895240	3901296	1	0	0	0	0	0	0	45	0	19	9	43		Q8VE01
ENSMUST00000109997	ENSMUSG00000052446	8	71951038	71993408	1	0	0	0	0	0	0	1	0	9	9	0	E9Q4R5	
ENSMUST00000110000	ENSMUSG00000002728	2	145902099	145916425	1	1	4	0	18	8	3	65	275	60	297	80		P61600
ENSMUST00000110001	ENSMUSG00000041645	12	103407976	103425867	-1	18	17	26	128	29	0	36	30	14	17	22	F8WJA0	
ENSMUST00000110002	ENSMUSG00000089857	8	71908608	71916354	1	29	16	53	48	30	24	7	42	14	13	8	E9Q4R4	
ENSMUST00000110003	ENSMUSG00000074895	13	54783998	54788459	1	39	38	72	229	56	36	0	8	0	0	2		Q3UTA9
ENSMUST00000110005	ENSMUSG00000001768	2	145784734	145887616	1	22	20	0	109	39	26	208	174	429	32	371		Q9D684
ENSMUST00000110007	ENSMUSG00000063873	2	145167754	145642166	1	0	0	0	68	0	0	20	0	0	0	20		Q99PD7
ENSMUST00000110009	ENSMUSG00000022602	15	74669083	74672570	-1	14	11	0	172	52	5	0	0	0	0	2		Q9WV31
ENSMUST00000110011	ENSMUSG00000020439	11	3517523	3540612	-1	0	0	9	0	23	7	0	18	15	0	6	D3Z3Q3	
ENSMUST00000110012	ENSMUSG00000031805	8	71676296	71690575	1	7	4	20	2	3	7	926	1589	789	39	937		
ENSMUST00000110013	ENSMUSG00000031805	8	71676296	71690575	1	2	3	7	183	21	9	0	0	0	0	0		
ENSMUST00000110017	ENSMUSG00000027427	2	144527718	144541995	1	9	9	23	24	10	7	1	12	15	3	10	Q9CZ23	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000110018	ENSMUSG00000034570	11	3494375	3504821	-1	0	0	0	0	0	0	0	67	0	13	0	D3Z3Q0	
ENSMUST00000110019	ENSMUSG00000034570	11	3494375	3504821	-1	4	3	9	5	3	2	22	25	27	0	0	D3Z3P9	
ENSMUST00000110020	ENSMUSG00000021190	12	102394084	102439813	-1	13	0	36	0	0	10	203	743	143	1134	492	A2RTI3	O89017
ENSMUST00000110021	ENSMUSG00000072487	15	73761410	73839699	-1	14	0	23	5	5	7	0	0	0	0	0	B9EKG2	
ENSMUST00000110027	ENSMUSG00000027424	2	144270663	144281227	1	5	5	5	25	0	0	0	0	9	7	0		Q9CXC3
ENSMUST00000110028	ENSMUSG00000027424	2	144270663	144281227	1	0	2	0	77	4	1	10	51	11	9	12		Q9CXC3
ENSMUST00000110029	ENSMUSG00000020451	11	3344256	3409189	-1	0	0	11	5	0	10	3	403	54	33	87		O54785
ENSMUST00000110030	ENSMUSG00000027423	2	144250123	144270906	-1	0	0	0	0	8	0	0	99	0	135	38		Q9D8U8
ENSMUST00000110031	ENSMUSG00000021460	13	52835119	52929681	-1	30	38	144	69	47	29	77	247	147	13	162	E9QMT1	
ENSMUST00000110032	ENSMUSG00000037307	2	144033059	144073979	1	0	0	0	0	0	0	0	0	0	0	0		Q8BVR0
ENSMUST00000110036	ENSMUSG00000022607	15	73205105	73423191	-1	13	11	28	13	17	9	0	12	5	43	147		P34152
ENSMUST00000110039	ENSMUSG00000021451	13	51701246	51793747	-1	29	15	65	0	31	14	2009	1341	1116	34	777		O09126
ENSMUST00000110040	ENSMUSG00000021451	13	51701246	51793747	-1	5	0	34	0	23	0	1	437	322	70	481		O09126
ENSMUST00000110042	ENSMUSG00000051107	13	51685529	51701041	-1	11	1	16	6	17	5	25	81	20	12	51	D3Z3P4	
ENSMUST00000110043	ENSMUSG00000020453	11	3288874	3309083	1	16	0	0	46	24	0	0	19	38	0	0	Q5NBY9	
ENSMUST00000110044	ENSMUSG00000035139	13	51651697	51684044	1	4	3	3	7	5	2	0	2	2	1	9	Q8BYU9	
ENSMUST00000110047	ENSMUSG00000021187	12	101645443	101718523	-1	2240	2273	5403	5116	2129	966	3	2	6	2	5		Q91XT6
ENSMUST00000110048	ENSMUSG00000020454	11	3202392	3244588	1	5	6	28	74	4	0	54	94	263	0	125		Q9EST3
ENSMUST00000110049	ENSMUSG00000020454	11	3202392	3244588	1	3	0	0	0	0	0	242	452	433	35	177		Q9EST3
ENSMUST00000110051	ENSMUSG00000002396	8	71371298	71379361	1	12	11	10	18	11	0	33	73	58	12	34	D3Z3P2	
ENSMUST00000110052	ENSMUSG00000002396	8	71371298	71379361	1	35	29	83	259	61	28	45	81	32	1	34	D3Z3P1	
ENSMUST00000110053	ENSMUSG00000002395	8	71366848	71369732	1	3	3	4	4	12	2	0	0	0	0	5	E9Q496	
ENSMUST00000110054	ENSMUSG00000002395	8	71366848	71369732	1	0	0	0	0	0	0	8	23	8	15	0		Q9CQ56
ENSMUST00000110057	ENSMUSG00000051379	2	140650914	140671469	-1	9	7	12	9	3	0	0	0	0	27	12	Q8BGT1	Q8BGT1
ENSMUST00000110061	ENSMUSG00000068205	2	140395309	142392966	1	0	0	5	0	0	1	0	10	1	2	2	Q05C81	
ENSMUST00000110062	ENSMUSG00000068205	2	140395309	142392966	1	1	3	0	3	3	4	0	0	0	0	0	Q05C81	
ENSMUST00000110063	ENSMUSG00000068205	2	140395309	142392966	1	1	2	0	141	2	1	0	0	0	0	0	B1AW12	
ENSMUST00000110064	ENSMUSG00000068205	2	140395309	142392966	1	0	19	0	0	1	4	0	0	0	0	0		Q3UYG8
ENSMUST00000110065	ENSMUSG00000047415	12	100876682	100908198	-1	27	0	0	110	32	0	16	22	23	10	25		Q8BFQ3
ENSMUST00000110066	ENSMUSG00000047415	12	100876682	100908198	-1	0	0	39	0	0	6	10	20	20	0	0		Q8BFQ3
ENSMUST00000110067	ENSMUSG00000068205	2	140395309	142392966	1	0	0	2	27	12	0	0	0	0	0	0	A2AS33	
ENSMUST00000110069	ENSMUSG00000021185	12	100779057	100896981	1	0	0	0	30	20	8	41	67	48	19	56		Q8BH86
ENSMUST00000110070	ENSMUSG00000021185	12	100779057	100896981	1	3	5	18	15	9	2	0	3	3	4	3		Q8BH86
ENSMUST00000110071	ENSMUSG00000035439	8	71248561	71272934	-1	0	0	0	0	0	0	170	497	121	48	104		Q99L00
ENSMUST00000110073	ENSMUSG00000021185	12	100779057	100896981	1	0	6	0	0	0	0	23	0	0	0	25	E9QMK9	
ENSMUST00000110078	ENSMUSG00000002908	8	70842049	70857008	-1	19	16	63	162	26	10	1	1	6	1	2		
ENSMUST00000110079	ENSMUSG00000039033	2	139833480	140066805	-1	0	0	0	22	8	0	0	20	17	0	0		Q8R1G1
ENSMUST00000110081	ENSMUSG00000002908	8	70842049	70857008	-1	9	8	29	76	13	5	0	0	3	0	1	Z4YL28	
ENSMUST00000110082	ENSMUSG00000001175	12	100199435	100209806	1	0	14	44	21	11	17	4134	21234	6881	16787	4404		P62204
ENSMUST00000110083	ENSMUSG00000039092	2	139493913	139637674	1	0	5	9	0	18	0	0	0	0	0	0		Q8BG54
ENSMUST00000110084	ENSMUSG00000037933	13	49341549	49387025	1	0	0	0	0	0	0	156	279	0	0	76	D3Z390	
ENSMUST00000110085	ENSMUSG00000037933	13	49341549	49387025	1	1	0	0	79	0	7	0	1	338	52	128		Q921C5
ENSMUST00000110086	ENSMUSG00000037946	13	49261554	49320311	-1	9	8	35	31	14	4	50	33	43	2	11		
ENSMUST00000110087	ENSMUSG00000037946	13	49261554	49320311	-1	23	16	40	35	24	15	2936	4964	3796	346	2913	Q3TNB8	
ENSMUST00000110089	ENSMUSG00000027274	2	136873780	136891389	-1	12	0	0	47	5	0	27	64	41	119	24		Q9JI70
ENSMUST00000110090	ENSMUSG00000031840	8	70754679	70758677	1	0	0	0	0	0	0	0	33	0	0	0	Q0PD63	P63011
ENSMUST00000110092	ENSMUSG00000031840	8	70754679	70758677	1	4	7	27	8	14	3	13	8	8	0	17	Q0PD63	P63011
ENSMUST00000110093	ENSMUSG00000031840	8	70754679	70758677	1	0	0	0	43	7	2	12	0	0	0	0	Q0PD63	P63011
ENSMUST00000110095	ENSMUSG00000031842	8	70723720	70751186	1	0	0	21	74	18	0	0	0	0	0	23		Q3UEI1
ENSMUST00000110096	ENSMUSG00000037989	13	49036303	49148014	-1	0	0	0	170	0	0	0	0	0	0	0	E9QMI9	
ENSMUST00000110097	ENSMUSG00000037989	13	49036303	49148014	-1	0	0	0	0	0	0	0	0	0	0	0	E9QMI8	
ENSMUST00000110098	ENSMUSG00000027273	2	136713453	136782428	1	55	46	423	58	38	35	0	0	0	0	1		P60879
ENSMUST00000110100	ENSMUSG00000079024	15	64979544	65014904	-1	589	417	5249	721	240	151	0	6	0	0	0	F6YUL9	
ENSMUST00000110103	ENSMUSG00000038508	8	70629393	70632456	-1	0	3	6	15	15	0	6	50	12	5	8		Q9Z0J7
ENSMUST00000110104	ENSMUSG00000021012	12	98746968	98787774	1	0	0	0	0	0	1	82	265	50	155	82		Q8BJ05
ENSMUST00000110105	ENSMUSG00000021012	12	98746968	98787774	1	8	15	23	15	35	18	309	1130	567	912	455		Q8BJ05
ENSMUST00000110109	ENSMUSG00000039943	2	135659011	136014593	1	38	24	13	7	0	16	18	18	9	0	0	Q91UZ1	
ENSMUST00000110110	ENSMUSG00000050954	13	48487647	48513451	-1	8	0	16	5	19	2	13	0	36	0	31	E9Q3R6	
ENSMUST00000110111	ENSMUSG00000038068	13	47122720	47247991	1	12	19	20	7	6	0	234	727	400	55	257		Q8BKD6
ENSMUST00000110113	ENSMUSG00000033854	12	98433994	98577940	-1	18	9	43	13	25	15	0	0	0	0	0	Q8BUW1	
ENSMUST00000110114	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	0	0	0	0	54	0	0	0	E9QMI7	
ENSMUST00000110115	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	1	0	0	59	124	425	0	169		Q9QWY8
ENSMUST00000110116	ENSMUSG00000051177	2	134786067	135475258	1	34	32	163	82	49	22	18	141	42	10	40		Q9Z1B3
ENSMUST00000110117	ENSMUSG00000047414	12	95692226	95785215	1	18	8	22	213	12	5	0	0	1	0	7	Q8BLU0	Q8BLU0
ENSMUST00000110118	ENSMUSG00000021376	13	47025170	47044737	-1	0	0	3	0	0	0	2	0	14	0	0	D3Z380	
ENSMUST00000110119	ENSMUSG00000034723	2	134594185	134644145	-1	0	0	2	0	0	1	1	0	0	0	0	A2ARI1	
ENSMUST00000110120	ENSMUSG00000034723	2	134594185	134644145	-1	214	167	1349	269	227	130	1	3	10	5	4	A2ARI0	
ENSMUST00000110122	ENSMUSG00000027357	2	132846666	132866785	1	2	0	3	94	3	2	0	0	0	0	0	E9PUH6	
ENSMUST00000110124	ENSMUSG00000003573	8	70282827	70294361	1	0	0	0	0	4	9	0	0	29	14	29		Q99JP6
ENSMUST00000110125	ENSMUSG00000079025	15	63775968	63808759	-1	19	12	19	41	17	19	0	0	0	0	1		Q99NB5
ENSMUST00000110127	ENSMUSG00000002346	8	70184340	70212305	-1	157	113	285	689	187	85	35	47	28	6	25		Q8R0Y8
ENSMUST00000110128	ENSMUSG00000057531	13	44922079	45002096	-1	7	2	8	24	11	6	0	0	0	0	0	K3W4R3	
ENSMUST00000110130	ENSMUSG00000066392	12	88722876	90334935	1	0	3	0	8	15	0	0	0	0	0	0		Q8C985
ENSMUST00000110132	ENSMUSG00000044991	2	132686931	132751055	1	4	4	7	4	4	3	3	10	4	0	7	B2RR16	Q9D112
ENSMUST00000110133	ENSMUSG00000066392	12	88722876	90334935	1	15	10	31	0	17	6	0	0	0	0	0	E9Q3Q4	
ENSMUST00000110135	ENSMUSG00000027346	2	132529082	132587729	-1	0	0	0	6	4	0	0	0	0	0	0	A2AMD7	
ENSMUST00000110136	ENSMUSG00000027346	2	132529082	132587729	-1	3	0	0	0	3	4	11	2712	0	0	0		Q8C0L9
ENSMUST00000110138						4	6	30	14	0	6	0	0	0	0	0		
ENSMUST00000110139	ENSMUSG00000002345	8	70139499	70167488	1	4	0	0	5	2	1	134	207	123	216	80	D3Z373	
ENSMUST00000110140	ENSMUSG00000079033	8	70152778	70167488	1	0	9	0	0	14	0	0	0	0	3	0	D3Z372	
ENSMUST00000110141	ENSMUSG00000079033	8	70152778	70167488	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2M6	
ENSMUST00000110142	ENSMUSG00000027346	2	132529082	132587729	-1	0	0	0	11	0	0	19	5	0	1035	2		Q8C0L9
ENSMUST00000110143	ENSMUSG00000079033	8	70152778	70167488	1	11	0	24	0	0	0	11	21	7	0	0	Q80VR4	
ENSMUST00000110145	ENSMUSG00000096276	12	87954080	87960672	1	0	0	0	0	0	0	0	0	0	0	0	Q5RJV9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000110146	ENSMUSG00000079033	8	70152778	70167488	1	0	0	0	128	0	0	0	0	0	0	0	K7N7F1	
ENSMUST00000110147	ENSMUSG00000072905	12	87874072	87877859	1	4	3	3	4	10	6	0	0	0	0	0	Q3TQZ4	
ENSMUST00000110148	ENSMUSG00000079030	12	87973528	87980224	1	4	1	0	2	3	2	0	0	0	0	0	D3Z367	
ENSMUST00000110149	ENSMUSG00000079031	12	87816577	87820676	1	11	11	0	0	12	6	0	0	0	0	0	Q3UT53	
ENSMUST00000110152	ENSMUSG00000079034	12	87514316	87518266	1	3	13	9	3	6	7	0	0	0	0	0	Q3UTA4	
ENSMUST00000110155	ENSMUSG00000050891	15	58890153	58933730	-1	9	3	21	16	6	4	25	130	31	128	31		
ENSMUST00000110156	ENSMUSG00000050558	2	132337733	132385447	-1	3	0	3	20	3	1	0	0	0	0	0		Q8K458
ENSMUST00000110157	ENSMUSG00000050558	2	132337733	132385447	-1	139	124	179	364	180	105	5	17	12	4	24	A2AMQ7	
ENSMUST00000110158	ENSMUSG00000058793	2	132263148	132312050	1	1	2	10	3	11	4	179	233	103	150	183	Q6PBC0	
ENSMUST00000110160	ENSMUSG00000036151	8	70072924	70080066	1	0	0	14	21	0	0	0	0	3	0	0	E9QM19	
ENSMUST00000110161	ENSMUSG00000054728	13	42680623	43138526	1	0	0	0	0	0	0	0	0	0	0	0		Q2M3X8
ENSMUST00000110163	ENSMUSG00000027341	2	132239492	132247807	-1	11	0	26	0	3	9	0	0	68	57	0		Q8CIB6
ENSMUST00000110164	ENSMUSG00000027341	2	132239492	132247807	-1	12	10	8	38	7	7	10	20	23	6	15		Q8CIB6
ENSMUST00000110167	ENSMUSG00000036199	8	69894188	69902558	-1	9	5	14	145	14	6	760	940	563	2652	440		Q9ERS2
ENSMUST00000110168	ENSMUSG00000022361	15	58047003	58076541	-1	15	12	0	0	0	6	0	45	0	41	0		P70121
ENSMUST00000110169	ENSMUSG00000027338	2	131950861	131956130	1	0	0	1	0	0	0	0	0	0	0	0	Q544A3	Q9QUG3
ENSMUST00000110170	ENSMUSG00000027338	2	131950861	131956130	1	0	2	0	0	3	0	0	0	0	0	0	Q544A3	Q9QUG3
ENSMUST00000110171	ENSMUSG00000027338	2	131950861	131956130	1	0	0	0	0	0	0	0	0	0	0	0	Q544A3	Q9QUG3
ENSMUST00000110172	ENSMUSG00000027338	2	131950861	131956130	1	26	0	121	14	0	13	0	1	2	0	0	Q544A3	Q9QUG3
ENSMUST00000110175						0	4	8	0	0	10	0	16	0	7	16		
ENSMUST00000110176	ENSMUSG00000021032	12	87097531	87102539	-1	6	8	20	6	10	7	0	0	0	0	0	D3YW07	
ENSMUST00000110177	ENSMUSG00000021032	12	87097531	87102539	-1	0	9	8	17	14	4	0	2	0	0	2	Q3USR6	
ENSMUST00000110179	ENSMUSG00000027333	2	131491496	131525922	1	0	0	0	0	0	0	0	0	0	0	0	A2ANQ4	
ENSMUST00000110180	ENSMUSG00000027333	2	131491496	131525922	1	0	0	0	0	0	0	43	52	0	0	10		Q99K82
ENSMUST00000110181	ENSMUSG00000027333	2	131491496	131525922	1	10	7	21	7	15	6	11	176	20	6	92	Q3TLR8	
ENSMUST00000110182	ENSMUSG00000027333	2	131491496	131525922	1	0	0	0	0	0	0	0	0	0	0	0		Q99K82
ENSMUST00000110183	ENSMUSG00000027333	2	131491496	131525922	1	0	0	0	0	0	0	14	0	0	5	20		Q99K82
ENSMUST00000110186	ENSMUSG00000027333	2	131491496	131525922	1	0	0	0	0	0	0	390	1957	287	27	961		Q99K82
ENSMUST00000110187	ENSMUSG00000034145	12	87021340	87090043	1	0	0	0	0	0	0	0	0	0	0	0		Q8CBX0
ENSMUST00000110188	ENSMUSG00000027333	2	131491496	131525922	1	7	0	0	0	8	0	41	0	61	0	125		Q99K82
ENSMUST00000110189	ENSMUSG00000027333	2	131491496	131525922	1	0	6	0	0	0	0	0	21	0	19	40		Q99K82
ENSMUST00000110191	ENSMUSG00000021360	13	40859768	40960891	1	20	13	63	41	27	15	25	46	55	10	24	Q6T5E4	
ENSMUST00000110193	ENSMUSG00000021359	13	40715675	40733823	-1	47	31	6	1111	60	52	2	0	5	7	11		
ENSMUST00000110194	ENSMUSG00000048911	2	131298064	131352892	-1	42	42	49	17	47	40	0	0	0	0	0	Q4VA59	Q8BGI1
ENSMUST00000110196	ENSMUSG00000022366	15	57243767	57477625	-1	7	8	0	0	4	3	0	0	0	0	0	Q8R0S9	
ENSMUST00000110199	ENSMUSG00000037523	2	131234063	131248025	1	31	19	40	64	22	0	0	0	9	0	29		Q8VCF0
ENSMUST00000110200	ENSMUSG00000060429	15	55638843	55906949	-1	2	3	3	104	0	1	0	0	0	0	0		Q99L88
ENSMUST00000110203	ENSMUSG00000021255	12	86361117	86521628	1	11	5	8	140	12	5	0	0	0	0	0	D3YW03	
ENSMUST00000110204	ENSMUSG00000021255	12	86361117	86521628	1	0	0	0	17	17	9	0	0	0	0	0	G5E8P8	
ENSMUST00000110206	ENSMUSG00000068264	2	131207078	131213514	1	0	1	0	0	0	0	0	11	16	3	3	A2ANC5	
ENSMUST00000110208	ENSMUSG00000068264	2	131207078	131213514	1	0	2	4	3	24	0	550	586	303	74	229	A2ANC6	
ENSMUST00000110210	ENSMUSG00000068264	2	131207078	131213514	1	0	4	5	0	0	0	24	44	0	0	0		Q9D742
ENSMUST00000110214	ENSMUSG00000090744	7	41545674	41573662	-1	0	0	0	0	0	0	0	0	0	0	0	L7N248	
ENSMUST00000110216	ENSMUSG00000059897	8	69226343	69228980	1	0	0	1	1	1	3	7	18	10	8	5	F6YAM1	
ENSMUST00000110217	ENSMUSG00000022371	15	55307750	55520803	1	4	0	0	6	0	15	0	0	0	1	23	K3W4R4	
ENSMUST00000110218	ENSMUSG00000027329	2	131170261	131187282	-1	17	19	47	14	23	9	31	53	28	4	15		Q99JL1
ENSMUST00000110220	ENSMUSG00000012609	12	85824659	86061893	1	12	6	17	26	11	1	0	0	0	0	2	Q8BUF0	
ENSMUST00000110221	ENSMUSG00000022371	15	55307750	55520803	1	18	31	0	28	36	0	1	0	0	5	0	B7ZNH7	
ENSMUST00000110224	ENSMUSG00000012609	12	85824659	86061893	1	8	0	11	3	0	5	0	0	0	0	22	D3YVZ5	
ENSMUST00000110225	ENSMUSG00000079039	2	131133497	131134215	1	0	0	0	0	0	0	0	0	0	0	0	F6YAE0	
ENSMUST00000110226	ENSMUSG00000027322	2	131069220	131086765	-1	5	1	11	8	6	3	0	0	0	0	2	H9KUZ2	
ENSMUST00000110227	ENSMUSG00000027322	2	131069220	131086765	-1	111	116	118	75	131	58	6	21	6	5	90	H9KUZ3	
ENSMUST00000110230	ENSMUSG00000053749	15	55099917	55113677	-1	5	3	7	5	3	3	0	2	0	0	0	D3YVZ2	
ENSMUST00000110231	ENSMUSG00000022422	15	55076099	55090491	-1	5	0	7	7	5	3	0	0	0	0	0	D3YVY9	
ENSMUST00000110232	ENSMUSG00000027318	2	131050591	131063814	-1	0	0	0	0	0	0	0	0	0	0	0		Q923W9
ENSMUST00000110233	ENSMUSG00000044566	13	38006052	38037069	-1	0	0	0	1	3	3	0	0	0	0	0		Q5IR70
ENSMUST00000110234	ENSMUSG00000027316	2	131039632	131043088	-1	0	0	0	22	2	0	0	0	0	0	0		Q9JJT2
ENSMUST00000110235	ENSMUSG00000027316	2	131039632	131043088	-1	0	1	2	0	0	0	0	0	1	0	0		Q9JJT2
ENSMUST00000110237	ENSMUSG00000039087	13	37778400	37952002	1	0	0	0	199	10	2	0	3	7	2	0		Q3UH06
ENSMUST00000110238	ENSMUSG00000039087	13	37778400	37952002	1	90	40	135	346	92	56	21	29	51	0	46		Q3UH06
ENSMUST00000110239	ENSMUSG00000027316	2	131039632	131043088	-1	0	0	0	40	0	0	0	0	0	0	0		Q9JJT2
ENSMUST00000110240	ENSMUSG00000027316	2	131039632	131043088	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JJT2
ENSMUST00000110241	ENSMUSG00000031864	8	68793929	68829410	1	0	0	2	3	2	2	46	150	86	37	77	E9Q361	
ENSMUST00000110242	ENSMUSG00000031864	8	68793929	68829410	1	0	0	0	0	32	0	0	9	0	19	0	E9Q360	
ENSMUST00000110243	ENSMUSG00000027309	2	130706200	130906406	-1	3	3	7	17	6	2	9	9	8	1	1	A2AKU3	
ENSMUST00000110244	ENSMUSG00000061731	15	53064038	53346159	-1	0	0	3	1	0	1	0	1	7	3	3	D3YVY6	
ENSMUST00000110249	ENSMUSG00000042320	12	85086385	85106431	-1	11	5	21	0	18	12	12	5	16	0	0		Q8BII1
ENSMUST00000110251	ENSMUSG00000021417	13	34977748	35027094	-1	0	0	0	0	0	0	89	269	105	431	151	Q3TCD4	
ENSMUST00000110253	ENSMUSG00000036469	8	65617900	66471637	1	0	0	0	0	0	8	174	1	272	503	154		Q6NZQ8
ENSMUST00000110254	ENSMUSG00000002020	12	84783212	84876532	-1	0	0	0	0	0	0	0	0	0	16	30	Q0VD84	
ENSMUST00000110255	ENSMUSG00000036469	8	65617900	66471637	1	0	0	0	23	0	0	38	53	0	52	17		Q6NZQ8
ENSMUST00000110256	ENSMUSG00000036469	8	65617900	66471637	1	16	13	40	4	7	0	4	38	41	83	41	D3YVY0	
ENSMUST00000110258	ENSMUSG00000036469	8	65617900	66471637	1	21	14	55	25	32	22	0	0	0	0	0		Q6NZQ8
ENSMUST00000110259	ENSMUSG00000036469	8	65617900	66471637	1	0	0	0	0	1	0	0	0	0	0	0		Q6NZQ8
ENSMUST00000110260	ENSMUSG00000037703	2	130632839	130642803	-1	51	11	39	801	83	31	12	0	18	0	0		A2AHG0
ENSMUST00000110261						9	2	62	17	8	3	0	0	0	0	0		
ENSMUST00000110262	ENSMUSG00000079043	2	130613840	130630027	-1	8	0	11	11	12	10	16	169	14	5	22		
ENSMUST00000110264						18	15	93	14	12	8	0	2	2	0	0		
ENSMUST00000110267	ENSMUSG00000022340	15	44671859	44788063	-1	5	11	12	4	12	10	0	0	0	0	0		Q8BHS8
ENSMUST00000110269	ENSMUSG00000022340	15	44671859	44788063	-1	0	5	32	0	6	6	1	1	0	4	9		Q8BHS8
ENSMUST00000110272	ENSMUSG00000021236	12	84373857	84409029	-1	0	0	0	13	0	0	67	526	377	51	269		Q9WUZ9
ENSMUST00000110273	ENSMUSG00000052180	13	33879816	33905708	-1	5	0	5	0	3	0	0	1	0	0	0	Q6P6K7	
ENSMUST00000110275	ENSMUSG00000069248	13	33832345	33843408	-1	8	8	4	4	9	2	0	0	0	0	0	I7HJI3	
ENSMUST00000110276	ENSMUSG00000021235	12	84361657	84373796	1	7	5	1	0	3	0	0	0	0	0	0		Q8R1S0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000110277	ENSMUSG00000037773	2	130417247	130424701	-1	0	0	0	0	0	0	53	57	51	7	40		Q6P1Z5
ENSMUST00000110278	ENSMUSG00000021235	12	84361657	84373796	1	0	0	0	0	0	0	0	8	19	0	0	D3YW66	
ENSMUST00000110281	ENSMUSG00000027409	2	130405259	130406074	1	1	2	0	0	3	1	0	0	0	0	0	Q9DA59	
ENSMUST00000110284	ENSMUSG00000021404	13	33149275	33159742	-1	0	0	2	2	1	0	0	0	0	1	0	Q9D6A7	
ENSMUST00000110286	ENSMUSG00000053552	2	130295169	130370481	1	0	0	45	0	36	0	0	0	0	0	0	B2RQX3	Q8K4J2
ENSMUST00000110287	ENSMUSG00000053552	2	130295169	130370481	1	0	0	0	46	0	0	0	0	0	0	0	A2BI84	
ENSMUST00000110288	ENSMUSG00000053552	2	130295169	130370481	1	0	0	0	19	0	0	0	0	0	0	0	A2BI80	
ENSMUST00000110289	ENSMUSG00000038760	15	44196135	44235912	1	0	0	9	0	0	0	0	0	0	0	0	Q32MS1	P21761
ENSMUST00000110293	ENSMUSG00000042842	13	32965209	32979067	1	11	10	9	25	9	7	0	0	0	0	0	O08804	
ENSMUST00000110294	ENSMUSG00000042507	12	84149176	84218881	-1	44	19	69	281	46	11	119	221	214	13	211	E9Q2I4	
ENSMUST00000110297	ENSMUSG00000022307	15	41447482	41861048	1	0	0	20	0	6	0	0	0	0	0	0		Q4KMM3
ENSMUST00000110298	ENSMUSG00000021224	12	83794034	83921934	-1	0	13	25	0	0	0	0	593	0	60	0	F8WJ71	
ENSMUST00000110299	ENSMUSG00000027401	2	130012349	130050399	1	50	48	70	61	39	33	15	66	15	6	22		Q08189
ENSMUST00000110301	ENSMUSG00000004319	8	60910389	60983300	-1	0	0	0	0	0	0	0	8	37	8	41		P51791
ENSMUST00000110302	ENSMUSG00000004319	8	60910389	60983300	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q2I1	
ENSMUST00000110305	ENSMUSG00000022305	15	39870603	39943994	-1	0	0	0	85	0	8	13	0	12	0	0		Q8BUJ9
ENSMUST00000110306	ENSMUSG00000022304	15	39768485	39857470	-1	6	7	0	1	8	0	0	0	0	1	0		Q9EQF5
ENSMUST00000110307	ENSMUSG00000021356	13	30749226	30766927	1	17	18	22	30	21	9	50	40	34	17	46	Q5SUZ5	Q64287
ENSMUST00000110310	ENSMUSG00000069255	13	30659999	30711231	1	2	3	4	10	10	1	0	1	0	0	0	Z4YL33	
ENSMUST00000110315	ENSMUSG00000027397	2	129198764	129211616	1	11	21	19	7	0	0	146	1361	0	51	5		Q61609
ENSMUST00000110316	ENSMUSG00000031608	8	57523828	57653032	-1	6	7	25	6	13	5	43	327	274	54	203		Q80VA0
ENSMUST00000110319	ENSMUSG00000042851	2	128967402	129018563	1	2	3	4	13	6	5	0	3	2	2	0		Q8BYK8
ENSMUST00000110320	ENSMUSG00000042851	2	128967402	129018563	1	18	15	30	17	13	12	29	94	97	32	89	A2AP88	
ENSMUST00000110322	ENSMUSG00000038206	8	56551090	56592393	1	5	4	0	68	6	0	0	4	28	45	22	Q921R9	
ENSMUST00000110323	ENSMUSG00000006191	13	29191746	29855674	-1	0	0	0	0	0	6	0	0	0	0	0	I7HPB3	
ENSMUST00000110324	ENSMUSG00000027386	2	128862981	128897034	1	0	13	0	39	20	10	0	0	0	0	0		Q501P1
ENSMUST00000110325	ENSMUSG00000014353	2	128818118	128854261	1	19	11	23	87	13	8	84	617	295	149	261		Q8BKU8
ENSMUST00000110328	ENSMUSG00000037458	15	38487430	38519266	-1	0	0	0	0	0	0	776	0	46	0	116	D3YW58	
ENSMUST00000110329	ENSMUSG00000037458	15	38487430	38519266	-1	0	0	0	0	0	7	1752	5663	2481	543	1214		O35484
ENSMUST00000110332	ENSMUSG00000014355	2	128610104	128687391	-1	4	2	0	18	4	1	0	1	1	0	0	Q6PG65	
ENSMUST00000110333	ENSMUSG00000014355	2	128610104	128687391	-1	2	11	15	13	12	5	49	0	167	0	146	A2ATQ5	
ENSMUST00000110335	ENSMUSG00000062551	13	27849344	27857793	1	0	1	2	0	0	0	0	0	0	0	0	Q5SVL9	
ENSMUST00000110336	ENSMUSG00000037487	15	37967328	38078853	-1	17	32	44	69	43	18	1849	4801	5461	323	2926	E9Q2H1	
ENSMUST00000110339						0	1	0	0	1	1	12	24	39	71	22		
ENSMUST00000110340	ENSMUSG00000091803	12	81359026	81485127	-1	0	2	0	0	4	3	0	78	19	115	14	Q497I8	Q9CR63
ENSMUST00000110341	ENSMUSG00000027381	2	128126038	128162547	1	33	30	77	46	38	0	685	1626	824	97	697	Q542N5	O54918
ENSMUST00000110343	ENSMUSG00000031561	8	48227682	48844026	-1	0	0	0	21	0	1	0	0	0	0	0	D3YW50	
ENSMUST00000110344	ENSMUSG00000027380	2	127838876	128123873	1	6	6	0	22	14	3	0	0	0	1	0		Q9DBS4
ENSMUST00000110345	ENSMUSG00000031561	8	48227682	48844026	-1	2	0	3	41	2	1	0	0	0	0	0	D3YW50	
ENSMUST00000110346	ENSMUSG00000031561	8	48227682	48844026	-1	20	17	84	178	12	10	0	0	0	0	0	D3YW49	
ENSMUST00000110347	ENSMUSG00000021136	12	81026808	81186414	1	0	0	32	132	38	0	0	2	0	0	0		
ENSMUST00000110350	ENSMUSG00000021346	13	27506968	27513215	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DAS4
ENSMUST00000110351	ENSMUSG00000021134	12	80945504	80950507	1	0	0	0	0	0	0	330	1960	424	900	400	Q9D8S5	
ENSMUST00000110352	ENSMUSG00000021134	12	80945504	80950507	1	0	0	0	0	0	0	261	2274	356	933	565		O35326
ENSMUST00000110354	ENSMUSG00000021134	12	80945504	80950507	1	0	0	0	0	0	0	0	0	0	0	0	Q9D8S5	
ENSMUST00000110355	ENSMUSG00000021345	13	27432681	27438688	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DAY2
ENSMUST00000110356	ENSMUSG00000021134	12	80945504	80950507	1	0	0	0	0	0	0	356	1267	385	0	316		O35326
ENSMUST00000110357	ENSMUSG00000027378	2	127740732	127788897	-1	0	0	0	28	0	0	0	0	0	0	0	Q3TWM5	
ENSMUST00000110359	ENSMUSG00000022285	15	36770770	36794547	-1	2	0	1	34	3	0	0	0	0	0	0	D3YW45	
ENSMUST00000110361	ENSMUSG00000022285	15	36770770	36794547	-1	7	5	11	58	24	3	0	0	0	26	0		P63101
ENSMUST00000110362	ENSMUSG00000022285	15	36770770	36794547	-1	0	0	0	13	0	0	2413	185	1800	1261	1150		P63101
ENSMUST00000110363	ENSMUSG00000018259	13	27345683	27354216	1	0	2	2	1	0	1	0	0	0	0	0	O35258	
ENSMUST00000110364	ENSMUSG00000017922	13	27196659	27203749	1	0	0	0	0	0	0	0	0	0	0	0	Z4YL38	
ENSMUST00000110366	ENSMUSG00000034800	2	127574662	127587094	-1	58	48	329	90	61	34	0	4	0	4	0		Q8BIQ3
ENSMUST00000110367	ENSMUSG00000038143	8	47180048	47352348	-1	32	24	107	5	39	13	7	18	10	0	2		Q499E5
ENSMUST00000110368	ENSMUSG00000034800	2	127574662	127587094	-1	2	7	2	2	6	0	0	11	4	7	0		Q8BIQ3
ENSMUST00000110369	ENSMUSG00000021342	13	27057570	27065204	1	0	0	0	0	0	0	0	0	0	0	0	Q9CPQ2	
ENSMUST00000110371	ENSMUSG00000018796	8	46471041	46536051	1	2	0	0	2	4	0	82	22	247	22	175	D3Z041	
ENSMUST00000110372	ENSMUSG00000018796	8	46471041	46536051	1	18	16	30	0	19	8	124	0	867	67	661		P41216
ENSMUST00000110374	ENSMUSG00000027367	2	127270218	127298932	1	39	35	171	43	39	13	7	36	29	3	34	Q8BXP7	
ENSMUST00000110375	ENSMUSG00000027367	2	127270218	127298932	1	0	0	5	138	7	1	182	295	300	146	148		Q8R1R3
ENSMUST00000110376	ENSMUSG00000031631	8	46151771	46195590	1	0	0	0	0	4	0	28	0	31	0	9	E9Q1K1	
ENSMUST00000110377	ENSMUSG00000038291	8	46033261	46152159	-1	0	0	6	0	0	0	4	0	0	0	0	D3Z040	
ENSMUST00000110378	ENSMUSG00000038291	8	46033261	46152159	-1	0	0	9	25	3	0	9	9	0	9	0	E9Q1K0	
ENSMUST00000110380	ENSMUSG00000031637	8	45999303	46029477	1	0	0	0	0	0	0	0	0	0	0	0		Q9D4C6
ENSMUST00000110381	ENSMUSG00000031637	8	45999303	46029477	1	0	7	2	7	0	0	0	0	0	0	0		Q9D4C6
ENSMUST00000110382	ENSMUSG00000006715	13	24751845	24761923	-1	0	0	0	30	0	0	123	231	92	350	82	Q3V295	O88513
ENSMUST00000110383	ENSMUSG00000036006	13	24582189	24733816	1	19	77	23	12	3	26	2817	5250	4237	710	3954	A6PW28	
ENSMUST00000110384	ENSMUSG00000036006	13	24582189	24733816	1	57	0	54	47	56	8	0	0	15	0	4		Q80U16
ENSMUST00000110386	ENSMUSG00000074825	2	127138772	127143442	-1	0	0	0	0	0	0	66	0	67	9	66		A2ASA8
ENSMUST00000110387	ENSMUSG00000034906	2	127103809	127133954	-1	0	4	16	31	6	3	73	60	136	10	62		Q8C156
ENSMUST00000110388	ENSMUSG00000047454	12	78226655	78684767	1	0	1	0	3	0	1	49	159	117	36	72	A0JNY3	
ENSMUST00000110389	ENSMUSG00000001999	2	127070665	127097084	1	0	0	0	0	0	0	0	0	0	0	0	A2ASB8	
ENSMUST00000110391	ENSMUSG00000016756	13	24327420	24477285	1	1983	1889	1531	1787	2320	1111	2119	7880	6190	250	4274		Q61419
ENSMUST00000110393	ENSMUSG00000001998	2	127008717	127067909	1	1	1	0	0	0	0	0	0	0	0	0	F6W7A9	
ENSMUST00000110394	ENSMUSG00000001998	2	127008717	127067909	1	5	5	7	3	5	2	2	3	2	0	1	A2ASB3	
ENSMUST00000110395	ENSMUSG00000059436	12	76937269	76962248	-1	23	19	0	0	0	0	771	1822	956	416	670	B2RS19	
ENSMUST00000110398	ENSMUSG00000021338	13	24012344	24280795	-1	7	16	17	8	22	8	0	0	4	0	9	D3Z030	
ENSMUST00000110399	ENSMUSG00000090258	12	76765538	76783180	1	134	166	203	143	58	99	0	51	11	49	29		Q6DG52
ENSMUST00000110407	ENSMUSG00000021336	13	23897738	23915007	-1	0	17	31	0	30	7	0	0	0	0	0		Q5NCM1
ENSMUST00000110408	ENSMUSG00000022236	15	31441210	31453689	-1	4	4	1	161	18	11	83	166	70	80	12		
ENSMUST00000110410	ENSMUSG00000022237	15	31291479	31367759	-1	11	24	90	144	11	28	204	551	640	248	394		Q3U0L2
ENSMUST00000110411	ENSMUSG00000079058	8	43650435	43699487	-1	10	6	3	17	8	3	0	0	0	0	0	A2RSG8	
ENSMUST00000110413	ENSMUSG00000021335	13	23867750	23895730	1	8	3	1	0	12	1	0	0	0	0	0		Q61983

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000110416	ENSMUSG00000027363	2	126707328	126759297	1	2	2	3	0	2	1	0	0	0	0	141	A2AI52	
ENSMUST00000110417	ENSMUSG00000031591	8	41340197	41374773	-1	0	1	0	0	0	0	94	256	117	100	50	D3Z015	
ENSMUST00000110421	ENSMUSG00000021055	12	76120419	76177259	-1	0	0	47	0	0	7	0	8	3	0	8		
ENSMUST00000110422	ENSMUSG00000036083	13	23839434	23860714	1	7	4	0	3	0	4	0	0	0	0	0	Q5SZ92	
ENSMUST00000110424	ENSMUSG00000027361	2	126627442	126676337	-1	0	0	0	0	0	0	235	835	350	51	194	Q3US22	Q00420
ENSMUST00000110425	ENSMUSG00000027361	2	126627442	126676337	-1	11	15	16	20	20	11	0	14	6	3	13		Q00420
ENSMUST00000110432	ENSMUSG00000053216	13	23477676	23488857	-1	0	0	19	0	8	0	0	0	0	0	0		A4QPC6
ENSMUST00000110433	ENSMUSG00000053216	13	23477676	23488857	-1	20	10	0	24	8	7	0	0	0	0	0		A4QPC6
ENSMUST00000110434	ENSMUSG00000000706	13	23456992	23465901	-1	4	6	5	53	10	0	0	0	0	0	0	Q921X1	
ENSMUST00000110437	ENSMUSG00000023330	2	126152141	126165279	1	6	9	8	0	6	0	5	0	0	61	7		Q9D8U7
ENSMUST00000110438	ENSMUSG00000022270	15	25843264	25973687	1	4	3	32	0	0	3	99	6	385	120	371		Q8VE91
ENSMUST00000110441	ENSMUSG00000079061	12	74315110	74316394	-1	59	44	569	90	29	16	0	0	0	0	0	F6VZP0	
ENSMUST00000110442	ENSMUSG00000027208	2	126034658	126091185	1	36	24	14	401	51	58	0	7	2	0	1	Q544I6	P36363
ENSMUST00000110446	ENSMUSG00000027209	2	125983483	126152004	-1	0	0	4	10	3	0	0	0	0	0	0		Q9D518
ENSMUST00000110448	ENSMUSG00000027209	2	125983483	126152004	-1	3	0	0	0	0	0	0	0	0	0	0	E9PUC3	
ENSMUST00000110449						3	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000110451	ENSMUSG00000044912	12	73997761	74267916	1	17	15	15	11	11	18	0	0	0	0	0		Q7TN83
ENSMUST00000110452	ENSMUSG00000069300	13	22043214	22043676	1	4	7	26	68	3	4	10	0	7	0	0		P10853
ENSMUST00000110454						2	3	0	0	1	1	0	0	0	0	0		
ENSMUST00000110455	ENSMUSG00000062727	13	22035870	22036345	1	12	6	10	67	15	4	60	6	24	61	44	B2RVD5	Q8CGP1
ENSMUST00000110456	ENSMUSG00000025731	17	25875464	25886007	1	12	0	0	71	13	10	0	0	7	0	0	D3YZM4	
ENSMUST00000110457	ENSMUSG00000022272	15	25622525	25813673	1	0	21	38	207	82	21	9	0	9	0	77		F8VQB6
ENSMUST00000110461	ENSMUSG00000021109	12	73901375	73947530	1	5	8	33	0	11	4	973	2363	737	214	606		
ENSMUST00000110462	ENSMUSG00000027206	2	125830304	125859139	-1	0	0	0	0	0	0	12	38	0	373	76	A2AQE4	
ENSMUST00000110463	ENSMUSG00000027206	2	125830304	125859139	-1	3	8	5	3	3	5	78	242	45	146	31	Q3V3N6	P61202
ENSMUST00000110464	ENSMUSG00000021109	12	73901375	73947530	1	3	0	0	126	2	3	0	2	6	0	0		
ENSMUST00000110467	ENSMUSG00000069303	13	21833743	21837530	1	0	0	0	0	0	0	0	232	10	0	21		P10853
ENSMUST00000110469	ENSMUSG00000069307	13	21806412	21810199	-1	34	16	175	0	14	1	41	405	59	11	113		P10853
ENSMUST00000110473	ENSMUSG00000069308	13	21787461	21789213	1	0	4	3	5	2	2	0	0	0	0	0		Q8CGP2
ENSMUST00000110476	ENSMUSG00000096807	13	21722098	21722478	1	5	2	3	59	6	0	0	0	0	4	0	B2RTK3	P10854
ENSMUST00000110477	ENSMUSG00000035109	2	125627447	125724148	-1	0	0	0	0	0	0	0	0	2	0	1	A2AUN0	
ENSMUST00000110480	ENSMUSG00000035109	2	125627447	125724148	-1	15	33	0	1396	73	46	8	4	7	0	4	A2AUN0	
ENSMUST00000110481	ENSMUSG00000063894	13	21513222	21531120	-1	6	0	2	26	2	2	2	0	0	2	3	Q78WV9	
ENSMUST00000110483	ENSMUSG00000016128	5	151037510	151233836	-1	26	1	90	1	51	23	0	0	0	0	12		Q923Q2
ENSMUST00000110485	ENSMUSG00000022228	13	21442175	21453730	-1	0	1	3	5	2	0	12	21	57	10	58		Q5RJ54
ENSMUST00000110486	ENSMUSG00000034021	5	150673739	150810690	1	2	10	2	0	1	0	8	0	19	0	19		Q4VA53
ENSMUST00000110489	ENSMUSG00000021098	12	72881109	72940774	-1	4	0	2	95	2	2	0	0	0	0	0	F8WHJ9	
ENSMUST00000110491	ENSMUSG00000004344	13	21286429	21292731	-1	6	14	0	0	10	8	0	0	0	0	0	F2Z3Y2	
ENSMUST00000110492	ENSMUSG00000050271	8	36094828	36147787	1	37	23	96	214	57	28	20	13	12	4	37	E9QLH9	
ENSMUST00000110494	ENSMUSG00000027202	2	125152505	125230002	1	13	20	0	0	0	14	0	0	0	0	0	A2AQ52	
ENSMUST00000110495	ENSMUSG00000027202	2	125152505	125230002	1	6	0	10	17	13	0	0	0	0	0	1	A2AQ51	
ENSMUST00000110496	ENSMUSG00000053368	5	150018675	150082184	1	8	9	20	15	0	6	0	0	0	0	0	E9Q0U9	
ENSMUST00000110498						2	0	13	26	0	1	3	47	12	54	113		
ENSMUST00000110501	ENSMUSG00000027201	2	125084628	125123661	-1	0	0	0	0	0	2	0	0	0	0	0		Q8C854
ENSMUST00000110502	ENSMUSG00000029658	5	149528679	149611894	1	16	0	0	19	0	9	3	4	1	3	2	E9PUB4	
ENSMUST00000110504	ENSMUSG00000022205	15	11981339	11996983	-1	1	1	4	2	4	5	1156	4413	845	1917	360		P11031
ENSMUST00000110505	ENSMUSG00000066551	5	149046702	149184489	-1	70	67	116	67	64	10	351	1535	206	370	152	Q58EV5	P63158
ENSMUST00000110506	ENSMUSG00000005803	2	122765237	122809569	1	0	4	8	0	0	3	0	0	0	7	7		Q9R112
ENSMUST00000110507						7	4	20	5	3	2	0	0	0	3	0		
ENSMUST00000110508						11	5	13	188	25	13	0	0	0	2	0		
ENSMUST00000110509	ENSMUSG00000041298	5	148871584	148929320	-1	6	4	6	169	8	3	0	2	0	2	0	G5E8P9	
ENSMUST00000110510	ENSMUSG00000021318	13	15463235	15730026	1	45	42	106	45	60	22	0	0	0	4	28	B2RUG4	Q61602
ENSMUST00000110512	ENSMUSG00000033213	2	122636986	122641191	1	0	0	2	0	0	0	872	1047	245	555	101	Q3UCF3	Q810Q5
ENSMUST00000110514	ENSMUSG00000029651	5	147957320	148316065	1	0	0	0	0	0	0	0	0	0	0	0	D3YZ69	
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ENSMUST00000110516	ENSMUSG00000021301	13	14226438	14523226	-1	60	48	80	47	56	31	1	3	0	1	4		Q8K4P8
ENSMUST00000110520	ENSMUSG00000021071	12	70244539	70347614	-1	13	19	0	364	27	14	12	22	27	2	33		Q8C7M3
ENSMUST00000110521	ENSMUSG00000079071	2	122484941	122528040	1	12	10	19	9	25	9	962	3277	1376	555	992	A2AWR5	
ENSMUST00000110522	ENSMUSG00000021071	12	70244539	70347614	-1	0	5	59	42	12	8	0	21	0	0	0	E9QLH4	
ENSMUST00000110523	ENSMUSG00000058914	15	10952332	10980150	1	3	3	46	9	8	6	0	0	0	0	0	D3YZ61	
ENSMUST00000110524	ENSMUSG00000027219	2	122426477	122461137	1	7	6	0	8	0	2	4339	11723	5788	1946	4183		O88627
ENSMUST00000110525	ENSMUSG00000027219	2	122426477	122461137	1	0	0	0	0	0	0	0	0	0	0	0		O88627
ENSMUST00000110527	ENSMUSG00000046152	8	31187331	31261738	1	5	2	2	0	5	2	0	0	0	3	0		Q5F2L2
ENSMUST00000110529	ENSMUSG00000029648	5	147561604	147726011	-1	60	46	73	458	48	54	0	2	4	0	14	O55095	
ENSMUST00000110530	ENSMUSG00000033256	2	122348892	122369162	-1	3	7	6	2	0	1	0	0	11	0	0		Q8CG80
ENSMUST00000110531	ENSMUSG00000033256	2	122348892	122369162	-1	0	0	0	85	0	0	4	8	0	0	0		Q8CG80
ENSMUST00000110532	ENSMUSG00000033256	2	122348892	122369162	-1	0	0	0	0	4	0	2	12	0	0	0	A2AQ88	
ENSMUST00000110533	ENSMUSG00000039219	13	14063232	14199603	1	6	5	0	57	5	5	0	0	0	0	5	Z4YL44	
ENSMUST00000110534	ENSMUSG00000039219	13	14063232	14199603	1	6	0	0	0	0	0	221	856	456	193	525		A2CG63
ENSMUST00000110536	ENSMUSG00000039219	13	14063232	14199603	1	0	0	10	93	11	2	37	0	7	0	0		A2CG63
ENSMUST00000110537	ENSMUSG00000027224	2	122302191	122313730	-1	0	0	0	2	0	0	0	0	0	0	0		Q8VE49
ENSMUST00000110538	ENSMUSG00000027224	2	122302191	122313730	-1	8	5	10	10	15	6	0	0	0	0	0	A2AQ96	
ENSMUST00000110540	ENSMUSG00000089678	15	10358532	10410153	1	0	1	31	6	8	3	0	0	0	0	0	D3YZ52	
ENSMUST00000110541	ENSMUSG00000089678	15	10358532	10410153	1	0	1	0	0	3	1	0	0	0	0	0	D3YZ49	
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ENSMUST00000110549						24	19	64	90	35	15	0	1	3	1	5		
ENSMUST00000110551	ENSMUSG00000027227	2	122234749	122265340	1	24	23	43	67	26	19	388	958	396	49	334		Q64442
ENSMUST00000110557	ENSMUSG00000029642	5	147077050	147111597	1	10	5	21	127	12	14	201	701	396	1378	281	Q9D1M1	
ENSMUST00000110559	ENSMUSG00000019726	13	13590409	13777440	1	37	36	82	116	58	33	4846	6948	12231	751	8819	G5E8Q0	
ENSMUST00000110560	ENSMUSG00000079076	12	69963473	69969721	1	2	3	12	2	4	1	0	2	1	1	2	Q05CB6	
ENSMUST00000110564	ENSMUSG00000016510	5	146951573	146963800	-1	4	0	6	0	2	2	66	157	37	0	0	A4QMQ0	Q9CZD5
ENSMUST00000110566	ENSMUSG00000016510	5	146951573	146963800	-1	0	0	4	4	0	0	18	106	97	98	46	A4QMQ0	Q9CZD5
ENSMUST00000110567	ENSMUSG00000034761	12	69803750	69893200	-1	0	8	4	0	0	4	0	151	43	4	0		Q8BPM2
ENSMUST00000110570	ENSMUSG00000034761	12	69803750	69893200	-1	0	0	0	23	0	0	0	0	0	0	0		Q8BPM2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000110572	ENSMUSG00000033411	2	121956001	122013642	1	3	0	0	0	0	0	16	94	27	46	17		Q8BG15
ENSMUST00000110573	ENSMUSG00000013878	8	26119368	26143871	1	2	3	3	1	2	2	0	1	0	0	0	D3YYB6	
ENSMUST00000110574	ENSMUSG00000033411	2	121956001	122013642	1	3	0	5	11	6	4	0	11	0	0	0		Q8BG15
ENSMUST00000110575	ENSMUSG00000013878	8	26119368	26143871	1	2	0	1	1	3	1	2	0	0	0	0		Q8CBG9
ENSMUST00000110576	ENSMUSG00000094303	JH584297.1	19740	22248	-1	10	4	6	0	13	0	0	0	0	0	0		
ENSMUST00000110578	ENSMUSG00000033411	2	121956001	122013642	1	4	2	0	0	0	0	69	217	93	120	43		Q8BG15
ENSMUST00000110579	ENSMUSG00000013878	8	26119368	26143871	1	0	3	77	0	0	0	0	0	24	0	0		Q8CBG9
ENSMUST00000110582	ENSMUSG00000079083	9	13242790	13245741	-1	6	7	6	10	12	0	176	632	271	91	118		B2RRL2
ENSMUST00000110583	ENSMUSG00000079084	9	13246982	13289409	1	5	5	2	8	0	5	102	324	157	76	131		Q6PG04
ENSMUST00000110585	ENSMUSG00000054115	15	9111985	9155425	-1	28	17	18	48	20	14	2	4	4	0	2		Q9Z0Z3
ENSMUST00000110586	ENSMUSG00000060227	2	121866970	121936220	1	113	99	403	166	84	62	11	26	12	0	0	E9PZJ6	
ENSMUST00000110592	ENSMUSG00000027238	2	121545529	121807087	-1	6	0	0	15	0	0	0	0	0	0	0	A2AR56	
ENSMUST00000110593	ENSMUSG00000027238	2	121545529	121807087	-1	15	0	0	0	13	0	0	0	0	0	0	B0R0D4	
ENSMUST00000110594	ENSMUSG00000079092	13	12996132	13005383	-1	4	3	0	0	0	0	0	0	0	8	3		P04095
ENSMUST00000110595	ENSMUSG00000095557	5	146556136	146558915	1	9	0	5	24	13	6	0	0	0	0	0	L7N249	
ENSMUST00000110596	ENSMUSG00000079091	5	146525801	146528553	1	30	29	56	40	55	17	0	0	0	0	0	Q9D506	
ENSMUST00000110597	ENSMUSG00000096664	5	146537647	146540427	1	0	4	0	0	0	5	0	0	0	0	0	D3YYA7	
ENSMUST00000110598	ENSMUSG00000079093	5	146502399	146505183	1	26	12	17	36	19	8	0	0	0	0	0	Q9D5E3	
ENSMUST00000110599	ENSMUSG00000096664	5	146537647	146540427	1	0	0	0	0	0	0	0	0	0	0	0	L7N464	
ENSMUST00000110600						0	0	0	9	0	0	0	0	0	0	0		
ENSMUST00000110602	ENSMUSG00000027242	2	121506723	121544860	1	31	31	132	39	30	27	24	81	47	20	29		A6PWY4
ENSMUST00000110603	ENSMUSG00000027242	2	121506723	121544860	1	2	0	0	17	4	0	13	1	2	0	5		A6PWY4
ENSMUST00000110608	ENSMUSG00000031575	8	25816191	25847694	-1	0	0	0	0	0	0	25	0	45	0	76	D3YYA0	
ENSMUST00000110609	ENSMUSG00000031575	8	25816191	25847694	-1	0	0	0	12	0	0	0	0	0	0	0	E9PU93	
ENSMUST00000110610	ENSMUSG00000031575	8	25816191	25847694	-1	1	5	1	1	4	0	0	22	0	0	0	E9PU93	
ENSMUST00000110611	ENSMUSG00000096527	5	146491363	146494132	1	21	16	72	10	0	15	0	0	0	0	0	L7N250	
ENSMUST00000110612	ENSMUSG00000027245	2	121453290	121458672	1	93	66	190	94	78	69	25	86	50	9	81		Q9CR41
ENSMUST00000110613	ENSMUSG00000046110	2	121439059	121456781	-1	0	0	0	0	0	0	0	0	0	0	9	A2ARQ6	
ENSMUST00000110615	ENSMUSG00000074884	2	121449195	121458313	1	0	0	5	4	0	0	50	114	0	23	41	A2ARQ2	
ENSMUST00000110616	ENSMUSG00000052374	13	12269426	12340760	-1	143	170	384	335	106	55	3	28	8	0	8	D3YY95	
ENSMUST00000110617	ENSMUSG00000039801	15	8169106	8271158	1	51	42	54	189	64	27	119	255	285	22	311		Q8CE72
ENSMUST00000110619	ENSMUSG00000049751	12	69182731	69184083	-1	12	3	5	100	13	8	0	13	6	32	7	Q5M9P1	P83882
ENSMUST00000110620	ENSMUSG00000049751	12	69182731	69184083	-1	0	0	0	32	0	0	7	9	5	11	6	Q5M9P1	P83882
ENSMUST00000110621	ENSMUSG00000034883	12	69168814	69179010	1	1	10	6	132	11	9	9	9	7	13	2	D3YY91	
ENSMUST00000110625	ENSMUSG00000033526	2	121310561	121355396	-1	0	0	0	17	23	0	23	27	84	8	0		A2ARP1
ENSMUST00000110626	ENSMUSG00000033526	2	121310561	121355396	-1	0	0	0	0	0	6	0	0	0	0	22		A2ARP1
ENSMUST00000110627	ENSMUSG00000033526	2	121310561	121355396	-1	27	16	21	5	0	0	38	0	15	0	0		A2ARP1
ENSMUST00000110628	ENSMUSG00000033526	2	121310561	121355396	-1	0	0	0	0	0	0	0	11	0	0	66		A2ARP1
ENSMUST00000110633	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	3	0	0	0	143	146	470	109	500	D3YY86	
ENSMUST00000110634	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	0	0	0	67	171	259	75	332		Q8R5C8
ENSMUST00000110635	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	0	0	0	54	294	0	0	0	D3YY85	
ENSMUST00000110636	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	15	46	0	0	0	0	0	0	0		Q8R5C8
ENSMUST00000110637	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	0	0	0	401	1219	673	163	698	Q8BJZ0	
ENSMUST00000110638	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	15	0	0	0	16	0	0	0	D3YXX1	
ENSMUST00000110639	ENSMUSG00000027254	2	121289600	121310832	1	34	10	0	6	24	1	2	0	0	0	42		Q9QYR6
ENSMUST00000110647	ENSMUSG00000043909	2	121193281	121271407	-1	31	39	46	0	39	0	59	180	34	20	0	A2AU89	
ENSMUST00000110648	ENSMUSG00000043909	2	121193281	121271407	-1	0	0	0	45	0	18	0	39	61	0	189	A2AU91	
ENSMUST00000110657	ENSMUSG00000027263	2	121170654	121198770	1	0	0	0	0	0	0	0	7	67	0	21	Q8BKL6	
ENSMUST00000110658	ENSMUSG00000027263	2	121170654	121198770	1	0	0	0	25	0	0	12	38	0	14	44	Q8BYN2	
ENSMUST00000110661	ENSMUSG00000050619	2	121158273	121171125	-1	67	53	466	86	64	62	261	1688	540	103	425	A2ARU5	
ENSMUST00000110662	ENSMUSG00000027259	2	121140428	121156680	1	0	3	2	5	0	0	3	13	0	7	8		Q80SY6
ENSMUST00000110663	ENSMUSG00000022150	15	6299788	6440712	1	8	0	0	0	0	0	8	0	0	0	77	Q3TRE6	
ENSMUST00000110664	ENSMUSG00000022150	15	6299788	6440712	1	0	0	0	0	0	0	0	0	0	15	0	E9QL31	
ENSMUST00000110665	ENSMUSG00000027259	2	121140428	121156680	1	4	3	0	2	0	0	0	0	0	0	0	Z4YL50	
ENSMUST00000110667	ENSMUSG00000031551	8	24584136	24597009	-1	10	15	19	4	9	3	0	0	0	7	2	D3YXV1	
ENSMUST00000110671	ENSMUSG00000035431	12	58211772	58214444	1	2	6	15	113	7	0	0	0	0	0	0	Q543T0	P30873
ENSMUST00000110672	ENSMUSG00000038770	5	144983519	145084030	-1	0	4	0	0	10	11	0	0	0	0	0		C0LLJ0
ENSMUST00000110673	ENSMUSG00000038770	5	144983519	145084030	-1	9	0	34	15	17	0	0	0	0	0	0		C0LLJ0
ENSMUST00000110674	ENSMUSG00000074890	2	121128307	121140653	-1	3	7	15	200	10	9	18	21	13	0	20		Q8BYR1
ENSMUST00000110675	ENSMUSG00000079103	2	121093565	121109795	-1	19	15	33	12	31	13	0	0	2	0	0	A2ART8	
ENSMUST00000110677	ENSMUSG00000038780	5	144876495	144965847	-1	22	0	0	0	0	0	0	0	0	0	48	E9PYU8	
ENSMUST00000110679	ENSMUSG00000041625	14	122816223	122913757	-1	6	2	1	1	2	1	0	0	0	0	0		Q923B0
ENSMUST00000110680	ENSMUSG00000035472	12	56712634	57197472	-1	1	0	0	1	0	0	0	0	0	0	0	B6CI26	
ENSMUST00000110686	ENSMUSG00000054484	2	120977017	121007852	1	6	5	0	44	14	3	83	409	76	30	60	A2AQ56	
ENSMUST00000110687	ENSMUSG00000021027	12	55602929	55821167	-1	24	5	0	8	10	17	562	926	1179	0	299		Q6GYP7
ENSMUST00000110688	ENSMUSG00000031543	8	22974844	23150497	1	0	13	4	0	0	0	0	0	0	0	0		Q02357
ENSMUST00000110689	ENSMUSG00000079105	15	4988762	5063773	-1	10	5	31	11	17	6	0	0	0	0	0	D3YXF5	
ENSMUST00000110690	ENSMUSG00000022186	15	4026383	4155344	1	20	14	5	239	15	5	177	757	317	282	201		Q9D0K2
ENSMUST00000110691	ENSMUSG00000045410	13	4590757	4609174	-1	151	109	859	172	172	83	2	9	8	3	21	Q8CEB6	
ENSMUST00000110695	ENSMUSG00000047843	5	144244437	144446757	1	6	4	22	4	9	3	530	947	238	55	168	E9PUB2	
ENSMUST00000110696	ENSMUSG00000031540	8	22859535	22943259	1	0	0	23	75	68	0	507	2172	664	86	689	G3X940	
ENSMUST00000110697	ENSMUSG00000055737	15	3317760	3583492	-1	0	3	4	0	0	0	0	0	0	0	0		P16882
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ENSMUST00000110700	ENSMUSG00000027284	2	120716154	120850128	-1	0	0	0	0	0	0	0	27	35	6	33	Z4YL55	
ENSMUST00000110701	ENSMUSG00000027284	2	120716154	120850128	-1	35	28	80	35	39	34	31	56	38	0	41		Q8CC12
ENSMUST00000110702	ENSMUSG00000029618	5	144019804	144026670	-1	5	0	0	0	1	1	0	2	0	0	0	D3YXE4	
ENSMUST00000110704	ENSMUSG00000021214	13	4132615	4150654	-1	0	2	4	3	0	0	13	7	0	0	8		Q8K023
ENSMUST00000110706	ENSMUSG00000027285	2	120609383	120621560	1	78	95	114	10	34	50	27	810	83	0	197		Q9CQS9
ENSMUST00000110707						0	0	0	0	0	0	14	44	22	22	25		
ENSMUST00000110708	ENSMUSG00000079108	12	55155104	55263020	1	22	23	66	238	30	15	122	317	277	236	218		P14576
ENSMUST00000110709	ENSMUSG00000079109	5	143909964	143933968	1	0	0	0	0	0	0	0	3	14	0	6	E9QLM4	
ENSMUST00000110710						0	0	0	0	0	0	0	15	0	8	12		
ENSMUST00000110711	ENSMUSG00000027287	2	120567671	120601255	1	41	0	0	55	0	0	1545	5923	1354	973	1081	A2AKH4	O09044
ENSMUST00000110713	ENSMUSG00000054302	12	54670340	54695897	-1	0	0	0	0	0	0	269	1169	359	1164	222		Q5BU09

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000110716	ENSMUSG00000079110	2	120456019	120504913	1	11	4	11	0	12	0	0	0	0	0	0	A2AVV7	
ENSMUST00000110717	ENSMUSG00000029607	5	143890741	143897685	-1	0	5	0	4	0	3	0	3	0	0	2		Q9CQM6
ENSMUST00000110718	ENSMUSG00000029607	5	143890741	143897685	-1	3	4	1	0	7	2	0	9	8	0	18	D3YXD2	
ENSMUST00000110719	ENSMUSG00000079110	2	120456019	120504913	1	0	4	0	19	0	0	0	0	0	0	0	A2AVV6	
ENSMUST00000110721	ENSMUSG00000079110	2	120456019	120504913	1	0	0	4	2	0	0	0	5	4	0	0		Q64691
ENSMUST00000110725	ENSMUSG00000035133	12	52516077	52567852	1	10	11	4	6	12	5	13	46	14	13	27	E9PYT0	
ENSMUST00000110727	ENSMUSG00000018001	5	143622447	143710250	1	14	5	16	7	6	10	0	0	0	0	0	G5E8Q4	
ENSMUST00000110729	ENSMUSG00000033808	2	120355312	120404113	-1	0	0	0	0	0	0	0	6	0	0	18	A2AQJ7	
ENSMUST00000110730	ENSMUSG00000031478	8	22128283	22166435	-1	0	0	0	0	0	0	0	0	0	0	0		Q9R0A5
ENSMUST00000110731	ENSMUSG00000079111	5	143403838	143421901	1	15	9	19	61	7	3	419	603	338	159	317		Q9CQM2
ENSMUST00000110733	ENSMUSG00000010825	5	143357338	143392152	1	17	9	19	328	48	19	0	0	0	0	0		Q0QWG9
ENSMUST00000110737	ENSMUSG00000063362	8	22060721	22071627	1	1	50	56	49	13	0	0	0	0	0	0		Q3TZM9
ENSMUST00000110738	ENSMUSG00000006567	8	21992785	22060305	-1	2	11	29	0	7	0	0	0	1	0	1	B1AQ57	
ENSMUST00000110741	ENSMUSG00000079112	8	21958714	21964303	1	14	7	85	27	17	8	0	0	0	0	0	A2A4E2	
ENSMUST00000110746	ENSMUSG00000089922	12	49385174	49394127	1	7	10	16	134	15	12	0	0	0	0	0	E9PYS1	
ENSMUST00000110748	ENSMUSG00000020598	12	44328885	44601846	1	0	55	0	71	60	25	2	12	7	9	20		Q810U4
ENSMUST00000110749	ENSMUSG00000079113	8	21593375	21594508	-1	0	0	0	0	0	0	0	0	0	0	0	D3YX03	
ENSMUST00000110752	ENSMUSG00000079114	8	21455445	21456560	-1	0	0	0	0	0	0	0	0	0	0	0	D3YX03	
ENSMUST00000110754	ENSMUSG00000079116	8	21201561	21202539	1	0	0	0	0	3	0	0	0	0	0	0	D3YX02	
ENSMUST00000110756	ENSMUSG00000074899	2	120046157	120085772	-1	23	19	44	46	46	17	0	0	0	0	3	A2AP58	
ENSMUST00000110758	ENSMUSG00000079120	8	20943693	20944748	-1	4	0	5	1	3	2	1	0	1	1	0	Q5ERI8	
ENSMUST00000110763	ENSMUSG00000039785	8	19247580	19250828	1	2	2	10	2	2	0	0	0	0	0	0		Q9EPV9
ENSMUST00000110766	ENSMUSG00000066640	5	142866946	142895421	-1	233	187	1655	1130	287	170	356	450	416	35	421	E9PYR1	
ENSMUST00000110767	ENSMUSG00000059463	8	19140759	19143010	1	9	9	5	7	6	5	0	0	0	0	0	Q3UW43	
ENSMUST00000110773	ENSMUSG00000033943	2	119897228	119969581	1	67	90	42	0	61	54	0	0	0	0	0		A2AWL7
ENSMUST00000110774	ENSMUSG00000033943	2	119897228	119969581	1	7	0	53	22	39	0	21	0	125	0	5	E9QLG3	
ENSMUST00000110778	ENSMUSG00000029578	5	142627698	142670588	1	0	0	0	0	0	0	288	138	240	55	103	D3YWK1	
ENSMUST00000110783	ENSMUSG00000027298	2	119797733	119818104	1	15	3	15	29	33	7	0	0	0	0	0		P55144
ENSMUST00000110784	ENSMUSG00000029576	5	142484839	142551098	-1	8	0	7	111	37	0	0	0	0	0	0		Q69Z89
ENSMUST00000110785	ENSMUSG00000029576	5	142484839	142551098	-1	8	0	12	0	0	13	0	0	0	0	0	D3YWJ9	
ENSMUST00000110793	ENSMUSG00000034032	2	119763304	119787537	-1	50	31	100	40	34	27	3	36	0	0	17		Q80TE0
ENSMUST00000110797						10	5	3	21	5	2	0	0	0	1	1		
ENSMUST00000110798						1	0	0	35	3	0	13	363	4	0	0		
ENSMUST00000110800	ENSMUSG00000071176	8	14911663	15001085	1	0	0	24	0	0	8	0	0	0	0	14		Q8C033
ENSMUST00000110801	ENSMUSG00000027305	2	119655446	119662827	-1	10	0	0	6	0	3	0	0	0	0	0	A2AQ17	
ENSMUST00000110802	ENSMUSG00000027305	2	119655446	119662827	-1	0	0	0	0	0	0	48	161	41	77	28	A2AQ17	
ENSMUST00000110805						16	13	20	35	11	8	0	12	7	5	5		
ENSMUST00000110806	ENSMUSG00000000148	5	140705011	140719379	1	34	13	117	30	37	11	59	42	37	0	78		Q8C3R1
ENSMUST00000110808	ENSMUSG00000034154	2	119373042	119477687	-1	3	3	3	0	2	2	0	0	0	0	0	Z4YL66	
ENSMUST00000110811	ENSMUSG00000019256	12	35497974	35535038	-1	0	2	1	0	1	0	3	11	109	0	35	A0A0B4J1L1	
ENSMUST00000110813	ENSMUSG00000051978	8	14027565	14090327	-1	36	41	147	89	38	12	85	237	152	147	89	E9PY43	
ENSMUST00000110815	ENSMUSG00000016494	1	194938819	194961279	1	15	9	7	3	12	0	13	136	28	12	31	Q543Y2	Q64314
ENSMUST00000110816	ENSMUSG00000027315	2	119237362	119249527	1	0	0	0	94	3	0	1	6	1	0	11		Q9R097
ENSMUST00000110817	ENSMUSG00000027315	2	119237362	119249527	1	9	0	25	152	12	7	0	0	64	0	0		Q9R097
ENSMUST00000110819	ENSMUSG00000004698	12	34371503	34528889	-1	19	13	17	7	19	9	0	2	4	18	8		
ENSMUST00000110820	ENSMUSG00000027317	2	119218119	119229906	-1	0	0	0	4	0	1	0	0	0	0	0		Q7TT52
ENSMUST00000110824	ENSMUSG00000020564	12	33147693	33375659	1	0	0	12	0	0	4	0	0	0	47	0		Q9CZ05
ENSMUST00000110825	ENSMUSG00000036639	5	140321656	140338137	1	4	0	3	5	3	1	0	0	0	0	2	D3YWH7	
ENSMUST00000110826	ENSMUSG00000036639	5	140321656	140338137	1	0	4	0	2	0	0	11	8	11	0	0		P53368
ENSMUST00000110827	ENSMUSG00000036639	5	140321656	140338137	1	0	0	2	4	2	0	7	0	0	37	0		P53368
ENSMUST00000110828						25	32	22	40	31	15	3	19	5	7	2		
ENSMUST00000110829	ENSMUSG00000029554	5	140008689	140321552	-1	0	0	49	0	0	13	0	0	0	0	0		Q9WTX8
ENSMUST00000110831	ENSMUSG00000079144	1	193168046	193177832	1	0	0	0	1	0	0	0	0	0	6	0		Q9DAE8
ENSMUST00000110832	ENSMUSG00000036687	5	139802485	139819917	-1	29	33	70	53	50	24	0	0	0	0	3		Q3UFJ6
ENSMUST00000110833	ENSMUSG00000039983	2	119017779	119029393	-1	2	0	0	3	0	0	0	0	0	0	0		Q8BS39
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ENSMUST00000110835	ENSMUSG00000036461	14	79481194	79582476	1	3	25	55	0	13	23	615	1927	1317	680	1062	Q3V1H4	Q60775
ENSMUST00000110836	ENSMUSG00000018143	5	139791513	139802653	1	11	7	47	24	29	9	0	32	22	0	54	Q3UP84	Q61827
ENSMUST00000110837	ENSMUSG00000074916	2	118926496	118928585	1	0	6	36	0	0	0	0	72	0	9	26	A2AQV2	
ENSMUST00000110838	ENSMUSG00000038506	8	13255963	13288131	-1	0	0	0	23	0	0	27	57	0	18	77	G5E8Q5	
ENSMUST00000110839	ENSMUSG00000038506	8	13255963	13288131	-1	0	0	0	0	0	0	14	0	0	0	0	G5E8Q6	
ENSMUST00000110840	ENSMUSG00000038506	8	13255963	13288131	-1	17	11	12	93	27	12	48	39	91	43	28		Q8BZJ7
ENSMUST00000110842	ENSMUSG00000027331	2	118814003	118853957	1	3	6	2	115	7	0	2	0	9	33	33	A3KGG8	
ENSMUST00000110843	ENSMUSG00000040035	2	118779719	118811293	1	38	30	295	45	51	31	2	0	0	0	1	A3KGG1	
ENSMUST00000110844	ENSMUSG00000058248	1	192190774	192510159	1	0	0	0	83	0	0	0	0	0	0	0	Q3UHC9	
ENSMUST00000110846	ENSMUSG00000040035	2	118779719	118811293	1	0	0	5	12	3	1	0	0	0	0	0		Q8CIP5
ENSMUST00000110849	ENSMUSG00000037395	1	192098546	192138062	-1	0	0	0	0	0	0	25	0	54	0	0		Q6PGA0
ENSMUST00000110851	ENSMUSG00000053581	5	139471211	139484549	-1	0	34	159	0	29	0	132	175	200	71	97		Q9JII7
ENSMUST00000110853	ENSMUSG00000074923	2	118663303	118698020	1	21	16	154	270	75	54	3	13	12	2	12		Q3ULB5
ENSMUST00000110854	ENSMUSG00000001225	12	31390871	31473917	1	0	0	0	0	0	1	0	0	0	0	0	E9PY22	
ENSMUST00000110855	ENSMUSG00000026623	1	191717834	191784255	1	21	19	47	34	27	16	928	2110	1665	136	1086		Q91YX5
ENSMUST00000110856	ENSMUSG00000026623	1	191717834	191784255	1	0	5	0	0	0	1	56	5	141	0	33	E9QL80	
ENSMUST00000110857	ENSMUSG00000020664	12	31331564	31351437	-1	8	7	18	46	9	5	286	1348	542	1022	308		O08749
ENSMUST00000110859	ENSMUSG00000040093	2	118528757	118549687	-1	13	6	63	15	13	6	8	8	31	0	0	A2AV74	
ENSMUST00000110862	ENSMUSG00000009549	2	118475850	118479711	-1	2	2	3	3	0	0	2	7	0	0	0	A2AUM6	
ENSMUST00000110865	ENSMUSG00000056413	5	139271876	139325622	-1	6	6	0	32	0	0	569	405	432	44	247	E9PY16	
ENSMUST00000110866	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	0	0	0	9	0	0	0	E9PY13	
ENSMUST00000110867	ENSMUSG00000031442	8	12873806	13020905	1	4	4	24	6	13	4	0	7	0	0	0	E9PY12	
ENSMUST00000110869	ENSMUSG00000005102	2	118388618	118475234	1	4	8	11	1	14	4	0	2	0	0	1		Q9QZ05
ENSMUST00000110870	ENSMUSG00000005102	2	118388618	118475234	1	11	6	37	16	25	10	0	0	0	0	0		Q9QZ05
ENSMUST00000110871	ENSMUSG00000031442	8	12873806	13020905	1	17	2	0	34	11	9	0	0	0	0	0	D3YUF4	
ENSMUST00000110872	ENSMUSG00000005102	2	118388618	118475234	1	3	0	0	3	0	2	11	35	16	0	29	A2AUM2	
ENSMUST00000110873	ENSMUSG00000031442	8	12873806	13020905	1	0	5	0	8	10	0	34	27	19	0	11	D3YUF3	
ENSMUST00000110874	ENSMUSG00000005102	2	118388618	118475234	1	7	7	6	9	21	6	0	0	0	9	0	A2AUM1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000110876	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	5	0	0	0	0	0	0	0	E9PXE2	
ENSMUST00000110877	ENSMUSG00000005102	2	118388618	118475234	1	9	9	4	37	12	0	0	0	0	0	0	A2AUL9	
ENSMUST00000110878	ENSMUSG00000025858	5	139252324	139270051	1	1	0	2	16	0	0	445	501	325	100	308		Q9D1H7
ENSMUST00000110879	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	0	0	6	0	0	0	0	E9PXE1	
ENSMUST00000110880	ENSMUSG00000020669	12	30911668	30960162	1	0	0	0	0	0	0	0	0	0	0	0		O08641
ENSMUST00000110882	ENSMUSG00000036817	5	139200637	139249840	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0V9	
ENSMUST00000110883	ENSMUSG00000036817	5	139200637	139249840	1	0	0	0	0	8	0	0	273	85	23	134		Q9D666
ENSMUST00000110884	ENSMUSG00000036817	5	139200637	139249840	1	11	0	9	0	0	0	106	86	18	5	71		Q9D666
ENSMUST00000110888	ENSMUSG00000022010	14	76414961	76507765	1	0	0	0	85	6	0	0	0	0	0	0	D3Z0V7	
ENSMUST00000110889	ENSMUSG00000025855	5	139017306	139150001	-1	11	17	0	4	28	18	1	3	0	1	0	D3Z0V6	
ENSMUST00000110890	ENSMUSG00000025855	5	139017306	139150001	-1	0	8	46	10	0	0	0	0	0	0	0		P12849
ENSMUST00000110891	ENSMUSG00000026632	1	191045826	191062932	-1	0	0	3	0	0	0	0	0	0	0	0	D3Z0V5	
ENSMUST00000110893	ENSMUSG00000026632	1	191045826	191062932	-1	0	0	2	16	0	5	0	16	0	0	26	E9QL22	
ENSMUST00000110894	ENSMUSG00000060126	14	75845093	75848525	1	0	0	10	185	0	9	559	8736	9083	13057	4991		P63028
ENSMUST00000110896	ENSMUSG00000025856	5	138976014	138997370	-1	5	0	3	78	11	3	0	0	0	0	0	Q99L56	
ENSMUST00000110897	ENSMUSG00000025856	5	138976014	138997370	-1	2	2	0	70	0	0	0	0	2	4	0	Q99L56	
ENSMUST00000110898						0	4	10	103	5	8	0	1	1	0	5		
ENSMUST00000110899	ENSMUSG00000026634	1	190925112	190946962	1	4	0	0	0	0	0	0	0	0	37	0		Q8K1C0
ENSMUST00000110901	ENSMUSG00000027351	2	117121374	117182279	1	3	4	0	15	1	0	0	0	0	0	0		Q924S8
ENSMUST00000110904	ENSMUSG00000031511	8	11728105	11835219	1	15	12	21	2	0	0	21	33	0	0	13	D3Z0V2	
ENSMUST00000110905	ENSMUSG00000058291	5	138603652	138619761	-1	5	0	7	22	7	0	40	349	40	51	50	Q9Z116	
ENSMUST00000110906	ENSMUSG00000027210	2	115863064	116065839	-1	0	30	36	139	32	0	0	0	0	0	0	B1AWK4	
ENSMUST00000110907	ENSMUSG00000027210	2	115863064	116065839	-1	0	2	3	0	0	7	0	0	0	0	4		P97367
ENSMUST00000110908	ENSMUSG00000027210	2	115863064	116065839	-1	0	0	0	43	4	0	0	3	0	0	0	Q3UJ35	P97367
ENSMUST00000110909	ENSMUSG00000031511	8	11728105	11835219	1	21	23	38	34	22	16	16	12	27	0	30		Q9ES28
ENSMUST00000110912	ENSMUSG00000036898	5	138441468	138460694	1	0	0	1	5	0	0	0	0	0	1	0	D3Z0U7	
ENSMUST00000110917	ENSMUSG00000020636	12	28553755	28582523	-1	0	9	11	0	0	7	0	0	0	0	0		Q9JHX6
ENSMUST00000110918	ENSMUSG00000040282	2	115581716	115778768	1	26	0	0	0	0	19	11	14	14	7	0		Q3U4G0
ENSMUST00000110920	ENSMUSG00000037624	1	189207930	189402273	-1	0	0	0	86	9	0	0	0	0	0	0		P97438
ENSMUST00000110929	ENSMUSG00000047592	5	138225898	138253363	1	0	0	0	0	0	0	0	0	0	53	0	E9PXC9	
ENSMUST00000110932	ENSMUSG00000036968	5	138187485	138193918	1	6	6	11	6	6	0	3	14	0	0	0	D3Z0T5	
ENSMUST00000110934	ENSMUSG00000036968	5	138187485	138193918	1	10	6	16	15	13	2	68	249	95	263	121		Q8BQ47
ENSMUST00000110936	ENSMUSG00000036980	5	138178617	138187451	-1	0	2	0	0	2	1	0	0	1	5	0		Q62311
ENSMUST00000110937	ENSMUSG00000036980	5	138178617	138187451	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z0T0	
ENSMUST00000110938	ENSMUSG00000026610	1	187608791	188214885	1	0	0	0	4	0	0	0	0	0	0	0		P62509
ENSMUST00000110939	ENSMUSG00000026610	1	187608791	188214885	1	11	17	32	70	21	10	0	0	0	0	0		P62509
ENSMUST00000110942	ENSMUSG00000020646	12	24831599	24960301	1	0	0	21	28	0	0	0	0	3	0	0		Q8R3I2
ENSMUST00000110943	ENSMUSG00000039210	1	187215508	187351704	1	0	0	0	0	20	19	0	73	18	0	14		Q7TQC7
ENSMUST00000110945	ENSMUSG00000026611	1	187044648	187215465	-1	0	0	0	0	0	4	0	0	0	0	0		Q9D552
ENSMUST00000110947	ENSMUSG00000041219	2	113831492	113848661	-1	0	3	0	6	0	0	21	7	0	26	23	A2AL19	
ENSMUST00000110948	ENSMUSG00000041219	2	113831492	113848661	-1	41	37	91	225	45	25	19	68	128	49	206	A2AL18	
ENSMUST00000110949	ENSMUSG00000041219	2	113831492	113848661	-1	11	9	10	0	7	0	37	288	209	0	94		Q80Y19
ENSMUST00000110951	ENSMUSG00000019494	5	138161071	138164646	1	0	0	0	5	0	0	394	688	315	430	236	D3Z0F5	
ENSMUST00000110952	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	0	2	0	19	58	69	130	66	G1EE51	Q99LJ7
ENSMUST00000110954						7	14	12	13	8	8	0	0	0	0	0		
ENSMUST00000110959	ENSMUSG00000037017	5	138116903	138134265	1	6	14	34	39	20	12	4	0	3	4	0		Q07231
ENSMUST00000110960	ENSMUSG00000037017	5	138116903	138134265	1	14	4	12	7	4	0	30	62	0	62	47		Q07231
ENSMUST00000110961	ENSMUSG00000037017	5	138116903	138134265	1	0	0	0	0	0	0	0	0	21	0	0		Q07231
ENSMUST00000110962	ENSMUSG00000029729	5	138085084	138107822	1	16	16	62	8	19	14	0	0	21	0	17		Q8BGS3
ENSMUST00000110963	ENSMUSG00000029729	5	138085084	138107822	1	0	9	46	19	0	0	45	81	82	0	46		Q8BGS3
ENSMUST00000110965	ENSMUSG00000026617	1	185332149	185357777	1	0	0	0	0	0	0	3	0	17	5	25	D3Z0E6	
ENSMUST00000110967	ENSMUSG00000075598	5	138053194	138066537	1	43	21	267	40	25	9	0	0	0	0	1	A0A087WSF2	
ENSMUST00000110969	ENSMUSG00000079157	8	9206001	9771018	-1	16	11	46	164	20	16	1	0	0	0	0		Q8CCS2
ENSMUST00000110971						24	20	109	775	59	28	0	0	1	0	1		
ENSMUST00000110973	ENSMUSG00000048280	13	67667437	67687071	-1	116	81	100	94	91	41	10	15	19	7	30	E9PWN4	
ENSMUST00000110974	ENSMUSG00000026618	1	185284726	185329396	-1	0	5	3	40	5	0	21	14	28	0	0	E9PWN3	
ENSMUST00000110975	ENSMUSG00000026618	1	185284726	185329396	-1	11	2	11	29	14	4	4	0	36	0	26	E9PWN2	
ENSMUST00000110978	ENSMUSG00000066684	5	137852147	137858106	-1	4	7	16	5	15	10	898	2592	938	2296	775		Q2YFS2
ENSMUST00000110980	ENSMUSG00000046245	5	137821952	137836281	-1	15	15	30	23	31	11	1048	1493	994	3777	909		Q2YFS3
ENSMUST00000110982	ENSMUSG00000023235	8	4325210	4360020	1	5	9	3	0	6	2	0	0	0	0	0	Q3V2F3	
ENSMUST00000110983	ENSMUSG00000029723	5	137745730	137768450	1	2	2	17	6	1	3	0	0	0	0	0	Q9DA18	
ENSMUST00000110984	ENSMUSG00000022099	14	70602184	70636048	-1	0	0	48	126	26	19	0	0	0	0	0		Q9WV69
ENSMUST00000110985	ENSMUSG00000029723	5	137745730	137768450	1	0	1	2	19	4	0	9	65	43	4	38	D3YZZ4	
ENSMUST00000110987	ENSMUSG00000027130	2	112265825	112363163	1	42	22	75	26	50	17	36	100	184	8	262	A2AGJ9	
ENSMUST00000110989						3	2	5	17	10	3	16	29	37	0	23		
ENSMUST00000110991	ENSMUSG00000027130	2	112265825	112363163	1	9	14	9	96	14	12	767	574	1890	40	1667	Q3V0N8	
ENSMUST00000110992	ENSMUSG00000026621	1	184786767	184811313	-1	4	2	11	84	14	11	0	0	0	0	0	D3YZZ3	
ENSMUST00000110993	ENSMUSG00000089736	8	4248214	4251423	1	0	2	24	124	10	5	11	28	14	0	31	D3YZZ2	
ENSMUST00000110994	ENSMUSG00000002948	8	4238740	4251423	1	0	11	15	0	0	8	85	57	66	65	100		Q8CE90
ENSMUST00000110995	ENSMUSG00000002948	8	4238740	4251423	1	0	0	0	5	0	7	0	0	0	0	0		Q8CE90
ENSMUST00000110996	ENSMUSG00000002948	8	4238740	4251423	1	0	0	2	2	4	0	5	0	30	0	40		Q8CE90
ENSMUST00000110997	ENSMUSG00000079164	1	182954788	182976044	1	0	0	0	0	14	0	99	246	126	16	162	E9QL10	
ENSMUST00000110998	ENSMUSG00000002948	8	4238740	4251423	1	0	0	0	124	0	0	80	282	239	0	226		Q8CE90
ENSMUST00000110999	ENSMUSG00000002948	8	4238740	4251423	1	0	0	0	0	0	0	0	0	0	0	0		Q8CE90
ENSMUST00000111002	ENSMUSG00000089984	5	137612503	137629002	-1	13	0	5	9	3	12	0	0	0	0	0	D3YZY9	
ENSMUST00000111004	ENSMUSG00000101322	2	111564504	111565442	-1	3	2	6	0	8	0	0	0	0	0	0	Q8VF48	
ENSMUST00000111007	ENSMUSG00000037221	5	137596645	137601058	-1	5	6	32	104	15	4	611	733	441	64	311	Q05DT5	Q8BGG6
ENSMUST00000111014	ENSMUSG00000065987	8	3917655	3926844	-1	0	0	0	0	13	0	0	0	0	7	3	Q8CJ85	
ENSMUST00000111016	ENSMUSG00000050808	2	110721340	110739527	1	10	21	10	21	21	0	0	0	0	0	0	Q0VEM9	Q8C6Z1
ENSMUST00000111017	ENSMUSG00000050808	2	110721340	110739527	1	15	0	90	0	7	9	1	0	0	0	2	A2AHK7	
ENSMUST00000111018	ENSMUSG00000026511	1	182124737	182132407	1	0	0	0	21	1	0	355	1162	519	983	176	D3YZX8	
ENSMUST00000111019						3	2	0	4	0	2	0	0	0	0	0		
ENSMUST00000111020	ENSMUSG00000029713	5	137528127	137533510	-1	0	0	2	3	0	0	2196	3111	2406	333	1774	D3YZX3	
ENSMUST00000111023	ENSMUSG00000029713	5	137528127	137533510	-1	0	0	1	0	0	0	0	0	0	0	0	D3YZX3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000111024	ENSMUSG00000022995	1	181896384	182019990	-1	0	0	0	0	0	0	16	0	38	4	22	E9QKR1	
ENSMUST00000111025	ENSMUSG00000022995	1	181896384	182019990	-1	0	0	0	0	0	0	0	0	0	0	0		Q03173
ENSMUST00000111026	ENSMUSG00000041644	2	110597298	110647779	1	0	0	0	0	0	0	0	0	0	0	0	B9EJ03	Q49B93
ENSMUST00000111027	ENSMUSG00000029713	5	137528127	137533510	-1	0	0	0	0	0	0	3286	2626	2336	513	2094	E9QKR0	
ENSMUST00000111030	ENSMUSG00000022995	1	181896384	182019990	-1	4	0	0	0	0	0	0	0	0	0	0	E9QKQ9	
ENSMUST00000111035	ENSMUSG00000029715	5	137501438	137502518	-1	4	3	20	28	11	6	14	46	6	4	10		Q9DCH2
ENSMUST00000111037	ENSMUSG00000050199	2	109917647	110014257	1	0	14	33	0	0	16	6	15	0	7	9		A2ARI4
ENSMUST00000111038	ENSMUSG00000029711	5	137483020	137533242	-1	0	4	8	40	0	0	0	0	0	0	0	Q0VED9	P07321
ENSMUST00000111039	ENSMUSG00000029711	5	137483020	137533242	-1	2	0	0	0	5	2	0	0	0	0	0	B7ZMY9	
ENSMUST00000111042	ENSMUSG00000048482	2	109674700	109727007	1	3	4	0	0	0	3	0	0	0	0	0	H9H9S8	
ENSMUST00000111043	ENSMUSG00000048482	2	109674700	109727007	1	0	5	0	7	4	3	0	0	0	0	0	Q541P3	P21237
ENSMUST00000111044	ENSMUSG00000048482	2	109674700	109727007	1	0	0	0	4	0	0	0	0	0	0	0	Q541P3	P21237
ENSMUST00000111045	ENSMUSG00000048482	2	109674700	109727007	1	6	2	10	139	8	10	0	0	0	0	0	Q541P3	P21237
ENSMUST00000111046	ENSMUSG00000048482	2	109674700	109727007	1	3	0	15	32	0	3	0	0	0	0	0	Q541P3	P21237
ENSMUST00000111047	ENSMUSG00000048482	2	109674700	109727007	1	0	0	0	0	0	2	0	0	0	0	0	Q541P3	P21237
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ENSMUST00000111050	ENSMUSG00000048482	2	109674700	109727007	1	6	9	0	2	2	2	0	0	0	0	0	Q541P3	P21237
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ENSMUST00000111054	ENSMUSG00000029710	5	137350109	137378669	1	12	13	17	0	13	5	0	0	2	0	9	E9PWK7	
ENSMUST00000111055	ENSMUSG00000029710	5	137350109	137378669	1	0	8	14	14	0	0	0	0	0	17	0	Q8C8K1	
ENSMUST00000111057						3	0	15	0	2	0	103	453	44	380	8		
ENSMUST00000111059	ENSMUSG00000062169	1	181144693	181168994	1	21	25	28	95	32	28	0	42	73	75	0	D3YZJ3	
ENSMUST00000111062						3	3	6	40	4	0	0	0	0	0	0		
ENSMUST00000111063	ENSMUSG00000016386	2	106693269	106868356	1	8	9	1	158	11	6	0	0	0	0	0	B1APT2	Q9CZJ0
ENSMUST00000111064	ENSMUSG00000020591	12	16653470	16660236	1	11	6	23	103	22	2	0	0	0	0	0		P70310
ENSMUST00000111067	ENSMUSG00000020593	12	16535669	16589770	-1	32	10	62	6	14	32	11	0	0	1	14	E9QKQ5	
ENSMUST00000111068	ENSMUSG00000038776	1	180976210	181020904	-1	0	0	18	0	11	4	0	19	0	24	22	E9PWK1	
ENSMUST00000111070	ENSMUSG00000004565	8	3515384	3544266	1	0	16	74	105	33	23	151	116	115	0	124		Q3TRM4
ENSMUST00000111072	ENSMUSG00000014725	14	68606027	68655842	-1	101	142	374	112	99	44	4	17	3	0	10		Q9JLN6
ENSMUST00000111079						0	0	0	0	1	0	0	1	0	0	0		
ENSMUST00000111080	ENSMUSG00000004849	5	137034993	137046135	-1	7	10	7	82	10	3	491	716	314	285	260		P61967
ENSMUST00000111081	ENSMUSG00000069633	8	3457105	3467680	-1	7	0	0	5	0	1	0	0	1	0	0		Q6P6M5
ENSMUST00000111082	ENSMUSG00000027168	2	105668900	105697364	1	0	0	0	0	0	0	0	0	0	0	0		P63015
ENSMUST00000111083	ENSMUSG00000027168	2	105668900	105697364	1	0	0	0	0	0	0	0	0	0	0	0		P63015
ENSMUST00000111085	ENSMUSG00000027168	2	105668900	105697364	1	0	0	0	0	0	0	0	0	0	0	0		P63015
ENSMUST00000111086	ENSMUSG00000027168	2	105668900	105697364	1	0	0	0	0	0	0	0	0	0	0	0		P63015
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ENSMUST00000111088	ENSMUSG00000027168	2	105668900	105697364	1	171	84	166	1646	297	149	1	2	5	2	5	A2A412	
ENSMUST00000111089	ENSMUSG00000022054	14	68082590	68124846	-1	42	26	60	1008	58	38	0	1	0	0	5	D3YZ35	
ENSMUST00000111090	ENSMUSG00000059518	5	136982164	136988021	-1	0	2	7	2	2	1	173	316	137	225	138	D3YZ34	
ENSMUST00000111091	ENSMUSG00000059518	5	136982164	136988021	-1	0	6	0	12	5	2	11	19	9	7	30	D3YZ33	
ENSMUST00000111093	ENSMUSG00000001739	5	136966616	136975858	1	20	16	25	21	0	0	36	0	0	0	36		Q9Z0S5
ENSMUST00000111094	ENSMUSG00000019054	5	136953275	136966234	1	5	5	9	11	16	5	45	183	65	119	58	G3X9U9	
ENSMUST00000111095	ENSMUSG00000015812	14	67745229	67749435	1	4	7	8	3	6	2	4	8	2	3	7	Q3UTE9	P13562
ENSMUST00000111097	ENSMUSG00000019054	5	136953275	136966234	1	0	0	0	0	0	0	21	13	13	37	22	D3YZ32	
ENSMUST00000111098	ENSMUSG00000016458	2	105126529	105173616	1	2	0	0	0	0	0	0	1	0	3	3	A2A404	
ENSMUST00000111099	ENSMUSG00000016458	2	105126529	105173616	1	0	2	9	0	0	2	0	0	0	0	0	A2A405	
ENSMUST00000111103	ENSMUSG00000004415	5	136741759	136883209	-1	6	12	0	26	0	0	0	0	0	0	0		Q91VF6
ENSMUST00000111104	ENSMUSG00000010609	1	180227004	180263438	-1	0	0	0	0	0	0	62	45	31	0	21		
ENSMUST00000111105	ENSMUSG00000010609	1	180227004	180263438	-1	0	0	8	0	2	0	0	0	18	0	18	Q3U4P5	
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ENSMUST00000111107	ENSMUSG00000079175	2	105092018	105093760	1	5	4	21	3	1	1	0	0	0	0	0	F6X9U9	
ENSMUST00000111108	ENSMUSG00000010609	1	180227004	180263438	-1	0	0	0	51	0	0	889	1491	670	135	587	Q3U4P5	
ENSMUST00000111110	ENSMUSG00000027170	2	104999656	105017080	-1	3	0	0	31	4	2	0	61	0	5	0	A2A702	
ENSMUST00000111113	ENSMUSG00000066643	12	8973892	9028847	1	2	11	0	0	0	0	5	22	9	28	16		Q8BND3
ENSMUST00000111114	ENSMUSG00000045106	2	104867805	105017904	1	10	10	22	6	11	6	2	0	4	2	4		Q8CDM4
ENSMUST00000111115	ENSMUSG00000022051	14	66985239	67008877	-1	0	0	0	0	0	0	0	37	0	0	23	Q91Z78	
ENSMUST00000111117	ENSMUSG00000026490	1	179960472	180165603	1	0	15	16	0	0	12	0	0	19	2	7	E9PVY0	
ENSMUST00000111118	ENSMUSG00000027175	2	104657288	104712169	-1	38	30	42	25	28	11	50	172	167	11	110		Q8BTG3
ENSMUST00000111121	ENSMUSG00000059456	14	66153257	66281052	-1	17	0	21	0	0	0	0	0	47	0	204	Q3UDE9	
ENSMUST00000111122	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	2	26	0	1	828	1126	165	353	Q3UR91	
ENSMUST00000111123	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	0	0	0	63	0	0	0	0	Q3UR91	
ENSMUST00000111124	ENSMUSG00000027177	2	104426481	104494446	-1	7	5	59	150	36	5	39	10	110	0	105		Q9ERH7
ENSMUST00000111125	ENSMUSG00000027177	2	104426481	104494446	-1	0	1	0	0	0	0	158	41	1044	23	538	A2AQH3	
ENSMUST00000111127	ENSMUSG00000039771	5	136116631	136122947	1	6	5	13	16	4	2	6	13	0	6	8	D3YZ20	
ENSMUST00000111129	ENSMUSG00000039771	5	136116631	136122947	1	3	0	3	27	0	0	0	7	17	14	0	D3YZ19	
ENSMUST00000111130	ENSMUSG00000068686	2	104069849	104091187	1	4	4	13	8	7	2	0	2	0	0	0		P58019
ENSMUST00000111131	ENSMUSG00000068686	2	104069849	104091187	1	366	337	166	221	358	180	40	181	73	37	96	A2BI28	
ENSMUST00000111132	ENSMUSG00000068686	2	104069849	104091187	1	192	169	85	37	176	94	0	1	5	6	0	Q6PBG1	
ENSMUST00000111134	ENSMUSG00000055067	1	178951960	179518041	-1	3	6	0	19	4	3	13	21	15	4	11	D3YZ17	
ENSMUST00000111135	ENSMUSG00000027180	2	104027721	104063240	1	0	3	0	6	0	0	0	36	0	0	0		Q9DC63
ENSMUST00000111136	ENSMUSG00000027180	2	104027721	104063240	1	0	1	0	2	11	6	146	0	32	14	95	A2BHN6	
ENSMUST00000111137	ENSMUSG00000006143	5	136054492	136064326	1	6	0	25	14	9	4	0	0	0	0	0	D3YZ16	
ENSMUST00000111139	ENSMUSG00000032698	2	103957986	103981878	1	0	0	0	96	4	1	0	76	0	0	0	A2BHP1	
ENSMUST00000111140	ENSMUSG00000032698	2	103957986	103981878	1	0	0	0	3	0	0	0	0	9	0	0	A2BHP3	
ENSMUST00000111142	ENSMUSG00000004947	5	135994800	136032872	1	5	0	0	33	9	0	211	264	51	30	151		Q8R3P2
ENSMUST00000111143	ENSMUSG00000032698	2	103957986	103981878	1	0	0	0	10	0	2	0	15	13	39	26	A2BHP5	
ENSMUST00000111144	ENSMUSG00000004947	5	135994800	136032872	1	0	8	0	0	0	0	0	0	0	0	0		Q8R3P2
ENSMUST00000111145	ENSMUSG00000004947	5	135994800	136032872	1	0	0	7	28	0	4	98	8	50	0	29		Q8R3P2
ENSMUST00000111147	ENSMUSG00000027184	2	103762941	103797649	-1	7	2	3	80	0	8	1039	3134	1663	385	1018		Q60865
ENSMUST00000111150	ENSMUSG00000029699	5	135960211	135974531	-1	3	4	5	2	0	0	0	0	9	0	0	D3YZ07	
ENSMUST00000111152	ENSMUSG00000029699	5	135960211	135974531	-1	0	1	13	109	0	3	0	2	0	0	0		A1L0T3
ENSMUST00000111153	ENSMUSG00000029699	5	135960211	135974531	-1	9	1	13	109	5	3	0	2	0	0	0		A1L0T3
ENSMUST00000111154	ENSMUSG00000079177	12	4713817	4738383	-1	17	12	48	48	22	10	1	1	1	0	1		Q8CDW1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000111155	ENSMUSG00000004951	5	135887919	135889563	1	5	4	6	40	9	8	0	0	0	0	0	D3YZ06	
ENSMUST00000111159	ENSMUSG00000019699	1	177020073	177258203	-1	31	21	18	29	24	5	29	65	76	0	114		Q9WUA6
ENSMUST00000111160	ENSMUSG00000019699	1	177020073	177258203	-1	0	0	0	0	4	0	21	88	0	23	0		Q9WUA6
ENSMUST00000111161	ENSMUSG00000019178	5	135747220	135778385	-1	0	0	0	0	0	0	0	0	0	0	0	Q9DAG7	
ENSMUST00000111162	ENSMUSG00000019178	5	135747220	135778385	-1	0	0	0	1	0	0	0	2	0	0	0	D3YZ02	
ENSMUST00000111163	ENSMUSG00000019178	5	135747220	135778385	-1	1	0	2	16	2	0	9	40	9	0	28	Q9DAR2	
ENSMUST00000111164	ENSMUSG00000019178	5	135747220	135778385	-1	0	0	0	0	0	0	0	12	9	21	8	Q9DAR2	
ENSMUST00000111166	ENSMUSG00000055214	1	175962306	176275312	-1	1	2	5	54	0	0	0	0	0	0	0	D3YZ01	
ENSMUST00000111167	ENSMUSG00000055214	1	175962306	176275312	-1	3	0	5	0	4	0	0	0	0	0	0	D3YYN6	
ENSMUST00000111168	ENSMUSG00000027187	2	103453849	103485160	-1	0	0	0	21	3	3	0	0	28	26	36	A2AL20	
ENSMUST00000111169	ENSMUSG00000020652	12	4196004	4234294	-1	6	4	3	3	1	5	0	4	6	0	14		Q8K015
ENSMUST00000111171	ENSMUSG00000053293	5	135376141	135394546	-1	0	0	113	278	82	0	678	487	672	0	566	Q3U425	Q8K3Z9
ENSMUST00000111174	ENSMUSG00000012350	2	103263433	103303278	-1	0	3	3	0	3	4	0	0	0	0	0		O70273
ENSMUST00000111176	ENSMUSG00000012350	2	103263433	103303278	-1	23	25	111	102	27	27	2	1	1	0	3	A2BIB5	
ENSMUST00000111178	ENSMUSG00000020658	12	3962554	4038915	-1	66	56	247	158	81	34	9	17	12	0	12		Q6ZQ18
ENSMUST00000111180	ENSMUSG00000053388	5	135353295	135368005	1	0	0	0	0	0	0	0	0	0	0	0	E9PVV5	
ENSMUST00000111183	ENSMUSG00000010914	2	103021075	103073513	-1	212	187	594	231	313	126	2	17	9	2	19	A2AWH8	
ENSMUST00000111186	ENSMUSG00000020661	12	3806007	3914443	1	6	0	0	0	0	0	0	0	0	0	0		O88508
ENSMUST00000111187	ENSMUSG00000029681	5	135168283	135181855	1	3	2	1	35	4	3	11	27	12	30	10		Q921K9
ENSMUST00000111188	ENSMUSG00000029681	5	135168283	135181855	1	4	4	10	0	4	2	0	0	0	6	0	D3YYL1	
ENSMUST00000111190	ENSMUSG00000005087	2	102811141	102901665	-1	0	0	0	0	0	0	15	0	18	0	0	A2APM3	
ENSMUST00000111191	ENSMUSG00000005087	2	102811141	102901665	-1	0	0	0	0	0	0	0	0	0	0	0	A2APM4	
ENSMUST00000111192	ENSMUSG00000005087	2	102811141	102901665	-1	0	0	0	0	4	0	784	59	1558	2356	2003	A2APM5	
ENSMUST00000111194	ENSMUSG00000005087	2	102811141	102901665	-1	0	0	68	49	26	8	4084	11852	3210	840	2530	E9QKM8	
ENSMUST00000111198	ENSMUSG00000005087	2	102811141	102901665	-1	0	0	0	0	0	0	5	3	11	5	13	A2APM1	
ENSMUST00000111203	ENSMUSG00000054763	14	63046991	63058149	1	0	2	0	2	0	1	0	0	0	0	0	Q8BVB5	Q8BVB5
ENSMUST00000111205	ENSMUSG00000005378	5	135052957	135064959	-1	0	0	0	0	0	0	22	55	5	26	76	D3YYK7	
ENSMUST00000111207	ENSMUSG00000075571	14	63034087	63049960	-1	3	0	0	0	3	0	0	0	0	0	0		Q30KN4
ENSMUST00000111208	ENSMUSG00000075571	14	63034087	63049960	-1	0	1	4	2	2	0	0	0	0	0	0	D3YYK2	
ENSMUST00000111209	ENSMUSG00000075571	14	63034087	63049960	-1	0	0	5	2	0	0	0	0	0	0	0	D3YYK2	
ENSMUST00000111210	ENSMUSG00000090272	1	173857220	173942491	-1	0	0	0	0	0	0	0	462	52	70	123		D0QMC3
ENSMUST00000111212	ENSMUSG00000005089	2	102658659	102790784	1	0	0	0	0	0	0	0	0	0	0	0	A2APL8	P43006
ENSMUST00000111213	ENSMUSG00000005089	2	102658659	102790784	1	0	0	5	1	0	3	0	0	0	0	1	A2APL5	
ENSMUST00000111214	ENSMUSG00000073489	1	173747293	173766943	-1	2	5	19	13	11	5	25	362	26	463	188	E9QKL6	
ENSMUST00000111215	ENSMUSG00000037486	12	3426857	3506852	1	0	0	0	0	0	0	140	398	183	47	117	F6WV21	
ENSMUST00000111216	ENSMUSG00000040532	5	135009152	135012175	1	3	0	1	2	0	0	181	259	184	183	112	D3YYK0	
ENSMUST00000111218	ENSMUSG00000040557	5	134932368	134942637	1	0	0	0	2	0	0	9	3	0	2	2	Q8BGM4	
ENSMUST00000111219	ENSMUSG00000040557	5	134932368	134942637	1	0	2	0	0	0	0	9	14	0	0	11	Q8BGM4	
ENSMUST00000111220	ENSMUSG00000005338	1	173333258	173367695	-1	27	29	80	55	33	17	0	0	0	0	0		Q99N28
ENSMUST00000111221	ENSMUSG00000040557	5	134932368	134942637	1	0	0	0	7	0	0	0	0	6	0	0	Q8BY07	
ENSMUST00000111222	ENSMUSG00000048058	2	101950203	102186385	-1	32	21	93	0	37	20	53	136	5	9	28		A2AR95
ENSMUST00000111224	ENSMUSG00000079180	1	173274382	173277777	-1	3	0	3	4	2	3	0	0	0	0	0	D3YYJ7	
ENSMUST00000111227	ENSMUSG00000032864	2	101624718	101632529	1	0	0	0	0	0	0	0	0	0	0	0	Q542D1	P21784
ENSMUST00000111228	ENSMUSG00000026547	1	172500047	172507380	1	1	0	1	2	2	3	1639	9	579	87	527		Q9WVA4
ENSMUST00000111230	ENSMUSG00000026547	1	172500047	172507380	1	37	28	67	551	82	55	9386	4719	4684	1336	4408		Q9WVA4
ENSMUST00000111231	ENSMUSG00000027165	2	101560781	101649532	-1	13	9	4	11	8	2	0	4	0	0	2		Q9CQI4
ENSMUST00000111233	ENSMUSG00000029674	5	134656039	134688598	-1	9	0	41	19	21	16	76	83	1	19	68	E9PVB6	
ENSMUST00000111234	ENSMUSG00000060548	14	60963834	61046855	-1	30	15	34	82	28	14	2	0	0	12	15		Q9JLL3
ENSMUST00000111235	ENSMUSG00000037995	1	172481788	172498878	1	39	0	0	118	25	0	0	0	0	0	0		Q05BQ1
ENSMUST00000111236	ENSMUSG00000060548	14	60963834	61046855	-1	7	0	0	49	8	16	0	0	1	0	20		Q9JLL3
ENSMUST00000111237	ENSMUSG00000027194	2	94300767	94406689	-1	0	12	25	0	24	0	0	0	0	0	0		E9PVB5
ENSMUST00000111238	ENSMUSG00000027194	2	94300767	94406689	-1	21	0	0	40	0	10	175	0	307	0	208		E9PVB5
ENSMUST00000111240	ENSMUSG00000040174	2	93980550	94010807	-1	3	0	10	53	7	6	24	47	10	0	18	A2AKV6	
ENSMUST00000111243	ENSMUSG00000007107	1	172223513	172258414	-1	33	16	54	43	32	13	0	0	0	0	1		Q9WV27
ENSMUST00000111244	ENSMUSG00000023079	5	134357656	134456716	-1	5	7	25	9	4	12	36	45	5	0	0	Q6PD35	
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ENSMUST00000111246	ENSMUSG00000040272	2	93833467	93849943	-1	55	34	222	84	52	24	9	30	11	8	29		A2AIG8
ENSMUST00000111247	ENSMUSG00000013698	1	172196728	172206804	-1	10	0	3	32	0	0	0	0	30	0	0		Q62048
ENSMUST00000111248	ENSMUSG00000027198	2	93661028	93822568	-1	0	0	0	0	0	0	2	0	0	0	0	A2AIG6	
ENSMUST00000111252	ENSMUSG00000003464	1	172126755	172136493	1	9	7	3	15	8	3	124	416	107	12	73		Q8VCI5
ENSMUST00000111253	ENSMUSG00000071350	14	59402009	59440884	-1	3	4	0	1	4	4	4	1	0	0	0		Q8C267
ENSMUST00000111254	ENSMUSG00000040310	2	93642384	93681339	1	51	19	47	58	58	34	0	0	0	0	0	A2AIK5	
ENSMUST00000111256	ENSMUSG00000027215	2	93419111	93463140	-1	0	0	5	56	4	3	0	2	0	0	2	A2AIJ3	
ENSMUST00000111257	ENSMUSG00000027215	2	93419111	93463140	-1	0	0	2	0	8	2	693	0	540	0	367	Q3UII2	P40237
ENSMUST00000111261	ENSMUSG00000060261	5	134237834	134314760	-1	0	3	0	0	0	2	0	0	0	0	0		Q9ESZ8
ENSMUST00000111263	ENSMUSG00000026556	1	172000960	172028444	-1	31	39	78	385	63	39	0	0	0	0	0		Q91ZD4
ENSMUST00000111264	ENSMUSG00000026556	1	172000960	172028444	-1	0	0	0	8	0	0	8	0	0	0	0	D3YY75	
ENSMUST00000111265	ENSMUSG00000027217	2	93201760	93334505	-1	195	155	1322	278	157	104	3	8	4	2	14		Q80WR1
ENSMUST00000111266	ENSMUSG00000068735	2	93187548	93201759	1	0	0	0	46	0	7	35	0	0	25	29		Q4QQM4
ENSMUST00000111267	ENSMUSG00000021963	14	57798180	57804980	1	0	0	0	0	0	0	0	0	0	0	0	D3YY73	
ENSMUST00000111268	ENSMUSG00000021963	14	57798180	57804980	1	0	0	0	0	3	0	0	11	0	0	2	D3YY73	
ENSMUST00000111269	ENSMUSG00000021963	14	57798180	57804980	1	0	0	0	40	0	0	0	0	6	21	0	D3YY55	
ENSMUST00000111272	ENSMUSG00000075028	2	92965151	93046167	-1	17	13	32	61	23	8	48	72	53	9	43	A0A0A0MQD9	
ENSMUST00000111274	ENSMUSG00000075028	2	92965151	93046167	-1	146	77	531	260	151	66	11	29	35	4	27		A2AGX3
ENSMUST00000111275	ENSMUSG00000015950	5	134220053	134229625	-1	60	36	47	0	59	53	26409	33823	23856	4963	11041		Q09014
ENSMUST00000111276	ENSMUSG00000038179	1	171632403	171653035	-1	0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000111277	ENSMUSG00000004707	1	171588624	171607410	-1	4	0	3	0	4	2	18	38	15	5	23	E9PV93	
ENSMUST00000111278	ENSMUSG00000068742	2	92403646	92434043	-1	3	2	3	14	3	0	7	0	0	0	5		Q9R194
ENSMUST00000111279	ENSMUSG00000027223	2	92383676	92401263	-1	0	12	42	282	4	7	0	0	0	0	0		Q9WVI9
ENSMUST00000111280	ENSMUSG00000044916	2	92382538	92385708	1	5	2	2	2	4	3	0	0	0	0	0	Z4YL72	
ENSMUST00000111283						37	36	38	35	23	15	17	24	11	0	6		
ENSMUST00000111284	ENSMUSG00000040434	2	92365046	92374869	-1	3	6	13	0	16	0	0	0	0	0	0	A2AHG6	
ENSMUST00000111285	ENSMUSG00000040123	14	56790585	56811716	-1	31	67	185	0	68	0	91	291	200	73	152		Q3U2E2
ENSMUST00000111286	ENSMUSG00000006411	1	171370099	171388598	1	0	17	0	0	30	13	11	15	0	0	18		Q8R007

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000111287	ENSMUSG00000060371	5	130369455	130847412	1	2	5	23	7	9	1	0	2	0	0	0	Q542R1	Q9JJG7
ENSMUST00000111288	ENSMUSG00000060371	5	130369455	130847412	1	9	1	0	184	13	4	0	0	0	0	0	Q542R1	Q9JJG7
ENSMUST00000111289	ENSMUSG00000013997	1	171338008	171345646	-1	14	6	4	2	0	11	49	478	75	35	25		Q8VDK1
ENSMUST00000111290	ENSMUSG00000058318	2	92093117	92364666	1	1	0	4	0	0	0	0	0	0	0	9	E9QKW9	
ENSMUST00000111291	ENSMUSG00000058318	2	92093117	92364666	1	0	0	5	0	0	0	0	55	212	14	48	D3Z764	
ENSMUST00000111292	ENSMUSG00000058318	2	92093117	92364666	1	0	0	0	0	0	0	62	0	167	0	69	A2AHG3	
ENSMUST00000111293	ENSMUSG00000058318	2	92093117	92364666	1	5	0	0	0	0	0	344	1714	526	133	516	A2AHG2	
ENSMUST00000111294	ENSMUSG00000058318	2	92093117	92364666	1	0	6	8	25	3	6	78	95	74	0	95	A2AHG4	
ENSMUST00000111295	ENSMUSG00000013997	1	171338008	171345646	-1	0	1	0	0	1	0	165	304	154	35	144		Q8VDK1
ENSMUST00000111296	ENSMUSG00000013997	1	171338008	171345646	-1	0	0	0	0	0	0	0	0	0	0	0	D3YY53	
ENSMUST00000111297	ENSMUSG00000058318	2	92093117	92364666	1	0	0	17	0	0	0	0	119	0	0	51	E9PV92	
ENSMUST00000111298	ENSMUSG00000053094	5	130217081	130243765	1	0	0	0	50	0	0	59	527	107	59	234		Q3TBN1
ENSMUST00000111299	ENSMUSG00000013973	1	171329145	171342331	1	0	0	4	5	2	0	80	38	52	12	58	Q3U001	Q9Z1L3
ENSMUST00000111300	ENSMUSG00000013973	1	171329145	171342331	1	0	2	0	40	3	7	11	17	11	0	24	Q3U001	Q9Z1L3
ENSMUST00000111302	ENSMUSG00000062963	1	171288563	171295024	-1	2	0	0	0	0	0	0	0	22	0	68		Q9CR09
ENSMUST00000111303	ENSMUSG00000040479	2	91932824	91975864	-1	32	3	28	107	32	0	59	144	220	6	215	A2AHK0	
ENSMUST00000111305	ENSMUSG00000053483	1	171281945	171287991	-1	0	0	0	40	0	0	0	0	0	0	0	E9PUE2	
ENSMUST00000111306	ENSMUSG00000053483	1	171281945	171287991	-1	0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000111307	ENSMUSG00000025534	5	129989011	130003049	-1	0	0	1	2	1	0	0	4	0	0	0	D3YY48	
ENSMUST00000111308	ENSMUSG00000025534	5	129989011	130003049	-1	4	7	20	11	9	8	9	17	12	0	26	Q99KJ6	
ENSMUST00000111309	ENSMUSG00000027239	2	91929805	91932297	-1	2	0	0	0	0	0	6	1	0	11	0		P12025
ENSMUST00000111313	ENSMUSG00000052423	1	171270328	171276896	1	0	0	0	0	0	0	74	368	0	16	0	Q3U260	Q91YY2
ENSMUST00000111314	ENSMUSG00000006403	1	171250421	171260637	1	45	23	57	81	22	0	0	8	5	2	0	E9PV91	
ENSMUST00000111315	ENSMUSG00000006403	1	171250421	171260637	1	19	17	117	67	49	34	7	0	0	0	12	Q3TNX8	
ENSMUST00000111316	ENSMUSG00000040506	2	91730134	91918849	1	0	0	0	0	3	14	0	0	0	0	0		A2AH22
ENSMUST00000111317	ENSMUSG00000040506	2	91730134	91918849	1	0	0	0	0	0	0	0	0	0	20	0		A2AH22
ENSMUST00000111318	ENSMUSG00000013593	1	171234853	171251388	-1	0	0	0	24	0	7	16	42	0	10	0	D3YXT0	
ENSMUST00000111319	ENSMUSG00000005681	1	171225054	171226379	1	0	0	9	0	3	4	0	0	0	0	5		P09813
ENSMUST00000111320	ENSMUSG00000005681	1	171225054	171226379	1	0	2	6	0	2	0	0	0	0	0	0		P09813
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ENSMUST00000111322	ENSMUSG00000027243	2	91710852	91721545	1	2	3	0	4	3	1	2	9	11	0	12		Q8BR93
ENSMUST00000111325	ENSMUSG00000022223	14	55897286	55900232	-1	7	6	24	29	19	9	357	1102	587	63	580		Q5M8N4
ENSMUST00000111326	ENSMUSG00000005674	1	171216011	171222514	-1	0	0	0	0	0	0	0	0	0	0	0	D3YXS8	
ENSMUST00000111327	ENSMUSG00000005674	1	171216011	171222514	-1	3	0	0	6	0	3	48	159	48	26	68		Q9CZR3
ENSMUST00000111328	ENSMUSG00000005677	1	171213970	171220701	1	0	0	0	0	0	0	0	0	0	0	0	Q5FW96	
ENSMUST00000111329	ENSMUSG00000027247	2	91649860	91672326	1	23	11	8	72	10	4	148	38	170	17	92		Q5FWK3
ENSMUST00000111330	ENSMUSG00000027247	2	91649860	91672326	1	9	12	39	13	22	9	13	83	48	14	51		Q5FWK3
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ENSMUST00000111333	ENSMUSG00000075040	2	91643669	91649791	-1	14	27	96	162	58	34	62	0	42	0	170	Q3V1D8	
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ENSMUST00000111335	ENSMUSG00000027249	2	91625320	91636414	-1	9	0	0	15	0	8	1	0	1	25	1	H7BX99	
ENSMUST00000111336	ENSMUSG00000058076	1	171127165	171150603	-1	39	23	52	43	54	29	262	340	199	70	148		Q9CZB0
ENSMUST00000111337	ENSMUSG00000040549	2	91526762	91620664	1	0	0	27	0	0	0	0	0	0	0	0	Z4YL78	
ENSMUST00000111338	ENSMUSG00000040549	2	91526762	91620664	1	20	10	0	38	27	13	145	73	218	73	258	K3W4R5	
ENSMUST00000111343	ENSMUSG00000029430	5	129020069	129024323	1	0	0	0	186	0	0	22	127	53	0	29		P62827
ENSMUST00000111346	ENSMUSG00000029420	5	128757791	128953486	-1	183	113	150	1924	315	237	0	6	0	0	3	D3YXR8	
ENSMUST00000111349	ENSMUSG00000027257	2	91255954	91264679	1	14	6	22	16	15	0	0	0	0	0	0	Q543N7	Q99JB8
ENSMUST00000111350	ENSMUSG00000026670	1	170141938	170174957	-1	0	0	0	13	0	0	194	531	254	254	267		
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ENSMUST00000111352	ENSMUSG00000002109	2	91211572	91236982	-1	0	0	0	0	0	0	39	284	48	8	49	A2AGR6	
ENSMUST00000111353	ENSMUSG00000026675	1	169949535	169969241	-1	3	4	6	57	17	7	0	0	0	0	0	Q8C5N9	
ENSMUST00000111354	ENSMUSG00000002108	2	91184061	91202834	-1	0	4	2	7	0	4	16	0	0	0	9	Q91X41	Q9Z0Y9
ENSMUST00000111355	ENSMUSG00000002108	2	91184061	91202834	-1	5	3	14	5	0	2	0	3	0	0	0	A2AGR4	
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ENSMUST00000111357	ENSMUSG00000038530	1	169741477	169747642	-1	0	0	12	0	9	2	0	0	0	0	2	D3YXR2	
ENSMUST00000111360	ENSMUSG00000079190	GL456211.1	167446	196478	1	50	28	151	63	76	32	8	28	17	22	28		
ENSMUST00000111364	ENSMUSG00000079192	GL456210.1	123792	124928	1	0	0	0	0	0	0	5	4	4	12	23		
ENSMUST00000111368	ENSMUSG00000026683	1	169497934	169531464	-1	41	39	65	59	28	22	6	65	29	22	21		Q99P69
ENSMUST00000111369	ENSMUSG00000040687	2	91137360	91183837	-1	115	0	0	0	0	0	0	1	103	1	159	A2AGR1	
ENSMUST00000111370	ENSMUSG00000040687	2	91137360	91183837	-1	22	16	0	0	0	26	0	55	259	21	179		
ENSMUST00000111371	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	0	0	96	0	0	0	0	0	0	A2AGQ9	
ENSMUST00000111372	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	0	0	0	0	371	284	465	0	449	A2AGQ7	
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ENSMUST00000111377	ENSMUSG00000026686	1	167689237	167848741	1	34	6	297	74	0	0	0	0	1	0	0	Q543W2	Q9JKU8
ENSMUST00000111378	ENSMUSG00000079197	14	55587441	55591113	-1	0	0	0	0	0	0	300	945	96	661	168	G3X9V0	
ENSMUST00000111380	ENSMUSG00000015843	1	167598384	167639623	1	0	5	4	1	2	1	0	0	0	0	0	E9Q9V9	
ENSMUST00000111381	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	0	0	0	0	0	1	0	0	13	A2AGQ5	
ENSMUST00000111384	ENSMUSG00000015843	1	167598384	167639623	1	0	0	0	0	0	0	0	0	0	0	0		P28705
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ENSMUST00000111388						7	11	0	0	22	17	9126	18737	9450	8424	7439		
ENSMUST00000111390	ENSMUSG00000037936	5	125277087	125341094	-1	19	11	19	19	13	0	138	22	233	0	84	D3Z2V4	
ENSMUST00000111393	ENSMUSG00000029478	5	125017153	125179219	-1	0	0	110	66	17	0	371	114	374	0	392	E9Q9V3	
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ENSMUST00000111404	ENSMUSG00000040632	14	55518978	55524981	-1	4	10	52	19	30	7	0	0	0	0	0	Q543Y0	P54846
ENSMUST00000111416	ENSMUSG00000040612	1	166254139	166316823	1	62	53	160	66	58	45	4	5	1	5	24		B5TVM2
ENSMUST00000111417	ENSMUSG00000079215	5	124862691	124902693	1	0	0	0	79	12	0	0	203	332	74	213	E9QPD3	
ENSMUST00000111423	ENSMUSG00000079222	GL456221.1	17591	30203	-1	49	55	58	65	63	28	9	101	16	14	19		
ENSMUST00000111426	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQE0	
ENSMUST00000111427	ENSMUSG00000026565	1	165865154	166002678	-1	0	4	45	0	4	2	0	0	2	0	0	F8VQL7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000111429	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	9	0	0	0	0		P25425
ENSMUST00000111430	ENSMUSG00000002100	2	91118144	91136516	1	26	0	0	56	0	0	0	1	0	0	0	E9Q9T8	
ENSMUST00000111432	ENSMUSG00000040713	1	165763746	165775308	1	0	0	26	115	0	9	471	2600	783	473	781		O88668
ENSMUST00000111435	ENSMUSG00000026566	1	165592240	165634538	-1	14	0	0	0	0	4	11	38	22	0	39		Q3TEW6
ENSMUST00000111436	ENSMUSG00000002105	2	91061791	91070417	-1	0	0	0	0	0	0	21	9	10	0	0		Q8BZH0
ENSMUST00000111438	ENSMUSG00000029389	5	124552864	124569660	1	29	29	49	3	0	0	1	37	1	0	0	E9Q9T6	
ENSMUST00000111439	ENSMUSG00000026567	1	165485183	165576774	1	0	0	0	0	0	0	0	0	0	0	0	E9Q9T4	
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ENSMUST00000111441	ENSMUSG00000002102	2	91054009	91066369	1	1	0	10	0	0	0	0	28	0	0	0	A2AGN7	
ENSMUST00000111442	ENSMUSG00000079227	9	124121543	124147699	1	14	6	7	11	15	14	130	479	228	1045	309		P51682
ENSMUST00000111445	ENSMUSG00000002104	2	91035620	91045729	1	10	9	0	2	11	0	0	0	3	1	3	A2AFX4	
ENSMUST00000111446	ENSMUSG00000002104	2	91035620	91045729	1	0	0	0	13	0	5	2	0	0	0	0	A2AFX6	
ENSMUST00000111448	ENSMUSG00000005506	2	90940382	91019497	1	0	0	0	0	0	0	38	37	19	8	76		P28659
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ENSMUST00000111450	ENSMUSG00000040836	1	165295789	165326745	1	38	32	145	49	61	29	1	3	1	4	6		
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ENSMUST00000111456	ENSMUSG00000040752	14	54941981	54966927	-1	0	1	0	1	0	1	0	0	0	0	0	B8JJH3	
ENSMUST00000111460	ENSMUSG00000033417	19	60524696	60581023	-1	0	0	0	147	0	0	0	0	0	1	0		Q8R0X2
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ENSMUST00000111464	ENSMUSG00000005505	2	90904740	90911626	1	2	14	26	11	25	0	56	64	0	34	32		Q8R179
ENSMUST00000111466	ENSMUSG00000040794	2	90885860	90890525	1	3	3	2	296	14	3	0	0	0	0	0		Q8R066
ENSMUST00000111467	ENSMUSG00000027282	2	90847155	90866810	1	0	5	7	0	2	0	25	278	137	0	2	A2AFW6	
ENSMUST00000111468	ENSMUSG00000027282	2	90847155	90866810	1	0	0	0	3	0	0	160	515	192	201	107	D6RCZ1	
ENSMUST00000111472	ENSMUSG00000029394	5	124345417	124363082	-1	7	0	0	6	7	3	171	181	123	36	114	F2Z4B3	
ENSMUST00000111473	ENSMUSG00000029394	5	124345417	124363082	-1	10	6	4	0	5	0	77	106	36	0	50	F2Z4B3	
ENSMUST00000111474	ENSMUSG00000029394	5	124345417	124363082	-1	17	6	61	16	25	18	5	27	7	0	14	F2Z4B3	
ENSMUST00000111477	ENSMUSG00000047635	5	124328089	124341844	1	11	8	30	8	11	9	1	1	1	0	0		Q80VP5
ENSMUST00000111481	ENSMUSG00000040812	2	90782727	90834437	1	0	0	0	0	0	0	0	0	0	0	0		Q8CDK2
ENSMUST00000111484	ENSMUSG00000022185	14	54642161	54686931	-1	0	0	0	0	0	0	0	0	453	0	93		Q9JIX8
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ENSMUST00000111493	ENSMUSG00000025314	2	90429754	90580647	-1	64	35	217	0	53	36	1829	3947	3025	325	2703	A2AWF8	
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ENSMUST00000111497	ENSMUSG00000032540	9	122351608	122381524	1	13	0	0	0	11	0	36	282	0	0	0		Q9DBL9
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ENSMUST00000111510	ENSMUSG00000040170	1	162874317	162898726	-1	7	2	5	0	8	3	0	0	0	0	0		Q8K2I3
ENSMUST00000111512	ENSMUSG00000042894	2	89974709	89978712	1	0	4	0	0	4	0	0	0	0	0	0	Q8VGN9	
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ENSMUST00000111515	ENSMUSG00000029422	5	123728426	123749414	-1	9	10	5	6	8	5	51	287	84	53	122	Q8BI46	
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ENSMUST00000111518	ENSMUSG00000040181	1	162829561	162866610	-1	356	389	319	214	232	109	642	1732	1094	739	925	Q8C9C1	
ENSMUST00000111519	ENSMUSG00000049057	2	89878444	89881809	1	0	3	0	1	0	0	0	0	0	0	0	Q8VGP0	
ENSMUST00000111520	ENSMUSG00000075073	2	89835023	89841133	-1	0	0	0	1	0	0	0	0	0	0	0	Q8VGP1	
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ENSMUST00000111524	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	0	25	1	2	0	0	0	0	0		Q8K4G5
ENSMUST00000111525	ENSMUSG00000026692	1	162793188	162813972	-1	11	6	9	10	18	9	0	0	0	0	0		Q8VHG0
ENSMUST00000111526	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	0	3	4	10	3	0	14	0	36	E9Q9Q7	
ENSMUST00000111527	ENSMUSG00000075078	2	89656395	89661216	-1	7	3	6	0	6	3	0	0	0	0	0	Q8VGM3	
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ENSMUST00000111529	ENSMUSG00000025085	19	57032733	57314919	-1	2	19	14	0	0	0	156	322	165	53	537	E9Q9D1	
ENSMUST00000111532	ENSMUSG00000075081	2	89609156	89614022	-1	5	4	2	2	5	2	0	0	0	0	0	A2AT78	
ENSMUST00000111535	ENSMUSG00000068250	6	149157147	149188712	-1	4	6	19	5	10	0	24	87	25	48	14	B8JKV0	
ENSMUST00000111540	ENSMUSG00000075085	2	89493294	89498213	-1	2	0	0	0	0	2	0	0	0	0	0	Q8VGM6	
ENSMUST00000111542	ENSMUSG00000057564	14	52462721	52467495	-1	8	7	10	14	7	2	0	0	0	0	0	Q9R0K4	
ENSMUST00000111543	ENSMUSG00000075090	2	89362483	89364865	-1	6	0	6	0	3	2	0	0	0	0	0	A2AVK5	
ENSMUST00000111544	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	0	38	0	0	0	0	0	0	0	E9Q9C7	
ENSMUST00000111546	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	0	0	0	0	3	0	0	0	0		Q8K4G5
ENSMUST00000111547	ENSMUSG00000039958	6	149139849	149151171	1	8	7	2	0	7	0	5	33	4	32	19	Q8BPB7	
ENSMUST00000111548	ENSMUSG00000039958	6	149139849	149151171	1	0	0	9	2	0	3	2	0	10	0	0	Q8BPB7	
ENSMUST00000111549	ENSMUSG00000075095	2	89282139	89287954	-1	0	3	2	2	3	2	0	0	0	0	0	A3KGY9	
ENSMUST00000111550	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	0	0	6	0	0	0	0	0	0	E9Q9C4	
ENSMUST00000111551	ENSMUSG00000039958	6	149139849	149151171	1	0	0	0	0	0	0	9	31	14	0	0		Q80ZM3
ENSMUST00000111555	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q9C2	
ENSMUST00000111557	ENSMUSG00000030313	6	148988071	149101680	-1	146	118	140	233	155	96	10	53	23	21	50		A2RSQ0
ENSMUST00000111558	ENSMUSG00000025085	19	57032733	57314919	-1	20	4	13	8	19	7	0	0	0	0	0	E9Q9C1	
ENSMUST00000111559	ENSMUSG00000025085	19	57032733	57314919	-1	0	0	3	0	0	0	0	0	0	0	0	E9Q9C0	
ENSMUST00000111560	ENSMUSG00000061536	9	121680047	121705490	-1	5	10	11	105	9	0	28	11	31	0	0		Q8BXT9
ENSMUST00000111561	ENSMUSG00000049550	5	123577795	123684618	-1	0	0	0	0	0	0	0	0	1	0	0	D3Z2Z1	
ENSMUST00000111562	ENSMUSG00000039985	6	148921035	148946467	-1	0	0	0	0	0	0	12	0	0	11	20		Q8C8M1
ENSMUST00000111564	ENSMUSG00000049550	5	123577795	123684618	-1	0	0	12	0	0	0	726	1893	1532	170	1084		Q922J3
ENSMUST00000111566	ENSMUSG00000049550	5	123577795	123684618	-1	10	9	12	113	32	9	0	23	71	0	42		Q922J3
ENSMUST00000111568	ENSMUSG00000068817	2	87746198	87747133	1	3	0	2	2	2	0	0	0	0	0	0	Q7TR39	
ENSMUST00000111569	ENSMUSG00000030309	6	148842492	148896237	-1	16	14	17	150	10	10	5	0	4	0	3	E4NKG5	Q05A80
ENSMUST00000111572	ENSMUSG00000025838	2	87506565	87510872	1	0	0	0	9	0	0	0	0	0	0	0	Q810Y9	
ENSMUST00000111574	ENSMUSG00000075169	2	86922583	86924498	-1	0	1	0	0	0	1	0	0	0	0	0	A2AVB0	
ENSMUST00000111576	ENSMUSG00000075170	2	86890226	86892163	-1	3	4	2	0	0	3	0	0	0	0	0	A2AVA9	
ENSMUST00000111578	ENSMUSG00000079239	2	86593885	86594826	-1	0	2	0	0	0	0	0	0	0	0	0	A2AK57	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000111581	ENSMUSG00000033565	15	77078990	77307053	-1	0	18	98	0	16	11	22	30	30	19	49		Q8BP71
ENSMUST00000111582	ENSMUSG00000075179	2	86537966	86542480	-1	0	3	4	0	0	0	0	0	0	0	0	Q8VF52	
ENSMUST00000111584	ENSMUSG00000025083	19	56912361	57008228	-1	10	0	60	0	26	0	0	0	0	0	0		Q5DTU0
ENSMUST00000111586	ENSMUSG00000029433	5	123509765	123525488	-1	0	0	0	0	0	0	1	14	0	25	9	D3Z2Q3	
ENSMUST00000111587	ENSMUSG00000029433	5	123509765	123525488	-1	0	0	22	18	0	0	265	548	236	283	160		Q9JIQ3
ENSMUST00000111589	ENSMUSG00000045392	2	86041317	86042249	1	0	5	4	5	3	0	0	0	0	0	0	Q8VFK5	
ENSMUST00000111594	ENSMUSG00000026698	1	161969186	161973435	1	0	0	7	16	3	0	35	145	59	35	13		Q9CXR4
ENSMUST00000111596	ENSMUSG00000038342	5	123394798	123457932	1	28	22	49	61	37	17	5	0	5	0	5	B2RQ56	
ENSMUST00000111597	ENSMUSG00000075222	2	85352925	85363058	-1	1	0	0	0	0	0	0	0	0	0	0	Q7TRA1	
ENSMUST00000111598	ENSMUSG00000075223	2	85330897	85339295	-1	5	4	2	0	4	0	0	0	0	0	0	Q7TRA2	
ENSMUST00000111600	ENSMUSG00000057132	14	52110704	52163546	1	0	0	0	0	0	0	0	0	0	0	0	E9QQ97	
ENSMUST00000111601	ENSMUSG00000075224	2	85162334	85196699	-1	12	3	13	14	21	4	0	0	0	0	0		Q3UY51
ENSMUST00000111603	ENSMUSG00000057132	14	52110704	52163546	1	0	0	5	3	12	0	0	0	0	0	0		Q9EPQ2
ENSMUST00000111604	ENSMUSG00000025081	19	56826209	56870012	1	52	23	22	4	40	29	0	0	0	0	0		Q99MV1
ENSMUST00000111605	ENSMUSG00000033955	2	85048022	85073048	1	3	0	42	25	25	22	66	48	108	0	96		P58871
ENSMUST00000111606	ENSMUSG00000025081	19	56826209	56870012	1	0	0	50	15	0	0	0	0	0	0	0		Q99MV1
ENSMUST00000111607	ENSMUSG00000030303	6	148047259	148182758	1	4	6	8	1	5	3	16	51	19	15	27		Q7TNT2
ENSMUST00000111608	ENSMUSG00000044835	1	161142691	161170498	1	12	12	17	13	8	7	0	0	0	0	0		Q810N6
ENSMUST00000111609						1	1	10	1	1	5	0	2	0	0	2		
ENSMUST00000111610	ENSMUSG00000060373	14	52073380	52104028	-1	27	35	49	33	0	11	1767	7574	2059	4159	1959		Q9Z204
ENSMUST00000111611	ENSMUSG00000026705	1	161088375	161131511	-1	17	8	5	10	23	1	93	158	104	20	102		Q8VCK5
ENSMUST00000111613	ENSMUSG00000027071	2	84998583	85037462	-1	0	4	0	31	0	0	0	0	0	0	0	A2AW04	
ENSMUST00000111614						1	3	3	5	4	2	0	0	0	0	0		
ENSMUST00000111616	ENSMUSG00000027071	2	84998583	85037462	-1	2	0	0	0	3	2	0	1	2	0	0	A2AW03	
ENSMUST00000111618	ENSMUSG00000026708	1	161070713	161086724	1	2	2	0	0	2	0	30	63	12	0	21	Q14A61	
ENSMUST00000111619	ENSMUSG00000054434	5	123068415	123117749	1	4	0	0	11	0	0	3	3	3	1	1		Q3TA38
ENSMUST00000111620	ENSMUSG00000026708	1	161070713	161086724	1	0	0	0	0	0	0	14	75	19	53	0	Q14A61	
ENSMUST00000111622	ENSMUSG00000040163	6	146950329	146954422	-1	0	0	5	0	0	0	0	1	0	0	0		Q80W69
ENSMUST00000111623	ENSMUSG00000016487	6	146888487	147032025	1	12	5	12	0	0	0	0	47	0	0	0		Q8C8U0
ENSMUST00000111624	ENSMUSG00000027075	2	84838850	84863594	1	4	4	41	104	11	8	0	0	0	0	0		Q8BSM7
ENSMUST00000111625	ENSMUSG00000027075	2	84838850	84863594	1	8	4	5	48	17	0	7	16	1	2	2	A2ATS4	
ENSMUST00000111627	ENSMUSG00000032517	9	120149742	120181484	1	90	74	506	126	53	0	4	10	3	0	4		Q9D2P8
ENSMUST00000111628	ENSMUSG00000025404	10	127380327	127499384	1	7	8	23	18	12	6	2	17	12	0	14	E9Q995	
ENSMUST00000111631	ENSMUSG00000027076	2	84826997	84830213	1	0	0	2	1	2	0	0	12	0	53	4		P62073
ENSMUST00000111632	ENSMUSG00000004558	14	51905271	51913488	-1	23	0	0	84	24	14	18	33	0	13	16		Q9QYG0
ENSMUST00000111634						0	1	1	6	10	0	0	0	0	0	0		
ENSMUST00000111635	ENSMUSG00000079243	9	120013755	120023598	-1	47	31	234	96	71	30	0	0	0	0	2	E9QQ93	
ENSMUST00000111636	ENSMUSG00000040187	6	146796055	146833529	1	0	0	0	0	0	0	0	0	0	0	0	E9Q994	
ENSMUST00000111638	ENSMUSG00000040187	6	146796055	146833529	1	0	0	0	0	0	0	0	0	0	0	0	E9Q993	
ENSMUST00000111639	ENSMUSG00000040187	6	146796055	146833529	1	26	20	36	33	39	15	10	11	8	5	25		Q2VPD4
ENSMUST00000111641	ENSMUSG00000023224	2	84765387	84775444	-1	9	12	1	0	10	0	0	0	0	0	0	A2ATR8	
ENSMUST00000111643	ENSMUSG00000034059	2	84734058	84738655	1	3	3	0	50	19	5	0	0	1	0	4	A2ATR6	
ENSMUST00000111644	ENSMUSG00000001630	6	146724995	146778812	1	22	22	30	12	10	8	20	50	24	35	36		Q7TSE6
ENSMUST00000111646	ENSMUSG00000024985	19	55741810	55933654	1	7	0	0	86	0	0	0	0	10	0	0		Q924A0
ENSMUST00000111649	ENSMUSG00000024985	19	55741810	55933654	1	0	0	0	27	0	0	0	0	0	1	0		
ENSMUST00000111650	ENSMUSG00000030291	6	146642547	146650732	1	0	0	1	2	1	0	0	4	0	0	0	B2KG29	
ENSMUST00000111651	ENSMUSG00000024985	19	55741810	55933654	1	10	0	24	8	14	9	2	0	0	0	0		
ENSMUST00000111652	ENSMUSG00000024985	19	55741810	55933654	1	0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000111653	ENSMUSG00000024985	19	55741810	55933654	1	0	0	0	0	0	0	0	0	0	0	0	D3Z2K5	
ENSMUST00000111654	ENSMUSG00000024985	19	55741810	55933654	1	19	7	16	19	16	5	0	4	5	0	11	Q3V1G9	
ENSMUST00000111656	ENSMUSG00000024985	19	55741810	55933654	1	0	0	0	0	0	0	0	0	0	0	0	E9QQ91	
ENSMUST00000111657	ENSMUSG00000024985	19	55741810	55933654	1	0	0	39	1	19	0	0	0	0	0	30	E9QQ90	
ENSMUST00000111658	ENSMUSG00000024985	19	55741810	55933654	1	0	2	0	0	1	0	2	9	0	0	0	E9Q990	
ENSMUST00000111659	ENSMUSG00000024985	19	55741810	55933654	1	0	0	0	12	0	0	0	0	0	7	5		
ENSMUST00000111662	ENSMUSG00000024985	19	55741810	55933654	1	0	6	0	0	0	0	0	13	0	0	0	E9QQ89	
ENSMUST00000111663	ENSMUSG00000040242	6	146577203	146599198	1	0	0	17	0	18	0	254	1065	0	86	87		Q9CRA9
ENSMUST00000111664	ENSMUSG00000050043	2	84671316	84679140	-1	0	23	24	0	45	2	0	32	5	0	20	D3Z2J6	
ENSMUST00000111665	ENSMUSG00000050043	2	84671316	84679140	-1	14	9	13	29	0	13	0	0	0	0	0		Q9D710
ENSMUST00000111668	ENSMUSG00000029471	5	122731170	122779409	-1	52	32	228	246	57	31	436	747	656	48	474		Q8C078
ENSMUST00000111669	ENSMUSG00000015829	1	159523769	159931729	1	0	0	0	0	0	0	0	0	0	0	0		Q8BYI9
ENSMUST00000111670	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	107	0	8	32	152	86	20	179	E9Q986	
ENSMUST00000111673						0	0	0	0	0	0	97	0	80	63	7		
ENSMUST00000111675	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	50	121	0	6	9	0	0	0	0	D3Z2H7	
ENSMUST00000111676	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	26	0	0	0	0	0	0	E9Q907	
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ENSMUST00000111678	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	2	0	0	0	0	0	0	E9Q905	
ENSMUST00000111684	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q904	
ENSMUST00000111685	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q903	
ENSMUST00000111686	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q8Z9	
ENSMUST00000111687	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	16	0	0	0	0	0	E9Q901	
ENSMUST00000111688	ENSMUSG00000034101	2	84600071	84650765	-1	8	0	0	0	0	0	0	0	0	0	0	E9Q8Z9	
ENSMUST00000111689	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2H2	
ENSMUST00000111690	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	8	0	0	0	19	0	0	E9Q8Z9	
ENSMUST00000111691	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	14	0	73	0	53	11	61		P30999
ENSMUST00000111692	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	G3X9V2	
ENSMUST00000111693	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	G3X9V2	
ENSMUST00000111694	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q8Z8	
ENSMUST00000111695	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q8Z6	
ENSMUST00000111696	ENSMUSG00000034101	2	84600071	84650765	-1	41	0	0	0	0	0	0	0	0	0	0	E9Q8Z5	
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ENSMUST00000111698	ENSMUSG00000034101	2	84600071	84650765	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q8Z4	
ENSMUST00000111700	ENSMUSG00000026589	1	157506728	157568425	1	13	7	37	9	21	10	12	20	10	7	16		Q91XT4
ENSMUST00000111701	ENSMUSG00000030255	6	145931641	145965223	1	6	12	14	8	13	3	0	0	0	0	0	E9Q8Y7	
ENSMUST00000111702	ENSMUSG00000030255	6	145931641	145965223	1	29	17	24	1	24	11	1	2	1	6	0	E9Q8Y7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000111703	ENSMUSG00000030256	6	145858243	145865558	-1	5	1	9	75	5	8	0	2	0	0	2	D3Z2G6	
ENSMUST00000111704	ENSMUSG00000030259	6	145746748	145821079	1	26	20	43	31	35	16	19	35	25	1	43		Q8CJ96
ENSMUST00000111706	ENSMUSG00000054966	6	145365134	145614319	-1	8	7	18	7	21	11	0	0	0	0	0	E9Q8Y6	
ENSMUST00000111708	ENSMUSG00000054966	6	145365134	145614319	-1	2	2	5	0	0	0	0	0	0	0	0		Q9D4C1
ENSMUST00000111710	ENSMUSG00000030265	6	145216699	145250239	-1	2	0	0	0	0	1	104	382	310	27	206	Q0VDV7	P32883
ENSMUST00000111711	ENSMUSG00000027082	2	84432855	84476775	-1	0	0	8	0	9	0	0	0	0	0	0	A2ARA3	
ENSMUST00000111713	ENSMUSG00000029465	5	122391878	122414184	1	0	0	6	5	3	0	7	59	24	6	24	D3Z2F8	
ENSMUST00000111714	ENSMUSG00000027082	2	84432855	84476775	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BSB7	
ENSMUST00000111716	ENSMUSG00000029465	5	122391878	122414184	1	3	1	7	3	0	0	17	27	23	0	13	D3Z2F7	
ENSMUST00000111717	ENSMUSG00000027082	2	84432855	84476775	-1	0	0	6	3	0	7	0	0	1	3	3	Q8BSB7	
ENSMUST00000111718	ENSMUSG00000027082	2	84432855	84476775	-1	5	3	0	13	6	1	0	0	0	0	0		O54819
ENSMUST00000111719	ENSMUSG00000040370	6	145211134	145216939	1	2	0	0	0	0	1	12	94	15	29	15		Q91V16
ENSMUST00000111720	ENSMUSG00000033544	1	156838562	156861078	1	0	3	9	2	4	0	0	0	0	0	0		Q640P2
ENSMUST00000111721	ENSMUSG00000040370	6	145211134	145216939	1	16	0	4	0	4	1	0	579	0	0	9		Q91V16
ENSMUST00000111722	ENSMUSG00000027082	2	84432855	84476775	-1	0	0	0	0	0	0	0	0	0	13	1	A2ARA0	
ENSMUST00000111723	ENSMUSG00000040370	6	145211134	145216939	1	0	0	0	0	0	0	13	15	4	15	0		Q91V16
ENSMUST00000111724	ENSMUSG00000040370	6	145211134	145216939	1	0	0	0	0	0	0	0	13	17	0	13		Q91V16
ENSMUST00000111725	ENSMUSG00000040370	6	145211134	145216939	1	1	2	2	46	4	2	22	15	32	51	14		Q91V16
ENSMUST00000111726	ENSMUSG00000040370	6	145211134	145216939	1	0	0	0	0	0	0	156	524	161	293	70		Q91V16
ENSMUST00000111727						16	21	34	22	43	13	10	63	20	2	57		
ENSMUST00000111728	ENSMUSG00000043541	6	145174834	145211005	-1	9	0	2	12	2	5	0	0	11	3	6		
ENSMUST00000111729	ENSMUSG00000029462	5	122354369	122364984	1	0	0	0	0	0	0	120	568	37	38	0	H7BXA2	
ENSMUST00000111735	ENSMUSG00000036339	14	48446128	48515135	1	16	9	24	14	20	8	153	527	267	38	189		Q8BMD6
ENSMUST00000111737	ENSMUSG00000025025	19	53310506	53375810	1	29	22	42	21	30	0	319	1924	107	48	29		P50540
ENSMUST00000111738	ENSMUSG00000038593	5	122237848	122264460	-1	16	0	21	23	17	1	187	85	248	0	236		Q8BZ64
ENSMUST00000111740	ENSMUSG00000027087	2	83724397	83806916	1	15	17	0	0	0	0	17	222	0	45	0	A2AKI5	
ENSMUST00000111741	ENSMUSG00000025026	19	53140445	53247399	1	11	14	33	6	26	5	1419	868	2610	458	1500		Q9QYB5
ENSMUST00000111742	ENSMUSG00000030268	6	144993835	145076184	-1	1	0	22	0	1	3	8	25	7	0	0	Q3TJN1	P24288
ENSMUST00000111746						1	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000111748	ENSMUSG00000041540	6	143828425	144781977	-1	17	11	69	212	43	18	0	4	0	0	9	Q3TVF9	P35710
ENSMUST00000111749	ENSMUSG00000041540	6	143828425	144781977	-1	0	0	0	0	0	0	0	0	0	0	0	B2KFM4	
ENSMUST00000111750	ENSMUSG00000013936	5	122100951	122113472	1	0	1	11	7	4	4	0	0	0	0	0	E9Q8Y0	
ENSMUST00000111751	ENSMUSG00000013936	5	122100951	122113472	1	10	3	4	5	0	1	11	35	14	17	16		P51667
ENSMUST00000111752	ENSMUSG00000042589	5	121856366	122050102	-1	23	21	115	81	27	24	0	1	0	0	0		P70298
ENSMUST00000111754	ENSMUSG00000050565	1	156035403	156068861	1	0	0	0	2	0	0	207	879	262	72	98		Q9ER81
ENSMUST00000111755	ENSMUSG00000091900	7	116082863	116084635	-1	7	0	2	0	0	0	20	48	22	31	0		Q8R4R6
ENSMUST00000111756	ENSMUSG00000043531	19	50143301	50678646	-1	0	11	0	44	13	0	0	0	0	0	0	E9QQ63	
ENSMUST00000111757	ENSMUSG00000050565	1	156035403	156068861	1	9	10	137	125	42	19	176	153	544	35	404		Q8BYU6
ENSMUST00000111758	ENSMUSG00000030279	6	143010920	143100141	-1	15	0	0	0	0	0	160	488	429	0	174		Q7TPS5
ENSMUST00000111760	ENSMUSG00000027002	2	80500512	80581380	-1	0	0	0	55	8	0	0	0	0	0	0	A2AS98	
ENSMUST00000111763	ENSMUSG00000032446	9	118478212	118486132	1	24	16	49	507	33	21	0	12	4	0	13		O54839
ENSMUST00000111764	ENSMUSG00000033684	1	155776029	155812889	-1	0	4	62	0	0	15	322	95	721	32	286		Q8BND5
ENSMUST00000111765	ENSMUSG00000029458	5	121660563	121687256	1	7	0	5	55	7	3	0	0	0	0	0		Q99MP8
ENSMUST00000111768	ENSMUSG00000048473	6	142785204	142804502	-1	0	0	7	6	0	0	0	13	8	3	2	B7ZWN4	
ENSMUST00000111769						6	4	9	10	17	1	1	1	0	0	0		
ENSMUST00000111770	ENSMUSG00000029456	5	121621026	121660514	-1	0	0	0	4	0	0	80	40	58	5	52		Q8K370
ENSMUST00000111771	ENSMUSG00000030249	6	142587862	142702315	-1	0	0	0	0	69	0	0	0	0	0	0	E9PUE8	
ENSMUST00000111772	ENSMUSG00000039607	9	116572746	117629913	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BWL5
ENSMUST00000111773	ENSMUSG00000039607	9	116572746	117629913	-1	23	22	40	9	29	17	0	0	1	0	1		Q8BWL5
ENSMUST00000111774	ENSMUSG00000026469	1	155275701	155417415	-1	0	0	0	62	0	0	39	0	166	0	77		Q9Z0U0
ENSMUST00000111775	ENSMUSG00000026469	1	155275701	155417415	-1	0	0	0	0	2	0	85	34	376	18	190	D3Z2B4	
ENSMUST00000111776	ENSMUSG00000042647	5	121596775	121618938	-1	24	22	189	68	33	17	0	3	9	0	4	D3Z2B3	
ENSMUST00000111778	ENSMUSG00000037544	14	47387779	47418407	-1	0	0	0	1	0	0	0	0	7	0	0	E9QQ48	
ENSMUST00000111780	ENSMUSG00000034683	2	79707780	79818496	1	0	0	0	0	0	0	0	0	0	0	0		Q8BKK4
ENSMUST00000111781						0	3	0	0	5	0	0	0	0	0	0		
ENSMUST00000111782	ENSMUSG00000029454	5	121525038	121545905	-1	0	0	0	0	0	0	0	0	0	5	0		O54992
ENSMUST00000111783	ENSMUSG00000029454	5	121525038	121545905	-1	0	0	0	0	0	0	144	338	151	59	61		O54992
ENSMUST00000111784	ENSMUSG00000027007	2	79635352	79672966	1	0	0	15	0	9	0	225	489	399	17	52	A2AQD5	
ENSMUST00000111785	ENSMUSG00000027007	2	79635352	79672966	1	0	0	0	23	0	0	49	0	546	138	1025		Q922B9
ENSMUST00000111786	ENSMUSG00000029454	5	121525038	121545905	-1	0	0	0	0	0	0	109	550	176	89	175		O54992
ENSMUST00000111788	ENSMUSG00000027007	2	79635352	79672966	1	13	0	0	20	0	0	0	0	0	0	0	A2AQD6	
ENSMUST00000111790	ENSMUSG00000037572	14	47240944	47276857	-1	25	28	27	26	31	18	0	12	12	0	15		P59328
ENSMUST00000111791	ENSMUSG00000037572	14	47240944	47276857	-1	0	0	13	0	15	0	52	0	65	0	6	E9QPB3	
ENSMUST00000111792	ENSMUSG00000037572	14	47240944	47276857	-1	12	15	0	0	0	3	0	127	43	54	65		
ENSMUST00000111795	ENSMUSG00000029452	5	121451893	121524183	1	6	4	8	45	9	2	0	20	23	2	29	Q8CA26	
ENSMUST00000111800	ENSMUSG00000053617	19	47260174	47464411	-1	91	0	42	0	1	0	0	28	32	9	0		O89032
ENSMUST00000111802	ENSMUSG00000029616	5	121428590	121452506	-1	0	1	2	4	3	2	455	618	341	191	335	F8WIM7	
ENSMUST00000111803	ENSMUSG00000030243	6	142350342	142387087	-1	2	3	5	6	0	3	0	106	42	0	41		Q9Z129
ENSMUST00000111807	ENSMUSG00000006435	19	47178820	47259440	1	25	11	70	181	11	13	0	0	0	1	6		Q923S6
ENSMUST00000111808	ENSMUSG00000006435	19	47178820	47259440	1	4	0	0	177	21	5	0	0	0	0	0		Q923S6
ENSMUST00000111810	ENSMUSG00000042671	1	153653025	153700323	1	25	21	23	0	38	0	0	0	0	0	0		Q8BXT1
ENSMUST00000111812	ENSMUSG00000042671	1	153653025	153700323	1	11	23	255	29	9	18	0	0	0	0	1		Q8BXT1
ENSMUST00000111813	ENSMUSG00000079258	19	47141035	47144174	-1	7	4	32	9	13	4	0	0	0	0	0		D3Z291
ENSMUST00000111814	ENSMUSG00000042671	1	153653025	153700323	1	0	0	0	0	0	0	0	0	0	0	0	D3Z289	
ENSMUST00000111815	ENSMUSG00000042671	1	153653025	153700323	1	0	2	0	1	0	0	0	0	0	0	0	D3Z289	
ENSMUST00000111816	ENSMUSG00000079259	9	114507133	114564369	-1	44	51	162	529	77	38	0	0	0	2	6		Q1PSW8
ENSMUST00000111817	ENSMUSG00000062014	14	46808149	46822242	-1	13	8	21	36	16	10	260	1143	437	581	394		Q9CQI3
ENSMUST00000111818	ENSMUSG00000027014	2	77881159	77946375	-1	0	5	0	2	0	0	0	7	0	0	0		Q8C5N3
ENSMUST00000111819	ENSMUSG00000027014	2	77881159	77946375	-1	1	0	0	0	0	6	89	247	193	270	134	B1AYU7	
ENSMUST00000111820	ENSMUSG00000079260	9	114401095	114411200	1	218	173	892	319	213	108	136	197	171	26	179	D3Z286	
ENSMUST00000111821	ENSMUSG00000027014	2	77881159	77946375	-1	0	0	0	12	0	0	0	0	53	0	0		Q8C5N3
ENSMUST00000111822						3	6	2	5	4	1	0	0	0	0	0		
ENSMUST00000111824	ENSMUSG00000027014	2	77881159	77946375	-1	6	0	6	1	2	0	0	0	0	0	0	B1AYU4	
ENSMUST00000111825	ENSMUSG00000063975	6	142234227	142322981	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDD1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000111826	ENSMUSG00000079261	14	46379414	46383608	1	5	0	11	4	2	5	0	0	0	0	0	A2CG07	
ENSMUST00000111827	ENSMUSG00000079262	6	142085761	142208521	-1	7	11	4	8	10	4	0	0	0	0	0		Q99J94
ENSMUST00000111828	ENSMUSG00000037697	14	45593174	45658143	-1	0	0	0	180	2	0	29	0	41	0	30	E9QQ38	
ENSMUST00000111829	ENSMUSG00000027016	2	77410634	77819639	-1	7	13	8	48	14	4	0	0	0	0	0	Q8BM98	
ENSMUST00000111830	ENSMUSG00000027016	2	77410634	77819639	-1	6	7	32	19	11	11	0	0	1	0	0		Q8BXJ8
ENSMUST00000111831	ENSMUSG00000027016	2	77410634	77819639	-1	0	2	0	40	0	0	0	0	0	0	0	A2AS57	Q8BXJ8
ENSMUST00000111832	ENSMUSG00000079263	6	141971845	142011414	-1	0	2	9	3	0	0	0	0	0	0	0	L7N251	
ENSMUST00000111833	ENSMUSG00000044033	2	77009902	77170636	-1	2	3	2	9	1	2	0	0	0	0	0	A2AK24	
ENSMUST00000111835	ENSMUSG00000053205	14	45351473	45373585	1	0	2	0	0	1	0	2	8	7	7	6		Q60969
ENSMUST00000111836	ENSMUSG00000042772	1	152836995	152902646	-1	0	0	0	8	0	0	0	3	0	0	17		Q5RJH6
ENSMUST00000111838	ENSMUSG00000033392	9	113812586	113919697	1	13	7	12	8	14	7	0	0	0	19	0	E9Q8N5	
ENSMUST00000111844	ENSMUSG00000079264	6	140729284	140756053	1	1	0	1	0	0	0	0	0	0	0	0	F6S4H3	
ENSMUST00000111846	ENSMUSG00000051747	2	76703980	76982547	-1	107	16	0	56	7	81	0	0	2	0	0	E9Q8N1	
ENSMUST00000111855	ENSMUSG00000047731	19	46599084	46657389	1	0	0	0	0	0	0	0	323	29	64	133		Q8BGW2
ENSMUST00000111857	ENSMUSG00000026482	1	152516760	152766351	-1	0	0	0	118	0	4	0	0	0	0	17	E9Q8N0	
ENSMUST00000111859	ENSMUSG00000026482	1	152516760	152766351	-1	10	19	91	100	21	14	0	0	10	0	0	E9Q8M9	
ENSMUST00000111860	ENSMUSG00000079265	14	44649204	44706456	-1	54	55	69	34	74	26	0	0	0	0	0	D3Z260	
ENSMUST00000111861	ENSMUSG00000032504	9	113651744	113708259	-1	8	0	13	92	0	0	1639	3172	2948	152	1459		Q9WU78
ENSMUST00000111862						5	0	4	3	3	0	0	0	0	0	0		
ENSMUST00000111863	ENSMUSG00000079267	14	44330442	44338584	-1	6	12	3	0	3	4	0	0	0	0	0	D3Z257	
ENSMUST00000111864						0	1	3	4	0	1	0	0	0	0	0		
ENSMUST00000111867	ENSMUSG00000025231	19	46396896	46488804	1	0	0	0	66	0	0	11	1	18	0	1	Q3U0Z8	Q9Z0P7
ENSMUST00000111868	ENSMUSG00000030228	6	139587221	139969284	1	3	0	20	12	7	1	0	0	0	0	0	E9QQ35	
ENSMUST00000111869	ENSMUSG00000079269	14	41641179	41646487	-1	0	6	0	3	0	0	0	0	0	0	0	D3Z236	
ENSMUST00000111870	ENSMUSG00000093945	14	41977873	41983325	-1	0	0	0	10	10	0	0	0	0	0	0	D3Z235	
ENSMUST00000111872	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DCB4
ENSMUST00000111873	ENSMUSG00000044378	6	137983586	138079916	-1	0	0	0	0	0	0	0	2	1	1	1	D3Z234	
ENSMUST00000111874	ENSMUSG00000072613	14	41570696	41576319	1	0	0	0	0	0	0	0	0	0	1	0	K9J7E8	
ENSMUST00000111875	ENSMUSG00000026483	1	151571186	151721939	1	3	3	11	4	5	1	0	3	13	4	15	D3Z233	
ENSMUST00000111878	ENSMUSG00000015766	6	137477245	137654876	-1	0	0	0	0	4	0	172	157	890	266	322		Q08509
ENSMUST00000111879	ENSMUSG00000032500	9	111439081	111489118	1	22	8	45	30	25	16	0	0	0	0	0		Q8BWQ5
ENSMUST00000111881	ENSMUSG00000025225	19	46304737	46312090	1	0	0	31	62	6	0	39	119	15	0	38	Q3UG25	Q9WTK5
ENSMUST00000111882	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q8K5	
ENSMUST00000111883	ENSMUSG00000052748	1	151367699	151428455	-1	0	3	0	0	2	0	0	4	0	0	0		Q9DBQ9
ENSMUST00000111884	ENSMUSG00000029600	5	120594305	120612589	-1	11	3	20	1	3	0	0	0	0	0	0	D3Z228	
ENSMUST00000111887	ENSMUSG00000023150	1	151344477	151364422	1	0	3	0	19	0	2	10	11	15	2	14		Q920Q8
ENSMUST00000111888	ENSMUSG00000043953	9	111054486	111057519	-1	12	11	25	17	22	4	163	1138	188	196	443		O35457
ENSMUST00000111889	ENSMUSG00000032754	5	120511168	120534024	1	0	0	0	0	0	0	23	0	75	0	0	D3Z226	
ENSMUST00000111890	ENSMUSG00000032754	5	120511168	120534024	1	42	5	242	0	32	24	112	308	173	0	93		Q925Q3
ENSMUST00000111891	ENSMUSG00000030220	6	136923655	136941899	-1	8	1	17	30	10	14	3418	3306	4381	11936	3900		Q61599
ENSMUST00000111892	ENSMUSG00000030220	6	136923655	136941899	-1	0	7	11	0	0	5	14897	59018	12474	29934	7243		Q61599
ENSMUST00000111894	ENSMUSG00000043298	6	136829927	136835452	-1	0	10	44	14	12	12	0	0	1	3	0		Q8BQM7
ENSMUST00000111895						0	0	3	2	0	1	40	511	223	46	114		
ENSMUST00000111898	ENSMUSG00000029597	5	120476526	120483932	1	1	3	4	2	6	1	0	0	0	1	0	D3Z221	
ENSMUST00000111899	ENSMUSG00000055491	19	46044886	46072915	1	0	0	55	181	0	0	37	62	67	0	18		Q6NZN1
ENSMUST00000111901	ENSMUSG00000006014	1	150449412	150466165	-1	0	0	10	0	0	0	3	6	10	4	354	E9QQ18	
ENSMUST00000111902	ENSMUSG00000006014	1	150449412	150466165	-1	0	0	0	0	0	0	0	0	0	65	0	E9QQ17	
ENSMUST00000111905	ENSMUSG00000030209	6	135713233	136173511	-1	82	72	631	118	51	46	0	2	0	0	4	G3X9V4	
ENSMUST00000111906						25	18	132	34	32	9	0	0	0	0	0		
ENSMUST00000111907	ENSMUSG00000030208	6	135362545	135383173	1	5	2	4	9	4	0	0	0	0	0	0	Q4FK43	P47801
ENSMUST00000111908	ENSMUSG00000041445	14	34375504	34404287	1	40	26	53	44	49	21	0	2	3	0	3		A6H6E2
ENSMUST00000111909	ENSMUSG00000030206	6	135237326	135254351	-1	6	2	10	9	0	2	11	14	12	49	7	E9QQ16	
ENSMUST00000111910	ENSMUSG00000030206	6	135237326	135254351	-1	3	2	20	0	10	0	0	0	0	0	0		Q8R1W2
ENSMUST00000111911	ENSMUSG00000030206	6	135237326	135254351	-1	0	0	0	4	0	7	0	0	0	0	0		Q8R1W2
ENSMUST00000111913	ENSMUSG00000006010	1	150361305	150393080	-1	0	0	0	0	0	0	45	41	43	0	19		Q4PJX1
ENSMUST00000111915	ENSMUSG00000030207	6	135197977	135244955	1	27	14	63	46	32	17	1099	2212	1363	184	1069		Q8BYI8
ENSMUST00000111916	ENSMUSG00000030207	6	135197977	135244955	1	16	7	22	38	21	10	0	1	0	2	8		Q8BYI8
ENSMUST00000111917	ENSMUSG00000041471	14	34237041	34310503	-1	18	17	12	68	15	4	43	157	84	79	57		Q3UEN2
ENSMUST00000111920	ENSMUSG00000002733	2	76675281	76696828	1	8	5	20	40	11	5	136	277	155	42	123		Q9ERS4
ENSMUST00000111922	ENSMUSG00000030205	6	135105991	135118283	-1	8	0	31	8	0	12	3	15	0	3	1	Q0VEL2	Q9JIL6
ENSMUST00000111924	ENSMUSG00000025219	19	45736798	45742915	-1	0	0	0	5	0	0	0	0	0	0	0	D3Z208	
ENSMUST00000111925	ENSMUSG00000025219	19	45736798	45742915	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z207	
ENSMUST00000111926	ENSMUSG00000056220	1	149829618	149961290	-1	0	0	0	0	14	0	0	0	0	0	7	Q9DBX5	
ENSMUST00000111927	ENSMUSG00000025219	19	45736798	45742915	-1	0	0	0	0	0	0	0	0	0	0	0		P37237
ENSMUST00000111928	ENSMUSG00000025219	19	45736798	45742915	-1	4	9	29	38	4	4	0	0	0	0	0	Q3V279	P37237
ENSMUST00000111929	ENSMUSG00000042359	2	76406508	76600647	1	43	52	110	61	66	24	0	8	5	2	4		Q8BXR9
ENSMUST00000111930	ENSMUSG00000042359	2	76406508	76600647	1	0	0	0	2	0	0	0	0	0	0	1		Q8BXR9
ENSMUST00000111932	ENSMUSG00000032641	6	134869093	134898578	-1	0	2	3	2	0	0	0	0	0	0	9		Q61121
ENSMUST00000111936	ENSMUSG00000025217	19	45363734	45533341	1	0	97	353	523	63	50	0	0	0	32	52		Q3ULA2
ENSMUST00000111937	ENSMUSG00000032652	6	134830154	134858931	1	0	1	0	14	0	0	12	2	25	2	16	D3Z200	
ENSMUST00000111941	ENSMUSG00000051079	1	144138654	144177372	-1	0	2	0	0	2	0	0	0	0	0	0		Q8K443
ENSMUST00000111942	ENSMUSG00000021936	14	33377898	33447158	-1	0	0	0	0	0	0	11	0	0	0	0	D3Z1Z4	
ENSMUST00000111943	ENSMUSG00000021936	14	33377898	33447158	-1	0	0	0	0	0	0	3	33	43	74	21	A6P3E4	
ENSMUST00000111944	ENSMUSG00000021936	14	33377898	33447158	-1	0	0	0	0	0	0	0	0	0	2	0	Q7TSJ7	
ENSMUST00000111945	ENSMUSG00000021936	14	33377898	33447158	-1	14	10	28	6	14	16	17	90	37	30	28	Q544A0	Q91Y86
ENSMUST00000111948	ENSMUSG00000025213	19	45075241	45079289	1	0	6	14	230	21	0	0	6	6	0	0		Q8BJ66
ENSMUST00000111950						17	8	13	4	13	2	0	0	0	0	0		
ENSMUST00000111952	ENSMUSG00000042410	2	75832177	75931350	1	1	6	1	10	3	2	4	4	2	0	0	A2AL49	
ENSMUST00000111953	ENSMUSG00000029363	5	117378103	117389047	-1	2	6	15	33	2	2	5	6	2	0	4	D3Z1Y6	
ENSMUST00000111954	ENSMUSG00000025212	19	45047576	45056383	1	41	0	13	0	0	0	0	104	0	0	30		Q91V61
ENSMUST00000111955	ENSMUSG00000063506	14	33214026	33369934	1	3	0	10	131	13	8	1	7	0	6	13	D3Z1Y5	
ENSMUST00000111956	ENSMUSG00000063506	14	33214026	33369934	1	12	20	35	16	15	0	6	0	0	11	32		Q8BL80
ENSMUST00000111957	ENSMUSG00000018196	1	143716338	143749676	1	0	0	0	0	0	0	48	285	66	97	30	Q3UQ95	Q923X4
ENSMUST00000111959	ENSMUSG00000029364	5	117357304	117378601	1	9	7	17	0	19	10	314	0	296	20	239	E9Q8J9	

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ENSMUST00000111960	ENSMUSG00000030200	6	134396318	134438736	1	0	0	0	10	0	0	0	3	0	1	3		Q9CPT0
ENSMUST00000111961	ENSMUSG00000059005	2	75659261	75669407	1	0	2	0	2	0	0	232	0	0	64	47	A2AL12	
ENSMUST00000111962	ENSMUSG00000059005	2	75659261	75669407	1	31	39	28	29	40	13	288	1419	400	477	408	Q0VG47	Q8BG05
ENSMUST00000111963	ENSMUSG00000030199	6	134035700	134270158	1	36	30	77	113	36	0	384	687	369	0	456	E9Q8J8	
ENSMUST00000111964	ENSMUSG00000059005	2	75659261	75669407	1	41	18	3	80	43	25	0	40	119	74	92	Q5FB19	Q8BG05
ENSMUST00000111967	ENSMUSG00000066894	5	117319083	117355005	1	0	0	0	114	0	6	185	216	273	37	226		D3YX43
ENSMUST00000111972	ENSMUSG00000059934	6	132569809	132572941	1	12	0	56	1275	0	0	0	0	0	0	0	D3Z1V5	
ENSMUST00000111973	ENSMUSG00000032959	5	117282654	117287625	-1	0	0	14	48	7	0	0	0	0	0	0	D3Z1V4	
ENSMUST00000111975	ENSMUSG00000061288	5	117120129	117275219	1	0	2	0	6	0	1	0	0	67	10	90	Q3V3K3	
ENSMUST00000111976	ENSMUSG00000026365	1	140084708	140183764	-1	0	0	0	0	2	0	6	182	22	248	114	E9Q8I0	
ENSMUST00000111977	ENSMUSG00000026365	1	140084708	140183764	-1	2	0	0	4	0	0	45	3	50	249	0	E9Q8H9	
ENSMUST00000111978	ENSMUSG00000061288	5	117120129	117275219	1	0	0	49	520	0	21	30	247	266	46	187		Q8BYC6
ENSMUST00000111980	ENSMUSG00000101174	2	74711929	74729160	1	0	4	0	38	0	0	0	0	0	0	0		P10628
ENSMUST00000111982	ENSMUSG00000079277	2	74711927	74748442	1	0	0	38	27	4	7	0	0	0	0	0	Q3UZR4	P09027
ENSMUST00000111983	ENSMUSG00000079277	2	74711927	74748442	1	8	7	4	266	10	0	0	0	0	0	0	Q3UZR4	P09027
ENSMUST00000111985	ENSMUSG00000051984	19	44516957	44545864	-1	11	23	0	0	0	3	4	0	13	2	2		Q3TZ89
ENSMUST00000111986	ENSMUSG00000070594	1	139697623	139781243	-1	0	4	4	2	0	5	0	0	0	0	0	E9Q8B6	
ENSMUST00000111989	ENSMUSG00000070594	1	139697623	139781243	-1	6	0	0	0	0	0	0	0	0	0	0	E9Q8B5	
ENSMUST00000111991	ENSMUSG00000032480	9	110084320	110117830	-1	0	16	5	0	0	0	0	1	0	0	0		Q99PU8
ENSMUST00000111993	ENSMUSG00000009207	2	74520291	74579435	-1	0	0	0	0	0	0	0	0	4	0	0	A2ASL8	
ENSMUST00000111994	ENSMUSG00000056234	14	32159865	32179855	1	0	0	8	8	13	1	1563	3941	2644	4031	1492	Q5U4H9	
ENSMUST00000111996	ENSMUSG00000018770	2	73908447	73911326	-1	0	0	0	24	10	0	591	568	218	142	128	Q14BC2	P56384
ENSMUST00000111997	ENSMUSG00000079278	5	116038755	116083244	-1	7	6	11	7	13	5	0	0	0	0	0	A0A0A0MQE1	
ENSMUST00000111998	ENSMUSG00000067591	6	130323289	130337574	-1	2	0	0	3	2	2	0	14	0	0	7		Q64329
ENSMUST00000111999	ENSMUSG00000029513	5	116013586	116024508	-1	0	0	2	59	5	3	18	6	45	0	0	Q542K0	Q9R078
ENSMUST00000112000	ENSMUSG00000021905	14	32080566	32085692	-1	3	4	13	5	5	2	53	106	27	183	16	D3Z1U2	
ENSMUST00000112001	ENSMUSG00000021905	14	32080566	32085692	-1	18	0	0	0	0	0	34	41	0	10	16	E9PZC5	
ENSMUST00000112007	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	27	52	21	0	109	Q543G2	P16951
ENSMUST00000112008	ENSMUSG00000029516	5	115845278	116008947	1	0	4	0	0	0	0	0	0	0	0	0	D3Z1U0	
ENSMUST00000112010	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	62	349	4	50	5	Q543G2	P16951
ENSMUST00000112013	ENSMUSG00000067599	6	130218605	130233322	-1	0	0	0	0	0	0	0	0	0	0	0	F8WJ94	
ENSMUST00000112016	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	88	0	0	47	221	45	0	118	Q640L6	P16951
ENSMUST00000112017	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	128	0	138	18	155		P16951
ENSMUST00000112020	ENSMUSG00000072718	6	130269194	130281928	-1	0	0	0	0	0	1	0	0	0	0	0	Q9R1G6	
ENSMUST00000112022	ENSMUSG00000038357	9	109847379	109849617	-1	4	7	11	42	7	7	19356	33677	10439	29921	6752		
ENSMUST00000112024	ENSMUSG00000056486	2	73610660	73775346	-1	0	0	0	0	0	0	0	0	0	0	0		Q91V57
ENSMUST00000112025	ENSMUSG00000079283	1	138851983	138856852	-1	0	0	0	38	0	0	6	18	19	24	9	D3Z1T2	
ENSMUST00000112026	ENSMUSG00000019230	1	138825186	138848577	-1	0	0	0	0	0	0	0	0	0	0	0		Q9WUH2
ENSMUST00000112027	ENSMUSG00000057606	14	31523082	31591343	-1	47	17	46	194	76	29	3	1	0	1	3		O35348
ENSMUST00000112028	ENSMUSG00000025198	19	44034944	44069785	-1	0	6	19	63	0	0	329	1534	445	402	369		
ENSMUST00000112030	ENSMUSG00000019230	1	138825186	138848577	-1	0	0	0	0	16	0	0	0	0	0	0		Q9WUH2
ENSMUST00000112032	ENSMUSG00000033024	6	130178675	130193112	-1	0	0	0	2	0	0	1	0	0	0	0	Q2TJJ8	
ENSMUST00000112036						22	19	14	20	32	0	561	764	288	54	407		
ENSMUST00000112039	ENSMUSG00000054087	9	109322886	109339659	-1	0	6	0	0	5	0	0	0	0	0	0	E9Q8A4	
ENSMUST00000112040	ENSMUSG00000054087	9	109322886	109339659	-1	20	13	34	25	18	15	0	0	1	0	0	Q3UPQ4	
ENSMUST00000112041	ENSMUSG00000105589	9	109270790	109287676	-1	12	7	0	5	5	3	0	0	0	0	0	Q4FZL9	
ENSMUST00000112043	ENSMUSG00000041762	2	73341506	73386572	-1	0	0	10	0	0	0	0	0	0	0	0	A2AWR3	
ENSMUST00000112044	ENSMUSG00000041762	2	73341506	73386572	-1	5	0	0	0	18	11	5	0	0	0	14	A2AWR2	
ENSMUST00000112046	ENSMUSG00000041483	1	136624901	136630053	1	4	6	10	187	29	6	11	356	362	0	249		Q99LI5
ENSMUST00000112047	ENSMUSG00000025193	19	43752996	43768638	1	3	3	5	0	3	0	27	143	15	70	18		Q9D8X1
ENSMUST00000112050	ENSMUSG00000008226	2	73312601	73337818	1	17	17	136	21	15	2	20	136	43	32	30	A2AWQ9	
ENSMUST00000112053	ENSMUSG00000049734	9	109057933	109059734	-1	0	3	0	0	0	0	290	649	183	131	330		Q91XB0
ENSMUST00000112055	ENSMUSG00000027108	2	73092801	73218924	-1	0	0	0	0	0	0	1	51	0	0	0	B1AYJ9	
ENSMUST00000112057	ENSMUSG00000052736	6	129647496	129660689	-1	0	0	0	0	0	0	0	0	0	0	0	Q9WTJ9	
ENSMUST00000112059	ENSMUSG00000025647	9	109038565	109057777	1	20	0	0	0	0	14	4093	5138	2659	677	2639		Q9D7I0
ENSMUST00000112062	ENSMUSG00000079286	2	72971548	72986716	-1	0	0	0	0	1	0	0	0	1	0	0	F6R5N3	
ENSMUST00000112063	ENSMUSG00000030165	6	129591782	129598775	1	0	0	0	0	0	0	0	0	2	3	0		O54707
ENSMUST00000112064	ENSMUSG00000026407	1	136052750	136119822	1	42	23	46	26	14	14	0	0	0	0	0	F8VQE0	
ENSMUST00000112066	ENSMUSG00000029524	5	115478010	115484725	-1	10	0	49	14	8	5	0	12	17	3	0		Q8R216
ENSMUST00000112067	ENSMUSG00000029524	5	115478010	115484725	-1	0	4	1	6	3	0	8	14	0	0	0		Q8R216
ENSMUST00000112068	ENSMUSG00000026407	1	136052750	136119822	1	12	15	0	6	49	0	0	0	0	0	0	E9QPX8	
ENSMUST00000112070	ENSMUSG00000025650	9	108953586	108984875	1	0	78	1	115	154	51	0	0	0	0	0		Q63870
ENSMUST00000112071	ENSMUSG00000029522	5	115466262	115474722	1	1	0	0	0	1	0	0	0	0	0	0	D3Z1N8	
ENSMUST00000112073						61	32	50	225	63	34	0	0	0	0	0		
ENSMUST00000112076	ENSMUSG00000079293	6	129461591	129472779	-1	1	1	3	3	1	1	0	91	88	0	133		Q6QLQ4
ENSMUST00000112079	ENSMUSG00000030159	6	129397297	129409335	1	0	0	0	0	0	0	0	0	0	0	0	A0T1G3	
ENSMUST00000112081	ENSMUSG00000030159	6	129397297	129409335	1	0	0	0	6	2	0	0	16	7	63	7		Q9JL99
ENSMUST00000112082	ENSMUSG00000030158	6	129375515	129385874	-1	0	0	7	0	0	0	0	0	0	0	0		
ENSMUST00000112085	ENSMUSG00000026414	1	135836354	135852260	1	7	0	16	7	0	0	0	0	0	0	0	K3W4R6	
ENSMUST00000112086	ENSMUSG00000026414	1	135836354	135852260	1	0	0	0	0	0	0	0	0	0	0	0	K3W4R7	
ENSMUST00000112087	ENSMUSG00000026414	1	135836354	135852260	1	0	0	0	0	0	0	0	0	0	0	0	Q54AB6	P50752
ENSMUST00000112090	ENSMUSG00000009013	5	115297110	115300999	-1	0	1	2	83	3	1	514	1441	683	1313	311		P63168
ENSMUST00000112091	ENSMUSG00000079316	X	166457253	166479867	-1	3	3	3	19	6	0	91	660	193	313	113	Q0PD48	Q9R0M6
ENSMUST00000112092	ENSMUSG00000042323	14	31019138	31121592	1	10	0	0	0	0	0	10	2	361	7	65	D3Z1N4	
ENSMUST00000112094	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	0	0	17	16	254	0	46		Q8BSQ9
ENSMUST00000112095	ENSMUSG00000042323	14	31019138	31121592	1	13	8	25	30	21	8	523	1049	813	126	562		Q8BSQ9
ENSMUST00000112096	ENSMUSG00000041740	5	115241412	115272898	-1	0	0	0	40	0	1	1904	3497	3477	350	1319		Q3UIW5
ENSMUST00000112097	ENSMUSG00000041740	5	115241412	115272898	-1	26	19	51	47	34	9	165	219	245	25	167	D3Z1N2	
ENSMUST00000112098	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	4	0	4	14	0	0	98	F8VQD1	
ENSMUST00000112099						0	0	0	0	0	0	64	0	162	55	112		
ENSMUST00000112101	ENSMUSG00000027111	2	71745616	71858416	1	17	6	22	22	7	5	22	0	0	21	160		Q61739
ENSMUST00000112102	ENSMUSG00000055357	X	169776257	169779635	-1	0	3	2	2	0	1	0	0	0	0	0	Q9CR52	
ENSMUST00000112104	ENSMUSG00000035299	X	169685199	170005736	1	0	0	0	0	0	0	0	0	0	0	0		O70583
ENSMUST00000112105	ENSMUSG00000035299	X	169685199	170005736	1	0	0	0	0	0	7	0	0	0	0	0		O70583

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112106	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	0	0	0	0	9	0	0	D3Z1M8	
ENSMUST00000112107	ENSMUSG00000035299	X	169685199	170005736	1	8	0	8	0	8	0	0	0	0	0	0	B1AUZ9	
ENSMUST00000112109						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000112110	ENSMUSG00000079299	6	128705836	128723059	-1	6	2	3	1	2	0	0	0	0	1	0		Q0ZUP1
ENSMUST00000112112	ENSMUSG00000029544	5	115168689	115194381	-1	0	0	0	2	0	0	0	0	0	0	0		Q9JLK7
ENSMUST00000112113	ENSMUSG00000029544	5	115168689	115194381	-1	0	0	3	125	3	3	0	0	0	0	0	D3Z1M4	
ENSMUST00000112115	ENSMUSG00000031352	X	169250193	169320372	-1	4	0	8	54	8	7	32	64	78	43	48		P53702
ENSMUST00000112118	ENSMUSG00000031354	X	169176114	169187200	-1	0	0	10	0	0	0	0	0	0	0	0		P63277
ENSMUST00000112119	ENSMUSG00000031354	X	169176114	169187200	-1	0	3	0	0	0	0	0	0	0	0	0		P63277
ENSMUST00000112120	ENSMUSG00000031354	X	169176114	169187200	-1	1	0	0	8	4	2	3	0	0	0	0	R9W2T8	P63277
ENSMUST00000112121	ENSMUSG00000048578	5	115142981	115158179	-1	13	12	52	307	16	7	64	223	73	0	0	D3Z1M3	Q6ZQI3
ENSMUST00000112122	ENSMUSG00000027018	2	71388958	71441622	1	0	0	7	67	3	10	5	9	15	19	0	A2ATU9	
ENSMUST00000112123	ENSMUSG00000034321	19	41922980	41933314	-1	0	12	26	89	8	3	0	0	0	0	0		Q9DAA6
ENSMUST00000112127	ENSMUSG00000031355	X	168795099	169304435	1	0	2	0	1	0	0	11	6	0	0	0		O54834
ENSMUST00000112129	ENSMUSG00000031355	X	168795099	169304435	1	45	35	74	67	71	24	3	6	7	0	9	A2ALX7	
ENSMUST00000112131	ENSMUSG00000031355	X	168795099	169304435	1	0	0	0	0	0	0	0	0	4	7	22		O54834
ENSMUST00000112132	ENSMUSG00000030359	6	128483567	128526720	-1	22	15	36	26	0	11	0	0	0	33	0		Q61838
ENSMUST00000112136	ENSMUSG00000027012	2	71211706	71263303	1	0	0	1	0	0	0	0	0	0	0	0	A2BFF5	
ENSMUST00000112137	ENSMUSG00000031358	X	168654117	168673898	-1	2	0	5	24	0	0	110	467	167	370	116		Q9WVG9
ENSMUST00000112138	ENSMUSG00000027012	2	71211706	71263303	1	0	2	0	0	0	2	489	1864	753	606	521	A2BFF7	O88487
ENSMUST00000112139	ENSMUSG00000027012	2	71211706	71263303	1	0	0	0	0	0	0	35	126	14	48	18	A2BFF8	
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ENSMUST00000112141						12	5	14	22	15	0	0	0	0	10	0		
ENSMUST00000112142	ENSMUSG00000027012	2	71211706	71263303	1	0	0	1	27	2	0	0	0	14	0	0	Q3TPJ8	
ENSMUST00000112143	ENSMUSG00000041827	5	114923240	114937915	1	12	0	22	15	23	0	261	599	69	34	461		Q8VI94
ENSMUST00000112144	ENSMUSG00000027012	2	71211706	71263303	1	0	0	0	0	0	0	0	0	0	0	0	A2BFF9	
ENSMUST00000112145	ENSMUSG00000049176	X	167471309	168577231	-1	14	0	0	0	0	0	0	0	0	0	0		A2AFR3
ENSMUST00000112146	ENSMUSG00000049176	X	167471309	168577231	-1	0	13	26	0	19	0	0	0	0	0	0		A2AFR3
ENSMUST00000112147	ENSMUSG00000049176	X	167471309	168577231	-1	0	8	16	6	5	3	0	0	0	0	0		A2AFR3
ENSMUST00000112148	ENSMUSG00000001517	6	128362967	128376146	1	4	5	0	0	6	4	7	0	20	0	49	E9Q7Y0	
ENSMUST00000112149	ENSMUSG00000049176	X	167471309	168577231	-1	16	0	9	66	10	7	0	0	0	0	0		A2AFR3
ENSMUST00000112150						2	2	3	3	2	0	1	5	4	13	0		
ENSMUST00000112151	ENSMUSG00000048668	6	128357000	128362911	-1	1	0	3	0	0	3	107	190	75	56	86	E9Q1D4	
ENSMUST00000112152	ENSMUSG00000048668	6	128357000	128362911	-1	4	0	4	29	5	2	16	45	10	7	8	E9Q1D4	
ENSMUST00000112153						32	14	28	28	27	14	0	1	2	0	0		
ENSMUST00000112155	ENSMUSG00000006673	9	108516806	108560163	1	0	12	0	0	6	6	275	1021	816	194	668	G3X8R5	
ENSMUST00000112157	ENSMUSG00000030353	6	128224288	128300823	-1	0	0	0	51	0	0	0	0	0	0	0		
ENSMUST00000112159	ENSMUSG00000041966	2	71055328	71099142	1	18	6	13	54	16	6	2	1	5	2	3		Q3TUL7
ENSMUST00000112160	ENSMUSG00000072694	5	114808196	114813976	-1	6	4	15	23	16	6	45	253	73	33	81	Q3V495	
ENSMUST00000112161	ENSMUSG00000044583	X	167304929	167330558	-1	0	0	0	0	0	0	56	229	0	31	0	Q548J0	P58681
ENSMUST00000112162	ENSMUSG00000096169	17	33215261	33216351	-1	18	15	9	20	16	6	0	0	0	0	0	K7N6V7	
ENSMUST00000112163	ENSMUSG00000073557	1	134754658	134955942	-1	9	1	4	148	7	5	0	0	2	0	0		Q8BG95
ENSMUST00000112164	ENSMUSG00000044583	X	167304929	167330558	-1	5	0	1	2	10	0	0	32	102	21	40	Q548J0	P58681
ENSMUST00000112165	ENSMUSG00000093884	17	33199062	33200009	1	3	5	3	0	8	2	0	0	0	0	0	A0PK55	
ENSMUST00000112167	ENSMUSG00000041966	2	71055328	71099142	1	0	0	0	0	0	0	8	61	42	5	0	F8WIJ2	
ENSMUST00000112168	ENSMUSG00000094891	17	33176416	33177363	1	29	12	36	17	15	8	0	0	0	0	0	K7N6Q1	
ENSMUST00000112170	ENSMUSG00000040522	X	167242696	167264329	-1	0	0	0	0	0	0	556	1780	1038	606	555		P58682
ENSMUST00000112171	ENSMUSG00000030352	6	127961396	128143594	-1	5	4	20	0	17	6	0	0	0	0	0		Q8BJU2
ENSMUST00000112172	ENSMUSG00000049775	X	167207093	167209315	-1	13	23	27	95	51	38	43376	265655	58139	247559	36418	Q6ZWX2	P20065
ENSMUST00000112173	ENSMUSG00000030352	6	127961396	128143594	-1	31	18	52	38	40	13	16	7	9	15	73		Q8BJU2
ENSMUST00000112175	ENSMUSG00000049775	X	167207093	167209315	-1	5	0	13	2	6	0	137	1518	422	157	458		P20065
ENSMUST00000112176	ENSMUSG00000049775	X	167207093	167209315	-1	0	0	61	49	9	4	1556	13698	1483	2890	1079		P20065
ENSMUST00000112177	ENSMUSG00000006527	14	30714849	30822713	1	0	0	3	37	8	4	0	0	49	18	13		Q9JMD1
ENSMUST00000112179	ENSMUSG00000041975	2	70964561	71055583	-1	0	0	0	0	0	0	0	54	0	19	0		A2AUU0
ENSMUST00000112182						0	0	6	42	1	0	26	625	102	1	4		
ENSMUST00000112183	ENSMUSG00000041890	5	114727407	114775517	-1	0	11	0	0	0	0	649	100	46	21	0	D3Z1I2	
ENSMUST00000112184	ENSMUSG00000006527	14	30714849	30822713	1	11	6	14	7	5	0	17	0	24	0	16		Q9JMD1
ENSMUST00000112185	ENSMUSG00000041890	5	114727407	114775517	-1	20	0	29	0	11	0	559	1592	1094	122	715		Q9JLQ2
ENSMUST00000112186	ENSMUSG00000041975	2	70964561	71055583	-1	0	0	0	0	0	0	22	0	0	0	1		A2AUU0
ENSMUST00000112187	ENSMUSG00000051224	X	166499812	166518567	-1	0	0	4	0	0	1	0	0	7	0	4	A2AFP8	
ENSMUST00000112188	ENSMUSG00000051224	X	166499812	166518567	-1	16	28	40	66	19	12	84	263	97	18	76		Q3US16
ENSMUST00000112191	ENSMUSG00000037997	6	127446840	127494261	1	80	76	542	77	55	20	0	107	19	9	18		Q8CFF0
ENSMUST00000112192	ENSMUSG00000079317	X	166440574	166453140	1	0	0	0	0	0	0	15	54	18	123	24	A2AFP1	
ENSMUST00000112193	ENSMUSG00000037997	6	127446840	127494261	1	6	3	3	0	3	0	3	13	3	0	11		Q8CFF0
ENSMUST00000112194	ENSMUSG00000079317	X	166440574	166453140	1	1	0	2	0	7	1	33	139	4	0	4	Q5J9A9	Q9CQP2
ENSMUST00000112195	ENSMUSG00000037997	6	127446840	127494261	1	1	0	0	1	6	0	0	0	0	0	0		Q8CFF0
ENSMUST00000112197						26	23	41	114	37	12	2	8	11	2	12		
ENSMUST00000112198	ENSMUSG00000042207	1	134560171	134635285	1	9	5	6	8	16	2	567	991	1379	72	996		Q80Y84
ENSMUST00000112199						7	8	32	0	15	0	8	23	6	0	18		
ENSMUST00000112200	ENSMUSG00000025014	19	41029275	41059523	1	8	0	0	0	22	9	5	8	0	12	7	Q3UZ80	P09838
ENSMUST00000112201	ENSMUSG00000014959	2	70661576	70712636	1	0	6	0	9	0	0	50	103	69	13	55	A2ATI9	
ENSMUST00000112202	ENSMUSG00000021948	14	30595356	30626210	-1	0	0	0	0	0	0	0	0	0	0	0	Q1MX40	
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ENSMUST00000112205	ENSMUSG00000014959	2	70661576	70712636	1	2	1	4	7	3	0	0	19	99	0	81	A2ATI6	
ENSMUST00000112206	ENSMUSG00000021948	14	30595356	30626210	-1	0	0	0	0	0	0	0	0	0	6	0	Q1MX42	
ENSMUST00000112207	ENSMUSG00000021948	14	30595356	30626210	-1	0	0	8	0	0	0	2226	4574	1141	242	846	Q1MX43	
ENSMUST00000112208	ENSMUSG00000021948	14	30595356	30626210	-1	0	0	0	85	0	0	0	90	0	47	0	Q53YN4	P28867
ENSMUST00000112210	ENSMUSG00000021948	14	30595356	30626210	-1	0	0	0	5	0	0	4055	5040	7091	376	3902	Q53YN4	P28867
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ENSMUST00000112212	ENSMUSG00000011884	5	114669398	114690984	-1	0	0	23	0	0	0	98	0	99	0	98	D3Z1H9	
ENSMUST00000112214	ENSMUSG00000011884	5	114669398	114690984	-1	4	0	1	31	0	0	0	0	0	0	0	D3Z1H8	
ENSMUST00000112216						11	28	68	23	11	11	0	0	0	0	0		
ENSMUST00000112217	ENSMUSG00000014158	5	114622152	114658421	-1	10	0	0	0	0	0	6	8	0	0	9	D3Z1H7	
ENSMUST00000112219	ENSMUSG00000014158	5	114622152	114658421	-1	0	4	32	5	20	6	0	0	0	0	0	D3Z1H6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112220	ENSMUSG00000030346	6	126923050	126939587	-1	3	6	16	5	11	5	0	43	7	15	11		
ENSMUST00000112221	ENSMUSG00000030346	6	126923050	126939587	-1	1	2	4	1	3	2	19	0	9	27	2		
ENSMUST00000112222	ENSMUSG00000014158	5	114622152	114658421	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7L7	
ENSMUST00000112223	ENSMUSG00000031342	X	166238911	166388988	1	3	0	0	0	0	0	0	0	0	0	0	A2AEG3	
ENSMUST00000112224	ENSMUSG00000031342	X	166238911	166388988	1	0	5	0	0	0	0	1	0	0	0	0		P35803
ENSMUST00000112225	ENSMUSG00000014158	5	114622152	114658421	-1	0	2	0	0	6	3	0	0	2	5	0		Q9EPK8
ENSMUST00000112226	ENSMUSG00000031342	X	166238911	166388988	1	0	0	0	0	0	0	0	0	0	0	0		P35803
ENSMUST00000112227	ENSMUSG00000031342	X	166238911	166388988	1	0	0	0	0	0	0	0	0	0	0	0	A2AEG3	
ENSMUST00000112228	ENSMUSG00000031342	X	166238911	166388988	1	0	0	0	0	0	0	0	0	0	0	0	Q3US81	P35803
ENSMUST00000112229	ENSMUSG00000031342	X	166238911	166388988	1	1	0	0	0	0	0	0	0	0	0	0	A2AEG6	
ENSMUST00000112231	ENSMUSG00000048120	19	40612366	40741602	1	15	16	55	17	24	19	431	2691	941	242	734	Q544U5	P55772
ENSMUST00000112232	ENSMUSG00000026455	1	134455531	134491018	1	11	0	0	16	0	0	0	243	0	0	78		Q8BZM0
ENSMUST00000112233	ENSMUSG00000031342	X	166238911	166388988	1	0	0	0	0	0	0	0	0	1	0	0	Q3V0Z9	P35803
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ENSMUST00000112237	ENSMUSG00000026457	1	134415378	134433351	1	17	6	0	150	63	0	3025	7402	5748	891	4683	Q53YY4	Q91VH1
ENSMUST00000112238	ENSMUSG00000034998	17	88440711	88490533	1	12	19	15	30	12	3	846	1989	1069	160	643	E9Q7L6	
ENSMUST00000112239	ENSMUSG00000041939	5	114444269	114460591	1	0	0	0	0	0	0	0	0	0	0	1	Q3UEB4	
ENSMUST00000112241	ENSMUSG00000042064	2	70039126	70429198	1	14	1	17	7	12	2	0	0	0	2	0	Q0P645	
ENSMUST00000112242	ENSMUSG00000038077	6	126708329	126740674	-1	0	9	11	0	4	0	0	0	0	0	0		Q61923
ENSMUST00000112243	ENSMUSG00000042064	2	70039126	70429198	1	34	29	52	0	49	20	0	3	0	1	3		Q1EG27
ENSMUST00000112244	ENSMUSG00000049107	6	126101412	126166910	-1	8	5	21	18	0	0	12	11	8	6	0	Q3V1A4	
ENSMUST00000112245	ENSMUSG00000029575	5	114431034	114444060	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1G7	
ENSMUST00000112247	ENSMUSG00000061778	X	164936169	164980375	-1	0	1	0	0	5	0	192	545	261	336	124		Q9CWP6
ENSMUST00000112248	ENSMUSG00000061778	X	164936169	164980375	-1	3	0	0	0	0	0	12	14	5	55	26		Q9CWP6
ENSMUST00000112249	ENSMUSG00000015968	14	30039949	30491156	-1	0	0	0	24	0	40	0	0	0	0	0		Q99246
ENSMUST00000112250	ENSMUSG00000015968	14	30039949	30491156	-1	61	61	148	48	73	0	48	93	234	21	98		Q99246
ENSMUST00000112251	ENSMUSG00000044308	2	69897246	70024013	1	3	4	4	3	6	3	154	511	426	94	394	F6QC57	
ENSMUST00000112253	ENSMUSG00000001930	6	125546774	125686679	1	10	0	5	5	14	0	0	0	0	0	0	Q3TPE1	
ENSMUST00000112254	ENSMUSG00000001930	6	125546774	125686679	1	48	26	111	4	7	28	6	1	6	0	8	E9QPU1	
ENSMUST00000112255	ENSMUSG00000031381	X	164419793	164433916	1	9	17	34	32	0	26	0	0	0	0	0	A2AIH5	Q64323
ENSMUST00000112256						48	39	83	37	44	18	4	21	9	4	6		
ENSMUST00000112257	ENSMUSG00000031381	X	164419793	164433916	1	104	59	217	369	117	69	63	296	59	13	43	M0QWH5	
ENSMUST00000112260	ENSMUSG00000068882	2	69861562	69871846	1	0	0	0	0	0	0	15	79	0	0	0	A2AR07	
ENSMUST00000112263	ENSMUSG00000031377	X	164192842	164258193	-1	0	2	2	6	0	0	146	0	331	157	197	B1AUL5	P97504
ENSMUST00000112264	ENSMUSG00000026463	1	133699457	133801041	-1	2	0	0	0	0	0	6	0	7	0	19	Q32ME1	
ENSMUST00000112265	ENSMUSG00000031377	X	164192842	164258193	-1	5	10	5	0	5	4	384	3442	1099	2375	856	B1AUL6	
ENSMUST00000112266	ENSMUSG00000027088	2	69789623	69800005	1	0	0	0	0	0	0	0	285	0	29	0		Q9D9M5
ENSMUST00000112268	ENSMUSG00000042682	14	29968308	29975074	1	12	5	17	36	11	12	614	1526	519	2251	439		Q9JLJ1
ENSMUST00000112271	ENSMUSG00000015405	X	164139332	164188420	1	0	0	0	0	0	0	0	0	0	0	0	Q3URC9	Q8R0I0
ENSMUST00000112272	ENSMUSG00000021994	14	28504750	28527447	1	0	0	0	0	0	0	0	0	0	3	0		P22725
ENSMUST00000112275	ENSMUSG00000029591	5	114130386	114139323	1	6	20	230	2	11	5	22	9	0	5	1	D3Z1G1	
ENSMUST00000112279	ENSMUSG00000044339	5	114123926	114128218	-1	2	3	0	16	5	0	14	12	8	18	2		Q6P6J4
ENSMUST00000112280	ENSMUSG00000015401	X	164088830	164118860	1	0	0	5	5	3	3	0	0	0	0	0		Q9ESG4
ENSMUST00000112281	ENSMUSG00000030336	6	125232622	125237010	-1	0	0	0	0	0	0	9	0	5	3	0	D3Z7W5	
ENSMUST00000112282	ENSMUSG00000030336	6	125232622	125237010	-1	0	0	0	0	0	0	6	6	0	1	0	B7ZW87	
ENSMUST00000112286	ENSMUSG00000063145	2	69647171	69667571	1	0	0	0	0	0	0	0	9	2	0	0	A2AUC6	
ENSMUST00000112287	ENSMUSG00000070645	1	133350510	133360325	1	0	0	0	0	0	0	0	0	0	0	0	Q9R259	
ENSMUST00000112289	ENSMUSG00000031370	X	163935443	163958661	-1	35	33	53	149	24	14	50	263	145	21	136	B1B0E8	
ENSMUST00000112292	ENSMUSG00000042096	5	114003703	114025682	1	0	0	17	26	0	5	0	0	0	0	0		
ENSMUST00000112294	ENSMUSG00000031367	X	163909017	163933666	1	1	1	6	6	3	2	228	445	142	55	159	Q8BW87	
ENSMUST00000112295	ENSMUSG00000070284	9	108049242	108052801	1	10	12	25	38	18	5	7	80	41	6	63		Q8BTZ7
ENSMUST00000112298	ENSMUSG00000042121	5	113937094	113993894	-1	0	0	2	0	0	0	164	0	256	6	62		Q76I79
ENSMUST00000112300	ENSMUSG00000031360	X	162901238	163032508	1	0	2	0	0	0	0	127	739	173	125	102	A2AEQ5	
ENSMUST00000112301	ENSMUSG00000031360	X	162901238	163032508	1	0	15	0	0	0	0	0	0	3	0	0		P70303
ENSMUST00000112302	ENSMUSG00000031360	X	162901238	163032508	1	21	0	25	4	8	16	15	41	36	25	22		P70303
ENSMUST00000112303	ENSMUSG00000031360	X	162901238	163032508	1	0	0	0	49	8	0	20	62	53	18	79		P70303
ENSMUST00000112304	ENSMUSG00000061130	17	84956741	85023991	1	29	18	53	67	17	10	211	602	263	46	199	Q546R1	P36993
ENSMUST00000112305	ENSMUSG00000061130	17	84956741	85023991	1	0	0	0	5	0	0	21	62	27	0	16		P36993
ENSMUST00000112307	ENSMUSG00000061130	17	84956741	85023991	1	0	12	13	0	6	0	75	173	223	23	195		P36993
ENSMUST00000112308	ENSMUSG00000024120	17	84705247	84790789	-1	135	91	569	161	71	41	38	201	110	55	156		Q6PB66
ENSMUST00000112311	ENSMUSG00000025825	5	113772748	113778288	1	41	47	83	49	50	37	39	113	62	32	63	D3Z7W0	
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ENSMUST00000112314	ENSMUSG00000038344	X	162778919	162829454	-1	8	12	32	10	10	10	0	4	3	3	2	A2AFJ4	
ENSMUST00000112315	ENSMUSG00000038344	X	162778919	162829454	-1	11	1	2	5	6	0	4	9	8	3	7	Q3TT61	Q8BHN1
ENSMUST00000112316	ENSMUSG00000038344	X	162778919	162829454	-1	1	6	1	1	0	0	43	0	0	0	0		Q8BHN1
ENSMUST00000112317	ENSMUSG00000005232	2	69211073	69227841	1	0	4	3	7	8	0	0	0	0	0	0		Q9Z186
ENSMUST00000112318	ENSMUSG00000021877	14	26638074	26665084	1	0	0	9	9	1	0	39	313	0	0	14	E9Q798	
ENSMUST00000112320	ENSMUSG00000005233	2	69193895	69206194	-1	10	4	4	104	6	1	7	25	25	12	0		Q3UA16
ENSMUST00000112324	ENSMUSG00000042216	5	113243220	113310786	-1	1	5	4	6	5	1	0	0	0	0	0	D3Z7V5	
ENSMUST00000112325	ENSMUSG00000042216	5	113243220	113310786	-1	0	3	7	3	0	0	0	0	0	0	0	D3Z7V4	
ENSMUST00000112326	ENSMUSG00000031353	X	162760402	162779092	1	1	0	0	8	4	0	23	24	69	41	89	A2AFI9	
ENSMUST00000112327	ENSMUSG00000031353	X	162760402	162779092	1	0	0	7	5	0	5	112	454	183	152	90	A2AFJ1	
ENSMUST00000112329	ENSMUSG00000024992	19	38132781	38183947	1	0	12	23	23	18	11	0	0	0	0	0		Q91ZQ1
ENSMUST00000112330	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	287	462	263	62	185	D3Z7V3	
ENSMUST00000112331	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	97	189	0	48	0	F8WIH0	
ENSMUST00000112332						45	35	63	28	62	29	2	1	0	0	3		
ENSMUST00000112334	ENSMUSG00000040855	X	162411954	162643649	-1	0	0	0	89	0	0	0	0	0	0	0	A2AFI8	
ENSMUST00000112335	ENSMUSG00000024990	19	38116620	38125321	-1	0	3	0	6	0	0	0	1	0	35	0		Q00724
ENSMUST00000112336	ENSMUSG00000042240	5	113058258	113070117	-1	6	2	11	10	0	0	0	0	0	0	0		P62696
ENSMUST00000112338	ENSMUSG00000043518	X	161717069	161779496	1	4	0	0	43	9	2	1	0	0	0	0		Q9QVY8
ENSMUST00000112340	ENSMUSG00000072672	14	26257962	26269436	1	0	5	20	8	7	0	0	0	0	0	0	Q3UY88	
ENSMUST00000112345	ENSMUSG00000000037	X	161117193	161258213	1	0	0	0	0	0	0	0	0	0	0	0	E9Q796	
ENSMUST00000112346	ENSMUSG00000034780	2	67565871	68122689	1	18	20	9	7	16	5	0	0	0	0	0	Q505A3	O54904
ENSMUST00000112347	ENSMUSG00000027022	2	67446002	67526614	1	5	6	10	6	7	3	0	0	0	0	0		Q4U4S6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112349	ENSMUSG00000055817	17	83706163	83821516	1	0	0	0	1	0	0	223	489	320	26	274	E9Q794	
ENSMUST00000112350	ENSMUSG00000055817	17	83706163	83821516	1	1	0	0	0	3	0	46	0	16	4	64	Q3U3A7	
ENSMUST00000112352	ENSMUSG00000055817	17	83706163	83821516	1	4	5	6	7	10	4	85	359	158	16	256	Q3UII8	
ENSMUST00000112354	ENSMUSG00000075316	2	66480080	66634962	-1	6	9	16	0	27	0	0	0	0	0	0	B1AYL0	
ENSMUST00000112355						1	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000112357	ENSMUSG00000079330	1	132191431	132259227	1	0	0	0	0	0	0	0	0	0	0	0		Q14C37
ENSMUST00000112359	ENSMUSG00000042328	5	112343083	112378414	1	11	6	8	53	0	0	161	281	149	0	111	Q541V2	Q99KG7
ENSMUST00000112362	ENSMUSG00000026437	1	132112237	132139684	-1	0	0	0	0	1	0	8	0	3	1	11	Q0VDL6	Q04899
ENSMUST00000112363	ENSMUSG00000032624	17	83350931	83480361	1	0	0	0	0	0	0	0	0	58	0	0		
ENSMUST00000112364	ENSMUSG00000021866	14	25842156	25886804	1	2	0	19	8	2	11	93	117	168	0	392	D3Z7U0	
ENSMUST00000112365	ENSMUSG00000059149	1	132022806	132068062	-1	0	0	4	0	0	3	0	0	0	0	0	F8WIG8	
ENSMUST00000112366	ENSMUSG00000064329	2	66270778	66440840	-1	32	21	61	13	24	12	0	0	0	0	0	A2APX8	
ENSMUST00000112368	ENSMUSG00000031293	X	160768013	160799663	1	0	0	0	0	0	0	0	0	0	0	0	B1AU64	
ENSMUST00000112370	ENSMUSG00000059149	1	132022806	132068062	-1	66	36	20	61	59	29	21	27	56	0	40		Q6PDC8
ENSMUST00000112371	ENSMUSG00000064329	2	66270778	66440840	-1	0	0	0	0	0	0	0	0	0	0	0	A2APX6	
ENSMUST00000112375	ENSMUSG00000029343	5	112255815	112269585	1	3	0	0	0	0	0	1	1	0	0	0		Q9WVJ5
ENSMUST00000112376	ENSMUSG00000031295	X	160502166	160598878	1	0	5	10	12	7	4	3	0	3	0	3	Q6PE66	
ENSMUST00000112377	ENSMUSG00000031295	X	160502166	160598878	1	0	0	0	4	0	0	103	260	152	23	174		Q8BWJ3
ENSMUST00000112380	ENSMUSG00000031295	X	160502166	160598878	1	4	0	5	10	6	0	20	48	23	0	18	A2AHQ7	
ENSMUST00000112383	ENSMUSG00000066975	5	112246493	112252518	-1	0	0	0	7	0	0	10	0	9	8	0	E9QAS6	
ENSMUST00000112384	ENSMUSG00000025290	14	24490681	24496146	1	8	1	21	78	11	4	2671	13768	3873	19074	2308		P62849
ENSMUST00000112385	ENSMUSG00000066975	5	112246493	112252518	-1	0	0	5	0	0	0	0	0	0	0	0	Q3V1A0	Q9JJV0
ENSMUST00000112386	ENSMUSG00000026433	1	131867224	131872887	1	7	7	4	78	3	5	83	248	205	179	94	E9QLQ7	
ENSMUST00000112387	ENSMUSG00000010051	9	107576927	107581710	1	4	4	3	0	0	0	4	0	2	3	2		Q91ZJ9
ENSMUST00000112389	ENSMUSG00000024242	17	80580512	80728093	-1	2	3	4	16	5	1	7	0	0	4	0	E9QNE9	
ENSMUST00000112390	ENSMUSG00000063870	6	125095981	125130591	1	31	27	104	2	62	0	1871	4134	4572	145	3411	E9QAS5	
ENSMUST00000112391	ENSMUSG00000023307	19	37207543	37222139	1	2	3	13	13	10	0	13	72	86	24	18		
ENSMUST00000112392	ENSMUSG00000063870	6	125095981	125130591	1	0	0	3	138	0	28	1200	1425	2178	129	1523	E9QAS4	
ENSMUST00000112393	ENSMUSG00000042251	1	131797381	131821473	1	264	241	1240	525	386	209	5	21	11	2	15		Q8C165
ENSMUST00000112394	ENSMUSG00000044647	2	65845767	66031546	1	0	0	0	11	0	1	0	0	1	0	0		P59055
ENSMUST00000112397	ENSMUSG00000044647	2	65845767	66031546	1	0	0	0	0	0	0	0	0	0	0	0	H3BJW4	
ENSMUST00000112398	ENSMUSG00000031298	X	160390690	160498070	1	4	0	4	0	3	0	0	0	0	2	0	A2AHQ2	
ENSMUST00000112400	ENSMUSG00000031298	X	160390690	160498070	1	0	0	0	0	0	0	0	0	0	0	0	Q14AX7	Q8CJ12
ENSMUST00000112401	ENSMUSG00000031298	X	160390690	160498070	1	0	0	0	0	0	0	0	0	0	0	0	Q14BH6	
ENSMUST00000112402	ENSMUSG00000031298	X	160390690	160498070	1	0	0	0	0	0	0	0	0	0	0	0		Q8CJ12
ENSMUST00000112404	ENSMUSG00000031298	X	160390690	160498070	1	10	10	18	0	0	6	0	2	0	0	1		Q8CJ12
ENSMUST00000112405	ENSMUSG00000031298	X	160390690	160498070	1	0	0	0	0	0	0	0	0	0	0	0		Q8CJ12
ENSMUST00000112408	ENSMUSG00000031298	X	160390690	160498070	1	0	0	0	44	13	0	0	0	0	0	0		Q8CJ12
ENSMUST00000112411	ENSMUSG00000004552	1	131638306	131675505	1	0	0	3	15	5	0	0	1137	45	0	0	D3Z6T3	
ENSMUST00000112412						6	2	6	0	4	2	11	172	27	8	45		
ENSMUST00000112413	ENSMUSG00000072770	6	125049689	125063267	1	0	2	8	0	2	0	0	0	0	0	0	F2Z440	
ENSMUST00000112414	ENSMUSG00000072770	6	125049689	125063267	1	2	1	11	35	4	2	28	112	37	0	76		Q3V140
ENSMUST00000112417	ENSMUSG00000030330	6	125039760	125049265	1	0	0	0	0	0	0	116	543	235	74	200		Q8C0D7
ENSMUST00000112420	ENSMUSG00000061171	2	65316430	65364034	-1	9	0	0	0	0	0	0	0	0	0	0		Q3USY0
ENSMUST00000112423	ENSMUSG00000063142	14	23289431	24004859	-1	0	0	0	0	2	2	0	0	0	0	0	F7BHL0	
ENSMUST00000112424	ENSMUSG00000038346	6	125009145	125037870	1	0	0	0	0	0	0	187	366	90	21	312	E9QAR6	
ENSMUST00000112425	ENSMUSG00000038346	6	125009145	125037870	1	0	1	0	0	0	5	87	502	388	0	235	E9QAR4	
ENSMUST00000112426	ENSMUSG00000029507	5	110773667	110780659	-1	14	6	45	10	15	1	0	0	0	0	13		Q9WU56
ENSMUST00000112427	ENSMUSG00000038346	6	125009145	125037870	1	0	0	0	7	0	0	0	0	0	0	0	E9Q1A5	
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ENSMUST00000112429	ENSMUSG00000034903	2	65088339	65239403	-1	0	18	28	0	0	0	0	0	0	0	0	B1AZ14	
ENSMUST00000112430	ENSMUSG00000034903	2	65088339	65239403	-1	0	0	0	16	0	0	0	0	0	0	0		Q3UMF0
ENSMUST00000112431	ENSMUSG00000034903	2	65088339	65239403	-1	0	0	0	33	32	0	0	0	0	0	0	B1AZ14	
ENSMUST00000112433	ENSMUSG00000029505	5	110664373	110770717	-1	9	9	15	48	0	7	3	4	5	0	2	D3Z6R8	
ENSMUST00000112435	ENSMUSG00000029505	5	110664373	110770717	-1	0	0	48	51	0	17	66	40	77	0	112		Q8CHI8
ENSMUST00000112436	ENSMUSG00000029505	5	110664373	110770717	-1	0	0	0	121	56	0	319	388	1964	0	1677		Q8CHI8
ENSMUST00000112437	ENSMUSG00000059811	17	79848392	79896123	-1	45	37	20	179	67	30	0	0	13	20	11	E9QND8	
ENSMUST00000112439	ENSMUSG00000030127	6	124958413	124965538	-1	2	0	5	32	6	0	71	60	27	25	37		Q9CZ04
ENSMUST00000112442	ENSMUSG00000026430	1	131176410	131245258	-1	0	0	0	0	0	0	0	0	8	0	0	D3Z6G2	
ENSMUST00000112446	ENSMUSG00000026427	1	131153181	131187658	1	0	0	5	14	4	2	5	44	26	4	2	E9PUG7	
ENSMUST00000112447						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000112451	ENSMUSG00000040990	X	159627272	159978069	1	0	3	0	0	0	3	0	275	6	24	0		Q8R550
ENSMUST00000112452	ENSMUSG00000059742	2	62693414	63184287	-1	10	7	3	0	10	4	0	0	0	0	0	Q8C782	
ENSMUST00000112453	ENSMUSG00000040990	X	159627272	159978069	1	1	0	0	0	1	0	0	180	0	60	0		Q8R550
ENSMUST00000112454	ENSMUSG00000059742	2	62693414	63184287	-1	0	0	0	23	0	0	0	0	0	0	0	Q8CC38	
ENSMUST00000112456	ENSMUSG00000040990	X	159627272	159978069	1	204	243	563	298	287	120	94	285	258	49	204	Q3TA88	Q8R550
ENSMUST00000112458	ENSMUSG00000021767	14	21481434	21672478	1	0	1	0	0	0	0	0	0	0	2	0	Q14AW2	
ENSMUST00000112459	ENSMUSG00000026896	2	62595798	62646255	-1	2	1	0	0	0	3	35	400	180	42	195		Q8R5F7
ENSMUST00000112460	ENSMUSG00000033610	19	34810894	34879455	-1	12	11	48	3	9	9	4	11	6	0	4	Q543J7	Q8K4K6
ENSMUST00000112463	ENSMUSG00000067297	19	34617049	34640743	-1	208	133	149	133	125	106	91	662	88	94	65	Q3U687	
ENSMUST00000112464	ENSMUSG00000044150	X	159526688	159593081	1	1	3	4	45	0	0	51	39	12	29	23		A2AG58
ENSMUST00000112465	ENSMUSG00000016524	1	130932656	130940115	-1	0	0	1	0	0	1	0	0	0	3	0	Q14BK1	Q8CJ70
ENSMUST00000112467	ENSMUSG00000079339	19	34592888	34601968	-1	9	0	0	0	0	0	8	50	5	0	7	D3Z6F0	
ENSMUST00000112470	ENSMUSG00000041020	X	159414572	159498757	1	4	0	0	0	0	0	0	0	0	0	0		A2AG50
ENSMUST00000112471	ENSMUSG00000041020	X	159414572	159498757	1	11	5	8	43	11	0	0	0	0	0	0		A2AG50
ENSMUST00000112472	ENSMUSG00000024778	19	34290659	34327770	1	1	3	0	0	0	2	4	17	9	11	7	Q8C350	
ENSMUST00000112473	ENSMUSG00000038451	6	124808661	124810619	1	7	8	20	10	5	3	36	117	49	15	44		O88838
ENSMUST00000112475	ENSMUSG00000030125	6	124769863	124779727	-1	0	0	10	15	0	3	3	10	0	2	2		O35125
ENSMUST00000112476	ENSMUSG00000004267	6	124760053	124769673	-1	0	0	0	0	0	0	0	7	2	1	0	D3Z6E4	
ENSMUST00000112477	ENSMUSG00000026415	1	130800902	130814740	1	22	0	31	7	7	7	0	0	0	0	0		Q2TB54
ENSMUST00000112478	ENSMUSG00000029503	5	110339812	110343212	-1	0	0	0	93	0	7	0	0	0	1	0		Q8K3P1
ENSMUST00000112479	ENSMUSG00000023249	9	106470322	106476949	-1	0	0	0	0	0	0	0	0	0	12	0	Q3ULW8	
ENSMUST00000112480	ENSMUSG00000026904	2	62046462	62326730	1	0	9	0	0	3	0	0	0	0	0	0		Q5DTL9
ENSMUST00000112481	ENSMUSG00000007080	5	110286306	110337474	1	2	0	0	0	0	0	4	5	0	15	0	E9QAP6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112482	ENSMUSG00000007080	5	110286306	110337474	1	0	0	0	25	0	2	1	4	0	3	0	E9QAP5	
ENSMUST00000112483						5	4	0	4	3	3	0	0	0	0	0		
ENSMUST00000112484	ENSMUSG00000004266	6	124720707	124738714	-1	7	0	7	26	8	3	10300	13527	10561	1421	6814		P29351
ENSMUST00000112487	ENSMUSG00000056121	17	78377885	78418131	-1	0	16	20	0	0	0	0	0	0	14	0	D3Z6D5	
ENSMUST00000112488	ENSMUSG00000026401	1	130388537	130423009	-1	0	0	3	4	8	1	0	0	0	0	0	E9QAP4	
ENSMUST00000112491	ENSMUSG00000031309	X	159210307	159368244	1	2	0	9	0	1	1	1	3	0	0	0	B1AXP0	
ENSMUST00000112492	ENSMUSG00000031309	X	159210307	159368244	1	0	0	0	1	0	0	5	2	0	0	3	B1AXN8	
ENSMUST00000112493	ENSMUSG00000031309	X	159210307	159368244	1	3	2	4	0	0	0	71	171	275	0	0	B1AXN9	
ENSMUST00000112494	ENSMUSG00000064289	2	61578585	61654171	1	6	5	7	2	5	2	62	144	57	80	70	A2AR78	
ENSMUST00000112495	ENSMUSG00000064289	2	61578585	61654171	1	0	0	0	16	0	0	200	954	523	670	177	Q8C2D3	
ENSMUST00000112498	ENSMUSG00000024074	17	78200248	78376592	1	44	28	99	220	47	26	13	9	12	9	71		Q9JLL0
ENSMUST00000112501	ENSMUSG00000064289	2	61578585	61654171	1	8	4	13	7	5	4	96	317	97	205	79		P70347
ENSMUST00000112502	ENSMUSG00000064289	2	61578585	61654171	1	1	0	3	0	0	2	0	0	0	20	0	A2AR76	
ENSMUST00000112503						13	22	145	24	22	12	2	18	9	0	23		
ENSMUST00000112504						0	1	74	3	5	2	0	0	0	0	0		
ENSMUST00000112505	ENSMUSG00000029500	5	110259130	110269913	-1	6	0	0	0	0	0	60	144	90	75	107		Q8BX10
ENSMUST00000112507	ENSMUSG00000002017	17	75537086	75551946	-1	17	15	20	37	24	10	46	176	110	94	78		Q3TJZ6
ENSMUST00000112508	ENSMUSG00000024766	19	33517740	33761951	-1	0	5	4	16	7	0	2	20	2	0	0	Q3UT41	
ENSMUST00000112509	ENSMUSG00000026970	2	60750193	60963192	-1	0	3	0	58	2	0	0	0	543	16	459	Q3TTX8	Q91W59
ENSMUST00000112511	ENSMUSG00000079344	19	33498037	33517780	-1	4	2	6	0	3	0	0	0	0	0	0	D3Z608	
ENSMUST00000112512	ENSMUSG00000029502	5	110176701	110226470	1	39	38	90	76	34	12	211	903	488	94	412		
ENSMUST00000112513	ENSMUSG00000025658	X	157821436	158043294	-1	1	2	2	33	2	1	0	1	0	0	0	A2AI78	
ENSMUST00000112514	ENSMUSG00000001870	17	75005568	75392512	1	0	0	4	0	0	5	0	5	0	37	148		Q8CG19
ENSMUST00000112516	ENSMUSG00000001870	17	75005568	75392512	1	0	13	0	0	0	0	0	0	0	0	70		Q8CG19
ENSMUST00000112517	ENSMUSG00000026971	2	60598292	60722643	-1	18	6	10	6	15	5	0	0	0	0	0	B1AYG6	
ENSMUST00000112519	ENSMUSG00000014668	5	110135842	110171972	1	17	2	5	21	6	3	790	2206	1218	376	1003		Q810L3
ENSMUST00000112520	ENSMUSG00000041476	X	157698910	157752591	1	0	0	1	3	0	0	0	0	0	0	0		Q9DC77
ENSMUST00000112521	ENSMUSG00000041476	X	157698910	157752591	1	0	0	0	0	2	0	0	0	0	0	0		Q9DC77
ENSMUST00000112522	ENSMUSG00000046873	X	157535371	157598715	-1	2	0	3	0	0	0	0	0	6	3	2	A0A0A0MQE2	
ENSMUST00000112523	ENSMUSG00000008153	6	124430759	124464794	-1	11	6	21	19	11	4	0	4	0	1	0	D3Z601	
ENSMUST00000112524	ENSMUSG00000032786	9	106233455	106248126	-1	15	13	12	74	23	17	0	19	0	0	4	Q3V0B2	Q8VC19
ENSMUST00000112525	ENSMUSG00000054580	2	60417543	60553308	-1	18	24	7	15	23	17	1	2	0	1	0	A0A0A0MQE3	Q62028
ENSMUST00000112528	ENSMUSG00000023284	5	110110092	110129794	1	36	32	60	39	38	24	21	170	43	40	53	E9QAH2	
ENSMUST00000112529	ENSMUSG00000071708	X	157443855	157492287	-1	8	15	12	66	14	7	2	35	10	9	9		P97355
ENSMUST00000112530	ENSMUSG00000005069	6	124396816	124415067	-1	9	0	19	0	15	5	177	0	0	41	3	D3Z600	
ENSMUST00000112531	ENSMUSG00000005069	6	124396816	124415067	-1	13	0	65	117	21	3	134	0	0	0	0		O09012
ENSMUST00000112532	ENSMUSG00000005069	6	124396816	124415067	-1	0	9	0	0	0	0	0	0	0	0	61		O09012
ENSMUST00000112533	ENSMUSG00000026980	2	60292103	60383303	-1	7	32	69	89	43	31	826	1742	1124	72	556	A2AW86	
ENSMUST00000112534	ENSMUSG00000064247	5	110099969	110105953	1	11	10	103	82	45	6	0	0	17	0	0	D3Z5Z4	
ENSMUST00000112536	ENSMUSG00000066613	5	109996521	110010411	1	7	15	8	6	11	5	0	12	4	0	0	D3Z5Z2	
ENSMUST00000112537	ENSMUSG00000079346	6	124347593	124357086	-1	1	2	2	3	2	1	0	0	0	0	0	Q0P521	
ENSMUST00000112538	ENSMUSG00000036086	1	127954184	128103047	-1	10	14	18	5	19	0	3	0	0	0	0		Q6NZP1
ENSMUST00000112540	ENSMUSG00000066613	5	109996521	110010411	1	11	3	3	0	0	0	12	40	0	10	0		E9QAG8
ENSMUST00000112541	ENSMUSG00000008845	6	124304656	124330527	1	0	0	0	0	45	0	0	10	0	63	130	B7ZMW6	Q2VLH6
ENSMUST00000112542	ENSMUSG00000055109	X	155624741	156345887	1	2	1	4	3	0	1	0	0	0	0	0	B1B034	
ENSMUST00000112543	ENSMUSG00000020258	9	106152857	106158138	-1	1	10	88	64	25	0	23	17	20	7	18		
ENSMUST00000112544	ENSMUSG00000090015	5	109923400	109943936	1	17	16	32	16	20	11	11	127	8	21	18	D3Z5Y8	
ENSMUST00000112547	ENSMUSG00000072762	5	109735990	109751886	-1	3	6	6	2	5	0	24	59	13	20	10	E9QAG4	
ENSMUST00000112550	ENSMUSG00000026987	2	59899363	60209839	-1	25	0	73	54	0	21	444	760	214	311	396	A2AUY4	
ENSMUST00000112551	ENSMUSG00000025283	X	155213132	155216449	-1	0	2	0	1	1	0	1112	4411	3215	14094	2381	A2BES2	
ENSMUST00000112552	ENSMUSG00000024817	19	30030513	30093722	1	19	5	0	35	15	17	4	4	0	0	0	Q3T995	
ENSMUST00000112554	ENSMUSG00000023349	6	123229843	123247021	1	4	0	0	0	0	2	49	148	0	154	14		Q9JKF4
ENSMUST00000112557						1	0	2	0	6	0	236	1628	447	41	183		
ENSMUST00000112558	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	0	2	0	0	18	90	56	22	55		Q80XR2
ENSMUST00000112559	ENSMUSG00000055746	X	155027201	155093666	-1	0	0	2	0	0	0	0	0	0	0	0	Q9R2A2	
ENSMUST00000112560	ENSMUSG00000008090	5	108692382	108706924	1	0	0	17	0	0	0	5	6	4	0	10		Q91V87
ENSMUST00000112562	ENSMUSG00000063728	X	154924012	154935987	-1	1	0	0	0	0	0	0	0	0	0	0	O89010	
ENSMUST00000112563	ENSMUSG00000033540	5	108660331	108684557	1	12	0	0	0	0	0	0	0	0	0	0	Q8BMG0	
ENSMUST00000112565	ENSMUSG00000094592	X	154109633	154120685	-1	0	9	4	2	0	0	0	0	0	0	0	A2BEE3	
ENSMUST00000112568	ENSMUSG00000035168	2	59612042	59846149	1	0	0	0	110	0	0	0	23	99	0	40	E9QAF9	
ENSMUST00000112570	ENSMUSG00000026349	1	127774164	127808061	1	0	0	0	19	1	2	250	929	466	152	466	E9QAF8	
ENSMUST00000112571	ENSMUSG00000024067	17	74299474	74323944	-1	4	4	7	107	9	4	63	208	79	310	41		Q99LT0
ENSMUST00000112572	ENSMUSG00000041633	X	153685154	153696391	-1	22	15	140	162	44	32	0	28	0	0	11	Q8C7J6	
ENSMUST00000112573	ENSMUSG00000048573	X	153558593	153559429	1	3	0	0	0	0	0	0	0	0	0	0	B1AY64	
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ENSMUST00000112576	ENSMUSG00000016498	19	29410919	29471157	1	12	7	20	16	10	6	7	2	2	0	5	Q3U304	Q9WUL5
ENSMUST00000112577	ENSMUSG00000026991	2	59160850	59355208	1	15	5	29	0	7	4	0	15	0	0	0	A2AS47	
ENSMUST00000112580	ENSMUSG00000012396	6	122707489	122714633	1	0	0	0	0	0	22	0	0	0	0	0		Q80Z64
ENSMUST00000112581	ENSMUSG00000012396	6	122707489	122714633	1	30	21	65	19	25	0	1	7	1	0	10		Q80Z64
ENSMUST00000112583	ENSMUSG00000049690	1	125913620	126830799	-1	0	0	0	0	0	0	0	0	0	0	0	E9QAE1	
ENSMUST00000112584	ENSMUSG00000025332	X	152233020	152274535	1	9	0	31	0	7	0	306	310	526	46	666		P41230
ENSMUST00000112585	ENSMUSG00000040613	6	122577792	122602444	-1	0	0	15	35	9	7	391	2367	625	1835	716	Q3U9G8	P51908
ENSMUST00000112586	ENSMUSG00000040613	6	122577792	122602444	-1	0	12	48	0	17	4	0	88	226	247	207	Q3U9G8	P51908
ENSMUST00000112587	ENSMUSG00000040613	6	122577792	122602444	-1	18	23	28	0	14	11	69	1525	115	631	257	Q3U9G8	P51908
ENSMUST00000112588	ENSMUSG00000025332	X	152233020	152274535	1	8	14	0	32	10	7	461	1343	598	28	477		P41230
ENSMUST00000112589	ENSMUSG00000079353	2	58859434	58907618	1	0	2	7	0	0	0	0	0	0	0	0	F7CV60	
ENSMUST00000112590	ENSMUSG00000032561	9	104288316	104337728	-1	12	11	66	19	13	4	48	74	66	87	75		Q8CE08
ENSMUST00000112591	ENSMUSG00000024064	17	73493228	73710453	-1	1	3	3	13	4	1	1	0	0	0	0		Q8BVG5
ENSMUST00000112595	ENSMUSG00000093979	14	19563801	19585135	-1	0	0	0	0	0	0	0	0	0	0	0	A6NAU1	
ENSMUST00000112597	ENSMUSG00000033623	5	108461232	108506976	1	8	5	8	25	8	2	0	11	9	0	7		Q8BTQ0
ENSMUST00000112598	ENSMUSG00000012405	14	18267823	18271391	-1	0	13	5	33	12	4	68	235	154	400	47	Q5M8Q0	Q9CZM2
ENSMUST00000112599	ENSMUSG00000026836	2	58388644	58567157	-1	0	0	0	0	1	4	0	10	0	6	0		P37172
ENSMUST00000112600	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	29	0	0	0	107	0	0	0	36	Q3V116	
ENSMUST00000112601	ENSMUSG00000026836	2	58388644	58567157	-1	0	0	0	0	6	0	3	19	5	0	0		P37172

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112603	ENSMUSG00000036815	1	123321471	124045559	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z5I7	
ENSMUST00000112604	ENSMUSG00000041115	X	152144268	152225236	1	0	12	21	54	32	19	0	0	0	0	14	D3Z5I6	
ENSMUST00000112605	ENSMUSG00000041115	X	152144268	152225236	1	0	0	0	0	0	0	0	0	0	0	0	E9QAD8	
ENSMUST00000112606	ENSMUSG00000036815	1	123321471	124045559	-1	4541	5590	5939	3646	5280	2451	40	211	76	74	131	E9QN98	
ENSMUST00000112607	ENSMUSG00000026834	2	58267453	58357895	-1	4	0	0	22	0	0	0	0	0	0	0	A2AJR6	
ENSMUST00000112608	ENSMUSG00000026834	2	58267453	58357895	-1	0	0	0	0	3	1	0	0	0	0	0	A2AJR5	
ENSMUST00000112610	ENSMUSG00000007458	6	122308720	122317680	1	19	23	0	0	33	5	0	33	0	0	0	Q3UKQ5	P24668
ENSMUST00000112612	ENSMUSG00000052942	19	28258851	28680077	-1	4	8	12	0	0	2	0	0	0	0	0		Q6XP49
ENSMUST00000112616	ENSMUSG00000026828	2	57997884	58045860	1	18	38	152	43	37	33	0	0	0	0	1		Q8C102
ENSMUST00000112617	ENSMUSG00000025260	X	152001845	152004442	1	4	4	0	0	0	0	0	0	15	10	0	A2AFQ2	
ENSMUST00000112618	ENSMUSG00000026827	2	57237635	57370719	1	26	0	0	137	0	16	0	0	0	0	0	A2AQR0	
ENSMUST00000112621	ENSMUSG00000026339	1	121431049	121506460	1	0	0	0	0	0	0	113	179	218	86	172	E9QAD4	
ENSMUST00000112622	ENSMUSG00000025261	X	151800807	151935417	1	20	0	51	28	42	17	371	1699	981	162	1001		Q7TMY8
ENSMUST00000112624	ENSMUSG00000021786	14	16238656	16249808	-1	1	0	1	11	0	1	17	15	0	14	37		Q9D404
ENSMUST00000112625	ENSMUSG00000021786	14	16238656	16249808	-1	0	0	1	11	1	0	34	34	84	5	16		Q9D404
ENSMUST00000112626	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	0	0	0	1	0	29	13	11	E9QAD3	
ENSMUST00000112627	ENSMUSG00000026826	2	57106830	57124003	-1	79	69	379	108	64	46	2	16	12	7	25	A2AQQ8	
ENSMUST00000112629	ENSMUSG00000026826	2	57106830	57124003	-1	19	0	0	0	0	0	0	0	0	0	0	Q3TYI4	Q06219
ENSMUST00000112630	ENSMUSG00000042567	14	14820765	15006743	1	13	0	13	9	11	0	0	3	0	1	2	K3W4R8	
ENSMUST00000112631	ENSMUSG00000042567	14	14820765	15006743	1	0	18	0	0	0	7	0	0	0	0	0		Q3UGM2
ENSMUST00000112632	ENSMUSG00000026824	2	55435970	55598145	1	0	0	0	0	0	0	0	3	0	0	2	B1AYE4	
ENSMUST00000112633	ENSMUSG00000026824	2	55435970	55598145	1	7	0	8	0	5	6	0	0	0	0	0	Q3ZAT1	P63250
ENSMUST00000112634	ENSMUSG00000060988	2	54436317	55118309	1	0	0	134	0	29	18	0	0	0	0	0		Q8CF93
ENSMUST00000112635	ENSMUSG00000060988	2	54436317	55118309	1	27	15	0	0	0	0	1	0	0	0	0	A2RRI8	Q8CF93
ENSMUST00000112636	ENSMUSG00000060988	2	54436317	55118309	1	31	17	0	394	48	24	1	0	0	1	0	A2RRI8	Q8CF93
ENSMUST00000112637	ENSMUSG00000024921	19	26605115	26778321	1	0	0	0	0	0	0	0	0	0	0	0	Q9D007	
ENSMUST00000112639	ENSMUSG00000026389	1	120190757	120272705	-1	0	0	11	0	2	0	0	0	0	0	0		
ENSMUST00000112640	ENSMUSG00000026389	1	120190757	120272705	-1	0	0	2	23	2	0	33	64	4	15	75		
ENSMUST00000112641	ENSMUSG00000026389	1	120190757	120272705	-1	32	23	44	32	30	30	4	15	2	9	31		
ENSMUST00000112642	ENSMUSG00000011831	5	107744795	107875107	-1	7	17	17	11	10	7	64	350	171	66	165	F8VPT6	
ENSMUST00000112643	ENSMUSG00000026389	1	120190757	120272705	-1	34	30	35	42	40	7	31	0	13	7	46	E9QN92	
ENSMUST00000112644	ENSMUSG00000026388	1	120121187	120188189	1	0	0	0	0	0	0	8	34	3	22	0		Q9CRW3
ENSMUST00000112645	ENSMUSG00000032554	9	103204001	103230444	-1	47	64	122	45	45	21	4949	5175	5371	0	3395		Q921I1
ENSMUST00000112648	ENSMUSG00000026385	1	120113280	120121078	-1	3	0	10	0	2	0	0	0	14	5	0	D3Z563	
ENSMUST00000112650	ENSMUSG00000033773	5	107597373	107661838	1	16	0	0	19	6	6	0	0	0	0	0		Q8VC34
ENSMUST00000112651	ENSMUSG00000033773	5	107597373	107661838	1	6	0	13	3	0	0	0	0	0	0	0		Q8VC34
ENSMUST00000112654	ENSMUSG00000033773	5	107597373	107661838	1	0	0	15	0	0	0	0	0	0	0	6		Q8VC34
ENSMUST00000112655	ENSMUSG00000033773	5	107597373	107661838	1	0	12	0	0	0	0	2	5	8	3	0		Q8VC34
ENSMUST00000112656	ENSMUSG00000056296	14	13284780	13615459	1	0	7	0	0	0	0	0	0	0	0	0		Q8BGN8
ENSMUST00000112657	ENSMUSG00000054423	14	12372563	12823079	-1	0	9	0	70	10	7	0	0	0	1	0	K4DI76	
ENSMUST00000112658	ENSMUSG00000054423	14	12372563	12823079	-1	0	5	0	40	6	4	0	0	0	0	0		Q80TJ1
ENSMUST00000112662	ENSMUSG00000041229	X	151520672	151633859	1	4	4	0	9	4	0	0	0	0	0	1	A2ABV3	Q80TJ7
ENSMUST00000112664						0	17	108	15	0	3	12	7	0	5	0		
ENSMUST00000112666	ENSMUSG00000041229	X	151520672	151633859	1	2	3	0	72	2	1	0	0	0	0	0		Q80TJ7
ENSMUST00000112668	ENSMUSG00000041229	X	151520672	151633859	1	80	81	236	84	85	47	0	4	0	3	5	A2ABV1	
ENSMUST00000112669	ENSMUSG00000033111	14	12284209	12303231	1	0	0	0	0	7	13	0	35	11	50	6		Q8BGD0
ENSMUST00000112670	ENSMUSG00000041229	X	151520672	151633859	1	0	1	0	0	0	1	6	3	6	0	0	Z4YL84	
ENSMUST00000112671	ENSMUSG00000044060	5	107497378	107512556	1	28	14	14	17	20	1	0	0	0	0	0	G3X9V7	
ENSMUST00000112673	ENSMUSG00000024867	19	24294794	24555872	-1	0	1	27	0	7	8	0	0	0	0	0		P70181
ENSMUST00000112674	ENSMUSG00000049672	17	69383050	69390750	1	15	0	0	44	10	25	0	31	140	20	31	Q544H8	Q08376
ENSMUST00000112676	ENSMUSG00000049672	17	69383050	69390750	1	18	21	68	114	42	0	27	41	39	11	55	Q544H8	Q08376
ENSMUST00000112677	ENSMUSG00000029279	5	107331159	107387058	1	8	3	2	0	8	0	0	0	0	0	0		Q91Y44
ENSMUST00000112680	ENSMUSG00000024044	17	69156810	69289985	1	0	0	0	0	0	16	0	0	0	0	0		Q9WV92
ENSMUST00000112682	ENSMUSG00000004902	6	120773578	120794336	1	8	6	21	35	8	3	6	2	15	3	13		Q9DB41
ENSMUST00000112683	ENSMUSG00000025264	X	151087094	151096543	-1	4	7	5	7	8	2	2	12	5	5	13	Z4YL87	
ENSMUST00000112685	ENSMUSG00000025265	X	151046150	151089521	1	0	8	13	2	9	3	0	0	0	4	10	A2ALP5	
ENSMUST00000112686	ENSMUSG00000071226	6	120666369	120771190	1	34	31	32	59	59	30	2	4	7	2	17	E9QA25	
ENSMUST00000112688	ENSMUSG00000026377	1	118321839	118333822	1	0	0	0	24	1	5	0	0	12	77	30		Q91VE6
ENSMUST00000112689	ENSMUSG00000033885	14	8098213	8165111	1	0	17	0	0	0	0	0	29	0	0	36		Q8BX57
ENSMUST00000112690	ENSMUSG00000043410	5	106840192	106926321	-1	0	0	0	0	0	0	0	0	0	0	0		D3Z4R1
ENSMUST00000112691	ENSMUSG00000025266	X	150983141	151017322	-1	33	33	49	39	29	16	117	277	215	52	229		Q6PGG6
ENSMUST00000112693	ENSMUSG00000036202	2	52072837	52122383	1	6	9	5	6	7	5	19	19	27	3	17		Q6PR54
ENSMUST00000112694						3	2	3	2	3	0	0	0	0	2	5		
ENSMUST00000112695	ENSMUSG00000049606	5	106616739	106697287	-1	0	1	0	2	0	0	0	0	0	0	0	E9QA23	
ENSMUST00000112696	ENSMUSG00000049606	5	106616739	106697287	-1	14	20	29	43	33	0	20	156	45	132	17	E9QA22	
ENSMUST00000112697	ENSMUSG00000025268	X	150806370	150814345	-1	0	0	7	0	2	0	0	6	12	6	11	Q9ER67	
ENSMUST00000112698	ENSMUSG00000049606	5	106616739	106697287	-1	0	0	0	0	0	14	0	0	50	0	0	E9Q624	
ENSMUST00000112699	ENSMUSG00000025268	X	150806370	150814345	-1	3	0	0	2	0	6	0	0	0	0	13	Q9ER67	
ENSMUST00000112700	ENSMUSG00000025268	X	150806370	150814345	-1	0	0	0	2	0	2	6	0	0	40	0	Q9ER67	
ENSMUST00000112701	ENSMUSG00000026312	1	109982431	110140157	1	63	50	234	98	35	33	0	3	0	0	2		Q8BM92
ENSMUST00000112703	ENSMUSG00000030177	6	120324323	120364374	-1	0	9	20	6	0	0	0	0	18	36	3		Q9CZH8
ENSMUST00000112705	ENSMUSG00000026946	2	51948487	51973494	-1	2	5	0	20	4	3	47	495	129	535	153	Q3UJ82	O35309
ENSMUST00000112706	ENSMUSG00000026315	1	107590006	107610484	1	13	23	9	14	20	14	4	0	3	6	6		O08800
ENSMUST00000112707	ENSMUSG00000070639	5	105415775	105490074	1	16	11	32	25	35	4	39	38	56	11	85		Q5DU41
ENSMUST00000112709	ENSMUSG00000025272	X	150645304	150657583	-1	19	0	0	12	0	10	0	0	0	0	0	Q6DIC6	
ENSMUST00000112711	ENSMUSG00000041377	6	120093350	120200339	1	11	0	8	3	0	0	0	0	0	0	0	Q3TQA7	Q9JL89
ENSMUST00000112712	ENSMUSG00000050447	2	50066429	50193569	1	0	0	14	32	0	4	0	1	1	0	0		Q8BPP5
ENSMUST00000112713	ENSMUSG00000025271	X	150588229	150643878	1	0	0	6	10	7	4	0	0	0	0	0		P70266
ENSMUST00000112715	ENSMUSG00000025270	X	150547375	150570638	1	0	0	28	21	1	14	171	39	39	445	470	A2AFM1	
ENSMUST00000112717	ENSMUSG00000044594	1	107045587	107052303	-1	4	4	4	3	6	9	0	0	0	0	0	G3X9V8	
ENSMUST00000112718	ENSMUSG00000034438	5	105014150	105139540	-1	1	0	0	0	0	0	0	0	1	4	9	Q2V6D6	
ENSMUST00000112719	ENSMUSG00000025269	X	150519519	150589868	-1	0	0	0	0	0	0	0	0	0	0	5	A2AFM5	
ENSMUST00000112720	ENSMUSG00000025269	X	150519519	150589868	-1	7	4	20	10	4	3	9	16	9	4	11	A2AFM3	
ENSMUST00000112721	ENSMUSG00000025269	X	150519519	150589868	-1	0	0	0	0	0	0	3	27	0	8	16	A2AFM4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112724	ENSMUSG00000059956	1	106934449	106957080	1	2	2	0	6	11	0	0	0	0	1	0		Q9D7P9
ENSMUST00000112725	ENSMUSG00000025269	X	150519519	150589868	-1	134	151	265	179	160	82	14	25	15	11	22		Q68G58
ENSMUST00000112726	ENSMUSG00000096828	14	6314876	6343678	-1	2	0	0	0	9	2	0	0	0	0	0	D3Z4P5	
ENSMUST00000112727	ENSMUSG00000025269	X	150519519	150589868	-1	0	0	0	0	0	0	0	0	0	0	0		Q68G58
ENSMUST00000112728	ENSMUSG00000095533	14	3395093	3403525	1	0	2	2	0	3	4	0	0	0	0	0	L7N465	
ENSMUST00000112729	ENSMUSG00000067006	1	106861173	106883348	1	8	6	0	0	7	0	0	0	0	3	0		P70124
ENSMUST00000112730	ENSMUSG00000067006	1	106861173	106883348	1	0	0	0	4	0	5	0	0	0	0	0		P70124
ENSMUST00000112736	ENSMUSG00000009907	1	106764071	106796728	-1	8	5	15	34	27	6	28	301	76	54	104	Q3TN07	P46467
ENSMUST00000112737	ENSMUSG00000094811	14	6296365	6304843	-1	7	0	0	0	0	0	0	0	0	0	0	L7N252	
ENSMUST00000112740	ENSMUSG00000095082	X	149941655	149984982	1	5	4	0	0	0	0	0	0	0	0	0	B1AZM2	
ENSMUST00000112741	ENSMUSG00000094378	X	149784473	149826694	1	0	0	0	0	0	0	0	0	0	0	0	E9QA14	
ENSMUST00000112742	ENSMUSG00000079371	14	6105321	6125807	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6M5	
ENSMUST00000112745	ENSMUSG00000036792	2	48949508	49325405	1	8	9	8	0	12	11	54	74	75	2	26	B1AYB7	
ENSMUST00000112746	ENSMUSG00000029304	5	104435118	104441050	1	0	0	0	0	0	0	0	0	0	11	10	D3Z4N2	
ENSMUST00000112747	ENSMUSG00000029304	5	104435118	104441050	1	0	0	3	0	5	0	0	0	0	0	7	Q547B5	P10923
ENSMUST00000112748	ENSMUSG00000029304	5	104435118	104441050	1	0	2	6	5	0	0	0	0	0	426	31	Q547B5	P10923
ENSMUST00000112751	ENSMUSG00000057329	1	106538178	106714274	-1	36	32	106	303	58	30	59	150	75	39	229		P10417
ENSMUST00000112753	ENSMUSG00000096834	X	148663598	148703849	1	0	0	0	0	0	0	0	0	0	0	0	E9Q1L3	
ENSMUST00000112754	ENSMUSG00000036792	2	48949508	49325405	1	0	9	0	0	0	6	90	344	253	48	201		B1AYB6
ENSMUST00000112755	ENSMUSG00000079374	X	148613253	148615153	-1	42	40	153	908	79	28	0	0	0	0	0	F7CD45	
ENSMUST00000112756	ENSMUSG00000055003	6	119315133	119330766	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BGX3
ENSMUST00000112758	ENSMUSG00000096629	14	5607620	5807982	-1	0	4	0	0	2	0	0	0	0	0	1	A6NAS6	
ENSMUST00000112767	ENSMUSG00000079378	14	5131519	5139959	1	0	0	0	0	0	0	0	0	0	0	0	Q497R9	
ENSMUST00000112770	ENSMUSG00000096197	14	5050629	5059243	1	9	24	0	5	5	0	0	0	0	0	0	L7N253	
ENSMUST00000112771	ENSMUSG00000053268	5	104170712	104180127	1	16	18	27	42	20	17	0	0	0	0	0	E9Q9Z9	
ENSMUST00000112772	ENSMUSG00000079382	19	21555674	21557657	1	1	1	0	4	2	1	4	5	3	3	1	F7CCV5	
ENSMUST00000112776	ENSMUSG00000079386	14	4430992	4519452	1	2	2	0	0	0	0	0	0	0	0	0	E9Q9Z8	
ENSMUST00000112777	ENSMUSG00000041477	6	119175253	119221616	1	0	5	46	92	6	4	4	5	7	0	9	B9EIX0	
ENSMUST00000112778	ENSMUSG00000079388	14	4334763	4354688	1	0	0	3	0	0	0	0	0	0	3	0	Q9D073	
ENSMUST00000112779	ENSMUSG00000079389	14	4317283	4325721	1	0	0	0	0	0	0	0	0	0	0	0	L7N254	
ENSMUST00000112781						2	2	0	0	6	0	0	0	0	0	0		
ENSMUST00000112785						5	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000112787	ENSMUSG00000095686	14	3998394	4007006	1	12	0	0	0	4	3	0	0	0	0	0	L7N255	
ENSMUST00000112788	ENSMUSG00000079395	X	148488949	148521446	1	0	0	0	0	0	0	0	0	0	0	0	B1B0X6	
ENSMUST00000112790	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	F8WJL1	
ENSMUST00000112792	ENSMUSG00000093887	14	3846245	3856085	1	0	0	0	0	0	0	0	0	0	0	0	E9Q9X9	
ENSMUST00000112793	ENSMUSG00000051331	6	118587240	119196418	-1	2	3	14	0	4	6	0	0	0	0	0	F7C376	
ENSMUST00000112796	ENSMUSG00000072930	X	148180724	148224710	1	0	0	0	0	0	0	0	0	0	0	0	B1B0X0	
ENSMUST00000112797	ENSMUSG00000096039	14	3224440	3234351	1	15	11	14	410	7	8	0	5	0	1	4	E9PYQ5	
ENSMUST00000112801	ENSMUSG00000079402	14	3652030	3673215	1	2	0	0	0	3	0	0	0	0	0	0	E9Q3J7	
ENSMUST00000112802	ENSMUSG00000095368	14	3634512	3642943	1	0	2	2	0	3	4	0	0	0	0	0	L7N465	
ENSMUST00000112803	ENSMUSG00000034528	5	103955440	103977410	-1	0	0	0	0	2	0	0	0	0	0	0		Q8VCR2
ENSMUST00000112804	ENSMUSG00000072931	X	147992993	148033174	1	1	0	17	0	2	1	0	0	0	0	0	A2BI02	
ENSMUST00000112810	ENSMUSG00000036890	2	44564412	44927657	-1	113	114	61	51	69	23	113	598	291	232	200		Q8BW56
ENSMUST00000112811	ENSMUSG00000029312	5	103861973	103911259	-1	0	0	0	2	0	0	0	0	0	0	0	A2AH59	
ENSMUST00000112814	ENSMUSG00000095872	X	147765991	147833456	1	7	9	9	3	5	8	0	0	0	0	0	A2ADW8	
ENSMUST00000112815	ENSMUSG00000029312	5	103861973	103911259	-1	0	0	0	0	5	11	6	10	0	0	0	A2AH60	
ENSMUST00000112819	ENSMUSG00000031290	X	147470375	147554081	-1	0	1	3	0	4	1	0	0	0	0	0		Q3UMG5
ENSMUST00000112822	ENSMUSG00000049744	2	43748824	44395953	1	6	0	0	0	0	0	75	549	323	657	219		Q811M1
ENSMUST00000112824	ENSMUSG00000049744	2	43748824	44395953	1	11	13	15	5	21	9	10	70	24	65	21	B1AW40	
ENSMUST00000112825	ENSMUSG00000051331	6	118587240	119196418	-1	5	6	14	10	8	0	0	0	0	0	0		Q01815
ENSMUST00000112826	ENSMUSG00000026866	2	43555329	43682715	1	0	0	0	0	2	0	0	17	3	34	0	Q6NSV5	
ENSMUST00000112827	ENSMUSG00000031289	X	147383476	147429192	-1	0	0	0	0	0	0	0	0	0	0	0		O88786
ENSMUST00000112828	ENSMUSG00000036192	19	18930605	19111196	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000112830	ENSMUSG00000007827	6	118501308	118562226	-1	27	22	27	69	32	9	4	20	11	11	35	D3Z482	
ENSMUST00000112831	ENSMUSG00000041380	X	146962513	147197277	1	0	0	0	0	0	2	0	0	0	0	0	B1ATN4	
ENSMUST00000112832	ENSMUSG00000036192	19	18930605	19111196	-1	45	14	189	245	78	0	0	0	0	0	0		Q8R1B8
ENSMUST00000112835	ENSMUSG00000041688	X	145446425	145505181	-1	14	5	30	29	24	12	0	0	6	0	9	A0A067XG49	
ENSMUST00000112836	ENSMUSG00000041688	X	145446425	145505181	-1	0	0	65	0	0	0	10	0	4	0	4		Q8VHG2
ENSMUST00000112839						6	0	5	1	0	0	0	0	0	0	0		
ENSMUST00000112840	ENSMUSG00000023965	17	63057452	63500017	-1	14	9	14	0	7	0	78	202	110	21	50	G3X9V9	
ENSMUST00000112841	ENSMUSG00000057710	9	101938481	101943219	1	3	3	2	5	8	2	0	0	0	0	0	D3Z3U4	
ENSMUST00000112842	ENSMUSG00000026333	1	97770172	97793709	1	9	7	10	8	11	4	0	7	8	25	10		Q8K259
ENSMUST00000112843	ENSMUSG00000071679	X	144688907	145122411	1	6	6	0	19	2	0	0	0	0	0	0		Q3URY0
ENSMUST00000112844	ENSMUSG00000026333	1	97770172	97793709	1	0	0	0	0	4	0	5	96	27	82	8		Q8K259
ENSMUST00000112845	ENSMUSG00000040648	1	97706048	97770411	-1	0	20	0	0	0	10	22	79	91	79	54	E9Q9J4	
ENSMUST00000112846	ENSMUSG00000046709	5	102907948	103211334	-1	11	7	5	5	3	1	0	0	0	0	0	Q3TQZ7	
ENSMUST00000112847	ENSMUSG00000046709	5	102907948	103211334	-1	0	0	0	0	0	0	0	0	0	0	0	Q8C9D4	
ENSMUST00000112848	ENSMUSG00000046709	5	102907948	103211334	-1	14	4	7	5	9	11	0	0	0	0	0	E9QN59	
ENSMUST00000112850	ENSMUSG00000026754	2	39016155	39065541	-1	24	15	19	0	0	0	0	3	6	0	0		Q9CW79
ENSMUST00000112851	ENSMUSG00000031285	X	143855842	143933311	-1	33	16	120	88	7	10	0	3	5	0	0	Q6PGI2	
ENSMUST00000112852	ENSMUSG00000057315	5	102481391	102897937	1	5	6	63	16	27	7	0	0	0	0	0		Q8C4V1
ENSMUST00000112853	ENSMUSG00000057315	5	102481391	102897937	1	0	6	0	0	3	3	8	27	0	0	7		Q8C4V1
ENSMUST00000112854	ENSMUSG00000057315	5	102481391	102897937	1	3	0	0	0	0	0	0	266	32	19	9		Q8C4V1
ENSMUST00000112856	ENSMUSG00000031285	X	143855842	143933311	-1	0	0	0	0	0	0	0	0	0	0	0	Q9CXL6	
ENSMUST00000112857						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000112858	ENSMUSG00000059689	6	117841180	117845956	1	0	0	0	0	0	0	5	0	0	0	0	D3Z3T2	
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ENSMUST00000112860	ENSMUSG00000059689	6	117841180	117845956	1	0	0	0	3	0	0	0	0	0	0	0		Q80V23
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ENSMUST00000112862	ENSMUSG00000026755	2	39005348	39015877	1	0	0	0	119	5	0	0	110	27	21	27	A3KGQ6	
ENSMUST00000112863	ENSMUSG00000031284	X	143518591	143797796	1	0	0	0	0	0	0	0	0	0	0	0		Q61036
ENSMUST00000112864	ENSMUSG00000031284	X	143518591	143797796	1	0	0	7	0	3	3	0	0	0	0	0		Q61036
ENSMUST00000112865	ENSMUSG00000031284	X	143518591	143797796	1	11	9	4	0	10	3	0	0	0	0	0		Q61036

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112866	ENSMUSG00000061353	6	117168535	117181367	1	3	0	4	42	10	5	0	0	0	2	4		P40224
ENSMUST00000112868	ENSMUSG00000031284	X	143518591	143797796	1	0	0	0	3	0	0	0	0	0	0	0		Q61036
ENSMUST00000112870	ENSMUSG00000034116	17	57279100	57328031	1	2	11	0	0	0	2	832	0	374	0	316	Q8VDU4	
ENSMUST00000112871	ENSMUSG00000061353	6	117168535	117181367	1	0	0	0	0	0	0	0	0	0	4	2		P40224
ENSMUST00000112872	ENSMUSG00000035295	2	38997476	39006168	1	4	5	31	1	4	7	1	0	1	0	0		Q9D994
ENSMUST00000112874	ENSMUSG00000032475	9	100492293	100546134	-1	4	4	0	0	0	0	290	1681	422	318	205	Q8BH99	
ENSMUST00000112877	ENSMUSG00000063972	2	38723370	38927688	-1	12	28	41	106	28	0	0	0	9	0	16		Q64249
ENSMUST00000112878	ENSMUSG00000031283	X	143285674	143394262	-1	5	4	6	47	9	0	0	0	0	0	0		Q920C1
ENSMUST00000112880	ENSMUSG00000059878	6	116624016	116628999	-1	3	2	17	56	3	4	0	14	34	0	0		Q9ERU3
ENSMUST00000112881	ENSMUSG00000073609	1	93824909	93852348	1	24	15	30	35	15	10	241	285	339	27	196	E9QN44	
ENSMUST00000112882	ENSMUSG00000032473	9	99689461	99717267	-1	0	0	0	0	0	0	0	0	0	0	0		P56857
ENSMUST00000112883	ENSMUSG00000026751	2	38692656	38714542	-1	0	0	21	67	4	9	0	0	0	0	0		P33242
ENSMUST00000112884	ENSMUSG00000037784	9	99629496	99669256	1	0	0	15	2	0	0	0	0	0	0	4		Q499E4
ENSMUST00000112885	ENSMUSG00000037784	9	99629496	99669256	1	24	22	40	159	46	27	0	0	0	0	0	B2RR42	Q499E4
ENSMUST00000112886	ENSMUSG00000037784	9	99629496	99669256	1	24	0	24	3	0	0	0	0	0	0	0		Q499E4
ENSMUST00000112887	ENSMUSG00000029314	5	100845713	100899102	1	0	0	0	131	7	6	0	72	0	0	0		Q8C0N2
ENSMUST00000112888	ENSMUSG00000047045	X	142681406	142843494	1	11	0	71	0	17	0	793	3630	1151	204	945	A2AHA2	
ENSMUST00000112889	ENSMUSG00000047045	X	142681406	142843494	1	0	0	0	15	0	0	0	85	18	11	7	A2AH99	
ENSMUST00000112890	ENSMUSG00000026281	1	93792576	93801934	-1	36	37	171	76	22	22	48	88	37	201	35	Q6GRA7	P97930
ENSMUST00000112891	ENSMUSG00000047045	X	142681406	142843494	1	0	0	0	0	0	0	40	0	18	0	13	A2AH98	
ENSMUST00000112893	ENSMUSG00000026281	1	93792576	93801934	-1	5	0	6	1	2	0	5	25	19	2	0	D3Z3R3	
ENSMUST00000112895	ENSMUSG00000026749	2	38511643	38594606	1	0	0	13	37	0	0	211	11	257	45	117		Q9ES70
ENSMUST00000112896	ENSMUSG00000047045	X	142681406	142843494	1	11	0	0	66	0	0	1048	442	636	0	456		Q6PHN7
ENSMUST00000112898	ENSMUSG00000016833	5	100798627	100804471	1	0	0	0	0	0	0	16	16	28	248	23	D3Z3D3	
ENSMUST00000112900	ENSMUSG00000042213	6	116264222	116330298	1	0	0	0	0	13	0	447	705	460	288	181	K3W4R9	
ENSMUST00000112901	ENSMUSG00000016833	5	100798627	100804471	1	163	151	252	135	334	129	0	159	41	16	61	Q8BTZ9	
ENSMUST00000112902	ENSMUSG00000026749	2	38511643	38594606	1	17	12	29	0	18	3	461	514	705	128	194	A2ATN9	
ENSMUST00000112903	ENSMUSG00000031278	X	142317993	142390535	-1	4	2	3	0	0	0	0	391	36	0	155	Q91YN3	Q9QUJ7
ENSMUST00000112904	ENSMUSG00000031278	X	142317993	142390535	-1	2	1	1	0	0	0	237	121	417	244	142	Q91YN3	Q9QUJ7
ENSMUST00000112905	ENSMUSG00000026279	1	93701935	93754864	-1	0	0	0	5	0	0	374	388	223	36	116		Q6P3Z3
ENSMUST00000112907	ENSMUSG00000031278	X	142317993	142390535	-1	6	0	0	0	0	0	7	143	0	0	0		Q9QUJ7
ENSMUST00000112908	ENSMUSG00000035273	5	100679484	100719716	-1	0	0	0	97	5	0	0	0	46	4	23	D3Z3C3	
ENSMUST00000112910	ENSMUSG00000029322	5	100553725	100572245	-1	9	9	12	8	16	11	5	29	15	2	34		Q9JI48
ENSMUST00000112911	ENSMUSG00000032463	9	98986373	99002021	1	0	3	0	0	0	0	0	0	0	0	0	D3Z3C1	
ENSMUST00000112912	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3C0	
ENSMUST00000112913	ENSMUSG00000042271	X	142226770	142239692	1	4	4	6	11	3	2	34	138	35	9	27		Q3UNA4
ENSMUST00000112914	ENSMUSG00000042271	X	142226770	142239692	1	0	0	0	5	2	0	24	0	0	81	13		Q3UNA4
ENSMUST00000112915	ENSMUSG00000079414	17	57092035	57105942	-1	10	13	11	12	21	4	0	2	1	4	7	Q3U4K9	
ENSMUST00000112916	ENSMUSG00000042271	X	142226770	142239692	1	2	0	0	0	0	0	0	0	53	50	18		Q3UNA4
ENSMUST00000112920	ENSMUSG00000035437	2	37443279	37566454	1	0	0	0	0	0	0	107	1638	186	124	0	B2RRC5	A2AWA9
ENSMUST00000112923	ENSMUSG00000030323	6	115853470	115926699	1	0	0	6	27	7	0	0	0	20	0	0	E9Q9G8	
ENSMUST00000112925	ENSMUSG00000030323	6	115853470	115926699	1	14	0	0	38	0	0	10	0	0	0	30		Q6NWV3
ENSMUST00000112930	ENSMUSG00000031274	X	141475385	141689234	1	10	0	0	0	11	7	0	0	0	9	16	Q63ZW6	
ENSMUST00000112931	ENSMUSG00000031274	X	141475385	141689234	1	0	10	19	17	0	0	0	0	0	0	26	Q63ZW6	
ENSMUST00000112932	ENSMUSG00000066798	2	37425500	37443171	-1	36	14	50	274	33	60	29	0	97	9	54		Q8K088
ENSMUST00000112933	ENSMUSG00000079415	19	12763660	12765632	-1	0	6	4	0	11	3	8	57	6	0	9	Q544D1	P51642
ENSMUST00000112934	ENSMUSG00000075376	2	37370069	37422903	-1	0	0	0	170	15	0	72	77	133	60	129	A2AVP4	
ENSMUST00000112935	ENSMUSG00000032456	9	98287435	98420438	1	0	13	0	89	14	14	0	0	0	5	10		Q99JR6
ENSMUST00000112936	ENSMUSG00000075376	2	37370069	37422903	-1	0	0	0	0	0	0	19	0	172	0	69		P0C090
ENSMUST00000112937	ENSMUSG00000032456	9	98287435	98420438	1	11	0	15	8	0	2	0	5	2	0	0	Q3V3C7	
ENSMUST00000112938	ENSMUSG00000032456	9	98287435	98420438	1	7	7	3	2	7	0	0	1	0	3	4	Q3V3F1	
ENSMUST00000112939	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	0	0	0	229	1036	486	0	19	G3X9W0	
ENSMUST00000112940	ENSMUSG00000009030	2	37350074	37359332	-1	17	9	30	18	23	11	29	75	68	35	67		Q9DBX2
ENSMUST00000112942	ENSMUSG00000026273	1	93299211	93305915	-1	11	5	16	15	17	8	14	28	17	9	9	D3Z3A4	
ENSMUST00000112944	ENSMUSG00000026273	1	93299211	93305915	-1	25	17	192	14	17	23	16	269	29	32	48	D3Z3A2	
ENSMUST00000112946	ENSMUSG00000059900	6	115729131	115762410	-1	11	5	25	29	13	2	317	376	312	134	150	E9QN39	
ENSMUST00000112949	ENSMUSG00000000441	6	115618067	115676635	-1	10	6	40	80	14	11	1717	3148	1082	295	1216		Q99N57
ENSMUST00000112950	ENSMUSG00000049315	2	36784276	36787468	1	0	2	0	0	8	2	0	0	0	0	0	Q8VGK3	
ENSMUST00000112951	ENSMUSG00000043587	9	96823336	96892669	-1	0	0	8	0	9	0	0	0	21	0	11		Q8BHA9
ENSMUST00000112952	ENSMUSG00000044994	19	12087612	12091847	-1	1	8	27	6	8	3	0	0	0	0	0	Q8VG74	
ENSMUST00000112956	ENSMUSG00000079416	5	98552695	98553744	1	0	0	0	0	0	0	0	0	0	0	0	F6YG85	
ENSMUST00000112957	ENSMUSG00000068011	6	115583544	115592576	-1	2	0	0	0	4	3	0	0	0	0	0	D3Z393	
ENSMUST00000112958	ENSMUSG00000014602	1	93015464	93101951	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q9G6	
ENSMUST00000112959	ENSMUSG00000035456	5	98180978	98188991	1	71	40	188	745	84	37	0	2	1	0	2	B2RU90	
ENSMUST00000112960	ENSMUSG00000026890	2	36081953	36105408	-1	0	0	0	0	0	0	0	0	0	0	0	H9H9T0	
ENSMUST00000112961	ENSMUSG00000026890	2	36081953	36105408	-1	42	46	63	88	31	27	0	0	0	0	0		Q9R1R0
ENSMUST00000112963	ENSMUSG00000026890	2	36081953	36105408	-1	0	0	0	140	0	0	0	0	0	0	0		Q9R1R0
ENSMUST00000112966	ENSMUSG00000026890	2	36081953	36105408	-1	0	0	73	51	24	0	1	1	0	1	0		Q9R1R0
ENSMUST00000112967	ENSMUSG00000026890	2	36081953	36105408	-1	0	0	0	63	0	0	0	0	0	0	7	E9QN32	
ENSMUST00000112968	ENSMUSG00000055725	5	97082329	97111596	-1	884	607	3686	910	978	459	8	83	57	20	46	D3Z181	
ENSMUST00000112969	ENSMUSG00000055725	5	97082329	97111596	-1	0	2	0	8	0	0	40	12	37	5	46	Q0VAZ2	Q6TCG8
ENSMUST00000112971	ENSMUSG00000079418	X	140956907	141164270	1	13	10	12	13	10	4	96	666	329	553	119	Q5EBK1	Q8C9S8
ENSMUST00000112974	ENSMUSG00000034663	5	96997689	97091867	1	3	3	84	22	2	0	334	795	436	48	279		Q91Z96
ENSMUST00000112975						7	0	6	11	7	10	0	0	0	0	0		
ENSMUST00000112976	ENSMUSG00000026885	2	35751241	35979913	-1	19	6	0	5	8	14	3	0	3	10	7		A4Q9F4
ENSMUST00000112978	ENSMUSG00000031429	X	140948429	140956728	-1	0	2	1	3	3	2	15	96	43	81	18	A2AG83	
ENSMUST00000112979	ENSMUSG00000040828	17	56628143	56664456	1	20	19	28	17	23	9	0	7	1	5	1		E9Q9F6
ENSMUST00000112981	ENSMUSG00000026883	2	35558266	35730994	1	0	3	19	7	0	0	0	0	3	0	0	F6Y0W2	
ENSMUST00000112983	ENSMUSG00000026883	2	35558266	35730994	1	7	9	23	4	8	0	521	705	633	40	455		Q3UHC7
ENSMUST00000112984	ENSMUSG00000024681	19	11629496	11640851	-1	0	0	25	0	0	0	46	82	57	121	13	Q53ZU3	Q920C4
ENSMUST00000112986	ENSMUSG00000026883	2	35558266	35730994	1	14	3	3	11	14	6	0	0	0	0	0		Q3UHC7
ENSMUST00000112987	ENSMUSG00000026883	2	35558266	35730994	1	5	5	7	0	0	0	212	27	1	0	74	A2AUX3	
ENSMUST00000112988	ENSMUSG00000000266	X	140664599	140767715	1	0	0	4	1	1	2	0	0	0	0	0	B1AVF5	
ENSMUST00000112990	ENSMUSG00000000266	X	140664599	140767715	1	0	0	6	28	0	0	0	0	0	0	0	B1AVF4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000112992	ENSMUSG00000026883	2	35558266	35730994	1	0	0	0	0	5	6	0	0	0	0	0		Q3UHC7
ENSMUST00000112993	ENSMUSG00000000266	X	140664599	140767715	1	9	9	0	0	9	2	1	0	0	1	0	B1AVF4	
ENSMUST00000112995						33	21	284	49	8	0	17	1076	65	10	210		
ENSMUST00000112996	ENSMUSG00000031431	X	140539528	140600659	-1	4	1	8	101	9	11	249	129	168	28	176		Q9Z2S7
ENSMUST00000112998	ENSMUSG00000034212	1	92870129	92902906	-1	24	14	33	19	28	17	2	0	1	0	0	E9PUG3	
ENSMUST00000112999	ENSMUSG00000073616	1	92637145	92641985	-1	5	3	13	1	4	5	4	11	6	2	7	D3Z159	
ENSMUST00000113001	ENSMUSG00000035778	2	35400179	35463231	-1	18	6	6	21	0	0	0	0	62	0	95	Q8C2H7	
ENSMUST00000113002	ENSMUSG00000035778	2	35400179	35463231	-1	4	0	0	0	8	0	0	111	77	3	0	Q3TXW0	P23336
ENSMUST00000113005	ENSMUSG00000034724	5	96070333	96164171	-1	0	0	0	0	0	0	217	340	240	65	169		Q8VEG6
ENSMUST00000113007	ENSMUSG00000031433	X	139889511	139998595	-1	8	12	20	8	4	4	23	0	0	0	30		Q8JZV4
ENSMUST00000113009	ENSMUSG00000079421	2	35375562	35397175	-1	0	0	4	0	0	4	0	1	0	0	0	Q14BP7	
ENSMUST00000113010	ENSMUSG00000079421	2	35375562	35397175	-1	5	6	0	2	8	0	0	0	0	0	0	A2AUQ8	
ENSMUST00000113011	ENSMUSG00000031433	X	139889511	139998595	-1	0	0	0	0	0	0	6	108	85	55	3	A2AG09	
ENSMUST00000113014						55	38	60	66	37	13	0	12	1	0	9		
ENSMUST00000113022	ENSMUSG00000056952	6	113697050	113711069	1	17	3	57	88	9	3	561	940	696	89	440	B7ZNL9	
ENSMUST00000113024						3	2	13	9	5	5	5	9	8	5	17		
ENSMUST00000113025	ENSMUSG00000026878	2	35180205	35201120	-1	3	22	0	7	12	3	35	676	114	39	192	A2AL34	
ENSMUST00000113026	ENSMUSG00000031438	X	139563316	139673145	1	4	2	7	132	14	7	0	55	12	15	32		Q9D304
ENSMUST00000113027	ENSMUSG00000031438	X	139563316	139673145	1	0	2	0	0	1	0	24	0	0	0	0	A2AGL8	
ENSMUST00000113028	ENSMUSG00000045414	9	94517864	94538081	-1	6	6	4	154	13	2	61	170	82	16	52		Q3USZ8
ENSMUST00000113029						1	2	5	0	1	2	1	14	0	0	4		
ENSMUST00000113030	ENSMUSG00000042498	X	139480367	139554582	1	0	0	4	2	7	1	1	1	0	3	1		Q8C779
ENSMUST00000113032	ENSMUSG00000057110	2	35109492	35178822	1	0	0	19	10	3	4	12	79	0	35	0	R4GML3	
ENSMUST00000113033	ENSMUSG00000057110	2	35109492	35178822	1	13	13	30	16	1	0	0	0	0	0	0	A2AS42	
ENSMUST00000113034	ENSMUSG00000057110	2	35109492	35178822	1	2	5	4	0	10	0	12	390	0	0	422	R4GML4	
ENSMUST00000113035	ENSMUSG00000001228	17	56303321	56323486	1	13	19	0	133	21	10	57	0	42	0	0		Q8VDF2
ENSMUST00000113037	ENSMUSG00000057110	2	35109492	35178822	1	4	8	7	0	16	0	0	0	243	0	0	E9Q9E7	
ENSMUST00000113038	ENSMUSG00000001228	17	56303321	56323486	1	0	0	35	0	0	9	45	221	159	0	110		Q8VDF2
ENSMUST00000113039	ENSMUSG00000001228	17	56303321	56323486	1	0	0	0	0	0	0	143	7	78	38	26		Q8VDF2
ENSMUST00000113041	ENSMUSG00000042515	X	139210042	139238335	1	0	0	0	6	0	0	0	0	0	0	0		Q4VA55
ENSMUST00000113042	ENSMUSG00000042515	X	139210042	139238335	1	6	4	8	0	7	1	0	0	0	0	0		Q4VA55
ENSMUST00000113043	ENSMUSG00000042515	X	139210042	139238335	1	0	1	0	6	0	0	0	0	0	0	0		Q4VA55
ENSMUST00000113044	ENSMUSG00000032372	9	92275602	92297752	1	1	0	0	0	0	0	0	81	3	9	7	D3Z7J3	
ENSMUST00000113045	ENSMUSG00000042515	X	139210042	139238335	1	0	0	0	0	0	0	0	0	0	0	0		Q4VA55
ENSMUST00000113046	ENSMUSG00000042525	X	139179228	139181009	1	1	1	1	4	1	0	0	0	0	0	0	Q9D3X3	
ENSMUST00000113051	ENSMUSG00000029381	5	92683435	92965318	1	0	0	0	593	0	0	0	0	0	0	0		
ENSMUST00000113052	ENSMUSG00000052854	X	138914430	139010532	1	35	20	146	32	29	9	0	0	1	0	0	B1B0C9	
ENSMUST00000113054	ENSMUSG00000029381	5	92683435	92965318	1	0	26	159	8	42	24	0	0	1	0	13		
ENSMUST00000113055	ENSMUSG00000029381	5	92683435	92965318	1	48	22	107	263	51	11	0	0	0	0	0	E9QMY5	
ENSMUST00000113059	ENSMUSG00000032363	9	90163069	90208071	1	36	24	0	172	19	0	0	0	0	0	0		Q68SA9
ENSMUST00000113060	ENSMUSG00000032363	9	90163069	90208071	1	0	0	59	0	0	33	0	0	0	0	0		Q68SA9
ENSMUST00000113062						0	5	15	4	0	0	0	0	0	3	6		
ENSMUST00000113063	ENSMUSG00000059203	X	137570608	138846946	1	3	3	0	23	11	0	0	0	0	0	0	Q0VBP3	Q9ERS6
ENSMUST00000113064	ENSMUSG00000026875	2	34941750	34961772	-1	2	1	4	64	11	5	0	23	0	0	0		P39428
ENSMUST00000113066	ENSMUSG00000023443	X	137115397	137122083	-1	13	0	6	59	5	0	0	0	0	0	0	A2AG22	
ENSMUST00000113067	ENSMUSG00000031428	X	136993155	136998472	1	0	0	0	7	0	3	4	0	0	0	10		Q8VD24
ENSMUST00000113068	ENSMUSG00000026870	2	34874396	34892132	1	17	0	0	17	0	0	0	0	0	0	0	Q9D1U5	
ENSMUST00000113069	ENSMUSG00000044348	X	136981116	137038302	-1	0	0	0	0	0	0	3	0	0	3	0	A2AF28	
ENSMUST00000113070	ENSMUSG00000044348	X	136981116	137038302	-1	0	0	0	0	4	0	0	0	9	0	10	A2AF28	
ENSMUST00000113071	ENSMUSG00000089768	X	136974022	136976874	-1	0	1	0	0	0	0	5	16	10	30	5	A2AF33	
ENSMUST00000113072	ENSMUSG00000011305	17	56111601	56117596	-1	30	4	77	56	22	9	18	44	0	30	73		Q8BVZ1
ENSMUST00000113075	ENSMUSG00000035949	2	34804514	34826311	-1	4	6	11	1	10	0	14	88	35	6	40	Q8BS25	
ENSMUST00000113077	ENSMUSG00000035949	2	34804514	34826311	-1	0	0	0	0	0	0	0	180	17	16	63	A2AUG1	
ENSMUST00000113078	ENSMUSG00000035949	2	34804514	34826311	-1	0	0	0	0	0	0	351	406	296	104	213	Q9QUH1	
ENSMUST00000113080	ENSMUSG00000035949	2	34804514	34826311	-1	0	0	0	0	0	0	0	0	187	96	63	Q9QUH1	
ENSMUST00000113083	ENSMUSG00000034842	5	92331827	92414628	1	0	0	2	0	0	2	0	0	0	0	0		Q8R2G4
ENSMUST00000113085	ENSMUSG00000031425	X	136822671	136839733	1	0	0	0	0	0	0	0	6	0	17	5		P60202
ENSMUST00000113086	ENSMUSG00000070953	2	34777556	34799912	-1	0	0	0	1	0	0	0	45	19	65	13	A2AUF7	
ENSMUST00000113089	ENSMUSG00000030278	6	113424634	113435760	-1	0	7	20	0	0	0	0	0	0	0	0		P56198
ENSMUST00000113091	ENSMUSG00000030278	6	113424634	113435760	-1	0	5	3	0	0	0	0	0	0	0	0	E9QMZ0	
ENSMUST00000113092	ENSMUSG00000051169	6	113415319	113419340	-1	0	0	0	10	0	0	18	21	0	0	7		Q14AI6
ENSMUST00000113093	ENSMUSG00000029417	5	92321347	92328079	-1	34	33	55	218	33	20	5	18	8	52	24		P18340
ENSMUST00000113094	ENSMUSG00000026301	1	90042132	90153401	-1	15	5	17	29	0	2	0	0	0	0	0	E9QMY8	
ENSMUST00000113095	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	7	0	0	0	0	0	0	A2AEB5	
ENSMUST00000113097	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	0	0	68	0	0	0	0		Q9R0Q4
ENSMUST00000113099	ENSMUSG00000026867	2	34674594	34755232	-1	0	0	0	0	0	0	0	0	30	0	0		Q6PAR5
ENSMUST00000113100	ENSMUSG00000044550	X	136590842	136668378	1	5	0	0	0	5	0	0	0	0	0	0		Q8R0A5
ENSMUST00000113101	ENSMUSG00000026867	2	34674594	34755232	-1	0	0	0	0	0	0	0	0	16	0	30	F7ADT6	
ENSMUST00000113102	ENSMUSG00000029413	5	92257659	92278170	-1	28	3	44	98	30	11	339	714	280	121	387		Q9D7V9
ENSMUST00000113103	ENSMUSG00000026867	2	34674594	34755232	-1	0	0	5	1	0	0	0	6	76	5	51	F7ADS7	
ENSMUST00000113104	ENSMUSG00000031424	X	136517999	136534309	1	0	1	0	0	0	0	0	0	0	0	0	D3Z751	
ENSMUST00000113105	ENSMUSG00000031424	X	136517999	136534309	1	4	0	4	0	5	0	0	0	0	0	0	Q673W4	
ENSMUST00000113106						7	10	36	11	12	7	34	61	35	4	39		
ENSMUST00000113107						12	7	26	35	23	0	11	12	0	0	12		
ENSMUST00000113108	ENSMUSG00000057439	X	136448107	136544056	-1	0	5	8	6	5	3	0	0	0	0	0	Q673W2	
ENSMUST00000113110	ENSMUSG00000079427	9	88688602	88720296	-1	0	2	0	0	3	0	237	1222	294	954	203	L7N466	
ENSMUST00000113111	ENSMUSG00000026867	2	34674594	34755232	-1	33	34	28	60	56	14	256	957	542	116	540	F7ADQ2	
ENSMUST00000113112	ENSMUSG00000046432	X	136270253	136271978	1	0	0	0	0	0	0	19	82	30	60	35		Q9WTZ9
ENSMUST00000113113	ENSMUSG00000046432	X	136270253	136271978	1	1	1	9	8	2	2	64	158	8	66	33		Q9WTZ9
ENSMUST00000113114	ENSMUSG00000036251	1	88277661	88389293	1	0	0	15	0	0	0	0	0	0	0	0		Q8R4D5
ENSMUST00000113115	ENSMUSG00000042712	X	136245079	136247139	1	0	3	0	4	3	0	42	0	0	0	0		Q9DD24
ENSMUST00000113116	ENSMUSG00000079428	X	136214779	136226100	1	0	5	2	0	1	0	0	0	0	0	0		A3KGA4
ENSMUST00000113117	ENSMUSG00000001632	6	113307137	113324860	1	23	12	68	3	8	0	956	1011	515	97	604	Q80XK2	
ENSMUST00000113118	ENSMUSG00000050071	X	136213972	136215513	-1	0	5	0	0	0	0	0	0	1	0	0		Q9R224

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000113119	ENSMUSG00000001632	6	113307137	113324860	1	0	0	0	0	21	0	0	0	59	0	131	Q3U109	
ENSMUST00000113120	ENSMUSG00000050071	X	136213972	136215513	-1	3	0	2	0	0	0	2	1	0	1	0		Q9R224
ENSMUST00000113121	ENSMUSG00000001632	6	113307137	113324860	1	0	0	32	0	0	0	408	909	1356	87	935	E9PXP1	
ENSMUST00000113122	ENSMUSG00000001632	6	113307137	113324860	1	0	0	0	304	6	22	3	385	356	42	137	B2RRD7	
ENSMUST00000113123	ENSMUSG00000038696	2	34406771	34624950	1	0	0	0	0	0	0	71	114	60	62	124		Q8BKH7
ENSMUST00000113124	ENSMUSG00000038696	2	34406771	34624950	1	0	0	0	0	0	0	0	141	73	1	0		Q8BKH7
ENSMUST00000113126	ENSMUSG00000038696	2	34406771	34624950	1	0	13	28	0	30	17	0	299	48	0	0		Q8BKH7
ENSMUST00000113127	ENSMUSG00000029405	5	92052146	92083719	-1	5	0	4	95	2	0	674	2405	1196	364	931	Q542W3	P97379
ENSMUST00000113130	ENSMUSG00000079429	1	88226986	88262289	1	0	149	345	391	273	0	128	352	195	11	165	F5H8M8	
ENSMUST00000113132	ENSMUSG00000038718	2	34171457	34373142	-1	0	8	16	10	22	8	8	79	19	10	15		O35317
ENSMUST00000113134	ENSMUSG00000054545	1	88134809	88218997	1	0	0	0	0	0	0	43	101	82	25	92		Q64435
ENSMUST00000113135	ENSMUSG00000090124	1	88095062	88220002	1	0	8	0	0	0	6	0	0	0	0	0		Q64435
ENSMUST00000113136	ENSMUSG00000072966	X	135839034	135844730	1	14	3	1	0	0	9	0	1	0	0	0		Q8BUY8
ENSMUST00000113137	ENSMUSG00000090145	1	88103252	88219003	1	4	8	13	5	0	0	61	216	28	49	104	K9J7B2	
ENSMUST00000113138	ENSMUSG00000090145	1	88103252	88219003	1	0	0	0	0	10	0	14	12	71	0	15	K9J7B2	
ENSMUST00000113139	ENSMUSG00000089675	1	88087813	88219004	1	2	7	8	5	5	5	0	0	0	0	0	D3Z748	
ENSMUST00000113140	ENSMUSG00000029403	5	92006074	92043883	-1	0	6	0	0	17	0	0	11	0	3	6	Q149A0	Q9QUK0
ENSMUST00000113142	ENSMUSG00000090165	1	88055388	88219004	1	4	4	0	0	12	5	0	0	0	0	0	E9PXN7	
ENSMUST00000113143	ENSMUSG00000029403	5	92006074	92043883	-1	11	0	31	23	0	4	3	0	0	0	0		Q9QUK0
ENSMUST00000113144	ENSMUSG00000043384	X	135742733	135803474	1	0	0	0	45	19	9	18	0	76	0	0		Q5U4C1
ENSMUST00000113145	ENSMUSG00000043384	X	135742733	135803474	1	0	0	0	0	0	0	0	31	0	16	83		Q5U4C1
ENSMUST00000113146	ENSMUSG00000030269	6	113237843	113281392	1	0	0	0	21	0	0	475	859	682	58	413		Q8VEL2
ENSMUST00000113147	ENSMUSG00000043384	X	135742733	135803474	1	0	0	24	0	0	0	0	0	0	0	0		Q5U4C1
ENSMUST00000113149	ENSMUSG00000042761	9	87144306	87184045	1	0	23	0	33	34	46	0	0	0	0	0		D3Z1Q2
ENSMUST00000113154	ENSMUSG00000060726	X	135718667	135725261	-1	1	3	0	4	3	2	0	0	0	0	0	A2AEH9	
ENSMUST00000113155	ENSMUSG00000034269	6	113077365	113153435	1	10	4	29	0	0	0	573	1481	179	76	65		Q5XJV7
ENSMUST00000113156	ENSMUSG00000026788	2	33450287	33468559	-1	0	0	0	5	0	0	19	3	40	0	21	G3X9N4	
ENSMUST00000113157	ENSMUSG00000034269	6	113077365	113153435	1	0	0	0	0	0	5	10	11	1088	39	795		Q5XJV7
ENSMUST00000113158	ENSMUSG00000068966	2	33406108	33431324	-1	0	0	0	0	0	0	0	0	71	42	0	A2ATY4	
ENSMUST00000113159	ENSMUSG00000031411	X	135613002	135627705	-1	8	8	17	11	5	1	0	0	0	0	0	Q9D4Z5	
ENSMUST00000113161	ENSMUSG00000024663	19	10001669	10038380	1	0	0	18	55	4	0	19	13	16	59	40		Q8VDV3
ENSMUST00000113163	ENSMUSG00000031410	X	135579555	135598777	-1	8	11	0	7	8	0	0	0	0	0	0	Q80SZ6	
ENSMUST00000113164						26	29	44	40	20	6	4	4	4	0	5		
ENSMUST00000113165	ENSMUSG00000038831	2	33133417	33371486	-1	0	0	0	33	23	0	40	57	0	0	0	A0A0A0MQE4	
ENSMUST00000113169	ENSMUSG00000030257	6	112717971	112947266	-1	0	0	0	0	0	0	0	0	0	7	0	E9QN14	
ENSMUST00000113172	ENSMUSG00000096508	X	135433835	135443830	1	0	5	0	3	7	4	0	0	0	0	0	A2AWL1	
ENSMUST00000113173	ENSMUSG00000094004	X	135373284	135383393	1	0	5	0	3	7	4	0	0	0	0	0	A2AWL1	
ENSMUST00000113176	ENSMUSG00000067360	X	135302307	135312652	1	0	8	2	4	0	0	0	0	0	0	0	Q99M97	
ENSMUST00000113179	ENSMUSG00000029369	5	90518932	90553543	1	4	7	4	6	5	0	0	0	0	7	0		O89020
ENSMUST00000113180	ENSMUSG00000030254	6	112619850	112696686	-1	0	0	14	0	3	1	7	7	0	0	16	D3Z734	
ENSMUST00000113182	ENSMUSG00000030254	6	112619850	112696686	-1	2	0	0	0	0	0	0	0	20	7	0	D3Z733	
ENSMUST00000113183	ENSMUSG00000079432	X	135167624	135177632	-1	13	0	24	0	26	4	0	0	0	0	0	L7MUB4	
ENSMUST00000113185	ENSMUSG00000052676	X	134971372	135009209	-1	0	1	26	0	0	0	15	65	2	0	0	Z4YL92	
ENSMUST00000113186	ENSMUSG00000026289	1	87755870	87792428	1	19	9	9	0	27	7	301	1011	491	144	471	Q3TDQ5	Q8C0J2
ENSMUST00000113187	ENSMUSG00000009941	X	134944526	134964754	-1	5	5	0	10	0	4	0	14	0	0	0	Q8R499	
ENSMUST00000113189	ENSMUSG00000009941	X	134944526	134964754	-1	0	0	0	0	0	0	0	0	0	0	0	Q99MW6	
ENSMUST00000113190	ENSMUSG00000026289	1	87755870	87792428	1	0	0	0	0	0	0	48	0	0	0	0	G9M4M6	Q8C0J2
ENSMUST00000113193	ENSMUSG00000033436	X	134804145	134809221	-1	11	0	0	10	0	6	24	5	0	0	0		Q6A058
ENSMUST00000113194	ENSMUSG00000050394	X	134748461	134751417	-1	0	18	10	0	15	15	0	0	0	0	0		Q8K3A6
ENSMUST00000113195	ENSMUSG00000039316	17	49992257	50190674	-1	4	16	21	3	21	3	106	150	70	14	132	D3Z731	
ENSMUST00000113197	ENSMUSG00000033460	X	134717963	134721917	1	0	0	0	0	0	0	0	0	0	0	0		Q9CX83
ENSMUST00000113198	ENSMUSG00000033460	X	134717963	134721917	1	0	2	0	0	0	0	1	3	0	2	0		Q9CX83
ENSMUST00000113199	ENSMUSG00000033460	X	134717963	134721917	1	0	0	0	0	5	0	0	0	0	0	0		Q9CX83
ENSMUST00000113200	ENSMUSG00000026792	2	32925216	32961614	-1	0	0	0	0	0	0	81	593	140	0	108		Q80ZI6
ENSMUST00000113201	ENSMUSG00000033460	X	134717963	134721917	1	2	0	5	0	0	0	0	0	0	0	0		Q9CX83
ENSMUST00000113202	ENSMUSG00000045427	X	134601179	134607060	1	29	38	102	50	37	18	50	118	74	19	146		P70333
ENSMUST00000113203	ENSMUSG00000045427	X	134601179	134607060	1	3	0	1	4	0	0	0	0	4	0	0		P70333
ENSMUST00000113205	ENSMUSG00000079433	9	85312773	85312860	1	0	0	3	0	0	0	0	0	0	0	0	F7A1V1	
ENSMUST00000113211	ENSMUSG00000079435	X	134585654	134588062	1	0	0	0	24	11	6	1126	2737	1231	7264	802	Q5M9P1	P83882
ENSMUST00000113212	ENSMUSG00000079436	1	87386363	87394729	-1	6	8	19	1	3	1	0	0	0	3	1		P86046
ENSMUST00000113213	ENSMUSG00000031264	X	134542336	134583570	-1	3	0	6	6	0	4	0	7	0	0	0	A2BDW0	
ENSMUST00000113215	ENSMUSG00000032261	9	83548327	83638801	1	27	23	23	17	26	11	13	33	22	130	92		Q8BG73
ENSMUST00000113216	ENSMUSG00000060961	5	88886818	89239653	1	17	6	21	7	12	11	0	0	0	1	0		O88343
ENSMUST00000113218	ENSMUSG00000060961	5	88886818	89239653	1	0	0	0	0	0	0	0	0	0	0	0	A7E1Z5	
ENSMUST00000113222						0	0	14	0	0	8	0	0	0	0	10		
ENSMUST00000113223	ENSMUSG00000009596	X	134460118	134476490	-1	0	0	0	4	0	0	0	0	0	0	1	B1AV36	
ENSMUST00000113224	ENSMUSG00000000223	X	134404551	134456573	1	28	21	50	199	53	18	2	3	0	0	0	B1AV35	
ENSMUST00000113226	ENSMUSG00000000223	X	134404551	134456573	1	1	0	0	0	0	0	0	0	0	0	0		Q05AA6
ENSMUST00000113228	ENSMUSG00000000223	X	134404551	134456573	1	0	0	6	1	0	0	0	0	1	0	0		Q05AA6
ENSMUST00000113229	ENSMUSG00000006262	5	88720855	88764220	1	31	32	201	50	37	17	200	549	241	55	279	Q3UDM0	
ENSMUST00000113230	ENSMUSG00000026254	1	87213914	87240488	1	6	0	14	47	6	0	0	8	4	3	4	D3Z730	
ENSMUST00000113231	ENSMUSG00000026254	1	87213914	87240488	1	3	0	0	2	2	1	364	988	523	244	395	Q0P688	
ENSMUST00000113232	ENSMUSG00000026254	1	87213914	87240488	1	0	4	0	0	0	0	71	119	37	72	88	Q3UUT0	
ENSMUST00000113233	ENSMUSG00000026254	1	87213914	87240488	1	7	8	85	21	14	8	15	29	21	0	13		Q8BMB3
ENSMUST00000113234	ENSMUSG00000044221	5	88659448	88676171	-1	3	2	1	38	3	2	303	1460	525	115	133	E9Q179	
ENSMUST00000113235	ENSMUSG00000026254	1	87213914	87240488	1	130	127	0	174	87	0	65	44	61	0	18	D3Z729	
ENSMUST00000113237	ENSMUSG00000023992	17	48346401	48354147	1	2	1	0	0	0	1	18	40	26	12	22		Q99NH8
ENSMUST00000113239	ENSMUSG00000005362	6	106780201	106800077	-1	0	0	0	30	6	0	162	572	245	426	107		Q8C7D2
ENSMUST00000113242	ENSMUSG00000059013	2	32721055	32755512	1	0	2	9	14	8	11	349	1573	341	70	400		Q9QZS8
ENSMUST00000113245	ENSMUSG00000032251	9	82829540	82847687	1	51	49	164	207	80	41	0	6	0	0	2		Q9ESJ7
ENSMUST00000113247	ENSMUSG00000013736	6	106769120	106782474	1	3	0	2	5	6	1	4	15	6	3	18		Q8K1J6
ENSMUST00000113248	ENSMUSG00000013736	6	106769120	106782474	1	6	0	0	0	0	0	40	85	40	123	57		Q8K1J6
ENSMUST00000113249	ENSMUSG00000013736	6	106769120	106782474	1	0	0	0	0	0	3	0	14	134	177	81		Q8K1J6
ENSMUST00000113250	ENSMUSG00000032343	9	80313330	80465481	-1	1	0	0	0	0	0	0	0	0	0	0		Q8R1W8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000113251	ENSMUSG00000042265	17	48232768	48246924	1	13	6	13	8	19	4	821	860	1144	365	828	Q14DT9	
ENSMUST00000113252	ENSMUSG00000067369	X	134222339	134276984	-1	31	29	35	17	26	11	47	187	0	21	21		Q8BQJ6
ENSMUST00000113255	ENSMUSG00000079438	5	88154023	88154099	-1	0	0	0	0	0	0	0	0	0	0	0	F6ZRA6	
ENSMUST00000113257	ENSMUSG00000079439	5	88110567	88111530	-1	1	0	0	0	1	0	0	0	0	0	0	F7A1G1	
ENSMUST00000113258	ENSMUSG00000064293	6	105677660	106699310	1	0	4	1	0	0	0	0	0	0	0	0		Q69Z26
ENSMUST00000113260	ENSMUSG00000064293	6	105677660	106699310	1	0	2	1	3	1	0	0	0	0	0	0		Q69Z26
ENSMUST00000113261	ENSMUSG00000064293	6	105677660	106699310	1	8	0	0	0	0	0	0	0	0	0	0		Q69Z26
ENSMUST00000113262	ENSMUSG00000023991	17	47867133	47924645	-1	0	0	7	0	0	1	148	69	84	4	66		
ENSMUST00000113263	ENSMUSG00000023991	17	47867133	47924645	-1	14	4	0	0	0	0	0	0	0	9	0	D3Z726	
ENSMUST00000113264	ENSMUSG00000064293	6	105677660	106699310	1	0	0	0	0	0	0	0	0	0	0	0		Q69Z26
ENSMUST00000113265	ENSMUSG00000023991	17	47867133	47924645	-1	5	5	44	168	30	10	34	54	37	5	23		Q9DBY0
ENSMUST00000113266	ENSMUSG00000033577	9	80165031	80311729	1	25	11	28	0	24	13	14	72	16	15	6	E9Q175	
ENSMUST00000113267	ENSMUSG00000001622	5	87925579	87932665	1	0	0	0	3	1	1	0	0	0	0	0		P06796
ENSMUST00000113268	ENSMUSG00000033577	9	80165031	80311729	1	0	0	0	0	0	0	0	0	0	0	0	E9Q174	
ENSMUST00000113270	ENSMUSG00000079440	1	87098002	87101606	-1	24	4	34	116	43	14	0	0	0	0	0	F8VPQ6	
ENSMUST00000113271	ENSMUSG00000001622	5	87925579	87932665	1	3	1	1	0	1	0	0	0	0	0	0		P06796
ENSMUST00000113272	ENSMUSG00000026814	2	32646595	32682669	1	17	10	21	229	28	6	15	16	9	0	128	F7A1B4	
ENSMUST00000113274	ENSMUSG00000009580	5	87885029	87894174	1	7	5	2	1	2	1	0	0	0	0	0		A1E960
ENSMUST00000113275	ENSMUSG00000031257	X	134086421	134221956	-1	0	0	6	0	5	0	0	0	0	0	0		Q8CIZ9
ENSMUST00000113277	ENSMUSG00000026817	2	32621758	32635058	1	0	0	25	15	11	0	0	0	0	0	10		Q9R0Y5
ENSMUST00000113278	ENSMUSG00000026817	2	32621758	32635058	1	15	4	11	6	10	12	0	0	0	0	0		Q9R0Y5
ENSMUST00000113279	ENSMUSG00000061388	5	87808082	87824426	1	0	1	3	2	0	2	0	0	0	0	0	Q3TP31	
ENSMUST00000113280	ENSMUSG00000032717	17	47815328	47834691	-1	0	0	0	0	0	2	0	4	1	0	0	D3Z6Q8	
ENSMUST00000113284	ENSMUSG00000023990	17	47737030	47792419	1	7	8	50	54	18	13	2	6	2	3	8	D3Z6Q7	
ENSMUST00000113286	ENSMUSG00000031256	X	134059187	134086819	1	15	25	14	33	29	19	25	42	29	0	22		Q8BIQ5
ENSMUST00000113287	ENSMUSG00000031256	X	134059187	134086819	1	0	0	0	29	0	0	14	0	114	13	78	A2AEK1	
ENSMUST00000113288	ENSMUSG00000023990	17	47737030	47792419	1	4	7	9	93	16	0	0	0	0	12	31		Q9R210
ENSMUST00000113290	ENSMUSG00000026811	2	32599709	32620806	1	0	0	0	8	0	0	0	17	0	0	0	E9PUI0	
ENSMUST00000113294	ENSMUSG00000031255	X	133936385	133981812	-1	185	122	1611	348	223	107	8	24	14	13	18		Q9R0Q1
ENSMUST00000113296	ENSMUSG00000023266	17	47689030	47704286	1	16	7	60	14	16	9	0	4	0	0	0		Q91WJ0
ENSMUST00000113297	ENSMUSG00000031255	X	133936385	133981812	-1	34	33	177	50	24	0	5	2	0	1	0		Q9R0Q1
ENSMUST00000113298	ENSMUSG00000075044	19	8160165	8218900	-1	12	5	0	5	0	1	0	0	0	0	0	Q8BWG6	
ENSMUST00000113299	ENSMUSG00000096549	17	47688517	47694736	-1	4	2	8	2	11	0	3	0	0	0	0	F6ZPB0	
ENSMUST00000113300	ENSMUSG00000096549	17	47688517	47694736	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z6Q6	
ENSMUST00000113301	ENSMUSG00000033475	17	47686646	47688386	-1	0	0	0	0	3	0	182	347	150	99	127		Q9CQN3
ENSMUST00000113302	ENSMUSG00000033475	17	47686646	47688386	-1	0	3	0	0	0	0	563	785	315	210	274		Q9CQN3
ENSMUST00000113304	ENSMUSG00000031253	X	133908426	133932446	1	10	5	0	5	6	0	0	0	0	0	0		Q8R054
ENSMUST00000113306	ENSMUSG00000079445	1	86302832	86307305	1	26	14	33	20	26	15	14	5	7	2	16		Q8K0J2
ENSMUST00000113307	ENSMUSG00000026819	2	32414487	32451445	-1	8	4	15	0	0	8	0	0	0	0	0		A2ASZ8
ENSMUST00000113308	ENSMUSG00000026819	2	32414487	32451445	-1	0	0	0	0	0	0	36	0	20	0	0		A2ASZ8
ENSMUST00000113309	ENSMUSG00000062590	1	86154780	86278284	1	0	0	0	0	0	0	0	0	0	0	0		Q9D2I5
ENSMUST00000113310	ENSMUSG00000026819	2	32414487	32451445	-1	3	0	0	47	0	0	0	117	75	24	55		A2ASZ8
ENSMUST00000113312	ENSMUSG00000035378	6	100568256	100671157	-1	2	2	0	11	4	0	4	10	5	8	2		Q7TMX5
ENSMUST00000113314	ENSMUSG00000029273	5	87554645	87569027	-1	2	6	0	2	3	2	0	0	0	0	0		Q3UZZ6
ENSMUST00000113320	ENSMUSG00000034480	X	129749742	130465834	1	103	118	986	0	0	59	361	803	386	0	187		O70566
ENSMUST00000113321						5	2	10	11	9	1	4	7	5	2	1		
ENSMUST00000113322	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	323	662	576	74	808		P58462
ENSMUST00000113324	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z6Q4	
ENSMUST00000113326	ENSMUSG00000030067	6	98925338	99522721	-1	14	14	30	21	23	15	225	529	466	74	0		
ENSMUST00000113328	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z6Q3	
ENSMUST00000113329	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	6	0	0	0		P58462
ENSMUST00000113331	ENSMUSG00000039205	2	32352327	32380970	1	0	0	0	0	0	0	0	1	155	64	44	A2AN61	
ENSMUST00000113332	ENSMUSG00000039205	2	32352327	32380970	1	0	0	0	79	12	6	167	59	137	0	67	Q3UUV0	
ENSMUST00000113333	ENSMUSG00000029260	5	86889767	86906937	-1	0	0	0	0	3	0	0	0	0	0	0	E9PZ30	
ENSMUST00000113334	ENSMUSG00000039205	2	32352327	32380970	1	5	3	17	105	8	9	0	0	0	0	0	Q8VEH2	
ENSMUST00000113335	ENSMUSG00000023977	17	46928292	47010532	-1	28	0	35	16	35	0	435	1453	896	0	1147	Q3UPU3	Q6WKZ8
ENSMUST00000113337	ENSMUSG00000023977	17	46928292	47010532	-1	28	30	35	327	35	25	791	1259	2191	210	1408		Q6WKZ8
ENSMUST00000113338	ENSMUSG00000039205	2	32352327	32380970	1	0	0	0	0	0	0	317	597	293	0	288	Q8VEH2	
ENSMUST00000113339	ENSMUSG00000035158	6	97807052	98021349	1	0	3	3	0	0	0	0	0	15	0	15	E9PZ28	
ENSMUST00000113343	ENSMUSG00000079450	X	123103495	123188795	1	0	1	1	450	1	1	0	0	0	0	0	Q8CCR8	
ENSMUST00000113344	ENSMUSG00000026226	1	86016816	86029958	1	0	5	14	5	5	7	0	0	0	0	0	Q3V2M5	Q9D9T6
ENSMUST00000113348	ENSMUSG00000079450	X	123103495	123188795	1	270	298	446	101	344	168	0	16	3	1	4	Q8K193	
ENSMUST00000113350	ENSMUSG00000026825	2	32308471	32353338	-1	0	0	0	0	0	0	0	0	0	0	0		P39053
ENSMUST00000113352	ENSMUSG00000026825	2	32308471	32353338	-1	16	19	41	26	35	19	0	0	0	2	6		P39053
ENSMUST00000113353						7	3	0	43	7	2	0	0	0	2	0		
ENSMUST00000113355	ENSMUSG00000030064	6	97286867	97617541	-1	0	0	0	80	21	4	0	11	0	8	16		Q920B0
ENSMUST00000113358	ENSMUSG00000034755	X	120290259	120910619	1	2	0	6	3	2	0	0	0	0	0	0	B1AZR7	
ENSMUST00000113359	ENSMUSG00000030064	6	97286867	97617541	-1	0	0	0	0	0	0	0	0	0	114	152	Q6ZQ04	
ENSMUST00000113360	ENSMUSG00000036707	1	85793441	85851576	1	14	16	26	51	16	7	1451	5151	2448	893	1620		Q06138
ENSMUST00000113364	ENSMUSG00000034755	X	120290259	120910619	1	0	0	0	1	0	0	0	0	0	0	0	F6ZNL5	
ENSMUST00000113365	ENSMUSG00000026825	2	32308471	32353338	-1	0	0	0	0	0	0	0	0	0	0	0		P39053
ENSMUST00000113366	ENSMUSG00000034732	X	119927196	119930165	1	2	1	0	2	3	0	0	0	0	0	0	Q8C7D3	
ENSMUST00000113367	ENSMUSG00000070291	9	78395777	78423587	1	3	6	3	58	3	4	0	5	1	1	1	D3Z6P9	
ENSMUST00000113369	ENSMUSG00000024968	19	7267325	7275225	1	12	3	36	0	23	9	1	4	0	2	13		
ENSMUST00000113370						0	7	29	0	0	0	0	0	0	0	0		
ENSMUST00000113371	ENSMUSG00000025597	X	114474333	114560829	1	4	0	0	0	8	0	0	0	0	0	0	B1AZQ9	
ENSMUST00000113372	ENSMUSG00000029255	5	86180754	86197901	-1	6	12	4	3	4	3	0	0	0	0	0	D3Z6P7	
ENSMUST00000113373	ENSMUSG00000035898	5	86109287	86172803	-1	3	9	2	9	9	3	28	56	91	12	37	D3Z061	
ENSMUST00000113376	ENSMUSG00000066463	9	78311972	78314797	-1	0	0	10	4	1	0	0	0	0	0	0	G3X9W2	
ENSMUST00000113377	ENSMUSG00000002546	2	32287384	32307921	1	29	17	65	85	22	8	363	240	370	0	74		Q921M4
ENSMUST00000113378	ENSMUSG00000025592	X	113297510	113836386	1	1	7	0	1	1	1	0	0	0	0	0	B1AXA6	
ENSMUST00000113379	ENSMUSG00000025592	X	113297510	113836386	1	0	0	0	0	0	0	0	0	0	1	0	B1AU60	
ENSMUST00000113380	ENSMUSG00000025592	X	113297510	113836386	1	4	0	5	4	0	0	0	0	0	0	0		Q925Q8
ENSMUST00000113382	ENSMUSG00000025592	X	113297510	113836386	1	0	0	0	0	3	0	0	0	0	0	0		Q925Q8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000113383	ENSMUSG00000047787	19	7092014	7105729	-1	82	52	376	153	94	32	2	2	1	0	5	Q6RKD8	Q6RKD8
ENSMUST00000113385	ENSMUSG00000070031	1	85600378	85645037	1	48	47	306	66	63	29	15	68	55	4	60	D3Z054	
ENSMUST00000113387	ENSMUSG00000035245	6	97110024	97149182	-1	0	0	0	0	0	0	1	0	2	0	2	D3Z052	
ENSMUST00000113388	ENSMUSG00000025531	X	113040593	113185517	-1	1	0	5	11	7	9	0	171	0	317	0	Q3UR39	
ENSMUST00000113395	ENSMUSG00000044627	2	32278816	32288075	-1	3	3	3	0	0	1	3	23	6	0	18	E3WH32	Q8K3D3
ENSMUST00000113397	ENSMUSG00000044627	2	32278816	32288075	-1	0	0	8	0	0	0	13	14	6	12	0	A2AN40	
ENSMUST00000113398	ENSMUSG00000029245	5	84054761	84417382	-1	0	0	0	112	0	0	0	0	4	0	0	E9PUQ4	
ENSMUST00000113399	ENSMUSG00000029245	5	84054761	84417382	-1	0	2	0	0	2	0	0	0	0	0	0	E9PUQ2	
ENSMUST00000113400	ENSMUSG00000044627	2	32278816	32288075	-1	0	0	0	0	8	0	107	609	141	411	130		Q8K3D3
ENSMUST00000113401	ENSMUSG00000029245	5	84054761	84417382	-1	187	143	351	4757	215	109	5	69	0	5	11	Q6PFV6	
ENSMUST00000113402						375	514	471	452	550	326	26	103	54	32	82		
ENSMUST00000113403	ENSMUSG00000029245	5	84054761	84417382	-1	6	7	9	0	3	0	0	0	0	0	0	E9PUQ0	
ENSMUST00000113406	ENSMUSG00000029245	5	84054761	84417382	-1	0	0	0	0	0	1	0	0	0	0	0	E9PUP9	
ENSMUST00000113407						0	0	0	0	0	0	0	1	0	4	0		
ENSMUST00000113409	ENSMUSG00000025529	X	112600526	112635070	1	2	0	0	5	0	0	0	0	0	0	0	E9PUP8	
ENSMUST00000113412	ENSMUSG00000025528	X	112495274	112558343	1	0	0	0	0	0	0	0	0	0	0	0	A2ANY3	
ENSMUST00000113415	ENSMUSG00000025525	X	112311334	112372755	1	0	0	0	0	0	0	6	101	24	12	0	B1AV14	
ENSMUST00000113421	ENSMUSG00000032352	9	77430823	77544870	-1	0	3	0	0	0	0	28	42	3	0	38	G3X9W3	
ENSMUST00000113422	ENSMUSG00000034551	X	111569931	111697079	-1	0	0	0	0	0	3	0	0	0	0	0		Q14B70
ENSMUST00000113423	ENSMUSG00000024959	19	6941861	6951898	1	8	0	20	6	7	2	612	603	286	174	77	Q3U9H3	
ENSMUST00000113426	ENSMUSG00000024959	19	6941861	6951898	1	0	1	5	0	0	0	0	0	0	0	0	D3YZR8	
ENSMUST00000113428	ENSMUSG00000025665	X	111388192	111537959	-1	0	5	0	7	0	1	0	0	0	0	0	E9PUP0	
ENSMUST00000113429	ENSMUSG00000002767	17	46646229	46650139	1	2	0	0	0	0	2	0	36	0	0	0	B1B1D7	
ENSMUST00000113430	ENSMUSG00000002767	17	46646229	46650139	1	2	2	5	4	6	0	119	21	0	0	0	B1B1D8	
ENSMUST00000113434	ENSMUSG00000079462	6	92869357	92884411	1	45	44	55	55	46	31	2	1	2	0	2	D3YZR0	
ENSMUST00000113436	ENSMUSG00000053161	1	83159752	83210574	1	0	4	0	0	1	1	0	0	0	0	0	D3YZQ8	
ENSMUST00000113437	ENSMUSG00000026166	1	83116766	83119167	1	0	0	0	0	0	0	0	0	0	0	0	Q54AI7	O89093
ENSMUST00000113438	ENSMUSG00000030022	6	92772699	92943492	-1	38	16	52	69	68	28	0	0	2	0	0	E9PUN6	
ENSMUST00000113440	ENSMUSG00000047810	19	6844623	6858211	-1	27	19	123	241	73	38	5420	6361	5610	331	4030		Q4QRL3
ENSMUST00000113442						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000113444	ENSMUSG00000026159	1	82839483	82901182	1	0	0	0	38	0	0	0	137	22	11	28		Q8K2K6
ENSMUST00000113445	ENSMUSG00000030020	6	92370908	92706155	-1	15	16	37	11	19	10	0	1	1	0	0		Q80Y24
ENSMUST00000113446	ENSMUSG00000030020	6	92370908	92706155	-1	6	29	15	26	40	25	0	0	0	0	8		Q80Y24
ENSMUST00000113447	ENSMUSG00000030020	6	92370908	92706155	-1	14	0	43	0	4	0	6	0	0	2	0		Q80Y24
ENSMUST00000113449	ENSMUSG00000029249	5	77265491	77286432	1	54	0	51	64	38	32	8	664	249	0	0		Q8VIG1
ENSMUST00000113451	ENSMUSG00000061742	19	6535845	6543019	-1	20	15	45	281	34	19	0	2	0	0	1		
ENSMUST00000113452						0	0	56	0	8	0	112	114	60	24	27		
ENSMUST00000113453	ENSMUSG00000059325	5	77086988	77115121	-1	0	0	4	30	0	0	929	2191	1004	1145	475		Q8R1H0
ENSMUST00000113457	ENSMUSG00000079465	1	82586921	82722059	1	59	38	68	31	43	32	0	3	5	1	2		Q9QZS0
ENSMUST00000113458	ENSMUSG00000033768	19	6418731	6544169	1	0	0	0	538	14	2	0	0	0	0	0	E9PUN2	
ENSMUST00000113459	ENSMUSG00000033768	19	6418731	6544169	1	18	11	34	24	28	10	0	0	0	0	1	E9PUN1	
ENSMUST00000113460	ENSMUSG00000005893	6	92091390	92174294	1	9	12	10	14	16	0	675	1304	1454	58	848	Q3ZAS1	P49117
ENSMUST00000113461	ENSMUSG00000033768	19	6418731	6544169	1	0	6	8	206	18	0	2	0	0	0	2	E9PUN0	
ENSMUST00000113462	ENSMUSG00000033768	19	6418731	6544169	1	0	0	0	39	20	0	0	0	0	0	0	E9PUM9	
ENSMUST00000113463	ENSMUSG00000005893	6	92091390	92174294	1	8	10	26	29	6	3	17	9	67	0	0	G3X9W4	
ENSMUST00000113465	ENSMUSG00000023968	17	46428926	46431776	1	7	0	7	5	3	0	0	0	0	0	0		
ENSMUST00000113466	ENSMUSG00000034037	6	91978878	92076004	1	0	23	17	0	17	10	0	0	2	0	5	E9QLU9	
ENSMUST00000113467	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	11	0	3	3	4	D3YZP4	
ENSMUST00000113468	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	23	0	0	0	6	0	0	0	D3YZP2	
ENSMUST00000113469	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	3	0	0	0	0	0	D3YZP1	
ENSMUST00000113470	ENSMUSG00000079466	2	31640037	31655795	1	33	32	201	238	34	13	0	3	0	0	0		A2AJ77
ENSMUST00000113471	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	218	334	121	258	87		Q9QUG9
ENSMUST00000113472	ENSMUSG00000032946	19	6399340	6415216	1	17	6	61	97	22	7	68	378	110	20	250		Q9QUG9
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ENSMUST00000113476	ENSMUSG00000032946	19	6399340	6415216	1	3	2	5	117	11	7	0	0	42	0	42		Q9QUG9
ENSMUST00000113480	ENSMUSG00000052821	X	106574346	106603679	-1	59	43	158	393	78	56	21	83	32	167	66		Q99JA4
ENSMUST00000113481	ENSMUSG00000015597	17	46383731	46420920	1	27	35	47	44	19	25	52	113	124	20	114	B0V2M3	
ENSMUST00000113482	ENSMUSG00000026843	2	31572651	31617526	1	29	23	36	230	30	15	30	27	38	18	42	A2AJ72	
ENSMUST00000113483	ENSMUSG00000032648	19	6384399	6398459	1	0	9	0	2	8	0	16	13	0	2	0	E9PUM3	
ENSMUST00000113485	ENSMUSG00000024949	19	6363690	6378030	1	0	0	21	0	0	4	442	847	425	57	619	F8WHF9	
ENSMUST00000113487	ENSMUSG00000024949	19	6363690	6378030	1	0	0	0	0	0	0	728	1694	659	48	486	E9Q4Q2	
ENSMUST00000113488	ENSMUSG00000024949	19	6363690	6378030	1	0	0	0	21	0	0	0	7	37	0	29	D3YZD0	
ENSMUST00000113489	ENSMUSG00000024949	19	6363690	6378030	1	0	0	0	0	0	0	0	0	0	0	0	D3YZC9	
ENSMUST00000113493	ENSMUSG00000036435	5	76529311	76570294	1	0	0	0	0	0	0	0	0	0	0	0	Q6P1Y9	
ENSMUST00000113494	ENSMUSG00000054976	1	81076950	81341764	1	6	11	14	5	14	5	0	0	0	0	0		
ENSMUST00000113495	ENSMUSG00000047242	X	106206883	106221158	-1	6	0	0	1	0	0	8	19	6	38	17	A2AP82	
ENSMUST00000113498	ENSMUSG00000064080	6	91212455	91272540	1	5	17	18	53	37	29	2	8	5	9	43	Q3TGL4	P37889
ENSMUST00000113500	ENSMUSG00000024947	19	6334979	6340891	1	8	0	19	0	0	0	290	17	7	48	0		O88559
ENSMUST00000113501	ENSMUSG00000024947	19	6334979	6340891	1	0	0	0	0	0	0	0	122	0	0	0	D3YZC2	
ENSMUST00000113502	ENSMUSG00000024947	19	6334979	6340891	1	3	0	0	21	0	0	234	292	327	0	0		
ENSMUST00000113503	ENSMUSG00000024947	19	6334979	6340891	1	2	0	0	0	0	3	0	5	0	0	2	F8WHD9	
ENSMUST00000113504	ENSMUSG00000024947	19	6334979	6340891	1	0	0	5	0	0	0	2	1	3	0	0		O88559
ENSMUST00000113505	ENSMUSG00000032215	9	73113426	73123333	1	1	0	0	0	0	0	0	0	0	104	49	E9Q4P7	
ENSMUST00000113506	ENSMUSG00000029233	5	76140271	76155504	1	98	54	53	1506	166	112	0	581	0	0	22	F6WPW1	
ENSMUST00000113507	ENSMUSG00000029233	5	76140271	76155504	1	22	29	137	0	6	0	664	312	475	106	283	F6WPW1	
ENSMUST00000113509	ENSMUSG00000030091	6	91013068	91116829	-1	44	2	0	0	0	0	0	246	0	24	0		
ENSMUST00000113510	ENSMUSG00000073643	1	79702262	79776143	-1	1	1	1	1	3	0	6	0	0	8	0	Q9DAD3	
ENSMUST00000113511	ENSMUSG00000073643	1	79702262	79776143	-1	1	1	1	1	3	0	6	0	0	8	0	Q9DAD3	
ENSMUST00000113512	ENSMUSG00000073643	1	79702262	79776143	-1	9	11	25	9	11	4	81	250	119	17	80	E9Q4P1	
ENSMUST00000113513	ENSMUSG00000073643	1	79702262	79776143	-1	9	11	25	9	11	4	81	250	119	17	80	E9Q4P1	
ENSMUST00000113514	ENSMUSG00000073643	1	79702262	79776143	-1	9	11	25	9	11	4	81	250	119	17	80	E9Q4P1	
ENSMUST00000113515	ENSMUSG00000073643	1	79702262	79776143	-1	9	11	25	9	11	4	81	250	119	17	80	E9Q4P1	
ENSMUST00000113516	ENSMUSG00000062960	5	75932827	75978458	-1	42	43	76	21	55	21	3	10	2	2	7	Q8VCD0	
ENSMUST00000113519	ENSMUSG00000023951	17	46016993	46032377	-1	0	0	0	0	0	0	7	9	0	0	19	E9Q4N9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000113520	ENSMUSG00000023951	17	46016993	46032377	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4N8	
ENSMUST00000113523	ENSMUSG00000036026	17	45660171	45686905	-1	11	9	23	45	18	7	177	355	211	26	268		Q3TWI9
ENSMUST00000113524	ENSMUSG00000012187	1	78510991	78538173	1	0	0	0	0	0	0	0	0	0	0	0		Q91ZV4
ENSMUST00000113526	ENSMUSG00000024784	19	6226380	6227768	1	5	3	48	14	0	5	0	0	0	0	0	A2RSW3	Q925Q5
ENSMUST00000113528	ENSMUSG00000024786	19	6184388	6224225	1	9	9	22	16	11	8	0	0	0	1	0	E9Q4N4	
ENSMUST00000113529	ENSMUSG00000079471	17	45600967	45602102	-1	4	2	10	15	0	0	0	0	0	0	0	Q2Q5T5	
ENSMUST00000113530	ENSMUSG00000030087	6	90462576	90475238	1	25	18	25	15	31	6	0	0	0	0	0		Q9EPW2
ENSMUST00000113531	ENSMUSG00000029228	5	74592447	74702912	-1	0	11	12	0	10	0	0	0	0	0	15	E9Q4N3	
ENSMUST00000113532	ENSMUSG00000055632	2	31314415	31460738	1	137	93	260	320	209	90	0	0	0	0	0		A2AJ76
ENSMUST00000113533	ENSMUSG00000024790	19	6116004	6118586	-1	5	0	5	409	14	8	20	32	15	4	10	G5E8Q7	
ENSMUST00000113534	ENSMUSG00000029227	5	74535449	74598800	1	3	9	0	4	4	0	0	17	0	0	0		Q9D824
ENSMUST00000113535	ENSMUSG00000029227	5	74535449	74598800	1	0	0	0	0	0	0	58	142	12	37	80		Q9D824
ENSMUST00000113536	ENSMUSG00000029227	5	74535449	74598800	1	2	0	0	0	0	0	213	186	322	0	232		Q9D824
ENSMUST00000113538						2	2	4	3	5	5	0	0	0	0	0		
ENSMUST00000113539	ENSMUSG00000034430	6	90369492	90403490	1	9	1	12	49	0	8	20	73	16	8	45	E9Q4N0	
ENSMUST00000113542	ENSMUSG00000062110	5	74204816	74531759	-1	0	0	0	0	0	0	12	0	10	5	3		Q8BTY8
ENSMUST00000113543	ENSMUSG00000024799	19	6062821	6068373	-1	3	0	17	0	0	0	0	9	17	0	13	E9Q4M8	
ENSMUST00000113547	ENSMUSG00000023949	17	45523434	45542679	1	44	25	174	106	48	19	0	0	0	0	0		A6H639
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ENSMUST00000113550	ENSMUSG00000030086	6	89383146	89595652	-1	0	0	0	43	0	0	0	0	0	16	11	E9Q4M4	
ENSMUST00000113552	ENSMUSG00000075415	2	31026206	31142008	-1	3	8	9	10	6	2	34	29	103	0	156		Q80TY0
ENSMUST00000113553	ENSMUSG00000026213	1	75521529	75537335	1	14	5	25	35	32	16	815	396	612	89	502		Q3TAA7
ENSMUST00000113555	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	0	0	0	0	0	0	0	0	0	A2AQ45	
ENSMUST00000113557	ENSMUSG00000033792	X	106027276	106124926	1	3	0	0	31	12	0	79	78	457	101	674		Q64430
ENSMUST00000113558	ENSMUSG00000051674	5	73481000	73560794	1	14	0	0	0	0	0	3	54	37	0	84	B7ZMU0	
ENSMUST00000113559	ENSMUSG00000075415	2	31026206	31142008	-1	0	5	79	0	11	19	0	118	0	2	0		Q80TY0
ENSMUST00000113560	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	0	66	11	0	0	40	0	16	31		Q80TY0
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ENSMUST00000113564	ENSMUSG00000075415	2	31026206	31142008	-1	2	3	1	5	8	10	384	39	1021	51	973		Q80TY0
ENSMUST00000113565	ENSMUSG00000026211	1	75479310	75506452	-1	0	0	2	9	0	3	0	0	0	0	0	A0A0B4J1L4	
ENSMUST00000113566	ENSMUSG00000031232	X	105968084	106011906	-1	0	0	0	0	0	0	12	0	0	0	10	F6WHL0	
ENSMUST00000113567	ENSMUSG00000026211	1	75479310	75506452	-1	9	13	66	118	30	5	0	0	0	0	0		D3YYU8
ENSMUST00000113568	ENSMUSG00000039153	17	44495987	44814797	-1	0	0	0	0	0	0	0	0	0	0	0	Q1PAG7	
ENSMUST00000113570	ENSMUSG00000032204	9	71110659	71168682	-1	0	0	3	0	0	0	5	0	0	0	0	Q4FK77	Q9JJJ3
ENSMUST00000113571	ENSMUSG00000039153	17	44495987	44814797	-1	33	26	63	0	0	22	164	468	178	0	0		Q08775
ENSMUST00000113572	ENSMUSG00000039153	17	44495987	44814797	-1	38	16	54	988	79	25	107	279	234	28	444	F8WHN7	
ENSMUST00000113573	ENSMUSG00000031229	X	105797615	105929403	-1	8	7	3	4	16	1	795	2131	1685	926	1173		Q61687
ENSMUST00000113575	ENSMUSG00000051703	1	75479532	75485705	1	10	0	0	132	10	6	10	9	9	1	2		Q8BG75
ENSMUST00000113577	ENSMUSG00000033007	1	75450436	75474343	1	9	9	26	293	22	0	0	0	0	0	0	D3YYS9	
ENSMUST00000113581	ENSMUSG00000033174	6	88724412	88828360	1	0	1	0	5	0	0	6	0	0	0	4	D3YYS6	
ENSMUST00000113582	ENSMUSG00000033174	6	88724412	88828360	1	2	0	0	0	0	0	0	0	0	0	0	Q3UFN1	
ENSMUST00000113584	ENSMUSG00000033021	1	75435930	75443179	1	0	0	0	0	0	0	80	109	59	11	17		Q922H4
ENSMUST00000113585	ENSMUSG00000033174	6	88724412	88828360	1	0	0	0	45	0	0	60	110	0	15	0		O35678
ENSMUST00000113587	ENSMUSG00000026207	1	75375297	75432320	1	5	4	0	19	4	0	0	0	0	0	0		
ENSMUST00000113588	ENSMUSG00000026207	1	75375297	75432320	1	2	0	12	0	3	7	0	0	0	0	5		
ENSMUST00000113589	ENSMUSG00000026207	1	75375297	75432320	1	10	4	18	99	10	5	0	0	0	2	0		
ENSMUST00000113590	ENSMUSG00000026207	1	75375297	75432320	1	5	0	0	3	0	0	0	0	0	0	0		Q62407
ENSMUST00000113592	ENSMUSG00000039476	2	30834972	30881251	1	14	0	4	6	16	2	1	0	0	5	0	Q9CY80	
ENSMUST00000113594	ENSMUSG00000029217	5	72755716	72868483	-1	5	0	0	0	3	0	0	103	0	10	29	Q3U436	
ENSMUST00000113595	ENSMUSG00000032217	9	70425429	70503725	-1	32	32	99	70	34	28	665	1654	936	98	981		Q99ML9
ENSMUST00000113596	ENSMUSG00000079477	6	87999106	88045270	-1	40	45	178	92	61	27	181	256	400	245	467	Q4FJQ0	P51150
ENSMUST00000113597	ENSMUSG00000079477	6	87999106	88045270	-1	3	5	7	2	7	0	121	238	81	11	80	Q4FJQ0	P51150
ENSMUST00000113598	ENSMUSG00000079477	6	87999106	88045270	-1	0	0	7	0	11	0	0	949	0	0	13	Q4FJQ0	P51150
ENSMUST00000113599	ENSMUSG00000056492	17	43389466	43459557	1	84	54	72	229	82	47	3	3	5	10	34		G5E8Q8
ENSMUST00000113600	ENSMUSG00000079477	6	87999106	88045270	-1	13	5	17	18	0	7	4645	11087	5065	1754	3407	Q4FJQ0	P51150
ENSMUST00000113601	ENSMUSG00000039515	2	30416039	30447806	1	3	0	31	0	9	0	22	143	28	46	24	A2AWF0	
ENSMUST00000113602	ENSMUSG00000079476	X	102908905	102909651	1	1	1	2	0	2	0	0	0	0	0	0	B1AX35	
ENSMUST00000113603	ENSMUSG00000039515	2	30416039	30447806	1	0	0	0	0	0	0	0	0	21	0	0	A2AWE9	
ENSMUST00000113604	ENSMUSG00000054892	5	72695978	72752777	-1	0	8	11	0	0	0	30	59	16	36	74		P42682
ENSMUST00000113605	ENSMUSG00000026209	1	75307896	75317990	-1	0	0	0	0	0	0	700	592	394	178	258		Q9Z2W0
ENSMUST00000113606	ENSMUSG00000030060	6	87913935	87936629	1	8	6	4	78	11	8	10	10	11	0	0		Q8R1M0
ENSMUST00000113607	ENSMUSG00000030058	6	87887814	87913595	1	7	12	40	16	17	7	709	1248	960	197	770		Q9QZE5
ENSMUST00000113609	ENSMUSG00000073027	X	102707865	102715209	1	0	0	0	0	0	0	0	0	0	0	0	Q2PMX6	
ENSMUST00000113610	ENSMUSG00000079479	X	102706890	102707635	-1	0	4	2	2	0	6	0	0	0	0	0	A2AI92	
ENSMUST00000113611	ENSMUSG00000034055	X	102513975	102644246	-1	0	0	0	0	0	0	0	0	0	0	0		P18826
ENSMUST00000113612	ENSMUSG00000026856	2	30392254	30400529	1	0	0	0	0	0	0	24	67	0	11	33	A2AWJ3	
ENSMUST00000113614	ENSMUSG00000057899	17	42708936	42742179	-1	8	9	26	13	20	7	0	0	0	0	0		E9Q4J9
ENSMUST00000113615	ENSMUSG00000054874	19	5664635	5688908	-1	7	20	0	147	40	5	921	289	830	35	939		Q8VI59
ENSMUST00000113617	ENSMUSG00000030057	6	87842615	87851106	-1	1	0	8	33	0	0	0	9	0	13	13	Q3ULK8	
ENSMUST00000113619	ENSMUSG00000030057	6	87842615	87851106	-1	0	0	0	22	4	0	827	3623	1049	2912	895	Q3U935	P53996
ENSMUST00000113620	ENSMUSG00000026860	2	30344809	30359337	-1	4	0	5	3	0	6	0	0	11	0	0	A2AWI9	
ENSMUST00000113621	ENSMUSG00000026860	2	30344809	30359337	-1	0	0	0	0	0	0	0	0	0	0	0	A2AWI7	
ENSMUST00000113623	ENSMUSG00000026200	1	75198236	75210813	-1	0	3	0	4	2	0	20	0	46	0	19		Q8VC60
ENSMUST00000113624	ENSMUSG00000032238	9	68653786	69388246	1	0	11	2	210	9	5	1	2	5	0	4	Q3U1P4	P51448
ENSMUST00000113627	ENSMUSG00000079480	X	102119447	102127669	1	2	0	1	0	0	0	87	504	131	929	132		Q9CWW6
ENSMUST00000113628						110	66	204	729	140	102	1656	2275	3237	163	1845		
ENSMUST00000113631	ENSMUSG00000049191	X	102066544	102071304	-1	9	12	0	12	5	0	15	14	0	0	11	Q8C065	Q5DTT4
ENSMUST00000113634	ENSMUSG00000052533	2	30286397	30344266	1	0	2	0	0	0	1	1	0	0	7	0	A2AWI5	
ENSMUST00000113636	ENSMUSG00000063240	17	38145393	38149590	1	0	4	2	3	5	1	0	0	0	0	0	Q8VG94	
ENSMUST00000113637	ENSMUSG00000030047	6	87458545	87533259	-1	0	12	39	18	19	14	707	1327	1138	143	1127		Q8BYW1
ENSMUST00000113641	ENSMUSG00000024926	19	5603017	5610094	-1	8	8	20	89	26	10	653	1306	691	247	445	Q3UJQ1	Q8CHK4
ENSMUST00000113643	ENSMUSG00000079484	2	30266203	30282149	1	0	0	0	0	0	0	0	0	0	0	0	A2AQZ7	
ENSMUST00000113645	ENSMUSG00000079484	2	30266203	30282149	1	2	0	4	1	0	0	0	8	0	0	0		Q9DB26
ENSMUST00000113651	ENSMUSG00000037685	5	67618140	67847434	-1	0	1	0	43	0	0	0	0	0	0	7	E9Q4J5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000113652	ENSMUSG00000037685	5	67618140	67847434	-1	0	0	0	0	0	0	19	71	13	4	0	Q3U9N5	
ENSMUST00000113654	ENSMUSG00000007476	2	30237715	30263790	1	48	31	182	79	21	33	117	103	0	33	0		Q80WG5
ENSMUST00000113655	ENSMUSG00000029992	6	87042846	87092197	1	0	13	0	0	0	0	0	0	0	0	0	D3YYE0	
ENSMUST00000113657	ENSMUSG00000029992	6	87042846	87092197	1	10	0	16	20	15	4	4	5	10	1	8	D3YYD9	
ENSMUST00000113658	ENSMUSG00000029992	6	87042846	87092197	1	40	44	138	46	37	20	159	411	300	34	244		P47856
ENSMUST00000113659	ENSMUSG00000039648	2	30185124	30205847	-1	2	0	0	0	4	1	0	0	15	0	0	A2AQY8	
ENSMUST00000113660	ENSMUSG00000039648	2	30185124	30205847	-1	0	1	3	2	0	0	0	0	0	0	0	A2AQY9	
ENSMUST00000113661	ENSMUSG00000039648	2	30185124	30205847	-1	18	18	178	41	34	13	0	0	0	4	11	Q05CI8	Q8BTY1
ENSMUST00000113662	ENSMUSG00000039648	2	30185124	30205847	-1	10	1	7	3	2	4	0	0	4	6	0	Q05CI8	Q8BTY1
ENSMUST00000113663	ENSMUSG00000039648	2	30185124	30205847	-1	0	0	0	0	0	0	6	0	0	0	0	Q05CI8	Q8BTY1
ENSMUST00000113667	ENSMUSG00000024459	17	36984061	36989537	-1	3	0	0	0	0	0	0	1	1	2	4	F6VXI7	
ENSMUST00000113668						5	8	0	87	0	6	47	40	104	0	80		
ENSMUST00000113669	ENSMUSG00000036315	17	36954356	36958559	-1	0	0	2	0	2	4	0	88	6	38	11		Q791N7
ENSMUST00000113672	ENSMUSG00000006542	1	74738922	74749221	-1	0	1	3	0	0	3	0	0	0	0	0		Q8BGM7
ENSMUST00000113673	ENSMUSG00000024914	19	5422805	5424979	-1	3	0	3	20	0	4	5	5	0	6	6	D3YYC2	
ENSMUST00000113674	ENSMUSG00000024914	19	5422805	5424979	-1	0	0	0	0	0	0	53	0	0	0	10	D3YY09	
ENSMUST00000113675	ENSMUSG00000029994	6	86736840	86793584	-1	0	0	0	0	0	0	0	0	0	0	0		P97429
ENSMUST00000113676	ENSMUSG00000029221	5	67306955	67358443	1	0	0	0	14	0	0	163	858	367	91	209	F8WHL1	
ENSMUST00000113677	ENSMUSG00000039686	2	30097283	30124585	-1	0	0	0	34	7	0	660	327	592	0	602	Q3UZ97	Q80ZJ6
ENSMUST00000113678	ENSMUSG00000033257	1	74661745	74703730	1	7	6	3	0	8	0	30	51	77	5	128	D3YY08	
ENSMUST00000113679	ENSMUSG00000001157	6	86691768	86733383	-1	5	1	0	68	0	3	0	0	6	0	2	Q3V0Z2	
ENSMUST00000113682	ENSMUSG00000001285	15	102331709	102338139	1	6	3	32	8	10	0	8	23	23	11	33		Q9JK81
ENSMUST00000113683	ENSMUSG00000001158	6	86675151	86684522	-1	2	3	2	6	3	3	0	2	0	3	0		Q8K194
ENSMUST00000113684	ENSMUSG00000032366	9	67022590	67049406	-1	0	1	0	0	0	0	0	0	0	0	0	E9Q456	
ENSMUST00000113685	ENSMUSG00000032366	9	67022590	67049406	-1	0	3	4	0	0	0	0	0	0	0	0	Q545Y3	P58771
ENSMUST00000113686	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	66	3	4	0	0	0	0	9	E9Q455	
ENSMUST00000113687	ENSMUSG00000032366	9	67022590	67049406	-1	1	0	2	0	0	0	0	0	0	19	4	E9Q454	
ENSMUST00000113689	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	0	1	0	2	0	6	0	0	E9Q453	
ENSMUST00000113690	ENSMUSG00000032366	9	67022590	67049406	-1	8	11	31	112	11	6	3	9	10	2	7	G5E8R0	
ENSMUST00000113693	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	0	1	0	0	0	0	0	0	E9Q452	
ENSMUST00000113694	ENSMUSG00000033276	1	74601445	74636894	1	0	3	0	0	4	3	11	26	9	16	2	Q9D9B2	
ENSMUST00000113695	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	0	0	0	22	71	5	108	85	G5E8R1	
ENSMUST00000113696	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	4	0	0	18	27	38	0	43	G5E8R2	
ENSMUST00000113697	ENSMUSG00000032366	9	67022590	67049406	-1	0	2	0	0	0	0	0	0	0	28	50	E9Q450	
ENSMUST00000113698	ENSMUSG00000046679	6	86438374	86473500	1	7	5	4	54	12	3	40	192	67	110	78		Q8R3C1
ENSMUST00000113700	ENSMUSG00000046679	6	86438374	86473500	1	0	0	0	7	0	0	56	96	55	0	17		Q8R3C1
ENSMUST00000113701	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	0	0	0	0	0	0	10	0	E9Q448	
ENSMUST00000113704						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000113705	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	66	3	4	0	0	0	0	0	B7ZNL3	
ENSMUST00000113706	ENSMUSG00000045409	17	36258873	36272247	-1	0	0	0	10	0	0	53	256	184	0	160	E9QLN4	
ENSMUST00000113707	ENSMUSG00000032366	9	67022590	67049406	-1	4	0	4	148	8	0	0	0	0	0	0	Q564G1	P58771
ENSMUST00000113708						0	0	0	0	0	0	0	0	0	4	15		
ENSMUST00000113710	ENSMUSG00000031297	X	101079210	101086020	-1	33	21	70	31	26	18	0	5	3	1	0		P70423
ENSMUST00000113711	ENSMUSG00000039715	2	30031546	30048881	-1	51	49	87	59	74	26	21	38	26	12	32	A2BE91	
ENSMUST00000113712	ENSMUSG00000071337	6	86404219	86433405	1	10	0	0	0	0	0	0	169	0	0	34	D3YY02	
ENSMUST00000113713	ENSMUSG00000071337	6	86404219	86433405	1	0	1	10	0	0	0	0	159	0	24	34	Q80ZW7	
ENSMUST00000113716	ENSMUSG00000009670	X	100838648	101059667	-1	0	1	0	0	0	0	0	0	1	0	0		Q14AT2
ENSMUST00000113717	ENSMUSG00000057738	2	29965560	30031451	1	0	0	0	0	31	0	0	0	0	0	0	A3KGU5	
ENSMUST00000113718	ENSMUSG00000009670	X	100838648	101059667	-1	0	0	0	0	0	6	0	0	0	0	0		Q14AT2
ENSMUST00000113719	ENSMUSG00000057738	2	29965560	30031451	1	0	0	0	82	0	0	0	0	0	0	0	E9Q447	
ENSMUST00000113720						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000113721	ENSMUSG00000026171	1	74593748	74601397	-1	0	2	0	10	0	0	74	543	150	67	54	E9Q446	
ENSMUST00000113724	ENSMUSG00000070780	5	66016549	66173118	-1	0	0	0	0	3	0	13	0	0	0	14		Q91WT8
ENSMUST00000113725						0	0	0	0	0	0	21	41	51	0	35		
ENSMUST00000113726	ENSMUSG00000070780	5	66016549	66173118	-1	26	16	0	33	16	15	0	66	66	0	49		Q91WT8
ENSMUST00000113727	ENSMUSG00000024862	19	5107746	5118560	-1	0	0	0	0	0	0	156	0	0	20	0	D3YXZ3	
ENSMUST00000113728	ENSMUSG00000024862	19	5107746	5118560	-1	0	0	0	0	0	0	43	129	0	0	0	D3YXZ3	
ENSMUST00000113729	ENSMUSG00000080717	16	97997323	98010000	1	0	0	0	0	0	0	2	14	5	27	9	L7N467	
ENSMUST00000113730	ENSMUSG00000032375	9	66775202	66795490	-1	0	0	2	29	4	0	42	13	8	0	22	F8WHK7	
ENSMUST00000113732	ENSMUSG00000026172	1	74588289	74592443	1	0	2	25	12	7	6	0	17	24	0	18		Q9CZP5
ENSMUST00000113733	ENSMUSG00000026172	1	74588289	74592443	1	0	3	6	5	4	0	97	215	28	21	38		Q9CZP5
ENSMUST00000113734	ENSMUSG00000046962	16	97947435	97962621	-1	0	0	0	0	0	0	0	0	80	0	91	E9Q444	
ENSMUST00000113735	ENSMUSG00000000881	X	100767722	100818410	1	6	0	0	33	0	2	9	0	0	0	0	A2BEF2	
ENSMUST00000113736	ENSMUSG00000000881	X	100767722	100818410	1	0	0	6	0	14	0	0	0	0	0	0	A2BEE9	
ENSMUST00000113737	ENSMUSG00000026135	1	74565127	74588246	-1	0	0	10	0	0	0	45	140	63	0	14	Q3V1C1	
ENSMUST00000113738						55	37	107	64	57	30	203	517	387	55	357		
ENSMUST00000113741	ENSMUSG00000057738	2	29965560	30031451	1	2	1	3	5	1	0	0	0	0	0	0	A3KGU4	
ENSMUST00000113742	ENSMUSG00000079492	17	36055816	36058371	-1	945	894	873	332	716	205	198	180	118	241	380	A7VMS2	
ENSMUST00000113743	ENSMUSG00000005251	16	97741933	97763737	-1	32	14	29	53	15	13	0	0	0	0	0	D3YXY4	
ENSMUST00000113744	ENSMUSG00000019359	X	100729873	100738895	1	8	6	5	9	6	3	0	0	0	0	5		Q9ESM6
ENSMUST00000113745						3	8	1	5	7	0	0	1	1	0	0		
ENSMUST00000113747	ENSMUSG00000026173	1	74542888	74567794	1	0	0	0	0	0	0	0	0	0	0	0		Q8K3R3
ENSMUST00000113749	ENSMUSG00000026173	1	74542888	74567794	1	29	0	0	0	0	0	0	15	0	0	17		Q8K3R3
ENSMUST00000113750	ENSMUSG00000026173	1	74542888	74567794	1	0	0	0	0	0	0	0	0	0	0	0		Q8K3R3
ENSMUST00000113751	ENSMUSG00000054226	6	85911865	85930284	1	2	0	1	0	1	1	4	3	7	11	9	D3YXX8	
ENSMUST00000113752	ENSMUSG00000054226	6	85911865	85930284	1	0	0	0	0	0	0	0	0	0	0	0		Q8QZZ7
ENSMUST00000113753	ENSMUSG00000054226	6	85911865	85930284	1	49	0	46	85	32	12	13	16	20	18	0		Q8QZZ7
ENSMUST00000113755	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	0	0	0	12	29	47	7	58		A3KGV1
ENSMUST00000113756	ENSMUSG00000026790	2	29889221	29931746	1	0	0	15	18	0	5	153	755	507	72	314		A3KGV1
ENSMUST00000113757	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	0	0	0	134	0	135	0	215		A3KGV1
ENSMUST00000113759	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	0	13	0	213	146	234	0	43		A3KGV1
ENSMUST00000113760	ENSMUSG00000053835	17	36005695	36020560	-1	41	21	38	31	37	26	663	2728	1265	337	1744	F8VQG4	
ENSMUST00000113762	ENSMUSG00000026790	2	29889221	29931746	1	0	7	0	0	8	0	0	0	0	0	0	A3KGV9	
ENSMUST00000113763	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	0	0	0	0	0	0	0	0		A3KGV1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000113764	ENSMUSG00000026790	2	29889221	29931746	1	6	0	14	144	15	10	0	0	0	0	0		A3KGV1
ENSMUST00000113765	ENSMUSG00000026790	2	29889221	29931746	1	7	0	0	0	0	0	0	0	21	0	0		A3KGV1
ENSMUST00000113767	ENSMUSG00000026790	2	29889221	29931746	1	0	0	2	31	3	0	0	0	43	0	26	A3KGW0	
ENSMUST00000113768	ENSMUSG00000000386	16	97447035	97462907	-1	5	3	0	4	0	0	2	37	0	0	31	Q3UD61	
ENSMUST00000113769	ENSMUSG00000060890	X	100605497	100618493	1	2	0	3	13	0	2	0	0	0	0	0		Q9EQP6
ENSMUST00000113770	ENSMUSG00000030008	6	85446810	85451970	-1	0	0	0	5	0	0	0	11	0	0	0	Q14C45	
ENSMUST00000113773	ENSMUSG00000000157	16	96422288	96443619	-1	9	4	20	32	0	14	124	950	430	138	369	D3YXH8	
ENSMUST00000113775	ENSMUSG00000059327	X	99975606	100400762	1	0	0	0	0	9	0	0	0	0	0	0	Q1L2D6	
ENSMUST00000113776	ENSMUSG00000059327	X	99975606	100400762	1	0	0	0	0	0	0	0	0	0	0	0	Q1L2D6	
ENSMUST00000113777	ENSMUSG00000059327	X	99975606	100400762	1	0	0	0	39	0	0	0	0	0	0	0	Q1L2D6	
ENSMUST00000113778	ENSMUSG00000059327	X	99975606	100400762	1	0	0	0	0	0	0	0	0	0	0	0		O54693
ENSMUST00000113779	ENSMUSG00000059327	X	99975606	100400762	1	0	0	0	0	0	0	0	0	0	0	0	Q3UV69	O54693
ENSMUST00000113780	ENSMUSG00000059327	X	99975606	100400762	1	19	0	0	13	14	3	0	2	0	0	0		O54693
ENSMUST00000113781	ENSMUSG00000059327	X	99975606	100400762	1	0	13	27	13	0	3	0	2	0	0	0	Q1L2D8	
ENSMUST00000113782	ENSMUSG00000024436	17	35910379	35916389	-1	4	5	24	15	8	0	9	0	0	17	0	Q542W5	Q99N84
ENSMUST00000113783	ENSMUSG00000059327	X	99975606	100400762	1	0	0	0	1	0	0	0	0	0	0	0	Q1L2D9	
ENSMUST00000113787	ENSMUSG00000033720	6	85213049	85333422	-1	7	2	10	98	15	7	35	49	56	17	44	D3YXH6	
ENSMUST00000113788	ENSMUSG00000033720	6	85213049	85333422	-1	0	1	0	46	0	0	9	33	17	30	15	D3YXH5	
ENSMUST00000113790	ENSMUSG00000034403	X	99465734	99471273	-1	0	0	0	0	0	0	6	40	16	6	5	B1AXU4	
ENSMUST00000113792	ENSMUSG00000034403	X	99465734	99471273	-1	0	2	14	34	6	0	0	0	0	8	0	Q05CG5	O55176
ENSMUST00000113793	ENSMUSG00000006456	19	4800569	4811634	-1	22	14	64	61	29	17	23	51	30	0	77	E9QL13	
ENSMUST00000113794	ENSMUSG00000000159	16	96361668	96525580	1	9	6	26	18	11	4	1	6	4	0	2	D3YXH1	
ENSMUST00000113795	ENSMUSG00000000159	16	96361668	96525580	1	0	0	0	0	0	0	0	0	0	0	0	D3YXH0	
ENSMUST00000113796	ENSMUSG00000006301	1	74288247	74305622	-1	177	151	501	629	248	134	8	21	25	1	43	Q3U717	
ENSMUST00000113797	ENSMUSG00000034403	X	99465734	99471273	-1	0	0	0	0	0	0	89	213	113	62	69	B1AXU3	
ENSMUST00000113800	ENSMUSG00000074892	16	96235801	96319859	1	24	36	39	3	8	12	0	0	0	0	0		Q9JI67
ENSMUST00000113802	ENSMUSG00000072952	6	85111416	85126125	-1	53	33	87	156	47	22	0	0	0	0	0	E9PUB3	
ENSMUST00000113803						1	1	2	0	0	3	7	3	7	0	6		
ENSMUST00000113804	ENSMUSG00000045275	16	96158407	96192257	-1	13	12	19	53	23	4	0	1	0	0	0	D3YXG9	
ENSMUST00000113805	ENSMUSG00000026179	1	74284930	74353694	1	5	0	10	18	5	0	129	191	59	146	43		
ENSMUST00000113807	ENSMUSG00000039826	2	29761224	29788502	-1	1	3	24	5	2	0	0	5	2	0	3	A2ARC1	
ENSMUST00000113809	ENSMUSG00000075425	2	29759312	29764089	1	0	0	0	0	0	0	0	0	0	0	0	F6VA34	
ENSMUST00000113810	ENSMUSG00000075425	2	29759312	29764089	1	8	5	7	2	5	2	1	2	3	0	3	A2ARC0	
ENSMUST00000113811	ENSMUSG00000047694	X	98936316	98949017	1	0	0	0	0	0	0	28	80	31	73	22		Q8BR70
ENSMUST00000113814	ENSMUSG00000034595	17	35865593	35875596	1	26	0	0	0	24	22	1639	2036	965	150	751		Q8BQ30
ENSMUST00000113818	ENSMUSG00000033788	6	84008590	84211060	1	0	0	0	7	48	0	0	0	0	0	0		Q9ESD7
ENSMUST00000113819	ENSMUSG00000006304	1	74236084	74268209	1	8	5	12	89	0	3	47	75	670	2780	118	D3YXG6	
ENSMUST00000113820	ENSMUSG00000006304	1	74236084	74268209	1	6	4	19	15	7	0	6343	19197	3723	12123	3164		Q9CVB6
ENSMUST00000113821	ENSMUSG00000033788	6	84008590	84211060	1	12	0	25	109	0	0	0	0	0	0	0	E9QL12	
ENSMUST00000113822	ENSMUSG00000045045	19	4611785	4615667	-1	15	4	61	430	10	11	6	7	2	7	6		Q80XU8
ENSMUST00000113823	ENSMUSG00000033788	6	84008590	84211060	1	15	23	27	1	17	12	0	0	0	0	0	E9Q423	
ENSMUST00000113824	ENSMUSG00000015357	9	65294260	65330658	1	9	12	6	0	13	0	0	259	93	28	32	Q6P8N8	
ENSMUST00000113825	ENSMUSG00000024892	19	4510472	4621752	1	49	32	59	7	34	24	0	20	28	6	20	G5E8R3	
ENSMUST00000113826	ENSMUSG00000031214	X	98554277	98891025	-1	0	0	0	0	0	0	1	15	2	12	5		Q99J31
ENSMUST00000113827	ENSMUSG00000022914	16	95992092	96082526	-1	5	9	21	38	7	5	25	68	28	2	19	Q8BPZ1	
ENSMUST00000113829	ENSMUSG00000022914	16	95992092	96082526	-1	17	17	109	37	22	24	92	393	306	88	325		Q921C3
ENSMUST00000113830	ENSMUSG00000026799	2	29346819	29524793	1	38	17	121	46	32	23	5	0	3	0	7		Q9DB40
ENSMUST00000113832	ENSMUSG00000034457	X	97333840	97377216	-1	2	0	0	0	4	2	0	0	0	2	0	Q3KP88	Q8BX35
ENSMUST00000113835	ENSMUSG00000030016	6	83867109	83989550	1	0	0	0	0	0	1	83	270	275	123	149		Q61464
ENSMUST00000113836	ENSMUSG00000030016	6	83867109	83989550	1	0	0	0	0	0	0	0	0	32	55	133	E9QKZ7	
ENSMUST00000113837	ENSMUSG00000024858	19	4286001	4306222	-1	23	16	33	53	23	11	499	1630	524	75	1040	E9Q419	
ENSMUST00000113838	ENSMUSG00000031209	X	96455359	96574485	1	0	0	0	6	0	0	0	0	0	0	0		Q9Z0Z4
ENSMUST00000113842						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000113843						1	1	0	0	1	0	0	0	0	1	0		
ENSMUST00000113846	ENSMUSG00000040732	16	95359169	95586593	-1	36	32	182	13	41	31	0	29	0	0	31		P81270
ENSMUST00000113847	ENSMUSG00000026805	2	28907679	28916668	-1	9	3	12	55	7	3	0	0	0	0	0		P63157
ENSMUST00000113848	ENSMUSG00000040732	16	95359169	95586593	-1	0	0	0	0	0	0	0	0	0	0	0		P81270
ENSMUST00000113849	ENSMUSG00000026805	2	28907679	28916668	-1	0	4	6	50	4	0	0	0	0	0	0		P63157
ENSMUST00000113850	ENSMUSG00000034744	6	83794982	83804018	1	10	4	17	10	1	0	2	2	5	0	2	D3YXG2	
ENSMUST00000113851	ENSMUSG00000034744	6	83794982	83804018	1	0	0	0	0	0	1	16	30	0	31	0	Q9D997	
ENSMUST00000113852	ENSMUSG00000034616	19	4261668	4269172	-1	0	2	45	0	31	1	68	186	64	0	110		Q8K330
ENSMUST00000113853	ENSMUSG00000026806	2	28840406	28905571	1	18	14	25	18	23	13	31	99	35	19	61	Q6NZQ2	
ENSMUST00000113854	ENSMUSG00000062609	16	95257558	95300260	1	0	0	179	0	3	10	0	1	1	1	0	Q53Z04	O88932
ENSMUST00000113855	ENSMUSG00000062609	16	95257558	95300260	1	0	0	0	0	7	0	0	0	0	0	0	Q53Z04	O88932
ENSMUST00000113856	ENSMUSG00000062609	16	95257558	95300260	1	0	0	0	1	0	0	0	0	0	0	0	Q53Z04	O88932
ENSMUST00000113858	ENSMUSG00000062609	16	95257558	95300260	1	16	9	50	12	22	23	0	0	0	0	0	Q3TNE6	
ENSMUST00000113859	ENSMUSG00000062609	16	95257558	95300260	1	0	0	0	0	0	0	0	0	0	0	0	Q3TNE6	
ENSMUST00000113861	ENSMUSG00000062609	16	95257558	95300260	1	0	0	0	0	0	0	0	0	0	0	1	Q3TNE6	
ENSMUST00000113862	ENSMUSG00000062609	16	95257558	95300260	1	78	77	50	1235	86	58	0	0	0	0	0	Q3TNE6	
ENSMUST00000113864	ENSMUSG00000057421	X	95935335	95956962	-1	0	0	0	0	7	0	0	0	0	0	0		A2BE28
ENSMUST00000113865	ENSMUSG00000039191	5	53466152	53657362	1	18	0	41	70	19	0	550	1445	739	136	355	Q3UM17	P31266
ENSMUST00000113867	ENSMUSG00000026812	2	28641228	28691167	1	0	0	0	0	0	0	58	82	124	69	0		Q9EP53
ENSMUST00000113869	ENSMUSG00000026812	2	28641228	28691167	1	33	0	0	50	55	43	0	0	0	0	241		Q9EP53
ENSMUST00000113870	ENSMUSG00000026812	2	28641228	28691167	1	0	33	103	0	17	0	140	219	0	0	0		Q9EP53
ENSMUST00000113873	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	0	0	4	0	0	0	0	0	0	B1AXI2	
ENSMUST00000113876	ENSMUSG00000025656	X	95048935	95196856	-1	0	6	27	0	13	0	0	0	0	0	0		Q3UTH8
ENSMUST00000113878	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	0	0	0	0	0	0	0	0	0		Q3UTH8
ENSMUST00000113879	ENSMUSG00000073409	17	35424850	35430055	1	0	0	0	0	0	0	583	621	306	203	671	P79568	
ENSMUST00000113882	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	0	0	0	0	0	0	0	0	0		Q3UTH8
ENSMUST00000113883	ENSMUSG00000025656	X	95048935	95196856	-1	21	0	0	15	0	0	0	0	0	0	0		Q3UTH8
ENSMUST00000113884	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	4	0	6	0	0	0	0	0	0	B1AXI6	
ENSMUST00000113885	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	0	0	0	5	1	0	0	0	0	B1AXI4	
ENSMUST00000113888	ENSMUSG00000014554	6	83480217	83506969	-1	0	2	0	26	0	2	0	0	0	0	0	Q504N4	
ENSMUST00000113889	ENSMUSG00000026816	2	28566311	28583751	-1	21	24	0	130	37	16	0	46	0	0	0		Q8R2T8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000113890	ENSMUSG00000032396	9	64306756	64341288	-1	6	6	14	57	12	0	0	0	0	0	0		Q8C0S1
ENSMUST00000113893	ENSMUSG00000026821	2	28513125	28553081	1	8	9	14	64	8	0	0	0	0	0	22	A2AK33	
ENSMUST00000113895	ENSMUSG00000079508	X	94367117	94417093	1	0	0	0	0	0	0	0	0	0	0	0		Q9DCZ4
ENSMUST00000113896	ENSMUSG00000079508	X	94367117	94417093	1	0	0	0	0	8	2	0	0	4	0	0		Q9DCZ4
ENSMUST00000113897	ENSMUSG00000079508	X	94367117	94417093	1	1	3	17	17	0	6	0	0	0	0	0		Q9DCZ4
ENSMUST00000113898	ENSMUSG00000079508	X	94367117	94417093	1	0	0	0	9	3	0	12	13	1	7	13		Q9DCZ4
ENSMUST00000113899	ENSMUSG00000068323	6	83219828	83304945	1	20	0	36	30	0	14	1	0	0	0	0	D3YX36	
ENSMUST00000113900	ENSMUSG00000068323	6	83219828	83304945	1	12	4	15	37	6	3	0	0	0	0	0	E9Q3M5	
ENSMUST00000113901						1	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000113902	ENSMUSG00000043549	X	94355053	94366777	-1	14	6	12	113	18	17	0	0	0	0	1	B1ASQ1	
ENSMUST00000113903	ENSMUSG00000043549	X	94355053	94366777	-1	5	0	20	0	3	2	0	0	1	0	0	Q9D4F3	
ENSMUST00000113904	ENSMUSG00000029179	5	52775409	52824665	1	10	13	27	27	20	5	13	109	25	24	42		Q8BKW4
ENSMUST00000113905	ENSMUSG00000022940	16	94358763	94371015	-1	0	0	0	0	1	0	0	0	0	5	0		Q9JHG1
ENSMUST00000113906	ENSMUSG00000022940	16	94358763	94371015	-1	0	0	0	8	0	0	0	7	0	24	10		Q9JHG1
ENSMUST00000113907	ENSMUSG00000031865	6	83165920	83200117	1	16	18	42	69	29	26	10	16	36	0	40	D3YX34	
ENSMUST00000113908	ENSMUSG00000043929	X	94234599	94277724	1	0	1	0	48	1	0	0	4	12	0	6	Q8K1Y4	
ENSMUST00000113910	ENSMUSG00000022940	16	94358763	94371015	-1	0	0	2	87	4	0	0	0	0	13	0	B8JK66	
ENSMUST00000113911	ENSMUSG00000043929	X	94234599	94277724	1	0	0	0	0	0	0	15	32	0	8	0	Q8K1Y4	
ENSMUST00000113913	ENSMUSG00000031865	6	83165920	83200117	1	0	0	19	0	0	0	48	14	0	0	18	E9Q3M3	
ENSMUST00000113914	ENSMUSG00000022940	16	94358763	94371015	-1	0	0	0	49	0	0	0	0	0	0	0	B8JK67	
ENSMUST00000113915	ENSMUSG00000043929	X	94234599	94277724	1	19	23	129	27	25	6	66	123	45	13	37	A2AAX3	
ENSMUST00000113916	ENSMUSG00000043929	X	94234599	94277724	1	0	0	0	0	0	0	0	0	0	0	5	A2AAX3	
ENSMUST00000113917	ENSMUSG00000022940	16	94358763	94371015	-1	2	2	9	3	0	1	0	0	0	0	1	B8JK65	
ENSMUST00000113918	ENSMUSG00000031865	6	83165920	83200117	1	14	0	16	0	7	0	0	0	0	0	0		O08788
ENSMUST00000113919	ENSMUSG00000031865	6	83165920	83200117	1	0	15	0	7	16	0	0	0	22	0	22		O08788
ENSMUST00000113920	ENSMUSG00000026833	2	28192992	28230736	1	8	12	39	0	13	0	0	0	1	0	0	A3KGE4	
ENSMUST00000113922	ENSMUSG00000035150	X	94188707	94212862	-1	0	0	0	0	0	0	0	0	0	0	0	A2AAW9	
ENSMUST00000113925	ENSMUSG00000079509	X	94074631	94123702	-1	1	1	5	0	1	0	9	33	36	0	0	Q8R2L1	
ENSMUST00000113926	ENSMUSG00000079509	X	94074631	94123702	-1	9	5	12	15	0	9	300	715	284	100	186	B1ASD1	P17012
ENSMUST00000113927	ENSMUSG00000079509	X	94074631	94123702	-1	0	0	0	29	19	0	0	40	0	121	121	B1ASD1	P17012
ENSMUST00000113930	ENSMUSG00000024563	18	76241580	76305731	1	2	4	0	0	4	0	0	53	18	32	7	E9Q3M0	
ENSMUST00000113933	ENSMUSG00000035246	X	93654863	93749951	1	15	6	75	287	48	0	4	27	9	2	24		Q811Q9
ENSMUST00000113934	ENSMUSG00000015846	2	27676440	27762957	1	0	0	6	20	0	0	0	0	0	0	0	Q6LC96	
ENSMUST00000113935	ENSMUSG00000030034	6	83121765	83125431	-1	8	0	28	91	13	5	113	201	76	52	57		Q99PT3
ENSMUST00000113936	ENSMUSG00000030035	6	83119044	83121559	-1	0	0	9	148	5	9	103	0	93	0	16		P97764
ENSMUST00000113938	ENSMUSG00000030037	6	83109040	83109939	1	0	1	0	12	0	0	107	224	73	177	33		Q9D1H8
ENSMUST00000113940	ENSMUSG00000053153	1	69826970	70725132	1	61	64	586	98	61	35	0	0	0	4	0		Q8K450
ENSMUST00000113941	ENSMUSG00000026918	2	27445579	27507662	-1	1	0	0	0	0	1	16	87	109	0	9	Q5CCJ9	Q8K2F0
ENSMUST00000113942	ENSMUSG00000034912	12	66469568	67222549	-1	0	3	26	0	0	2	0	0	0	0	0	Q3UUB8	
ENSMUST00000113947	ENSMUSG00000035277	X	93286445	93298357	1	4	0	0	0	15	6	0	1	0	0	0		O35085
ENSMUST00000113951	ENSMUSG00000022948	16	93583457	93604063	-1	2	0	0	0	5	0	0	12	0	0	0	G3X9W6	
ENSMUST00000113952	ENSMUSG00000026917	2	27515157	27536535	1	12	11	78	52	20	6	1138	2228	1234	190	602		P61965
ENSMUST00000113954						99	91	714	142	71	51	1	18	9	0	3		
ENSMUST00000113955	ENSMUSG00000067649	X	92118879	92599572	-1	11	9	23	18	16	7	0	0	0	0	0	Q8BQR7	
ENSMUST00000113956	ENSMUSG00000022952	16	92601466	92826149	-1	0	0	6	146	6	0	121	128	118	3	75	G3X9W7	
ENSMUST00000113958	ENSMUSG00000079513	X	89752268	89755491	1	1	1	0	0	1	2	0	0	0	0	0	A2ADI4	
ENSMUST00000113959	ENSMUSG00000035395	X	89403848	89409689	-1	0	2	4	4	4	0	0	0	0	0	0	A2AHY8	
ENSMUST00000113960	ENSMUSG00000035395	X	89403848	89409689	-1	8	3	6	6	4	1	0	0	0	0	0	A2AHY8	
ENSMUST00000113962	ENSMUSG00000068329	6	83051266	83055273	-1	0	0	0	0	2	0	0	0	0	10	49	D3YX28	
ENSMUST00000113963	ENSMUSG00000068329	6	83051266	83055273	-1	1	0	0	0	0	0	0	0	0	0	0	D3YX27	
ENSMUST00000113964	ENSMUSG00000052372	X	86740870	88115645	-1	2	3	0	0	0	0	0	0	0	0	0	Q0VDP7	
ENSMUST00000113966	ENSMUSG00000052372	X	86740870	88115645	-1	6	6	23	11	8	6	0	0	0	0	0	B1ASU0	
ENSMUST00000113968	ENSMUSG00000045098	19	3767421	3818303	1	10	5	14	26	4	6	10	36	29	3	34		Q3U8K7
ENSMUST00000113969	ENSMUSG00000035427	X	86250254	86305093	-1	1	2	5	1	2	1	0	0	0	0	0	A2A9R3	
ENSMUST00000113970	ENSMUSG00000045098	19	3767421	3818303	1	0	23	17	0	0	5	35	163	74	13	75		Q3U8K7
ENSMUST00000113971	ENSMUSG00000039672	16	92292389	92298129	1	4	6	2	8	4	0	0	0	0	0	0		
ENSMUST00000113972	ENSMUSG00000045098	19	3767421	3818303	1	0	0	0	0	0	0	0	0	53	0	0		Q3U8K7
ENSMUST00000113973	ENSMUSG00000045098	19	3767421	3818303	1	19	0	0	35	13	0	296	1176	518	0	383		Q3U8K7
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ENSMUST00000113975	ENSMUSG00000089774	16	92058322	92087473	1	48	36	96	107	59	28	2	10	10	6	27		Q9JKZ2
ENSMUST00000113976	ENSMUSG00000025058	X	85870354	85891499	1	67	58	142	95	82	41	37	592	85	212	105	Q08EG0	Q9D3J9
ENSMUST00000113977	ENSMUSG00000045098	19	3767421	3818303	1	1	19	82	0	0	4	16	7	0	92	50		Q3U8K7
ENSMUST00000113978	ENSMUSG00000025059	X	85701937	85776819	-1	0	0	0	0	0	0	0	70	40	0	25		Q64516
ENSMUST00000113979	ENSMUSG00000026000	1	67000517	67038872	-1	23	14	32	114	33	19	12	26	10	7	14		O89112
ENSMUST00000113980	ENSMUSG00000030041	6	82946902	83030309	1	14	13	21	11	14	13	7	35	15	25	5		Q9Z0E1
ENSMUST00000113982						8	1	33	15	13	4	0	2	0	0	2		
ENSMUST00000113987	ENSMUSG00000026004	1	66719248	66817562	-1	0	0	0	6	0	0	0	54	99	0	0	E9QLE2	
ENSMUST00000113990	ENSMUSG00000032278	9	61953481	62026856	-1	1	0	14	3	4	3	5	12	0	2	1	Q497J6	
ENSMUST00000113991	ENSMUSG00000045103	X	82948870	85206141	1	46	36	366	43	23	20	1	5	4	0	1	A2A9Z2	
ENSMUST00000113992	ENSMUSG00000045103	X	82948870	85206141	1	0	0	0	0	0	0	0	0	0	0	0	A2A9Z1	
ENSMUST00000113993	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	0	0	0	69	0	51	12	157	E9Q3I9	
ENSMUST00000113995	ENSMUSG00000026005	1	66700831	66719805	1	0	0	0	0	0	0	21	70	0	28	15	B2KGF0	
ENSMUST00000113996	ENSMUSG00000022957	16	91729281	91920597	1	1	0	0	0	8	0	0	0	0	0	0	E9Q3I8	
ENSMUST00000113997	ENSMUSG00000024908	19	3454933	3575749	-1	0	0	0	0	0	0	743	1492	1257	168	948	G5E8R4	
ENSMUST00000113999	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	2	0	0	0	0	0	0	0	E9Q3I5	
ENSMUST00000114000	ENSMUSG00000045103	X	82948870	85206141	1	6	12	26	4	13	6	0	0	0	0	0		P11531
ENSMUST00000114001	ENSMUSG00000022957	16	91729281	91920597	1	0	0	1	13	1	0	0	0	71	0	35	E9Q3I4	
ENSMUST00000114002	ENSMUSG00000022957	16	91729281	91920597	1	288	418	519	375	395	191	4	21	5	8	22		Q9Z0R4
ENSMUST00000114003	ENSMUSG00000015488	2	27009926	27021089	1	2	0	1	1	0	4	4	0	0	0	6	A6PWX1	
ENSMUST00000114004	ENSMUSG00000015488	2	27009926	27021089	1	6	0	18	8	8	0	7	34	11	0	18		Q8BG21
ENSMUST00000114005	ENSMUSG00000015488	2	27009926	27021089	1	10	5	0	12	1	6	11	33	13	3	3		Q8BG21
ENSMUST00000114006	ENSMUSG00000015488	2	27009926	27021089	1	0	0	0	0	0	0	0	0	7	0	0		Q8BG21
ENSMUST00000114007	ENSMUSG00000015488	2	27009926	27021089	1	52	35	286	97	45	18	163	234	168	25	156		Q8BG21
ENSMUST00000114008	ENSMUSG00000055567	1	66468367	66699866	1	0	0	0	1	0	0	0	0	0	0	0	I6L9J4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114011	ENSMUSG00000007050	17	34981862	34985891	1	0	0	0	0	1	0	27	139	43	0	54	Q3U9X2	O35900
ENSMUST00000114012	ENSMUSG00000015222	1	66175273	66442583	1	0	5	0	0	8	2	0	0	0	0	0	Q80X35	
ENSMUST00000114013	ENSMUSG00000015222	1	66175273	66442583	1	29	28	43	32	27	14	0	0	0	0	0		P20357
ENSMUST00000114015	ENSMUSG00000015222	1	66175273	66442583	1	0	0	0	0	0	0	0	0	0	0	0	Q80ZL4	
ENSMUST00000114016	ENSMUSG00000046942	X	79623231	79671435	-1	0	3	0	0	0	0	0	0	0	0	0		Q9CWV4
ENSMUST00000114017	ENSMUSG00000015222	1	66175273	66442583	1	0	0	6	8	0	0	0	0	1	0	0	Q3TLQ0	
ENSMUST00000114018	ENSMUSG00000015222	1	66175273	66442583	1	0	0	0	0	0	0	0	0	0	0	0	Q3TLQ0	
ENSMUST00000114020	ENSMUSG00000052406	2	26953563	26964386	-1	15	9	17	25	11	8	85	282	172	72	136		Q6PAQ4
ENSMUST00000114021	ENSMUSG00000073077	X	79266559	79517285	-1	15	10	9	5	10	2	0	0	1	0	2	B1AXF0	
ENSMUST00000114023	ENSMUSG00000058240	16	91689322	91728975	-1	1	1	3	2	3	0	24	149	37	40	77		Q921W4
ENSMUST00000114024	ENSMUSG00000047996	X	78449613	78583896	-1	0	0	0	5	0	0	0	0	0	0	0	A2BFE8	
ENSMUST00000114025	ENSMUSG00000047996	X	78449613	78583896	-1	0	0	0	0	0	0	0	0	0	0	0	A2BFE8	
ENSMUST00000114026	ENSMUSG00000079519	X	78240462	78245921	-1	0	0	0	1	1	0	0	0	0	0	0	A2BHD2	
ENSMUST00000114027	ENSMUSG00000025945	1	65926520	65928307	1	0	5	0	0	5	4	0	0	0	0	0	E9Q3I1	
ENSMUST00000114030	ENSMUSG00000079521	X	78125467	78130403	1	1	0	0	0	1	0	0	0	0	0	0	A2AEN9	
ENSMUST00000114031	ENSMUSG00000022960	16	91677268	91688765	-1	0	2	0	51	0	0	0	0	16	0	0	D3YWN6	
ENSMUST00000114032	ENSMUSG00000047766	9	60568859	60688158	-1	0	0	0	0	0	0	22	58	0	13	0	D3YWN5	
ENSMUST00000114033	ENSMUSG00000013787	17	34898469	34914052	1	0	0	37	0	0	0	468	255	224	73	10		Q9Z148
ENSMUST00000114034	ENSMUSG00000047766	9	60568859	60688158	-1	0	0	3	0	0	0	0	28	0	26	0	G5E8R5	
ENSMUST00000114036	ENSMUSG00000022961	16	91647506	91679221	1	14	13	78	24	27	18	693	2045	1530	143	1094		Q9QX47
ENSMUST00000114037	ENSMUSG00000022961	16	91647506	91679221	1	0	0	0	0	0	0	555	0	2301	77	1750		Q9QX47
ENSMUST00000114038						9	4	9	5	2	0	0	0	0	0	0		
ENSMUST00000114039	ENSMUSG00000079522	X	77864758	77870033	1	0	6	0	2	7	0	0	0	0	0	0	B1AVU4	
ENSMUST00000114040	ENSMUSG00000052861	6	73017606	73221651	-1	76	60	28	16	57	31	2	18	2	7	8	E9Q3H7	
ENSMUST00000114041	ENSMUSG00000000003	X	77837901	77853623	-1	1	1	0	1	0	0	0	0	0	0	0	B1AVU3	
ENSMUST00000114043	ENSMUSG00000036160	2	26888628	26902879	-1	56	61	43	37	60	33	9	20	19	0	0	A2ALA0	
ENSMUST00000114044	ENSMUSG00000035725	X	77761411	77796278	-1	3	3	5	13	6	0	6	5	7	0	23	B1AVU1	
ENSMUST00000114045	ENSMUSG00000015787	2	26842503	26864979	-1	7	4	7	7	14	7	0	0	0	0	0	Z4YLB0	
ENSMUST00000114047	ENSMUSG00000039753	5	43744615	43821638	-1	0	0	0	0	5	0	3250	13672	6231	5142	2729		Q8C2S5
ENSMUST00000114048	ENSMUSG00000079523	6	72957347	72958748	-1	0	0	4	27	3	3	0	8	0	0	0	A6H6H4	Q6ZWY8
ENSMUST00000114049	ENSMUSG00000079523	6	72957347	72958748	-1	5	3	13	113	14	6	20	32	13	14	35	A6H6H4	Q6ZWY8
ENSMUST00000114050	ENSMUSG00000079523	6	72957347	72958748	-1	0	1	0	14	0	0	1231	2517	1137	5300	1041	A6H6H4	Q6ZWY8
ENSMUST00000114053	ENSMUSG00000055799	6	72626378	72789254	-1	8	1	12	122	13	7	1	0	0	0	1	A1A549	
ENSMUST00000114054	ENSMUSG00000079525	X	76582610	76602924	-1	3	0	0	2	1	1	0	0	0	0	0	A2AGU5	
ENSMUST00000114057	ENSMUSG00000016382	X	75785654	75875182	-1	4	0	3	0	0	0	0	0	0	66	0		Q99K51
ENSMUST00000114058	ENSMUSG00000016382	X	75785654	75875182	-1	0	8	0	0	1	0	0	34	0	0	0	B1AX58	
ENSMUST00000114059	ENSMUSG00000016382	X	75785654	75875182	-1	5	0	3	1	2	3	11	53	97	259	78		Q99K51
ENSMUST00000114064	ENSMUSG00000025952	1	65071525	65073689	-1	0	0	2	4	1	0	0	0	0	0	0	A3RLD5	
ENSMUST00000114065	ENSMUSG00000039782	5	43233170	43289724	1	0	0	0	0	0	2	308	668	217	46	281	A0A0H2UH22	
ENSMUST00000114066	ENSMUSG00000039782	5	43233170	43289724	1	5	1	16	0	5	0	42	53	200	13	153	D3YUJ4	
ENSMUST00000114069	ENSMUSG00000056698	6	72565922	72598413	-1	17	5	0	14	25	5	51	139	35	0	70		Q91YP6
ENSMUST00000114070	ENSMUSG00000031197	X	75514299	75534942	1	4	6	5	2	1	2	0	0	44	86	15	Q3TIR6	
ENSMUST00000114071	ENSMUSG00000056737	6	72544391	72562983	1	5	2	9	7	10	4	1370	1277	568	328	845	Q99LB4	
ENSMUST00000114072	ENSMUSG00000056737	6	72544391	72562983	1	2	0	0	0	2	2	9	0	9	0	0	Q99LB4	
ENSMUST00000114074	ENSMUSG00000031201	X	75416628	75454001	1	2	0	0	0	0	0	0	11	0	9	4		P46737
ENSMUST00000114076	ENSMUSG00000039851	16	91053935	91095122	-1	0	0	0	0	5	3	0	0	0	0	0		Q9D4G1
ENSMUST00000114077	ENSMUSG00000070871	1	64690455	64725644	1	9	0	32	30	23	9	27	43	60	44	24	D3YUJ3	
ENSMUST00000114079	ENSMUSG00000025956	1	64606473	64617242	-1	4	8	14	16	0	0	16	90	28	8	23		Q9CQL0
ENSMUST00000114081	ENSMUSG00000031200	X	75410444	75416588	-1	0	0	2	0	0	0	2	6	18	7	15		Q60945
ENSMUST00000114082	ENSMUSG00000026924	2	26409431	26445216	-1	0	0	131	20	48	0	240	258	379	0	509	A2AIX1	
ENSMUST00000114085	ENSMUSG00000031196	X	75172715	75382615	-1	10	5	17	0	0	6	4	2	2	0	4	B2RRC9	
ENSMUST00000114086	ENSMUSG00000025959	1	64029447	64122282	-1	28	38	96	62	51	19	1596	4595	4269	206	2170		Q99JB0
ENSMUST00000114090	ENSMUSG00000026925	2	26396249	26409203	-1	0	0	15	0	0	0	42	10	18	0	37	A2AIX0	
ENSMUST00000114091	ENSMUSG00000031402	X	75109733	75131016	-1	0	0	0	0	0	2	629	753	1650	634	816	A2AN84	
ENSMUST00000114092	ENSMUSG00000031402	X	75109733	75131016	-1	0	0	2	0	0	0	1025	3670	1663	1434	1066	B7ZCL8	
ENSMUST00000114093	ENSMUSG00000026926	2	26389339	26397122	1	21	12	57	47	26	14	15	28	31	7	56	A2AIW9	
ENSMUST00000114094	ENSMUSG00000025963	1	63698819	63730318	-1	10	3	5	6	14	2	0	0	0	0	0		Q5F204
ENSMUST00000114095	ENSMUSG00000055850	6	72359714	72366956	-1	0	0	0	0	0	0	5	0	0	0	7	D3YUJ1	
ENSMUST00000114099	ENSMUSG00000051596	5	38275972	38304217	1	0	0	0	134	0	8	0	0	0	0	0		
ENSMUST00000114100	ENSMUSG00000026927	2	26382802	26389316	-1	0	0	0	0	0	8	0	0	82	36	119	A2AIW3	
ENSMUST00000114101						18	6	13	9	4	6	0	0	0	0	0		
ENSMUST00000114102	ENSMUSG00000026927	2	26382802	26389316	-1	0	0	0	18	0	0	87	183	0	0	0		A2AIW0
ENSMUST00000114103	ENSMUSG00000025964	1	63445891	63596276	1	0	0	0	0	0	0	0	0	0	0	0		Q9R1V7
ENSMUST00000114104	ENSMUSG00000032750	X	74966843	75085458	-1	0	0	0	0	0	0	6	0	35	30	32	B1AYB9	
ENSMUST00000114106	ENSMUSG00000067367	5	38220470	38234306	1	2	2	0	6	0	0	22	138	43	0	0		Q08288
ENSMUST00000114107	ENSMUSG00000025964	1	63445891	63596276	1	0	0	0	0	0	0	0	0	0	0	0		Q9R1V7
ENSMUST00000114109	ENSMUSG00000032750	X	74966843	75085458	-1	44	23	116	168	41	4	4	5	5	2	2	Q3V3J9	
ENSMUST00000114112	ENSMUSG00000056091	6	72097592	72154571	1	0	0	13	116	13	13	0	0	24	0	0		
ENSMUST00000114113	ENSMUSG00000029127	5	38189735	38220457	-1	13	7	27	5	16	1	12	20	25	2	11	E9Q2Y5	
ENSMUST00000114115	ENSMUSG00000036281	2	26362765	26380653	-1	15	12	0	0	33	21	9	0	70	1	20	A2AIV6	
ENSMUST00000114116	ENSMUSG00000079531	X	74837196	74843355	1	15	10	20	28	25	8	2	1	4	2	4	A2BG95	
ENSMUST00000114117	ENSMUSG00000079532	X	74740927	74742188	1	6	0	1	0	10	4	0	0	0	0	0	A2BG94	
ENSMUST00000114119	ENSMUSG00000079534	X	74639119	74645635	-1	19	10	46	28	34	18	0	0	1	0	0	A3KG49	
ENSMUST00000114121	ENSMUSG00000032336	9	58582240	58657955	1	0	6	0	0	0	2	0	30	317	1042	427	Z4YLB7	
ENSMUST00000114122	ENSMUSG00000002489	16	89787111	89980080	-1	0	0	0	0	0	0	0	241	0	0	0	E9Q2Y4	
ENSMUST00000114124	ENSMUSG00000002489	16	89787111	89980080	-1	0	25	66	63	62	0	0	0	0	0	0	G3UWG2	
ENSMUST00000114125	ENSMUSG00000079536	X	74480287	74481399	-1	0	2	4	5	8	3	0	0	0	0	0	A3KG45	
ENSMUST00000114126	ENSMUSG00000029125	5	38038742	38137765	1	18	22	33	45	35	11	68	220	116	27	69		Q8VDS8
ENSMUST00000114127	ENSMUSG00000004221	X	74393290	74453854	1	3	0	6	5	5	0	425	255	192	13	27		O88522
ENSMUST00000114128	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	0	0	0	14	141	60	121		O88522
ENSMUST00000114129	ENSMUSG00000004221	X	74393290	74453854	1	0	0	3	0	0	0	0	0	0	4	1	Q8VC91	
ENSMUST00000114130	ENSMUSG00000004221	X	74393290	74453854	1	0	22	0	0	25	26	11	209	131	0	85	E9Q2Y3	
ENSMUST00000114132	ENSMUSG00000027520	1	63273265	63314576	1	0	0	0	90	0	21	0	0	0	0	0		Q5SS00
ENSMUST00000114133	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	0	0	0	91	0	0	0		O88522

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114134	ENSMUSG00000026930	2	26315515	26348237	1	0	0	14	0	9	0	0	34	0	0	0	A2AIV3	
ENSMUST00000114136	ENSMUSG00000036986	9	58218076	58249786	-1	0	0	3	0	10	10	66	54	0	19	50		Q60953
ENSMUST00000114137	ENSMUSG00000022935	16	87896196	88056176	-1	10	10	0	10	10	9	0	0	0	0	0	E9Q2Y1	
ENSMUST00000114138	ENSMUSG00000031399	X	74384719	74393272	-1	0	0	0	0	0	0	6	0	0	0	0	J3JS95	
ENSMUST00000114139	ENSMUSG00000031399	X	74384719	74393272	-1	0	2	0	0	0	0	0	0	16	0	0	I7HPY1	
ENSMUST00000114140	ENSMUSG00000034254	17	34604262	34613449	1	0	12	0	3	19	10	77	386	0	0	117		
ENSMUST00000114141	ENSMUSG00000031399	X	74384719	74393272	-1	0	0	0	0	0	0	0	0	0	0	0	I7HJS7	
ENSMUST00000114142	ENSMUSG00000031399	X	74384719	74393272	-1	0	0	0	0	0	0	41	0	33	0	0		Q9D8T0
ENSMUST00000114143	ENSMUSG00000031399	X	74384719	74393272	-1	3	4	12	12	7	6	110	137	99	29	127		Q9D8T0
ENSMUST00000114144	ENSMUSG00000051243	9	58196298	58204319	-1	2	2	5	12	0	0	0	0	0	0	0		Q5RKR3
ENSMUST00000114146	ENSMUSG00000032806	X	74369217	74373349	-1	0	3	0	0	0	9	29	10	177	0	0		P21129
ENSMUST00000114147	ENSMUSG00000032806	X	74369217	74373349	-1	5	0	0	0	0	0	0	84	0	0	0	J3JSA1	
ENSMUST00000114148	ENSMUSG00000029122	5	37289098	37336894	-1	2	3	5	2	0	0	0	0	0	0	0	E9Q2E6	
ENSMUST00000114151	ENSMUSG00000052337	6	71831331	71877388	1	0	0	0	2	0	0	187	592	325	107	188		Q8CAQ8
ENSMUST00000114152	ENSMUSG00000015289	X	74351276	74353618	-1	0	0	0	0	0	0	19	8	0	24	0	J3JS94	
ENSMUST00000114153	ENSMUSG00000015289	X	74351276	74353618	-1	54	32	46	48	48	27	0	9	5	3	5	J3JS94	
ENSMUST00000114154	ENSMUSG00000029122	5	37289098	37336894	-1	14	5	6	7	9	6	0	0	0	0	0	D3YUJ0	
ENSMUST00000114155	ENSMUSG00000025969	1	62703285	62818695	1	58	44	59	1145	99	35	45	207	99	17	81	Q3U5I8	O35375
ENSMUST00000114157	ENSMUSG00000025969	1	62703285	62818695	1	11	7	62	0	1	3	2	0	0	1	0		O35375
ENSMUST00000114158	ENSMUSG00000029121	5	37241940	37292133	1	0	0	0	68	14	8	0	0	0	0	0	Q6P1J1	
ENSMUST00000114159	ENSMUSG00000026932	2	26055535	26123220	-1	112	45	61	326	67	63	0	0	22	0	16		Q9DCM7
ENSMUST00000114160	ENSMUSG00000001962	X	74313033	74320149	1	0	2	0	38	1	0	259	1131	348	456	322		Q9WV03
ENSMUST00000114165	ENSMUSG00000004661	9	57790353	57836793	-1	0	0	0	0	0	0	0	0	0	0	0	Q3V3M5	
ENSMUST00000114167	ENSMUSG00000026933	2	25926838	25983282	-1	33	33	129	152	53	52	8	62	9	4	11	A0A0A0MQE5	
ENSMUST00000114170						4	4	4	28	14	4	0	0	0	0	0		
ENSMUST00000114171	ENSMUSG00000019087	X	74297097	74304721	1	3	0	0	16	9	0	197	4	88	0	44	Q3TKX1	
ENSMUST00000114172	ENSMUSG00000058740	2	25863734	25918273	1	0	0	0	0	0	0	0	0	0	0	0	A2AHB9	Q6ZPR4
ENSMUST00000114174	ENSMUSG00000041134	16	85421533	85553397	-1	36	35	45	329	33	19	0	4	0	0	0		Q8VIH7
ENSMUST00000114175	ENSMUSG00000057246	17	34398820	34460734	1	4	0	0	15	3	0	0	3	0	2	4	Q80XD0	
ENSMUST00000114176	ENSMUSG00000058740	2	25863734	25918273	1	33	29	66	39	46	16	0	0	0	0	0	A2AHB7	
ENSMUST00000114178	ENSMUSG00000052656	6	71493894	71510881	1	0	0	18	15	9	0	0	12	10	0	19	D3Z0Y5	
ENSMUST00000114179	ENSMUSG00000052656	6	71493894	71510881	1	15	3	22	0	5	0	170	593	287	58	186		Q9R1W3
ENSMUST00000114180	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	0	0	0	13	102	24	40	83	I7HJS2	
ENSMUST00000114182	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	0	0	0	35	0	36	3	22	H3BKZ8	
ENSMUST00000114184	ENSMUSG00000008976	16	84834925	84863779	1	0	2	0	0	0	0	113	179	359	116	198		Q00422
ENSMUST00000114185						29	9	53	20	26	11	2	5	5	2	4		
ENSMUST00000114186	ENSMUSG00000055027	6	71213940	71322233	-1	0	6	0	11	0	0	0	0	0	0	0	Q3UQT9	P97443
ENSMUST00000114188	ENSMUSG00000055027	6	71213940	71322233	-1	0	2	0	0	0	2	0	0	0	0	0	G5E8R7	
ENSMUST00000114189	ENSMUSG00000019088	X	74273217	74282337	-1	0	0	0	0	0	0	10	28	0	35	13	I7HPX5	
ENSMUST00000114191	ENSMUSG00000022890	16	84827866	84835625	-1	0	4	10	0	6	0	50	135	62	219	39		P97450
ENSMUST00000114192	ENSMUSG00000079539	2	25737009	25740097	1	9	5	13	6	10	11	0	0	0	0	0	A2BHR0	
ENSMUST00000114193	ENSMUSG00000022890	16	84827866	84835625	-1	0	0	0	0	0	0	0	34	32	4	8		P97450
ENSMUST00000114195	ENSMUSG00000053062	16	84774123	84825928	1	26	30	48	105	32	11	6	5	5	28	17		Q9JI59
ENSMUST00000114197	ENSMUSG00000045684	2	25676786	25681608	1	2	0	0	0	0	1	0	0	0	0	0	A2AJC1	
ENSMUST00000114199	ENSMUSG00000045684	2	25676786	25681608	1	5	2	16	1	7	4	0	0	0	0	0	A2AJB9	
ENSMUST00000114200	ENSMUSG00000032305	9	57537528	57543187	1	40	22	98	0	0	25	77	123	142	0	31		Q14DQ1
ENSMUST00000114201	ENSMUSG00000090935	12	81497941	81532911	-1	3	2	5	8	6	0	0	3	0	0	0		Q9D6K5
ENSMUST00000114202						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000114203	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0Y4	
ENSMUST00000114204	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	0	0	0	0	0	0	0	1		Q8BL65
ENSMUST00000114205	ENSMUSG00000029095	5	35757880	35884973	1	16	0	0	0	0	7	2	3	0	1	0		Q8BL65
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ENSMUST00000114209						0	1	0	0	3	1	0	0	0	0	0		
ENSMUST00000114210	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	0	0	0	0	0	0	0	0		Q8BL65
ENSMUST00000114212	ENSMUSG00000079543	6	68930269	68930734	-1	0	1	2	0	1	1	0	0	0	0	1	A0A075B666	
ENSMUST00000114214						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000114216	ENSMUSG00000022860	16	78930948	78951733	1	5	0	3	0	4	0	0	0	0	0	0	F2Z3Y6	
ENSMUST00000114217	ENSMUSG00000029419	2	25575416	25581757	-1	24	0	53	190	38	20	0	0	0	0	0		A2AJA9
ENSMUST00000114218	ENSMUSG00000022864	16	78544012	78576657	-1	13	2	0	74	6	10	51	209	70	100	101		Q9D7G4
ENSMUST00000114219	ENSMUSG00000022864	16	78544012	78576657	-1	0	0	0	0	0	0	23	8	2	9	28		Q9D7G4
ENSMUST00000114220	ENSMUSG00000022864	16	78544012	78576657	-1	6	4	14	118	14	2	15	61	33	6	39		Q9D7G4
ENSMUST00000114222	ENSMUSG00000036402	6	66896397	67021350	1	3	1	16	158	6	1	12	22	46	18	18		Q9DAS9
ENSMUST00000114223	ENSMUSG00000026941	2	25563115	25574845	-1	0	3	31	5	0	3	0	0	0	0	0		A2AJA7
ENSMUST00000114224	ENSMUSG00000036402	6	66896397	67021350	1	0	0	0	0	0	0	95	191	159	417	90		Q9DAS9
ENSMUST00000114225	ENSMUSG00000036402	6	66896397	67021350	1	0	0	5	0	0	2	11	0	143	9	117		Q9DAS9
ENSMUST00000114226	ENSMUSG00000036402	6	66896397	67021350	1	0	0	0	0	0	0	0	35	0	0	0		Q9DAS9
ENSMUST00000114227	ENSMUSG00000036402	6	66896397	67021350	1	0	0	0	0	0	0	228	741	60	314	61		Q9DAS9
ENSMUST00000114228	ENSMUSG00000036402	6	66896397	67021350	1	0	0	0	9	0	0	308	688	311	675	243		Q9DAS9
ENSMUST00000114229	ENSMUSG00000022865	16	78301496	78359785	1	7	8	14	15	7	5	0	4	7	26	16		P97792
ENSMUST00000114230						9	8	51	29	34	19	40	239	61	11	124		
ENSMUST00000114231	ENSMUSG00000079546	16	77588578	77602094	-1	0	0	0	0	0	0	0	0	0	0	0	F6WTR5	
ENSMUST00000114232	ENSMUSG00000079547	17	34153072	34160230	1	6	2	14	0	6	3	31	65	23	39	155	Q31094	
ENSMUST00000114233	ENSMUSG00000029096	5	35652023	35679782	-1	8	8	33	37	12	4	0	2	0	1	8		Q9D236
ENSMUST00000114234	ENSMUSG00000026942	2	25517982	25546940	-1	0	0	2	0	2	1	498	417	310	92	181		P39429
ENSMUST00000114236	ENSMUSG00000044162	6	65590398	65634040	1	10	5	9	6	10	7	7	1	8	21	2	Q3SXA6	
ENSMUST00000114237	ENSMUSG00000029098	5	35583040	35615352	1	0	0	4	29	0	0	171	26	231	0	135		Q9EPL9
ENSMUST00000114238	ENSMUSG00000029098	5	35583040	35615352	1	2	0	2	0	0	0	7	11	31	6	30	E9Q296	
ENSMUST00000114239	ENSMUSG00000022876	16	75858793	76022270	-1	0	0	5	2	2	0	944	4532	2060	5745	1549		P57725
ENSMUST00000114240	ENSMUSG00000022876	16	75858793	76022270	-1	4	7	4	4	7	5	0	0	0	0	0	D3Z0Y1	
ENSMUST00000114242	ENSMUSG00000024335	17	34112023	34122634	-1	0	0	24	0	0	0	4	27	0	0	0	B2RS09	Q7JJ13
ENSMUST00000114243	ENSMUSG00000047361	1	59516264	59636417	1	17	9	22	16	31	12	0	2	1	0	2	E9Q295	
ENSMUST00000114244	ENSMUSG00000032932	16	75755190	75766821	-1	12	0	0	0	4	1	13	97	121	265	93	D3Z0Y0	
ENSMUST00000114245	ENSMUSG00000026943	2	25490845	25493911	-1	0	5	0	0	9	2	0	0	0	0	0	Q9D265	
ENSMUST00000114246	ENSMUSG00000041075	1	59482424	59486955	1	28	22	74	622	42	28	96	203	113	12	188		Q61090

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114247	ENSMUSG00000049556	9	56618475	56685253	-1	13	4	21	0	0	0	0	0	0	0	0		Q9D1T0
ENSMUST00000114248	ENSMUSG00000026023	1	59256906	59352993	1	0	0	0	0	0	0	0	0	0	0	0		Q3V3A1
ENSMUST00000114249	ENSMUSG00000032940	16	75592844	75602829	1	0	0	52	31	0	0	0	0	0	0	0	H9KUZ7	
ENSMUST00000114251	ENSMUSG00000015090	2	25466709	25470046	-1	2	0	0	0	5	0	0	0	0	0	0		O09114
ENSMUST00000114252	ENSMUSG00000024330	17	34039437	34066685	1	0	13	0	78	30	12	29	44	39	3	49		Q64739
ENSMUST00000114253	ENSMUSG00000032940	16	75592844	75602829	1	21	16	6	0	22	11	4	26	12	2	11		Q80YT9
ENSMUST00000114255	ENSMUSG00000024330	17	34039437	34066685	1	0	10	50	0	0	12	23	8	13	0	132		Q64739
ENSMUST00000114256	ENSMUSG00000049556	9	56618475	56685253	-1	4	0	0	348	23	0	0	0	0	0	0	A9DA50	
ENSMUST00000114259	ENSMUSG00000015090	2	25466709	25470046	-1	0	0	2	0	3	0	0	0	0	0	0		O09114
ENSMUST00000114261	ENSMUSG00000047617	2	25455141	25461094	-1	0	0	0	5	0	0	117	51	37	30	11		Q8K0Y7
ENSMUST00000114265	ENSMUSG00000015093	2	25456838	25458776	1	0	2	15	0	0	0	0	0	0	0	0		Q9D7P7
ENSMUST00000114268	ENSMUSG00000025889	6	60731575	60829855	-1	9	5	8	44	26	9	30	0	13	379	73		O55042
ENSMUST00000114270	ENSMUSG00000044716	5	35056766	35087839	1	0	0	0	0	0	0	0	0	0	0	0		Q18PE0
ENSMUST00000114275	ENSMUSG00000079550	1	59120935	59163389	-1	14	7	4	8	15	4	0	2	0	0	0	D3Z0G8	
ENSMUST00000114276	ENSMUSG00000032320	9	56041845	56061882	1	0	6	0	0	1	3	89	284	125	64	150		Q8BP92
ENSMUST00000114278	ENSMUSG00000036587	2	25423267	25426374	1	0	0	0	0	0	0	69	142	40	5	32	Q3SWS0	Q11131
ENSMUST00000114280	ENSMUSG00000029101	5	34949445	35039644	1	0	0	0	11	0	0	0	0	1	0	9	Q3TTW9	
ENSMUST00000114281	ENSMUSG00000029101	5	34949445	35039644	1	0	0	0	4	10	3	0	11	0	0	0	E9Q1K7	
ENSMUST00000114283	ENSMUSG00000029101	5	34949445	35039644	1	0	0	12	0	0	0	0	0	0	0	0	D3Z0G7	
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ENSMUST00000114285	ENSMUSG00000029101	5	34949445	35039644	1	5	0	2	0	0	0	0	0	0	0	0	D3Z0G5	
ENSMUST00000114290	ENSMUSG00000032318	9	55538672	55546180	1	4	3	0	0	3	6	0	1	0	0	1	Q0VAX2	
ENSMUST00000114292	ENSMUSG00000064115	16	66655421	67620908	-1	54	53	171	73	36	20	0	1	0	0	2		Q8BLQ9
ENSMUST00000114293	ENSMUSG00000026955	2	25372321	25378213	1	0	0	0	0	0	0	1	0	0	2	9		Q9D818
ENSMUST00000114294	ENSMUSG00000029802	6	58584523	58695676	1	0	0	0	0	0	0	8	23	0	0	16		
ENSMUST00000114296	ENSMUSG00000026027	1	58973522	58995715	1	2	1	8	94	0	0	26	63	33	5	14		Q8K4T3
ENSMUST00000114297	ENSMUSG00000037788	6	57727807	57825159	-1	13	5	38	69	19	5	90	330	159	63	240		Q8R1C3
ENSMUST00000114299	ENSMUSG00000031328	X	74223461	74249820	-1	0	0	42	121	0	0	86	79	334	0	163	B7FAU9	
ENSMUST00000114303	ENSMUSG00000073422	17	34026033	34028060	-1	5	0	1	42	4	0	0	11	0	0	0	G3UX44	
ENSMUST00000114306	ENSMUSG00000032311	9	55220222	55326844	-1	10	3	2	5	3	3	0	0	0	0	0	D3Z0G2	
ENSMUST00000114307	ENSMUSG00000026959	2	25291181	25319187	-1	0	0	0	137	0	0	0	0	0	0	0	A2AI19	
ENSMUST00000114308	ENSMUSG00000026959	2	25291181	25319187	-1	0	0	0	0	0	0	0	0	0	0	0	A2AI20	
ENSMUST00000114309	ENSMUSG00000026031	1	58711508	58758884	1	5	0	7	0	6	0	64	171	65	38	44	Q5U4G3	
ENSMUST00000114310	ENSMUSG00000026959	2	25291181	25319187	-1	0	0	0	0	0	0	0	0	0	0	0	A2AI21	
ENSMUST00000114311						0	0	3	20	5	0	177	1873	245	52	525		
ENSMUST00000114312	ENSMUSG00000026959	2	25291181	25319187	-1	0	0	0	106	36	0	0	0	0	0	0		P35438
ENSMUST00000114313	ENSMUSG00000026031	1	58711508	58758884	1	180	130	617	263	175	92	813	2876	1994	231	1527	Q812G4	
ENSMUST00000114314	ENSMUSG00000026959	2	25291181	25319187	-1	0	16	46	0	0	0	0	0	0	0	0	A2AI17	
ENSMUST00000114317	ENSMUSG00000026959	2	25291181	25319187	-1	29	0	0	0	0	17	0	0	0	0	0	A2AI16	
ENSMUST00000114318	ENSMUSG00000026959	2	25291181	25319187	-1	0	0	0	0	0	0	0	0	0	0	0	A2AI14	
ENSMUST00000114321	ENSMUSG00000059486	6	56777524	56797813	-1	0	0	63	34	0	0	51	132	0	0	28	G3X9X1	
ENSMUST00000114323	ENSMUSG00000059486	6	56777524	56797813	-1	32	32	1	0	21	13	318	1285	623	126	305	G3X9X1	
ENSMUST00000114325	ENSMUSG00000026037	1	58462771	58505109	-1	0	0	2	0	0	0	0	34	2	0	4	Q59IX1	
ENSMUST00000114327	ENSMUSG00000004347	6	56069804	56569103	-1	14	0	3	6	6	6	0	0	0	0	0		Q64338
ENSMUST00000114328	ENSMUSG00000062564	X	74150944	74167838	-1	2	2	5	1	1	1	0	0	0	0	0	B1AYN9	
ENSMUST00000114329	ENSMUSG00000001082	5	34633642	34637212	-1	3	0	0	0	0	0	167	58	51	16	84		Q9D2V8
ENSMUST00000114331	ENSMUSG00000001082	5	34633642	34637212	-1	0	3	4	7	7	0	381	355	250	46	82		Q9D2V8
ENSMUST00000114335	ENSMUSG00000029106	5	34573664	34632308	1	10	7	20	108	28	11	170	351	271	38	225	E9Q1K3	
ENSMUST00000114336	ENSMUSG00000048707	2	25262618	25269885	1	10	13	53	584	40	10	127	138	106	9	68		A2AI08
ENSMUST00000114337	ENSMUSG00000026036	1	58445151	58481816	1	0	0	16	11	4	1	25	12	31	77	6	D3Z0G0	
ENSMUST00000114338	ENSMUSG00000029106	5	34573664	34632308	1	0	6	0	17	0	0	0	0	0	0	0		Q9QYC0
ENSMUST00000114340	ENSMUSG00000029106	5	34573664	34632308	1	0	0	0	0	0	2	4898	5592	5975	300	3428		Q9QYC0
ENSMUST00000114341	ENSMUSG00000074991	16	59407332	59461889	1	8	8	7	1	17	5	0	0	0	0	0	B2RXA8	
ENSMUST00000114345	ENSMUSG00000026035	1	58430994	58445486	-1	2	0	2	21	5	0	3	11	2	0	0		Q9D6L8
ENSMUST00000114348	ENSMUSG00000026035	1	58430994	58445486	-1	0	0	0	0	0	0	16	47	34	57	21		Q9D6L8
ENSMUST00000114349	ENSMUSG00000006471	2	25244821	25256022	-1	0	0	0	0	0	5	27	0	28	0	16		A2AI05
ENSMUST00000114352	ENSMUSG00000031392	X	74013914	74023918	-1	21	26	22	8	20	10	198	932	805	1	367	Q540G0	Q62406
ENSMUST00000114353	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	0	0	0	0	0	B1AUW8	
ENSMUST00000114354	ENSMUSG00000031392	X	74013914	74023918	-1	2	2	1	1	2	1	240	822	42	108	188	Q8BR10	
ENSMUST00000114355	ENSMUSG00000044628	2	25242255	25244262	1	3	13	23	37	14	12	0	0	0	0	0		Q8K0W3
ENSMUST00000114356	ENSMUSG00000036731	2	25238818	25242452	-1	0	0	0	0	0	0	0	0	0	1	0	A0A0A0MQE7	
ENSMUST00000114357	ENSMUSG00000022747	16	58468125	58524243	-1	0	0	9	0	3	0	45	77	21	0	49		Q8VIB3
ENSMUST00000114358	ENSMUSG00000022747	16	58468125	58524243	-1	7	1	3	1	0	2	89	1467	220	260	188		Q8VIB3
ENSMUST00000114359	ENSMUSG00000059866	5	34496087	34513991	-1	5	1	10	0	0	0	0	154	0	0	0	D3Z039	
ENSMUST00000114360	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	0	0	0	0	0		Q62406
ENSMUST00000114361	ENSMUSG00000079553	17	33875666	33890661	-1	0	0	0	0	0	0	0	79	0	0	0		Q9QWT9
ENSMUST00000114363	ENSMUSG00000036770	2	25212207	25214637	-1	0	3	0	0	4	4	0	0	0	0	0	Q8CDQ3	
ENSMUST00000114366	ENSMUSG00000079554	1	58278326	58380259	1	53	59	50	37	62	23	0	0	0	0	0		Q5SGK3
ENSMUST00000114368	ENSMUSG00000037224	5	34194893	34288449	-1	0	1	0	11	3	0	0	0	0	0	0	D3Z3F0	
ENSMUST00000114369						1	1	9	43	1	1	0	0	0	0	0		
ENSMUST00000114370						50	50	107	50	70	20	1	21	4	0	6		
ENSMUST00000114371	ENSMUSG00000022748	16	57302199	57606825	-1	2	5	18	71	11	4	3	24	4	59	9		Q9CZT6
ENSMUST00000114372	ENSMUSG00000031386	X	73942792	73966357	-1	18	0	80	27	46	0	462	133	422	22	427	B1AUX2	
ENSMUST00000114373	ENSMUSG00000036805	2	25085667	25095149	-1	15	9	0	0	0	0	0	0	0	0	0		Q8CJ00
ENSMUST00000114374	ENSMUSG00000003476	6	55090049	55133016	-1	0	0	0	0	0	0	0	0	0	0	0	E9QNK5	
ENSMUST00000114376	ENSMUSG00000036813	2	25080304	25085716	1	0	2	0	0	9	0	0	0	0	0	0		Q8K0L2
ENSMUST00000114379	ENSMUSG00000031387	X	73922121	73930850	-1	0	0	4	2	0	0	16	19	0	11	0		P82343
ENSMUST00000114380	ENSMUSG00000036813	2	25080304	25085716	1	0	0	0	0	0	2	0	0	0	0	0		Q8K0L2
ENSMUST00000114382	ENSMUSG00000070858	5	33983433	33985013	1	0	0	0	0	0	0	0	0	0	8	0		Q3UR78
ENSMUST00000114383	ENSMUSG00000070858	5	33983433	33985013	1	0	0	0	0	0	0	6	9	8	4	5		Q3UR78
ENSMUST00000114384	ENSMUSG00000070858	5	33983433	33985013	1	0	0	1	289	3	4	0	2	0	0	0		Q3UR78
ENSMUST00000114385	ENSMUSG00000059208	17	33646233	33686860	-1	15	0	0	1	0	0	143	456	418	105	557	B8JK32	
ENSMUST00000114386	ENSMUSG00000006476	2	25054355	25062881	1	0	0	0	0	1	0	0	0	0	0	0	A2AJ95	
ENSMUST00000114387	ENSMUSG00000031388	X	73916873	73921944	-1	0	0	3	0	0	0	31	46	41	35	0	B1AUY9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114388	ENSMUSG00000006476	2	25054355	25062881	1	0	0	0	0	9	0	0	0	0	0	0	A2AJ96	
ENSMUST00000114389	ENSMUSG00000031388	X	73916873	73921944	-1	4	0	0	9	12	0	104	137	75	33	103	Q3V4D5	
ENSMUST00000114390	ENSMUSG00000031388	X	73916873	73921944	-1	0	0	0	0	0	0	27	41	0	16	2	B1AUY7	
ENSMUST00000114391	ENSMUSG00000031388	X	73916873	73921944	-1	0	0	0	0	0	0	0	0	0	0	0	B1AUY8	
ENSMUST00000114395	ENSMUSG00000031390	X	73892102	73895502	1	0	0	0	0	0	1	0	0	0	0	0	Q3KNZ4	
ENSMUST00000114397	ENSMUSG00000057406	5	33820725	33897975	1	9	20	13	12	9	1	20	12	16	0	28	D3Z3E4	
ENSMUST00000114399	ENSMUSG00000057406	5	33820725	33897975	1	0	0	0	0	0	0	25	0	0	0	0	D3Z3E0	
ENSMUST00000114401	ENSMUSG00000004633	6	54039554	54301810	1	2	0	0	3	3	4	0	0	0	5	0	Q3TVA5	Q80XD1
ENSMUST00000114402	ENSMUSG00000004633	6	54039554	54301810	1	0	0	0	2	2	0	5	0	5	1	4	H7BXA9	
ENSMUST00000114403						75	65	79	50	87	42	6	8	5	8	11		
ENSMUST00000114404	ENSMUSG00000031389	X	73891442	73921870	-1	0	0	0	0	0	0	577	22	111	0	58	B1AUY2	
ENSMUST00000114405	ENSMUSG00000031389	X	73891442	73921870	-1	18	4	39	55	23	8	41	110	114	5	189	B1AUY3	
ENSMUST00000114406	ENSMUSG00000031389	X	73891442	73921870	-1	0	0	0	0	0	0	297	1758	144	51	345	Q3TE27	
ENSMUST00000114407	ENSMUSG00000031389	X	73891442	73921870	-1	0	0	0	0	0	0	1056	815	703	0	86	B1AUX5	
ENSMUST00000114410	ENSMUSG00000054770	1	57955101	58018956	-1	0	0	6	36	0	0	32	347	25	21	26	E0CZ26	
ENSMUST00000114411	ENSMUSG00000054252	5	33721674	33737068	1	0	0	0	0	0	0	0	0	0	0	0	E9QNJ9	
ENSMUST00000114415	ENSMUSG00000038331	1	56793981	56978650	-1	23	3	33	0	31	26	5	0	1	1	0	Q546B3	Q8VI24
ENSMUST00000114416	ENSMUSG00000038203	6	52257694	52260880	-1	0	0	0	2	0	0	0	0	0	0	0	Q496S0	
ENSMUST00000114418	ENSMUSG00000036893	2	24789928	24919614	-1	0	23	69	40	10	0	114	142	0	13	0	E9Q5A3	
ENSMUST00000114423	ENSMUSG00000025977	1	55248658	55363469	-1	1	0	8	27	3	2	0	0	0	0	0	E9PWH1	
ENSMUST00000114425	ENSMUSG00000038227	6	52223100	52231089	-1	2	0	0	137	1	2	0	0	2	2	2		P09631
ENSMUST00000114426	ENSMUSG00000037313	5	33658128	33678995	1	0	0	0	0	0	0	216	412	356	42	206	Q6NV52	
ENSMUST00000114427	ENSMUSG00000079559	9	51270258	51278554	-1	4	7	10	11	12	8	0	0	0	4	10	F8VPY8	
ENSMUST00000114428	ENSMUSG00000025978	1	55170159	55226782	-1	7	1	5	4	4	2	0	2	0	1	4		Q8CHX7
ENSMUST00000114430	ENSMUSG00000031391	X	73853778	73896105	-1	2	2	0	0	0	19	581	1675	883	51	984	A2AFG8	
ENSMUST00000114431	ENSMUSG00000032056	9	51116001	51119700	1	8	3	13	7	16	5	0	0	0	0	0		O70552
ENSMUST00000114432	ENSMUSG00000036893	2	24789928	24919614	-1	0	0	0	0	0	0	20	63	65	10	0		Q5DW34
ENSMUST00000114434	ENSMUSG00000079560	6	52169062	52213336	-1	6	7	53	349	17	13	3	1	0	1	5		P02831
ENSMUST00000114437	ENSMUSG00000032058	9	50845301	50894229	1	5	17	26	15	10	5	207	440	212	31	174		Q7TNP2
ENSMUST00000114438	ENSMUSG00000002006	X	73793359	73824969	-1	0	0	10	0	0	0	16	8	24	4	4	A2AFG3	
ENSMUST00000114439	ENSMUSG00000038301	6	51523901	51590679	1	3	2	7	3	6	0	31	177	154	167	82	Q4FJX6	Q9CWT3
ENSMUST00000114444	ENSMUSG00000071533	16	56007245	56029739	-1	0	0	0	59	0	0	191	494	120	38	169	Q3UCC5	Q6P8I4
ENSMUST00000114445	ENSMUSG00000029836	6	51470360	51483704	1	0	17	30	0	0	0	0	0	0	0	0	D3Z1A9	
ENSMUST00000114446	ENSMUSG00000029836	6	51470360	51483704	1	36	0	0	0	49	20	139	417	0	0	27	Q9DCC5	
ENSMUST00000114447	ENSMUSG00000004113	2	24603887	24763152	-1	1	0	0	0	0	0	2	0	1	0	0	A2AIR7	
ENSMUST00000114449	ENSMUSG00000079562	5	33335509	33373296	1	18	12	26	49	25	12	2232	3182	2168	513	1376		Q4VC33
ENSMUST00000114455	ENSMUSG00000079563	17	32413100	32424167	-1	16	0	2	18	7	0	18	7	13	4	20		Q8VCS0
ENSMUST00000114457	ENSMUSG00000035356	16	55811375	55838899	-1	14	10	4	0	0	0	0	0	12	16	8		Q9EST8
ENSMUST00000114458	ENSMUSG00000035356	16	55811375	55838899	-1	0	0	0	260	4	9	391	2141	543	145	973		Q9EST8
ENSMUST00000114459	ENSMUSG00000004980	6	51460932	51469894	-1	5	8	20	11	6	9	995	4835	864	435	1024		O88569
ENSMUST00000114461	ENSMUSG00000031378	X	73716597	73738534	1	25	14	87	38	29	13	47	69	101	3	207	A2ALN0	
ENSMUST00000114464	ENSMUSG00000019558	X	73673150	73682502	1	16	22	52	0	4	0	2	1	2	8	12	F7C668	
ENSMUST00000114465	ENSMUSG00000019558	X	73673150	73682502	1	8	0	0	0	0	0	0	0	0	0	0	A2ALM6	Q8VBW1
ENSMUST00000114466	ENSMUSG00000029822	6	50293330	50456201	-1	4	0	12	0	0	0	17	15	0	4	5	D3Z194	
ENSMUST00000114467	ENSMUSG00000019558	X	73673150	73682502	1	0	0	0	0	0	0	0	0	0	0	0	A2ALM6	Q8VBW1
ENSMUST00000114468	ENSMUSG00000029822	6	50293330	50456201	-1	16	17	7	20	19	15	7	12	0	0	19		Q9DBS9
ENSMUST00000114471	ENSMUSG00000022637	16	52031549	52208047	1	49	28	63	81	46	27	151	291	222	27	188	B9EKI5	
ENSMUST00000114472	ENSMUSG00000002012	X	73655994	73660117	-1	0	0	0	0	0	3	0	0	0	0	0	Q3TYC1	Q9QYK9
ENSMUST00000114473	ENSMUSG00000002012	X	73655994	73660117	-1	4	3	15	29	8	0	0	0	0	0	0	Q3TYC1	Q9QYK9
ENSMUST00000114474	ENSMUSG00000032068	9	50494525	50505482	1	33	27	146	46	20	19	5	1	3	7	12		Q8VEN2
ENSMUST00000114475	ENSMUSG00000024002	17	32196274	32284722	-1	0	0	18	13	0	2	18	8	144	0	76	B2RSE4	Q9ESU6
ENSMUST00000114476	ENSMUSG00000039542	9	49502136	49798925	-1	52	41	197	100	44	25	8	5	9	0	10	E9Q589	
ENSMUST00000114477	ENSMUSG00000022641	16	50191844	50432390	-1	7	10	10	154	12	2	2	3	11	0	4	B8JK50	
ENSMUST00000114479	ENSMUSG00000031376	X	73503086	73571005	1	0	0	0	60	54	28	0	0	0	0	0	A2ALL9	
ENSMUST00000114482	ENSMUSG00000026981	2	24336853	24351494	1	47	23	208	54	33	12	567	2454	381	250	526	Q542C7	P25085
ENSMUST00000114484	ENSMUSG00000026096	1	53313624	53326343	1	2	3	3	3	2	2	7	9	18	27	5		Q6PEB4
ENSMUST00000114485	ENSMUSG00000026981	2	24336853	24351494	1	0	0	1	0	0	0	80	138	144	164	264	Q3TBV5	
ENSMUST00000114486						10	5	9	5	8	5	0	0	0	0	0		
ENSMUST00000114487	ENSMUSG00000026981	2	24336853	24351494	1	0	9	32	10	15	5	99	697	77	28	88	Q542W1	P25085
ENSMUST00000114488	ENSMUSG00000022641	16	50191844	50432390	-1	0	3	0	0	1	0	9	0	143	0	126		Q8VBW5
ENSMUST00000114490	ENSMUSG00000026983	2	24276954	24283426	1	0	0	0	0	0	0	0	0	0	0	0		Q9QYY1
ENSMUST00000114491	ENSMUSG00000050786	6	49319274	49341582	1	0	0	0	10	0	0	0	0	12	0	0		Q8BIS8
ENSMUST00000114492	ENSMUSG00000043629	1	52922324	53020179	-1	2	12	10	46	11	3	3	4	1	2	1		Q9CPS8
ENSMUST00000114493	ENSMUSG00000043629	1	52922324	53020179	-1	10	10	2	0	0	0	0	0	0	0	0		Q9CPS8
ENSMUST00000114496	ENSMUSG00000055447	16	49855618	49915010	1	0	0	0	0	0	0	1728	6480	2818	616	1072	D3Z187	
ENSMUST00000114497	ENSMUSG00000026986	2	24002910	24049394	-1	0	0	0	1	0	0	19	363	80	98	31	A2AQK4	Q91VF2
ENSMUST00000114498	ENSMUSG00000026986	2	24002910	24049394	-1	2	5	0	2	5	0	55	0	0	0	42	A2AQK4	Q91VF2
ENSMUST00000114499	ENSMUSG00000031365	X	73342621	73359080	1	0	10	43	63	27	14	5	207	106	34	84	Q3UQ14	
ENSMUST00000114500	ENSMUSG00000029815	6	49073795	49086751	1	5	0	0	0	0	0	16	32	13	12	8	D3Z186	
ENSMUST00000114503	ENSMUSG00000067764	X	73282896	73292976	-1	5	4	26	20	10	0	0	13	1	0	0	A2AIE6	
ENSMUST00000114505	ENSMUSG00000026774	2	23207476	23267129	1	4	0	0	8	3	0	0	3	1	0	0	A2ASY2	
ENSMUST00000114506	ENSMUSG00000067768	X	73214333	73222453	1	0	0	0	0	0	0	0	0	9	12	16	B1B0R4	
ENSMUST00000114507	ENSMUSG00000052139	5	31697684	32084962	1	0	4	0	1	0	0	187	3	43	0	0		Q8K3W0
ENSMUST00000114509						0	0	0	0	0	0	69	13	0	27	63		
ENSMUST00000114510	ENSMUSG00000026103	1	52163448	52233232	-1	24	32	57	275	52	25	0	10	8	0	24		D3Z7P3
ENSMUST00000114512	ENSMUSG00000026103	1	52163448	52233232	-1	1	3	2	52	4	4	30	0	101	0	0	D3Z7P4	
ENSMUST00000114513	ENSMUSG00000026103	1	52163448	52233232	-1	62	54	258	82	43	23	314	1095	601	82	537		D3Z7P3
ENSMUST00000114514						7	3	5	9	18	5	0	3	2	2	2		
ENSMUST00000114515	ENSMUSG00000052139	5	31697684	32084962	1	0	0	0	0	0	0	198	384	256	183	25	D3Z7P0	
ENSMUST00000114516	ENSMUSG00000064061	16	48924232	48994165	-1	5	0	0	0	4	0	21	17	17	4	0		Q7TPV2
ENSMUST00000114517	ENSMUSG00000079566	X	73175302	73176989	-1	41	37	160	95	51	30	0	0	0	0	0	B1B0R2	
ENSMUST00000114518	ENSMUSG00000072479	X	73148796	73158872	1	2	2	12	0	3	9	0	0	0	0	0	A2BI50	
ENSMUST00000114520	ENSMUSG00000058328	X	73107635	73292976	-1	0	4	0	10	4	0	0	0	0	0	0	A2BI45	
ENSMUST00000114521	ENSMUSG00000058328	X	73107635	73292976	-1	16	0	0	0	0	0	0	0	2	0	1	A2BI46	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114523	ENSMUSG00000026781	2	23068168	23114510	1	0	0	0	0	6	0	3	481	88	183	0		Q5XG73
ENSMUST00000114524	ENSMUSG00000057836	X	73086293	73097095	-1	0	0	0	0	0	0	0	0	0	0	0	Q78PE0	Q60595
ENSMUST00000114526	ENSMUSG00000026781	2	23068168	23114510	1	0	6	7	91	7	0	95	275	169	123	81		Q5XG73
ENSMUST00000114528	ENSMUSG00000031362	X	73233688	73243130	-1	0	0	0	0	0	0	0	0	8	5	0	L7MUB7	
ENSMUST00000114529	ENSMUSG00000026781	2	23068168	23114510	1	13	5	5	0	5	0	184	48	326	32	175	E9QNH7	
ENSMUST00000114530	ENSMUSG00000031362	X	73233688	73243130	-1	2	0	3	4	0	1	0	37	4	11	0	Q3TKR2	
ENSMUST00000114531	ENSMUSG00000031362	X	73233688	73243130	-1	0	0	0	0	0	0	7	30	0	0	7	Q3TKR2	
ENSMUST00000114533	ENSMUSG00000029141	5	31526995	31556932	1	0	0	0	0	0	0	104	360	271	108	187	E9Q585	
ENSMUST00000114534	ENSMUSG00000079845	X	73074345	73082478	-1	0	0	1	0	0	1	0	3	2	0	1	A2BI42	
ENSMUST00000114537	ENSMUSG00000018417	1	51749765	51916071	-1	0	0	0	0	0	5	0	0	0	0	56	E9QNH6	
ENSMUST00000114540	ENSMUSG00000050424	X	73033981	73037103	-1	0	0	18	0	0	0	0	0	0	0	0		Q5DTT8
ENSMUST00000114541	ENSMUSG00000018417	1	51749765	51916071	-1	14	13	17	3	16	0	0	0	0	0	0	E9Q580	
ENSMUST00000114544	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	15	0	0	0	1109	2805	1287	467	715		Q8CBW3
ENSMUST00000114545	ENSMUSG00000073096	6	48554796	48570722	1	24	24	33	369	33	36	313	325	252	41	206		
ENSMUST00000114546	ENSMUSG00000031351	X	72987339	73031543	1	10	10	29	0	0	3	0	0	0	1	1	A2BI37	
ENSMUST00000114547	ENSMUSG00000032076	9	47530173	47857637	1	27	20	58	0	11	6	0	4	5	10	2		Q8R5M8
ENSMUST00000114548	ENSMUSG00000032076	9	47530173	47857637	1	0	0	0	46	20	0	0	0	0	0	0		Q8R5M8
ENSMUST00000114549	ENSMUSG00000024034	17	31179272	31198975	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TZ06	Q8K1T0
ENSMUST00000114550	ENSMUSG00000031347	X	72913532	72918411	-1	0	0	0	0	0	0	0	0	0	0	0	Z4YJH1	
ENSMUST00000114551	ENSMUSG00000031347	X	72913532	72918411	-1	1	0	1	10	0	6	72	125	101	470	91		Q9R1K9
ENSMUST00000114552	ENSMUSG00000032078	9	46273064	46282643	1	0	0	6	0	0	0	112	278	76	80	107	F8WHU9	
ENSMUST00000114553	ENSMUSG00000031344	X	72825178	72842602	1	51	28	403	73	43	13	1	0	1	0	1	B1AUQ5	
ENSMUST00000114554	ENSMUSG00000031343	X	72432681	72656848	-1	0	3	0	4	0	0	0	0	0	0	0	B1AVY2	
ENSMUST00000114555	ENSMUSG00000054134	17	30954679	31010708	1	20	0	0	0	0	0	0	0	0	0	0		Q5DID3
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ENSMUST00000114558	ENSMUSG00000068551	6	48427697	48445825	-1	0	9	0	0	0	3	10	62	11	7	0	G3X9X3	
ENSMUST00000114559	ENSMUSG00000068551	6	48427697	48445825	-1	0	0	0	0	0	3	0	0	0	0	0	G3X9X3	
ENSMUST00000114560	ENSMUSG00000068551	6	48427697	48445825	-1	16	17	75	229	18	23	0	169	0	0	10	B2RU53	Q8JZL0
ENSMUST00000114561	ENSMUSG00000068551	6	48427697	48445825	-1	38	5	57	159	20	9	65	94	55	0	58	B2RU53	Q8JZL0
ENSMUST00000114562	ENSMUSG00000033177	16	45656315	45693658	-1	9	10	18	0	20	6	0	0	0	0	0		Q8BIK6
ENSMUST00000114563	ENSMUSG00000068551	6	48427697	48445825	-1	1	4	18	2	2	0	6	8	0	5	3	D3Z7M0	
ENSMUST00000114564	ENSMUSG00000068551	6	48427697	48445825	-1	0	1	0	0	0	0	1	5	0	3	1	D3Z7L9	
ENSMUST00000114565	ENSMUSG00000026109	1	50900647	51187270	1	73	83	146	143	75	51	1	3	0	1	3		
ENSMUST00000114566	ENSMUSG00000068551	6	48427697	48445825	-1	3	2	2	10	2	0	13	6	12	2	3	Q3USQ2	
ENSMUST00000114569	ENSMUSG00000053593	X	71972986	71989046	1	0	1	0	8	0	1	0	0	0	0	0		Q8CEK7
ENSMUST00000114570						1	1	2	5	4	2	11	34	18	0	23		
ENSMUST00000114571	ENSMUSG00000042810	6	48395586	48419781	1	0	0	30	37	0	5	0	0	0	0	0	D3Z4B8	
ENSMUST00000114572	ENSMUSG00000042810	6	48395586	48419781	1	0	0	0	50	18	0	5	0	3	0	5		Q6NXZ1
ENSMUST00000114573	ENSMUSG00000034908	9	45937857	45955247	-1	20	17	64	0	0	0	7348	7424	6334	404	5562		Q8CIF6
ENSMUST00000114574	ENSMUSG00000024027	17	30901867	30936510	1	13	8	39	66	22	9	0	0	0	0	0		O35659
ENSMUST00000114575	ENSMUSG00000073131	X	71815924	71839757	1	0	2	0	34	0	4	0	0	0	0	0	F2Z447	
ENSMUST00000114576	ENSMUSG00000073131	X	71815924	71839757	1	0	0	0	13	0	0	61	68	32	84	33		Q78T54
ENSMUST00000114577	ENSMUSG00000073131	X	71815924	71839757	1	12	12	6	60	18	11	0	0	0	8	0	F2Z446	
ENSMUST00000114578	ENSMUSG00000061619	4	52496939	52497244	-1	3	0	0	1	1	1	0	0	0	0	0		
ENSMUST00000114579						79	41	338	58	39	22	0	3	0	0	2		
ENSMUST00000114582	ENSMUSG00000015217	X	71555918	71560676	1	0	0	0	79	11	0	0	0	0	0	26	Q544R9	O54879
ENSMUST00000114583	ENSMUSG00000071477	6	48024188	48048911	-1	21	16	74	18	0	0	123	212	97	18	120	B9EKF4	
ENSMUST00000114585	ENSMUSG00000053182	16	45411768	45492969	-1	1	2	3	0	2	0	0	0	0	0	0	E9Q573	
ENSMUST00000114586	ENSMUSG00000035776	X	71420060	71492849	-1	13	5	17	11	15	10	0	0	0	0	0	I7HJQ8	
ENSMUST00000114587	ENSMUSG00000035776	X	71420060	71492849	-1	0	0	2	36	0	0	3	0	3	0	3	A2AP74	
ENSMUST00000114588						206	197	172	196	265	125	4	1	12	0	38		
ENSMUST00000114590	ENSMUSG00000043059	5	31198981	31202303	-1	0	0	6	146	13	0	119	296	108	39	200		Q6PD29
ENSMUST00000114594	ENSMUSG00000036591	2	20847919	20968881	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQE8	
ENSMUST00000114598	ENSMUSG00000062519	6	47835661	47873537	1	22	23	56	111	33	10	28	10	32	4	56	E9Q569	
ENSMUST00000114600	ENSMUSG00000022664	16	45139573	45158706	-1	0	0	0	0	0	0	63	127	76	70	73	D3Z784	
ENSMUST00000114601	ENSMUSG00000015214	X	71364760	71419196	1	1	1	0	0	0	1	0	0	0	0	0	I7HJQ9	
ENSMUST00000114603	ENSMUSG00000029145	5	31187558	31193430	-1	5	3	16	196	24	11	44	18	58	19	19		Q61749
ENSMUST00000114604	ENSMUSG00000036617	2	19909780	20810713	1	0	0	0	0	0	0	0	0	0	0	0	D3Z781	
ENSMUST00000114605						0	0	0	0	0	0	119	161	64	9	0		
ENSMUST00000114606	ENSMUSG00000036617	2	19909780	20810713	1	8	10	22	7	12	5	0	7	0	0	3		A2AQ25
ENSMUST00000114607	ENSMUSG00000036617	2	19909780	20810713	1	0	0	3	0	0	0	0	0	0	0	5		A2AQ25
ENSMUST00000114608	ENSMUSG00000036617	2	19909780	20810713	1	5	16	28	7	26	6	7	11	21	0	7		A2AQ25
ENSMUST00000114610	ENSMUSG00000036617	2	19909780	20810713	1	8	5	8	58	20	5	0	0	0	0	0	Q8BHR1	
ENSMUST00000114611	ENSMUSG00000036172	16	44943678	44981380	1	0	0	0	0	0	0	0	0	8	4	21		Q5UKY4
ENSMUST00000114612	ENSMUSG00000036172	16	44943678	44981380	1	0	0	0	0	0	0	0	0	0	10	0		Q5UKY4
ENSMUST00000114613	ENSMUSG00000036172	16	44943678	44981380	1	0	0	0	0	0	0	4	9	0	0	0		Q5UKY4
ENSMUST00000114614	ENSMUSG00000036617	2	19909780	20810713	1	7	3	0	77	12	2	0	0	0	0	0		A2AQ25
ENSMUST00000114616	ENSMUSG00000029687	6	47530139	47595341	-1	0	0	0	22	4	5	61	160	0	1	55	D3Z774	
ENSMUST00000114617	ENSMUSG00000031337	X	71210767	71315691	1	0	0	0	4	0	0	0	0	47	0	33		Q9Z2C5
ENSMUST00000114618	ENSMUSG00000029687	6	47530139	47595341	-1	3	0	0	0	0	0	14	35	12	22	0	Q6AXH7	
ENSMUST00000114621	ENSMUSG00000031337	X	71210767	71315691	1	0	0	0	0	0	0	0	0	0	2	0	B1AW21	
ENSMUST00000114622	ENSMUSG00000036172	16	44943678	44981380	1	0	0	0	0	0	0	2	9	5	0	0		Q5UKY4
ENSMUST00000114626	ENSMUSG00000062082	16	44811733	44839150	1	0	0	0	4	0	0	23	180	32	39	0		Q6XJV4
ENSMUST00000114627	ENSMUSG00000036617	2	19909780	20810713	1	3	0	0	0	0	0	0	0	0	0	0	E9QAU4	
ENSMUST00000114629	ENSMUSG00000059401	X	71050256	71156056	1	9	8	90	44	16	0	0	0	0	0	0	D3Z768	
ENSMUST00000114630	ENSMUSG00000073139	X	70459753	70477180	-1	0	0	0	26	0	0	0	0	26	0	0		A2AF53
ENSMUST00000114631						2	4	4	1	3	1	0	0	0	0	0		
ENSMUST00000114632						0	0	0	0	0	0	0	0	0	10	0		
ENSMUST00000114634	ENSMUSG00000022687	16	44485045	44558897	-1	0	0	0	244	1	0	0	0	0	0	0	D3Z763	
ENSMUST00000114637						17	0	0	11	9	0	0	0	0	0	0		
ENSMUST00000114640	ENSMUSG00000037683	2	19199302	19310241	1	0	11	0	0	20	0	0	0	0	0	0		A2AU72
ENSMUST00000114641	ENSMUSG00000039419	6	45060061	47304213	1	34	27	31	31	46	21	0	0	0	0	0	E9QNF7	
ENSMUST00000114643						0	2	1	7	4	3	0	0	1	0	0		
ENSMUST00000114644	ENSMUSG00000029735	6	43345001	43666278	-1	10	11	6	0	9	0	0	9	0	0	13		Q9R0M5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114646						19	5	26	13	13	4	0	0	4	0	0		
ENSMUST00000114647	ENSMUSG00000062170	X	68761839	68804567	1	3	1	7	2	0	2	0	0	0	0	0	B7ZW84	
ENSMUST00000114653	ENSMUSG00000000838	X	68678541	68717963	1	0	2	0	0	0	1	136	210	25	47	113	E9QAT0	
ENSMUST00000114654	ENSMUSG00000000838	X	68678541	68717963	1	0	1	0	0	0	1	0	0	0	0	0	E9QAS9	
ENSMUST00000114655	ENSMUSG00000000838	X	68678541	68717963	1	0	0	0	0	0	0	0	0	0	0	8	E9QAS8	
ENSMUST00000114656	ENSMUSG00000000838	X	68678541	68717963	1	0	0	0	0	0	0	0	0	0	0	0	D3Z6U8	
ENSMUST00000114657	ENSMUSG00000000838	X	68678541	68717963	1	0	0	0	0	4	0	137	210	135	38	88	E9QNF5	
ENSMUST00000114659						1	1	2	6	1	0	0	9	0	3	13		
ENSMUST00000114660						0	5	0	0	0	1	0	105	19	23	0		
ENSMUST00000114663	ENSMUSG00000070305	9	45055186	45077436	1	1	0	0	0	0	2	15	16	23	20	39	A0A0A0MQE9	
ENSMUST00000114664	ENSMUSG00000070305	9	45055186	45077436	1	14	16	41	26	21	9	998	3460	1019	250	693		Q3V3F6
ENSMUST00000114665						34	15	23	18	38	16	0	0	0	0	0		
ENSMUST00000114666	ENSMUSG00000052459	16	44085402	44139705	-1	17	8	3	19	15	8	1098	2086	919	431	599		P50516
ENSMUST00000114668	ENSMUSG00000006641	5	31036036	31048924	-1	8	0	0	66	15	14	0	17	0	0	0		Q5U4D8
ENSMUST00000114669	ENSMUSG00000026743	2	18055237	18212388	1	6	3	22	0	12	14	0	362	262	118	138	A2AS72	
ENSMUST00000114671	ENSMUSG00000026743	2	18055237	18212388	1	0	0	0	40	12	0	214	256	173	34	70	A2AS70	
ENSMUST00000114672	ENSMUSG00000079577	X	67695698	67706350	1	0	1	0	1	1	0	0	0	0	0	0	A2BH01	
ENSMUST00000114674	ENSMUSG00000041607	18	82475146	82585637	1	0	0	0	0	0	0	0	0	0	0	0		P04370
ENSMUST00000114675	ENSMUSG00000079578	X	67682900	67693562	-1	0	1	0	1	1	0	0	0	0	0	0	A2BH01	
ENSMUST00000114676	ENSMUSG00000041607	18	82475146	82585637	1	14	11	10	54	7	1	33	84	49	12	32	D3Z6U4	
ENSMUST00000114677	ENSMUSG00000036292	16	43980350	44027945	-1	0	13	0	12	16	0	0	0	0	0	0		Q8CI52
ENSMUST00000114679	ENSMUSG00000046699	X	64264885	64276996	-1	0	0	0	0	0	0	0	0	0	0	0	Q149A4	Q810B8
ENSMUST00000114680	ENSMUSG00000026743	2	18055237	18212388	1	0	0	0	0	0	0	36	0	381	0	153		O54826
ENSMUST00000114682	ENSMUSG00000079579	X	64151405	64152198	-1	3	1	3	1	2	0	0	0	0	0	0	Q0ZNK3	
ENSMUST00000114683	ENSMUSG00000079580	17	29526033	29549593	-1	2	0	3	0	0	3	0	1	0	0	0	Q14AF1	
ENSMUST00000114684						14	14	19	16	18	13	2	6	2	1	12		
ENSMUST00000114687	ENSMUSG00000079583	X	60436052	60539249	-1	0	0	0	0	0	0	0	0	0	0	0	E9QAS1	
ENSMUST00000114689	ENSMUSG00000002028	9	44803355	44881296	-1	14	9	37	85	127	10	0	26	30	5	593		P55200
ENSMUST00000114690	ENSMUSG00000022708	16	42875881	43642602	1	0	0	0	33	0	0	0	0	0	0	6		Q8K0L9
ENSMUST00000114691	ENSMUSG00000022708	16	42875881	43642602	1	3	3	8	0	4	0	0	0	0	0	0		Q8K0L9
ENSMUST00000114694	ENSMUSG00000022708	16	42875881	43642602	1	215	230	1098	350	206	119	55	118	144	18	229		Q8K0L9
ENSMUST00000114695	ENSMUSG00000022708	16	42875881	43642602	1	0	0	0	0	0	0	0	0	8	0	0		Q8K0L9
ENSMUST00000114696						4	3	4	0	0	0	22	8	0	0	19		
ENSMUST00000114699	ENSMUSG00000024011	17	29318877	29329413	1	0	0	0	0	0	0	911	526	535	140	397	D3Z6T6	
ENSMUST00000114700	ENSMUSG00000029165	5	30888694	30906965	1	0	0	0	0	0	0	0	0	0	0	0		Q09M02
ENSMUST00000114701	ENSMUSG00000024011	17	29318877	29329413	1	6	10	22	6	21	5	5614	6979	4837	877	3154	E9QNE5	
ENSMUST00000114702	ENSMUSG00000026748	2	16356304	16755839	1	0	0	0	0	0	0	2	9	5	19	59	B1AY85	
ENSMUST00000114703	ENSMUSG00000026748	2	16356304	16755839	1	0	0	13	0	0	0	0	0	0	0	49	B1AY86	
ENSMUST00000114704						0	0	16	2	0	0	0	0	0	0	6		
ENSMUST00000114705	ENSMUSG00000002032	9	44793776	44799307	-1	34	0	0	68	27	11	0	7	0	0	3		Q9DCF1
ENSMUST00000114706	ENSMUSG00000022790	16	38901471	39027159	1	3	2	0	1	2	0	0	0	0	0	0	D3Z6S7	
ENSMUST00000114708	ENSMUSG00000022793	16	38742264	38769049	1	0	0	0	0	0	0	3	0	0	0	1	A6X8Z8	
ENSMUST00000114709	ENSMUSG00000041684	1	44118957	44144770	1	3	0	11	0	0	6	0	0	0	0	19		Q8CBX9
ENSMUST00000114710	ENSMUSG00000022793	16	38742264	38769049	1	0	2	0	1	3	6	0	0	0	0	0	A6X8Z8	
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ENSMUST00000114712	ENSMUSG00000022793	16	38742264	38769049	1	0	0	0	94	12	0	0	0	0	0	0		Q9JJ04
ENSMUST00000114713	ENSMUSG00000026707	2	14995131	15055069	-1	4	3	2	0	6	0	0	5	1	3	1	Q8BXZ8	
ENSMUST00000114715	ENSMUSG00000026707	2	14995131	15055069	-1	0	0	0	0	0	0	9	34	10	38	10	A2ASK1	
ENSMUST00000114716	ENSMUSG00000038828	5	30868012	30879180	1	0	0	0	0	0	0	284	128	211	15	143	D3Z6S1	
ENSMUST00000114718						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000114719	ENSMUSG00000057914	2	14603088	14987908	1	3	0	1	2	12	4	0	0	0	0	0		Q8CC27
ENSMUST00000114723	ENSMUSG00000057914	2	14603088	14987908	1	8	0	0	5	0	10	2	3	0	1	0	Q32MF3	Q8CC27
ENSMUST00000114724						0	0	0	0	0	0	37	114	21	3	47		
ENSMUST00000114725	ENSMUSG00000079584	X	57409154	57488767	1	2	3	4	1	3	4	0	0	2	0	0	A2AFI6	
ENSMUST00000114726	ENSMUSG00000031134	X	57383530	57393036	-1	0	0	0	0	0	0	123	196	89	75	127		Q9WV02
ENSMUST00000114729	ENSMUSG00000029168	5	30711564	30799375	1	0	15	71	147	31	10	0	0	0	0	0		Q9EQF6
ENSMUST00000114730	ENSMUSG00000031134	X	57383530	57393036	-1	0	0	0	0	0	0	31	177	128	0	3		Q9WV02
ENSMUST00000114731	ENSMUSG00000036949	2	14388316	14494977	1	11	6	5	5	8	1	0	0	0	2	0		Q5FWH7
ENSMUST00000114732	ENSMUSG00000029869	6	41605482	41620509	1	32	17	38	122	28	19	6	8	2	2	20		O08644
ENSMUST00000114735	ENSMUSG00000031133	X	57231485	57338729	-1	0	4	0	1	4	2	10	0	52	0	0	A2AFJ8	
ENSMUST00000114737	ENSMUSG00000043286	17	28858411	28890308	1	77	56	105	82	109	56	150	247	225	16	108	B2KF06	Q3V1D5
ENSMUST00000114739	ENSMUSG00000022803	16	38362209	38378216	1	11	0	4	0	0	0	1	12	1	3	3		Q9ES82
ENSMUST00000114740	ENSMUSG00000022805	16	38297754	38342143	-1	482	500	634	403	523	230	7	53	34	4	37		Q8BRC6
ENSMUST00000114741	ENSMUSG00000025429	18	77794545	77882007	1	8	6	8	175	17	9	440	1403	1062	95	693		Q99M15
ENSMUST00000114743	ENSMUSG00000029182	5	30466047	30484088	1	2	0	8	3	0	4	0	0	0	0	0	D3Z6F6	
ENSMUST00000114744	ENSMUSG00000066877	1	43444579	43570515	1	0	0	1	0	0	0	0	0	2	0	0	A0A0A0MQF0	
ENSMUST00000114745	ENSMUSG00000031131	X	57088106	57106540	1	5	2	0	0	0	0	0	0	0	0	0		Q99NC0
ENSMUST00000114746	ENSMUSG00000031131	X	57088106	57106540	1	0	0	7	5	7	4	0	0	0	0	0		Q99NC0
ENSMUST00000114747	ENSMUSG00000062372	5	30367062	30461932	-1	0	0	1	0	60	27	0	0	1	3	0		
ENSMUST00000114748	ENSMUSG00000025428	18	77773729	77782869	1	3	3	32	371	17	6	11	45	20	20	135	D3Z6F5	
ENSMUST00000114750	ENSMUSG00000022812	16	38089001	38246084	1	0	0	0	0	0	0	230	332	427	41	304	E9QAQ5	
ENSMUST00000114751	ENSMUSG00000067873	X	57053583	57067183	1	23	32	68	48	27	8	16	42	7	15	24		Q8BGC0
ENSMUST00000114752	ENSMUSG00000053436	17	28691342	28748404	1	21	20	60	3	18	14	4208	8203	4913	453	3571		P47811
ENSMUST00000114753	ENSMUSG00000063275	2	13850282	14056135	-1	5	2	0	0	4	0	0	0	0	0	0	B9EHK9	
ENSMUST00000114754	ENSMUSG00000053436	17	28691342	28748404	1	0	0	0	0	0	0	91	261	145	16	83		P47811
ENSMUST00000114758	ENSMUSG00000053436	17	28691342	28748404	1	2	1	30	91	8	2	58	86	160	10	295	B2KF35	
ENSMUST00000114761	ENSMUSG00000041907	1	42952872	43035456	1	8	2	0	1	4	4	0	0	0	0	0	Q148B5	Q9EQQ4
ENSMUST00000114763	ENSMUSG00000022816	16	37776873	37836514	1	25	10	26	62	13	9	2	2	1	19	21		Q62356
ENSMUST00000114764	ENSMUSG00000036196	17	28637783	28689987	-1	18	9	74	63	14	8	6	24	8	1	7		Q8R0C3
ENSMUST00000114765	ENSMUSG00000079588	1	40805601	40856887	1	18	11	42	10	15	6	0	0	0	0	0		B2RVY9
ENSMUST00000114766	ENSMUSG00000067878	X	56797858	56822326	-1	5	8	14	0	4	0	1	14	0	4	5		A2AEY4
ENSMUST00000114767	ENSMUSG00000004865	17	28587648	28622521	-1	1	1	4	19	3	0	4	3	4	5	9	B2KF32	
ENSMUST00000114768	ENSMUSG00000023092	X	56731787	56793346	1	0	0	0	0	0	1	0	0	0	0	0	A2AEX7	
ENSMUST00000114769	ENSMUSG00000023092	X	56731787	56793346	1	128	68	564	265	80	49	11	28	18	0	41	A2AEY2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114772	ENSMUSG00000023092	X	56731787	56793346	1	1	1	0	0	0	0	0	0	0	29	0	A2AEX8	
ENSMUST00000114773	ENSMUSG00000023092	X	56731787	56793346	1	2	1	2	0	0	0	0	0	0	0	0	A2AEX6	
ENSMUST00000114774						21	19	42	24	38	14	2	3	0	0	0		
ENSMUST00000114775	ENSMUSG00000022829	16	37114942	37384962	-1	0	0	0	0	0	0	0	0	0	0	0		Q5DQR4
ENSMUST00000114776	ENSMUSG00000025423	18	77065208	77155708	1	2	2	0	28	3	2	56	120	119	0	58	F8WHS8	
ENSMUST00000114777	ENSMUSG00000025423	18	77065208	77155708	1	0	20	0	19	15	0	91	408	154	57	129		Q8C5D8
ENSMUST00000114779	ENSMUSG00000029911	6	40471352	40484700	1	3	2	3	24	5	1	4	10	0	0	2	Q8R2K3	
ENSMUST00000114780	ENSMUSG00000022829	16	37114942	37384962	-1	0	0	0	30	5	2	0	0	0	0	0		Q5DQR4
ENSMUST00000114781	ENSMUSG00000022829	16	37114942	37384962	-1	0	0	0	0	0	0	0	0	0	0	0		Q5DQR4
ENSMUST00000114782	ENSMUSG00000022829	16	37114942	37384962	-1	12	0	0	4	2	0	0	0	0	0	0		Q5DQR4
ENSMUST00000114783	ENSMUSG00000059447	5	30155248	30184593	1	6	6	9	20	5	3	0	184	0	66	0		Q99JY0
ENSMUST00000114784	ENSMUSG00000060681	X	56609757	56664230	1	0	0	33	0	0	4	242	707	415	93	227	B0QZV3	
ENSMUST00000114785	ENSMUSG00000024225	17	28558210	28560766	-1	0	2	0	0	0	0	0	0	0	0	0	B2KF29	
ENSMUST00000114786	ENSMUSG00000059447	5	30155248	30184593	1	10	0	13	33	13	0	45	160	213	460	70		Q99JY0
ENSMUST00000114787	ENSMUSG00000022829	16	37114942	37384962	-1	0	6	3	0	6	5	0	0	0	0	0		Q5DQR4
ENSMUST00000114791	ENSMUSG00000026727	2	13076821	13271415	-1	0	0	0	0	0	0	76	63	91	104	16	A2AUR7	
ENSMUST00000114792	ENSMUSG00000024222	17	28399095	28517524	-1	0	0	0	0	20	13	21	1	2	122	59	Q4FJN2	Q64378
ENSMUST00000114794	ENSMUSG00000037446	17	28351515	28365182	-1	11	6	11	9	10	6	0	0	0	0	0	Q8K0Y6	
ENSMUST00000114795	ENSMUSG00000026072	1	40225080	40317257	1	0	0	4	42	3	3	16	24	11	24	13	Q8C833	
ENSMUST00000114796	ENSMUSG00000026730	2	12924041	13003455	1	0	0	0	0	0	0	0	0	3	0	0	A2AUR5	
ENSMUST00000114797	ENSMUSG00000029918	6	39801804	39810988	-1	0	3	0	0	0	0	99	275	53	290	48	Q8R2K5	
ENSMUST00000114799	ENSMUSG00000002249	17	28331671	28350805	-1	0	0	0	2	0	0	0	0	0	2	0	F8VPU0	
ENSMUST00000114801	ENSMUSG00000007570	17	28313530	28326568	1	0	0	0	0	0	0	19	20	12	5	16	B8JJD5	
ENSMUST00000114803	ENSMUSG00000007570	17	28313530	28326568	1	0	0	8	218	0	0	0	0	0	2	0	B8JJD3	
ENSMUST00000114804	ENSMUSG00000007570	17	28313530	28326568	1	0	5	0	0	0	0	37	0	17	0	0	Q8R3Z2	
ENSMUST00000114806	ENSMUSG00000047746	16	36963460	36990467	-1	5	6	0	3	0	0	0	0	0	0	0	Q3KN92	P62932
ENSMUST00000114810	ENSMUSG00000054626	X	53777118	53797706	-1	0	0	0	2	0	0	0	13	0	8	1	Q544L6	P05531
ENSMUST00000114812	ENSMUSG00000034243	16	36875140	36933085	1	63	30	57	88	82	0	157	367	1071	0	1039	E9QAH1	
ENSMUST00000114815	ENSMUSG00000079592	9	44107245	44109187	1	0	0	0	0	0	0	1	0	0	2	0	Q4ZJN4	Q8K479
ENSMUST00000114816	ENSMUSG00000079592	9	44107245	44109187	1	0	0	1	0	0	0	0	0	0	0	0	Q4ZJN4	Q8K479
ENSMUST00000114818	ENSMUSG00000079592	9	44107245	44109187	1	0	0	0	0	0	0	0	7	0	0	0	Q4ZJN4	Q8K479
ENSMUST00000114819	ENSMUSG00000022837	16	36828385	36872721	1	5	4	0	3	0	0	0	10	0	3	0		Q8BP00
ENSMUST00000114821	ENSMUSG00000079592	9	44107245	44109187	1	0	2	0	13	0	0	0	0	1	0	1	F8WHS3	Q8K479
ENSMUST00000114822	ENSMUSG00000029922	6	39397804	39420462	-1	0	2	7	62	16	0	273	796	269	537	211	Q8C5B6	Q9QXP6
ENSMUST00000114823	ENSMUSG00000029922	6	39397804	39420462	-1	10	12	16	87	17	0	27	183	63	0	24	E9QAG7	
ENSMUST00000114825	ENSMUSG00000022838	16	36792884	36875003	-1	0	0	0	0	0	1	0	0	0	1	0		Q91ZD6
ENSMUST00000114829	ENSMUSG00000022838	16	36792884	36875003	-1	2	1	9	119	4	0	0	3	0	5	0		Q91ZD6
ENSMUST00000114830	ENSMUSG00000032010	9	44067021	44095627	1	4	0	0	0	0	4	0	0	0	0	0		O88623
ENSMUST00000114831	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	0	0	0	0	0	3		Q60819
ENSMUST00000114832	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	0	0	0	0	4	5		Q60819
ENSMUST00000114833	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	0	8	30	0	0	9		Q60819
ENSMUST00000114834	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	0	0	0	0	0	0		Q60819
ENSMUST00000114835	ENSMUSG00000036013	X	53273424	53331185	1	1	1	0	3	4	0	0	0	0	0	0	Q9D5J5	
ENSMUST00000114836	ENSMUSG00000062859	17	28066747	28080639	-1	10	0	11	0	0	0	43	2	0	0	22	Q5FWA2	
ENSMUST00000114838	ENSMUSG00000036022	X	53243415	53269805	-1	0	0	4	0	0	0	15	62	7	7	2	G1UD78	Q6NZE7
ENSMUST00000114839	ENSMUSG00000029131	5	29735688	29818134	1	0	0	0	0	4	8	351	1388	356	697	190		O54946
ENSMUST00000114840	ENSMUSG00000032011	9	44043384	44048579	1	8	8	20	26	17	9	185	160	81	56	181		P01831
ENSMUST00000114841	ENSMUSG00000036022	X	53243415	53269805	-1	0	7	0	1	0	3	13	11	0	0	0		Q6NZE7
ENSMUST00000114842	ENSMUSG00000024219	17	27909340	28062600	1	0	0	0	218	0	0	1449	679	1456	24	970		P59672
ENSMUST00000114843	ENSMUSG00000061082	X	53069995	53240111	-1	0	2	0	1	4	2	0	0	0	0	0		Q9JI83
ENSMUST00000114844	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	45	0	0	3	6	20	0	15	A2AUP4	
ENSMUST00000114845	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	0	0	0	0	0	Q7TS91	
ENSMUST00000114846	ENSMUSG00000026773	2	11471433	11554077	-1	0	17	0	0	0	20	1963	1532	3055	273	1973	A2AUP1	
ENSMUST00000114847	ENSMUSG00000051980	16	36493696	36562141	-1	6	21	19	37	1	3	0	0	0	0	0		Q9QY96
ENSMUST00000114848	ENSMUSG00000024218	17	27901122	27909242	-1	2	4	7	124	22	4	22	77	35	22	29		Q99JX1
ENSMUST00000114849	ENSMUSG00000039512	17	27856490	27900040	1	67	46	181	314	113	45	44	81	73	10	130	B2KF50	
ENSMUST00000114850	ENSMUSG00000079594	16	36321665	36334332	-1	3	6	5	11	0	5	5691	21770	12064	56729	6488	L7N257	
ENSMUST00000114851	ENSMUSG00000079595	16	36308045	36312653	1	0	0	0	0	0	0	1	2	0	4	0	L7N258	
ENSMUST00000114853						1251	1121	1389	948	1112	482	82	305	167	83	255		
ENSMUST00000114855						6	11	66	5	8	12	27	64	38	13	23		
ENSMUST00000114857	ENSMUSG00000055653	X	52272426	52613950	-1	0	8	3	104	8	3	11	5	36	6	5	B1ATR5	
ENSMUST00000114858	ENSMUSG00000079597	16	36184212	36188111	1	3	11	29	45	8	7	20860	54130	35604	99207	17097	B2RV77	
ENSMUST00000114859	ENSMUSG00000056692	17	27751232	27820558	-1	23	15	40	67	42	0	745	685	341	93	338	B2KF54	
ENSMUST00000114861	ENSMUSG00000061186	2	10370510	10595253	1	0	8	4	3	0	0	0	0	0	0	0	Q8BG70	
ENSMUST00000114862	ENSMUSG00000061186	2	10370510	10595253	1	8	0	0	0	4	0	0	0	0	0	0	Q8BG70	
ENSMUST00000114863	ENSMUSG00000056692	17	27751232	27820558	-1	0	6	38	0	0	17	1566	2221	2124	165	1407		Q3TT38
ENSMUST00000114864	ENSMUSG00000061186	2	10370510	10595253	1	3	0	0	0	0	1	0	0	0	0	0	Q8BG70	
ENSMUST00000114865	ENSMUSG00000032017	9	42518135	42944493	-1	127	92	470	566	132	73	0	3	4	0	2		Q8BMF5
ENSMUST00000114866	ENSMUSG00000031118	X	51968695	51972772	-1	4	5	3	7	3	5	0	0	0	0	0	Q9D9G4	
ENSMUST00000114869	ENSMUSG00000055780	X	51753959	51801233	-1	0	0	1	0	1	0	0	0	0	0	0		Q99MX1
ENSMUST00000114870	ENSMUSG00000024215	17	27714352	27728951	-1	0	12	19	0	0	0	0	0	0	0	0		Q9WTP3
ENSMUST00000114871	ENSMUSG00000062184	X	51387212	51681856	-1	0	0	0	38	7	0	0	0	0	0	0		Q80UW0
ENSMUST00000114872	ENSMUSG00000040276	17	27655509	27711106	1	4	0	8	0	0	1	3	4	4	0	8	Q543Y7	Q61644
ENSMUST00000114873	ENSMUSG00000040276	17	27655509	27711106	1	0	0	0	140	14	9	0	0	0	0	0	Q543Y7	Q61644
ENSMUST00000114874	ENSMUSG00000079598	6	38663069	38680864	1	11	8	16	15	7	1	0	0	0	0	0		P0C7M9
ENSMUST00000114875	ENSMUSG00000036109	X	51117269	51206532	-1	1	0	10	16	7	0	40	31	55	6	43	Q3TJQ3	
ENSMUST00000114876	ENSMUSG00000036109	X	51117269	51206532	-1	0	0	1	55	2	1	17	0	27	0	11	Q542D8	Q8R003
ENSMUST00000114877	ENSMUSG00000022906	16	35938470	35972605	1	3	3	0	1	0	0	0	20	27	0	14		Q8CAS9
ENSMUST00000114878	ENSMUSG00000022906	16	35938470	35972605	1	14	18	22	91	20	17	85	152	186	153	247		Q8CAS9
ENSMUST00000114881	ENSMUSG00000052146	17	27630422	27636629	-1	5	0	0	0	0	0	20	13	0	27	0	Q5M9K7	P63325
ENSMUST00000114882	ENSMUSG00000052146	17	27630422	27636629	-1	3	17	0	40	10	3	3531	3930	2231	7578	1297	Q5M9K7	P63325
ENSMUST00000114884	ENSMUSG00000048271	5	28317121	28419239	1	55	40	92	0	20	0	135	1195	936	0	738	D3Z5I9	
ENSMUST00000114885	ENSMUSG00000049502	16	35926511	35939151	-1	26	23	29	68	31	8	10	44	73	5	95		Q3UIR3
ENSMUST00000114886	ENSMUSG00000024213	17	27579382	27623465	-1	0	0	0	23	0	0	19	0	40	0	1	B2KF67	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000114887	ENSMUSG00000031112	X	50841047	50893097	1	0	0	0	0	0	0	264	224	0	0	0	A2AD84	
ENSMUST00000114888	ENSMUSG00000046711	17	27556620	27563674	1	0	0	0	0	0	0	172	148	84	48	206	Q3TVP0	P17095
ENSMUST00000114890	ENSMUSG00000079600	X	165003765	165004829	-1	300	147	158	3444	410	277	2	6	2	0	2	E9QAD7	
ENSMUST00000114891	ENSMUSG00000031111	X	49782536	49797749	-1	5	3	2	0	8	2	0	0	0	0	0		Q7TQA1
ENSMUST00000114893	ENSMUSG00000031111	X	49782536	49797749	-1	3	5	2	0	0	0	0	0	0	0	0		Q7TQA1
ENSMUST00000114894	ENSMUSG00000026085	1	37946736	37957759	-1	3	1	2	0	4	1	0	0	0	0	0	Q0VE18	Q9D7Q0
ENSMUST00000114895	ENSMUSG00000035394	18	74283090	74359986	1	8	7	7	12	8	3	0	0	0	0	1		Q9D439
ENSMUST00000114896	ENSMUSG00000025781	2	10056016	10080510	-1	10	0	2	65	4	12	0	0	15	0	0	Q8C2Q8	
ENSMUST00000114897	ENSMUSG00000025781	2	10056016	10080510	-1	0	0	0	43	0	3	727	2738	901	1849	526	Q3UD06	Q91VR2
ENSMUST00000114898	ENSMUSG00000029826	6	38305286	38354603	-1	9	9	9	252	0	0	0	1043	116	0	73	G3X9X5	
ENSMUST00000114900	ENSMUSG00000029826	6	38305286	38354603	-1	56	49	97	43	84	14	927	4132	1644	145	970	D3Z5I1	
ENSMUST00000114902	ENSMUSG00000060771	1	37754776	37866429	-1	0	3	0	0	0	0	0	24	9	26	4		Q6NY15
ENSMUST00000114904	ENSMUSG00000036198	X	49463945	49500244	1	7	0	5	46	10	3	0	0	0	0	0		B1AUC7
ENSMUST00000114906	ENSMUSG00000025782	2	9914552	10048596	-1	2	1	2	0	0	0	1	0	9	3	0	A2ASX8	
ENSMUST00000114907	ENSMUSG00000025782	2	9914552	10048596	-1	2	3	5	9	7	0	0	0	0	0	0	A2ASX9	
ENSMUST00000114908	ENSMUSG00000038600	6	38048483	38124586	-1	13	0	16	11	17	5	0	0	0	0	0		Q920R6
ENSMUST00000114909	ENSMUSG00000025782	2	9914552	10048596	-1	50	60	199	43	42	25	32	10	8	1	35	A2ASY0	
ENSMUST00000114911	ENSMUSG00000031109	X	49009707	49288259	-1	1	2	7	0	0	2	7	88	57	60	44		Q8R0Z2
ENSMUST00000114912	ENSMUSG00000031109	X	49009707	49288259	-1	0	0	0	0	0	0	0	75	27	12	11		Q8R0Z2
ENSMUST00000114913	ENSMUSG00000022840	16	35154877	35305737	1	34	17	60	636	64	33	1	3	1	2	5		P84309
ENSMUST00000114914	ENSMUSG00000031109	X	49009707	49288259	-1	0	9	0	5	5	0	0	0	0	0	0		Q8R0Z2
ENSMUST00000114915	ENSMUSG00000079602	2	9883041	9889540	-1	3	0	3	3	1	0	0	0	0	6	0	A2ASX7	
ENSMUST00000114918	ENSMUSG00000031109	X	49009707	49288259	-1	0	0	0	0	0	0	37	1	23	50	39		Q8R0Z2
ENSMUST00000114919	ENSMUSG00000025783	2	9881252	9883921	1	0	3	1	0	3	0	0	0	0	0	0	A2ASX5	
ENSMUST00000114922						0	0	0	0	1	1	1	0	0	7	0		
ENSMUST00000114923	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	0	0	0	0	5	A3KGT0	
ENSMUST00000114924	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	1	18	0	0	0	0	0		Q9Z0H4
ENSMUST00000114925	ENSMUSG00000026111	1	37430139	37439124	1	0	3	7	7	2	3	248	787	200	280	126		Q9CQ61
ENSMUST00000114927	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	0	0	732	74	399		Q9Z0H4
ENSMUST00000114928	ENSMUSG00000079606	X	48841466	48877713	-1	4	1	6	4	3	0	0	0	0	0	0	A2AF73	
ENSMUST00000114933	ENSMUSG00000026113	1	37299865	37410736	1	0	0	3	0	8	0	30	0	158	0	10	E9QAD0	
ENSMUST00000114934	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	1109	2108	1195	225	957		Q9Z0H4
ENSMUST00000114935	ENSMUSG00000024194	17	26937973	26939478	-1	4	5	12	5	0	4	354	367	105	110	63	D5MCW4	
ENSMUST00000114936	ENSMUSG00000031105	X	48623413	48662294	1	0	0	0	0	0	0	0	0	0	1	0		Q9Z2B2
ENSMUST00000114937	ENSMUSG00000039046	2	6322667	6446390	1	41	36	172	84	67	46	71	220	190	31	221		Q80XC3
ENSMUST00000114939	ENSMUSG00000024515	18	73639009	73703780	-1	5	2	17	0	5	1	101	82	528	36	234		P97471
ENSMUST00000114940	ENSMUSG00000036916	X	48541625	48594504	-1	0	4	23	0	0	7	0	0	0	0	0		Q6P3Y5
ENSMUST00000114941						7	5	17	31	10	5	3	0	8	0	5		
ENSMUST00000114942	ENSMUSG00000045319	2	6097607	6130211	-1	13	15	13	52	16	8	2	3	0	0	6		Q8C5R2
ENSMUST00000114943	ENSMUSG00000060534	18	71258738	72351069	-1	24	13	51	0	0	11	0	0	0	0	0		P70211
ENSMUST00000114945	ENSMUSG00000036932	X	48474944	48513563	-1	0	0	6	0	10	0	0	0	0	0	0	B1AU25	
ENSMUST00000114946	ENSMUSG00000024513	18	70568189	70626131	1	9	14	48	24	10	9	0	6	3	1	3		Q9Z2E1
ENSMUST00000114947	ENSMUSG00000061751	16	33974258	34573532	-1	5	6	5	3	0	0	0	0	0	0	0	D3Z560	
ENSMUST00000114949	ENSMUSG00000061751	16	33974258	34573532	-1	7	18	5	5	19	10	0	0	0	0	0	D3Z559	
ENSMUST00000114950	ENSMUSG00000038072	5	25221904	25265918	1	0	0	12	0	0	0	0	0	0	0	40		Q921L8
ENSMUST00000114952	ENSMUSG00000038072	5	25221904	25265918	1	36	37	15	49	35	26	63	202	69	21	0		Q921L8
ENSMUST00000114953	ENSMUSG00000061751	16	33974258	34573532	-1	0	0	0	5	0	0	0	0	0	0	0		A2CG49
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ENSMUST00000114956	ENSMUSG00000049281	9	40269216	40291618	1	46	41	101	108	24	27	0	0	0	0	0	Q0P666	Q8BHK2
ENSMUST00000114958	ENSMUSG00000031103	X	48411046	48463132	-1	0	0	0	99	21	17	176	201	723	50	627		Q9Z2U4
ENSMUST00000114959	ENSMUSG00000079608	18	70472454	70501066	1	3	1	2	28	0	3	0	4	0	2	0	Q9CPT8	P59096
ENSMUST00000114960	ENSMUSG00000061751	16	33974258	34573532	-1	0	18	29	0	0	0	0	0	0	0	0		A2CG49
ENSMUST00000114961	ENSMUSG00000061751	16	33974258	34573532	-1	18	0	42	84	24	5	0	0	0	0	0	A0A0A0MQF1	
ENSMUST00000114963	ENSMUSG00000061751	16	33974258	34573532	-1	11	0	14	12	14	4	0	0	0	0	0	D3Z535	
ENSMUST00000114964	ENSMUSG00000061751	16	33974258	34573532	-1	0	0	0	27	0	0	1	10	4	1	9	D3Z534	
ENSMUST00000114965	ENSMUSG00000028938	5	25181460	25220297	1	0	3	3	8	0	5	0	0	0	0	0	D3Z533	
ENSMUST00000114966	ENSMUSG00000061751	16	33974258	34573532	-1	14	23	26	131	25	20	0	0	0	0	0	D3Z532	
ENSMUST00000114972	ENSMUSG00000036959	X	48341358	48408049	1	19	8	7	2	19	0	101	12	183	5	100	F8WJL9	
ENSMUST00000114973	ENSMUSG00000061751	16	33974258	34573532	-1	33	25	80	35	27	20	0	0	0	0	0	D3Z4R2	
ENSMUST00000114975	ENSMUSG00000028944	5	24862744	25100642	-1	0	0	0	0	0	0	71	393	41	5	0	Q3TMN8	Q91WG5
ENSMUST00000114976	ENSMUSG00000024188	17	26252910	26285504	1	38	42	96	46	29	18	117	490	212	40	229		Q9CYI4
ENSMUST00000114977	ENSMUSG00000053477	18	69343356	69689079	1	0	0	0	0	0	0	0	5	0	16	7	Q91YV0	
ENSMUST00000114978	ENSMUSG00000053477	18	69343356	69689079	1	4	7	2	1	8	3	19	19	48	4	86	Q91XK1	Q60722
ENSMUST00000114980	ENSMUSG00000053477	18	69343356	69689079	1	0	0	0	6	0	0	7	0	25	0	23		Q60722
ENSMUST00000114981	ENSMUSG00000046337	1	36562692	36683183	-1	8	5	43	109	14	7	1	0	2	0	0	E9PUL8	
ENSMUST00000114982	ENSMUSG00000053477	18	69343356	69689079	1	0	0	0	0	0	0	9	0	1	0	0		Q60722
ENSMUST00000114985	ENSMUSG00000053477	18	69343356	69689079	1	0	0	0	0	0	0	0	69	22	0	49		Q60722
ENSMUST00000114987	ENSMUSG00000039145	2	5293457	5714515	-1	0	2	5	12	5	1	24	0	76	0	75		Q8BW96
ENSMUST00000114988	ENSMUSG00000024187	17	26211822	26244223	-1	20	21	34	47	30	7	253	169	233	13	219		Q8C0Z1
ENSMUST00000114989	ENSMUSG00000038784	6	35022065	35133724	-1	0	10	40	0	12	13	10	234	102	80	62	E9QA19	
ENSMUST00000114991	ENSMUSG00000026121	1	36548639	36558349	-1	0	0	0	135	0	21	0	0	0	0	13		Q64151
ENSMUST00000114993	ENSMUSG00000038784	6	35022065	35133724	-1	14	0	17	43	0	0	120	320	129	57	109		
ENSMUST00000114996	ENSMUSG00000026672	2	5020642	5064051	-1	13	6	13	8	9	7	232	379	357	111	200		Q8K3K8
ENSMUST00000114997	ENSMUSG00000029848	6	34920163	34939344	1	0	0	0	11	3	0	0	0	0	0	0	F2Z435	
ENSMUST00000114998	ENSMUSG00000037005	X	48108725	48136981	1	342	312	910	259	426	181	1	31	15	11	18	Q8BU59	
ENSMUST00000114999	ENSMUSG00000029848	6	34920163	34939344	1	0	0	0	3	0	7	0	0	0	0	0		P70278
ENSMUST00000115000	ENSMUSG00000037005	X	48108725	48136981	1	0	1	0	0	7	0	1	6	0	2	2	B1AVD2	
ENSMUST00000115004	ENSMUSG00000063350	9	37746136	37747068	1	3	1	3	10	2	3	0	0	0	0	0	Q7TRE6	
ENSMUST00000115006	ENSMUSG00000046806	6	34871771	34878060	-1	0	0	0	4	0	2	11	0	11	0	0		Q8BHZ5
ENSMUST00000115007	ENSMUSG00000046806	6	34871771	34878060	-1	0	2	0	28	8	0	13	201	99	19	74		Q8BHZ5
ENSMUST00000115009	ENSMUSG00000038836	6	34780432	34859459	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4P1	
ENSMUST00000115010	ENSMUSG00000026668	2	4976122	4985748	1	0	0	0	0	0	0	0	0	0	0	0		Q14BU0
ENSMUST00000115011	ENSMUSG00000001143	1	36419871	36445271	-1	0	0	3	0	0	0	41	0	61	0	93	D3Z4P2	
ENSMUST00000115012	ENSMUSG00000038836	6	34780432	34859459	1	0	1	2	0	2	0	1	0	0	0	0	D3Z4P1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000115013	ENSMUSG00000001173	X	47912387	47965868	1	8	6	5	2	10	11	20	96	28	18	0	Q7TPR1	
ENSMUST00000115014	ENSMUSG00000038836	6	34780432	34859459	1	0	0	0	0	0	0	2	5	6	6	1		Q8CDP0
ENSMUST00000115016	ENSMUSG00000038836	6	34780432	34859459	1	0	0	4	0	0	0	0	0	0	0	0		Q8CDP0
ENSMUST00000115017	ENSMUSG00000038836	6	34780432	34859459	1	0	0	0	16	0	2	4	0	4	0	0		Q8CDP0
ENSMUST00000115019	ENSMUSG00000026662	2	4881564	4910557	1	0	0	0	14	3	0	129	187	162	114	100		Q8BH69
ENSMUST00000115020	ENSMUSG00000001173	X	47912387	47965868	1	0	0	0	0	0	0	0	0	7	0	7		Q6NVF0
ENSMUST00000115021	ENSMUSG00000029761	6	34598500	34775473	1	0	9	5	14	13	7	1	1	4	41	39	Q8VCQ8	
ENSMUST00000115022	ENSMUSG00000048186	2	4717831	4802142	1	4	0	0	68	6	0	0	0	0	0	0	A2AMN2	
ENSMUST00000115026	ENSMUSG00000029761	6	34598500	34775473	1	0	0	0	0	0	0	0	0	0	0	0	E9QA16	
ENSMUST00000115027	ENSMUSG00000029761	6	34598500	34775473	1	0	0	0	0	0	0	0	0	0	0	0	E9QA15	
ENSMUST00000115028	ENSMUSG00000022817	16	33829665	33949153	1	16	0	27	187	30	0	235	249	128	73	326	Q6PE70	
ENSMUST00000115029	ENSMUSG00000037447	1	36307733	36324029	1	28	0	0	18	8	0	39	172	0	17	1		Q3U108
ENSMUST00000115031	ENSMUSG00000037447	1	36307733	36324029	1	0	0	0	0	0	0	63	0	97	0	78		Q3U108
ENSMUST00000115032	ENSMUSG00000037447	1	36307733	36324029	1	0	0	0	0	0	0	1610	2571	1458	116	1638		Q3U108
ENSMUST00000115033	ENSMUSG00000028958	5	24445458	24447854	-1	8	4	12	80	4	4	44	31	18	0	0		Q9JMG3
ENSMUST00000115036	ENSMUSG00000028958	5	24445458	24447854	-1	0	5	0	6	4	0	41	72	24	6	30	E9QN77	
ENSMUST00000115037	ENSMUSG00000026657	2	4017717	4614043	1	0	0	1	1	0	0	0	0	0	0	0	F7CDA2	
ENSMUST00000115038	ENSMUSG00000032128	9	37415669	37433163	-1	12	0	11	129	9	0	0	0	0	0	0	D3Z4M6	
ENSMUST00000115039						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000115041	ENSMUSG00000028959	5	24438440	24445287	-1	0	0	0	0	0	0	0	0	0	0	0	E9QA06	
ENSMUST00000115043	ENSMUSG00000028959	5	24438440	24445287	-1	3	3	13	0	0	0	27	116	46	8	81	D3Z4M5	
ENSMUST00000115044	ENSMUSG00000022824	16	33794037	33819934	1	0	0	0	51	0	0	15	0	62	0	0	Q3V1S6	P19467
ENSMUST00000115046	ENSMUSG00000032125	9	37401897	37414023	1	30	14	29	31	33	17	0	0	0	0	0	D3Z4M4	
ENSMUST00000115047	ENSMUSG00000028962	5	24423837	24440950	1	14	16	58	36	21	6	0	0	12	0	12		
ENSMUST00000115048	ENSMUSG00000032125	9	37401897	37414023	1	5	0	30	10	9	0	0	4	0	0	0	E9QN68	
ENSMUST00000115049	ENSMUSG00000028962	5	24423837	24440950	1	15	0	0	7	8	0	725	778	419	85	306		
ENSMUST00000115050	ENSMUSG00000024533	18	67488209	67552777	-1	0	0	0	0	6	0	4	9	6	7	5	D3Z495	
ENSMUST00000115051	ENSMUSG00000061758	6	34384218	34396950	1	4	0	0	0	0	0	0	19	1	32	17	D3Z494	
ENSMUST00000115052	ENSMUSG00000026655	2	3613758	3782142	1	5	0	4	3	0	4	0	11	0	0	0	H9H9T1	
ENSMUST00000115053	ENSMUSG00000026655	2	3613758	3782142	1	0	0	5	40	7	0	0	0	6	6	7		Q3TGF2
ENSMUST00000115054	ENSMUSG00000026655	2	3613758	3782142	1	0	2	0	0	0	0	0	0	0	0	0		Q3TGF2
ENSMUST00000115055	ENSMUSG00000026655	2	3613758	3782142	1	0	0	2	4	3	0	68	0	136	44	102		Q3TGF2
ENSMUST00000115056	ENSMUSG00000045284	X	44786570	44790197	-1	3	6	12	0	12	3	0	1	0	0	0		Q8CBW4
ENSMUST00000115057	ENSMUSG00000050926	X	44365458	44368342	-1	44	41	51	306	65	42	0	2	1	0	0		Q8BGW4
ENSMUST00000115058	ENSMUSG00000016150	X	42527866	43429126	-1	37	21	23	17	25	11	0	0	0	0	0	A2ANL9	
ENSMUST00000115059	ENSMUSG00000016150	X	42527866	43429126	-1	2	1	1	1	1	1	0	0	0	0	0	A2ANM0	Q9WTS4
ENSMUST00000115066	ENSMUSG00000026648	2	3424131	3464130	1	2	0	0	0	0	0	27	102	38	18	37		Q8K4J0
ENSMUST00000115068	ENSMUSG00000032122	9	37229149	37255738	-1	20	16	36	88	38	19	84	316	109	36	124		Q9WU81
ENSMUST00000115070	ENSMUSG00000005696	X	42502453	42529330	1	0	0	0	0	0	0	0	0	4	0	0		O88890
ENSMUST00000115071	ENSMUSG00000037529	1	34543968	34560943	-1	8	9	17	43	4	6	0	0	0	0	0	E9Q9Y0	
ENSMUST00000115072	ENSMUSG00000025862	X	42149317	42277185	1	0	0	0	0	0	0	0	0	0	0	0		O35638
ENSMUST00000115073	ENSMUSG00000025862	X	42149317	42277185	1	32	35	126	32	35	29	209	1774	557	511	373	A2AFF6	
ENSMUST00000115074						7	11	22	0	7	1	0	0	0	3	9		
ENSMUST00000115075	ENSMUSG00000060636	16	33056453	33060189	1	0	2	0	0	0	0	0	0	6	3	0	Q6ZWX1	O55142
ENSMUST00000115076	ENSMUSG00000060636	16	33056453	33060189	1	0	0	0	0	0	0	3	14	0	0	0	Q6ZWX1	O55142
ENSMUST00000115077	ENSMUSG00000028973	5	24393663	24410054	1	0	0	0	20	12	5	22	0	0	0	0		Q9CXJ4
ENSMUST00000115078	ENSMUSG00000060636	16	33056453	33060189	1	0	0	0	0	0	0	3	24	3	32	6	Q6ZWX1	O55142
ENSMUST00000115079	ENSMUSG00000060636	16	33056453	33060189	1	4	3	6	17	8	0	83	211	93	459	54	Q6ZWX1	O55142
ENSMUST00000115080	ENSMUSG00000029763	6	33249085	33973979	1	3	3	2	3	1	1	0	0	0	3	0	Q8C391	
ENSMUST00000115081	ENSMUSG00000026650	2	3409043	3422648	-1	0	0	0	0	3	0	3	8	3	8	0		Q61845
ENSMUST00000115082	ENSMUSG00000026650	2	3409043	3422648	-1	0	5	0	18	0	0	3	11	0	3	0		Q61845
ENSMUST00000115083	ENSMUSG00000026650	2	3409043	3422648	-1	3	5	6	9	3	0	0	0	0	0	0		Q61845
ENSMUST00000115084	ENSMUSG00000026650	2	3409043	3422648	-1	3	0	0	0	0	3	0	4	0	0	0		Q61845
ENSMUST00000115086	ENSMUSG00000062762	9	36779159	36797361	-1	6	7	15	0	4	0	398	833	382	71	190		
ENSMUST00000115087	ENSMUSG00000026645	2	3341982	3397210	-1	0	0	0	0	2	0	0	1	0	1	0		Q8R197
ENSMUST00000115089	ENSMUSG00000026644	2	3336168	3340993	1	5	2	2	3	4	0	0	0	0	0	0		Q9D258
ENSMUST00000115090	ENSMUSG00000028978	5	24364810	24384474	1	17	18	43	78	3	23	0	0	0	0	3	E9Q9X4	
ENSMUST00000115091	ENSMUSG00000053768	6	32790976	33060260	-1	4	0	4	0	2	0	13	12	6	13	9	Q9D9P1	
ENSMUST00000115094	ENSMUSG00000025860	X	42059679	42109656	1	16	0	1	2	11	0	181	472	781	188	537		Q60989
ENSMUST00000115095	ENSMUSG00000025860	X	42059679	42109656	1	0	10	17	69	7	4	24	200	411	0	187		Q60989
ENSMUST00000115096	ENSMUSG00000029765	6	32144268	32588192	-1	96	51	231	335	135	38	3	4	7	11	42		Q80UG2
ENSMUST00000115097	ENSMUSG00000046610	18	65698268	65751601	1	17	18	19	0	44	28	0	0	0	0	0	Q8BML2	
ENSMUST00000115098	ENSMUSG00000038319	5	24319589	24351604	-1	11	9	18	122	26	8	2	0	0	0	0		
ENSMUST00000115099	ENSMUSG00000050530	2	3114224	3227806	1	0	0	0	0	0	0	0	0	0	0	12	A2ATK9	
ENSMUST00000115100	ENSMUSG00000035578	16	33015385	33056218	-1	79	56	487	122	65	27	1	7	3	3	2		Q80W32
ENSMUST00000115101	ENSMUSG00000048439	5	24164963	24184013	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000115103	ENSMUSG00000001986	X	41400854	41678601	1	0	0	0	5	0	0	0	5	0	2	0	B0QZW1	
ENSMUST00000115104	ENSMUSG00000026131	1	33908225	34308661	1	0	0	0	0	0	33	0	0	0	0	4	E9Q9X1	
ENSMUST00000115105	ENSMUSG00000035629	16	32821703	32877766	-1	0	0	40	60	17	0	0	0	0	2	44		Q80U62
ENSMUST00000115108	ENSMUSG00000025739	17	25717171	25719406	1	2	0	0	1	0	4	0	0	0	0	0		Q9JMF3
ENSMUST00000115109	ENSMUSG00000028995	5	23915276	24030690	-1	7	0	21	2	8	0	12	2	40	0	33	D3Z481	
ENSMUST00000115110	ENSMUSG00000050555	9	35560820	35570398	-1	10	8	32	145	17	2	22	126	51	159	47		
ENSMUST00000115113	ENSMUSG00000028999	5	23787711	23820369	1	0	2	0	4	2	14	0	0	0	31	0		Q8BZ36
ENSMUST00000115114	ENSMUSG00000079619	X	39346267	39346963	1	0	2	3	0	1	2	0	0	0	0	0	B1AXS0	
ENSMUST00000115116	ENSMUSG00000035638	16	32777419	32797435	-1	22	7	37	21	21	16	0	0	0	0	0	E9PUF1	
ENSMUST00000115118	ENSMUSG00000031095	X	38533274	38576196	-1	0	0	9	17	2	5	1	90	43	104	82		A2A432
ENSMUST00000115119						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000115120	ENSMUSG00000022791	16	32643874	32683493	1	4	0	42	83	17	0	0	96	1	9	25	D3Z3U7	
ENSMUST00000115121	ENSMUSG00000022791	16	32643874	32683493	1	0	0	0	0	0	0	0	0	0	0	0	E9QN61	
ENSMUST00000115122	ENSMUSG00000022791	16	32643874	32683493	1	1	0	1	0	2	0	0	0	0	0	0	E9QN60	
ENSMUST00000115123	ENSMUSG00000022791	16	32643874	32683493	1	0	0	0	0	0	0	66	129	142	9	117	D3Z3U6	
ENSMUST00000115124	ENSMUSG00000022791	16	32643874	32683493	1	0	0	38	0	0	27	31	6	53	0	0	G3X9X7	
ENSMUST00000115125	ENSMUSG00000022791	16	32643874	32683493	1	19	23	8	382	15	0	205	1	72	0	155		
ENSMUST00000115126	ENSMUSG00000022791	16	32643874	32683493	1	0	0	0	0	0	0	0	84	0	0	0	D3Z3U5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000115127	ENSMUSG00000051855	6	30723547	30748465	1	0	0	0	0	1	0	0	0	0	0	0	D3Z3U2	
ENSMUST00000115128	ENSMUSG00000029004	5	23434441	23504235	1	44	0	132	206	51	23	487	501	970	0	810		Q3UG20
ENSMUST00000115130	ENSMUSG00000029790	6	30653457	30693749	-1	2	0	4	2	1	1	1	0	2	2	0		Q99NF3
ENSMUST00000115131	ENSMUSG00000029790	6	30653457	30693749	-1	0	1	6	5	12	0	0	0	0	9	9	H9KUZ8	
ENSMUST00000115134	ENSMUSG00000016327	X	38316184	38336769	1	7	5	15	6	9	2	1	0	4	1	4	B1APX1	Q99ME6
ENSMUST00000115137	ENSMUSG00000005615	16	32430921	32475070	1	14	15	0	68	0	11	0	0	37	76	14	D3Z3T5	
ENSMUST00000115138	ENSMUSG00000029788	6	30611010	30631745	1	7	4	9	0	1	0	0	0	0	0	0	D3Z3T4	
ENSMUST00000115139	ENSMUSG00000029788	6	30611010	30631745	1	7	3	13	16	19	0	0	0	0	0	0	B2RQW9	Q8R4H4
ENSMUST00000115140	ENSMUSG00000005615	16	32430921	32475070	1	4	0	20	33	13	3	0	0	0	0	9		P49586
ENSMUST00000115142	ENSMUSG00000048047	X	38189793	38197046	1	3	2	0	0	0	0	12	57	73	0	42	A2A3Z3	Q8BN78
ENSMUST00000115145	ENSMUSG00000045991	18	64340364	64398488	1	58	62	412	245	61	29	1	2	0	1	0		Q6XBJ3
ENSMUST00000115146	ENSMUSG00000071766	X	38104077	38110907	-1	0	0	0	0	0	0	0	0	0	0	0	Q4TU81	
ENSMUST00000115148	ENSMUSG00000032036	9	34485894	35036716	1	0	0	0	0	0	0	0	0	0	4	0		Q8BR86
ENSMUST00000115149	ENSMUSG00000079625	16	32400506	32408227	1	6	6	30	14	9	1	0	0	4	1	6	E9Q9H8	
ENSMUST00000115150	ENSMUSG00000053909	X	38066475	38071691	1	3	2	8	4	3	5	0	0	0	0	0	Q4TU83	
ENSMUST00000115151	ENSMUSG00000053774	16	32332252	32393747	1	49	52	123	103	54	31	547	1546	908	224	855	G5E8R8	
ENSMUST00000115154	ENSMUSG00000035521	17	25233331	25240124	-1	0	0	19	0	0	0	27	259	0	19	22		
ENSMUST00000115156	ENSMUSG00000079626	X	37886439	37897232	-1	2	3	3	7	2	1	0	0	0	0	0	A6PW38	
ENSMUST00000115157	ENSMUSG00000029782	6	30479053	30509783	-1	0	0	0	0	0	0	0	22	3	94	0		Q8BRG8
ENSMUST00000115160	ENSMUSG00000029782	6	30479053	30509783	-1	48	42	83	49	47	17	56	204	67	43	62		Q8BRG8
ENSMUST00000115161	ENSMUSG00000042182	1	33852052	33907816	-1	0	3	0	6	6	0	0	0	4	25	7		Q6PFX2
ENSMUST00000115162	ENSMUSG00000079627	X	37668989	37673277	-1	4	2	0	1	0	2	0	0	0	0	0	K7N6P1	
ENSMUST00000115163	ENSMUSG00000052384	16	32142785	32165594	-1	1	89	234	0	3	62	588	2470	835	60	1345		Q8BMT4
ENSMUST00000115165	ENSMUSG00000052384	16	32142785	32165594	-1	0	0	0	0	0	0	2016	3770	1249	229	891		Q8BMT4
ENSMUST00000115166	ENSMUSG00000079628	X	37646500	37651327	-1	3	2	3	3	0	0	0	0	0	0	0	Q2MDF7	
ENSMUST00000115167	ENSMUSG00000042197	1	33761545	33814595	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q9H6	
ENSMUST00000115168	ENSMUSG00000035790	16	32099800	32108069	1	0	8	18	80	13	8	709	2852	1630	1337	599		Q9CQA8
ENSMUST00000115169	ENSMUSG00000079629	X	37639115	37643470	-1	2	1	1	0	19	0	0	0	0	0	0	L7MUB9	
ENSMUST00000115170	ENSMUSG00000079630	X	37602894	37607704	-1	0	0	6	1	6	0	0	0	0	0	0	Q2MDF8	
ENSMUST00000115172	ENSMUSG00000095510	X	37580992	37585496	1	0	0	0	0	1	0	0	0	0	0	0	A2ANE1	
ENSMUST00000115173	ENSMUSG00000095741	X	37571405	37576163	1	3	2	0	0	2	1	0	0	0	0	0	A2ANE0	
ENSMUST00000115174	ENSMUSG00000004768	1	33719887	33742564	1	11	15	17	39	19	10	0	106	0	0	20	Q9D4I9	
ENSMUST00000115175	ENSMUSG00000079633	X	37514359	37519176	1	0	3	7	1	0	0	0	0	0	0	0	Q2MDG0	
ENSMUST00000115176	ENSMUSG00000029015	5	21810655	21865604	-1	17	5	17	0	0	0	0	0	0	0	0	Q32MT6	
ENSMUST00000115178	ENSMUSG00000022774	16	31948513	31961781	1	0	0	0	25	0	1	17	20	14	121	10	D3Z3D2	
ENSMUST00000115179	ENSMUSG00000095698	X	37493428	37497623	1	0	2	4	0	3	2	0	0	0	0	0	W4VSN9	
ENSMUST00000115181	ENSMUSG00000024170	17	25099570	25115967	-1	0	0	0	0	0	0	12	0	0	0	13		Q9DC40
ENSMUST00000115183	ENSMUSG00000079635	X	37480337	37485124	1	0	1	0	0	0	0	0	0	0	0	0	Q2MDG1	
ENSMUST00000115184	ENSMUSG00000039130	6	30366380	30391028	-1	3	0	3	5	6	2	0	8	0	0	0	D3Z3D0	
ENSMUST00000115188	ENSMUSG00000079636	X	37458585	37473964	1	2	0	0	0	0	0	0	0	0	0	0	A2AWM0	
ENSMUST00000115189	ENSMUSG00000079636	X	37458585	37473964	1	0	0	0	0	4	0	0	0	0	0	0	A2AWM0	
ENSMUST00000115190	ENSMUSG00000079637	X	37453680	37469861	1	0	0	0	0	0	0	0	0	0	0	0	A2AWL9	
ENSMUST00000115191	ENSMUSG00000079638	X	37412067	37416806	1	5	0	0	0	2	0	0	0	0	0	0	A2A447	
ENSMUST00000115192	ENSMUSG00000029014	5	21757267	21785251	-1	2	0	7	24	3	3	0	4	2	0	2	Q3TRX6	
ENSMUST00000115193	ENSMUSG00000029014	5	21757267	21785251	-1	4	0	6	4	6	0	0	6	7	5	6	E9Q9H3	
ENSMUST00000115194	ENSMUSG00000079639	X	37265338	37270132	1	0	0	0	0	0	0	0	0	0	0	0	Q9D3I8	
ENSMUST00000115195	ENSMUSG00000029014	5	21757267	21785251	-1	0	0	0	69	8	0	66	414	68	160	109	E9Q9H2	
ENSMUST00000115196	ENSMUSG00000022770	16	31663443	31873356	1	8	4	4	1	5	7	32	16	46	6	37	D3Z3B8	
ENSMUST00000115198	ENSMUSG00000059626	X	37542019	37551082	1	0	0	10	6	7	7	0	0	0	0	0	Q4TU90	
ENSMUST00000115199	ENSMUSG00000058440	6	30047988	30153458	1	1	2	15	0	0	0	0	0	0	0	0	Q3UXF4	
ENSMUST00000115200	ENSMUSG00000058440	6	30047988	30153458	1	12	23	95	19	19	5	3	17	12	3	22	E9Q7X0	
ENSMUST00000115201	ENSMUSG00000022770	16	31663443	31873356	1	0	0	0	78	0	0	0	0	23	0	0	E9Q9H0	
ENSMUST00000115203	ENSMUSG00000071772	X	37249919	37258983	1	0	14	0	6	0	0	0	0	0	0	0	Q4TU90	
ENSMUST00000115204	ENSMUSG00000058440	6	30047988	30153458	1	0	3	9	6	4	0	0	0	6	0	7	G3XA39	
ENSMUST00000115205	ENSMUSG00000022770	16	31663443	31873356	1	10	18	24	8	13	10	28	673	79	19	77		Q811D0
ENSMUST00000115206	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	0	29	0	59	20	0	Q99K73	
ENSMUST00000115208	ENSMUSG00000058440	6	30047988	30153458	1	0	0	1	0	0	1	4	11	13	0	29	D3Z3B4	
ENSMUST00000115209	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	0	54	0	0	0	0		Q9WU00
ENSMUST00000115210	ENSMUSG00000071773	X	37213804	37222258	-1	2	2	2	6	7	3	0	0	0	0	0	B1APN4	
ENSMUST00000115211	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	7	314	702	360	94	289		Q9WU00
ENSMUST00000115212	ENSMUSG00000058440	6	30047988	30153458	1	21	9	43	22	20	0	113	211	65	14	33		Q9WU00
ENSMUST00000115217	ENSMUSG00000044968	5	21662901	21701396	-1	85	84	85	83	84	17	0	0	0	0	12		Q8BH82
ENSMUST00000115222	ENSMUSG00000047412	9	31030644	31075879	1	71	96	162	200	105	42	218	826	385	90	318		Q8R0A2
ENSMUST00000115224	ENSMUSG00000039629	6	29917012	29959681	1	24	28	57	52	33	7	6	3	9	1	3	E9QN41	
ENSMUST00000115226	ENSMUSG00000046598	16	31422280	31458901	1	9	1	12	107	18	2	3	0	0	0	0		Q80XN0
ENSMUST00000115227	ENSMUSG00000046598	16	31422280	31458901	1	67	48	171	76	31	22	17	75	33	6	25		Q80XN0
ENSMUST00000115228	ENSMUSG00000024163	17	24892153	24936977	-1	10	0	0	0	0	0	308	343	353	0	481		Q9ESN9
ENSMUST00000115229	ENSMUSG00000024163	17	24892153	24936977	-1	0	0	0	0	1	0	0	0	0	0	0	K3W4S4	
ENSMUST00000115230	ENSMUSG00000022548	16	31296192	31314808	-1	0	0	0	0	0	0	0	0	0	0	0		P51910
ENSMUST00000115231	ENSMUSG00000079641	X	37082520	37085402	-1	2	3	3	9	9	2	2258	5015	1796	7812	704	Q505A8	P62892
ENSMUST00000115233	ENSMUSG00000047714	16	31251537	31275277	-1	0	2	0	0	0	1	679	2491	1206	186	744	D3Z3A0	
ENSMUST00000115234	ENSMUSG00000048520	5	21483847	21645634	-1	0	0	1	0	0	0	0	0	0	0	0	D3Z399	
ENSMUST00000115236	ENSMUSG00000059974	9	28994750	29963141	-1	0	0	3	2	1	0	0	0	0	0	0	D3Z396	
ENSMUST00000115237	ENSMUSG00000059974	9	28994750	29963141	-1	8	0	19	56	12	4	0	0	0	0	0		Q99PJ0
ENSMUST00000115238	ENSMUSG00000029772	6	29768011	29912310	1	12	20	54	0	36	8	2	0	0	0	0		Q68FL4
ENSMUST00000115239	ENSMUSG00000050379	X	36911326	36991794	-1	0	0	0	22	2	0	108	69	170	188	160		Q9R1T4
ENSMUST00000115242	ENSMUSG00000029772	6	29768011	29912310	1	0	0	5	0	0	0	0	120	282	23	0		Q68FL4
ENSMUST00000115243	ENSMUSG00000062257	9	27790775	28925410	1	22	30	21	24	29	19	0	0	0	0	0	Q6DFY2	
ENSMUST00000115244	ENSMUSG00000026141	1	24261890	24587472	-1	0	0	2	45	11	1	0	0	0	0	0		Q0VF58
ENSMUST00000115245	ENSMUSG00000064280	5	21292961	21424677	-1	15	8	17	14	18	6	6	55	18	31	64	E9Q9F7	
ENSMUST00000115246	ENSMUSG00000024576	18	61555274	61590061	1	0	0	0	173	0	0	0	0	32	0	0	H7BXB1	
ENSMUST00000115247	ENSMUSG00000034275	9	27299228	27334763	1	13	16	102	21	16	8	0	0	0	0	0	D3Z169	
ENSMUST00000115248	ENSMUSG00000006423	X	36823737	36874111	-1	45	3	63	206	8	0	211	647	284	170	205		Q8VDP2
ENSMUST00000115249	ENSMUSG00000006423	X	36823737	36874111	-1	0	3	0	2	3	0	0	0	0	0	0	Z4YLD0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000115250	ENSMUSG00000001763	6	29694222	29718559	1	11	0	17	0	0	1	6	2	2	1	6		Q8R3S2
ENSMUST00000115251	ENSMUSG00000012535	6	29540827	29609887	-1	15	0	0	0	0	0	3	741	7	0	0		Q6P2B1
ENSMUST00000115253	ENSMUSG00000079642	X	36403477	36404655	1	2	0	0	0	0	0	0	0	0	0	0	A2A3U9	
ENSMUST00000115256	ENSMUSG00000036699	X	36195904	36199158	1	3	5	0	3	10	5	0	0	0	0	0		Q9CZA5
ENSMUST00000115257	ENSMUSG00000036699	X	36195904	36199158	1	0	0	0	0	0	0	0	14	3	2	9		Q9CZA5
ENSMUST00000115258	ENSMUSG00000036699	X	36195904	36199158	1	9	0	7	6	10	2	0	0	0	0	0		Q9CZA5
ENSMUST00000115259	ENSMUSG00000045435	5	20882191	20886870	1	8	7	10	43	7	4	49	135	39	112	24		Q8K174
ENSMUST00000115261	ENSMUSG00000079644	9	26879567	26923081	-1	12	13	4	20	15	5	0	0	0	0	0	Q0Q237	
ENSMUST00000115262	ENSMUSG00000075705	17	24736642	24742778	1	9	0	6	22	15	12	16632	25923	10513	16490	8559		Q9JLC3
ENSMUST00000115264	ENSMUSG00000031093	X	35888832	36076562	1	2	0	1	0	0	1	50	1076	0	52	0	A2AF65	
ENSMUST00000115266	ENSMUSG00000031093	X	35888832	36076562	1	0	9	0	2	0	0	382	2039	348	95	82	A2AF67	
ENSMUST00000115267	ENSMUSG00000040003	5	19227036	20704792	1	0	0	0	0	0	0	0	0	0	0	0		Q9WVQ1
ENSMUST00000115268	ENSMUSG00000024621	18	61105572	61132149	1	13	14	44	14	19	7	58	287	95	53	182	Q0P635	P09581
ENSMUST00000115269	ENSMUSG00000045994	9	26733728	26763101	1	9	10	9	6	13	0	0	0	0	0	0	Q8R531	
ENSMUST00000115271						6	3	26	0	6	3	0	0	0	0	0		
ENSMUST00000115272	ENSMUSG00000001833	9	25252439	25308571	1	3	2	0	10	2	0	0	0	0	0	0	E9Q9F5	
ENSMUST00000115273	ENSMUSG00000041670	1	22286251	22805724	-1	0	19	0	0	11	20	0	0	0	0	0	F6Y0S3	
ENSMUST00000115274	ENSMUSG00000024620	18	61045150	61085061	1	3	0	49	13	0	0	1	0	0	0	0	E9QN12	
ENSMUST00000115275	ENSMUSG00000029769	6	29396309	29426994	1	0	6	0	30	0	0	0	0	0	0	6	D3Z165	
ENSMUST00000115277	ENSMUSG00000043067	9	24411776	24503140	-1	38	31	32	42	33	17	0	115	27	14	39		A6X919
ENSMUST00000115278						24	7	48	0	16	7	5	66	8	12	28		
ENSMUST00000115281	ENSMUSG00000040118	5	15934691	16374511	1	4	0	0	14	0	1	0	0	0	0	1	Q14BH8	O08532
ENSMUST00000115286	ENSMUSG00000079652	6	29279593	29290680	1	0	7	16	0	4	5	0	0	0	0	0	B2RXB0	
ENSMUST00000115289	ENSMUSG00000043421	6	29272488	29275446	1	3	0	15	42	7	4	6	3	0	0	0		Q9JLS0
ENSMUST00000115295	ENSMUSG00000024617	18	60925618	60988152	1	13	4	6	9	11	3	1	0	0	0	0		P11798
ENSMUST00000115297	ENSMUSG00000024617	18	60925618	60988152	1	0	0	0	1	0	1	0	0	0	0	0	D3Z7K9	
ENSMUST00000115299						0	1	2	34	2	5	0	1	0	0	0		
ENSMUST00000115300	ENSMUSG00000028033	1	21398403	21961942	-1	13	9	0	164	26	15	0	0	0	0	0	E9Q9F1	
ENSMUST00000115302	ENSMUSG00000038148	16	26463135	26482765	1	2	0	0	0	0	0	0	0	0	0	0	Q14BW2	Q925N4
ENSMUST00000115304	ENSMUSG00000022510	16	25683763	25892102	1	7	4	4	10	7	8	0	0	0	1	0		
ENSMUST00000115305	ENSMUSG00000022510	16	25683763	25892102	1	0	2	8	0	13	4	0	0	0	0	0	Q569E5	
ENSMUST00000115306	ENSMUSG00000022510	16	25683763	25892102	1	13	11	13	11	4	0	0	0	0	0	1	Q3UVI3	
ENSMUST00000115307	ENSMUSG00000022510	16	25683763	25892102	1	7	8	17	11	3	3	0	0	0	0	0	D3Z7K2	
ENSMUST00000115308	ENSMUSG00000022510	16	25683763	25892102	1	7	0	0	11	0	0	0	0	0	0	0		O88898
ENSMUST00000115310	ENSMUSG00000022510	16	25683763	25892102	1	0	0	0	0	0	0	0	0	0	0	0		O88898
ENSMUST00000115313	ENSMUSG00000036782	X	23219271	23365082	-1	2	0	0	7	3	2	0	0	0	4	0		Q80TF4
ENSMUST00000115314	ENSMUSG00000033306	16	24393350	24992576	1	1	175	298	0	261	113	0	0	0	0	0		Q8BFW7
ENSMUST00000115315	ENSMUSG00000001348	9	22126731	22135746	-1	0	0	22	2	7	3	143	73	27	85	119		Q05117
ENSMUST00000115316	ENSMUSG00000036782	X	23219271	23365082	-1	0	5	3	0	0	2	0	0	0	0	0		Q80TF4
ENSMUST00000115317	ENSMUSG00000036782	X	23219271	23365082	-1	0	0	1	3	3	2	0	0	0	0	0		Q80TF4
ENSMUST00000115318	ENSMUSG00000043079	18	60593973	60660142	-1	0	34	82	13	16	0	0	0	0	0	0	Q3URF1	Q8CC35
ENSMUST00000115319	ENSMUSG00000036782	X	23219271	23365082	-1	0	0	0	0	5	0	0	0	0	0	0		Q80TF4
ENSMUST00000115320	ENSMUSG00000039841	6	28239927	28398005	-1	0	0	0	0	0	0	27	0	0	10	7	B7ZMR9	Q0VEE6
ENSMUST00000115321	ENSMUSG00000039841	6	28239927	28398005	-1	0	0	14	0	0	4	50	193	142	28	61	B7ZMR9	Q0VEE6
ENSMUST00000115323	ENSMUSG00000024211	6	27275119	28135178	-1	19	7	15	6	27	8	0	0	0	0	0	Q05BD6	
ENSMUST00000115324	ENSMUSG00000024211	6	27275119	28135178	-1	0	1	0	0	0	0	0	0	0	0	0	Q05BD6	
ENSMUST00000115327	ENSMUSG00000029676	6	25743737	25809246	-1	4	7	6	2	10	2	2	7	3	0	3	Q3UXR7	
ENSMUST00000115329						3	2	0	2	3	0	5	17	12	0	11		
ENSMUST00000115330	ENSMUSG00000029676	6	25743737	25809246	-1	16	16	75	13	10	12	121	756	199	233	147		Q91WC1
ENSMUST00000115331	ENSMUSG00000003402	9	22003035	22014219	1	18	0	0	22	22	0	226	360	237	82	176		O08795
ENSMUST00000115333	ENSMUSG00000054737	X	21028939	21062316	-1	0	0	5	5	0	0	0	19	0	0	42	A2AE18	
ENSMUST00000115334	ENSMUSG00000054737	X	21028939	21062316	-1	0	0	0	2	0	0	28	26	11	46	23	A2AE19	
ENSMUST00000115335	ENSMUSG00000022885	16	23224740	23360350	1	19	3	8	9	10	0	0	0	12	0	33		Q64685
ENSMUST00000115336	ENSMUSG00000039632	9	21989871	22002634	-1	4	2	7	8	6	5	0	0	0	0	0		
ENSMUST00000115337	ENSMUSG00000022881	16	23113943	23127737	-1	0	0	0	0	2	0	0	0	0	18	2	D3Z7I8	
ENSMUST00000115338	ENSMUSG00000022881	16	23113943	23127737	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UI84	
ENSMUST00000115340	ENSMUSG00000025774	1	18115191	18145902	-1	0	0	0	0	0	0	0	0	0	0	0	Q9D259	
ENSMUST00000115341	ENSMUSG00000022884	16	23107444	23114136	1	0	0	0	0	0	0	198	474	147	187	93		P10630
ENSMUST00000115342	ENSMUSG00000001131	X	20870166	20874735	1	0	0	10	0	9	2	0	0	0	195	0		P12032
ENSMUST00000115344	ENSMUSG00000025774	1	18115191	18145902	-1	7	2	7	7	12	5	0	0	0	0	0	E9PVG4	
ENSMUST00000115345	ENSMUSG00000037217	X	20860511	20921004	-1	0	0	23	250	0	0	0	37	0	0	0		O88935
ENSMUST00000115348	ENSMUSG00000056004	5	9266118	9481825	1	4	2	6	0	4	0	0	0	0	1	4		Q3UZV7
ENSMUST00000115349	ENSMUSG00000060459	16	22985854	23029101	-1	5	9	4	0	5	5	0	0	0	20	1	Q6S9I0	
ENSMUST00000115351	ENSMUSG00000019066	9	21907491	21918192	-1	34	0	22	125	16	0	4535	5339	3085	317	1861	Q543Q4	P35276
ENSMUST00000115352	ENSMUSG00000079658	1	16641725	16657042	-1	0	0	0	3	0	0	36	0	0	0	0		P83940
ENSMUST00000115354	ENSMUSG00000051956	6	23648869	23650305	-1	11	8	21	0	7	4	0	0	0	0	0		Q14B02
ENSMUST00000115355						3	5	1	13	2	1	0	0	0	0	0		
ENSMUST00000115356	ENSMUSG00000017978	6	23262773	23839421	-1	17	18	139	54	14	18	0	6	3	2	4		Q8BYR5
ENSMUST00000115357						7	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000115358	ENSMUSG00000017978	6	23262773	23839421	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BYR5
ENSMUST00000115359	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	5	6	2	0	2	0	2	0	3		Q8CJ67
ENSMUST00000115360						6	5	0	5	0	0	0	12	0	0	1		
ENSMUST00000115361	ENSMUSG00000017978	6	23262773	23839421	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BYR5
ENSMUST00000115364	ENSMUSG00000031065	X	20687954	20699880	1	5	0	18	5	6	5	25	109	22	16	12	Q3TM24	Q04735
ENSMUST00000115365	ENSMUSG00000079659	5	9100668	9160986	1	2	3	6	50	5	4	229	866	280	92	150	B2RVB9	
ENSMUST00000115366	ENSMUSG00000024597	18	57878678	57946821	1	17	20	18	167	24	11	6	6	3	12	44	E9QM38	
ENSMUST00000115367	ENSMUSG00000067795	1	16065979	16093325	-1	11	8	19	5	14	7	0	0	1	0	1	D3YUR1	
ENSMUST00000115371	ENSMUSG00000034681	17	24414675	24425895	1	0	0	0	0	4	3	44	154	0	2	66		Q99M28
ENSMUST00000115374	ENSMUSG00000031060	X	20617503	20650901	1	12	11	16	23	0	20	0	0	0	0	3		Q99KG3
ENSMUST00000115375	ENSMUSG00000031060	X	20617503	20650901	1	5	0	29	161	35	0	35	12	91	25	18		Q99KG3
ENSMUST00000115378	ENSMUSG00000040570	5	8490334	8622952	-1	5	1	0	118	0	4	2	0	0	0	3	D3YUQ5	
ENSMUST00000115379	ENSMUSG00000033581	16	22059009	22163299	-1	5	2	4	40	10	9	0	6	2	3	16	A6X8Z3	
ENSMUST00000115382	ENSMUSG00000062980	6	21985916	22256404	1	3	5	0	0	0	1	0	0	0	0	0	D3YUQ2	
ENSMUST00000115383	ENSMUSG00000062980	6	21985916	22256404	1	15	3	57	23	15	5	29	190	83	74	10	B2RX70	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000115384	ENSMUSG00000037315	X	20425688	20519939	1	4	7	12	67	16	12	24	81	18	14	28		
ENSMUST00000115385	ENSMUSG00000040537	5	8072352	8368160	-1	4	1	2	2	6	0	0	0	0	0	0	D3YUQ0	
ENSMUST00000115386	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	12	0	0	25	0	0	D3YUP9	
ENSMUST00000115387	ENSMUSG00000060090	X	20364481	20405653	1	0	12	27	10	12	9	69	0	92	62	42		Q9EPK2
ENSMUST00000115388	ENSMUSG00000040537	5	8072352	8368160	-1	0	21	63	30	10	0	0	0	0	0	0		Q9R1V6
ENSMUST00000115389	ENSMUSG00000029670	6	21949571	21976038	1	0	0	0	0	0	0	64	154	35	108	51	D3YUP8	
ENSMUST00000115390	ENSMUSG00000072082	17	24223232	24251409	-1	27	14	63	49	35	10	291	122	216	17	103		P51944
ENSMUST00000115391	ENSMUSG00000060090	X	20364481	20405653	1	0	1	0	29	0	0	118	578	528	258	107		Q9EPK2
ENSMUST00000115393	ENSMUSG00000037341	X	20105755	20291807	-1	149	156	140	191	189	119	8	19	13	10	19		Q8BLV3
ENSMUST00000115394	ENSMUSG00000032185	9	21546894	21589487	1	0	1	9	48	0	0	0	39	0	0	82	D3YUP1	
ENSMUST00000115395	ENSMUSG00000032185	9	21546894	21589487	1	0	0	0	0	0	0	0	268	92	0	84		Q9WVG6
ENSMUST00000115396	ENSMUSG00000029517	6	18866318	18879586	1	0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000115397	ENSMUSG00000033653	16	21423118	21644680	1	0	0	0	0	2	0	0	0	18	0	0	D3YUP0	
ENSMUST00000115398	ENSMUSG00000069378	18	53464546	53575907	1	0	2	4	0	2	0	0	0	0	0	0		Q3UZD5
ENSMUST00000115399	ENSMUSG00000069378	18	53464546	53575907	1	9	8	12	0	8	0	0	0	0	0	0		Q3UZD5
ENSMUST00000115402	ENSMUSG00000025938	1	12866549	12992650	-1	3	2	3	49	15	5	0	0	0	0	0	E9PVE0	
ENSMUST00000115403	ENSMUSG00000025938	1	12866549	12992650	-1	13	7	1	0	13	0	0	0	0	0	0	E9PVD9	
ENSMUST00000115404	ENSMUSG00000033335	9	21424908	21507759	1	3	0	0	0	0	1	0	221	127	0	42	F8WIV5	
ENSMUST00000115405	ENSMUSG00000041301	6	18170687	18322768	1	0	0	0	0	0	0	0	0	0	0	0		P26361
ENSMUST00000115406	ENSMUSG00000041301	6	18170687	18322768	1	6	0	12	0	0	1	0	0	0	0	0	E9PVD7	
ENSMUST00000115407	ENSMUSG00000024122	17	24073680	24150924	-1	0	0	0	1	0	0	0	0	0	0	0	F2Z400	
ENSMUST00000115409	ENSMUSG00000024122	17	24073680	24150924	-1	40	21	167	44	34	35	0	0	543	0	405	F2Z3Z9	
ENSMUST00000115410	ENSMUSG00000024534	18	52767709	52915935	1	15	17	20	1	23	0	0	0	3	0	0	Q3V1N2	
ENSMUST00000115411	ENSMUSG00000024122	17	24073680	24150924	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TRL2	
ENSMUST00000115414	ENSMUSG00000032178	9	21368019	21405361	1	11	9	14	15	13	13	36	101	46	13	64	Q45VK5	
ENSMUST00000115417	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	5	18	0	6	0	11		Q99M96
ENSMUST00000115418	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	0	0	0	0	0	D3YUN2	
ENSMUST00000115419	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	0	0	0	0	0		Q99M96
ENSMUST00000115420	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	0	0	0	0	0	D3YUM7	
ENSMUST00000115421	ENSMUSG00000012428	5	7960457	7982213	1	11	10	34	34	22	17	9514	40815	16488	4592	12346		Q923B6
ENSMUST00000115422	ENSMUSG00000023257	X	16522869	16523689	1	0	2	4	4	1	1	0	0	0	0	0	Q8CH20	
ENSMUST00000115423	ENSMUSG00000006958	16	20733127	20742384	1	13	7	22	108	12	5	0	0	0	0	1	A2CG33	
ENSMUST00000115424	ENSMUSG00000015653	5	5664829	5694578	-1	0	0	0	0	0	0	0	0	0	0	7	B2RX33	Q8BWB6
ENSMUST00000115425	ENSMUSG00000015653	5	5664829	5694578	-1	10	4	1	131	6	2	0	0	0	2	0	B2RX33	Q8BWB6
ENSMUST00000115426	ENSMUSG00000015653	5	5664829	5694578	-1	86	62	240	239	92	69	0	8	5	14	27	B2RX33	Q8BWB6
ENSMUST00000115427	ENSMUSG00000015653	5	5664829	5694578	-1	0	0	0	0	0	3	0	0	0	0	3	D3YUM6	
ENSMUST00000115428	ENSMUSG00000057417	17	23917458	23919441	1	0	2	2	0	0	0	0	0	0	0	0	L7N259	
ENSMUST00000115433	ENSMUSG00000003309	9	21295457	21312333	-1	0	1	1	1	1	0	0	34	0	0	0		
ENSMUST00000115435	ENSMUSG00000031012	X	13517080	13851367	-1	0	0	0	0	0	0	0	5	0	2	0	B1AUH6	
ENSMUST00000115436	ENSMUSG00000031012	X	13517080	13851367	-1	0	56	40	0	59	15	0	0	0	0	0		O70589
ENSMUST00000115437	ENSMUSG00000022847	16	20725158	20734511	-1	3	12	14	30	15	4	0	0	0	0	0	Q543R9	P40226
ENSMUST00000115438	ENSMUSG00000031012	X	13517080	13851367	-1	51	0	0	80	0	0	48	236	134	35	195		O70589
ENSMUST00000115441	ENSMUSG00000040464	5	5537454	5559538	-1	6	8	15	31	5	5	14	61	22	91	17		Q8K013
ENSMUST00000115442	ENSMUSG00000009376	6	17463800	17573980	1	21	18	36	0	28	13	4	0	0	0	1	F8VQL0	
ENSMUST00000115443	ENSMUSG00000009376	6	17463800	17573980	1	0	9	0	85	17	10	3	74	13	17	50	F8VQL0	
ENSMUST00000115444	ENSMUSG00000049620	17	23833360	23836056	-1	0	0	0	0	0	0	0	0	0	0	1	Z4YLD7	
ENSMUST00000115445	ENSMUSG00000046798	5	5489537	5514958	-1	22	15	13	69	21	8	0	0	20	12	43		Q9ET43
ENSMUST00000115446	ENSMUSG00000046798	5	5489537	5514958	-1	0	0	0	0	0	0	0	91	0	0	0		Q9ET43
ENSMUST00000115447	ENSMUSG00000079666	5	5437827	5479143	-1	3	3	1	3	0	0	0	0	0	0	0	D3YUK8	
ENSMUST00000115449	ENSMUSG00000019647	18	47235598	47368870	-1	0	14	43	57	35	12	0	0	0	0	0	K3W4S5	
ENSMUST00000115450	ENSMUSG00000028926	5	4803391	5420312	-1	0	4	7	2	0	3	0	0	7	0	0	Q6NVF8	O35495
ENSMUST00000115451	ENSMUSG00000028926	5	4803391	5420312	-1	18	16	37	0	19	0	0	0	0	16	15	Q6NVF8	O35495
ENSMUST00000115452	ENSMUSG00000028926	5	4803391	5420312	-1	7	0	0	0	0	3	0	0	1	0	0	E9PVC7	
ENSMUST00000115453	ENSMUSG00000007655	6	17306335	17341452	1	0	0	2	15	14	11	0	0	0	0	0		P49817
ENSMUST00000115454	ENSMUSG00000007655	6	17306335	17341452	1	3	0	0	0	0	1	0	0	0	3	0		P49817
ENSMUST00000115455	ENSMUSG00000007655	6	17306335	17341452	1	0	0	0	0	0	0	0	0	0	0	2	D3Z148	
ENSMUST00000115456	ENSMUSG00000007655	6	17306335	17341452	1	0	7	0	3	0	0	0	0	0	0	0		P49817
ENSMUST00000115457	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	626	185	1278	113	700	E9PVC6	
ENSMUST00000115458	ENSMUSG00000032177	9	21165714	21213248	1	6	0	0	0	0	0	7	0	4	0	0		O89084
ENSMUST00000115459	ENSMUSG00000000058	6	17281185	17289115	1	8	5	27	11	6	3	0	0	0	7	0	Q924U4	
ENSMUST00000115460	ENSMUSG00000045983	16	20668313	20692884	1	17	10	66	37	22	20	18	38	77	0	72		Q6NZJ6
ENSMUST00000115461	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	1	0	520	0	657	E9PVC5	
ENSMUST00000115462	ENSMUSG00000000058	6	17281185	17289115	1	1	0	2	0	0	0	3	2	4	14	8	D3Z147	
ENSMUST00000115463	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	0	1	1	0	141		Q6NZJ6
ENSMUST00000115467	ENSMUSG00000029552	6	17065149	17105828	1	5	0	18	15	0	10	592	1427	861	1226	675	Q921W7	
ENSMUST00000115468	ENSMUSG00000025912	1	9667415	9700209	-1	3	4	0	0	0	0	2	0	3	1	13	E9QLX9	
ENSMUST00000115469	ENSMUSG00000029563	6	14901349	15441977	1	1	2	0	0	0	3	0	0	0	0	0	D3Z146	
ENSMUST00000115470	ENSMUSG00000029563	6	14901349	15441977	1	9	13	38	9	10	5	0	0	1	0	0	Q3TPK1	
ENSMUST00000115472	ENSMUSG00000029563	6	14901349	15441977	1	0	3	3	9	7	4	0	0	0	0	0		P58463
ENSMUST00000115474	ENSMUSG00000029563	6	14901349	15441977	1	0	0	0	0	0	0	0	0	0	0	0	D3Z142	
ENSMUST00000115475	ENSMUSG00000029563	6	14901349	15441977	1	0	0	0	0	0	0	0	0	0	0	0	F6UMM1	
ENSMUST00000115477	ENSMUSG00000029563	6	14901349	15441977	1	27	24	76	81	15	9	0	5	2	0	0		P58463
ENSMUST00000115479						2	4	0	1	4	3	0	0	0	0	0		
ENSMUST00000115481	ENSMUSG00000064127	X	12675369	12762073	-1	6	8	0	3	3	5	18	35	28	0	61	A2BDP0	
ENSMUST00000115484						5	0	13	0	0	0	0	0	0	0	0		
ENSMUST00000115487	ENSMUSG00000010205	9	21074168	21091988	-1	21	13	57	181	44	21	987	788	799	56	699		Q9CW46
ENSMUST00000115488	ENSMUSG00000025909	1	8361475	9299878	-1	0	1	0	0	0	2	0	0	0	0	0	Q8BNW6	
ENSMUST00000115489	ENSMUSG00000041319	17	23668614	23673882	-1	0	0	0	0	0	0	0	0	4	40	2	D3Z132	
ENSMUST00000115490	ENSMUSG00000041319	17	23668614	23673882	-1	0	0	0	0	0	0	0	0	0	6	0	D3Z131	
ENSMUST00000115491	ENSMUSG00000048216	6	13834458	13839942	-1	0	12	0	3	3	9	1	3	0	2	1	Q6ZWR2	P60894
ENSMUST00000115492	ENSMUSG00000048216	6	13834458	13839942	-1	8	4	0	9	3	5	0	0	0	0	0	Q6ZWR2	P60894
ENSMUST00000115494	ENSMUSG00000079681	9	21062393	21067093	-1	5	4	17	40	10	5	0	1	0	1	1		Q1WG82
ENSMUST00000115496	ENSMUSG00000101053	Y	8832821	8835169	-1	0	0	0	0	22	5	0	0	0	0	0	J3KMI0	
ENSMUST00000115498	ENSMUSG00000024471	18	44334074	44355724	1	0	6	0	1	8	8	0	0	0	0	0	A0A509	Q9JIF9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000115509	ENSMUSG00000023902	17	23600856	23611019	1	0	0	0	99	17	0	0	0	0	0	0		Q3URR7
ENSMUST00000115510	ENSMUSG00000029629	6	11907809	12081205	1	0	4	0	49	9	5	24	37	41	0	67	G5E8S0	
ENSMUST00000115511	ENSMUSG00000029629	6	11907809	12081205	1	4	0	24	2	1	0	135	1018	408	153	220		Q9D4H9
ENSMUST00000115512	ENSMUSG00000040363	X	12036740	12160355	-1	0	9	0	0	0	0	0	0	0	12	0		Q8CGN4
ENSMUST00000115513	ENSMUSG00000040363	X	12036740	12160355	-1	0	0	0	0	0	0	89	130	214	0	372		Q8CGN4
ENSMUST00000115515						7	0	6	3	5	3	0	0	0	0	0		
ENSMUST00000115516	ENSMUSG00000062012	17	23575845	23599487	-1	24	10	46	147	29	20	2	2	0	0	3	D7F2B3	P10754
ENSMUST00000115518	ENSMUSG00000062995	6	8630527	8778488	-1	0	1	3	1	3	0	0	0	11	0	5	D3Z119	
ENSMUST00000115519	ENSMUSG00000062995	6	8630527	8778488	-1	0	0	0	0	0	0	59	94	80	82	17	D3Z118	
ENSMUST00000115520	ENSMUSG00000062995	6	8630527	8778488	-1	0	0	0	0	0	0	20	64	0	0	9		P97411
ENSMUST00000115522	ENSMUSG00000022842	16	20611593	20646485	1	6	0	3	21	6	4	74	81	27	30	37		Q80Z60
ENSMUST00000115524	ENSMUSG00000008035	X	10715013	10719690	1	13	1	6	35	4	1	564	736	398	40	202	Q4FK31	Q9CQ20
ENSMUST00000115526	ENSMUSG00000058254	X	10485158	10596605	1	77	26	51	0	0	0	0	0	0	0	0	Q3UHG5	
ENSMUST00000115527	ENSMUSG00000058503	5	3543833	3570238	1	8	7	28	20	15	4	67	295	145	200	111		Q9CVI2
ENSMUST00000115528	ENSMUSG00000031173	X	10252305	10321024	1	4	4	4	5	7	2	0	0	0	0	0	Q8R1A8	
ENSMUST00000115529	ENSMUSG00000025903	1	4807788	4848410	1	0	0	0	0	0	0	0	132	28	0	0	D3Z111	
ENSMUST00000115532	ENSMUSG00000031174	X	10073621	10216920	-1	4	0	2	8	6	0	0	0	0	0	4	Q8CDM3	
ENSMUST00000115533	ENSMUSG00000031174	X	10073621	10216920	-1	0	0	0	12	0	2	0	27	0	0	9	Q3UWJ5	
ENSMUST00000115534	ENSMUSG00000031174	X	10073621	10216920	-1	0	3	0	0	0	0	9	0	20	0	0	Q3UTY5	
ENSMUST00000115535	ENSMUSG00000033972	17	22337989	22361400	-1	9	6	9	47	7	5	85	318	89	151	89	E9PUS4	
ENSMUST00000115537	ENSMUSG00000068794	6	7997808	8192617	-1	23	7	24	17	37	13	0	1	0	0	0		Q2UY11
ENSMUST00000115538						0	0	0	5	0	0	43	136	68	87	43		
ENSMUST00000115542	ENSMUSG00000029752	6	7675169	7693254	-1	7	0	0	10	4	4	0	0	0	0	0		Q61024
ENSMUST00000115543	ENSMUSG00000090084	X	10037977	10117709	-1	0	0	0	0	0	0	0	0	0	0	2		Q9R0M3
ENSMUST00000115544	ENSMUSG00000090084	X	10037977	10117709	-1	0	4	1	4	3	0	0	0	0	0	0	A2BE45	
ENSMUST00000115547	ENSMUSG00000022822	16	20331303	20426394	-1	0	0	0	0	0	0	96	0	1	0	54		Q9R1X5
ENSMUST00000115553	ENSMUSG00000079694	X	9250928	9256899	-1	4	4	33	3	5	1	0	0	1	0	1	B1AV28	
ENSMUST00000115554	ENSMUSG00000029757	6	5725639	6028039	1	0	0	0	0	0	8	0	0	0	1	0		O88485
ENSMUST00000115555	ENSMUSG00000029757	6	5725639	6028039	1	0	19	0	0	23	0	0	0	0	0	0	D3Z0M6	
ENSMUST00000115556	ENSMUSG00000029757	6	5725639	6028039	1	0	0	0	151	5	0	0	0	0	0	0	Q3TYJ3	
ENSMUST00000115557	ENSMUSG00000058192	9	20581325	20595194	1	10	5	21	90	14	7	2	0	0	0	0	G3X996	
ENSMUST00000115559	ENSMUSG00000029757	6	5725639	6028039	1	13	0	26	0	0	0	0	0	0	0	0		O88485
ENSMUST00000115560	ENSMUSG00000041215	16	20141063	20232573	1	49	0	0	51	51	27	149	51	255	0	294		Q3TUF7
ENSMUST00000115561	ENSMUSG00000079697	X	8874253	8880750	1	5	0	0	3	0	1	0	1	0	0	1	A2AHC8	
ENSMUST00000115562	ENSMUSG00000059475	9	20468549	20492746	-1	0	2	0	0	2	0	39	60	88	55	64		Q8R1D1
ENSMUST00000115563	ENSMUSG00000079699	X	8843994	8849607	1	0	1	3	0	0	0	0	0	0	0	1	A2AHC7	
ENSMUST00000115565	ENSMUSG00000079700	17	17887852	17971677	1	0	5	24	12	6	1	1	10	4	5	2		O08790
ENSMUST00000115567	ENSMUSG00000024431	18	39410545	39491301	-1	0	0	0	13	20	0	176	117	528	117	352	E9PUR6	
ENSMUST00000115571	ENSMUSG00000024431	18	39410545	39491301	-1	14	12	14	0	0	13	1397	3271	1511	526	1151	E9PUR6	
ENSMUST00000115573	ENSMUSG00000079704	X	8514052	8524954	-1	2	0	0	2	0	0	0	0	0	0	0	A2BI73	
ENSMUST00000115574						4	4	7	230	11	9	0	2	2	3	2		
ENSMUST00000115576	ENSMUSG00000047786	17	17402672	17459387	1	31	28	48	42	45	22	0	0	0	0	0		Q6P566
ENSMUST00000115577	ENSMUSG00000004631	6	4674350	4747207	-1	0	0	0	0	0	0	0	0	0	0	0		O70258
ENSMUST00000115578	ENSMUSG00000005262	16	18811779	18835261	1	0	0	0	0	0	0	0	0	0	0	0		P70362
ENSMUST00000115579	ENSMUSG00000004631	6	4674350	4747207	-1	4	0	0	33	3	0	0	0	0	7	0		O70258
ENSMUST00000115580						21	28	50	22	34	19	2	4	1	0	0		
ENSMUST00000115582	ENSMUSG00000036585	18	38838673	38929404	-1	7	0	11	11	13	0	2	0	0	0	0	Q6ZWS1	P61148
ENSMUST00000115584	ENSMUSG00000068218	X	8366978	8375390	1	0	2	0	0	0	1	0	0	0	0	0	A2BI93	
ENSMUST00000115585	ENSMUSG00000000028	16	18780447	18811987	-1	5	2	6	2	3	2	10	17	9	3	4	D3Z0L5	
ENSMUST00000115588	ENSMUSG00000043885	9	15709738	15742384	1	0	0	4	19	0	0	0	7	63	0	16	D3Z0L1	
ENSMUST00000115590	ENSMUSG00000031170	X	8271133	8280179	1	58	23	85	510	94	53	0	0	2	4	0		Q3U1J0
ENSMUST00000115591	ENSMUSG00000031170	X	8271133	8280179	1	1	0	0	0	0	0	1	0	0	0	0		Q3U1J0
ENSMUST00000115592	ENSMUSG00000039977	9	15559864	15627933	-1	45	9	151	0	0	11	1	2	1	1	0		Q7M6Y5
ENSMUST00000115593	ENSMUSG00000039977	9	15559864	15627933	-1	0	30	58	81	30	0	0	0	0	0	0		Q7M6Y5
ENSMUST00000115594	ENSMUSG00000031171	X	8238668	8252406	-1	0	0	0	0	0	0	0	71	33	9	0	A2ALH2	
ENSMUST00000115595	ENSMUSG00000031171	X	8238668	8252406	-1	0	0	0	0	0	0	70	110	60	75	73	Q8JZY1	
ENSMUST00000115600	ENSMUSG00000000884	16	18498768	18566679	1	2	0	0	0	0	2	5	5	4	0	4		Q9EQ15
ENSMUST00000115601	ENSMUSG00000000884	16	18498768	18566679	1	19	8	0	0	15	0	0	2	0	1	3	Q3TM20	
ENSMUST00000115604	ENSMUSG00000075704	16	18426384	18479073	1	1	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000115605	ENSMUSG00000075704	16	18426384	18479073	1	0	0	0	0	0	0	0	0	2	0	12	D3Z0K8	
ENSMUST00000115606	ENSMUSG00000075704	16	18426384	18479073	1	0	0	0	0	5	0	0	12	10	8	11		
ENSMUST00000115609	ENSMUSG00000000326	16	18406886	18426852	-1	1	0	3	161	7	5	0	28	5	0	10		O88587
ENSMUST00000115610	ENSMUSG00000000325	16	18348182	18407076	1	21	15	34	80	30	6	1	0	2	0	4		P98203
ENSMUST00000115612	ENSMUSG00000000325	16	18348182	18407076	1	0	0	0	0	4	6	0	0	0	0	6		P98203
ENSMUST00000115613	ENSMUSG00000000325	16	18348182	18407076	1	0	7	0	5	33	0	0	0	0	0	0		P98203
ENSMUST00000115614	ENSMUSG00000000325	16	18348182	18407076	1	28	0	88	236	0	12	0	0	0	0	0		P98203
ENSMUST00000115615	ENSMUSG00000031167	X	8138975	8145880	-1	0	0	0	0	10	0	1071	1689	1029	7326	707	Q545K5	O89086
ENSMUST00000115616	ENSMUSG00000031167	X	8138975	8145880	-1	0	0	0	0	0	0	1228	2062	1078	7298	1046	Q8BG13	
ENSMUST00000115617	ENSMUSG00000031167	X	8138975	8145880	-1	2	6	3	0	0	3	484	0	0	0	0	Q8BG13	
ENSMUST00000115619	ENSMUSG00000031167	X	8138975	8145880	-1	0	0	0	0	0	0	0	158	515	514	258	Q545K5	O89086
ENSMUST00000115621	ENSMUSG00000031167	X	8138975	8145880	-1	5	0	0	32	0	0	0	0	0	0	0	Q545K5	O89086
ENSMUST00000115622	ENSMUSG00000023964	6	3685680	3764714	-1	20	7	17	2	9	7	0	0	0	0	0		Q60755
ENSMUST00000115623	ENSMUSG00000031166	X	8123301	8132892	-1	0	0	0	0	0	0	0	0	9	0	0	Q32P16	Q91V09
ENSMUST00000115624	ENSMUSG00000031932	9	14860210	14870789	1	21	6	8	0	0	3	0	0	5	2	10	Q544C4	P30731
ENSMUST00000115628	ENSMUSG00000013539	16	18300825	18348103	-1	0	0	0	3	0	0	67	103	57	58	53	Q8BTN3	
ENSMUST00000115629	ENSMUSG00000024456	18	37843601	37935476	-1	36	30	63	0	0	0	2611	6373	507	293	636	D3Z074	
ENSMUST00000115631	ENSMUSG00000024456	18	37843601	37935476	-1	0	0	0	0	18	0	0	0	0	0	38	Q6NS79	
ENSMUST00000115632	ENSMUSG00000031928	9	14784654	14837123	1	77	66	98	66	65	23	27	156	91	25	78		Q61216
ENSMUST00000115633	ENSMUSG00000022718	16	18253948	18289249	-1	4	3	12	21	7	5	0	0	33	0	0		Q9EQM6
ENSMUST00000115634	ENSMUSG00000024456	18	37843601	37935476	-1	0	0	0	143	24	33	1690	5813	8351	80	5797		O08808
ENSMUST00000115636	ENSMUSG00000039231	X	8061171	8074760	-1	15	8	66	31	15	15	0	7	12	3	6		O54864
ENSMUST00000115637	ENSMUSG00000039231	X	8061171	8074760	-1	0	2	8	0	2	6	197	196	111	27	74	A2AC19	
ENSMUST00000115638	ENSMUSG00000039231	X	8061171	8074760	-1	6	0	3	0	9	0	12	0	16	0	5		O54864
ENSMUST00000115640	ENSMUSG00000022721	16	18248679	18254772	1	0	0	0	0	0	0	54	28	33	2	48	Q3UYU2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000115642	ENSMUSG00000031161	X	7930120	7947889	-1	0	0	9	0	0	0	268	481	273	24	303		Q9Z2V5
ENSMUST00000115643	ENSMUSG00000036912	9	14696230	14740733	-1	21	15	76	100	20	7	0	0	0	6	18	Z4YLE4	
ENSMUST00000115644	ENSMUSG00000036912	9	14696230	14740733	-1	7	0	25	32	3	6	0	2	0	0	0		Q8CGT6
ENSMUST00000115645	ENSMUSG00000005732	16	18239784	18248732	-1	0	0	0	41	4	1	6	61	42	349	45		P34022
ENSMUST00000115647	ENSMUSG00000053914	9	14462548	14500482	-1	0	0	0	0	13	0	0	1	2	1	0	Z4YLE9	
ENSMUST00000115649						0	2	0	4	0	0	0	0	0	0	0		
ENSMUST00000115654	ENSMUSG00000031157	X	7894519	7899269	-1	29	25	343	55	34	27	0	7	0	3	11	A2AER7	Q91VJ5
ENSMUST00000115655	ENSMUSG00000031157	X	7894519	7899269	-1	0	0	1	0	0	0	116	109	112	64	33	A2AER7	Q91VJ5
ENSMUST00000115657	ENSMUSG00000102206	18	37010712	37187657	1	0	0	0	0	0	0	0	0	0	0	0	Q91Y19	
ENSMUST00000115658	ENSMUSG00000007440	18	37005203	37187657	1	20	8	27	62	18	4	0	0	0	0	0		Q91Y20
ENSMUST00000115659	ENSMUSG00000103770	18	36997880	37187657	1	30	13	38	133	18	10	0	0	0	0	0		Q91Y11
ENSMUST00000115660	ENSMUSG00000031156	X	7884041	7894492	1	8	9	25	43	10	7	36	33	18	0	0	Q3UIP1	Q9R0M8
ENSMUST00000115661	ENSMUSG00000103458	18	36952741	37840200	1	17	0	24	0	0	13	0	0	0	0	0		O88689
ENSMUST00000115662	ENSMUSG00000104148	18	36939205	37187657	1	0	0	0	0	0	0	0	0	0	0	0	Q91Y17	
ENSMUST00000115663	ENSMUSG00000031156	X	7884041	7894492	1	5	0	0	23	0	0	122	149	131	25	114	A2AER4	
ENSMUST00000115665	ENSMUSG00000031154	X	7841364	7876626	1	0	6	2	0	0	0	0	0	0	0	0	A2AES3	
ENSMUST00000115666	ENSMUSG00000031154	X	7841364	7876626	1	0	5	0	94	2	3	503	530	826	94	904	A2AES5	
ENSMUST00000115667	ENSMUSG00000031154	X	7841364	7876626	1	0	0	0	0	0	0	0	0	0	0	0	A2AES4	
ENSMUST00000115668	ENSMUSG00000031154	X	7841364	7876626	1	0	0	0	0	0	0	297	678	393	20	409		Q3U2S4
ENSMUST00000115672	ENSMUSG00000032000	9	7848699	7873186	-1	67	66	110	117	83	53	24	107	83	20	134	A2CGA3	
ENSMUST00000115673	ENSMUSG00000032000	9	7848699	7873186	-1	2	1	13	18	8	0	64	107	209	109	164	E0CZ20	
ENSMUST00000115675	ENSMUSG00000031153	X	7789765	7820567	1	0	0	13	0	0	0	286	1194	951	447	866	A2AEW8	
ENSMUST00000115677	ENSMUSG00000000134	X	7762560	7775202	1	0	0	1	0	2	3	2200	1495	1299	118	830		Q64092
ENSMUST00000115678	ENSMUSG00000000134	X	7762560	7775202	1	0	1	0	0	0	0	428	2681	319	72	205		Q64092
ENSMUST00000115679	ENSMUSG00000000134	X	7762560	7775202	1	0	0	0	0	0	0	800	577	904	1	448		Q64092
ENSMUST00000115680	ENSMUSG00000000134	X	7762560	7775202	1	2	0	1	0	0	0	59	67	0	0	202	Z4YLF7	
ENSMUST00000115681	ENSMUSG00000022761	16	17508688	17526333	1	4	6	0	42	0	8	10	8	9	0	17	E9PUQ1	
ENSMUST00000115682	ENSMUSG00000044719	18	36684923	36695925	-1	14	11	31	16	29	9	0	0	0	0	1	G5E8S3	
ENSMUST00000115685	ENSMUSG00000022763	16	17489611	17507485	1	0	0	0	2	0	0	0	0	0	0	0		Q3TY86
ENSMUST00000115687	ENSMUSG00000039382	X	7721973	7728201	1	0	0	9	0	0	0	130	84	214	70	50		Q91VM3
ENSMUST00000115688	ENSMUSG00000039382	X	7721973	7728201	1	0	0	0	13	0	1	42	0	95	49	0		Q91VM3
ENSMUST00000115689	ENSMUSG00000039382	X	7721973	7728201	1	3	0	0	0	0	0	126	540	111	128	144		Q91VM3
ENSMUST00000115694	ENSMUSG00000024485	18	36528157	36541293	1	35	25	38	17	31	10	0	0	0	0	0	E9PUP3	
ENSMUST00000115695	ENSMUSG00000031147	X	7673164	7681251	-1	3	4	2	25	3	1	1	0	0	0	5		Q4KL35
ENSMUST00000115698	ENSMUSG00000050240	16	17233572	17263430	1	0	0	0	0	0	0	0	4	0	0	0		Q9JLZ6
ENSMUST00000115699	ENSMUSG00000038965	16	17152013	17202649	-1	19	10	44	48	29	10	0	0	0	0	0	Q561N4	P68037
ENSMUST00000115700	ENSMUSG00000038965	16	17152013	17202649	-1	5	0	0	0	0	0	0	57	12	153	28	D3YZS3	
ENSMUST00000115702	ENSMUSG00000041774	16	17144621	17160701	1	3	3	8	4	5	0	1	0	2	0	0		Q14BV6
ENSMUST00000115705	ENSMUSG00000060275	18	36017707	36197380	-1	0	0	0	4	0	1	5	0	0	0	2	E9PUN9	
ENSMUST00000115706	ENSMUSG00000041774	16	17144621	17160701	1	7	6	24	11	12	9	6	7	5	4	6	D3YZR5	
ENSMUST00000115708	ENSMUSG00000023868	17	8525372	8986648	1	7	0	14	2	8	0	4	1	1	0	0	D3YZR4	
ENSMUST00000115709	ENSMUSG00000022768	16	17139064	17147229	-1	0	0	0	0	0	0	7	0	1	2	3		Q80X53
ENSMUST00000115711	ENSMUSG00000022768	16	17139064	17147229	-1	0	2	18	0	0	2	0	0	0	0	0		Q80X53
ENSMUST00000115712	ENSMUSG00000060275	18	36017707	36197380	-1	18	10	55	194	19	13	1	5	6	0	0	D3YZR3	
ENSMUST00000115713	ENSMUSG00000060275	18	36017707	36197380	-1	0	0	0	150	18	0	0	0	0	0	7	D3YZR2	
ENSMUST00000115715	ENSMUSG00000023868	17	8525372	8986648	1	9	6	23	15	6	4	0	0	0	0	0	F8WHK3	
ENSMUST00000115716	ENSMUSG00000024347	18	35964830	36014715	1	0	9	19	133	34	5	0	9	0	0	0		Q6P1I6
ENSMUST00000115717	ENSMUSG00000023868	17	8525372	8986648	1	28	26	70	31	0	13	0	0	1	2	3	S4R197	
ENSMUST00000115719	ENSMUSG00000022771	16	17086555	17111257	-1	4	2	2	0	2	1	21	54	29	3	37	D3YZQ4	
ENSMUST00000115720	ENSMUSG00000023868	17	8525372	8986648	1	7	0	0	4	2	2	0	0	0	0	0		Q8CA95
ENSMUST00000115721	ENSMUSG00000022771	16	17086555	17111257	-1	8	11	21	21	17	11	39	123	66	9	99		Q9D787
ENSMUST00000115722	ENSMUSG00000023868	17	8525372	8986648	1	17	14	50	32	35	16	0	0	1	0	1	F2Z3Z4	
ENSMUST00000115724	ENSMUSG00000023868	17	8525372	8986648	1	12	3	4	15	11	5	0	0	0	0	0		Q8CA95
ENSMUST00000115725	ENSMUSG00000031142	X	7607083	7635196	1	0	0	0	0	0	12	19	17	12	18	9	B1AVA4	
ENSMUST00000115726	ENSMUSG00000031142	X	7607083	7635196	1	0	1	0	0	0	0	0	0	0	0	0	Q7TNI3	
ENSMUST00000115728	ENSMUSG00000024349	18	35733678	35740554	-1	29	13	89	39	51	17	366	884	535	324	420		Q3TBT3
ENSMUST00000115729	ENSMUSG00000022773	16	17069696	17087045	1	49	50	81	70	65	28	3	42	19	11	29	D3YZQ1	
ENSMUST00000115731	ENSMUSG00000063358	16	16983382	17047453	1	4	2	0	0	4	1	275	595	305	39	64		P63085
ENSMUST00000115733	ENSMUSG00000041624	9	3532354	3897342	1	10	13	11	175	22	10	0	0	0	0	0	F8VQK3	
ENSMUST00000115734	ENSMUSG00000037058	18	35598617	35617186	1	2	7	0	4	7	2	27	23	31	0	64		Q9D6V8
ENSMUST00000115735	ENSMUSG00000037058	18	35598617	35617186	1	6	0	9	0	0	0	41	195	54	74	27		Q9D6V8
ENSMUST00000115736	ENSMUSG00000037058	18	35598617	35617186	1	0	0	0	0	0	0	54	421	310	198	60		Q9D6V8
ENSMUST00000115737	ENSMUSG00000037058	18	35598617	35617186	1	0	0	0	23	0	4	0	37	32	223	0		Q9D6V8
ENSMUST00000115738	ENSMUSG00000039521	X	7579676	7595243	1	0	0	0	0	6	7	0	0	0	0	0	Q53Z59	Q99JB6
ENSMUST00000115739	ENSMUSG00000039521	X	7579676	7595243	1	0	0	0	0	18	0	0	0	26	0	56	Q53Z59	Q99JB6
ENSMUST00000115740	ENSMUSG00000039521	X	7579676	7595243	1	14	0	12	0	0	0	0	0	0	0	21	Q53Z59	Q99JB6
ENSMUST00000115742	ENSMUSG00000039556	X	7557296	7574283	-1	0	0	0	151	0	0	15	22	27	0	36		Q9JIG4
ENSMUST00000115744	ENSMUSG00000046269	X	7371276	7375830	-1	0	0	0	150	0	0	6	46	21	6	12		Q8CEG8
ENSMUST00000115746	ENSMUSG00000004317	X	7153810	7319358	-1	0	0	0	0	0	0	6	0	4	0	1	B1ATV0	
ENSMUST00000115747	ENSMUSG00000079722	17	7350904	7352696	-1	40	26	58	31	60	18	0	6	4	0	3		A4Q9E4
ENSMUST00000115749	ENSMUSG00000022789	16	16312235	16359030	-1	0	0	0	0	0	0	44	268	146	68	75		Q8K1M6
ENSMUST00000115750	ENSMUSG00000050089	X	7067519	7078609	1	0	0	15	0	0	0	0	0	0	0	0		Q60662
ENSMUST00000115751	ENSMUSG00000050089	X	7067519	7078609	1	5	7	0	4	4	4	6	21	10	17	5		Q60662
ENSMUST00000115752	ENSMUSG00000051592	X	6979652	7041619	-1	9	5	17	11	5	0	0	0	0	0	0	A2AEP2	
ENSMUST00000115763	ENSMUSG00000041831	17	6673458	6738042	1	27	8	21	19	18	17	0	0	2	0	10	F8WHG0	
ENSMUST00000115765	ENSMUSG00000003778	18	34598615	34624601	-1	6	2	8	6	2	2	75	230	175	18	191	D3YZC8	
ENSMUST00000115766	ENSMUSG00000003778	18	34598615	34624601	-1	10	9	3	12	12	6	34	169	59	23	0	D3YZC7	
ENSMUST00000115772						23	13	61	15	25	4	20	39	29	7	40		
ENSMUST00000115776	ENSMUSG00000022674	16	15552677	15594524	-1	0	0	0	2	8	0	10	70	21	89	33		Q9D2M8
ENSMUST00000115777	ENSMUSG00000022674	16	15552677	15594524	-1	15	13	33	37	13	3	17	67	21	43	5	Q4VBX4	Q9D2M8
ENSMUST00000115781	ENSMUSG00000005871	18	34220924	34322189	1	39	39	74	28	21	7	125	488	112	45	161	E9QLQ9	
ENSMUST00000115784	ENSMUSG00000023805	17	5941280	6044290	1	8	0	5	4	9	0	0	9	0	0	25		Q9D2G5
ENSMUST00000115785	ENSMUSG00000023805	17	5941280	6044290	1	0	0	3	0	0	0	0	22	9	13	0	E9Q4P5	
ENSMUST00000115786	ENSMUSG00000023805	17	5941280	6044290	1	25	26	140	37	24	18	6	7	12	15	4	D3YZB5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000115787	ENSMUSG00000023805	17	5941280	6044290	1	2	4	0	3	4	4	0	0	0	0	0	D3YZB4	
ENSMUST00000115788	ENSMUSG00000023805	17	5941280	6044290	1	0	0	7	0	0	0	0	0	0	0	0	D3YZB3	
ENSMUST00000115789	ENSMUSG00000023805	17	5941280	6044290	1	9	0	11	7	0	2	44	102	40	17	56		Q9D2G5
ENSMUST00000115790	ENSMUSG00000023805	17	5941280	6044290	1	0	0	0	0	0	0	71	0	83	0	41	D3YZB2	
ENSMUST00000115791	ENSMUSG00000023805	17	5941280	6044290	1	16	19	32	49	38	10	0	0	0	0	21	F8WHD8	
ENSMUST00000115795	ENSMUSG00000022678	16	14163275	14192928	1	10	0	22	1	7	4	120	189	108	35	84		Q9CZA6
ENSMUST00000115797	ENSMUSG00000069729	17	4994332	5347656	1	51	81	168	74	66	27	0	0	0	0	0	E9Q4N7	
ENSMUST00000115799	ENSMUSG00000069729	17	4994332	5347656	1	0	0	0	0	0	0	233	359	276	18	245	E9Q4N6	
ENSMUST00000115800	ENSMUSG00000023802	17	3635240	3696261	-1	7	8	17	10	18	3	0	0	0	0	0		Q672J9
ENSMUST00000115802	ENSMUSG00000022680	16	13833148	13903131	-1	44	55	250	78	45	25	16	20	13	0	25		Q99K01
ENSMUST00000115803	ENSMUSG00000022680	16	13833148	13903131	-1	1	0	0	0	0	0	6	0	0	0	0	D3YZA7	
ENSMUST00000115804	ENSMUSG00000022680	16	13833148	13903131	-1	0	0	0	0	0	0	0	0	32	0	24		Q99K01
ENSMUST00000115805	ENSMUSG00000022681	16	13819251	13835451	1	0	1	0	0	0	2	0	17	0	0	0	D3YZ99	
ENSMUST00000115807	ENSMUSG00000022683	16	13715057	13730983	-1	1	0	3	5	4	6	0	0	0	1	0	Q8K130	
ENSMUST00000115808	ENSMUSG00000041915	18	31759824	31784071	1	29	33	103	126	37	14	411	848	550	61	396		Q8JZZ6
ENSMUST00000115809	ENSMUSG00000009569	16	13256481	13417529	1	0	0	0	4	0	0	0	0	0	0	0	Q8R2L3	
ENSMUST00000115811	ENSMUSG00000033628	18	30272747	30348126	1	3	2	3	8	9	5	16	8	14	0	17	D3YZ98	
ENSMUST00000115812	ENSMUSG00000033628	18	30272747	30348126	1	5	5	32	28	7	0	279	963	525	190	316		Q6PF93
ENSMUST00000115814	ENSMUSG00000071669	16	11322908	11755472	1	11	7	6	0	10	6	0	2	8	1	0	D3YZ90	
ENSMUST00000115816	ENSMUSG00000024268	18	25477632	25753983	-1	0	0	0	0	62	0	0	0	18	0	0		Q7TSY6
ENSMUST00000115817	ENSMUSG00000024269	18	25127223	25169007	-1	21	24	66	54	31	17	28	104	31	27	34	E9QLP0	
ENSMUST00000115821	ENSMUSG00000073682	4	155614413	155645408	-1	91	56	193	571	89	84	4	4	2	1	4	F6WIE4	
ENSMUST00000115822	ENSMUSG00000079740	16	10812915	10812994	1	4	3	9	182	11	7	0	1	0	0	1	F6ZH14	
ENSMUST00000115823	ENSMUSG00000068663	16	10545339	10744878	1	0	6	16	4	7	13	14	2	10	0	6		Q80U30
ENSMUST00000115824	ENSMUSG00000068663	16	10545339	10744878	1	0	0	29	34	0	0	0	0	0	0	0	Z4YLG3	
ENSMUST00000115827	ENSMUSG00000068663	16	10545339	10744878	1	0	0	0	0	5	0	0	0	0	0	0		Q80U30
ENSMUST00000115828	ENSMUSG00000068663	16	10545339	10744878	1	0	0	0	0	0	0	74	0	89	0	48	H7BXB6	
ENSMUST00000115829	ENSMUSG00000024274	18	23970975	23981555	-1	4	3	1	2	6	1	0	0	1	2	0	Q149X8	
ENSMUST00000115830	ENSMUSG00000024277	18	23752333	23893861	1	7	5	21	0	11	4	296	724	275	53	241		Q8R001
ENSMUST00000115831	ENSMUSG00000039179	16	10357948	10395490	-1	6	2	0	0	0	2	0	0	0	0	0	Q14BE9	
ENSMUST00000115832	ENSMUSG00000024302	18	23415415	23659714	1	46	38	100	56	33	30	0	0	1	1	0	Q8CFR5	
ENSMUST00000115835	ENSMUSG00000059003	16	9567898	9995560	-1	28	38	16	120	41	22	0	0	0	0	0		P35436
ENSMUST00000115837	ENSMUSG00000024306	18	21810897	22171396	-1	0	0	0	0	3	0	0	0	0	0	0		Q8CDV0
ENSMUST00000115838	ENSMUSG00000057880	16	8513429	8621568	1	0	0	0	16	0	0	0	0	0	0	1	Q3TUE8	
ENSMUST00000115839	ENSMUSG00000057880	16	8513429	8621568	1	16	0	11	0	2	6	0	0	0	1	0		P61922
ENSMUST00000115841	ENSMUSG00000008658	16	6809222	7412479	1	4	0	15	31	9	1	0	0	0	0	0		Q9JJ43
ENSMUST00000115844	ENSMUSG00000022536	16	5013906	5049910	-1	24	0	0	0	0	0	1909	4858	2661	293	1752	D3YYT1	
ENSMUST00000115848	ENSMUSG00000059898	18	19960930	20002097	-1	22	21	28	19	30	10	0	0	0	0	0	G5E8S6	
ENSMUST00000115850	ENSMUSG00000024304	18	16588877	16809246	-1	3	0	0	0	3	0	0	0	0	0	13	D3YYT0	
ENSMUST00000115851	ENSMUSG00000063445	16	4710059	4719356	-1	3	0	2	0	6	0	25	25	25	40	3	G5E8S7	
ENSMUST00000115854	ENSMUSG00000004069	16	4639989	4707695	1	0	10	19	0	0	1	54	138	81	14	96	Q3TJA9	Q99M87
ENSMUST00000115857	ENSMUSG00000024430	18	12741324	12755146	1	8	7	0	23	0	0	0	4	0	0	1		Q9D424
ENSMUST00000115859	ENSMUSG00000005983	16	3895179	3908689	-1	80	68	169	86	63	43	29	71	40	8	75		Q8BT88
ENSMUST00000115860	ENSMUSG00000005982	16	3872375	3904780	1	0	0	15	16	0	6	1085	1861	9	0	0		Q9DBU2
ENSMUST00000115861	ENSMUSG00000041238	18	11633276	11743207	1	0	9	0	1	3	6	0	267	0	0	0		Q80YR6
ENSMUST00000115864	ENSMUSG00000024293	18	10566602	10610352	-1	0	0	0	0	0	0	14	0	0	0	0		Q69Z69
ENSMUST00000115869	ENSMUSG00000057440	18	7347962	7626863	-1	52	30	122	59	42	15	112	294	226	46	116	G5E8S8	
ENSMUST00000115870	ENSMUSG00000024240	18	6435951	6516108	-1	9	12	0	24	11	7	42	157	58	0	17		Q8C9X6
ENSMUST00000115885	ENSMUSG00000043051	8	125054195	125261858	1	0	0	0	0	0	0	0	0	0	0	0	Z4YLG9	
ENSMUST00000115891	ENSMUSG00000000103	Y	2106015	2170409	-1	1	4	0	1	3	0	0	0	0	0	0		P20662
ENSMUST00000115894	ENSMUSG00000069053	Y	818649	844224	1	608	560	1911	615	816	451	7	71	25	12	43		P31254
ENSMUST00000115902						3	4	0	0	16	0	0	0	0	0	0		
ENSMUST00000115904	ENSMUSG00000096506	JH584293.1	103128	104629	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000115907	ENSMUSG00000079773	GL456350.1	173252	174286	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000115912	ENSMUSG00000079774	GL456350.1	144079	149877	-1	4	0	1	0	0	0	0	0	0	0	4		A2APU8
ENSMUST00000115924	ENSMUSG00000079808	GL456212.1	128555	150452	-1	253	200	703	671	275	127	20	96	29	27	45		
ENSMUST00000115928	ENSMUSG00000094799	GL456210.1	147792	149707	1	2	0	0	8	3	5	0	0	0	0	0		
ENSMUST00000115931	ENSMUSG00000079794	GL456210.1	135395	136519	-1	1	0	4	0	1	1	0	2	2	0	0		
ENSMUST00000115940	ENSMUSG00000079806	Y	6680421	6682872	-1	0	0	0	0	0	0	0	0	0	0	0	J3KMI9	
ENSMUST00000115964	ENSMUSG00000079834	GL456233.1	159647	334183	1	82	85	386	97	80	34	3	14	6	19	13		Q91ZE0
ENSMUST00000115977						4	5	17	8	5	5	0	0	0	0	0		
ENSMUST00000115979	ENSMUSG00000084128	8	106130319	106136974	-1	15	13	33	235	29	6	6	20	18	6	18		Q8K0G8
ENSMUST00000115986						1	1	16	0	2	2	0	1	0	1	0		
ENSMUST00000115987						2	1	2	0	4	0	0	0	0	0	2		
ENSMUST00000115991	ENSMUSG00000079875	11	73954692	73955628	1	5	5	2	2	6	4	0	0	0	0	0		
ENSMUST00000115992						1	3	2	1	4	0	0	2	0	1	0		
ENSMUST00000115995	ENSMUSG00000024664	19	10041548	10059671	1	11	15	33	182	34	16	4	10	1	6	15	Q3T9H9	Q9JJE7
ENSMUST00000116005						6	3	9	8	10	5	12	5	11	14	6		
ENSMUST00000116006						18	13	139	24	18	8	0	8	1	0	2		
ENSMUST00000116008						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000116009						0	0	1	2	0	1	0	0	0	0	0		
ENSMUST00000116010						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000116022						6	4	9	4	5	2	3	4	2	1	1		
ENSMUST00000116032						9	2	12	7	5	3	1	3	0	0	1		
ENSMUST00000116034						0	0	0	4	2	0	1	0	0	0	1		
ENSMUST00000116054						7	1	16	5	8	2	0	0	0	0	0		
ENSMUST00000116058						0	0	0	0	0	0	0	0	2	7	7		
ENSMUST00000116078						0	1	4	3	12	4	1	0	0	10	0		
ENSMUST00000116079						2	5	5	7	4	0	0	0	0	0	0		
ENSMUST00000116081						0	2	7	3	2	0	0	2	2	1	0		
ENSMUST00000116082						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000116094	ENSMUSG00000070661	4	138967112	138968360	1	7	4	23	21	9	4	1	0	0	0	1	A2ALL3	
ENSMUST00000116102						12	10	38	320	45	23	49	82	38	22	56		
ENSMUST00000116105						4	5	3	2	4	3	0	4	0	2	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000116110						9	3	41	6	7	5	0	0	0	0	1		
ENSMUST00000116114						2	2	5	1	2	0	0	0	0	1	0		
ENSMUST00000116115						0	5	0	0	12	6	3109	7242	3244	15313	2174		
ENSMUST00000116118						9	5	15	4	8	4	0	0	0	1	1		
ENSMUST00000116122						5	3	3	1	5	2	2	0	0	5	1		
ENSMUST00000116133	ENSMUSG00000045005	1	64730558	64737751	-1	0	0	0	448	0	0	0	0	1	0	0		Q9EQD0
ENSMUST00000116136						4	5	8	2	12	4	8	6	11	11	9		
ENSMUST00000116160						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000116162						4	3	45	7	6	5	0	1	0	0	1		
ENSMUST00000116164						5	4	6	7	4	0	0	0	0	0	0		
ENSMUST00000116165						2	3	12	0	7	0	0	0	0	0	0		
ENSMUST00000116168						4	5	16	6	5	5	0	0	0	8	0		
ENSMUST00000116171						15	9	31	16	11	8	0	0	1	0	0		
ENSMUST00000116172	ENSMUSG00000080058	8	70699538	70700080	-1	0	0	0	6	0	0	402	492	498	219	446	Q3UXY7	
ENSMUST00000116174						4	2	16	2	11	5	0	6	10	9	5		
ENSMUST00000116179						5	6	17	7	10	10	0	0	0	0	0		
ENSMUST00000116183						4	4	2	2	5	0	0	0	0	0	0		
ENSMUST00000116185						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000116186						9	14	55	20	28	9	0	0	0	0	0		
ENSMUST00000116187						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000116189						1	3	1	9	4	1	1	0	0	0	0		
ENSMUST00000116191						32	36	96	44	34	15	0	0	55	19	106		
ENSMUST00000116229	ENSMUSG00000040415	10	127190378	127195728	-1	18	5	22	18	15	9	38	183	60	5	101	E9Q3J1	
ENSMUST00000116231	ENSMUSG00000080115	10	127031004	127041513	-1	106	122	293	245	115	61	5	13	6	2	16	D3YWP0	
ENSMUST00000116234	ENSMUSG00000060904	10	88730858	88744094	1	8	12	12	15	13	8	206	871	293	536	347	Q14AC7	P61211
ENSMUST00000116237						0	0	0	0	0	0	12	11	0	0	0		
ENSMUST00000116238	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	37	5	30	20	0	0	0	0	0		P17710
ENSMUST00000116247	ENSMUSG00000048200	7	141461094	141466613	1	49	38	95	0	35	35	1	25	4	2	8	F6VRL7	
ENSMUST00000116257	ENSMUSG00000028965	4	150914562	150946102	1	0	0	0	30	14	13	0	0	0	0	0	Q3U3R1	P20334
ENSMUST00000116259	ENSMUSG00000019996	10	20148471	20281589	1	20	10	25	5	29	6	10	27	10	1	7	D3YWN7	
ENSMUST00000116269	ENSMUSG00000030720	7	126571207	126585817	-1	0	0	0	0	0	0	0	0	0	0	0		Q61124
ENSMUST00000116273	ENSMUSG00000036940	4	136550540	136602723	-1	4	2	0	59	5	0	1	0	29	0	0		Q6ZQ88
ENSMUST00000116278						1	1	2	3	4	3	0	0	0	0	0		
ENSMUST00000116279	ENSMUSG00000046671	4	134525550	134535387	-1	0	8	0	0	0	0	327	459	269	100	141		Q9CWE0
ENSMUST00000116280	ENSMUSG00000030980	7	118842222	118856254	-1	48	43	92	0	44	25	66	271	110	68	160	E9QKQ3	
ENSMUST00000116284	ENSMUSG00000046793	3	108148321	108154882	-1	0	0	68	0	21	0	3	10	0	1	0		Q8C010
ENSMUST00000116286	ENSMUSG00000042608	4	126103957	126141029	1	30	0	52	14	21	0	191	299	270	0	289		Q7TNL3
ENSMUST00000116287	ENSMUSG00000030701	7	100642892	100662414	-1	0	0	0	0	7	5	0	0	0	0	0		Q9QYE9
ENSMUST00000116304	ENSMUSG00000038642	3	95526786	95556403	1	4	4	7	15	3	4	1113	5228	1587	15960	3399		O70370
ENSMUST00000116305	ENSMUSG00000025156	11	120784272	120789102	1	0	0	15	0	0	5	338	378	228	142	179	Q3MIA8	
ENSMUST00000116306						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000116307	ENSMUSG00000028601	4	108165437	108179308	1	0	0	0	0	0	0	0	0	0	0	5		Q3TLP5
ENSMUST00000116309	ENSMUSG00000028601	4	108165437	108179308	1	0	0	0	0	0	0	0	0	0	3	0		Q3TLP5
ENSMUST00000116315						13	4	22	27	10	6	0	0	0	0	0		
ENSMUST00000116316	ENSMUSG00000035126	4	103038065	103114555	-1	0	0	0	0	3	0	20	0	0	7	0		E9PYY5
ENSMUST00000116317	ENSMUSG00000028523	4	102986379	103005594	1	0	0	0	3	0	0	0	0	0	0	0	B7ZNE0	Q9D5I4
ENSMUST00000116318	ENSMUSG00000075410	11	116653534	116668389	1	2	3	9	0	0	0	0	0	0	0	0		Q00LT2
ENSMUST00000116324	ENSMUSG00000055102	7	43607169	43618285	1	7	5	26	0	1	0	2	0	5	3	0	Q80V81	
ENSMUST00000116341	ENSMUSG00000045973	4	45395923	45408766	-1	39	38	62	156	37	14	53	106	69	22	53		Q5HZI9
ENSMUST00000116343	ENSMUSG00000040857	7	25242561	25250761	-1	3	0	10	4	10	2	14	21	0	0	23	D3YXK6	
ENSMUST00000116349	ENSMUSG00000020868	11	94663851	94677515	-1	25	10	33	55	22	7	60	79	53	20	108		Q9EPL0
ENSMUST00000116350						2	0	0	0	4	1	0	0	0	0	0		
ENSMUST00000116354	ENSMUSG00000074406	7	4915217	4922003	1	18	11	87	457	27	15	277	312	193	22	157		Q8CJ78
ENSMUST00000116358	ENSMUSG00000023170	11	69913888	69916591	1	0	0	0	0	0	2	505	890	420	367	410	Q921N8	
ENSMUST00000116359	ENSMUSG00000020898	11	69015911	69036473	1	7	6	0	9	0	6	158	450	195	13	141		Q5SUQ9
ENSMUST00000116361						4	4	2	8	11	0	0	10	10	0	4		
ENSMUST00000116363	ENSMUSG00000020910	11	67037905	67052594	-1	0	0	0	0	0	0	229	1005	357	573	205		Q99KS6
ENSMUST00000116365	ENSMUSG00000000826	2	181520485	181555133	1	4	0	25	7	9	0	735	784	1394	161	1149	G5E8T0	
ENSMUST00000116366	ENSMUSG00000027582	2	181364928	181383628	1	0	0	7	0	0	0	296	741	348	56	357		Q8VDM1
ENSMUST00000116371	ENSMUSG00000005417	11	59661305	59780860	1	86	1	1	28	1	0	0	0	0	0	0		P97434
ENSMUST00000116375	ENSMUSG00000027498	2	172370681	172382448	1	22	15	70	95	39	17	219	357	220	67	204		Q99LC2
ENSMUST00000116376	ENSMUSG00000013646	11	58330724	58347728	1	5	0	42	0	0	0	409	313	199	47	199		Q99LH9
ENSMUST00000116378	ENSMUSG00000049321	11	50898712	50916165	-1	0	0	0	0	0	2	0	0	0	0	0		P08043
ENSMUST00000116380	ENSMUSG00000027642	2	157279017	157326319	1	0	0	0	64	27	11	98	221	172	18	171		Q9DBG6
ENSMUST00000116383						1	0	0	0	0	0	0	8	3	31	7		
ENSMUST00000116388	ENSMUSG00000037896	12	111039351	111115901	1	2	3	0	0	8	3	52	0	165	0	110		
ENSMUST00000116389	ENSMUSG00000027593	2	154791096	154867261	1	5	0	0	0	5	0	272	0	0	0	0		Q64012
ENSMUST00000116393						0	0	0	0	4	0	0	0	0	6	1		
ENSMUST00000116395						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000116400	ENSMUSG00000022992	15	98518821	98534244	-1	11	5	33	37	16	7	196	348	181	31	159		Q8BQR4
ENSMUST00000116402	ENSMUSG00000021255	12	86361117	86521628	1	52	19	61	10	30	5	0	0	0	0	0	E9QKA2	
ENSMUST00000116403	ENSMUSG00000021546	13	58391142	58403343	-1	6	0	6	36	9	13	60	0	41	0	40	Q5FWJ5	P61979
ENSMUST00000116408	ENSMUSG00000022475	15	97792664	97844502	-1	0	5	6	5	4	4	0	0	0	0	0		Q8C2B3
ENSMUST00000116409	ENSMUSG00000022475	15	97792664	97844502	-1	7	4	11	1	16	0	88	50	35	0	0		Q8C2B3
ENSMUST00000116410						8	6	10	8	8	3	0	2	0	2	1		
ENSMUST00000116412	ENSMUSG00000049482	8	122476143	122484138	1	0	0	13	96	5	0	130	143	80	26	110		Q3U308
ENSMUST00000116415	ENSMUSG00000031816	8	121091628	121108392	-1	5	0	0	0	0	6	31	43	30	8	14		Q3URQ7
ENSMUST00000116420	ENSMUSG00000034442	12	73280410	73286711	-1	8	8	8	3	7	3	14	63	19	83	19		Q9D0C4
ENSMUST00000116423	ENSMUSG00000022456	15	82274935	82294442	1	126	89	619	117	69	56	0	0	2	1	7		Q9Z1S5
ENSMUST00000116425	ENSMUSG00000031921	8	107069400	107096547	-1	18	4	12	132	28	12	9	27	22	0	9		O35144
ENSMUST00000116429	ENSMUSG00000017765	8	105943590	105966115	-1	23	21	46	0	44	0	88	50	54	7	138	Q3TWZ6	Q9JIS8
ENSMUST00000116432	ENSMUSG00000027246	2	121439010	121444278	-1	0	0	3	0	0	0	3	0	0	5	0		Q80VR2
ENSMUST00000116433	ENSMUSG00000021327	13	21387013	21402755	-1	0	0	0	0	0	0	0	2	0	0	3	Q5RJ53	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000116434	ENSMUSG00000021327	13	21387013	21402755	-1	0	0	0	18	3	0	42	291	152	65	171		
ENSMUST00000116436	ENSMUSG00000019256	12	35497974	35535038	-1	30	26	51	142	36	22	357	437	519	68	302	Q3U5D9	
ENSMUST00000116437	ENSMUSG00000027287	2	120567671	120601255	1	0	0	75	0	0	0	0	0	15	12	28	Q9D3L3	
ENSMUST00000116438						2	0	1	1	1	2	0	0	0	2	1		
ENSMUST00000116440	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	0	0	0	314	353	248	472	257		
ENSMUST00000116442	ENSMUSG00000028785	4	129111570	129122036	-1	4	7	27	43	6	6	0	0	0	0	0		P84075
ENSMUST00000116444	ENSMUSG00000028785	4	129111570	129122036	-1	3	4	9	21	14	6	0	0	0	0	0		P84075
ENSMUST00000116445	ENSMUSG00000051359	15	37366175	37792570	-1	0	0	0	0	0	0	0	0	0	0	0		Q91X97
ENSMUST00000116454	ENSMUSG00000038770	5	144983519	145084030	-1	18	2	0	1	0	0	0	2	0	0	0		C0LLJ0
ENSMUST00000116456	ENSMUSG00000018001	5	143622447	143710250	1	15	18	25	47	27	6	86	154	138	40	144	Q3TXK1	O08967
ENSMUST00000116457	ENSMUSG00000027215	2	93419111	93463140	-1	0	0	0	0	0	0	0	1877	0	140	0	Q3UII2	P40237
ENSMUST00000116463	ENSMUSG00000036180	8	69907069	69996379	-1	46	28	84	50	0	27	1419	2038	1184	162	828		Q8CHY6
ENSMUST00000116468	ENSMUSG00000079184	14	56668248	56697430	1	6	9	6	140	9	7	45	241	129	111	77		Q3TYA6
ENSMUST00000116469						0	1	0	0	0	0	0	2	0	0	1		
ENSMUST00000116473	ENSMUSG00000031640	8	45269442	45294859	-1	0	0	22	11	7	8	0	0	0	0	0		P26262
ENSMUST00000116474						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000116476	ENSMUSG00000022194	14	54892500	54898169	1	9	0	33	18	0	8	25	240	137	17	22		Q8CCS6
ENSMUST00000116491						5	1	16	9	10	5	0	0	3	0	1		
ENSMUST00000116492	ENSMUSG00000009741	9	113930934	113977199	1	0	0	0	3	0	1	175	0	167	0	214		Q811S7
ENSMUST00000116495	ENSMUSG00000079317	X	166440574	166453140	1	0	3	1	26	0	0	0	56	45	37	14	Q5J9A9	Q9CQP2
ENSMUST00000116499						3	0	6	0	2	2	0	0	0	0	0		
ENSMUST00000116506	ENSMUSG00000024989	19	38055025	38074425	1	0	1	3	0	0	0	0	17	50	33	15		Q8BT07
ENSMUST00000116514	ENSMUSG00000030216	6	136813654	136828233	-1	21	15	65	103	22	16	812	1628	1027	124	764		Q923D5
ENSMUST00000116515	ENSMUSG00000032641	6	134869093	134898578	-1	0	7	5	0	11	0	0	0	17	0	0		Q61121
ENSMUST00000116517	ENSMUSG00000032803	9	103353094	103365840	-1	91	49	109	125	99	25	0	0	0	0	0	F8WGL9	
ENSMUST00000116522	ENSMUSG00000032475	9	100492293	100546134	-1	7	5	3	47	15	11	23	124	73	97	62		Q99M51
ENSMUST00000116523						2	1	4	0	2	1	0	0	0	0	0		
ENSMUST00000116527	ENSMUSG00000047844	X	136138996	136140443	1	5	2	0	13	8	10	1	0	0	0	0	Q14BB8	Q9CWT2
ENSMUST00000116528	ENSMUSG00000026455	1	134455531	134491018	1	0	4	34	0	9	5	254	760	476	63	98		Q8BZM0
ENSMUST00000116535						0	0	6	2	5	3	0	1	0	0	0		
ENSMUST00000116542	ENSMUSG00000024742	19	10199132	10204169	-1	0	0	0	0	0	0	130	129	17	98	40	Q91Z50	
ENSMUST00000116543	ENSMUSG00000026858	2	30364233	30385521	1	6	0	10	2	1	0	1	0	0	0	0	H3BJU3	
ENSMUST00000116546	ENSMUSG00000069476	11	74069955	74087292	1	0	0	0	0	0	0	0	0	0	0	0	A7DTG8	
ENSMUST00000116547	ENSMUSG00000031327	X	103356476	103396092	1	85	95	200	455	135	74	6	28	11	10	32	A2RT09	Q8CBW7
ENSMUST00000116551	ENSMUSG00000038812	19	6909698	6911049	1	0	0	12	104	2	8	0	0	154	0	0		Q9DCG9
ENSMUST00000116552	ENSMUSG00000033543	9	70012550	70022866	1	0	0	0	0	0	0	44	279	61	22	27	Q05C74	
ENSMUST00000116553	ENSMUSG00000048764	5	86521898	86632424	-1	15	10	7	19	10	5	0	0	0	3	0		Q8BHM9
ENSMUST00000116556	ENSMUSG00000024101	17	66111546	66120503	1	221	185	232	109	183	118	195	188	221	0	87		Q8VDD8
ENSMUST00000116558	ENSMUSG00000024939	19	5728087	5729653	-1	0	0	3	8	10	0	269	277	133	0	126	Q05DI7	
ENSMUST00000116560	ENSMUSG00000056201	19	5490485	5494029	1	13	13	21	118	31	15	21531	48292	22043	12039	14850	F8WGL3	
ENSMUST00000116562						1	1	1	0	0	1	0	0	0	0	0		
ENSMUST00000116563	ENSMUSG00000024862	19	5107746	5118560	-1	5	6	18	296	41	16	57	194	145	0	137	Q91YS4	
ENSMUST00000116567	ENSMUSG00000080268	19	5041404	5049917	1	14	4	26	45	21	10	937	1095	661	434	489	Q547N0	Q99N20
ENSMUST00000116571	ENSMUSG00000054611	19	4314419	4398285	-1	5	4	2	10	1	0	0	4	0	0	4	A0A087WP68	
ENSMUST00000116574	ENSMUSG00000006476	2	25054355	25062881	1	0	0	0	0	0	0	0	0	0	0	0	F6TKU5	
ENSMUST00000116578	ENSMUSG00000031387	X	73922121	73930850	-1	0	0	0	0	0	2	77	134	26	41	87		P82343
ENSMUST00000116584	ENSMUSG00000022889	16	84717576	84735742	-1	28	12	30	131	41	32	50	317	117	229	97		Q9JKF7
ENSMUST00000116586	ENSMUSG00000052516	16	73892306	74411825	-1	10	11	31	30	16	5	0	0	0	1	0	E9PYK2	
ENSMUST00000116594	ENSMUSG00000061186	2	10370510	10595253	1	43	42	133	53	56	0	0	20	0	6	0	Q3UH07	
ENSMUST00000116595	ENSMUSG00000036309	11	52231995	52246858	1	0	0	0	0	0	0	5	100	0	12	0	F6TGP8	
ENSMUST00000116596	ENSMUSG00000023092	X	56731787	56793346	1	0	0	0	0	0	0	0	0	0	0	4		P97447
ENSMUST00000116598	ENSMUSG00000060550	17	35439155	35443773	1	3	3	5	386	3	0	41	0	0	27	24	L7N260	
ENSMUST00000116605	ENSMUSG00000029910	6	66535390	66547220	1	0	1	11	17	0	1	65	176	83	151	42	Q5HZH8	Q9Z1B5
ENSMUST00000116606						2	3	8	5	7	3	0	0	0	0	0		
ENSMUST00000116612	ENSMUSG00000039656	17	34031812	34038393	1	16	2	37	0	27	9	1174	1520	809	219	713		P28704
ENSMUST00000116613	ENSMUSG00000022245	9	63138170	63148961	-1	0	7	0	242	0	0	0	0	0	0	0	D3YX64	
ENSMUST00000116614	ENSMUSG00000068113	X	23882553	23907607	1	0	6	0	0	0	0	0	0	0	0	0	B1AXB9	
ENSMUST00000116615	ENSMUSG00000032033	9	31846044	31913462	-1	15	15	28	161	16	11	0	1	0	1	1		O08686
ENSMUST00000116619	ENSMUSG00000032739	17	33638056	33645706	1	8	13	17	31	15	5	874	1242	933	156	594	E9PYJ5	
ENSMUST00000116621	ENSMUSG00000031059	X	20615326	20617619	-1	13	2	13	33	8	3	1481	2411	1154	4757	702		O09111
ENSMUST00000116625	ENSMUSG00000022871	16	22918382	22939766	1	7	4	20	0	10	0	0	0	0	19	0	Q6YJU1	
ENSMUST00000116629	ENSMUSG00000037447	1	36307733	36324029	1	0	0	0	0	0	0	2101	2820	1672	197	1507	J3KMU9	
ENSMUST00000116633	ENSMUSG00000039382	X	7721973	7728201	1	0	0	0	3	0	0	0	0	0	0	0	A2AEV2	
ENSMUST00000116634	ENSMUSG00000039382	X	7721973	7728201	1	0	0	3	0	0	0	54	138	8	0	0	A2AEV5	
ENSMUST00000116639	ENSMUSG00000073565	18	51117898	51304641	1	5	3	41	36	10	5	0	0	0	1	0		A3KMN5
ENSMUST00000116640						4	4	1	2	2	1	0	2	0	1	0		
ENSMUST00000116641	ENSMUSG00000002279	17	25579174	25662826	1	0	0	6	0	0	0	21	23	21	9	38		Q3U3R4
ENSMUST00000116642						2	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000116643						49	15	247	81	55	30	0	0	0	0	0		
ENSMUST00000116648						8	0	15	9	14	6	4	4	2	0	0		
ENSMUST00000116649						4	5	3	4	2	0	0	2	0	0	0		
ENSMUST00000116652	ENSMUSG00000025902	1	4490931	4497354	-1	0	0	0	187	0	4	0	0	0	0	0		Q61473
ENSMUST00000116653	ENSMUSG00000024483	18	36559987	36665917	1	3	0	0	1	0	4	6	5	0	0	4	F6TF24	
ENSMUST00000116665						4	1	2	0	5	1	0	0	0	0	0		
ENSMUST00000116666	ENSMUSG00000055602	17	13061104	13082481	1	15	15	36	38	40	1	0	0	0	0	0	E9PYJ0	
ENSMUST00000116669	ENSMUSG00000047879	18	9995432	10045119	-1	0	1	0	0	0	2	31	99	0	13	0	E9PYI8	
ENSMUST00000116671						13	8	8	10	14	3	0	0	0	0	0		
ENSMUST00000117044	ENSMUSG00000022913	16	95979933	95990960	-1	5	0	0	10	3	0	0	0	11	12	0	D3Z795	
ENSMUST00000117045						0	0	0	0	0	0	392	681	369	1244	232		
ENSMUST00000117046						1	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000117047						2	1	1	3	0	1	1	4	1	1	2		
ENSMUST00000117049						4	1	2	2	1	0	0	0	0	0	0		
ENSMUST00000117050						32	9	91	45	35	31	0	0	0	0	0		
ENSMUST00000117051						0	2	3	4	2	0	0	2	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117052						1	2	0	0	8	0	0	0	0	0	0		
ENSMUST00000117053	ENSMUSG00000021081	12	103688044	103695529	-1	21	24	42	18	25	15	0	0	1	0	1	E9PUC6	
ENSMUST00000117055						2	5	10	12	5	4	0	0	0	0	0		
ENSMUST00000117056						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117057						1	5	4	4	3	1	1	2	2	0	5		
ENSMUST00000117058						5	6	13	8	1	1	53	56	63	1	34		
ENSMUST00000117059						1	2	1	3	2	0	0	0	0	0	0		
ENSMUST00000117060						10	9	22	26	42	7	1	0	1	0	3		
ENSMUST00000117061	ENSMUSG00000018398	11	53519257	53549565	1	25	0	36	18	41	12	14	0	0	0	26		Q8CHH9
ENSMUST00000117062						3	1	0	1	2	0	0	0	0	0	0		
ENSMUST00000117063						2	2	1	1	0	1	0	0	0	0	0		
ENSMUST00000117064	ENSMUSG00000050875	18	59062248	59076962	1	4	7	16	10	10	0	0	0	0	0	0	I1E4Y1	
ENSMUST00000117065						6	6	9	5	10	2	0	0	0	0	0		
ENSMUST00000117066	ENSMUSG00000017721	2	164497520	164508301	1	0	0	0	0	0	0	38	0	26	0	0	B7ZC19	
ENSMUST00000117067						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000117068						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000117069	ENSMUSG00000026035	1	58430994	58445486	-1	5	5	18	11	7	8	4	3	10	4	7		Q9D6L8
ENSMUST00000117070						0	4	1	1	2	2	0	0	0	0	0		
ENSMUST00000117071						16	20	32	47	29	6	2	2	0	4	2		
ENSMUST00000117072						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000117073	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9PX60	
ENSMUST00000117074						0	2	8	4	3	2	0	0	0	0	0		
ENSMUST00000117075						1	4	4	3	3	1	0	0	0	0	0		
ENSMUST00000117076						25	10	158	28	11	5	0	5	2	1	0		
ENSMUST00000117077	ENSMUSG00000031596	8	40862396	40922308	1	33	30	64	0	21	0	7	11	13	2	29		P18581
ENSMUST00000117078						3	2	1	1	2	1	0	0	0	0	0		
ENSMUST00000117079						34	24	67	41	35	12	0	0	0	0	0		
ENSMUST00000117080						4	3	6	3	0	3	0	0	0	0	0		
ENSMUST00000117081						7	4	21	9	6	2	0	0	0	0	0		
ENSMUST00000117082	ENSMUSG00000003166	16	17839482	17894145	-1	0	3	0	0	5	8	55	0	0	0	0	E9QNU3	
ENSMUST00000117083	ENSMUSG00000032386	9	65828930	65908794	-1	0	0	0	0	1	1	148	512	375	364	263		Q9QXN3
ENSMUST00000117084						0	2	4	0	3	1	0	0	0	0	0		
ENSMUST00000117085	ENSMUSG00000038459	7	84109356	84151893	-1	14	4	20	110	16	5	177	254	178	29	114		Q8VCV1
ENSMUST00000117086	ENSMUSG00000037846	10	67979570	68059740	1	0	0	8	0	0	0	9	8	10	3	5		Q14B46
ENSMUST00000117087						7	5	9	3	10	0	0	0	0	0	4		
ENSMUST00000117088						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117089	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVU6	
ENSMUST00000117090						2	3	4	0	2	0	0	0	0	0	0		
ENSMUST00000117091						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117092						1	0	0	56	2	1	0	0	0	0	0		
ENSMUST00000117093	ENSMUSG00000032064	9	50662752	50739517	-1	2	12	24	26	7	0	0	3	0	0	0		Q80Y83
ENSMUST00000117094						2	1	14	3	0	0	1	0	4	0	0		
ENSMUST00000117095	ENSMUSG00000003363	7	27532000	27553218	-1	6	0	0	0	0	11	570	517	485	109	469		O35405
ENSMUST00000117096	ENSMUSG00000021364	13	41182495	41220405	-1	0	0	9	33	23	15	0	0	0	0	0		
ENSMUST00000117097						2	1	3	6	8	4	0	0	0	0	0		
ENSMUST00000117098	ENSMUSG00000044681	5	28200819	28245792	-1	4	6	4	98	2	5	0	0	0	0	0		Q4VAB4
ENSMUST00000117099	ENSMUSG00000022945	16	93883901	93906115	1	6	5	0	2	0	0	0	87	52	0	28		Q9D0N7
ENSMUST00000117100	ENSMUSG00000022243	15	11000721	11029233	1	25	11	4	13	25	2	0	0	0	0	0	Q541S3	P58355
ENSMUST00000117101						2	4	4	2	3	0	0	0	0	2	2		
ENSMUST00000117102	ENSMUSG00000081683	5	128600844	128604093	1	13	14	56	331	25	6	0	0	0	0	0	Q149J3	Q8BKG4
ENSMUST00000117103						3	0	0	15	0	0	0	0	0	0	0		
ENSMUST00000117104						1	2	1	4	1	0	0	0	1	0	0		
ENSMUST00000117105						59	75	86	145	108	77	3	12	8	3	10		
ENSMUST00000117106						1	1	1	0	4	0	0	0	0	0	0		
ENSMUST00000117107						4	2	6	11	5	1	1	0	2	2	4		
ENSMUST00000117108	ENSMUSG00000034842	5	92331827	92414628	1	0	0	5	0	0	2	0	0	0	0	0	E9Q7Q8	
ENSMUST00000117109						18	14	191	28	13	20	1	2	1	0	3		
ENSMUST00000117110	ENSMUSG00000051037	13	67194506	67209298	1	0	4	0	2	6	2	2	0	0	0	2	Q8BMT6	
ENSMUST00000117111						3	3	1	0	6	2	0	0	0	0	0		
ENSMUST00000117112						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000117113						2	1	4	11	0	1	0	472	91	30	44		
ENSMUST00000117114						0	1	8	3	6	2	0	0	0	0	0		
ENSMUST00000117115						0	6	0	0	1	0	0	0	0	0	0		
ENSMUST00000117116						7	5	15	14	12	3	1	0	0	0	0		
ENSMUST00000117117						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000117118						6	6	54	8	11	2	0	0	1	0	0		
ENSMUST00000117119						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117120						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000117121						5	3	28	2	5	0	6	20	3	11	5		
ENSMUST00000117123	ENSMUSG00000017868	2	162987330	163014127	1	21	24	35	25	25	9	0	0	0	0	0		Q9QZS5
ENSMUST00000117124						20	26	203	30	12	8	0	0	1	0	0		
ENSMUST00000117125						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117126						1	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000117127						1	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000117128						1	1	7	6	9	1	0	0	0	0	0		
ENSMUST00000117129						1	0	0	0	6	1	326	0	751	164	711		
ENSMUST00000117130	ENSMUSG00000023349	6	123229843	123247021	1	0	0	0	0	0	0	0	0	0	0	0	Q3U3M9	
ENSMUST00000117131						2	8	7	10	7	0	0	0	0	4	2		
ENSMUST00000117132						0	0	0	0	0	0	0	0	0	6	0		
ENSMUST00000117133						0	3	0	1	1	0	0	6	3	4	2		
ENSMUST00000117134	ENSMUSG00000035506	16	33517328	33664135	1	0	2	5	1	2	0	0	0	0	1	0	D3YTS8	
ENSMUST00000117135						2	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000117136	ENSMUSG00000022671	16	15848441	15863369	-1	0	2	3	0	3	0	15	11	6	12	11		Q9CQ25
ENSMUST00000117137	ENSMUSG00000023914	17	43474324	43502812	-1	14	21	0	0	0	0	0	0	0	0	0		P28825

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117138	ENSMUSG00000008822	12	85272398	85288438	-1	2	2	17	41	3	2	3	3	0	0	0		P56376
ENSMUST00000117139						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000117140	ENSMUSG00000028468	4	43578715	43587487	1	0	0	0	71	7	0	0	0	11	0	6	Q3TDM6	
ENSMUST00000117141						5	8	11	4	0	1	0	0	0	0	0		
ENSMUST00000117142						4	0	2	2	0	9	2	0	0	5	0		
ENSMUST00000117143	ENSMUSG00000029352	5	113075839	113081584	-1	0	6	0	0	0	0	0	0	0	1	0		Q9JJU9
ENSMUST00000117144						3	2	2	1	0	0	0	0	1	0	0		
ENSMUST00000117145						1	3	5	2	3	3	0	1	3	5	0		
ENSMUST00000117146	ENSMUSG00000025939	1	16540790	16619489	-1	6	6	5	44	5	4	161	840	183	206	100	A0A0A0MQF3	
ENSMUST00000117147						0	1	4	5	1	1	0	0	1	0	0		
ENSMUST00000117148						1	0	1	9	1	0	170	474	186	331	129		
ENSMUST00000117149						3	4	18	1	3	1	1	0	0	0	0		
ENSMUST00000117150	ENSMUSG00000058388	3	103968110	104024598	1	3	4	21	14	9	4	43	220	129	39	100	Q5IBN5	Q9QZ09
ENSMUST00000117151						53	49	126	24	53	21	0	0	0	1	1		
ENSMUST00000117152						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117153						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117154						0	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000117155						0	0	1	0	0	0	33	66	31	93	10		
ENSMUST00000117156						1	0	1	1	3	1	0	0	0	0	0		
ENSMUST00000117157						7	5	3	3	5	8	0	0	0	0	0		
ENSMUST00000117158						0	1	0	24	1	1	0	0	4	0	0		
ENSMUST00000117159	ENSMUSG00000022960	16	91677268	91688765	-1	0	0	0	0	0	0	0	20	22	0	32	D3Z6I5	
ENSMUST00000117160	ENSMUSG00000031841	8	118283733	119324921	1	16	8	18	26	23	7	1	0	0	0	1		Q9WTR5
ENSMUST00000117161						3	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000117162						50	47	105	43	52	19	0	0	1	2	5		
ENSMUST00000117163						2	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000117164	ENSMUSG00000040998	3	132881745	132950291	-1	4	6	15	2	0	0	0	1	0	0	0		Q91V88
ENSMUST00000117165						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117166						10	8	26	11	7	6	0	0	0	0	0		
ENSMUST00000117167	ENSMUSG00000056071	3	90692632	90695721	-1	35	24	124	351	40	78	74051	405073	124291	584637	62482	Q3UP42	P31725
ENSMUST00000117168						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000117169						0	1	3	0	3	1	0	0	0	0	0		
ENSMUST00000117170						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000117171	ENSMUSG00000030170	6	119432531	119544347	-1	14	8	47	13	18	0	0	0	0	0	0		P22726
ENSMUST00000117172	ENSMUSG00000050122	1	37026596	37187613	1	7	6	0	0	0	6	0	0	0	0	0	Q8BH17	
ENSMUST00000117173	ENSMUSG00000043832	6	122952515	122969875	1	0	5	0	0	0	1	61	457	47	65	0	Q8JZX6	
ENSMUST00000117174						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000117176						5	4	0	6	8	2	0	3	4	3	3		
ENSMUST00000117177	ENSMUSG00000032850	5	118190736	118245116	-1	0	14	45	0	46	13	0	2	0	0	2		Q3UF64
ENSMUST00000117178						2	2	2	0	1	2	0	0	0	0	0		
ENSMUST00000117179	ENSMUSG00000031565	8	25513654	25575714	1	0	0	0	0	0	0	0	5	0	25	125	Q8CIM9	P16092
ENSMUST00000117180						0	3	2	0	1	0	0	0	0	0	0		
ENSMUST00000117181						1	8	19	5	2	6	0	0	0	0	0		
ENSMUST00000117182						2	1	4	4	3	5	0	0	0	0	0		
ENSMUST00000117183						4	2	5	6	3	1	0	0	0	0	0		
ENSMUST00000117184						1	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000117185						2	3	14	8	6	4	0	4	3	5	3		
ENSMUST00000117186						2	1	5	15	6	2	0	0	0	0	0		
ENSMUST00000117187						2	1	0	1	2	0	0	0	0	0	0		
ENSMUST00000117188						5	7	11	14	9	5	0	0	0	1	0		
ENSMUST00000117189	ENSMUSG00000054715	7	12897815	12909083	1	10	13	13	25	16	8	8	54	20	9	23	Q3TQC3	
ENSMUST00000117190						5	3	10	6	4	1	0	0	0	0	0		
ENSMUST00000117192	ENSMUSG00000022750	16	17759618	17793382	1	1	3	4	105	10	4	4	0	17	0	3	H9KV05	
ENSMUST00000117193	ENSMUSG00000001166	5	120800194	120812514	-1	20	9	28	16	25	8	64	275	110	180	108	Q924S2	
ENSMUST00000117194	ENSMUSG00000043987	9	45766946	45828691	-1	40	33	101	95	72	30	265	307	477	36	327	D3YVU3	
ENSMUST00000117195						12	15	10	13	17	14	1	4	0	0	6		
ENSMUST00000117196	ENSMUSG00000029283	5	106964322	106984432	1	0	0	0	0	0	0	9	19	22	1	0		Q9Z0H0
ENSMUST00000117197						6	0	0	2	5	0	0	0	0	0	0		
ENSMUST00000117198						4	1	2	2	3	1	1	3	1	7	2		
ENSMUST00000117199						1	3	0	0	2	1	0	2	1	1	1		
ENSMUST00000117200	ENSMUSG00000052516	16	73892306	74411825	-1	0	0	11	0	0	0	0	0	0	0	0	E9Q6A0	
ENSMUST00000117201						1	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000117202	ENSMUSG00000083929	4	42240639	42242685	1	16	16	40	39	14	4	0	6	0	1	1	Q8BQ57	
ENSMUST00000117203	ENSMUSG00000079487	X	101274030	101297465	1	0	0	0	0	0	0	4	0	280	0	4	A2AGH9	
ENSMUST00000117204						2	1	8	2	4	1	0	0	0	0	1		
ENSMUST00000117205						10	19	65	15	13	9	1	8	1	0	3		
ENSMUST00000117206						3	3	0	3	0	0	0	0	2	0	1		
ENSMUST00000117207						8	3	15	9	9	6	92	135	90	200	92		
ENSMUST00000117208						9	11	177	15	10	4	0	1	0	0	1		
ENSMUST00000117209						5	4	5	6	3	0	0	0	0	0	0		
ENSMUST00000117210						3	3	27	1	0	1	0	0	0	0	0		
ENSMUST00000117211						1	1	4	0	1	3	0	0	0	0	0		
ENSMUST00000117212						4	4	1	1	4	0	0	0	0	2	0		
ENSMUST00000117213						8	1	10	72	10	4	1	1	1	0	0		
ENSMUST00000117214						5	2	8	10	4	2	2	1	0	0	0		
ENSMUST00000117215						1	0	3	3	1	0	0	0	0	0	0		
ENSMUST00000117216						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000117217	ENSMUSG00000021224	12	83794034	83921934	-1	11	0	0	42	18	12	2126	4540	3011	371	1913		Q9QZS3
ENSMUST00000117218						6	2	12	6	4	6	0	0	0	0	0		
ENSMUST00000117219						11	7	4	8	6	4	18	48	31	125	39		
ENSMUST00000117220	ENSMUSG00000039200	16	10192712	10243051	1	4	0	0	0	0	0	0	0	0	0	0		Q3UL97
ENSMUST00000117221	ENSMUSG00000027849	3	103575231	103645569	1	0	0	0	26	0	0	0	0	0	0	0	Q6P1H9	Q9R0N8
ENSMUST00000117222	ENSMUSG00000044709	7	19564946	19573823	-1	7	3	12	40	7	4	38	90	30	19	40		Q9CWY4
ENSMUST00000117223	ENSMUSG00000027679	3	34056020	34081321	-1	3	1	0	0	0	0	0	0	2	13	9		Q9CQV7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117224						2	1	1	4	0	0	0	0	0	0	0		
ENSMUST00000117225						3	1	2	0	2	1	0	0	0	0	0		
ENSMUST00000117226						6	13	10	6	12	4	0	0	0	0	0		
ENSMUST00000117227						22	0	12	27	15	3	12	0	0	7	0		
ENSMUST00000117228						3	5	4	1	3	0	0	0	0	0	0		
ENSMUST00000117229						6	1	2	2	4	0	0	0	0	0	0		
ENSMUST00000117230						7	8	3	4	4	0	0	0	0	0	0		
ENSMUST00000117231						3	2	2	1	1	3	0	1	0	0	0		
ENSMUST00000117232						2	3	1	0	3	0	0	1	0	0	0		
ENSMUST00000117233						0	1	1	5	4	2	0	1	0	0	2		
ENSMUST00000117234						3	5	2	1	0	1	2	0	0	0	0		
ENSMUST00000117235						1	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000117236	ENSMUSG00000022214	14	55560006	55570065	1	0	5	0	4	3	0	360	796	319	109	239		Q91VU6
ENSMUST00000117237	ENSMUSG00000074994	2	104754795	104816696	-1	36	40	43	62	30	17	30	54	52	12	58	A2BIE1	
ENSMUST00000117238						1	3	4	2	5	1	0	0	0	0	0		
ENSMUST00000117239						8	7	11	6	11	8	0	0	0	0	0		
ENSMUST00000117240						8	2	31	3	5	4	1	0	0	5	2		
ENSMUST00000117241	ENSMUSG00000044934	13	64133022	64153202	-1	7	4	10	192	9	3	0	2	0	0	6		Q0VDT2
ENSMUST00000117242	ENSMUSG00000034109	3	75875084	75956949	-1	0	0	0	33	7	0	222	236	464	72	334	D3YVW2	
ENSMUST00000117243	ENSMUSG00000031516	8	34090420	34108796	-1	2	0	0	0	2	0	77	29	159	312	69	D3Z4E5	
ENSMUST00000117244						6	7	9	0	7	6	1	13	2	4	4		
ENSMUST00000117245	ENSMUSG00000026510	1	182409172	182462432	1	20	14	26	136	44	18	271	580	596	42	395	E9QJU8	
ENSMUST00000117246	ENSMUSG00000032235	9	69397906	69433122	1	2	0	0	0	0	2	0	0	0	0	0		Q3UZ18
ENSMUST00000117247						1	0	0	8	0	1	0	0	0	0	0		
ENSMUST00000117248						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117250						3	1	12	4	5	2	0	0	0	0	0		
ENSMUST00000117252	ENSMUSG00000054102	7	26535023	26575615	1	4	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000117253	ENSMUSG00000037605	5	81020138	81825133	1	10	7	0	2	9	0	0	0	0	0	0	D3YWR3	
ENSMUST00000117254	ENSMUSG00000046711	17	27556620	27563674	1	5	4	6	251	8	9	0	0	0	0	0	Q566K0	P17095
ENSMUST00000117255						41	31	42	98	38	47	1	0	1	2	3		
ENSMUST00000117256						1	1	0	1	4	3	0	0	0	0	0		
ENSMUST00000117257						11	8	29	31	13	2	0	0	0	0	0		
ENSMUST00000117258						5	2	1	2	1	0	0	0	0	0	1		
ENSMUST00000117259						4	4	0	5	2	3	0	0	0	0	0		
ENSMUST00000117260						1	1	6	66	6	2	0	0	0	0	0		
ENSMUST00000117261						4	5	8	5	3	2	0	0	0	0	0		
ENSMUST00000117262						0	2	4	10	4	0	15	289	63	36	70		
ENSMUST00000117263	ENSMUSG00000038569	5	122323223	122354233	-1	14	6	10	4	6	0	0	17	0	15	20	D3Z3W7	
ENSMUST00000117264						5	0	1	5	7	3	3	19	7	4	1		
ENSMUST00000117265						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000117266						0	2	4	0	0	0	0	0	0	0	0		
ENSMUST00000117267	ENSMUSG00000078880	2	176613364	176636344	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BHI0	
ENSMUST00000117268	ENSMUSG00000040550	4	14809498	14826587	-1	12	5	5	69	10	7	34	94	98	245	73	A0A0A0MQF5	
ENSMUST00000117269	ENSMUSG00000021277	12	111166370	111267153	1	0	0	0	120	0	0	0	69	81	0	0	Q3UHJ1	
ENSMUST00000117270	ENSMUSG00000031543	8	22974844	23150497	1	12	0	0	0	19	9	0	0	5	0	0	D3Z5M4	
ENSMUST00000117271	ENSMUSG00000087119	3	103643954	103646068	-1	6	2	0	0	2	2	0	0	5	0	4	A0A0G2JFS9	
ENSMUST00000117272						2	1	4	3	3	0	0	0	0	0	0		
ENSMUST00000117273						2	0	0	2	4	2	0	0	0	0	0		
ENSMUST00000117274	ENSMUSG00000035545	7	4137039	4148177	1	3	2	2	4	0	1	2	9	9	1	16		Q8CBY3
ENSMUST00000117275						1	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000117276	ENSMUSG00000046822	10	81028538	81037426	-1	11	16	63	281	32	0	97	48	107	0	22		Q99K24
ENSMUST00000117277						3	2	8	3	4	1	0	0	0	1	1		
ENSMUST00000117278	ENSMUSG00000032657	3	89183143	89189295	1	0	0	0	0	5	0	14	31	0	0	0	E9Q6C9	
ENSMUST00000117279						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117280	ENSMUSG00000028312	4	52439243	52488260	1	0	9	15	0	0	0	54	140	9	30	49		Q8CG48
ENSMUST00000117281						16	7	53	324	28	7	58	63	119	15	94		
ENSMUST00000117282	ENSMUSG00000038406	7	45002948	45016363	-1	0	0	0	0	0	4	971	1032	768	85	661		Q5U4C3
ENSMUST00000117283						0	1	0	0	2	0	0	1	0	0	1		
ENSMUST00000117284						2	0	3	2	2	3	0	0	0	0	0		
ENSMUST00000117285						1	2	11	3	11	2	0	0	0	0	0		
ENSMUST00000117286	ENSMUSG00000021236	12	84373857	84409029	-1	0	9	0	20	12	6	78	37	194	12	129		Q9WUZ9
ENSMUST00000117287						21	19	142	57	18	17	0	4	0	3	8		
ENSMUST00000117288						12	0	17	7	11	0	3791	3317	2145	11777	1663		
ENSMUST00000117289						2	1	11	2	3	1	0	0	0	0	0		
ENSMUST00000117290						4	5	0	3	2	1	0	0	0	0	0		
ENSMUST00000117291	ENSMUSG00000040675	10	3973118	4167081	1	19	0	25	114	15	14	91	166	36	30	54		Q3V3R1
ENSMUST00000117292						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000117293	ENSMUSG00000003382	3	87525407	87540156	1	0	2	0	0	0	0	10	24	17	1	10	D3YVU8	
ENSMUST00000117295						34	0	0	128	0	0	0	0	7	0	0		
ENSMUST00000117296	ENSMUSG00000031543	8	22974844	23150497	1	0	0	0	0	19	0	0	0	0	0	0	Q0VGY9	
ENSMUST00000117297						1	4	2	1	1	2	0	0	0	0	0		
ENSMUST00000117298						0	1	2	4	2	0	0	0	0	0	0		
ENSMUST00000117299	ENSMUSG00000076437	2	84669215	84670770	-1	3	4	10	46	3	8	114	199	78	103	13		Q3UQA7
ENSMUST00000117300						2	1	5	4	6	4	0	0	0	0	0		
ENSMUST00000117301	ENSMUSG00000003534	17	35681567	35704621	-1	14	0	65	52	26	16	0	0	0	0	0		Q03146
ENSMUST00000117302						4	0	2	0	4	1	0	0	0	0	0		
ENSMUST00000117303						0	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000117304						1	3	4	1	0	0	0	1	0	0	0		
ENSMUST00000117305						8	1	3	4	5	0	0	0	0	0	0		
ENSMUST00000117306						4	1	2	1	4	2	0	0	0	0	0		
ENSMUST00000117307						0	2	0	0	4	0	0	0	0	0	0		
ENSMUST00000117308						1	0	12	2	1	1	0	0	0	1	0		
ENSMUST00000117309						1	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000117310	ENSMUSG00000073008	X	107255878	107296769	1	0	0	0	1	0	1	0	0	0	0	0		Q3U507

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117311						1	2	4	4	4	3	0	0	0	0	0		
ENSMUST00000117312						6	4	11	3	3	3	0	0	0	0	0		
ENSMUST00000117313						1	0	0	0	1	1	0	1	0	0	0		
ENSMUST00000117314						0	0	2	0	3	3	13	0	0	16	7		
ENSMUST00000117315						2	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000117316	ENSMUSG00000081769	11	53783418	53859256	-1	1	6	33	6	22	2	0	7	0	1	3	A8Y5C0	
ENSMUST00000117317						10	6	6	11	12	4	5	2	3	3	0		
ENSMUST00000117318						7	7	10	12	13	6	0	0	2	0	1		
ENSMUST00000117319						4	3	21	5	4	1	6	20	12	0	25		
ENSMUST00000117320						3	3	2	0	2	1	0	0	0	2	0		
ENSMUST00000117321						1	0	0	1	1	0	0	1	1	2	2		
ENSMUST00000117322						2	1	3	1	1	0	0	1	1	1	0		
ENSMUST00000117324	ENSMUSG00000038695	7	44467980	44471662	1	0	0	0	0	0	0	75	100	12	0	14		Q9CR30
ENSMUST00000117325						2	2	2	2	1	2	0	0	0	0	0		
ENSMUST00000117326						2	2	6	2	6	1	0	0	0	0	0		
ENSMUST00000117327						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000117328						6	3	5	4	1	1	0	0	3	0	0		
ENSMUST00000117330	ENSMUSG00000009828	9	78109192	78172107	1	8	5	10	5	8	10	0	0	0	0	0	Q3UZZ3	
ENSMUST00000117331						1	1	3	2	1	1	0	0	0	0	0		
ENSMUST00000117332						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000117333						4	1	3	0	3	0	0	0	0	0	0		
ENSMUST00000117334						1	0	0	4	2	0	0	0	0	0	0		
ENSMUST00000117335						9	6	2	8	6	2	0	0	2	0	0		
ENSMUST00000117337	ENSMUSG00000024130	17	24351950	24410201	1	21	7	0	11	20	0	243	717	233	27	420	Q6AXE3	
ENSMUST00000117338	ENSMUSG00000040811	7	19176421	19206482	1	11	0	14	114	11	3	0	15	0	0	11	E9QK48	
ENSMUST00000117339						44	8	30	43	33	13	0	0	0	0	0		
ENSMUST00000117340						1	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000117341	ENSMUSG00000036580	3	55112108	55137322	1	13	16	39	20	22	17	2	0	0	0	0	D3Z3F8	
ENSMUST00000117342						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117343						9	4	8	10	14	6	0	0	0	0	0		
ENSMUST00000117344						1	1	1	2	0	2	0	0	0	0	0		
ENSMUST00000117345						6	2	3	4	3	0	0	0	2	0	0		
ENSMUST00000117346	ENSMUSG00000037418	19	9985174	10001633	-1	22	9	25	15	13	9	0	3	0	2	0		O88870
ENSMUST00000117347						0	3	3	1	1	1	0	1	0	1	0		
ENSMUST00000117348						2	3	2	0	1	2	0	0	0	0	0		
ENSMUST00000117349	ENSMUSG00000084387	11	73433291	73434224	-1	0	8	3	2	4	4	0	0	0	0	0	Q8VGT2	
ENSMUST00000117350	ENSMUSG00000040928	4	129148005	129189727	-1	4	3	9	2	6	9	3	0	3	0	7		Q9D5K4
ENSMUST00000117351						0	2	2	3	2	2	0	0	0	0	0		
ENSMUST00000117352						4	7	0	4	6	0	0	0	0	0	0		
ENSMUST00000117353						1	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000117354	ENSMUSG00000062797	7	89917529	89941199	-1	2	1	7	11	0	0	13	76	27	43	20	D3YU13	
ENSMUST00000117355	ENSMUSG00000005625	3	95032694	95042614	-1	0	0	0	0	0	0	20	201	12	3	26		O35226
ENSMUST00000117356						3	1	4	0	3	0	184	376	108	1035	145		
ENSMUST00000117357	ENSMUSG00000030849	7	130162451	133123350	-1	0	1	4	0	0	0	0	0	0	0	0	E9PX90	
ENSMUST00000117358						1	0	4	1	6	1	0	0	0	0	0		
ENSMUST00000117359						6	0	0	14	0	0	0	0	0	0	0		
ENSMUST00000117360	ENSMUSG00000022500	16	10959275	11066157	-1	2	0	5	2	5	0	143	44	80	77	252		Q9JLJ0
ENSMUST00000117361	ENSMUSG00000044252	18	12755314	12941841	-1	2	2	1	5	0	0	0	0	0	0	0		Q91XL9
ENSMUST00000117362						9	3	28	10	4	3	0	3	7	0	1		
ENSMUST00000117363	ENSMUSG00000022538	16	30560494	30587592	-1	13	4	32	13	17	14	0	0	13	6	12		Q3UM18
ENSMUST00000117364	ENSMUSG00000035234	5	100805192	100820965	-1	0	0	0	0	0	0	0	0	0	17	7		Q8BPZ8
ENSMUST00000117365						8	4	17	18	6	6	0	2	1	0	0		
ENSMUST00000117366	ENSMUSG00000030826	7	45570153	45589710	1	0	3	6	1	4	7	0	0	0	0	0	O88374	
ENSMUST00000117367						0	0	3	4	3	0	0	0	0	0	0		
ENSMUST00000117368						5	3	10	1	5	0	0	0	0	0	0		
ENSMUST00000117369						0	0	0	0	2	10	0	0	0	0	0		
ENSMUST00000117371						5	1	9	10	6	7	0	0	0	0	0		
ENSMUST00000117372						2	0	7	4	7	1	0	2	0	0	0		
ENSMUST00000117373	ENSMUSG00000027750	3	54361109	54391037	1	16	0	14	0	9	5	0	0	0	5	0		Q62009
ENSMUST00000117374						3	1	2	0	5	0	1	0	1	0	0		
ENSMUST00000117375	ENSMUSG00000038074	6	54577604	54597308	-1	2	0	0	0	0	3	0	0	0	0	0	D3YWB6	
ENSMUST00000117376						2	1	2	3	1	1	0	0	0	0	0		
ENSMUST00000117377	ENSMUSG00000054162	8	62951009	63357103	1	3	0	0	4	0	1	0	0	0	0	0		Q8BKV0
ENSMUST00000117378						5	3	18	5	10	3	0	0	0	0	0		
ENSMUST00000117379	ENSMUSG00000089773	4	112006269	112029538	1	3	2	4	2	0	0	0	0	0	0	0		A7TZE6
ENSMUST00000117380						1	1	1	2	3	0	0	0	0	0	0		
ENSMUST00000117381						11	4	15	4	10	3	0	1	0	0	0		
ENSMUST00000117382						1	0	6	2	4	1	0	0	0	0	0		
ENSMUST00000117383	ENSMUSG00000025724	7	80904889	80947780	-1	0	0	0	6	0	0	33	91	45	65	76	D3Z569	
ENSMUST00000117384						7	12	2	5	5	5	1	3	0	0	1		
ENSMUST00000117385						5	7	10	11	3	4	0	0	0	0	1		
ENSMUST00000117386	ENSMUSG00000039376	14	20658946	20668354	-1	0	5	144	155	15	7	0	0	0	0	0	B2RQK7	
ENSMUST00000117387						3	2	47	35	6	2	0	0	1	0	2		
ENSMUST00000117388	ENSMUSG00000029228	5	74592447	74702912	-1	0	4	4	8	5	0	6	0	19	3	25		O70263
ENSMUST00000117389	ENSMUSG00000042496	9	31280538	31378543	1	5	0	6	24	3	3	9	14	36	1	22		Q3UTQ7
ENSMUST00000117390						1	5	23	1	4	4	1	0	0	0	0		
ENSMUST00000117391						2	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000117392	ENSMUSG00000045374	11	75440944	75454717	-1	0	25	73	0	0	11	1228	480	902	45	54	K4DI77	
ENSMUST00000117393						1	5	3	1	1	1	0	0	0	0	0		
ENSMUST00000117394	ENSMUSG00000059981	7	126865678	126884703	-1	27	11	48	94	44	12	576	1029	916	74	915		Q6ZQ29
ENSMUST00000117395						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117396	ENSMUSG00000015880	5	45669919	45700546	1	5	2	7	53	7	1	71	135	105	66	28	E9PWG6	
ENSMUST00000117397						32	44	38	110	23	24	0	11	2	1	4		
ENSMUST00000117398						4	1	27	6	5	5	10	36	15	5	21		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117399	ENSMUSG00000031207	X	96096042	96168552	1	14	15	35	95	46	27	19877	47012	31740	4836	23856		P26041
ENSMUST00000117400	ENSMUSG00000005649	7	13398132	13408887	1	1	9	6	2	3	4	0	0	0	0	0	D3YWT5	
ENSMUST00000117401						7	5	3	4	4	2	0	0	0	0	0		
ENSMUST00000117402						2	0	4	2	2	0	3	2	3	0	2		
ENSMUST00000117403						0	1	0	0	0	0	0	0	0	1	0		
ENSMUST00000117404	ENSMUSG00000040139	7	137375574	137410762	-1	16	10	13	10	0	1	9	5	2	7	6	D3YTU4	
ENSMUST00000117405						15	7	15	40	64	17	4202	18395	9712	6023	7656		
ENSMUST00000117406	ENSMUSG00000023289	6	42038394	42042851	1	1	2	5	0	2	1	0	0	0	0	0	E9PX96	
ENSMUST00000117407	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0		Q80TS3
ENSMUST00000117408						1	1	0	1	3	0	0	0	0	0	0		
ENSMUST00000117409	ENSMUSG00000048997	3	108202222	108210934	-1	0	0	0	28	0	0	0	48	23	0	0	B7ZCC3	
ENSMUST00000117410	ENSMUSG00000046027	7	83631959	83653127	1	15	25	265	38	29	22	59	263	63	50	134	D3YU00	
ENSMUST00000117411	ENSMUSG00000029911	6	40471352	40484700	1	0	0	0	0	1	0	46	223	83	220	63	Q8R2K3	
ENSMUST00000117413	ENSMUSG00000034087	7	10687793	10730168	1	12	0	8	0	0	0	0	0	0	0	0		Q8C6J9
ENSMUST00000117414						5	6	12	6	4	4	0	0	0	0	0		
ENSMUST00000117415	ENSMUSG00000056763	1	10037987	10136768	1	0	0	1	0	0	0	0	0	0	0	0		B2RX88
ENSMUST00000117416						1	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000117417						15	11	230	18	28	11	0	1	0	1	0		
ENSMUST00000117418						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000117419	ENSMUSG00000040940	7	24902912	24926594	1	0	0	0	0	0	0	6653	89	39	0	3		Q61210
ENSMUST00000117420	ENSMUSG00000021699	13	108449948	109953461	1	1	1	0	1	0	0	0	0	0	0	0	A6XDB0	
ENSMUST00000117421						2	3	4	1	3	1	0	0	0	0	0		
ENSMUST00000117422	ENSMUSG00000035041	10	81084324	81098874	-1	17	12	60	50	17	14	17	72	22	30	13		Q91XE9
ENSMUST00000117423	ENSMUSG00000021693	13	106958996	107022126	-1	0	0	0	0	0	0	229	898	736	127	195		P28740
ENSMUST00000117424	ENSMUSG00000036686	8	84132828	84147936	-1	20	4	6	3	29	8	0	42	0	0	0	E9PX94	
ENSMUST00000117425	ENSMUSG00000015806	5	45434021	45450236	-1	7	0	13	5	4	0	17	23	10	21	5	D3YWR7	
ENSMUST00000117426						0	4	3	1	4	0	0	0	0	0	0		
ENSMUST00000117427						3	3	12	2	7	3	0	0	0	0	0		
ENSMUST00000117428						7	6	3	1	6	4	0	0	0	0	0		
ENSMUST00000117429						2	1	16	2	1	0	0	0	0	0	0		
ENSMUST00000117430						0	0	0	2	2	0	15	0	0	19	8		
ENSMUST00000117431						0	1	0	0	3	1	0	0	0	0	0		
ENSMUST00000117432						1	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000117433						2	1	9	1	2	2	0	0	0	0	0		
ENSMUST00000117434						6	5	7	5	1	5	0	0	0	0	0		
ENSMUST00000117435						0	0	0	0	0	0	87	0	62	84	19		
ENSMUST00000117436						4	1	1	8	2	0	1	0	2	0	0		
ENSMUST00000117437						0	0	1	0	0	0	0	0	0	0	1		
ENSMUST00000117438	ENSMUSG00000026019	1	60069785	60098645	-1	1	2	6	163	6	3	0	32	8	32	8	Q4V9X1	Q9JJA4
ENSMUST00000117439						10	12	52	3	8	5	0	0	1	0	0		
ENSMUST00000117440	ENSMUSG00000060002	10	88452745	88504073	-1	93	96	288	76	83	42	13	54	14	4	22	D3YU39	
ENSMUST00000117441	ENSMUSG00000018341	6	67291318	67376188	-1	41	30	224	197	70	34	4	14	8	0	5	D3Z6H5	
ENSMUST00000117442	ENSMUSG00000016257	2	174465067	174473081	-1	2	0	4	0	0	0	17	298	55	106	51	B0QZU2	
ENSMUST00000117443						3	3	1	2	7	4	0	0	0	0	0		
ENSMUST00000117444						1	1	2	2	1	1	212	801	248	1450	181		
ENSMUST00000117445	ENSMUSG00000069825	11	73329741	73355913	1	33	41	94	34	30	18	7	25	7	3	13	B0QZP0	
ENSMUST00000117446	ENSMUSG00000020415	11	43420250	43426251	-1	35	20	174	82	31	28	6	73	5	5	25		Q9CQJ7
ENSMUST00000117447						0	0	0	0	0	0	1	14	0	4	0		
ENSMUST00000117448						72	49	53	2793	129	54	0	3	0	0	2		
ENSMUST00000117449	ENSMUSG00000005078	12	72085589	72101461	1	9	8	11	3	9	6	47	284	49	151	70		Q8BI36
ENSMUST00000117450	ENSMUSG00000011958	9	69989466	70008317	1	5	5	0	7	10	4	12	70	79	21	135	G5E8U9	
ENSMUST00000117451						6	5	9	6	9	4	0	0	0	0	0		
ENSMUST00000117452	ENSMUSG00000053550	7	4825552	4844696	-1	13	6	112	0	12	0	0	0	0	0	0	F6T9T6	
ENSMUST00000117453						3	3	1	2	3	0	0	0	0	0	0		
ENSMUST00000117454						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000117455	ENSMUSG00000029269	5	87513339	87538195	-1	0	3	0	0	0	5	0	0	0	0	0		Q9QWG7
ENSMUST00000117456	ENSMUSG00000040998	3	132881745	132950291	-1	7	10	0	17	0	31	0	0	0	9	0	D3YTX1	
ENSMUST00000117457						7	5	26	107	12	4	0	0	0	0	0		
ENSMUST00000117458						0	2	6	0	0	0	0	0	0	0	0		
ENSMUST00000117459						23	15	29	16	26	10	1	0	0	0	1		
ENSMUST00000117460	ENSMUSG00000020023	10	94311949	94590956	1	0	0	0	0	0	0	0	0	1	0	0		Q8R310
ENSMUST00000117461						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117462	ENSMUSG00000041845	19	4425459	4439432	-1	5	6	9	25	14	3	0	0	0	0	3	G3X9Y4	
ENSMUST00000117463	ENSMUSG00000040429	5	3890581	3893933	-1	18	18	42	58	23	19	7	71	22	45	18		Q8CHZ9
ENSMUST00000117464						2	3	2	6	1	3	3	2	6	7	3		
ENSMUST00000117465						15	6	95	15	7	3	0	0	0	0	0		
ENSMUST00000117466						0	1	4	1	1	1	0	0	0	0	0		
ENSMUST00000117467	ENSMUSG00000026705	1	161088375	161131511	-1	0	0	0	0	0	0	0	0	5	0	0		Q8VCK5
ENSMUST00000117468	ENSMUSG00000022604	16	55899888	55934855	-1	0	0	0	0	0	0	3	6	8	13	7		Q9CZ62
ENSMUST00000117469						0	1	0	67	0	0	151	1108	255	354	126		
ENSMUST00000117470						3	2	7	3	6	7	0	0	0	0	0		
ENSMUST00000117471						2	2	1	1	5	2	0	0	0	0	0		
ENSMUST00000117472						5016	7598	5468	24643	26406	3946	3111	4649	11179	19360	5283		
ENSMUST00000117473						4	3	2	1	2	4	0	0	0	0	0		
ENSMUST00000117474						2	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000117475						2	0	0	4	1	2	0	0	0	0	0		
ENSMUST00000117476						1	2	0	0	3	0	5	3	0	17	0		
ENSMUST00000117477						3	3	0	3	3	1	0	0	0	0	0		
ENSMUST00000117478						6	2	1	3	4	1	0	0	0	0	0		
ENSMUST00000117479						2	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000117480						3	1	6	2	3	1	0	0	0	0	0		
ENSMUST00000117481						19	17	0	0	16	6	0	0	0	0	0		
ENSMUST00000117482						6	2	8	2	1	0	0	0	0	0	0		
ENSMUST00000117483						0	0	0	0	1	0	9	5	78	3	42		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117484						14	7	18	18	15	9	0	0	0	0	0		
ENSMUST00000117485						2	3	4	0	0	0	0	0	1	7	1		
ENSMUST00000117486	ENSMUSG00000026835	2	28076378	28084885	-1	0	0	11	4	1	4	85	36	121	104	36	Q3U9R5	
ENSMUST00000117487						5	3	4	75	4	2	2	1	0	0	0		
ENSMUST00000117488	ENSMUSG00000004933	10	81252935	81263365	1	3	2	7	44	6	1	0	0	0	0	14		
ENSMUST00000117489	ENSMUSG00000061759	10	4432467	4455141	1	0	0	0	0	0	0	0	0	0	0	0		A6H630
ENSMUST00000117490						2	5	1	0	4	1	0	0	0	0	0		
ENSMUST00000117491						2	7	6	0	8	0	0	1	0	3	0		
ENSMUST00000117492	ENSMUSG00000025437	3	152346478	152393617	1	0	5	20	6	4	1	322	1108	676	317	574		Q8R5K2
ENSMUST00000117493						2	1	6	3	3	1	0	0	0	0	0		
ENSMUST00000117494						2	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000117495						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000117496						5	7	6	2	0	0	0	0	0	0	0		
ENSMUST00000117497	ENSMUSG00000040928	4	129148005	129189727	-1	0	0	0	0	0	0	0	0	17	5	8	E9Q5M3	
ENSMUST00000117498						2	2	15	6	7	5	0	0	0	0	0		
ENSMUST00000117499						10	1	8	39	2	2	0	3	1	0	1		
ENSMUST00000117500						6	3	0	2	1	0	1	12	6	0	4		
ENSMUST00000117501						3	3	4	0	1	3	0	0	0	0	0		
ENSMUST00000117502						1	2	4	0	3	0	0	0	0	0	0		
ENSMUST00000117503						0	3	13	2	2	0	0	0	0	1	0		
ENSMUST00000117504						3	6	11	46	8	1	0	0	0	1	0		
ENSMUST00000117505						0	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000117506	ENSMUSG00000059890	9	44923131	44965600	-1	17	13	16	18	19	12	582	1970	794	182	470		E9Q735
ENSMUST00000117507	ENSMUSG00000028108	3	95734147	95739569	-1	1	4	37	2	15	12	1334	438	1196	354	1699		Q61508
ENSMUST00000117508						1	1	1	3	2	0	0	0	0	0	0		
ENSMUST00000117509	ENSMUSG00000024163	17	24892153	24936977	-1	1	2	0	0	1	0	0	0	0	0	0		Q9ESN9
ENSMUST00000117510	ENSMUSG00000049041	11	73983662	73990290	-1	0	10	7	10	9	4	0	0	0	0	0	Q8VFY0	
ENSMUST00000117511						8	5	15	8	10	2	0	0	0	0	0		
ENSMUST00000117512						4	8	7	6	10	9	1	2	0	1	1		
ENSMUST00000117513	ENSMUSG00000020100	10	60712072	60752794	-1	200	179	322	180	222	82	328	474	297	46	231		Q99P65
ENSMUST00000117514						11	7	33	12	16	6	1	3	2	0	7		
ENSMUST00000117515						2	3	3	4	5	0	0	0	0	0	0		
ENSMUST00000117516						13	12	29	0	8	18	0	198	174	194	0		
ENSMUST00000117517						0	0	9	25	0	0	0	0	0	0	0		
ENSMUST00000117518	ENSMUSG00000030861	7	131410601	131446211	1	6	9	3	10	11	0	16	22	57	10	42	E9Q5L3	
ENSMUST00000117519						3	1	0	4	1	0	0	0	0	0	0		
ENSMUST00000117520						2	2	0	2	1	1	0	0	0	0	0		
ENSMUST00000117521						2	2	2	1	1	0	0	0	0	0	0		
ENSMUST00000117522						10	12	8	9	15	6	0	0	0	0	0		
ENSMUST00000117523						2	1	5	7	5	1	0	0	0	0	0		
ENSMUST00000117524						5	1	5	5	1	3	0	0	0	0	0		
ENSMUST00000117525	ENSMUSG00000029228	5	74592447	74702912	-1	0	0	0	0	0	0	0	2	0	0	0	A4QPD4	O70263
ENSMUST00000117526						2	5	5	4	2	7	0	0	0	0	0		
ENSMUST00000117527						4	0	0	0	4	2	0	0	0	5	6		
ENSMUST00000117528						0	4	1	2	4	0	0	0	0	0	0		
ENSMUST00000117529	ENSMUSG00000027601	3	19187327	19220817	1	4	3	10	2	0	0	0	1	52	0	0	Q3TTQ5	Q99MB2
ENSMUST00000117530						3	4	4	3	1	2	0	0	0	0	0		
ENSMUST00000117531						3	4	0	0	1	0	0	0	0	2	0		
ENSMUST00000117532						8	4	12	3	8	5	0	0	0	0	0		
ENSMUST00000117533						3	3	6	0	2	0	0	0	0	0	0		
ENSMUST00000117534	ENSMUSG00000031749	8	110919922	110972480	1	5	7	5	0	4	6	48	8	14	4	24	D3Z3V2	
ENSMUST00000117535						16	13	65	18	22	0	0	0	0	0	0		
ENSMUST00000117536	ENSMUSG00000029247	5	76951307	76967509	1	0	12	3	0	4	0	116	506	191	996	253		Q9DCL9
ENSMUST00000117537	ENSMUSG00000032507	9	113963637	114046191	-1	0	0	0	21	0	0	21	0	0	5	24	Q4VA21	Q8BH16
ENSMUST00000117538						5	2	6	3	6	4	0	0	0	0	0		
ENSMUST00000117539	ENSMUSG00000021693	13	106958996	107022126	-1	4	2	1	4	2	1	60	49	62	57	86	F8VQ42	
ENSMUST00000117540						2	2	1	2	1	1	1	0	0	0	0		
ENSMUST00000117541						1	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000117542						2	0	3	0	0	0	43	211	0	0	0		
ENSMUST00000117543	ENSMUSG00000048782	7	114743694	114850383	1	0	5	23	6	0	0	0	0	0	0	0	G3UW77	
ENSMUST00000117544	ENSMUSG00000073294	X	6081219	6083419	-1	6	0	27	239	12	6	0	0	0	0	0	B1B0V2	
ENSMUST00000117545						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117546						9	3	0	57	0	7	24	8	15	52	30		
ENSMUST00000117547						1	0	2	4	2	1	0	0	0	0	0		
ENSMUST00000117548						3	0	0	2	0	0	0	0	7	0	0		
ENSMUST00000117549	ENSMUSG00000059890	9	44923131	44965600	-1	1	0	14	9	6	3	227	269	643	75	533	G3X9Y5	
ENSMUST00000117550	ENSMUSG00000070873	7	4237754	4243463	1	8	7	13	13	8	10	3	10	1	90	15	D3Z7A9	
ENSMUST00000117551	ENSMUSG00000031453	8	13566950	13677603	-1	26	22	34	98	31	13	3608	4194	4828	494	4742		Q60790
ENSMUST00000117552						3	0	9	7	0	0	0	0	0	0	0		
ENSMUST00000117553						6	4	9	8	8	3	0	0	0	0	0		
ENSMUST00000117554						1	4	7	6	1	3	0	0	0	0	0		
ENSMUST00000117555	ENSMUSG00000053687	8	105984944	105996423	-1	1	2	0	3	0	3	127	698	74	318	46		Q8C255
ENSMUST00000117556	ENSMUSG00000063455	6	38123174	38254009	-1	23	22	10	12	0	0	0	3	0	0	0	D3YTS3	
ENSMUST00000117557	ENSMUSG00000015656	9	40800984	40805200	1	3	27	15	0	0	9	2602	8279	6083	5873	5931	Q504P4	
ENSMUST00000117558						1	1	2	28	4	0	0	1	1	0	1		
ENSMUST00000117559						1	2	1	4	3	0	2	3	1	7	2		
ENSMUST00000117560						0	1	0	1	3	1	0	0	0	1	0		
ENSMUST00000117561						3	4	6	9	7	1	0	0	0	0	0		
ENSMUST00000117562						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117563						2	2	15	9	4	0	37	494	0	230	83		
ENSMUST00000117564	ENSMUSG00000079173	5	137378637	137477064	-1	16	13	177	23	24	13	0	0	0	0	1	E9PWQ7	
ENSMUST00000117565	ENSMUSG00000031489	8	27225776	27229588	-1	2	2	19	293	9	4	0	0	0	0	0		P25962
ENSMUST00000117566	ENSMUSG00000036585	18	38838673	38929404	-1	0	0	0	0	0	0	0	0	0	0	1	D3Z6H1	
ENSMUST00000117567						16	4	27	74	14	8	0	1	3	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117568						1	0	4	3	2	0	0	0	0	0	0		
ENSMUST00000117569						1	3	1	1	6	2	0	0	0	0	0		
ENSMUST00000117570						10	11	10	5	8	2	0	1	1	0	0		
ENSMUST00000117571						1	1	2	2	1	1	212	801	248	1450	181		
ENSMUST00000117572						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000117573						17	13	46	24	12	12	0	0	0	0	0		
ENSMUST00000117574						0	0	3	4	0	0	0	0	0	0	0		
ENSMUST00000117575						8	10	18	5	12	1	0	0	1	0	0		
ENSMUST00000117576						123	112	264	1214	163	85	2	7	2	0	3		
ENSMUST00000117577	ENSMUSG00000038187	7	113315626	113369392	-1	3	4	0	1	16	0	0	0	0	0	0	E9Q6Y9	
ENSMUST00000117578						2	2	5	4	2	0	0	0	0	0	0		
ENSMUST00000117579	ENSMUSG00000060002	10	88452745	88504073	-1	3	1	0	0	6	2	0	0	0	0	0	D3Z6W4	
ENSMUST00000117580	ENSMUSG00000055553	8	70508272	70527956	-1	0	0	0	42	0	0	3	5	5	1	5	D3YWA5	
ENSMUST00000117581						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000117582						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117583	ENSMUSG00000029993	6	87009236	87028461	1	0	0	0	0	0	0	115	343	171	351	102		Q9QZ23
ENSMUST00000117584						7	3	9	9	4	3	0	0	0	0	0		
ENSMUST00000117585						3	2	6	13	1	6	1	1	1	0	1		
ENSMUST00000117586						2	5	1	1	2	2	0	0	0	0	0		
ENSMUST00000117587						42	29	157	61	41	19	0	1	1	0	0		
ENSMUST00000117588	ENSMUSG00000043410	5	106840192	106926321	-1	8	6	1	12	8	7	0	0	0	0	0		D3Z4R1
ENSMUST00000117589	ENSMUSG00000020738	11	115523102	115536276	-1	0	17	0	4	0	0	11	24	0	0	0	D3YW94	
ENSMUST00000117590						0	0	0	1	1	0	1	0	2	0	6		
ENSMUST00000117591						7	4	22	18	10	4	5	11	1	2	2		
ENSMUST00000117592	ENSMUSG00000080907	3	116968267	116984406	1	5	4	4	14	4	0	0	0	0	0	0	D3Z622	
ENSMUST00000117593	ENSMUSG00000014767	17	15499888	15528379	1	1	1	2	70	3	2	0	0	5	0	0	Q6RI65	P29037
ENSMUST00000117594						5	2	2	11	3	3	0	3	1	0	1		
ENSMUST00000117595						4	3	4	12	4	0	0	1	0	0	1		
ENSMUST00000117596						6	6	4	1	8	1	0	0	0	0	0		
ENSMUST00000117597	ENSMUSG00000001786	10	86021972	86051873	1	0	7	0	0	3	3	66	304	79	35	79	Q3UGI9	
ENSMUST00000117598	ENSMUSG00000033653	16	21423118	21644680	1	0	0	0	0	0	0	80	221	256	0	222		Q0P5W1
ENSMUST00000117599						3	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000117600	ENSMUSG00000046711	17	27556620	27563674	1	5	8	0	58	0	4	12	21	11	17	38	Q566K0	P17095
ENSMUST00000117601	ENSMUSG00000037736	5	66745827	67057158	1	10	0	6	0	0	0	0	0	0	0	2	D3Z589	
ENSMUST00000117602						1	2	4	0	1	0	0	82	0	3	0		
ENSMUST00000117603						43	39	338	28	31	29	0	0	2	0	2		
ENSMUST00000117605						1	0	0	3	1	2	0	0	0	0	0		
ENSMUST00000117606	ENSMUSG00000023902	17	23600856	23611019	1	0	2	0	0	0	2	0	2	0	2	0	D3YWR9	
ENSMUST00000117607						2	2	5	1	17	3	0	0	0	0	0		
ENSMUST00000117608						0	1	9	5	2	2	0	0	0	0	0		
ENSMUST00000117609						1	2	4	1	2	3	0	0	0	0	0		
ENSMUST00000117610	ENSMUSG00000032235	9	69397906	69433122	1	0	0	0	0	2	0	0	0	0	0	0	B0V2N3	
ENSMUST00000117611	ENSMUSG00000003363	7	27532000	27553218	-1	0	6	12	40	18	0	66	0	0	0	0		O35405
ENSMUST00000117612						2	3	7	5	8	3	0	0	0	0	0		
ENSMUST00000117613						22	13	12	0	30	8	0	0	0	0	0		
ENSMUST00000117614						6	5	26	9	9	6	1	3	0	5	1		
ENSMUST00000117616						1	4	1	0	1	0	0	0	0	0	0		
ENSMUST00000117617						10	3	17	10	7	5	0	0	0	0	0		
ENSMUST00000117618						1	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000117619						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117620	ENSMUSG00000031933	9	14885814	14903949	-1	5	8	2	6	3	0	0	0	2	0	0	G5E8D3	
ENSMUST00000117621						2	3	0	5	1	0	0	0	2	12	2		
ENSMUST00000117622						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000117623						7	0	14	6	0	1	0	0	0	0	0		
ENSMUST00000117624	ENSMUSG00000037300	8	124671335	124721983	-1	8	0	15	11	0	5	100	183	152	51	113	D3YVV0	
ENSMUST00000117625						3	0	7	7	4	8	0	0	0	0	1		
ENSMUST00000117626						1	3	4	1	1	4	0	0	1	0	1		
ENSMUST00000117627						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000117628						13	22	22	274	26	16	3	0	0	0	0		
ENSMUST00000117629						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117630						1	2	3	0	0	0	0	0	0	0	0		
ENSMUST00000117631						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000117632	ENSMUSG00000073988	4	20007938	20030785	1	0	0	0	92	6	0	0	0	0	0	0	A2AIT6	
ENSMUST00000117633	ENSMUSG00000022961	16	91647506	91679221	1	0	8	0	104	0	7	115	0	100	51	169	H9KV00	
ENSMUST00000117634	ENSMUSG00000025511	7	141475240	141493427	1	0	0	22	10	5	2	37	29	6	83	64	Q4FJW7	Q9DCK3
ENSMUST00000117635						0	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000117636						0	0	2	5	2	0	0	1	0	0	0		
ENSMUST00000117637	ENSMUSG00000031310	X	101404384	101420849	-1	0	0	0	0	0	0	0	0	22	14	0	Q32P02	
ENSMUST00000117638	ENSMUSG00000062518	4	147673502	147702553	-1	13	19	10	15	6	12	0	0	0	0	0	A2A7A1	
ENSMUST00000117639						3	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000117640						3	3	1	4	2	1	0	0	0	1	0		
ENSMUST00000117641	ENSMUSG00000024663	19	10001669	10038380	1	3	3	0	0	0	0	16	14	4	2	68	D3Z585	
ENSMUST00000117642						74	96	444	70	34	34	0	32	35	1	0		
ENSMUST00000117643	ENSMUSG00000001062	8	123242356	123254348	-1	0	0	0	0	0	0	0	0	0	0	0	Q3U280	
ENSMUST00000117644	ENSMUSG00000058240	16	91689322	91728975	-1	0	2	0	0	0	0	52	64	39	106	5	D3Z6I4	
ENSMUST00000117645	ENSMUSG00000049624	9	78536488	78588041	-1	14	22	24	0	44	22	0	211	0	0	1		Q8BN82
ENSMUST00000117646	ENSMUSG00000032064	9	50662752	50739517	-1	14	2	2	46	20	6	0	1	1	1	0		Q80Y83
ENSMUST00000117647						0	1	3	0	1	0	0	1	1	0	0		
ENSMUST00000117648	ENSMUSG00000040785	16	94370618	94469222	1	12	20	14	36	12	0	16	64	38	54	97	G5E8T2	
ENSMUST00000117649						7	3	10	3	3	4	0	0	0	0	0		
ENSMUST00000117650						26	20	17	15	21	16	0	0	0	0	1		
ENSMUST00000117651						3	5	2	1	2	0	0	0	0	0	0		
ENSMUST00000117653						2	3	0	0	3	0	0	0	0	0	0		
ENSMUST00000117654	ENSMUSG00000011114	9	37649182	37657312	-1	8	0	8	64	0	3	545	1092	765	381	644		Q3UB74

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117655						0	11	53	374	19	6	0	5	3	0	0		
ENSMUST00000117656						15	13	62	23	37	19	1	2	4	0	4		
ENSMUST00000117657						0	1	0	2	2	1	0	0	0	0	0		
ENSMUST00000117658	ENSMUSG00000043051	8	125054195	125261858	1	0	0	0	33	4	0	0	3	0	0	3		Q811T9
ENSMUST00000117659						2	2	7	1	1	1	0	0	0	0	0		
ENSMUST00000117660						0	0	3	4	3	0	0	0	0	0	0		
ENSMUST00000117661	ENSMUSG00000039156	5	53998499	54121057	1	11	11	7	56	8	5	10	41	24	0	10	A5CVE4	P83093
ENSMUST00000117662	ENSMUSG00000031543	8	22974844	23150497	1	0	11	21	21	2	7	0	0	0	0	0	E9QNT8	
ENSMUST00000117663						5	2	2	5	5	2	0	0	0	0	0		
ENSMUST00000117664						0	0	0	0	0	0	2	153	191	708	146		
ENSMUST00000117665						2	3	3	1	2	6	0	2	0	1	3		
ENSMUST00000117666						2	3	6	6	4	1	0	0	0	0	0		
ENSMUST00000117667						130	77	205	778	189	68	2	4	0	2	3		
ENSMUST00000117668						4	3	3	1	3	1	0	0	0	0	0		
ENSMUST00000117669						17	25	57	12	21	6	2	0	2	0	1		
ENSMUST00000117670						1	2	1	2	2	0	0	0	0	0	0		
ENSMUST00000117672	ENSMUSG00000005936	17	28951950	28969549	1	4	0	0	1	0	0	0	0	0	7	0		Q8CDD8
ENSMUST00000117673						1	0	2	5	1	0	0	1	1	1	0		
ENSMUST00000117674						1	0	4	0	0	0	14	0	13	2	16		
ENSMUST00000117675	ENSMUSG00000038271	6	125145241	125161782	1	0	0	0	0	0	0	43	0	0	0	0	D3Z7B0	Q8BXL9
ENSMUST00000117676	ENSMUSG00000019775	10	5825663	5922400	-1	84	55	30	171	67	81	3	34	9	5	5		Q9QZB0
ENSMUST00000117677						2	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000117678						3	6	10	5	5	2	0	0	0	0	0		
ENSMUST00000117679						0	3	1	1	4	0	0	0	0	0	2		
ENSMUST00000117680						0	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000117681						4	3	2	0	2	1	0	0	0	0	0		
ENSMUST00000117682						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000117683						4	12	4	4	7	3	0	0	0	0	0		
ENSMUST00000117684						1	2	3	1	3	1	0	0	0	0	0		
ENSMUST00000117685						9	5	59	9	17	6	0	0	0	0	0		
ENSMUST00000117686						5	7	3	4	4	4	0	0	0	0	0		
ENSMUST00000117687	ENSMUSG00000024500	18	42637432	43059471	-1	0	6	0	0	0	8	0	0	0	0	0		Q6ZWR4
ENSMUST00000117688	ENSMUSG00000029685	6	24528144	24573164	1	17	17	19	10	29	14	0	0	0	0	0		Q8VHS6
ENSMUST00000117689						3	3	8	3	3	1	0	0	0	0	0		
ENSMUST00000117690						0	0	0	0	3	2	0	0	0	2	0		
ENSMUST00000117691	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	17	E9Q7E8	
ENSMUST00000117692	ENSMUSG00000024511	18	69979131	70141605	-1	0	0	0	0	12	0	0	0	0	0	0	Q549X4	Q99P58
ENSMUST00000117693						0	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000117694	ENSMUSG00000046610	18	65698268	65751601	1	14	0	123	44	0	0	0	2	0	0	2	E9Q6M1	
ENSMUST00000117695	ENSMUSG00000061132	19	40928927	40994535	-1	3	4	22	9	10	8	8	7	14	4	12	D3YWR2	
ENSMUST00000117696						6	3	10	2	4	3	0	0	0	1	0		
ENSMUST00000117697						5	3	3	4	1	0	0	0	0	0	0		
ENSMUST00000117698						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117699	ENSMUSG00000070687	4	136423524	136444398	1	8	15	60	17	10	10	0	0	0	0	0		Q61224
ENSMUST00000117700						25	33	33	37	50	19	7	7	5	4	18		
ENSMUST00000117701	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4U8	
ENSMUST00000117702	ENSMUSG00000019478	8	123805985	123835287	1	3	0	17	2	4	4	0	2	4	0	2		P56371
ENSMUST00000117703						0	1	1	1	3	0	0	0	0	0	0		
ENSMUST00000117704						0	7	1	3	2	1	0	0	0	0	0		
ENSMUST00000117706	ENSMUSG00000079487	X	101274030	101297465	1	0	0	0	102	31	0	70	114	204	0	282	A2AGH8	
ENSMUST00000117707						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000117708						2	1	14	0	0	0	0	0	0	1	3		
ENSMUST00000117709						5	0	3	2	1	0	0	0	0	0	0		
ENSMUST00000117710	ENSMUSG00000020267	11	54866383	54870501	1	3	2	17	8	5	1	4	2	0	2	0	B0R1E3	
ENSMUST00000117711						8	7	13	23	18	6	0	0	0	0	0		
ENSMUST00000117712						1	5	2	9	5	0	0	0	0	0	0		
ENSMUST00000117713	ENSMUSG00000004071	16	4750348	4790292	-1	1	0	0	0	1	0	35	5	17	17	49		Q9DB75
ENSMUST00000117714						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117715						1	0	2	3	7	0	3	12	4	0	1		
ENSMUST00000117716						3	1	8	2	4	0	2	0	0	0	0		
ENSMUST00000117717						6	1	5	2	2	1	0	0	0	0	0		
ENSMUST00000117718	ENSMUSG00000031070	7	145300828	145309557	1	0	14	21	7	28	13	0	0	0	5	1	D3Z3Y0	
ENSMUST00000117719						1	1	1	6	1	0	0	0	0	0	0		
ENSMUST00000117720						3	1	8	4	3	0	0	0	1	0	1		
ENSMUST00000117721	ENSMUSG00000021327	13	21387013	21402755	-1	528	458	1470	723	610	274	161	321	399	53	272	D3YTV4	
ENSMUST00000117722						2	2	2	1	3	2	0	0	1	0	1		
ENSMUST00000117723						0	0	0	0	0	0	0	1	0	4	0		
ENSMUST00000117724						57	59	471	73	36	32	1	1	0	0	1		
ENSMUST00000117725	ENSMUSG00000016552	15	77940522	77956722	-1	11	0	33	0	5	2	0	0	0	0	38		Q3USW5
ENSMUST00000117726	ENSMUSG00000002475	18	10644411	10706771	-1	0	0	0	0	0	0	0	0	0	0	0	D3YU06	
ENSMUST00000117727						4	2	5	5	2	2	0	0	0	0	0		
ENSMUST00000117728	ENSMUSG00000027660	3	31095058	31122577	1	2	0	0	0	0	0	17	1	94	0	30	D3Z7C5	
ENSMUST00000117729						1	1	0	2	3	1	0	0	0	0	0		
ENSMUST00000117730						1	0	0	0	0	1	0	720	0	6	0		
ENSMUST00000117731	ENSMUSG00000025576	11	118489762	118911597	-1	9	4	0	119	27	11	0	0	0	0	0		Q8BIF2
ENSMUST00000117732						8	3	4	10	8	3	14	3	9	12	7		
ENSMUST00000117733						5	5	32	3	5	2	0	0	0	0	0		
ENSMUST00000117734						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117735	ENSMUSG00000045636	8	40990914	41133726	-1	3	1	6	18	5	1	30	62	104	19	157	D3Z7B3	
ENSMUST00000117736	ENSMUSG00000092463	X	101261405	101269023	-1	2	0	0	0	0	0	0	0	0	2	0	A2AGH5	
ENSMUST00000117737						0	1	4	4	4	0	0	0	0	0	0		
ENSMUST00000117738						1	1	3	1	2	2	0	0	0	0	0		
ENSMUST00000117739						22	12	31	10	22	1	0	0	0	0	0		
ENSMUST00000117740						2	1	8	2	4	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117741						1	1	3	0	1	0	0	0	0	0	0		
ENSMUST00000117742						7	4	13	10	4	4	0	0	0	0	0		
ENSMUST00000117743	ENSMUSG00000002814	11	60740058	60777365	-1	0	14	6	0	0	0	0	0	18	0	0	Q5NCT0	
ENSMUST00000117744						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117745						4	1	6	2	2	1	0	0	0	0	0		
ENSMUST00000117746						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117747						49	42	184	71	57	33	0	0	0	0	0		
ENSMUST00000117748	ENSMUSG00000022967	16	91485238	91507441	1	0	16	11	22	0	0	274	711	303	55	192		P33896
ENSMUST00000117749						4	2	4	5	2	0	0	1	0	0	1		
ENSMUST00000117750						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000117751						0	5	7	5	0	2	0	1	0	0	0		
ENSMUST00000117752						3	0	3	1	3	0	0	0	1	1	0		
ENSMUST00000117753						2	0	0	4	4	0	0	0	0	0	0		
ENSMUST00000117754	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7E6	
ENSMUST00000117755						7	6	8	5	3	4	0	0	0	0	0		
ENSMUST00000117756						10	6	29	20	9	5	1	0	0	0	1		
ENSMUST00000117757	ENSMUSG00000057666	6	125161715	125166467	-1	0	42	0	0	0	11	12828	6133	5667	5754	3146	A0A0A0MQF6	
ENSMUST00000117758						2	2	3	2	2	4	0	0	0	0	0		
ENSMUST00000117759	ENSMUSG00000063406	5	108106366	108132620	-1	0	1	4	39	4	0	0	4	28	79	37	Q3V440	
ENSMUST00000117760						8	2	6	7	10	3	0	0	0	0	0		
ENSMUST00000117761						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000117762	ENSMUSG00000030830	7	127296260	127335138	1	2	11	0	26	0	0	2758	2955	1738	14	1603	E9QNL8	
ENSMUST00000117763						4	3	0	4	3	3	0	0	0	0	0		
ENSMUST00000117765						15	9	21	37	28	15	0	0	0	0	0		
ENSMUST00000117766	ENSMUSG00000029486	5	96209493	96266727	1	0	0	35	28	0	0	0	0	0	56	0		Q99N96
ENSMUST00000117767						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000117768						0	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000117769						3	2	1	1	9	4	0	0	0	0	0		
ENSMUST00000117770						8	8	57	19	17	7	0	0	0	0	0		
ENSMUST00000117771						5	4	7	10	5	5	0	0	0	0	0		
ENSMUST00000117772						0	0	0	0	0	0	3	69	24	55	32		
ENSMUST00000117773						1	0	12	2	2	0	0	0	0	0	0		
ENSMUST00000117774						2	1	6	0	4	1	0	1	0	0	0		
ENSMUST00000117775	ENSMUSG00000036810	8	88118769	88135110	1	0	0	0	0	0	0	2	6	0	7	0	D3Z6J3	
ENSMUST00000117776						1	0	0	7	2	1	0	0	0	0	0		
ENSMUST00000117777						0	0	0	5	0	1	0	0	0	0	0		
ENSMUST00000117778						7	2	4	8	7	4	0	0	0	0	0		
ENSMUST00000117779						0	2	14	2	6	0	1	0	0	0	0		
ENSMUST00000117780	ENSMUSG00000020894	11	69088490	69092384	1	5	3	9	15	1	4	52	228	101	8	181	B0QZN5	
ENSMUST00000117781	ENSMUSG00000050106	11	117782076	117793110	1	0	0	3	0	0	0	0	0	68	8	106	B0QZP7	
ENSMUST00000117782	ENSMUSG00000015850	3	95676201	95687917	-1	21	0	31	142	42	20	281	79	465	22	170		Q80T21
ENSMUST00000117783	ENSMUSG00000028999	5	23787711	23820369	1	21	17	25	23	15	7	5	16	16	3	13	D3YU07	
ENSMUST00000117784	ENSMUSG00000048997	3	108202222	108210934	-1	0	0	0	0	0	0	97	83	73	0	88	Q8C8K6	
ENSMUST00000117785	ENSMUSG00000052516	16	73892306	74411825	-1	15	12	18	3	11	4	0	0	0	0	0	Q19AB2	
ENSMUST00000117786	ENSMUSG00000022433	15	79417856	79443919	-1	73	55	56	402	113	50	492	1693	748	90	854		Q9JMK2
ENSMUST00000117787						7	5	19	8	12	2	0	0	0	0	0		
ENSMUST00000117788						1	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000117789						10	6	20	5	7	1	1	1	0	1	0		
ENSMUST00000117790						3	1	2	1	3	1	0	0	0	0	0		
ENSMUST00000117791						2	3	1	2	5	3	0	0	0	0	0		
ENSMUST00000117792						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000117793						1	2	1	1	0	1	0	0	0	0	0		
ENSMUST00000117794						5	4	8	0	10	5	0	0	0	0	0		
ENSMUST00000117795						1	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000117796	ENSMUSG00000040940	7	24902912	24926594	1	0	0	0	54	21	0	48	461	289	0	315	E9PUF7	
ENSMUST00000117797						4	2	2	2	4	1	0	0	0	0	0		
ENSMUST00000117798	ENSMUSG00000034949	10	81233155	81252123	1	0	0	0	0	5	10	4	4	0	0	4	E9Q5M4	
ENSMUST00000117799						5	11	19	10	5	8	0	0	0	0	0		
ENSMUST00000117800						2	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000117801	ENSMUSG00000005580	16	4287529	4420498	-1	0	0	75	19	36	0	0	0	0	0	0		P51830
ENSMUST00000117802						0	1	0	0	0	0	0	1	0	0	0		
ENSMUST00000117803	ENSMUSG00000065968	16	13981702	13986855	-1	67	59	128	58	104	49	4	6	5	3	3	G3X9Z2	
ENSMUST00000117804						5	3	6	3	4	2	0	0	0	2	0		
ENSMUST00000117805	ENSMUSG00000048240	10	80948624	81014945	-1	28	0	0	41	0	0	0	0	0	0	0	Q3UGN1	Q61016
ENSMUST00000117806						7	4	3	5	3	4	0	1	0	0	0		
ENSMUST00000117807						7	5	13	3	5	8	0	0	0	0	0		
ENSMUST00000117808						0	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000117809						1	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000117810						4	7	13	5	3	0	0	3	0	1	4		
ENSMUST00000117811	ENSMUSG00000040998	3	132881745	132950291	-1	19	0	44	99	0	0	0	0	0	0	0	D3Z4D3	
ENSMUST00000117812	ENSMUSG00000030452	7	55931287	55962476	-1	0	0	0	0	0	0	87	133	147	45	55		Q9JJC8
ENSMUST00000117813						2	3	14	0	3	2	0	0	0	0	4		
ENSMUST00000117814	ENSMUSG00000026270	1	92934376	92947941	1	9	3	2	21	11	6	11	31	18	10	24	Q9CPY2	
ENSMUST00000117815						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117816						1	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000117817						3	2	4	5	1	1	0	0	0	0	0		
ENSMUST00000117818	ENSMUSG00000020741	11	74649495	74670847	1	0	0	0	6	15	0	12	0	27	0	64	Z4YLI8	
ENSMUST00000117819						3	0	3	0	2	0	0	0	0	0	0		
ENSMUST00000117820						1	0	2	2	1	2	0	0	0	0	0		
ENSMUST00000117821						6	3	4	5	4	0	0	0	1	0	0		
ENSMUST00000117822						1	0	1	2	3	0	0	0	0	0	0		
ENSMUST00000117823						3	1	27	3	4	0	0	0	0	0	0		
ENSMUST00000117824						5	3	4	0	3	2	0	0	0	0	0		
ENSMUST00000117825						0	1	3	3	5	3	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117826						4	1	11	4	2	2	0	0	1	0	0		
ENSMUST00000117827						36	43	181	38	43	26	3	5	2	0	4		
ENSMUST00000117828	ENSMUSG00000002475	18	10644411	10706771	-1	8	0	0	113	17	0	0	0	0	0	0	D3Z6Y2	
ENSMUST00000117829						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117830	ENSMUSG00000029911	6	40471352	40484700	1	3	0	0	0	0	0	0	7	0	0	0	D3Z3Y3	
ENSMUST00000117831	ENSMUSG00000024847	19	4114446	4125858	-1	0	2	9	8	6	2	162	223	90	17	54		O08915
ENSMUST00000117832						1	3	2	3	5	1	0	0	0	0	0		
ENSMUST00000117833						1	2	4	1	2	3	0	0	0	0	0		
ENSMUST00000117834						7	2	1	5	6	4	0	0	0	0	0		
ENSMUST00000117835						4	5	16	9	6	2	0	1	0	0	0		
ENSMUST00000117836	ENSMUSG00000022971	16	91372783	91405589	1	2	0	0	6	5	0	424	1581	354	179	210	Q9D1R7	O35664
ENSMUST00000117837						3	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000117838						0	3	10	4	4	1	0	1	1	0	1		
ENSMUST00000117839						4	1	2	1	3	3	0	0	0	0	0		
ENSMUST00000117840						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000117842						6	10	1	8	12	9	1	0	1	4	1		
ENSMUST00000117843						4	7	9	8	1	6	0	0	0	0	0		
ENSMUST00000117845	ENSMUSG00000037101	8	78213297	78394326	1	0	0	4	0	0	1	0	0	0	0	0		Q80VM3
ENSMUST00000117846						1	0	9	2	1	1	0	0	0	0	0		
ENSMUST00000117847						7	2	14	4	11	6	1	0	0	0	1		
ENSMUST00000117848						1	1	2	7	1	0	0	2	0	1	0		
ENSMUST00000117849	ENSMUSG00000032384	9	65908924	66045015	1	18	17	41	59	39	22	26	0	72	2	48	Q6P2B2	
ENSMUST00000117850						10	4	12	7	9	2	0	0	0	0	0		
ENSMUST00000117851						9	3	9	9	0	1	1	5	1	9	5		
ENSMUST00000117852	ENSMUSG00000039428	7	89139723	89404222	-1	5	13	6	11	14	5	0	4	0	0	2	Q8C8G3	
ENSMUST00000117853						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000117854						7	1	6	10	5	3	0	1	1	0	1		
ENSMUST00000117855						7	2	7	3	2	1	1	0	1	0	3		
ENSMUST00000117856						49	67	112	44	43	15	0	0	2	0	3		
ENSMUST00000117857						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000117858	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9PX67	
ENSMUST00000117859	ENSMUSG00000052563	11	51650954	51657681	1	32	22	106	92	48	13	2	10	0	1	9	B0QZN8	
ENSMUST00000117860						4	0	1	3	4	1	0	0	0	0	0		
ENSMUST00000117861						2	0	3	0	3	0	0	0	0	0	0		
ENSMUST00000117862						9	1	13	6	8	3	0	0	0	0	0		
ENSMUST00000117863						6	1	8	4	9	2	0	0	1	0	0		
ENSMUST00000117864						25	10	63	238	27	8	0	4	1	0	0		
ENSMUST00000117865						1	1	1	39	2	3	0	0	0	0	0		
ENSMUST00000117866						4	3	0	2	0	3	0	0	0	0	0		
ENSMUST00000117867						2	2	3	4	2	0	0	0	0	0	0		
ENSMUST00000117868	ENSMUSG00000029462	5	122354369	122364984	1	3	2	0	3	1	0	62	82	63	633	90	D3Z645	
ENSMUST00000117869						7	1	1	1	5	5	0	0	0	0	0		
ENSMUST00000117870	ENSMUSG00000015656	9	40800984	40805200	1	0	0	2	0	0	0	5	3	0	0	8	D3YW43	
ENSMUST00000117871						7	23	7	52	10	10	0	6	5	0	1		
ENSMUST00000117872	ENSMUSG00000030849	7	130162451	133123350	-1	14	11	7	5	0	1	0	0	0	0	0	E9Q5C2	
ENSMUST00000117873						2	3	3	3	2	2	0	0	0	0	0		
ENSMUST00000117874						5	4	3	2	5	3	0	0	0	0	1		
ENSMUST00000117875						2	1	0	6	1	2	0	0	0	0	0		
ENSMUST00000117876						4	11	12	5	9	4	0	0	0	0	1		
ENSMUST00000117877						10	5	15	10	15	1	0	0	0	0	0		
ENSMUST00000117878	ENSMUSG00000041264	5	149184350	149215434	1	0	0	0	0	0	0	170	819	218	259	100		Q3ULM6
ENSMUST00000117879	ENSMUSG00000021699	13	108449948	109953461	1	1	6	2	0	4	4	0	0	0	0	0	A6XDB1	
ENSMUST00000117880	ENSMUSG00000029248	5	77016023	77061529	1	0	0	17	34	0	0	0	1	1	0	0		Q9DA15
ENSMUST00000117881						3	2	7	7	11	2	0	1	1	1	2		
ENSMUST00000117882	ENSMUSG00000016982	13	21981194	21988734	1	8	6	16	347	17	19	2	19	8	10	3	Q3V0N0	
ENSMUST00000117883	ENSMUSG00000020305	11	30885416	31102704	1	24	23	24	64	24	9	26	30	52	52	31	A8Y5I6	
ENSMUST00000117884						5	3	16	3	4	4	0	0	0	0	0		
ENSMUST00000117885						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000117886						0	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000117887						11	6	11	4	8	3	0	0	0	0	0		
ENSMUST00000117888						1	0	9	50	5	4	0	0	0	1	0		
ENSMUST00000117889						0	1	11	2	3	0	0	0	0	0	0		
ENSMUST00000117890	ENSMUSG00000024160	17	24886643	24892152	1	0	0	0	12	0	0	446	466	222	48	155		Q571F5
ENSMUST00000117891						3	1	0	3	0	2	0	0	0	0	0		
ENSMUST00000117892	ENSMUSG00000081534	15	97784355	97792692	1	15	13	26	74	35	18	790	926	613	194	569		Q9D8M3
ENSMUST00000117893						4	7	8	25	9	5	0	0	0	2	0		
ENSMUST00000117894						0	5	0	1	1	2	0	1	1	1	0		
ENSMUST00000117895						79	75	1916	184	93	39	1	1	0	1	0		
ENSMUST00000117896						3	6	4	9	5	2	0	0	0	0	0		
ENSMUST00000117897						1	2	3	4	8	6	0	0	0	0	1		
ENSMUST00000117898						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000117899						1	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000117900	ENSMUSG00000038204	5	24532697	24540978	-1	3	4	20	42	7	3	0	0	0	0	0	D3YU18	
ENSMUST00000117901	ENSMUSG00000031310	X	101404384	101420849	-1	0	2	0	0	0	0	0	23	0	8	0	B1AXS6	
ENSMUST00000117902						3	3	5	2	1	0	0	0	0	0	0		
ENSMUST00000117903						5	5	14	1	8	6	1	1	0	2	0		
ENSMUST00000117904						1	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000117905						5	7	9	9	9	4	0	0	0	1	1		
ENSMUST00000117906						3	0	2	10	3	5	0	1	0	0	0		
ENSMUST00000117907						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117908						5	2	2	0	1	0	0	0	0	3	0		
ENSMUST00000117909	ENSMUSG00000060508	7	20008023	20073306	1	5	0	3	0	0	0	0	0	0	0	0		Q66X22
ENSMUST00000117910						3	2	8	2	4	4	0	0	0	0	0		
ENSMUST00000117911	ENSMUSG00000032511	9	119483408	119579016	-1	0	0	0	253	15	0	0	0	0	0	38		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000117912						0	1	2	3	3	0	0	0	0	0	0		
ENSMUST00000117913	ENSMUSG00000078945	13	100144063	100202092	-1	41	59	28	42	45	35	336	839	1469	336	759		Q9QUK4
ENSMUST00000117914						1	1	1	4	0	4	0	2	0	2	0		
ENSMUST00000117915	ENSMUSG00000027677	3	33799832	33814860	1	0	0	22	81	18	2	0	0	0	0	0	E9PXW3	
ENSMUST00000117916						1	0	0	3	3	1	0	0	0	0	0		
ENSMUST00000117917	ENSMUSG00000027530	3	10244209	10301183	-1	0	0	0	0	2	1	0	0	0	0	0		Q9DAK4
ENSMUST00000117918						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000117919	ENSMUSG00000030222	6	137054825	137170497	-1	0	0	3	39	18	3	0	0	0	6	8		Q8R367
ENSMUST00000117920						7	2	6	4	6	2	0	0	0	0	0		
ENSMUST00000117921						12	6	16	4	7	8	0	8	2	0	0		
ENSMUST00000117923						1	1	1	9	2	0	0	0	0	0	0		
ENSMUST00000117924						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000117925						1	1	8	3	3	0	0	0	0	0	0		
ENSMUST00000117926						4	2	2	4	4	3	0	0	0	1	0		
ENSMUST00000117927						0	2	3	4	3	0	6	5	6	3	9		
ENSMUST00000117928						1	0	0	1	1	0	0	0	0	4	1		
ENSMUST00000117929	ENSMUSG00000020023	10	94311949	94590956	1	4	10	12	5	23	14	1	0	0	5	24		Q8R310
ENSMUST00000117930						7	4	2	5	6	1	0	1	2	0	1		
ENSMUST00000117931						8	4	10	11	5	2	0	2	3	1	1		
ENSMUST00000117932	ENSMUSG00000094793	4	60737383	60741326	-1	0	0	0	0	0	0	0	0	0	0	0	Q58ES8	P11588
ENSMUST00000117933						11	3	7	0	9	0	3	0	1	3	1		
ENSMUST00000117934						3	0	4	8	3	1	1	1	2	0	1		
ENSMUST00000117935						4	5	0	1	2	2	0	0	0	0	0		
ENSMUST00000117937						17	11	20	21	23	14	13	21	10	1	5		
ENSMUST00000117938						4	3	10	1	4	3	0	0	0	0	0		
ENSMUST00000117939						8	0	2	1	2	4	0	0	0	4	0		
ENSMUST00000117940						1	0	1	0	2	1	0	0	0	0	0		
ENSMUST00000117941						9	7	17	10	2	1	5	7	9	8	4		
ENSMUST00000117942						0	0	0	4	2	0	0	0	33	0	0		
ENSMUST00000117943						7	10	21	14	22	9	6	2	6	1	2		
ENSMUST00000117944	ENSMUSG00000051022	5	39613935	39755475	-1	34	37	86	32	32	17	0	6	0	0	4		O35310
ENSMUST00000117945	ENSMUSG00000003166	16	17839482	17894145	-1	0	0	0	0	0	0	595	550	330	78	313		
ENSMUST00000117946						2	2	2	2	2	4	0	0	0	0	0		
ENSMUST00000117947						8	4	1	10	2	5	0	1	0	0	0		
ENSMUST00000117948						2	2	7	4	1	0	5	27	9	1	50		
ENSMUST00000117949						4	3	2	1	9	2	0	0	0	0	0		
ENSMUST00000117950	ENSMUSG00000026411	1	136008150	136035342	1	0	4	2	55	6	3	7	0	4	0	20		Q9CR23
ENSMUST00000117951						2	2	3	0	5	2	0	1	1	0	1		
ENSMUST00000117952						10	9	9	9	7	6	10	122	35	33	29		
ENSMUST00000117953						2	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000117954						7	10	29	4	7	4	0	0	0	0	0		
ENSMUST00000117955						7	3	9	12	4	4	0	0	0	0	1		
ENSMUST00000117956	ENSMUSG00000035011	10	81135220	81152995	1	0	0	0	80	0	0	0	0	110	0	76		O88939
ENSMUST00000117957						6	1	0	1	8	0	1	0	2	3	0		
ENSMUST00000117958	ENSMUSG00000022678	16	14163275	14192928	1	0	1	0	0	1	0	16	44	55	13	57		Q9CZA6
ENSMUST00000117959						10	5	8	3	10	7	0	0	0	0	0		
ENSMUST00000117960						4	1	11	3	1	2	0	0	0	0	0		
ENSMUST00000117961						0	1	3	7	2	0	0	0	0	4	0		
ENSMUST00000117962						2	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000117963						4	2	30	38	8	2	1	4	0	0	0		
ENSMUST00000117964						27149	47126	39572	15896	25357	10495	257	2346	640	442	787		
ENSMUST00000117965	ENSMUSG00000040928	4	129148005	129189727	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q5M3	
ENSMUST00000117966	ENSMUSG00000055053	10	81396186	81431005	-1	6	2	13	28	3	6	4	0	12	0	5		P70255
ENSMUST00000117967						1	1	6	4	3	3	1	1	2	0	0		
ENSMUST00000117969						4	0	6	2	1	2	0	0	0	0	0		
ENSMUST00000117970						1	1	4	1	2	0	0	0	0	0	0		
ENSMUST00000117971	ENSMUSG00000029438	5	123343834	123374992	1	65	47	141	124	79	44	5	8	11	2	16		Q9CXE2
ENSMUST00000117972						5	0	27	3	8	2	0	0	0	0	0		
ENSMUST00000117973						5	2	60	20	3	2	0	0	0	0	0		
ENSMUST00000117975						4	2	9	2	5	1	0	0	0	0	0		
ENSMUST00000117977						41	40	247	37	37	20	1	6	2	1	0		
ENSMUST00000117978						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000117979						2	1	0	2	0	6	0	13	1	2	0		
ENSMUST00000117980						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000117981	ENSMUSG00000007908	9	76014855	76136350	1	0	0	0	0	0	0	0	0	0	0	0	D3YVU9	
ENSMUST00000117982						0	4	5	0	1	0	0	0	0	0	0		
ENSMUST00000117983						1	6	4	10	4	4	0	0	0	0	0		
ENSMUST00000117984	ENSMUSG00000000530	15	101128522	101145336	1	0	0	0	0	0	0	0	0	73	0	41		Q61288
ENSMUST00000117985	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3G4	
ENSMUST00000117986						0	4	5	0	3	0	0	0	0	0	0		
ENSMUST00000117987						1	5	0	0	0	0	78	97	86	35	83		
ENSMUST00000117988						0	0	0	1	2	1	1	2	2	1	2		
ENSMUST00000117989	ENSMUSG00000047084	7	80261215	80265374	1	1	0	0	11	0	0	282	756	357	225	267		Q99KS2
ENSMUST00000117990						2	3	7	5	3	2	0	0	0	0	0		
ENSMUST00000117991						1	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000117992	ENSMUSG00000019893	10	52045721	52195244	-1	0	0	0	0	21	0	0	0	0	0	0	E9PWG5	
ENSMUST00000117993						3	1	3	2	4	0	2	4	2	6	3		
ENSMUST00000117994	ENSMUSG00000033031	16	48994185	49019709	1	0	1	5	28	0	0	16	0	0	0	0	D3Z7B5	
ENSMUST00000117995						1	0	6	0	4	0	0	0	0	0	0		
ENSMUST00000117996						1	1	2	5	3	1	0	0	0	0	0		
ENSMUST00000117997	ENSMUSG00000039838	4	150628572	150652174	-1	50	33	182	65	67	38	4	0	3	0	1	B0QZL3	
ENSMUST00000117998	ENSMUSG00000040189	7	45924072	45948956	1	0	0	0	0	0	0	0	0	0	6	0	D3Z6I9	
ENSMUST00000117999						7	2	3	7	5	5	0	0	0	0	0		
ENSMUST00000118000	ENSMUSG00000002459	1	4909576	5070285	-1	35	23	65	27	28	18	0	0	0	0	0	E9Q720	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118001	ENSMUSG00000014767	17	15499888	15528379	1	0	0	0	0	0	0	130	254	92	154	68	Q91YM5	
ENSMUST00000118002	ENSMUSG00000037143	2	145934784	146215039	1	8	10	26	12	11	9	0	0	0	0	0	B2FDE9	
ENSMUST00000118003	ENSMUSG00000054162	8	62951009	63357103	1	0	1	1	0	1	0	0	0	0	0	0		Q8BKV0
ENSMUST00000118004						0	1	3	4	7	2	0	0	0	0	2		
ENSMUST00000118005						27	33	183	34	8	0	117	537	187	53	353		
ENSMUST00000118006	ENSMUSG00000034855	5	92346638	92348889	-1	3	1	1	1	3	0	0	2	0	0	0	D3YW23	
ENSMUST00000118007						2	2	9	2	1	1	0	0	0	0	0		
ENSMUST00000118008						5	10	13	1	0	1	0	0	0	0	0		
ENSMUST00000118009	ENSMUSG00000014907	8	66860217	66890564	1	9	12	8	278	13	3	9	32	21	2	16	E9QJT2	
ENSMUST00000118010						3	6	12	4	14	10	5	0	5	13	5		
ENSMUST00000118011						2	0	0	3	1	1	3	21	4	1	5		
ENSMUST00000118012	ENSMUSG00000078877	2	176798612	176811223	1	0	1	0	4	0	0	0	0	0	0	0	A2BG90	
ENSMUST00000118013						6	0	9	4	2	2	0	0	0	0	0		
ENSMUST00000118014						3	5	1	0	0	0	0	0	0	0	0		
ENSMUST00000118015	ENSMUSG00000019528	3	20122084	20155317	-1	0	15	0	168	18	11	0	109	17	8	34	K3W4S6	
ENSMUST00000118016						4	2	3	5	6	3	0	0	0	0	0		
ENSMUST00000118017						15	22	61	23	14	11	1	1	0	0	0		
ENSMUST00000118018						8	6	20	9	10	6	0	0	0	0	0		
ENSMUST00000118019						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000118020						2	2	2	10	0	1	0	0	0	0	0		
ENSMUST00000118021						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118022	ENSMUSG00000021944	14	63198922	63271692	-1	0	0	0	0	0	9	0	0	0	0	0		Q08369
ENSMUST00000118023						13	11	4	10	10	7	0	0	0	0	0		
ENSMUST00000118024						7	4	1	2	5	5	3	4	0	0	3		
ENSMUST00000118025						3	2	4	5	2	1	0	0	0	2	0		
ENSMUST00000118026						1	1	0	4	1	0	0	0	0	0	0		
ENSMUST00000118027	ENSMUSG00000029475	5	122870665	122989823	-1	9	5	20	212	26	3	0	26	0	0	0	D3YVU4	
ENSMUST00000118029						1	2	0	3	0	0	0	4	1	1	3		
ENSMUST00000118030						0	0	10	2	4	2	0	0	0	0	0		
ENSMUST00000118031						1	2	8	3	2	3	0	0	0	0	0		
ENSMUST00000118032						3	2	1	1	5	1	0	0	0	1	0		
ENSMUST00000118033						8	2	2	3	7	4	0	0	0	0	0		
ENSMUST00000118034	ENSMUSG00000037605	5	81020138	81825133	1	2	0	0	0	6	0	0	0	0	0	0	D3Z593	
ENSMUST00000118035						0	3	1	1	4	0	0	0	1	0	0		
ENSMUST00000118036	ENSMUSG00000063406	5	108106366	108132620	-1	3	0	3	0	2	0	4	7	0	20	8	Q8C5H9	
ENSMUST00000118037						2	1	0	0	3	1	0	0	0	0	0		
ENSMUST00000118038						8	2	11	8	4	3	0	0	0	0	0		
ENSMUST00000118039						2	3	1	5	2	0	0	0	0	0	0		
ENSMUST00000118040						10	4	15	14	11	4	0	0	0	1	0		
ENSMUST00000118041						0	0	0	4	1	1	0	0	0	0	0		
ENSMUST00000118042						17	12	36	14	14	7	1	0	0	0	1		
ENSMUST00000118043	ENSMUSG00000024501	18	43320979	43438286	-1	2	0	4	0	6	4	0	0	0	0	6	Q3TT92	
ENSMUST00000118044						9	14	120	20	11	10	2	1	0	0	2		
ENSMUST00000118045						5	3	21	7	7	3	0	0	0	0	0		
ENSMUST00000118046						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118047						0	0	26	3	4	0	45	560	104	154	40		
ENSMUST00000118048						0	0	10	0	0	0	557	1307	470	845	258		
ENSMUST00000118049						6	9	12	2	3	1	0	0	0	0	0		
ENSMUST00000118050						6	6	15	78	3	4	3	3	1	0	2		
ENSMUST00000118051	ENSMUSG00000032579	9	107327084	107338350	-1	0	0	0	0	0	0	0	0	4	0	0	B0QZV0	
ENSMUST00000118052						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118053						3	4	6	5	9	4	0	1	0	0	1		
ENSMUST00000118054						3	4	9	5	2	3	0	0	0	0	0		
ENSMUST00000118055						56	20	42	429	93	39	0	0	0	0	1		
ENSMUST00000118056						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000118057						0	2	2	2	0	0	0	0	0	0	1		
ENSMUST00000118058						6	1	1	1	5	2	0	1	1	0	1		
ENSMUST00000118059	ENSMUSG00000026111	1	37430139	37439124	1	0	0	0	0	1	0	20	0	74	51	67		Q9CQ61
ENSMUST00000118060	ENSMUSG00000030173	6	129898996	129917650	-1	3	2	0	0	0	1	0	0	0	0	0	Q548A2	Q60652
ENSMUST00000118061						11	8	15	7	8	6	3	3	2	0	0		
ENSMUST00000118062						0	2	1	0	1	0	0	9	0	1	0		
ENSMUST00000118063						1	3	10	4	12	2	0	0	0	0	0		
ENSMUST00000118064	ENSMUSG00000051989	16	92301286	92313041	1	4	4	13	14	7	6	4	0	6	2	2		Q99J19
ENSMUST00000118065						3	2	16	4	6	3	0	0	0	0	0		
ENSMUST00000118066						8	7	21	13	9	1	680	2024	1116	345	805		
ENSMUST00000118067						497	495	247	377	435	195	7	25	16	11	21		
ENSMUST00000118068	ENSMUSG00000081665	7	3731630	3739889	-1	3	0	2	0	0	0	1561	3359	2458	1641	1757		
ENSMUST00000118069						4	0	2	4	5	3	0	0	1	4	0		
ENSMUST00000118070						0	1	9	2	0	0	0	0	0	0	0		
ENSMUST00000118071	ENSMUSG00000024501	18	43320979	43438286	-1	1	0	0	0	0	1	0	0	0	0	0	D3Z567	
ENSMUST00000118072	ENSMUSG00000043183	13	54503779	54551290	1	0	0	0	12	0	0	0	73	0	5	0	E9PYI6	
ENSMUST00000118073						5	0	4	0	3	0	0	0	0	0	0		
ENSMUST00000118075	ENSMUSG00000061143	3	51685907	52105076	-1	25	47	186	0	2	2	0	44	0	1	0	E9Q6E8	
ENSMUST00000118076	ENSMUSG00000049680	11	5713417	5762376	-1	18	0	18	35	0	0	0	0	18	0	30		Q5NCI0
ENSMUST00000118077	ENSMUSG00000036099	10	93939165	94035817	-1	4	3	1	1	3	2	14	1	10	10	17		Q3ZK22
ENSMUST00000118078	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3YU23	
ENSMUST00000118079						2	3	5	2	2	1	0	0	0	0	0		
ENSMUST00000118080						1	1	1	0	1	0	1	2	0	0	0		
ENSMUST00000118081						6	1	0	2	5	4	0	4	0	2	0		
ENSMUST00000118082						40	29	50	37	39	26	1	7	3	0	8		
ENSMUST00000118083						1	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000118084						23	33	59	28	32	11	1	2	0	0	0		
ENSMUST00000118085						5	3	12	4	7	5	0	0	0	0	0		
ENSMUST00000118086						2	0	8	0	2	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118087						2	0	11	6	3	0	1	0	1	1	2		
ENSMUST00000118088						8	1	4	2	2	2	0	0	0	2	0		
ENSMUST00000118089						4	5	4	7	8	11	0	0	0	0	0		
ENSMUST00000118090						3	5	31	7	4	2	0	0	0	0	0		
ENSMUST00000118091	ENSMUSG00000008540	6	138140316	138156755	1	3	2	10	3	4	2	14	24	3	12	4	E9QJW0	
ENSMUST00000118092	ENSMUSG00000031310	X	101404384	101420849	-1	0	2	0	0	0	0	0	0	0	0	0	Q32P02	
ENSMUST00000118093						10	5	1	5	5	4	0	0	0	0	0		
ENSMUST00000118094						8	5	5	2	6	2	0	0	0	0	0		
ENSMUST00000118095						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000118096	ENSMUSG00000021567	13	73818534	73847631	-1	0	0	15	0	0	0	0	0	0	0	0		Q8VE28
ENSMUST00000118097	ENSMUSG00000015806	5	45434021	45450236	-1	3	3	2	1	0	0	0	3	0	0	0	D3YWR7	
ENSMUST00000118098	ENSMUSG00000046101	1	9908638	9942085	1	5	3	0	0	1	2	3	5	0	0	0	A0A0A0MQF4	
ENSMUST00000118099						2	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000118100	ENSMUSG00000062232	3	79062516	79286517	-1	0	0	20	0	51	20	0	0	0	0	0		Q8CHG7
ENSMUST00000118101	ENSMUSG00000021081	12	103688044	103695529	-1	0	2	7	10	6	0	0	0	0	0	0	G3X9Z5	
ENSMUST00000118102						3	0	4	2	2	0	0	1	1	1	0		
ENSMUST00000118103						8	3	9	36	7	4	0	0	0	0	0		
ENSMUST00000118104						4	5	7	7	4	1	4	11	3	4	3		
ENSMUST00000118105						0	9	31	0	25	7	0	0	0	0	0		
ENSMUST00000118106	ENSMUSG00000034842	5	92331827	92414628	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118107						7	5	7	10	8	2	0	1	0	0	1		
ENSMUST00000118108	ENSMUSG00000070953	2	34777556	34799912	-1	9	6	9	39	6	5	65	41	0	0	16	B0R0S4	
ENSMUST00000118109						3	2	7	1	4	0	0	0	0	0	0		
ENSMUST00000118110	ENSMUSG00000042659	7	68737045	68749241	-1	0	0	0	170	5	0	0	0	48	114	70	Q8VD69	
ENSMUST00000118111	ENSMUSG00000031302	X	101299168	101325963	1	80	55	232	114	63	0	4	13	0	0	0	A2AGI3	
ENSMUST00000118112	ENSMUSG00000020481	11	5569684	5689337	1	0	0	0	0	0	3	0	0	1	0	0	Q5QNR3	
ENSMUST00000118113	ENSMUSG00000040732	16	95359169	95586593	-1	18	0	123	116	10	4	131	289	221	43	61	D3YU51	
ENSMUST00000118114						1	3	2	2	4	0	0	0	0	0	0		
ENSMUST00000118115	ENSMUSG00000044442	16	87354185	87368742	1	13	9	12	3	8	14	0	0	3	1	4	D3Z6J0	
ENSMUST00000118116						11	8	0	4	4	3	0	0	0	0	0		
ENSMUST00000118117	ENSMUSG00000027849	3	103575231	103645569	1	4	3	23	6	7	6	0	0	0	0	0	Q8C8S6	
ENSMUST00000118118	ENSMUSG00000036580	3	55112108	55137322	1	23	0	22	210	25	7	0	0	0	0	0	Q3TVW1	Q8R1X6
ENSMUST00000118119						3	0	11	3	3	3	12	34	17	2	0		
ENSMUST00000118120	ENSMUSG00000030170	6	119432531	119544347	-1	3	4	13	10	3	7	0	4	2	0	5	D3YTW9	
ENSMUST00000118121	ENSMUSG00000083012	5	143548706	143564531	1	3	3	1	30	5	4	83	159	34	36	33	Q91X57	
ENSMUST00000118122						1	1	1	1	0	1	0	0	0	0	0		
ENSMUST00000118124						12	6	16	13	4	6	0	0	0	0	0		
ENSMUST00000118125	ENSMUSG00000074141	7	44816088	44840809	1	8	0	27	238	11	0	6	0	26	9	0	D3Z4E0	
ENSMUST00000118126						0	0	10	0	3	0	11	340	51	15	71		
ENSMUST00000118127						8	11	12	6	8	1	3	13	3	2	17		
ENSMUST00000118128						4	1	0	1	2	1	0	0	0	0	0		
ENSMUST00000118129	ENSMUSG00000036242	14	49681560	49783383	-1	20	0	0	0	0	3	0	0	0	2	1	D3Z566	
ENSMUST00000118130						31	32	98	43	34	25	0	0	0	0	2		
ENSMUST00000118131						5	1	3	23	4	0	0	0	0	0	0		
ENSMUST00000118132						1	0	1	1	1	1	0	0	4	0	6		
ENSMUST00000118133						0	3	11	9	6	2	0	0	0	0	0		
ENSMUST00000118134	ENSMUSG00000037300	8	124671335	124721983	-1	11	11	22	15	22	8	205	369	403	54	315	E9Q723	
ENSMUST00000118135						1	1	0	3	1	1	0	0	0	0	0		
ENSMUST00000118136	ENSMUSG00000031822	8	120230536	120581390	1	0	0	0	418	15	18	369	98	334	24	319		Q3U3C9
ENSMUST00000118137						7	3	8	4	1	3	0	0	0	0	0		
ENSMUST00000118138	ENSMUSG00000033653	16	21423118	21644680	1	7	2	7	9	5	6	0	51	0	0	4	D3Z5P1	
ENSMUST00000118139	ENSMUSG00000049971	5	127632262	127709374	1	16	15	23	69	8	9	2	3	1	0	2		A4FUP9
ENSMUST00000118140						1	0	5	41	6	1	0	0	0	0	0		
ENSMUST00000118142						3	2	21	5	8	7	0	0	0	0	0		
ENSMUST00000118143						18	9	32	23	21	4	5	8	6	0	7		
ENSMUST00000118144	ENSMUSG00000023186	9	38718268	38743337	1	9	9	0	1	14	9	129	687	458	863	347		Q99KC8
ENSMUST00000118145						1	3	1	0	0	1	0	0	0	0	0		
ENSMUST00000118146						2	1	10	2	4	1	0	0	0	0	0		
ENSMUST00000118147						1	1	2	2	0	0	1	1	3	0	0		
ENSMUST00000118148						7	5	8	9	13	5	0	2	0	0	0		
ENSMUST00000118149						4	2	5	2	3	1	0	0	0	0	0		
ENSMUST00000118151						20	22	47	9	21	10	0	0	0	0	0		
ENSMUST00000118152	ENSMUSG00000009575	15	103191544	103239816	-1	51	63	97	82	55	39	187	303	259	65	222		Q61686
ENSMUST00000118153						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000118154						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000118155	ENSMUSG00000020738	11	115523102	115536276	-1	1	0	0	0	0	0	0	26	0	0	10	D3Z794	
ENSMUST00000118156						2	1	5	4	2	2	0	0	0	0	0		
ENSMUST00000118157	ENSMUSG00000041343	7	92581723	92637142	-1	0	8	0	107	0	9	0	0	0	0	0		
ENSMUST00000118158						41	41	55	40	36	13	5	37	9	3	8		
ENSMUST00000118159	ENSMUSG00000040111	9	40293233	40531383	-1	1	4	20	16	3	2	0	0	0	0	0		Q80TI0
ENSMUST00000118160	ENSMUSG00000037846	10	67979570	68059740	1	0	12	0	72	7	0	0	0	0	0	7		Q14B46
ENSMUST00000118161	ENSMUSG00000063239	17	27422387	27513341	-1	29	10	75	218	28	14	0	0	0	0	0	G3XA00	
ENSMUST00000118162	ENSMUSG00000048012	7	44731481	44751050	-1	0	0	0	0	0	0	24	0	20	1	16	Q4VA40	
ENSMUST00000118163	ENSMUSG00000041268	9	54365158	54501760	-1	0	10	27	0	0	18	1674	2586	3077	307	1821	B0V2P5	
ENSMUST00000118164	ENSMUSG00000032297	9	59577917	59607292	1	0	0	0	0	0	0	0	0	0	0	0	D3YX51	
ENSMUST00000118165						2	0	4	4	3	0	0	0	0	0	0		
ENSMUST00000118166						2	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000118167						0	0	0	1	0	0	0	0	0	1	0		
ENSMUST00000118168						3	0	0	47	2	2	2	0	0	0	0		
ENSMUST00000118169	ENSMUSG00000030781	7	128265657	128272430	1	8	15	44	9	29	8	0	0	0	0	0		Q923I7
ENSMUST00000118171	ENSMUSG00000031772	8	112570043	112882717	1	1	1	0	0	1	3	0	0	0	0	0	D3YWB9	
ENSMUST00000118172						72	66	173	47	104	38	0	0	0	0	0		
ENSMUST00000118173						9	3	6	4	5	3	1	3	4	17	4		
ENSMUST00000118174	ENSMUSG00000039987	5	20758663	20882124	-1	2	4	0	14	11	6	24	92	68	14	55		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118175						3	5	7	6	3	1	0	0	0	0	0		
ENSMUST00000118176						0	3	3	16	4	1	0	0	0	0	0		
ENSMUST00000118177						8	2	3	1	3	1	0	0	0	0	0		
ENSMUST00000118178						2	3	3	2	1	0	0	0	0	0	0		
ENSMUST00000118179						2	0	0	0	0	0	1	0	1	0	0		
ENSMUST00000118180						1	4	3	2	2	0	0	0	0	0	0		
ENSMUST00000118181						1	0	0	0	0	1	0	1	0	0	0		
ENSMUST00000118182						2	5	3	6	3	2	44	10	41	16	10		
ENSMUST00000118183						0	3	3	8	0	0	0	0	0	0	0		
ENSMUST00000118184						9	4	5	7	8	3	0	0	0	0	0		
ENSMUST00000118185						2	2	4	4	2	2	0	0	0	0	0		
ENSMUST00000118186	ENSMUSG00000002031	9	44767908	44792714	1	0	0	0	0	0	0	198	435	188	205	162		Q9DB07
ENSMUST00000118187						6	4	3	5	6	2	0	0	0	0	0		
ENSMUST00000118188						2	2	2	4	2	2	0	0	0	0	0		
ENSMUST00000118189						16	13	46	54	16	12	0	2	0	0	0		
ENSMUST00000118190	ENSMUSG00000038646	7	81762925	81769491	1	0	0	1	37	7	0	0	0	8	0	0		Q9CQY2
ENSMUST00000118191						0	0	1	19	3	0	11	17	6	43	6		
ENSMUST00000118192	ENSMUSG00000023286	4	155943831	155959604	1	0	0	0	0	2	0	42	357	99	27	73	B0QZM1	
ENSMUST00000118193	ENSMUSG00000022151	15	5185525	5218336	1	0	2	3	3	0	0	138	214	116	193	24		Q9D6K7
ENSMUST00000118194	ENSMUSG00000069633	8	3457105	3467680	-1	25	21	48	35	28	17	0	8	1	4	4	Q3TN90	
ENSMUST00000118195	ENSMUSG00000045312	13	94057796	94195409	1	15	14	25	2	30	11	0	0	0	0	0		Q8BGA2
ENSMUST00000118196	ENSMUSG00000038866	1	105990406	106034074	1	12	0	0	355	16	16	88	757	304	5	402		Q69ZB8
ENSMUST00000118197						11	12	44	23	61	31	0	0	0	0	0		
ENSMUST00000118198	ENSMUSG00000033543	9	70012550	70022866	1	0	0	0	57	0	2	85	1	0	113	0	Q3TE88	Q80ZM7
ENSMUST00000118199	ENSMUSG00000028779	4	130102558	130128135	1	5	0	46	21	29	10	5	5	0	0	0		Q8BFY6
ENSMUST00000118200						2	2	1	1	2	0	0	2	0	0	0		
ENSMUST00000118201						1	1	11	3	3	2	0	0	0	0	0		
ENSMUST00000118202						6	9	5	6	5	4	0	0	0	0	0		
ENSMUST00000118203						70	47	131	38	50	11	0	0	0	0	5		
ENSMUST00000118204	ENSMUSG00000027660	3	31095058	31122577	1	0	1	2	0	0	0	124	130	304	81	217		Q60665
ENSMUST00000118205	ENSMUSG00000036099	10	93939165	94035817	-1	11	13	8	11	16	14	0	5	5	2	5		Q3ZK22
ENSMUST00000118206	ENSMUSG00000078439	10	81393051	81395392	1	12	6	8	3	14	5	107	167	60	0	37	D3Z3Y2	
ENSMUST00000118207	ENSMUSG00000026592	1	157099139	157108680	-1	3	0	0	0	13	0	0	0	0	0	0		
ENSMUST00000118208						3	2	2	0	1	2	0	0	0	0	0		
ENSMUST00000118209	ENSMUSG00000000563	3	105942698	105960099	-1	1	3	9	75	2	0	777	1626	1177	3191	1093	Q5I0W0	Q9CQQ7
ENSMUST00000118210						3	6	9	4	11	4	1	2	0	2	1		
ENSMUST00000118211						0	0	2	6	0	1	0	0	0	0	0		
ENSMUST00000118212						4	5	7	0	6	1	0	0	0	2	32		
ENSMUST00000118213						1	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000118214						0	0	1	7	0	2	0	0	0	0	0		
ENSMUST00000118215	ENSMUSG00000032401	9	64117147	64138118	1	0	2	0	0	0	0	0	0	0	0	0	D3YTQ7	
ENSMUST00000118216	ENSMUSG00000012777	7	44252148	44257378	-1	8	0	11	95	1	12	0	0	0	0	0	D3YTS9	
ENSMUST00000118217						4	0	1	3	3	2	0	0	0	0	0		
ENSMUST00000118218	ENSMUSG00000067562	X	102802963	102809942	1	0	4	17	33	20	2	0	0	0	0	0	Q9D410	
ENSMUST00000118219						1	0	0	0	2	1	0	2	3	0	3		
ENSMUST00000118220						6	1	16	4	10	1	0	0	0	0	0		
ENSMUST00000118221						14	18	59	35	19	4	0	4	0	0	0		
ENSMUST00000118222						0	0	0	7	0	0	0	0	0	0	1		
ENSMUST00000118223						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000118224						2	0	3	3	1	0	9	34	18	52	16		
ENSMUST00000118225						9	2	6	11	10	5	0	0	0	0	0		
ENSMUST00000118226	ENSMUSG00000029352	5	113075839	113081584	-1	0	0	0	0	11	0	0	0	0	0	0		Q9JJU9
ENSMUST00000118227						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000118228	ENSMUSG00000032501	15	59648350	59656550	1	15	11	34	207	30	12	4	285	3	3	15		Q8K4K4
ENSMUST00000118229	ENSMUSG00000052751	6	48593883	48599082	1	0	0	0	227	27	0	0	0	0	0	31		Q5U4E2
ENSMUST00000118230						0	0	0	0	0	0	0	0	0	5	0		
ENSMUST00000118231						8	5	1	2	9	3	0	0	0	0	0		
ENSMUST00000118232						0	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000118233	ENSMUSG00000048240	10	80948624	81014945	-1	0	1	60	1	3	0	0	0	0	0	0	Q3UGN1	Q61016
ENSMUST00000118234	ENSMUSG00000067825	6	121183667	121198837	1	1	3	8	32	2	0	3	42	20	0	0	D3Z3F5	
ENSMUST00000118235						3	2	1	1	3	0	0	0	0	0	0		
ENSMUST00000118236	ENSMUSG00000022674	16	15552677	15594524	-1	0	4	0	0	0	2	20	51	0	0	0	B2KF55	
ENSMUST00000118237						6	3	6	6	3	2	1	0	0	0	1		
ENSMUST00000118238						1	0	6	3	0	2	0	0	0	0	0		
ENSMUST00000118239						5	0	0	5	4	0	0	0	0	0	0		
ENSMUST00000118240						8	4	12	5	10	1	0	0	0	0	0		
ENSMUST00000118242	ENSMUSG00000037736	5	66745827	67057158	1	0	0	28	98	19	6	0	0	0	0	0	D3YU22	
ENSMUST00000118243	ENSMUSG00000038188	11	75513540	75526582	1	0	5	14	123	0	5	5	11	6	11	0	B7ZC28	
ENSMUST00000118245						1	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000118246						5	1	0	0	6	0	112	195	298	14	0		
ENSMUST00000118247						17	5	17	10	24	9	0	0	0	0	0		
ENSMUST00000118248						5	5	31	0	10	0	0	0	0	5	0		
ENSMUST00000118249						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118250						2	1	4	2	1	1	0	0	0	0	0		
ENSMUST00000118251						0	0	0	2	2	2	0	0	1	0	0		
ENSMUST00000118252						6	2	11	1	6	1	1	0	1	4	1		
ENSMUST00000118253						1	2	5	1	2	0	0	0	0	0	0		
ENSMUST00000118254	ENSMUSG00000074452	9	35570284	35690318	1	7	5	5	3	4	1	0	0	1	0	0		Q3UW31
ENSMUST00000118255						8	2	11	7	6	1	0	0	0	0	0		
ENSMUST00000118256						4	3	4	0	0	2	0	0	0	0	0		
ENSMUST00000118257						6	3	31	19	18	8	295	188	325	14	231		
ENSMUST00000118259						0	1	4	0	0	0	0	0	1	1	0		
ENSMUST00000118260						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118261	ENSMUSG00000029283	5	106964322	106984432	1	14	2	20	130	9	4	0	0	0	0	7		Q9Z0H0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118262						3	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000118263	ENSMUSG00000056763	1	10037987	10136768	1	0	0	2	12	2	2	0	2	4	2	0		B2RX88
ENSMUST00000118264						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000118265						0	1	0	0	1	2	0	0	1	0	1		
ENSMUST00000118266						832	783	579	715	968	492	41	105	53	12	81		
ENSMUST00000118267						0	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000118268	ENSMUSG00000029446	5	129765558	129787449	-1	2	0	0	0	0	0	0	4	0	0	3	D3Z4T3	
ENSMUST00000118269						17	4	8	29	15	0	2	0	0	0	2		
ENSMUST00000118270						1	0	1	4	1	0	0	0	0	0	0		
ENSMUST00000118271						22	9	25	13	9	23	0	0	0	0	0		
ENSMUST00000118272						2	0	2	0	4	0	0	2	3	9	0		
ENSMUST00000118273						5	3	5	2	6	6	0	0	0	0	0		
ENSMUST00000118274						5	2	3	4	1	3	0	0	0	0	0		
ENSMUST00000118275						2	0	4	3	2	1	0	0	0	0	0		
ENSMUST00000118276	ENSMUSG00000031098	7	142434850	142440396	1	8	0	8	11	6	11	2	60	22	0	26		Q9R0N6
ENSMUST00000118277						3	3	3	4	1	0	0	0	0	0	1		
ENSMUST00000118278	ENSMUSG00000083138	4	115242084	115254557	1	5	6	11	6	12	4	0	0	0	0	0	A0A087WPC3	
ENSMUST00000118279	ENSMUSG00000001062	8	123242356	123254348	-1	0	0	0	0	0	0	108	73	0	4	20	Q3U280	
ENSMUST00000118280	ENSMUSG00000068523	3	146499807	146505572	1	5	4	3	1	1	0	5	38	10	19	22	Q3UKC8	Q80SZ7
ENSMUST00000118281						10	5	11	6	20	4	2	0	0	0	2		
ENSMUST00000118282	ENSMUSG00000034218	9	53439149	53536740	-1	31	41	96	31	57	20	32	52	63	29	76		Q62388
ENSMUST00000118283	ENSMUSG00000047407	17	70844205	70853546	-1	0	2	4	1	3	2	0	26	12	5	15	Q3TVD4	P70284
ENSMUST00000118284						10	5	11	15	13	7	0	1	1	0	1		
ENSMUST00000118285						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118286	ENSMUSG00000027668	3	32529465	32579239	1	73	80	202	86	102	40	74	307	219	20	147		Q811U4
ENSMUST00000118287	ENSMUSG00000023007	15	99295087	99317018	1	0	0	0	0	0	0	0	0	0	0	0	E9QP07	
ENSMUST00000118288						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118289						6	5	9	7	4	3	0	0	0	0	0		
ENSMUST00000118290						0	0	0	0	0	0	0	9	0	1	1		
ENSMUST00000118291						10	6	45	10	13	4	0	0	3	0	1		
ENSMUST00000118292						0	2	1	1	3	1	0	0	0	0	0		
ENSMUST00000118293						0	1	2	2	1	0	0	0	0	0	0		
ENSMUST00000118294	ENSMUSG00000022475	15	97792664	97844502	-1	3	0	18	78	0	11	35	126	0	0	89		Q8C2B3
ENSMUST00000118295						3	3	4	3	2	1	0	0	0	0	0		
ENSMUST00000118296	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9PXV8	
ENSMUST00000118297						4	2	3	1	6	1	0	0	0	0	0		
ENSMUST00000118298						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000118299						1	2	2	5	2	2	0	0	0	0	0		
ENSMUST00000118300	ENSMUSG00000090102	X	23957702	23958934	-1	5	4	3	3	5	2	0	0	0	0	0	A2ALC6	
ENSMUST00000118301						3	2	3	2	5	2	0	3	2	0	1		
ENSMUST00000118302						4	9	45	28	23	14	45	88	57	10	53		
ENSMUST00000118303						4	10	26	19	10	3	0	0	0	0	1		
ENSMUST00000118304						7	5	2	2	6	1	0	1	0	0	1		
ENSMUST00000118305	ENSMUSG00000046180	X	58909360	58920304	1	4	0	3	5	3	2	0	0	0	0	0	Q99PA7	
ENSMUST00000118306						6	8	9	3	6	1	0	0	0	0	0		
ENSMUST00000118307						0	0	0	0	0	0	1352	2451	1063	626	682		
ENSMUST00000118308						0	2	1	1	0	1	0	0	0	0	0		
ENSMUST00000118310	ENSMUSG00000044442	16	87354185	87368742	1	38	37	83	0	42	30	3	30	0	17	16	Q6PRU9	
ENSMUST00000118311						0	0	0	1	1	0	0	0	0	2	0		
ENSMUST00000118312						2	3	9	0	2	1	0	0	0	0	0		
ENSMUST00000118313	ENSMUSG00000044252	18	12755314	12941841	-1	0	0	4	19	0	0	0	0	0	9	7		Q91XL9
ENSMUST00000118314	ENSMUSG00000046449	X	104077434	104201185	-1	0	0	0	22	17	0	0	0	0	0	0	Q003Y7	Q5DTT1
ENSMUST00000118315	ENSMUSG00000039552	10	33905111	33916021	1	0	3	0	0	0	0	0	0	1	0	0	D3Z590	
ENSMUST00000118316	ENSMUSG00000029655	5	150608007	150666183	-1	29	49	93	40	42	35	65	216	91	111	119		Q8JZS6
ENSMUST00000118317	ENSMUSG00000008730	3	103739815	103791563	-1	54	40	115	117	35	20	9716	12742	12639	928	7690		O88904
ENSMUST00000118318						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000118319						1	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000118320						3	3	1	2	3	0	0	0	0	0	0		
ENSMUST00000118321	ENSMUSG00000020674	12	29938036	30017658	1	5	0	0	4	1	3	0	0	0	0	0	D3Z5M7	
ENSMUST00000118322						16	12	34	16	10	5	0	0	0	0	0		
ENSMUST00000118323						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000118324						0	0	0	2	0	0	0	17	0	3	4		
ENSMUST00000118325						13	22	33	21	16	11	1	2	0	0	2		
ENSMUST00000118326	ENSMUSG00000045348	5	137729899	137741607	-1	9	5	27	4	22	20	0	7	7	0	21		Q6PFX7
ENSMUST00000118327						7	5	11	6	2	1	0	0	0	0	0		
ENSMUST00000118328						4	4	3	3	3	0	0	0	0	0	0		
ENSMUST00000118329						41	34	94	35	45	19	1	0	3	0	0		
ENSMUST00000118330						7	1	14	27	4	1	0	0	0	0	0		
ENSMUST00000118332	ENSMUSG00000089859	2	90322222	90325208	1	0	0	0	0	3	4	0	0	0	0	0	A2ATW2	
ENSMUST00000118333						1	2	12	0	4	0	0	0	0	0	0		
ENSMUST00000118334						1	0	0	3	0	1	0	0	0	0	0		
ENSMUST00000118335						1	2	4	0	0	0	0	0	0	0	0		
ENSMUST00000118336	ENSMUSG00000080781	11	73723960	73725022	-1	2	3	11	6	2	3	0	0	0	0	0		
ENSMUST00000118337						5	2	7	12	2	1	2	13	7	1	13		
ENSMUST00000118338						36	17	30	725	83	89	0	0	0	0	0		
ENSMUST00000118339						8	1	18	13	7	6	2	2	2	0	5		
ENSMUST00000118340	ENSMUSG00000062232	3	79062516	79286517	-1	24	22	43	0	0	0	0	147	0	0	47	E9QNQ4	
ENSMUST00000118341	ENSMUSG00000027951	3	89715022	89753446	1	0	0	0	0	0	0	0	0	0	0	0		Q99MU3
ENSMUST00000118342						4	5	16	6	6	1	0	0	0	0	0		
ENSMUST00000118343						1	3	3	1	1	0	0	0	0	0	0		
ENSMUST00000118344						6	7	5	6	6	7	0	0	0	0	0		
ENSMUST00000118345						1	2	3	0	2	0	0	0	0	0	0		
ENSMUST00000118346						0	0	0	0	0	0	6	24	3	15	5		
ENSMUST00000118347						0	0	0	0	1	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118348						2	2	22	4	6	0	0	0	0	0	2		
ENSMUST00000118349						3	2	9	76	9	4	0	0	0	0	2		
ENSMUST00000118350						25	22	36	246	42	24	0	2	0	1	1		
ENSMUST00000118351						5	1	0	133	16	5	28	15	28	24	42		
ENSMUST00000118352						5	5	33	3	0	7	3	0	0	5	0		
ENSMUST00000118353	ENSMUSG00000018395	11	53567379	53601967	1	0	7	8	0	8	0	5	0	0	27	0	B1AQZ2	
ENSMUST00000118354						3	1	3	1	3	1	0	0	0	0	0		
ENSMUST00000118355						9	7	64	12	8	8	3	0	5	0	3		
ENSMUST00000118356						2	0	1	1	0	1	0	0	0	0	0		
ENSMUST00000118357						6	1	15	7	6	0	0	0	0	0	0		
ENSMUST00000118358						4	5	54	5	6	1	0	0	0	0	0		
ENSMUST00000118359						8	2	23	58	7	4	0	0	0	1	1		
ENSMUST00000118360	ENSMUSG00000040896	3	105452330	105674002	1	16	7	20	44	11	11	0	0	0	0	0	B2RUE0	Q9Z0V1
ENSMUST00000118361						4	3	15	8	13	1	1	2	0	0	2		
ENSMUST00000118362	ENSMUSG00000022498	16	11074911	11134650	-1	19	18	17	14	16	16	28	46	35	4	48	Q3TWZ5	
ENSMUST00000118363						38	27	86	37	43	27	0	2	3	1	4		
ENSMUST00000118364	ENSMUSG00000049093	6	67422932	67491855	-1	15	11	19	8	12	7	3	14	12	5	3	G5E8U4	
ENSMUST00000118365	ENSMUSG00000041849	15	5095981	5108539	-1	53	38	281	72	37	44	565	1556	1010	99	908	E9PWH2	
ENSMUST00000118366	ENSMUSG00000024012	17	29332072	29347904	-1	0	3	0	52	6	2	961	1016	710	164	538		Q791T5
ENSMUST00000118367	ENSMUSG00000066760	7	17074040	17133450	1	3	4	4	0	3	2	0	0	0	0	0	D0VY58	
ENSMUST00000118368	ENSMUSG00000020415	11	43420250	43426251	-1	0	0	0	0	0	0	65	169	26	226	77		Q9CQJ7
ENSMUST00000118369	ENSMUSG00000023902	17	23600856	23611019	1	0	0	0	0	0	0	0	0	0	0	0	E9PX93	
ENSMUST00000118370	ENSMUSG00000055994	8	88647315	88688474	1	3	0	8	0	1	0	112	240	43	0	35	Q80SY9	
ENSMUST00000118371						4	0	2	2	3	1	0	0	0	0	0		
ENSMUST00000118372						4	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000118373						0	1	7	0	3	2	0	0	0	0	0		
ENSMUST00000118374	ENSMUSG00000034194	14	69697307	69707584	-1	1	13	1	3	0	0	6	6	3	3	0	E9PUE1	
ENSMUST00000118375	ENSMUSG00000038517	11	97136171	97151495	-1	0	0	0	0	0	0	625	532	207	38	384	Z4YKN2	
ENSMUST00000118376						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000118377						17	12	30	13	14	15	0	0	0	0	0		
ENSMUST00000118378						0	2	1	5	7	1	0	0	0	0	0		
ENSMUST00000118379						56	64	70	82	46	20	3	7	3	0	9		
ENSMUST00000118380						9	8	7	1	5	5	0	0	0	0	0		
ENSMUST00000118381	ENSMUSG00000060733	10	71347763	71433327	1	14	3	2	9	8	7	28	51	31	7	29		Q7TT16
ENSMUST00000118382						2	2	7	1	4	1	0	0	0	0	0		
ENSMUST00000118383	ENSMUSG00000030492	7	35448796	35466036	1	0	0	0	0	3	0	0	0	0	0	0	Q3UQE3	Q9QXA6
ENSMUST00000118384	ENSMUSG00000024403	17	35233660	35238767	1	1	0	1	0	0	0	7	14	15	2	2	B0V2H4	
ENSMUST00000118385						3	4	2	1	1	2	0	0	0	0	0		
ENSMUST00000118386						0	3	8	0	2	0	0	0	0	0	0		
ENSMUST00000118387						7	7	17	11	18	5	0	0	0	0	0		
ENSMUST00000118388						4	3	11	12	2	4	0	3	0	0	0		
ENSMUST00000118389						2	0	7	2	1	1	1	1	1	1	4		
ENSMUST00000118390	ENSMUSG00000022973	16	90936092	91011308	-1	0	10	0	0	0	8	89	0	895	0	930	F7BQW7	
ENSMUST00000118391						1	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000118392						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000118393						5	2	8	0	1	3	0	0	0	0	0		
ENSMUST00000118394						2	4	17	4	1	1	0	0	0	0	0		
ENSMUST00000118395	ENSMUSG00000032815	8	123268300	123318576	-1	139	115	748	222	89	69	2	6	9	0	6	D3Z6Y5	
ENSMUST00000118396						3	1	2	3	3	2	0	0	0	0	1		
ENSMUST00000118398						4	0	3	5	0	0	0	0	0	0	0		
ENSMUST00000118399						75	76	95	133	124	65	2	2	10	0	9		
ENSMUST00000118400						5	2	8	2	3	1	0	0	0	0	0		
ENSMUST00000118401	ENSMUSG00000052736	6	129647496	129660689	-1	0	0	0	0	0	0	0	5	0	1	0	Q9WVJ7	
ENSMUST00000118402						2	1	8	11	3	0	0	0	0	0	0		
ENSMUST00000118403						1	2	2	1	0	1	0	0	0	0	0		
ENSMUST00000118404						5	1	10	3	7	3	0	0	0	0	0		
ENSMUST00000118405	ENSMUSG00000030830	7	127296260	127335138	1	16	0	12	0	21	13	57	5543	228	352	765	D3YW95	
ENSMUST00000118406						5	1	11	2	3	0	0	0	0	0	0		
ENSMUST00000118407						9	6	50	19	15	0	0	0	0	1	3		
ENSMUST00000118408	ENSMUSG00000051000	3	85660061	85817291	-1	15	8	38	0	27	0	0	0	0	0	0		Q505K2
ENSMUST00000118409						3	1	0	2	2	0	0	0	0	0	0		
ENSMUST00000118410	ENSMUSG00000027531	3	10311956	10331439	-1	6	2	27	25	16	4	199	618	200	377	158	Q80ZJ2	
ENSMUST00000118411	ENSMUSG00000044313	3	101813076	101848959	-1	14	6	22	11	19	0	1	1	0	0	0		Q8CI17
ENSMUST00000118412	ENSMUSG00000044117	16	13986604	14101500	1	2	0	0	0	6	1	0	0	1	0	0	D3YWS4	
ENSMUST00000118413	ENSMUSG00000046460	9	54538984	54545020	1	3	4	0	7	0	5	0	0	0	0	3		Q8BI17
ENSMUST00000118414						0	0	1	0	0	0	0	2	0	1	0		
ENSMUST00000118415						8	2	3	2	0	0	0	0	9	36	4		
ENSMUST00000118416						1	6	13	2	4	2	0	0	0	0	0		
ENSMUST00000118417						3	3	5	2	6	2	4	2	1	3	3		
ENSMUST00000118418						15	14	27	37	28	4	0	0	0	0	0		
ENSMUST00000118419	ENSMUSG00000031554	8	24727093	24824369	-1	8	8	57	0	4	0	0	0	0	0	0		Q3TTE0
ENSMUST00000118420	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	0	0	0	53	0	76	162	0		Q9CQE3
ENSMUST00000118421						0	1	2	10	4	3	0	0	0	0	0		
ENSMUST00000118422	ENSMUSG00000032551	9	122945089	122951000	-1	0	0	0	17	0	0	42	87	19	83	17	D3YWR8	
ENSMUST00000118424						81	66	105	88	78	32	63	268	147	13	165		
ENSMUST00000118425						1	1	6	4	1	0	0	0	1	0	1		
ENSMUST00000118426	ENSMUSG00000022044	14	66344296	66361680	1	2	1	3	0	5	0	0	0	0	0	0	Q05DI3	
ENSMUST00000118427						6	3	4	7	6	1	1	0	0	0	0		
ENSMUST00000118428	ENSMUSG00000031201	X	75416628	75454001	1	0	0	0	0	0	0	8	0	0	29	0		P46737
ENSMUST00000118429	ENSMUSG00000047554	7	109972187	109986929	-1	12	13	4	14	0	0	11	0	0	103	37		Q8K1A5
ENSMUST00000118430						0	2	6	74	10	2	0	12	4	18	2		
ENSMUST00000118431						0	0	0	0	0	4	15	49	14	145	27		
ENSMUST00000118432	ENSMUSG00000031596	8	40862396	40922308	1	3	1	2	3	10	5	0	0	0	0	0	E9QJY0	
ENSMUST00000118433						28	21	16	30	22	12	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118434						3	2	2	0	1	0	0	0	0	0	0		
ENSMUST00000118435						1	1	1	0	0	0	0	0	0	1	0		
ENSMUST00000118436						4	3	3	1	3	2	0	0	0	1	0		
ENSMUST00000118437						0	2	0	2	0	0	0	0	0	0	0		
ENSMUST00000118438	ENSMUSG00000022722	16	59612949	59639391	-1	0	0	0	0	1	0	2	6	0	4	0		O88848
ENSMUST00000118440	ENSMUSG00000025231	19	46396896	46488804	1	11	4	13	17	13	12	4	10	8	4	16	D3Z7B6	
ENSMUST00000118441						6	3	15	9	13	4	2	8	17	24	13		
ENSMUST00000118442	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3X6	
ENSMUST00000118443						1	1	0	8	1	3	0	1	1	2	0		
ENSMUST00000118444	ENSMUSG00000001802	7	35200027	35215498	-1	11	0	41	215	11	7	0	0	0	0	0	E9Q711	
ENSMUST00000118445						2	0	1	4	1	2	0	0	0	2	0		
ENSMUST00000118446						6	7	19	13	7	6	1	4	0	0	3		
ENSMUST00000118447	ENSMUSG00000030167	6	129666015	129678973	-1	1	1	3	0	0	0	0	8	0	4	8	Q9WU32	
ENSMUST00000118448						5	2	30	5	1	4	113	381	147	759	88		
ENSMUST00000118450						13	6	4	21	9	7	0	0	1	0	0		
ENSMUST00000118451						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000118452						1	1	4	4	3	1	2	16	6	11	12		
ENSMUST00000118453						2	2	7	1	1	1	0	0	0	0	0		
ENSMUST00000118454						3	1	4	1	3	1	0	0	0	0	0		
ENSMUST00000118455	ENSMUSG00000040249	10	127538161	127621148	-1	10	9	26	62	14	14	2	6	0	0	6	D3Z5M3	
ENSMUST00000118456						5	0	14	3	1	1	0	0	0	0	0		
ENSMUST00000118457						2	3	0	7	3	0	3	3	7	0	2		
ENSMUST00000118458						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118459						0	0	0	0	0	0	137	793	203	439	106		
ENSMUST00000118460						95	84	147	112	136	76	2	17	13	0	7		
ENSMUST00000118461						1	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000118463	ENSMUSG00000061984	11	73814118	73816880	-1	4	2	1	0	3	1	0	0	0	0	0	Q7TRX6	
ENSMUST00000118464						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000118465	ENSMUSG00000048240	10	80948624	81014945	-1	4	5	6	2	11	4	0	0	0	0	0	Q3UGN1	Q61016
ENSMUST00000118466	ENSMUSG00000021792	14	40993740	41013788	-1	0	0	0	48	0	11	0	0	0	0	51	Q3U125	
ENSMUST00000118467						2	2	5	4	4	2	0	0	0	0	0		
ENSMUST00000118469						5	3	4	4	6	5	0	0	0	1	0		
ENSMUST00000118470	ENSMUSG00000027660	3	31095058	31122577	1	10	0	0	27	0	12	434	969	545	130	511	Q3TB81	Q60665
ENSMUST00000118471	ENSMUSG00000021288	12	111758849	111807844	1	0	15	0	43	0	3	29	0	57	5	49	Q5UE59	
ENSMUST00000118472						2	3	4	4	5	1	0	0	0	0	0		
ENSMUST00000118473						5	7	8	5	7	5	0	0	0	0	0		
ENSMUST00000118474						7	2	3	7	2	1	0	0	0	0	0		
ENSMUST00000118475						1	1	6	1	2	5	0	1	2	1	0		
ENSMUST00000118476						0	3	3	2	2	0	0	0	0	0	0		
ENSMUST00000118477						4	15	9	10	9	0	0	1	1	0	0		
ENSMUST00000118478						3	1	6	5	2	0	0	0	0	0	0		
ENSMUST00000118479						0	1	1	0	0	2	0	0	0	0	0		
ENSMUST00000118480						61	25	31	645	80	60	1	0	0	0	0		
ENSMUST00000118481						1	2	0	3	4	2	41	173	110	199	85		
ENSMUST00000118482						6	1	8	4	6	5	4	5	2	2	6		
ENSMUST00000118483	ENSMUSG00000024830	19	4156713	4163354	-1	0	0	0	0	0	0	0	0	0	0	34	D3YWB8	
ENSMUST00000118484						4	2	5	5	8	3	0	0	0	0	0		
ENSMUST00000118485	ENSMUSG00000036466	9	64385626	64709205	1	0	0	0	45	0	0	0	0	0	0	1		Q80T91
ENSMUST00000118486						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000118487	ENSMUSG00000024187	17	26211822	26244223	-1	0	0	14	1	6	4	829	1384	679	108	609		Q8C0Z1
ENSMUST00000118488						1	0	0	1	1	1	0	3	0	0	0		
ENSMUST00000118489	ENSMUSG00000063239	17	27422387	27513341	-1	6	12	28	87	26	6	0	0	0	0	0		
ENSMUST00000118490						0	1	0	2	1	1	191	519	812	238	902		
ENSMUST00000118491						4	1	8	12	7	2	0	0	0	0	0		
ENSMUST00000118492						1	0	2	1	0	1	0	0	0	0	0		
ENSMUST00000118493	ENSMUSG00000038695	7	44467980	44471662	1	0	0	0	12	0	0	0	0	19	0	6		Q9CR30
ENSMUST00000118494						3	3	6	6	5	5	0	0	0	0	0		
ENSMUST00000118496						3	1	4	4	4	0	0	0	0	0	0		
ENSMUST00000118497						53	55	60	43	45	26	5	12	21	6	34		
ENSMUST00000118498	ENSMUSG00000020238	10	81486249	81496392	-1	0	1	0	0	0	0	1976	1914	1273	102	1119	D3YU17	
ENSMUST00000118499						0	0	7	0	0	0	1990	8631	2324	11347	2175		
ENSMUST00000118500	ENSMUSG00000022604	16	55899888	55934855	-1	20	9	32	33	21	5	0	0	0	0	13		Q9CZ62
ENSMUST00000118501	ENSMUSG00000030417	7	35641982	35647521	-1	0	0	0	22	0	1	42	158	42	346	48	Q564F6	P56812
ENSMUST00000118503						2	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000118504	ENSMUSG00000024039	17	31612623	31637199	-1	0	0	0	0	0	0	0	0	0	1	0		Q91WT9
ENSMUST00000118505						7	5	16	1	3	7	0	0	0	0	0		
ENSMUST00000118506						678	723	2518	1102	1056	488	5	2	3	0	10		
ENSMUST00000118507						5	3	4	6	3	1	0	0	0	0	0		
ENSMUST00000118508						21	0	6	259	12	2	0	0	10	0	4		
ENSMUST00000118509						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000118510	ENSMUSG00000050875	18	59062248	59076962	1	0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000118511						2	8	18	7	17	6	1	14	3	1	4		
ENSMUST00000118512						40	27	45	23	22	23	0	0	0	0	0		
ENSMUST00000118513						2	2	0	2	3	2	0	0	0	0	0		
ENSMUST00000118514						0	2	0	3	3	1	0	0	0	0	0		
ENSMUST00000118515	ENSMUSG00000008140	7	44489937	44496529	-1	0	6	0	0	1	3	560	542	286	62	255		Q3TAS6
ENSMUST00000118516						1	1	3	2	5	3	0	0	0	0	0		
ENSMUST00000118517						0	0	6	7	0	2	0	0	0	0	0		
ENSMUST00000118518						12	7	10	11	12	7	4	1	1	0	3		
ENSMUST00000118519						3	3	0	2	4	2	0	0	0	0	0		
ENSMUST00000118520						0	2	5	1	2	3	0	0	1	2	0		
ENSMUST00000118521						0	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000118522	ENSMUSG00000022974	16	91014037	91044543	-1	54	36	318	186	62	37	33	159	91	22	163		P58501
ENSMUST00000118523						3	3	3	0	4	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118524						0	0	2	3	0	1	0	0	0	0	0		
ENSMUST00000118525	ENSMUSG00000057766	18	12252362	12305720	-1	12	4	0	0	12	0	0	0	0	0	0	D3YVV3	
ENSMUST00000118526						2	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000118527	ENSMUSG00000029650	5	147878437	147894815	-1	0	2	0	1	0	0	0	39	0	2	0		Q9DC26
ENSMUST00000118528						12	9	49	18	1	5	0	2	0	0	1		
ENSMUST00000118529						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118530						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000118531	ENSMUSG00000063600	3	29082023	29691209	1	0	0	3	0	1	0	0	0	0	0	0		Q8C088
ENSMUST00000118532	ENSMUSG00000071158	6	129766568	129784270	-1	6	9	5	4	8	3	0	0	0	0	0	Q3UU75	
ENSMUST00000118533						16	12	18	42	29	7	2291	4968	2497	15763	1865		
ENSMUST00000118534						3	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000118535	ENSMUSG00000019478	8	123805985	123835287	1	11	14	14	24	10	0	19	29	7	6	18		P56371
ENSMUST00000118536						6	4	5	2	3	3	0	0	0	0	0		
ENSMUST00000118537						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118538						74	92	567	148	114	51	0	6	5	0	4		
ENSMUST00000118539	ENSMUSG00000028179	3	157894248	157925077	-1	14	5	5	23	10	5	1	2	0	9	2		Q8VCN5
ENSMUST00000118540	ENSMUSG00000094661	JH584294.1	102539	104139	-1	0	0	0	0	0	0	0	0	0	0	0	Q548P0	O70460
ENSMUST00000118541						3	4	5	7	8	3	0	0	0	0	0		
ENSMUST00000118542						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118543	ENSMUSG00000047215	5	65388364	65391444	-1	0	4	0	0	0	0	13	113	0	14	0	D3Z629	
ENSMUST00000118544	ENSMUSG00000061759	10	4432467	4455141	1	159	140	750	232	127	51	54	200	114	77	187		A6H630
ENSMUST00000118545	ENSMUSG00000054520	5	34525838	34563641	1	0	0	0	104	30	0	0	51	16	0	15	E9QJU7	
ENSMUST00000118546						1	0	1	2	2	0	0	3	0	3	1		
ENSMUST00000118547						0	0	2	10	8	3	0	2	0	1	0		
ENSMUST00000118548						5	1	3	3	4	2	0	0	0	0	0		
ENSMUST00000118549	ENSMUSG00000032297	9	59577917	59607292	1	0	0	0	0	0	0	0	0	0	0	0	D3YU11	
ENSMUST00000118550						2	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000118551	ENSMUSG00000024608	18	60774510	60778546	1	0	0	0	25	0	0	10	9	0	20	20		P62264
ENSMUST00000118553						1	5	3	3	1	0	0	2	1	2	0		
ENSMUST00000118554						0	0	0	0	0	0	0	8	0	24	9		
ENSMUST00000118556	ENSMUSG00000031075	7	144588549	144751974	-1	38	1	48	60	20	1	0	0	0	0	0	G8JL82	
ENSMUST00000118557	ENSMUSG00000028102	3	96635376	96645366	1	0	4	16	47	16	8	0	25	0	25	0		Q9Z210
ENSMUST00000118558	ENSMUSG00000023089	6	24518666	24528013	-1	0	0	0	0	3	0	3	4	0	17	5	D3YTQ8	
ENSMUST00000118559	ENSMUSG00000046806	6	34871771	34878060	-1	0	2	6	0	2	3	0	9	5	0	0	D3Z648	
ENSMUST00000118560						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118561						2	2	2	3	1	2	0	0	0	0	0		
ENSMUST00000118562						9	6	62	12	16	3	1	1	0	1	1		
ENSMUST00000118563	ENSMUSG00000027849	3	103575231	103645569	1	0	0	0	18	0	0	0	0	0	0	0	Q3UY13	
ENSMUST00000118564	ENSMUSG00000062044	7	45783738	45804144	1	3	20	21	505	49	20	0	0	0	0	0	E9QNZ5	
ENSMUST00000118565						2	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000118566	ENSMUSG00000027940	3	90072649	90100902	1	0	0	0	0	0	0	437	1750	791	238	475	E9Q7Q3	
ENSMUST00000118567						1	1	11	5	4	1	0	0	0	0	0		
ENSMUST00000118568						4	5	1	3	7	3	0	0	0	0	0		
ENSMUST00000118569						1	1	5	2	0	1	0	0	1	0	0		
ENSMUST00000118570	ENSMUSG00000046711	17	27556620	27563674	1	0	0	0	0	0	0	18	10	9	7	9	Q3TVP0	P17095
ENSMUST00000118571	ENSMUSG00000031021	7	109735834	109752875	-1	0	4	11	81	5	6	136	108	46	40	5	D3Z6W5	
ENSMUST00000118573						2	7	1	1	5	0	0	0	0	0	0		
ENSMUST00000118574	ENSMUSG00000078942	13	100281121	100317674	-1	54	46	0	0	0	0	20	141	57	0	103		Q9JIB6
ENSMUST00000118576	ENSMUSG00000041609	5	115648175	115731621	-1	16	7	14	26	20	0	12	6	11	0	4	D3YTR9	
ENSMUST00000118577						0	0	1	1	1	1	0	0	0	0	0		
ENSMUST00000118578	ENSMUSG00000021848	14	48657679	48667644	-1	4	4	10	60	12	1	0	0	0	0	0	Q8VD35	
ENSMUST00000118579						7	4	11	10	12	3	0	0	0	0	0		
ENSMUST00000118580	ENSMUSG00000042594	5	121815488	121837646	-1	0	0	0	94	0	0	0	0	0	0	0	D3Z3Y5	
ENSMUST00000118581						2	2	5	1	6	5	0	0	0	0	0		
ENSMUST00000118582						6	3	22	25	5	4	1	0	0	0	0		
ENSMUST00000118583	ENSMUSG00000040488	7	27305136	27337692	-1	0	7	0	7	0	0	0	0	0	6	50	D3Z598	
ENSMUST00000118584						11	8	15	7	8	6	3	3	2	0	0		
ENSMUST00000118585						5	3	5	9	5	7	0	0	0	0	0		
ENSMUST00000118586						2	1	2	1	2	1	0	0	0	0	0		
ENSMUST00000118587	ENSMUSG00000027954	3	89271733	89281142	-1	8	5	46	84	13	7	0	0	0	0	0	D3YTT5	
ENSMUST00000118588						7	1	3	3	9	2	0	0	0	0	0		
ENSMUST00000118589						7	5	8	3	6	4	0	0	0	0	3		
ENSMUST00000118590						2	0	5	1	3	2	0	0	0	0	0		
ENSMUST00000118591						0	1	2	8	4	1	1	0	1	0	0		
ENSMUST00000118592	ENSMUSG00000035173	19	56787481	56822190	-1	30	21	49	15	33	21	296	1420	805	145	605		Q8C9S4
ENSMUST00000118593	ENSMUSG00000014599	3	107741048	107760469	-1	0	8	0	0	0	0	462	2482	438	97	335		P07141
ENSMUST00000118594						0	7	9	0	0	2	0	0	0	0	0		
ENSMUST00000118595						1	0	0	3	1	3	0	0	0	0	0		
ENSMUST00000118596						3	0	0	2	6	0	0	0	0	0	0		
ENSMUST00000118597						3	1	0	3	2	0	0	0	0	0	0		
ENSMUST00000118598						2	0	8	3	3	2	0	0	1	0	1		
ENSMUST00000118599	ENSMUSG00000046711	17	27556620	27563674	1	1	0	9	0	3	0	0	0	0	1	5	Q566K0	P17095
ENSMUST00000118600	ENSMUSG00000041268	9	54365158	54501760	-1	6	21	39	39	38	0	507	457	3177	177	2555		Q8BPN8
ENSMUST00000118601						0	0	0	2	1	2	0	0	0	0	0		
ENSMUST00000118602	ENSMUSG00000046768	12	75308322	75401456	1	0	0	15	2	0	0	0	0	0	0	0	D3YX61	
ENSMUST00000118604	ENSMUSG00000021062	12	76797960	76822908	-1	4	3	17	3	3	2	0	0	0	0	0	D3YTZ8	
ENSMUST00000118605	ENSMUSG00000042105	7	128611328	128696425	1	18	11	43	36	16	3	4	20	0	5	14		Q8CDA1
ENSMUST00000118606						4	2	2	5	6	2	0	0	0	0	0		
ENSMUST00000118607	ENSMUSG00000042202	4	155601416	155623340	1	1	0	0	75	5	0	12	4	47	7	22		Q8C811
ENSMUST00000118608						1	3	30	6	2	2	0	0	0	0	0		
ENSMUST00000118609						2	7	13	20	3	2	0	0	0	0	0		
ENSMUST00000118610						8	2	2	0	3	1	0	0	0	0	0		
ENSMUST00000118611						0	0	3	0	1	0	6	10	0	6	6		
ENSMUST00000118612	ENSMUSG00000040195	10	127666901	127701049	1	2	1	2	84	6	2	4	7	12	2	0	Q8K2N3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118613	ENSMUSG00000024208	17	27122663	27133916	-1	4	0	3	5	1	0	0	0	0	0	0	D3Z4D6	
ENSMUST00000118614						3	2	5	1	5	5	1	3	0	1	2		
ENSMUST00000118615						5	0	31	2	5	3	0	0	0	0	0		
ENSMUST00000118616	ENSMUSG00000082482	X	116681178	116681525	1	1	3	2	2	2	3	0	0	0	0	0	S4R1M3	
ENSMUST00000118617						1	1	10	8	1	0	0	1	1	3	0		
ENSMUST00000118618						8	0	5	9	8	1	0	0	0	0	0		
ENSMUST00000118619						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000118620						116	138	68	118	113	23	260	1472	413	93	754		
ENSMUST00000118621						0	1	2	1	0	0	0	0	0	0	0		
ENSMUST00000118622	ENSMUSG00000037134	8	77549397	77581338	1	9	8	9	0	6	3	0	2	2	16	7		Q3U3W5
ENSMUST00000118623	ENSMUSG00000024826	19	5896516	5913010	-1	1	0	0	0	0	0	875	881	634	87	434	D3Z5N6	
ENSMUST00000118624						12	9	15	8	17	1	0	0	0	0	0		
ENSMUST00000118625						0	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000118626	ENSMUSG00000030116	6	122505845	122529290	1	0	0	0	0	0	0	0	0	0	2	0	D3Z4D7	
ENSMUST00000118627	ENSMUSG00000023764	11	3131850	3193463	-1	115	76	170	274	145	76	18	82	18	39	13	A8Y5K5	
ENSMUST00000118628	ENSMUSG00000038695	7	44467980	44471662	1	0	0	0	0	0	0	122	162	28	18	55		Q9CR30
ENSMUST00000118629						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000118630						0	1	0	0	2	0	5	0	0	0	5		
ENSMUST00000118631						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000118632	ENSMUSG00000050856	5	108433244	108434448	-1	0	0	0	0	0	0	0	0	3	7	2	Q8BTB6	
ENSMUST00000118633						2	2	14	5	5	1	0	0	0	0	0		
ENSMUST00000118634						9	6	8	104	17	6	0	3	0	0	0		
ENSMUST00000118636						3	1	6	8	2	3	0	0	0	0	0		
ENSMUST00000118637						0	0	1	2	0	0	1	6	1	0	1		
ENSMUST00000118638						8	4	43	2	6	3	0	0	3	3	0		
ENSMUST00000118639	ENSMUSG00000031603	8	40279166	40308331	-1	0	0	0	0	0	0	0	0	0	0	0	D3YU10	
ENSMUST00000118640						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118641						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118642						0	1	4	0	3	0	15	0	0	20	7		
ENSMUST00000118643						3	2	2	1	3	2	0	0	0	0	0		
ENSMUST00000118644						1	4	3	0	5	1	0	1	2	1	0		
ENSMUST00000118645						4	2	0	2	4	2	0	0	0	0	0		
ENSMUST00000118646						7	2	20	5	4	6	0	1	0	0	0		
ENSMUST00000118647						2	5	2	2	5	2	0	0	0	0	0		
ENSMUST00000118648	ENSMUSG00000039713	4	152072498	152115400	1	0	0	0	101	0	0	14	15	0	2	34	B1AS67	
ENSMUST00000118649	ENSMUSG00000032081	9	46232933	46235636	-1	2	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000118650						8	12	14	12	15	1	4	15	8	9	0		
ENSMUST00000118652						0	1	3	1	0	1	6	18	5	27	2		
ENSMUST00000118653						5	5	5	6	9	1	5	11	3	3	3		
ENSMUST00000118654						5	6	1	7	4	4	0	0	0	0	0		
ENSMUST00000118655						7	10	10	4	11	5	27	8	17	20	15		
ENSMUST00000118656						6	2	3	1	2	4	0	0	0	0	0		
ENSMUST00000118657	ENSMUSG00000020622	12	10369973	10390173	1	0	0	0	12	5	0	0	0	0	0	0	Q6P906	Q91YE9
ENSMUST00000118658						2	0	5	2	3	0	0	11	3	0	0		
ENSMUST00000118659						5	4	3	4	5	0	0	0	1	0	1		
ENSMUST00000118660						8	3	6	5	5	4	0	0	0	0	0		
ENSMUST00000118661						19	2	21	120	21	4	2	14	5	0	4		
ENSMUST00000118662						0	0	4	1	0	2	0	0	0	0	0		
ENSMUST00000118663	ENSMUSG00000071551	13	4228700	4248681	1	0	3	0	2	7	4	0	0	0	0	0	G3X9Y6	
ENSMUST00000118664						1	0	0	0	0	0	1	1	0	4	3		
ENSMUST00000118665						7	8	42	15	6	4	0	0	0	0	1		
ENSMUST00000118666	ENSMUSG00000050921	X	107088492	107104974	1	0	0	0	0	0	0	0	0	0	0	0		Q8BFU7
ENSMUST00000118667						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118668						2	3	2	2	2	0	0	0	0	0	0		
ENSMUST00000118669						4	4	3	1	2	1	0	0	0	0	0		
ENSMUST00000118670						4	0	0	1	3	1	0	0	0	1	1		
ENSMUST00000118671						3	2	26	3	5	0	0	0	0	0	0		
ENSMUST00000118672						1	1	2	2	3	0	0	0	0	0	0		
ENSMUST00000118673						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000118674						0	1	2	34	2	0	7	10	0	23	0		
ENSMUST00000118675						5	2	4	6	7	6	0	1	1	0	0		
ENSMUST00000118676						5	7	0	15	2	0	0	0	0	0	0		
ENSMUST00000118677						1	0	5	0	0	1	0	0	0	0	0		
ENSMUST00000118678						3	4	0	3	6	0	0	0	0	1	0		
ENSMUST00000118679	ENSMUSG00000022498	16	11074911	11134650	-1	98	76	105	82	92	58	10	32	12	3	35	D3YU69	
ENSMUST00000118680						16	15	16	49	18	0	0	0	0	0	0		
ENSMUST00000118681						0	10	17	65	12	6	59	498	207	474	199		
ENSMUST00000118682						2	7	3	5	5	4	0	0	0	0	0		
ENSMUST00000118683						1	3	1	2	3	4	4	22	10	16	14		
ENSMUST00000118684						26	19	126	11	11	10	0	0	4	0	1		
ENSMUST00000118685						7	0	1	1	2	2	0	0	0	0	0		
ENSMUST00000118686						0	2	2	0	0	1	0	0	0	0	0		
ENSMUST00000118687	ENSMUSG00000026255	1	87264363	87310839	1	0	0	21	127	0	0	0	0	0	1	1		Q9D4J1
ENSMUST00000118688						5	7	9	6	7	5	0	0	0	0	0		
ENSMUST00000118689						21	10	58	46	22	8	0	0	1	0	3		
ENSMUST00000118690						6	1	6	7	5	5	0	2	0	2	0		
ENSMUST00000118691						2	4	36	17	4	3	0	0	0	0	0		
ENSMUST00000118692						2	7	8	10	5	2	1	1	0	1	0		
ENSMUST00000118693						3	3	1	0	2	0	0	0	0	0	0		
ENSMUST00000118694	ENSMUSG00000025512	7	141493136	141539857	-1	25	5	0	0	27	0	0	0	0	0	0		Q922Q9
ENSMUST00000118696						4	2	5	0	2	2	0	0	0	0	0		
ENSMUST00000118697						3	0	3	5	3	0	0	0	0	0	0		
ENSMUST00000118698	ENSMUSG00000037426	5	32863701	32994236	1	0	0	0	0	0	0	0	4	8	0	2	E9PWF2	
ENSMUST00000118699						1	3	5	4	1	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118700						4	7	1	5	4	2	6	4	1	2	2		
ENSMUST00000118701						5	3	0	4	6	1	0	0	0	0	0		
ENSMUST00000118702						0	0	4	0	4	0	0	0	0	0	0		
ENSMUST00000118703	ENSMUSG00000004071	16	4750348	4790292	-1	2	0	2	29	0	0	54	135	49	0	29		Q9DB75
ENSMUST00000118704	ENSMUSG00000039936	4	149649168	149702571	-1	5	0	0	0	0	8	0	424	91	0	179	Q3TBW3	
ENSMUST00000118705						1	0	1	3	1	0	0	3	0	0	2		
ENSMUST00000118706						3	1	6	5	1	0	0	0	0	0	0		
ENSMUST00000118707	ENSMUSG00000032064	9	50662752	50739517	-1	43	15	329	100	32	25	0	1	0	0	0	F2Z453	
ENSMUST00000118708						9	1	17	7	3	0	7	5	14	278	54		
ENSMUST00000118709						7	5	6	0	3	1	0	0	0	0	0		
ENSMUST00000118710	ENSMUSG00000035596	7	3677789	3693523	-1	0	0	0	99	1	0	0	0	0	33	116	D3YU33	
ENSMUST00000118711						5	4	4	0	3	0	12	28	13	7	6		
ENSMUST00000118712						1	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000118713						1	3	6	0	5	0	0	1	2	0	4		
ENSMUST00000118714						16	10	40	15	10	8	0	0	2	0	0		
ENSMUST00000118716						8	4	35	8	8	3	0	0	0	0	0		
ENSMUST00000118717	ENSMUSG00000033715	13	4049011	4090422	1	7	11	0	5	0	0	0	0	0	0	0	Q91WT7	
ENSMUST00000118718						0	1	3	0	11	2	2	1	1	2	0		
ENSMUST00000118719						1	1	2	2	4	1	0	0	0	0	0		
ENSMUST00000118720						9	13	19	51	18	4	2	4	0	0	0		
ENSMUST00000118721						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000118722						10	12	23	8	13	7	0	4	0	0	4		
ENSMUST00000118723						4	0	6	3	4	0	0	3	4	10	0		
ENSMUST00000118724	ENSMUSG00000024532	18	52646209	52663733	1	0	0	0	0	9	0	0	0	0	0	0	Q9D2T6	
ENSMUST00000118725						0	3	8	3	0	0	0	0	0	1	0		
ENSMUST00000118726	ENSMUSG00000044465	7	105371211	105400054	-1	0	0	0	25	0	20	0	16	0	0	0		Q3U2I3
ENSMUST00000118727						3	2	2	0	1	0	1	0	0	0	0		
ENSMUST00000118728	ENSMUSG00000040195	10	127666901	127701049	1	1	1	2	8	2	3	3	2	3	4	9	E9Q6Z3	
ENSMUST00000118729	ENSMUSG00000046897	15	102203648	102215606	1	22	1	0	76	0	8	1415	2064	1624	234	1476		Q6NZQ6
ENSMUST00000118730						12	4	12	4	8	8	0	0	0	0	0		
ENSMUST00000118731	ENSMUSG00000034488	13	88821472	89323223	1	5	0	0	26	8	3	0	0	0	0	0	Q8C8K0	
ENSMUST00000118732	ENSMUSG00000050074	9	109812280	109826633	1	4	3	2	4	2	2	0	0	0	0	0	Q8C1F8	
ENSMUST00000118733	ENSMUSG00000031543	8	22974844	23150497	1	0	0	0	0	0	0	0	0	0	0	0	D3YTV8	
ENSMUST00000118734						12	5	23	20	10	10	0	0	1	0	1		
ENSMUST00000118735	ENSMUSG00000027606	3	19508595	19610862	1	7	4	11	7	4	5	0	0	0	0	0		Q9CQ94
ENSMUST00000118736						2	1	0	1	1	2	0	0	0	0	0		
ENSMUST00000118737	ENSMUSG00000030917	7	120102376	120120992	1	0	0	2	0	6	8	0	19	0	0	0		Q922Z1
ENSMUST00000118738						4	4	0	1	2	1	0	0	0	0	0		
ENSMUST00000118739						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118740						9	0	80	26	9	2	0	0	0	0	0		
ENSMUST00000118741						1	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000118742						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000118744						1	2	0	1	2	2	0	0	0	0	0		
ENSMUST00000118745						1	2	0	1	1	0	0	0	0	0	0		
ENSMUST00000118746						4	6	4	1	9	3	0	3	0	2	1		
ENSMUST00000118747						1	0	1	2	2	0	0	0	0	0	0		
ENSMUST00000118749						3	4	21	3	5	2	0	0	0	0	0		
ENSMUST00000118750						0	0	0	0	0	0	0	48	5	0	0		
ENSMUST00000118751						0	0	15	5	5	0	0	0	0	0	0		
ENSMUST00000118752						2	5	6	3	9	5	0	1	1	1	0		
ENSMUST00000118753						3	1	0	2	4	5	0	0	0	0	0		
ENSMUST00000118755	ENSMUSG00000070371	7	127932638	127946725	-1	14	7	35	101	30	20	0	0	0	0	0	E9QJT0	
ENSMUST00000118756	ENSMUSG00000021457	13	52583173	52648792	1	8	9	8	6	13	5	151	95	215	5	275	E9PWE9	
ENSMUST00000118757						0	2	0	1	1	2	0	0	0	0	0		
ENSMUST00000118758						1	2	4	9	4	5	0	0	0	0	0		
ENSMUST00000118759	ENSMUSG00000078686	4	60418046	60421952	-1	0	0	0	0	0	0	0	0	0	0	0	A9C496	
ENSMUST00000118760						12	7	13	56	0	0	0	0	0	0	0		
ENSMUST00000118761						6	6	9	7	4	0	62	238	133	99	107		
ENSMUST00000118762	ENSMUSG00000005936	17	28951950	28969549	1	40	38	148	68	60	29	4898	12186	5685	562	3244		Q8CDD8
ENSMUST00000118763	ENSMUSG00000034818	10	81459227	81482709	-1	0	0	0	196	38	0	0	0	0	0	0	D3Z4T1	
ENSMUST00000118764						0	0	0	1	3	0	0	0	0	0	1		
ENSMUST00000118765	ENSMUSG00000029462	5	122354369	122364984	1	0	0	0	0	0	1	25	33	27	22	0	D3YW98	
ENSMUST00000118766						7	3	12	6	10	5	0	0	0	0	0		
ENSMUST00000118767						2	1	2	2	1	3	0	0	0	0	0		
ENSMUST00000118768	ENSMUSG00000024070	17	78949405	79020816	-1	1	2	0	0	0	8	0	5	8	50	54	D3Z6I0	
ENSMUST00000118769	ENSMUSG00000056586	5	150507055	150518164	-1	8	7	17	6	10	8	0	0	0	0	0	C3VD30	
ENSMUST00000118770						17	9	66	244	34	10	0	0	0	0	1		
ENSMUST00000118771	ENSMUSG00000061559	9	54714735	54734519	-1	9	8	11	7	16	11	0	10	3	0	0	Q8BVQ0	
ENSMUST00000118772						9	4	65	11	10	8	1	3	0	5	5		
ENSMUST00000118774						2	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000118775						0	0	17	1	1	0	3	5	3	0	2		
ENSMUST00000118776						6	9	19	14	15	17	13	9	2	0	1		
ENSMUST00000118777						4	0	15	4	4	0	0	0	0	0	0		
ENSMUST00000118778						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118779						1	3	6	1	3	2	0	0	0	0	0		
ENSMUST00000118780						44	53	228	72	63	35	0	0	1	0	0		
ENSMUST00000118781						0	1	4	0	1	0	0	4	1	3	0		
ENSMUST00000118782						3	4	2	7	6	2	0	0	0	0	1		
ENSMUST00000118784	ENSMUSG00000023723	11	88204388	88211507	1	5	0	4	0	0	3	25	41	9	21	15	Q3TI14	
ENSMUST00000118785	ENSMUSG00000045655	14	78081021	78089007	-1	0	0	0	0	0	2	0	0	0	0	0	D3Z583	
ENSMUST00000118786						4	9	13	41	8	3	109	257	104	99	82		
ENSMUST00000118787						0	4	0	6	0	0	0	0	0	0	0		
ENSMUST00000118788	ENSMUSG00000024158	17	24840143	24864450	1	0	0	0	42	0	7	49	109	128	182	73	G5E8T9	
ENSMUST00000118789						5	3	7	5	7	6	0	0	1	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118790						3	3	12	2	5	0	0	0	0	0	0		
ENSMUST00000118791						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000118792						5	2	11	10	13	4	3	1	3	1	1		
ENSMUST00000118793	ENSMUSG00000081650	17	35220834	35224134	1	29	19	38	30	30	15	14	10	7	1	16	B0V2H2	
ENSMUST00000118794						1	0	3	2	1	0	0	0	0	0	0		
ENSMUST00000118795	ENSMUSG00000006019	7	16197147	16222037	-1	12	0	64	26	6	0	0	0	0	0	0	D3YTV3	
ENSMUST00000118796						11	4	20	42	15	11	0	0	0	0	0		
ENSMUST00000118797						26	19	54	153	37	13	0	0	0	0	0		
ENSMUST00000118798						0	1	4	5	0	0	3	0	0	1	0		
ENSMUST00000118800	ENSMUSG00000025083	19	56912361	57008228	-1	0	14	0	0	0	0	0	0	0	0	0		Q5DTU0
ENSMUST00000118801						5	3	4	0	3	1	0	0	0	0	0		
ENSMUST00000118802	ENSMUSG00000054435	6	48684549	48692060	1	0	0	1	0	0	1	6	0	9	87	47	D3YWB5	
ENSMUST00000118803						0	3	0	1	1	1	0	0	0	0	0		
ENSMUST00000118804						4	4	5	12	3	3	26	88	41	6	51		
ENSMUST00000118805						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000118807						1	4	2	0	3	1	0	0	0	0	0		
ENSMUST00000118808	ENSMUSG00000008140	7	44489937	44496529	-1	0	0	15	67	0	0	0	0	0	0	0		Q3TAS6
ENSMUST00000118809	ENSMUSG00000083886	11	74317027	74317997	1	7	3	13	4	7	6	0	0	0	0	0		
ENSMUST00000118810	ENSMUSG00000041775	7	138835823	138846273	-1	0	5	41	9	0	0	26	73	0	40	78		Q9D7G9
ENSMUST00000118811	ENSMUSG00000031516	8	34090420	34108796	-1	0	0	0	0	0	0	19	0	26	0	33	D3Z6H3	
ENSMUST00000118812	ENSMUSG00000020235	10	81366222	81378516	-1	0	0	5	5	0	0	208	145	139	10	56	D3YTV2	
ENSMUST00000118813						4	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000118814						1	1	5	2	4	1	0	0	0	0	0		
ENSMUST00000118815						9	4	35	20	14	4	0	0	0	0	0		
ENSMUST00000118816	ENSMUSG00000035505	5	90214724	90224001	-1	4	0	4	0	0	0	0	21	35	9	41	G5E8U6	
ENSMUST00000118817						1	5	8	4	3	1	2	0	1	1	0		
ENSMUST00000118818						3	3	4	5	7	1	0	1	0	0	0		
ENSMUST00000118819						17	11	83	18	12	11	1	0	0	0	0		
ENSMUST00000118820	ENSMUSG00000073008	X	107255878	107296769	1	0	0	0	0	0	0	3	0	0	0	0		Q3U507
ENSMUST00000118821	ENSMUSG00000067360	X	135302307	135312652	1	15	0	0	0	0	6	0	0	0	0	0	A2AHA7	
ENSMUST00000118822						5	5	4	2	4	0	0	0	0	0	1		
ENSMUST00000118823	ENSMUSG00000005124	15	66891320	66923201	1	3	4	12	6	7	1	0	0	0	0	2	D3Z6X6	
ENSMUST00000118824						4	4	0	6	7	2	0	1	0	2	1		
ENSMUST00000118825						2	0	4	6	2	1	0	0	2	0	0		
ENSMUST00000118826	ENSMUSG00000024277	18	23752333	23893861	1	36	29	205	53	31	14	0	6	4	0	5	Q3TG90	
ENSMUST00000118827						4	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000118828	ENSMUSG00000037098	17	25989036	26069409	-1	24	19	15	0	18	0	0	16	0	2	11		Q8CHD8
ENSMUST00000118829						3	10	51	8	11	2	800	1094	837	4155	592		
ENSMUST00000118830	ENSMUSG00000029462	5	122354369	122364984	1	0	0	0	0	0	0	150	378	153	325	70		Q9QZ88
ENSMUST00000118831	ENSMUSG00000030731	7	44384102	44400187	1	12	12	15	8	0	15	0	0	0	0	0	G3X9Y1	
ENSMUST00000118832						7	1	8	3	5	3	0	0	1	0	0		
ENSMUST00000118833	ENSMUSG00000015804	5	45520229	45529276	1	0	0	0	0	0	0	148	323	138	517	95	D3Z7D6	
ENSMUST00000118834						2	3	3	8	4	5	0	0	0	1	0		
ENSMUST00000118835	ENSMUSG00000045636	8	40990914	41133726	-1	16	8	60	0	0	0	92	263	216	101	114		
ENSMUST00000118836						6	3	3	0	2	2	0	0	0	0	1		
ENSMUST00000118837						1	3	7	2	8	2	0	0	5	0	0		
ENSMUST00000118838						16	6	77	14	26	4	0	0	0	1	2		
ENSMUST00000118839						749	738	436	737	781	386	41	78	105	12	141		
ENSMUST00000118840						0	3	2	1	4	1	0	1	0	0	0		
ENSMUST00000118841						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000118842	ENSMUSG00000073027	X	102707865	102715209	1	0	3	0	0	2	0	0	0	0	0	0	Q2PMX7	
ENSMUST00000118843						6	16	14	8	2	9	0	0	0	0	0		
ENSMUST00000118844						5	3	8	1	5	3	0	0	0	0	0		
ENSMUST00000118845						2	5	20	2	8	3	0	0	0	0	0		
ENSMUST00000118846						2	6	1	3	4	5	0	0	0	0	2		
ENSMUST00000118847						1	1	0	0	0	1	0	0	0	0	1		
ENSMUST00000118848						2	3	3	0	7	1	0	2	0	0	0		
ENSMUST00000118849						2	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000118850	ENSMUSG00000055553	8	70508272	70527956	-1	0	0	6	6	2	5	150	20	55	204	75	G3X9Z9	
ENSMUST00000118851						1	5	5	3	1	1	0	0	0	0	0		
ENSMUST00000118852						1	1	3	1	2	0	0	0	0	0	0		
ENSMUST00000118853	ENSMUSG00000027955	3	79884533	79946280	1	0	56	0	0	74	22	0	0	0	0	0		Q3UPI1
ENSMUST00000118855						11	0	4	61	21	6	0	0	0	0	0		
ENSMUST00000118856	ENSMUSG00000008129	8	84148025	84172590	1	12	0	35	17	23	11	1	0	0	0	0	E9QNR8	
ENSMUST00000118857						8	4	10	12	12	7	0	0	0	0	0		
ENSMUST00000118858						2	5	12	4	6	0	0	0	0	0	0		
ENSMUST00000118859						0	0	6	1	0	4	0	0	0	0	0		
ENSMUST00000118860	ENSMUSG00000027954	3	89271733	89281142	-1	7	0	12	0	8	0	0	2	1	5	0	D3Z7A6	
ENSMUST00000118861						0	1	2	2	4	1	0	0	0	0	1		
ENSMUST00000118862						1	3	16	2	6	4	0	0	0	0	0		
ENSMUST00000118863						0	3	8	0	6	6	0	4	0	7	0		
ENSMUST00000118864						2	1	1	0	2	2	0	0	0	0	0		
ENSMUST00000118865	ENSMUSG00000043964	7	127769815	127775150	1	0	0	0	103	0	0	0	0	0	0	0	D3YX58	
ENSMUST00000118866						0	0	2	7	1	0	0	0	0	0	0		
ENSMUST00000118867	ENSMUSG00000039236	7	78913424	78920396	1	0	0	0	2	0	0	17	0	0	73	27	Q4FK39	Q9JL16
ENSMUST00000118868						11	12	22	21	15	9	0	1	0	1	2		
ENSMUST00000118869	ENSMUSG00000009828	9	78109192	78172107	1	7	7	0	48	0	0	9	15	10	2	13		Q9JKV2
ENSMUST00000118870	ENSMUSG00000066442	9	89210676	89377713	1	4	0	1	91	0	4	0	0	0	0	0	B2KF83	
ENSMUST00000118871						9	3	20	4	9	4	4	0	0	0	1		
ENSMUST00000118872						28	30	74	526	62	24	0	6	0	0	1		
ENSMUST00000118873						2	3	0	2	4	1	0	0	0	0	0		
ENSMUST00000118874						42	27	62	49	33	18	10	14	13	0	3		
ENSMUST00000118875	ENSMUSG00000057666	6	125161715	125166467	-1	16	6	8	76	33	0	6848	10624	1492	4562	889	D2KHZ9	P16858
ENSMUST00000118876						3	0	10	3	0	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118877						0	4	2	3	4	2	0	0	0	0	0		
ENSMUST00000118878	ENSMUSG00000031314	X	101532734	101601789	1	0	0	0	0	0	0	184	240	492	77	323		Q80UV9
ENSMUST00000118879						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118880						0	1	1	2	2	0	0	0	0	0	1		
ENSMUST00000118881						4	2	2	4	0	1	0	0	0	0	0		
ENSMUST00000118882	ENSMUSG00000044681	5	28200819	28245792	-1	0	2	0	24	9	0	0	0	1	0	2		Q4VAB4
ENSMUST00000118883						0	8	11	0	6	10	0	0	0	0	0		
ENSMUST00000118884						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118885	ENSMUSG00000004070	16	4726361	4766742	1	3	0	0	17	0	1	0	15	22	0	0	Q544R7	O70252
ENSMUST00000118886	ENSMUSG00000038145	9	122117283	122169702	1	0	0	0	115	0	0	117	15	415	5	175		Q8VDU5
ENSMUST00000118887						5	8	9	4	7	5	7	45	16	51	13		
ENSMUST00000118888						3	1	1	4	4	2	0	0	0	0	0		
ENSMUST00000118889						5	7	5	3	4	3	1	0	1	0	0		
ENSMUST00000118890						4	1	9	6	3	1	0	0	0	0	0		
ENSMUST00000118891						5	3	7	0	6	4	0	4	0	2	1		
ENSMUST00000118892						7	3	63	37	14	8	0	0	1	0	0		
ENSMUST00000118893						5	4	10	13	10	4	0	1	0	0	0		
ENSMUST00000118894						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000118895						7	1	1	2	6	1	0	0	0	0	0		
ENSMUST00000118896	ENSMUSG00000039539	8	37522298	38661508	-1	0	8	28	31	9	0	0	0	0	0	0		Q8BX51
ENSMUST00000118897						4	0	3	4	0	0	0	0	0	0	0		
ENSMUST00000118898	ENSMUSG00000020069	10	63014664	63024217	-1	1	4	4	3	4	2	12	117	29	0	37	D3YWT1	
ENSMUST00000118899						4	3	3	3	4	7	0	0	0	0	0		
ENSMUST00000118900						2	0	2	4	1	8	0	0	0	0	0		
ENSMUST00000118901						5	10	8	2	6	7	0	0	0	0	0		
ENSMUST00000118902	ENSMUSG00000032897	4	120757438	120831572	-1	9	3	0	9	10	0	117	0	0	0	0		P70353
ENSMUST00000118903						7	5	10	13	3	2	0	1	0	0	0		
ENSMUST00000118904	ENSMUSG00000024182	17	26138688	26195811	1	0	0	0	0	0	10	50	0	46	0	222	Q14DJ8	
ENSMUST00000118905						3	1	5	11	1	0	0	0	0	0	0		
ENSMUST00000118906						3	2	1	0	1	1	0	0	0	0	0		
ENSMUST00000118907						3	0	9	1	5	0	0	0	0	0	0		
ENSMUST00000118908						26	27	96	35	41	21	0	0	0	0	0		
ENSMUST00000118909						0	0	3	0	12	7	1737	3625	2108	271	957		
ENSMUST00000118910	ENSMUSG00000029263	5	108312609	108349355	1	9	0	139	0	0	3	0	0	0	3	0	D3YTQ6	
ENSMUST00000118911						20	17	14	152	19	8	9	5	4	0	8		
ENSMUST00000118912						1	1	4	7	3	0	0	0	0	0	0		
ENSMUST00000118913						1	1	4	4	0	0	0	0	0	0	0		
ENSMUST00000118914						0	4	54	0	14	0	0	0	0	0	0		
ENSMUST00000118915						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118917	ENSMUSG00000015970	14	30009023	30040466	1	20	6	12	5	3	1	2	9	6	0	3		Q8BJ64
ENSMUST00000118918						1	2	5	5	7	5	0	0	0	1	0		
ENSMUST00000118919	ENSMUSG00000050821	16	20693282	20703048	1	5	0	0	0	0	0	0	24	0	3	0	D3Z4E4	
ENSMUST00000118920	ENSMUSG00000044287	8	105893567	105895023	1	1	2	0	12	0	0	0	3	0	2	6		Q8C4W3
ENSMUST00000118921						3	2	5	4	1	1	0	0	0	0	0		
ENSMUST00000118922						10	9	6	49	11	7	0	0	0	0	0		
ENSMUST00000118923	ENSMUSG00000033653	16	21423118	21644680	1	5	0	0	0	0	0	35	12	0	36	0		Q0P5W1
ENSMUST00000118924						33	16	175	55	26	7	23	0	54	131	29		
ENSMUST00000118925						7	6	27	12	10	2	0	0	0	0	0		
ENSMUST00000118926						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118927	ENSMUSG00000030471	7	48789003	48827440	1	3	6	5	16	4	5	119	864	354	401	279		Q9CWU2
ENSMUST00000118928						2	14	17	21	16	6	18	14	25	63	24		
ENSMUST00000118929						1	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000118930						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118931						1	3	5	2	2	2	0	0	0	0	0		
ENSMUST00000118932						2	2	1	3	2	1	0	0	0	0	0		
ENSMUST00000118933						0	4	4	1	0	3	0	0	0	0	0		
ENSMUST00000118934						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118935						2	1	24	3	3	1	0	0	0	0	0		
ENSMUST00000118936	ENSMUSG00000033416	10	75351111	75517972	-1	0	0	7	0	0	0	3596	4968	2599	447	1757	Q05CJ4	
ENSMUST00000118937						3	5	1	8	6	5	0	0	0	0	0		
ENSMUST00000118938						7	2	0	0	0	2	0	0	0	0	0		
ENSMUST00000118939						8	10	14	6	11	2	0	0	0	0	0		
ENSMUST00000118940						0	3	0	0	2	1	0	0	0	0	0		
ENSMUST00000118941	ENSMUSG00000029248	5	77016023	77061529	1	2	0	6	10	6	3	0	0	0	0	0	D3YU57	
ENSMUST00000118942	ENSMUSG00000043051	8	125054195	125261858	1	19	2	7	0	24	12	0	0	0	0	0		Q811T9
ENSMUST00000118943						4	5	15	0	12	0	0	0	0	0	0		
ENSMUST00000118944						3	5	4	3	1	1	0	1	0	0	0		
ENSMUST00000118945						1	2	3	4	5	2	0	0	0	0	0		
ENSMUST00000118946						2	2	0	7	0	1	0	0	0	0	0		
ENSMUST00000118947						3	2	0	0	0	2	6	32	6	15	5		
ENSMUST00000118948						0	4	5	5	2	4	15	28	31	4	14		
ENSMUST00000118949						11	8	12	2	4	0	6	0	158	241	200		
ENSMUST00000118950						1	0	0	2	2	2	0	0	8	5	0		
ENSMUST00000118951						118	129	64	92	78	50	0	0	0	0	0		
ENSMUST00000118952	ENSMUSG00000036779	8	88199213	88259722	1	0	0	0	0	0	0	31	345	264	42	41	E9QJT6	
ENSMUST00000118953						0	2	1	3	2	0	0	0	0	0	0		
ENSMUST00000118954						5	1	0	3	2	1	0	0	0	1	0		
ENSMUST00000118955	ENSMUSG00000000861	11	24078056	24174123	1	2	2	2	17	0	4	6	13	0	7	14		Q9QYE3
ENSMUST00000118956						3	0	2	6	4	0	59	223	92	15	42		
ENSMUST00000118957						4	0	7	12	9	1	0	0	0	0	0		
ENSMUST00000118958						8	8	1	2	7	4	0	0	0	0	0		
ENSMUST00000118959	ENSMUSG00000039187	7	79391929	79450264	1	21	17	88	29	17	12	0	3	4	1	4	F2Z414	
ENSMUST00000118960	ENSMUSG00000090236	16	17835276	17838364	-1	4	6	3	2	6	6	14	53	18	6	9		Q99N23
ENSMUST00000118961	ENSMUSG00000108715	7	27311715	27333604	-1	15	6	10	135	28	6	0	0	0	0	0	E9Q6B8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000118962	ENSMUSG00000030731	7	44384102	44400187	1	0	1	0	59	23	0	0	1	0	0	0	G3X9Y1	
ENSMUST00000118963	ENSMUSG00000048655	3	55137339	55172935	1	1	4	1	2	10	1	0	0	0	0	0	D3YWT6	
ENSMUST00000118964	ENSMUSG00000064068	3	89209081	89227088	-1	2	2	11	159	0	2	0	5	9	0	0	D3YVW0	
ENSMUST00000118965						2	0	7	2	4	4	0	0	0	0	0		
ENSMUST00000118966	ENSMUSG00000046768	12	75308322	75401456	1	32	28	87	37	40	17	0	0	0	0	0	F2Z463	
ENSMUST00000118967						6	1	4	2	2	1	0	0	0	0	0		
ENSMUST00000118968	ENSMUSG00000027606	3	19508595	19610862	1	2	0	0	0	0	0	0	0	0	0	0		Q9CQ94
ENSMUST00000118969	ENSMUSG00000030492	7	35448796	35466036	1	0	0	0	0	0	0	0	0	0	0	0	Q3UQE3	Q9QXA6
ENSMUST00000118970						12	0	30	11	15	13	5	6	1	3	7		
ENSMUST00000118971						7	1	7	14	5	3	1	0	0	0	0		
ENSMUST00000118973						6	8	33	6	3	3	0	0	0	0	0		
ENSMUST00000118974						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118975						3	3	5	4	5	0	0	0	0	1	0		
ENSMUST00000118976	ENSMUSG00000041375	7	16274042	16286795	-1	0	2	0	60	0	0	147	229	119	22	119	D3YW42	
ENSMUST00000118977						2	2	0	3	0	1	0	0	0	0	0		
ENSMUST00000118978						9	6	6	8	16	0	0	0	0	0	0		
ENSMUST00000118979						0	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000118980						1	3	5	9	2	0	0	0	0	1	0		
ENSMUST00000118982						2	0	7	2	4	0	0	0	0	0	0		
ENSMUST00000118983						2	3	5	3	10	0	0	0	0	0	0		
ENSMUST00000118984						2	1	0	0	5	2	0	0	0	0	0		
ENSMUST00000118985						0	0	3	0	0	0	0	3	0	0	0		
ENSMUST00000118986	ENSMUSG00000031241	X	107667964	107688978	1	11	9	15	229	36	26	0	0	1	0	3		Q8K402
ENSMUST00000118987	ENSMUSG00000039741	11	120232947	120292296	1	57	60	14	893	124	88	13	5	6	0	13		Q3UHR0
ENSMUST00000118988						8	6	17	7	14	7	0	0	0	0	0		
ENSMUST00000118989						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118990	ENSMUSG00000024378	18	33199355	33213862	-1	0	1	3	0	0	0	0	0	0	0	9	D3YW24	
ENSMUST00000118991	ENSMUSG00000024070	17	78949405	79020816	-1	0	2	0	0	0	0	0	0	0	0	0	D3YU02	
ENSMUST00000118992						1	2	6	0	1	1	1	3	3	1	1		
ENSMUST00000118993	ENSMUSG00000034118	5	130073326	130135729	1	19	10	15	8	20	9	14	24	20	14	35	Q4FK50	O70281
ENSMUST00000118994						6	6	7	2	9	2	0	0	0	0	0		
ENSMUST00000118995						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000118996						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000118997						5	0	4	5	6	7	0	0	1	1	0		
ENSMUST00000118998						2	0	3	3	1	4	141	211	75	326	38		
ENSMUST00000118999						9	6	4	5	9	6	0	0	0	0	0		
ENSMUST00000119000						2	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000119001						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000119002	ENSMUSG00000028062	3	88549819	88553074	-1	0	0	0	2	0	3	14	27	8	38	4	D3YTS4	
ENSMUST00000119003	ENSMUSG00000066880	8	71908635	71934629	1	33	34	57	74	32	16	118	553	139	213	130	Q91WM0	
ENSMUST00000119004						2	4	4	11	7	3	2	1	0	0	0		
ENSMUST00000119005						2	4	1	10	6	3	0	1	0	0	0		
ENSMUST00000119006						0	0	12	1	2	0	0	0	0	0	0		
ENSMUST00000119007						3	2	3	6	1	2	0	0	2	0	0		
ENSMUST00000119008						15	13	10	21	13	0	3	4	5	0	21		
ENSMUST00000119009						4	2	1	2	1	0	0	0	0	0	0		
ENSMUST00000119010	ENSMUSG00000033436	X	134804145	134809221	-1	0	0	0	0	0	3	0	22	3	3	8		Q6A058
ENSMUST00000119011						1	0	1	0	3	0	0	1	0	0	2		
ENSMUST00000119012						1	1	7	8	1	1	1	1	1	3	0		
ENSMUST00000119013						14	6	16	11	9	5	0	0	0	0	0		
ENSMUST00000119014	ENSMUSG00000029263	5	108312609	108349355	1	0	16	3	0	4	12	20	62	55	9	50	D3Z3Y1	
ENSMUST00000119015	ENSMUSG00000038582	5	122284365	122324281	1	9	8	21	0	17	0	130	0	284	27	238		Q6NVE9
ENSMUST00000119016						1	6	1	2	0	2	7	23	24	1	47		
ENSMUST00000119017						2	2	4	1	2	1	0	0	0	0	0		
ENSMUST00000119018						9	10	15	6	7	5	0	0	0	0	0		
ENSMUST00000119019						0	2	0	1	2	0	0	0	0	0	0		
ENSMUST00000119020						1	0	14	1	0	0	0	0	0	0	0		
ENSMUST00000119022						3	1	1	1	2	0	0	0	0	0	0		
ENSMUST00000119023	ENSMUSG00000039200	16	10192712	10243051	1	0	1	0	0	1	2	0	0	0	0	0		Q3UL97
ENSMUST00000119024						0	4	3	0	8	7	711	564	508	2820	342		
ENSMUST00000119025	ENSMUSG00000029311	5	103989762	104021919	-1	10	4	13	11	9	4	13	31	28	8	39		Q9EQ06
ENSMUST00000119026	ENSMUSG00000034324	5	127241808	127565793	1	16	15	33	70	36	7	0	0	0	0	1	E9QP73	
ENSMUST00000119027	ENSMUSG00000025340	5	130171798	130214342	1	3	0	2	0	0	0	0	0	0	0	0	D3YWB4	
ENSMUST00000119028						1	5	0	1	0	0	0	0	0	0	0		
ENSMUST00000119030						10	5	41	8	8	5	0	0	0	0	0		
ENSMUST00000119031	ENSMUSG00000027259	2	121140428	121156680	1	0	0	0	0	0	0	7	0	0	0	0		Q80SY6
ENSMUST00000119032						8	7	3	3	4	7	0	24	7	6	7		
ENSMUST00000119033	ENSMUSG00000036779	8	88199213	88259722	1	23	0	0	0	0	0	295	0	33	0	150	E9QJT6	
ENSMUST00000119034						0	0	2	1	2	1	0	0	0	2	0		
ENSMUST00000119035	ENSMUSG00000045802	X	96306178	96456294	-1	0	0	1	0	3	0	0	0	0	0	1	Q8BL67	
ENSMUST00000119036						0	2	0	0	3	2	0	0	0	0	0		
ENSMUST00000119037						7	14	38	8	4	2	0	2	0	0	1		
ENSMUST00000119038						2	0	13	0	2	0	0	0	0	0	0		
ENSMUST00000119039						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000119040						1	0	1	0	0	1	0	0	1	0	0		
ENSMUST00000119041	ENSMUSG00000030452	7	55931287	55962476	-1	0	0	0	0	0	0	188	405	0	0	0		Q9JJC8
ENSMUST00000119042						0	0	0	3	0	0	7	8	1	8	6		
ENSMUST00000119043	ENSMUSG00000044252	18	12755314	12941841	-1	7	2	3	2	6	6	0	6	0	10	0		Q91XL9
ENSMUST00000119044						1	2	32	2	6	4	0	0	0	1	0		
ENSMUST00000119045						5	1	2	5	8	4	0	0	0	0	0		
ENSMUST00000119046						0	6	12	61	5	3	0	0	0	0	0		
ENSMUST00000119047	ENSMUSG00000067365	5	38260185	38269634	1	2	0	0	6	0	0	7	13	0	88	0		Q9CZB9
ENSMUST00000119048						6	5	16	10	8	5	0	1	2	0	5		
ENSMUST00000119049						1	0	3	2	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119050						46	26	40	409	112	63	0	2	3	0	1		
ENSMUST00000119051						0	1	18	8	3	0	25	0	0	17	9		
ENSMUST00000119052						2	5	4	4	0	0	2	2	0	0	0		
ENSMUST00000119053	ENSMUSG00000055933	19	11697055	11711874	1	1	0	0	0	0	1	0	0	0	0	0	D3YTU9	
ENSMUST00000119054						4	2	0	2	3	2	0	0	0	0	0		
ENSMUST00000119055	ENSMUSG00000019066	9	21907491	21918192	-1	2	0	11	0	0	0	11	0	0	0	12	D3YW33	
ENSMUST00000119056						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000119057						10	4	12	4	6	2	0	16	3	14	3		
ENSMUST00000119058						8	7	26	4	19	9	0	0	0	0	0		
ENSMUST00000119060	ENSMUSG00000034818	10	81459227	81482709	-1	43	42	57	0	11	37	1	10	3	0	3	D3Z588	
ENSMUST00000119061						11	3	56	0	0	3	0	2	0	0	3		
ENSMUST00000119062						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000119063	ENSMUSG00000000530	15	101128522	101145336	1	0	0	0	24	0	0	115	11	28	9	34		Q61288
ENSMUST00000119064						2	3	6	4	4	4	30	193	56	75	10		
ENSMUST00000119065						4	4	0	2	0	1	0	0	0	0	0		
ENSMUST00000119066						5	1	0	1	5	2	0	0	0	0	0		
ENSMUST00000119067						12	10	62	13	7	4	0	0	0	0	1		
ENSMUST00000119068	ENSMUSG00000054162	8	62951009	63357103	1	0	0	0	0	0	0	0	0	0	0	0		Q8BKV0
ENSMUST00000119069						0	2	3	4	3	0	0	0	0	0	0		
ENSMUST00000119070	ENSMUSG00000021848	14	48657679	48667644	-1	0	0	0	0	0	0	0	0	0	0	0	Q8R0B5	
ENSMUST00000119071						3	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000119072						0	1	2	2	2	2	2	2	0	0	1		
ENSMUST00000119073						1	2	0	0	3	1	0	0	0	0	0		
ENSMUST00000119074						7	9	5	3	7	2	1	0	0	0	0		
ENSMUST00000119075						0	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000119076	ENSMUSG00000049191	X	102066544	102071304	-1	3	0	13	52	10	5	0	18	14	2	23	Q8C065	Q5DTT4
ENSMUST00000119077	ENSMUSG00000051000	3	85660061	85817291	-1	15	0	17	38	6	0	0	0	0	0	0	E9PX40	
ENSMUST00000119078	ENSMUSG00000025409	10	127281956	127289018	-1	0	0	0	88	0	0	293	596	515	33	556		Q3TY92
ENSMUST00000119079						2	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000119080	ENSMUSG00000047797	X	101376378	101385629	1	0	2	0	28	10	0	0	0	0	6	0		P28230
ENSMUST00000119081	ENSMUSG00000048170	7	128696441	128740495	-1	0	0	0	66	0	0	622	956	1031	82	641	H9KV04	
ENSMUST00000119082	ENSMUSG00000083947	17	37768607	37772789	1	5	0	7	7	2	2	0	0	0	0	0	W4VSP0	
ENSMUST00000119083	ENSMUSG00000025726	7	81114799	81170416	1	35	0	52	22	0	0	0	0	0	0	0	E9PXX9	
ENSMUST00000119084	ENSMUSG00000028047	3	89215180	89226837	1	0	0	8	1	0	1	0	24	0	0	69	E9PWF0	
ENSMUST00000119085						3	2	1	2	0	1	0	0	0	0	0		
ENSMUST00000119086						9	3	3	4	1	7	0	0	0	0	0		
ENSMUST00000119087						1	4	3	9	5	1	0	0	0	0	0		
ENSMUST00000119088						28	34	37	34	29	22	0	0	0	0	2		
ENSMUST00000119089						0	1	0	1	2	3	0	5	1	0	0		
ENSMUST00000119090						5	7	14	4	3	3	0	2	2	1	4		
ENSMUST00000119091						3	4	2	4	8	3	0	0	0	0	0		
ENSMUST00000119092	ENSMUSG00000021108	12	73584797	73778185	1	23	12	33	76	29	17	9	21	0	0	11	D3YWQ8	
ENSMUST00000119093	ENSMUSG00000048661	10	120923413	120979332	-1	18	9	15	573	19	15	37	259	216	10	153	D3YU56	
ENSMUST00000119094						0	0	2	4	1	0	0	0	0	1	0		
ENSMUST00000119095						2	2	0	1	0	2	1	0	0	0	0		
ENSMUST00000119096	ENSMUSG00000079852	6	130043731	130067271	-1	1	0	0	3	0	1	0	2	0	0	0	Q542S4	Q60651
ENSMUST00000119097						9	10	28	8	14	5	0	0	0	0	0		
ENSMUST00000119098						2	1	0	0	3	0	0	0	1	0	0		
ENSMUST00000119099						1	3	2	4	1	0	1	3	0	0	6		
ENSMUST00000119100	ENSMUSG00000070933	5	15619064	15623864	1	5	5	3	11	7	3	0	0	0	0	0	L7N261	
ENSMUST00000119101						2	4	9	4	1	1	0	0	0	0	0		
ENSMUST00000119102	ENSMUSG00000006019	7	16197147	16222037	-1	0	19	0	72	18	14	12	23	25	0	0	D3YTV3	
ENSMUST00000119103	ENSMUSG00000032066	9	50533087	50555181	-1	11	15	13	8	18	9	8	131	17	16	13	Q3KNZ2	Q99NF1
ENSMUST00000119104						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119105						9	10	16	22	8	3	2	0	2	0	0		
ENSMUST00000119106						1	1	0	0	3	1	0	0	0	0	0		
ENSMUST00000119107						5	1	5	4	5	2	0	1	0	0	1		
ENSMUST00000119108	ENSMUSG00000024430	18	12741324	12755146	1	0	0	0	0	7	0	0	0	0	0	0		Q9D424
ENSMUST00000119109	ENSMUSG00000003382	3	87525407	87540156	1	17	0	29	56	0	7	54	29	174	0	69		Q8R4Z4
ENSMUST00000119110						5	4	75	7	17	2	0	0	0	0	0		
ENSMUST00000119111						7	1	13	7	4	3	0	0	0	0	0		
ENSMUST00000119112						9	21	15	14	19	7	0	0	0	0	0		
ENSMUST00000119114						8	3	22	7	9	4	0	0	0	0	0		
ENSMUST00000119115	ENSMUSG00000024163	17	24892153	24936977	-1	0	0	0	0	0	0	0	0	50	0	0		Q9ESN9
ENSMUST00000119116						9	17	17	4	7	6	0	0	0	0	0		
ENSMUST00000119117						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119118	ENSMUSG00000030518	7	64756091	65156570	-1	0	0	0	28	3	0	0	0	0	0	0		Q6A044
ENSMUST00000119119						2	2	2	2	2	2	0	0	0	0	0		
ENSMUST00000119120	ENSMUSG00000040712	11	70669463	70688105	-1	0	0	0	0	0	0	1014	746	947	56	599	B0QZH4	
ENSMUST00000119121	ENSMUSG00000062444	7	81460399	81493925	-1	8	9	3	89	5	3	0	0	0	0	0	E9Q1S6	
ENSMUST00000119122						1	4	1	1	1	0	0	0	0	0	0		
ENSMUST00000119123	ENSMUSG00000024002	17	32196274	32284722	-1	0	0	0	0	0	21	0	0	0	0	0		Q9ESU6
ENSMUST00000119124						9	1	11	10	3	1	0	0	0	1	0		
ENSMUST00000119125						4	6	6	4	2	2	0	1	0	0	0		
ENSMUST00000119126						1	6	29	5	2	2	3	0	0	0	1		
ENSMUST00000119127	ENSMUSG00000061322	4	41569775	41638158	1	0	0	0	0	0	0	0	0	0	2	0	Q8BMY8	
ENSMUST00000119128						1	0	3	1	4	6	29	232	66	11	109		
ENSMUST00000119129	ENSMUSG00000038119	9	35421128	35507652	1	0	0	65	89	55	2	0	0	0	0	25		Q32MD9
ENSMUST00000119130	ENSMUSG00000068523	3	146499807	146505572	1	4	0	0	64	5	4	7	12	4	23	6	D3Z7Q3	
ENSMUST00000119131	ENSMUSG00000040785	16	94370618	94469222	1	0	0	6	0	0	0	0	0	0	0	0	G5E8U3	
ENSMUST00000119132						2	0	1	1	2	2	0	0	0	0	0		
ENSMUST00000119133	ENSMUSG00000082766	3	19610368	19628677	-1	2	3	0	12	7	0	0	1	0	1	0	D3Z4D4	
ENSMUST00000119134	ENSMUSG00000011154	7	83774101	83794880	-1	5	15	9	11	11	9	0	0	0	0	0	D3YVU5	
ENSMUST00000119135						11	11	7	9	11	3	11	11	18	12	6		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119136						1	3	30	21	5	3	0	2	0	1	0		
ENSMUST00000119137						0	4	20	6	3	1	1	3	2	2	0		
ENSMUST00000119138						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119139	ENSMUSG00000070814	7	13258967	13278721	-1	23	12	29	22	20	0	0	0	5	0	0		Q6DI92
ENSMUST00000119140						6	9	22	1	8	4	3	0	3	0	0		
ENSMUST00000119141	ENSMUSG00000043587	9	96823336	96892669	-1	16	15	23	2	6	5	77	0	85	25	0		Q8BHA9
ENSMUST00000119142	ENSMUSG00000062209	1	68032186	69108059	-1	0	11	30	0	0	0	0	0	0	0	0		Q61527
ENSMUST00000119143						1	1	1	0	2	1	0	0	0	0	0		
ENSMUST00000119144						0	1	0	1	2	1	0	0	0	0	0		
ENSMUST00000119145						0	7	19	5	6	0	2	1	0	2	0		
ENSMUST00000119146	ENSMUSG00000022245	9	63138170	63148961	-1	7	0	0	391	16	12	0	0	0	0	0		Q8BX46
ENSMUST00000119147						2	3	8	3	2	2	0	0	0	1	0		
ENSMUST00000119148						1	1	0	0	3	1	0	0	0	0	0		
ENSMUST00000119149	ENSMUSG00000078880	2	176613364	176636344	-1	0	0	3	0	0	0	3	0	0	0	3	Q8BHI0	
ENSMUST00000119150						1	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000119152						3	0	2	2	3	2	0	0	0	0	0		
ENSMUST00000119153						1	3	1	6	1	3	0	0	0	0	0		
ENSMUST00000119154	ENSMUSG00000054814	5	73998453	74068431	-1	0	30	72	15	0	16	36	0	0	0	0	D3YVU0	
ENSMUST00000119155						33	39	483	57	22	24	0	0	1	0	0		
ENSMUST00000119156						0	1	0	4	0	0	0	0	0	3	0		
ENSMUST00000119157						5	6	7	8	7	7	0	0	0	0	0		
ENSMUST00000119158	ENSMUSG00000027940	3	90072649	90100902	1	4	7	0	0	14	0	29	173	74	26	156	D3Z6I8	
ENSMUST00000119159						14	17	16	29	13	12	0	0	0	0	1		
ENSMUST00000119160						2	2	11	0	3	0	0	0	0	0	0		
ENSMUST00000119161	ENSMUSG00000006005	1	150392838	150449935	1	0	0	0	67	0	0	206	205	686	0	0	Q7M739	
ENSMUST00000119162						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119163						6	2	18	13	8	2	1	0	0	0	0		
ENSMUST00000119164						1	0	10	0	1	0	0	0	0	0	0		
ENSMUST00000119165						6	5	5	3	3	9	0	13	3	2	2		
ENSMUST00000119166	ENSMUSG00000038866	1	105990406	106034074	1	25	28	11	34	32	6	368	1114	679	71	481		Q69ZB8
ENSMUST00000119167	ENSMUSG00000054659	4	33174230	33189737	-1	6	6	6	187	6	0	0	0	0	0	0		A3KG59
ENSMUST00000119168	ENSMUSG00000046897	15	102203648	102215606	1	0	0	0	0	14	0	116	97	107	0	243	D3Z4S9	
ENSMUST00000119169						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000119170						1	1	2	0	3	1	0	0	0	0	0		
ENSMUST00000119171	ENSMUSG00000037235	5	34173883	34187720	-1	0	0	0	0	0	0	64	4	23	0	8	Q3UZ22	
ENSMUST00000119172	ENSMUSG00000014077	2	119547697	119587027	1	5	0	29	13	29	0	55	109	27	0	110	B0R091	
ENSMUST00000119173	ENSMUSG00000035506	16	33517328	33664135	1	2	0	0	0	4	0	0	0	0	0	0		Q8VI23
ENSMUST00000119174						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000119175						6	0	62	6	16	4	0	0	0	5	1		
ENSMUST00000119176						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119177						2	2	0	3	5	1	0	0	0	0	0		
ENSMUST00000119178						0	1	6	1	0	0	0	0	1	2	0		
ENSMUST00000119179						0	0	0	0	4	2	0	0	0	0	0		
ENSMUST00000119180	ENSMUSG00000084174	7	28540885	28542210	1	4	2	3	6	5	4	0	0	0	0	0		Q8VCK7
ENSMUST00000119181						0	0	0	1	9	0	0	0	0	0	0		
ENSMUST00000119182						22	16	183	187	29	16	0	9	1	0	1		
ENSMUST00000119183						23	19	17	19	34	7	9	17	7	8	6		
ENSMUST00000119185	ENSMUSG00000020061	10	88518279	88605152	-1	0	13	10	0	0	13	0	0	0	0	0	D3YU50	
ENSMUST00000119187						3	1	4	2	1	1	2	13	9	2	4		
ENSMUST00000119188						2	1	0	4	4	1	0	0	0	0	0		
ENSMUST00000119189						1	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000119190	ENSMUSG00000047797	X	101376378	101385629	1	8	0	3	0	0	0	0	0	0	0	0		P28230
ENSMUST00000119191						4	2	6	3	1	0	0	0	0	0	0		
ENSMUST00000119192						0	5	1	1	3	2	0	0	0	0	0		
ENSMUST00000119193						10	5	10	8	12	3	0	1	0	0	0		
ENSMUST00000119194						13	15	83	38	19	6	0	0	2	0	2		
ENSMUST00000119195						8	8	15	5	4	6	0	0	0	0	0		
ENSMUST00000119196						4	5	26	6	8	9	0	0	0	0	1		
ENSMUST00000119197	ENSMUSG00000001964	X	74254687	74261548	1	0	0	0	21	2	0	13	29	16	0	0	B7FAU5	
ENSMUST00000119198						2	0	6	7	4	2	0	0	0	0	0		
ENSMUST00000119199						5	4	5	4	5	2	0	1	1	0	0		
ENSMUST00000119200	ENSMUSG00000014039	16	97791467	97851850	-1	2	0	0	0	2	1	2	0	0	0	0	D3Z7Q9	
ENSMUST00000119201	ENSMUSG00000030452	7	55931287	55962476	-1	3	8	34	77	16	9	14	7	5	8	14		Q9JJC8
ENSMUST00000119203						1	0	12	0	3	0	0	0	0	0	0		
ENSMUST00000119204						1	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000119205						6	3	9	6	9	3	0	0	0	0	0		
ENSMUST00000119206	ENSMUSG00000070509	7	73375509	73419899	1	0	0	0	0	33	4	0	0	0	0	14	Q8C4C4	
ENSMUST00000119208						3	3	0	1	3	1	0	0	0	0	0		
ENSMUST00000119209						2	1	1	1	2	3	0	0	0	0	0		
ENSMUST00000119210						3	3	4	3	3	2	0	0	0	0	0		
ENSMUST00000119211	ENSMUSG00000035293	12	51348061	51376986	1	0	0	0	3	0	0	0	0	13	0	8	E9Q7C2	
ENSMUST00000119212	ENSMUSG00000033540	5	108660331	108684557	1	21	0	0	0	0	0	74	225	87	4	89	Q8BLF6	
ENSMUST00000119213	ENSMUSG00000049624	9	78536488	78588041	-1	351	432	166	462	396	162	8	47	5	4	25		Q8BN82
ENSMUST00000119214						16	3	0	4	9	0	0	0	0	0	0		
ENSMUST00000119215	ENSMUSG00000038145	9	122117283	122169702	1	0	0	0	0	0	0	26	74	48	0	25	D3Z3V0	
ENSMUST00000119216						2	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000119217						11	2	26	4	13	6	0	0	0	0	0		
ENSMUST00000119218						12	7	10	18	8	6	0	0	0	0	0		
ENSMUST00000119219						1	2	1	0	1	1	0	0	0	0	0		
ENSMUST00000119220						2	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000119221						1	0	3	0	3	1	0	0	0	0	1		
ENSMUST00000119222	ENSMUSG00000064068	3	89209081	89227088	-1	4	1	0	0	1	1	38	114	39	34	4	D3Z3F4	
ENSMUST00000119223	ENSMUSG00000046179	7	48866429	48881596	-1	28	43	457	40	16	26	134	200	294	12	168		Q58FA4
ENSMUST00000119224	ENSMUSG00000022842	16	20611593	20646485	1	3	3	15	8	0	5	0	0	0	0	0	F7DDS0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119226						5	4	5	3	5	3	0	0	0	0	0		
ENSMUST00000119227	ENSMUSG00000024208	17	27122663	27133916	-1	0	0	0	2	0	0	0	0	0	0	0	D3Z4C9	
ENSMUST00000119228						4	7	2	5	6	2	0	0	0	0	0		
ENSMUST00000119229	ENSMUSG00000034055	X	102513975	102644246	-1	13	0	0	0	0	0	11	0	0	0	0	A2AI89	
ENSMUST00000119230						0	0	1	2	1	1	0	0	0	0	0		
ENSMUST00000119231	ENSMUSG00000080725	X	26912743	26935697	-1	0	3	0	0	0	0	0	0	0	0	0	L7MUF1	
ENSMUST00000119232						4	2	2	1	2	0	0	0	0	0	0		
ENSMUST00000119233						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119234						5	3	31	9	2	0	0	0	1	0	0		
ENSMUST00000119236						2	1	3	4	2	1	0	0	0	0	0		
ENSMUST00000119237						9	6	2	8	8	6	0	1	1	0	2		
ENSMUST00000119238						4	1	2	16	3	1	0	0	0	0	0		
ENSMUST00000119239	ENSMUSG00000064036	18	73859385	73881333	1	0	0	0	1	2	1	0	0	0	0	0	E9PUF9	
ENSMUST00000119241						8	5	58	6	19	14	7	12	0	11	0		
ENSMUST00000119242						5	2	16	6	4	3	0	1	0	1	0		
ENSMUST00000119243						6	4	16	6	4	1	0	0	0	0	0		
ENSMUST00000119244						6	4	14	18	9	8	0	0	0	0	0		
ENSMUST00000119245	ENSMUSG00000032386	9	65828930	65908794	-1	0	0	0	0	0	0	18	0	0	31	0		Q9QXN3
ENSMUST00000119246						8	4	5	11	10	0	29	27	15	27	5		
ENSMUST00000119247						7	4	20	24	11	3	0	2	2	0	0		
ENSMUST00000119248						3	1	4	6	4	2	0	0	0	0	0		
ENSMUST00000119249						3	4	4	2	6	2	0	0	0	0	0		
ENSMUST00000119250						26	11	109	30	15	7	0	0	0	0	0		
ENSMUST00000119251	ENSMUSG00000001419	3	88142372	88172086	1	11	0	17	43	15	0	557	336	383	16	453	E9Q5E0	
ENSMUST00000119252						2	0	4	4	0	1	12	20	6	3	5		
ENSMUST00000119253						8	5	27	8	5	4	0	0	0	0	0		
ENSMUST00000119254	ENSMUSG00000071064	8	79028437	79193766	1	0	0	0	4	0	0	0	0	0	1	0	G5E8U2	
ENSMUST00000119255						8	4	9	15	3	3	2	1	0	0	9		
ENSMUST00000119256	ENSMUSG00000002459	1	4909576	5070285	-1	3	1	1	14	5	2	0	0	0	0	0	Q8C5J7	
ENSMUST00000119257						3	4	6	8	4	0	0	1	1	0	0		
ENSMUST00000119258						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119259						0	2	3	2	4	1	0	0	0	0	0		
ENSMUST00000119260	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7T0	
ENSMUST00000119261	ENSMUSG00000036270	8	105880881	105894908	1	0	0	0	0	0	0	190	117	196	0	0		
ENSMUST00000119262						0	5	18	4	0	5	0	0	0	3	0		
ENSMUST00000119263						3	6	1	7	7	5	0	0	0	0	0		
ENSMUST00000119264						4	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119265						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119266						0	0	2	0	6	0	11	6	0	0	0		
ENSMUST00000119267						4	6	4	0	5	5	0	0	0	0	0		
ENSMUST00000119268						2	0	5	0	4	0	0	0	0	0	2		
ENSMUST00000119269	ENSMUSG00000023707	5	124112297	124115483	1	0	4	32	0	11	6	29	64	96	0	0	D3YU42	
ENSMUST00000119270	ENSMUSG00000046959	5	108669878	108675569	-1	0	0	6	0	0	0	0	0	0	0	0	G5E8U1	
ENSMUST00000119271						1	4	1	2	2	0	0	1	0	0	0		
ENSMUST00000119272						3	0	0	7	2	3	189	475	259	652	119		
ENSMUST00000119273	ENSMUSG00000022706	16	18872018	18876767	-1	0	0	0	1	0	0	68	288	119	419	48	D3Z7C0	
ENSMUST00000119274	ENSMUSG00000024006	17	28970885	29007945	-1	0	0	0	0	0	1	46	21	603	14	196		Q91VJ4
ENSMUST00000119275						3	3	0	1	0	1	0	7	6	3	0		
ENSMUST00000119276						0	2	1	5	1	1	1	0	3	0	7		
ENSMUST00000119277						8	9	11	9	11	6	0	0	0	0	0		
ENSMUST00000119278	ENSMUSG00000038187	7	113315626	113369392	-1	0	4	14	25	0	6	118	307	160	32	62	E9Q6L8	
ENSMUST00000119279						7	2	0	1	9	1	0	0	0	0	0		
ENSMUST00000119280						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119281						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000119282						7	12	11	10	8	4	1	0	1	0	1		
ENSMUST00000119283						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119284	ENSMUSG00000024070	17	78949405	79020816	-1	0	0	0	0	0	0	31	22	127	0	92	Q5FWX6	
ENSMUST00000119285	ENSMUSG00000081218	X	24552250	24574895	-1	85	79	238	149	99	61	0	3	0	1	4	D3YWB7	
ENSMUST00000119286						57	54	156	59	62	42	4	15	13	3	36		
ENSMUST00000119287						3	0	4	6	5	2	0	1	1	0	0		
ENSMUST00000119288						8	3	4	1	9	10	24	57	29	6	33		
ENSMUST00000119289						0	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000119290						3	0	1	1	2	0	0	0	0	0	0		
ENSMUST00000119291	ENSMUSG00000056880	9	115909455	116076176	1	2	0	2	1	3	0	0	0	0	0	0	D3YWS5	
ENSMUST00000119292	ENSMUSG00000024831	19	3260924	3283017	-1	12	30	22	0	1	0	0	0	20	0	0	D3Z5P5	
ENSMUST00000119293						2	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000119294	ENSMUSG00000039137	4	63414910	63495991	-1	0	2	0	0	0	0	0	0	1	0	0		Q80VW5
ENSMUST00000119295						5	4	6	9	3	3	1	1	2	3	2		
ENSMUST00000119296						408	296	746	467	512	235	10	42	35	18	72		
ENSMUST00000119297						3	7	0	0	2	2	0	0	0	0	0		
ENSMUST00000119298						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000119299	ENSMUSG00000034160	X	101640060	101684351	1	4	0	2	0	6	0	163	372	1227	328	1519		Q8CGY8
ENSMUST00000119300						5	9	20	16	6	4	0	0	0	0	0		
ENSMUST00000119301						2	1	3	1	2	2	0	0	0	0	0		
ENSMUST00000119302						14	14	25	21	17	6	0	0	0	0	0		
ENSMUST00000119303						2	0	5	1	2	0	0	0	0	0	0		
ENSMUST00000119304	ENSMUSG00000027937	3	90231597	90235838	1	5	3	9	0	0	2	0	5	0	0	0	D3Z4D1	
ENSMUST00000119305						6	0	16	53	0	7	3	6	4	0	0		
ENSMUST00000119306	ENSMUSG00000031137	X	59062145	59568071	-1	16	0	43	53	21	13	4	6	0	2	1		P70377
ENSMUST00000119307	ENSMUSG00000042198	4	3938888	3951046	1	0	2	2	141	8	0	3	20	3	8	10		Q8K2Q5
ENSMUST00000119308						0	2	0	2	2	2	0	0	0	0	0		
ENSMUST00000119309						1	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000119310	ENSMUSG00000037610	3	31902507	32200180	1	10	0	6	0	5	7	0	0	0	0	0		Q9CZM9
ENSMUST00000119311	ENSMUSG00000021460	13	52835119	52929681	-1	63	48	73	82	52	29	55	245	106	18	113	E9Q6L3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119313						8	10	10	4	14	6	0	0	5	0	8		
ENSMUST00000119314						5	0	3	3	1	0	0	0	0	0	0		
ENSMUST00000119315	ENSMUSG00000047867	6	48701582	48708225	-1	70	89	129	103	80	50	21	81	33	31	173	D3Z3H3	
ENSMUST00000119316	ENSMUSG00000025010	19	40831279	40848572	1	12	9	33	201	30	16	9	5	35	0	31		Q3TZI6
ENSMUST00000119317						4	1	5	8	3	0	3	5	3	8	11		
ENSMUST00000119318						3	1	5	0	4	0	0	0	0	0	0		
ENSMUST00000119319						2	0	3	3	1	4	0	0	0	0	0		
ENSMUST00000119320						1	5	3	0	4	4	0	0	1	0	0		
ENSMUST00000119321						2	2	0	3	0	0	0	0	0	0	0		
ENSMUST00000119322						6	9	1	9	5	1	0	4	0	1	0		
ENSMUST00000119323						3	2	22	4	4	3	0	0	2	0	0		
ENSMUST00000119324	ENSMUSG00000034748	10	81621785	81627797	-1	8	6	8	16	7	8	43	128	84	14	76	Q3UKP1	
ENSMUST00000119325						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000119326						3	3	3	1	1	3	0	0	0	0	0		
ENSMUST00000119328						0	0	12	0	0	0	0	0	0	0	0		
ENSMUST00000119329	ENSMUSG00000014504	18	34330847	34336599	1	0	0	0	27	0	0	51	202	70	409	54	G5E8T3	
ENSMUST00000119330						2	1	4	1	1	1	0	0	0	0	0		
ENSMUST00000119331						3	5	2	1	1	2	0	0	0	0	0		
ENSMUST00000119332						6	9	6	0	0	2	1	0	1	1	0		
ENSMUST00000119333						95	75	158	98	79	33	1	2	1	1	0		
ENSMUST00000119334						6	0	5	5	6	1	0	0	0	0	0		
ENSMUST00000119335						2	2	10	3	4	2	0	0	1	0	0		
ENSMUST00000119336	ENSMUSG00000054708	10	81628540	81647610	1	2	0	0	0	2	0	0	0	0	1	0		Q80VM7
ENSMUST00000119337						4	2	0	2	4	1	0	71	12	3	0		
ENSMUST00000119339	ENSMUSG00000035851	5	86804221	86836659	1	7	0	8	69	0	4	34	37	207	7	99		E9Q5K9
ENSMUST00000119340						4	4	5	0	3	0	0	0	0	0	0		
ENSMUST00000119341	ENSMUSG00000021373	13	46501848	46649642	1	0	8	10	0	0	5	0	0	0	0	0	D3YTR7	
ENSMUST00000119342						9	5	12	10	7	6	0	0	0	0	0		
ENSMUST00000119343						5	6	3	2	7	1	0	0	0	0	0		
ENSMUST00000119344	ENSMUSG00000027805	3	57841895	57848079	-1	0	0	0	77	11	7	0	0	0	0	0		Q9JJV2
ENSMUST00000119345						1	0	1	0	0	1	0	1	1	0	2		
ENSMUST00000119346	ENSMUSG00000020682	11	83440768	83463071	-1	0	5	8	37	8	3	0	3	0	0	0	Q5SSG2	
ENSMUST00000119347						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000119348						4	6	2	0	8	3	0	0	0	0	0		
ENSMUST00000119349						5	11	21	12	13	7	0	0	1	0	0		
ENSMUST00000119350						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000119351						10	2	4	6	2	1	0	0	0	1	0		
ENSMUST00000119352						0	2	5	0	1	1	0	0	0	0	1		
ENSMUST00000119353	ENSMUSG00000019428	8	70527724	70535328	1	0	4	8	0	11	5	612	606	375	199	268		O35465
ENSMUST00000119354	ENSMUSG00000028789	4	128930233	128962442	-1	15	7	35	29	8	3	0	0	2	2	6	A8Y5E7	
ENSMUST00000119355						3	1	3	1	1	0	0	0	1	0	0		
ENSMUST00000119356						6	6	7	0	7	0	1	5	9	1	6		
ENSMUST00000119357						1	2	3	4	2	4	0	0	0	0	0		
ENSMUST00000119358						1	3	1	2	3	1	2	2	3	0	0		
ENSMUST00000119359						1	1	5	2	0	0	0	2	1	0	3		
ENSMUST00000119360						3	4	13	24	5	5	0	0	0	0	0		
ENSMUST00000119361	ENSMUSG00000019088	X	74273217	74282337	-1	0	2	2	0	3	0	6	0	0	0	0	I7HIQ0	
ENSMUST00000119362	ENSMUSG00000095546	X	27472031	27494882	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000119363						295	292	494	300	382	192	12	55	10	9	12		
ENSMUST00000119364						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000119365	ENSMUSG00000090210	3	96645584	96664519	1	17	0	40	27	13	13	2	2	2	0	17	E9PXZ3	
ENSMUST00000119366	ENSMUSG00000024675	19	11404770	11427246	1	12	12	93	18	9	7	29	464	33	103	60	Q3U5N6	
ENSMUST00000119367						7	7	17	21	14	11	0	1	1	0	0		
ENSMUST00000119368	ENSMUSG00000022961	16	91647506	91679221	1	22	11	67	82	22	4	510	2251	1462	195	1547	H9KV01	
ENSMUST00000119369	ENSMUSG00000030170	6	119432531	119544347	-1	0	0	0	0	0	0	0	0	0	4	0		
ENSMUST00000119370						2	0	3	4	3	1	0	0	1	2	0		
ENSMUST00000119371						3	0	4	14	2	4	0	0	0	0	1		
ENSMUST00000119372						1	4	1	5	4	0	0	0	1	0	0		
ENSMUST00000119373	ENSMUSG00000040111	9	40293233	40531383	-1	6	1	6	70	7	3	0	0	0	0	10	D3YWR0	
ENSMUST00000119374	ENSMUSG00000055761	4	20118874	20778866	-1	21	22	26	18	13	10	0	0	0	0	0		Q3URJ8
ENSMUST00000119375						5	1	14	7	4	3	0	0	0	0	0		
ENSMUST00000119377						7	3	19	3	6	5	0	0	0	0	0		
ENSMUST00000119378						2	2	0	2	4	0	0	0	0	0	0		
ENSMUST00000119379	ENSMUSG00000002416	6	39592574	39603382	1	0	0	6	0	0	0	34	174	54	350	21		Q9CPU2
ENSMUST00000119380						0	2	3	0	3	0	0	0	0	0	0		
ENSMUST00000119381						9	4	8	7	6	5	0	3	0	0	0		
ENSMUST00000119382						3	4	5	2	3	4	0	0	0	0	0		
ENSMUST00000119383						4	6	27	13	10	1	7	0	6	15	0		
ENSMUST00000119384						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000119385	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z6H9	
ENSMUST00000119386	ENSMUSG00000040601	7	26435113	26476142	1	0	0	3	0	0	3	0	0	0	0	0	B2RUQ7	Q8BU40
ENSMUST00000119387						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119388						6	3	9	2	3	4	0	0	0	0	0		
ENSMUST00000119389						2	5	2	3	5	4	10	12	0	14	4		
ENSMUST00000119390						11	8	11	15	14	4	0	1	2	0	0		
ENSMUST00000119391						8	4	12	7	5	4	2	1	0	0	2		
ENSMUST00000119392						0	1	2	1	0	1	0	0	0	0	0		
ENSMUST00000119393						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000119394	ENSMUSG00000028608	4	107889813	107899384	1	0	0	0	0	0	0	1	4	2	0	7	B7ZC72	
ENSMUST00000119395						9	4	20	25	14	8	1	0	9	2	1		
ENSMUST00000119396						3	2	10	4	5	9	0	0	1	0	0		
ENSMUST00000119397						10	9	7	14	23	7	0	9	0	0	4		
ENSMUST00000119398	ENSMUSG00000031565	8	25513654	25575714	1	0	0	0	0	0	0	39	5	6	3	168		P16092
ENSMUST00000119399						0	8	2	1	3	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119400						6	4	3	7	3	1	0	0	0	0	0		
ENSMUST00000119401						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119402						3	3	3	2	2	1	0	0	0	0	0		
ENSMUST00000119403	ENSMUSG00000042198	4	3938888	3951046	1	1	0	1	0	0	0	0	13	2	0	1		Q8K2Q5
ENSMUST00000119404						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000119405						0	0	37	0	7	0	0	0	0	0	0		
ENSMUST00000119406						5	5	13	6	8	3	0	0	0	0	0		
ENSMUST00000119407	ENSMUSG00000022753	16	57266139	57292865	-1	6	1	0	3	1	1	0	0	0	0	0		Q9D4D7
ENSMUST00000119408						3	3	16	4	6	2	0	0	0	0	0		
ENSMUST00000119409						6	3	2	2	5	2	0	0	0	0	0		
ENSMUST00000119410						1	0	2	1	0	0	0	0	0	1	0		
ENSMUST00000119411						12	10	70	11	11	9	2	1	0	3	0		
ENSMUST00000119412						0	1	1	4	5	1	0	0	0	0	0		
ENSMUST00000119413	ENSMUSG00000033543	9	70012550	70022866	1	1	0	0	118	4	2	0	9	10	7	18	Q3TE88	Q80ZM7
ENSMUST00000119414						8	5	13	10	7	6	0	0	0	0	0		
ENSMUST00000119415						0	2	1	1	3	2	0	2	4	2	2		
ENSMUST00000119416						1	2	4	4	4	2	0	0	0	0	1		
ENSMUST00000119417						5	6	3	4	6	7	0	0	0	5	0		
ENSMUST00000119418						15	7	7	5	13	5	18	11	19	10	10		
ENSMUST00000119419						3	6	2	5	3	4	0	0	0	0	0		
ENSMUST00000119420						4	1	3	4	2	0	0	0	0	0	0		
ENSMUST00000119421						2	3	4	4	4	1	0	0	0	0	0		
ENSMUST00000119422	ENSMUSG00000027309	2	130706200	130906406	-1	5	5	21	13	5	10	0	2	0	0	0	Q3V0A7	
ENSMUST00000119423	ENSMUSG00000028778	4	130130217	130139359	-1	9	5	31	214	28	5	0	0	0	0	0		P58307
ENSMUST00000119424						3	6	9	1	1	3	0	1	0	0	0		
ENSMUST00000119425	ENSMUSG00000019428	8	70527724	70535328	1	23	33	90	46	43	22	16	50	22	1	24	D3Z597	
ENSMUST00000119426	ENSMUSG00000032271	9	48591877	48605153	-1	0	0	0	0	0	0	0	0	0	0	4	D3YX59	
ENSMUST00000119427	ENSMUSG00000049719	9	110844506	110856522	1	9	7	0	0	5	0	0	0	0	0	1	F6U6W2	
ENSMUST00000119428	ENSMUSG00000025723	7	80902227	80905076	-1	0	1	0	0	3	1	0	11	0	0	10	D3Z621	
ENSMUST00000119429	ENSMUSG00000061816	1	66924295	66945404	-1	0	0	0	7	0	0	0	0	0	0	0	Q545G5	P05977
ENSMUST00000119430	ENSMUSG00000021770	14	21750531	21798725	1	75	64	209	78	72	38	495	1661	1090	85	569	Q3UH82	
ENSMUST00000119431						0	0	0	1	2	1	1	0	1	0	6		
ENSMUST00000119432	ENSMUSG00000026401	1	130388537	130423009	-1	1	5	0	2	2	0	3	6	5	0	3	E9Q731	
ENSMUST00000119433	ENSMUSG00000053550	7	4825552	4844696	-1	0	0	0	332	8	12	0	0	0	0	1		Q8C3Q5
ENSMUST00000119434						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000119435						3	2	4	4	0	1	0	0	0	0	0		
ENSMUST00000119437	ENSMUSG00000063406	5	108106366	108132620	-1	47	45	45	42	33	11	9	13	21	7	13	E9PXY3	
ENSMUST00000119438						0	0	3	0	0	0	320	436	7	164	1		
ENSMUST00000119439						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000119440						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000119441						6	1	3	2	9	5	0	0	0	0	1		
ENSMUST00000119442						16	4	37	17	7	6	12	14	15	3	51		
ENSMUST00000119443						6	16	7	3	14	7	0	0	0	0	0		
ENSMUST00000119444						2	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000119445						5	3	6	3	8	3	0	0	0	0	0		
ENSMUST00000119446						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000119447						3	5	0	3	5	0	0	6	0	9	0		
ENSMUST00000119448						35	39	137	17	20	8	3	13	4	1	0		
ENSMUST00000119449						0	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000119450	ENSMUSG00000027854	3	102995708	103008459	1	0	0	0	4	0	0	47	60	67	26	29	D3YTU7	
ENSMUST00000119451						1	2	2	0	3	0	0	0	0	0	0		
ENSMUST00000119452						3	3	12	6	6	0	0	0	0	0	0		
ENSMUST00000119453	ENSMUSG00000027517	2	173568666	173578365	-1	0	0	0	20	0	0	0	0	0	0	0	A2AMD2	
ENSMUST00000119454						12	10	17	11	13	4	0	0	0	0	0		
ENSMUST00000119455	ENSMUSG00000050106	11	117782076	117793110	1	21	18	49	66	29	22	167	381	190	7	229	B0QZP6	Q7TN58
ENSMUST00000119456						3	5	16	6	7	1	0	0	0	0	0		
ENSMUST00000119457						1	0	2	0	0	0	0	0	0	1	0		
ENSMUST00000119458						5	0	0	0	5	1	0	2	0	0	0		
ENSMUST00000119459						3	0	0	5	3	0	0	1772	0	14	4		
ENSMUST00000119460						18	16	43	20	18	14	0	0	1	0	0		
ENSMUST00000119461						6	1	12	99	9	1	0	1	0	0	0		
ENSMUST00000119462						3	1	1	1	3	3	0	0	0	0	0		
ENSMUST00000119463						2	3	0	4	4	0	3	0	7	0	5		
ENSMUST00000119464	ENSMUSG00000022900	16	36693978	36726804	1	5	0	17	0	0	0	0	0	0	0	0		Q8CBR1
ENSMUST00000119465						66	26	38	720	101	42	0	2	0	0	1		
ENSMUST00000119466						2	2	14	2	1	1	0	0	0	0	0		
ENSMUST00000119467						4	2	10	5	8	4	8	116	23	137	104		
ENSMUST00000119468	ENSMUSG00000022686	16	19760208	19772753	1	0	2	0	107	8	5	3	4	2	1	21		Q8BGY6
ENSMUST00000119469	ENSMUSG00000089942	7	3836812	3845051	-1	0	0	0	0	0	0	11	35	22	26	31	D3Z3W9	
ENSMUST00000119471						23	21	22	9	19	3	0	2	0	0	0		
ENSMUST00000119472	ENSMUSG00000032470	9	99385420	99437381	-1	1	2	3	0	3	2	0	0	0	0	0	Q3TPX5	O08989
ENSMUST00000119473						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000119474	ENSMUSG00000031028	7	109010825	109034460	1	5	0	0	17	5	3	0	0	0	0	0		
ENSMUST00000119475	ENSMUSG00000054690	3	137341067	137432185	1	5	3	8	4	0	2	1	4	0	3	0		Q9R0H2
ENSMUST00000119476						11	5	31	9	13	1	0	0	0	0	0		
ENSMUST00000119477	ENSMUSG00000031226	X	105079756	105117090	1	1	3	5	3	1	0	12	58	34	51	0		Q9D0B6
ENSMUST00000119478						1	6	2	2	2	1	1	2	0	2	0		
ENSMUST00000119479						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119480	ENSMUSG00000057572	4	129335695	129354547	1	0	0	0	0	1	0	47	265	78	508	58	A8Y5E9	
ENSMUST00000119481	ENSMUSG00000035653	12	61523150	61858342	1	0	12	0	1	7	0	0	0	0	0	0		Q8BXA0
ENSMUST00000119482						0	0	1	1	4	0	0	0	0	0	0		
ENSMUST00000119483	ENSMUSG00000039376	14	20658946	20668354	-1	36	29	181	185	13	0	1	6	1	1	4	D3YU08	
ENSMUST00000119484						2	0	10	1	2	1	0	0	1	0	0		
ENSMUST00000119485	ENSMUSG00000008435	7	4424770	4445649	-1	11	8	19	15	7	5	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119486	ENSMUSG00000046711	17	27556620	27563674	1	5	0	28	51	0	0	4	2	11	0	55	Q566K0	P17095
ENSMUST00000119487						4	3	2	4	2	2	0	0	0	0	1		
ENSMUST00000119488	ENSMUSG00000083012	5	143548706	143564531	1	5	6	0	17	58	4	270	47	30	10	14	Q5U425	
ENSMUST00000119489						0	2	0	0	2	2	0	0	0	0	0		
ENSMUST00000119490						1	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000119491						1	2	2	2	5	1	7	6	5	6	5		
ENSMUST00000119492	ENSMUSG00000074862	10	81606270	81620703	1	1	3	0	3	1	1	0	0	0	3	2	Q3US60	
ENSMUST00000119493						0	2	4	0	3	2	0	0	0	0	0		
ENSMUST00000119494						13	10	37	20	35	9	13	7	8	0	4		
ENSMUST00000119495						0	2	7	1	3	1	0	0	0	0	0		
ENSMUST00000119496						4	5	0	5	6	5	0	0	4	6	2		
ENSMUST00000119497						13	13	11	195	18	2	1	4	1	1	1		
ENSMUST00000119498						6	2	9	0	0	3	0	0	0	0	0		
ENSMUST00000119499	ENSMUSG00000037606	7	143688762	143756985	-1	6	0	7	41	18	5	26	24	8	8	64		Q9ER64
ENSMUST00000119500						3	3	4	3	0	0	0	0	0	0	0		
ENSMUST00000119501						1	1	0	11	0	1	0	0	0	1	0		
ENSMUST00000119502						1	3	4	4	3	2	0	0	0	0	0		
ENSMUST00000119503						4	3	0	9	2	5	0	0	0	0	0		
ENSMUST00000119504	ENSMUSG00000025616	16	87454703	87483517	1	0	0	0	0	0	0	35	83	76	65	77	D3YVU1	
ENSMUST00000119505						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000119506						2	4	13	5	2	2	0	0	1	0	0		
ENSMUST00000119507	ENSMUSG00000021699	13	108449948	109953461	1	2	3	0	0	3	3	0	0	0	0	0	B2KF84	
ENSMUST00000119508						4	0	8	3	2	0	0	0	0	0	0		
ENSMUST00000119509	ENSMUSG00000048279	14	61138457	61240695	1	6	6	24	19	12	6	0	0	0	0	1	B2RRL5	
ENSMUST00000119510						8	2	8	2	5	0	0	0	0	0	0		
ENSMUST00000119511						1	2	0	0	2	0	0	0	0	1	0		
ENSMUST00000119512	ENSMUSG00000044252	18	12755314	12941841	-1	2	7	5	70	10	3	0	8	3	0	0	Q3V156	
ENSMUST00000119513						1	4	53	8	5	6	0	0	0	0	2		
ENSMUST00000119514						4	3	2	9	5	3	0	0	0	0	0		
ENSMUST00000119515						11	6	21	10	9	6	1	1	2	2	1		
ENSMUST00000119516						13	14	84	19	14	12	1	2	1	0	0		
ENSMUST00000119517						0	0	1	1	0	1	0	0	0	0	0		
ENSMUST00000119518						4	1	7	1	4	3	0	0	0	0	0		
ENSMUST00000119519						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000119520	ENSMUSG00000030165	6	129591782	129598775	1	0	0	0	0	0	0	0	0	0	0	0	D3Z626	
ENSMUST00000119521	ENSMUSG00000040464	5	5537454	5559538	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z4U2	
ENSMUST00000119522						0	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000119523	ENSMUSG00000039753	5	43744615	43821638	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z584	
ENSMUST00000119524						5	5	4	3	3	2	0	0	0	0	0		
ENSMUST00000119525						6	1	8	6	5	3	0	8	0	5	3		
ENSMUST00000119526	ENSMUSG00000026592	1	157099139	157108680	-1	4	1	0	0	0	0	0	0	0	0	0	D3Z652	
ENSMUST00000119527	ENSMUSG00000038271	6	125145241	125161782	1	0	0	0	0	0	0	0	0	0	2	0	D3Z633	
ENSMUST00000119528						1	2	6	0	2	0	0	0	0	0	0		
ENSMUST00000119529						1	1	1	0	1	0	0	0	1	0	0		
ENSMUST00000119530						2	1	2	3	1	0	0	0	0	0	0		
ENSMUST00000119531						0	1	0	0	1	3	0	0	0	0	0		
ENSMUST00000119532						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119533	ENSMUSG00000052736	6	129647496	129660689	-1	0	0	0	0	0	0	0	0	0	0	0	Q9WTJ9	
ENSMUST00000119534						0	0	1	0	0	0	1	0	0	0	0		
ENSMUST00000119535						1	0	3	0	0	2	0	0	0	0	0		
ENSMUST00000119536						1	0	0	2	0	1	0	0	0	0	0		
ENSMUST00000119537						7	4	14	11	6	5	0	0	0	0	0		
ENSMUST00000119538						1	1	1	2	2	0	0	0	0	0	0		
ENSMUST00000119539						8	5	9	13	9	4	0	0	0	0	0		
ENSMUST00000119540						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119541						4	0	18	0	0	0	0	6	0	16	12		
ENSMUST00000119542						3	0	21	10	7	6	0	7	1	0	1		
ENSMUST00000119543	ENSMUSG00000038623	7	81859001	81884434	1	0	0	6	0	1	1	387	2282	949	400	455	D3YX52	
ENSMUST00000119544						7	0	6	0	3	4	6	5	0	3	0		
ENSMUST00000119545						3	2	5	2	5	0	0	0	0	0	0		
ENSMUST00000119546						0	2	3	5	0	0	2	18	6	14	3		
ENSMUST00000119547	ENSMUSG00000004933	10	81252935	81263365	1	6	3	16	32	4	2	0	0	0	0	0		
ENSMUST00000119548						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119549						18	19	24	23	33	12	0	0	0	0	0		
ENSMUST00000119550						4	5	5	6	2	0	0	0	0	0	0		
ENSMUST00000119551						21	0	0	0	10	0	0	0	0	0	0		
ENSMUST00000119552						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000119553						2	1	2	0	0	0	0	1	1	1	3		
ENSMUST00000119554						4	1	6	5	4	2	0	2	0	0	0		
ENSMUST00000119555						5	3	1	0	7	1	0	0	0	0	0		
ENSMUST00000119556						1	0	10	1	0	0	0	0	0	0	0		
ENSMUST00000119557	ENSMUSG00000033377	3	116918258	116968987	-1	8	13	3	12	5	11	0	0	0	0	0	Q3UVT7	
ENSMUST00000119558	ENSMUSG00000070814	7	13258967	13278721	-1	21	0	0	0	0	11	2	24	0	9	20	D3YTW6	
ENSMUST00000119559	ENSMUSG00000026000	1	67000517	67038872	-1	1	0	0	0	0	1	91	188	66	89	60		O89112
ENSMUST00000119560						0	3	17	0	3	0	3	0	8	9	0		
ENSMUST00000119561						0	0	1	1	2	0	0	0	0	0	0		
ENSMUST00000119562						8	6	11	10	6	5	0	2	1	0	0		
ENSMUST00000119563						1	1	0	0	2	0	0	0	0	4	0		
ENSMUST00000119564	ENSMUSG00000070691	4	135120652	135177990	1	0	0	0	206	3	0	0	3	5	0	0		Q64131
ENSMUST00000119565						0	4	1	1	0	0	0	0	0	0	0		
ENSMUST00000119566						2	1	4	1	6	0	0	0	0	0	0		
ENSMUST00000119567	ENSMUSG00000020070	10	62980223	63017210	1	16	15	28	20	19	9	29	124	55	31	58	B2RQ36	Q8R4C2
ENSMUST00000119568						0	3	1	0	4	0	0	0	0	0	0		
ENSMUST00000119569						2	1	19	4	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119570	ENSMUSG00000027940	3	90072649	90100902	1	0	0	0	0	4	2	16	29	0	0	0	E9Q5J9	
ENSMUST00000119571						4	0	2	0	0	0	0	0	0	2	0		
ENSMUST00000119572	ENSMUSG00000025766	3	41742611	41803320	1	1	0	2	5	0	0	3	0	0	0	0		
ENSMUST00000119573						2	4	0	3	4	0	1	0	0	0	0		
ENSMUST00000119574						16	15	43	20	13	9	1	5	0	0	3		
ENSMUST00000119575	ENSMUSG00000054435	6	48684549	48692060	1	0	2	0	2	0	2	0	41	3	10	4	D3Z3F3	
ENSMUST00000119576	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	10	0	0	0	0	11	0	0		Q9CQE3
ENSMUST00000119577						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000119578						11	4	20	8	7	3	0	0	0	0	0		
ENSMUST00000119579	ENSMUSG00000015804	5	45520229	45529276	1	0	0	0	22	0	0	0	0	2	14	0	D3YWT4	
ENSMUST00000119580						2	2	2	5	3	0	0	0	0	0	0		
ENSMUST00000119581	ENSMUSG00000032625	6	12311610	12749410	-1	0	0	0	99	9	0	0	0	0	0	0	E9Q6P0	
ENSMUST00000119582	ENSMUSG00000030031	6	95117240	95129790	1	0	7	0	0	9	0	10	0	0	5	10		Q3UQV5
ENSMUST00000119584						5	4	16	1	10	8	0	2	0	3	3		
ENSMUST00000119585						2	3	6	0	1	0	0	0	0	0	0		
ENSMUST00000119586						0	0	1	0	3	0	0	0	0	0	0		
ENSMUST00000119587	ENSMUSG00000034842	5	92331827	92414628	1	0	0	0	0	0	0	0	0	0	0	0		Q8R2G4
ENSMUST00000119588						8	3	2	5	7	3	0	2	0	0	0		
ENSMUST00000119589						8	3	49	13	8	7	1	0	1	0	0		
ENSMUST00000119590	ENSMUSG00000083628	X	26286977	26310044	-1	0	0	4	3	3	0	0	0	0	0	0	D3Z7C4	
ENSMUST00000119591	ENSMUSG00000025199	19	44073335	44107480	-1	13	3	0	0	3	0	0	477	151	32	141	E9Q605	
ENSMUST00000119592						2	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000119593						5	8	4	9	4	3	0	0	0	0	0		
ENSMUST00000119594						3	0	0	1	1	4	0	0	0	0	0		
ENSMUST00000119595	ENSMUSG00000020100	10	60712072	60752794	-1	68	47	155	79	122	72	47	0	102	0	124	D3YWS9	
ENSMUST00000119596						1	2	0	0	1	0	0	1	0	1	0		
ENSMUST00000119597	ENSMUSG00000037455	10	23796986	23827968	1	506	554	1470	426	560	203	9	62	17	9	43	E9PU92	
ENSMUST00000119598	ENSMUSG00000063600	3	29082023	29691209	1	8	7	3	6	4	3	0	0	0	0	0	B7ZCE7	
ENSMUST00000119599						0	0	0	72	9	5	44	94	159	21	64		
ENSMUST00000119600						3	1	4	1	1	2	0	0	0	0	0		
ENSMUST00000119601						6	0	8	3	5	3	0	0	0	0	0		
ENSMUST00000119602						1	7	8	11	4	4	0	0	0	0	0		
ENSMUST00000119603	ENSMUSG00000024776	19	34192229	34240333	1	0	0	0	0	0	0	150	1066	304	147	139		Q76N33
ENSMUST00000119604	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	0	0	0	1	7	0	0	24		Q9CQE3
ENSMUST00000119605						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119606	ENSMUSG00000035011	10	81135220	81152995	1	0	0	0	244	0	0	45	5	109	0	48		O88939
ENSMUST00000119607						3	1	5	0	1	0	0	0	0	0	0		
ENSMUST00000119608						7	0	11	4	3	0	4	0	3	8	0		
ENSMUST00000119609						2	2	2	1	2	1	0	0	0	0	0		
ENSMUST00000119610	ENSMUSG00000030222	6	137054825	137170497	-1	2	3	7	6	6	4	0	0	1	1	1	E9PUF8	
ENSMUST00000119611						3	5	8	4	6	3	0	3	0	0	1		
ENSMUST00000119612	ENSMUSG00000025903	1	4807788	4848410	1	0	0	0	0	0	0	0	64	13	0	0	J3QQ63	
ENSMUST00000119613						11	13	42	21	26	7	1	1	1	0	0		
ENSMUST00000119614	ENSMUSG00000002578	10	128630843	128645991	-1	5	4	6	7	8	0	0	0	0	0	0		Q8C208
ENSMUST00000119615						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119616						2	2	8	2	4	2	0	0	0	3	0		
ENSMUST00000119617						2	2	0	0	4	0	0	0	0	0	0		
ENSMUST00000119618						3	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000119619						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000119620						2	0	2	1	2	2	0	0	0	0	0		
ENSMUST00000119621						0	0	1	0	2	2	0	0	0	0	0		
ENSMUST00000119622						1	2	2	1	1	1	0	0	0	0	0		
ENSMUST00000119623						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119624	ENSMUSG00000031323	X	102903216	102908687	-1	2	1	0	0	2	0	0	0	0	0	0	B1AX33	
ENSMUST00000119625						9	6	21	5	11	2	0	1	2	0	3		
ENSMUST00000119626						1	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000119627	ENSMUSG00000029352	5	113075839	113081584	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JJU9
ENSMUST00000119628	ENSMUSG00000018401	11	87592162	87616302	1	32	6	6	3	15	11	87	0	354	0	301		Q91XS1
ENSMUST00000119629						6	4	47	18	5	5	0	1	0	1	0		
ENSMUST00000119630						0	0	2	0	1	0	0	1	1	0	2		
ENSMUST00000119631						40	44	56	36	66	18	0	0	1	0	2		
ENSMUST00000119632						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119633	ENSMUSG00000024993	19	60811585	60836227	1	3	0	0	2	3	4	96	178	126	68	86	Q3TH34	
ENSMUST00000119634						4	1	17	6	2	1	0	0	0	0	0		
ENSMUST00000119635						1	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000119636						9	8	3	2	11	1	0	0	0	0	0		
ENSMUST00000119637						26	23	31	23	15	0	0	4	1	0	3		
ENSMUST00000119638						1	1	0	2	1	1	0	0	0	0	0		
ENSMUST00000119639						8	4	5	6	4	3	0	1	0	0	0		
ENSMUST00000119640	ENSMUSG00000035062	X	95639193	95658509	-1	0	0	11	2	0	0	2	11	1	0	5		Q68FG0
ENSMUST00000119641						5	1	13	3	1	3	0	0	0	0	4		
ENSMUST00000119642						0	0	0	0	1	0	0	0	1	0	0		
ENSMUST00000119643						6	8	28	12	5	0	0	0	0	0	0		
ENSMUST00000119644						1	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000119645						7	5	15	7	6	2	0	0	0	0	0		
ENSMUST00000119646						15	13	48	15	19	7	0	2	1	0	1		
ENSMUST00000119647	ENSMUSG00000047248	7	100372233	100470152	1	4	0	0	6	11	5	0	5	18	0	12	D3Z640	
ENSMUST00000119648						2	2	0	1	3	1	0	0	0	0	1		
ENSMUST00000119649	ENSMUSG00000071788	X	26672777	26702638	-1	0	2	0	0	0	0	0	0	0	0	0	B1AZA0	
ENSMUST00000119650	ENSMUSG00000048997	3	108202222	108210934	-1	0	0	0	7	10	0	7	0	0	15	0	B7ZCC4	
ENSMUST00000119651						4	15	9	4	14	4	0	0	0	0	0		
ENSMUST00000119652						0	6	0	0	2	0	0	2	0	4	3		
ENSMUST00000119653						7	12	1	89	5	4	0	0	0	1	0		
ENSMUST00000119654	ENSMUSG00000028583	4	143267431	143299564	-1	1	2	9	0	1	1	0	0	0	3	0	A8Y5F6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119655						1	7	7	5	5	3	0	0	0	0	0		
ENSMUST00000119656						2	2	4	3	3	2	0	0	0	0	0		
ENSMUST00000119657	ENSMUSG00000038204	5	24532697	24540978	-1	10	6	24	7	7	5	0	0	0	0	0	D3Z651	
ENSMUST00000119658						12	3	27	29	8	9	0	0	0	0	1		
ENSMUST00000119659						0	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000119660						3	1	8	0	5	2	0	1	1	4	1		
ENSMUST00000119661	ENSMUSG00000030428	7	4119408	4136708	1	0	0	0	0	0	0	0	0	0	0	0		Q9D3A9
ENSMUST00000119663						1	4	3	5	6	3	0	0	2	0	0		
ENSMUST00000119664	ENSMUSG00000041775	7	138835823	138846273	-1	10	10	3	21	19	11	44	111	118	4	166		Q9D7G9
ENSMUST00000119665	ENSMUSG00000037716	9	58028677	58118823	-1	0	0	0	0	0	5	0	0	0	0	0	D3YU68	
ENSMUST00000119666						1	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000119667						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119668						0	0	16	6	2	0	1	2	0	0	0		
ENSMUST00000119669						0	1	0	1	2	0	0	4	3	4	1		
ENSMUST00000119670	ENSMUSG00000022475	15	97792664	97844502	-1	0	0	0	0	0	0	51	106	104	0	6	E9PXW1	
ENSMUST00000119671						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000119672	ENSMUSG00000021699	13	108449948	109953461	1	0	0	0	74	4	0	0	0	0	0	7	F7BK43	
ENSMUST00000119673						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000119674						2	2	2	2	4	2	0	1	0	0	0		
ENSMUST00000119675						1	1	2	11	0	0	0	0	0	0	0		
ENSMUST00000119676						0	1	3	32	3	1	0	0	0	1	4		
ENSMUST00000119677						1	6	1	1	1	0	0	0	0	0	0		
ENSMUST00000119678						3	2	2	1	2	0	0	0	0	0	0		
ENSMUST00000119679						0	1	0	15	0	0	0	0	0	0	0		
ENSMUST00000119680						2	1	18	0	12	1	0	0	0	0	0		
ENSMUST00000119681						2	5	8	2	5	4	1	2	3	0	3		
ENSMUST00000119682						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119683						3	4	8	3	1	0	1	0	0	4	0		
ENSMUST00000119684						4	3	6	1	5	0	0	1	0	0	0		
ENSMUST00000119685	ENSMUSG00000041264	5	149184350	149215434	1	0	0	0	0	0	0	7	0	0	142	0	D3YW34	
ENSMUST00000119686	ENSMUSG00000038173	8	46986925	47094895	1	9	0	1	3	6	0	0	0	0	0	0	D3YU63	
ENSMUST00000119687						8	8	7	8	15	4	0	0	0	0	0		
ENSMUST00000119688						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119689						4	4	2	6	0	1	0	0	0	0	0		
ENSMUST00000119690						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000119691						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119692						2	4	1	1	5	2	0	2	0	0	0		
ENSMUST00000119693	ENSMUSG00000041479	14	34219595	34230421	1	3	8	27	10	9	1	0	0	0	0	0		Q8C6N3
ENSMUST00000119694	ENSMUSG00000083282	19	4855129	4860912	1	14	13	28	74	27	10	15	11	1	16	24		Q9R013
ENSMUST00000119695						10	9	12	6	10	3	0	0	0	0	0		
ENSMUST00000119696						0	0	0	1	0	0	23	30	4	0	48		
ENSMUST00000119697						6	0	0	8	4	3	0	0	0	0	0		
ENSMUST00000119698	ENSMUSG00000019428	8	70527724	70535328	1	0	2	0	38	0	0	250	227	172	81	188		O35465
ENSMUST00000119699	ENSMUSG00000031310	X	101404384	101420849	-1	0	0	0	0	0	4	0	0	0	5	0	B0R077	
ENSMUST00000119700						0	2	4	25	1	1	0	0	0	0	0		
ENSMUST00000119701						2	3	7	2	4	1	0	0	0	0	0		
ENSMUST00000119703	ENSMUSG00000043843	7	25306106	25316195	1	0	8	9	0	0	0	0	1	0	0	0	D3YU53	
ENSMUST00000119704	ENSMUSG00000095464	16	38347040	38362297	1	3	3	0	2	3	4	0	0	0	0	0	Q54AC6	P56394
ENSMUST00000119705	ENSMUSG00000037426	5	32863701	32994236	1	0	0	0	0	0	0	0	0	63	0	0		P61460
ENSMUST00000119706	ENSMUSG00000005225	6	54595111	54645839	1	37	42	61	37	53	26	30	51	25	3	29		Q80W71
ENSMUST00000119707	ENSMUSG00000032657	3	89183143	89189295	1	0	3	0	24	0	0	31	32	0	16	0	E9Q6P6	
ENSMUST00000119708						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000119709						1	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000119710	ENSMUSG00000084234	7	50599190	50600530	1	8	7	5	11	6	5	0	0	0	0	0		Q8BPC6
ENSMUST00000119711						3	1	9	0	0	0	4	29	11	0	0		
ENSMUST00000119712	ENSMUSG00000030670	7	114550166	114562972	-1	0	0	0	0	0	0	0	0	0	0	0	D3YTX0	
ENSMUST00000119713						4	7	5	3	2	4	0	0	0	0	0		
ENSMUST00000119714	ENSMUSG00000056763	1	10037987	10136768	1	3	0	0	0	0	0	0	0	1	0	2		B2RX88
ENSMUST00000119715						6	5	6	2	5	4	0	0	2	7	0		
ENSMUST00000119716						0	12	18	10	6	6	0	0	0	0	0		
ENSMUST00000119717	ENSMUSG00000070374	11	74283736	74289646	1	11	0	18	7	8	3	0	0	0	0	0	B1ARL3	
ENSMUST00000119718	ENSMUSG00000078502	4	145585166	145625345	1	13	14	9	8	12	5	8	28	16	24	10	B1ASQ6	
ENSMUST00000119719						3	1	3	3	3	0	0	0	0	0	0		
ENSMUST00000119720	ENSMUSG00000037437	8	24836140	24948804	-1	0	0	5	0	8	0	0	4	1	0	0		Q8K410
ENSMUST00000119721	ENSMUSG00000021384	13	49230690	49248706	-1	11	5	23	27	18	1	20	68	14	4	12		Q9D176
ENSMUST00000119722	ENSMUSG00000038112	9	39587396	39604403	-1	11	0	0	7	13	13	0	0	0	0	0	Q8BGF0	
ENSMUST00000119723						0	1	3	1	4	2	0	0	0	0	0		
ENSMUST00000119724						2	2	13	3	7	3	1	0	1	1	1		
ENSMUST00000119725						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000119726						0	1	3	3	1	1	0	0	0	1	0		
ENSMUST00000119727						10	9	11	9	9	7	4	28	0	0	0		
ENSMUST00000119728						3	2	1	7	4	0	0	0	0	0	2		
ENSMUST00000119729						16	5	23	279	30	9	0	3	0	0	0		
ENSMUST00000119730	ENSMUSG00000051359	15	37366175	37792570	-1	5	0	0	0	0	0	0	6	1	4	6		Q91X97
ENSMUST00000119731						1	0	7	2	5	4	0	1	0	0	1		
ENSMUST00000119732						5	0	7	4	3	4	0	0	0	0	0		
ENSMUST00000119733						7	0	2	2	0	3	207	180	281	72	151		
ENSMUST00000119734						2	0	1	3	1	0	0	0	0	0	0		
ENSMUST00000119735						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119736	ENSMUSG00000031901	8	105991337	106053840	1	0	0	0	4	8	3	39	46	0	15	0	D3Z4C7	
ENSMUST00000119737						0	1	1	1	4	0	0	1	1	0	0		
ENSMUST00000119738						0	0	3	1	1	0	0	0	0	6	0		
ENSMUST00000119739	ENSMUSG00000021848	14	48657679	48667644	-1	1	2	0	5	1	0	0	0	0	0	0	D3Z581	
ENSMUST00000119740						5	0	0	2	2	0	0	0	0	2	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119741						1	2	1	8	6	4	0	0	0	0	0		
ENSMUST00000119742						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000119743						0	5	0	0	1	1	0	0	0	0	0		
ENSMUST00000119744						10	6	17	5	9	7	40	52	30	37	19		
ENSMUST00000119745						11	2	18	5	19	0	6	0	0	2	0		
ENSMUST00000119746	ENSMUSG00000068284	16	44173246	44227465	1	0	0	0	128	85	0	192	244	1497	0	955	B2RUQ2	
ENSMUST00000119747						3	4	1	4	9	0	0	0	0	0	0		
ENSMUST00000119749						8	3	5	8	8	2	0	0	0	0	0		
ENSMUST00000119750						4	0	39	4	2	3	0	0	0	0	0		
ENSMUST00000119751						5	4	3	1	4	2	0	4	2	5	0		
ENSMUST00000119752						3	6	8	3	2	5	0	0	0	0	0		
ENSMUST00000119753	ENSMUSG00000074862	10	81606270	81620703	1	0	0	0	0	0	0	0	0	0	4	0	Q3US60	
ENSMUST00000119754	ENSMUSG00000030741	7	126370060	126377450	-1	0	4	0	32	0	0	0	0	22	0	0	D3YWA9	
ENSMUST00000119755						6	3	2	1	6	2	0	0	0	0	0		
ENSMUST00000119756	ENSMUSG00000029174	5	64156305	64351486	1	0	13	6	20	9	10	0	752	243	88	130	E9Q6L4	
ENSMUST00000119757						0	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000119758						11	5	2	2	2	2	0	0	0	0	0		
ENSMUST00000119759						8	3	16	4	6	5	0	0	0	0	0		
ENSMUST00000119760	ENSMUSG00000049493	9	95752642	95845311	-1	1	0	3	2	0	0	0	0	0	0	0	D3Z6J7	
ENSMUST00000119761	ENSMUSG00000027530	3	10244209	10301183	-1	2	0	1	0	2	0	0	0	1	0	0		Q9DAK4
ENSMUST00000119762						1	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000119763						2	1	11	2	1	1	0	0	0	0	0		
ENSMUST00000119764						300	280	1090	276	325	151	5	100	30	16	30		
ENSMUST00000119765						9	2	30	20	4	5	0	1	0	0	0		
ENSMUST00000119766						5	2	9	5	3	3	0	2	0	0	1		
ENSMUST00000119767						0	6	0	0	4	6	0	0	0	11	0		
ENSMUST00000119768						8	7	1	15	9	0	10	55	19	13	4		
ENSMUST00000119769						1	3	6	1	0	0	0	1	0	0	0		
ENSMUST00000119770						3	2	7	3	6	7	0	0	0	0	0		
ENSMUST00000119771						5	6	14	7	7	2	1	0	0	2	0		
ENSMUST00000119772						2	3	22	6	3	3	0	0	0	0	0		
ENSMUST00000119773						1	2	0	0	0	0	1	1	0	5	0		
ENSMUST00000119774						4	1	1	3	2	1	0	0	0	0	0		
ENSMUST00000119775						25	18	61	31	17	8	1	1	0	2	1		
ENSMUST00000119776						2	1	1	1	2	0	0	0	0	0	0		
ENSMUST00000119777						7	1	7	13	4	0	0	1	0	0	0		
ENSMUST00000119778						7	7	24	7	12	5	0	0	0	0	0		
ENSMUST00000119779						7	3	2	2	4	1	0	0	0	0	0		
ENSMUST00000119780						0	0	14	0	0	0	1616	10564	1927	8031	1312		
ENSMUST00000119781	ENSMUSG00000060538	7	126886171	126922917	-1	0	0	0	5	0	0	0	0	0	0	0	G5E8V1	
ENSMUST00000119782						2	1	5	22	8	1	0	0	0	0	1		
ENSMUST00000119783	ENSMUSG00000007415	5	3632932	3657185	-1	4	4	10	26	8	3	70	143	100	31	18		Q920S3
ENSMUST00000119784	ENSMUSG00000063406	5	108106366	108132620	-1	0	2	2	3	1	2	0	0	6	3	3	D3Z615	
ENSMUST00000119785						1	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000119786	ENSMUSG00000052726	1	140246158	140612067	1	0	0	0	0	0	0	0	0	0	0	0	D3Z592	
ENSMUST00000119787	ENSMUSG00000022779	16	16870736	16892990	1	0	0	0	0	0	0	222	99	0	0	126	Q3UJF5	Q9Z321
ENSMUST00000119788	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3YVT9	
ENSMUST00000119789						1	4	36	5	9	2	0	2	0	2	0		
ENSMUST00000119790						4	6	10	3	7	7	3	4	1	22	3		
ENSMUST00000119791						11	32	33	72	0	20	0	0	0	0	0		
ENSMUST00000119792	ENSMUSG00000029466	5	122421693	122444912	1	58	47	92	167	79	40	18	63	43	8	32	D3YU58	
ENSMUST00000119793						0	0	2	4	1	2	0	0	0	0	0		
ENSMUST00000119794						0	1	4	0	2	2	0	1	0	0	0		
ENSMUST00000119795						7	2	5	1	4	5	0	0	0	0	0		
ENSMUST00000119796						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000119797	ENSMUSG00000025340	5	130171798	130214342	1	9	1	24	15	14	1	161	479	256	39	210		Q9JM13
ENSMUST00000119798	ENSMUSG00000096719	7	47463806	47528862	-1	0	0	0	0	0	4	3791	13664	3415	2230	3004	E9QNZ7	
ENSMUST00000119799						1094	1003	4199	1669	1411	688	2	7	9	9	39		
ENSMUST00000119800	ENSMUSG00000046897	15	102203648	102215606	1	0	11	21	0	0	0	745	2360	965	110	472		Q6NZQ6
ENSMUST00000119801						6	5	48	11	8	8	0	0	0	2	0		
ENSMUST00000119802						0	0	2	1	0	0	0	0	1	0	0		
ENSMUST00000119803						3	3	5	1	2	1	0	0	0	1	0		
ENSMUST00000119804						3	1	0	3	1	1	0	0	0	0	0		
ENSMUST00000119805						0	1	2	2	3	0	3	2	0	0	4		
ENSMUST00000119806						6	1	6	18	12	5	0	0	0	0	0		
ENSMUST00000119807						0	1	0	0	1	0	0	0	0	1	0		
ENSMUST00000119808						2	0	1	0	2	3	0	0	0	0	0		
ENSMUST00000119809						2	1	7	1	2	0	0	0	0	0	0		
ENSMUST00000119810	ENSMUSG00000035629	16	32821703	32877766	-1	12	0	3	82	7	0	5	6	5	3	18	D3Z7B1	
ENSMUST00000119811						4	1	2	0	1	3	0	1	1	0	0		
ENSMUST00000119812						10	4	23	7	14	10	0	0	0	0	0		
ENSMUST00000119813						2	2	4	3	7	4	0	0	0	0	0		
ENSMUST00000119814	ENSMUSG00000020069	10	63014664	63024217	-1	0	0	0	0	2	1	0	98	8	9	25	D3Z6Y3	
ENSMUST00000119815						1	3	4	2	9	1	0	0	0	1	1		
ENSMUST00000119816	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	0	0	0	0	0	0	0	8	D6RCV1	
ENSMUST00000119817						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000119818	ENSMUSG00000036099	10	93939165	94035817	-1	35	33	57	35	27	22	5	13	3	2	7	D3Z4E6	
ENSMUST00000119819						2	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000119820	ENSMUSG00000053693	8	84911903	84937359	-1	4	7	7	70	4	0	0	0	0	0	0	E9Q6Q5	
ENSMUST00000119821						6	4	6	4	4	1	1	1	0	0	0		
ENSMUST00000119822						18	8	15	0	9	10	8	6	0	19	0		
ENSMUST00000119823	ENSMUSG00000074179	9	78289923	78305525	1	13	10	14	26	14	6	2	2	1	0	3	E9Q6L7	
ENSMUST00000119824	ENSMUSG00000029320	5	103648039	103656010	-1	5	4	5	44	5	6	0	0	0	0	0		Q9DAA3
ENSMUST00000119825	ENSMUSG00000003534	17	35681567	35704621	-1	0	0	0	124	0	0	0	0	0	0	0		Q03146

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119826	ENSMUSG00000004383	8	72814599	73353540	-1	32	9	38	254	44	19	0	5	8	5	18	Q059X9	Q9Z1M7
ENSMUST00000119827	ENSMUSG00000019942	10	69336635	69352938	-1	2	0	0	2	0	2	180	173	156	479	90		P11440
ENSMUST00000119828						5	1	17	2	1	0	0	0	0	0	0		
ENSMUST00000119829	ENSMUSG00000024160	17	24886643	24892152	1	0	0	10	0	3	0	35	44	60	0	30	D3YW96	
ENSMUST00000119830						0	4	72	0	23	0	147	510	188	23	377		
ENSMUST00000119832						5	7	17	4	13	3	0	3	0	0	0		
ENSMUST00000119833	ENSMUSG00000031137	X	59062145	59568071	-1	15	25	0	26	10	0	0	0	0	0	0	B1AU20	
ENSMUST00000119834						2	1	2	2	2	0	0	0	0	0	0		
ENSMUST00000119835						1	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000119836						17	13	13	13	12	6	4	35	8	15	19		
ENSMUST00000119837						3	3	7	5	10	1	0	0	1	6	0		
ENSMUST00000119838	ENSMUSG00000078864	2	177759288	177770472	1	0	0	0	0	0	0	0	0	0	0	0	A2AW66	
ENSMUST00000119839						0	2	1	8	2	1	3	19	1	2	0		
ENSMUST00000119840						5	12	6	70	12	8	0	0	0	0	0		
ENSMUST00000119841	ENSMUSG00000034729	17	47368887	47381417	1	0	0	0	0	0	0	0	0	5	0	0	E9QJS0	
ENSMUST00000119842						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119843						3	4	0	6	3	0	0	0	0	0	0		
ENSMUST00000119844						3	4	6	41	2	3	0	0	0	0	0		
ENSMUST00000119845						4	7	10	0	12	3	0	0	0	0	0		
ENSMUST00000119846	ENSMUSG00000030741	7	126370060	126377450	-1	0	0	0	125	0	0	0	162	80	41	22	D3YTR6	
ENSMUST00000119847	ENSMUSG00000032040	9	35124408	35176061	-1	14	4	15	0	0	0	42	110	59	17	116	Q3TBW9	
ENSMUST00000119848	ENSMUSG00000073436	17	24888486	24895087	-1	22	21	46	24	21	15	101	222	110	15	114	D3Z6X0	
ENSMUST00000119849						17	6	6	73	18	11	0	0	0	0	0		
ENSMUST00000119850						3	2	27	13	8	2	0	1	1	2	2		
ENSMUST00000119851						8	5	4	13	13	3	7	8	5	8	0		
ENSMUST00000119853						2	0	6	0	3	0	5	5	9	21	4		
ENSMUST00000119854	ENSMUSG00000037736	5	66745827	67057158	1	0	9	0	0	0	0	0	0	0	0	0	D3YU59	
ENSMUST00000119855						9	3	8	7	3	0	0	0	0	0	0		
ENSMUST00000119856						1	2	0	3	4	3	0	0	0	0	0		
ENSMUST00000119857						1	2	5	6	3	0	0	0	0	0	0		
ENSMUST00000119858						0	0	1	6	0	1	0	0	18	0	0		
ENSMUST00000119859						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000119860						1	6	0	1	0	2	0	2	0	0	1		
ENSMUST00000119862						2	7	6	4	8	2	0	0	0	1	0		
ENSMUST00000119863	ENSMUSG00000072708	11	73485887	73491477	-1	8	0	0	0	7	0	0	0	0	0	0	Q5SSP0	
ENSMUST00000119864						58	44	60	37	89	34	12	47	31	6	50		
ENSMUST00000119865	ENSMUSG00000027601	3	19187327	19220817	1	0	0	0	0	0	0	69	172	65	167	101	Q3TTQ5	Q99MB2
ENSMUST00000119866	ENSMUSG00000021768	14	21733394	21751181	-1	10	4	13	17	10	1	0	0	0	0	0	Z4YLI2	
ENSMUST00000119867						0	1	4	0	3	1	0	0	0	0	0		
ENSMUST00000119868						1	3	12	1	1	0	0	0	0	0	0		
ENSMUST00000119869						3	4	4	2	7	0	0	0	0	0	0		
ENSMUST00000119870	ENSMUSG00000031789	8	95239045	95306585	-1	37	58	79	145	88	32	2	7	0	0	5	E1AZ71	
ENSMUST00000119871						5	3	10	5	6	5	0	0	0	0	0		
ENSMUST00000119872						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000119873						1	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000119875						3	7	5	2	11	9	0	0	0	0	0		
ENSMUST00000119876						12	0	10	0	5	0	4	0	5	19	0		
ENSMUST00000119877						0	1	1	0	4	3	41	139	54	187	68		
ENSMUST00000119878	ENSMUSG00000022897	16	94570010	94695517	1	0	0	4	21	0	0	483	991	821	31	414	A9C475	Q61214
ENSMUST00000119879	ENSMUSG00000014767	17	15499888	15528379	1	0	0	0	0	0	0	42	34	104	97	61	F8WJ67	
ENSMUST00000119880						244	242	687	4269	287	171	3	30	10	4	8		
ENSMUST00000119881						0	1	0	3	1	1	0	0	0	0	0		
ENSMUST00000119883						5	0	0	0	1	0	0	6	0	3	1		
ENSMUST00000119884						3	0	0	0	4	0	11	0	56	80	0		
ENSMUST00000119885						2	2	5	0	3	3	2	2	2	10	2		
ENSMUST00000119886						3	3	7	3	7	2	1	1	3	0	2		
ENSMUST00000119887						5	1	1	2	6	2	0	0	0	0	0		
ENSMUST00000119888	ENSMUSG00000021745	14	11553532	12242041	1	7	10	1	0	8	3	0	0	0	0	1	E9Q6E7	
ENSMUST00000119889						0	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000119890						3	3	11	3	9	4	0	0	0	0	0		
ENSMUST00000119891	ENSMUSG00000033488	1	157458577	157492638	1	423	410	538	453	489	235	9	60	28	8	39		Q3UNZ8
ENSMUST00000119892						43	23	101	94	62	28	156	193	379	12	321		
ENSMUST00000119893						0	2	3	0	0	1	0	0	0	0	0		
ENSMUST00000119894						4	3	0	1	2	0	0	0	0	0	0		
ENSMUST00000119895						0	1	0	2	1	0	0	0	0	0	0		
ENSMUST00000119896	ENSMUSG00000027828	3	65379655	65392623	-1	2	1	3	13	0	0	14	16	10	12	9		Q9DCF9
ENSMUST00000119897						2	2	4	2	4	3	0	3	0	0	0		
ENSMUST00000119898						3	8	8	4	4	0	6	12	3	55	9		
ENSMUST00000119899						1	2	1	0	3	0	0	0	0	0	0		
ENSMUST00000119900						2	3	3	4	5	3	5	37	12	7	10		
ENSMUST00000119901	ENSMUSG00000023067	17	29090979	29100722	1	0	0	3	13	4	3	0	0	5	7	0	Q564P6	P39689
ENSMUST00000119902	ENSMUSG00000027858	3	102734529	102801513	1	5	2	11	42	4	3	13	0	24	5	20	Q9D1X8	
ENSMUST00000119903						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119904						9	3	14	11	7	4	0	0	0	0	0		
ENSMUST00000119905	ENSMUSG00000033543	9	70012550	70022866	1	1	0	0	0	0	0	0	100	41	210	29	D3Z7C2	
ENSMUST00000119906						2	0	0	2	0	1	0	0	0	0	0		
ENSMUST00000119907						2	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000119908						2	1	9	4	0	1	1	0	0	0	0		
ENSMUST00000119909						3	6	23	6	9	2	1	1	0	0	0		
ENSMUST00000119910						2	1	0	0	1	1	0	0	0	1	0		
ENSMUST00000119911						3	6	1	1	5	3	0	0	0	0	0		
ENSMUST00000119912	ENSMUSG00000044709	7	19564946	19573823	-1	0	1	0	8	1	0	13	12	5	0	17		Q9CWY4
ENSMUST00000119913						2	2	1	0	0	0	0	0	1	0	1		
ENSMUST00000119915						1	1	2	3	0	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000119916	ENSMUSG00000029196	5	36473670	36484285	-1	1	4	0	0	4	0	27	0	19	0	52	D3YW26	
ENSMUST00000119917	ENSMUSG00000020027	10	95385362	95417180	-1	0	2	0	18	5	5	0	0	0	3	3	Q548Q7	O35717
ENSMUST00000119919						0	7	0	0	0	0	0	0	0	0	0		
ENSMUST00000119920						9	8	0	14	12	9	0	0	0	0	0		
ENSMUST00000119921	ENSMUSG00000028992	4	149467572	149485202	-1	66	86	280	123	84	53	7	46	5	24	31	B0QZL2	
ENSMUST00000119922	ENSMUSG00000096145	7	127893063	127895617	-1	0	0	0	0	0	0	0	0	0	0	0	D3YWB2	
ENSMUST00000119923						9	6	2	4	3	4	0	0	0	0	0		
ENSMUST00000119924						2	2	4	2	3	0	0	0	0	0	0		
ENSMUST00000119925						2	1	0	1	6	1	0	0	0	0	0		
ENSMUST00000119926						0	0	0	2	1	0	2	29	1	1	8		
ENSMUST00000119927						1	3	6	0	1	7	0	1	2	1	0		
ENSMUST00000119928	ENSMUSG00000024188	17	26252910	26285504	1	0	0	0	0	0	0	0	0	25	0	9		
ENSMUST00000119929	ENSMUSG00000047554	7	109972187	109986929	-1	0	0	0	0	0	4	29	269	56	0	0		Q8K1A5
ENSMUST00000119930						0	1	3	9	3	4	0	0	0	0	0		
ENSMUST00000119931						6	3	2	11	2	5	0	0	0	0	0		
ENSMUST00000119932	ENSMUSG00000024136	17	24440081	24443105	-1	2	2	31	0	6	2	12	21	9	0	13		Q9D1G0
ENSMUST00000119933						1	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000119934						5	8	6	3	5	3	8	82	17	0	33		
ENSMUST00000119935						3	2	10	4	4	7	0	0	0	0	0		
ENSMUST00000119936						16	7	26	13	8	6	0	0	0	0	0		
ENSMUST00000119937						3	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000119938						3	2	3	2	3	3	0	4	1	0	2		
ENSMUST00000119939						4	0	2	1	3	0	0	0	0	0	0		
ENSMUST00000119941	ENSMUSG00000022656	16	46387706	46498525	-1	3	1	0	0	5	1	0	0	0	0	0	D3Z657	
ENSMUST00000119942						3	2	2	3	2	1	0	0	0	0	0		
ENSMUST00000119943	ENSMUSG00000048279	14	61138457	61240695	1	40	40	63	47	45	22	35	66	61	15	62	E9QNY8	
ENSMUST00000119944	ENSMUSG00000048661	10	120923413	120979332	-1	0	0	0	0	0	0	151	197	130	50	117	E9QP59	
ENSMUST00000119945	ENSMUSG00000034729	17	47368887	47381417	1	0	0	0	0	0	0	32	90	44	69	0	G5E8U5	
ENSMUST00000119946	ENSMUSG00000057541	5	23740648	23783711	-1	0	12	0	104	3	8	0	50	12	0	0	Q91VU7	
ENSMUST00000119947						0	0	0	0	0	0	8	0	62	0	30		
ENSMUST00000119948						1	0	1	0	2	0	2	0	1	0	0		
ENSMUST00000119949						1	0	2	0	0	0	135	288	121	449	136		
ENSMUST00000119950	ENSMUSG00000067847	2	156144039	156145797	1	0	0	0	0	0	0	22	0	0	114	0		P60603
ENSMUST00000119952						8	4	29	12	11	6	0	1	0	0	1		
ENSMUST00000119953	ENSMUSG00000005846	16	11192970	11203331	-1	5	12	15	40	9	2	54	461	108	577	165		Q8BVY0
ENSMUST00000119954	ENSMUSG00000041328	7	92643712	92669933	-1	20	7	5	124	33	16	309	838	631	121	802	G3X9Z4	
ENSMUST00000119955						5	2	4	5	0	1	0	0	0	0	0		
ENSMUST00000119956						3	2	0	5	5	4	0	0	0	0	0		
ENSMUST00000119957						0	0	0	0	3	5	2	0	0	2	0		
ENSMUST00000119958	ENSMUSG00000084346	4	115452604	115471062	1	9	8	1	9	6	3	0	0	0	0	0	A0A087WS15	
ENSMUST00000119959						0	0	3	1	0	0	0	5	1	0	1		
ENSMUST00000119960	ENSMUSG00000063683	19	12633308	12653911	1	40	33	22	29	43	17	5	6	4	2	12		Q91XE0
ENSMUST00000119961						2	2	1	1	1	2	0	0	0	0	0		
ENSMUST00000119962	ENSMUSG00000019823	10	41476314	41487032	1	4	3	9	81	8	9	16	1	93	0	0		Q8VDP3
ENSMUST00000119963						2	2	3	8	5	1	0	0	0	2	0		
ENSMUST00000119964						3	1	0	5	2	1	0	0	0	0	0		
ENSMUST00000119965	ENSMUSG00000080933	X	37623318	37628612	-1	0	3	0	1	2	0	0	0	0	0	0	B9EJQ9	
ENSMUST00000119966						2	0	3	4	6	1	0	0	0	0	0		
ENSMUST00000119967						2	4	3	1	4	1	0	0	0	0	0		
ENSMUST00000119968	ENSMUSG00000019710	3	87919506	87923672	1	0	2	8	3	4	1	177	413	230	431	235		Q9CQ06
ENSMUST00000119969						2	2	2	1	4	1	0	0	0	0	0		
ENSMUST00000119970	ENSMUSG00000037610	3	31902507	32200180	1	0	1	0	1	0	0	0	0	0	0	0		Q9CZM9
ENSMUST00000119972	ENSMUSG00000081984	1	88204732	88205782	-1	1	5	9	180	15	6	0	0	3	1	7	Q5RL26	
ENSMUST00000119973	ENSMUSG00000035067	14	63606503	63820809	1	15	14	48	156	27	14	0	0	2	0	0		E9Q6C8
ENSMUST00000119975	ENSMUSG00000029022	4	147860778	147868816	-1	12	7	25	27	24	9	33	76	44	23	76		A2A7Y5
ENSMUST00000119976	ENSMUSG00000046295	8	71406010	71409904	1	105	84	700	41	61	39	5	46	14	0	20	A8VU90	
ENSMUST00000119977						8	3	7	9	8	2	5	13	14	0	15		
ENSMUST00000119978						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000119980	ENSMUSG00000025724	7	80904889	80947780	-1	1	0	0	20	0	0	0	0	0	0	0	D3YWT0	
ENSMUST00000119981	ENSMUSG00000071533	16	56007245	56029739	-1	0	1	0	0	0	0	0	9	12	23	0	D3YWA4	
ENSMUST00000119982						5	3	9	1	7	5	0	0	0	0	0		
ENSMUST00000119984						2	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000119985	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	0	0	0	0	0	0	0	0		Q9CQE3
ENSMUST00000119987						2	3	8	4	1	0	1	32	16	10	9		
ENSMUST00000119988						3	2	3	1	5	3	0	0	0	0	0		
ENSMUST00000119989	ENSMUSG00000054715	7	12897815	12909083	1	3	0	0	0	0	0	0	0	18	0	9	Q3TQC3	
ENSMUST00000119990	ENSMUSG00000037552	7	28359604	28372599	-1	0	0	0	0	0	0	184	79	240	0	90	G5E8T4	
ENSMUST00000119991	ENSMUSG00000024378	18	33199355	33213862	-1	0	0	4	0	2	1	7	2	29	7	14	D3YW30	
ENSMUST00000119992						4	8	4	4	11	2	0	0	0	0	0		
ENSMUST00000119993	ENSMUSG00000028152	3	138742195	138907905	1	5	0	2	0	10	0	222	114	246	0	110	D3Z641	
ENSMUST00000119994						5	4	10	3	3	0	0	1	1	1	3		
ENSMUST00000119995	ENSMUSG00000014104	6	41852989	41864413	1	0	0	0	1	0	0	0	0	0	0	0	D3Z4E7	
ENSMUST00000119996						24	16	47	15	35	12	0	0	0	0	1		
ENSMUST00000119997	ENSMUSG00000050982	15	77477047	77491069	1	6	3	21	2	6	7	0	0	0	0	0	Q8CCA5	
ENSMUST00000119998						1	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000119999						14	7	32	10	10	11	0	0	0	1	0		
ENSMUST00000120000						2	0	3	1	1	3	2	4	2	4	2		
ENSMUST00000120001						7	10	4	4	2	0	0	0	0	0	0		
ENSMUST00000120002						2	1	3	1	2	1	0	0	0	0	0		
ENSMUST00000120003						425	355	315	387	378	198	12	53	13	4	42		
ENSMUST00000120004	ENSMUSG00000057093	7	27689340	27706484	1	40	39	82	38	37	21	4	13	6	6	7	G3X9H3	
ENSMUST00000120005	ENSMUSG00000062044	7	45783738	45804144	1	22	0	0	581	0	0	0	0	0	0	0		
ENSMUST00000120006	ENSMUSG00000052675	7	24112314	24127952	1	16	9	12	12	9	6	8	18	0	7	0		Q0VAW7
ENSMUST00000120007	ENSMUSG00000060538	7	126886171	126922917	-1	1	3	5	4	2	3	38	124	53	70	48	G3X9Z3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120008						2	2	8	5	4	1	1	1	5	0	3		
ENSMUST00000120009	ENSMUSG00000005980	16	4036942	4040024	1	0	0	0	0	0	0	0	0	1	0	0	Q14BW6	P49183
ENSMUST00000120010						4	4	32	24	4	0	0	0	0	0	0		
ENSMUST00000120011						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000120012						1	0	2	0	0	1	1	0	1	0	1		
ENSMUST00000120013						3	6	7	6	4	6	0	0	0	0	0		
ENSMUST00000120014						0	0	0	3	0	3	3	3	9	0	6		
ENSMUST00000120015						0	1	0	0	2	0	0	0	0	1	0		
ENSMUST00000120016	ENSMUSG00000079605	17	26973167	26976205	1	7	0	0	75	1	15	202	447	202	38	188		Q8CDC7
ENSMUST00000120017						0	6	14	0	8	4	0	0	0	8	0		
ENSMUST00000120018						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000120019						1	2	2	6	5	3	0	0	0	0	0		
ENSMUST00000120021						8	2	3	5	6	0	0	0	0	0	0		
ENSMUST00000120022						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120023						37	35	63	41	44	20	3	2	14	2	16		
ENSMUST00000120024						6	5	10	7	5	3	1	1	0	0	0		
ENSMUST00000120025						1	10	0	1	1	0	6	15	9	0	12		
ENSMUST00000120026						0	0	3	2	0	0	0	0	0	0	0		
ENSMUST00000120027						3	4	5	1	4	2	0	0	0	0	0		
ENSMUST00000120028	ENSMUSG00000000530	15	101128522	101145336	1	0	0	12	2	0	0	0	0	0	0	0		Q61288
ENSMUST00000120029						7	7	10	16	7	5	2	0	0	0	0		
ENSMUST00000120030						2	0	5	6	2	0	0	0	1	1	0		
ENSMUST00000120031						0	0	0	1	4	3	0	0	0	0	0		
ENSMUST00000120032						8	11	48	9	12	5	1	0	0	2	1		
ENSMUST00000120033	ENSMUSG00000064036	18	73859385	73881333	1	2	2	0	0	0	1	0	0	0	0	0	E9QNX2	
ENSMUST00000120034	ENSMUSG00000025466	7	140096770	140102441	-1	1	2	0	3	3	5	0	0	0	0	0	D3YWS7	
ENSMUST00000120035	ENSMUSG00000024163	17	24892153	24936977	-1	0	0	0	0	0	0	0	0	0	0	0		Q9ESN9
ENSMUST00000120036						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120037						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120038						1	1	0	3	1	1	0	0	0	0	0		
ENSMUST00000120039						0	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000120040	ENSMUSG00000045160	6	83349147	83360136	1	2	1	4	24	4	0	0	0	3	16	0	E9PX89	
ENSMUST00000120041	ENSMUSG00000002320	14	55635965	55643806	-1	6	0	0	0	0	0	56	220	25	10	0		Q9DBU0
ENSMUST00000120042						14	17	41	128	26	22	0	0	0	0	0		
ENSMUST00000120043						1	3	0	1	1	1	0	0	0	0	0		
ENSMUST00000120044	ENSMUSG00000031789	8	95239045	95306585	-1	0	6	0	40	0	3	0	0	0	0	0	E9PXX0	
ENSMUST00000120045						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000120046						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000120047						1	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000120048						11	4	3	6	9	1	0	0	0	0	0		
ENSMUST00000120049	ENSMUSG00000071550	16	44394796	44482428	1	25	15	37	26	23	15	0	0	0	0	0	E9Q5M6	
ENSMUST00000120050						37	38	64	50	64	42	3	11	16	2	50		
ENSMUST00000120051	ENSMUSG00000045312	13	94057796	94195409	1	5	0	0	0	2	0	0	0	0	0	0	D3Z4C4	
ENSMUST00000120052	ENSMUSG00000041044	14	37054830	37064946	1	24	23	25	64	32	17	0	0	0	0	0		Q8K099
ENSMUST00000120053						7	7	5	3	6	2	0	1	0	1	1		
ENSMUST00000120054						1	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000120055						4	2	2	10	4	0	0	0	0	0	0		
ENSMUST00000120056	ENSMUSG00000063445	16	4710059	4719356	-1	40	38	54	55	48	21	21	57	27	14	61	D3YU12	
ENSMUST00000120057	ENSMUSG00000025010	19	40831279	40848572	1	3	5	0	16	0	0	0	0	0	0	0		Q3TZI6
ENSMUST00000120058						7	0	4	0	5	0	0	0	0	0	0		
ENSMUST00000120059						3	4	10	6	4	4	2	4	1	1	3		
ENSMUST00000120060						1	2	1	0	1	0	0	0	0	0	0		
ENSMUST00000120061	ENSMUSG00000025576	11	118489762	118911597	-1	0	0	0	39	0	3	0	0	0	0	0		Q8BIF2
ENSMUST00000120062						5	4	13	4	10	2	0	0	0	0	0		
ENSMUST00000120063						4	2	7	1	3	1	0	0	0	0	0		
ENSMUST00000120064						1	1	3	1	9	2	0	0	0	0	0		
ENSMUST00000120065						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000120066	ENSMUSG00000067825	6	121183667	121198837	1	5	0	94	8	19	0	35	64	43	12	66		Q8BGI5
ENSMUST00000120067						0	2	0	2	2	2	0	0	0	0	0		
ENSMUST00000120068	ENSMUSG00000044681	5	28200819	28245792	-1	16	7	9	1	6	4	0	0	0	0	0		Q4VAB4
ENSMUST00000120069						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000120071	ENSMUSG00000030465	8	67689082	68062286	-1	39	57	119	316	61	35	4	7	7	10	13	E9PUC5	
ENSMUST00000120072						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000120073						3	3	3	12	0	3	0	0	0	0	0		
ENSMUST00000120074	ENSMUSG00000048012	7	44731481	44751050	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BI67
ENSMUST00000120075						7	0	9	2	4	0	0	0	0	0	0		
ENSMUST00000120076						2	6	12	11	8	0	0	1	1	1	0		
ENSMUST00000120077	ENSMUSG00000021950	14	34085981	34100571	1	0	0	10	0	3	0	0	1	1	0	7	Q921D0	
ENSMUST00000120078						0	0	2	1	1	0	0	0	0	0	0		
ENSMUST00000120079						4	3	5	3	2	1	0	0	0	0	0		
ENSMUST00000120080	ENSMUSG00000005580	16	4287529	4420498	-1	0	5	0	309	27	7	0	0	6	0	12	E9Q706	
ENSMUST00000120081	ENSMUSG00000069818	11	73782966	73787875	1	0	5	10	6	8	0	0	0	0	0	0	Q8VEZ7	
ENSMUST00000120082						4	4	8	6	3	2	1	1	3	1	1		
ENSMUST00000120083	ENSMUSG00000028700	4	116123840	116159849	1	0	0	0	0	1	0	0	0	0	0	0		Q91X88
ENSMUST00000120085						10	13	20	10	13	7	1	0	0	1	1		
ENSMUST00000120086						6	8	9	16	15	8	0	1	0	0	0		
ENSMUST00000120087	ENSMUSG00000047735	6	3372257	3399572	-1	13	17	9	17	14	7	1155	7469	2068	1312	1247	E9PX59	
ENSMUST00000120088						9	8	38	7	8	6	3	2	0	0	3		
ENSMUST00000120089						8	0	4	0	5	1	0	0	0	0	0		
ENSMUST00000120090						3	0	0	3	2	1	0	2	0	3	4		
ENSMUST00000120092						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000120093						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000120094	ENSMUSG00000047215	5	65388364	65391444	-1	1	0	0	0	0	6	32	175	61	104	42	Q5EBQ6	P51410
ENSMUST00000120095	ENSMUSG00000028391	4	62448653	62470896	-1	9	9	12	11	10	6	0	0	0	0	0		Q9JHB4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120096						1	0	4	1	2	1	0	0	0	0	0		
ENSMUST00000120097						0	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000120098						8	5	14	18	12	6	2	21	9	4	6		
ENSMUST00000120099	ENSMUSG00000022843	16	20702964	20717746	-1	0	0	0	0	0	0	1	0	0	0	0	A9C437	
ENSMUST00000120100						4	1	0	0	5	1	0	0	0	0	0		
ENSMUST00000120101	ENSMUSG00000043587	9	96823336	96892669	-1	0	0	0	26	0	0	16	0	0	0	0		Q8BHA9
ENSMUST00000120102	ENSMUSG00000044393	18	20558074	20604521	1	37	49	33	33	45	20	0	1	2	1	0	Q811I1	
ENSMUST00000120103						8	4	10	7	4	0	0	0	0	0	0		
ENSMUST00000120104						11	6	39	8	12	8	0	1	2	2	0		
ENSMUST00000120105	ENSMUSG00000009555	2	32705784	32713076	-1	0	0	2	26	0	1	629	1829	648	150	704		Q99J95
ENSMUST00000120106						36	32	75	53	44	23	6	18	9	8	56		
ENSMUST00000120107	ENSMUSG00000031310	X	101404384	101420849	-1	19	2	34	0	15	0	0	0	0	0	9	B1AXS8	
ENSMUST00000120108	ENSMUSG00000029320	5	103648039	103656010	-1	2	1	0	23	3	0	0	0	0	0	0		Q9DAA3
ENSMUST00000120109						2	3	3	3	3	0	0	0	0	0	0		
ENSMUST00000120110						15	4	18	8	9	7	2	5	0	0	11		
ENSMUST00000120111						8	6	2	10	10	2	0	0	0	0	0		
ENSMUST00000120112	ENSMUSG00000022753	16	57266139	57292865	-1	76	68	159	176	93	46	0	20	0	2	14	A9C448	
ENSMUST00000120113						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000120114						6	7	2	7	5	3	0	0	0	0	0		
ENSMUST00000120115						5	4	2	2	8	4	1	1	0	1	2		
ENSMUST00000120116						1	2	2	2	2	1	0	0	0	1	0		
ENSMUST00000120117						7	5	6	15	9	5	0	0	0	0	0		
ENSMUST00000120118						0	3	5	0	0	1	0	0	0	0	0		
ENSMUST00000120119	ENSMUSG00000030990	7	102210208	102238567	1	6	4	34	11	11	5	11	36	25	0	31		
ENSMUST00000120120	ENSMUSG00000027957	3	116669470	116712831	-1	5	0	2	2	3	3	21	149	61	4	26		Q8R1T4
ENSMUST00000120121						0	1	6	1	5	4	0	0	0	0	0		
ENSMUST00000120122	ENSMUSG00000032030	9	53614582	53670014	-1	3	11	11	3	0	0	9	150	15	0	0	E9Q6Z0	
ENSMUST00000120123						27	24	79	29	19	11	83	252	83	36	151		
ENSMUST00000120124						3	2	1	2	2	4	0	0	0	0	0		
ENSMUST00000120125						6	2	19	6	4	3	0	0	0	0	0		
ENSMUST00000120126	ENSMUSG00000023232	4	130253495	130279205	-1	0	0	0	1	0	3	0	0	2	0	0	E9Q7Q6	
ENSMUST00000120127						1	2	0	0	0	2	0	0	0	0	0		
ENSMUST00000120128	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z6J2	
ENSMUST00000120129	ENSMUSG00000054280	5	32789820	32854256	-1	71	65	169	70	75	38	497	1175	1286	77	849	E9Q7C4	
ENSMUST00000120130						2	0	0	0	3	0	0	0	0	0	2		
ENSMUST00000120131						0	2	2	0	0	1	0	0	0	0	0		
ENSMUST00000120132						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120133	ENSMUSG00000074764	2	140229855	140389706	-1	1	1	1	0	0	0	0	0	0	0	0	B0QZY1	
ENSMUST00000120134						1	0	0	7	4	1	0	0	0	0	0		
ENSMUST00000120135	ENSMUSG00000021457	13	52583173	52648792	1	39	32	15	342	59	22	4712	5119	10230	692	8337	Q3UPF7	P48025
ENSMUST00000120136						3	2	7	6	7	2	0	0	1	1	0		
ENSMUST00000120137	ENSMUSG00000062128	11	73350839	73354795	1	0	1	0	2	2	0	0	0	0	0	0	Q7TRX9	
ENSMUST00000120138						1	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000120139						5	1	6	8	2	0	0	0	0	0	0		
ENSMUST00000120141	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q708	
ENSMUST00000120142						2	3	11	0	3	1	0	0	0	0	0		
ENSMUST00000120143	ENSMUSG00000027506	3	8925593	9004723	-1	25	18	59	109	36	26	218	1612	749	344	1234		Q62393
ENSMUST00000120144	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4V0	
ENSMUST00000120145						2	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000120146						0	3	8	0	5	0	0	1	0	0	0		
ENSMUST00000120147						7	2	3	6	4	4	0	1	0	0	0		
ENSMUST00000120148						1	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000120149						13	12	5	0	18	2	0	239	18	79	39		
ENSMUST00000120150	ENSMUSG00000029269	5	87513339	87538195	-1	0	0	2	1	0	0	0	0	0	0	0		Q9QWG7
ENSMUST00000120151						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000120152						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120154	ENSMUSG00000028778	4	130130217	130139359	-1	17	8	13	7	10	6	0	2	0	0	0		P58307
ENSMUST00000120156						1	2	3	0	0	0	0	0	0	0	0		
ENSMUST00000120157	ENSMUSG00000028657	4	122836242	122859175	1	14	11	11	9	0	0	192	560	457	66	328	F7CTA8	
ENSMUST00000120158						3	5	11	2	2	0	0	0	0	0	0		
ENSMUST00000120159						6	3	7	4	6	2	0	0	0	0	0		
ENSMUST00000120160						8	14	44	34	13	3	0	0	0	0	0		
ENSMUST00000120161						20	12	66	49	25	20	0	0	0	0	0		
ENSMUST00000120162						0	1	1	0	0	0	0	0	1	0	0		
ENSMUST00000120163						24	18	41	18	30	20	0	5	4	1	3		
ENSMUST00000120164						12	7	30	16	14	6	0	0	0	0	0		
ENSMUST00000120165						6	2	13	10	9	5	1	1	1	0	0		
ENSMUST00000120166						61	30	23	391	82	60	2	5	2	0	0		
ENSMUST00000120167	ENSMUSG00000025766	3	41742611	41803320	1	0	0	0	8	0	0	0	0	0	0	0	A0A0B4J1L5	
ENSMUST00000120168						12	13	19	16	14	3	1	0	0	3	0		
ENSMUST00000120169						510	414	1342	565	634	323	2	3	5	0	8		
ENSMUST00000120170						5	1	1	4	1	0	0	0	0	0	2		
ENSMUST00000120171						4	3	3	0	2	0	0	0	0	0	0		
ENSMUST00000120172						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000120173	ENSMUSG00000038145	9	122117283	122169702	1	44	46	94	82	75	32	1188	3168	2071	224	1752		Q8VDU5
ENSMUST00000120174						4	2	5	1	7	4	0	0	0	1	0		
ENSMUST00000120175						5	6	24	8	2	2	1	7	0	7	0		
ENSMUST00000120176						5	1	6	191	12	7	0	1	0	0	0		
ENSMUST00000120177	ENSMUSG00000001663	10	75783813	75798584	-1	9	5	9	3	7	3	0	0	0	0	0	D3Z3X5	
ENSMUST00000120178						0	0	5	3	4	0	0	0	0	0	0		
ENSMUST00000120179						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000120180						4	2	10	1	1	0	1	0	0	0	2		
ENSMUST00000120181						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000120182						8	1	4	0	3	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120183						2	7	11	5	9	2	3	7	6	1	9		
ENSMUST00000120184						3	2	0	0	1	0	0	0	0	2	0		
ENSMUST00000120185						2	0	1	0	2	2	0	0	0	0	0		
ENSMUST00000120186						1	1	1	2	2	0	0	0	0	0	0		
ENSMUST00000120187	ENSMUSG00000030849	7	130162451	133123350	-1	1	1	0	63	5	0	0	0	0	0	0	E9Q7C7	
ENSMUST00000120188						49	17	168	52	27	11	0	0	0	0	3		
ENSMUST00000120189						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000120190						2	0	5	2	2	0	0	0	0	0	0		
ENSMUST00000120191						18	8	24	14	19	0	3	5	0	3	0		
ENSMUST00000120192						13	7	4	19	19	8	0	3	0	0	0		
ENSMUST00000120193	ENSMUSG00000034842	5	92331827	92414628	1	0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000120194	ENSMUSG00000041629	11	113661319	113684155	-1	11	9	27	174	23	12	505	1110	521	235	398	A2A6P4	
ENSMUST00000120195						3	3	2	1	7	2	0	0	0	0	1		
ENSMUST00000120196	ENSMUSG00000047248	7	100372233	100470152	1	15	7	24	3	0	1	0	62	12	0	24	D3Z4D9	
ENSMUST00000120197						8	1	3	4	8	6	1	0	0	0	0		
ENSMUST00000120198						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000120199						11	10	6	9	7	4	4	2	1	1	1		
ENSMUST00000120200						23	11	10	10	21	4	7	4	1	5	1		
ENSMUST00000120201	ENSMUSG00000031310	X	101404384	101420849	-1	0	0	0	0	0	0	31	6	0	6	0	Q8CG95	
ENSMUST00000120202						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000120203						8	5	20	31	6	9	0	1	1	1	0		
ENSMUST00000120204	ENSMUSG00000028782	4	129984870	130022633	1	4	5	9	135	0	0	0	0	0	0	3	B1ASC0	
ENSMUST00000120205						7	4	31	8	6	4	0	0	0	0	0		
ENSMUST00000120206						1	2	1	1	2	0	0	0	0	0	0		
ENSMUST00000120207						4	6	28	6	10	1	0	0	0	0	0		
ENSMUST00000120208						5	6	1	9	10	0	0	0	0	0	0		
ENSMUST00000120209						1	1	0	3	2	2	0	0	0	0	0		
ENSMUST00000120210						5	2	1	0	2	0	0	0	0	0	0		
ENSMUST00000120211						1	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000120212						6	0	0	14	0	0	0	0	0	0	0		
ENSMUST00000120213	ENSMUSG00000031667	8	91112041	91134465	-1	3	0	0	3	3	0	119	483	122	90	63		Q64362
ENSMUST00000120214						3	1	4	3	7	2	0	0	0	0	0		
ENSMUST00000120215						4	1	5	2	8	0	0	0	0	0	0		
ENSMUST00000120216						4	2	2	0	2	0	0	0	0	0	0		
ENSMUST00000120217						6	5	23	5	3	3	0	0	0	0	0		
ENSMUST00000120219						3	3	5	1	3	1	0	0	0	1	0		
ENSMUST00000120220	ENSMUSG00000034071	7	12415153	12422751	-1	0	0	0	5	0	3	0	2	0	0	0	D3YU41	
ENSMUST00000120221						3	2	19	18	2	0	0	1	0	0	0		
ENSMUST00000120222	ENSMUSG00000071266	17	22424222	22456689	1	0	0	5	4	0	3	4	4	0	18	17	Q8K3B4	
ENSMUST00000120223	ENSMUSG00000045215	18	22344883	22530227	1	0	0	160	52	63	34	0	0	0	0	0		Q8C4A5
ENSMUST00000120224						1	2	3	3	2	1	0	0	0	0	0		
ENSMUST00000120225						0	0	0	4	1	3	0	0	0	0	0		
ENSMUST00000120226	ENSMUSG00000006728	10	127063534	127067920	1	0	0	0	13	0	0	0	0	0	0	20	D3YWB0	
ENSMUST00000120227						1	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000120228						3	7	4	0	1	0	0	1	0	1	3		
ENSMUST00000120229	ENSMUSG00000022044	14	66344296	66361680	1	2	1	3	0	0	4	0	0	0	0	0	G3X9Z6	
ENSMUST00000120230	ENSMUSG00000008540	6	138140316	138156755	1	7	4	0	3	6	0	0	34	6	12	20	Q53ZD4	Q91VS7
ENSMUST00000120231						6	6	9	4	10	5	0	0	0	0	0		
ENSMUST00000120232	ENSMUSG00000004070	16	4726361	4766742	1	0	3	18	0	2	0	444	1656	332	1318	335	Q544R7	O70252
ENSMUST00000120233						11	9	0	4	12	6	0	0	0	0	0		
ENSMUST00000120234						2	0	14	0	0	0	1946	2225	1201	3560	970		
ENSMUST00000120235						2	1	6	4	2	2	0	0	0	0	0		
ENSMUST00000120236						5	9	53	8	12	3	0	0	0	0	0		
ENSMUST00000120238	ENSMUSG00000029833	6	37870811	37966296	1	11	1	12	0	12	0	45	31	103	20	24	E9Q1U8	
ENSMUST00000120239	ENSMUSG00000020063	10	63319005	63381704	-1	11	9	5	9	7	7	0	0	0	0	0	Q53Z05	Q923E4
ENSMUST00000120240	ENSMUSG00000029993	6	87009236	87028461	1	14	13	13	61	18	7	6	37	0	9	5		
ENSMUST00000120241						7	10	13	6	4	1	0	0	0	11	1		
ENSMUST00000120242						29	38	108	39	56	35	0	2	1	0	1		
ENSMUST00000120243	ENSMUSG00000014599	3	107741048	107760469	-1	10	3	9	7	3	0	73	134	117	0	40		P07141
ENSMUST00000120244						66	41	78	49	61	26	1	31	7	13	20		
ENSMUST00000120245						346	230	2073	421	406	214	3	19	11	4	20		
ENSMUST00000120246						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000120247	ENSMUSG00000034135	9	46012820	46224194	1	7	0	37	0	12	13	72	0	131	0	190	F6U6U5	
ENSMUST00000120248						9	0	0	7	7	0	0	1	0	0	0		
ENSMUST00000120249						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000120250						4	8	4	8	4	4	4	6	2	0	3		
ENSMUST00000120251	ENSMUSG00000063232	12	103980243	103989957	-1	7	0	13	0	0	7	5	0	15	0	0	E9QK54	
ENSMUST00000120252						3	4	4	6	8	1	0	0	0	0	0		
ENSMUST00000120253						1	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000120254						7	5	18	12	11	4	0	0	0	0	0		
ENSMUST00000120255						2	1	5	2	5	5	1	0	0	0	0		
ENSMUST00000120256						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120257						1	1	8	0	6	2	0	0	2	0	0		
ENSMUST00000120258						40	22	42	575	56	17	1	2	2	1	3		
ENSMUST00000120259	ENSMUSG00000071369	10	19934472	20142753	1	10	4	6	145	21	8	94	18	962	66	895	E9PWG9	
ENSMUST00000120260						5	5	17	25	8	2	24	5	16	0	15		
ENSMUST00000120261	ENSMUSG00000040712	11	70669463	70688105	-1	0	0	0	0	0	0	0	0	17	0	0	B0QZH6	
ENSMUST00000120262	ENSMUSG00000030731	7	44384102	44400187	1	0	2	49	0	0	0	1	0	0	1	1	G3X9Y1	
ENSMUST00000120263						3	2	14	1	4	3	2	2	1	2	0		
ENSMUST00000120264						140	164	904	94	109	53	0	14	0	0	2		
ENSMUST00000120265	ENSMUSG00000004933	10	81252935	81263365	1	0	0	0	0	0	0	61	61	18	0	4	D3Z4T5	
ENSMUST00000120266						1	2	2	3	3	1	0	0	0	0	0		
ENSMUST00000120267	ENSMUSG00000047767	7	101289392	101302251	-1	0	0	0	0	0	0	201	62	125	0	139	G9M4M8	Q6KAU8
ENSMUST00000120268	ENSMUSG00000073267	X	25548296	25570452	-1	0	0	0	0	0	0	0	0	0	0	0	A6X8I0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120269	ENSMUSG00000021922	14	30886476	30901981	1	0	0	42	0	0	0	0	0	0	0	0		
ENSMUST00000120270	ENSMUSG00000034055	X	102513975	102644246	-1	0	0	0	0	0	0	0	0	0	0	0	A2AI88	
ENSMUST00000120271						9	8	11	77	13	5	0	0	0	0	0		
ENSMUST00000120272	ENSMUSG00000028175	3	159495433	159529955	1	13	12	12	0	9	0	9	17	0	7	0	D3Z6J1	
ENSMUST00000120273						2	3	2	0	9	0	0	0	0	0	0		
ENSMUST00000120274	ENSMUSG00000040624	10	3740364	3967303	1	0	0	0	59	0	0	0	11	40	0	0	Q3UX37	
ENSMUST00000120275						0	1	0	0	0	1	2	12	4	68	10		
ENSMUST00000120276	ENSMUSG00000024002	17	32196274	32284722	-1	31	24	77	36	28	18	212	580	402	19	279	B0V2V8	
ENSMUST00000120277						3	2	3	2	1	1	0	0	0	0	0		
ENSMUST00000120278						2	0	4	2	1	1	0	0	0	0	1		
ENSMUST00000120279	ENSMUSG00000002147	10	127642986	127660957	1	12	5	8	55	6	3	0	0	0	0	0	D3YU28	
ENSMUST00000120280						4	3	6	4	4	0	0	0	0	0	0		
ENSMUST00000120281	ENSMUSG00000000901	10	75923222	75932502	-1	1	7	5	0	9	0	2	0	0	0	6	Q3UQT3	Q02853
ENSMUST00000120282						1	0	0	20	4	6	0	0	0	0	0		
ENSMUST00000120283						3	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000120284	ENSMUSG00000044442	16	87354185	87368742	1	61	51	300	109	59	39	0	5	4	0	10	E9PXT7	
ENSMUST00000120285	ENSMUSG00000025724	7	80904889	80947780	-1	1	4	0	1	4	0	0	0	5	4	12	D3YTS1	
ENSMUST00000120286	ENSMUSG00000090110	X	75404846	75416584	-1	0	1	0	0	0	0	0	12	2	0	2	A3KGA5	Q61908
ENSMUST00000120287						9	5	41	10	15	0	2	0	1	0	0		
ENSMUST00000120288						3	5	1	1	3	0	0	0	0	0	0		
ENSMUST00000120289	ENSMUSG00000027805	3	57841895	57848079	-1	1	0	0	46	5	1	1	1	0	0	0	D3YWS3	
ENSMUST00000120290						5	1	2	2	2	4	0	1	0	0	0		
ENSMUST00000120291						12	15	14	10	20	13	50	100	178	10	87		
ENSMUST00000120292	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3YWB1	
ENSMUST00000120293						2	0	5	3	1	1	0	0	0	0	1		
ENSMUST00000120294						4	3	23	5	1	6	0	0	0	0	0		
ENSMUST00000120295						1	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000120296	ENSMUSG00000030826	7	45570153	45589710	1	11	1	9	13	3	3	0	0	0	4	5	O88374	
ENSMUST00000120297						3	0	1	4	8	2	0	0	0	0	0		
ENSMUST00000120298						9	15	28	7	14	4	0	0	0	0	0		
ENSMUST00000120299	ENSMUSG00000040231	7	45885222	45896714	-1	4	3	0	7	3	0	0	0	0	1	0	D3Z3G3	
ENSMUST00000120300						3	0	9	7	4	4	0	0	0	0	0		
ENSMUST00000120301	ENSMUSG00000034066	1	93512079	93621976	1	25	8	30	28	20	13	6	6	14	1	9		Q91VS8
ENSMUST00000120302	ENSMUSG00000008540	6	138140316	138156755	1	0	2	5	4	1	0	939	3393	1764	6296	1091	Q53ZD4	Q91VS7
ENSMUST00000120303	ENSMUSG00000069823	11	73395076	73399495	-1	1	2	0	0	4	2	0	0	0	0	0		Q8VGI1
ENSMUST00000120304						22	24	183	28	15	12	0	2	0	0	0		
ENSMUST00000120306	ENSMUSG00000049680	11	5713417	5762376	-1	11	6	68	250	31	15	249	248	208	41	184		Q5NCI0
ENSMUST00000120307						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000120308						3	2	5	5	2	1	0	2	1	0	0		
ENSMUST00000120309						29	19	21	1662	54	17	0	5	0	0	3		
ENSMUST00000120310	ENSMUSG00000028194	3	145758675	145894277	1	0	0	0	0	0	5	0	0	0	0	0	D3YU15	
ENSMUST00000120311						6	2	2	10	7	1	0	3	2	3	0		
ENSMUST00000120312						5	0	14	1	2	1	0	0	0	0	0		
ENSMUST00000120313						6	2	13	1	1	3	2	4	0	2	1		
ENSMUST00000120314	ENSMUSG00000067561	X	102847639	102854616	-1	0	4	17	33	20	2	0	0	0	0	0	Q9D410	
ENSMUST00000120315						8	6	8	4	6	0	0	1	1	0	0		
ENSMUST00000120316	ENSMUSG00000027309	2	130706200	130906406	-1	0	0	0	27	0	0	0	0	0	0	0	B0R038	
ENSMUST00000120317						1	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000120318						0	0	0	4	2	0	2	1	0	13	0		
ENSMUST00000120319						4	10	60	17	8	6	0	2	2	0	3		
ENSMUST00000120320	ENSMUSG00000034528	5	103955440	103977410	-1	4	1	0	2	2	2	0	1	0	3	0	A8Y5N4	
ENSMUST00000120322						11	0	10	7	6	2	33	19	41	0	1		
ENSMUST00000120323						3	5	28	0	8	3	0	0	0	0	0		
ENSMUST00000120324						5	5	20	41	1	3	0	0	0	0	0		
ENSMUST00000120325						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000120326						9	15	15	16	17	12	0	4	2	0	4		
ENSMUST00000120327	ENSMUSG00000013495	5	108629770	108648782	1	8	6	14	0	12	12	133	23	111	36	101		Q9CXY1
ENSMUST00000120328						1	1	0	0	3	2	0	0	0	0	0		
ENSMUST00000120330						0	0	0	0	0	0	1	11	4	3	2		
ENSMUST00000120331	ENSMUSG00000039236	7	78913424	78920396	1	4	0	5	3	3	2	0	0	15	97	13	Q4FK39	Q9JL16
ENSMUST00000120332						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120333	ENSMUSG00000024184	17	26195999	26199087	-1	0	0	0	0	0	7	0	0	0	0	0		D3Z6P0
ENSMUST00000120334						2	3	1	0	0	2	0	0	0	0	0		
ENSMUST00000120335						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120336	ENSMUSG00000059901	10	61197112	61273438	-1	0	0	0	0	0	0	0	0	0	0	0	E9PX39	
ENSMUST00000120337						17	9	71	35	15	13	0	0	0	0	0		
ENSMUST00000120338						3	0	2	0	6	0	2	0	0	2	0		
ENSMUST00000120339	ENSMUSG00000041605	1	136213531	136234264	-1	24	13	74	262	32	12	0	1	0	0	3	G3X9Z8	
ENSMUST00000120340	ENSMUSG00000040139	7	137375574	137410762	-1	0	0	0	0	0	18	4	8	21	2	19	G5E8T7	
ENSMUST00000120341						0	0	3	1	1	0	0	0	0	0	0		
ENSMUST00000120342						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120343						3	0	3	9	6	4	0	0	0	1	1		
ENSMUST00000120344	ENSMUSG00000001786	10	86021972	86051873	1	3	0	0	106	8	0	60	140	44	23	29	Q3UD93	
ENSMUST00000120345	ENSMUSG00000022800	16	32877500	32908963	1	0	1	2	1	1	1	0	0	0	0	4	D3Z591	
ENSMUST00000120346	ENSMUSG00000052712	17	29268788	29302881	1	0	0	0	0	0	0	108	581	163	347	150		Q99KU6
ENSMUST00000120347						2	1	0	5	0	0	0	0	0	0	0		
ENSMUST00000120348						3	1	8	4	4	4	0	0	0	0	0		
ENSMUST00000120349	ENSMUSG00000031667	8	91112041	91134465	-1	0	5	6	10	3	0	0	0	2	0	0		Q64362
ENSMUST00000120350						3	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000120351						3	6	6	4	10	1	0	3	0	0	0		
ENSMUST00000120352						9	6	21	6	7	4	0	0	0	0	0		
ENSMUST00000120353						3	1	1	2	1	1	0	0	0	0	0		
ENSMUST00000120354						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120355	ENSMUSG00000030786	7	128062640	128118491	1	6	0	0	6	6	0	495	564	490	29	845	E9Q5K8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120356	ENSMUSG00000001127	X	20797814	20860519	1	6	4	0	0	1	0	11	27	0	79	0	Q8CAD1	
ENSMUST00000120357						4	6	5	10	8	1	0	9	4	4	3		
ENSMUST00000120358						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000120359						12	3	14	10	7	4	0	1	1	0	0		
ENSMUST00000120360						12	2	0	0	0	7	1579	2875	1261	7628	1107		
ENSMUST00000120361						2	0	4	1	2	2	0	0	0	0	0		
ENSMUST00000120362						2	1	5	1	2	1	1	3	0	1	0		
ENSMUST00000120363	ENSMUSG00000029844	6	52155590	52158317	-1	0	0	11	0	0	0	0	4	3	0	5	D3Z4E1	
ENSMUST00000120365						2	2	1	1	2	0	0	0	0	0	0		
ENSMUST00000120366						1	2	1	0	3	0	0	0	0	0	0		
ENSMUST00000120367	ENSMUSG00000031969	9	26974135	26999566	-1	11	8	0	13	0	0	0	0	0	0	0	D3YTT4	
ENSMUST00000120368						2	1	5	0	0	0	0	0	0	0	0		
ENSMUST00000120369						5	3	14	1	9	4	0	0	1	0	0		
ENSMUST00000120371						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120372						3	3	17	10	7	10	1	1	1	1	1		
ENSMUST00000120373						0	0	0	5	0	0	0	5	2	7	0		
ENSMUST00000120374	ENSMUSG00000020389	11	52004221	52089784	1	0	0	0	0	0	0	0	8	7	0	20	B1AU43	
ENSMUST00000120375	ENSMUSG00000001507	11	95044474	95076801	-1	0	24	0	0	29	10	0	2	0	6	38		Q62470
ENSMUST00000120376						4	3	18	6	7	8	1	2	1	1	0		
ENSMUST00000120377	ENSMUSG00000028063	3	88480147	88509956	-1	0	8	3	5	0	0	190	68	243	176	621		P48678
ENSMUST00000120378						8	5	6	1	4	2	0	0	0	0	0		
ENSMUST00000120379						1	2	3	4	2	2	0	2	1	3	1		
ENSMUST00000120380						0	3	1	0	0	3	0	0	1	0	0		
ENSMUST00000120381	ENSMUSG00000032116	9	36729344	36767679	-1	24	31	68	37	36	13	501	1968	817	640	680	Q3U573	P46978
ENSMUST00000120382						2	5	8	5	2	1	0	0	0	0	0		
ENSMUST00000120383						2	2	9	1	1	0	0	0	0	0	0		
ENSMUST00000120384						2	3	37	5	12	1	1	1	0	0	0		
ENSMUST00000120385						0	1	0	0	1	0	0	3	0	1	6		
ENSMUST00000120386						5	5	7	1	3	4	0	0	0	0	0		
ENSMUST00000120387						7	4	4	0	9	3	0	0	0	0	0		
ENSMUST00000120388	ENSMUSG00000024810	19	29925114	29960718	1	6	6	10	0	0	6	0	0	0	147	9		Q8BVZ5
ENSMUST00000120389	ENSMUSG00000046032	X	101097786	101222563	-1	22	13	143	51	25	19	286	593	269	34	203	Q6ZWQ5	
ENSMUST00000120390						5	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120391						4	3	7	9	7	5	0	0	0	0	0		
ENSMUST00000120392						2	3	3	1	1	1	0	0	0	0	1		
ENSMUST00000120394	ENSMUSG00000022842	16	20611593	20646485	1	0	0	0	2	2	0	0	0	0	0	0	E9PUE3	
ENSMUST00000120395						3	6	2	2	2	1	0	0	0	0	0		
ENSMUST00000120396						7	4	7	2	0	5	0	0	0	0	0		
ENSMUST00000120397	ENSMUSG00000028167	3	135281221	135304426	1	5	5	8	0	6	0	0	0	0	0	0	G3UWD3	
ENSMUST00000120398						2	0	0	6	2	0	0	15	5	0	7		
ENSMUST00000120399						0	2	0	0	4	0	0	0	0	0	0		
ENSMUST00000120400						4	5	4	3	0	3	0	0	1	4	0		
ENSMUST00000120401	ENSMUSG00000063881	11	73371246	73375704	1	4	2	4	2	4	0	0	0	0	0	0	Q8VGI2	
ENSMUST00000120402						0	2	3	0	2	1	0	0	0	0	0		
ENSMUST00000120403						10	6	14	12	7	4	0	0	0	0	0		
ENSMUST00000120404						4	2	4	0	2	1	0	0	0	0	0		
ENSMUST00000120405	ENSMUSG00000001520	6	128399296	128416427	1	0	0	0	0	0	0	0	0	0	0	0		Q9JHR9
ENSMUST00000120406						2	6	7	5	4	0	0	0	0	0	1		
ENSMUST00000120407						1	2	1	1	1	0	0	0	0	0	0		
ENSMUST00000120408						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000120410						0	4	3	1	0	0	0	39	0	0	0		
ENSMUST00000120411	ENSMUSG00000021750	14	8296274	8318023	-1	4	5	102	106	34	0	0	1	0	0	0	Q78TU8	
ENSMUST00000120412						3	1	4	1	0	0	0	0	0	0	0		
ENSMUST00000120413						10	2	8	13	5	3	1	2	1	0	2		
ENSMUST00000120414						28	23	69	38	25	22	0	0	0	3	0		
ENSMUST00000120415	ENSMUSG00000061816	1	66924295	66945404	-1	0	0	0	0	0	0	0	0	0	0	0	E9PWG4	
ENSMUST00000120416	ENSMUSG00000034842	5	92331827	92414628	1	0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000120417	ENSMUSG00000002814	11	60740058	60777365	-1	0	0	1	8	9	0	0	0	0	0	0	B0QZI1	
ENSMUST00000120418						0	9	6	4	6	4	0	12	3	11	0		
ENSMUST00000120419						1	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000120420	ENSMUSG00000032511	9	119483408	119579016	-1	0	44	0	0	15	35	0	0	0	10	15		Q9JJV9
ENSMUST00000120421						0	0	0	0	0	0	686	3120	1535	6465	1092		
ENSMUST00000120422						0	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000120423						20	2	15	3	17	7	3	7	7	15	0		
ENSMUST00000120424						2	0	7	0	2	0	0	0	0	0	0		
ENSMUST00000120425	ENSMUSG00000030960	7	132827457	132852673	-1	0	0	0	0	0	0	14	0	8	32	0	D3Z7D0	
ENSMUST00000120426	ENSMUSG00000031667	8	91112041	91134465	-1	3	1	0	3	4	0	0	0	5	0	11	D3Z632	
ENSMUST00000120427						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120428	ENSMUSG00000029833	6	37870811	37966296	1	0	0	0	5	5	3	6	204	27	31	67		Q64127
ENSMUST00000120429	ENSMUSG00000053030	5	77205107	77211471	-1	2	1	3	0	6	2	0	0	0	5	0	D3YTY0	
ENSMUST00000120430						25	16	36	22	37	12	32	26	26	15	10		
ENSMUST00000120431						4	16	10	18	11	6	0	0	0	1	1		
ENSMUST00000120432	ENSMUSG00000012519	8	111311797	111338177	-1	0	0	0	65	25	9	6	50	21	96	38		Q9D2Y4
ENSMUST00000120433						7	5	11	7	9	6	3	1	0	1	3		
ENSMUST00000120434						5	1	0	2	4	3	0	0	0	0	0		
ENSMUST00000120435						3	2	5	4	5	1	0	1	0	1	0		
ENSMUST00000120436						3	10	24	16	15	0	0	0	0	0	0		
ENSMUST00000120437						0	3	6	1	1	1	0	0	0	0	0		
ENSMUST00000120438						2	6	11	6	4	4	3	8	6	2	12		
ENSMUST00000120439						0	0	18	6	12	0	0	0	0	0	0		
ENSMUST00000120440						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000120441	ENSMUSG00000040268	7	130865756	130913312	1	8	0	0	31	16	0	11	179	93	49	16	D3YU01	
ENSMUST00000120442						0	2	5	1	1	2	0	1	0	0	2		
ENSMUST00000120443						4	2	17	6	6	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120444						2	3	6	5	3	1	0	0	0	0	0		
ENSMUST00000120445	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z6H7	
ENSMUST00000120447	ENSMUSG00000026577	1	164289800	164307489	-1	0	2	0	0	10	0	71	314	122	164	88		Q8R2X8
ENSMUST00000120448						9	7	7	3	7	5	0	0	0	0	0		
ENSMUST00000120449						0	0	5	1	3	1	0	0	0	0	0		
ENSMUST00000120450	ENSMUSG00000022962	16	91621186	91646952	-1	2	2	20	0	10	1	20	66	44	19	35	Q3TH49	Q64737
ENSMUST00000120451						14	10	38	19	19	3	0	0	0	0	0		
ENSMUST00000120452	ENSMUSG00000032285	9	54698873	54716315	1	10	4	29	384	23	7	0	0	0	0	0		Q9JMC3
ENSMUST00000120453						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120454	ENSMUSG00000044881	7	100537100	100540369	1	0	4	14	25	2	1	25	0	20	86	3		Q8BT51
ENSMUST00000120455						1	0	3	0	0	0	0	0	2	4	0		
ENSMUST00000120456						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000120457	ENSMUSG00000031949	8	111966908	111992302	-1	0	0	0	0	0	0	0	0	0	4	0	D3Z6J6	
ENSMUST00000120458						1	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000120459						6	3	36	5	4	0	0	0	0	0	0		
ENSMUST00000120460						10	3	2	9	6	7	0	1	1	0	1		
ENSMUST00000120461	ENSMUSG00000041891	18	65980754	66022580	-1	3	1	0	80	3	3	8	24	28	4	42		Q9D0F3
ENSMUST00000120462						1	1	0	3	4	1	0	1	0	0	0		
ENSMUST00000120463	ENSMUSG00000034135	9	46012820	46224194	1	9	0	1	41	13	0	195	0	329	0	211	F6S7W6	
ENSMUST00000120464						1	2	10	4	2	1	0	0	0	0	0		
ENSMUST00000120465						7	3	9	5	7	7	0	0	0	0	0		
ENSMUST00000120466						2	0	1	1	0	0	0	0	1	2	0		
ENSMUST00000120467						4	2	1	33	2	1	0	0	1	0	0		
ENSMUST00000120468						2	0	5	4	1	2	1	0	0	0	0		
ENSMUST00000120469						2	0	0	0	3	1	0	0	0	0	1		
ENSMUST00000120470						8	4	4	7	3	3	0	0	0	0	0		
ENSMUST00000120471						3	3	5	7	4	2	0	0	0	0	0		
ENSMUST00000120472	ENSMUSG00000033032	18	61730261	61786702	-1	7	19	5	64	12	0	13	6	12	0	14	B2RSM5	Q8BZI0
ENSMUST00000120473	ENSMUSG00000028608	4	107889813	107899384	1	0	0	4	0	3	0	2	0	7	0	5	B7ZC71	
ENSMUST00000120474						0	2	3	2	4	1	0	0	0	0	0		
ENSMUST00000120475	ENSMUSG00000024901	19	4930651	4943127	-1	20	9	56	29	20	14	0	0	1	0	1	D3Z6V8	
ENSMUST00000120476						5	3	28	13	7	3	0	0	0	0	0		
ENSMUST00000120477						0	5	19	6	5	0	0	0	0	0	0		
ENSMUST00000120478						5	5	4	2	6	2	0	0	0	0	0		
ENSMUST00000120479						3	0	1	0	5	0	0	0	0	0	1		
ENSMUST00000120480						0	1	0	0	0	0	0	1	0	0	0		
ENSMUST00000120481						7	2	21	3	6	0	0	0	0	0	0		
ENSMUST00000120482						7	5	9	2	3	1	0	0	1	0	1		
ENSMUST00000120483						0	3	11	1	3	1	0	0	0	1	0		
ENSMUST00000120484	ENSMUSG00000039710	3	14480697	14505830	1	1	0	0	2	0	1	0	0	0	0	0	D3YTZ6	
ENSMUST00000120485						3	2	1	2	2	6	0	0	0	0	0		
ENSMUST00000120486						0	5	0	3	3	2	0	0	0	0	0		
ENSMUST00000120487						2	2	11	3	1	3	0	0	0	0	1		
ENSMUST00000120488	ENSMUSG00000022750	16	17759618	17793382	1	37	29	44	27	50	18	44	60	25	31	56		Q99JN2
ENSMUST00000120489						1	1	5	0	1	1	0	1	0	0	0		
ENSMUST00000120490	ENSMUSG00000051900	7	120409647	120544813	1	3	2	3	1	2	4	0	0	0	0	0	E9PWJ7	
ENSMUST00000120491						2	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000120492						1	5	3	6	3	4	0	0	0	0	0		
ENSMUST00000120493	ENSMUSG00000031822	8	120230536	120581390	1	0	0	3	80	11	0	0	19	0	0	0		Q3U3C9
ENSMUST00000120494						3	2	6	3	3	3	0	0	0	0	0		
ENSMUST00000120495	ENSMUSG00000046516	16	38346991	38352763	1	29	7	60	35	35	20	35	159	68	22	148	Q54AC6	P56394
ENSMUST00000120497						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000120498	ENSMUSG00000035851	5	86804221	86836659	1	0	0	7	0	0	0	130	374	351	129	513		E9Q5K9
ENSMUST00000120499						1	4	4	3	4	1	0	0	0	0	0		
ENSMUST00000120500						25	33	71	28	18	4	0	0	8	0	3		
ENSMUST00000120501						1	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000120502						1	1	0	5	3	1	0	0	0	0	0		
ENSMUST00000120503						7	6	6	11	11	5	0	0	1	0	1		
ENSMUST00000120504						10	3	32	11	7	5	0	0	0	0	0		
ENSMUST00000120505	ENSMUSG00000083361	2	37065746	37069260	1	4	6	0	6	3	0	0	0	0	0	0	Q8VFP3	
ENSMUST00000120506	ENSMUSG00000029352	5	113075839	113081584	-1	0	0	0	10	0	0	0	0	0	0	0		Q9JJU9
ENSMUST00000120507						6	12	11	4	3	2	0	1	0	1	0		
ENSMUST00000120508	ENSMUSG00000034818	10	81459227	81482709	-1	0	0	4	1	0	0	0	0	0	0	0	D3Z580	
ENSMUST00000120509	ENSMUSG00000019970	10	21882184	21999903	1	2	13	27	32	5	4	32	65	18	11	42		Q9WVC6
ENSMUST00000120511						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120512	ENSMUSG00000041390	6	15720661	15802169	1	3	0	10	82	6	5	6	23	19	30	44		Q8BX65
ENSMUST00000120513						1	3	8	7	6	2	0	1	0	1	1		
ENSMUST00000120514						6	6	17	4	0	3	0	0	0	0	0		
ENSMUST00000120515						5	0	7	2	0	0	3	2	0	2	1		
ENSMUST00000120516	ENSMUSG00000040428	7	45526330	45554229	1	0	2	23	0	3	6	0	0	0	0	3	D3YW21	
ENSMUST00000120518						8	4	4	1	2	0	0	0	0	0	0		
ENSMUST00000120519						2	0	0	7	5	3	0	0	0	0	0		
ENSMUST00000120520	ENSMUSG00000030760	7	98206389	98321208	-1	0	15	0	0	0	0	65	75	0	16	0	D3YTU8	
ENSMUST00000120521	ENSMUSG00000078881	2	176473278	176486783	-1	0	0	0	0	0	2	0	0	3	0	1	Q8BHI0	
ENSMUST00000120522	ENSMUSG00000053303	19	7781041	7802667	-1	7	0	0	0	13	10	0	0	0	0	0	E9Q6M5	
ENSMUST00000120523						1	0	10	2	3	1	0	0	0	0	0		
ENSMUST00000120524	ENSMUSG00000024736	19	10857822	10869940	-1	24	17	93	44	44	28	100	192	140	21	234	D3Z4S6	
ENSMUST00000120525						1	3	4	2	2	0	0	0	0	0	0		
ENSMUST00000120526						5	2	8	2	6	4	0	1	0	0	0		
ENSMUST00000120527						1	0	1	1	0	2	0	0	0	1	0		
ENSMUST00000120528						5	1	3	1	4	1	1	6	3	0	7		
ENSMUST00000120530						8	6	26	18	12	6	0	5	0	0	0		
ENSMUST00000120531	ENSMUSG00000046314	12	44852488	45074493	-1	8	14	27	95	21	10	3	19	13	6	23	Q3TYA4	
ENSMUST00000120532	ENSMUSG00000022702	16	18877037	18970309	1	2	0	14	41	3	2	38	62	28	0	14		Q61666

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120533						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000120534						11	2	9	7	10	3	0	2	0	0	0		
ENSMUST00000120535	ENSMUSG00000021460	13	52835119	52929681	-1	11	8	20	12	14	2	21	159	48	22	43		
ENSMUST00000120536						3	0	6	0	4	1	0	0	0	0	0		
ENSMUST00000120537	ENSMUSG00000053175	7	19808462	19822770	-1	5	8	11	89	8	5	2240	2545	1513	104	1109		Q9Z2F6
ENSMUST00000120538						2	1	5	10	4	2	0	0	0	0	0		
ENSMUST00000120539	ENSMUSG00000028266	3	144188530	144205220	-1	0	0	0	175	0	0	704	2400	1611	459	1019	Q542S1	P61969
ENSMUST00000120540	ENSMUSG00000052562	19	8335371	8405111	-1	62	36	36	751	76	35	0	3	3	0	2	Q3V3G0	
ENSMUST00000120541	ENSMUSG00000027875	3	98280435	98310738	1	0	0	0	0	0	0	0	3	0	0	0		P54869
ENSMUST00000120542	ENSMUSG00000006732	10	127041414	127046365	1	8	7	0	12	5	4	4	0	2	2	16	D3Z7D2	
ENSMUST00000120544	ENSMUSG00000021288	12	111758849	111807844	1	10	0	23	0	13	0	32	57	60	12	166	E9Q7C9	
ENSMUST00000120545						2	0	3	5	2	0	0	0	0	18	4		
ENSMUST00000120546						2	3	1	4	1	3	0	0	0	0	0		
ENSMUST00000120547	ENSMUSG00000040521	10	127011572	127030840	-1	6	4	12	4	6	4	0	17	16	2	18	Q9CX33	
ENSMUST00000120548						0	0	0	0	0	0	0	1	1	0	0		
ENSMUST00000120549	ENSMUSG00000019810	10	13499540	13519035	1	0	0	0	0	0	0	0	10	0	3	0	D3YVV4	
ENSMUST00000120550	ENSMUSG00000036323	5	76974683	76999937	1	0	0	0	0	3	0	144	42	390	649	340	E9Q740	
ENSMUST00000120551						4	1	10	2	3	1	0	0	0	0	0		
ENSMUST00000120552						3	3	3	1	1	0	0	0	0	0	0		
ENSMUST00000120553						1	0	1	2	1	1	0	0	0	0	0		
ENSMUST00000120554						2	3	5	8	3	3	0	0	0	0	0		
ENSMUST00000120555	ENSMUSG00000061576	5	26817203	27727505	1	26	35	165	24	24	18	0	0	0	0	2	Q5U4C2	
ENSMUST00000120556						3	0	1	0	0	0	6	10	0	3	0		
ENSMUST00000120557						18	14	0	0	16	3	2009	3771	2129	8719	2540		
ENSMUST00000120558						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000120559						15	16	16	11	11	8	0	0	0	0	0		
ENSMUST00000120560						1	0	3	0	0	2	41	0	13	7	36		
ENSMUST00000120561						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000120562						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120563	ENSMUSG00000039942	15	5206661	5244187	-1	0	0	0	0	16	11	59	70	30	0	35	Q91VE4	
ENSMUST00000120564	ENSMUSG00000039323	1	72824503	72852474	1	4	1	2	4	3	0	0	0	0	2	0	D3YU40	
ENSMUST00000120565						3	3	11	2	7	7	0	0	0	0	0		
ENSMUST00000120566						4	7	13	6	10	1	2	17	6	0	6		
ENSMUST00000120567						3	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000120568						1	2	0	0	3	2	0	0	0	0	0		
ENSMUST00000120569						3	4	5	8	2	2	0	0	0	0	0		
ENSMUST00000120570						1	2	0	3	0	0	0	0	0	0	0		
ENSMUST00000120571						1	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000120572						7	2	10	2	4	0	0	0	0	0	0		
ENSMUST00000120573	ENSMUSG00000021592	13	76060422	76098660	-1	10	6	14	22	5	4	49	196	63	131	25		
ENSMUST00000120574						0	0	0	0	1	0	22	0	0	0	0		
ENSMUST00000120575						13	13	7	9	8	6	0	2	4	0	1		
ENSMUST00000120576						1	4	2	5	2	3	0	0	0	0	0		
ENSMUST00000120577						3	1	1	5	0	0	0	0	0	0	0		
ENSMUST00000120578						2	0	2	2	1	2	0	0	0	0	0		
ENSMUST00000120579						3	4	7	3	2	0	0	4	0	0	0		
ENSMUST00000120580	ENSMUSG00000035597	12	65036333	65063386	1	8	4	3	21	5	0	135	616	163	95	139	E9QJV4	
ENSMUST00000120581						2	6	38	9	15	2	0	0	0	0	0		
ENSMUST00000120582						3	0	28	3	5	1	1	1	0	2	0		
ENSMUST00000120583						5	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000120584						4	2	11	0	5	2	37	232	56	316	36		
ENSMUST00000120585	ENSMUSG00000040675	10	3973118	4167081	1	8	28	24	65	23	3	0	0	0	0	0		Q3V3R1
ENSMUST00000120586	ENSMUSG00000022945	16	93883901	93906115	1	0	0	0	0	0	0	0	0	0	0	0	D3Z616	
ENSMUST00000120587						4	1	0	3	2	2	0	0	0	0	0		
ENSMUST00000120588	ENSMUSG00000041673	14	32991382	33015292	1	1	0	0	0	1	0	0	0	1	0	1	D3Z3X8	
ENSMUST00000120589						30	25	41	15	29	13	0	0	0	1	11		
ENSMUST00000120590						2	3	8	1	2	2	0	4	0	0	0		
ENSMUST00000120591	ENSMUSG00000023452	5	32736301	32785646	-1	8	8	22	0	6	5	411	435	378	68	333	E9PX91	
ENSMUST00000120592	ENSMUSG00000005716	15	78191114	78206400	-1	11	6	10	4	8	11	0	0	0	0	0	Q545M7	P32848
ENSMUST00000120593						14	8	34	137	19	13	0	0	0	0	5		
ENSMUST00000120594	ENSMUSG00000064115	16	66655421	67620908	-1	0	0	0	6	0	0	0	0	0	0	0		Q8BLQ9
ENSMUST00000120595	ENSMUSG00000040811	7	19176421	19206482	1	0	0	0	6	0	6	250	320	109	57	99	D3YWS2	
ENSMUST00000120596						10	0	22	2	6	2	3	5	2	14	1		
ENSMUST00000120597						1	2	5	1	3	0	0	0	0	0	0		
ENSMUST00000120598						1	0	4	1	2	0	0	0	0	0	0		
ENSMUST00000120599						1	0	3	2	1	0	0	0	0	0	0		
ENSMUST00000120600						0	0	0	10	1	0	0	0	0	0	0		
ENSMUST00000120601						1	3	6	1	1	0	0	0	0	0	0		
ENSMUST00000120602						0	2	3	2	0	0	0	0	0	0	0		
ENSMUST00000120603						2	1	0	2	2	2	0	0	0	0	0		
ENSMUST00000120604						3	3	3	3	5	1	0	0	0	0	0		
ENSMUST00000120605	ENSMUSG00000014104	6	41852989	41864413	1	1	0	0	0	0	0	0	0	0	0	0	D3Z617	
ENSMUST00000120606						4	7	11	6	12	2	0	0	0	0	0		
ENSMUST00000120607						3	3	6	2	2	1	0	1	1	3	0		
ENSMUST00000120608						1	0	2	4	6	3	0	0	0	0	0		
ENSMUST00000120609						20	16	10	30	29	8	0	0	0	0	0		
ENSMUST00000120610						3	0	4	0	4	0	0	0	0	0	0		
ENSMUST00000120611						0	0	1	0	3	2	0	0	0	0	1		
ENSMUST00000120613	ENSMUSG00000018395	11	53567379	53601967	1	15	14	10	0	6	13	13	49	41	74	43		P28741
ENSMUST00000120614						2	3	2	3	3	1	0	2	0	0	0		
ENSMUST00000120615						2	2	3	3	1	1	0	0	0	0	0		
ENSMUST00000120616						2	1	2	9	6	5	0	0	0	0	1		
ENSMUST00000120617						0	2	0	1	1	0	0	0	0	0	0		
ENSMUST00000120618	ENSMUSG00000029227	5	74535449	74598800	1	0	1	1	0	0	0	0	0	2	0	0	D3Z3F1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120619						2	4	20	6	3	0	0	0	0	0	0		
ENSMUST00000120620	ENSMUSG00000035062	X	95639193	95658509	-1	3	8	0	0	10	2	0	0	0	15	0	Q05BE0	
ENSMUST00000120621						0	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000120622	ENSMUSG00000032064	9	50662752	50739517	-1	9	5	2	3	9	4	0	0	0	0	1		Q80Y83
ENSMUST00000120623						0	3	5	7	2	0	0	0	0	0	0		
ENSMUST00000120624	ENSMUSG00000081044	X	93968659	93975470	1	0	0	1	1	0	0	0	0	0	0	0	B2FDE5	
ENSMUST00000120625						20	13	6	16	10	10	0	0	0	0	2		
ENSMUST00000120626						12	4	10	23	13	7	2	0	2	0	0		
ENSMUST00000120627						5	3	1	2	4	0	0	0	0	0	0		
ENSMUST00000120628						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000120629						8	5	2	4	2	3	0	0	0	0	0		
ENSMUST00000120630	ENSMUSG00000050022	5	140724127	140761439	1	24	14	91	70	39	17	63	46	53	9	107	A1L312	Q8BVF9
ENSMUST00000120631						0	0	0	8	0	0	0	3	0	0	0		
ENSMUST00000120632	ENSMUSG00000024500	18	42637432	43059471	-1	4	0	6	26	0	0	0	0	0	0	0		Q6ZWR4
ENSMUST00000120633	ENSMUSG00000023008	15	99317225	99370482	-1	0	17	9	6	0	0	0	0	0	0	0	D3Z7A7	
ENSMUST00000120635						2	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000120636						5	1	18	1	3	0	0	0	0	0	0		
ENSMUST00000120637						3	8	9	6	7	5	0	1	0	2	0		
ENSMUST00000120638	ENSMUSG00000059602	10	86055125	86498896	-1	6	5	33	14	13	7	0	6	5	0	7		Q8JZP2
ENSMUST00000120639	ENSMUSG00000036377	5	76656512	76873554	1	19	9	0	461	5	0	21	0	0	0	0	E9Q3Y7	
ENSMUST00000120640						2	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000120641						4	4	12	5	11	4	323	730	273	138	216		
ENSMUST00000120642	ENSMUSG00000047642	10	121641588	121692892	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3G0	
ENSMUST00000120643	ENSMUSG00000040189	7	45924072	45948956	1	159	191	351	270	201	115	26	65	43	11	43	D3Z3W5	
ENSMUST00000120644						0	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000120645	ENSMUSG00000025069	19	47865545	47886324	1	7	3	0	42	7	0	1	0	1	0	0		Q8K2Q2
ENSMUST00000120646						0	4	11	4	1	2	1	0	0	0	0		
ENSMUST00000120647						13	16	27	19	7	15	0	8	4	2	6		
ENSMUST00000120648						8	2	12	3	4	1	0	0	0	0	0		
ENSMUST00000120649						6	6	10	6	9	7	0	0	0	0	0		
ENSMUST00000120650						0	0	3	2	1	0	0	3	0	0	0		
ENSMUST00000120651						0	0	10	3	2	0	1	0	0	0	0		
ENSMUST00000120652						1	2	8	1	1	0	0	0	0	0	0		
ENSMUST00000120653	ENSMUSG00000031576	8	25849623	25937933	1	3	7	2	9	0	0	0	0	0	0	0	D3Z5P2	
ENSMUST00000120654	ENSMUSG00000014599	3	107741048	107760469	-1	4	3	6	4	7	7	2	30	7	0	11	D3YTW1	
ENSMUST00000120655	ENSMUSG00000049723	9	7344381	7369499	1	0	0	0	0	0	0	0	0	1	15	2	Q3TCW6	
ENSMUST00000120656						0	0	0	0	1	0	0	0	1	0	0		
ENSMUST00000120657						4	4	8	9	10	4	0	1	0	0	1		
ENSMUST00000120658						2	2	5	3	3	2	0	10	4	6	6		
ENSMUST00000120659						4	0	0	5	1	1	1	1	1	0	0		
ENSMUST00000120660						4	3	2	1	2	0	0	0	0	0	0		
ENSMUST00000120661						1	0	3	1	3	2	0	0	0	0	0		
ENSMUST00000120662						3	3	0	0	2	0	0	0	0	0	0		
ENSMUST00000120663						1	0	5	5	3	1	0	0	0	0	0		
ENSMUST00000120664	ENSMUSG00000021699	13	108449948	109953461	1	15	15	42	109	15	6	32	51	50	5	61	A6XDA6	Q01063
ENSMUST00000120666						2	0	0	2	3	3	0	0	0	0	0		
ENSMUST00000120667	ENSMUSG00000022724	16	59471775	59492461	1	21	27	64	25	24	14	2	0	4	0	1	Q8CCK9	
ENSMUST00000120668						4	7	13	1	8	4	0	0	0	0	0		
ENSMUST00000120669						40	46	181	49	59	19	3	9	9	1	8		
ENSMUST00000120670						6	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000120671	ENSMUSG00000021699	13	108449948	109953461	1	0	0	0	0	0	0	0	0	0	0	0	E9PVU7	
ENSMUST00000120672	ENSMUSG00000021694	13	108158731	108195364	1	0	4	0	0	2	0	0	0	0	0	0	D3YU16	
ENSMUST00000120673	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5M6	
ENSMUST00000120674	ENSMUSG00000022724	16	59471775	59492461	1	5	3	0	0	7	0	0	0	4	0	3	D3YTU3	
ENSMUST00000120675						2	1	1	2	3	3	0	0	0	0	0		
ENSMUST00000120676						8	17	98	17	30	8	2	3	3	7	2		
ENSMUST00000120677						3	5	1	2	7	7	1	0	0	1	0		
ENSMUST00000120678	ENSMUSG00000066113	4	86053915	86428385	1	6	0	3	4	0	1	2	0	0	0	0	A9Z1Z6	
ENSMUST00000120679	ENSMUSG00000028252	4	21727701	21759922	1	1	1	0	0	2	1	0	0	0	21	0	Q3UXL9	
ENSMUST00000120680	ENSMUSG00000022797	16	32608920	32632794	1	2	4	9	2	4	0	0	11	21	12	26	Q8C872	
ENSMUST00000120681						2	7	8	6	8	1	0	0	0	0	0		
ENSMUST00000120682						1	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000120683	ENSMUSG00000022475	15	97792664	97844502	-1	5	4	6	5	4	0	13	29	75	21	72	E9PXW8	
ENSMUST00000120684						4	4	4	5	10	4	0	0	0	1	0		
ENSMUST00000120685						5	3	2	1	1	0	0	0	0	0	0		
ENSMUST00000120686						2	0	6	0	2	0	0	0	0	0	0		
ENSMUST00000120687						102	114	163	108	133	53	0	0	0	0	5		
ENSMUST00000120688	ENSMUSG00000029320	5	103648039	103656010	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DAA3
ENSMUST00000120689	ENSMUSG00000031644	8	60993195	61131346	1	0	0	0	26	0	0	0	0	0	0	0	B7ZWK0	
ENSMUST00000120690	ENSMUSG00000032328	9	79768943	79793507	-1	7	8	9	51	6	6	17	31	11	0	0	D3YVV1	
ENSMUST00000120691	ENSMUSG00000037098	17	25989036	26069409	-1	0	0	29	133	0	0	0	0	27	0	9		Q8CHD8
ENSMUST00000120692						1	4	1	3	5	1	0	0	0	0	0		
ENSMUST00000120693						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000120694						2	2	3	2	4	1	0	0	0	0	0		
ENSMUST00000120695						0	0	7	0	2	2	0	0	0	0	0		
ENSMUST00000120696						11	4	35	12	14	5	0	0	0	0	0		
ENSMUST00000120697	ENSMUSG00000028049	3	89177473	89182765	1	0	3	20	0	3	6	510	565	445	145	318	Q3UXS0	
ENSMUST00000120698						38	22	81	40	33	16	2	5	2	1	1		
ENSMUST00000120699	ENSMUSG00000020843	11	76406952	76416292	1	0	1	3	1	0	0	58	54	30	14	35	B0QZS8	
ENSMUST00000120700						1	3	15	7	7	0	0	0	0	0	0		
ENSMUST00000120701						0	0	0	0	1	0	0	0	8	5	7		
ENSMUST00000120702						4	12	32	15	23	8	7	6	15	22	1		
ENSMUST00000120703						3	1	0	4	1	2	0	0	0	0	0		
ENSMUST00000120704	ENSMUSG00000083361	2	37065746	37069260	1	10	0	7	0	2	6	0	0	0	0	0	Q8VFP3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120705	ENSMUSG00000042492	7	127197459	127208468	-1	20	18	91	415	31	18	4328	4553	3610	260	2277		Q8BHL3
ENSMUST00000120706						0	3	1	0	2	1	0	0	0	0	0		
ENSMUST00000120707	ENSMUSG00000022677	16	14299244	14317375	-1	0	9	11	0	10	2	0	2	0	0	88	D3Z644	
ENSMUST00000120708						27	30	138	51	41	21	17	78	36	4	61		
ENSMUST00000120709	ENSMUSG00000052726	1	140246158	140612067	1	3	0	0	9	0	0	0	0	0	0	0	D3YTU6	
ENSMUST00000120710						2	2	7	4	2	4	0	0	0	0	0		
ENSMUST00000120711						2	0	5	6	2	0	1	0	1	0	1		
ENSMUST00000120712						7	8	7	16	12	4	0	0	0	0	0		
ENSMUST00000120713						2	1	3	7	8	1	0	0	0	0	0		
ENSMUST00000120714	ENSMUSG00000030417	7	35641982	35647521	-1	2	2	2	110	6	4	0	4	4	0	3	D3Z7Q5	
ENSMUST00000120715	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	2	D3Z5M8	
ENSMUST00000120716						0	0	0	0	0	0	0	0	0	17	0		
ENSMUST00000120717	ENSMUSG00000058626	17	45630204	45659325	-1	11	16	30	34	34	19	0	0	0	0	0		Q6J756
ENSMUST00000120718						12	7	14	4	18	3	140	76	90	14	72		
ENSMUST00000120719						12	23	53	33	12	12	0	0	1	0	0		
ENSMUST00000120720						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120721	ENSMUSG00000020454	11	3202392	3244588	1	4	1	0	1	3	0	0	98	10	0	0	A8Y5K6	
ENSMUST00000120722	ENSMUSG00000031242	X	107782751	107816334	-1	21	18	23	62	18	14	91	261	140	64	66		Q9CQD4
ENSMUST00000120723						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000120724						3	0	5	0	2	0	0	0	0	0	0		
ENSMUST00000120725	ENSMUSG00000046295	8	71406010	71409904	1	0	0	0	0	0	0	0	0	0	1	0	G5E8T1	
ENSMUST00000120726						2	5	2	2	4	4	0	0	0	0	0		
ENSMUST00000120727						0	2	8	0	0	0	0	1	0	1	1		
ENSMUST00000120728						5	4	4	8	8	7	1	1	1	0	1		
ENSMUST00000120729						6	5	7	8	13	13	0	0	6	1	5		
ENSMUST00000120730						1	3	2	2	3	2	0	1	0	0	0		
ENSMUST00000120731						8	15	21	17	6	8	0	0	0	0	0		
ENSMUST00000120732	ENSMUSG00000042198	4	3938888	3951046	1	0	0	0	0	0	0	0	0	0	0	0	Q3TFT3	
ENSMUST00000120733	ENSMUSG00000037966	13	49187485	49196244	1	1	0	2	6	6	0	18	7	7	0	15	D3YW25	
ENSMUST00000120734	ENSMUSG00000084063	X	24474308	24500760	-1	168	113	510	201	122	92	1	9	1	0	1	D3Z4U6	
ENSMUST00000120735						3	0	5	0	3	0	1	1	0	12	0		
ENSMUST00000120737	ENSMUSG00000034729	17	47368887	47381417	1	0	0	0	15	0	1	0	0	0	36	40	G5E8U8	
ENSMUST00000120738						1	3	1	2	3	1	0	0	0	0	0		
ENSMUST00000120739						3	1	0	2	4	0	0	0	0	0	0		
ENSMUST00000120740						0	0	0	0	0	1	0	0	0	1	0		
ENSMUST00000120741						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000120742						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000120743						3	2	7	3	1	2	0	0	0	0	0		
ENSMUST00000120744						4	0	4	5	5	3	0	0	0	0	0		
ENSMUST00000120745						3	1	6	8	2	2	0	2	0	6	0		
ENSMUST00000120746	ENSMUSG00000051359	15	37366175	37792570	-1	0	21	45	0	32	14	0	0	0	0	0		Q91X97
ENSMUST00000120747						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000120748	ENSMUSG00000019888	10	101681487	102391469	1	2	3	6	2	0	2	0	0	0	0	1		Q9D306
ENSMUST00000120749						6	5	5	4	4	4	0	0	0	0	0		
ENSMUST00000120750						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000120751						1	0	2	0	2	3	0	0	0	0	0		
ENSMUST00000120752						1	1	0	0	1	1	1	2	0	2	0		
ENSMUST00000120753	ENSMUSG00000030530	7	80388585	80405436	-1	8	2	7	15	18	7	0	76	103	0	100		P23188
ENSMUST00000120754	ENSMUSG00000000530	15	101128522	101145336	1	0	13	45	0	15	0	1063	868	1501	62	584		Q61288
ENSMUST00000120755						1	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000120756	ENSMUSG00000052133	16	35541145	35664732	1	31	0	31	197	47	0	0	0	0	0	0		Q60519
ENSMUST00000120757	ENSMUSG00000020226	10	76057494	76110961	-1	116	111	168	83	117	80	2	6	5	1	11	Q91ZP4	
ENSMUST00000120758						0	3	5	2	2	0	0	0	0	0	0		
ENSMUST00000120759						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120760	ENSMUSG00000032396	9	64306756	64341288	-1	3	0	5	306	33	20	0	0	6	0	0		Q8C0S1
ENSMUST00000120761						8	6	5	9	7	3	2	9	14	1	8		
ENSMUST00000120762						2	0	5	11	2	0	0	0	0	16	0		
ENSMUST00000120763						7	2	4	2	5	2	0	0	0	0	0		
ENSMUST00000120764						5	4	25	3	2	5	0	1	0	0	0		
ENSMUST00000120765						1	2	0	1	1	1	0	0	0	1	0		
ENSMUST00000120766						5	1	2	2	3	1	0	0	0	0	0		
ENSMUST00000120767						5	7	5	7	3	2	0	0	0	0	0		
ENSMUST00000120768						4	3	3	3	2	0	0	2	0	0	0		
ENSMUST00000120769						34	16	30	31	25	18	0	0	0	0	0		
ENSMUST00000120770						0	2	0	2	8	0	32	101	45	152	35		
ENSMUST00000120771						2	4	5	6	5	3	0	0	0	0	1		
ENSMUST00000120773						4	3	35	8	6	2	0	0	0	0	0		
ENSMUST00000120774						4	2	8	2	2	0	0	0	0	0	0		
ENSMUST00000120775						1	2	2	0	2	1	0	0	0	0	0		
ENSMUST00000120776	ENSMUSG00000081769	11	53783418	53859256	-1	3	1	2	27	3	2	0	0	1	0	0	A8Y5C1	
ENSMUST00000120777						14	16	42	191	23	12	0	1	0	0	0		
ENSMUST00000120778	ENSMUSG00000025231	19	46396896	46488804	1	10	7	25	32	22	8	2	2	2	2	4		
ENSMUST00000120779	ENSMUSG00000032897	4	120757438	120831572	-1	6	5	11	6	3	8	0	13	0	0	0		P70353
ENSMUST00000120780						2	0	4	1	4	0	1	7	1	16	2		
ENSMUST00000120781	ENSMUSG00000034842	5	92331827	92414628	1	0	0	1	0	0	0	0	1	0	1	3	E9Q7Z7	
ENSMUST00000120782						71	78	366	129	68	55	0	0	1	0	0		
ENSMUST00000120783						0	3	1	0	1	1	0	0	0	0	0		
ENSMUST00000120784	ENSMUSG00000042726	5	121371725	121385632	-1	0	3	0	0	0	3	412	1214	485	141	611		Q3UDK1
ENSMUST00000120785						3	3	2	3	7	1	0	0	0	0	0		
ENSMUST00000120786						3	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000120787						3	0	4	8	0	0	10	40	15	22	7		
ENSMUST00000120788						6	5	7	1	4	2	17	19	0	0	7		
ENSMUST00000120789	ENSMUSG00000029209	5	69573108	69592340	-1	3	0	1	14	8	0	1	0	0	7	12	D3YWR1	
ENSMUST00000120790						1	0	0	0	3	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120791						0	4	26	5	0	4	0	0	0	0	0		
ENSMUST00000120792						3	3	2	1	2	3	0	0	0	0	0		
ENSMUST00000120793						7	6	12	3	9	5	1	3	3	0	1		
ENSMUST00000120794	ENSMUSG00000029034	4	155869546	155889103	1	0	0	11	10	0	0	291	90	130	47	153	A8Y5J3	
ENSMUST00000120795						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000120796	ENSMUSG00000052726	1	140246158	140612067	1	6	8	22	0	7	3	0	0	0	2	0	D3Z649	
ENSMUST00000120797						0	1	1	2	3	0	0	0	0	0	0		
ENSMUST00000120798	ENSMUSG00000048012	7	44731481	44751050	-1	0	0	0	0	0	0	1	95	0	4	1	Q4VA40	
ENSMUST00000120799						2	5	1	3	2	0	0	0	0	0	0		
ENSMUST00000120800						103	93	132	174	132	75	4	2	21	4	21		
ENSMUST00000120801	ENSMUSG00000039710	3	14480697	14505830	1	0	0	0	0	3	0	0	0	0	0	0	D3YTZ6	
ENSMUST00000120802						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120803						2	3	0	2	6	4	0	0	0	0	0		
ENSMUST00000120804						1	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000120805	ENSMUSG00000027679	3	34056020	34081321	-1	0	0	0	0	0	0	18	73	7	41	7	D3Z5K6	
ENSMUST00000120806						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000120807						0	2	2	0	3	0	0	0	0	0	0		
ENSMUST00000120808	ENSMUSG00000031323	X	102903216	102908687	-1	0	0	0	5	0	0	0	0	0	0	0		Q9D9R7
ENSMUST00000120809	ENSMUSG00000054715	7	12897815	12909083	1	0	0	30	0	0	0	0	1	5	2	14	Q8BGS5	
ENSMUST00000120811						2	5	20	0	1	6	0	0	0	0	0		
ENSMUST00000120812						3	1	4	0	0	2	0	0	0	0	0		
ENSMUST00000120813						3	4	11	2	8	2	0	0	0	0	0		
ENSMUST00000120814						2	4	5	3	3	3	0	6	1	3	1		
ENSMUST00000120815						1	1	5	0	0	0	0	1	0	0	0		
ENSMUST00000120816						5	4	5	8	15	3	0	0	0	0	0		
ENSMUST00000120817						0	1	5	4	2	1	0	0	0	0	0		
ENSMUST00000120818	ENSMUSG00000036377	5	76656512	76873554	1	6	0	0	0	4	5	0	0	6	0	0	D3YTS2	
ENSMUST00000120819						3	1	0	1	2	2	0	0	1	0	0		
ENSMUST00000120820	ENSMUSG00000035067	14	63606503	63820809	1	4	4	24	4	9	8	0	0	0	0	0		E9Q6C8
ENSMUST00000120821						1	1	0	0	3	2	0	0	0	0	0		
ENSMUST00000120822	ENSMUSG00000016257	2	174465067	174473081	-1	0	0	0	1	3	0	3	0	0	77	0	B0QZU2	
ENSMUST00000120823						5	1	1	3	2	1	0	0	0	0	0		
ENSMUST00000120824						6	7	4	13	10	3	0	0	0	0	0		
ENSMUST00000120825	ENSMUSG00000010825	5	143357338	143392152	1	21	22	25	79	31	8	0	0	0	0	0		Q0QWG9
ENSMUST00000120826						0	0	0	0	0	0	0	6	0	6	0		
ENSMUST00000120827	ENSMUSG00000059325	5	77086988	77115121	-1	2	2	6	174	9	9	0	160	101	29	23		Q8R1H0
ENSMUST00000120828						3	5	3	8	8	3	0	0	0	0	0		
ENSMUST00000120829						5	3	7	1	6	5	0	0	0	0	0		
ENSMUST00000120830						6	4	16	8	7	0	0	0	0	1	1		
ENSMUST00000120831						6	2	3	7	5	5	0	0	0	0	0		
ENSMUST00000120832						5	1	6	5	4	3	0	0	0	0	0		
ENSMUST00000120833						0	0	28	6	0	0	0	0	4	8	0		
ENSMUST00000120834	ENSMUSG00000027695	3	27938695	28133362	1	0	0	0	39	5	0	334	347	721	55	257	Q6NVF2	
ENSMUST00000120836	ENSMUSG00000035390	7	4690604	4715997	1	11	15	0	13	22	0	2	0	1	0	17	D3Z5P0	
ENSMUST00000120837	ENSMUSG00000024233	18	4165832	4182232	1	0	0	0	0	0	0	0	0	0	0	0	D3Z796	
ENSMUST00000120838						4	4	7	3	4	3	0	1	0	4	0		
ENSMUST00000120839						1	1	4	0	2	0	0	0	0	0	0		
ENSMUST00000120840						4	6	8	6	4	1	0	0	0	0	0		
ENSMUST00000120842						6	7	4	3	4	4	0	2	0	1	1		
ENSMUST00000120843						8	4	13	6	7	1	0	0	0	0	0		
ENSMUST00000120844						2	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000120845						1	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000120846						0	0	0	0	1	0	0	1	0	1	0		
ENSMUST00000120847	ENSMUSG00000046079	5	105699969	105832436	1	5	35	112	62	35	5	1181	2022	1360	102	809		Q8BGR2
ENSMUST00000120848						1	2	0	4	1	0	0	0	0	0	0		
ENSMUST00000120849						5	3	6	1	3	0	0	3	3	0	0		
ENSMUST00000120850						1	1	8	5	3	0	0	0	0	0	0		
ENSMUST00000120851						7	1	9	10	4	2	0	0	0	0	0		
ENSMUST00000120852	ENSMUSG00000038695	7	44467980	44471662	1	0	0	0	0	0	0	0	0	42	0	0		Q9CR30
ENSMUST00000120853						287	242	307	270	349	137	7	14	18	6	49		
ENSMUST00000120854	ENSMUSG00000090150	9	104063377	104127656	1	12	2	0	0	9	7	5	463	75	93	0	D3YTQ5	
ENSMUST00000120855						1	0	0	1	2	0	0	0	0	0	4		
ENSMUST00000120856	ENSMUSG00000034818	10	81459227	81482709	-1	13	6	54	52	21	9	0	0	0	0	0	D3Z4C5	
ENSMUST00000120857	ENSMUSG00000030830	7	127296260	127335138	1	21	12	49	34	49	10	333	613	571	39	1149	D3Z627	
ENSMUST00000120859	ENSMUSG00000022433	15	79417856	79443919	-1	0	0	0	0	0	0	141	19	172	22	65		Q9JMK2
ENSMUST00000120860						11	19	111	21	27	12	6	6	5	0	7		
ENSMUST00000120861	ENSMUSG00000051037	13	67194506	67209298	1	7	10	11	7	5	0	0	20	5	15	0	Q7M6X9	
ENSMUST00000120862						6	3	8	6	13	3	2	1	0	0	0		
ENSMUST00000120863						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000120864	ENSMUSG00000030826	7	45570153	45589710	1	0	0	0	0	0	0	37	104	30	7	98	D3Z7C8	
ENSMUST00000120865						2	1	2	0	3	4	0	0	0	0	0		
ENSMUST00000120866	ENSMUSG00000041673	14	32991382	33015292	1	0	3	21	15	6	6	0	0	0	0	0		Q9CQ07
ENSMUST00000120867	ENSMUSG00000015806	5	45434021	45450236	-1	5	0	4	41	0	4	3	0	2	0	13	D3YWR7	
ENSMUST00000120868						9	5	12	8	6	2	0	0	2	0	1		
ENSMUST00000120869	ENSMUSG00000028999	5	23787711	23820369	1	54	38	52	379	51	38	0	8	6	1	7	D3YU54	
ENSMUST00000120870						7	4	3	6	7	1	0	0	0	2	0		
ENSMUST00000120871						4	2	3	5	8	5	0	0	0	0	0		
ENSMUST00000120872						4	5	2	1	3	2	0	0	0	0	0		
ENSMUST00000120873						3	2	6	9	0	1	0	1	0	0	0		
ENSMUST00000120874	ENSMUSG00000094362	8	21391811	21392698	1	1	0	0	0	1	0	0	0	0	0	0	Q8C1N9	
ENSMUST00000120875	ENSMUSG00000044864	3	38449259	38484844	-1	12	5	10	16	6	4	42	56	49	5	36	D3Z643	
ENSMUST00000120876	ENSMUSG00000048330	7	109034312	109083331	-1	0	0	0	5	2	0	1	0	2	0	0	D3YTZ9	
ENSMUST00000120877						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000120878	ENSMUSG00000018398	11	53519257	53549565	1	6	0	14	0	5	0	0	0	0	0	10	B7ZC46	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120879	ENSMUSG00000030990	7	102210208	102238567	1	0	3	0	0	0	0	70	36	0	0	0		Q3TQR0
ENSMUST00000120880						2	0	2	0	3	1	0	0	0	0	0		
ENSMUST00000120881						0	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000120882						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000120883						42	35	42	31	44	13	0	2	2	0	2		
ENSMUST00000120884						5	4	4	4	6	4	0	0	0	0	0		
ENSMUST00000120885						3	0	1	3	2	0	0	0	0	0	0		
ENSMUST00000120886						1	2	5	0	4	3	8	0	8	2	2		
ENSMUST00000120887						5	3	4	11	6	7	0	0	0	0	0		
ENSMUST00000120888						4	3	10	3	3	0	0	12	4	95	0		
ENSMUST00000120890						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000120891						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000120892						2	2	0	4	1	0	0	0	0	0	0		
ENSMUST00000120893						79	45	465	99	54	21	0	2	1	0	0		
ENSMUST00000120894						4	6	27	17	17	1	1	2	13	2	17		
ENSMUST00000120896						6	10	6	9	6	2	0	0	0	0	0		
ENSMUST00000120897						3	6	5	3	6	3	0	0	0	0	0		
ENSMUST00000120898	ENSMUSG00000064115	16	66655421	67620908	-1	0	0	1	137	0	1	0	0	0	0	0		Q8BLQ9
ENSMUST00000120899						6	1	7	4	2	0	0	0	0	0	1		
ENSMUST00000120900	ENSMUSG00000070323	9	7571396	7581885	1	0	10	0	2	0	2	14	43	0	0	7	D3Z6I1	
ENSMUST00000120901						0	0	0	0	0	0	0	11	3	5	0		
ENSMUST00000120902	ENSMUSG00000037426	5	32863701	32994236	1	0	0	0	0	0	0	152	110	205	4	195		P61460
ENSMUST00000120903	ENSMUSG00000030382	7	12988346	12998192	-1	10	5	5	5	8	1	0	0	0	0	0	E9PXV4	
ENSMUST00000120904	ENSMUSG00000042807	1	53806876	54195168	-1	0	0	0	46	0	27	0	0	0	0	0		Q6I6G8
ENSMUST00000120905						6	8	2	4	9	3	0	0	0	0	0		
ENSMUST00000120906						10	7	6	10	14	6	0	0	0	0	0		
ENSMUST00000120908						1	0	0	3	2	0	0	0	0	0	0		
ENSMUST00000120909						39	19	37	681	61	36	0	12	3	0	4		
ENSMUST00000120911						0	1	2	2	9	0	14	24	23	26	18		
ENSMUST00000120912	ENSMUSG00000029247	5	76951307	76967509	1	0	0	0	0	0	0	62	143	40	32	0		Q9DCL9
ENSMUST00000120913						5	4	8	4	9	5	0	2	0	0	0		
ENSMUST00000120914						2	3	3	0	3	0	0	0	0	0	0		
ENSMUST00000120915						6	6	5	7	6	1	0	0	0	0	0		
ENSMUST00000120916						8	0	16	14	5	4	0	0	0	0	0		
ENSMUST00000120917						14	10	43	10	16	5	0	0	0	0	0		
ENSMUST00000120918	ENSMUSG00000032530	9	121577843	121642096	-1	8	6	19	83	0	0	0	1	0	0	0	Q78ID0	Q9D925
ENSMUST00000120919						3	3	3	0	1	6	0	0	0	1	0		
ENSMUST00000120920						0	0	0	0	2	0	0	191	222	27	105		
ENSMUST00000120921						5	2	2	4	3	1	0	0	0	0	0		
ENSMUST00000120922						0	0	0	2	0	0	0	17	0	3	4		
ENSMUST00000120923						7	2	1	17	5	4	0	0	0	0	0		
ENSMUST00000120925						0	2	6	0	2	0	0	2	6	50	1		
ENSMUST00000120926						0	2	6	1	1	1	0	0	0	0	0		
ENSMUST00000120927	ENSMUSG00000021228	12	84052144	84059565	1	0	2	16	90	9	0	0	0	0	0	0		Q9QYR7
ENSMUST00000120928	ENSMUSG00000048277	11	117809668	117814283	1	0	6	10	0	11	5	284	332	0	25	48	B0QZP8	
ENSMUST00000120929	ENSMUSG00000059891	7	44943240	44958033	1	17	15	27	110	9	12	0	0	0	0	0		O54887
ENSMUST00000120930						5	2	2	0	2	1	0	0	0	0	0		
ENSMUST00000120931						7	0	0	6	3	0	1	2	0	4	0		
ENSMUST00000120932						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000120933	ENSMUSG00000033182	6	88545114	88637950	-1	7	0	0	0	0	3	0	0	0	0	0		Q9D618
ENSMUST00000120934	ENSMUSG00000024539	18	67665511	67724595	-1	4	3	3	29	5	4	0	0	15	0	0	D3Z6W2	
ENSMUST00000120935	ENSMUSG00000055102	7	43607169	43618285	1	0	1	6	29	19	6	6	28	9	5	4	E9Q5X9	
ENSMUST00000120936	ENSMUSG00000024979	19	55180733	55196313	1	2	0	0	1	18	4	0	0	0	0	0	D3Z3Y6	
ENSMUST00000120937						3	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000120938						0	0	0	18	0	0	269	443	238	1250	102		
ENSMUST00000120939	ENSMUSG00000008540	6	138140316	138156755	1	0	0	0	0	0	1	1177	2685	738	2282	428	D3YU60	
ENSMUST00000120940	ENSMUSG00000009894	11	59407134	59451186	-1	2	0	6	15	5	0	6	6	11	7	11	B2FDF6	
ENSMUST00000120941						4	6	6	3	3	3	0	0	0	0	0		
ENSMUST00000120942	ENSMUSG00000021236	12	84373857	84409029	-1	0	0	0	0	0	0	194	429	239	27	75		Q9WUZ9
ENSMUST00000120943	ENSMUSG00000024160	17	24886643	24892152	1	1	0	0	1	0	0	0	0	0	0	0		Q571F5
ENSMUST00000120944						4	0	5	21	2	0	10	0	13	0	0		
ENSMUST00000120945						0	0	0	3	3	0	0	0	0	0	0		
ENSMUST00000120946	ENSMUSG00000028796	4	128654702	128752881	1	2	0	0	0	2	0	2	1	0	0	0	B1ASA0	
ENSMUST00000120947						2	1	4	3	2	4	0	0	0	0	1		
ENSMUST00000120948						5	3	4	2	6	0	0	0	0	0	0		
ENSMUST00000120949						2	2	4	6	3	0	0	0	1	0	1		
ENSMUST00000120950						1	0	0	4	3	0	0	0	0	0	0		
ENSMUST00000120951	ENSMUSG00000041673	14	32991382	33015292	1	2	0	11	3	2	2	1	0	0	0	0	D3Z3F9	
ENSMUST00000120952						2	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000120953						3	6	3	3	5	1	0	0	0	0	1		
ENSMUST00000120954						5	1	33	14	11	1	0	4	0	1	0		
ENSMUST00000120955						2	6	13	5	8	4	0	0	0	0	0		
ENSMUST00000120956	ENSMUSG00000021768	14	21733394	21751181	-1	0	3	2	2	2	3	0	0	1	0	0	Q7TNW3	
ENSMUST00000120957						1	0	3	0	6	1	0	0	0	0	0		
ENSMUST00000120958						99	52	117	946	133	96	6	9	5	1	9		
ENSMUST00000120959	ENSMUSG00000078881	2	176473278	176486783	-1	0	0	3	0	0	0	3	0	0	0	3	Q8BHI0	
ENSMUST00000120960						3	0	0	1	3	3	0	0	0	0	0		
ENSMUST00000120961						8	5	5	4	3	2	0	0	0	1	0		
ENSMUST00000120962						19	17	16	5	16	8	0	0	0	0	0		
ENSMUST00000120963	ENSMUSG00000055923	5	76873659	76905514	-1	0	0	0	21	11	10	0	35	18	0	2		Q80WC9
ENSMUST00000120964						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120965	ENSMUSG00000029669	6	21771395	21852515	-1	0	0	4	0	0	0	0	0	0	0	0		Q8BKT6
ENSMUST00000120966						4	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000120967	ENSMUSG00000023902	17	23600856	23611019	1	27	11	12	48	13	5	0	0	0	0	0		Q3URR7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000120969						13	6	0	6	13	3	0	0	0	0	0		
ENSMUST00000120970						3	2	15	5	1	1	0	0	1	2	2		
ENSMUST00000120971	ENSMUSG00000073008	X	107255878	107296769	1	0	0	0	0	0	0	0	0	0	0	0		Q3U507
ENSMUST00000120972						7	1	5	1	0	0	0	0	0	0	0		
ENSMUST00000120973						6	6	0	0	0	7	0	0	0	0	0		
ENSMUST00000120974						1	1	0	2	3	3	1	0	0	2	0		
ENSMUST00000120975						0	2	2	1	1	2	0	0	0	0	0		
ENSMUST00000120976						6	1	16	9	8	4	1	20	6	7	5		
ENSMUST00000120977	ENSMUSG00000027803	3	57455649	57575910	-1	0	0	7	97	12	27	0	7	0	30	0		Q9EPK5
ENSMUST00000120978						4	6	4	6	7	2	0	0	0	0	0		
ENSMUST00000120979						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000120980						5	3	7	1	5	0	75	250	88	44	36		
ENSMUST00000120981						6	7	17	9	5	5	0	0	0	0	0		
ENSMUST00000120982						6	2	21	15	8	4	0	3	0	0	0		
ENSMUST00000120983						2	1	3	1	6	1	0	0	0	0	0		
ENSMUST00000120984	ENSMUSG00000021768	14	21733394	21751181	-1	4	4	2	0	4	5	0	1	0	0	1		Q9QYJ7
ENSMUST00000120985	ENSMUSG00000040428	7	45526330	45554229	1	8	0	13	73	19	0	0	5	0	0	0	E9QJX8	
ENSMUST00000120986						126	125	266	152	96	69	7	19	13	4	18		
ENSMUST00000120987	ENSMUSG00000038102	8	47490115	47533470	-1	10	12	26	11	9	6	2	7	7	0	4		B2RXC1
ENSMUST00000120988	ENSMUSG00000028165	3	135406412	135423925	-1	5	5	24	8	3	4	17	27	45	18	59	D3Z3X4	
ENSMUST00000120989						3	0	4	0	0	0	1	1	1	0	0		
ENSMUST00000120990	ENSMUSG00000051041	7	107567446	107591094	1	16	8	15	9	25	11	0	0	0	1	1	Q8BSH2	
ENSMUST00000120991						4	1	0	4	14	0	0	0	0	0	0		
ENSMUST00000120992	ENSMUSG00000027809	3	79603788	79629500	-1	5	0	7	0	5	4	89	528	103	75	168	Q6PF96	
ENSMUST00000120993						35	19	105	45	39	15	1	1	0	0	1		
ENSMUST00000120994						6	0	0	2	0	0	0	1	0	0	0		
ENSMUST00000120995						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000120997	ENSMUSG00000054855	15	98663421	98677461	-1	403	272	3086	550	209	128	142	409	160	41	87		Q8BLR7
ENSMUST00000120998						5	4	3	5	3	2	0	0	0	0	0		
ENSMUST00000120999						0	3	8	3	3	0	0	0	0	0	0		
ENSMUST00000121000						10	6	7	11	11	5	1	2	0	0	0		
ENSMUST00000121001						12	9	0	9	13	0	27	0	0	16	0		
ENSMUST00000121002						5	2	3	5	8	2	0	0	0	0	0		
ENSMUST00000121003						3	0	0	5	3	1	0	0	0	0	2		
ENSMUST00000121004	ENSMUSG00000030815	7	127573340	127583307	1	0	0	6	37	0	0	0	60	0	4	15		Q9DB30
ENSMUST00000121005						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000121006	ENSMUSG00000022043	14	66297031	66311424	1	9	5	5	106	4	0	0	3	6	0	3	F6U6G6	
ENSMUST00000121007						6	8	0	11	9	5	0	0	0	0	1		
ENSMUST00000121008						3	4	25	11	5	0	1	2	1	2	5		
ENSMUST00000121009						10	4	11	11	3	3	0	12	5	8	11		
ENSMUST00000121010	ENSMUSG00000063646	5	37028335	37148001	1	15	10	21	27	11	5	0	0	0	0	13	D3Z4U5	
ENSMUST00000121011						43	9	183	27	26	19	1	0	0	1	1		
ENSMUST00000121012						4	1	4	4	3	3	0	0	0	0	0		
ENSMUST00000121013						0	3	2	2	0	0	0	0	0	0	0		
ENSMUST00000121014						7	3	0	5	3	2	0	0	0	0	0		
ENSMUST00000121015						5	18	0	4	4	8	0	0	0	0	0		
ENSMUST00000121016						0	7	11	11	7	2	53	130	162	12	155		
ENSMUST00000121017	ENSMUSG00000038292	7	45183624	45204892	-1	25	9	45	76	44	19	0	1	1	0	0		Q80VJ8
ENSMUST00000121018	ENSMUSG00000024430	18	12741324	12755146	1	6	7	6	14	0	7	3	3	5	3	6	Q3KNH8	Q9D424
ENSMUST00000121019						1	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000121020						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121021	ENSMUSG00000018604	5	119670669	119684724	1	0	11	30	20	0	0	0	0	0	0	0	Q4VA43	P70324
ENSMUST00000121022						5	5	6	4	4	5	0	2	0	6	0		
ENSMUST00000121023						1	1	5	4	0	2	0	0	0	0	0		
ENSMUST00000121024	ENSMUSG00000053367	7	6252710	6282066	1	2	3	7	3	0	0	0	0	0	0	0	E9Q7F5	
ENSMUST00000121025						4	1	20	3	2	2	0	0	0	0	0		
ENSMUST00000121026						2	0	18	5	2	2	0	0	0	0	0		
ENSMUST00000121027						9	4	11	4	7	2	0	1	1	0	0		
ENSMUST00000121028						5	0	5	4	4	2	0	0	0	0	0		
ENSMUST00000121029						3	3	6	4	3	0	0	0	0	0	0		
ENSMUST00000121030						8	6	10	3	9	3	0	0	0	1	0		
ENSMUST00000121031						9	4	4	13	11	7	0	0	8	0	2		
ENSMUST00000121032						1	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000121033	ENSMUSG00000040167	7	131388652	131410521	-1	0	0	5	0	0	0	29	5	39	50	35		Q8BU00
ENSMUST00000121034	ENSMUSG00000027900	3	106547798	106575890	1	0	0	0	2	0	0	22	13	0	36	0		Q9CR48
ENSMUST00000121035						85	57	222	62	55	20	135	239	111	54	182		
ENSMUST00000121036						7	12	11	14	14	3	1	0	0	0	0		
ENSMUST00000121037						0	1	1	0	5	3	0	0	0	0	0		
ENSMUST00000121038	ENSMUSG00000027506	3	8925593	9004723	-1	5	0	1	5	0	2	11	20	375	648	543	D3Z637	
ENSMUST00000121039						1	2	2	1	2	0	0	0	0	0	0		
ENSMUST00000121040	ENSMUSG00000026420	1	130882074	130887454	-1	4	0	20	0	0	0	0	0	1	4	0		
ENSMUST00000121041						0	0	1	0	0	1	0	3	2	0	2		
ENSMUST00000121042						35	26	61	39	43	22	69	96	55	49	45		
ENSMUST00000121043	ENSMUSG00000000938	6	52231197	52240854	-1	20	7	24	5	11	13	0	0	0	5	5		P31310
ENSMUST00000121044	ENSMUSG00000082361	5	91357261	91402994	-1	33	28	44	39	39	18	2	3	2	1	8	Q543J8	Q05928
ENSMUST00000121045						1	4	12	0	0	0	0	0	0	0	0		
ENSMUST00000121046						2	14	7	10	18	14	6522	16538	10917	24981	6101		
ENSMUST00000121047	ENSMUSG00000078440	10	81384428	81391560	1	4	0	28	52	12	3	0	3	3	0	9	D3Z6Y9	
ENSMUST00000121048	ENSMUSG00000019710	3	87919506	87923672	1	51	37	133	47	47	15	41	661	98	87	146		Q9CQ06
ENSMUST00000121049	ENSMUSG00000028782	4	129984870	130022633	1	0	0	0	5	20	0	0	0	0	2	0		Q8CGM1
ENSMUST00000121050						2	2	2	2	0	0	0	0	0	0	0		
ENSMUST00000121051						2	2	1	3	2	0	3	3	1	1	0		
ENSMUST00000121052	ENSMUSG00000028700	4	116123840	116159849	1	3	0	7	6	0	0	0	85	53	0	0		Q91X88
ENSMUST00000121053						2	1	2	1	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121054						3	8	3	4	4	2	0	0	0	0	0		
ENSMUST00000121055						0	2	0	0	3	0	0	1	0	0	0		
ENSMUST00000121056						1	2	7	4	5	3	0	3	0	1	0		
ENSMUST00000121057						2	0	22	8	3	2	1	0	2	0	1		
ENSMUST00000121058						4	0	25	4	6	0	0	29	5	8	7		
ENSMUST00000121059						6	1	3	7	6	0	7	7	7	21	9		
ENSMUST00000121060						0	0	0	0	1	0	0	190	35	0	0		
ENSMUST00000121061						63	35	336	402	41	35	3	45	8	1	6		
ENSMUST00000121062						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000121063						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121064	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q700	
ENSMUST00000121065	ENSMUSG00000083188	11	74239566	74240537	1	4	2	6	5	2	0	0	0	0	0	0		
ENSMUST00000121066						8	2	34	12	4	5	0	0	0	0	0		
ENSMUST00000121067						2	3	1	0	1	1	0	0	0	0	0		
ENSMUST00000121068						6	2	11	23	4	5	0	0	0	0	0		
ENSMUST00000121069						0	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000121070						0	0	1	1	0	2	0	0	0	0	0		
ENSMUST00000121071						0	2	0	3	2	1	0	0	3	3	0		
ENSMUST00000121072						5	0	1	2	4	2	0	18	4	9	0		
ENSMUST00000121073						1	2	2	21	4	6	0	0	0	0	1		
ENSMUST00000121075	ENSMUSG00000031543	8	22974844	23150497	1	3	0	0	0	4	2	0	0	0	1	1		Q02357
ENSMUST00000121076						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000121077	ENSMUSG00000043587	9	96823336	96892669	-1	0	0	2	0	2	3	9	0	0	0	0	D3Z7C3	
ENSMUST00000121078	ENSMUSG00000032899	6	131299142	131353597	-1	0	4	9	3	0	8	0	1	0	4	0		Q6J9G1
ENSMUST00000121079						1	4	2	0	3	5	0	0	0	0	0		
ENSMUST00000121080	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	0	0	E9PX88	
ENSMUST00000121081						7	16	19	16	5	5	0	0	0	0	0		
ENSMUST00000121082						2	1	3	3	0	2	0	0	0	0	0		
ENSMUST00000121083	ENSMUSG00000036667	6	42668002	42710088	-1	0	0	0	17	5	6	0	1	0	6	1		Q8BNE1
ENSMUST00000121084						0	0	2	0	3	1	0	0	0	0	0		
ENSMUST00000121085	ENSMUSG00000037552	7	28359604	28372599	-1	6	10	27	68	20	12	0	0	0	0	0	D3Z5N8	
ENSMUST00000121086						16	6	15	6	8	1	0	1	2	0	4		
ENSMUST00000121087						1	3	2	1	3	1	1	6	1	12	3		
ENSMUST00000121088						1	7	1	8	4	1	0	0	0	0	0		
ENSMUST00000121089						2	8	1	8	3	5	0	0	0	0	0		
ENSMUST00000121090						33	36	205	76	29	7	0	0	0	0	0		
ENSMUST00000121091	ENSMUSG00000048279	14	61138457	61240695	1	12	18	13	179	17	11	0	0	0	0	3	D3Z3H1	
ENSMUST00000121092						5	6	13	7	6	3	0	0	1	0	0		
ENSMUST00000121093	ENSMUSG00000034930	6	83135463	83152579	1	0	0	6	58	4	0	0	0	0	0	4		Q8C6B2
ENSMUST00000121094	ENSMUSG00000027951	3	89715022	89753446	1	0	0	0	0	0	5	142	737	183	76	292		Q99MU3
ENSMUST00000121095	ENSMUSG00000035509	13	56522472	56537898	1	0	0	0	37	0	0	0	2	0	1	0		
ENSMUST00000121096	ENSMUSG00000034842	5	92331827	92414628	1	0	0	0	0	0	0	0	0	0	0	0	E9QNU1	
ENSMUST00000121097	ENSMUSG00000036810	8	88118769	88135110	1	10	3	8	14	17	7	11	22	23	12	8		Q3UJ81
ENSMUST00000121098						6	4	4	8	0	2	0	0	0	0	0		
ENSMUST00000121099						76	99	177	77	63	0	0	0	0	0	0		
ENSMUST00000121100						1	2	0	1	3	4	0	0	0	0	0		
ENSMUST00000121101	ENSMUSG00000050079	8	94601955	94660275	1	6	8	7	154	6	6	0	6	3	0	2		Q8BVR6
ENSMUST00000121102						1	3	2	2	0	0	0	0	0	0	0		
ENSMUST00000121103						10	19	9	9	11	4	0	0	0	0	0		
ENSMUST00000121104						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000121105						5	3	1	2	1	0	0	0	0	0	0		
ENSMUST00000121106						0	1	10	0	2	0	48	111	35	236	37		
ENSMUST00000121107						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121108						0	0	13	0	13	0	0	0	0	0	0		
ENSMUST00000121109	ENSMUSG00000073721	4	144372760	144377933	-1	6	4	3	5	3	2	0	0	0	0	0	B1ARV6	
ENSMUST00000121110	ENSMUSG00000042198	4	3938888	3951046	1	0	0	0	14	1	0	0	0	0	0	0		Q8K2Q5
ENSMUST00000121111	ENSMUSG00000028641	4	119232915	119248975	1	0	0	6	71	10	16	9	17	6	2	32		Q3V1T4
ENSMUST00000121112	ENSMUSG00000028266	3	144188530	144205220	-1	7	6	8	111	17	4	88	238	89	30	148	Q542S1	P61969
ENSMUST00000121113						4	4	21	30	3	3	0	0	0	0	1		
ENSMUST00000121114	ENSMUSG00000027075	2	84838850	84863594	1	7	0	18	105	10	14	0	0	0	0	5		Q8BSM7
ENSMUST00000121115	ENSMUSG00000025466	7	140096770	140102441	-1	5	1	5	8	12	3	0	0	0	0	0		Q8R2K1
ENSMUST00000121116	ENSMUSG00000031933	9	14885814	14903949	-1	0	2	5	0	0	0	0	0	0	0	0	D3Z631	
ENSMUST00000121117						5	10	32	6	7	0	1	4	1	0	0		
ENSMUST00000121118						1	4	1	1	3	2	3	6	5	21	3		
ENSMUST00000121120						4	1	8	4	1	0	0	0	0	0	0		
ENSMUST00000121121						5	2	6	3	7	5	0	0	0	0	0		
ENSMUST00000121122						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000121123	ENSMUSG00000006019	7	16197147	16222037	-1	0	0	10	15	0	0	3	0	4	20	0	D3YTV3	
ENSMUST00000121125						0	4	3	2	4	1	2	9	3	0	4		
ENSMUST00000121126						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000121127	ENSMUSG00000029385	5	93267257	93276231	1	0	3	7	11	8	8	881	1800	487	53	356	Q5HZK4	O08918
ENSMUST00000121128	ENSMUSG00000048583	7	142650766	142666816	-1	34	29	56	444	42	17	0	0	0	0	0	E9QLW5	
ENSMUST00000121129	ENSMUSG00000022604	16	55899888	55934855	-1	0	3	0	0	4	3	0	0	2	1	0	Q8BH46	
ENSMUST00000121130						5	2	8	4	2	1	0	0	0	0	1		
ENSMUST00000121131						0	2	3	1	0	0	0	1	0	0	0		
ENSMUST00000121132						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000121133	ENSMUSG00000028186	3	146570426	146632305	1	0	0	0	0	0	2	0	0	0	12	2	D3Z4U1	
ENSMUST00000121134						0	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000121135						4	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000121136						2	2	0	0	0	3	0	0	0	0	0		
ENSMUST00000121137	ENSMUSG00000022580	15	75704280	75714410	1	0	0	0	17	0	0	0	3	0	0	0	E9Q7Q7	
ENSMUST00000121138	ENSMUSG00000074862	10	81606270	81620703	1	0	1	0	0	0	0	0	0	0	0	0	Q3US60	
ENSMUST00000121139						5	4	2	3	9	2	0	0	0	0	0		
ENSMUST00000121140						8	2	8	9	5	3	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121141						9	8	21	4	5	4	0	0	0	0	0		
ENSMUST00000121142	ENSMUSG00000034194	14	69697307	69707584	-1	17	0	27	157	39	17	0	8	8	0	8	E9PUE1	
ENSMUST00000121143						7	2	10	9	5	5	0	0	0	1	0		
ENSMUST00000121144						3	1	4	3	2	0	0	0	1	1	0		
ENSMUST00000121145						0	1	5	1	0	0	0	0	0	0	0		
ENSMUST00000121146	ENSMUSG00000060985	1	156255296	156303664	-1	20	18	7	50	22	0	0	0	0	0	0		Q5VCS6
ENSMUST00000121147						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000121148	ENSMUSG00000035296	14	61221059	61258490	-1	1	0	0	0	2	5	0	0	0	0	0	Q9EQ83	P82348
ENSMUST00000121149						1	0	0	2	3	0	0	2	0	0	0		
ENSMUST00000121150						3	2	4	6	7	4	0	0	0	0	0		
ENSMUST00000121151	ENSMUSG00000000903	10	75943057	75949657	1	7	4	11	4	5	2	0	0	0	0	0	D3Z6J4	
ENSMUST00000121152						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000121153	ENSMUSG00000056537	X	103957163	103981284	-1	4	3	7	16	3	3	2	228	346	317	151		Q9WTV7
ENSMUST00000121154						0	2	2	2	1	0	1	0	0	0	0		
ENSMUST00000121155						4	0	5	0	1	0	0	0	0	0	0		
ENSMUST00000121156						3	2	1	2	2	0	0	0	1	1	2		
ENSMUST00000121157						301	278	293	279	416	246	0	6	4	2	6		
ENSMUST00000121158						4	3	4	0	3	2	0	0	0	0	0		
ENSMUST00000121159						6	5	18	82	20	5	0	0	0	0	0		
ENSMUST00000121160	ENSMUSG00000036377	5	76656512	76873554	1	32	20	166	148	75	30	81	39	291	7	65	E9Q5L4	
ENSMUST00000121161	ENSMUSG00000020053	10	87858265	87937042	1	0	0	0	0	0	0	0	0	0	0	0	E9Q138	
ENSMUST00000121162	ENSMUSG00000031789	8	95239045	95306585	-1	12	0	29	71	21	0	0	0	0	0	0	E9PXX0	
ENSMUST00000121163						5	3	8	1	5	1	0	0	0	0	0		
ENSMUST00000121164						1	3	0	4	7	2	0	0	0	0	0		
ENSMUST00000121165						0	0	4	1	2	0	0	3	0	0	0		
ENSMUST00000121166						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121167						2	3	5	2	6	5	1	1	1	0	1		
ENSMUST00000121168						2	0	0	0	1	0	0	0	0	3	0		
ENSMUST00000121169						3	2	0	79	3	0	0	3	3	0	0		
ENSMUST00000121170						3	2	2	4	4	2	0	3	3	2	10		
ENSMUST00000121172						1	1	4	0	5	0	0	0	0	0	0		
ENSMUST00000121173						4	11	21	8	9	3	0	0	0	0	0		
ENSMUST00000121175	ENSMUSG00000040488	7	27305136	27337692	-1	0	0	0	11	0	0	0	0	0	0	0		Q8K4G1
ENSMUST00000121176						0	0	5	0	1	0	0	0	0	1	0		
ENSMUST00000121177						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000121178						6	3	4	5	4	3	0	0	0	0	0		
ENSMUST00000121179						0	3	3	0	10	8	0	0	0	0	0		
ENSMUST00000121180						1	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000121181						5	1	6	2	2	1	0	1	0	0	1		
ENSMUST00000121182	ENSMUSG00000040767	11	32205415	32208984	1	6	1	4	0	0	1	0	0	5	0	0	A7M7T4	
ENSMUST00000121183						5	5	8	11	7	2	0	0	0	0	0		
ENSMUST00000121184	ENSMUSG00000025478	7	139086001	139102704	1	5	5	0	1	2	0	0	0	0	0	0		
ENSMUST00000121185	ENSMUSG00000020738	11	115523102	115536276	-1	0	0	0	5	0	0	50	179	6	0	0	D3YW94	
ENSMUST00000121186						3	1	1	2	2	0	0	0	0	0	0		
ENSMUST00000121187						0	0	0	0	0	9	0	0	0	0	0		
ENSMUST00000121188						9	9	15	11	11	4	0	2	2	2	0		
ENSMUST00000121189	ENSMUSG00000032415	9	86307306	86464950	-1	1	2	4	82	2	2	0	0	0	0	0	D3Z587	
ENSMUST00000121190						11	4	33	25	17	8	0	25	11	1	12		
ENSMUST00000121191						1	0	1	0	1	3	0	0	0	0	0		
ENSMUST00000121192						7	4	27	6	7	0	0	0	0	0	0		
ENSMUST00000121193						1	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000121194						8	2	8	5	5	0	0	0	0	0	0		
ENSMUST00000121195						0	0	0	0	1	0	0	0	0	0	1		
ENSMUST00000121196						6	4	5	5	5	2	0	0	0	0	0		
ENSMUST00000121197	ENSMUSG00000031323	X	102903216	102908687	-1	3	3	6	0	0	3	0	0	0	0	0		Q9D9R7
ENSMUST00000121198	ENSMUSG00000052539	3	104013259	104220374	-1	28	8	46	0	12	13	83	202	290	18	140	G5E8T6	
ENSMUST00000121199						6	5	20	12	13	4	0	0	0	0	1		
ENSMUST00000121200	ENSMUSG00000058056	8	61513246	61902690	-1	7	0	0	413	14	0	90	105	258	9	56		Q9ET54
ENSMUST00000121201						6	2	9	9	4	3	0	1	0	0	0		
ENSMUST00000121202						10	15	14	8	4	3	0	0	2	0	2		
ENSMUST00000121204	ENSMUSG00000061559	9	54714735	54734519	-1	0	0	12	20	2	0	46	42	0	26	35	A0MNP4	Q9ERF3
ENSMUST00000121205	ENSMUSG00000004933	10	81252935	81263365	1	0	0	0	57	0	0	0	0	4	12	11	D3Z4T5	
ENSMUST00000121206	ENSMUSG00000046897	15	102203648	102215606	1	0	2	0	3	7	0	0	0	0	0	0	D3Z5P3	
ENSMUST00000121207						3	5	8	2	2	2	0	0	0	0	0		
ENSMUST00000121208						2	1	3	62	6	2	0	0	7	0	8		
ENSMUST00000121209	ENSMUSG00000072709	11	73453275	73457458	-1	0	5	0	0	0	0	0	0	0	0	0	Q8VGT3	
ENSMUST00000121210	ENSMUSG00000042198	4	3938888	3951046	1	1	2	0	0	0	0	2	6	0	8	1	B1AXC5	
ENSMUST00000121211						331	285	1128	656	490	284	6	24	11	8	33		
ENSMUST00000121212	ENSMUSG00000068917	3	89164795	89176921	1	0	0	0	12	0	0	0	0	0	0	0		O35491
ENSMUST00000121213						7	0	15	10	11	7	0	0	0	0	0		
ENSMUST00000121214						0	1	3	2	2	2	0	0	0	0	0		
ENSMUST00000121215	ENSMUSG00000057894	7	12804977	12818858	-1	0	0	0	0	0	0	0	16	22	6	11	B2RSV9	Q6GQR8
ENSMUST00000121216						2	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000121217						3	3	0	1	2	0	11	79	34	104	15		
ENSMUST00000121218						4	2	11	5	4	3	0	0	0	0	0		
ENSMUST00000121219	ENSMUSG00000027238	2	121545529	121807087	-1	0	8	16	0	10	7	0	0	0	0	0		Q6P5H6
ENSMUST00000121220						1	1	2	0	2	0	0	0	1	2	0		
ENSMUST00000121221						1	2	3	3	5	0	0	0	0	0	0		
ENSMUST00000121222						2	1	5	1	2	0	0	2	0	3	0		
ENSMUST00000121223						2	1	0	0	0	1	1	0	0	2	0		
ENSMUST00000121224						3	1	5	0	0	1	0	1	0	1	0		
ENSMUST00000121225						0	2	1	0	0	1	0	0	0	0	0		
ENSMUST00000121226	ENSMUSG00000035435	17	24264259	24351029	-1	21	31	55	76	50	20	0	0	0	0	0	E9PX95	
ENSMUST00000121227	ENSMUSG00000032332	9	79598991	79718831	-1	9	0	28	14	13	23	0	0	0	0	6	E9PX70	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121228	ENSMUSG00000057534	11	88964658	88966931	-1	0	0	0	0	0	0	0	0	0	0	0	A6PWE0	
ENSMUST00000121229						9	5	11	2	14	6	181	203	321	43	216		
ENSMUST00000121230						8	2	22	4	7	1	0	0	0	0	0		
ENSMUST00000121231	ENSMUSG00000040774	3	106502260	106547802	-1	0	0	0	0	0	0	476	1667	313	374	160		Q8BGS7
ENSMUST00000121232						4	0	13	9	6	5	0	0	0	0	0		
ENSMUST00000121233						1	0	1	1	0	0	0	0	0	0	1		
ENSMUST00000121234						3	6	6	4	10	3	0	0	0	0	0		
ENSMUST00000121235						4	3	2	0	3	2	0	0	0	0	0		
ENSMUST00000121236						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000121237	ENSMUSG00000033256	2	122348892	122369162	-1	0	0	0	0	3	0	6	5	0	0	0	B0R096	
ENSMUST00000121238						6	5	7	26	1	6	3	5	3	0	1		
ENSMUST00000121239						0	1	0	0	3	0	156	260	181	37	66		
ENSMUST00000121240						2	7	4	7	7	2	0	0	0	0	0		
ENSMUST00000121241						3	5	12	7	5	2	0	0	0	0	0		
ENSMUST00000121242						2	2	4	1	5	5	0	0	0	0	0		
ENSMUST00000121243						3	0	3	1	1	1	0	0	0	0	0		
ENSMUST00000121244						4	2	2	6	2	1	0	0	0	0	0		
ENSMUST00000121245	ENSMUSG00000022656	16	46387706	46498525	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z6X5	
ENSMUST00000121246	ENSMUSG00000032103	9	35558595	35567401	1	0	0	8	0	2	10	2	3	0	0	0	Q9D0F7	
ENSMUST00000121247						2	0	2	2	2	0	0	0	0	0	0		
ENSMUST00000121248						3	2	8	0	4	4	0	0	0	0	0		
ENSMUST00000121249	ENSMUSG00000025081	19	56826209	56870012	1	0	16	61	122	20	0	0	0	0	0	0		Q99MV1
ENSMUST00000121250						0	3	0	0	2	0	5	0	0	0	2		
ENSMUST00000121251						9	7	3	2	13	3	0	3	0	2	3		
ENSMUST00000121252						0	4	9	8	7	5	2	1	1	1	0		
ENSMUST00000121253						2	3	12	2	5	3	0	0	0	0	0		
ENSMUST00000121254						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121255						3	2	24	0	2	0	0	0	0	0	0		
ENSMUST00000121256						0	0	0	0	1	0	0	1	0	0	0		
ENSMUST00000121257						6	12	0	6	5	5	0	0	0	0	0		
ENSMUST00000121258						7	4	4	5	12	3	0	0	0	0	0		
ENSMUST00000121259						2	0	3	0	0	0	3	26	3	12	4		
ENSMUST00000121260						3	2	5	8	5	2	0	0	0	2	0		
ENSMUST00000121261						1	0	0	5	2	0	0	7	0	4	0		
ENSMUST00000121262						4	6	1	4	1	1	0	0	0	0	0		
ENSMUST00000121263						0	0	0	1	4	0	0	0	0	0	0		
ENSMUST00000121264						4	4	13	2	3	1	0	0	0	0	0		
ENSMUST00000121265	ENSMUSG00000054746	7	120328684	120407687	1	9	5	7	12	9	6	0	0	0	0	0	E9PWH4	
ENSMUST00000121266	ENSMUSG00000032297	9	59577917	59607292	1	20	13	51	24	0	18	0	2	0	0	0		Q7TN33
ENSMUST00000121267						0	1	2	1	0	0	0	1	0	1	0		
ENSMUST00000121268						4	2	4	3	4	2	0	0	0	0	0		
ENSMUST00000121269						7	4	1	10	4	0	0	0	0	0	0		
ENSMUST00000121270	ENSMUSG00000035545	7	4137039	4148177	1	0	0	0	56	0	0	311	487	471	51	289	D3YWS8	
ENSMUST00000121271						1	4	4	0	0	1	0	0	0	0	0		
ENSMUST00000121272						10	1	6	4	5	0	0	0	0	0	0		
ENSMUST00000121273	ENSMUSG00000074179	9	78289923	78305525	1	2	0	0	0	0	0	0	0	0	0	0	E9Q6L7	
ENSMUST00000121274						0	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000121275						0	1	0	0	1	0	0	0	1	0	0		
ENSMUST00000121276						0	1	0	5	6	4	0	0	0	0	0		
ENSMUST00000121277						5	3	6	16	5	7	1	2	0	0	0		
ENSMUST00000121278						6	10	66	15	9	7	1	0	0	1	0		
ENSMUST00000121279						257	182	504	169	265	144	1	12	3	2	17		
ENSMUST00000121280	ENSMUSG00000057050	11	73964530	73965620	1	0	5	3	4	2	0	0	0	0	0	0	B2FDE2	
ENSMUST00000121281						1	0	6	5	2	3	0	0	0	0	0		
ENSMUST00000121282						2	3	16	7	5	0	0	1	0	0	0		
ENSMUST00000121283						2	2	1	1	6	3	0	0	0	0	0		
ENSMUST00000121284						4	2	7	6	9	8	0	0	0	0	0		
ENSMUST00000121285	ENSMUSG00000024002	17	32196274	32284722	-1	27	26	90	141	31	0	1729	2709	2263	135	1978		Q9ESU6
ENSMUST00000121286						0	0	6	2	2	0	0	0	0	0	0		
ENSMUST00000121287	ENSMUSG00000020847	11	75830999	75938429	-1	11	12	30	21	17	8	7	11	5	1	12		Q768S4
ENSMUST00000121288	ENSMUSG00000035095	14	63436394	63465498	1	26	16	40	43	40	22	57	93	76	10	17		Q6P1G6
ENSMUST00000121289						2	1	3	1	0	0	0	0	0	0	0		
ENSMUST00000121290						5	3	59	19	8	3	0	0	0	0	0		
ENSMUST00000121291	ENSMUSG00000005907	5	3596066	3637232	1	0	12	8	11	0	0	37	157	107	20	74		Q5BL07
ENSMUST00000121292	ENSMUSG00000039209	16	10170226	10174911	1	0	4	11	3	8	0	0	5	1	3	0	Q9CQD0	
ENSMUST00000121293						3	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000121294						77	58	282	54	34	20	4	0	5	0	18		
ENSMUST00000121296	ENSMUSG00000070855	2	87268819	87269814	1	2	3	0	3	4	4	0	0	0	0	0		
ENSMUST00000121297	ENSMUSG00000020096	10	61171954	61188841	1	0	0	4	0	0	0	0	0	0	0	0		Q7TSD4
ENSMUST00000121298						0	1	12	7	6	2	0	1	0	0	0		
ENSMUST00000121299						50	71	229	89	77	48	14	38	31	5	33		
ENSMUST00000121302						0	3	0	0	0	0	12	145	0	0	1		
ENSMUST00000121303	ENSMUSG00000009350	11	87793581	87804413	1	42	54	302	52	52	25	2692	2692	2209	103	894		P11247
ENSMUST00000121304	ENSMUSG00000000902	10	75896769	75921617	-1	2	1	0	0	0	0	232	263	122	46	188	Q3UDA4	Q9Z0H3
ENSMUST00000121305						11	2	26	12	6	2	0	1	0	4	3		
ENSMUST00000121306						7	4	2	7	7	4	0	0	0	0	0		
ENSMUST00000121307						3	2	6	0	4	1	0	2	0	1	0		
ENSMUST00000121308						3	0	1	1	2	0	0	146	0	0	0		
ENSMUST00000121309						0	0	0	0	0	0	122	13	129	650	106		
ENSMUST00000121310						0	3	2	4	3	0	1	1	0	0	0		
ENSMUST00000121311						4	3	5	4	6	3	0	0	0	0	0		
ENSMUST00000121312	ENSMUSG00000021944	14	63198922	63271692	-1	13	13	17	6	4	18	0	0	0	0	6	Q3UYJ1	
ENSMUST00000121313						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000121314						4	3	0	0	2	3	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121315	ENSMUSG00000044501	17	22361453	22377281	1	1	0	0	0	0	0	6	9	0	0	0	E9Q462	
ENSMUST00000121316						4	5	11	4	10	5	0	1	0	0	2		
ENSMUST00000121317						1	1	0	2	3	2	91	939	114	157	12		
ENSMUST00000121318						6	5	0	0	3	1	0	0	0	0	0		
ENSMUST00000121319						2	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000121320						1	1	4	16	3	1	832	664	656	5791	520		
ENSMUST00000121321						5	0	11	0	4	0	42	9	0	25	0		
ENSMUST00000121322	ENSMUSG00000032232	9	71626509	71771602	-1	4	0	11	26	0	0	136	408	265	120	66	D3Z3H4	
ENSMUST00000121323						5	8	3	4	5	1	244	212	198	167	98		
ENSMUST00000121324						0	0	0	11	0	2	183	18	728	15	497		
ENSMUST00000121325	ENSMUSG00000019817	10	13060504	13131694	1	0	0	0	0	0	2	0	0	0	0	0	Q3UQW2	
ENSMUST00000121326	ENSMUSG00000055436	3	158010473	158036639	-1	4	0	0	21	3	2	9	13	8	0	36	E9Q6E5	
ENSMUST00000121327						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000121328						3	5	10	6	8	5	0	0	0	0	0		
ENSMUST00000121329						8	3	2	2	6	1	0	0	0	0	0		
ENSMUST00000121330						1	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000121331	ENSMUSG00000078656	11	101253707	101259549	1	4	0	16	87	11	0	0	0	6	0	10	A8XY17	
ENSMUST00000121332						0	0	0	3	0	5	0	0	0	0	0		
ENSMUST00000121333						4	1	4	2	4	2	0	0	0	0	0		
ENSMUST00000121334	ENSMUSG00000018398	11	53519257	53549565	1	9	7	4	23	12	5	18	16	15	2	19	B1AQZ0	
ENSMUST00000121335						171	342	1732	425	212	83	2	6	1	0	2		
ENSMUST00000121336						4	2	6	0	4	5	0	0	0	0	0		
ENSMUST00000121337	ENSMUSG00000066363	12	104214544	104221129	1	0	0	23	0	0	6	0	0	0	0	0		Q80X76
ENSMUST00000121338						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121339	ENSMUSG00000034211	5	129715497	129722556	1	19	10	27	16	15	8	25	80	29	26	24		Q9CQE3
ENSMUST00000121340						7	6	12	5	6	0	0	0	0	0	0		
ENSMUST00000121341						0	0	1	0	2	1	0	0	0	0	0		
ENSMUST00000121342						21	14	6	84	10	3	0	0	0	0	0		
ENSMUST00000121343						4	2	6	5	1	1	0	0	0	0	0		
ENSMUST00000121344	ENSMUSG00000022686	16	19760208	19772753	1	10	3	12	21	9	1	7	20	15	12	25		Q8BGY6
ENSMUST00000121345						1	4	9	0	1	1	0	0	0	0	0		
ENSMUST00000121346						9	4	12	7	4	1	0	0	0	1	0		
ENSMUST00000121347						5	6	9	10	5	4	0	0	1	0	0		
ENSMUST00000121348						14	22	18	35	24	7	3	1	1	1	5		
ENSMUST00000121349						6	3	14	8	3	1	0	0	0	0	0		
ENSMUST00000121350						5	2	2	2	6	2	0	0	0	0	0		
ENSMUST00000121351						2	0	5	3	1	0	0	0	1	0	0		
ENSMUST00000121352						0	0	0	0	0	0	0	69	10	36	14		
ENSMUST00000121353						0	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000121354						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121355						2	5	0	2	0	0	0	0	0	0	0		
ENSMUST00000121356						1	2	1	1	1	0	0	0	0	0	0		
ENSMUST00000121357	ENSMUSG00000040111	9	40293233	40531383	-1	127	87	171	1547	332	161	530	1408	861	57	755		Q80TI0
ENSMUST00000121358						134	122	325	130	151	75	9	24	12	10	15		
ENSMUST00000121359						22	14	21	33	18	9	16	18	32	3	18		
ENSMUST00000121360	ENSMUSG00000029911	6	40471352	40484700	1	0	3	1	55	5	3	13	138	45	27	20	Q8R2K3	
ENSMUST00000121361						14	10	18	14	15	6	0	1	1	0	0		
ENSMUST00000121363						1	1	0	1	0	2	0	0	0	0	0		
ENSMUST00000121364						6	5	4	9	5	1	0	0	0	0	0		
ENSMUST00000121365						0	0	0	0	0	0	0	27	0	0	0		
ENSMUST00000121366						0	0	6	0	1	2	0	0	0	2	0		
ENSMUST00000121367						7	3	2	0	2	2	2	0	0	14	0		
ENSMUST00000121368						3	1	2	0	2	3	139	235	136	686	79		
ENSMUST00000121369	ENSMUSG00000032850	5	118190736	118245116	-1	35	12	54	72	0	0	0	0	0	0	0		Q3UF64
ENSMUST00000121370	ENSMUSG00000029174	5	64156305	64351486	1	0	0	0	0	0	0	721	20	184	12	516	Q3U3T9	Q60949
ENSMUST00000121371						4	5	12	1	8	2	0	0	0	0	0		
ENSMUST00000121372						0	1	1	0	2	0	0	0	0	0	1		
ENSMUST00000121373						4	1	2	1	1	1	0	0	0	0	0		
ENSMUST00000121374						7	1	3	5	3	2	0	0	0	1	0		
ENSMUST00000121375						3	2	7	3	3	2	0	0	0	0	0		
ENSMUST00000121376						1	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000121377	ENSMUSG00000039804	2	165000357	165034867	-1	9	0	27	0	0	4	13	81	44	18	61	B7ZC23	
ENSMUST00000121378	ENSMUSG00000031027	7	109279223	109439081	-1	0	0	0	0	0	0	0	0	0	0	0	D3YWA6	
ENSMUST00000121379						3	3	1	1	3	1	0	0	0	0	0		
ENSMUST00000121380						4	1	5	6	7	6	0	0	0	0	0		
ENSMUST00000121381						2	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000121382						1	1	0	1	1	0	5	8	0	8	0		
ENSMUST00000121383						4	6	16	15	10	3	0	0	1	0	9		
ENSMUST00000121384						4	2	11	9	6	9	4	4	3	4	2		
ENSMUST00000121385						5	5	8	5	9	8	0	0	0	0	0		
ENSMUST00000121386						17	19	13	37	21	3	0	5	1	3	3		
ENSMUST00000121387						2	0	0	1	2	1	0	3	1	1	2		
ENSMUST00000121388						6	5	19	4	12	2	0	0	0	0	0		
ENSMUST00000121389						5	3	5	10	6	4	0	1	0	1	1		
ENSMUST00000121390	ENSMUSG00000034656	8	84388440	84640246	1	22	0	0	49	45	9	0	9	0	0	0		P97445
ENSMUST00000121391	ENSMUSG00000012123	4	134065912	134092504	1	43	20	90	223	66	31	0	0	3	1	3	B7ZCC2	
ENSMUST00000121392						1	0	0	2	1	3	0	0	0	0	0		
ENSMUST00000121393	ENSMUSG00000078899	2	175321955	175338197	-1	224	184	274	170	188	107	53	249	55	119	96	A2ART4	
ENSMUST00000121394	ENSMUSG00000044139	7	127885841	127890970	-1	3	12	7	17	31	10	0	5	0	0	8	B2RX64	Q571E5
ENSMUST00000121395						3	3	3	0	2	0	0	0	0	0	0		
ENSMUST00000121396						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121397						2	5	5	2	4	0	0	0	0	0	0		
ENSMUST00000121398						0	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000121399						2	10	2	6	9	6	1	1	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121400						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000121401	ENSMUSG00000043183	13	54503779	54551290	1	18	15	58	42	20	10	48	128	81	18	151	E9Q6E9	
ENSMUST00000121402	ENSMUSG00000024847	19	4114446	4125858	-1	0	0	0	0	0	0	69	21	56	13	20	D3YW40	
ENSMUST00000121403						3	2	15	1	6	4	0	0	0	1	0		
ENSMUST00000121404	ENSMUSG00000058022	13	41763148	41847684	-1	4	1	0	13	2	0	18	78	17	17	1		Q8C138
ENSMUST00000121405						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000121406						0	1	3	0	2	1	0	0	0	0	0		
ENSMUST00000121407						8	9	59	21	12	3	0	2	1	0	1		
ENSMUST00000121408						4	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000121409	ENSMUSG00000037606	7	143688762	143756985	-1	5	1	10	6	6	2	0	0	0	0	0		Q9ER64
ENSMUST00000121410						3	0	4	9	0	0	4	4	3	2	8		
ENSMUST00000121411						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121412	ENSMUSG00000073795	7	139972303	139978755	-1	6	8	16	12	7	2	29	11	30	0	25	Q3TNW9	
ENSMUST00000121413						4	2	6	1	3	4	42	104	31	137	31		
ENSMUST00000121414						3	2	4	7	9	4	0	0	1	0	5		
ENSMUST00000121416	ENSMUSG00000041264	5	149184350	149215434	1	0	0	5	27	0	0	0	60	95	14	0		
ENSMUST00000121417						5	5	9	80	6	4	0	0	0	0	0		
ENSMUST00000121418	ENSMUSG00000024663	19	10001669	10038380	1	14	19	68	11	25	7	0	0	0	0	4		Q8VDV3
ENSMUST00000121419						6	3	0	1	3	3	0	0	0	0	0		
ENSMUST00000121420						5	6	11	36	15	3	1	0	0	0	0		
ENSMUST00000121421						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000121422						5	2	11	9	6	3	4	205	321	1837	45		
ENSMUST00000121423						6	2	7	2	5	3	0	0	0	0	0		
ENSMUST00000121424						1	2	6	2	1	1	0	0	0	0	0		
ENSMUST00000121425						19	17	89	31	25	13	0	1	0	0	2		
ENSMUST00000121426	ENSMUSG00000031446	8	13105621	13147940	1	2	7	8	9	4	3	0	0	0	0	0	E9PXT5	
ENSMUST00000121427						2	3	5	8	0	5	0	0	0	0	0		
ENSMUST00000121428						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000121429	ENSMUSG00000031310	X	101404384	101420849	-1	0	0	0	0	0	0	0	0	0	0	0	Q8CG95	
ENSMUST00000121430						6	0	6	3	0	4	33	16	72	0	21		
ENSMUST00000121431						1	4	2	2	1	0	0	0	0	0	0		
ENSMUST00000121432						15	6	14	3	12	7	0	0	0	0	0		
ENSMUST00000121433	ENSMUSG00000027011	2	78868124	78921293	1	3	1	13	94	6	3	125	552	179	57	86		P52483
ENSMUST00000121434						19	9	46	27	8	9	0	1	0	1	2		
ENSMUST00000121435	ENSMUSG00000081769	11	53783418	53859256	-1	8	0	4	39	0	0	0	0	0	0	0	A8Y5C2	
ENSMUST00000121436						3	1	1	1	2	4	0	0	0	0	0		
ENSMUST00000121437						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121438	ENSMUSG00000037437	8	24836140	24948804	-1	8	2	0	3	0	5	0	0	0	0	0		Q8K410
ENSMUST00000121439						4	3	1	0	1	0	0	0	0	1	0		
ENSMUST00000121440	ENSMUSG00000061143	3	51685907	52105076	-1	66	37	242	445	100	56	52	93	153	15	135	D4QGC2	
ENSMUST00000121441						8	4	2	126	5	2	0	0	0	0	0		
ENSMUST00000121442	ENSMUSG00000040795	4	129615126	129619099	-1	3	0	12	15	5	0	91	126	39	196	40	A8Y5J7	
ENSMUST00000121443						34	34	13	10	21	10	0	2	3	3	6		
ENSMUST00000121444	ENSMUSG00000063409	5	123489305	123508205	1	0	0	23	0	0	0	1	0	0	0	0		Q3V0L5
ENSMUST00000121445						6	4	22	19	12	2	0	1	0	0	1		
ENSMUST00000121446	ENSMUSG00000060733	10	71347763	71433327	1	0	0	0	0	0	3	170	51	339	8	159	D3YWA2	
ENSMUST00000121448						2	2	19	10	11	3	0	0	0	0	0		
ENSMUST00000121449						1	1	1	0	0	0	2	8	2	1	3		
ENSMUST00000121450						1	5	0	5	1	0	1	1	0	0	0		
ENSMUST00000121451						2	0	2	0	0	0	0	2	1	2	0		
ENSMUST00000121452						5	1	7	9	1	0	0	0	0	0	0		
ENSMUST00000121453						4	9	2	10	9	3	0	1	0	0	0		
ENSMUST00000121454						0	0	0	0	0	0	2	7	0	0	1		
ENSMUST00000121455						2	11	12	5	7	0	20	11	22	19	21		
ENSMUST00000121456						13	9	17	17	17	8	19	43	21	11	4		
ENSMUST00000121457						0	10	4	8	4	5	0	0	0	0	0		
ENSMUST00000121458						30	38	227	30	27	14	1	2	1	0	3		
ENSMUST00000121459						1	1	2	4	0	1	0	0	0	0	0		
ENSMUST00000121461						2	3	10	37	0	0	0	0	0	0	2		
ENSMUST00000121462						3	8	9	9	14	8	1	0	1	4	0		
ENSMUST00000121463						1	2	7	1	2	0	0	0	0	0	0		
ENSMUST00000121465	ENSMUSG00000019810	10	13499540	13519035	1	54	48	225	72	73	37	115	525	149	39	207	Q505Q3	Q99KR8
ENSMUST00000121466						2	3	2	9	2	3	0	0	0	0	0		
ENSMUST00000121467						3	1	4	4	4	3	0	0	0	0	0		
ENSMUST00000121468						3	4	2	1	6	1	0	0	0	0	2		
ENSMUST00000121469	ENSMUSG00000052852	6	71707561	71810710	1	26	19	53	78	47	10	0	0	0	1	0		Q8BGH4
ENSMUST00000121470						0	1	2	5	0	2	0	0	0	0	0		
ENSMUST00000121471	ENSMUSG00000020023	10	94311949	94590956	1	8	0	14	2	7	2	0	0	0	0	0		Q8R310
ENSMUST00000121472						3	4	0	2	5	2	0	0	0	0	0		
ENSMUST00000121473	ENSMUSG00000062209	1	68032186	69108059	-1	26	9	0	120	33	16	0	0	0	0	0		Q61527
ENSMUST00000121474						9	4	35	15	20	10	0	7	0	0	2		
ENSMUST00000121475						1	1	1	1	0	1	0	0	0	0	0		
ENSMUST00000121476						3	1	10	4	3	0	0	0	0	0	0		
ENSMUST00000121477	ENSMUSG00000029486	5	96209493	96266727	1	14	21	14	14	17	4	18	158	30	36	20	Q9D3F3	
ENSMUST00000121478						63	86	5	53	63	35	0	0	0	0	7		
ENSMUST00000121479						2	1	3	0	1	0	0	0	0	0	0		
ENSMUST00000121480						2	1	3	2	5	0	0	0	0	0	0		
ENSMUST00000121481						0	3	8	23	3	4	0	0	0	0	0		
ENSMUST00000121482						3	1	2	3	4	1	0	1	0	2	0		
ENSMUST00000121483						0	1	1	0	1	2	0	0	0	0	0		
ENSMUST00000121484	ENSMUSG00000027580	2	181227615	181242027	-1	0	14	69	57	105	20	0	0	69	0	155	A2AS05	
ENSMUST00000121485						6	6	6	4	3	0	0	0	0	0	1		
ENSMUST00000121486						3	3	0	1	1	0	0	0	0	0	0		
ENSMUST00000121487						6	1	29	18	11	3	0	2	0	7	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121488						10	2	5	8	2	0	7	58	8	27	9		
ENSMUST00000121489	ENSMUSG00000029468	5	122643911	122691432	1	0	1	0	0	0	11	0	11	0	32	5	Q3UN00	
ENSMUST00000121490						6	3	11	5	7	3	0	0	0	0	0		
ENSMUST00000121491	ENSMUSG00000073988	4	20007938	20030785	1	1	5	0	23	5	2	1	3	1	0	0	A8Y5N9	
ENSMUST00000121492	ENSMUSG00000051504	7	55768178	55778925	1	18	17	53	24	0	6	0	6	0	0	0	B7ZMQ5	
ENSMUST00000121493	ENSMUSG00000058056	8	61513246	61902690	-1	0	0	0	56	0	0	0	0	0	0	0		Q9ET54
ENSMUST00000121494	ENSMUSG00000039013	7	43351341	43359531	1	3	0	6	0	6	2	15	8	98	35	56	Q80ZE2	
ENSMUST00000121495						0	0	3	1	2	1	0	1	2	1	4		
ENSMUST00000121496						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121497						0	4	0	0	2	1	1244	1669	876	2051	575		
ENSMUST00000121498						11	2	7	3	11	4	0	0	0	0	0		
ENSMUST00000121499						5	4	39	4	4	3	0	0	0	0	0		
ENSMUST00000121500						6	2	0	0	4	2	0	0	0	0	0		
ENSMUST00000121501						4	2	4	5	6	1	0	0	0	0	0		
ENSMUST00000121502						1	3	2	1	1	2	0	0	0	1	0		
ENSMUST00000121503	ENSMUSG00000027940	3	90072649	90100902	1	2	4	3	6	3	0	9	38	25	41	39		
ENSMUST00000121504	ENSMUSG00000043964	7	127769815	127775150	1	18	0	22	11	9	0	109	70	50	11	56	D3Z6X8	
ENSMUST00000121505						3	3	10	0	8	4	0	0	0	0	0		
ENSMUST00000121506						5	1	7	7	7	3	10	4	2	3	3		
ENSMUST00000121507						0	0	9	7	1	0	0	0	0	0	0		
ENSMUST00000121508						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000121509						2	3	5	7	6	3	0	0	2	0	8		
ENSMUST00000121510						9	4	2	13	8	3	0	0	0	0	0		
ENSMUST00000121511						3	1	10	9	12	6	0	0	0	0	0		
ENSMUST00000121512						4	5	6	0	4	3	0	1	4	3	0		
ENSMUST00000121513						2	2	1	2	2	4	0	0	0	1	0		
ENSMUST00000121514	ENSMUSG00000022475	15	97792664	97844502	-1	6	2	5	21	3	2	70	0	4	0	66	E9PX62	
ENSMUST00000121515						5	7	4	5	10	2	0	0	0	1	0		
ENSMUST00000121516						4	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000121517						4	0	3	1	1	2	0	1	0	0	0		
ENSMUST00000121518						49	41	98	52	34	23	1	5	7	1	19		
ENSMUST00000121519						10	8	3	5	10	7	0	0	0	0	0		
ENSMUST00000121520	ENSMUSG00000031310	X	101404384	101420849	-1	0	0	2	32	10	3	102	239	167	0	133	B1AXS7	
ENSMUST00000121521	ENSMUSG00000035293	12	51348061	51376986	1	0	0	0	0	0	0	12	0	0	0	0	E9Q7E5	
ENSMUST00000121522						1	2	6	11	3	2	0	0	0	0	0		
ENSMUST00000121523						7	13	17	7	10	4	1	1	0	0	1		
ENSMUST00000121524						2	3	9	4	7	1	0	0	0	0	0		
ENSMUST00000121525						2	3	12	16	0	2	19	66	17	21	15		
ENSMUST00000121526						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000121527						75	68	106	94	79	38	5	2	1	0	8		
ENSMUST00000121528						1	0	2	2	1	2	0	0	0	0	0		
ENSMUST00000121529	ENSMUSG00000004070	16	4726361	4766742	1	0	4	0	0	4	1	102	65	143	177	24	D3YX62	
ENSMUST00000121530						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000121532	ENSMUSG00000060538	7	126886171	126922917	-1	0	0	0	0	0	0	251	416	194	350	113		Q9D123
ENSMUST00000121533	ENSMUSG00000032666	1	151852403	152090125	-1	0	0	2	3	1	0	6	11	5	3	1	A0A0A0MQF7	
ENSMUST00000121534	ENSMUSG00000026240	1	86582904	86609375	1	61	57	142	69	66	29	7	27	14	0	17		Q8BV13
ENSMUST00000121535						0	1	19	2	3	2	0	0	0	0	0		
ENSMUST00000121536						3	0	5	0	2	0	0	0	0	0	0		
ENSMUST00000121537						0	0	33	0	1	3	0	1	1	0	1		
ENSMUST00000121538						6	6	28	10	3	1	1	0	0	0	1		
ENSMUST00000121539						11	7	7	22	11	0	1	1	3	0	0		
ENSMUST00000121540						1	2	1	1	3	0	1	0	0	0	0		
ENSMUST00000121541						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121542	ENSMUSG00000073436	17	24888486	24895087	-1	0	0	0	0	0	0	16	6	10	14	0		Q56A04
ENSMUST00000121543						11	7	9	4	10	6	0	0	0	0	0		
ENSMUST00000121544						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121545						5	0	19	9	13	0	0	0	0	0	19		
ENSMUST00000121546						3	2	5	6	7	5	0	1	0	1	0		
ENSMUST00000121547						4	1	2	2	7	2	0	1	0	3	0		
ENSMUST00000121548						6	0	5	5	5	3	0	0	0	0	0		
ENSMUST00000121549						6	7	11	8	19	9	0	0	0	0	0		
ENSMUST00000121550						10	2	16	5	9	2	0	0	0	0	0		
ENSMUST00000121551						1	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000121552						3345	4063	5857	2777	3999	1787	26	261	92	52	88		
ENSMUST00000121554	ENSMUSG00000022757	16	56690332	56717450	-1	0	0	0	6	0	0	0	0	0	0	0	B8JJG6	
ENSMUST00000121555						3	0	2	1	0	0	4	0	1	5	0		
ENSMUST00000121556						4	1	3	2	9	4	0	0	0	0	0		
ENSMUST00000121557						7	2	3	3	9	2	0	0	0	0	0		
ENSMUST00000121558						8	5	9	5	4	2	0	0	0	0	0		
ENSMUST00000121559						2	2	24	6	4	3	0	0	1	0	1		
ENSMUST00000121560	ENSMUSG00000053111	7	133776861	133881532	1	0	0	0	0	1	0	0	0	0	0	0	D3YW22	
ENSMUST00000121561						2	2	2	2	3	1	0	0	0	0	0		
ENSMUST00000121562						11	13	17	16	6	5	0	0	0	0	0		
ENSMUST00000121563						6	0	5	2	2	2	0	4	4	11	0		
ENSMUST00000121564	ENSMUSG00000050471	9	35216965	35267805	-1	0	0	0	0	0	0	0	14	0	0	0		Q8C569
ENSMUST00000121565	ENSMUSG00000081044	X	93968659	93975470	1	0	15	0	6	0	11	0	0	0	0	0	B1ASY6	
ENSMUST00000121566	ENSMUSG00000037443	4	134129858	134187112	-1	22	0	60	0	0	0	0	45	52	10	8	A2A9K3	
ENSMUST00000121567						22	16	66	26	42	15	0	0	0	0	0		
ENSMUST00000121568						1	0	3	1	3	0	4	4	3	2	9		
ENSMUST00000121569						0	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000121570						8	9	11	9	11	6	0	0	0	0	0		
ENSMUST00000121571	ENSMUSG00000070687	4	136423524	136444398	1	6	0	0	8	16	2	0	0	0	0	0		Q61224
ENSMUST00000121572						7	5	6	0	3	1	0	0	0	0	0		
ENSMUST00000121573	ENSMUSG00000015882	5	45697181	45857615	-1	0	6	28	13	5	1	0	0	4	0	0	E9PXY2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121574						0	0	0	0	0	0	7	28	0	0	0		
ENSMUST00000121575						5	4	14	10	12	4	0	2	0	0	1		
ENSMUST00000121577						4	3	8	8	3	3	0	0	1	0	1		
ENSMUST00000121578						2	8	19	5	2	4	0	0	0	0	0		
ENSMUST00000121579						1	6	7	8	3	0	0	0	0	0	0		
ENSMUST00000121581						0	0	15	15	4	10	0	0	0	0	0		
ENSMUST00000121582						58	44	111	34	63	34	0	0	2	1	0		
ENSMUST00000121583	ENSMUSG00000034690	7	6045161	6105149	1	4	3	0	15	3	7	0	0	0	0	0		Q3TKR3
ENSMUST00000121584	ENSMUSG00000014039	16	97791467	97851850	-1	0	0	0	41	28	0	96	241	193	0	135	E9Q6A1	
ENSMUST00000121585						0	4	7	3	6	0	76	926	255	254	119		
ENSMUST00000121586	ENSMUSG00000041975	2	70964561	71055583	-1	1	0	0	0	0	0	0	0	0	0	6		A2AUU0
ENSMUST00000121587						9	0	15	3	5	2	0	0	0	0	0		
ENSMUST00000121588						5	4	4	0	2	3	0	0	0	0	0		
ENSMUST00000121589						7	6	13	7	5	0	0	0	0	1	0		
ENSMUST00000121590						4	0	0	13	1	0	0	0	0	0	0		
ENSMUST00000121591	ENSMUSG00000020389	11	52004221	52089784	1	0	0	0	6	0	0	0	0	3	5	0		Q8BLF2
ENSMUST00000121592						1	2	2	2	1	2	0	0	0	0	0		
ENSMUST00000121593						0	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000121594						4	4	8	10	6	1	248	1084	336	130	158		
ENSMUST00000121595						4	4	6	3	2	2	0	1	0	0	0		
ENSMUST00000121596						9	6	9	17	8	2	1	2	1	3	3		
ENSMUST00000121597						5	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000121598	ENSMUSG00000032079	9	46268633	46271919	1	25	17	12	37	9	7	0	0	0	0	0		Q8C7G5
ENSMUST00000121599						5	7	36	9	8	3	0	0	0	0	0		
ENSMUST00000121600						0	1	0	8	0	1	10	0	0	0	1		
ENSMUST00000121601						1	0	3	3	2	3	0	0	0	0	0		
ENSMUST00000121602						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000121603						1	1	0	0	2	0	0	0	1	2	2		
ENSMUST00000121604						2	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000121605						0	3	7	3	0	3	0	0	0	0	0		
ENSMUST00000121606						1	3	3	6	3	1	0	0	0	0	0		
ENSMUST00000121607						6	8	4	7	8	4	0	0	0	0	0		
ENSMUST00000121608	ENSMUSG00000083193	12	111159850	111184491	-1	7	2	8	3	8	11	6	12	6	3	3	D3Z642	
ENSMUST00000121609						2	0	4	3	2	2	0	0	0	1	0		
ENSMUST00000121610						1	4	4	6	7	1	0	0	0	0	0		
ENSMUST00000121611						1	0	1	1	2	1	0	3	0	0	0		
ENSMUST00000121612	ENSMUSG00000060538	7	126886171	126922917	-1	2	0	2	1	0	0	0	0	0	0	0	D3Z6H6	
ENSMUST00000121613						1	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000121614						3	5	3	4	5	4	0	0	0	0	0		
ENSMUST00000121615						7	8	12	197	4	2	0	0	0	0	0		
ENSMUST00000121616	ENSMUSG00000030795	7	127967457	127985701	1	0	0	0	0	0	0	204	706	518	92	513	Q91VQ2	
ENSMUST00000121617						1	2	19	2	6	1	0	0	0	3	0		
ENSMUST00000121618	ENSMUSG00000045312	13	94057796	94195409	1	13	6	32	27	16	3	72	41	28	17	86		Q8BGA2
ENSMUST00000121619						1	0	0	0	3	1	0	0	0	0	0		
ENSMUST00000121620						3	5	18	12	5	3	11	17	9	4	16		
ENSMUST00000121621						6	1	3	2	6	7	1	0	0	1	0		
ENSMUST00000121622	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	72	0	41	3	0		Q91VU6
ENSMUST00000121623	ENSMUSG00000055553	8	70508272	70527956	-1	0	0	0	0	0	0	0	0	0	62	0	E9QNP0	
ENSMUST00000121624						1	2	1	2	3	4	0	0	0	0	0		
ENSMUST00000121625	ENSMUSG00000061947	12	103614786	103631444	-1	0	0	0	0	0	0	0	0	0	2	0		Q8R121
ENSMUST00000121626						2	2	3	3	5	1	0	0	0	0	0		
ENSMUST00000121627						3	2	9	2	0	2	0	29	0	0	0		
ENSMUST00000121628						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000121629	ENSMUSG00000020061	10	88518279	88605152	-1	10	0	0	8	21	0	0	0	0	0	0	Q6P6L5	
ENSMUST00000121630						4	2	10	3	3	3	0	0	1	0	0		
ENSMUST00000121631						1	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000121633						5	7	4	3	3	4	0	0	0	0	0		
ENSMUST00000121634	ENSMUSG00000032064	9	50662752	50739517	-1	2	3	3	44	8	0	0	0	0	0	0		Q80Y83
ENSMUST00000121635						1	1	0	1	3	2	44	487	0	38	44		
ENSMUST00000121636						4	11	3	22	5	8	0	0	0	0	0		
ENSMUST00000121637						2	0	2	4	5	0	0	0	0	5	3		
ENSMUST00000121638	ENSMUSG00000020415	11	43420250	43426251	-1	0	0	0	0	0	0	0	0	0	0	0		Q9CQJ7
ENSMUST00000121639						3	2	2	1	4	0	0	2	0	0	0		
ENSMUST00000121640						1	4	0	1	1	1	0	0	0	0	0		
ENSMUST00000121641	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4S7	
ENSMUST00000121642						1	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000121643						0	0	4	1	3	2	0	0	0	1	0		
ENSMUST00000121644						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000121645	ENSMUSG00000039236	7	78913424	78920396	1	3	3	12	3	4	1	7	34	7	0	5		Q9JL16
ENSMUST00000121646	ENSMUSG00000019817	10	13060504	13131694	1	19	8	53	16	22	10	0	0	0	0	3	Q9JLQ4	
ENSMUST00000121647						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121648						2	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000121649						0	2	2	1	3	0	0	0	0	0	0		
ENSMUST00000121650						2	2	0	2	9	4	0	0	0	0	0		
ENSMUST00000121651	ENSMUSG00000042198	4	3938888	3951046	1	0	0	0	4	0	0	0	17	0	27	0		Q8K2Q5
ENSMUST00000121652	ENSMUSG00000049686	5	123015074	123030456	1	9	5	14	28	15	3	619	1546	473	76	246	A3KCG1	Q8BWG9
ENSMUST00000121653						4	2	10	2	6	1	0	0	0	0	0		
ENSMUST00000121654						0	2	3	0	6	4	0	0	0	0	0		
ENSMUST00000121655						1	5	4	9	4	3	2	0	7	0	7		
ENSMUST00000121656	ENSMUSG00000030116	6	122505845	122529290	1	0	0	0	0	0	2	0	0	0	0	0	D3YW93	
ENSMUST00000121657						10	5	14	76	6	11	0	2	0	0	0		
ENSMUST00000121658						29	15	10	24	16	23	47189	46050	31356	34094	19102		
ENSMUST00000121659						91	59	172	804	129	97	2	9	9	0	4		
ENSMUST00000121660						1	0	3	0	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121661	ENSMUSG00000037822	5	65446844	65537184	-1	2	2	4	40	3	4	4	2	8	32	5		Q91VT8
ENSMUST00000121662						4	3	6	0	2	2	0	0	0	0	0		
ENSMUST00000121663						1	2	2	2	2	0	0	0	0	0	0		
ENSMUST00000121664						3	1	6	30	6	1	0	0	0	0	0		
ENSMUST00000121665						4	2	3	2	4	1	0	0	0	0	0		
ENSMUST00000121666						4	3	4	2	3	1	0	0	0	0	0		
ENSMUST00000121667						9	7	10	32	10	0	0	0	71	4	13		
ENSMUST00000121668						5	4	1	6	7	2	0	0	0	0	0		
ENSMUST00000121669						7	3	7	2	3	0	0	1	4	3	7		
ENSMUST00000121670						2	5	2	10	2	5	0	0	0	0	0		
ENSMUST00000121671	ENSMUSG00000023973	17	46735705	46752214	-1	5	0	3	32	11	3	4	52	17	16	8	B0V2V1	
ENSMUST00000121672						3	0	8	2	3	3	0	0	0	0	0		
ENSMUST00000121673	ENSMUSG00000047866	8	86624043	86723873	1	0	1	0	0	10	0	11	686	0	124	24	Q8BK80	
ENSMUST00000121674	ENSMUSG00000038425	18	70508680	70530620	-1	1	0	4	20	0	0	0	0	15	0	0	E9QJU6	
ENSMUST00000121675						34	16	30	14	19	8	0	0	0	1	0		
ENSMUST00000121676	ENSMUSG00000025934	1	21240589	21265661	1	5	3	4	2	9	1	0	0	0	6	0		P30115
ENSMUST00000121677	ENSMUSG00000032307	9	55148854	55207529	1	0	0	12	0	0	3	0	0	62	0	25	D3Z647	
ENSMUST00000121678						1	1	3	0	2	1	0	2	0	0	0		
ENSMUST00000121679						0	0	0	7	0	2	0	0	0	0	0		
ENSMUST00000121680						0	1	0	2	3	0	0	0	0	0	0		
ENSMUST00000121681						1	3	8	2	2	3	0	0	0	0	1		
ENSMUST00000121682						3	2	1	1	1	3	0	0	0	0	0		
ENSMUST00000121683						5	6	11	2	4	2	0	1	0	0	1		
ENSMUST00000121684						7	3	5	7	7	5	0	0	0	0	0		
ENSMUST00000121685	ENSMUSG00000003923	10	71225464	71238280	-1	5	4	7	60	8	4	0	4	0	0	4		
ENSMUST00000121686						3	2	5	28	5	0	0	0	0	0	0		
ENSMUST00000121687						0	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000121688						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000121689						1	0	0	0	1	0	1	2	1	2	1		
ENSMUST00000121690	ENSMUSG00000029228	5	74592447	74702912	-1	0	0	0	0	3	0	0	0	0	0	0	E9Q6Q0	
ENSMUST00000121691						24	9	18	18	25	10	4	3	5	19	6		
ENSMUST00000121692						2	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000121693	ENSMUSG00000024511	18	69979131	70141605	-1	37	29	51	21	32	15	7	13	3	0	7	Q549X4	Q99P58
ENSMUST00000121694	ENSMUSG00000081225	4	96099318	96141152	-1	7	12	7	7	13	0	0	0	0	0	0	G3UZ89	
ENSMUST00000121695						5	7	14	4	11	6	9	28	8	4	4		
ENSMUST00000121696						68	40	716	220	64	44	0	0	4	3	5		
ENSMUST00000121697						0	2	14	1	4	3	0	1	0	0	0		
ENSMUST00000121698						2	1	2	2	8	0	0	0	0	0	0		
ENSMUST00000121699						0	4	1	5	4	0	0	0	0	0	0		
ENSMUST00000121700						3	5	1	4	2	2	0	0	0	0	0		
ENSMUST00000121701						2	0	3	2	0	0	0	2	1	0	1		
ENSMUST00000121702						3	1	0	2	0	1	0	0	0	0	0		
ENSMUST00000121703	ENSMUSG00000022604	16	55899888	55934855	-1	0	0	0	0	0	0	2	2	1	4	2	Q8BJR7	
ENSMUST00000121704						17	11	13	7	9	5	0	0	1	0	0		
ENSMUST00000121705	ENSMUSG00000030805	7	127824294	127849019	1	9	2	4	3	2	3	26	253	60	107	152		P70452
ENSMUST00000121706						9	6	32	42	7	5	0	0	1	0	0		
ENSMUST00000121707	ENSMUSG00000037605	5	81020138	81825133	1	6	0	14	51	6	0	0	0	0	0	0	D3YTW7	
ENSMUST00000121708						1	2	3	4	1	1	0	0	0	0	0		
ENSMUST00000121709						1	0	4	2	4	0	1	6	2	0	13		
ENSMUST00000121710						3	4	10	6	12	4	0	0	0	0	0		
ENSMUST00000121711						1	1	0	0	0	0	0	2	1	0	0		
ENSMUST00000121712						1	2	0	3	4	1	0	0	0	0	0		
ENSMUST00000121713						11	5	21	83	15	3	4	0	9	5	4		
ENSMUST00000121714						2	2	31	2	1	0	0	0	0	0	0		
ENSMUST00000121715	ENSMUSG00000030650	7	118597297	118675086	1	8	2	0	21	0	5	0	0	0	0	0		Q32NZ6
ENSMUST00000121716	ENSMUSG00000021062	12	76797960	76822908	-1	2	0	5	1	2	0	1	0	0	0	0	D3YTZ8	
ENSMUST00000121717	ENSMUSG00000074771	2	136501910	136562091	1	12	11	13	0	0	5	0	0	0	0	0		Q9D2J7
ENSMUST00000121718	ENSMUSG00000000530	15	101128522	101145336	1	0	0	0	0	0	0	0	3	0	0	11		Q61288
ENSMUST00000121719						4	3	13	5	4	2	1	5	0	10	0		
ENSMUST00000121720	ENSMUSG00000082229	X	103184176	103186640	-1	8	5	2	6	8	1	4	33	5	5	10		P51860
ENSMUST00000121721						1	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000121722						9	10	12	117	11	8	7	0	4	0	7		
ENSMUST00000121723	ENSMUSG00000024163	17	24892153	24936977	-1	4	7	0	0	4	12	0	45	0	81	0	E9Q6E0	
ENSMUST00000121724						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000121725	ENSMUSG00000058624	19	21391307	21473445	-1	2	0	7	0	4	0	2405	38	6370	277	3151	D3YU09	
ENSMUST00000121726						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000121727						6	2	2	2	9	2	0	0	0	0	0		
ENSMUST00000121728						11	12	8	0	0	2	0	0	2	0	3		
ENSMUST00000121729						9	2	4	3	1	0	0	0	0	0	0		
ENSMUST00000121730						5	2	9	0	3	3	1	0	1	2	6		
ENSMUST00000121731	ENSMUSG00000059430	6	83512905	83536265	-1	2	3	0	3	0	0	0	2	0	0	0	Q3UJ36	P63268
ENSMUST00000121732						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121733	ENSMUSG00000021223	12	83763634	83792382	1	27	0	70	164	0	0	0	1	0	0	0	B7ZN28	
ENSMUST00000121734						1	4	9	2	1	4	0	0	0	0	0		
ENSMUST00000121735						1	2	2	6	1	1	112	113	75	12	64		
ENSMUST00000121736	ENSMUSG00000039753	5	43744615	43821638	-1	0	0	0	0	0	2	270	3094	1128	391	0		Q8C2S5
ENSMUST00000121737						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121738	ENSMUSG00000001323	11	74906359	74925948	-1	0	0	0	47	5	0	0	44	0	27	30		Q9QZX7
ENSMUST00000121739	ENSMUSG00000029475	5	122870665	122989823	-1	6	3	0	0	0	10	0	0	0	0	0	D3YVU7	
ENSMUST00000121740						7	3	6	9	5	1	0	0	0	0	0		
ENSMUST00000121741						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121742						3	5	1	2	2	0	1	1	2	10	0		
ENSMUST00000121743	ENSMUSG00000019734	7	3665790	3677553	-1	0	0	3	4	0	3	25	321	108	30	250	D3YWB3	
ENSMUST00000121744	ENSMUSG00000030650	7	118597297	118675086	1	3	2	0	0	17	0	0	0	0	0	0		Q32NZ6

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121745						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000121746	ENSMUSG00000041609	5	115648175	115731621	-1	0	0	0	0	0	10	0	68	0	8	9	D3YTR9	
ENSMUST00000121747						0	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000121748	ENSMUSG00000031027	7	109279223	109439081	-1	8	0	20	66	9	2	0	0	0	0	0		Q924X7
ENSMUST00000121749						6	3	2	23	2	1	0	0	0	0	0		
ENSMUST00000121750	ENSMUSG00000065979	16	11803721	11909445	-1	10	8	14	13	16	5	20	0	1	26	6		Q8BFS6
ENSMUST00000121751						2	3	8	19	4	2	0	1	1	0	1		
ENSMUST00000121752						6	1	0	1	5	1	0	13	13	33	17		
ENSMUST00000121753						0	0	0	5	1	0	0	0	0	1	0		
ENSMUST00000121754						2	1	3	11	5	3	0	0	0	2	0		
ENSMUST00000121755						2	0	6	0	2	0	0	0	2	1	6		
ENSMUST00000121756						4	3	7	7	5	3	0	0	0	1	0		
ENSMUST00000121757						10	2	31	48	18	8	0	7	4	1	5		
ENSMUST00000121758	ENSMUSG00000031075	7	144588549	144751974	-1	0	15	0	0	0	16	0	0	1	0	9	A0A0A0MQF2	
ENSMUST00000121759	ENSMUSG00000022973	16	90936092	91011308	-1	0	0	47	43	0	0	684	1568	1230	91	569	D3Z656	
ENSMUST00000121760						1	1	0	0	0	2	4	8	3	2	2		
ENSMUST00000121761						7	5	12	10	9	2	0	0	0	0	0		
ENSMUST00000121764						2	2	4	1	4	1	0	0	1	0	0		
ENSMUST00000121765						71	52	260	87	88	36	0	6	6	0	9		
ENSMUST00000121766	ENSMUSG00000019817	10	13060504	13131694	1	11	10	71	65	28	0	2	0	1	0	0	Q3UQW2	
ENSMUST00000121767						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000121768						5	2	5	4	0	3	2	7	6	14	7		
ENSMUST00000121769						2	0	1	24	7	2	0	0	0	0	0		
ENSMUST00000121770	ENSMUSG00000056880	9	115909455	116076176	1	0	0	0	0	0	0	0	0	0	0	0	E9QP13	
ENSMUST00000121771						0	6	14	154	9	16	0	0	0	0	0		
ENSMUST00000121772						3795	4918	5538	2985	4764	2451	49	310	144	74	209		
ENSMUST00000121773						0	0	0	0	0	2	12	47	7	8	20		
ENSMUST00000121774	ENSMUSG00000044252	18	12755314	12941841	-1	7	3	0	60	8	3	0	0	3	0	0		Q91XL9
ENSMUST00000121775						1	3	1	4	3	1	0	0	0	0	0		
ENSMUST00000121776						2	3	1	1	0	2	0	1	0	0	0		
ENSMUST00000121777	ENSMUSG00000053091	7	66689889	66717256	1	2	0	0	0	0	0	56	162	30	0	0		Q3U1D0
ENSMUST00000121778	ENSMUSG00000027673	3	32736990	32751566	1	0	0	0	0	0	0	115	187	119	657	77	D3Z6W9	
ENSMUST00000121779						1	1	2	2	1	1	212	801	248	1450	181		
ENSMUST00000121780						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000121781						6	4	19	4	3	1	0	2	0	5	3		
ENSMUST00000121782	ENSMUSG00000034177	11	87662722	87735539	1	6	0	18	12	13	5	6	0	3	0	0	E9PWJ5	
ENSMUST00000121783	ENSMUSG00000015341	8	23241353	23257074	-1	12	0	15	243	35	19	11	90	50	105	52		Q91W53
ENSMUST00000121784						10	4	61	8	15	6	0	0	1	6	2		
ENSMUST00000121785	ENSMUSG00000058056	8	61513246	61902690	-1	0	0	19	16	0	9	6	6	8	0	4		Q9ET54
ENSMUST00000121786						137	144	131	125	189	112	0	9	3	8	6		
ENSMUST00000121787	ENSMUSG00000024163	17	24892153	24936977	-1	0	0	50	0	0	0	359	639	506	1	496	E9Q6B6	
ENSMUST00000121788						5	5	9	3	11	2	1	0	0	2	1		
ENSMUST00000121789	ENSMUSG00000059602	10	86055125	86498896	-1	25	18	27	30	24	14	0	1	0	0	0	D3Z620	
ENSMUST00000121790						1	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000121791	ENSMUSG00000002320	14	55635965	55643806	-1	0	3	0	0	0	0	120	100	0	0	0		Q9DBU0
ENSMUST00000121792						8	1	0	3	3	7	0	3	0	0	0		
ENSMUST00000121793	ENSMUSG00000055895	19	11647279	11660559	-1	5	0	26	3	5	0	0	0	0	0	0		Q4FZG8
ENSMUST00000121794						5	4	0	0	2	0	0	0	0	0	0		
ENSMUST00000121795						0	1	4	1	5	0	0	0	0	0	0		
ENSMUST00000121796	ENSMUSG00000028266	3	144188530	144205220	-1	0	0	0	0	0	0	964	1493	288	145	139	Q542S1	P61969
ENSMUST00000121797	ENSMUSG00000037600	4	133518963	133530790	1	12	11	20	15	23	4	0	0	0	3	0	A8Y5H9	
ENSMUST00000121798						0	2	0	0	0	3	0	10	0	0	3		
ENSMUST00000121799	ENSMUSG00000049807	11	97415533	97502402	1	26	16	98	637	30	24	836	418	936	11	798	B1AQY2	
ENSMUST00000121800						4	0	3	0	0	0	0	1	0	0	0		
ENSMUST00000121801						1	5	23	88	8	0	1	18	5	8	6		
ENSMUST00000121802	ENSMUSG00000031543	8	22974844	23150497	1	0	0	7	153	0	0	0	0	0	0	0		
ENSMUST00000121803	ENSMUSG00000022656	16	46387706	46498525	-1	0	0	0	0	0	0	0	0	0	0	0	D3YWA3	
ENSMUST00000121805	ENSMUSG00000024501	18	43320979	43438286	-1	42	32	127	179	36	30	3	5	2	20	40	E9PWE8	
ENSMUST00000121806						3	5	9	7	14	4	0	0	0	0	0		
ENSMUST00000121807						10	9	22	19	16	4	0	0	1	0	1		
ENSMUST00000121808	ENSMUSG00000044252	18	12755314	12941841	-1	0	0	10	157	0	0	0	0	0	0	0		Q91XL9
ENSMUST00000121809	ENSMUSG00000040732	16	95359169	95586593	-1	0	0	0	0	0	0	6	0	33	4	25	I1E4Y2	
ENSMUST00000121810						0	0	2	2	1	0	0	0	0	0	0		
ENSMUST00000121811						6	3	10	6	4	2	0	0	0	0	0		
ENSMUST00000121813	ENSMUSG00000034211	5	129715497	129722556	1	0	0	1	16	7	1	0	46	0	57	51		Q9CQE3
ENSMUST00000121814						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000121815						8	5	3	2	12	6	1	4	2	1	4		
ENSMUST00000121816						13	0	19	11	13	0	0	0	0	0	0		
ENSMUST00000121817						3	1	4	4	3	1	0	0	0	0	0		
ENSMUST00000121818						4	4	1	5	5	5	0	0	0	0	0		
ENSMUST00000121819						1	2	2	3	6	5	0	0	1	1	3		
ENSMUST00000121820	ENSMUSG00000058297	10	60106219	60135198	1	36	17	81	71	54	34	7	3	0	3	20		Q9ER58
ENSMUST00000121821						0	0	0	13	5	3	0	0	0	9	9		
ENSMUST00000121822						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121823						8	4	48	16	8	11	1	0	0	0	1		
ENSMUST00000121824						1	2	1	0	0	1	0	0	0	0	0		
ENSMUST00000121825	ENSMUSG00000053030	5	77205107	77211471	-1	0	0	4	3	4	4	0	0	0	0	0	D3Z3X9	
ENSMUST00000121826	ENSMUSG00000028152	3	138742195	138907905	1	1	2	8	0	6	3	31	14	31	0	23	D3Z641	
ENSMUST00000121827						3	1	4	6	1	6	2	0	0	2	0		
ENSMUST00000121828						1	5	11	3	8	1	0	0	0	1	1		
ENSMUST00000121829	ENSMUSG00000040249	10	127538161	127621148	-1	6	0	2	27	5	2	0	1	3	0	0	Q3U5J2	
ENSMUST00000121830						11	9	85	24	10	9	0	1	0	0	1		
ENSMUST00000121831						0	0	0	0	0	0	0	7	0	0	6		
ENSMUST00000121832						1	0	3	0	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121833						0	1	1	0	0	1	0	0	0	0	0		
ENSMUST00000121834	ENSMUSG00000027849	3	103575231	103645569	1	0	0	0	106	14	8	0	0	0	0	0		Q9R0N8
ENSMUST00000121835						1	1	5	2	0	0	0	0	0	0	0		
ENSMUST00000121836						14	15	17	17	7	0	0	0	0	0	0		
ENSMUST00000121837	ENSMUSG00000044393	18	20558074	20604521	1	0	0	0	0	0	0	1	0	0	0	1	Q8VCE3	
ENSMUST00000121838	ENSMUSG00000031489	8	27225776	27229588	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UP63	P25962
ENSMUST00000121839	ENSMUSG00000066129	7	139894696	139941537	1	0	0	14	59	16	2	0	0	0	0	0	D3Z3X0	
ENSMUST00000121840	ENSMUSG00000035011	10	81135220	81152995	1	6	8	9	20	11	0	9	12	10	0	9	D3Z4C3	
ENSMUST00000121841						0	4	2	5	4	0	0	0	0	0	0		
ENSMUST00000121842						1	4	1	3	6	3	0	0	0	0	0		
ENSMUST00000121843						5	13	5	2	17	0	0	3	0	0	0		
ENSMUST00000121844						1	1	5	1	1	0	0	0	0	0	0		
ENSMUST00000121845						0	3	2	1	2	2	0	0	0	0	0		
ENSMUST00000121847						24	4	91	13	6	4	0	0	0	0	0		
ENSMUST00000121848	ENSMUSG00000089661	7	27179742	27181157	-1	0	0	0	2	0	0	0	0	0	0	0	G5E8V2	
ENSMUST00000121849						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121850						1	0	0	0	0	0	0	7	0	5	3		
ENSMUST00000121851	ENSMUSG00000036377	5	76656512	76873554	1	3	6	8	4	3	3	1	3	0	0	0	D3YTS2	
ENSMUST00000121852						2	1	0	3	1	0	0	0	0	0	1		
ENSMUST00000121853						8	8	14	8	7	4	2	3	5	0	0		
ENSMUST00000121854						2	4	11	13	9	1	0	0	0	0	0		
ENSMUST00000121855						9	10	6	22	13	2	0	0	0	0	0		
ENSMUST00000121856						1	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000121857						9	2	5	4	3	0	5	9	7	10	4		
ENSMUST00000121858						2	2	0	4	5	3	0	0	0	0	0		
ENSMUST00000121859						2	2	4	4	3	2	0	1	0	0	0		
ENSMUST00000121860						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000121861						6	3	2	31	5	3	0	4	0	0	0		
ENSMUST00000121862	ENSMUSG00000009248	7	142966822	142969264	-1	6	8	5	318	18	0	2	9	1	2	1	D3Z7Q6	
ENSMUST00000121863	ENSMUSG00000038181	5	24586741	24594556	1	17	18	50	227	0	8	908	973	692	82	541	Q3UU43	
ENSMUST00000121864						8	9	0	7	6	0	0	0	0	0	0		
ENSMUST00000121865						2	2	1	1	5	0	0	0	0	0	0		
ENSMUST00000121866						2	1	0	3	3	1	1	0	1	1	1		
ENSMUST00000121867						2	3	14	3	3	2	0	0	0	0	0		
ENSMUST00000121868						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000121869	ENSMUSG00000064061	16	48924232	48994165	-1	7	7	8	189	7	4	0	26	22	0	6	E9QNZ2	
ENSMUST00000121870	ENSMUSG00000028657	4	122836242	122859175	1	8	3	9	30	9	4	13	39	32	14	72	B1B0P8	
ENSMUST00000121871	ENSMUSG00000035509	13	56522472	56537898	1	6	0	4	3	9	2	1	0	0	0	0	G3X9Y3	
ENSMUST00000121872	ENSMUSG00000061535	5	43515538	43618803	1	0	5	0	0	4	6	0	0	0	4	0	Q5BKS0	Q8BVD7
ENSMUST00000121873						7	3	14	9	10	1	0	0	0	0	0		
ENSMUST00000121874						11	6	14	12	8	4	0	0	0	0	0		
ENSMUST00000121875	ENSMUSG00000025885	18	74440936	74771493	1	16	17	67	5	21	11	0	0	0	0	4	G3X9Y9	
ENSMUST00000121876						12	11	17	2	0	7	1	24	0	0	2		
ENSMUST00000121877	ENSMUSG00000040302	5	3583978	3596585	-1	0	2	0	0	5	1	0	1	0	2	0	I1E4Y0	
ENSMUST00000121878						0	1	2	0	1	2	0	0	0	0	0		
ENSMUST00000121879						2	2	5	0	2	1	0	0	0	0	0		
ENSMUST00000121880	ENSMUSG00000048617	8	84946991	84956603	1	0	0	0	0	0	0	0	0	0	0	0		Q8QZY4
ENSMUST00000121881						0	0	4	4	0	0	0	0	0	0	0		
ENSMUST00000121882	ENSMUSG00000038930	7	80293229	80324454	-1	0	0	0	0	0	0	0	0	8	0	10		Q8BTU7
ENSMUST00000121883						0	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000121884						10	12	18	10	20	4	0	0	0	0	0		
ENSMUST00000121885						155	134	477	187	202	105	11	49	22	12	34		
ENSMUST00000121886	ENSMUSG00000060427	8	69610857	69625548	-1	3	9	8	7	3	2	165	930	272	203	291	Q3UTQ6	
ENSMUST00000121887	ENSMUSG00000021750	14	8296274	8318023	-1	54	0	54	72	54	18	0	0	0	0	0	Q78TU8	
ENSMUST00000121888	ENSMUSG00000044252	18	12755314	12941841	-1	0	0	0	0	0	0	0	23	0	0	0		Q91XL9
ENSMUST00000121889						4	7	33	17	11	4	0	0	0	0	0		
ENSMUST00000121890						3	2	3	1	1	0	0	0	0	1	0		
ENSMUST00000121891						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121892						2	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000121893						11	5	11	3	8	0	0	0	0	0	0		
ENSMUST00000121894						2	1	0	13	2	1	0	0	0	0	0		
ENSMUST00000121895						5	3	22	2	17	4	21	57	27	7	17		
ENSMUST00000121897						4	1	5	0	2	0	0	0	0	1	0		
ENSMUST00000121898						2	1	1	7	3	0	0	0	0	0	0		
ENSMUST00000121899						0	0	0	0	1	0	0	1	1	1	5		
ENSMUST00000121900	ENSMUSG00000082639	X	26200678	26231355	-1	8	11	1	14	6	1	0	0	0	0	0	B1B0R1	
ENSMUST00000121901						7	3	6	38	8	5	0	0	0	0	0		
ENSMUST00000121902	ENSMUSG00000052794	8	72443880	72461001	1	12	8	0	17	7	8	0	0	0	19	20	E9Q7C0	
ENSMUST00000121903	ENSMUSG00000047115	6	49367739	49390539	1	0	0	5	0	1	0	3	11	5	9	4		Q8C790
ENSMUST00000121904						1	1	0	0	4	2	0	0	0	0	0		
ENSMUST00000121905						4	2	4	0	3	0	0	0	0	0	0		
ENSMUST00000121906						0	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000121907						4	4	8	10	0	0	0	42	15	11	12		
ENSMUST00000121908						2	1	0	3	4	1	0	0	0	0	2		
ENSMUST00000121909						5	8	6	8	9	1	0	0	0	0	0		
ENSMUST00000121910						5	3	1	7	6	4	1	4	1	0	0		
ENSMUST00000121911	ENSMUSG00000026592	1	157099139	157108680	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z4U7	
ENSMUST00000121912	ENSMUSG00000074679	2	152518255	152521447	1	1	2	1	1	0	2	0	0	0	0	0	Q3V2L0	
ENSMUST00000121913						0	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000121914						4	2	5	4	4	1	0	0	0	0	0		
ENSMUST00000121915						6	14	3	8	13	3	0	0	6	0	20		
ENSMUST00000121916	ENSMUSG00000032081	9	46232933	46235636	-1	5	4	31	8	8	0	0	0	0	0	0	E9QP56	
ENSMUST00000121917						2	0	2	0	3	2	0	0	0	0	0		
ENSMUST00000121918						7	0	0	1	4	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000121919						0	0	0	0	2	0	1	0	3	0	2		
ENSMUST00000121920	ENSMUSG00000019710	3	87919506	87923672	1	0	0	0	0	0	0	31	159	34	323	24		Q9CQ06
ENSMUST00000121921						2	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000121922	ENSMUSG00000038695	7	44467980	44471662	1	0	0	0	0	2	0	0	0	4	0	0	D3YTZ7	
ENSMUST00000121923						3	2	4	4	2	1	0	0	0	0	0		
ENSMUST00000121924						6	4	16	126	14	2	12	34	30	10	16		
ENSMUST00000121925	ENSMUSG00000035506	16	33517328	33664135	1	6	0	8	67	2	2	0	0	0	0	0		Q8VI23
ENSMUST00000121926						1	2	2	2	2	3	0	0	0	0	0		
ENSMUST00000121927	ENSMUSG00000048490	16	76287400	76373827	-1	12	16	9	8	26	2	40	61	24	16	89		Q8CBD1
ENSMUST00000121928						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000121929						5	6	28	19	14	2	0	0	0	0	0		
ENSMUST00000121930	ENSMUSG00000008822	12	85272398	85288438	-1	2	0	11	3	9	8	0	0	0	0	0	E9QJT5	
ENSMUST00000121931	ENSMUSG00000068917	3	89164795	89176921	1	0	0	0	0	0	0	163	265	220	21	87	E9Q5Y1	
ENSMUST00000121932	ENSMUSG00000040428	7	45526330	45554229	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3Y7	
ENSMUST00000121933						6	3	5	3	4	0	4	45	4	17	9		
ENSMUST00000121934						2	3	5	1	5	1	5	0	0	7	0		
ENSMUST00000121935						1	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000121936						0	0	2	3	2	0	0	0	0	0	0		
ENSMUST00000121937	ENSMUSG00000002320	14	55635965	55643806	-1	0	0	0	0	0	0	54	0	0	0	0	D3Z6X7	
ENSMUST00000121938						2	0	4	0	2	3	0	0	0	0	0		
ENSMUST00000121939						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121940						1	2	1	5	2	2	0	0	0	0	0		
ENSMUST00000121941						1	2	13	2	0	3	0	1	0	0	1		
ENSMUST00000121942						0	14	54	23	0	7	0	0	0	19	8		
ENSMUST00000121943						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000121944						4	1	2	1	4	1	0	0	0	0	0		
ENSMUST00000121945						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000121946						3	5	10	4	10	4	0	0	1	0	0		
ENSMUST00000121947						1	1	1	1	0	1	0	0	0	0	0		
ENSMUST00000121948						1	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000121949	ENSMUSG00000031657	8	88137855	88172027	1	0	0	32	0	0	0	17	78	0	2	0	E9PWH6	
ENSMUST00000121950						0	0	9	0	0	4	31	235	128	26	41		
ENSMUST00000121951	ENSMUSG00000069094	3	19223108	19311322	-1	2	1	9	0	2	1	0	0	0	0	0	D3Z6W6	
ENSMUST00000121952	ENSMUSG00000020053	10	87858265	87937042	1	2	3	10	2	1	0	0	0	0	19	0	E9Q138	
ENSMUST00000121953	ENSMUSG00000043051	8	125054195	125261858	1	5	3	14	22	0	0	0	0	0	0	0		Q811T9
ENSMUST00000121954						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000121955	ENSMUSG00000022044	14	66344296	66361680	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4C2	
ENSMUST00000121956	ENSMUSG00000078879	2	176670522	176719085	1	1	0	0	2	1	0	8	3	1	4	2	A2BE19	
ENSMUST00000121957	ENSMUSG00000054435	6	48684549	48692060	1	0	0	0	0	0	0	0	11	0	3	3	D3Z7Q4	
ENSMUST00000121958	ENSMUSG00000081649	6	116540455	116541438	1	10	4	18	5	6	4	0	0	0	0	0	Q7TS32	
ENSMUST00000121959	ENSMUSG00000073433	17	26196226	26207786	-1	0	0	0	32	0	0	0	0	0	0	0	D3Z6W0	
ENSMUST00000121960						1	4	12	4	4	0	0	0	0	0	1		
ENSMUST00000121961						4	8	16	9	10	4	0	0	0	0	0		
ENSMUST00000121962						1	6	6	4	4	1	0	0	0	0	0		
ENSMUST00000121963	ENSMUSG00000032572	9	105989454	106096783	-1	56	37	65	100	66	32	83	159	138	10	263		A2AX52
ENSMUST00000121964	ENSMUSG00000029442	5	123252102	123327484	1	40	30	95	1160	80	38	1	14	0	0	4	E9Q743	
ENSMUST00000121965						0	0	0	0	0	0	10	182	17	0	9		
ENSMUST00000121966						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000121967						0	1	0	1	4	0	0	0	0	0	6		
ENSMUST00000121968						3	1	2	0	1	1	0	0	0	0	0		
ENSMUST00000121969						2	1	2	0	1	1	0	0	0	0	0		
ENSMUST00000121970						0	5	26	3	1	2	0	0	0	0	0		
ENSMUST00000121971						0	0	3	0	2	0	13	22	24	58	6		
ENSMUST00000121972	ENSMUSG00000031698	8	85324303	85386345	-1	15	0	14	16	11	0	0	4	1	0	2		Q3UIZ8
ENSMUST00000121973						49	77	44	141	99	119	0	1	0	0	3		
ENSMUST00000121974						4	0	1	2	4	1	0	0	0	0	0		
ENSMUST00000121975						0	1	0	0	1	2	0	0	0	0	0		
ENSMUST00000121976						0	2	7	5	3	1	0	0	0	0	0		
ENSMUST00000121977						4	5	27	10	12	5	0	0	0	0	0		
ENSMUST00000121978						2	3	4	2	1	0	0	0	0	0	0		
ENSMUST00000121979	ENSMUSG00000036403	5	76588698	76646466	1	0	0	0	6	6	8	8	0	116	1	16		Q6P5D4
ENSMUST00000121980						1	0	4	0	0	1	0	0	0	0	0		
ENSMUST00000121981						2	0	5	7	3	1	0	0	0	0	0		
ENSMUST00000121982						14	7	63	18	20	20	0	0	0	0	0		
ENSMUST00000121983	ENSMUSG00000031620	8	75448694	75984503	1	3	0	3	0	2	4	0	0	0	0	0	Q149I8	
ENSMUST00000121984						3	1	3	2	6	2	1	2	1	1	0		
ENSMUST00000121985						3	1	10	4	9	0	0	0	1	1	0		
ENSMUST00000121986						4	1	5	5	5	2	0	0	0	0	0		
ENSMUST00000121987	ENSMUSG00000051727	7	97451323	97459557	1	18	7	79	0	12	10	3	3	0	4	8	Q5EER8	
ENSMUST00000121989						7	7	6	1	3	4	0	0	0	0	0		
ENSMUST00000121990	ENSMUSG00000026452	1	134646677	134762593	1	41	29	119	166	76	26	2	0	1	0	0		
ENSMUST00000121991						0	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000121992	ENSMUSG00000031549	8	24531894	24576333	-1	13	0	4	22	20	4	0	0	0	2	2	A4UHF3	Q8R0V5
ENSMUST00000121993						2	2	3	3	2	0	0	0	0	0	0		
ENSMUST00000121994						3	0	1	4	5	1	0	0	0	0	0		
ENSMUST00000121995	ENSMUSG00000081512	17	34211312	34214459	-1	4	3	12	11	7	0	15	55	25	1	22	A6X8J8	
ENSMUST00000121996						7	6	5	1	9	1	0	0	0	0	0		
ENSMUST00000121997						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000121998						1	0	5	0	3	0	0	9	0	0	0		
ENSMUST00000121999						5	3	6	2	3	3	0	0	0	0	0		
ENSMUST00000122000						0	2	0	0	4	0	60	290	95	612	107		
ENSMUST00000122001	ENSMUSG00000041954	4	156026164	156028895	1	2	1	4	2	3	0	0	25	0	37	25	B1ASL6	
ENSMUST00000122003	ENSMUSG00000034724	5	96070333	96164171	-1	3	3	1	251	9	6	0	51	213	23	103		Q8VEG6
ENSMUST00000122004						1	1	1	1	1	0	1	2	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122005						3	1	19	4	5	2	0	0	0	0	0		
ENSMUST00000122006	ENSMUSG00000001240	11	101246028	101259546	1	0	2	5	3	0	0	0	0	0	1	1	A8XY18	
ENSMUST00000122007						3	3	19	32	3	7	0	0	0	0	0		
ENSMUST00000122008						0	3	3	3	0	0	0	3	0	0	2		
ENSMUST00000122009	ENSMUSG00000021848	14	48657679	48667644	-1	0	3	0	0	5	0	0	0	0	0	0	Q8VD35	
ENSMUST00000122010	ENSMUSG00000029466	5	122421693	122444912	1	11	8	18	63	13	4	0	0	0	0	0		Q9WVM3
ENSMUST00000122011						0	1	0	2	1	1	2	8	9	4	9		
ENSMUST00000122012						4	0	6	1	4	3	0	0	0	2	1		
ENSMUST00000122013						2	6	3	5	10	7	0	0	0	0	0		
ENSMUST00000122014	ENSMUSG00000022701	16	43889800	43964314	1	15	8	6	3	7	4	3	0	9	0	0	A9C445	
ENSMUST00000122015						3	3	4	3	4	1	0	0	0	0	0		
ENSMUST00000122016						3	3	5	1	2	0	0	0	0	0	0		
ENSMUST00000122017						0	1	0	1	2	1	0	0	0	0	0		
ENSMUST00000122018						10	10	4	5	9	6	0	0	0	0	0		
ENSMUST00000122019						8	1	3	3	3	6	0	0	0	0	0		
ENSMUST00000122020						3	4	3	10	6	6	0	0	0	0	0		
ENSMUST00000122021						12	23	39	29	11	7	0	0	3	0	3		
ENSMUST00000122022	ENSMUSG00000034055	X	102513975	102644246	-1	0	0	0	0	0	0	0	0	0	0	0	A2AI87	
ENSMUST00000122023						2	2	1	1	6	0	0	0	0	0	0		
ENSMUST00000122024						0	1	2	2	0	0	0	0	0	0	0		
ENSMUST00000122025	ENSMUSG00000082976	8	20900606	20902444	-1	0	0	0	0	0	0	0	2	0	0	0	E9Q8Z3	
ENSMUST00000122026	ENSMUSG00000029199	5	65391497	65410693	1	0	1	0	0	0	0	96	298	148	178	112	D3Z6I3	Q99M04
ENSMUST00000122027						4	0	10	2	2	1	0	0	0	0	1		
ENSMUST00000122029						5	0	16	4	6	2	0	1	0	0	3		
ENSMUST00000122030						4	6	6	3	4	0	0	0	0	0	0		
ENSMUST00000122031						37	46	501	71	61	15	0	0	0	0	0		
ENSMUST00000122032						0	3	1	2	5	0	3	1	1	0	0		
ENSMUST00000122033						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122034						2	1	2	4	2	1	0	0	0	0	0		
ENSMUST00000122035						10	10	31	21	19	3	0	1	0	0	1		
ENSMUST00000122036	ENSMUSG00000080990	17	37672025	37672990	1	7	5	3	12	7	5	0	0	0	0	0	Q7TRJ6	
ENSMUST00000122037	ENSMUSG00000037605	5	81020138	81825133	1	0	7	44	0	0	0	0	0	0	0	0	D3Z634	
ENSMUST00000122038	ENSMUSG00000026019	1	60069785	60098645	-1	0	0	0	0	0	0	18	86	32	181	9	Q4V9X1	Q9JJA4
ENSMUST00000122039						0	0	2	4	1	0	0	2	0	2	0		
ENSMUST00000122040	ENSMUSG00000054102	7	26535023	26575615	1	0	9	5	0	0	0	0	0	0	0	0	E9QKM4	
ENSMUST00000122041	ENSMUSG00000021699	13	108449948	109953461	1	0	0	0	0	8	0	13	38	10	16	11	A2RSH1	Q01063
ENSMUST00000122042						6	1	1	1	2	0	0	0	0	0	0		
ENSMUST00000122043						0	0	3	0	3	0	0	0	0	0	0		
ENSMUST00000122044	ENSMUSG00000022433	15	79417856	79443919	-1	19	13	74	153	17	13	210	383	303	40	246	Q3TYE1	
ENSMUST00000122045						2	2	3	3	4	0	0	0	0	0	0		
ENSMUST00000122046						1	11	1	0	1	1	0	0	0	0	0		
ENSMUST00000122047						2	1	6	6	4	1	0	0	0	0	0		
ENSMUST00000122048						8	5	27	8	10	5	0	0	0	0	0		
ENSMUST00000122049						3	2	3	35	4	1	0	0	0	0	0		
ENSMUST00000122050	ENSMUSG00000083616	X	120312748	120313095	-1	3	0	3	0	4	0	0	0	0	0	0	S4R1G7	
ENSMUST00000122051						0	2	8	5	4	0	32	59	6	11	14		
ENSMUST00000122052						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000122053	ENSMUSG00000034656	8	84388440	84640246	1	14	39	139	364	40	20	2	0	6	1	21	E9Q1R5	
ENSMUST00000122054	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	9	0	0	0	0	0	0	24	E9QK53	
ENSMUST00000122055	ENSMUSG00000044709	7	19564946	19573823	-1	1	0	0	0	0	0	0	38	0	0	6		Q9CWY4
ENSMUST00000122056						2	2	0	2	0	2	0	0	0	0	0		
ENSMUST00000122057						0	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000122058	ENSMUSG00000024186	17	26202951	26211324	1	0	0	0	0	0	0	0	1	0	0	0	E9QNN3	
ENSMUST00000122059	ENSMUSG00000039936	4	149649168	149702571	-1	0	18	17	0	44	0	661	1409	764	0	758	B0QZL5	
ENSMUST00000122061						4	2	16	4	6	4	1	2	0	4	1		
ENSMUST00000122062						2	1	3	2	1	0	0	0	0	0	0		
ENSMUST00000122063	ENSMUSG00000040040	14	57424062	57517936	1	0	0	0	11	0	0	18	35	23	27	9	G3X9Z7	
ENSMUST00000122064	ENSMUSG00000054690	3	137341067	137432185	1	7	8	8	0	6	6	0	0	0	0	0		Q9R0H2
ENSMUST00000122065	ENSMUSG00000032232	9	71626509	71771602	-1	15	9	47	128	21	8	0	0	0	3	14	B2RSU6	
ENSMUST00000122066	ENSMUSG00000045639	7	127607031	127615797	-1	0	0	0	20	21	0	0	0	0	0	10		Q6A085
ENSMUST00000122067	ENSMUSG00000020486	11	87568903	87590539	1	0	0	0	0	0	0	0	0	0	0	0		P28661
ENSMUST00000122068						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122069						8	1	11	6	8	2	0	0	0	0	0		
ENSMUST00000122070	ENSMUSG00000039804	2	165000357	165034867	-1	11	13	0	0	23	0	106	409	314	36	386	B7ZC24	
ENSMUST00000122071						6	0	4	0	0	4	0	0	0	0	0		
ENSMUST00000122072						3	1	1	0	2	3	0	0	0	0	0		
ENSMUST00000122073						3	4	9	4	7	1	0	2	0	0	0		
ENSMUST00000122074						3	7	20	1	4	5	0	0	0	0	0		
ENSMUST00000122075						4	6	8	6	4	0	0	0	0	0	0		
ENSMUST00000122076						3	2	7	20	7	5	1	0	1	0	1		
ENSMUST00000122077						0	0	0	1	0	3	0	0	0	0	0		
ENSMUST00000122078	ENSMUSG00000022798	16	38812205	38828749	-1	10	2	54	0	0	0	0	0	0	0	0	A6X8Z9	
ENSMUST00000122079	ENSMUSG00000024647	18	86711110	86718283	1	0	10	8	9	10	0	0	0	0	0	0		Q8BGU2
ENSMUST00000122080						1	1	2	2	1	2	0	0	0	0	0		
ENSMUST00000122081						2	2	0	4	4	1	0	0	0	0	0		
ENSMUST00000122082						3	3	0	3	5	3	1	0	0	0	0		
ENSMUST00000122083						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122084						2	2	6	0	4	0	0	0	0	0	0		
ENSMUST00000122085						9	4	1	2	7	2	1	0	0	0	0		
ENSMUST00000122086						1	2	4	8	5	0	0	0	0	0	0		
ENSMUST00000122087	ENSMUSG00000033543	9	70012550	70022866	1	2	4	15	4	6	0	14	17	45	9	16	D3Z793	
ENSMUST00000122088	ENSMUSG00000045087	9	21242912	21248443	-1	14	6	57	652	36	21	0	16	0	0	5		Q91X56
ENSMUST00000122089						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000122090						11	11	0	179	13	16	0	1	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122091	ENSMUSG00000032400	9	64137144	64173104	-1	5	7	10	6	5	4	20	37	23	11	24	G3X9Z0	
ENSMUST00000122092	ENSMUSG00000066150	4	62360727	62391769	1	8	10	36	9	24	14	5	25	10	8	4	A8Y5P1	
ENSMUST00000122093						2	4	16	4	4	0	0	0	0	0	0		
ENSMUST00000122094						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122095						14	7	16	15	12	2	0	0	0	0	0		
ENSMUST00000122096	ENSMUSG00000107906	6	116551141	116552502	1	34	24	27	57	29	17	0	0	0	0	0		
ENSMUST00000122097	ENSMUSG00000078881	2	176473278	176486783	-1	0	0	0	0	0	0	0	0	0	0	0	A2ART4	
ENSMUST00000122098						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122099						1	6	3	4	7	3	0	0	0	0	0		
ENSMUST00000122100	ENSMUSG00000020053	10	87858265	87937042	1	0	0	0	0	0	0	0	0	0	17	0	E9PU89	
ENSMUST00000122101	ENSMUSG00000055407	7	99267447	99337137	1	15	11	0	609	12	12	0	0	0	0	0	D3Z6W1	
ENSMUST00000122102						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000122103	ENSMUSG00000037098	17	25989036	26069409	-1	10	14	7	0	19	21	44	29	5	6	45		Q8CHD8
ENSMUST00000122104						1	2	4	0	0	1	0	0	0	0	0		
ENSMUST00000122105						1	5	4	1	2	2	0	0	0	0	0		
ENSMUST00000122106	ENSMUSG00000048731	17	26973217	27036378	1	0	0	1	0	2	1	0	0	0	0	0	D3Z3W4	
ENSMUST00000122107						1	3	4	1	0	4	0	0	0	0	0		
ENSMUST00000122108						7	9	11	6	9	1	0	0	0	0	0		
ENSMUST00000122109						2	1	18	1	3	1	0	0	0	0	0		
ENSMUST00000122110	ENSMUSG00000038429	6	124815019	124829484	-1	0	1	0	0	4	0	808	877	684	96	475	Q3U4W8	
ENSMUST00000122112						1	0	5	0	4	1	3	45	9	4	0		
ENSMUST00000122113	ENSMUSG00000005514	5	135670033	135735326	1	8	0	43	289	17	4	76	491	112	0	134	Q05DV1	
ENSMUST00000122114						2	0	1	7	4	0	0	0	0	0	0		
ENSMUST00000122115	ENSMUSG00000020545	12	36208345	36253398	-1	1	2	1	3	3	2	0	0	0	0	0	D3Z5A1	
ENSMUST00000122116	ENSMUSG00000047767	7	101289392	101302251	-1	0	0	0	0	0	2	0	129	0	23	0	D3Z653	
ENSMUST00000122117						2	1	7	3	4	1	0	0	0	0	0		
ENSMUST00000122119						0	0	1	0	3	0	47	177	66	352	55		
ENSMUST00000122120	ENSMUSG00000059187	6	96113154	96657198	1	15	15	0	0	12	8	0	0	0	0	0		Q7TPG8
ENSMUST00000122121						5	5	11	7	10	2	0	0	0	0	0		
ENSMUST00000122122						0	2	3	1	2	1	0	0	0	0	0		
ENSMUST00000122123						5	5	6	3	6	1	0	0	0	0	0		
ENSMUST00000122124						2	3	1	1	2	0	0	0	0	0	0		
ENSMUST00000122125						7	3	9	2	9	6	19	24	13	29	15		
ENSMUST00000122126						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122127	ENSMUSG00000044709	7	19564946	19573823	-1	0	2	4	1	4	0	16	15	21	0	34		Q9CWY4
ENSMUST00000122128	ENSMUSG00000027998	3	83055522	83072355	1	7	6	0	0	0	4	64	228	140	421	48	D3Z4V1	
ENSMUST00000122129	ENSMUSG00000028849	4	126232167	126256343	-1	0	9	22	0	0	0	1927	1818	1568	99	1350	A8Y5P4	
ENSMUST00000122131						1	2	3	1	3	3	0	1	0	0	2		
ENSMUST00000122132						1	4	4	11	5	3	1	2	0	0	1		
ENSMUST00000122133						1	1	1	0	3	0	2	13	1	2	0		
ENSMUST00000122134						4	2	19	9	4	2	0	0	0	0	0		
ENSMUST00000122135						1	2	1	1	1	2	0	0	0	2	0		
ENSMUST00000122136	ENSMUSG00000030981	7	133674270	133680061	-1	0	0	0	0	1	2	0	0	1	0	0	Q3KP74	
ENSMUST00000122137						2	1	2	3	7	2	0	0	0	1	0		
ENSMUST00000122138						7	7	4	4	10	9	0	3	0	0	0		
ENSMUST00000122139						0	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000122140						6	4	31	13	10	6	0	0	0	0	0		
ENSMUST00000122141						0	0	0	0	3	0	3	4	0	2	0		
ENSMUST00000122142						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122143	ENSMUSG00000038611	7	141228784	141262750	1	25	10	48	0	34	0	32	71	77	0	132		A6H619
ENSMUST00000122144						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000122145						0	1	2	2	3	1	0	0	0	1	0		
ENSMUST00000122147						0	1	0	1	1	1	0	1	0	1	3		
ENSMUST00000122148	ENSMUSG00000039741	11	120232947	120292296	1	57	0	275	0	0	0	13	5	6	0	13		Q3UHR0
ENSMUST00000122149						11	6	19	13	15	6	2	2	3	1	1		
ENSMUST00000122150						15	13	18	8	15	8	0	0	1	0	4		
ENSMUST00000122151						13	11	0	6	6	12	1732	12959	4020	12769	2536		
ENSMUST00000122152						7	4	10	4	4	3	0	1	0	1	7		
ENSMUST00000122153						2	5	12	1	4	2	0	0	0	0	0		
ENSMUST00000122154						4	6	4	8	4	4	0	0	0	0	0		
ENSMUST00000122155						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000122156	ENSMUSG00000056763	1	10037987	10136768	1	0	4	0	0	0	0	5	0	0	0	14		B2RX88
ENSMUST00000122157						3	6	9	7	4	3	1	0	1	0	0		
ENSMUST00000122158						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000122159						0	0	2	1	1	1	0	0	0	0	0		
ENSMUST00000122160	ENSMUSG00000041264	5	149184350	149215434	1	0	3	0	0	0	0	0	94	109	14	38	E9QLC6	
ENSMUST00000122161						0	0	3	0	4	0	0	0	2	0	0		
ENSMUST00000122162						14	3	8	0	11	7	27	141	15	90	43		
ENSMUST00000122163	ENSMUSG00000005936	17	28951950	28969549	1	8	5	0	90	0	12	0	10	98	12	77		Q8CDD8
ENSMUST00000122164						0	2	2	1	0	1	0	0	0	0	0		
ENSMUST00000122165						1	1	7	1	4	1	0	0	0	0	0		
ENSMUST00000122166						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122167						7	6	22	56	10	6	2	1	3	0	8		
ENSMUST00000122168	ENSMUSG00000071669	16	11322908	11755472	1	3	4	23	3	0	1	0	3	11	0	10	E9Q6P3	
ENSMUST00000122169						6	4	14	8	8	5	0	1	0	0	0		
ENSMUST00000122170						0	3	0	0	0	0	201	307	202	1033	153		
ENSMUST00000122171	ENSMUSG00000061576	5	26817203	27727505	1	9	8	4	132	10	5	0	0	0	0	0	E9PWX1	
ENSMUST00000122172						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000122173						7	2	10	7	6	4	5	20	16	0	16		
ENSMUST00000122175	ENSMUSG00000044252	18	12755314	12941841	-1	3	4	3	0	0	0	0	6	0	0	0	Q8K2D2	
ENSMUST00000122176						3	9	3	5	2	3	0	0	0	0	0		
ENSMUST00000122177						0	8	0	1	0	0	0	0	0	0	0		
ENSMUST00000122178						0	0	0	0	2	2	0	0	1	0	0		
ENSMUST00000122179						3	2	0	2	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122180						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122181	ENSMUSG00000029883	6	40920437	40940557	-1	1	3	0	1	0	2	0	0	0	0	0	Q9D9G7	
ENSMUST00000122182	ENSMUSG00000009575	15	103191544	103239816	-1	0	0	0	0	0	0	0	0	20	11	12		Q61686
ENSMUST00000122183						43	34	36	45	37	7	0	1	0	0	0		
ENSMUST00000122184						1	0	4	0	0	1	0	0	0	0	0		
ENSMUST00000122185						4	2	3	1	0	0	0	0	0	0	0		
ENSMUST00000122186						2	2	2	4	1	0	0	0	0	0	0		
ENSMUST00000122187						5	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000122188	ENSMUSG00000047866	8	86624043	86723873	1	0	0	0	0	0	1	0	0	0	74	102		Q9DBN5
ENSMUST00000122189						2	1	0	2	1	1	0	0	0	1	0		
ENSMUST00000122190						8	7	2	3	12	7	0	0	0	0	0		
ENSMUST00000122191						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122192						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000122193						3	4	4	3	0	0	0	0	0	0	0		
ENSMUST00000122194	ENSMUSG00000021236	12	84373857	84409029	-1	5	0	9	4	0	0	93	44	15	1	0		Q9WUZ9
ENSMUST00000122195						2	3	0	1	1	0	0	0	0	0	0		
ENSMUST00000122196						2	3	6	1	3	1	0	0	0	0	0		
ENSMUST00000122197						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122198						2	4	1	0	3	0	0	0	0	0	0		
ENSMUST00000122199	ENSMUSG00000040732	16	95359169	95586593	-1	0	2	0	0	3	0	16	25	54	0	0	Q3UQJ4	P81270
ENSMUST00000122200						0	6	8	0	0	10	0	0	0	0	0		
ENSMUST00000122201						0	0	3	2	1	0	1	3	0	0	0		
ENSMUST00000122202	ENSMUSG00000061479	7	27187005	27196271	-1	0	0	6	0	0	4	38	136	80	0	82		Q62189
ENSMUST00000122203						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000122204	ENSMUSG00000033036	5	43913144	43913917	1	0	15	0	11	0	0	15	58	9	92	27	Q4G0C5	Q9D868
ENSMUST00000122205	ENSMUSG00000015966	14	29996141	30008896	-1	0	0	1	35	4	0	0	0	0	0	3	D3Z4T0	
ENSMUST00000122206						2	1	1	0	1	1	0	0	1	0	0		
ENSMUST00000122207						7	6	9	10	13	9	0	0	0	0	0		
ENSMUST00000122208						2	3	1	3	2	2	0	0	0	0	0		
ENSMUST00000122209						1	1	0	2	1	2	0	0	0	0	0		
ENSMUST00000122210	ENSMUSG00000027805	3	57841895	57848079	-1	1	2	1	0	2	0	1	0	0	2	0		Q9JJV2
ENSMUST00000122211	ENSMUSG00000019066	9	21907491	21918192	-1	24	41	75	4	39	35	327	123	488	39	144	Q543Q4	P35276
ENSMUST00000122212						1	0	2	4	4	2	0	0	0	0	0		
ENSMUST00000122213	ENSMUSG00000029235	5	76312115	76331156	-1	2	0	1	0	0	0	0	0	0	0	0		Q78Y63
ENSMUST00000122214						0	2	6	74	10	2	0	12	4	18	2		
ENSMUST00000122215						3	2	0	13	4	1	0	0	0	0	0		
ENSMUST00000122216	ENSMUSG00000045160	6	83349147	83360136	1	2	0	9	19	1	2	12	33	8	102	4	E9Q705	
ENSMUST00000122217						1	3	3	5	6	1	0	0	0	0	0		
ENSMUST00000122218	ENSMUSG00000078876	2	176831140	176836730	1	0	2	0	0	0	0	0	0	0	0	0	E9Q6B9	
ENSMUST00000122219	ENSMUSG00000014543	6	129831154	129876672	-1	3	4	4	2	7	1	449	5026	1267	646	732	Q8BJS9	
ENSMUST00000122220						1	0	0	14	4	0	0	1	0	0	0		
ENSMUST00000122221						1	0	17	6	2	3	0	0	0	0	0		
ENSMUST00000122222	ENSMUSG00000028977	4	148804429	148954889	1	26	17	122	756	49	24	76	154	199	9	113	B1AS46	
ENSMUST00000122223						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122224	ENSMUSG00000070383	11	73776387	73780589	-1	0	4	0	0	2	0	0	0	0	0	0	Q7TRX7	
ENSMUST00000122225	ENSMUSG00000010067	9	107551555	107562267	1	0	0	0	7	0	0	0	25	50	0	12	B0QZV7	
ENSMUST00000122226						0	0	0	0	0	4	1014	1757	1235	2168	1122		
ENSMUST00000122227	ENSMUSG00000021123	12	79208914	79222665	1	0	2	0	0	1	0	30	141	25	208	91		
ENSMUST00000122228						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000122229	ENSMUSG00000072849	12	103946931	103958975	-1	0	1	4	0	0	0	0	0	0	0	0		Q00898
ENSMUST00000122230						3	5	13	6	6	5	0	0	0	1	0		
ENSMUST00000122231	ENSMUSG00000020070	10	62980223	63017210	1	0	0	0	0	7	15	0	0	0	0	0	D3Z4D2	
ENSMUST00000122232	ENSMUSG00000030530	7	80388585	80405436	-1	0	0	0	8	0	0	811	1840	3442	177	1993		P23188
ENSMUST00000122233	ENSMUSG00000021693	13	106958996	107022126	-1	81	75	66	80	94	42	207	801	345	128	232		P28740
ENSMUST00000122234						6	3	26	5	3	3	0	2	1	0	0		
ENSMUST00000122235	ENSMUSG00000033653	16	21423118	21644680	1	20	23	19	27	33	12	6	4	6	1	6	D3YU67	
ENSMUST00000122236						6	8	18	13	4	2	1	0	0	0	0		
ENSMUST00000122237						6	4	9	0	5	3	1	0	0	0	3		
ENSMUST00000122238						4	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000122239						3	3	6	5	4	3	0	0	0	0	0		
ENSMUST00000122240						1	3	1	3	3	1	0	0	0	0	0		
ENSMUST00000122241						7	0	8	2	9	4	0	0	0	2	0		
ENSMUST00000122242	ENSMUSG00000060519	1	156653617	156674356	-1	2	0	4	0	0	0	26	4	32	10	41		Q9ER38
ENSMUST00000122243						2	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000122244						8	4	22	2	11	6	0	0	0	0	0		
ENSMUST00000122245						2	3	10	14	5	0	26	202	149	26	37		
ENSMUST00000122246						0	1	0	3	1	0	0	0	0	0	0		
ENSMUST00000122247						0	0	1	0	0	0	0	4	0	2	0		
ENSMUST00000122248						5	2	1	0	2	3	0	0	0	0	0		
ENSMUST00000122249						2	1	5	2	6	1	0	0	0	0	0		
ENSMUST00000122250						5	3	11	3	4	3	0	0	0	0	0		
ENSMUST00000122251						3	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000122252						4	1	5	0	0	0	0	0	0	0	1		
ENSMUST00000122253	ENSMUSG00000071533	16	56007245	56029739	-1	6	2	6	16	4	3	8	36	11	9	26	Q3TM89	
ENSMUST00000122254	ENSMUSG00000058240	16	91689322	91728975	-1	1	0	0	0	0	0	22	110	69	113	39	D3YU21	
ENSMUST00000122255	ENSMUSG00000030527	7	80586627	80688877	-1	57	45	132	72	85	45	925	1098	1207	93	1018		Q91X84
ENSMUST00000122256						0	2	22	1	9	5	0	1	0	0	1		
ENSMUST00000122257						1	3	0	6	7	1	0	0	0	0	0		
ENSMUST00000122258						4	7	15	12	8	2	0	0	1	0	3		
ENSMUST00000122259	ENSMUSG00000020097	10	61098642	61147703	-1	0	0	0	53	0	14	696	1882	1193	340	1261		Q8R0X7
ENSMUST00000122260						4	3	20	5	3	7	0	2	0	0	0		
ENSMUST00000122261	ENSMUSG00000020096	10	61171954	61188841	1	0	0	2	0	3	0	0	0	0	0	0		Q7TSD4
ENSMUST00000122262						1	3	2	2	3	3	0	0	0	0	0		
ENSMUST00000122263						1	0	0	1	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122265						3	2	3	10	0	0	0	1409	485	6823	505		
ENSMUST00000122266	ENSMUSG00000026207	1	75375297	75432320	1	0	0	14	0	3	0	0	0	0	0	0		
ENSMUST00000122267						3	2	0	2	1	2	0	0	0	0	0		
ENSMUST00000122268						2	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000122269						3	0	5	3	3	0	0	1	0	1	0		
ENSMUST00000122271						7	7	0	2	2	0	0	0	0	0	0		
ENSMUST00000122272						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122273						8	6	22	7	4	6	0	0	0	0	0		
ENSMUST00000122274						0	1	0	2	0	2	1	0	0	0	0		
ENSMUST00000122275						4	1	2	3	9	9	0	0	0	0	0		
ENSMUST00000122278						1	1	0	1	1	4	0	0	0	0	0		
ENSMUST00000122279	ENSMUSG00000024608	18	60774510	60778546	1	7	0	7	3	4	8	5	15	23	20	7		P62264
ENSMUST00000122280	ENSMUSG00000022604	16	55899888	55934855	-1	8	0	12	8	0	0	0	2	0	0	2	Q6P077	
ENSMUST00000122281						0	0	1	3	0	0	0	0	0	0	0		
ENSMUST00000122282						10	10	21	10	22	14	0	0	0	0	0		
ENSMUST00000122283						8	0	11	6	5	3	1	1	0	0	0		
ENSMUST00000122284	ENSMUSG00000022897	16	94570010	94695517	1	9	15	67	36	13	0	236	377	539	18	334	A1L341	
ENSMUST00000122285	ENSMUSG00000023902	17	23600856	23611019	1	0	0	0	0	0	0	0	0	0	0	0	E9PX93	
ENSMUST00000122286	ENSMUSG00000039114	13	36725625	36734477	-1	4	0	0	27	5	2	0	0	1	0	0	D3Z4E2	
ENSMUST00000122287						4	13	6	5	9	5	0	0	0	0	0		
ENSMUST00000122288	ENSMUSG00000027879	3	97901190	97923276	1	6	1	1	3	4	3	7	19	18	14	19	E9Q6R3	
ENSMUST00000122289						2	1	0	0	1	0	0	2	0	0	4		
ENSMUST00000122290	ENSMUSG00000027673	3	32736990	32751566	1	2	0	0	7	0	0	132	504	111	490	85	D3Z568	
ENSMUST00000122291						4	1	2	2	2	3	0	0	0	1	0		
ENSMUST00000122292						0	0	4	0	0	4	0	0	0	0	0		
ENSMUST00000122293						225	226	523	909	178	82	1	24	7	0	3		
ENSMUST00000122294						1	0	4	0	3	0	0	0	0	0	0		
ENSMUST00000122295						313	325	296	310	377	177	3	66	48	1	31		
ENSMUST00000122296						8	9	27	16	7	6	0	0	0	0	0		
ENSMUST00000122297						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122298						0	1	1	0	2	1	0	0	0	0	0		
ENSMUST00000122299						3	2	6	5	2	6	0	0	1	0	2		
ENSMUST00000122300	ENSMUSG00000021288	12	111758849	111807844	1	5	0	0	0	0	0	415	450	383	86	307	Q7TNF4	
ENSMUST00000122301						5	1	0	1	1	2	0	0	0	0	0		
ENSMUST00000122302	ENSMUSG00000022961	16	91647506	91679221	1	0	0	0	1	0	0	17	2251	0	88	0	H9KV02	
ENSMUST00000122303	ENSMUSG00000052539	3	104013259	104220374	-1	0	3	0	114	0	0	0	0	13	0	18		Q9EQJ9
ENSMUST00000122304						0	0	3	1	12	0	0	0	0	0	0		
ENSMUST00000122305						15	5	29	20	25	0	27	29	36	5	29		
ENSMUST00000122306	ENSMUSG00000022842	16	20611593	20646485	1	5	4	5	0	6	3	0	0	2	0	0	E9Q1S5	
ENSMUST00000122307						3	0	2	3	2	3	0	0	0	0	0		
ENSMUST00000122308						4	2	17	6	4	1	0	0	0	0	0		
ENSMUST00000122309	ENSMUSG00000078495	4	147753974	147809788	-1	16	22	26	22	9	4	31	169	13	24	0	A2A7A2	
ENSMUST00000122310						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122311						6	2	11	10	6	2	0	0	0	0	0		
ENSMUST00000122312	ENSMUSG00000001127	X	20797814	20860519	1	6	8	31	30	13	8	55	205	95	4	130	Q8CAD1	
ENSMUST00000122313						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000122314	ENSMUSG00000035506	16	33517328	33664135	1	11	5	6	20	0	17	1	9	3	0	3	D3Z3V1	
ENSMUST00000122315						2	0	2	34	8	8	0	0	0	0	0		
ENSMUST00000122316						5	2	1	5	2	1	0	1	0	0	0		
ENSMUST00000122317						5	4	10	2	6	0	0	0	0	0	0		
ENSMUST00000122318	ENSMUSG00000081724	17	38054599	38059784	-1	0	0	4	7	4	4	0	0	0	0	0	Q8VEY1	
ENSMUST00000122319						2	1	2	0	5	1	0	0	0	0	0		
ENSMUST00000122320						4	4	8	9	4	4	0	0	0	2	0		
ENSMUST00000122321						5	2	8	6	4	2	0	0	0	0	0		
ENSMUST00000122322						1	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000122323						2	4	2	2	2	1	0	0	0	0	0		
ENSMUST00000122324						0	1	2	1	0	0	0	0	0	0	0		
ENSMUST00000122325						1	0	6	1	3	2	0	0	0	0	0		
ENSMUST00000122326						1	1	2	7	2	1	0	3	0	1	1		
ENSMUST00000122327	ENSMUSG00000044465	7	105371211	105400054	-1	11	13	15	0	0	0	463	860	721	73	315		Q3U2I3
ENSMUST00000122328	ENSMUSG00000020674	12	29938036	30017658	1	33	28	43	92	55	16	0	1	0	12	140		Q3UQ28
ENSMUST00000122329						1	1	5	3	0	0	0	0	0	0	0		
ENSMUST00000122330	ENSMUSG00000027746	3	53853376	53863830	-1	1	0	1	0	1	1	0	0	1	0	3	D3YW97	
ENSMUST00000122331						7	4	2	2	0	0	0	0	0	0	3		
ENSMUST00000122332						3	4	23	6	10	6	0	0	0	0	0		
ENSMUST00000122333	ENSMUSG00000042514	18	21550377	21654718	-1	23	16	27	199	15	10	0	2	0	0	0		Q69ZK5
ENSMUST00000122334	ENSMUSG00000028013	3	133310110	133378235	1	0	0	0	0	0	0	0	6	8	0	5	D3Z636	
ENSMUST00000122335						0	1	3	0	0	0	0	0	0	0	0		
ENSMUST00000122336						0	1	6	2	3	0	69	226	80	274	94		
ENSMUST00000122337						15	12	22	8	30	15	0	16	0	0	14		
ENSMUST00000122338						76	78	44	73	91	71	2	7	1	1	1		
ENSMUST00000122339						1	1	2	1	0	2	0	0	0	0	0		
ENSMUST00000122340						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000122341						1	0	0	2	0	0	2	4	0	2	0		
ENSMUST00000122342	ENSMUSG00000020834	11	78032280	78037866	1	0	0	0	23	0	0	0	0	0	0	0	B0QZT2	
ENSMUST00000122344						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122345						1	3	2	3	1	2	0	0	0	0	0		
ENSMUST00000122346						5	3	21	8	6	8	0	0	0	0	0		
ENSMUST00000122348	ENSMUSG00000023067	17	29090979	29100722	1	4	0	4	87	4	0	0	12	10	0	20	Q564P6	P39689
ENSMUST00000122349						5	4	2	13	7	7	0	0	0	0	0		
ENSMUST00000122350						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000122351						1	3	1	2	1	0	1	4	1	0	2		
ENSMUST00000122352						8	4	8	8	12	6	14	4	6	7	5		
ENSMUST00000122353						0	0	4	2	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122354						2	4	4	1	0	1	0	0	0	0	0		
ENSMUST00000122355						9	6	52	4	14	4	0	1	0	3	1		
ENSMUST00000122356	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	6	0	0	0	0	0		Q80TS3
ENSMUST00000122357						1	2	1	2	3	2	0	0	0	0	0		
ENSMUST00000122358	ENSMUSG00000002320	14	55635965	55643806	-1	0	0	4	161	15	5	12	0	22	4	8		Q9DBU0
ENSMUST00000122359	ENSMUSG00000025083	19	56912361	57008228	-1	18	0	0	18	4	12	0	0	0	0	22		
ENSMUST00000122360						4	2	5	0	3	2	8	35	3	58	10		
ENSMUST00000122361						4	2	10	4	11	3	110	482	174	461	203		
ENSMUST00000122362						0	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000122363	ENSMUSG00000001062	8	123242356	123254348	-1	0	0	0	0	0	0	0	0	0	0	0		Q8C190
ENSMUST00000122364						2	5	18	2	0	0	3	98	0	967	0		
ENSMUST00000122366						1	2	3	2	1	0	0	3	0	1	2		
ENSMUST00000122367	ENSMUSG00000074764	2	140229855	140389706	-1	4	5	0	8	7	2	0	0	0	0	0		Q3V172
ENSMUST00000122368						1	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000122369						0	0	3	2	2	0	0	0	0	0	0		
ENSMUST00000122370						1	0	2	2	1	3	0	0	0	0	0		
ENSMUST00000122371						0	0	2	0	0	1	0	2	0	1	1		
ENSMUST00000122372						2	2	9	1	6	0	0	0	0	0	0		
ENSMUST00000122373						8	0	9	2	5	4	2601	1948	1650	512	1154		
ENSMUST00000122374	ENSMUSG00000023232	4	130253495	130279205	-1	9	14	21	81	13	7	0	0	0	1	0	B2KFY0	
ENSMUST00000122375	ENSMUSG00000042532	19	42247574	42270348	1	36	23	0	23	1	38	0	0	0	0	0		Q9D428
ENSMUST00000122376						4	2	19	7	7	2	0	0	0	0	0		
ENSMUST00000122377	ENSMUSG00000061259	5	86302217	86373420	-1	41	14	94	33	40	27	2	4	5	3	10		Q8VHK8
ENSMUST00000122378						10	9	54	16	17	9	3	2	4	4	0		
ENSMUST00000122379						3	6	29	4	6	2	0	3	1	0	1		
ENSMUST00000122380						2	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000122381	ENSMUSG00000078686	4	60418046	60421952	-1	0	0	0	0	0	0	0	0	0	0	0	A2CGB6	P02762
ENSMUST00000122382						3	2	6	0	3	1	0	0	0	0	0		
ENSMUST00000122383	ENSMUSG00000041440	9	96119362	96184608	1	23	19	51	44	16	17	82	223	150	9	89		Q8BX05
ENSMUST00000122384	ENSMUSG00000032470	9	99385420	99437381	-1	0	0	0	0	0	0	5	1	1	5	3	Q3TPX5	O08989
ENSMUST00000122385						0	7	5	5	6	0	35	150	34	6	19		
ENSMUST00000122386	ENSMUSG00000020053	10	87858265	87937042	1	10	12	28	7	9	14	0	0	0	0	0	Q4VJC0	P05017
ENSMUST00000122387	ENSMUSG00000047473	7	29783998	29794702	1	17	12	0	69	43	13	0	1	0	3	0	D3Z614	
ENSMUST00000122388						18	15	23	18	29	19	1	0	0	0	0		
ENSMUST00000122389	ENSMUSG00000043051	8	125054195	125261858	1	79	69	156	106	77	39	7	9	12	0	18		Q811T9
ENSMUST00000122390						2	0	0	4	3	2	0	0	1	0	0		
ENSMUST00000122391						0	1	0	0	1	1	1	0	0	0	0		
ENSMUST00000122392						2	1	0	1	2	3	0	0	0	0	0		
ENSMUST00000122393	ENSMUSG00000031098	7	142434850	142440396	1	2	2	7	9	4	0	6	44	17	0	22		Q9R0N6
ENSMUST00000122394	ENSMUSG00000029404	5	124116089	124118196	1	0	0	0	66	0	0	0	34	0	0	0	D3YWC2	
ENSMUST00000122395						10	8	8	5	11	6	0	0	0	0	0		
ENSMUST00000122396						4	5	0	2	1	2	0	0	0	0	0		
ENSMUST00000122397						2	1	3	3	1	1	0	0	0	2	0		
ENSMUST00000122398						0	0	4	2	1	1	1	0	2	0	4		
ENSMUST00000122399	ENSMUSG00000042385	13	113171608	113225908	-1	4	2	3	8	3	0	0	0	0	0	0	D3Z594	
ENSMUST00000122400						1	5	1	1	10	5	0	0	0	0	0		
ENSMUST00000122401						15	25	61	20	32	16	0	2	0	0	0		
ENSMUST00000122402	ENSMUSG00000034066	1	93512079	93621976	1	13	8	24	11	12	7	0	3	5	0	20	D3Z4C0	
ENSMUST00000122403						1	1	8	1	3	0	0	0	0	0	0		
ENSMUST00000122404						23	12	12	5	9	8	8	11	7	8	7		
ENSMUST00000122405						3	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000122406						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122407						4	2	1	3	3	0	1	5	1	0	0		
ENSMUST00000122408	ENSMUSG00000057766	18	12252362	12305720	-1	5	2	3	9	3	1	0	0	0	1	0	D3YTU5	
ENSMUST00000122409	ENSMUSG00000001802	7	35200027	35215498	-1	9	15	0	15	30	6	0	0	0	0	2	E9Q1T6	
ENSMUST00000122410	ENSMUSG00000032386	9	65828930	65908794	-1	0	0	0	0	0	0	123	716	160	144	73		Q9QXN3
ENSMUST00000122411						0	0	1	0	1	0	0	3	0	0	0		
ENSMUST00000122412	ENSMUSG00000024539	18	67665511	67724595	-1	8	4	2	12	7	4	20	86	27	35	24		Q06180
ENSMUST00000122413						3	5	14	8	3	1	0	0	0	0	0		
ENSMUST00000122414						6	3	10	2	3	1	0	0	0	0	0		
ENSMUST00000122415						8	10	85	28	16	2	17	52	17	19	33		
ENSMUST00000122416						7	1	2	11	0	1	0	0	3	0	6		
ENSMUST00000122417						0	3	0	0	1	0	16	16	21	3	6		
ENSMUST00000122418						3	0	8	0	7	4	0	0	0	0	0		
ENSMUST00000122419	ENSMUSG00000021062	12	76797960	76822908	-1	4	3	2	3	3	3	0	0	0	0	0	D3YWS1	
ENSMUST00000122420						4	1	4	0	1	0	0	0	0	0	0		
ENSMUST00000122421	ENSMUSG00000031971	8	123840831	123860209	-1	11	2	0	43	7	3	15	53	14	0	23		Q8QZT2
ENSMUST00000122422						0	0	38	0	18	0	10	0	0	9	0		
ENSMUST00000122423	ENSMUSG00000039013	7	43351341	43359531	1	0	0	17	46	15	0	0	150	75	17	89		Q920G3
ENSMUST00000122424	ENSMUSG00000033557	1	156678532	156719086	-1	0	0	0	18	7	0	373	422	294	97	279		Q8VCS3
ENSMUST00000122426	ENSMUSG00000042594	5	121815488	121837646	-1	11	7	39	22	26	12	61	10	98	0	149		O09039
ENSMUST00000122427	ENSMUSG00000035506	16	33517328	33664135	1	0	4	22	3	2	0	0	0	0	0	0	D3Z6X1	
ENSMUST00000122428						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000122429						8	3	6	3	7	6	0	0	0	0	0		
ENSMUST00000122430						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122431	ENSMUSG00000046204	14	66911170	66920054	1	0	0	0	0	0	0	0	0	0	0	0		Q8BHK0
ENSMUST00000122432	ENSMUSG00000002266	7	6671456	6696450	-1	6	11	47	0	0	0	0	0	0	0	0	Q8C393	
ENSMUST00000122433						9	4	5	5	8	8	8	3	2	8	2		
ENSMUST00000122434						6	8	2	9	6	5	0	3	1	3	1		
ENSMUST00000122435						107	80	804	138	69	66	0	0	1	0	2		
ENSMUST00000122436						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000122437						3	1	5	4	0	1	0	0	0	0	0		
ENSMUST00000122438						1	0	0	0	0	1	2	3	1	0	0		
ENSMUST00000122439						4	0	0	0	0	6	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122440	ENSMUSG00000022701	16	43889800	43964314	1	12	0	17	2	0	1	6	8	0	0	0	F7D3E1	
ENSMUST00000122441	ENSMUSG00000032307	9	55148854	55207529	1	9	5	4	18	8	0	66	220	132	45	60		Q8K2Z8
ENSMUST00000122442						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000122443						1	1	1	2	2	0	0	0	0	0	0		
ENSMUST00000122444						3	1	2	0	4	0	0	6	1	2	7		
ENSMUST00000122445						7	4	1	3	5	4	0	0	0	0	0		
ENSMUST00000122446	ENSMUSG00000067441	X	117014757	117015104	1	0	0	0	4	1	2	0	0	0	0	0	S4R1E0	
ENSMUST00000122447						2	1	9	88	2	5	0	0	0	0	0		
ENSMUST00000122448	ENSMUSG00000030849	7	130162451	133123350	-1	2	0	0	0	0	0	0	0	0	0	0	E9Q5C3	
ENSMUST00000122449						8	1	8	3	7	4	0	0	0	0	0		
ENSMUST00000122450	ENSMUSG00000080717	16	97997323	98010000	1	3	0	6	11	6	1	3	6	4	20	6	Q8BLB2	
ENSMUST00000122451						4	3	14	8	3	2	0	0	0	0	0		
ENSMUST00000122452	ENSMUSG00000031698	8	85324303	85386345	-1	0	15	4	0	0	0	1	0	0	0	0	D3Z630	
ENSMUST00000122453						8	6	3	11	13	4	1	4	1	3	2		
ENSMUST00000122454						6	1	7	3	2	2	0	3	0	5	0		
ENSMUST00000122455						1	0	1	1	2	0	0	1	0	0	0		
ENSMUST00000122456	ENSMUSG00000026889	2	36116079	36136773	-1	2	2	3	0	0	0	0	36	51	48	13	B0R043	
ENSMUST00000122457						1	1	2	3	0	0	1	2	1	0	1		
ENSMUST00000122458						2	2	6	2	3	2	0	4	2	0	0		
ENSMUST00000122459						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122460						2	4	5	7	8	15	0	0	0	0	0		
ENSMUST00000122462						5	2	2	1	5	1	0	1	0	0	0		
ENSMUST00000122463						0	3	0	0	2	3	0	0	0	0	0		
ENSMUST00000122464	ENSMUSG00000024647	18	86711110	86718283	1	10	6	7	219	20	7	0	0	0	0	0		Q8BGU2
ENSMUST00000122465						3	5	20	6	11	3	0	0	0	0	0		
ENSMUST00000122466						5	1	17	8	14	7	0	0	0	0	0		
ENSMUST00000122467						8	7	30	5	7	2	0	0	0	0	0		
ENSMUST00000122805	ENSMUSG00000025529	X	112600526	112635070	1	2	0	2	0	0	1	0	0	0	0	0	F6VDX0	
ENSMUST00000122807						0	6	4	270	8	0	126	309	344	54	189		
ENSMUST00000122808	ENSMUSG00000060183	5	92359544	92365485	-1	12	17	52	23	23	12	0	0	0	0	0		
ENSMUST00000122809						0	5	3	103	25	1	0	17	3	0	13		
ENSMUST00000122810						1	0	1	1	3	0	56	85	32	93	33		
ENSMUST00000122811						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122812	ENSMUSG00000037736	5	66745827	67057158	1	2	0	2	5	5	2	0	0	0	0	0		
ENSMUST00000122814						2	0	2	0	0	0	5	7	18	11	17		
ENSMUST00000122815						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000122816	ENSMUSG00000030322	6	115840697	115853371	-1	5	0	0	1	1	3	19	14	21	11	21		
ENSMUST00000122817						0	0	0	0	0	0	171	599	155	44	75		
ENSMUST00000122818	ENSMUSG00000022438	15	84232043	84315688	1	1	0	3	70	6	1	2	0	0	10	1	F2Z417	
ENSMUST00000122819	ENSMUSG00000000739	8	123142847	123158315	-1	8	9	0	8	0	0	0	0	0	0	0	Q3UQP7	
ENSMUST00000122820						8	3	8	3	0	1	0	10	11	0	3		
ENSMUST00000122822						3	2	4	3	0	0	0	7	4	0	0		
ENSMUST00000122823						6	0	1	1	6	5	0	7	5	0	5		
ENSMUST00000122824						2	1	4	0	2	0	0	0	0	0	0		
ENSMUST00000122825						27	13	35	17	25	11	1	5	7	0	12		
ENSMUST00000122826						22	19	36	11	21	13	3	10	3	0	0		
ENSMUST00000122827						15	15	16	114	10	4	0	0	0	0	0		
ENSMUST00000122828						21	0	59	22	0	33	0	2	2	0	0		
ENSMUST00000122829						40	42	145	40	38	19	4	4	0	2	4		
ENSMUST00000122830						16	12	89	0	0	8	0	6	0	0	0		
ENSMUST00000122832						7	3	12	5	7	6	0	0	0	0	0		
ENSMUST00000122833						6	6	9	6	5	2	0	12	7	29	14		
ENSMUST00000122835	ENSMUSG00000018995	7	96951505	97064758	1	0	1	11	1	0	1	31	32	38	69	33		
ENSMUST00000122836						0	2	6	19	1	0	0	0	0	0	0		
ENSMUST00000122838						7	0	4	2	1	2	0	0	6	7	0		
ENSMUST00000122840	ENSMUSG00000021998	14	75131101	75230842	1	4	0	0	0	4	5	0	7	0	0	5	D3YVW8	
ENSMUST00000122841	ENSMUSG00000036792	2	48949508	49325405	1	0	8	13	8	0	8	24	130	79	18	38	F6Q8U1	
ENSMUST00000122842	ENSMUSG00000039087	13	37778400	37952002	1	1	2	1	76	5	3	5	1	11	1	4	B8JJE5	
ENSMUST00000122843						1	0	3	1	2	1	14	31	9	6	6		
ENSMUST00000122844						5	7	22	12	19	8	0	0	0	0	0		
ENSMUST00000122845						0	4	0	0	0	1	0	383	0	0	0		
ENSMUST00000122846						4	8	8	44	11	5	5	10	4	0	4		
ENSMUST00000122847						1	5	7	99	5	3	0	0	0	1	0		
ENSMUST00000122849	ENSMUSG00000027993	3	84160439	84306877	-1	4	2	2	0	4	0	0	0	0	0	0	D3YZJ0	
ENSMUST00000122850	ENSMUSG00000001127	X	20797814	20860519	1	0	0	0	0	0	0	6	2	0	5	0	B1AUN8	
ENSMUST00000122852						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122855						3	0	0	0	0	0	0	7	26	0	30		
ENSMUST00000122856						101	100	65	101	116	39	16	39	20	5	27		
ENSMUST00000122857						0	0	0	0	0	0	0	0	0	0	63		
ENSMUST00000122859	ENSMUSG00000068134	2	150114406	150136708	-1	0	0	0	0	0	0	0	115	0	0	0	F2Z412	
ENSMUST00000122860	ENSMUSG00000000085	4	120405281	120530186	1	0	0	8	0	0	0	0	7	0	1	3	F6UK33	
ENSMUST00000122861	ENSMUSG00000020570	12	32953891	32979050	1	0	0	4	32	0	0	4	8	17	26	18	D6RFU9	
ENSMUST00000122862						3	0	1	1	2	2	21	271	35	15	62		
ENSMUST00000122863	ENSMUSG00000019850	10	19000910	19015657	-1	0	0	0	1	0	0	0	0	0	0	0	D3Z5R6	
ENSMUST00000122864						3	0	0	0	0	0	4	41	14	2	9		
ENSMUST00000122865	ENSMUSG00000034135	9	46012820	46224194	1	8	6	9	6	6	2	178	352	283	30	205	F6U8X4	
ENSMUST00000122866						67	32	345	61	32	19	7	16	12	2	14		
ENSMUST00000122868						0	0	5	8	2	0	13	18	6	0	20		
ENSMUST00000122869						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000122870	ENSMUSG00000022906	16	35938470	35972605	1	0	0	0	3	0	0	1	20	16	20	0	E0CYZ7	
ENSMUST00000122871	ENSMUSG00000020808	11	72042032	72047370	1	7	3	2	65	5	1	0	0	0	0	0	Q5RIU2	
ENSMUST00000122872	ENSMUSG00000055313	13	21421275	21441058	-1	11	0	33	0	12	14	0	0	0	0	0	E9Q2C6	
ENSMUST00000122873						19	11	60	29	13	10	1	18	2	1	12		
ENSMUST00000122874						0	1	0	1	2	1	0	17	10	0	27		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122875						4	0	4	0	0	0	0	0	0	0	1		
ENSMUST00000122876	ENSMUSG00000036892	7	30493622	30513402	1	31	27	57	24	39	16	0	2	3	7	5	F6ZBU4	
ENSMUST00000122877						7	13	17	12	12	4	0	8	0	0	7		
ENSMUST00000122878						0	0	2	0	4	0	107	988	169	495	61		
ENSMUST00000122880						4	4	4	10	6	3	0	0	5	0	3		
ENSMUST00000122883						3	0	8	3	5	1	8	0	0	0	0		
ENSMUST00000122884	ENSMUSG00000026240	1	86582904	86609375	1	0	0	0	0	0	0	15	38	0	4	11	D6RI85	
ENSMUST00000122885	ENSMUSG00000001750	19	3896050	3907133	-1	0	0	8	0	0	0	101	651	28	63	91	F6ZFB8	
ENSMUST00000122886						32	27	61	66	37	20	11	13	13	19	60		
ENSMUST00000122887	ENSMUSG00000004952	5	136083916	136111860	1	7	1	1	0	2	1	2	6	0	0	4	F6W8M5	
ENSMUST00000122888						1	1	1	14	2	2	0	0	0	0	0		
ENSMUST00000122889						0	0	3	1	0	0	9	79	111	45	67		
ENSMUST00000122890	ENSMUSG00000030759	7	113513834	113571511	1	0	0	5	150	6	2	1	3	11	4	13	D3Z072	
ENSMUST00000122892						14	18	65	70	25	13	0	1	3	0	10		
ENSMUST00000122893						0	0	2	1	0	0	0	0	8	1	0		
ENSMUST00000122894	ENSMUSG00000031399	X	74384719	74393272	-1	2	0	0	0	0	0	16	0	18	0	0	I7HLV5	
ENSMUST00000122895	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	D6RDD2	
ENSMUST00000122896						23	10	94	16	37	8	6	9	2	4	0		
ENSMUST00000122897						1	0	0	0	3	1	0	0	0	0	0		
ENSMUST00000122899	ENSMUSG00000034595	17	35865593	35875596	1	14	0	18	116	25	4	242	579	348	44	203		Q8BQ30
ENSMUST00000122900						29	29	245	153	30	14	10	19	2	0	17		
ENSMUST00000122901						5	1	3	1	4	2	0	5	5	0	13		
ENSMUST00000122902	ENSMUSG00000036257	12	44221370	44312343	1	23167	21020	26634	79427	15514	3035	126	864	536	340	400	E9PXB0	
ENSMUST00000122903						2	2	0	0	2	0	99	0	29	0	34		
ENSMUST00000122905						0	0	9	8	0	2	22	180	8	0	41		
ENSMUST00000122907						0	0	0	3	0	0	0	9	0	0	0		
ENSMUST00000122908						585	482	744	370	862	344	3	13	7	4	17		
ENSMUST00000122909						9	5	20	7	12	8	0	0	0	1	0		
ENSMUST00000122912	ENSMUSG00000044647	2	65845767	66031546	1	49	57	122	36	45	34	0	0	1	0	5		P59055
ENSMUST00000122913	ENSMUSG00000029001	4	148152800	148160482	-1	0	0	0	0	0	0	0	0	1	0	0	D6RHP0	
ENSMUST00000122914						1	1	0	0	0	3	0	0	0	0	0		
ENSMUST00000122915						4	0	10	3	4	0	1108	1162	737	228	475		
ENSMUST00000122916	ENSMUSG00000029571	6	13069759	13089269	1	5	1	2	2	1	1	23	40	51	14	23	D3Z191	
ENSMUST00000122917						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000122918						24	20	147	69	21	19	0	2	1	0	2		
ENSMUST00000122919						0	3	0	0	0	0	51	138	7	29	35		
ENSMUST00000122920	ENSMUSG00000044712	12	73286779	73354049	1	0	0	0	1	2	1	0	0	0	0	0	E0CY99	
ENSMUST00000122921						0	0	3	0	3	0	0	0	0	0	0		
ENSMUST00000122922	ENSMUSG00000019900	10	51677756	51730429	1	17	0	23	2	13	8	0	0	0	0	0		Q8C7R7
ENSMUST00000122924	ENSMUSG00000024869	19	4000580	4005816	1	7	4	19	24	9	0	20	42	28	3	31	D3Z5H8	
ENSMUST00000122925						3	1	5	14	14	6	1	2	1	0	1		
ENSMUST00000122928						0	3	3	0	1	2	28	49	22	29	33		
ENSMUST00000122929	ENSMUSG00000060568	1	167001417	167091302	1	4	3	0	12	0	0	8	0	2	6	18	F6SII3	
ENSMUST00000122930						0	0	4	0	0	0	2	39	0	12	1		
ENSMUST00000122931						1	2	2	0	0	4	0	13	0	0	0		
ENSMUST00000122932						0	0	9	14	7	4	29	0	0	0	0		
ENSMUST00000122933						0	1	0	0	0	0	0	0	6	2	9		
ENSMUST00000122934						0	1	3	0	2	0	0	8	0	3	3		
ENSMUST00000122935	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	12	0	0	0	0	0	0	0	0	D3Z6D0	
ENSMUST00000122936	ENSMUSG00000024114	17	23836785	23844172	-1	4	7	0	4	10	3	0	2	0	0	1	F2Z3Y8	
ENSMUST00000122937						6	7	3	3	3	10	2	8	1	0	4		
ENSMUST00000122938	ENSMUSG00000030031	6	95117240	95129790	1	2	0	18	5	1	0	0	0	0	0	0		
ENSMUST00000122939						0	1	0	0	1	0	0	0	0	1	0		
ENSMUST00000122941	ENSMUSG00000022201	15	12117831	12185683	1	8	13	13	43	17	6	441	1111	945	284	492		O88532
ENSMUST00000122942						3	9	9	3	1	3	0	1	1	0	3		
ENSMUST00000122943	ENSMUSG00000031169	X	8193848	8206525	-1	2	2	20	10	0	17	0	3	0	0	7	S4R2F8	
ENSMUST00000122944						0	0	1	0	0	2	0	0	3	1	0		
ENSMUST00000122945	ENSMUSG00000020486	11	87568903	87590539	1	0	0	0	0	0	0	1	0	0	0	0	Q5ND18	
ENSMUST00000122946	ENSMUSG00000018858	11	115403752	115412674	1	0	0	0	10	0	0	0	0	10	0	0	D6RHR8	
ENSMUST00000122949						2	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000122950						0	0	2	0	0	0	9	38	32	0	29		
ENSMUST00000122951						28	20	49	15	24	13	4	9	6	0	6		
ENSMUST00000122954						0	0	0	0	0	21	0	0	0	0	0		
ENSMUST00000122955	ENSMUSG00000068329	6	83051266	83055273	-1	0	2	0	0	0	0	24	35	18	20	37	S4R1B3	
ENSMUST00000122956						0	6	0	72	0	0	584	8128	459	63	95		
ENSMUST00000122957						4	0	0	52	4	0	1	0	1	0	0		
ENSMUST00000122958	ENSMUSG00000063889	18	3266048	3337748	-1	2	0	8	0	3	0	0	2	2	0	0	E9PV35	
ENSMUST00000122959						1	1	2	2	4	0	0	1	0	0	0		
ENSMUST00000122960	ENSMUSG00000038354	3	96670131	96691032	1	14	8	14	0	0	13	0	0	2	8	5	D6RGN5	
ENSMUST00000122961	ENSMUSG00000027994	3	129914960	129970206	-1	0	0	0	27	0	0	2	5	2	8	0	D6RI54	
ENSMUST00000122962	ENSMUSG00000022160	14	52294668	52305128	-1	4	4	9	3	5	3	0	3	0	3	0	G3UY98	
ENSMUST00000122963						3	6	14	8	15	1	1	0	0	0	0		
ENSMUST00000122964						79	55	531	142	52	34	4	4	7	1	9		
ENSMUST00000122965	ENSMUSG00000027167	2	105701027	105904564	-1	12	13	6	28	7	4	4	7	10	5	6		Q9ER73
ENSMUST00000122966						0	0	0	0	0	0	0	0	0	7	0		
ENSMUST00000122967	ENSMUSG00000051043	11	114851152	114872617	1	14	13	40	157	19	12	0	0	0	0	2	E9PZP1	
ENSMUST00000122970	ENSMUSG00000005107	5	38349273	38503143	-1	0	4	0	8	6	0	31	73	11	31	3	D6REU9	
ENSMUST00000122971						3	0	7	1	6	0	0	0	0	1	0		
ENSMUST00000122973						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000122974						0	0	0	0	0	0	0	20	0	0	7		
ENSMUST00000122975						0	0	0	0	0	0	1	0	0	0	5		
ENSMUST00000122976	ENSMUSG00000047583	3	154576431	154597104	-1	0	0	0	34	0	0	0	0	0	0	0	D3YVH5	
ENSMUST00000122977						0	3	0	14	4	2	0	0	0	0	0		
ENSMUST00000122979	ENSMUSG00000006143	5	136054492	136064326	1	0	2	0	1	0	0	0	0	0	0	0	F7BUZ0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000122980	ENSMUSG00000049606	5	106616739	106697287	-1	0	0	0	0	0	0	0	0	0	0	0	D3YY78	
ENSMUST00000122981	ENSMUSG00000029804	6	58831465	58920398	1	0	0	0	128	5	0	0	3	6	0	0	D3Z2S3	
ENSMUST00000122982						0	7	0	0	0	5	0	0	0	0	0		
ENSMUST00000122983						3	2	0	46	1	1	0	0	0	0	0		
ENSMUST00000122984	ENSMUSG00000025420	18	76977148	77047308	-1	0	0	3	4	0	0	0	0	0	0	0	D6RI39	
ENSMUST00000122985	ENSMUSG00000079334	9	107578887	107584050	1	40	18	74	31	13	7	0	0	0	0	0	B7ZCE0	
ENSMUST00000122986						2	2	2	0	7	3	22	91	39	0	27		
ENSMUST00000122989						3	0	39	0	0	8	38	82	34	22	28		
ENSMUST00000122991	ENSMUSG00000023911	17	23776916	23786081	-1	0	3	0	0	0	0	0	1	0	0	0	F6VCP8	
ENSMUST00000122992						6	4	18	5	11	3	0	0	6	17	21		
ENSMUST00000122993	ENSMUSG00000020232	10	81346048	81350480	-1	0	0	0	0	0	2	45	0	23	0	0	Q05DT2	
ENSMUST00000122994						50	39	331	140	43	28	4	11	4	3	18		
ENSMUST00000122995	ENSMUSG00000062732	7	24864620	24869941	-1	2	0	8	0	6	1	0	0	0	0	0	D3Z162	
ENSMUST00000122996	ENSMUSG00000029922	6	39397804	39420462	-1	2	0	0	36	2	6	154	525	148	83	127	F6S742	
ENSMUST00000122997						0	0	0	0	0	2	7	44	5	3	19		
ENSMUST00000122998						2	0	6	2	2	0	0	0	0	0	0		
ENSMUST00000122999	ENSMUSG00000030409	7	19083849	19093821	1	2	0	15	28	2	4	0	1	0	0	1	D3YYG5	
ENSMUST00000123000						1	1	0	17	2	0	0	0	0	0	0		
ENSMUST00000123001						4	2	4	3	5	4	2	0	0	0	0		
ENSMUST00000123002						0	1	0	0	1	2	10	12	0	1	2		
ENSMUST00000123003						3	2	6	2	10	4	0	0	0	0	0		
ENSMUST00000123004	ENSMUSG00000040363	X	12036740	12160355	-1	0	0	4	17	3	1	0	0	0	0	0	F6XPR4	
ENSMUST00000123005	ENSMUSG00000010051	9	107576927	107581710	1	0	0	0	0	0	0	0	0	0	0	0	D6RFV7	
ENSMUST00000123006	ENSMUSG00000015745	3	95988429	95996001	-1	4	0	7	0	5	0	167	320	81	106	201	F6XQM2	
ENSMUST00000123007						3	4	0	1	3	3	0	0	0	0	0		
ENSMUST00000123008	ENSMUSG00000043962	4	126164082	126202760	-1	0	1	0	3	0	0	0	20	40	0	19	E9Q494	
ENSMUST00000123010						1	0	0	0	0	1	0	39	11	20	17		
ENSMUST00000123011						3	6	9	60	8	1	0	0	0	0	0		
ENSMUST00000123012						1	2	2	2	1	0	2	2	0	0	2		
ENSMUST00000123013	ENSMUSG00000033099	15	78934933	78943634	1	0	1	1	5	0	2	4	15	7	0	11	B7ZCM5	
ENSMUST00000123015	ENSMUSG00000002963	7	44857139	44862992	1	0	0	0	0	6	0	2333	3356	1494	209	1224		
ENSMUST00000123017						53	28	148	34	44	21	0	0	0	0	0		
ENSMUST00000123018						7	0	0	1	6	0	0	0	0	0	0		
ENSMUST00000123019						11	5	26	29	21	9	64	267	93	59	147		
ENSMUST00000123020						5	5	16	29	16	8	12	17	24	1	37		
ENSMUST00000123021						8	24	65	22	36	23	16	45	16	10	16		
ENSMUST00000123022						2	1	1	0	2	0	0	63	0	0	0		
ENSMUST00000123023						5	3	2	32	9	7	0	1	5	0	6		
ENSMUST00000123025	ENSMUSG00000056394	7	13277283	13311433	1	0	0	0	0	0	0	0	0	0	0	0	D3YUW4	
ENSMUST00000123026						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000123027	ENSMUSG00000028602	4	145267137	145315164	-1	11	0	0	50	14	8	0	0	0	0	13	D6RHK4	
ENSMUST00000123028	ENSMUSG00000063052	3	158036662	158068487	1	0	0	0	0	0	0	0	0	1	0	4	F6RGS7	
ENSMUST00000123029						1	6	2	0	2	2	0	0	56	0	44		
ENSMUST00000123030						1	3	2	1	1	1	0	0	0	2	0		
ENSMUST00000123031						38	35	87	57	55	38	6	16	12	0	14		
ENSMUST00000123032						335	369	339	266	262	114	52	109	135	34	101		
ENSMUST00000123033						0	0	0	2	0	4	0	149	47	2	3		
ENSMUST00000123034	ENSMUSG00000079593	X	53577087	53608979	-1	0	1	0	5	3	0	0	0	0	0	0	B1AXE0	
ENSMUST00000123035						4	0	0	0	3	0	0	0	0	3	3		
ENSMUST00000123036	ENSMUSG00000045671	11	19924375	20024026	1	2	0	5	0	0	2	0	0	0	0	0	Q5SRF9	
ENSMUST00000123037						167	105	588	802	202	93	8	22	16	6	39		
ENSMUST00000123038						0	0	0	0	3	2	0	0	0	0	0		
ENSMUST00000123039						2	2	4	2	3	8	5	35	10	0	19		
ENSMUST00000123041						6	5	4	27	6	3	2	6	0	0	3		
ENSMUST00000123042						0	0	0	0	0	0	0	0	0	1	1		
ENSMUST00000123043	ENSMUSG00000022124	14	103080239	103099566	-1	3	2	2	0	1	2	13	15	15	4	37	D3Z388	
ENSMUST00000123045						4	0	6	0	4	4	1	3	2	0	0		
ENSMUST00000123046						1	0	0	0	0	0	13	31	63	5	88		
ENSMUST00000123047	ENSMUSG00000022708	16	42875881	43642602	1	4	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000123049						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123050						0	0	0	0	0	0	2	3	0	0	0		
ENSMUST00000123052						2	0	12	0	5	0	37	70	48	18	46		
ENSMUST00000123053	ENSMUSG00000026983	2	24276954	24283426	1	2	0	5	0	0	0	0	0	0	0	0	A2AIA8	
ENSMUST00000123054						1	0	6	0	3	0	59	133	134	5	152		
ENSMUST00000123056						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123057	ENSMUSG00000000214	7	142892752	142931128	-1	2	0	3	0	3	0	0	0	0	0	0	D6RGQ9	
ENSMUST00000123058						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000123059						9	8	4	2	15	5	2	7	5	0	2		
ENSMUST00000123061						68	45	527	102	56	37	6	6	7	0	10		
ENSMUST00000123062						6	4	52	8	10	4	0	4	0	0	0		
ENSMUST00000123063						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000123064						0	0	3	2	2	1	0	0	4	0	4		
ENSMUST00000123066						13	0	9	30	7	12	0	0	0	0	0		
ENSMUST00000123068						13	10	14	57	17	6	0	0	1	0	0		
ENSMUST00000123069	ENSMUSG00000035297	5	100518309	100547803	1	1	1	1	0	0	0	0	0	0	0	0	D6RG47	
ENSMUST00000123070						8	4	3	2	8	6	2	33	7	5	14		
ENSMUST00000123071						0	1	0	0	0	0	11	9	0	21	12		
ENSMUST00000123072	ENSMUSG00000003810	4	116306762	116464183	-1	0	0	0	0	0	0	0	0	0	0	0	B1AST5	
ENSMUST00000123073						0	0	3	8	1	1	0	0	0	0	0		
ENSMUST00000123074						1	0	1	0	0	5	0	2	2	11	3		
ENSMUST00000123076	ENSMUSG00000021338	13	24012344	24280795	-1	4	2	4	1	3	0	0	0	0	0	0	E9Q7X4	
ENSMUST00000123077						0	1	0	0	0	0	0	0	0	0	1		
ENSMUST00000123078						2	1	3	35	12	3	0	0	1	0	0		
ENSMUST00000123079						9	15	9	15	15	10	5	27	36	0	12		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123080						4	3	12	98	10	9	37	28	36	6	36		
ENSMUST00000123081						0	0	0	2	9	0	0	0	0	0	0		
ENSMUST00000123082	ENSMUSG00000060771	1	37754776	37866429	-1	10	6	24	87	9	4	18	79	18	6	6	Q3TR21	
ENSMUST00000123083	ENSMUSG00000027472	2	153008890	153015427	-1	0	0	0	0	0	0	0	0	0	4	0	D6RFQ5	
ENSMUST00000123084						0	7	2	0	1	0	8	61	6	7	20		
ENSMUST00000123085						0	2	0	2	5	0	24	58	44	0	28		
ENSMUST00000123086	ENSMUSG00000026315	1	107590006	107610484	1	0	0	0	0	0	0	0	5	4	4	4	F6Y0I8	
ENSMUST00000123088	ENSMUSG00000035585	7	3692863	3701024	1	5	0	0	8	5	0	10	0	0	5	0	D3YY06	
ENSMUST00000123089						0	0	0	0	0	0	2	0	2	0	6		
ENSMUST00000123090						13	8	12	9	7	5	3	3	2	1	5		
ENSMUST00000123091	ENSMUSG00000048763	11	96323326	96347930	1	12	16	20	213	27	16	0	0	0	0	1	G3UZC2	
ENSMUST00000123092						0	0	0	0	0	0	0	10	0	2	6		
ENSMUST00000123093						20	10	22	16	8	14	27	146	56	20	93		
ENSMUST00000123095						0	0	0	0	0	0	0	4	3	6	3		
ENSMUST00000123096						0	0	0	0	0	1	4	30	82	16	32		
ENSMUST00000123097	ENSMUSG00000025877	13	55005985	55021385	-1	0	0	0	0	0	0	342	1273	759	0	559	E9Q8S8	
ENSMUST00000123098	ENSMUSG00000039841	6	28239927	28398005	-1	0	0	0	158	2	0	0	0	0	1	0	D3YV79	
ENSMUST00000123099						1	0	0	2	3	0	0	0	0	0	0		
ENSMUST00000123100	ENSMUSG00000015217	X	71555918	71560676	1	0	0	0	1	0	0	0	0	10	4	0	A2AP78	
ENSMUST00000123101	ENSMUSG00000022443	15	77760587	77842175	-1	5	2	5	6	3	1	0	2	0	0	4	F2Z494	
ENSMUST00000123102	ENSMUSG00000025665	X	111388192	111537959	-1	3	3	0	18	1	2	0	0	0	0	0	E9Q3H1	
ENSMUST00000123103						0	0	0	0	4	0	0	8	4	0	1		
ENSMUST00000123104	ENSMUSG00000027331	2	118814003	118853957	1	3	0	0	4	0	0	0	9	10	0	0	H3BKK2	
ENSMUST00000123105	ENSMUSG00000018401	11	87592162	87616302	1	2	3	7	12	2	2	1	1	1	0	1	A7M7R0	
ENSMUST00000123106	ENSMUSG00000029127	5	38189735	38220457	-1	0	0	1	35	0	1	0	0	0	0	0		
ENSMUST00000123108	ENSMUSG00000078786	7	27195781	27210186	1	2	0	3	0	5	0	3	1	1	1	5	F7BUA2	
ENSMUST00000123109						6	0	13	63	10	0	0	14	0	3	8		
ENSMUST00000123111						0	7	4	14	6	2	9	216	167	63	125		
ENSMUST00000123112						6	6	62	15	3	0	0	0	0	0	0		
ENSMUST00000123113						1	1	2	4	3	0	6	16	11	0	7		
ENSMUST00000123114						2	2	3	2	1	0	0	0	0	0	0		
ENSMUST00000123115						7	1	3	6	4	0	24	71	36	6	40		
ENSMUST00000123116	ENSMUSG00000029669	6	21771395	21852515	-1	2	2	0	8	0	0	0	0	0	0	0	D3YW00	
ENSMUST00000123118						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123119						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000123121	ENSMUSG00000042662	2	152940997	152951698	-1	0	0	0	43	0	0	0	0	0	0	0		Q8R4V2
ENSMUST00000123123	ENSMUSG00000048537	9	44686304	44735198	-1	14	4	27	31	4	9	0	0	0	0	0	F7CB18	
ENSMUST00000123124						0	0	0	0	1	4	0	0	0	0	0		
ENSMUST00000123125						1	4	1	1	2	0	0	0	0	0	2		
ENSMUST00000123126						4	2	0	0	4	0	0	22	2	5	6		
ENSMUST00000123128	ENSMUSG00000034593	9	75071015	75223688	1	65	77	145	613	108	53	321	739	518	56	458		Q99104
ENSMUST00000123130						11	11	12	13	6	5	2	12	3	0	9		
ENSMUST00000123131						5	1	3	0	2	0	0	0	0	0	0		
ENSMUST00000123132						3	3	5	4	1	2	17	33	6	0	5		
ENSMUST00000123133						6	5	12	19	16	0	0	0	0	1	0		
ENSMUST00000123134						3	1	18	20	5	1	0	0	0	0	0		
ENSMUST00000123135						0	0	0	121	1	0	0	0	0	0	0		
ENSMUST00000123137						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000123138	ENSMUSG00000021694	13	108158731	108195364	1	0	0	0	0	0	0	0	0	0	1	0	F6QPY9	
ENSMUST00000123139						0	1	0	0	0	1	10	27	0	8	8		
ENSMUST00000123140						0	0	0	0	8	0	0	0	0	0	7		
ENSMUST00000123141	ENSMUSG00000048696	10	80380355	80387659	-1	0	0	3	0	0	0	4	25	9	4	1	F6TY75	
ENSMUST00000123142	ENSMUSG00000002107	2	6539694	7509563	-1	1	2	0	6	1	2	0	0	0	0	0	S4R2J2	
ENSMUST00000123143	ENSMUSG00000028108	3	95734147	95739569	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z038	
ENSMUST00000123144						0	2	0	0	0	0	6	0	0	0	17		
ENSMUST00000123145						5	0	2	64	2	2	0	0	0	0	0		
ENSMUST00000123146	ENSMUSG00000071632	16	18836578	18840160	1	2	1	0	22	1	1	0	7	2	0	2	A0A087WS89	
ENSMUST00000123147						40	22	284	31	19	14	0	0	0	1	0		
ENSMUST00000123148						1	6	5	0	3	2	5	14	11	0	15		
ENSMUST00000123150	ENSMUSG00000006219	4	141576062	141606096	-1	0	0	0	0	0	0	0	0	0	0	0	A2ADF2	
ENSMUST00000123151						2	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000123152						1	1	4	5	0	0	12	0	0	0	8		
ENSMUST00000123153						1	1	0	0	2	4	0	0	0	0	0		
ENSMUST00000123154						9	14	5	0	6	4	9	34	6	0	0		
ENSMUST00000123156	ENSMUSG00000027546	2	168634438	168742409	-1	0	2	33	8	1	0	0	0	0	0	0	A2AUZ0	
ENSMUST00000123157						0	4	3	17	3	1	0	0	0	0	0		
ENSMUST00000123158						9	15	17	26	28	10	3	8	11	0	14		
ENSMUST00000123159	ENSMUSG00000052738	6	73248382	73276911	1	0	2	3	12	0	0	0	3	10	0	8	G3UYP8	
ENSMUST00000123161						2	0	0	1	0	0	6	0	0	3	0		
ENSMUST00000123163						3	3	0	6	4	2	0	0	0	0	0		
ENSMUST00000123164	ENSMUSG00000020381	11	50174444	50200115	1	0	2	1	2	5	2	0	0	4	0	0	F6S5X0	
ENSMUST00000123165						11	12	15	12	7	11	0	2	1	0	0		
ENSMUST00000123166	ENSMUSG00000032818	18	77281958	77442341	1	0	1	0	0	8	2	0	0	0	0	0	F6QGA9	
ENSMUST00000123167	ENSMUSG00000028958	5	24445458	24447854	-1	4	2	0	21	3	0	0	0	21	0	0	D3Z5X7	
ENSMUST00000123168	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	0	0	0	1	0	0	F7BXL9	
ENSMUST00000123169						3	2	11	0	5	2	4	1	2	2	0		
ENSMUST00000123170	ENSMUSG00000009555	2	32705784	32713076	-1	0	0	0	24	0	0	0	80	24	7	29	D6RGN3	
ENSMUST00000123171						6	0	19	0	5	0	0	0	0	0	2		
ENSMUST00000123172						12	12	16	23	9	6	130	539	198	4	292		
ENSMUST00000123173						0	2	2	0	1	0	0	0	0	0	0		
ENSMUST00000123174						3	5	20	7	4	5	24	35	184	55	103		
ENSMUST00000123175						2	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000123176	ENSMUSG00000032782	11	69299487	69323775	-1	0	15	26	0	32	0	0	48	0	6	38	D6RGB4	
ENSMUST00000123177						3	0	0	7	3	0	5	18	20	172	141		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123178						19	23	34	7	26	15	43	67	42	3	53		
ENSMUST00000123179	ENSMUSG00000066107	4	92190744	92191749	-1	5	3	13	0	15	9	0	3	2	14	3	A2AMD0	
ENSMUST00000123180						3	2	28	4	6	0	0	8	7	0	20		
ENSMUST00000123181	ENSMUSG00000018509	11	62524946	62539261	-1	0	1	1	4	4	0	2	3	0	0	0	F6SS03	
ENSMUST00000123182	ENSMUSG00000021694	13	108158731	108195364	1	2	0	1	10	1	0	0	0	0	0	1	D6RET0	
ENSMUST00000123183						4	0	0	14	10	1	5	23	3	3	8		
ENSMUST00000123184						8	10	6	20	8	2	2	17	2	2	5		
ENSMUST00000123185						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123186						2	0	8	46	3	2	9	1	6	0	1		
ENSMUST00000123187	ENSMUSG00000052551	13	8202866	8768747	1	3	21	147	20	7	0	0	0	1	0	0	Q6PB89	
ENSMUST00000123188	ENSMUSG00000002210	7	24399619	24422778	1	0	0	0	0	0	0	0	0	0	0	0	F6YIT4	
ENSMUST00000123189	ENSMUSG00000038930	7	80293229	80324454	-1	0	0	0	1	1	4	0	0	0	0	2	D3Z1Y2	
ENSMUST00000123190						0	0	0	5	11	4	391	426	288	48	144		
ENSMUST00000123191						0	0	0	0	0	1	0	0	0	0	2		
ENSMUST00000123192						734	734	3736	874	1094	431	24	167	62	5	85		
ENSMUST00000123193						2	3	4	6	3	0	2	0	0	0	2		
ENSMUST00000123194	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	7	0	0	15	4	4	0	8	D3YV66	
ENSMUST00000123195						5	4	6	30	9	2	0	0	0	0	0		
ENSMUST00000123196	ENSMUSG00000022967	16	91485238	91507441	1	26	0	16	10	5	0	65	138	230	8	271		P33896
ENSMUST00000123197						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000123198	ENSMUSG00000001946	9	37528078	37538319	1	5	5	7	6	5	4	0	0	0	0	0	D3Z5S5	
ENSMUST00000123199						4	0	5	53	8	5	0	0	0	0	1		
ENSMUST00000123200						30	23	69	22	29	14	0	2	0	0	3		
ENSMUST00000123201	ENSMUSG00000036099	10	93939165	94035817	-1	0	0	0	0	0	0	0	0	0	0	1	D3YVB1	
ENSMUST00000123202	ENSMUSG00000026856	2	30392254	30400529	1	6	4	18	7	10	5	37	0	0	0	0		
ENSMUST00000123203						53	40	424	153	89	32	7	5	17	0	15		
ENSMUST00000123204						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000123205						0	0	2	0	3	0	0	6	0	0	0		
ENSMUST00000123206	ENSMUSG00000032224	9	70089310	70142560	-1	1	0	0	4	0	0	0	0	0	0	0	D3YYF8	
ENSMUST00000123207	ENSMUSG00000067367	5	38220470	38234306	1	2	0	0	0	0	0	0	0	0	7	0	D3YU83	
ENSMUST00000123208						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123209						0	4	26	73	10	11	0	0	0	0	0		
ENSMUST00000123211						5	0	9	0	2	4	45	407	151	10	326		
ENSMUST00000123213	ENSMUSG00000025665	X	111388192	111537959	-1	0	0	0	4	2	0	0	0	0	0	0	A2CEE8	
ENSMUST00000123214	ENSMUSG00000074771	2	136501910	136562091	1	0	1	3	0	0	0	0	0	0	0	0	Q8BLU6	
ENSMUST00000123215						1	0	1	0	0	2	11	5	14	0	17		
ENSMUST00000123216						4	4	0	42	1	4	3	2	0	0	0		
ENSMUST00000123217						5	2	0	1	2	1	0	3	0	4	3		
ENSMUST00000123219						3	1	1	7	4	0	10	42	33	0	41		
ENSMUST00000123220						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123221						3	3	8	4	16	3	3	0	0	0	0		
ENSMUST00000123222						6	3	4	193	13	4	0	0	0	0	0		
ENSMUST00000123223						3	3	1	0	3	2	0	0	0	0	0		
ENSMUST00000123225	ENSMUSG00000051344	1	64785983	64956824	-1	0	0	0	90	13	0	0	1	0	0	1	D3Z0F2	
ENSMUST00000123226						15	10	100	19	20	7	1	4	1	0	0		
ENSMUST00000123227	ENSMUSG00000040532	5	135009152	135012175	1	4	2	4	8	6	2	71	166	52	11	45		
ENSMUST00000123228	ENSMUSG00000019647	18	47235598	47368870	-1	5	4	8	5	10	7	0	0	0	0	0	F6WLW8	
ENSMUST00000123229						0	0	2	0	0	2	0	10	7	6	31		
ENSMUST00000123230						2	1	1	0	0	1	0	0	6	0	0		
ENSMUST00000123232						0	2	5	0	0	0	2	5	0	7	0		
ENSMUST00000123233						3	2	3	117	7	3	0	2	1	1	0		
ENSMUST00000123234	ENSMUSG00000003038	4	133964738	133968650	-1	0	0	2	0	0	0	0	0	8	0	0	F6W687	
ENSMUST00000123235	ENSMUSG00000005983	16	3895179	3908689	-1	0	0	0	3	0	1	8	11	3	2	7	H3BK34	
ENSMUST00000123236						6	4	6	2	12	0	0	0	0	0	0		
ENSMUST00000123237	ENSMUSG00000025437	3	152346478	152393617	1	21	24	52	22	30	18	0	8	5	0	14	D6RES0	
ENSMUST00000123238	ENSMUSG00000026365	1	140084708	140183764	-1	0	7	0	0	0	0	26	46	0	0	0	D6RGQ0	
ENSMUST00000123239						2	7	5	3	5	6	0	0	0	0	0		
ENSMUST00000123240						18	13	39	90	33	19	25	132	38	5	65		
ENSMUST00000123241						3	2	5	5	2	0	12	46	24	6	30		
ENSMUST00000123242						0	1	0	1	5	2	0	0	0	0	0		
ENSMUST00000123243						2	0	0	32	1	0	8	30	7	1	8		
ENSMUST00000123244	ENSMUSG00000020059	10	88459569	88473236	1	4	0	0	0	0	0	0	0	0	0	0	M0QW86	
ENSMUST00000123245	ENSMUSG00000025862	X	42149317	42277185	1	0	0	0	5	0	0	0	2	10	0	0	B7ZCD2	
ENSMUST00000123246						9	7	20	8	1	0	5	8	0	0	14		
ENSMUST00000123247						4	0	5	1	2	0	7	37	20	0	35		
ENSMUST00000123248	ENSMUSG00000007570	17	28313530	28326568	1	0	0	0	0	0	0	4	0	0	0	3	B8JJD7	
ENSMUST00000123250						3	1	5	0	0	2	1	0	1	1	0		
ENSMUST00000123251	ENSMUSG00000041607	18	82475146	82585637	1	0	0	4	3	0	0	0	0	8	0	0	F6RT34	
ENSMUST00000123252						0	0	4	1	2	0	0	0	0	0	0		
ENSMUST00000123253						0	0	0	22	0	0	0	0	0	0	0		
ENSMUST00000123254						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000123255						7	5	11	60	5	2	24	86	68	14	128		
ENSMUST00000123256	ENSMUSG00000029575	5	114431034	114444060	-1	10	11	12	0	12	2	2	0	2	0	4		Q9D273
ENSMUST00000123257	ENSMUSG00000002871	6	88902251	88912238	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123259						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000123260	ENSMUSG00000020546	11	90476492	90638084	-1	12	10	13	7	9	3	0	0	5	0	0	F7AX23	
ENSMUST00000123261						0	0	0	3	0	0	0	0	0	0	3		
ENSMUST00000123262	ENSMUSG00000028483	4	83417724	83467676	1	1	7	3	5	2	3	29	37	24	0	50		Q9D2C9
ENSMUST00000123264	ENSMUSG00000046550	X	153832225	153834243	1	0	0	0	0	0	1	0	0	0	0	0	B1AXT5	
ENSMUST00000123265						3	5	0	11	4	0	6	0	1	3	0		
ENSMUST00000123266	ENSMUSG00000064115	16	66655421	67620908	-1	0	0	0	80	7	2	0	0	0	0	0	D3Z0N3	
ENSMUST00000123267	ENSMUSG00000071337	6	86404219	86433405	1	0	1	0	2	0	0	3	0	0	0	0		
ENSMUST00000123268						2	0	5	3	6	1	0	0	0	0	0		
ENSMUST00000123270						0	3	2	4	5	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123271	ENSMUSG00000026761	2	48902824	48950277	-1	1	1	3	5	3	1	8	22	7	11	7	A2AI42	
ENSMUST00000123273						23	10	83	54	28	13	5	68	34	4	76		
ENSMUST00000123274						0	0	4	8	2	1	0	0	0	10	0		
ENSMUST00000123275						1	0	0	0	5	2	13	46	15	17	11		
ENSMUST00000123276						34	46	41	27	46	20	0	5	8	0	13		
ENSMUST00000123277	ENSMUSG00000031156	X	7884041	7894492	1	0	0	0	0	0	0	0	0	0	0	0	F6QH15	
ENSMUST00000123279	ENSMUSG00000030538	7	80227147	80232813	-1	0	1	7	71	4	0	278	353	183	117	80	D3YY46	
ENSMUST00000123280						0	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000123281						1	0	0	0	0	0	2	11	0	0	0		
ENSMUST00000123282						3	1	7	0	4	3	6	6	8	4	11		
ENSMUST00000123283	ENSMUSG00000031389	X	73891442	73921870	-1	4	6	8	9	8	7	7	24	3	1	36	D6RFT8	
ENSMUST00000123284						3	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000123285	ENSMUSG00000054976	1	81076950	81341764	1	29	23	172	53	22	13	1	0	0	0	0		
ENSMUST00000123286	ENSMUSG00000022538	16	30560494	30587592	-1	0	0	0	0	0	0	5	0	3	0	12	F7AMG0	
ENSMUST00000123287	ENSMUSG00000034235	14	20548912	20618354	-1	0	0	0	0	0	0	1	0	0	0	1	F6ZXV1	
ENSMUST00000123288	ENSMUSG00000043079	18	60593973	60660142	-1	3	0	22	3	3	0	0	0	0	0	0	E0CYK1	
ENSMUST00000123289						0	1	1	0	3	3	8	6	34	15	7		
ENSMUST00000123290						0	0	0	0	1	0	6	16	4	1	8		
ENSMUST00000123291	ENSMUSG00000044005	10	128194457	128210004	1	0	0	0	88	5	2	0	0	0	0	0	E0CXA4	
ENSMUST00000123292						0	0	5	2	2	0	260	1096	166	69	52		
ENSMUST00000123293	ENSMUSG00000038369	2	155390656	155473894	-1	16	16	90	0	20	0	0	0	0	0	0	A2AQM9	
ENSMUST00000123294						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123296	ENSMUSG00000030869	7	122085403	122101886	-1	169	142	444	182	211	99	6	16	5	6	6	Q569N0	Q9CR21
ENSMUST00000123297						1	1	3	1	0	1	0	0	0	0	0		
ENSMUST00000123299						25	23	33	11	30	9	0	6	1	0	4		
ENSMUST00000123300	ENSMUSG00000047907	2	169633013	170071816	1	0	0	0	0	5	0	0	0	0	0	0	A0A0A0MQI3	
ENSMUST00000123301	ENSMUSG00000026027	1	58973522	58995715	1	7	0	0	0	0	0	431	1093	654	163	270		
ENSMUST00000123302	ENSMUSG00000037286	9	100597798	100959375	1	0	0	0	0	5	0	53	0	130	0	0	D6REF2	
ENSMUST00000123303						0	0	2	0	3	2	0	0	0	0	0		
ENSMUST00000123305	ENSMUSG00000054708	10	81628540	81647610	1	0	0	1	0	0	1	0	0	0	0	0	F6WJT5	
ENSMUST00000123306	ENSMUSG00000025261	X	151800807	151935417	1	0	0	0	0	0	0	0	0	0	0	4	F6UYC1	
ENSMUST00000123307						0	0	0	0	0	0	0	5	9	7	0		
ENSMUST00000123308						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123309						2	3	26	183	14	2	0	0	0	0	0		
ENSMUST00000123310	ENSMUSG00000048537	9	44686304	44735198	-1	0	0	0	0	0	0	2	3	0	0	0	F7AWU3	
ENSMUST00000123311	ENSMUSG00000071074	17	46248080	46252537	1	0	0	0	29	0	0	67	53	32	9	0	D3YXM6	
ENSMUST00000123313						5	1	7	8	1	3	1	2	10	0	27		
ENSMUST00000123314						9	0	0	19	0	0	19	45	75	3	111		
ENSMUST00000123315						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000123316	ENSMUSG00000032604	9	108507713	108515941	1	0	0	0	0	0	0	101	435	162	90	160	Q8R1V9	
ENSMUST00000123317						0	0	0	23	1	0	0	0	0	0	0		
ENSMUST00000123319						28	23	48	94	27	10	0	0	1	0	2		
ENSMUST00000123320	ENSMUSG00000032359	9	90054152	90076089	1	0	0	0	0	0	0	340	1549	293	1463	454	D7UEQ9	
ENSMUST00000123321	ENSMUSG00000001827	7	101858331	101870788	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123322						13	16	14	12	25	11	0	0	0	0	0		
ENSMUST00000123323						13	2	14	16	9	6	0	26	6	2	10		
ENSMUST00000123324						1	5	3	1	1	0	0	3	0	7	0		
ENSMUST00000123325	ENSMUSG00000022237	15	31291479	31367759	-1	26	0	0	0	26	0	1053	2991	2033	1	1652		Q3U0L2
ENSMUST00000123326						4	0	7	0	3	0	0	0	7	0	0		
ENSMUST00000123327						1	3	8	0	0	0	0	18	0	8	0		
ENSMUST00000123328						0	1	3	3	2	0	0	0	0	0	1		
ENSMUST00000123329						49	34	105	44	49	30	3	31	10	1	20		
ENSMUST00000123330	ENSMUSG00000070880	2	70553072	70602014	1	4	1	14	127	5	3	0	0	0	0	0	D3Z5S3	
ENSMUST00000123331	ENSMUSG00000049008	8	15041444	15046078	-1	0	3	0	2	2	0	0	0	0	0	0	D3Z6N0	
ENSMUST00000123332						5	0	0	5	0	3	0	35	35	0	11		
ENSMUST00000123333						2	0	7	36	3	0	3	1	3	0	10		
ENSMUST00000123334						3	7	8	22	3	5	0	1	1	0	1		
ENSMUST00000123335	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	1	0	0	0	4	0	1	0	A3KGV2	
ENSMUST00000123336						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123337						4	2	8	0	7	6	20	170	68	62	130		
ENSMUST00000123338						8	5	15	12	4	0	13	0	0	0	0		
ENSMUST00000123339	ENSMUSG00000020719	11	106780355	106789185	-1	5	5	5	81	12	4	61	53	162	63	129	B1ARC0	
ENSMUST00000123340						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000123342						6	0	6	1	0	1	0	2	0	0	1		
ENSMUST00000123343						7	5	8	3	7	0	2	1	1	0	2		
ENSMUST00000123344						4	3	7	2	8	1	17	50	34	3	41		
ENSMUST00000123345	ENSMUSG00000016940	11	115420128	115431274	1	0	0	0	0	0	0	9	21	7	3	7	F6SH71	
ENSMUST00000123346						3	3	5	4	4	3	0	0	0	0	0		
ENSMUST00000123347						3	2	6	4	4	2	0	0	4	2	5		
ENSMUST00000123349	ENSMUSG00000035900	15	86057695	86137634	1	25	11	54	32	49	26	0	57	20	0	57	D6RET7	
ENSMUST00000123350						556	611	267	2635	584	384	9	62	27	10	17		
ENSMUST00000123351	ENSMUSG00000028469	4	43631935	43651244	1	4	0	0	0	0	0	0	0	0	0	0	F6YN80	
ENSMUST00000123352						4	0	4	4	1	0	0	0	0	0	0		
ENSMUST00000123353						4	2	14	4	7	4	0	0	1	0	5		
ENSMUST00000123354						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123355						0	0	0	0	6	0	42	57	31	12	26		
ENSMUST00000123356						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123357						0	1	1	1	3	2	0	1	0	0	0		
ENSMUST00000123358						4	0	3	136	4	0	70	290	178	24	202		
ENSMUST00000123359						4	0	0	0	0	0	0	0	1	0	3		
ENSMUST00000123360						0	1	0	296	0	4	0	0	0	0	0		
ENSMUST00000123362	ENSMUSG00000031393	X	74026592	74135363	-1	0	0	0	0	0	5	58	61	81	10	43	D3YY81	
ENSMUST00000123364	ENSMUSG00000019892	10	103063198	103236322	-1	2	0	5	8	4	3	0	0	0	0	0	D3Z1J9	
ENSMUST00000123365	ENSMUSG00000015702	3	95296096	95307176	-1	2	1	2	3	3	0	0	0	0	0	0	D3Z1V0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123366						0	2	1	0	0	0	0	1	0	4	0		
ENSMUST00000123367	ENSMUSG00000072662	6	147075060	147087032	-1	1	0	2	4	3	0	0	0	0	0	0		
ENSMUST00000123369	ENSMUSG00000020884	11	70054085	70057894	1	3	0	3	2	4	1	0	0	0	0	0	J3QPT6	
ENSMUST00000123370	ENSMUSG00000005373	5	135089890	135138382	1	16	16	22	17	29	2	0	1	1	4	3	F6Q4B6	
ENSMUST00000123371						0	0	9	6	0	0	6	428	172	190	373		
ENSMUST00000123372	ENSMUSG00000070425	7	102065713	102096864	1	0	0	26	41	31	25	0	4	0	0	13	E9PVR2	
ENSMUST00000123373						4	1	5	93	7	2	0	3	5	0	0		
ENSMUST00000123374						3	4	8	7	6	4	0	0	0	0	0		
ENSMUST00000123375						2	4	11	11	1	4	0	30	12	0	13		
ENSMUST00000123376	ENSMUSG00000018899	11	53770014	53778374	1	0	0	0	0	0	0	11	0	0	0	18	Q5SX14	
ENSMUST00000123378						3	3	24	2	5	0	3	0	11	0	6		
ENSMUST00000123379						18	19	27	72	33	16	2	2	2	0	6		
ENSMUST00000123380						1	2	3	2	4	0	8	8	0	0	31		
ENSMUST00000123381						0	0	0	3	0	1	26	128	36	0	16		
ENSMUST00000123382						0	3	0	0	0	0	0	22	0	0	2		
ENSMUST00000123383						4	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000123384	ENSMUSG00000026634	1	190925112	190946962	1	0	0	0	36	0	0	27	35	12	1	15		Q8K1C0
ENSMUST00000123385						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123386						2	2	9	72	6	5	1	1	2	2	1		
ENSMUST00000123387	ENSMUSG00000041708	15	83779467	83858494	1	26	23	21	24	18	0	0	0	0	0	1	F2Z3Z7	
ENSMUST00000123389	ENSMUSG00000044037	9	110879870	110900530	1	0	1	0	67	2	1	0	0	0	0	2	A0A0G2JEP6	
ENSMUST00000123391						0	1	5	1	1	1	0	0	0	0	0		
ENSMUST00000123392						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000123393						103	126	157	88	88	52	2	10	5	0	9		
ENSMUST00000123394						1	0	9	3	4	4	6	26	0	4	0		
ENSMUST00000123395						0	0	0	8	0	0	4	0	0	1	4		
ENSMUST00000123396						0	0	0	0	0	0	1	18	1	11	6		
ENSMUST00000123397						10	12	40	22	14	8	0	7	0	0	5		
ENSMUST00000123398						3	1	0	142	2	0	0	0	0	0	0		
ENSMUST00000123399	ENSMUSG00000026667	1	170193420	170215397	-1	43	0	0	45	47	15	0	53	86	0	67	D3YUF5	
ENSMUST00000123400						0	0	0	0	0	0	0	0	4	0	6		
ENSMUST00000123401						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123404	ENSMUSG00000028669	4	135975460	135987264	-1	2	0	1	5	2	0	0	4	0	0	3	B1AV58	
ENSMUST00000123405	ENSMUSG00000025702	6	116338024	116409540	1	5	0	2	1	4	0	0	2	2	0	5		
ENSMUST00000123406	ENSMUSG00000048537	9	44686304	44735198	-1	0	0	0	17	0	0	2	0	0	0	0	D3YVQ3	
ENSMUST00000123407						9	9	8	0	7	3	0	0	0	0	0		
ENSMUST00000123408	ENSMUSG00000031342	X	166238911	166388988	1	0	0	0	3	0	0	0	0	0	0	0	H3BIV8	
ENSMUST00000123409	ENSMUSG00000026504	1	176814660	177020437	1	3	0	0	0	0	0	0	0	0	0	0	Q05DD9	
ENSMUST00000123410	ENSMUSG00000032818	18	77281958	77442341	1	5	0	19	6	12	0	0	0	0	0	0	F6XPZ0	
ENSMUST00000123411						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000123412	ENSMUSG00000037492	8	23636019	24156585	1	11	5	4	25	12	4	0	0	1	0	0		Q8BZ94
ENSMUST00000123413	ENSMUSG00000022884	16	23107444	23114136	1	0	0	0	0	10	0	51	784	62	134	40	Q8BTU6	
ENSMUST00000123414						3	6	15	1	7	2	0	0	1	0	1		
ENSMUST00000123415	ENSMUSG00000036980	5	138178617	138187451	-1	6	4	50	30	2	4	9	0	3	0	5	D3Z5H6	
ENSMUST00000123416	ENSMUSG00000030590	7	29152511	29156234	-1	0	0	0	0	0	0	0	0	0	0	0	F7AR27	
ENSMUST00000123417						5	4	1	2	1	5	1	4	1	0	0		
ENSMUST00000123418	ENSMUSG00000031543	8	22974844	23150497	1	30	6	20	166	51	24	0	0	0	0	0	D6RJ51	
ENSMUST00000123419						0	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000123421						3	2	2	0	0	0	6	19	1	1	8		
ENSMUST00000123424						0	2	0	0	0	1	2	0	9	0	2		
ENSMUST00000123425	ENSMUSG00000070000	8	71708387	71725716	-1	0	2	0	5	10	0	0	0	0	0	0	F6VQ30	
ENSMUST00000123426						5	0	4	1	1	0	8	29	8	0	10		
ENSMUST00000123427						0	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000123428	ENSMUSG00000034586	11	115347707	115367756	-1	0	0	0	5	0	0	1	1	0	0	0	F6RGN1	
ENSMUST00000123429	ENSMUSG00000046323	6	122626410	122630272	1	8	3	0	5	4	2	0	0	0	0	0	K4DID3	
ENSMUST00000123430						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123431	ENSMUSG00000053765	5	120847367	120857986	1	1	2	0	0	4	1	0	0	0	0	0	F7AC31	
ENSMUST00000123432						0	1	0	94	1	0	0	0	0	0	0		
ENSMUST00000123433	ENSMUSG00000040990	X	159627272	159978069	1	1	0	2	0	0	0	7	5	8	3	49	B1AZ85	
ENSMUST00000123434	ENSMUSG00000048070	11	66911981	66929876	1	71	40	124	244	104	54	0	9	5	1	12		Q8BFY0
ENSMUST00000123435						2	2	8	2	0	3	0	0	0	0	0		
ENSMUST00000123436						1	8	25	0	9	5	0	0	0	1	0		
ENSMUST00000123437	ENSMUSG00000032698	2	103957986	103981878	1	2	0	5	47	8	3	5	6	12	27	24	Q544Z2	P25801
ENSMUST00000123439	ENSMUSG00000007655	6	17306335	17341452	1	0	2	1	0	3	0	0	0	0	0	0	D3Z0J2	
ENSMUST00000123440						32	33	198	11	65	37	344	1590	194	116	263		
ENSMUST00000123442						0	2	0	1	0	0	23	7	46	8	35		
ENSMUST00000123443	ENSMUSG00000041700	X	145290359	145349089	-1	2	1	4	3	2	0	0	0	0	0	0	B1B0D3	
ENSMUST00000123444						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123446						10	4	20	95	12	4	0	0	1	0	0		
ENSMUST00000123447						0	0	5	1	1	3	0	0	0	0	2		
ENSMUST00000123448						14	5	14	6	6	4	1	0	2	0	1		
ENSMUST00000123449						43	36	307	128	51	22	1	3	0	0	4		
ENSMUST00000123450						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123453	ENSMUSG00000036246	8	69808679	69821870	1	0	9	16	31	15	2	606	1469	622	58	867		Q6PGG2
ENSMUST00000123454	ENSMUSG00000053930	11	66211725	66525964	-1	73	43	195	83	55	24	0	2	0	0	4	F6VQZ6	
ENSMUST00000123456						7	2	11	5	8	3	0	0	4	3	3		
ENSMUST00000123458						1	2	2	0	1	0	0	8	3	3	10		
ENSMUST00000123460	ENSMUSG00000078500	4	145868794	145899975	1	21	21	8	16	15	14	2	1	0	0	0	L7MUC9	
ENSMUST00000123461	ENSMUSG00000023030	15	100387898	100425072	-1	3	2	0	1	7	2	0	0	0	0	0	D3Z314	
ENSMUST00000123464						0	0	0	0	0	1	3	5	7	0	13		
ENSMUST00000123465						0	0	0	0	0	0	0	12	18	43	23		
ENSMUST00000123466	ENSMUSG00000041623	11	113684412	113694647	1	0	0	0	27	0	0	0	5	0	0	14	A2A6P6	
ENSMUST00000123467						0	1	4	32	5	2	7	12	8	0	0		
ENSMUST00000123468						3	0	1	0	6	0	37	0	0	2	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123469						3	4	2	1	3	0	0	2	0	0	0		
ENSMUST00000123470	ENSMUSG00000032231	9	69453620	69491795	1	0	0	6	4	3	0	0	0	0	9	0	B0V2N7	
ENSMUST00000123471	ENSMUSG00000026842	2	31688376	31804227	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY65	
ENSMUST00000123472						4	4	16	6	3	4	0	6	5	0	0		
ENSMUST00000123474						3	0	18	8	3	0	0	0	0	0	12		
ENSMUST00000123475						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123476	ENSMUSG00000028347	4	48585174	48663131	1	3	0	1	24	3	0	0	0	1	2	3		Q6PFE7
ENSMUST00000123477						0	0	12	27	0	0	0	4	0	0	5		
ENSMUST00000123478						6	2	5	4	2	1	4	1	6	0	15		
ENSMUST00000123479						6	2	41	30	9	4	3	3	3	0	10		
ENSMUST00000123481						25	26	41	27	35	15	0	0	0	1	2		
ENSMUST00000123484						13	11	25	28	25	3	2	0	0	0	0		
ENSMUST00000123485						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000123487	ENSMUSG00000046020	2	153241533	153270247	1	33	27	127	26	33	23	0	14	0	0	20	E9PZ15	
ENSMUST00000123488						0	1	0	0	0	0	165	390	155	762	71		
ENSMUST00000123489						0	2	0	0	0	0	59	51	22	6	15		
ENSMUST00000123490	ENSMUSG00000045968	1	153849542	153900228	-1	0	0	0	48	4	8	1	0	1	0	3	D3YXN9	
ENSMUST00000123491	ENSMUSG00000042523	12	84114366	84147498	1	76	62	160	974	103	42	3	8	4	6	22		Q05A62
ENSMUST00000123492	ENSMUSG00000035297	5	100518309	100547803	1	0	0	4	0	3	1	0	16	0	0	5	F6QTS1	
ENSMUST00000123493	ENSMUSG00000038215	8	56531522	56551047	-1	3	2	0	0	1	0	6	24	37	33	14	F7BA57	
ENSMUST00000123494	ENSMUSG00000029775	6	30401868	30455179	1	0	0	0	0	0	0	36	1	21	5	25		
ENSMUST00000123495	ENSMUSG00000035439	8	71248561	71272934	-1	514	608	3165	677	614	343	45	230	61	13	67	D6RCV2	
ENSMUST00000123496						0	22	71	79	41	20	0	0	0	0	0		
ENSMUST00000123497						0	1	0	0	0	0	26	0	0	6	20		
ENSMUST00000123498	ENSMUSG00000047022	12	57230427	57497199	1	3	3	6	2	0	2	0	0	0	12	0	G3UVV8	
ENSMUST00000123499						0	2	0	88	0	1	0	0	1	0	0		
ENSMUST00000123500						2	0	4	0	0	1	2	59	0	0	0		
ENSMUST00000123501						0	0	0	50	1	0	8	6	4	1	0		
ENSMUST00000123502	ENSMUSG00000024018	17	29689378	29717012	-1	17	8	35	25	11	0	34	107	62	8	69		Q9D162
ENSMUST00000123503						35	26	26	30	15	16	4	3	7	1	5		
ENSMUST00000123504						1	1	3	1	0	1	3	12	4	0	4		
ENSMUST00000123505	ENSMUSG00000033416	10	75351111	75517972	-1	0	0	0	0	0	0	5	0	5	0	11	D3Z5D9	
ENSMUST00000123506	ENSMUSG00000034354	11	4480868	4594863	-1	0	0	42	9	25	0	2982	5655	4520	360	3143	R4GML8	
ENSMUST00000123507	ENSMUSG00000020804	11	116586432	116597680	1	0	5	0	4	4	3	0	0	0	1	7	F2Z3V1	
ENSMUST00000123510						11	6	49	26	9	4	3	16	9	0	20		
ENSMUST00000123511						3	2	7	0	4	0	132	165	157	29	227		
ENSMUST00000123512						0	0	5	0	0	0	0	15	77	14	52		
ENSMUST00000123513						6	0	7	43	0	0	0	0	0	0	0		
ENSMUST00000123514	ENSMUSG00000042333	4	154922210	154928563	-1	6	0	13	8	8	0	78	14	38	23	103	Q80WM9	
ENSMUST00000123515						0	0	5	44	3	0	0	0	0	0	0		
ENSMUST00000123516						0	0	0	0	0	0	1	1	0	0	0		
ENSMUST00000123518						9	5	13	6	7	6	0	2	2	1	0		
ENSMUST00000123519	ENSMUSG00000026095	1	53344617	53352752	-1	4	0	1	11	0	1	188	1021	272	1827	300	Q3TGY6	
ENSMUST00000123520						0	0	4	3	5	2	0	0	0	1	0		
ENSMUST00000123521						1	2	5	3	5	0	0	0	0	1	0		
ENSMUST00000123522						2	3	4	0	2	0	0	0	0	0	0		
ENSMUST00000123523						12	4	13	15	11	8	0	0	0	0	0		
ENSMUST00000123524						19	2	15	67	13	2	0	1	1	0	4		
ENSMUST00000123525	ENSMUSG00000025498	7	141262706	141266481	-1	1	3	0	0	6	2	0	32	0	18	12	F6TQ89	
ENSMUST00000123526						7	0	0	10	11	5	1	0	3	0	5		
ENSMUST00000123528						8	2	26	7	8	9	10	12	15	1	36		
ENSMUST00000123529						0	0	0	6	0	3	7	11	0	3	0		
ENSMUST00000123530	ENSMUSG00000033688	9	103250521	103305082	-1	0	0	2	0	0	1	0	0	0	0	0	D3YY36	
ENSMUST00000123531	ENSMUSG00000034593	9	75071015	75223688	1	0	0	0	0	0	0	0	0	0	0	0	D6RFU0	
ENSMUST00000123532	ENSMUSG00000027660	3	31095058	31122577	1	0	1	0	8	0	2	0	0	0	0	5	D3YYG2	
ENSMUST00000123533						21	13	68	13	38	0	9	13	0	0	0		
ENSMUST00000123534	ENSMUSG00000021852	14	49298519	49526046	-1	9	12	10	128	14	2	0	0	0	0	0		Q8BZK4
ENSMUST00000123536						1	1	7	1	1	4	0	0	0	0	0		
ENSMUST00000123537	ENSMUSG00000029464	5	122371876	122382902	1	2	1	37	0	3	0	0	7	8	0	18	F6WZX5	
ENSMUST00000123538						5	8	10	5	5	0	10	16	19	0	42		
ENSMUST00000123539	ENSMUSG00000027695	3	27938695	28133362	1	0	0	20	0	9	2	72	15	142	0	108	D6RH77	
ENSMUST00000123540						0	0	0	0	0	1	15	27	4	48	8		
ENSMUST00000123541	ENSMUSG00000005575	7	13035120	13038275	-1	3	3	3	2	3	0	16	50	25	0	22	F6WMC0	
ENSMUST00000123542						0	0	0	0	2	2	10	14	2	8	9		
ENSMUST00000123543						6	4	5	24	4	3	0	0	0	0	0		
ENSMUST00000123545						3	0	0	0	0	0	1	0	19	0	0		
ENSMUST00000123546						9	4	5	3	10	3	1	1	6	1	5		
ENSMUST00000123547						4	3	3	0	4	1	0	0	0	1	1		
ENSMUST00000123550						4	3	13	3	1	0	8	18	18	0	19		
ENSMUST00000123551						2	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000123552	ENSMUSG00000049538	13	70727802	70841811	-1	12	32	44	45	24	0	0	0	0	0	0	D6RGS8	
ENSMUST00000123553						9	6	15	4	7	4	44	112	65	23	36		
ENSMUST00000123554						1	0	9	28	5	0	4	11	0	0	0		
ENSMUST00000123555	ENSMUSG00000023249	9	106470322	106476949	-1	0	2	1	5	6	2	92	356	112	11	66	Q8CFB8	
ENSMUST00000123556	ENSMUSG00000049565	3	108739658	108782309	1	6	0	22	6	0	0	0	0	0	1	0	Q8BI23	
ENSMUST00000123557	ENSMUSG00000031995	9	31089402	31131853	-1	10	1	17	117	0	0	0	0	1	0	0	D6RIN3	
ENSMUST00000123558	ENSMUSG00000017119	11	101552149	101581951	1	0	0	0	0	0	0	142	317	128	37	315	Q05BC8	
ENSMUST00000123559						5	7	3	1	6	0	2	18	5	0	10		
ENSMUST00000123560						0	0	0	0	0	0	0	6	0	0	0		
ENSMUST00000123561	ENSMUSG00000032740	11	29373658	29510808	1	5	2	3	0	0	0	4	26	9	3	2	F6R1B7	
ENSMUST00000123562						8	7	12	30	8	3	0	0	0	2	0		
ENSMUST00000123563						0	0	0	2	2	0	13	193	102	0	185		
ENSMUST00000123564						0	0	0	0	0	0	0	35	0	0	0		
ENSMUST00000123565	ENSMUSG00000027215	2	93419111	93463140	-1	0	0	5	0	2	0	0	7	0	0	5	A2AIJ1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123566						8	7	8	21	5	2	0	5	0	0	5		
ENSMUST00000123567						15	11	25	13	23	5	0	0	0	0	0		
ENSMUST00000123568						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000123569						3	0	1	2	3	0	2	3	2	0	3		
ENSMUST00000123570						0	1	1	6	1	4	0	0	4	0	0		
ENSMUST00000123571						3	2	1	44	0	0	0	0	0	3	0		
ENSMUST00000123572	ENSMUSG00000035310	5	100441918	100500639	-1	0	0	2	0	11	0	171	0	56	40	83		Q571G4
ENSMUST00000123573						18	17	19	35	39	13	1	1	4	2	11		
ENSMUST00000123575						0	1	0	2	1	0	2	4	0	0	0		
ENSMUST00000123576						2	3	9	200	3	4	0	0	0	0	0		
ENSMUST00000123577						0	0	3	3	0	3	0	0	0	0	0		
ENSMUST00000123578						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000123580						9	11	14	1	6	1	149	1035	265	238	300		
ENSMUST00000123582	ENSMUSG00000025736	17	25828867	25831842	1	0	0	0	0	4	0	0	0	0	0	0	D3Z1G6	
ENSMUST00000123583	ENSMUSG00000001143	1	36419871	36445271	-1	21	34	114	63	27	11	5	9	18	0	10	J3QPK9	
ENSMUST00000123584						2	1	10	3	1	4	2	0	0	4	0		
ENSMUST00000123585	ENSMUSG00000062044	7	45783738	45804144	1	0	0	0	0	0	0	0	0	0	0	0	D3Z2L9	
ENSMUST00000123586						3	1	2	4	1	1	0	5	0	0	1		
ENSMUST00000123587						3	2	3	40	11	3	0	0	0	0	4		
ENSMUST00000123588						0	2	0	1	1	0	0	0	0	0	0		
ENSMUST00000123589						33	21	22	172	24	13	0	4	5	0	10		
ENSMUST00000123590						0	0	0	0	0	5	95	863	86	181	92		
ENSMUST00000123591						4	2	3	2	5	3	28	25	53	17	44		
ENSMUST00000123593						0	0	6	1	1	0	0	0	0	0	0		
ENSMUST00000123594	ENSMUSG00000024767	19	7198202	7206316	-1	0	0	5	28	13	0	0	0	0	0	0	D3YWF6	
ENSMUST00000123596						0	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000123597						2	4	0	0	1	1	0	0	0	0	0		
ENSMUST00000123598	ENSMUSG00000027355	2	116878691	116892494	1	0	0	0	0	0	0	0	0	0	0	0	Z4YLS6	
ENSMUST00000123599	ENSMUSG00000021460	13	52835119	52929681	-1	0	3	0	23	3	1	51	10	83	8	66	F6R307	
ENSMUST00000123600	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	0	9	0	44	20	46	E9QA82	
ENSMUST00000123601						4	3	25	4	3	0	11	84	5	4	8		
ENSMUST00000123602						9	0	54	41	18	4	76	381	94	14	109		
ENSMUST00000123603						4	2	0	7	5	2	0	31	0	0	9		
ENSMUST00000123604	ENSMUSG00000066042	4	132458731	132463921	-1	7	2	0	1	4	1	0	0	0	0	0	A8Y5Q6	
ENSMUST00000123605	ENSMUSG00000031730	8	109591343	109608673	-1	0	0	0	0	0	0	15	47	25	3	20		O35435
ENSMUST00000123607						2	1	5	17	5	1	0	0	0	0	0		
ENSMUST00000123608						1	3	3	0	0	0	0	0	0	0	4		
ENSMUST00000123609						0	0	0	0	0	1	8	0	0	0	9		
ENSMUST00000123611	ENSMUSG00000058388	3	103968110	104024598	1	0	0	0	68	0	0	0	0	12	0	12	D3Z6K3	
ENSMUST00000123612						1	0	14	5	3	0	0	0	0	0	0		
ENSMUST00000123614	ENSMUSG00000072946	12	84285232	84315832	1	12	11	35	9	16	5	99	454	224	143	145		Q8VDQ1
ENSMUST00000123615						2	0	4	5	1	2	0	0	0	0	0		
ENSMUST00000123616	ENSMUSG00000025825	5	113772748	113778288	1	0	0	0	39	0	0	5	19	6	5	8	D6RE47	
ENSMUST00000123617	ENSMUSG00000040690	4	130047840	130099283	1	2	2	2	1	1	0	0	0	0	1	0	A3KFV6	
ENSMUST00000123618						16	10	25	16	18	2	0	0	0	0	0		
ENSMUST00000123619	ENSMUSG00000027966	3	114030540	114220718	1	5	2	12	9	6	6	0	0	0	0	0	E9PVT8	
ENSMUST00000123621						0	0	0	0	0	0	0	35	9	14	3		
ENSMUST00000123622						178	144	443	659	203	117	12	53	24	7	24		
ENSMUST00000123624						0	0	0	0	0	0	0	2	7	0	0		
ENSMUST00000123625						0	0	1	0	4	2	10	263	0	65	0		
ENSMUST00000123626	ENSMUSG00000048175	15	98134637	98165625	-1	0	0	0	38	2	0	40	17	87	13	50		
ENSMUST00000123627						29	28	82	28	14	15	2	0	2	0	0		
ENSMUST00000123628						1	0	0	1	0	5	0	3	0	2	0		
ENSMUST00000123629						2	4	0	22	1	1	0	0	0	0	0		
ENSMUST00000123630	ENSMUSG00000001827	7	101858331	101870788	-1	1	3	5	0	0	4	0	0	0	0	0		
ENSMUST00000123631						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123632	ENSMUSG00000043924	4	135369576	135398227	-1	0	0	7	0	0	1	0	0	0	0	2	A2A990	
ENSMUST00000123634						0	0	0	12	0	0	5	0	0	0	0		
ENSMUST00000123635						0	0	2	3	0	0	0	0	0	0	0		
ENSMUST00000123636	ENSMUSG00000041143	4	138972888	139059171	1	2	1	0	17	5	0	30	10	16	0	11	A2ALL4	
ENSMUST00000123637	ENSMUSG00000035390	7	4690604	4715997	1	2	4	4	1	8	1	1	1	0	0	1		
ENSMUST00000123638	ENSMUSG00000030945	7	119554469	119600694	1	0	0	1	0	1	0	0	0	0	0	0	F6XLJ8	
ENSMUST00000123639						5	2	0	5	3	1	0	0	0	0	0		
ENSMUST00000123640						4	2	0	0	4	6	2	0	1	1	21		
ENSMUST00000123641						23	19	22	27	29	14	3	6	6	2	9		
ENSMUST00000123642						0	4	0	4	3	0	200	1058	390	98	322		
ENSMUST00000123643						0	0	0	131	4	2	0	0	0	0	0		
ENSMUST00000123645						6	3	0	5	13	0	5	29	23	148	31		
ENSMUST00000123646	ENSMUSG00000023967	17	46110986	46128910	1	0	0	0	6	0	0	4	0	6	0	1	D3Z603	
ENSMUST00000123647	ENSMUSG00000015222	1	66175273	66442583	1	2	0	0	2	1	0	0	0	0	0	0	E9Q8Y2	
ENSMUST00000123648						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000123649						16	15	70	27	27	10	0	5	0	0	2		
ENSMUST00000123650	ENSMUSG00000025420	18	76977148	77047308	-1	0	1	0	0	0	2	0	0	0	0	0	D3Z087	
ENSMUST00000123651						3	5	50	15	9	3	0	0	0	0	0		
ENSMUST00000123652	ENSMUSG00000029053	4	155260129	155361361	-1	2	0	1	16	3	0	0	0	0	0	0	A2AD72	
ENSMUST00000123653						1	2	7	4	3	0	2	30	17	4	15		
ENSMUST00000123655						3	2	6	3	2	5	0	0	0	0	0		
ENSMUST00000123656						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123657	ENSMUSG00000021694	13	108158731	108195364	1	5	8	3	36	10	5	0	0	8	0	0	D6RET0	
ENSMUST00000123658						5	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123659						18	9	22	6	12	12	2	4	2	2	1		
ENSMUST00000123660						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123661						0	0	0	5	0	0	124	81	106	10	156		
ENSMUST00000123662	ENSMUSG00000037791	11	77982754	78030539	1	0	0	2	0	0	0	9	13	18	0	23	F7AKS4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123664						2	1	5	0	1	4	2	2	0	0	3		
ENSMUST00000123665						0	0	0	105	0	1	0	3	1	0	2		
ENSMUST00000123666	ENSMUSG00000030846	7	128439777	128461717	-1	0	2	0	38	0	1	19	76	14	11	25	D6RGU1	
ENSMUST00000123667						0	0	9	0	4	0	0	0	0	2	3		
ENSMUST00000123669						15	0	57	9	7	6	23	47	15	0	26		
ENSMUST00000123670						10	12	30	116	14	15	0	5	3	0	0		
ENSMUST00000123671						25	10	26	12	19	0	3	19	7	0	30		
ENSMUST00000123672	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123673	ENSMUSG00000036208	16	44724301	44737284	1	0	0	0	6	0	0	0	0	2	0	0	D6RFS8	
ENSMUST00000123674						5	6	15	14	13	3	0	1	0	0	0		
ENSMUST00000123675						0	1	2	0	0	1	6	0	11	0	17		
ENSMUST00000123676	ENSMUSG00000017221	11	98682554	98695979	1	1	2	1	1	3	1	0	16	15	0	12	F7B7L8	
ENSMUST00000123677						6	3	43	84	10	4	0	0	2	0	0		
ENSMUST00000123678	ENSMUSG00000042323	14	31019138	31121592	1	0	5	9	0	0	6	0	0	0	0	0	D6RIL0	
ENSMUST00000123679						2	4	2	2	5	3	0	8	6	3	16		
ENSMUST00000123680	ENSMUSG00000010607	9	22156846	22158358	1	0	0	2	13	0	0	112	173	81	220	45		P0C1P0
ENSMUST00000123681						0	0	0	1	1	1	0	0	3	3	5		
ENSMUST00000123682	ENSMUSG00000055923	5	76873659	76905514	-1	11	9	11	7	20	6	4	10	5	0	10	E9PUJ1	
ENSMUST00000123683						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000123684	ENSMUSG00000059363	19	24261453	24280605	-1	38	20	9	0	8	0	0	0	0	0	0	E9Q2P9	
ENSMUST00000123685						0	0	0	38	0	0	0	0	0	0	0		
ENSMUST00000123686	ENSMUSG00000024048	17	70993656	71002878	-1	4	5	3	7	5	5	0	0	751	1116	769	Q6ZWQ9	
ENSMUST00000123687	ENSMUSG00000020886	11	70017085	70045532	1	5	2	2	0	9	4	2	3	4	2	2	G3UZL5	
ENSMUST00000123688						4	5	7	1	6	4	2	4	0	2	2		
ENSMUST00000123689						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123690	ENSMUSG00000039285	9	118040499	118069794	1	3	1	1	0	0	0	26	240	118	12	35	F6SY96	
ENSMUST00000123691						2	1	7	53	1	0	0	0	0	0	0		
ENSMUST00000123692						3	0	2	4	0	3	0	0	0	0	0		
ENSMUST00000123693	ENSMUSG00000072946	12	84285232	84315832	1	0	0	0	0	0	0	27	49	22	0	22	D6RGL6	
ENSMUST00000123694						0	3	3	0	3	0	1	25	0	3	4		
ENSMUST00000123695						21	8	52	24	25	15	1	0	1	2	3		
ENSMUST00000123696						11	7	37	52	9	7	43	64	25	9	9		
ENSMUST00000123697						1	0	0	77	0	2	0	0	0	0	0		
ENSMUST00000123698						0	0	3	0	1	2	0	0	0	0	0		
ENSMUST00000123701						0	2	2	2	0	0	58	83	102	229	42		
ENSMUST00000123702						0	2	17	7	14	9	6	6	6	0	16		
ENSMUST00000123704						0	0	0	0	0	0	12	0	37	0	0		
ENSMUST00000123705	ENSMUSG00000026466	1	156004599	156036480	-1	2	0	0	0	6	2	16	0	0	0	9	D3YXF8	
ENSMUST00000123706						5	5	0	2	9	3	2	2	4	0	0		
ENSMUST00000123708	ENSMUSG00000039997	1	173920407	173942672	-1	14	0	350	107	0	0	0	0	17	1	46	E9PUG6	
ENSMUST00000123709	ENSMUSG00000041268	9	54365158	54501760	-1	22	0	0	0	9	0	145	1432	86	8	4	F6RYL8	
ENSMUST00000123710	ENSMUSG00000041718	X	144317804	144374450	1	1	2	13	13	2	2	0	0	4	0	0	E9Q161	
ENSMUST00000123712	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z7N2	
ENSMUST00000123713						4	3	12	3	3	0	0	0	1	0	0		
ENSMUST00000123714	ENSMUSG00000026820	2	32395896	32405772	1	2	0	0	11	1	0	9	28	6	0	5	A0A0A6YWP8	
ENSMUST00000123715	ENSMUSG00000024457	17	36837134	36859398	1	0	0	0	0	0	0	0	6	0	0	0		Q99PN3
ENSMUST00000123716	ENSMUSG00000040938	11	70212752	70216417	1	9	0	17	4	10	2	0	0	0	0	0	D6RDF0	
ENSMUST00000123717						17	11	35	154	25	11	16	12	38	0	26		
ENSMUST00000123718						0	2	0	0	0	0	0	17	13	0	2		
ENSMUST00000123719						5	0	0	4	4	8	0	0	0	0	0		
ENSMUST00000123720	ENSMUSG00000054976	1	81076950	81341764	1	0	0	8	6	0	6	0	0	0	0	0	D3Z3N9	
ENSMUST00000123721						258	262	270	177	364	149	4	17	7	2	16		
ENSMUST00000123723						7	0	4	0	1	0	17	61	49	0	43		
ENSMUST00000123724	ENSMUSG00000022487	15	103402405	103430470	-1	0	0	0	1	0	0	0	0	0	0	0	D3YV29	
ENSMUST00000123725	ENSMUSG00000014418	7	46760466	46796064	-1	1	0	3	0	0	0	0	0	0	0	0	D3Z3L4	
ENSMUST00000123726	ENSMUSG00000017421	11	80383279	80405733	1	9	7	23	3	7	11	180	413	217	51	273	M0QWF0	
ENSMUST00000123727	ENSMUSG00000039652	19	37021291	37208601	-1	27	21	26	150	72	24	0	5	11	3	14	D3Z1R6	
ENSMUST00000123728	ENSMUSG00000040666	16	96200470	96228933	1	0	4	0	0	0	0	0	0	0	0	0	K4DI78	
ENSMUST00000123730						0	0	2	0	0	2	0	75	6	11	18		
ENSMUST00000123731	ENSMUSG00000035623	7	97579889	97692778	1	0	0	0	0	3	0	54	278	44	155	116		
ENSMUST00000123732	ENSMUSG00000029994	6	86736840	86793584	-1	0	0	0	0	0	0	24	0	27	222	71	D3Z0S1	
ENSMUST00000123733						1	0	2	0	1	0	0	2	2	0	2		
ENSMUST00000123735	ENSMUSG00000026254	1	87213914	87240488	1	0	0	7	0	0	0	21	0	20	0	0	M0QWD1	
ENSMUST00000123736	ENSMUSG00000029516	5	115845278	116008947	1	0	2	11	28	15	6	9	6	5	2	10	H3BJ74	
ENSMUST00000123737						0	0	1	0	4	2	3	7	13	0	6		
ENSMUST00000123738	ENSMUSG00000034023	6	113531682	113597017	1	2	0	0	2	2	1	0	0	1	0	0	F7CAP1	
ENSMUST00000123739	ENSMUSG00000031842	8	70723720	70751186	1	3	4	9	4	11	2	0	0	0	0	0	D3Z2G1	
ENSMUST00000123740	ENSMUSG00000039254	2	32236590	32255005	1	0	1	6	0	0	0	7	0	0	0	0	B0R071	
ENSMUST00000123743						1	0	4	3	3	1	10	23	28	4	28		
ENSMUST00000123744						29	41	152	140	38	27	15	51	20	12	36		
ENSMUST00000123745						2	0	1	52	2	1	0	0	0	0	0		
ENSMUST00000123746						9	4	37	11	12	8	0	0	0	0	0		
ENSMUST00000123748						4	0	1	0	0	6	11	23	5	17	8		
ENSMUST00000123749	ENSMUSG00000028944	5	24862744	25100642	-1	0	0	1	38	2	1	0	0	0	0	0	D3Z5V5	
ENSMUST00000123750	ENSMUSG00000034006	18	80253292	80292725	1	0	3	7	1	2	7	1264	1331	781	256	392		Q80XM9
ENSMUST00000123751						2	2	0	1	3	2	5	11	6	23	3		
ENSMUST00000123752						0	0	4	3	4	4	0	0	2	0	0		
ENSMUST00000123753	ENSMUSG00000028064	3	88435959	88461182	-1	7	0	0	4	1	0	3	0	4	1	7	D3YWK5	
ENSMUST00000123754						2	3	28	7	1	3	0	0	0	0	0		
ENSMUST00000123755						3	5	20	3	5	2	0	0	0	0	0		
ENSMUST00000123756						11	9	9	8	21	0	2	3	0	0	6		
ENSMUST00000123758						3	5	5	0	0	0	0	12	3	10	12		
ENSMUST00000123759	ENSMUSG00000005089	2	102658659	102790784	1	0	0	0	0	0	0	0	0	0	0	0	A2AQI7	
ENSMUST00000123760	ENSMUSG00000002345	8	70139499	70167488	1	0	4	2	8	9	4	0	0	0	4	0	D6RJ21	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123761						2	2	13	2	11	0	0	0	3	0	3		
ENSMUST00000123762						0	1	2	0	0	0	51	177	85	36	24		
ENSMUST00000123763						3	3	9	4	3	2	0	0	0	0	0		
ENSMUST00000123765	ENSMUSG00000028649	4	123349633	123684360	-1	0	0	0	0	5	0	2	82	0	7	0	F6RCJ3	
ENSMUST00000123766	ENSMUSG00000021608	13	73467197	73516422	1	15	3	0	0	0	11	125	317	0	45	99	D6RE48	
ENSMUST00000123767						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000123768	ENSMUSG00000031444	8	13037308	13056676	1	2	3	4	3	2	1	23	18	16	9	10	D3Z7R3	
ENSMUST00000123769	ENSMUSG00000042198	4	3938888	3951046	1	0	0	0	0	1	0	0	17	4	0	0	B1AXC7	
ENSMUST00000123770	ENSMUSG00000071708	X	157443855	157492287	-1	0	0	0	22	4	2	0	0	0	0	0	A2AC81	
ENSMUST00000123771	ENSMUSG00000032470	9	99385420	99437381	-1	1	0	1	0	0	0	0	0	0	0	0	D3Z2V6	
ENSMUST00000123772						0	0	7	4	0	0	6	0	12	18	4		
ENSMUST00000123773						0	2	9	0	5	0	0	26	14	15	5		
ENSMUST00000123774	ENSMUSG00000033809	16	20605451	20610768	-1	0	5	29	0	0	7	3	0	6	4	0	D6RCW8	
ENSMUST00000123775						5	1	7	4	7	0	0	0	0	0	0		
ENSMUST00000123776						2	4	0	1	0	0	0	2	0	0	7		
ENSMUST00000123778						3	0	5	0	6	1	35	93	6	14	37		
ENSMUST00000123779						1	1	5	3	2	2	0	0	0	0	0		
ENSMUST00000123780						0	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000123781						7	7	0	4	1	6	10	4	9	6	1		
ENSMUST00000123782						26	21	14	189	49	0	2	1	1	0	6		
ENSMUST00000123783						12	24	29	12	8	5	0	0	0	0	0		
ENSMUST00000123785						21	19	58	10	20	12	4	10	7	1	3		
ENSMUST00000123786	ENSMUSG00000030352	6	127961396	128143594	-1	2	0	6	80	6	3	1	1	1	0	2	D3YXN7	
ENSMUST00000123787						4	4	13	10	10	0	0	5	0	0	0		
ENSMUST00000123788	ENSMUSG00000024667	19	10533865	10556238	-1	4	7	2	0	2	0	3	42	22	0	12		Q9CQC4
ENSMUST00000123789						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123790						12	8	13	19	2	6	2	6	0	0	2		
ENSMUST00000123791	ENSMUSG00000036529	15	89288236	89315311	-1	31	0	39	146	0	0	0	19	259	12	238		Q6ZPE2
ENSMUST00000123792						3	0	0	1	3	3	0	12	3	0	3		
ENSMUST00000123793						7	2	11	16	5	2	0	0	0	0	0		
ENSMUST00000123794						5	3	1	1	2	1	4	0	0	1	0		
ENSMUST00000123795						0	0	0	9	2	0	115	237	98	86	12		
ENSMUST00000123796						0	0	3	2	5	0	2	15	20	15	3		
ENSMUST00000123797	ENSMUSG00000037446	17	28351515	28365182	-1	0	0	0	0	0	0	0	0	0	0	0	B8JJC6	
ENSMUST00000123798						0	0	2	0	5	2	7	109	17	8	38		
ENSMUST00000123799						4	3	1	7	1	0	0	0	0	0	0		
ENSMUST00000123801						2	1	1	1	1	1	0	1	0	2	0		
ENSMUST00000123802						2	0	0	0	0	0	6	40	1	0	7		
ENSMUST00000123803						5	12	6	8	5	9	6	25	23	5	11		
ENSMUST00000123804						9	8	13	8	13	0	0	0	0	0	0		
ENSMUST00000123805						8	2	32	7	7	1	0	0	0	0	0		
ENSMUST00000123806						51	63	236	42	29	29	16	89	33	0	65		
ENSMUST00000123807						5	9	0	8	6	3	4	1	19	3	21		
ENSMUST00000123809						3	3	0	6	3	1	4	3	0	0	12		
ENSMUST00000123811	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	0	0	33	34	25	5	27	F6WPM5	
ENSMUST00000123813						3	2	1	1	5	0	0	0	0	0	0		
ENSMUST00000123814						1	2	1	9	1	2	0	0	0	0	0		
ENSMUST00000123815						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000123816						0	3	9	2	0	0	12	44	42	11	75		
ENSMUST00000123817						0	0	0	9	0	2	3	0	0	0	0		
ENSMUST00000123818	ENSMUSG00000072980	2	119609512	119618469	-1	0	0	0	0	0	0	10	14	6	4	3		A2AQ14
ENSMUST00000123819	ENSMUSG00000038188	11	75513540	75526582	1	24	0	0	35	12	11	8	0	0	0	0	D6RJK6	
ENSMUST00000123820						1	2	9	4	0	0	0	92	0	0	0		
ENSMUST00000123821						0	0	4	19	5	1	7	0	0	0	2		
ENSMUST00000123822	ENSMUSG00000041673	14	32991382	33015292	1	1	2	3	3	3	2	0	0	0	0	0	D3Z0P1	
ENSMUST00000123823	ENSMUSG00000029761	6	34598500	34775473	1	0	0	1	2	0	0	0	0	0	0	0	F6ZAW1	
ENSMUST00000123824						15	22	52	37	43	20	17	119	23	34	50		
ENSMUST00000123825	ENSMUSG00000026201	1	75210838	75215606	1	0	0	0	0	0	0	11	28	29	7	30	D3YXM1	
ENSMUST00000123826	ENSMUSG00000056153	18	88665224	88927481	-1	0	15	0	0	0	0	68	117	44	0	0		Q9JLY0
ENSMUST00000123827	ENSMUSG00000041025	4	139530548	139620382	1	9	12	4	9	25	11	16	23	19	2	23	B1AZL1	
ENSMUST00000123830						33	39	83	122	38	18	4	24	9	6	7		
ENSMUST00000123831						0	0	2	0	0	0	0	0	21	0	68		
ENSMUST00000123832						0	0	0	0	0	0	0	1	0	0	1		
ENSMUST00000123833						108	88	136	450	129	73	7	18	15	2	15		
ENSMUST00000123835						1	0	8	12	2	0	1	11	2	0	6		
ENSMUST00000123836	ENSMUSG00000001134	X	20941722	20962017	-1	0	2	4	0	6	6	7	34	10	20	0	Q8CEJ2	
ENSMUST00000123837						2	2	7	0	5	1	0	0	0	0	2		
ENSMUST00000123838						205	103	955	544	144	77	6	18	14	2	29		
ENSMUST00000123839						3	4	29	6	1	0	3	75	13	0	8		
ENSMUST00000123842						0	0	2	0	0	2	7	0	0	0	0		
ENSMUST00000123843	ENSMUSG00000026771	2	23506220	23572106	-1	0	0	0	48	2	0	0	0	0	2	0	A0A0A6YXV6	
ENSMUST00000123844						0	1	2	0	5	1	0	0	3	0	0		
ENSMUST00000123845						0	4	0	4	1	0	0	0	44	15	16		
ENSMUST00000123846						1	16	46	62	2	17	0	0	0	0	0		
ENSMUST00000123848						0	3	6	21	5	2	0	2	0	5	0		
ENSMUST00000123849						20	20	70	15	19	18	4	19	7	0	10		
ENSMUST00000123851	ENSMUSG00000079636	X	37458585	37473964	1	0	0	0	0	0	0	0	0	0	0	0	K7N6R6	
ENSMUST00000123852						6	5	5	9	8	1	1	4	2	0	1		
ENSMUST00000123853	ENSMUSG00000022016	14	78492246	78536860	-1	62	56	109	0	61	21	52	126	113	69	8	E9Q777	
ENSMUST00000123854	ENSMUSG00000028591	4	144391674	144408464	-1	0	1	0	0	2	3	0	0	0	0	0	B1ARV8	
ENSMUST00000123855	ENSMUSG00000001323	11	74906359	74925948	-1	0	0	0	4	0	0	3	1	3	0	0	Z4YMF3	
ENSMUST00000123856	ENSMUSG00000029173	5	52640087	52669708	-1	1	0	0	0	2	0	0	0	0	0	0	F6ZFG8	
ENSMUST00000123857						5	1	13	38	3	3	0	1	4	6	11		
ENSMUST00000123858						7	5	5	3	4	3	0	0	2	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123859						0	1	2	86	6	1	0	0	0	0	0		
ENSMUST00000123860						3	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000123861	ENSMUSG00000000766	10	6758506	7038198	1	2	0	4	2	1	1	0	0	0	0	0	A1KZZ4	
ENSMUST00000123862						1	0	4	3	0	0	0	0	0	0	0		
ENSMUST00000123863	ENSMUSG00000078889	2	175789357	175801093	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q9W0	
ENSMUST00000123864	ENSMUSG00000035172	11	101162679	101171351	-1	7	5	13	35	14	11	4	1	0	0	1	A2A4L0	
ENSMUST00000123865						0	0	1	0	0	7	0	1	0	1	0		
ENSMUST00000123866	ENSMUSG00000023902	17	23600856	23611019	1	10	0	7	3	7	0	0	0	0	0	0	D3Z3Z6	
ENSMUST00000123867	ENSMUSG00000001520	6	128399296	128416427	1	3	0	0	0	3	0	0	0	0	0	0	E9QAD1	
ENSMUST00000123868						0	0	0	0	0	0	0	0	2	0	1		
ENSMUST00000123869						0	0	2	14	0	0	0	0	0	0	0		
ENSMUST00000123870	ENSMUSG00000001829	7	101663633	101790168	1	0	1	2	38	2	0	0	0	0	0	0	D6RIQ2	
ENSMUST00000123871						2	0	1	3	2	0	0	0	7	0	0		
ENSMUST00000123872	ENSMUSG00000058925	18	57533780	57731065	1	0	2	3	6	1	0	0	0	0	0	0	F7AIZ1	
ENSMUST00000123873						1	1	4	2	6	1	6	0	5	2	0		
ENSMUST00000123874	ENSMUSG00000024835	19	4148619	4154035	1	0	0	0	4	0	0	28	0	17	3	2	D3YUG6	
ENSMUST00000123875	ENSMUSG00000022185	14	54642161	54686931	-1	0	0	0	0	2	0	0	0	0	0	2	B8JJ90	
ENSMUST00000123876	ENSMUSG00000045576	3	104864005	104930064	1	0	0	0	0	0	0	0	0	0	3	0	S4R2B4	
ENSMUST00000123877						0	2	7	6	0	0	0	0	1	0	0		
ENSMUST00000123878						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123879	ENSMUSG00000021830	14	45134448	45220328	-1	9	9	20	5	8	4	0	0	0	0	0		Q7TN22
ENSMUST00000123880						6	0	3	0	1	1	0	0	0	0	0		
ENSMUST00000123881						7	5	10	1	0	6	0	0	0	0	1		
ENSMUST00000123883						33	27	90	37	50	19	1	0	1	0	1		
ENSMUST00000123884	ENSMUSG00000057110	2	35109492	35178822	1	10	2	10	0	17	8	18	69	25	0	56	F6QP53	
ENSMUST00000123885						0	3	5	6	0	0	83	178	57	101	65		
ENSMUST00000123887						0	2	7	0	0	2	0	0	0	0	0		
ENSMUST00000123888						35	34	69	29	37	9	6	20	12	2	23		
ENSMUST00000123889						2	0	0	5	2	0	45	39	32	0	21		
ENSMUST00000123890						14	4	33	9	12	1	0	17	2	0	7		
ENSMUST00000123892						7	3	7	4	3	1	0	0	0	0	0		
ENSMUST00000123893						3	0	0	0	4	0	12	82	46	9	69		
ENSMUST00000123895	ENSMUSG00000017309	11	102041509	102055620	1	0	0	0	0	0	2	6	0	5	0	18	X1WI18	
ENSMUST00000123896	ENSMUSG00000054708	10	81628540	81647610	1	0	0	8	3	2	0	0	0	0	0	0	D3Z4H0	
ENSMUST00000123897						43	43	65	38	56	21	1	5	3	3	6		
ENSMUST00000123898	ENSMUSG00000031431	X	140539528	140600659	-1	0	0	0	0	0	0	0	0	395	353	460	B1AVF2	
ENSMUST00000123900						1	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000123901						5	3	0	0	0	12	0	0	0	0	0		
ENSMUST00000123902						9	9	10	3	14	0	0	0	3	0	3		
ENSMUST00000123903						0	3	9	5	5	5	0	0	0	0	0		
ENSMUST00000123906						0	0	0	0	0	0	0	5	0	1	2		
ENSMUST00000123907	ENSMUSG00000004631	6	4674350	4747207	-1	0	0	0	0	0	0	0	0	0	0	0	F6ULV5	
ENSMUST00000123908	ENSMUSG00000026991	2	59160850	59355208	1	0	0	0	55	0	0	0	0	0	0	0	A2AS44	
ENSMUST00000123909	ENSMUSG00000042208	11	23564961	23633639	-1	5	6	1	0	3	1	1	12	5	18	1	Z4YM60	
ENSMUST00000123910						0	0	2	0	0	2	0	0	0	0	0		
ENSMUST00000123912	ENSMUSG00000030243	6	142350342	142387087	-1	0	0	0	0	0	0	0	0	0	0	0	F7DB73	
ENSMUST00000123913						0	0	8	0	0	0	0	2	0	3	0		
ENSMUST00000123914	ENSMUSG00000074259	9	59680144	59718874	1	0	0	4	57	6	5	0	0	0	0	0	D3YVC0	
ENSMUST00000123915						5	4	9	47	4	0	0	2	0	5	0		
ENSMUST00000123916						0	3	7	22	0	2	0	0	0	0	4		
ENSMUST00000123917						0	0	0	0	0	0	0	0	0	11	0		
ENSMUST00000123918	ENSMUSG00000022747	16	58468125	58524243	-1	0	0	0	0	0	0	0	0	0	0	0	A6X953	
ENSMUST00000123919						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000123921	ENSMUSG00000039737	5	136178127	136198963	-1	4	1	0	2	2	0	16	72	22	53	22	F7ATT9	
ENSMUST00000123922	ENSMUSG00000048175	15	98134637	98165625	-1	0	1	0	1	2	0	0	0	0	0	0		
ENSMUST00000123923						0	1	1	0	6	2	0	0	2	0	0		
ENSMUST00000123924	ENSMUSG00000021661	13	98263158	98274750	1	0	0	0	0	0	6	52	412	87	51	123	Q6NZJ1	
ENSMUST00000123925						0	2	7	13	3	8	1104	1747	976	207	973		
ENSMUST00000123926	ENSMUSG00000057969	9	107597674	107609229	-1	8	5	25	35	5	7	0	0	2	0	0	M0QWQ7	
ENSMUST00000123927	ENSMUSG00000043687	8	120608602	120647632	-1	3	0	7	26	4	2	2	2	1	0	0	E9PUE0	
ENSMUST00000123928						1	3	2	4	2	1	0	0	1	0	0		
ENSMUST00000123929	ENSMUSG00000025728	17	25926427	25944510	-1	2	2	13	5	0	3	0	12	10	0	14	F6VRD3	
ENSMUST00000123930	ENSMUSG00000030268	6	144993835	145076184	-1	0	6	3	2	2	0	0	0	0	0	0	B2KFA8	
ENSMUST00000123931						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123932	ENSMUSG00000027639	2	157097533	157135265	-1	29	23	48	36	33	14	1002	4818	1974	365	4143	E0CXZ5	
ENSMUST00000123934	ENSMUSG00000036281	2	26362765	26380653	-1	0	0	0	0	0	0	0	0	2	0	0	F7D5X7	
ENSMUST00000123935						5	2	0	5	8	4	0	0	0	0	1		
ENSMUST00000123936						3	3	9	10	4	0	0	2	1	0	0		
ENSMUST00000123937	ENSMUSG00000025786	9	123066160	123113205	-1	0	0	0	0	0	0	0	11	14	0	14	D6RDS4	
ENSMUST00000123939						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000123940	ENSMUSG00000000730	10	78041947	78063622	1	3	4	0	0	11	0	0	0	0	0	0	D3YUQ4	
ENSMUST00000123941	ENSMUSG00000015942	5	134184019	134224355	1	45	27	131	174	55	29	93	298	194	22	187	D6RI26	
ENSMUST00000123942						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123943						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000123945						0	0	1	0	1	0	0	0	0	8	2		
ENSMUST00000123946						1	1	18	6	1	3	0	0	0	0	26		
ENSMUST00000123947						3	3	4	2	1	0	3	8	15	1	13		
ENSMUST00000123948	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	0	0	0	0	0	0	0	0		Q8CBW3
ENSMUST00000123950						0	2	11	6	0	1	20	65	17	2	27		
ENSMUST00000123951	ENSMUSG00000025665	X	111388192	111537959	-1	2	1	0	9	0	0	0	0	0	0	0	B1B0X3	
ENSMUST00000123952	ENSMUSG00000078490	4	155409190	155466823	1	194	209	302	157	178	53	0	20	10	0	8	G3UWF6	
ENSMUST00000123953						4	1	2	1	2	0	0	3	9	0	13		
ENSMUST00000123954						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000123955						2	1	2	1	0	0	0	7	3	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000123956						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000123957	ENSMUSG00000025089	19	58235604	58455909	-1	1	1	0	37	0	0	0	0	0	0	0	D3YWL3	
ENSMUST00000123958						9	6	4	0	0	0	0	255	40	0	0		
ENSMUST00000123959						3	2	0	18	4	1	7	16	17	31	2		
ENSMUST00000123960						3	0	1	0	0	0	5	2	0	0	14		
ENSMUST00000123961						0	1	1	0	1	2	0	0	9	3	0		
ENSMUST00000123962						1	0	1	72	1	0	0	0	0	0	0		
ENSMUST00000123963						0	0	0	0	0	0	2	3	0	0	0		
ENSMUST00000123964						0	0	0	59	0	0	0	0	3	0	24		
ENSMUST00000123965						10	4	10	5	15	7	1	1	7	0	1		
ENSMUST00000123966						3	1	0	1	3	0	2	1	2	1	2		
ENSMUST00000123967	ENSMUSG00000035640	10	80130451	80140835	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q5J1	
ENSMUST00000123968						59	53	549	116	63	54	9	48	16	0	11		
ENSMUST00000123969						3	4	5	7	6	5	0	1	0	0	0		
ENSMUST00000123970						0	0	0	0	0	0	1	12	1	0	0		
ENSMUST00000123971						4	4	4	2	3	0	0	0	2	0	0		
ENSMUST00000123972						4	0	3	2	0	0	133	658	275	52	218		
ENSMUST00000123973	ENSMUSG00000073599	18	35713086	35722356	-1	3	3	13	2	0	3	0	0	0	0	0	F6W6D3	
ENSMUST00000123974						2	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000123975						1	2	6	0	3	0	0	0	0	2	0		
ENSMUST00000123976						8	3	5	3	0	0	185	219	130	270	96		
ENSMUST00000123977						0	0	0	19	0	1	0	17	0	0	26		
ENSMUST00000123978	ENSMUSG00000040428	7	45526330	45554229	1	0	2	2	2	4	0	0	2	0	1	2	D3YVL5	
ENSMUST00000123979						0	1	6	3	8	3	0	0	0	0	0		
ENSMUST00000123980	ENSMUSG00000059447	5	30155248	30184593	1	0	0	4	5	2	0	0	0	0	0	0	D3YXU1	
ENSMUST00000123981						4	4	18	9	6	6	0	0	0	1	0		
ENSMUST00000123982						1	1	0	0	0	0	0	0	1	0	1		
ENSMUST00000123983						0	0	9	0	0	2	0	0	1	0	26		
ENSMUST00000123984						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000123985						3	1	3	71	7	4	19	38	18	46	25		
ENSMUST00000123986						6	4	14	41	2	4	0	0	8	4	1		
ENSMUST00000123987						1	3	0	0	3	0	0	0	0	0	0		
ENSMUST00000123988						9	4	3	12	14	9	0	0	0	0	0		
ENSMUST00000123989	ENSMUSG00000024013	17	29360914	29379660	1	14	11	33	14	34	14	0	12	20	0	21	E9PVB8	
ENSMUST00000123990	ENSMUSG00000026317	8	14881335	14901720	1	0	0	0	8	4	4	15	7	5	0	20	D3Z332	
ENSMUST00000123992	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	2	0	0	0	D3Z454	
ENSMUST00000123993	ENSMUSG00000054708	10	81628540	81647610	1	42	56	159	68	43	26	1	1	3	0	7	D6RE46	
ENSMUST00000123994	ENSMUSG00000028542	4	117834506	117875198	1	0	0	0	0	0	0	6	0	0	0	0	E9Q036	
ENSMUST00000123995						25	23	70	50	44	26	18	228	60	68	122		
ENSMUST00000123996	ENSMUSG00000056724	9	110624789	110654161	-1	0	1	0	0	0	0	0	0	10	0	0	F7CGQ9	
ENSMUST00000123997						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000123999						33	31	0	0	27	33	11	102	0	2	40		
ENSMUST00000124000	ENSMUSG00000038860	2	32986224	33131654	-1	0	0	0	43	0	0	0	0	0	0	0	A2AUQ6	
ENSMUST00000124001	ENSMUSG00000052525	17	71552061	71589533	1	1	0	4	30	1	3	0	0	0	0	0	B2RWC8	Q5IBH7
ENSMUST00000124002						0	8	16	19	0	0	0	90	6	11	20		
ENSMUST00000124004						1	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000124005						6	1	5	6	5	0	0	2	2	0	4		
ENSMUST00000124006						3	3	10	2	5	7	1	11	8	2	25		
ENSMUST00000124007						3	4	12	9	3	3	0	6	19	31	14		
ENSMUST00000124008	ENSMUSG00000034563	9	72985429	73016340	1	7	10	0	0	0	0	0	7056	457	289	1261	G3UVW4	
ENSMUST00000124009						0	2	2	0	0	1	0	0	13	0	2		
ENSMUST00000124010	ENSMUSG00000047694	X	98936316	98949017	1	0	0	4	34	0	1	2	0	4	0	0	B1AV65	
ENSMUST00000124011	ENSMUSG00000035944	15	85832306	85858822	1	0	0	0	0	0	0	0	0	2	0	0	D6RH59	
ENSMUST00000124012						7	9	27	46	7	7	15	26	39	9	38		
ENSMUST00000124014	ENSMUSG00000057606	14	31523082	31591343	-1	1	2	9	1	5	0	0	0	0	0	0	D3Z1C2	
ENSMUST00000124016						6	0	12	0	9	4	0	0	0	0	0		
ENSMUST00000124017						0	0	6	2	0	1	0	0	0	0	0		
ENSMUST00000124019						4	2	12	4	0	0	0	0	0	0	0		
ENSMUST00000124020	ENSMUSG00000032401	9	64117147	64138118	1	12	3	0	15	0	6	0	0	0	0	0	D6RI22	
ENSMUST00000124022	ENSMUSG00000025266	X	150983141	151017322	-1	0	0	0	0	0	0	0	0	0	0	0	S4R289	
ENSMUST00000124023	ENSMUSG00000023861	17	8282904	8297661	1	0	0	0	0	0	0	0	44	36	191	0	D3YWY6	
ENSMUST00000124024	ENSMUSG00000020265	10	77606097	77641543	1	3	3	16	0	2	0	60	106	165	53	32	G3UXQ9	
ENSMUST00000124025						13	9	23	8	14	12	0	0	0	0	0		
ENSMUST00000124026	ENSMUSG00000001827	7	101858331	101870788	-1	7	1	3	5	2	5	0	0	0	0	0		
ENSMUST00000124027						0	0	0	0	0	1	4	0	6	1	2		
ENSMUST00000124029						10	6	4	19	8	3	0	0	0	0	0		
ENSMUST00000124030						4	2	7	12	2	2	5	82	34	4	44		
ENSMUST00000124031						1	0	6	4	4	1	0	0	0	0	0		
ENSMUST00000124032						2	2	2	7	0	1	6	0	6	0	0		
ENSMUST00000124033	ENSMUSG00000040363	X	12036740	12160355	-1	0	0	0	207	30	0	0	0	0	0	0		Q8CGN4
ENSMUST00000124034	ENSMUSG00000011831	5	107744795	107875107	-1	5	0	2	215	4	0	0	7	12	0	0	Q3TMK4	
ENSMUST00000124035	ENSMUSG00000040952	7	24884371	24889806	1	2	0	10	69	5	2	0	0	0	228	41	D3Z5R8	
ENSMUST00000124036	ENSMUSG00000029192	5	36490604	36593276	-1	0	0	6	2	5	0	0	3	0	0	0	G3UVU5	
ENSMUST00000124037						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000124038						3	3	10	27	6	2	0	10	3	2	3		
ENSMUST00000124039						0	0	0	3	0	0	4	0	12	0	22		
ENSMUST00000124040						4	2	0	0	0	1	0	0	0	2	0		
ENSMUST00000124041						0	0	0	0	0	0	0	0	4	0	2		
ENSMUST00000124042	ENSMUSG00000032997	1	75474569	75479307	-1	1	0	0	59	0	0	0	0	0	0	0	D6RGS3	
ENSMUST00000124043						0	0	0	3	0	0	0	0	0	0	1		
ENSMUST00000124044						2	0	2	1	6	0	21	5	28	0	39		
ENSMUST00000124045	ENSMUSG00000048922	14	67676331	67715841	-1	0	0	0	4	0	0	7	0	7	0	0	D3Z5P7	
ENSMUST00000124046	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	6	0	0	0	0	0		Q99PJ1
ENSMUST00000124048						156	155	108	112	175	95	8	39	11	4	15		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124050	ENSMUSG00000030064	6	97286867	97617541	-1	0	2	2	0	0	0	1	0	0	1	2		
ENSMUST00000124051	ENSMUSG00000010311	1	133897199	133907999	-1	6	7	20	14	7	4	0	0	0	0	0	G3UVW2	
ENSMUST00000124052						1	0	2	151	2	2	1	0	2	0	4		
ENSMUST00000124053						3	0	14	20	7	0	0	98	264	0	106		
ENSMUST00000124054						2	2	0	10	2	1	20	13	21	95	22		
ENSMUST00000124057	ENSMUSG00000030562	7	87246096	87398710	1	1	0	4	2	0	0	0	0	0	0	0	D3Z2E1	
ENSMUST00000124058	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z0J5	
ENSMUST00000124059						13	5	1	0	3	0	0	0	0	0	1		
ENSMUST00000124060						0	0	0	16	0	0	0	0	0	0	2		
ENSMUST00000124062						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000124063	ENSMUSG00000036986	9	58218076	58249786	-1	0	0	0	0	1	0	0	0	0	1	0	F6XUT1	
ENSMUST00000124064						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124065	ENSMUSG00000086022	12	11456079	11462928	1	11	2	8	65	8	2	0	0	0	0	0	G3UW63	
ENSMUST00000124066						3	1	1	1	2	1	0	0	0	0	0		
ENSMUST00000124067						0	0	0	0	0	1	22	83	10	77	17		
ENSMUST00000124069						0	0	14	53	14	2	0	0	0	0	0		
ENSMUST00000124070						4	3	0	1	1	1	0	0	0	0	3		
ENSMUST00000124071	ENSMUSG00000028707	4	115915119	115939926	-1	35	0	0	423	72	43	0	4	1	1	0		Q91ZK4
ENSMUST00000124072	ENSMUSG00000058756	11	98740638	98769006	1	0	0	0	0	9	0	1	21	3	0	22		
ENSMUST00000124073						0	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000124074						6	4	0	7	2	2	0	0	3	0	0		
ENSMUST00000124075	ENSMUSG00000072944	X	140006805	140062712	-1	1	1	1	32	1	0	0	0	0	0	0	A2AG14	
ENSMUST00000124076						0	5	0	0	7	2	0	0	0	13	0		
ENSMUST00000124077	ENSMUSG00000008855	11	102194432	102230166	-1	6	0	15	10	5	0	801	382	389	30	541	D6RH93	
ENSMUST00000124078						2	1	7	4	5	3	0	0	3	0	0		
ENSMUST00000124079						1	0	0	28	8	0	0	0	0	0	0		
ENSMUST00000124080						0	0	2	40	2	0	0	0	0	0	0		
ENSMUST00000124081	ENSMUSG00000057110	2	35109492	35178822	1	0	0	0	0	0	0	0	0	0	3	22	A0A0G2JFA2	
ENSMUST00000124082	ENSMUSG00000059810	4	62559847	62704001	1	7	0	39	3	2	2	180	0	0	0	0	I7HFV2	
ENSMUST00000124083						3	1	1	0	4	0	137	193	243	32	265		
ENSMUST00000124084						14	15	53	35	26	9	23	73	41	8	64		
ENSMUST00000124085						2	1	30	11	6	5	0	0	1	1	0		
ENSMUST00000124086						0	1	0	0	1	0	8	15	24	2	9		
ENSMUST00000124087						0	0	3	0	0	0	43	67	74	0	38		
ENSMUST00000124088						6	9	7	17	7	3	0	0	2	0	0		
ENSMUST00000124089	ENSMUSG00000026842	2	31688376	31804227	1	0	1	8	28	6	1	0	0	0	0	0	A2AV23	
ENSMUST00000124090						2	0	0	7	5	2	0	0	0	0	0		
ENSMUST00000124091						2	0	2	5	3	2	0	0	0	0	0		
ENSMUST00000124092						6	4	11	10	9	4	5	40	14	0	42		
ENSMUST00000124093	ENSMUSG00000038651	13	41114307	41171684	1	10	9	15	10	13	4	0	0	0	1	0	D3YWV8	
ENSMUST00000124094						4	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000124096	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	0	0	0	0	0	1	0	F2Z480	
ENSMUST00000124097						27	17	49	37	29	17	4	15	0	2	6		
ENSMUST00000124098	ENSMUSG00000026883	2	35558266	35730994	1	0	0	0	0	9	5	4	0	79	0	137	F6RK07	
ENSMUST00000124099						0	0	0	0	0	0	223	801	348	61	441		
ENSMUST00000124100	ENSMUSG00000098754	2	131909957	131956130	1	0	0	0	0	0	0	0	0	0	2	0	A0A075B668	
ENSMUST00000124101						6	6	16	21	2	3	9	43	28	2	66		
ENSMUST00000124102	ENSMUSG00000052459	16	44085402	44139705	-1	0	0	0	0	0	0	0	0	222	12	148	D3YWH3	
ENSMUST00000124103						1	2	2	5	0	0	0	0	0	0	3		
ENSMUST00000124105						4	2	1	1	0	2	0	0	0	0	0		
ENSMUST00000124107	ENSMUSG00000027346	2	132529082	132587729	-1	0	0	0	0	0	0	0	0	459	10	104	A2AMD6	
ENSMUST00000124109						2	0	2	3	0	0	0	7	0	0	0		
ENSMUST00000124110						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000124111	ENSMUSG00000042625	17	56560965	56584585	-1	16	6	20	14	23	11	24	61	42	5	97	F6VRR0	
ENSMUST00000124112						2	3	6	16	6	0	89	304	156	14	287		
ENSMUST00000124113	ENSMUSG00000031889	8	105225145	105253053	1	11	3	0	0	4	5	0	41	37	49	34	D6RI91	
ENSMUST00000124114						14	6	24	13	19	13	0	13	2	5	9		
ENSMUST00000124115	ENSMUSG00000024431	18	39410545	39491301	-1	0	2	2	11	0	0	2	0	0	0	0	E9Q8A6	
ENSMUST00000124116						7	9	21	6	8	4	0	0	0	0	0		
ENSMUST00000124117	ENSMUSG00000037605	5	81020138	81825133	1	9	0	0	0	8	3	0	0	0	0	0		
ENSMUST00000124119						5	3	4	2	7	5	0	0	0	0	0		
ENSMUST00000124120	ENSMUSG00000027011	2	78868124	78921293	1	23	14	17	386	31	24	0	0	0	0	0	B2FDH7	
ENSMUST00000124121	ENSMUSG00000040537	5	8072352	8368160	-1	2	1	2	0	3	2	0	2	0	0	2	F7CDH3	
ENSMUST00000124123						0	3	30	0	0	0	0	57	40	40	47		
ENSMUST00000124124						5	1	17	7	9	3	0	0	1	2	0		
ENSMUST00000124125						5	0	0	2	8	2	0	0	0	0	0		
ENSMUST00000124126						3	3	8	25	2	2	0	3	1	0	1		
ENSMUST00000124127						21	19	75	51	21	9	0	4	3	6	5		
ENSMUST00000124128						2	0	0	2	3	3	0	0	0	0	0		
ENSMUST00000124129						0	0	0	0	0	0	0	0	0	0	7		
ENSMUST00000124130						0	0	1	3	1	1	0	0	0	0	0		
ENSMUST00000124131						6	5	18	7	17	9	86	64	92	82	106		
ENSMUST00000124132						0	0	0	47	0	0	0	0	0	0	0		
ENSMUST00000124133						0	0	6	0	1	1	20	28	26	0	16		
ENSMUST00000124134	ENSMUSG00000051985	1	135953578	136006342	-1	0	0	0	3	0	0	0	0	0	0	0	F6QKE4	
ENSMUST00000124135	ENSMUSG00000068115	2	150934519	151039382	-1	0	0	0	0	0	0	0	0	0	0	2	A2ANB6	
ENSMUST00000124136	ENSMUSG00000024457	17	36837134	36859398	1	0	0	3	0	0	3	14	19	41	7	27	B8JJ53	
ENSMUST00000124137	ENSMUSG00000036013	X	53273424	53331185	1	0	0	0	0	0	0	0	0	0	0	0	Q9D5J5	
ENSMUST00000124138						0	1	4	2	0	0	0	3	2	0	0		
ENSMUST00000124139						24	20	52	34	27	13	3	10	7	1	9		
ENSMUST00000124140	ENSMUSG00000029276	5	107548967	107597888	-1	2	1	4	67	7	2	0	0	0	0	0	D3Z0L3	
ENSMUST00000124141						0	0	0	0	3	0	0	0	0	1	0		
ENSMUST00000124142	ENSMUSG00000036599	5	140505550	140525724	1	4	5	10	23	4	0	144	28	127	12	94	D3YUY0	
ENSMUST00000124143						19	16	18	24	19	7	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124144						0	3	0	1	2	0	0	0	0	0	0		
ENSMUST00000124145						69	47	41	43	60	18	3	10	7	1	5		
ENSMUST00000124146						3	0	5	0	2	1	0	0	0	0	0		
ENSMUST00000124147						1	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000124148						28	22	52	40	34	25	2	18	4	0	4		
ENSMUST00000124149						0	5	1	7	5	0	0	28	0	4	7		
ENSMUST00000124150						3	0	6	0	0	0	0	0	0	0	0		
ENSMUST00000124151	ENSMUSG00000000530	15	101128522	101145336	1	1	0	2	1	0	0	5	3	10	0	7	D3YUY5	
ENSMUST00000124152						0	0	0	0	0	0	0	11	0	1	0		
ENSMUST00000124154						2	0	21	8	5	0	0	0	3	0	0		
ENSMUST00000124155	ENSMUSG00000036002	4	43032414	43046220	-1	0	0	1	0	1	0	0	0	0	0	5	B0QZW7	
ENSMUST00000124156	ENSMUSG00000021270	12	110690605	110702728	-1	0	0	1	27	1	0	0	0	0	0	0	B7ZC49	
ENSMUST00000124157	ENSMUSG00000026649	1	171113918	171126967	1	0	0	0	0	0	0	0	4	2	0	0	F6VF16	
ENSMUST00000124158	ENSMUSG00000039652	19	37021291	37208601	-1	2	0	0	0	0	0	1	27	17	4	13	F6T0J8	
ENSMUST00000124159						0	0	1	1	1	2	4	14	12	0	16		
ENSMUST00000124161						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000124162						4	0	9	3	1	0	0	7	6	3	3		
ENSMUST00000124163						0	0	0	0	0	0	1	26	19	57	18		
ENSMUST00000124164	ENSMUSG00000033987	11	118021723	118129219	-1	8	5	1	11	7	4	0	0	0	0	0	A2A521	
ENSMUST00000124165						6	2	9	2	4	3	0	0	0	0	0		
ENSMUST00000124168	ENSMUSG00000002963	7	44857139	44862992	1	10	2	13	18	11	2	34	116	33	3	116		
ENSMUST00000124169	ENSMUSG00000001986	X	41400854	41678601	1	0	0	3	0	0	0	0	0	0	0	0	B0QZW2	
ENSMUST00000124170						2	1	12	6	3	2	0	0	0	0	0		
ENSMUST00000124171						0	1	2	1	2	4	0	0	0	1	0		
ENSMUST00000124172						0	0	19	20	14	6	22	192	13	0	55		
ENSMUST00000124173	ENSMUSG00000030059	6	97152997	97179122	-1	0	1	0	0	1	8	1	0	0	0	0	D6RJK7	
ENSMUST00000124174						4	1	6	6	3	5	0	0	0	2	0		
ENSMUST00000124175						3	5	15	5	2	4	2	3	0	0	0		
ENSMUST00000124176						0	2	1	3	3	2	0	0	0	0	0		
ENSMUST00000124177						2	4	1	5	3	2	196	1026	188	31	331		
ENSMUST00000124178						22	23	64	33	19	13	3	6	3	1	5		
ENSMUST00000124179						0	0	0	22	4	0	0	21	23	2	5		
ENSMUST00000124180						2	2	0	1	3	1	0	0	0	0	0		
ENSMUST00000124181						1	9	26	0	9	5	0	0	0	0	0		
ENSMUST00000124183	ENSMUSG00000004113	2	24603887	24763152	-1	0	0	0	0	2	1	0	0	0	0	0	A2AJ01	
ENSMUST00000124185	ENSMUSG00000022779	16	16870736	16892990	1	0	2	0	0	0	0	0	0	0	0	0	F7A473	
ENSMUST00000124186						3	1	9	3	4	0	0	0	0	0	0		
ENSMUST00000124187	ENSMUSG00000027285	2	120609383	120621560	1	47	0	246	122	94	0	487	853	735	646	304		Q9CQS9
ENSMUST00000124188						2	0	0	8	0	3	1	9	23	5	10		
ENSMUST00000124189	ENSMUSG00000100254	7	102083116	102096396	1	22	17	26	3	19	8	2	7	0	0	0		Q9R244
ENSMUST00000124190						11	18	22	31	18	17	0	2	0	0	4		
ENSMUST00000124192	ENSMUSG00000055003	6	119315133	119330766	-1	0	3	19	7	3	0	0	0	0	0	1	D3YY28	
ENSMUST00000124193						30	22	199	35	47	14	0	1	0	1	2		
ENSMUST00000124194						2	2	7	11	3	3	0	0	0	0	0		
ENSMUST00000124195	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	0	0	0	1	0	0	0	6	E9PZQ6	
ENSMUST00000124196						0	0	0	133	0	0	0	0	0	0	0		
ENSMUST00000124197						1	1	0	12	2	1	0	17	4	0	1		
ENSMUST00000124199	ENSMUSG00000025371	11	119913441	119919548	1	0	1	3	29	3	0	0	3	0	0	0	B1AZ40	
ENSMUST00000124200	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	0	0	0	281	1070	266	149	233	Q810E8	
ENSMUST00000124201						0	0	0	18	0	0	0	0	0	0	0		
ENSMUST00000124202						0	0	1	0	1	0	0	0	0	5	0		
ENSMUST00000124203	ENSMUSG00000019970	10	21882184	21999903	1	1	0	0	0	1	0	0	0	0	0	0	F6RKM6	
ENSMUST00000124204						0	3	21	5	3	2	14	90	10	0	9		
ENSMUST00000124205						8	4	10	12	14	8	18	27	15	4	23		
ENSMUST00000124206						2	0	0	177	5	0	0	1	7	0	0		
ENSMUST00000124207	ENSMUSG00000024501	18	43320979	43438286	-1	5	2	0	0	0	4	0	0	0	0	0	D3YUS0	
ENSMUST00000124208						3	3	3	5	7	0	0	0	2	0	0		
ENSMUST00000124209	ENSMUSG00000028555	4	109406623	109444745	1	1	1	2	13	1	0	0	0	0	0	0	A0A0A0MQI5	
ENSMUST00000124211						2	2	0	1	1	0	3	2	1	4	10		
ENSMUST00000124212						61	52	198	29	47	36	4	24	10	5	9		
ENSMUST00000124213						104	74	598	184	64	39	1	1	1	0	3		
ENSMUST00000124215	ENSMUSG00000004035	3	107926334	107931817	-1	0	0	0	0	0	0	0	0	0	0	0	D3YZ29	
ENSMUST00000124216						2	4	6	0	14	2	0	0	0	0	0		
ENSMUST00000124217						19	17	41	35	20	9	11	39	23	16	20		
ENSMUST00000124218						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000124219						16	18	42	33	33	11	1	4	3	2	9		
ENSMUST00000124220						9	5	7	5	8	3	4	4	3	5	16		
ENSMUST00000124221	ENSMUSG00000063652	11	53949965	53980332	-1	0	7	33	20	3	0	0	0	0	0	1	D6RDB6	
ENSMUST00000124222	ENSMUSG00000023927	17	51736187	51833290	-1	3	5	7	159	4	7	0	0	2	0	8	D3Z4F8	
ENSMUST00000124223	ENSMUSG00000032743	7	125707888	125874793	1	14	0	38	45	31	12	0	220	32	7	14	F6XQI1	
ENSMUST00000124224						0	2	3	20	1	1	0	0	0	0	1		
ENSMUST00000124225						14	7	36	26	16	9	1	17	14	2	43		
ENSMUST00000124226	ENSMUSG00000049804	X	134686519	134696757	1	27	17	54	67	25	15	10	38	41	4	10	E9PWM3	
ENSMUST00000124227						1	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000124228	ENSMUSG00000031565	8	25513654	25575714	1	3	3	27	16	7	1	0	0	0	0	3	D3Z4V6	
ENSMUST00000124229						5	5	11	2	15	5	9	10	14	4	14		
ENSMUST00000124231	ENSMUSG00000020315	11	30099395	30268175	-1	15	12	16	46	23	4	0	0	269	0	50	A0A0A0MQG2	
ENSMUST00000124232						0	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000124233	ENSMUSG00000041540	6	143828425	144781977	-1	3	0	2	1	4	1	0	0	0	0	2	B2KFM8	
ENSMUST00000124234	ENSMUSG00000029571	6	13069759	13089269	1	0	0	0	4	1	0	0	44	23	17	4	D3Z0M2	
ENSMUST00000124235						0	0	0	22	1	0	0	8	0	0	0		
ENSMUST00000124236						6	20	39	16	6	9	0	1	0	7	12		
ENSMUST00000124237						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000124239	ENSMUSG00000045349	4	138250403	138261332	1	4	0	16	38	4	2	0	0	16	0	0	A2AM66	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124240						0	0	0	0	4	3	82	3	101	0	26		
ENSMUST00000124242						25	3	25	6	31	30	0	0	0	0	0		
ENSMUST00000124243	ENSMUSG00000022797	16	32608920	32632794	1	0	0	0	86	1	0	0	0	0	0	0	D3YZB9	
ENSMUST00000124244						3	3	5	2	2	3	0	0	0	0	0		
ENSMUST00000124245						31	15	53	24	33	20	0	1	1	0	4		
ENSMUST00000124247	ENSMUSG00000029452	5	121451893	121524183	1	3	0	0	0	8	0	0	0	0	0	0	G3UZ41	
ENSMUST00000124248	ENSMUSG00000019254	7	4481520	4501680	-1	0	0	19	0	4	3	1964	2050	1562	299	1397	F6XWD4	
ENSMUST00000124249						1	1	1	0	0	3	0	0	0	0	0		
ENSMUST00000124250	ENSMUSG00000032449	9	97074961	97111157	-1	9	9	10	7	6	1	31	8	12	2	27	F6R114	
ENSMUST00000124251						2	1	0	0	4	0	0	0	0	0	0		
ENSMUST00000124252						0	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000124253						0	0	5	2	1	1	0	0	1	0	0		
ENSMUST00000124254						3	3	1	0	0	0	4	22	0	14	21		
ENSMUST00000124255						2	0	0	0	0	1	0	3	2	6	0		
ENSMUST00000124256						0	1	0	109	3	1	0	0	0	0	0		
ENSMUST00000124257						14	18	35	32	18	6	0	3	9	0	5		
ENSMUST00000124258						0	0	0	0	0	0	0	0	19	0	0		
ENSMUST00000124259	ENSMUSG00000006345	10	75561604	75586200	1	0	2	0	0	0	3	0	9	12	0	0	D3Z4Q6	
ENSMUST00000124260	ENSMUSG00000041939	5	114444269	114460591	1	0	3	4	0	5	0	18	20	0	4	4	A0A0G2JFX8	
ENSMUST00000124261						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000124262						10	4	13	5	16	6	0	0	0	0	1		
ENSMUST00000124263	ENSMUSG00000049606	5	106616739	106697287	-1	0	1	3	0	3	1	2	1	0	0	2	D3Z7X8	
ENSMUST00000124264	ENSMUSG00000035576	2	162943472	162974522	1	0	0	0	0	2	0	0	0	0	0	0	A2A6Y5	
ENSMUST00000124265						1	0	0	22	5	3	0	0	0	0	0		
ENSMUST00000124266	ENSMUSG00000019082	7	141429744	141437892	-1	0	0	0	0	0	0	65	90	34	0	23	E9Q579	
ENSMUST00000124267	ENSMUSG00000059741	9	110741861	110769798	1	0	0	0	2	0	0	0	0	0	0	0	A0A0G2JDM3	
ENSMUST00000124268	ENSMUSG00000039087	13	37778400	37952002	1	36	23	90	35	30	24	45	39	64	0	41	Q3UHQ4	
ENSMUST00000124269						575	590	2519	1031	596	331	11	13	15	2	9		
ENSMUST00000124270	ENSMUSG00000053702	2	17343909	17731464	-1	32	8	14	7	6	7	0	0	3	0	5	B7ZCI2	
ENSMUST00000124271						8	6	5	2	0	4	74	187	92	5	117		
ENSMUST00000124272						45	42	132	39	33	26	5	30	9	1	20		
ENSMUST00000124273						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000124275						3	0	21	19	7	1	0	0	0	0	0		
ENSMUST00000124277						0	0	0	0	6	0	0	0	0	0	0		
ENSMUST00000124278						1	0	0	2	0	0	1	0	5	0	0		
ENSMUST00000124279	ENSMUSG00000079481	X	101849385	102092055	1	0	0	1	74	0	0	4	1	1	0	3	B1AXG8	
ENSMUST00000124280						15	23	76	34	38	25	61	216	97	5	244		
ENSMUST00000124281	ENSMUSG00000020792	11	116288001	116307233	-1	2	1	0	0	1	3	0	0	0	0	0	A2AAN5	
ENSMUST00000124282	ENSMUSG00000058240	16	91689322	91728975	-1	0	0	0	0	0	0	65	377	108	259	106	D3YZD6	
ENSMUST00000124283						0	0	4	0	0	0	2	2	0	2	0		
ENSMUST00000124284						1	0	3	6	1	2	4	2	1	0	1		
ENSMUST00000124285						1	1	15	0	2	3	0	0	0	0	0		
ENSMUST00000124286						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000124287						1	0	0	2	0	0	12	72	0	0	0		
ENSMUST00000124288	ENSMUSG00000024294	18	10725548	10818704	1	1	0	0	0	0	0	12	23	15	7	6	F6ZBL2	
ENSMUST00000124289	ENSMUSG00000026553	1	172082529	172122330	1	0	0	0	0	0	0	0	0	0	0	5	D6RH55	
ENSMUST00000124290						7	6	19	8	11	7	0	0	0	0	1		
ENSMUST00000124291						0	2	0	0	0	0	10	2	5	2	0		
ENSMUST00000124292						111	118	270	251	122	73	12	36	34	3	41		
ENSMUST00000124293	ENSMUSG00000040856	12	109452823	109463336	1	2	3	15	5	4	4	0	0	0	0	0	G3UX30	
ENSMUST00000124294						6	5	5	1	3	1	0	4	0	0	1		
ENSMUST00000124295						141	148	467	242	164	58	12	51	24	3	8		
ENSMUST00000124297						9	11	11	9	9	1	2	14	4	1	2		
ENSMUST00000124300						0	0	0	0	0	0	33	0	0	50	20		
ENSMUST00000124301	ENSMUSG00000032400	9	64137144	64173104	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJF6	
ENSMUST00000124302						0	0	0	101	0	5	0	3	8	0	20		
ENSMUST00000124303	ENSMUSG00000021905	14	32080566	32085692	-1	5	5	0	0	2	0	104	239	42	363	66	D3YXV3	
ENSMUST00000124304						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124305	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	0	0	0	0	0	0	0	0	A2AM62	
ENSMUST00000124306						5	2	59	120	0	0	0	1	1	0	2		
ENSMUST00000124307						1	1	1	26	3	2	0	0	1	0	0		
ENSMUST00000124308						43	31	115	96	57	22	204	198	198	31	142		
ENSMUST00000124309						0	2	3	3	5	2	6	19	6	3	18		
ENSMUST00000124310	ENSMUSG00000032556	9	103424920	103480420	-1	9	3	27	19	20	15	0	0	0	4	0		Q6NVD9
ENSMUST00000124311						34	43	105	48	47	22	3	10	9	5	14		
ENSMUST00000124312						1	1	0	0	1	2	0	2	6	0	17		
ENSMUST00000124313						60	48	77	60	62	30	4	11	5	0	5		
ENSMUST00000124314						6	3	1	3	0	0	42	1	20	0	26		
ENSMUST00000124315						8	3	8	7	5	4	10	58	48	6	52		
ENSMUST00000124316	ENSMUSG00000066952	5	114289166	114365357	1	17	13	26	17	25	0	0	0	2	0	0	E9PVB9	Q9D6A1
ENSMUST00000124317	ENSMUSG00000063870	6	125095981	125130591	1	0	0	0	13	4	0	53	476	195	8	194	F6WR45	
ENSMUST00000124318						9	6	15	5	12	3	0	0	0	0	0		
ENSMUST00000124321						0	1	1	1	4	3	2	9	0	1	4		
ENSMUST00000124323						4	3	4	3	6	6	0	0	0	0	2		
ENSMUST00000124324	ENSMUSG00000023030	15	100387898	100425072	-1	0	0	10	0	2	3	0	0	1	0	0	F6ZM31	
ENSMUST00000124325						22	23	35	38	36	25	1	0	2	0	5		
ENSMUST00000124327						2	0	1	4	2	2	0	2	0	0	0		
ENSMUST00000124330						9	4	42	9	5	3	0	9	6	2	15		
ENSMUST00000124331	ENSMUSG00000051396	2	3488850	3512814	-1	32	16	68	22	42	16	27	60	60	12	61	F6QKP8	
ENSMUST00000124332	ENSMUSG00000045917	4	63558781	63586357	1	1	1	12	5	8	7	130	71	181	19	142	Z4YMT7	
ENSMUST00000124333						0	0	0	34	4	0	0	0	0	0	0		
ENSMUST00000124334	ENSMUSG00000024906	19	5482345	5488402	-1	0	0	0	0	0	0	223	284	125	3	80		Q91ZJ0
ENSMUST00000124335	ENSMUSG00000025527	X	112384303	112406779	-1	0	2	0	0	0	0	0	1	0	0	0	F7BXA4	
ENSMUST00000124337						2	4	4	6	5	5	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124338	ENSMUSG00000027650	2	157981803	158028433	-1	0	0	23	0	4	0	3	2	0	0	0	A0A0A0MQH1	
ENSMUST00000124339						4	4	0	1	4	3	0	0	0	0	0		
ENSMUST00000124340	ENSMUSG00000058454	7	143823145	143848410	1	10	5	0	7	18	11	74	41	41	13	66		O88455
ENSMUST00000124341	ENSMUSG00000006576	1	75546266	75562172	1	40	23	90	52	49	32	0	0	0	0	0		P16283
ENSMUST00000124342	ENSMUSG00000029432	5	129725063	129758327	1	1	0	0	0	0	0	10	84	45	19	60	Q7TMG8	
ENSMUST00000124343						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000124344	ENSMUSG00000028245	4	6396207	6454271	-1	1	0	0	0	0	0	4	0	0	0	0	A2AKK2	
ENSMUST00000124346	ENSMUSG00000027589	2	181837854	181857461	1	0	0	0	1	0	0	0	20	64	26	35	F6SPX7	
ENSMUST00000124347						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124348						5	4	12	4	4	2	8	10	14	4	17		
ENSMUST00000124349						21	13	49	34	34	13	10	51	14	0	20		
ENSMUST00000124350	ENSMUSG00000019970	10	21882184	21999903	1	0	0	0	0	6	0	45	18	318	0	66	D3YV51	
ENSMUST00000124351						0	0	0	0	0	0	2	1	0	0	0		
ENSMUST00000124352	ENSMUSG00000020380	11	53649519	53707319	-1	0	0	0	104	0	0	2	0	0	0	0	A8Y5I3	
ENSMUST00000124353	ENSMUSG00000058317	14	18573575	18894267	-1	1	1	8	15	5	5	0	1	0	0	0	D3YW10	
ENSMUST00000124355	ENSMUSG00000013033	8	83900105	83941954	1	0	0	0	271	0	0	0	0	0	0	0	D6RI60	
ENSMUST00000124356						0	6	27	12	23	6	14	100	10	0	10		
ENSMUST00000124358						7	9	4	8	10	4	0	0	0	0	1		
ENSMUST00000124359						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124360	ENSMUSG00000039115	9	118606690	118901003	1	2	3	0	2	3	2	0	0	0	0	0	E9QAP0	
ENSMUST00000124361						3	1	0	2	2	0	0	0	0	1	6		
ENSMUST00000124362						0	0	0	13	0	0	0	0	8	0	3		
ENSMUST00000124364						28	20	62	16	45	13	1	1	2	0	0		
ENSMUST00000124365						0	0	0	0	2	0	2	10	1	3	1		
ENSMUST00000124367						6	5	5	3	0	6	0	0	0	0	1		
ENSMUST00000124368						3	0	15	0	0	0	1	128	11	14	11		
ENSMUST00000124369						0	0	0	2	2	2	0	0	0	0	0		
ENSMUST00000124370	ENSMUSG00000022914	16	95992092	96082526	-1	0	0	0	0	0	2	0	0	0	0	0	F6WJH7	
ENSMUST00000124371						1	2	5	5	4	2	0	7	0	0	0		
ENSMUST00000124372						4	1	0	17	0	1	0	5	3	0	3		
ENSMUST00000124373	ENSMUSG00000039087	13	37778400	37952002	1	0	1	0	5	2	0	0	0	0	0	0	Q3UHQ4	
ENSMUST00000124375	ENSMUSG00000015095	2	25500750	25505471	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQH6	
ENSMUST00000124377	ENSMUSG00000026999	2	80617236	80658906	1	0	0	2	12	3	3	0	5	3	0	5	A2ATJ2	
ENSMUST00000124379	ENSMUSG00000029621	5	145083830	145108761	1	0	0	6	27	2	0	0	0	0	0	0	D3YVI5	
ENSMUST00000124380	ENSMUSG00000036062	4	42916660	42944752	1	0	0	0	4	0	0	0	0	0	0	0	S4R2C8	
ENSMUST00000124381						3	0	0	5	4	0	0	0	0	6	0		
ENSMUST00000124382						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124383	ENSMUSG00000026975	2	24962400	24972163	1	0	4	7	1	1	2	0	2	0	0	0	A0A0A6YY05	
ENSMUST00000124384	ENSMUSG00000027884	3	108653913	108678840	1	0	0	0	0	0	0	7	4	10	18	16	Z4YMG1	
ENSMUST00000124385	ENSMUSG00000047126	11	86694351	86757565	-1	4	0	1	0	0	0	0	618	0	120	0	F6Z1R4	
ENSMUST00000124386						2	0	0	0	0	5	44	234	123	49	56		
ENSMUST00000124387	ENSMUSG00000004500	7	12965838	12974236	1	20	0	23	79	28	0	11	14	16	0	0	E0CYR3	
ENSMUST00000124388						4	3	0	34	2	4	3	0	0	1	0		
ENSMUST00000124389						29	37	109	55	33	20	9	32	11	1	33		
ENSMUST00000124390						1	0	0	252	13	3	0	0	0	0	0		
ENSMUST00000124391						1	3	5	0	6	1	0	0	0	0	0		
ENSMUST00000124396						5	3	16	9	9	3	7	89	28	0	253		
ENSMUST00000124397						5	5	0	4	6	0	6	5	1	0	3		
ENSMUST00000124398						5	2	8	3	3	6	0	90	49	1	64		
ENSMUST00000124399						0	2	1	4	1	2	0	0	0	0	0		
ENSMUST00000124400	ENSMUSG00000027577	2	181018380	181043546	-1	2	2	4	4	3	6	0	0	0	0	0	B7ZBV1	
ENSMUST00000124401	ENSMUSG00000025583	11	119602905	119899576	1	0	0	0	0	0	1	0	0	1	0	0	F7BQS0	
ENSMUST00000124402	ENSMUSG00000031137	X	59062145	59568071	-1	0	0	1	17	1	2	0	1	0	0	0	A0A067XG51	
ENSMUST00000124403						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124404	ENSMUSG00000050122	1	37026596	37187613	1	0	3	6	15	0	1	1	1	0	0	2	A0A0A6YWT6	
ENSMUST00000124405						18	33	26	247	36	13	0	1	8	0	3		
ENSMUST00000124406	ENSMUSG00000021565	13	73679745	73704865	-1	3	3	0	5	0	0	0	0	0	0	0	D6RJ80	
ENSMUST00000124407						0	3	0	0	8	0	0	462	0	0	0		
ENSMUST00000124408						45	43	214	53	24	22	0	5	1	0	5		
ENSMUST00000124409						31	44	126	75	65	36	275	734	452	32	431		
ENSMUST00000124410						31	33	67	28	26	14	4	20	17	0	21		
ENSMUST00000124411						9	3	13	0	8	8	0	0	4	0	3		
ENSMUST00000124412						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000124413	ENSMUSG00000028990	4	149485229	149496668	1	2	0	0	7	0	1	0	12	12	13	6	B1AS03	
ENSMUST00000124414						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124415						0	0	8	180	10	5	0	0	0	0	0		
ENSMUST00000124417	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	11	6	21	1	7	B1AUW1	
ENSMUST00000124418						0	3	2	0	1	0	0	11	7	7	8		
ENSMUST00000124419						131	103	1034	228	101	53	2	15	3	6	7		
ENSMUST00000124420						14	4	47	50	16	13	33	95	21	9	48		
ENSMUST00000124421						2	1	5	0	1	1	512	739	571	331	549		
ENSMUST00000124422						3	0	3	0	2	2	0	0	0	0	3		
ENSMUST00000124423						13	7	138	0	0	1	0	2	0	0	3		
ENSMUST00000124424						0	0	0	0	6	1	0	0	0	0	0		
ENSMUST00000124426						4	1	0	4	0	2	0	0	0	0	0		
ENSMUST00000124427						0	2	12	0	3	1	4	8	17	0	25		
ENSMUST00000124428						0	1	0	18	0	0	0	0	0	0	0		
ENSMUST00000124429						0	0	0	0	4	0	0	0	12	0	17		
ENSMUST00000124430						1	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000124431	ENSMUSG00000039987	5	20758663	20882124	-1	0	0	0	1	0	0	0	0	3	0	0	F6W0Y3	
ENSMUST00000124433						0	0	5	4	4	1	0	0	0	0	0		
ENSMUST00000124436	ENSMUSG00000053768	6	32790976	33060260	-1	0	4	6	0	0	0	0	0	0	0	0	S4R238	
ENSMUST00000124437	ENSMUSG00000020238	10	81486249	81496392	-1	1	0	2	0	0	0	11	0	3	0	4	F6S731	
ENSMUST00000124438						2	6	7	10	0	5	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124440						2	0	3	24	0	5	0	0	0	0	0		
ENSMUST00000124441						8	9	12	6	22	9	0	0	1	1	0		
ENSMUST00000124442						0	0	2	5	5	2	0	0	8	5	9		
ENSMUST00000124443	ENSMUSG00000038696	2	34406771	34624950	1	0	0	0	53	3	0	1	64	121	24	44	A2AR15	
ENSMUST00000124444	ENSMUSG00000060240	7	141426446	141429491	-1	8	7	14	45	5	0	0	0	0	0	0		Q9JKC6
ENSMUST00000124445						13	7	11	129	11	1	0	24	68	13	118		
ENSMUST00000124446						3	1	3	1	6	4	4	13	2	0	3		
ENSMUST00000124447						0	0	0	0	0	0	0	2	4	3	0		
ENSMUST00000124448						10	18	35	18	33	12	19	47	90	5	94		
ENSMUST00000124449						2	5	2	1	2	2	15	31	30	2	49		
ENSMUST00000124450	ENSMUSG00000056486	2	73610660	73775346	-1	0	0	0	2	0	0	0	0	0	0	0	F7C3N6	
ENSMUST00000124451						5	2	0	13	1	0	24	16	61	2	93		
ENSMUST00000124453						7	0	9	8	5	10	6	4	0	0	1		
ENSMUST00000124454						4	0	1	27	0	0	3	8	0	0	0		
ENSMUST00000124455						4	1	1	2	0	0	0	6	2	0	0		
ENSMUST00000124456						3	1	0	0	0	0	2	0	4	0	3		
ENSMUST00000124457						0	0	0	0	0	0	6	58	0	0	11		
ENSMUST00000124458	ENSMUSG00000037475	X	41794991	41920674	-1	0	0	3	0	3	0	13	154	18	21	7	Q8C690	
ENSMUST00000124459						0	0	0	30	5	0	0	0	0	0	0		
ENSMUST00000124460	ENSMUSG00000005803	2	122765237	122809569	1	3	1	1	56	4	0	1	2	4	2	5	H3BJJ7	
ENSMUST00000124461						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000124463						0	0	2	0	0	0	1	5	0	0	0		
ENSMUST00000124464	ENSMUSG00000040620	11	70984091	71004437	-1	0	0	0	0	0	0	0	0	0	0	8	A3QK59	
ENSMUST00000124465						0	4	2	3	2	0	0	1	0	0	0		
ENSMUST00000124466	ENSMUSG00000028556	4	98936671	99120915	-1	0	0	0	0	9	0	0	12	8	2	36		
ENSMUST00000124467						8	13	10	4	9	2	10	5	20	0	29		
ENSMUST00000124468						0	1	10	6	3	2	7	14	5	0	11		
ENSMUST00000124470	ENSMUSG00000005268	15	10177238	10349180	1	204	191	341	133	241	105	0	5	3	0	3		Q08501
ENSMUST00000124472						15	16	21	27	23	12	4	34	7	1	24		
ENSMUST00000124474	ENSMUSG00000029175	5	30647933	30659729	1	0	0	0	0	0	0	18	0	88	30	60	D6RHL1	
ENSMUST00000124475						2	3	2	0	4	0	0	0	0	0	1		
ENSMUST00000124476						0	0	2	18	0	0	0	0	0	0	5		
ENSMUST00000124477						0	1	0	44	6	0	0	0	0	0	0		
ENSMUST00000124478						1	0	0	0	0	3	0	0	0	18	0		
ENSMUST00000124479						0	0	5	5	5	1	2	260	0	6	4		
ENSMUST00000124480						0	4	0	0	0	3	0	0	0	0	0		
ENSMUST00000124481						2	2	7	5	5	1	0	0	0	0	0		
ENSMUST00000124482	ENSMUSG00000030879	7	105806658	105811099	-1	19	13	23	58	24	16	35	108	21	11	22		Q9D8P4
ENSMUST00000124483						13	31	59	30	33	9	9	11	26	1	51		
ENSMUST00000124484	ENSMUSG00000006005	1	150392838	150449935	1	0	3	2	0	0	0	0	182	15	19	50	F6R5D8	
ENSMUST00000124485						19	11	20	71	16	12	3	82	17	5	53		
ENSMUST00000124486						2	1	14	1	5	1	0	10	0	0	0		
ENSMUST00000124487	ENSMUSG00000037286	9	100597798	100959375	1	2	0	5	3	2	2	0	0	0	0	0	D3YYD4	
ENSMUST00000124488	ENSMUSG00000026723	2	13509014	13544668	-1	24	24	82	37	26	14	51	250	56	212	108	Q5I0V6	O55055
ENSMUST00000124490						7	1	3	5	2	2	2	27	14	3	22		
ENSMUST00000124491						0	2	10	5	3	0	0	0	0	0	4		
ENSMUST00000124492	ENSMUSG00000026792	2	32925216	32961614	-1	0	0	0	0	0	0	0	0	2	0	4	A2AHX3	
ENSMUST00000124493	ENSMUSG00000022208	14	55106830	55116935	-1	0	2	18	383	23	4	0	0	0	0	0		Q80WT0
ENSMUST00000124494						0	3	4	2	2	1	0	19	41	26	30		
ENSMUST00000124495	ENSMUSG00000033671	1	155844964	155973255	-1	0	0	0	8	0	0	0	0	5	0	3	D3YTP2	
ENSMUST00000124496	ENSMUSG00000009628	8	33516738	33585582	1	1	0	0	15	4	6	10	0	3	0	0	E9PY31	
ENSMUST00000124497						1	4	1	2	3	5	0	1	2	0	0		
ENSMUST00000124499	ENSMUSG00000021998	14	75131101	75230842	1	0	0	0	0	0	0	901	54	3178	1	10126		Q61233
ENSMUST00000124500	ENSMUSG00000042671	1	153653025	153700323	1	0	0	2	0	5	4	0	0	0	0	0	D3Z5I4	
ENSMUST00000124501	ENSMUSG00000009628	8	33516738	33585582	1	0	2	4	57	2	0	8	119	7	14	16	M0QWY2	
ENSMUST00000124502						0	0	0	0	0	0	0	18	0	16	58		
ENSMUST00000124504						5	2	0	0	0	0	0	52	7	0	20		
ENSMUST00000124505	ENSMUSG00000020654	12	4133103	4213525	1	0	0	0	34	16	0	0	0	3	0	31	B8JK56	
ENSMUST00000124506						2	6	1	23	4	3	0	4	0	0	2		
ENSMUST00000124507						15	9	75	20	21	10	1	0	2	0	0		
ENSMUST00000124508						3	1	6	39	0	1	14	19	17	2	10		
ENSMUST00000124509	ENSMUSG00000034842	5	92331827	92414628	1	2	0	0	0	0	1	0	0	0	0	0	E9Q9Q8	
ENSMUST00000124510						2	3	2	0	0	0	9	11	9	11	1		
ENSMUST00000124511						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124512						0	0	0	93	0	0	0	0	2	0	0		
ENSMUST00000124514						4	3	14	5	8	1	0	0	0	2	0		
ENSMUST00000124515	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	7	9	3	0	5	0	28	3	41	D3Z0Z1	
ENSMUST00000124516	ENSMUSG00000056328	11	67200052	67224575	1	27	0	46	0	42	0	0	0	0	0	0		Q5SX40
ENSMUST00000124517	ENSMUSG00000029055	4	154983115	155056784	-1	0	0	0	33	0	0	0	0	0	0	0	F7C512	
ENSMUST00000124518						2	5	10	36	8	2	14	35	26	2	10		
ENSMUST00000124519						18	14	24	22	27	11	0	16	5	2	14		
ENSMUST00000124520						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124521						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000124523						1	1	1	2	2	2	0	1	0	0	5		
ENSMUST00000124524						979	1075	1908	559	594	264	3	9	4	0	14		
ENSMUST00000124525						2	2	1	0	0	2	0	0	36	17	6		
ENSMUST00000124526	ENSMUSG00000072812	12	112772194	112802657	-1	24	15	27	714	29	12	0	2	0	0	24	E9PYB0	
ENSMUST00000124527						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124528						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000124529	ENSMUSG00000029390	5	124540695	124550506	1	1	0	2	35	3	2	18	0	15	0	18	F6V6T4	
ENSMUST00000124530						4	6	5	6	6	1	8	28	18	1	29		
ENSMUST00000124531	ENSMUSG00000030321	6	115810729	115838412	-1	31	19	51	24	42	11	0	0	4	0	7	I6L9E6	
ENSMUST00000124532	ENSMUSG00000006191	13	29191746	29855674	-1	1	0	1	16	3	0	0	0	0	0	0	B7FAT1	
ENSMUST00000124533	ENSMUSG00000030802	7	127904082	127910221	1	0	0	1	0	0	3	99	108	108	7	30		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124534						9	2	7	1	12	4	2	10	4	7	17		
ENSMUST00000124535						18	14	27	10	20	11	0	0	0	0	0		
ENSMUST00000124536	ENSMUSG00000013858	10	79974948	79984330	-1	1	5	12	0	7	6	984	754	639	69	534	F6RN19	
ENSMUST00000124537						0	0	5	1	2	0	0	2	0	0	0		
ENSMUST00000124538						6	4	7	167	13	2	0	0	0	0	0		
ENSMUST00000124539						9	0	9	10	7	3	2	13	0	0	3		
ENSMUST00000124540						2	0	2	0	0	0	0	0	0	30	0		
ENSMUST00000124541	ENSMUSG00000018362	11	106988629	106999541	-1	2	5	0	1	0	0	0	3	0	0	0	A2A601	
ENSMUST00000124542						0	1	1	55	1	1	0	0	0	0	0		
ENSMUST00000124543	ENSMUSG00000041565	17	68273797	68777961	1	0	0	1	0	0	0	0	4	0	5	18	A0A0A0MQK6	
ENSMUST00000124544						30	32	19	20	12	16	0	3	1	0	1		
ENSMUST00000124545	ENSMUSG00000024979	19	55180733	55196313	1	0	0	0	0	0	1	0	0	0	0	0	F6Z818	
ENSMUST00000124546	ENSMUSG00000029276	5	107548967	107597888	-1	0	0	0	0	3	0	0	0	0	0	7	D6RGR3	
ENSMUST00000124547	ENSMUSG00000073791	4	99829198	99912788	1	4	0	0	1	2	0	0	1	0	4	1	B1B0D1	
ENSMUST00000124548						1	0	3	0	0	2	0	0	0	0	0		
ENSMUST00000124549	ENSMUSG00000021773	14	21845861	21848977	-1	11	10	24	62	21	5	13	28	14	6	15		Q8BIG7
ENSMUST00000124550						2	0	2	3	1	0	3	7	0	2	0		
ENSMUST00000124551						0	2	3	0	2	0	11	37	22	8	26		
ENSMUST00000124552	ENSMUSG00000035642	7	97550331	97579497	-1	0	0	2	2	0	0	0	0	2	3	4	D3YX09	
ENSMUST00000124553						0	0	0	0	2	0	44	35	114	0	55		
ENSMUST00000124554	ENSMUSG00000043909	2	121193281	121271407	-1	1	0	0	4	3	0	1	0	0	0	0	F7CE65	
ENSMUST00000124556	ENSMUSG00000024948	19	6341135	6355615	1	0	0	0	0	0	0	189	1788	1538	68	1615	D6RCZ7	
ENSMUST00000124557	ENSMUSG00000024118	17	24215054	24220851	-1	0	0	0	0	0	0	17	10	18	6	6	F6PZ19	
ENSMUST00000124558	ENSMUSG00000042641	1	153779381	153844142	-1	9	9	6	14	12	4	0	0	0	0	0	H3BL40	
ENSMUST00000124559						6	2	2	2	2	0	14	71	13	3	34		
ENSMUST00000124560	ENSMUSG00000031391	X	73853778	73896105	-1	0	1	0	0	0	0	0	50	21	1	26	F6UIL7	
ENSMUST00000124561						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124562						7	3	2	1	8	2	0	1	0	0	1		
ENSMUST00000124563						3	0	7	14	9	5	19	44	28	6	72		
ENSMUST00000124564						0	0	0	0	0	2	4	0	6	0	3		
ENSMUST00000124565	ENSMUSG00000086158	9	72979722	72985382	-1	7	1	11	4	5	1	71	231	75	161	49	V9GXK1	
ENSMUST00000124566	ENSMUSG00000030872	7	121986722	122021222	-1	10	8	45	0	12	0	16	52	0	0	0		Q6P5E6
ENSMUST00000124567						0	2	0	0	0	0	5	59	4	14	11		
ENSMUST00000124568	ENSMUSG00000020886	11	70017085	70045532	1	1	0	0	2	0	0	0	0	0	0	0	F6TPQ6	
ENSMUST00000124569	ENSMUSG00000029416	5	127595664	127632897	-1	0	3	7	0	3	3	268	373	195	41	137	F6QFB4	
ENSMUST00000124570	ENSMUSG00000044252	18	12755314	12941841	-1	4	3	9	2	5	3	0	0	0	0	0	D3Z754	
ENSMUST00000124573						0	0	4	0	0	0	3	32	5	0	19		
ENSMUST00000124574						2	4	3	81	17	2	0	0	0	0	0		
ENSMUST00000124576	ENSMUSG00000036529	15	89288236	89315311	-1	0	0	11	49	0	25	225	130	0	1	88	D6RG52	
ENSMUST00000124578						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000124579						1	4	2	15	4	3	3	3	20	2	8		
ENSMUST00000124580	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	12	1	0	0	0	F7ANU5	
ENSMUST00000124581	ENSMUSG00000038729	4	57717657	57896982	1	2	0	0	22	3	3	0	0	0	0	5	A2APJ1	
ENSMUST00000124582						0	0	3	5	1	0	0	0	3	1	4		
ENSMUST00000124583						4	1	4	4	2	0	1	0	5	0	2		
ENSMUST00000124584						18	11	54	29	22	10	124	450	251	14	87		
ENSMUST00000124585						0	0	0	18	0	0	0	0	0	0	0		
ENSMUST00000124587						4	4	0	2	0	2	0	0	0	0	0		
ENSMUST00000124588						2	3	10	3	8	7	0	2	2	0	6		
ENSMUST00000124590						1	0	3	1	1	1	0	0	0	0	0		
ENSMUST00000124591						0	0	3	0	0	1	1	9	0	0	0		
ENSMUST00000124592	ENSMUSG00000032894	X	102859186	102867971	-1	3	4	0	3	3	0	0	0	0	0	0	B1AX30	
ENSMUST00000124593						7	2	16	8	8	7	3	0	5	0	3		
ENSMUST00000124594						0	5	2	5	2	9	0	23	6	0	8		
ENSMUST00000124595						13	10	12	4	5	2	16	97	42	0	46		
ENSMUST00000124596						0	0	0	1	1	1	21	155	37	7	94		
ENSMUST00000124597						3	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000124598						3	8	10	43	12	9	12	15	18	4	25		
ENSMUST00000124599	ENSMUSG00000027551	2	168893331	168955587	-1	2	6	0	123	8	2	0	0	0	0	0	A2AQR2	
ENSMUST00000124600						2	2	0	3	2	0	0	0	0	0	0		
ENSMUST00000124601						0	0	1	3	2	0	0	0	0	0	0		
ENSMUST00000124602	ENSMUSG00000022656	16	46387706	46498525	-1	1	2	3	6	5	1	0	0	0	0	0	F6UII7	
ENSMUST00000124603	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	1	33	0	1	76	63	62	0	10	D6REU0	
ENSMUST00000124604						0	4	1	4	3	0	0	0	0	0	6		
ENSMUST00000124605						0	1	12	0	2	4	5	0	0	1	0		
ENSMUST00000124607						0	0	0	0	6	0	0	0	0	2	0		
ENSMUST00000124608						935	1020	2976	954	1027	518	29	114	98	20	82		
ENSMUST00000124610	ENSMUSG00000039753	5	43744615	43821638	-1	0	2	0	0	1	0	29	95	83	253	295	F7BZC4	
ENSMUST00000124611	ENSMUSG00000053702	2	17343909	17731464	-1	1	0	0	0	0	0	0	0	1	0	0	F6RM14	
ENSMUST00000124612						5	0	3	57	3	1	0	2	0	0	0		
ENSMUST00000124613						0	0	0	0	0	0	28	273	129	92	91		
ENSMUST00000124614						5	7	8	43	7	4	7	25	5	6	10		
ENSMUST00000124615	ENSMUSG00000020083	10	62107655	62143920	-1	0	2	8	131	16	3	0	0	0	0	0		Q9D882
ENSMUST00000124616						26	8	104	43	16	12	134	541	347	24	394		
ENSMUST00000124617						4	0	10	1	9	1	0	22	0	5	0		
ENSMUST00000124618	ENSMUSG00000034151	3	75037907	75165034	-1	1	5	3	1	1	1	0	0	0	0	0	D3Z5Y6	
ENSMUST00000124619						5	2	5	7	4	6	11	19	9	4	14		
ENSMUST00000124621						3	2	0	25	3	0	1	3	1	2	4		
ENSMUST00000124623						0	2	0	0	1	1	0	0	2	0	0		
ENSMUST00000124624						8	4	21	8	14	6	26	8	48	2	89		
ENSMUST00000124625						1	0	1	6	2	0	0	0	0	0	0		
ENSMUST00000124626	ENSMUSG00000028644	4	119175457	119190011	-1	1	0	0	0	1	0	0	0	0	0	0	A2A7P8	
ENSMUST00000124627						1	3	9	3	2	1	0	0	0	0	0		
ENSMUST00000124628						2	0	0	0	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124629						4	2	10	3	7	1	4	6	6	1	5		
ENSMUST00000124630						0	3	0	0	0	1	0	22	9	0	9		
ENSMUST00000124631						2	0	30	0	0	0	0	2	0	0	17		
ENSMUST00000124632	ENSMUSG00000027346	2	132529082	132587729	-1	1	1	0	0	0	0	31	113	88	45	109	F6YDB7	
ENSMUST00000124633						3	3	11	3	4	4	0	10	0	3	3		
ENSMUST00000124634						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000124635	ENSMUSG00000014550	6	92186712	92214925	-1	0	0	0	0	0	0	5	0	0	0	4		
ENSMUST00000124636						3	0	0	2	2	1	5	0	17	0	6		
ENSMUST00000124637						4	1	2	5	8	2	70	770	146	44	213		
ENSMUST00000124638						24	19	27	22	25	14	69	301	173	9	170		
ENSMUST00000124639						2	0	0	3	2	1	0	0	0	0	0		
ENSMUST00000124640	ENSMUSG00000020289	11	32225628	32267707	-1	10	4	10	156	22	7	0	4	5	0	3	F2Z3V7	
ENSMUST00000124641						0	0	0	0	0	0	1441	1755	1068	7456	860		
ENSMUST00000124642	ENSMUSG00000036529	15	89288236	89315311	-1	2	0	3	0	1	0	0	0	0	0	0	F6S251	
ENSMUST00000124644						52	46	44	56	62	38	0	7	2	0	9		
ENSMUST00000124645						0	0	0	0	4	0	15	0	0	0	0		
ENSMUST00000124646						2	1	4	0	3	4	0	0	5	0	0		
ENSMUST00000124647						2	5	0	2	4	1	0	0	0	0	0		
ENSMUST00000124648	ENSMUSG00000029359	5	118027743	118061878	1	0	0	0	0	0	0	10	0	0	0	11	D0EM46	
ENSMUST00000124649						13	12	26	24	16	6	0	1	0	0	1		
ENSMUST00000124650	ENSMUSG00000057375	4	107314363	107359823	1	1	3	6	3	1	6	0	0	0	0	0	D3Z2S7	
ENSMUST00000124651						0	0	2	59	2	1	1	0	1	0	2		
ENSMUST00000124652						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124653						1	1	0	0	1	1	18	73	50	7	52		
ENSMUST00000124655	ENSMUSG00000067148	17	46243920	46248054	-1	0	0	0	3	0	2	0	72	17	0	15	D3Z3D6	
ENSMUST00000124656						1	0	0	3	0	1	0	0	0	0	2		
ENSMUST00000124657						3	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000124658						0	1	6	23	3	0	0	0	0	0	1		
ENSMUST00000124659						16	16	35	29	24	12	9	5	4	0	5		
ENSMUST00000124660	ENSMUSG00000028750	4	138724792	138746132	1	2	4	6	14	2	1	0	0	0	0	0	E0CYB5	
ENSMUST00000124661						0	3	31	18	0	0	0	0	0	0	0		
ENSMUST00000124662						1	0	0	1	0	1	4	11	2	1	4		
ENSMUST00000124663						81	44	125	155	76	44	7	16	12	3	20		
ENSMUST00000124665	ENSMUSG00000051855	6	30723547	30748465	1	0	0	0	0	0	2	0	0	0	0	0	D3Z383	
ENSMUST00000124666	ENSMUSG00000038848	2	180904377	180920949	-1	2	1	0	8	0	0	0	0	24	0	21	A2AWN7	
ENSMUST00000124667	ENSMUSG00000024949	19	6363690	6378030	1	4	0	0	3	0	2	0	10	6	0	11	F6Z9W2	
ENSMUST00000124668	ENSMUSG00000001082	5	34633642	34637212	-1	3	0	3	71	6	5	0	0	0	0	0	D3Z2Z9	
ENSMUST00000124669						3	2	0	1	2	2	0	0	0	0	0		
ENSMUST00000124670	ENSMUSG00000003581	11	4135202	4141172	1	0	0	0	53	3	0	0	1	0	0	0	Z4YLJ7	
ENSMUST00000124671	ENSMUSG00000027635	2	156995265	157007154	-1	1	4	0	0	1	0	0	0	0	10	0	B0QZT4	
ENSMUST00000124672						9	4	0	2	6	3	0	5	3	0	0		
ENSMUST00000124674						0	1	3	0	0	0	0	0	0	0	0		
ENSMUST00000124675						0	2	0	2	2	0	0	0	0	0	1		
ENSMUST00000124677	ENSMUSG00000067855	5	13791619	13796820	1	8	7	8	12	9	7	0	0	0	0	0	W4VSP1	
ENSMUST00000124678						0	0	0	2	3	0	0	0	7	0	34		
ENSMUST00000124680						59	63	136	41	53	0	21	23	43	0	0		
ENSMUST00000124681						2	2	1	3	3	0	7	46	24	9	41		
ENSMUST00000124682	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	0	0	0	0	0	0	0	0	B1AT86	
ENSMUST00000124683						3	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000124684						6	3	8	20	2	9	18	10	27	2	22		
ENSMUST00000124685						18	15	35	24	14	11	0	0	3	0	1		
ENSMUST00000124686						4	3	0	3	2	0	0	0	0	0	0		
ENSMUST00000124687						5	3	3	0	4	7	0	0	4	0	0		
ENSMUST00000124688						17	15	55	51	19	13	1	3	1	0	1		
ENSMUST00000124689						1	2	3	0	2	1	0	0	2	0	0		
ENSMUST00000124690						0	0	1	18	1	0	0	2	0	0	0		
ENSMUST00000124691						2	2	0	4	2	1	7	25	29	4	28		
ENSMUST00000124692						14	9	3	17	8	3	0	0	0	0	0		
ENSMUST00000124693	ENSMUSG00000029718	5	137605103	137613784	-1	0	0	0	0	0	0	0	0	0	0	4	D3YWH0	
ENSMUST00000124694						1	0	0	1	0	0	0	14	0	0	2		
ENSMUST00000124695						3	4	8	5	5	1	2	6	10	0	1		
ENSMUST00000124696						15	21	48	55	21	4	6	11	7	1	13		
ENSMUST00000124698						2	0	1	0	0	1	1	0	0	6	0		
ENSMUST00000124699						8	4	8	43	10	4	33	64	71	0	120		
ENSMUST00000124701						8	11	21	9	11	6	0	2	2	0	0		
ENSMUST00000124702						2	4	3	2	5	1	0	0	0	0	0		
ENSMUST00000124703						9	13	0	4	7	6	0	0	0	4	0		
ENSMUST00000124704						15	8	44	34	17	7	55	370	188	17	434		
ENSMUST00000124707						2	1	0	0	3	3	36	36	10	7	40		
ENSMUST00000124708						7	5	17	9	7	9	0	1	0	0	2		
ENSMUST00000124709						1	0	1	82	0	0	0	0	1	0	0		
ENSMUST00000124710	ENSMUSG00000031012	X	13517080	13851367	-1	0	0	0	0	0	0	1	7	7	2	0	B1AUH5	
ENSMUST00000124711	ENSMUSG00000029119	5	36806921	36830653	-1	0	0	23	0	0	2	13	93	12	0	38	F6TMZ3	
ENSMUST00000124712						0	0	0	0	3	0	2	5	10	0	22		
ENSMUST00000124713						6	3	4	8	7	7	0	0	0	0	0		
ENSMUST00000124714	ENSMUSG00000018800	11	110269369	110337716	-1	2	0	14	13	4	1	0	0	0	0	1	A2AEP5	
ENSMUST00000124715						4	7	10	5	5	5	0	1	0	0	0		
ENSMUST00000124716	ENSMUSG00000029561	5	114896936	114912234	1	0	0	0	3	0	2	0	5	0	4	31	F6VMV6	
ENSMUST00000124717	ENSMUSG00000066366	12	103853589	103863562	-1	16	10	12	19	13	6	0	0	0	0	0	D3YZL0	
ENSMUST00000124718						1	0	1	8	1	0	23	79	75	109	72		
ENSMUST00000124719						1	0	1	0	0	0	0	4	5	0	4		
ENSMUST00000124720	ENSMUSG00000036339	14	48446128	48515135	1	7	3	7	25	5	2	30	31	49	5	22		Q8BMD6
ENSMUST00000124721	ENSMUSG00000040963	11	70092644	70106187	1	4	0	16	8	9	9	0	0	0	0	0	B1AR35	
ENSMUST00000124722						0	0	3	1	3	0	0	1	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124723	ENSMUSG00000032462	9	99036654	99140621	-1	6	0	8	58	9	5	2	1	0	0	0	D3Z2Z7	
ENSMUST00000124724						1	4	10	11	9	4	0	0	2	0	1		
ENSMUST00000124725						0	0	4	1	2	0	0	0	1	0	6		
ENSMUST00000124726						8	10	20	9	5	4	0	6	5	1	4		
ENSMUST00000124727						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000124729	ENSMUSG00000082932	4	96444596	96507386	-1	3	6	3	3	9	0	0	0	0	0	0	G3UZ38	
ENSMUST00000124730						55	76	270	45	52	37	0	0	4	0	8		
ENSMUST00000124731	ENSMUSG00000040389	3	108591279	108645719	1	0	0	0	6	0	0	0	0	0	0	0	A0A0G2JFW8	
ENSMUST00000124732	ENSMUSG00000002393	8	71374123	71381960	-1	0	0	0	0	0	0	0	0	0	0	0	F7DC78	
ENSMUST00000124733						0	0	0	151	0	0	0	0	0	1	0		
ENSMUST00000124734	ENSMUSG00000040473	5	5579278	5664239	-1	0	1	0	0	1	0	0	0	0	5	0	F6Q7Y3	
ENSMUST00000124735	ENSMUSG00000047181	11	95009879	95026087	1	1	0	3	61	2	2	0	0	0	0	0	B7ZC59	
ENSMUST00000124736						0	0	0	0	0	0	45	0	0	0	0		
ENSMUST00000124737	ENSMUSG00000027104	2	73816509	73892639	-1	31	21	170	0	21	14	0	43	0	0	0	F6Z2B2	
ENSMUST00000124739						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000124740						4	1	12	0	2	4	1	1	0	0	1		
ENSMUST00000124741	ENSMUSG00000001482	8	123442986	123463270	1	2	0	0	0	0	0	2	0	0	0	0	D3Z5H7	
ENSMUST00000124742						3	4	7	0	4	4	0	3	0	0	0		
ENSMUST00000124743	ENSMUSG00000036745	3	146852367	146984009	1	2	1	15	2	1	0	2	12	0	2	0	A0A0G2JFF6	
ENSMUST00000124744						4	2	4	2	1	9	0	1	0	0	2		
ENSMUST00000124745	ENSMUSG00000074247	8	71469199	71476098	1	0	0	0	0	0	0	576	744	220	9	309		Q9D9Z5
ENSMUST00000124747	ENSMUSG00000063889	18	3266048	3337748	-1	5	0	5	0	3	0	6	0	6	10	0	D3Z326	
ENSMUST00000124748						1	8	6	7	6	3	1	0	0	0	0		
ENSMUST00000124749						8	12	61	45	6	15	0	0	0	0	0		
ENSMUST00000124750						4	6	5	17	7	3	14	64	20	1	29		
ENSMUST00000124751						165	168	183	162	188	111	0	11	8	1	10		
ENSMUST00000124752	ENSMUSG00000025873	13	54621784	54664068	1	0	1	0	0	0	7	6	0	7	15	12	D3Z2H4	
ENSMUST00000124755	ENSMUSG00000018677	11	102402985	102407946	-1	0	0	4	13	2	2	0	0	0	0	0	B0QZI6	
ENSMUST00000124756						1	0	12	0	3	2	0	0	0	0	0		
ENSMUST00000124757	ENSMUSG00000013878	8	26119368	26143871	1	0	0	0	0	0	0	0	0	0	2	0	E9PUJ5	
ENSMUST00000124758	ENSMUSG00000033295	4	118208213	118291405	-1	0	0	20	0	0	0	0	0	0	0	12	F6S1X8	
ENSMUST00000124759	ENSMUSG00000030979	7	133686243	133710072	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q9B5	
ENSMUST00000124760	ENSMUSG00000027931	3	90450591	90465866	-1	1	4	0	5	0	0	0	0	0	0	0	F6W125	
ENSMUST00000124761	ENSMUSG00000039307	11	121204433	121222655	1	3	0	4	0	3	1	4	10	10	3	9	F7B4F0	
ENSMUST00000124763	ENSMUSG00000032589	9	108096022	108190384	-1	7	33	201	215	10	16	9	15	10	1	0	V9GX98	
ENSMUST00000124764	ENSMUSG00000031570	8	25720061	25724887	1	0	0	0	0	0	0	0	13	0	0	9	D6RCW4	
ENSMUST00000124765						0	1	0	2	1	2	0	0	0	0	0		
ENSMUST00000124766						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124767						0	0	2	5	2	2	0	0	0	0	0		
ENSMUST00000124768	ENSMUSG00000039307	11	121204433	121222655	1	469	636	613	174	540	243	23	86	48	40	67	B1AXL0	
ENSMUST00000124769						0	1	3	10	1	0	0	0	0	0	0		
ENSMUST00000124770						0	4	1	0	4	0	0	2	0	0	0		
ENSMUST00000124771	ENSMUSG00000039410	4	154316125	154636873	-1	0	2	0	32	0	0	0	0	0	0	0	A2A929	
ENSMUST00000124772						1	3	3	1	1	3	1	4	0	2	2		
ENSMUST00000124773	ENSMUSG00000094950	7	84994645	85012020	-1	4	4	3	3	4	1	0	0	0	0	0	K7N6R9	
ENSMUST00000124775						0	0	4	0	0	0	0	0	0	1	0		
ENSMUST00000124776						0	0	0	15	3	0	7	4	0	0	0		
ENSMUST00000124777						4	2	2	0	2	0	0	0	0	0	0		
ENSMUST00000124778						2	0	3	18	10	0	11	17	25	5	31		
ENSMUST00000124779						5	1	0	12	2	2	6	26	3	0	6		
ENSMUST00000124780	ENSMUSG00000037426	5	32863701	32994236	1	0	4	7	6	0	0	0	0	1	0	0	F6X8H7	
ENSMUST00000124781						1	1	0	7	0	3	0	0	0	0	1		
ENSMUST00000124782						6	6	10	0	1	5	0	18	3	0	17		
ENSMUST00000124783	ENSMUSG00000028042	3	89377644	89394776	-1	3	0	1	3	1	4	84	75	74	6	84	D3YXC8	
ENSMUST00000124784	ENSMUSG00000020072	10	63024315	63077962	1	1	1	6	4	3	1	0	0	1	0	1	D3Z2D7	
ENSMUST00000124785						0	7	0	0	4	0	1	0	0	1	0		
ENSMUST00000124787						2	9	3	6	2	0	0	4	0	0	4		
ENSMUST00000124788						12	0	9	6	6	4	0	0	0	0	0		
ENSMUST00000124789						0	0	0	243	0	0	0	0	0	2	0		
ENSMUST00000124790	ENSMUSG00000079042	8	65012976	65037336	-1	2	4	1	6	2	0	0	0	0	0	0		P0DMC4
ENSMUST00000124791	ENSMUSG00000074698	2	152226839	152281852	1	0	0	0	0	0	1	0	0	27	0	0	A2ANR6	
ENSMUST00000124793						4	2	0	1	0	0	14	29	22	3	15		
ENSMUST00000124794						2	0	0	0	1	0	0	5	4	2	3		
ENSMUST00000124796						1	3	8	323	10	5	0	0	0	0	0		
ENSMUST00000124797	ENSMUSG00000019087	X	74297097	74304721	1	0	0	0	0	0	6	0	3	0	0	0	F6X9J0	
ENSMUST00000124798	ENSMUSG00000031389	X	73891442	73921870	-1	0	2	0	1	0	0	8	6	3	0	33	B1AUY1	
ENSMUST00000124799						2	1	0	4	6	5	0	2	0	0	2		
ENSMUST00000124800						2	3	4	0	1	0	0	0	0	0	0		
ENSMUST00000124801						1	0	1	0	0	0	7	38	44	12	23		
ENSMUST00000124802	ENSMUSG00000032841	2	101714285	101883027	-1	2	1	0	5	0	0	0	18	5	2	10	B0R102	
ENSMUST00000124803	ENSMUSG00000027977	3	123526166	123690853	-1	3	0	0	0	0	1	0	0	0	0	0	D3YXE5	
ENSMUST00000124804	ENSMUSG00000027215	2	93419111	93463140	-1	2	1	8	32	5	3	0	0	1	1	4	A2AIJ4	
ENSMUST00000124805						1	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000124806						0	0	0	0	0	0	0	0	56	0	32		
ENSMUST00000124807						92	70	690	210	71	41	2	7	4	1	10		
ENSMUST00000124808						10	6	12	27	16	6	48	135	77	10	98		
ENSMUST00000124809	ENSMUSG00000063600	3	29082023	29691209	1	3	1	3	1	1	0	0	0	0	0	0	D3YVN3	
ENSMUST00000124810						0	0	0	0	0	0	2	0	18	0	0		
ENSMUST00000124812	ENSMUSG00000074646	2	155973279	156007977	-1	15	9	20	11	13	13	0	5	2	6	1	D6RHS0	
ENSMUST00000124815						1	0	4	1	0	3	0	1	0	0	0		
ENSMUST00000124816						3	5	2	8	3	3	0	0	0	0	0		
ENSMUST00000124817						53	39	62	7	51	28	6	7	4	4	4		
ENSMUST00000124819						2	2	1	3	0	0	0	0	0	0	0		
ENSMUST00000124820						72	79	211	92	58	49	0	84	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124821	ENSMUSG00000047554	7	109972187	109986929	-1	0	0	0	60	0	0	2	0	16	45	4	D6RIR0	
ENSMUST00000124822						0	1	2	1	0	3	4	16	17	0	30		
ENSMUST00000124823						324	264	449	224	312	142	7	37	18	10	26		
ENSMUST00000124824						2	4	1	1	5	1	3	10	0	0	0		
ENSMUST00000124825	ENSMUSG00000075270	2	75989141	76338774	-1	10	4	21	9	11	8	1	3	0	0	1	F7AAG1	
ENSMUST00000124826	ENSMUSG00000025809	8	128685654	128733200	1	0	1	20	6	0	0	60	164	391	532	458	D6RJL5	
ENSMUST00000124827						0	0	0	1	0	0	0	0	0	0	4		
ENSMUST00000124828	ENSMUSG00000020776	11	116142285	116168166	-1	0	0	0	0	0	0	5	0	0	0	0	Z4YLK3	
ENSMUST00000124830	ENSMUSG00000054889	13	38151328	38198577	1	68	48	138	34	79	35	11	11	21	0	11		E9Q557
ENSMUST00000124831	ENSMUSG00000056962	11	116837432	116843449	-1	0	0	0	0	0	0	17	81	14	25	7	F7BDP4	
ENSMUST00000124832	ENSMUSG00000026307	1	91298338	91321075	1	0	0	0	1	0	1	0	0	0	0	0	F7BB44	
ENSMUST00000124834	ENSMUSG00000027357	2	132846666	132866785	1	0	3	0	0	0	0	0	0	0	7	0	E9PUW6	
ENSMUST00000124835						15	15	103	126	31	6	4	2	0	0	6		
ENSMUST00000124836	ENSMUSG00000027357	2	132846666	132866785	1	0	0	0	0	2	0	36	38	19	26	14	A0A0C3SFZ5	
ENSMUST00000124837						78	59	101	64	94	44	9	14	25	6	28		
ENSMUST00000124838	ENSMUSG00000040006	10	7767947	7792824	-1	6	0	4	0	8	2	235	924	334	819	309	Q3UN36	
ENSMUST00000124839						0	2	0	0	0	1	5	6	10	9	12		
ENSMUST00000124840	ENSMUSG00000026809	2	28692080	28699727	-1	0	0	9	0	0	0	0	16	0	0	0		Q7TPM5
ENSMUST00000124841	ENSMUSG00000071493	13	22772327	22773325	-1	0	0	0	4	5	0	0	0	0	0	0	Q8R275	
ENSMUST00000124843						2	2	1	30	3	2	0	1	1	0	3		
ENSMUST00000124844						0	0	1	1	0	0	0	4	0	0	4		
ENSMUST00000124845						0	0	0	0	0	0	0	55	1	10	0		
ENSMUST00000124846	ENSMUSG00000013787	17	34898469	34914052	1	2	0	0	2	0	0	13	4	16	0	11	A2CG77	
ENSMUST00000124847						3	4	19	10	0	8	3	3	3	0	0		
ENSMUST00000124849	ENSMUSG00000014232	16	3908801	3941147	1	0	2	0	0	0	2	5	7	23	0	16	E9Q8M4	
ENSMUST00000124851						12	12	14	17	12	5	0	5	1	0	2		
ENSMUST00000124852						26	14	50	56	46	22	39	205	78	67	117		
ENSMUST00000124854	ENSMUSG00000034771	10	81574561	81590845	1	0	0	2	0	2	1	0	0	0	0	0	F6X5U5	
ENSMUST00000124856	ENSMUSG00000028483	4	83417724	83467676	1	0	0	0	0	0	0	0	0	0	0	0		Q9D2C9
ENSMUST00000124857						17	2	7	3	15	6	0	0	1	3	6		
ENSMUST00000124858						29	47	55	27	46	14	0	0	0	0	5		
ENSMUST00000124859						3	0	4	1	0	0	4	6	4	0	6		
ENSMUST00000124860						2	2	1	3	5	4	0	9	0	0	0		
ENSMUST00000124861	ENSMUSG00000017446	11	118428203	118449963	1	150	89	192	5305	425	270	0	4	5	1	8	A2A4W1	
ENSMUST00000124862						22	15	88	21	22	3	0	0	1	0	0		
ENSMUST00000124864						1	0	0	0	0	0	2	4	0	0	0		
ENSMUST00000124866						11	8	16	24	7	5	0	0	1	1	0		
ENSMUST00000124867	ENSMUSG00000013878	8	26119368	26143871	1	1	3	0	0	2	0	8	4	6	0	0	F6UDR6	
ENSMUST00000124868						6	0	4	103	3	0	1	0	0	0	0		
ENSMUST00000124869						0	1	0	0	1	0	2	0	6	6	2		
ENSMUST00000124870						4	0	0	11	11	0	0	20	8	0	0		
ENSMUST00000124872						1	0	3	3	3	1	8	21	11	4	13		
ENSMUST00000124873						2	0	1	43	0	0	0	0	0	0	0		
ENSMUST00000124874	ENSMUSG00000025916	1	9968624	10009136	-1	0	0	0	0	0	0	26	169	25	31	21	E9PUJ7	
ENSMUST00000124875						0	0	1	0	2	1	0	0	0	7	8		
ENSMUST00000124876						6	2	2	0	0	5	0	0	0	0	0		
ENSMUST00000124877						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124878	ENSMUSG00000009073	11	4765845	4849536	-1	1	0	0	0	1	0	0	0	0	0	0	F6X089	
ENSMUST00000124879						2	2	8	56	0	0	0	0	0	0	0		
ENSMUST00000124880						21	25	122	20	20	10	0	9	0	1	0		
ENSMUST00000124881	ENSMUSG00000036466	9	64385626	64709205	1	0	0	0	0	0	0	0	0	0	0	0	F6UPK0	
ENSMUST00000124882						2	2	1	1	6	4	0	0	0	0	0		
ENSMUST00000124883	ENSMUSG00000031922	9	13807792	13827107	-1	3	0	5	0	0	0	12	214	64	270	89		Q8CEE0
ENSMUST00000124884						0	5	0	0	0	1	0	1	0	0	0		
ENSMUST00000124885						0	0	0	0	0	0	0	0	1	0	10		
ENSMUST00000124886	ENSMUSG00000053436	17	28691342	28748404	1	3	0	0	0	0	2	248	0	356	0	146	B2KF34	
ENSMUST00000124887	ENSMUSG00000032077	9	46283008	46298783	1	4	2	2	0	2	1	0	0	0	3	0	F6ZBW5	
ENSMUST00000124888	ENSMUSG00000057554	13	12439415	12464944	-1	7	0	15	50	4	2	0	0	0	0	54	Q542M5	Q9JL15
ENSMUST00000124889						0	0	0	0	0	0	5	87	21	3	39		
ENSMUST00000124890	ENSMUSG00000075370	16	16860671	16863985	-1	0	0	0	0	0	0	0	0	0	0	0	F7CFU6	
ENSMUST00000124891						0	0	0	1	0	0	0	0	1	0	13		
ENSMUST00000124892						9	12	33	23	21	6	10	3	3	0	21		
ENSMUST00000124894						0	0	0	0	0	0	31	330	28	64	48		
ENSMUST00000124895						1	2	0	0	2	2	0	0	1	0	0		
ENSMUST00000124896						2	3	5	79	8	1	0	0	0	0	1		
ENSMUST00000124898	ENSMUSG00000018372	11	106789252	106819930	1	1	1	7	3	4	1	5	27	3	21	11	A2A5Z4	
ENSMUST00000124899	ENSMUSG00000030509	7	66644565	66689596	-1	15	0	84	104	17	11	636	643	1227	123	768		Q91ZU0
ENSMUST00000124900	ENSMUSG00000013465	2	25199712	25211489	-1	2	0	0	0	1	0	1	0	0	0	0	F6UFF7	
ENSMUST00000124902	ENSMUSG00000041119	17	31386234	31476310	1	0	0	0	0	0	8	0	0	0	0	0	D6RH57	
ENSMUST00000124903						2	0	2	0	1	0	3	8	0	4	3		
ENSMUST00000124904						14	7	10	5	14	9	3	43	17	11	47		
ENSMUST00000124905						2	1	9	48	5	0	2	40	18	0	23		
ENSMUST00000124906						5	7	10	8	14	5	0	8	2	0	4		
ENSMUST00000124907						14	17	58	23	16	9	0	0	0	0	0		
ENSMUST00000124908						0	1	3	0	0	0	0	0	0	0	6		
ENSMUST00000124909						2	2	10	3	4	0	6	21	30	0	26		
ENSMUST00000124910	ENSMUSG00000039842	8	18595131	18803189	1	14	15	46	38	12	12	0	0	0	0	0	G3UWE9	
ENSMUST00000124911						1	1	0	0	0	3	0	0	0	0	0		
ENSMUST00000124913						3	1	5	53	3	0	0	0	0	0	0		
ENSMUST00000124915	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	0	0	0	0	0	0	0	0	F6TQ32	
ENSMUST00000124916						0	3	0	0	1	0	0	0	0	0	1		
ENSMUST00000124917						3	3	10	3	4	0	0	0	0	0	0		
ENSMUST00000124918	ENSMUSG00000061171	2	65316430	65364034	-1	0	4	0	0	0	0	0	0	0	0	0	F6X0X3	
ENSMUST00000124920						1	3	9	2	2	4	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000124921	ENSMUSG00000063698	19	60837277	60861479	-1	1	0	0	0	0	1	0	4	0	0	1	D6RHK7	
ENSMUST00000124922						15	2	9	13	14	0	45	250	93	46	53		
ENSMUST00000124923	ENSMUSG00000043587	9	96823336	96892669	-1	2	0	0	0	0	0	0	0	0	0	0	D3YZM5	
ENSMUST00000124924						4	0	7	42	3	0	0	0	0	0	2		
ENSMUST00000124925						5963	6003	7346	5369	5439	2530	330	1422	799	190	891		
ENSMUST00000124926	ENSMUSG00000024240	18	6435951	6516108	-1	5	0	36	0	0	0	2	10	19	24	31	D3Z3Q6	
ENSMUST00000124927	ENSMUSG00000070383	11	73776387	73780589	-1	2	0	1	2	0	1	0	0	0	0	0	B7ZC58	
ENSMUST00000124928	ENSMUSG00000043372	11	103132429	103139876	1	0	0	0	0	0	0	0	0	0	0	0	A2AB67	
ENSMUST00000124930	ENSMUSG00000040752	14	54941981	54966927	-1	3	1	7	3	2	0	0	0	0	0	0	Q1WNP4	
ENSMUST00000124931	ENSMUSG00000048652	3	146645195	146685592	-1	87	71	177	328	135	62	0	9	1	0	4		D3YUG0
ENSMUST00000124932						0	0	0	4	0	0	0	26	0	50	22		
ENSMUST00000124933						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000124934						7	3	9	13	13	2	0	0	0	0	0		
ENSMUST00000124935						0	0	5	159	8	2	0	6	0	0	2		
ENSMUST00000124936						6	7	33	17	13	6	33	61	18	0	0		
ENSMUST00000124937						2	0	3	39	6	1	0	0	0	1	1		
ENSMUST00000124938						3	4	8	148	6	6	0	0	0	0	0		
ENSMUST00000124939						124	97	828	200	123	44	2	16	10	2	18		
ENSMUST00000124941	ENSMUSG00000051736	10	39118804	39133914	-1	0	0	0	0	0	0	0	0	0	2	0	B2RVF6	Q8CF36
ENSMUST00000124942						0	0	0	0	0	0	4	15	9	3	20		
ENSMUST00000124943	ENSMUSG00000060216	11	70432635	70440828	1	0	5	6	0	4	3	34	88	87	5	110	J3QNV6	
ENSMUST00000124944						9	15	16	25	20	10	4	20	7	0	9		
ENSMUST00000124945						14	0	0	7	1	5	0	0	0	10	0		
ENSMUST00000124946						0	1	9	2	5	0	29	91	26	4	56		
ENSMUST00000124947	ENSMUSG00000022679	16	13903161	13949619	1	0	0	0	0	0	0	0	0	0	0	0		Q99MS3
ENSMUST00000124948	ENSMUSG00000021376	13	47025170	47044737	-1	2	0	0	0	0	0	0	0	0	1	0	D3Z0R1	
ENSMUST00000124949						11	9	29	10	13	7	5	24	8	19	8		
ENSMUST00000124950						0	0	5	1	0	1	77	211	134	18	278		
ENSMUST00000124951	ENSMUSG00000000214	7	142892752	142931128	-1	0	0	4	0	8	2	0	0	0	0	0	E9Q9G5	
ENSMUST00000124954						2	0	0	9	1	0	2	1	3	2	6		
ENSMUST00000124955						3	0	3	1	3	0	5	27	0	3	0		
ENSMUST00000124956	ENSMUSG00000027506	3	8925593	9004723	-1	22	29	23	11	15	19	2	11	10	3	15	D3Z2U2	
ENSMUST00000124957	ENSMUSG00000021185	12	100779057	100896981	1	1	3	0	3	3	0	0	3	0	0	0	F7CUW7	
ENSMUST00000124958	ENSMUSG00000020717	11	106654217	106750628	-1	6	0	0	0	0	0	0	0	0	0	0	B1ARA9	
ENSMUST00000124959						4	0	2	0	3	0	3	0	6	2	9		
ENSMUST00000124960	ENSMUSG00000022779	16	16870736	16892990	1	4	0	6	101	7	1	0	0	17	0	4	D3YY65	
ENSMUST00000124961	ENSMUSG00000019796	10	7589800	7625483	1	3	2	28	4	4	4	1	0	2	1	0	F6XYG6	
ENSMUST00000124962						0	1	2	0	4	0	4	0	0	0	0		
ENSMUST00000124963						0	4	0	52	0	0	0	0	0	4	0		
ENSMUST00000124964						6	2	0	2	3	2	16	4	5	0	0		
ENSMUST00000124965						5	1	9	0	8	1	48	56	33	13	17		
ENSMUST00000124966	ENSMUSG00000022272	15	25622525	25813673	1	0	0	0	0	2	0	0	0	0	0	0	D3Z0V4	
ENSMUST00000124967	ENSMUSG00000090137	8	70508263	70510801	-1	4	2	1	4	4	2	10	31	10	10	6	E9Q9J0	
ENSMUST00000124968	ENSMUSG00000021496	13	55727368	55776830	1	0	0	4	11	0	0	1	1	1	1	0		
ENSMUST00000124969						5	8	6	5	7	3	3	5	10	0	12		
ENSMUST00000124970						0	0	0	0	0	0	6	40	13	25	4		
ENSMUST00000124971	ENSMUSG00000025499	7	141189105	141194005	-1	0	0	5	4	6	3	34	68	40	0	32	C0H5X4	
ENSMUST00000124972	ENSMUSG00000027361	2	126627442	126676337	-1	0	2	0	13	0	0	0	0	0	2	0	A2AQ71	
ENSMUST00000124973	ENSMUSG00000006005	1	150392838	150449935	1	14	12	17	0	22	10	653	1526	2284	171	1618		F6ZDS4
ENSMUST00000124974						1	2	4	13	0	8	59	523	111	11	157		
ENSMUST00000124977						5	6	4	2	3	2	3	3	0	0	2		
ENSMUST00000124978						1	0	4	25	5	0	0	1	1	0	0		
ENSMUST00000124979	ENSMUSG00000002068	7	38097984	38107534	-1	5	1	3	12	0	2	1	3	2	0	0		
ENSMUST00000124980						5	1	0	1	8	0	0	0	0	0	0		
ENSMUST00000124981	ENSMUSG00000035509	13	56522472	56537898	1	15	13	24	12	24	5	0	1	0	0	0	D6RE27	
ENSMUST00000124982	ENSMUSG00000036986	9	58218076	58249786	-1	0	0	0	34	0	2	0	0	0	0	0	D3Z2V0	
ENSMUST00000124983						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000124984	ENSMUSG00000032245	9	62838785	62852006	1	5	0	5	2	0	0	0	0	0	0	0	F6SXC2	
ENSMUST00000124985						0	0	0	0	0	2	4	0	3	0	4		
ENSMUST00000124986	ENSMUSG00000026017	1	60098247	60153953	1	0	0	0	0	0	0	0	2	0	3	5	D3Z2W4	
ENSMUST00000124987						0	3	2	0	3	1	0	0	2	0	7		
ENSMUST00000124990	ENSMUSG00000025934	1	21240589	21265661	1	2	5	2	6	2	0	0	0	0	6	2	A0A087WQI6	
ENSMUST00000124991						1	5	11	0	14	0	0	30	0	3	2		
ENSMUST00000124992	ENSMUSG00000028277	4	33031416	33052363	1	0	10	0	17	8	5	521	1267	711	377	507		Q9JJZ4
ENSMUST00000124993						2	2	0	1	2	2	219	505	45	192	114		
ENSMUST00000124994						0	0	2	1	0	1	0	2	2	0	0		
ENSMUST00000124995						0	0	7	5	0	0	0	1	0	0	0		
ENSMUST00000124996	ENSMUSG00000071451	13	34162964	34178172	1	0	4	3	42	0	0	16	41	11	15	16	D3Z016	
ENSMUST00000124997						8	4	7	7	6	4	14	27	12	3	11		
ENSMUST00000124998						0	0	6	7	6	4	1	2	1	1	0		
ENSMUST00000124999						4	0	0	11	6	2	0	0	0	0	0		
ENSMUST00000125000						0	0	0	49	0	1	0	0	0	0	0		
ENSMUST00000125002						0	2	0	0	9	1	0	1	0	0	2		
ENSMUST00000125003						0	0	0	0	0	0	6	0	13	0	6		
ENSMUST00000125004						15	21	34	14	21	8	4	17	11	0	16		
ENSMUST00000125005						2	7	0	15	5	10	7	15	42	166	30		
ENSMUST00000125006	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000125007						28	18	63	161	35	21	42	0	31	0	55		
ENSMUST00000125008	ENSMUSG00000040413	11	46668960	46707061	-1	3	2	2	1	3	0	0	0	0	0	0	D3YUN5	
ENSMUST00000125009	ENSMUSG00000049583	7	87602544	88134907	1	14	9	71	7	9	12	0	0	0	0	0	F6WSV0	
ENSMUST00000125013						0	0	0	0	0	2	0	4	8	2	2		
ENSMUST00000125014						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000125015						12	6	23	13	12	4	0	0	0	0	0		
ENSMUST00000125016						0	1	2	2	0	0	0	2	2	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125017						0	0	6	0	0	6	0	3	0	0	0		
ENSMUST00000125018	ENSMUSG00000044835	1	161142691	161170498	1	0	0	3	0	0	2	0	0	0	0	0	D3YVW9	
ENSMUST00000125019						908	1088	4405	977	1079	657	21	99	56	17	87		
ENSMUST00000125021						0	4	3	1	2	0	0	0	0	2	1		
ENSMUST00000125023	ENSMUSG00000016386	2	106693269	106868356	1	4	0	0	1	6	0	0	0	0	0	0	B1APT1	
ENSMUST00000125024						19	21	0	0	0	14	165	576	178	34	298		
ENSMUST00000125025						4	3	7	5	8	7	11	60	37	0	44		
ENSMUST00000125026						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000125027						1	0	0	2	0	0	0	0	0	0	1		
ENSMUST00000125028						2	4	3	1	2	1	0	0	2	0	0		
ENSMUST00000125029						2	0	10	3	1	2	9	11	10	0	6		
ENSMUST00000125030						1	0	0	0	0	0	0	4	3	30	6		
ENSMUST00000125031						10	11	35	9	16	9	8	9	41	1	67		
ENSMUST00000125032	ENSMUSG00000022973	16	90936092	91011308	-1	1	0	0	0	0	1	17	38	92	3	94	F6VSS8	
ENSMUST00000125033						3	4	22	6	5	1	0	0	0	0	0		
ENSMUST00000125034	ENSMUSG00000028563	4	98355370	98383306	-1	0	0	0	0	0	0	0	0	0	0	0	F6TRH6	
ENSMUST00000125035						0	2	0	0	0	0	10	52	24	0	47		
ENSMUST00000125036	ENSMUSG00000042626	3	89418443	89430027	1	0	0	0	0	0	0	43	11	39	0	17	D3YZV5	
ENSMUST00000125037	ENSMUSG00000021411	13	34627840	34652681	-1	0	0	0	161	31	0	0	0	0	0	0	D6REG6	
ENSMUST00000125038	ENSMUSG00000021693	13	106958996	107022126	-1	4	2	19	16	6	4	6	24	22	0	39	Q9D481	
ENSMUST00000125040	ENSMUSG00000071533	16	56007245	56029739	-1	4	11	30	0	13	4	149	820	294	434	139	D6RDQ3	
ENSMUST00000125041						17	12	37	11	24	7	0	0	5	0	2		
ENSMUST00000125042	ENSMUSG00000051736	10	39118804	39133914	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2A8	
ENSMUST00000125043						2	6	7	4	8	1	0	1	3	0	3		
ENSMUST00000125045						5	4	4	0	7	8	0	0	0	0	0		
ENSMUST00000125046						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000125047						1	3	0	8	0	2	5	24	7	0	0		
ENSMUST00000125048						45	55	250	92	84	43	0	24	12	0	29		
ENSMUST00000125049	ENSMUSG00000027367	2	127270218	127298932	1	17	13	24	0	12	2	272	1405	311	233	392	F7BBA2	
ENSMUST00000125050						6	0	12	2	8	6	0	0	0	0	0		
ENSMUST00000125051	ENSMUSG00000017723	2	164562413	164568510	1	0	5	8	4	3	2	0	0	1	0	0	A2A5G6	
ENSMUST00000125052	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	0	0	0	0	0	0	0	0	F6U8U1	
ENSMUST00000125053	ENSMUSG00000029478	5	125017153	125179219	-1	0	0	0	453	0	0	0	292	0	33	0	F6Z4B2	
ENSMUST00000125054						22	13	71	65	42	29	268	306	364	25	654		
ENSMUST00000125055	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000125057						1	0	0	5	1	0	0	0	0	0	1		
ENSMUST00000125058						51	53	100	57	58	43	98	284	90	8	87		
ENSMUST00000125059	ENSMUSG00000033285	3	100138180	100162407	-1	0	0	2	0	0	0	2	0	0	2	0	H3BLC1	
ENSMUST00000125060	ENSMUSG00000058793	2	132263148	132312050	1	1	1	2	0	1	0	0	0	0	0	3	H3BLA1	
ENSMUST00000125061						4	1	13	5	3	1	0	0	0	0	0		
ENSMUST00000125063						5	4	4	3	4	1	3	116	19	21	35		
ENSMUST00000125064						29	18	74	26	45	15	25	64	43	3	65		
ENSMUST00000125065						12	0	23	47	31	12	13	0	54	11	45		
ENSMUST00000125066						8	6	18	7	17	10	0	0	0	0	5		
ENSMUST00000125067						0	1	9	2	3	5	0	0	0	0	0		
ENSMUST00000125069						0	0	0	0	0	0	4	0	0	2	0		
ENSMUST00000125070						0	3	27	0	2	0	61	224	87	8	90		
ENSMUST00000125072						0	4	6	30	4	0	10	3	4	0	7		
ENSMUST00000125074						0	0	0	40	3	0	187	169	128	166	93		
ENSMUST00000125075	ENSMUSG00000032530	9	121577843	121642096	-1	0	5	0	1	0	0	0	0	0	0	0	D3YUC1	
ENSMUST00000125076						3	2	2	73	7	4	30	17	70	934	506		
ENSMUST00000125077	ENSMUSG00000052407	4	83525545	83864670	1	25	0	0	0	15	0	0	0	9	0	0	A2BI14	
ENSMUST00000125078						0	2	10	3	3	3	0	6	0	0	1		
ENSMUST00000125079						1	3	14	4	2	0	6	172	35	15	86		
ENSMUST00000125080						2	3	0	140	3	2	1	1	0	0	0		
ENSMUST00000125081						43	18	153	166	41	31	1	4	0	0	2		
ENSMUST00000125082						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000125083	ENSMUSG00000026226	1	86016816	86029958	1	0	0	0	0	0	0	0	0	0	0	0		Q9D9T6
ENSMUST00000125084	ENSMUSG00000027207	2	125859109	125984299	1	3	0	0	4	0	3	1	0	0	0	0	B7ZCT5	
ENSMUST00000125085						0	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000125086	ENSMUSG00000045503	2	164456964	164479638	1	15	10	23	23	27	10	36	130	31	0	62		Q78S06
ENSMUST00000125087	ENSMUSG00000050471	9	35216965	35267805	-1	0	0	0	0	0	1	0	0	0	5	9	D3Z1L4	
ENSMUST00000125088						52	43	101	38	52	22	3	19	14	0	20		
ENSMUST00000125089						0	0	0	0	0	0	5	0	0	0	7		
ENSMUST00000125090						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125091						1	2	1	0	2	1	0	0	0	0	2		
ENSMUST00000125092	ENSMUSG00000070000	8	71708387	71725716	-1	0	3	9	1	1	0	17	16	16	1	15	D3YYE9	
ENSMUST00000125093						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125094	ENSMUSG00000018339	11	54902453	54910377	1	0	1	0	15	3	3	0	6	10	0	1	D3Z2Y7	
ENSMUST00000125096						7	11	26	17	5	10	0	0	0	0	0		
ENSMUST00000125097	ENSMUSG00000020740	11	115584255	115604051	-1	1	0	1	0	0	0	0	15	8	0	4	A2A9W5	
ENSMUST00000125098						0	2	0	0	3	2	33	280	86	44	102		
ENSMUST00000125099						1	0	5	7	2	2	16	67	14	0	34		
ENSMUST00000125100						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000125103						5	5	0	3	8	0	0	0	0	0	0		
ENSMUST00000125104	ENSMUSG00000028560	4	98923810	98935543	1	2	0	4	0	0	1	9	0	0	0	0	H3BKR6	
ENSMUST00000125105						0	0	0	4	0	0	0	0	0	7	0		
ENSMUST00000125106						4	14	4	3	10	10	1	8	3	3	1		
ENSMUST00000125107	ENSMUSG00000028608	4	107889813	107899384	1	0	0	0	26	0	0	57	307	64	150	53		Q8BHG2
ENSMUST00000125108						18	14	81	30	15	12	8	43	9	11	8		
ENSMUST00000125109						0	0	0	0	0	0	0	0	2	2	0		
ENSMUST00000125110	ENSMUSG00000046798	5	5489537	5514958	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125111						2	2	10	2	2	4	0	21	3	0	6		
ENSMUST00000125112	ENSMUSG00000025808	8	128980019	129065517	-1	1	1	0	0	0	0	0	0	0	0	0	D3YVX2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125113	ENSMUSG00000021838	14	46882854	47105817	1	6	3	3	0	7	3	0	0	0	0	3		Q8CBY1
ENSMUST00000125114	ENSMUSG00000024818	19	5877808	5885766	1	0	0	22	19	21	17	44	137	52	12	27		Q8CFJ7
ENSMUST00000125115						6	3	2	5	6	3	0	0	0	0	0		
ENSMUST00000125116						4	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000125118						0	3	7	123	11	2	0	0	0	0	0		
ENSMUST00000125119						70	75	45	38	75	41	27	83	19	34	20		
ENSMUST00000125120						23	26	57	39	36	5	6	9	0	5	17		
ENSMUST00000125122						63	40	82	47	61	33	159	1314	306	104	570		
ENSMUST00000125123	ENSMUSG00000060317	4	49379840	49408151	-1	0	6	11	2	2	1	0	0	0	0	0	A2BH60	
ENSMUST00000125124						8	7	5	2	5	3	0	1	0	0	0		
ENSMUST00000125125	ENSMUSG00000048118	12	71015990	71098592	1	3	0	4	34	4	0	0	4	15	0	22	Q8BY40	
ENSMUST00000125127	ENSMUSG00000024571	18	80206765	80212741	1	0	0	0	0	0	0	427	2206	1010	405	838	Q9CQX6	
ENSMUST00000125128						0	0	0	51	0	0	0	0	0	0	0		
ENSMUST00000125129						3	0	3	0	2	0	5	12	0	0	0		
ENSMUST00000125132	ENSMUSG00000018906	11	54100095	54131665	1	0	2	0	39	0	2	0	0	0	0	0	D6RCG8	
ENSMUST00000125133						3	0	4	73	6	4	0	0	0	1	0		
ENSMUST00000125134	ENSMUSG00000032921	11	68921835	68927081	-1	0	3	0	7	3	5	0	0	0	0	0		
ENSMUST00000125135	ENSMUSG00000039911	4	149896283	149955043	-1	13	2	41	4	4	2	0	0	0	0	0	A2A7B1	
ENSMUST00000125136						6	4	11	0	0	2	21	3	0	0	2		
ENSMUST00000125137						5	1	2	6	2	0	31	86	54	16	60		
ENSMUST00000125138						5	2	2	1	1	0	0	0	0	0	0		
ENSMUST00000125139	ENSMUSG00000033963	6	113596761	113600715	-1	0	0	0	17	2	8	0	2	0	0	0		
ENSMUST00000125140						10	2	8	8	9	7	0	0	5	0	0		
ENSMUST00000125141						6	5	48	70	11	2	0	0	0	0	0		
ENSMUST00000125142						1	4	11	7	1	1	0	0	0	0	2		
ENSMUST00000125144						1	4	1	2	1	0	0	5	4	0	0		
ENSMUST00000125145	ENSMUSG00000020840	11	76924809	76987379	1	0	0	1	1	1	1	0	0	5	0	0	E9PY26	
ENSMUST00000125146						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000125148						0	0	3	2	0	0	0	2	0	4	0		
ENSMUST00000125149	ENSMUSG00000026303	1	90915085	90951142	1	1	0	1	4	3	1	0	0	0	0	0	D3Z049	
ENSMUST00000125150						14	14	10	21	17	13	0	0	0	0	0		
ENSMUST00000125151						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125152						0	0	0	0	0	2	6	18	0	0	8		
ENSMUST00000125153	ENSMUSG00000027624	2	156420909	156543214	1	23	26	70	313	63	25	0	2	3	2	7	E9PV14	
ENSMUST00000125154						0	1	1	2	3	3	0	0	0	0	0		
ENSMUST00000125155						3	0	7	4	6	0	0	3	0	0	3		
ENSMUST00000125156						2	2	5	0	3	2	0	0	0	0	2		
ENSMUST00000125157						0	4	0	0	0	0	18	43	0	8	11		
ENSMUST00000125159						0	0	0	10	0	0	0	0	0	0	0		
ENSMUST00000125160						55	64	129	70	84	37	9	26	19	2	26		
ENSMUST00000125162						0	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000125163	ENSMUSG00000069456	10	127801152	127846565	1	100	96	95	91	94	54	15	65	27	4	22	D6RFT0	
ENSMUST00000125164						0	0	0	0	0	0	19	0	108	29	99		
ENSMUST00000125165						8	3	51	40	12	3	0	37	19	37	23		
ENSMUST00000125166						5	12	0	0	8	4	432	1521	325	606	208		
ENSMUST00000125167	ENSMUSG00000039230	11	121451949	121617164	1	4	2	3	2	2	2	0	3	0	0	0	F6UI15	
ENSMUST00000125169	ENSMUSG00000047989	18	24104757	24121953	-1	7	6	5	0	3	0	0	0	15	61	15	D3Z3N1	
ENSMUST00000125171						2	3	0	15	1	0	2	24	29	0	7		
ENSMUST00000125172	ENSMUSG00000038845	11	95666957	95680773	1	18	9	34	23	27	11	27	77	15	45	65		P67778
ENSMUST00000125174	ENSMUSG00000043740	17	48316141	48327024	1	131	126	146	189	105	74	1162	2663	1388	405	1484	D6RJI6	
ENSMUST00000125175						0	2	2	0	6	0	0	0	0	0	0		
ENSMUST00000125176	ENSMUSG00000069171	13	78188973	78199757	-1	0	0	0	23	0	0	0	0	0	2	0	F7CII1	
ENSMUST00000125177	ENSMUSG00000023990	17	47737030	47792419	1	1	1	9	9	3	3	6	3	3	2	3	D3Z1X9	
ENSMUST00000125179						39	45	48	42	43	30	1	9	5	5	1		
ENSMUST00000125180						7	1	15	5	3	0	24	71	0	12	15		
ENSMUST00000125181						0	3	0	7	0	0	0	0	0	0	0		
ENSMUST00000125182						2	0	1	5	1	3	0	0	0	0	0		
ENSMUST00000125183	ENSMUSG00000028099	3	96711490	96727628	-1	0	0	0	2	5	2	10	0	0	0	4	D3YYS2	
ENSMUST00000125184	ENSMUSG00000090137	8	70508263	70510801	-1	5	0	0	37	11	6	94	126	84	492	46	Q66JP1	P62984
ENSMUST00000125187						2	0	7	1	1	0	0	0	0	0	0		
ENSMUST00000125188	ENSMUSG00000042289	7	127800604	127803802	1	1	0	0	0	3	0	1	4	0	0	8		
ENSMUST00000125189						1	1	0	2	1	0	13	41	0	12	9		
ENSMUST00000125192	ENSMUSG00000020564	12	33147693	33375659	1	11	22	15	9	13	8	430	1215	776	92	951	F6X2K7	
ENSMUST00000125193						3	3	0	2	2	0	0	0	1	0	0		
ENSMUST00000125195	ENSMUSG00000023328	5	137287519	137294466	1	0	0	0	0	0	0	0	0	0	0	0	D3Z064	
ENSMUST00000125196						3	5	1	3	4	3	0	0	0	0	0		
ENSMUST00000125197						3	0	1	5	0	2	0	0	0	0	5		
ENSMUST00000125199						4	2	16	142	11	5	0	0	0	0	0		
ENSMUST00000125200	ENSMUSG00000019790	10	9755547	9901079	-1	0	2	0	0	0	6	201	49	556	26	187	D3Z2Q2	
ENSMUST00000125201						16	15	19	26	18	8	0	1	2	1	6		
ENSMUST00000125202						0	0	11	0	0	0	5	0	0	0	22		
ENSMUST00000125203						14	8	3	13	4	5	16	86	40	8	81		
ENSMUST00000125205						1	0	0	7	1	0	0	3	12	0	3		
ENSMUST00000125206						4	0	6	0	2	2	0	0	0	0	0		
ENSMUST00000125207						0	0	0	0	0	0	5	12	0	8	4		
ENSMUST00000125208						0	0	0	0	0	0	45	414	196	99	355		
ENSMUST00000125209	ENSMUSG00000021596	13	76384535	77031810	1	15	12	11	337	18	10	263	598	188	188	103	E9PV86	
ENSMUST00000125210						0	0	0	0	0	5	3	11	3	1	4		
ENSMUST00000125211						0	0	0	16	1	0	0	2	5	0	5		
ENSMUST00000125212	ENSMUSG00000034327	14	67715937	67742310	1	0	1	0	0	0	0	3	6	0	1	0		
ENSMUST00000125213	ENSMUSG00000066613	5	109996521	110010411	1	0	0	0	0	0	0	6	3	0	0	1	D3Z1G5	
ENSMUST00000125215						0	1	1	3	0	0	0	1	0	0	1		
ENSMUST00000125216						7	6	3	82	9	1	0	0	0	0	0		
ENSMUST00000125217	ENSMUSG00000016510	5	146951573	146963800	-1	0	1	6	18	2	0	0	0	0	0	0	D3Z0H9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125218						0	0	0	0	0	0	8	11	0	6	1		
ENSMUST00000125220	ENSMUSG00000019254	7	4481520	4501680	-1	0	1	0	48	0	2	2	3	10	0	7		
ENSMUST00000125221	ENSMUSG00000000308	2	121357714	121363737	1	0	0	0	0	0	0	0	0	0	0	0	B0R0E8	
ENSMUST00000125222						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000125223	ENSMUSG00000037143	2	145934784	146215039	1	1	0	0	1	2	0	0	0	0	0	0	B7ZCG4	
ENSMUST00000125224						37	30	30	42	39	40	7	16	14	0	22		
ENSMUST00000125225						3	0	0	6	5	7	3	0	0	6	4		
ENSMUST00000125226						68	52	158	23	42	26	4	17	18	4	32		
ENSMUST00000125227						113	34	481	20	0	0	0	0	0	0	51		
ENSMUST00000125228						8	3	65	18	8	9	0	0	1	0	0		
ENSMUST00000125229						2	0	0	0	2	0	0	0	9	13	4		
ENSMUST00000125231						78	65	242	237	98	54	0	13	6	1	11		
ENSMUST00000125232						17	14	33	9	15	7	11	89	39	12	48		
ENSMUST00000125233						0	1	0	0	2	0	1	1	7	0	1		
ENSMUST00000125235						0	0	0	0	5	1	13	22	12	0	13		
ENSMUST00000125238						5	1	0	0	1	0	2	0	1	6	0		
ENSMUST00000125239	ENSMUSG00000032078	9	46273064	46282643	1	0	0	0	0	0	1	9	0	0	0	7	F6WPJ5	
ENSMUST00000125241						5	0	5	6	3	4	0	1	0	0	0		
ENSMUST00000125242						10	3	5	8	5	0	8	22	8	0	0		
ENSMUST00000125243	ENSMUSG00000061136	2	53134704	53191284	-1	0	1	0	12	0	0	55	92	277	103	116	A2AQW6	
ENSMUST00000125245						3	2	7	0	10	7	3	4	0	0	0		
ENSMUST00000125246						4	8	8	9	10	2	0	0	0	0	0		
ENSMUST00000125247						2	2	4	4	5	4	0	0	0	0	1		
ENSMUST00000125248						0	2	0	0	2	0	0	0	0	0	1		
ENSMUST00000125249	ENSMUSG00000086784	7	4877053	4895717	1	5	7	31	15	18	1	87	74	37	65	50		P85094
ENSMUST00000125251						0	2	0	1	3	0	0	1	0	0	0		
ENSMUST00000125252	ENSMUSG00000045031	3	37307749	37312708	-1	0	0	0	36	3	0	0	0	0	0	1	E9PVN5	
ENSMUST00000125254						1	0	0	1	1	1	1	2	1	0	3		
ENSMUST00000125256						2	0	2	2	1	0	1	0	3	0	2		
ENSMUST00000125257	ENSMUSG00000031667	8	91112041	91134465	-1	0	0	6	12	0	0	10	20	27	17	9	D3Z2J4	
ENSMUST00000125258						4	3	3	7	3	0	0	0	0	0	2		
ENSMUST00000125259						3	0	7	4	5	2	0	0	0	0	0		
ENSMUST00000125260						41	26	168	48	42	14	0	0	0	0	0		
ENSMUST00000125261	ENSMUSG00000035011	10	81135220	81152995	1	2	1	6	193	6	3	9	6	8	0	13	D3YVF8	
ENSMUST00000125262						0	4	0	12	0	0	0	0	0	0	0		
ENSMUST00000125263						3	5	4	2	2	3	0	0	0	0	0		
ENSMUST00000125264						0	1	2	2	0	0	0	0	0	0	0		
ENSMUST00000125265	ENSMUSG00000022185	14	54642161	54686931	-1	8	6	8	21	6	11	17	98	26	0	17	B8JJ89	
ENSMUST00000125266						0	0	0	0	3	0	7	26	31	64	28		
ENSMUST00000125267						2	0	4	0	1	3	0	0	0	0	0		
ENSMUST00000125268	ENSMUSG00000031960	8	111033144	111057664	1	1	5	2	11	4	1	1	3	0	0	0		
ENSMUST00000125270						2	2	0	6	3	3	1	4	5	0	9		
ENSMUST00000125271	ENSMUSG00000041688	X	145446425	145505181	-1	8	16	34	0	0	5	0	20	0	4	0	F6QYS7	
ENSMUST00000125272						3	0	6	0	2	1	0	0	0	0	0		
ENSMUST00000125273						8	10	12	15	17	5	0	0	0	0	0		
ENSMUST00000125274						10	0	51	8	17	1	1	0	0	0	5		
ENSMUST00000125276	ENSMUSG00000049922	2	92452764	92460538	-1	0	13	19	36	10	0	270	637	329	38	133	Q8R2I1	
ENSMUST00000125278	ENSMUSG00000033031	16	48994185	49019709	1	4	1	3	41	5	1	0	0	0	7	0	D6RGL3	
ENSMUST00000125279						1	3	1	4	7	4	0	0	0	0	0		
ENSMUST00000125280	ENSMUSG00000030471	7	48789003	48827440	1	0	0	0	3	0	0	25	0	0	0	0	D3YY07	
ENSMUST00000125281						0	0	1	3	2	0	0	0	0	0	0		
ENSMUST00000125282	ENSMUSG00000073842	4	60066469	60070475	-1	0	0	0	0	0	0	0	0	0	0	0	L7MUC7	
ENSMUST00000125283						3	6	0	6	0	0	0	0	0	0	2		
ENSMUST00000125284						0	0	0	0	0	1	133	359	144	31	138		
ENSMUST00000125285						0	1	0	0	0	0	0	71	0	2	0		
ENSMUST00000125286						8	9	12	8	6	3	0	7	2	1	1		
ENSMUST00000125287	ENSMUSG00000013539	16	18300825	18348103	-1	0	1	2	12	2	0	0	0	0	0	0	D6RH68	
ENSMUST00000125288	ENSMUSG00000028402	4	81278500	81442815	-1	0	0	0	0	3	2	0	0	0	0	0	A3KG80	
ENSMUST00000125289	ENSMUSG00000039994	10	128232065	128252941	1	3	1	0	0	0	0	3	0	0	0	0	E9Q302	
ENSMUST00000125290						16	9	95	391	26	17	17	0	0	0	0		
ENSMUST00000125291	ENSMUSG00000024679	19	11586604	11604849	-1	4984	4424	6037	17361	2786	552	12	14	25	9	54	F6V7U2	
ENSMUST00000125292	ENSMUSG00000020524	11	57011387	57330244	1	0	4	0	5	3	0	0	0	0	0	0		
ENSMUST00000125293						1	0	5	1	2	0	0	0	0	0	0		
ENSMUST00000125294	ENSMUSG00000046101	1	9908638	9942085	1	0	0	0	0	1	0	2	0	0	0	0	H9KV11	
ENSMUST00000125295	ENSMUSG00000031626	8	45507788	45827906	1	0	19	40	18	17	6	0	0	0	0	0		
ENSMUST00000125296						2	0	0	5	0	1	0	0	0	0	0		
ENSMUST00000125297						3	1	3	2	7	3	4	2	3	0	2		
ENSMUST00000125298						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125299						31	30	25	30	40	18	6	30	14	0	14		
ENSMUST00000125300	ENSMUSG00000022090	14	70164218	70177681	-1	0	0	0	0	0	0	0	0	0	0	0	F7C957	
ENSMUST00000125301						5	0	0	34	5	0	0	3	2	7	0		
ENSMUST00000125302	ENSMUSG00000020321	11	21556787	21572367	-1	0	0	0	1	0	0	65	88	63	436	51	B1ATQ3	
ENSMUST00000125303	ENSMUSG00000028441	4	41505009	41517333	-1	3	0	0	43	4	4	0	4	0	0	1	F7CUE2	
ENSMUST00000125304	ENSMUSG00000001143	1	36419871	36445271	-1	16	10	29	22	10	7	100	244	147	11	140		P59481
ENSMUST00000125306	ENSMUSG00000026207	1	75375297	75432320	1	0	2	0	2	2	0	0	0	0	0	0	D6RI69	
ENSMUST00000125307	ENSMUSG00000043648	11	59783897	59787645	-1	3	2	5	115	4	2	2	0	0	0	0		Q5SWZ9
ENSMUST00000125310						0	0	3	21	4	3	1	0	0	0	0		
ENSMUST00000125311						2	0	9	0	1	0	0	0	0	0	0		
ENSMUST00000125312	ENSMUSG00000033423	4	117550365	117674297	1	2	2	12	3	5	3	2	0	0	0	0		
ENSMUST00000125314	ENSMUSG00000031537	8	22659212	22706589	-1	0	5	5	0	0	2	0	105	0	20	0	Q3U141	
ENSMUST00000125315						2	4	3	1	5	1	0	0	0	0	0		
ENSMUST00000125316						5	0	10	18	8	8	6	13	7	16	9		
ENSMUST00000125319	ENSMUSG00000038225	8	46575579	46617212	-1	0	0	0	0	0	0	0	0	0	0	0	D3YXL5	
ENSMUST00000125320						4	1	3	0	2	0	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125321						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125322						1	0	0	0	1	0	0	44	7	19	20		
ENSMUST00000125323						0	0	0	0	0	0	4	15	1	4	0		
ENSMUST00000125325	ENSMUSG00000029505	5	110664373	110770717	-1	0	1	4	19	4	0	33	18	47	1	52	F6R9G0	
ENSMUST00000125326	ENSMUSG00000041390	6	15720661	15802169	1	6	13	10	13	13	5	0	0	0	0	0	A0A087WPB2	
ENSMUST00000125327						0	0	1	0	0	0	0	0	0	0	25		
ENSMUST00000125328	ENSMUSG00000046351	13	23353103	23369208	-1	0	0	0	0	0	0	4	16	5	5	7	B7ZCB3	
ENSMUST00000125329						4	2	0	15	5	5	0	0	0	0	0		
ENSMUST00000125330	ENSMUSG00000037348	4	134496697	134510235	1	0	0	0	0	0	0	4	0	0	0	0	D3Z5A3	
ENSMUST00000125331						3	2	16	3	2	7	0	0	0	0	0		
ENSMUST00000125332						2	2	2	1	0	1	5	121	34	4	87		
ENSMUST00000125334						9	9	12	7	6	3	2	2	5	0	5		
ENSMUST00000125335						4	1	0	0	2	2	3	5	9	0	4		
ENSMUST00000125337						0	0	0	5	0	0	0	0	18	14	1		
ENSMUST00000125338	ENSMUSG00000027695	3	27938695	28133362	1	0	0	3	0	5	2	0	0	0	0	0	D3Z2V2	
ENSMUST00000125339	ENSMUSG00000043243	8	71597648	71607936	1	5	10	13	104	13	11	1	35	0	0	0	F6QUK2	
ENSMUST00000125340						5	4	0	0	1	1	0	328	0	9	0		
ENSMUST00000125341						26	17	61	32	53	24	1	0	0	0	1		
ENSMUST00000125342	ENSMUSG00000028614	4	107367784	107416346	1	0	0	0	0	2	1	0	0	0	0	0	J3QMD9	
ENSMUST00000125343						27	34	21	25	33	27	4	8	4	5	8		
ENSMUST00000125344						27	29	103	43	29	11	8	12	6	0	14		
ENSMUST00000125346	ENSMUSG00000026785	2	30077684	30091022	1	3	0	0	52	6	8	0	0	0	0	2	A2BE96	
ENSMUST00000125347						1	4	8	4	0	1	0	0	0	0	0		
ENSMUST00000125348						7	4	17	15	5	1	0	0	0	0	0		
ENSMUST00000125349						0	4	2	0	5	0	15	28	1	0	0		
ENSMUST00000125350	ENSMUSG00000017978	6	23262773	23839421	-1	0	0	0	0	0	0	1	2	0	0	3	F6SH36	
ENSMUST00000125351						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125352						0	0	0	24	2	4	0	0	0	0	0		
ENSMUST00000125356	ENSMUSG00000030757	7	123475384	123500449	-1	8	0	0	1	0	2	0	0	0	0	0	F7BPE8	
ENSMUST00000125357						0	2	0	21	0	0	5	4	10	38	26		
ENSMUST00000125359						0	0	0	38	6	0	0	0	0	0	0		
ENSMUST00000125360						4	1	10	39	5	0	1	0	0	0	0		
ENSMUST00000125361						3	6	5	5	6	1	0	9	5	2	5		
ENSMUST00000125362	ENSMUSG00000056153	18	88665224	88927481	-1	6	0	0	126	11	8	39	270	142	50	103		Q9JLY0
ENSMUST00000125363						0	0	7	0	0	1	18	41	9	0	7		
ENSMUST00000125364						2	0	2	22	0	0	3	0	0	0	0		
ENSMUST00000125366	ENSMUSG00000019188	2	152669461	152708670	1	30	12	66	486	28	25	708	1061	606	126	483		Q9D8V0
ENSMUST00000125367	ENSMUSG00000067642	5	30193431	30205722	-1	2	0	0	0	1	0	0	2	0	1	0	F6UJY6	
ENSMUST00000125369						3	5	14	4	7	0	136	495	77	32	61		
ENSMUST00000125370	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	4	2	0	0	9	0	0	0	H3BKS8	
ENSMUST00000125371						1	1	0	0	0	0	3	2	1	0	2		
ENSMUST00000125372						2	1	11	9	7	3	0	1	2	0	6		
ENSMUST00000125375						41	31	156	53	35	21	29	101	32	7	43		
ENSMUST00000125376						7	10	6	6	0	0	0	11	17	5	5		
ENSMUST00000125377						0	0	0	4	6	0	0	3	0	0	9		
ENSMUST00000125378	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	0	0	0	0	0	0	0	0	F6UI99	
ENSMUST00000125379						0	3	1	3	0	0	0	0	0	0	0		
ENSMUST00000125380						8	5	0	6	16	8	0	1	0	3	6		
ENSMUST00000125381						500	599	353	550	596	352	13	27	13	3	41		
ENSMUST00000125383	ENSMUSG00000078622	11	106197408	106216344	-1	6	8	52	27	11	8	20	82	52	22	56	F7C265	
ENSMUST00000125385	ENSMUSG00000071477	6	48024188	48048911	-1	0	0	0	27	2	0	0	0	0	0	0	D3YYD3	
ENSMUST00000125386						0	0	0	4	3	0	4	16	21	7	22		
ENSMUST00000125387						0	0	2	34	0	2	0	0	0	0	0		
ENSMUST00000125388						1	1	0	0	0	0	1	198	10	2	2		
ENSMUST00000125389	ENSMUSG00000018761	11	69656697	69662642	-1	0	0	0	0	0	0	17	4	0	0	0	F6ZGG4	
ENSMUST00000125390						8	13	19	70	13	13	4	0	0	2	6		
ENSMUST00000125391						3	1	2	33	4	2	0	0	0	0	0		
ENSMUST00000125392	ENSMUSG00000028919	4	141239499	141257564	1	0	0	12	10	0	3	0	0	0	0	0	A2A829	
ENSMUST00000125393						19	17	39	53	46	14	0	10	0	0	0		
ENSMUST00000125394						0	0	1	30	1	0	0	1	0	0	0		
ENSMUST00000125395						0	0	3	0	0	0	0	0	0	5	0		
ENSMUST00000125397						0	2	1	50	0	1	0	0	22	7	0		
ENSMUST00000125398	ENSMUSG00000027425	2	144368983	144407676	1	5	2	0	1	1	2	0	2	2	0	0	E9Q3Q5	
ENSMUST00000125399	ENSMUSG00000035969	4	43381979	43427088	1	1	0	0	0	0	0	0	0	0	0	0	B0QZZ9	
ENSMUST00000125402	ENSMUSG00000027087	2	83724397	83806916	1	3	1	3	1	3	0	0	0	19	0	12	F6W6Q6	
ENSMUST00000125403						1	1	1	2	1	0	0	0	0	0	1		
ENSMUST00000125404	ENSMUSG00000055214	1	175962306	176275312	-1	9	15	54	81	12	5	0	0	0	0	1	D6RCJ9	
ENSMUST00000125405						0	0	0	164	0	0	0	0	0	0	0		
ENSMUST00000125407	ENSMUSG00000027198	2	93661028	93822568	-1	0	0	2	0	0	5	0	0	6	0	0	E9Q1M5	
ENSMUST00000125408						0	0	1	27	6	3	10	13	0	38	17		
ENSMUST00000125409						0	0	3	16	0	0	0	0	0	0	0		
ENSMUST00000125410	ENSMUSG00000056648	11	96281905	96285315	1	0	0	0	64	5	0	0	0	0	0	0	F6W0B3	
ENSMUST00000125411						7	4	1	67	6	2	2	1	5	1	14		
ENSMUST00000125414						4	0	8	5	3	3	0	23	15	10	35		
ENSMUST00000125415						0	0	0	0	0	0	0	0	0	11	0		
ENSMUST00000125416	ENSMUSG00000022371	15	55307750	55520803	1	4	0	14	11	15	3	1	0	0	4	0	F7D5Y4	
ENSMUST00000125417	ENSMUSG00000028523	4	102986379	103005594	1	0	1	0	0	0	0	0	0	0	0	1	A2AIZ3	
ENSMUST00000125418	ENSMUSG00000031162	X	7959260	7978071	-1	0	1	0	3	0	0	1	0	0	0	0	B1AUB3	
ENSMUST00000125420						38	35	147	115	58	23	0	2	0	0	4		
ENSMUST00000125421						42	51	46	1427	144	75	0	2	0	0	3		
ENSMUST00000125422						1	0	0	0	0	0	0	0	0	0	16		
ENSMUST00000125423						0	0	2	2	0	3	0	0	3	0	9		
ENSMUST00000125424						49	58	127	62	40	20	8	16	14	4	20		
ENSMUST00000125425						9	3	0	1	4	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125426	ENSMUSG00000051682	17	48264295	48275360	1	2	0	8	4	0	0	12	10	0	0	21		Q3LRV9
ENSMUST00000125427						0	0	0	0	0	0	0	32	17	23	1		
ENSMUST00000125429						8	6	0	12	0	0	0	0	0	0	0		
ENSMUST00000125430						5	4	3	56	13	5	4	9	0	0	0		
ENSMUST00000125432						22	14	41	37	25	14	10	42	18	2	26		
ENSMUST00000125433						2	0	2	62	6	1	0	0	0	0	0		
ENSMUST00000125434	ENSMUSG00000041798	11	5900820	5950081	-1	3	0	3	34	4	5	0	0	0	0	0	F6V339	
ENSMUST00000125435	ENSMUSG00000058571	14	116925297	117979529	1	0	1	4	0	1	0	0	0	0	0	0	Q8R3X6	
ENSMUST00000125436						0	0	0	0	8	0	0	0	0	0	0		
ENSMUST00000125437	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	1	0	0	0	0	3	0	D3Z0N1	
ENSMUST00000125439						2	0	5	1	1	1	0	0	0	0	0		
ENSMUST00000125440						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000125441						0	0	14	12	14	1	0	0	0	0	0		
ENSMUST00000125442	ENSMUSG00000028410	4	40722150	40737149	1	0	0	0	47	0	7	0	0	0	0	0	B1AXY0	
ENSMUST00000125443						6	1	16	5	5	3	0	3	7	0	3		
ENSMUST00000125444						2	2	0	110	6	2	0	0	0	0	0		
ENSMUST00000125445	ENSMUSG00000053730	4	129676355	129696838	-1	0	0	0	9	15	0	31	38	14	7	38	D6RCH5	
ENSMUST00000125446	ENSMUSG00000034848	2	66184327	66256617	-1	0	0	0	0	0	6	0	0	0	0	7	E9PVK4	
ENSMUST00000125447						0	0	0	0	0	1	0	6	0	0	0		
ENSMUST00000125448						1	4	0	3	3	0	62	500	64	30	190		
ENSMUST00000125449						18	9	57	38	27	4	2	1	3	0	7		
ENSMUST00000125450	ENSMUSG00000048410	18	84128027	84589725	-1	0	0	2	3	2	0	0	0	0	0	0	S4R2G4	
ENSMUST00000125451						0	0	195	51	23	11	0	0	3	4	0		
ENSMUST00000125452						1	2	0	3	5	1	0	14	2	1	8		
ENSMUST00000125453						70	77	71	75	92	39	11	81	88	35	139		
ENSMUST00000125454	ENSMUSG00000062580	1	135295213	135313778	-1	31	22	315	45	23	16	6	14	8	0	6	D3Z1K5	
ENSMUST00000125455	ENSMUSG00000040488	7	27305136	27337692	-1	0	0	0	0	2	0	0	0	0	0	0	F6W6Z0	
ENSMUST00000125456						1	4	4	2	3	0	0	0	2	0	0		
ENSMUST00000125457						0	0	1	0	1	0	0	0	0	0	1		
ENSMUST00000125458						1	1	5	3	1	0	0	0	0	0	0		
ENSMUST00000125459						3	2	7	253	15	7	1	0	5	0	7		
ENSMUST00000125460						84	59	206	82	71	35	0	12	8	0	4		
ENSMUST00000125461	ENSMUSG00000073830	4	61300023	61304000	-1	0	0	0	0	0	0	0	0	0	0	0	B8JI96	
ENSMUST00000125462	ENSMUSG00000034842	5	92331827	92414628	1	4	0	0	1	0	0	0	0	0	0	0	E9Q1U7	
ENSMUST00000125463						5	3	0	92	10	6	0	3	5	0	0		
ENSMUST00000125466	ENSMUSG00000031557	8	25039144	25102194	-1	0	0	0	0	0	0	0	0	9	0	9	D3Z3L8	
ENSMUST00000125467						2	7	0	1	0	0	0	16	8	0	13		
ENSMUST00000125468						2	2	3	14	6	4	4	31	7	0	15		
ENSMUST00000125469						0	2	2	0	0	0	8	34	4	3	0		
ENSMUST00000125470						5	6	0	0	11	4	0	0	0	0	0		
ENSMUST00000125471						14	8	30	23	14	8	1	0	0	0	0		
ENSMUST00000125472						1	1	2	27	2	0	0	0	0	0	1		
ENSMUST00000125473						0	0	0	0	1	0	0	6	0	0	0		
ENSMUST00000125475						6	2	15	0	4	5	0	0	0	0	0		
ENSMUST00000125476	ENSMUSG00000038861	3	94974731	95006843	1	0	10	10	0	5	0	346	584	305	75	254	E9Q8A3	
ENSMUST00000125477						5	4	12	11	1	0	0	0	3	0	0		
ENSMUST00000125479	ENSMUSG00000057933	9	78331018	78355788	-1	0	0	11	13	3	0	0	0	0	0	0	D3YZV3	
ENSMUST00000125480						8	12	9	68	10	2	0	1	6	1	0		
ENSMUST00000125481	ENSMUSG00000038047	4	86578855	86612055	-1	0	1	4	134	2	0	0	0	1	0	0	B1AXR2	
ENSMUST00000125482	ENSMUSG00000039205	2	32352327	32380970	1	0	0	3	0	0	0	21	0	44	7	13	F6XWQ4	
ENSMUST00000125483						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125484	ENSMUSG00000076671	12	114357759	114358218	-1	2	4	3	0	3	0	0	0	0	0	0	A0A0A6YWN3	
ENSMUST00000125485						3	0	0	1	1	2	0	0	0	0	0		
ENSMUST00000125486						8	13	5	5	10	6	0	0	0	0	0		
ENSMUST00000125487	ENSMUSG00000033653	16	21423118	21644680	1	2	7	12	7	10	5	6	50	22	0	45	F6ZLN8	
ENSMUST00000125488						6	9	10	13	12	8	1	0	2	0	1		
ENSMUST00000125489	ENSMUSG00000029712	5	137553517	137569582	1	0	0	1	48	2	4	0	0	0	0	0	D3Z2E2	
ENSMUST00000125490						3	2	2	1	10	5	0	0	0	1	0		
ENSMUST00000125491						0	1	0	0	0	0	0	0	16	19	6		
ENSMUST00000125492						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000125493						1	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000125495	ENSMUSG00000048280	13	67667437	67687071	-1	0	0	2	4	1	3	0	0	2	2	0	Q8BPD8	
ENSMUST00000125497						4	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000125498	ENSMUSG00000004996	8	84249906	84257326	-1	6	4	13	2	12	7	6	26	9	1	12	F6YY88	
ENSMUST00000125499						3	2	0	1	6	0	0	0	0	0	0		
ENSMUST00000125500						0	0	0	0	0	0	0	9	3	0	13		
ENSMUST00000125501						1	0	3	3	3	2	8	0	0	5	7		
ENSMUST00000125502	ENSMUSG00000039263	2	174110349	174123070	1	6	0	3	2	4	0	0	2	4	0	9	F6T2H5	
ENSMUST00000125503						1	4	1	0	2	0	0	2	0	0	2		
ENSMUST00000125504						14	14	59	147	27	22	0	0	0	0	0		
ENSMUST00000125505	ENSMUSG00000020251	10	82650433	82690650	-1	0	0	0	0	0	0	2	0	0	0	1	H3BLS5	
ENSMUST00000125506						0	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000125507						0	0	4	4	4	0	0	0	0	0	0		
ENSMUST00000125508	ENSMUSG00000030720	7	126571207	126585817	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z448	
ENSMUST00000125509	ENSMUSG00000028465	4	43531519	43562691	-1	0	2	0	5	1	0	2	2	0	0	0	F6SX70	
ENSMUST00000125510						11	24	61	26	18	10	3	4	7	0	7		
ENSMUST00000125511						3	0	3	8	4	4	0	4	0	0	0		
ENSMUST00000125512	ENSMUSG00000024236	18	4920540	5119299	1	0	0	0	0	0	0	310	4096	992	167	1069	F6R6A4	
ENSMUST00000125513	ENSMUSG00000028898	4	132311763	132329538	-1	7	6	8	4	8	7	0	7	5	3	3	E9PYW1	
ENSMUST00000125514	ENSMUSG00000031446	8	13105621	13147940	1	17	11	28	6	18	5	56	196	196	43	185	F6UV36	
ENSMUST00000125515	ENSMUSG00000028115	3	95241271	95251193	-1	0	4	4	0	0	0	0	0	0	0	0	D3YY90	
ENSMUST00000125516	ENSMUSG00000024949	19	6363690	6378030	1	0	0	0	0	0	0	17	0	0	30	110	F6YR19	
ENSMUST00000125517	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000125519	ENSMUSG00000022972	16	90925809	90934927	-1	4	0	6	43	10	3	0	0	0	0	0	D6REH7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125520						0	0	0	0	2	0	5	15	0	0	0		
ENSMUST00000125521						3	0	0	1	2	0	21	43	34	0	64		
ENSMUST00000125522						81	45	436	107	69	34	4	7	12	3	21		
ENSMUST00000125523	ENSMUSG00000033055	15	79053094	79062893	-1	0	2	0	0	0	0	0	0	0	0	0	F6UYM2	
ENSMUST00000125524						2	1	17	14	4	2	11	99	14	0	79		
ENSMUST00000125525						0	1	0	150	0	0	0	0	0	0	0		
ENSMUST00000125526	ENSMUSG00000028064	3	88435959	88461182	-1	3	0	2	3	5	0	77	46	109	0	113	D3Z336	
ENSMUST00000125527						11	3	12	62	12	3	11	2	3	5	7		
ENSMUST00000125528						2	1	16	6	7	4	1	52	1	3	8		
ENSMUST00000125530						0	2	0	40	2	0	0	0	0	0	0		
ENSMUST00000125531						47	42	53	15	42	25	46	71	47	4	75		
ENSMUST00000125532						0	0	0	0	0	0	1	0	0	2	0		
ENSMUST00000125533	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	13	22	0	0	0	0	0	3	0		P0C8K7
ENSMUST00000125534						2	3	2	2	8	2	0	0	1	0	0		
ENSMUST00000125535						0	0	3	7	7	1	3	33	1	2	13		
ENSMUST00000125536	ENSMUSG00000063049	8	47667178	47675556	-1	2	0	4	0	0	0	50	308	87	46	77	E0CXA7	
ENSMUST00000125537	ENSMUSG00000037965	16	11136592	11176393	-1	1	0	4	1	1	0	0	0	3	0	4	D3Z5I3	
ENSMUST00000125539						0	1	1	12	1	0	10	5	0	32	0		
ENSMUST00000125540	ENSMUSG00000026049	1	44086613	44102441	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2U8	
ENSMUST00000125541	ENSMUSG00000056596	4	133491100	133498550	-1	2	3	2	182	8	3	2	0	0	2	9		Q80ZI1
ENSMUST00000125542	ENSMUSG00000030541	7	80094846	80115392	-1	0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000125543						7	3	7	49	13	5	0	0	2	0	2		
ENSMUST00000125544	ENSMUSG00000089739	2	167607850	167661496	-1	0	0	21	0	6	0	279	0	345	0	59	E9PY39	
ENSMUST00000125545						0	0	0	0	1	0	1	19	11	6	6		
ENSMUST00000125546						3	9	26	7	14	3	0	0	0	0	1		
ENSMUST00000125547	ENSMUSG00000001166	5	120800194	120812514	-1	0	0	1	5	5	2	5	1	4	7	1	D3YWG4	
ENSMUST00000125548						0	0	0	0	0	0	127	129	133	42	37		
ENSMUST00000125549						1	0	0	2	4	3	6	44	10	10	9		
ENSMUST00000125550						6	4	11	4	4	4	0	17	10	7	19		
ENSMUST00000125551						37	18	279	61	22	15	0	4	4	0	1		
ENSMUST00000125552						2	2	20	7	4	2	114	1371	18	0	24		
ENSMUST00000125553						0	0	2	0	5	1	3	66	0	7	9		
ENSMUST00000125554	ENSMUSG00000055850	6	72359714	72366956	-1	3	0	0	0	2	0	0	0	0	0	10	S4R1H9	
ENSMUST00000125555	ENSMUSG00000020377	11	50236469	50238616	-1	6	0	5	20	0	9	0	0	0	0	23	Q5SVR6	
ENSMUST00000125556						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125557						22	15	214	38	19	9	0	1	0	0	0		
ENSMUST00000125559						9	2	28	260	11	5	0	0	0	0	0		
ENSMUST00000125560						10	8	33	9	10	8	0	1	0	0	3		
ENSMUST00000125561	ENSMUSG00000039515	2	30416039	30447806	1	0	3	3	1	5	3	5	5	0	0	7	F6Z6I0	
ENSMUST00000125562	ENSMUSG00000039176	7	79446231	79466362	-1	1	0	0	142	2	0	0	0	2	0	0		
ENSMUST00000125563	ENSMUSG00000079465	1	82586921	82722059	1	0	0	0	0	0	0	0	0	0	0	0	M0QWQ2	
ENSMUST00000125564						1	2	0	2	0	1	0	0	0	0	0		
ENSMUST00000125565						0	0	0	4	0	2	0	0	0	0	0		
ENSMUST00000125566						2	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000125567	ENSMUSG00000035735	19	10245265	10304877	-1	49	34	0	0	0	0	10	3	4	4	0	S4R2M3	
ENSMUST00000125568	ENSMUSG00000029522	5	115466262	115474722	1	2	2	0	1	0	1	0	0	0	0	0	D3YWH2	
ENSMUST00000125570						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125571	ENSMUSG00000001583	11	69851005	69858730	-1	0	0	5	27	0	0	0	0	0	1	0	A2ARN2	
ENSMUST00000125572						2	1	28	1	2	1	1	7	2	0	1		
ENSMUST00000125573						0	8	14	0	8	6	0	0	0	0	0		
ENSMUST00000125574	ENSMUSG00000037426	5	32863701	32994236	1	1	0	0	7	1	0	0	0	0	0	0	D3Z7M7	
ENSMUST00000125576	ENSMUSG00000044770	10	42860370	42960780	1	3	0	0	2	0	0	2	0	4	0	7	D3YY47	
ENSMUST00000125579						0	1	0	1	1	0	0	0	0	1	0		
ENSMUST00000125580	ENSMUSG00000039208	11	121701544	121716306	1	2	1	2	19	5	0	0	0	21	0	0	A2AAV6	
ENSMUST00000125581	ENSMUSG00000000938	6	52231197	52240854	-1	0	3	18	335	14	8	0	1	0	0	0		P31310
ENSMUST00000125583						6	3	4	121	3	4	4	0	0	0	0		
ENSMUST00000125584						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000125586						1	2	13	0	10	2	2	7	0	2	6		
ENSMUST00000125587	ENSMUSG00000024782	19	29020833	29047961	-1	4	2	3	1	3	2	16	62	33	5	39	F6RP11	
ENSMUST00000125588						27	27	121	2	22	13	0	0	0	0	0		
ENSMUST00000125589						0	0	0	0	2	0	0	6	6	0	11		
ENSMUST00000125590						2	0	13	5	3	1	0	0	0	0	0		
ENSMUST00000125591	ENSMUSG00000017428	11	80428615	80473248	1	0	0	0	0	2	0	0	0	5	0	0	G3UZ28	
ENSMUST00000125592						39	34	183	29	41	22	23	35	53	12	71		
ENSMUST00000125593						2	3	0	3	2	1	0	3	1	0	2		
ENSMUST00000125594						3	2	13	3	4	1	0	0	0	0	0		
ENSMUST00000125595						41	23	86	35	61	33	2	4	6	2	8		
ENSMUST00000125596						1	0	13	1	2	0	0	98	10	13	28		
ENSMUST00000125597						8	4	10	4	14	0	74	397	169	37	286		
ENSMUST00000125598	ENSMUSG00000033352	11	65688243	65788297	-1	0	0	0	0	2	0	0	12	0	0	0	M0QW52	
ENSMUST00000125599						3	3	7	4	5	3	0	0	0	0	0		
ENSMUST00000125601	ENSMUSG00000026854	2	30982279	31023586	1	1	1	2	2	0	0	0	0	0	0	0	A2AQ34	
ENSMUST00000125602						1	0	0	2	1	1	0	0	1	0	0		
ENSMUST00000125603						0	0	0	0	0	0	0	395	0	23	0		
ENSMUST00000125604						9	3	10	0	6	2	0	25	0	6	3		
ENSMUST00000125605	ENSMUSG00000066551	5	149046702	149184489	-1	0	7	0	30	3	0	0	0	0	0	0	D3YVC6	
ENSMUST00000125606	ENSMUSG00000000167	9	50617321	50625000	1	2	0	5	4	4	0	0	0	2	0	0	D3YTM2	
ENSMUST00000125608						0	1	0	0	0	0	0	0	3	1	0		
ENSMUST00000125610						3	0	11	5	4	4	0	0	0	0	0		
ENSMUST00000125612	ENSMUSG00000020059	10	88459569	88473236	1	0	0	0	0	0	0	0	0	0	0	0	M0QWF4	
ENSMUST00000125613						8	7	0	30	4	0	6	2	0	0	2		
ENSMUST00000125614						27	24	52	44	47	19	26	61	17	3	54		
ENSMUST00000125615	ENSMUSG00000009828	9	78109192	78172107	1	0	0	2	0	0	0	1	0	0	0	0	D3YZV1	
ENSMUST00000125616						0	0	17	6	8	8	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125617						2	2	11	112	8	1	0	0	5	0	0		
ENSMUST00000125618						1	0	20	16	6	0	25	0	9	0	6		
ENSMUST00000125619	ENSMUSG00000075376	2	37370069	37422903	-1	0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000125620						3	1	6	3	2	0	0	1	0	0	2		
ENSMUST00000125621	ENSMUSG00000079324	2	68656486	68748467	1	389	391	874	2012	573	187	1	1	2	1	10	A2AQL4	
ENSMUST00000125622	ENSMUSG00000053317	4	47474658	47483242	1	0	2	2	68	4	3	0	4	0	0	0	A8Y5P9	
ENSMUST00000125623						0	0	0	0	2	0	0	0	1	0	0		
ENSMUST00000125624						4	4	7	108	17	8	41	52	77	19	69		
ENSMUST00000125625	ENSMUSG00000025337	5	130245731	130255530	-1	7	3	42	7	13	2	3	36	24	0	40	F6TN03	
ENSMUST00000125627						0	2	1	0	4	1	0	8	27	4	0		
ENSMUST00000125628						3	2	2	5	11	3	0	11	0	0	0		
ENSMUST00000125629	ENSMUSG00000028883	5	13125414	13602565	1	1	0	0	0	1	2	0	0	0	0	0	D3Z2A7	
ENSMUST00000125630						11	7	27	15	0	0	12	0	0	0	0		
ENSMUST00000125632						4	2	3	1	2	0	0	11	3	50	7		
ENSMUST00000125633	ENSMUSG00000067825	6	121183667	121198837	1	0	4	3	20	5	2	0	4	0	0	4		Q8BGI5
ENSMUST00000125634						3	0	7	0	3	4	0	0	0	0	0		
ENSMUST00000125635						3	1	12	10	3	0	0	4	2	2	0		
ENSMUST00000125637	ENSMUSG00000020454	11	3202392	3244588	1	0	0	0	17	1	0	2	11	38	2	26	Q5NBZ7	
ENSMUST00000125638						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000125639						6	3	8	3	3	1	0	0	0	0	0		
ENSMUST00000125640	ENSMUSG00000024843	19	3851773	3894369	1	0	0	0	0	0	0	2	2	0	0	0	F6S062	
ENSMUST00000125641	ENSMUSG00000073643	1	79702262	79776143	-1	4	0	1	62	2	0	0	0	0	2	2	D3YWG9	
ENSMUST00000125642	ENSMUSG00000059890	9	44923131	44965600	-1	0	1	0	0	0	0	0	2	14	0	10	D3YXR7	
ENSMUST00000125643						1	3	3	0	2	3	0	0	0	0	0		
ENSMUST00000125644						0	4	0	0	0	1	0	0	0	0	0		
ENSMUST00000125645	ENSMUSG00000053510	4	109000655	109061777	1	2	1	1	3	4	2	56	109	58	2	73	Q3V3G9	
ENSMUST00000125646						3	6	123	3	7	1	0	245	5	16	0		
ENSMUST00000125647	ENSMUSG00000028601	4	108165437	108179308	1	0	0	0	0	0	0	0	0	0	0	0	E0CYT3	
ENSMUST00000125648						0	1	2	0	0	2	12	5	0	0	18		
ENSMUST00000125649						0	0	0	0	0	0	1	28	0	12	12		
ENSMUST00000125650	ENSMUSG00000041939	5	114444269	114460591	1	0	0	0	0	0	2	3	0	13	0	0	D3YV77	
ENSMUST00000125651						22	33	110	14	31	16	0	2	0	0	5		
ENSMUST00000125652	ENSMUSG00000029433	5	123509765	123525488	-1	26	12	20	20	42	20	6	10	7	0	0		Q9JIQ3
ENSMUST00000125655	ENSMUSG00000020808	11	72042032	72047370	1	0	0	1	1	5	4	0	0	0	1	0	Q5RIU1	
ENSMUST00000125656						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125658						1	1	3	8	4	0	0	3	0	2	0		
ENSMUST00000125659	ENSMUSG00000026463	1	133699457	133801041	-1	4	2	0	0	2	0	0	0	0	0	6	E9Q828	
ENSMUST00000125660						25	27	34	0	30	14	0	0	0	0	11		
ENSMUST00000125661						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125663						2	2	10	1	3	4	0	0	0	0	0		
ENSMUST00000125664						0	10	45	27	18	15	0	3	1	0	0		
ENSMUST00000125665						0	0	9	4	5	8	2	14	0	1	12		
ENSMUST00000125666						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000125667	ENSMUSG00000022272	15	25622525	25813673	1	7	3	17	6	5	2	0	1	1	0	3	D3YXW4	
ENSMUST00000125668						4	2	14	3	0	8	0	0	0	2	15		
ENSMUST00000125669	ENSMUSG00000030683	7	126950563	126970606	1	4	3	1	3	2	0	0	0	0	0	4		
ENSMUST00000125670	ENSMUSG00000001103	11	78503447	78505081	1	16	3	7	10	8	0	0	0	0	0	1	E9Q4C2	
ENSMUST00000125671	ENSMUSG00000028689	4	116708509	116751206	1	0	0	0	0	0	0	6	0	0	0	0	A2AGD5	
ENSMUST00000125672						7	12	11	13	18	4	4	7	4	0	7		
ENSMUST00000125673	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	26	0	1	0	0	0	0	9	D6RFD8	
ENSMUST00000125674	ENSMUSG00000074578	2	167062934	167065862	1	0	0	0	0	0	0	101	265	76	526	66	Q3V494	
ENSMUST00000125675						0	2	0	2	4	0	26	107	98	117	86		
ENSMUST00000125676	ENSMUSG00000054293	X	107148927	107173661	1	0	0	0	0	2	0	0	3	0	19	0	A2ASC4	
ENSMUST00000125677						9	5	7	19	5	1	0	1	0	0	1		
ENSMUST00000125678	ENSMUSG00000072944	X	140006805	140062712	-1	1	0	0	0	0	1	0	0	0	0	0	A2AG13	
ENSMUST00000125679						3	1	1	0	0	0	236	3	546	0	817		
ENSMUST00000125682	ENSMUSG00000006728	10	127063534	127067920	1	10	11	70	41	20	16	5	10	5	5	3	E9PZX7	
ENSMUST00000125683						5	3	45	5	4	1	0	40	0	0	0		
ENSMUST00000125684						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000125686	ENSMUSG00000029759	6	5220852	5256286	-1	0	0	0	0	0	0	1	0	5	19	1	H3BL07	
ENSMUST00000125687						17	11	39	9	29	4	190	690	259	0	466		
ENSMUST00000125688	ENSMUSG00000021838	14	46882854	47105817	1	4	1	0	2	2	0	0	0	0	0	5		Q8CBY1
ENSMUST00000125689						3	4	3	1	1	1	0	3	2	0	6		
ENSMUST00000125690						2	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000125691						20	22	44	50	37	9	0	1	0	0	0		
ENSMUST00000125692	ENSMUSG00000051497	11	110968033	111027968	1	0	0	0	0	0	0	0	0	0	0	0	A2A5W8	
ENSMUST00000125693						14	12	28	16	16	9	23	167	63	11	82		
ENSMUST00000125694	ENSMUSG00000020402	11	52360860	52389397	1	0	0	9	0	4	0	6	23	6	7	14	F2Z471	
ENSMUST00000125695						0	0	0	204	1	0	0	0	0	0	0		
ENSMUST00000125696	ENSMUSG00000066037	4	136310942	136359447	1	8	5	7	106	4	0	0	0	11	0	7	S4R1E9	
ENSMUST00000125697						0	4	5	1	2	2	3	0	3	0	0		
ENSMUST00000125698	ENSMUSG00000069170	13	81095068	81633154	-1	16	22	24	5	6	1	0	0	0	0	0		
ENSMUST00000125699	ENSMUSG00000002608	7	25711106	25719088	-1	2	2	6	9	10	1	49	33	34	5	58		
ENSMUST00000125701						0	1	0	1	1	0	8	0	0	0	0		
ENSMUST00000125702						0	2	2	9	0	0	0	0	0	0	0		
ENSMUST00000125703						4	0	8	0	4	0	35	214	66	75	43		
ENSMUST00000125704	ENSMUSG00000020083	10	62107655	62143920	-1	25	3	54	31	17	10	0	11	3	2	4		Q9D882
ENSMUST00000125705	ENSMUSG00000002205	7	44748413	44777515	1	3	3	2	11	1	1	30	94	42	5	50	D3Z188	
ENSMUST00000125707						0	4	0	0	1	0	2	2	2	2	1		
ENSMUST00000125708	ENSMUSG00000035683	4	44300876	44364675	1	0	2	0	0	0	0	0	0	0	0	0	A2ALQ9	
ENSMUST00000125709						0	0	0	0	0	0	5	8	5	8	1		
ENSMUST00000125710						0	0	0	0	0	0	149	166	128	58	64		
ENSMUST00000125711						5	2	13	20	0	0	0	4	0	0	0		
ENSMUST00000125712						2	1	6	141	2	2	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125714						0	0	10	0	6	4	0	87	70	9	71		
ENSMUST00000125715						0	0	0	0	0	0	0	0	5	0	0		
ENSMUST00000125716	ENSMUSG00000031748	8	93809966	93969388	1	22	14	80	27	20	11	0	0	0	1	6	Q543S2	P18872
ENSMUST00000125717						0	0	1	45	0	0	3	0	0	0	0		
ENSMUST00000125718						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125719	ENSMUSG00000071550	16	44394796	44482428	1	1	0	0	0	0	0	0	0	0	0	0	F6THM3	
ENSMUST00000125720						9	5	6	0	9	8	280	509	249	272	103		
ENSMUST00000125721	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	0	0	0	27	0	0	0	0		Q9WV30
ENSMUST00000125722						12	14	47	22	19	13	0	2	2	0	2		
ENSMUST00000125723						1	1	2	69	3	1	0	0	0	0	1		
ENSMUST00000125724						3	0	7	3	5	2	1	0	0	0	0		
ENSMUST00000125726						3	3	7	14	3	6	5	30	23	0	38		
ENSMUST00000125727						0	0	0	38	0	0	0	0	0	0	0		
ENSMUST00000125728	ENSMUSG00000030116	6	122505845	122529290	1	3	1	0	4	1	0	0	0	0	0	0	D3Z0U1	
ENSMUST00000125729						2	10	0	72	6	0	0	0	0	0	0		
ENSMUST00000125730						1	0	1	0	3	1	0	1	6	0	5		
ENSMUST00000125731						0	1	2	0	3	3	0	3	0	0	0		
ENSMUST00000125732						0	0	0	0	1	0	0	6	0	4	3		
ENSMUST00000125733	ENSMUSG00000050671	12	87278638	87299705	-1	13	4	42	91	21	16	1	0	0	0	0	D3Z6A3	
ENSMUST00000125734						48	44	53	39	53	23	6	65	23	7	37		
ENSMUST00000125735						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125737	ENSMUSG00000074899	2	120046157	120085772	-1	8	3	10	5	8	5	0	0	0	0	0	F6TMY4	
ENSMUST00000125738	ENSMUSG00000061288	5	117120129	117275219	1	1	3	0	1	0	0	0	0	0	0	0	E9Q364	
ENSMUST00000125739	ENSMUSG00000041708	15	83779467	83858494	1	1	2	0	1	2	0	0	0	0	0	0	E9PYE1	
ENSMUST00000125740	ENSMUSG00000008307	5	3571566	3584356	1	0	0	2	0	0	2	0	4	0	0	0	F6YAH5	
ENSMUST00000125741						2	0	0	4	0	2	80	99	24	23	95		
ENSMUST00000125742						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000125743						35	20	84	25	26	10	40	119	37	3	81		
ENSMUST00000125744						1	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000125745						0	0	3	5	1	0	0	0	0	0	0		
ENSMUST00000125747						1	0	1	0	0	0	7	16	0	23	0		
ENSMUST00000125748						38	13	36	195	8	14	36	100	0	1	42		
ENSMUST00000125749	ENSMUSG00000048728	11	50872720	50887651	-1	5	0	4	0	6	3	0	0	0	0	0	Q5NCH5	
ENSMUST00000125750						1	0	2	0	1	1	1	0	0	0	0		
ENSMUST00000125751						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000125752	ENSMUSG00000093989	11	70238124	70239842	-1	0	3	3	14	8	2	16	45	17	2	25	H3BLR9	
ENSMUST00000125753	ENSMUSG00000027482	2	154130336	154138356	1	3	1	0	2	1	2	0	0	0	0	0	H3BLP6	
ENSMUST00000125754						1	4	0	137	5	4	0	0	0	0	0		
ENSMUST00000125755						3	1	14	14	1	0	0	0	1	0	0		
ENSMUST00000125756						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125757	ENSMUSG00000036257	12	44221370	44312343	1	2	0	1	0	0	0	0	2	0	0	0	D3Z5W9	
ENSMUST00000125758	ENSMUSG00000005611	7	110868266	110982461	-1	24	0	21	11	0	11	0	0	12	0	0	G5E8V5	
ENSMUST00000125760						0	0	0	24	0	0	0	0	2	0	0		
ENSMUST00000125761						7	9	17	16	11	2	0	0	0	0	0		
ENSMUST00000125762						81	78	530	128	116	46	29	270	87	49	112		
ENSMUST00000125763	ENSMUSG00000048410	18	84128027	84589725	-1	30	25	37	92	49	19	199	450	518	105	454	G3UVV3	
ENSMUST00000125764	ENSMUSG00000005078	12	72085589	72101461	1	5	3	0	13	1	0	5	7	12	2	0	B8JJ81	
ENSMUST00000125765						1	0	1	0	0	0	11	0	9	0	3		
ENSMUST00000125766						3	0	6	4	5	0	0	9	15	0	14		
ENSMUST00000125767						0	0	1	2	4	0	0	0	0	1	0		
ENSMUST00000125768						1	1	4	1	2	4	0	0	0	0	0		
ENSMUST00000125769						1	0	0	44	5	0	0	15	0	2	17		
ENSMUST00000125770	ENSMUSG00000006345	10	75561604	75586200	1	3	5	3	4	1	2	0	0	2	0	2	D3YVX1	
ENSMUST00000125771						0	1	5	0	0	0	0	0	0	0	0		
ENSMUST00000125772						18	8	28	13	16	12	0	0	2	0	0		
ENSMUST00000125773						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125774	ENSMUSG00000026426	1	135146824	135156269	1	14	9	33	11	13	4	596	1097	165	1	242	F6QKK2	
ENSMUST00000125775						0	0	0	0	0	0	35	208	56	23	45		
ENSMUST00000125776	ENSMUSG00000078570	4	124849080	124851196	-1	0	0	0	0	0	0	0	0	0	0	0	V9GWZ1	
ENSMUST00000125777						2	0	0	0	2	5	3	3	0	0	0		
ENSMUST00000125778						2	2	8	5	2	1	11	69	21	5	15		
ENSMUST00000125779						0	0	0	0	0	0	0	1	3	3	5		
ENSMUST00000125780						5	3	5	14	4	4	32	75	67	14	64		
ENSMUST00000125782	ENSMUSG00000008373	7	3629985	3642486	1	8	12	27	11	14	10	0	0	6	1	7		
ENSMUST00000125783	ENSMUSG00000036591	2	20847919	20968881	-1	0	3	1	4	0	0	0	0	0	0	0	F6WQR2	
ENSMUST00000125784						12	6	18	19	6	0	28	77	27	0	71		
ENSMUST00000125785						7	8	19	6	8	3	2	2	4	2	0		
ENSMUST00000125786						21	8	28	3	18	11	14	27	31	6	47		
ENSMUST00000125787						22	11	8	20	36	14	1	4	2	0	1		
ENSMUST00000125788	ENSMUSG00000012350	2	103263433	103303278	-1	1	0	4	0	1	0	0	0	0	0	0	B0S7M9	
ENSMUST00000125789						7	2	7	4	0	1	0	2	4	0	6		
ENSMUST00000125790	ENSMUSG00000022875	16	23057865	23082068	1	2	2	0	6	5	0	0	0	0	0	0	D3Z2B2	
ENSMUST00000125791						0	1	0	2	6	2	5	3	9	3	18		
ENSMUST00000125792						6	0	0	9	0	0	35	109	107	0	170		
ENSMUST00000125793	ENSMUSG00000027489	2	154544399	154558890	-1	0	0	2	41	0	2	0	0	0	0	0	A2AKF0	
ENSMUST00000125794	ENSMUSG00000003518	11	101971143	101987013	-1	0	0	0	0	3	0	0	0	0	4	0	H3BKD1	
ENSMUST00000125795						0	0	0	0	3	0	0	0	0	4	0		
ENSMUST00000125796						4	0	5	0	1	0	0	0	0	0	0		
ENSMUST00000125797						50	41	87	68	62	46	30	82	87	5	131		
ENSMUST00000125798	ENSMUSG00000004113	2	24603887	24763152	-1	0	0	0	0	0	0	1	0	0	0	0	A0A0A6YWZ5	
ENSMUST00000125799	ENSMUSG00000073988	4	20007938	20030785	1	0	1	3	47	3	4	0	1	0	1	0	A8Y5P0	
ENSMUST00000125800						31	38	167	49	74	42	12	18	5	4	11		
ENSMUST00000125801						2	2	0	113	0	0	3	3	5	0	0		
ENSMUST00000125802	ENSMUSG00000089857	8	71908608	71916354	1	1	0	1	14	1	1	0	1	2	1	0	D3Z2V3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125803						0	0	0	11	1	2	3	8	15	28	0		
ENSMUST00000125804	ENSMUSG00000029602	5	120648812	120679597	1	2	2	6	57	1	0	0	1	1	0	0	D3Z7V8	
ENSMUST00000125805	ENSMUSG00000033852	2	120027493	120043033	1	0	1	0	2	1	0	0	0	0	3	1	F6YGA3	
ENSMUST00000125806						0	0	0	0	0	0	0	0	0	9	5		
ENSMUST00000125807						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000125808						0	0	0	1	0	0	0	16	0	0	0		
ENSMUST00000125809						0	0	0	0	0	0	7	2	0	1	0		
ENSMUST00000125810	ENSMUSG00000008540	6	138140316	138156755	1	2	1	9	3	7	2	0	2	5	0	0	D3YVR3	
ENSMUST00000125812	ENSMUSG00000000308	2	121357714	121363737	1	0	0	15	0	2	0	0	0	0	0	0	B0R0E9	
ENSMUST00000125813						0	0	1	1	1	0	0	1	0	0	0		
ENSMUST00000125814						2	0	1	0	1	0	195	828	722	750	826		
ENSMUST00000125815						1	3	1	26	2	2	2	6	0	31	26		
ENSMUST00000125816	ENSMUSG00000026491	1	179744894	179803680	-1	3	3	3	1	1	0	3	93	10	29	19	F6QTR3	
ENSMUST00000125817	ENSMUSG00000054520	5	34525838	34563641	1	7	0	3	31	8	2	2	1	5	0	5	D3Z107	
ENSMUST00000125818	ENSMUSG00000039205	2	32352327	32380970	1	0	0	0	3	0	0	0	150	18	17	12	F7AT58	
ENSMUST00000125819	ENSMUSG00000034708	11	102430315	102437048	1	0	0	0	0	0	0	99	1378	282	136	198	H3BJE0	
ENSMUST00000125821						2	2	7	45	9	0	2	63	4	7	23		
ENSMUST00000125824						14	8	5	18	9	7	14	0	0	0	0		
ENSMUST00000125825						5	4	19	3	7	0	0	0	0	0	0		
ENSMUST00000125826	ENSMUSG00000033256	2	122348892	122369162	-1	0	0	0	38	0	0	0	0	0	0	0	A2AQ87	
ENSMUST00000125827	ENSMUSG00000004947	5	135994800	136032872	1	9	0	17	7	5	3	0	0	104	0	0		Q8R3P2
ENSMUST00000125828						4	3	1	1	7	4	1	0	1	0	2		
ENSMUST00000125830						0	0	3	0	0	4	0	0	0	0	0		
ENSMUST00000125831						0	0	5	130	2	5	147	68	351	6	271		
ENSMUST00000125832						0	0	0	12	3	0	0	0	0	0	0		
ENSMUST00000125833	ENSMUSG00000021998	14	75131101	75230842	1	0	0	0	0	0	0	30	71	37	11	54	D3Z7D9	
ENSMUST00000125834						0	0	0	0	0	0	0	4	0	0	2		
ENSMUST00000125835	ENSMUSG00000034427	11	115858406	115892603	1	0	0	4	0	0	0	0	0	2	0	0		
ENSMUST00000125836						1	0	3	0	1	0	10	4	0	0	10		
ENSMUST00000125837						0	3	0	7	18	3	0	0	0	0	0		
ENSMUST00000125838						1	3	26	4	5	3	108	832	323	220	237		
ENSMUST00000125839						2	1	1	0	0	0	0	0	1	0	0		
ENSMUST00000125840						14	0	0	0	0	4	0	0	0	0	0		
ENSMUST00000125841						0	0	0	0	0	0	45	121	22	100	41		
ENSMUST00000125842	ENSMUSG00000033373	12	76765589	76921412	1	0	0	12	0	0	0	37	1	11	0	10	D6RGU2	
ENSMUST00000125843						0	0	0	0	0	0	4	10	9	0	6		
ENSMUST00000125844						2	0	3	0	4	1	0	0	0	0	0		
ENSMUST00000125846	ENSMUSG00000009894	11	59407134	59451186	-1	0	0	0	0	4	0	0	0	0	0	1	A0A0G2JDA4	
ENSMUST00000125847	ENSMUSG00000062609	16	95257558	95300260	1	0	0	0	0	0	0	0	0	0	0	0	D3YV68	
ENSMUST00000125848						33	22	142	2	28	17	11	0	0	5	15		
ENSMUST00000125849						8	6	7	18	18	8	9	57	11	15	38		
ENSMUST00000125850	ENSMUSG00000023249	9	106470322	106476949	-1	0	0	4	1	0	2	0	0	12	0	0	E9Q992	
ENSMUST00000125851						0	1	0	5	0	2	0	2	0	0	0		
ENSMUST00000125855						10	6	7	5	2	3	4	3	5	0	13		
ENSMUST00000125856	ENSMUSG00000039976	11	119143045	119228499	-1	1	2	0	5	3	2	0	0	0	0	0	A2AFK9	
ENSMUST00000125858						4	8	6	6	10	3	6	8	9	0	9		
ENSMUST00000125859						32	43	89	53	44	21	9	43	26	0	36		
ENSMUST00000125860						0	0	1	1	0	0	0	0	0	0	3		
ENSMUST00000125861						0	7	8	3	4	8	0	1	0	0	0		
ENSMUST00000125862						0	1	1	0	0	0	7	16	6	0	4		
ENSMUST00000125864						0	0	0	0	0	0	1	1	0	2	2		
ENSMUST00000125865						0	3	0	1	0	0	0	0	0	0	0		
ENSMUST00000125866	ENSMUSG00000039765	5	43662346	43740972	1	0	0	20	11	0	1	0	9	2	10	10	F6YZ61	
ENSMUST00000125868						6	5	6	6	7	2	63	307	67	0	130		
ENSMUST00000125870						6	4	7	4	6	0	0	0	0	3	2		
ENSMUST00000125871	ENSMUSG00000034928	13	54679399	54693907	-1	5	0	33	120	23	0	106	154	350	0	56	E9PUC0	
ENSMUST00000125872	ENSMUSG00000027593	2	154791096	154867261	1	1	0	0	0	0	0	0	0	0	0	0	A2AU60	
ENSMUST00000125874						1	4	4	15	3	1	0	3	2	0	12		
ENSMUST00000125875	ENSMUSG00000036918	17	87282886	87381769	1	24	33	132	33	28	18	20	34	50	3	71	D3Z0R8	
ENSMUST00000125876						20	19	130	126	40	16	1	6	4	0	3		
ENSMUST00000125877	ENSMUSG00000002031	9	44767908	44792714	1	5	3	6	0	11	0	0	0	7	0	0	D3Z4B1	
ENSMUST00000125878						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000125879						0	1	0	0	2	3	0	0	0	0	0		
ENSMUST00000125880	ENSMUSG00000030341	6	125349362	125362484	1	2	0	2	0	4	0	45	30	22	5	47	F6R6K0	
ENSMUST00000125881						21	12	35	71	28	18	3	27	8	0	21		
ENSMUST00000125882	ENSMUSG00000025885	18	74440936	74771493	1	2	0	0	1	0	4	0	0	0	0	0	D3Z135	
ENSMUST00000125883	ENSMUSG00000039356	2	31670715	31681349	1	3	0	0	3	0	0	0	0	0	0	2	A0A0A6YW57	
ENSMUST00000125885						2	1	0	5	0	0	0	19	23	2	13		
ENSMUST00000125886						1	0	6	3	1	1	0	0	0	0	5		
ENSMUST00000125887						3	1	9	4	6	5	0	0	0	0	0		
ENSMUST00000125888						0	1	8	3	1	0	0	0	0	0	5		
ENSMUST00000125889						3	1	14	29	6	2	0	0	0	0	1		
ENSMUST00000125890	ENSMUSG00000041654	11	113244853	113650079	-1	0	0	0	0	0	0	0	0	0	0	0	B1ARC2	
ENSMUST00000125891	ENSMUSG00000039021	2	32757026	32775633	-1	36	30	34	95	55	29	0	0	1	0	0	E0CXL5	
ENSMUST00000125892						3	2	2	0	4	2	0	50	0	0	14		
ENSMUST00000125893	ENSMUSG00000005161	8	84969587	84974834	1	0	1	8	6	8	5	9	21	1	10	13	D3Z4A4	
ENSMUST00000125894	ENSMUSG00000030032	6	83149361	83156397	-1	0	0	0	0	0	0	2	0	0	0	0	D3Z394	
ENSMUST00000125895						0	0	0	41	0	0	0	4	0	10	0		
ENSMUST00000125896						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000125897	ENSMUSG00000022893	16	85793827	85803113	-1	2	13	16	42	20	11	0	0	1	2	6	E9PY08	
ENSMUST00000125898						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000125899	ENSMUSG00000024002	17	32196274	32284722	-1	1	0	0	2	0	0	40	16	100	1	72	D6RGP2	
ENSMUST00000125900						8	16	36	14	18	14	0	0	0	0	0		
ENSMUST00000125901	ENSMUSG00000021338	13	24012344	24280795	-1	3	0	8	0	8	0	1	5	0	0	5	F7AI27	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125904						0	3	0	2	0	0	0	0	0	0	0		
ENSMUST00000125905	ENSMUSG00000030209	6	135713233	136173511	-1	0	0	0	0	0	0	0	0	0	0	0	Q8CG69	
ENSMUST00000125906	ENSMUSG00000002342	8	70172356	70183681	1	1	1	9	0	0	0	0	2	0	0	5	M0QWE7	
ENSMUST00000125907						1	1	2	6	3	0	0	0	0	0	0		
ENSMUST00000125910						0	0	8	6	2	0	0	0	0	0	0		
ENSMUST00000125911	ENSMUSG00000029772	6	29768011	29912310	1	2	5	12	4	13	5	0	0	0	0	0	H3BKT5	
ENSMUST00000125912						0	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000125913						3	2	0	7	8	0	0	0	0	0	0		
ENSMUST00000125914						0	0	0	7	0	0	0	0	0	0	0		
ENSMUST00000125915						3	5	9	10	1	0	2	3	4	0	2		
ENSMUST00000125916	ENSMUSG00000056770	12	108106431	108179314	-1	0	0	0	22	2	0	0	2	0	0	5	F2Z438	
ENSMUST00000125918	ENSMUSG00000020747	11	115765433	115799366	1	3	3	0	3	7	0	51	7	27	0	22	B1ATA0	
ENSMUST00000125919						2	0	0	0	0	2	26	127	39	3	19		
ENSMUST00000125920						4	3	16	146	4	1	12	26	16	1	15		
ENSMUST00000125922						3	5	1	1	4	3	0	6	0	1	3		
ENSMUST00000125923	ENSMUSG00000039754	5	136136146	136141615	1	2	0	0	30	4	8	21	16	8	3	21	D6RFB6	
ENSMUST00000125924						0	13	13	0	0	0	0	0	0	0	0		
ENSMUST00000125925	ENSMUSG00000026433	1	131867224	131872887	1	2	0	5	4	0	0	13	6	0	0	0	M0QW55	
ENSMUST00000125926						0	0	0	10	1	0	0	0	0	0	3		
ENSMUST00000125927	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	27	0	0	0	0	0	0	0	D3Z6V1	
ENSMUST00000125928	ENSMUSG00000022439	15	84324026	84342978	1	0	0	10	0	0	1	0	0	0	0	0	A6PW97	
ENSMUST00000125929						6	5	3	2	1	1	3	95	9	24	14		
ENSMUST00000125931	ENSMUSG00000028785	4	129111570	129122036	-1	0	0	0	13	0	0	0	0	0	0	0	E9PV73	
ENSMUST00000125933	ENSMUSG00000000215	7	142678656	142699510	-1	0	2	0	0	0	0	0	0	0	0	0	D3YWU5	
ENSMUST00000125935						0	4	0	2	3	0	0	0	0	0	0		
ENSMUST00000125936						0	5	1	12	4	0	1291	2273	1137	5897	873		
ENSMUST00000125937						3	3	3	5	2	1	3	14	5	0	10		
ENSMUST00000125938	ENSMUSG00000032235	9	69397906	69433122	1	0	0	1	54	4	0	0	0	0	0	0	B0V2P0	
ENSMUST00000125939						10	9	23	26	13	6	54	269	84	6	200		
ENSMUST00000125940						0	1	2	0	0	1	3	12	11	0	4		
ENSMUST00000125941	ENSMUSG00000030378	7	14410686	14446769	-1	0	0	0	0	1	2	0	0	0	0	0	E9QAK1	
ENSMUST00000125942						0	1	0	3	4	0	7	65	19	4	10		
ENSMUST00000125943	ENSMUSG00000048772	4	117251951	117268582	1	0	0	3	0	0	0	0	0	6	0	0	A0A0A0MQK8	
ENSMUST00000125944						6	5	16	27	9	0	0	4	2	2	0		
ENSMUST00000125945						1	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000125946	ENSMUSG00000105340	5	121518613	121545482	-1	33	34	80	26	41	11	14	43	29	0	42	A0A0G2JDU2	
ENSMUST00000125947	ENSMUSG00000064284	15	85806972	85811697	-1	2	0	7	2	3	0	0	0	5	0	0		Q8R3A2
ENSMUST00000125948						3	3	0	0	6	2	0	0	0	0	0		
ENSMUST00000125949						2	5	5	2	0	4	0	9	0	7	0		
ENSMUST00000125950						5	0	7	4	4	6	30	92	73	17	74		
ENSMUST00000125951						6	2	8	0	3	0	0	0	0	0	0		
ENSMUST00000125952	ENSMUSG00000042766	3	89234177	89246309	-1	1	0	3	0	0	0	0	0	2	0	0	D3YYF9	
ENSMUST00000125953						2	1	0	5	0	1	21	7	3	0	9		
ENSMUST00000125954						10	7	27	11	7	9	5	9	27	1	29		
ENSMUST00000125955						2	2	4	1	5	0	0	0	0	0	0		
ENSMUST00000125957						20	25	35	56	38	12	2	10	8	2	5		
ENSMUST00000125958						11	13	14	14	9	8	9	78	11	8	34		
ENSMUST00000125959						1	1	0	36	8	1	176	207	227	902	170		
ENSMUST00000125961						0	2	1	4	2	6	1	2	0	0	0		
ENSMUST00000125963	ENSMUSG00000034729	17	47368887	47381417	1	0	0	0	0	0	0	0	1	0	2	0	D3Z6K5	
ENSMUST00000125964	ENSMUSG00000005575	7	13035120	13038275	-1	3	2	3	21	0	0	692	735	453	96	273	F7CDT0	
ENSMUST00000125965	ENSMUSG00000048652	3	146645195	146685592	-1	3	0	0	34	6	3	0	5	2	0	1		D3YUG0
ENSMUST00000125966						271	246	387	244	289	154	13	43	22	11	45		
ENSMUST00000125968						0	0	0	0	0	0	2	0	5	1	15		
ENSMUST00000125969						0	0	0	2	0	0	0	66	5	12	5		
ENSMUST00000125970						2	0	5	0	1	2	0	1	0	0	8		
ENSMUST00000125971	ENSMUSG00000022842	16	20611593	20646485	1	21	24	99	23	36	14	0	0	1	0	0	F6WM66	
ENSMUST00000125972						0	0	0	0	0	0	0	11	23	3	37		
ENSMUST00000125973						2	1	10	4	2	0	4	4	19	5	7		
ENSMUST00000125974						6	0	13	2	0	2	0	3	0	0	0		
ENSMUST00000125975	ENSMUSG00000000738	8	123062942	123097760	1	0	0	0	0	0	0	206	307	207	16	101	D3YZN4	
ENSMUST00000125976						43	30	94	25	30	19	0	5	1	0	4		
ENSMUST00000125977						4	0	21	5	0	0	0	0	0	0	0		
ENSMUST00000125978						3	0	3	6	8	4	7	7	6	0	14		
ENSMUST00000125979						0	2	28	4	6	2	0	0	2	1	0		
ENSMUST00000125980						5	5	0	20	19	0	5	2	0	5	6		
ENSMUST00000125981	ENSMUSG00000028849	4	126232167	126256343	-1	0	0	0	0	0	0	339	1634	575	104	417	F6WF36	
ENSMUST00000125982	ENSMUSG00000000753	11	75409769	75422701	-1	0	2	0	7	4	2	0	0	0	0	0	E9PWS2	
ENSMUST00000125983						0	2	1	2	0	0	0	0	0	0	0		
ENSMUST00000125984	ENSMUSG00000020122	11	16752203	16918158	1	0	0	0	0	0	0	0	0	0	0	0	Q5SVE7	
ENSMUST00000125985	ENSMUSG00000032841	2	101714285	101883027	-1	0	0	0	0	0	0	0	0	0	0	0	B0R106	
ENSMUST00000125986						0	0	0	0	0	0	5	12	9	0	28		
ENSMUST00000125987						3	2	7	79	5	2	0	0	0	0	0		
ENSMUST00000125988						4	0	9	0	0	0	0	0	0	0	0		
ENSMUST00000125989						8	4	6	12	5	3	7	19	5	0	30		
ENSMUST00000125990	ENSMUSG00000053198	7	27499324	27520214	1	33	5	16	26	23	26	0	13	4	4	0		
ENSMUST00000125991	ENSMUSG00000039382	X	7721973	7728201	1	0	0	0	0	0	0	9	16	7	0	4	F6QP00	
ENSMUST00000125992						3	1	0	0	0	0	2	6	2	3	3		
ENSMUST00000125993	ENSMUSG00000074365	7	15882617	15904020	1	8	26	24	39	11	8	0	0	0	0	0	V9GXY9	
ENSMUST00000125994						1	0	2	0	0	0	0	0	0	0	4		
ENSMUST00000125995	ENSMUSG00000037287	9	42412316	42507809	-1	6	11	10	0	17	9	308	611	477	62	317		Q8C5W3
ENSMUST00000125996						33	35	98	262	50	33	1	3	6	0	7		
ENSMUST00000125997						17	14	8	8	11	11	0	0	0	0	0		
ENSMUST00000125998						2	0	5	0	3	4	2	3	10	2	13		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000125999						8	4	29	6	12	2	0	1	0	0	1		
ENSMUST00000126000						1	0	8	3	2	3	21	13	37	0	29		
ENSMUST00000126001						1	1	8	4	2	0	3	19	4	1	7		
ENSMUST00000126004	ENSMUSG00000030851	7	46861203	46878142	1	2	0	0	8	0	1	0	0	0	0	0	D3YZE4	
ENSMUST00000126005	ENSMUSG00000052581	6	80018877	80810143	1	0	13	41	0	0	21	0	0	0	0	0		Q80XG9
ENSMUST00000126006	ENSMUSG00000013936	5	122100951	122113472	1	0	0	6	0	0	2	0	0	1	0	0	F6XCE3	
ENSMUST00000126007						1	2	0	1	0	3	0	3	6	0	2		
ENSMUST00000126008	ENSMUSG00000057363	1	43746966	43827800	-1	18	9	15	17	26	12	10	43	14	14	23		Q91XL3
ENSMUST00000126010	ENSMUSG00000003731	4	129643980	129672767	-1	1	0	0	61	1	0	0	0	0	0	0	A2ADZ6	
ENSMUST00000126012	ENSMUSG00000028218	4	12153409	12172015	-1	0	0	0	0	0	0	0	4	0	16	2	G3UY30	
ENSMUST00000126013						0	0	1	0	2	0	4	0	2	0	0		
ENSMUST00000126014						11	1	8	6	7	7	3	0	4	1	7		
ENSMUST00000126015						4	3	2	1	2	3	8	14	0	3	19		
ENSMUST00000126017						6	0	12	4	2	2	19	11	12	0	8		
ENSMUST00000126018						2	2	0	0	2	4	0	2	2	5	3		
ENSMUST00000126019						2	4	0	4	2	0	14	34	18	25	35		
ENSMUST00000126020						4	0	0	4	1	7	1	5	2	6	1		
ENSMUST00000126021						2	4	2	188	15	0	9	25	22	2	26		
ENSMUST00000126022						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126023						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000126024						4	1	4	0	4	2	0	0	0	0	0		
ENSMUST00000126026						3	2	2	51	6	6	0	2	2	0	0		
ENSMUST00000126027	ENSMUSG00000028042	3	89377644	89394776	-1	0	0	0	3	0	0	50	5	14	0	24	D3YZR6	
ENSMUST00000126028						0	3	3	0	3	0	28	285	75	13	128		
ENSMUST00000126029						2	0	1	1	0	0	2	7	5	9	8		
ENSMUST00000126030						35	39	26	27	36	14	1	3	5	0	4		
ENSMUST00000126031						0	0	0	0	0	0	0	74	35	9	0		
ENSMUST00000126032	ENSMUSG00000023960	17	44078813	44086567	1	20	21	42	17	24	26	4	11	10	6	4	D6RH39	
ENSMUST00000126033	ENSMUSG00000028293	4	34663257	34687438	-1	3	0	0	1	0	0	0	7	0	5	5	F6R7Y0	
ENSMUST00000126034						0	2	15	5	0	0	0	0	0	0	0		
ENSMUST00000126035						2	1	0	6	1	0	0	0	0	0	12		
ENSMUST00000126036						0	0	0	0	0	0	14	11	23	25	14		
ENSMUST00000126037						4	6	19	14	7	0	0	1	3	0	3		
ENSMUST00000126038						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126039	ENSMUSG00000062995	6	8630527	8778488	-1	0	1	2	0	0	2	0	0	0	0	0	D3Z020	
ENSMUST00000126040						0	0	0	5	0	0	10	57	16	7	0		
ENSMUST00000126041						1	1	0	21	6	1	0	20	0	4	4		
ENSMUST00000126042						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126043						0	0	10	2	4	3	27	44	11	0	101		
ENSMUST00000126044						0	2	1	0	0	1	0	0	0	0	0		
ENSMUST00000126045	ENSMUSG00000027331	2	118814003	118853957	1	0	0	5	0	0	0	0	7	6	0	5	F7BE71	
ENSMUST00000126046						14	17	16	111	11	6	7	152	197	39	81		
ENSMUST00000126047						4	3	3	0	3	1	0	0	0	0	0		
ENSMUST00000126048						5	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000126049						3	4	11	14	2	1	87	96	36	7	37		
ENSMUST00000126050						3	2	10	7	3	1	0	0	0	0	1		
ENSMUST00000126051						5	1	0	29	2	2	5	13	5	0	11		
ENSMUST00000126053						0	0	0	0	0	0	0	1	6	0	5		
ENSMUST00000126054						0	0	5	108	0	3	12	8	7	4	11		
ENSMUST00000126056						0	0	1	1	0	2	0	0	0	0	0		
ENSMUST00000126057						3	6	6	66	5	2	3	1	7	0	5		
ENSMUST00000126058	ENSMUSG00000018654	11	11685003	11772926	1	2	0	5	1	0	2	6	16	7	0	0	Q5SWT7	
ENSMUST00000126059						0	0	1	49	3	3	0	2	0	0	2		
ENSMUST00000126060	ENSMUSG00000070382	11	73798753	73803052	-1	2	2	0	1	1	1	0	0	0	0	0		
ENSMUST00000126061	ENSMUSG00000023467	7	45486262	45523632	1	0	0	0	0	0	0	0	0	0	0	0	D3YZV6	
ENSMUST00000126062						1	3	4	13	0	6	2	6	0	6	27		
ENSMUST00000126064						0	1	0	0	0	1	2	4	7	5	10		
ENSMUST00000126065	ENSMUSG00000055850	6	72359714	72366956	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1P6	
ENSMUST00000126066	ENSMUSG00000040433	9	96682770	96752831	-1	0	2	31	3	0	0	0	0	32	0	23	F6Z595	
ENSMUST00000126067	ENSMUSG00000031626	8	45507788	45827906	1	0	1	0	0	0	1	0	0	0	0	0	D3Z0E9	
ENSMUST00000126068	ENSMUSG00000037034	2	147361925	147393295	1	9	10	4	30	8	2	0	0	0	0	0	A2ALK0	
ENSMUST00000126069						3	4	2	4	5	2	13	64	20	28	43		
ENSMUST00000126070	ENSMUSG00000001750	19	3896050	3907133	-1	10	8	38	43	27	10	152	84	112	0	167	Q9JHF5	
ENSMUST00000126071	ENSMUSG00000025873	13	54621784	54664068	1	27	30	69	53	44	16	364	771	585	105	393		Q3TDN2
ENSMUST00000126073	ENSMUSG00000020262	10	77290726	77418270	-1	0	0	0	0	0	0	0	0	0	0	0	D6RDS5	
ENSMUST00000126074	ENSMUSG00000060002	10	88452745	88504073	-1	0	0	0	0	0	0	0	0	0	0	0	D6RCW3	
ENSMUST00000126075						0	0	0	1	0	0	2	0	0	0	0		
ENSMUST00000126076						6	2	6	3	0	0	0	0	0	0	0		
ENSMUST00000126077	ENSMUSG00000029192	5	36490604	36593276	-1	30	19	62	88	22	25	201	60	362	0	362	E9PYB1	
ENSMUST00000126078						0	0	5	2	2	0	0	13	0	0	24		
ENSMUST00000126079						0	0	0	0	0	3	0	2	3	0	3		
ENSMUST00000126081						2	2	4	3	7	2	5	15	3	0	36		
ENSMUST00000126082						107	67	223	73	54	27	5	17	11	0	14		
ENSMUST00000126083						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000126084						1	3	5	8	4	0	0	0	0	0	0		
ENSMUST00000126085	ENSMUSG00000035642	7	97550331	97579497	-1	0	3	0	0	1	0	0	0	0	0	0	D6RJK8	
ENSMUST00000126087	ENSMUSG00000003526	16	18060357	18090203	-1	4	0	0	1	2	3	0	1	0	0	7	F6PYI8	
ENSMUST00000126088						1	1	11	5	4	4	33	64	33	1	65		
ENSMUST00000126089	ENSMUSG00000006392	4	118409337	118415782	1	0	0	0	1	0	0	0	0	0	0	0	A2A9C5	
ENSMUST00000126090						0	0	0	0	0	0	0	0	15	0	0		
ENSMUST00000126091	ENSMUSG00000017548	11	79993106	80034123	1	0	0	0	0	0	1	0	0	0	0	0	F6Z494	
ENSMUST00000126092						0	2	2	0	2	2	0	0	0	0	0		
ENSMUST00000126093						0	0	0	0	0	0	0	0	2	0	7		
ENSMUST00000126094						0	0	7	35	3	1	0	0	0	9	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126096						7	3	3	9	7	3	0	0	0	0	0		
ENSMUST00000126097						0	0	0	2	0	0	2	35	10	32	15		
ENSMUST00000126098	ENSMUSG00000029055	4	154983115	155056784	-1	1	1	8	15	3	5	0	0	0	0	0	A6PWW4	
ENSMUST00000126100	ENSMUSG00000022708	16	42875881	43642602	1	0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000126101	ENSMUSG00000056737	6	72544391	72562983	1	2	3	2	2	0	2	367	28	292	40	226	D3YTL5	
ENSMUST00000126102	ENSMUSG00000019763	10	4401915	4432388	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVL9	
ENSMUST00000126103						0	0	0	21	0	0	0	0	0	2	0		
ENSMUST00000126105	ENSMUSG00000040829	11	70459433	70466202	1	0	1	10	0	1	0	0	0	0	0	0	G3UZR2	
ENSMUST00000126106						6	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000126107						3	1	7	5	3	7	0	0	0	0	0		
ENSMUST00000126108						3	5	58	8	10	2	2	0	1	0	6		
ENSMUST00000126109						2	3	4	0	4	0	1	0	0	0	1		
ENSMUST00000126110						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000126111						7	4	9	2	7	3	0	0	0	0	1		
ENSMUST00000126112	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TJ64	Q8CBW3
ENSMUST00000126113						6	2	2	0	5	7	3	0	0	0	5		
ENSMUST00000126114	ENSMUSG00000057054	11	70688361	70700155	-1	7	7	0	0	18	15	0	6	0	0	0		Q6PKN7
ENSMUST00000126115						4	2	15	2	13	6	0	4	3	0	0		
ENSMUST00000126116	ENSMUSG00000001794	7	30186942	30195164	-1	0	0	1	5	0	2	600	558	484	86	249	D3YW48	
ENSMUST00000126117						10	1	2	0	0	0	0	21	0	13	0		
ENSMUST00000126118						12	2	31	21	14	6	0	0	2	0	26		
ENSMUST00000126119	ENSMUSG00000078350	4	154020470	154026230	-1	6	0	29	0	26	0	0	0	0	0	0		P0C8K7
ENSMUST00000126120						1	2	2	1	0	0	21	54	31	8	65		
ENSMUST00000126121						1	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000126123	ENSMUSG00000010311	1	133897199	133907999	-1	3	0	1	0	0	2	0	0	0	0	0	F6Z4X6	
ENSMUST00000126124	ENSMUSG00000056737	6	72544391	72562983	1	0	3	0	5	0	0	17	0	12	0	0	D3YU77	
ENSMUST00000126125						66	46	144	151	105	55	9	20	19	5	35		
ENSMUST00000126126	ENSMUSG00000029725	5	137778849	137780110	1	2	1	0	30	0	0	20	8	0	0	0	F6XYC5	
ENSMUST00000126127	ENSMUSG00000055491	19	46044886	46072915	1	4	7	6	37	1	0	0	0	0	0	0	D3Z2D9	
ENSMUST00000126128	ENSMUSG00000020409	11	43433744	43447981	1	0	3	0	0	1	0	5	23	3	0	19	B0QZT9	
ENSMUST00000126129	ENSMUSG00000022577	15	75551268	75567255	-1	0	0	0	0	0	0	0	0	0	0	0	Q544M1	Q9WUC3
ENSMUST00000126130	ENSMUSG00000000308	2	121357714	121363737	1	0	0	0	6	3	0	0	0	0	0	0	D6RET9	
ENSMUST00000126131	ENSMUSG00000020385	11	51261730	51281766	1	0	0	0	0	0	0	0	9	0	33	0	D6RH46	
ENSMUST00000126132						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126133						5	0	0	9	6	0	0	0	0	0	0		
ENSMUST00000126134						0	0	4	35	2	1	0	0	4	0	3		
ENSMUST00000126135						17	0	37	48	21	13	11	484	25	0	110		
ENSMUST00000126136						20	0	6	134	18	2	57	105	65	6	43		
ENSMUST00000126137						1	1	2	2	1	0	4	22	7	1	5		
ENSMUST00000126139						2	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000126142	ENSMUSG00000061742	19	6535845	6543019	-1	5	0	4	3	8	2	0	0	0	0	0	F7A0H7	
ENSMUST00000126144	ENSMUSG00000027671	3	32706298	32726973	1	0	0	0	0	6	0	5	27	28	9	9	D3YVN1	
ENSMUST00000126145						0	0	0	0	0	0	0	1	1	0	0		
ENSMUST00000126146						1	0	0	3	2	0	0	13	0	0	2		
ENSMUST00000126147	ENSMUSG00000016239	X	36328353	36362341	1	1	0	3	2	1	2	0	0	5	2	0	A2A3U8	
ENSMUST00000126148						4	0	3	35	4	1	4	3	0	0	6		
ENSMUST00000126149						1	1	2	3	0	0	3	53	12	0	63		
ENSMUST00000126150	ENSMUSG00000098488	2	120033417	120043030	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCM8	
ENSMUST00000126151	ENSMUSG00000004631	6	4674350	4747207	-1	0	0	0	0	0	0	0	0	0	0	0	F6WKE4	
ENSMUST00000126153	ENSMUSG00000025420	18	76977148	77047308	-1	3	0	3	0	0	2	0	0	0	0	2		Q9D3R6
ENSMUST00000126154						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126155						2	1	2	5	2	0	6	0	1	1	0		
ENSMUST00000126156						5	5	20	4	11	0	2	7	2	0	8		
ENSMUST00000126157	ENSMUSG00000039396	8	53586867	53639065	-1	0	0	0	3	2	0	0	0	0	0	0	D3YXA4	
ENSMUST00000126158						38	48	132	117	71	28	0	10	6	7	11		
ENSMUST00000126159						3	7	11	62	11	3	31	67	59	6	110		
ENSMUST00000126160						25	24	234	55	30	18	8	48	34	4	38		
ENSMUST00000126161						12	10	52	16	5	5	0	1	0	0	3		
ENSMUST00000126162						1	0	3	0	1	1	5	37	4	2	6		
ENSMUST00000126163	ENSMUSG00000016921	2	162931528	162937121	1	0	0	0	1	0	0	0	2	0	0	0	A0A0A6YXX6	
ENSMUST00000126164						12	12	56	16	21	9	1	1	1	0	1		
ENSMUST00000126165						3	0	3	0	0	0	21	268	19	42	28		
ENSMUST00000126166	ENSMUSG00000022185	14	54642161	54686931	-1	0	0	10	0	0	0	0	682	0	67	0		Q9JIX8
ENSMUST00000126167						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000126168	ENSMUSG00000041264	5	149184350	149215434	1	11	0	0	0	0	0	48	326	36	1	43	D6RI24	
ENSMUST00000126169						0	1	0	17	9	0	0	0	0	0	0		
ENSMUST00000126171	ENSMUSG00000007613	4	47353222	47414931	1	0	0	0	1	0	1	0	3	0	0	3	E9Q418	
ENSMUST00000126172	ENSMUSG00000037101	8	78213297	78394326	1	1	1	0	5	0	0	0	0	0	0	0		
ENSMUST00000126173						2	4	0	0	0	0	9	5	3	21	3		
ENSMUST00000126174						2	0	4	0	0	0	0	20	6	8	6		
ENSMUST00000126175	ENSMUSG00000020694	11	105178807	105283959	1	0	0	0	0	0	0	143	739	239	6	95	D6RHM1	
ENSMUST00000126177						0	0	0	0	0	0	3	5	6	0	7		
ENSMUST00000126178						7	9	31	30	24	9	75	11649	926	71	3909		
ENSMUST00000126179						0	6	7	69	8	11	0	4	0	0	4		
ENSMUST00000126180	ENSMUSG00000031792	8	95332292	95347507	1	6	7	6	16	6	4	0	4	2	0	4	D3Z5I2	
ENSMUST00000126181	ENSMUSG00000029761	6	34598500	34775473	1	0	0	0	0	0	0	1	0	0	0	0	F6RGN9	
ENSMUST00000126182	ENSMUSG00000035268	2	163658386	163726158	1	0	0	0	0	7	0	0	0	0	0	0	Q3TP50	O70139
ENSMUST00000126183						11	11	3	9	4	2	1	0	1	0	0		
ENSMUST00000126184	ENSMUSG00000022285	15	36770770	36794547	-1	2	0	4	23	1	2	0	8	0	0	3	D3YXN6	
ENSMUST00000126185						11	12	32	26	17	15	2	9	4	4	9		
ENSMUST00000126186						4	3	10	0	9	0	0	0	0	0	0		
ENSMUST00000126188	ENSMUSG00000039652	19	37021291	37208601	-1	2	0	24	105	9	0	0	0	5	0	6		Q7TN99
ENSMUST00000126191						1	1	2	5	4	4	0	3	0	0	6		
ENSMUST00000126192						0	0	0	0	0	0	3	4	16	16	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126193						4	0	15	10	0	4	194	426	303	31	363		
ENSMUST00000126194						2	2	14	142	13	1	17	107	57	27	122		
ENSMUST00000126195	ENSMUSG00000035086	11	101285952	101302286	-1	0	0	0	0	0	0	2	0	25	6	0	F7C090	
ENSMUST00000126196						4	4	5	2	2	1	0	0	0	0	0		
ENSMUST00000126197						4	5	29	0	7	7	0	29	0	0	0		
ENSMUST00000126198	ENSMUSG00000060568	1	167001417	167091302	1	9	6	3	25	7	0	0	0	0	0	12		Q8BQN5
ENSMUST00000126199						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000126200						1	3	4	0	1	0	4	55	10	3	0		
ENSMUST00000126201	ENSMUSG00000020718	11	106768253	106779537	-1	0	0	0	62	0	0	0	0	0	0	0	F2Z482	
ENSMUST00000126202	ENSMUSG00000020692	11	82900768	82908411	-1	3	2	12	1	4	4	0	9	0	0	3	F6QAD9	
ENSMUST00000126203	ENSMUSG00000090124	1	88095062	88220002	1	0	0	0	0	0	0	170	664	381	237	579	D6RH94	
ENSMUST00000126204	ENSMUSG00000001827	7	101858331	101870788	-1	0	0	0	4	0	0	0	0	0	0	0	E9PYD9	
ENSMUST00000126206						0	0	0	0	0	0	43	0	124	0	389		
ENSMUST00000126207	ENSMUSG00000028621	4	107066988	107088268	1	33	23	76	26	54	39	3	14	0	2	19	F6RAM1	
ENSMUST00000126208						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126209						2	1	3	0	1	1	1	4	0	0	2		
ENSMUST00000126210						0	2	0	3	2	2	0	2	9	0	14		
ENSMUST00000126211	ENSMUSG00000061479	7	27187005	27196271	-1	0	8	17	18	8	0	11	8	0	0	21	D3Z0S6	
ENSMUST00000126213						5	0	0	0	4	0	0	6	11	0	0		
ENSMUST00000126214	ENSMUSG00000039578	6	61180324	62382865	1	40	22	172	78	49	19	1	1	0	0	1		Q8C0C4
ENSMUST00000126215						0	1	0	0	3	1	24	21	37	38	19		
ENSMUST00000126216	ENSMUSG00000013921	7	30291672	30308367	1	0	0	0	0	0	0	1	0	0	0	0	D3YXY6	
ENSMUST00000126217						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000126218						0	0	0	61	2	1	0	0	0	0	1		
ENSMUST00000126220						0	0	1	0	0	0	75	0	42	80	35		
ENSMUST00000126221						3	3	3	0	0	0	2	5	7	0	5		
ENSMUST00000126222						0	20	19	30	14	16	6	0	12	0	10		
ENSMUST00000126223						6	2	2	0	2	1	0	0	0	0	0		
ENSMUST00000126224						0	1	2	73	6	0	5	6	27	0	29		
ENSMUST00000126226	ENSMUSG00000031576	8	25849623	25937933	1	0	0	5	0	0	0	0	0	0	0	0	D3Z073	
ENSMUST00000126227						0	4	0	2	3	0	0	0	0	0	0		
ENSMUST00000126228						1	0	1	1	0	1	0	5	1	4	1		
ENSMUST00000126230						0	3	13	2	3	1	17	191	59	59	86		
ENSMUST00000126232	ENSMUSG00000039860	5	135806890	135874772	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3C2	
ENSMUST00000126233						0	8	8	4	7	0	0	0	0	0	0		
ENSMUST00000126234	ENSMUSG00000025877	13	55005985	55021385	-1	0	0	41	0	0	0	1224	1	1159	24	349		Q3TRM8
ENSMUST00000126235						56	50	94	180	53	19	3	3	6	0	15		
ENSMUST00000126236						4	1	10	0	2	2	0	1	0	0	1		
ENSMUST00000126239	ENSMUSG00000036054	8	70234226	70279915	1	28	21	54	42	35	18	3	28	14	0	11	F6X398	
ENSMUST00000126241	ENSMUSG00000060600	11	70657202	70662513	1	0	0	0	0	0	0	0	4	4	0	3	Q5SX61	
ENSMUST00000126242						7	5	0	2	4	2	0	0	0	0	0		
ENSMUST00000126243	ENSMUSG00000025409	10	127281956	127289018	-1	9	3	34	59	0	12	255	1164	414	43	456	F6S711	
ENSMUST00000126244						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000126245	ENSMUSG00000068922	3	88905107	88913999	-1	0	1	0	14	0	0	45	40	41	27	54	E9PUB7	
ENSMUST00000126246						5	4	6	73	10	0	18	31	81	410	26		
ENSMUST00000126247						41	35	332	95	31	13	3	21	6	5	18		
ENSMUST00000126248						3	0	13	0	0	0	175	0	67	0	74		
ENSMUST00000126249						0	1	0	2	4	0	0	0	0	0	0		
ENSMUST00000126250	ENSMUSG00000027628	2	156547584	156568972	1	5	0	1	0	0	4	3	0	0	0	0	B7ZD24	
ENSMUST00000126251	ENSMUSG00000038775	9	119052778	119071525	1	0	0	0	0	0	0	11	7	0	0	0	D3Z669	
ENSMUST00000126253						0	0	0	2	2	0	2	8	0	0	0		
ENSMUST00000126254						6	7	10	18	4	0	0	0	0	0	0		
ENSMUST00000126255						2	2	0	0	0	0	0	0	0	3	5		
ENSMUST00000126256						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000126257	ENSMUSG00000001082	5	34633642	34637212	-1	0	0	0	0	0	0	0	5	0	0	4		
ENSMUST00000126258	ENSMUSG00000023990	17	47737030	47792419	1	0	0	1	63	0	3	0	0	0	0	0	D3Z219	
ENSMUST00000126259						0	1	0	2	1	0	0	0	0	0	0		
ENSMUST00000126261						3	0	3	64	1	1	0	0	0	2	0		
ENSMUST00000126262						0	0	4	6	0	4	4	5	3	0	14		
ENSMUST00000126263	ENSMUSG00000030780	7	128271379	128298170	-1	0	0	0	15	0	0	0	0	0	0	0	D6RDS0	
ENSMUST00000126264						1	0	0	15	0	1	0	1	0	1	3		
ENSMUST00000126266						0	0	0	19	3	0	47	3	30	0	0		
ENSMUST00000126267	ENSMUSG00000029127	5	38189735	38220457	-1	0	0	0	0	0	0	12	24	3	6	7	D6RGS0	
ENSMUST00000126268						1	0	4	0	6	0	0	0	0	0	4		
ENSMUST00000126269						2	0	0	0	0	1	15	0	24	11	78		
ENSMUST00000126271						1	0	5	0	4	2	0	0	0	0	0		
ENSMUST00000126272						5	2	20	1	0	1	85	188	61	61	27		
ENSMUST00000126274						8	2	3	0	10	0	0	0	0	0	0		
ENSMUST00000126275						26	11	66	28	24	8	39	61	80	4	142		
ENSMUST00000126276						3	11	20	0	34	18	36	608	38	0	0		
ENSMUST00000126277						3	4	2	0	2	2	0	35	7	11	18		
ENSMUST00000126278						0	8	0	0	2	0	0	0	0	0	0		
ENSMUST00000126279						2	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000126280						18	11	57	18	9	3	78	201	164	7	203		
ENSMUST00000126281	ENSMUSG00000034842	5	92331827	92414628	1	0	0	0	6	0	0	0	0	0	1	0	F6RER8	
ENSMUST00000126282						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000126283						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126284						3	2	3	1	3	2	0	0	0	0	0		
ENSMUST00000126285						334	440	308	225	336	168	5	18	10	2	9		
ENSMUST00000126287	ENSMUSG00000038453	11	97509340	97575226	-1	4	0	0	180	1	1	0	0	0	0	0	B1AQX8	
ENSMUST00000126288						6	1	14	0	4	0	5	23	10	0	7		
ENSMUST00000126290	ENSMUSG00000027186	2	103411688	103450989	1	0	0	0	0	3	0	0	0	0	0	0	A2AL22	
ENSMUST00000126291	ENSMUSG00000034785	4	107291465	107307169	-1	2	0	0	10	2	2	0	0	0	0	0	D6RDQ6	
ENSMUST00000126292	ENSMUSG00000029804	6	58831465	58920398	1	0	0	0	49	0	0	0	0	4	1	4	D3Z6D4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126293						0	1	3	4	2	0	0	2	0	1	0		
ENSMUST00000126295	ENSMUSG00000025871	13	54551218	54565435	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1U8	
ENSMUST00000126296	ENSMUSG00000040938	11	70212752	70216417	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCB4	
ENSMUST00000126297	ENSMUSG00000006649	7	30458315	30487223	1	1	4	0	6	5	4	0	0	0	0	0	E9QPI7	
ENSMUST00000126299						21	15	35	29	5	0	0	14	0	5	27		
ENSMUST00000126301	ENSMUSG00000001855	2	31974436	32053975	1	0	0	2	0	0	2	0	0	2	0	2	A0A0A6YW83	
ENSMUST00000126302						2	0	1	3	1	3	0	0	0	0	2		
ENSMUST00000126303	ENSMUSG00000029752	6	7675169	7693254	-1	2	1	3	106	6	4	0	0	0	0	0	D3Z0C2	
ENSMUST00000126304						7	4	7	37	9	3	0	0	0	0	0		
ENSMUST00000126305	ENSMUSG00000041343	7	92581723	92637142	-1	0	0	8	32	11	0	0	0	0	0	0	D6RCX7	
ENSMUST00000126306						16	6	49	612	27	8	0	0	5	0	0		
ENSMUST00000126307	ENSMUSG00000020097	10	61098642	61147703	-1	2	0	3	428	17	11	1	1	2	0	6	D3YY13	
ENSMUST00000126308						3	5	15	0	13	0	0	0	0	0	0		
ENSMUST00000126309						60	38	39	79	69	10	0	0	0	0	0		
ENSMUST00000126310						0	4	1	0	2	0	0	0	0	0	0		
ENSMUST00000126311						4	0	10	0	1	0	0	0	0	0	0		
ENSMUST00000126312						3	6	15	6	12	5	18	8	31	4	53		
ENSMUST00000126313						0	0	4	3	1	0	0	4	4	0	6		
ENSMUST00000126315						25	18	33	31	38	14	8	20	5	0	28		
ENSMUST00000126316						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000126317	ENSMUSG00000048240	10	80948624	81014945	-1	0	2	6	5	2	0	0	0	0	0	0	D3Z483	
ENSMUST00000126318	ENSMUSG00000017670	2	165288031	165326479	-1	0	0	0	0	0	0	0	0	0	0	0	D6RHT3	
ENSMUST00000126319	ENSMUSG00000040688	17	24697949	24707660	-1	13	22	30	32	40	8	0	11	3	0	4		Q8C4J7
ENSMUST00000126320						3	1	1	8	5	0	4	32	0	0	43		
ENSMUST00000126321						0	0	0	8	0	0	0	1	0	0	0		
ENSMUST00000126322	ENSMUSG00000027610	2	155563181	155592810	-1	0	0	3	1	0	0	0	0	0	0	3	A2AQN7	
ENSMUST00000126323	ENSMUSG00000054708	10	81628540	81647610	1	0	0	0	3	0	0	0	0	0	0	0	D3YXU5	
ENSMUST00000126324	ENSMUSG00000054362	4	106590909	106617241	-1	0	0	0	0	0	0	0	0	0	0	0	F6X5R4	
ENSMUST00000126327						0	2	4	4	1	1	0	0	0	0	1		
ENSMUST00000126328						0	0	0	0	0	0	26	104	50	8	26		
ENSMUST00000126330						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126331						19	15	78	15	19	3	0	3	0	0	0		
ENSMUST00000126332						1	0	0	4	3	0	0	1	0	5	2		
ENSMUST00000126333	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	0	0	0	0	0	0	0	0	F6VCW7	
ENSMUST00000126334	ENSMUSG00000038623	7	81859001	81884434	1	9	5	19	0	6	2	86	649	68	80	85	D6RD09	
ENSMUST00000126335						6	0	20	76	10	4	48	10	95	0	54		
ENSMUST00000126336	ENSMUSG00000028538	4	117932154	118134914	-1	0	0	0	2	8	0	7	0	0	0	0	B1AS81	
ENSMUST00000126337	ENSMUSG00000050447	2	50066429	50193569	1	1	1	2	0	3	3	0	0	0	0	0	A2AQT3	
ENSMUST00000126338	ENSMUSG00000059810	4	62559847	62704001	1	7	1	9	6	4	2	9	5	14	0	25	I7HJI7	
ENSMUST00000126340						1	4	3	0	1	3	0	0	0	1	0		
ENSMUST00000126341						27	33	31	19	31	12	28	156	129	34	123		
ENSMUST00000126342						2	1	4	0	0	0	0	0	0	0	2		
ENSMUST00000126343						2	3	8	7	4	5	2334	2466	2876	704	2591		
ENSMUST00000126344						11	11	23	138	21	9	0	0	0	0	2		
ENSMUST00000126345						7	7	20	12	17	13	10	3	15	4	16		
ENSMUST00000126346	ENSMUSG00000029068	4	155812489	155824543	1	4	6	0	0	0	4	435	2904	813	216	1523	F6RXL0	
ENSMUST00000126347						101	94	346	114	92	55	0	14	11	1	13		
ENSMUST00000126348						0	1	1	13	3	0	0	0	0	0	0		
ENSMUST00000126349						5	1	3	2	6	4	0	0	0	0	0		
ENSMUST00000126350						1	3	3	0	6	0	5	3	2	0	6		
ENSMUST00000126351						0	0	0	1	0	1	0	0	8	0	6		
ENSMUST00000126352						7	10	60	20	4	4	0	12	13	2	16		
ENSMUST00000126353	ENSMUSG00000028496	4	87769925	88033364	-1	2	1	0	0	5	0	5	21	9	1	3	Q9D2P1	
ENSMUST00000126354						1	2	2	1	2	0	0	2	0	0	0		
ENSMUST00000126355	ENSMUSG00000040268	7	130865756	130913312	1	2	2	6	0	7	0	0	0	3	8	18	F6YLP9	
ENSMUST00000126356	ENSMUSG00000030753	7	98703103	98718062	1	0	0	0	13	0	0	0	2	3	0	5	D6RI43	
ENSMUST00000126357						22	14	17	13	11	9	0	2	0	0	0		
ENSMUST00000126358	ENSMUSG00000078875	2	177000956	177012787	1	0	0	0	0	1	0	0	0	0	1	0	A2ARL5	
ENSMUST00000126359	ENSMUSG00000032554	9	103204001	103230444	-1	1	5	4	3	8	1	0	0	6	0	0	D3YYR8	
ENSMUST00000126360						0	0	0	0	0	0	0	17	0	7	4		
ENSMUST00000126362	ENSMUSG00000033361	X	71962624	71972722	1	1	1	0	25	1	1	0	0	0	0	0	I7HPX7	
ENSMUST00000126363						2	0	15	0	0	1	0	0	0	0	0		
ENSMUST00000126364						0	0	4	61	2	2	0	0	0	0	0		
ENSMUST00000126365						1	0	2	2	1	2	1	20	4	3	8		
ENSMUST00000126366	ENSMUSG00000048012	7	44731481	44751050	-1	21	24	22	18	23	13	8	6	10	2	15	E9Q4I9	
ENSMUST00000126367	ENSMUSG00000033533	7	119607026	119662515	1	2	4	0	2	6	0	0	0	0	0	0	D3YV36	
ENSMUST00000126368						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126370						3	0	50	0	21	6	0	0	0	0	0		
ENSMUST00000126371						3	0	9	10	9	1	4	44	6	2	12		
ENSMUST00000126372						5	1	0	8	1	0	9	11	11	9	5		
ENSMUST00000126373	ENSMUSG00000020114	10	119199255	119240055	-1	1	0	4	41	2	0	19	0	27	0	42	D3YWC5	
ENSMUST00000126374	ENSMUSG00000022957	16	91729281	91920597	1	0	1	0	0	0	0	3	3	0	0	9	F6ZLP6	
ENSMUST00000126375	ENSMUSG00000025860	X	42059679	42109656	1	0	0	0	26	0	0	0	0	5	0	8	A2BGY5	
ENSMUST00000126376	ENSMUSG00000025702	6	116338024	116409540	1	0	0	0	8	0	0	0	0	0	0	0		
ENSMUST00000126377						3	2	1	1	1	2	0	1	4	6	8		
ENSMUST00000126378	ENSMUSG00000040174	2	93980550	94010807	-1	1	2	0	0	0	0	7	15	4	3	0	A2AKV7	
ENSMUST00000126381						51	37	420	93	75	40	125	313	191	44	487		
ENSMUST00000126382						2	0	1	0	7	0	0	0	2	1	0		
ENSMUST00000126383						0	0	0	270	0	0	0	0	0	0	0		
ENSMUST00000126384	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	0	0	0	0	0	0	F6VJ78	
ENSMUST00000126386						4	2	8	66	5	3	11	0	4	32	5		
ENSMUST00000126387						5	0	6	6	19	3	0	2	0	2	2		
ENSMUST00000126388	ENSMUSG00000040938	11	70212752	70216417	1	3	0	8	32	0	0	0	3	0	0	0		Q5NC32
ENSMUST00000126389						0	0	0	0	0	0	0	0	0	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126390	ENSMUSG00000019854	10	18055861	18125155	1	0	0	0	0	2	0	161	368	236	60	225		O54916
ENSMUST00000126391	ENSMUSG00000018920	11	70453983	70459984	-1	0	0	0	0	1	2	8	5	4	78	16	I7HIQ2	
ENSMUST00000126393						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126394						0	0	0	0	0	0	0	0	5	0	0		
ENSMUST00000126395						0	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000126396						4	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000126397						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126398						1	2	2	3	2	0	2	1	0	0	3		
ENSMUST00000126399	ENSMUSG00000052581	6	80018877	80810143	1	0	0	0	0	0	0	0	0	0	0	0		Q80XG9
ENSMUST00000126400	ENSMUSG00000041911	2	71528113	71533981	1	1	3	0	85	0	2	0	0	0	0	0	G3UX87	
ENSMUST00000126402						2	1	13	2	6	0	0	0	0	0	0		
ENSMUST00000126403	ENSMUSG00000005803	2	122765237	122809569	1	0	0	0	0	0	0	364	1989	689	546	300	F6ZKZ3	
ENSMUST00000126404						1	0	0	0	0	0	0	18	41	0	13		
ENSMUST00000126405	ENSMUSG00000032422	9	88376750	88438958	-1	0	2	0	7	5	5	0	0	27	0	0	D6RH84	
ENSMUST00000126406	ENSMUSG00000039958	6	149139849	149151171	1	0	0	0	0	0	0	2	0	0	0	0	B8JKU4	
ENSMUST00000126407	ENSMUSG00000026836	2	58388644	58567157	-1	0	0	1	0	1	1	0	0	0	0	0	B1AW87	
ENSMUST00000126408	ENSMUSG00000090258	12	76765538	76783180	1	10	7	64	0	80	24	15	30	0	35	18	D3Z553	
ENSMUST00000126409						3	0	1	0	1	5	0	0	0	0	2		
ENSMUST00000126410						4	0	7	1	4	1	0	0	0	0	0		
ENSMUST00000126411	ENSMUSG00000043587	9	96823336	96892669	-1	3	5	8	4	4	1	0	0	10	0	2	D3Z2N0	
ENSMUST00000126412	ENSMUSG00000026098	1	53189187	53297018	-1	0	0	0	45	0	0	0	0	0	5	0	D3Z012	
ENSMUST00000126413	ENSMUSG00000037447	1	36307733	36324029	1	0	0	0	10	0	0	257	76	109	0	183	D3Z085	
ENSMUST00000126414						0	0	0	0	4	1	0	5	0	0	0		
ENSMUST00000126415	ENSMUSG00000037143	2	145934784	146215039	1	13	8	0	8	8	4	0	0	0	0	0	B7ZCD7	
ENSMUST00000126416						1	3	2	0	3	2	0	0	0	0	0		
ENSMUST00000126417	ENSMUSG00000062524	7	4337724	4345164	1	14	0	4	8	7	0	0	91	0	8	6		
ENSMUST00000126418						1	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000126419						0	0	0	0	0	0	0	33	16	24	0		
ENSMUST00000126420						3	2	0	132	13	0	0	0	0	0	0		
ENSMUST00000126421	ENSMUSG00000059842	2	154613297	154646821	1	0	18	3	38	14	0	20	96	0	12	23	D6REV2	
ENSMUST00000126422	ENSMUSG00000047867	6	48701582	48708225	-1	0	0	0	0	0	0	0	0	5	0	7		
ENSMUST00000126423						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126424						1	2	5	0	2	0	1	0	0	0	1		
ENSMUST00000126425						8	2	11	1	6	4	234	108	232	3	206		
ENSMUST00000126426						2	1	6	0	2	0	0	0	1	1	0		
ENSMUST00000126428						6	9	2	6	4	1	4	14	3	1	7		
ENSMUST00000126429	ENSMUSG00000052407	4	83525545	83864670	1	1	0	1	16	1	0	0	5	0	2	0	S4R1F3	
ENSMUST00000126430	ENSMUSG00000062995	6	8630527	8778488	-1	3	3	1	6	3	0	2	0	0	0	0	F7BG11	
ENSMUST00000126431	ENSMUSG00000031816	8	121091628	121108392	-1	0	0	6	120	7	5	0	0	0	0	0	D3Z1R2	
ENSMUST00000126432	ENSMUSG00000024516	18	65800549	65817665	1	0	0	0	0	0	0	20	95	24	108	38	D6RFV4	
ENSMUST00000126433						65	42	96	46	42	21	0	1	1	0	1		
ENSMUST00000126434						17	10	26	17	19	9	0	0	0	0	0		
ENSMUST00000126435	ENSMUSG00000004996	8	84249906	84257326	-1	8	14	17	36	19	10	20	29	4	0	9		Q9CQT1
ENSMUST00000126436	ENSMUSG00000019823	10	41476314	41487032	1	0	0	0	0	0	0	0	19	0	0	35	E9PUI4	
ENSMUST00000126438						2	8	0	29	0	0	0	0	0	0	0		
ENSMUST00000126439						16	17	28	26	23	13	1	1	1	0	2		
ENSMUST00000126440						1	0	1	5	2	0	0	7	28	0	19		
ENSMUST00000126441						2	0	3	0	2	0	0	0	0	0	2		
ENSMUST00000126442	ENSMUSG00000026788	2	33450287	33468559	-1	0	0	1	79	0	0	7	5	8	2	14	A2AUS2	
ENSMUST00000126444	ENSMUSG00000069170	13	81095068	81633154	-1	0	0	0	0	0	0	0	0	0	0	0	D3YYF1	
ENSMUST00000126445						9	5	58	6	5	5	3	0	2	2	1		
ENSMUST00000126446						0	1	2	68	3	1	0	0	0	0	0		
ENSMUST00000126449						3	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000126451						0	4	4	7	3	0	232	199	174	450	145		
ENSMUST00000126452						2	0	0	17	2	0	0	5	0	0	0		
ENSMUST00000126453						7	3	3	6	5	0	10	30	2	0	10		
ENSMUST00000126454						0	0	2	0	3	0	0	0	1	0	0		
ENSMUST00000126455						8	2	6	0	3	4	0	5	0	0	0		
ENSMUST00000126456	ENSMUSG00000039187	7	79391929	79450264	1	101	93	224	128	90	61	2	4	2	0	6	D3YVC7	
ENSMUST00000126457						2	0	4	21	2	0	0	0	0	0	4		
ENSMUST00000126458						0	0	0	0	0	0	65	355	142	581	103		
ENSMUST00000126460						3	3	6	0	0	0	0	0	0	2	10		
ENSMUST00000126461						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126463						1	1	0	3	1	0	1	3	1	2	0		
ENSMUST00000126464						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000126465	ENSMUSG00000089945	4	57568179	57896984	1	3	0	0	0	0	2	0	0	0	0	0	G3X9P1	
ENSMUST00000126466						0	2	0	0	0	0	0	12	20	8	18		
ENSMUST00000126468						4	4	5	0	0	0	7	11	0	9	6		
ENSMUST00000126469						3	0	0	9	3	1	0	35	8	4	18		
ENSMUST00000126471	ENSMUSG00000024906	19	5482345	5488402	-1	2	1	9	6	0	0	3	0	6	0	1	D6RCJ5	
ENSMUST00000126473						0	3	4	0	3	0	107	0	54	0	44		
ENSMUST00000126474						2	5	5	9	7	8	0	0	0	0	0		
ENSMUST00000126475						64	68	140	377	97	13	7659	35865	12982	2956	10387		
ENSMUST00000126477						3	2	6	37	2	2	0	10	9	0	3		
ENSMUST00000126478						2	1	1	20	0	0	0	2	1	0	0		
ENSMUST00000126481	ENSMUSG00000029217	5	72755716	72868483	-1	0	0	0	0	0	7	0	0	0	0	0	D6RJM5	
ENSMUST00000126483						0	0	0	0	0	0	3	21	21	4	6		
ENSMUST00000126484						4	0	7	12	8	3	11	27	16	0	29		
ENSMUST00000126485						10	5	24	43	11	8	17	3	19	4	16		
ENSMUST00000126486	ENSMUSG00000019843	10	39368855	39565381	1	4	0	0	64	11	0	0	0	0	0	0		P39688
ENSMUST00000126487						0	0	0	0	0	0	1	0	1	0	2		
ENSMUST00000126488	ENSMUSG00000044712	12	73286779	73354049	1	0	0	0	0	1	0	0	0	0	0	0	Q3USV8	
ENSMUST00000126489						4	2	4	5	6	0	5	111	14	20	33		
ENSMUST00000126490	ENSMUSG00000020053	10	87858265	87937042	1	0	0	0	0	0	0	0	0	0	0	1	D3Z7M4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126491						0	0	1	0	0	0	9	15	10	20	13		
ENSMUST00000126493						1	0	6	1	0	0	27	89	40	11	14		
ENSMUST00000126494						4	0	3	0	3	3	0	0	1	5	6		
ENSMUST00000126495						2	0	3	0	2	0	2	9	15	0	9		
ENSMUST00000126496						4	9	17	13	7	2	9	49	33	1	49		
ENSMUST00000126497						0	0	0	286	5	0	0	0	0	0	0		
ENSMUST00000126499						5	0	14	9	5	12	0	2	0	4	1		
ENSMUST00000126501	ENSMUSG00000079049	13	32881833	32898161	-1	8	7	13	7	10	4	0	1	0	0	0		
ENSMUST00000126503						4	4	7	0	0	0	0	39	3	4	7		
ENSMUST00000126504						67	52	61	199	75	43	8	5	15	8	21		
ENSMUST00000126505	ENSMUSG00000024191	17	26781079	26792565	1	0	2	0	0	0	0	6	0	0	0	0	F6WZQ6	
ENSMUST00000126506						6	5	0	1	2	4	0	8	6	1	0		
ENSMUST00000126507						8	6	21	3	5	1	119	626	42	33	42		
ENSMUST00000126508	ENSMUSG00000047295	15	91838265	91861438	1	0	7	7	0	1	0	0	0	0	0	0	D3Z0U8	
ENSMUST00000126509						6	4	17	7	10	2	0	0	0	0	0		
ENSMUST00000126510	ENSMUSG00000025505	7	141327739	141337156	1	0	0	0	3	0	0	0	0	0	0	0		Q9D3H0
ENSMUST00000126511						13	3	34	8	9	3	3	8	2	2	5		
ENSMUST00000126512	ENSMUSG00000042489	4	126556935	126593903	1	0	1	0	0	0	0	0	0	3	0	6	F6S522	
ENSMUST00000126513						3	0	1	0	0	0	0	6	0	0	0		
ENSMUST00000126514						1	0	0	0	0	0	0	15	0	14	0		
ENSMUST00000126515	ENSMUSG00000051747	2	76703980	76982547	-1	0	1	0	1	0	0	0	0	0	0	0	A2AT63	
ENSMUST00000126517						20	14	16	20	24	14	5	18	9	5	8		
ENSMUST00000126518						1	0	1	64	2	0	0	0	0	9	0		
ENSMUST00000126519						0	0	1	0	1	0	0	0	0	0	3		
ENSMUST00000126520						0	3	0	12	8	0	0	14	29	0	72		
ENSMUST00000126521	ENSMUSG00000071112	6	142413441	142419730	1	0	0	0	0	1	0	0	0	0	0	0	D3YZM2	D3Z752
ENSMUST00000126522	ENSMUSG00000042678	11	60469339	60528369	1	0	28	0	2	12	5	0	0	1	0	0	F6VXK7	
ENSMUST00000126523						0	6	7	15	12	3	17	64	46	14	68		
ENSMUST00000126524						0	0	0	0	0	0	0	0	0	11	0		
ENSMUST00000126525	ENSMUSG00000074895	13	54783998	54788459	1	0	0	0	0	0	0	0	0	0	0	0	Q27ZI6	
ENSMUST00000126526						4	0	0	89	4	0	0	1	0	0	0		
ENSMUST00000126527						4	6	6	7	5	4	0	0	0	1	0		
ENSMUST00000126528						0	1	1	15	0	1	0	0	0	0	0		
ENSMUST00000126529						3	0	6	0	6	9	179	277	40	106	46		
ENSMUST00000126530						6	5	8	2	4	2	0	4	0	0	0		
ENSMUST00000126531						0	0	0	2	0	0	0	0	1	0	3		
ENSMUST00000126532	ENSMUSG00000075254	16	33684466	33771576	1	10	8	65	9	19	11	2	0	0	0	23		E9Q7X6
ENSMUST00000126533						10	3	12	46	6	2	129	125	91	36	133		
ENSMUST00000126534	ENSMUSG00000033685	7	100493337	100502020	1	40	25	77	71	61	32	16071	13237	8973	1282	7717	Q549J5	P70406
ENSMUST00000126535						0	1	3	9	0	1	1	0	0	0	0		
ENSMUST00000126536	ENSMUSG00000021824	14	21031442	21052508	-1	0	0	0	0	0	0	7	14	15	10	0	D6RI63	
ENSMUST00000126539						5	2	11	0	5	2	4	15	2	3	13		
ENSMUST00000126540	ENSMUSG00000055360	13	13182715	13191923	1	5	4	0	3	4	0	0	0	0	0	0	Q3UKX5	
ENSMUST00000126541						0	1	4	0	0	0	7	11	18	0	18		
ENSMUST00000126542						0	2	0	5	3	0	0	0	1	0	3		
ENSMUST00000126543						0	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000126544						0	0	0	0	0	0	3	2	6	0	3		
ENSMUST00000126545	ENSMUSG00000005907	5	3596066	3637232	1	0	0	0	1	0	1	0	0	3	0	0	F6RUH9	
ENSMUST00000126546						2	0	5	0	1	0	2	0	0	0	0		
ENSMUST00000126547						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000126548						0	0	0	0	0	0	4	53	4	0	0		
ENSMUST00000126550						5	2	8	13	11	0	0	1	1	0	4		
ENSMUST00000126551	ENSMUSG00000045319	2	6097607	6130211	-1	3	2	6	50	0	0	0	0	0	0	1	A2AT36	
ENSMUST00000126552						1	2	11	6	4	2	0	0	0	0	0		
ENSMUST00000126553						0	0	0	0	0	2	0	6	0	1	0		
ENSMUST00000126554						4	1	12	9	15	4	4	0	0	0	5		
ENSMUST00000126555						14	9	13	0	0	0	0	0	0	7	5		
ENSMUST00000126557						3	2	0	1	1	4	6	41	13	0	10		
ENSMUST00000126558						0	0	8	4	2	0	0	27	3	0	0		
ENSMUST00000126559	ENSMUSG00000043243	8	71597648	71607936	1	2	0	3	0	0	0	3	7	2	1	0	G5E8W2	
ENSMUST00000126560						0	1	0	8	4	0	0	55	55	0	79		
ENSMUST00000126561						5	7	43	11	2	5	185	1400	43	0	10		
ENSMUST00000126562	ENSMUSG00000006333	7	3703993	3706897	1	3	0	21	8	5	4	47	194	115	35	136	D3YWH9	
ENSMUST00000126563						7	5	2	133	3	0	0	0	0	0	6		
ENSMUST00000126564						0	1	1	2	1	1	0	0	1	0	0		
ENSMUST00000126565	ENSMUSG00000017210	11	98704591	98729435	-1	0	1	2	0	1	0	0	0	0	2	0	A6PW46	
ENSMUST00000126566						1	1	16	5	8	5	0	0	0	0	0		
ENSMUST00000126567						0	0	1	0	1	3	0	0	0	0	0		
ENSMUST00000126568	ENSMUSG00000022479	15	97854425	97910630	-1	0	0	0	0	8	2	0	0	3	0	0	D3Z3H9	
ENSMUST00000126569	ENSMUSG00000050931	3	131318985	131491411	-1	0	0	0	2	0	8	5	3	18	0	0	D3YVS9	
ENSMUST00000126570	ENSMUSG00000030714	7	126649309	126672925	1	1	0	0	0	1	0	0	0	0	0	2		
ENSMUST00000126573	ENSMUSG00000028613	4	107802261	107876840	1	0	21	60	1	6	13	10	0	0	0	0	B1AXJ6	
ENSMUST00000126574	ENSMUSG00000029173	5	52640087	52669708	-1	0	1	3	0	1	1	0	3	2	0	0	F6YLP3	
ENSMUST00000126575	ENSMUSG00000031641	8	61487734	61503482	1	0	0	1	4	1	1	0	0	0	0	0	D3Z6C4	
ENSMUST00000126576						0	2	5	9	6	5	0	2	0	2	0		
ENSMUST00000126578	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	2	7	0	1	E9PWV9	
ENSMUST00000126579	ENSMUSG00000062590	1	86154780	86278284	1	1	2	1	4	5	1	0	0	0	0	5	F7AY77	
ENSMUST00000126580						4	0	0	2	0	0	0	0	4	4	2		
ENSMUST00000126581						8	3	7	126	4	3	0	1	8	2	3		
ENSMUST00000126582						0	1	3	114	3	0	3	7	0	0	0		
ENSMUST00000126583	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	28	0	0	0	30	F6THK7	
ENSMUST00000126584						21	11	20	16	17	8	2	28	2	4	9		
ENSMUST00000126585						0	1	1	3	1	0	0	0	0	0	0		
ENSMUST00000126586	ENSMUSG00000029004	5	23434441	23504235	1	0	1	0	0	0	0	31	31	399	0	161	A0A087WSN9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126587	ENSMUSG00000092367	7	27352649	27357419	-1	0	0	0	0	0	0	0	2	10	0	0	D3Z4P8	
ENSMUST00000126588						3	1	5	1	5	2	0	0	0	3	0		
ENSMUST00000126589						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000126590	ENSMUSG00000026098	1	53189187	53297018	-1	1	0	0	0	0	0	0	0	3	0	1	D3YX04	
ENSMUST00000126592	ENSMUSG00000031284	X	143518591	143797796	1	0	0	0	12	0	0	0	0	0	0	0	A3KGC2	
ENSMUST00000126593	ENSMUSG00000058135	3	108012255	108017973	-1	1	0	3	0	0	0	12	0	14	0	8	A2AE89	
ENSMUST00000126594	ENSMUSG00000027695	3	27938695	28133362	1	2	0	1	0	0	1	0	0	0	12	8	F6QJR6	
ENSMUST00000126595						17	0	6	14	5	0	0	0	0	0	0		
ENSMUST00000126597						8	0	5	4	10	3	0	0	0	0	0		
ENSMUST00000126598						2	0	0	0	1	0	0	3	2	1	2		
ENSMUST00000126599						4	1	3	0	5	0	0	0	0	0	0		
ENSMUST00000126600	ENSMUSG00000022750	16	17759618	17793382	1	0	0	0	1	0	1	0	0	0	0	0	D3YZH5	
ENSMUST00000126601						0	0	0	0	0	0	5	0	0	0	0		
ENSMUST00000126602						2	2	0	1	2	1	0	5	0	0	0		
ENSMUST00000126603						5	5	13	12	14	9	0	103	20	0	30		
ENSMUST00000126604	ENSMUSG00000030452	7	55931287	55962476	-1	0	0	0	0	0	0	0	31	51	22	36	D3Z682	
ENSMUST00000126605						12	8	78	18	15	4	4	13	0	0	23		
ENSMUST00000126606						92	78	57	60	122	59	1	9	3	3	7		
ENSMUST00000126607	ENSMUSG00000089857	8	71908608	71916354	1	4	6	10	7	7	2	0	0	0	0	1	D3Z7G7	
ENSMUST00000126608						5	1	0	0	4	0	9	0	1	43	11		
ENSMUST00000126609						0	0	4	0	0	0	0	0	0	0	1		
ENSMUST00000126610	ENSMUSG00000038900	2	32961559	32965345	1	2	3	14	67	0	4	17	22	12	53	17	Q5BLK0	P35979
ENSMUST00000126611	ENSMUSG00000090077	2	181380078	181383628	1	0	0	0	0	0	0	88	238	2	63	25	F6QX71	
ENSMUST00000126612						4	0	10	1	1	0	0	0	0	0	0		
ENSMUST00000126613						0	0	3	14	0	2	0	0	0	0	0		
ENSMUST00000126614						0	8	0	5	18	0	17	55	17	16	69		
ENSMUST00000126615	ENSMUSG00000055401	4	148145716	148152140	-1	0	3	3	0	0	0	0	0	0	0	0	A2A7H1	
ENSMUST00000126616						0	0	0	0	0	0	2	0	0	0	6		
ENSMUST00000126617	ENSMUSG00000034591	10	83230848	83337882	-1	0	0	0	30	0	0	0	0	0	0	0	D3YWW0	
ENSMUST00000126618						64	38	30	39	46	6	59	309	93	6	174		
ENSMUST00000126619						14	11	10	7	10	4	53	191	111	6	141		
ENSMUST00000126620						4	1	6	4	1	4	5	64	5	5	32		
ENSMUST00000126621	ENSMUSG00000107071	6	39585753	39596595	1	0	0	0	0	0	0	0	30	0	6	10		
ENSMUST00000126623						2	0	0	0	0	0	0	15	0	0	6		
ENSMUST00000126624						0	0	0	1	0	0	0	0	0	0	1		
ENSMUST00000126625						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126626	ENSMUSG00000033569	1	25067476	25829707	-1	0	0	0	0	0	2	0	0	0	0	0	Q8BJ13	
ENSMUST00000126627						10	8	22	14	9	5	0	0	0	0	0		
ENSMUST00000126628	ENSMUSG00000048416	3	67374097	67400003	1	1	1	2	0	0	0	0	0	0	5	2	A0A0A6YVP7	
ENSMUST00000126629						2	3	0	0	2	0	0	0	0	0	2		
ENSMUST00000126630						1	0	10	0	4	0	0	0	0	0	0		
ENSMUST00000126631						1	0	2	0	0	2	0	0	0	0	3		
ENSMUST00000126632						0	1	0	0	1	1	3	0	11	0	17		
ENSMUST00000126633						0	1	0	1	0	0	0	4	0	9	0		
ENSMUST00000126634						0	7	20	0	11	4	1	0	12	0	15		
ENSMUST00000126636	ENSMUSG00000026811	2	32599709	32620806	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW64	
ENSMUST00000126637	ENSMUSG00000086040	6	54429603	54503768	1	0	6	0	221	23	18	0	0	0	0	0	D3Z5R4	
ENSMUST00000126638						5	6	14	7	3	6	1	0	2	2	1		
ENSMUST00000126639						0	0	0	10	0	0	1	9	9	21	13		
ENSMUST00000126641	ENSMUSG00000028676	4	135855747	135869908	1	14	8	13	12	7	7	54	138	25	16	39	Q3UA07	Q9R0U0
ENSMUST00000126643						142	169	307	177	172	80	20	118	46	16	88		
ENSMUST00000126644						0	0	2	0	1	0	0	0	10	0	0		
ENSMUST00000126645	ENSMUSG00000028712	4	115563649	115579015	1	0	0	0	0	0	0	0	0	0	0	0	A2A8S9	
ENSMUST00000126648						11	9	14	36	13	6	1	2	6	1	5		
ENSMUST00000126650						36	40	104	46	49	34	4	9	4	1	11		
ENSMUST00000126651						0	0	0	0	0	0	0	260	0	0	0		
ENSMUST00000126652						17	2	48	10	23	5	0	1	4	0	0		
ENSMUST00000126654						0	2	0	2	1	0	0	0	0	1	0		
ENSMUST00000126655						0	3	0	5	2	0	9	47	21	30	38		
ENSMUST00000126656	ENSMUSG00000044083	2	153780879	153844752	1	13	7	19	6	12	8	1	1	8	1	2	H3BL58	
ENSMUST00000126657						20	18	92	44	17	13	0	2	3	0	3		
ENSMUST00000126658	ENSMUSG00000074653	3	30679058	30699843	-1	8	1	13	4	8	4	0	0	0	0	0	F6VYM1	
ENSMUST00000126660	ENSMUSG00000020696	11	82802449	82871210	-1	4	0	18	4	8	4	5	2	0	0	3	B1AT06	
ENSMUST00000126661						3	0	1	4	2	1	13	4	15	2	2		
ENSMUST00000126662	ENSMUSG00000030804	7	127886227	127895454	-1	20	0	26	0	0	0	1	0	0	0	0	F6W3F3	
ENSMUST00000126663						9	3	10	2	12	2	9	73	30	48	12		
ENSMUST00000126666	ENSMUSG00000062210	18	49979427	50107173	1	3	7	0	4	9	4	0	5	4	6	0	D3Z312	
ENSMUST00000126670						10	7	13	71	14	5	0	0	3	0	0		
ENSMUST00000126671						2	2	12	3	0	0	9	49	39	3	62		
ENSMUST00000126673						8	3	18	2	8	6	0	0	0	0	0		
ENSMUST00000126674						4	0	5	9	4	4	12	32	22	8	25		
ENSMUST00000126675						6	6	4	4	6	0	22	26	23	0	47		
ENSMUST00000126676						11	10	34	14	7	3	7	37	16	0	15		
ENSMUST00000126678						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126680						1	2	0	1	1	1	0	5	1	5	3		
ENSMUST00000126681	ENSMUSG00000024052	17	71182560	71249817	1	10	5	9	0	8	4	0	0	79	0	14	E9PWN0	
ENSMUST00000126682						3	5	4	0	3	0	0	0	0	0	0		
ENSMUST00000126683						174	189	338	146	173	71	30	138	55	10	78		
ENSMUST00000126684	ENSMUSG00000019647	18	47235598	47368870	-1	0	0	0	0	0	0	0	0	0	0	0	D3YZJ8	
ENSMUST00000126685						1	3	1	2	1	4	0	0	0	0	0		
ENSMUST00000126686	ENSMUSG00000031309	X	159210307	159368244	1	0	0	1	49	0	0	5	9	13	1	9	B1AXN7	
ENSMUST00000126687						1	1	3	2	3	1	0	0	0	0	0		
ENSMUST00000126688						0	0	0	8	0	0	0	1	0	0	0		
ENSMUST00000126689						4	0	2	2	2	0	4	0	2	3	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126690	ENSMUSG00000036986	9	58218076	58249786	-1	0	6	0	0	0	0	0	3	0	0	0	F7BTZ2	
ENSMUST00000126691						0	0	0	24	10	0	0	0	23	43	6		
ENSMUST00000126692						6	2	19	3	0	4	0	351	0	0	13		
ENSMUST00000126694						29	24	78	38	27	29	76	188	109	7	134		
ENSMUST00000126695						0	1	4	4	2	1	0	0	0	0	0		
ENSMUST00000126697						2	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000126698	ENSMUSG00000030304	6	148179079	148212374	-1	0	0	0	0	0	0	3	0	33	51	2	B2KFC9	
ENSMUST00000126699	ENSMUSG00000052423	1	171270328	171276896	1	0	0	0	0	0	0	197	2042	138	54	0	A0A0A6YXE7	
ENSMUST00000126700						2	0	2	1	4	1	3	1	1	0	9		
ENSMUST00000126701						0	0	2	1	2	0	0	0	13	0	0		
ENSMUST00000126702						0	1	2	47	4	2	0	4	0	0	2		
ENSMUST00000126703	ENSMUSG00000020400	11	54910785	54962917	-1	0	2	2	8	3	0	59	33	64	4	41	D3Z3B6	
ENSMUST00000126704						0	0	0	0	0	1	0	10	3	0	0		
ENSMUST00000126705	ENSMUSG00000014856	8	105326354	105335219	1	4	2	7	5	3	2	19	168	50	41	44	S4R1H6	
ENSMUST00000126706	ENSMUSG00000028484	4	83455680	83486459	-1	0	0	0	0	0	1	0	0	0	0	0	F6W677	
ENSMUST00000126707	ENSMUSG00000028965	4	150914562	150946102	1	0	0	0	0	0	0	0	0	0	0	2	A2A888	
ENSMUST00000126708						2	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000126709						6	1	2	1	2	1	0	0	0	1	1		
ENSMUST00000126710	ENSMUSG00000024770	19	34067358	34084918	1	3	0	0	0	3	1	0	0	0	2	2	D3YVB0	
ENSMUST00000126713						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126714						0	0	0	0	0	0	0	0	0	0	5		
ENSMUST00000126715						4	5	14	46	9	8	2	4	4	0	16		
ENSMUST00000126716	ENSMUSG00000055436	3	158010473	158036639	-1	0	0	0	0	0	0	0	36	52	3	38	D6RE22	
ENSMUST00000126717	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	0	0	0	42	0	9	0	0	D3Z721	
ENSMUST00000126718						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000126720						0	0	0	8	0	1	0	2	3	0	0		
ENSMUST00000126721						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000126722						5	3	6	6	8	1	0	1	0	0	3		
ENSMUST00000126723						0	0	0	0	1	0	0	2	0	0	0		
ENSMUST00000126724						8	5	8	2	3	0	0	0	0	0	4		
ENSMUST00000126725						0	8	11	7	7	8	0	23	0	0	6		
ENSMUST00000126726	ENSMUSG00000078876	2	176831140	176836730	1	0	0	0	0	0	0	0	0	0	0	0	D3Z288	
ENSMUST00000126727						12	12	20	14	17	5	3	13	8	5	37		
ENSMUST00000126728						2	0	2	17	0	0	0	0	0	0	0		
ENSMUST00000126729						6	3	31	7	3	3	12	94	17	0	23		
ENSMUST00000126730						0	0	1	0	0	0	0	0	0	1	0		
ENSMUST00000126731	ENSMUSG00000020792	11	116288001	116307233	-1	1	0	3	14	8	0	59	33	89	2	56	A2AAN3	
ENSMUST00000126733						0	0	0	0	0	0	21	0	0	3	0		
ENSMUST00000126734						1	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000126736						7	1	8	0	16	2	5	15	7	4	10		
ENSMUST00000126737						4	7	0	0	7	9	227	0	0	0	0		
ENSMUST00000126738						0	0	0	23	2	1	4	2	6	5	18		
ENSMUST00000126739						98	90	134	420	119	50	92	149	206	12	154		
ENSMUST00000126740	ENSMUSG00000053552	2	130295169	130370481	1	23	0	0	0	0	0	0	0	0	0	0		Q8K4J2
ENSMUST00000126741	ENSMUSG00000055923	5	76873659	76905514	-1	0	0	0	0	0	0	7	0	0	3	0	E9PUI6	
ENSMUST00000126742						5	2	4	6	2	3	6	4	14	4	6		
ENSMUST00000126743						0	0	0	1	2	0	18	78	13	52	20		
ENSMUST00000126744	ENSMUSG00000024426	17	35897595	35910075	-1	0	0	1	0	0	4	0	49	13	2	11	F7BUT2	
ENSMUST00000126745						4	4	25	4	11	0	0	156	32	10	77		
ENSMUST00000126746	ENSMUSG00000023764	11	3131850	3193463	-1	0	0	6	0	0	0	0	0	0	37	0	F7CL63	
ENSMUST00000126747						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000126748						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000126749						5	3	15	2	9	1	0	0	0	0	0		
ENSMUST00000126750						0	2	2	11	2	0	0	0	5	0	3		
ENSMUST00000126751						0	0	0	0	0	0	0	459	0	150	0		
ENSMUST00000126752						4	3	0	1	5	0	0	0	0	0	1		
ENSMUST00000126753						0	0	0	3	6	0	6	9	0	0	5		
ENSMUST00000126754						8	5	22	20	7	2	0	0	0	0	0		
ENSMUST00000126755						854	706	1223	791	770	333	48	258	102	33	138		
ENSMUST00000126756	ENSMUSG00000045251	7	127418967	127422068	-1	0	0	0	0	0	0	9	18	11	8	5	F6QTX1	
ENSMUST00000126757						17	15	12	32	20	8	0	1	0	0	0		
ENSMUST00000126758						1	4	11	1	3	4	0	4	0	1	0		
ENSMUST00000126759						0	2	0	109	0	0	0	0	0	0	0		
ENSMUST00000126760						9	5	1	2	6	0	0	0	0	0	0		
ENSMUST00000126761	ENSMUSG00000042308	7	127776670	127800122	1	0	0	0	6	0	0	0	0	0	0	0	D3YX07	
ENSMUST00000126762						0	0	4	4	4	0	0	0	0	0	0		
ENSMUST00000126763	ENSMUSG00000008333	2	143063039	143072853	1	6	5	5	79	7	1	0	0	0	0	14	A2CES4	
ENSMUST00000126764	ENSMUSG00000027245	2	121453290	121458672	1	2	0	0	0	2	1	18	43	12	0	3		Q9CR41
ENSMUST00000126765						0	0	0	0	6	3	12	26	26	0	30		
ENSMUST00000126766	ENSMUSG00000020904	11	67924806	67965651	-1	15	2	7	5	8	4	0	0	0	0	0		Q5F201
ENSMUST00000126767						0	0	0	0	1	0	0	42	5	10	0		
ENSMUST00000126768						0	0	0	0	0	0	13	0	0	0	33		
ENSMUST00000126770	ENSMUSG00000016128	5	151037510	151233836	-1	0	0	0	98	7	4	0	0	0	0	0	D3Z5Y1	
ENSMUST00000126772						0	0	4	0	0	0	0	0	0	6	0		
ENSMUST00000126773						0	0	0	0	0	0	9	44	0	0	0		
ENSMUST00000126774						3	1	2	0	0	4	0	0	0	0	0		
ENSMUST00000126775						1	0	0	0	0	0	0	0	4	0	2		
ENSMUST00000126776						7	1	28	15	12	3	0	0	0	0	0		
ENSMUST00000126777						4	0	1	0	3	1	2	20	5	3	4		
ENSMUST00000126778	ENSMUSG00000075704	16	18426384	18479073	1	2	0	0	0	1	0	0	0	0	0	0	Q9D8I4	
ENSMUST00000126780						0	0	30	33	0	6	8	17	10	1	28		
ENSMUST00000126781	ENSMUSG00000039652	19	37021291	37208601	-1	7	4	5	122	3	0	0	0	0	0	0		Q7TN99
ENSMUST00000126782						0	0	4	0	0	0	0	0	9	0	0		
ENSMUST00000126784						2	0	2	6	3	1	0	1	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126785	ENSMUSG00000074895	13	54783998	54788459	1	0	0	0	0	0	0	0	0	0	0	0	E9PVZ9	
ENSMUST00000126786						4	3	12	71	8	5	22	42	20	3	28		
ENSMUST00000126787						10	10	19	11	11	4	23	88	30	49	233		
ENSMUST00000126788						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126790						8	2	6	28	10	4	0	2	2	2	0		
ENSMUST00000126791						5	1	0	76	4	3	2	0	0	0	0		
ENSMUST00000126792	ENSMUSG00000030980	7	118842222	118856254	-1	0	0	0	0	0	0	16	0	0	0	0	F6ZLH4	
ENSMUST00000126793						3	0	2	3	1	3	1	0	0	0	0		
ENSMUST00000126794	ENSMUSG00000030432	7	4792874	4795066	1	4	1	0	0	0	0	0	0	0	0	0	F6Z0X0	
ENSMUST00000126795	ENSMUSG00000025967	1	63176825	63180486	1	3	2	0	0	0	0	11	109	11	10	12	G3UZ47	
ENSMUST00000126796						26	11	78	42	26	7	2	5	5	1	18		
ENSMUST00000126797						9	1	0	6	3	0	0	0	0	0	0		
ENSMUST00000126799	ENSMUSG00000067220	5	72603696	72644275	-1	10	9	21	13	9	11	0	0	1	0	1	A0A0G2JG06	
ENSMUST00000126800	ENSMUSG00000016495	19	29348599	29367390	-1	5	2	1	33	0	1	0	18	6	10	10	D3YXU2	
ENSMUST00000126801						4	0	2	1	4	0	0	0	0	0	0		
ENSMUST00000126802						18	16	53	31	35	14	0	9	6	1	3		
ENSMUST00000126803						0	0	12	28	0	2	0	6	0	0	0		
ENSMUST00000126804						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000126805	ENSMUSG00000030008	6	85446810	85451970	-1	1	0	3	0	0	0	0	73	16	35	29		
ENSMUST00000126806	ENSMUSG00000001911	8	84699876	84800344	-1	4	0	11	13	8	2	0	0	0	0	0	D3YZ00	
ENSMUST00000126807						20	27	32	0	0	0	0	7	0	0	0		
ENSMUST00000126808						19	20	15	19	26	10	0	3	4	0	1		
ENSMUST00000126809						0	1	0	0	0	0	2	1	0	0	0		
ENSMUST00000126810						19	18	72	31	41	21	107	229	114	4	138		
ENSMUST00000126811	ENSMUSG00000079428	X	136214779	136226100	1	2	0	0	9	0	1	0	0	0	0	0	A3KGA3	
ENSMUST00000126812						4	0	6	0	1	3	0	0	0	0	0		
ENSMUST00000126813						24	14	46	27	17	13	2	0	8	0	17		
ENSMUST00000126814						0	0	1	2	2	1	0	0	2	0	8		
ENSMUST00000126815						0	0	0	0	0	0	0	0	4	15	26		
ENSMUST00000126816	ENSMUSG00000025432	10	127000709	127020994	1	0	1	0	1	3	0	0	1	0	0	3	D3YXP4	
ENSMUST00000126817						5	4	4	4	3	2	2	4	5	0	2		
ENSMUST00000126818						7	3	2	5	4	0	0	0	0	0	0		
ENSMUST00000126819						12	14	58	83	21	7	38	86	128	4	137		
ENSMUST00000126820						1	2	9	7	2	2	0	0	0	0	0		
ENSMUST00000126821						6	0	0	49	0	0	0	6	0	0	0		
ENSMUST00000126822						25	13	49	21	29	31	23	66	38	12	68		
ENSMUST00000126824	ENSMUSG00000027171	2	104830741	104849876	-1	5	4	7	116	6	3	0	0	1	0	0	A2A6Z6	
ENSMUST00000126825						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126827						2	3	6	18	4	0	4	59	18	1	20		
ENSMUST00000126828						0	2	0	4	2	0	0	0	0	0	0		
ENSMUST00000126829						2	2	10	2	0	1	4	0	0	0	0		
ENSMUST00000126830						8	2	6	0	1	1	5	8	4	0	1		
ENSMUST00000126831	ENSMUSG00000020096	10	61171954	61188841	1	8	8	21	17	10	7	0	0	0	0	0	F6RYN6	
ENSMUST00000126832						4	1	6	4	1	0	7	11	7	0	10		
ENSMUST00000126833						30	20	29	27	22	14	29	267	69	12	120		
ENSMUST00000126834	ENSMUSG00000032815	8	123268300	123318576	-1	10	2	6	0	1	1	0	0	0	2	0	D3Z403	
ENSMUST00000126835						0	0	0	0	0	5	0	6	5	0	3		
ENSMUST00000126836	ENSMUSG00000030201	6	134446476	134566965	-1	1	1	0	28	6	0	0	0	0	0	0		
ENSMUST00000126837	ENSMUSG00000057182	2	65457118	65567627	-1	0	0	0	0	2	0	0	0	0	0	0	F6U9Y2	
ENSMUST00000126838						7	0	11	3	9	5	0	0	0	0	0		
ENSMUST00000126839						23	21	0	143	50	0	863	599	794	27	930		
ENSMUST00000126840	ENSMUSG00000018906	11	54100095	54131665	1	0	0	0	0	0	0	0	0	0	0	0	B0QZH1	
ENSMUST00000126841						6	3	2	4	5	2	26	67	23	0	60		
ENSMUST00000126842						0	0	13	2	0	1	0	0	2	0	3		
ENSMUST00000126843						3	4	0	0	0	0	0	0	0	0	2		
ENSMUST00000126844						2	2	1	4	6	1	2	11	2	0	9		
ENSMUST00000126845						604	670	2153	521	695	316	4	45	15	9	32		
ENSMUST00000126846						5	0	6	2	5	0	0	0	0	0	4		
ENSMUST00000126848	ENSMUSG00000019803	10	42561963	42583632	-1	2	1	0	11	2	0	0	0	0	0	0	D3Z5B6	
ENSMUST00000126850						26	9	63	31	25	14	7	5	16	1	17		
ENSMUST00000126851						0	4	2	1	3	4	0	0	0	0	0		
ENSMUST00000126853						0	0	5	0	2	0	34	0	94	0	0		
ENSMUST00000126854	ENSMUSG00000022469	15	97744770	97767972	-1	0	0	53	122	14	19	0	0	5	0	17		Q8VCC8
ENSMUST00000126855	ENSMUSG00000040464	5	5537454	5559538	-1	0	1	0	0	2	0	0	0	0	0	0	F6WSS0	
ENSMUST00000126856	ENSMUSG00000029408	5	124061530	124095798	-1	0	0	5	0	0	1	0	0	0	1	0	D6RFD9	
ENSMUST00000126857						3	0	10	0	3	0	7	23	0	0	4		
ENSMUST00000126859						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126860						3	5	11	1	8	0	0	63	0	0	13		
ENSMUST00000126861						10	17	20	93	38	12	2	0	3	9	5		
ENSMUST00000126862						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126863						5	0	24	13	8	0	0	0	4	0	0		
ENSMUST00000126864						32	30	15	19	32	22	0	0	0	0	6		
ENSMUST00000126865	ENSMUSG00000034135	9	46012820	46224194	1	26	25	13	39	15	17	825	778	985	49	1094	E9PU87	
ENSMUST00000126866						0	0	1	2	0	1	0	0	0	0	0		
ENSMUST00000126867	ENSMUSG00000041594	14	122918971	122984035	-1	7	9	0	0	2	0	0	0	0	0	0		Q8BG19
ENSMUST00000126868						2	1	1	0	1	1	0	0	4	0	0		
ENSMUST00000126869	ENSMUSG00000052384	16	32142785	32165594	-1	1	3	11	3	7	3	302	381	278	0	414		Q8BMT4
ENSMUST00000126870						1	0	4	18	1	0	0	2	7	0	5		
ENSMUST00000126871						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000126872						2	0	4	0	0	2	0	0	3	0	3		
ENSMUST00000126873						0	0	0	1	3	1	0	13	0	2	0		
ENSMUST00000126874						0	0	25	7	15	0	0	10	0	0	0		
ENSMUST00000126875						3	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000126876						0	0	0	0	0	0	0	0	0	0	30		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126877						0	1	0	0	1	3	0	0	0	21	0		
ENSMUST00000126878						1	1	0	122	5	0	0	0	1	0	0		
ENSMUST00000126879	ENSMUSG00000021514	13	65278814	65304221	1	13	5	23	25	21	7	22	42	101	5	83	F8VQL6	
ENSMUST00000126880						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126881	ENSMUSG00000023805	17	5941280	6044290	1	6	9	11	2	5	0	0	9	0	0	11	F6U4I6	
ENSMUST00000126882						2	1	1	25	2	1	0	0	0	0	0		
ENSMUST00000126884						18	27	71	32	36	19	0	2	3	0	4		
ENSMUST00000126885	ENSMUSG00000003033	8	72240018	72257385	1	0	0	0	18	0	0	7	11	24	0	27	D3YZ71	
ENSMUST00000126887	ENSMUSG00000030562	7	87246096	87398710	1	0	4	2	0	0	0	0	0	0	0	0	S4R1R3	
ENSMUST00000126888						5	3	12	20	5	6	1	6	0	0	3		
ENSMUST00000126889						1	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000126890						3	0	13	6	12	0	0	0	0	0	0		
ENSMUST00000126892						50	38	489	74	35	12	0	1	0	0	0		
ENSMUST00000126893						9	13	27	56	22	11	208	486	436	28	580		
ENSMUST00000126894						0	0	0	31	2	0	0	2	5	0	0		
ENSMUST00000126895						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000126896	ENSMUSG00000028992	4	149467572	149485202	-1	0	1	0	0	1	0	1	0	0	0	0	B1AS01	
ENSMUST00000126897						9	6	4	12	4	3	0	7	9	8	12		
ENSMUST00000126898						0	7	2	1	4	0	0	0	0	0	0		
ENSMUST00000126899						3	3	1	2	11	2	0	0	0	2	1		
ENSMUST00000126900	ENSMUSG00000028601	4	108165437	108179308	1	0	0	0	0	0	0	0	0	0	0	0	F6VA02	
ENSMUST00000126901						3	5	10	4	3	5	7	13	16	2	17		
ENSMUST00000126903	ENSMUSG00000063450	12	75818134	76110926	1	3	0	0	0	0	3	3	0	6	0	0	D6RH38	
ENSMUST00000126904						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126905	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	0	0	0	25	0	0	24	F6VR53	
ENSMUST00000126907						6	0	3	0	0	2	32	201	0	0	0		
ENSMUST00000126908						1	0	4	39	0	0	33	160	59	20	57		
ENSMUST00000126909	ENSMUSG00000026975	2	24962400	24972163	1	0	0	0	0	0	0	30	0	0	4	18	A0A0A6YWH1	
ENSMUST00000126911	ENSMUSG00000032372	9	92275602	92297752	1	10	8	3	0	8	1	2	8	8	0	4	D3Z2S8	
ENSMUST00000126912						2	0	4	2	2	1	61	372	405	40	230		
ENSMUST00000126913						0	0	0	0	0	0	0	33	0	8	10		
ENSMUST00000126914	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	22	0	2	0	0	1	0	3	D3YUX4	
ENSMUST00000126915	ENSMUSG00000092544	8	69742862	69774886	-1	2	0	5	0	3	1	4	0	15	8	9	F7BDX4	
ENSMUST00000126916						3	0	0	4	3	1	0	0	3	0	2		
ENSMUST00000126917						65	63	210	55	37	21	0	4	4	5	9		
ENSMUST00000126918						2	3	5	10	2	2	3	43	7	0	0		
ENSMUST00000126919						4	3	8	7	6	6	0	0	0	0	0		
ENSMUST00000126920	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000126921						3	3	10	7	12	5	0	2	1	0	4		
ENSMUST00000126923	ENSMUSG00000033313	8	105264648	105269326	1	0	0	29	52	7	7	0	7	38	0	8	D6RGN0	
ENSMUST00000126924						1	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000126925	ENSMUSG00000057229	7	25619414	25625551	1	0	0	0	0	1	0	0	5	0	0	0		
ENSMUST00000126927	ENSMUSG00000059149	1	132022806	132068062	-1	0	2	14	2	0	4	0	0	2	1	2		Q6PDC8
ENSMUST00000126928						0	3	1	2	0	0	8	123	18	10	39		
ENSMUST00000126929						2	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000126930						0	2	2	1	2	2	0	0	0	1	0		
ENSMUST00000126931						1	1	5	46	7	1	0	0	0	0	0		
ENSMUST00000126932	ENSMUSG00000027520	1	63273265	63314576	1	0	0	0	3	0	0	0	0	0	0	0	B1AU71	
ENSMUST00000126933						2	1	10	1	0	0	0	13	0	4	0		
ENSMUST00000126934						1	1	0	2	0	2	118	138	154	11	159		
ENSMUST00000126935						0	2	21	6	9	9	0	0	0	0	0		
ENSMUST00000126937						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126938						2	0	4	3	2	2	1	0	0	0	6		
ENSMUST00000126939	ENSMUSG00000030244	6	142422613	142473109	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000126940						3	1	2	1	2	1	0	0	0	1	0		
ENSMUST00000126941						0	8	6	117	9	2	0	0	0	0	0		
ENSMUST00000126942						0	0	0	52	0	0	4	2	4	0	2		
ENSMUST00000126943	ENSMUSG00000021224	12	83794034	83921934	-1	1	1	1	47	0	0	0	3	11	6	16	D3Z7J1	
ENSMUST00000126945						1	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000126946						4	4	14	5	6	0	0	0	0	0	0		
ENSMUST00000126947						0	0	17	5	0	0	8	49	22	1	29		
ENSMUST00000126949	ENSMUSG00000038615	11	96817414	96829968	-1	0	0	0	13	0	0	0	0	0	0	0	A2A6D0	
ENSMUST00000126950						2	0	3	4	0	0	0	0	0	0	0		
ENSMUST00000126951						4	0	4	3	8	6	0	0	0	0	0		
ENSMUST00000126952						1	3	35	1	0	1	0	0	0	0	0		
ENSMUST00000126954						33	41	154	32	44	19	1	0	0	1	1		
ENSMUST00000126955	ENSMUSG00000023007	15	99295087	99317018	1	0	1	0	0	0	0	1	0	1	0	3	F6W479	
ENSMUST00000126956						3	0	1	2	3	1	0	0	0	0	0		
ENSMUST00000126957	ENSMUSG00000025451	13	119428601	119458218	1	0	0	0	0	0	0	0	25	20	25	15	F6Y616	
ENSMUST00000126960	ENSMUSG00000021596	13	76384535	77031810	1	5	7	8	1	6	2	136	379	186	329	137	E9PYR7	
ENSMUST00000126961						294	265	1660	1198	545	273	71	223	111	43	259		
ENSMUST00000126962	ENSMUSG00000036707	1	85793441	85851576	1	0	0	1	12	0	3	0	0	0	0	0	D3Z704	
ENSMUST00000126963						3	2	8	66	0	1	0	0	0	0	0		
ENSMUST00000126964	ENSMUSG00000025083	19	56912361	57008228	-1	0	0	5	0	0	2	0	0	0	1	0	D3YZD3	
ENSMUST00000126968	ENSMUSG00000035649	4	44755877	44932215	1	0	0	12	3	0	0	6	8	23	1	0	F7CLJ4	
ENSMUST00000126969	ENSMUSG00000052915	11	98795516	98807859	1	0	0	2	0	1	0	179	335	203	30	273	F7CR37	
ENSMUST00000126970						78	57	132	186	80	31	10	23	9	1	11		
ENSMUST00000126971						1	1	10	35	5	2	0	0	0	0	0		
ENSMUST00000126972						0	0	0	0	0	0	17	46	16	0	0		
ENSMUST00000126973						1	0	10	13	0	3	0	0	0	2	0		
ENSMUST00000126974						5	5	2	1	2	3	2	1	5	2	4		
ENSMUST00000126975						30	27	109	40	38	25	0	5	4	0	2		
ENSMUST00000126976	ENSMUSG00000029082	5	43818885	43843986	1	6	1	14	1	5	0	118	66	290	220	345	A0A0G2JG11	
ENSMUST00000126977	ENSMUSG00000024236	18	4920540	5119299	1	4	0	0	40	0	0	245	320	961	57	651		Q8K4L3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000126978	ENSMUSG00000022747	16	58468125	58524243	-1	0	0	0	0	2	0	0	0	0	0	0	A6X952	
ENSMUST00000126979	ENSMUSG00000036923	10	62659043	62726128	-1	5	7	20	8	6	5	0	0	0	0	0	F6YZ72	
ENSMUST00000126980	ENSMUSG00000003344	10	80642617	80657071	-1	0	0	0	0	0	5	310	243	156	11	141	E9PY28	
ENSMUST00000126981	ENSMUSG00000029319	5	100654723	100675140	-1	0	0	0	2	0	0	0	0	0	0	0	D6RGA8	
ENSMUST00000126982						5	5	278	419	19	5	0	0	0	0	7		
ENSMUST00000126983						21	24	65	34	23	24	5	13	4	0	19		
ENSMUST00000126984						2	3	8	2	2	0	3	6	6	0	5		
ENSMUST00000126985						0	3	1	0	1	0	0	0	0	0	0		
ENSMUST00000126986						9	10	85	18	12	3	249	838	267	117	413		
ENSMUST00000126987						7	2	21	6	6	2	2	0	0	4	0		
ENSMUST00000126989						9	7	21	26	12	10	0	3	9	0	3		
ENSMUST00000126990						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000126991						0	0	0	0	3	2	0	0	0	0	0		
ENSMUST00000126992	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	0	0	0	2	9	71	88	85	110	B7ZD61	
ENSMUST00000126993						0	8	27	16	17	0	3	2	0	1	3		
ENSMUST00000126994						4	0	0	7	1	1	0	0	0	0	0		
ENSMUST00000126995	ENSMUSG00000046093	4	123183227	123194701	1	0	0	0	0	0	0	0	0	0	0	0	F2Z450	
ENSMUST00000126996						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000126998						3	0	1	0	4	4	0	0	1	0	1		
ENSMUST00000127000	ENSMUSG00000022094	14	70303469	70351425	-1	2	0	0	35	0	1	1	0	0	0	2	D3Z354	
ENSMUST00000127002						0	0	0	0	0	0	0	0	0	0	21		
ENSMUST00000127003	ENSMUSG00000056260	3	106684987	106736577	1	0	0	0	2	3	0	0	0	22	0	0		Q8CDD9
ENSMUST00000127004						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127005						3	6	0	0	9	13	8	40	11	0	6		
ENSMUST00000127007						3	2	3	2	3	1	0	0	6	0	0		
ENSMUST00000127008						3	1	5	0	2	2	0	0	0	0	0		
ENSMUST00000127009						41	42	32	33	45	19	1	6	0	1	12		
ENSMUST00000127011						0	0	0	23	2	2	39	77	37	15	33		
ENSMUST00000127012						2	0	0	0	1	0	0	0	0	1	0		
ENSMUST00000127013						0	0	0	0	1	0	0	0	0	0	1		
ENSMUST00000127014	ENSMUSG00000001281	15	102215995	102231935	-1	0	1	15	0	3	1	2	2	2	0	7	D3Z0L2	
ENSMUST00000127016						0	1	4	19	6	1	2	1	2	0	6		
ENSMUST00000127018						2	0	0	0	1	0	1	1	0	0	2		
ENSMUST00000127019						5	0	2	1	0	0	24	41	0	46	55		
ENSMUST00000127021	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	37	0	0	0	0	D3YZP1	
ENSMUST00000127022						1	2	2	0	2	1	0	5	4	0	2		
ENSMUST00000127023	ENSMUSG00000031402	X	75109733	75131016	-1	0	0	0	1	0	0	10	8	21	11	16	D6RFD5	
ENSMUST00000127024						5	5	5	7	10	10	0	0	0	0	0		
ENSMUST00000127026						0	0	9	0	0	0	0	0	0	0	0		
ENSMUST00000127027	ENSMUSG00000096696	17	17064113	17089628	1	12	12	17	16	6	4	0	117	19	11	10	L7N267	
ENSMUST00000127028						2	0	2	1	11	0	13	37	21	0	74		
ENSMUST00000127029						0	0	0	0	0	3	4	7	3	5	2		
ENSMUST00000127030						3	4	27	15	10	4	0	35	8	3	34		
ENSMUST00000127031						27	33	44	62	32	32	6	27	13	0	13		
ENSMUST00000127032	ENSMUSG00000038347	17	13482553	13761825	-1	9	10	0	0	0	1	0	0	0	0	0	D3YY45	
ENSMUST00000127033	ENSMUSG00000038366	11	97799000	97838764	1	0	0	0	1	0	1	0	1	0	1	0	E9Q0N6	
ENSMUST00000127034						0	2	4	1	2	1	0	0	0	0	0		
ENSMUST00000127035						5	3	16	173	20	8	0	0	0	0	0		
ENSMUST00000127036						196	145	103	146	256	141	246	162	1438	71	1104		
ENSMUST00000127037						0	3	2	0	0	2	3	9	0	0	0		
ENSMUST00000127038	ENSMUSG00000035399	2	163405822	163424697	-1	0	0	0	0	0	0	0	0	0	2	0	A2A478	
ENSMUST00000127039						0	4	0	12	5	0	0	0	0	0	1		
ENSMUST00000127041						2	2	5	1	3	0	0	0	0	0	0		
ENSMUST00000127042						6	1	0	0	5	1	9	0	1	16	0		
ENSMUST00000127043						0	0	0	0	0	0	0	13	4	0	0		
ENSMUST00000127044						2	1	5	4	0	0	0	0	2	3	0		
ENSMUST00000127045	ENSMUSG00000036817	5	139200637	139249840	1	0	0	0	0	1	0	0	0	0	0	0	D3Z0L7	
ENSMUST00000127046						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000127047	ENSMUSG00000028655	4	122946850	122961188	-1	0	8	3	123	4	0	0	0	0	0	0	B1ARS3	
ENSMUST00000127048	ENSMUSG00000018669	11	96907426	96916496	-1	1	0	2	91	7	0	15	8	7	2	13	B0QZI8	
ENSMUST00000127050						5	5	5	73	6	3	0	1	3	0	2		
ENSMUST00000127051						3	3	10	101	11	6	0	1	0	0	1		
ENSMUST00000127052	ENSMUSG00000037995	1	172481788	172498878	1	0	1	0	1	2	0	0	0	0	0	0	D3YZD2	
ENSMUST00000127053						9	3	18	13	11	4	0	0	0	0	0		
ENSMUST00000127054	ENSMUSG00000033880	11	118392751	118402092	-1	1	1	2	0	3	1	2	1	1	0	1		
ENSMUST00000127055						5	5	4	2	2	4	0	0	0	0	0		
ENSMUST00000127056						0	1	0	0	0	0	21	88	19	0	38		
ENSMUST00000127057						59	48	53	187	35	32	0	26	9	22	20		
ENSMUST00000127058	ENSMUSG00000041237	3	89136142	89146784	1	3	0	0	0	4	0	0	0	0	0	0	D3Z2C4	
ENSMUST00000127059						19	17	1	0	7	8	0	0	0	0	0		
ENSMUST00000127061	ENSMUSG00000020718	11	106768253	106779537	-1	0	2	7	49	7	0	5	23	7	0	33	D6REU1	
ENSMUST00000127062	ENSMUSG00000031166	X	8123301	8132892	-1	0	0	0	0	0	0	0	0	0	0	0	S4R258	
ENSMUST00000127063						3	2	2	11	2	0	1	0	3	0	0		
ENSMUST00000127064						3	0	1	126	0	1	0	0	0	0	0		
ENSMUST00000127065	ENSMUSG00000036026	17	45660171	45686905	-1	3	0	0	36	0	0	0	0	0	0	0	D3YYJ8	
ENSMUST00000127066						1	3	6	3	3	1	0	0	0	0	0		
ENSMUST00000127067						1	0	0	1	0	0	3	0	2	6	9		
ENSMUST00000127068						0	4	2	5	4	1	1	0	3	0	0		
ENSMUST00000127069						1	1	0	0	5	5	0	0	0	0	0		
ENSMUST00000127071						6	4	10	187	16	6	0	49	9	31	0		
ENSMUST00000127072						2	4	10	99	10	5	0	2	0	0	0		
ENSMUST00000127073						0	1	3	0	1	3	0	0	0	0	0		
ENSMUST00000127075						0	0	1	6	1	0	1	0	0	0	0		
ENSMUST00000127076						2	4	3	4	4	0	0	0	0	0	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127077	ENSMUSG00000026609	1	188262023	188965041	1	3	4	0	0	0	0	0	0	0	0	0	F6TQ19	
ENSMUST00000127078						0	0	0	0	0	2	0	0	5	0	0		
ENSMUST00000127079						0	0	1	39	0	3	0	0	32	12	34		
ENSMUST00000127080	ENSMUSG00000050106	11	117782076	117793110	1	4	4	10	67	2	0	0	3	0	0	6	B1ATB9	
ENSMUST00000127081						0	0	4	236	3	2	6	8	11	0	24		
ENSMUST00000127082						0	0	0	57	0	8	315	8	464	2	386		
ENSMUST00000127083						6	5	27	27	14	2	0	0	0	0	0		
ENSMUST00000127084						8	0	3	0	9	0	64	118	19	97	3		
ENSMUST00000127085						0	0	0	2	3	0	11	19	55	4	37		
ENSMUST00000127086						2	4	7	6	2	1	0	0	0	0	0		
ENSMUST00000127087						2	3	0	5	0	1	0	0	3	0	0		
ENSMUST00000127088						5	5	35	0	11	2	0	0	0	4	0		
ENSMUST00000127089						19	17	20	23	19	16	4	24	7	2	19		
ENSMUST00000127090						58	47	94	68	63	24	40	134	126	4	232		
ENSMUST00000127091	ENSMUSG00000030849	7	130162451	133123350	-1	4	2	2	1	3	2	0	0	0	1	0	F7BDU9	
ENSMUST00000127092						1	1	0	13	0	1	0	0	0	0	0		
ENSMUST00000127093						8	0	4	4	6	0	0	8	3	0	8		
ENSMUST00000127094						1	0	1	0	2	2	30	78	24	5	32		
ENSMUST00000127095	ENSMUSG00000022577	15	75551268	75567255	-1	0	1	4	71	11	7	0	0	0	0	0	Q8K356	
ENSMUST00000127096	ENSMUSG00000005514	5	135670033	135735326	1	1	1	4	3	1	3	1	3	7	0	11	F6R7H8	
ENSMUST00000127097	ENSMUSG00000085795	8	26977336	26981461	1	13	19	37	755	43	21	63	40	47	0	83	E9PXD8	
ENSMUST00000127098						1	2	10	9	4	3	0	0	0	0	0		
ENSMUST00000127099						0	0	3	0	0	0	20	119	7	14	10		
ENSMUST00000127100	ENSMUSG00000004846	5	136987019	136996648	1	6	3	16	2	11	3	37	144	52	10	75	F6W3Q8	
ENSMUST00000127101						2	2	39	0	13	1	0	5	6	2	8		
ENSMUST00000127102						2	1	2	3	4	6	0	0	0	0	1		
ENSMUST00000127103	ENSMUSG00000031170	X	8271133	8280179	1	0	0	0	1	0	0	0	0	0	0	0	A2ALH6	
ENSMUST00000127104						0	0	0	5	2	5	0	0	0	0	0		
ENSMUST00000127105	ENSMUSG00000030352	6	127961396	128143594	-1	3	1	3	4	1	8	0	0	0	0	0	D3YU98	
ENSMUST00000127106	ENSMUSG00000035596	7	3677789	3693523	-1	0	0	65	0	0	4	3815	7809	3533	385	2402	D6RHB6	
ENSMUST00000127109						2	3	1	1	2	3	0	0	0	0	0		
ENSMUST00000127110						0	3	9	1	6	2	2	2	0	0	4		
ENSMUST00000127111						0	0	3	0	5	0	0	0	1	0	0		
ENSMUST00000127112						4	0	0	18	0	4	0	0	0	0	0		
ENSMUST00000127113						1	2	13	3	6	7	23	82	173	43	133		
ENSMUST00000127114						4	1	4	2	12	4	17	44	23	5	73		
ENSMUST00000127116	ENSMUSG00000025817	2	5845019	5871895	1	0	0	0	0	0	0	0	0	12	78	14	A2ATT5	
ENSMUST00000127118						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127119						1	1	8	11	0	4	4	0	0	0	0		
ENSMUST00000127120						0	2	6	123	6	2	0	1	1	0	3		
ENSMUST00000127121						10	5	4	6	12	8	5	13	7	22	38		
ENSMUST00000127122	ENSMUSG00000036053	2	52857860	53134202	1	0	0	0	2	3	5	18	32	0	11	43	F6XR20	
ENSMUST00000127123						8	1	14	2	2	4	64	218	123	50	176		
ENSMUST00000127124						4	3	12	5	2	4	0	2	0	0	2		
ENSMUST00000127125						2	3	11	0	0	1	12	24	17	0	18		
ENSMUST00000127126						3	0	9	3	2	1	0	0	0	0	0		
ENSMUST00000127128	ENSMUSG00000030726	7	100082111	100121565	-1	0	1	0	0	0	0	13	0	27	124	1	D6RG54	
ENSMUST00000127130	ENSMUSG00000058925	18	57533780	57731065	1	0	3	0	3	3	2	0	0	0	0	0	F6ZQZ7	
ENSMUST00000127131						105	118	289	178	150	64	25	76	56	8	61		
ENSMUST00000127132						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127133						4	0	13	0	5	0	7	8	12	2	9		
ENSMUST00000127134	ENSMUSG00000061815	1	74125541	74148223	1	6	0	0	0	0	4	363	610	566	157	642		Q3TYX8
ENSMUST00000127135	ENSMUSG00000029167	5	51454250	51567726	-1	1	2	0	2	2	0	0	0	0	0	0	D3YZS8	
ENSMUST00000127136	ENSMUSG00000020392	11	51967661	51977334	1	2	3	0	2	3	5	0	0	3	3	0	F6XNW8	
ENSMUST00000127137	ENSMUSG00000069171	13	78188973	78199757	-1	0	0	6	32	6	0	0	0	0	0	0	B8JJI9	
ENSMUST00000127138						6	10	0	4	9	8	0	0	0	0	0		
ENSMUST00000127139						1	2	5	1	2	0	4	0	2	0	0		
ENSMUST00000127140						27	9	183	0	26	0	32	0	0	0	10		
ENSMUST00000127141	ENSMUSG00000026275	1	93342854	93373489	1	0	2	5	2	4	3	0	8	18	39	15	F6TGJ2	
ENSMUST00000127142	ENSMUSG00000024905	19	3388857	3407823	1	9	6	0	6	3	2	3	19	6	3	2		Q9WTJ6
ENSMUST00000127143						0	1	0	0	1	0	0	0	0	3	0		
ENSMUST00000127144	ENSMUSG00000023911	17	23776916	23786081	-1	7	0	22	15	11	12	0	0	0	0	0	D6RJ61	
ENSMUST00000127145						5	1	22	6	4	2	0	0	0	0	0		
ENSMUST00000127146	ENSMUSG00000030177	6	120324323	120364374	-1	0	0	0	0	14	0	0	31	0	19	20	D6RHN3	
ENSMUST00000127148	ENSMUSG00000037936	5	125277087	125341094	-1	2	0	6	0	0	2	48	108	4	0	28	F7C5U2	
ENSMUST00000127149						0	3	2	0	5	0	0	0	0	0	0		
ENSMUST00000127151						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127152	ENSMUSG00000029994	6	86736840	86793584	-1	80	40	65	173	76	60	41	166	63	17	88	S4R1F2	
ENSMUST00000127153	ENSMUSG00000042104	14	118985039	119099430	-1	8	3	0	0	1	1	0	0	0	0	0	F6YNY8	
ENSMUST00000127154						7	2	0	15	4	2	2	3	0	0	2		
ENSMUST00000127155						6	5	52	16	2	0	6	22	10	2	27		
ENSMUST00000127156						3	1	9	0	3	0	33	15	0	0	24		
ENSMUST00000127157	ENSMUSG00000048997	3	108202222	108210934	-1	9	5	11	10	9	6	10	12	3	0	15	A2AE44	
ENSMUST00000127158						8	0	2	0	4	6	0	2	0	4	0		
ENSMUST00000127159						6	8	18	9	7	7	0	0	1	0	4		
ENSMUST00000127161						0	0	0	2	0	0	4	142	15	0	40		
ENSMUST00000127162						19	27	62	112	40	22	33	99	50	3	91		
ENSMUST00000127163						0	0	0	0	0	3	0	45	0	0	0		
ENSMUST00000127164						5	2	12	18	1	0	0	0	0	0	0		
ENSMUST00000127165						11	2	21	7	8	4	14	32	15	2	27		
ENSMUST00000127167						25	38	38	85	41	11	43	65	41	11	24		
ENSMUST00000127168						12	9	16	168	8	11	0	13	2	0	5		
ENSMUST00000127170						0	2	0	0	1	0	0	86	0	0	11		
ENSMUST00000127171						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127172						2	1	0	14	6	1	0	0	0	0	0		
ENSMUST00000127173						12	0	53	0	52	10	0	0	0	0	2		
ENSMUST00000127175						4	5	7	2	5	1	8	47	8	16	19		
ENSMUST00000127176						9	2	9	16	6	1	7	21	20	21	4		
ENSMUST00000127178						0	2	0	0	0	0	1	8	7	0	4		
ENSMUST00000127179						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000127181						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000127182						2	1	0	0	4	0	0	0	3	0	2		
ENSMUST00000127183						0	3	0	1	4	0	0	0	0	0	0		
ENSMUST00000127184	ENSMUSG00000037736	5	66745827	67057158	1	0	0	0	0	0	0	0	0	0	0	0	D3YV55	
ENSMUST00000127185	ENSMUSG00000020566	12	17284721	17329359	-1	0	0	1	29	0	0	0	0	1	1	0	D3YZX0	
ENSMUST00000127186	ENSMUSG00000072553	11	89073841	89093040	1	2	2	9	3	4	0	0	0	0	0	0	A7M7S0	
ENSMUST00000127187						27	15	35	203	36	24	0	1	5	0	1		
ENSMUST00000127188	ENSMUSG00000084845	4	155734800	155740564	1	0	0	0	63	0	0	0	0	0	2	0		B2RWJ3
ENSMUST00000127189						0	1	0	0	2	0	18	68	31	7	48		
ENSMUST00000127190	ENSMUSG00000032344	9	78430526	78443237	-1	0	0	0	0	5	0	11	0	0	8	0	F6ZBV6	
ENSMUST00000127191	ENSMUSG00000009575	15	103191544	103239816	-1	0	0	0	4	0	0	0	0	0	2	1	D3Z0U2	
ENSMUST00000127192						3	5	6	4	0	0	0	0	0	1	0		
ENSMUST00000127193						2	0	5	2	2	0	0	0	0	0	3		
ENSMUST00000127194	ENSMUSG00000028958	5	24445458	24447854	-1	0	0	0	0	0	0	0	0	1	0	11	D3Z108	
ENSMUST00000127195	ENSMUSG00000025878	13	55027880	55100300	-1	1	0	0	5	1	0	0	0	0	0	0	E9Q577	
ENSMUST00000127196						2	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000127197						0	3	5	16	11	0	0	4	0	0	27		
ENSMUST00000127198						1	3	5	0	3	0	0	3	0	0	9		
ENSMUST00000127199						6	3	2	8	2	3	0	0	0	0	0		
ENSMUST00000127200						16	5	44	24	12	9	0	0	0	0	2		
ENSMUST00000127201	ENSMUSG00000035877	2	160748708	160872998	-1	0	0	0	7	0	0	0	0	0	0	0	F6V503	
ENSMUST00000127202						1	4	3	4	1	2	0	0	0	0	0		
ENSMUST00000127203						2	2	3	0	5	2	0	0	2	0	0		
ENSMUST00000127204	ENSMUSG00000021884	14	31552905	31641286	-1	0	1	0	0	0	0	35	79	23	48	19	D3YZ54	
ENSMUST00000127205						11	8	28	199	15	15	0	0	0	0	0		
ENSMUST00000127206	ENSMUSG00000026360	1	143999338	144004161	-1	17	16	45	34	14	12	1848	21222	2406	8367	1927		O08849
ENSMUST00000127207						5	4	3	1	4	1	0	31	21	2	35		
ENSMUST00000127208	ENSMUSG00000033728	15	76710623	76717699	1	44	45	154	52	47	22	20	42	25	0	13		Q8VC16
ENSMUST00000127209						1	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000127210	ENSMUSG00000054808	7	28893248	28962340	-1	0	0	0	66	7	0	0	0	106	0	111	E9Q2W9	
ENSMUST00000127211						85	98	180	86	81	60	14	38	24	34	42		
ENSMUST00000127212						49	47	284	89	73	34	1	4	2	0	11		
ENSMUST00000127213						2	1	4	18	0	2	7	6	1	0	5		
ENSMUST00000127214						59	36	103	79	80	24	0	0	0	0	0		
ENSMUST00000127215						1	1	10	0	4	3	13	94	17	44	19		
ENSMUST00000127217						54	47	127	62	66	26	1	2	3	1	2		
ENSMUST00000127219						0	0	0	1	0	0	0	0	0	1	0		
ENSMUST00000127220	ENSMUSG00000029469	5	122550204	122614518	-1	0	0	0	29	8	6	0	0	0	0	0	D3Z5A8	
ENSMUST00000127221	ENSMUSG00000031229	X	105797615	105929403	-1	0	0	0	0	0	0	0	0	3	0	0	A0A0G2JGR1	
ENSMUST00000127222						0	3	0	0	1	0	9	28	2	0	16		
ENSMUST00000127223						0	0	2	0	2	1	34	118	39	13	86		
ENSMUST00000127226	ENSMUSG00000038178	11	75531694	75577575	1	0	0	0	5	1	0	4	0	9	0	0	Q5ND23	
ENSMUST00000127227	ENSMUSG00000025572	11	117765988	117782198	-1	1	3	0	47	6	1	5	2	3	0	4	A0A0G2JDA0	
ENSMUST00000127228						2	3	1	1	2	2	3	39	32	3	20		
ENSMUST00000127229						4	2	10	6	2	0	0	0	0	0	0		
ENSMUST00000127231						6	3	5	1	7	5	1	6	0	0	4		
ENSMUST00000127232						1	1	4	1	2	3	6	36	13	0	18		
ENSMUST00000127233	ENSMUSG00000024985	19	55741810	55933654	1	0	0	0	0	0	0	0	0	0	0	0	F6WPX2	
ENSMUST00000127234	ENSMUSG00000024571	18	80206765	80212741	1	3	6	0	15	11	1	19	102	55	0	0	Q9CQX6	
ENSMUST00000127235						2	0	0	3	5	0	0	0	0	0	0		
ENSMUST00000127236						1	4	3	0	0	0	0	0	0	0	8		
ENSMUST00000127238						23	19	42	24	41	17	82	651	231	16	318		
ENSMUST00000127239						2	4	6	113	13	0	3	23	5	3	4		
ENSMUST00000127240	ENSMUSG00000003363	7	27532000	27553218	-1	2	0	0	52	0	4	6	0	0	0	8	D3YY25	
ENSMUST00000127241						6	5	12	5	6	1	3	17	11	0	10		
ENSMUST00000127242	ENSMUSG00000026979	2	24367580	24414954	1	4	1	0	2	4	2	13	10	24	0	13	A0A0A6YX36	
ENSMUST00000127243	ENSMUSG00000005233	2	69193895	69206194	-1	0	3	0	0	0	0	15	18	0	0	0	A2AUT4	
ENSMUST00000127244						1	3	0	1	1	0	5	8	9	3	6		
ENSMUST00000127245						4	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000127246						3	3	16	7	3	3	3	8	3	0	1		
ENSMUST00000127247	ENSMUSG00000048022	6	24951141	24956297	-1	10	14	63	313	21	23	2	3	4	0	5		B9EJI9
ENSMUST00000127248						3	7	10	60	8	3	19	126	82	0	95		
ENSMUST00000127249						2	0	5	4	9	5	2	0	2	1	0		
ENSMUST00000127250	ENSMUSG00000026491	1	179744894	179803680	-1	5	0	3	1	1	0	3	27	10	4	21	F6XUM6	
ENSMUST00000127251						12	18	3	0	0	39	2	0	0	0	0		
ENSMUST00000127252						6	8	6	0	0	0	861	1622	852	309	996		
ENSMUST00000127253						1179	1332	12166	1572	1466	744	10	36	22	0	25		
ENSMUST00000127254						0	11	9	16	12	7	6	10	0	5	23		
ENSMUST00000127255	ENSMUSG00000033526	2	121310561	121355396	-1	5	0	0	1	3	2	0	5	1	0	3	F6VID9	
ENSMUST00000127259						6	3	12	1	0	8	0	0	0	0	0		
ENSMUST00000127260	ENSMUSG00000024513	18	70568189	70626131	1	0	2	6	0	2	4	260	1865	1050	574	631	F6UPR7	
ENSMUST00000127261						16	5	2	7	14	5	0	0	0	0	0		
ENSMUST00000127262						2	0	0	2	1	1	0	1	11	0	13		
ENSMUST00000127264	ENSMUSG00000038119	9	35421128	35507652	1	0	0	0	0	0	1	0	0	0	0	3	F6SDC3	
ENSMUST00000127265						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127266						4	3	5	5	6	0	0	0	0	0	3		
ENSMUST00000127267						0	3	0	1	3	3	0	0	0	0	0		
ENSMUST00000127268	ENSMUSG00000048120	19	40612366	40741602	1	0	0	0	0	0	0	46	262	188	0	111	F7B9M9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127269	ENSMUSG00000025142	11	120672973	120709447	1	0	0	19	25	0	0	2	0	0	3	0	A2AC00	
ENSMUST00000127270						0	0	3	0	5	4	6	33	0	16	24		
ENSMUST00000127271						9	9	10	21	18	4	0	1	0	0	0		
ENSMUST00000127272						2	0	16	0	0	0	0	0	1	0	2		
ENSMUST00000127273	ENSMUSG00000039936	4	149649168	149702571	-1	0	0	3	0	0	0	0	0	0	0	0	B1AS25	
ENSMUST00000127274	ENSMUSG00000004267	6	124760053	124769673	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127275						1	1	0	1	1	0	4	9	7	2	9		
ENSMUST00000127276						0	0	0	13	0	2	3	7	4	0	0		
ENSMUST00000127277						34	30	240	28	20	14	9	16	3	6	16		
ENSMUST00000127278	ENSMUSG00000029233	5	76140271	76155504	1	0	0	0	0	0	0	14	7	19	2	6	H9KV08	
ENSMUST00000127279	ENSMUSG00000028832	4	134468320	134473843	1	0	0	3	0	0	0	4	0	0	0	0	D3Z1Z8	
ENSMUST00000127280						18	22	27	21	17	8	0	0	0	0	4		
ENSMUST00000127281	ENSMUSG00000021287	12	111803192	111813873	-1	101	90	561	184	88	52	17	0	21	0	28	Q80W51	
ENSMUST00000127282						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127283						1	0	0	1	0	3	19	735	25	12	21		
ENSMUST00000127285						1	0	0	0	0	0	11	15	11	1	30		
ENSMUST00000127286						0	1	0	0	0	0	0	26	0	0	0		
ENSMUST00000127287						1	0	1	94	4	0	11	19	7	2	10		
ENSMUST00000127288	ENSMUSG00000036553	5	35697180	35739987	-1	0	10	0	0	0	0	76	129	10	0	0	F6UWL1	
ENSMUST00000127289	ENSMUSG00000027014	2	77881159	77946375	-1	2	2	0	38	1	2	2	0	0	0	0	B1AYU8	
ENSMUST00000127291	ENSMUSG00000037907	11	77470485	77489678	-1	0	0	0	0	0	0	0	0	1	0	0	F6XU77	
ENSMUST00000127292						3	5	0	30	0	2	0	472	14	0	22		
ENSMUST00000127293						6	1	2	9	7	3	0	2	6	0	8		
ENSMUST00000127294						0	0	0	6	0	0	0	4	0	0	2		
ENSMUST00000127295						20	21	98	288	43	24	0	0	0	0	2		
ENSMUST00000127296	ENSMUSG00000035919	9	22475715	22888280	1	4	0	0	0	7	2	6	35	7	0	0	D6RIM6	
ENSMUST00000127297	ENSMUSG00000024236	18	4920540	5119299	1	13	2	35	0	0	0	0	18	163	0	573	E9Q3Z5	
ENSMUST00000127298	ENSMUSG00000030890	7	105736592	105742925	1	0	0	0	0	0	0	50	126	69	10	0	F6Q5Z1	
ENSMUST00000127300						1	0	6	9	4	1	640	2341	1186	2995	889		
ENSMUST00000127302						7	3	20	7	10	6	4	3	2	0	13		
ENSMUST00000127303						68	60	394	110	54	29	0	0	2	0	1		
ENSMUST00000127304						5	4	6	9	9	5	7	8	7	56	111		
ENSMUST00000127305	ENSMUSG00000010080	11	94489599	94499974	-1	31	29	66	162	42	28	1	3	0	1	3		Q91W69
ENSMUST00000127306	ENSMUSG00000028445	4	41638144	41640324	-1	7	6	32	66	15	10	0	7	4	5	2		Q8K1D8
ENSMUST00000127308						0	1	18	58	8	7	0	8	0	0	24		
ENSMUST00000127309						7	0	12	10	11	7	0	1	0	0	0		
ENSMUST00000127310	ENSMUSG00000036817	5	139200637	139249840	1	0	4	0	4	0	1	0	0	0	0	1	F7AJ01	
ENSMUST00000127311						2	0	4	1	0	0	0	0	0	0	3		
ENSMUST00000127312						10	3	22	4	8	4	70	95	109	14	137		
ENSMUST00000127313						3	3	11	65	5	3	0	1	1	0	2		
ENSMUST00000127314						0	1	1	62	4	2	0	2	1	0	0		
ENSMUST00000127315						1	0	0	0	2	3	0	0	0	0	0		
ENSMUST00000127316	ENSMUSG00000055371	2	52691664	52742281	-1	8	1	2	52	0	4	51	118	129	168	102		O88811
ENSMUST00000127318						8	4	2	0	1	6	0	0	0	0	0		
ENSMUST00000127319						2	1	16	1	3	2	0	0	0	0	0		
ENSMUST00000127320	ENSMUSG00000055235	5	24711738	24730727	-1	0	0	0	0	0	0	0	0	0	0	1	F6RAR9	
ENSMUST00000127321	ENSMUSG00000026792	2	32925216	32961614	-1	1	0	1	3	0	0	0	0	6	3	2	A2AHX6	
ENSMUST00000127322						0	0	1	0	0	0	0	0	0	1	6		
ENSMUST00000127323	ENSMUSG00000004633	6	54039554	54301810	1	0	0	0	0	0	0	0	0	0	0	0	D3YXQ4	
ENSMUST00000127324						2	2	2	54	0	0	0	0	0	0	0		
ENSMUST00000127325						2	0	2	0	4	0	0	12	2	0	1		
ENSMUST00000127326	ENSMUSG00000030527	7	80586627	80688877	-1	0	0	0	0	0	0	0	0	16	0	0	F6Y626	
ENSMUST00000127329						5	0	3	8	3	3	81	187	99	1	122		
ENSMUST00000127331	ENSMUSG00000058446	6	54816916	54893500	1	0	1	0	1	0	2	0	0	0	0	3	F6X469	
ENSMUST00000127332						0	0	0	34	0	0	0	0	0	0	0		
ENSMUST00000127334						1	0	3	0	1	1	0	23	48	5	0		
ENSMUST00000127338						6	0	2	36	4	0	0	0	0	0	0		
ENSMUST00000127339						4	1	2	0	1	3	0	0	0	0	0		
ENSMUST00000127340						16	5	27	18	25	12	3	11	3	0	2		
ENSMUST00000127341						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127342						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000127343						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127344						1	3	7	105	6	4	0	0	0	0	0		
ENSMUST00000127345						0	0	4	2	0	0	0	0	4	0	0		
ENSMUST00000127346						0	0	1	0	0	1	40	18	134	65	184		
ENSMUST00000127347						0	0	0	0	0	0	0	11	0	0	0		
ENSMUST00000127348	ENSMUSG00000028085	3	85574119	85655622	1	51	41	47	570	70	26	3	24	17	3	0		Q99JT1
ENSMUST00000127349						8	6	12	39	11	7	0	0	0	0	0		
ENSMUST00000127351						4	3	26	7	9	5	0	0	0	0	0		
ENSMUST00000127352						2	5	5	46	3	3	0	0	14	2	4		
ENSMUST00000127353	ENSMUSG00000038718	2	34171457	34373142	-1	0	4	0	36	6	2	0	0	0	0	0	B2FDH2	
ENSMUST00000127354						0	0	0	2	2	0	0	7	0	3	0		
ENSMUST00000127355						14	6	17	21	22	0	0	12	0	0	4		
ENSMUST00000127356						2	2	7	0	0	0	0	0	0	0	0		
ENSMUST00000127357						14	22	85	51	25	11	0	3	2	2	8		
ENSMUST00000127358						1	3	0	5	2	3	0	0	0	0	0		
ENSMUST00000127360						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127361						0	0	0	4	2	1	0	0	0	2	0		
ENSMUST00000127362						122	99	396	124	91	58	0	11	2	0	11		
ENSMUST00000127363						0	0	3	13	6	1	0	0	6	0	0		
ENSMUST00000127364						81	71	179	85	74	27	5	8	9	6	17		
ENSMUST00000127365						16	9	18	16	15	3	2	13	4	2	7		
ENSMUST00000127366						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000127367						0	0	3	1	0	0	0	17	4	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127368						2	0	0	1	1	1	0	0	0	0	0		
ENSMUST00000127369						5	1	0	4	5	4	0	0	1	0	4		
ENSMUST00000127370	ENSMUSG00000031370	X	163935443	163958661	-1	0	0	0	12	0	0	0	11	20	3	16	B1B0F1	
ENSMUST00000127371	ENSMUSG00000020435	11	3703731	3863903	-1	0	0	0	0	0	0	0	0	0	0	1	Q5F209	
ENSMUST00000127372						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127373						54	45	75	98	54	22	3	31	7	2	12		
ENSMUST00000127374						0	0	1	2	2	0	0	0	0	0	0		
ENSMUST00000127375	ENSMUSG00000020876	11	96767555	96777559	-1	8	9	8	2	10	2	48	65	81	6	43	A2A880	
ENSMUST00000127376						3	2	6	1	5	3	1	2	0	0	1		
ENSMUST00000127377						0	3	0	3	1	0	0	10	2	2	3		
ENSMUST00000127378	ENSMUSG00000071074	17	46248080	46252537	1	3	1	0	0	0	0	306	279	137	0	0	F6YIY0	
ENSMUST00000127379						0	2	21	1	2	0	0	0	0	0	0		
ENSMUST00000127380	ENSMUSG00000079334	9	107578887	107584050	1	0	0	0	0	0	0	32	3	7	0	15	B7ZCE0	
ENSMUST00000127381	ENSMUSG00000017311	11	102106676	102107832	-1	4	0	2	29	5	2	0	0	0	0	0	H3BK86	
ENSMUST00000127382	ENSMUSG00000020328	11	40733667	40740046	1	0	0	0	0	0	0	0	0	0	33	13	E0CYQ2	
ENSMUST00000127383	ENSMUSG00000059248	11	117199661	117362325	1	6	2	3	3	4	8	95	18	120	14	86	A2A6U5	
ENSMUST00000127384						4	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000127385						7	23	0	47	16	28	3	0	0	0	15		
ENSMUST00000127386						10	2	11	4	13	6	0	0	2	0	2		
ENSMUST00000127387	ENSMUSG00000022037	14	65968483	65981548	1	1	1	3	2	0	2	0	0	0	0	0	E9PXG5	
ENSMUST00000127388						10	13	29	5	22	8	0	0	0	0	0		
ENSMUST00000127389						2	1	2	3	5	4	0	0	0	0	0		
ENSMUST00000127390						6	10	12	2	8	2	0	7	1	2	3		
ENSMUST00000127392						8	3	13	5	3	4	0	0	0	0	0		
ENSMUST00000127393						10	5	16	3	20	13	0	0	0	0	1		
ENSMUST00000127394	ENSMUSG00000026649	1	171113918	171126967	1	3	5	6	1	4	3	0	0	0	0	0	D3Z5E0	
ENSMUST00000127395						54	42	41	40	77	36	3	1	11	2	7		
ENSMUST00000127396	ENSMUSG00000029228	5	74592447	74702912	-1	6	0	0	9	0	2	0	12	0	0	0	D6RHN7	
ENSMUST00000127397	ENSMUSG00000074796	2	130684113	130697519	-1	0	0	0	1	0	1	0	0	0	0	1	A2AJN8	
ENSMUST00000127398	ENSMUSG00000062995	6	8630527	8778488	-1	0	0	0	0	0	0	0	0	0	0	3	F6UY19	
ENSMUST00000127399						0	0	1	4	0	0	0	0	0	0	0		
ENSMUST00000127400						2	2	11	12	2	0	0	0	0	0	0		
ENSMUST00000127401						0	8	33	125	0	23	0	22	0	0	0		
ENSMUST00000127402	ENSMUSG00000028898	4	132311763	132329538	-1	0	0	0	0	1	0	0	0	0	0	0	A2CEQ8	
ENSMUST00000127403	ENSMUSG00000029475	5	122870665	122989823	-1	8	0	13	22	7	5	7	0	1	3	0	D6RHM8	
ENSMUST00000127404	ENSMUSG00000072955	X	136954988	136976869	-1	0	0	3	0	1	0	0	15	0	6	0	Q8C0W0	
ENSMUST00000127405	ENSMUSG00000001056	11	51619735	51623714	1	3	10	12	22	5	4	65	120	32	319	69		Q9CRB2
ENSMUST00000127407						0	2	7	0	5	2	3	7	10	2	14		
ENSMUST00000127410						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000127411						0	0	0	3	0	0	0	10	0	0	1		
ENSMUST00000127412	ENSMUSG00000026456	1	134405559	134411740	1	3	0	4	0	0	3	0	0	0	0	3	G3UZ57	
ENSMUST00000127414						2	1	5	2	8	4	0	0	0	0	0		
ENSMUST00000127415						2	3	10	4	8	7	11	40	8	0	22		
ENSMUST00000127416						0	3	0	7	1	1	4	0	8	0	4		
ENSMUST00000127417	ENSMUSG00000028556	4	98936671	99120915	-1	3	4	0	0	0	0	0	33	5	21	7	A2A9M4	
ENSMUST00000127418						4	0	0	3	2	1	0	4	4	0	20		
ENSMUST00000127419						3	2	0	0	0	1	1	0	0	2	0		
ENSMUST00000127420	ENSMUSG00000025920	1	16228674	16520112	-1	0	4	3	0	4	0	0	0	0	0	0	D6RGR9	
ENSMUST00000127421	ENSMUSG00000017119	11	101552149	101581951	1	0	0	0	1	1	0	0	0	0	0	2	A2A4R0	
ENSMUST00000127423						3	3	1	0	5	1	37	38	29	10	19		
ENSMUST00000127425						0	1	0	5	1	0	0	0	0	0	0		
ENSMUST00000127426						3	0	6	0	2	0	2	9	3	0	4		
ENSMUST00000127427						0	0	5	0	0	0	4	0	3	1	0		
ENSMUST00000127428						2	1	1	1	1	1	10	11	28	0	28		
ENSMUST00000127430	ENSMUSG00000024054	17	71344489	71475343	-1	16	7	13	19	13	9	229	669	534	50	509		Q6P5D8
ENSMUST00000127431						23	18	48	18	27	12	0	0	1	0	1		
ENSMUST00000127432						0	0	0	0	0	0	6	0	0	2	0		
ENSMUST00000127433	ENSMUSG00000085601	7	19099046	19118368	-1	39	27	60	42	49	26	0	0	0	0	0	D6RG70	
ENSMUST00000127434	ENSMUSG00000049606	5	106616739	106697287	-1	2	2	0	0	1	1	3	0	13	0	9	Q3UMJ0	
ENSMUST00000127435	ENSMUSG00000046110	2	121439059	121456781	-1	0	0	0	0	0	0	0	2	0	0	0	F6Q288	
ENSMUST00000127436	ENSMUSG00000028064	3	88435959	88461182	-1	0	2	9	5	3	1	0	0	9	0	0	D3YZ30	
ENSMUST00000127437	ENSMUSG00000018565	11	69968222	69982517	-1	27	20	57	19	31	11	7	0	11	2	10	J3QN35	
ENSMUST00000127438						0	0	0	5	0	0	2	0	3	11	7		
ENSMUST00000127439						0	1	0	30	5	1	0	6	0	0	0		
ENSMUST00000127440						4	5	34	82	14	3	21	42	31	1	64		
ENSMUST00000127442	ENSMUSG00000034595	17	35865593	35875596	1	13	11	23	58	20	8	106	851	182	27	288		Q8BQ30
ENSMUST00000127443						0	0	1	109	1	0	0	5	0	0	0		
ENSMUST00000127444						0	0	3	0	7	4	0	0	0	0	1		
ENSMUST00000127445	ENSMUSG00000031394	X	74127464	74150760	1	0	0	0	0	0	4	0	0	0	0	0	B1AYN8	
ENSMUST00000127446	ENSMUSG00000044783	1	88262471	88277633	-1	5	3	24	12	7	3	0	2	0	0	0	F6XR06	
ENSMUST00000127447						11	7	5	41	15	3	0	0	0	0	0		
ENSMUST00000127448						5	3	2	6	1	2	0	0	0	0	0		
ENSMUST00000127449						0	1	3	6	2	0	57	12	80	64	51		
ENSMUST00000127451	ENSMUSG00000061559	9	54714735	54734519	-1	4	3	1	2	0	0	0	0	16	20	1	D6RJ72	
ENSMUST00000127452						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000127453	ENSMUSG00000026930	2	26315515	26348237	1	0	0	0	0	3	0	0	0	0	0	0	A2AIV4	
ENSMUST00000127454	ENSMUSG00000033809	16	20605451	20610768	-1	9	0	0	0	0	0	0	7	0	0	0	F6XUH0	
ENSMUST00000127455	ENSMUSG00000006219	4	141576062	141606096	-1	0	0	0	3	1	0	0	0	0	0	0	A2ADE8	
ENSMUST00000127457	ENSMUSG00000029049	4	155086577	155145505	1	1	0	1	2	0	1	1	7	4	0	5	B1AUE8	
ENSMUST00000127458						13	17	20	110	19	8	0	0	0	1	0		
ENSMUST00000127459						2	0	23	5	0	1	0	0	0	0	0		
ENSMUST00000127460	ENSMUSG00000023235	8	4325210	4360020	1	0	0	0	2	0	0	1	0	0	8	7	D3YWJ1	
ENSMUST00000127461	ENSMUSG00000035045	X	95711678	95932637	1	1	0	0	0	0	0	0	0	0	0	0	A2BE29	
ENSMUST00000127463	ENSMUSG00000031328	X	74223461	74249820	-1	0	0	0	1	3	0	44	1279	98	8	99	F6Z2C0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127464						1	0	4	55	0	0	35	0	113	21	216		
ENSMUST00000127465						3	2	6	4	3	0	0	0	0	0	0		
ENSMUST00000127467	ENSMUSG00000005268	15	10177238	10349180	1	0	1	0	0	0	0	0	0	0	0	0	E9Q631	
ENSMUST00000127468						8	3	3	5	13	5	0	5	0	0	2		
ENSMUST00000127469						1	0	2	0	2	0	0	108	154	43	7		
ENSMUST00000127470						1	8	18	11	6	2	1	0	0	0	0		
ENSMUST00000127471	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	2	114	2	2	18	28	65	13	75	E9Q8K6	
ENSMUST00000127472	ENSMUSG00000030491	7	35469098	35537745	-1	2	2	8	9	2	5	0	0	0	0	0	D3YZI6	
ENSMUST00000127473						25	27	75	112	38	13	3	15	24	13	42		
ENSMUST00000127474						5	0	7	6	0	1	0	0	0	0	0		
ENSMUST00000127475						16	24	17	35	33	12	0	8	3	1	7		
ENSMUST00000127476	ENSMUSG00000041235	4	8690406	8867659	1	0	0	0	205	0	0	0	0	24	0	12		
ENSMUST00000127477	ENSMUSG00000027673	3	32736990	32751566	1	2	3	2	8	6	0	29	55	45	128	30		Q9CQH3
ENSMUST00000127478						0	0	0	0	0	0	24	91	55	12	39		
ENSMUST00000127479						5	0	0	0	6	0	4	2	0	0	0		
ENSMUST00000127480						5	4	19	4	16	3	0	0	0	0	0		
ENSMUST00000127481	ENSMUSG00000020719	11	106780355	106789185	-1	0	3	0	0	0	0	96	7158	2471	1887	2155	S4R1E3	
ENSMUST00000127482	ENSMUSG00000037995	1	172481788	172498878	1	0	21	14	0	25	19	0	2	1	0	0		Q05BQ1
ENSMUST00000127484						0	0	5	14	7	3	0	0	0	5	0		
ENSMUST00000127485	ENSMUSG00000037788	6	57727807	57825159	-1	16	12	9	15	10	4	0	0	0	0	0		Q8R1C3
ENSMUST00000127486						5	0	0	173	5	4	0	0	0	0	0		
ENSMUST00000127487						2	2	13	6	2	4	28	229	69	2	208		
ENSMUST00000127489	ENSMUSG00000026610	1	187608791	188214885	1	3	1	0	24	1	0	0	0	0	0	0	D3Z2J0	
ENSMUST00000127490	ENSMUSG00000036810	8	88118769	88135110	1	3	0	0	5	0	0	0	62	0	0	38		Q3UJ81
ENSMUST00000127491						4	2	11	7	2	0	0	0	0	0	0		
ENSMUST00000127492						48	26	168	84	51	21	0	6	2	0	7		
ENSMUST00000127493						1	1	4	0	5	1	0	0	0	0	0		
ENSMUST00000127494						3	1	0	1	5	1	0	0	0	0	0		
ENSMUST00000127495						0	0	0	0	1	0	0	0	0	0	1		
ENSMUST00000127496						1	0	0	2	0	2	12	54	12	0	11		
ENSMUST00000127497	ENSMUSG00000027782	3	69067149	69127113	-1	0	0	3	12	0	0	0	0	0	0	0	D3YTN1	
ENSMUST00000127499						5	17	22	0	6	16	0	25	0	0	11		
ENSMUST00000127501						4	2	53	11	8	2	0	0	0	0	0		
ENSMUST00000127502						1	0	0	0	6	1	7	25	0	11	11		
ENSMUST00000127503						0	9	18	154	8	5	41	64	98	3	99		
ENSMUST00000127504	ENSMUSG00000019888	10	101681487	102391469	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5V6	
ENSMUST00000127505						5	1	8	16	6	2	163	202	272	41	270		
ENSMUST00000127506						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000127507						8	4	5	7	21	9	1	0	0	0	4		
ENSMUST00000127508	ENSMUSG00000048794	6	90403479	90428797	-1	5	2	6	0	2	0	0	0	0	1	0		
ENSMUST00000127509	ENSMUSG00000038860	2	32986224	33131654	-1	0	2	6	0	0	2	0	0	0	0	0	A0A0A6YWF1	
ENSMUST00000127510						8	4	32	22	2	0	0	0	0	0	0		
ENSMUST00000127511	ENSMUSG00000039375	8	54629055	54887184	-1	2	3	0	0	5	0	0	0	0	0	0	E9Q271	
ENSMUST00000127512						0	1	1	0	3	1	0	0	0	0	0		
ENSMUST00000127514	ENSMUSG00000063316	11	101442298	101445529	1	0	0	0	0	0	0	0	8	0	2	0	A2A4Q0	
ENSMUST00000127515						0	1	3	56	1	3	0	0	0	0	0		
ENSMUST00000127516						0	3	5	3	2	1	0	0	22	0	23		
ENSMUST00000127517						2	1	7	1	0	0	0	0	2	0	6		
ENSMUST00000127518						2	0	3	6	7	2	0	0	0	0	0		
ENSMUST00000127519						0	2	2	2	0	0	3	7	6	0	9		
ENSMUST00000127520	ENSMUSG00000026872	2	44983632	45117395	-1	0	0	0	0	0	1	18	15	20	139	24	F6X889	
ENSMUST00000127522						3	1	9	0	3	5	0	0	0	0	1		
ENSMUST00000127523						0	0	0	0	0	1	0	0	0	0	1		
ENSMUST00000127524	ENSMUSG00000054555	7	133883199	134232146	-1	5	0	1	0	3	0	0	0	0	0	1	D3YUK3	
ENSMUST00000127526						0	0	0	0	1	0	0	0	0	0	2		
ENSMUST00000127529	ENSMUSG00000040234	6	146602352	146642824	-1	0	3	0	7	4	3	0	0	0	0	0	D6RI14	
ENSMUST00000127530						0	1	3	3	3	0	0	0	5	0	9		
ENSMUST00000127531						1	1	0	0	4	7	3	3	0	0	1		
ENSMUST00000127532						13	9	20	8	12	5	1	4	5	0	4		
ENSMUST00000127534						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000127535						3	2	1	24	4	0	4	2	1	4	3		
ENSMUST00000127536						64	54	61	91	68	32	7	24	10	7	21		
ENSMUST00000127537	ENSMUSG00000098715	6	48718607	48752644	1	0	0	0	0	0	0	0	1	0	1	0	D3YZL2	
ENSMUST00000127538						1	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000127539						0	1	0	78	2	5	0	2	4	0	0		
ENSMUST00000127540	ENSMUSG00000026646	2	3455815	3475031	-1	0	0	0	38	0	0	0	0	0	11	0	E0CZC9	
ENSMUST00000127541						0	0	0	2	1	0	1	5	0	0	0		
ENSMUST00000127542						0	0	9	2	7	1	2	0	0	0	0		
ENSMUST00000127543						11	4	23	41	14	4	1531	2771	1496	167	1601		
ENSMUST00000127544						1	0	0	0	0	0	0	0	0	6	2		
ENSMUST00000127545						2	4	2	6	9	5	5	45	44	0	19		
ENSMUST00000127546	ENSMUSG00000034758	10	81590904	81601073	-1	1	0	6	21	0	0	0	0	0	1	0	D3YV26	
ENSMUST00000127547						8	4	19	11	6	1	6	35	12	5	10		
ENSMUST00000127548						5	3	0	2	7	1	22	164	73	5	122		
ENSMUST00000127549						3	3	11	8	0	3	4	6	3	0	2		
ENSMUST00000127550	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	2	0	0	0	0	0	0	0	0	Q9CVV2	
ENSMUST00000127551						2	2	3	0	3	2	4	5	3	0	3		
ENSMUST00000127552						22	12	21	37	21	7	44	140	40	20	27		
ENSMUST00000127553						40	41	120	94	45	22	0	2	1	1	10		
ENSMUST00000127554						4	3	11	20	0	0	0	2	0	0	0		
ENSMUST00000127556						9	3	0	0	24	9	0	79	0	2	0		
ENSMUST00000127557						6	7	6	3	10	4	3	2	1	1	6		
ENSMUST00000127558						3	2	0	72	8	2	0	0	0	0	0		
ENSMUST00000127559						29	25	58	25	38	19	81	311	115	16	199		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127560						3	1	6	23	2	2	0	0	0	0	5		
ENSMUST00000127561						13	22	16	24	23	15	0	1	0	0	1		
ENSMUST00000127562	ENSMUSG00000015806	5	45434021	45450236	-1	0	1	0	55	4	3	0	0	0	0	0	D3Z099	
ENSMUST00000127565						0	0	3	75	8	0	0	0	0	0	0		
ENSMUST00000127566	ENSMUSG00000026857	2	30807826	30823033	1	0	0	1	0	1	0	0	0	0	0	0	A0A0A6YXY1	
ENSMUST00000127567	ENSMUSG00000022696	16	44240180	44333196	-1	0	5	17	1	0	0	25	42	14	4	35		Q6AXF6
ENSMUST00000127568	ENSMUSG00000024608	18	60774510	60778546	1	9	0	5	7	5	0	0	19	0	9	11	D3YVF4	
ENSMUST00000127569	ENSMUSG00000032376	9	66514637	66593142	-1	87	71	262	165	63	35	161	471	268	32	229		Q91W36
ENSMUST00000127570						2	0	0	1	0	0	0	1	0	0	0		
ENSMUST00000127571						0	0	3	19	0	0	0	0	0	0	0		
ENSMUST00000127572						0	0	0	1	2	0	0	0	3	4	3		
ENSMUST00000127573						425	448	889	341	527	209	27	162	34	20	80		
ENSMUST00000127574						6	7	5	8	9	2	0	0	0	0	0		
ENSMUST00000127575						0	0	5	5	3	0	0	7	0	0	7		
ENSMUST00000127577						2	1	2	0	0	0	4	6	0	0	4		
ENSMUST00000127578						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000127579						0	0	0	0	0	0	0	0	4	0	8		
ENSMUST00000127580						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000127581						12	8	8	25	14	13	0	1	0	0	0		
ENSMUST00000127582						0	2	0	3	5	0	0	3	0	0	0		
ENSMUST00000127583						0	2	74	7	1	3	0	0	0	0	0		
ENSMUST00000127584						0	2	8	3	2	4	0	5	0	0	4		
ENSMUST00000127585						1	1	0	3	4	0	0	8	13	0	20		
ENSMUST00000127586	ENSMUSG00000032649	1	152399830	152510695	1	0	0	20	124	5	4	0	0	0	0	0	D6RCH2	
ENSMUST00000127587	ENSMUSG00000019437	11	78176711	78181909	1	0	0	0	0	0	0	0	43	0	0	5		Q99JT6
ENSMUST00000127588						0	3	1	4	2	0	10	61	19	3	38		
ENSMUST00000127589	ENSMUSG00000048497	11	62648664	62666354	1	0	0	0	0	1	0	0	1	0	0	0	G3UWB0	
ENSMUST00000127590						0	6	5	2	3	1	0	4	3	0	4		
ENSMUST00000127591	ENSMUSG00000032900	18	56588350	56594782	1	0	0	1	2	0	1	0	0	0	0	0	F6YCE8	
ENSMUST00000127592	ENSMUSG00000040165	8	3940222	3954746	-1	3	1	6	1	4	0	0	0	0	0	0	D6RJ18	
ENSMUST00000127593						14	12	20	20	20	6	4	5	2	0	5		
ENSMUST00000127594						22	14	40	11	30	16	1	5	2	0	0		
ENSMUST00000127595						0	0	0	0	2	0	0	1	0	0	3		
ENSMUST00000127596	ENSMUSG00000040596	1	166384622	166409863	-1	5	3	6	0	3	4	1	0	2	0	0	D3YZK0	
ENSMUST00000127597						5	4	8	0	4	3	0	0	0	0	0		
ENSMUST00000127598						4	4	11	5	0	0	3	2	15	0	8		
ENSMUST00000127599						0	1	1	0	4	0	0	0	7	0	3		
ENSMUST00000127601	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	3	2	0	0	0	F6XRJ7	
ENSMUST00000127602						3	3	0	0	1	1	3	6	0	4	29		
ENSMUST00000127605	ENSMUSG00000024830	19	4156713	4163354	-1	0	1	0	0	0	0	12	114	77	9	1	E9PUN3	
ENSMUST00000127606						1	0	0	0	1	1	1	1	8	0	1		
ENSMUST00000127607						8	0	8	5	6	2	0	2	1	0	2		
ENSMUST00000127608	ENSMUSG00000029464	5	122371876	122382902	1	3	2	11	174	8	6	0	19	11	0	10	A0A0G2JG32	
ENSMUST00000127609						33	5	0	0	5	0	0	0	0	0	0		
ENSMUST00000127610	ENSMUSG00000020790	11	72690006	72772146	1	0	0	0	0	0	0	985	1554	2021	19	1307		Q810B6
ENSMUST00000127611						3	1	3	0	4	0	0	0	0	0	0		
ENSMUST00000127613						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000127614						0	0	0	0	0	0	0	12	0	0	0		
ENSMUST00000127615	ENSMUSG00000035311	10	88379132	88447329	1	0	0	0	17	2	0	0	0	0	0	0	D3Z1C3	
ENSMUST00000127616						1	4	6	15	10	7	0	0	0	0	0		
ENSMUST00000127617						1	0	0	25	0	1	0	0	0	0	0		
ENSMUST00000127618	ENSMUSG00000025862	X	42149317	42277185	1	0	0	0	4	0	0	3	0	4	0	0	A2AFF3	
ENSMUST00000127619						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127621	ENSMUSG00000020463	11	29172890	29220797	1	0	0	0	0	0	0	0	4	0	0	0	Q5M6W0	
ENSMUST00000127622						0	0	2	2	10	4	1	0	0	0	0		
ENSMUST00000127623	ENSMUSG00000061171	2	65316430	65364034	-1	0	1	10	14	8	3	0	0	0	0	0	F6WJL8	
ENSMUST00000127624						11	15	10	14	12	8	0	3	3	0	7		
ENSMUST00000127625	ENSMUSG00000026199	1	75192151	75199387	1	0	0	0	0	0	1	13	0	0	0	0	J3QPB4	
ENSMUST00000127626	ENSMUSG00000031807	8	71592176	71601092	1	0	0	0	0	0	0	6	0	0	0	0	Q8CBG6	
ENSMUST00000127628						0	0	4	0	0	0	135	433	32	0	164		
ENSMUST00000127629						4	5	11	2	8	0	0	0	0	0	0		
ENSMUST00000127630	ENSMUSG00000027160	2	110017817	110173360	1	0	0	0	0	0	4	0	0	11	3	0	F6QKZ7	
ENSMUST00000127632						6	2	7	4	6	2	5	23	11	0	5		
ENSMUST00000127633						27	15	40	59	40	31	0	0	0	0	0		
ENSMUST00000127634						0	0	0	0	0	0	5	0	22	0	4		
ENSMUST00000127635						0	0	0	0	0	0	32	9	23	20	31		
ENSMUST00000127636						1	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000127637						0	0	0	15	0	1	130	42	111	0	72		
ENSMUST00000127638	ENSMUSG00000004040	11	100885098	100939540	-1	0	0	0	28	0	0	6134	14214	10036	838	7539		P42227
ENSMUST00000127639						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000127641						137	150	430	163	177	92	9	56	21	10	49		
ENSMUST00000127643						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000127644	ENSMUSG00000022965	16	91547072	91565169	1	2	1	2	0	7	0	142	238	181	35	133	D6RIP6	
ENSMUST00000127645						6	0	10	123	11	1	3	9	0	0	12		
ENSMUST00000127646						1	5	4	0	3	0	0	2	0	0	0		
ENSMUST00000127647	ENSMUSG00000024181	17	26123520	26126613	1	0	0	2	0	0	0	0	0	8	10	0	F6U4U1	
ENSMUST00000127648	ENSMUSG00000002992	7	19671579	19681423	-1	0	2	0	8	4	5	0	0	0	0	3	D3YXE8	
ENSMUST00000127649						7	9	9	18	5	2	0	11	14	0	13		
ENSMUST00000127650	ENSMUSG00000017760	2	164832873	164841032	1	0	0	0	0	0	0	0	0	0	0	0	A2A5J8	
ENSMUST00000127651						0	3	11	27	2	0	2	24	0	0	9		
ENSMUST00000127652						0	0	3	0	0	0	1349	4544	1023	331	745		
ENSMUST00000127653						0	1	0	14	0	0	0	0	0	0	0		
ENSMUST00000127654						2	1	4	0	6	0	1	0	0	1	0		
ENSMUST00000127655	ENSMUSG00000030769	7	123214780	123273253	1	1	0	6	0	0	0	0	0	0	0	0	D3YW46	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127656	ENSMUSG00000028577	4	94567514	94603244	-1	0	0	0	0	0	0	0	0	0	0	0	F7D1R5	
ENSMUST00000127657						5	2	3	10	6	6	0	2	0	0	0		
ENSMUST00000127658	ENSMUSG00000030443	7	6315660	6331285	-1	0	0	0	11	1	0	0	0	0	1	0	D3YXW6	
ENSMUST00000127659						19	6	56	21	17	7	0	12	3	0	5		
ENSMUST00000127660						53	54	92	49	71	31	8	61	13	5	30		
ENSMUST00000127661						28	18	52	12	1	12	0	0	0	0	0		
ENSMUST00000127662						8	10	16	10	26	8	5	10	3	0	24		
ENSMUST00000127664	ENSMUSG00000092329	8	119910841	124345722	1	18	20	59	14	37	10	1061	1147	1225	97	569		Q6PB93
ENSMUST00000127665						0	3	2	1	3	5	13	114	36	16	56		
ENSMUST00000127666	ENSMUSG00000053768	6	32790976	33060260	-1	4	0	1	16	0	0	0	0	35	88	47	D3Z0L4	
ENSMUST00000127667	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	F7DAQ7	
ENSMUST00000127669						1	0	12	2	2	0	3	14	2	2	0		
ENSMUST00000127670						3	0	2	0	2	2	0	0	0	1	0		
ENSMUST00000127671						0	1	4	1	3	1	0	0	0	0	0		
ENSMUST00000127674						11	8	10	0	18	6	0	29	0	0	0		
ENSMUST00000127675						9	12	10	7	24	7	0	0	2	0	0		
ENSMUST00000127676						4	4	8	8	4	1	0	0	0	0	0		
ENSMUST00000127677						0	0	0	43	0	0	0	2	4	0	13		
ENSMUST00000127679						0	0	5	58	0	0	0	0	0	0	0		
ENSMUST00000127680	ENSMUSG00000032712	6	149309414	149335663	1	22	20	25	14	29	15	15	38	57	3	60	B2KFD0	
ENSMUST00000127681						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127682						0	0	0	0	0	0	0	0	0	0	11		
ENSMUST00000127683	ENSMUSG00000026831	2	28462001	28466332	-1	2	3	6	31	0	4	0	0	0	0	0	B0R017	
ENSMUST00000127685						2	0	5	3	3	1	2	0	0	0	0		
ENSMUST00000127686	ENSMUSG00000046079	5	105699969	105832436	1	0	0	0	37	0	0	0	0	0	0	0	D3Z6C1	
ENSMUST00000127687	ENSMUSG00000089951	2	176423594	176435761	1	0	1	0	2	1	0	0	0	0	0	0	A2BDM8	
ENSMUST00000127689	ENSMUSG00000079484	2	30266203	30282149	1	0	0	0	0	0	0	0	0	0	0	0	D6RIQ3	
ENSMUST00000127690						2	0	5	0	0	0	0	0	0	0	3		
ENSMUST00000127691						6	5	14	2	9	3	3	0	0	0	1		
ENSMUST00000127692						3	0	6	2	1	4	0	0	0	0	0		
ENSMUST00000127693						0	0	9	0	2	0	1	0	0	0	0		
ENSMUST00000127694	ENSMUSG00000029621	5	145083830	145108761	1	54	40	94	48	59	24	106	551	138	82	285	A0A0G2JF52	
ENSMUST00000127695						3	2	12	4	0	1	15	40	15	0	8		
ENSMUST00000127696						0	1	1	11	1	1	0	0	0	0	0		
ENSMUST00000127698	ENSMUSG00000071359	10	22703879	22731938	-1	10	8	24	34	5	4	212	900	293	130	248		P62340
ENSMUST00000127699						0	1	11	0	0	0	0	3	3	0	0		
ENSMUST00000127700						49	38	298	79	54	34	0	4	1	0	5		
ENSMUST00000127701						0	1	0	0	1	0	1	3	0	0	0		
ENSMUST00000127702						0	0	0	0	0	3	1	18	16	0	0		
ENSMUST00000127703						17	6	12	2	11	8	29	967	337	69	156		
ENSMUST00000127704						31	30	212	192	32	26	1	4	2	0	8		
ENSMUST00000127705						0	1	1	1	2	0	0	0	1	0	0		
ENSMUST00000127707						0	2	0	29	3	0	2	0	1	0	1		
ENSMUST00000127710	ENSMUSG00000030672	7	127208890	127214298	1	0	0	0	0	0	0	0	7	7	4	1	F6ULR7	
ENSMUST00000127712						9	11	8	11	15	5	120	375	290	96	809		
ENSMUST00000127713	ENSMUSG00000057522	11	95414080	95493406	1	0	0	0	0	0	0	8	12	11	0	13	B1ATK7	
ENSMUST00000127714						1	0	4	7	5	0	0	0	4	1	0		
ENSMUST00000127715						1	2	12	10	7	3	4	11	4	20	5		
ENSMUST00000127717	ENSMUSG00000020525	11	85311244	85347066	1	9	1	11	1	7	4	16	20	30	0	36	B1B0B1	
ENSMUST00000127718						81	61	172	57	64	38	2	19	9	3	7		
ENSMUST00000127719	ENSMUSG00000047407	17	70844205	70853546	-1	3	0	0	0	0	0	5	0	0	9	14	D3Z0Q5	
ENSMUST00000127720	ENSMUSG00000028619	4	107134155	107179116	-1	0	0	0	0	0	0	75	201	132	133	120	D6RH96	
ENSMUST00000127721						1	2	3	5	1	1	0	0	0	0	0		
ENSMUST00000127722	ENSMUSG00000049723	9	7344381	7369499	1	0	3	23	4	0	2	0	2	0	0	0	D6RJI9	
ENSMUST00000127723						35	28	90	85	42	25	143	474	340	17	632		
ENSMUST00000127724						3	5	20	5	2	3	0	4	0	0	4		
ENSMUST00000127725						15	19	89	14	15	9	8	19	23	3	16		
ENSMUST00000127726						0	3	0	0	1	0	0	78	1	22	9		
ENSMUST00000127727	ENSMUSG00000030313	6	148988071	149101680	-1	0	0	0	59	1	0	0	0	0	0	0	B8JKU3	
ENSMUST00000127728						0	0	0	0	0	0	35	0	0	0	0		
ENSMUST00000127729						2	1	5	2	3	3	0	0	0	0	0		
ENSMUST00000127730	ENSMUSG00000073490	1	173723430	173741809	-1	51	13	190	21	41	14	0	0	5	0	122	D3Z2E7	
ENSMUST00000127731						21	19	42	62	32	20	0	0	0	0	0		
ENSMUST00000127732						3	7	3	26	8	3	0	0	0	0	0		
ENSMUST00000127733						0	0	0	0	0	0	1	0	0	0	1		
ENSMUST00000127734						1	0	19	5	3	0	10	20	10	2	13		
ENSMUST00000127735						0	0	0	0	6	1	12	11	5	0	10		
ENSMUST00000127736						0	2	0	2	0	0	0	2	0	0	1		
ENSMUST00000127737	ENSMUSG00000028639	4	119277981	119294604	-1	16	6	8	2	0	0	649	1004	651	273	490	A2BGG7	
ENSMUST00000127738						1	0	1	1	0	0	0	7	11	0	0		
ENSMUST00000127740	ENSMUSG00000061589	10	80755206	80795461	1	0	1	2	13	0	0	0	4	26	0	0	E9Q6I8	
ENSMUST00000127741	ENSMUSG00000007610	8	71488103	71499583	1	0	6	50	0	0	12	12	47	3	17	17	D6RDC6	
ENSMUST00000127742						2	0	13	98	5	1	2	16	3	2	0		
ENSMUST00000127743						61	40	58	42	46	27	7	18	16	3	32		
ENSMUST00000127745						39	40	110	352	46	17	1	8	3	2	7		
ENSMUST00000127746						0	0	0	8	0	0	0	0	0	0	0		
ENSMUST00000127747						14	10	28	32	19	13	3	5	4	0	6		
ENSMUST00000127748	ENSMUSG00000043496	6	53815468	53820830	-1	51	44	157	1136	76	30	0	0	0	1	0		Q9DBY4
ENSMUST00000127749	ENSMUSG00000086815	5	30103584	30106086	-1	0	0	0	33	1	1	0	0	0	0	0	F6Z6Z2	
ENSMUST00000127750						1	0	2	7	2	1	0	0	0	0	0		
ENSMUST00000127751						0	0	2	9	0	0	26	23	31	1	33		
ENSMUST00000127753						0	0	0	16	0	4	0	0	0	1	0		
ENSMUST00000127755						5	0	8	9	3	1	0	0	5	0	10		
ENSMUST00000127756	ENSMUSG00000020654	12	4133103	4213525	1	0	0	0	0	0	0	0	0	0	0	0		Q8VHH7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127758	ENSMUSG00000037958	11	77044292	77078435	-1	0	1	1	1	1	0	3	4	11	8	11	Q5NCR8	
ENSMUST00000127759						1	0	0	1	1	0	1	12	9	0	7		
ENSMUST00000127760						0	0	0	0	2	2	39	131	29	97	8		
ENSMUST00000127761						23	15	34	21	22	5	4	7	23	1	36		
ENSMUST00000127762						0	2	5	5	2	3	0	0	0	0	0		
ENSMUST00000127765	ENSMUSG00000055102	7	43607169	43618285	1	6	3	6	5	7	0	0	1	3	0	0	D3Z4F2	
ENSMUST00000127766						0	3	3	0	0	1	0	0	0	0	0		
ENSMUST00000127767						0	0	2	2	0	0	0	0	1	0	1		
ENSMUST00000127768						3	5	13	13	1	2	0	0	0	0	0		
ENSMUST00000127769						0	0	0	0	0	0	0	0	0	6	6		
ENSMUST00000127770						0	0	2	0	1	0	0	6	17	0	0		
ENSMUST00000127771						0	0	1	0	0	0	0	0	1	0	1		
ENSMUST00000127772	ENSMUSG00000028152	3	138742195	138907905	1	0	0	0	28	1	0	0	0	0	0	0	D6RG91	
ENSMUST00000127773						7	0	17	51	22	6	1	0	0	3	9		
ENSMUST00000127774						0	1	1	4	0	1	1	13	2	6	2		
ENSMUST00000127775	ENSMUSG00000086727	1	31135226	31222684	-1	66	62	61	56	66	27	1	1	4	1	5	Q9D4J5	
ENSMUST00000127776						4	1	13	5	10	6	0	1	1	0	0		
ENSMUST00000127777						1	6	6	0	3	2	0	2	0	0	5		
ENSMUST00000127778						2	0	0	0	0	0	32	545	214	106	233		
ENSMUST00000127779	ENSMUSG00000033577	9	80165031	80311729	1	5	7	0	0	0	0	0	0	0	0	3	V9GXM4	
ENSMUST00000127780						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000127781						6	0	31	0	6	2	3	0	0	3	0		
ENSMUST00000127782						219	102	1411	233	125	61	0	3	1	0	4		
ENSMUST00000127783	ENSMUSG00000011096	7	44848991	44855421	1	0	0	0	0	0	0	0	0	0	0	0	F6R8S6	
ENSMUST00000127784						0	0	0	51	0	1	2	34	0	0	0		
ENSMUST00000127785	ENSMUSG00000040734	7	19359749	19378533	1	4	2	21	50	8	2	0	1	0	0	5	D3Z5Q5	
ENSMUST00000127787						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127788						3	4	1	7	2	1	2	15	4	3	17		
ENSMUST00000127789	ENSMUSG00000063881	11	73371246	73375704	1	0	7	7	3	0	0	0	0	0	0	0	B0QZP1	
ENSMUST00000127790	ENSMUSG00000047085	7	44429018	44463351	1	0	0	0	6	0	1	0	0	0	0	0	D3YZP3	
ENSMUST00000127791						0	0	0	17	1	0	1	0	0	3	0		
ENSMUST00000127793						4	9	0	11	0	0	7	0	0	19	0		
ENSMUST00000127794	ENSMUSG00000070280	9	119169455	119365553	-1	2	0	5	1	0	1	0	0	0	0	0	D3YUH1	
ENSMUST00000127795						0	0	13	0	0	0	0	0	1	0	0		
ENSMUST00000127796						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127797						13	6	5	15	6	0	20	51	6	13	10		
ENSMUST00000127798	ENSMUSG00000038954	17	44777152	45119290	1	0	0	0	0	1	0	14	2	5	0	12	B0QZW5	
ENSMUST00000127799	ENSMUSG00000087153	8	19682268	19698275	1	57	55	85	58	55	36	21	104	18	0	17	D3Z1Y8	
ENSMUST00000127800	ENSMUSG00000041530	4	126435012	126468583	-1	0	4	19	12	5	5	0	0	0	0	12	H3BL59	
ENSMUST00000127801						5	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000127802						8	2	0	54	0	2	1	0	9	0	23		
ENSMUST00000127803						2	2	11	2	0	4	0	3	3	0	3		
ENSMUST00000127804						0	1	0	0	0	0	6	8	0	2	0		
ENSMUST00000127805						3	2	6	5	7	0	0	0	0	1	2		
ENSMUST00000127806	ENSMUSG00000063145	2	69647171	69667571	1	0	0	0	1	2	0	1	0	4	0	0	F6Q242	
ENSMUST00000127807						1	2	5	5	1	1	4	14	10	2	4		
ENSMUST00000127808						0	0	11	0	9	5	0	0	4	0	0		
ENSMUST00000127809						0	0	0	0	0	0	4	8	21	0	32		
ENSMUST00000127810						2	0	0	3	1	1	21	79	27	3	26		
ENSMUST00000127811	ENSMUSG00000029319	5	100654723	100675140	-1	2	4	27	3	3	0	0	0	0	0	1	D3YZF3	
ENSMUST00000127812	ENSMUSG00000009566	2	32682609	32704145	-1	0	0	0	3	3	0	0	0	2	0	0	A2AK70	
ENSMUST00000127813						3	0	0	0	2	0	0	0	3	0	5		
ENSMUST00000127814	ENSMUSG00000061288	5	117120129	117275219	1	2	0	0	0	5	0	0	0	0	0	0	F6RXB5	
ENSMUST00000127815	ENSMUSG00000029182	5	30466047	30484088	1	7	5	8	33	12	0	0	0	0	0	0		Q9DAS2
ENSMUST00000127816						3	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000127818						0	1	6	0	0	0	14	0	0	0	0		
ENSMUST00000127819						7	0	11	73	2	3	13	10	11	2	3		
ENSMUST00000127820	ENSMUSG00000037868	10	67535475	67542188	1	10	0	31	103	10	14	0	2	11	0	0	D3Z3K7	
ENSMUST00000127821						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000127822						6	17	10	9	21	7	0	0	0	0	0		
ENSMUST00000127823	ENSMUSG00000026933	2	25926838	25983282	-1	1	2	0	2	1	0	1	0	3	0	4	V9GWZ6	
ENSMUST00000127824						4	1	0	4	2	0	12	45	40	2	23		
ENSMUST00000127825	ENSMUSG00000036553	5	35697180	35739987	-1	0	0	0	0	0	0	0	0	0	0	0	F6U4F1	
ENSMUST00000127826						198	144	216	172	180	98	0	0	2	0	3		
ENSMUST00000127827	ENSMUSG00000000805	11	84957786	84966044	1	0	0	15	56	4	0	3	0	0	0	0	D6RCZ3	
ENSMUST00000127828	ENSMUSG00000048120	19	40612366	40741602	1	1	0	41	1	0	0	63	55	90	91	221	D6RFA9	
ENSMUST00000127830	ENSMUSG00000013973	1	171329145	171342331	1	0	0	0	0	0	0	0	0	5	0	0	D3Z4Q1	
ENSMUST00000127831	ENSMUSG00000028842	4	126331704	126429556	-1	0	0	0	0	0	0	0	0	2	0	0	A3KFX7	
ENSMUST00000127832						0	0	0	16	0	0	3	67	25	24	12		
ENSMUST00000127833	ENSMUSG00000036622	4	140986873	141007330	1	0	0	0	0	0	0	2613	2063	3150	221	1463	E9Q2A4	
ENSMUST00000127835						1	3	7	0	1	1	10	1	8	0	9		
ENSMUST00000127836	ENSMUSG00000022090	14	70164218	70177681	-1	4	0	9	16	7	1	19	35	16	4	22	A0A087WPL1	
ENSMUST00000127837						1	1	1	9	1	1	6	2	13	0	1		
ENSMUST00000127838						1	1	2	2	1	0	0	2	0	7	0		
ENSMUST00000127839						8	6	15	10	10	2	0	0	0	0	0		
ENSMUST00000127840	ENSMUSG00000045106	2	104867805	105017904	1	0	0	2	1	2	0	0	0	0	0	0	A2A6Z7	
ENSMUST00000127841	ENSMUSG00000037455	10	23796986	23827968	1	0	0	0	0	0	0	0	0	0	1	0	F6WI82	
ENSMUST00000127842						57	60	202	113	93	47	10	163	62	2	151		
ENSMUST00000127843	ENSMUSG00000041669	12	103196908	103242150	-1	0	4	0	0	0	0	0	0	0	0	0	D6RE30	
ENSMUST00000127845						0	7	7	0	7	0	1	0	2	0	1		
ENSMUST00000127846						3	4	5	0	6	0	4	3	7	11	4		
ENSMUST00000127847						0	1	0	0	1	1	0	8	4	0	13		
ENSMUST00000127848	ENSMUSG00000037458	15	38487430	38519266	-1	2	0	13	5	2	2	0	0	0	3	0	D3YUY1	
ENSMUST00000127850						6	0	13	26	3	2	0	2	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127851	ENSMUSG00000021768	14	21733394	21751181	-1	0	0	3	0	4	0	0	0	0	0	0	D6RHL3	
ENSMUST00000127853						5	0	1	2	13	0	0	118	17	0	13		
ENSMUST00000127854						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000127855						4	3	2	15	6	6	2	1	0	0	4		
ENSMUST00000127856						2	0	0	58	4	0	0	8	4	0	5		
ENSMUST00000127857	ENSMUSG00000050890	4	134275002	134287895	-1	2	3	7	19	5	1	0	0	4	2	4	F6YU83	
ENSMUST00000127858						1	1	1	0	2	1	0	3	0	0	2		
ENSMUST00000127859						4	0	4	2	2	3	0	0	0	0	0		
ENSMUST00000127860						4	3	0	2	6	0	3	29	10	0	15		
ENSMUST00000127861	ENSMUSG00000025980	1	55077835	55088243	-1	0	3	0	63	4	3	11	5	31	39	15	D3Z2F2	
ENSMUST00000127862	ENSMUSG00000074793	2	131127280	131146321	1	3	1	23	58	12	0	0	0	0	0	0	S4R176	
ENSMUST00000127863						0	0	0	0	0	0	0	2	0	5	3		
ENSMUST00000127864						0	0	0	1	0	1	0	0	1	0	0		
ENSMUST00000127865	ENSMUSG00000030200	6	134396318	134438736	1	1	0	7	4	0	0	0	0	0	0	0	D3YZF2	
ENSMUST00000127866						29	22	43	25	24	11	0	5	6	2	0		
ENSMUST00000127867						9	2	6	13	3	0	0	0	0	0	2		
ENSMUST00000127868						1	1	0	0	0	0	0	3	3	0	0		
ENSMUST00000127869						1	0	0	0	1	0	0	0	0	0	1		
ENSMUST00000127870	ENSMUSG00000040701	14	55098578	55106593	-1	0	0	0	0	0	0	0	88	26	0	0	D6RFT7	
ENSMUST00000127871						0	0	0	6	0	0	0	0	0	0	3		
ENSMUST00000127872						1	2	0	2	0	0	0	27	4	6	5		
ENSMUST00000127873	ENSMUSG00000032812	7	101348067	101412586	1	0	0	0	4	0	0	7	4	3	0	0	D3Z2X3	
ENSMUST00000127874	ENSMUSG00000047215	5	65388364	65391444	-1	4	0	4	156	11	3	7	0	0	0	5	D3YZT0	
ENSMUST00000127876	ENSMUSG00000054874	19	5664635	5688908	-1	2	4	10	10	3	0	22	7	24	2	29	F6VNK1	
ENSMUST00000127877						1	1	2	2	4	4	0	0	0	0	0		
ENSMUST00000127878						6	4	15	14	14	8	3	96	22	13	39		
ENSMUST00000127879						2	1	2	7	2	1	0	0	0	0	0		
ENSMUST00000127880	ENSMUSG00000041268	9	54365158	54501760	-1	0	3	0	0	0	1	64	40	174	0	91	B0V2P6	
ENSMUST00000127881						3	0	0	8	0	2	19	18	19	50	41		
ENSMUST00000127882						6	5	29	53	30	6	74	358	107	23	137		
ENSMUST00000127884						134	120	1174	234	130	53	23	81	44	4	68		
ENSMUST00000127885						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127886	ENSMUSG00000059049	4	82897920	83052339	-1	44	27	208	37	39	14	1	1	0	0	1	F7D5I3	
ENSMUST00000127887						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000127888						50	56	204	108	68	35	0	7	8	3	8		
ENSMUST00000127889	ENSMUSG00000001039	11	61505144	61512931	1	0	2	0	0	2	0	0	0	0	0	0	Q5NCM9	
ENSMUST00000127890						441	399	2667	578	559	296	10	38	27	16	67		
ENSMUST00000127891	ENSMUSG00000035623	7	97579889	97692778	1	0	0	3	29	0	0	5	3	0	0	0		
ENSMUST00000127892						6	2	0	15	3	0	0	2	0	0	1		
ENSMUST00000127893	ENSMUSG00000024002	17	32196274	32284722	-1	0	2	9	9	0	0	23	4	71	0	65	B0V2V6	
ENSMUST00000127894						1	2	4	0	3	2	11	19	8	0	21		
ENSMUST00000127895						1	3	6	1	2	1	4	22	5	0	8		
ENSMUST00000127896	ENSMUSG00000036781	9	66946086	66949516	1	0	0	0	0	0	0	7	22	12	36	0	D3YYB0	
ENSMUST00000127897						5	0	2	198	0	3	2	0	2	0	3		
ENSMUST00000127898						0	6	14	75	20	0	37	0	18	18	71		
ENSMUST00000127899						5	10	5	4	3	0	0	0	1	0	2		
ENSMUST00000127900	ENSMUSG00000031748	8	93809966	93969388	1	0	0	0	0	0	0	0	0	0	1	0	F7BLT7	
ENSMUST00000127901						77	60	153	111	108	36	3	10	9	1	3		
ENSMUST00000127902						1	0	0	0	2	0	3	0	0	0	4		
ENSMUST00000127903						5	3	1	11	5	6	0	0	0	0	0		
ENSMUST00000127904	ENSMUSG00000032815	8	123268300	123318576	-1	0	2	22	0	8	0	0	0	0	0	0	F7CK17	
ENSMUST00000127905						2	2	1	1	1	1	0	0	0	0	0		
ENSMUST00000127906	ENSMUSG00000054889	13	38151328	38198577	1	0	6	0	151	14	0	3	1	2	0	16	E9PZW0	
ENSMUST00000127907						0	1	0	33	0	0	0	2	0	0	0		
ENSMUST00000127908						27	30	160	20	31	20	0	6	6	3	4		
ENSMUST00000127909						3	1	1	1	4	2	0	1	0	0	1		
ENSMUST00000127910						5	0	0	1	2	2	0	74	0	0	0		
ENSMUST00000127911						0	0	3	0	2	2	0	0	0	0	0		
ENSMUST00000127912						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000127914						8	10	16	4	11	5	0	0	0	0	5		
ENSMUST00000127915						4	4	1	0	4	0	0	0	0	0	0		
ENSMUST00000127916	ENSMUSG00000028621	4	107066988	107088268	1	0	0	0	0	0	0	1	0	0	1	0	B1AS45	
ENSMUST00000127917						0	0	0	10	0	0	0	0	0	0	0		
ENSMUST00000127918	ENSMUSG00000079170	2	111088372	111105982	-1	3	3	2	0	1	0	0	0	0	0	0	A2AJ38	
ENSMUST00000127919	ENSMUSG00000028797	4	129600668	129624059	1	1	0	0	6	0	0	3	6	0	0	4	D6RDC0	
ENSMUST00000127921	ENSMUSG00000026135	1	74565127	74588246	-1	0	0	19	0	0	0	128	0	214	0	156	M0QWM7	
ENSMUST00000127923	ENSMUSG00000026049	1	44086613	44102441	-1	1	3	0	3	0	0	0	0	6	0	0	D3Z7L3	
ENSMUST00000127924	ENSMUSG00000031328	X	74223461	74249820	-1	2	0	1	0	0	0	56	851	0	11	0	F7AVL7	
ENSMUST00000127925						62	0	4	89	32	16	0	0	0	0	0		
ENSMUST00000127926						1	0	4	0	2	1	0	2	3	1	0		
ENSMUST00000127927						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000127928						0	6	0	3	0	0	0	0	0	0	0		
ENSMUST00000127929	ENSMUSG00000041119	17	31386234	31476310	1	0	0	0	0	0	0	0	0	0	0	0		O70628
ENSMUST00000127931						4	0	30	7	5	4	0	3	6	0	8		
ENSMUST00000127932						5	4	0	7	2	0	5	0	6	0	4		
ENSMUST00000127933						0	2	0	0	0	0	2	0	0	0	0		
ENSMUST00000127934						3	5	14	2	5	0	0	0	0	0	0		
ENSMUST00000127935	ENSMUSG00000005611	7	110868266	110982461	-1	0	0	0	15	3	0	7	77	0	19	5	Q3UR44	
ENSMUST00000127937	ENSMUSG00000061462	11	58994256	59136402	-1	5	4	0	4	14	0	0	0	0	0	0	F6X8F4	
ENSMUST00000127938	ENSMUSG00000026171	1	74593748	74601397	-1	0	2	0	0	0	3	0	0	3	0	0	D3Z7S2	
ENSMUST00000127939	ENSMUSG00000006418	2	167492645	167516173	1	11	3	15	0	0	0	1583	3475	1120	340	1130	S4R1Z0	
ENSMUST00000127940						10	3	10	3	3	3	0	3	3	0	4		
ENSMUST00000127941	ENSMUSG00000030309	6	148842492	148896237	-1	0	0	0	0	0	0	0	2	1	1	0		
ENSMUST00000127943						0	0	18	7	5	4	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000127944						26	16	62	50	32	29	236	651	345	42	675		
ENSMUST00000127946	ENSMUSG00000028556	4	98936671	99120915	-1	3	0	4	0	3	0	0	0	0	0	0	A2AW79	
ENSMUST00000127947						1	0	6	0	2	2	9	50	22	4	42		
ENSMUST00000127948						6	0	8	3	4	2	0	0	0	0	0		
ENSMUST00000127949						12	8	4	10	15	2	9	35	6	6	15		
ENSMUST00000127950						0	4	1	1	0	2	8	5	11	0	11		
ENSMUST00000127952						5	4	7	0	6	2	0	0	0	0	0		
ENSMUST00000127953						4	0	2	1	1	0	5	13	5	2	4		
ENSMUST00000127954						0	2	6	10	4	0	42	55	50	8	20		
ENSMUST00000127955	ENSMUSG00000027940	3	90072649	90100902	1	1	1	6	5	1	4	4	8	15	6	9		
ENSMUST00000127956	ENSMUSG00000098950	2	156071845	156127092	-1	0	17	0	0	0	0	179	631	254	25	146	F6YJB6	
ENSMUST00000127957	ENSMUSG00000033576	15	77044729	77057107	1	34	33	64	31	55	31	0	2	2	2	8	B7ZC55	
ENSMUST00000127958						0	0	0	5	4	0	1	0	1	2	0		
ENSMUST00000127959						1	1	2	4	0	1	1	0	0	0	2		
ENSMUST00000127960						719	721	580	495	752	361	21	128	55	16	57		
ENSMUST00000127961	ENSMUSG00000026819	2	32414487	32451445	-1	0	0	0	0	0	0	0	0	0	0	0	F6RC04	
ENSMUST00000127962						0	2	10	0	0	0	0	1	0	0	0		
ENSMUST00000127963						0	0	0	1	2	0	0	4	0	0	3		
ENSMUST00000127964						0	3	0	26	0	0	0	0	0	0	0		
ENSMUST00000127965						3	0	0	1	0	0	2	3	0	0	5		
ENSMUST00000127966						138	127	286	1151	194	78	15	62	48	6	67		
ENSMUST00000127968						1	2	0	0	0	0	7	0	4	5	6		
ENSMUST00000127970						9	0	10	0	2	3	8	0	7	0	13		
ENSMUST00000127971						5	0	10	20	0	2	0	4	22	0	0		
ENSMUST00000127972	ENSMUSG00000065979	16	11803721	11909445	-1	0	5	0	33	3	7	0	0	0	0	2	D3Z7F7	
ENSMUST00000127973	ENSMUSG00000022684	16	13671858	13703612	1	0	1	9	17	3	0	4	11	21	4	12	D6RG73	
ENSMUST00000127974	ENSMUSG00000052593	12	21323509	21373632	-1	0	8	0	0	0	0	197	384	0	513	137	J3QNB3	
ENSMUST00000127975	ENSMUSG00000029015	5	21810655	21865604	-1	0	0	21	9	11	0	0	0	0	0	0	D3Z013	
ENSMUST00000127976						4	0	2	1	1	1	0	0	0	0	0		
ENSMUST00000127977						0	0	0	49	0	0	0	0	0	0	0		
ENSMUST00000127978						0	0	3	7	2	0	0	15	14	0	3		
ENSMUST00000127979	ENSMUSG00000071281	13	67705306	67729119	-1	29	0	84	30	0	92	32	47	32	27	8	B8JJX9	
ENSMUST00000127980						0	0	0	39	0	0	1	0	1	0	0		
ENSMUST00000127982	ENSMUSG00000032657	3	89183143	89189295	1	14	5	47	30	26	16	0	57	8	0	31	D6RDQ0	
ENSMUST00000127983	ENSMUSG00000007888	8	70493158	70504081	1	0	0	0	6	2	2	0	0	0	0	0	F6T1W4	
ENSMUST00000127984	ENSMUSG00000006362	8	122628739	122699109	-1	23	13	62	41	31	12	71	121	49	3	84	B7ZP57	
ENSMUST00000127986						0	3	7	3	12	2	0	0	0	0	0		
ENSMUST00000127987	ENSMUSG00000027329	2	131170261	131187282	-1	0	0	0	24	0	2	0	2	4	2	3	F6ZW13	
ENSMUST00000127988	ENSMUSG00000038671	2	181357690	181365404	-1	0	0	0	0	0	0	117	621	50	4	102		Q8BXL7
ENSMUST00000127991						0	0	0	1	0	0	1	6	0	0	7		
ENSMUST00000127992						3	2	1	13	6	4	0	0	0	0	0		
ENSMUST00000127993						0	0	1	0	1	0	13	46	35	16	29		
ENSMUST00000127994	ENSMUSG00000022757	16	56690332	56717450	-1	4	2	15	0	3	0	36	9	51	28	42	F6QJV5	
ENSMUST00000127995						1	2	9	0	0	0	0	0	0	0	0		
ENSMUST00000127996	ENSMUSG00000039048	9	35204206	35211055	-1	0	0	0	20	5	0	118	306	201	69	0		Q3TQB2
ENSMUST00000127997	ENSMUSG00000030533	7	80325292	80341005	-1	0	0	0	0	0	0	0	0	0	0	10	D3YVI2	
ENSMUST00000127998						3	0	13	0	3	0	6	7	3	0	0		
ENSMUST00000127999						33	24	66	168	40	24	13	105	16	14	27		
ENSMUST00000128001						0	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000128002						0	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000128003	ENSMUSG00000055681	8	70302518	70312993	1	3	2	3	0	2	2	43	229	28	14	88	F6YFR7	
ENSMUST00000128004						6	0	4	0	8	2	0	0	0	0	3		
ENSMUST00000128005	ENSMUSG00000000561	3	105959369	105970037	1	0	0	0	0	0	0	199	387	243	31	295	F7D5L2	
ENSMUST00000128006						3	4	6	0	5	2	5	5	0	0	0		
ENSMUST00000128007	ENSMUSG00000028784	4	129947547	129957115	1	1	3	6	1	6	4	0	0	0	0	0	B1ASB5	
ENSMUST00000128008						10	3	19	8	10	9	1	3	0	0	0		
ENSMUST00000128009	ENSMUSG00000036676	10	100443902	100487350	-1	0	0	0	0	0	0	0	0	0	0	2	D3Z2Z3	
ENSMUST00000128010						35	36	123	49	39	22	21	149	34	4	35		
ENSMUST00000128011						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128012	ENSMUSG00000031012	X	13517080	13851367	-1	0	0	0	0	0	0	0	0	36	19	60	F6ZQR2	
ENSMUST00000128014						5	0	0	0	0	0	12	0	17	4	5		
ENSMUST00000128015						39	15	86	29	32	21	18	111	32	4	150		
ENSMUST00000128016	ENSMUSG00000020923	11	102304560	102319742	-1	3	0	9	46	3	3	0	2	2	1	4	E9Q4A8	
ENSMUST00000128018	ENSMUSG00000059851	7	4740115	4747514	1	3	0	0	36	2	0	12	15	5	0	18	F6XZN9	
ENSMUST00000128019						0	0	22	8	3	0	26	50	22	8	15		
ENSMUST00000128020						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000128021	ENSMUSG00000032327	9	58063788	58153996	1	0	1	0	1	0	0	0	0	0	0	0	D3YVZ1	
ENSMUST00000128022						1	1	1	7	2	3	0	3	0	0	0		
ENSMUST00000128023						4	5	3	6	4	2	0	0	0	0	0		
ENSMUST00000128024	ENSMUSG00000045205	4	11261315	11322137	-1	0	0	0	48	0	0	4	0	23	0	0	A2AJQ1	
ENSMUST00000128025						2	4	8	10	7	6	2	5	2	0	10		
ENSMUST00000128027						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000128028						0	2	0	6	7	0	0	21	10	0	5		
ENSMUST00000128029						0	5	16	0	15	7	14	54	18	4	26		
ENSMUST00000128030						1	1	52	9	6	2	0	0	1	0	1		
ENSMUST00000128031						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000128032						0	0	0	0	2	0	14	0	9	13	0		
ENSMUST00000128033						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128034						2	1	2	7	2	4	0	0	0	0	0		
ENSMUST00000128035	ENSMUSG00000003813	8	84834019	84840665	-1	0	1	0	54	9	4	20	0	52	0	2	Q3TN85	
ENSMUST00000128036						12	8	1	8	6	1	5	2	0	0	11		
ENSMUST00000128037						0	0	0	0	0	0	10	12	6	0	0		
ENSMUST00000128038						3	3	10	3	6	0	31	34	42	5	73		
ENSMUST00000128039						2	3	6	8	9	1	36	42	32	6	40		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128040	ENSMUSG00000044550	X	136590842	136668378	1	4	0	22	4	8	6	0	0	0	1	1	A2AEC2	
ENSMUST00000128041	ENSMUSG00000025227	19	46341121	46375252	1	8	7	25	0	0	3	0	209	20	0	92		Q6PDE8
ENSMUST00000128042	ENSMUSG00000034610	4	108459426	108559421	1	0	0	0	0	1	0	7	66	22	20	50	A2A8R1	
ENSMUST00000128043	ENSMUSG00000031021	7	109735834	109752875	-1	0	0	1	46	5	2	0	0	0	0	0	D3YU78	
ENSMUST00000128044						8	4	16	12	10	4	0	0	0	0	2		
ENSMUST00000128045	ENSMUSG00000022721	16	18248679	18254772	1	0	0	0	0	0	0	0	0	0	0	0	F6SY41	
ENSMUST00000128046	ENSMUSG00000018570	11	69897352	69900987	-1	0	0	0	0	0	0	0	0	2	0	3	J3QPY8	
ENSMUST00000128047						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000128048						1	1	4	1	6	0	0	0	0	0	0		
ENSMUST00000128049						2	4	2	2	0	3	39	94	31	6	42		
ENSMUST00000128050	ENSMUSG00000022885	16	23224740	23360350	1	2	1	0	0	0	2	3	0	0	0	0	D3Z1Z5	
ENSMUST00000128051						2	2	9	3	8	5	0	0	0	0	0		
ENSMUST00000128052						0	0	24	0	14	2	0	35	1	0	0		
ENSMUST00000128054						4	12	5	5	8	4	0	0	0	0	0		
ENSMUST00000128055	ENSMUSG00000062825	11	120345690	120348542	-1	0	4	2	184	14	2	12	93	43	2	78	G3UZ07	
ENSMUST00000128057	ENSMUSG00000031072	7	144915100	144930748	1	10	3	23	15	24	8	32	45	42	3	19	Q8BQU0	
ENSMUST00000128058						9	13	13	10	10	6	0	0	0	0	0		
ENSMUST00000128059	ENSMUSG00000028692	4	116636510	116651680	-1	0	0	0	0	0	2	0	0	0	0	8	B1AXW3	
ENSMUST00000128060						0	0	0	0	9	0	0	0	0	0	0		
ENSMUST00000128061	ENSMUSG00000037270	3	36863104	37053033	1	0	0	0	0	0	0	0	6	13	0	12	F6Q4Y5	
ENSMUST00000128062	ENSMUSG00000105383	9	109057933	109074120	-1	0	0	0	0	0	0	0	0	0	0	0	D3YUE0	
ENSMUST00000128064						3901	3005	3517	3114	8161	1299	4	34	10	4	71		
ENSMUST00000128065	ENSMUSG00000043411	4	137593755	137658537	1	0	3	2	0	6	2	9	15	20	5	22	F6TGT8	
ENSMUST00000128066						3	2	1	4	3	1	0	0	0	0	0		
ENSMUST00000128067						23	21	88	21	43	17	9	5	4	0	6		
ENSMUST00000128068						15	16	47	11	15	8	0	0	0	0	3		
ENSMUST00000128069						3	0	1	0	2	2	0	0	0	0	0		
ENSMUST00000128070						0	1	2	4	0	0	1	0	0	2	2		
ENSMUST00000128071	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	0	0	0	0	0	0	0	0	A2AT68	
ENSMUST00000128072						2	0	3	1	4	1	4	3	2	0	9		
ENSMUST00000128073						0	3	0	3	0	0	78	0	0	16	0		
ENSMUST00000128074						0	0	0	6	0	7	0	28	0	0	12		
ENSMUST00000128075	ENSMUSG00000028964	4	150897133	150914437	-1	7	0	20	10	3	2	3	13	8	3	12	A2A815	
ENSMUST00000128076						0	0	6	0	2	1	0	0	0	0	0		
ENSMUST00000128077						2	0	0	1	3	1	0	0	0	0	0		
ENSMUST00000128079						1	0	1	2	3	3	0	2	1	0	1		
ENSMUST00000128081						28	18	13	14	16	10	0	0	1	0	0		
ENSMUST00000128082	ENSMUSG00000030243	6	142350342	142387087	-1	2	0	0	9	0	0	2	0	1	2	9	D3YZW9	
ENSMUST00000128083	ENSMUSG00000037965	16	11136592	11176393	-1	6	5	21	3	2	0	0	0	0	0	13	E9Q0D3	
ENSMUST00000128084						2	2	9	3	2	5	0	0	0	1	0		
ENSMUST00000128085	ENSMUSG00000037216	1	37871738	37876228	1	5	6	4	5	5	3	0	0	0	0	3	D3Z2L3	
ENSMUST00000128086						1	1	7	6	3	0	0	0	0	0	0		
ENSMUST00000128087						0	0	2	0	0	2	0	4	0	0	8		
ENSMUST00000128088	ENSMUSG00000074115	7	46740501	46742980	-1	3	7	3	6	8	6	102	79	69	149	4	Q5I0U6	P05366
ENSMUST00000128089	ENSMUSG00000068744	3	108383839	108388231	1	3	0	3	6	0	1	0	0	0	0	2	A2AEF3	
ENSMUST00000128090	ENSMUSG00000003762	7	27233023	27257950	1	2	0	3	2	0	0	25	64	20	0	7		
ENSMUST00000128092						0	0	0	0	0	0	0	0	2	0	1		
ENSMUST00000128093						0	0	0	0	0	0	0	156	53	14	62		
ENSMUST00000128095	ENSMUSG00000031012	X	13517080	13851367	-1	0	0	0	0	0	0	3	141	35	72	4	F7CD87	
ENSMUST00000128096						11	22	109	10	6	9	0	0	3	0	5		
ENSMUST00000128097	ENSMUSG00000022149	15	6445327	6498751	1	0	1	1	0	4	2	0	0	0	0	0	H3BL17	
ENSMUST00000128098	ENSMUSG00000050854	4	118540941	118544044	-1	3	1	11	47	3	3	0	0	0	0	0	A8WIT1	
ENSMUST00000128099	ENSMUSG00000020230	10	76207222	76237865	-1	0	0	0	0	0	0	0	0	0	0	0	M0QW88	
ENSMUST00000128100	ENSMUSG00000028394	4	62522649	62525068	-1	14	14	63	96	0	19	11	19	0	6	14	D6RDT4	
ENSMUST00000128101	ENSMUSG00000043036	5	122108040	122140823	-1	2	0	2	0	0	0	0	0	0	0	0	D3YUZ2	
ENSMUST00000128102	ENSMUSG00000101298	6	52163359	52213339	-1	0	2	0	11	0	0	0	0	0	2	0	A0A087WRU5	
ENSMUST00000128103						4	5	1	0	3	0	1	3	3	0	1		
ENSMUST00000128105						23	11	39	6	27	10	7	5	6	2	0		
ENSMUST00000128106						0	0	0	0	0	0	0	0	9	1	0		
ENSMUST00000128107						5	3	1	15	0	1	0	0	0	3	0		
ENSMUST00000128108						26	23	20	12	13	4	0	0	0	0	0		
ENSMUST00000128109						1	8	7	1	4	1	0	0	0	0	0		
ENSMUST00000128110	ENSMUSG00000017754	2	164839518	164857711	-1	0	0	0	12	0	0	0	3	0	0	5	A2A5K3	
ENSMUST00000128112	ENSMUSG00000036377	5	76656512	76873554	1	0	0	0	0	0	0	3	0	22	1	1	D3Z1J3	
ENSMUST00000128113						2	1	11	3	2	0	0	0	0	0	1		
ENSMUST00000128114						0	1	3	2	2	0	0	0	0	0	0		
ENSMUST00000128115	ENSMUSG00000067369	X	134222339	134276984	-1	540	458	2109	566	678	293	24	124	84	34	111	S4R2E5	
ENSMUST00000128116						3	1	2	4	3	1	0	0	0	0	0		
ENSMUST00000128117						10	10	11	9	10	6	0	0	0	0	0		
ENSMUST00000128118						2	5	2	0	2	0	1	74	4	3	5		
ENSMUST00000128119	ENSMUSG00000045039	7	25317164	25365917	1	103	54	284	607	160	60	52	16	43	5	112		P60882
ENSMUST00000128120	ENSMUSG00000069170	13	81095068	81633154	-1	0	0	0	3	0	0	0	8	0	5	3	Q8C1E5	
ENSMUST00000128122	ENSMUSG00000028677	4	117271463	117497052	-1	2	3	1	18	6	0	16	0	0	0	0	A2APN9	
ENSMUST00000128123	ENSMUSG00000028618	4	107178399	107200996	1	0	0	0	0	0	1	0	0	0	0	0	D3Z0H8	
ENSMUST00000128124						0	0	0	12	0	0	0	0	0	0	1		
ENSMUST00000128127						32	37	30	31	19	0	8	33	1	0	37		
ENSMUST00000128128	ENSMUSG00000042554	1	130576713	130629621	-1	0	0	0	9	0	3	0	0	0	0	0	E9PZ07	
ENSMUST00000128129						0	0	0	31	0	0	0	0	0	0	0		
ENSMUST00000128130						1	2	8	9	5	2	3	10	1	1	3		
ENSMUST00000128132						2	1	3	2	1	4	0	0	0	0	0		
ENSMUST00000128133						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000128134						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128135						0	3	11	2	6	0	77	245	112	0	115		
ENSMUST00000128136	ENSMUSG00000031386	X	73942792	73966357	-1	0	0	0	0	0	0	62	631	63	47	63	F6SJS2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128137						0	3	2	0	0	3	0	0	0	0	0		
ENSMUST00000128139	ENSMUSG00000000392	2	62500943	62574075	-1	0	2	0	0	0	3	0	0	0	2	0	G3UYG3	
ENSMUST00000128140	ENSMUSG00000027243	2	91710852	91721545	1	0	0	1	6	0	0	0	0	0	0	0	B7ZCF6	
ENSMUST00000128141						3	5	6	0	3	2	0	20	22	0	10		
ENSMUST00000128142						0	0	0	0	1	0	0	1	2	2	0		
ENSMUST00000128144						2	3	14	5	3	3	0	0	0	0	4		
ENSMUST00000128145						3	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000128146						21	28	42	33	45	14	0	0	0	0	0		
ENSMUST00000128148						2	1	0	5	0	0	0	0	0	0	0		
ENSMUST00000128149						0	0	6	0	3	0	0	8	2	46	7		
ENSMUST00000128150	ENSMUSG00000002031	9	44767908	44792714	1	23	18	37	20	20	10	23	38	29	18	27	D3YYR2	
ENSMUST00000128151	ENSMUSG00000079666	5	5437827	5479143	-1	0	0	0	0	1	0	0	0	0	0	0	F6RPA1	
ENSMUST00000128152	ENSMUSG00000040479	2	91932824	91975864	-1	0	13	19	24	15	12	953	618	963	24	736	D6RHK9	
ENSMUST00000128153						3	3	2	9	0	2	0	0	1	0	0		
ENSMUST00000128154						1	2	0	0	0	0	0	25	13	0	3		
ENSMUST00000128155						0	0	0	2	0	0	0	0	0	0	3		
ENSMUST00000128156	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	0	30	109	125	40	89	Q501M1	Q60819
ENSMUST00000128157						8	11	15	33	12	6	10	32	18	5	37		
ENSMUST00000128158						0	0	0	0	0	1	0	0	0	0	3		
ENSMUST00000128161						6	20	57	24	38	16	2	0	0	0	0		
ENSMUST00000128162						3	1	7	87	0	3	0	0	0	0	0		
ENSMUST00000128163	ENSMUSG00000032281	9	54604877	54661870	-1	0	1	4	0	1	2	0	0	0	0	0	D3Z1Z2	
ENSMUST00000128164						1	2	2	1	0	0	2	15	6	0	7		
ENSMUST00000128166	ENSMUSG00000039470	8	40423815	40510268	1	0	0	0	0	0	0	0	0	8	0	1		P59267
ENSMUST00000128167						1	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000128168	ENSMUSG00000064115	16	66655421	67620908	-1	0	2	0	0	0	0	0	0	0	0	0	G3UZM4	
ENSMUST00000128169						0	0	9	3	1	0	0	0	0	0	0		
ENSMUST00000128170	ENSMUSG00000024948	19	6341135	6355615	1	0	0	0	0	0	0	270	222	241	25	257	F6RPB0	
ENSMUST00000128171						0	0	0	0	0	0	0	3	3	0	0		
ENSMUST00000128172	ENSMUSG00000007659	2	152780668	152831728	-1	12	2	8	89	17	8	30	5	35	0	15	Q9QWX2	
ENSMUST00000128173						4	3	36	14	10	5	0	0	1	0	4		
ENSMUST00000128174						3	3	29	5	10	7	0	28	19	42	0		
ENSMUST00000128175						0	4	6	3	4	0	11	28	23	0	28		
ENSMUST00000128177						5	10	9	10	6	6	0	0	0	0	0		
ENSMUST00000128179	ENSMUSG00000024048	17	70993656	71002878	-1	1	3	1	78	10	1	8	2	7	0	2	D3Z249	
ENSMUST00000128182						69	46	153	234	59	27	0	1	5	0	0		
ENSMUST00000128184	ENSMUSG00000024986	19	37434810	37440731	1	27	13	45	32	27	15	362	1223	309	83	238	G3UXH1	
ENSMUST00000128185						3	1	0	1	1	0	0	0	0	0	3		
ENSMUST00000128187	ENSMUSG00000029328	5	100033577	100039664	-1	0	5	0	0	0	0	86	1215	160	222	232	D3YTQ3	
ENSMUST00000128188						18	16	45	9	13	9	0	44	4	0	31		
ENSMUST00000128189						0	0	0	0	1	1	7	35	37	417	158		
ENSMUST00000128190	ENSMUSG00000026049	1	44086613	44102441	-1	4	0	10	0	7	7	3	0	0	0	12		Q3TUU5
ENSMUST00000128192						0	1	3	22	3	0	0	0	0	0	0		
ENSMUST00000128193						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128194	ENSMUSG00000038347	17	13482553	13761825	-1	0	2	3	2	0	3	0	0	0	0	0	D6RFB5	
ENSMUST00000128195	ENSMUSG00000029097	5	35557313	35575070	-1	0	0	0	0	0	0	0	7	0	0	0		
ENSMUST00000128196						14	15	19	15	7	0	0	0	0	0	0		
ENSMUST00000128197						79	50	97	917	145	85	3	7	1	0	14		
ENSMUST00000128199						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000128200	ENSMUSG00000043241	2	5951469	6056703	1	0	0	0	0	0	0	15	840	104	270	128	F6Q3G7	
ENSMUST00000128201	ENSMUSG00000060098	8	106210936	106252794	1	9	2	5	6	4	5	0	0	0	0	12	F6RXJ8	
ENSMUST00000128202						11	4	2	3	5	4	0	0	0	0	0		
ENSMUST00000128203						0	3	4	12	3	0	567	1075	648	315	539		
ENSMUST00000128204						14	2	0	10	11	10	9	10	21	0	0		
ENSMUST00000128205						0	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000128206	ENSMUSG00000027651	2	158028497	158132297	1	4	0	0	0	0	0	17	0	26	0	22	F6YB25	
ENSMUST00000128207						0	0	2	0	0	0	1	0	0	0	0		
ENSMUST00000128208						158	98	723	540	178	102	2	3	5	0	3		
ENSMUST00000128210						8	10	10	0	7	10	0	59	0	56	124		
ENSMUST00000128211						7	5	5	0	0	0	0	0	0	0	0		
ENSMUST00000128212						14	16	14	17	8	5	0	0	0	0	0		
ENSMUST00000128215						17	10	10	5	12	10	1	0	2	0	0		
ENSMUST00000128217	ENSMUSG00000030757	7	123475384	123500449	-1	8	5	2	47	6	2	0	0	0	0	0	G3UZ80	
ENSMUST00000128219	ENSMUSG00000059857	3	109780040	110144011	-1	8	14	16	0	7	9	0	0	0	0	0	F7CVQ1	
ENSMUST00000128220						3	3	0	5	0	0	0	0	0	0	0		
ENSMUST00000128221						2	3	0	4	0	4	12	175	97	18	270		
ENSMUST00000128222						7	10	12	17	7	4	1	0	2	0	3		
ENSMUST00000128223						1	1	4	2	3	4	7	9	3	1	10		
ENSMUST00000128224						5	15	0	8	3	3	0	0	0	0	0		
ENSMUST00000128225						0	0	0	0	0	0	23	0	24	0	48		
ENSMUST00000128226						8	4	27	10	0	6	0	0	0	0	0		
ENSMUST00000128227						8	11	0	0	9	6	10	3	6	1	11		
ENSMUST00000128228						5	3	3	37	4	0	0	0	8	0	4		
ENSMUST00000128229						7	0	3	1	4	7	94	526	145	78	176		
ENSMUST00000128230	ENSMUSG00000038335	11	74898071	74909342	1	0	4	0	3	0	0	2	0	0	0	13	D6RCZ2	
ENSMUST00000128231	ENSMUSG00000022174	14	54235479	54254104	-1	27	27	120	52	45	28	8	17	10	1	17		P61804
ENSMUST00000128232						1	0	4	2	2	0	0	2	0	2	0		
ENSMUST00000128234	ENSMUSG00000000738	8	123062942	123097760	1	0	0	2	0	0	0	8	29	0	11	8	F6W695	
ENSMUST00000128236	ENSMUSG00000021792	14	40993740	41013788	-1	2	0	0	23	5	2	2	0	0	0	0	D3YWL4	
ENSMUST00000128237						2	1	4	1	0	1	0	0	0	0	0		
ENSMUST00000128238	ENSMUSG00000042626	3	89418443	89430027	1	0	0	0	0	1	0	0	0	0	0	0	D3Z2I8	
ENSMUST00000128239						10	7	6	5	13	2	5	52	8	4	21		
ENSMUST00000128241	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0	B2MVU6	Q9Z0E3
ENSMUST00000128243						2	0	0	4	0	2	29	42	28	3	38		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128244	ENSMUSG00000049491	11	55124815	55151708	-1	12	7	20	0	8	0	10	60	0	6	25	D6R158	
ENSMUST00000128245	ENSMUSG00000029671	6	22288227	22298522	1	15	15	48	37	14	1	0	2	0	0	3	H3BJ29	
ENSMUST00000128246	ENSMUSG00000034842	5	92331827	92414628	1	11	0	4	5	9	0	0	1	0	1	0	E9Q8Z0	
ENSMUST00000128247	ENSMUSG00000099009	10	127759787	127792694	1	0	0	0	0	0	0	14	0	17	0	0	E9Q9P8	
ENSMUST00000128248						0	0	0	0	0	0	7	0	0	3	0		
ENSMUST00000128249						0	0	0	0	24	0	0	0	0	90	0		
ENSMUST00000128250	ENSMUSG00000001127	X	20797814	20860519	1	2	2	6	4	0	1	30	108	0	0	38	B1AUP0	
ENSMUST00000128251						1	0	2	0	1	0	0	0	0	1	1		
ENSMUST00000128252						16	9	12	426	11	9	0	0	0	0	0		
ENSMUST00000128253	ENSMUSG00000026274	1	93308770	93343482	-1	0	0	1	0	0	0	0	0	0	0	0	D3YUI8	
ENSMUST00000128254						2	4	10	8	4	0	0	3	0	2	12		
ENSMUST00000128255	ENSMUSG00000029703	5	136122772	136136074	-1	3	0	1	0	2	0	0	0	0	0	3	F6RP62	
ENSMUST00000128256	ENSMUSG00000034354	11	4480868	4594863	-1	3	12	0	0	3	15	139	9	297	0	191	B1ATD4	
ENSMUST00000128257	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	3	10	0	0	0	0	0	7		Q3UHJ8
ENSMUST00000128258	ENSMUSG00000072812	12	112772194	112802657	-1	48	34	127	219	89	21	0	0	0	2	65	F7DBB3	
ENSMUST00000128259	ENSMUSG00000079324	2	68656486	68748467	1	14	13	31	11	21	6	0	0	0	0	0	Q8CEQ9	
ENSMUST00000128260	ENSMUSG00000001240	11	101246028	101259546	1	2	1	0	27	6	10	0	0	0	7	0	E9Q0S5	
ENSMUST00000128261	ENSMUSG00000057363	1	43746966	43827800	-1	0	0	3	39	0	0	0	0	4	0	0	D3Z411	
ENSMUST00000128262						7	0	8	5	4	0	0	18	5	1	7		
ENSMUST00000128264	ENSMUSG00000027852	3	103058285	103067914	1	0	0	0	0	0	0	76	175	136	260	150	E9PVD5	
ENSMUST00000128265						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000128266						2	2	0	129	1	5	4	9	0	0	2		
ENSMUST00000128267						1	0	0	2	1	0	3	9	6	0	0		
ENSMUST00000128268						0	0	3	0	0	0	4	0	0	0	0		
ENSMUST00000128269	ENSMUSG00000040433	9	96682770	96752831	-1	0	0	4	0	0	2	2	0	0	1	3	D3Z1Y7	
ENSMUST00000128270	ENSMUSG00000032116	9	36729344	36767679	-1	0	0	0	8	0	0	49	46	59	37	49	D6RDS9	
ENSMUST00000128271						0	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000128272						65	53	342	233	66	38	0	5	1	1	1		
ENSMUST00000128273	ENSMUSG00000050821	16	20693282	20703048	1	3	0	19	43	8	2	1	0	0	0	0	D3YXU9	
ENSMUST00000128275						0	0	0	0	0	0	0	1	5	0	0		
ENSMUST00000128276	ENSMUSG00000045589	4	56957173	56990391	-1	0	0	0	0	0	0	0	0	0	0	0	F6Q3S1	
ENSMUST00000128277						72	89	85	56	87	45	16	116	52	29	69		
ENSMUST00000128278						10	5	7	4	10	5	0	0	0	0	0		
ENSMUST00000128279						4	2	1	1	2	0	5	8	0	0	0		
ENSMUST00000128280						0	0	1	0	0	1	0	0	0	0	1		
ENSMUST00000128281						0	0	3	0	6	0	12	23	6	20	1		
ENSMUST00000128282						6	0	8	3	6	7	0	0	4	2	0		
ENSMUST00000128283						8	7	9	115	9	7	0	1	0	0	0		
ENSMUST00000128284	ENSMUSG00000057375	4	107314363	107359823	1	0	0	0	0	0	0	0	0	0	0	0	A2A8S2	
ENSMUST00000128285						0	2	0	0	0	3	0	110	0	0	0		
ENSMUST00000128286						0	0	6	80	2	0	0	0	0	0	0		
ENSMUST00000128287						3	3	2	57	0	2	0	10	0	6	4		
ENSMUST00000128288	ENSMUSG00000050908	16	10420557	10447362	-1	0	0	0	0	0	0	0	0	0	0	0	D6RI57	
ENSMUST00000128289	ENSMUSG00000031150	X	7731714	7750905	-1	1	1	3	0	2	0	0	0	0	0	1	A2AEV8	
ENSMUST00000128290						1	8	0	0	3	2	8	13	0	0	34		
ENSMUST00000128291						2	3	2	8	0	3	0	0	0	0	0		
ENSMUST00000128293	ENSMUSG00000004500	7	12965838	12974236	1	22	22	0	0	42	16	30	0	24	10	34	E0CXY6	
ENSMUST00000128294	ENSMUSG00000061723	7	142498836	142516009	1	0	0	5	0	0	0	2	0	0	0	0	A2A6J2	
ENSMUST00000128295	ENSMUSG00000026854	2	30982279	31023586	1	2	4	5	2	4	0	0	0	0	1	0	A2AQ35	
ENSMUST00000128296						3	0	13	13	2	2	0	0	0	0	0		
ENSMUST00000128297						0	0	6	6	1	0	0	2	0	0	0		
ENSMUST00000128299						2	0	6	15	0	0	1	0	0	0	0		
ENSMUST00000128300	ENSMUSG00000001729	12	112653821	112674884	-1	3	0	0	0	1	0	1314	0	1053	57	935	D3Z783	
ENSMUST00000128302	ENSMUSG00000055067	1	178951960	179518041	-1	124	87	401	277	142	63	15	79	55	5	69		Q9CWR2
ENSMUST00000128303	ENSMUSG00000026857	2	30807826	30823033	1	0	0	0	0	0	0	0	0	0	0	4	A2APZ2	
ENSMUST00000128304	ENSMUSG00000014633	8	116888685	116921455	-1	1	0	0	0	0	0	0	8	0	0	1	D3YZZ0	
ENSMUST00000128306						0	2	0	108	2	0	0	0	0	0	0		
ENSMUST00000128308	ENSMUSG00000061577	8	94923694	94943290	1	0	16	33	0	7	0	0	14	5	0	52	D6RJJ2	
ENSMUST00000128309	ENSMUSG00000004455	5	122158278	122175273	1	6	7	4	0	30	0	146	798	183	86	563	A0A0G2JGC1	
ENSMUST00000128311	ENSMUSG00000020279	11	32187541	32200279	-1	1	0	0	0	0	0	0	0	0	0	4	A2AVE0	
ENSMUST00000128312						2	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000128313						0	2	0	36	2	0	0	0	0	0	0		
ENSMUST00000128314						7	2	24	5	4	0	1	0	0	0	0		
ENSMUST00000128315						4	2	3	2	2	0	0	0	0	0	0		
ENSMUST00000128316						0	4	4	1	3	2	0	0	0	0	0		
ENSMUST00000128317						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128318	ENSMUSG00000068917	3	89164795	89176921	1	0	0	0	0	0	0	0	642	157	53	195	D6RG48	
ENSMUST00000128319	ENSMUSG00000004317	X	7153810	7319358	-1	3	1	0	46	0	0	7	0	37	0	12	B1ATV1	
ENSMUST00000128320						1	2	1	0	6	1	11	0	2	1	0		
ENSMUST00000128321						0	2	0	5	3	2	6	10	10	0	5		
ENSMUST00000128323						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128324						2	0	4	0	1	1	0	0	0	0	0		
ENSMUST00000128325						0	0	0	0	0	0	6	0	0	0	0		
ENSMUST00000128326	ENSMUSG00000048537	9	44686304	44735198	-1	0	0	0	0	0	0	0	0	0	10	23	F6RYD0	
ENSMUST00000128329						0	0	0	0	1	0	0	6	0	0	0		
ENSMUST00000128330	ENSMUSG00000038224	11	75431732	75439591	-1	0	0	5	5	0	0	0	0	0	0	0	Q5ND35	
ENSMUST00000128331						3	4	0	4	0	0	0	0	0	0	0		
ENSMUST00000128332						0	10	35	21	21	31	43	263	116	0	757		
ENSMUST00000128333						2	1	6	0	1	0	0	2	4	3	5		
ENSMUST00000128334						2	3	3	2	4	0	3	4	13	4	5		
ENSMUST00000128335						27	21	43	25	26	22	2	15	4	5	8		
ENSMUST00000128336						2	0	0	18	0	0	104	24	71	0	180		
ENSMUST00000128337	ENSMUSG00000026098	1	53189187	53297018	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z0R7	
ENSMUST00000128338						10	9	10	10	21	7	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128339						350	318	418	366	529	210	49	383	110	15	227		
ENSMUST00000128340	ENSMUSG00000028544	4	111875375	111902918	-1	1	0	0	0	0	0	0	0	0	0	0	I7HPX2	
ENSMUST00000128341	ENSMUSG00000039585	9	59750896	59928866	1	0	29	0	135	0	0	87	184	111	61	26		Q8C170
ENSMUST00000128343						4	0	2	9	0	5	0	2	0	2	1		
ENSMUST00000128344						2	0	11	5	6	3	26	66	51	11	39		
ENSMUST00000128345	ENSMUSG00000035131	1	146494760	146902472	1	0	0	0	0	3	0	0	0	0	0	0	F2Z476	
ENSMUST00000128346	ENSMUSG00000032413	9	96539300	96631617	-1	0	0	15	0	1	0	26	1	54	15	15	D3YZE9	
ENSMUST00000128347	ENSMUSG00000052133	16	35541145	35664732	1	0	0	0	0	0	0	0	0	0	0	0	F6PZQ7	
ENSMUST00000128348	ENSMUSG00000033157	16	45729725	45742955	-1	1	0	5	0	0	0	15	55	23	18	8	F6X5P5	
ENSMUST00000128349						0	0	0	1	5	0	0	0	0	0	0		
ENSMUST00000128350	ENSMUSG00000031730	8	109591343	109608673	-1	4	0	1	13	1	0	6	2	4	4	5	D3YZY5	
ENSMUST00000128351						2	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000128352	ENSMUSG00000023007	15	99295087	99317018	1	0	0	0	20	0	0	0	0	0	0	0	D3Z1Y9	
ENSMUST00000128353	ENSMUSG00000037904	12	110975353	110979040	-1	19	9	55	51	28	10	7	9	2	0	15		Q8BH83
ENSMUST00000128354						2	2	3	0	0	1	35	136	42	3	69		
ENSMUST00000128355						1	2	13	2	4	5	11	95	36	0	21		
ENSMUST00000128356						7	4	5	23	6	5	0	0	0	0	0		
ENSMUST00000128357	ENSMUSG00000024993	19	60811585	60836227	1	0	0	0	32	1	0	12	29	53	165	33	D3YUG1	
ENSMUST00000128358						0	0	0	6	7	0	0	0	0	0	0		
ENSMUST00000128359						1	1	0	0	3	2	0	0	1	0	0		
ENSMUST00000128360						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128361						0	2	11	0	0	0	0	0	0	0	0		
ENSMUST00000128362						1	1	3	0	1	2	0	0	0	0	0		
ENSMUST00000128363						0	0	0	26	0	0	0	0	2	0	0		
ENSMUST00000128364	ENSMUSG00000035596	7	3677789	3693523	-1	1	0	0	0	0	4	1290	312	915	118	841	F6UP63	
ENSMUST00000128365						0	2	2	3	0	0	0	0	0	0	0		
ENSMUST00000128367						7	6	16	10	15	13	7	0	2	0	4		
ENSMUST00000128369						4	4	5	2	2	0	0	0	4	2	2		
ENSMUST00000128370	ENSMUSG00000005267	11	62700356	62731905	-1	14	7	13	3	8	10	1	4	1	0	1	B7ZC81	
ENSMUST00000128371						1	1	0	12	0	0	0	0	4	0	0		
ENSMUST00000128372	ENSMUSG00000020288	11	23487882	23498030	-1	5	0	7	0	0	0	114	880	0	0	79	F6S1R2	
ENSMUST00000128373	ENSMUSG00000060568	1	167001417	167091302	1	19	0	52	7	14	9	0	0	0	0	5	F6ZXE6	
ENSMUST00000128374						3	1	8	1	3	0	28	72	29	28	0		
ENSMUST00000128375						18	18	43	17	39	0	0	60	9	0	28		
ENSMUST00000128376						0	0	0	49	3	1	88	166	151	7	89		
ENSMUST00000128377	ENSMUSG00000062210	18	49979427	50107173	1	0	0	0	0	0	0	0	0	7	174	25	J3QM73	
ENSMUST00000128378	ENSMUSG00000032327	9	58063788	58153996	1	0	0	1	1	0	0	0	0	0	0	0	E9Q283	
ENSMUST00000128379						0	1	1	3	4	3	0	0	1	1	4		
ENSMUST00000128380						9	7	36	14	7	6	29	152	44	6	60		
ENSMUST00000128381						1	3	0	4	2	3	8	7	0	0	9		
ENSMUST00000128382						7	1	3	2	0	3	0	56	33	0	37		
ENSMUST00000128383	ENSMUSG00000014444	8	122481698	122551329	-1	0	0	0	0	0	0	108	0	150	0	32	F6QY99	
ENSMUST00000128384	ENSMUSG00000046826	7	30973790	30989726	1	1	4	10	11	0	1	0	1	0	0	0		
ENSMUST00000128386						0	3	16	174	6	7	0	0	0	0	0		
ENSMUST00000128387						0	0	0	10	0	0	4	0	0	0	0		
ENSMUST00000128388						1	0	0	4	1	1	0	9	13	1	9		
ENSMUST00000128389						3	1	6	4	3	0	1	3	0	0	2		
ENSMUST00000128390						6	2	2	5	8	9	0	3	5	1	8		
ENSMUST00000128391						4	3	14	15	7	0	78	145	61	9	26		
ENSMUST00000128392						4	0	5	3	8	3	0	0	0	0	5		
ENSMUST00000128393						3	2	2	3	1	2	3	0	0	0	0		
ENSMUST00000128394						1	4	14	2	5	1	0	1	0	0	0		
ENSMUST00000128395	ENSMUSG00000035960	14	50924968	50927139	1	0	5	0	0	0	0	0	14	0	0	0	F6QA74	
ENSMUST00000128396						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128397						5	6	9	6	5	2	2	5	0	0	4		
ENSMUST00000128398						0	0	0	22	0	0	0	0	0	0	0		
ENSMUST00000128399	ENSMUSG00000020151	10	116018213	116274932	1	11	10	15	8	16	6	0	11	20	12	1		Q62132
ENSMUST00000128400						9	9	18	413	13	6	52	214	93	72	77		
ENSMUST00000128401						0	2	0	26	0	0	0	1	0	0	6		
ENSMUST00000128402	ENSMUSG00000021294	12	112146208	112181747	1	55	29	157	916	93	42	0	0	0	0	0		Q52KG5
ENSMUST00000128403						26	8	48	25	18	6	106	489	87	9	223		
ENSMUST00000128405						0	1	10	43	2	2	0	0	0	0	0		
ENSMUST00000128406						8	0	41	51	12	0	0	0	0	0	3		
ENSMUST00000128407						11	9	5	26	10	7	31	0	0	7	62		
ENSMUST00000128408						4	0	0	0	1	0	104	663	23	320	28		
ENSMUST00000128409						46	68	64	87	59	30	1	2	5	2	17		
ENSMUST00000128410						3	1	5	3	0	0	416	140	340	26	229		
ENSMUST00000128411						2	4	5	3	2	1	0	4	3	9	10		
ENSMUST00000128414						14	8	18	12	15	6	16	96	38	17	59		
ENSMUST00000128416						1	0	0	0	0	0	0	0	0	1	3		
ENSMUST00000128417						0	0	0	0	0	0	12	372	10	109	43		
ENSMUST00000128418	ENSMUSG00000031444	8	13037308	13056676	1	0	0	0	0	0	0	1	99	0	125	35	D3Z215	
ENSMUST00000128419	ENSMUSG00000033416	10	75351111	75517972	-1	0	0	0	0	0	0	21	0	0	0	0	F6RDQ0	
ENSMUST00000128420	ENSMUSG00000006599	7	46796103	46823800	1	0	2	0	0	0	2	0	48	14	0	0	D6RJL7	
ENSMUST00000128421						0	1	0	0	0	0	0	0	2	1	0		
ENSMUST00000128422						0	0	0	0	2	0	0	0	0	0	1		
ENSMUST00000128423						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000128424	ENSMUSG00000001482	8	123442986	123463270	1	0	0	6	2	0	0	20	0	6	0	9	D3YWV3	
ENSMUST00000128425						2	4	2	0	0	2	0	0	0	4	6		
ENSMUST00000128426	ENSMUSG00000035696	4	44126210	44233789	-1	0	0	0	0	0	0	0	12	109	0	213	B1AWE8	
ENSMUST00000128427						5	19	7	0	20	14	3	12	0	0	7		
ENSMUST00000128428	ENSMUSG00000027238	2	121545529	121807087	-1	0	0	6	23	8	3	0	0	0	2	0	F2Z484	
ENSMUST00000128429						4	4	8	7	3	2	1	1	0	0	4		
ENSMUST00000128430						0	0	0	0	0	0	8	33	4	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128431	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	1	0	0	0	4	10	24	0	39	A0A0A6YWT1	
ENSMUST00000128432	ENSMUSG00000040167	7	131388652	131410521	-1	3	2	1	50	2	3	6	17	17	0	18	A0A087WNW9	
ENSMUST00000128433						0	0	2	1	0	0	4	27	5	1	0		
ENSMUST00000128434	ENSMUSG00000019763	10	4401915	4432388	-1	5	2	0	2	0	2	2	17	2	8	6	F6QWS3	
ENSMUST00000128435	ENSMUSG00000056174	4	126286793	126314330	1	3	3	5	6	2	0	0	0	0	0	0	A3KFY1	
ENSMUST00000128436	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	2	0	0	5	0	0	0	0	0	B1AUV9	
ENSMUST00000128437						0	0	0	0	0	0	3	0	11	0	0		
ENSMUST00000128438	ENSMUSG00000019338	3	95006590	95015448	-1	0	0	5	0	0	0	0	0	0	0	0	D3Z2E5	
ENSMUST00000128439	ENSMUSG00000028479	4	44034075	44084177	-1	0	1	0	0	0	0	0	0	0	0	0	F6SHH4	
ENSMUST00000128440						10	13	128	28	21	3	0	3	5	0	3		
ENSMUST00000128441						0	1	1	5	0	1	0	0	0	0	0		
ENSMUST00000128442	ENSMUSG00000019066	9	21907491	21918192	-1	0	1	3	0	1	0	40	5	23	0	20	D3YWL1	
ENSMUST00000128444						3	2	0	9	0	0	34	11	11	51	24		
ENSMUST00000128445	ENSMUSG00000073650	1	74362108	74369321	1	0	0	0	0	0	0	0	0	2	0	0	F7AAT1	
ENSMUST00000128446	ENSMUSG00000063975	6	142234227	142322981	-1	0	0	1	0	0	0	0	0	0	0	0	E0CX25	
ENSMUST00000128447						2	0	7	3	4	0	3	0	1	0	0		
ENSMUST00000128448						0	2	4	0	3	0	8	8	15	2	22		
ENSMUST00000128449	ENSMUSG00000031162	X	7959260	7978071	-1	0	0	0	2	0	1	0	1	0	0	0	B1AUB4	
ENSMUST00000128450	ENSMUSG00000005268	15	10177238	10349180	1	0	0	0	0	0	0	0	0	0	0	0		Q08501
ENSMUST00000128451	ENSMUSG00000050447	2	50066429	50193569	1	0	2	0	22	0	3	1	0	0	0	0	A2AQT4	
ENSMUST00000128452						0	0	9	9	17	1	28	49	6	10	10		
ENSMUST00000128454	ENSMUSG00000058454	7	143823145	143848410	1	0	0	0	0	0	0	0	0	0	0	0	Q711T1	
ENSMUST00000128455	ENSMUSG00000025227	19	46341121	46375252	1	0	2	0	6	3	0	0	0	0	0	0	D3Z2Z0	
ENSMUST00000128456						9	5	3	7	10	7	2	28	13	0	37		
ENSMUST00000128457						0	1	0	0	5	0	0	0	0	4	0		
ENSMUST00000128459						1	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000128460	ENSMUSG00000030630	7	84585159	84606722	-1	3	3	9	2	5	1	4	6	0	0	0	D3Z2R9	
ENSMUST00000128461						0	0	0	0	0	0	1	0	1	1	0		
ENSMUST00000128462						0	2	1	5	0	1	1	0	0	0	0		
ENSMUST00000128463						0	23	0	92	11	10	0	0	0	0	0		
ENSMUST00000128464	ENSMUSG00000024331	18	20030633	20059554	-1	0	13	25	9	3	12	0	0	0	0	0	D6RDD6	
ENSMUST00000128465						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128466	ENSMUSG00000020652	12	4196004	4234294	-1	3	0	0	6	2	2	10	15	23	8	15	B8JK51	
ENSMUST00000128467	ENSMUSG00000039128	2	5794294	5845164	-1	3	0	2	1	3	0	15	52	13	59	26	A0A0A6YVX4	
ENSMUST00000128468						12	12	11	62	15	8	0	0	0	0	0		
ENSMUST00000128470						6	7	43	68	7	9	0	0	2	0	3		
ENSMUST00000128471	ENSMUSG00000070509	7	73375509	73419899	1	0	0	0	14	0	0	0	0	0	0	0	D3Z4W0	
ENSMUST00000128472						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128474	ENSMUSG00000028608	4	107889813	107899384	1	0	0	0	8	0	0	0	0	0	0	0	A2A8E4	
ENSMUST00000128475	ENSMUSG00000022201	15	12117831	12185683	1	0	0	19	7	0	0	0	0	33	10	48	D3Z5G4	
ENSMUST00000128477						3	1	0	0	1	0	1	0	0	0	0		
ENSMUST00000128478						15	17	68	48	57	14	67	112	88	16	82		
ENSMUST00000128479						8	2	14	5	15	3	0	0	0	0	0		
ENSMUST00000128480						0	0	0	0	3	1	0	0	0	0	0		
ENSMUST00000128481						1	0	1	2	3	0	2	4	2	0	4		
ENSMUST00000128482	ENSMUSG00000008683	7	118104372	118116188	-1	0	0	0	0	0	0	699	1513	657	3637	413	D3YVB4	
ENSMUST00000128483	ENSMUSG00000020380	11	53649519	53707319	-1	0	0	0	13	2	0	0	0	0	0	0	E9PUJ2	
ENSMUST00000128484						0	0	0	0	0	0	0	7	2	0	7		
ENSMUST00000128485	ENSMUSG00000028656	4	122859047	122886056	-1	0	0	0	8	0	0	96	50	177	15	185	B1ARS0	
ENSMUST00000128486						5	3	5	5	5	0	21	62	29	15	47		
ENSMUST00000128487						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000128488						1	0	0	8	4	0	0	0	2	0	0		
ENSMUST00000128490	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	8	0	22	1	5	D3YVR5	
ENSMUST00000128491						2	5	1	4	0	0	13	40	11	2	11		
ENSMUST00000128492						3	1	0	3	4	2	0	0	0	0	0		
ENSMUST00000128493	ENSMUSG00000072244	7	104218793	104235152	1	1	0	1	0	1	0	0	0	0	0	1	D3YY77	
ENSMUST00000128494						0	0	4	34	0	0	0	0	0	0	0		
ENSMUST00000128495	ENSMUSG00000044876	7	6172226	6191349	1	2	2	1	3	2	2	0	0	0	0	0	D3Z2T1	
ENSMUST00000128496						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000128497						3	5	8	6	2	2	7	13	8	4	15		
ENSMUST00000128498						2	1	0	13	5	0	23	44	22	1	24		
ENSMUST00000128499	ENSMUSG00000089824	2	156091958	156111978	-1	0	0	0	1	0	0	0	0	0	0	0	B7ZCQ0	
ENSMUST00000128500	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	0	0	0	0	78	0	181	18	121	F6VVN1	
ENSMUST00000128501						4	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000128502	ENSMUSG00000058740	2	25863734	25918273	1	3	0	10	14	7	0	0	0	0	0	0	A0A0G2JG91	
ENSMUST00000128503						2	1	3	4	2	0	0	0	0	3	0		
ENSMUST00000128504	ENSMUSG00000010554	11	74770830	74828525	1	2	4	5	55	4	2	0	0	0	0	0	Q5SW13	
ENSMUST00000128505	ENSMUSG00000006301	1	74288247	74305622	-1	2	0	12	4	1	4	0	0	0	0	2	F6YG30	
ENSMUST00000128506						0	0	0	0	0	0	0	0	40	4	11		
ENSMUST00000128507						5	3	6	1	7	1	4	5	5	4	0		
ENSMUST00000128508	ENSMUSG00000038034	1	172261641	172319841	1	5	2	3	4	0	1	0	3	0	0	0	D3Z4Q8	
ENSMUST00000128509						1	0	6	24	3	3	0	0	0	0	0		
ENSMUST00000128510						1	0	1	1	0	1	0	0	37	0	60		
ENSMUST00000128511	ENSMUSG00000029310	5	104046306	104065379	1	0	1	0	20	0	0	0	0	0	0	10	A2AH28	
ENSMUST00000128512						103	48	128	810	63	51	0	0	1	0	0		
ENSMUST00000128513						3	1	24	7	9	4	5	8	3	8	6		
ENSMUST00000128514						4	7	12	7	7	2	0	0	0	0	0		
ENSMUST00000128515						20	19	114	45	20	14	0	0	0	3	5		
ENSMUST00000128516						9	2	28	7	8	3	8	5	4	0	16		
ENSMUST00000128517						2	0	2	1	3	0	11	158	38	5	73		
ENSMUST00000128518						1	7	0	0	0	6	6	28	7	30	31		
ENSMUST00000128519						0	0	0	0	0	0	50	342	37	134	175		
ENSMUST00000128522						5	3	11	0	6	6	0	0	0	0	0		
ENSMUST00000128523						44	35	94	181	42	36	64	199	95	12	239		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128524						2	1	5	54	8	3	3	20	17	6	11		
ENSMUST00000128525						0	3	0	5	4	0	5	3	11	0	6		
ENSMUST00000128526						2	2	6	0	2	2	0	4	0	0	1		
ENSMUST00000128527	ENSMUSG00000025466	7	140096770	140102441	-1	2	1	4	1	2	1	0	4	0	0	0	F6X9P4	
ENSMUST00000128528						8	8	0	42	0	0	0	2	0	15	2		
ENSMUST00000128529						2	2	3	27	4	0	4	2	1	2	15		
ENSMUST00000128530	ENSMUSG00000023307	19	37207543	37222139	1	0	0	0	0	0	5	75	467	90	22	48	F6W8T3	
ENSMUST00000128531	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	12	0	0	0	0	A2AQF0	
ENSMUST00000128532						16	3	7	12	7	3	46	43	66	3	45		
ENSMUST00000128533	ENSMUSG00000071322	17	7324646	7345974	1	14	12	43	14	22	15	0	0	0	0	0	Q80W76	
ENSMUST00000128534						8	3	6	4	8	5	2	0	0	0	0		
ENSMUST00000128535						18	11	9	10	17	17	0	0	0	0	0		
ENSMUST00000128536						4	4	6	8	3	3	19	45	25	2	39		
ENSMUST00000128537						0	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000128538						3	3	10	3	3	1	0	0	0	0	0		
ENSMUST00000128539	ENSMUSG00000022037	14	65968483	65981548	1	1	0	5	0	0	1	0	2	0	0	0	E9Q9B8	
ENSMUST00000128540	ENSMUSG00000004056	7	27591552	27640826	1	0	1	8	5	5	2	0	0	0	0	4	D3Z490	
ENSMUST00000128541						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000128542						11	12	16	19	17	3	0	1	1	1	1		
ENSMUST00000128543						7	9	11	4	0	3	4	19	0	0	0		
ENSMUST00000128544						0	1	0	3	1	0	0	16	0	0	5		
ENSMUST00000128546						96	65	559	102	63	45	2	14	9	0	5		
ENSMUST00000128547						3	3	7	4	2	3	0	1	0	0	0		
ENSMUST00000128548						5	15	27	9	12	3	7	54	14	12	13		
ENSMUST00000128549	ENSMUSG00000028469	4	43631935	43651244	1	0	0	0	0	0	0	0	2	0	1	1	F6YT88	
ENSMUST00000128550	ENSMUSG00000045482	5	144767732	144859778	1	0	0	5	50	0	0	0	0	2	0	8	D3YY11	
ENSMUST00000128551	ENSMUSG00000022757	16	56690332	56717450	-1	0	0	0	1	0	0	0	0	0	0	0	B8JJG7	
ENSMUST00000128553	ENSMUSG00000000823	2	181582103	181592803	-1	36	0	114	37	51	19	115	247	258	18	213	Q6PHP4	
ENSMUST00000128555						2	1	6	0	9	0	242	1271	262	236	246		
ENSMUST00000128556	ENSMUSG00000001323	11	74906359	74925948	-1	1	0	0	6	0	0	0	0	0	7	0		Q9QZX7
ENSMUST00000128557	ENSMUSG00000047710	8	13869641	13881639	1	0	2	8	52	8	1	0	0	38	0	33		
ENSMUST00000128558						1	3	2	179	11	3	0	0	0	0	0		
ENSMUST00000128559	ENSMUSG00000020288	11	23487882	23498030	-1	3	2	0	2	3	4	18	17	47	20	36	A2AF82	
ENSMUST00000128560						0	0	4	0	0	0	0	21	16	10	6		
ENSMUST00000128561						0	1	0	0	0	0	13	15	26	28	9		
ENSMUST00000128564						1	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000128565	ENSMUSG00000025656	X	95048935	95196856	-1	5	3	33	26	0	0	0	0	0	0	0	S4R1K5	
ENSMUST00000128566						0	0	0	0	0	0	2	0	5	0	0		
ENSMUST00000128567	ENSMUSG00000029563	6	14901349	15441977	1	0	0	0	68	0	0	0	0	0	0	0	D3YUM2	
ENSMUST00000128568						9	4	23	11	14	7	0	0	0	0	0		
ENSMUST00000128570	ENSMUSG00000039087	13	37778400	37952002	1	0	0	0	0	0	0	411	205	412	0	188		Q3UH06
ENSMUST00000128572						9	4	4	4	6	2	0	1	0	0	0		
ENSMUST00000128573	ENSMUSG00000021933	14	62392676	62456289	-1	1	2	2	0	0	0	0	0	0	0	0	D3Z022	
ENSMUST00000128574						6	5	18	9	13	9	0	0	0	0	0		
ENSMUST00000128575						2	0	2	3	0	0	0	0	0	0	0		
ENSMUST00000128576	ENSMUSG00000004933	10	81252935	81263365	1	13	10	16	37	22	10	20	17	10	0	4	D6RGA0	
ENSMUST00000128578						28	21	21	29	25	16	0	40	3	7	13		
ENSMUST00000128579						3	3	4	4	2	0	0	0	0	0	0		
ENSMUST00000128580	ENSMUSG00000013539	16	18300825	18348103	-1	0	1	8	0	1	1	11	56	7	8	0	Q99K56	
ENSMUST00000128581						2	2	0	0	0	0	3	8	2	7	2		
ENSMUST00000128582						129	173	174	149	126	74	19	93	34	15	37		
ENSMUST00000128583						4	5	9	7	5	0	0	0	0	0	0		
ENSMUST00000128584						1	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000128585	ENSMUSG00000069170	13	81095068	81633154	-1	3	4	0	3	4	2	0	0	0	0	0		Q8VHN7
ENSMUST00000128586						0	0	0	0	0	0	72	269	0	0	0		
ENSMUST00000128587	ENSMUSG00000030670	7	114550166	114562972	-1	0	0	0	0	0	2	0	0	0	0	0	F6RCB2	
ENSMUST00000128590	ENSMUSG00000029550	5	115011137	115098790	1	6	1	0	1	3	1	135	115	149	10	121		
ENSMUST00000128592						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000128593						4	1	0	91	0	2	14	2	14	2	13		
ENSMUST00000128594	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	0	4	85	0	0		
ENSMUST00000128595						4	3	2	3	8	2	0	0	0	0	0		
ENSMUST00000128596						0	0	0	0	0	0	78	409	205	2	276		
ENSMUST00000128597	ENSMUSG00000024180	17	26113316	26123254	1	0	0	7	0	0	0	0	30	5	0	0	F6Q3Y1	
ENSMUST00000128598						5	0	1	0	2	1	0	0	0	0	0		
ENSMUST00000128599						7	4	14	6	9	1	0	0	0	0	0		
ENSMUST00000128600						0	1	0	46	2	3	0	32	12	6	22		
ENSMUST00000128604						0	0	0	0	1	0	1	5	0	0	0		
ENSMUST00000128605	ENSMUSG00000028238	4	19876841	19922605	-1	0	0	2	2	0	0	0	0	0	0	0	B1AWC2	
ENSMUST00000128606						0	1	5	4	2	2	0	0	0	0	0		
ENSMUST00000128607						6	0	7	0	2	2	0	0	0	0	0		
ENSMUST00000128609	ENSMUSG00000028268	3	142560026	142573209	1	2	0	3	2	3	0	0	0	0	0	0	D3YVW6	
ENSMUST00000128610						4	3	5	3	5	1	0	0	2	0	0		
ENSMUST00000128611						0	0	1	2	3	3	4	0	0	0	9		
ENSMUST00000128612	ENSMUSG00000000308	2	121357714	121363737	1	0	3	5	6	0	0	0	0	0	0	0	D6RG68	
ENSMUST00000128613						4	3	10	3	15	4	0	0	0	0	0		
ENSMUST00000128614	ENSMUSG00000034947	11	101582242	101591788	1	4	6	2	5	3	3	54	31	21	2	60	A2A4M9	
ENSMUST00000128615						4	4	0	9	10	7	0	0	0	0	0		
ENSMUST00000128616	ENSMUSG00000029815	6	49073795	49086751	1	0	2	0	4	3	2	0	0	0	0	0	F7ASG0	Q9CWV0
ENSMUST00000128617						0	0	0	92	2	2	7	58	16	0	31		
ENSMUST00000128618						0	0	0	0	0	1	6	37	0	1	0		
ENSMUST00000128619	ENSMUSG00000037375	1	192496711	192771223	-1	30	19	20	57	34	22	4	30	17	10	19		Q8BMT9
ENSMUST00000128620						10	1	16	80	8	6	0	2	5	0	4		
ENSMUST00000128621						0	0	0	0	0	0	4	42	6	37	0		
ENSMUST00000128622						4	0	2	2	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128623						4	0	17	5	3	1	63	113	76	7	45		
ENSMUST00000128624	ENSMUSG00000032281	9	54604877	54661870	-1	2	0	2	0	1	0	0	0	0	0	0	D3Z2G8	
ENSMUST00000128625						3	3	5	6	9	1	0	0	0	0	0		
ENSMUST00000128626						2	4	0	0	0	0	13	39	14	4	16		
ENSMUST00000128627	ENSMUSG00000068115	2	150934519	151039382	-1	0	3	0	5	6	0	0	0	1	0	1	A2ANB9	
ENSMUST00000128628	ENSMUSG00000031142	X	7607083	7635196	1	1	1	0	1	0	0	0	0	0	0	0	B1AVA5	
ENSMUST00000128629	ENSMUSG00000021884	14	31552905	31641286	-1	1	0	0	0	0	0	0	0	1	0	0	E9Q5P5	
ENSMUST00000128630						3	0	0	4	3	0	0	58	19	8	0		
ENSMUST00000128631						17	18	119	57	31	30	2	9	4	1	7		
ENSMUST00000128632						3	1	3	8	6	0	0	10	0	2	2		
ENSMUST00000128633						8	4	14	4	13	7	9	31	19	2	24		
ENSMUST00000128635						1	0	2	0	0	1	11	0	12	0	0		
ENSMUST00000128636	ENSMUSG00000032249	9	62341293	62378812	1	0	4	0	6	5	0	85	115	109	35	75	D3YYE1	
ENSMUST00000128637						7	5	5	3	5	3	0	0	0	0	0		
ENSMUST00000128638						8	3	19	15	28	4	0	0	0	0	0		
ENSMUST00000128640						0	1	1	105	0	2	0	5	5	0	7		
ENSMUST00000128641						0	0	0	2	0	0	5	0	0	0	0		
ENSMUST00000128642	ENSMUSG00000039652	19	37021291	37208601	-1	2	0	1	5	7	3	0	0	0	2	1	D3YXB8	
ENSMUST00000128643						3	0	9	6	10	2	0	0	8	0	0		
ENSMUST00000128644	ENSMUSG00000020577	12	36014557	36042500	-1	1	1	2	92	0	0	5	19	82	108	133	E0CY97	
ENSMUST00000128645						15	4	19	32	14	5	37	183	88	10	144		
ENSMUST00000128646	ENSMUSG00000054728	13	42680623	43138526	1	0	22	28	26	35	13	0	0	0	0	0		Q2M3X8
ENSMUST00000128648						0	0	0	2	2	0	2	5	3	0	0		
ENSMUST00000128649						4	4	0	1	0	0	38	89	28	17	18		
ENSMUST00000128650	ENSMUSG00000020937	11	103070304	103101658	-1	3	5	7	0	6	1	0	0	3	6	0	F7AAE0	
ENSMUST00000128651						3	3	4	1	3	1	2	6	10	11	16		
ENSMUST00000128653	ENSMUSG00000020131	10	80321283	80329498	-1	9	0	0	0	0	0	0	0	0	0	0	M0QWG0	
ENSMUST00000128655						17	12	77	0	8	10	4	3	2	2	0		
ENSMUST00000128656						1	2	2	3	0	0	0	0	0	0	0		
ENSMUST00000128657	ENSMUSG00000078867	2	177387124	177398320	-1	0	0	0	0	0	0	0	0	0	0	0	A2ARR6	
ENSMUST00000128658	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	33	1	0	0	0	0	0	0	D3Z2K4	
ENSMUST00000128659						5	2	22	9	6	0	12	77	21	0	36		
ENSMUST00000128660						9	5	3	10	3	3	1	1	4	0	4		
ENSMUST00000128661						3	7	16	48	7	3	5	40	16	7	39		
ENSMUST00000128663						21	4	25	24	33	21	17	8	0	0	0		
ENSMUST00000128664	ENSMUSG00000040652	9	65668001	65690300	1	8	5	8	7	2	4	26	124	69	14	59	J3QPT5	
ENSMUST00000128665						5	3	7	0	2	4	3	32	9	2	10		
ENSMUST00000128666						2	0	6	3	5	1	0	3	0	0	0		
ENSMUST00000128667	ENSMUSG00000028414	4	53713998	53765785	1	33	13	60	47	25	13	12	67	29	13	56		Q8R507
ENSMUST00000128668	ENSMUSG00000035509	13	56522472	56537898	1	0	3	0	0	0	1	0	0	0	0	0	D6RE27	
ENSMUST00000128669						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000128670						0	0	3	6	16	15	6	59	16	4	27		
ENSMUST00000128671	ENSMUSG00000026988	2	59852364	59882591	-1	0	0	0	1	5	0	0	0	6	0	2	A2AUY0	
ENSMUST00000128673						11	11	14	11	15	3	0	0	0	0	0		
ENSMUST00000128674						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000128676	ENSMUSG00000039501	2	167035793	167063015	-1	0	0	0	0	0	0	65	26	183	0	221	A2A5R4	
ENSMUST00000128677						2	0	0	3	2	0	0	0	0	4	0		
ENSMUST00000128678						27	33	62	28	38	24	49	162	50	12	89		
ENSMUST00000128679						0	0	0	19	4	0	65	109	93	551	71		
ENSMUST00000128680						13	2	4	5	8	3	0	0	1	0	1		
ENSMUST00000128682	ENSMUSG00000017418	2	15049395	15082456	1	0	1	1	35	0	0	0	6	37	3	20	D6RJJ6	
ENSMUST00000128683	ENSMUSG00000038241	2	155956458	155998900	1	0	0	0	0	0	0	15	0	19	0	7	F6QCB4	
ENSMUST00000128684	ENSMUSG00000027257	2	91255954	91264679	1	8	3	13	5	9	6	0	0	0	0	0	F6W8Y8	
ENSMUST00000128685						5	3	13	18	15	5	0	1	0	0	1		
ENSMUST00000128686						1	0	2	0	0	1	1	0	0	0	2		
ENSMUST00000128688						0	3	0	0	16	2	0	0	0	0	5		
ENSMUST00000128689						9	5	18	2	11	4	0	0	0	0	0		
ENSMUST00000128690	ENSMUSG00000017670	2	165288031	165326479	-1	0	0	0	7	6	0	0	0	0	0	0	A2A5A7	
ENSMUST00000128691	ENSMUSG00000005373	5	135089890	135138382	1	0	0	0	0	0	0	0	0	0	0	0		Q99MZ3
ENSMUST00000128692						0	0	0	8	0	2	0	0	0	1	2		
ENSMUST00000128693						0	2	0	18	0	0	0	0	2	0	3		
ENSMUST00000128694	ENSMUSG00000024843	19	3851773	3894369	1	0	0	0	51	0	0	0	0	0	0	0	Q5J2U5	
ENSMUST00000128695						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000128696						5	1	0	9	1	1	0	0	1	0	0		
ENSMUST00000128697	ENSMUSG00000030125	6	124769863	124779727	-1	3	0	0	0	0	0	0	0	0	0	0	D3Z6G0	
ENSMUST00000128698						1	4	5	137	12	3	0	0	0	33	16		
ENSMUST00000128699						0	0	0	0	1	1	1	0	0	20	4		
ENSMUST00000128700	ENSMUSG00000057751	4	154170730	154275713	1	0	0	0	0	0	1	0	0	0	0	0	F6YCL7	
ENSMUST00000128701						1	3	16	0	0	4	0	0	0	0	0		
ENSMUST00000128702						8	4	14	71	8	2	0	0	0	0	0		
ENSMUST00000128703	ENSMUSG00000025507	7	141438113	141444025	-1	0	0	0	0	0	0	6	0	8	0	5	A0A087WNT6	
ENSMUST00000128704						2	1	0	45	0	0	0	0	7	82	11		
ENSMUST00000128705						0	5	18	0	3	0	1	0	0	0	0		
ENSMUST00000128706	ENSMUSG00000053477	18	69343356	69689079	1	7	4	16	8	5	10	0	5	2	0	0	Q8BPX7	
ENSMUST00000128707						0	0	0	108	5	0	0	0	0	1	0		
ENSMUST00000128708						0	3	4	0	1	0	2	2	1	0	0		
ENSMUST00000128709						0	2	0	9	4	0	9	27	15	0	10		
ENSMUST00000128710						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000128711						27	35	67	40	30	8	4	22	11	8	32		
ENSMUST00000128712						266	246	3035	614	345	186	7	1	5	7	10		
ENSMUST00000128713						4	2	5	11	7	4	5	0	2	0	2		
ENSMUST00000128714						0	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000128715	ENSMUSG00000031557	8	25039144	25102194	-1	33	17	44	280	19	18	883	2587	1167	205	750		Q9ERS5
ENSMUST00000128716	ENSMUSG00000027845	3	103800605	103809444	-1	0	0	0	0	0	0	0	0	0	0	0	D6RFP8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128717	ENSMUSG00000047773	11	89420987	89639631	-1	18	0	15	0	17	9	0	0	0	0	0	F6RWQ6	
ENSMUST00000128718	ENSMUSG00000052581	6	80018877	80810143	1	2	0	0	1	0	0	0	0	0	0	0	D3YVI4	
ENSMUST00000128719						0	1	0	0	0	0	0	0	1	0	0		
ENSMUST00000128720						7	10	14	11	14	7	0	0	0	0	1		
ENSMUST00000128721	ENSMUSG00000004270	6	124663027	124704418	1	0	0	5	8	0	0	32	0	68	12	65		
ENSMUST00000128722						13	37	78	16	0	0	20	16	0	0	8		
ENSMUST00000128723	ENSMUSG00000011831	5	107744795	107875107	-1	0	4	0	12	0	4	0	0	0	0	32	E9PWR7	
ENSMUST00000128724						0	0	0	4	0	2	10	6	0	2	5		
ENSMUST00000128725						26	19	63	49	35	16	11	82	21	45	21		
ENSMUST00000128726						1	1	1	5	4	0	0	0	0	0	0		
ENSMUST00000128727	ENSMUSG00000056367	5	25759997	25850688	1	0	0	13	36	15	5	3	0	4	2	2		Q641P0
ENSMUST00000128729						0	0	26	0	1	0	18	132	108	31	177		
ENSMUST00000128731	ENSMUSG00000045639	7	127607031	127615797	-1	3	0	0	25	2	1	0	0	0	0	0	A0A087WR77	
ENSMUST00000128732						9	4	16	6	7	4	0	0	0	0	0		
ENSMUST00000128733						0	1	5	22	3	4	81	247	235	1943	260		
ENSMUST00000128734						2	0	3	4	2	0	0	0	0	0	0		
ENSMUST00000128735						40	20	35	22	13	18	3	3	1	0	3		
ENSMUST00000128737	ENSMUSG00000032680	2	152415587	152444330	1	1	0	0	0	1	1	0	0	0	1	1	B0R090	
ENSMUST00000128738						0	4	1	0	5	0	3	49	12	7	16		
ENSMUST00000128739						6	6	0	6	5	0	1	1	0	5	2		
ENSMUST00000128740	ENSMUSG00000029369	5	90518932	90553543	1	5	4	4	3	17	4	0	0	0	1	0		O89020
ENSMUST00000128741						1	3	11	2	1	1	0	0	0	0	0		
ENSMUST00000128742						1	1	2	0	0	1	0	0	0	0	1		
ENSMUST00000128744						0	2	1	31	3	6	1	0	0	0	0		
ENSMUST00000128745						1	0	7	2	3	0	2	5	0	0	3		
ENSMUST00000128746						73	76	311	110	75	40	3	5	5	0	17		
ENSMUST00000128747						5	1	18	4	8	5	0	0	0	0	0		
ENSMUST00000128748	ENSMUSG00000060216	11	70432635	70440828	1	4	0	2	0	0	0	170	105	211	20	112	G3UZ54	
ENSMUST00000128749						4	2	18	7	4	0	1	2	5	0	3		
ENSMUST00000128750						0	0	0	0	0	0	3	0	68	19	31		
ENSMUST00000128751	ENSMUSG00000024018	17	29689378	29717012	-1	5	4	0	2	5	0	13	0	4	113	0		Q9D162
ENSMUST00000128752						4	3	3	143	5	5	0	2	0	0	0		
ENSMUST00000128753						2	0	3	0	6	2	0	0	0	0	27		
ENSMUST00000128754						18	10	39	14	23	9	0	7	6	0	4		
ENSMUST00000128755						18	19	43	23	23	4	0	3	1	2	5		
ENSMUST00000128756	ENSMUSG00000035545	7	4137039	4148177	1	2	0	0	22	2	1	46	12	61	1	115	D3YY84	
ENSMUST00000128757	ENSMUSG00000022679	16	13903161	13949619	1	119	124	396	51	99	63	5	44	26	27	34		Q99MS3
ENSMUST00000128758						0	0	0	104	0	0	7	0	12	8	23		
ENSMUST00000128759						0	0	0	12	3	0	0	0	0	0	1		
ENSMUST00000128761						375	397	574	382	494	213	28	88	60	21	96		
ENSMUST00000128762						6	3	9	111	4	6	0	0	0	0	3		
ENSMUST00000128763						1	1	0	0	0	0	4	28	8	0	1		
ENSMUST00000128764	ENSMUSG00000021963	14	57798180	57804980	1	66	42	99	67	64	36	119	548	143	48	153	E9Q317	
ENSMUST00000128765						0	2	4	0	3	0	0	3	0	0	0		
ENSMUST00000128766						8	5	7	7	7	4	0	0	0	0	0		
ENSMUST00000128767	ENSMUSG00000090231	17	34856374	34862518	-1	0	0	0	19	0	0	0	29	0	0	106	Q3UEG8	P04186
ENSMUST00000128768	ENSMUSG00000002028	9	44803355	44881296	-1	3	0	0	94	5	0	0	0	0	0	0	D3Z5H5	
ENSMUST00000128769						1	1	1	5	1	0	0	0	0	0	0		
ENSMUST00000128770						6	5	1	1	8	0	21	4	11	16	10		
ENSMUST00000128771						3	1	5	5	1	1	0	68	25	109	13		
ENSMUST00000128772						3	3	41	4	5	5	6	12	7	1	19		
ENSMUST00000128773						0	1	2	22	1	2	0	0	0	0	0		
ENSMUST00000128774	ENSMUSG00000047909	2	11777876	11790329	1	0	0	0	0	0	0	0	125	20	0	0	F6T2W3	
ENSMUST00000128775	ENSMUSG00000022469	15	97744770	97767972	-1	7	9	53	0	16	20	14	0	0	2	6	E9Q2E5	
ENSMUST00000128776						0	1	9	4	4	0	0	0	0	0	0		
ENSMUST00000128777						0	0	0	0	0	0	3	14	11	0	2		
ENSMUST00000128778						0	0	0	0	0	2	10	17	0	0	13		
ENSMUST00000128780	ENSMUSG00000025402	10	127660918	127668568	-1	0	1	5	5	6	1	1	0	0	0	0	D3Z292	
ENSMUST00000128781	ENSMUSG00000058318	2	92093117	92364666	1	3	0	3	11	9	3	0	32	8	0	22		
ENSMUST00000128782						0	0	0	0	1	0	0	8	6	0	11		
ENSMUST00000128783						8	6	26	33	12	6	0	0	0	0	0		
ENSMUST00000128784						3	0	3	7	16	7	0	8	0	0	4		
ENSMUST00000128785						0	0	0	4	0	3	0	3	0	2	0		
ENSMUST00000128786						3	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000128787	ENSMUSG00000037916	19	4007497	4012806	-1	0	0	0	0	0	0	186	449	106	22	124	D3YUM1	
ENSMUST00000128788	ENSMUSG00000001105	11	78536361	78541737	1	6	9	40	71	14	5	72	332	92	395	75		Q61025
ENSMUST00000128789	ENSMUSG00000038298	3	96829284	96870926	1	4	1	3	5	1	3	0	0	0	0	0	D3Z114	
ENSMUST00000128790	ENSMUSG00000002871	6	88902251	88912238	1	0	4	6	3	0	0	0	18	0	0	11		
ENSMUST00000128791	ENSMUSG00000030560	7	88278085	88310888	1	0	1	7	0	0	2	164	459	378	167	357	D3Z220	
ENSMUST00000128792	ENSMUSG00000028383	4	59581563	59618689	1	0	2	0	0	0	0	0	6	5	0	0	B1AX77	
ENSMUST00000128793						6	4	1	0	1	3	19	13	22	0	26		
ENSMUST00000128794						1	4	0	2	0	0	0	0	0	0	0		
ENSMUST00000128795						4	0	2	0	1	2	2	1	0	2	7		
ENSMUST00000128796						2	0	0	2	8	1	0	4	0	0	0		
ENSMUST00000128797						2	2	4	0	4	2	0	0	0	0	0		
ENSMUST00000128798						2	1	3	1	2	2	2	30	6	0	18		
ENSMUST00000128799	ENSMUSG00000025862	X	42149317	42277185	1	0	0	0	1	0	0	0	0	40	0	12	Q3UQG8	
ENSMUST00000128801	ENSMUSG00000071415	11	97777527	97782437	-1	0	0	0	0	0	0	0	4	3	0	2	A2A6F8	
ENSMUST00000128802						12	7	9	18	17	2	18	63	37	0	84		
ENSMUST00000128803						22	20	68	38	27	8	9	70	54	8	87		
ENSMUST00000128805						7	2	4	2	2	0	0	4	4	0	6		
ENSMUST00000128808						5	6	56	23	14	2	0	0	3	0	0		
ENSMUST00000128809	ENSMUSG00000000266	X	140664599	140767715	1	0	3	4	3	0	2	0	0	0	0	0	B1AVF6	
ENSMUST00000128810						0	1	1	0	1	0	0	3	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128811	ENSMUSG00000026811	2	32599709	32620806	1	0	0	0	0	0	0	0	0	0	0	0	Z4YMI1	
ENSMUST00000128812	ENSMUSG00000035919	9	22475715	22888280	1	0	0	2	5	0	1	6	0	0	0	0	D3Z389	
ENSMUST00000128813						0	0	0	0	0	0	2	37	23	4	24		
ENSMUST00000128814						2	0	8	1	0	0	0	22	0	0	0		
ENSMUST00000128816						7	5	36	11	6	0	0	22	0	9	6		
ENSMUST00000128817	ENSMUSG00000036817	5	139200637	139249840	1	1	3	11	0	1	2	18	6	22	2	32	F6RMJ1	
ENSMUST00000128818						1	2	0	115	2	2	7	0	5	0	25		
ENSMUST00000128819	ENSMUSG00000025665	X	111388192	111537959	-1	0	1	0	0	0	0	0	0	0	0	0	B1B0X1	
ENSMUST00000128820						28	16	13	30	36	14	20	12	22	7	18		
ENSMUST00000128821						0	0	3	1	0	0	6	8	18	0	7		
ENSMUST00000128822						7	8	0	11	5	0	9	47	24	0	44		
ENSMUST00000128823						0	0	0	2	2	0	18	11	0	35	29		
ENSMUST00000128824						5	6	9	32	11	2	0	4	0	0	3		
ENSMUST00000128825	ENSMUSG00000018677	11	102402985	102407946	-1	5	3	4	0	7	4	42	36	0	12	0	F6S0J8	
ENSMUST00000128826	ENSMUSG00000020782	11	115824049	115855780	1	0	0	0	0	0	0	0	12	0	7	0	F6X6X1	
ENSMUST00000128827						11	11	67	29	21	17	0	0	0	0	0		
ENSMUST00000128828						11	8	36	25	18	7	0	2	0	2	0		
ENSMUST00000128829						2	3	4	2	3	1	0	0	0	0	0		
ENSMUST00000128830						0	0	0	0	0	0	30	51	4	19	10		
ENSMUST00000128831						3	0	3	14	2	0	0	0	0	0	0		
ENSMUST00000128833						4	3	3	1	0	0	10	44	14	4	12		
ENSMUST00000128834						12	21	12	21	12	9	0	13	0	2	3		
ENSMUST00000128835	ENSMUSG00000034659	19	10870660	10882001	-1	0	0	0	1	0	3	0	0	0	0	0	D3Z7P2	
ENSMUST00000128836						3	0	6	0	2	0	0	2	8	0	5		
ENSMUST00000128837						0	0	2	0	0	0	0	4	0	0	0		
ENSMUST00000128838						14	11	15	31	14	1	0	0	0	0	0		
ENSMUST00000128839	ENSMUSG00000026317	8	14881335	14901720	1	2	0	8	5	0	0	0	0	0	3	0	D3Z2H1	
ENSMUST00000128840	ENSMUSG00000045983	16	20668313	20692884	1	0	0	2	1	0	1	0	0	0	0	0		
ENSMUST00000128842						1	0	2	1	1	0	0	0	2	0	0		
ENSMUST00000128843						1	6	0	0	1	0	0	0	0	0	0		
ENSMUST00000128845						33	18	49	89	47	19	1	0	1	0	11		
ENSMUST00000128847						11	12	10	13	13	9	5	23	30	9	44		
ENSMUST00000128849	ENSMUSG00000041390	6	15720661	15802169	1	6	2	6	0	1	2	0	1	4	15	0	A0A087WRW6	
ENSMUST00000128850						0	0	1	0	0	3	0	0	0	0	0		
ENSMUST00000128851						10	12	30	8	15	12	122	1047	265	34	493		
ENSMUST00000128852						1	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000128853	ENSMUSG00000020389	11	52004221	52089784	1	7	4	12	5	5	6	0	3	0	2	6	F6RBI5	
ENSMUST00000128854						0	1	0	0	4	0	0	0	0	0	0		
ENSMUST00000128855	ENSMUSG00000026867	2	34674594	34755232	-1	0	0	0	0	0	0	0	5	0	0	0	F6YRL2	
ENSMUST00000128856						13	4	13	0	11	1	0	5	8	3	11		
ENSMUST00000128857						4	5	1	6	4	1	207	355	256	44	259		
ENSMUST00000128860	ENSMUSG00000036510	8	99024471	99416471	-1	17	5	0	26	16	0	0	0	0	0	0		P97291
ENSMUST00000128861	ENSMUSG00000040596	1	166384622	166409863	-1	23	16	106	67	38	4	0	0	3	0	38		
ENSMUST00000128862	ENSMUSG00000031618	8	76899442	77245012	1	1	4	4	83	8	2	0	0	0	0	0	D3Z7F2	
ENSMUST00000128863						2	0	0	2	4	0	0	0	0	0	0		
ENSMUST00000128864						0	0	1	0	0	5	0	0	0	0	0		
ENSMUST00000128865						1	0	0	0	0	0	5	39	0	0	1		
ENSMUST00000128866						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000128868						0	1	10	6	3	0	0	0	3	0	0		
ENSMUST00000128869	ENSMUSG00000046709	5	102907948	103211334	-1	8	2	9	7	8	4	0	0	0	0	0	A0A0G2JG69	
ENSMUST00000128870						3	0	6	2	4	0	10	27	5	7	3		
ENSMUST00000128871						46	30	123	21	4	3	0	0	2	0	3		
ENSMUST00000128873	ENSMUSG00000000253	13	45507444	45546382	1	0	6	4	0	0	2	7	16	1	2	0	F6VY18	
ENSMUST00000128874	ENSMUSG00000037410	9	90202027	90270804	-1	41	41	212	135	47	28	46	160	52	56	79	A0A087WRL5	
ENSMUST00000128876						7	0	29	159	20	16	16	84	80	13	104		
ENSMUST00000128877						3	4	6	11	13	0	0	0	0	0	0		
ENSMUST00000128878						5	5	22	11	4	2	0	0	4	0	16		
ENSMUST00000128879						0	2	1	3	0	0	0	0	0	0	0		
ENSMUST00000128880	ENSMUSG00000036737	9	119238432	119322427	-1	8	3	0	49	0	0	76	5	68	0	48	D6RFV0	
ENSMUST00000128881						45	46	140	52	63	34	5	6	7	2	8		
ENSMUST00000128882						0	0	0	0	0	0	3	0	0	0	3		
ENSMUST00000128883						0	0	0	0	0	0	8	0	53	76	27		
ENSMUST00000128884						2	1	0	0	1	5	104	21	40	2	81		
ENSMUST00000128885	ENSMUSG00000028108	3	95734147	95739569	-1	0	0	6	0	0	0	10	14	15	0	0	D3Z0U9	
ENSMUST00000128886	ENSMUSG00000006345	10	75561604	75586200	1	0	0	0	0	0	0	0	0	0	0	0	D3YXV6	
ENSMUST00000128887	ENSMUSG00000040464	5	5537454	5559538	-1	0	0	0	0	0	0	0	0	0	0	0	F6TIN5	
ENSMUST00000128889						3	0	2	25	10	0	0	1032	32	5414	114		
ENSMUST00000128890	ENSMUSG00000031144	X	7638471	7653256	1	0	1	0	5	0	0	0	1	0	0	0	F6VR28	
ENSMUST00000128891						3	5	10	5	3	2	0	5	7	0	7		
ENSMUST00000128892	ENSMUSG00000021213	13	4191184	4205596	1	0	0	1	1	2	0	6	5	9	37	3	D6RGB1	
ENSMUST00000128893						14	10	7	10	11	4	0	0	2	0	0		
ENSMUST00000128895						7	2	43	24	10	5	2	2	6	0	4		
ENSMUST00000128897	ENSMUSG00000038208	11	98388677	98400490	-1	0	0	13	41	1	4	0	0	6	0	0		A2A559
ENSMUST00000128898	ENSMUSG00000027165	2	101560781	101649532	-1	0	4	0	0	0	0	0	0	0	0	1	I1E4Y3	
ENSMUST00000128899	ENSMUSG00000027340	2	132052496	132145108	-1	0	1	0	0	3	0	0	0	0	1	0	A2ANL1	
ENSMUST00000128900						2	5	5	3	8	2	0	0	0	2	3		
ENSMUST00000128901	ENSMUSG00000039990	7	133637543	133672971	1	0	3	0	0	0	0	136	612	311	47	239	D3YZE7	
ENSMUST00000128902						0	0	0	0	0	0	0	27	26	0	30		
ENSMUST00000128903						0	0	2	0	0	0	0	0	0	0	1		
ENSMUST00000128905						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000128906	ENSMUSG00000025505	7	141327739	141337156	1	8	5	7	8	11	3	19	44	29	6	30		Q9D3H0
ENSMUST00000128908						0	0	0	1	0	0	0	0	0	0	5		
ENSMUST00000128909	ENSMUSG00000028132	3	121201761	121283098	-1	0	0	0	68	0	0	0	0	0	0	0		Q8CGF5
ENSMUST00000128910						0	0	0	0	0	0	69	227	85	7	102		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000128911						0	0	2	0	4	0	2	5	2	0	3		
ENSMUST00000128912	ENSMUSG00000027531	3	10311956	10331439	-1	1	2	2	11	4	2	0	0	0	0	0	D3Z703	
ENSMUST00000128913						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128915						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128916						2	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000128917						49	40	226	61	69	44	2	3	4	1	8		
ENSMUST00000128918	ENSMUSG00000028099	3	96711490	96727628	-1	0	0	1	2	0	0	0	21	13	4	23	F6QK97	
ENSMUST00000128920	ENSMUSG00000029388	5	124570213	124579131	-1	0	0	0	0	0	0	0	0	0	0	0	D3YZ05	
ENSMUST00000128921	ENSMUSG00000005268	15	10177238	10349180	1	117	90	693	242	105	67	0	12	7	8	7	G3UVW6	
ENSMUST00000128922						1	0	0	2	1	1	4	21	12	0	8		
ENSMUST00000128923	ENSMUSG00000031969	9	26974135	26999566	-1	0	4	0	0	0	0	39	51	40	16	23	D6RDD5	
ENSMUST00000128924						1	1	6	22	3	0	7	3	2	12	0		
ENSMUST00000128926						0	0	0	0	0	0	3	18	4	0	14		
ENSMUST00000128927	ENSMUSG00000029772	6	29768011	29912310	1	0	0	0	0	0	0	0	0	0	0	0	H3BL31	
ENSMUST00000128928						1	0	5	4	0	3	0	0	0	0	0		
ENSMUST00000128929						3	0	9	6	9	2	2	12	3	0	15		
ENSMUST00000128930						3	0	59	73	0	0	7	9	1	6	5		
ENSMUST00000128931	ENSMUSG00000053411	15	79915807	79971119	-1	0	0	9	6	0	0	0	0	0	0	0	D3YYK4	
ENSMUST00000128932						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000128933	ENSMUSG00000040548	11	106502147	106613423	-1	2	6	0	13	0	6	0	0	0	0	2	B1ATR3	
ENSMUST00000128934						0	0	0	0	0	1	0	0	0	1	3		
ENSMUST00000128935						29	18	42	73	20	4	2	1	1	0	0		
ENSMUST00000128936	ENSMUSG00000039262	2	32151082	32234537	1	0	1	0	0	0	0	7	0	25	2	19	F6Q3E1	
ENSMUST00000128937						10	4	35	13	12	6	11	63	13	4	39		
ENSMUST00000128938						46	61	77	80	53	18	0	7	4	0	5		
ENSMUST00000128939						0	0	10	4	5	5	0	0	0	0	0		
ENSMUST00000128940	ENSMUSG00000020397	11	46436925	46442721	1	0	0	5	24	4	1	0	20	21	17	10	F2Z466	
ENSMUST00000128941	ENSMUSG00000050565	1	156035403	156068861	1	15	8	12	22	20	6	16	17	13	0	27		Q9ER81
ENSMUST00000128942						1	2	2	0	0	3	0	26	4	0	4		
ENSMUST00000128944	ENSMUSG00000074259	9	59680144	59718874	1	6	0	9	5	7	0	118	387	176	14	120		Q3V3G7
ENSMUST00000128945						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000128946						0	1	0	0	3	5	0	1	2	0	0		
ENSMUST00000128947						9	7	4	8	5	3	0	0	0	0	0		
ENSMUST00000128948						0	2	0	0	2	0	1	0	0	0	0		
ENSMUST00000128949						17	24	128	23	24	7	2	11	1	1	8		
ENSMUST00000128951						0	0	3	0	0	2	0	51	15	0	34		
ENSMUST00000128952	ENSMUSG00000060938	11	68901583	68906989	1	0	0	0	0	0	0	3	10	0	0	6	B1ARA3	
ENSMUST00000128953						0	5	7	17	2	2	0	0	0	0	0		
ENSMUST00000128954						6	0	2	3	1	1	10	76	26	7	26		
ENSMUST00000128955						0	0	0	15	3	2	0	0	17	63	14		
ENSMUST00000128957	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	7	0	0	0	0	0	0	0	0	D3Z6D2	
ENSMUST00000128958						2	4	3	1	0	0	0	173	27	15	26		
ENSMUST00000128959	ENSMUSG00000037287	9	42412316	42507809	-1	6	0	0	39	3	3	0	0	0	0	0		Q8C5W3
ENSMUST00000128961						2	7	11	27	10	2	33	63	19	0	79		
ENSMUST00000128962						6	5	20	18	14	1	0	1	0	0	6		
ENSMUST00000128963	ENSMUSG00000027014	2	77881159	77946375	-1	0	0	0	0	0	0	7	4	25	39	17	B1AYU9	
ENSMUST00000128965						0	2	14	1	1	2	0	0	0	0	0		
ENSMUST00000128966						1	1	1	4	2	7	0	0	0	0	0		
ENSMUST00000128967						2	2	1	2	2	0	0	0	0	0	4		
ENSMUST00000128968	ENSMUSG00000031229	X	105797615	105929403	-1	2	0	7	9	1	2	25	16	270	0	188	F6RDB7	
ENSMUST00000128969	ENSMUSG00000041594	14	122918971	122984035	-1	0	0	0	8	2	0	1	0	4	0	0	D6RH66	
ENSMUST00000128970	ENSMUSG00000030720	7	126571207	126585817	-1	0	0	0	0	0	0	322	409	259	25	231	D3YUU4	
ENSMUST00000128971						7	4	4	4	4	2	4	23	18	8	10		
ENSMUST00000128972	ENSMUSG00000052926	8	84956610	84969767	-1	2	0	8	6	2	0	10	0	26	44	55	F6RP29	
ENSMUST00000128973	ENSMUSG00000035637	4	44981395	44990734	1	0	0	0	11	0	0	0	0	0	0	0	B0R075	
ENSMUST00000128974						0	0	0	0	0	0	0	0	9	0	0		
ENSMUST00000128975						389	322	45	26	77	41	1	2	0	0	5		
ENSMUST00000128977						3	4	9	0	5	0	4	0	0	0	3		
ENSMUST00000128978						4	2	11	3	2	0	2	18	3	0	16		
ENSMUST00000128980						5	5	6	7	0	2	0	0	0	2	0		
ENSMUST00000128981	ENSMUSG00000018474	11	69343273	69369406	-1	29	19	48	0	54	23	19	23	67	17	194	F7C528	
ENSMUST00000128983						3	0	0	10	3	1	0	0	0	0	0		
ENSMUST00000128985						15	13	21	16	14	9	0	0	0	0	0		
ENSMUST00000128986						18	11	32	44	33	18	47	284	182	13	307		
ENSMUST00000128987						6	4	3	0	1	6	0	0	0	0	0		
ENSMUST00000128988						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000128989						1	2	2	111	8	1	0	0	0	0	0		
ENSMUST00000128991						2	0	3	50	3	1	0	0	9	0	0		
ENSMUST00000128992						3	0	17	23	2	6	170	76	58	12	87		
ENSMUST00000128993						11	3	38	35	18	4	23	61	32	4	21		
ENSMUST00000128994	ENSMUSG00000027411	2	130424339	130444269	1	0	0	3	3	2	0	0	11	13	0	61	A2BI90	
ENSMUST00000128995						3	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000128997	ENSMUSG00000024122	17	24073680	24150924	-1	3	1	8	22	6	0	2	4	0	0	0	F2Z3X9	
ENSMUST00000128999	ENSMUSG00000074607	2	163203125	163324170	1	0	2	0	59	2	1	0	0	0	0	0	A2A474	
ENSMUST00000129001						2	0	25	3	9	0	250	931	92	130	54		
ENSMUST00000129002	ENSMUSG00000027829	3	65946151	65958249	-1	6	0	4	3	2	0	65	436	169	95	298	F6WYR6	
ENSMUST00000129003						0	0	0	11	0	0	11	26	47	6	35		
ENSMUST00000129004						2	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000129005						0	1	0	0	0	0	0	57	33	215	58		
ENSMUST00000129006	ENSMUSG00000059540	2	181680310	181688071	1	0	0	9	0	2	1	0	0	7	0	0	F6XMY4	
ENSMUST00000129008	ENSMUSG00000005373	5	135089890	135138382	1	0	0	0	0	0	0	0	0	0	4	16		Q99MZ3
ENSMUST00000129009						1	1	7	1	4	1	2	6	2	1	1		
ENSMUST00000129010	ENSMUSG00000020289	11	32225628	32267707	-1	0	0	0	5	2	1	1	0	0	2	1	A2AAX8	
ENSMUST00000129011						0	8	3	2	4	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129012						1	1	2	1	3	4	1	0	0	0	0		
ENSMUST00000129013						266	217	2763	525	158	84	5	0	8	2	9		
ENSMUST00000129014	ENSMUSG00000021643	13	100107997	100114571	1	1	3	4	3	0	0	0	0	0	0	0		O88892
ENSMUST00000129015						0	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000129016						9	8	42	6	9	9	0	0	0	0	0		
ENSMUST00000129017						1	4	0	2	2	0	0	0	0	0	0		
ENSMUST00000129018	ENSMUSG00000056328	11	67200052	67224575	1	3	1	0	6	4	1	0	1	0	0	1	Q1WNQ6	
ENSMUST00000129019						6	2	0	3	3	0	4	11	17	3	18		
ENSMUST00000129020	ENSMUSG00000006345	10	75561604	75586200	1	3	0	3	0	0	1	192	87	235	7	147	F6WUX1	
ENSMUST00000129021	ENSMUSG00000028411	4	40682382	40703194	-1	0	0	0	0	0	0	69	229	83	306	75	E0CXB7	
ENSMUST00000129022						0	2	2	3	1	3	2	7	10	0	5		
ENSMUST00000129023						0	0	0	0	0	3	8	83	12	0	14		
ENSMUST00000129024	ENSMUSG00000041733	5	115279666	115296972	1	0	2	0	0	5	0	16	26	0	2	7	F6X4L9	
ENSMUST00000129025						6	2	30	0	0	1	215	482	589	86	374		
ENSMUST00000129026						0	0	0	0	0	0	0	0	222	0	0		
ENSMUST00000129027						8	3	6	75	13	3	0	9	4	0	3		
ENSMUST00000129028						2	1	7	2	1	0	0	0	0	1	2		
ENSMUST00000129029						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000129030						85	57	235	703	143	68	2	0	1	0	3		
ENSMUST00000129031	ENSMUSG00000022191	15	12824815	12935290	1	3	0	0	0	15	0	23	49	8	23	28	F6QX82	
ENSMUST00000129032	ENSMUSG00000040606	4	142102390	142239401	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZCA7	
ENSMUST00000129033						1	2	0	13	0	0	589	801	1317	297	798		
ENSMUST00000129034						3	0	7	4	9	3	0	0	0	1	0		
ENSMUST00000129035	ENSMUSG00000030079	6	88465409	88497572	1	4	0	15	18	8	0	0	0	0	0	0	D3YW60	
ENSMUST00000129038	ENSMUSG00000045251	7	127418967	127422068	-1	1	3	0	36	0	1	0	0	5	0	0		
ENSMUST00000129039						4	1	11	8	8	8	0	4	5	0	0		
ENSMUST00000129040	ENSMUSG00000033615	5	108518554	108550024	-1	0	1	4	26	6	2	0	0	0	0	0	D3YZ72	
ENSMUST00000129041						0	0	0	0	0	0	15	11	80	2	67		
ENSMUST00000129042						0	7	6	0	4	3	0	0	0	0	0		
ENSMUST00000129043	ENSMUSG00000034006	18	80253292	80292725	1	0	0	0	28	0	0	651	987	523	92	368		Q80XM9
ENSMUST00000129044						6	0	0	0	0	4	0	123	0	0	6		
ENSMUST00000129045						15	8	31	287	37	5	0	0	0	0	2		
ENSMUST00000129046	ENSMUSG00000062859	17	28066747	28080639	-1	0	2	0	15	0	0	0	5	0	0	6	B2KF24	
ENSMUST00000129047	ENSMUSG00000051169	6	113415319	113419340	-1	0	0	11	3	8	1	0	0	8	0	7		Q14AI6
ENSMUST00000129048						1	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000129049	ENSMUSG00000022545	16	13109684	13150617	1	60	50	39	36	69	28	40	110	42	6	62	F7A043	
ENSMUST00000129050						8	10	40	14	9	9	0	0	0	1	0		
ENSMUST00000129051						3	2	7	3	4	2	0	0	0	0	0		
ENSMUST00000129052						2	5	0	5	4	1	0	0	0	0	0		
ENSMUST00000129053						0	0	0	0	0	0	5	10	19	8	27		
ENSMUST00000129054						0	15	4	0	3	0	83	816	72	136	65		
ENSMUST00000129055	ENSMUSG00000064068	3	89209081	89227088	-1	1	0	1	0	0	0	0	0	1	0	0		
ENSMUST00000129057						22	28	48	32	17	9	2	16	11	5	11		
ENSMUST00000129058						8	7	23	10	10	2	0	0	0	0	1		
ENSMUST00000129060						0	0	0	39	0	0	0	0	0	1	0		
ENSMUST00000129061						41	39	69	45	50	32	5	25	8	4	15		
ENSMUST00000129062						0	0	0	0	3	1	8	11	14	3	8		
ENSMUST00000129064						0	2	0	8	1	2	0	0	0	0	0		
ENSMUST00000129066						3	1	0	6	0	2	0	0	0	0	0		
ENSMUST00000129068	ENSMUSG00000041684	1	44118957	44144770	1	1	1	10	8	7	3	0	0	0	2	0		
ENSMUST00000129069	ENSMUSG00000053768	6	32790976	33060260	-1	2	0	4	0	1	1	0	0	0	0	0	F6QFL0	
ENSMUST00000129070						0	0	0	0	0	0	1	55	5	0	2		
ENSMUST00000129071	ENSMUSG00000056666	6	72598475	72608425	1	2	1	9	7	3	1	3	7	7	4	7	F7CW61	
ENSMUST00000129072						12	19	44	51	22	7	0	0	0	0	0		
ENSMUST00000129073						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129074						1	3	8	60	8	4	0	0	0	0	5		
ENSMUST00000129076						1	0	5	1	1	3	2	7	3	0	7		
ENSMUST00000129077						4	3	12	30	7	2	0	0	0	0	0		
ENSMUST00000129078						3	4	2	0	4	2	0	2	0	0	1		
ENSMUST00000129079	ENSMUSG00000036817	5	139200637	139249840	1	1	0	0	1	1	1	0	0	0	0	0	D3Z1X3	
ENSMUST00000129080						9	5	18	5	9	0	2	4	3	0	4		
ENSMUST00000129081	ENSMUSG00000024807	19	6046576	6053712	1	10	3	4	69	1	3	7	0	0	0	6	D3YZH4	
ENSMUST00000129083						0	0	7	0	0	1	0	0	0	4	0		
ENSMUST00000129085						36	26	84	33	21	8	3	8	10	2	11		
ENSMUST00000129087	ENSMUSG00000030759	7	113513834	113571511	1	0	0	0	45	5	0	0	0	0	0	7	D3Z5W6	
ENSMUST00000129088	ENSMUSG00000016128	5	151037510	151233836	-1	0	1	0	0	2	0	0	0	0	0	0	D3Z418	
ENSMUST00000129090						14	10	35	8	28	10	0	0	0	0	8		
ENSMUST00000129091	ENSMUSG00000024018	17	29689378	29717012	-1	0	0	0	6	9	14	27	114	44	0	30		Q9D162
ENSMUST00000129092	ENSMUSG00000029651	5	147957320	148316065	1	0	0	0	107	1	0	0	0	0	0	0	D3YZ59	
ENSMUST00000129093						2	2	14	1	1	0	449	209	240	292	190		
ENSMUST00000129094						4	3	2	7	4	4	13	15	51	1	79		
ENSMUST00000129095						2	0	13	3	1	1	27	42	24	2	37		
ENSMUST00000129096	ENSMUSG00000004864	17	28769307	28778698	1	5	0	21	87	4	9	0	104	219	0	57	D6RG58	
ENSMUST00000129098						49	40	215	99	85	27	3	24	20	4	24		
ENSMUST00000129099	ENSMUSG00000005107	5	38349273	38503143	-1	0	0	0	0	10	3	0	0	0	0	0	B9EHN5	
ENSMUST00000129100	ENSMUSG00000025089	19	58235604	58455909	-1	7	3	0	2	0	4	0	0	0	2	0		P97785
ENSMUST00000129101						0	0	0	0	0	0	16	16	21	10	6		
ENSMUST00000129103						14	10	15	7	17	4	0	0	0	2	0		
ENSMUST00000129104						7	3	5	0	6	3	6	8	11	0	20		
ENSMUST00000129105						4	9	11	85	7	5	0	0	1	0	0		
ENSMUST00000129106						0	0	4	1	0	0	0	2	1	0	0		
ENSMUST00000129107	ENSMUSG00000026103	1	52163448	52233232	-1	0	0	0	0	0	0	14	61	51	16	34	F6RDM4	
ENSMUST00000129109						2	3	7	0	5	0	0	8	14	0	24		
ENSMUST00000129110						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129111						217	184	484	311	219	123	6	14	8	4	14		
ENSMUST00000129112						6	0	12	6	0	3	0	0	0	0	0		
ENSMUST00000129113	ENSMUSG00000041977	3	87617559	87738034	1	33	0	37	33	15	16	212	63	275	0	133	E9Q0A3	
ENSMUST00000129115	ENSMUSG00000020413	11	8993137	9011191	-1	7	18	8	0	10	9	0	68	10	0	2		Q8BQY8
ENSMUST00000129116	ENSMUSG00000013973	1	171329145	171342331	1	0	0	0	0	0	0	64	39	55	6	23	D3Z0I1	
ENSMUST00000129117	ENSMUSG00000021694	13	108158731	108195364	1	4	2	12	1	3	2	0	0	1	0	3	D6RET0	
ENSMUST00000129118						2	1	4	0	1	1	0	0	0	0	0		
ENSMUST00000129119						3	0	6	7	0	2	0	0	0	0	0		
ENSMUST00000129120						2	0	2	2	2	1	0	0	0	21	13		
ENSMUST00000129121						1	3	9	7	6	5	7	46	16	0	25		
ENSMUST00000129122						2	0	0	6	2	0	0	43	0	4	12		
ENSMUST00000129123						41	47	45	39	56	42	7	18	15	11	23		
ENSMUST00000129124						2	0	0	0	4	3	0	12	3	2	3		
ENSMUST00000129125						2	0	10	13	9	3	0	3	2	0	12		
ENSMUST00000129127						5	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000129128						0	0	0	0	0	0	11	17	0	0	0		
ENSMUST00000129129	ENSMUSG00000074259	9	59680144	59718874	1	0	0	1	0	0	1	1	3	14	1	2	F6W980	
ENSMUST00000129130	ENSMUSG00000000308	2	121357714	121363737	1	2	0	0	0	0	0	0	0	0	0	0	B0R0F0	
ENSMUST00000129131						4	5	8	10	2	0	21	14	12	3	27		
ENSMUST00000129132	ENSMUSG00000039375	8	54629055	54887184	-1	0	2	0	0	0	0	0	0	0	0	0	Q9CXX5	
ENSMUST00000129133						3	0	3	3	1	4	0	0	0	0	0		
ENSMUST00000129134						0	0	6	2	0	2	12	9	22	0	21		
ENSMUST00000129135						0	0	1	1	0	3	0	0	0	0	0		
ENSMUST00000129136	ENSMUSG00000033498	2	121363728	121387168	-1	0	0	6	0	0	0	0	0	0	0	0	F6UNX5	
ENSMUST00000129137	ENSMUSG00000027593	2	154791096	154867261	1	0	0	0	0	0	0	612	14	183	0	0	A2AU61	
ENSMUST00000129138	ENSMUSG00000034785	4	107291465	107307169	-1	0	0	0	0	0	0	0	0	0	0	0	D3YX15	
ENSMUST00000129140						0	0	13	6	4	0	16	187	37	0	85		
ENSMUST00000129141						2	3	0	3	0	7	0	0	0	0	1		
ENSMUST00000129142	ENSMUSG00000019997	10	24595442	24598683	1	1	0	0	66	2	0	0	0	0	0	0	H3BK14	
ENSMUST00000129143	ENSMUSG00000027333	2	131491496	131525922	1	1	2	3	23	0	0	0	11	0	0	0	A2ANQ3	
ENSMUST00000129144						2	0	0	3	0	1	0	0	0	0	0		
ENSMUST00000129145						6	4	25	21	20	7	30	273	86	8	103		
ENSMUST00000129147						0	0	0	4	1	3	17	19	13	0	7		
ENSMUST00000129148						0	0	7	0	1	0	0	0	0	0	0		
ENSMUST00000129150						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000129151						33	32	166	108	36	10	7	5	15	0	19		
ENSMUST00000129152						6	3	20	12	2	3	0	71	32	26	26		
ENSMUST00000129153						5	11	47	84	19	6	26	227	56	3	119		
ENSMUST00000129154						10	7	65	14	12	1	0	0	0	1	1		
ENSMUST00000129156	ENSMUSG00000026825	2	32308471	32353338	-1	0	0	0	0	0	0	0	2	0	0	0	F6W8Z8	
ENSMUST00000129157						14	11	46	18	15	8	3	12	3	0	8		
ENSMUST00000129159						0	2	3	0	0	0	0	0	0	0	0		
ENSMUST00000129160						2	0	0	18	3	2	0	0	0	0	0		
ENSMUST00000129161	ENSMUSG00000029127	5	38189735	38220457	-1	4	0	2	0	4	4	4	0	8	0	7		
ENSMUST00000129162	ENSMUSG00000048497	11	62648664	62666354	1	3	12	18	14	10	6	29	82	30	38	26		Q8R3L0
ENSMUST00000129163						25	12	62	45	35	11	16	36	56	19	53		
ENSMUST00000129165	ENSMUSG00000026811	2	32599709	32620806	1	2	1	5	3	2	0	2	0	0	0	0	Z4YN31	
ENSMUST00000129166	ENSMUSG00000078681	7	65691169	65701913	1	0	2	0	0	0	0	8	0	13	0	0		
ENSMUST00000129167						5	0	46	6	4	3	12	20	108	12	202		
ENSMUST00000129168						0	0	4	0	4	3	0	0	0	0	0		
ENSMUST00000129169						1	1	0	3	4	2	0	0	0	0	0		
ENSMUST00000129170	ENSMUSG00000025702	6	116338024	116409540	1	1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129171						8	7	20	126	7	11	5	26	12	2	12		
ENSMUST00000129172						5	0	0	0	0	1	0	11	0	4	5		
ENSMUST00000129173	ENSMUSG00000025432	10	127000709	127020994	1	20	5	16	12	16	7	20	8	20	7	40		O88398
ENSMUST00000129174	ENSMUSG00000022090	14	70164218	70177681	-1	0	0	6	0	0	0	174	455	230	80	117	A0A087WPL1	
ENSMUST00000129176						2	0	4	2	3	0	0	0	0	0	0		
ENSMUST00000129177						9	11	61	33	20	6	8	28	12	0	21		
ENSMUST00000129178						12	8	23	5	6	8	3	116	9	3	25		
ENSMUST00000129179	ENSMUSG00000040594	11	33211795	33513746	-1	5	3	4	9	7	0	0	1	1	0	1	M0QWL9	
ENSMUST00000129180						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129181						8	4	11	5	10	5	17	63	20	20	22		
ENSMUST00000129182						4	4	11	1	5	3	0	0	0	0	0		
ENSMUST00000129183						0	6	24	33	31	9	0	5	0	0	0		
ENSMUST00000129184						0	0	4	0	0	0	0	2	0	2	1		
ENSMUST00000129185						13	4	33	13	4	5	23	4	37	4	46		
ENSMUST00000129186						2	5	5	9	4	3	0	0	0	0	0		
ENSMUST00000129187	ENSMUSG00000060131	2	126320973	126500674	-1	7	2	9	8	9	1	12	6	47	28	48	A2ANX2	
ENSMUST00000129188						1	1	7	49	4	3	0	1	0	0	2		
ENSMUST00000129189						0	4	0	1	5	0	0	0	0	0	0		
ENSMUST00000129190	ENSMUSG00000026004	1	66719248	66817562	-1	3	5	0	3	1	5	55	274	84	52	94	F6ULJ7	
ENSMUST00000129192						2	4	15	5	0	2	0	0	0	0	0		
ENSMUST00000129193	ENSMUSG00000002546	2	32287384	32307921	1	0	0	0	0	0	0	18	0	32	0	36	A2AN48	
ENSMUST00000129194						2	4	1	1	2	1	0	6	13	0	4		
ENSMUST00000129195						0	0	0	71	0	2	0	0	0	0	0		
ENSMUST00000129197						4	4	5	1	6	2	4	10	2	0	5		
ENSMUST00000129198						1	0	0	0	0	0	0	0	0	0	8		
ENSMUST00000129199	ENSMUSG00000022750	16	17759618	17793382	1	0	0	0	10	1	0	0	0	2	6	6	D3Z2R6	
ENSMUST00000129200	ENSMUSG00000023973	17	46735705	46752214	-1	0	0	0	6	0	0	76	57	116	39	49	D6RI28	
ENSMUST00000129201						5	6	0	3	2	2	3	3	0	1	2		
ENSMUST00000129202						0	0	5	1	0	1	0	0	0	0	0		
ENSMUST00000129203						42	28	152	40	19	15	6	3	6	0	10		
ENSMUST00000129204						12	5	18	26	11	8	55	474	89	33	136		
ENSMUST00000129205	ENSMUSG00000023927	17	51736187	51833290	-1	1	1	1	0	3	0	0	0	0	0	0	D3YZD1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129206						0	0	0	33	0	2	3	0	0	0	6		
ENSMUST00000129209						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129210	ENSMUSG00000017664	2	165276554	165287869	-1	1	0	3	0	3	1	98	64	73	11	64	Q5GMG7	
ENSMUST00000129211	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	0	0	0	0	D3YYB1	
ENSMUST00000129212	ENSMUSG00000029576	5	142484839	142551098	-1	2	0	0	9	7	1	0	0	0	0	0	D3YYI1	
ENSMUST00000129213	ENSMUSG00000070644	1	133363572	133380336	1	11	6	12	0	13	6	0	0	0	5	1	H9KV13	
ENSMUST00000129214						2	2	3	3	0	0	4	3	4	1	0		
ENSMUST00000129217	ENSMUSG00000026418	1	135779434	135810989	1	2	0	10	0	10	2	0	0	0	0	0	F6QC77	
ENSMUST00000129218						1	0	0	4	13	0	0	4	0	3	0		
ENSMUST00000129219						2	2	5	3	1	2	0	11	3	3	7		
ENSMUST00000129220						0	0	0	0	0	0	20	78	18	30	15		
ENSMUST00000129221	ENSMUSG00000000766	10	6758506	7038198	1	0	2	0	0	0	0	0	0	0	0	0	E9PVC1	
ENSMUST00000129222						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129223	ENSMUSG00000022469	15	97744770	97767972	-1	23	0	27	0	0	0	0	8	13	0	0		Q8VCC8
ENSMUST00000129224	ENSMUSG00000018761	11	69656697	69662642	-1	0	0	0	0	2	0	47	275	38	0	10	F6XX36	
ENSMUST00000129225						0	6	13	0	0	0	0	0	0	0	0		
ENSMUST00000129226						3	0	0	0	3	0	0	0	0	5	0		
ENSMUST00000129227	ENSMUSG00000023902	17	23600856	23611019	1	0	0	0	9	0	0	3	1	1	4	4	E9PV84	
ENSMUST00000129228	ENSMUSG00000032046	2	150832493	150904741	-1	0	0	0	70	0	2	0	0	0	0	0	D6RI21	
ENSMUST00000129229						3	0	0	0	2	0	25	85	46	5	38		
ENSMUST00000129230	ENSMUSG00000001089	4	136469761	136554780	1	0	2	0	2	0	0	0	0	0	0	0	E9Q9L3	
ENSMUST00000129231	ENSMUSG00000006191	13	29191746	29855674	-1	0	0	1	0	2	1	0	0	2	0	0	D6RJ19	
ENSMUST00000129232	ENSMUSG00000006345	10	75561604	75586200	1	0	0	4	0	1	0	0	0	5	0	0	D3YWW2	
ENSMUST00000129233	ENSMUSG00000055850	6	72359714	72366956	-1	0	0	0	0	0	0	0	0	12	29	5	S4R1T4	
ENSMUST00000129234	ENSMUSG00000018570	11	69897352	69900987	-1	0	3	9	19	1	3	0	17	7	0	0	J3QNJ8	
ENSMUST00000129235						4	2	45	7	0	2	4	4	0	0	5		
ENSMUST00000129236						3	1	3	0	4	3	0	0	0	0	1		
ENSMUST00000129238						4	0	1	2	2	2	0	0	0	0	0		
ENSMUST00000129239						0	1	7	2	0	1	10	117	35	21	34		
ENSMUST00000129240						12	6	11	9	5	6	1	1	1	3	1		
ENSMUST00000129241	ENSMUSG00000057738	2	29965560	30031451	1	11	2	13	8	13	4	59	557	51	185	107	A3KGU9	
ENSMUST00000129242						0	0	1	1	2	0	10	0	0	0	1		
ENSMUST00000129243	ENSMUSG00000005503	6	52313498	52318378	1	0	1	6	82	7	1	0	0	0	0	0	F6R8N2	
ENSMUST00000129244						358	348	467	665	358	164	39	138	77	11	69		
ENSMUST00000129246						0	0	0	19	1	1	1	1	1	0	0		
ENSMUST00000129247	ENSMUSG00000057933	9	78331018	78355788	-1	3	8	2	0	0	2	0	0	0	2	1	D3Z6A6	
ENSMUST00000129248						5	3	7	5	2	3	0	0	0	1	0		
ENSMUST00000129249	ENSMUSG00000030400	7	19382010	19395694	1	12	3	0	85	0	8	7	0	43	0	0	F6YA33	
ENSMUST00000129250	ENSMUSG00000003032	4	55527143	55532466	-1	2	0	2	126	0	1	0	0	4	0	0	B7ZCH2	
ENSMUST00000129251						3	5	7	0	1	0	0	0	0	1	0		
ENSMUST00000129252	ENSMUSG00000025402	10	127660918	127668568	-1	0	0	0	3	0	0	0	0	2	2	0	D3Z008	
ENSMUST00000129253	ENSMUSG00000029001	4	148152800	148160482	-1	0	4	4	6	0	2	0	0	0	3	0	E9PUJ0	
ENSMUST00000129254	ENSMUSG00000026155	1	23844846	23922317	-1	0	0	0	0	0	0	1	0	233	56	105	D3YVX4	
ENSMUST00000129255	ENSMUSG00000048108	6	116679063	116716913	-1	2	0	0	1	4	0	0	0	0	0	0	D6RGB3	
ENSMUST00000129256	ENSMUSG00000017288	11	76046226	76179647	-1	4	3	5	29	5	5	44	68	17	25	11	E9Q124	
ENSMUST00000129257						40	31	82	472	42	21	10	11	24	4	30		
ENSMUST00000129258						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129260						136	96	301	297	190	111	2	10	10	0	13		
ENSMUST00000129262						2	8	5	4	7	14	0	0	1	0	0		
ENSMUST00000129263						1	0	2	2	0	1	0	6	6	5	5		
ENSMUST00000129264						1	0	1	0	1	0	2	60	8	0	3		
ENSMUST00000129265						3	0	9	12	5	3	36	91	70	4	77		
ENSMUST00000129266						3	2	18	8	6	3	5	9	7	2	5		
ENSMUST00000129267	ENSMUSG00000015714	3	95314791	95323599	1	3	0	5	23	1	1	27	7	22	5	10	D3YTM0	
ENSMUST00000129268						7	1	0	0	2	0	1	3	0	16	0		
ENSMUST00000129269	ENSMUSG00000037286	9	100597798	100959375	1	0	0	0	0	0	0	61	97	106	101	164		Q9D3E6
ENSMUST00000129270						6	3	9	23	5	3	99	82	92	1	55		
ENSMUST00000129271						35	29	102	52	32	16	2	4	6	3	13		
ENSMUST00000129272						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129273	ENSMUSG00000027881	3	108902805	108911727	-1	12	6	0	4	14	5	52	173	41	41	117	A0A0G2JGW4	
ENSMUST00000129274						5	12	20	14	12	2	0	0	0	3	0		
ENSMUST00000129276						41	34	156	94	53	29	0	13	0	0	15		
ENSMUST00000129277						0	0	0	0	0	0	2	0	0	1	0		
ENSMUST00000129278						2	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000129279						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129280						0	0	5	4	5	2	2	5	0	0	7		
ENSMUST00000129281	ENSMUSG00000034593	9	75071015	75223688	1	0	0	1	0	0	0	25	32	53	3	8	B8JK05	
ENSMUST00000129282						1	3	0	0	5	0	1	1	0	4	0		
ENSMUST00000129283						1	0	0	2	0	0	3	0	1	0	0		
ENSMUST00000129284						0	0	1	0	1	0	21	139	38	72	20		
ENSMUST00000129285	ENSMUSG00000028019	3	81036416	81214040	1	2	3	4	0	0	0	0	0	0	10	7	D6RGS6	
ENSMUST00000129287						4	5	0	0	1	3	0	0	0	0	0		
ENSMUST00000129288						1	3	3	0	0	0	0	0	0	0	0		
ENSMUST00000129289						309	330	94	41	120	63	5	3	3	0	15		
ENSMUST00000129290						3	6	2	3	3	0	10	4	10	3	15		
ENSMUST00000129291						2	2	3	2	11	3	0	7	1	0	0		
ENSMUST00000129292						3	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000129293						8	3	0	1	5	0	27	84	90	11	54		
ENSMUST00000129294						0	5	13	4	5	0	61	151	63	11	135		
ENSMUST00000129295						2	0	4	59	9	2	0	15	6	5	23		
ENSMUST00000129296						4	0	9	5	3	1	0	0	0	0	0		
ENSMUST00000129297						0	0	0	15	0	4	34	76	31	14	14		
ENSMUST00000129298						13	8	18	28	14	6	14	11	67	1	75		
ENSMUST00000129299						5	3	3	1	3	0	0	0	0	0	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129300	ENSMUSG00000026965	2	25272478	25285915	1	0	1	0	0	0	0	81	68	73	0	30	A2AI11	
ENSMUST00000129301						0	0	0	0	0	0	2	5	2	2	3		
ENSMUST00000129303						2	2	5	2	4	1	25	435	38	27	46		
ENSMUST00000129304						4	5	31	1	0	3	4	4	9	0	4		
ENSMUST00000129305	ENSMUSG00000050627	9	114899341	114933987	-1	8	0	24	0	0	0	139	0	237	32	125	D3Z0L6	
ENSMUST00000129306	ENSMUSG00000029581	5	142960343	142973185	1	0	0	0	0	0	0	1	0	2	9	25	F7BDR1	
ENSMUST00000129307						6	2	8	4	3	4	27	23	15	0	45		
ENSMUST00000129308	ENSMUSG00000042642	3	89401004	89411870	-1	14	15	0	10	3	8	123	321	128	24	115		Q8R123
ENSMUST00000129309						1	0	1	145	1	0	0	0	0	0	0		
ENSMUST00000129310						33	44	120	94	55	32	16	75	47	6	62		
ENSMUST00000129311						44	27	58	67	48	32	15	27	11	11	20		
ENSMUST00000129312						11	13	49	10	15	8	16	91	11	5	18		
ENSMUST00000129313						0	1	7	1	6	0	24	24	28	0	19		
ENSMUST00000129314						12	25	91	6	12	0	459	836	57	62	179		
ENSMUST00000129315	ENSMUSG00000028691	4	116685544	116700822	1	7	3	11	17	6	1	0	0	0	0	0	B1AXW4	
ENSMUST00000129316	ENSMUSG00000034930	6	83135463	83152579	1	3	4	1	17	4	0	0	0	0	0	0	D3YXC9	
ENSMUST00000129317	ENSMUSG00000028719	4	114959336	114987241	-1	0	0	0	5	1	0	0	8	7	3	4	F6TY56	
ENSMUST00000129318						0	0	0	7	0	0	1	0	2	0	0		
ENSMUST00000129319						0	0	0	0	1	0	0	0	0	0	2		
ENSMUST00000129320						68	64	126	69	89	46	22	83	44	6	63		
ENSMUST00000129322						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129323						1	1	4	4	2	0	0	5	1	0	0		
ENSMUST00000129324	ENSMUSG00000033685	7	100493337	100502020	1	1	4	4	1	8	6	107	51	79	0	189	D3YZE5	
ENSMUST00000129325						19	17	100	175	23	14	0	1	0	0	0		
ENSMUST00000129326						1	0	2	0	0	2	0	0	12	0	4		
ENSMUST00000129327	ENSMUSG00000039850	11	119491347	119511437	1	0	0	0	0	0	0	9	38	27	0	0		Q8C9A2
ENSMUST00000129328						3	0	6	1	3	5	0	0	0	0	0		
ENSMUST00000129330						0	3	32	12	0	0	0	0	0	0	0		
ENSMUST00000129331						3	5	11	4	4	1	3	0	0	0	4		
ENSMUST00000129332						3	1	0	5	3	0	0	3	1	0	0		
ENSMUST00000129333						1	2	3	1	3	3	0	31	2	0	4		
ENSMUST00000129334						2	6	1	14	3	1	0	0	0	0	0		
ENSMUST00000129335	ENSMUSG00000021224	12	83794034	83921934	-1	0	0	0	0	0	0	0	0	0	0	0		Q9QZS3
ENSMUST00000129336	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	0	0	0	0	0	Q5GMG9	
ENSMUST00000129338						2	0	1	0	2	0	2	13	4	0	8		
ENSMUST00000129339	ENSMUSG00000025967	1	63176825	63180486	1	18	19	19	48	18	12	26	49	12	8	8		O70251
ENSMUST00000129340	ENSMUSG00000030990	7	102210208	102238567	1	5	0	0	4	0	0	12	37	7	0	32	D6RG97	
ENSMUST00000129341	ENSMUSG00000070709	7	27907392	27929460	-1	0	0	0	0	0	1	1	0	0	2	0	Q9CVS5	
ENSMUST00000129342	ENSMUSG00000028790	4	129703164	129742303	-1	5	4	12	18	11	0	22	375	430	93	450		Q60749
ENSMUST00000129344	ENSMUSG00000029759	6	5220852	5256286	-1	6	10	22	5	7	7	0	0	8	23	14	D6RJ12	
ENSMUST00000129345	ENSMUSG00000022972	16	90925809	90934927	-1	0	0	0	1	0	0	1	2	0	2	0	F7C0A6	
ENSMUST00000129346						2	1	2	2	0	3	47	1178	155	412	253		
ENSMUST00000129347	ENSMUSG00000029095	5	35757880	35884973	1	7	3	0	0	0	0	0	0	0	0	0	E9Q4K0	
ENSMUST00000129348	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	0	0	0	0	22	40	21	4	12	F6S1I0	
ENSMUST00000129349						28	27	33	86	37	16	121	459	303	38	627		
ENSMUST00000129350						3	1	0	1	0	0	5	6	0	0	0		
ENSMUST00000129351	ENSMUSG00000070730	2	119137001	119157034	-1	1	0	0	0	0	0	0	0	0	0	0	A3KGH6	
ENSMUST00000129352	ENSMUSG00000021377	13	47084775	47106201	-1	2	0	0	29	4	0	0	30	224	0	81	D3YVJ6	
ENSMUST00000129354						0	0	0	11	0	0	0	0	2	0	0		
ENSMUST00000129355	ENSMUSG00000020032	10	84370905	84440597	-1	0	0	0	0	2	0	1	0	0	0	3	F6XZX4	
ENSMUST00000129356	ENSMUSG00000004849	5	137034993	137046135	-1	3	2	4	5	4	5	3	0	0	0	2	D3Z268	
ENSMUST00000129357	ENSMUSG00000032297	9	59577917	59607292	1	0	0	0	0	0	0	0	0	0	0	0	D6RGB9	
ENSMUST00000129358	ENSMUSG00000035234	5	100805192	100820965	-1	0	0	0	0	0	0	0	0	3	0	0	D6RFD4	
ENSMUST00000129359						4	5	1	5	5	3	0	0	0	0	2		
ENSMUST00000129360	ENSMUSG00000032717	17	47815328	47834691	-1	0	0	0	0	0	0	0	0	0	0	0	D3YUT8	
ENSMUST00000129361						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129362	ENSMUSG00000021136	12	81026808	81186414	1	0	0	0	0	0	9	0	0	2	2	4	D3Z3A3	
ENSMUST00000129363						0	0	1	1	0	3	2	3	0	0	3		
ENSMUST00000129367						0	1	0	0	0	0	0	0	2	0	0		
ENSMUST00000129368	ENSMUSG00000056342	11	23306895	23490560	1	0	0	0	0	0	0	7	202	12	30	0	Z4YN11	
ENSMUST00000129369						0	2	1	0	0	1	1	0	0	2	0		
ENSMUST00000129370						1	1	2	5	2	0	0	0	0	0	0		
ENSMUST00000129371						0	0	8	2	1	0	0	0	0	0	0		
ENSMUST00000129372	ENSMUSG00000041815	15	83125978	83149384	-1	0	0	1	7	7	0	23	0	37	0	9	F6VR84	
ENSMUST00000129374						11	12	74	77	22	5	0	0	1	0	2		
ENSMUST00000129375	ENSMUSG00000037446	17	28351515	28365182	-1	0	0	0	0	0	0	0	0	0	0	0	F6R7T6	
ENSMUST00000129376	ENSMUSG00000034601	12	71136848	71243303	1	1	1	9	0	2	5	12	76	10	11	14	F7BDN4	
ENSMUST00000129377	ENSMUSG00000027474	2	153065955	153081735	1	0	0	0	0	0	0	0	0	0	0	0	A2ATH4	
ENSMUST00000129378						0	0	0	0	0	0	0	8	0	0	0		
ENSMUST00000129380						13	0	13	7	0	14	6	72	11	64	22		
ENSMUST00000129381						3	0	11	7	6	0	0	1	0	2	0		
ENSMUST00000129382						0	0	0	0	0	0	1	0	0	1	0		
ENSMUST00000129383						1	0	1	18	3	4	10	14	32	2	58		
ENSMUST00000129384						6	14	29	14	13	4	5	4	3	1	4		
ENSMUST00000129385						10	13	55	81	26	14	0	0	0	0	0		
ENSMUST00000129386						5	2	8	8	7	2	0	0	4	6	6		
ENSMUST00000129387						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129388						1	0	0	141	7	4	4	11	10	31	13		
ENSMUST00000129389						5	0	3	32	8	0	0	2	0	0	2		
ENSMUST00000129390						5	1	7	9	5	4	0	0	2	0	0		
ENSMUST00000129391						1	0	2	3	4	0	0	3	2	0	1		
ENSMUST00000129392	ENSMUSG00000026224	1	85928483	85940624	1	3	3	0	2	5	0	0	0	0	1	0	D3Z3J4	
ENSMUST00000129393						1	0	16	1	1	0	15	77	23	34	0		
ENSMUST00000129394						3	4	11	3	5	4	0	8	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129395						3	2	4	6	2	2	0	0	0	0	2		
ENSMUST00000129396						4	3	9	4	5	4	5	17	4	0	1		
ENSMUST00000129398						0	0	0	5	0	0	0	0	0	18	0		
ENSMUST00000129399						0	1	8	7	3	0	108	357	78	10	131		
ENSMUST00000129400	ENSMUSG00000007646	11	87376645	87404954	-1	0	0	0	0	0	0	7	0	0	0	0	F2Z4A1	
ENSMUST00000129401	ENSMUSG00000024136	17	24440081	24443105	-1	1	10	6	3	5	1	0	4	0	0	0	F7A4S2	
ENSMUST00000129402						5	1	8	10	7	5	0	0	0	2	0		
ENSMUST00000129403						7	0	0	16	5	9	0	0	0	0	0		
ENSMUST00000129404	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000129405						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129406						31	33	114	23	36	22	3	14	4	0	14		
ENSMUST00000129411	ENSMUSG00000107478	6	124739189	124756021	-1	0	8	0	222	0	20	373	51	407	28	379		O35126
ENSMUST00000129412						0	0	0	11	0	2	3	0	0	0	0		
ENSMUST00000129413	ENSMUSG00000020048	10	86690209	86705509	-1	0	0	0	0	0	0	0	0	65	0	0	F7C312	
ENSMUST00000129414	ENSMUSG00000084786	9	20642878	20647140	1	8	5	24	0	1	0	106	162	71	85	75		Q9EPV8
ENSMUST00000129415						0	2	1	2	0	1	5	4	3	0	2		
ENSMUST00000129416	ENSMUSG00000038954	17	44777152	45119290	1	5	5	2	0	0	2	17	56	22	12	8	B0QZW4	
ENSMUST00000129417						0	0	0	0	0	0	0	0	0	65	0		
ENSMUST00000129419						0	0	3	0	0	4	2	35	6	0	5		
ENSMUST00000129420						6	4	16	5	5	4	0	0	4	2	4		
ENSMUST00000129421	ENSMUSG00000020017	10	93488768	93519304	1	164	104	141	4539	233	111	47	179	130	123	185	B2RXW1	P35492
ENSMUST00000129422						1	0	10	8	4	0	3	12	9	0	8		
ENSMUST00000129423	ENSMUSG00000030428	7	4119408	4136708	1	81	92	387	110	79	44	5	13	6	4	16		Q9D3A9
ENSMUST00000129424						17	17	35	27	30	17	0	3	2	0	5		
ENSMUST00000129426						0	0	1	0	0	0	0	0	0	7	0		
ENSMUST00000129427						4	0	0	0	1	1	0	0	3	3	0		
ENSMUST00000129428						14	5	13	14	24	4	140	609	651	84	668		
ENSMUST00000129429						2	2	0	3	1	1	26	26	20	3	18		
ENSMUST00000129430	ENSMUSG00000035547	7	98121559	98178274	-1	3	5	22	12	0	2	0	0	0	0	0	D3YU84	
ENSMUST00000129431						1	3	1	1	2	0	0	5	0	0	8		
ENSMUST00000129433	ENSMUSG00000030203	6	134715468	134792625	-1	0	0	0	0	0	0	8	0	15	0	0	F6UIK0	
ENSMUST00000129434	ENSMUSG00000018287	11	70663771	70669416	-1	0	0	0	0	0	0	25	2	28	76	1	Q5SX56	
ENSMUST00000129435	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	1	0	0	0	0	D3Z4K8	
ENSMUST00000129436						1	0	0	2	9	1	0	1	1	0	0		
ENSMUST00000129437	ENSMUSG00000071369	10	19934472	20142753	1	2	3	7	4	8	2	0	0	3	0	3	D3YVC4	
ENSMUST00000129439						0	1	13	7	4	2	3	4	3	0	10		
ENSMUST00000129442						6	6	8	74	10	7	0	0	1	0	0		
ENSMUST00000129443						0	0	0	0	3	0	8	5	0	2	0		
ENSMUST00000129444						0	0	13	4	4	0	0	0	0	0	2		
ENSMUST00000129445						11	18	14	27	16	12	0	0	0	0	0		
ENSMUST00000129446	ENSMUSG00000030127	6	124958413	124965538	-1	0	1	1	0	3	0	0	4	0	0	0	D3YVI6	
ENSMUST00000129447						7	3	14	56	11	5	48	63	48	8	67		
ENSMUST00000129448						0	0	0	0	0	0	0	0	11	7	0		
ENSMUST00000129449	ENSMUSG00000087370	13	41606216	41641347	1	37	27	85	83	39	24	732	1690	1500	112	690		P86050
ENSMUST00000129450						0	0	0	27	0	0	20	6	5	0	3		
ENSMUST00000129451						1	0	0	2	1	0	0	23	5	6	12		
ENSMUST00000129452	ENSMUSG00000041301	6	18170687	18322768	1	4	2	4	4	6	1	0	0	1	0	0	F6U9G7	
ENSMUST00000129453						13	8	32	29	13	8	7	16	46	1	69		
ENSMUST00000129454						4	3	28	8	13	10	0	0	0	0	0		
ENSMUST00000129455						1	0	0	0	0	0	0	14	7	2	8		
ENSMUST00000129456	ENSMUSG00000047648	10	11281330	11298052	1	34	35	39	47	40	25	90	123	61	14	51		Q8BJL1
ENSMUST00000129457						0	0	0	0	0	0	28	30	37	5	17		
ENSMUST00000129458	ENSMUSG00000026189	1	72259167	72284314	-1	5	2	0	4	0	2	0	0	0	0	0	D6RIP0	
ENSMUST00000129459	ENSMUSG00000029096	5	35652023	35679782	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129462	ENSMUSG00000034023	6	113531682	113597017	1	3	1	0	2	3	0	1	0	1	0	0		
ENSMUST00000129463	ENSMUSG00000018334	11	79013440	79146407	-1	2	2	7	3	3	2	0	0	2	0	6	Q5SXE1	
ENSMUST00000129464	ENSMUSG00000042182	1	33852052	33907816	-1	7	3	6	76	6	9	2	4	0	0	0	A0A087WSH8	
ENSMUST00000129465						9	4	28	8	7	4	0	0	0	0	0		
ENSMUST00000129466						8	11	4	6	7	1	0	7	4	0	4		
ENSMUST00000129467	ENSMUSG00000021281	12	111442469	111455018	1	0	2	1	0	0	1	40	3	35	0	36	G3XA62	
ENSMUST00000129468	ENSMUSG00000033576	15	77044729	77057107	1	0	1	2	0	0	1	0	0	0	1	0	B7ZC56	
ENSMUST00000129469	ENSMUSG00000089917	2	181569149	181584892	-1	0	0	0	0	0	0	286	357	177	71	197	D6RJ84	
ENSMUST00000129471						3	2	6	4	7	4	0	0	0	0	1		
ENSMUST00000129473	ENSMUSG00000025161	11	120948480	120960868	1	0	0	2	25	0	3	0	0	40	0	205	B1ATM2	
ENSMUST00000129474	ENSMUSG00000020340	11	46193850	46312859	-1	4	1	0	93	1	2	0	0	0	1	0	F7C3H9	
ENSMUST00000129475	ENSMUSG00000047284	11	69901072	69913820	1	0	0	0	0	11	0	0	6	0	0	0	H3BLC3	
ENSMUST00000129476	ENSMUSG00000010751	7	143634806	143649661	-1	0	1	0	9	4	1	4	0	0	0	0	D3YVF3	
ENSMUST00000129477	ENSMUSG00000063358	16	16983382	17047453	1	0	2	2	0	0	0	0	18	0	0	25	F6VEI7	
ENSMUST00000129478						1	5	3	1	1	4	0	0	0	0	0		
ENSMUST00000129480						0	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000129481						2	1	0	16	1	1	0	0	0	0	1		
ENSMUST00000129482						0	3	13	8	3	0	7	68	9	6	14		
ENSMUST00000129483	ENSMUSG00000033773	5	107597373	107661838	1	0	0	0	0	0	0	0	0	2	0	0	A0A0G2JDU8	
ENSMUST00000129484						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129487						9	15	0	0	10	9	39	504	54	66	23		
ENSMUST00000129488	ENSMUSG00000039219	13	14063232	14199603	1	0	0	3	37	4	0	0	0	106	0	38	Z4YMH1	
ENSMUST00000129489	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	0	0	0	0	0	0	46	0	76	D6RG90	
ENSMUST00000129490						8	7	16	10	10	4	3	0	0	0	3		
ENSMUST00000129491						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000129492	ENSMUSG00000020265	10	77606097	77641543	1	0	0	0	0	0	0	0	5	0	16	6	G3UZA7	
ENSMUST00000129493						0	0	0	0	0	0	677	1069	875	118	772		
ENSMUST00000129494	ENSMUSG00000026853	2	30400471	30415813	-1	9	3	7	13	4	0	1	3	4	1	5	A2AWE5	
ENSMUST00000129495						0	0	0	0	0	0	3	63	4	27	26		
ENSMUST00000129496						0	0	0	2	0	3	0	0	0	0	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129497						0	0	0	2	0	0	2	0	0	0	0		
ENSMUST00000129498						1	0	0	0	2	0	0	6	2	2	0		
ENSMUST00000129499	ENSMUSG00000018906	11	54100095	54131665	1	0	0	4	0	0	0	0	0	0	0	0	B0QZH0	
ENSMUST00000129500	ENSMUSG00000017428	11	80428615	80473248	1	0	0	0	0	0	0	0	0	0	5	0	G3UWW7	
ENSMUST00000129502						1	2	0	1	0	1	1	9	2	19	5		
ENSMUST00000129503						2	4	9	1	10	4	122	343	102	10	77		
ENSMUST00000129504						2	0	1	1	1	0	0	1	0	0	3		
ENSMUST00000129505						2	1	0	0	1	0	3	15	6	0	4		
ENSMUST00000129506						0	3	0	4	0	0	0	0	0	0	0		
ENSMUST00000129507	ENSMUSG00000054161	7	45721212	45729492	1	0	0	17	87	19	0	0	0	0	0	0		Q80XS7
ENSMUST00000129508						14	20	18	18	11	9	0	0	0	0	1		
ENSMUST00000129509	ENSMUSG00000017418	2	15049395	15082456	1	0	0	0	0	0	0	7	0	0	0	0	F6Y333	
ENSMUST00000129510						0	4	0	27	20	0	0	13	0	0	6		
ENSMUST00000129511						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000129512						0	3	0	0	0	0	0	6	4	0	2		
ENSMUST00000129514	ENSMUSG00000015846	2	27676440	27762957	1	0	0	6	36	7	4	11	0	0	0	0	A2AJP2	
ENSMUST00000129515	ENSMUSG00000028797	4	129600668	129624059	1	12	42	0	48	18	0	30	0	24	0	23	D6RDC0	
ENSMUST00000129516						0	2	4	3	4	0	0	27	9	0	31		
ENSMUST00000129517						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000129518						1	1	3	3	1	0	0	0	0	0	0		
ENSMUST00000129519						3	0	2	2	5	1	12	26	12	0	31		
ENSMUST00000129520						12	15	30	83	23	9	1	4	1	1	0		
ENSMUST00000129521						0	1	6	2	1	0	0	0	0	0	0		
ENSMUST00000129522	ENSMUSG00000024220	17	28177207	28205886	1	1	0	11	0	0	0	12	75	0	20	16	F7B631	
ENSMUST00000129523	ENSMUSG00000036820	17	24155833	24163766	-1	0	0	3	5	3	0	9	15	11	0	12	F6UP77	
ENSMUST00000129525						2	0	2	0	3	6	0	0	0	0	1		
ENSMUST00000129528	ENSMUSG00000029345	5	112326358	112338073	1	2	3	6	85	7	3	0	2	8	0	2	D3YWC8	
ENSMUST00000129529						0	3	0	1	1	0	5	58	7	10	9		
ENSMUST00000129530	ENSMUSG00000042002	5	114254164	114273807	-1	2	1	12	5	5	0	0	0	0	0	0	F6ZBN9	
ENSMUST00000129531						3	0	2	10	2	0	14	40	26	4	25		
ENSMUST00000129532						6	3	9	8	16	5	16	43	21	5	56		
ENSMUST00000129533						0	0	0	2	0	0	370	1318	732	4573	455		
ENSMUST00000129534						2	7	0	1	3	3	2	15	4	2	15		
ENSMUST00000129535	ENSMUSG00000024776	19	34192229	34240333	1	1	1	1	14	1	0	33	32	44	15	8	D3Z0S7	
ENSMUST00000129536						83	104	356	36	83	34	2	13	2	0	2		
ENSMUST00000129537						0	0	0	0	9	0	3	0	0	5	14		
ENSMUST00000129539						0	0	1	1	0	1	0	0	0	0	0		
ENSMUST00000129540						5	4	2	5	6	2	18	223	50	46	62		
ENSMUST00000129541						1	1	0	0	2	0	1	5	4	0	5		
ENSMUST00000129542						5	4	8	5	3	1	0	0	0	0	0		
ENSMUST00000129543						44	27	40	429	80	43	46	1231	175	153	180		
ENSMUST00000129544	ENSMUSG00000043535	2	29124181	29182471	1	0	0	2	5	0	0	0	0	0	1	4	A0A0A0MQJ0	
ENSMUST00000129545						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129547						1272	1518	2316	1007	1194	602	35	114	65	19	61		
ENSMUST00000129548						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000129549						34	48	100	30	61	32	28	15	21	0	41		
ENSMUST00000129550						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000129552	ENSMUSG00000030965	7	132859225	132885111	1	0	0	0	0	0	0	0	168	0	332	136	D6RJ39	
ENSMUST00000129553						1	0	0	0	0	2	2	6	3	0	12		
ENSMUST00000129554						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000129555						20	19	123	54	13	18	0	0	1	0	4		
ENSMUST00000129556						0	2	1	0	2	0	0	2	3	2	0		
ENSMUST00000129557						39	46	62	148	44	41	19	52	41	14	30		
ENSMUST00000129558	ENSMUSG00000038366	11	97799000	97838764	1	1	3	9	45	2	4	2	0	0	0	0	A2A6G8	
ENSMUST00000129560	ENSMUSG00000051169	6	113415319	113419340	-1	0	0	1	0	1	0	0	0	0	1	0	D3YVC8	
ENSMUST00000129561						3	0	3	3	2	2	0	7	0	0	0		
ENSMUST00000129562						0	0	1	0	1	0	0	0	0	0	1		
ENSMUST00000129563						3	2	0	1	2	0	3	0	16	0	0		
ENSMUST00000129564	ENSMUSG00000042404	3	90265185	90280669	1	0	0	0	186	23	10	0	20	0	0	16		Q3U1Y4
ENSMUST00000129565						0	0	1	0	0	1	5	83	5	80	0		
ENSMUST00000129566	ENSMUSG00000049357	18	34579846	34597468	-1	17	0	18	10	15	0	0	141	41	168	47	D6RFA1	
ENSMUST00000129567						5	5	26	84	11	8	0	0	0	0	0		
ENSMUST00000129568						4	3	3	5	2	1	0	2	0	0	0		
ENSMUST00000129571						2	4	10	0	8	2	0	1	3	0	2		
ENSMUST00000129572	ENSMUSG00000020838	11	76998603	77032340	1	3	4	0	4	7	4	0	0	0	0	0	Q5NCR5	
ENSMUST00000129573						6	9	52	10	9	4	1	1	2	0	3		
ENSMUST00000129575						0	0	3	0	0	0	133	143	127	20	102		
ENSMUST00000129577						20	20	44	24	32	16	270	545	521	695	820		
ENSMUST00000129580						0	0	6	0	1	0	9	0	0	0	16		
ENSMUST00000129581						13	6	19	15	13	15	3	69	5	4	16		
ENSMUST00000129582						9	12	2	3	8	0	5	23	13	0	19		
ENSMUST00000129583						0	0	0	66	0	0	0	0	0	0	6		
ENSMUST00000129585	ENSMUSG00000020719	11	106780355	106789185	-1	3	0	0	53	6	2	15	37	382	292	422	B1ARB9	
ENSMUST00000129586						5	0	3	4	0	0	0	1	3	0	3		
ENSMUST00000129587						1	3	0	2	4	1	0	0	0	0	0		
ENSMUST00000129588	ENSMUSG00000020346	11	49244191	49263030	1	3	0	0	0	4	0	7	0	0	0	0	J3JS24	
ENSMUST00000129589	ENSMUSG00000037458	15	38487430	38519266	-1	4	0	0	3	0	0	328	2782	235	24	99	D6RE45	
ENSMUST00000129590						4	2	10	67	6	5	0	3	0	0	0		
ENSMUST00000129591						35	64	121	77	66	33	47	177	53	152	69		
ENSMUST00000129592						5	4	3	85	4	2	0	0	0	0	5		
ENSMUST00000129593	ENSMUSG00000020311	11	30930774	30954335	-1	2	0	0	0	0	0	46	265	92	39	40	F6Z458	
ENSMUST00000129594						4	1	13	3	5	3	0	0	0	0	0		
ENSMUST00000129595						0	4	0	23	8	9	14	123	27	0	30		
ENSMUST00000129596						4	3	18	3	7	2	0	3	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129598	ENSMUSG00000023186	9	38718268	38743337	1	8	3	1	3	5	3	0	0	13	0	0	D3Z671	
ENSMUST00000129599						3	3	8	0	2	1	92	248	107	0	100		
ENSMUST00000129600						3	4	14	15	13	4	23	1	0	6	11		
ENSMUST00000129602	ENSMUSG00000006219	4	141576062	141606096	-1	0	0	0	0	0	0	0	0	0	0	0	A2ADE8	
ENSMUST00000129603	ENSMUSG00000054641	6	60924976	60989378	1	19	13	28	18	18	2	4	11	9	43	22	G3UVV6	
ENSMUST00000129604	ENSMUSG00000030498	7	51862015	51994975	1	1	3	16	17	7	1	3	35	8	4	0	D6RDR2	
ENSMUST00000129605						0	0	5	0	2	0	2	0	0	0	2		
ENSMUST00000129606						3	3	5	4	1	0	0	0	0	0	1		
ENSMUST00000129607						3	4	1	13	4	2	0	0	0	0	0		
ENSMUST00000129608						7	2	6	26	4	4	5	5	12	3	24		
ENSMUST00000129610						2	2	18	8	4	0	0	0	2	0	2		
ENSMUST00000129611						4	3	1	1	10	3	0	0	0	0	0		
ENSMUST00000129612						82	54	893	183	89	42	14	41	28	1	38		
ENSMUST00000129613	ENSMUSG00000071064	8	79028437	79193766	1	0	0	0	0	0	1	0	0	1	0	2	F6RU08	
ENSMUST00000129614						3	4	4	95	3	3	0	0	0	0	0		
ENSMUST00000129615						4	3	3	4	6	1	0	2	3	3	5		
ENSMUST00000129616	ENSMUSG00000024150	17	87254658	87265935	-1	0	0	0	13	1	2	26	27	30	13	55	D0EW11	Q8K5B2
ENSMUST00000129618						3	4	7	5	4	0	126	292	105	184	77		
ENSMUST00000129619						20	17	239	96	24	5	0	0	1	1	1		
ENSMUST00000129620						12	5	8	2	12	5	0	0	0	0	0		
ENSMUST00000129621						0	0	0	67	0	1	3	0	3	0	6		
ENSMUST00000129622	ENSMUSG00000054708	10	81628540	81647610	1	4	2	0	2	0	4	0	0	2	0	0		
ENSMUST00000129623						5	1	12	3	15	6	0	0	0	0	0		
ENSMUST00000129624						0	0	0	7	0	1	2	0	2	0	2		
ENSMUST00000129625	ENSMUSG00000036764	10	63382443	63408840	1	3	3	13	8	4	0	17	26	36	101	13	D3Z0D9	
ENSMUST00000129626						1	0	0	0	0	1	0	1	5	0	0		
ENSMUST00000129628	ENSMUSG00000039483	2	30823097	30830333	-1	0	0	0	58	6	0	92	28	16	17	36	A0A0A6YY11	
ENSMUST00000129629						0	2	5	5	1	0	0	0	0	0	0		
ENSMUST00000129630	ENSMUSG00000055027	6	71213940	71322233	-1	0	2	0	2	1	3	0	0	0	0	0	Q8BMV4	
ENSMUST00000129631						0	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000129632						24	26	64	23	30	17	27	26	22	6	28		
ENSMUST00000129633						2	1	0	0	6	3	30	27	52	32	44		
ENSMUST00000129635	ENSMUSG00000024052	17	71182560	71249817	1	20	16	49	40	17	6	244	991	447	81	639		Q99PI5
ENSMUST00000129636						1	0	0	0	1	0	3	44	6	2	27		
ENSMUST00000129637						4	2	0	2	0	0	1	3	0	0	9		
ENSMUST00000129638						0	0	3	0	0	0	6	0	0	0	0		
ENSMUST00000129639						0	0	0	3	1	1	1	0	0	0	0		
ENSMUST00000129640						0	0	0	0	0	0	0	2	6	23	13		
ENSMUST00000129641						0	0	8	0	0	2	0	10	0	0	0		
ENSMUST00000129642						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129643	ENSMUSG00000075395	16	14562316	14621300	1	20	16	85	56	19	10	0	0	0	0	0	A9C474	
ENSMUST00000129644	ENSMUSG00000025142	11	120672973	120709447	1	0	0	3	0	0	0	0	2	0	1	0	E9PUH8	
ENSMUST00000129646	ENSMUSG00000034724	5	96070333	96164171	-1	3	0	1	133	6	2	3	0	7	0	0	D3YXZ0	
ENSMUST00000129647						0	0	0	0	0	0	0	3	0	3	0		
ENSMUST00000129648	ENSMUSG00000054752	4	53631471	53707009	1	1	0	0	31	0	0	1	0	0	0	0	E9PV06	
ENSMUST00000129650						5	2	40	14	13	4	1	0	3	0	1		
ENSMUST00000129651	ENSMUSG00000026649	1	171113918	171126967	1	3	5	34	62	9	2	0	0	4	0	5	F6YI90	
ENSMUST00000129652						2	1	7	0	8	2	15	6	24	0	10		
ENSMUST00000129653	ENSMUSG00000018196	1	143716338	143749676	1	723	671	3692	390	858	433	23	71	16	0	46	Q3UQ95	Q923X4
ENSMUST00000129654						2	0	0	1	3	0	2	0	0	5	0		
ENSMUST00000129655	ENSMUSG00000041235	4	8690406	8867659	1	4	0	6	6	4	1	0	0	1	0	0	A2AJK7	
ENSMUST00000129656						5	0	4	117	6	1	0	21	0	0	7		
ENSMUST00000129657	ENSMUSG00000026648	2	3424131	3464130	1	0	0	3	3	0	0	2	36	14	13	39	F7BA65	
ENSMUST00000129658						1	2	1	1	8	1	0	0	0	0	0		
ENSMUST00000129659						3	0	8	15	0	6	0	0	0	0	0		
ENSMUST00000129660	ENSMUSG00000004535	6	52713729	52766780	1	0	0	0	0	0	0	0	0	0	0	0	D3Z152	
ENSMUST00000129662	ENSMUSG00000031145	X	7657260	7668186	1	3	0	4	6	5	0	341	427	55	0	66	Q8BNH2	
ENSMUST00000129664	ENSMUSG00000036553	5	35697180	35739987	-1	7	0	0	0	14	14	14	16	57	19	43	F6QD49	
ENSMUST00000129665						0	4	3	0	0	0	107	170	87	46	38		
ENSMUST00000129666						0	2	0	1	0	2	0	0	0	0	0		
ENSMUST00000129667	ENSMUSG00000023927	17	51736187	51833290	-1	0	0	0	0	0	0	90	977	823	58	650		Q60611
ENSMUST00000129668	ENSMUSG00000002345	8	70139499	70167488	1	0	0	5	0	0	0	0	17	15	123	10	D6RJ21	
ENSMUST00000129669	ENSMUSG00000000416	6	18366478	18514843	-1	0	1	2	0	0	0	0	0	0	0	0	D3Z1E3	
ENSMUST00000129670	ENSMUSG00000050830	11	11114223	11268931	1	9	6	12	3	11	2	0	0	0	0	0		Q8C8N3
ENSMUST00000129671						4	9	59	16	6	2	0	0	0	0	1		
ENSMUST00000129672						24	33	134	29	41	13	13	23	39	3	59		
ENSMUST00000129673						1	4	6	9	8	16	10	63	15	11	26		
ENSMUST00000129674	ENSMUSG00000040350	11	48826140	48852209	1	2	0	0	0	0	0	1	0	0	0	2	Q5NCB9	
ENSMUST00000129676						3	1	4	3	0	2	0	13	0	0	28		
ENSMUST00000129677						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000129678						2	0	0	0	0	1	2	1	3	2	3		
ENSMUST00000129679	ENSMUSG00000098789	2	120027483	120032594	1	0	2	3	4	4	5	0	0	0	0	1	F6SBG7	
ENSMUST00000129680	ENSMUSG00000001240	11	101246028	101259546	1	2	1	4	148	8	5	0	0	0	0	0		Q9WUP0
ENSMUST00000129682	ENSMUSG00000015790	2	26913381	26916530	-1	2	1	0	6	1	0	0	2	2	0	5	A0A0A6YXB3	
ENSMUST00000129683						1	1	3	0	0	0	0	4	4	4	14		
ENSMUST00000129685	ENSMUSG00000033852	2	120027493	120043033	1	0	0	0	0	0	0	0	0	0	3	0	B7ZCM9	
ENSMUST00000129686						6	10	17	267	20	7	2	56	20	2	39		
ENSMUST00000129688						2	2	1	2	0	1	0	0	0	0	0		
ENSMUST00000129689						6	7	19	9	11	3	0	0	1	0	0		
ENSMUST00000129690						0	0	3	26	4	0	61	0	25	69	29		
ENSMUST00000129691	ENSMUSG00000005378	5	135052957	135064959	-1	3	3	2	3	2	1	3	23	3	0	5	F6VT90	
ENSMUST00000129693						2	0	3	3	0	1	0	6	1	0	1		
ENSMUST00000129694	ENSMUSG00000030243	6	142350342	142387087	-1	2	3	8	37	1	1	0	0	0	0	0	D3Z6T0	
ENSMUST00000129695	ENSMUSG00000016346	2	181075579	181135300	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZBV3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129697						6	3	0	2	0	0	0	0	0	0	0		
ENSMUST00000129698						0	0	7	3	4	0	0	0	0	0	1		
ENSMUST00000129700						1	0	0	1	0	0	18	111	69	5	133		
ENSMUST00000129702	ENSMUSG00000026049	1	44086613	44102441	-1	0	0	0	8	1	1	0	9	5	5	0	D3Z094	
ENSMUST00000129703						0	0	0	13	0	0	0	0	0	0	0		
ENSMUST00000129704	ENSMUSG00000036555	5	140661827	140702378	-1	0	0	0	0	0	0	13	2	12	0	12	F6R782	
ENSMUST00000129705						4	1	4	2	6	7	2	0	0	0	14		
ENSMUST00000129706	ENSMUSG00000037916	19	4007497	4012806	-1	0	3	0	3	0	0	10	45	39	8	22	D6RG60	
ENSMUST00000129707						2	3	2	2	0	1	3	32	12	0	33		
ENSMUST00000129708	ENSMUSG00000068749	3	108256926	108279974	1	1	3	1	0	0	3	0	0	0	0	0	A0A0G2JF97	
ENSMUST00000129709	ENSMUSG00000071322	17	7324646	7345974	1	0	0	0	0	0	0	0	0	0	0	0	Q80W76	
ENSMUST00000129710						0	0	0	0	0	0	0	1	3	0	15		
ENSMUST00000129711						0	0	0	0	0	0	0	2	4	3	5		
ENSMUST00000129712	ENSMUSG00000026857	2	30807826	30823033	1	6	2	20	53	8	2	0	0	0	0	0	A0A0A6YVQ9	
ENSMUST00000129714						3	1	28	12	8	4	0	0	0	0	0		
ENSMUST00000129715						1	0	0	0	2	0	0	12	12	0	2		
ENSMUST00000129716						5	5	0	66	3	1	5	0	0	5	0		
ENSMUST00000129717						2	5	0	0	2	1	4	6	0	0	4		
ENSMUST00000129718						0	0	1	0	3	5	0	14	55	12	28		
ENSMUST00000129719						1	1	6	39	6	1	0	0	0	0	0		
ENSMUST00000129720						4	8	8	3	11	3	0	0	2	3	0		
ENSMUST00000129721						3	0	0	0	1	1	0	0	1	0	2		
ENSMUST00000129722						4	2	1	2	10	6	2	7	5	2	10		
ENSMUST00000129725						19	6	47	13	8	6	0	0	0	0	0		
ENSMUST00000129726	ENSMUSG00000055805	11	103171107	103198901	1	4	3	0	5	3	0	203	1686	153	51	311	G3UWI1	
ENSMUST00000129727	ENSMUSG00000040249	10	127538161	127621148	-1	5	2	10	3	7	0	32	47	2	0	31	F6XU19	
ENSMUST00000129728						5	1	1	2	1	3	0	0	0	0	0		
ENSMUST00000129729						2	2	1	0	0	0	0	7	9	0	3		
ENSMUST00000129730						1	2	14	17	6	0	0	2	1	0	1		
ENSMUST00000129731						3	2	5	5	2	2	0	0	1	0	0		
ENSMUST00000129732						0	1	1	2	0	0	0	0	0	0	0		
ENSMUST00000129733	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	1	0	2	0	0	0	0	13	S4R2U0	
ENSMUST00000129734						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129736						0	0	17	2	1	1	2	3	6	12	4		
ENSMUST00000129737	ENSMUSG00000048078	7	96171246	96911093	1	0	3	0	0	3	0	0	0	0	0	0	F6UP10	
ENSMUST00000129738						0	0	7	2	3	0	0	0	0	0	7		
ENSMUST00000129741	ENSMUSG00000034931	11	101732919	101767358	1	0	0	0	0	0	0	0	0	46	0	94	A2A4N9	
ENSMUST00000129743	ENSMUSG00000022973	16	90936092	91011308	-1	0	0	0	0	2	0	0	0	0	0	4	F6XIX0	
ENSMUST00000129744	ENSMUSG00000019124	6	54501173	54566489	-1	2	0	0	0	4	0	0	0	0	0	0	D3YXW0	
ENSMUST00000129745	ENSMUSG00000059540	2	181680310	181688071	1	0	0	0	1	0	0	6	2	0	19	12	B7ZCS4	
ENSMUST00000129746						0	0	4	5	2	0	0	0	4	0	9		
ENSMUST00000129747						2	1	8	4	1	0	0	0	0	0	0		
ENSMUST00000129748						21	21	39	18	19	7	31	88	27	15	19		
ENSMUST00000129749	ENSMUSG00000068686	2	104069849	104091187	1	0	0	0	0	0	0	0	0	0	1	0		P58019
ENSMUST00000129751						3	1	8	4	6	2	0	0	0	0	0		
ENSMUST00000129752	ENSMUSG00000043909	2	121193281	121271407	-1	3	0	2	0	0	2	1	0	0	0	7	F6VCK5	
ENSMUST00000129753	ENSMUSG00000029455	5	121566027	121593824	-1	5	0	9	11	0	0	8911	10891	9524	514	4895	A0A0G2JEU1	
ENSMUST00000129754						2	4	18	4	7	0	0	0	0	0	0		
ENSMUST00000129755						2	3	5	4	3	2	11	35	30	2	47		
ENSMUST00000129756						0	2	6	27	0	0	0	2	0	0	0		
ENSMUST00000129757	ENSMUSG00000009580	5	87885029	87894174	1	0	0	0	0	0	0	0	0	0	0	0		A1E960
ENSMUST00000129759	ENSMUSG00000026036	1	58445151	58481816	1	0	2	3	0	0	0	8	0	0	17	3	E9PWJ6	
ENSMUST00000129760						7	0	4	0	0	0	5	0	4	0	5		
ENSMUST00000129761						11	9	28	23	11	8	16	56	31	6	33		
ENSMUST00000129762						21	19	9	11	11	22	6	115	14	37	17		
ENSMUST00000129765						0	1	10	44	3	0	0	0	0	0	0		
ENSMUST00000129766	ENSMUSG00000030945	7	119554469	119600694	1	0	0	0	0	0	0	0	0	0	0	0	F6V4U2	
ENSMUST00000129767	ENSMUSG00000044551	14	70154405	70159502	-1	0	1	8	0	0	0	0	27	2	0	0	F6Q9I6	
ENSMUST00000129768	ENSMUSG00000025268	X	150806370	150814345	-1	0	0	0	0	2	0	0	0	0	0	0	A2AG48	
ENSMUST00000129769	ENSMUSG00000079593	X	53577087	53608979	-1	2	0	10	0	6	4	0	0	0	0	0	A2CFG5	
ENSMUST00000129770						1	0	2	79	0	0	0	0	0	0	0		
ENSMUST00000129771						7	9	15	7	7	4	0	0	0	0	0		
ENSMUST00000129772						7	8	24	23	14	2	0	1	0	0	2		
ENSMUST00000129773	ENSMUSG00000046826	7	30973790	30989726	1	8	6	9	94	8	1	6	11	4	4	10		Q0VAY3
ENSMUST00000129774	ENSMUSG00000041440	9	96119362	96184608	1	0	1	0	0	5	0	0	0	15	15	8	D6RCU4	
ENSMUST00000129775	ENSMUSG00000040213	3	142701051	142746870	1	0	0	2	3	2	3	0	0	0	0	0	D6RJ70	
ENSMUST00000129776						4	1	10	0	2	1	0	0	0	0	0		
ENSMUST00000129777						2	0	1	3	2	0	0	0	0	0	0		
ENSMUST00000129778						5	3	0	21	6	4	0	0	0	0	0		
ENSMUST00000129779	ENSMUSG00000066036	4	139352609	139489588	1	0	2	2	3	2	0	21	4	32	0	11	Z4YLP1	
ENSMUST00000129781						2	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000129782	ENSMUSG00000031262	X	134308084	134362639	1	1	3	5	4	0	0	0	0	4	0	1	B1AV88	
ENSMUST00000129783						16	11	25	18	22	5	0	0	0	0	0		
ENSMUST00000129784						0	0	0	0	0	0	13	9	0	8	13		
ENSMUST00000129785						26	26	53	18	32	12	39	110	55	0	103		
ENSMUST00000129786	ENSMUSG00000030714	7	126649309	126672925	1	0	0	5	4	2	0	5	5	0	2	3		
ENSMUST00000129787						0	0	0	0	0	0	1	0	5	0	0		
ENSMUST00000129788	ENSMUSG00000040187	6	146796055	146833529	1	0	0	0	0	0	0	0	0	0	0	0		Q2VPD4
ENSMUST00000129789						13	7	33	25	5	5	6	6	0	2	0		
ENSMUST00000129790						2	0	1	0	7	4	0	0	22	0	41		
ENSMUST00000129792						1	3	6	10	7	2	2	0	10	0	6		
ENSMUST00000129793						6	5	8	2	9	3	54	123	85	9	128		
ENSMUST00000129794						0	0	0	1	1	0	27	4	47	0	0		
ENSMUST00000129795	ENSMUSG00000042489	4	126556935	126593903	1	0	1	0	0	1	0	0	0	0	0	1	B1ARX7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129796						1	5	0	3	3	0	0	0	0	0	0		
ENSMUST00000129797						0	0	0	0	1	0	12	26	13	0	6		
ENSMUST00000129798						20	17	31	155	35	13	0	0	0	0	4		
ENSMUST00000129799						11	7	47	227	27	11	0	0	0	0	0		
ENSMUST00000129800						3	0	1	0	6	2	4	7	0	0	0		
ENSMUST00000129801						1	1	3	3	4	2	0	0	0	0	0		
ENSMUST00000129803	ENSMUSG00000071226	6	120666369	120771190	1	2	0	3	0	0	0	0	0	0	0	0	F6VR46	
ENSMUST00000129804	ENSMUSG00000075081	2	89609156	89614022	-1	0	3	0	0	2	1	0	0	0	0	0	A2AT79	
ENSMUST00000129805						2	0	6	3	3	0	0	0	0	4	0		
ENSMUST00000129806						2	0	0	1	0	0	1	0	0	3	15		
ENSMUST00000129807	ENSMUSG00000044348	X	136981116	137038302	-1	0	0	6	20	6	1	0	0	0	0	0	A2AF35	
ENSMUST00000129808						3	7	17	13	8	8	3	27	8	0	10		
ENSMUST00000129809						2	3	43	11	7	3	0	1	0	0	0		
ENSMUST00000129810						6	1	3	0	4	3	0	0	0	0	0		
ENSMUST00000129811	ENSMUSG00000016024	2	158306493	158332852	1	0	0	0	0	0	0	112	237	219	10	71	F6XKX9	
ENSMUST00000129812	ENSMUSG00000030689	7	126850960	126862377	-1	0	0	6	0	1	2	2	9	8	0	9	D3YV78	
ENSMUST00000129814						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000129815	ENSMUSG00000040797	6	121372933	121473678	-1	90	22	304	88	79	34	0	0	0	0	0	D6RHQ8	
ENSMUST00000129816						2	4	2	6	8	6	14	45	15	5	34		
ENSMUST00000129817	ENSMUSG00000037652	3	30899371	30969415	-1	0	0	0	0	0	0	0	0	0	0	0		Q8CHP6
ENSMUST00000129818						8	10	25	17	16	4	0	1	0	0	1		
ENSMUST00000129819	ENSMUSG00000032558	9	104002544	104153483	1	14	5	0	0	0	11	0	0	3	0	0	H9KV07	
ENSMUST00000129820	ENSMUSG00000044847	11	45928269	45944935	-1	94	71	182	104	107	36	21	87	62	6	59	Q5SUH5	Q8BUV6
ENSMUST00000129821	ENSMUSG00000031561	8	48227682	48844026	-1	0	0	3	59	0	0	0	0	0	0	2	F6RJC1	
ENSMUST00000129822	ENSMUSG00000015790	2	26913381	26916530	-1	0	0	0	0	0	0	151	170	89	118	79	A0A0A6YVX3	
ENSMUST00000129823						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129824	ENSMUSG00000040850	11	30771726	30880361	1	1	0	0	1	0	0	0	9	4	0	1	Q5SSW0	
ENSMUST00000129825	ENSMUSG00000043740	17	48316141	48327024	1	0	0	1	1	4	2	547	306	586	79	284	A6XA72	
ENSMUST00000129826						2	0	2	26	5	2	20	42	19	0	30		
ENSMUST00000129827	ENSMUSG00000008398	10	93247414	93311135	-1	0	0	0	0	2	0	90	115	63	9	98	G3UVX2	
ENSMUST00000129828	ENSMUSG00000038366	11	97799000	97838764	1	6	4	26	31	11	5	3	8	2	1	10	A2A6G9	
ENSMUST00000129829	ENSMUSG00000039997	1	173920407	173942672	-1	37	30	205	40	35	23	23	219	45	221	159	E9QAN9	
ENSMUST00000129830	ENSMUSG00000027613	2	155819832	155826925	-1	0	0	0	0	0	0	0	0	0	0	0	D6RJJ3	
ENSMUST00000129831						0	2	0	8	6	2	0	0	0	0	0		
ENSMUST00000129832	ENSMUSG00000058291	5	138603652	138619761	-1	4	1	25	5	3	2	0	0	0	19	8	D3Z6N7	
ENSMUST00000129835						5	4	20	9	6	7	126	508	104	8	375		
ENSMUST00000129836						9	4	31	24	5	4	3	2	3	0	10		
ENSMUST00000129837	ENSMUSG00000022487	15	103402405	103430470	-1	0	0	1	0	1	0	0	0	0	0	1	D3YWV9	
ENSMUST00000129838						4	3	0	2	1	0	4	0	0	0	0		
ENSMUST00000129839						5	1	10	0	4	0	0	1	2	0	4		
ENSMUST00000129840						0	3	3	2	2	1	0	3	0	2	0		
ENSMUST00000129841						3	3	11	3	8	3	0	0	0	0	0		
ENSMUST00000129842						2	0	0	0	0	1	9	14	3	0	6		
ENSMUST00000129843	ENSMUSG00000010505	2	181763332	181827797	1	0	0	0	0	0	0	3	0	0	0	0	F6SWU2	
ENSMUST00000129844						1	1	1	5	5	0	0	0	0	0	0		
ENSMUST00000129845						4	0	8	1	4	0	13	40	66	27	79		
ENSMUST00000129846						0	0	0	30	0	3	1	0	0	0	0		
ENSMUST00000129847	ENSMUSG00000040952	7	24884371	24889806	1	0	0	0	0	0	0	1275	1950	1154	5903	730	S4R223	
ENSMUST00000129848						2	0	5	0	8	0	0	2	0	0	0		
ENSMUST00000129849	ENSMUSG00000009535	18	68300355	68324852	1	2	1	0	0	1	0	0	0	0	0	4	D3Z4K1	
ENSMUST00000129850						5	9	26	6	12	10	208	758	444	13	683		
ENSMUST00000129851	ENSMUSG00000025855	5	139017306	139150001	-1	2	1	3	22	6	0	0	0	0	0	0	D3YTM5	
ENSMUST00000129852						70	53	154	79	58	32	22	76	42	9	59		
ENSMUST00000129853	ENSMUSG00000069808	11	76179671	76214827	1	5	5	1	89	3	6	2	0	0	0	0	B7ZC15	
ENSMUST00000129854						7	5	57	119	5	0	80	30	400	11	44		
ENSMUST00000129855						1	3	7	5	7	3	0	1	0	0	0		
ENSMUST00000129856	ENSMUSG00000010505	2	181763332	181827797	1	0	1	0	0	0	1	0	0	0	0	0	F7CGS5	
ENSMUST00000129857						1	0	0	3	8	5	81	0	335	0	0		
ENSMUST00000129858						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000129859						35	33	104	565	49	21	5	15	9	1	19		
ENSMUST00000129860						3	3	9	0	1	2	23	118	111	123	58		
ENSMUST00000129861						2	1	0	84	2	0	0	2	0	3	19		
ENSMUST00000129862	ENSMUSG00000025786	9	123066160	123113205	-1	0	0	0	0	0	0	38	0	0	0	0	F6Q2M4	
ENSMUST00000129863	ENSMUSG00000035086	11	101285952	101302286	-1	0	0	0	0	0	0	0	0	0	0	0	F7CVL9	
ENSMUST00000129864	ENSMUSG00000024019	17	29660595	29705979	1	2	2	0	0	2	0	14	28	17	2	19	G3UZ59	
ENSMUST00000129865						2	0	10	0	4	0	0	0	58	0	21		
ENSMUST00000129866						0	0	5	21	0	0	0	0	0	0	0		
ENSMUST00000129867						1	2	7	1	2	3	0	1	0	1	0		
ENSMUST00000129869						1	0	8	0	6	9	0	9	4	0	2		
ENSMUST00000129870	ENSMUSG00000056938	11	103101682	103112200	1	0	0	0	0	3	0	79	46	41	1	30	E0CXU7	
ENSMUST00000129871						3	3	22	2	5	4	0	12	0	3	2		
ENSMUST00000129872						0	1	4	1	5	0	2	4	0	0	2		
ENSMUST00000129873						1	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000129874						70	86	805	149	72	38	54	357	155	31	127		
ENSMUST00000129877						4	2	8	6	7	1	0	0	5	0	2		
ENSMUST00000129878	ENSMUSG00000022967	16	91485238	91507441	1	0	0	0	0	0	0	0	0	0	0	0	E9PWM1	
ENSMUST00000129880	ENSMUSG00000070565	1	157135182	157412595	-1	9	8	30	8	12	6	0	0	0	0	0	D3YWZ9	
ENSMUST00000129881	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	0	0	0	0	0	26	0	0	D3Z7N0	
ENSMUST00000129882						8	3	22	19	10	9	0	1	0	1	1		
ENSMUST00000129883	ENSMUSG00000030269	6	113237843	113281392	1	2	12	16	22	11	0	29	129	56	25	31	D6RDS6	
ENSMUST00000129884						2	1	6	0	1	0	2	0	0	0	0		
ENSMUST00000129885						0	2	2	0	2	1	0	0	0	0	0		
ENSMUST00000129886	ENSMUSG00000035296	14	61221059	61258490	-1	2	0	7	1	3	1	0	1	0	0	0	F6YKG7	
ENSMUST00000129887						1	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129888						0	0	21	7	9	5	5	36	7	0	3		
ENSMUST00000129890	ENSMUSG00000033257	1	74661745	74703730	1	0	0	0	0	0	0	0	0	0	0	0	D3Z7H1	
ENSMUST00000129891	ENSMUSG00000092511	17	34856412	34882042	-1	0	0	0	0	0	0	0	0	0	7	15	F6VQX8	
ENSMUST00000129892						3	0	0	54	8	3	0	0	0	0	0		
ENSMUST00000129893						1	0	0	0	1	1	0	0	0	0	2		
ENSMUST00000129894						5	2	2	3	1	1	0	4	11	0	10		
ENSMUST00000129895	ENSMUSG00000035172	11	101162679	101171351	-1	0	0	0	0	0	0	12	6	0	0	0		Q8VCE9
ENSMUST00000129896						7	0	14	4	8	0	0	7	33	0	36		
ENSMUST00000129897						6	3	4	1	8	5	0	0	2	0	4		
ENSMUST00000129898	ENSMUSG00000036872	8	86482260	86580686	-1	24	31	29	28	14	14	0	0	0	0	0		Q80WJ6
ENSMUST00000129899						0	0	0	0	0	0	12	0	20	105	13		
ENSMUST00000129900	ENSMUSG00000022772	16	31962506	32003287	-1	0	0	0	1	0	0	15	30	27	13	11	F6S6C3	
ENSMUST00000129901						1	0	8	22	2	0	11	42	34	0	47		
ENSMUST00000129902						28	15	53	55	38	12	2	5	6	0	7		
ENSMUST00000129903	ENSMUSG00000026843	2	31572651	31617526	1	3	0	3	0	4	0	2	0	9	0	7	F7AM43	
ENSMUST00000129904	ENSMUSG00000040666	16	96200470	96228933	1	69	35	79	1281	137	82	0	9	1	0	1	D3Z3Z9	
ENSMUST00000129905	ENSMUSG00000052688	1	131688695	131715439	1	0	0	0	0	0	0	4	0	0	0	0	D3Z4X4	
ENSMUST00000129906	ENSMUSG00000032020	9	41011098	41161697	-1	0	0	0	0	0	0	1	0	0	0	10	H3BJB9	
ENSMUST00000129907						61	56	148	712	113	62	0	4	2	0	3		
ENSMUST00000129909	ENSMUSG00000090137	8	70508263	70510801	-1	0	0	0	14	0	0	33	58	12	11	13	Q66JP1	P62984
ENSMUST00000129911						24	18	33	47	18	11	4	3	2	0	2		
ENSMUST00000129912						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129913						7	8	26	18	28	17	0	0	0	0	0		
ENSMUST00000129914						0	0	0	0	0	0	0	28	18	1	0		
ENSMUST00000129915	ENSMUSG00000037475	X	41794991	41920674	-1	0	0	0	4	1	0	0	0	0	0	0	F6RBN0	
ENSMUST00000129916						8	5	1	2	2	4	3	21	13	4	12		
ENSMUST00000129917						5	7	25	42	27	0	11	90	28	0	27		
ENSMUST00000129918						3	1	0	0	1	0	0	0	0	1	0		
ENSMUST00000129920						12	8	9	6	12	3	0	0	8	1	13		
ENSMUST00000129921	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	0	0	0	0	0	9	0	2	M0QWI3	
ENSMUST00000129922						0	2	0	2	4	0	33	24	41	4	23		
ENSMUST00000129923	ENSMUSG00000026312	1	109982431	110140157	1	0	0	0	0	0	0	0	0	0	0	0	Q8BLT5	
ENSMUST00000129925	ENSMUSG00000045934	3	96162004	96171718	1	0	3	0	0	0	0	0	0	0	0	0	D6RIK1	
ENSMUST00000129926						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000129927						5	1	5	2	13	3	16	60	30	4	60		
ENSMUST00000129928						8	1	10	63	5	2	38	72	106	2	198		
ENSMUST00000129929	ENSMUSG00000035495	4	46114746	46138694	-1	5	1	9	3	2	1	1	10	4	0	6	E0CZ46	
ENSMUST00000129930						5	1	7	90	6	0	0	0	0	0	0		
ENSMUST00000129931						0	3	0	0	3	0	1	1	3	5	2		
ENSMUST00000129934	ENSMUSG00000029477	5	123035769	123047016	-1	1	0	0	3	0	0	1	10	4	0	4	F7CPM9	
ENSMUST00000129935	ENSMUSG00000037805	17	28328471	28331032	1	0	0	3	0	6	4	19	123	40	39	111	D6RE43	
ENSMUST00000129936						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000129937						4	3	3	3	5	1	0	0	0	0	0		
ENSMUST00000129938	ENSMUSG00000029283	5	106964322	106984432	1	0	0	0	0	0	0	0	6	6	2	5	G3UVV7	
ENSMUST00000129939	ENSMUSG00000052748	1	151367699	151428455	-1	0	0	0	0	0	0	0	0	8	6	6	F6V527	
ENSMUST00000129940						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000129941						1	1	6	14	2	4	0	0	0	0	0		
ENSMUST00000129942	ENSMUSG00000020027	10	95385362	95417180	-1	0	0	7	195	8	0	0	0	0	0	0	D3Z441	
ENSMUST00000129943						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000129944						0	0	7	1	1	0	0	2	3	2	0		
ENSMUST00000129945						11	16	14	1	10	6	7	2	3	1	0		
ENSMUST00000129946						0	1	0	0	1	1	2	1	0	0	0		
ENSMUST00000129947	ENSMUSG00000031167	X	8138975	8145880	-1	5	0	0	0	0	0	0	0	0	0	0	S4R2M6	
ENSMUST00000129948	ENSMUSG00000029915	6	40574894	40585821	-1	0	0	5	1	0	2	166	798	372	317	173		Q9R007
ENSMUST00000129949	ENSMUSG00000066036	4	139352609	139489588	1	4	0	16	0	8	3	58	0	168	0	0	F6SSP6	
ENSMUST00000129951						6	15	63	30	21	9	0	36	0	11	0		
ENSMUST00000129952						0	0	0	75	9	0	0	0	1	0	0		
ENSMUST00000129954	ENSMUSG00000000766	10	6758506	7038198	1	1	4	5	0	1	1	0	1	4	0	5	E9QAQ1	
ENSMUST00000129955	ENSMUSG00000025155	11	120789201	120796403	-1	0	3	0	157	5	0	22	9	20	0	0	B1ATU7	
ENSMUST00000129956	ENSMUSG00000035597	12	65036333	65063386	1	0	0	0	0	0	4	85	408	140	95	196	D6RDR5	
ENSMUST00000129957	ENSMUSG00000028718	4	115000159	115043196	1	0	0	0	12	0	0	0	0	7	0	0	Q8BQI9	
ENSMUST00000129958						3	1	1	3	3	3	8	27	16	2	31		
ENSMUST00000129959						36	33	36	30	32	30	14	73	38	5	100		
ENSMUST00000129960						3	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000129961						3	6	36	1	4	14	0	0	0	3	3		
ENSMUST00000129962						5	2	4	1	5	1	0	4	0	29	0		
ENSMUST00000129964						2	2	0	2	0	0	0	11	0	0	1		
ENSMUST00000129966	ENSMUSG00000028911	4	131873617	131901706	1	0	1	0	3	5	3	24	4	52	0	33	A0A0A6YWA5	
ENSMUST00000129967						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000129968						0	1	0	1	0	0	6	28	2	10	17		
ENSMUST00000129969						0	0	1	8	0	0	2	5	2	0	7		
ENSMUST00000129970						12	2	32	31	22	9	0	0	0	0	0		
ENSMUST00000129972						7	6	6	6	6	2	3	0	3	1	2		
ENSMUST00000129973						2	0	13	2	0	0	0	162	5	7	16		
ENSMUST00000129974						34	33	29	25	27	14	0	1	2	0	0		
ENSMUST00000129975	ENSMUSG00000009614	2	27188393	27248337	-1	0	0	0	3	1	0	0	0	0	0	1	A2AH55	
ENSMUST00000129976	ENSMUSG00000030127	6	124958413	124965538	-1	3	0	1	39	0	9	0	0	29	2	28	D3Z440	
ENSMUST00000129977						12	7	33	7	5	3	24	63	51	4	63		
ENSMUST00000129978	ENSMUSG00000036825	3	146404642	146440144	1	0	0	1	42	0	0	0	0	0	0	0	D3Z474	
ENSMUST00000129979	ENSMUSG00000002871	6	88902251	88912238	1	5	2	0	0	4	0	72	74	0	6	22		
ENSMUST00000129981						0	1	0	9	0	0	0	0	0	0	0		
ENSMUST00000129982						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000129983						1	0	1	0	0	1	0	0	0	4	0		
ENSMUST00000129984						5	6	3	4	5	6	4	40	11	5	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000129985						3	15	56	19	18	5	294	1273	376	11	552		
ENSMUST00000129986	ENSMUSG00000030230	6	139989673	140041457	-1	6	0	0	3	0	0	0	0	0	0	0	D6RCJ4	
ENSMUST00000129987						2	0	4	0	0	2	0	0	0	0	0		
ENSMUST00000129989						0	3	3	6	0	1	0	0	0	0	0		
ENSMUST00000129990	ENSMUSG00000049571	7	139600951	139683817	-1	0	15	0	2	0	17	0	0	0	0	0	E9Q2C0	
ENSMUST00000129992						0	0	0	0	0	0	64	283	105	457	62		
ENSMUST00000129993	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	0	44	0	2	12	15	21	6	26	A0A0A6YWB5	
ENSMUST00000129995						0	0	0	8	0	0	0	0	0	0	2		
ENSMUST00000129996						0	1	3	2	4	2	0	0	0	0	0		
ENSMUST00000129997	ENSMUSG00000034708	11	102430315	102437048	1	4	0	13	5	10	0	24	55	95	7	68	H3BLC9	
ENSMUST00000129998						2	5	0	3	1	2	0	2	0	0	0		
ENSMUST00000129999						0	0	1	0	0	0	0	2	0	2	13		
ENSMUST00000130000						0	0	3	2	0	0	0	2	1	8	0		
ENSMUST00000130001						0	2	0	1	2	0	0	0	0	3	3		
ENSMUST00000130002						5	5	6	2	9	3	0	30	55	0	47		
ENSMUST00000130005						4	6	8	1	3	0	1	7	9	23	4		
ENSMUST00000130006						0	1	0	0	0	0	13	285	9	7	43		
ENSMUST00000130007	ENSMUSG00000031328	X	74223461	74249820	-1	0	0	0	0	0	12	150	0	1877	0	224	B7FAV1	
ENSMUST00000130008	ENSMUSG00000058498	4	152307019	152318993	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4D7	
ENSMUST00000130009	ENSMUSG00000033352	11	65688243	65788297	-1	0	0	0	5	0	0	4	8	5	5	3	M0QWG5	
ENSMUST00000130010						0	0	1	0	0	0	0	0	10	0	0		
ENSMUST00000130011	ENSMUSG00000031626	8	45507788	45827906	1	7	0	4	2	0	0	0	0	0	1	0	B2RXQ9	
ENSMUST00000130012	ENSMUSG00000020532	11	84129672	84401651	1	0	0	0	0	0	0	0	0	0	0	0	V9GWS0	
ENSMUST00000130013						0	2	4	0	2	4	2	2	0	0	7		
ENSMUST00000130014	ENSMUSG00000047295	15	91838265	91861438	1	0	0	0	0	0	0	0	0	0	0	0	F6VRN1	
ENSMUST00000130016	ENSMUSG00000032812	7	101348067	101412586	1	5	0	12	3	3	1	0	0	0	0	13	D3YY40	
ENSMUST00000130017	ENSMUSG00000053841	4	129626078	129641065	-1	0	2	2	101	6	1	0	0	0	0	0	A8Y5J8	
ENSMUST00000130018						11	4	9	9	11	4	0	0	0	2	1		
ENSMUST00000130019						1	0	0	1	0	0	0	0	0	0	1		
ENSMUST00000130020						1	0	6	0	4	3	28	22	8	14	9		
ENSMUST00000130023						2	6	20	8	6	6	33	91	32	6	78		
ENSMUST00000130024	ENSMUSG00000056724	9	110624789	110654161	-1	29	5	17	0	17	0	735	300	1054	5	622	F6VTL9	
ENSMUST00000130026	ENSMUSG00000028600	4	108014791	108096445	-1	0	0	0	4	0	0	0	0	0	0	0	F6XS92	
ENSMUST00000130027						2	0	0	19	0	0	0	9	0	4	3		
ENSMUST00000130028	ENSMUSG00000022827	16	37539885	37572385	1	15	27	86	16	17	13	27	0	7	19	19		Q9D4V7
ENSMUST00000130029						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130031						0	5	0	0	0	0	0	8	7	5	0		
ENSMUST00000130032	ENSMUSG00000032185	9	21546894	21589487	1	0	0	0	0	26	8	0	61	47	21	123	D6RFA7	
ENSMUST00000130033	ENSMUSG00000038347	17	13482553	13761825	-1	17	11	56	0	34	24	0	0	1	0	0	D3Z5S1	
ENSMUST00000130034						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000130035	ENSMUSG00000024483	18	36559987	36665917	1	0	0	0	0	0	0	3	0	0	0	2	F6YYD3	
ENSMUST00000130036						38	44	45	44	63	32	6	11	24	6	55		
ENSMUST00000130037	ENSMUSG00000018395	11	53567379	53601967	1	0	0	0	0	0	0	0	0	0	0	0	B1AQZ5	
ENSMUST00000130038						4	9	5	2	4	0	3	0	3	0	7		
ENSMUST00000130039						0	1	5	2	6	0	0	0	0	0	0		
ENSMUST00000130040						3	2	1	4	1	2	0	0	1	0	0		
ENSMUST00000130041	ENSMUSG00000060961	5	88886818	89239653	1	9	0	0	1	6	0	0	0	0	0	4	E1AWU4	O88343
ENSMUST00000130042	ENSMUSG00000026304	1	90958133	90969661	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVQ6	
ENSMUST00000130043	ENSMUSG00000015745	3	95988429	95996001	-1	0	1	5	24	0	0	79	155	39	41	132	F6VV25	
ENSMUST00000130044	ENSMUSG00000043079	18	60593973	60660142	-1	0	0	1	24	27	8	0	2	2	0	0	Q3U336	Q8CC35
ENSMUST00000130045						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000130046						5	2	3	13	7	4	0	0	0	0	0		
ENSMUST00000130047						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000130048	ENSMUSG00000024962	19	6982473	6987651	-1	0	1	0	0	0	0	13	2	0	0	2		P49766
ENSMUST00000130049						14	8	18	30	23	2	4	0	3	0	2		
ENSMUST00000130050						0	0	0	2	4	2	5	14	10	0	19		
ENSMUST00000130051						23	25	57	21	39	14	4	16	0	7	11		
ENSMUST00000130052						3	3	0	1	1	1	0	0	0	0	0		
ENSMUST00000130053	ENSMUSG00000079334	9	107578887	107584050	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCE0	
ENSMUST00000130056						6	3	3	9	12	5	0	0	0	0	0		
ENSMUST00000130057						1	1	1	1	0	0	2	18	7	2	12		
ENSMUST00000130058						5	4	7	5	3	4	0	23	10	0	10		
ENSMUST00000130059	ENSMUSG00000000290	10	77530252	77565708	1	0	0	0	0	0	0	139	58	237	11	167	D3YYP8	
ENSMUST00000130060						3	3	4	3	12	3	1	10	4	0	4		
ENSMUST00000130061						0	1	0	1	3	0	0	3	0	0	0		
ENSMUST00000130062						2	0	3	3	3	2	0	0	0	0	0		
ENSMUST00000130064	ENSMUSG00000055850	6	72359714	72366956	-1	0	0	0	0	0	0	7	10	9	0	0	F6SLH0	
ENSMUST00000130065	ENSMUSG00000021318	13	15463235	15730026	1	0	0	0	5	0	1	0	0	0	1	1	Q3UMJ8	
ENSMUST00000130066	ENSMUSG00000008763	3	100562208	100685503	-1	0	0	2	0	0	2	12	42	80	2	42	A2A723	
ENSMUST00000130067	ENSMUSG00000025781	2	10056016	10080510	-1	1	1	0	0	8	6	2	0	0	0	5	A2AKV0	
ENSMUST00000130068	ENSMUSG00000002814	11	60740058	60777365	-1	0	0	0	28	0	0	0	0	0	0	0	Q5NCT1	
ENSMUST00000130069						3	0	3	3	2	1	0	0	7	0	12		
ENSMUST00000130070						7	11	21	27	23	11	1	4	1	2	1		
ENSMUST00000130071	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	11	1	0	0	3	0	0	0	A2AM69	
ENSMUST00000130072						4	0	45	10	5	7	29	107	31	7	56		
ENSMUST00000130073						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130074	ENSMUSG00000070426	7	102019137	102065469	-1	6	4	15	8	3	1	0	0	0	0	0	D3YWK0	
ENSMUST00000130075	ENSMUSG00000026017	1	60098247	60153953	1	0	0	0	0	1	0	0	0	6	0	0	M0QWJ8	
ENSMUST00000130076						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130077	ENSMUSG00000040272	2	93833467	93849943	-1	0	0	0	0	0	0	7	4	0	1	0	A2AIG9	
ENSMUST00000130078						6	2	9	6	10	3	0	0	0	0	0		
ENSMUST00000130079						16	20	3	11	9	9	0	0	0	0	0		
ENSMUST00000130080						303	252	1703	384	425	198	4	73	22	23	16		
ENSMUST00000130081						0	5	39	10	23	15	60	260	65	0	116		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130084						0	0	0	36	2	1	0	0	0	0	0		
ENSMUST00000130087						1	2	4	4	0	2	0	0	8	0	0		
ENSMUST00000130090						2	0	4	0	7	4	0	0	2	2	2		
ENSMUST00000130091	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	0	0	0	0	0	0	0	0	0	B4YB29	
ENSMUST00000130093						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000130096						0	1	2	1	0	0	0	0	1	0	0		
ENSMUST00000130097						3	2	4	31	0	0	25	4	28	0	12		
ENSMUST00000130098						0	5	0	31	0	0	34	23	26	0	33		
ENSMUST00000130100						0	2	0	2	3	4	0	0	0	0	0		
ENSMUST00000130101						3	1	2	2	3	1	2	9	3	0	5		
ENSMUST00000130102	ENSMUSG00000025916	1	9968624	10009136	-1	3	0	0	0	0	0	0	3	0	3	0		Q8R1Z4
ENSMUST00000130103	ENSMUSG00000038503	7	83884466	83901532	1	0	0	0	0	0	0	3	15	6	11	9	D3YVR4	
ENSMUST00000130104						0	2	7	1	3	1	0	0	0	0	0		
ENSMUST00000130105	ENSMUSG00000056260	3	106684987	106736577	1	0	0	3	2	2	1	7	4	2	5	0	D3YWW6	
ENSMUST00000130106						4	0	5	2	4	3	13	18	22	4	20		
ENSMUST00000130107						1	0	3	3	7	0	0	0	0	0	2		
ENSMUST00000130108	ENSMUSG00000025609	6	31398735	31516811	1	0	0	0	0	0	0	3	0	0	2	3	F6UW85	
ENSMUST00000130110						4	2	2	3	0	2	0	27	12	0	19		
ENSMUST00000130111						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130112						13	18	0	104	29	4	0	34	0	0	0		
ENSMUST00000130113						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000130114						0	0	0	0	0	0	1	1	2	0	3		
ENSMUST00000130115						1	0	3	0	1	1	0	0	6	0	2		
ENSMUST00000130116						4	5	13	16	11	6	0	0	0	6	0		
ENSMUST00000130118						7	9	21	4	15	11	0	529	44	53	63		
ENSMUST00000130119						0	0	0	5	0	1	0	5	3	0	0		
ENSMUST00000130120						15	17	85	41	50	19	54	216	44	17	73		
ENSMUST00000130121						1	0	4	0	1	0	182	372	132	47	79		
ENSMUST00000130122						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130124						0	1	0	12	1	0	0	0	0	0	0		
ENSMUST00000130125						0	0	0	3	8	1	0	4	0	0	0		
ENSMUST00000130126						4	0	0	0	6	5	0	4	0	0	0		
ENSMUST00000130127	ENSMUSG00000032400	9	64137144	64173104	-1	0	0	0	16	0	0	0	0	0	2	0	D3Z6K4	
ENSMUST00000130128						3	0	0	23	0	1	0	12	4	8	0		
ENSMUST00000130129						34	26	47	38	28	17	2	5	1	0	2		
ENSMUST00000130130						0	0	0	0	0	0	68	125	45	3	29		
ENSMUST00000130131	ENSMUSG00000056342	11	23306895	23490560	1	4	6	5	5	10	4	5	58	8	9	20	Z4YLQ1	
ENSMUST00000130132						4	4	16	3	10	3	18	124	0	24	47		
ENSMUST00000130133						7	9	16	7	24	14	2	1	6	0	5		
ENSMUST00000130134	ENSMUSG00000054280	5	32789820	32854256	-1	0	3	0	49	3	2	2	1	2	0	0	H3BKZ4	
ENSMUST00000130135						0	0	0	19	0	7	2	3	0	2	1		
ENSMUST00000130136						10	9	45	18	10	10	0	0	0	0	0		
ENSMUST00000130137						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000130138						9	10	29	6	11	3	1	0	1	1	1		
ENSMUST00000130139	ENSMUSG00000057143	7	104338754	104353362	-1	0	0	0	0	0	0	66	128	341	261	308	D3Z3L3	
ENSMUST00000130140						0	7	26	100	15	0	0	47	38	0	38		
ENSMUST00000130141	ENSMUSG00000054764	8	45069137	45088356	1	0	0	0	0	0	0	0	0	0	0	0	F6SP87	
ENSMUST00000130142						1	0	5	0	1	0	17	62	60	227	43		
ENSMUST00000130143						0	0	1	1	4	0	0	0	0	0	0		
ENSMUST00000130144						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130145	ENSMUSG00000038290	11	74925823	75164448	1	5	0	32	0	0	2	42	186	6	31	41	F6WT10	
ENSMUST00000130146						0	0	4	8	1	0	0	2	5	0	5		
ENSMUST00000130147						47	42	237	75	58	36	0	8	7	2	12		
ENSMUST00000130148						1	0	7	8	0	0	0	4	2	0	0		
ENSMUST00000130149						7	11	20	9	17	5	0	0	2	1	2		
ENSMUST00000130150						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130151	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	0	0	2	0	6	22	0	14	D3YXR0	
ENSMUST00000130152						0	0	0	0	0	0	4	0	13	0	0		
ENSMUST00000130155						2	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000130156	ENSMUSG00000034826	5	92415540	92435219	-1	3	1	7	34	3	0	0	0	0	0	0	F6UKR5	
ENSMUST00000130157						1	5	8	85	6	4	1	2	1	0	1		
ENSMUST00000130158	ENSMUSG00000032311	9	55220222	55326844	-1	0	0	0	0	0	0	0	0	0	0	0		Q9WTX4
ENSMUST00000130160	ENSMUSG00000038451	6	124808661	124810619	1	0	0	0	35	0	11	42	33	0	0	9	D3Z7N7	
ENSMUST00000130161	ENSMUSG00000053091	7	66689889	66717256	1	16	31	12	0	7	0	21	0	0	0	0	D6RFA2	
ENSMUST00000130162						4	0	3	0	5	0	0	0	0	0	0		
ENSMUST00000130163	ENSMUSG00000008301	18	56562443	56587712	1	3	4	2	20	3	0	39	286	52	203	102	G5E8V8	
ENSMUST00000130164						8	5	39	28	4	15	0	7	18	14	15		
ENSMUST00000130165						19	6	40	21	14	8	5	36	10	4	25		
ENSMUST00000130166	ENSMUSG00000021792	14	40993740	41013788	-1	1	2	5	0	0	0	0	0	0	0	0	D3Z398	
ENSMUST00000130167						61	52	126	53	79	30	18	35	21	10	41		
ENSMUST00000130168	ENSMUSG00000037143	2	145934784	146215039	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCD5	
ENSMUST00000130169	ENSMUSG00000029577	5	114380607	114421169	1	42	0	80	0	0	10	1192	1860	1211	90	766	S4R2P2	
ENSMUST00000130170						4	2	18	21	10	5	6	32	13	0	13		
ENSMUST00000130171						0	0	11	0	0	11	0	0	0	0	0		
ENSMUST00000130172						0	0	0	0	0	0	162	1094	0	0	0		
ENSMUST00000130173						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130174	ENSMUSG00000020419	11	4345814	4441105	-1	0	3	6	10	2	1	0	0	0	0	0	B1ATD3	
ENSMUST00000130175	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	0	0	0	0	0	0	0	0		P0C8K7
ENSMUST00000130176						4	0	2	5	0	0	0	0	1	0	3		
ENSMUST00000130178						2	3	4	4	1	2	0	0	0	0	2		
ENSMUST00000130179						0	1	3	3	6	0	0	72	48	0	12		
ENSMUST00000130180						0	1	1	4	7	2	3	2	2	2	5		
ENSMUST00000130181	ENSMUSG00000006219	4	141576062	141606096	-1	3	2	0	4	2	2	0	0	0	0	0	A2ADE6	
ENSMUST00000130182	ENSMUSG00000030986	7	133720942	133782726	-1	0	0	1	81	6	3	0	0	0	0	0	D3YZD7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130183						10	8	12	3	12	3	13	147	43	23	96		
ENSMUST00000130185						3	7	7	3	1	1	0	0	0	0	3		
ENSMUST00000130186	ENSMUSG00000047909	2	11777876	11790329	1	3	5	11	78	9	0	11	12	29	9	32	A0A0A6YWT3	
ENSMUST00000130187						16	22	51	409	32	25	12	60	14	1	36		
ENSMUST00000130188	ENSMUSG00000029066	4	155802878	155809975	1	49	46	160	84	54	27	14	22	11	24	15	V9GX65	
ENSMUST00000130190	ENSMUSG00000019966	10	100015630	100100413	1	0	2	0	67	6	0	0	0	0	0	2	Q8C9K1	
ENSMUST00000130191	ENSMUSG00000030270	6	113282307	113305627	1	4	1	3	24	3	0	0	0	0	0	0	S4R2U2	
ENSMUST00000130192						4	1	2	3	0	0	0	0	0	0	0		
ENSMUST00000130194	ENSMUSG00000024160	17	24886643	24892152	1	0	0	0	0	0	0	6	0	23	0	20	D6RI75	
ENSMUST00000130195						4	0	2	2	1	0	0	0	0	1	1		
ENSMUST00000130196						1	0	8	4	1	0	0	0	0	0	0		
ENSMUST00000130197						3	0	19	17	4	0	0	0	0	0	0		
ENSMUST00000130198	ENSMUSG00000020224	10	120227070	120232071	1	9	2	8	134	8	7	5	19	7	9	12	D3YXW1	
ENSMUST00000130200						2	0	2	1	0	2	10	9	21	0	18		
ENSMUST00000130201	ENSMUSG00000033845	1	4773206	4785739	-1	0	1	0	0	8	0	7	0	0	2	4		Q9CPR5
ENSMUST00000130202						0	0	0	0	0	1	1	0	0	1	0		
ENSMUST00000130203						0	0	0	2	1	0	0	0	5	0	0		
ENSMUST00000130204						3	2	2	16	3	2	0	0	0	0	2		
ENSMUST00000130207						3	2	6	3	8	2	0	0	0	0	0		
ENSMUST00000130208	ENSMUSG00000023990	17	47737030	47792419	1	2	0	0	1	1	1	0	0	0	0	0	D3Z782	
ENSMUST00000130209						0	4	4	1	4	6	0	0	0	0	1		
ENSMUST00000130210						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000130211	ENSMUSG00000021335	13	23867750	23895730	1	1	1	10	2	2	5	0	0	0	0	0	Q5SZ94	
ENSMUST00000130212	ENSMUSG00000031865	6	83165920	83200117	1	6	0	0	13	0	3	0	0	4	0	0	D3YYG9	
ENSMUST00000130213						13	5	16	8	11	6	16	31	29	0	54		
ENSMUST00000130214	ENSMUSG00000036356	8	68356781	68735146	-1	5	16	0	0	18	4	0	0	0	0	4		Q8BJQ9
ENSMUST00000130215	ENSMUSG00000059851	7	4740115	4747514	1	0	0	0	0	0	0	0	0	8	0	0	D3Z2F5	
ENSMUST00000130216	ENSMUSG00000071172	17	29032673	29043366	1	5	11	0	13	5	0	128	213	103	744	125		P84104
ENSMUST00000130217						1	1	0	1	0	0	0	23	18	17	5		
ENSMUST00000130218						3	2	6	46	7	2	1	2	0	0	0		
ENSMUST00000130219						1	0	3	7	1	1	22	34	24	154	35		
ENSMUST00000130220						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000130221						0	0	0	30	17	14	0	0	5	0	0		
ENSMUST00000130222						0	4	3	1	1	0	0	0	0	0	0		
ENSMUST00000130223	ENSMUSG00000051351	4	136284683	136293942	1	0	0	0	0	0	0	0	0	1	0	0	A2AW47	
ENSMUST00000130224						0	3	27	1	0	1	5	4	4	2	8		
ENSMUST00000130225						0	0	0	0	0	0	93	112	229	25	94		
ENSMUST00000130227						9	3	11	16	6	10	1	5	2	0	1		
ENSMUST00000130228	ENSMUSG00000037736	5	66745827	67057158	1	0	0	1	41	1	2	0	0	0	0	0	D6RHT2	
ENSMUST00000130229						5	13	8	0	6	0	0	228	33	60	0		
ENSMUST00000130230	ENSMUSG00000027953	3	89268246	89270570	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z071	
ENSMUST00000130231	ENSMUSG00000037214	8	26158212	26162940	1	0	0	0	0	0	1	0	0	0	0	1	D3YTK5	
ENSMUST00000130232	ENSMUSG00000009207	2	74520291	74579435	-1	1	1	3	79	7	1	0	0	0	0	0	A2ASM1	
ENSMUST00000130233	ENSMUSG00000029095	5	35757880	35884973	1	6	4	8	8	0	2	0	0	0	0	0	D3YYR9	
ENSMUST00000130234						2	0	3	1	1	0	1	6	44	0	38		
ENSMUST00000130235	ENSMUSG00000021464	13	53109312	53286124	-1	22	18	64	33	37	21	0	0	0	0	2	E9PUN5	
ENSMUST00000130236						1	3	0	1	3	0	0	0	0	4	0		
ENSMUST00000130237						2	1	7	2	2	4	3	19	10	0	12		
ENSMUST00000130238	ENSMUSG00000037643	3	30995747	31052959	1	0	3	3	0	2	0	0	0	6	0	8	D3YXY0	
ENSMUST00000130239						1	0	2	1	3	0	5	3	0	0	3		
ENSMUST00000130241						0	6	24	14	8	1	0	0	0	0	0		
ENSMUST00000130242	ENSMUSG00000030304	6	148179079	148212374	-1	0	0	3	1	0	0	20	23	14	30	49	D6RGS9	
ENSMUST00000130243						6	0	0	137	9	9	6	28	20	1	24		
ENSMUST00000130245						0	3	1	31	3	1	0	0	5	0	6		
ENSMUST00000130246						0	0	0	0	3	0	0	0	2	0	0		
ENSMUST00000130247	ENSMUSG00000034555	X	112011007	112127326	1	0	0	0	0	0	0	0	0	0	0	0	F6WNY1	
ENSMUST00000130248						15	15	15	17	22	9	4	5	0	0	8		
ENSMUST00000130249						4	1	5	2	3	7	0	0	0	0	0		
ENSMUST00000130250						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130252						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130253						1	3	0	3	4	1	0	1	0	0	1		
ENSMUST00000130254						6	4	1	5	5	2	0	0	1	0	2		
ENSMUST00000130255	ENSMUSG00000020836	11	77462411	77470484	1	1	1	0	27	3	2	0	0	0	0	0	F6WME2	
ENSMUST00000130257	ENSMUSG00000030341	6	125349362	125362484	1	1	0	2	18	0	1	0	0	0	0	0	D3YXL4	
ENSMUST00000130258						0	0	0	0	0	0	4	0	0	0	5		
ENSMUST00000130260	ENSMUSG00000020156	10	80226434	80243903	1	3	3	0	0	7	0	6	0	0	0	2	D3Z468	
ENSMUST00000130261						0	1	3	2	5	1	9	73	17	4	15		
ENSMUST00000130263						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000130265	ENSMUSG00000057133	2	160946978	161109075	-1	0	0	9	9	4	0	0	0	0	12	15	A3KFM6	
ENSMUST00000130267	ENSMUSG00000040935	4	140727355	140742643	-1	2	3	14	5	4	3	0	0	0	0	1	A2AMU1	
ENSMUST00000130268						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130269	ENSMUSG00000018932	11	60932033	60952811	1	11	6	37	0	2	0	1	2	0	194	0		
ENSMUST00000130270						8	11	7	10	9	4	0	0	0	0	0		
ENSMUST00000130271	ENSMUSG00000032921	11	68921835	68927081	-1	7	0	0	0	0	6	0	0	0	0	0		Q8VI88
ENSMUST00000130272						1	0	4	0	1	1	0	0	0	0	0		
ENSMUST00000130273	ENSMUSG00000028684	4	116989965	116994413	-1	0	0	0	0	0	0	8	0	6	5	0	A0A0A0MQG7	
ENSMUST00000130274						4	0	0	0	4	0	0	393	0	205	76		
ENSMUST00000130275						6	5	24	2	0	3	0	3	10	0	16		
ENSMUST00000130276						7	3	7	0	4	7	0	0	0	0	0		
ENSMUST00000130277						0	0	20	194	28	9	6	36	6	0	6		
ENSMUST00000130278	ENSMUSG00000027074	2	84936579	84958509	1	2	0	0	19	5	0	0	0	6	0	0	A6PWZ8	
ENSMUST00000130279	ENSMUSG00000004264	6	124712336	124716950	1	0	0	0	0	0	0	93	100	0	3	13	F6QPR1	
ENSMUST00000130281						0	1	2	3	4	0	0	0	0	0	0		
ENSMUST00000130282	ENSMUSG00000004933	10	81252935	81263365	1	3	0	0	71	0	1	0	0	0	0	0	D3YVQ8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130283						29	25	41	50	38	17	0	0	0	0	3		
ENSMUST00000130284						0	0	0	3	7	0	13	8	0	0	31		
ENSMUST00000130285						0	0	0	0	0	0	0	6	4	0	5		
ENSMUST00000130286						3	0	0	21	3	1	0	0	0	1	0		
ENSMUST00000130287						11	6	15	15	8	8	4	7	8	2	8		
ENSMUST00000130288						0	0	0	0	4	0	0	0	0	0	4		
ENSMUST00000130289						0	0	9	67	7	2	0	0	2	1	0		
ENSMUST00000130290						4	10	13	2	0	0	20	359	337	183	125		
ENSMUST00000130291	ENSMUSG00000021824	14	21031442	21052508	-1	0	0	0	0	0	0	4	0	36	11	5	D3YXV9	
ENSMUST00000130292	ENSMUSG00000041966	2	71055328	71099142	1	0	0	0	1	0	0	3	5	0	0	0	F6YAD1	
ENSMUST00000130293	ENSMUSG00000046804	2	118772769	118778165	1	0	5	0	0	0	0	0	0	0	0	0		Q8K0G7
ENSMUST00000130294						9	6	13	9	9	5	2	1	5	0	5		
ENSMUST00000130295						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130297						0	0	0	0	0	0	0	0	0	0	7		
ENSMUST00000130298	ENSMUSG00000026634	1	190925112	190946962	1	1	1	0	1	2	3	0	0	0	0	0	A0A0A6YY82	
ENSMUST00000130299						11	6	4	8	12	4	0	0	0	0	1		
ENSMUST00000130300	ENSMUSG00000046318	18	66045302	66302739	-1	0	0	0	62	5	0	0	0	1	3	3		Q3MI99
ENSMUST00000130301	ENSMUSG00000035311	10	88379132	88447329	1	0	0	0	0	0	0	1	0	2	0	0	D3YXC6	
ENSMUST00000130302						31	22	41	24	34	9	0	12	0	2	3		
ENSMUST00000130303						1	0	2	7	0	0	2	32	14	5	12		
ENSMUST00000130305	ENSMUSG00000000631	11	77763246	77865980	1	0	0	0	6	0	0	0	0	58	0	0		Q9JMH9
ENSMUST00000130306						1	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000130308						0	1	0	0	0	0	23	67	92	236	23		
ENSMUST00000130309						2	1	0	5	1	1	4	0	0	0	0		
ENSMUST00000130310	ENSMUSG00000025586	7	81347026	81455465	-1	13	10	11	0	15	0	0	1	0	0	1	F6X7Z3	
ENSMUST00000130311						6	1	2	3	0	2	0	0	0	0	0		
ENSMUST00000130312						1	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000130313	ENSMUSG00000019817	10	13060504	13131694	1	0	1	0	0	0	0	0	0	0	0	0	B0QZX4	
ENSMUST00000130314						16	13	6	10	9	7	0	0	0	0	2		
ENSMUST00000130315	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	0	0	0	0	0	0	F6TDF4	
ENSMUST00000130316						4	0	2	2	1	4	0	0	0	0	0		
ENSMUST00000130318						1	1	8	3	3	0	11	17	25	0	61		
ENSMUST00000130319	ENSMUSG00000002343	8	70220172	70234466	-1	0	3	12	20	5	0	0	0	4	0	3	D3Z3J0	
ENSMUST00000130320	ENSMUSG00000001786	10	86021972	86051873	1	11	13	51	100	23	2	13	38	24	5	22		Q3U7U3
ENSMUST00000130321						2	3	3	2	2	0	4	8	2	0	5		
ENSMUST00000130322	ENSMUSG00000015755	10	7905653	7956230	-1	3	3	17	0	2	0	0	0	3	0	7	D3Z564	
ENSMUST00000130323						3	0	8	1	4	2	6	45	17	5	44		
ENSMUST00000130324	ENSMUSG00000036572	X	37091678	37110322	-1	0	0	2	2	1	0	0	0	5	0	0	F6Q8N5	
ENSMUST00000130325	ENSMUSG00000031683	8	78804865	78821140	-1	217	146	274	158	210	115	58	147	82	108	76	Q542U7	P62313
ENSMUST00000130326	ENSMUSG00000025858	5	139252324	139270051	1	0	0	0	0	0	0	83	23	64	10	43	D3Z4J5	
ENSMUST00000130327						9	10	21	20	20	5	0	0	0	0	0		
ENSMUST00000130328	ENSMUSG00000023118	7	19024377	19054618	1	0	4	0	0	0	0	0	0	0	0	0	F6UJ99	
ENSMUST00000130329	ENSMUSG00000002068	7	38097984	38107534	-1	1	0	3	52	6	0	8	1	0	0	0	D3Z3N8	
ENSMUST00000130330						2	1	0	0	1	0	3	5	1	4	1		
ENSMUST00000130332	ENSMUSG00000049148	15	4375491	4575553	1	52	40	71	339	77	37	1	0	0	0	1	D6RDF3	
ENSMUST00000130333						7	7	10	6	14	1	3	9	7	2	14		
ENSMUST00000130334	ENSMUSG00000043962	4	126164082	126202760	-1	0	0	0	0	0	0	4	0	2	0	0	A2AJI6	
ENSMUST00000130335						9	3	14	1	13	4	6	6	7	0	7		
ENSMUST00000130336						0	2	0	1	2	1	0	16	11	0	21		
ENSMUST00000130337						4	0	17	3	12	6	0	0	0	0	0		
ENSMUST00000130338	ENSMUSG00000033740	1	6487231	6860940	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVU2	
ENSMUST00000130339						0	0	0	1	0	0	4	23	9	40	3		
ENSMUST00000130340						2	5	3	6	4	4	1	0	0	0	4		
ENSMUST00000130341	ENSMUSG00000043372	11	103132429	103139876	1	0	0	0	0	2	0	1	0	1	1	0	A2AB65	
ENSMUST00000130342	ENSMUSG00000001729	12	112653821	112674884	-1	0	0	1	41	1	2	5	11	3	0	9	D3YYP9	
ENSMUST00000130343						0	4	3	6	2	0	0	30	5	0	0		
ENSMUST00000130344						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000130345	ENSMUSG00000004947	5	135994800	136032872	1	0	0	14	0	1	0	0	0	0	0	0		
ENSMUST00000130346						2	0	10	0	0	0	18	79	8	0	27		
ENSMUST00000130347						2	3	6	2	3	0	32	52	0	9	22		
ENSMUST00000130348	ENSMUSG00000042997	3	53448583	53463332	-1	0	0	48	51	38	18	0	183	34	10	46	D6RE41	
ENSMUST00000130349	ENSMUSG00000025289	X	155323918	155340754	-1	2	0	1	2	1	0	0	0	0	0	0	B1AZS9	
ENSMUST00000130350						19	19	32	25	37	24	1	1	1	0	0		
ENSMUST00000130351						0	0	2	4	4	1	0	12	0	0	0		
ENSMUST00000130352						23	13	20	50	14	13	6	16	6	2	15		
ENSMUST00000130353	ENSMUSG00000028465	4	43531519	43562691	-1	9	3	7	0	0	0	27	0	9	2	10	A2AIM2	
ENSMUST00000130354						0	4	3	1	5	0	15	543	42	44	49		
ENSMUST00000130355	ENSMUSG00000037965	16	11136592	11176393	-1	0	0	0	0	0	0	0	0	0	2	0	D3YZY2	
ENSMUST00000130356	ENSMUSG00000027364	2	126709096	126783458	-1	0	0	0	0	1	0	0	0	0	0	0	B0QZZ0	
ENSMUST00000130357						0	0	0	0	0	0	0	0	11	0	0		
ENSMUST00000130358						1	0	5	8	5	12	0	2	0	0	0		
ENSMUST00000130359	ENSMUSG00000028687	4	116807723	116819440	1	0	1	0	7	1	3	0	0	1	0	0	A8Y5N1	
ENSMUST00000130360	ENSMUSG00000043079	18	60593973	60660142	-1	0	5	62	0	0	11	0	0	0	5	81	E9Q3E2	
ENSMUST00000130363						1	2	1	2	1	0	2	9	2	3	4		
ENSMUST00000130364	ENSMUSG00000017631	11	76416734	76622314	-1	0	0	6	0	3	0	0	0	0	0	0	H3BJY3	
ENSMUST00000130365	ENSMUSG00000014418	7	46760466	46796064	-1	0	0	0	0	0	0	0	0	0	0	0	F6YT95	
ENSMUST00000130366	ENSMUSG00000053646	9	109095389	109119917	1	2	0	6	1	4	1	0	0	0	0	0	D3YUD0	
ENSMUST00000130367	ENSMUSG00000024457	17	36837134	36859398	1	0	0	0	0	0	0	127	103	250	22	25		Q99PN3
ENSMUST00000130368	ENSMUSG00000061559	9	54714735	54734519	-1	0	0	0	0	0	0	0	45	3	0	0	D6RDC7	
ENSMUST00000130369						2	1	9	3	0	0	0	0	0	0	0		
ENSMUST00000130370	ENSMUSG00000021824	14	21031442	21052508	-1	0	0	0	79	6	2	0	0	0	0	0	D3YWU3	
ENSMUST00000130371						2	2	12	49	4	4	37	123	54	15	81		
ENSMUST00000130372	ENSMUSG00000079168	8	4134733	4137707	1	7	1	7	2	6	6	1	0	0	0	0	D3Z5D4	
ENSMUST00000130374						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130375	ENSMUSG00000055632	2	31314415	31460738	1	0	2	2	1	4	0	0	0	0	0	0	F6VSY0	
ENSMUST00000130376						1	1	1	45	2	0	0	0	0	0	1		
ENSMUST00000130377						0	0	0	4	3	1	0	0	0	0	0		
ENSMUST00000130378						15	19	47	8	17	8	0	0	2	0	5		
ENSMUST00000130379	ENSMUSG00000005371	17	87990859	88065291	-1	4	2	15	0	0	10	447	1114	332	45	235	F6T356	
ENSMUST00000130380						0	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000130381						3	2	4	41	3	2	0	0	0	0	0		
ENSMUST00000130382	ENSMUSG00000024948	19	6341135	6355615	1	0	0	0	0	0	0	31	0	18	0	0	D3YUH9	
ENSMUST00000130383						2	2	15	4	4	5	4	13	0	0	5		
ENSMUST00000130384	ENSMUSG00000034593	9	75071015	75223688	1	0	0	0	0	0	0	0	0	0	3	0	F6Z2S4	
ENSMUST00000130385						1	2	4	2	2	4	0	5	0	0	7		
ENSMUST00000130386	ENSMUSG00000044037	9	110879870	110900530	1	3	14	0	0	63	11	52	26	46	10	118		
ENSMUST00000130387	ENSMUSG00000034813	10	119454034	120087261	1	0	4	0	2	2	3	0	0	0	0	0	D3Z066	
ENSMUST00000130390						18	11	52	112	16	13	0	2	0	2	6		
ENSMUST00000130393	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	45	0	0	0	0	0	0	0	Q5GMG6	
ENSMUST00000130394						29	17	45	208	43	18	0	0	0	0	0		
ENSMUST00000130395						2	2	7	15	10	11	0	17	10	0	30		
ENSMUST00000130396						0	0	21	0	2	2	0	0	0	0	0		
ENSMUST00000130397	ENSMUSG00000021907	14	32142026	32158370	1	1	0	0	0	2	0	0	0	0	1	0	F6R7D9	
ENSMUST00000130398						0	0	9	26	0	0	0	0	1	0	0		
ENSMUST00000130399						0	0	0	0	0	0	0	0	9	3	0		
ENSMUST00000130400						3	1	8	1	4	0	60	66	50	9	79		
ENSMUST00000130401						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130402						7	1	4	3	3	3	3	2	0	0	0		
ENSMUST00000130403						0	0	2	0	4	2	1	23	15	3	0		
ENSMUST00000130404						50	37	105	9	70	43	32	217	7	10	31		
ENSMUST00000130405	ENSMUSG00000053199	9	51765337	51853856	1	8	5	15	89	5	4	0	0	0	0	0	D3YUH8	
ENSMUST00000130406	ENSMUSG00000023944	17	45567775	45573271	-1	1	0	2	38	3	4	0	0	0	0	0	D3Z1R1	
ENSMUST00000130407	ENSMUSG00000057530	4	137862237	137965229	1	0	0	0	9	2	0	1	0	0	0	1	E0CZB7	
ENSMUST00000130408						57	35	422	66	44	34	9	30	26	11	24		
ENSMUST00000130409						49	33	68	52	0	21	0	0	0	0	0		
ENSMUST00000130410	ENSMUSG00000052384	16	32142785	32165594	-1	0	0	2	41	3	1	30	4	15	3	7	D3Z755	
ENSMUST00000130411	ENSMUSG00000016921	2	162931528	162937121	1	13	10	6	11	5	1	325	1192	286	88	217		Q3TWW8
ENSMUST00000130412						3	3	4	0	0	0	75	548	84	118	79		
ENSMUST00000130413						0	0	0	4	4	2	4	40	34	17	18		
ENSMUST00000130414	ENSMUSG00000062542	7	107370728	107548656	1	9	1	17	8	0	14	0	0	0	0	0	D6RGS5	
ENSMUST00000130415						1	0	4	3	6	3	30	62	49	6	38		
ENSMUST00000130417	ENSMUSG00000029192	5	36490604	36593276	-1	0	5	0	0	0	0	0	0	0	0	0	G3UVU5	
ENSMUST00000130418	ENSMUSG00000030088	6	90486427	90600203	1	24	18	42	26	59	23	0	0	0	4	0		Q8R0Y6
ENSMUST00000130419						2	0	3	102	0	0	0	0	52	43	6		
ENSMUST00000130420	ENSMUSG00000033389	11	65002039	65162961	-1	17	11	37	0	11	0	0	0	0	0	0	F6T1Y2	
ENSMUST00000130421						1	2	3	0	0	0	0	15	17	69	10		
ENSMUST00000130422	ENSMUSG00000037012	10	62268855	62379908	-1	4	0	0	0	5	10	567	0	984	21	642	G3UVV4	
ENSMUST00000130423	ENSMUSG00000024019	17	29660595	29705979	1	3	3	23	60	6	1	101	8	50	0	57	D3Z491	
ENSMUST00000130425	ENSMUSG00000042389	6	115544664	115578628	1	3	1	10	13	3	0	0	0	1	0	0		
ENSMUST00000130426						15	19	33	8	16	15	0	3	2	0	4		
ENSMUST00000130427						2	5	13	3	7	4	0	0	0	0	0		
ENSMUST00000130428						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000130429						0	5	0	0	4	2	0	0	0	0	0		
ENSMUST00000130430						10	9	59	4	20	5	289	315	224	19	120		
ENSMUST00000130432	ENSMUSG00000000530	15	101128522	101145336	1	0	0	4	0	0	0	1	0	2	0	0	D3Z7H9	
ENSMUST00000130433						2	2	14	3	4	5	0	6	0	0	6		
ENSMUST00000130435						2	1	1	4	3	4	0	0	0	0	0		
ENSMUST00000130436	ENSMUSG00000018677	11	102402985	102407946	-1	3	1	5	4	7	0	0	0	0	0	0	B0QZI5	
ENSMUST00000130438						4	2	2	4	3	1	0	0	2	0	2		
ENSMUST00000130439	ENSMUSG00000025139	7	141874813	141918507	-1	0	0	0	10	0	0	9	4	4	0	2	F7AT44	
ENSMUST00000130440						0	0	0	0	0	0	2	4	8	0	0		
ENSMUST00000130441						1886	2119	4838	1612	2098	1047	17	104	49	29	82		
ENSMUST00000130443	ENSMUSG00000028467	4	43566928	43578873	-1	5	5	5	5	11	1	0	6	16	0	0	B1AWI3	
ENSMUST00000130444						1	0	0	0	2	0	0	0	1	0	0		
ENSMUST00000130445						0	3	19	7	5	0	0	0	0	0	2		
ENSMUST00000130447	ENSMUSG00000047022	12	57230427	57497199	1	1	0	0	0	0	0	0	0	2	0	0	G3UVV8	
ENSMUST00000130448						3	0	9	5	4	4	0	0	0	0	0		
ENSMUST00000130449						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000130450						9	6	2	9	7	7	5	3	12	0	10		
ENSMUST00000130451	ENSMUSG00000029616	5	121428590	121452506	-1	48	47	124	70	46	32	107	212	102	62	99		P57759
ENSMUST00000130452						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000130453	ENSMUSG00000049571	7	139600951	139683817	-1	0	0	0	4	0	0	0	0	0	0	0	D3Z0A9	
ENSMUST00000130454	ENSMUSG00000030353	6	128224288	128300823	-1	4	4	9	2	6	1	0	13	2	0	6		
ENSMUST00000130455	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	15	0	0	2	F6QKL8	
ENSMUST00000130456						5	3	0	0	3	3	2	0	0	0	0		
ENSMUST00000130457						12	13	18	17	13	8	0	0	3	1	4		
ENSMUST00000130458	ENSMUSG00000092260	8	69741639	69749970	-1	11	6	15	9	16	6	14	165	24	34	30	D3Z2T8	
ENSMUST00000130459	ENSMUSG00000036986	9	58218076	58249786	-1	2	1	2	20	0	7	0	0	0	0	0	F6RQM1	
ENSMUST00000130460						3	2	7	0	7	6	456	2842	505	1973	496		
ENSMUST00000130461	ENSMUSG00000037426	5	32863701	32994236	1	0	1	0	0	0	0	0	0	0	0	0	F6XIK0	
ENSMUST00000130462	ENSMUSG00000025487	7	140881968	140898643	1	0	5	6	2	7	0	31	193	60	37	127	F6ZQQ3	
ENSMUST00000130463						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130464	ENSMUSG00000012117	4	133969028	134000918	-1	1	0	0	0	0	0	0	0	0	5	0	A3KGK9	
ENSMUST00000130465						0	0	3	4	3	0	0	0	0	0	0		
ENSMUST00000130466	ENSMUSG00000006932	9	120929216	120960507	1	0	0	0	0	1	0	0	0	0	0	0	D3Z7S6	
ENSMUST00000130467						5	6	3	3	8	0	2	26	18	10	17		
ENSMUST00000130468						2	0	5	5	7	0	0	0	2	0	0		
ENSMUST00000130469	ENSMUSG00000024830	19	4156713	4163354	-1	0	0	0	11	0	0	24	51	7	3	42	Q80X26	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130470						0	1	3	3	0	0	0	0	0	0	0		
ENSMUST00000130471						1	2	5	14	2	0	0	0	6	0	0		
ENSMUST00000130472	ENSMUSG00000035392	2	37798991	38287390	-1	0	0	2	0	0	2	0	0	0	0	0	A2AUP6	
ENSMUST00000130473						13	20	43	17	8	7	13	62	12	4	18		
ENSMUST00000130474						1	0	4	2	0	1	0	1	0	0	0		
ENSMUST00000130475	ENSMUSG00000038705	2	181251449	181288035	-1	0	3	0	0	2	2	22	2	18	0	7	A2AS07	
ENSMUST00000130476						1	2	5	0	7	2	0	1	0	0	1		
ENSMUST00000130477						0	0	6	7	0	0	5	0	2	0	2		
ENSMUST00000130479						15	9	2	11	18	10	0	1	0	0	0		
ENSMUST00000130480						11	4	16	0	0	0	40	198	75	3	93		
ENSMUST00000130481	ENSMUSG00000087141	16	45959263	46010218	-1	36	32	55	53	48	34	16	52	41	16	63	B2RXA1	
ENSMUST00000130482						0	0	3	0	0	0	5	36	0	11	17		
ENSMUST00000130483						3	0	0	0	0	0	1	0	0	1	0		
ENSMUST00000130484						8	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130487						3	0	8	4	3	0	4	71	10	19	11		
ENSMUST00000130488						0	2	0	0	3	4	0	0	0	0	0		
ENSMUST00000130489						55	21	163	1137	170	62	0	3	0	1	1		
ENSMUST00000130490						27	26	44	109	50	11	4	0	0	0	4		
ENSMUST00000130491	ENSMUSG00000056216	7	35046422	35056573	-1	34	17	105	42	42	11	330	1361	440	61	331	Q54AJ1	P53568
ENSMUST00000130492						1	7	5	5	2	0	0	2	0	0	3		
ENSMUST00000130494						1	2	2	5	5	4	4	9	9	0	20		
ENSMUST00000130495						75	61	494	132	84	44	4	13	6	8	16		
ENSMUST00000130496						10	2	9	5	8	2	0	0	0	0	0		
ENSMUST00000130497						0	0	0	0	0	0	0	6	5	0	0		
ENSMUST00000130498	ENSMUSG00000047721	7	126695401	126699798	1	2	4	1	5	0	0	13	40	45	36	25		Q8BGS2
ENSMUST00000130499						1	1	0	0	1	4	0	0	0	1	0		
ENSMUST00000130500						3	0	0	2	5	2	38	114	203	544	152		
ENSMUST00000130502	ENSMUSG00000038126	5	124250959	124327972	-1	1	0	10	3	0	0	0	0	0	0	10	D6RI17	
ENSMUST00000130503						43	50	90	87	67	22	0	33	20	0	54		
ENSMUST00000130504	ENSMUSG00000026226	1	86016816	86029958	1	0	0	0	0	0	0	0	0	0	0	0	Q3V2M5	Q9D9T6
ENSMUST00000130505						5	1	13	1	0	1	0	0	0	0	0		
ENSMUST00000130506						5	2	4	2	0	0	0	3	5	1	6		
ENSMUST00000130507						1	1	1	25	2	0	0	0	0	0	1		
ENSMUST00000130508						22	7	42	22	10	10	0	0	3	0	6		
ENSMUST00000130509	ENSMUSG00000051506	14	32959547	33185508	-1	75	28	103	81	113	36	2301	2670	4205	137	3506	E9Q2M9	
ENSMUST00000130510						1	2	7	1	3	1	2	6	3	2	3		
ENSMUST00000130511						3	7	3	10	0	2	0	2	4	0	16		
ENSMUST00000130512						3	2	0	2	3	1	0	0	1	0	0		
ENSMUST00000130514						0	0	0	0	0	0	0	2	5	2	0		
ENSMUST00000130515	ENSMUSG00000020728	11	108425192	108860615	1	0	0	0	0	0	0	0	0	0	0	0		Q5PR68
ENSMUST00000130516						13	11	12	20	12	3	6	37	2	0	17		
ENSMUST00000130517						0	0	1	0	0	5	0	0	0	0	0		
ENSMUST00000130518						0	0	0	0	0	3	5	0	0	0	3		
ENSMUST00000130519	ENSMUSG00000035847	X	70343069	70365084	-1	0	0	2	0	1	1	0	15	33	0	24	F6X9C5	
ENSMUST00000130520						3	0	0	4	4	2	0	0	0	0	17		
ENSMUST00000130521						3	2	12	12	5	4	6	8	2	1	3		
ENSMUST00000130522	ENSMUSG00000020407	11	9118103	9136170	1	2	0	0	0	0	1	0	295	0	0	0	Q5SUC6	
ENSMUST00000130523						0	0	0	48	2	2	0	0	0	0	0		
ENSMUST00000130524						2	5	1	188	5	4	0	2	0	0	0		
ENSMUST00000130525						55	75	242	117	82	42	5	14	3	3	11		
ENSMUST00000130526	ENSMUSG00000049421	7	30094777	30107622	1	0	2	0	0	2	3	0	0	0	0	0	D3Z766	
ENSMUST00000130527						0	3	5	55	5	4	0	0	0	0	0		
ENSMUST00000130528						19	10	7	9	13	10	208	2091	505	44	538		
ENSMUST00000130529						4	4	5	11	4	3	2	10	6	6	7		
ENSMUST00000130530						0	0	0	0	0	0	71	21	24	87	347		
ENSMUST00000130531						3	6	8	3	5	2	0	1	0	0	0		
ENSMUST00000130533						5	2	0	0	0	0	0	0	0	5	1		
ENSMUST00000130534						4	5	16	15	7	5	11	17	2	0	13		
ENSMUST00000130535						5	5	8	66	8	10	0	0	0	0	0		
ENSMUST00000130536						0	0	4	1	3	0	3	0	0	0	0		
ENSMUST00000130537						0	1	0	0	0	0	2	65	2	9	9		
ENSMUST00000130538						0	1	0	2	2	0	0	0	0	0	0		
ENSMUST00000130539						14	14	36	12	8	3	8	10	14	2	21		
ENSMUST00000130540						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130541	ENSMUSG00000028573	4	95557507	95926939	1	0	0	3	0	1	0	30	61	21	42	1	B7ZCH9	
ENSMUST00000130542						23	12	64	24	21	8	0	1	0	0	0		
ENSMUST00000130543						1	1	2	22	1	0	1	14	2	0	8		
ENSMUST00000130544						0	3	14	10	3	5	0	0	0	0	0		
ENSMUST00000130545						3	3	12	0	5	3	0	5	0	0	0		
ENSMUST00000130547						2	2	3	1	7	0	0	0	0	0	0		
ENSMUST00000130548						2	1	0	3	3	0	0	0	0	0	0		
ENSMUST00000130549	ENSMUSG00000025207	19	44989101	45003397	1	7	17	18	102	38	8	0	0	2	0	0		Q9WUH7
ENSMUST00000130550						1	0	0	2	0	2	0	4	0	0	0		
ENSMUST00000130551						3	2	2	6	8	5	0	0	0	0	0		
ENSMUST00000130552						3	0	0	0	9	5	2	0	0	2	2		
ENSMUST00000130553	ENSMUSG00000047161	18	15451924	15760157	-1	5	10	4	23	3	5	0	0	0	0	0	D6RCI1	
ENSMUST00000130555	ENSMUSG00000031302	X	101299168	101325963	1	0	0	0	0	0	0	0	0	1	1	0	A2AGI0	
ENSMUST00000130557						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130558	ENSMUSG00000036198	X	49463945	49500244	1	2	1	4	0	1	0	0	0	0	0	0	Z4YMR3	
ENSMUST00000130559	ENSMUSG00000023861	17	8282904	8297661	1	1	0	0	0	0	0	79	438	155	223	46	D3Z5S0	
ENSMUST00000130560	ENSMUSG00000022548	16	31296192	31314808	-1	13	17	47	23	24	6	0	9	1	4	1		P51910
ENSMUST00000130561						1	1	5	0	3	1	0	0	0	6	0		
ENSMUST00000130562						2	2	1	0	3	0	0	0	0	1	0		
ENSMUST00000130563	ENSMUSG00000018796	8	46471041	46536051	1	0	0	0	0	0	0	0	0	0	0	0	D3YVF6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130565						3	1	1	0	0	4	11	325	8	0	49		
ENSMUST00000130566	ENSMUSG00000074365	7	15882617	15904020	1	0	0	4	0	9	0	0	0	0	0	0	V9GWZ5	
ENSMUST00000130568	ENSMUSG00000025875	13	54789377	54796776	1	0	0	0	0	0	0	11	0	15	5	0	F6VW20	
ENSMUST00000130569						8	8	18	14	16	6	72	40	76	10	57		
ENSMUST00000130572						19	8	18	16	17	4	0	0	0	0	0		
ENSMUST00000130573						1	1	5	99	3	3	0	0	0	0	0		
ENSMUST00000130574	ENSMUSG00000054469	17	73107985	73243368	1	5	0	0	64	0	2	1	0	0	0	0	B0V2Q8	
ENSMUST00000130575						0	0	2	32	6	0	0	0	0	0	0		
ENSMUST00000130577						0	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000130578	ENSMUSG00000026843	2	31572651	31617526	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW42	
ENSMUST00000130579						112	107	102	98	137	78	2	6	9	1	11		
ENSMUST00000130580						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000130581	ENSMUSG00000015291	X	74304998	74311862	1	0	0	0	0	0	0	0	708	0	0	0	B7FAU8	
ENSMUST00000130583	ENSMUSG00000030945	7	119554469	119600694	1	0	0	0	0	0	0	0	0	0	0	0	D3YXB1	
ENSMUST00000130585						4	2	5	0	0	1	1	0	0	0	0		
ENSMUST00000130586	ENSMUSG00000009207	2	74520291	74579435	-1	2	1	0	0	0	0	0	0	0	0	0	A2ASM0	
ENSMUST00000130587						1	1	7	0	1	0	0	0	1	0	1		
ENSMUST00000130588	ENSMUSG00000061086	11	104550663	104595753	1	0	0	0	0	2	0	0	0	0	0	0	D6RFU4	
ENSMUST00000130589	ENSMUSG00000051159	X	102247381	102252181	-1	0	1	0	12	3	0	0	0	0	0	0	A0A0A0MQI7	
ENSMUST00000130590	ENSMUSG00000019796	10	7589800	7625483	1	14	0	27	0	0	0	1	0	5	0	3	D3Z2B1	
ENSMUST00000130591						1	0	7	1	4	4	0	38	6	0	9		
ENSMUST00000130593						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130594						1	3	0	0	2	0	2	4	3	0	6		
ENSMUST00000130596						4	2	19	2	2	1	0	0	5	0	0		
ENSMUST00000130597	ENSMUSG00000037523	2	131234063	131248025	1	4	0	9	6	8	5	0	0	32	0	0	S4R1W6	
ENSMUST00000130598						5	3	17	10	17	2	0	4	0	0	0		
ENSMUST00000130599	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	7	0		
ENSMUST00000130600						1	1	1	0	0	4	0	0	0	0	0		
ENSMUST00000130601						0	0	0	1	0	0	3	0	0	0	0		
ENSMUST00000130602	ENSMUSG00000032531	9	102716672	102733418	1	0	0	0	0	0	0	385	660	125	41	42	B8JK81	
ENSMUST00000130603						3	1	7	1	1	0	0	0	0	0	0		
ENSMUST00000130604	ENSMUSG00000070880	2	70553072	70602014	1	0	0	0	21	0	3	0	0	0	0	0	D3Z1L8	
ENSMUST00000130605						4	2	2	0	2	0	0	1	0	0	0		
ENSMUST00000130606	ENSMUSG00000015733	6	17636234	17666972	1	0	0	0	0	0	0	323	1283	689	820	283	D6RCW7	
ENSMUST00000130608	ENSMUSG00000027400	2	129686565	129699844	-1	0	2	3	0	1	1	0	0	0	0	0	A2ANF0	
ENSMUST00000130609						0	0	0	8	1	2	0	0	0	0	0		
ENSMUST00000130610						0	0	0	0	0	0	359	693	348	98	257		
ENSMUST00000130611						0	1	2	3	1	4	0	0	0	0	0		
ENSMUST00000130612	ENSMUSG00000030207	6	135197977	135244955	1	1	0	0	78	7	3	0	0	0	0	0	E0CXF9	
ENSMUST00000130613						5	3	14	2	6	4	2	2	6	3	4		
ENSMUST00000130614						1	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000130615	ENSMUSG00000015619	2	9857078	9890034	-1	0	0	0	43	4	0	0	0	0	0	0	F6QTY0	
ENSMUST00000130616						0	0	0	27	0	0	7	0	10	3	22		
ENSMUST00000130617						0	1	2	52	3	5	0	0	0	0	0		
ENSMUST00000130618	ENSMUSG00000070880	2	70553072	70602014	1	1	2	3	17	0	0	0	0	0	0	0	D3Z466	
ENSMUST00000130620	ENSMUSG00000027879	3	97901190	97923276	1	1	2	2	22	1	0	0	0	13	33	0	A0A0G2JF08	
ENSMUST00000130621						7	13	12	90	12	3	11	20	26	6	36		
ENSMUST00000130622	ENSMUSG00000034930	6	83135463	83152579	1	5	0	4	63	3	0	0	0	0	0	0	D3Z4N1	
ENSMUST00000130623						65	68	152	62	60	33	6	7	2	2	1		
ENSMUST00000130624						29	22	117	71	37	20	79	372	319	17	419		
ENSMUST00000130626	ENSMUSG00000028484	4	83455680	83486459	-1	0	1	1	49	3	0	0	2	0	0	2	F6RB63	
ENSMUST00000130627	ENSMUSG00000000631	11	77763246	77865980	1	0	0	0	0	0	0	8	8	0	0	0		Q9JMH9
ENSMUST00000130628						0	0	10	0	5	0	0	0	0	0	11		
ENSMUST00000130629						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000130631						0	2	4	3	0	0	0	0	3	0	0		
ENSMUST00000130632						9	6	43	16	12	5	21	62	36	12	45		
ENSMUST00000130633	ENSMUSG00000040688	17	24697949	24707660	-1	1	0	10	2	2	0	11	29	5	6	10	F6YAR3	
ENSMUST00000130635	ENSMUSG00000021098	12	72881109	72940774	-1	4	2	2	2	3	1	0	0	0	0	0	D3YUI5	
ENSMUST00000130636	ENSMUSG00000059921	3	141465216	141834924	1	1	0	5	18	3	0	0	0	0	0	0	E9PVI4	
ENSMUST00000130637	ENSMUSG00000026987	2	59899363	60209839	-1	3	0	0	0	1	2	14	90	52	11	127	F6R4Y5	
ENSMUST00000130638						2	5	26	16	16	4	0	0	0	0	0		
ENSMUST00000130640						0	1	0	21	0	0	0	0	0	0	0		
ENSMUST00000130641	ENSMUSG00000020385	11	51261730	51281766	1	0	0	0	2	0	0	0	0	0	0	0	B0QZP9	
ENSMUST00000130642						5	5	4	0	8	5	0	0	0	0	0		
ENSMUST00000130643	ENSMUSG00000004865	17	28587648	28622521	-1	79	67	254	78	67	45	175	910	312	126	349	Q3UB06	O70551
ENSMUST00000130644	ENSMUSG00000029299	5	104935057	104982718	-1	7	0	0	1	0	0	3	3	0	0	0	D3Z0Z4	
ENSMUST00000130645	ENSMUSG00000027601	3	19187327	19220817	1	69	59	58	78	115	49	83	316	109	67	158	Q3TTQ5	Q99MB2
ENSMUST00000130646						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130647						0	0	0	63	0	0	0	0	0	0	0		
ENSMUST00000130648						9	8	10	5	3	3	0	0	0	0	0		
ENSMUST00000130649						2	2	50	12	9	4	12	52	10	2	20		
ENSMUST00000130650	ENSMUSG00000022779	16	16870736	16892990	1	0	0	0	0	0	0	0	0	0	0	0	D3YW63	
ENSMUST00000130651						51	37	95	105	39	16	17	54	82	25	83		
ENSMUST00000130652						0	0	0	0	0	0	7	9	8	0	2		
ENSMUST00000130653						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000130654						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000130655						0	0	0	0	0	0	0	0	6	0	0		
ENSMUST00000130656						261	257	585	339	316	169	17	31	27	10	38		
ENSMUST00000130658	ENSMUSG00000051351	4	136284683	136293942	1	0	0	0	0	0	0	8	2	0	0	3	A2AW48	
ENSMUST00000130660						0	2	0	84	3	0	0	0	0	0	0		
ENSMUST00000130661						1	0	0	0	0	1	0	5	0	4	2		
ENSMUST00000130662						1	1	0	0	1	0	0	1	3	0	1		
ENSMUST00000130663	ENSMUSG00000033088	15	78947724	79005867	1	8	1	16	42	9	3	114	150	82	12	65	G5E8W1	
ENSMUST00000130664	ENSMUSG00000032712	6	149309414	149335663	1	0	0	0	88	0	2	23	20	115	2	38		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130665						0	2	1	0	0	1	0	0	0	0	0		
ENSMUST00000130666						11	9	18	23	14	9	6	21	10	1	31		
ENSMUST00000130667						0	0	0	0	2	0	0	10	6	0	0		
ENSMUST00000130668						0	2	1	0	0	1	35	24	5	13	0		
ENSMUST00000130669						3	4	7	5	8	1	0	0	0	0	0		
ENSMUST00000130670						0	0	2	9	7	2	11	9	12	0	38		
ENSMUST00000130671	ENSMUSG00000023088	16	14361558	14475737	1	0	0	0	0	0	0	0	0	0	0	37	E9Q1I5	
ENSMUST00000130672						3	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000130674						2	3	0	0	1	0	4	4	0	3	3		
ENSMUST00000130675						4	2	0	0	0	0	60	146	34	25	17		
ENSMUST00000130676						7	7	10	5	9	3	20	54	32	7	43		
ENSMUST00000130678	ENSMUSG00000020828	11	70540064	70558110	1	0	0	0	0	0	0	0	0	0	0	0	J3QN26	
ENSMUST00000130681						3	0	9	1	2	1	2	0	0	0	0		
ENSMUST00000130682						0	0	6	0	0	0	2	7	7	21	9		
ENSMUST00000130685						4	2	11	3	10	2	0	0	0	0	0		
ENSMUST00000130686						1	1	2	4	1	1	2	3	0	0	2		
ENSMUST00000130687	ENSMUSG00000038611	7	141228784	141262750	1	0	0	5	1	3	0	37	208	0	18	53	F6WXS6	
ENSMUST00000130688						6	2	7	3	6	0	4	15	3	6	10		
ENSMUST00000130689						4	0	9	10	2	0	8	19	20	0	38		
ENSMUST00000130690						0	0	7	0	0	0	0	4	0	2	17		
ENSMUST00000130692						3	2	8	2	6	0	0	0	0	0	0		
ENSMUST00000130693						60	37	263	91	46	35	0	8	3	0	5		
ENSMUST00000130694						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130697	ENSMUSG00000002325	14	55603571	55610030	1	0	0	0	4	0	0	320	659	465	242	580	Q3UKQ7	Q61179
ENSMUST00000130698						5	5	19	6	8	0	0	36	28	8	45		
ENSMUST00000130700	ENSMUSG00000035757	15	89089084	89100340	1	13	22	34	102	32	15	24	80	43	8	67	S4R1U9	
ENSMUST00000130701						1	2	0	2	2	6	4	17	9	2	19		
ENSMUST00000130702	ENSMUSG00000064141	4	120930137	120951699	-1	4	2	0	1	2	0	0	0	6	0	4	G3UWJ2	
ENSMUST00000130703	ENSMUSG00000001436	10	77032241	77061002	1	0	0	0	0	0	0	0	0	0	0	0	D3YZE1	
ENSMUST00000130704	ENSMUSG00000020220	4	144972622	145195005	-1	13	9	86	47	19	6	0	894	0	50	0	F6XI52	
ENSMUST00000130705	ENSMUSG00000034640	3	65528410	65555518	1	0	0	0	0	0	0	9	0	0	0	0	D3Z7U2	
ENSMUST00000130706						0	0	1	2	1	2	4	1	0	0	4		
ENSMUST00000130707	ENSMUSG00000030731	7	44384102	44400187	1	1	0	5	28	1	2	0	0	0	0	0	D3Z1B8	
ENSMUST00000130708						4	0	0	53	0	1	2	2	3	5	0		
ENSMUST00000130709						2	3	1	3	0	0	16	8	55	0	58		
ENSMUST00000130711						0	0	4	0	2	0	14	61	13	0	7		
ENSMUST00000130712						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130713						0	1	0	0	0	0	0	4	0	0	0		
ENSMUST00000130714						0	0	1	0	0	0	0	0	1	0	1		
ENSMUST00000130715						0	1	0	2	0	0	2	2	0	0	13		
ENSMUST00000130716	ENSMUSG00000034354	11	4480868	4594863	-1	0	0	0	21	0	0	0	0	39	0	172	M0QW74	
ENSMUST00000130717	ENSMUSG00000025786	9	123066160	123113205	-1	4	5	5	27	3	4	9	16	16	1	10	D3Z2A6	
ENSMUST00000130718						4	1	0	0	3	0	2	2	4	0	3		
ENSMUST00000130719						0	0	2	1	1	1	0	64	0	35	0		
ENSMUST00000130720	ENSMUSG00000005268	15	10177238	10349180	1	0	1	0	0	0	0	0	0	0	0	0	E9Q2L5	
ENSMUST00000130721	ENSMUSG00000067367	5	38220470	38234306	1	0	0	0	0	0	0	0	0	5	0	6	D3Z7N3	
ENSMUST00000130723						2	0	3	1	2	0	2	3	3	5	13		
ENSMUST00000130725						15	9	24	152	18	13	0	0	0	0	0		
ENSMUST00000130726						7	6	15	23	5	4	0	0	0	0	0		
ENSMUST00000130727						36	9	25	68	23	16	15	126	34	10	23		
ENSMUST00000130728						31	23	33	13	29	20	0	5	4	0	7		
ENSMUST00000130729	ENSMUSG00000027067	2	85037234	85047109	1	0	0	0	0	0	0	55	0	25	0	72	A2AW05	
ENSMUST00000130730						3	2	0	4	3	2	0	4	2	0	2		
ENSMUST00000130731						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000130732	ENSMUSG00000031274	X	141475385	141689234	1	0	0	1	0	0	0	0	0	0	0	0	F7CK55	
ENSMUST00000130735	ENSMUSG00000039285	9	118040499	118069794	1	0	0	0	0	0	0	100	225	165	9	57	F7A092	
ENSMUST00000130736						24	11	47	65	28	28	275	915	556	60	1213		
ENSMUST00000130737						1	3	2	6	9	5	0	0	0	0	5		
ENSMUST00000130738						2	6	6	0	0	1	5	0	3	4	32		
ENSMUST00000130739	ENSMUSG00000056752	11	65831282	66168551	-1	0	2	3	0	0	2	0	0	0	0	0	B7FAT5	
ENSMUST00000130740	ENSMUSG00000020564	12	33147693	33375659	1	1	0	0	0	0	1	0	0	2	0	0	F6RPR7	
ENSMUST00000130741						0	0	8	0	0	0	0	0	0	0	0		
ENSMUST00000130742						3	6	16	16	4	2	0	5	0	2	2		
ENSMUST00000130743						3	3	4	6	3	6	26	114	40	9	71		
ENSMUST00000130747						2	0	12	8	4	3	14	19	55	0	35		
ENSMUST00000130748						37	24	54	26	31	24	4	7	9	0	7		
ENSMUST00000130749						0	0	0	0	0	0	5	0	1	6	3		
ENSMUST00000130750						2	3	1	0	0	2	4	6	8	0	6		
ENSMUST00000130751						2	0	1	1	0	0	0	3	0	0	0		
ENSMUST00000130752	ENSMUSG00000013539	16	18300825	18348103	-1	0	0	0	11	2	0	6	1	2	1	1	D3Z2V8	
ENSMUST00000130754	ENSMUSG00000036707	1	85793441	85851576	1	4	1	0	3	1	2	4	0	0	0	0	D3YV52	
ENSMUST00000130755						0	0	0	24	0	0	3	0	3	0	9		
ENSMUST00000130756						0	0	0	0	0	0	0	0	11	0	0		
ENSMUST00000130757						3	0	1	2	5	1	2	2	2	1	8		
ENSMUST00000130758						2	0	3	3	2	0	0	0	0	0	0		
ENSMUST00000130759						0	0	0	3	1	0	12	321	58	31	41		
ENSMUST00000130760						1	3	11	0	3	0	18	78	13	11	18		
ENSMUST00000130761	ENSMUSG00000027523	2	174284320	174346744	1	0	0	0	0	0	0	1	5	4	0	0	A6PW71	
ENSMUST00000130762						0	0	0	67	3	0	0	0	0	0	0		
ENSMUST00000130763	ENSMUSG00000006301	1	74288247	74305622	-1	11	10	19	10	9	8	0	0	0	0	0	D3Z225	
ENSMUST00000130764	ENSMUSG00000013338	2	156019139	156052947	-1	6	0	2	0	0	1	0	0	0	0	0	F6YZT0	
ENSMUST00000130765	ENSMUSG00000079020	15	73577424	73645762	-1	0	0	0	12	0	0	15	2	11	5	2	D3Z0C0	
ENSMUST00000130767						5	2	7	6	2	2	0	10	7	0	10		
ENSMUST00000130768						0	0	0	0	0	0	0	0	0	8	17		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130769						0	0	0	308	7	6	0	2	1	0	0		
ENSMUST00000130772						17	5	31	16	17	9	6	23	6	5	29		
ENSMUST00000130774	ENSMUSG00000018669	11	96907426	96916496	-1	1	3	0	0	0	0	4	7	0	0	3	A2A6E0	
ENSMUST00000130775						1	2	0	7	1	0	0	0	0	0	0		
ENSMUST00000130776	ENSMUSG00000028603	4	108043839	108144998	-1	0	0	0	0	1	1	0	0	0	0	0	A2APS5	
ENSMUST00000130778	ENSMUSG00000027879	3	97901190	97923276	1	2	0	0	43	6	2	253	1019	367	581	282	D6RES2	
ENSMUST00000130779						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130780	ENSMUSG00000032782	11	69299487	69323775	-1	0	0	0	0	0	0	0	6	0	0	1	H3BJ47	
ENSMUST00000130782	ENSMUSG00000073468	17	8311102	8396852	1	0	0	0	0	1	0	4	0	6	2	5	D6RFQ7	
ENSMUST00000130784						15	9	19	24	13	3	0	2	2	1	1		
ENSMUST00000130785	ENSMUSG00000079304	6	128375456	128385144	1	2	7	15	10	11	4	0	0	1	0	1		
ENSMUST00000130786	ENSMUSG00000039364	11	121053458	121063569	-1	1	3	8	2	2	0	0	0	0	0	0	A2ABP5	
ENSMUST00000130787						1	0	0	0	3	0	0	0	0	0	2		
ENSMUST00000130788						0	1	5	23	2	0	2	4	4	0	10		
ENSMUST00000130789						14	16	43	11	27	13	17	111	32	8	111		
ENSMUST00000130790						1	2	6	2	4	1	0	0	3	0	0		
ENSMUST00000130793						1	0	1	0	2	0	0	0	4	0	4		
ENSMUST00000130795						9	4	9	5	6	1	4	6	4	4	12		
ENSMUST00000130796						0	0	0	0	0	0	0	2	0	4	0		
ENSMUST00000130797						12	10	8	22	11	5	0	4	0	0	5		
ENSMUST00000130798	ENSMUSG00000032384	9	65908924	66045015	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130799	ENSMUSG00000021514	13	65278814	65304221	1	11	2	17	6	9	3	39	54	53	48	24	E9Q628	
ENSMUST00000130800						2	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000130801	ENSMUSG00000024457	17	36837134	36859398	1	0	0	0	0	0	0	0	0	0	2	0	B8JJ57	
ENSMUST00000130802	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	0	0	3	0	12	3	0	A3KG40	
ENSMUST00000130803	ENSMUSG00000028793	4	129058271	129085886	1	2	6	0	0	6	0	9	0	20	0	22	F6TQN1	
ENSMUST00000130804						4	1	5	0	0	0	4	19	2	14	20		
ENSMUST00000130805						60	86	94	55	48	22	3	15	9	1	28		
ENSMUST00000130806	ENSMUSG00000027601	3	19187327	19220817	1	0	0	4	0	0	0	0	0	0	0	0	D3YZ89	
ENSMUST00000130807						2	4	5	10	1	1	0	2	2	0	0		
ENSMUST00000130808						4	3	8	100	7	4	2	0	0	0	2		
ENSMUST00000130809						0	0	2	0	0	6	37	335	209	90	160		
ENSMUST00000130810						5	0	8	7	0	4	0	0	0	0	0		
ENSMUST00000130811	ENSMUSG00000020283	11	23646479	23665959	-1	0	0	0	84	0	0	3	39	18	29	14	D6RH41	
ENSMUST00000130813	ENSMUSG00000022973	16	90936092	91011308	-1	0	0	0	0	0	0	95	0	304	18	300	D3Z1M7	
ENSMUST00000130814						0	0	3	0	0	0	0	0	1	0	1		
ENSMUST00000130815						2	1	0	0	0	2	0	6	2	0	3		
ENSMUST00000130816						1	0	3	7	2	2	0	0	0	0	0		
ENSMUST00000130817	ENSMUSG00000030246	6	142490249	142507957	-1	0	0	0	2	0	0	0	3	0	0	0		
ENSMUST00000130818	ENSMUSG00000071533	16	56007245	56029739	-1	0	0	0	2	0	0	84	298	142	134	107	D6RGL8	
ENSMUST00000130819	ENSMUSG00000028708	4	115839198	115879250	1	0	0	0	0	0	0	0	0	0	0	0	F6VT22	
ENSMUST00000130820						13	10	13	15	9	7	4	10	19	0	36		
ENSMUST00000130821						0	0	0	194	0	0	0	0	0	0	0		
ENSMUST00000130822	ENSMUSG00000035208	11	83002158	83020810	-1	0	1	1	6	0	0	14	10	41	15	48	A0A0A0MQG0	
ENSMUST00000130823						0	0	0	1	0	0	0	0	0	0	1		
ENSMUST00000130824						2	6	13	0	1	0	0	0	0	0	1		
ENSMUST00000130825	ENSMUSG00000063245	4	146610961	146658160	1	27	17	33	33	31	7	5	22	43	80	22	A2A8V4	
ENSMUST00000130826						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130828	ENSMUSG00000028689	4	116708509	116751206	1	0	0	0	0	0	0	0	0	0	0	0	A2AGD6	
ENSMUST00000130829	ENSMUSG00000038112	9	39587396	39604403	-1	0	1	0	0	3	0	0	0	0	0	0	D3Z5E6	
ENSMUST00000130830						17	14	19	10	17	9	0	1	0	3	3		
ENSMUST00000130831						7	1	5	21	12	2	0	0	0	0	0		
ENSMUST00000130832	ENSMUSG00000031166	X	8123301	8132892	-1	0	14	28	14	13	0	186	484	245	0	360	S4R225	
ENSMUST00000130833						0	1	0	3	0	0	12	12	0	0	0		
ENSMUST00000130834	ENSMUSG00000028347	4	48585174	48663131	1	0	6	7	8	8	4	0	0	0	1	6	A0A0A0MQL0	
ENSMUST00000130835						2	1	1	0	7	0	8	4	14	0	11		
ENSMUST00000130836						0	0	0	0	0	0	0	2	6	0	0		
ENSMUST00000130838						1	0	5	0	2	3	13	34	29	2	50		
ENSMUST00000130839	ENSMUSG00000036892	7	30493622	30513402	1	0	0	0	0	0	0	0	0	0	0	0	D6RET3	
ENSMUST00000130841						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130842	ENSMUSG00000029234	5	76183880	76209245	1	0	2	0	0	0	3	0	0	0	19	0	D3YV67	
ENSMUST00000130843						2	2	1	138	13	0	4	11	0	6	0		
ENSMUST00000130844	ENSMUSG00000030731	7	44384102	44400187	1	3	1	0	4	0	0	0	0	0	0	0	D3YYS0	
ENSMUST00000130845	ENSMUSG00000006932	9	120929216	120960507	1	0	0	0	0	0	0	0	4	0	0	0	D3Z5Q1	
ENSMUST00000130846	ENSMUSG00000048126	1	90765923	90843971	-1	0	15	0	0	17	4	0	0	0	0	0	D3YWD1	
ENSMUST00000130848						3	0	3	2	5	0	0	4	8	0	2		
ENSMUST00000130849						4	5	4	1	11	2	0	0	0	0	0		
ENSMUST00000130850	ENSMUSG00000031626	8	45507788	45827906	1	1	0	0	0	0	0	0	0	0	0	0	D3Z0N2	
ENSMUST00000130851	ENSMUSG00000030204	6	135011612	135023776	1	0	2	1	1	2	0	0	0	0	0	0	D3YWF9	
ENSMUST00000130852						0	0	17	0	0	0	0	0	0	0	0		
ENSMUST00000130853	ENSMUSG00000021850	14	49226358	49245428	-1	6	9	0	3	3	5	0	0	0	0	0	A9C480	
ENSMUST00000130854						77	48	101	74	72	59	4	59	13	6	45		
ENSMUST00000130855	ENSMUSG00000040415	10	127190378	127195728	-1	0	3	20	22	8	5	0	15	0	0	0	D3YV13	
ENSMUST00000130856						5	9	9	5	0	3	0	0	8	0	7		
ENSMUST00000130857						11	4	20	17	12	2	9	50	13	5	21		
ENSMUST00000130858	ENSMUSG00000042613	3	89436706	89450952	1	0	0	0	0	0	0	0	0	0	0	0	D3YUE1	
ENSMUST00000130861						6	4	4	4	4	3	0	0	4	0	0		
ENSMUST00000130864	ENSMUSG00000041642	1	136131389	136177998	1	27	46	66	6	72	0	47	0	86	0	48	E9Q0A4	
ENSMUST00000130865	ENSMUSG00000019810	10	13499540	13519035	1	0	0	0	14	0	1	0	0	0	0	0		
ENSMUST00000130867						4	0	15	0	6	5	4	0	1	0	2		
ENSMUST00000130868	ENSMUSG00000039903	16	90826719	90905109	1	7	5	6	110	3	4	0	0	0	2	0	D6RCJ7	
ENSMUST00000130869						1	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000130870	ENSMUSG00000084897	2	155018266	155027104	1	796	751	670	677	995	563	9	116	47	19	95	Q3TZL0	
ENSMUST00000130871	ENSMUSG00000098374	17	29614876	29703359	1	57	61	115	42	62	33	409	1133	614	55	768	E0CXC2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130873						7	7	14	22	8	3	0	0	0	0	0		
ENSMUST00000130876	ENSMUSG00000026623	1	191717834	191784255	1	0	0	0	4	4	1	28	34	94	0	53	D3YVK0	
ENSMUST00000130877						60	54	246	189	75	27	8	8	6	0	11		
ENSMUST00000130878						2	0	15	3	0	0	0	0	0	0	0		
ENSMUST00000130879						37	20	210	62	33	18	0	8	2	1	8		
ENSMUST00000130880	ENSMUSG00000040621	X	166170454	166190512	1	92	61	431	112	61	42	15	33	12	24	16		Q8BHE1
ENSMUST00000130881	ENSMUSG00000027610	2	155563181	155592810	-1	2	0	5	0	0	4	32	73	30	3	11	Q3UEE2	
ENSMUST00000130883						13	8	23	15	12	7	0	1	1	0	0		
ENSMUST00000130885						0	0	1	0	1	0	0	20	5	0	0		
ENSMUST00000130886						19	20	49	32	21	11	16	84	18	151	23		
ENSMUST00000130887						43	19	143	210	31	12	1	0	0	0	0		
ENSMUST00000130888						2	2	15	8	6	2	0	0	0	0	2		
ENSMUST00000130889						6	7	6	3	8	5	0	0	0	0	0		
ENSMUST00000130890						275	283	152	174	302	139	10	26	20	18	38		
ENSMUST00000130891	ENSMUSG00000071281	13	67705306	67729119	-1	0	0	6	1	0	0	0	2	12	3	4	B8JJY0	
ENSMUST00000130893						2	0	8	7	4	0	2	3	5	0	5		
ENSMUST00000130894						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000130896						5	2	10	7	3	1	0	0	1	0	0		
ENSMUST00000130897						3	2	1	7	0	0	8	24	16	0	12		
ENSMUST00000130899						2	3	2	2	4	3	0	0	0	0	2		
ENSMUST00000130900	ENSMUSG00000038764	4	57190841	57301837	-1	5	5	43	3	6	2	3	9	1	0	1	A2ALL0	
ENSMUST00000130901	ENSMUSG00000050944	11	77089915	77188968	-1	6	0	69	0	0	3	6	0	1	0	13	A0A0A0MQI1	
ENSMUST00000130902	ENSMUSG00000052926	8	84956610	84969767	-1	0	5	23	0	2	3	0	0	0	0	6	D3Z6L4	
ENSMUST00000130903						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000130904						2	2	0	0	1	0	18	59	0	6	10		
ENSMUST00000130905						1	3	11	2	2	1	0	2	0	3	0		
ENSMUST00000130906						0	0	0	0	2	0	0	3	0	0	0		
ENSMUST00000130907	ENSMUSG00000030505	7	49778346	49858265	1	0	1	3	1	2	0	0	0	0	0	0	F6ZU11	
ENSMUST00000130908						1	0	4	1	0	0	49	298	70	10	136		
ENSMUST00000130909	ENSMUSG00000015214	X	71364760	71419196	1	0	0	0	0	0	0	0	0	0	0	0	Q8CIU5	
ENSMUST00000130910						0	0	9	3	0	0	3	0	0	4	0		
ENSMUST00000130911	ENSMUSG00000020248	10	82748701	82764144	-1	3	3	1	19	3	0	216	900	406	498	241		P63139
ENSMUST00000130913						3	0	3	2	2	3	0	0	0	0	0		
ENSMUST00000130914	ENSMUSG00000027011	2	78868124	78921293	1	0	0	20	0	1	0	0	0	0	18	36	B2FDH0	
ENSMUST00000130915	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	4	0	0	0	0	0	0	0	0	A2AT67	
ENSMUST00000130916	ENSMUSG00000035086	11	101285952	101302286	-1	24	29	24	64	26	14	14	120	22	14	41		O88597
ENSMUST00000130917						3	7	5	3	11	2	2	30	12	3	19		
ENSMUST00000130918						1	1	2	2	1	1	4	28	17	0	31		
ENSMUST00000130920	ENSMUSG00000022770	16	31663443	31873356	1	0	0	0	0	0	0	8	38	30	1	8	S4R2V5	
ENSMUST00000130921						112	134	177	165	157	97	5	64	20	20	41		
ENSMUST00000130922	ENSMUSG00000048922	14	67676331	67715841	-1	19	26	14	8	19	5	4	24	16	5	10	F6RTJ7	
ENSMUST00000130923						3	0	3	42	13	4	0	0	0	0	1		
ENSMUST00000130924	ENSMUSG00000038205	3	97658193	97673812	1	0	0	0	4	11	0	0	0	0	0	0	D6RH98	
ENSMUST00000130925	ENSMUSG00000041890	5	114727407	114775517	-1	1	2	4	0	0	2	62	8	180	0	96	F6SLJ2	
ENSMUST00000130926						0	2	0	0	0	1	48	0	17	0	48		
ENSMUST00000130927	ENSMUSG00000025911	1	9547948	9580673	1	2	3	0	0	2	1	0	0	5	0	0	M0QWG3	
ENSMUST00000130928						0	3	1	4	0	2	2	5	1	0	9		
ENSMUST00000130929						0	1	0	35	3	0	0	2	0	0	2		
ENSMUST00000130930	ENSMUSG00000038215	8	56531522	56551047	-1	0	0	2	13	0	2	0	13	7	0	0	D3YXR3	
ENSMUST00000130931						0	4	2	92	6	0	0	3	3	0	8		
ENSMUST00000130932						13	8	54	31	16	3	6	24	25	4	31		
ENSMUST00000130933	ENSMUSG00000037868	10	67535475	67542188	1	0	0	5	6	0	5	0	0	0	0	1	D3Z4X9	
ENSMUST00000130934						3	3	0	2	4	4	0	62	10	7	18		
ENSMUST00000130935						0	0	4	3	0	0	5	3	5	0	8		
ENSMUST00000130936						4	1	1	46	4	0	0	0	0	0	0		
ENSMUST00000130938						0	1	0	24	0	1	2	0	0	0	0		
ENSMUST00000130939						0	0	2	6	1	0	0	0	0	0	0		
ENSMUST00000130940	ENSMUSG00000027523	2	174284320	174346744	1	0	0	0	0	0	0	0	0	0	0	0	A6PW70	
ENSMUST00000130941						6	1	8	3	6	1	0	0	0	0	0		
ENSMUST00000130942	ENSMUSG00000028601	4	108165437	108179308	1	3	0	9	5	5	2	0	3	0	0	0	E0CXC8	
ENSMUST00000130944						2	4	10	24	7	0	0	0	0	0	0		
ENSMUST00000130946	ENSMUSG00000059208	17	33646233	33686860	-1	0	0	0	0	0	0	11	76	2	0	0	F7C9U3	
ENSMUST00000130947						5	3	0	0	3	0	0	0	0	0	2		
ENSMUST00000130948						0	0	0	16	0	0	6	0	0	0	0		
ENSMUST00000130949						0	0	0	0	0	0	0	0	5	0	2		
ENSMUST00000130950	ENSMUSG00000051236	10	120781096	120899101	-1	2	3	4	14	8	3	0	0	1	0	1	D3YUC9	
ENSMUST00000130951						0	0	0	0	0	0	0	0	2	0	3		
ENSMUST00000130954						0	4	4	6	1	0	24	49	29	5	75		
ENSMUST00000130955						2	0	3	63	4	3	0	0	0	0	0		
ENSMUST00000130956						2	0	5	1	0	3	0	0	0	0	0		
ENSMUST00000130957						38	40	316	55	32	6	11	63	17	1	25		
ENSMUST00000130958						2	1	2	0	3	0	2	0	0	0	0		
ENSMUST00000130959						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000130960						0	0	0	42	1	2	0	0	0	0	0		
ENSMUST00000130962						0	0	0	0	1	0	0	0	0	0	2		
ENSMUST00000130964						0	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000130965						1	2	3	0	1	0	0	0	2	0	4		
ENSMUST00000130967	ENSMUSG00000071337	6	86404219	86433405	1	0	0	0	0	0	0	0	2	17	0	13	Q8CII5	
ENSMUST00000130968						24	8	95	15	14	5	2	3	0	0	2		
ENSMUST00000130969						55	56	47	59	57	18	15	109	53	7	37		
ENSMUST00000130970						6	3	5	3	0	1	0	0	0	0	1		
ENSMUST00000130971						0	0	13	0	0	0	0	0	0	0	0		
ENSMUST00000130972	ENSMUSG00000000731	10	78030022	78043610	-1	1	0	0	2	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000130973						2	0	0	2	2	0	0	0	0	0	14		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000130974						3	2	3	0	6	0	0	0	0	0	0		
ENSMUST00000130975						0	0	5	28	0	0	0	0	0	2	0		
ENSMUST00000130976	ENSMUSG00000031389	X	73891442	73921870	-1	2	0	3	3	0	0	0	118	46	35	209	E9PYS6	
ENSMUST00000130978						24	15	39	172	33	17	16	4	26	0	164		
ENSMUST00000130979						2	1	0	0	7	0	0	0	0	0	2		
ENSMUST00000130980	ENSMUSG00000031229	X	105797615	105929403	-1	1	0	0	58	2	0	0	5	21	15	13	A6PWL2	
ENSMUST00000130981						1	6	0	0	4	0	3	49	13	3	24		
ENSMUST00000130982						1	1	4	0	0	0	4	13	3	2	0		
ENSMUST00000130983						2	0	6	8	3	3	0	0	0	0	0		
ENSMUST00000130984						2	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000130985						8	4	8	8	5	1	0	0	0	0	0		
ENSMUST00000130986	ENSMUSG00000038914	2	180657964	180709999	-1	16	6	0	0	20	0	0	0	0	0	0		Q8C9B9
ENSMUST00000130987						0	0	0	0	0	1	0	0	0	6	0		
ENSMUST00000130989	ENSMUSG00000024158	17	24840143	24864450	1	1	0	6	19	0	0	0	27	19	13	11	D3YWI0	
ENSMUST00000130990	ENSMUSG00000037169	12	12936096	12941914	-1	14	8	22	35	19	0	4	6	1	0	2	Q3UII1	P03966
ENSMUST00000130991	ENSMUSG00000036890	2	44564412	44927657	-1	0	0	0	0	0	0	0	0	10	23	0	B1AY87	
ENSMUST00000130992	ENSMUSG00000024403	17	35233660	35238767	1	1	1	1	37	5	0	10	20	19	1	10	G5E923	
ENSMUST00000130993						0	1	0	0	0	0	1	0	0	0	4		
ENSMUST00000130994	ENSMUSG00000000561	3	105959369	105970037	1	60	43	102	56	77	45	44	545	51	13	84	D6RIL4	
ENSMUST00000130995	ENSMUSG00000026466	1	156004599	156036480	-1	0	0	0	187	0	0	0	0	0	0	0	Q3UE61	
ENSMUST00000130996						2	2	0	1	0	3	0	4	0	0	0		
ENSMUST00000130997	ENSMUSG00000037640	7	27731389	27753702	1	1	0	0	2	1	1	0	0	0	4	0	D3YUF8	
ENSMUST00000130998	ENSMUSG00000070880	2	70553072	70602014	1	2	7	3	12	14	0	0	0	0	0	0	D3Z1L8	
ENSMUST00000130999	ENSMUSG00000058070	12	108370957	108539617	1	0	0	2	0	0	0	0	0	4	0	0	D6RII3	
ENSMUST00000131000	ENSMUSG00000049739	7	127876221	127885996	1	11	5	8	85	17	2	84	36	126	3	68	D3Z083	
ENSMUST00000131001						1	0	0	1	0	3	0	0	0	0	2		
ENSMUST00000131002	ENSMUSG00000006307	7	30568858	30588726	-1	1	7	66	0	13	9	484	1148	520	58	767	F6W623	
ENSMUST00000131003	ENSMUSG00000033149	16	45746243	45953598	-1	0	0	0	0	0	0	2	0	4	10	6	F6QU68	
ENSMUST00000131004						4	0	10	0	3	0	0	0	0	0	0		
ENSMUST00000131005						0	1	0	0	5	0	0	39	8	0	9		
ENSMUST00000131008						7	0	7	0	0	1	0	50	5	0	16		
ENSMUST00000131009						0	0	0	2	2	1	0	0	0	0	0		
ENSMUST00000131010						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000131011	ENSMUSG00000017778	13	86044816	86046904	-1	6	5	9	20	12	3	174	140	31	140	27		P17665
ENSMUST00000131012						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000131014						1	0	2	17	0	0	1	1	0	49	3		
ENSMUST00000131015						4	0	4	6	10	3	0	0	21	6	35		
ENSMUST00000131016	ENSMUSG00000041890	5	114727407	114775517	-1	3	1	0	15	2	1	0	0	13	0	8	D3Z409	
ENSMUST00000131017	ENSMUSG00000056724	9	110624789	110654161	-1	0	0	0	3	9	8	804	2372	539	107	758	F6ZZB1	
ENSMUST00000131018	ENSMUSG00000013033	8	83900105	83941954	1	0	0	2	96	0	0	3	0	0	1	0		
ENSMUST00000131020						6	3	1	0	2	3	0	0	0	0	0		
ENSMUST00000131022						2	4	3	54	6	0	1	5	1	0	6		
ENSMUST00000131023	ENSMUSG00000000290	10	77530252	77565708	1	0	0	0	1	0	0	6	5	28	6	29	D3Z1S4	
ENSMUST00000131024	ENSMUSG00000010358	11	101448407	101458698	1	3	0	6	0	0	8	23	98	20	13	35	D6RFB1	
ENSMUST00000131025						0	0	0	0	0	0	92	143	48	27	29		
ENSMUST00000131026						5	0	1	6	2	0	0	0	0	0	0		
ENSMUST00000131027	ENSMUSG00000059857	3	109780040	110144011	-1	0	0	0	0	0	0	0	0	0	0	0		Q8R4G0
ENSMUST00000131028	ENSMUSG00000000731	10	78030022	78043610	-1	306	226	541	810	345	119	4	8	0	4	10	D6RDQ5	
ENSMUST00000131030						0	1	4	1	0	2	2	12	10	0	12		
ENSMUST00000131031	ENSMUSG00000001436	10	77032241	77061002	1	2	2	5	1	1	5	0	0	0	0	0	F6YWA3	
ENSMUST00000131032						3	2	20	23	3	0	0	0	0	0	9		
ENSMUST00000131033	ENSMUSG00000021098	12	72881109	72940774	-1	3	3	5	9	2	0	0	0	0	0	0		Q9CTN5
ENSMUST00000131034						0	0	17	14	2	1	3	18	5	17	5		
ENSMUST00000131035	ENSMUSG00000070327	11	119393100	119487418	1	111	0	0	101	81	0	0	4	0	23	2		E9Q555
ENSMUST00000131036						1	1	2	0	0	1	1	28	5	7	15		
ENSMUST00000131037						0	5	34	0	20	12	0	0	0	0	0		
ENSMUST00000131039						39	30	146	128	68	32	1	0	1	0	3		
ENSMUST00000131040	ENSMUSG00000036892	7	30493622	30513402	1	0	0	0	0	0	0	0	0	0	0	0	F7CED2	
ENSMUST00000131041	ENSMUSG00000095545	2	175692223	175703646	-1	0	0	0	0	0	0	0	0	0	3	0	E9PXD4	
ENSMUST00000131043						25	23	33	16	19	8	1	2	2	7	0		
ENSMUST00000131045						0	1	0	3	0	1	4	13	2	2	4		
ENSMUST00000131046						55	71	246	186	66	37	5	3	4	0	11		
ENSMUST00000131047						4	2	2	3	0	0	0	0	0	0	0		
ENSMUST00000131048	ENSMUSG00000030495	7	35186385	35201114	1	0	4	0	19	10	5	0	0	0	0	0	D6RII2	
ENSMUST00000131049						2	0	3	0	0	0	0	35	7	0	6		
ENSMUST00000131050						0	0	2	15	0	0	0	0	0	0	0		
ENSMUST00000131051						1	1	0	0	0	0	0	15	5	0	7		
ENSMUST00000131052						4	6	7	1	2	0	21	25	9	0	12		
ENSMUST00000131053						4	2	7	6	1	0	1	1	5	0	1		
ENSMUST00000131054						36	20	51	63	31	16	3	15	9	0	23		
ENSMUST00000131055						3	10	7	56	9	4	0	0	0	0	0		
ENSMUST00000131056	ENSMUSG00000042625	17	56560965	56584585	-1	0	1	0	18	0	2	46	458	126	41	232	F6WIZ2	
ENSMUST00000131058	ENSMUSG00000040181	1	162829561	162866610	-1	3	9	0	3	4	1	0	0	0	0	0	D3Z0T2	
ENSMUST00000131059						6	7	10	68	0	3	11	21	14	0	38		
ENSMUST00000131060						0	3	0	0	5	2	0	0	0	0	0		
ENSMUST00000131062						4	3	1	4	11	1	0	0	0	0	0		
ENSMUST00000131063	ENSMUSG00000022779	16	16870736	16892990	1	0	0	0	6	0	0	0	0	3	0	4	D3Z758	
ENSMUST00000131065						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000131066	ENSMUSG00000044566	13	38006052	38037069	-1	0	0	0	0	0	0	0	0	1	0	0	A6X912	
ENSMUST00000131068						1	2	0	0	4	1	0	0	0	0	0		
ENSMUST00000131069						66	52	178	283	98	51	14	56	9	23	82		
ENSMUST00000131070	ENSMUSG00000056999	19	37268743	37337852	-1	11	10	34	7	19	8	62	178	129	43	128	F6RPJ9	
ENSMUST00000131071						0	0	13	9	3	3	0	0	0	0	9		
ENSMUST00000131072	ENSMUSG00000051313	2	90000145	90003322	1	0	8	0	0	6	0	0	0	0	0	0	A2ATM2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131073						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131074						7	6	17	0	2	4	0	0	1	0	1		
ENSMUST00000131075	ENSMUSG00000009535	18	68300355	68324852	1	0	2	0	0	0	0	0	2	0	3	0	D3Z478	
ENSMUST00000131076						2	3	6	0	4	2	502	132	467	0	323		
ENSMUST00000131077	ENSMUSG00000039382	X	7721973	7728201	1	0	2	0	0	0	0	0	0	0	0	10	F6YHS5	
ENSMUST00000131078						4	0	0	2	0	0	17	70	0	0	31		
ENSMUST00000131079	ENSMUSG00000054256	5	115429599	115455698	1	0	2	4	43	2	1	0	0	0	0	0		
ENSMUST00000131081						2	0	6	81	3	0	0	0	0	0	0		
ENSMUST00000131082						196	216	327	195	274	106	7	26	13	15	22		
ENSMUST00000131083						0	0	0	11	0	0	0	0	3	0	0		
ENSMUST00000131084						2	5	3	4	6	2	0	3	10	0	18		
ENSMUST00000131086						6	1	7	35	5	2	0	0	0	1	5		
ENSMUST00000131087	ENSMUSG00000048481	7	18991245	19001766	1	11	0	20	144	3	7	25	41	4	6	20		Q8R4U1
ENSMUST00000131088						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131089						1	1	22	53	5	0	0	0	0	0	0		
ENSMUST00000131090						5	3	3	4	5	0	0	0	0	0	0		
ENSMUST00000131091						0	0	1	4	0	0	0	0	16	0	0		
ENSMUST00000131092	ENSMUSG00000027238	2	121545529	121807087	-1	0	0	0	0	3	0	0	1	0	0	0	F6XLQ6	
ENSMUST00000131094						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131095	ENSMUSG00000037784	9	99629496	99669256	1	0	0	1	58	0	1	0	0	0	0	0	D3Z4F5	
ENSMUST00000131096						4	8	1	1	2	1	1	0	0	0	0		
ENSMUST00000131097	ENSMUSG00000052395	14	30654360	30691317	1	3	28	0	0	0	0	0	35	41	0	82	E9Q0V1	
ENSMUST00000131098	ENSMUSG00000089774	16	92058322	92087473	1	2	1	1	0	0	0	0	0	0	0	0	V9GXD5	
ENSMUST00000131100						0	0	0	27	3	2	0	0	3	16	6		
ENSMUST00000131101						0	3	0	44	0	0	23	205	94	5	214		
ENSMUST00000131102						14	5	12	13	18	4	0	0	0	0	0		
ENSMUST00000131103	ENSMUSG00000062825	11	120345690	120348542	-1	0	0	0	0	0	0	109	0	2968	13	2954	G3UYG0	
ENSMUST00000131104	ENSMUSG00000070426	7	102019137	102065469	-1	1	0	1	0	0	0	2	0	0	0	2	F6XTP0	
ENSMUST00000131105	ENSMUSG00000024339	17	34203527	34216321	1	0	0	1	3	3	0	0	0	0	0	10	A6X8J6	
ENSMUST00000131106	ENSMUSG00000003363	7	27532000	27553218	-1	0	1	0	0	3	2	3	2	0	0	3	D6RCG9	
ENSMUST00000131107						20	9	37	35	22	16	1	1	2	2	7		
ENSMUST00000131108						21	12	25	29	24	5	188	630	200	186	149		
ENSMUST00000131109	ENSMUSG00000026925	2	26396249	26409203	-1	5	6	12	0	5	0	0	61	0	2	0	F6X9A4	
ENSMUST00000131111						6	5	7	3	6	5	0	0	0	0	1		
ENSMUST00000131112	ENSMUSG00000026921	2	26580014	26593120	1	0	0	0	0	0	0	2	11	0	0	1	F7BU34	
ENSMUST00000131113	ENSMUSG00000028845	4	126322121	126325688	-1	0	0	0	9	0	0	0	0	0	0	0	A3KFY5	
ENSMUST00000131114						3	1	1	0	1	0	7	0	3	0	17		
ENSMUST00000131115						0	0	2	2	2	0	0	0	0	0	10		
ENSMUST00000131116	ENSMUSG00000009995	X	74281912	74290151	1	2	0	0	0	3	0	0	183	0	11	0	B7FAU2	
ENSMUST00000131117						3	0	6	1	3	1	0	0	0	0	1		
ENSMUST00000131118	ENSMUSG00000019564	10	79927043	79955018	1	2	2	13	119	0	8	26	19	78	2	39	D3YVQ2	
ENSMUST00000131119	ENSMUSG00000025903	1	4807788	4848410	1	0	0	0	2	0	1	11	33	96	25	20	D3YUG4	
ENSMUST00000131120						0	0	11	15	11	3	0	3	0	0	1		
ENSMUST00000131121						2	4	3	36	5	0	0	19	0	0	9		
ENSMUST00000131122						21	18	37	18	19	9	14	140	17	0	47		
ENSMUST00000131123						7	2	10	4	6	1	0	0	0	0	1		
ENSMUST00000131124	ENSMUSG00000048047	X	38189793	38197046	1	1	0	4	21	5	0	0	13	139	7	25	A2A3Z2	
ENSMUST00000131125						0	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000131126	ENSMUSG00000055541	7	4003402	4063204	-1	5	0	1	0	5	0	37	102	63	129	68	D6RGS7	Q8BG84
ENSMUST00000131127	ENSMUSG00000060212	8	125751508	125898317	-1	23	34	94	51	24	15	0	0	0	0	0		Q5DU28
ENSMUST00000131128	ENSMUSG00000066892	9	20618118	20644767	-1	0	0	18	252	29	21	17	67	23	0	242		
ENSMUST00000131130						0	0	0	0	0	0	7	0	0	40	0		
ENSMUST00000131131						0	0	8	0	8	3	178	13	129	50	244		
ENSMUST00000131132						1	0	1	12	2	2	0	0	0	0	4		
ENSMUST00000131134	ENSMUSG00000024330	17	34039437	34066685	1	7	0	17	41	6	12	0	7	11	0	16	I7HPY2	
ENSMUST00000131135	ENSMUSG00000020319	11	21572235	21898989	1	2	3	0	0	4	0	0	0	0	0	1	B1ATQ4	
ENSMUST00000131136	ENSMUSG00000022770	16	31663443	31873356	1	0	0	0	0	0	0	0	0	0	0	10	F6UDT8	
ENSMUST00000131137						0	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000131138	ENSMUSG00000013878	8	26119368	26143871	1	0	0	0	29	0	0	4	0	3	0	0	D3Z0A0	
ENSMUST00000131139						1	0	2	1	0	0	0	1	1	5	1		
ENSMUST00000131140						0	0	2	0	0	0	0	5	0	3	0		
ENSMUST00000131141						0	1	3	2	3	0	0	2	0	0	0		
ENSMUST00000131142						3	0	1	6	5	1	0	0	0	0	0		
ENSMUST00000131143	ENSMUSG00000063808	7	35276536	35318440	-1	26	9	0	0	0	1	0	0	72	12	24	D6RJ67	
ENSMUST00000131144	ENSMUSG00000038180	2	156065175	156070617	1	0	0	0	0	0	0	0	0	0	0	0	F6XNA5	
ENSMUST00000131145	ENSMUSG00000049488	4	12039355	12090020	-1	0	3	0	4	2	0	0	0	0	0	0	D6RGQ2	
ENSMUST00000131148						1	4	6	2	2	2	0	0	0	0	0		
ENSMUST00000131149						5	1	2	0	2	0	0	4	3	0	3		
ENSMUST00000131150						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000131151	ENSMUSG00000026226	1	86016816	86029958	1	2	0	18	9	0	0	0	0	0	0	0	F6UTK3	
ENSMUST00000131152	ENSMUSG00000039205	2	32352327	32380970	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVQ0	
ENSMUST00000131153						0	1	2	1	2	0	0	0	0	0	0		
ENSMUST00000131154						0	0	28	72	30	14	0	0	0	0	0		
ENSMUST00000131155	ENSMUSG00000031403	X	75095854	75109777	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCL7	
ENSMUST00000131156						3	3	35	8	4	2	0	5	2	0	0		
ENSMUST00000131157	ENSMUSG00000061689	2	156613705	156764363	1	0	0	0	8	0	0	63	31	31	0	57	H3BJD4	
ENSMUST00000131158						10	9	15	17	13	2	5	3	0	4	8		
ENSMUST00000131159						0	0	2	0	0	0	0	4	3	0	0		
ENSMUST00000131162						0	0	0	3	1	0	0	0	0	0	1		
ENSMUST00000131163						0	5	0	0	0	1	0	0	0	0	0		
ENSMUST00000131164						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000131165						0	0	2	2	2	0	0	0	0	0	5		
ENSMUST00000131166	ENSMUSG00000057068	5	92555069	92591279	1	0	0	5	6	0	0	0	0	0	0	0	E9Q0Z5	
ENSMUST00000131167						6	3	11	11	10	4	0	0	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131168						3	0	4	4	4	3	9	6	0	0	10		
ENSMUST00000131169						0	0	6	2	1	2	0	7	21	0	11		
ENSMUST00000131170						0	2	0	0	0	2	0	7	0	13	0		
ENSMUST00000131171						0	0	0	4	4	0	0	0	0	0	0		
ENSMUST00000131173	ENSMUSG00000029055	4	154983115	155056784	-1	5	0	16	3	1	1	0	0	0	0	0	F6UKG4	
ENSMUST00000131174						18	7	14	21	21	11	5	91	18	27	15		
ENSMUST00000131175	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	0	34	0	0	F6WYM0	
ENSMUST00000131176						96	87	101	88	140	83	6	68	13	92	35		
ENSMUST00000131177						21	0	25	15	0	12	0	11	16	22	10		
ENSMUST00000131178						0	0	0	0	0	0	5	0	3	0	2		
ENSMUST00000131179	ENSMUSG00000048922	14	67676331	67715841	-1	0	3	0	0	0	0	1	6	11	0	1	F6VP65	
ENSMUST00000131180	ENSMUSG00000074165	7	41633203	41651530	1	0	1	0	0	0	0	3	4	10	4	7	D3YVB5	
ENSMUST00000131181						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000131182						6	0	2	21	0	0	0	0	2	0	0		
ENSMUST00000131183						18	10	15	0	16	8	0	0	30	9	0		
ENSMUST00000131184	ENSMUSG00000023051	15	102518192	102523676	1	0	3	0	20	0	1	3	31	15	13	24	D6RE49	
ENSMUST00000131185						3	0	2	2	0	0	1	0	0	0	7		
ENSMUST00000131186	ENSMUSG00000019841	10	39732118	39875211	1	12	0	38	0	0	0	55	0	55	0	152	Q9Z281	
ENSMUST00000131187						3	3	1	0	1	1	0	0	0	0	0		
ENSMUST00000131191						3	6	7	0	0	5	5	9	8	52	15		
ENSMUST00000131192	ENSMUSG00000027087	2	83724397	83806916	1	1	0	0	0	0	0	0	13	2	1	0	F6RWM8	
ENSMUST00000131193	ENSMUSG00000020873	11	95384692	95391776	1	0	4	0	0	0	1	103	391	173	278	136	E0CXH1	
ENSMUST00000131194						0	0	0	0	1	0	8	27	10	0	17		
ENSMUST00000131195						4	0	19	94	13	7	0	35	647	4	544		
ENSMUST00000131196						0	0	1	34	0	0	0	0	0	0	0		
ENSMUST00000131197	ENSMUSG00000028402	4	81278500	81442815	-1	0	0	0	0	0	0	0	0	0	0	0	F7D0H8	
ENSMUST00000131199						3	0	3	5	3	3	0	0	0	0	0		
ENSMUST00000131200						1	0	6	3	4	1	3	5	13	0	3		
ENSMUST00000131201						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131202						0	0	6	0	0	1	10	1	0	0	0		
ENSMUST00000131203						0	0	5	4	0	3	31	79	28	113	30		
ENSMUST00000131204						9	4	5	10	8	5	28	297	42	73	90		
ENSMUST00000131205						5	0	6	2	3	2	1	0	1	2	0		
ENSMUST00000131206						1	1	1	0	2	4	4	50	4	6	11		
ENSMUST00000131208						0	0	4	9	3	3	0	3	3	0	13		
ENSMUST00000131209	ENSMUSG00000030769	7	123214780	123273253	1	0	0	33	2	5	0	0	1	1	0	0	F6WZD3	
ENSMUST00000131210						5	7	12	183	17	6	231	137	600	9	594		
ENSMUST00000131211						2	1	2	0	2	0	5	23	0	3	5		
ENSMUST00000131212						3	4	12	14	6	2	0	0	0	0	0		
ENSMUST00000131213	ENSMUSG00000063808	7	35276536	35318440	-1	0	7	26	9	15	8	0	0	0	15	0	D6RET6	
ENSMUST00000131214						1	0	4	0	0	0	97	84	87	44	0		
ENSMUST00000131217	ENSMUSG00000025583	11	119602905	119899576	1	3	0	0	3	1	0	0	0	0	0	3	F7B6I3	
ENSMUST00000131218						3	3	2	6	4	0	1	2	0	0	1		
ENSMUST00000131219						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000131220						2	4	9	3	5	0	3	40	16	4	46		
ENSMUST00000131224	ENSMUSG00000039936	4	149649168	149702571	-1	0	0	6	0	7	1	0	0	0	0	0	B1AS24	
ENSMUST00000131225						8	7	10	8	4	5	0	2	1	0	0		
ENSMUST00000131226						0	1	0	0	3	1	2	2	0	2	0		
ENSMUST00000131227						0	0	2	10	3	0	19	102	50	444	49		
ENSMUST00000131228	ENSMUSG00000035268	2	163658386	163726158	1	0	0	0	0	0	0	3	3	1	2	0	B7ZC22	
ENSMUST00000131229	ENSMUSG00000026811	2	32599709	32620806	1	2	0	6	0	3	1	0	0	4	0	0	Z4YLR0	
ENSMUST00000131230						5	0	20	9	7	5	12	20	8	0	14		
ENSMUST00000131231						1	2	4	0	1	3	0	0	0	0	0		
ENSMUST00000131232	ENSMUSG00000029016	4	148004259	148038821	-1	3	0	8	38	7	2	1	1	2	0	7	D6RHT0	
ENSMUST00000131233	ENSMUSG00000032235	9	69397906	69433122	1	1	0	0	0	0	0	0	0	0	0	0	D6RH44	
ENSMUST00000131234	ENSMUSG00000036062	4	42916660	42944752	1	3	0	0	0	1	2	0	0	0	0	0	S4R1R0	
ENSMUST00000131235	ENSMUSG00000042292	15	81012281	81190757	-1	0	0	14	27	13	0	32	0	28	0	104	D3YUI2	
ENSMUST00000131236						21	11	21	16	20	7	0	1	0	0	3		
ENSMUST00000131237	ENSMUSG00000052446	8	71951038	71993408	1	0	0	0	6	4	0	14	90	16	0	6	E9Q9F0	
ENSMUST00000131238	ENSMUSG00000022791	16	32643874	32683493	1	2	1	25	6	6	1	8	3	3	0	4	E9PWA3	
ENSMUST00000131239						2	1	6	0	6	1	0	0	0	0	2		
ENSMUST00000131240						3	1	0	0	1	0	21	0	37	14	2		
ENSMUST00000131241	ENSMUSG00000025268	X	150806370	150814345	-1	0	0	0	0	1	0	0	0	0	1	0	A2AG49	
ENSMUST00000131243						41	23	185	67	21	17	0	0	0	1	0		
ENSMUST00000131244						6	2	2	3	0	1	6	82	23	21	24		
ENSMUST00000131245	ENSMUSG00000043909	2	121193281	121271407	-1	0	0	0	0	0	0	0	0	39	0	45	A2AU90	
ENSMUST00000131246						0	0	5	56	4	2	1	2	4	0	7		
ENSMUST00000131247						3	0	7	6	7	3	4	18	0	0	11		
ENSMUST00000131250						3	3	3	0	1	3	0	4	2	2	0		
ENSMUST00000131251						60	51	121	68	86	36	3	8	2	1	6		
ENSMUST00000131252	ENSMUSG00000024949	19	6363690	6378030	1	12	11	30	131	24	19	127	600	194	40	231	Q3UI45	Q64213
ENSMUST00000131253	ENSMUSG00000069823	11	73395076	73399495	-1	1	4	3	3	2	4	0	0	0	0	0	B0QZP2	
ENSMUST00000131254	ENSMUSG00000008855	11	102194432	102230166	-1	0	0	0	33	0	0	0	0	0	0	1	B7ZDF6	
ENSMUST00000131255						17	11	51	42	26	16	313	1749	575	338	1171		
ENSMUST00000131256						0	0	0	0	0	0	13	5	0	0	0		
ENSMUST00000131257	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	0	8	0	0	0	0	5	0	0	E2QRQ3	
ENSMUST00000131258						18	18	25	18	28	16	1	10	4	3	12		
ENSMUST00000131259	ENSMUSG00000037475	X	41794991	41920674	-1	0	0	0	0	0	0	0	0	0	0	1	F6QCT0	
ENSMUST00000131260	ENSMUSG00000020812	11	116671660	116675799	1	2	0	0	0	1	0	0	4	2	0	0	E9PV55	
ENSMUST00000131261	ENSMUSG00000039678	2	30133746	30152013	1	1	1	3	0	1	0	0	6	2	0	0	D6RI34	
ENSMUST00000131262						0	1	0	0	0	0	4	11	9	0	15		
ENSMUST00000131263	ENSMUSG00000029201	5	65413221	65435949	-1	0	1	2	0	0	1	15	8	29	5	13	D3YXP9	
ENSMUST00000131264						9	5	10	0	11	0	0	74	36	30	18		
ENSMUST00000131265	ENSMUSG00000024851	19	4099998	4113965	1	2	2	0	78	3	5	19	16	16	0	63	D3YXW5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131266						9	17	24	8	16	1	0	14	1	1	2		
ENSMUST00000131267						0	0	0	48	0	0	0	0	0	0	0		
ENSMUST00000131268						0	0	0	0	0	0	0	0	1	1	0		
ENSMUST00000131269						2	1	5	2	1	0	2	2	2	7	1		
ENSMUST00000131270						41	42	259	93	55	34	6	6	2	6	14		
ENSMUST00000131271	ENSMUSG00000090247	10	128917882	128924035	-1	0	3	3	0	0	0	0	0	0	0	7	D3YVM8	
ENSMUST00000131272						0	0	0	0	2	0	1	2	1	0	0		
ENSMUST00000131273	ENSMUSG00000052430	3	141837136	142169425	-1	3	1	0	0	0	3	0	0	0	0	0	D6RET5	
ENSMUST00000131276						1	0	6	0	6	0	0	0	0	0	0		
ENSMUST00000131278						2	0	8	6	4	4	17	45	48	2	77		
ENSMUST00000131279						0	1	9	0	0	0	0	0	0	0	5		
ENSMUST00000131280	ENSMUSG00000037966	13	49187485	49196244	1	4	1	4	4	0	1	14	18	5	12	27	D6RFN5	
ENSMUST00000131281						8	7	15	12	14	5	0	0	0	0	2		
ENSMUST00000131282	ENSMUSG00000045751	4	24496451	24602950	1	4	3	17	4	4	1	0	5	0	0	0	G3UXR9	
ENSMUST00000131283	ENSMUSG00000020850	11	75486816	75509449	1	15	11	0	60	1	1	8	0	0	0	0	B7ZC27	
ENSMUST00000131284						25	35	99	67	50	13	31	97	43	20	103		
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ENSMUST00000131286						0	0	3	0	0	0	97	297	76	28	23		
ENSMUST00000131287						4	1	0	2	4	1	0	6	0	0	0		
ENSMUST00000131288	ENSMUSG00000018326	2	163994960	164018588	1	2	3	3	73	5	3	0	15	17	0	10	A2A5N1	
ENSMUST00000131289						0	3	3	3	2	0	8	0	8	0	2		
ENSMUST00000131290	ENSMUSG00000030798	7	45233632	45239115	-1	8	5	0	6	3	0	1022	532	804	49	612	D3Z0N6	
ENSMUST00000131291						0	0	4	19	0	0	13	38	28	36	33		
ENSMUST00000131292	ENSMUSG00000027439	2	148681023	148692949	1	3	0	11	108	9	0	0	2	0	0	3	A2ASL5	
ENSMUST00000131293						6	9	17	4	7	3	4	1	9	0	0		
ENSMUST00000131294						4	1	9	7	6	4	4	8	0	5	0		
ENSMUST00000131295						0	0	1	7	1	0	0	4	0	0	0		
ENSMUST00000131298	ENSMUSG00000038831	2	33133417	33371486	-1	11	19	0	0	0	2	0	119	220	16	201		A2AR50
ENSMUST00000131300						2	4	0	13	6	0	73	1868	1352	449	601		
ENSMUST00000131301	ENSMUSG00000028809	4	135320484	135353321	-1	0	0	28	0	0	0	26	0	0	0	6	F7BWM1	
ENSMUST00000131302						6	6	9	28	4	0	0	0	0	0	0		
ENSMUST00000131303	ENSMUSG00000075704	16	18426384	18479073	1	2	1	0	1	2	1	4	5	0	1	1		
ENSMUST00000131304	ENSMUSG00000034555	X	112011007	112127326	1	0	0	0	0	0	0	0	0	0	0	0	F6Z198	
ENSMUST00000131305						5	4	9	7	4	2	4	7	0	0	8		
ENSMUST00000131306	ENSMUSG00000021493	13	55495795	55513676	-1	14	5	22	49	15	6	6	83	22	0	54	B8JJB3	
ENSMUST00000131307						3	0	0	6	1	0	4	5	2	1	0		
ENSMUST00000131308						5	10	34	8	7	6	0	0	0	0	1		
ENSMUST00000131309	ENSMUSG00000007989	14	65201026	65262463	-1	26	24	19	23	25	6	2	12	4	2	5		Q61086
ENSMUST00000131310						2	0	3	0	0	0	20	16	47	20	34		
ENSMUST00000131311						1	3	1	0	1	0	0	0	0	0	0		
ENSMUST00000131312						953	781	3203	935	1090	453	21	62	54	7	68		
ENSMUST00000131313						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131315						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000131316	ENSMUSG00000027714	3	36552606	36565727	1	0	1	9	0	0	0	3	60	29	17	12	F6Y747	
ENSMUST00000131317	ENSMUSG00000006219	4	141576062	141606096	-1	3	0	12	1	1	1	0	0	0	0	0	A2ADF1	
ENSMUST00000131318	ENSMUSG00000045639	7	127607031	127615797	-1	0	0	5	2	0	0	0	0	0	0	0	D3Z5P9	
ENSMUST00000131319	ENSMUSG00000031137	X	59062145	59568071	-1	0	2	0	0	0	0	0	0	0	0	0	B1AU23	
ENSMUST00000131320	ENSMUSG00000030509	7	66644565	66689596	-1	8	25	0	0	15	0	631	3996	840	303	683	Q8BQC5	
ENSMUST00000131321	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000131322	ENSMUSG00000022914	16	95992092	96082526	-1	0	0	0	0	5	0	5	0	37	0	0	F6X674	
ENSMUST00000131323	ENSMUSG00000040701	14	55098578	55106593	-1	5	5	16	18	12	4	0	0	0	0	0	D6RFT7	
ENSMUST00000131325	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	5	3	0	0	0	0	0	0	S4R2T3	
ENSMUST00000131326						6	4	7	105	6	3	0	0	0	0	0		
ENSMUST00000131327						2	2	0	5	8	2	160	759	169	24	274		
ENSMUST00000131329						0	0	0	12	2	0	0	0	0	0	0		
ENSMUST00000131330						2	5	26	50	13	6	24	2	15	1	29		
ENSMUST00000131332	ENSMUSG00000025287	X	155262443	155297654	1	5	0	4	0	4	0	0	270	25	41	19	S4R266	
ENSMUST00000131333						2	3	0	58	3	0	0	0	1	0	0		
ENSMUST00000131335						0	2	4	0	0	0	0	0	0	0	0		
ENSMUST00000131337						2	4	0	6	0	0	0	0	0	0	0		
ENSMUST00000131338	ENSMUSG00000042647	5	121596775	121618938	-1	52	49	108	43	44	27	11	19	18	0	21	F6RGT6	
ENSMUST00000131339						0	1	0	1	1	0	14	61	32	32	54		
ENSMUST00000131340	ENSMUSG00000018442	11	71007164	71019841	-1	0	0	0	20	3	0	0	0	0	0	0	J3KMR6	
ENSMUST00000131341						0	2	1	6	2	3	0	0	0	0	1		
ENSMUST00000131343	ENSMUSG00000066892	9	20618118	20644767	-1	0	0	0	0	0	0	13	0	0	0	12	D3YY70	
ENSMUST00000131348	ENSMUSG00000036585	18	38838673	38929404	-1	21	15	0	11	24	18	0	0	0	2	3	D6RCX9	
ENSMUST00000131349						6	5	3	0	1	0	0	0	0	0	1		
ENSMUST00000131350						2	2	0	0	2	1	6	31	16	2	9		
ENSMUST00000131351	ENSMUSG00000059820	9	50605240	50617464	-1	6	8	11	55	15	4	77	467	136	127	98	E9PUQ3	
ENSMUST00000131352						1	4	11	13	3	1	1	3	0	0	0		
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ENSMUST00000131354						2	2	19	18	7	10	131	613	300	20	444		
ENSMUST00000131355						15	21	96	25	18	8	3	27	5	3	13		
ENSMUST00000131356	ENSMUSG00000025616	16	87454703	87483517	1	1	0	1	37	0	0	0	0	0	0	1	D3Z6E6	
ENSMUST00000131358						13	10	19	44	24	6	422	847	823	55	544		
ENSMUST00000131359						0	0	0	0	2	1	12	4	22	38	36		
ENSMUST00000131360						1	0	2	3	2	0	0	0	0	0	0		
ENSMUST00000131361						2	2	3	5	2	2	0	3	0	0	0		
ENSMUST00000131362						4	3	3	0	12	0	0	0	0	9	17		
ENSMUST00000131363						0	0	1	92	0	0	1	0	1	0	0		
ENSMUST00000131364	ENSMUSG00000058794	15	103248212	103258403	-1	0	0	8	0	2	0	55	39	36	5	79	D3Z6L9	
ENSMUST00000131366						0	3	0	0	0	0	0	0	1	0	0		
ENSMUST00000131367						35	44	86	43	36	15	3	11	3	3	14		
ENSMUST00000131368						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131369						0	1	0	0	0	0	2	2	0	0	2		
ENSMUST00000131371						3	0	3	0	2	0	0	6	0	0	0		
ENSMUST00000131372						3	2	10	6	3	0	13	7	5	1	15		
ENSMUST00000131373	ENSMUSG00000028809	4	135320484	135353321	-1	0	0	0	2	0	0	11	0	55	0	0	A2A983	
ENSMUST00000131374	ENSMUSG00000008683	7	118104372	118116188	-1	1	0	1	12	6	0	486	1011	523	2419	295	Q5M9M4	P62245
ENSMUST00000131375						0	0	0	0	0	0	65	36	63	1	27		
ENSMUST00000131376	ENSMUSG00000028108	3	95734147	95739569	-1	0	0	0	0	0	0	35	16	0	5	40	D3YV64	
ENSMUST00000131377	ENSMUSG00000089824	2	156091958	156111978	-1	5	1	0	0	7	4	1	0	49	2	53	B7ZCP9	
ENSMUST00000131379	ENSMUSG00000054272	7	11005722	11010547	1	3	3	10	0	0	0	0	0	0	0	0		Q80VJ6
ENSMUST00000131380						2	0	8	0	4	0	0	2	0	0	1		
ENSMUST00000131382						3	0	5	33	12	8	3	0	0	2	0		
ENSMUST00000131384	ENSMUSG00000053801	7	45825227	45830944	-1	0	0	15	0	0	10	0	0	0	0	0		Q810D6
ENSMUST00000131385						2	0	0	0	0	4	13	1	0	0	17		
ENSMUST00000131386	ENSMUSG00000028556	4	98936671	99120915	-1	0	0	0	0	1	0	3	2	0	0	0		
ENSMUST00000131389	ENSMUSG00000090100	2	120732816	120850604	-1	0	0	0	40	4	0	0	0	0	0	0	A2AW14	
ENSMUST00000131390	ENSMUSG00000041945	1	40772038	40790687	-1	19	11	22	58	26	8	0	0	45	0	22	M0QWK7	
ENSMUST00000131391						101	104	109	86	107	34	0	104	0	0	0		
ENSMUST00000131392	ENSMUSG00000028926	5	4803391	5420312	-1	0	0	0	0	0	0	0	0	0	0	0	D3YV23	
ENSMUST00000131393						22	24	100	114	41	29	2	9	5	4	7		
ENSMUST00000131394						0	0	0	9	0	0	1	0	1	0	1		
ENSMUST00000131395						1	0	0	0	1	1	0	16	0	0	7		
ENSMUST00000131396						18	13	29	18	17	3	6	12	7	0	8		
ENSMUST00000131397	ENSMUSG00000028527	4	101419277	101466995	1	0	0	0	96	5	2	0	0	0	0	2	A2ARF6	
ENSMUST00000131398	ENSMUSG00000020849	11	75732869	75765845	1	0	0	0	46	3	0	0	67	6	0	0	F6WA09	
ENSMUST00000131399						3	5	0	4	0	0	7	142	0	0	44		
ENSMUST00000131400						6	7	22	5	3	0	296	1575	569	1639	506		
ENSMUST00000131402						7	2	5	0	7	4	195	441	180	134	131		
ENSMUST00000131404	ENSMUSG00000057541	5	23740648	23783711	-1	0	0	0	0	0	0	3	0	0	5	0	F7CG42	
ENSMUST00000131405	ENSMUSG00000033628	18	30272747	30348126	1	10	8	0	0	8	7	2	0	2	2	0	E9Q824	
ENSMUST00000131406	ENSMUSG00000038822	10	45577829	45712345	1	0	0	7	0	0	0	1	45	1	1	0	H9KV10	
ENSMUST00000131407	ENSMUSG00000024663	19	10001669	10038380	1	0	1	3	57	0	2	0	0	3	0	0	D3YXL8	
ENSMUST00000131408						17	8	18	24	22	17	23	49	25	2	33		
ENSMUST00000131409	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	6	0	0	0	0	A2A5A3	
ENSMUST00000131410	ENSMUSG00000037492	8	23636019	24156585	1	0	2	3	0	0	2	0	0	0	0	0	D3YYX6	
ENSMUST00000131411	ENSMUSG00000034771	10	81574561	81590845	1	0	1	1	0	0	0	0	0	0	0	0	F6YM15	
ENSMUST00000131412	ENSMUSG00000062590	1	86154780	86278284	1	0	0	0	0	0	0	3	0	0	5	0		Q9D2I5
ENSMUST00000131413						17	12	16	7	16	6	0	0	0	1	0		
ENSMUST00000131414	ENSMUSG00000029563	6	14901349	15441977	1	0	0	0	0	0	0	0	0	0	0	0	D3YUQ7	
ENSMUST00000131415	ENSMUSG00000030707	7	126699773	126707787	-1	0	2	2	0	3	2	1519	470	845	164	501	D3YW57	
ENSMUST00000131417	ENSMUSG00000041119	17	31386234	31476310	1	0	0	0	0	0	0	0	0	0	0	0	D6RGP8	
ENSMUST00000131418						4	3	1	2	6	3	0	0	0	0	0		
ENSMUST00000131419						0	0	0	0	8	0	0	0	0	0	0		
ENSMUST00000131420						1	0	1	1	6	2	4	19	10	0	2		
ENSMUST00000131422	ENSMUSG00000036875	10	62947026	62974185	1	0	0	0	55	0	0	199	465	281	34	176		Q6ZQJ5
ENSMUST00000131423	ENSMUSG00000036872	8	86482260	86580686	-1	0	8	5	0	2	0	0	0	0	0	0		Q80WJ6
ENSMUST00000131424						1	0	2	4	3	1	0	0	0	0	0		
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ENSMUST00000131426						0	1	0	1	1	2	0	0	0	0	0		
ENSMUST00000131427	ENSMUSG00000029559	5	114942158	114949783	1	0	0	7	0	21	0	0	0	0	0	0	H3BLG8	
ENSMUST00000131428	ENSMUSG00000026304	1	90958133	90969661	-1	4	5	6	5	19	0	1	1	0	3	1	Q0PD39	P35292
ENSMUST00000131429						8	21	10	5	11	7	0	0	0	0	0		
ENSMUST00000131430	ENSMUSG00000041762	2	73341506	73386572	-1	0	1	0	1	2	3	0	6	0	0	2	F6Z6G4	
ENSMUST00000131431						0	1	0	0	3	1	0	0	0	0	0		
ENSMUST00000131432						1	4	0	3	9	0	0	0	0	1	1		
ENSMUST00000131433						4	4	8	7	7	5	24	79	42	5	109		
ENSMUST00000131434						0	1	1	0	3	1	0	0	2	0	2		
ENSMUST00000131435						3	6	24	6	7	0	0	48	0	35	15		
ENSMUST00000131436	ENSMUSG00000018001	5	143622447	143710250	1	0	2	0	0	0	0	0	0	0	0	0	D3YXU3	
ENSMUST00000131437						1	1	0	112	3	0	0	0	0	0	0		
ENSMUST00000131439						0	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000131440	ENSMUSG00000061887	4	106910701	107049694	1	1	1	1	1	1	0	0	0	12	0	0	B1AS33	
ENSMUST00000131442						0	5	0	1	0	0	0	0	0	0	0		
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ENSMUST00000131444						0	0	3	3	0	0	0	3	8	6	0		
ENSMUST00000131445	ENSMUSG00000014329	10	70922832	71159700	-1	0	0	0	0	0	0	0	0	0	0	0		Q99MQ1
ENSMUST00000131446	ENSMUSG00000030881	7	105634203	105640416	-1	0	0	6	0	0	0	27	137	88	26	55		Q8K221
ENSMUST00000131448	ENSMUSG00000074063	8	119434124	119446256	1	3	4	0	1	2	2	34	34	60	0	66	D3YYR6	
ENSMUST00000131450						0	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000131451	ENSMUSG00000067562	X	102802963	102809942	1	0	0	7	0	0	0	0	0	0	0	0	B1AX27	
ENSMUST00000131452	ENSMUSG00000041268	9	54365158	54501760	-1	0	0	0	22	0	0	0	0	0	0	0	D6RFA6	
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ENSMUST00000131455						3	0	5	85	5	0	0	2	0	0	6		
ENSMUST00000131456						7	1	73	24	10	2	0	0	0	0	2		
ENSMUST00000131458	ENSMUSG00000002280	17	25773776	25783332	1	0	0	0	0	0	0	0	0	0	0	14	D6RJ43	
ENSMUST00000131460						0	2	0	5	4	2	0	0	0	0	0		
ENSMUST00000131461	ENSMUSG00000030769	7	123214780	123273253	1	1	2	7	1	0	0	0	0	1	0	1	D3YUP3	
ENSMUST00000131462	ENSMUSG00000053646	9	109095389	109119917	1	5	2	1	35	0	3	0	0	0	0	0	D3YUD0	
ENSMUST00000131463						0	0	0	0	9	4	5	3	0	0	19		
ENSMUST00000131464	ENSMUSG00000026312	1	109982431	110140157	1	1	4	4	14	3	3	0	0	0	0	0	M0QWW8	
ENSMUST00000131465						2	2	1	89	2	3	0	0	0	1	0		
ENSMUST00000131467	ENSMUSG00000033740	1	6487231	6860940	1	0	1	0	0	13	0	0	0	0	0	0	D3YUH3	
ENSMUST00000131468						0	0	7	60	10	0	0	0	0	0	1		
ENSMUST00000131469						0	3	1	0	4	1	0	4	0	4	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131470						0	0	2	0	9	6	31	14	36	3	107		
ENSMUST00000131471						6	2	4	41	5	4	0	0	2	0	0		
ENSMUST00000131472						2	3	2	37	5	2	8	11	2	0	0		
ENSMUST00000131473						3	0	5	2	4	1	0	6	0	0	0		
ENSMUST00000131474						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131475	ENSMUSG00000002797	6	54982580	54992950	-1	17	19	41	38	15	9	3	31	17	37	11		Q9D7X8
ENSMUST00000131476	ENSMUSG00000039515	2	30416039	30447806	1	7	2	6	0	6	5	34	17	4	2	13	B7ZDE0	
ENSMUST00000131477						0	0	3	5	3	1	33	30	23	0	30		
ENSMUST00000131478						0	0	0	2	0	1	0	4	2	0	5		
ENSMUST00000131479						0	0	10	3	0	0	0	0	0	0	0		
ENSMUST00000131480	ENSMUSG00000063450	12	75818134	76110926	1	8	1	0	0	4	0	0	1	0	0	0	D3YVK9	
ENSMUST00000131482						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000131483	ENSMUSG00000041064	9	65587160	65595967	1	0	0	0	18	0	0	16	8	35	3	3		Q80SX8
ENSMUST00000131485	ENSMUSG00000029784	6	30509849	30520254	1	4	0	0	0	0	2	0	0	0	0	0	D3Z3E1	
ENSMUST00000131486	ENSMUSG00000028944	5	24862744	25100642	-1	2	0	0	0	0	0	0	0	0	0	3	D3YYW4	
ENSMUST00000131487	ENSMUSG00000040596	1	166384622	166409863	-1	22	18	17	59	33	0	0	0	0	12	0		
ENSMUST00000131488	ENSMUSG00000041598	11	113726850	113751881	-1	0	4	12	2	0	0	0	0	0	0	7	A2A6Q2	
ENSMUST00000131489	ENSMUSG00000036054	8	70234226	70279915	1	0	8	15	6	7	0	0	150	70	0	67		Q8CH09
ENSMUST00000131492						5	0	12	5	1	1	0	6	4	1	2		
ENSMUST00000131493						2	3	2	2	4	4	15	56	17	0	55		
ENSMUST00000131494	ENSMUSG00000033740	1	6487231	6860940	1	0	0	0	0	0	0	0	0	0	0	0	Q148A0	Q80TY4
ENSMUST00000131495						0	0	0	41	11	0	0	0	0	0	0		
ENSMUST00000131496						13	19	67	51	39	13	5	25	12	6	7		
ENSMUST00000131497						0	2	0	0	3	0	0	3	0	0	2		
ENSMUST00000131499						2	2	5	5	4	0	0	0	0	0	0		
ENSMUST00000131500	ENSMUSG00000029998	6	86386006	86397154	-1	0	0	0	0	0	4	2	31	20	0	19	F7CIP8	
ENSMUST00000131503						4	3	0	0	2	0	0	1	2	0	0		
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ENSMUST00000131505						3	3	0	0	1	0	0	0	0	0	0		
ENSMUST00000131506						0	2	0	0	0	0	2	5	0	0	8		
ENSMUST00000131507	ENSMUSG00000003528	16	17925211	17928219	-1	0	0	0	0	0	0	0	10	0	21	5	F6VVY4	
ENSMUST00000131508						0	2	3	3	4	0	0	0	0	0	0		
ENSMUST00000131510	ENSMUSG00000054034	X	136200948	136203876	-1	0	0	0	3	1	2	1	0	0	0	1	A2AJS2	
ENSMUST00000131511						11	13	28	33	10	16	69	161	85	24	230		
ENSMUST00000131513						2	0	0	2	2	3	0	10	2	0	9		
ENSMUST00000131515	ENSMUSG00000044629	11	17051586	17079371	1	6	4	9	6	6	2	0	0	0	0	0	Q9CW19	
ENSMUST00000131517						19	22	24	21	27	8	1	3	4	0	0		
ENSMUST00000131518	ENSMUSG00000063052	3	158036662	158068487	1	4	2	6	40	3	3	5	20	10	0	4	F6RDA7	
ENSMUST00000131519	ENSMUSG00000017400	11	98036623	98053462	-1	2	3	4	1	7	3	1	0	0	0	0	F6V5E7	
ENSMUST00000131520	ENSMUSG00000038827	4	56802345	56809601	1	0	0	0	0	18	0	0	0	0	16	6	D6RGQ6	
ENSMUST00000131521						1	2	14	6	7	5	0	0	0	0	0		
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ENSMUST00000131523						0	0	0	1	2	0	4	0	12	0	0		
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ENSMUST00000131527						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000131529						7	2	12	5	5	5	0	0	0	0	0		
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ENSMUST00000131534						3	4	4	22	5	2	37	173	64	24	46		
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ENSMUST00000131538						60	39	270	163	36	21	2	0	0	0	2		
ENSMUST00000131540	ENSMUSG00000042185	9	31386192	31421333	1	0	4	4	13	3	0	3	3	6	0	0	D6RIN8	
ENSMUST00000131541						13	13	13	19	27	13	0	0	0	0	0		
ENSMUST00000131542						3	5	21	2	2	2	0	1	0	0	2		
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ENSMUST00000131546	ENSMUSG00000020807	11	72153929	72207459	-1	0	0	0	0	0	0	0	154	38	11	82	F2Z444	
ENSMUST00000131547	ENSMUSG00000028402	4	81278500	81442815	-1	2	0	0	0	0	0	0	0	0	1	2	A3KG83	
ENSMUST00000131549						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000131550	ENSMUSG00000090115	17	47630690	47686738	1	0	0	0	0	0	0	0	7	0	0	1	F6VK47	
ENSMUST00000131551						6	2	60	4	4	3	0	1	0	0	2		
ENSMUST00000131552	ENSMUSG00000051177	2	134786067	135475258	1	0	0	3	3	3	0	1	6	0	0	3	F6X322	Q9Z1B3
ENSMUST00000131553	ENSMUSG00000044308	2	69897246	70024013	1	0	0	0	95	0	1	0	0	0	0	7	F6RDS0	
ENSMUST00000131554						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131555						0	0	7	0	2	0	19	9	8	2	4		
ENSMUST00000131556	ENSMUSG00000067851	1	10137571	10232670	-1	0	0	0	214	0	2	7	0	16	0	0	D3YYK9	
ENSMUST00000131557						2	1	0	0	0	3	1	0	2	0	0		
ENSMUST00000131558	ENSMUSG00000075297	10	22158586	22288849	1	7	0	0	116	11	2	0	0	0	0	0	B1B212	
ENSMUST00000131559						0	0	9	11	0	0	5	6	7	4	2		
ENSMUST00000131560	ENSMUSG00000022483	15	97975602	98004695	-1	0	0	0	7	0	0	0	0	0	0	0	D3Z7T2	
ENSMUST00000131561						13	4	18	0	14	0	0	12	3	0	0		
ENSMUST00000131562						4	5	22	8	7	5	14	15	13	3	13		
ENSMUST00000131563	ENSMUSG00000004948	5	135980099	135988624	1	3	0	8	27	7	2	0	0	0	0	0	F6VD35	
ENSMUST00000131565	ENSMUSG00000006345	10	75561604	75586200	1	0	0	0	0	0	0	0	0	0	0	0	D3YXV6	
ENSMUST00000131566	ENSMUSG00000048442	11	115899966	115906269	1	2	2	4	2	6	3	2	3	3	0	1	V9GXR9	
ENSMUST00000131567	ENSMUSG00000000157	16	96422288	96443619	-1	0	0	0	0	18	0	440	1132	504	121	487		Q3UV74
ENSMUST00000131568	ENSMUSG00000038822	10	45577829	45712345	1	0	0	0	0	0	0	0	0	0	0	0	F6T851	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131569						919	963	1523	423	461	158	20	49	20	0	37		
ENSMUST00000131571						5	4	2	0	5	6	0	0	0	0	2		
ENSMUST00000131572						2	3	9	59	4	7	0	0	0	0	0		
ENSMUST00000131573						0	0	0	0	0	0	0	0	13	5	3		
ENSMUST00000131574						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000131575						0	0	4	2	0	1	1	1	2	0	0		
ENSMUST00000131576						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000131578	ENSMUSG00000020752	11	115892595	115933477	-1	4	0	0	7	5	0	4	7	4	0	20	J3QM90	
ENSMUST00000131579						0	2	17	83	4	0	0	21	79	0	41		
ENSMUST00000131580						0	1	0	0	1	0	0	0	0	5	0		
ENSMUST00000131582						0	1	0	17	1	1	0	0	2	0	2		
ENSMUST00000131583						0	0	1	41	0	0	0	0	0	0	0		
ENSMUST00000131584						3	0	13	0	1	3	0	0	5	4	0		
ENSMUST00000131585						0	0	0	0	2	4	0	0	0	0	0		
ENSMUST00000131589	ENSMUSG00000030824	7	45492874	45510406	-1	0	0	0	0	0	0	87	0	69	0	58	D3Z7D7	
ENSMUST00000131590	ENSMUSG00000030123	6	115954811	115995005	-1	4	3	9	0	6	2	0	0	0	0	3	F6T0L5	
ENSMUST00000131591						0	0	1	0	2	0	7	2	5	0	4		
ENSMUST00000131594						59	53	152	74	43	28	14	97	33	19	29		
ENSMUST00000131595						0	3	4	35	3	1	0	0	0	0	0		
ENSMUST00000131596						4	2	4	8	1	0	6	0	0	0	0		
ENSMUST00000131597	ENSMUSG00000005628	3	95124476	95129209	1	2	2	4	3	2	7	0	5	11	0	5	D3Z5Q9	
ENSMUST00000131598						63	79	85	65	54	49	2	17	13	5	23		
ENSMUST00000131599						6	0	12	65	8	4	0	0	0	0	0		
ENSMUST00000131600	ENSMUSG00000039852	4	150281646	150621966	1	0	0	17	0	1	0	0	0	0	0	4	B1AS11	
ENSMUST00000131601	ENSMUSG00000046909	11	80136678	80142175	-1	9	12	6	12	10	3	5	14	7	8	8	B7ZCA9	
ENSMUST00000131602						3	0	0	71	8	4	0	0	0	0	0		
ENSMUST00000131604						0	1	8	25	12	2	0	0	0	0	0		
ENSMUST00000131605	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	13	0	0	0	0	0	0	0	A2AL71	
ENSMUST00000131606	ENSMUSG00000025572	11	117765988	117782198	-1	28	9	70	23	24	15	111	193	58	0	146	D6RCY1	
ENSMUST00000131607						25	22	78	40	36	14	31	502	293	16	377		
ENSMUST00000131608	ENSMUSG00000044117	16	13986604	14101500	1	0	0	5	2	0	1	0	0	0	0	0	D3Z3S8	
ENSMUST00000131609	ENSMUSG00000024236	18	4920540	5119299	1	32	4	0	0	0	8	0	0	30	0	27	Q8K4L2	
ENSMUST00000131610	ENSMUSG00000028164	3	135485611	135571404	1	2	0	10	39	0	1	7	8	16	0	32	D6RGR1	
ENSMUST00000131611						1	4	5	0	5	3	0	0	0	8	7		
ENSMUST00000131612	ENSMUSG00000042208	11	23564961	23633639	-1	0	0	1	36	2	2	2	0	2	0	0	Z4YN77	
ENSMUST00000131613	ENSMUSG00000046671	4	134525550	134535387	-1	4	0	0	32	0	0	0	159	0	0	0	D6RCX5	
ENSMUST00000131614						3	6	8	20	3	3	0	0	0	0	0		
ENSMUST00000131615	ENSMUSG00000075324	2	63971507	64098038	-1	132	122	589	781	195	100	1	7	4	1	5		Q9ERZ6
ENSMUST00000131616	ENSMUSG00000014633	8	116888685	116921455	-1	0	0	0	0	0	0	54	34	29	47	9	D6RD08	
ENSMUST00000131617						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000131618						8	5	18	9	8	11	1	2	0	0	2		
ENSMUST00000131620	ENSMUSG00000038777	3	95160457	95174024	1	0	0	0	0	0	0	1	0	0	0	0	S4R1B4	
ENSMUST00000131621						1	3	10	3	4	0	0	0	0	1	0		
ENSMUST00000131622						2	0	8	0	0	0	4	3	0	0	0		
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ENSMUST00000131624	ENSMUSG00000063362	8	22060721	22071627	1	0	1	0	0	0	0	2	5	3	4	6	F6R220	
ENSMUST00000131625						1	2	0	0	0	1	5	18	19	23	39		
ENSMUST00000131626						0	1	0	61	0	0	0	0	0	0	0		
ENSMUST00000131627						1	1	0	0	0	2	45	86	66	0	46		
ENSMUST00000131628						83	70	169	127	70	41	7	31	12	5	22		
ENSMUST00000131629						1	0	0	0	1	2	0	2	1	1	3		
ENSMUST00000131631	ENSMUSG00000029389	5	124552864	124569660	1	40	37	140	74	54	32	21	73	45	7	90	A0A0G2JG82	
ENSMUST00000131632						1	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000131633						0	1	2	2	3	0	3	5	3	0	10		
ENSMUST00000131635						0	0	0	0	0	0	3	1	0	6	2		
ENSMUST00000131636						7	10	14	9	9	0	3	8	6	3	4		
ENSMUST00000131637	ENSMUSG00000031860	8	69832491	69872292	1	0	0	0	22	0	0	0	0	0	0	3	D3Z318	
ENSMUST00000131638						2	2	1	1	2	1	0	0	0	2	1		
ENSMUST00000131641						0	0	0	0	0	0	2	15	15	0	0		
ENSMUST00000131643	ENSMUSG00000027207	2	125859109	125984299	1	0	0	0	0	0	0	0	6	0	0	0	D6RJ57	
ENSMUST00000131644	ENSMUSG00000028607	4	107903981	107923610	-1	0	2	0	94	2	1	0	1	0	0	0	A2A8E9	
ENSMUST00000131645						8	7	26	32	14	7	8	18	13	2	15		
ENSMUST00000131647	ENSMUSG00000038775	9	119052778	119071525	1	1	2	8	4	2	1	0	0	0	0	0	D3YWZ2	
ENSMUST00000131648						13	5	11	2	12	4	6	14	8	7	41		
ENSMUST00000131650	ENSMUSG00000068877	3	94693556	94704413	1	0	0	0	0	0	0	0	0	0	0	0	G3UWX5	
ENSMUST00000131651						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131652						0	1	0	0	0	2	0	0	0	1	0		
ENSMUST00000131653						13	13	24	22	26	10	11	43	16	1	19		
ENSMUST00000131654	ENSMUSG00000028573	4	95557507	95926939	1	0	0	0	0	0	0	0	0	0	0	0	D6RHR3	
ENSMUST00000131655	ENSMUSG00000032563	9	105053239	105079888	1	2	0	0	0	4	0	0	0	0	0	0	F6W7C7	
ENSMUST00000131656	ENSMUSG00000048351	4	108328140	108341544	1	49	50	105	53	59	27	14	39	36	9	35		Q921H9
ENSMUST00000131657	ENSMUSG00000044702	7	122107262	122132985	-1	0	0	0	0	0	1	0	6	0	0	0	F6VTV6	
ENSMUST00000131658						4	0	9	3	3	0	0	0	0	0	2		
ENSMUST00000131659						30	13	53	88	57	20	1	0	0	0	0		
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ENSMUST00000131661						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000131662	ENSMUSG00000040250	6	146549632	146577835	-1	0	6	0	0	0	0	51	200	100	54	61	F6W761	
ENSMUST00000131664						3	2	3	2	6	5	0	2	0	0	2		
ENSMUST00000131665						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000131666	ENSMUSG00000001418	3	88325023	88331313	1	0	0	0	0	0	0	13	4	57	0	7	D6RJI7	
ENSMUST00000131667						12	5	9	5	14	4	0	0	0	0	0		
ENSMUST00000131668	ENSMUSG00000035969	4	43381979	43427088	1	2	0	13	0	7	2	10	0	0	4	28	G8JL85	
ENSMUST00000131669						0	0	0	0	0	0	0	188	8	15	8		
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131671	ENSMUSG00000066037	4	136310942	136359447	1	0	0	0	24	14	2	132	434	245	172	212	F7B5B5	
ENSMUST00000131672						74	84	119	136	106	47	5	4	9	2	3		
ENSMUST00000131673	ENSMUSG00000029343	5	112255815	112269585	1	3	0	6	2	5	0	0	0	0	0	0	E9PYP8	
ENSMUST00000131674						7	2	4	41	7	4	0	5	6	10	11		
ENSMUST00000131676	ENSMUSG00000078898	2	175372436	175384201	1	0	3	3	0	0	0	6	0	0	0	1	E9PXD4	
ENSMUST00000131677						0	0	3	4	4	1	4	7	5	0	1		
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ENSMUST00000131679	ENSMUSG00000002486	5	114707760	114722327	1	2	2	11	13	2	0	1	0	0	4	1	F6Q720	
ENSMUST00000131680	ENSMUSG00000037791	11	77982754	78030539	1	0	0	6	0	0	0	8	118	22	4	36	F6U3I4	
ENSMUST00000131681						4	5	7	2	0	2	12	33	5	5	0		
ENSMUST00000131682						2	1	0	4	2	1	0	0	0	0	2		
ENSMUST00000131683						0	0	5	52	3	2	454	300	214	60	176		
ENSMUST00000131684						14	0	0	15	4	6	16	11	3	10	0		
ENSMUST00000131685						3	1	7	1	8	3	26	20	0	0	18		
ENSMUST00000131686						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131688						8	7	20	58	18	8	573	1254	862	52	740		
ENSMUST00000131689						6	1	23	4	7	2	0	0	0	0	0		
ENSMUST00000131691						2	0	0	0	2	0	0	5	34	0	44		
ENSMUST00000131692	ENSMUSG00000025875	13	54789377	54796776	1	0	0	0	43	0	0	0	0	0	7	0	Q3TLW9	
ENSMUST00000131693						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000131694						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000131695						0	0	9	28	5	0	0	0	0	0	21		
ENSMUST00000131696	ENSMUSG00000028948	4	152039321	152061494	1	33	22	49	0	45	21	0	85	125	18	55		
ENSMUST00000131697						2	0	3	1	6	3	6	16	0	8	6		
ENSMUST00000131698	ENSMUSG00000027333	2	131491496	131525922	1	0	0	1	184	6	2	0	9	2	0	3	A2AP08	
ENSMUST00000131699	ENSMUSG00000023930	17	40764734	40807003	-1	0	1	0	0	0	0	0	0	0	0	0	Q9D2T2	
ENSMUST00000131700	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	0	0	0	0	0	D6RG86	
ENSMUST00000131701						3	0	0	50	0	0	0	0	0	0	0		
ENSMUST00000131702	ENSMUSG00000078861	2	178067695	178078476	-1	0	0	0	0	1	0	0	1	0	0	1	D3YWJ2	
ENSMUST00000131703						26	11	70	32	13	14	0	0	4	0	4		
ENSMUST00000131704						15	4	10	17	16	4	1	0	1	1	0		
ENSMUST00000131706	ENSMUSG00000006527	14	30714849	30822713	1	5	0	0	37	12	2	19	0	18	0	26	E9Q354	
ENSMUST00000131708	ENSMUSG00000029352	5	113075839	113081584	-1	0	0	1	0	0	0	0	0	0	0	0	D3YYW5	
ENSMUST00000131709						248	291	1016	314	195	106	4	5	2	0	7		
ENSMUST00000131711	ENSMUSG00000027257	2	91255954	91264679	1	0	0	8	0	0	0	0	0	0	0	0	B1AW94	
ENSMUST00000131712	ENSMUSG00000002546	2	32287384	32307921	1	0	0	0	0	0	0	1	0	0	0	0	A2AN46	
ENSMUST00000131713						0	0	1	16	0	0	31	252	55	162	52		
ENSMUST00000131714	ENSMUSG00000036617	2	19909780	20810713	1	3	3	0	4	3	3	0	0	0	0	0	B1AY50	
ENSMUST00000131715						2	0	4	14	3	4	4	9	3	4	7		
ENSMUST00000131716	ENSMUSG00000087236	1	179695297	179745185	-1	29	24	35	30	49	13	3	5	4	0	4	R4GML7	
ENSMUST00000131717	ENSMUSG00000013033	8	83900105	83941954	1	0	0	7	66	24	0	0	0	5	0	4		Q80TR1
ENSMUST00000131718	ENSMUSG00000020070	10	62980223	63017210	1	5	9	2	14	0	0	0	0	0	0	0	Q8BR30	
ENSMUST00000131719						27	37	72	34	38	24	18	31	29	4	35		
ENSMUST00000131720						0	0	5	81	7	3	0	0	0	0	0		
ENSMUST00000131721						42	31	175	122	68	43	13	61	26	3	49		
ENSMUST00000131722	ENSMUSG00000067424	17	33089310	33106203	1	6	6	2	3	4	1	9	16	6	5	3	B8JJZ9	
ENSMUST00000131723	ENSMUSG00000010122	11	61343401	61378345	-1	22	14	36	28	19	12	0	0	0	0	0	D6RGQ3	
ENSMUST00000131724	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000131725						9	4	3	52	10	3	0	7	5	0	24		
ENSMUST00000131726						7	4	24	25	14	12	0	0	0	0	7		
ENSMUST00000131727	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	0	0	0	0	0	3	0	0	A2AC02	
ENSMUST00000131728	ENSMUSG00000025364	10	128557766	128565934	-1	0	3	2	0	4	0	67	146	83	34	62	D3YVH7	
ENSMUST00000131729						27	26	66	20	38	13	1	7	5	3	7		
ENSMUST00000131730	ENSMUSG00000063275	2	13850282	14056135	-1	886	969	1746	900	993	495	16	126	32	13	40	A2AQ81	
ENSMUST00000131731	ENSMUSG00000031075	7	144588549	144751974	-1	0	0	0	52	0	0	0	0	0	0	0	D3YYA4	
ENSMUST00000131732						40	51	38	39	81	45	3	2	7	7	7		
ENSMUST00000131734						0	0	0	0	0	0	2	0	4	0	0		
ENSMUST00000131736	ENSMUSG00000020234	10	81363067	81365816	-1	1	5	17	119	5	8	9	23	6	0	14	F6UVB2	
ENSMUST00000131737						1	3	0	1	2	0	8	23	15	64	10		
ENSMUST00000131738						0	1	4	0	0	1	27	0	4	9	0		
ENSMUST00000131739	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	2	0	0	0	0	0	0	0	F6ZX53	
ENSMUST00000131741						21	12	41	38	20	12	21	131	64	4	65		
ENSMUST00000131742	ENSMUSG00000038777	3	95160457	95174024	1	1	0	0	0	3	3	0	0	0	0	0	A0A0G2JDV7	
ENSMUST00000131743						4	4	8	6	8	2	14	64	35	5	44		
ENSMUST00000131744						38	37	58	57	71	24	3	4	0	0	14		
ENSMUST00000131745	ENSMUSG00000035778	2	35400179	35463231	-1	3	3	8	5	0	0	0	0	3	0	0	B2FDI6	
ENSMUST00000131746	ENSMUSG00000042198	4	3938888	3951046	1	0	0	0	0	0	0	0	7	0	0	0	D6REE9	
ENSMUST00000131747						9	8	48	0	20	7	8	23	12	4	19		
ENSMUST00000131748						0	0	0	0	0	1	0	2	1	0	0		
ENSMUST00000131749	ENSMUSG00000074575	2	168260117	168281736	-1	4	4	7	52	5	3	0	0	0	0	0	A2BDX5	
ENSMUST00000131750						30	15	122	39	19	14	0	7	6	0	2		
ENSMUST00000131751						0	3	8	0	3	4	0	0	0	0	0		
ENSMUST00000131752						49	42	0	0	29	35	0	103	179	0	50		
ENSMUST00000131753						22	17	106	21	20	8	0	0	0	0	4		
ENSMUST00000131754						0	1	0	1	4	1	0	15	4	0	0		
ENSMUST00000131755	ENSMUSG00000043411	4	137593755	137658537	1	1	1	7	1	4	0	3	15	4	0	27	F6Z2T3	
ENSMUST00000131758	ENSMUSG00000058183	4	154869585	154895528	1	1	3	2	0	1	1	0	0	0	0	0	B1AS18	
ENSMUST00000131759						0	0	0	0	0	0	0	76	0	0	38		
ENSMUST00000131760						17	19	56	28	29	11	0	0	0	0	0		
ENSMUST00000131761						6	1	5	0	1	3	0	19	0	3	5		
ENSMUST00000131762						1	1	11	15	0	2	0	0	0	0	0		
ENSMUST00000131763						5	3	3	1	6	1	4	10	5	1	10		
ENSMUST00000131764						5	10	0	36	2	0	0	14	0	1	17		
ENSMUST00000131765						0	0	0	0	0	0	5	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131766						103	98	176	207	80	47	14	36	25	6	33		
ENSMUST00000131767	ENSMUSG00000031537	8	22659212	22706589	-1	1	0	0	1	1	2	0	0	0	0	0	F6ULQ4	
ENSMUST00000131768						1	0	7	5	0	0	30	53	52	18	40		
ENSMUST00000131769						0	3	5	93	11	8	1	4	0	0	0		
ENSMUST00000131770						7	0	0	1	4	2	3	0	0	9	0		
ENSMUST00000131771	ENSMUSG00000029559	5	114942158	114949783	1	0	1	2	0	0	2	17	12	7	5	4	D6RDR6	
ENSMUST00000131772						1	3	3	7	3	2	0	0	0	0	0		
ENSMUST00000131773						15	9	50	28	18	7	39	32	74	3	68		
ENSMUST00000131774						4	1	5	52	5	1	0	2	0	0	0		
ENSMUST00000131775	ENSMUSG00000008601	3	88542029	88548300	-1	0	0	0	0	0	0	0	3	3	1	5	D3YYB3	
ENSMUST00000131776	ENSMUSG00000028610	4	107676290	107684230	-1	3	3	10	31	7	2	1	0	0	0	0	B1ASP8	
ENSMUST00000131777						0	0	6	0	2	0	5	13	0	3	18		
ENSMUST00000131778						0	11	25	8	6	6	0	0	0	0	0		
ENSMUST00000131779						0	0	0	57	0	0	8	3	0	0	3		
ENSMUST00000131780	ENSMUSG00000034006	18	80253292	80292725	1	10	14	39	30	13	7	0	275	81	38	106		Q80XM9
ENSMUST00000131781						1	1	4	0	1	1	0	1	1	0	1		
ENSMUST00000131782						0	1	5	2	2	3	0	0	0	0	2		
ENSMUST00000131784	ENSMUSG00000043090	8	69761326	69791178	-1	21	18	30	31	28	6	35	174	89	21	88	E9Q810	
ENSMUST00000131785						5	7	4	8	13	4	0	2	2	0	0		
ENSMUST00000131786						1	0	1	0	0	0	5	0	20	0	13		
ENSMUST00000131788						0	4	5	20	0	10	29	209	66	13	67		
ENSMUST00000131789						0	0	5	0	0	4	0	0	0	0	0		
ENSMUST00000131791						68	50	66	48	69	38	4	30	16	5	8		
ENSMUST00000131792						3	2	1	2	5	0	0	0	0	0	0		
ENSMUST00000131793						1	1	2	14	3	1	0	4	2	1	5		
ENSMUST00000131794	ENSMUSG00000034771	10	81574561	81590845	1	0	1	2	0	1	0	0	0	1	0	0	D3Z0X0	
ENSMUST00000131795						0	3	3	6	2	1	0	1	0	0	1		
ENSMUST00000131796						7	5	0	2	0	0	0	13	20	164	0		
ENSMUST00000131797						15	0	2	297	12	3	0	0	0	0	0		
ENSMUST00000131798						1	0	0	1	0	2	7	4	0	0	7		
ENSMUST00000131799						2	2	1	29	3	0	0	0	0	0	0		
ENSMUST00000131800						98	68	334	92	109	41	0	5	6	1	10		
ENSMUST00000131802	ENSMUSG00000021998	14	75131101	75230842	1	15	45	0	118	53	0	28136	138770	48306	12675	26090		Q61233
ENSMUST00000131803						5	3	8	0	0	0	0	2338	42	23	27		
ENSMUST00000131804	ENSMUSG00000031441	8	12757014	12868728	1	2	1	15	1	7	0	63	73	171	4	225	F6QJS5	
ENSMUST00000131805						2	3	14	2	8	2	29	146	26	36	48		
ENSMUST00000131806	ENSMUSG00000036872	8	86482260	86580686	-1	0	0	17	0	9	5	0	0	0	0	0	D6RGU5	
ENSMUST00000131807	ENSMUSG00000024018	17	29689378	29717012	-1	0	0	1	0	0	0	0	0	0	0	0	F6WM75	
ENSMUST00000131808						1	2	6	1	3	3	5	0	0	0	0		
ENSMUST00000131809						0	6	0	3	7	0	0	0	0	0	5		
ENSMUST00000131810	ENSMUSG00000020109	10	59879556	59899302	1	0	0	0	23	0	0	143	0	100	46	54	D6RHR9	
ENSMUST00000131811						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000131813						2	0	0	0	2	1	19	8	4	0	2		
ENSMUST00000131814						0	0	0	2	2	2	26	148	66	46	27		
ENSMUST00000131815						0	0	1	0	3	1	7	11	5	0	10		
ENSMUST00000131816	ENSMUSG00000035745	10	79970715	79977190	1	0	0	0	0	0	0	0	0	0	1	0	F7ARC5	
ENSMUST00000131817						0	0	0	0	0	0	6	0	0	0	0		
ENSMUST00000131818	ENSMUSG00000017677	11	79239372	79254671	-1	0	0	0	0	0	1	41	487	264	34	99	F6ZUJ8	
ENSMUST00000131819						0	0	0	0	0	0	5	2	9	0	13		
ENSMUST00000131820						2	0	20	3	0	2	441	305	823	1403	665		
ENSMUST00000131822						6	0	2	2	13	0	0	0	0	0	0		
ENSMUST00000131823						3	0	0	0	3	0	1	77	24	0	37		
ENSMUST00000131824	ENSMUSG00000037110	2	146239879	146512026	-1	0	0	0	0	0	0	14	0	0	0	4		A3KGS3
ENSMUST00000131825	ENSMUSG00000000730	10	78041947	78063622	1	0	3	0	2	2	4	28	53	20	19	3	D3YUQ4	
ENSMUST00000131826						5	2	10	4	5	1	0	7	10	0	0		
ENSMUST00000131827						3	0	0	3	3	0	0	0	0	0	2		
ENSMUST00000131828						0	2	12	0	6	4	20	41	40	0	45		
ENSMUST00000131829	ENSMUSG00000052854	X	138914430	139010532	1	0	0	0	0	0	2	0	0	0	0	0	D6RFR0	
ENSMUST00000131830	ENSMUSG00000038866	1	105990406	106034074	1	0	1	1	0	0	0	0	0	0	0	7	A0A087WRA5	
ENSMUST00000131831						49	40	65	72	60	24	12	18	11	0	11		
ENSMUST00000131832						6	5	6	2	7	3	0	0	1	0	0		
ENSMUST00000131833						0	3	2	2	0	2	0	0	0	0	0		
ENSMUST00000131834	ENSMUSG00000022272	15	25622525	25813673	1	5	2	0	2	0	1	0	0	0	1	0	D3Z2P4	
ENSMUST00000131835	ENSMUSG00000030257	6	112717971	112947266	-1	2	4	8	5	3	5	0	0	0	0	0	F6QZR7	
ENSMUST00000131836						4	3	3	10	5	0	0	0	1	0	0		
ENSMUST00000131837						0	0	0	2	0	0	151	228	30	27	36		
ENSMUST00000131838						2	1	3	1	2	0	2	0	3	1	9		
ENSMUST00000131839						10	9	9	14	17	10	14	13	10	36	3		
ENSMUST00000131840	ENSMUSG00000008683	7	118104372	118116188	-1	1	1	9	99	7	3	0	2	0	3	0	D3Z712	
ENSMUST00000131842						731	850	1138	687	788	369	21	79	77	25	77		
ENSMUST00000131843	ENSMUSG00000029312	5	103861973	103911259	-1	0	7	17	0	0	0	0	6	0	2	0	D6REH9	
ENSMUST00000131844						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131847	ENSMUSG00000023505	6	124829547	124833701	1	3	2	8	0	2	3	9	0	4	26	15	D3YZ81	
ENSMUST00000131848	ENSMUSG00000017677	11	79239372	79254671	-1	0	0	14	0	0	1	8	0	118	0	0	E9Q647	
ENSMUST00000131849						1	1	4	9	0	6	3	1	0	0	0		
ENSMUST00000131850						24	10	29	16	21	11	96	1181	146	36	319		
ENSMUST00000131852						9	6	4	18	16	4	0	0	0	0	0		
ENSMUST00000131853	ENSMUSG00000019763	10	4401915	4432388	-1	0	0	0	1	0	0	0	0	0	0	0	D3YZC3	
ENSMUST00000131854						0	0	0	0	0	0	10	0	2	0	22		
ENSMUST00000131855	ENSMUSG00000026427	1	131153181	131187658	1	11	10	58	43	24	15	16	10	61	6	110		
ENSMUST00000131856	ENSMUSG00000009108	3	108092789	108101432	1	3	0	3	0	0	5	1	0	2	0	4	F6QPU5	
ENSMUST00000131857						1	0	0	27	0	0	0	0	0	0	0		
ENSMUST00000131858						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131860	ENSMUSG00000042759	7	126584942	126589112	1	0	0	0	3	0	0	0	3	0	4	8		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131861	ENSMUSG00000004113	2	24603887	24763152	-1	0	0	0	0	0	0	0	1	0	0	0	A0A0A6YWR0	
ENSMUST00000131862						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000131863						4	5	3	6	4	0	9	0	0	16	10		
ENSMUST00000131865						0	4	0	0	1	2	0	4	0	0	0		
ENSMUST00000131866						0	1	4	13	4	1	3	2	1	0	18		
ENSMUST00000131867						0	0	0	0	0	0	0	0	0	5	0		
ENSMUST00000131868	ENSMUSG00000001017	3	90498956	90509498	-1	3	2	11	33	6	1	0	0	0	0	0	D3YZA1	
ENSMUST00000131869						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131870						1	2	1	2	0	0	2	119	19	23	12		
ENSMUST00000131871	ENSMUSG00000022884	16	23107444	23114136	1	0	0	0	0	0	1	58	1367	181	184	71	D6RJ11	
ENSMUST00000131872						0	3	0	1	2	0	0	2	0	0	0		
ENSMUST00000131873						0	0	0	110	0	0	120	453	142	179	73		
ENSMUST00000131875						0	0	0	0	0	0	9	6	0	0	0		
ENSMUST00000131876	ENSMUSG00000003344	10	80642617	80657071	-1	0	1	3	2	10	0	1	8	20	4	14	F6WBW4	
ENSMUST00000131877	ENSMUSG00000025089	19	58235604	58455909	-1	3	4	10	65	8	5	0	0	0	0	0	D3Z3C9	
ENSMUST00000131878	ENSMUSG00000034145	12	87021340	87090043	1	0	7	5	14	13	5	0	2	0	0	0		Q8CBX0
ENSMUST00000131879	ENSMUSG00000020096	10	61171954	61188841	1	0	0	0	0	0	0	0	0	0	0	0	D6RH51	
ENSMUST00000131880						1	0	3	0	6	4	22	34	27	16	13		
ENSMUST00000131881						9	12	9	4	7	0	0	0	0	0	0		
ENSMUST00000131882						20	16	33	23	19	10	0	0	0	0	0		
ENSMUST00000131883	ENSMUSG00000035208	11	83002158	83020810	-1	0	0	0	0	0	0	0	0	0	0	0	F6RTS1	
ENSMUST00000131884						0	0	0	0	2	0	7	3	13	5	12		
ENSMUST00000131885	ENSMUSG00000024431	18	39410545	39491301	-1	0	1	1	103	7	1	0	2	8	0	8	D3YTK8	
ENSMUST00000131887						78	103	72	36	43	28	12	12	6	1	8		
ENSMUST00000131888	ENSMUSG00000040365	11	48806404	48817353	-1	5	1	11	0	8	4	28	17	28	3	59	Q5NCC4	
ENSMUST00000131889						0	2	3	0	0	1	45	0	0	0	29		
ENSMUST00000131890	ENSMUSG00000030287	6	146108299	146502223	-1	5	3	0	0	1	0	5	3	7	0	0	B2KF89	
ENSMUST00000131891						0	0	0	10	0	0	2	9	0	5	0		
ENSMUST00000131892						1	0	2	3	0	2	0	0	0	0	0		
ENSMUST00000131893	ENSMUSG00000058594	2	11742573	11777582	-1	0	0	0	0	0	0	11	234	18	18	0	A2AS52	
ENSMUST00000131894						21	16	26	32	37	10	0	0	0	0	0		
ENSMUST00000131895						12	3	33	80	5	7	16	5	50	0	78		
ENSMUST00000131897	ENSMUSG00000024211	6	27275119	28135178	-1	0	3	0	0	0	0	0	0	0	0	0	D3YZL1	
ENSMUST00000131899	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	7	0	0	0	0	F6Q346	
ENSMUST00000131900						1	1	0	43	0	0	4	3	0	0	0		
ENSMUST00000131901						3	0	1	14	4	0	0	0	0	0	0		
ENSMUST00000131902						0	1	3	11	2	0	3	9	6	1	12		
ENSMUST00000131903						2	1	4	3	5	1	0	32	3	4	0		
ENSMUST00000131905						7	8	6	12	9	5	6	26	21	2	33		
ENSMUST00000131906						0	2	2	0	2	0	0	0	0	0	0		
ENSMUST00000131909						0	0	0	0	0	0	20	92	15	0	8		
ENSMUST00000131910						0	2	4	0	6	6	0	0	0	0	0		
ENSMUST00000131911						1	0	0	0	0	0	0	10	0	0	0		
ENSMUST00000131912	ENSMUSG00000028745	4	139192899	139291818	1	0	3	9	8	0	4	6	34	31	11	43	F6YHZ8	
ENSMUST00000131913						1	0	0	0	0	2	25	39	14	3	27		
ENSMUST00000131914						2	1	7	1	3	0	4	14	9	2	6		
ENSMUST00000131915						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000131916	ENSMUSG00000001741	7	83642848	83745726	-1	5	4	10	4	5	7	0	0	0	0	0	D3Z3C7	
ENSMUST00000131917	ENSMUSG00000039652	19	37021291	37208601	-1	2	6	5	10	2	0	0	0	1	0	0	D3YUL6	
ENSMUST00000131918						19	11	8	14	15	8	16	52	34	6	24		
ENSMUST00000131919	ENSMUSG00000026725	1	160085029	160153580	-1	18	13	26	111	16	4	0	3	0	1	0	E9Q1F6	
ENSMUST00000131920	ENSMUSG00000023267	4	33062999	33095865	1	6	0	0	2	8	0	0	0	2	0	0	A3KG54	
ENSMUST00000131921						5	0	14	1	2	2	0	11	6	45	6		
ENSMUST00000131922	ENSMUSG00000032473	9	99689461	99717267	-1	6	1	8	6	4	2	0	0	0	0	0		P56857
ENSMUST00000131923	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	1	0	1	25	11	0	3	A2AEB9	
ENSMUST00000131924						2	6	10	4	1	2	3	94	22	2	42		
ENSMUST00000131926						0	3	0	0	0	0	1	0	0	0	0		
ENSMUST00000131927	ENSMUSG00000005951	11	73199460	73224511	1	19	14	0	0	11	9	0	47	0	0	0	D6RJM2	
ENSMUST00000131928						0	0	4	5	1	0	0	0	1	0	0		
ENSMUST00000131929						2	1	2	4	3	0	3	13	20	2	27		
ENSMUST00000131930	ENSMUSG00000026979	2	24367580	24414954	1	6	7	2	13	0	4	24	26	34	4	22	A0A0A6YY70	
ENSMUST00000131932	ENSMUSG00000066007	4	146156824	146198755	1	2	7	0	5	5	4	0	0	0	0	0	A2A7U9	
ENSMUST00000131933	ENSMUSG00000030769	7	123214780	123273253	1	5	2	9	4	0	4	0	0	1	0	0	D3Z300	
ENSMUST00000131934						0	3	3	0	6	2	9	34	12	5	7		
ENSMUST00000131935	ENSMUSG00000028952	4	152019774	152027671	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQG8	
ENSMUST00000131936	ENSMUSG00000030035	6	83119044	83121559	-1	0	0	7	1	0	0	17	0	0	0	0		
ENSMUST00000131937						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000131938	ENSMUSG00000078588	4	117866524	117872557	-1	0	0	3	2	0	0	0	0	0	0	0	E9PZ77	
ENSMUST00000131939						0	10	0	9	0	0	44	72	29	0	21		
ENSMUST00000131940						7	7	22	0	7	4	1539	1413	721	223	426		
ENSMUST00000131941						1	3	0	0	3	0	0	0	0	0	0		
ENSMUST00000131942	ENSMUSG00000054728	13	42680623	43138526	1	2	6	10	1	9	3	0	0	0	2	0	B1B1B8	
ENSMUST00000131943						11	8	11	40	19	16	3	5	3	2	9		
ENSMUST00000131945						2	2	4	3	3	0	0	0	0	0	0		
ENSMUST00000131946						0	0	0	13	0	2	0	0	0	0	0		
ENSMUST00000131948	ENSMUSG00000014592	4	150917322	151861876	-1	1	2	0	94	0	1	0	0	0	0	0	B0QZL6	
ENSMUST00000131949	ENSMUSG00000089917	2	181569149	181584892	-1	2	2	3	12	5	0	0	4	11	0	7	B7ZCR0	
ENSMUST00000131950						45	32	76	62	53	18	83	857	222	23	337		
ENSMUST00000131951						5	6	26	6	0	2	4	0	5	6	5		
ENSMUST00000131952						1	0	1	0	2	0	8	45	9	0	9		
ENSMUST00000131953						0	0	0	0	0	0	0	0	0	0	24		
ENSMUST00000131954	ENSMUSG00000048602	17	33135588	33139683	-1	23	5	59	12	26	7	0	0	0	0	0		Q8C5W4
ENSMUST00000131955						0	0	0	23	3	2	0	0	0	0	0		
ENSMUST00000131956						31	3	0	0	0	0	0	5	0	6	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000131957	ENSMUSG00000053702	2	17343909	17731464	-1	0	0	0	0	4	0	0	2	0	0	0	B7ZCI3	
ENSMUST00000131958						1	1	5	3	0	0	0	0	0	0	0		
ENSMUST00000131959						2	0	0	5	6	1	0	0	0	0	0		
ENSMUST00000131960						155	27	18	80	959	52	3128	1592	611	36132	4050		
ENSMUST00000131962						0	0	2	3	1	1	0	14	0	4	23		
ENSMUST00000131963						0	0	3	1	1	1	0	12	16	0	13		
ENSMUST00000131964						2	2	4	100	8	4	0	0	0	0	0		
ENSMUST00000131965	ENSMUSG00000045636	8	40990914	41133726	-1	2	0	0	3	0	1	56	93	154	153	176	D3Z2H5	
ENSMUST00000131966	ENSMUSG00000039391	7	89866148	89903629	-1	12	8	17	8	2	4	0	0	0	0	0	D6REG7	
ENSMUST00000131967						0	6	0	2	0	7	0	0	1	0	0		
ENSMUST00000131968	ENSMUSG00000078440	10	81384428	81391560	1	3	0	0	9	0	0	0	0	0	0	0	F6TY47	
ENSMUST00000131969						10	4	11	12	11	3	0	0	0	0	0		
ENSMUST00000131970						56	44	41	216	77	65	2	27	8	1	12		
ENSMUST00000131971	ENSMUSG00000032717	17	47815328	47834691	-1	1	0	1	28	4	2	0	0	0	0	0	D3YZ53	
ENSMUST00000131972						0	0	0	14	0	0	0	0	0	0	0		
ENSMUST00000131973	ENSMUSG00000010342	11	87405065	87555823	1	2	2	0	0	3	1	0	16	1	3	2	Q5ND21	
ENSMUST00000131974	ENSMUSG00000040154	2	164176327	164182742	-1	6	3	6	3	3	0	0	0	0	0	0	F6TTH9	
ENSMUST00000131975	ENSMUSG00000029053	4	155260129	155361361	-1	3	2	2	3	5	4	0	0	0	0	0	A2AD74	
ENSMUST00000131976						0	2	8	5	5	0	10	14	12	0	10		
ENSMUST00000131977						5	5	4	10	4	4	7	7	17	11	7		
ENSMUST00000131978						4	4	1	3	7	0	9	27	31	0	28		
ENSMUST00000131979						5	2	12	8	14	2	1	0	1	1	2		
ENSMUST00000131980						6	7	0	8	14	6	0	0	0	0	0		
ENSMUST00000131981	ENSMUSG00000041729	9	62419492	62537044	-1	4	5	7	0	11	5	0	1	0	0	0	G3UWZ2	
ENSMUST00000131982						2	2	1	0	5	1	1	0	1	7	2		
ENSMUST00000131983						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000131986						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000131987						18	21	58	37	29	14	0	5	2	3	13		
ENSMUST00000131988						2	2	0	2	0	1	0	7	5	6	4		
ENSMUST00000131989						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000131990	ENSMUSG00000022814	16	33954782	33967038	-1	3	0	0	38	9	9	0	66	0	39	54	D6RJ62	
ENSMUST00000131991	ENSMUSG00000049657	4	44991242	45012412	-1	0	0	2	63	0	0	0	0	0	0	0	B1AXQ4	
ENSMUST00000131992	ENSMUSG00000057541	5	23740648	23783711	-1	14	0	21	6	45	0	0	0	0	0	0	Q91VU7	
ENSMUST00000131993	ENSMUSG00000041890	5	114727407	114775517	-1	0	1	3	1	0	1	20	0	178	0	132	F6WV69	
ENSMUST00000131995	ENSMUSG00000052139	5	31697684	32084962	1	0	0	0	0	0	0	9	597	171	0	128		Q8K3W0
ENSMUST00000131996	ENSMUSG00000019775	10	5825663	5922400	-1	32	36	95	0	31	18	0	2	0	0	1		Q9QZB0
ENSMUST00000131998						1	2	6	2	4	1	0	0	0	0	0		
ENSMUST00000131999						1	4	0	4	6	3	0	0	0	0	0		
ENSMUST00000132000	ENSMUSG00000031403	X	75095854	75109777	1	0	0	0	0	2	0	0	0	0	0	0	A2AN81	
ENSMUST00000132001	ENSMUSG00000026317	8	14881335	14901720	1	2	2	7	4	6	1	0	0	0	0	0		
ENSMUST00000132002						19	18	47	22	31	22	0	0	0	0	0		
ENSMUST00000132003						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000132004	ENSMUSG00000022124	14	103080239	103099566	-1	0	3	0	17	7	0	14	0	0	8	9		Q8C4V4
ENSMUST00000132005	ENSMUSG00000074895	13	54783998	54788459	1	0	0	0	0	0	0	0	0	0	0	0	E9Q929	
ENSMUST00000132006						6	3	22	15	3	2	0	1	2	0	3		
ENSMUST00000132008						11	10	11	45	9	11	0	11	3	2	5		
ENSMUST00000132009	ENSMUSG00000030180	6	120364124	120444574	1	0	0	0	0	0	0	45	11	103	0	26	Q921T5	
ENSMUST00000132010						16	0	34	0	0	0	2035	3206	2787	1762	1460		
ENSMUST00000132011						0	0	7	1	1	0	0	0	3	1	5		
ENSMUST00000132012	ENSMUSG00000062115	11	60105013	60199197	1	0	0	0	1	0	0	0	0	0	0	0	B1AU85	
ENSMUST00000132013						4	2	9	1	4	2	0	26	6	9	11		
ENSMUST00000132014						1	0	3	20	2	2	0	2	1	4	5		
ENSMUST00000132015						6	5	7	3	0	1	0	0	0	0	3		
ENSMUST00000132016						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132017	ENSMUSG00000020128	11	21239281	21321136	1	0	0	0	0	2	0	185	1031	600	124	379	Q5SRW8	
ENSMUST00000132018						1	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000132020						0	19	56	0	0	0	0	0	0	0	0		
ENSMUST00000132021	ENSMUSG00000064080	6	91212455	91272540	1	0	1	0	0	1	1	0	0	0	1	0	D3Z5B0	
ENSMUST00000132022						64	49	208	54	48	29	20	57	37	8	70		
ENSMUST00000132024	ENSMUSG00000018068	11	86210681	86257575	-1	0	0	0	7	0	0	0	0	0	1	0	A0A0A0MQG3	
ENSMUST00000132025						3	6	10	0	8	2	8	7	6	0	4		
ENSMUST00000132026	ENSMUSG00000032925	14	123659971	123975618	1	0	0	0	0	0	1	0	0	0	0	0	B1B1E3	
ENSMUST00000132027						10	4	35	23	12	2	0	0	0	0	8		
ENSMUST00000132028	ENSMUSG00000039205	2	32352327	32380970	1	0	0	0	0	0	0	31	0	23	0	5	A0A0A0MQJ7	
ENSMUST00000132029						13	7	13	109	8	4	1	4	0	0	2		
ENSMUST00000132030						9	4	10	5	9	2	0	0	0	0	7		
ENSMUST00000132031						3	3	8	66	7	1	0	0	4	7	32		
ENSMUST00000132032	ENSMUSG00000031601	8	40492540	40515847	-1	2	0	4	0	2	0	255	84	49	0	0	Q543X5	Q60809
ENSMUST00000132033						4	2	9	8	3	2	0	0	0	0	0		
ENSMUST00000132034	ENSMUSG00000038803	5	30905885	30907788	-1	7	2	13	30	6	3	622	1169	328	1936	273		Q99LX8
ENSMUST00000132035	ENSMUSG00000027601	3	19187327	19220817	1	1	3	0	71	5	4	5	14	7	0	3	D3Z5W5	
ENSMUST00000132036						5	2	0	0	6	2	0	0	0	5	0		
ENSMUST00000132037	ENSMUSG00000079460	X	112239049	112243852	1	0	0	0	3	0	0	0	0	0	0	0	F6RU76	
ENSMUST00000132038	ENSMUSG00000002602	7	25757273	25788705	-1	0	1	15	0	2	2	0	1	0	0	3	F6YPR4	
ENSMUST00000132039						0	0	3	0	0	0	2	0	0	0	0		
ENSMUST00000132040						3	0	4	0	5	2	0	0	1	0	0		
ENSMUST00000132041	ENSMUSG00000027932	3	90385239	90389938	-1	0	0	0	0	0	0	2	37	0	8	16	F7CPA3	
ENSMUST00000132042	ENSMUSG00000026887	2	36136389	36190647	1	0	3	9	2	1	0	0	1	3	9	0	E0CYT0	
ENSMUST00000132043	ENSMUSG00000028542	4	117834506	117875198	1	9	0	8	0	3	0	0	0	2	0	0	E9QA02	
ENSMUST00000132044						0	0	2	7	2	0	0	0	0	0	0		
ENSMUST00000132045						5	3	1	0	6	2	0	0	0	0	0		
ENSMUST00000132046						7	6	10	17	11	4	9	74	31	1	52		
ENSMUST00000132047	ENSMUSG00000022436	15	78899667	78919517	1	0	0	0	0	0	0	0	0	0	0	0	S4R2D3	
ENSMUST00000132048	ENSMUSG00000039176	7	79446231	79466362	-1	3	1	8	0	0	0	15	6	0	0	26		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132049						1	1	4	5	2	4	0	8	1	0	4		
ENSMUST00000132050						20	26	172	38	34	23	0	0	0	0	0		
ENSMUST00000132051						0	0	0	50	0	0	0	0	0	0	0		
ENSMUST00000132053	ENSMUSG00000021643	13	100107997	100114571	1	2	1	1	10	1	3	0	0	0	0	0	B2KF71	
ENSMUST00000132054						4	1	0	2	4	2	7	0	6	0	14		
ENSMUST00000132055	ENSMUSG00000025978	1	55170159	55226782	-1	0	4	0	4	5	6	3	5	0	6	2	M0QWQ1	
ENSMUST00000132057						72	67	481	114	83	43	2	12	9	4	21		
ENSMUST00000132058						8	10	47	47	12	10	0	2	4	1	6		
ENSMUST00000132059	ENSMUSG00000058656	15	53461621	53902537	-1	4	0	5	0	1	0	0	0	0	1	0	D6RCW1	
ENSMUST00000132060						4	4	6	15	10	5	0	0	0	1	0		
ENSMUST00000132061	ENSMUSG00000025505	7	141327739	141337156	1	0	0	10	0	0	0	1	0	1	0	2		Q9D3H0
ENSMUST00000132062						12	35	24	12	43	16	4	19	2	1	13		
ENSMUST00000132063	ENSMUSG00000001482	8	123442986	123463270	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0I7	
ENSMUST00000132064	ENSMUSG00000025909	1	8361475	9299878	-1	3	0	0	0	0	0	0	0	0	0	0	Q8C415	
ENSMUST00000132065	ENSMUSG00000042190	5	113612354	113650426	-1	3	3	0	4	2	0	0	0	5	0	22	E9Q8N2	
ENSMUST00000132066						2	0	0	0	10	0	43	30	0	0	64		
ENSMUST00000132067	ENSMUSG00000021098	12	72881109	72940774	-1	1	2	5	131	5	2	0	0	0	0	0	D3YZ78	
ENSMUST00000132068						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132071						0	0	8	24	8	0	0	0	0	0	0		
ENSMUST00000132072						1	3	2	39	0	1	0	0	0	0	0		
ENSMUST00000132073	ENSMUSG00000033379	4	117884326	117887333	-1	0	0	0	0	0	0	9	144	45	0	40	M0QW50	
ENSMUST00000132074	ENSMUSG00000026972	2	24925352	24935252	-1	0	0	0	0	0	0	0	0	0	0	0	F6Q4G2	
ENSMUST00000132075						1	1	0	40	0	0	0	2	6	0	2		
ENSMUST00000132078						1	4	0	0	7	0	0	0	0	0	0		
ENSMUST00000132079	ENSMUSG00000020859	11	93996091	94126085	1	6	0	10	8	8	7	0	0	0	0	0	F6WNT4	
ENSMUST00000132080						28	29	91	118	37	11	22	78	43	3	49		
ENSMUST00000132081	ENSMUSG00000026171	1	74593748	74601397	-1	2	0	4	3	3	5	0	7	2	1	9	D3Z0R9	
ENSMUST00000132082						11	4	1	16	7	1	284	2681	325	251	397		
ENSMUST00000132083	ENSMUSG00000055401	4	148145716	148152140	-1	0	0	0	0	0	0	2	0	0	1	3	A2A7H3	
ENSMUST00000132084						2	0	9	46	3	4	24	132	19	4	78		
ENSMUST00000132085						9	9	95	20	23	8	0	0	0	0	0		
ENSMUST00000132086	ENSMUSG00000035545	7	4137039	4148177	1	0	0	0	8	0	0	0	0	0	1	4	D3YTL3	
ENSMUST00000132087						3	5	11	266	6	4	0	4	5	0	4		
ENSMUST00000132088						18	14	7	37	18	6	0	0	0	0	0		
ENSMUST00000132089						6	3	9	1	8	2	0	0	0	1	0		
ENSMUST00000132091	ENSMUSG00000039187	7	79391929	79450264	1	1	17	0	0	0	3	0	14	20	0	34		Q8K368
ENSMUST00000132092						2	1	5	4	3	5	0	1	0	2	2		
ENSMUST00000132093						8	0	0	2	0	0	3	0	0	0	3		
ENSMUST00000132094						59	55	445	81	55	42	0	3	5	0	1		
ENSMUST00000132095						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132096						2	0	7	2	4	1	5	22	3	2	18		
ENSMUST00000132098	ENSMUSG00000020530	11	84832361	84870817	-1	2	0	1	1	0	0	11	185	26	13	27	F6Y247	
ENSMUST00000132099	ENSMUSG00000068329	6	83051266	83055273	-1	0	0	0	0	0	0	0	50	17	10	16	S4R1A8	
ENSMUST00000132102	ENSMUSG00000016503	5	146948657	146955614	1	0	0	0	0	0	0	87	122	75	34	72	F6SIJ4	
ENSMUST00000132103						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000132104						4	3	5	5	2	2	0	0	0	0	0		
ENSMUST00000132105						0	1	4	19	5	1	0	41	0	0	0		
ENSMUST00000132107						1	1	3	18	0	1	0	14	3	2	2		
ENSMUST00000132109						4	0	1	0	0	0	16	17	4	7	28		
ENSMUST00000132110	ENSMUSG00000006576	1	75546266	75562172	1	4	0	6	28	0	0	0	0	0	0	0	F6S265	
ENSMUST00000132112	ENSMUSG00000027977	3	123526166	123690853	-1	0	1	0	3	5	0	0	0	0	0	0	D3YXE5	
ENSMUST00000132113						0	6	0	0	0	8	0	0	1	0	0		
ENSMUST00000132114	ENSMUSG00000033526	2	121310561	121355396	-1	3	1	0	4	1	1	3	0	0	0	0	F7AST3	
ENSMUST00000132115						0	0	0	0	0	0	0	0	0	2	2		
ENSMUST00000132116	ENSMUSG00000000085	4	120405281	120530186	1	0	3	3	0	7	0	0	4	1	0	1	B1AS49	
ENSMUST00000132117						3	5	2	3	2	0	0	0	0	0	0		
ENSMUST00000132118	ENSMUSG00000026385	1	120113280	120121078	-1	0	0	0	0	0	0	0	6	0	0	0	M0QWU8	
ENSMUST00000132119	ENSMUSG00000087444	15	100422147	100428150	1	16	15	10	241	40	9	0	2	0	0	0	D3YV11	
ENSMUST00000132120						79	65	920	187	63	44	0	0	0	0	3		
ENSMUST00000132121	ENSMUSG00000056899	12	41024090	41955588	1	0	0	3	1	0	0	0	0	0	7	0		Q8BPT6
ENSMUST00000132122	ENSMUSG00000021944	14	63198922	63271692	-1	4	3	33	0	6	3	0	0	0	0	0	D3YTQ2	
ENSMUST00000132123	ENSMUSG00000028842	4	126331704	126429556	-1	1	1	1	4	0	1	2	0	0	0	7	A3KFX6	
ENSMUST00000132124						1	4	5	7	4	0	33	412	38	36	86		
ENSMUST00000132125	ENSMUSG00000032717	17	47815328	47834691	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVA0	
ENSMUST00000132126						0	1	0	1	3	1	0	4	0	2	4		
ENSMUST00000132127						70	44	340	96	33	26	0	0	0	0	2		
ENSMUST00000132128	ENSMUSG00000006471	2	25244821	25256022	-1	0	0	1	63	2	0	0	0	0	0	0	E0CX27	
ENSMUST00000132129						42	28	168	31	33	26	1	0	1	0	6		
ENSMUST00000132131						2	6	2	0	3	4	0	0	5	0	8		
ENSMUST00000132132						3	6	28	10	13	6	0	0	0	0	0		
ENSMUST00000132133	ENSMUSG00000034472	8	75213944	75224113	1	6	6	1	3	5	0	0	0	0	0	0		P63032
ENSMUST00000132134						3	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000132135						1	0	6	13	4	3	0	14	0	1	0		
ENSMUST00000132136	ENSMUSG00000025871	13	54551218	54565435	-1	2	0	0	78	4	0	4	5	12	0	0	D3YTM8	
ENSMUST00000132139	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0	D3Z080	
ENSMUST00000132141						0	1	0	3	0	5	0	0	0	0	0		
ENSMUST00000132142						3	0	3	0	3	0	2	1	0	0	0		
ENSMUST00000132143						153	145	472	241	165	94	18	78	38	23	45		
ENSMUST00000132144	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	0	0	0	0	0	F6ZGQ1	
ENSMUST00000132145						0	0	1	0	0	1	0	17	0	18	8		
ENSMUST00000132146						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000132147	ENSMUSG00000004394	11	6270369	6274870	-1	0	0	0	0	0	0	28	3	5	16	13	Q5SVW9	
ENSMUST00000132148						7	4	3	0	5	3	0	0	0	0	0		
ENSMUST00000132150	ENSMUSG00000000282	11	74830920	74845725	1	2	1	4	0	0	2	20	0	0	4	20	Q5SWE2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132151	ENSMUSG00000054752	4	53631471	53707009	1	0	0	0	64	5	0	0	0	0	0	0		Q8BYN5
ENSMUST00000132152						19	28	59	27	30	15	4	40	7	2	20		
ENSMUST00000132153	ENSMUSG00000051506	14	32959547	33185508	-1	4	4	0	0	3	0	0	2	0	0	2	F6X8K3	
ENSMUST00000132155						10	0	0	5	5	2	0	0	0	2	1		
ENSMUST00000132156						0	6	0	0	0	1	0	0	0	0	0		
ENSMUST00000132157						0	0	0	0	0	0	0	16	38	0	0		
ENSMUST00000132158	ENSMUSG00000026696	1	162570515	162599084	1	0	0	12	73	22	11	0	133	269	78	301	Q8BSN6	
ENSMUST00000132159	ENSMUSG00000020457	11	3187360	3266415	-1	0	1	0	34	0	0	0	0	0	0	0	D6RHA5	
ENSMUST00000132161	ENSMUSG00000063450	12	75818134	76110926	1	0	7	0	9	19	8	69	166	0	31	0	F7BX34	
ENSMUST00000132162						5	14	12	13	5	8	0	0	0	0	0		
ENSMUST00000132163	ENSMUSG00000038797	7	80860920	80876537	1	0	4	0	47	0	0	0	0	1	0	7	D3YYN4	
ENSMUST00000132164	ENSMUSG00000001750	19	3896050	3907133	-1	0	2	0	0	0	0	1	0	0	0	0	F6XRE6	
ENSMUST00000132165	ENSMUSG00000028552	4	109280268	109387817	1	3	0	0	0	3	0	13	182	3	0	0	F6W2Q5	
ENSMUST00000132166						14	12	4	16	3	4	0	0	0	0	1		
ENSMUST00000132168	ENSMUSG00000018882	11	97315716	97329920	1	0	7	5	9	8	12	12	0	0	4	9	F6QAU7	
ENSMUST00000132169	ENSMUSG00000029208	5	69556923	69575973	1	27	37	67	30	32	13	2	19	9	0	27		
ENSMUST00000132170						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132171						1	5	9	2	3	2	0	0	0	1	0		
ENSMUST00000132172	ENSMUSG00000006476	2	25054355	25062881	1	0	1	0	4	0	0	0	0	0	0	0	A2AJ90	
ENSMUST00000132173	ENSMUSG00000036062	4	42916660	42944752	1	2	0	0	13	1	0	0	1	0	0	0	S4R202	
ENSMUST00000132174						37	34	115	109	79	17	0	4	5	0	0		
ENSMUST00000132175						6	10	8	2	7	1	0	0	0	0	0		
ENSMUST00000132176	ENSMUSG00000022770	16	31663443	31873356	1	0	0	0	9	0	0	34	68	0	0	11	S4R2T8	
ENSMUST00000132177						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132178						11	8	16	32	15	6	0	7	0	0	2		
ENSMUST00000132179	ENSMUSG00000004815	5	108646693	108669672	-1	3	0	0	99	0	0	0	0	49	0	37	D6RI30	
ENSMUST00000132180	ENSMUSG00000031554	8	24727093	24824369	-1	0	5	0	2	2	7	0	0	0	0	0	F6S1B5	
ENSMUST00000132181						85	55	126	89	115	41	116	604	170	30	143		
ENSMUST00000132182						2	1	6	1	2	1	0	0	0	0	1		
ENSMUST00000132183	ENSMUSG00000047284	11	69901072	69913820	1	0	1	1	3	8	1	54	76	26	7	27	F6WND1	
ENSMUST00000132185						16	13	13	14	20	8	3	4	5	0	9		
ENSMUST00000132186	ENSMUSG00000068882	2	69861562	69871846	1	0	0	0	0	4	0	55	695	384	650	213	D6RI87	
ENSMUST00000132187	ENSMUSG00000000167	9	50617321	50625000	1	0	0	0	0	0	0	0	0	0	0	0		Q8CHR9
ENSMUST00000132188						0	0	21	103	6	6	0	0	8	0	9		
ENSMUST00000132189						1	0	0	2	5	0	9	140	64	9	38		
ENSMUST00000132190	ENSMUSG00000067367	5	38220470	38234306	1	1	0	3	55	5	0	0	0	0	0	3	D3Z345	
ENSMUST00000132191	ENSMUSG00000023328	5	137287519	137294466	1	0	1	7	5	1	3	0	0	1	0	0	D3Z064	
ENSMUST00000132192						1	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000132193						0	0	0	30	0	0	1	117	24	23	38		
ENSMUST00000132194						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132195	ENSMUSG00000019338	3	95006590	95015448	-1	10	2	5	45	2	1	16	4	14	0	25	D3Z524	
ENSMUST00000132196						4	0	3	3	4	4	1	0	0	0	0		
ENSMUST00000132197	ENSMUSG00000025371	11	119913441	119919548	1	1	1	2	0	3	1	0	0	18	4	7	B1AZ42	
ENSMUST00000132198	ENSMUSG00000018442	11	71007164	71019841	-1	0	0	0	4	0	0	10	0	0	0	0	J3QMQ7	
ENSMUST00000132199						27	17	58	24	26	12	0	0	0	0	0		
ENSMUST00000132200						0	0	0	0	0	1	5	58	11	0	0		
ENSMUST00000132201						1	2	3	42	3	3	0	3	1	0	0		
ENSMUST00000132202	ENSMUSG00000047731	19	46599084	46657389	1	0	0	145	9	39	32	325	589	797	0	839		Q8BGW2
ENSMUST00000132204	ENSMUSG00000032743	7	125707888	125874793	1	0	3	0	0	2	0	0	0	0	0	0	F6UDS6	
ENSMUST00000132205						4	3	0	5	14	0	5	186	37	3	63		
ENSMUST00000132206						2	0	1	2	7	0	0	0	0	0	0		
ENSMUST00000132207	ENSMUSG00000033740	1	6487231	6860940	1	2	2	0	0	3	0	0	0	0	0	0	A0A0A6YY81	
ENSMUST00000132208						2	1	1	1	3	1	0	1	3	0	0		
ENSMUST00000132209						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132212	ENSMUSG00000027509	2	173000117	173015739	1	0	1	0	0	0	1	7	5	43	0	26	A2ASC6	
ENSMUST00000132213						2	0	0	0	0	1	6	0	2	4	2		
ENSMUST00000132214						16	7	11	3	8	6	0	0	0	0	0		
ENSMUST00000132215						20	17	35	16	15	16	17	28	64	0	53		
ENSMUST00000132216						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000132217	ENSMUSG00000053841	4	129626078	129641065	-1	0	0	0	0	2	0	26	0	31	0	0	A2ADZ3	
ENSMUST00000132220						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000132222						2	4	5	356	16	7	0	0	0	0	1		
ENSMUST00000132224						0	1	5	2	2	2	3	5	11	0	3		
ENSMUST00000132225						48	62	314	76	58	36	9	0	4	0	0		
ENSMUST00000132227	ENSMUSG00000023110	14	54507187	54517525	-1	0	0	0	16	0	0	2	0	0	0	0	S4R295	
ENSMUST00000132228	ENSMUSG00000026207	1	75375297	75432320	1	0	0	0	0	0	1	0	0	0	0	0	F6RU40	
ENSMUST00000132229	ENSMUSG00000031824	8	120114152	120165306	1	2	0	0	0	0	0	0	0	2	0	2	D3Z5E4	
ENSMUST00000132230						0	0	4	44	1	3	1	0	0	0	2		
ENSMUST00000132231	ENSMUSG00000017765	8	105943590	105966115	-1	0	0	0	0	0	1	0	0	0	0	0	F6TQE2	
ENSMUST00000132232						3	2	4	14	4	2	0	0	0	0	1		
ENSMUST00000132233	ENSMUSG00000017778	13	86044816	86046904	-1	4	1	0	15	1	1	6	40	6	14	5	B8JJA9	
ENSMUST00000132234						1	4	7	4	6	3	6	7	3	0	9		
ENSMUST00000132235	ENSMUSG00000028437	4	41348996	41390525	1	5	1	0	0	3	0	46	324	122	16	68	F6WHE1	
ENSMUST00000132236						4	2	5	7	3	2	0	0	0	0	0		
ENSMUST00000132237	ENSMUSG00000028392	4	62480053	62497298	1	0	1	0	92	3	3	0	0	0	0	0	D6RIR4	
ENSMUST00000132238	ENSMUSG00000061462	11	58994256	59136402	-1	0	0	0	0	0	0	0	0	0	0	0	F7DCJ0	
ENSMUST00000132239						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132240						0	0	0	0	0	0	9	36	37	16	30		
ENSMUST00000132241	ENSMUSG00000003526	16	18060357	18090203	-1	6	1	4	3	7	0	0	5	0	0	1	F6XMC0	
ENSMUST00000132242						0	0	0	3	1	0	0	0	2	0	2		
ENSMUST00000132243	ENSMUSG00000055912	6	72355447	72359762	1	4	4	4	14	6	5	4	5	0	2	4	S4R204	
ENSMUST00000132244						1	1	5	6	0	0	10	6	10	5	0		
ENSMUST00000132245	ENSMUSG00000018411	11	104231390	104332090	1	1	0	0	0	0	0	0	0	0	0	0	B1AQW6	
ENSMUST00000132246						0	0	2	0	0	0	0	0	0	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132249	ENSMUSG00000034218	9	53439149	53536740	-1	0	0	0	0	0	0	1	3	0	0	5	F6UXV2	
ENSMUST00000132250						25	19	22	60	14	7	1	0	1	1	4		
ENSMUST00000132251	ENSMUSG00000040690	4	130047840	130099283	1	3	0	8	12	2	1	0	0	0	0	0	A3KFV1	
ENSMUST00000132252	ENSMUSG00000026211	1	75479310	75506452	-1	3	2	0	51	9	0	0	0	0	0	0	F7AGE9	
ENSMUST00000132253	ENSMUSG00000038803	5	30905885	30907788	-1	1	2	3	17	0	3	329	559	265	1265	146		Q99LX8
ENSMUST00000132255						2	0	0	0	1	0	0	14	2	7	0		
ENSMUST00000132256	ENSMUSG00000057123	3	96904693	97077416	1	0	0	2	6	0	0	0	0	0	0	0	Q6TPI9	
ENSMUST00000132257						2	1	2	0	0	0	0	0	0	0	3		
ENSMUST00000132258						6	8	7	6	6	2	4	12	3	4	13		
ENSMUST00000132259						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000132260						0	1	0	1	0	1	4	5	0	0	5		
ENSMUST00000132263	ENSMUSG00000028391	4	62448653	62470896	-1	0	0	0	2	0	0	0	1	0	0	0	B7ZCH4	
ENSMUST00000132265						36	44	44	36	49	17	6	10	2	0	7		
ENSMUST00000132266						1	2	6	2	4	0	0	0	0	0	2		
ENSMUST00000132268						7	0	5	3	7	4	2	0	0	0	0		
ENSMUST00000132269						1	5	27	3	3	2	0	25	0	5	0		
ENSMUST00000132270	ENSMUSG00000017664	2	165276554	165287869	-1	8	0	0	0	7	9	56	663	0	28	219	E0CYZ1	
ENSMUST00000132271						0	0	0	0	0	0	1	0	0	0	2		
ENSMUST00000132272						0	0	0	28	0	0	2	2	4	2	1		
ENSMUST00000132273						3	3	6	41	4	0	0	0	2	0	0		
ENSMUST00000132274						50	0	0	130	0	0	0	0	0	0	0		
ENSMUST00000132275						0	0	0	0	0	0	0	10	0	0	0		
ENSMUST00000132276						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000132277						20	28	27	16	20	3	44	99	75	9	142		
ENSMUST00000132278						8	12	10	5	6	10	40	26	40	2	37		
ENSMUST00000132279	ENSMUSG00000031537	8	22659212	22706589	-1	5	3	1	0	0	0	3	22	12	0	2	F6XPL0	
ENSMUST00000132280	ENSMUSG00000020681	11	105967945	105989964	1	11	6	29	44	8	0	12	22	9	3	36	F6QCP8	
ENSMUST00000132281	ENSMUSG00000029059	4	154895504	154899135	-1	0	2	8	12	1	0	0	0	0	0	0	B1AS14	
ENSMUST00000132282	ENSMUSG00000017764	2	164822686	164826871	1	5	0	9	24	4	2	0	0	0	0	0	A2A5J2	
ENSMUST00000132283	ENSMUSG00000027993	3	84160439	84306877	-1	0	1	3	0	0	1	0	0	0	0	0	D3YY69	
ENSMUST00000132284						5	0	3	2	6	2	0	0	0	0	0		
ENSMUST00000132285						1	1	12	78	3	3	3	19	2	2	4		
ENSMUST00000132286						13	11	17	37	12	4	0	0	1	0	0		
ENSMUST00000132287						2	1	10	2	1	0	0	0	0	0	0		
ENSMUST00000132288						0	0	7	0	2	0	145	255	156	44	127		
ENSMUST00000132289						1	4	4	0	2	5	0	2	0	3	2		
ENSMUST00000132290						0	0	0	1	2	0	0	0	0	0	9		
ENSMUST00000132291						1	0	4	4	4	3	0	18	0	0	0		
ENSMUST00000132292						4	1	4	2	0	0	11	11	22	3	47		
ENSMUST00000132293	ENSMUSG00000031969	9	26974135	26999566	-1	0	0	7	5	0	0	0	0	0	0	0	D6RDD5	
ENSMUST00000132295						0	0	0	40	0	2	0	14	0	0	0		
ENSMUST00000132298	ENSMUSG00000093485	11	117809668	117839904	1	9	4	33	23	21	10	0	56	18	0	32	H3BKF4	
ENSMUST00000132299						2	1	18	2	3	0	0	0	0	0	0		
ENSMUST00000132300						2	0	0	0	3	1	0	0	5	2	0		
ENSMUST00000132301						0	6	23	32	6	3	2	6	2	0	5		
ENSMUST00000132302						0	2	0	0	9	0	0	0	0	0	0		
ENSMUST00000132303						4	7	57	8	6	5	3	0	3	0	5		
ENSMUST00000132304	ENSMUSG00000025451	13	119428601	119458218	1	0	0	0	48	6	0	0	0	0	0	0	G3UZS6	
ENSMUST00000132305						6	7	16	38	18	6	4	14	2	2	38		
ENSMUST00000132306						7	6	5	30	6	3	8	57	29	4	55		
ENSMUST00000132307	ENSMUSG00000020044	10	86300372	86349506	1	1	2	1	0	6	0	0	0	0	0	0	E9QAB2	
ENSMUST00000132308	ENSMUSG00000020549	11	64979038	65002069	1	0	0	6	1	2	3	0	0	0	0	0	B1ATP9	
ENSMUST00000132309	ENSMUSG00000025877	13	55005985	55021385	-1	0	0	0	0	0	0	358	3421	817	314	911	D6RFA3	
ENSMUST00000132310						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132311						3	0	0	0	0	2	0	0	9	0	0		
ENSMUST00000132312						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000132313						6	7	15	95	15	12	52	221	96	3	113		
ENSMUST00000132314						5	1	2	5	5	3	0	20	9	0	10		
ENSMUST00000132315						9	16	20	17	7	4	3	0	0	0	0		
ENSMUST00000132316	ENSMUSG00000022678	16	14163275	14192928	1	9	0	0	0	0	0	0	0	0	0	0	D6RJ36	
ENSMUST00000132317						0	0	9	0	6	3	0	1	0	0	0		
ENSMUST00000132318	ENSMUSG00000037007	5	138139702	138155744	-1	0	0	1	0	1	3	2	0	0	3	0	D3Z3H8	
ENSMUST00000132319	ENSMUSG00000025665	X	111388192	111537959	-1	0	0	0	0	0	0	0	0	0	0	0	B1B0X2	
ENSMUST00000132320						18	18	13	12	16	9	0	696	0	64	112		
ENSMUST00000132322						1	1	8	1	4	0	0	0	0	0	0		
ENSMUST00000132324						4	1	7	0	1	1	31	45	23	10	28		
ENSMUST00000132325	ENSMUSG00000027849	3	103575231	103645569	1	0	5	0	0	0	11	0	0	1	0	0	D6RHQ5	
ENSMUST00000132327						2	3	4	0	7	0	0	6	0	0	0		
ENSMUST00000132328	ENSMUSG00000034164	11	5106265	5152257	-1	0	5	15	0	0	4	0	0	4	0	0	F6YMU2	
ENSMUST00000132329	ENSMUSG00000042185	9	31386192	31421333	1	16	5	40	17	12	0	77	43	91	0	179	D6RHP5	
ENSMUST00000132330	ENSMUSG00000028020	3	80843599	80913660	-1	0	2	3	13	1	2	0	0	0	0	0	E9PV81	
ENSMUST00000132331						1	3	7	3	0	2	0	0	0	0	1		
ENSMUST00000132333						2	0	1	6	2	5	0	0	0	0	0		
ENSMUST00000132334						2	3	2	26	5	3	0	3	2	1	1		
ENSMUST00000132335						2	0	0	1	0	2	1	0	0	0	2		
ENSMUST00000132338	ENSMUSG00000002320	14	55635965	55643806	-1	0	2	16	36	0	5	0	0	56	0	37	D3YWH4	
ENSMUST00000132339						12	15	18	9	14	7	2	12	15	3	56		
ENSMUST00000132340						86	74	126	106	117	52	18	24	14	3	18		
ENSMUST00000132341						1	0	0	0	11	1	0	2	1	0	0		
ENSMUST00000132342						1	3	4	0	1	0	0	0	0	0	0		
ENSMUST00000132343						0	1	1	3	0	1	0	0	0	0	0		
ENSMUST00000132344	ENSMUSG00000035632	7	3645268	3661109	1	0	0	0	0	0	0	76	103	54	0	56	F6YBV1	
ENSMUST00000132345						20	19	39	24	26	17	0	6	0	1	3		
ENSMUST00000132346						1	0	0	3	0	0	8	19	400	5	123		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132347						31	25	34	18	24	16	0	36	101	0	84		
ENSMUST00000132348						0	0	5	2	0	0	0	0	0	0	0		
ENSMUST00000132349						1	0	3	1	2	0	0	0	5	0	5		
ENSMUST00000132350						1	0	1	4	3	1	20	58	14	0	14		
ENSMUST00000132351	ENSMUSG00000053091	7	66689889	66717256	1	0	0	0	0	1	3	11	4	18	0	0	F6SLL8	
ENSMUST00000132352						2	2	34	10	7	2	1	0	4	0	9		
ENSMUST00000132353	ENSMUSG00000070360	3	113529403	113532428	-1	5	0	0	0	0	0	0	0	0	0	0	E9PV85	
ENSMUST00000132354						4	2	17	12	6	5	3	13	6	1	8		
ENSMUST00000132355						1	0	14	6	8	0	0	0	0	0	0		
ENSMUST00000132356						0	2	0	0	1	1	0	7	4	4	5		
ENSMUST00000132357						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132358	ENSMUSG00000028329	4	46155347	46196311	-1	0	0	3	0	4	1	22	144	35	26	29	S4R260	
ENSMUST00000132359						3	2	11	93	6	2	0	10	0	0	0		
ENSMUST00000132360						4	0	10	1	13	3	10	13	0	14	1		
ENSMUST00000132361						1	4	3	0	2	1	0	0	0	0	0		
ENSMUST00000132362						2	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000132363						4	0	10	0	2	0	0	0	0	0	0		
ENSMUST00000132364						7	3	0	0	5	2	5	47	39	0	37		
ENSMUST00000132365						0	0	0	9	5	0	0	0	0	0	2		
ENSMUST00000132366	ENSMUSG00000047766	9	60568859	60688158	-1	3	0	7	1	2	0	0	0	0	0	0	D3Z2Y1	
ENSMUST00000132367	ENSMUSG00000029049	4	155086577	155145505	1	9	6	8	16	13	5	2	0	0	0	12	F2Z475	
ENSMUST00000132368	ENSMUSG00000034854	10	81357491	81366225	1	0	0	0	69	0	0	0	0	0	0	0	D6RJ45	
ENSMUST00000132369	ENSMUSG00000041607	18	82475146	82585637	1	0	0	0	0	0	6	0	0	0	0	0	F6ZIA4	
ENSMUST00000132371						0	1	0	41	0	0	0	8	0	4	0		
ENSMUST00000132372						8	4	9	14	10	4	0	0	0	0	0		
ENSMUST00000132373						15	7	5	8	13	6	12	132	52	8	29		
ENSMUST00000132374	ENSMUSG00000021772	14	18271136	18283942	1	51	50	139	70	62	18	12	16	11	6	14		Q8CEC5
ENSMUST00000132375	ENSMUSG00000037605	5	81020138	81825133	1	0	0	0	0	0	0	0	0	0	0	0	D6RFB0	
ENSMUST00000132376	ENSMUSG00000053898	7	28825217	28832247	1	0	0	0	0	0	0	0	0	0	0	0	F7B227	
ENSMUST00000132377						2	2	1	1	2	1	0	0	0	0	0		
ENSMUST00000132379						5	6	2	9	5	1	0	4	0	0	0		
ENSMUST00000132380						1	1	8	2	1	0	0	41	8	0	8		
ENSMUST00000132381						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132382						3	1	3	5	3	0	9	14	25	2	83		
ENSMUST00000132383	ENSMUSG00000029190	5	36600485	36696024	-1	21	14	81	28	43	29	0	413	84	15	14	F7D143	
ENSMUST00000132384						24	0	1	331	39	11	5	5	7	3	7		
ENSMUST00000132385						2	2	15	9	6	4	18	41	20	2	27		
ENSMUST00000132386						0	0	16	0	0	0	3	7	2	8	0		
ENSMUST00000132387						610	549	655	357	707	274	12	44	34	19	51		
ENSMUST00000132388						2	0	7	6	0	2	0	0	0	0	0		
ENSMUST00000132390						650	885	3394	1020	845	432	18	67	23	6	37		
ENSMUST00000132391						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000132392						0	3	6	2	2	1	2	21	6	0	6		
ENSMUST00000132393	ENSMUSG00000005774	3	94954075	94961561	1	0	0	0	0	0	2	0	0	0	0	0	D3YVW1	
ENSMUST00000132395						3	1	0	3	1	0	0	0	0	0	0		
ENSMUST00000132396						0	0	0	0	0	0	73	34	9	0	33		
ENSMUST00000132397	ENSMUSG00000023984	17	47611589	47683861	1	0	0	0	123	0	0	0	5	13	0	0	G3UVU6	
ENSMUST00000132398						4	0	0	1	1	1	0	5	3	2	7		
ENSMUST00000132399						4	1	2	12	5	3	0	0	0	0	1		
ENSMUST00000132400						4	4	1	4	3	1	0	0	0	0	0		
ENSMUST00000132401	ENSMUSG00000026113	1	37299865	37410736	1	0	0	0	15	13	0	241	118	509	0	321	D3YUL8	
ENSMUST00000132402						2	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000132403						2	2	8	2	0	0	0	0	0	0	0		
ENSMUST00000132404	ENSMUSG00000075703	5	30232581	30272427	1	1	0	19	0	0	0	64	147	70	11	22	Q8CET7	
ENSMUST00000132405						0	1	3	0	0	0	0	0	0	1	0		
ENSMUST00000132406						7	4	3	1	0	0	0	0	0	0	0		
ENSMUST00000132408						126	75	177	78	130	66	6	22	5	0	23		
ENSMUST00000132409	ENSMUSG00000045794	2	181696793	181698442	-1	0	0	1	0	0	0	0	0	0	0	0	F6RL86	
ENSMUST00000132410						65	69	151	33	33	25	3	10	2	0	7		
ENSMUST00000132411						5	7	12	3	5	2	0	0	0	0	4		
ENSMUST00000132412						0	0	1	4	0	0	0	0	0	2	10		
ENSMUST00000132413						1	2	0	1	2	0	3	20	7	0	2		
ENSMUST00000132415	ENSMUSG00000074895	13	54783998	54788459	1	0	0	3	0	0	0	1	2	5	0	5	Q27ZI8	
ENSMUST00000132416						0	0	0	19	0	2	1	23	3	0	0		
ENSMUST00000132417	ENSMUSG00000028608	4	107889813	107899384	1	18	11	61	43	10	6	12	67	12	19	15	D6REH4	
ENSMUST00000132418	ENSMUSG00000053702	2	17343909	17731464	-1	3	0	0	0	5	0	0	0	0	0	0		Q0II04
ENSMUST00000132419						4	1	6	0	0	0	3	2	16	4	9		
ENSMUST00000132420						0	1	1	10	2	0	2	4	2	0	4		
ENSMUST00000132421						0	4	4	0	4	0	3	3	0	0	0		
ENSMUST00000132422						3	2	3	19	8	4	2	9	4	0	11		
ENSMUST00000132423						2	0	0	4	0	0	2	0	0	0	2		
ENSMUST00000132424	ENSMUSG00000040666	16	96200470	96228933	1	2	0	0	0	0	0	0	0	0	2	0	F6X737	
ENSMUST00000132425						1	0	0	0	0	0	0	5	0	0	2		
ENSMUST00000132426						6	0	0	0	4	2	0	0	0	0	0		
ENSMUST00000132427						3	0	12	5	6	0	1	0	0	5	0		
ENSMUST00000132428	ENSMUSG00000035967	X	56454857	56507843	1	0	1	0	5	2	0	24	9	2	135	155		Q8BND4
ENSMUST00000132429	ENSMUSG00000027198	2	93661028	93822568	-1	0	1	3	2	4	0	0	9	0	0	1	F6WHC9	
ENSMUST00000132430	ENSMUSG00000043987	9	45766946	45828691	-1	8	5	20	30	3	11	17	9	44	0	29	F7AUV3	
ENSMUST00000132431						2	3	13	8	3	1	3	42	19	2	33		
ENSMUST00000132433						1	3	15	5	3	0	0	49	9	4	14		
ENSMUST00000132434						16	22	57	20	22	16	10	15	27	4	45		
ENSMUST00000132435	ENSMUSG00000042066	1	132356315	132391281	-1	10	6	46	22	8	5	9	0	0	0	0	Q3TZY4	
ENSMUST00000132436						25	11	61	30	12	10	0	0	0	0	3		
ENSMUST00000132437	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	0	0	0	0	0	0	0	0	H3BK99	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132438	ENSMUSG00000058794	15	103248212	103258403	-1	1	0	4	1	0	0	2	4	0	0	0	D3Z706	
ENSMUST00000132439						3	1	2	20	2	5	0	0	0	0	5		
ENSMUST00000132441	ENSMUSG00000044005	10	128194457	128210004	1	0	1	4	0	0	0	0	0	0	5	0	F6SJZ7	
ENSMUST00000132442	ENSMUSG00000045374	11	75440944	75454717	-1	0	3	24	4	4	0	125	523	27	26	71	F6XD87	
ENSMUST00000132443						1	0	6	0	1	0	0	1	0	0	0		
ENSMUST00000132444	ENSMUSG00000041650	14	122534324	122891100	1	0	0	0	0	0	0	0	0	0	0	0	H3BJR0	
ENSMUST00000132445						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132446						5	3	6	3	1	2	4	12	5	5	6		
ENSMUST00000132447						0	6	4	2	6	3	5	0	0	0	0		
ENSMUST00000132448	ENSMUSG00000014077	2	119547697	119587027	1	0	0	1	0	3	4	0	1	5	0	0	B0R092	
ENSMUST00000132449	ENSMUSG00000010914	2	103021075	103073513	-1	0	0	0	0	1	0	5	0	0	13	5	A2AWH7	
ENSMUST00000132450						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000132451	ENSMUSG00000006527	14	30714849	30822713	1	0	0	0	0	0	0	0	35	0	0	1	F6W207	
ENSMUST00000132452	ENSMUSG00000025008	19	40596446	40612233	-1	3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132453						1	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000132454						4	0	4	0	5	0	0	2	6	0	8		
ENSMUST00000132455						3	5	8	4	2	2	0	0	4	0	1		
ENSMUST00000132456						10	0	9	9	12	4	127	1106	449	54	772		
ENSMUST00000132457	ENSMUSG00000029304	5	104435118	104441050	1	0	1	0	0	0	1	0	0	0	0	0	D3Z116	
ENSMUST00000132458	ENSMUSG00000054708	10	81628540	81647610	1	4	3	3	0	0	2	1	2	1	9	3	F6PZI9	
ENSMUST00000132459	ENSMUSG00000039262	2	32151082	32234537	1	0	0	0	2	6	0	30	0	137	0	87	F7AYW2	
ENSMUST00000132460						0	0	0	2	1	0	8	0	1	2	6		
ENSMUST00000132461						5	0	0	0	5	2	0	0	0	0	0		
ENSMUST00000132462	ENSMUSG00000020893	11	69095217	69109960	1	0	0	2	24	0	0	0	0	21	0	0	B0QZN6	
ENSMUST00000132463						0	1	8	9	0	0	0	112	36	0	83		
ENSMUST00000132464	ENSMUSG00000079169	2	111134114	111152936	-1	0	0	0	0	1	1	0	0	0	0	0	F6PYN5	
ENSMUST00000132466						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000132467	ENSMUSG00000068739	3	108424865	108445209	-1	0	0	0	0	0	3	20	0	0	0	10	A2AFS0	
ENSMUST00000132468						18	38	41	42	34	19	7	16	7	3	26		
ENSMUST00000132469						0	0	0	2	4	0	0	6	0	2	7		
ENSMUST00000132471						0	0	0	0	0	0	16	0	65	0	0		
ENSMUST00000132472						6	6	2	12	4	6	0	1	7	1	3		
ENSMUST00000132473						1	1	5	0	5	1	1	0	0	0	2		
ENSMUST00000132475	ENSMUSG00000079620	16	32735886	32782391	1	0	1	17	0	0	0	0	0	0	0	0	E9Q9U1	
ENSMUST00000132476						3	0	16	3	3	1	0	0	8	0	6		
ENSMUST00000132477						0	1	4	128	5	0	0	0	0	0	0		
ENSMUST00000132478						1	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000132479						32	57	77	25	47	24	11	9	15	3	18		
ENSMUST00000132480						7	4	13	251	12	11	33	106	64	0	37		
ENSMUST00000132481						6	5	9	1	4	0	0	0	0	0	1		
ENSMUST00000132482						0	0	7	0	2	0	0	0	0	0	0		
ENSMUST00000132483						6	0	8	8	9	4	0	0	0	0	0		
ENSMUST00000132484	ENSMUSG00000026771	2	23506220	23572106	-1	13	8	18	12	22	11	25	34	34	16	38		Q2M2N2
ENSMUST00000132486						0	1	8	3	3	0	23	69	36	28	35		
ENSMUST00000132490						3	1	0	0	0	1	0	0	0	0	7		
ENSMUST00000132491						17	19	91	39	18	14	4	31	12	0	24		
ENSMUST00000132492						2	5	8	2	6	1	2	2	0	2	1		
ENSMUST00000132493	ENSMUSG00000028497	4	88396144	88438928	-1	12	14	38	20	12	7	30	141	16	10	26	Z4YMP4	
ENSMUST00000132494	ENSMUSG00000098950	2	156071845	156127092	-1	19	11	0	0	0	6	20	0	62	0	0	V9GXJ1	
ENSMUST00000132495						0	1	1	2	2	0	26	5	19	0	51		
ENSMUST00000132496	ENSMUSG00000018395	11	53567379	53601967	1	0	0	8	8	4	2	0	0	0	0	0	F6V6Z9	
ENSMUST00000132497	ENSMUSG00000038729	4	57717657	57896982	1	0	0	0	0	4	0	0	0	0	0	0	A2API9	
ENSMUST00000132498						1	2	3	1	3	0	16	27	8	0	26		
ENSMUST00000132499						2	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000132500	ENSMUSG00000013033	8	83900105	83941954	1	5	0	4	7	0	5	0	0	0	0	0	E9Q9Q9	
ENSMUST00000132501	ENSMUSG00000031402	X	75109733	75131016	-1	0	0	0	0	0	1	0	1	0	53	29	B7ZCL9	
ENSMUST00000132502						4	1	3	33	4	1	0	1	1	0	0		
ENSMUST00000132503						5	10	9	14	6	1	0	13	1	0	12		
ENSMUST00000132504						3	3	6	2	3	2	0	14	14	11	14		
ENSMUST00000132505						3	3	22	3	5	4	7	16	12	0	8		
ENSMUST00000132506						5	4	8	7	8	3	0	0	2	2	0		
ENSMUST00000132507						0	0	9	0	0	0	0	0	0	3	8		
ENSMUST00000132508						0	1	2	1	2	4	0	0	2	0	2		
ENSMUST00000132509	ENSMUSG00000033917	7	118688545	118705778	-1	4	3	13	27	5	2	21	18	22	0	0	D3Z3E2	
ENSMUST00000132510	ENSMUSG00000040473	5	5579278	5664239	-1	0	0	0	0	0	0	0	0	0	0	0	D6RFV9	
ENSMUST00000132511						1	1	2	0	0	2	0	0	0	0	0		
ENSMUST00000132512						0	4	2	2	0	0	0	0	0	0	0		
ENSMUST00000132513	ENSMUSG00000028571	4	96027534	96077546	-1	2	3	2	1	3	0	0	0	0	0	0	F6R6R4	
ENSMUST00000132514	ENSMUSG00000026848	2	30952959	30959015	1	0	0	0	0	0	0	0	0	0	0	0	F6ZDX6	
ENSMUST00000132515						3	0	2	1	7	3	13	7	2	0	0		
ENSMUST00000132516	ENSMUSG00000039254	2	32236590	32255005	1	0	0	0	2	4	0	3	5	0	4	0	D6RI46	
ENSMUST00000132517	ENSMUSG00000035722	10	79996494	80015572	1	68	0	82	204	28	0	2222	1979	1804	94	2336		Q91V24
ENSMUST00000132518						4	2	5	39	1	3	0	0	0	0	0		
ENSMUST00000132519						0	0	2	0	0	3	40	0	59	0	56		
ENSMUST00000132520	ENSMUSG00000031090	7	143795584	143822849	-1	7	1	31	0	14	9	14	8	39	0	0	G5E8V4	
ENSMUST00000132521						0	2	0	2	0	0	117	211	74	7	54		
ENSMUST00000132522						0	4	0	0	1	0	0	42	34	11	69		
ENSMUST00000132523	ENSMUSG00000035640	10	80130451	80140835	-1	0	1	0	0	0	0	0	0	2	0	1	E9Q6U0	
ENSMUST00000132524	ENSMUSG00000045639	7	127607031	127615797	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSE9	
ENSMUST00000132525	ENSMUSG00000029713	5	137528127	137533510	-1	0	0	0	0	0	0	1190	183	307	0	61	D3Z1M1	
ENSMUST00000132526						0	1	1	0	1	0	0	4	0	0	2		
ENSMUST00000132527	ENSMUSG00000027570	2	180597790	180622189	1	6	5	15	43	15	0	0	0	0	0	0	A2ACT7	
ENSMUST00000132528	ENSMUSG00000018750	11	69765912	69784023	1	1	0	0	78	5	1	0	0	0	0	0	Q5F295	
ENSMUST00000132529						0	0	6	0	0	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132530						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000132531						0	1	4	0	4	4	0	0	0	0	0		
ENSMUST00000132533						44	29	98	61	64	39	15	18	18	0	43		
ENSMUST00000132534						2	7	27	3	16	4	0	0	0	0	0		
ENSMUST00000132535						54	45	161	34	26	15	1	2	2	0	8		
ENSMUST00000132536						4	1	2	3	0	0	0	4	0	0	0		
ENSMUST00000132537						3	2	5	0	2	2	2	7	23	7	36		
ENSMUST00000132538	ENSMUSG00000000823	2	181582103	181592803	-1	0	1	0	0	0	2	1	0	0	0	4	F6R5G3	
ENSMUST00000132539						0	0	0	0	0	0	6	0	5	0	0		
ENSMUST00000132540						0	1	3	0	2	4	4	3	0	0	7		
ENSMUST00000132541	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	0	0	0	0	0	0	3	0		P0C8K7
ENSMUST00000132542						0	0	0	1	2	0	0	0	55	0	5		
ENSMUST00000132543	ENSMUSG00000020929	11	102838473	102880985	-1	0	2	0	0	1	0	0	25	0	5	0	G3UXK8	
ENSMUST00000132544						2	2	0	2	8	0	0	0	0	0	0		
ENSMUST00000132545	ENSMUSG00000028776	4	130164454	130175122	-1	6	5	24	69	15	6	0	0	2	0	2	H3BKM8	
ENSMUST00000132546						0	0	50	0	25	14	0	18	10	0	0		
ENSMUST00000132547						8	13	0	6	8	4	5	10	0	4	5		
ENSMUST00000132548	ENSMUSG00000041346	11	69561758	69580255	-1	0	0	4	0	0	0	27	22	26	8	19	I7HJ86	
ENSMUST00000132550						19	21	23	4	19	11	0	0	0	0	0		
ENSMUST00000132551						7	4	2	48	7	0	17	96	50	2	58		
ENSMUST00000132552						4	0	1	2	3	0	0	4	6	0	0		
ENSMUST00000132554						21	9	57	16	23	3	0	0	0	0	0		
ENSMUST00000132555	ENSMUSG00000004455	5	122158278	122175273	1	0	1	9	30	0	0	0	0	0	0	0	A0A0G2JGC1	
ENSMUST00000132556						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000132557						1	3	4	1	2	1	0	8	0	4	0		
ENSMUST00000132558						0	0	0	0	0	0	2	14	19	9	0		
ENSMUST00000132561						0	3	2	0	0	2	53	97	18	43	35		
ENSMUST00000132562						2	1	2	0	3	0	0	18	7	0	7		
ENSMUST00000132563	ENSMUSG00000041578	7	15865947	15879968	-1	2	0	1	12	4	2	0	0	0	0	0	G3UXU9	
ENSMUST00000132565						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132566						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132567						54	48	316	90	52	27	1	1	2	0	5		
ENSMUST00000132569						2	2	18	9	6	3	0	0	0	0	0		
ENSMUST00000132570	ENSMUSG00000020491	11	58867216	58883288	1	0	0	11	2	0	7	0	4	4	0	4	Q5NC62	
ENSMUST00000132572						1	3	3	0	0	0	0	3	0	0	3		
ENSMUST00000132573	ENSMUSG00000050994	10	10335703	10472326	-1	0	0	6	8	0	0	0	0	0	0	3	D3YZ77	
ENSMUST00000132574						10	6	27	4	14	0	168	644	211	47	345		
ENSMUST00000132575						4	2	9	4	6	2	0	0	2	0	7		
ENSMUST00000132576						3	0	1	2	0	3	0	0	0	0	0		
ENSMUST00000132577						6	3	5	6	14	2	0	0	0	0	0		
ENSMUST00000132578	ENSMUSG00000020282	11	32209585	32222300	-1	0	0	0	4	0	0	0	0	0	0	0	F2Z3W3	
ENSMUST00000132580	ENSMUSG00000039652	19	37021291	37208601	-1	0	0	0	22	0	0	0	0	4	0	0		
ENSMUST00000132581	ENSMUSG00000029775	6	30401868	30455179	1	0	2	0	1	0	2	19	24	0	0	11		
ENSMUST00000132582						0	0	0	0	0	0	0	0	0	6	0		
ENSMUST00000132583	ENSMUSG00000031825	8	119992438	120052793	1	23	13	38	64	33	10	4859	3270	4754	447	3544		Q8BZQ2
ENSMUST00000132585						4	4	2	6	6	1	0	3	3	0	3		
ENSMUST00000132586						1	0	0	0	0	0	0	0	0	6	3		
ENSMUST00000132588						0	0	0	0	0	0	0	28	0	0	0		
ENSMUST00000132590						7	12	14	11	7	4	19	60	45	12	7		
ENSMUST00000132591						4	0	6	49	5	2	0	10	7	0	8		
ENSMUST00000132592						15	16	47	11	15	8	0	0	0	0	3		
ENSMUST00000132593	ENSMUSG00000090266	11	116843278	116854263	1	0	0	0	0	0	0	3	13	5	31	0	H3BKP4	
ENSMUST00000132594						7	6	5	37	12	0	0	0	0	6	0		
ENSMUST00000132595						0	0	1	0	0	0	0	1	0	0	0		
ENSMUST00000132596						2	3	0	0	6	3	5	89	21	9	18		
ENSMUST00000132597	ENSMUSG00000020886	11	70017085	70045532	1	2	0	1	3	3	1	0	0	0	2	0	B1AR31	
ENSMUST00000132598						0	0	0	0	0	2	0	0	0	0	3		
ENSMUST00000132599						10	9	8	15	13	6	18	44	48	17	51		
ENSMUST00000132600						15	21	19	15	21	7	15	71	25	31	16		
ENSMUST00000132601						0	1	0	1	5	0	0	0	0	0	0		
ENSMUST00000132602						13	11	31	4	12	10	39	104	56	10	89		
ENSMUST00000132603	ENSMUSG00000068882	2	69861562	69871846	1	1	1	1	0	0	1	19	416	71	298	63	F6SXM5	
ENSMUST00000132604						1	2	1	4	1	1	1	4	1	0	9		
ENSMUST00000132605						47	35	55	39	70	23	5	7	15	0	9		
ENSMUST00000132606						14	19	35	52	19	19	10	4	22	5	45		
ENSMUST00000132607	ENSMUSG00000079020	15	73577424	73645762	-1	26	6	64	54	13	21	0	0	0	3	0		Q0P5V9
ENSMUST00000132608	ENSMUSG00000027611	2	155751117	155755471	1	0	0	0	0	0	3	0	0	1	0	1	A2AUV5	
ENSMUST00000132610	ENSMUSG00000036208	16	44724301	44737284	1	0	0	0	0	0	0	0	0	0	0	0	F6RAK6	
ENSMUST00000132611						2	2	0	0	7	0	40	469	54	68	126		
ENSMUST00000132612						37	14	57	81	50	15	0	0	0	0	0		
ENSMUST00000132613	ENSMUSG00000033526	2	121310561	121355396	-1	0	4	6	12	4	3	0	0	0	0	0	F6RMX0	
ENSMUST00000132614						1	2	10	0	5	0	28	0	0	0	20		
ENSMUST00000132615	ENSMUSG00000026113	1	37299865	37410736	1	0	0	0	0	0	0	0	0	0	0	0	D3YUD3	
ENSMUST00000132617						107	137	146	86	100	62	10	27	12	9	12		
ENSMUST00000132618						15	11	1	10	11	3	1039	2858	350	10	182		
ENSMUST00000132619						0	0	0	0	0	2	0	0	1	1	0		
ENSMUST00000132620	ENSMUSG00000005417	11	59661305	59780860	1	0	0	0	0	0	0	153	574	189	74	348	F6S5I0	
ENSMUST00000132621						4	2	0	3	6	1	0	0	0	0	3		
ENSMUST00000132622						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132623	ENSMUSG00000020863	11	94287890	94321988	-1	0	0	0	0	0	0	0	95	7	23	0	F7A7G1	
ENSMUST00000132624						1	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000132625						0	0	0	41	0	0	0	0	0	0	0		
ENSMUST00000132627						0	0	3	0	2	0	1	0	0	1	3		
ENSMUST00000132628	ENSMUSG00000008301	18	56562443	56587712	1	0	0	0	0	0	3	15	112	53	172	33	F6RPD4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132629						439	459	1104	433	589	297	2	22	8	13	19		
ENSMUST00000132630						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000132631	ENSMUSG00000028466	4	43562332	43567060	1	0	1	3	0	2	0	40	75	54	17	0	E0CYW8	
ENSMUST00000132632						0	1	0	2	0	3	0	26	4	8	9		
ENSMUST00000132633						2	0	0	2	0	0	32	228	133	31	110		
ENSMUST00000132634						9	1	7	54	7	3	0	0	0	0	0		
ENSMUST00000132635						0	0	0	0	0	0	1	0	5	0	0		
ENSMUST00000132636						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000132637						0	0	3	4	0	0	0	0	0	0	0		
ENSMUST00000132638						4	3	3	5	8	3	0	0	0	0	0		
ENSMUST00000132639	ENSMUSG00000019494	5	138161071	138164646	1	5	0	1	0	0	1	12	28	8	0	5	F6QK86	
ENSMUST00000132640						3	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000132641	ENSMUSG00000026222	1	85649988	85709998	1	0	0	0	0	0	0	233	1545	499	138	475	F6WL90	
ENSMUST00000132642						3	6	2	5	3	4	0	0	0	0	0		
ENSMUST00000132643	ENSMUSG00000042675	7	126776955	126780514	1	0	0	0	0	0	0	0	8	9	0	6	D3YUC6	
ENSMUST00000132644						6	0	0	0	2	0	0	9	1	0	8		
ENSMUST00000132645						3	0	3	2	2	1	0	0	0	0	0		
ENSMUST00000132646						2	2	12	14	6	0	7	16	9	1	11		
ENSMUST00000132647						2	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000132648	ENSMUSG00000007888	8	70493158	70504081	1	4	1	1	0	2	0	0	0	0	0	0	F6RP70	
ENSMUST00000132649						0	0	2	2	1	0	0	0	0	0	0		
ENSMUST00000132650						7	1	7	0	5	4	17	27	12	15	11		
ENSMUST00000132651						5	3	12	47	3	2	0	4	4	0	6		
ENSMUST00000132652						1	2	0	0	5	1	9	31	10	2	4		
ENSMUST00000132653	ENSMUSG00000018395	11	53567379	53601967	1	3	0	0	0	1	0	0	0	0	0	0	F6VT70	
ENSMUST00000132654	ENSMUSG00000059713	4	135412308	135433853	-1	0	0	0	0	0	2	2	8	0	2	6	B0QZL9	
ENSMUST00000132655	ENSMUSG00000040734	7	19359749	19378533	1	2	2	4	4	2	0	0	0	1	0	0	D3YXE7	
ENSMUST00000132656						10	10	13	3	10	3	0	9	18	4	13		
ENSMUST00000132658	ENSMUSG00000037366	4	134396320	134427413	1	2	0	7	1	2	0	4	2	2	0	0	D3Z3Q4	
ENSMUST00000132659						1	0	1	1	0	0	0	0	0	0	1		
ENSMUST00000132660	ENSMUSG00000028830	4	126753544	126870070	1	0	0	0	0	0	0	0	0	0	0	0	A2A787	
ENSMUST00000132661	ENSMUSG00000050423	13	35958839	35970388	1	27	11	47	486	43	11	0	1	0	0	0		Q9CW07
ENSMUST00000132663						0	0	0	0	0	0	3	6	2	3	3		
ENSMUST00000132664						0	4	0	0	3	0	27	23	38	0	90		
ENSMUST00000132666						8	9	2	6	8	3	5	8	5	0	0		
ENSMUST00000132667	ENSMUSG00000070704	5	87065927	87092555	-1	0	0	0	1	0	0	0	0	0	0	0	D3YUP6	
ENSMUST00000132668	ENSMUSG00000028163	3	135584655	135691547	-1	0	0	0	0	0	0	200	366	126	6	99	F6Z9G5	
ENSMUST00000132669						8	8	15	7	5	2	2	2	3	12	15		
ENSMUST00000132670	ENSMUSG00000038677	17	28142316	28174852	1	28	28	63	43	46	28	0	0	2	0	2	F7A487	
ENSMUST00000132672						2	2	3	0	2	0	0	0	0	0	0		
ENSMUST00000132674	ENSMUSG00000047295	15	91838265	91861438	1	6	6	2	3	0	0	0	0	0	0	0	F6XMP1	
ENSMUST00000132675						2	2	19	37	1	2	2	7	8	0	4		
ENSMUST00000132676	ENSMUSG00000017715	11	117986292	118024011	1	10	6	10	61	14	10	224	291	142	36	128	B9EKS7	Q8BHF7
ENSMUST00000132677						5	2	27	13	9	5	0	0	1	0	0		
ENSMUST00000132678						2	1	4	0	6	2	0	76	27	91	34		
ENSMUST00000132679						0	0	0	0	0	2	44	53	110	35	66		
ENSMUST00000132680	ENSMUSG00000036270	8	105880881	105894908	1	5	0	0	0	7	0	21	9	30	5	24	F6ZJ27	
ENSMUST00000132681						0	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000132682	ENSMUSG00000056770	12	108106431	108179314	-1	0	0	0	0	0	0	189	419	274	29	223	D6RCY6	
ENSMUST00000132683						8	7	52	10	16	4	0	0	0	1	1		
ENSMUST00000132684						0	0	0	0	0	0	152	94	32	0	144		
ENSMUST00000132685	ENSMUSG00000033987	11	118021723	118129219	-1	42	44	87	35	33	25	0	0	4	0	7	A2A520	
ENSMUST00000132686						0	0	2	0	1	3	0	3	0	0	1		
ENSMUST00000132687						2	1	6	1	1	2	0	0	0	1	1		
ENSMUST00000132688						17	7	87	21	8	7	0	0	0	0	0		
ENSMUST00000132689	ENSMUSG00000036006	13	24582189	24733816	1	7	0	47	8	16	5	24	70	43	13	78	F2Z3V4	
ENSMUST00000132693						2	1	4	12	3	1	39	23	154	20	100		
ENSMUST00000132694						0	0	13	2	4	0	0	0	0	0	0		
ENSMUST00000132696	ENSMUSG00000039985	6	148921035	148946467	-1	0	0	30	9	2	0	1	0	2	0	0	D3Z0C1	
ENSMUST00000132697						330	317	534	241	261	138	8	17	26	7	40		
ENSMUST00000132698	ENSMUSG00000029003	4	148130384	148145699	1	0	0	0	0	0	0	0	0	0	0	0	A2A7G6	
ENSMUST00000132699	ENSMUSG00000070565	1	157135182	157412595	-1	0	0	0	0	13	0	0	0	0	0	4	D3YUS5	
ENSMUST00000132700						146	138	705	273	123	95	1	9	4	0	13		
ENSMUST00000132701	ENSMUSG00000043036	5	122108040	122140823	-1	1	1	2	25	2	0	0	0	0	0	0	D3YVN4	
ENSMUST00000132702						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000132703						0	3	10	10	5	0	12	26	35	66	29		
ENSMUST00000132704						13	10	13	8	13	5	4	36	7	1	18		
ENSMUST00000132705	ENSMUSG00000048922	14	67676331	67715841	-1	0	0	0	55	0	0	0	0	1	0	0	D3YZE8	
ENSMUST00000132706	ENSMUSG00000025579	11	119267887	119285454	1	2	2	0	3	0	3	0	4	0	0	0	A2AFL5	
ENSMUST00000132707						0	0	2	39	5	0	0	2	0	0	0		
ENSMUST00000132708	ENSMUSG00000004815	5	108646693	108669672	-1	26	16	76	25	24	9	17	70	0	0	27	D6RFT1	
ENSMUST00000132709						8	4	9	11	8	3	1	0	0	0	2		
ENSMUST00000132710						51	46	68	56	62	47	0	0	3	0	3		
ENSMUST00000132711						1	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000132712						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132713						2	0	3	2	4	0	10	5	11	2	21		
ENSMUST00000132714	ENSMUSG00000002455	2	181591868	181655660	1	1	2	0	0	0	0	0	3	0	0	0	B7ZCS1	
ENSMUST00000132715						0	0	0	0	1	0	0	46	11	4	0		
ENSMUST00000132717	ENSMUSG00000036792	2	48949508	49325405	1	3	5	21	11	12	10	5	19	7	0	15	Q3TTF1	
ENSMUST00000132718	ENSMUSG00000032359	9	90054152	90076089	1	1	3	5	0	5	0	16	73	134	365	70	D3Z437	
ENSMUST00000132719						0	0	14	0	4	0	0	0	20	0	57		
ENSMUST00000132720						1664	1934	2617	1473	1448	755	47	161	82	6	64		
ENSMUST00000132721						0	2	8	0	3	4	0	15	0	2	4		
ENSMUST00000132722	ENSMUSG00000075023	2	93855361	93869157	-1	1	0	0	1	0	1	0	0	0	0	0	F6Q926	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132723						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132724						4	3	3	11	3	1	0	0	0	0	0		
ENSMUST00000132725						0	3	4	2	1	0	0	1	2	2	5		
ENSMUST00000132726	ENSMUSG00000029726	5	137781906	137787655	-1	0	2	0	7	2	1	87	85	33	20	33	F6XIE4	
ENSMUST00000132727						1	3	7	9	5	6	0	6	6	0	4		
ENSMUST00000132728	ENSMUSG00000074895	13	54783998	54788459	1	0	0	0	309	0	0	0	0	0	0	0		Q3UTA9
ENSMUST00000132730						1	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000132732						3	3	16	0	2	0	0	0	0	0	0		
ENSMUST00000132733						0	0	0	0	0	0	0	0	4	0	3		
ENSMUST00000132734	ENSMUSG00000029167	5	51454250	51567726	-1	42	37	104	216	49	20	0	2	0	2	3		O70343
ENSMUST00000132735						46	67	149	57	68	44	1	1	5	0	5		
ENSMUST00000132736						1	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000132737						33	40	79	77	61	26	0	2	10	0	4		
ENSMUST00000132738						1	3	10	0	0	0	2	0	0	0	13		
ENSMUST00000132739						0	3	1	0	1	0	0	0	0	0	0		
ENSMUST00000132740						0	3	0	0	0	0	0	32	26	6	19		
ENSMUST00000132741	ENSMUSG00000002111	2	91082390	91115756	1	1	0	2	34	2	6	1136	851	660	28	611	E9QAI9	
ENSMUST00000132742						0	2	2	1	0	1	8	29	5	0	16		
ENSMUST00000132743	ENSMUSG00000020023	10	94311949	94590956	1	0	0	0	0	0	0	0	0	0	0	0	D3Z1L1	
ENSMUST00000132744	ENSMUSG00000047642	10	121641588	121692892	1	0	0	0	0	4	0	0	1	0	0	0	F6XLN3	
ENSMUST00000132745						0	2	0	3	2	0	1	4	0	3	4		
ENSMUST00000132746	ENSMUSG00000003032	4	55527143	55532466	-1	0	0	0	14	3	0	0	0	0	0	0	B7ZCH1	
ENSMUST00000132747						3	6	31	5	9	5	7	28	14	2	11		
ENSMUST00000132748						0	0	0	74	3	0	0	0	0	0	0		
ENSMUST00000132749	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	0	0	0	7	0	0	4	D3YYY3	
ENSMUST00000132750						3	2	8	0	5	0	0	1	0	0	2		
ENSMUST00000132751	ENSMUSG00000040940	7	24902912	24926594	1	0	3	0	0	4	0	42	88	118	9	95	F6ZN61	
ENSMUST00000132752						1	0	2	3	1	1	1	2	7	0	14		
ENSMUST00000132753						4	4	7	5	1	0	1	5	5	0	5		
ENSMUST00000132754						8	2	6	4	6	4	0	1	0	0	0		
ENSMUST00000132755	ENSMUSG00000024211	6	27275119	28135178	-1	1	1	0	2	0	2	0	0	0	0	0	D3YZK8	
ENSMUST00000132756						4	0	9	0	2	2	0	2	13	0	4		
ENSMUST00000132757	ENSMUSG00000033282	8	91217030	91313262	-1	0	0	0	2	2	1	0	0	1	5	3	D3Z0V3	
ENSMUST00000132758						0	0	1	17	0	0	0	0	0	0	0		
ENSMUST00000132760						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000132763						0	0	0	3	0	2	0	0	2	0	0		
ENSMUST00000132764						3	3	4	1	1	0	0	0	1	0	0		
ENSMUST00000132765						0	0	0	1	0	0	4	0	0	0	0		
ENSMUST00000132766						0	2	0	1	0	2	0	12	3	2	6		
ENSMUST00000132767						3	0	2	3	1	3	0	0	0	0	0		
ENSMUST00000132768	ENSMUSG00000069892	11	49015874	49051242	-1	2	0	3	2	1	1	0	3	7	7	22	Q5SVN9	
ENSMUST00000132769						6	4	9	161	13	2	21	199	40	7	102		
ENSMUST00000132770						2	0	11	55	6	1	0	0	3	0	0		
ENSMUST00000132771	ENSMUSG00000019312	11	98446394	98455373	1	0	0	7	0	4	1	0	0	0	0	2	A2A555	
ENSMUST00000132772						0	0	0	47	0	0	0	0	9	0	3		
ENSMUST00000132773	ENSMUSG00000074825	2	127138772	127143442	-1	32	42	127	43	54	29	206	449	239	34	152	A2ASB0	
ENSMUST00000132774						99	100	80	91	137	46	5	6	7	0	6		
ENSMUST00000132775	ENSMUSG00000029477	5	123035769	123047016	-1	0	0	0	0	4	0	3	2	6	0	2		Q8C5T4
ENSMUST00000132776						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132777						28	18	54	31	68	45	39	553	141	16	286		
ENSMUST00000132778						49	63	88	123	65	25	15	37	18	8	25		
ENSMUST00000132780	ENSMUSG00000034471	11	115799183	115813639	-1	2	2	9	5	10	0	0	0	0	0	0	F6R2B3	
ENSMUST00000132781						15	4	27	6	9	1	0	0	0	0	0		
ENSMUST00000132782						5	1	4	23	8	4	6	8	12	2	21		
ENSMUST00000132783	ENSMUSG00000020459	11	29526408	29545279	1	0	0	0	0	0	0	0	2	0	0	0	F6RR02	
ENSMUST00000132784						0	2	0	15	1	0	0	0	0	0	0		
ENSMUST00000132785						2	0	3	1	1	3	6	5	12	0	19		
ENSMUST00000132786						0	0	0	0	0	0	111	1096	268	66	162		
ENSMUST00000132787	ENSMUSG00000031452	8	13550733	13562461	-1	0	0	0	6	1	0	0	0	0	0	0	E9Q7I5	
ENSMUST00000132788	ENSMUSG00000039556	X	7557296	7574283	-1	0	0	2	0	0	3	7	1	4	0	1	F6RXH3	
ENSMUST00000132789						0	0	6	4	2	0	0	2	2	0	2		
ENSMUST00000132790						10	5	25	127	30	2	5	2	6	0	6		
ENSMUST00000132791						1	2	6	2	2	1	0	0	0	0	0		
ENSMUST00000132793						4	3	3	2	6	5	0	0	0	0	0		
ENSMUST00000132794						2	0	0	1	2	1	4	22	12	0	30		
ENSMUST00000132795	ENSMUSG00000026418	1	135779434	135810989	1	0	0	0	0	0	0	0	0	0	0	0	D3YTL4	
ENSMUST00000132796						0	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000132797						3	3	0	2	2	0	0	0	2	0	0		
ENSMUST00000132798						0	0	4	24	4	0	0	0	0	0	0		
ENSMUST00000132799	ENSMUSG00000032042	9	35200175	35247973	1	4	2	2	1	0	0	0	0	0	0	0	F6VF36	
ENSMUST00000132800						0	1	0	0	2	0	91	312	89	4	187		
ENSMUST00000132801						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000132802						1	1	0	0	0	0	0	6	0	1	0		
ENSMUST00000132803						2	0	0	3	2	0	2	21	0	0	4		
ENSMUST00000132804						89	107	118	96	97	34	39	175	61	5	62		
ENSMUST00000132805						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132806						0	3	4	48	3	1	0	0	0	0	0		
ENSMUST00000132807						0	5	0	0	2	0	5	58	4	0	5		
ENSMUST00000132808	ENSMUSG00000042606	7	126861972	126865377	1	2	0	3	3	3	0	5	4	6	7	8	D3YWU7	
ENSMUST00000132809						1	0	0	2	0	0	1	57	9	8	4		
ENSMUST00000132810						2	6	8	1	8	0	0	12	5	1	5		
ENSMUST00000132812						7	3	22	1	4	0	0	4	0	3	10		
ENSMUST00000132813						0	0	0	1	0	0	0	0	0	0	2		
ENSMUST00000132815	ENSMUSG00000045973	4	45395923	45408766	-1	0	0	0	2	0	0	30	0	36	13	39		Q5HZI9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132816	ENSMUSG00000055296	4	56866923	56947437	-1	0	0	0	0	0	0	0	0	2	0	2	B1AZA8	
ENSMUST00000132817	ENSMUSG00000026563	1	166379097	166393621	1	0	3	2	14	2	0	0	1	0	0	0	D6RGB8	
ENSMUST00000132818						0	0	6	0	1	1	0	8	2	5	5		
ENSMUST00000132819	ENSMUSG00000030822	7	127459611	127476759	1	0	3	0	0	0	0	25	0	41	0	68		
ENSMUST00000132820	ENSMUSG00000026923	2	26457903	26516663	-1	4	4	7	1	4	1	0	0	0	0	0	A2AIX5	
ENSMUST00000132821	ENSMUSG00000053411	15	79915807	79971119	-1	0	5	0	0	3	3	0	0	0	0	0	D3YY71	
ENSMUST00000132825						3	3	0	6	1	2	0	0	0	0	0		
ENSMUST00000132827	ENSMUSG00000026771	2	23506220	23572106	-1	2	2	3	0	1	0	6	40	34	0	0	A0A0A6YXL9	
ENSMUST00000132828						2	2	1	4	3	2	36	5	30	0	33		
ENSMUST00000132829	ENSMUSG00000078686	4	60418046	60421952	-1	0	0	0	0	0	0	0	0	0	0	0	A2BIN0	
ENSMUST00000132830						1	3	0	8	4	3	13	24	5	0	12		
ENSMUST00000132831	ENSMUSG00000032850	5	118190736	118245116	-1	12	5	28	12	11	5	1	0	1	0	1	F6V638	
ENSMUST00000132832						7	9	1	4	5	0	0	0	0	0	0		
ENSMUST00000132833						4	2	2	2	4	5	0	0	2	0	0		
ENSMUST00000132835						3	0	0	0	2	0	5	0	4	0	0		
ENSMUST00000132836	ENSMUSG00000058794	15	103248212	103258403	-1	0	0	0	0	0	0	35	20	32	0	43	D3Z0J1	
ENSMUST00000132837	ENSMUSG00000015214	X	71364760	71419196	1	0	0	0	0	1	0	0	0	0	0	0	F6T9H9	
ENSMUST00000132838	ENSMUSG00000034224	8	119479602	119501698	-1	4	0	9	1	12	2	0	0	0	0	0	F6S1U6	
ENSMUST00000132839						2	1	1	3	1	0	0	0	0	0	0		
ENSMUST00000132841						3	5	11	7	5	3	21	137	68	7	58		
ENSMUST00000132842						25	29	210	53	29	17	6	6	11	2	0		
ENSMUST00000132843						2	0	12	5	2	1	0	0	0	0	0		
ENSMUST00000132844						2	0	11	2	3	5	1	0	0	0	0		
ENSMUST00000132846	ENSMUSG00000071866	11	6415443	6419817	1	4	0	6	108	8	0	11	21	21	106	11	Q5SVY2	P17742
ENSMUST00000132847	ENSMUSG00000035131	1	146494760	146902472	1	0	0	11	2	0	0	0	0	0	1	0	B1AQT5	
ENSMUST00000132848	ENSMUSG00000052446	8	71951038	71993408	1	72	67	49	51	59	33	0	6	6	5	5	D3YV32	
ENSMUST00000132851						13	11	12	16	18	6	0	0	0	0	0		
ENSMUST00000132852						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132853						7	4	5	1	1	2	5	1	0	0	1		
ENSMUST00000132854						1	2	0	26	3	1	4	4	8	0	11		
ENSMUST00000132855	ENSMUSG00000086040	6	54429603	54503768	1	0	0	0	61	0	0	0	0	0	0	0	E9Q2D0	
ENSMUST00000132856						2	1	2	13	6	0	0	0	0	0	5		
ENSMUST00000132859	ENSMUSG00000022701	16	43889800	43964314	1	0	6	6	23	29	0	0	27	0	0	10	B8JJH0	
ENSMUST00000132860						10	11	12	10	11	9	12	120	7	6	28		
ENSMUST00000132862	ENSMUSG00000078762	7	30653711	30664994	-1	0	0	0	0	0	0	0	8	0	0	0		Q9D786
ENSMUST00000132863						4	0	20	9	3	5	8	29	25	3	39		
ENSMUST00000132864						5	2	12	4	6	10	1	5	5	0	10		
ENSMUST00000132865						5	0	0	2	6	1	0	0	0	0	0		
ENSMUST00000132866	ENSMUSG00000058440	6	30047988	30153458	1	13	2	10	10	6	4	11	58	16	28	21	F6XZB0	
ENSMUST00000132867	ENSMUSG00000055553	8	70508272	70527956	-1	0	0	0	0	4	0	1	0	0	0	0	D3YXX6	
ENSMUST00000132868						12	17	6	21	19	11	0	1	0	1	6		
ENSMUST00000132869	ENSMUSG00000000901	10	75923222	75932502	-1	0	1	0	0	0	0	0	3	0	0	0		
ENSMUST00000132870						11	1	70	0	20	13	0	3	0	0	4		
ENSMUST00000132872						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132873	ENSMUSG00000064246	1	134182176	134190181	1	0	0	0	0	0	0	23	5	0	9	0	D3YXU4	
ENSMUST00000132874						0	0	0	7	0	0	0	61	18	103	21		
ENSMUST00000132875	ENSMUSG00000030824	7	45492874	45510406	-1	4	2	22	22	7	0	2	2	0	0	0	D3Z1N1	
ENSMUST00000132876						3	0	0	32	0	1	0	0	0	0	0		
ENSMUST00000132877						8	10	3	10	16	5	6	43	3	12	4		
ENSMUST00000132878	ENSMUSG00000021013	12	98920574	98983238	1	2	3	4	4	0	3	0	0	0	0	5	D3YYH2	
ENSMUST00000132879						1	1	5	2	3	0	0	0	0	1	1		
ENSMUST00000132881						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132882						6	0	2	2	4	4	0	12	11	0	7		
ENSMUST00000132883	ENSMUSG00000078877	2	176798612	176811223	1	4	3	8	3	0	1	0	0	4	0	1	A2BG91	
ENSMUST00000132884	ENSMUSG00000011096	7	44848991	44855421	1	2	3	1	2	4	4	9	6	2	2	11	D3Z4V8	
ENSMUST00000132885						0	1	1	5	2	1	0	0	0	3	5		
ENSMUST00000132886						1	1	0	5	0	0	23	80	72	8	90		
ENSMUST00000132887						2	3	1	5	5	1	2	12	0	0	2		
ENSMUST00000132888						0	0	1	3	0	0	0	7	6	43	0		
ENSMUST00000132889						2	1	2	4	0	0	5	6	4	1	9		
ENSMUST00000132890						24	14	43	36	37	24	163	984	217	21	421		
ENSMUST00000132891						2	1	8	4	7	2	2	2	8	1	3		
ENSMUST00000132893	ENSMUSG00000023764	11	3131850	3193463	-1	150	72	253	170	60	9	11	0	26	0	49	E9PY38	
ENSMUST00000132894						45	43	210	41	47	15	1	0	1	0	0		
ENSMUST00000132895						16	22	136	62	31	17	1	10	0	0	1		
ENSMUST00000132896						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000132897						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132899	ENSMUSG00000031860	8	69832491	69872292	1	0	1	0	0	0	0	0	4	0	0	0		Q99NE9
ENSMUST00000132900						0	0	3	5	5	1	0	0	0	0	0		
ENSMUST00000132901						5	7	26	5	6	4	0	3	0	1	2		
ENSMUST00000132902						7	2	11	85	7	8	0	4	2	0	3		
ENSMUST00000132903						1	0	4	3	5	0	65	460	94	4	301		
ENSMUST00000132904						2	0	2	2	2	0	2	2	13	0	5		
ENSMUST00000132905	ENSMUSG00000020546	11	90476492	90638084	-1	0	0	2	2	0	3	0	0	0	0	0	B1ATH0	
ENSMUST00000132906						0	1	0	0	19	0	0	37	0	0	0		
ENSMUST00000132907						2	3	5	218	7	0	1	0	0	0	0		
ENSMUST00000132908	ENSMUSG00000025816	2	5870987	5895432	-1	0	0	5	0	0	0	1	9	2	0	0	A0A0A6YVQ7	
ENSMUST00000132909						0	0	0	0	0	0	0	14	0	0	0		
ENSMUST00000132910						87	41	94	952	161	69	0	2	2	0	9		
ENSMUST00000132911						0	0	2	5	0	0	0	0	1	0	0		
ENSMUST00000132912	ENSMUSG00000013338	2	156019139	156052947	-1	4	0	0	0	4	0	0	0	0	0	0	F6UNQ3	
ENSMUST00000132914						2	2	10	5	6	4	0	0	0	0	0		
ENSMUST00000132915	ENSMUSG00000046862	4	143412426	143421091	1	0	0	0	0	0	1	2	1	4	0	2	A6PW90	
ENSMUST00000132916	ENSMUSG00000029596	5	120458186	120472810	-1	0	0	0	3	0	0	4	0	0	0	5	D3Z0F6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000132917	ENSMUSG00000053119	6	71543797	71582609	1	0	2	2	15	0	0	0	5	0	0	8		
ENSMUST00000132918						7	11	41	8	7	0	13	66	80	57	30		
ENSMUST00000132919						2	8	6	15	8	1	0	0	0	2	6		
ENSMUST00000132920	ENSMUSG00000015766	6	137477245	137654876	-1	0	3	0	0	2	0	0	0	0	0	17	D3Z5I5	
ENSMUST00000132922						3	0	0	4	0	0	0	3	2	0	3		
ENSMUST00000132923	ENSMUSG00000027900	3	106547798	106575890	1	0	0	0	0	0	0	7	46	12	0	0	D3YZH9	
ENSMUST00000132924						0	0	0	5	1	0	0	4	0	0	0		
ENSMUST00000132925	ENSMUSG00000045482	5	144767732	144859778	1	0	18	78	0	35	31	119	971	791	53	786	F7CGG2	
ENSMUST00000132926	ENSMUSG00000037012	10	62268855	62379908	-1	8	5	12	0	3	3	0	0	0	0	0	B4YB29	
ENSMUST00000132927						2	1	0	1	5	2	0	1	0	0	0		
ENSMUST00000132928						3	1	3	3	1	2	0	0	0	2	0		
ENSMUST00000132929						2	0	7	0	4	3	31	101	73	13	57		
ENSMUST00000132930						5	2	10	4	5	0	3	5	0	4	0		
ENSMUST00000132932	ENSMUSG00000031700	8	85492576	85527560	1	34	47	176	49	54	27	2	0	0	0	5	D6RFQ8	
ENSMUST00000132933						3	2	8	5	4	4	0	0	0	0	0		
ENSMUST00000132934						2	4	3	98	7	4	1	0	0	0	0		
ENSMUST00000132935						0	1	0	0	0	0	0	50	15	4	37		
ENSMUST00000132936						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132937						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132938						4	3	6	5	3	0	2	0	2	0	0		
ENSMUST00000132939						10	4	8	35	17	5	0	2	0	0	0		
ENSMUST00000132940						2	0	3	21	4	4	0	0	0	0	0		
ENSMUST00000132941						1	0	4	4	3	0	4	5	7	0	20		
ENSMUST00000132942						9	1	4	22	6	5	1	1	2	0	1		
ENSMUST00000132943						1	0	3	2	0	0	0	0	0	0	0		
ENSMUST00000132944						1	0	8	1	0	0	16	18	11	1	0		
ENSMUST00000132945	ENSMUSG00000057672	8	83669762	83699179	-1	0	5	8	42	6	0	13	64	0	0	0	D6RH37	
ENSMUST00000132946						1	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000132947						4	7	7	3	6	0	0	0	0	0	0		
ENSMUST00000132948	ENSMUSG00000030263	6	145115653	145174934	1	0	0	0	7	7	0	158	1718	256	1	207	F6WLY0	
ENSMUST00000132949	ENSMUSG00000026017	1	60098247	60153953	1	0	0	0	0	0	0	2	5	1	0	1	A0A087WPQ8	
ENSMUST00000132950						0	0	0	3	0	1	0	0	3	0	5		
ENSMUST00000132951						9	4	14	4	6	7	12	11	13	5	16		
ENSMUST00000132952						4	6	3	38	5	6	6	56	20	2	25		
ENSMUST00000132953						0	0	0	2	0	0	0	0	1	0	0		
ENSMUST00000132955						0	0	0	8	9	0	0	0	0	0	0		
ENSMUST00000132956						2	1	11	68	13	3	0	3	10	9	23		
ENSMUST00000132957						1	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000132958						0	2	0	0	0	0	0	0	1	0	0		
ENSMUST00000132959	ENSMUSG00000036596	5	35502218	35525698	-1	0	2	2	20	0	0	0	0	0	0	0	D3YYF7	
ENSMUST00000132960						14	14	49	22	7	6	14	9	9	0	5		
ENSMUST00000132961	ENSMUSG00000075420	11	115912017	115913920	1	5	10	19	14	10	3	18	13	4	16	8	Q3U0I6	
ENSMUST00000132962						14	8	23	8	7	8	2	24	4	6	19		
ENSMUST00000132963						1	4	5	8	4	0	0	4	0	2	0		
ENSMUST00000132964	ENSMUSG00000031889	8	105225145	105253053	1	0	0	4	1	1	1	0	6	4	0	0	D3YYD8	
ENSMUST00000132966						30	17	32	166	40	15	13	81	20	5	45		
ENSMUST00000132967	ENSMUSG00000075249	2	82943634	83008937	1	0	16	0	0	5	6	0	0	0	0	0	F7BGZ6	
ENSMUST00000132968						5	2	0	1	3	2	0	0	0	0	0		
ENSMUST00000132969	ENSMUSG00000009894	11	59407134	59451186	-1	0	0	0	0	0	0	5	2	0	0	0	J3JS29	
ENSMUST00000132970						35	52	153	51	38	24	3	5	4	2	7		
ENSMUST00000132971	ENSMUSG00000010803	11	42130939	42182930	-1	0	0	0	10	0	0	0	0	0	0	0	E9PXL4	
ENSMUST00000132972						1	3	5	0	1	0	0	0	54	72	64		
ENSMUST00000132974	ENSMUSG00000031441	8	12757014	12868728	1	145	92	169	49	67	22	172	4785	113	152	474	F6Z4J2	
ENSMUST00000132975						0	0	0	1	1	0	6	0	0	0	3		
ENSMUST00000132976						0	0	0	0	0	0	11	71	17	0	43		
ENSMUST00000132977	ENSMUSG00000018411	11	104231390	104332090	1	0	0	0	0	0	0	0	0	0	0	0	B1AQW5	
ENSMUST00000132978	ENSMUSG00000020728	11	108425192	108860615	1	4	1	4	2	6	4	0	0	0	0	0	S4R188	
ENSMUST00000132979						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000132980	ENSMUSG00000038495	3	96104527	96161129	1	0	0	0	16	0	0	0	0	11	0	10	D3YYZ8	
ENSMUST00000132981	ENSMUSG00000026853	2	30400471	30415813	-1	0	3	0	0	2	0	13	5	11	1	3	B7ZDD7	
ENSMUST00000132982						6	6	8	5	4	5	0	0	4	1	4		
ENSMUST00000132983						0	0	4	0	0	1	27	59	45	2	61		
ENSMUST00000132984	ENSMUSG00000001436	10	77032241	77061002	1	4	0	0	2	3	0	5	0	0	0	0	D3Z4F3	
ENSMUST00000132985						0	3	2	5	0	0	3	0	2	0	1		
ENSMUST00000132987	ENSMUSG00000032380	9	66158223	66272242	1	0	2	5	0	3	3	0	6	0	0	1	F6YX98	
ENSMUST00000132989						21	11	34	114	20	11	0	0	0	0	0		
ENSMUST00000132990	ENSMUSG00000034087	7	10687793	10730168	1	5	2	1	18	6	4	0	0	0	0	0	F6SI62	
ENSMUST00000132991	ENSMUSG00000037736	5	66745827	67057158	1	0	2	1	1	0	0	0	0	0	0	0	F6X3N8	
ENSMUST00000132992						5	3	0	2	8	8	0	0	0	0	0		
ENSMUST00000132993						10	12	18	16	13	3	3	11	11	0	12		
ENSMUST00000132994	ENSMUSG00000035694	10	112163621	112216555	1	1743	1580	9323	7541	1546	1088	9	8	6	2	25	E9Q7K6	
ENSMUST00000132995	ENSMUSG00000053460	6	72414308	72430712	1	0	2	2	1	3	1	2	1	2	0	1		
ENSMUST00000132996						12	18	12	9	10	6	3	32	14	26	0		
ENSMUST00000132997						2	0	0	0	0	3	0	0	2	0	0		
ENSMUST00000132998						1	1	3	0	0	0	12	21	14	5	24		
ENSMUST00000132999						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133000						8	10	7	20	5	4	0	0	0	0	0		
ENSMUST00000133001						36	29	32	21	28	7	50	172	91	28	120		
ENSMUST00000133002	ENSMUSG00000032342	9	78448208	78475348	1	1	3	3	3	2	1	2	8	5	0	2	F6WQ99	
ENSMUST00000133003						2	3	0	0	0	0	0	2	0	0	3		
ENSMUST00000133004						8	3	12	12	8	0	20	42	8	10	41		
ENSMUST00000133006	ENSMUSG00000066000	4	147611937	147642513	-1	1	0	0	0	0	1	0	3	0	1	0	A2A7A0	
ENSMUST00000133007						8	3	8	11	5	0	5	12	3	2	23		
ENSMUST00000133008						0	0	1	90	0	1	0	2	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133009						2	2	2	1	2	0	0	0	0	0	0		
ENSMUST00000133010	ENSMUSG00000085576	9	24557048	24696293	-1	12	6	12	78	14	4	0	0	0	0	0		P0CW70
ENSMUST00000133011						4	9	45	12	6	7	0	0	0	0	0		
ENSMUST00000133012	ENSMUSG00000025505	7	141327739	141337156	1	0	0	0	0	0	0	0	0	0	10	0		Q9D3H0
ENSMUST00000133013						0	0	0	0	1	0	10	69	7	9	17		
ENSMUST00000133014						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000133016						20	26	28	12	28	0	0	0	9	0	0		
ENSMUST00000133017						1	10	5	7	6	3	0	0	0	0	0		
ENSMUST00000133018						5	9	8	21	6	2	0	2	0	0	4		
ENSMUST00000133019						16	17	41	36	18	21	0	7	6	10	4		
ENSMUST00000133020						2	0	0	3	4	0	29	67	29	5	47		
ENSMUST00000133021	ENSMUSG00000019082	7	141429744	141437892	-1	0	1	3	0	0	0	0	0	0	0	0	G3UX09	
ENSMUST00000133022						3	3	0	2	0	0	0	0	6	0	0		
ENSMUST00000133023						9	10	15	14	12	16	123	2636	512	113	1094		
ENSMUST00000133026	ENSMUSG00000003847	8	107293470	107379517	1	20	0	22	5	0	0	176	76	221	0	686	D6RH97	
ENSMUST00000133027						3	6	1	2	4	0	0	0	0	0	0		
ENSMUST00000133028						2	4	0	5	2	0	1	0	0	0	0		
ENSMUST00000133029	ENSMUSG00000025161	11	120948480	120960868	1	6	3	3	6	6	1	14	19	16	0	36	A0A0G2JD98	
ENSMUST00000133030						3	0	6	4	2	0	0	0	0	0	0		
ENSMUST00000133031						1	1	0	0	1	0	0	108	0	0	0		
ENSMUST00000133032						3	0	5	4	3	5	35	152	41	0	40		
ENSMUST00000133033						6	4	13	16	18	7	107	409	178	15	164		
ENSMUST00000133034	ENSMUSG00000038646	7	81762925	81769491	1	4	1	0	96	6	0	0	3	0	0	2	D3YZS0	
ENSMUST00000133035						0	3	0	0	0	3	29	72	33	3	16		
ENSMUST00000133036	ENSMUSG00000004043	11	100859351	100885169	1	3	1	0	2	3	1	0	0	0	0	0	A2A5D4	
ENSMUST00000133037	ENSMUSG00000031816	8	121091628	121108392	-1	0	0	0	19	0	1	23	39	25	3	5	D3Z4L1	
ENSMUST00000133038						2	0	4	1	6	0	0	12	5	13	3		
ENSMUST00000133039						0	1	0	0	0	0	0	0	0	1	0		
ENSMUST00000133040	ENSMUSG00000061462	11	58994256	59136402	-1	0	0	14	0	6	8	0	0	0	0	0	J9JIB2	
ENSMUST00000133041	ENSMUSG00000021196	13	6579768	6648777	-1	0	4	1	0	5	5	69	112	67	29	76	F6VP95	
ENSMUST00000133042						4	3	3	10	13	1	5	28	12	4	15		
ENSMUST00000133043	ENSMUSG00000029687	6	47530139	47595341	-1	0	0	0	31	1	0	0	2	0	0	2	E9PWK3	
ENSMUST00000133044	ENSMUSG00000033685	7	100493337	100502020	1	0	0	0	0	0	0	90	47	117	20	21	D3YZG5	
ENSMUST00000133045	ENSMUSG00000043131	6	83326016	83343776	1	0	0	0	76	0	0	0	0	0	0	0		
ENSMUST00000133046	ENSMUSG00000066568	7	34344646	34393315	-1	5	3	11	33	9	1	17	27	26	9	30	A2BH69	
ENSMUST00000133047						1	4	7	5	4	4	1	6	5	1	17		
ENSMUST00000133048						1	2	5	0	2	0	73	18	47	11	27		
ENSMUST00000133049						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133050						6	2	12	7	5	2	3	13	16	0	13		
ENSMUST00000133051						3	1	0	0	0	0	0	0	4	0	0		
ENSMUST00000133052	ENSMUSG00000038633	1	182275772	182282804	-1	3	0	0	9	2	0	319	500	445	87	104	F6S3U4	
ENSMUST00000133053						7	5	20	4	10	6	35	139	54	15	75		
ENSMUST00000133054						2	0	8	4	1	1	0	0	2	0	0		
ENSMUST00000133055	ENSMUSG00000028527	4	101419277	101466995	1	0	0	0	45	2	0	0	0	1	0	0	A2ARF5	
ENSMUST00000133056						4	2	28	15	8	3	4	8	6	0	8		
ENSMUST00000133057						4	5	7	51	14	4	2	2	0	1	2		
ENSMUST00000133058						3	5	4	2	4	1	0	0	0	0	1		
ENSMUST00000133059	ENSMUSG00000001436	10	77032241	77061002	1	1	0	6	2	0	0	0	0	0	0	0	D3Z0I6	
ENSMUST00000133060	ENSMUSG00000032116	9	36729344	36767679	-1	1	1	5	28	4	4	0	0	0	0	0	D3YZN5	
ENSMUST00000133061						15	12	13	9	14	5	6	10	5	1	14		
ENSMUST00000133062						10	2	9	114	6	4	10	9	30	0	15		
ENSMUST00000133063						75	65	145	60	76	33	0	14	10	0	11		
ENSMUST00000133064	ENSMUSG00000073599	18	35713086	35722356	-1	0	0	0	0	3	0	0	0	0	33	5	G3UVV5	
ENSMUST00000133065						0	1	2	1	3	0	0	0	0	3	0		
ENSMUST00000133066	ENSMUSG00000028719	4	114959336	114987241	-1	0	0	0	0	0	0	83	535	195	110	66	D6RIL5	
ENSMUST00000133067						0	3	0	6	1	0	8	328	9	35	62		
ENSMUST00000133068						1	0	7	18	2	2	0	0	0	0	2		
ENSMUST00000133069	ENSMUSG00000046709	5	102907948	103211334	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JGL2	
ENSMUST00000133070	ENSMUSG00000075595	11	95712673	95835115	1	29	18	83	69	46	30	116	145	121	15	202	F2Z443	
ENSMUST00000133071	ENSMUSG00000061046	17	25779843	25785673	-1	0	0	0	0	0	0	51	69	0	18	0	D3YZU6	
ENSMUST00000133072						33	40	131	72	50	29	2	10	9	2	23		
ENSMUST00000133074	ENSMUSG00000030557	7	67231163	67372858	-1	0	0	0	1	0	0	0	0	45	0	0	D3Z6M5	
ENSMUST00000133075	ENSMUSG00000005677	1	171213970	171220701	1	0	0	0	0	3	2	0	0	0	0	0	M0QWI8	
ENSMUST00000133076	ENSMUSG00000026623	1	191717834	191784255	1	0	0	0	26	0	0	0	0	0	0	0	D3YUD1	
ENSMUST00000133077						0	0	0	0	0	0	0	0	7	0	0		
ENSMUST00000133078	ENSMUSG00000078497	4	147361303	147391004	1	12	6	28	7	10	8	1	0	0	5	3	A2A7I0	
ENSMUST00000133079						5	2	5	2	2	1	0	0	0	0	0		
ENSMUST00000133080						2	4	2	2	2	2	0	0	0	1	0		
ENSMUST00000133081						2	2	2	1	0	0	3	0	5	3	4		
ENSMUST00000133083						0	2	7	0	0	3	3	5	1	1	10		
ENSMUST00000133084						0	4	8	5	6	4	0	2	4	0	0		
ENSMUST00000133085						6	3	0	0	6	4	0	0	0	0	0		
ENSMUST00000133086	ENSMUSG00000031981	8	124576111	124618731	1	0	0	0	0	0	0	0	0	0	0	0	D3Z7U6	
ENSMUST00000133088						5	5	5	24	6	3	0	0	0	0	0		
ENSMUST00000133089	ENSMUSG00000030846	7	128439777	128461717	-1	0	1	0	0	0	0	22	212	74	0	63		
ENSMUST00000133090						4	4	4	0	5	1	125	152	137	8	177		
ENSMUST00000133092						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000133093						7	0	13	6	0	2	39	84	129	0	79		
ENSMUST00000133094						0	0	2	64	3	0	0	0	4	0	3		
ENSMUST00000133095						1	2	2	16	8	5	3	15	3	5	7		
ENSMUST00000133096						8	10	5	8	8	6	7	14	32	3	31		
ENSMUST00000133097						2	0	0	1	1	0	0	2	2	0	5		
ENSMUST00000133098	ENSMUSG00000029513	5	116013586	116024508	-1	0	0	0	35	4	0	0	0	0	0	0	S4R2R1	
ENSMUST00000133099						0	0	0	0	0	0	0	6	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133100						2	2	0	1	2	0	0	0	0	0	0		
ENSMUST00000133101						3	3	4	0	3	1	0	2	1	0	3		
ENSMUST00000133102						0	2	8	0	2	1	0	0	0	0	2		
ENSMUST00000133103	ENSMUSG00000032673	11	29511757	29515033	-1	5	7	2	4	9	3	18	72	13	67	24	A0A0A0MQH9	
ENSMUST00000133104						2	7	0	6	1	0	0	0	0	0	0		
ENSMUST00000133105						0	0	0	0	0	0	0	2	5	0	2		
ENSMUST00000133106						4	0	0	1	0	3	14	10	0	0	1		
ENSMUST00000133107						688	643	1454	591	818	401	59	191	139	166	94		
ENSMUST00000133108	ENSMUSG00000032402	9	63646767	63757994	-1	0	0	0	0	0	0	6	0	0	0	0	F7BUP2	
ENSMUST00000133109	ENSMUSG00000028488	4	85205126	85639195	1	0	0	0	0	0	0	0	0	0	0	0	F6ZL13	
ENSMUST00000133110						4	0	0	2	5	4	0	2	0	1	2		
ENSMUST00000133111						0	0	0	2	0	0	0	0	1	0	2		
ENSMUST00000133112						54	30	179	136	79	50	4	18	10	0	18		
ENSMUST00000133115	ENSMUSG00000006728	10	127063534	127067920	1	0	0	0	0	0	0	95	0	21	1	0	E9Q9E4	
ENSMUST00000133116						4	0	5	19	5	3	0	0	1	0	0		
ENSMUST00000133117						0	0	0	0	0	0	0	45	14	24	0		
ENSMUST00000133118	ENSMUSG00000030353	6	128224288	128300823	-1	0	0	0	49	0	0	0	0	0	0	0	F6UKF4	
ENSMUST00000133119	ENSMUSG00000074698	2	152226839	152281852	1	0	0	0	21	0	0	0	4	11	5	0	Q6NSS6	
ENSMUST00000133120						0	1	1	0	0	0	0	0	0	0	3		
ENSMUST00000133121						0	7	2	5	3	2	23	86	24	54	18		
ENSMUST00000133122						1	0	0	4	2	0	0	1	3	0	3		
ENSMUST00000133123	ENSMUSG00000039354	1	72583251	72633134	1	0	0	0	0	0	0	0	0	0	0	0	D3YUX5	
ENSMUST00000133124						0	2	3	0	2	0	0	0	0	0	0		
ENSMUST00000133126						0	0	0	0	0	0	1	1	0	0	3		
ENSMUST00000133127	ENSMUSG00000090231	17	34856374	34862518	-1	0	0	0	0	0	0	0	6	5	0	24	F6WZA2	
ENSMUST00000133128						0	0	0	0	0	0	4	34	8	1	3		
ENSMUST00000133129						3	4	6	6	7	4	9	20	10	0	18		
ENSMUST00000133130						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133131	ENSMUSG00000020708	11	106256154	106263120	1	18	0	41	25	14	0	9	46	9	0	45	Q8K1K2	
ENSMUST00000133132						19	22	33	12	30	9	0	5	7	1	5		
ENSMUST00000133133	ENSMUSG00000005893	6	92091390	92174294	1	1	1	4	0	1	2	0	0	0	0	1		
ENSMUST00000133134	ENSMUSG00000001521	6	128321161	128355851	-1	2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000133135	ENSMUSG00000038860	2	32986224	33131654	-1	0	0	0	0	1	0	0	0	0	0	0	B1AW31	
ENSMUST00000133136	ENSMUSG00000054874	19	5664635	5688908	-1	0	0	4	6	0	0	0	0	0	4	0	F6VP43	
ENSMUST00000133137	ENSMUSG00000051674	5	73481000	73560794	1	2	2	1	1	5	1	0	0	0	0	0	D6RJL1	
ENSMUST00000133138						6	4	11	14	7	3	11	132	16	4	53		
ENSMUST00000133140	ENSMUSG00000020886	11	70017085	70045532	1	2	0	0	2	2	0	0	0	0	0	0	E9PXG2	
ENSMUST00000133141						11	2	9	8	16	4	0	11	2	0	0		
ENSMUST00000133142						12	15	22	125	29	10	0	0	0	0	0		
ENSMUST00000133143						13	11	71	17	19	8	30	358	100	7	99		
ENSMUST00000133144	ENSMUSG00000087247	1	6359218	6394731	1	0	5	1	65	2	1	0	1	0	0	0	J3QPP8	
ENSMUST00000133145						0	0	0	0	0	0	10	0	0	0	0		
ENSMUST00000133146						2	0	0	1	1	1	0	1	0	0	2		
ENSMUST00000133148						3	0	0	0	0	0	2	0	52	20	27		
ENSMUST00000133149						1	4	0	14	8	3	1	1	2	0	1		
ENSMUST00000133150	ENSMUSG00000046311	11	49203292	49218816	1	4	8	24	42	8	3	0	1	4	0	5	Q3UGK1	
ENSMUST00000133151						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000133152	ENSMUSG00000050565	1	156035403	156068861	1	0	0	0	21	0	0	0	2	17	0	5		
ENSMUST00000133153	ENSMUSG00000033918	16	20279820	20302387	-1	0	0	0	0	0	0	0	0	0	0	0	D6RCZ6	
ENSMUST00000133154	ENSMUSG00000061175	3	79455974	79567796	-1	52	62	149	84	88	36	567	1327	895	57	545	D3YUC5	
ENSMUST00000133155						4	0	3	38	8	1	0	0	0	0	0		
ENSMUST00000133156						3	0	12	1	5	4	0	22	14	1	38		
ENSMUST00000133157	ENSMUSG00000028318	4	45018583	45036565	1	24	25	51	31	34	7	0	17	5	10	8	Q3V1B9	Q8K202
ENSMUST00000133158						5	19	3	11	24	4	0	14	21	2	16		
ENSMUST00000133159						6	0	15	12	3	5	0	12	0	0	0		
ENSMUST00000133161						4	4	10	5	2	0	0	1	5	0	7		
ENSMUST00000133162						0	0	4	0	0	0	0	35	0	0	0		
ENSMUST00000133164						2	3	18	58	6	4	0	0	0	0	0		
ENSMUST00000133165						0	4	6	26	2	1	38	95	49	9	53		
ENSMUST00000133166						0	0	13	0	0	0	0	97	28	13	52		
ENSMUST00000133167						17	17	37	32	12	8	2	17	10	1	7		
ENSMUST00000133168						0	0	0	0	8	0	8	51	21	17	22		
ENSMUST00000133169						0	0	2	0	0	0	0	6	0	0	0		
ENSMUST00000133170	ENSMUSG00000020680	11	83473086	83506743	1	0	0	7	0	0	0	14	278	17	67	102	F6QCI0	
ENSMUST00000133172	ENSMUSG00000030681	7	126986860	127014621	-1	0	1	3	0	0	3	20	11	10	0	5	D3Z2N7	
ENSMUST00000133173	ENSMUSG00000041794	9	120303936	120474841	1	7	8	2	0	7	2	0	0	0	0	0	F7CFT8	
ENSMUST00000133174						0	3	2	2	4	1	9	104	53	2	112		
ENSMUST00000133175						9	8	5	4	9	3	50	466	49	26	59		
ENSMUST00000133176	ENSMUSG00000021504	13	55599896	55610443	1	0	0	0	0	0	0	0	0	0	0	0	D3Z065	
ENSMUST00000133177						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133178						1	1	5	0	1	0	0	13	0	2	2		
ENSMUST00000133180	ENSMUSG00000022964	16	91574503	91597800	-1	0	0	2	0	2	2	15	5	12	0	10	D6RJK9	
ENSMUST00000133181	ENSMUSG00000024370	18	34630951	34651735	-1	8	2	12	0	7	5	100	203	61	7	88		
ENSMUST00000133182						1	2	0	3	0	0	0	2	3	16	0		
ENSMUST00000133184						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133185						1	1	0	11	0	0	0	1	4	1	0		
ENSMUST00000133186						4	5	0	1	0	1	0	0	0	0	0		
ENSMUST00000133187						6	9	14	0	2	4	9	50	13	19	31		
ENSMUST00000133188						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133189						0	0	0	802	0	0	15	41	20	2	21		
ENSMUST00000133190						35	28	80	23	42	18	1	18	3	0	7		
ENSMUST00000133191	ENSMUSG00000056724	9	110624789	110654161	-1	15	0	0	0	53	39	0	0	0	81	0		Q6ZQA0
ENSMUST00000133192						0	0	0	45	0	0	0	0	0	0	0		
ENSMUST00000133193	ENSMUSG00000041607	18	82475146	82585637	1	0	0	0	0	0	0	0	24	0	0	36	F6RWW8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133194						5	0	3	1	1	0	3	7	5	0	4		
ENSMUST00000133195						8	6	9	3	7	0	26	98	64	2	66		
ENSMUST00000133197						2	2	0	14	2	0	0	13	0	0	9		
ENSMUST00000133198						5	3	2	0	6	0	0	7	6	0	4		
ENSMUST00000133199	ENSMUSG00000053091	7	66689889	66717256	1	0	0	0	0	0	0	0	0	0	0	0	D6RGQ4	
ENSMUST00000133200						0	0	0	100	1	0	3	15	11	0	15		
ENSMUST00000133201						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000133202	ENSMUSG00000020486	11	87568903	87590539	1	0	0	2	2	0	0	0	0	0	0	0	Q5ND09	
ENSMUST00000133203	ENSMUSG00000047284	11	69901072	69913820	1	7	3	0	3	0	12	0	70	51	10	139	H9H9T3	
ENSMUST00000133205	ENSMUSG00000017670	2	165288031	165326479	-1	1	1	0	2	1	3	0	0	0	0	0	Q5GMG0	
ENSMUST00000133206	ENSMUSG00000019082	7	141429744	141437892	-1	0	0	0	0	0	0	0	0	0	0	0	V9GWV4	
ENSMUST00000133207						0	1	5	1	2	0	0	0	0	0	1		
ENSMUST00000133208						5	7	21	15	17	3	2	0	2	0	0		
ENSMUST00000133209						12	13	18	17	13	8	0	0	3	1	4		
ENSMUST00000133210						3	0	8	0	6	0	0	0	0	0	7		
ENSMUST00000133211						0	0	0	37	4	0	0	0	0	0	1		
ENSMUST00000133212						0	0	1	10	4	0	0	0	1	0	0		
ENSMUST00000133213	ENSMUSG00000034275	9	27299228	27334763	1	16	11	79	377	51	10	0	0	0	0	0	E9PZ19	
ENSMUST00000133215						7	0	7	6	1	1	0	7	4	4	5		
ENSMUST00000133216						0	0	0	0	0	0	1	0	0	0	1		
ENSMUST00000133217						2	0	0	16	0	0	42	0	0	0	3		
ENSMUST00000133218						1	3	0	2	3	1	0	17	0	0	4		
ENSMUST00000133219						1	2	2	2	0	0	0	1	1	0	0		
ENSMUST00000133220						7	3	13	44	3	0	2	0	2	0	0		
ENSMUST00000133222						9	11	51	28	19	9	0	0	0	0	0		
ENSMUST00000133223						0	1	0	0	0	1	102	151	72	7	92		
ENSMUST00000133224	ENSMUSG00000022010	14	76414961	76507765	1	0	0	0	2	0	1	0	0	0	0	0	H3BLI9	
ENSMUST00000133225						0	1	0	1	2	0	0	4	0	2	6		
ENSMUST00000133226						0	0	1	0	0	0	0	0	1	2	0		
ENSMUST00000133227						4	4	5	61	9	1	2	1	4	0	3		
ENSMUST00000133228						3	3	18	9	3	1	0	0	0	0	0		
ENSMUST00000133229						3	5	4	8	3	5	154	530	193	702	117		
ENSMUST00000133230						33	24	69	262	93	51	0	2	3	0	9		
ENSMUST00000133232						2	1	0	4	5	3	0	0	10	0	0		
ENSMUST00000133233	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	16	0	0	0	0	0	0	0	A3KGV3	
ENSMUST00000133234						2	2	5	0	5	3	43	20	2	3	3		
ENSMUST00000133235	ENSMUSG00000095315	2	150323702	150363071	1	3	1	8	0	1	1	0	3	0	2	1	F6ZHM5	
ENSMUST00000133236	ENSMUSG00000040865	1	62958418	63114667	-1	11	10	13	3	25	9	0	0	5	0	25	B1AT32	
ENSMUST00000133237	ENSMUSG00000015721	7	23385889	23441922	1	0	9	0	19	0	0	0	0	0	0	0		Q9R1M5
ENSMUST00000133238						0	0	0	1	3	0	0	11	0	13	11		
ENSMUST00000133239						0	1	1	0	2	0	0	1	0	0	3		
ENSMUST00000133240						0	0	3	3	2	2	2	0	1	4	1		
ENSMUST00000133241						0	0	0	0	0	1	2	30	0	0	0		
ENSMUST00000133242	ENSMUSG00000030825	7	45554893	45567752	1	20	9	47	27	18	8	3	3	4	0	3	D3YTP9	
ENSMUST00000133245	ENSMUSG00000051043	11	114851152	114872617	1	0	0	0	4	2	0	0	0	0	0	0	B7FAU0	
ENSMUST00000133246						4	7	6	8	12	4	3	29	8	0	22		
ENSMUST00000133247						10	1	4	6	3	0	1	3	17	0	9		
ENSMUST00000133248	ENSMUSG00000030282	6	142756686	142775714	1	0	0	0	35	0	0	0	0	11	4	0		
ENSMUST00000133249						4	1	9	7	6	3	0	0	0	0	5		
ENSMUST00000133250	ENSMUSG00000020782	11	115824049	115855780	1	2	2	7	5	4	4	0	2	0	0	0	B1ATA8	
ENSMUST00000133251						0	0	10	2	8	1	5	22	6	5	5		
ENSMUST00000133252						2	0	0	39	1	1	12	86	97	457	82		
ENSMUST00000133253						0	0	0	0	0	3	0	0	0	1	8		
ENSMUST00000133254	ENSMUSG00000024901	19	4930651	4943127	-1	0	0	0	0	0	0	0	0	0	0	0	D3YYQ7	
ENSMUST00000133255						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133256	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	11	0	0	0	20	D3YWI9	
ENSMUST00000133257	ENSMUSG00000048731	17	26973217	27036378	1	25	22	39	29	38	8	16	63	44	4	56		Q6K1E7
ENSMUST00000133258	ENSMUSG00000036949	2	14388316	14494977	1	0	0	1	1	4	4	0	0	0	0	0	A2AQ77	
ENSMUST00000133260						0	1	0	1	0	0	0	6	0	2	1		
ENSMUST00000133261						0	0	9	12	1	3	0	0	0	0	0		
ENSMUST00000133262						13	18	25	151	17	11	0	1	0	0	1		
ENSMUST00000133263						2	3	9	198	6	2	0	13	3	0	17		
ENSMUST00000133265						2	2	2	0	3	2	0	4	0	1	4		
ENSMUST00000133266						13	13	55	7	37	16	350	846	282	41	0		
ENSMUST00000133267						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000133268	ENSMUSG00000059857	3	109780040	110144011	-1	7	7	8	130	28	5	0	0	0	0	0		Q8R4G0
ENSMUST00000133269						1	0	0	78	2	0	1	0	0	2	2		
ENSMUST00000133271						3	0	13	4	7	0	1	0	0	0	0		
ENSMUST00000133272	ENSMUSG00000085272	7	4965260	4971168	-1	19	5	8	11	7	6	0	0	0	0	0		P0C5K0
ENSMUST00000133275						2	0	0	29	1	1	1	1	0	0	1		
ENSMUST00000133276						1	0	2	4	4	0	2	11	7	4	9		
ENSMUST00000133277						1	0	0	0	0	0	0	4	6	0	0		
ENSMUST00000133278						15	22	32	14	19	9	0	15	0	1	5		
ENSMUST00000133279	ENSMUSG00000074141	7	44816088	44840809	1	2	2	14	73	1	0	2	5	2	0	1	G3UXA7	
ENSMUST00000133280						4	1	3	0	2	2	11	71	22	41	17		
ENSMUST00000133281						2	0	1	2	0	0	0	10	3	0	8		
ENSMUST00000133282	ENSMUSG00000021221	12	83213745	83487716	-1	0	0	9	0	0	2	0	0	0	0	0	F6T820	
ENSMUST00000133283						0	3	5	2	2	0	0	0	1	0	2		
ENSMUST00000133284						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000133285						32	26	95	24	41	25	2	39	9	0	18		
ENSMUST00000133286						0	0	5	0	0	0	33	373	128	280	88		
ENSMUST00000133287	ENSMUSG00000032327	9	58063788	58153996	1	0	0	0	0	0	0	0	0	0	0	0	E9PZN4	
ENSMUST00000133288						0	1	0	0	0	0	0	0	0	0	5		
ENSMUST00000133289	ENSMUSG00000037455	10	23796986	23827968	1	3	0	19	4	0	1	0	0	0	0	0	D3Z2W5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133290						3	3	6	4	3	0	0	4	0	0	0		
ENSMUST00000133291	ENSMUSG00000018899	11	53770014	53778374	1	0	0	0	0	0	0	0	2	0	0	0	Q5SX15	
ENSMUST00000133292	ENSMUSG00000031166	X	8123301	8132892	-1	0	0	0	0	0	0	0	181	22	1	0	S4R258	
ENSMUST00000133293	ENSMUSG00000020051	10	87521795	87584136	1	0	3	0	0	2	1	0	0	0	0	0	D3Z270	
ENSMUST00000133294						1	0	1	1	4	0	0	0	3	0	0		
ENSMUST00000133295						0	0	2	0	0	0	5	44	3	1	0		
ENSMUST00000133296						0	6	12	11	9	3	5	42	27	0	0		
ENSMUST00000133297	ENSMUSG00000038861	3	94974731	95006843	1	0	2	0	0	0	1	42	132	47	9	51	F6W459	
ENSMUST00000133298	ENSMUSG00000047495	8	14095865	14847680	1	10	11	13	0	22	20	0	0	0	0	0		Q8BJ42
ENSMUST00000133300						7	9	22	41	15	6	6	61	15	3	21		
ENSMUST00000133301	ENSMUSG00000078870	2	177183453	177206421	-1	1	1	0	4	0	0	4	2	0	1	0	A2ARW1	
ENSMUST00000133303	ENSMUSG00000034659	19	10870660	10882001	-1	1	2	19	0	3	0	0	4	0	0	7	D3Z0I8	
ENSMUST00000133304						0	3	6	0	16	9	0	0	0	0	0		
ENSMUST00000133305						271	216	2138	964	335	228	19	72	69	7	101		
ENSMUST00000133306	ENSMUSG00000004631	6	4674350	4747207	-1	0	0	0	0	0	0	0	0	0	0	0	F6R6P2	
ENSMUST00000133307						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000133308	ENSMUSG00000002076	17	31944769	32034508	-1	0	0	0	0	0	0	4	6	0	2	0	F6UJ67	
ENSMUST00000133309						23	29	61	30	30	12	0	3	2	0	9		
ENSMUST00000133310						3	4	0	0	0	0	3	0	0	0	15		
ENSMUST00000133311						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000133312						2	4	9	7	3	0	0	0	0	0	0		
ENSMUST00000133313	ENSMUSG00000048271	5	28317121	28419239	1	3	0	0	0	0	0	8	0	0	0	0	F6Y0Q7	
ENSMUST00000133314						7	1	1	4	9	4	0	0	1	0	0		
ENSMUST00000133315	ENSMUSG00000004633	6	54039554	54301810	1	1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133316	ENSMUSG00000029177	5	30666777	30674830	1	2	0	6	22	0	0	57	71	86	35	41	D6RCV6	
ENSMUST00000133317	ENSMUSG00000040481	11	107033081	107132127	-1	2	2	3	19	8	3	7	33	14	3	24	A2A652	
ENSMUST00000133318	ENSMUSG00000036892	7	30493622	30513402	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5H4	
ENSMUST00000133319						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000133320	ENSMUSG00000000563	3	105942698	105960099	-1	1	0	5	0	0	6	914	6156	1127	2556	452	D6RGL7	
ENSMUST00000133321						1	2	0	0	0	2	0	3	6	6	0		
ENSMUST00000133322						5	4	12	7	12	4	0	0	1	0	0		
ENSMUST00000133323						1	6	0	0	2	1	17	23	21	0	25		
ENSMUST00000133324	ENSMUSG00000020672	12	30174482	30373375	-1	0	0	0	0	12	0	0	0	0	0	0	D6RE37	
ENSMUST00000133325	ENSMUSG00000025190	19	43499752	43524605	-1	3	0	0	1	3	0	82	133	111	24	64	F7ALS6	
ENSMUST00000133326	ENSMUSG00000038302	10	42312585	42478565	-1	10	11	6	3	7	0	0	0	0	0	0	E9Q4K2	
ENSMUST00000133327						1	0	0	7	1	2	0	0	0	0	0		
ENSMUST00000133328						3	0	5	1	4	2	0	2	0	0	0		
ENSMUST00000133329						0	0	2	1	1	0	0	0	0	0	0		
ENSMUST00000133330						2	5	6	44	27	4	0	0	0	0	0		
ENSMUST00000133331						0	1	1	5	1	0	0	0	0	0	0		
ENSMUST00000133332						18	16	101	25	19	19	1	1	2	2	2		
ENSMUST00000133335						5	4	1	0	3	3	0	0	0	0	0		
ENSMUST00000133336	ENSMUSG00000058486	6	34880426	34910876	-1	4	2	2	36	3	2	0	0	0	0	0	D3Z0V8	
ENSMUST00000133338	ENSMUSG00000031441	8	12757014	12868728	1	5	8	13	15	13	3	616	179	1374	0	1081	D6RII8	
ENSMUST00000133339						4	2	9	10	8	4	0	0	0	0	2		
ENSMUST00000133340	ENSMUSG00000010609	1	180227004	180263438	-1	1	0	1	0	0	1	4	15	5	1	4	D3Z0X1	
ENSMUST00000133342	ENSMUSG00000002578	10	128630843	128645991	-1	141	82	736	266	111	75	4	10	6	0	16		Q8C208
ENSMUST00000133343						0	0	0	0	0	0	0	168	0	0	0		
ENSMUST00000133344	ENSMUSG00000022842	16	20611593	20646485	1	0	6	4	36	4	0	0	0	0	0	0	E9Q896	
ENSMUST00000133345						0	1	0	1	3	2	1	0	3	0	5		
ENSMUST00000133346	ENSMUSG00000031134	X	57383530	57393036	-1	0	0	3	3	1	0	0	0	0	0	0	A2AFI4	
ENSMUST00000133347	ENSMUSG00000037020	7	30240138	30280419	-1	3	4	4	2	6	3	7	3	0	0	0	F6SP69	
ENSMUST00000133348	ENSMUSG00000030278	6	113424634	113435760	-1	4	0	1	0	4	0	0	0	0	0	0	D3Z1A6	
ENSMUST00000133349	ENSMUSG00000031161	X	7930120	7947889	-1	0	0	0	0	0	3	0	0	3	0	0	B1AUA8	
ENSMUST00000133351						0	0	0	0	0	0	1	0	9	0	1		
ENSMUST00000133352	ENSMUSG00000029917	6	65381105	65458150	1	0	0	4	168	8	0	0	0	0	0	0	D3Z612	
ENSMUST00000133353	ENSMUSG00000031730	8	109591343	109608673	-1	36	42	68	23	31	27	3	19	2	2	4	F6ZQJ5	
ENSMUST00000133354						24	22	24	0	0	0	0	0	0	0	17		
ENSMUST00000133355						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133356						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133357						22	16	55	19	17	12	0	3	1	3	3		
ENSMUST00000133358	ENSMUSG00000026098	1	53189187	53297018	-1	0	4	4	1	3	1	0	0	0	0	0	D3Z611	
ENSMUST00000133359						20	28	22	32	32	26	1	11	3	2	6		
ENSMUST00000133361						0	1	1	0	0	0	0	0	0	1	63		
ENSMUST00000133362	ENSMUSG00000061731	15	53064038	53346159	-1	0	1	0	0	9	7	6	33	9	24	46	D6RE56	
ENSMUST00000133364						2	1	0	2	6	4	4	2	0	0	3		
ENSMUST00000133365						3	7	12	0	7	4	0	0	0	0	3		
ENSMUST00000133366	ENSMUSG00000039157	2	32535332	32569756	1	0	0	10	10	0	0	0	2	0	0	0	A2ASZ7	
ENSMUST00000133367						9	0	12	7	8	1	3	4	2	0	3		
ENSMUST00000133368						0	0	0	0	0	2	0	0	2	0	0		
ENSMUST00000133369	ENSMUSG00000025085	19	57032733	57314919	-1	0	1	5	3	2	0	0	0	0	0	0	F6YHE5	
ENSMUST00000133370						0	2	6	4	0	0	0	0	0	0	0		
ENSMUST00000133371	ENSMUSG00000036923	10	62659043	62726128	-1	19	28	46	75	40	19	0	3	3	0	0		B2RQL2
ENSMUST00000133372	ENSMUSG00000032850	5	118190736	118245116	-1	1	0	0	2	1	2	0	0	0	0	0	D3Z7E1	
ENSMUST00000133373	ENSMUSG00000029790	6	30653457	30693749	-1	3	2	0	1	1	1	0	0	0	0	0	D3Z672	
ENSMUST00000133374						3	5	7	3	1	4	31	40	14	0	30		
ENSMUST00000133375						1	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000133376						35	47	134	112	49	37	1	1	1	0	2		
ENSMUST00000133377						0	0	0	0	0	0	1	1	0	0	0		
ENSMUST00000133378						2	3	5	157	7	2	0	0	0	0	0		
ENSMUST00000133379						7	4	8	3	5	7	0	0	0	0	0		
ENSMUST00000133380						3	0	9	4	5	2	0	0	0	0	0		
ENSMUST00000133381	ENSMUSG00000044716	5	35056766	35087839	1	0	0	0	0	0	0	0	0	0	0	0	D3Z7E3	
ENSMUST00000133382						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133383	ENSMUSG00000000049	11	108343354	108414396	1	2	0	1	64	0	2	0	0	0	0	0	I7HPW5	
ENSMUST00000133384						1	0	0	4	0	0	43	423	204	117	85		
ENSMUST00000133386						30	26	128	74	42	25	3	17	22	3	8		
ENSMUST00000133388	ENSMUSG00000037286	9	100597798	100959375	1	0	0	0	0	0	0	0	0	26	2	31	D3Z1T1	
ENSMUST00000133389						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000133390						53	44	259	66	40	23	0	4	5	0	6		
ENSMUST00000133392						1	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000133393	ENSMUSG00000038545	17	46650337	46664364	1	12	18	14	0	30	15	27	24	12	10	0	F6Q1R4	
ENSMUST00000133394						1	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000133395						1	0	3	30	6	1	0	0	0	0	1		
ENSMUST00000133396						2	6	5	34	4	2	25	120	36	6	46		
ENSMUST00000133397	ENSMUSG00000089682	14	54883377	54888234	1	34	18	79	80	51	18	6	0	0	7	18		P70345
ENSMUST00000133398						0	0	0	0	0	0	0	5	3	0	4		
ENSMUST00000133399						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000133401						2	0	5	3	1	0	0	1	0	0	0		
ENSMUST00000133403						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000133404						0	0	0	3	2	0	0	0	0	0	0		
ENSMUST00000133405						1	1	3	5	4	1	0	4	0	0	0		
ENSMUST00000133406						0	1	4	2	3	0	0	0	2	0	0		
ENSMUST00000133407						1	1	0	0	2	0	2	1	0	0	0		
ENSMUST00000133408						11	17	19	15	15	5	0	3	0	0	8		
ENSMUST00000133409	ENSMUSG00000015094	2	25399351	25409494	1	6	0	2	0	2	0	0	0	0	8	4	A2AJ23	
ENSMUST00000133410	ENSMUSG00000045752	7	143069249	143071093	1	10	6	9	72	12	6	0	5	0	0	11	D3YYU6	
ENSMUST00000133411						0	0	0	0	3	0	1	3	0	1	0		
ENSMUST00000133412						0	0	4	0	1	2	730	940	334	471	394		
ENSMUST00000133413	ENSMUSG00000040599	11	71019611	71027371	1	5	0	0	0	0	3	0	2	4	8	0	A3QK65	
ENSMUST00000133414						0	2	5	0	4	1	1	0	0	0	3		
ENSMUST00000133415						1	0	1	45	6	2	0	0	0	0	0		
ENSMUST00000133416						5	3	3	5	6	2	0	0	0	0	0		
ENSMUST00000133417	ENSMUSG00000039842	8	18595131	18803189	1	3	0	0	1	0	1	0	2	3	0	0	F6Q8J5	
ENSMUST00000133418	ENSMUSG00000033021	1	75435930	75443179	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5Z5	
ENSMUST00000133419						4	4	7	1	6	2	1	0	2	0	0		
ENSMUST00000133420	ENSMUSG00000000538	11	60226714	60352905	-1	0	0	1	0	0	0	0	0	0	0	0	F6ZDJ1	
ENSMUST00000133421						6	3	8	0	4	2	0	7	0	1	10		
ENSMUST00000133422						0	1	6	0	0	4	3	4	15	0	0		
ENSMUST00000133423	ENSMUSG00000032812	7	101348067	101412586	1	4	0	12	5	10	5	169	75	146	0	107	D3Z2S2	
ENSMUST00000133425	ENSMUSG00000039137	4	63414910	63495991	-1	2	3	2	4	3	7	0	0	2	0	0	I7HNW6	
ENSMUST00000133426	ENSMUSG00000020719	11	106780355	106789185	-1	7	5	21	15	14	3	5291	24220	9452	3731	9158	S4R1I6	
ENSMUST00000133427	ENSMUSG00000002980	7	19756131	19771016	-1	0	0	0	0	1	0	0	0	0	0	0	D6RE44	
ENSMUST00000133428	ENSMUSG00000062044	7	45783738	45804144	1	2	0	0	0	0	0	0	0	0	0	0	D3Z7K7	
ENSMUST00000133429	ENSMUSG00000037012	10	62268855	62379908	-1	2	2	0	5	2	0	0	0	1	0	0	B4YB29	
ENSMUST00000133430						1	1	3	1	1	0	0	0	0	0	0		
ENSMUST00000133432	ENSMUSG00000014959	2	70661576	70712636	1	1	3	2	0	9	6	2	8	0	3	0	A2ATI8	
ENSMUST00000133433	ENSMUSG00000037143	2	145934784	146215039	1	0	5	25	0	0	0	0	0	0	0	0	A8Y5L4	
ENSMUST00000133434	ENSMUSG00000035437	2	37443279	37566454	1	2	2	0	104	0	0	9	0	0	0	0	A2AWA7	
ENSMUST00000133435						0	0	4	0	0	1	9	0	0	0	5		
ENSMUST00000133436	ENSMUSG00000024906	19	5482345	5488402	-1	6	3	2	8	4	2	0	29	0	5	6	F6VIY4	
ENSMUST00000133437	ENSMUSG00000086598	2	84659079	84668780	1	29	18	72	31	24	13	1	0	0	0	0	A0A0A6YY25	
ENSMUST00000133438						1	0	8	4	0	3	0	8	6	0	6		
ENSMUST00000133439	ENSMUSG00000028796	4	128654702	128752881	1	0	3	0	17	0	1	0	0	0	0	0	B1ASA1	
ENSMUST00000133440						0	3	0	9	0	1	2	0	3	0	0		
ENSMUST00000133441						6	2	7	0	0	2	0	0	0	0	0		
ENSMUST00000133442						1	1	1	1	2	0	1	7	3	0	3		
ENSMUST00000133443						2	1	0	4	3	0	0	0	0	0	0		
ENSMUST00000133444	ENSMUSG00000030846	7	128439777	128461717	-1	0	0	0	0	0	0	6	14	9	0	23		
ENSMUST00000133445						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133446						0	12	0	10	15	0	0	0	0	0	0		
ENSMUST00000133447	ENSMUSG00000025597	X	114474333	114560829	1	0	0	0	2	0	0	1	0	0	0	0	Q8BLJ6	
ENSMUST00000133448						6	0	6	2	4	0	134	4	101	0	65		
ENSMUST00000133452	ENSMUSG00000020459	11	29526408	29545279	1	0	0	0	17	0	0	0	0	0	0	6	Q5M6W9	
ENSMUST00000133453						0	0	0	0	2	0	2	2	0	0	0		
ENSMUST00000133454	ENSMUSG00000023088	16	14361558	14475737	1	0	5	31	0	15	0	4	0	0	0	32	E9Q1I5	
ENSMUST00000133456						0	0	5	4	7	0	0	10	8	1	10		
ENSMUST00000133457						0	0	0	0	0	0	13	12	1	0	0		
ENSMUST00000133458						0	1	1	3	4	3	2	11	0	2	1		
ENSMUST00000133459	ENSMUSG00000004630	8	3623371	3625545	-1	0	1	0	1	0	0	0	0	0	0	0		P12660
ENSMUST00000133460	ENSMUSG00000021772	14	18271136	18283942	1	0	0	0	1	0	0	0	3	0	14	2	F7BUB1	
ENSMUST00000133461						6	6	15	1	8	0	4	75	9	0	9		
ENSMUST00000133462						2	0	0	111	0	0	0	0	0	0	0		
ENSMUST00000133464	ENSMUSG00000047248	7	100372233	100470152	1	51	40	229	82	51	27	11	19	29	0	25	D6RH58	
ENSMUST00000133465						65	55	207	271	94	78	0	1	0	0	2		
ENSMUST00000133466						33	14	50	32	38	10	15	13	28	4	78		
ENSMUST00000133468	ENSMUSG00000020792	11	116288001	116307233	-1	1	0	0	25	4	4	0	0	0	0	6	A2AAN4	
ENSMUST00000133469						0	0	2	0	0	0	1	0	26	24	25		
ENSMUST00000133470	ENSMUSG00000016458	2	105126529	105173616	1	0	0	0	0	0	5	0	0	0	0	0	A2A400	
ENSMUST00000133472						10	8	0	8	7	2	449	2343	841	121	279		
ENSMUST00000133473	ENSMUSG00000028766	4	137741733	137796384	-1	2	1	2	1	3	1	0	0	0	0	0	B1AXF6	
ENSMUST00000133474	ENSMUSG00000037916	19	4007497	4012806	-1	0	0	0	17	0	0	48	0	22	18	10	D3Z0K1	
ENSMUST00000133477						0	0	1	0	0	0	1	2	0	0	2		
ENSMUST00000133478						4	10	7	0	0	0	0	0	0	0	0		
ENSMUST00000133479	ENSMUSG00000021848	14	48657679	48667644	-1	0	1	0	0	0	0	0	0	0	0	0	D3Z7L5	
ENSMUST00000133480						0	2	1	3	0	0	0	0	0	0	0		
ENSMUST00000133481						50	65	59	34	46	18	19	19	32	6	40		
ENSMUST00000133482						4	4	7	6	5	4	0	10	2	0	8		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133484						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133485	ENSMUSG00000018572	11	69995777	70000009	1	10	0	17	111	7	6	638	0	625	76	462		Q8BSN5
ENSMUST00000133486						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133487						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000133488						0	2	4	1	2	0	0	0	0	0	0		
ENSMUST00000133490						6	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000133491						2	3	0	0	2	1	0	0	0	0	1		
ENSMUST00000133492						0	0	0	10	0	0	4	1	0	0	8		
ENSMUST00000133493	ENSMUSG00000069733	4	100478849	100550147	1	0	14	0	0	0	9	0	0	0	0	0	B1AUC4	
ENSMUST00000133495						0	0	0	0	0	0	7	0	0	0	0		
ENSMUST00000133497						6	2	12	2	5	1	0	2	0	0	1		
ENSMUST00000133498						0	0	0	7	1	0	12	7	11	6	12		
ENSMUST00000133500	ENSMUSG00000040189	7	45924072	45948956	1	0	0	0	0	0	0	7	12	16	6	0	D3YVK8	
ENSMUST00000133501						0	0	0	0	0	0	0	0	73	0	99		
ENSMUST00000133502						0	0	0	25	0	0	0	0	0	0	0		
ENSMUST00000133503	ENSMUSG00000044033	2	77009902	77170636	-1	4	2	0	1	1	0	0	0	0	0	0	D6RJ38	
ENSMUST00000133504						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133505						2	2	3	67	5	4	0	2	0	0	1		
ENSMUST00000133506	ENSMUSG00000074358	7	18890883	18910415	-1	5	3	9	7	1	2	12	34	24	3	6	F6XT04	
ENSMUST00000133507						0	0	0	64	0	2	33	0	8	0	33		
ENSMUST00000133508						0	0	0	0	0	0	0	0	1	0	3		
ENSMUST00000133509						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000133511						8	2	0	24	11	0	0	0	0	0	0		
ENSMUST00000133512	ENSMUSG00000039157	2	32535332	32569756	1	0	0	0	38	1	0	0	0	0	0	1	A2ASZ6	
ENSMUST00000133513	ENSMUSG00000015790	2	26913381	26916530	-1	1	0	3	21	0	0	0	0	0	0	0	A0A0A6YVY3	
ENSMUST00000133514	ENSMUSG00000030695	7	126795234	126800751	-1	0	0	0	0	0	1	0	16	0	0	15	D3YV98	
ENSMUST00000133515						0	3	0	0	0	0	0	11	0	0	0		
ENSMUST00000133516						0	2	1	1	0	1	4	8	0	1	13		
ENSMUST00000133517						1	2	2	2	0	0	0	1	1	0	0		
ENSMUST00000133518						0	1	2	0	2	0	0	0	0	1	0		
ENSMUST00000133519	ENSMUSG00000030881	7	105634203	105640416	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2F3	
ENSMUST00000133520						13	2	7	11	19	5	4	18	17	0	20		
ENSMUST00000133521						0	1	4	0	3	2	0	0	0	0	0		
ENSMUST00000133522						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000133524						0	0	0	51	2	1	0	6	0	0	0		
ENSMUST00000133526						2	2	0	0	4	2	0	0	0	0	0		
ENSMUST00000133527	ENSMUSG00000007570	17	28313530	28326568	1	0	0	0	0	0	0	2	0	2	1	0	B8JJD8	
ENSMUST00000133530						7	0	13	0	6	0	0	0	0	0	0		
ENSMUST00000133532	ENSMUSG00000044221	5	88659448	88676171	-1	0	0	0	0	0	0	0	0	0	0	13	D3YV30	
ENSMUST00000133533	ENSMUSG00000029026	4	154056253	154140208	-1	24	10	33	0	30	19	0	0	0	1	0		Q9JJP2
ENSMUST00000133535						9	12	17	18	14	10	36	168	78	13	166		
ENSMUST00000133536						7	0	2	1	3	1	0	1	1	0	5		
ENSMUST00000133538						14	10	4	9	20	15	31	160	76	130	112		
ENSMUST00000133539						7	0	23	236	15	4	0	1	1	0	2		
ENSMUST00000133540						74	42	242	99	78	43	5	10	12	3	25		
ENSMUST00000133541						15	11	35	34	26	13	20	128	10	0	47		
ENSMUST00000133542						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000133543						0	1	0	0	1	0	0	0	0	1	0		
ENSMUST00000133544						27	20	133	33	45	6	103	320	172	15	172		
ENSMUST00000133545						1	1	0	0	1	0	0	26	14	0	12		
ENSMUST00000133546						2	0	11	2	1	0	5	16	2	0	6		
ENSMUST00000133547						1	0	0	0	4	0	257	966	397	50	535		
ENSMUST00000133549	ENSMUSG00000020564	12	33147693	33375659	1	2	0	0	5	0	0	92	34	83	11	118	D3YXW3	
ENSMUST00000133551						0	0	0	0	3	0	24	7	5	2	0		
ENSMUST00000133552						6	6	2	20	13	8	0	1	0	0	0		
ENSMUST00000133553	ENSMUSG00000030611	7	78783119	78792989	1	0	0	6	3	1	1	75	40	37	39	35		
ENSMUST00000133554						15	8	17	83	31	12	0	0	0	0	0		
ENSMUST00000133555						0	1	2	3	5	2	0	0	0	0	0		
ENSMUST00000133556						12	0	0	304	0	6	0	0	0	0	0		
ENSMUST00000133557						1	1	3	2	1	0	9	0	4	0	0		
ENSMUST00000133558	ENSMUSG00000017446	11	118428203	118449963	1	10	3	30	3	5	3	0	0	0	0	0	A2A4W2	
ENSMUST00000133559						5	0	1	4	0	0	0	1	2	0	2		
ENSMUST00000133561	ENSMUSG00000070375	11	74269356	74270444	1	7	7	9	3	3	4	0	0	0	0	0	Q7TRX0	
ENSMUST00000133562	ENSMUSG00000075023	2	93855361	93869157	-1	0	0	4	8	1	0	0	0	0	0	0	A2AIH1	
ENSMUST00000133563						0	0	0	3	0	0	6	0	6	4	14		
ENSMUST00000133564	ENSMUSG00000021055	12	76120419	76177259	-1	34	31	0	29	36	0	0	0	0	0	0	S4R2G7	
ENSMUST00000133565	ENSMUSG00000026812	2	28641228	28691167	1	0	0	0	14	0	0	45	0	0	0	26	F2Z3X2	
ENSMUST00000133566						3	3	9	1	0	0	0	0	0	0	0		
ENSMUST00000133567	ENSMUSG00000045573	4	4133531	4138819	-1	0	0	0	54	4	1	1	2	0	0	7	B1AZQ0	
ENSMUST00000133568	ENSMUSG00000004455	5	122158278	122175273	1	2	0	9	4	3	0	80	146	35	0	15	A0A0G2JF34	
ENSMUST00000133569						0	0	0	0	0	4	0	5	6	0	0		
ENSMUST00000133571						7	0	8	46	14	5	0	0	0	0	0		
ENSMUST00000133572						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133573						0	1	0	4	1	1	0	0	0	0	0		
ENSMUST00000133574	ENSMUSG00000023927	17	51736187	51833290	-1	0	0	2	49	0	0	396	0	73	16	119		Q60611
ENSMUST00000133575						6	0	5	0	7	2	5	57	29	12	45		
ENSMUST00000133576						0	0	0	0	0	0	0	0	7	0	2		
ENSMUST00000133577						2	0	0	24	0	1	0	0	0	0	0		
ENSMUST00000133578	ENSMUSG00000026317	8	14881335	14901720	1	0	1	8	6	2	0	0	0	0	3	6	D3Z3T9	
ENSMUST00000133579						3	13	14	25	27	11	11	0	5	0	3		
ENSMUST00000133580	ENSMUSG00000039285	9	118040499	118069794	1	0	0	0	0	0	0	0	0	0	0	0		Q9QYP6
ENSMUST00000133581						0	0	3	0	0	0	0	2	2	0	0		
ENSMUST00000133582						2	0	1	2	12	1	2	0	0	0	1		
ENSMUST00000133583						0	0	0	1	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133584	ENSMUSG00000023791	16	32084418	32099738	-1	0	0	0	0	0	0	46	208	109	177	101	F6QPF7	
ENSMUST00000133585						4	6	6	3	10	1	3	0	3	0	2		
ENSMUST00000133587						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133588	ENSMUSG00000042846	10	63928472	64090277	-1	0	0	0	0	0	0	0	0	0	0	0	D3YV09	
ENSMUST00000133589						2	1	9	0	1	1	0	0	72	19	66		
ENSMUST00000133590						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000133591						0	1	6	0	0	0	0	146	11	11	12		
ENSMUST00000133592						1	0	1	39	5	6	0	0	0	0	0		
ENSMUST00000133593						3	0	4	3	0	0	8	6	13	4	19		
ENSMUST00000133594						3	2	2	1	1	0	0	0	2	2	3		
ENSMUST00000133595	ENSMUSG00000025736	17	25828867	25831842	1	17	10	24	13	12	1	0	16	0	0	13		Q3TA59
ENSMUST00000133597						30	54	133	46	43	32	0	9	11	2	14		
ENSMUST00000133598						3	2	1	19	2	0	0	0	8	0	7		
ENSMUST00000133600	ENSMUSG00000058794	15	103248212	103258403	-1	0	0	0	0	0	0	125	566	0	85	0	D3Z224	
ENSMUST00000133601	ENSMUSG00000001100	11	78512193	78522736	1	3	0	20	4	5	0	28	0	60	2	12	F6SQH7	
ENSMUST00000133602	ENSMUSG00000027327	2	131146324	131160081	-1	2	0	2	3	3	0	6	3	3	0	0	H7BXB9	
ENSMUST00000133603						6	6	0	4	6	1	0	0	0	2	5		
ENSMUST00000133604	ENSMUSG00000042625	17	56560965	56584585	-1	7	5	19	34	11	6	0	0	1	0	71	D6RJ78	
ENSMUST00000133605						0	0	6	5	8	0	0	29	25	5	43		
ENSMUST00000133606						0	0	0	16	0	0	2	0	0	0	3		
ENSMUST00000133607						0	0	5	0	0	0	3	4	0	0	7		
ENSMUST00000133608	ENSMUSG00000041660	2	110262697	110314560	-1	1	2	10	5	3	1	0	0	0	0	0	A2AGK3	
ENSMUST00000133609						0	0	2	2	4	0	177	832	262	24	428		
ENSMUST00000133610						2	2	4	1	4	2	0	0	0	0	0		
ENSMUST00000133611						12	5	22	70	10	14	0	1	0	0	3		
ENSMUST00000133612	ENSMUSG00000027286	2	120604238	120609520	-1	6	1	2	31	0	0	26	10	23	58	38	A2AKH7	
ENSMUST00000133613						0	0	7	2	3	0	0	13	4	5	4		
ENSMUST00000133614						0	0	1	1	0	0	2	0	91	207	36		
ENSMUST00000133615						0	0	0	42	7	0	1	161	161	69	155		
ENSMUST00000133617	ENSMUSG00000032786	9	106233455	106248126	-1	3	0	2	9	4	0	224	29	130	0	86	D6RGR8	
ENSMUST00000133618	ENSMUSG00000071715	15	78244801	78262580	1	0	3	0	0	0	0	1805	1305	2489	156	1305	A8XU21	
ENSMUST00000133619	ENSMUSG00000060090	X	20364481	20405653	1	17	13	0	0	0	11	23	17	0	0	18		Q9EPK2
ENSMUST00000133620	ENSMUSG00000040249	10	127538161	127621148	-1	0	0	2	0	4	0	0	0	0	0	2	F6UAC8	
ENSMUST00000133621						27	20	103	10	21	7	36	205	64	5	104		
ENSMUST00000133623						6	0	1	8	2	2	4	0	2	1	0		
ENSMUST00000133624						1	4	1	1	2	0	0	0	0	0	0		
ENSMUST00000133625						0	4	0	0	12	5	130	387	257	26	305		
ENSMUST00000133626	ENSMUSG00000073724	4	144059126	144069327	1	3	0	16	4	3	0	0	0	0	0	0	E0CXV0	
ENSMUST00000133627						109	57	497	232	66	42	5	5	5	0	3		
ENSMUST00000133628						7	2	8	79	11	3	658	2164	588	910	470		
ENSMUST00000133629						0	1	0	0	0	0	0	2	0	0	0		
ENSMUST00000133631						4	8	6	2	13	2	0	0	1	0	0		
ENSMUST00000133632						2	5	7	0	2	1	0	0	0	0	1		
ENSMUST00000133633						3	7	2	5	4	2	0	0	0	0	0		
ENSMUST00000133634	ENSMUSG00000047045	X	142681406	142843494	1	0	0	0	36	0	4	3	11	0	0	20		Q6PHN7
ENSMUST00000133635	ENSMUSG00000020397	11	46436925	46442721	1	0	2	10	0	0	0	0	44	8	0	11	F2Z3X8	
ENSMUST00000133636						0	0	0	0	2	0	0	0	0	0	5		
ENSMUST00000133637	ENSMUSG00000031142	X	7607083	7635196	1	2	0	12	6	5	0	0	0	0	0	0	Q8C8Q4	
ENSMUST00000133638						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133639	ENSMUSG00000025939	1	16540790	16619489	-1	0	0	3	0	1	0	0	0	21	95	22	D6RCG4	
ENSMUST00000133640						5	4	47	5	4	4	6	21	6	1	16		
ENSMUST00000133641						1	3	2	13	3	1	5	77	19	6	13		
ENSMUST00000133642						0	0	1	0	0	0	17	11	40	0	7		
ENSMUST00000133645	ENSMUSG00000034156	11	87760541	87785928	1	0	2	4	1	0	1	3	0	6	0	0	F7AUI0	
ENSMUST00000133647						0	1	1	2	0	0	0	0	0	0	0		
ENSMUST00000133649						0	0	0	0	0	0	12	0	20	0	6		
ENSMUST00000133650	ENSMUSG00000025728	17	25926427	25944510	-1	0	0	0	3	2	0	32	0	19	0	32	F6YYP1	
ENSMUST00000133651						2	0	5	5	3	2	18	37	23	10	16		
ENSMUST00000133652						7	7	15	31	6	2	0	3	0	0	0		
ENSMUST00000133654	ENSMUSG00000027605	2	155517948	155585724	1	12	0	16	0	5	0	0	0	0	26	22	D6RHA7	
ENSMUST00000133655	ENSMUSG00000005994	4	80834123	80851719	1	4	1	3	3	12	8	0	0	0	0	0	A2ADJ4	
ENSMUST00000133656						3	0	9	0	0	0	0	0	0	0	0		
ENSMUST00000133657						1	0	1	2	1	0	0	0	0	1	0		
ENSMUST00000133659						7	13	14	8	11	7	0	0	0	0	0		
ENSMUST00000133660						2	1	2	55	0	1	0	0	0	0	0		
ENSMUST00000133661	ENSMUSG00000000247	2	38339281	38369733	1	0	3	2	3	3	1	0	0	0	0	0	F6SM03	
ENSMUST00000133662						0	0	0	0	0	0	0	0	0	6	0		
ENSMUST00000133663						2	3	0	5	3	4	0	1	0	4	0		
ENSMUST00000133664	ENSMUSG00000047909	2	11777876	11790329	1	2	1	0	1	3	0	0	51	13	3	16	F6SD06	
ENSMUST00000133665						0	3	8	4	2	0	0	0	0	0	0		
ENSMUST00000133666						3	1	9	5	3	3	4	13	11	0	14		
ENSMUST00000133667						7	0	52	5	9	0	0	61	88	669	93		
ENSMUST00000133668	ENSMUSG00000048647	2	119516505	119547627	-1	0	0	0	9	0	0	0	0	5	0	0	A2AQ12	
ENSMUST00000133669						1	1	0	0	0	1	0	0	0	1	0		
ENSMUST00000133670	ENSMUSG00000020728	11	108425192	108860615	1	0	0	0	0	0	0	0	0	0	6	0	A2ABQ5	
ENSMUST00000133671						2	3	1	0	0	0	0	0	0	0	0		
ENSMUST00000133672						0	3	21	5	3	1	0	0	0	0	0		
ENSMUST00000133673						0	2	8	6	0	1	0	0	0	0	0		
ENSMUST00000133674						4	4	2	4	2	1	0	0	0	0	0		
ENSMUST00000133676	ENSMUSG00000033770	4	141384610	141398724	-1	0	0	2	13	17	4	0	0	0	0	0	A2ADB4	
ENSMUST00000133677	ENSMUSG00000026049	1	44086613	44102441	-1	0	0	0	0	0	0	0	0	0	0	0		Q3TUU5
ENSMUST00000133679						7	5	14	9	9	5	0	1	1	0	1		
ENSMUST00000133680						0	0	0	78	0	0	9	1	8	0	8		
ENSMUST00000133681						0	0	0	0	0	0	8	25	3	0	17		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133682						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000133683						0	0	0	0	0	2	6	23	3	31	3		
ENSMUST00000133685						0	0	0	0	0	0	7	22	6	0	0		
ENSMUST00000133686						11	9	13	78	18	7	20	168	65	6	73		
ENSMUST00000133688						0	5	4	72	3	2	0	0	0	0	0		
ENSMUST00000133689	ENSMUSG00000006932	9	120929216	120960507	1	3	1	4	3	3	3	48	190	172	88	322	F7CRC6	
ENSMUST00000133690						9	6	0	3	3	0	0	0	0	0	0		
ENSMUST00000133692						0	0	12	0	1	2	0	0	0	0	0		
ENSMUST00000133695						21	9	52	23	37	20	20	133	30	0	76		
ENSMUST00000133696						14	0	54	38	19	3	154	292	153	0	240		
ENSMUST00000133697						3	2	6	0	0	0	89	54	49	171	33		
ENSMUST00000133699						32	47	61	114	59	51	6	24	9	0	16		
ENSMUST00000133700						4	1	28	10	6	0	0	0	0	0	0		
ENSMUST00000133701	ENSMUSG00000064246	1	134182176	134190181	1	9	4	7	17	7	3	779	849	449	132	412	D3Z2Z5	
ENSMUST00000133703						1	0	2	9	0	0	0	0	0	0	0		
ENSMUST00000133704						0	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000133705	ENSMUSG00000037221	5	137596645	137601058	-1	0	0	0	34	3	0	0	0	3	2	2	D3Z5Y3	
ENSMUST00000133706						0	5	4	3	4	1	5	47	8	0	21		
ENSMUST00000133707	ENSMUSG00000002320	14	55635965	55643806	-1	2	0	0	21	0	1	4	0	0	0	7	D3YYW1	
ENSMUST00000133708						14	9	26	0	31	15	0	0	11	0	20		
ENSMUST00000133709	ENSMUSG00000028479	4	44034075	44084177	-1	0	0	0	0	0	0	7	4	5	0	0	G3UX49	
ENSMUST00000133710						21	15	39	25	26	15	0	4	3	0	8		
ENSMUST00000133711						0	0	0	16	0	2	0	0	0	0	0		
ENSMUST00000133712						0	0	0	0	0	0	6	18	46	61	14		
ENSMUST00000133714						0	0	0	26	0	0	2	2	4	1	7		
ENSMUST00000133715						26	35	58	33	40	15	56	140	79	16	116		
ENSMUST00000133716						5	11	24	16	29	5	0	0	0	0	0		
ENSMUST00000133717	ENSMUSG00000003279	17	69969073	70821413	1	0	0	0	132	1	0	0	0	0	0	0	D3Z6F4	
ENSMUST00000133718						0	8	0	0	0	0	66	6651	101	23	105		
ENSMUST00000133719						5	7	14	1	1	3	0	0	7	0	3		
ENSMUST00000133720						3	10	3	4	4	2	3	0	2	0	12		
ENSMUST00000133721						37	50	131	96	51	23	4	9	17	0	13		
ENSMUST00000133722	ENSMUSG00000040522	X	167242696	167264329	-1	0	0	0	0	0	1	0	0	46	0	3	A2AHI8	
ENSMUST00000133724	ENSMUSG00000004359	10	88674772	88685015	-1	1	0	0	0	1	0	0	0	0	0	0	D6RE28	
ENSMUST00000133725						0	2	1	1	0	0	15	49	0	2	35		
ENSMUST00000133726	ENSMUSG00000005882	2	155846894	155930310	-1	0	0	0	0	0	0	0	0	0	0	7	D6RJ83	
ENSMUST00000133727	ENSMUSG00000010362	11	101627195	101636100	1	0	0	3	1	5	0	0	3	0	4	0	F6W1D5	
ENSMUST00000133728	ENSMUSG00000030533	7	80325292	80341005	-1	0	0	0	0	0	0	20	12	14	0	0	D3YZN8	
ENSMUST00000133729						17	36	78	28	25	7	12	19	32	0	51		
ENSMUST00000133730						2	0	0	0	0	0	0	0	0	0	10		
ENSMUST00000133731	ENSMUSG00000039763	16	91614257	91619026	-1	0	0	0	1	2	0	0	3	2	1	0	D3Z0T8	
ENSMUST00000133732						12	6	36	4	10	7	2	2	2	0	2		
ENSMUST00000133733						7	4	19	8	5	0	10	13	2	0	29		
ENSMUST00000133734						0	0	0	8	0	0	0	6	0	0	14		
ENSMUST00000133736						0	0	4	28	3	0	123	187	117	117	67		
ENSMUST00000133737						0	0	0	0	3	2	1	0	36	0	14		
ENSMUST00000133738						9	4	27	12	16	11	0	4	4	0	2		
ENSMUST00000133739	ENSMUSG00000050471	9	35216965	35267805	-1	0	2	2	1	2	0	29	121	7	71	32	F6Q255	
ENSMUST00000133740						2	1	0	0	2	0	0	15	0	1	0		
ENSMUST00000133741	ENSMUSG00000036026	17	45660171	45686905	-1	1	0	0	0	0	0	0	0	0	0	0	D3Z0P2	
ENSMUST00000133743						0	0	5	0	0	0	0	1350	0	24	5		
ENSMUST00000133744						8	13	16	58	20	7	0	17	7	0	15		
ENSMUST00000133745						3	3	3	1	0	2	2	9	0	0	8		
ENSMUST00000133746						0	4	2	3	3	1	0	0	0	0	0		
ENSMUST00000133747						10	9	13	19	14	10	0	5	0	0	2		
ENSMUST00000133748						3	0	1	17	0	0	27	60	44	0	57		
ENSMUST00000133749						1	2	8	0	1	3	0	2	0	0	1		
ENSMUST00000133750	ENSMUSG00000040466	7	27447978	27466144	1	0	3	2	30	7	0	0	0	10	0	16		
ENSMUST00000133753	ENSMUSG00000046679	6	86438374	86473500	1	0	3	12	16	6	3	0	0	0	0	0		Q8R3C1
ENSMUST00000133754						1	1	0	0	3	0	0	0	0	2	0		
ENSMUST00000133756						61	80	120	88	88	48	23	163	47	18	46		
ENSMUST00000133757	ENSMUSG00000032349	9	77917364	77984519	1	2	0	1	5	1	0	0	0	8	0	34	D3Z136	
ENSMUST00000133758	ENSMUSG00000030924	7	119794006	119848943	1	0	0	0	0	0	0	0	8	0	4	5	D6RFP2	
ENSMUST00000133760						65	50	66	99	61	19	4	10	3	1	11		
ENSMUST00000133761						8	4	7	5	9	3	0	0	1	1	4		
ENSMUST00000133762						0	4	0	7	0	3	54	537	75	118	135		
ENSMUST00000133763	ENSMUSG00000038618	7	141215860	141218658	1	4	3	2	83	4	3	0	3	3	0	2	D3YXD9	
ENSMUST00000133764						0	0	0	1	3	0	0	0	0	0	0		
ENSMUST00000133767						12	10	54	17	10	7	4	3	0	0	3		
ENSMUST00000133768	ENSMUSG00000026766	2	50279881	50296801	-1	0	3	1	15	0	1	0	3	16	9	0	A2AQT8	
ENSMUST00000133769	ENSMUSG00000026277	1	93619751	93658659	-1	0	0	0	78	0	2	44	21	35	6	42	D3Z359	
ENSMUST00000133770						0	2	0	11	1	0	0	0	0	0	0		
ENSMUST00000133771	ENSMUSG00000053091	7	66689889	66717256	1	0	0	0	0	0	1	0	56	70	16	0	D6RFA2	
ENSMUST00000133773						0	0	0	0	0	1	1	0	0	0	29		
ENSMUST00000133774	ENSMUSG00000034187	11	103821782	103954056	-1	0	0	11	0	0	0	11	0	0	0	0	G3UX86	
ENSMUST00000133775						34	20	46	34	42	31	5	15	6	1	15		
ENSMUST00000133776	ENSMUSG00000029629	6	11907809	12081205	1	0	0	12	0	0	0	4	25	0	4	0	F6TN92	
ENSMUST00000133777						8	6	13	12	12	7	9	11	24	4	26		
ENSMUST00000133778						0	0	3	0	1	0	0	0	2	0	0		
ENSMUST00000133779	ENSMUSG00000017499	11	98907801	98923940	1	12	15	20	11	12	0	7	20	0	0	17	E9PY34	
ENSMUST00000133780	ENSMUSG00000072944	X	140006805	140062712	-1	0	2	4	26	2	2	0	0	0	0	0	A2AG12	
ENSMUST00000133781	ENSMUSG00000031201	X	75416628	75454001	1	0	0	0	0	0	0	0	5	9	0	0	A3KGA8	
ENSMUST00000133782						1	0	1	0	0	1	0	0	2	0	3		
ENSMUST00000133783						3	2	4	3	0	7	9	161	8	24	58		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133784						1	1	0	0	3	0	0	0	1	3	0		
ENSMUST00000133785						10	9	46	22	11	2	9	72	6	11	19		
ENSMUST00000133786						4	0	13	24	6	3	9	77	86	0	10		
ENSMUST00000133787	ENSMUSG00000043659	9	24097996	24316398	1	0	6	4	2	6	1	0	0	0	0	0	B1B1A4	
ENSMUST00000133788						2	0	6	6	6	0	0	0	1	0	0		
ENSMUST00000133789						6	2	4	0	0	4	0	9	0	0	0		
ENSMUST00000133790						10	10	19	4	12	4	4	33	11	7	20		
ENSMUST00000133791						7	2	5	11	6	3	6	0	12	0	7		
ENSMUST00000133792	ENSMUSG00000026417	1	130826684	130852249	1	0	0	0	0	4	2	0	0	0	0	0	D3Z2D3	
ENSMUST00000133793						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133795	ENSMUSG00000032309	9	55208925	55224433	1	0	0	2	0	1	1	4	3	9	0	18	D3Z2G9	
ENSMUST00000133796						1	4	9	0	0	4	0	53	0	0	10		
ENSMUST00000133797						7	8	5	7	8	1	0	6	4	0	6		
ENSMUST00000133799						0	1	0	1	0	0	0	0	0	17	0		
ENSMUST00000133800						2	0	0	2	0	0	1	0	1	0	2		
ENSMUST00000133801						3	5	17	17	15	5	0	0	0	0	0		
ENSMUST00000133802	ENSMUSG00000062006	3	130726831	130730398	-1	2	4	57	8	5	7	4	29	2	0	10	A0A0G2JEY6	
ENSMUST00000133803	ENSMUSG00000053841	4	129626078	129641065	-1	6	0	1	30	0	0	0	0	45	0	32	A2ADZ2	
ENSMUST00000133804						10	8	86	0	12	9	36	145	67	3	79		
ENSMUST00000133806						1	2	14	4	5	0	0	0	0	0	0		
ENSMUST00000133807	ENSMUSG00000015488	2	27009926	27021089	1	2	3	0	1	2	2	0	3	6	1	3	F7CPS9	
ENSMUST00000133809	ENSMUSG00000026988	2	59852364	59882591	-1	1	0	0	4	1	2	0	0	0	0	0	A2AUX9	
ENSMUST00000133810						43	23	98	35	28	17	0	0	0	0	3		
ENSMUST00000133811	ENSMUSG00000020532	11	84129672	84401651	1	0	0	0	14	0	2	0	0	0	0	0		
ENSMUST00000133812						3	5	4	1	6	1	0	0	0	0	0		
ENSMUST00000133813	ENSMUSG00000031381	X	164419793	164433916	1	0	0	0	0	0	0	0	0	50	71	4	A2AIH4	
ENSMUST00000133814						0	0	0	0	0	0	15	27	22	2	28		
ENSMUST00000133816						8	0	18	70	3	0	0	0	5	0	5		
ENSMUST00000133817	ENSMUSG00000030822	7	127459611	127476759	1	0	0	0	1	0	0	6	0	4	0	13		
ENSMUST00000133818						0	0	0	15	3	0	0	0	0	0	0		
ENSMUST00000133820	ENSMUSG00000044456	12	102283048	102390855	1	39	21	97	18	43	25	9615	9301	7835	509	5877	Q3U332	
ENSMUST00000133821	ENSMUSG00000034224	8	119479602	119501698	-1	2	0	0	0	0	0	0	0	0	0	0	D3YUL2	
ENSMUST00000133822						4	2	25	3	4	3	2	3	4	0	4		
ENSMUST00000133825						1	1	3	5	7	0	0	0	0	0	0		
ENSMUST00000133826						2	0	0	21	0	1	223	40	562	2792	327		
ENSMUST00000133827						1	1	0	1	2	0	6	78	34	2	10		
ENSMUST00000133828						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000133830						185	243	86	100	130	66	0	1	32	0	16		
ENSMUST00000133832	ENSMUSG00000026792	2	32925216	32961614	-1	0	0	0	0	0	0	2	0	0	0	0	A2AHX5	
ENSMUST00000133833	ENSMUSG00000006546	1	74889934	74893143	-1	14	8	52	88	17	3	0	1	0	0	0	A0A087WQQ2	
ENSMUST00000133834						0	0	2	0	3	3	0	2	0	0	0		
ENSMUST00000133835						4	0	2	0	8	0	0	0	0	0	0		
ENSMUST00000133836						7	0	0	0	0	6	0	0	0	48	0		
ENSMUST00000133837						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133838						5	3	0	4	6	2	0	0	0	0	0		
ENSMUST00000133839	ENSMUSG00000063524	4	150236721	150248879	1	0	0	0	0	0	0	533	8	324	0	148	B0QZL1	
ENSMUST00000133840						6	6	12	3	11	5	0	9	10	2	8		
ENSMUST00000133841						1	2	1	0	6	2	0	0	0	0	0		
ENSMUST00000133842						7	9	43	103	17	10	2	3	4	2	8		
ENSMUST00000133843	ENSMUSG00000007891	7	142371148	142388038	-1	4	0	10	5	3	5	4048	5091	2892	194	1670	F6Y6L6	
ENSMUST00000133845	ENSMUSG00000035266	5	100762145	100798598	-1	6	10	4	0	7	2	5	0	1	0	0	F7DCU7	
ENSMUST00000133846						1	0	1	4	1	0	0	8	0	0	6		
ENSMUST00000133847	ENSMUSG00000022881	16	23113943	23127737	-1	2	0	6	24	5	5	0	0	0	0	0	D6RGM1	
ENSMUST00000133848						3	0	19	7	8	0	0	0	0	0	0		
ENSMUST00000133849						6	0	5	6	2	0	0	13	0	0	6		
ENSMUST00000133850						0	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000133851						3	2	8	2	4	1	3	6	0	4	5		
ENSMUST00000133852						8	4	12	8	10	5	6	44	5	2	9		
ENSMUST00000133853	ENSMUSG00000061080	16	39984361	42181679	1	0	1	0	0	2	0	0	0	0	0	0	A0A087WP70	
ENSMUST00000133854						17	16	28	26	15	5	4	12	8	0	6		
ENSMUST00000133855						1	0	6	1	0	0	0	1	2	0	3		
ENSMUST00000133856	ENSMUSG00000038685	2	181319739	181356616	1	1	0	0	0	0	0	0	0	0	0	0	F6X1P9	
ENSMUST00000133857						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133858						12	9	2	13	12	4	0	0	0	0	0		
ENSMUST00000133859						1	2	0	1	2	1	1	0	0	0	0		
ENSMUST00000133861	ENSMUSG00000005417	11	59661305	59780860	1	3	3	14	10	13	2	99	141	202	15	246	F6RND9	
ENSMUST00000133862	ENSMUSG00000020721	11	107547930	107693826	1	8	9	117	22	11	10	0	0	0	0	7	A2AAU5	
ENSMUST00000133863						5	3	2	3	10	0	0	0	0	0	0		
ENSMUST00000133864						0	0	0	3	2	0	0	0	0	0	0		
ENSMUST00000133865						6	1	1	0	2	3	0	19	15	0	18		
ENSMUST00000133866						0	4	0	0	4	0	0	0	0	34	0		
ENSMUST00000133868	ENSMUSG00000024220	17	28177207	28205886	1	0	3	0	0	0	1	11	0	18	0	0	B2KF19	
ENSMUST00000133869	ENSMUSG00000001665	10	75774115	75781414	-1	79	72	756	160	55	42	0	1	0	0	0	G3UYL6	
ENSMUST00000133870						0	2	3	1	1	0	0	0	2	0	0		
ENSMUST00000133872	ENSMUSG00000032030	9	53614582	53670014	-1	3	0	3	1	2	1	0	0	0	0	0	F8VQI6	
ENSMUST00000133874	ENSMUSG00000006219	4	141576062	141606096	-1	1	0	0	2	1	2	0	0	0	0	0	A2ADF4	
ENSMUST00000133875						8	3	3	1	3	7	10	3	15	0	21		
ENSMUST00000133876						85	79	557	128	89	71	1	2	0	1	4		
ENSMUST00000133877	ENSMUSG00000079484	2	30266203	30282149	1	0	0	4	0	0	0	0	0	0	0	0	A2AQZ2	
ENSMUST00000133879						8	13	26	22	14	5	0	0	0	1	1		
ENSMUST00000133880						4	3	3	6	3	0	0	1	0	0	3		
ENSMUST00000133881						0	0	0	5	2	2	0	0	20	16	22		
ENSMUST00000133882						83	66	84	32	91	49	0	0	0	2	5		
ENSMUST00000133883						38	27	72	12	34	29	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133885	ENSMUSG00000040681	16	96120618	96127729	-1	0	0	5	0	1	3	3	1	3	16	12	D3Z607	
ENSMUST00000133886						1	1	21	3	4	5	0	0	0	0	0		
ENSMUST00000133887						2	5	1	2	0	0	0	0	0	0	0		
ENSMUST00000133888						15	21	85	19	24	12	0	2	0	0	1		
ENSMUST00000133889						2	4	1	0	4	2	0	10	5	0	4		
ENSMUST00000133890	ENSMUSG00000026490	1	179960472	180165603	1	0	0	0	0	0	0	0	9	13	0	13	F6Q5A5	
ENSMUST00000133891						1	2	3	0	1	0	0	6	0	0	2		
ENSMUST00000133892	ENSMUSG00000004113	2	24603887	24763152	-1	0	0	0	0	0	0	1	2	0	0	0	A2AIZ9	
ENSMUST00000133893						6	6	16	15	6	0	11	20	19	2	14		
ENSMUST00000133894						2	0	8	0	4	0	5	15	0	0	4		
ENSMUST00000133895	ENSMUSG00000060206	4	54945048	55083563	1	4	2	4	12	2	1	0	0	0	0	3	B1AWL3	
ENSMUST00000133896						1	0	0	0	3	0	19	62	5	0	44		
ENSMUST00000133897						8	2	24	15	9	2	0	0	0	0	0		
ENSMUST00000133898	ENSMUSG00000027238	2	121545529	121807087	-1	3	15	133	0	16	9	0	4	0	0	0	F6XM46	
ENSMUST00000133899	ENSMUSG00000024172	17	55445382	55514581	1	4	4	5	88	3	2	0	0	0	0	0	A9C433	
ENSMUST00000133900						2	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000133901						3	1	3	19	0	2	6	5	0	18	6		
ENSMUST00000133902						23	8	86	29	0	8	0	20	0	0	0		
ENSMUST00000133903						1	2	1	5	2	1	2	48	3	0	15		
ENSMUST00000133904						0	0	7	0	0	2	0	0	0	0	0		
ENSMUST00000133905						2	1	2	2	0	3	2	9	0	1	0		
ENSMUST00000133906						0	0	9	0	0	0	33	67	13	16	7		
ENSMUST00000133907						1427	1397	1583	315	797	334	20	285	95	29	133		
ENSMUST00000133908						0	0	4	0	2	1	0	0	0	0	0		
ENSMUST00000133909						7	16	18	12	18	9	1	9	3	0	9		
ENSMUST00000133910						3	0	0	0	20	4	249	84	581	3433	750		
ENSMUST00000133911						3	1	4	0	2	4	29	291	61	7	92		
ENSMUST00000133912						2	1	1	0	0	3	0	0	0	0	0		
ENSMUST00000133913	ENSMUSG00000000486	7	127214447	127233130	-1	0	0	0	0	0	0	0	1	2	26	71		
ENSMUST00000133914						0	0	0	47	2	0	0	0	0	0	0		
ENSMUST00000133915						7	4	12	18	8	3	0	0	0	0	0		
ENSMUST00000133916						0	0	0	5	1	0	6	4	0	0	0		
ENSMUST00000133918	ENSMUSG00000052581	6	80018877	80810143	1	2	0	0	7	0	0	0	0	0	0	0		Q80XG9
ENSMUST00000133919						0	3	2	4	3	0	52	45	0	0	0		
ENSMUST00000133920						4	2	12	5	2	2	0	0	0	0	0		
ENSMUST00000133921	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	2	0	4	0	48	4	42	B7ZCP7	
ENSMUST00000133922						1	3	3	5	1	1	0	9	11	3	9		
ENSMUST00000133923						1	0	5	0	0	0	18	23	15	16	37		
ENSMUST00000133924						0	0	0	0	0	0	0	28	0	0	0		
ENSMUST00000133925	ENSMUSG00000031921	8	107069400	107096547	-1	0	0	0	7	0	0	20	0	38	0	1	D3YZ08	
ENSMUST00000133926						0	0	1	1	1	0	0	1	0	0	0		
ENSMUST00000133927	ENSMUSG00000019868	10	14654755	14705560	-1	0	1	4	0	0	2	4	0	6	53	5	F6RYM7	
ENSMUST00000133928	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	0	0	0	18	4	5	D3YVX7	
ENSMUST00000133929						4	10	6	7	9	7	0	0	0	0	0		
ENSMUST00000133930	ENSMUSG00000034773	11	102248882	102265187	1	13	21	66	21	34	16	10	13	21	0	10		Q32P12
ENSMUST00000133931	ENSMUSG00000049565	3	108739658	108782309	1	9	10	5	15	13	4	0	0	0	0	0	E9Q8N6	
ENSMUST00000133932	ENSMUSG00000005994	4	80834123	80851719	1	0	0	1	0	2	0	0	0	0	0	0	A2ADJ6	
ENSMUST00000133933						3	2	1	0	2	5	0	0	0	0	0		
ENSMUST00000133934	ENSMUSG00000026972	2	24925352	24935252	-1	2	0	0	22	0	2	27	49	55	0	44	A2AIS9	
ENSMUST00000133935						0	1	1	0	0	1	0	0	0	0	0		
ENSMUST00000133936						3	3	3	1	8	1	0	0	0	0	2		
ENSMUST00000133937						72	76	113	58	86	37	3	13	4	1	4		
ENSMUST00000133938	ENSMUSG00000030822	7	127459611	127476759	1	0	0	0	58	0	5	7	6	24	0	3	D3Z5U4	
ENSMUST00000133939	ENSMUSG00000030877	7	120982509	121014787	1	0	0	4	0	0	0	1	3	0	0	1	F6RDL4	
ENSMUST00000133942	ENSMUSG00000022960	16	91677268	91688765	-1	4	2	7	0	0	2	32	56	69	0	87	F6RJK8	
ENSMUST00000133943						4	1	3	18	4	4	0	0	0	0	2		
ENSMUST00000133944						4	7	6	9	5	1	7	6	0	0	2		
ENSMUST00000133946						0	0	1	1	0	1	0	0	0	0	0		
ENSMUST00000133947	ENSMUSG00000004035	3	107926334	107931817	-1	13	9	154	28	18	10	0	0	0	0	0	E9QAC8	
ENSMUST00000133949						0	1	3	1	5	3	0	0	0	0	9		
ENSMUST00000133950						4	1	13	3	0	0	2	4	0	0	2		
ENSMUST00000133951	ENSMUSG00000045438	5	139336189	139351418	-1	1	1	0	0	1	0	5	12	3	0	4	S4R231	
ENSMUST00000133952	ENSMUSG00000040407	5	3928054	4081310	1	3	2	0	0	0	0	0	0	0	0	0	A0A0G2JFW0	
ENSMUST00000133953						0	1	8	0	1	2	80	0	0	0	5		
ENSMUST00000133954						17	8	28	110	28	12	1	1	4	0	9		
ENSMUST00000133955	ENSMUSG00000035473	17	80127471	80185101	1	1	3	0	3	1	0	0	8	0	0	11	F6XWR4	
ENSMUST00000133956	ENSMUSG00000028644	4	119175457	119190011	-1	1	1	0	0	0	1	0	0	0	0	0	A2A7P5	
ENSMUST00000133957	ENSMUSG00000021694	13	108158731	108195364	1	0	0	0	0	0	0	0	6	2	0	1	F6QML7	
ENSMUST00000133958						8	10	3	11	10	11	0	2	1	0	3		
ENSMUST00000133959						2	3	2	0	1	0	0	0	0	0	0		
ENSMUST00000133961	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	0	0	0	0	0	Q5GMG8	
ENSMUST00000133962						5	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000133964	ENSMUSG00000015656	9	40800984	40805200	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5E2	
ENSMUST00000133965						8	0	13	24	20	15	0	2	3	0	5		
ENSMUST00000133966						8	2	6	19	12	9	0	0	3	1	2		
ENSMUST00000133967	ENSMUSG00000070394	11	69838514	69839618	1	0	1	0	4	0	0	158	444	147	577	79	F6YWB5	
ENSMUST00000133968						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133969						0	0	0	0	4	3	0	0	0	0	0		
ENSMUST00000133970						1	2	9	3	4	2	0	0	0	0	0		
ENSMUST00000133971						0	0	0	38	1	0	36	58	58	9	45		
ENSMUST00000133972						3	1	4	2	3	1	0	5	2	0	5		
ENSMUST00000133973						2	0	3	1	3	0	0	0	0	0	0		
ENSMUST00000133975						0	0	0	2	0	3	1	1	0	3	0		
ENSMUST00000133976						4	3	4	11	6	0	3	2	2	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000133977	ENSMUSG00000030382	7	12988346	12998192	-1	5	0	2	0	0	0	0	0	0	0	0	F6YDR6	
ENSMUST00000133978						2	0	2	7	1	0	13	18	17	4	18		
ENSMUST00000133979						0	0	0	0	0	0	12	0	7	8	0		
ENSMUST00000133980	ENSMUSG00000059708	X	36608314	36645395	-1	1	1	4	0	2	0	0	0	0	0	6	Z4YN92	
ENSMUST00000133982						4	2	3	36	5	3	0	0	0	0	0		
ENSMUST00000133983	ENSMUSG00000003279	17	69969073	70821413	1	0	5	0	116	0	0	0	0	0	0	0	Q3UHD8	Q9D415
ENSMUST00000133984						2005	2323	2205	1932	1705	851	37	190	93	12	54		
ENSMUST00000133985						9	12	21	11	13	9	0	0	0	0	1		
ENSMUST00000133986	ENSMUSG00000046897	15	102203648	102215606	1	0	2	2	0	7	4	0	0	0	0	10	D3Z606	
ENSMUST00000133987	ENSMUSG00000062814	X	21115820	21121192	1	1	1	0	2	2	0	0	0	0	0	0	B1AUS7	
ENSMUST00000133988	ENSMUSG00000039652	19	37021291	37208601	-1	0	0	0	205	0	0	0	0	0	0	0	D3Z3Z5	
ENSMUST00000133989						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000133990						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000133991						1	0	7	4	3	0	3	0	0	0	3		
ENSMUST00000133992	ENSMUSG00000028811	4	129189760	129219607	1	4	2	3	0	0	0	0	19	15	0	13	F6VXZ2	
ENSMUST00000133993						25	16	33	53	24	17	14	91	47	4	56		
ENSMUST00000133994						62	37	179	193	65	39	0	13	6	2	14		
ENSMUST00000133995						0	1	16	0	0	0	0	0	6	0	0		
ENSMUST00000133996						2	0	0	19	3	1	0	1	5	0	0		
ENSMUST00000133997	ENSMUSG00000031010	X	13071498	13173328	1	3	0	4	1	0	0	49	406	56	62	54	G3UZS3	
ENSMUST00000133998	ENSMUSG00000003199	17	56005711	56016790	1	5	2	4	0	6	4	0	0	0	2	0	B8JJA2	
ENSMUST00000134000						4	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000134001						1	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000134002						3	5	3	1	8	4	0	0	0	0	0		
ENSMUST00000134003						9	11	35	10	12	7	0	3	2	0	3		
ENSMUST00000134004						2	3	0	0	0	0	4	2	1	0	5		
ENSMUST00000134005	ENSMUSG00000031310	X	101404384	101420849	-1	0	0	0	9	0	0	6	0	2	0	0	B1AXS9	
ENSMUST00000134008						0	0	0	0	0	1	0	15	0	6	0		
ENSMUST00000134009	ENSMUSG00000052613	10	73099342	74649737	1	4	2	1	1	4	3	0	0	0	0	0		Q99PJ1
ENSMUST00000134010						23	13	48	27	21	8	113	350	88	10	210		
ENSMUST00000134011	ENSMUSG00000069824	11	73388081	73392214	-1	0	0	0	1	3	2	0	0	0	0	0		
ENSMUST00000134012	ENSMUSG00000028573	4	95557507	95926939	1	0	0	0	0	0	0	0	0	0	0	0	D6RG41	
ENSMUST00000134013						0	0	12	4	2	2	0	6	0	0	0		
ENSMUST00000134015						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134016						95	91	73	50	124	85	5	30	6	7	30		
ENSMUST00000134017						6	4	13	52	8	4	17	45	17	0	19		
ENSMUST00000134018						1	0	0	2	2	1	0	0	0	1	3		
ENSMUST00000134019						0	0	0	3	2	0	12	22	9	0	17		
ENSMUST00000134020						3	0	0	3	1	0	0	2	0	0	0		
ENSMUST00000134021	ENSMUSG00000002489	16	89787111	89980080	-1	17	11	31	11	8	6	15	13	28	0	34	J3QQ55	
ENSMUST00000134022						5	3	4	5	9	4	0	0	0	0	0		
ENSMUST00000134023	ENSMUSG00000031452	8	13550733	13562461	-1	10	7	0	37	11	3	0	2	0	2	5	Q9D9Y4	
ENSMUST00000134024						8	8	9	8	6	5	0	2	3	0	7		
ENSMUST00000134025						1	0	0	3	1	0	0	0	0	0	5		
ENSMUST00000134026	ENSMUSG00000029267	5	108065674	108109004	1	1	0	0	0	0	0	0	96	50	50	18	E9Q8G7	
ENSMUST00000134027	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	1	0	3	0	0	3	0	D6RG82	
ENSMUST00000134028						2	4	2	6	2	0	0	0	0	0	3		
ENSMUST00000134029	ENSMUSG00000020718	11	106768253	106779537	-1	35	37	73	47	33	22	29	209	81	41	79	D6RFU3	
ENSMUST00000134030						12	14	19	13	13	10	0	0	0	0	0		
ENSMUST00000134031						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134032						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000134033						0	0	0	0	0	0	1	0	0	0	2		
ENSMUST00000134034	ENSMUSG00000023007	15	99295087	99317018	1	0	0	0	0	0	1	0	3	0	1	0	F6XW22	
ENSMUST00000134035						2	2	2	55	2	2	0	0	0	0	0		
ENSMUST00000134036	ENSMUSG00000022773	16	17069696	17087045	1	0	0	0	0	0	0	0	0	0	0	0	Q65Z96	Q9ESC7
ENSMUST00000134037						0	2	0	0	0	0	0	0	0	0	4		
ENSMUST00000134038						138	157	468	126	120	87	7	32	18	11	33		
ENSMUST00000134039						4	2	5	3	7	4	0	0	0	0	0		
ENSMUST00000134040						17	1	16	0	16	0	8606	40751	3907	0	0		
ENSMUST00000134041						0	0	0	0	0	0	0	0	0	0	8		
ENSMUST00000134042						4	2	3	10	5	5	167	197	123	1591	678		
ENSMUST00000134043						1	0	2	1	0	0	2	16	0	0	5		
ENSMUST00000134044	ENSMUSG00000068290	2	130653960	130664659	-1	2	0	0	1	6	2	0	0	0	0	0	F7AIJ1	
ENSMUST00000134045	ENSMUSG00000006362	8	122628739	122699109	-1	0	0	0	39	0	0	0	0	0	0	0	D3Z3P7	
ENSMUST00000134046	ENSMUSG00000024410	18	12168717	12189997	1	0	1	0	2	3	1	0	0	0	0	0	F6X2I0	
ENSMUST00000134047						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000134048						7	7	6	0	7	5	5	103	1	0	22		
ENSMUST00000134049						5	3	1	5	8	3	0	21	4	0	4		
ENSMUST00000134050						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134051						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000134053						0	0	0	2	2	0	785	1260	794	72	213		
ENSMUST00000134054	ENSMUSG00000026933	2	25926838	25983282	-1	3	0	2	0	0	0	0	0	0	0	5	F6Q2D3	
ENSMUST00000134055	ENSMUSG00000050818	11	58528929	58534836	-1	11	7	23	8	6	6	0	0	0	0	0		
ENSMUST00000134056	ENSMUSG00000037606	7	143688762	143756985	-1	0	3	16	12	9	0	0	0	1	0	0	D3YWU9	
ENSMUST00000134057	ENSMUSG00000038611	7	141228784	141262750	1	2	0	0	0	2	0	0	0	17	0	0	D3YWH5	
ENSMUST00000134058						16	8	22	11	14	7	0	0	0	0	0		
ENSMUST00000134061	ENSMUSG00000033356	15	94522688	94543547	-1	1	0	2	2	0	0	0	0	0	0	0	D3Z0X6	
ENSMUST00000134062						1	1	0	1	0	0	4	0	3	0	0		
ENSMUST00000134063	ENSMUSG00000048120	19	40612366	40741602	1	6	2	0	0	0	5	855	3987	1391	1481	2009	Q8CDV7	
ENSMUST00000134064						2	1	0	23	0	0	0	0	0	0	0		
ENSMUST00000134065						14	6	16	20	9	14	20	157	32	4	53		
ENSMUST00000134067						22	19	43	42	26	5	0	0	0	1	0		
ENSMUST00000134068						0	0	0	3	3	1	0	0	0	0	0		
ENSMUST00000134070						5	1	5	11	5	2	3	4	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134071						2	5	23	198	21	4	5	16	16	2	18		
ENSMUST00000134072	ENSMUSG00000032349	9	77917364	77984519	1	0	0	2	1	0	0	0	0	0	0	0	D3Z0Z6	
ENSMUST00000134073						12	6	8	25	22	12	0	0	0	3	0		
ENSMUST00000134074	ENSMUSG00000047671	4	117126794	117128738	1	2	0	0	21	0	1	0	0	1	1	0	A0A0A0MQF8	
ENSMUST00000134075						5	6	3	6	2	0	0	0	0	0	0		
ENSMUST00000134076						0	0	0	0	6	0	0	0	0	0	0		
ENSMUST00000134077	ENSMUSG00000092232	14	54883441	54898137	1	0	0	0	2	0	0	6	0	8	3	8	D3Z5F7	
ENSMUST00000134078	ENSMUSG00000018209	2	164070322	164155524	1	3	0	4	46	3	6	0	0	4	0	11	A2A5M9	
ENSMUST00000134079	ENSMUSG00000020774	11	73304992	73329596	-1	0	0	0	0	0	0	0	0	0	0	0	B0QZP3	
ENSMUST00000134080						0	5	9	0	2	0	0	39	32	22	5		
ENSMUST00000134081						4	1	9	2	2	2	2	6	4	0	4		
ENSMUST00000134082						1	0	2	1	1	0	0	3	0	0	0		
ENSMUST00000134083						2	5	7	3	4	1	13	0	6	4	9		
ENSMUST00000134084						1	0	1	0	0	0	10	41	33	32	36		
ENSMUST00000134085						7	9	5	10	8	2	0	3	1	0	1		
ENSMUST00000134086						2	1	7	11	0	0	70	31	22	8	32		
ENSMUST00000134087	ENSMUSG00000060600	11	70657202	70662513	1	2	2	0	1	2	0	0	16	2	0	2	Q5SX60	
ENSMUST00000134088	ENSMUSG00000062580	1	135295213	135313778	-1	4	2	5	98	10	1	7	22	13	157	28	D3Z1Z0	
ENSMUST00000134089	ENSMUSG00000020453	11	3288874	3309083	1	0	0	0	0	0	0	10	51	0	0	0	Q7TNQ3	
ENSMUST00000134090						4	7	2	4	11	3	0	0	4	6	0		
ENSMUST00000134091						4	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000134092	ENSMUSG00000051674	5	73481000	73560794	1	2	0	0	16	0	0	0	0	0	3	4	D6RHK6	
ENSMUST00000134093	ENSMUSG00000029674	5	134656039	134688598	-1	16	9	29	0	26	0	0	6	0	0	23	F6PZ73	
ENSMUST00000134094						6	14	38	17	7	2	20	151	31	20	30		
ENSMUST00000134095						0	0	0	0	4	2	0	0	0	0	0		
ENSMUST00000134096						3	11	28	3	14	15	0	33	32	0	0		
ENSMUST00000134097						0	0	3	3	2	2	0	0	0	0	0		
ENSMUST00000134098	ENSMUSG00000040181	1	162829561	162866610	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UNX7	
ENSMUST00000134100						3	3	4	11	7	8	11	34	19	0	16		
ENSMUST00000134101						0	0	0	6	8	1	4	12	9	18	13		
ENSMUST00000134102						30	0	45	0	54	22	34	88	9	36	0		
ENSMUST00000134103						0	0	0	0	0	0	0	114	1	6	26		
ENSMUST00000134104	ENSMUSG00000044005	10	128194457	128210004	1	0	0	0	0	0	0	0	0	0	0	3	F6WPK7	
ENSMUST00000134105	ENSMUSG00000028645	4	119108711	119137983	1	0	3	0	34	0	0	9	8	13	4	25	A2A7P3	
ENSMUST00000134106						2	0	0	0	1	0	0	0	11	0	0		
ENSMUST00000134107						26	24	77	36	39	15	9	13	19	2	15		
ENSMUST00000134108	ENSMUSG00000002280	17	25773776	25783332	1	0	0	0	0	11	0	388	433	282	69	149		Q7TMW6
ENSMUST00000134109	ENSMUSG00000022010	14	76414961	76507765	1	4	3	7	7	6	3	0	2	0	2	4	H3BJV9	
ENSMUST00000134110	ENSMUSG00000034891	13	54758860	54766595	-1	4	3	3	39	4	0	0	0	0	0	0		Q91ZZ3
ENSMUST00000134111						18	20	9	0	14	13	0	0	13	0	24		
ENSMUST00000134112						3	7	7	4	8	5	0	0	3	0	3		
ENSMUST00000134113						127	120	112	75	151	77	6	20	12	4	16		
ENSMUST00000134114	ENSMUSG00000021998	14	75131101	75230842	1	0	0	4	0	1	0	46	20	122	14	271	D3Z311	
ENSMUST00000134115	ENSMUSG00000062169	1	181144693	181168994	1	0	0	0	0	0	1	120	365	55	283	133		Q9CX13
ENSMUST00000134116	ENSMUSG00000002992	7	19671579	19681423	-1	0	1	4	0	0	4	10	0	0	18	0	Q3UJG0	Q05020
ENSMUST00000134117						0	1	1	0	1	1	0	0	2	0	0		
ENSMUST00000134118	ENSMUSG00000020709	11	80154105	80178958	1	0	0	0	41	0	0	1	0	0	1	0	E9QAL8	
ENSMUST00000134119						4	6	36	7	4	6	0	0	1	0	2		
ENSMUST00000134120	ENSMUSG00000026853	2	30400471	30415813	-1	0	0	0	3	3	0	6	0	9	2	5	B7ZDD8	
ENSMUST00000134121						1	2	3	3	1	0	0	0	0	0	0		
ENSMUST00000134122						2	2	1	11	4	10	0	0	0	0	0		
ENSMUST00000134123						53	20	177	43	43	17	2	4	5	0	8		
ENSMUST00000134124						6	9	16	42	6	4	0	0	0	0	0		
ENSMUST00000134125						25	20	41	80	61	31	0	0	0	0	3		
ENSMUST00000134126						2	0	2	7	1	0	0	0	3	0	2		
ENSMUST00000134127	ENSMUSG00000049482	8	122476143	122484138	1	0	0	0	0	6	3	10	34	18	0	11	D3Z2M0	
ENSMUST00000134128						4	3	8	8	4	0	0	0	0	0	0		
ENSMUST00000134131						5	5	9	8	2	3	0	0	0	0	0		
ENSMUST00000134132						2	3	4	7	2	1	0	2	0	10	5		
ENSMUST00000134133						3	0	0	0	4	0	56	169	10	0	12		
ENSMUST00000134134	ENSMUSG00000060538	7	126886171	126922917	-1	0	3	0	0	6	1	0	0	0	0	0	D3Z3J3	
ENSMUST00000134135						4	12	14	30	13	0	504	798	428	34	393		
ENSMUST00000134136						0	2	0	0	0	2	0	2	0	0	3		
ENSMUST00000134137						1	0	0	13	4	0	0	3	0	5	0		
ENSMUST00000134138						11	3	18	0	5	7	185	314	268	37	303		
ENSMUST00000134139						17	6	23	55	21	5	0	0	0	0	0		
ENSMUST00000134141						15	12	45	28	16	10	16	122	65	7	88		
ENSMUST00000134142						0	2	0	7	0	0	26	27	11	0	28		
ENSMUST00000134143	ENSMUSG00000032812	7	101348067	101412586	1	0	0	0	0	0	0	0	0	0	0	0	D3YWW7	
ENSMUST00000134144						1	2	3	2	0	0	6	0	0	0	13		
ENSMUST00000134145	ENSMUSG00000001827	7	101858331	101870788	-1	0	1	8	0	0	0	0	0	0	0	0	E9PXB5	
ENSMUST00000134146	ENSMUSG00000024483	18	36559987	36665917	1	0	0	0	2	0	1	0	6	0	0	17	F7C545	
ENSMUST00000134147						3	2	1	7	2	0	1	0	0	0	0		
ENSMUST00000134148						0	1	0	14	0	0	0	0	3	0	0		
ENSMUST00000134149						3	3	12	1	3	1	1	0	0	0	2		
ENSMUST00000134150						0	4	22	18	11	0	0	0	0	0	0		
ENSMUST00000134151						0	0	10	0	6	2	0	3	4	0	0		
ENSMUST00000134152	ENSMUSG00000039787	2	29869164	29882840	1	1	0	5	21	4	1	0	0	0	0	0	A3KGW6	
ENSMUST00000134153						0	3	2	10	0	1	5	6	9	43	7		
ENSMUST00000134154						6	2	13	3	5	3	0	0	0	0	0		
ENSMUST00000134155	ENSMUSG00000038330	4	88627320	88634411	-1	0	2	0	4	5	0	0	0	0	0	0	S4R292	
ENSMUST00000134156	ENSMUSG00000001082	5	34633642	34637212	-1	4	0	7	0	15	4	0	22	0	0	0		
ENSMUST00000134157						1	1	3	96	0	0	0	0	1	0	0		
ENSMUST00000134158						0	0	0	0	0	0	2	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134159	ENSMUSG00000028772	4	130315383	130359943	-1	15	11	16	28	26	8	123	269	173	233	104	Q3TG23	Q9ESX4
ENSMUST00000134160						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134161	ENSMUSG00000057400	8	93099015	93131283	-1	0	0	0	3	0	3	0	0	0	0	0	F6XTA4	
ENSMUST00000134162	ENSMUSG00000038215	8	56531522	56551047	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z464	
ENSMUST00000134163						1	1	0	14	0	5	0	0	0	0	0		
ENSMUST00000134164						18	22	65	21	16	3	2	2	0	0	1		
ENSMUST00000134165						1	4	4	17	2	2	0	0	0	0	0		
ENSMUST00000134166	ENSMUSG00000062609	16	95257558	95300260	1	0	0	0	0	0	0	0	0	0	0	0	D3YXQ3	
ENSMUST00000134167						9	0	18	42	3	3	0	0	0	2	0		
ENSMUST00000134168	ENSMUSG00000009207	2	74520291	74579435	-1	1	1	0	155	6	0	0	1	7	1	2	A2ASM2	
ENSMUST00000134170	ENSMUSG00000037455	10	23796986	23827968	1	1	0	1	0	2	0	0	0	0	0	0	D6RGT8	
ENSMUST00000134171						1	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000134172	ENSMUSG00000029020	4	147873599	147904704	-1	0	1	2	0	0	0	0	0	7	0	0	A8Y5E5	
ENSMUST00000134173						4	0	1	1	2	4	41	3	24	0	14		
ENSMUST00000134174	ENSMUSG00000028010	3	129824912	129831396	-1	0	0	3	0	0	0	14	0	5	0	0	F6SL78	
ENSMUST00000134175						64	67	22	39	95	38	0	0	3	0	2		
ENSMUST00000134176	ENSMUSG00000030590	7	29152511	29156234	-1	0	0	0	0	0	0	17	0	0	0	0	D3Z100	
ENSMUST00000134177	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	2	0	0	2	0	5	0	0	9	D3YXW8	
ENSMUST00000134178	ENSMUSG00000057133	2	160946978	161109075	-1	10	2	0	2	0	4	0	0	21	0	0	A3KFM8	
ENSMUST00000134179	ENSMUSG00000079451	5	86485876	86518600	-1	53	36	40	29	61	32	0	0	1	0	4		Q8BZ10
ENSMUST00000134180						0	0	3	0	6	0	6	26	0	12	10		
ENSMUST00000134181						0	0	0	0	0	0	0	17	0	2	0		
ENSMUST00000134182	ENSMUSG00000070331	11	116441325	116455237	-1	0	12	24	9	5	8	0	0	0	0	0	F6UEA3	
ENSMUST00000134183						0	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000134184						2	0	2	1	2	0	41	201	36	5	32		
ENSMUST00000134185						1	0	0	5	0	0	5	3	0	0	15		
ENSMUST00000134186						4	7	8	24	7	6	0	0	0	0	2		
ENSMUST00000134187						3	0	0	7	0	0	0	2	0	0	10		
ENSMUST00000134188						0	0	0	0	0	0	0	17	0	0	0		
ENSMUST00000134189						1	6	1	1	0	2	42	15	13	0	58		
ENSMUST00000134191	ENSMUSG00000030246	6	142490249	142507957	-1	5	2	10	2	7	3	0	0	0	0	0	D3Z7F0	
ENSMUST00000134192						0	2	3	0	0	0	1	14	10	0	13		
ENSMUST00000134193	ENSMUSG00000058794	15	103248212	103258403	-1	3	0	0	0	0	4	488	305	303	25	253	D3YUM3	
ENSMUST00000134194						0	3	0	2	0	0	0	0	13	0	0		
ENSMUST00000134196						0	2	3	0	5	0	0	0	0	0	0		
ENSMUST00000134197	ENSMUSG00000063820	5	77004055	77010606	1	3	4	1	2	1	0	0	10	0	0	0	F7BE40	
ENSMUST00000134198						6	3	4	5	6	3	38	5	25	0	10		
ENSMUST00000134199						0	0	0	20	0	0	0	0	0	0	0		
ENSMUST00000134200						2	4	8	6	5	3	0	0	0	0	0		
ENSMUST00000134201						0	0	0	0	0	0	11	2	40	6	24		
ENSMUST00000134202	ENSMUSG00000068874	3	94933056	94944758	1	2	5	0	0	0	0	0	8	0	0	0	D6RHN2	
ENSMUST00000134203						0	1	0	0	0	0	0	68	0	0	10		
ENSMUST00000134204						7	0	14	98	6	3	0	0	0	0	0		
ENSMUST00000134205						0	1	0	34	2	2	0	0	0	0	0		
ENSMUST00000134207						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134208	ENSMUSG00000020752	11	115892595	115933477	-1	10	6	22	17	6	7	11	14	10	0	12	J3QP94	
ENSMUST00000134209						1	0	5	2	2	0	2	5	0	2	6		
ENSMUST00000134210						2	3	6	22	4	1	0	0	0	0	0		
ENSMUST00000134211						36	27	26	17	25	9	2	2	4	0	3		
ENSMUST00000134212						7	2	16	0	0	3	1	0	0	0	0		
ENSMUST00000134213						3	0	2	145	6	1	0	0	0	0	0		
ENSMUST00000134214						1	12	8	0	2	2	12	0	0	0	0		
ENSMUST00000134215						0	0	0	0	0	0	0	3	0	0	3		
ENSMUST00000134216	ENSMUSG00000018401	11	87592162	87616302	1	1	0	0	69	2	1	0	0	0	0	0	Q5ND05	
ENSMUST00000134217						1	1	2	2	3	1	0	16	11	0	15		
ENSMUST00000134218	ENSMUSG00000038375	2	155381059	155389850	1	5	4	4	39	7	5	17	11	14	0	2	A2ARD0	
ENSMUST00000134219						0	0	0	0	0	0	50	486	0	0	0		
ENSMUST00000134220	ENSMUSG00000020003	10	19859929	19907689	-1	0	0	5	0	4	0	28	126	74	50	55	F6QU40	
ENSMUST00000134221						59	76	84	45	52	45	20	58	32	10	44		
ENSMUST00000134222						3	5	10	2	13	2	0	28	5	6	0		
ENSMUST00000134223						1	0	0	25	5	0	0	0	0	0	0		
ENSMUST00000134224	ENSMUSG00000048794	6	90403479	90428797	-1	0	0	0	25	6	8	0	0	0	0	0		
ENSMUST00000134225						10	5	27	26	14	12	0	3	1	0	5		
ENSMUST00000134227	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	0	0	0	0	0	0	0	F7BZ65	
ENSMUST00000134228						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000134229						6	4	3	3	8	7	0	0	0	3	4		
ENSMUST00000134230						0	0	0	0	0	0	80	758	385	787	460		
ENSMUST00000134231						2	0	8	21	1	6	0	0	0	0	1		
ENSMUST00000134233						13	6	0	7	25	0	23	166	14	0	43		
ENSMUST00000134234						3	0	0	0	0	3	0	0	1	0	1		
ENSMUST00000134235						0	6	5	43	0	13	0	3	0	0	0		
ENSMUST00000134237						2	2	13	3	3	3	3	30	3	0	21		
ENSMUST00000134239						0	1	2	16	0	1	1	4	2	0	5		
ENSMUST00000134240						8	5	21	13	16	7	0	0	0	0	1		
ENSMUST00000134241						0	0	0	52	0	0	0	0	0	0	0		
ENSMUST00000134242						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000134243						3	2	3	1	1	3	0	0	0	1	0		
ENSMUST00000134244						12	7	3	4	7	6	0	0	0	0	0		
ENSMUST00000134246						0	0	3	0	1	3	0	10	15	0	32		
ENSMUST00000134247						15	9	16	9	18	10	3	7	8	0	6		
ENSMUST00000134248						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000134249						1	6	29	128	14	6	0	0	0	0	0		
ENSMUST00000134253	ENSMUSG00000032456	9	98287435	98420438	1	1	0	0	1	0	2	0	0	0	0	1	A0A087WSM7	
ENSMUST00000134254	ENSMUSG00000028608	4	107889813	107899384	1	4	0	0	0	0	0	0	4	0	0	0	B7ZC73	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134255						0	0	0	39	0	0	0	40	0	8	0		
ENSMUST00000134256	ENSMUSG00000040752	14	54941981	54966927	-1	0	0	0	0	0	0	0	0	0	0	0	Q1WNP4	
ENSMUST00000134257	ENSMUSG00000031105	X	48623413	48662294	1	0	0	0	0	0	0	6	0	9	0	0	A0A0A0MQJ8	
ENSMUST00000134258	ENSMUSG00000022475	15	97792664	97844502	-1	0	0	6	11	7	0	11	23	0	0	24	F6VIB5	
ENSMUST00000134259	ENSMUSG00000036587	2	25423267	25426374	1	10	5	8	9	6	0	35	20	9	2	8	A2AJ24	
ENSMUST00000134261	ENSMUSG00000055401	4	148145716	148152140	-1	0	1	2	4	0	0	20	21	0	0	0	A2A7G9	
ENSMUST00000134262						0	0	8	0	2	0	1	18	7	0	0		
ENSMUST00000134263						3	1	8	2	12	1	0	7	8	10	0		
ENSMUST00000134265						2	1	0	2	0	2	0	0	0	0	0		
ENSMUST00000134266	ENSMUSG00000018412	11	104333229	104468861	-1	1	6	10	1	8	1	2	1	5	0	6	B1AQV9	
ENSMUST00000134267	ENSMUSG00000034175	11	5098926	5106093	1	0	0	0	0	0	0	0	0	0	0	0	Q5SUT8	
ENSMUST00000134268						0	0	4	0	0	0	0	0	0	1	0		
ENSMUST00000134269						47	40	81	93	70	23	4	3	5	0	7		
ENSMUST00000134270						1	1	4	1	1	2	0	0	0	0	0		
ENSMUST00000134272	ENSMUSG00000040749	X	164070705	164076493	-1	3	0	5	47	0	1	3	3	9	2	5	A2AHZ3	
ENSMUST00000134273						0	0	0	0	0	0	1	2	0	0	4		
ENSMUST00000134274	ENSMUSG00000057181	11	80360492	80378034	-1	0	2	1	115	8	3	0	0	0	3	0	B1AQG3	
ENSMUST00000134277	ENSMUSG00000022201	15	12117831	12185683	1	0	0	0	38	0	0	0	0	7	0	0	D3Z7V6	
ENSMUST00000134278	ENSMUSG00000027613	2	155819832	155826925	-1	0	2	0	0	1	0	0	0	0	0	0	A6PWZ2	
ENSMUST00000134279	ENSMUSG00000051736	10	39118804	39133914	-1	0	0	0	0	3	0	0	0	0	0	0	B2RVF6	Q8CF36
ENSMUST00000134280	ENSMUSG00000035615	4	45184875	45285936	1	9	1	0	7	3	0	0	0	0	0	0	A2AKB3	
ENSMUST00000134281						5	5	11	7	5	5	0	0	0	0	0		
ENSMUST00000134282						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000134283						1	0	0	0	1	1	4	7	14	0	2		
ENSMUST00000134286						4	6	4	5	2	1	0	1	2	0	0		
ENSMUST00000134287	ENSMUSG00000038936	1	179668210	179687189	1	4	0	10	23	4	0	0	0	3	0	14	J3QNN5	
ENSMUST00000134288						0	2	7	0	2	3	0	3	0	0	0		
ENSMUST00000134290						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134291						2	6	0	8	0	3	33	62	30	2	48		
ENSMUST00000134292						1	2	30	16	2	0	0	0	0	0	0		
ENSMUST00000134293	ENSMUSG00000042302	11	22005828	22342292	-1	0	0	3	0	0	0	0	0	0	0	0	Q5SS55	
ENSMUST00000134295						9	0	15	9	17	5	0	1	0	0	6		
ENSMUST00000134296						5	0	3	13	3	1	0	0	1	0	0		
ENSMUST00000134298						4	1	1	0	2	1	2	0	0	97	0		
ENSMUST00000134299						3	0	2	0	6	4	102	394	132	20	174		
ENSMUST00000134300	ENSMUSG00000024371	17	34862604	34898265	-1	1	3	2	0	0	1	0	0	0	0	0	F6ZCY7	
ENSMUST00000134301	ENSMUSG00000026312	1	109982431	110140157	1	1	1	2	2	0	0	0	0	0	0	0	F6WWT2	
ENSMUST00000134303	ENSMUSG00000060961	5	88886818	89239653	1	0	4	0	0	0	0	0	0	0	0	0	D3Z7G8	
ENSMUST00000134304						0	0	4	0	3	0	0	17	0	12	0		
ENSMUST00000134306	ENSMUSG00000039958	6	149139849	149151171	1	0	0	0	0	0	0	4	10	2	0	0	B8JKU6	
ENSMUST00000134307						1	0	3	1	5	2	3	2	2	0	5		
ENSMUST00000134309						0	2	1	2	0	0	0	0	0	0	2		
ENSMUST00000134310	ENSMUSG00000039943	2	135659011	136014593	1	0	0	0	4	11	0	7	8	4	5	1	A2AT91	
ENSMUST00000134311						0	0	0	0	0	0	12	0	7	7	37		
ENSMUST00000134313	ENSMUSG00000029310	5	104046306	104065379	1	1	2	0	19	4	3	0	0	0	0	0	A2AH29	
ENSMUST00000134314						0	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000134315						10	4	14	12	10	5	0	3	3	2	3		
ENSMUST00000134316						6	4	4	8	7	3	0	0	2	0	2		
ENSMUST00000134317						6	2	9	184	2	1	0	0	0	0	0		
ENSMUST00000134318	ENSMUSG00000060002	10	88452745	88504073	-1	0	0	0	0	0	1	0	0	0	0	0	F7DAN4	
ENSMUST00000134319						0	0	3	0	0	0	6	0	2	0	2		
ENSMUST00000134321	ENSMUSG00000031626	8	45507788	45827906	1	5	0	0	0	3	6	0	0	0	0	0	D3YY43	
ENSMUST00000134322						0	0	8	16	5	2	0	0	0	0	0		
ENSMUST00000134323						19	21	101	28	17	13	6	13	10	0	22		
ENSMUST00000134324						914	609	5031	1298	598	294	3	36	21	6	44		
ENSMUST00000134325						102	108	283	134	128	51	70	197	127	9	252		
ENSMUST00000134326	ENSMUSG00000042589	5	121856366	122050102	-1	0	0	2	4	0	2	0	0	0	0	0	D3YUK2	
ENSMUST00000134327						0	0	0	0	0	0	26	23	18	14	8		
ENSMUST00000134328	ENSMUSG00000030541	7	80094846	80115392	-1	0	6	4	0	1	0	0	0	0	0	0	D6RIL6	
ENSMUST00000134329						6	3	10	8	4	4	0	11	15	2	23		
ENSMUST00000134330						0	0	0	0	0	0	11	140	14	11	16		
ENSMUST00000134331						6	0	2	4	5	0	16	49	38	3	84		
ENSMUST00000134332						17	6	0	36	27	3	0	0	0	0	0		
ENSMUST00000134334						1	2	6	2	6	5	2	1	0	0	0		
ENSMUST00000134335						11	0	21	5	15	4	50	65	0	1	10		
ENSMUST00000134336	ENSMUSG00000000409	4	129548344	129573641	-1	0	0	0	3	0	0	0	0	0	0	8	B2KG65	
ENSMUST00000134337	ENSMUSG00000027207	2	125859109	125984299	1	6	0	0	0	1	0	0	10	0	0	0	B7ZCT3	
ENSMUST00000134338	ENSMUSG00000032386	9	65828930	65908794	-1	0	0	0	25	0	0	0	1	0	4	0	D3Z3P3	
ENSMUST00000134339						0	1	4	4	2	1	7	17	4	6	6		
ENSMUST00000134340	ENSMUSG00000089917	2	181569149	181584892	-1	0	0	0	0	0	0	0	0	0	9	0	F7CAK3	
ENSMUST00000134341						0	1	0	15	0	0	0	0	0	0	0		
ENSMUST00000134342						0	0	0	0	0	0	2	31	0	130	24		
ENSMUST00000134343						3	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000134344	ENSMUSG00000024191	17	26781079	26792565	1	0	0	0	0	0	0	7	0	0	0	0	F7C279	
ENSMUST00000134346	ENSMUSG00000019796	10	7589800	7625483	1	2	0	0	178	0	0	0	0	0	0	0	D3Z3A7	
ENSMUST00000134347						0	0	5	15	5	1	0	0	0	0	0		
ENSMUST00000134348	ENSMUSG00000062210	18	49979427	50107173	1	2	1	2	125	3	0	1	0	0	0	0	D3Z205	
ENSMUST00000134349	ENSMUSG00000060090	X	20364481	20405653	1	0	0	6	9	19	0	0	30	22	25	23		Q9EPK2
ENSMUST00000134350						6	4	31	16	7	1	17	63	36	0	39		
ENSMUST00000134351						2	3	4	95	2	3	3	4	10	0	6		
ENSMUST00000134352	ENSMUSG00000044951	13	32700827	32783954	-1	0	0	0	0	0	0	0	0	0	0	0		Q5SUV5
ENSMUST00000134353	ENSMUSG00000068391	15	73090392	73097554	1	0	0	0	27	0	0	0	14	0	5	6	D3Z0U4	
ENSMUST00000134354						1	1	8	5	5	5	0	2	0	0	5		
ENSMUST00000134355						3	2	0	4	3	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134356						0	0	0	0	0	0	19	33	22	62	0		
ENSMUST00000134357	ENSMUSG00000007659	2	152780668	152831728	-1	0	0	0	0	0	0	0	0	16	3	31	A2AHX9	
ENSMUST00000134358						82	60	0	12	68	34	0	0	0	0	1		
ENSMUST00000134360						4	2	9	3	1	3	0	0	4	0	5		
ENSMUST00000134361						0	0	1	0	0	0	25	51	26	7	28		
ENSMUST00000134362						0	1	1	0	0	0	0	2	3	0	5		
ENSMUST00000134363						0	0	0	0	0	0	7	0	0	0	2		
ENSMUST00000134364	ENSMUSG00000054766	2	30057378	30072577	1	0	0	0	0	0	0	0	0	12	32	19	A2BE93	
ENSMUST00000134365						0	0	0	2	0	1	0	1	0	0	0		
ENSMUST00000134366	ENSMUSG00000034785	4	107291465	107307169	-1	0	0	0	0	0	0	0	0	0	0	0	D6RCH6	
ENSMUST00000134367	ENSMUSG00000038236	6	52214491	52221854	-1	1	1	0	0	0	0	1	0	0	0	0	G3UZS1	
ENSMUST00000134368						0	0	0	26	1	0	0	0	0	0	0		
ENSMUST00000134369						3	1	0	1	4	2	0	4	5	0	15		
ENSMUST00000134370						0	3	6	3	5	1	20	19	284	0	197		
ENSMUST00000134371	ENSMUSG00000022469	15	97744770	97767972	-1	0	1	0	0	2	0	0	0	0	0	0	F7BXV7	
ENSMUST00000134372						2	0	6	2	3	1	10	38	22	4	23		
ENSMUST00000134373						1	0	0	0	0	1	0	59	9	8	9		
ENSMUST00000134374	ENSMUSG00000037287	9	42412316	42507809	-1	1	0	0	2	2	0	0	0	0	0	0	D3YVP4	
ENSMUST00000134375						0	1	0	27	1	1	0	0	0	0	1		
ENSMUST00000134376	ENSMUSG00000020886	11	70017085	70045532	1	0	0	0	24	0	0	0	0	2	0	0	E9Q3Z8	
ENSMUST00000134377						3	1	28	22	0	2	0	0	0	1	3		
ENSMUST00000134378						2	1	0	1	1	0	29	3	0	0	11		
ENSMUST00000134379						8	6	8	15	5	5	0	0	0	0	0		
ENSMUST00000134380						5	8	22	27	22	12	0	2	2	0	5		
ENSMUST00000134381	ENSMUSG00000031229	X	105797615	105929403	-1	0	2	0	0	0	2	5	6	24	0	0	A6PWK8	
ENSMUST00000134382						0	0	6	4	4	2	84	287	90	4	138		
ENSMUST00000134383						3	5	6	4	9	8	4	3	1	1	11		
ENSMUST00000134384	ENSMUSG00000025903	1	4807788	4848410	1	137	122	198	188	121	65	13	158	59	0	68	J3QP56	
ENSMUST00000134385						16	9	23	21	12	10	1	1	3	1	5		
ENSMUST00000134386						0	0	0	3	0	0	8	15	0	0	0		
ENSMUST00000134387						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134388						0	4	2	3	2	0	0	0	0	0	0		
ENSMUST00000134389	ENSMUSG00000029564	5	114853664	114883880	1	0	0	0	10	1	0	0	0	0	0	0	Q9DAB8	
ENSMUST00000134390						2	0	12	5	4	1	0	0	1	0	0		
ENSMUST00000134392						1	4	13	6	7	1	8	7	9	4	35		
ENSMUST00000134394						0	0	0	0	0	0	0	2	3	27	6		
ENSMUST00000134395						0	0	4	0	0	1	0	0	0	0	0		
ENSMUST00000134396	ENSMUSG00000027900	3	106547798	106575890	1	0	0	0	1	0	0	0	0	0	0	0	D3Z2M3	
ENSMUST00000134398	ENSMUSG00000038695	7	44467980	44471662	1	4	0	2	0	0	1	0	0	0	0	6		
ENSMUST00000134399						0	0	4	13	4	0	0	0	0	0	0		
ENSMUST00000134400						1	3	4	0	6	4	0	0	0	0	0		
ENSMUST00000134401						0	1	4	4	1	2	0	1	0	1	0		
ENSMUST00000134402	ENSMUSG00000031284	X	143518591	143797796	1	3	0	0	0	1	0	0	0	0	0	0	A3KGC5	
ENSMUST00000134403						0	0	7	7	0	0	2	0	0	0	3		
ENSMUST00000134404	ENSMUSG00000029478	5	125017153	125179219	-1	13	19	47	242	32	13	21	0	20	0	21	D3Z2J5	
ENSMUST00000134405						3	0	7	3	8	2	0	2	0	0	5		
ENSMUST00000134406						8	4	3	5	7	4	11	66	37	1	50		
ENSMUST00000134407						2	0	0	0	4	0	4	0	0	0	0		
ENSMUST00000134408						6	12	11	47	17	3	0	0	65	0	21		
ENSMUST00000134410	ENSMUSG00000005268	15	10177238	10349180	1	1	1	2	0	0	0	0	0	0	0	0	E9Q0U8	
ENSMUST00000134412						18	5	43	37	27	5	75	692	168	13	200		
ENSMUST00000134413						32	2	7	0	0	6	72	316	61	10	54		
ENSMUST00000134414						0	1	3	21	1	0	0	122	607	3850	417		
ENSMUST00000134415	ENSMUSG00000040451	19	32122727	32389714	-1	0	0	4	0	0	0	8	187	105	274	12	E3W996	
ENSMUST00000134417	ENSMUSG00000001674	1	121553835	121567989	-1	0	0	0	0	0	0	0	0	0	2	0	F6ZX28	
ENSMUST00000134418	ENSMUSG00000018661	11	113649169	113667054	1	4	0	6	1	4	3	8	10	9	0	15	F6V3F1	
ENSMUST00000134419						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000134420	ENSMUSG00000030796	7	45215753	45233635	1	0	0	0	0	0	0	0	0	0	0	0	D3Z6C5	
ENSMUST00000134421	ENSMUSG00000028796	4	128654702	128752881	1	0	0	1	0	3	0	0	0	0	0	0	B1ASA2	
ENSMUST00000134423	ENSMUSG00000069855	11	61301631	61342860	-1	4	0	0	43	11	4	0	0	0	0	0	Z4YMV2	
ENSMUST00000134424						0	0	0	0	0	0	9	18	4	0	0		
ENSMUST00000134425						0	0	5	55	4	0	0	11	3	0	0		
ENSMUST00000134426						4	3	1	3	6	2	0	0	0	0	2		
ENSMUST00000134428	ENSMUSG00000038366	11	97799000	97838764	1	1	2	0	1	0	0	3	1	2	0	2	A2A6G3	
ENSMUST00000134429						8	17	60	13	12	6	0	1	0	0	1		
ENSMUST00000134430						1	0	1	0	4	0	0	0	0	0	0		
ENSMUST00000134431						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134432	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	1	0	0	17	0	12	0	8	F6V7B7	
ENSMUST00000134433	ENSMUSG00000039285	9	118040499	118069794	1	51	43	1031	194	47	16	49	101	114	25	155		Q9QYP6
ENSMUST00000134434						0	0	0	0	0	0	0	0	0	0	15		
ENSMUST00000134435						0	0	0	6	0	0	1	2	1	5	5		
ENSMUST00000134437						3	1	7	1	4	1	0	23	2	2	15		
ENSMUST00000134438	ENSMUSG00000029772	6	29768011	29912310	1	0	0	0	0	0	1	0	0	0	0	0	D3YYM7	
ENSMUST00000134439	ENSMUSG00000035310	5	100441918	100500639	-1	0	0	0	0	2	2	1	0	50	0	21	F6XQ46	
ENSMUST00000134440	ENSMUSG00000022044	14	66344296	66361680	1	0	0	0	0	0	0	0	0	0	0	0	D3YUL4	
ENSMUST00000134441						3	0	35	6	5	7	153	167	76	41	18		
ENSMUST00000134442						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134443						0	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000134444						0	0	0	1	0	1	19	0	56	28	51		
ENSMUST00000134445	ENSMUSG00000004018	11	26386135	26471876	1	0	0	0	0	0	0	2	17	1	4	7	F6Q7G3	
ENSMUST00000134446	ENSMUSG00000045639	7	127607031	127615797	-1	2	0	13	45	2	0	0	0	0	0	2	A0A087WSE9	
ENSMUST00000134447	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	0	0	0	0	0	0	0	0	0	B4YB29	
ENSMUST00000134449						7	4	7	0	17	0	10	54	8	0	33		
ENSMUST00000134450	ENSMUSG00000032327	9	58063788	58153996	1	2	1	9	9	4	0	0	0	0	0	0	D3YXW9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134451	ENSMUSG00000028232	4	3549041	3574853	-1	1	0	1	1	1	5	0	0	3	0	5	A8Y5P2	
ENSMUST00000134452						0	0	0	0	0	5	0	0	0	0	0		
ENSMUST00000134453						4	0	3	1	2	0	2	4	6	0	12		
ENSMUST00000134454						0	0	0	1	1	1	0	0	0	0	4		
ENSMUST00000134455						3	4	6	3	5	3	0	0	0	0	0		
ENSMUST00000134457						0	2	9	0	4	2	3	0	0	3	0		
ENSMUST00000134458	ENSMUSG00000028649	4	123349633	123684360	-1	0	0	0	0	0	0	107	717	634	15	810	F6Q750	
ENSMUST00000134459	ENSMUSG00000036053	2	52857860	53134202	1	1	3	0	1	0	3	3	0	7	6	16	A2AQW3	
ENSMUST00000134460						5	5	14	4	6	6	0	0	0	0	0		
ENSMUST00000134461						4	8	10	4	8	2	0	0	0	0	0		
ENSMUST00000134462						0	0	20	15	0	0	111	937	211	68	422		
ENSMUST00000134463						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000134464						3	2	9	0	3	0	0	0	0	0	4		
ENSMUST00000134465	ENSMUSG00000048537	9	44686304	44735198	-1	0	0	0	0	0	0	0	0	0	0	45	E9PWB1	
ENSMUST00000134466	ENSMUSG00000053819	3	126596302	126846326	1	2	2	5	7	1	1	2	4	6	0	6	D6RDQ8	
ENSMUST00000134468						0	7	20	0	11	4	1	0	12	0	15		
ENSMUST00000134469	ENSMUSG00000042292	15	81012281	81190757	-1	0	10	0	0	0	0	0	0	0	0	0		Q8K4J6
ENSMUST00000134470						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134471						0	1	7	6	3	1	0	4	3	0	4		
ENSMUST00000134472						1	1	0	2	3	1	0	0	0	0	0		
ENSMUST00000134473						24	12	33	3	20	16	227	414	36	0	107		
ENSMUST00000134474						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000134475						4	5	3	4	6	0	0	0	0	0	0		
ENSMUST00000134477	ENSMUSG00000036676	10	100443902	100487350	-1	0	3	0	52	5	1	2	0	0	0	0	D3YWM5	
ENSMUST00000134478						1	1	2	2	1	0	0	0	2	0	0		
ENSMUST00000134479	ENSMUSG00000037916	19	4007497	4012806	-1	4	0	0	12	2	6	0	0	0	0	0	D3Z1U9	
ENSMUST00000134480						0	0	0	0	0	0	24	58	0	28	26		
ENSMUST00000134481						7	3	11	4	6	0	0	0	0	0	0		
ENSMUST00000134482						4	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000134483	ENSMUSG00000032531	9	102716672	102733418	1	0	2	7	6	0	1	0	0	0	0	0	B8JK85	
ENSMUST00000134484						0	0	6	4	0	0	0	0	0	0	0		
ENSMUST00000134485						10	4	2	156	6	6	1	1	1	0	0		
ENSMUST00000134486						0	6	0	0	3	0	0	0	0	0	0		
ENSMUST00000134487						17	15	11	5	12	11	13	27	6	0	6		
ENSMUST00000134488						4	2	3	7	6	0	0	4	0	0	13		
ENSMUST00000134489	ENSMUSG00000020437	11	6506548	6520965	-1	0	0	3	0	1	2	1	5	6	1	7	A8Y5I5	
ENSMUST00000134490						17	10	33	0	0	4	0	7	0	0	4		
ENSMUST00000134491	ENSMUSG00000022971	16	91372783	91405589	1	0	2	0	62	3	0	34	57	40	104	90	H3BJ04	
ENSMUST00000134492						0	0	0	11	0	0	0	0	11	0	16		
ENSMUST00000134495						0	0	0	0	0	0	0	0	33	30	20		
ENSMUST00000134496						11	9	11	21	17	8	0	0	0	0	0		
ENSMUST00000134497						2	1	1	0	3	0	8	14	15	0	19		
ENSMUST00000134498						1	1	28	20	7	2	4	50	16	0	33		
ENSMUST00000134499	ENSMUSG00000026483	1	151571186	151721939	1	0	0	3	34	6	0	0	0	0	0	0	D3YYZ9	
ENSMUST00000134500						0	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000134501						10	6	18	6	12	4	0	0	0	0	0		
ENSMUST00000134502						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000134503	ENSMUSG00000006345	10	75561604	75586200	1	0	0	18	0	0	0	5280	5675	4175	385	1457	Q4FK56	Q60928
ENSMUST00000134504	ENSMUSG00000054555	7	133883199	134232146	-1	0	1	1	0	0	2	0	0	0	0	0	D3Z117	
ENSMUST00000134505						136	87	860	172	96	27	4	5	2	0	2		
ENSMUST00000134506	ENSMUSG00000037348	4	134496697	134510235	1	37	25	57	31	42	16	72	170	79	6	64	D3YZW6	
ENSMUST00000134507	ENSMUSG00000031229	X	105797615	105929403	-1	0	0	7	0	0	0	0	7	7	6	12	Q3UY26	
ENSMUST00000134508						0	0	0	0	0	0	2	0	1	0	4		
ENSMUST00000134509						4	0	4	14	9	8	0	0	6	0	30		
ENSMUST00000134510						43	46	173	47	51	27	2	10	9	1	10		
ENSMUST00000134511						6	0	0	4	15	3	0	0	0	0	3		
ENSMUST00000134513						0	0	1	9	3	2	0	5	0	1	2		
ENSMUST00000134514						0	2	0	4	0	2	0	2	5	0	0		
ENSMUST00000134515						2	1	0	0	2	0	0	23	10	0	13		
ENSMUST00000134516						3	0	1	3	4	0	0	15	0	0	6		
ENSMUST00000134517						1	0	0	1	1	0	0	8	6	3	7		
ENSMUST00000134518						11	13	66	71	14	4	32	18	36	2	31		
ENSMUST00000134519						5	1	4	0	9	3	0	7	1	0	2		
ENSMUST00000134520						5	8	15	1	9	0	0	6	5	2	0		
ENSMUST00000134521	ENSMUSG00000036435	5	76529311	76570294	1	0	0	2	1	2	1	0	4	0	0	0	G3UVW9	
ENSMUST00000134522						0	0	0	0	8	1	0	0	0	0	0		
ENSMUST00000134523						103	101	512	214	114	45	4	9	11	0	9		
ENSMUST00000134524	ENSMUSG00000066037	4	136310942	136359447	1	0	0	0	0	4	7	9	0	19	0	9	A2AW41	
ENSMUST00000134525	ENSMUSG00000041119	17	31386234	31476310	1	0	0	0	21	0	0	0	0	0	0	0	D3YTQ4	
ENSMUST00000134526	ENSMUSG00000059689	6	117841180	117845956	1	0	0	0	0	0	5	0	0	13	24	0	D3YYX3	
ENSMUST00000134528						56	62	70	58	73	19	8	55	24	4	11		
ENSMUST00000134529						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000134530	ENSMUSG00000031918	9	13748410	13806481	1	0	0	0	1	0	0	3	5	0	0	7	F6T2Q0	
ENSMUST00000134531						11	3	12	0	10	0	5	14	3	1	7		
ENSMUST00000134532	ENSMUSG00000001098	5	114363567	114380508	-1	6	8	49	21	18	0	150	0	23	1	83	S4R2A3	
ENSMUST00000134533	ENSMUSG00000028522	4	103114390	103165754	1	2	0	2	0	2	1	0	0	0	0	0	B1AY31	
ENSMUST00000134534	ENSMUSG00000039936	4	149649168	149702571	-1	2	4	9	62	2	5	6	0	7	0	9	B1AS27	
ENSMUST00000134535						74	85	73	33	71	20	3	8	2	2	8		
ENSMUST00000134536						32	16	109	37	34	22	0	0	0	0	0		
ENSMUST00000134537						1	1	4	1	0	0	1	0	0	0	0		
ENSMUST00000134538	ENSMUSG00000041064	9	65587160	65595967	1	5	0	16	0	0	5	0	0	0	0	0		Q80SX8
ENSMUST00000134539	ENSMUSG00000025790	7	74275419	74554780	-1	0	0	0	2	0	0	0	0	0	3	4	F7B851	
ENSMUST00000134540						3	1	12	3	8	5	11	25	19	0	64		
ENSMUST00000134542	ENSMUSG00000021660	13	98309896	98317006	-1	4	3	4	3	3	0	0	2	0	10	0	Q3UJR8	Q64152

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134543	ENSMUSG00000070565	1	157135182	157412595	-1	2	2	0	0	4	3	0	0	1	0	0	D3Z1T6	
ENSMUST00000134544						307	319	672	314	416	168	8	25	22	4	43		
ENSMUST00000134545						8	0	64	11	0	4	0	0	11	0	4		
ENSMUST00000134546						5	2	30	9	0	9	0	0	0	0	0		
ENSMUST00000134547	ENSMUSG00000047242	X	106206883	106221158	-1	5	6	0	18	5	1	0	0	0	0	0	A2AP81	
ENSMUST00000134548						6	0	0	0	5	2	7	1	2	1	1		
ENSMUST00000134549						2	0	3	4	3	3	0	9	9	1	6		
ENSMUST00000134550	ENSMUSG00000092305	12	34984761	34986436	1	13	11	0	0	17	0	6	80	13	27	0	Q8C5R8	
ENSMUST00000134551	ENSMUSG00000026727	2	13076821	13271415	-1	2	0	0	0	4	1	0	0	34	71	72	E0CXG5	
ENSMUST00000134553	ENSMUSG00000026843	2	31572651	31617526	1	3	0	16	15	14	5	0	7	4	4	11	A0A0A6YVV5	
ENSMUST00000134554	ENSMUSG00000058794	15	103248212	103258403	-1	3	3	14	6	0	0	69	223	138	44	172		
ENSMUST00000134555						12	22	20	9	19	8	0	0	0	0	0		
ENSMUST00000134556						7	4	23	7	6	5	0	2	0	0	2		
ENSMUST00000134557						3	2	4	0	0	0	0	0	0	0	1		
ENSMUST00000134558						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134559						2	0	12	2	4	5	0	2	0	0	6		
ENSMUST00000134560						9	3	8	5	8	0	14	131	52	13	109		
ENSMUST00000134561						0	1	0	0	4	1	0	0	0	0	1		
ENSMUST00000134562						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134564						202	240	917	181	187	113	8	58	19	7	47		
ENSMUST00000134565						13	7	11	6	15	3	0	0	0	0	0		
ENSMUST00000134566	ENSMUSG00000032883	1	78657825	78707743	1	0	0	0	55	2	3	23	114	38	29	46	E9PUC2	
ENSMUST00000134568						90	81	249	103	86	62	5	5	9	3	13		
ENSMUST00000134569	ENSMUSG00000003812	8	84908560	84922915	1	0	0	0	0	0	0	33	13	39	19	0	D3Z5U3	
ENSMUST00000134570	ENSMUSG00000037020	7	30240138	30280419	-1	0	0	33	0	0	1	20	36	22	5	25	F6R9F0	
ENSMUST00000134571						2	2	2	1	0	0	0	0	0	2	0		
ENSMUST00000134572	ENSMUSG00000028402	4	81278500	81442815	-1	0	0	1	1	0	0	0	0	0	0	0	A3KG82	
ENSMUST00000134573						0	0	0	0	0	0	16	34	16	5	14		
ENSMUST00000134574						0	0	0	0	0	0	1	0	1	1	1		
ENSMUST00000134575	ENSMUSG00000036873	3	145938014	145944829	1	0	0	0	0	6	0	35	224	0	0	6	D6RCI4	
ENSMUST00000134576						14	14	33	0	38	3	50	107	25	0	29		
ENSMUST00000134577						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000134578	ENSMUSG00000021288	12	111758849	111807844	1	0	0	1	1	0	0	43	102	20	15	0	F6UYN4	
ENSMUST00000134579	ENSMUSG00000027331	2	118814003	118853957	1	0	0	0	10	0	0	0	53	33	29	21	F6UVD3	
ENSMUST00000134581	ENSMUSG00000023170	11	69913888	69916591	1	0	0	7	5	1	2	9	50	8	4	17	J3QNR4	
ENSMUST00000134582						1	1	0	54	6	0	0	0	0	0	0		
ENSMUST00000134583						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134585	ENSMUSG00000018666	11	96789127	96808640	1	8	6	11	28	27	9	98	528	151	91	126	Q7TPM0	
ENSMUST00000134587						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000134588	ENSMUSG00000031351	X	72987339	73031543	1	0	0	0	2	1	1	0	0	0	0	0	B1AXE7	
ENSMUST00000134589						0	0	1	0	0	0	8	4	13	0	13		
ENSMUST00000134590						2	0	0	6	1	1	0	8	1	1	2		
ENSMUST00000134591						0	6	7	3	9	3	0	0	0	0	0		
ENSMUST00000134592	ENSMUSG00000078440	10	81384428	81391560	1	2	1	2	1	2	1	0	0	6	0	0	D3YZM0	
ENSMUST00000134593	ENSMUSG00000031767	8	114133557	114154739	1	3	3	1	1	1	2	6	14	19	39	27		Q99P30
ENSMUST00000134594						151	147	285	199	152	97	29	152	81	24	156		
ENSMUST00000134595						0	0	0	28	4	7	0	0	0	0	0		
ENSMUST00000134596						18	11	32	22	23	19	2	1	2	0	2		
ENSMUST00000134597						7	0	5	3	0	1	0	0	0	0	0		
ENSMUST00000134598						0	0	0	0	0	0	0	21	1	0	12		
ENSMUST00000134599	ENSMUSG00000020462	11	29221532	29247409	-1	3	1	2	7	4	3	0	4	0	1	0	Q5SNY8	
ENSMUST00000134600						0	58	0	0	0	0	0	17	0	0	8		
ENSMUST00000134601						1	0	0	0	0	2	0	0	0	1	0		
ENSMUST00000134602	ENSMUSG00000047996	X	78449613	78583896	-1	0	0	0	0	0	0	0	0	0	0	0	A2BFE9	
ENSMUST00000134603						0	0	0	5	0	0	0	0	3	1	0		
ENSMUST00000134604						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000134605						15	27	34	30	35	24	3	13	1	1	8		
ENSMUST00000134606	ENSMUSG00000068329	6	83051266	83055273	-1	0	0	0	0	0	0	10	0	0	0	0	F6TCV0	
ENSMUST00000134607	ENSMUSG00000075302	2	70508819	70540884	1	0	0	0	14	0	0	0	0	0	0	0	D3Z5X9	
ENSMUST00000134609						28	21	51	27	32	14	2	1	1	0	3		
ENSMUST00000134610						36	25	102	184	44	15	0	0	0	0	1		
ENSMUST00000134611	ENSMUSG00000017307	2	164792768	164804882	-1	0	3	7	13	1	0	22	19	27	7	30	G3UXJ8	
ENSMUST00000134612						3	0	0	0	0	2	2	2	0	0	0		
ENSMUST00000134613						2	2	0	1	0	0	0	7	3	0	0		
ENSMUST00000134614	ENSMUSG00000078872	2	177074320	177087347	1	0	0	0	0	0	0	0	0	0	0	0	A2ARV7	
ENSMUST00000134616	ENSMUSG00000034243	16	36875140	36933085	1	0	1	0	0	0	0	0	0	0	0	0	Q9CTU9	
ENSMUST00000134617						2	2	5	2	4	0	0	16	0	0	0		
ENSMUST00000134618						2	0	0	6	2	0	0	4	0	1	3		
ENSMUST00000134619						1	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000134621						2	3	6	1	0	3	7	2	11	2	8		
ENSMUST00000134622						8	5	5	4	5	1	7	37	23	3	34		
ENSMUST00000134623	ENSMUSG00000028465	4	43531519	43562691	-1	0	0	0	0	0	0	0	0	0	0	0	F6S1V7	
ENSMUST00000134625	ENSMUSG00000022667	16	44765736	44794978	1	2	2	0	3	0	0	15	846	275	405	197	M0QWY6	
ENSMUST00000134626	ENSMUSG00000021884	14	31552905	31641286	-1	1	1	6	5	0	0	0	5	3	0	2	D6RDE9	
ENSMUST00000134628						3	9	9	5	3	3	0	3	3	0	2		
ENSMUST00000134629						1	2	3	0	1	3	8	127	80	49	71		
ENSMUST00000134630	ENSMUSG00000015766	6	137477245	137654876	-1	0	0	0	22	1	0	0	0	0	0	0	D3YXC3	
ENSMUST00000134631	ENSMUSG00000064284	15	85806972	85811697	-1	2	4	0	1	0	2	0	5	0	0	0		Q8R3A2
ENSMUST00000134632						0	2	0	84	3	0	1	0	40	59	30		
ENSMUST00000134635	ENSMUSG00000029669	6	21771395	21852515	-1	4	0	1	26	5	0	0	0	0	0	0	D3YYV7	
ENSMUST00000134636						2	0	24	2	2	0	0	8	0	0	0		
ENSMUST00000134637						0	1	19	2	13	3	54	86	82	17	33		
ENSMUST00000134638						6	2	8	6	2	3	0	0	0	0	0		
ENSMUST00000134639						2	3	4	2	9	4	16	93	30	5	28		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134641						0	0	0	0	0	0	72	120	106	37	45		
ENSMUST00000134642						3	2	16	52	5	4	2	0	0	0	0		
ENSMUST00000134643						5	4	7	17	0	0	0	0	0	0	0		
ENSMUST00000134644						6	5	13	5	2	8	0	0	6	0	5		
ENSMUST00000134645						4	2	18	84	5	0	4	0	4	2	5		
ENSMUST00000134647						12	12	13	22	29	7	0	1	0	0	1		
ENSMUST00000134648						5	0	8	0	2	4	0	0	0	0	0		
ENSMUST00000134650						1	0	1	0	0	1	1	0	0	1	0		
ENSMUST00000134651	ENSMUSG00000038685	2	181319739	181356616	1	0	0	0	0	0	0	4	1	7	0	0	F6UWJ0	
ENSMUST00000134652	ENSMUSG00000046196	17	80207460	80217936	1	6	10	6	14	10	5	0	0	0	0	0	Q0VF76	
ENSMUST00000134653						0	1	0	0	1	2	0	0	0	2	0		
ENSMUST00000134654	ENSMUSG00000047407	17	70844205	70853546	-1	1	0	28	6	0	0	0	0	0	0	3	E0CXJ4	
ENSMUST00000134655	ENSMUSG00000007833	7	45140684	45154584	-1	0	0	0	0	0	0	119	177	81	11	53	F6RQF0	
ENSMUST00000134656	ENSMUSG00000073599	18	35713086	35722356	-1	0	0	0	0	0	0	0	0	0	0	0	F6RF12	
ENSMUST00000134657						0	1	2	0	2	0	9	16	0	12	4		
ENSMUST00000134658						0	0	2	1	0	0	0	0	1	0	0		
ENSMUST00000134659	ENSMUSG00000063145	2	69647171	69667571	1	3	2	2	28	1	2	0	0	0	10	0	D6RJ69	
ENSMUST00000134660	ENSMUSG00000020538	11	60199089	60222581	-1	0	0	30	0	0	0	38	477	63	0	27	F6XZS9	
ENSMUST00000134661	ENSMUSG00000027331	2	118814003	118853957	1	17	17	34	82	24	18	17	47	42	48	15		Q9D9Z1
ENSMUST00000134662						3	0	9	25	5	0	2	5	1	8	13		
ENSMUST00000134663	ENSMUSG00000024388	18	31959234	32036961	-1	68	31	99	59	91	38	0	0	0	0	0		Q99MZ6
ENSMUST00000134664						0	6	4	5	4	4	2	10	0	3	8		
ENSMUST00000134665						2	0	0	0	2	0	0	2	0	0	1		
ENSMUST00000134666						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000134667	ENSMUSG00000024807	19	6046576	6053712	1	5	8	5	119	8	1	187	246	190	8	206		
ENSMUST00000134668	ENSMUSG00000026889	2	36116079	36136773	-1	0	0	0	0	0	2	25	6	37	60	37	D6REF9	
ENSMUST00000134669	ENSMUSG00000018677	11	102402985	102407946	-1	0	0	0	13	0	0	0	0	0	0	8	D6RDT5	
ENSMUST00000134670						3	3	1	0	5	0	0	0	0	0	0		
ENSMUST00000134671						1	2	12	7	4	3	24	154	54	5	54		
ENSMUST00000134674	ENSMUSG00000031918	9	13748410	13806481	1	0	1	0	0	0	0	111	188	108	81	166	B8JJF6	
ENSMUST00000134675	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0		Q3UTJ2
ENSMUST00000134676						3	3	36	14	7	5	0	3	5	0	5		
ENSMUST00000134677						0	1	1	0	1	0	13	93	3	10	13		
ENSMUST00000134678						6	9	7	13	8	2	12	5	23	0	8		
ENSMUST00000134680						22	18	59	23	28	13	0	0	0	1	1		
ENSMUST00000134681						5	3	7	0	6	2	0	0	0	0	0		
ENSMUST00000134682	ENSMUSG00000032577	9	107254927	107289877	-1	9	3	16	3	6	3	2	1	2	0	0	B0QZU6	
ENSMUST00000134683	ENSMUSG00000035674	7	3617373	3620327	1	0	0	0	0	0	0	0	0	0	0	0	F7BLS8	
ENSMUST00000134684						12	9	36	16	14	10	0	3	0	0	6		
ENSMUST00000134685						0	0	1	0	0	0	3	3	1	1	4		
ENSMUST00000134686						6	6	5	10	8	4	10	64	21	5	31		
ENSMUST00000134687						3	4	11	10	5	1	7	30	16	2	24		
ENSMUST00000134689						0	1	0	8	0	0	0	0	10	0	8		
ENSMUST00000134690						35	28	37	251	48	19	1	0	0	0	6		
ENSMUST00000134691						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134693						0	0	0	76	3	0	0	0	0	0	0		
ENSMUST00000134694	ENSMUSG00000108596	7	128062683	128128160	1	2	4	9	7	5	3	257	1011	404	142	389	F6YXU0	
ENSMUST00000134695						0	0	0	3	3	0	0	0	0	0	0		
ENSMUST00000134696						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000134697						0	2	2	6	0	0	14	103	58	0	70		
ENSMUST00000134698						1	2	20	1	4	1	11	48	15	0	30		
ENSMUST00000134699	ENSMUSG00000027257	2	91255954	91264679	1	2	0	2	30	2	4	0	0	0	0	0	B1AW91	
ENSMUST00000134700	ENSMUSG00000020831	11	70235206	70237914	-1	0	0	0	0	0	0	0	41	0	18	0	F6S0D5	
ENSMUST00000134701						18	13	16	59	27	4	0	1	0	0	2		
ENSMUST00000134702						3	5	8	10	0	2	13	177	62	11	140		
ENSMUST00000134703						0	0	0	127	0	3	27	33	24	7	58		
ENSMUST00000134704						1	0	0	2	2	2	0	0	0	0	0		
ENSMUST00000134706						14	12	44	171	16	8	0	3	0	0	0		
ENSMUST00000134707	ENSMUSG00000018656	6	42584866	42597692	-1	6	0	0	0	3	0	1	1	2	1	0	D3Z045	
ENSMUST00000134708						23	14	30	14	14	15	1	2	1	2	1		
ENSMUST00000134709						0	0	0	1	0	0	3	0	2	3	0		
ENSMUST00000134710	ENSMUSG00000039578	6	61180324	62382865	1	2	1	0	2	1	0	0	0	0	0	0	F7CDW2	
ENSMUST00000134711						9	7	19	7	8	5	5	16	3	1	15		
ENSMUST00000134712						2	2	0	2	0	0	0	0	0	0	0		
ENSMUST00000134713						11	3	12	6	10	4	0	0	0	0	0		
ENSMUST00000134714						3	6	23	11	4	1	2	2	4	0	1		
ENSMUST00000134715	ENSMUSG00000021792	14	40993740	41013788	-1	5	7	6	10	8	7	0	0	3	8	6	D3Z0A8	
ENSMUST00000134716						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134717						2	2	0	0	2	4	0	0	0	0	0		
ENSMUST00000134718						0	4	0	40	4	0	4	0	3	0	0		
ENSMUST00000134719	ENSMUSG00000004455	5	122158278	122175273	1	8	10	11	0	0	3	271	637	366	68	176	A0A0G2JEB0	
ENSMUST00000134720	ENSMUSG00000051747	2	76703980	76982547	-1	26	92	58	0	4	4	0	0	0	0	0	F7CR78	
ENSMUST00000134721	ENSMUSG00000018800	11	110269369	110337716	-1	0	0	0	0	0	0	0	0	0	0	0	A2AEP6	
ENSMUST00000134723						1	5	7	15	2	3	0	0	0	0	0		
ENSMUST00000134724						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134725						0	0	0	20	0	1	0	0	1	0	0		
ENSMUST00000134726	ENSMUSG00000028402	4	81278500	81442815	-1	0	2	0	0	0	0	0	0	0	0	4	A3KG84	
ENSMUST00000134727	ENSMUSG00000066149	4	62383654	62408642	-1	43	53	74	74	68	31	50	210	63	110	52		Q99JP4
ENSMUST00000134728						0	17	0	315	0	21	0	0	0	0	0		
ENSMUST00000134729	ENSMUSG00000031826	8	119910360	119957560	1	3	5	0	0	3	0	0	4	0	0	0	G3UYQ8	
ENSMUST00000134730						0	0	0	0	0	0	3	4	22	0	3		
ENSMUST00000134731						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000134732	ENSMUSG00000018669	11	96907426	96916496	-1	9	4	26	52	2	16	0	51	36	0	52	D6RJ46	
ENSMUST00000134733						2	2	2	2	0	1	0	0	2	0	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134734	ENSMUSG00000026739	2	18677018	18686629	1	0	0	3	8	0	0	0	0	0	0	0	A2ASR6	
ENSMUST00000134735						2	0	24	25	0	1	0	9	0	11	0		
ENSMUST00000134737						4	3	1	2	10	5	35	89	45	6	65		
ENSMUST00000134738						2	2	4	5	5	0	4	28	1	0	13		
ENSMUST00000134739	ENSMUSG00000059173	2	79834453	80129458	-1	1	0	0	0	0	0	0	0	0	0	0	F6X0V1	
ENSMUST00000134740						1	3	3	5	0	1	3	0	0	2	0		
ENSMUST00000134741						14	21	50	16	23	7	25	145	77	15	112		
ENSMUST00000134742						0	10	0	0	10	3	0	0	0	0	1		
ENSMUST00000134743						3	4	39	124	13	4	0	1	0	0	0		
ENSMUST00000134744	ENSMUSG00000006476	2	25054355	25062881	1	9	1	2	0	21	6	68	495	58	22	93	F6VTS9	
ENSMUST00000134745	ENSMUSG00000020849	11	75732869	75765845	1	0	0	0	73	2	0	201	50	653	201	435	D6REF3	
ENSMUST00000134746	ENSMUSG00000031922	9	13807792	13827107	-1	0	0	0	0	0	0	4	51	86	118	29	D6RH89	
ENSMUST00000134747	ENSMUSG00000028975	4	148960535	149099876	-1	0	0	1	0	2	0	0	0	0	0	2	D6RH82	
ENSMUST00000134748	ENSMUSG00000034601	12	71136848	71243303	1	4	0	2	5	3	2	2	2	0	0	0	F6ZIY2	
ENSMUST00000134749						12	0	11	4	17	10	0	0	4	0	0		
ENSMUST00000134750						2	3	16	10	2	1	15	16	13	5	32		
ENSMUST00000134751	ENSMUSG00000028964	4	150897133	150914437	-1	1	2	2	12	1	0	11	0	0	0	0	A2A816	
ENSMUST00000134752						0	0	0	0	0	0	0	25	0	8	0		
ENSMUST00000134753						1	6	6	4	9	2	0	0	0	0	0		
ENSMUST00000134754						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134756						0	2	0	0	1	2	3	79	14	6	12		
ENSMUST00000134757	ENSMUSG00000031105	X	48623413	48662294	1	0	0	0	0	0	0	0	0	21	55	5	F2Z407	
ENSMUST00000134758						0	1	0	2	0	0	0	4	6	9	3		
ENSMUST00000134759	ENSMUSG00000002728	2	145902099	145916425	1	12	15	24	18	3	10	7	13	9	6	15	G5E8X4	
ENSMUST00000134760						0	0	0	0	1	0	4	13	6	14	0		
ENSMUST00000134761	ENSMUSG00000033439	3	116581093	116614587	-1	0	1	2	1	0	1	0	0	0	0	0	S4R2S3	
ENSMUST00000134762	ENSMUSG00000025855	5	139017306	139150001	-1	0	0	0	0	0	1	0	0	0	0	0	D3Z7E4	
ENSMUST00000134763	ENSMUSG00000040430	11	107207892	107470699	-1	0	2	0	0	4	2	45	24	50	0	17	X1WI19	
ENSMUST00000134764						0	2	2	0	2	0	0	0	0	0	0		
ENSMUST00000134765						2	5	3	9	11	1	3	0	3	0	11		
ENSMUST00000134766						0	1	0	31	1	0	0	0	0	0	0		
ENSMUST00000134767	ENSMUSG00000023805	17	5941280	6044290	1	10	4	20	10	10	2	0	0	25	0	0	S4R207	
ENSMUST00000134769						0	0	0	8	0	0	9	0	6	12	26		
ENSMUST00000134770						4	0	1	2	0	1	23	9	36	1	13		
ENSMUST00000134771						0	0	6	3	0	0	0	0	0	1	9		
ENSMUST00000134772	ENSMUSG00000031916	8	107046289	107056689	-1	1	0	2	46	0	0	3	0	0	0	0	M0QW66	
ENSMUST00000134773	ENSMUSG00000061246	11	73660090	73665542	1	3	1	1	0	2	2	0	0	0	0	0		
ENSMUST00000134774						1	6	5	6	9	0	0	0	0	0	0		
ENSMUST00000134775	ENSMUSG00000036893	2	24789928	24919614	-1	0	0	0	0	10	6	0	82	0	9	15	A0A0A6YXD1	
ENSMUST00000134776	ENSMUSG00000023088	16	14361558	14475737	1	0	0	0	0	0	0	2	0	0	0	4	D3YZY1	
ENSMUST00000134777	ENSMUSG00000031860	8	69832491	69872292	1	0	0	0	0	0	0	0	4	0	0	0	D6RGB0	
ENSMUST00000134778	ENSMUSG00000040354	10	127296221	127311786	-1	1	0	0	0	0	0	0	12	0	0	0	F6W0G8	
ENSMUST00000134779						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000134780						1	5	1	39	5	0	0	0	0	0	0		
ENSMUST00000134781	ENSMUSG00000028857	4	133266045	133277792	-1	2	0	5	4	4	1	23	11	13	0	13	F6XVJ2	
ENSMUST00000134782	ENSMUSG00000028433	4	41194313	41275144	-1	0	0	0	0	0	0	0	0	6	0	0	F6PYV5	
ENSMUST00000134783						8	7	11	8	5	6	5	33	0	2	4		
ENSMUST00000134784						0	0	0	0	0	0	0	0	9	0	0		
ENSMUST00000134785						2	3	9	7	3	3	2	13	6	6	12		
ENSMUST00000134786	ENSMUSG00000047115	6	49367739	49390539	1	0	1	0	10	1	0	0	0	0	0	0	D3YVA9	
ENSMUST00000134788	ENSMUSG00000027506	3	8925593	9004723	-1	0	0	0	0	0	0	28	52	156	127	162	D3Z7X7	
ENSMUST00000134789						10	7	13	0	5	7	36	321	0	88	71		
ENSMUST00000134790						14	14	16	18	23	0	5	22	15	0	31		
ENSMUST00000134791	ENSMUSG00000057637	4	143107391	143212995	-1	0	0	0	2	0	0	0	0	0	0	0	Q8C2W5	
ENSMUST00000134792	ENSMUSG00000022704	16	43861407	43926809	-1	0	0	0	0	0	0	0	0	0	0	0	D6RGP3	
ENSMUST00000134793						6	2	2	0	3	0	0	9	30	0	16		
ENSMUST00000134794	ENSMUSG00000026730	2	12924041	13003455	1	7	3	6	5	0	1	0	0	0	0	0		Q60866
ENSMUST00000134796	ENSMUSG00000033526	2	121310561	121355396	-1	1	0	1	71	4	3	0	0	0	0	0	B0R0E7	
ENSMUST00000134797	ENSMUSG00000020225	10	120201590	120224917	1	0	4	7	77	8	8	5	27	41	30	40	Q8K191	
ENSMUST00000134798	ENSMUSG00000027207	2	125859109	125984299	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCT4	
ENSMUST00000134802	ENSMUSG00000033149	16	45746243	45953598	-1	5	0	0	0	15	9	0	0	2	3	4	D3Z069	
ENSMUST00000134803						1	0	0	0	0	0	46	301	58	10	77		
ENSMUST00000134804						3	5	7	3	11	0	57	55	43	0	35		
ENSMUST00000134805						1	1	3	58	0	2	2	1	0	0	0		
ENSMUST00000134806						65	26	279	66	38	20	8	21	10	1	7		
ENSMUST00000134807						0	1	0	0	1	1	0	2	0	0	5		
ENSMUST00000134808						64	56	689	170	44	42	0	4	0	0	9		
ENSMUST00000134809	ENSMUSG00000056737	6	72544391	72562983	1	1	2	7	3	3	4	0	20	6	0	4	D3Z014	
ENSMUST00000134811						0	0	0	0	1	1	3	6	0	6	4		
ENSMUST00000134812						0	0	5	6	5	6	80	7324	157	54	125		
ENSMUST00000134813						0	0	0	0	0	0	0	7	0	4	0		
ENSMUST00000134814	ENSMUSG00000069805	13	62864753	62888282	-1	2	5	10	31	7	7	0	0	0	0	0	E9Q0T7	
ENSMUST00000134815	ENSMUSG00000001555	11	100415697	100424824	1	0	1	8	1	0	0	0	0	1	0	0	F6W360	
ENSMUST00000134816						5	0	0	0	4	12	0	21	23	5	27		
ENSMUST00000134817						8	2	0	0	1	1	4	183	29	34	43		
ENSMUST00000134818	ENSMUSG00000020812	11	116671660	116675799	1	8	1	14	6	6	1	0	4	3	0	2	E9Q255	
ENSMUST00000134819	ENSMUSG00000029478	5	125017153	125179219	-1	2	0	18	29	0	0	12	9	14	0	13	F6SK53	
ENSMUST00000134820						11	13	20	10	17	6	5	2	6	1	33		
ENSMUST00000134821						13	6	65	40	33	8	20	38	8	5	12		
ENSMUST00000134822						0	4	28	16	22	6	25	69	27	11	37		
ENSMUST00000134823						30	34	108	51	31	24	0	0	0	0	1		
ENSMUST00000134824	ENSMUSG00000018379	11	88047373	88053755	1	0	0	0	0	0	0	0	386	154	43	108	F7AI47	
ENSMUST00000134825	ENSMUSG00000090122	X	142304752	142306294	-1	4	4	12	99	9	3	0	0	0	0	0		Q9QZ26
ENSMUST00000134826						0	0	0	10	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134827						5	4	6	5	4	4	0	0	0	0	0		
ENSMUST00000134828	ENSMUSG00000018068	11	86210681	86257575	-1	0	0	0	0	4	0	0	0	0	1	0	H3BK92	
ENSMUST00000134829	ENSMUSG00000032373	9	66713686	66766845	1	0	0	7	2	0	0	0	0	1	0	0	F6W0I8	
ENSMUST00000134830						0	1	0	10	0	0	0	0	0	0	5		
ENSMUST00000134831	ENSMUSG00000079560	6	52169062	52213336	-1	0	0	0	0	3	0	0	0	0	0	0	D3YV38	
ENSMUST00000134832						16	14	14	10	15	6	0	0	0	0	0		
ENSMUST00000134834						69	45	137	576	89	43	2	5	2	2	15		
ENSMUST00000134835						0	0	0	3	0	0	5	3	0	0	6		
ENSMUST00000134836						0	0	10	6	5	0	0	5	0	0	0		
ENSMUST00000134837						1	3	7	2	13	1	2	15	7	0	27		
ENSMUST00000134839						44	34	92	45	50	25	28	100	55	0	59		
ENSMUST00000134840	ENSMUSG00000026189	1	72259167	72284314	-1	0	3	4	0	9	3	0	0	4	0	0	D6RHN4	
ENSMUST00000134841						2	4	1	3	5	2	12	61	41	59	75		
ENSMUST00000134842	ENSMUSG00000021639	13	100460218	100492579	-1	0	0	0	0	0	0	3	10	5	26	13	S4R2R0	
ENSMUST00000134843						10	9	7	8	11	7	0	1	0	1	4		
ENSMUST00000134844	ENSMUSG00000028582	4	108619940	108634123	1	0	0	0	0	1	0	126	142	48	95	57	F6XC25	
ENSMUST00000134846	ENSMUSG00000029177	5	30666777	30674830	1	0	0	12	19	4	3	52	119	52	15	68	D6RJ71	
ENSMUST00000134847	ENSMUSG00000064036	18	73859385	73881333	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0V1	
ENSMUST00000134848	ENSMUSG00000050812	4	58798911	58912749	-1	0	0	0	0	0	0	0	0	5	0	0	A2ALV9	
ENSMUST00000134849						1	2	3	2	0	1	0	0	1	0	1		
ENSMUST00000134850						6	2	10	2	4	0	1	3	2	0	3		
ENSMUST00000134851						0	0	1	0	3	0	8	13	4	4	12		
ENSMUST00000134852						0	0	2	0	0	0	2	0	0	0	0		
ENSMUST00000134853						4	0	8	3	1	0	0	3	0	0	0		
ENSMUST00000134854						5	1	21	5	7	7	0	7	16	1	19		
ENSMUST00000134855						0	0	0	0	0	0	56	1764	52	10	37		
ENSMUST00000134856	ENSMUSG00000052997	7	34140688	34169599	-1	0	0	0	0	2	0	0	0	0	0	0	H3BLM2	
ENSMUST00000134857						1	0	5	39	0	0	0	24	4	6	12		
ENSMUST00000134858						28	17	46	16	12	11	0	5	6	1	3		
ENSMUST00000134859						359	372	887	211	433	173	15	58	44	22	62		
ENSMUST00000134860						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000134861						0	0	4	158	1	0	9	10	76	0	80		
ENSMUST00000134862	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	31	0	20	1	1	989	238	130		Q3UHJ8
ENSMUST00000134863	ENSMUSG00000002325	14	55603571	55610030	1	7	2	14	8	22	12	105	310	185	48	231	E9PZJ2	
ENSMUST00000134864	ENSMUSG00000036585	18	38838673	38929404	-1	3	0	4	8	3	3	0	0	0	0	0	D3Z192	
ENSMUST00000134865						23	9	54	35	27	12	0	1	0	0	2		
ENSMUST00000134866						9	9	10	5	9	0	0	0	0	0	0		
ENSMUST00000134867						4	4	2	1	3	5	3	0	0	0	3		
ENSMUST00000134868						0	0	0	0	0	0	8	0	12	6	0		
ENSMUST00000134869						3	0	7	116	5	2	0	0	0	0	0		
ENSMUST00000134870						0	0	0	0	1	0	6	96	72	7	30		
ENSMUST00000134871						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000134872						0	1	21	0	6	0	0	6	3	0	0		
ENSMUST00000134873						0	0	0	0	0	0	4	0	6	0	0		
ENSMUST00000134874						13	5	22	7	10	3	0	0	0	0	0		
ENSMUST00000134875	ENSMUSG00000035984	18	34562634	34579115	-1	0	1	0	1	3	5	0	8	0	0	2		Q99MH5
ENSMUST00000134876	ENSMUSG00000027522	2	174076308	174099771	1	1	1	0	0	0	0	1	2	4	0	6	B7ZCB7	
ENSMUST00000134877	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	0	0	2	1	0	0	0	0	0	B4YB29	
ENSMUST00000134878						20	16	107	27	39	23	2	3	18	4	29		
ENSMUST00000134879	ENSMUSG00000028382	4	59471868	59549364	-1	0	0	0	0	0	0	0	0	0	0	10	G3UZG7	
ENSMUST00000134880						0	1	1	64	2	1	0	0	0	0	0		
ENSMUST00000134881	ENSMUSG00000025825	5	113772748	113778288	1	0	0	0	0	0	1	71	0	0	31	17	F6XUL3	
ENSMUST00000134882	ENSMUSG00000026933	2	25926838	25983282	-1	0	0	0	0	0	0	0	0	0	0	0	A2AHC4	
ENSMUST00000134883						26	29	49	17	26	28	3	6	4	0	0		
ENSMUST00000134884	ENSMUSG00000056938	11	103101682	103112200	1	0	0	0	0	1	0	0	0	0	0	0	B0QZY2	
ENSMUST00000134885	ENSMUSG00000022469	15	97744770	97767972	-1	0	0	0	0	0	0	1	7	1	1	0	H3BKA8	
ENSMUST00000134886						3	2	0	1	1	2	0	0	0	0	0		
ENSMUST00000134887	ENSMUSG00000051159	X	102247381	102252181	-1	0	0	0	31	1	1	0	0	0	0	0	F6YUL1	
ENSMUST00000134888						4	0	2	104	1	0	0	0	0	0	0		
ENSMUST00000134890						86	76	679	185	87	57	86	144	185	8	200		
ENSMUST00000134891						0	1	3	5	1	0	3	9	2	2	9		
ENSMUST00000134892						3	3	4	49	4	8	2	4	2	5	8		
ENSMUST00000134893	ENSMUSG00000019428	8	70527724	70535328	1	1	1	7	1	4	0	11	33	0	0	12	F6WP10	
ENSMUST00000134894	ENSMUSG00000017686	11	80209019	80267907	1	0	0	0	0	0	0	4	180	42	26	35	F7ASU3	
ENSMUST00000134895						0	5	34	10	0	3	0	8	1	3	9		
ENSMUST00000134896	ENSMUSG00000020515	11	58104153	58118594	1	9	4	10	86	8	0	4	3	6	0	9	A2AFQ7	
ENSMUST00000134897						0	2	0	0	0	0	0	0	0	0	12		
ENSMUST00000134898						3	0	1	7	4	1	0	0	0	0	0		
ENSMUST00000134900						5	7	21	6	10	3	6	0	1	2	7		
ENSMUST00000134901	ENSMUSG00000061859	4	98395785	98719603	1	4	3	4	0	7	2	0	3	0	1	0	A2ADT1	
ENSMUST00000134902	ENSMUSG00000007659	2	152780668	152831728	-1	22	10	27	0	20	6	0	5	4	0	11		Q64373
ENSMUST00000134903						10	2	8	3	6	2	19	63	39	10	34		
ENSMUST00000134904						42	27	56	44	40	23	5	7	3	4	9		
ENSMUST00000134905						24	6	28	5	11	9	70	110	76	14	116		
ENSMUST00000134906						1	0	6	83	8	3	4	4	3	0	1		
ENSMUST00000134907	ENSMUSG00000032231	9	69453620	69491795	1	8	2	11	54	3	11	143	121	153	100	21	B0V2N8	
ENSMUST00000134908						0	8	1	0	0	0	3	0	8	19	9		
ENSMUST00000134909						12	10	18	28	16	10	15	30	29	9	17		
ENSMUST00000134910						0	0	0	2	0	0	1	0	2	2	15		
ENSMUST00000134912						20	12	47	10	26	6	0	3	2	7	0		
ENSMUST00000134913						3	2	5	1	2	0	33	39	32	0	15		
ENSMUST00000134914						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000134915						0	2	1	2	0	3	0	0	0	0	0		
ENSMUST00000134916						2	0	5	2	1	0	0	8	4	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000134917						8	16	18	31	10	3	2	4	0	0	2		
ENSMUST00000134918						1	1	1	109	7	2	2	0	0	0	0		
ENSMUST00000134919						0	3	0	3	2	3	7	73	75	6	88		
ENSMUST00000134922						0	0	0	0	0	1	23	18	21	0	10		
ENSMUST00000134923						8	12	12	2	8	7	0	0	0	0	0		
ENSMUST00000134924						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000134925						0	2	0	0	3	2	7	111	0	16	0		
ENSMUST00000134926	ENSMUSG00000029320	5	103648039	103656010	-1	0	0	0	0	3	2	0	0	0	0	0		Q9DAA3
ENSMUST00000134927						47	38	85	58	54	24	3	25	15	4	17		
ENSMUST00000134928						2	0	0	2	2	1	0	0	0	0	0		
ENSMUST00000134929						7	4	11	80	3	3	13	20	6	6	22		
ENSMUST00000134930						3	1	2	1	4	3	0	0	0	0	0		
ENSMUST00000134931						1	4	3	51	3	0	2	1	2	1	1		
ENSMUST00000134932						1	0	0	0	4	0	46	36	0	0	7		
ENSMUST00000134933	ENSMUSG00000044876	7	6172226	6191349	1	0	0	1	0	0	0	0	8	4	0	0	E9Q3H2	
ENSMUST00000134935	ENSMUSG00000074899	2	120046157	120085772	-1	24	16	30	76	32	10	0	0	0	0	2	F7BYG3	
ENSMUST00000134936						2	0	0	0	0	0	10	0	11	9	70		
ENSMUST00000134937						18	11	56	15	0	0	0	0	0	0	0		
ENSMUST00000134938						0	0	0	0	0	0	0	0	4	11	0		
ENSMUST00000134939	ENSMUSG00000032604	9	108507713	108515941	1	18	10	22	21	16	5	64	689	172	52	280	D3Z158	
ENSMUST00000134940	ENSMUSG00000035875	2	35084046	35101543	-1	0	0	0	0	0	0	3	7	1	0	0		
ENSMUST00000134941						3	3	21	5	8	3	0	0	0	0	0		
ENSMUST00000134942	ENSMUSG00000005204	11	69673115	69682084	-1	0	0	0	0	0	0	19	111	0	0	0	F6Z9L5	
ENSMUST00000134943	ENSMUSG00000028911	4	131873617	131901706	1	2	2	0	0	0	0	77	89	80	12	91	A0A0A6YXU8	
ENSMUST00000134945	ENSMUSG00000030269	6	113237843	113281392	1	0	0	0	0	0	0	102	207	51	38	48	F6W741	
ENSMUST00000134946	ENSMUSG00000030956	7	132712082	132813886	-1	0	0	0	42	0	0	0	0	10	0	15	D3YXR6	
ENSMUST00000134947	ENSMUSG00000012187	1	78510991	78538173	1	0	0	0	4	0	0	0	0	0	0	0	D3Z6K9	
ENSMUST00000134948						0	2	3	2	3	2	0	0	2	0	1		
ENSMUST00000134949	ENSMUSG00000038145	9	122117283	122169702	1	0	0	0	0	0	0	75	0	59	0	36	D3Z1F6	
ENSMUST00000134950						3	2	3	0	3	0	0	0	2	0	0		
ENSMUST00000134951						1	1	5	1	0	0	0	0	3	1	3		
ENSMUST00000134952						0	9	14	1	11	3	0	0	0	0	0		
ENSMUST00000134953	ENSMUSG00000037275	11	58120002	58168539	-1	0	6	1	1	4	0	0	0	0	0	0	F7CKD6	
ENSMUST00000134954						2	1	0	9	0	0	0	13	0	1	0		
ENSMUST00000134955	ENSMUSG00000032327	9	58063788	58153996	1	0	0	2	0	0	0	0	0	0	0	0	E9PZT7	
ENSMUST00000134956						0	2	0	0	4	0	0	8	0	0	0		
ENSMUST00000134957						0	0	5	0	3	0	5	2	1	0	0		
ENSMUST00000134958						0	0	0	0	0	0	3	25	7	0	0		
ENSMUST00000134959	ENSMUSG00000026490	1	179960472	180165603	1	2	0	0	0	0	0	4	0	0	0	0	A0A0A6YXJ5	
ENSMUST00000134960						11	6	10	8	4	4	0	2	0	0	6		
ENSMUST00000134961						5	3	6	44	11	2	8	45	14	2	20		
ENSMUST00000134962						34	29	115	62	40	21	55	246	95	13	146		
ENSMUST00000134963	ENSMUSG00000037138	1	38177326	38664955	-1	0	3	0	0	2	0	0	0	0	0	0	D6RHR2	
ENSMUST00000134964						0	0	0	21	0	0	0	0	0	0	0		
ENSMUST00000134965	ENSMUSG00000056899	12	41024090	41955588	1	6	1	3	67	1	2	1	1	1	8	1		Q8BPT6
ENSMUST00000134967						0	0	5	0	0	5	0	22	0	3	0		
ENSMUST00000134968	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	0	0	0	G3UX39	
ENSMUST00000134969						2	3	0	3	2	0	0	0	0	0	0		
ENSMUST00000134970						1	2	0	3	2	3	2	1	0	0	3		
ENSMUST00000134972	ENSMUSG00000028933	5	25689812	25705825	-1	2	0	0	0	0	0	1	0	0	0	0	A0A0G2JF58	
ENSMUST00000134973						4	5	5	0	3	1	0	0	0	0	0		
ENSMUST00000134974	ENSMUSG00000064080	6	91212455	91272540	1	2	1	2	2	0	1	0	0	0	0	0	D3Z5S2	
ENSMUST00000134975						2	1	0	6	0	4	0	0	0	0	0		
ENSMUST00000134977						0	0	0	4	0	8	36	103	107	28	130		
ENSMUST00000134978	ENSMUSG00000001525	17	35833921	35838306	-1	0	0	0	9	6	3	22	79	32	10	33	G3UZR1	
ENSMUST00000134979	ENSMUSG00000032897	4	120757438	120831572	-1	0	0	0	0	1	0	0	3	15	0	0	A2A762	
ENSMUST00000134980						6	0	4	157	10	1	0	0	1	0	0		
ENSMUST00000134981						0	2	8	10	0	3	6	26	12	0	8		
ENSMUST00000134982	ENSMUSG00000074527	2	176892509	176927809	-1	502	456	547	696	696	398	13	30	28	11	52	E9Q3Y3	
ENSMUST00000134983						0	2	0	0	0	3	0	0	4	0	0		
ENSMUST00000134984						4	3	17	6	2	1	3	1	2	1	3		
ENSMUST00000134985	ENSMUSG00000033237	15	96287518	96404992	1	2	0	7	94	0	3	5	0	10	0	2	Q9D982	
ENSMUST00000134986						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000134987						23	31	19	502	49	25	3	27	9	0	5		
ENSMUST00000134988						4	6	17	51	11	0	4	28	13	93	0		
ENSMUST00000134989						81	48	555	82	66	34	7	9	9	1	5		
ENSMUST00000134990						2	0	12	3	5	2	0	0	5	0	0		
ENSMUST00000134991	ENSMUSG00000056004	5	9266118	9481825	1	0	0	10	0	0	0	0	0	0	0	0		Q3UZV7
ENSMUST00000134993	ENSMUSG00000033233	3	100922202	100936920	1	0	0	0	0	7	0	9	3	7	0	10	F6SXK7	Q6PFY8
ENSMUST00000134994						4	0	8	4	7	3	1	0	0	0	0		
ENSMUST00000134995	ENSMUSG00000003534	17	35681567	35704621	-1	0	3	0	0	3	2	1	0	0	0	0	B0V2H8	
ENSMUST00000134996	ENSMUSG00000032363	9	90163069	90208071	1	0	0	20	0	15	0	0	0	0	0	0	D6RI90	
ENSMUST00000134999						1	1	0	0	0	0	0	0	3	0	0		
ENSMUST00000135000						17	6	18	24	33	2	0	0	0	0	0		
ENSMUST00000135001	ENSMUSG00000072946	12	84285232	84315832	1	0	2	0	0	0	0	16	9	37	102	53	Q3TXN1	
ENSMUST00000135002						46	22	242	70	38	21	18	65	27	2	23		
ENSMUST00000135003	ENSMUSG00000042446	4	126861939	126968135	-1	20	17	20	0	6	5	10	74	32	30	76	F6VYE2	
ENSMUST00000135004						1	3	4	4	2	0	0	0	0	0	0		
ENSMUST00000135005						17	15	27	58	23	13	7	0	0	0	0		
ENSMUST00000135006						1	2	1	4	0	1	0	0	0	0	0		
ENSMUST00000135007	ENSMUSG00000047407	17	70844205	70853546	-1	0	4	1	3	8	1	0	0	2	0	5	E0CYI0	
ENSMUST00000135008						0	0	0	4	4	3	0	0	0	0	2		
ENSMUST00000135009	ENSMUSG00000032332	9	79598991	79718831	-1	2	0	3	3	1	4	0	0	0	0	3	F6WIM8	
ENSMUST00000135010	ENSMUSG00000025555	14	121035200	121283744	1	1	0	0	49	4	0	0	0	0	0	0	E9Q805	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135011						10	7	11	33	4	2	0	0	0	0	5		
ENSMUST00000135012						0	1	0	0	0	0	4	0	0	0	0		
ENSMUST00000135013						1	1	17	2	3	7	4	15	10	2	5		
ENSMUST00000135014	ENSMUSG00000057715	1	11414105	11975901	1	0	43	22	7	0	36	0	0	0	0	0		Q8BZJ8
ENSMUST00000135015	ENSMUSG00000025873	13	54621784	54664068	1	0	1	0	52	3	2	0	0	2	0	0	D6RE51	
ENSMUST00000135016	ENSMUSG00000025069	19	47865545	47886324	1	0	1	0	1	3	3	0	0	0	3	0	D3Z1Q9	
ENSMUST00000135017	ENSMUSG00000005687	3	103171655	103179166	1	9	21	17	3	19	0	43	237	94	0	69	D6RGA5	
ENSMUST00000135018						31	24	24	19	20	10	7	7	8	1	13		
ENSMUST00000135019						4	3	2	3	3	4	9	31	8	2	4		
ENSMUST00000135020						0	0	0	2	0	0	0	37	11	8	14		
ENSMUST00000135021	ENSMUSG00000027955	3	79884533	79946280	1	0	2	0	1	0	1	0	0	0	0	0		
ENSMUST00000135022						0	0	0	0	0	0	1	0	3	0	4		
ENSMUST00000135023						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135024						11	7	6	14	14	2	0	0	0	0	0		
ENSMUST00000135025						21	0	24	3	29	10	48	770	24	103	183		
ENSMUST00000135026						5	2	11	0	2	0	3	28	0	0	2		
ENSMUST00000135027						1	1	1	3	2	3	5	1	10	0	9		
ENSMUST00000135028	ENSMUSG00000036555	5	140661827	140702378	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JG25	
ENSMUST00000135029	ENSMUSG00000025420	18	76977148	77047308	-1	3	4	0	3	4	0	0	0	0	0	5	D6RGM7	
ENSMUST00000135031	ENSMUSG00000038298	3	96829284	96870926	1	2	0	1	0	0	3	0	0	0	0	0	D3YW13	
ENSMUST00000135032						0	2	0	0	1	0	0	25	0	1	15		
ENSMUST00000135034						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135035	ENSMUSG00000030839	7	46443168	46639807	-1	0	0	0	65	9	0	0	0	0	0	0	D3Z5A9	
ENSMUST00000135036						2	2	2	1	3	2	8	34	11	0	18		
ENSMUST00000135038	ENSMUSG00000031304	X	101264378	101268255	-1	1	1	0	0	0	0	24	121	32	5	14	B0QZX1	
ENSMUST00000135039						5	8	6	3	6	1	3	2	4	0	11		
ENSMUST00000135040						0	4	14	0	0	0	11	4	3	24	7		
ENSMUST00000135041						0	0	0	0	0	0	50	657	126	0	0		
ENSMUST00000135043	ENSMUSG00000028020	3	80843599	80913660	-1	2	2	0	3	5	0	0	0	0	0	0	E9Q9K1	
ENSMUST00000135044						4	4	10	3	1	1	2	13	20	12	8		
ENSMUST00000135045						0	1	0	3	5	0	3	24	21	8	20		
ENSMUST00000135046						1	2	0	6	4	3	0	0	0	0	0		
ENSMUST00000135047	ENSMUSG00000042292	15	81012281	81190757	-1	14	8	40	18	11	9	843	311	1080	21	715	D3YUG5	
ENSMUST00000135049						118	86	195	509	151	128	44	113	55	6	83		
ENSMUST00000135050						19	0	0	2	8	5	3	14	6	0	0		
ENSMUST00000135051						0	3	4	2	5	0	27	44	37	0	49		
ENSMUST00000135052						0	0	0	0	0	0	44	83	165	103	44		
ENSMUST00000135053	ENSMUSG00000030534	7	80269649	80291754	1	113	0	507	0	72	52	0	0	48	14	0	S4R227	
ENSMUST00000135054	ENSMUSG00000039048	9	35204206	35211055	-1	0	0	0	0	0	0	0	24	8	0	8	F6UAF9	
ENSMUST00000135055	ENSMUSG00000028798	4	129591960	129600648	-1	0	0	0	0	0	0	6	0	0	8	13	A2AE03	
ENSMUST00000135056	ENSMUSG00000026490	1	179960472	180165603	1	0	0	2	0	3	0	7	0	1	0	0	F6YZJ7	
ENSMUST00000135057	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	0	0	0	0	0	0	0	0	D3Z6P4	
ENSMUST00000135058						0	1	1	1	0	1	4	3	0	9	0		
ENSMUST00000135059						1	1	1	3	2	1	0	0	0	0	1		
ENSMUST00000135060						2	0	0	1	1	3	6	7	14	11	39		
ENSMUST00000135061						0	1	4	1	0	0	0	0	0	8	10		
ENSMUST00000135062						0	0	7	0	0	0	11	0	1	0	0		
ENSMUST00000135063						0	0	12	3	2	3	0	28	0	3	13		
ENSMUST00000135064						0	1	1	0	0	2	0	0	0	0	0		
ENSMUST00000135065	ENSMUSG00000059923	11	115644045	115708597	-1	2	0	0	2	4	1	360	236	386	11	241	B1AT95	
ENSMUST00000135066						0	1	0	0	1	3	0	0	0	0	0		
ENSMUST00000135067	ENSMUSG00000036002	4	43032414	43046220	-1	14	0	0	47	31	4	0	71	48	0	0	E9Q9G4	
ENSMUST00000135069						8	7	19	20	10	1	0	0	0	1	0		
ENSMUST00000135070	ENSMUSG00000001750	19	3896050	3907133	-1	0	0	6	0	0	10	0	0	14	0	0	D6RFN1	
ENSMUST00000135071	ENSMUSG00000020131	10	80321283	80329498	-1	3	0	9	126	5	6	0	0	0	0	0	M0QW95	
ENSMUST00000135072	ENSMUSG00000068290	2	130653960	130664659	-1	1	2	2	2	2	6	8	9	7	0	4	B0R015	
ENSMUST00000135073	ENSMUSG00000081534	15	97784355	97792692	1	0	1	12	18	1	2	0	0	2	0	2	D6RG96	
ENSMUST00000135074	ENSMUSG00000062646	2	120403896	120461700	1	17	6	39	26	20	12	66	357	95	16	106	A2AQJ8	
ENSMUST00000135075	ENSMUSG00000025959	1	64029447	64122282	-1	7	3	7	45	5	9	0	0	14	9	14	A2AAB6	
ENSMUST00000135076	ENSMUSG00000020389	11	52004221	52089784	1	0	0	0	0	0	0	0	0	6	3	2	B1AU42	
ENSMUST00000135077						443	448	768	194	337	93	4	2	4	0	16		
ENSMUST00000135078	ENSMUSG00000003534	17	35681567	35704621	-1	4	2	9	13	4	4	0	0	0	0	0	F7BZR8	
ENSMUST00000135079	ENSMUSG00000027248	2	121413775	121438687	1	0	0	0	0	0	0	172	396	271	41	184	F6Q404	
ENSMUST00000135080	ENSMUSG00000022469	15	97744770	97767972	-1	0	0	0	36	0	0	0	0	0	1	0	D3Z514	
ENSMUST00000135081						2	0	0	2	3	0	0	12	0	0	4		
ENSMUST00000135083						0	0	0	38	2	3	0	0	0	0	0		
ENSMUST00000135084						1	0	0	6	2	0	0	21	2	0	0		
ENSMUST00000135087	ENSMUSG00000030707	7	126699773	126707787	-1	5	4	2	58	3	0	125	172	106	21	136	D3YXM2	
ENSMUST00000135088	ENSMUSG00000076432	12	21390071	21417637	-1	6	11	9	65	0	0	0	101	0	0	0	F6VW30	
ENSMUST00000135089						10	5	54	18	14	4	2	10	2	0	13		
ENSMUST00000135090						3	5	6	7	8	1	13	47	57	8	108		
ENSMUST00000135091	ENSMUSG00000051319	2	127791388	127792488	-1	8	3	16	85	11	7	12	37	4	232	21		Q8BT35
ENSMUST00000135092						7	2	4	8	5	5	0	0	2	0	2		
ENSMUST00000135093	ENSMUSG00000005982	16	3872375	3904780	1	3	5	0	0	3	1	22	61	17	0	18	D6RDS3	
ENSMUST00000135094						1	1	2	0	0	0	11	39	17	4	21		
ENSMUST00000135095						0	0	0	11	0	0	0	0	0	0	0		
ENSMUST00000135096	ENSMUSG00000021763	13	113317084	113379711	1	4	6	2	7	3	5	0	0	0	0	0	F6Z6Y0	
ENSMUST00000135097						0	0	0	0	0	0	7	8	4	4	0		
ENSMUST00000135098						8	12	32	10	9	7	0	4	3	2	4		
ENSMUST00000135099						4	7	6	40	13	2	5	16	3	0	12		
ENSMUST00000135100						2	0	0	0	1	0	70	6	48	0	46		
ENSMUST00000135101						7	12	22	77	10	18	2	7	12	3	10		
ENSMUST00000135102						2	0	4	0	1	0	0	1	0	1	0		
ENSMUST00000135103						6	8	17	14	13	7	88	316	109	6	209		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135104						4	0	11	2	0	3	0	0	0	0	0		
ENSMUST00000135105						1	2	10	1	6	4	0	5	10	4	8		
ENSMUST00000135106	ENSMUSG00000020227	10	120141648	120202130	-1	4	0	4	0	0	7	51	8	243	55	303	D6RCU1	
ENSMUST00000135107	ENSMUSG00000045179	X	60891366	60893430	-1	3	3	3	159	9	2	0	0	0	0	0	A2AM37	
ENSMUST00000135108	ENSMUSG00000049606	5	106616739	106697287	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z3E3	
ENSMUST00000135109						0	0	0	16	0	0	0	0	0	0	0		
ENSMUST00000135111						1	6	13	4	4	2	0	0	0	1	0		
ENSMUST00000135112	ENSMUSG00000034826	5	92415540	92435219	-1	0	0	0	4	0	0	0	0	3	0	1	D3Z5F5	
ENSMUST00000135113						6	0	6	2	1	0	0	0	0	0	0		
ENSMUST00000135117						2	0	0	7	2	3	63	4	33	0	13		
ENSMUST00000135119						26	10	74	814	39	30	11	66	121	0	62		
ENSMUST00000135120						1	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000135121						4	1	17	0	5	2	0	0	0	0	3		
ENSMUST00000135123	ENSMUSG00000024007	17	29250803	29264158	-1	6	1	29	4	5	3	0	0	0	0	15	F6SSV9	
ENSMUST00000135124	ENSMUSG00000020456	11	6291633	6356642	1	0	0	2	11	1	1	2	4	9	0	3	Q5SVY1	
ENSMUST00000135125						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135126						0	0	0	0	0	0	0	14	19	24	5		
ENSMUST00000135127	ENSMUSG00000023191	6	124841089	124857752	-1	21	0	0	28	20	9	0	0	0	0	0	D6RHQ3	
ENSMUST00000135128						15	9	28	0	10	9	127	103	149	60	76		
ENSMUST00000135129	ENSMUSG00000030752	7	125444676	125462269	1	0	0	0	0	0	0	8	3	0	0	0	D3YUV8	
ENSMUST00000135130	ENSMUSG00000012640	7	43296197	43313294	-1	0	0	0	0	0	0	0	2	0	25	16	D3Z3C8	
ENSMUST00000135131	ENSMUSG00000037904	12	110975353	110979040	-1	0	0	0	0	0	0	0	16	18	0	0		Q8BH83
ENSMUST00000135133						6	0	15	15	6	6	0	0	0	0	0		
ENSMUST00000135134						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135135						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135136						7	0	0	67	5	3	9	54	9	17	0		
ENSMUST00000135137						4	1	12	11	0	1	17	19	29	6	55		
ENSMUST00000135139						0	0	4	1	1	0	0	0	0	0	0		
ENSMUST00000135140	ENSMUSG00000026171	1	74593748	74601397	-1	18	4	0	0	14	3	0	265	0	15	30	M0QWW2	
ENSMUST00000135141	ENSMUSG00000020902	11	68209364	68400823	-1	0	0	0	72	0	2	0	0	0	0	0	B0QZL0	
ENSMUST00000135142	ENSMUSG00000090206	8	95310566	95326323	1	0	2	3	0	2	0	0	0	0	0	1	D3YY82	
ENSMUST00000135146	ENSMUSG00000029319	5	100654723	100675140	-1	0	0	0	0	0	2	0	0	0	0	0	F7CDY3	
ENSMUST00000135148	ENSMUSG00000018921	11	70392883	70410031	-1	0	1	0	148	0	0	0	0	0	0	0	Q9D4T3	
ENSMUST00000135149	ENSMUSG00000027318	2	131050591	131063814	-1	0	0	0	0	0	0	0	0	0	0	0	F7CIM2	
ENSMUST00000135150	ENSMUSG00000013973	1	171329145	171342331	1	0	2	2	3	0	1	0	1	0	0	4	D3YZI2	
ENSMUST00000135151	ENSMUSG00000052751	6	48593883	48599082	1	0	0	0	0	0	1	4	0	0	0	0	D3YY67	
ENSMUST00000135152						2	1	4	2	3	2	1	0	2	0	1		
ENSMUST00000135154						4	1	7	4	0	1	0	4	0	1	6		
ENSMUST00000135155						0	0	0	20	0	0	0	2	0	0	2		
ENSMUST00000135156						7	4	4	6	0	2	0	0	0	0	0		
ENSMUST00000135157						3	1	6	1	4	2	0	0	0	0	2		
ENSMUST00000135158	ENSMUSG00000057337	10	60181532	60219260	-1	66	39	68	747	101	51	0	14	42	0	0	G5E8X5	
ENSMUST00000135159	ENSMUSG00000038664	9	66350450	66508775	1	5	6	23	1	9	1	0	13	68	0	78	F6RXM1	
ENSMUST00000135160						0	0	1	3	1	1	1	0	3	0	2		
ENSMUST00000135161	ENSMUSG00000025350	10	128913593	128922888	-1	2	0	1	1	6	2	0	15	6	13	2	D3YWG0	
ENSMUST00000135162						4	3	23	85	7	2	20	22	24	1	22		
ENSMUST00000135163	ENSMUSG00000029388	5	124570213	124579131	-1	1	6	1	16	0	1	0	0	0	0	0	D6RI38	
ENSMUST00000135164						2	2	6	8	9	0	10	19	7	0	4		
ENSMUST00000135165	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	1	0	0	0	0	0	0	A3KG41	
ENSMUST00000135166	ENSMUSG00000057554	13	12439415	12464944	-1	0	0	0	0	0	0	0	471	1	50	0	Q8C6H0	
ENSMUST00000135167						1	1	3	0	1	0	2	10	2	0	0		
ENSMUST00000135168						4	2	8	5	3	1	0	0	0	0	0		
ENSMUST00000135169	ENSMUSG00000028965	4	150914562	150946102	1	3	5	1	21	1	2	0	0	0	0	0	A2A887	
ENSMUST00000135170						0	3	0	0	0	5	3	0	0	0	0		
ENSMUST00000135171						5	0	5	0	5	0	7	34	1	3	3		
ENSMUST00000135172						0	2	1	0	1	0	0	0	2	0	0		
ENSMUST00000135173	ENSMUSG00000022272	15	25622525	25813673	1	0	2	0	1	0	0	0	0	0	0	0	D3YZ13	
ENSMUST00000135174						5	3	1	2	5	0	3	2	0	0	0		
ENSMUST00000135175						8	6	17	7	2	2	0	0	0	0	0		
ENSMUST00000135176						2	3	3	6	2	0	0	0	1	0	0		
ENSMUST00000135177						4	2	11	28	0	2	0	0	0	0	0		
ENSMUST00000135179						0	0	1	20	3	0	0	0	2	13	0		
ENSMUST00000135181						0	1	0	2	2	0	5	21	0	5	4		
ENSMUST00000135182	ENSMUSG00000074139	9	92309377	92357876	1	5	6	2	2	1	2	0	0	0	0	0	A0A087WRL7	
ENSMUST00000135184	ENSMUSG00000000386	16	97447035	97462907	-1	136	95	249	115	170	78	9	40	16	12	38	V9GWS9	
ENSMUST00000135185	ENSMUSG00000028943	4	152120331	152152371	-1	0	4	0	0	0	0	0	0	0	1	0	B1AWQ1	
ENSMUST00000135187						0	0	0	0	0	0	1	0	0	2	6		
ENSMUST00000135188						1	0	8	17	1	0	4	311	19	48	35		
ENSMUST00000135189						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135191						7	3	8	3	8	4	10	103	34	4	72		
ENSMUST00000135192	ENSMUSG00000026553	1	172082529	172122330	1	7	13	25	31	14	0	849	1181	1753	175	1148		Q8CIE6
ENSMUST00000135193	ENSMUSG00000022801	16	32914100	33015647	1	9	3	12	4	3	0	0	10	30	0	40	E9QAU9	
ENSMUST00000135194						4	5	4	9	2	4	52	764	168	36	125		
ENSMUST00000135195						5	0	8	1	4	3	24	92	83	22	142		
ENSMUST00000135196	ENSMUSG00000015869	11	116470845	116494202	-1	0	0	0	78	0	0	6	3	9	0	0	B1AT83	
ENSMUST00000135197	ENSMUSG00000094638	1	86133637	86162788	1	0	0	4	34	6	12	0	6	0	3	0	J3QN38	
ENSMUST00000135198						1	4	0	4	3	0	0	0	0	0	0		
ENSMUST00000135199						34	29	170	45	32	18	0	0	0	0	0		
ENSMUST00000135200	ENSMUSG00000026950	2	52136647	52338798	-1	0	0	0	3	0	0	3	8	3	8	23	F6X9B6	
ENSMUST00000135201						4	1	4	6	5	1	0	58	44	0	36		
ENSMUST00000135202	ENSMUSG00000005950	11	73160421	73172685	1	2	0	0	9	0	0	0	0	0	0	0	B1AUD6	
ENSMUST00000135204						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000135205						2	0	1	1	1	0	2	0	4	0	13		
ENSMUST00000135206						34	24	67	48	33	18	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135207						0	3	0	3	0	1	27	35	17	92	41		
ENSMUST00000135208						87	65	169	131	93	55	3	12	8	1	11		
ENSMUST00000135209						1	1	3	3	5	2	49	206	123	7	169		
ENSMUST00000135210						3	1	3	0	2	1	1	0	0	0	0		
ENSMUST00000135211	ENSMUSG00000034771	10	81574561	81590845	1	0	0	0	0	0	0	0	0	0	0	0	Q3UN01	
ENSMUST00000135212						2	11	0	1	2	0	0	0	0	0	0		
ENSMUST00000135213						1	0	0	7	2	1	0	0	0	0	5		
ENSMUST00000135214						0	1	2	74	7	0	0	0	2	0	0		
ENSMUST00000135215						0	0	0	0	0	0	2	5	1	0	0		
ENSMUST00000135216	ENSMUSG00000035969	4	43381979	43427088	1	5	8	20	0	0	3	0	0	0	0	0	B0R002	
ENSMUST00000135217	ENSMUSG00000057246	17	34398820	34460734	1	0	0	0	0	0	0	0	0	0	0	0	A6X8K8	
ENSMUST00000135218	ENSMUSG00000032498	9	111228228	111271791	-1	14	9	12	23	24	10	0	5	0	0	10	A0A0G2JH14	
ENSMUST00000135219						0	0	0	0	0	0	12	0	0	2	0		
ENSMUST00000135220						1	1	7	23	0	2	0	0	0	0	0		
ENSMUST00000135221	ENSMUSG00000002319	14	55625400	55637895	-1	0	8	0	89	0	21	0	0	20	0	101	Q5U4C5	
ENSMUST00000135222	ENSMUSG00000070644	1	133363572	133380336	1	9	5	5	156	9	4	0	0	0	0	0		A7MCT6
ENSMUST00000135223	ENSMUSG00000020454	11	3202392	3244588	1	0	0	0	0	0	0	0	12	0	0	10	Q5NBZ4	
ENSMUST00000135224	ENSMUSG00000047230	X	139800828	139811386	1	5	4	1	3	3	0	0	0	0	0	0	A3KGB5	
ENSMUST00000135225	ENSMUSG00000062234	5	108569411	108629755	-1	0	0	0	116	4	12	0	0	0	0	0	D6RHK5	
ENSMUST00000135226						0	0	0	0	0	0	52	11	58	0	41		
ENSMUST00000135227						16	9	32	35	1	4	0	0	0	0	7		
ENSMUST00000135229						49	25	69	28	56	28	61	100	58	0	60		
ENSMUST00000135230						0	0	0	13	0	1	11	13	52	45	21		
ENSMUST00000135231	ENSMUSG00000025793	11	120467635	120483984	1	5	2	0	0	1	3	0	0	17	0	2	F6VV02	
ENSMUST00000135232	ENSMUSG00000025873	13	54621784	54664068	1	0	0	0	0	0	2	5	0	0	17	0	D3YUP4	
ENSMUST00000135233	ENSMUSG00000026842	2	31688376	31804227	1	7	9	5	9	11	10	8	2	2	0	8	A0A0A6YVY6	
ENSMUST00000135234						4	0	24	1	3	1	29	68	21	1	31		
ENSMUST00000135235						43	44	24	41	57	29	2	3	8	4	7		
ENSMUST00000135236						0	0	4	0	4	1	0	0	0	0	0		
ENSMUST00000135237						0	0	3	2	0	0	0	0	0	0	0		
ENSMUST00000135239						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135240						12	13	11	37	9	9	0	0	1	0	4		
ENSMUST00000135241	ENSMUSG00000026696	1	162570515	162599084	1	0	0	0	0	3	0	330	1000	396	272	184		O70480
ENSMUST00000135242	ENSMUSG00000019843	10	39368855	39565381	1	0	13	20	2	0	0	29	74	71	0	134		P39688
ENSMUST00000135243						28	19	80	38	33	12	251	1532	737	67	1169		
ENSMUST00000135245	ENSMUSG00000086727	1	31135226	31222684	-1	1	3	2	8	1	0	0	0	0	0	0	Q9D4S9	
ENSMUST00000135246	ENSMUSG00000026098	1	53189187	53297018	-1	0	0	5	0	3	0	2	0	0	14	0	E9Q8A5	
ENSMUST00000135247						0	0	0	0	0	0	0	0	5	0	0		
ENSMUST00000135248	ENSMUSG00000023452	5	32736301	32785646	-1	2	0	10	5	3	0	95	72	65	9	41	D3Z0X7	
ENSMUST00000135249						0	0	3	109	0	0	29	74	47	13	37		
ENSMUST00000135250						153	80	188	1000	195	103	1	0	3	2	3		
ENSMUST00000135251	ENSMUSG00000039285	9	118040499	118069794	1	2	0	2	4	1	0	3	0	38	9	42	D3Z7S3	
ENSMUST00000135252	ENSMUSG00000040473	5	5579278	5664239	-1	0	0	0	0	1	0	0	0	0	0	0	F6ZXD8	Q8BH53
ENSMUST00000135253	ENSMUSG00000025728	17	25926427	25944510	-1	0	0	2	0	2	0	0	0	0	0	4	F7BU94	
ENSMUST00000135254						4	3	13	8	10	6	0	0	0	0	0		
ENSMUST00000135255						0	3	3	4	4	2	0	0	0	0	1		
ENSMUST00000135258						7	5	5	8	6	4	626	1305	363	191	176		
ENSMUST00000135259	ENSMUSG00000041319	17	23668614	23673882	-1	10	4	6	1	12	7	0	0	0	0	0	F6S2T7	
ENSMUST00000135260						0	0	15	7	8	10	6	63	26	27	0		
ENSMUST00000135261						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135263						0	2	8	0	0	0	7	2	0	2	5		
ENSMUST00000135264						0	4	5	0	10	4	117	205	211	17	272		
ENSMUST00000135265						0	0	0	17	0	0	0	0	0	0	0		
ENSMUST00000135266	ENSMUSG00000027787	3	69721985	69756373	1	0	0	0	0	2	0	0	0	4	5	0	A0A0A6YY59	
ENSMUST00000135267	ENSMUSG00000037995	1	172481788	172498878	1	0	0	3	7	3	0	0	0	0	0	0	D3Z7T6	
ENSMUST00000135269	ENSMUSG00000031601	8	40492540	40515847	-1	0	0	0	0	0	0	0	0	15	0	0	Q3TLK9	
ENSMUST00000135270	ENSMUSG00000035623	7	97579889	97692778	1	2	0	0	1	0	0	1	6	22	10	13		
ENSMUST00000135271						2	2	10	8	10	5	0	0	0	0	0		
ENSMUST00000135272						5	6	17	5	9	5	3	8	5	0	16		
ENSMUST00000135273						5	6	19	4	3	1	0	0	1	0	0		
ENSMUST00000135274						1	0	0	1	2	3	0	5	0	2	2		
ENSMUST00000135275	ENSMUSG00000021699	13	108449948	109953461	1	0	1	0	0	3	1	0	0	0	0	0	B2KF57	
ENSMUST00000135276						6	3	11	17	9	3	0	0	0	0	0		
ENSMUST00000135277						0	1	0	0	0	1	22	210	51	18	45		
ENSMUST00000135278	ENSMUSG00000021377	13	47084775	47106201	-1	0	0	0	32	0	0	0	0	0	41	0	E9Q8Y1	
ENSMUST00000135279	ENSMUSG00000021848	14	48657679	48667644	-1	5	1	12	3	0	0	0	0	0	0	0	D3YUN4	
ENSMUST00000135280	ENSMUSG00000022901	16	36603869	36666081	-1	3	1	10	3	2	0	2	0	2	14	0	D3Z363	
ENSMUST00000135281						1	1	6	13	3	1	0	0	0	0	0		
ENSMUST00000135282						0	1	0	7	0	1	0	0	0	2	0		
ENSMUST00000135283						10	5	8	28	3	3	0	0	0	0	0		
ENSMUST00000135284						2	3	3	2	1	1	0	0	0	0	0		
ENSMUST00000135285						0	0	0	0	0	0	7	20	4	0	14		
ENSMUST00000135287						0	0	0	0	3	0	6	0	0	0	0		
ENSMUST00000135288						0	3	13	3	7	2	0	0	0	0	0		
ENSMUST00000135289						0	0	5	0	0	0	0	3	0	0	2		
ENSMUST00000135290						0	0	1	73	4	1	0	0	0	0	0		
ENSMUST00000135292	ENSMUSG00000020022	10	94198955	94221443	1	0	0	0	0	0	0	0	1	0	0	0	F6RBR6	
ENSMUST00000135293						4	1	8	6	10	0	0	0	0	0	0		
ENSMUST00000135294						7	5	35	6	5	3	4	4	3	1	11		
ENSMUST00000135295						4	0	0	140	0	0	0	0	0	0	0		
ENSMUST00000135296						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000135298	ENSMUSG00000039585	9	59750896	59928866	1	0	0	74	0	0	18	0	87	122	0	158		Q8C170
ENSMUST00000135299	ENSMUSG00000028886	4	132638987	132724765	1	1	4	8	67	8	0	21	12	25	0	17	A2A953	
ENSMUST00000135300						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135301						0	0	0	55	0	0	0	0	0	0	0		
ENSMUST00000135302	ENSMUSG00000033624	8	111094630	111137074	1	0	0	0	66	0	0	2	2	5	0	5	D3Z443	
ENSMUST00000135303						2	0	2	2	1	0	4	0	3	2	0		
ENSMUST00000135304	ENSMUSG00000038836	6	34780432	34859459	1	1	0	2	7	3	4	0	2	5	2	0	D6RI59	
ENSMUST00000135305						23	22	92	27	26	11	3	11	0	2	0		
ENSMUST00000135306	ENSMUSG00000030530	7	80388585	80405436	-1	2	0	4	3	1	0	0	0	0	0	0	D3Z401	
ENSMUST00000135307						0	3	7	0	0	0	0	0	0	0	0		
ENSMUST00000135308						0	0	0	1	0	0	16	41	20	2	13		
ENSMUST00000135309	ENSMUSG00000061894	4	128583539	128610098	-1	0	0	7	0	23	7	5	3	13	1	2	E9Q8Y3	
ENSMUST00000135310	ENSMUSG00000036986	9	58218076	58249786	-1	0	0	0	0	0	0	25	53	0	0	0	D3Z3A6	
ENSMUST00000135311						1	0	0	0	0	0	0	13	0	0	3		
ENSMUST00000135312						9	0	3	25	5	13	181	920	235	88	849		
ENSMUST00000135314						9	1	6	3	3	3	6	9	13	0	17		
ENSMUST00000135315						6	0	4	0	8	1	0	0	0	0	0		
ENSMUST00000135316						2	2	1	0	2	1	0	0	0	0	0		
ENSMUST00000135317	ENSMUSG00000037012	10	62268855	62379908	-1	1	0	8	1	0	0	0	0	0	0	0	B4YB29	
ENSMUST00000135318	ENSMUSG00000072889	5	72513301	72559684	-1	2	1	12	0	2	0	0	63	0	0	2	E9PZN0	
ENSMUST00000135319						4	5	15	12	8	10	1	21	2	0	10		
ENSMUST00000135320						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000135321	ENSMUSG00000029106	5	34573664	34632308	1	0	0	0	0	0	0	0	0	12	0	0	F6V4G5	
ENSMUST00000135322						3	4	5	1	3	0	0	0	0	0	0		
ENSMUST00000135323	ENSMUSG00000028433	4	41194313	41275144	-1	3	3	24	9	0	0	0	0	0	0	0	A2AMY7	
ENSMUST00000135324	ENSMUSG00000029093	5	36017180	36398139	-1	3	0	0	0	3	0	0	0	0	0	0	D3YYF4	
ENSMUST00000135325						17	1	31	48	8	0	0	0	0	0	0		
ENSMUST00000135326	ENSMUSG00000031537	8	22659212	22706589	-1	2	0	0	3	14	0	14	203	46	15	154	Q3U141	
ENSMUST00000135327	ENSMUSG00000055491	19	46044886	46072915	1	0	0	0	0	0	0	2	0	0	0	1	D3Z1R3	
ENSMUST00000135328						2	1	0	10	4	0	6	18	8	0	22		
ENSMUST00000135330						7	2	0	4	5	2	3	5	0	0	2		
ENSMUST00000135331						0	0	0	0	0	0	6	0	10	41	20		
ENSMUST00000135332						2	0	0	0	3	0	7	3	6	0	0		
ENSMUST00000135333						277	283	697	224	276	112	15	62	22	15	46		
ENSMUST00000135334						64	37	19	20	21	8	0	0	0	0	2		
ENSMUST00000135335						47	24	52	41	50	0	0	0	0	0	0		
ENSMUST00000135336	ENSMUSG00000031626	8	45507788	45827906	1	12	0	0	0	4	0	0	0	0	0	0	E9Q0B0	
ENSMUST00000135337	ENSMUSG00000038215	8	56531522	56551047	-1	0	1	0	0	1	0	3	10	0	11	8	D3Z3B7	
ENSMUST00000135338	ENSMUSG00000086596	9	114057354	114098733	1	38	18	82	104	50	23	0	0	1	1	0	G3UW60	
ENSMUST00000135339	ENSMUSG00000026975	2	24962400	24972163	1	1	2	0	0	0	0	0	0	0	0	0	A0A0A6YY79	
ENSMUST00000135340						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000135341	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	0	11	0	42	100	70	Q501M1	Q60819
ENSMUST00000135342						0	0	2	0	0	0	5	11	3	1	5		
ENSMUST00000135343	ENSMUSG00000069227	13	54736671	54749874	-1	0	0	0	190	0	6	0	0	0	0	0		Q3UNH4
ENSMUST00000135344						0	0	0	0	0	0	16	7	0	0	0		
ENSMUST00000135345						3	4	33	1	5	2	9	61	18	155	17		
ENSMUST00000135346	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	32	5	4	38	15	15	0	22	A2AC03	
ENSMUST00000135349						0	1	0	0	4	4	0	0	0	0	0		
ENSMUST00000135350	ENSMUSG00000020159	11	33550781	33578959	-1	0	0	6	1	1	0	0	0	0	0	0	A8Y5I7	
ENSMUST00000135351						2	0	0	0	0	0	6	61	21	302	62		
ENSMUST00000135352						27	9	31	37	29	17	26	131	61	18	86		
ENSMUST00000135353						8	7	11	9	17	3	11	13	17	0	29		
ENSMUST00000135354						2	1	14	6	6	8	0	1	0	0	1		
ENSMUST00000135355						0	3	0	6	2	0	2	7	0	0	3		
ENSMUST00000135356						13	13	91	44	20	8	27	45	63	0	101		
ENSMUST00000135357	ENSMUSG00000041966	2	71055328	71099142	1	0	0	0	10	0	0	0	0	4	0	0	B0R0U2	
ENSMUST00000135359						0	2	0	0	1	2	0	4	3	2	2		
ENSMUST00000135361	ENSMUSG00000029388	5	124570213	124579131	-1	0	1	0	4	0	0	2	7	7	0	5	D3Z151	
ENSMUST00000135362						0	1	2	0	2	0	0	0	0	1	0		
ENSMUST00000135364	ENSMUSG00000026634	1	190925112	190946962	1	0	0	0	0	0	0	13	5	46	2	11	F6SBQ6	
ENSMUST00000135365	ENSMUSG00000098789	2	120027483	120032594	1	10	0	4	88	7	0	0	0	0	0	0	D6RGQ7	
ENSMUST00000135367						3	1	3	0	2	0	2	6	11	4	13		
ENSMUST00000135368	ENSMUSG00000003573	8	70282827	70294361	1	0	0	0	57	0	0	0	0	0	0	0	J3QQ00	
ENSMUST00000135369						0	0	2	0	6	2	0	3	2	0	1		
ENSMUST00000135370						1	3	1	0	2	0	3	10	1	1	3		
ENSMUST00000135371						4133	4483	6184	3793	5085	2404	64	428	149	100	213		
ENSMUST00000135372						1	0	2	0	1	0	3	17	7	1	17		
ENSMUST00000135373	ENSMUSG00000039620	8	36457548	36514320	1	7	3	11	133	10	4	0	0	0	0	0	D3YYA2	
ENSMUST00000135374						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135375	ENSMUSG00000000631	11	77763246	77865980	1	2	2	13	53	6	5	0	0	0	1	1	F6ZGN3	
ENSMUST00000135376						29	39	54	25	42	25	2	9	0	0	0		
ENSMUST00000135377						17	19	67	183	26	22	4	2	2	1	6		
ENSMUST00000135379						1	0	2	15	2	0	0	0	95	242	149		
ENSMUST00000135380						0	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000135381						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000135382						4	2	16	6	14	2	1	5	0	0	2		
ENSMUST00000135383	ENSMUSG00000033857	11	118476829	118489209	1	0	0	0	51	0	0	0	21	0	6	21		Q8BX80
ENSMUST00000135384						0	2	5	4	2	0	0	9	0	0	11		
ENSMUST00000135386	ENSMUSG00000038147	1	171839697	171890718	1	30	14	192	65	30	9	154	174	418	17	656		
ENSMUST00000135387						116	168	108	61	94	42	11	7	11	7	24		
ENSMUST00000135388						2	4	12	10	5	3	29	6	19	0	10		
ENSMUST00000135389						2	0	2	0	2	0	0	0	4	2	3		
ENSMUST00000135390	ENSMUSG00000020831	11	70235206	70237914	-1	6	1	6	2	2	0	3	22	0	0	6	H3BJI0	
ENSMUST00000135392						5	0	7	0	4	0	0	0	0	0	0		
ENSMUST00000135393						3	5	9	8	7	1	0	0	0	0	0		
ENSMUST00000135394						3	0	0	1	2	6	5	3	0	5	0		
ENSMUST00000135395	ENSMUSG00000032249	9	62341293	62378812	1	4	2	28	19	10	3	138	345	162	393	200	D3Z7M9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135396						10	12	23	0	4	6	0	0	0	0	0		
ENSMUST00000135397	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	2	3	0	2	36	71	5	8	49	F6Z9V3	
ENSMUST00000135398						23	0	30	0	20	8	0	0	0	0	1		
ENSMUST00000135399						34	19	100	27	36	15	8	41	26	14	28		
ENSMUST00000135400						3	8	11	2	2	2	0	6	1	0	1		
ENSMUST00000135402	ENSMUSG00000084957	19	53929677	53944627	-1	23	28	38	65	29	14	302	1912	440	1278	281	J3QMK2	
ENSMUST00000135403						6	3	5	7	6	7	0	0	0	0	0		
ENSMUST00000135404						2	0	0	79	2	0	0	0	0	0	0		
ENSMUST00000135405						4	3	1	16	5	3	0	0	0	0	0		
ENSMUST00000135406	ENSMUSG00000034243	16	36875140	36933085	1	3	4	9	55	4	5	12	2	13	0	21	E9Q028	
ENSMUST00000135407						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135408						3	4	1	5	3	0	0	0	0	0	0		
ENSMUST00000135409	ENSMUSG00000033434	5	110103975	110108197	-1	0	0	4	88	2	0	7	34	12	6	10	D3YW02	
ENSMUST00000135410						4	0	1	2	1	0	3	3	0	1	0		
ENSMUST00000135411						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000135412						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135413						5	0	7	4	3	0	0	0	0	0	0		
ENSMUST00000135414						7	0	14	0	0	0	0	0	12	2	13		
ENSMUST00000135415						0	0	0	0	63	0	0	0	0	0	0		
ENSMUST00000135416						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135417						1	5	12	4	5	4	19	119	8	28	16		
ENSMUST00000135418						37	20	91	153	56	13	1	14	5	4	10		
ENSMUST00000135419	ENSMUSG00000070730	2	119137001	119157034	-1	0	0	1	0	0	0	0	0	0	0	0	A3KGH7	
ENSMUST00000135420						3	0	0	3	6	1	9	24	7	2	17		
ENSMUST00000135422						1	0	6	10	9	6	0	0	3	0	5		
ENSMUST00000135424						3	2	3	0	3	2	17	51	0	0	0		
ENSMUST00000135425	ENSMUSG00000024039	17	31612623	31637199	-1	0	0	0	0	0	0	0	0	0	0	0	D3YYN0	
ENSMUST00000135426						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000135428						6	1	5	1	6	3	0	0	0	1	0		
ENSMUST00000135429	ENSMUSG00000029063	4	155562378	155591001	1	1	0	0	29	0	0	21	20	12	0	25	A2A9N9	
ENSMUST00000135430	ENSMUSG00000078894	2	176226569	176240328	1	0	0	0	0	0	0	0	0	0	0	0	A2ARV8	
ENSMUST00000135431	ENSMUSG00000050587	2	96318169	97631666	1	0	4	12	21	5	0	0	0	0	0	0		Q8C031
ENSMUST00000135432	ENSMUSG00000031629	8	46552055	46580007	1	0	4	6	4	5	0	0	30	39	0	17	D6RJ34	
ENSMUST00000135435						3	0	1	5	5	0	0	0	0	1	0		
ENSMUST00000135436	ENSMUSG00000048537	9	44686304	44735198	-1	0	3	0	0	11	0	0	0	0	0	4	E9Q340	
ENSMUST00000135437	ENSMUSG00000018566	11	69942539	69948188	-1	0	0	0	0	0	0	0	0	0	0	0	J3QP46	
ENSMUST00000135439	ENSMUSG00000058056	8	61513246	61902690	-1	0	1	1	2	4	6	35	6	28	4	41	D3Z1J5	
ENSMUST00000135440	ENSMUSG00000026226	1	86016816	86029958	1	4	4	10	1	0	5	0	0	0	0	0	Q6P8X3	
ENSMUST00000135441						7	0	14	0	0	0	0	0	0	0	1		
ENSMUST00000135442	ENSMUSG00000015001	15	65876053	65912397	-1	0	3	0	0	0	4	0	0	0	0	0	F6ZCJ0	
ENSMUST00000135443	ENSMUSG00000039396	8	53586867	53639065	-1	2	2	0	7	2	1	0	0	0	0	0	D3Z1T7	
ENSMUST00000135445						108	85	162	82	124	63	5	22	9	30	12		
ENSMUST00000135446	ENSMUSG00000090137	8	70508263	70510801	-1	18	4	15	0	17	6	30	15	30	13	13	Q66JP1	P62984
ENSMUST00000135447	ENSMUSG00000001870	17	75005568	75392512	1	8	0	11	3	7	0	3	0	2	0	6	B1B1E2	
ENSMUST00000135448	ENSMUSG00000023147	16	96145407	96157852	1	5	2	4	119	6	1	0	0	0	0	0	D3Z1B0	
ENSMUST00000135449						0	5	0	3	2	0	0	10	0	2	4		
ENSMUST00000135450						0	0	1	1	2	0	0	0	0	0	0		
ENSMUST00000135452	ENSMUSG00000030495	7	35186385	35201114	1	0	3	21	48	11	3	0	0	0	0	0	E9Q248	
ENSMUST00000135453						0	3	3	0	0	0	0	17	0	9	4		
ENSMUST00000135454	ENSMUSG00000028608	4	107889813	107899384	1	22	13	35	14	23	13	0	36	2	13	4		Q8BHG2
ENSMUST00000135455	ENSMUSG00000060152	5	115235836	115245351	1	5	3	19	9	7	3	14	100	37	4	33		Q9DB28
ENSMUST00000135456						0	0	1	0	3	0	4	0	4	0	15		
ENSMUST00000135457	ENSMUSG00000032028	9	48318006	48353454	-1	0	0	0	0	0	0	0	6	3	2	2	E9Q4V1	
ENSMUST00000135458						2	0	6	4	1	2	5	10	2	2	6		
ENSMUST00000135459						0	0	0	0	0	0	0	0	1	0	2		
ENSMUST00000135460						2	0	6	3	5	2	0	0	0	0	0		
ENSMUST00000135461						5	5	0	0	12	10	0	0	0	0	0		
ENSMUST00000135462						0	6	1	11	7	0	0	1	0	0	3		
ENSMUST00000135463						7	3	20	45	8	3	4	3	0	2	8		
ENSMUST00000135464	ENSMUSG00000029390	5	124540695	124550506	1	21	13	107	0	0	14	1638	5151	1466	465	900	Q8BPI2	
ENSMUST00000135465	ENSMUSG00000027286	2	120604238	120609520	-1	0	0	0	0	0	0	5	28	48	27	45	B0R031	
ENSMUST00000135466	ENSMUSG00000001288	15	102234938	102257517	-1	9	4	14	60	9	5	0	0	0	3	1	D3YZY4	
ENSMUST00000135467	ENSMUSG00000074358	7	18890883	18910415	-1	0	3	0	0	0	1	0	23	10	0	0	D6RHL6	
ENSMUST00000135469	ENSMUSG00000004085	2	72285637	72442610	1	100	107	684	169	93	53	22	63	31	5	45	Q3TRG2	Q9ESL4
ENSMUST00000135470						17	19	76	18	17	13	5	10	0	0	3		
ENSMUST00000135471						0	0	7	21	0	0	35	34	74	34	95		
ENSMUST00000135472	ENSMUSG00000026835	2	28076378	28084885	-1	3	4	0	2	0	0	0	0	5	4	0	B2FDG6	
ENSMUST00000135473						2	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000135474						7	3	0	6	6	4	0	0	0	0	0		
ENSMUST00000135475						2	4	1	2	3	0	7	32	2	0	14		
ENSMUST00000135477						4	3	4	1	6	3	0	0	0	0	0		
ENSMUST00000135479						2	0	1	1	0	0	0	1	0	0	0		
ENSMUST00000135480						17	14	100	16	25	9	20	12	24	11	25		
ENSMUST00000135481						0	4	10	1	3	2	0	4	0	0	0		
ENSMUST00000135482						3	0	18	12	12	2	0	4	0	0	4		
ENSMUST00000135484						0	0	2	0	0	0	73	444	75	0	102		
ENSMUST00000135486	ENSMUSG00000006216	4	141404353	141416014	-1	0	2	5	0	2	0	0	0	0	0	0	F6RJZ6	
ENSMUST00000135487						13	11	28	17	16	6	7	18	20	2	26		
ENSMUST00000135488						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000135489						1	1	0	4	0	0	9	4	0	0	0		
ENSMUST00000135490	ENSMUSG00000034930	6	83135463	83152579	1	0	1	8	0	4	3	0	0	0	0	0	D3Z7S7	
ENSMUST00000135492						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000135493	ENSMUSG00000030557	7	67231163	67372858	-1	0	0	31	0	7	4	0	0	180	11	211		Q60929
ENSMUST00000135494						0	0	0	0	0	0	4	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135495	ENSMUSG00000037979	5	124834418	124862424	-1	11	16	23	76	22	11	51	9	0	0	25	D6RJ58	
ENSMUST00000135497						4	4	5	2	2	0	0	5	6	6	9		
ENSMUST00000135498						1	0	0	2	1	0	200	322	61	41	68		
ENSMUST00000135499	ENSMUSG00000028689	4	116708509	116751206	1	0	0	0	7	5	0	0	5	4	0	0	A8Y5M6	
ENSMUST00000135500	ENSMUSG00000059070	7	45715457	45720835	1	7	5	8	97	10	7	23	60	37	10	44	G3UZK4	
ENSMUST00000135501	ENSMUSG00000068009	2	153900388	153912795	1	6	1	5	2	8	5	0	0	0	0	0	A6PWW6	
ENSMUST00000135502	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	0	0	0	0	0	0	0	0		P42866
ENSMUST00000135503						0	2	14	108	4	0	0	0	0	0	0		
ENSMUST00000135504	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	0	0	0	0	0	4	0	0	J3JS92	
ENSMUST00000135505	ENSMUSG00000014039	16	97791467	97851850	-1	0	0	13	22	1	3	0	0	0	0	0	D3YYH8	
ENSMUST00000135506						22	26	63	41	49	24	6	18	3	12	15		
ENSMUST00000135507	ENSMUSG00000026848	2	30952959	30959015	1	0	0	0	78	0	0	3	0	0	2	3	D6REF0	
ENSMUST00000135508						0	0	0	0	0	0	0	37	0	0	0		
ENSMUST00000135509	ENSMUSG00000015980	7	139212988	139242979	1	0	1	0	0	0	0	5	16	5	1	4	D3Z3I5	
ENSMUST00000135510	ENSMUSG00000038187	7	113315626	113369392	-1	5	0	0	0	0	0	0	154	0	28	0	D6RDQ7	
ENSMUST00000135511						3	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000135513						2	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000135514	ENSMUSG00000032519	9	120110374	120124504	1	1	2	6	2	2	0	0	0	4	0	0	D3Z284	
ENSMUST00000135515						0	7	23	5	12	0	0	12	12	0	0		
ENSMUST00000135516						0	0	0	25	3	9	0	0	0	0	0		
ENSMUST00000135517						5	4	25	7	0	2	23	51	17	0	54		
ENSMUST00000135518	ENSMUSG00000033569	1	25067476	25829707	-1	0	0	0	0	0	0	0	0	0	0	0		Q80ZF8
ENSMUST00000135519	ENSMUSG00000022433	15	79417856	79443919	-1	0	0	0	0	0	0	0	0	0	0	0	A8Y2Z5	
ENSMUST00000135520						3	0	0	2	3	0	0	0	0	0	0		
ENSMUST00000135521						3	5	0	15	0	2	5	0	6	0	0		
ENSMUST00000135522						30	24	48	54	33	26	0	0	1	0	1		
ENSMUST00000135523						20	0	42	118	43	8	3	7	1	0	4		
ENSMUST00000135524						13	13	11	13	9	10	0	0	0	0	0		
ENSMUST00000135525						1	2	0	0	0	0	4	17	38	5	20		
ENSMUST00000135526	ENSMUSG00000037990	10	58813359	59138916	1	0	5	2	166	8	5	0	0	0	0	0		Q8C120
ENSMUST00000135528						24	15	87	33	33	24	2	3	8	2	5		
ENSMUST00000135529	ENSMUSG00000001999	2	127070665	127097084	1	6	1	38	15	4	0	0	0	0	0	6	A2ASB7	
ENSMUST00000135530						2	4	7	5	4	0	0	0	0	0	0		
ENSMUST00000135531	ENSMUSG00000032311	9	55220222	55326844	-1	2	6	8	4	4	5	1	10	3	2	2	D6RE18	
ENSMUST00000135532						0	0	0	0	0	0	2	0	36	2	51		
ENSMUST00000135533						1	4	11	4	5	6	0	0	1	0	2		
ENSMUST00000135534						0	1	6	2	2	1	0	210	10	10	4		
ENSMUST00000135536						0	0	1	6	1	1	7	0	12	0	11		
ENSMUST00000135537	ENSMUSG00000035268	2	163658386	163726158	1	4	1	0	5	2	0	0	0	0	0	0	B7ZC21	
ENSMUST00000135538						2	2	3	0	0	1	0	0	0	1	0		
ENSMUST00000135539						6	5	12	4	0	7	9	25	4	7	19		
ENSMUST00000135540						2	0	8	25	7	0	0	6	0	8	0		
ENSMUST00000135541						0	0	0	5	1	1	5	0	0	0	7		
ENSMUST00000135542	ENSMUSG00000067878	X	56797858	56822326	-1	0	0	1	3	0	3	0	0	3	2	0		
ENSMUST00000135543						0	1	1	4	0	2	0	0	0	0	0		
ENSMUST00000135545						4	2	2	2	0	0	7	0	5	0	0		
ENSMUST00000135546						4	0	0	7	3	3	0	1	0	0	0		
ENSMUST00000135547						0	0	0	0	6	2	0	1	0	0	7		
ENSMUST00000135548						0	2	4	25	6	2	0	0	0	0	1		
ENSMUST00000135549	ENSMUSG00000024124	17	23972126	23975230	-1	0	2	7	0	0	0	0	0	0	0	0	D3YVP0	
ENSMUST00000135550						2	1	4	17	2	0	40	96	104	10	58		
ENSMUST00000135551						0	0	0	0	2	0	0	3	0	0	0		
ENSMUST00000135552	ENSMUSG00000020744	11	115614178	115628295	-1	6	2	0	3	3	2	14	16	0	0	24	A2A9V7	
ENSMUST00000135554	ENSMUSG00000002781	7	45896941	45917413	1	0	0	0	3	0	0	14	25	5	0	3	S4R1U1	
ENSMUST00000135555						0	0	0	0	0	0	0	0	0	0	8		
ENSMUST00000135556						1	0	12	2	7	1	0	0	1	0	0		
ENSMUST00000135557						0	1	0	1	0	0	0	1	0	0	0		
ENSMUST00000135558	ENSMUSG00000029780	6	56882400	56923932	-1	4	0	0	0	2	0	12	0	0	0	0		
ENSMUST00000135559						18	15	28	17	16	9	42	232	76	12	63		
ENSMUST00000135560						8	3	17	11	7	1	0	0	0	0	0		
ENSMUST00000135561	ENSMUSG00000000823	2	181582103	181592803	-1	0	3	0	5	0	3	0	0	1	0	0	F6PYY4	
ENSMUST00000135562	ENSMUSG00000030235	6	141524368	141570177	1	10	9	2	12	2	0	0	0	0	0	0	Q66L38	
ENSMUST00000135563						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135565	ENSMUSG00000047554	7	109972187	109986929	-1	0	0	0	5	0	0	25	66	22	30	9	D6RFP3	
ENSMUST00000135566	ENSMUSG00000029775	6	30401868	30455179	1	3	0	2	0	3	0	0	0	0	0	3		
ENSMUST00000135567	ENSMUSG00000042269	8	120166397	120177466	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYC8	
ENSMUST00000135568						0	0	0	0	0	2	6	47	13	11	0		
ENSMUST00000135569	ENSMUSG00000028713	4	115624725	115647723	-1	0	10	0	1	0	0	0	0	0	2	0	A0A0A6YY50	
ENSMUST00000135570						1	2	4	24	0	2	104	1405	541	1311	161		
ENSMUST00000135571						2	0	13	0	0	0	17	13	0	0	9		
ENSMUST00000135573	ENSMUSG00000028691	4	116685544	116700822	1	39	22	82	58	49	34	309	1402	301	1891	341		P35700
ENSMUST00000135574	ENSMUSG00000052551	13	8202866	8768747	1	460	393	199	255	391	209	31	52	112	39	211		Q9JI20
ENSMUST00000135575	ENSMUSG00000026869	2	34849734	34874968	-1	0	2	0	0	0	0	20	56	15	57	1	F7BA91	
ENSMUST00000135576						16	10	10	16	10	6	1	5	1	1	6		
ENSMUST00000135577						0	3	1	0	2	1	0	0	0	0	0		
ENSMUST00000135578	ENSMUSG00000041650	14	122534324	122891100	1	0	0	0	0	0	0	0	0	0	0	0	D3YZC0	
ENSMUST00000135579	ENSMUSG00000028906	4	131923413	132075321	-1	6	10	0	0	10	4	12	21	17	19	24	F6S4K9	
ENSMUST00000135580						4	0	4	2	2	1	0	0	0	0	2		
ENSMUST00000135581						0	3	4	2	4	2	0	1	0	0	0		
ENSMUST00000135582						5	1	3	0	0	0	28	50	36	8	48		
ENSMUST00000135584						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000135585	ENSMUSG00000057236	4	129307100	129335370	-1	0	0	0	12	0	0	0	0	0	19	13	A8Y5E8	
ENSMUST00000135586						120	105	439	137	85	77	1	24	22	7	28		
ENSMUST00000135587						34	24	47	39	29	10	0	5	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135588	ENSMUSG00000015942	5	134184019	134224355	1	1	3	0	2	3	5	34	100	28	6	55	F6XRH9	
ENSMUST00000135589	ENSMUSG00000024052	17	71182560	71249817	1	3	4	4	5	0	0	0	0	0	0	2	D6RH34	
ENSMUST00000135590						0	0	5	0	4	2	0	0	0	0	0		
ENSMUST00000135591						0	0	0	148	2	1	0	1	0	0	0		
ENSMUST00000135592						0	0	0	0	0	0	2	18	6	0	4		
ENSMUST00000135593						1	0	0	0	2	0	3	15	14	2	8		
ENSMUST00000135594						11	12	9	6	9	6	0	0	0	0	0		
ENSMUST00000135595						0	2	0	0	1	0	2	72	2	4	4		
ENSMUST00000135596						0	0	0	0	2	0	0	0	0	0	4		
ENSMUST00000135597						0	0	0	0	0	0	6	160	51	0	0		
ENSMUST00000135598						21	19	19	8	33	19	1	0	4	2	15		
ENSMUST00000135599						2	1	0	1	0	0	0	8	3	0	2		
ENSMUST00000135600						7	15	15	4	5	6	5	54	16	1	15		
ENSMUST00000135601						4	2	2	2	1	0	3	2	0	0	2		
ENSMUST00000135602						0	0	1	14	2	3	0	47	0	7	0		
ENSMUST00000135603	ENSMUSG00000027651	2	158028497	158132297	1	0	1	1	1	0	0	7	0	7	0	0	F7DAY5	
ENSMUST00000135604						46	31	79	48	28	25	0	0	0	0	0		
ENSMUST00000135605						0	0	0	14	0	0	0	0	0	2	0		
ENSMUST00000135606						23	33	51	20	38	23	2	5	6	0	6		
ENSMUST00000135607	ENSMUSG00000048701	10	70097121	70193200	1	15	15	15	0	31	15	0	0	3	0	0	F7B4D5	
ENSMUST00000135608						7	4	13	9	9	10	1	9	3	0	7		
ENSMUST00000135609	ENSMUSG00000053175	7	19808462	19822770	-1	4	0	26	10	9	5	184	574	179	14	117	F6YNH8	
ENSMUST00000135611						113	81	514	121	80	68	4	62	18	2	27		
ENSMUST00000135613						0	0	0	0	0	0	0	7	6	0	0		
ENSMUST00000135614	ENSMUSG00000026096	1	53313624	53326343	1	5	6	11	3	6	1	21	114	43	0	21		Q6PEB4
ENSMUST00000135615						4	6	23	67	8	0	0	0	0	0	0		
ENSMUST00000135616						0	0	0	0	0	0	12	0	0	8	5		
ENSMUST00000135617						5	1	14	10	4	0	0	0	2	4	14		
ENSMUST00000135618	ENSMUSG00000052142	17	32390659	32403583	-1	0	0	0	0	0	0	273	0	133	0	162	D3Z6Z7	
ENSMUST00000135619						1	1	2	0	2	1	9	19	13	53	9		
ENSMUST00000135620						4	2	1	1	3	0	0	1	1	0	1		
ENSMUST00000135621	ENSMUSG00000026784	2	22895522	22940266	1	0	0	0	0	1	2	0	0	0	0	0	D6RHT8	
ENSMUST00000135622						6	11	15	5	8	5	12	44	17	2	53		
ENSMUST00000135623	ENSMUSG00000028919	4	141239499	141257564	1	2	0	4	18	0	2	0	0	0	0	0	A2A826	
ENSMUST00000135624						0	0	0	0	0	7	0	0	0	0	0		
ENSMUST00000135625	ENSMUSG00000027288	2	120506820	120563843	-1	2	0	1	24	0	0	2	3	44	0	21	E9PVH6	
ENSMUST00000135626	ENSMUSG00000004267	6	124760053	124769673	-1	3	0	0	0	0	0	0	0	1	0	0	D3YVD3	
ENSMUST00000135627						0	0	0	24	0	0	0	66	23	0	0		
ENSMUST00000135628	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	0	6	27	0	0	D6RDC0	
ENSMUST00000135629	ENSMUSG00000028152	3	138742195	138907905	1	0	1	0	1	2	1	0	0	0	0	0	D3YZK1	
ENSMUST00000135631	ENSMUSG00000053838	11	6105691	6200415	-1	0	0	14	2	0	0	207	117	249	0	207	A0A0A0MQL8	
ENSMUST00000135632						0	0	11	8	2	1	0	0	0	0	0		
ENSMUST00000135633						0	1	0	1	0	0	2	0	65	38	22		
ENSMUST00000135634						0	1	4	50	2	0	23	57	311	2	94		
ENSMUST00000135635						18	12	87	58	31	7	36	91	41	13	50		
ENSMUST00000135636	ENSMUSG00000068747	3	108284082	108361511	1	1	0	12	0	11	0	287	158	551	32	359	A2AEF0	Q6PHU5
ENSMUST00000135637						19	12	30	25	19	10	0	0	0	0	3		
ENSMUST00000135638						29	12	110	16	0	5	39	67	47	0	32		
ENSMUST00000135639	ENSMUSG00000005371	17	87990859	88065291	-1	4	4	10	0	0	2	51	932	250	33	73	S4R2I0	
ENSMUST00000135640						0	2	10	0	1	0	0	0	0	0	0		
ENSMUST00000135641						1	0	9	95	7	2	0	0	1	1	0		
ENSMUST00000135642	ENSMUSG00000032883	1	78657825	78707743	1	0	0	0	0	0	0	1	4	5	2	4	D3Z4I4	
ENSMUST00000135644						4	10	16	9	7	3	12	118	42	3	100		
ENSMUST00000135645						7	3	14	0	0	2	23	22	18	7	14		
ENSMUST00000135646						4	2	0	5	5	4	4	14	5	10	11		
ENSMUST00000135647						2	0	15	1	0	0	1	0	0	0	2		
ENSMUST00000135648						0	0	0	0	0	0	1	0	0	0	9		
ENSMUST00000135649						0	1	2	4	3	0	0	10	0	0	11		
ENSMUST00000135650						5	4	5	0	1	2	3	16	2	2	9		
ENSMUST00000135651	ENSMUSG00000022475	15	97792664	97844502	-1	0	0	8	0	0	0	0	0	15	0	0	F6RY11	
ENSMUST00000135652						0	0	5	2	4	2	0	0	0	0	0		
ENSMUST00000135653	ENSMUSG00000018906	11	54100095	54131665	1	2	0	4	70	5	2	0	0	0	0	0	Q5SX76	
ENSMUST00000135654	ENSMUSG00000000983	11	83709015	83711348	1	0	0	0	0	0	0	0	0	0	0	0	M0QWG9	
ENSMUST00000135655						13	10	19	34	22	8	0	1	5	2	12		
ENSMUST00000135658						5	2	5	4	3	1	2	0	0	0	0		
ENSMUST00000135660	ENSMUSG00000028455	4	43027690	43031710	-1	0	0	0	0	0	5	101	134	109	127	73	F6WI02	
ENSMUST00000135661						0	0	0	30	2	0	0	3	0	0	5		
ENSMUST00000135662						2	3	0	3	4	0	0	7	0	0	0		
ENSMUST00000135663	ENSMUSG00000042109	15	81936759	81950941	1	2	3	8	10	8	3	0	0	0	0	0	D3YTN0	
ENSMUST00000135664	ENSMUSG00000026640	1	194618218	194816869	1	3	1	2	1	4	0	0	0	0	0	0	F6VSI0	
ENSMUST00000135665	ENSMUSG00000029055	4	154983115	155056784	-1	0	0	0	105	0	2	0	0	0	0	0		A2AP18
ENSMUST00000135666	ENSMUSG00000035173	19	56787481	56822190	-1	4	0	0	0	1	0	11	13	6	4	12	F7CUD4	
ENSMUST00000135667						3	1	8	2	6	3	0	4	4	0	7		
ENSMUST00000135668						2	0	12	30	3	0	0	0	1	0	0		
ENSMUST00000135669						2	0	0	21	1	0	0	0	2	0	0		
ENSMUST00000135671	ENSMUSG00000002416	6	39592574	39603382	1	39	44	77	37	40	25	9	57	19	15	20		Q9CPU2
ENSMUST00000135672	ENSMUSG00000022754	16	56805161	56886166	-1	3	3	0	2	0	2	0	0	0	0	0	A9C432	
ENSMUST00000135673	ENSMUSG00000040596	1	166384622	166409863	-1	6	2	35	14	4	3	0	2	8	0	15	E9Q3B2	
ENSMUST00000135675						6	1	5	10	0	2	0	0	0	3	0		
ENSMUST00000135676	ENSMUSG00000025413	4	106662256	106678944	-1	2	0	1	0	3	0	0	0	0	0	0	A2AVR1	
ENSMUST00000135677						644	665	1191	589	729	356	18	101	41	17	49		
ENSMUST00000135678	ENSMUSG00000025428	18	77773729	77782869	1	0	0	0	0	0	0	0	875	0	0	0	D6RJ16	
ENSMUST00000135680	ENSMUSG00000058267	1	160195215	160202170	1	102	82	415	132	69	42	83	129	69	295	55		Q9CR88
ENSMUST00000135681						0	0	0	0	0	0	0	0	0	5	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135683	ENSMUSG00000033533	7	119607026	119662515	1	0	0	17	2	0	5	0	0	0	0	0	D3Z106	
ENSMUST00000135684						0	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000135685						0	1	0	2	2	0	0	1	0	0	1		
ENSMUST00000135686	ENSMUSG00000060791	7	28437447	28448233	1	5	3	13	12	14	5	513	1408	549	1540	466	D3Z2F6	
ENSMUST00000135688	ENSMUSG00000024575	18	61220482	61289924	1	20	22	396	15	18	16	4	8	0	2	4	F6UDG9	
ENSMUST00000135689						4	1	13	14	1	2	0	0	0	0	1		
ENSMUST00000135690	ENSMUSG00000008682	X	74270812	74273135	1	0	0	0	19	0	0	34	110	7	18	0	B7FAU6	
ENSMUST00000135691						0	0	0	4	0	4	0	33	12	16	5		
ENSMUST00000135692						7	6	8	10	9	3	0	7	0	0	7		
ENSMUST00000135693						2	2	6	3	16	1	0	20	0	8	5		
ENSMUST00000135694						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000135695	ENSMUSG00000032498	9	111228228	111271791	-1	0	0	3	1	3	1	0	0	0	0	0	F6R1G0	
ENSMUST00000135696						0	0	1	0	1	0	4	0	0	0	0		
ENSMUST00000135697						5	4	69	14	6	2	0	13	4	2	4		
ENSMUST00000135698						0	1	1	162	1	1	0	0	0	0	0		
ENSMUST00000135699						2	4	9	7	3	8	0	0	0	0	0		
ENSMUST00000135701	ENSMUSG00000067220	5	72603696	72644275	-1	0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000135702						1	0	4	4	1	1	8	24	3	0	9		
ENSMUST00000135703						4	0	9	0	6	4	186	476	495	700	357		
ENSMUST00000135704	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	0	0	0	0	0	0	0	F6THL5	
ENSMUST00000135705						5	0	32	80	17	11	0	0	0	0	0		
ENSMUST00000135706						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135707						0	3	6	0	3	0	13	33	0	0	12		
ENSMUST00000135708	ENSMUSG00000040048	17	24722060	24724478	-1	0	3	0	0	0	0	0	0	0	0	0	D3YUK4	
ENSMUST00000135709	ENSMUSG00000048118	12	71015990	71098592	1	2	0	12	0	0	0	0	10	148	0	136	E9Q9V1	
ENSMUST00000135710						4	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000135711						5	7	0	11	17	0	0	4	0	0	4		
ENSMUST00000135712						1	0	0	0	0	0	0	0	0	8	0		
ENSMUST00000135713	ENSMUSG00000057457	X	157162075	157415312	-1	138	152	379	1601	149	80	11	15	1	3	7	F6S0V7	
ENSMUST00000135714						2	1	0	1	0	2	22	119	76	0	77		
ENSMUST00000135715						6	6	9	16	15	4	8	5	6	0	15		
ENSMUST00000135717						3	1	0	0	0	0	1	0	5	0	0		
ENSMUST00000135718	ENSMUSG00000028601	4	108165437	108179308	1	0	0	6	3	0	0	0	0	0	0	0	F6YTG0	
ENSMUST00000135719	ENSMUSG00000027829	3	65946151	65958249	-1	0	2	0	0	0	0	131	1796	539	229	377	F6WST0	
ENSMUST00000135720	ENSMUSG00000036817	5	139200637	139249840	1	0	0	0	0	0	0	3	0	0	0	2	F7BX07	
ENSMUST00000135721						4	3	7	1	4	0	0	14	5	2	14		
ENSMUST00000135722						12	20	40	14	22	5	6	2	7	1	4		
ENSMUST00000135723	ENSMUSG00000028199	3	154596711	154623182	1	0	0	1	0	0	0	0	0	0	0	0	A0A0G2JFU5	
ENSMUST00000135724						8	6	12	18	11	2	2	6	1	15	2		
ENSMUST00000135725						0	0	0	0	2	0	3	0	0	4	25		
ENSMUST00000135726						2	0	1	1	1	1	0	0	0	0	0		
ENSMUST00000135727	ENSMUSG00000022415	15	80091334	80119501	1	4	2	9	27	6	3	0	0	0	1	0	F6PZA3	
ENSMUST00000135730	ENSMUSG00000025089	19	58235604	58455909	-1	2	1	6	70	7	1	0	0	0	0	0		
ENSMUST00000135731	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	1	0	0	0	6	0	0	0	5	A2AEB7	
ENSMUST00000135732						3	0	1	11	3	1	89	360	115	2	322		
ENSMUST00000135733						1	2	0	0	2	4	7	0	4	0	4		
ENSMUST00000135734						0	0	2	46	3	0	0	0	0	0	0		
ENSMUST00000135736						84	65	347	138	70	39	18	15	24	6	28		
ENSMUST00000135737						15	9	5	24	17	3	0	0	0	0	0		
ENSMUST00000135740						0	0	0	0	0	0	11	186	142	177	38		
ENSMUST00000135741	ENSMUSG00000026883	2	35558266	35730994	1	8	0	2	176	2	6	0	0	0	0	27	B7ZD29	
ENSMUST00000135742	ENSMUSG00000072479	X	73148796	73158872	1	0	0	0	1	0	0	0	0	0	0	0	A2BI49	
ENSMUST00000135743						6	7	11	2	14	4	0	2	0	0	0		
ENSMUST00000135744	ENSMUSG00000010505	2	181763332	181827797	1	0	0	0	0	2	0	0	0	0	0	0	B0R0C6	
ENSMUST00000135745						3	3	3	0	0	2	0	0	10	0	0		
ENSMUST00000135746						20	20	94	29	28	11	4	33	4	1	3		
ENSMUST00000135747	ENSMUSG00000037492	8	23636019	24156585	1	1	0	2	0	2	0	0	0	0	0	0	D3Z339	
ENSMUST00000135748	ENSMUSG00000058908	4	138831857	138835186	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135750						13	4	29	4	12	13	0	3	2	19	4		
ENSMUST00000135751						0	0	4	9	5	1	2	0	0	0	1		
ENSMUST00000135752						2	0	32	0	6	4	0	0	9	0	8		
ENSMUST00000135753	ENSMUSG00000079620	16	32735886	32782391	1	0	0	0	0	0	0	0	0	0	0	0	F6R2G3	
ENSMUST00000135754						14	0	49	172	19	16	2508	7362	2995	348	4115		
ENSMUST00000135755						0	0	0	0	3	0	0	4	0	0	8		
ENSMUST00000135756						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000135757	ENSMUSG00000048794	6	90403479	90428797	-1	0	1	6	4	6	1	0	0	0	0	0		
ENSMUST00000135758						0	2	2	189	12	1	0	1	3	0	1		
ENSMUST00000135759						2	1	5	2	0	0	0	1	0	0	1		
ENSMUST00000135760						6	2	10	7	11	5	26	64	20	9	29		
ENSMUST00000135761						0	2	3	0	0	0	0	0	0	0	4		
ENSMUST00000135762						32	26	68	24	43	10	49	82	105	0	133		
ENSMUST00000135763	ENSMUSG00000028785	4	129111570	129122036	-1	0	0	0	0	0	0	0	0	0	0	0	A2A7R6	
ENSMUST00000135764	ENSMUSG00000039539	8	37522298	38661508	-1	26	9	0	0	17	11	0	0	0	0	0	D6RFA5	
ENSMUST00000135765	ENSMUSG00000004934	10	81153266	81167923	-1	0	0	0	0	0	0	0	0	0	0	0	F6RKH8	
ENSMUST00000135766						0	0	0	49	0	0	0	0	0	0	0		
ENSMUST00000135768						5	0	2	27	4	0	0	31	0	11	7		
ENSMUST00000135769						1	7	12	8	3	0	0	0	0	0	1		
ENSMUST00000135770						11	8	21	5	13	0	23	30	34	16	68		
ENSMUST00000135771						15	10	55	11	21	4	1	1	2	0	4		
ENSMUST00000135772	ENSMUSG00000020629	12	28675231	28682175	1	0	0	0	0	0	0	0	0	0	0	0	F7ARY2	
ENSMUST00000135773						0	0	2	68	4	4	0	0	3	0	0		
ENSMUST00000135774						0	6	1	1	1	4	0	0	0	0	0		
ENSMUST00000135776						157	123	347	370	145	39	81	204	216	124	231		
ENSMUST00000135778						3	0	4	0	0	0	14	0	16	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135779						2	0	1	3	0	1	0	0	0	0	2		
ENSMUST00000135780						0	0	0	3	0	1	15	52	8	11	5		
ENSMUST00000135782						2	3	0	3	5	0	0	0	0	4	1		
ENSMUST00000135783						6	0	0	1	1	0	20	75	12	23	0		
ENSMUST00000135784	ENSMUSG00000021384	13	49230690	49248706	-1	0	0	0	2	4	1	0	0	0	0	0	D3YY27	
ENSMUST00000135785	ENSMUSG00000051736	10	39118804	39133914	-1	2	0	0	1	1	1	0	0	0	2	0	B2RVF6	Q8CF36
ENSMUST00000135786						0	0	0	0	0	0	0	0	3	22	1		
ENSMUST00000135787						8	3	3	4	0	3	0	0	0	0	5		
ENSMUST00000135788	ENSMUSG00000043207	4	121059237	121098241	-1	0	0	6	1	0	0	4	3	28	0	14	I7HIP5	
ENSMUST00000135789						0	3	3	3	6	0	184	0	220	540	69		
ENSMUST00000135790	ENSMUSG00000019647	18	47235598	47368870	-1	0	42	0	0	0	0	0	0	0	0	0	D3YWM8	
ENSMUST00000135791						0	1	4	0	3	0	20	14	10	0	0		
ENSMUST00000135793						3	5	2	5	6	0	20	22	25	8	26		
ENSMUST00000135794						0	0	34	0	4	1	11	81	16	11	12		
ENSMUST00000135795	ENSMUSG00000025008	19	40596446	40612233	-1	7	0	11	0	0	0	0	0	0	0	0		Q8R2Q6
ENSMUST00000135796						4	2	11	8	6	1	0	0	0	0	0		
ENSMUST00000135797						2	1	7	3	11	0	0	0	0	0	0		
ENSMUST00000135798	ENSMUSG00000059423	4	147822986	147848366	-1	0	0	0	0	0	0	0	0	0	14	4	Q3V2G0	
ENSMUST00000135800						2	2	1	1	2	0	0	2	3	0	3		
ENSMUST00000135801	ENSMUSG00000029319	5	100654723	100675140	-1	5	6	18	19	12	0	2	20	12	4	18	D3Z296	
ENSMUST00000135802	ENSMUSG00000030180	6	120364124	120444574	1	0	0	0	0	0	0	0	0	245	0	87		
ENSMUST00000135803	ENSMUSG00000026821	2	28513125	28553081	1	0	0	0	14	0	0	0	0	0	0	0	B0R018	
ENSMUST00000135804						0	4	2	0	7	4	0	2	0	0	7		
ENSMUST00000135805						0	0	0	0	1	1	5	0	3	0	5		
ENSMUST00000135806	ENSMUSG00000058925	18	57533780	57731065	1	0	0	0	0	0	3	0	0	0	0	0	D3YYW6	
ENSMUST00000135807	ENSMUSG00000046785	9	111271929	111279093	1	0	0	6	189	4	0	5	71	53	13	26		Q8VEH5
ENSMUST00000135808	ENSMUSG00000063698	19	60837277	60861479	-1	0	0	0	3	1	0	0	0	0	0	1		Q925N1
ENSMUST00000135809						2	1	6	2	1	1	0	0	0	0	0		
ENSMUST00000135810						0	0	0	5	2	1	0	0	0	0	0		
ENSMUST00000135811	ENSMUSG00000028391	4	62448653	62470896	-1	0	1	0	31	4	0	0	0	0	0	0	B7ZCH6	
ENSMUST00000135812						5	0	0	0	1	1	0	104	3	21	12		
ENSMUST00000135813						4	5	3	1	3	1	3	5	7	3	10		
ENSMUST00000135814	ENSMUSG00000018572	11	69995777	70000009	1	6	0	6	148	19	6	52	140	44	15	43		Q8BSN5
ENSMUST00000135815						0	4	0	0	0	0	0	0	1	7	1		
ENSMUST00000135816						0	0	1	59	1	2	0	0	0	0	0		
ENSMUST00000135817						1	0	15	1	2	1	0	0	0	0	0		
ENSMUST00000135818	ENSMUSG00000028132	3	121201761	121283098	-1	10	6	3	0	6	3	0	0	0	0	0		Q8CGF5
ENSMUST00000135819						0	3	1	0	0	0	0	0	0	0	0		
ENSMUST00000135820						1	0	0	2	2	1	0	0	0	0	0		
ENSMUST00000135821						4	4	6	1	3	1	4	6	6	0	10		
ENSMUST00000135822	ENSMUSG00000020027	10	95385362	95417180	-1	0	0	12	63	0	2	0	0	0	0	0	D3YZ26	
ENSMUST00000135823	ENSMUSG00000039637	16	4626133	4679777	-1	3	0	4	12	6	0	689	144	772	9	469	E9PYU1	
ENSMUST00000135824	ENSMUSG00000024191	17	26781079	26792565	1	1	0	1	0	0	0	3	5	0	13	0	B8JJI4	
ENSMUST00000135826						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135827						2	2	3	1	2	1	2	0	0	1	0		
ENSMUST00000135828						0	3	0	21	3	0	0	0	0	0	0		
ENSMUST00000135830						0	2	0	2	5	1	0	0	0	0	0		
ENSMUST00000135831						9	0	12	5	5	2	14	39	8	22	14		
ENSMUST00000135832						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000135833						0	1	4	35	3	4	39	332	83	152	39		
ENSMUST00000135834						5	4	14	1	6	0	2	1	0	0	0		
ENSMUST00000135835	ENSMUSG00000034762	4	107434591	107635061	1	0	0	0	0	0	0	0	0	0	0	0	A2A8S0	
ENSMUST00000135836						0	2	21	14	0	3	0	0	3	0	15		
ENSMUST00000135837						6	5	6	2	6	8	0	0	0	0	0		
ENSMUST00000135838						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000135839						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135840						1	0	10	0	2	4	0	0	5	4	5		
ENSMUST00000135841						2	2	7	7	8	0	0	0	0	0	0		
ENSMUST00000135842	ENSMUSG00000025465	7	140105710	140116476	-1	1	0	0	0	0	0	27	109	52	34	31	F6T930	
ENSMUST00000135843						2	5	12	22	7	0	0	0	0	0	0		
ENSMUST00000135844						0	1	1	0	0	0	4	19	0	12	3		
ENSMUST00000135845						10	10	25	35	15	6	0	0	0	0	0		
ENSMUST00000135846	ENSMUSG00000037370	10	24637914	24712159	-1	5	11	2	0	0	0	0	4	4	4	32		
ENSMUST00000135847						7	3	10	34	7	1	12	3	9	0	9		
ENSMUST00000135848						2	3	7	11	5	2	0	0	0	0	0		
ENSMUST00000135849						10	7	19	3	11	5	3	6	5	0	7		
ENSMUST00000135850						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000135851						7	4	0	26	7	9	19	626	61	31	28		
ENSMUST00000135852						4	6	6	19	9	1	0	0	0	0	1		
ENSMUST00000135853						1	3	0	1	0	0	0	0	1	0	1		
ENSMUST00000135854						0	0	0	2	0	1	2	45	22	45	8		
ENSMUST00000135855						1	1	0	3	0	0	4	9	2	0	14		
ENSMUST00000135856	ENSMUSG00000062168	X	160623094	160735765	-1	45	22	152	109	57	21	7	28	14	2	34	Q3UQZ5	
ENSMUST00000135859						4	6	4	5	0	1	1	0	1	2	1		
ENSMUST00000135861						3	2	25	0	4	0	3	21	22	2	13		
ENSMUST00000135862						0	1	0	0	5	5	0	0	0	0	0		
ENSMUST00000135863						4	0	3	1	5	0	2	28	14	0	29		
ENSMUST00000135864						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000135865	ENSMUSG00000087279	11	70615848	70616890	1	0	0	4	2	2	0	0	0	0	0	0	J3KMM3	
ENSMUST00000135866	ENSMUSG00000039031	10	26753421	26918648	1	0	1	0	0	0	0	0	0	0	0	0	H3BLG9	
ENSMUST00000135867						0	0	1	0	1	0	0	0	4	0	0		
ENSMUST00000135868	ENSMUSG00000050567	11	50255634	50292311	-1	20	21	81	0	40	15	1156	1881	1527	108	1118	F6UY95	
ENSMUST00000135869	ENSMUSG00000050708	7	45457944	45459884	-1	0	0	18	86	0	10	296	815	265	163	912	H3BKD3	
ENSMUST00000135870						2	0	4	2	0	0	0	0	7	1	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135871	ENSMUSG00000028298	4	34893779	34907370	1	3	2	3	0	0	4	0	0	0	0	0	A2AVN2	
ENSMUST00000135872						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000135874						98	93	173	134	110	78	5	12	4	0	13		
ENSMUST00000135875						0	0	4	1	0	0	0	0	0	0	0		
ENSMUST00000135876	ENSMUSG00000027810	3	58525821	58557501	1	0	0	0	0	0	0	19	53	54	103	24	D6RGA6	
ENSMUST00000135877	ENSMUSG00000025967	1	63176825	63180486	1	0	4	7	0	5	0	1309	4552	1203	3893	962	M0QW60	
ENSMUST00000135878						1	3	3	8	7	1	0	0	0	0	0		
ENSMUST00000135879						3	2	0	3	4	0	0	0	0	0	0		
ENSMUST00000135880						23	20	47	264	27	7	6	11	3	1	0		
ENSMUST00000135881	ENSMUSG00000008384	7	27486910	27490316	1	0	0	0	46	5	1	4	3	0	2	10	D3Z2X7	
ENSMUST00000135882						1	1	0	27	3	2	2	11	0	0	12		
ENSMUST00000135884	ENSMUSG00000037601	11	93956979	93968521	-1	20	10	30	70	31	14	179	384	109	554	146	Q5NC81	P15532
ENSMUST00000135885						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000135886						23	16	57	43	30	11	25	201	64	6	78		
ENSMUST00000135887	ENSMUSG00000020427	11	7206086	7213923	-1	3	1	4	55	17	0	0	0	0	0	0		P47878
ENSMUST00000135888	ENSMUSG00000015966	14	29996141	30008896	-1	0	0	1	0	0	0	11	6	5	2	0	D6RCY5	
ENSMUST00000135889						1139	801	924	27069	1696	521	22	114	41	25	152		
ENSMUST00000135890						6	7	12	0	12	2	0	17	30	5	0		
ENSMUST00000135891						1	2	2	2	1	1	4	9	9	1	26		
ENSMUST00000135892						4	2	7	3	5	3	8	17	15	1	20		
ENSMUST00000135893						5	2	15	3	5	0	0	9	0	0	0		
ENSMUST00000135894						0	0	0	3	2	1	4	13	20	3	14		
ENSMUST00000135895						0	1	3	0	0	0	7	0	6	1	5		
ENSMUST00000135896						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135897	ENSMUSG00000021404	13	33149275	33159742	-1	3	1	0	0	0	0	0	0	0	0	0	J3JSA2	
ENSMUST00000135898						15	22	61	28	21	24	0	1	3	0	1		
ENSMUST00000135899						69	45	190	347	112	65	8	33	17	0	50		
ENSMUST00000135900						2	0	0	0	0	0	0	0	0	0	14		
ENSMUST00000135901	ENSMUSG00000025702	6	116338024	116409540	1	0	0	0	0	0	0	0	0	11	0	0	F6THH9	
ENSMUST00000135903						2	1	2	0	0	0	0	4	13	0	0		
ENSMUST00000135904	ENSMUSG00000056486	2	73610660	73775346	-1	6	2	0	0	2	1	0	0	0	0	0	B2FDI2	
ENSMUST00000135905						0	0	0	0	0	0	5	32	3	0	6		
ENSMUST00000135906						0	4	6	0	0	0	0	0	0	7	0		
ENSMUST00000135907	ENSMUSG00000019796	10	7589800	7625483	1	0	0	0	2	0	2	0	0	0	1	1	F7AX87	
ENSMUST00000135908						1	1	3	1	1	0	0	0	0	0	0		
ENSMUST00000135909						3	7	13	47	14	8	8	68	21	0	57		
ENSMUST00000135910						28	37	41	25	35	23	12	44	20	3	40		
ENSMUST00000135911						0	0	9	0	0	0	8	63	18	3	0		
ENSMUST00000135912	ENSMUSG00000070044	8	45336717	45382291	-1	5	8	3	26	18	0	0	0	0	0	0	F6X0J3	
ENSMUST00000135913						3	7	13	5	3	0	34	64	93	1	82		
ENSMUST00000135914						0	0	6	3	2	3	66	369	156	16	202		
ENSMUST00000135915						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000135916	ENSMUSG00000020886	11	70017085	70045532	1	1	2	5	19	1	0	2	0	0	0	0	J3KMS4	
ENSMUST00000135917						6	8	28	0	2	0	0	0	0	0	4		
ENSMUST00000135918						8	6	16	7	4	0	0	0	1	0	2		
ENSMUST00000135919						2	0	0	0	1	0	11	3	404	1	285		
ENSMUST00000135920						0	6	5	26	0	0	0	0	0	0	0		
ENSMUST00000135921						67	46	285	85	51	26	0	3	2	7	2		
ENSMUST00000135922						0	0	0	1	3	1	0	0	0	0	0		
ENSMUST00000135923						2	4	5	10	7	3	3	0	0	0	1		
ENSMUST00000135924	ENSMUSG00000028277	4	33031416	33052363	1	17	2	22	0	4	6	195	221	152	19	65	F6SPK0	
ENSMUST00000135925						2	0	15	1	3	4	0	0	0	0	0		
ENSMUST00000135926	ENSMUSG00000036817	5	139200637	139249840	1	2	0	1	0	0	0	0	0	0	0	0	F6XYA0	
ENSMUST00000135927						0	5	0	0	0	0	0	116	27	0	0		
ENSMUST00000135928						5	2	9	14	3	5	10	87	29	6	80		
ENSMUST00000135929						0	0	0	0	0	0	34	0	24	0	34		
ENSMUST00000135930	ENSMUSG00000037685	5	67618140	67847434	-1	0	0	0	0	1	0	0	0	180	0	164	F6WYQ5	P70704
ENSMUST00000135931						5	3	8	38	5	0	4	17	4	0	8		
ENSMUST00000135932						3	2	4	11	6	4	4	8	0	2	1		
ENSMUST00000135934	ENSMUSG00000032116	9	36729344	36767679	-1	1	0	0	0	0	0	41	182	28	36	52	F6YHG5	
ENSMUST00000135935						3	3	4	0	3	1	3	0	1	1	1		
ENSMUST00000135937						6	4	4	2	10	5	9	2	15	2	8		
ENSMUST00000135938	ENSMUSG00000003279	17	69969073	70821413	1	0	0	0	0	0	0	0	0	0	0	0		Q9D415
ENSMUST00000135939						3	0	0	0	1	1	0	0	0	4	0		
ENSMUST00000135941	ENSMUSG00000006412	1	171345670	171359254	1	31	27	38	70	42	12	27	118	57	51	47		O70591
ENSMUST00000135943						74	77	82	40	69	40	10	24	20	22	25		
ENSMUST00000135944						30	39	131	60	45	17	16	43	24	5	58		
ENSMUST00000135945						1	1	2	11	3	1	0	0	0	0	0		
ENSMUST00000135946						3	0	2	0	6	3	0	0	1	0	0		
ENSMUST00000135947						5	2	3	9	4	2	4	10	3	0	8		
ENSMUST00000135948	ENSMUSG00000079429	1	88226986	88262289	1	0	8	41	15	2	7	3	24	15	4	25	F6W219	
ENSMUST00000135949	ENSMUSG00000062070	X	106187100	106203699	1	3	13	0	0	49	0	0	0	75	4225	923	S4R2M7	
ENSMUST00000135950						10	7	18	3	18	7	0	3	0	0	1		
ENSMUST00000135952						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000135953	ENSMUSG00000078683	4	60498012	60501960	-1	5	7	0	3	6	2	0	0	0	0	0	A2CEK9	
ENSMUST00000135954	ENSMUSG00000055923	5	76873659	76905514	-1	0	0	0	0	0	0	1	0	0	0	0	D3YXV2	
ENSMUST00000135955	ENSMUSG00000018796	8	46471041	46536051	1	0	3	3	4	3	0	9	10	0	0	6	D3Z457	
ENSMUST00000135956						4	4	8	0	2	1	4	0	0	0	0		
ENSMUST00000135957						10	2	11	43	3	1	3	0	1	0	2		
ENSMUST00000135959						0	0	1	38	2	0	0	0	8	2	0		
ENSMUST00000135960	ENSMUSG00000004233	3	99141068	99239186	1	0	0	206	10	30	0	10	84	23	19	3	A0A0G2JDR5	
ENSMUST00000135961	ENSMUSG00000038342	5	123394798	123457932	1	118	82	675	108	89	34	260	1853	311	107	554	F6UPM1	
ENSMUST00000135962	ENSMUSG00000021224	12	83794034	83921934	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z7I6	
ENSMUST00000135963	ENSMUSG00000018841	11	82876434	82890614	-1	0	7	0	0	0	0	14	39	0	0	0	E9QAG0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000135964						0	2	0	0	0	0	0	14	0	7	2		
ENSMUST00000135966						1	0	1	0	0	0	10	10	9	0	11		
ENSMUST00000135967						30	23	102	65	36	29	10	15	30	0	61		
ENSMUST00000135968						1	0	2	103	4	1	5	39	13	0	14		
ENSMUST00000135969						13	27	37	78	22	14	87	265	284	13	356		
ENSMUST00000135970	ENSMUSG00000031778	8	94772009	94782423	1	0	0	0	0	1	0	0	0	0	0	0	E0CXC3	
ENSMUST00000135971						1	0	0	0	0	0	8	17	5	0	12		
ENSMUST00000135972	ENSMUSG00000002043	7	19508670	19516145	1	0	1	5	2	0	2	41	0	0	0	0	F6VKM0	
ENSMUST00000135973						26	11	56	40	27	10	6	4	15	0	18		
ENSMUST00000135974						14	29	19	36	22	16	0	5	2	2	7		
ENSMUST00000135975	ENSMUSG00000020679	11	83850063	83905819	1	4	1	14	67	1	1	0	0	0	0	0	A0A0A0MQH4	
ENSMUST00000135976	ENSMUSG00000070985	4	49447105	49473912	-1	0	0	3	0	1	0	0	0	0	0	0	A2AKK6	
ENSMUST00000135977	ENSMUSG00000035632	7	3645268	3661109	1	14	11	59	5	29	1	0	31	46	23	38	F6WUZ2	
ENSMUST00000135978						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000135979	ENSMUSG00000032782	11	69299487	69323775	-1	1	0	0	3	0	0	0	0	0	0	0	F6TUD4	
ENSMUST00000135980						0	0	0	0	0	0	0	2	0	1	0		
ENSMUST00000135981	ENSMUSG00000022272	15	25622525	25813673	1	0	0	0	1	0	0	0	0	0	0	3	F6UVU0	
ENSMUST00000135982						0	0	0	3	3	1	0	0	0	0	1		
ENSMUST00000135983	ENSMUSG00000025877	13	55005985	55021385	-1	3	3	0	5	6	4	44	73	71	14	79	D6RCV7	
ENSMUST00000135984	ENSMUSG00000030263	6	145115653	145174934	1	4	5	6	0	0	2	558	1429	1014	536	426	D6RIN0	
ENSMUST00000135985						0	3	8	7	5	2	0	0	0	0	0		
ENSMUST00000135986	ENSMUSG00000079235	9	121797627	121839461	-1	12	13	37	93	38	20	0	0	0	0	1		D3YV10
ENSMUST00000135988	ENSMUSG00000022472	15	81992523	82033862	-1	0	3	6	40	11	0	17	13	0	7	7	Q3TCG9	
ENSMUST00000135989	ENSMUSG00000030986	7	133720942	133782726	-1	7	1	8	66	8	2	0	0	0	0	1		
ENSMUST00000135991	ENSMUSG00000000738	8	123062942	123097760	1	0	0	0	0	0	0	0	0	0	0	0	F6VTG4	
ENSMUST00000135992						0	0	0	3	4	0	9	0	0	0	3		
ENSMUST00000135993						2	1	5	18	3	0	0	0	0	0	5		
ENSMUST00000135994	ENSMUSG00000055895	19	11647279	11660559	-1	0	0	0	0	1	0	0	0	0	0	0	D6RCH7	
ENSMUST00000135995						3	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000135996						3	2	4	6	7	0	0	0	0	0	0		
ENSMUST00000135997						16	7	41	21	22	4	0	3	0	0	0		
ENSMUST00000135998	ENSMUSG00000035642	7	97550331	97579497	-1	0	1	5	4	1	2	0	3	0	0	1	D3YWY5	
ENSMUST00000135999						6	3	7	5	9	5	284	119	129	0	122		
ENSMUST00000136000						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000136001						1	0	6	0	2	0	21	5	17	2	11		
ENSMUST00000136002						3	1	0	1	1	0	0	2	0	0	5		
ENSMUST00000136003						0	0	2	2	0	0	119	0	4	6	70		
ENSMUST00000136004						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136005	ENSMUSG00000051517	4	43496142	43499695	-1	0	0	0	0	0	0	0	0	0	0	0	F6V695	
ENSMUST00000136006						0	3	1	0	2	0	1	0	0	0	1		
ENSMUST00000136008	ENSMUSG00000030304	6	148179079	148212374	-1	27	11	40	28	13	8	135	614	206	430	185		Q9CR89
ENSMUST00000136009	ENSMUSG00000039515	2	30416039	30447806	1	0	2	3	3	1	1	9	28	2	2	19	B7ZDE0	
ENSMUST00000136010						0	1	7	3	0	0	0	129	0	25	29		
ENSMUST00000136011						43	24	51	41	52	21	3	10	6	0	12		
ENSMUST00000136012	ENSMUSG00000020818	11	116852440	116875635	1	13	11	9	24	15	10	3	25	20	1	27	E9PZJ5	
ENSMUST00000136013						0	2	0	1	2	3	19	134	24	25	26		
ENSMUST00000136016	ENSMUSG00000029917	6	65381105	65458150	1	4	0	3	1	0	0	0	0	0	0	0	F6RNN2	
ENSMUST00000136017						2	1	11	5	6	0	2	0	3	1	13		
ENSMUST00000136018						35	36	354	62	34	13	4	1	3	0	0		
ENSMUST00000136019						5	2	0	1	3	1	0	8	2	0	0		
ENSMUST00000136020	ENSMUSG00000001054	11	51623671	51635896	-1	0	0	1	0	0	0	179	520	29	26	10	D6RII5	
ENSMUST00000136021	ENSMUSG00000020389	11	52004221	52089784	1	3	4	1	0	3	0	0	0	6	0	4	F6Y3R0	
ENSMUST00000136023	ENSMUSG00000060227	2	121866970	121936220	1	0	0	0	0	0	0	0	0	0	0	0	A2AR60	
ENSMUST00000136024	ENSMUSG00000029469	5	122550204	122614518	-1	2	0	2	13	2	0	0	2	0	0	0	D6RHM7	
ENSMUST00000136026	ENSMUSG00000003824	8	84872111	84888221	1	7	0	11	16	9	6	2	7	0	3	0		Q505B8
ENSMUST00000136028	ENSMUSG00000089984	5	137612503	137629002	-1	0	0	0	0	0	0	0	0	0	4	0	D6RFP4	
ENSMUST00000136029						22	24	57	127	27	22	0	5	0	0	2		
ENSMUST00000136030	ENSMUSG00000024483	18	36559987	36665917	1	0	0	0	0	0	0	12	8	45	0	52	F6SI14	
ENSMUST00000136031	ENSMUSG00000029772	6	29768011	29912310	1	2	5	1	5	1	2	0	0	0	0	0	H3BKE9	
ENSMUST00000136032						21	14	13	28	10	12	0	0	0	3	24		
ENSMUST00000136033						8	10	11	12	16	13	0	0	0	0	0		
ENSMUST00000136034						2	3	8	5	3	3	0	0	0	0	0		
ENSMUST00000136035						1	0	0	19	1	1	0	0	0	0	0		
ENSMUST00000136037						2	0	0	4	1	1	0	0	0	0	0		
ENSMUST00000136039						7	0	0	7	5	0	0	0	0	0	0		
ENSMUST00000136041						80	88	361	166	133	47	4	29	9	4	14		
ENSMUST00000136042						1	0	1	6	2	1	0	0	0	0	0		
ENSMUST00000136043						2	0	7	5	0	2	2	1	2	1	4		
ENSMUST00000136044						5	5	11	4	9	2	1	6	3	0	6		
ENSMUST00000136045						16	12	24	116	23	8	1	2	0	0	0		
ENSMUST00000136047						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136048	ENSMUSG00000036270	8	105880881	105894908	1	15	10	17	2	8	10	6	18	0	0	0	D6RE33	
ENSMUST00000136049	ENSMUSG00000027849	3	103575231	103645569	1	0	0	0	0	0	0	0	0	0	0	0	D6RHQ5	
ENSMUST00000136050						0	0	0	1	3	1	0	0	0	0	0		
ENSMUST00000136054						5	2	11	2	4	2	3	11	7	1	8		
ENSMUST00000136055						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000136056	ENSMUSG00000019087	X	74297097	74304721	1	0	0	0	0	2	0	0	8	5	0	0	F6ZE56	
ENSMUST00000136057	ENSMUSG00000028433	4	41194313	41275144	-1	1	0	5	77	5	5	0	0	2	3	0	F6WTC8	
ENSMUST00000136058	ENSMUSG00000040812	2	90782727	90834437	1	0	0	0	0	0	0	0	0	0	0	0	A0A0B4J1L6	
ENSMUST00000136059						8	3	12	14	3	2	0	0	0	0	3		
ENSMUST00000136060	ENSMUSG00000036356	8	68356781	68735146	-1	5	3	0	0	6	0	0	0	0	0	0		
ENSMUST00000136061						3	2	1	1	4	0	5	0	0	4	4		
ENSMUST00000136063						2	3	4	2	4	4	27	100	103	5	54		
ENSMUST00000136064						28	24	133	31	33	20	0	3	5	0	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136065						5	6	6	55	12	6	0	0	4	0	3		
ENSMUST00000136066	ENSMUSG00000016757	15	83575119	83595157	-1	12	9	49	11	10	7	0	0	8	0	0	F2Z423	
ENSMUST00000136067						0	1	0	40	1	1	0	0	0	0	3		
ENSMUST00000136068						3	0	15	4	2	0	0	4	8	0	41		
ENSMUST00000136069						0	4	0	0	0	1	30	130	44	96	50		
ENSMUST00000136070						0	2	25	4	3	0	0	0	3	0	0		
ENSMUST00000136071						4	1	0	1	2	1	0	6	1	1	14		
ENSMUST00000136072						4	4	10	26	4	1	0	2	0	2	0		
ENSMUST00000136073						1	0	3	2	2	0	1	0	3	0	3		
ENSMUST00000136074	ENSMUSG00000029622	5	145114215	145130705	1	1	3	0	0	7	0	1658	2223	1724	438	1265	F6VVE6	
ENSMUST00000136075	ENSMUSG00000021098	12	72881109	72940774	-1	13	9	23	26	11	14	0	0	1	2	0	D3Z202	
ENSMUST00000136076						7	0	2	20	9	0	1	35	16	0	20		
ENSMUST00000136077						10	6	10	6	10	1	6	8	0	0	8		
ENSMUST00000136078	ENSMUSG00000026171	1	74593748	74601397	-1	0	0	0	0	0	0	13	0	0	0	0	F6Z123	
ENSMUST00000136079	ENSMUSG00000039205	2	32352327	32380970	1	0	0	0	0	0	0	0	0	0	0	0	F7BM53	
ENSMUST00000136080						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136081						0	0	0	0	0	0	0	26	0	0	3		
ENSMUST00000136082						2	3	36	3	0	2	4	3	7	0	34		
ENSMUST00000136084	ENSMUSG00000035919	9	22475715	22888280	1	1	0	0	0	0	0	0	17	0	0	0	F6XSQ3	
ENSMUST00000136085						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000136086	ENSMUSG00000037643	3	30995747	31052959	1	0	0	0	0	0	0	0	2	0	0	0	F6QWV4	
ENSMUST00000136087						1	0	1	5	0	0	0	0	0	0	0		
ENSMUST00000136088	ENSMUSG00000029712	5	137553517	137569582	1	0	0	0	26	0	0	0	0	0	0	0	D3Z5W4	
ENSMUST00000136089						19	14	142	29	16	9	0	0	0	0	1		
ENSMUST00000136090	ENSMUSG00000034083	6	91878053	91899843	1	18	21	38	35	20	9	5	13	3	2	5		
ENSMUST00000136091						2	2	0	3	6	3	0	0	0	3	1		
ENSMUST00000136092						0	0	0	13	0	0	0	2	0	0	0		
ENSMUST00000136093						4	1	2	2	2	0	0	0	0	0	0		
ENSMUST00000136094						4	3	12	11	8	3	0	5	7	0	12		
ENSMUST00000136095						3	5	4	6	3	2	0	4	4	0	12		
ENSMUST00000136096	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000136097						3	1	0	0	0	1	2	0	0	0	0		
ENSMUST00000136098	ENSMUSG00000038005	8	60890418	60907580	1	2	4	4	2	7	2	0	31	8	5	8	D6RIJ8	
ENSMUST00000136099						0	0	0	0	0	0	0	55	0	0	0		
ENSMUST00000136100						0	3	3	9	11	6	6	62	7	0	19		
ENSMUST00000136101	ENSMUSG00000044328	11	77508099	77515980	-1	0	2	0	0	0	0	3	0	2	0	7	F6YFL2	
ENSMUST00000136102						9	7	6	21	9	7	5	16	4	0	12		
ENSMUST00000136103						3	0	1	3	7	0	0	0	3	0	0		
ENSMUST00000136104						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000136105	ENSMUSG00000004630	8	3623371	3625545	-1	0	0	0	0	0	0	1	1	1	0	0	A8IK50	
ENSMUST00000136106						0	0	0	2	0	1	0	0	0	0	0		
ENSMUST00000136107						5	8	4	25	2	4	610	1937	700	151	941		
ENSMUST00000136108	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	1	0	0	0	0	1	35	6	D3Z198	
ENSMUST00000136109						8	9	5	10	12	3	10	8	14	2	19		
ENSMUST00000136111						7	5	8	5	5	8	0	0	0	0	0		
ENSMUST00000136112						1	2	8	1	3	1	0	0	0	0	0		
ENSMUST00000136113						2	5	4	12	1	0	2	0	2	0	0		
ENSMUST00000136114						0	1	0	19	2	0	0	0	0	0	0		
ENSMUST00000136116						2	1	0	3	2	1	0	0	0	0	0		
ENSMUST00000136118						12	8	24	98	14	0	0	0	0	0	1		
ENSMUST00000136119						24	21	14	9	17	12	0	0	0	0	0		
ENSMUST00000136120						3	2	0	0	3	1	0	0	0	1	1		
ENSMUST00000136121						4	3	3	0	2	1	3	12	2	4	6		
ENSMUST00000136122						0	4	11	6	4	1	0	925	94	0	449		
ENSMUST00000136123						0	0	0	54	5	0	17	13	14	26	16		
ENSMUST00000136124						2	1	9	0	2	1	0	1	0	0	1		
ENSMUST00000136125						2	0	13	9	0	2	0	0	0	0	0		
ENSMUST00000136126						247	272	554	289	245	141	7	36	19	5	20		
ENSMUST00000136128						0	0	1	10	5	2	17	7	20	5	15		
ENSMUST00000136129	ENSMUSG00000022313	15	51877429	51884614	1	0	0	0	16	2	0	3	81	36	63	11	G3XA22	
ENSMUST00000136130						0	0	0	0	0	0	1	6	0	2	1		
ENSMUST00000136131						1	0	0	0	1	0	154	615	168	2455	486		
ENSMUST00000136132						0	0	0	0	2	0	4	2	6	1	12		
ENSMUST00000136133						3	2	5	7	2	0	1	2	0	2	1		
ENSMUST00000136134						2	1	3	3	0	1	0	0	0	0	0		
ENSMUST00000136135						5	0	0	3	4	1	2	9	3	0	3		
ENSMUST00000136136						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000136137	ENSMUSG00000040599	11	71019611	71027371	1	0	0	2	0	0	0	0	0	4	0	4	A3QK66	
ENSMUST00000136138						5	4	19	15	12	17	0	0	0	0	5		
ENSMUST00000136139	ENSMUSG00000038766	3	95181766	95217916	-1	0	0	0	46	0	0	213	362	520	216	453		P81069
ENSMUST00000136141	ENSMUSG00000041476	X	157698910	157752591	1	3	1	3	1	0	0	0	0	0	1	0	B1AW13	
ENSMUST00000136142						7	2	4	13	10	8	0	0	1	0	0		
ENSMUST00000136143						3	4	4	80	0	3	0	28	8	0	0		
ENSMUST00000136144						101	103	118	70	87	82	13	63	29	4	64		
ENSMUST00000136145						3	0	0	0	0	0	12	18	28	3	3		
ENSMUST00000136146						0	0	2	2	0	1	0	0	0	0	0		
ENSMUST00000136147						8	5	17	11	16	10	0	0	0	0	5		
ENSMUST00000136148	ENSMUSG00000002227	3	104794836	104818563	-1	0	0	4	74	0	0	0	0	0	0	18	D3YYR1	
ENSMUST00000136150	ENSMUSG00000001436	10	77032241	77061002	1	0	4	0	1	4	0	0	0	0	0	0	D3YU74	
ENSMUST00000136151						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136153						0	0	0	58	4	0	0	0	0	0	0		
ENSMUST00000136154	ENSMUSG00000032327	9	58063788	58153996	1	4	1	0	0	0	0	0	0	0	0	0	E9Q9S7	
ENSMUST00000136155						13	0	4	0	7	0	0	237	52	24	107		
ENSMUST00000136156						3	3	0	2	4	0	0	0	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136157	ENSMUSG00000043962	4	126164082	126202760	-1	1	2	4	0	3	0	0	0	2	0	0	A2AJI3	
ENSMUST00000136158	ENSMUSG00000030759	7	113513834	113571511	1	1	0	11	0	0	1	27	99	176	145	90	D3Z4N9	
ENSMUST00000136159	ENSMUSG00000042523	12	84114366	84147498	1	0	1	0	0	2	0	0	0	0	0	0	D3YYU7	
ENSMUST00000136160						0	1	1	4	4	2	0	0	0	0	0		
ENSMUST00000136161						0	0	0	0	0	1	26	83	34	25	4		
ENSMUST00000136162						0	0	0	3	0	0	35	0	10	0	0		
ENSMUST00000136163						5	0	4	6	5	2	0	1	0	0	0		
ENSMUST00000136164						1	1	2	2	1	2	0	0	0	2	1		
ENSMUST00000136165						0	0	3	9	6	0	31	39	45	6	50		
ENSMUST00000136166	ENSMUSG00000040652	9	65668001	65690300	1	0	2	0	54	0	0	3	11	0	8	3	J3QJW9	
ENSMUST00000136167						0	0	0	0	0	0	0	0	17	0	15		
ENSMUST00000136168	ENSMUSG00000023030	15	100387898	100425072	-1	0	0	0	0	0	0	0	0	0	0	10	D6RGP0	
ENSMUST00000136169	ENSMUSG00000025409	10	127281956	127289018	-1	0	0	0	0	0	0	0	0	0	3	0	F7CV40	
ENSMUST00000136171	ENSMUSG00000037348	4	134496697	134510235	1	0	0	0	0	0	0	5	0	0	0	0	D3Z7K5	
ENSMUST00000136172	ENSMUSG00000047295	15	91838265	91861438	1	0	1	0	0	0	0	0	0	0	0	0	F6RMZ4	
ENSMUST00000136173						84	77	82	66	84	33	5	18	13	5	12		
ENSMUST00000136174						4	4	2	133	17	0	0	9	5	2	0		
ENSMUST00000136175	ENSMUSG00000084883	12	108206345	108275417	-1	7	6	17	128	9	1	0	1	2	0	7		E9Q6B2
ENSMUST00000136176						2427	2006	12100	5999	2634	1136	24	48	51	20	47		
ENSMUST00000136177						0	0	6	5	0	0	11	31	3	0	18		
ENSMUST00000136178						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000136179						4	6	5	5	7	1	0	7	0	0	0		
ENSMUST00000136180						10	7	11	0	13	6	0	3	2	0	2		
ENSMUST00000136181	ENSMUSG00000075415	2	31026206	31142008	-1	0	0	2	59	0	1	0	5	25	0	0	A2AQ47	
ENSMUST00000136182	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	0	7	0	0	F6UKN5	
ENSMUST00000136183	ENSMUSG00000039678	2	30133746	30152013	1	0	0	0	0	0	0	17	11	19	5	22	D6RJI8	
ENSMUST00000136184						0	1	0	2	0	3	0	0	0	0	0		
ENSMUST00000136185	ENSMUSG00000017119	11	101552149	101581951	1	2	0	6	1	0	1	0	0	0	0	0	G3UZH6	
ENSMUST00000136186	ENSMUSG00000043872	4	127047094	127061152	-1	7	1	24	36	12	0	0	0	5	0	4	A2A7U0	
ENSMUST00000136188						0	0	9	0	1	2	0	0	0	0	0		
ENSMUST00000136189	ENSMUSG00000029192	5	36490604	36593276	-1	10	0	0	56	28	6	99	1640	2169	543	3330	E9Q2V7	
ENSMUST00000136191	ENSMUSG00000023235	8	4325210	4360020	1	0	0	0	5	0	0	0	0	0	0	0	D3Z470	
ENSMUST00000136192						0	2	0	2	1	1	0	0	0	0	0		
ENSMUST00000136193						13	11	20	30	15	14	1	0	0	0	0		
ENSMUST00000136194	ENSMUSG00000010796	6	18050964	18109061	-1	0	0	0	0	0	1	0	0	0	0	0	D6RFV1	
ENSMUST00000136197	ENSMUSG00000025938	1	12866549	12992650	-1	8	18	5	27	4	4	0	0	0	0	0	A0A087WNX4	
ENSMUST00000136198						78	59	402	92	54	25	0	16	5	0	10		
ENSMUST00000136199						6	2	3	0	4	0	47	551	101	81	129		
ENSMUST00000136200	ENSMUSG00000029670	6	21949571	21976038	1	3	0	0	6	0	0	29	57	160	86	3	S4R2I3	
ENSMUST00000136202	ENSMUSG00000075249	2	82943634	83008937	1	2	2	0	1	1	1	0	0	0	0	0	F6ZQI5	
ENSMUST00000136203						6	2	5	1	3	3	0	19	37	0	13		
ENSMUST00000136205	ENSMUSG00000041064	9	65587160	65595967	1	0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000136207						0	0	1	2	1	1	0	3	2	0	1		
ENSMUST00000136208						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000136209						2	0	3	26	8	2	2	5	0	0	0		
ENSMUST00000136210						0	5	0	0	1	0	2	0	0	0	0		
ENSMUST00000136212						3	0	0	0	0	0	0	33	0	4	0		
ENSMUST00000136213	ENSMUSG00000003269	7	45806637	45814581	-1	0	1	0	0	0	1	0	0	0	0	0	D3Z5C3	
ENSMUST00000136214						20	15	41	196	21	6	0	14	9	0	3		
ENSMUST00000136215						4	1	6	4	10	2	8	4	0	0	4		
ENSMUST00000136216						13	13	57	24	16	15	93	529	199	40	470		
ENSMUST00000136219						0	9	15	5	4	6	73	112	42	0	65		
ENSMUST00000136220						3	3	5	5	11	4	0	0	0	0	0		
ENSMUST00000136221						1	1	2	4	4	0	0	0	0	0	0		
ENSMUST00000136222						23	15	60	39	45	10	0	0	0	0	0		
ENSMUST00000136223	ENSMUSG00000056148	10	127776386	127792697	1	190	147	536	346	254	74	2	3	2	1	9	Q6PHA1	
ENSMUST00000136225						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136226	ENSMUSG00000024925	19	5601873	5603439	1	2	0	0	0	2	0	63	0	0	3	0	F6ZDT4	
ENSMUST00000136227	ENSMUSG00000046959	5	108669878	108675569	-1	6	0	0	3	3	0	0	1	0	0	5	D3Z4W4	
ENSMUST00000136228	ENSMUSG00000026976	2	24420560	24475599	-1	0	0	0	0	2	6	0	0	0	0	0	A2AIU7	
ENSMUST00000136229						3	0	4	0	0	5	0	0	0	0	0		
ENSMUST00000136230						2	4	4	3	7	4	0	2	10	0	6		
ENSMUST00000136231	ENSMUSG00000008318	7	100845848	100863446	-1	0	0	0	67	1	0	2	5	2	0	9	D3Z306	
ENSMUST00000136232	ENSMUSG00000011096	7	44848991	44855421	1	0	0	1	23	0	0	0	4	0	2	3	D3Z4W3	
ENSMUST00000136233						1	0	9	3	4	0	0	8	0	0	6		
ENSMUST00000136234						1	1	3	0	3	2	1	0	0	2	0		
ENSMUST00000136235	ENSMUSG00000020290	11	23256041	23298249	1	5	4	9	6	7	3	0	0	0	4	15	A2AKT6	
ENSMUST00000136236	ENSMUSG00000032897	4	120757438	120831572	-1	0	0	0	0	0	0	0	0	0	0	0	A2A763	
ENSMUST00000136237	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	0	0	0	0	0	0	0	D6RI94	
ENSMUST00000136238						0	0	9	2	11	0	7609	23672	11819	6176	9499		
ENSMUST00000136239						0	0	3	49	1	0	0	0	1	0	6		
ENSMUST00000136240						0	0	7	8	5	4	0	0	0	0	4		
ENSMUST00000136241						0	0	0	0	0	0	0	4	0	0	0		
ENSMUST00000136242						23	20	54	48	27	19	2	18	4	6	12		
ENSMUST00000136243	ENSMUSG00000020439	11	3517523	3540612	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z525	
ENSMUST00000136244	ENSMUSG00000061086	11	104550663	104595753	1	1	2	2	0	3	2	0	0	0	0	0	F6XL79	
ENSMUST00000136245	ENSMUSG00000036646	2	25332338	25352212	1	2	2	10	54	8	4	0	3	0	0	0	A2AJ14	
ENSMUST00000136246	ENSMUSG00000040557	5	134932368	134942637	1	5	6	9	39	0	4	0	2	2	0	0	D3Z271	
ENSMUST00000136247	ENSMUSG00000052688	1	131688695	131715439	1	0	1	6	3	4	0	0	0	0	0	1	D3YZQ6	
ENSMUST00000136248						0	2	4	1	5	1	1	0	1	0	0		
ENSMUST00000136249						0	1	8	1	1	0	3	0	4	0	0		
ENSMUST00000136250						0	0	3	1	0	4	0	0	7	0	5		
ENSMUST00000136251						3	0	0	0	0	0	5	41	7	0	8		
ENSMUST00000136252	ENSMUSG00000033918	16	20279820	20302387	-1	0	0	5	0	0	0	0	0	23	0	0	D6RJ50	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136253	ENSMUSG00000049482	8	122476143	122484138	1	0	0	0	0	0	0	0	0	0	0	0	F6RF61	
ENSMUST00000136254						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136255	ENSMUSG00000039130	6	30366380	30391028	-1	0	0	0	0	3	0	0	0	3	0	1	D3Z0B2	
ENSMUST00000136256	ENSMUSG00000030590	7	29152511	29156234	-1	0	0	0	49	2	0	0	0	4	0	5	D3YXS7	
ENSMUST00000136257						4	4	0	3	5	4	0	0	0	0	0		
ENSMUST00000136258						0	0	1	0	1	0	14	11	54	3	82		
ENSMUST00000136259						8	6	21	11	7	9	32	46	51	3	46		
ENSMUST00000136260						2	1	17	24	4	0	0	0	0	0	0		
ENSMUST00000136261						2	1	10	0	2	0	4	15	4	0	0		
ENSMUST00000136262	ENSMUSG00000028457	4	43267159	43373833	1	1	0	0	0	2	0	0	0	0	0	0	D6RHC0	
ENSMUST00000136263	ENSMUSG00000030271	6	113326972	113335068	1	15	3	10	0	0	0	97	53	34	22	17		
ENSMUST00000136264						0	0	2	2	4	2	0	0	0	0	0		
ENSMUST00000136265	ENSMUSG00000042042	6	118107452	118139140	-1	0	0	0	0	3	0	6	200	48	22	0	D3Z5Q0	
ENSMUST00000136266						2	2	0	18	0	2	0	0	0	0	0		
ENSMUST00000136267						53	53	30	38	72	38	6	15	7	0	6		
ENSMUST00000136268	ENSMUSG00000051674	5	73481000	73560794	1	0	1	0	0	1	0	0	0	1	0	2	D3Z7G2	
ENSMUST00000136269						8	0	0	107	10	4	47	62	71	28	77		
ENSMUST00000136270						0	0	0	3	9	0	0	2	0	0	2		
ENSMUST00000136271						5	2	4	113	3	2	0	0	0	1	0		
ENSMUST00000136272	ENSMUSG00000051682	17	48264295	48275360	1	0	0	0	0	0	0	6	5	0	0	4	D3YY88	
ENSMUST00000136273						3	0	0	3	0	1	0	0	0	4	4		
ENSMUST00000136274	ENSMUSG00000046603	9	122805539	122836334	1	17	21	63	0	28	0	19	16	0	38	36	D6RHM0	
ENSMUST00000136275						80	52	153	210	110	36	32	130	52	12	106		
ENSMUST00000136277	ENSMUSG00000051159	X	102247381	102252181	-1	0	0	0	12	1	0	0	0	0	0	0	F6ZC52	
ENSMUST00000136278	ENSMUSG00000028641	4	119232915	119248975	1	7	5	26	13	8	0	0	7	13	0	0	F2Z499	
ENSMUST00000136279						4	9	5	4	14	7	0	0	0	0	0		
ENSMUST00000136280						2	2	0	0	9	4	0	0	0	0	0		
ENSMUST00000136281						2	3	7	0	0	3	0	3	0	0	2		
ENSMUST00000136282	ENSMUSG00000032231	9	69453620	69491795	1	7	2	0	4	7	5	0	131	51	0	52	B0V2N5	
ENSMUST00000136283						7	3	11	21	7	3	1	6	4	1	7		
ENSMUST00000136284						4	2	3	61	4	1	2	3	4	0	2		
ENSMUST00000136285						5	3	8	1	11	3	0	5	0	4	0		
ENSMUST00000136286	ENSMUSG00000039652	19	37021291	37208601	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z5R9	
ENSMUST00000136287						0	0	1	36	0	0	0	0	0	0	0		
ENSMUST00000136289						0	1	0	1	0	0	63	378	86	0	75		
ENSMUST00000136290						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136291						0	1	0	0	0	0	2	3	0	3	0		
ENSMUST00000136292	ENSMUSG00000000159	16	96361668	96525580	1	0	0	5	11	5	0	0	1	0	0	0	F7ATS8	
ENSMUST00000136293						0	2	0	0	0	0	8	72	0	0	16		
ENSMUST00000136295						38	24	138	43	24	17	7	11	16	1	50		
ENSMUST00000136296	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	0	0	0	0	246	0	207	A3KGK7	
ENSMUST00000136297						2	2	2	1	2	1	0	0	0	0	0		
ENSMUST00000136298						3	2	8	0	4	1	47	51	39	0	23		
ENSMUST00000136299	ENSMUSG00000041966	2	71055328	71099142	1	582	614	468	383	413	191	18	94	74	13	93	F6XZ79	
ENSMUST00000136300						0	1	0	0	0	0	0	11	5	5	6		
ENSMUST00000136301						4	2	2	1	3	0	0	1	0	0	0		
ENSMUST00000136303						0	0	10	60	3	1	0	3	0	0	6		
ENSMUST00000136304						0	0	0	0	0	0	0	31	10	11	4		
ENSMUST00000136307	ENSMUSG00000018900	11	53864542	53891660	-1	4	2	35	143	10	3	0	0	6	0	0	D6RH54	
ENSMUST00000136308						0	1	8	0	8	2	0	0	0	0	3		
ENSMUST00000136309	ENSMUSG00000078503	4	145510759	145539188	1	18	10	16	16	21	21	5	8	1	3	5	B1AVN4	
ENSMUST00000136310						3	0	35	7	3	4	42	157	22	11	29		
ENSMUST00000136311						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000136312	ENSMUSG00000008348	5	125385965	125390202	-1	1	0	4	9	0	0	309	980	661	51	498		P0CG50
ENSMUST00000136313	ENSMUSG00000072814	5	95742014	95746617	1	0	0	0	0	0	0	0	0	0	0	0	K9J7D1	
ENSMUST00000136314						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000136316						2	0	0	3	2	1	0	0	0	0	0		
ENSMUST00000136317						0	3	8	3	6	6	0	0	0	0	0		
ENSMUST00000136318						0	10	33	17	18	7	0	33	24	0	8		
ENSMUST00000136319	ENSMUSG00000027364	2	126709096	126783458	-1	16	17	48	29	15	6	2	10	5	11	4	D6RCG3	
ENSMUST00000136320	ENSMUSG00000066113	4	86053915	86428385	1	3	0	0	3	0	0	0	0	0	0	0	F6WY46	
ENSMUST00000136321						0	0	1	58	4	2	0	0	2	0	0		
ENSMUST00000136323						22	22	17	34	40	19	3	6	3	1	0		
ENSMUST00000136324	ENSMUSG00000019790	10	9755547	9901079	-1	2	1	0	1	0	0	0	0	0	0	0	F6WXQ4	
ENSMUST00000136325						2	0	12	0	7	2	0	0	2	0	8		
ENSMUST00000136326	ENSMUSG00000028455	4	43027690	43031710	-1	0	0	0	0	9	0	0	6	0	0	0	A2AG39	
ENSMUST00000136327	ENSMUSG00000003038	4	133964738	133968650	-1	0	3	0	0	0	0	36	113	81	0	50	B7ZCQ3	
ENSMUST00000136328	ENSMUSG00000040938	11	70212752	70216417	1	0	0	0	2	0	0	2	0	0	0	0	B7ZCB5	
ENSMUST00000136329						0	0	0	2	0	0	55	534	0	0	43		
ENSMUST00000136330						0	0	0	0	0	0	3	3	0	0	4		
ENSMUST00000136331	ENSMUSG00000026466	1	156004599	156036480	-1	0	1	7	0	10	1	623	1196	1023	409	1151	J3QQ40	
ENSMUST00000136332						9	6	11	2	1	6	0	0	0	0	0		
ENSMUST00000136333						6	7	9	57	6	3	0	0	0	0	0		
ENSMUST00000136334						1	3	0	3	5	0	2	1	4	2	0		
ENSMUST00000136335						0	13	16	7	11	10	44	47	43	10	76		
ENSMUST00000136336						7	6	13	5	13	3	1	2	4	0	7		
ENSMUST00000136337						3	5	25	12	5	2	0	0	0	0	0		
ENSMUST00000136338	ENSMUSG00000032327	9	58063788	58153996	1	2	3	9	1	6	3	0	0	0	0	1	D3YUA2	
ENSMUST00000136339						4	2	6	36	7	8	5	20	12	0	3		
ENSMUST00000136340						0	1	7	3	0	0	2	0	0	0	2		
ENSMUST00000136341	ENSMUSG00000034771	10	81574561	81590845	1	0	0	0	0	0	0	0	0	0	0	1	D3Z2J7	
ENSMUST00000136342	ENSMUSG00000028809	4	135320484	135353321	-1	4	5	2	8	0	0	72	0	625	0	584	E9PUK6	
ENSMUST00000136343	ENSMUSG00000020781	11	115814724	115823094	1	0	4	12	0	5	0	10	5	0	1	11	B1ATA6	
ENSMUST00000136344						3	0	3	1	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136345						0	1	4	6	5	2	0	0	0	0	0		
ENSMUST00000136346						1	3	4	25	0	1	47	127	40	158	49		
ENSMUST00000136347						3	0	11	2	0	0	0	0	0	0	0		
ENSMUST00000136348	ENSMUSG00000036959	X	48341358	48408049	1	0	0	11	30	0	0	68	57	46	0	116		A2AQH4
ENSMUST00000136351	ENSMUSG00000020459	11	29526408	29545279	1	0	0	2	17	6	0	0	0	0	0	0	Q5M6W8	
ENSMUST00000136352	ENSMUSG00000029352	5	113075839	113081584	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2L5	
ENSMUST00000136353						0	0	0	0	0	14	3116	3917	1698	250	1118		
ENSMUST00000136354	ENSMUSG00000019082	7	141429744	141437892	-1	0	2	3	4	5	1	0	0	0	0	0	E9PV90	
ENSMUST00000136355						12	14	21	12	9	6	1	6	3	0	10		
ENSMUST00000136356						1	0	5	8	5	1	0	16	5	0	4		
ENSMUST00000136358						8	8	21	13	4	4	0	12	0	0	0		
ENSMUST00000136360	ENSMUSG00000035969	4	43381979	43427088	1	0	0	5	3	6	0	0	0	0	0	0	B0R003	
ENSMUST00000136361	ENSMUSG00000026819	2	32414487	32451445	-1	0	0	0	0	0	0	0	0	0	0	5	Z4YLR9	
ENSMUST00000136362						0	0	4	5	3	0	0	0	0	0	0		
ENSMUST00000136363						1	0	0	14	3	0	0	0	0	0	0		
ENSMUST00000136365						3	3	15	3	2	0	0	4	2	2	0		
ENSMUST00000136366						1	0	0	0	0	0	1	10	6	17	6		
ENSMUST00000136367						0	0	0	0	0	0	4	20	1	2	7		
ENSMUST00000136368						0	0	0	0	0	0	0	32	5	7	20		
ENSMUST00000136369	ENSMUSG00000018733	11	83294642	83302586	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SWQ9	
ENSMUST00000136370						3	9	1	2	4	0	15	38	39	3	75		
ENSMUST00000136372						0	1	0	12	1	1	0	0	0	0	0		
ENSMUST00000136373	ENSMUSG00000037640	7	27731389	27753702	1	0	2	0	0	0	0	0	0	0	4	0	D6RFC9	
ENSMUST00000136374						0	0	3	0	0	0	99	34	152	34	62		
ENSMUST00000136375	ENSMUSG00000052142	17	32390659	32403583	-1	0	0	14	184	23	0	0	69	0	0	12		
ENSMUST00000136377	ENSMUSG00000028796	4	128654702	128752881	1	3	3	0	26	2	0	0	0	0	0	0	B1AS97	
ENSMUST00000136378						11	11	5	7	13	18	14	12	5	7	10		
ENSMUST00000136379						25	15	106	130	23	10	14	10	46	0	49		
ENSMUST00000136381	ENSMUSG00000022696	16	44240180	44333196	-1	0	0	0	24	26	0	23	35	14	0	55		Q6AXF6
ENSMUST00000136383	ENSMUSG00000014606	11	70644196	70647479	-1	2	0	8	28	4	3	11	2	0	0	0	Q5SX48	
ENSMUST00000136384	ENSMUSG00000041119	17	31386234	31476310	1	1	1	2	1	1	1	0	0	0	0	0	D3Z408	
ENSMUST00000136385						62	57	161	125	85	41	12	29	23	6	31		
ENSMUST00000136386						3	0	2	5	1	2	0	0	0	0	0		
ENSMUST00000136387						28	28	45	24	39	26	27	28	32	6	37		
ENSMUST00000136388						5	3	42	7	0	0	0	2	0	9	6		
ENSMUST00000136389						0	0	0	0	1	2	0	3	0	0	0		
ENSMUST00000136390	ENSMUSG00000022568	15	76047158	76069784	-1	0	0	0	0	0	6	60	374	57	28	113	F6RIN9	
ENSMUST00000136391						2	0	3	0	2	0	4	0	8	4	5		
ENSMUST00000136392	ENSMUSG00000041654	11	113244853	113650079	-1	0	0	1	0	1	2	0	1	3	0	0	B1ARC3	
ENSMUST00000136393						3	0	2	3	4	2	0	0	0	0	0		
ENSMUST00000136394	ENSMUSG00000022757	16	56690332	56717450	-1	0	0	0	0	1	0	0	4	0	2	0	B8JJG8	
ENSMUST00000136395						2	2	2	5	0	0	1	9	3	0	3		
ENSMUST00000136396	ENSMUSG00000053852	X	56870163	57001558	1	12	0	16	11	0	7	0	0	0	0	0	B7ZCD1	
ENSMUST00000136397	ENSMUSG00000026466	1	156004599	156036480	-1	0	1	0	0	0	0	41	40	46	38	0	D3YZJ9	
ENSMUST00000136398	ENSMUSG00000028957	4	151003652	151044665	-1	12	13	23	46	0	0	0	0	5	2	8	E9PV88	
ENSMUST00000136399	ENSMUSG00000036912	9	14696230	14740733	-1	3	4	9	6	14	2	0	0	0	1	1	F6VRE5	
ENSMUST00000136402						1	3	4	47	5	0	2	10	8	0	3		
ENSMUST00000136403						0	3	0	0	0	2	0	0	0	0	1		
ENSMUST00000136404	ENSMUSG00000036109	X	51117269	51206532	-1	0	0	0	0	0	0	9	15	0	0	0	S4R267	
ENSMUST00000136405	ENSMUSG00000033149	16	45746243	45953598	-1	2	0	2	0	0	0	0	0	0	0	0	D3Z231	
ENSMUST00000136407						0	1	0	25	4	0	0	0	0	0	0		
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ENSMUST00000136409	ENSMUSG00000028809	4	135320484	135353321	-1	3	0	0	1	0	0	0	6	0	0	10	F6T4M4	
ENSMUST00000136410						14	0	2	0	0	0	15	113	10	8	10		
ENSMUST00000136411						3	2	9	3	1	1	0	0	0	0	0		
ENSMUST00000136412						12	6	10	14	6	2	24	17	28	3	15		
ENSMUST00000136413	ENSMUSG00000015522	3	95434388	95497240	1	0	0	0	0	0	0	0	0	0	0	16	F7C9F6	
ENSMUST00000136414						1	0	10	11	6	2	0	0	0	1	2		
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ENSMUST00000136416						2	1	14	13	7	2	0	0	0	0	2		
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ENSMUST00000136420						6	0	2	20	0	1	0	0	0	0	0		
ENSMUST00000136421	ENSMUSG00000052581	6	80018877	80810143	1	0	6	5	4	15	0	0	0	0	0	0	E9Q8Y9	
ENSMUST00000136423	ENSMUSG00000001909	8	84686307	84699808	1	3	3	3	0	0	0	0	4	0	0	4	G3V019	
ENSMUST00000136424						0	0	0	54	2	0	0	0	0	0	0		
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ENSMUST00000136426						7	4	15	20	11	8	3	5	5	0	17		
ENSMUST00000136427						1	0	4	51	6	0	0	0	0	0	0		
ENSMUST00000136429	ENSMUSG00000032473	9	99689461	99717267	-1	2	0	6	13	4	2	0	0	0	0	0		P56857
ENSMUST00000136430						0	0	48	0	9	1	0	0	0	0	0		
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ENSMUST00000136432	ENSMUSG00000053684	10	121739937	121752878	1	42	3	3	575	23	47	46	220	99	12	0	D3Z5F2	
ENSMUST00000136433						1	0	1	0	1	0	0	0	0	0	0		
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ENSMUST00000136435						15	9	13	16	8	8	0	2	0	0	0		
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ENSMUST00000136437						3	1	3	1	5	1	0	0	0	0	0		
ENSMUST00000136439						1	2	0	0	4	0	7	0	0	0	10		
ENSMUST00000136440						0	0	1	3	2	0	0	0	0	0	2		
ENSMUST00000136441	ENSMUSG00000047446	12	40005447	40038025	-1	834	927	513	992	912	372	9	36	32	4	44	G3UVX1	
ENSMUST00000136442						3	1	24	6	9	1	0	3	2	0	3		
ENSMUST00000136443						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136444						0	0	1	9	5	0	3	9	4	0	10		
ENSMUST00000136445						0	2	1	4	2	0	0	0	0	3	0		
ENSMUST00000136446	ENSMUSG00000009356	11	87806428	87828289	-1	0	0	5	2	0	1	0	0	0	0	0	A7M7R7	
ENSMUST00000136448						352	434	445	275	431	194	39	95	90	14	92		
ENSMUST00000136449						0	0	1	4	0	0	0	0	0	0	0		
ENSMUST00000136450						5	1	1	1	0	2	0	0	1	1	1		
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ENSMUST00000136453						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000136455						33	22	26	23	37	3	8	18	7	2	17		
ENSMUST00000136457						1	1	1	37	1	2	0	0	0	0	0		
ENSMUST00000136459						21	11	61	19	27	12	2	8	0	0	9		
ENSMUST00000136460	ENSMUSG00000035392	2	37798991	38287390	-1	4	0	35	2	7	0	0	2	0	0	0	A2ALU3	
ENSMUST00000136461						1	0	0	0	0	3	0	0	0	0	1		
ENSMUST00000136462						4	0	11	2	3	0	0	0	0	0	0		
ENSMUST00000136463	ENSMUSG00000020532	11	84129672	84401651	1	0	1	1	9	2	0	0	0	0	0	0	V9GWR9	
ENSMUST00000136464						1	3	12	4	1	1	0	0	0	0	0		
ENSMUST00000136465	ENSMUSG00000060675	19	7557459	7588545	1	23	22	51	28	22	22	0	0	7	0	5		Q8R3U1
ENSMUST00000136466						0	0	6	0	0	0	14	1	0	16	0		
ENSMUST00000136467						2	1	2	5	2	3	0	0	0	0	0		
ENSMUST00000136468						5	2	0	2	1	0	1	1	1	1	1		
ENSMUST00000136469	ENSMUSG00000018068	11	86210681	86257575	-1	0	0	10	0	3	0	0	0	0	0	0	Q5SXZ7	
ENSMUST00000136470						0	0	0	0	0	0	0	0	8	0	4		
ENSMUST00000136471	ENSMUSG00000032745	13	111425680	111490111	-1	0	0	6	0	0	0	134	1377	333	313	72	D6RCY3	
ENSMUST00000136473						5	2	13	7	7	3	0	0	0	0	0		
ENSMUST00000136474	ENSMUSG00000034614	11	3330401	3342971	1	0	1	3	0	0	2	71	18	90	0	34	Z4YMN3	
ENSMUST00000136475	ENSMUSG00000029127	5	38189735	38220457	-1	0	3	0	0	0	0	8	0	16	3	0	D6RFB4	
ENSMUST00000136476						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000136479	ENSMUSG00000038147	1	171839697	171890718	1	0	0	0	0	0	0	661	5910	2385	5990	2152	E9Q9E8	
ENSMUST00000136480	ENSMUSG00000022487	15	103402405	103430470	-1	2	3	0	0	0	1	0	0	0	0	0		Q9DAN6
ENSMUST00000136481	ENSMUSG00000002455	2	181591868	181655660	1	18	10	16	12	44	12	568	1395	904	240	793		Q91YR7
ENSMUST00000136482						2	0	4	1	4	1	0	0	0	0	0		
ENSMUST00000136483	ENSMUSG00000029507	5	110773667	110780659	-1	6	3	20	34	8	5	0	0	0	2	1	D3YWU8	
ENSMUST00000136484						4	1	7	6	5	1	0	1	2	0	1		
ENSMUST00000136485						6	0	8	9	11	8	7	12	3	0	6		
ENSMUST00000136487						1	3	16	3	4	3	0	15	2	2	8		
ENSMUST00000136488	ENSMUSG00000005089	2	102658659	102790784	1	1	0	0	0	0	1	0	0	0	1	0	F7CAM6	
ENSMUST00000136490	ENSMUSG00000029192	5	36490604	36593276	-1	1	4	11	2	5	0	0	0	0	0	0	D3YVW3	
ENSMUST00000136491	ENSMUSG00000034255	11	103331497	103363692	-1	0	0	10	11	0	0	0	0	0	0	0	E9Q6V8	
ENSMUST00000136492	ENSMUSG00000023286	4	155943831	155959604	1	0	0	0	51	0	0	2	4	8	0	13	B0QZM0	
ENSMUST00000136493	ENSMUSG00000070390	11	71153102	71230733	-1	0	0	1	14	0	0	0	0	0	0	0	Q2LK61	
ENSMUST00000136494	ENSMUSG00000037533	11	54522847	54699285	1	7	2	10	0	5	4	37	48	128	10	131	F7ACB1	
ENSMUST00000136495	ENSMUSG00000004788	12	85219481	85226628	1	0	0	0	0	0	0	108	0	68	0	62	D3Z487	
ENSMUST00000136496						2	2	17	7	3	3	0	0	0	0	0		
ENSMUST00000136497						4	4	2	4	4	1	0	0	0	0	0		
ENSMUST00000136498						18	0	25	24	27	0	34	6	58	1	56		
ENSMUST00000136499	ENSMUSG00000029883	6	40920437	40940557	-1	2	4	7	2	2	0	0	0	0	0	0	D3Z4W5	
ENSMUST00000136501	ENSMUSG00000045160	6	83349147	83360136	1	12	9	38	18	11	4	0	14	10	32	18	Q14A77	Q8CEI1
ENSMUST00000136502	ENSMUSG00000034349	3	69004738	69034623	1	0	4	1	82	0	2	0	0	0	0	7	Q3U763	
ENSMUST00000136504						0	1	8	0	0	0	4	19	4	0	16		
ENSMUST00000136505						8	5	11	4	7	1	5	0	0	0	0		
ENSMUST00000136506						3	0	0	0	0	0	7	47	36	16	39		
ENSMUST00000136507	ENSMUSG00000029446	5	129765558	129787449	-1	4	0	0	0	2	2	29	19	17	34	10	D3Z666	
ENSMUST00000136508						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000136509						18	6	15	10	13	8	406	1055	612	65	608		
ENSMUST00000136510	ENSMUSG00000031256	X	134059187	134086819	1	0	0	0	0	0	0	2	0	0	0	8	A2AEK3	
ENSMUST00000136511						3	0	5	2	8	3	0	0	1	2	0		
ENSMUST00000136512	ENSMUSG00000034317	3	69035288	69044755	-1	4	4	0	0	1	0	0	0	0	0	3	D3Z0I5	
ENSMUST00000136513	ENSMUSG00000027438	2	148693985	148732467	-1	32	0	149	0	30	12	1	17	4	5	6	D6RHL2	
ENSMUST00000136514						1	0	3	0	2	0	0	0	0	0	0		
ENSMUST00000136516	ENSMUSG00000052446	8	71951038	71993408	1	0	0	0	0	0	0	0	0	0	0	0	D3Z552	
ENSMUST00000136517						0	1	4	3	2	0	1	0	0	0	0		
ENSMUST00000136519						1	2	0	0	1	1	5	60	35	17	18		
ENSMUST00000136520						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000136521	ENSMUSG00000053963	1	180432387	180483504	-1	32	23	157	57	63	35	0	0	0	0	0		Q0VBF8
ENSMUST00000136522						1	1	3	0	0	1	0	0	5	0	2		
ENSMUST00000136523	ENSMUSG00000005043	11	119343425	119355536	-1	0	30	0	34	0	21	0	183	0	0	0	G3XA02	
ENSMUST00000136524	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	4	3	0	0	0	0	0	0	0	F7AYY9	
ENSMUST00000136526						2	0	0	4	0	2	2	0	0	0	0		
ENSMUST00000136527						1	0	4	25	2	2	4	0	3	18	3		
ENSMUST00000136528						0	4	6	1	2	3	1	12	2	0	6		
ENSMUST00000136529						2	2	2	1	2	1	0	0	12	0	7		
ENSMUST00000136530	ENSMUSG00000032020	9	41011098	41161697	-1	0	0	1	138	3	2	0	1	0	0	2	D3YVT5	
ENSMUST00000136532						6	1	1	27	9	3	175	268	450	49	270		
ENSMUST00000136533	ENSMUSG00000051579	X	136168984	136172342	-1	0	0	1	0	1	3	0	2	0	0	2	A2AJR9	
ENSMUST00000136535						2	8	12	3	1	2	15	190	46	21	83		
ENSMUST00000136536	ENSMUSG00000034614	11	3330401	3342971	1	0	0	0	0	0	0	7	0	50	12	64	Z4YN57	
ENSMUST00000136537						71	68	129	71	88	49	7	16	3	17	8		
ENSMUST00000136539	ENSMUSG00000046311	11	49203292	49218816	1	6	7	0	9	5	4	49	227	124	46	42	J3JS23	
ENSMUST00000136540						0	3	0	8	3	2	0	0	0	0	1		
ENSMUST00000136541						0	0	0	0	0	1	0	50	10	0	0		
ENSMUST00000136543						0	0	0	0	0	0	0	0	2	0	2		
ENSMUST00000136544						0	0	3	0	0	0	0	7	0	11	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136545						17	30	16	12	8	11	2	17	15	7	11		
ENSMUST00000136546	ENSMUSG00000051736	10	39118804	39133914	-1	0	1	1	0	0	0	0	0	0	0	0	B2RVF6	Q8CF36
ENSMUST00000136547						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136548	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	0	0	0	0	0	0	0	0	0	B4YB29	
ENSMUST00000136549	ENSMUSG00000020173	11	12236608	12464960	-1	3	0	0	0	1	2	0	0	0	0	0	F6ZEZ1	
ENSMUST00000136550						4	3	1	4	1	1	31	62	59	1	52		
ENSMUST00000136551	ENSMUSG00000025576	11	118489762	118911597	-1	2	2	0	109	8	3	0	0	0	0	0	A2A4W9	
ENSMUST00000136552	ENSMUSG00000034285	11	4873951	4894200	1	6	12	12	3	7	3	2	22	6	0	19	F2Z416	
ENSMUST00000136553						0	0	3	0	0	2	0	0	0	0	0		
ENSMUST00000136554						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136556						149	134	161	139	199	98	4	17	15	6	25		
ENSMUST00000136558						0	13	12	15	12	0	15	13	5	9	10		
ENSMUST00000136559						29	24	61	37	25	12	3	7	2	0	12		
ENSMUST00000136560	ENSMUSG00000042055	7	129591863	129635738	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136561	ENSMUSG00000038775	9	119052778	119071525	1	2	2	4	0	2	2	0	13	2	1	0	D3YZN9	
ENSMUST00000136562						9	7	18	8	15	12	14	56	5	0	16		
ENSMUST00000136563						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136564						4	2	3	4	1	2	2	0	2	0	0		
ENSMUST00000136565	ENSMUSG00000029712	5	137553517	137569582	1	0	0	0	0	1	0	0	0	0	0	0	D3Z4L2	
ENSMUST00000136567	ENSMUSG00000029402	5	124483134	124491124	1	3	0	20	17	3	2	0	0	0	0	2	D3YTL6	
ENSMUST00000136568	ENSMUSG00000031928	9	14784654	14837123	1	4	0	0	2	4	0	2	0	0	0	1	B2KF75	
ENSMUST00000136569						11	8	33	77	11	3	0	0	0	0	0		
ENSMUST00000136570						2	1	8	2	4	4	2	15	6	0	11		
ENSMUST00000136572						0	0	0	0	0	0	0	6	5	0	15		
ENSMUST00000136573						0	0	3	59	0	0	2	0	5	1	3		
ENSMUST00000136574						4	1	19	53	15	2	0	0	0	0	0		
ENSMUST00000136575	ENSMUSG00000035245	6	97110024	97149182	-1	0	0	0	0	0	2	0	0	0	0	0	D3Z459	
ENSMUST00000136576						25	15	54	166	28	20	0	0	0	0	0		
ENSMUST00000136577	ENSMUSG00000030562	7	87246096	87398710	1	3	0	0	0	0	0	0	0	0	0	0	S4R1R3	
ENSMUST00000136579	ENSMUSG00000024914	19	5422805	5424979	-1	0	0	0	0	3	0	812	1613	693	348	578	G3UXH5	
ENSMUST00000136580						1	2	10	12	0	2	0	0	0	0	0		
ENSMUST00000136581						0	0	2	1	1	0	1	0	0	0	0		
ENSMUST00000136582						100	128	362	113	98	61	30	231	94	23	153		
ENSMUST00000136583						1	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000136584	ENSMUSG00000043857	11	116918863	116986948	1	2	3	0	0	0	0	0	0	0	0	0	F7BPB5	
ENSMUST00000136585	ENSMUSG00000021196	13	6579768	6648777	-1	3	2	5	2	2	0	14	6	16	6	6	D3YUA3	
ENSMUST00000136586	ENSMUSG00000054256	5	115429599	115455698	1	3	1	7	8	0	1	0	0	0	0	0		
ENSMUST00000136587						0	0	0	0	0	0	34	0	63	9	12		
ENSMUST00000136588	ENSMUSG00000026854	2	30982279	31023586	1	0	0	0	0	0	0	0	0	3	0	5	F6QWP5	
ENSMUST00000136589						5	4	5	4	2	2	1	0	26	0	1		
ENSMUST00000136590						1	0	0	0	0	0	103	127	0	1	0		
ENSMUST00000136591	ENSMUSG00000044224	15	10446756	10470516	-1	1	0	10	14	1	1	32	149	73	65	76	E9Q8D0	
ENSMUST00000136592	ENSMUSG00000065952	8	3567990	3584939	1	3	0	0	0	4	0	0	0	0	0	0	Q8C7T0	
ENSMUST00000136593						9	13	16	37	20	14	15	41	36	5	31		
ENSMUST00000136594						0	0	0	0	0	0	5	0	2	1	2		
ENSMUST00000136595						1	0	1	2	2	1	0	0	0	0	0		
ENSMUST00000136596	ENSMUSG00000033379	4	117884326	117887333	-1	0	0	7	6	0	0	36	35	23	0	17	A0A0A0MQI2	
ENSMUST00000136597						7	0	0	12	4	1	10	0	0	0	0		
ENSMUST00000136598						2	6	9	3	6	4	1	5	1	1	1		
ENSMUST00000136599						3	1	7	4	4	0	0	0	0	0	0		
ENSMUST00000136601	ENSMUSG00000027165	2	101560781	101649532	-1	0	0	0	0	1	0	0	0	0	2	0	H3BJ20	
ENSMUST00000136602	ENSMUSG00000009246	7	143069153	143094642	-1	0	2	1	0	3	4	0	0	0	0	0	F7CCW2	
ENSMUST00000136603						2	2	7	5	3	1	2	9	0	0	10		
ENSMUST00000136604						4	0	2	0	2	0	26	821	50	117	0		
ENSMUST00000136605						23	11	17	22	12	17	112	427	288	11	450		
ENSMUST00000136606						5	5	21	13	9	3	0	5	0	0	3		
ENSMUST00000136607						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000136608						0	0	7	0	1	0	0	0	0	0	0		
ENSMUST00000136609	ENSMUSG00000038695	7	44467980	44471662	1	0	0	0	0	0	0	11	16	0	4	0	Q8VCY7	
ENSMUST00000136610						6	2	0	0	4	0	0	0	0	0	0		
ENSMUST00000136611						1	0	0	1	1	0	3	24	5	0	17		
ENSMUST00000136612						1	0	0	0	0	0	4	3	0	0	2		
ENSMUST00000136613	ENSMUSG00000028159	3	137931007	137981545	-1	0	30	112	10	0	0	0	0	0	0	0	Q3TEK6	
ENSMUST00000136614	ENSMUSG00000042708	1	153425162	153452574	1	14	13	66	83	29	14	1	2	0	0	1	J3QQ47	
ENSMUST00000136615						3	2	6	3	3	1	2	0	6	1	7		
ENSMUST00000136616	ENSMUSG00000055541	7	4003402	4063204	-1	2	0	4	0	0	0	0	47	0	0	23	D6RGS7	Q8BG84
ENSMUST00000136617						0	0	0	8	0	1	2	0	3	0	1		
ENSMUST00000136618						0	0	2	0	0	0	99	564	122	382	67		
ENSMUST00000136619						12	8	49	31	7	6	0	0	1	1	1		
ENSMUST00000136621	ENSMUSG00000027405	2	130274430	130279313	1	0	0	0	0	0	0	0	22	0	9	0	E0CXZ0	
ENSMUST00000136622						0	0	0	0	0	0	0	14	5	2	0		
ENSMUST00000136623						0	3	0	2	0	0	0	0	7	4	0		
ENSMUST00000136624						11	8	12	4	17	4	5	9	7	0	4		
ENSMUST00000136625						0	0	1	0	0	0	0	2	0	0	9		
ENSMUST00000136626						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000136627						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136628	ENSMUSG00000074754	2	144594054	144595366	1	1	6	4	2	5	3	6	26	9	80	12	Q3V460	
ENSMUST00000136629						2	0	0	118	0	1	0	0	3	0	0		
ENSMUST00000136630						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000136631						73	61	84	74	72	23	6	16	12	2	27		
ENSMUST00000136633						2	0	4	0	4	2	18	6	9	0	20		
ENSMUST00000136634	ENSMUSG00000039754	5	136136146	136141615	1	0	0	3	3	2	1	0	0	9	2	0	D3Z7X9	
ENSMUST00000136635	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	5	111	73	50	91	D3YV81	
ENSMUST00000136636						2	0	0	0	0	0	2	1	1	15	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136637						1	2	2	7	6	1	10	20	24	0	21		
ENSMUST00000136638						2	2	9	6	3	4	0	10	0	0	0		
ENSMUST00000136640	ENSMUSG00000070000	8	71708387	71725716	-1	6	0	0	74	12	0	12	58	25	0	18	D6RCG0	
ENSMUST00000136641						0	0	1	0	2	2	0	2	0	0	0		
ENSMUST00000136642	ENSMUSG00000060988	2	54436317	55118309	1	0	0	0	32	4	0	0	0	0	0	0	B1AY79	
ENSMUST00000136643	ENSMUSG00000023791	16	32084418	32099738	-1	0	0	0	0	0	0	0	0	0	11	0	F6XTT6	
ENSMUST00000136644						0	0	0	28	0	8	0	0	0	0	0		
ENSMUST00000136645	ENSMUSG00000048782	7	114743694	114850383	1	0	0	1	56	8	0	0	0	0	1	0	D3Z267	
ENSMUST00000136646	ENSMUSG00000039852	4	150281646	150621966	1	0	0	7	0	0	2	57	96	80	1	92	A2A7T1	
ENSMUST00000136647						0	4	0	7	2	2	0	0	0	0	0		
ENSMUST00000136648						0	0	0	51	0	0	0	0	0	0	0		
ENSMUST00000136649						3	0	0	0	2	0	2	2	4	0	18		
ENSMUST00000136650	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	0	0	0	0	0	0	0	A2AEB6	
ENSMUST00000136651						52	54	98	163	77	37	1	2	1	0	6		
ENSMUST00000136652	ENSMUSG00000030615	7	90450700	90457229	-1	3	0	0	0	5	2	0	0	12	48	9	D6RG44	
ENSMUST00000136653						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000136654						0	0	2	2	2	1	2	5	0	0	6		
ENSMUST00000136655						65	42	485	110	36	17	2	16	10	2	9		
ENSMUST00000136656						25	14	45	54	17	9	7	5	0	0	0		
ENSMUST00000136657						7	3	2	1	7	3	0	0	0	0	0		
ENSMUST00000136659	ENSMUSG00000019843	10	39368855	39565381	1	8	0	0	0	4	4	39	55	20	17	37	D3YZ57	
ENSMUST00000136660						5	4	5	1	1	0	0	0	0	0	0		
ENSMUST00000136661	ENSMUSG00000021792	14	40993740	41013788	-1	1	0	2	4	1	0	2	0	0	15	14	D3Z252	
ENSMUST00000136662	ENSMUSG00000025583	11	119602905	119899576	1	13	12	24	12	19	13	11	0	18	0	0	F7CN67	
ENSMUST00000136663	ENSMUSG00000020827	11	70562881	70614483	1	0	14	36	0	0	0	68	227	112	5	41	F7AMS7	
ENSMUST00000136664						11	4	0	10	10	7	0	11	7	0	6		
ENSMUST00000136665						0	0	5	2	2	1	5	11	7	0	7		
ENSMUST00000136666						5	5	3	1	3	4	11	5	0	0	0		
ENSMUST00000136667						0	0	1	0	4	0	153	44	395	128	294		
ENSMUST00000136668						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000136669						0	4	0	3	0	2	0	2	0	0	7		
ENSMUST00000136670						4	4	5	4	6	4	0	11	2	0	18		
ENSMUST00000136671	ENSMUSG00000040624	10	3740364	3967303	1	18	0	13	11	22	0	0	0	0	0	23	F6S200	
ENSMUST00000136674						0	0	0	0	0	0	3	0	0	0	4		
ENSMUST00000136675						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000136676						1	0	1	0	0	1	0	204	65	4	21		
ENSMUST00000136677						0	0	2	0	0	0	6	0	20	6	25		
ENSMUST00000136678						8	5	16	3	2	3	35	310	58	4	109		
ENSMUST00000136679	ENSMUSG00000038695	7	44467980	44471662	1	1	0	4	2	3	2	10	29	5	0	13	D6RDE6	
ENSMUST00000136680						18	27	66	185	45	29	16	64	20	7	59		
ENSMUST00000136681						4	5	4	5	2	6	9	25	13	2	26		
ENSMUST00000136682	ENSMUSG00000000384	11	6615598	6626067	-1	0	0	0	3	2	0	0	0	3	0	0	Q5SWP1	
ENSMUST00000136684						1	5	18	0	5	3	0	0	0	0	0		
ENSMUST00000136685						7	4	16	7	7	5	2	2	3	0	5		
ENSMUST00000136686	ENSMUSG00000000394	2	62474530	62483650	-1	1	0	1	2	4	0	0	0	0	1	0	A2AS86	
ENSMUST00000136687	ENSMUSG00000030890	7	105736592	105742925	1	4	2	26	144	7	2	5	10	5	2	19	D3YZA5	
ENSMUST00000136688						3	1	6	0	5	0	0	96	34	20	16		
ENSMUST00000136689						0	0	5	0	1	0	0	0	1	0	0		
ENSMUST00000136691	ENSMUSG00000046311	11	49203292	49218816	1	0	0	0	0	0	0	0	0	1	0	0	I7HPA9	
ENSMUST00000136692						7	6	28	10	0	2	0	0	0	0	0		
ENSMUST00000136694						95	81	60	119	125	66	2	14	5	4	9		
ENSMUST00000136695	ENSMUSG00000059741	9	110741861	110769798	1	2	0	5	4	2	0	0	0	0	0	0	A0A0G2JDM3	
ENSMUST00000136696						0	0	0	0	0	0	0	32	0	0	0		
ENSMUST00000136698						25	22	56	25	23	11	0	0	0	0	0		
ENSMUST00000136699	ENSMUSG00000022960	16	91677268	91688765	-1	0	0	0	0	4	0	81	33	90	14	39	F7BX63	
ENSMUST00000136700						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000136701						0	6	0	0	1	3	0	0	0	0	0		
ENSMUST00000136702						0	0	0	0	1	1	0	0	3	0	0		
ENSMUST00000136703						7	1	22	8	1	0	0	85	84	0	107		
ENSMUST00000136704	ENSMUSG00000057363	1	43746966	43827800	-1	1	3	0	0	0	0	0	0	0	0	2	D6RIQ1	
ENSMUST00000136705						0	1	0	151	5	0	8	11	18	3	12		
ENSMUST00000136706						25	14	28	55	37	19	80	182	167	8	177		
ENSMUST00000136707						2	0	0	1	1	0	5	10	4	0	9		
ENSMUST00000136708						132	116	152	87	128	70	8	18	13	0	18		
ENSMUST00000136709						3	0	0	1	0	0	2	5	0	0	2		
ENSMUST00000136710	ENSMUSG00000052406	2	26953563	26964386	-1	0	0	0	0	0	0	0	0	0	0	12	A2ALB1	
ENSMUST00000136711	ENSMUSG00000066043	4	132355923	132422489	-1	5	0	0	0	6	1	0	0	0	0	0	A0A0A0MQL5	
ENSMUST00000136712						2	0	0	0	0	0	5	0	5	0	12		
ENSMUST00000136713	ENSMUSG00000045983	16	20668313	20692884	1	0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000136714						5	0	7	8	5	0	0	0	0	0	0		
ENSMUST00000136715						8	2	0	4	2	0	0	0	6	0	6		
ENSMUST00000136716						2	4	13	7	0	1	0	2	0	0	1		
ENSMUST00000136717						1	4	0	0	2	1	5	20	0	1	0		
ENSMUST00000136718	ENSMUSG00000049922	2	92452764	92460538	-1	2	0	0	0	2	3	0	0	0	0	0	M0QWB9	
ENSMUST00000136719	ENSMUSG00000078894	2	176226569	176240328	1	0	0	0	0	0	0	0	0	0	0	0	D3YYR3	
ENSMUST00000136720	ENSMUSG00000020747	11	115765433	115799366	1	0	0	0	0	0	0	0	0	0	0	0	B1AT96	
ENSMUST00000136721						0	0	0	0	0	0	230	70	158	18	97		
ENSMUST00000136722						0	0	0	0	0	0	7	8	17	0	0		
ENSMUST00000136723	ENSMUSG00000038366	11	97799000	97838764	1	0	0	0	4	0	0	0	0	0	0	0	A2A6G5	
ENSMUST00000136724						0	0	1	1	4	3	0	3	0	0	1		
ENSMUST00000136725						0	0	0	58	0	0	0	0	0	0	0		
ENSMUST00000136726	ENSMUSG00000015966	14	29996141	30008896	-1	26	33	95	17	22	16	0	6	5	0	6	D6REG3	
ENSMUST00000136727						1	0	0	6	2	0	0	0	0	0	0		
ENSMUST00000136728						1	0	0	0	1	0	0	1	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136729	ENSMUSG00000025572	11	117765988	117782198	-1	2	1	0	0	3	1	4	7	0	0	2	B1ATB6	
ENSMUST00000136730	ENSMUSG00000035696	4	44126210	44233789	-1	0	0	0	54	0	0	0	0	0	0	8	E9Q959	
ENSMUST00000136731	ENSMUSG00000034593	9	75071015	75223688	1	0	0	0	0	0	0	214	294	734	84	485	D3YZ62	
ENSMUST00000136732						3	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000136733						28	16	158	23	35	13	0	0	5	1	4		
ENSMUST00000136734						17	14	20	19	12	17	0	3	0	0	3		
ENSMUST00000136735						0	0	0	46	0	3	0	0	0	0	0		
ENSMUST00000136736						0	1	9	2	5	0	0	0	0	0	0		
ENSMUST00000136737						5	0	4	1	3	6	2	2	7	1	5		
ENSMUST00000136738						4	6	8	5	6	3	2	0	5	0	4		
ENSMUST00000136739						2	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000136740	ENSMUSG00000039585	9	59750896	59928866	1	45	0	1	0	55	0	0	0	0	0	0	D3Z3A8	
ENSMUST00000136741						0	4	2	43	5	1	0	0	0	0	5		
ENSMUST00000136742						1	0	0	0	0	1	0	0	0	4	0		
ENSMUST00000136743	ENSMUSG00000035027	10	81105915	81124697	1	0	2	0	2	5	0	49	0	71	0	86	D3Z446	
ENSMUST00000136746						9	3	15	3	12	1	4	22	16	17	35		
ENSMUST00000136748	ENSMUSG00000039917	5	135632618	135646448	1	11	0	20	50	55	0	0	76	22	0	33	D6RCZ4	
ENSMUST00000136750	ENSMUSG00000036352	2	25998543	26021747	-1	10	3	1	0	5	0	2	0	6	0	5	F6UMH9	
ENSMUST00000136751						4	8	0	86	0	0	0	0	0	0	1		
ENSMUST00000136752						3	4	6	28	2	0	0	0	0	0	0		
ENSMUST00000136753	ENSMUSG00000035960	14	50924968	50927139	1	3	1	9	0	0	0	0	0	0	0	8	D3Z124	
ENSMUST00000136754						0	3	0	0	0	0	0	0	7	0	0		
ENSMUST00000136755	ENSMUSG00000021763	13	113317084	113379711	1	57	37	104	65	71	40	0	0	0	0	0	F6RXI4	
ENSMUST00000136756	ENSMUSG00000060675	19	7557459	7588545	1	0	0	0	0	0	0	12	38	11	224	43		Q8R3U1
ENSMUST00000136757	ENSMUSG00000035642	7	97550331	97579497	-1	0	0	0	0	0	0	0	0	0	0	0		Q8R0P4
ENSMUST00000136758						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136760						5	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000136761						0	0	0	1	0	0	0	3	0	0	0		
ENSMUST00000136762						6	2	10	0	1	1	0	0	0	0	0		
ENSMUST00000136763	ENSMUSG00000033416	10	75351111	75517972	-1	0	0	0	20	0	1	42	66	65	15	51	D6RDT9	
ENSMUST00000136764						0	1	1	106	10	3	0	0	0	0	0		
ENSMUST00000136765						10	9	10	32	11	12	0	0	1	0	1		
ENSMUST00000136766	ENSMUSG00000048775	1	106980984	107001195	1	8	11	43	1	8	8	1	0	0	0	0	D6RHN5	
ENSMUST00000136767						4	4	4	2	5	2	21	19	15	0	36		
ENSMUST00000136768						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136769						66	44	83	48	96	35	0	0	2	2	0		
ENSMUST00000136770	ENSMUSG00000026127	1	34439851	34449356	1	0	0	0	2	2	0	77	74	49	43	33	F6VY64	
ENSMUST00000136771						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136773	ENSMUSG00000032384	9	65908924	66045015	1	1	1	3	0	2	1	0	1	2	0	5		
ENSMUST00000136774						17	6	37	17	24	8	22	148	38	0	69		
ENSMUST00000136775						0	0	0	17	17	0	0	0	0	0	0		
ENSMUST00000136776	ENSMUSG00000003526	16	18060357	18090203	-1	3	0	11	1	6	0	13	27	2	20	17		
ENSMUST00000136777	ENSMUSG00000044876	7	6172226	6191349	1	2	2	0	6	0	0	0	0	0	0	10	D3Z1T3	
ENSMUST00000136778						1	4	5	11	4	1	0	0	0	0	1		
ENSMUST00000136780						0	0	0	20	1	0	0	0	0	0	0		
ENSMUST00000136781	ENSMUSG00000002083	7	16309616	16318205	1	0	0	1	90	0	1	1	0	1	0	0	D3Z2M5	
ENSMUST00000136782						2	0	3	0	0	0	11	8	13	1	19		
ENSMUST00000136783	ENSMUSG00000098754	2	131909957	131956130	1	11	32	15	37	55	0	0	0	0	0	10	A0A075B668	
ENSMUST00000136784						5	0	17	6	13	0	0	0	1	0	0		
ENSMUST00000136785	ENSMUSG00000051043	11	114851152	114872617	1	0	0	0	0	0	0	0	0	0	0	0	B7FAT8	
ENSMUST00000136786						0	0	0	0	0	0	84	36	112	0	92		
ENSMUST00000136787						6	3	23	1	7	3	0	1	1	0	0		
ENSMUST00000136788						0	0	0	5	0	4	64	1857	125	147	255		
ENSMUST00000136789	ENSMUSG00000031290	X	147470375	147554081	-1	0	0	0	51	0	0	0	0	0	0	0	F6VQ19	
ENSMUST00000136790						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000136791						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136792						0	0	0	0	0	0	1	0	1	0	0		
ENSMUST00000136795						38	26	323	67	45	20	3	4	1	1	2		
ENSMUST00000136796						0	0	0	0	0	0	6	0	0	0	0		
ENSMUST00000136797	ENSMUSG00000025173	11	121327224	121354445	-1	0	0	0	4	0	0	0	0	9	0	23	F6RIG8	
ENSMUST00000136798						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136799						7	4	7	10	7	3	11	41	33	1	50		
ENSMUST00000136800						0	0	14	6	5	0	0	64	26	75	14		
ENSMUST00000136801						4	3	0	0	0	0	28	72	5	17	28		
ENSMUST00000136802						13	25	50	38	30	17	0	5	5	2	6		
ENSMUST00000136803						6	3	12	11	4	3	0	0	7	0	15		
ENSMUST00000136804						0	0	1	31	5	3	122	246	114	333	54		
ENSMUST00000136805						10	9	5	3	6	6	0	0	0	0	0		
ENSMUST00000136808	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	1	0	0	0	0	0	F7DAP1	
ENSMUST00000136809						1	3	2	2	1	1	7	11	18	1	10		
ENSMUST00000136810						4	1	2	0	2	0	1	0	0	0	0		
ENSMUST00000136811						1	4	5	0	0	0	0	0	0	0	0		
ENSMUST00000136812						4	5	16	31	7	1	0	0	0	0	3		
ENSMUST00000136813						5	2	5	1	3	2	0	0	0	0	0		
ENSMUST00000136814						4	0	0	4	5	1	0	0	0	0	0		
ENSMUST00000136815						3	2	0	0	3	1	2	0	0	0	3		
ENSMUST00000136816						28	24	107	73	70	24	53	58	56	3	82		
ENSMUST00000136817						14	16	42	6	15	14	6	8	12	3	23		
ENSMUST00000136819	ENSMUSG00000030268	6	144993835	145076184	-1	32	12	19	162	40	26	0	0	0	0	0	F6YUH3	
ENSMUST00000136821	ENSMUSG00000026890	2	36081953	36105408	-1	0	0	0	37	0	0	0	0	0	0	0	H3BLG4	
ENSMUST00000136822	ENSMUSG00000069920	8	105252638	105255153	-1	0	14	27	159	24	15	6	18	0	0	13		Q8VI16
ENSMUST00000136823	ENSMUSG00000108815	7	127785608	127803802	1	0	0	0	0	0	0	0	0	6	0	0		
ENSMUST00000136824	ENSMUSG00000041769	7	138846079	138883057	1	0	0	0	0	0	0	0	0	0	0	3	G3UWQ1	
ENSMUST00000136825						6	7	7	3	6	3	0	0	5	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136826	ENSMUSG00000042567	14	14820765	15006743	1	5	0	2	0	2	9	1	0	5	0	3	F6XT14	
ENSMUST00000136827						1	0	2	48	1	0	0	0	0	0	0		
ENSMUST00000136828						2	0	11	49	7	0	1	0	0	0	1		
ENSMUST00000136829	ENSMUSG00000030177	6	120324323	120364374	-1	0	0	0	0	0	0	0	0	0	0	0	E9PY84	
ENSMUST00000136830	ENSMUSG00000004018	11	26386135	26471876	1	0	0	0	7	1	0	0	0	0	4	0	D3Z6C0	
ENSMUST00000136831	ENSMUSG00000006219	4	141576062	141606096	-1	0	0	0	0	0	0	0	0	0	0	0	A2ADF3	
ENSMUST00000136832						6	9	34	13	18	12	4	18	4	0	0		
ENSMUST00000136833	ENSMUSG00000024818	19	5877808	5885766	1	0	1	3	2	0	0	3	5	3	0	5	D3Z2H6	
ENSMUST00000136835	ENSMUSG00000039478	8	40307458	40386308	1	5	5	2	1	6	1	0	0	4	2	6	F6WMX7	
ENSMUST00000136836						4	4	8	2	1	2	0	0	0	0	0		
ENSMUST00000136837	ENSMUSG00000016487	6	146888487	147032025	1	0	1	3	0	0	0	0	0	0	0	0	F6YZ95	
ENSMUST00000136838						6	6	11	5	16	9	9	59	4	0	25		
ENSMUST00000136839	ENSMUSG00000052033	2	170496428	170519123	1	0	0	0	0	0	0	25	107	20	128	21	E9Q6U4	
ENSMUST00000136840	ENSMUSG00000033728	15	76710623	76717699	1	0	0	0	112	0	0	0	0	0	0	0	D3Z1R4	
ENSMUST00000136841	ENSMUSG00000044770	10	42860370	42960780	1	7	3	4	2	3	5	0	0	0	0	0	F6SBH7	
ENSMUST00000136842	ENSMUSG00000039671	2	165784152	165899016	-1	1	1	3	2	1	1	0	0	0	0	0	A2A486	
ENSMUST00000136843						4	6	17	16	7	5	0	7	2	0	2		
ENSMUST00000136845						0	8	22	0	27	17	0	0	0	0	0		
ENSMUST00000136846	ENSMUSG00000026113	1	37299865	37410736	1	0	0	0	0	0	0	0	0	0	0	0	E9Q9A0	
ENSMUST00000136848	ENSMUSG00000021224	12	83794034	83921934	-1	0	0	0	0	0	0	102	53	221	0	141	D3Z549	
ENSMUST00000136849						0	3	0	0	1	0	0	6	0	0	0		
ENSMUST00000136850	ENSMUSG00000024810	19	29925114	29960718	1	0	0	0	0	0	0	0	0	0	0	0	H3BKB5	
ENSMUST00000136851						2	3	6	12	5	0	0	0	0	2	0		
ENSMUST00000136852	ENSMUSG00000025876	13	54949411	55006018	1	2	2	0	0	0	2	0	0	0	0	0	F7CVI0	
ENSMUST00000136854						6	5	10	8	14	5	0	4	4	0	0		
ENSMUST00000136855						11	6	9	9	22	9	0	0	0	0	0		
ENSMUST00000136856						5	0	0	0	0	0	12	29	21	2	5		
ENSMUST00000136858						0	0	5	0	0	0	74	151	88	45	121		
ENSMUST00000136859						7	4	0	0	1	0	0	0	0	0	0		
ENSMUST00000136861						0	1	9	2	2	3	0	0	0	0	5		
ENSMUST00000136863						4	2	4	9	3	1	19	67	30	6	66		
ENSMUST00000136864	ENSMUSG00000021376	13	47025170	47044737	-1	1	0	0	35	4	0	0	0	0	8	0	D3YWK6	
ENSMUST00000136865						11	13	55	8	24	16	22	0	45	0	34		
ENSMUST00000136866						1	4	0	19	0	0	46	80	43	43	33		
ENSMUST00000136867						10	6	13	10	14	10	0	0	0	0	0		
ENSMUST00000136868						0	0	4	2	0	0	6	48	0	0	40		
ENSMUST00000136870						0	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000136871						3	3	1	3	1	0	0	4	5	0	0		
ENSMUST00000136872	ENSMUSG00000027282	2	90847155	90866810	1	5	0	0	53	0	0	0	24	14	0	0		Q791V5
ENSMUST00000136873	ENSMUSG00000002043	7	19508670	19516145	1	5	0	0	36	7	0	4	16	14	5	0	D6RD01	
ENSMUST00000136874	ENSMUSG00000073791	4	99829198	99912788	1	0	0	0	0	0	0	0	0	0	2	0	A2CEK1	
ENSMUST00000136875	ENSMUSG00000089917	2	181569149	181584892	-1	4	3	3	2	4	2	0	17	17	0	10	B7ZCR1	
ENSMUST00000136876	ENSMUSG00000020690	11	105063592	105117537	1	0	4	2	5	2	0	0	0	0	0	0	B2FDE4	
ENSMUST00000136877						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000136878						6	4	18	11	6	1	10	37	13	4	44		
ENSMUST00000136880						3	2	1	5	5	1	0	0	0	0	0		
ENSMUST00000136881	ENSMUSG00000028047	3	89215180	89226837	1	0	0	0	0	0	0	4	0	0	0	0	F6W6J3	
ENSMUST00000136882	ENSMUSG00000029287	5	107106570	107289629	-1	0	0	0	0	4	1	0	0	0	0	0	F6VPT9	
ENSMUST00000136883						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136884	ENSMUSG00000032469	9	99575799	99584501	1	1	4	14	8	1	0	3	4	0	0	0	F6ZYX6	
ENSMUST00000136885						83	0	40	40	40	32	0	0	0	0	0		
ENSMUST00000136887	ENSMUSG00000042831	7	30308717	30314304	1	0	0	0	0	0	0	13	29	19	4	24	D3Z1T0	
ENSMUST00000136888	ENSMUSG00000062168	X	160623094	160735765	-1	0	0	0	2	1	0	0	0	0	0	0	B7ZCG2	
ENSMUST00000136889	ENSMUSG00000059689	6	117841180	117845956	1	0	0	0	74	6	0	0	0	0	0	4	D3YYX3	
ENSMUST00000136890	ENSMUSG00000027714	3	36552606	36565727	1	0	0	0	0	0	0	0	0	0	0	0	D3YTN9	
ENSMUST00000136891						0	2	11	3	3	1	0	3	0	0	0		
ENSMUST00000136892	ENSMUSG00000050751	8	124369049	124439658	-1	0	0	0	0	0	0	15	0	12	0	0	D3Z077	
ENSMUST00000136893						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000136894	ENSMUSG00000005950	11	73160421	73172685	1	0	0	0	0	2	0	0	0	0	0	0	B1AUD7	
ENSMUST00000136895						0	0	1	0	1	2	19	16	0	10	10		
ENSMUST00000136896						30	23	59	32	41	17	6	12	16	0	11		
ENSMUST00000136897						0	0	0	1	0	1	1	1	0	0	0		
ENSMUST00000136898						3	2	3	3	0	1	0	0	2	1	0		
ENSMUST00000136899						3	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000136900						38	32	57	38	45	30	4	14	8	4	9		
ENSMUST00000136901						7	5	8	6	11	7	4	16	10	0	0		
ENSMUST00000136902						4	4	1	2	4	1	4	18	4	0	13		
ENSMUST00000136903	ENSMUSG00000020289	11	32225628	32267707	-1	26	34	24	18	36	14	11	57	13	0	15	F2Z404	
ENSMUST00000136904	ENSMUSG00000050912	9	7764041	7794333	1	0	1	8	59	4	0	1	2	4	3	5	D6REH0	
ENSMUST00000136905						0	1	4	20	3	3	0	0	0	0	0		
ENSMUST00000136907	ENSMUSG00000029761	6	34598500	34775473	1	5	8	17	14	6	4	0	0	0	4	6	F6T2Z7	
ENSMUST00000136909						0	0	3	0	0	0	14	27	24	1	46		
ENSMUST00000136910						3	2	1	13	1	1	0	0	4	0	6		
ENSMUST00000136912						2	6	4	1	7	1	9	29	8	4	12		
ENSMUST00000136913	ENSMUSG00000058833	8	70504292	70506752	-1	0	0	1	3	0	0	17	58	24	14	9	D3YZ60	
ENSMUST00000136914	ENSMUSG00000034120	11	116849901	116853094	-1	0	0	0	0	0	0	0	0	0	0	0		Q62093
ENSMUST00000136915						0	0	0	1	0	3	13	977	38	34	10		
ENSMUST00000136916						7	4	11	9	11	4	0	0	0	0	0		
ENSMUST00000136917						13	14	11	11	7	3	0	2	0	0	1		
ENSMUST00000136918						0	0	0	4	0	0	2	14	0	3	13		
ENSMUST00000136920						2	5	1	2	7	0	0	0	0	0	0		
ENSMUST00000136921	ENSMUSG00000037916	19	4007497	4012806	-1	0	0	0	1	0	0	0	0	5	0	5	D3YXX5	
ENSMUST00000136922	ENSMUSG00000062327	17	8434423	8442496	1	5	2	12	9	10	3	0	1	0	0	0	D3Z1X4	
ENSMUST00000136923						4	2	17	11	12	4	0	4	1	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000136924						13	5	48	107	15	10	0	0	1	0	2		
ENSMUST00000136925	ENSMUSG00000001436	10	77032241	77061002	1	23	5	34	17	19	10	0	3	0	0	3	E9Q8X6	
ENSMUST00000136926	ENSMUSG00000029822	6	50293330	50456201	-1	0	0	5	2	0	0	0	0	0	2	2		
ENSMUST00000136929						41	26	99	29	42	26	4	1	5	1	6		
ENSMUST00000136930	ENSMUSG00000031153	X	7789765	7820567	1	0	0	0	0	0	0	2	0	0	0	0	A2AEW5	
ENSMUST00000136932						5	0	0	0	0	0	0	6	0	0	0		
ENSMUST00000136933	ENSMUSG00000005882	2	155846894	155930310	-1	0	0	0	0	0	0	0	38	22	0	0	D6RHP7	
ENSMUST00000136934						0	0	3	0	0	0	0	17	26	2	9		
ENSMUST00000136935	ENSMUSG00000017774	11	75650504	75673910	1	0	0	1	70	1	1	0	1	1	0	2	Q5ND45	
ENSMUST00000136936	ENSMUSG00000015837	11	50199366	50210827	-1	0	0	6	0	1	0	90	1110	2	96	0	F6VD69	
ENSMUST00000136937						7	11	11	10	17	4	15	59	33	11	45		
ENSMUST00000136938	ENSMUSG00000019505	11	62551171	62553213	1	0	0	6	42	6	0	3479	2628	3230	2121	3015	Q5SX22	
ENSMUST00000136939						1	2	1	5	1	0	0	0	0	0	0		
ENSMUST00000136942						2	1	22	5	8	0	0	176	12	0	5		
ENSMUST00000136943						5	3	12	3	5	2	0	0	0	0	0		
ENSMUST00000136944						3	3	15	71	7	8	0	0	0	0	3		
ENSMUST00000136945						1	1	0	0	2	0	0	6	0	2	0		
ENSMUST00000136946	ENSMUSG00000028717	4	115056426	115071755	1	1	0	2	145	0	1	3	0	0	0	1	A2AD40	
ENSMUST00000136947						1	3	3	3	1	2	2	7	3	0	7		
ENSMUST00000136948	ENSMUSG00000068099	15	82252397	82260753	1	0	5	4	11	5	5	0	0	0	0	0	D3YYW9	
ENSMUST00000136949						0	0	16	2	0	1	0	0	2	0	0		
ENSMUST00000136951						1	3	0	3	2	0	0	0	0	0	0		
ENSMUST00000136952						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136953	ENSMUSG00000056486	2	73610660	73775346	-1	3	0	1	0	1	0	0	0	0	0	0	B2FDI1	
ENSMUST00000136954						14	9	39	5	13	6	0	4	12	37	13		
ENSMUST00000136955						0	1	0	0	0	2	61	32	1	7	0		
ENSMUST00000136957						30	24	15	21	14	11	0	0	0	0	0		
ENSMUST00000136958	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	0	0	0	0	0	A2AQE9	
ENSMUST00000136959						3	3	8	3	4	2	7	69	6	9	23		
ENSMUST00000136960	ENSMUSG00000042594	5	121815488	121837646	-1	23	0	0	21	17	16	927	3302	1138	128	1254	D6RCY9	
ENSMUST00000136961	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z0R0	
ENSMUST00000136962	ENSMUSG00000004056	7	27591552	27640826	1	0	0	4	11	4	0	0	0	0	0	0	D3Z3N2	
ENSMUST00000136963						1	1	0	0	0	0	0	0	2	0	4		
ENSMUST00000136964	ENSMUSG00000027365	2	126791565	126876230	-1	0	0	2	0	2	0	0	57	13	0	8	F6QKC0	
ENSMUST00000136965	ENSMUSG00000032462	9	99036654	99140621	-1	17	8	28	70	20	7	561	1235	1062	69	606	S4R1S1	
ENSMUST00000136966						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000136967						10	6	4	1	14	6	0	0	0	0	1		
ENSMUST00000136968						17	9	80	16	27	23	10	16	9	2	13		
ENSMUST00000136970						0	2	8	25	0	0	236	988	175	33	302		
ENSMUST00000136971						77	53	530	135	73	44	1	1	3	0	4		
ENSMUST00000136972						0	0	0	0	0	0	0	3	3	0	10		
ENSMUST00000136973						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000136974						6	5	9	6	7	1	23	51	33	0	24		
ENSMUST00000136975						0	0	0	1	0	1	2	6	4	0	6		
ENSMUST00000136976						0	4	4	12	0	0	17	115	18	0	63		
ENSMUST00000136977						0	0	0	0	1	0	0	3	0	0	0		
ENSMUST00000136978						0	0	5	1	0	0	5	7	6	0	8		
ENSMUST00000136979						5	5	11	12	8	8	0	0	0	0	0		
ENSMUST00000136980	ENSMUSG00000023007	15	99295087	99317018	1	4	0	3	0	0	0	0	8	2	0	0	D3Z4N6	
ENSMUST00000136981						12	8	31	5	9	2	11	34	16	2	23		
ENSMUST00000136982						32	23	65	108	31	24	11	34	20	9	13		
ENSMUST00000136983	ENSMUSG00000024826	19	5896516	5913010	-1	12	16	34	46	17	11	33	83	73	0	33		Q61103
ENSMUST00000136984						0	0	0	0	0	0	0	8	4	0	0		
ENSMUST00000136985						4	1	18	60	2	0	94	174	112	12	125		
ENSMUST00000136986						3	1	0	2	1	0	0	0	0	0	0		
ENSMUST00000136987						4	4	14	4	6	3	0	0	0	0	0		
ENSMUST00000136988						1	8	0	0	0	4	1	0	4	0	0		
ENSMUST00000136989						5	3	0	33	6	4	0	0	1	0	1		
ENSMUST00000136993						0	0	0	0	0	0	0	104	19	37	111		
ENSMUST00000136994						0	0	0	153	0	0	3	10	2	2	6		
ENSMUST00000136995	ENSMUSG00000036282	14	49172226	49191031	1	1	3	0	0	0	0	9	32	22	1	15	F6QNU4	
ENSMUST00000136996	ENSMUSG00000046909	11	80136678	80142175	-1	2	2	0	0	0	0	0	0	7	0	2	F7CPB7	
ENSMUST00000136997						3	0	11	2	3	1	19	102	19	7	27		
ENSMUST00000136999						26	27	46	46	16	10	10	6	13	4	22		
ENSMUST00000137001						0	0	3	6	0	0	21	23	0	3	6		
ENSMUST00000137004						23	34	23	26	32	18	9	5	7	0	8		
ENSMUST00000137005						0	2	0	0	0	0	0	6	0	0	0		
ENSMUST00000137006						0	2	0	0	0	1	7	0	2	0	9		
ENSMUST00000137007						5	4	9	0	5	2	0	2	0	1	3		
ENSMUST00000137008						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000137009						13	15	34	11	7	6	12	19	32	2	40		
ENSMUST00000137011						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137012						3	1	27	4	3	3	0	0	3	0	0		
ENSMUST00000137013						3	3	0	1	7	2	0	5	2	5	0		
ENSMUST00000137014						3	1	9	40	2	3	3	7	13	1	22		
ENSMUST00000137015						104	107	249	115	93	52	4	11	11	0	17		
ENSMUST00000137016						0	0	0	32	0	0	0	0	0	0	0		
ENSMUST00000137017						1	0	4	0	2	0	0	0	0	0	1		
ENSMUST00000137018						3	3	3	3	5	0	5	2	9	0	13		
ENSMUST00000137019	ENSMUSG00000063646	5	37028335	37148001	1	0	0	0	45	0	0	2	0	4	0	0	D3Z555	
ENSMUST00000137021	ENSMUSG00000038696	2	34406771	34624950	1	0	0	0	0	1	0	0	0	0	0	0	A0A0A6YY51	
ENSMUST00000137022						0	1	0	0	0	3	2	0	2	0	0		
ENSMUST00000137023						6	0	9	8	2	8	0	0	0	0	0		
ENSMUST00000137024	ENSMUSG00000025486	7	140863670	140882309	-1	0	0	0	0	0	0	21	0	13	0	7	D3YVQ5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137025						1	0	2	7	6	1	0	0	0	0	0		
ENSMUST00000137027						5	0	15	65	1	0	0	0	0	0	0		
ENSMUST00000137028						0	0	0	0	1	1	17	10	2	4	22		
ENSMUST00000137029						5	8	12	4	17	5	0	8	2	2	5		
ENSMUST00000137031						5	0	0	1	0	3	0	0	0	0	0		
ENSMUST00000137032						0	0	12	0	11	0	53	249	48	1	86		
ENSMUST00000137033	ENSMUSG00000071723	X	94636069	94643244	1	3	5	7	79	8	3	20	205	32	10	46	Q8BQF5	
ENSMUST00000137035	ENSMUSG00000022747	16	58468125	58524243	-1	0	7	2	18	10	5	2	23	10	14	8		Q8VIB3
ENSMUST00000137037						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137038	ENSMUSG00000030781	7	128265657	128272430	1	0	0	7	1	0	0	0	0	0	0	0	F6TFB9	
ENSMUST00000137039						2	2	1	5	9	5	0	1	0	0	3		
ENSMUST00000137040						12	13	13	14	11	9	0	0	0	0	0		
ENSMUST00000137041						0	0	1	9	0	3	0	2	0	0	7		
ENSMUST00000137042						5	2	4	5	1	1	0	0	0	0	0		
ENSMUST00000137043						7	6	6	4	7	5	0	0	0	0	0		
ENSMUST00000137044						6	0	14	0	8	5	0	0	0	0	0		
ENSMUST00000137045						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000137046						0	0	0	0	0	0	4	0	0	0	0		
ENSMUST00000137047						13	5	43	6	15	14	0	0	0	0	0		
ENSMUST00000137048	ENSMUSG00000068457	Y	1096861	1245759	-1	0	0	0	0	0	0	5	0	0	3	0	D3Z2A3	
ENSMUST00000137050						0	0	57	35	10	0	0	0	0	6	0		
ENSMUST00000137051						16	17	28	23	24	8	0	2	2	0	0		
ENSMUST00000137052						2	12	10	3	1	0	24	98	35	34	18		
ENSMUST00000137053	ENSMUSG00000012123	4	134065912	134092504	1	0	3	5	6	3	2	0	1	0	0	0	I7HIQ4	
ENSMUST00000137054						0	0	4	0	0	0	25	291	20	7	8		
ENSMUST00000137055						1	1	2	5	6	0	2	0	0	0	0		
ENSMUST00000137058	ENSMUSG00000002393	8	71374123	71381960	-1	2	0	0	108	6	3	0	6	0	0	0	F6Q454	
ENSMUST00000137059						3	3	2	12	4	3	0	0	0	0	0		
ENSMUST00000137060						49	45	70	29	25	23	6	93	22	4	45		
ENSMUST00000137061	ENSMUSG00000046311	11	49203292	49218816	1	3	0	1	47	0	1	0	0	0	0	0	J3JS21	
ENSMUST00000137062						0	0	6	11	0	4	0	0	0	0	0		
ENSMUST00000137063	ENSMUSG00000034377	17	6106437	6251128	1	558	499	1126	675	687	366	16	59	49	25	142	F6UMF8	
ENSMUST00000137064	ENSMUSG00000021460	13	52835119	52929681	-1	9	3	4	1	6	4	23	158	51	16	103	F6RT60	
ENSMUST00000137065						5	1	0	5	2	5	0	0	0	0	0		
ENSMUST00000137066						0	1	0	1	1	0	0	0	0	0	1		
ENSMUST00000137067						7	11	28	6	9	7	0	0	2	0	5		
ENSMUST00000137068						46	30	171	107	24	16	0	4	2	0	12		
ENSMUST00000137069						0	0	0	0	0	0	3	0	0	2	0		
ENSMUST00000137070	ENSMUSG00000017943	2	163438476	163455324	1	0	0	0	26	2	4	0	0	0	0	0	A2A5H8	
ENSMUST00000137071	ENSMUSG00000013787	17	34898469	34914052	1	0	0	0	0	0	0	0	71	0	0	0	H3BIW5	
ENSMUST00000137072						1	0	0	0	0	0	9	27	15	5	0		
ENSMUST00000137074	ENSMUSG00000026307	1	91298338	91321075	1	17	5	6	17	11	5	26	53	27	4	28	F7D651	
ENSMUST00000137075	ENSMUSG00000008305	4	72117142	72200919	-1	3	0	3	0	6	1	0	0	0	2	0	Q5SQA5	
ENSMUST00000137076						27	47	87	23	32	25	1	4	1	1	4		
ENSMUST00000137078	ENSMUSG00000008730	3	103739815	103791563	-1	0	0	12	71	11	7	60	16	118	4	109		
ENSMUST00000137079	ENSMUSG00000024018	17	29689378	29717012	-1	73	61	139	90	85	57	0	9	5	0	9	D6RG69	
ENSMUST00000137080						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137082						1	0	0	0	0	0	16	207	120	0	20		
ENSMUST00000137083						41	47	276	48	42	23	5	14	8	1	3		
ENSMUST00000137084						0	0	0	3	2	3	0	50	0	7	16		
ENSMUST00000137085						14	18	24	90	18	13	0	0	0	0	0		
ENSMUST00000137086	ENSMUSG00000020690	11	105063592	105117537	1	1	4	0	1	8	1	0	0	0	0	0	B1ASN7	
ENSMUST00000137087	ENSMUSG00000033526	2	121310561	121355396	-1	0	0	0	0	0	0	0	0	0	0	0	F6VU93	
ENSMUST00000137088	ENSMUSG00000005774	3	94954075	94961561	1	7	0	3	0	0	0	0	2	0	0	0		Q9JL61
ENSMUST00000137090	ENSMUSG00000028797	4	129600668	129624059	1	8	2	21	63	15	1	18	60	20	11	23	D6RDC0	
ENSMUST00000137091	ENSMUSG00000027201	2	125084628	125123661	-1	0	0	3	0	0	0	0	0	1	0	0	F6XJA1	
ENSMUST00000137092	ENSMUSG00000026312	1	109982431	110140157	1	0	4	5	29	5	1	0	0	0	0	0	Q8BLT5	
ENSMUST00000137093						30	24	140	38	38	18	33	211	85	5	209		
ENSMUST00000137094						2	4	6	3	0	0	0	0	0	1	0		
ENSMUST00000137095						7	2	18	20	3	2	126	764	221	22	364		
ENSMUST00000137097						5	4	13	3	4	0	0	0	4	0	2		
ENSMUST00000137098						3	0	4	14	0	0	19	41	27	8	21		
ENSMUST00000137100						2	2	2	0	1	0	0	0	0	0	4		
ENSMUST00000137101						4	0	0	3	10	0	0	0	0	0	0		
ENSMUST00000137102						0	0	0	0	0	0	13	20	38	3	12		
ENSMUST00000137103	ENSMUSG00000000753	11	75409769	75422701	-1	0	0	0	0	2	0	0	0	0	0	1	B7ZC25	
ENSMUST00000137104						2	4	3	3	3	1	17	109	16	4	29		
ENSMUST00000137105						27	25	62	1308	58	24	0	17	1	1	10		
ENSMUST00000137106						2	0	1	0	1	3	20	68	25	9	16		
ENSMUST00000137107	ENSMUSG00000054293	X	107148927	107173661	1	0	0	2	0	0	0	0	0	0	0	0	A2ASC2	
ENSMUST00000137108						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137109						2	0	0	0	5	0	14	57	70	37	71		
ENSMUST00000137110						2	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000137111						4	5	15	104	15	9	0	0	0	0	0		
ENSMUST00000137112						2	2	4	3	2	0	0	3	0	0	4		
ENSMUST00000137113						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000137116	ENSMUSG00000022313	15	51877429	51884614	1	402	325	414	630	456	237	164	556	220	107	222		Q9CX11
ENSMUST00000137117	ENSMUSG00000053896	2	68582413	68616387	1	0	0	5	1	0	1	0	0	0	0	0	F6YRC2	
ENSMUST00000137118						4	0	1	0	5	0	12	49	39	2	86		
ENSMUST00000137119	ENSMUSG00000020821	11	70700548	70731964	1	51	33	206	93	54	34	132	348	118	4	53		O35071
ENSMUST00000137120						1	0	0	0	0	0	6	4	29	23	4		
ENSMUST00000137121	ENSMUSG00000030595	7	28758251	28767512	-1	1	0	0	29	4	0	0	0	0	0	0	D3Z358	
ENSMUST00000137122						0	2	0	25	9	3	0	0	0	4	0		
ENSMUST00000137124						8	5	14	6	11	5	0	0	2	0	5		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137125						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000137126	ENSMUSG00000023328	5	137287519	137294466	1	0	0	0	0	0	0	0	2	0	0	1	D3Z064	
ENSMUST00000137128						6	7	2	11	5	1	0	0	0	0	0		
ENSMUST00000137129						0	0	0	0	0	0	0	83	0	0	0		
ENSMUST00000137130						1	1	5	1	0	1	0	0	0	0	0		
ENSMUST00000137131						0	0	0	4	0	0	0	0	0	0	2		
ENSMUST00000137132	ENSMUSG00000051736	10	39118804	39133914	-1	2	0	0	0	1	3	1	7	0	0	0	B2RVF6	Q8CF36
ENSMUST00000137133	ENSMUSG00000021750	14	8296274	8318023	-1	1	0	0	1	0	0	0	0	0	0	0	A9C450	
ENSMUST00000137135						1	0	1	5	0	0	0	0	0	0	0		
ENSMUST00000137137						0	3	8	0	0	0	0	58	13	0	0		
ENSMUST00000137138	ENSMUSG00000033855	17	88597684	88662586	1	0	0	1	1	0	0	0	0	0	0	0	D3Z0U0	
ENSMUST00000137139						2	6	9	0	7	8	79	259	131	40	202		
ENSMUST00000137140						0	4	12	10	0	0	0	2	0	0	20		
ENSMUST00000137141	ENSMUSG00000041482	18	63010213	63387183	-1	12	11	185	8	7	9	9	57	14	2	12	F6YYK4	
ENSMUST00000137142	ENSMUSG00000051022	5	39613935	39755475	-1	4	2	2	3	2	2	0	0	0	0	5	D3YUR4	
ENSMUST00000137143						27	20	29	26	30	9	18	68	17	6	9		
ENSMUST00000137144						2	1	5	2	3	2	0	9	6	2	4		
ENSMUST00000137145	ENSMUSG00000026864	2	34771970	34777547	1	0	0	0	65	1	0	19	65	124	166	179	A0A0A6YXF5	
ENSMUST00000137146						2	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000137147						0	0	0	0	3	6	0	0	0	0	0		
ENSMUST00000137148	ENSMUSG00000030230	6	139989673	140041457	-1	0	0	0	0	0	0	0	0	0	0	0	D6RIP4	
ENSMUST00000137149						14	5	23	87	9	7	0	5	2	0	5		
ENSMUST00000137150	ENSMUSG00000001082	5	34633642	34637212	-1	0	0	0	0	0	0	0	81	13	42	0	D6RI23	
ENSMUST00000137151	ENSMUSG00000040415	10	127190378	127195728	-1	0	0	0	0	0	0	0	0	0	0	0	D3YUA4	
ENSMUST00000137152						1	0	0	3	0	0	0	7	10	0	11		
ENSMUST00000137155						30	20	222	164	54	26	0	0	0	0	0		
ENSMUST00000137156	ENSMUSG00000039356	2	31670715	31681349	1	1	0	0	0	0	0	0	0	0	0	0	A2AV19	
ENSMUST00000137157						7	1	8	6	10	0	0	0	0	0	0		
ENSMUST00000137158	ENSMUSG00000044465	7	105371211	105400054	-1	0	0	0	0	0	0	1231	1473	935	65	643	D6RCH8	
ENSMUST00000137159						1	4	7	0	5	1	0	0	0	0	0		
ENSMUST00000137160						0	0	0	0	7	0	0	0	0	0	0		
ENSMUST00000137161						2	0	9	6	5	3	0	5	6	2	9		
ENSMUST00000137163						0	2	6	0	5	4	0	0	0	0	0		
ENSMUST00000137164						5	4	1	4	0	2	0	0	0	0	0		
ENSMUST00000137165						0	0	0	0	0	0	3	0	0	3	4		
ENSMUST00000137166	ENSMUSG00000033768	19	6418731	6544169	1	24	0	4	0	0	20	0	0	0	0	0	E9Q7X7	
ENSMUST00000137167	ENSMUSG00000041939	5	114444269	114460591	1	4	0	0	7	0	3	0	1	7	0	9	A0A0G2JEG0	
ENSMUST00000137168						7	11	77	22	3	5	21	151	61	4	92		
ENSMUST00000137169	ENSMUSG00000037426	5	32863701	32994236	1	0	0	0	0	3	0	0	133	13	26	36	F6TK47	
ENSMUST00000137170	ENSMUSG00000085793	12	84451508	84531533	1	14	19	16	28	26	18	48	147	40	42	54	B2RQ11	Q8CD94
ENSMUST00000137171						0	0	9	2	4	0	0	0	2	0	0		
ENSMUST00000137172						1	0	0	159	3	6	0	0	0	0	0		
ENSMUST00000137173						1	3	9	5	4	1	0	0	1	0	0		
ENSMUST00000137174						0	0	5	0	0	0	0	0	0	0	2		
ENSMUST00000137177						0	1	26	85	22	0	0	0	0	0	0		
ENSMUST00000137178						7	4	16	13	5	2	2	0	0	0	12		
ENSMUST00000137179						0	1	0	87	3	1	0	0	0	0	0		
ENSMUST00000137181						6	0	0	0	10	0	0	76	0	6	0		
ENSMUST00000137182	ENSMUSG00000024426	17	35897595	35910075	-1	0	0	1	40	0	2	1	6	0	0	6	F7CID0	
ENSMUST00000137183	ENSMUSG00000060508	7	20008023	20073306	1	0	0	0	0	0	0	0	0	0	0	0	D3YWU2	
ENSMUST00000137185						2	2	7	73	4	7	4	13	4	0	7		
ENSMUST00000137187						5	0	6	25	2	2	3	13	6	0	17		
ENSMUST00000137188	ENSMUSG00000017670	2	165288031	165326479	-1	0	0	0	0	0	0	0	0	0	0	0	F6XD63	
ENSMUST00000137189						2	1	17	2	2	3	0	0	0	0	0		
ENSMUST00000137190						0	0	1	55	1	0	4	9	15	1	5		
ENSMUST00000137191	ENSMUSG00000057406	5	33820725	33897975	1	0	0	0	0	8	0	0	21	0	30	70	D3Z3E0	
ENSMUST00000137192	ENSMUSG00000016382	X	75785654	75875182	-1	0	0	5	0	1	0	2	0	14	233	69		
ENSMUST00000137194						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000137195	ENSMUSG00000072812	12	112772194	112802657	-1	5	0	9	6822	114	49	0	0	1	0	0	F7CVJ5	
ENSMUST00000137196						0	0	0	87	0	0	0	0	0	0	0		
ENSMUST00000137197	ENSMUSG00000066842	1	150562524	150993435	-1	71	31	71	0	40	49	0	0	1	0	6	D3Z2Q7	
ENSMUST00000137200	ENSMUSG00000038119	9	35421128	35507652	1	0	0	0	4	1	0	0	0	0	0	0	D6RHA1	
ENSMUST00000137201	ENSMUSG00000002279	17	25579174	25662826	1	0	0	13	21	16	6	19	29	0	0	18	D6RDS1	
ENSMUST00000137202	ENSMUSG00000031748	8	93809966	93969388	1	3	5	0	8	8	1	0	0	0	0	1	D3Z2M7	
ENSMUST00000137204	ENSMUSG00000035585	7	3692863	3701024	1	0	2	1	27	6	2	3	8	5	2	11	D3YZ84	
ENSMUST00000137206	ENSMUSG00000028753	4	138565360	138635884	-1	0	0	0	0	0	0	0	0	0	0	0	F7D0T1	
ENSMUST00000137207	ENSMUSG00000034724	5	96070333	96164171	-1	2	0	3	0	2	0	0	0	0	3	3	D3Z2G5	
ENSMUST00000137208						0	0	3	0	0	0	2	2	0	7	5		
ENSMUST00000137209	ENSMUSG00000028681	4	117096075	117116101	1	1	5	7	5	11	3	0	0	0	0	0	F6XYY1	
ENSMUST00000137210						1	0	3	0	4	1	0	0	0	0	3		
ENSMUST00000137211						3	1	3	0	4	0	0	0	0	0	0		
ENSMUST00000137212	ENSMUSG00000038301	6	51523901	51590679	1	0	0	0	2	0	0	0	0	0	0	22	D3YW62	
ENSMUST00000137213						0	0	1	0	0	3	0	0	0	0	0		
ENSMUST00000137214						5	2	0	44	3	0	0	0	0	0	0		
ENSMUST00000137215	ENSMUSG00000026821	2	28513125	28553081	1	2	3	1	0	0	1	0	0	0	0	3	F6QRS4	
ENSMUST00000137216						18	7	20	6	9	5	0	2	1	0	0		
ENSMUST00000137217						13	8	19	0	11	12	0	1	0	2	0		
ENSMUST00000137219						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137220						0	0	0	0	0	0	12	0	0	2	23		
ENSMUST00000137222	ENSMUSG00000024055	17	32924688	32947402	-1	5	0	0	0	0	0	48	95	28	6	28	E9Q4L9	
ENSMUST00000137223						2	0	0	12	7	0	6	0	1	0	0		
ENSMUST00000137224	ENSMUSG00000059689	6	117841180	117845956	1	0	0	6	0	0	0	4	0	6	5	2	D3Z0E5	
ENSMUST00000137225	ENSMUSG00000006191	13	29191746	29855674	-1	3	3	7	4	3	5	0	0	0	0	0		Q91WE6
ENSMUST00000137226						2	1	3	15	5	4	1	2	8	0	6		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137227						0	0	0	0	0	1	0	0	0	0	3		
ENSMUST00000137228						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000137230						2	1	14	0	0	2	0	0	20	0	0		
ENSMUST00000137231						17	11	45	21	28	6	3	13	12	2	6		
ENSMUST00000137232						5	1	8	79	1	1	0	0	0	0	0		
ENSMUST00000137233						0	0	0	0	0	0	0	9	8	0	7		
ENSMUST00000137234	ENSMUSG00000028132	3	121201761	121283098	-1	0	0	0	3	2	0	0	0	0	0	0	D3Z3E6	
ENSMUST00000137235						3	1	1	1	0	1	9	70	14	0	17		
ENSMUST00000137238						6	4	8	67	10	5	0	0	3	0	0		
ENSMUST00000137240						21	0	0	0	0	0	0	0	10	0	10		
ENSMUST00000137242	ENSMUSG00000027597	2	155059310	155074497	-1	0	0	0	0	0	0	0	0	0	0	0	A2ALT5	
ENSMUST00000137243						58	34	261	63	40	13	3	78	10	10	30		
ENSMUST00000137244	ENSMUSG00000021944	14	63198922	63271692	-1	5	6	38	10	4	0	0	0	0	0	0	A4K4Z6	
ENSMUST00000137245	ENSMUSG00000038957	9	57708540	57752499	1	5	0	0	0	0	0	288	184	249	51	61	D6RCX6	
ENSMUST00000137246	ENSMUSG00000028410	4	40722150	40737149	1	0	0	0	0	0	0	81	327	310	599	262	B1AXY1	
ENSMUST00000137247						0	1	7	27	0	1	0	0	0	0	0		
ENSMUST00000137248	ENSMUSG00000026856	2	30392254	30400529	1	3	0	10	0	0	0	0	0	0	7	0	F6QGX7	
ENSMUST00000137249						2	2	1	1	1	0	44	79	11	29	14		
ENSMUST00000137250	ENSMUSG00000028115	3	95241271	95251193	-1	6	0	3	3	2	0	0	3	0	0	0		Q99JU7
ENSMUST00000137252						4	2	10	0	1	0	0	0	0	0	0		
ENSMUST00000137253						0	1	0	0	0	0	0	0	1	0	0		
ENSMUST00000137254						0	0	0	9	0	0	69	171	78	25	34		
ENSMUST00000137255	ENSMUSG00000042303	15	80977765	81012289	1	0	1	0	0	1	0	0	0	0	0	0	D3Z190	
ENSMUST00000137256						17	15	25	29	30	10	8	17	6	1	24		
ENSMUST00000137260						0	0	14	0	2	0	0	0	0	0	0		
ENSMUST00000137261						11	5	36	90	19	4	35	49	42	9	52		
ENSMUST00000137262						1	3	17	6	0	0	0	3	7	0	11		
ENSMUST00000137263						5	3	3	7	0	1	7	28	9	0	17		
ENSMUST00000137264						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137265						3	4	0	0	2	3	0	0	0	0	0		
ENSMUST00000137266	ENSMUSG00000026113	1	37299865	37410736	1	9	6	9	0	0	0	0	0	0	10	0	D3Z230	
ENSMUST00000137267						0	0	0	50	0	0	0	7	0	3	0		
ENSMUST00000137268	ENSMUSG00000032727	13	111686178	111718596	1	11	0	20	0	5	0	175	434	80	107	88	D6RET2	
ENSMUST00000137269	ENSMUSG00000028621	4	107066988	107088268	1	0	0	0	0	0	0	0	7	0	0	0	B1AS44	
ENSMUST00000137270						0	0	0	0	2	3	0	0	0	0	0		
ENSMUST00000137271						369	380	489	398	441	253	13	37	46	7	50		
ENSMUST00000137272	ENSMUSG00000059518	5	136982164	136988021	-1	0	0	0	1	0	1	9	13	13	2	0	D3Z017	
ENSMUST00000137274	ENSMUSG00000027574	2	180934772	180954699	-1	1	3	4	1	1	0	0	0	0	0	0	F6X001	
ENSMUST00000137276	ENSMUSG00000026405	1	130634773	130661632	-1	2	1	1	0	0	0	0	0	0	0	0	E9PUZ8	
ENSMUST00000137277						0	0	0	22	1	1	0	0	0	102	52		
ENSMUST00000137278						0	5	0	0	0	0	0	0	0	0	7		
ENSMUST00000137279						3	4	0	2	4	1	0	0	0	0	0		
ENSMUST00000137280	ENSMUSG00000074736	2	149829211	150004392	1	0	0	0	0	0	0	0	0	0	0	0	B1AYD4	
ENSMUST00000137284						4	0	22	12	7	5	89	76	46	14	0		
ENSMUST00000137285	ENSMUSG00000049606	5	106616739	106697287	-1	0	0	0	10	0	0	0	0	1	0	0	E9PXI9	
ENSMUST00000137286						0	1	0	0	1	0	0	16	4	0	0		
ENSMUST00000137287						92	90	128	80	117	67	13	56	36	24	47		
ENSMUST00000137288						0	0	0	0	0	2	1	0	0	1	0		
ENSMUST00000137289						59	54	33	57	66	32	4	61	11	6	11		
ENSMUST00000137290	ENSMUSG00000031698	8	85324303	85386345	-1	5	7	6	3	1	4	0	0	0	0	0	D3YZQ0	
ENSMUST00000137291						6	1	6	167	2	5	2	2	2	0	5		
ENSMUST00000137292						0	0	0	51	0	0	6	0	14	0	6		
ENSMUST00000137293	ENSMUSG00000040455	4	21767156	21837872	1	33	28	83	73	47	17	0	30	0	0	0	F7CLE5	
ENSMUST00000137294						0	1	30	9	14	6	0	0	0	0	0		
ENSMUST00000137296	ENSMUSG00000047098	14	55591708	55603693	1	38	35	136	167	56	31	23	142	64	0	151	D6RFE2	
ENSMUST00000137297						0	0	3	0	0	0	27	96	80	0	3		
ENSMUST00000137298						1	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000137299	ENSMUSG00000039294	11	121222588	121229322	-1	4	7	25	2	6	6	71	126	77	12	116	A0A0A0MQK0	
ENSMUST00000137300						11	7	41	15	18	7	0	2	0	0	0		
ENSMUST00000137301						0	1	0	30	1	1	0	5	1	0	0		
ENSMUST00000137302						93	82	924	399	69	40	0	31	0	0	0		
ENSMUST00000137303	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	0	0	0	0	0	0	0	0	F7AWQ5	
ENSMUST00000137304						6	0	0	0	0	0	0	223	18	0	0		
ENSMUST00000137305						1	2	0	1	0	0	0	0	1	0	0		
ENSMUST00000137306	ENSMUSG00000020305	11	30885416	31102704	1	2	0	0	0	4	0	0	84	18	40	13	D6RDR7	
ENSMUST00000137307						3	1	12	9	1	4	388	142	22	24	83		
ENSMUST00000137309						4	5	9	2	3	0	0	0	0	0	0		
ENSMUST00000137310						4	3	14	4	3	0	0	2	0	0	2		
ENSMUST00000137311	ENSMUSG00000022861	16	22468461	22657221	-1	14	5	3	43	10	7	8	20	42	7	33	F2Z409	
ENSMUST00000137312	ENSMUSG00000028648	4	123712710	123718202	-1	0	0	0	0	0	0	0	0	0	71	0	B1ARW4	
ENSMUST00000137313	ENSMUSG00000054874	19	5664635	5688908	-1	9	2	10	0	0	0	5	0	0	6	0	F6SDA4	
ENSMUST00000137314						4	2	16	0	5	0	23	57	282	578	82		
ENSMUST00000137316						2	0	0	8	7	0	0	0	0	0	0		
ENSMUST00000137317						0	0	0	0	0	0	0	24	5	8	4		
ENSMUST00000137318						0	0	2	3	0	0	426	466	109	307	39		
ENSMUST00000137320						138	100	574	129	142	78	5	29	18	4	27		
ENSMUST00000137321	ENSMUSG00000028910	4	131843470	131867786	1	2	2	0	0	0	3	0	0	0	0	11	A2A845	
ENSMUST00000137322						0	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000137323						27	13	78	4	26	15	0	86	4	3	19		
ENSMUST00000137324						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137325						9	8	5	9	8	14	18	160	33	3	31		
ENSMUST00000137326						0	0	2	8	22	6	2	0	0	0	0		
ENSMUST00000137327						2	0	5	18	10	6	0	0	0	0	0		
ENSMUST00000137328						8	4	14	58	11	3	8	4	11	0	16		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137329	ENSMUSG00000012848	7	12922290	12926686	1	0	0	5	0	0	0	0	0	0	171	108	D3YYM6	
ENSMUST00000137331						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137332						0	0	0	0	0	0	18	33	23	17	21		
ENSMUST00000137333	ENSMUSG00000027596	2	154791402	155051012	1	0	0	0	0	0	0	0	0	0	0	0	A2ALT1	
ENSMUST00000137334						2	0	0	0	0	0	0	0	0	2	1		
ENSMUST00000137335	ENSMUSG00000027361	2	126627442	126676337	-1	1	0	2	0	1	1	5	6	2	0	6	A2AQ72	
ENSMUST00000137336	ENSMUSG00000087642	12	113271174	113273248	-1	15	11	77	21	20	4	1	0	0	0	1	F6W6U3	
ENSMUST00000137337	ENSMUSG00000037336	12	4862440	4874359	-1	0	2	3	2	0	2	0	0	5	0	0	B8JK42	
ENSMUST00000137338						1	0	5	0	3	3	3	15	3	4	12		
ENSMUST00000137339						0	4	1	76	5	11	0	0	0	0	0		
ENSMUST00000137340						0	0	1	8	0	0	0	34	38	7	15		
ENSMUST00000137342						5	6	2	1	1	0	0	3	0	0	0		
ENSMUST00000137344						3	4	4	3	5	1	4	11	14	3	15		
ENSMUST00000137345						2	0	9	8	0	0	0	0	1	35	13		
ENSMUST00000137346						0	4	0	0	1	0	0	2	0	0	2		
ENSMUST00000137347						42	32	76	61	40	13	0	1	0	4	0		
ENSMUST00000137348						0	0	0	0	0	0	0	3	9	4	0		
ENSMUST00000137354	ENSMUSG00000025420	18	76977148	77047308	-1	2	4	17	7	7	0	0	0	0	0	0	D3Z0U5	
ENSMUST00000137355						2	1	5	2	3	1	2	2	2	0	8		
ENSMUST00000137356	ENSMUSG00000061689	2	156613705	156764363	1	0	0	0	23	6	0	0	0	0	0	0	H3BL90	
ENSMUST00000137357	ENSMUSG00000025538	5	129846986	129864050	1	0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000137358						2	0	0	0	3	1	0	21	0	25	32		
ENSMUST00000137360						1	5	3	3	3	2	0	35	0	12	9		
ENSMUST00000137361						0	0	0	0	0	0	10	4	0	5	0		
ENSMUST00000137362						0	1	3	6	2	1	0	0	0	1	0		
ENSMUST00000137363	ENSMUSG00000049550	5	123577795	123684618	-1	0	0	0	0	0	3	0	446	0	16	0	F6RCU2	
ENSMUST00000137365						26	12	50	27	31	17	0	0	0	4	14		
ENSMUST00000137366						2	0	1	30	4	1	0	0	2	3	0		
ENSMUST00000137367						8	5	11	11	6	1	11	46	52	4	67		
ENSMUST00000137368						9	2	5	27	15	4	0	2	0	0	5		
ENSMUST00000137369						5	0	16	27	7	4	0	0	0	0	0		
ENSMUST00000137370						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137372						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137374						1	0	0	2	3	0	0	1	0	1	0		
ENSMUST00000137375						55	25	204	294	68	39	1	0	4	0	6		
ENSMUST00000137376						10	6	13	0	10	0	43	78	28	23	49		
ENSMUST00000137377						47	55	177	139	45	23	7	12	6	4	18		
ENSMUST00000137378						0	0	0	0	0	0	12	119	0	7	31		
ENSMUST00000137380						0	0	0	0	2	0	4	3	9	0	0		
ENSMUST00000137381	ENSMUSG00000038860	2	32986224	33131654	-1	5	2	10	11	4	0	0	0	2	0	0		Q3V0G7
ENSMUST00000137382						3	4	2	1	2	7	25	59	13	5	40		
ENSMUST00000137383						0	0	1	0	7	0	0	0	0	0	0		
ENSMUST00000137384	ENSMUSG00000032812	7	101348067	101412586	1	0	2	10	36	2	0	72	52	92	2	80	D3YZJ7	
ENSMUST00000137385						2	1	0	6	0	0	0	0	0	0	0		
ENSMUST00000137386	ENSMUSG00000024169	17	25016091	25099495	1	0	0	0	0	0	0	40	19	17	0	23	E9Q682	
ENSMUST00000137387	ENSMUSG00000059995	11	102289300	102296631	-1	0	0	0	0	20	5	1514	1830	1681	94	1073	Z4YN62	
ENSMUST00000137388	ENSMUSG00000037443	4	134129858	134187112	-1	0	0	0	0	0	0	0	0	0	0	0	Q8C1L6	
ENSMUST00000137389						1	2	4	1	1	1	1	2	0	0	9		
ENSMUST00000137390						0	0	0	1	0	0	4	0	0	7	12		
ENSMUST00000137391						15	10	36	35	14	7	25	44	48	1	83		
ENSMUST00000137392						2	2	11	4	0	1	0	0	0	0	0		
ENSMUST00000137393						1	0	1	31	0	0	2	0	0	0	0		
ENSMUST00000137394						5	0	1	19	0	1	0	0	0	0	0		
ENSMUST00000137395						4	0	15	3	0	0	0	0	0	0	0		
ENSMUST00000137396						8	6	1	6	4	1	0	3	15	3	6		
ENSMUST00000137399						7	2	3	7	2	1	2	0	0	0	0		
ENSMUST00000137400	ENSMUSG00000024608	18	60774510	60778546	1	0	6	0	0	0	0	1829	2161	698	7139	672	D3Z7I1	
ENSMUST00000137401	ENSMUSG00000028710	4	115784812	115818828	1	0	0	0	0	0	0	4	5	0	0	3	H3BKR0	
ENSMUST00000137402	ENSMUSG00000029591	5	114130386	114139323	1	0	0	0	0	0	0	0	2	0	0	0	D3YW18	
ENSMUST00000137403						6	0	6	7	13	5	0	17	5	8	10		
ENSMUST00000137404	ENSMUSG00000027977	3	123526166	123690853	-1	19	17	0	42	0	10	0	0	0	0	0		Q9EQH7
ENSMUST00000137406						5	5	7	4	7	3	0	0	0	0	0		
ENSMUST00000137407						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000137408						0	9	0	16	40	0	54	86	0	0	19		
ENSMUST00000137409						11	3	18	10	16	0	2	7	2	0	0		
ENSMUST00000137410						0	2	0	0	0	0	0	0	0	4	0		
ENSMUST00000137412						0	4	0	0	0	1	0	4	8	4	0		
ENSMUST00000137413	ENSMUSG00000025873	13	54621784	54664068	1	0	0	2	1	0	0	0	0	0	0	0	D3Z4G9	
ENSMUST00000137414						6	3	13	23	6	4	0	0	0	0	0		
ENSMUST00000137415						0	3	6	4	1	1	0	0	0	0	1		
ENSMUST00000137416						0	0	0	0	0	0	5	0	0	4	0		
ENSMUST00000137417						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000137419						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137420						3	0	4	4	0	0	0	0	0	0	0		
ENSMUST00000137423						6	2	5	0	0	1	0	106	0	0	3		
ENSMUST00000137424						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137425						23	34	100	21	31	14	1	2	4	0	7		
ENSMUST00000137426	ENSMUSG00000055762	15	75894796	75909556	-1	1	0	9	0	12	6	8	6	0	0	18	F6ZFU0	
ENSMUST00000137427						48	28	72	260	60	30	0	1	1	0	4		
ENSMUST00000137428						307	274	447	236	276	100	7	16	18	4	25		
ENSMUST00000137429						1	1	1	4	0	0	3	59	10	12	7		
ENSMUST00000137430						2	2	0	44	5	3	23	47	14	32	20		
ENSMUST00000137431	ENSMUSG00000024830	19	4156713	4163354	-1	0	0	0	0	0	0	23	0	0	0	0	D6RH86	
ENSMUST00000137432	ENSMUSG00000067825	6	121183667	121198837	1	0	0	0	18	0	0	0	0	0	0	0	D3Z323	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137433	ENSMUSG00000049287	11	59155369	59163739	-1	0	0	0	34	0	0	0	0	0	0	0	B2FDE8	
ENSMUST00000137434						9	6	9	0	4	14	0	5	2	0	0		
ENSMUST00000137435						3	2	8	11	3	2	61	88	84	0	37		
ENSMUST00000137436						21	12	77	40	15	12	0	0	0	0	0		
ENSMUST00000137437	ENSMUSG00000062980	6	21985916	22256404	1	2	5	0	0	2	0	0	8	22	12	13	E9Q7L8	
ENSMUST00000137438	ENSMUSG00000035476	X	85574022	85634469	1	0	0	0	2	0	0	0	0	0	0	0	F7AT87	
ENSMUST00000137439	ENSMUSG00000003282	4	3900996	3938423	-1	0	0	0	25	0	0	0	1	0	0	1	D6RES7	
ENSMUST00000137440						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000137441						10	12	6	18	19	4	0	0	0	0	1		
ENSMUST00000137444	ENSMUSG00000055436	3	158010473	158036639	-1	1	0	1	39	0	3	3	2	0	0	0	D3Z4B0	
ENSMUST00000137445						7	3	12	2	4	2	219	577	165	420	179		
ENSMUST00000137446						3	5	4	16	11	0	0	45	0	0	0		
ENSMUST00000137447						0	1	0	0	0	1	47	35	71	6	169		
ENSMUST00000137448						30	30	43	22	38	28	6	11	0	0	11		
ENSMUST00000137449	ENSMUSG00000017950	2	163506808	163572910	1	0	0	0	6	3	2	0	0	0	0	0	A2A5I6	
ENSMUST00000137450	ENSMUSG00000044876	7	6172226	6191349	1	3	2	8	5	5	4	1	2	1	0	1	D3Z381	
ENSMUST00000137451	ENSMUSG00000027544	2	168476410	168601657	-1	3	0	0	234	8	6	0	0	0	0	0	A2AQC8	
ENSMUST00000137452						2	6	16	7	5	1	0	0	2	0	1		
ENSMUST00000137453	ENSMUSG00000031229	X	105797615	105929403	-1	0	0	0	10	0	0	0	0	0	0	0	A6PWK9	
ENSMUST00000137454	ENSMUSG00000040111	9	40293233	40531383	-1	0	0	0	0	0	0	0	160	70	25	83	F7BFL8	
ENSMUST00000137456						0	0	0	0	0	0	203	500	252	185	179		
ENSMUST00000137458	ENSMUSG00000052142	17	32390659	32403583	-1	8	4	29	72	14	7	136	424	247	38	291		Q8C2K5
ENSMUST00000137459						152	132	346	207	183	118	5	62	12	5	11		
ENSMUST00000137461	ENSMUSG00000053317	4	47474658	47483242	1	0	3	9	4	0	0	0	36	0	0	0	A8Y5P8	
ENSMUST00000137464						0	0	0	19	0	1	24	0	99	0	118		
ENSMUST00000137465						23	22	41	28	26	11	2	50	17	3	14		
ENSMUST00000137466						3	5	2	2	1	1	0	0	0	0	0		
ENSMUST00000137467	ENSMUSG00000000134	X	7762560	7775202	1	2	0	11	64	3	3	12	0	36	0	0		Q64092
ENSMUST00000137468						6	1	5	3	5	3	0	6	2	6	0		
ENSMUST00000137469						0	0	3	0	4	0	10	8	4	0	24		
ENSMUST00000137472	ENSMUSG00000011958	9	69989466	70008317	1	0	1	0	0	1	0	17	27	11	4	23	F6VF29	
ENSMUST00000137473						141	135	201	161	169	74	14	65	37	14	37		
ENSMUST00000137474						18	0	0	2	0	4	4	31	31	2	31		
ENSMUST00000137475						0	1	0	0	2	0	0	83	0	13	0		
ENSMUST00000137476						0	2	2	6	1	3	53	118	106	390	103		
ENSMUST00000137479						7	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000137480						0	0	4	22	0	0	46	38	97	22	126		
ENSMUST00000137481						8	6	48	20	7	4	0	5	0	0	7		
ENSMUST00000137482						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137483						11	10	19	89	7	5	0	2	1	0	0		
ENSMUST00000137484						2	1	1	3	1	1	1	0	0	0	1		
ENSMUST00000137485						2	1	3	2	6	3	0	0	0	0	0		
ENSMUST00000137486	ENSMUSG00000003644	4	133847290	133887797	-1	11	5	5	97	16	2	781	303	982	20	445	F6Q8A4	
ENSMUST00000137487	ENSMUSG00000029066	4	155802878	155809975	1	0	1	0	0	5	0	5	39	5	5	8		Q9CQL4
ENSMUST00000137488	ENSMUSG00000060240	7	141426446	141429491	-1	5	3	15	16	0	7	0	0	0	0	0		Q9JKC6
ENSMUST00000137490	ENSMUSG00000029477	5	123035769	123047016	-1	0	0	0	0	1	0	3	0	0	2	0	F6Z6W0	
ENSMUST00000137491						152	110	1005	244	113	75	2	23	12	0	18		
ENSMUST00000137492	ENSMUSG00000044583	X	167304929	167330558	-1	0	0	0	0	2	0	1	0	2	0	0	A2AHJ2	
ENSMUST00000137493						3	3	2	2	4	0	1	0	1	0	1		
ENSMUST00000137494						16	8	34	0	5	0	39	237	27	131	44		
ENSMUST00000137495						29	25	80	44	26	19	0	5	5	0	0		
ENSMUST00000137496	ENSMUSG00000048280	13	67667437	67687071	-1	1	5	4	6	7	3	35	145	62	35	37	B8JJX8	
ENSMUST00000137497	ENSMUSG00000036452	18	38601534	39376284	1	0	11	0	0	0	0	828	2336	774	96	571	Q3U860	
ENSMUST00000137498	ENSMUSG00000025420	18	76977148	77047308	-1	0	0	0	0	0	0	0	0	0	8	0	D3Z4J2	
ENSMUST00000137499						23	29	36	26	31	15	23	90	52	10	82		
ENSMUST00000137500	ENSMUSG00000020532	11	84129672	84401651	1	0	0	0	11	0	1	0	3	4	0	6	V9GWS1	
ENSMUST00000137501						14	11	30	19	14	4	0	0	0	0	0		
ENSMUST00000137502						0	0	1	0	2	0	0	7	0	1	0		
ENSMUST00000137503						1	3	3	1	2	1	0	0	0	0	2		
ENSMUST00000137504						12	13	26	16	12	6	1	0	0	0	0		
ENSMUST00000137506	ENSMUSG00000001082	5	34633642	34637212	-1	6	3	23	9	5	5	2	6	7	0	23		
ENSMUST00000137507						1	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000137508						0	3	1	2	1	3	0	0	0	0	6		
ENSMUST00000137510						7	8	25	23	18	3	26	86	55	63	36		
ENSMUST00000137511	ENSMUSG00000040865	1	62958418	63114667	-1	0	0	0	7	0	0	0	0	0	0	23	B1AT33	
ENSMUST00000137512	ENSMUSG00000028483	4	83417724	83467676	1	0	0	5	0	0	0	0	13	8	3	0	E0CY59	
ENSMUST00000137513						24	8	35	8	18	26	0	0	0	0	0		
ENSMUST00000137514	ENSMUSG00000028294	4	34688559	34730206	-1	0	0	0	0	0	1	0	0	0	0	0	Z4YM47	
ENSMUST00000137515						0	2	5	3	3	1	0	0	0	0	0		
ENSMUST00000137516						1	3	4	3	4	2	217	756	276	20	355		
ENSMUST00000137517						14	5	11	167	26	22	0	0	0	1	3		
ENSMUST00000137518						0	0	0	3	0	0	0	2	0	0	0		
ENSMUST00000137519	ENSMUSG00000041870	5	114774677	114806200	1	4	0	12	0	4	5	1414	1055	1917	96	1501	F7B209	
ENSMUST00000137520	ENSMUSG00000028898	4	132311763	132329538	-1	0	1	3	2	0	0	0	0	0	0	2	E9Q0Q0	
ENSMUST00000137521						0	0	0	0	0	0	0	0	3	0	3		
ENSMUST00000137522						5	0	25	9	4	7	41	221	84	10	90		
ENSMUST00000137523						3	1	0	9	8	7	0	7	2	0	10		
ENSMUST00000137525						3	1	4	25	2	1	0	0	0	3	3		
ENSMUST00000137526	ENSMUSG00000038533	2	154436481	154539356	1	127	112	984	10	117	66	0	195	0	29	58	F6WYU8	
ENSMUST00000137527						0	0	5	0	0	1	4	3	7	0	2		
ENSMUST00000137528	ENSMUSG00000026867	2	34674594	34755232	-1	4	0	0	0	0	0	50	14	90	3	33	F6X819	
ENSMUST00000137529						0	1	1	3	1	0	0	0	0	0	0		
ENSMUST00000137530	ENSMUSG00000040774	3	106502260	106547802	-1	0	0	5	0	0	0	0	10	9	13	4	D6RFR8	
ENSMUST00000137531	ENSMUSG00000068036	17	13760539	13906150	1	0	0	11	0	3	0	11	3	0	11	14	F7C3I9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137533						0	0	3	7	1	2	0	0	8	6	8		
ENSMUST00000137534						14	15	53	44	22	10	0	3	3	1	5		
ENSMUST00000137536	ENSMUSG00000027547	2	168748332	168767943	-1	3	0	35	39	9	1	0	0	0	0	0	A2AUZ7	
ENSMUST00000137537						4	0	18	6	4	8	62	361	103	26	76		
ENSMUST00000137538						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137540						0	4	0	57	0	2	2	9	11	8	0		
ENSMUST00000137541						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137542	ENSMUSG00000032382	9	66088133	66126587	-1	2	2	1	3	3	1	56	61	122	10	43	D3YWH1	
ENSMUST00000137543	ENSMUSG00000021838	14	46882854	47105817	1	15	19	85	108	39	19	0	0	0	0	0		Q8CBY1
ENSMUST00000137544						0	0	0	6	0	6	75	68	72	47	26		
ENSMUST00000137545						4	0	9	4	0	2	2	3	6	2	7		
ENSMUST00000137547						1	1	1	2	1	3	0	0	0	0	0		
ENSMUST00000137548						6	4	11	5	5	3	6	7	7	0	8		
ENSMUST00000137550	ENSMUSG00000042831	7	30308717	30314304	1	0	0	7	0	3	1	0	0	0	0	0	D6RFR9	
ENSMUST00000137552						0	2	2	1	3	0	0	0	0	0	3		
ENSMUST00000137553						73	64	304	90	64	54	37	118	19	9	18		
ENSMUST00000137554						2	1	1	0	2	1	0	0	0	0	0		
ENSMUST00000137555						2	1	5	29	0	0	8	47	42	7	52		
ENSMUST00000137556	ENSMUSG00000040112	6	147042764	147073991	1	0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000137557	ENSMUSG00000052459	16	44085402	44139705	-1	0	0	4	3	0	0	0	2	0	0	0	D3Z1B9	
ENSMUST00000137558	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	0	0	0	11	4	0	0	0	F6Y325	
ENSMUST00000137559						0	1	3	2	2	0	0	0	0	0	0		
ENSMUST00000137560	ENSMUSG00000032998	4	119537004	119629119	1	0	1	5	2	3	1	0	0	0	0	0	E0CYX1	
ENSMUST00000137562						1	1	0	4	3	2	0	2	5	3	15		
ENSMUST00000137563						0	1	3	4	1	0	3	49	18	8	7		
ENSMUST00000137564	ENSMUSG00000106447	3	96635474	96653101	1	17	14	21	42	33	14	0	0	0	0	3	D6RFQ2	
ENSMUST00000137565	ENSMUSG00000027668	3	32529465	32579239	1	0	0	0	1	0	0	0	0	0	0	15	D3Z4L5	
ENSMUST00000137566	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	0	0	0	0	0	0	0	0	0	D6RCZ8	
ENSMUST00000137568	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	27	12	0	0	F6U9F5	
ENSMUST00000137569						0	0	2	0	0	0	2	0	0	0	0		
ENSMUST00000137570	ENSMUSG00000055198	4	114821722	114856166	1	10	11	25	73	19	8	0	0	0	0	0	F6XVH0	
ENSMUST00000137571						3	0	8	3	6	0	0	0	0	0	0		
ENSMUST00000137572						0	0	0	0	0	0	0	4	0	1	0		
ENSMUST00000137573	ENSMUSG00000043090	8	69761326	69791178	-1	40	38	58	52	37	23	71	154	145	51	103	Q6PGD2	
ENSMUST00000137574						18	0	10	44	16	7	4	9	0	5	4		
ENSMUST00000137575						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137576						7	12	12	218	17	14	0	0	0	0	1		
ENSMUST00000137577						3	3	2	4	5	1	0	0	0	0	0		
ENSMUST00000137578	ENSMUSG00000003863	7	45339126	45367019	-1	0	0	30	0	1	0	0	4	1	0	0	F6UYF1	
ENSMUST00000137580						0	0	0	2	0	4	0	2	0	0	0		
ENSMUST00000137581						117	135	336	146	145	70	18	42	13	5	43		
ENSMUST00000137583						0	0	0	1	2	1	1	0	2	0	7		
ENSMUST00000137584						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137585						2	0	0	2	0	2	87	0	108	0	102		
ENSMUST00000137586	ENSMUSG00000079537	2	26251757	26257554	-1	4	5	8	8	8	6	0	0	0	0	0	F6VUL6	
ENSMUST00000137587						0	0	7	5	6	1	27	53	7	5	14		
ENSMUST00000137588						4	0	12	6	8	5	0	0	0	0	0		
ENSMUST00000137589						0	0	0	0	2	2	125	190	184	29	94		
ENSMUST00000137590						0	0	5	20	16	12	0	0	4	0	0		
ENSMUST00000137591						2	0	0	0	0	0	15	0	18	15	34		
ENSMUST00000137592						1	1	1	3	1	0	0	0	0	0	0		
ENSMUST00000137594						0	1	4	0	1	2	0	0	0	0	0		
ENSMUST00000137595	ENSMUSG00000075101	2	89124794	89125731	-1	5	1	1	4	2	4	0	0	0	0	0	A3KGY3	
ENSMUST00000137596						29	40	85	36	52	25	3	4	3	0	7		
ENSMUST00000137597						0	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000137599						7	3	14	7	12	0	0	0	0	0	0		
ENSMUST00000137600						0	0	15	1	3	1	0	2	0	0	5		
ENSMUST00000137601	ENSMUSG00000022272	15	25622525	25813673	1	12	5	0	48	11	0	3	0	0	0	0	D3YXU7	
ENSMUST00000137602						8	9	6	3	9	2	0	229	8	62	115		
ENSMUST00000137604						3	3	0	5	2	3	8	12	19	2	15		
ENSMUST00000137605	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	5	1	0	2	67	75	147	705	179	A2AEB4	
ENSMUST00000137608						0	1	8	48	3	3	5	3	13	0	8		
ENSMUST00000137609						7	1	3	3	4	1	0	34	4	0	13		
ENSMUST00000137610	ENSMUSG00000055553	8	70508272	70527956	-1	0	0	0	0	2	0	0	0	1	7	0	D3Z2M8	
ENSMUST00000137611						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000137612						1	0	0	59	2	4	2	15	13	10	22		
ENSMUST00000137613	ENSMUSG00000011263	7	19489056	19496760	1	4	5	10	78	12	12	0	1	0	0	0	D3YUP5	
ENSMUST00000137614						1	6	5	22	8	3	2	0	0	0	4		
ENSMUST00000137615						0	30	15	0	17	0	15	0	18	8	28		
ENSMUST00000137616						2	2	0	4	2	0	0	0	0	0	0		
ENSMUST00000137618						2	0	0	2	3	0	0	0	0	0	0		
ENSMUST00000137619						1	2	6	6	4	1	39	16	0	16	12		
ENSMUST00000137620						4	0	3	2	3	0	4	3	0	0	4		
ENSMUST00000137621						33	24	25	20	26	11	6	18	11	1	10		
ENSMUST00000137622	ENSMUSG00000028857	4	133266045	133277792	-1	0	0	6	0	0	0	0	0	6	0	6	F6ZS99	
ENSMUST00000137623						4	2	1	1	4	0	3	0	1	0	2		
ENSMUST00000137625						1	0	4	1	6	3	0	0	0	0	0		
ENSMUST00000137626	ENSMUSG00000017737	2	164940780	164955850	1	2	0	3	4	1	5	0	2	0	0	10	A2A5K8	
ENSMUST00000137627						5	9	31	6	8	7	0	19	6	6	2		
ENSMUST00000137628	ENSMUSG00000029563	6	14901349	15441977	1	5	2	0	0	0	1	0	0	0	0	0	D3Z4F4	
ENSMUST00000137630						1	0	0	21	0	1	65	658	121	9	128		
ENSMUST00000137631						4	3	0	3	4	2	0	0	0	0	0		
ENSMUST00000137632	ENSMUSG00000039670	11	120456606	120458068	-1	0	0	0	0	0	0	4	0	4	0	0	H3BK04	
ENSMUST00000137633						0	0	0	0	0	0	50	264	73	18	147		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137634	ENSMUSG00000061718	11	98348404	98357796	1	0	0	0	0	0	0	0	0	0	0	0		Q60829
ENSMUST00000137635						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000137636	ENSMUSG00000022292	15	37923952	37961318	-1	2	0	0	1	0	0	2	5	6	0	0	D3Z2A4	
ENSMUST00000137637	ENSMUSG00000024663	19	10001669	10038380	1	2	0	4	0	0	0	0	0	0	0	0	D3YZN2	
ENSMUST00000137638						0	0	0	35	0	0	0	0	17	0	31		
ENSMUST00000137639						0	0	3	25	1	0	0	3	0	0	0		
ENSMUST00000137640	ENSMUSG00000053730	4	129676355	129696838	-1	0	0	0	24	2	0	0	0	2	0	0	A8Y5J9	
ENSMUST00000137641						28	31	47	24	24	16	1	1	8	1	3		
ENSMUST00000137642						0	3	1	0	4	0	0	0	0	0	0		
ENSMUST00000137644						6	0	6	3	3	0	0	0	0	9	0		
ENSMUST00000137645	ENSMUSG00000018381	11	95830074	95842476	-1	0	0	0	0	0	0	29	0	0	3	0	F6RXN4	
ENSMUST00000137646	ENSMUSG00000042759	7	126584942	126589112	1	0	0	0	0	0	1	20	21	6	4	7		
ENSMUST00000137647						0	3	0	3	0	0	0	0	0	0	0		
ENSMUST00000137648						0	1	10	46	6	0	0	21	8	0	7		
ENSMUST00000137649	ENSMUSG00000033728	15	76710623	76717699	1	3	3	7	128	11	14	13	21	60	5	29		Q8VC16
ENSMUST00000137650						5	5	1	4	5	4	0	0	0	0	0		
ENSMUST00000137652						4	0	2	1	0	0	3	7	5	8	0		
ENSMUST00000137653	ENSMUSG00000021177	12	99884517	99955219	1	2	3	0	3	0	2	0	0	2	0	0	D3Z075	
ENSMUST00000137654						0	0	4	3	1	1	0	0	0	0	0		
ENSMUST00000137655						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137656						3	3	3	0	0	0	0	0	0	0	0		
ENSMUST00000137657						8	7	2	5	16	1	76	341	141	17	135		
ENSMUST00000137658						5	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000137659						2	1	7	8	4	2	5	13	0	0	2		
ENSMUST00000137660						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000137663	ENSMUSG00000062542	7	107370728	107548656	1	0	0	0	54	1	0	0	0	0	0	0	D3YVX0	
ENSMUST00000137664						1	2	6	0	2	0	0	38	4	11	0		
ENSMUST00000137665	ENSMUSG00000031290	X	147470375	147554081	-1	0	1	1	0	0	0	0	0	0	0	0	F7AAC3	
ENSMUST00000137667	ENSMUSG00000039187	7	79391929	79450264	1	0	2	6	0	3	4	1	0	0	0	0	F7ALG5	
ENSMUST00000137668						0	0	2	22	3	2	0	0	0	0	3		
ENSMUST00000137669						5	1	3	0	10	1	0	1	0	0	0		
ENSMUST00000137670	ENSMUSG00000026727	2	13076821	13271415	-1	1	0	0	0	0	0	17	4	185	286	88	B1AYQ0	
ENSMUST00000137671						4	0	3	5	9	2	1	5	3	0	1		
ENSMUST00000137672						1	0	1	45	3	0	0	0	0	0	0		
ENSMUST00000137674						0	1	2	16	0	1	8	26	0	4	20		
ENSMUST00000137675	ENSMUSG00000032311	9	55220222	55326844	-1	1	0	1	0	1	0	0	0	0	0	0	D6RE18	
ENSMUST00000137676						6	5	9	9	3	0	10	94	24	0	32		
ENSMUST00000137677	ENSMUSG00000030780	7	128271379	128298170	-1	1	0	0	1	4	4	0	0	0	0	0	F6ZSG8	
ENSMUST00000137679						7	0	12	0	16	5	0	0	0	0	0		
ENSMUST00000137682	ENSMUSG00000042594	5	121815488	121837646	-1	2	0	6	156	1	1	2	1	4	0	1	D3Z0T9	
ENSMUST00000137683						281	281	618	404	274	146	52	200	95	33	112		
ENSMUST00000137684						2	2	6	5	4	1	0	0	0	0	0		
ENSMUST00000137685						1	0	0	15	0	0	18	31	32	49	13		
ENSMUST00000137686						0	1	1	0	3	2	0	0	0	0	0		
ENSMUST00000137687	ENSMUSG00000067860	X	58022700	58041736	1	0	1	1	12	2	1	0	0	0	0	0	A2AWK4	
ENSMUST00000137688						0	0	0	0	1	0	16	18	0	0	49		
ENSMUST00000137689	ENSMUSG00000044072	11	29743048	30026033	-1	5	6	0	2	11	3	0	1	0	0	1	F6QY72	
ENSMUST00000137690						0	1	4	17	0	0	0	0	0	0	2		
ENSMUST00000137691						1	2	1	1	1	1	30	34	33	41	31		
ENSMUST00000137692						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137693						5	2	10	0	1	6	0	0	0	0	0		
ENSMUST00000137694						7	6	21	239	21	7	37	75	48	23	81		
ENSMUST00000137695						5	5	0	65	9	1	0	23	6	0	0		
ENSMUST00000137696						5	3	7	9	9	4	27	106	71	0	61		
ENSMUST00000137697						0	2	4	8	4	0	7	14	11	3	15		
ENSMUST00000137698						42	41	85	45	65	38	3	19	5	15	14		
ENSMUST00000137699						5	4	4	0	9	0	5	0	5	0	1		
ENSMUST00000137700	ENSMUSG00000038685	2	181319739	181356616	1	0	0	0	0	0	0	0	3	0	0	0	F6RDU0	
ENSMUST00000137701	ENSMUSG00000020805	11	72241994	72267222	-1	2	3	6	28	6	5	0	0	0	0	0	Q5NBV0	
ENSMUST00000137702	ENSMUSG00000045411	7	44246722	44252319	1	0	0	0	26	4	0	0	0	0	0	5	D3Z276	
ENSMUST00000137703	ENSMUSG00000035683	4	44300876	44364675	1	0	0	0	0	0	0	0	0	2	0	2	A2ALR0	
ENSMUST00000137704						8	3	16	3	1	2	0	0	0	0	0		
ENSMUST00000137705	ENSMUSG00000037339	5	33600347	33629635	-1	6	9	6	5	11	4	0	0	8	0	2	D6REV4	
ENSMUST00000137707	ENSMUSG00000028826	4	134802759	134853345	-1	8	0	17	7	4	5	17	0	0	0	17	E0CY55	
ENSMUST00000137708	ENSMUSG00000068036	17	13760539	13906150	1	3	13	36	14	13	5	12	0	39	12	13	E9PYX7	
ENSMUST00000137709						0	0	0	0	0	0	48	109	220	34	89		
ENSMUST00000137710	ENSMUSG00000025486	7	140863670	140882309	-1	5	3	1	7	0	0	5	0	2	0	0	D3YWD6	
ENSMUST00000137711						0	0	6	2	7	0	4	0	0	0	1		
ENSMUST00000137712	ENSMUSG00000025665	X	111388192	111537959	-1	1	0	2	7	4	0	0	0	0	0	0	A2CEE5	
ENSMUST00000137713	ENSMUSG00000032402	9	63646767	63757994	-1	0	0	4	1	0	0	0	0	1	0	0	A2CG45	
ENSMUST00000137715						3	3	5	5	3	2	2	0	2	0	2		
ENSMUST00000137716	ENSMUSG00000029528	5	115506676	115555987	1	0	3	4	4	4	0	710	116	416	16	370		
ENSMUST00000137717						12	16	32	36	16	12	14	52	47	7	82		
ENSMUST00000137718						5	0	2	0	3	1	0	6	0	0	5		
ENSMUST00000137719						2	0	2	2	4	2	8	3	3	0	11		
ENSMUST00000137720						12	4	25	227	15	11	0	3	0	0	1		
ENSMUST00000137721						1	3	9	9	3	4	0	0	0	0	0		
ENSMUST00000137722						0	0	0	18	0	3	0	0	0	0	0		
ENSMUST00000137723	ENSMUSG00000039428	7	89139723	89404222	-1	2	0	9	94	3	4	0	0	2	0	1	D3YUX0	
ENSMUST00000137724	ENSMUSG00000029016	4	148004259	148038821	-1	46	27	81	82	56	25	104	213	135	25	188	A2A7F6	
ENSMUST00000137725						0	1	1	22	1	2	0	0	0	0	0		
ENSMUST00000137726						20	15	24	18	7	0	149	350	124	6	171		
ENSMUST00000137727	ENSMUSG00000024008	17	29156550	29237797	-1	0	3	7	15	3	0	0	0	0	0	0	E9Q1V2	
ENSMUST00000137732						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137733	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	1	1	3	1	0	0	0	0	0	S4R2L5	
ENSMUST00000137734						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137735						2	0	0	0	2	0	0	0	9	0	9		
ENSMUST00000137736						0	0	0	0	0	0	35	0	23	0	18		
ENSMUST00000137737						3	3	1	3	4	0	0	0	0	0	0		
ENSMUST00000137739						4	3	16	106	6	3	0	4	2	0	19		
ENSMUST00000137740						4	5	5	1	0	1	0	0	0	0	0		
ENSMUST00000137741						0	0	3	2	4	0	9	9	0	0	0		
ENSMUST00000137743						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000137744						7	8	93	25	2	0	4	13	1	0	6		
ENSMUST00000137745						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137746						11	7	3	6	7	2	0	0	0	0	0		
ENSMUST00000137747	ENSMUSG00000025350	10	128913593	128922888	-1	0	0	2	0	0	0	2	4	0	1	4	F7CWI9	
ENSMUST00000137748	ENSMUSG00000005980	16	4036942	4040024	1	0	0	0	0	2	0	0	0	0	0	4	E9Q797	
ENSMUST00000137750	ENSMUSG00000035310	5	100441918	100500639	-1	3	4	0	11	0	0	0	0	21	0	0	E9PV28	
ENSMUST00000137751						0	0	0	60	0	0	2	0	0	0	0		
ENSMUST00000137753						0	0	2	31	0	3	34	0	78	6	78		
ENSMUST00000137754	ENSMUSG00000034566	11	115415689	115419962	-1	0	0	0	0	0	0	0	0	0	71	0	B1ASE2	
ENSMUST00000137755	ENSMUSG00000022619	15	89453913	89464468	1	0	3	4	2	4	0	0	0	0	0	0	D3Z2R7	
ENSMUST00000137757						0	1	0	0	0	0	1	0	3	2	1		
ENSMUST00000137758						11	6	18	2	4	4	20	26	3	5	16		
ENSMUST00000137759						0	3	0	0	0	0	0	0	3	0	0		
ENSMUST00000137760						5	0	2	2	0	0	0	0	0	0	2		
ENSMUST00000137762						0	8	15	54	11	0	0	0	0	0	0		
ENSMUST00000137763						2	0	0	3	0	1	9	13	9	1	12		
ENSMUST00000137764	ENSMUSG00000022366	15	57243767	57477625	-1	0	0	2	0	1	0	0	0	0	0	0	D3YXY3	
ENSMUST00000137766						0	0	11	103	16	0	0	44	4	4	4		
ENSMUST00000137767						1	1	0	1	0	0	3	2	25	68	21		
ENSMUST00000137768	ENSMUSG00000064330	6	136923832	136968865	1	244	181	875	283	182	89	12	43	28	5	54		P61249
ENSMUST00000137769	ENSMUSG00000078570	4	124849080	124851196	-1	0	0	0	42	3	2	30	65	25	41	41	E9Q9M4	
ENSMUST00000137770						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000137771	ENSMUSG00000025223	19	46032593	46045214	-1	0	4	12	2	2	2	216	885	286	32	361		P70662
ENSMUST00000137772	ENSMUSG00000030269	6	113237843	113281392	1	0	0	0	0	0	4	0	0	0	1	15	F6RV41	
ENSMUST00000137773						2	0	11	0	2	0	0	0	6	7	4		
ENSMUST00000137774						2	3	2	0	1	0	0	0	0	2	0		
ENSMUST00000137775	ENSMUSG00000019710	3	87919506	87923672	1	0	1	0	0	0	0	58	62	65	144	65	A0A0A6YXP0	
ENSMUST00000137777						3	3	1	1	0	5	3	5	5	5	0		
ENSMUST00000137778						1	1	4	6	1	0	0	9	2	0	3		
ENSMUST00000137779						3	11	16	3	6	2	11	53	14	1	11		
ENSMUST00000137780	ENSMUSG00000073991	4	18860454	19122526	-1	3	1	5	0	0	1	0	0	0	0	0	B1AWM0	
ENSMUST00000137781						7	5	37	10	9	1	1	10	0	0	5		
ENSMUST00000137782	ENSMUSG00000026417	1	130826684	130852249	1	0	0	0	0	0	0	0	0	0	0	1	D3YVM4	
ENSMUST00000137783	ENSMUSG00000037936	5	125277087	125341094	-1	2	1	3	2	5	2	0	0	0	0	0	D3Z5U8	
ENSMUST00000137784	ENSMUSG00000068036	17	13760539	13906150	1	7	0	0	20	0	0	111	50	93	16	135	E9Q9C3	
ENSMUST00000137785						1	0	4	2	2	0	0	0	0	0	0		
ENSMUST00000137786						3	1	7	7	8	1	0	4	0	1	1		
ENSMUST00000137787						0	5	2	2	7	2	21	136	34	0	47		
ENSMUST00000137788						5	4	1	0	11	3	0	0	0	0	0		
ENSMUST00000137789						0	0	0	12	5	4	0	29	0	1	1		
ENSMUST00000137791						5	6	11	64	10	3	0	0	0	0	0		
ENSMUST00000137792	ENSMUSG00000020641	12	26442753	26456452	-1	7	12	30	10	31	0	0	0	0	0	0	D6RJ49	
ENSMUST00000137793	ENSMUSG00000042626	3	89418443	89430027	1	0	0	0	0	1	0	11	2	0	3	0	D3Z5U6	
ENSMUST00000137794	ENSMUSG00000026127	1	34439851	34449356	1	0	0	0	0	0	0	12	12	0	6	0	D6RCI8	
ENSMUST00000137795						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000137796						0	0	1	234	8	0	0	0	0	0	0		
ENSMUST00000137797						3	12	43	12	8	4	4	9	2	2	3		
ENSMUST00000137798	ENSMUSG00000028883	5	13125414	13602565	1	118	89	626	157	83	24	5	6	9	3	14	E9Q668	
ENSMUST00000137799	ENSMUSG00000019338	3	95006590	95015448	-1	0	1	0	0	1	0	0	0	118	0	68		Q9D2D7
ENSMUST00000137803						4	0	8	4	8	5	7	10	11	2	13		
ENSMUST00000137804						12	7	89	52	27	13	1	0	0	0	0		
ENSMUST00000137805	ENSMUSG00000024617	18	60925618	60988152	1	0	4	6	3	1	1	0	0	0	0	0	F6WHR9	
ENSMUST00000137806						39	26	64	26	44	20	3	5	3	8	8		
ENSMUST00000137807						4	8	4	3	7	1	0	0	0	0	0		
ENSMUST00000137808						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000137809						18	13	46	21	19	18	0	0	0	0	0		
ENSMUST00000137811						4	0	0	40	0	0	53	39	0	119	0		
ENSMUST00000137812						1	0	0	3	2	3	0	0	0	1	0		
ENSMUST00000137813						0	1	9	4	2	0	0	2	37	8	53		
ENSMUST00000137814						0	0	8	6	0	0	0	6	0	0	0		
ENSMUST00000137815						0	1	8	3	0	0	0	0	0	0	4		
ENSMUST00000137816						7	5	4	14	13	10	0	0	0	0	1		
ENSMUST00000137817						0	0	1	0	0	0	7	47	9	0	0		
ENSMUST00000137819						18	20	34	20	25	7	0	0	0	0	0		
ENSMUST00000137821	ENSMUSG00000033768	19	6418731	6544169	1	0	0	0	6	0	0	0	0	0	0	0	F6Y027	
ENSMUST00000137822						4	6	23	4	11	10	0	2817	0	200	203		
ENSMUST00000137823	ENSMUSG00000056342	11	23306895	23490560	1	34	38	102	28	43	8	780	1444	1668	213	953	F6WJB7	
ENSMUST00000137824	ENSMUSG00000057715	1	11414105	11975901	1	0	0	0	0	0	0	0	0	0	0	0	B2RQF6	
ENSMUST00000137825						2	2	0	0	4	3	2	0	0	0	2		
ENSMUST00000137826	ENSMUSG00000033373	12	76765589	76921412	1	7	0	0	8	10	0	0	0	0	0	0	D3YWJ4	
ENSMUST00000137827						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137828						0	0	0	4	0	3	1	18	12	0	21		
ENSMUST00000137829						0	0	0	0	0	0	0	21	11	19	27		
ENSMUST00000137831						0	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000137832						0	0	3	8	0	1	21	39	124	14	45		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137833	ENSMUSG00000020097	10	61098642	61147703	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1Z3	
ENSMUST00000137834						5	2	12	2	4	0	6	17	5	2	7		
ENSMUST00000137835						2	8	5	3	0	2	82	215	158	68	158		
ENSMUST00000137836						2	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000137837						6	6	1	0	0	2	0	40	0	1	0		
ENSMUST00000137840						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000137841	ENSMUSG00000020265	10	77606097	77641543	1	0	0	0	0	0	0	20	65	19	0	47	G3UWI9	
ENSMUST00000137843						6	2	21	3	6	5	22	59	9	0	7		
ENSMUST00000137844						66	50	197	107	41	23	2	9	2	1	2		
ENSMUST00000137845	ENSMUSG00000023990	17	47737030	47792419	1	2	2	0	1	4	2	6	8	0	0	3	D3Z219	
ENSMUST00000137846	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	0	0	1	22	1	0	0	21	A2A838	
ENSMUST00000137847						0	0	0	0	4	0	3	0	0	1	0		
ENSMUST00000137848	ENSMUSG00000030584	7	29303951	29317588	1	3	2	6	6	0	3	0	0	0	0	0	F6UJZ6	
ENSMUST00000137849						0	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000137850						2	2	4	0	3	3	0	5	0	5	0		
ENSMUST00000137851	ENSMUSG00000028759	4	138216296	138244683	1	0	1	0	15	0	0	0	0	4	0	3	A2AM63	
ENSMUST00000137852						0	0	5	2	3	2	0	8	3	0	5		
ENSMUST00000137853	ENSMUSG00000079509	X	94074631	94123702	-1	0	0	0	32	0	0	0	0	0	0	0	B1ASD2	
ENSMUST00000137854	ENSMUSG00000051747	2	76703980	76982547	-1	1	0	0	0	2	0	0	0	0	0	0	A2AT62	
ENSMUST00000137855						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000137856	ENSMUSG00000045752	7	143069249	143071093	1	0	1	1	0	4	0	0	17	25	0	5	D3YZR1	
ENSMUST00000137857	ENSMUSG00000020230	10	76207222	76237865	-1	9	4	21	6	0	7	0	4	0	0	0	M0QW88	
ENSMUST00000137858						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000137859						13	4	4	20	13	0	0	0	0	0	0		
ENSMUST00000137860						1	1	0	0	1	2	8	27	5	0	7		
ENSMUST00000137861						3	3	5	1	5	2	0	0	1	0	1		
ENSMUST00000137862	ENSMUSG00000054976	1	81076950	81341764	1	2	4	2	0	0	0	0	0	0	0	0		
ENSMUST00000137863						1	0	0	0	2	1	1	8	0	0	0		
ENSMUST00000137864						1	5	9	2	5	5	0	9	2	0	0		
ENSMUST00000137865	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	0	0	0	5	3	24	8	19	A2AM70	
ENSMUST00000137866	ENSMUSG00000018209	2	164070322	164155524	1	2	0	0	2	2	1	0	4	16	56	18	F7BYZ4	
ENSMUST00000137867	ENSMUSG00000005268	15	10177238	10349180	1	0	0	0	0	0	0	3	0	0	0	0		Q08501
ENSMUST00000137868	ENSMUSG00000026207	1	75375297	75432320	1	0	0	0	0	26	0	0	0	0	3	2	A0A087WSE3	
ENSMUST00000137870						6	7	10	0	12	4	0	0	5	3	0		
ENSMUST00000137871						3	0	5	18	2	0	0	0	4	0	0		
ENSMUST00000137872						14	8	33	1	6	2	11	9	5	3	17		
ENSMUST00000137873	ENSMUSG00000052301	7	126847416	126852705	1	0	4	12	17	9	2	0	0	0	0	0	D3Z1K1	
ENSMUST00000137874						3	0	7	4	7	3	48	49	36	35	24		
ENSMUST00000137875						2	4	3	6	6	3	2	28	6	5	21		
ENSMUST00000137876						4	0	3	5	8	3	0	0	0	0	3		
ENSMUST00000137878	ENSMUSG00000018661	11	113649169	113667054	1	0	0	0	0	0	0	12	37	10	8	16	F6RK91	
ENSMUST00000137880						5	0	0	0	0	0	0	59	15	2	0		
ENSMUST00000137881						5	6	5	9	6	6	2	4	5	0	3		
ENSMUST00000137884						14	5	10	52	8	1	0	0	0	0	0		
ENSMUST00000137885						7	0	6	5	0	0	0	0	0	0	0		
ENSMUST00000137887	ENSMUSG00000025903	1	4807788	4848410	1	0	0	0	0	0	0	0	8	0	58	12	D3Z269	
ENSMUST00000137888	ENSMUSG00000048787	7	119853163	119896291	-1	3	0	15	0	0	0	0	0	0	0	3	D3Z0Q3	
ENSMUST00000137889	ENSMUSG00000026843	2	31572651	31617526	1	0	0	0	30	0	0	0	0	0	0	0	A2AJ71	
ENSMUST00000137890						0	1	0	3	1	1	49	28	24	3	17		
ENSMUST00000137891	ENSMUSG00000049969	4	10988662	11007927	-1	8	10	4	13	2	0	14	0	89	9	65	A8Y5N8	
ENSMUST00000137892						1	2	0	1	0	0	0	107	8	13	37		
ENSMUST00000137893						0	3	0	0	6	0	6	58	77	104	73		
ENSMUST00000137894						18	10	20	10	11	8	0	0	0	0	1		
ENSMUST00000137895						1	4	4	1	6	2	0	0	0	0	0		
ENSMUST00000137896						31	19	44	39	30	29	363	2528	665	159	911		
ENSMUST00000137897						40	29	94	265	60	30	1	6	0	1	4		
ENSMUST00000137898						1	0	0	25	1	0	9	8	6	0	4		
ENSMUST00000137899	ENSMUSG00000030760	7	98206389	98321208	-1	0	1	0	105	3	0	21	10	39	87	30	D6RJ31	
ENSMUST00000137900	ENSMUSG00000020782	11	115824049	115855780	1	0	0	0	0	0	0	0	0	1	0	4	B1ATA9	
ENSMUST00000137901						0	1	0	0	4	2	0	0	2	0	0		
ENSMUST00000137902						0	0	0	0	0	2	0	0	3	0	6		
ENSMUST00000137903						26	15	47	23	23	8	45	631	132	25	163		
ENSMUST00000137904						0	0	0	0	0	0	0	0	1	1	0		
ENSMUST00000137905	ENSMUSG00000058022	13	41763148	41847684	-1	2	0	4	1	2	0	20	67	36	45	31	H9KV14	
ENSMUST00000137906	ENSMUSG00000037447	1	36307733	36324029	1	28	21	114	59	57	29	415	721	687	127	882		Q3U108
ENSMUST00000137908						39	19	78	71	49	21	3	27	31	5	4		
ENSMUST00000137909						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000137910						0	0	1	7	4	2	6	0	3	0	3		
ENSMUST00000137911						0	0	0	1	0	0	0	0	0	1	0		
ENSMUST00000137912	ENSMUSG00000028108	3	95734147	95739569	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z772	
ENSMUST00000137913	ENSMUSG00000036833	2	24976033	25054057	1	9	0	0	0	15	9	264	603	337	0	481	A0A0A6YWJ6	
ENSMUST00000137914	ENSMUSG00000030737	7	99657804	99711340	-1	0	0	0	2	0	0	0	0	0	0	0	D3YY31	
ENSMUST00000137915	ENSMUSG00000078622	11	106197408	106216344	-1	3	1	0	0	0	0	0	5	5	0	6	B1AR93	
ENSMUST00000137916						4	0	2	1	3	0	2	5	2	2	5		
ENSMUST00000137917						0	0	0	0	1	2	10	13	6	10	4		
ENSMUST00000137918						0	0	1	19	2	2	0	1	0	0	0		
ENSMUST00000137919						4	1	6	0	0	0	1	0	1	1	0		
ENSMUST00000137920	ENSMUSG00000059555	2	25192966	25196886	-1	1	0	0	35	0	3	2	1	2	0	2	A0A0A6YWQ0	
ENSMUST00000137921						6	2	7	5	5	3	0	0	0	0	0		
ENSMUST00000137922						0	1	0	0	2	0	0	0	0	0	1		
ENSMUST00000137924						7	3	5	1	4	0	0	0	0	0	0		
ENSMUST00000137925						60	53	108	75	66	23	5	26	10	2	12		
ENSMUST00000137926	ENSMUSG00000009073	11	4765845	4849536	-1	0	0	0	0	0	0	5	0	0	2	0	F7D6P2	
ENSMUST00000137927	ENSMUSG00000041119	17	31386234	31476310	1	0	0	3	0	0	0	0	0	0	0	0	D6RFN9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000137928						0	1	5	32	7	3	0	0	0	0	0		
ENSMUST00000137929						9	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000137930						0	5	0	0	2	0	0	0	3	70	16		
ENSMUST00000137931	ENSMUSG00000030881	7	105634203	105640416	-1	0	0	6	0	0	0	0	0	0	0	0	D6RHM6	
ENSMUST00000137932						15	16	6	18	25	16	39	147	74	3	199		
ENSMUST00000137933	ENSMUSG00000020481	11	5569684	5689337	1	4	1	35	9	8	3	0	0	0	0	0	Q5QNR4	
ENSMUST00000137934						40	28	42	49	26	20	2	3	7	1	8		
ENSMUST00000137935	ENSMUSG00000029096	5	35652023	35679782	-1	0	1	0	9	12	3	0	0	0	0	2		
ENSMUST00000137936	ENSMUSG00000027457	2	151590549	151632593	-1	1	0	0	109	0	4	0	0	0	0	0	Z4YN82	
ENSMUST00000137937						4	4	2	15	4	3	1	3	0	2	0		
ENSMUST00000137938						3	7	7	7	4	2	1	4	0	0	6		
ENSMUST00000137939						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137940						4	0	5	7	4	2	1	7	2	2	1		
ENSMUST00000137942	ENSMUSG00000002100	2	91118144	91136516	1	0	18	0	0	36	22	93	497	135	0	203	Q3TF37	
ENSMUST00000137943						11	10	49	25	28	19	16	13	27	0	80		
ENSMUST00000137944						19	27	91	34	40	25	20	331	64	63	88		
ENSMUST00000137945						4	1	5	2	0	1	0	0	0	0	0		
ENSMUST00000137946						0	0	0	27	4	0	0	0	0	0	0		
ENSMUST00000137947						5	4	1	105	10	5	0	0	0	0	0		
ENSMUST00000137948						0	2	7	12	0	6	0	0	0	0	0		
ENSMUST00000137949						2	2	7	1	1	2	3	8	6	0	1		
ENSMUST00000137950	ENSMUSG00000020289	11	32225628	32267707	-1	0	0	0	0	0	0	0	0	0	5	4	F2Z3V7	
ENSMUST00000137951						0	0	0	14	0	0	7	8	0	0	3		
ENSMUST00000137952	ENSMUSG00000029516	5	115845278	116008947	1	0	0	0	0	0	0	0	0	0	5	0	D3Z477	
ENSMUST00000137953						12	21	35	35	26	8	6	50	12	3	40		
ENSMUST00000137954						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000137955						3	6	3	5	4	2	0	0	0	0	0		
ENSMUST00000137956						7	2	8	129	14	3	33	36	29	5	44		
ENSMUST00000137957						5	5	3	7	4	1	0	0	0	0	0		
ENSMUST00000137959						2	0	0	1	0	0	41	7	105	2	51		
ENSMUST00000137960						1	1	17	94	2	2	1	6	0	0	0		
ENSMUST00000137961						0	0	0	0	0	0	6	8	7	2	0		
ENSMUST00000137963	ENSMUSG00000022603	15	74606029	74636353	-1	16	0	0	0	0	0	0	0	0	0	0	E9PZ22	
ENSMUST00000137965						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000137966	ENSMUSG00000038180	2	156065175	156070617	1	0	0	0	0	0	0	1	0	0	0	0	B7ZCP3	
ENSMUST00000137967	ENSMUSG00000025876	13	54949411	55006018	1	0	0	0	0	0	0	0	2	0	0	4	F6TGW0	
ENSMUST00000137968	ENSMUSG00000042793	1	134983301	135105276	-1	0	0	4	166	2	0	0	0	0	0	14	D3Z6S4	
ENSMUST00000137969						0	1	3	0	1	0	0	0	0	0	0		
ENSMUST00000137971						6	3	32	15	7	4	0	3	0	0	2		
ENSMUST00000137972	ENSMUSG00000023186	9	38718268	38743337	1	0	2	0	0	6	1	0	0	0	6	0	F6TIL5	
ENSMUST00000137973						55	47	54	50	68	31	4	18	2	0	5		
ENSMUST00000137974						2	2	1	2	1	3	0	0	0	0	0		
ENSMUST00000137975						11	1	23	30	9	2	6	0	0	15	0		
ENSMUST00000137976	ENSMUSG00000032028	9	48318006	48353454	-1	10	0	9	4	4	0	0	1	0	1	2	D3Z433	
ENSMUST00000137977	ENSMUSG00000031410	X	135579555	135598777	-1	0	0	0	0	4	0	0	0	0	0	0	F7AR15	
ENSMUST00000137978						69	47	469	449	67	56	0	10	3	1	9		
ENSMUST00000137979						0	0	1	0	0	0	0	2	2	0	0		
ENSMUST00000137980						1	0	6	6	2	4	1	15	1	1	8		
ENSMUST00000137982						4	2	29	13	6	2	54	90	95	7	94		
ENSMUST00000137983						3	1	11	89	9	3	2	1	6	0	8		
ENSMUST00000137984						4	2	5	8	3	4	0	0	0	0	0		
ENSMUST00000137985						3	0	5	1	1	0	4	0	13	0	15		
ENSMUST00000137986						2	0	3	3	5	2	0	29	5	3	5		
ENSMUST00000137987						3	0	18	7	8	5	14	46	26	6	44		
ENSMUST00000137988						4	4	3	5	3	0	0	0	0	0	0		
ENSMUST00000137989	ENSMUSG00000024191	17	26781079	26792565	1	6	3	0	9	4	7	15	44	0	0	0	F6QGF9	
ENSMUST00000137990	ENSMUSG00000021087	12	72211752	72409054	-1	0	0	0	0	0	0	0	0	0	0	1	A3QM89	
ENSMUST00000137991						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000137992						19	14	20	16	16	7	5	7	7	1	5		
ENSMUST00000137993						1	0	10	3	4	0	4	15	17	4	7		
ENSMUST00000137994						32	37	19	34	19	15	1	0	3	0	4		
ENSMUST00000137996	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	0	0	0	0	5	2	0	0	F6Q1Z6	
ENSMUST00000137997	ENSMUSG00000020716	11	79339693	79581612	1	4	0	13	0	0	0	92	186	220	20	162	Q5SYH9	
ENSMUST00000137998	ENSMUSG00000000739	8	123142847	123158315	-1	4	0	0	0	4	0	0	0	0	1	0	D3Z6D1	
ENSMUST00000137999	ENSMUSG00000034949	10	81233155	81252123	1	0	0	0	7	0	0	0	0	0	1	0	F6VRB4	
ENSMUST00000138000						2	2	11	4	8	5	0	4	9	0	10		
ENSMUST00000138001						2	6	12	4	5	3	16	5	22	0	6		
ENSMUST00000138002	ENSMUSG00000032469	9	99575799	99584501	1	0	0	2	0	0	0	2	0	0	0	0	F6S2R9	
ENSMUST00000138003	ENSMUSG00000034842	5	92331827	92414628	1	0	0	1	0	7	0	0	3	0	0	0	F6W3A0	
ENSMUST00000138004						2	1	0	2	4	1	0	0	4	0	0		
ENSMUST00000138005						9	4	21	85	11	2	19	63	43	10	31		
ENSMUST00000138006						0	7	29	0	1	0	304	1183	328	47	680		
ENSMUST00000138008						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138009						0	3	2	0	3	0	0	0	0	0	0		
ENSMUST00000138010						0	0	0	29	0	3	11	302	31	8	19		
ENSMUST00000138012	ENSMUSG00000001855	2	31974436	32053975	1	45	31	162	55	51	22	24	77	51	25	53	A2ATN3	
ENSMUST00000138013	ENSMUSG00000040859	4	129461581	129488498	1	1	0	3	87	1	1	2	0	0	0	0	B2KGE3	
ENSMUST00000138014	ENSMUSG00000038298	3	96829284	96870926	1	3	1	5	0	7	2	0	0	0	0	0	D3YZS9	
ENSMUST00000138015						1	0	7	20	6	1	0	0	1	0	1		
ENSMUST00000138016	ENSMUSG00000019888	10	101681487	102391469	1	0	0	0	0	0	0	0	0	0	0	0	D3Z1C7	
ENSMUST00000138017						2	1	5	47	4	1	0	0	0	0	0		
ENSMUST00000138018						5	4	1	2	3	0	0	0	0	0	0		
ENSMUST00000138019	ENSMUSG00000040365	11	48806404	48817353	-1	2	0	0	0	0	0	44	0	29	0	43	F6X2H0	
ENSMUST00000138020						0	1	0	82	3	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138021	ENSMUSG00000038718	2	34171457	34373142	-1	0	0	1	2	1	0	0	0	0	0	0	H3BK27	
ENSMUST00000138022						2	0	2	63	1	0	17	7	36	53	43		
ENSMUST00000138023	ENSMUSG00000025261	X	151800807	151935417	1	0	3	0	0	0	0	0	0	0	0	0	F6XP90	
ENSMUST00000138024	ENSMUSG00000004768	1	33719887	33742564	1	0	0	0	0	0	0	0	16	39	0	17	M0QWL7	
ENSMUST00000138025						12	16	29	18	15	9	0	3	2	0	0		
ENSMUST00000138026						1	0	3	2	0	1	0	0	0	0	0		
ENSMUST00000138027						7	4	5	24	1	2	0	0	0	0	0		
ENSMUST00000138028						5	4	3	0	0	0	0	0	0	0	0		
ENSMUST00000138029						4	1	0	44	4	3	0	1	0	1	0		
ENSMUST00000138030	ENSMUSG00000028455	4	43027690	43031710	-1	0	0	0	0	0	0	38	57	42	44	24	A2AG41	
ENSMUST00000138031						0	0	0	0	0	0	0	3	0	1	0		
ENSMUST00000138032						4	5	20	4	10	3	42	145	64	8	116		
ENSMUST00000138033						4	4	5	0	5	0	0	0	0	0	1		
ENSMUST00000138034						1	1	0	11	4	0	0	10	6	0	9		
ENSMUST00000138035	ENSMUSG00000001211	10	78269178	78352489	-1	1	0	6	9	1	0	0	0	0	0	0	D3YTN7	
ENSMUST00000138036						11	4	7	3	9	13	0	0	0	0	8		
ENSMUST00000138037	ENSMUSG00000002325	14	55603571	55610030	1	0	0	0	0	0	0	486	3134	424	91	400	E9Q8M6	
ENSMUST00000138038						41	43	296	98	39	33	10	29	7	8	47		
ENSMUST00000138039						3	1	2	0	5	0	8	34	25	0	61		
ENSMUST00000138040	ENSMUSG00000004535	6	52713729	52766780	1	3	2	25	33	7	5	4	6	5	1	1	D3Z213	
ENSMUST00000138041	ENSMUSG00000014550	6	92186712	92214925	-1	4	2	29	108	10	4	0	0	0	0	0	D3Z0E7	
ENSMUST00000138042						5	4	0	0	4	2	0	0	0	0	0		
ENSMUST00000138043	ENSMUSG00000039087	13	37778400	37952002	1	1	0	0	32	0	0	0	0	2	0	2		
ENSMUST00000138044						0	0	3	23	0	2	5	4	11	0	26		
ENSMUST00000138045	ENSMUSG00000028745	4	139192899	139291818	1	5	0	0	2	5	0	1186	66	1676	557	1182	F7CAZ6	
ENSMUST00000138046						2	0	0	0	2	1	1	15	13	7	4		
ENSMUST00000138047	ENSMUSG00000044550	X	136590842	136668378	1	0	0	0	0	1	0	0	2	0	0	0	A2AEC1	
ENSMUST00000138048						0	2	2	0	0	0	3	0	0	0	0		
ENSMUST00000138049	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138050	ENSMUSG00000020287	11	32226505	32232700	1	11	9	36	21	24	7	8	16	14	0	24	F2Z3Y1	
ENSMUST00000138051	ENSMUSG00000016495	19	29348599	29367390	-1	1	0	1	18	3	0	3	28	0	12	15		
ENSMUST00000138052						17	9	47	27	15	12	4	30	8	8	8		
ENSMUST00000138053						9	5	21	20	10	3	0	0	0	0	0		
ENSMUST00000138054						0	0	0	0	0	0	1	0	1	11	12		
ENSMUST00000138055	ENSMUSG00000090219	7	103998800	104137405	-1	8	2	0	5	4	1	0	0	0	0	0	V9GXN4	
ENSMUST00000138056						2	5	0	1	3	0	0	0	3	1	0		
ENSMUST00000138057						3	3	4	9	7	2	0	0	0	0	0		
ENSMUST00000138058						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138059						0	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000138060	ENSMUSG00000035642	7	97550331	97579497	-1	0	0	0	0	0	0	6	0	0	24	4		Q8R0P4
ENSMUST00000138061	ENSMUSG00000034224	8	119479602	119501698	-1	0	2	1	5	3	0	0	0	0	0	0	D3Z7F9	
ENSMUST00000138062	ENSMUSG00000030610	7	78821547	78847263	-1	0	1	17	7	1	0	5	5	1	1	0		
ENSMUST00000138063						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000138064						7	4	15	11	13	9	0	0	0	0	0		
ENSMUST00000138065						13	15	34	21	24	22	0	4	0	0	6		
ENSMUST00000138066						7	0	2	0	1	4	0	0	0	1	2		
ENSMUST00000138067						0	6	9	78	15	2	0	0	0	0	0		
ENSMUST00000138068	ENSMUSG00000089824	2	156091958	156111978	-1	0	0	0	0	0	0	1	6	0	0	0	B7ZCQ1	
ENSMUST00000138069						4	2	2	0	4	2	2	13	3	0	9		
ENSMUST00000138070						2	1	9	4	2	2	0	0	0	0	0		
ENSMUST00000138071						4	4	2	3	0	1	0	0	0	0	2		
ENSMUST00000138072						2	3	2	3	2	2	4	0	0	0	3		
ENSMUST00000138073	ENSMUSG00000028463	4	43506966	43513729	1	0	0	0	0	0	0	0	0	0	0	0	F6XXU0	
ENSMUST00000138074						15	10	12	8	9	3	0	0	0	0	0		
ENSMUST00000138075						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138076						1	3	3	2	1	0	6	35	17	23	0		
ENSMUST00000138078						0	0	11	14	10	2	3	0	0	0	0		
ENSMUST00000138079						7	0	2	120	1	0	0	0	0	0	30		
ENSMUST00000138081						4	1	2	3	1	1	0	0	0	3	0		
ENSMUST00000138083	ENSMUSG00000004043	11	100859351	100885169	1	0	0	4	79	8	3	0	3	0	0	0	A2A5D3	
ENSMUST00000138084						1	1	0	199	2	3	0	0	0	0	10		
ENSMUST00000138085	ENSMUSG00000002320	14	55635965	55643806	-1	0	0	0	0	7	0	0	0	4	0	6	D3Z279	
ENSMUST00000138086						6	0	9	33	7	3	0	21	0	0	0		
ENSMUST00000138087						3	4	10	5	4	4	0	0	0	0	0		
ENSMUST00000138088						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138089						0	0	0	8	7	0	16	117	44	8	19		
ENSMUST00000138090	ENSMUSG00000040663	19	4214238	4223490	1	0	3	8	4	0	4	0	0	0	0	0	D6RIL9	
ENSMUST00000138091	ENSMUSG00000027893	3	107663118	107696560	-1	0	0	0	0	0	0	128	908	185	80	25	F7ATQ6	
ENSMUST00000138092	ENSMUSG00000025511	7	141475240	141493427	1	4	0	0	0	0	0	1	7	0	0	5	D3Z0B7	
ENSMUST00000138093						30	23	175	43	21	14	0	2	8	0	3		
ENSMUST00000138094						5	2	17	20	6	3	1927	2276	941	173	578		
ENSMUST00000138095						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000138096	ENSMUSG00000028919	4	141239499	141257564	1	1	0	6	11	5	0	0	0	1	0	0	A2A827	
ENSMUST00000138097						21	20	60	47	20	11	1	10	3	3	2		
ENSMUST00000138098						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138099	ENSMUSG00000025790	7	74275419	74554780	-1	5	2	23	9	9	4	0	0	2	0	0	D3YUC4	
ENSMUST00000138100						0	0	0	0	0	1	1	0	0	0	18		
ENSMUST00000138101	ENSMUSG00000019179	5	135778480	135790398	1	6	0	14	44	7	8	2575	5831	1951	802	1834	J3QMC8	
ENSMUST00000138102						1	6	14	9	3	3	0	2	6	0	3		
ENSMUST00000138103						3	4	1	4	9	0	0	0	0	0	4		
ENSMUST00000138104						0	1	0	2	7	4	0	0	0	0	12		
ENSMUST00000138106						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138107						0	1	0	0	0	1	0	2	0	0	0		
ENSMUST00000138109	ENSMUSG00000100838	9	89199379	89215471	1	0	0	2	0	1	0	10	29	5	12	0	F6Q785	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138110	ENSMUSG00000039087	13	37778400	37952002	1	0	0	0	10	1	0	2	0	2	1	0	B8JJE4	
ENSMUST00000138111	ENSMUSG00000011831	5	107744795	107875107	-1	0	0	0	0	0	0	13	0	0	0	0	E9Q9B1	
ENSMUST00000138112	ENSMUSG00000019767	10	4482502	4562231	1	45	46	198	53	49	33	5	4	5	0	4	D3YXL0	
ENSMUST00000138113						3	5	43	19	8	0	1	0	0	0	0		
ENSMUST00000138115						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000138116						4	9	8	84	17	10	8	5	9	0	9		
ENSMUST00000138117						21	8	29	28	16	10	3	7	6	3	11		
ENSMUST00000138118						0	0	10	0	0	1	43	39	15	137	10		
ENSMUST00000138119	ENSMUSG00000002028	9	44803355	44881296	-1	8	9	24	9	8	8	3	0	39	0	72	S4R199	
ENSMUST00000138121						1	1	6	16	0	0	0	0	0	0	9		
ENSMUST00000138122	ENSMUSG00000033416	10	75351111	75517972	-1	0	0	0	0	0	0	0	0	21	0	0	D6RI82	
ENSMUST00000138123						6	1	4	2	3	2	5	11	10	5	21		
ENSMUST00000138124						59	82	47	61	68	42	1	2	3	0	3		
ENSMUST00000138125						0	2	12	8	5	3	11	30	13	4	50		
ENSMUST00000138126						0	0	0	0	0	0	0	45	0	0	89		
ENSMUST00000138127	ENSMUSG00000015597	17	46383731	46420920	1	11	8	33	67	25	0	0	4	0	0	9	B8JJA0	
ENSMUST00000138128	ENSMUSG00000030588	7	29238329	29247593	1	0	0	5	5	0	3	0	0	0	0	0	D3Z5F9	
ENSMUST00000138129						3	3	4	0	6	0	0	0	0	0	0		
ENSMUST00000138130						3	2	2	2	7	3	0	0	0	0	0		
ENSMUST00000138131						3	0	21	4	5	3	48	306	88	8	130		
ENSMUST00000138132						0	0	0	0	0	0	0	6	9	4	10		
ENSMUST00000138133	ENSMUSG00000002550	2	32255002	32260159	-1	1	3	10	1	2	0	38	24	15	0	29	F7CBX2	
ENSMUST00000138134	ENSMUSG00000035900	15	86057695	86137634	1	4	0	34	5	6	0	13	15	0	24	19	D3YUE7	
ENSMUST00000138135						1	1	2	1	2	1	0	0	0	0	0		
ENSMUST00000138138						11	4	7	1	12	7	0	0	0	1	0		
ENSMUST00000138139						4	1	12	12	6	9	102	330	127	9	260		
ENSMUST00000138140	ENSMUSG00000034639	6	108065045	108077122	1	4	0	5	5	0	1	2	6	11	20	8		
ENSMUST00000138141	ENSMUSG00000030741	7	126370060	126377450	-1	0	0	0	0	0	0	0	135	0	24	0	D6REG2	
ENSMUST00000138142	ENSMUSG00000026333	1	97770172	97793709	1	2	0	0	0	0	2	5	0	0	0	19	M0QWB3	
ENSMUST00000138143						63	65	132	48	69	28	4	11	6	1	15		
ENSMUST00000138144						1	0	3	0	2	0	0	4	0	0	4		
ENSMUST00000138145						0	3	2	0	3	5	3873	7311	3316	24572	3965		
ENSMUST00000138146						0	0	34	0	0	0	0	0	0	0	0		
ENSMUST00000138147						3	4	5	3	10	3	0	8	5	11	2		
ENSMUST00000138148						1	2	1	3	3	4	0	8	24	23	12		
ENSMUST00000138149						0	0	0	0	0	0	0	0	6	0	2		
ENSMUST00000138150						0	0	0	0	0	0	203	118	125	37	80		
ENSMUST00000138151						0	1	0	4	0	3	6	56	42	16	26		
ENSMUST00000138152	ENSMUSG00000037270	3	36863104	37053033	1	0	0	0	0	0	0	0	5	0	2	13	F6YB09	
ENSMUST00000138154						8	2	10	5	8	3	0	4	14	0	7		
ENSMUST00000138155						0	0	0	0	0	1	0	0	0	0	1		
ENSMUST00000138157	ENSMUSG00000027238	2	121545529	121807087	-1	0	12	9	91	0	9	0	0	0	0	0		Q6P5H6
ENSMUST00000138158						0	0	0	0	2	0	6	0	11	0	16		
ENSMUST00000138159	ENSMUSG00000020057	10	88322804	88379080	-1	3	3	1	3	1	0	0	0	0	0	0	D3Z5R7	
ENSMUST00000138160						8	0	1	0	10	4	451	1646	703	1197	568		
ENSMUST00000138161	ENSMUSG00000026854	2	30982279	31023586	1	0	0	0	7	1	4	0	0	0	0	0	A2AQ35	
ENSMUST00000138162						3	2	12	2	0	1	0	0	0	0	0		
ENSMUST00000138163						3	0	2	10	0	1	0	0	0	0	0		
ENSMUST00000138165						10	7	6	17	6	1	1	4	3	1	11		
ENSMUST00000138166	ENSMUSG00000022641	16	50191844	50432390	-1	26	23	39	30	39	18	249	849	514	75	399		Q8VBW5
ENSMUST00000138167	ENSMUSG00000030609	7	78895854	78911209	1	5	5	6	4	8	1	0	0	0	2	0	D3Z516	
ENSMUST00000138168	ENSMUSG00000028973	5	24393663	24410054	1	0	2	11	3	0	0	0	0	0	0	0	D3Z1J6	
ENSMUST00000138169						1	3	9	3	5	3	0	0	2	0	0		
ENSMUST00000138171						1	1	3	47	4	2	0	1	2	0	6		
ENSMUST00000138172						0	1	0	0	5	0	0	0	0	2	0		
ENSMUST00000138174						0	0	0	0	0	0	0	5	3	0	4		
ENSMUST00000138175	ENSMUSG00000060445	2	178345293	178407685	-1	0	0	0	0	0	3	0	0	0	0	0	A2AJW3	
ENSMUST00000138176						0	2	5	3	5	2	0	0	0	0	0		
ENSMUST00000138177	ENSMUSG00000030877	7	120982509	121014787	1	4	1	5	0	5	0	0	0	0	1	0	D3YWD7	
ENSMUST00000138178	ENSMUSG00000038180	2	156065175	156070617	1	0	0	0	21	0	0	0	0	0	0	0	F6S430	
ENSMUST00000138179						7	6	8	1	6	4	2955	434	2147	356	2211		
ENSMUST00000138181	ENSMUSG00000028960	4	149328416	149426749	-1	1	0	0	0	0	0	0	97	100	15	35	H7BXC2	
ENSMUST00000138182	ENSMUSG00000090165	1	88055388	88219004	1	0	0	20	0	0	0	0	0	0	0	0	D3Z7G0	
ENSMUST00000138183						1	6	4	0	3	2	3	11	16	0	5		
ENSMUST00000138184	ENSMUSG00000005674	1	171216011	171222514	-1	2	0	0	0	0	0	2	0	0	3	6	D3YY29	
ENSMUST00000138185	ENSMUSG00000037965	16	11136592	11176393	-1	2	0	0	91	4	2	0	0	16	0	0	E9Q8M5	
ENSMUST00000138186	ENSMUSG00000018572	11	69995777	70000009	1	0	5	0	55	0	0	0	0	0	0	0	B0QZH9	
ENSMUST00000138187	ENSMUSG00000041688	X	145446425	145505181	-1	5	0	4	1	2	0	0	0	0	0	5	F6YMV1	
ENSMUST00000138189						0	0	2	15	0	0	0	42	0	8	11		
ENSMUST00000138190	ENSMUSG00000041319	17	23668614	23673882	-1	4	1	1	0	0	0	30	0	6	1	15	D3YUL7	
ENSMUST00000138191	ENSMUSG00000022037	14	65968483	65981548	1	3	1	3	5	2	0	0	0	0	0	0	E9PUU2	
ENSMUST00000138192						0	0	0	1	0	1	0	0	7	4	0		
ENSMUST00000138193						22	14	55	26	25	12	0	133	6	54	33		
ENSMUST00000138194	ENSMUSG00000058793	2	132263148	132312050	1	0	0	0	0	0	0	0	0	9	0	13	F6S4G2	
ENSMUST00000138196						0	1	2	0	0	0	0	3	0	2	5		
ENSMUST00000138197						1	0	2	19	4	1	0	0	0	0	0		
ENSMUST00000138198						5	7	11	65	5	2	0	1	0	0	0		
ENSMUST00000138199						0	0	0	0	0	0	45	0	45	0	31		
ENSMUST00000138200						65	74	129	75	89	29	1	8	2	2	6		
ENSMUST00000138202						29	11	31	10	26	19	46	365	166	69	60		
ENSMUST00000138203	ENSMUSG00000026867	2	34674594	34755232	-1	0	0	0	1	2	2	0	0	0	0	16	F6UFP6	
ENSMUST00000138204						6	1	0	3	0	2	3	38	5	0	3		
ENSMUST00000138205						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000138206	ENSMUSG00000038495	3	96104527	96161129	1	1	0	0	0	1	0	23	0	14	0	34	D3Z210	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138208	ENSMUSG00000018648	11	84048041	84069261	-1	4	0	8	9	6	4	0	0	0	0	0	B1AT24	
ENSMUST00000138209	ENSMUSG00000038861	3	94974731	95006843	1	0	0	0	0	0	0	6	0	0	0	0	D6RI80	
ENSMUST00000138210						8	8	13	1	3	5	0	0	0	0	0		
ENSMUST00000138211						3	0	13	1	2	0	2	0	0	0	0		
ENSMUST00000138212						3	0	1	0	2	0	8	4	5	0	0		
ENSMUST00000138213						1	0	3	0	0	0	4	7	0	0	0		
ENSMUST00000138214						3	3	29	37	10	8	0	3	1	1	0		
ENSMUST00000138215						0	0	11	1	2	1	0	0	1	0	0		
ENSMUST00000138216	ENSMUSG00000027792	3	73635808	73708415	-1	3	1	2	0	0	0	0	0	0	0	0	A0A0A6YVZ5	
ENSMUST00000138217						1	2	0	3	0	0	0	0	0	0	0		
ENSMUST00000138218						2	1	1	3	0	0	0	19	5	0	4		
ENSMUST00000138219						4	4	7	8	6	4	15	14	25	2	14		
ENSMUST00000138220						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138221						3	1	10	13	3	0	0	0	0	0	0		
ENSMUST00000138222	ENSMUSG00000071322	17	7324646	7345974	1	7	2	2	0	2	2	0	0	0	0	0	E9Q2X0	
ENSMUST00000138223						0	0	7	68	5	0	0	0	6	1	0		
ENSMUST00000138224						10	7	19	10	18	8	5	18	0	4	13		
ENSMUST00000138225						2	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000138226						0	0	0	0	0	0	200	2375	521	964	223		
ENSMUST00000138227						0	5	0	0	1	0	0	0	0	0	0		
ENSMUST00000138228						1	0	2	0	0	0	3	2	0	0	0		
ENSMUST00000138229						1	0	10	4	0	2	0	0	0	0	0		
ENSMUST00000138230						0	0	1	0	3	2	0	0	0	2	0		
ENSMUST00000138231						0	0	0	0	0	0	19	248	0	0	6		
ENSMUST00000138232						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138233						5	3	5	7	7	1	48	54	14	0	29		
ENSMUST00000138234						2	0	0	1	0	0	16	5	6	0	27		
ENSMUST00000138235						3	0	5	3	2	2	103	475	158	17	220		
ENSMUST00000138237						2	0	9	2	3	4	0	13	8	0	6		
ENSMUST00000138238						11	4	20	15	15	1	38	754	102	14	508		
ENSMUST00000138239						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000138240	ENSMUSG00000037313	5	33658128	33678995	1	0	1	0	0	1	0	2	20	2	0	2	F6TNB3	
ENSMUST00000138241						0	1	0	0	0	0	1	0	0	0	1		
ENSMUST00000138242						4	4	9	12	7	1	3	128	17	12	32		
ENSMUST00000138243	ENSMUSG00000040390	7	27656375	27674598	-1	3	4	0	142	11	7	63	113	45	33	42		
ENSMUST00000138244	ENSMUSG00000029650	5	147878437	147894815	-1	1	0	0	33	3	1	0	3	0	2	1	D3YWM2	
ENSMUST00000138245						0	0	12	4	0	0	0	0	0	4	5		
ENSMUST00000138246						1	0	6	4	3	0	0	25	4	2	4		
ENSMUST00000138247	ENSMUSG00000020794	11	72607283	72686481	1	0	0	0	0	7	5	18	106	16	54	14	D6RES1	
ENSMUST00000138248						2	0	1	25	2	0	0	0	0	0	1		
ENSMUST00000138249						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138250	ENSMUSG00000018999	6	34153380	34177111	-1	5	6	0	50	5	0	25	10	19	0	8	S4R2P0	
ENSMUST00000138251						5	3	5	1	6	0	0	0	0	0	2		
ENSMUST00000138252						0	2	15	0	5	3	0	0	0	0	0		
ENSMUST00000138254	ENSMUSG00000079484	2	30266203	30282149	1	0	2	3	3	2	1	4	11	4	0	15	D6RI61	
ENSMUST00000138255	ENSMUSG00000021687	13	94201310	94285857	-1	1	0	5	0	2	1	0	0	35	0	0	D3YTP4	
ENSMUST00000138257	ENSMUSG00000041313	5	148327410	148399904	-1	0	1	0	0	0	0	0	0	0	0	11	E9Q3N1	
ENSMUST00000138258						0	0	4	0	0	0	54	47	159	0	22		
ENSMUST00000138260	ENSMUSG00000055553	8	70508272	70527956	-1	0	0	0	0	0	0	0	0	0	4	4	E9Q4P0	
ENSMUST00000138261						3	1	0	4	2	0	10	72	24	0	8		
ENSMUST00000138263						103	66	453	265	101	56	118	435	115	22	254		
ENSMUST00000138264	ENSMUSG00000033623	5	108461232	108506976	1	0	0	0	6	0	0	0	0	5	1	0	A0A0G2JDR0	
ENSMUST00000138265						8	13	15	14	7	2	13	43	15	3	28		
ENSMUST00000138266						2	4	2	2	7	1	0	0	0	0	0		
ENSMUST00000138267						0	0	0	0	0	0	2	0	3	0	0		
ENSMUST00000138268	ENSMUSG00000045503	2	164456964	164479638	1	3	3	0	20	0	0	0	9	2	6	8	D6RE24	
ENSMUST00000138269						0	0	0	0	0	4	26	15	30	0	66		
ENSMUST00000138271						2	1	8	87	6	4	0	0	0	0	1		
ENSMUST00000138272	ENSMUSG00000053522	7	28863853	28866284	1	1	0	1	0	5	0	1	0	0	17	2	D3Z141	
ENSMUST00000138273						1	0	1	4	0	1	0	0	0	0	0		
ENSMUST00000138274	ENSMUSG00000028538	4	117932154	118134914	-1	2	0	0	0	5	0	0	0	4	0	0	F6XZQ5	
ENSMUST00000138276	ENSMUSG00000032245	9	62838785	62852006	1	4	2	0	0	5	7	6	0	0	0	0	F6YAC1	
ENSMUST00000138278	ENSMUSG00000030264	6	113046225	113068273	1	0	1	3	27	3	0	0	2	5	10	0		
ENSMUST00000138279	ENSMUSG00000022890	16	84827866	84835625	-1	0	0	0	0	0	0	12	0	0	175	0	E9QAD6	
ENSMUST00000138280	ENSMUSG00000026240	1	86582904	86609375	1	0	0	0	0	0	2	56	19	12	27	79	D6RH36	
ENSMUST00000138281						0	2	0	0	0	0	2	0	0	0	0		
ENSMUST00000138282						0	0	5	0	0	2	32	578	76	85	75		
ENSMUST00000138283	ENSMUSG00000053253	14	105258573	105309298	1	0	0	0	0	0	0	188	383	358	158	199	F6RT43	
ENSMUST00000138284						49	50	234	88	61	43	10	27	31	1	36		
ENSMUST00000138285						0	0	0	0	0	0	0	22	0	28	0		
ENSMUST00000138286	ENSMUSG00000038665	6	36846022	37300184	-1	0	0	0	1	0	0	0	0	0	0	0	S4R2G0	
ENSMUST00000138287						0	0	0	0	0	0	0	0	80	0	44		
ENSMUST00000138290	ENSMUSG00000055371	2	52691664	52742281	-1	0	0	0	3	2	0	0	0	4	1	6	B0R0N7	
ENSMUST00000138292						3	0	5	164	5	3	0	0	0	0	0		
ENSMUST00000138293						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138294						0	0	6	0	2	5	10	28	0	13	16		
ENSMUST00000138296						6	4	11	14	13	6	32	18	13	0	55		
ENSMUST00000138297						11	3	10	13	35	11	0	0	0	0	0		
ENSMUST00000138299	ENSMUSG00000025571	11	117654289	117763439	1	0	0	119	0	0	0	272	83	605	26	648	B7ZC94	
ENSMUST00000138300						1	0	2	2	0	0	0	8	3	0	0		
ENSMUST00000138301						0	1	2	0	2	4	0	0	0	3	2		
ENSMUST00000138302	ENSMUSG00000047731	19	46599084	46657389	1	88	74	136	453	41	0	785	1818	840	422	560		Q8BGW2
ENSMUST00000138304						10	0	6	0	0	7	1	1	0	6	14		
ENSMUST00000138305	ENSMUSG00000028689	4	116708509	116751206	1	0	0	0	0	0	0	20	14	4	23	11	A8Y5M8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138306						2	3	0	45	6	6	39	18	147	8	172		
ENSMUST00000138307	ENSMUSG00000044349	2	158375638	158386145	1	0	0	0	0	0	0	0	0	0	0	0	D6RCZ9	
ENSMUST00000138308						2	0	6	0	0	2	0	3	0	43	0		
ENSMUST00000138309						10	3	17	58	9	3	13	68	9	16	28		
ENSMUST00000138310	ENSMUSG00000075704	16	18426384	18479073	1	4	1	3	2	6	1	0	0	0	0	0		
ENSMUST00000138311						0	0	0	2	0	0	6	9	9	0	21		
ENSMUST00000138312						2	0	0	0	1	1	0	3	4	2	1		
ENSMUST00000138313						80	84	93	83	90	47	5	33	13	5	21		
ENSMUST00000138314	ENSMUSG00000009030	2	37350074	37359332	-1	0	6	0	0	2	0	0	0	2	11	8		
ENSMUST00000138315	ENSMUSG00000032281	9	54604877	54661870	-1	0	0	6	3	3	3	0	0	0	0	0	D3YZ56	
ENSMUST00000138316						5	7	21	411	8	0	2	6	3	3	2		
ENSMUST00000138317						8	2	0	5	2	0	0	0	0	0	0		
ENSMUST00000138318						16	13	66	19	10	6	10	587	0	28	40		
ENSMUST00000138319						0	0	1	0	0	0	0	0	1	0	1		
ENSMUST00000138320						5	1	10	0	1	3	0	0	1	0	0		
ENSMUST00000138321	ENSMUSG00000022185	14	54642161	54686931	-1	7	3	22	8	9	5	7	62	16	5	40	F6Q8C0	
ENSMUST00000138322						12	7	15	3	19	3	0	0	0	0	0		
ENSMUST00000138323						0	4	5	0	0	4	76	159	95	320	92		
ENSMUST00000138324	ENSMUSG00000022724	16	59471775	59492461	1	2	2	3	1	1	3	2	0	0	0	0	D3Z287	
ENSMUST00000138325	ENSMUSG00000026840	2	31887291	31946539	1	0	4	36	174	15	18	0	0	0	0	0	A2ATM9	
ENSMUST00000138326						1	0	8	4	5	5	1	3	0	0	0		
ENSMUST00000138327						0	0	0	0	0	0	1	0	3	0	0		
ENSMUST00000138328	ENSMUSG00000008140	7	44489937	44496529	-1	0	0	2	31	10	0	0	0	6	0	0	D3Z665	
ENSMUST00000138329	ENSMUSG00000062609	16	95257558	95300260	1	1	2	0	3	0	0	0	0	0	0	0	D3Z370	
ENSMUST00000138330						5	3	0	6	7	3	0	0	0	0	1		
ENSMUST00000138331						2	1	16	2	7	0	0	1	0	0	0		
ENSMUST00000138332						0	1	8	2	5	1	0	0	1	0	0		
ENSMUST00000138333						15	13	28	18	19	3	0	0	0	0	0		
ENSMUST00000138334	ENSMUSG00000054405	4	132535550	132553742	1	0	0	0	0	0	0	12	196	35	5	34	F6QIL6	
ENSMUST00000138335						0	1	5	0	3	0	0	0	0	0	0		
ENSMUST00000138336						9	9	10	6	16	12	1	4	1	0	1		
ENSMUST00000138337						0	0	4	6	1	0	0	0	0	0	0		
ENSMUST00000138338	ENSMUSG00000034135	9	46012820	46224194	1	0	0	0	0	0	0	0	0	0	1	0	F6SBP3	
ENSMUST00000138339						8	3	8	108	10	3	0	0	0	0	0		
ENSMUST00000138340	ENSMUSG00000010021	11	114765388	114790739	1	1	4	8	41	3	3	1	0	0	0	7	F7BXY3	
ENSMUST00000138342						0	0	10	32	0	1	0	0	0	0	0		
ENSMUST00000138343						15	5	36	65	20	10	39	103	43	2	89		
ENSMUST00000138344	ENSMUSG00000059857	3	109780040	110144011	-1	1	0	0	0	2	0	0	0	0	0	0		Q8R4G0
ENSMUST00000138345						102	72	95	88	90	38	13	41	39	14	35		
ENSMUST00000138346						0	0	3	1	8	0	0	0	0	0	0		
ENSMUST00000138347						0	0	2	1	2	3	0	0	0	0	3		
ENSMUST00000138348						5	2	21	4	8	7	0	0	0	0	0		
ENSMUST00000138349	ENSMUSG00000023206	2	11705290	11734317	1	2	7	6	6	15	3	0	50	5	5	0	Q501M1	Q60819
ENSMUST00000138350	ENSMUSG00000033676	7	57419692	57828802	1	0	0	0	0	0	0	0	0	0	0	0	F6WUM4	
ENSMUST00000138351						4	1	3	4	2	0	3	49	7	1	16		
ENSMUST00000138352						0	0	10	8	0	4	0	0	0	0	0		
ENSMUST00000138353						0	0	0	85	0	3	27	0	0	0	0		
ENSMUST00000138354						1	1	11	3	1	1	1	16	0	0	0		
ENSMUST00000138355						3	5	36	0	3	1	1	4	0	2	2		
ENSMUST00000138356	ENSMUSG00000048537	9	44686304	44735198	-1	22	5	23	0	0	0	0	0	0	3	0	D3Z0X5	
ENSMUST00000138357						1	1	1	2	2	1	123	144	94	6	80		
ENSMUST00000138358						1	0	4	0	0	2	0	0	0	0	2		
ENSMUST00000138359						1	1	3	0	5	0	2	0	0	0	4		
ENSMUST00000138360						3	2	8	9	5	0	3	12	0	1	12		
ENSMUST00000138362						0	0	2	3	0	6	0	0	0	0	0		
ENSMUST00000138363	ENSMUSG00000054555	7	133883199	134232146	-1	0	0	0	78	23	7	0	0	0	0	0	F6YWH6	
ENSMUST00000138364						4	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000138365						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138366						0	3	3	0	0	4	0	0	0	0	0		
ENSMUST00000138367						5	4	15	7	3	0	2	10	4	0	0		
ENSMUST00000138368						3	2	13	0	1	0	0	0	0	0	0		
ENSMUST00000138369	ENSMUSG00000020863	11	94287890	94321988	-1	0	0	0	0	0	0	3	0	0	0	0	F7CR21	
ENSMUST00000138370	ENSMUSG00000039990	7	133637543	133672971	1	1	7	0	0	1	2	12	8	8	4	20	H3BJ09	
ENSMUST00000138371						2	0	4	10	0	1	1	0	0	0	0		
ENSMUST00000138375						7	2	3	1	11	0	0	0	0	0	0		
ENSMUST00000138376	ENSMUSG00000042404	3	90265185	90280669	1	0	6	16	40	1	2	0	0	0	0	0	F6RXE7	
ENSMUST00000138380						0	0	0	3	3	0	0	0	2	0	0		
ENSMUST00000138381						0	0	0	0	0	0	11	7	0	33	72		
ENSMUST00000138384						4	8	5	17	8	1	0	0	0	0	0		
ENSMUST00000138385						3	4	10	8	5	5	0	0	0	0	0		
ENSMUST00000138386						1	2	2	3	0	6	30	24	25	0	23		
ENSMUST00000138387						0	4	2	0	3	2	0	2	0	0	0		
ENSMUST00000138388						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138389						11	0	7	0	0	3	0	1	0	0	1		
ENSMUST00000138392	ENSMUSG00000047730	7	28071236	28120862	1	34	11	52	41	51	21	0	0	0	0	0	E9Q0B5	
ENSMUST00000138393	ENSMUSG00000020577	12	36014557	36042500	-1	5	1	10	2	9	3	38	99	35	130	91	A7NSI0	
ENSMUST00000138394						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000138395	ENSMUSG00000028644	4	119175457	119190011	-1	0	26	0	0	37	0	0	0	0	0	0	A2A7P7	
ENSMUST00000138396	ENSMUSG00000057457	X	157162075	157415312	-1	1	6	0	0	0	0	0	0	0	0	0	A2AC80	
ENSMUST00000138397	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	16	0	75	5	46	F6TQF4	
ENSMUST00000138398						22	21	64	81	24	11	3	3	4	8	2		
ENSMUST00000138399						2	2	2	19	0	0	0	9	7	0	10		
ENSMUST00000138400						6	8	6	2	5	3	5	32	11	10	5		
ENSMUST00000138401						1	4	4	2	3	3	51	80	32	13	16		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138403	ENSMUSG00000086848	3	92620081	92621660	-1	2	0	2	7	2	0	0	0	0	0	0	D3YV94	
ENSMUST00000138404						0	0	0	0	0	0	0	18	0	0	0		
ENSMUST00000138405	ENSMUSG00000037286	9	100597798	100959375	1	2	0	6	4	0	0	0	0	0	0	3	D6RHQ7	
ENSMUST00000138407						16	5	11	49	8	0	10	14	12	2	21		
ENSMUST00000138408						2	2	0	0	3	0	10	32	0	0	20		
ENSMUST00000138409						3	3	0	1	7	0	0	0	0	0	22		
ENSMUST00000138410	ENSMUSG00000034813	10	119454034	120087261	1	0	0	0	0	0	0	0	0	0	0	0		Q925T6
ENSMUST00000138412						1	0	0	8	0	1	3	0	0	5	0		
ENSMUST00000138413						2	2	0	0	2	0	2	6	3	0	3		
ENSMUST00000138414						0	4	0	2	6	0	2	0	3	0	7		
ENSMUST00000138415						2	1	2	69	4	0	0	0	0	0	2		
ENSMUST00000138417						2	0	0	1	1	0	3	5	3	3	1		
ENSMUST00000138418						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138419						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000138420	ENSMUSG00000056952	6	113697050	113711069	1	0	2	0	1	4	0	0	3	3	0	0	F7CWI0	
ENSMUST00000138421						0	0	1	0	4	1	0	0	0	0	0		
ENSMUST00000138423	ENSMUSG00000059439	11	85353167	85826058	1	1	0	7	6	0	2	7	0	1	0	3	B1B0B3	
ENSMUST00000138425	ENSMUSG00000036062	4	42916660	42944752	1	0	1	10	13	5	6	0	0	0	0	0	F6SBE4	
ENSMUST00000138428						3	0	0	0	0	3	5	7	0	5	0		
ENSMUST00000138429						5	3	5	0	0	0	0	0	0	0	0		
ENSMUST00000138432	ENSMUSG00000042289	7	127800604	127803802	1	1	1	3	0	0	0	0	0	0	0	0	D3YVB8	
ENSMUST00000138433						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138434	ENSMUSG00000021134	12	80945504	80950507	1	9	7	108	26	1	13	8	34	31	3	45	S4R2G3	
ENSMUST00000138435						21	17	35	39	36	17	0	1	0	0	0		
ENSMUST00000138436						14	17	24	7	26	11	13	60	20	6	66		
ENSMUST00000138437	ENSMUSG00000042903	X	101254528	101260873	1	5	0	10	0	4	3	8	0	0	0	0	B1AUT2	
ENSMUST00000138438	ENSMUSG00000004040	11	100885098	100939540	-1	0	2	0	46	7	0	0	0	0	0	0	B7ZC18	
ENSMUST00000138439	ENSMUSG00000051906	8	4102787	4105835	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1H5	
ENSMUST00000138440						2	0	0	0	1	0	0	47	0	4	1		
ENSMUST00000138441						49	38	159	79	51	21	2	8	1	3	5		
ENSMUST00000138443						6	14	31	39	15	9	8	132	40	2	49		
ENSMUST00000138445	ENSMUSG00000028796	4	128654702	128752881	1	0	0	0	22	4	0	0	0	0	0	0	D6REH8	
ENSMUST00000138446						12	10	59	17	15	6	0	1	3	0	2		
ENSMUST00000138448						0	0	0	48	0	0	8	3	4	14	4		
ENSMUST00000138449						0	0	0	2	0	0	3	0	8	0	46		
ENSMUST00000138450						2	4	8	0	13	6	0	3	7	0	1		
ENSMUST00000138451						0	5	2	0	4	0	7	35	15	2	13		
ENSMUST00000138452						0	1	8	6	4	0	0	0	0	0	0		
ENSMUST00000138453						8	9	24	13	6	1	0	0	0	0	1		
ENSMUST00000138454						2	2	0	2	5	0	0	0	0	1	0		
ENSMUST00000138455						2	0	0	0	5	1	0	0	0	0	0		
ENSMUST00000138456						249	251	465	281	226	125	10	28	23	7	42		
ENSMUST00000138457						3	3	8	105	8	3	3	5	2	1	2		
ENSMUST00000138458						2	3	0	49	2	0	22	35	3	0	10		
ENSMUST00000138459	ENSMUSG00000004056	7	27591552	27640826	1	1	3	8	15	5	3	1	0	5	0	1	D3Z0M3	
ENSMUST00000138463						1	0	5	60	5	4	0	0	0	0	0		
ENSMUST00000138464						0	0	0	124	5	1	0	0	0	0	0		
ENSMUST00000138465	ENSMUSG00000051048	7	100285520	100319699	1	85	45	425	34	49	27	3	16	15	3	20	F6R2A2	
ENSMUST00000138466						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000138468						69	49	66	91	94	34	26	91	64	15	56		
ENSMUST00000138469						13	2	42	11	13	5	4	0	2	0	4		
ENSMUST00000138470	ENSMUSG00000027257	2	91255954	91264679	1	5	2	0	4	4	2	0	0	0	2	5	A6PWR1	
ENSMUST00000138473						45	36	102	40	39	27	7	25	24	1	77		
ENSMUST00000138474						1	1	0	1	0	0	0	0	1	0	1		
ENSMUST00000138475						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138476						0	0	0	16	1	0	0	0	0	1	0		
ENSMUST00000138477	ENSMUSG00000018906	11	54100095	54131665	1	0	0	0	1	0	0	0	0	0	0	0	B0QZH3	
ENSMUST00000138478						0	2	10	0	3	0	61	94	21	0	10		
ENSMUST00000138479	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	0	0	0	0	0	6	2	0	A0A0E3D6L5	
ENSMUST00000138480						0	0	0	0	0	0	0	51	20	29	3		
ENSMUST00000138482	ENSMUSG00000000214	7	142892752	142931128	-1	0	1	0	0	0	0	0	0	0	0	0	F6VPB5	
ENSMUST00000138483	ENSMUSG00000020929	11	102838473	102880985	-1	0	0	0	0	2	0	0	0	0	0	0	G3V021	
ENSMUST00000138484						9	8	53	21	13	6	257	1510	327	63	389		
ENSMUST00000138485						1	1	2	27	3	1	0	2	0	0	1		
ENSMUST00000138487	ENSMUSG00000023902	17	23600856	23611019	1	0	0	0	0	0	0	0	0	0	0	0	D3YVM1	
ENSMUST00000138488	ENSMUSG00000003992	13	91460283	91703429	1	9	6	13	47	7	2	1	4	0	0	2	D6RG78	
ENSMUST00000138489						2	0	10	2	0	1	0	0	0	0	0		
ENSMUST00000138490						2	2	0	0	1	0	8	17	9	2	10		
ENSMUST00000138491	ENSMUSG00000024339	17	34203527	34216321	1	0	0	0	28	0	0	0	10	26	1	17	A6X8J5	
ENSMUST00000138493	ENSMUSG00000040964	4	140514485	140666012	-1	0	0	0	0	0	0	23	124	51	0	20	F6S3V7	
ENSMUST00000138494						0	0	0	5	0	1	0	12	3	0	0		
ENSMUST00000138495						18	13	28	37	17	12	4	11	9	0	3		
ENSMUST00000138497						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000138498						241	160	823	429	217	84	5	69	54	7	33		
ENSMUST00000138499						0	2	0	1	0	1	0	0	8	0	0		
ENSMUST00000138500						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000138502	ENSMUSG00000028234	4	3831334	3835665	-1	43	35	139	73	45	34	1294	1384	1206	7637	811	Q5BLK2	P60867
ENSMUST00000138503						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000138504						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000138505	ENSMUSG00000061589	10	80755206	80795461	1	7	2	9	55	21	0	8	32	15	1	30	F6S070	
ENSMUST00000138506	ENSMUSG00000037287	9	42412316	42507809	-1	0	0	4	7	4	0	10	0	48	0	33		Q8C5W3
ENSMUST00000138507						0	0	0	13	0	2	58	30	21	17	23		
ENSMUST00000138508	ENSMUSG00000025858	5	139252324	139270051	1	6	2	6	0	5	2	0	0	0	0	0	D3Z7S0	
ENSMUST00000138509						0	0	4	34	3	2	55	189	50	24	72		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138510						1	3	3	0	4	1	0	0	0	0	0		
ENSMUST00000138511						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138512						5	0	9	3	4	2	0	207	13	0	33		
ENSMUST00000138513						7	4	9	2	1	0	0	0	0	0	0		
ENSMUST00000138514	ENSMUSG00000022940	16	94358763	94371015	-1	3	4	1	64	5	2	3	12	2	6	0	B8JK63	
ENSMUST00000138515	ENSMUSG00000020333	11	54303798	54364756	1	0	1	0	29	5	0	0	0	0	0	0	B0QZJ6	
ENSMUST00000138517						3	7	4	18	2	2	0	2	2	0	2		
ENSMUST00000138518						7	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000138519						4	1	7	4	2	1	0	0	0	0	0		
ENSMUST00000138520						4	1	8	1	2	0	0	0	0	0	0		
ENSMUST00000138521						2	0	0	3	0	1	0	3	1	0	2		
ENSMUST00000138522	ENSMUSG00000019888	10	101681487	102391469	1	0	0	0	0	0	0	0	0	0	0	0	D3YZM8	
ENSMUST00000138523						4	3	4	0	3	1	0	2	0	0	0		
ENSMUST00000138524						7	4	9	17	4	7	0	0	4	0	2		
ENSMUST00000138525						6	0	2	31	8	0	0	0	0	0	0		
ENSMUST00000138526						0	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000138527						1	4	0	40	3	0	0	0	0	0	0		
ENSMUST00000138529						0	0	0	0	0	0	0	0	0	4	0		
ENSMUST00000138530	ENSMUSG00000025089	19	58235604	58455909	-1	0	1	4	70	4	2	0	0	0	0	0	D3YUD5	
ENSMUST00000138531						3	0	4	0	2	0	0	0	4	0	3		
ENSMUST00000138532	ENSMUSG00000024807	19	6046576	6053712	1	10	0	0	140	30	14	79	212	349	0	0		
ENSMUST00000138533						0	2	9	4	6	0	0	0	0	0	0		
ENSMUST00000138536						10	4	16	8	8	2	49	256	104	5	119		
ENSMUST00000138537						1	0	4	19	1	0	5	0	0	0	0		
ENSMUST00000138538	ENSMUSG00000020728	11	108425192	108860615	1	4	2	1	40	0	2	0	0	0	0	0	I7HLS4	
ENSMUST00000138540						1	2	1	0	2	1	0	0	1	0	0		
ENSMUST00000138541						0	0	0	2	0	1	129	0	26	0	38		
ENSMUST00000138542	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	0	0	2	0	0	0	0	0	F6RSJ3	
ENSMUST00000138543						7	3	10	7	16	8	0	0	0	0	0		
ENSMUST00000138544						0	2	7	0	6	0	22	31	123	0	61		
ENSMUST00000138545	ENSMUSG00000024694	19	12695786	12719902	1	0	0	0	0	2	1	0	0	0	0	0	D3Z4V9	
ENSMUST00000138546						7	3	26	361	11	5	0	0	0	0	0		
ENSMUST00000138547						0	0	1	0	0	0	0	6	0	0	0		
ENSMUST00000138548						0	3	0	0	0	0	17	102	27	11	0		
ENSMUST00000138549						21	20	25	29	20	13	5	20	18	3	14		
ENSMUST00000138550						4	0	5	7	3	2	0	10	5	0	8		
ENSMUST00000138551						1	3	8	3	6	10	0	0	0	0	0		
ENSMUST00000138552	ENSMUSG00000027882	3	108793176	108840526	-1	7	5	10	20	3	3	6	14	6	10	12	A0A0G2JEQ3	
ENSMUST00000138553	ENSMUSG00000066551	5	149046702	149184489	-1	0	0	0	0	0	0	0	0	0	3	0	D3YZ18	
ENSMUST00000138554						5	0	14	2	1	0	0	0	0	0	0		
ENSMUST00000138555	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	0	79	0	15	11	D3Z2F9	
ENSMUST00000138556						4	1	21	4	0	0	11	11	5	0	18		
ENSMUST00000138557	ENSMUSG00000060441	7	104263386	104288094	-1	18	14	1	273	28	9	0	106	10	17	0	D6RCJ3	
ENSMUST00000138558	ENSMUSG00000042759	7	126584942	126589112	1	0	0	0	0	0	0	4	0	3	0	0		
ENSMUST00000138559						28	36	143	23	34	13	13	26	25	1	41		
ENSMUST00000138560	ENSMUSG00000022960	16	91677268	91688765	-1	0	0	0	8	2	0	0	0	73	16	58	F6QFE2	
ENSMUST00000138561	ENSMUSG00000039298	4	70216856	70410443	-1	0	0	0	0	5	2	7	12	8	6	3	Q5SP75	
ENSMUST00000138562						0	0	0	0	2	0	19	0	0	66	0		
ENSMUST00000138563	ENSMUSG00000037225	3	37348346	37410108	1	1	4	3	38	10	7	0	0	0	0	0	Q541T2	P15655
ENSMUST00000138564	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	0	0	0	0	8	0	0	A3KG37	
ENSMUST00000138565						4	7	4	48	10	3	3	0	2	1	0		
ENSMUST00000138566	ENSMUSG00000025261	X	151800807	151935417	1	0	0	0	0	0	0	0	6	7	0	15	D6RDF2	
ENSMUST00000138567	ENSMUSG00000045751	4	24496451	24602950	1	2	0	0	145	0	6	9	0	0	0	5	G5E925	
ENSMUST00000138568						0	1	4	0	12	0	0	0	0	0	0		
ENSMUST00000138569						6	2	1	2	0	0	4	5	42	0	22		
ENSMUST00000138571						0	0	5	0	2	1	7	1	12	3	19		
ENSMUST00000138572						2	1	0	0	1	3	0	0	0	0	0		
ENSMUST00000138575						0	1	0	0	0	0	0	5	25	0	0		
ENSMUST00000138576						1	0	2	1	0	6	0	0	0	0	0		
ENSMUST00000138577						21	14	18	20	14	7	0	0	4	0	2		
ENSMUST00000138578						0	1	3	2	1	0	0	0	0	0	0		
ENSMUST00000138579	ENSMUSG00000029361	5	117781032	117958840	1	0	0	1	10	0	0	0	0	0	0	0	S4R1D5	
ENSMUST00000138580						1	0	0	3	0	3	0	2	2	2	0		
ENSMUST00000138581						0	0	0	0	0	0	0	0	0	7	24		
ENSMUST00000138582						2	0	0	131	1	3	0	0	0	0	0		
ENSMUST00000138583						80	69	57	64	85	44	0	8	2	2	6		
ENSMUST00000138584						50	47	154	65	61	44	0	0	2	0	12		
ENSMUST00000138585						0	0	0	0	0	0	0	0	0	12	14		
ENSMUST00000138586						12	4	13	11	4	5	1	2	0	0	5		
ENSMUST00000138587	ENSMUSG00000061462	11	58994256	59136402	-1	16	36	94	4	36	40	0	0	0	0	1	F6TJX7	
ENSMUST00000138588						5	2	14	25	14	9	0	6	2	0	4		
ENSMUST00000138589						6	2	8	3	14	1	17	397	62	19	51		
ENSMUST00000138590	ENSMUSG00000029674	5	134656039	134688598	-1	0	0	0	0	0	1	2	1	1	0	2	F6XM68	
ENSMUST00000138591	ENSMUSG00000023328	5	137287519	137294466	1	0	0	0	0	1	1	2	3	0	0	0	D3Z064	
ENSMUST00000138594						4	7	9	82	10	2	0	0	0	0	0		
ENSMUST00000138595	ENSMUSG00000084989	1	93168725	93231072	1	68	45	165	159	110	44	0	0	0	0	1	F6XLV1	
ENSMUST00000138596	ENSMUSG00000041313	5	148327410	148399904	-1	3	2	9	6	7	1	0	0	0	0	0	D3Z161	
ENSMUST00000138597						22	14	30	15	16	7	3	4	4	2	5		
ENSMUST00000138598						971	730	978	823	909	516	251	1151	535	279	646		
ENSMUST00000138599						0	0	0	0	0	0	2	4	0	0	2		
ENSMUST00000138601						1	0	2	0	0	0	26	14	0	9	0		
ENSMUST00000138602						7	0	0	19	8	0	12	52	56	3	57		
ENSMUST00000138603	ENSMUSG00000006930	11	100347327	100356128	-1	18	9	79	149	40	27	2	9	1	2	23		O35668
ENSMUST00000138604						2	5	10	40	9	2	0	2	2	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138605						0	5	1	0	7	5	0	79	5	0	0		
ENSMUST00000138607						0	1	1	0	0	1	0	0	1	0	0		
ENSMUST00000138608						3	5	10	16	0	4	3	18	7	0	11		
ENSMUST00000138609						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000138610						1	0	2	7	5	3	4	8	7	10	9		
ENSMUST00000138612	ENSMUSG00000001323	11	74906359	74925948	-1	2	0	0	0	0	0	0	5	4	0	9	A8Y5D6	
ENSMUST00000138613						7	5	4	3	8	2	0	35	5	0	18		
ENSMUST00000138615	ENSMUSG00000029290	5	105876565	105915818	1	6	5	4	48	11	4	0	82	10	13	8	D6RG92	
ENSMUST00000138616	ENSMUSG00000030750	7	125467640	125491596	-1	3	3	1	18	5	1	17	0	0	5	0	F6VZ99	
ENSMUST00000138618						1	2	0	1	3	0	0	7	10	0	0		
ENSMUST00000138619						0	0	0	0	0	0	2	0	0	0	1		
ENSMUST00000138620						2	0	5	12	9	6	4	0	1	0	0		
ENSMUST00000138621						0	3	3	8	12	3	8	26	13	0	7		
ENSMUST00000138622	ENSMUSG00000025786	9	123066160	123113205	-1	17	17	27	23	8	5	59	68	70	11	50	D6RDS4	
ENSMUST00000138623						5	4	19	6	9	4	0	4	5	0	2		
ENSMUST00000138624						2	2	5	0	0	0	0	5	0	0	0		
ENSMUST00000138625						3	2	2	1	8	4	0	0	0	0	0		
ENSMUST00000138627	ENSMUSG00000030761	7	98051060	98119524	-1	0	0	0	0	0	0	0	0	0	0	0	D3YUT5	
ENSMUST00000138628	ENSMUSG00000032812	7	101348067	101412586	1	3	3	15	1	6	7	16	8	4	0	5	D3YVS8	
ENSMUST00000138629						6	9	6	1	0	0	5	33	7	91	28		
ENSMUST00000138630						0	0	0	0	0	0	16	30	18	7	7		
ENSMUST00000138631	ENSMUSG00000044197	5	139377697	139396415	1	4	4	0	14	7	0	8	0	19	7	3	D3Z262	
ENSMUST00000138632						2	2	7	1	0	1	1	9	2	0	5		
ENSMUST00000138633						5	2	13	3	2	2	8	35	30	0	17		
ENSMUST00000138634						9	10	4	125	18	7	0	0	0	0	0		
ENSMUST00000138635						17	12	7	19	9	9	3	5	3	0	0		
ENSMUST00000138636						17	21	23	13	16	14	0	0	3	1	0		
ENSMUST00000138637						2	0	0	50	5	0	1	0	0	0	0		
ENSMUST00000138638						42	16	81	56	35	25	117	212	185	19	163		
ENSMUST00000138639						1	0	2	6	1	3	122	143	98	7	81		
ENSMUST00000138640						1	0	2	6	2	0	0	0	0	0	0		
ENSMUST00000138642	ENSMUSG00000079702	X	8542608	8548255	-1	3	0	0	1	0	2	0	0	0	0	0	A2BI74	
ENSMUST00000138643	ENSMUSG00000053166	2	165111507	165234853	-1	0	7	8	0	0	0	0	0	0	0	0	I6L9J1	
ENSMUST00000138645	ENSMUSG00000025665	X	111388192	111537959	-1	0	0	0	0	0	0	0	0	0	0	0	B2GVN8	
ENSMUST00000138646						14	14	0	42	24	0	241	2633	593	107	872		
ENSMUST00000138647						0	0	0	23	0	0	0	0	1	2	0		
ENSMUST00000138648						6	0	10	111	12	7	8	24	4	10	6		
ENSMUST00000138650						1	0	2	0	5	7	15	45	18	25	25		
ENSMUST00000138651						0	0	0	0	0	0	0	1	0	2	0		
ENSMUST00000138652						1	0	2	1	11	6	0	0	0	0	0		
ENSMUST00000138654						1	3	2	2	0	3	0	0	0	0	0		
ENSMUST00000138656						0	0	0	0	0	3	6	27	0	1	12		
ENSMUST00000138657						1	1	0	7	0	0	6	156	5	19	39		
ENSMUST00000138658						0	0	0	5	3	1	0	33	0	5	8		
ENSMUST00000138659						12	6	28	11	18	9	0	0	0	1	10		
ENSMUST00000138660						0	0	0	1	0	0	0	0	0	7	0		
ENSMUST00000138661	ENSMUSG00000000753	11	75409769	75422701	-1	0	0	0	0	0	0	1	1	0	0	0	Q5ND37	
ENSMUST00000138662						14	20	121	43	32	12	12	31	13	8	11		
ENSMUST00000138665	ENSMUSG00000022037	14	65968483	65981548	1	0	0	0	0	0	0	0	0	0	0	0	D6RFP9	
ENSMUST00000138666	ENSMUSG00000052533	2	30286397	30344266	1	0	0	0	0	0	1	0	0	0	0	0	J3JSA4	
ENSMUST00000138667	ENSMUSG00000093752	2	168180986	168230364	-1	0	0	0	0	0	0	764	2143	1096	162	649		O70152
ENSMUST00000138668	ENSMUSG00000038871	6	34476207	34505613	1	0	2	5	4	7	0	0	0	0	0	0	D3YYH3	
ENSMUST00000138669						0	2	0	0	0	0	3	16	16	0	12		
ENSMUST00000138671	ENSMUSG00000038909	11	95274259	95310246	-1	0	4	5	0	0	0	8	49	36	7	38	F6S4B9	
ENSMUST00000138673						2	2	3	9	8	3	11	109	6	4	34		
ENSMUST00000138674						2	2	7	27	2	2	149	83	184	23	120		
ENSMUST00000138676	ENSMUSG00000034940	11	83964428	84044578	1	2	2	1	0	0	1	2	0	0	0	0	F6YUG5	
ENSMUST00000138677						5	0	20	0	0	0	0	0	8	0	1		
ENSMUST00000138679						9	0	12	3	6	8	6150	1270	4599	1178	2997		
ENSMUST00000138680						6	4	4	4	3	2	0	0	0	0	0		
ENSMUST00000138681						5	0	0	1	2	0	9	11	29	0	27		
ENSMUST00000138682						2	3	9	0	0	1	0	0	0	0	5		
ENSMUST00000138683	ENSMUSG00000032997	1	75474569	75479307	-1	0	0	11	0	0	0	40	35	12	26	24	D6RFA4	
ENSMUST00000138685	ENSMUSG00000036820	17	24155833	24163766	-1	3	4	2	2	4	4	8	23	3	0	10	F7CUP3	
ENSMUST00000138686						4	0	7	4	5	2	0	0	0	0	0		
ENSMUST00000138687	ENSMUSG00000034842	5	92331827	92414628	1	0	2	0	0	0	0	0	1	0	0	0	E9PVX7	
ENSMUST00000138688						9	9	64	12	12	2	20	97	18	0	23		
ENSMUST00000138689						3	0	0	0	0	0	0	1	1	0	0		
ENSMUST00000138690						4	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000138692	ENSMUSG00000039048	9	35204206	35211055	-1	0	0	0	0	0	0	0	0	0	0	22	D6RCV5	
ENSMUST00000138693	ENSMUSG00000026918	2	27445579	27507662	-1	0	0	0	0	0	0	82	50	100	0	64	A2AKA9	
ENSMUST00000138694	ENSMUSG00000041329	11	69599736	69605942	-1	0	0	0	0	0	0	0	0	0	0	0	I7HIF3	
ENSMUST00000138695						1	1	0	1	3	1	3	1	0	1	0		
ENSMUST00000138696						0	0	0	0	2	0	0	15	21	4	2		
ENSMUST00000138698						7	5	4	1	3	2	0	0	0	0	1		
ENSMUST00000138699						9	8	18	14	16	5	9	16	28	3	17		
ENSMUST00000138700						3	3	0	13	0	2	0	0	0	0	0		
ENSMUST00000138701						4	4	4	5	1	4	0	2	0	0	3		
ENSMUST00000138703	ENSMUSG00000021196	13	6579768	6648777	-1	5	3	0	26	9	0	139	201	99	50	121		Q9WUA3
ENSMUST00000138704						6	4	7	4	7	1	0	2	5	2	12		
ENSMUST00000138705						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000138706						5	2	28	4	6	3	2	12	6	0	6		
ENSMUST00000138707						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138708						0	0	0	0	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138709						2	0	1	0	2	1	0	19	11	0	0		
ENSMUST00000138710						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000138712	ENSMUSG00000030670	7	114550166	114562972	-1	0	0	0	0	0	0	0	0	0	0	0	D6RCU9	
ENSMUST00000138713						4	0	5	8	2	4	5	0	0	0	4		
ENSMUST00000138714	ENSMUSG00000026556	1	172000960	172028444	-1	3	1	3	51	2	0	0	0	0	0	0	D3Z374	
ENSMUST00000138716						15	8	27	1	13	11	8	5	1	1	1		
ENSMUST00000138717						36	38	118	69	53	38	6	0	14	0	31		
ENSMUST00000138718						2	0	0	0	0	0	0	29	0	0	0		
ENSMUST00000138719	ENSMUSG00000027074	2	84936579	84958509	1	0	2	0	0	0	0	0	0	0	2	0	A6PWZ9	
ENSMUST00000138720						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138721						3	5	3	12	10	5	0	3	1	0	0		
ENSMUST00000138722						8	2	15	12	1	0	2637	4655	1970	201	1227		
ENSMUST00000138724	ENSMUSG00000033737	X	106420041	106485401	-1	1	0	0	1	0	1	0	0	0	0	0	A2AMR3	
ENSMUST00000138725	ENSMUSG00000058093	13	67589443	67609707	-1	0	0	5	0	0	0	4	0	28	3	18	B8JK40	
ENSMUST00000138726						3	7	0	0	5	0	0	0	0	0	0		
ENSMUST00000138728						2	3	13	34	5	7	0	133	0	0	60		
ENSMUST00000138730						9	6	19	25	10	2	0	0	0	1	1		
ENSMUST00000138731						0	0	0	0	0	0	0	6	0	0	0		
ENSMUST00000138732						0	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000138733						83	106	106	52	93	39	5	13	19	12	42		
ENSMUST00000138734	ENSMUSG00000004359	10	88674772	88685015	-1	0	0	0	0	0	0	0	0	0	0	0	D3YYM5	
ENSMUST00000138735						1	1	0	0	4	1	0	0	0	0	0		
ENSMUST00000138736						2	7	1	2	4	2	0	0	2	0	0		
ENSMUST00000138737						1	0	0	0	0	3	0	14	8	2	17		
ENSMUST00000138738						8	3	12	10	7	6	0	2	4	0	0		
ENSMUST00000138739						3	4	30	28	5	2	7	41	15	5	31		
ENSMUST00000138740	ENSMUSG00000037486	12	3426857	3506852	1	0	1	2	0	0	0	4	0	0	0	5	G3UXC9	
ENSMUST00000138741						11	6	16	31	12	7	275	1399	419	115	456		
ENSMUST00000138742	ENSMUSG00000031807	8	71592176	71601092	1	0	0	0	0	2	0	14	6	0	0	0	F6X8L5	
ENSMUST00000138743						0	2	0	1	0	2	7	60	17	56	35		
ENSMUST00000138745						1	0	1	0	0	0	0	17	0	0	0		
ENSMUST00000138746						12	0	0	104	37	0	11	0	0	0	0		
ENSMUST00000138748						6	4	8	3	1	2	0	0	0	0	0		
ENSMUST00000138749						19	24	43	62	23	15	5	15	6	2	5		
ENSMUST00000138750	ENSMUSG00000017210	11	98704591	98729435	-1	0	0	0	0	0	0	0	6	0	0	0	F6XX22	
ENSMUST00000138752						100	79	686	173	75	49	135	689	299	15	1860		
ENSMUST00000138753	ENSMUSG00000030990	7	102210208	102238567	1	0	1	13	17	14	2	0	0	4	0	0	D3Z1F0	
ENSMUST00000138754						1	0	10	8	9	0	0	0	0	0	3		
ENSMUST00000138756						3	0	1	2	6	2	0	0	0	0	0		
ENSMUST00000138757						13	23	116	273	36	19	0	0	0	0	1		
ENSMUST00000138758	ENSMUSG00000027309	2	130706200	130906406	-1	0	0	4	0	4	0	0	0	2	0	0	F6VYF3	
ENSMUST00000138759	ENSMUSG00000061046	17	25779843	25785673	-1	0	0	0	0	0	0	8	212	75	0	68	D3YZU6	
ENSMUST00000138760	ENSMUSG00000048078	7	96171246	96911093	1	0	0	0	41	0	0	0	0	0	0	0	D3YVP2	
ENSMUST00000138762	ENSMUSG00000033671	1	155844964	155973255	-1	56	46	79	61	54	26	902	1778	2394	132	1967	E9Q309	
ENSMUST00000138765						0	0	0	0	0	0	0	0	15	8	11		
ENSMUST00000138766						8	7	47	3	14	5	26	68	85	5	35		
ENSMUST00000138768						0	0	2	28	0	1	1	0	0	0	0		
ENSMUST00000138769						1	0	6	15	4	0	5	5	0	0	3		
ENSMUST00000138770	ENSMUSG00000004267	6	124760053	124769673	-1	0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000138771						833	460	4732	880	404	172	3	12	17	0	27		
ENSMUST00000138772						0	0	0	49	0	0	0	0	0	0	2		
ENSMUST00000138773						3	0	13	75	10	1	62	47	123	5	78		
ENSMUST00000138774	ENSMUSG00000037143	2	145934784	146215039	1	82	77	328	75	80	29	3	10	9	0	9	Q6ZWM9	
ENSMUST00000138775						0	2	2	5	1	2	0	5	0	0	0		
ENSMUST00000138776						1	1	1	11	6	1	0	0	0	0	0		
ENSMUST00000138777	ENSMUSG00000027601	3	19187327	19220817	1	0	0	0	0	0	0	3	3	4	0	0	D6RFQ6	
ENSMUST00000138778						0	0	0	3	0	0	1	0	0	0	0		
ENSMUST00000138779						4	2	5	3	2	5	8	45	14	2	24		
ENSMUST00000138780						2	1	0	115	4	2	0	0	1	0	0		
ENSMUST00000138781	ENSMUSG00000026796	2	32876114	32925254	1	0	0	0	2	1	0	0	0	0	0	0	A2ARS6	
ENSMUST00000138782						5	2	3	62	6	4	0	1	3	0	0		
ENSMUST00000138783						1	2	13	19	3	0	0	1	1	0	0		
ENSMUST00000138784						0	0	0	20	0	0	0	1	0	0	0		
ENSMUST00000138785	ENSMUSG00000000730	10	78041947	78063622	1	14	10	7	21	7	4	0	0	0	0	0	A3EWM2	Q9CWR8
ENSMUST00000138786						16	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138787						4	0	0	4	1	0	1	1	1	0	1		
ENSMUST00000138788						3	6	7	7	9	1	1	15	6	0	7		
ENSMUST00000138789						1	4	9	6	9	1	28	33	30	10	59		
ENSMUST00000138790						21	10	31	10	15	7	0	0	1	0	0		
ENSMUST00000138791	ENSMUSG00000031353	X	162760402	162779092	1	1	3	4	18	1	0	0	26	0	0	0	F6ZLC6	
ENSMUST00000138792						0	0	0	0	0	0	35	65	0	0	55		
ENSMUST00000138793						8	1	40	1	8	7	6	7	1	7	17		
ENSMUST00000138794						1	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000138796	ENSMUSG00000071561	16	36359382	36367748	-1	0	7	0	24	12	10	1641	14128	6050	5305	427	D6REU3	
ENSMUST00000138797	ENSMUSG00000069793	11	82979629	82991830	-1	2	0	2	2	3	1	0	2	3	5	19	A0A0A0MQG6	
ENSMUST00000138798	ENSMUSG00000008435	7	4424770	4445649	-1	0	0	0	0	0	0	0	0	0	1	3	D3YVJ8	
ENSMUST00000138799						3	5	3	1	3	1	6	4	0	4	0		
ENSMUST00000138800						0	0	0	152	8	0	55	48	20	21	37		
ENSMUST00000138801						94	61	287	130	112	41	14	24	14	6	9		
ENSMUST00000138803						6	2	11	133	5	7	12	6	28	7	25		
ENSMUST00000138804	ENSMUSG00000010021	11	114765388	114790739	1	0	0	5	147	0	0	0	0	2	0	0	A2AC95	
ENSMUST00000138805						1	0	4	4	2	5	0	0	0	0	2		
ENSMUST00000138806						2	1	4	3	5	2	4	13	2	3	11		
ENSMUST00000138807	ENSMUSG00000028890	4	124802104	124849800	1	0	0	0	20	0	0	10	0	6	4	0	B1ARW6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138808	ENSMUSG00000040945	4	140700541	140723220	1	0	0	6	10	0	0	0	0	0	0	0	A2AWQ2	
ENSMUST00000138809						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000138810	ENSMUSG00000020516	11	86498871	86544805	-1	3	1	2	33	2	0	4	5	26	21	17	Q5SWG2	
ENSMUST00000138811						3	0	8	1	2	0	0	1	0	1	0		
ENSMUST00000138812	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	0	0	1	8	16	6	10	0	D3YX95	
ENSMUST00000138813						2	0	0	17	0	0	0	0	0	0	0		
ENSMUST00000138814	ENSMUSG00000006576	1	75546266	75562172	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3U9	
ENSMUST00000138815	ENSMUSG00000032698	2	103957986	103981878	1	0	0	0	12	0	0	0	0	0	0	0	A2BHP4	
ENSMUST00000138818						3	2	2	24	5	1	2	0	2	0	0		
ENSMUST00000138820	ENSMUSG00000029127	5	38189735	38220457	-1	0	0	11	0	0	0	0	0	8	0	0	D6RE57	
ENSMUST00000138821						2	4	0	70	2	4	0	0	0	0	0		
ENSMUST00000138822						13	5	60	73	22	13	61	385	88	10	237		
ENSMUST00000138823	ENSMUSG00000029782	6	30479053	30509783	-1	0	0	0	0	0	0	22	0	34	0	20		Q8BRG8
ENSMUST00000138824						3	3	8	32	1	1	0	0	0	0	0		
ENSMUST00000138825						1	0	9	2	0	2	0	0	1	1	0		
ENSMUST00000138826						5	5	7	37	7	3	0	0	0	0	0		
ENSMUST00000138827						255	266	634	13616	265	168	5	37	9	5	28		
ENSMUST00000138828						19	20	27	76	19	11	0	5	7	0	4		
ENSMUST00000138829						0	2	0	46	0	0	0	0	0	0	0		
ENSMUST00000138830	ENSMUSG00000030701	7	100642892	100662414	-1	1	0	0	0	0	0	0	0	0	0	0	D3Z1E2	
ENSMUST00000138831	ENSMUSG00000028868	4	133130505	133199756	1	0	0	5	33	2	2	13	3	32	0	24	B1AUN0	
ENSMUST00000138833						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138834						3	0	0	0	3	1	0	0	0	0	0		
ENSMUST00000138835						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138836						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000138837						1	0	9	2	1	0	42	486	164	75	144		
ENSMUST00000138839						14	14	22	17	15	13	0	1	1	0	1		
ENSMUST00000138840	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	0	0	0	0	0	0	0	0	B1AT87	
ENSMUST00000138841	ENSMUSG00000022329	15	34875496	35155806	-1	0	1	0	25	0	1	0	0	0	0	0	D6RHQ9	
ENSMUST00000138842	ENSMUSG00000029217	5	72755716	72868483	-1	0	3	16	36	12	0	0	150	2	106	121		
ENSMUST00000138843	ENSMUSG00000023030	15	100387898	100425072	-1	44	42	84	38	40	19	3	19	10	0	23		P49282
ENSMUST00000138845	ENSMUSG00000032998	4	119537004	119629119	1	0	4	5	1	0	0	0	0	0	0	0	Q3TAY5	
ENSMUST00000138846						1	1	8	5	1	4	0	0	0	0	0		
ENSMUST00000138847	ENSMUSG00000024099	17	66078795	66101559	-1	1	0	0	0	1	2	0	20	11	0	12	M0QWP9	
ENSMUST00000138848	ENSMUSG00000027810	3	58525821	58557501	1	2	0	0	1	0	1	0	0	0	0	0	D3YZZ6	
ENSMUST00000138849						0	7	10	0	8	0	2	16	6	2	7		
ENSMUST00000138850						3	5	10	12	4	1	0	0	0	0	0		
ENSMUST00000138851						3	0	0	0	0	0	7	0	25	2	47		
ENSMUST00000138852						0	0	0	0	1	0	0	0	0	1	0		
ENSMUST00000138853	ENSMUSG00000005952	11	73234292	73261242	1	4	2	0	11	0	0	0	1	0	0	1	Z4YLZ2	
ENSMUST00000138854						1	0	0	1	0	0	0	0	0	0	2		
ENSMUST00000138856	ENSMUSG00000023206	2	11705290	11734317	1	2	2	8	140	8	3	1	0	2	5	0	A2AP38	
ENSMUST00000138857						4	8	17	28	7	1	14	206	34	34	31		
ENSMUST00000138858						0	0	1	28	7	0	0	0	0	2	0		
ENSMUST00000138859						0	2	12	56	2	0	0	465	0	79	0		
ENSMUST00000138860						2	0	3	0	3	1	124	861	426	142	213		
ENSMUST00000138862						0	0	0	0	0	0	0	11	5	0	0		
ENSMUST00000138863	ENSMUSG00000025716	2	22227503	22618252	1	5	5	20	0	6	3	0	0	0	0	0	A2ASW0	
ENSMUST00000138864						1	0	3	0	2	0	0	0	3	13	3		
ENSMUST00000138865	ENSMUSG00000019082	7	141429744	141437892	-1	5	4	22	8	1	1	9	0	0	0	13	E9PY45	
ENSMUST00000138866	ENSMUSG00000024410	18	12168717	12189997	1	0	0	0	0	0	0	4	15	0	0	17	F6RDF1	
ENSMUST00000138867						0	3	13	195	8	0	6	2	14	3	15		
ENSMUST00000138868						105	82	233	100	142	87	13	59	15	16	27		
ENSMUST00000138869	ENSMUSG00000043183	13	54503779	54551290	1	0	0	0	0	0	0	3	0	0	0	4	E0CY56	
ENSMUST00000138870	ENSMUSG00000029630	5	145977194	146009618	-1	0	1	0	0	1	0	0	0	0	1	0	D3Z707	
ENSMUST00000138873						14	7	4	31	15	7	0	11	0	0	0		
ENSMUST00000138874						42	40	148	84	48	22	1	3	12	2	19		
ENSMUST00000138876						2	1	0	1	0	0	2	14	8	3	10		
ENSMUST00000138877						1	0	6	10	2	2	0	0	0	11	8		
ENSMUST00000138878	ENSMUSG00000057000	X	136072099	136085255	-1	0	0	0	0	0	0	0	0	0	0	0	B1AUS0	
ENSMUST00000138879						3	6	14	154	15	0	5	12	5	0	21		
ENSMUST00000138880	ENSMUSG00000033099	15	78934933	78943634	1	60	44	95	70	69	18	18	42	28	43	48		Q8BG17
ENSMUST00000138881						0	1	0	0	0	0	0	2	0	0	3		
ENSMUST00000138884	ENSMUSG00000021852	14	49298519	49526046	-1	3	1	3	0	0	0	0	0	0	0	0		Q8BZK4
ENSMUST00000138885	ENSMUSG00000029518	5	115631908	115647736	1	0	2	5	0	5	0	293	22	504	41	355	S4R1W7	
ENSMUST00000138886						1	0	5	4	1	1	1	1	0	5	0		
ENSMUST00000138887						2	1	0	1	3	2	2	23	11	8	7		
ENSMUST00000138888						4	0	19	3	0	1	0	0	0	0	0		
ENSMUST00000138889	ENSMUSG00000026857	2	30807826	30823033	1	0	0	0	0	4	0	34	20	5	15	19	A0A0A6YVQ9	
ENSMUST00000138890	ENSMUSG00000029478	5	125017153	125179219	-1	1	0	7	0	0	0	25	28	23	4	34	F6YAU7	
ENSMUST00000138892	ENSMUSG00000074247	8	71469199	71476098	1	1	0	0	0	0	0	0	0	0	0	0	D3Z6F8	
ENSMUST00000138894						0	2	4	0	8	0	4	53	7	4	23		
ENSMUST00000138895						1	6	6	188	9	3	0	10	12	1	17		
ENSMUST00000138897						2	1	0	1	4	0	3	0	0	0	0		
ENSMUST00000138898						0	0	0	0	0	0	0	150	0	0	0		
ENSMUST00000138899						5	4	10	45	11	1	0	0	0	0	0		
ENSMUST00000138900						0	0	0	0	0	0	3256	5144	3527	941	2521		
ENSMUST00000138901						10	19	28	10	10	5	0	0	0	0	0		
ENSMUST00000138903						0	0	0	0	4	0	0	0	5	9	2		
ENSMUST00000138904						2	3	6	104	3	4	29	79	39	2	109		
ENSMUST00000138905						0	2	10	3	1	3	0	0	0	1	0		
ENSMUST00000138906						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000138907	ENSMUSG00000034614	11	3330401	3342971	1	0	2	2	0	1	0	30	12	48	24	14	F6S185	
ENSMUST00000138908						0	0	0	0	0	0	0	1	0	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000138909	ENSMUSG00000020135	10	80295977	80318263	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3K9	
ENSMUST00000138910	ENSMUSG00000064329	2	66270778	66440840	-1	2	0	0	2	1	2	0	0	0	0	0	A2APX9	
ENSMUST00000138912	ENSMUSG00000054520	5	34525838	34563641	1	0	0	0	0	0	0	4	11	8	0	12	D6RDU0	
ENSMUST00000138913	ENSMUSG00000018899	11	53770014	53778374	1	6	4	13	112	5	2	7	21	24	2	40	Q5SX16	
ENSMUST00000138914	ENSMUSG00000048550	2	21205724	21215009	1	3	2	24	19	11	6	0	2	2	3	6	A2AUG4	
ENSMUST00000138916						2	2	0	1	1	6	0	2	3	0	6		
ENSMUST00000138917						4	0	16	0	0	0	0	6	0	0	3		
ENSMUST00000138918						9	10	0	12	0	8	7	61	0	0	13		
ENSMUST00000138919	ENSMUSG00000038366	11	97799000	97838764	1	0	0	2	1	1	0	0	0	0	0	0	A2A6G2	
ENSMUST00000138920						18	13	32	27	26	11	3	9	12	3	26		
ENSMUST00000138921						0	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000138922	ENSMUSG00000029622	5	145114215	145130705	1	0	2	11	6	5	2	1392	1537	1307	438	941	F6THG2	
ENSMUST00000138923						2	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000138924						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000138925						19	15	33	24	13	17	0	0	0	0	1		
ENSMUST00000138927	ENSMUSG00000022186	15	4026383	4155344	1	0	0	6	0	0	0	0	0	119	31	89	Q3UJQ9	
ENSMUST00000138929						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138930						1	0	0	173	6	4	0	0	0	0	0		
ENSMUST00000138931	ENSMUSG00000024787	19	6119399	6128304	-1	0	0	3	23	2	0	0	0	0	0	0	D3YVT2	
ENSMUST00000138933						2	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000138934	ENSMUSG00000032511	9	119483408	119579016	-1	4	2	6	1	2	2	0	0	0	0	0	D3YXW2	
ENSMUST00000138935						19	12	19	26	9	3	0	11	5	1	3		
ENSMUST00000138936						4	0	5	42	8	3	3	16	17	91	28		
ENSMUST00000138938						0	0	6	87	1	0	0	0	0	0	0		
ENSMUST00000138939						0	0	0	0	0	0	1579	3072	1479	284	1151		
ENSMUST00000138941	ENSMUSG00000014554	6	83480217	83506969	-1	4	2	2	0	3	0	0	30	15	20	10		
ENSMUST00000138942						3	2	6	131	8	4	0	0	0	1	0		
ENSMUST00000138944						8	3	11	0	5	3	377	5983	647	273	356		
ENSMUST00000138945						2	2	7	2	8	0	0	0	0	0	2		
ENSMUST00000138946						5	3	6	5	7	5	0	0	0	0	0		
ENSMUST00000138947	ENSMUSG00000027698	3	27182965	27284608	1	0	1	0	64	2	0	0	0	0	0	0	D6RGP7	
ENSMUST00000138948						8	3	12	14	7	0	0	0	0	0	0		
ENSMUST00000138949	ENSMUSG00000050174	3	37404910	37420211	-1	2	2	4	0	3	3	4	0	2	0	0	F6WJF1	
ENSMUST00000138950	ENSMUSG00000037270	3	36863104	37053033	1	0	0	0	0	0	0	146	1659	371	495	183	A2AB97	
ENSMUST00000138951						6	1	5	2	5	5	0	0	0	0	1		
ENSMUST00000138952						4	3	4	1	2	1	0	7	3	0	2		
ENSMUST00000138953	ENSMUSG00000059857	3	109780040	110144011	-1	0	0	0	0	0	0	0	0	0	0	0		Q8R4G0
ENSMUST00000138954						0	0	0	0	0	0	5	60	0	0	0		
ENSMUST00000138955						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138957						0	0	3	155	6	5	2	0	3	0	0		
ENSMUST00000138958						2	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000138959						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000138960						0	0	8	0	0	0	0	15	0	0	0		
ENSMUST00000138961						3	3	3	2	7	3	0	0	0	0	0		
ENSMUST00000138962						0	0	10	45	4	5	174	116	116	30	71		
ENSMUST00000138963						0	0	2	0	0	0	3	3	2	3	0		
ENSMUST00000138964						0	2	8	9	3	3	1	0	2	0	0		
ENSMUST00000138965	ENSMUSG00000048550	2	21205724	21215009	1	0	0	0	0	0	0	3	5	3	0	0	A2AUG6	
ENSMUST00000138966	ENSMUSG00000087194	4	112804616	113286973	-1	0	0	0	0	0	0	0	0	0	0	0		A7XUZ6
ENSMUST00000138967						0	5	0	0	6	0	0	0	0	0	0		
ENSMUST00000138968						5	5	0	0	3	5	0	7	5	0	12		
ENSMUST00000138969						12	1	15	6	9	1	0	4	0	0	1		
ENSMUST00000138970	ENSMUSG00000024215	17	27714352	27728951	-1	3	0	2	48	7	2	0	0	0	0	0	B2KF87	
ENSMUST00000138971						5	0	0	0	3	1	1	5	3	0	2		
ENSMUST00000138972	ENSMUSG00000028546	4	110203722	110351909	-1	0	5	20	8	5	1	0	0	0	0	0	A2A9R4	
ENSMUST00000138973						5	4	6	6	3	0	2	2	2	0	3		
ENSMUST00000138974						9	3	31	11	10	0	4	22	3	7	7		
ENSMUST00000138975						5	4	1	2	1	3	0	0	0	0	0		
ENSMUST00000138976						6	1	3	48	3	0	0	0	0	0	0		
ENSMUST00000138977	ENSMUSG00000078627	11	105360798	105456735	-1	23	13	59	7	9	0	0	0	0	0	0	E9PX79	
ENSMUST00000138978						6	0	6	185	3	2	0	0	0	0	5		
ENSMUST00000138979						0	0	1	6	1	0	21	43	33	57	31		
ENSMUST00000138980						9	16	69	9	7	0	0	0	0	0	0		
ENSMUST00000138981	ENSMUSG00000028458	4	43441939	43448064	1	0	0	16	0	0	5	41	21	34	8	79	D6RFP6	
ENSMUST00000138982						2	4	4	1	0	2	14	246	43	13	49		
ENSMUST00000138983						2	2	6	0	11	3	0	0	1	1	7		
ENSMUST00000138984						3	2	6	1	6	1	0	0	0	0	0		
ENSMUST00000138985						0	0	7	2	3	1	0	2	6	8	2		
ENSMUST00000138986						16	4	29	27	23	11	26	84	18	3	56		
ENSMUST00000138987	ENSMUSG00000057880	16	8513429	8621568	1	2	3	0	0	0	0	0	0	0	0	0	F7C9G3	
ENSMUST00000138989	ENSMUSG00000026718	2	14074098	14149634	1	2	2	0	39	3	0	1	27	22	1	11	A2ARJ0	
ENSMUST00000138990	ENSMUSG00000027309	2	130706200	130906406	-1	0	0	0	0	0	0	0	0	0	0	0	B0R037	
ENSMUST00000138991						3	0	3	72	8	2	0	0	0	0	0		
ENSMUST00000138993						0	0	0	0	0	5	0	0	0	0	0		
ENSMUST00000138994						0	1	4	1	0	1	0	3	0	0	2		
ENSMUST00000138995	ENSMUSG00000058318	2	92093117	92364666	1	0	4	0	0	1	0	12	13	23	0	8	E0CZ36	
ENSMUST00000138996						0	0	0	0	0	0	11	22	23	2	0		
ENSMUST00000138997						0	4	0	0	2	2	0	0	0	1	1		
ENSMUST00000138998						3	4	2	0	3	0	0	58	17	30	0		
ENSMUST00000138999						1	1	4	0	0	2	132	520	19	0	0		
ENSMUST00000139000						6	3	13	22	8	3	0	0	0	0	0		
ENSMUST00000139001	ENSMUSG00000028197	3	145292472	145552011	1	1	0	0	1	1	1	0	0	0	0	0	D3Z1L7	
ENSMUST00000139002						5	2	6	0	2	3	0	0	0	1	4		
ENSMUST00000139003	ENSMUSG00000002963	7	44857139	44862992	1	0	0	0	5	0	0	425	317	529	13	302		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139004						1	0	0	2	2	3	0	0	0	0	0		
ENSMUST00000139007						1	1	3	13	0	2	3	7	5	2	4		
ENSMUST00000139009						4	2	12	5	2	2	0	0	0	0	0		
ENSMUST00000139013						30	14	136	48	24	13	3	3	0	0	0		
ENSMUST00000139015	ENSMUSG00000068373	2	104143073	104410334	-1	0	2	6	0	0	0	0	0	0	0	0	F6SUT5	
ENSMUST00000139016						5	8	39	9	4	6	2	2	4	0	4		
ENSMUST00000139018						3	1	3	2	4	1	2	0	2	0	0		
ENSMUST00000139020	ENSMUSG00000020776	11	116142285	116168166	-1	0	2	0	0	1	0	0	0	2	0	0	A2A872	
ENSMUST00000139021						10	10	4	27	3	2	0	0	0	0	7		
ENSMUST00000139022						27	14	211	66	25	13	0	3	2	0	7		
ENSMUST00000139023						1	0	3	4	2	1	1	2	4	1	1		
ENSMUST00000139024	ENSMUSG00000038770	5	144983519	145084030	-1	2	5	0	0	9	0	0	0	0	0	0	D3Z2P7	
ENSMUST00000139026						57	81	134	48	58	28	0	268	15	2	70		
ENSMUST00000139028						18	19	22	27	31	7	5	4	7	0	8		
ENSMUST00000139029						0	0	0	4	2	3	0	0	0	3	0		
ENSMUST00000139030	ENSMUSG00000028857	4	133266045	133277792	-1	0	0	0	0	0	0	2	3	0	0	8	D6RIQ5	
ENSMUST00000139031						0	2	14	0	3	1	11	3	14	1	17		
ENSMUST00000139032						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139033						0	0	0	7	0	0	0	0	4	0	0		
ENSMUST00000139035						4	2	19	9	6	0	14	11	3	0	18		
ENSMUST00000139036						4	2	0	1	0	1	2	0	0	0	0		
ENSMUST00000139037						3	3	12	60	2	2	0	3	5	0	8		
ENSMUST00000139038	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZCU5	
ENSMUST00000139039						4	2	0	2	5	2	0	0	0	0	0		
ENSMUST00000139040						4	3	0	14	2	0	0	0	3	7	6		
ENSMUST00000139041						0	0	1	2	0	0	4	0	8	3	10		
ENSMUST00000139044						4	1	9	1	2	0	7	11	28	2	37		
ENSMUST00000139045						19	13	18	0	13	8	6	20	13	7	37		
ENSMUST00000139046	ENSMUSG00000032366	9	67022590	67049406	-1	0	0	0	0	0	0	0	24	0	0	0	S4R261	
ENSMUST00000139047	ENSMUSG00000027339	2	131989415	132030258	-1	1	1	0	76	3	0	29	13	86	9	57	A2APB1	
ENSMUST00000139048	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	0	0	0	0	0	0	F7BZ55	
ENSMUST00000139049	ENSMUSG00000079104	12	57230412	57239882	1	2	7	7	17	8	3	68	128	94	103	68	G3UXL2	
ENSMUST00000139050						1	0	0	9	0	0	0	0	1	0	1		
ENSMUST00000139051						1	1	5	4	5	0	0	0	0	0	1		
ENSMUST00000139052						302	232	506	234	379	202	4	17	8	0	17		
ENSMUST00000139053						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000139054						214	214	594	224	146	75	27	75	29	8	62		
ENSMUST00000139057						1	0	9	2	0	0	0	0	0	0	0		
ENSMUST00000139059						2	2	5	0	8	0	7	0	20	5	26		
ENSMUST00000139060						3	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000139061	ENSMUSG00000012640	7	43296197	43313294	-1	2	2	0	56	1	1	0	0	42	9	21	D3YV82	
ENSMUST00000139062						2	2	0	34	3	0	6	19	5	3	9		
ENSMUST00000139063	ENSMUSG00000057246	17	34398820	34460734	1	0	0	0	0	0	0	0	0	0	0	0	A2CG25	
ENSMUST00000139064	ENSMUSG00000009734	13	18121101	18382041	-1	44	30	164	32	39	23	0	0	0	0	1	F6ZW42	
ENSMUST00000139066						7	0	13	0	0	0	700	4331	1081	183	1997		
ENSMUST00000139067	ENSMUSG00000038871	6	34476207	34505613	1	5	0	0	0	0	0	0	0	0	0	0	D3YUE8	
ENSMUST00000139068	ENSMUSG00000042289	7	127800604	127803802	1	0	2	0	0	0	0	2	2	0	1	0	D3YU71	
ENSMUST00000139069	ENSMUSG00000039768	4	151933691	151982137	1	0	0	0	0	0	0	0	0	20	0	10	E9Q8B3	
ENSMUST00000139070						2	2	9	5	4	3	0	0	0	0	0		
ENSMUST00000139071						142	125	279	290	159	82	39	157	91	20	108		
ENSMUST00000139072						3	0	2	0	3	3	0	7	4	0	7		
ENSMUST00000139073						0	0	3	0	3	2	3	11	3	2	8		
ENSMUST00000139074	ENSMUSG00000054405	4	132535550	132553742	1	0	0	4	24	2	0	12	30	17	5	12	E9Q592	
ENSMUST00000139075	ENSMUSG00000021870	14	26413168	26534931	-1	19	7	16	566	34	12	0	0	420	24	222		Q3URD3
ENSMUST00000139076						0	0	1	3	1	0	2	2	0	1	0		
ENSMUST00000139077	ENSMUSG00000074358	7	18890883	18910415	-1	2	1	11	0	0	0	0	0	0	0	0	D3YY03	
ENSMUST00000139078						3	4	5	1	3	0	6	18	4	4	12		
ENSMUST00000139079						3	0	1	38	1	0	2	7	1	6	0		
ENSMUST00000139081						0	0	0	27	0	0	0	0	0	0	3		
ENSMUST00000139082						14	13	20	4	11	9	5	35	11	15	7		
ENSMUST00000139083						0	0	0	0	0	0	10	0	0	2	0		
ENSMUST00000139084						2	3	10	2	7	4	0	0	0	0	0		
ENSMUST00000139085						5	5	24	28	0	1	0	29	9	5	13		
ENSMUST00000139086	ENSMUSG00000062778	3	106113229	106132120	1	3	0	6	0	0	0	0	0	0	0	0	D3Z1S6	
ENSMUST00000139087						2	4	7	5	0	2	0	0	0	0	0		
ENSMUST00000139088						2	6	0	3	4	0	4	12	4	0	7		
ENSMUST00000139090						4	3	31	11	5	1	0	0	0	0	0		
ENSMUST00000139091	ENSMUSG00000025408	10	127290774	127296288	1	0	1	0	0	0	0	42	137	0	1	41	D3YX14	
ENSMUST00000139092	ENSMUSG00000070501	1	173519717	173535957	-1	10	11	18	7	8	2	0	22	0	5	5		
ENSMUST00000139093						1	0	3	11	1	0	0	0	0	0	6		
ENSMUST00000139094						1	3	8	54	10	4	10	13	14	0	12		
ENSMUST00000139096						136	171	285	197	178	117	5	7	4	0	5		
ENSMUST00000139097						0	1	0	0	4	0	0	7	2	0	0		
ENSMUST00000139098						5	5	6	12	16	6	2	2	2	1	2		
ENSMUST00000139099						5	6	6	2	5	0	3	0	0	2	3		
ENSMUST00000139100	ENSMUSG00000036062	4	42916660	42944752	1	1	1	5	4	7	3	0	0	0	0	0	S4R193	
ENSMUST00000139101						0	0	0	0	0	1	2	23	7	8	8		
ENSMUST00000139102	ENSMUSG00000072821	5	94076385	94080997	1	3	2	0	0	0	0	0	0	0	0	0	D3YXK9	
ENSMUST00000139103	ENSMUSG00000031626	8	45507788	45827906	1	1	0	1	0	0	0	0	0	0	0	0	D3Z2C7	
ENSMUST00000139104	ENSMUSG00000070425	7	102065713	102096864	1	0	0	0	0	0	0	0	0	0	4	0	F7D6D1	
ENSMUST00000139105						1	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000139106						0	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000139108						0	0	0	0	0	0	0	15	11	0	0		
ENSMUST00000139109	ENSMUSG00000060002	10	88452745	88504073	-1	0	0	0	0	0	0	6	27	0	2	4		Q8C025

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139110						6	1	2	5	0	1	2	6	2	0	20		
ENSMUST00000139111	ENSMUSG00000009535	18	68300355	68324852	1	4	6	22	9	4	3	0	0	0	0	0	D3YYS7	
ENSMUST00000139113	ENSMUSG00000033282	8	91217030	91313262	-1	9	0	0	0	1	0	11	0	18	16	8	D6RIK9	
ENSMUST00000139114						3	1	2	3	2	3	4	4	4	3	0		
ENSMUST00000139115	ENSMUSG00000047193	9	6928503	7184446	-1	4	2	14	19	13	2	3	1	3	0	2	D3Z025	
ENSMUST00000139116	ENSMUSG00000074646	2	155973279	156007977	-1	3	0	0	0	1	0	0	0	0	0	0	B7ZCN6	
ENSMUST00000139117						3	3	0	0	0	2	3	0	5	3	23		
ENSMUST00000139118						0	0	3	26	0	12	0	53	0	13	12		
ENSMUST00000139120						3	2	15	40	18	5	9	76	29	0	89		
ENSMUST00000139121						1	1	3	1	2	2	1	5	4	4	6		
ENSMUST00000139122	ENSMUSG00000037822	5	65446844	65537184	-1	19	12	37	57	23	15	234	667	237	85	194		Q91VT8
ENSMUST00000139123	ENSMUSG00000063077	4	149176319	149307693	-1	25	26	71	121	29	16	15	0	0	0	0	F6XNB6	
ENSMUST00000139124						45	32	122	40	38	21	0	13	5	3	10		
ENSMUST00000139125						0	0	1	38	1	0	0	0	3	7	3		
ENSMUST00000139126						2	6	1	0	2	0	0	0	0	2	3		
ENSMUST00000139127	ENSMUSG00000028451	4	42969604	42983640	1	9	7	12	4	1	2	0	5	0	0	0	Q3V0W6	
ENSMUST00000139128						67	36	176	62	64	37	4	14	20	1	19		
ENSMUST00000139129	ENSMUSG00000018379	11	88047373	88053755	1	6	1	3	62	2	1	97	149	48	10	77		Q6PDM2
ENSMUST00000139130						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000139131						1	3	17	2	4	0	0	0	0	0	0		
ENSMUST00000139132						1	0	0	0	2	2	0	0	0	16	0		
ENSMUST00000139133						1	0	4	0	0	0	2	0	5	0	11		
ENSMUST00000139134						0	0	5	0	0	0	0	0	11	0	14		
ENSMUST00000139135						0	0	0	0	0	0	0	0	1	1	0		
ENSMUST00000139137						4	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000139138						2	2	3	0	6	0	4	20	21	8	56		
ENSMUST00000139139						0	0	0	0	0	0	0	0	5	0	14		
ENSMUST00000139141						1	4	2	0	1	0	0	0	0	0	0		
ENSMUST00000139142						0	5	11	2	3	0	0	3	17	22	12		
ENSMUST00000139143	ENSMUSG00000042197	1	33761545	33814595	-1	12	0	36	20	13	9	24	174	48	7	52	M0QWT6	
ENSMUST00000139145						5	2	4	4	10	4	0	0	3	0	0		
ENSMUST00000139146	ENSMUSG00000031355	X	168795099	169304435	1	3	0	0	0	0	1	0	0	0	0	0	G3UZI7	
ENSMUST00000139147						19	16	43	33	38	16	12	58	25	8	7		
ENSMUST00000139148						17	1	39	22	17	10	0	0	2	0	8		
ENSMUST00000139149						3	1	2	4	2	2	57	281	163	29	403		
ENSMUST00000139150						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139151						36	30	88	61	50	26	20	220	78	6	133		
ENSMUST00000139152						4	3	0	1	2	3	1	0	3	0	3		
ENSMUST00000139153						0	1	0	16	0	0	5	3	3	0	4		
ENSMUST00000139154						4	0	23	3	1	2	6	13	12	0	21		
ENSMUST00000139155						22	16	24	21	29	8	13	39	15	0	17		
ENSMUST00000139156	ENSMUSG00000061758	6	34384218	34396950	1	0	3	1	7	0	0	23	8	1	0	0	S4R2G9	
ENSMUST00000139157						5	3	6	2	0	1	0	0	1	0	0		
ENSMUST00000139158	ENSMUSG00000041857	19	11667460	11691150	-1	2	0	0	0	0	0	0	0	0	0	0		Q925U0
ENSMUST00000139159						0	0	6	26	0	0	0	0	0	0	0		
ENSMUST00000139160	ENSMUSG00000050315	3	123076519	123236149	-1	0	10	0	0	0	0	0	0	0	0	1	F6WWS1	
ENSMUST00000139161						0	0	0	0	0	0	1	21	0	6	0		
ENSMUST00000139162	ENSMUSG00000021277	12	111166370	111267153	1	2	1	2	18	1	2	13	3	15	2	9	D3Z343	
ENSMUST00000139164						0	0	0	1	2	2	17	27	9	0	12		
ENSMUST00000139165						0	0	0	0	0	0	0	0	0	11	0		
ENSMUST00000139166						0	0	1	21	1	2	7	76	24	15	9		
ENSMUST00000139167	ENSMUSG00000029536	5	115333239	115341178	-1	25	21	88	290	40	17	60	242	120	39	123		Q8CBY0
ENSMUST00000139168						0	0	0	51	0	2	0	0	0	0	0		
ENSMUST00000139169						4	3	30	5	0	4	1	1	1	0	3		
ENSMUST00000139170	ENSMUSG00000023723	11	88204388	88211507	1	1	0	8	34	3	2	2	0	0	0	1	A7M7Q8	
ENSMUST00000139171						0	1	1	17	1	2	0	1	0	0	0		
ENSMUST00000139172						0	8	0	0	7	3	0	0	0	0	2		
ENSMUST00000139173						0	12	28	22	11	4	1	870	146	68	190		
ENSMUST00000139174	ENSMUSG00000052301	7	126847416	126852705	1	0	0	0	0	0	0	0	0	0	0	0	A0A0E3D6L4	
ENSMUST00000139176						11	5	27	15	18	5	10	65	34	5	64		
ENSMUST00000139177						0	4	0	2	0	0	115	770	199	483	78		
ENSMUST00000139178						3	4	9	1	0	0	0	10	0	0	0		
ENSMUST00000139179						4	7	3	3	4	2	42	20	63	0	97		
ENSMUST00000139180						4	0	11	1	3	1	0	0	0	5	2		
ENSMUST00000139181	ENSMUSG00000038145	9	122117283	122169702	1	0	0	0	16	0	0	0	2	6	0	2	D3YXV4	
ENSMUST00000139182	ENSMUSG00000029192	5	36490604	36593276	-1	0	0	0	1	0	0	0	0	0	0	0	D3Z5Y9	
ENSMUST00000139183						4	1	15	5	3	9	0	0	0	0	0		
ENSMUST00000139184	ENSMUSG00000074895	13	54783998	54788459	1	0	0	0	0	0	0	0	0	0	0	0	E9Q8Z2	
ENSMUST00000139186						1	2	8	12	3	0	0	0	0	0	0		
ENSMUST00000139187						3	2	4	9	5	1	0	0	0	0	0		
ENSMUST00000139188	ENSMUSG00000042608	4	126103957	126141029	1	3	4	6	2	5	3	50	31	44	0	69	B1AW00	
ENSMUST00000139189						4	2	7	34	6	0	0	0	0	0	0		
ENSMUST00000139191	ENSMUSG00000079845	X	73074345	73082478	-1	0	0	0	0	0	0	0	0	0	8	4	A2BI41	
ENSMUST00000139192	ENSMUSG00000030929	7	119768679	119794058	-1	0	0	0	0	0	0	0	24	0	1	0	D6RE53	
ENSMUST00000139193	ENSMUSG00000061536	9	121680047	121705490	-1	0	0	0	0	0	0	0	0	0	1	11	D6RE35	
ENSMUST00000139195						0	0	4	5	0	0	0	6	0	1	1		
ENSMUST00000139196						3	0	2	5	3	2	0	0	0	0	0		
ENSMUST00000139197						2	0	0	25	5	2	0	0	0	0	0		
ENSMUST00000139198	ENSMUSG00000035969	4	43381979	43427088	1	0	0	2	0	0	0	0	0	1	0	0	B0R004	
ENSMUST00000139199						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139200	ENSMUSG00000035172	11	101162679	101171351	-1	0	4	0	0	0	0	0	0	0	0	0	M0QWE8	
ENSMUST00000139201						5	1	12	2	1	1	0	1	0	0	0		
ENSMUST00000139202						0	1	7	18	1	0	10	0	9	0	10		
ENSMUST00000139203						8	4	3	0	9	0	0	2	4	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139204	ENSMUSG00000063450	12	75818134	76110926	1	0	0	36	0	8	0	39	221	20	0	88	F6W8R9	
ENSMUST00000139205						12	6	26	13	0	0	1	1	0	0	0		
ENSMUST00000139206						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139208						2	2	2	4	0	0	8	0	25	0	54		
ENSMUST00000139209						0	1	0	2	2	0	0	2	0	0	0		
ENSMUST00000139210	ENSMUSG00000020027	10	95385362	95417180	-1	19	19	32	16	17	3	0	0	0	0	0	F6RVG2	
ENSMUST00000139211	ENSMUSG00000025337	5	130245731	130255530	-1	5	0	6	47	6	3	33	39	34	103	56	D6REV5	
ENSMUST00000139212						13	10	20	14	23	14	14	126	29	25	34		
ENSMUST00000139213	ENSMUSG00000013936	5	122100951	122113472	1	0	0	0	0	0	0	0	0	0	0	0	D3YW14	
ENSMUST00000139215	ENSMUSG00000041180	19	36554639	36621135	1	6	12	22	6	13	8	0	4	0	0	0	D6REW0	
ENSMUST00000139216						0	3	5	0	0	4	0	9	12	0	30		
ENSMUST00000139217						1	2	7	7	2	0	4	22	5	1	10		
ENSMUST00000139219						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000139220						8	0	37	5	7	3	1	0	0	1	0		
ENSMUST00000139221						0	0	0	0	0	0	0	21	0	0	8		
ENSMUST00000139223						0	0	0	0	3	0	0	6	11	0	6		
ENSMUST00000139224	ENSMUSG00000004328	7	17031507	17062427	-1	0	2	5	0	4	2	1	0	0	0	0		
ENSMUST00000139225						5	11	28	1	16	9	2	46	6	7	6		
ENSMUST00000139226	ENSMUSG00000025728	17	25926427	25944510	-1	2	0	0	3	3	0	0	0	0	0	9	D3Z0A4	
ENSMUST00000139227	ENSMUSG00000047090	10	128800036	128804370	-1	0	0	0	0	5	0	10	7	4	0	0	D6RJ24	
ENSMUST00000139228	ENSMUSG00000037012	10	62268855	62379908	-1	4	2	12	6	13	4	5	2	13	0	18	D3YYR4	
ENSMUST00000139229						2	12	0	3	7	3	0	5	0	0	6		
ENSMUST00000139230						2	1	1	0	5	0	1	2	0	2	0		
ENSMUST00000139231	ENSMUSG00000052419	6	13867735	13871518	-1	10	10	15	7	15	8	36	86	40	71	12	F2Z3Y9	
ENSMUST00000139232	ENSMUSG00000005882	2	155846894	155930310	-1	0	0	0	0	0	0	4	0	1	0	0	F6V305	
ENSMUST00000139233						0	1	1	0	2	1	0	7	0	0	0		
ENSMUST00000139234	ENSMUSG00000035310	5	100441918	100500639	-1	0	6	0	3	0	0	0	34	0	0	0	E9PUI8	
ENSMUST00000139235	ENSMUSG00000022439	15	84324026	84342978	1	3	0	0	1	0	0	2	0	0	0	3	F2Z401	
ENSMUST00000139236						0	2	3	5	2	0	0	0	0	0	0		
ENSMUST00000139237	ENSMUSG00000028555	4	109406623	109444745	1	0	0	1	6	1	1	0	0	0	0	0	A0A0A0MQL1	
ENSMUST00000139238	ENSMUSG00000026825	2	32308471	32353338	-1	3	0	6	97	10	1	0	0	0	0	0	D6RH60	
ENSMUST00000139239						1	5	5	4	1	1	0	0	0	0	0		
ENSMUST00000139240						3	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000139242						6	5	7	12	11	8	1	0	0	0	2		
ENSMUST00000139243	ENSMUSG00000024592	18	56955833	56975368	-1	0	0	0	5	2	0	8	23	8	5	1		Q9CWB7
ENSMUST00000139244						0	1	0	0	0	0	6	29	26	19	7		
ENSMUST00000139245						1	2	0	2	1	0	2	28	7	3	7		
ENSMUST00000139246						0	4	4	3	2	2	0	0	0	0	0		
ENSMUST00000139247	ENSMUSG00000039834	2	164891882	164911757	-1	2	0	3	9	2	0	0	0	3	2	3	S4R2J0	
ENSMUST00000139248						4	1	4	6	3	4	0	0	0	0	0		
ENSMUST00000139249						1	0	15	6	0	0	139	22	31	0	68		
ENSMUST00000139250	ENSMUSG00000022897	16	94570010	94695517	1	0	0	0	19	1	0	6	0	0	3	0	A9C477	
ENSMUST00000139251						0	2	2	0	0	2	0	0	0	0	0		
ENSMUST00000139252	ENSMUSG00000056486	2	73610660	73775346	-1	0	0	0	3	0	0	0	0	0	0	0	D6RCX8	
ENSMUST00000139253	ENSMUSG00000074884	2	121449195	121458313	1	2	6	3	39	5	3	1196	2110	750	934	498		P84102
ENSMUST00000139254						0	0	0	0	3	0	34	62	28	10	27		
ENSMUST00000139255						0	0	0	53	0	0	0	0	0	0	0		
ENSMUST00000139256	ENSMUSG00000038709	4	57984027	58009124	-1	0	0	1	1	0	0	0	0	0	0	0	A2AV98	
ENSMUST00000139257						3	0	7	5	1	1	7	8	9	0	5		
ENSMUST00000139258						4	0	0	0	4	1	0	6	0	1	0		
ENSMUST00000139259	ENSMUSG00000048621	X	109196756	109200439	1	0	0	0	0	0	0	0	1	0	0	2	A2ALN9	
ENSMUST00000139260						0	0	0	0	0	2	0	0	2	0	0		
ENSMUST00000139261						0	4	0	13	6	3	5	17	0	14	17		
ENSMUST00000139262						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139263	ENSMUSG00000027639	2	157097533	157135265	-1	0	0	0	0	0	0	3609	11147	6597	5616	5657	F6TVP2	
ENSMUST00000139264						0	0	0	0	0	0	44	119	253	241	265		
ENSMUST00000139266						0	1	4	10	0	4	0	0	0	0	0		
ENSMUST00000139267						1	1	0	0	1	3	0	4	6	0	8		
ENSMUST00000139268						0	1	0	0	0	0	0	0	5	4	0		
ENSMUST00000139269						0	0	1	0	0	4	1	0	0	2	0		
ENSMUST00000139270						9	9	6	11	7	3	3	7	3	6	0		
ENSMUST00000139273						0	0	0	0	0	0	7	4	0	0	21		
ENSMUST00000139274	ENSMUSG00000079334	9	107578887	107584050	1	0	0	2	3	0	1	0	0	0	0	0		
ENSMUST00000139275	ENSMUSG00000034675	13	55473429	55488111	-1	0	0	0	28	2	0	0	0	0	0	0	F7CPL2	
ENSMUST00000139276	ENSMUSG00000036980	5	138178617	138187451	-1	4	0	0	0	6	0	5	1	9	0	0	D3Z4X5	
ENSMUST00000139277						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000139278	ENSMUSG00000029576	5	142484839	142551098	-1	0	5	9	1	3	1	0	0	0	0	0	D3YUE9	
ENSMUST00000139279						5	17	49	24	15	12	0	0	0	0	8		
ENSMUST00000139280						0	2	4	2	5	3	1	0	1	0	1		
ENSMUST00000139281						41	37	60	297	42	23	4	9	1	0	11		
ENSMUST00000139282	ENSMUSG00000001211	10	78269178	78352489	-1	0	0	2	0	0	1	0	0	4	0	1	D3Z1M6	
ENSMUST00000139283						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000139284	ENSMUSG00000022094	14	70303469	70351425	-1	0	1	4	1	0	0	0	0	0	0	0	D3Z4Q7	
ENSMUST00000139285	ENSMUSG00000018068	11	86210681	86257575	-1	0	2	0	2	0	0	0	0	0	1	2	X1WI16	
ENSMUST00000139287	ENSMUSG00000021326	13	21179445	21194724	1	0	1	3	0	0	0	71	227	82	26	69	F6U3T5	
ENSMUST00000139289						1	0	0	0	6	1	0	8	0	0	0		
ENSMUST00000139290	ENSMUSG00000039176	7	79446231	79466362	-1	1	1	0	0	1	0	0	0	0	1	0		
ENSMUST00000139291	ENSMUSG00000026825	2	32308471	32353338	-1	0	0	0	52	0	0	0	0	0	0	0	F6TH70	
ENSMUST00000139292						2	3	2	0	0	0	0	9	3	1	0		
ENSMUST00000139293						0	0	1	0	4	0	5	49	4	5	27		
ENSMUST00000139294	ENSMUSG00000014232	16	3908801	3941147	1	6	0	4	27	7	2	0	9	0	0	0	F6TQ80	
ENSMUST00000139295						37	47	152	21	47	21	6	41	14	2	14		
ENSMUST00000139296						2	3	2	6	2	0	0	7	4	0	9		
ENSMUST00000139297						7	6	0	0	0	0	50	137	64	7	73		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139298						5	0	0	0	7	3	0	0	0	0	2		
ENSMUST00000139299						0	0	3	2	0	1	0	0	0	0	0		
ENSMUST00000139300						3	0	6	2	3	0	0	0	0	0	0		
ENSMUST00000139301						0	0	0	0	1	0	1	0	0	6	0		
ENSMUST00000139302	ENSMUSG00000059208	17	33646233	33686860	-1	0	3	52	79	13	0	0	11	0	20	0	B8JK33	
ENSMUST00000139303	ENSMUSG00000062234	5	108569411	108629755	-1	3	0	0	0	0	0	13	12	5	0	21	F7BG02	
ENSMUST00000139304						4	4	13	7	6	5	0	0	0	0	0		
ENSMUST00000139305						1	0	3	39	2	0	3	3	3	1	5		
ENSMUST00000139306	ENSMUSG00000038400	2	173224458	173276533	-1	1	3	2	43	3	1	1	4	0	0	8	A2APF5	
ENSMUST00000139307						2	4	0	32	0	0	7	0	7	0	0		
ENSMUST00000139308						14	15	57	37	23	11	362	1871	520	281	359		
ENSMUST00000139310						2	0	4	6	4	3	0	0	0	0	0		
ENSMUST00000139311						26	16	35	25	33	11	24	47	58	12	57		
ENSMUST00000139312	ENSMUSG00000009614	2	27188393	27248337	-1	0	5	11	4	0	0	0	0	0	0	0	A2AH52	
ENSMUST00000139313						0	0	0	0	0	0	0	7	0	0	0		
ENSMUST00000139314						8	4	13	4	12	4	19	19	31	0	13		
ENSMUST00000139315						134	99	265	792	156	80	1	4	1	0	6		
ENSMUST00000139316						2	0	2	8	2	2	0	0	2	0	8		
ENSMUST00000139318						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139319						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139320						0	0	1	0	0	0	3	0	0	0	3		
ENSMUST00000139321						3	4	6	2	6	1	0	3	2	0	3		
ENSMUST00000139322						0	0	0	0	0	0	37	238	48	40	65		
ENSMUST00000139323						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000139324	ENSMUSG00000022960	16	91677268	91688765	-1	4	0	2	0	0	0	0	150	22	16	20	D6RHL8	
ENSMUST00000139325						7	3	23	1	7	6	0	0	0	0	2		
ENSMUST00000139326						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000139328	ENSMUSG00000052033	2	170496428	170519123	1	13	6	19	11	10	4	0	9	0	0	1	E9Q2U7	
ENSMUST00000139329						1	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000139330						0	0	0	0	0	1	0	0	3	1	0		
ENSMUST00000139332						9	7	16	29	5	6	0	37	17	0	0		
ENSMUST00000139333						0	0	0	22	33	12	0	16	8	0	16		
ENSMUST00000139336						13	8	19	15	10	3	0	0	0	0	0		
ENSMUST00000139337	ENSMUSG00000072915	11	58847158	58861956	1	14	13	30	14	19	6	51	71	68	27	64	Q5NC63	
ENSMUST00000139339						2	2	2	0	1	3	9	0	8	0	5		
ENSMUST00000139340	ENSMUSG00000062510	1	191063012	191086474	1	0	0	0	2	0	0	0	2	0	3	0	E9Q3W6	
ENSMUST00000139341	ENSMUSG00000017747	11	100766032	100770957	-1	1	2	0	2	3	0	0	0	2	0	0	A2A5D6	
ENSMUST00000139342						0	0	0	0	0	0	5	102	3	33	26		
ENSMUST00000139343						0	0	1	0	0	0	0	0	37	0	11		
ENSMUST00000139344	ENSMUSG00000024143	17	86963082	87000069	1	0	0	1	27	4	1	3	0	15	0	6	D3Z3L1	
ENSMUST00000139346						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000139347	ENSMUSG00000068036	17	13760539	13906150	1	1	0	0	0	7	3	0	0	13	0	4	D3YUD2	
ENSMUST00000139349						3	1	0	2	6	2	0	10	4	12	3		
ENSMUST00000139350						6	5	4	4	8	2	6	4	5	1	8		
ENSMUST00000139352						21	25	30	7	18	31	0	0	0	0	0		
ENSMUST00000139353	ENSMUSG00000024055	17	32924688	32947402	-1	0	0	1	13	0	11	35	42	0	32	51	B8JK07	
ENSMUST00000139354						1	2	4	1	0	0	0	0	0	0	0		
ENSMUST00000139355	ENSMUSG00000039985	6	148921035	148946467	-1	0	2	0	2	1	0	0	0	0	0	3	D3Z1Z9	
ENSMUST00000139358						2	0	6	7	4	0	0	0	0	0	0		
ENSMUST00000139359						0	1	0	5	0	1	0	0	0	0	0		
ENSMUST00000139360						0	0	0	1	0	0	0	0	0	0	2		
ENSMUST00000139362						2	3	5	2	5	2	3	4	4	7	14		
ENSMUST00000139364						0	1	0	66	0	4	0	0	0	0	0		
ENSMUST00000139365	ENSMUSG00000068457	Y	1096861	1245759	-1	0	0	0	0	0	0	33	0	5	27	0	E9PWW8	
ENSMUST00000139366	ENSMUSG00000029185	5	64970071	65041886	1	0	2	8	0	0	0	7	3	0	7	0	D3Z2J2	
ENSMUST00000139367						9	4	10	10	14	7	0	10	5	0	0		
ENSMUST00000139368						0	0	0	0	0	0	0	7	16	9	8		
ENSMUST00000139369						4	1	12	1	5	2	0	0	0	0	0		
ENSMUST00000139370						5	2	7	10	4	7	0	0	0	0	0		
ENSMUST00000139371	ENSMUSG00000019578	17	56067045	56075028	-1	3	5	6	18	5	3	164	180	164	25	82	B8JJA4	
ENSMUST00000139372						4	4	6	10	3	0	0	1	0	0	0		
ENSMUST00000139373						7	8	12	104	21	5	3	5	0	0	1		
ENSMUST00000139374						0	0	0	0	0	0	21	26	0	0	0		
ENSMUST00000139375						8	4	0	7	3	6	0	6	0	0	2		
ENSMUST00000139376	ENSMUSG00000003269	7	45806637	45814581	-1	0	0	0	0	0	1	144	449	107	78	43	D6RCZ5	
ENSMUST00000139378						3	0	0	228	5	3	17	707	161	599	384		
ENSMUST00000139379						5	7	7	2	7	2	0	0	0	0	0		
ENSMUST00000139380						1	0	0	1	0	0	1	2	6	1	1		
ENSMUST00000139381						0	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000139382						0	1	8	4	0	0	0	0	0	0	2		
ENSMUST00000139383	ENSMUSG00000041565	17	68273797	68777961	1	9	7	5	6	16	3	0	0	0	0	0	D6REI4	
ENSMUST00000139384	ENSMUSG00000020175	10	75037058	75054748	1	4	0	0	8	1	0	0	0	0	0	0	D3YZ27	
ENSMUST00000139385	ENSMUSG00000045205	4	11261315	11322137	-1	30	27	111	0	0	0	0	38	0	3	0	A2AJQ2	
ENSMUST00000139386						0	0	0	13	0	1	0	0	1	0	3		
ENSMUST00000139387						2	0	0	0	0	0	85	223	0	0	0		
ENSMUST00000139388						1	3	9	3	8	6	43	75	35	10	106		
ENSMUST00000139389	ENSMUSG00000032098	9	44673233	44686305	1	0	0	0	21	30	0	0	0	0	0	0	D6RI51	
ENSMUST00000139390						1	3	3	4	2	0	0	22	10	0	11		
ENSMUST00000139391						1	0	0	2	1	3	31	80	55	8	65		
ENSMUST00000139393						8	7	15	29	13	3	0	3	3	0	7		
ENSMUST00000139394						3	3	0	1	5	3	8	18	12	5	35		
ENSMUST00000139395	ENSMUSG00000029712	5	137553517	137569582	1	0	0	0	0	0	9	0	0	0	0	0		Q99MR0
ENSMUST00000139396						2	3	9	51	4	0	0	19	12	5	43		
ENSMUST00000139398	ENSMUSG00000029433	5	123509765	123525488	-1	0	0	3	0	0	0	0	6	2	0	0	Q8R1D8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139399						1	2	15	28	2	1	4	2	0	1	8		
ENSMUST00000139400						2	2	0	2	2	0	0	48	6	0	0		
ENSMUST00000139401	ENSMUSG00000028403	4	82798738	82859958	-1	4	3	5	0	8	2	0	0	0	0	0	Q5SRN8	
ENSMUST00000139402						0	1	0	0	2	1	0	149	89	54	66		
ENSMUST00000139403						0	0	2	9	4	3	0	0	0	0	0		
ENSMUST00000139404						4	10	21	6	3	3	3	30	6	11	14		
ENSMUST00000139405						2	5	9	18	12	5	0	1	0	0	0		
ENSMUST00000139406						2	1	3	33	3	4	0	0	2	1	1		
ENSMUST00000139407						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000139408						0	3	7	1	2	0	0	101	14	0	5		
ENSMUST00000139410						3	3	18	8	11	3	2	3	0	0	12		
ENSMUST00000139412						6	1	15	0	2	1	23	86	40	14	96		
ENSMUST00000139413						4	2	0	5	1	3	4	1	0	0	3		
ENSMUST00000139414						0	0	0	0	0	0	26	0	1	21	14		
ENSMUST00000139415						0	0	8	2	3	0	1	0	0	0	0		
ENSMUST00000139416						5	3	8	68	10	4	0	3	0	0	0		
ENSMUST00000139417						5	2	0	0	0	0	11	0	19	12	21		
ENSMUST00000139418						2	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000139419						3	2	0	68	2	6	0	8	3	0	4		
ENSMUST00000139420	ENSMUSG00000041939	5	114444269	114460591	1	0	4	0	3	3	0	0	1	0	0	0	A0A0G2JDI0	
ENSMUST00000139421	ENSMUSG00000031232	X	105968084	106011906	-1	0	0	0	0	0	0	0	0	28	31	5	F6TBV1	
ENSMUST00000139422	ENSMUSG00000010142	11	61126755	61149372	1	3	5	4	0	4	2	0	0	0	0	0	B1ATI4	
ENSMUST00000139425	ENSMUSG00000063919	5	116439275	116591817	-1	7	9	50	24	7	0	0	0	0	0	0		Q8BKA3
ENSMUST00000139426						0	0	2	1	0	0	4	0	13	0	12		
ENSMUST00000139427						0	1	4	1	1	2	6	11	2	0	12		
ENSMUST00000139428	ENSMUSG00000054484	2	120977017	121007852	1	8	0	0	235	10	0	0	149	0	13	49	D6RH67	
ENSMUST00000139430						0	2	4	1	5	0	0	207	0	0	0		
ENSMUST00000139431						0	0	0	0	0	1	0	1	0	0	0		
ENSMUST00000139432						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139433						0	0	0	2	1	3	0	0	0	0	0		
ENSMUST00000139434	ENSMUSG00000027589	2	181837854	181857461	1	0	2	2	0	3	2	0	0	17	28	18	B0R0D0	
ENSMUST00000139435						0	0	0	0	0	0	4	1	4	0	0		
ENSMUST00000139436						6	4	30	2	10	0	0	0	0	0	0		
ENSMUST00000139437						10	3	12	35	7	5	3	4	3	0	6		
ENSMUST00000139438	ENSMUSG00000052551	13	8202866	8768747	1	3	6	7	10	1	0	0	0	0	0	0	D3Z321	
ENSMUST00000139439						1	0	9	46	4	0	0	0	0	0	0		
ENSMUST00000139441						0	3	2	3	3	0	0	0	0	0	0		
ENSMUST00000139442	ENSMUSG00000002578	10	128630843	128645991	-1	0	0	0	0	2	1	0	0	0	0	0	F6VUB6	
ENSMUST00000139443	ENSMUSG00000066551	5	149046702	149184489	-1	4	0	0	0	1	0	5	8	16	104	49		
ENSMUST00000139445						5	3	7	2	5	4	3	3	5	3	2		
ENSMUST00000139446						0	0	0	1	0	0	0	0	75	13	77		
ENSMUST00000139447						2	3	2	0	4	1	0	0	0	0	0		
ENSMUST00000139448						29	23	47	86	46	32	0	6	0	0	0		
ENSMUST00000139450	ENSMUSG00000028785	4	129111570	129122036	-1	0	0	0	1	0	0	0	0	4	0	0		P84075
ENSMUST00000139451	ENSMUSG00000057363	1	43746966	43827800	-1	0	0	0	15	0	0	33	82	93	141	62	D3YUF9	
ENSMUST00000139452						5	2	15	0	0	2	0	0	1	0	3		
ENSMUST00000139453						8	7	5	6	7	3	0	0	0	0	0		
ENSMUST00000139454	ENSMUSG00000099041	2	30240567	30282148	1	0	0	8	6	8	2	0	9	20	0	46		Q80WG5
ENSMUST00000139456	ENSMUSG00000030869	7	122085403	122101886	-1	0	0	0	0	2	0	54	91	22	19	0	F6ZFT1	
ENSMUST00000139457						8	4	5	102	11	5	0	2	0	0	7		
ENSMUST00000139458						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139459	ENSMUSG00000006345	10	75561604	75586200	1	0	0	0	3	6	0	0	0	0	0	32	D3Z266	
ENSMUST00000139460						1	0	2	0	2	0	25	53	26	13	18		
ENSMUST00000139461						5	2	6	4	8	3	2	14	5	2	0		
ENSMUST00000139462	ENSMUSG00000035158	6	97807052	98021349	1	0	0	0	0	16	0	0	0	7	0	0	D6RCW2	
ENSMUST00000139463						5	1	8	0	4	1	0	3	0	0	0		
ENSMUST00000139464						0	2	5	1	0	3	0	0	0	0	0		
ENSMUST00000139465						1	1	4	0	6	1	0	0	0	0	0		
ENSMUST00000139466						5	0	4	18	3	0	0	0	0	0	0		
ENSMUST00000139467						197	232	384	126	174	70	11	19	18	3	21		
ENSMUST00000139468						2	5	11	11	7	3	0	0	1	1	1		
ENSMUST00000139472						6	4	5	3	4	1	7	41	10	7	9		
ENSMUST00000139473	ENSMUSG00000033653	16	21423118	21644680	1	1	0	0	86	4	1	0	1	0	0	0	D3Z2G2	
ENSMUST00000139474	ENSMUSG00000041264	5	149184350	149215434	1	1	0	0	3	0	0	0	0	4	0	6	D3Z5G1	
ENSMUST00000139475						0	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000139476	ENSMUSG00000026473	1	153899944	153909723	1	0	0	0	23	5	1	126	0	201	12	267	D3YVK1	
ENSMUST00000139477	ENSMUSG00000018415	11	60417145	60450927	1	29	10	96	229	7	18	0	3	0	0	0		Q9CPY6
ENSMUST00000139478						0	0	0	0	0	0	0	0	0	1	1		
ENSMUST00000139480						34	28	219	118	44	22	0	1	0	0	4		
ENSMUST00000139481						2	1	13	34	2	0	2	9	3	0	7		
ENSMUST00000139482						4	2	10	5	3	4	8	44	22	8	24		
ENSMUST00000139484	ENSMUSG00000020333	11	54303798	54364756	1	0	0	0	0	0	0	1	2	0	0	0	F6WYN6	
ENSMUST00000139485						10	8	15	7	12	6	4	17	4	1	16		
ENSMUST00000139486	ENSMUSG00000006732	10	127041414	127046365	1	2	14	26	0	12	16	0	0	0	4	0	F6WMV8	
ENSMUST00000139487	ENSMUSG00000035112	11	101260567	101277409	1	0	2	13	195	7	4	1	0	0	1	0	E9Q470	
ENSMUST00000139489						1	0	0	0	0	1	10	89	5	20	4		
ENSMUST00000139490						0	0	1	3	0	0	0	0	0	5	0		
ENSMUST00000139491						20	21	68	17	30	12	4	0	3	1	3		
ENSMUST00000139494	ENSMUSG00000002546	2	32287384	32307921	1	0	0	1	13	0	1	0	0	0	0	0	A2AN42	
ENSMUST00000139495						2	2	0	0	1	4	0	0	1	0	6		
ENSMUST00000139496						16	6	11	0	7	7	25	92	65	11	61		
ENSMUST00000139498	ENSMUSG00000015714	3	95314791	95323599	1	1	0	0	0	3	0	0	0	0	0	0	D3Z4M2	
ENSMUST00000139499						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139501						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139502						3	0	0	1	2	3	0	2	0	0	0		
ENSMUST00000139503	ENSMUSG00000022971	16	91372783	91405589	1	2	0	2	3	0	0	4	2	3	0	5	H3BKB3	
ENSMUST00000139504						2	2	2	233	11	2	0	3	34	0	7		
ENSMUST00000139505						0	0	6	4	0	2	0	1	0	0	1		
ENSMUST00000139506						0	0	0	4	1	0	7	0	0	0	2		
ENSMUST00000139507						3	0	2	2	2	0	21	36	24	0	30		
ENSMUST00000139509						3	0	0	0	1	0	0	0	2	1	0		
ENSMUST00000139510						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139511						2	1	0	1	4	0	204	211	484	65	319		
ENSMUST00000139513	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	D6REF1	
ENSMUST00000139515						3	5	25	3	11	5	0	0	1	0	4		
ENSMUST00000139516						2	0	0	0	3	0	0	0	0	0	5		
ENSMUST00000139517	ENSMUSG00000042303	15	80977765	81012289	1	18	7	18	36	15	15	26	0	42	0	63		Q8VCZ6
ENSMUST00000139518	ENSMUSG00000004642	5	33634952	33652574	-1	1	2	8	6	3	0	0	11	0	12	5		
ENSMUST00000139519	ENSMUSG00000070730	2	119137001	119157034	-1	2	0	3	159	6	1	0	1	0	0	0	A3KGH5	
ENSMUST00000139520	ENSMUSG00000050640	5	100077872	100159808	-1	0	0	0	5	0	0	0	0	0	0	0	H9KV06	
ENSMUST00000139521						5	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000139522	ENSMUSG00000032946	19	6399340	6415216	1	0	0	10	6	1	0	12	46	38	0	27	D6RDD3	
ENSMUST00000139523						0	3	1	9	1	0	0	0	2	0	2		
ENSMUST00000139524	ENSMUSG00000042608	4	126103957	126141029	1	0	0	0	41	0	0	2	3	6	1	6	B1AVZ9	
ENSMUST00000139526	ENSMUSG00000021830	14	45134448	45220328	-1	0	1	0	0	0	3	67	200	133	119	128		Q7TN22
ENSMUST00000139527	ENSMUSG00000057375	4	107314363	107359823	1	0	0	2	2	1	0	0	28	0	0	56	A2A8S3	
ENSMUST00000139528	ENSMUSG00000038034	1	172261641	172319841	1	13	5	6	18	0	8	0	4	0	0	4	G3UYZ1	
ENSMUST00000139531						0	0	5	0	0	0	0	0	1	0	0		
ENSMUST00000139532	ENSMUSG00000018548	11	87127077	87220683	1	0	0	0	76	0	0	0	0	2	0	0	Q5SQY9	
ENSMUST00000139533						1	3	2	0	0	0	2	0	1	0	3		
ENSMUST00000139534						5	2	4	2	0	1	2	8	0	4	4		
ENSMUST00000139535						8	2	44	9	6	1	11	25	9	2	26		
ENSMUST00000139536						0	1	0	0	0	1	0	71	13	14	3		
ENSMUST00000139537	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	10	10	D3Z7P7	
ENSMUST00000139538						10	4	21	24	9	6	196	1426	454	154	541		
ENSMUST00000139539	ENSMUSG00000000730	10	78041947	78063622	1	0	0	60	6	0	0	0	0	0	0	0	D3YUQ4	
ENSMUST00000139540						0	7	31	8	3	0	0	0	0	0	11		
ENSMUST00000139541	ENSMUSG00000002395	8	71366848	71369732	1	12	9	9	51	7	6	0	0	0	2	0	D3Z6D3	
ENSMUST00000139542						0	0	0	25	0	0	0	0	0	0	3		
ENSMUST00000139544						0	2	0	3	5	1	0	0	0	0	0		
ENSMUST00000139545						1	0	1	0	5	5	56	73	219	2	273		
ENSMUST00000139546						0	4	2	0	4	0	12	48	13	0	20		
ENSMUST00000139547	ENSMUSG00000032376	9	66514637	66593142	-1	0	0	0	0	0	0	211	1002	415	87	202	D6RG67	
ENSMUST00000139548						21	22	40	34	23	20	6	58	36	0	33		
ENSMUST00000139549						3	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000139550	ENSMUSG00000029122	5	37289098	37336894	-1	6	1	10	12	4	3	0	0	0	0	0	F6X0M4	
ENSMUST00000139551						2	0	2	1	1	0	0	0	0	1	0		
ENSMUST00000139553	ENSMUSG00000026816	2	28566311	28583751	-1	1	0	13	10	9	0	0	1	0	0	1	H3BJX5	
ENSMUST00000139554						4	2	3	4	3	2	0	6	1	1	7		
ENSMUST00000139555						42	33	67	191	54	28	14	53	19	3	48		
ENSMUST00000139556						0	0	0	28	2	0	0	0	0	3	0		
ENSMUST00000139557						11	16	78	13	22	10	0	0	0	0	0		
ENSMUST00000139558						2	0	0	98	3	3	4	18	6	14	0		
ENSMUST00000139559						4	0	12	7	8	5	0	0	0	0	0		
ENSMUST00000139560	ENSMUSG00000028614	4	107367784	107416346	1	24	16	31	75	30	0	9	102	67	12	49		Q8VCB1
ENSMUST00000139561						5	5	18	10	4	2	0	0	0	0	0		
ENSMUST00000139562						0	0	15	0	4	0	0	0	0	0	4		
ENSMUST00000139563						0	1	4	52	7	3	19	69	43	3	93		
ENSMUST00000139564						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000139565	ENSMUSG00000005374	5	135149657	135165760	1	1	4	3	92	5	5	0	5	2	0	3	D6RI48	
ENSMUST00000139566	ENSMUSG00000022914	16	95992092	96082526	-1	0	0	0	0	0	0	0	0	0	0	0	F6TDU4	
ENSMUST00000139568						4	6	9	3	6	5	0	0	0	0	0		
ENSMUST00000139569	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	0	0	0	0	0	0	0	0	S4R191	
ENSMUST00000139570						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000139571						0	1	0	15	4	4	0	0	0	0	0		
ENSMUST00000139572						23	9	13	9	17	0	0	0	0	0	0		
ENSMUST00000139573						2	2	4	77	6	3	2	0	0	0	0		
ENSMUST00000139574						2	0	4	1	1	0	0	0	0	0	0		
ENSMUST00000139575						2	0	3	0	2	5	2	0	0	0	0		
ENSMUST00000139577						0	2	0	34	2	3	0	2	0	0	0		
ENSMUST00000139578						16	11	52	23	30	14	15	131	24	14	37		
ENSMUST00000139579						3	1	4	3	0	1	0	0	2	0	0		
ENSMUST00000139580						12	5	12	4	10	3	3	8	2	0	2		
ENSMUST00000139581	ENSMUSG00000079334	9	107578887	107584050	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCE0	
ENSMUST00000139582	ENSMUSG00000035713	7	97309380	97332020	-1	19	11	34	252	33	18	40	30	39	0	44	M0QWN7	
ENSMUST00000139583						6	4	3	7	4	0	8	13	14	2	13		
ENSMUST00000139584	ENSMUSG00000022544	16	5244152	5255983	-1	0	0	0	4	1	0	16	7	0	12	14	D3YYE2	
ENSMUST00000139585	ENSMUSG00000016458	2	105126529	105173616	1	6	10	0	0	9	1	0	0	0	0	2	F6VXG5	
ENSMUST00000139586						1	1	5	0	0	2	0	2	2	0	7		
ENSMUST00000139587	ENSMUSG00000031295	X	160502166	160598878	1	3	0	0	9	1	0	0	0	5	0	0	A2AHQ8	
ENSMUST00000139589						4	0	6	51	4	4	0	0	0	0	5		
ENSMUST00000139590	ENSMUSG00000029469	5	122550204	122614518	-1	0	7	0	0	0	0	0	0	1	0	0	A0A0G2JFG8	
ENSMUST00000139593	ENSMUSG00000027673	3	32736990	32751566	1	1	0	15	1	2	0	0	0	0	0	0	D3YX99	
ENSMUST00000139594						9	0	41	4	8	5	10	6	0	2	0		
ENSMUST00000139595						0	1	5	0	0	0	0	0	0	0	0		
ENSMUST00000139596	ENSMUSG00000029752	6	7675169	7693254	-1	0	1	0	0	0	1	0	0	0	0	0	D3YYR0	
ENSMUST00000139597						6	3	12	5	6	4	6	24	18	0	24		
ENSMUST00000139598						2	0	2	2	1	1	0	0	14	0	6		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139599						4	2	4	1	2	0	2	0	3	0	0		
ENSMUST00000139601						2	2	8	0	0	0	0	7	0	1	6		
ENSMUST00000139602						1	1	2	0	6	3	33	244	0	0	0		
ENSMUST00000139603						4	5	10	9	6	4	1	0	4	0	0		
ENSMUST00000139604	ENSMUSG00000008318	7	100845848	100863446	-1	5	2	6	0	6	0	18	29	20	2	34	D3YWL9	
ENSMUST00000139605						5	4	9	1	0	4	11	39	19	0	14		
ENSMUST00000139606						1	0	1	0	4	0	8	65	6	2	25		
ENSMUST00000139607						81	83	142	65	87	52	1	5	3	4	3		
ENSMUST00000139608						0	8	11	10	0	8	0	34	0	0	12		
ENSMUST00000139609	ENSMUSG00000047767	7	101289392	101302251	-1	4	2	19	57	14	4	4	0	0	0	0		Q6KAU8
ENSMUST00000139610						0	0	0	0	0	0	5	0	12	0	0		
ENSMUST00000139611	ENSMUSG00000029502	5	110176701	110226470	1	1	1	3	54	1	3	2	1	2	0	3	D3Z0Q8	
ENSMUST00000139613						3	1	4	2	2	0	0	0	0	3	0		
ENSMUST00000139615						2	2	3	0	1	1	1	0	0	0	3		
ENSMUST00000139616						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139617						1	0	0	2	4	1	0	1	0	0	1		
ENSMUST00000139619	ENSMUSG00000019302	11	101009452	101063719	1	1	1	5	3	0	2	0	0	4	0	0	A2A599	
ENSMUST00000139620						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000139622	ENSMUSG00000056812	18	64254359	64276146	1	1	0	1	11	0	1	0	0	0	0	0	D3Z320	
ENSMUST00000139623						4	3	12	62	14	10	2440	3694	2195	3787	2470		
ENSMUST00000139624	ENSMUSG00000026825	2	32308471	32353338	-1	0	0	0	85	5	0	0	0	0	0	8		P39053
ENSMUST00000139625	ENSMUSG00000000884	16	18498768	18566679	1	1	0	5	0	0	2	1	0	1	0	0	D3Z0D5	
ENSMUST00000139626						0	3	0	88	6	2	0	0	0	0	0		
ENSMUST00000139627						3	3	2	38	5	6	11	43	3	4	8		
ENSMUST00000139628						0	0	1	1	2	0	0	4	0	0	5		
ENSMUST00000139629	ENSMUSG00000050592	2	32050055	32084857	-1	11	11	42	306	25	11	2	17	9	5	26	A2ATN4	Q8C552
ENSMUST00000139630						0	1	0	1	0	0	0	0	0	1	1		
ENSMUST00000139631	ENSMUSG00000029470	5	122707544	122729738	1	0	0	0	16	0	0	0	0	0	0	0	D3YYR5	
ENSMUST00000139632	ENSMUSG00000029209	5	69573108	69592340	-1	0	0	0	0	0	0	0	0	40	105	7		Q9CRC9
ENSMUST00000139633						0	1	5	3	0	0	0	1	0	0	0		
ENSMUST00000139634	ENSMUSG00000029026	4	154056253	154140208	-1	2	0	16	51	3	0	0	0	0	0	0	B1AX91	
ENSMUST00000139635						2	0	6	0	5	0	1	2	0	0	2		
ENSMUST00000139637	ENSMUSG00000039205	2	32352327	32380970	1	4	1	48	0	0	0	0	0	0	0	14	F7D5G9	
ENSMUST00000139638	ENSMUSG00000014606	11	70644196	70647479	-1	0	0	0	0	0	4	9	2	5	0	0	Q5SX46	
ENSMUST00000139639						8	3	12	7	7	0	0	0	1	2	0		
ENSMUST00000139640	ENSMUSG00000030315	6	114860628	114969994	-1	6	5	3	139	17	7	0	0	0	3	0	D3YZY3	
ENSMUST00000139641						2	3	5	6	4	1	0	0	0	0	0		
ENSMUST00000139642						5	1	3	3	5	2	3	1	0	0	4		
ENSMUST00000139643						11	6	12	17	19	5	142	874	237	191	335		
ENSMUST00000139644	ENSMUSG00000022033	14	65805837	65817822	1	5	1	6	17	3	2	0	1	0	0	0	D3YVF2	
ENSMUST00000139645						1	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000139646						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000139647						2	5	4	0	5	0	0	0	0	0	0		
ENSMUST00000139648						0	2	0	0	1	0	0	16	1	4	0		
ENSMUST00000139649	ENSMUSG00000051344	1	64785983	64956824	-1	69	111	354	92	88	52	12	55	42	7	29		Q8BM47
ENSMUST00000139650						45	43	53	253	88	32	5	19	13	2	14		
ENSMUST00000139651	ENSMUSG00000065990	4	155831272	155833130	1	0	0	0	0	5	1	5	4	6	0	0	A0A0A0MQH8	
ENSMUST00000139654						8	5	24	9	21	8	0	2	0	0	4		
ENSMUST00000139655	ENSMUSG00000024843	19	3851773	3894369	1	0	0	0	0	0	0	0	0	0	0	0	F7AYX1	
ENSMUST00000139656						3	5	8	3	5	1	0	0	0	0	0		
ENSMUST00000139657						12	6	16	17	10	0	210	203	115	8	109		
ENSMUST00000139658						6	0	2	0	3	4	0	16	29	0	24		
ENSMUST00000139660	ENSMUSG00000027663	3	32334792	32366014	-1	0	0	0	44	2	0	0	0	0	0	0	A0A0A6YWE0	
ENSMUST00000139661	ENSMUSG00000015721	7	23385889	23441922	1	16	15	0	7	19	0	0	0	0	0	0		Q9R1M5
ENSMUST00000139663						0	0	0	3	2	0	0	0	0	0	0		
ENSMUST00000139664						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000139665						2	2	0	4	4	5	0	0	0	0	0		
ENSMUST00000139666	ENSMUSG00000068036	17	13760539	13906150	1	10	8	0	0	17	10	0	0	0	0	0		Q9QZQ1
ENSMUST00000139668	ENSMUSG00000039176	7	79446231	79466362	-1	0	1	2	0	2	0	0	0	0	0	5	F6YLN2	
ENSMUST00000139669						2	5	0	24	1	0	0	0	0	8	0		
ENSMUST00000139670						6	5	16	4	6	3	0	0	0	0	0		
ENSMUST00000139671	ENSMUSG00000047193	9	6928503	7184446	-1	0	2	0	0	0	0	1	0	4	0	4	F6QLS2	
ENSMUST00000139672	ENSMUSG00000026950	2	52136647	52338798	-1	0	3	0	0	0	0	2	0	0	0	13	F6RDH3	
ENSMUST00000139673						0	0	0	0	0	0	0	0	0	0	55		
ENSMUST00000139674						49	46	327	92	52	29	10	26	31	4	36		
ENSMUST00000139675						5	6	3	10	5	1	4	29	3	4	20		
ENSMUST00000139676						1	1	6	76	5	3	0	0	0	0	0		
ENSMUST00000139678						1090	1157	1180	689	977	367	18	79	52	22	81		
ENSMUST00000139679	ENSMUSG00000024201	17	56326062	56402870	1	1	0	4	9	10	0	14	5	21	5	9	B0V2M7	
ENSMUST00000139680	ENSMUSG00000053175	7	19808462	19822770	-1	6	1	5	0	0	0	64	4	11	0	7	D3Z6Z2	
ENSMUST00000139682						0	3	0	4	4	0	2	2	2	0	0		
ENSMUST00000139683						1	1	0	0	4	0	18	22	12	13	4		
ENSMUST00000139684	ENSMUSG00000027309	2	130706200	130906406	-1	0	0	4	0	0	0	0	0	0	0	0	F7ATN7	
ENSMUST00000139685	ENSMUSG00000028936	4	152325742	152334071	1	11	1	5	3	3	2	10	16	18	18	8	Q4VAG4	P67984
ENSMUST00000139686						9	10	39	16	21	6	3	8	5	0	9		
ENSMUST00000139687						0	6	27	5	6	0	0	0	1	0	1		
ENSMUST00000139689	ENSMUSG00000026988	2	59852364	59882591	-1	0	0	0	0	0	0	9	12	7	0	3	F6R860	
ENSMUST00000139690						3	3	12	1	3	2	0	15	7	0	6		
ENSMUST00000139691						3	1	0	1	1	0	0	9	0	0	9		
ENSMUST00000139692						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000139693						3	1	7	20	7	1	0	0	0	0	0		
ENSMUST00000139694						4	3	0	0	3	0	0	0	0	0	0		
ENSMUST00000139696						6	5	10	3	4	2	0	0	0	0	0		
ENSMUST00000139697						3	2	0	0	1	1	0	6	3	0	8		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139698						9	14	13	13	12	2	6	13	15	4	33		
ENSMUST00000139699						13	11	26	35	19	0	18	25	63	0	10		
ENSMUST00000139700						9	5	5	15	9	6	1	3	4	5	4		
ENSMUST00000139702						3	0	0	0	3	2	147	40	157	0	156		
ENSMUST00000139703	ENSMUSG00000039048	9	35204206	35211055	-1	0	0	0	0	0	0	0	18	16	0	0	D6RG85	
ENSMUST00000139705						1	0	0	1	4	3	11	99	9	0	20		
ENSMUST00000139706	ENSMUSG00000025140	11	120635712	120643769	-1	0	0	0	5	1	0	0	0	0	0	0	A2ABZ3	
ENSMUST00000139707						1	0	2	0	1	0	6	20	6	3	3		
ENSMUST00000139708	ENSMUSG00000030701	7	100642892	100662414	-1	0	0	2	0	3	0	0	0	0	0	0	D3Z6S5	
ENSMUST00000139709	ENSMUSG00000007880	4	133679008	133756769	-1	13	25	44	33	31	16	3	0	2	0	4	E9Q495	
ENSMUST00000139710						0	2	9	0	0	0	0	4	1	0	0		
ENSMUST00000139711						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000139712						3	2	0	2	2	0	4	0	10	8	15		
ENSMUST00000139713	ENSMUSG00000020467	11	28853204	28926743	1	1	0	0	0	0	0	0	0	0	4	1	F6ZFS0	
ENSMUST00000139714						2	0	5	48	8	5	0	0	0	0	0		
ENSMUST00000139715	ENSMUSG00000026229	1	86064387	86139151	1	0	0	0	0	0	8	0	0	0	0	0	D6RGR5	
ENSMUST00000139716						0	1	3	3	2	0	5	7	10	2	0		
ENSMUST00000139717						70	97	118	76	71	40	8	26	20	11	33		
ENSMUST00000139719	ENSMUSG00000079484	2	30266203	30282149	1	2	0	7	3	2	1	4	0	0	0	0	A0A0A0MQG9	
ENSMUST00000139720	ENSMUSG00000030770	7	112427505	112591692	1	1003	1218	1262	764	1383	655	10	27	15	1	47	D6RHM9	
ENSMUST00000139721						13	0	77	0	20	0	0	46	30	22	23		
ENSMUST00000139722						0	1	0	91	2	1	0	0	0	1	0		
ENSMUST00000139723						0	1	0	9	2	0	0	0	0	0	0		
ENSMUST00000139724	ENSMUSG00000001663	10	75783813	75798584	-1	0	0	0	0	0	2	0	0	1	0	0	D3Z5W7	
ENSMUST00000139725	ENSMUSG00000026088	1	37874801	37890411	-1	0	0	4	0	5	0	0	7	0	0	0		Q8VDV8
ENSMUST00000139726						0	0	0	1	2	0	2	17	7	2	2		
ENSMUST00000139727	ENSMUSG00000046727	18	36345619	36402980	1	1	1	0	0	2	0	0	0	0	0	0	D3YWV2	
ENSMUST00000139728	ENSMUSG00000025583	11	119602905	119899576	1	0	0	1	3	1	0	0	0	0	0	0	F6U5L3	
ENSMUST00000139729						2	2	8	5	8	1	21	42	26	9	67		
ENSMUST00000139730						100	76	225	67	108	74	16	48	29	9	19		
ENSMUST00000139731						0	28	0	89	0	0	0	61	18	18	14		
ENSMUST00000139732	ENSMUSG00000030287	6	146108299	146502223	-1	0	4	0	44	0	0	19	0	119	8	70	B2KF92	
ENSMUST00000139733						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139734	ENSMUSG00000033540	5	108660331	108684557	1	4	6	5	0	0	4	33	158	57	17	19	D6REH5	
ENSMUST00000139735	ENSMUSG00000031012	X	13517080	13851367	-1	0	0	0	0	0	0	15	193	100	70	50	F6Y9I5	
ENSMUST00000139736						3	3	1	0	9	0	0	0	0	0	0		
ENSMUST00000139737	ENSMUSG00000034285	11	4873951	4894200	1	0	0	9	0	2	0	2	0	1	0	2	Q5SVG6	
ENSMUST00000139738	ENSMUSG00000026927	2	26382802	26389316	-1	0	0	0	11	0	1	15	13	10	5	23	A2AIW4	
ENSMUST00000139739						0	0	5	44	8	3	0	0	0	0	0		
ENSMUST00000139740	ENSMUSG00000022779	16	16870736	16892990	1	0	0	0	0	0	0	63	0	73	0	17	D3YWY3	
ENSMUST00000139741						1	0	7	1	3	3	0	0	0	0	0		
ENSMUST00000139742	ENSMUSG00000034175	11	5098926	5106093	1	1	2	0	26	3	0	2	6	0	0	0	Q5SUT9	
ENSMUST00000139743	ENSMUSG00000051736	10	39118804	39133914	-1	0	0	0	0	0	0	0	0	0	0	0	B2RVF6	Q8CF36
ENSMUST00000139744						4	4	3	8	2	1	0	2	0	0	0		
ENSMUST00000139746						7	4	25	73	7	5	0	0	0	0	0		
ENSMUST00000139747	ENSMUSG00000029451	4	143846497	143853637	1	0	2	8	1	3	2	0	0	0	0	0	A6PWA1	
ENSMUST00000139748						55	82	81	49	69	24	0	0	5	0	9		
ENSMUST00000139749						0	4	2	65	14	0	14	71	22	0	33		
ENSMUST00000139750	ENSMUSG00000046314	12	44852488	45074493	-1	1	2	1	0	0	0	0	0	0	0	0	D6RJ81	
ENSMUST00000139753	ENSMUSG00000015766	6	137477245	137654876	-1	3	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000139754	ENSMUSG00000073436	17	24888486	24895087	-1	0	0	0	2	0	0	0	0	0	0	0	D6RIK4	
ENSMUST00000139755						0	2	0	0	5	0	0	0	0	0	0		
ENSMUST00000139756	ENSMUSG00000033740	1	6487231	6860940	1	0	0	0	0	0	1	0	0	0	0	0	A0A0A6YXN3	
ENSMUST00000139757						7	7	12	15	15	3	0	4	0	0	0		
ENSMUST00000139758						9	13	14	4	7	6	0	0	0	0	0		
ENSMUST00000139759	ENSMUSG00000028760	4	137993022	138208508	1	0	0	0	122	0	0	0	0	0	0	0	A2AMI4	
ENSMUST00000139760						100	80	168	67	120	62	1	4	5	9	12		
ENSMUST00000139761						2	0	6	7	0	2	0	3	9	0	5		
ENSMUST00000139762						7	6	3	4	5	0	37	144	87	197	89		
ENSMUST00000139763						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000139764						1	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000139765						6	0	8	5	8	3	0	32	0	0	15		
ENSMUST00000139766						0	0	0	3	3	1	10	125	22	5	18		
ENSMUST00000139767						5	0	6	8	7	3	0	4	4	0	7		
ENSMUST00000139768	ENSMUSG00000041720	16	17280351	17406314	-1	4	0	4	0	0	0	0	0	52	0	32	F6WIX7	
ENSMUST00000139770						1	2	3	2	1	2	0	0	0	0	0		
ENSMUST00000139772						0	0	0	16	0	0	0	0	0	1	0		
ENSMUST00000139774						8	4	17	34	12	0	17	75	51	0	15		
ENSMUST00000139775						1	2	1	5	2	5	0	12	0	3	2		
ENSMUST00000139776	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	0	0	0	0	0	0	0	F6UKC6	
ENSMUST00000139777						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139778						35	15	29	13	29	8	2	57	20	15	23		
ENSMUST00000139779						1	1	0	0	1	1	3	1	4	0	0		
ENSMUST00000139780	ENSMUSG00000070509	7	73375509	73419899	1	31	22	121	40	16	12	0	0	0	3	0		
ENSMUST00000139781						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139782	ENSMUSG00000031816	8	121091628	121108392	-1	0	0	0	4	0	0	29	15	0	16	35	D3Z0Q4	
ENSMUST00000139783	ENSMUSG00000055865	3	104767406	104781840	-1	44	17	96	57	41	17	5	12	7	0	4		Q7TPG6
ENSMUST00000139784	ENSMUSG00000065999	4	147553277	147585198	1	1	4	9	0	6	4	0	0	0	0	0	A2A7A4	
ENSMUST00000139785						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000139786						85	86	492	145	87	52	6	27	12	1	14		
ENSMUST00000139787						0	2	0	1	0	0	16	39	0	1	3		
ENSMUST00000139788						0	1	20	64	3	0	0	119	1	3	23		
ENSMUST00000139789						7	5	44	14	6	2	0	1	0	5	0		
ENSMUST00000139790	ENSMUSG00000051048	7	100285520	100319699	1	15	22	0	132	20	12	0	0	0	0	0	D6RFD3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139792						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000139793	ENSMUSG00000040396	8	9977707	9992155	1	24	22	30	88	17	17	115	284	177	44	150		Q80UX8
ENSMUST00000139795						5	4	6	0	2	0	0	0	0	2	0		
ENSMUST00000139796	ENSMUSG00000032469	9	99575799	99584501	1	3	3	4	0	7	1	17	32	30	12	16	F6SDN8	
ENSMUST00000139797						0	0	1	1	1	1	73	928	200	38	539		
ENSMUST00000139798						1	0	4	0	2	0	0	0	0	0	0		
ENSMUST00000139799	ENSMUSG00000073792	4	99715664	99763460	1	0	0	0	0	0	0	0	0	0	0	0	A2BDX8	
ENSMUST00000139800						8	8	51	16	12	1	0	0	0	0	2		
ENSMUST00000139801	ENSMUSG00000026921	2	26580014	26593120	1	6	1	38	16	6	2	0	0	2	0	0	E9Q4M7	
ENSMUST00000139802						4	1	0	0	4	1	0	4	2	0	0		
ENSMUST00000139803	ENSMUSG00000019841	10	39732118	39875211	1	9	0	6	0	4	0	22	345	127	65	53	F6T1D2	
ENSMUST00000139805						1	0	0	0	5	2	0	0	0	0	0		
ENSMUST00000139806	ENSMUSG00000028977	4	148804429	148954889	1	27	4	55	31	22	10	2	6	8	1	2	B1AS48	
ENSMUST00000139807						1	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000139809						4	0	3	32	10	7	0	0	0	0	0		
ENSMUST00000139810	ENSMUSG00000025781	2	10056016	10080510	-1	0	0	0	0	0	0	11	0	2	6	0	A2AKV1	
ENSMUST00000139811						3	1	2	11	8	2	0	6	0	0	2		
ENSMUST00000139812	ENSMUSG00000027425	2	144368983	144407676	1	2	0	0	0	0	0	0	0	0	0	0	F7C4S8	
ENSMUST00000139813						1	0	6	1	5	0	0	2	0	0	8		
ENSMUST00000139814						7	6	6	3	5	2	0	0	4	0	2		
ENSMUST00000139815	ENSMUSG00000015776	2	26905262	26910677	-1	1	1	0	75	0	2	7	6	12	2	6	A2ALA4	
ENSMUST00000139816						0	0	2	0	1	0	0	2	2	0	0		
ENSMUST00000139817						1	0	0	3	0	2	8	8	20	0	17		
ENSMUST00000139818	ENSMUSG00000006333	7	3703993	3706897	1	0	0	0	0	0	0	80	25	12	0	0	D3YUV6	
ENSMUST00000139819	ENSMUSG00000033256	2	122348892	122369162	-1	2	0	15	4	0	3	0	0	3	0	2	A2AQ89	
ENSMUST00000139820	ENSMUSG00000031949	8	111966908	111992302	-1	68	62	75	58	84	19	6	26	21	0	16		Q9JHI2
ENSMUST00000139821						10	11	27	13	14	8	0	2	1	0	0		
ENSMUST00000139824						11	18	28	23	6	5	0	0	0	0	0		
ENSMUST00000139826	ENSMUSG00000028965	4	150914562	150946102	1	5	3	0	1	12	6	0	0	0	10	0	A2A886	
ENSMUST00000139828	ENSMUSG00000072821	5	94076385	94080997	1	24	11	20	16	27	10	0	0	0	0	0	K9J7D1	
ENSMUST00000139829						2	2	4	0	4	4	0	0	0	0	0		
ENSMUST00000139830						1	3	5	3	4	0	0	0	0	0	5		
ENSMUST00000139831						0	0	7	20	4	0	0	0	0	0	0		
ENSMUST00000139832						3	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000139833						0	2	1	0	4	0	0	6	0	0	0		
ENSMUST00000139834						0	0	0	0	0	0	0	2	0	0	7		
ENSMUST00000139836	ENSMUSG00000031570	8	25720061	25724887	1	5	0	4	4	0	0	9	0	0	0	7		Q3UMZ3
ENSMUST00000139837						9	3	6	7	11	3	7	13	0	0	17		
ENSMUST00000139838	ENSMUSG00000033740	1	6487231	6860940	1	2	4	20	1	1	4	0	0	0	0	0	D3YZ65	
ENSMUST00000139839	ENSMUSG00000039384	1	184013302	184075636	1	0	1	0	7	5	0	0	0	0	0	0	D3Z2S1	
ENSMUST00000139840	ENSMUSG00000028744	4	139294029	139310708	-1	20	6	24	14	17	12	40	221	95	9	74		Q8C4N4
ENSMUST00000139841	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	4	0	0	0	0	0	0	0	0	F6SK63	
ENSMUST00000139842						2	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000139843						1	0	15	1	4	2	4	8	7	2	5		
ENSMUST00000139844						0	0	4	0	5	0	0	0	0	3	0		
ENSMUST00000139845	ENSMUSG00000057406	5	33820725	33897975	1	0	0	0	0	20	0	0	0	0	0	0	D3Z3E0	
ENSMUST00000139846						1	0	2	8	0	0	642	1557	300	39	148		
ENSMUST00000139847						6	7	15	12	13	4	7	15	12	3	11		
ENSMUST00000139848	ENSMUSG00000034472	8	75213944	75224113	1	73	30	106	862	150	65	2	5	5	0	1		P63032
ENSMUST00000139849						1	2	1	5	3	0	0	0	0	0	4		
ENSMUST00000139850						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139852						3	3	9	12	3	1	1	15	0	0	3		
ENSMUST00000139853	ENSMUSG00000041740	5	115241412	115272898	-1	2	7	0	0	9	0	4060	5487	3056	313	2065	F7AN16	
ENSMUST00000139854						56	42	105	47	48	27	2	8	5	0	18		
ENSMUST00000139855	ENSMUSG00000001508	11	94962791	94976327	-1	0	0	0	0	6	0	0	0	0	0	0	Q5SWB0	
ENSMUST00000139856	ENSMUSG00000006127	11	75630988	75648871	1	0	0	5	0	0	0	31	141	35	5	34	Q5ND44	
ENSMUST00000139857						0	0	2	0	0	0	46	105	78	0	61		
ENSMUST00000139858						223	213	528	228	262	124	12	41	28	8	59		
ENSMUST00000139859						3	4	1	0	4	0	2	0	0	0	3		
ENSMUST00000139860						2	8	4	0	4	0	2	44	9	0	24		
ENSMUST00000139861	ENSMUSG00000003526	16	18060357	18090203	-1	17	10	46	114	24	10	2	19	6	5	9	E9PUR5	
ENSMUST00000139862						0	0	19	3	2	0	0	0	0	4	2		
ENSMUST00000139863	ENSMUSG00000035168	2	59612042	59846149	1	0	0	37	0	19	0	47	0	0	6	58		Q0VGY8
ENSMUST00000139865						0	0	0	1	3	5	0	0	0	0	4		
ENSMUST00000139866	ENSMUSG00000015714	3	95314791	95323599	1	1	5	2	4	13	4	10	0	0	0	5	D3Z0Z2	
ENSMUST00000139867	ENSMUSG00000026879	2	35256380	35307892	1	0	0	0	12	0	1	11	5	5	0	0		
ENSMUST00000139868						3	1	9	3	7	4	7	70	41	0	37		
ENSMUST00000139869	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139870	ENSMUSG00000032508	9	119335934	119341411	-1	3	2	4	81	0	0	0	0	0	0	0	F6SPW1	
ENSMUST00000139871						0	0	2	2	1	0	3	10	4	0	11		
ENSMUST00000139872						6	8	4	3	3	0	11	31	18	3	19		
ENSMUST00000139873						2	4	13	0	3	3	0	0	0	0	0		
ENSMUST00000139875						7	0	0	8	5	0	0	0	13	4	19		
ENSMUST00000139876	ENSMUSG00000028545	4	111415006	111460298	1	3	3	2	0	0	0	0	2	0	0	0	F6Q2G7	
ENSMUST00000139877						77	63	147	85	66	35	4	31	16	0	19		
ENSMUST00000139878						0	0	0	0	0	0	0	2	0	1	1		
ENSMUST00000139881						0	0	0	0	0	0	1	0	0	0	3		
ENSMUST00000139882						1	4	5	2	9	3	0	0	0	7	0		
ENSMUST00000139883						2	4	3	0	4	2	0	0	0	0	0		
ENSMUST00000139885	ENSMUSG00000052102	18	38327558	38339003	-1	1	2	1	39	0	2	0	0	4	2	15	D3Z0R5	
ENSMUST00000139886						2	8	2	0	4	4	69	530	187	22	199		
ENSMUST00000139887						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000139888	ENSMUSG00000037313	5	33658128	33678995	1	7	0	6	0	11	0	3	0	6	6	0	F7AGT6	
ENSMUST00000139889						0	5	35	0	15	16	0	0	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139890						1	1	2	8	0	0	0	0	0	0	0		
ENSMUST00000139892	ENSMUSG00000024593	18	57133090	57297467	1	10	4	28	3	14	11	0	0	0	0	0		
ENSMUST00000139893	ENSMUSG00000051790	11	69823122	69837784	-1	2	0	0	16	0	0	0	0	0	0	0	F6VE93	
ENSMUST00000139896						4	4	1	3	5	1	0	0	0	0	0		
ENSMUST00000139897						0	0	0	0	0	0	2	0	0	0	3		
ENSMUST00000139898						3	2	5	0	2	2	1	2	0	0	0		
ENSMUST00000139899						3	1	1	3	0	0	0	0	0	0	0		
ENSMUST00000139900						0	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000139901						21	17	25	36	26	17	8	44	20	3	16		
ENSMUST00000139902						0	0	32	5	0	0	58	54	0	11	0		
ENSMUST00000139903						4	0	2	0	7	0	0	2	2	0	0		
ENSMUST00000139904						0	0	7	3	0	4	0	14	11	1	15		
ENSMUST00000139905						2	0	8	2	10	0	0	0	0	0	0		
ENSMUST00000139906	ENSMUSG00000050541	11	43774606	43901210	-1	0	3	0	3	0	2	0	0	0	0	0	B1AU41	
ENSMUST00000139907						0	1	5	1	3	2	0	3	0	0	9		
ENSMUST00000139908						6	4	53	30	20	11	3	16	6	0	5		
ENSMUST00000139909						0	0	0	0	1	0	2	5	5	0	2		
ENSMUST00000139910						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000139911						2	3	5	27	3	4	2	0	10	0	7		
ENSMUST00000139913						2	1	2	4	4	2	0	0	0	0	2		
ENSMUST00000139914	ENSMUSG00000030309	6	148842492	148896237	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2D4	
ENSMUST00000139915						0	0	0	60	2	0	0	0	0	0	0		
ENSMUST00000139916						8	11	57	10	13	10	7	11	21	2	12		
ENSMUST00000139917	ENSMUSG00000033857	11	118476829	118489209	1	28	26	57	10	32	17	0	9	0	0	0	E9PY27	
ENSMUST00000139918						1	1	1	0	0	3	0	0	0	0	0		
ENSMUST00000139920						1	1	1	0	3	1	0	0	0	0	0		
ENSMUST00000139922						0	2	0	0	4	0	0	0	0	0	0		
ENSMUST00000139923						58	40	120	98	75	39	8	14	0	3	23		
ENSMUST00000139924	ENSMUSG00000057455	18	30973489	31317290	-1	1	1	5	0	2	0	0	1	0	0	0	F2Z432	
ENSMUST00000139925						27	21	62	1	23	14	7	35	22	2	23		
ENSMUST00000139926						0	0	0	0	0	0	0	0	8	10	1		
ENSMUST00000139928						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000139929	ENSMUSG00000027574	2	180934772	180954699	-1	0	0	8	0	0	0	0	0	0	3	0	F7B7M8	
ENSMUST00000139930						11	10	9	113	16	14	2	2	7	0	6		
ENSMUST00000139931						0	0	8	3	1	3	172	135	131	15	125		
ENSMUST00000139932						0	0	0	0	0	0	22	0	27	0	7		
ENSMUST00000139933						0	2	0	0	6	0	4	5	0	1	0		
ENSMUST00000139934	ENSMUSG00000020812	11	116671660	116675799	1	0	0	0	0	0	0	4	6	0	0	5	Q9D8U9	
ENSMUST00000139935						2	0	0	0	0	1	4	15	9	2	18		
ENSMUST00000139936						3	2	2	1	0	1	2	0	0	1	0		
ENSMUST00000139937	ENSMUSG00000026933	2	25926838	25983282	-1	0	0	0	82	0	0	0	0	0	0	0	V9GXT0	
ENSMUST00000139938						4	6	11	1	9	2	0	0	0	0	0		
ENSMUST00000139939						4	3	6	2	7	2	8	5	12	6	6		
ENSMUST00000139940	ENSMUSG00000020653	12	24651371	24662774	1	0	1	1	13	2	1	0	0	0	0	0	D3YZX6	
ENSMUST00000139942						1	1	0	0	3	0	0	0	2	0	3		
ENSMUST00000139943						0	1	0	0	2	0	0	5	2	0	0		
ENSMUST00000139944	ENSMUSG00000035093	2	125736986	125782870	-1	10	9	22	12	8	12	15	28	18	2	46	F6QQ13	
ENSMUST00000139945						1	0	5	3	4	0	0	3	0	2	7		
ENSMUST00000139946	ENSMUSG00000031575	8	25816191	25847694	-1	0	0	0	0	0	0	0	0	0	0	0	D6RI55	
ENSMUST00000139947						21	5	28	18	28	6	132	362	62	0	51		
ENSMUST00000139949						2	0	4	5	4	0	0	0	0	0	2		
ENSMUST00000139950						42	45	28	30	40	64	0	0	0	0	0		
ENSMUST00000139951	ENSMUSG00000028766	4	137741733	137796384	-1	2	2	4	6	7	3	0	0	0	0	0	E9Q7P8	
ENSMUST00000139952						0	0	0	0	0	1	40	102	75	3	27		
ENSMUST00000139953						39	14	24	436	76	41	0	11	8	3	2		
ENSMUST00000139954	ENSMUSG00000020818	11	116852440	116875635	1	0	0	0	16	1	0	108	175	0	0	0	E9PZJ5	
ENSMUST00000139955						7	12	11	8	0	0	3	0	19	0	7		
ENSMUST00000139956						0	5	0	0	3	3	182	17	93	30	127		
ENSMUST00000139957						3	1	7	3	0	0	0	2	0	0	0		
ENSMUST00000139958	ENSMUSG00000078789	11	75177643	75191241	-1	4	0	9	0	0	3	0	0	0	0	5	B1ARH1	
ENSMUST00000139959						0	0	0	0	0	0	74	797	188	255	413		
ENSMUST00000139960	ENSMUSG00000046897	15	102203648	102215606	1	0	0	0	0	0	0	18	9	39	0	15	D3Z6P2	
ENSMUST00000139961						1	0	0	13	9	4	0	0	0	0	0		
ENSMUST00000139962	ENSMUSG00000028582	4	108619940	108634123	1	8	3	21	3	14	0	0	4	0	0	5	H3BKI0	
ENSMUST00000139963						5	5	7	10	6	7	0	4	4	1	9		
ENSMUST00000139964	ENSMUSG00000023110	14	54507187	54517525	-1	4	3	0	0	2	0	0	0	0	0	0	F6QQQ6	
ENSMUST00000139965	ENSMUSG00000001986	X	41400854	41678601	1	17	23	58	0	0	8	18	0	0	5	0	F2Z488	
ENSMUST00000139966	ENSMUSG00000054823	8	25601601	25719667	1	2	0	0	5	6	0	105	14	420	24	449	D3Z197	
ENSMUST00000139967						3	3	11	3	0	0	2	1	2	0	0		
ENSMUST00000139968						1	2	19	56	2	3	0	0	0	0	0		
ENSMUST00000139969	ENSMUSG00000080316	17	17830719	17843009	1	0	3	3	0	5	2	3	7	3	12	2	D3Z1S3	
ENSMUST00000139970						9	8	12	16	17	6	4	1	9	1	15		
ENSMUST00000139971						20	11	36	20	15	7	6	27	7	4	24		
ENSMUST00000139972	ENSMUSG00000036585	18	38838673	38929404	-1	1	0	0	2	1	0	0	0	0	0	0	D3Z6E2	
ENSMUST00000139974						2	0	7	2	2	0	0	0	0	0	0		
ENSMUST00000139975						3	1	2	0	4	4	1	2	0	0	3		
ENSMUST00000139976	ENSMUSG00000029055	4	154983115	155056784	-1	0	0	21	13	8	3	0	0	0	0	0	F7C3A0	
ENSMUST00000139977						0	0	0	30	0	0	0	2	0	0	0		
ENSMUST00000139978						0	4	0	0	1	0	0	0	0	0	0		
ENSMUST00000139979	ENSMUSG00000040250	6	146549632	146577835	-1	0	0	0	0	0	1	55	360	77	81	37	F7BP94	
ENSMUST00000139980						1	0	2	36	6	0	0	0	0	0	0		
ENSMUST00000139981						3	0	3	4	8	1	0	0	1	0	0		
ENSMUST00000139982						11	6	16	15	7	7	1878	33877	4950	8302	7625		
ENSMUST00000139983	ENSMUSG00000029730	5	138164583	138172422	-1	0	0	0	0	0	0	2	0	11	0	11	D3Z0J6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000139984						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000139985	ENSMUSG00000022194	14	54892500	54898169	1	0	2	4	19	2	0	7	14	5	0	15	D3Z055	
ENSMUST00000139986	ENSMUSG00000026418	1	135779434	135810989	1	0	0	0	0	0	0	0	0	0	0	0	D3YUN3	
ENSMUST00000139988						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000139989	ENSMUSG00000022723	16	59490775	59555752	-1	29	30	176	47	25	19	2	3	7	0	3	D3Z4M9	
ENSMUST00000139990						21	18	58	6	7	12	12	2	0	0	11		
ENSMUST00000139991						14	8	27	68	17	11	0	0	0	0	5		
ENSMUST00000139992						2	2	0	0	1	0	34	87	26	279	36		
ENSMUST00000139993						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000139994						0	4	16	0	2	5	0	0	4	0	3		
ENSMUST00000139995						0	2	2	2	0	0	0	0	5	0	0		
ENSMUST00000139996						0	0	2	0	0	0	1	1	4	0	1		
ENSMUST00000139997						13	8	37	20	30	11	118	686	215	14	500		
ENSMUST00000139998						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000139999						0	0	7	2	0	2	0	0	0	7	0		
ENSMUST00000140001						9	10	8	10	10	8	3	14	19	19	43		
ENSMUST00000140002	ENSMUSG00000021892	14	31359880	31436078	-1	7	1	0	201	4	4	0	5	4	0	118		Q9Z131
ENSMUST00000140004						52	53	286	83	62	35	1	7	1	0	3		
ENSMUST00000140005						6	4	0	10	6	5	0	5	7	0	0		
ENSMUST00000140006						4	4	0	1	5	2	0	0	0	0	0		
ENSMUST00000140007						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000140008	ENSMUSG00000048232	4	45034247	45084604	-1	0	0	0	0	3	8	0	0	0	0	0	F6Q7Q7	
ENSMUST00000140011						2	0	5	7	0	0	111	362	60	29	42		
ENSMUST00000140012	ENSMUSG00000050751	8	124369049	124439658	-1	0	0	0	128	19	9	0	0	8	0	0	D3YZI9	
ENSMUST00000140013						13	9	20	48	10	9	0	3	2	0	4		
ENSMUST00000140014						16	6	27	150	11	7	41	39	144	0	128		
ENSMUST00000140015						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140016						6	8	10	21	2	4	0	0	0	0	0		
ENSMUST00000140017						0	0	0	0	0	0	11	0	7	0	0		
ENSMUST00000140018						2	0	4	11	11	1	0	3	0	0	0		
ENSMUST00000140019						1	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000140020	ENSMUSG00000026142	1	82316452	82445366	1	17	9	30	0	39	12	0	0	0	0	0		Q8BHC7
ENSMUST00000140022						2	7	0	6	10	1	5	15	3	0	8		
ENSMUST00000140024						106	101	74	92	100	51	16	69	30	7	39		
ENSMUST00000140025						16	11	18	8	18	0	0	0	0	0	7		
ENSMUST00000140026	ENSMUSG00000031725	8	93256236	93279747	-1	0	2	0	1	2	2	0	0	0	0	0	D6RHA4	
ENSMUST00000140027	ENSMUSG00000020397	11	46436925	46442721	1	0	0	0	0	0	0	0	0	0	0	0	F2Z3Z0	
ENSMUST00000140029						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000140030	ENSMUSG00000014592	4	150917322	151861876	-1	0	13	18	0	0	4	4	3	4	0	5	Z4YMK8	
ENSMUST00000140031						5	0	1	0	5	1	0	0	0	0	0		
ENSMUST00000140032						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140033						0	3	0	0	0	3	0	0	0	0	0		
ENSMUST00000140034						0	3	1	9	1	0	0	0	0	0	0		
ENSMUST00000140035						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000140036						3	0	0	0	0	1	0	0	0	22	0		
ENSMUST00000140037						5	2	6	5	7	4	73	186	115	8	192		
ENSMUST00000140038						8	7	24	6	10	6	2	0	0	0	1		
ENSMUST00000140039						0	0	0	0	0	0	222	282	156	0	124		
ENSMUST00000140040						4	2	5	1	5	5	0	2	1	0	0		
ENSMUST00000140042	ENSMUSG00000021338	13	24012344	24280795	-1	3	1	0	30	6	0	0	0	0	0	0	E9Q4H6	
ENSMUST00000140043						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000140045						0	1	0	0	0	2	8	0	13	16	31		
ENSMUST00000140046						29	27	44	301	29	18	2	3	7	0	7		
ENSMUST00000140047						0	0	2	78	3	3	0	0	0	0	0		
ENSMUST00000140048						36	11	44	19	23	13	9	0	19	5	9		
ENSMUST00000140049	ENSMUSG00000029003	4	148130384	148145699	1	0	0	5	7	0	0	11	5	3	0	0	A2A7G5	
ENSMUST00000140050	ENSMUSG00000028809	4	135320484	135353321	-1	6	0	32	0	3	5	0	0	12	31	0	F6UK16	
ENSMUST00000140051						5	2	1	0	1	4	0	3	3	0	3		
ENSMUST00000140053						0	2	0	3	0	4	25	0	0	0	0		
ENSMUST00000140054	ENSMUSG00000090019	6	48739054	48743795	1	1	0	1	1	0	0	2	5	0	5	2	D3YX11	
ENSMUST00000140056						0	0	0	0	0	0	81	371	109	160	155		
ENSMUST00000140057	ENSMUSG00000028771	5	20986645	21055911	-1	2	0	0	0	1	0	6	73	32	5	43	F6Z0X5	
ENSMUST00000140058	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	0	5	2	0	0	0	0	0	D6RG97	
ENSMUST00000140059	ENSMUSG00000047767	7	101289392	101302251	-1	0	1	0	1	0	0	0	3	0	0	0	F6QTU9	
ENSMUST00000140060						3	0	2	0	3	2	0	8	6	0	10		
ENSMUST00000140061	ENSMUSG00000024483	18	36559987	36665917	1	4	9	36	0	10	4	114	835	246	150	299	F6RUI8	
ENSMUST00000140062						10	8	4	0	9	4	0	0	0	0	0		
ENSMUST00000140063						0	0	0	14	0	0	8	15	0	6	0		
ENSMUST00000140064						0	1	2	43	0	0	0	0	0	0	0		
ENSMUST00000140065						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000140066						15	12	13	12	17	12	0	0	0	0	0		
ENSMUST00000140067						7	4	0	1	3	7	0	0	6	10	0		
ENSMUST00000140068	ENSMUSG00000001827	7	101858331	101870788	-1	4	0	5	13	3	2	0	1	0	0	0	E9PXL5	
ENSMUST00000140070	ENSMUSG00000009376	6	17463800	17573980	1	0	0	0	64	4	0	1	0	0	0	0	D3YVY2	
ENSMUST00000140071						29	16	84	37	20	12	0	1	1	0	2		
ENSMUST00000140072						6	1	6	4	12	5	0	0	0	0	0		
ENSMUST00000140073						1	4	8	5	3	2	10	22	23	1	29		
ENSMUST00000140074						3	3	4	50	4	0	6	7	3	0	0		
ENSMUST00000140075	ENSMUSG00000026858	2	30364233	30385521	1	10	10	20	5	17	4	0	0	0	0	0		Q8BK03
ENSMUST00000140076	ENSMUSG00000029246	5	76913249	76951578	-1	0	0	0	7	0	11	9	66	0	21	18	Q8CIH9	
ENSMUST00000140077	ENSMUSG00000030826	7	45570153	45589710	1	0	1	4	1	2	0	0	0	0	0	0	D3Z3D7	
ENSMUST00000140078						0	0	6	0	0	1	0	10	6	2	2		
ENSMUST00000140079	ENSMUSG00000033740	1	6487231	6860940	1	16	19	0	0	0	0	0	0	0	0	0	Q148A0	Q80TY4
ENSMUST00000140081						1	0	9	3	0	0	0	2	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140082						2	0	1	1	0	0	0	0	5	0	2		
ENSMUST00000140083						0	0	0	0	0	0	8	18	7	13	13		
ENSMUST00000140084	ENSMUSG00000029228	5	74592447	74702912	-1	0	1	5	8	0	0	0	0	2	0	0	F7AT68	
ENSMUST00000140085						7	0	20	66	23	8	0	0	0	0	2		
ENSMUST00000140086						0	0	0	0	0	0	9	9	39	1	0		
ENSMUST00000140088	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	2	0	0	0	0	0	F6ZWT0	
ENSMUST00000140089	ENSMUSG00000056300	4	146502027	146539395	1	11	6	28	6	3	5	0	0	0	0	0	A2A8V6	
ENSMUST00000140090						5	2	3	15	3	2	0	0	0	0	0		
ENSMUST00000140091	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	2	0	0	0	0	0	0	0	Q8BUJ6	
ENSMUST00000140092	ENSMUSG00000054545	1	88134809	88218997	1	0	0	0	0	0	0	0	119	0	8	0	D3YZE6	
ENSMUST00000140093						3	2	0	3	0	2	0	3	0	0	4		
ENSMUST00000140094						5	2	5	2	1	0	0	0	0	1	0		
ENSMUST00000140095	ENSMUSG00000079451	5	86485876	86518600	-1	0	0	0	0	0	0	0	0	0	0	0	D3YZU3	
ENSMUST00000140096						26	17	35	3	26	0	47	70	33	15	33		
ENSMUST00000140097						0	1	2	0	0	3	0	66	6	12	8		
ENSMUST00000140098						1	1	7	0	2	0	1	17	11	1	22		
ENSMUST00000140099						1	1	1	7	3	0	0	7	32	0	7		
ENSMUST00000140100						0	0	1	4	4	1	0	0	0	0	0		
ENSMUST00000140102						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000140103	ENSMUSG00000000823	2	181582103	181592803	-1	2	0	2	6	4	0	1	1	0	0	2	B7ZCR5	
ENSMUST00000140106						35	31	97	49	53	28	0	2	2	0	5		
ENSMUST00000140107	ENSMUSG00000038215	8	56531522	56551047	-1	3	0	0	0	3	0	3	0	5	4	0	D3YVD2	
ENSMUST00000140108	ENSMUSG00000039298	4	70216856	70410443	-1	0	0	0	81	0	0	0	0	0	0	0	F6R2K5	
ENSMUST00000140109	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	3	0	3	4	0	0	0	18	0	F6R587	
ENSMUST00000140110						30	34	138	51	33	19	0	0	0	0	0		
ENSMUST00000140111						807	654	1871	2321	907	474	84	279	188	110	290		
ENSMUST00000140112						6	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000140114						4	0	0	29	3	2	12	25	19	21	7		
ENSMUST00000140115						4	1	5	0	5	0	0	0	0	0	0		
ENSMUST00000140117						0	0	3	0	3	3	0	0	0	0	0		
ENSMUST00000140118	ENSMUSG00000059974	9	28994750	29963141	-1	3	0	0	0	0	0	0	0	0	0	0	F6Z2M6	
ENSMUST00000140119						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000140120						5	1	5	11	8	1	1	0	0	0	0		
ENSMUST00000140121	ENSMUSG00000040433	9	96682770	96752831	-1	8	2	27	129	16	7	0	3	12	4	0	Q8BW24	
ENSMUST00000140122	ENSMUSG00000020286	11	23516203	23521155	-1	2	0	5	3	3	6	0	0	1	1	0	A2AF84	
ENSMUST00000140123						2	1	5	11	5	4	3	5	2	0	2		
ENSMUST00000140124						1	0	0	50	5	3	0	0	0	0	0		
ENSMUST00000140125						161	128	455	157	129	53	25	67	32	5	36		
ENSMUST00000140126						6	6	19	8	14	4	0	0	1	0	1		
ENSMUST00000140127	ENSMUSG00000003271	7	45729983	45759612	-1	0	0	0	0	1	0	0	0	0	0	0	D3Z2X1	
ENSMUST00000140128						2	0	1	0	2	3	0	0	2	0	0		
ENSMUST00000140129						2	0	0	2	8	2	0	3	0	0	6		
ENSMUST00000140130						0	0	4	0	0	0	0	10	24	0	43		
ENSMUST00000140131	ENSMUSG00000030330	6	125039760	125049265	1	2	0	12	2	3	3	198	372	300	148	264		Q8C0D7
ENSMUST00000140134						88	94	226	76	76	42	2	20	6	6	8		
ENSMUST00000140135	ENSMUSG00000046110	2	121439059	121456781	-1	0	0	0	0	0	0	0	0	0	0	0	F6ZBF6	
ENSMUST00000140136	ENSMUSG00000035469	14	59201209	59237265	1	0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000140137						6	3	7	72	12	14	0	0	0	0	0		
ENSMUST00000140138						2	0	8	28	7	1	0	0	1	0	2		
ENSMUST00000140139	ENSMUSG00000029713	5	137528127	137533510	-1	2	1	7	166	4	5	198	489	314	55	305	D3Z1T4	
ENSMUST00000140140	ENSMUSG00000048078	7	96171246	96911093	1	0	0	0	40	0	0	0	0	0	0	0		
ENSMUST00000140141	ENSMUSG00000025089	19	58235604	58455909	-1	3	0	0	12	10	0	0	0	0	0	0	D6RDD4	
ENSMUST00000140142	ENSMUSG00000047547	13	54592401	54611344	-1	0	0	0	0	0	0	24	0	0	0	0	F7BHJ0	
ENSMUST00000140143						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140144						162	97	129	5457	383	302	0	0	4	0	0		
ENSMUST00000140145						1	1	0	58	2	0	0	0	0	0	0		
ENSMUST00000140146						7	4	23	58	15	3	0	0	0	0	0		
ENSMUST00000140147						12	4	24	47	16	14	4	4	0	2	0		
ENSMUST00000140149						0	2	1	0	8	0	0	0	0	0	0		
ENSMUST00000140150						1	4	1	1	2	1	1	2	0	0	10		
ENSMUST00000140151						15	4	16	9	15	3	0	0	0	0	0		
ENSMUST00000140152						0	0	4	4	0	0	3	0	2	1	4		
ENSMUST00000140153						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000140154	ENSMUSG00000008305	4	72117142	72200919	-1	1	2	9	3	0	5	0	0	0	0	0	Q5SQA7	
ENSMUST00000140155						4	15	0	0	3	1	2186	3768	1152	5567	907		
ENSMUST00000140156						0	2	6	2	5	2	0	0	0	0	0		
ENSMUST00000140157						0	0	0	0	0	0	7	0	20	3	0		
ENSMUST00000140158						1	5	9	0	1	0	0	0	4	0	5		
ENSMUST00000140159						3	4	2	3	2	0	21	20	0	0	15		
ENSMUST00000140160						0	0	0	18	0	0	1	0	0	0	0		
ENSMUST00000140162						56	70	149	81	58	40	10	10	24	6	38		
ENSMUST00000140163						0	0	0	0	0	0	1	0	2	3	1		
ENSMUST00000140164	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TJR5	Q8CBW3
ENSMUST00000140165						5	0	3	155	11	6	0	0	0	0	0		
ENSMUST00000140166						2	3	0	6	4	3	0	0	0	0	0		
ENSMUST00000140167	ENSMUSG00000020805	11	72241994	72267222	-1	0	1	0	10	0	0	0	0	0	0	0	Q5NBV1	
ENSMUST00000140168						9	5	1	8	7	1	0	0	0	0	1		
ENSMUST00000140169	ENSMUSG00000053552	2	130295169	130370481	1	0	0	0	0	0	0	0	0	0	0	1		Q8K4J2
ENSMUST00000140170						1	0	2	3	0	1	15	20	28	0	62		
ENSMUST00000140171						99	116	215	0	112	34	0	450	0	45	16		
ENSMUST00000140172						0	0	0	36	0	0	0	0	0	0	7		
ENSMUST00000140173						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140174	ENSMUSG00000020752	11	115892595	115933477	-1	0	10	25	0	8	0	67	68	21	0	31	J3QMY1	
ENSMUST00000140175						0	0	0	0	0	0	0	0	0	15	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140177						0	1	5	3	2	3	2	17	3	2	12		
ENSMUST00000140178	ENSMUSG00000047098	14	55591708	55603693	1	11	7	10	0	8	8	508	806	97	43	236	F6XVP7	
ENSMUST00000140179	ENSMUSG00000029192	5	36490604	36593276	-1	3	0	11	1	3	2	0	0	0	0	0	D3Z400	
ENSMUST00000140180						2	0	6	2	4	1	0	0	0	0	7		
ENSMUST00000140181						2	0	15	90	4	1	6	6	12	2	22		
ENSMUST00000140182						18	0	22	0	47	4	0	0	0	0	0		
ENSMUST00000140183	ENSMUSG00000027243	2	91710852	91721545	1	0	0	0	0	1	0	0	0	6	0	0	B7ZCF7	
ENSMUST00000140184						0	0	0	63	1	3	0	14	29	5	12		
ENSMUST00000140186						0	0	0	1	0	0	0	0	6	7	0		
ENSMUST00000140187						35	39	71	36	48	14	37	185	65	10	68		
ENSMUST00000140188						14	2	43	28	16	8	0	0	0	0	0		
ENSMUST00000140189						0	2	1	1	3	0	2	0	0	0	4		
ENSMUST00000140190	ENSMUSG00000025946	1	65282056	65389244	1	4	0	0	2	6	1	0	0	0	0	0	D3YV95	
ENSMUST00000140191						0	2	7	5	3	0	0	0	1	1	0		
ENSMUST00000140192	ENSMUSG00000071322	17	7324646	7345974	1	0	0	0	0	0	0	0	0	0	0	0	L7N265	
ENSMUST00000140193						68	81	161	55	43	25	10	37	8	3	14		
ENSMUST00000140194	ENSMUSG00000032740	11	29373658	29510808	1	0	0	0	0	0	0	0	0	6	0	7	Z4YLN8	
ENSMUST00000140197	ENSMUSG00000038290	11	74925823	75164448	1	0	0	0	2	2	0	7	0	13	0	0	B1ARG9	
ENSMUST00000140198						1	0	0	4	3	0	0	4	0	0	0		
ENSMUST00000140199						1	0	1	3	3	0	39	335	63	57	63		
ENSMUST00000140201	ENSMUSG00000026885	2	35751241	35979913	-1	5	0	0	0	1	0	0	0	0	0	0	E0CY35	
ENSMUST00000140202						6	10	9	3	9	2	0	0	0	0	0		
ENSMUST00000140204						0	1	0	1	0	0	5	10	9	30	8		
ENSMUST00000140205	ENSMUSG00000054693	9	70678997	70780229	1	4	0	16	47	1	4	0	0	1284	90	536	E9PYF2	
ENSMUST00000140206	ENSMUSG00000022721	16	18248679	18254772	1	1	2	2	4	2	4	2	30	5	0	0		Q8BNV1
ENSMUST00000140207	ENSMUSG00000025269	X	150519519	150589868	-1	0	0	0	0	0	0	0	0	0	0	0	F7CPY7	
ENSMUST00000140208						1	2	3	6	3	3	1	1	0	1	0		
ENSMUST00000140209						2	2	0	3	0	3	0	0	0	0	0		
ENSMUST00000140210						0	0	4	9	0	2	0	3	1	1	1		
ENSMUST00000140211	ENSMUSG00000029790	6	30653457	30693749	-1	5	15	0	0	7	5	0	0	0	0	4	S4R2L7	
ENSMUST00000140212	ENSMUSG00000003573	8	70282827	70294361	1	0	6	13	10	8	0	0	0	0	0	0		Q99JP6
ENSMUST00000140213						0	1	0	2	0	2	47	203	67	17	89		
ENSMUST00000140214	ENSMUSG00000036853	3	146117450	146141806	1	0	5	12	29	4	0	0	0	0	1	0	D3YZE2	
ENSMUST00000140215						2	3	0	1	0	1	0	0	0	0	0		
ENSMUST00000140216	ENSMUSG00000078923	2	167607638	167632095	-1	0	0	0	0	0	0	0	0	0	13	0	B7ZBY6	
ENSMUST00000140217						0	0	0	21	0	0	1	0	0	0	0		
ENSMUST00000140218						0	0	0	0	0	1	5	0	1	0	0		
ENSMUST00000140219	ENSMUSG00000006345	10	75561604	75586200	1	1	0	0	0	2	3	0	0	0	0	0	D3YXV6	
ENSMUST00000140220						1	0	1	0	0	0	0	0	0	0	1		
ENSMUST00000140221						13	8	11	2	0	4	0	21	7	84	46		
ENSMUST00000140222	ENSMUSG00000062609	16	95257558	95300260	1	0	0	4	7	2	0	0	0	0	0	0	D3YVH1	
ENSMUST00000140223						2	3	11	0	2	0	17	0	0	0	0		
ENSMUST00000140224	ENSMUSG00000027297	2	119751320	119760431	-1	0	0	0	1	0	0	0	0	0	0	0	F6V2R5	
ENSMUST00000140225						1	2	2	0	4	0	0	0	0	0	0		
ENSMUST00000140226						16	6	65	106	24	17	6	38	5	11	12		
ENSMUST00000140227						0	0	0	1	1	4	20	84	0	44	25		
ENSMUST00000140228						22	4	38	151	31	21	0	0	0	2	0		
ENSMUST00000140229						20	12	0	6	9	4	0	124	0	16	16		
ENSMUST00000140230	ENSMUSG00000036591	2	20847919	20968881	-1	0	3	0	0	0	1	0	0	0	0	0	A2BHQ2	
ENSMUST00000140231						14	7	7	3	12	6	0	1	0	0	1		
ENSMUST00000140232						9	4	4	5	5	6	0	0	0	0	0		
ENSMUST00000140233						7	2	6	1	13	2	0	2	0	0	0		
ENSMUST00000140234						31	31	59	34	58	20	2	3	3	0	3		
ENSMUST00000140235						4	4	51	8	8	8	0	0	0	0	0		
ENSMUST00000140236						0	0	0	0	3	0	59	125	21	95	58		
ENSMUST00000140237						4	0	0	1	3	1	2	5	4	1	14		
ENSMUST00000140239	ENSMUSG00000087408	8	70315775	70331592	1	18	7	24	0	22	0	0	0	1	0	2	A2RT05	P27545
ENSMUST00000140240						8	4	11	2	3	6	0	0	1	0	0		
ENSMUST00000140242	ENSMUSG00000034543	11	3649494	3690477	1	0	1	0	0	0	3	0	0	0	0	0	Q5QNQ8	
ENSMUST00000140243	ENSMUSG00000002781	7	45896941	45917413	1	0	0	0	0	0	0	9	2	0	3	0	F6ZAS5	
ENSMUST00000140244						3	2	3	0	0	0	1	7	0	1	0		
ENSMUST00000140245						2	1	5	4	3	1	0	0	0	0	0		
ENSMUST00000140246						4	0	3	1	0	2	11	8	23	0	47		
ENSMUST00000140247						16	24	42	94	41	0	18	35	0	42	57		
ENSMUST00000140248						2	1	4	0	2	1	0	0	5	0	2		
ENSMUST00000140249						0	1	2	0	0	0	0	51	0	0	0		
ENSMUST00000140250						5	8	21	44	0	4	0	0	0	0	0		
ENSMUST00000140251	ENSMUSG00000022010	14	76414961	76507765	1	4	0	0	0	0	3	0	0	4	31	4	H3BLI9	
ENSMUST00000140252	ENSMUSG00000029790	6	30653457	30693749	-1	1	1	5	2	1	1	0	0	0	0	0		
ENSMUST00000140254						25	28	33	37	35	24	79	578	144	214	221		
ENSMUST00000140255	ENSMUSG00000078619	11	106263179	106272972	-1	0	0	0	0	0	0	199	29	24	13	101	G3UXC0	
ENSMUST00000140256						7	2	10	4	13	12	1	0	0	0	6		
ENSMUST00000140257						2	0	1	0	3	0	20	22	35	5	30		
ENSMUST00000140258						2	2	2	0	0	1	0	15	2	0	0		
ENSMUST00000140259						12	0	26	26	13	12	0	0	0	0	0		
ENSMUST00000140260						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000140261						2	0	11	162	9	1	0	0	0	0	5		
ENSMUST00000140262	ENSMUSG00000029344	5	112276691	112315361	1	0	0	5	0	5	7	16	19	13	0	15	F7BM44	
ENSMUST00000140264	ENSMUSG00000026113	1	37299865	37410736	1	6	6	6	34	10	7	97	31	340	4	214	Q3UEQ1	
ENSMUST00000140265	ENSMUSG00000033543	9	70012550	70022866	1	0	0	0	0	0	0	16	117	10	7	0	D6RIQ7	
ENSMUST00000140266						5	1	3	3	3	1	2	15	2	0	7		
ENSMUST00000140268						4	6	14	14	5	4	4	20	8	0	8		
ENSMUST00000140269						3	3	11	16	9	2	4	30	5	0	13		
ENSMUST00000140270						3	0	1	0	3	3	0	0	0	0	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140272						0	0	1	2	2	0	0	6	0	0	1		
ENSMUST00000140274	ENSMUSG00000026692	1	162793188	162813972	-1	3	4	4	4	0	0	0	0	0	0	0	D3YUF0	
ENSMUST00000140276						0	0	0	3	2	2	0	0	0	0	10		
ENSMUST00000140277						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000140278	ENSMUSG00000006191	13	29191746	29855674	-1	9	3	4	7	7	3	0	0	0	0	0		Q91WE6
ENSMUST00000140279						26	16	38	35	23	13	18	56	34	9	66		
ENSMUST00000140280						8	5	43	9	13	9	2	74	11	2	36		
ENSMUST00000140281						1	3	0	11	1	0	6	8	13	19	7		
ENSMUST00000140282						5	0	5	1	2	3	0	15	0	0	0		
ENSMUST00000140283						0	0	0	0	0	0	12	0	8	0	21		
ENSMUST00000140284						2	1	0	0	3	2	0	5	0	0	0		
ENSMUST00000140285						13	6	12	8	10	7	0	3	0	0	1		
ENSMUST00000140286						0	0	0	0	0	0	71	51	173	75	190		
ENSMUST00000140287	ENSMUSG00000033021	1	75435930	75443179	1	0	0	0	3	0	0	0	7	0	0	0	D3Z2L8	
ENSMUST00000140288	ENSMUSG00000063600	3	29082023	29691209	1	0	3	0	0	0	0	0	0	0	0	0	F6ZMV2	
ENSMUST00000140289						3	1	7	1	5	2	0	0	0	0	0		
ENSMUST00000140291						0	0	0	0	0	0	218	155	82	13	27		
ENSMUST00000140292	ENSMUSG00000024426	17	35897595	35910075	-1	0	3	2	16	3	2	0	12	6	0	3	F6RPX5	
ENSMUST00000140293	ENSMUSG00000041975	2	70964561	71055583	-1	0	2	4	2	3	0	0	2	2	0	0	F6W103	
ENSMUST00000140294						3	0	2	5	3	0	0	2	0	0	0		
ENSMUST00000140295	ENSMUSG00000025909	1	8361475	9299878	-1	0	8	0	4	8	0	0	0	0	0	0	Q8BNW6	
ENSMUST00000140296						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000140297						1	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000140299	ENSMUSG00000034620	10	122078114	122097371	-1	12	14	20	73	16	10	3	3	10	13	10		Q8VDX6
ENSMUST00000140300	ENSMUSG00000078218	X	4037674	4039616	1	6	0	0	0	17	0	0	0	0	0	0	A2CGC2	
ENSMUST00000140301	ENSMUSG00000033352	11	65688243	65788297	-1	0	0	0	24	0	0	0	0	0	0	0	M0QWR0	
ENSMUST00000140302	ENSMUSG00000025909	1	8361475	9299878	-1	15	0	5	114	12	9	0	0	0	0	0	D6REU8	
ENSMUST00000140303	ENSMUSG00000026979	2	24367580	24414954	1	0	0	2	0	3	1	0	4	0	0	2	A0A0A6YXQ2	
ENSMUST00000140304						12	5	10	12	13	7	0	6	11	0	22		
ENSMUST00000140305	ENSMUSG00000033543	9	70012550	70022866	1	0	0	0	0	0	0	11	18	11	7	9	D3Z7S8	
ENSMUST00000140306	ENSMUSG00000022750	16	17759618	17793382	1	0	0	0	0	0	0	4	0	0	0	0	D3Z7N9	
ENSMUST00000140308						0	1	0	6	0	0	0	0	0	0	2		
ENSMUST00000140309						2	1	3	1	0	0	0	0	0	0	0		
ENSMUST00000140310						0	1	0	1	1	0	3	5	3	2	7		
ENSMUST00000140311						0	5	1	0	0	0	0	0	0	0	2		
ENSMUST00000140312	ENSMUSG00000022961	16	91647506	91679221	1	0	0	8	0	0	9	1201	1667	2763	134	3497	H9KV15	
ENSMUST00000140313	ENSMUSG00000002617	17	23173869	23193252	-1	0	0	0	0	0	0	0	0	0	0	0	G3UVW7	
ENSMUST00000140314						0	2	14	2	13	3	3	65	4	0	12		
ENSMUST00000140315	ENSMUSG00000028708	4	115839198	115879250	1	3	1	5	3	2	0	9	9	10	0	16	F7B478	
ENSMUST00000140316	ENSMUSG00000038236	6	52214491	52221854	-1	3	1	2	64	5	1	1	1	0	1	0	S4R2U5	
ENSMUST00000140317						2	2	0	0	1	1	0	12	0	0	13		
ENSMUST00000140318						133	118	340	126	169	79	9	54	14	9	41		
ENSMUST00000140322						7	9	19	23	12	5	94	244	147	41	114		
ENSMUST00000140323	ENSMUSG00000039850	11	119491347	119511437	1	0	0	0	0	0	0	0	0	2	6	8	F6XV41	
ENSMUST00000140324	ENSMUSG00000042385	13	113171608	113225908	-1	0	2	3	0	0	0	1	5	0	2	0	D6RE36	
ENSMUST00000140325						2	1	3	5	3	1	0	1	0	0	1		
ENSMUST00000140326	ENSMUSG00000038060	9	119102478	119148246	1	39	23	27	119	47	24	0	0	0	0	1	D3Z6E8	
ENSMUST00000140327	ENSMUSG00000021221	12	83213745	83487716	-1	1	0	0	1	2	2	0	0	0	0	1	B8JJH9	
ENSMUST00000140328						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000140329	ENSMUSG00000032754	5	120511168	120534024	1	2	0	1	0	0	0	0	0	0	0	0	D3Z5E7	
ENSMUST00000140330						2	1	4	1	3	0	5	12	1	6	2		
ENSMUST00000140331	ENSMUSG00000005774	3	94954075	94961561	1	0	0	0	0	0	0	0	0	0	0	0	D6RDE5	
ENSMUST00000140332	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z0B6	
ENSMUST00000140333						2	1	0	23	0	0	0	0	0	0	3		
ENSMUST00000140334	ENSMUSG00000040044	4	34570796	34614944	-1	0	0	0	0	0	0	0	0	0	0	0	A2AT40	
ENSMUST00000140335						2	0	4	3	0	0	0	0	0	0	1		
ENSMUST00000140336						2	2	1	3	5	0	0	30	10	4	16		
ENSMUST00000140337						18	8	36	4	26	7	0	86	0	0	0		
ENSMUST00000140338						1	1	0	0	0	0	2	41	2	1	3		
ENSMUST00000140339						6	7	25	9	11	5	178	150	314	16	724		
ENSMUST00000140340						9	5	14	3	10	5	0	1	0	3	0		
ENSMUST00000140341	ENSMUSG00000028309	4	49632006	49656887	1	0	0	0	0	0	0	0	0	0	0	4	A2AIR0	
ENSMUST00000140342						0	2	18	4	5	1	0	0	0	0	0		
ENSMUST00000140343						4	2	0	2	0	1	1	2	1	0	4		
ENSMUST00000140344	ENSMUSG00000000214	7	142892752	142931128	-1	3	11	13	5	4	4	0	0	0	0	0	D3Z0B1	
ENSMUST00000140345	ENSMUSG00000054708	10	81628540	81647610	1	0	0	3	0	0	0	0	0	0	2	0	D3YY05	
ENSMUST00000140346	ENSMUSG00000067714	6	125067920	125082472	1	5	4	3	0	3	0	0	0	0	0	4	F6S365	
ENSMUST00000140347						1	0	3	0	4	0	7	4	5	1	14		
ENSMUST00000140348	ENSMUSG00000005625	3	95032694	95042614	-1	0	0	0	0	4	2	0	0	0	0	26	F7AI87	
ENSMUST00000140349	ENSMUSG00000056962	11	116837432	116843449	-1	0	0	0	0	0	0	0	0	33	35	0	F6VRF7	
ENSMUST00000140350						62	41	89	341	59	48	23	93	70	7	90		
ENSMUST00000140351						5	8	21	41	9	2	0	0	0	0	0		
ENSMUST00000140352	ENSMUSG00000029352	5	113075839	113081584	-1	0	0	0	2	0	1	0	0	0	0	0	D3Z1U1	
ENSMUST00000140354						16	8	7	10	10	9	5	6	16	0	30		
ENSMUST00000140355						0	0	0	0	0	0	0	0	68	0	116		
ENSMUST00000140356						5	3	11	2	4	4	0	0	0	0	0		
ENSMUST00000140357						6	1	9	5	8	2	0	1	0	0	0		
ENSMUST00000140358						0	7	12	27	16	0	0	0	0	0	0		
ENSMUST00000140359						0	3	2	46	2	0	0	0	0	0	0		
ENSMUST00000140360						136	68	205	261	145	63	9	49	10	1	23		
ENSMUST00000140361						2	2	5	0	2	0	0	0	0	0	0		
ENSMUST00000140362	ENSMUSG00000018362	11	106988629	106999541	-1	0	0	0	0	0	0	4	0	0	0	0	A6PW68	
ENSMUST00000140363						8	0	0	4	0	4	5	76	11	3	35		
ENSMUST00000140364	ENSMUSG00000046947	6	39573873	39588769	1	20	9	23	273	41	25	23	62	13	19	23		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140365						0	1	0	0	0	6	2	2	0	0	0		
ENSMUST00000140366						0	0	0	0	0	0	0	6	17	0	1		
ENSMUST00000140367	ENSMUSG00000004070	16	4726361	4766742	1	0	0	0	13	0	0	0	0	0	3	0	D3YXN4	
ENSMUST00000140368						6	5	9	2	6	4	0	4	1	0	8		
ENSMUST00000140369						30	15	28	23	33	13	10	31	15	7	13		
ENSMUST00000140370						51	40	49	52	72	31	3	38	19	14	50		
ENSMUST00000140372	ENSMUSG00000056938	11	103101682	103112200	1	0	0	1	0	0	0	0	5	26	2	0	B0QZY4	
ENSMUST00000140373						10	11	7	8	16	4	0	0	0	0	9		
ENSMUST00000140374	ENSMUSG00000092252	5	114809036	114823460	-1	1	0	5	0	0	0	0	0	10	0	4	D3Z4G5	
ENSMUST00000140375	ENSMUSG00000032309	9	55208925	55224433	1	21	20	29	16	0	0	0	17	1	49	71	D6REV6	
ENSMUST00000140376	ENSMUSG00000029131	5	29735688	29818134	1	3	2	3	191	6	3	25	40	17	2	26	F6YRQ2	
ENSMUST00000140377						1	2	4	1	1	1	0	0	0	2	0		
ENSMUST00000140378						2	6	11	4	8	0	0	0	0	0	5		
ENSMUST00000140379						0	0	3	3	0	1	4	3	5	0	5		
ENSMUST00000140381						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140382	ENSMUSG00000028494	4	86648386	86670060	-1	2	1	0	0	4	2	172	0	111	0	48	B1AXR5	
ENSMUST00000140383	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	0	0	0	0	0	0	0	0	0	B4YB29	
ENSMUST00000140384	ENSMUSG00000031134	X	57383530	57393036	-1	0	2	4	1	5	4	53	323	154	54	104		Q9WV02
ENSMUST00000140385						0	1	7	5	3	0	71	273	204	397	98		
ENSMUST00000140386						9	4	5	56	3	0	3	17	24	4	11		
ENSMUST00000140387						6	0	3	46	7	0	0	0	5	0	0		
ENSMUST00000140388	ENSMUSG00000000902	10	75896769	75921617	-1	0	0	0	43	2	1	0	0	0	0	0	D6RDC4	
ENSMUST00000140389	ENSMUSG00000061451	19	5070859	5085531	-1	1	0	0	5	0	0	0	0	0	0	0	D3Z5V1	
ENSMUST00000140390						56	37	186	73	54	43	10	118	40	0	68		
ENSMUST00000140391						0	10	5	16	9	3	5	5	0	0	5		
ENSMUST00000140392						12	9	54	12	21	12	0	7	10	3	12		
ENSMUST00000140393	ENSMUSG00000031389	X	73891442	73921870	-1	0	0	2	0	0	0	81	136	51	0	81	E9Q4R3	
ENSMUST00000140394						3	0	1	8	1	0	0	1	0	0	0		
ENSMUST00000140395						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140396	ENSMUSG00000026917	2	27515157	27536535	1	2	3	0	3	5	2	56	0	0	6	36	F6Q3W0	
ENSMUST00000140397	ENSMUSG00000038902	3	94837567	94882326	1	0	1	0	0	0	0	0	0	0	0	0	F7D0L1	
ENSMUST00000140398						1	1	0	23	10	0	0	0	0	0	0		
ENSMUST00000140399	ENSMUSG00000031393	X	74026592	74135363	-1	1	0	3	0	2	0	0	0	0	0	1	D3Z7U4	
ENSMUST00000140400	ENSMUSG00000026399	1	130439027	130462744	-1	0	0	0	0	0	0	16	0	0	0	0	F7BP06	
ENSMUST00000140402	ENSMUSG00000022537	16	30511855	30550842	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4M0	
ENSMUST00000140403	ENSMUSG00000040964	4	140514485	140666012	-1	0	3	3	0	2	0	4	2	0	0	0	F6ZH54	
ENSMUST00000140404						52	41	99	58	48	14	8	11	2	2	19		
ENSMUST00000140406	ENSMUSG00000044627	2	32278816	32288075	-1	0	1	2	3	0	1	2	31	10	14	20	V9GXX7	
ENSMUST00000140407	ENSMUSG00000041301	6	18170687	18322768	1	0	0	0	0	0	0	0	0	0	0	0		P26361
ENSMUST00000140408						234	259	691	242	298	179	19	40	38	8	57		
ENSMUST00000140410	ENSMUSG00000063838	7	4151260	4164860	-1	3	3	5	3	3	3	0	0	0	0	0		
ENSMUST00000140411						0	3	2	2	0	0	12	8	0	0	3		
ENSMUST00000140413	ENSMUSG00000028339	4	47208161	47313167	1	2	3	0	0	3	0	0	0	0	0	0	A2AJY4	
ENSMUST00000140414						10	6	13	2	2	0	0	0	0	0	0		
ENSMUST00000140416						1	3	0	45	1	1	0	0	0	0	0		
ENSMUST00000140417						24	15	67	16	23	0	0	0	0	0	0		
ENSMUST00000140418						63	72	133	72	71	50	3	36	21	41	22		
ENSMUST00000140419						1	0	4	2	1	1	34	175	45	13	93		
ENSMUST00000140420						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140422						2	3	1	3	1	1	0	0	0	0	0		
ENSMUST00000140423						20	27	126	35	33	17	46	232	93	15	114		
ENSMUST00000140424	ENSMUSG00000035458	7	4518305	4524229	-1	4	0	9	3	4	0	2	13	6	2	6	D3YXP5	
ENSMUST00000140425						3	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000140426						0	0	0	0	0	0	1273	6134	1922	787	3397		
ENSMUST00000140427	ENSMUSG00000024188	17	26252910	26285504	1	0	0	0	0	1	0	0	13	0	0	19	D3Z765	
ENSMUST00000140428						3	14	6	13	14	7	0	0	0	0	0		
ENSMUST00000140429						0	2	0	0	3	1	0	19	3	68	19		
ENSMUST00000140430						14	18	22	15	14	3	0	0	1	0	0		
ENSMUST00000140431						0	0	0	1	0	2	0	15	4	0	0		
ENSMUST00000140433						8	0	33	213	17	13	0	0	0	0	0		
ENSMUST00000140434	ENSMUSG00000020415	11	43420250	43426251	-1	0	0	0	0	0	0	0	0	3	0	0	B0QZU1	
ENSMUST00000140435						3	7	14	113	15	10	0	0	0	0	1		
ENSMUST00000140436	ENSMUSG00000007659	2	152780668	152831728	-1	0	3	44	9	7	7	2	0	0	1	0		Q64373
ENSMUST00000140438	ENSMUSG00000014551	6	92169525	92184033	-1	40	23	62	47	32	24	108	667	121	78	105		Q9D125
ENSMUST00000140439						1	3	2	2	0	0	11	166	10	88	50		
ENSMUST00000140440						35	25	64	371	47	23	3	2	0	0	5		
ENSMUST00000140441						44	46	115	40	44	24	9	13	12	6	24		
ENSMUST00000140442	ENSMUSG00000024968	19	7267325	7275225	1	0	1	2	100	4	2	0	0	0	0	2	D3YUX3	
ENSMUST00000140444						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140446						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000140448	ENSMUSG00000024236	18	4920540	5119299	1	0	17	0	4	37	15	0	0	0	7	20		Q8K4L3
ENSMUST00000140449						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140452	ENSMUSG00000037432	1	36372291	36422110	1	0	0	10	4	0	1	27	96	37	7	42		
ENSMUST00000140453						1	0	0	0	1	1	0	1	0	0	1		
ENSMUST00000140454						0	0	0	37	3	8	0	4	37	272	92		
ENSMUST00000140455	ENSMUSG00000033152	6	88842558	88875044	-1	2	1	2	44	2	0	0	0	0	0	0	D3YZ50	
ENSMUST00000140456						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140457						27	38	54	29	34	26	1	5	4	1	1		
ENSMUST00000140458						17	11	16	0	37	12	4	14	10	0	29		
ENSMUST00000140459						5	3	7	0	2	0	0	0	0	0	0		
ENSMUST00000140460						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000140461						91	70	530	236	89	45	3	11	5	0	11		
ENSMUST00000140462						6	0	7	13	9	4	5	8	8	2	5		
ENSMUST00000140463						1	0	8	6	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140466	ENSMUSG00000047193	9	6928503	7184446	-1	53	32	52	30	54	12	41	25	106	41	109		Q45VK7
ENSMUST00000140467						3	2	9	12	5	2	28	27	25	1	73		
ENSMUST00000140468						1	2	2	3	2	0	0	6	131	233	138		
ENSMUST00000140469						0	1	1	0	0	0	81	30	24	14	37		
ENSMUST00000140470						0	0	0	0	0	0	1	46	31	32	54		
ENSMUST00000140471						17	21	27	24	22	13	21	497	35	5	145		
ENSMUST00000140472						5	4	0	3	2	1	0	0	0	0	0		
ENSMUST00000140473	ENSMUSG00000032657	3	89183143	89189295	1	2	2	8	4	7	1	5	2	0	1	2	D3Z5C1	
ENSMUST00000140474	ENSMUSG00000039783	1	175620381	175662116	1	2	5	6	7	1	7	0	2	3	0	0	Q3V0K6	
ENSMUST00000140475	ENSMUSG00000026988	2	59852364	59882591	-1	0	0	0	0	0	0	0	0	0	1	0	A2AUY0	
ENSMUST00000140476						4	3	4	8	9	1	0	0	0	0	1		
ENSMUST00000140477						1	1	0	1	4	2	2	0	0	0	3		
ENSMUST00000140478						16	12	8	0	19	9	1	2	1	4	3		
ENSMUST00000140479						0	1	0	1	0	0	1	2	0	0	0		
ENSMUST00000140480						380	367	1339	401	315	168	16	24	29	4	49		
ENSMUST00000140481						3	0	5	3	0	0	27	97	3	3	30		
ENSMUST00000140482						31	0	44	0	31	15	54	129	65	0	135		
ENSMUST00000140483	ENSMUSG00000048490	16	76287400	76373827	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140484						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000140485	ENSMUSG00000026014	1	60482292	60567104	-1	51	40	144	60	65	18	56	83	44	12	126	F2Z3U3	
ENSMUST00000140486	ENSMUSG00000031103	X	48411046	48463132	-1	0	0	0	0	3	2	0	0	138	0	56	Q3U1U8	
ENSMUST00000140487						9	18	3	6	8	9	7	24	13	4	24		
ENSMUST00000140489	ENSMUSG00000026491	1	179744894	179803680	-1	2	0	0	0	1	0	0	140	2	0	0	F6S6E4	
ENSMUST00000140490	ENSMUSG00000026389	1	120190757	120272705	-1	0	2	0	46	4	0	2	0	4	0	0	D3YTP0	
ENSMUST00000140491	ENSMUSG00000055436	3	158010473	158036639	-1	1	0	0	0	0	0	8	14	0	0	0	F6X2U6	
ENSMUST00000140492						0	0	0	131	7	3	0	0	0	0	0		
ENSMUST00000140493						4	0	1	3	2	1	0	8	2	0	4		
ENSMUST00000140494	ENSMUSG00000051396	2	3488850	3512814	-1	0	3	5	20	0	5	0	0	0	0	0	D6RJ26	
ENSMUST00000140496						0	0	0	2	1	1	0	0	8	0	0		
ENSMUST00000140497	ENSMUSG00000025786	9	123066160	123113205	-1	52	43	86	75	49	18	974	2474	1758	157	963	D6RFV6	
ENSMUST00000140498						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000140500						5	2	5	40	3	3	0	0	2	2	4		
ENSMUST00000140502						2	1	0	2	0	5	0	0	1	0	0		
ENSMUST00000140503	ENSMUSG00000012350	2	103263433	103303278	-1	1	0	4	5	1	0	0	0	0	0	0	A2BIB7	
ENSMUST00000140504						4	4	15	4	4	1	0	0	0	0	0		
ENSMUST00000140505						0	0	7	0	0	0	15	0	0	2	39		
ENSMUST00000140507						6	0	11	3	2	0	4	5	4	6	0		
ENSMUST00000140508						0	2	0	0	0	0	5	5	4	4	0		
ENSMUST00000140511						4	2	8	0	6	4	23	126	32	21	48		
ENSMUST00000140512	ENSMUSG00000033033	19	47105353	47138294	-1	14	17	71	38	33	23	0	0	0	0	0	D3Z2E8	
ENSMUST00000140513	ENSMUSG00000056962	11	116837432	116843449	-1	0	0	0	0	0	0	52	189	0	0	35	F6VMC4	
ENSMUST00000140514						1	0	0	0	0	0	0	48	7	2	5		
ENSMUST00000140515						3	2	10	4	5	0	0	6	0	6	3		
ENSMUST00000140516	ENSMUSG00000041390	6	15720661	15802169	1	4	8	17	125	6	8	0	4	0	0	2	D6REI0	
ENSMUST00000140517						6	4	9	1	9	3	0	0	1	0	0		
ENSMUST00000140518						1	1	3	0	1	0	2	14	3	3	0		
ENSMUST00000140519	ENSMUSG00000050373	2	164785823	164793816	1	0	0	0	0	0	0	0	0	0	3	10	G3UYX2	
ENSMUST00000140520						2	1	5	0	1	1	0	0	0	0	3		
ENSMUST00000140521	ENSMUSG00000005481	8	83715177	83726892	1	0	0	0	0	0	0	0	0	0	82	0	D6RHT5	
ENSMUST00000140522						20	26	84	80	22	15	2	6	0	8	0		
ENSMUST00000140523	ENSMUSG00000044712	12	73286779	73354049	1	78	102	463	115	81	55	57	203	100	59	67	G3UVW3	
ENSMUST00000140524						0	0	0	0	0	0	0	4	0	1	15		
ENSMUST00000140525						3	0	0	0	6	0	0	0	6	10	189		
ENSMUST00000140526	ENSMUSG00000016510	5	146951573	146963800	-1	0	0	0	0	0	0	0	0	0	0	5	D3YWL2	
ENSMUST00000140527						11	5	3	0	2	0	545	1120	625	5204	598		
ENSMUST00000140528						7	5	11	5	12	5	6	2	19	6	17		
ENSMUST00000140529						0	4	13	6	2	3	9	2	1	0	9		
ENSMUST00000140530						0	11	9	2	14	0	0	0	5	0	0		
ENSMUST00000140531						4	1	3	1	5	0	0	0	0	2	3		
ENSMUST00000140532						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140534						2	1	0	0	1	2	1	0	0	0	0		
ENSMUST00000140535						0	0	5	2	0	0	5	2	1	2	0		
ENSMUST00000140536						5	4	8	6	18	7	0	0	0	0	2		
ENSMUST00000140537						11	4	15	5	13	5	0	0	0	0	0		
ENSMUST00000140538	ENSMUSG00000033434	5	110103975	110108197	-1	0	0	0	0	0	0	18	0	0	0	7	D3YXC1	
ENSMUST00000140539						1	1	1	4	3	0	0	5	3	0	7		
ENSMUST00000140540	ENSMUSG00000031153	X	7789765	7820567	1	0	0	0	0	0	0	63	81	171	42	86	A2AEW6	
ENSMUST00000140541	ENSMUSG00000034853	4	106744555	106804998	-1	2	0	0	0	0	2	0	0	0	0	0	F6SS52	
ENSMUST00000140542						4	2	8	11	8	0	0	0	0	0	0		
ENSMUST00000140543						7	3	7	9	11	4	2	100	21	5	24		
ENSMUST00000140544						4	0	10	5	3	4	24	37	79	6	259		
ENSMUST00000140545						9	3	0	5	4	3	8	9	3	8	22		
ENSMUST00000140546	ENSMUSG00000071005	4	42754525	42756577	-1	7	7	16	15	12	3	0	0	0	0	0		
ENSMUST00000140547	ENSMUSG00000026979	2	24367580	24414954	1	0	0	0	48	0	3	4	0	4	0	3	A0A0A6YXD4	
ENSMUST00000140548						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000140549						0	4	1	0	2	3	0	1	1	0	1		
ENSMUST00000140550						2	0	10	13	6	2	0	7	18	0	3		
ENSMUST00000140551						42	28	43	164	46	24	0	4	2	0	2		
ENSMUST00000140552	ENSMUSG00000035392	2	37798991	38287390	-1	0	0	0	7	0	0	6	0	0	0	0	D6RHL0	
ENSMUST00000140553	ENSMUSG00000047767	7	101289392	101302251	-1	0	0	0	12	0	0	0	0	0	0	4	D6RHC1	
ENSMUST00000140554	ENSMUSG00000029600	5	120594305	120612589	-1	0	2	0	0	0	0	5	0	0	0	1	D3Z5Q7	
ENSMUST00000140555						1	0	1	2	1	1	9	32	7	5	9		
ENSMUST00000140557	ENSMUSG00000029563	6	14901349	15441977	1	0	0	0	0	0	0	0	0	0	0	0	D3Z2Q6	
ENSMUST00000140558	ENSMUSG00000015519	10	28972288	28986303	-1	8	8	13	5	5	4	0	0	0	0	0	D3YTP1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140559						1	0	2	1	2	2	0	0	0	0	0		
ENSMUST00000140560	ENSMUSG00000038301	6	51523901	51590679	1	0	0	0	3	0	2	0	0	0	0	0	D3Z4P6	
ENSMUST00000140561	ENSMUSG00000052926	8	84956610	84969767	-1	3	0	3	4	0	0	0	9	0	3	0	D3YWG3	
ENSMUST00000140562						0	0	0	0	2	0	0	0	3	0	0		
ENSMUST00000140563						0	0	0	90	2	0	0	12	0	6	0		
ENSMUST00000140564						1	1	0	2	3	0	0	15	0	0	0		
ENSMUST00000140565						15	14	17	121	54	28	0	0	0	0	0		
ENSMUST00000140566						3	0	5	3	2	0	0	0	14	0	0		
ENSMUST00000140567						0	1	3	6	1	0	0	0	0	0	0		
ENSMUST00000140568						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140570						0	0	0	0	0	0	12	0	0	0	0		
ENSMUST00000140571						4	2	4	7	4	4	0	0	0	0	0		
ENSMUST00000140572						0	1	2	0	1	2	0	0	0	0	0		
ENSMUST00000140573	ENSMUSG00000037437	8	24836140	24948804	-1	0	1	6	0	0	0	0	1	0	0	0	G3UXV9	
ENSMUST00000140574						4	5	0	5	7	0	1	0	0	0	0		
ENSMUST00000140576	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	0	0	0	0	10	D3Z439	
ENSMUST00000140577						2	2	4	15	5	2	0	0	0	22	4		
ENSMUST00000140579						7	4	0	4	11	2	0	0	0	3	2		
ENSMUST00000140580						6	8	11	1	5	0	8	4	7	0	5		
ENSMUST00000140581	ENSMUSG00000027300	2	130590002	130630038	-1	5	22	0	0	1	0	19	0	6	0	0	F2Z402	
ENSMUST00000140582						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140583	ENSMUSG00000026156	1	23761753	23849158	1	3	3	0	440	10	0	0	0	0	0	0		P59270
ENSMUST00000140584	ENSMUSG00000001827	7	101858331	101870788	-1	1	0	0	0	0	1	0	0	0	1	0	D3Z711	
ENSMUST00000140585						0	2	3	2	6	2	13	2	21	0	14		
ENSMUST00000140586						3	1	8	4	4	0	0	0	0	0	0		
ENSMUST00000140587						4	1	3	0	2	0	7	0	22	0	0		
ENSMUST00000140590						0	0	5	1	3	0	1	0	0	0	0		
ENSMUST00000140591						1	1	0	0	3	0	1	0	5	0	5		
ENSMUST00000140592	ENSMUSG00000026810	2	32570858	32573579	1	5	3	19	7	13	4	39	176	40	7	85	E0CXW3	
ENSMUST00000140593						17	23	5	4	18	3	0	0	0	0	8		
ENSMUST00000140594	ENSMUSG00000034006	18	80253292	80292725	1	7	4	14	356	27	7	34	133	144	23	90		Q80XM9
ENSMUST00000140595						0	2	1	1	0	0	3	1	0	0	0		
ENSMUST00000140596	ENSMUSG00000028649	4	123349633	123684360	-1	0	1	8	0	0	6	28	85	112	6	127	A0A0A0MQH5	
ENSMUST00000140597						6	0	0	9	0	0	0	114	1	0	0		
ENSMUST00000140598						0	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000140599	ENSMUSG00000048012	7	44731481	44751050	-1	3	0	4	6	3	1	1	0	2	0	0	E9Q0R5	
ENSMUST00000140600	ENSMUSG00000040687	2	91137360	91183837	-1	0	0	0	0	0	0	0	0	0	0	0	A6PWP7	
ENSMUST00000140601	ENSMUSG00000032878	11	28385685	28584324	-1	1	0	0	0	3	2	0	0	0	0	0	F6TRJ8	
ENSMUST00000140602						9	15	42	40	16	16	0	37	15	0	29		
ENSMUST00000140603	ENSMUSG00000053754	14	52198151	52257723	-1	0	0	0	0	1	0	9	24	28	0	11	F6W5S9	
ENSMUST00000140604						0	0	10	0	0	0	0	0	0	0	0		
ENSMUST00000140605						0	1	0	0	1	0	0	1	1	0	1		
ENSMUST00000140606						0	0	3	0	0	1	205	447	500	17	823		
ENSMUST00000140607	ENSMUSG00000029192	5	36490604	36593276	-1	0	0	0	0	0	0	1029	0	1370	0	0	E9Q8K4	
ENSMUST00000140608						0	0	0	16	0	0	0	0	0	0	0		
ENSMUST00000140609	ENSMUSG00000031403	X	75095854	75109777	1	0	0	0	0	0	0	0	0	1	0	5	F6YUI5	
ENSMUST00000140610						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000140612						38	34	90	488	53	30	6	21	21	4	3		
ENSMUST00000140615						1	2	0	0	3	0	0	1	0	0	0		
ENSMUST00000140616						80	84	202	65	60	39	8	40	21	6	26		
ENSMUST00000140617						2	5	11	206	13	7	0	0	0	0	0		
ENSMUST00000140619						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000140620	ENSMUSG00000033540	5	108660331	108684557	1	0	0	22	0	27	8	0	19	0	0	23	D6RIN7	
ENSMUST00000140621	ENSMUSG00000059355	8	85080740	85082339	1	0	3	4	4	5	9	93	149	70	0	28	F7AME8	
ENSMUST00000140622	ENSMUSG00000054808	7	28893248	28962340	-1	6	4	0	0	2	0	186	0	178	0	89	D3Z0L8	
ENSMUST00000140623						12	6	27	126	10	8	0	0	0	1	4		
ENSMUST00000140624						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000140625						4	2	0	2	4	2	0	0	0	0	0		
ENSMUST00000140626						0	0	1	5	0	2	5350	4739	4645	5941	4413		
ENSMUST00000140628						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140629						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140630	ENSMUSG00000000632	11	77930800	77979048	1	6	0	0	2	3	2	0	0	0	0	0	F6SXT0	
ENSMUST00000140631	ENSMUSG00000030990	7	102210208	102238567	1	0	1	0	1	0	1	0	0	0	0	0	D3Z1Q8	
ENSMUST00000140632						1	0	3	1	0	1	0	14	0	0	13		
ENSMUST00000140633						1	3	6	6	4	0	0	0	0	0	0		
ENSMUST00000140634	ENSMUSG00000039795	3	10339953	10351317	-1	0	0	1	0	0	0	0	1	11	68	24	F7CFT1	
ENSMUST00000140635						0	1	0	4	5	0	6	0	7	0	0		
ENSMUST00000140636	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000140637						0	0	1	1	0	2	0	0	0	1	0		
ENSMUST00000140638						0	0	5	2	4	5	28	235	25	4	53		
ENSMUST00000140640						4	3	2	0	4	2	111	51	43	10	49		
ENSMUST00000140641						0	12	13	67	14	0	0	9	6	0	15		
ENSMUST00000140642						8	4	10	28	8	1	0	0	0	0	1		
ENSMUST00000140643	ENSMUSG00000003458	1	172066013	172082795	-1	24	0	30	0	20	12	36	0	46	0	189	D6RCJ2	
ENSMUST00000140644	ENSMUSG00000028199	3	154596711	154623182	1	0	1	0	0	1	0	1	0	0	0	0	D3YWU6	
ENSMUST00000140647						37	41	109	82	48	27	2	5	7	1	7		
ENSMUST00000140648						0	2	0	55	1	0	0	0	0	0	0		
ENSMUST00000140649						1	0	3	22	1	1	0	0	0	0	0		
ENSMUST00000140651						0	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000140652	ENSMUSG00000040387	4	24612554	24851124	-1	1	1	0	0	0	0	0	0	0	0	0	J3QPI3	
ENSMUST00000140653	ENSMUSG00000029190	5	36600485	36696024	-1	28	24	22	34	43	16	30	75	25	47	36		Q80U59
ENSMUST00000140654	ENSMUSG00000028523	4	102986379	103005594	1	0	3	1	0	0	0	0	1	0	0	0	A2AIZ4	
ENSMUST00000140655						0	0	5	0	6	3	0	0	0	0	0		
ENSMUST00000140656	ENSMUSG00000030505	7	49778346	49858265	1	2	0	2	5	2	2	0	5	0	0	0	Q9D8D8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140657	ENSMUSG00000074646	2	155973279	156007977	-1	0	0	4	12	3	0	0	0	0	0	0	A3KGJ9	
ENSMUST00000140658						25	17	34	38	24	17	1	3	2	0	4		
ENSMUST00000140659						3	3	7	4	4	3	3	36	7	25	19		
ENSMUST00000140660						1	0	1	3	2	0	10	169	37	36	38		
ENSMUST00000140661						0	0	2	0	0	0	6	2	0	0	0		
ENSMUST00000140662						0	0	0	5	3	1	0	0	0	1	0		
ENSMUST00000140663	ENSMUSG00000070953	2	34777556	34799912	-1	3	3	8	12	6	1	2	13	2	0	7	D6RGR6	
ENSMUST00000140664						2	5	2	3	3	0	0	3	9	0	8		
ENSMUST00000140665						4	0	8	1	2	0	0	26	0	2	21		
ENSMUST00000140666	ENSMUSG00000079277	2	74711927	74748442	1	6	0	9	0	1	0	0	0	0	0	0	G3UZS5	
ENSMUST00000140667	ENSMUSG00000025537	5	129863421	129898549	-1	0	1	0	0	2	2	0	0	0	0	0	D3Z472	
ENSMUST00000140668	ENSMUSG00000058192	9	20581325	20595194	1	2	0	0	3	4	0	0	23	10	15	11	D6RFR2	
ENSMUST00000140670						7	4	11	0	12	13	42	304	115	35	89		
ENSMUST00000140671						4	3	17	5	5	3	4	2	5	3	8		
ENSMUST00000140672	ENSMUSG00000105103	3	116641902	116681260	-1	0	0	15	0	2	0	18	0	0	0	0	F6YIH5	
ENSMUST00000140674	ENSMUSG00000061533	12	90998492	91384409	-1	0	0	0	2	0	0	0	8	15	5	0	F6Q1Q5	
ENSMUST00000140675	ENSMUSG00000034563	9	72985429	73016340	1	0	0	0	0	6	10	300	1154	1618	617	1254	D3Z7R9	
ENSMUST00000140676						4	5	1	1	2	4	0	1	3	0	0		
ENSMUST00000140677	ENSMUSG00000000339	3	116488963	116508208	-1	0	1	0	7	5	0	0	0	0	0	0	D6REI7	
ENSMUST00000140678						2	8	15	6	3	0	0	3	0	0	7		
ENSMUST00000140679	ENSMUSG00000090137	8	70508263	70510801	-1	0	4	0	0	0	0	4	8	16	0	0	Q66JP1	P62984
ENSMUST00000140680						7	4	22	7	4	8	3	0	5	0	6		
ENSMUST00000140681						2	2	11	4	3	2	6	0	18	1	20		
ENSMUST00000140682						0	3	2	0	2	0	166	534	487	17	161		
ENSMUST00000140683						5	0	6	47	5	5	0	5	0	0	2		
ENSMUST00000140684	ENSMUSG00000000869	11	53602982	53618669	-1	1	1	2	4	1	0	0	4	0	0	0	G3UXB0	
ENSMUST00000140685	ENSMUSG00000026473	1	153899944	153909723	1	1	0	1	0	0	2	0	0	9	0	0	D3Z121	
ENSMUST00000140687						0	0	0	0	0	0	432	1024	0	0	0		
ENSMUST00000140688						0	4	9	123	0	0	0	4	0	0	1		
ENSMUST00000140690						72	62	154	82	53	10	5	4	3	0	4		
ENSMUST00000140691	ENSMUSG00000022194	14	54892500	54898169	1	4	1	4	0	1	0	0	0	0	6	3	D3YUB9	
ENSMUST00000140692						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140693						5	3	1	0	7	1	6	5	4	3	7		
ENSMUST00000140694						0	0	2	0	1	1	3	0	0	5	0		
ENSMUST00000140695						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000140696						0	2	8	6	5	3	0	0	0	0	0		
ENSMUST00000140697						3	1	1	11	5	3	0	0	1	0	0		
ENSMUST00000140698						3	0	3	0	0	2	0	0	0	2	1		
ENSMUST00000140699	ENSMUSG00000047907	2	169633013	170071816	1	0	0	0	0	0	0	0	0	0	0	0	Q8K350	
ENSMUST00000140700						9	5	11	15	17	7	1	4	4	0	5		
ENSMUST00000140701						4	3	3	10	9	6	190	1870	359	27	543		
ENSMUST00000140702	ENSMUSG00000066892	9	20618118	20644767	-1	3	2	12	22	11	9	60	408	72	28	89		
ENSMUST00000140703	ENSMUSG00000051985	1	135953578	136006342	-1	4	0	7	38	10	8	0	0	0	0	0	A0A087WPK2	
ENSMUST00000140704	ENSMUSG00000026821	2	28513125	28553081	1	2	0	9	0	0	2	3	7	2	2	6	B0R019	
ENSMUST00000140705						0	4	1	5	5	0	2	11	15	1	24		
ENSMUST00000140706	ENSMUSG00000035086	11	101285952	101302286	-1	3	2	9	109	10	2	0	0	17	0	2	F7DB15	
ENSMUST00000140707	ENSMUSG00000033737	X	106420041	106485401	-1	0	0	1	2	1	1	0	0	0	0	0	A2AMR4	
ENSMUST00000140708						6	2	2	3	3	4	9	3	7	3	3		
ENSMUST00000140710						0	8	2	0	2	2	0	0	29	183	0		
ENSMUST00000140711						3	0	3	12	2	0	0	0	0	0	0		
ENSMUST00000140712						24	19	65	46	32	14	43	192	95	10	169		
ENSMUST00000140713	ENSMUSG00000027593	2	154791096	154867261	1	0	0	0	0	5	0	43	567	346	48	268	A2AU62	
ENSMUST00000140714						2	2	0	0	1	0	60	40	34	16	49		
ENSMUST00000140715						4	2	9	27	9	6	4	27	5	0	35		
ENSMUST00000140718						3	0	3	0	1	2	3	0	0	0	0		
ENSMUST00000140719	ENSMUSG00000045466	6	47953390	47965300	1	0	18	18	0	16	0	27	41	12	0	29	D6RE39	
ENSMUST00000140720						5	2	3	5	5	1	0	0	0	0	0		
ENSMUST00000140721						2	2	2	1	1	1	0	0	0	0	0		
ENSMUST00000140722						5	3	6	3	3	3	0	59	9	8	4		
ENSMUST00000140723						4	3	0	3	2	1	0	0	0	0	0		
ENSMUST00000140724	ENSMUSG00000028479	4	44034075	44084177	-1	4	0	5	14	3	1	0	0	0	0	0	F7BWW0	
ENSMUST00000140725						31	17	312	87	39	9	56	265	160	104	115		
ENSMUST00000140727						2	0	6	0	0	1	0	3	0	0	0		
ENSMUST00000140728	ENSMUSG00000003279	17	69969073	70821413	1	0	0	0	0	0	0	0	0	0	0	0	D3Z508	
ENSMUST00000140729						7	1	11	1	3	1	0	0	0	0	5		
ENSMUST00000140730						2	0	21	10	0	6	0	0	0	0	0		
ENSMUST00000140731						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000140732						21	18	64	38	32	19	47	189	116	0	113		
ENSMUST00000140733						6	8	25	14	13	3	18	48	18	1	39		
ENSMUST00000140734						5	5	1	3	0	5	20	187	46	4	33		
ENSMUST00000140735						2	2	11	1	0	3	11	21	20	0	0		
ENSMUST00000140737	ENSMUSG00000006476	2	25054355	25062881	1	0	2	5	0	0	0	0	7	0	0	0	A0A0A6YW62	
ENSMUST00000140738	ENSMUSG00000061046	17	25779843	25785673	-1	3	2	4	1	7	1	39	26	9	0	10		Q9DB32
ENSMUST00000140739						14	9	30	10	10	13	0	0	3	0	2		
ENSMUST00000140740						40	34	47	32	48	29	3	10	12	0	20		
ENSMUST00000140741						2	1	2	2	3	0	0	0	0	0	0		
ENSMUST00000140742						2	1	9	85	2	8	0	0	0	0	2		
ENSMUST00000140743	ENSMUSG00000020069	10	63014664	63024217	-1	5	0	0	117	3	6	53	415	114	69	129	D3Z6Y3	
ENSMUST00000140744						0	0	2	44	0	0	0	0	0	0	0		
ENSMUST00000140745	ENSMUSG00000021645	13	100124852	100137690	1	1	0	2	31	6	0	4	9	4	0	2	D6RI18	
ENSMUST00000140747						3	2	10	2	11	4	1	0	2	0	1		
ENSMUST00000140748						3	3	14	16	8	1	1	0	0	0	0		
ENSMUST00000140749						2	0	0	1	3	0	0	0	0	0	0		
ENSMUST00000140750						2	1	0	0	0	1	0	0	2	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140751	ENSMUSG00000020566	12	17284721	17329359	-1	10	0	0	10	5	4	1	0	0	0	0	D6RCW6	
ENSMUST00000140752	ENSMUSG00000046110	2	121439059	121456781	-1	0	2	2	0	3	0	0	0	0	0	1	F7C9Q7	
ENSMUST00000140753						1	0	6	0	0	1	0	0	0	0	0		
ENSMUST00000140755	ENSMUSG00000037965	16	11136592	11176393	-1	0	0	0	0	0	0	0	0	0	0	15	D6RI42	
ENSMUST00000140756						3	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000140757	ENSMUSG00000068874	3	94933056	94944758	1	0	0	0	0	22	0	0	0	0	0	0	D6RHN2	
ENSMUST00000140758						0	0	0	1	1	2	3	8	8	0	5		
ENSMUST00000140759						26	12	359	3	18	20	0	0	0	0	0		
ENSMUST00000140760	ENSMUSG00000021553	13	58545399	58610877	-1	2	2	3	7	5	0	0	0	0	0	0	F6VNY5	
ENSMUST00000140761	ENSMUSG00000020253	9	106194172	106199746	-1	0	0	0	71	0	0	2343	3012	1514	264	883	E9Q2I3	
ENSMUST00000140762	ENSMUSG00000051373	2	32095528	32110820	1	2	0	3	37	0	1	0	0	1	0	0	A0A0A6YWL5	
ENSMUST00000140763						2	2	3	6	1	1	0	1	2	0	1		
ENSMUST00000140764						0	0	0	0	0	0	0	2	2	7	0		
ENSMUST00000140765	ENSMUSG00000020456	11	6291633	6356642	1	2	0	0	50	2	0	4	2	10	0	0	Q5SVY0	
ENSMUST00000140766						22	19	76	40	27	15	1	0	1	0	2		
ENSMUST00000140768	ENSMUSG00000032557	9	104046599	104063134	-1	1	0	0	30	0	0	0	13	0	0	0	D6RH76	
ENSMUST00000140769	ENSMUSG00000040713	1	165763746	165775308	1	14	4	7	7	10	0	7	33	0	0	8	J3QP41	
ENSMUST00000140770	ENSMUSG00000066438	12	80692591	80724214	1	32	19	55	180	49	19	0	1	0	0	0		B2RPU2
ENSMUST00000140772	ENSMUSG00000017493	11	99041244	99054392	1	0	0	1	2	0	0	0	0	0	0	0	H3BLB7	
ENSMUST00000140773						4	1	2	6	0	2	0	0	0	0	0		
ENSMUST00000140774						0	0	0	0	0	0	68	53	65	17	142		
ENSMUST00000140775						18	18	188	24	11	6	41	186	39	14	72		
ENSMUST00000140776						0	0	4	0	3	0	0	0	0	0	2		
ENSMUST00000140777	ENSMUSG00000074968	2	110655201	110950923	-1	0	1	5	1	2	0	0	0	0	0	0	A2AHK9	
ENSMUST00000140778						0	0	0	0	1	0	0	0	0	1	2		
ENSMUST00000140779						0	0	0	28	0	0	0	0	0	0	0		
ENSMUST00000140780						4	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000140781	ENSMUSG00000020840	11	76924809	76987379	1	4	0	0	1	0	1	0	0	0	0	0	E9PYU0	
ENSMUST00000140783						0	1	8	5	3	0	7	31	22	0	25		
ENSMUST00000140784						2	2	9	4	4	4	0	0	1	0	0		
ENSMUST00000140785						1	0	0	100	0	2	0	0	0	0	0		
ENSMUST00000140786	ENSMUSG00000040322	3	109123149	109168457	1	0	0	0	90	9	0	0	0	24	1	21	A0A0G2JFB9	
ENSMUST00000140787						0	3	0	0	0	1	0	40	7	0	0		
ENSMUST00000140788	ENSMUSG00000037904	12	110975353	110979040	-1	5	0	8	56	7	0	0	0	40	0	0		Q8BH83
ENSMUST00000140789						179	103	1482	370	139	64	2	5	2	1	4		
ENSMUST00000140790						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000140791	ENSMUSG00000027339	2	131989415	132030258	-1	7	1	2	10	5	5	10	2	19	2	17	A2AVI0	
ENSMUST00000140792						1	0	23	1	8	2	0	0	0	0	3		
ENSMUST00000140793						0	0	11	0	0	0	17	0	0	0	0		
ENSMUST00000140794						3	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000140795						22	20	15	22	45	23	0	1	0	0	2		
ENSMUST00000140796	ENSMUSG00000028760	4	137993022	138208508	1	23	21	0	33	13	10	0	125	0	40	0	A2AMI7	
ENSMUST00000140797	ENSMUSG00000030306	6	148232430	148444389	-1	3	3	0	0	0	4	0	0	0	0	0	D6RG80	
ENSMUST00000140798						8	7	3	7	4	5	0	1	0	0	3		
ENSMUST00000140799						0	4	2	2	2	5	3	0	0	0	3		
ENSMUST00000140800	ENSMUSG00000040365	11	48806404	48817353	-1	0	0	0	0	0	0	32	0	75	0	32	Q5NCC2	
ENSMUST00000140801						0	1	0	0	5	0	4	0	5	0	0		
ENSMUST00000140802	ENSMUSG00000047642	10	121641588	121692892	1	13	17	40	99	16	12	1	0	1	0	0	D6RIN2	
ENSMUST00000140803						0	5	0	0	7	2	0	0	0	0	0		
ENSMUST00000140804						2	0	6	2	0	0	0	17	0	0	0		
ENSMUST00000140805						0	2	0	0	3	0	2	0	1	3	5		
ENSMUST00000140806	ENSMUSG00000023007	15	99295087	99317018	1	0	0	0	0	0	0	3	2	0	0	0	D6RD12	
ENSMUST00000140808						6	2	1	3	3	4	6	39	12	4	21		
ENSMUST00000140809						83	94	118	140	115	72	55	54	168	18	253		
ENSMUST00000140810						2	1	3	2	5	1	0	0	0	0	4		
ENSMUST00000140811						1	3	18	0	2	2	0	0	0	0	2		
ENSMUST00000140812	ENSMUSG00000042523	12	84114366	84147498	1	4	7	3	4	7	3	0	0	0	0	1	D3YTL1	
ENSMUST00000140814						2	0	0	5	0	1	0	0	0	0	0		
ENSMUST00000140816						2	2	6	0	4	0	0	0	0	0	0		
ENSMUST00000140818						0	0	0	0	0	1	7	25	42	6	11		
ENSMUST00000140819	ENSMUSG00000013878	8	26119368	26143871	1	0	1	0	101	3	0	3	0	5	0	6	D3Z0A0	
ENSMUST00000140820	ENSMUSG00000049571	7	139600951	139683817	-1	11	0	0	38	33	0	0	0	0	0	0	G3UVW5	
ENSMUST00000140821	ENSMUSG00000000142	11	108920349	108950783	1	0	1	2	110	0	0	0	0	0	0	1	A2ABQ8	
ENSMUST00000140822						0	0	0	2	0	0	2	0	0	0	2		
ENSMUST00000140823	ENSMUSG00000021123	12	79208914	79222665	1	1	2	4	1	0	1	0	10	4	0	11	D3YY80	
ENSMUST00000140824	ENSMUSG00000032289	9	59966931	60522046	-1	0	0	0	21	0	0	0	1	0	0	0	D3Z044	
ENSMUST00000140825						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000140828	ENSMUSG00000020135	10	80295977	80318263	1	0	0	0	0	0	0	0	0	0	0	0	D3Z344	
ENSMUST00000140829	ENSMUSG00000067424	17	33089310	33106203	1	3	0	22	20	3	2	0	6	7	10	0	B8JK01	
ENSMUST00000140830	ENSMUSG00000028249	4	6365650	6408423	1	3	2	25	0	1	1	21	35	22	54	36	A2AKJ5	
ENSMUST00000140831						0	1	2	0	1	0	2	0	0	5	0		
ENSMUST00000140832						5	5	2	5	5	3	16	102	79	4	61		
ENSMUST00000140834						7	6	8	0	0	5	0	0	0	0	0		
ENSMUST00000140835						10	11	11	0	4	0	0	27	0	0	0		
ENSMUST00000140836	ENSMUSG00000040734	7	19359749	19378533	1	0	0	0	0	0	0	0	0	0	0	0	D3YVH2	
ENSMUST00000140837						85	59	157	50	74	40	1	10	3	0	2		
ENSMUST00000140838	ENSMUSG00000064215	12	103434211	103440239	1	0	0	0	1	0	0	22	33	15	18	4	D3Z4L8	
ENSMUST00000140840	ENSMUSG00000022269	15	26309048	26409576	1	0	0	0	0	0	0	0	0	0	0	0		Q8CBH7
ENSMUST00000140841						5	1	16	39	4	4	11	14	18	2	47		
ENSMUST00000140842	ENSMUSG00000040483	11	72301629	72313733	1	18	19	13	4	20	12	5	129	10	96	50		Q5NBU8
ENSMUST00000140843	ENSMUSG00000033705	2	120629126	120731895	1	83	37	177	90	9	4	12	64	221	11	546	A2AKH9	
ENSMUST00000140844						0	3	1	5	4	2	5	2	0	0	5		
ENSMUST00000140845	ENSMUSG00000031367	X	163909017	163933666	1	2	6	0	0	0	0	22	36	0	0	5	B1B0F6	
ENSMUST00000140846	ENSMUSG00000023764	11	3131850	3193463	-1	150	96	362	31	121	83	0	0	0	0	0	E9Q799	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140847						1	2	6	2	4	1	6	23	13	0	10		
ENSMUST00000140848						18	10	27	17	4	11	0	4	0	1	4		
ENSMUST00000140849						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000140850						0	0	2	130	0	0	2	0	0	0	0		
ENSMUST00000140851	ENSMUSG00000035032	9	105162156	105395524	-1	0	0	0	0	0	0	1	0	0	0	0	D3Z1E7	
ENSMUST00000140852						7	3	23	0	4	2	0	0	0	0	0		
ENSMUST00000140853	ENSMUSG00000027472	2	153008890	153015427	-1	1	0	0	54	0	0	1	3	0	0	1	D6RFC3	
ENSMUST00000140854						0	1	2	0	3	4	0	0	0	0	0		
ENSMUST00000140855						3	1	0	5	3	0	6	15	9	0	3		
ENSMUST00000140856						14	8	15	7	7	4	0	0	0	0	0		
ENSMUST00000140857						8	2	3	5	6	9	17	21	37	10	46		
ENSMUST00000140858	ENSMUSG00000025511	7	141475240	141493427	1	1	0	5	62	4	2	0	0	0	0	0	D3YXS4	
ENSMUST00000140860						123	92	678	147	135	69	7	27	14	4	21		
ENSMUST00000140861						0	0	10	0	0	0	0	0	32	160	44		
ENSMUST00000140862	ENSMUSG00000025793	11	120467635	120483984	1	5	0	2	0	0	2	0	0	0	0	7	B1ATY9	
ENSMUST00000140863						5	2	13	7	16	4	0	0	0	0	0		
ENSMUST00000140864						0	1	0	13	1	1	0	6	0	0	0		
ENSMUST00000140865	ENSMUSG00000030956	7	132712082	132813886	-1	2	0	3	1	0	1	0	0	0	0	0	D3Z4V7	
ENSMUST00000140866	ENSMUSG00000018899	11	53770014	53778374	1	0	0	2	16	1	0	17	3	26	0	0	A8Y5B9	
ENSMUST00000140867						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000140868						0	0	0	0	1	2	3	0	0	0	10		
ENSMUST00000140869	ENSMUSG00000090266	11	116843278	116854263	1	0	0	0	0	0	0	14	68	23	86	22	H3BKB2	
ENSMUST00000140870	ENSMUSG00000074736	2	149829211	150004392	1	0	0	0	0	0	1	0	0	0	0	0	B1AYD5	
ENSMUST00000140871	ENSMUSG00000007415	5	3632932	3657185	-1	6	8	9	8	7	6	45	110	60	13	56	F7CAN4	
ENSMUST00000140872						5	7	7	0	5	1	0	0	4	2	3		
ENSMUST00000140873						68	52	152	55	58	29	2	16	7	0	4		
ENSMUST00000140874						3	8	16	7	12	5	0	0	0	0	0		
ENSMUST00000140875						0	2	3	3	0	3	0	0	0	0	0		
ENSMUST00000140876						3	6	12	5	9	3	4	1	0	4	8		
ENSMUST00000140877						0	2	0	2	0	4	6	81	22	23	0		
ENSMUST00000140878						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140879						17	7	92	77	29	3	3	58	30	29	26		
ENSMUST00000140880						1	0	0	0	0	0	0	0	14	0	0		
ENSMUST00000140882						0	0	0	3	0	0	2	3	7	0	7		
ENSMUST00000140883						10	7	12	9	28	5	40	241	129	12	184		
ENSMUST00000140884	ENSMUSG00000025702	6	116338024	116409540	1	0	0	0	1	1	2	0	0	0	0	0		
ENSMUST00000140885						2	1	18	6	1	1	20	3	4	4	3		
ENSMUST00000140886						3	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000140887	ENSMUSG00000056018	8	129067134	129183732	1	0	0	0	0	0	0	0	0	0	6	0	D6RD02	
ENSMUST00000140888						0	0	0	0	9	3	4	4	0	0	0		
ENSMUST00000140889						9	3	13	42	6	6	0	0	0	0	0		
ENSMUST00000140890						4	3	2	8	8	2	0	0	0	0	0		
ENSMUST00000140891						0	0	5	0	0	0	0	4	0	0	0		
ENSMUST00000140893						0	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000140894						1	0	0	0	1	0	0	1	0	1	0		
ENSMUST00000140895	ENSMUSG00000027185	2	103721256	103761270	-1	3	0	10	5	0	0	0	0	0	0	7	A2BH46	
ENSMUST00000140896						2	0	8	14	5	6	296	757	385	30	597		
ENSMUST00000140897	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJV1	
ENSMUST00000140898	ENSMUSG00000037965	16	11136592	11176393	-1	0	2	1	0	0	3	22	286	58	13	25	F6X2N3	
ENSMUST00000140899						4	0	6	3	0	0	0	13	1	0	18		
ENSMUST00000140900	ENSMUSG00000004788	12	85219481	85226628	1	0	4	0	0	0	0	7	0	11	28	0	D3Z7J6	
ENSMUST00000140901	ENSMUSG00000020235	10	81366222	81378516	-1	11	4	53	37	27	13	320	376	218	23	164	Q3U3D4	Q9R1K5
ENSMUST00000140902						4	2	15	6	2	0	11	46	20	2	22		
ENSMUST00000140904						2	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000140905						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140906						1	0	0	0	1	0	0	0	19	0	0		
ENSMUST00000140907						0	0	0	3	0	0	12	14	20	0	10		
ENSMUST00000140908	ENSMUSG00000027524	2	174760619	174784042	1	2	0	0	14	0	0	0	0	0	0	1	E0CZ86	
ENSMUST00000140910	ENSMUSG00000075044	19	8160165	8218900	-1	0	0	0	0	9	1	0	0	0	0	0	E9Q4Q3	
ENSMUST00000140911	ENSMUSG00000036459	7	34109543	34133268	-1	2	7	0	0	2	0	0	0	0	0	1		
ENSMUST00000140912						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140913						3	0	14	4	9	0	0	1	1	0	0		
ENSMUST00000140914	ENSMUSG00000032965	16	49699233	49765126	1	3	2	0	4	1	0	67	338	158	68	104	F7B458	
ENSMUST00000140915						36	32	236	72	46	14	2	4	3	1	10		
ENSMUST00000140916	ENSMUSG00000055053	10	81396186	81431005	-1	0	0	0	23	0	0	2	0	1	0	21	F6XYU7	
ENSMUST00000140917						5	0	0	0	0	0	26	54	39	0	25		
ENSMUST00000140918						4	5	53	15	12	6	1	2	3	2	9		
ENSMUST00000140920	ENSMUSG00000039929	16	90751527	90810413	-1	61	40	105	82	57	44	30	60	39	7	75	E9PU96	
ENSMUST00000140921						82	54	199	448	95	44	0	8	1	0	7		
ENSMUST00000140922	ENSMUSG00000049680	11	5713417	5762376	-1	2	0	0	2	0	2	7	0	0	0	1	B0QZL8	
ENSMUST00000140923						10	7	25	10	9	5	0	0	0	0	8		
ENSMUST00000140924	ENSMUSG00000021983	14	59647531	60197179	-1	0	1	0	44	1	3	0	0	1	0	0	D3Z2Z6	
ENSMUST00000140925	ENSMUSG00000028382	4	59471868	59549364	-1	4	2	1	45	3	4	18	6	14	3	5	F7C521	
ENSMUST00000140926						0	3	5	2	0	1	13	20	10	2	7		
ENSMUST00000140927						1	0	4	0	2	0	3	3	5	0	7		
ENSMUST00000140929						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140930						5	5	7	2	8	2	0	0	0	0	0		
ENSMUST00000140931						6	1	18	0	0	3	32	0	0	37	0		
ENSMUST00000140932	ENSMUSG00000008540	6	138140316	138156755	1	0	0	0	0	0	0	1064	75	0	0	0		
ENSMUST00000140933						45	27	140	36	34	28	20	76	23	6	49		
ENSMUST00000140934	ENSMUSG00000013465	2	25199712	25211489	-1	3	1	6	1	0	0	11	0	39	1	48	F6SWS9	
ENSMUST00000140935						1	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000140936						13	16	20	43	20	8	0	16	8	1	16		
ENSMUST00000140938						6	1	4	3	2	5	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000140939	ENSMUSG00000027323	2	119112793	119147445	1	0	0	0	104	1	1	0	0	0	0	3	A3KGI2	
ENSMUST00000140940						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000140942						4	5	7	15	5	4	0	0	0	0	2		
ENSMUST00000140943	ENSMUSG00000090077	2	181380078	181383628	1	0	0	0	0	0	0	0	0	0	6	0	F6ZRC5	
ENSMUST00000140944						0	2	4	1	2	2	126	55	128	163	64		
ENSMUST00000140945						0	1	3	1	0	0	0	5	10	5	7		
ENSMUST00000140947						38	26	0	57	27	9	0	0	0	0	0		
ENSMUST00000140948	ENSMUSG00000046101	1	9908638	9942085	1	3	2	2	2	6	0	0	9	0	0	0	H7BXC1	
ENSMUST00000140950						3	0	0	47	1	1	0	0	0	2	0		
ENSMUST00000140951	ENSMUSG00000017652	2	165055627	165072948	1	0	1	0	1	0	0	0	0	0	0	0	A2A5L7	
ENSMUST00000140955						5	0	0	0	4	2	14	71	34	3	28		
ENSMUST00000140956	ENSMUSG00000045031	3	37307749	37312708	-1	54	43	410	110	61	34	3	22	4	0	16	A0A0A0MQN3	
ENSMUST00000140959						7	0	9	2	3	4	0	0	0	0	0		
ENSMUST00000140960						0	0	0	0	9	4	44	237	70	5	32		
ENSMUST00000140961						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000140962	ENSMUSG00000008855	11	102194432	102230166	-1	0	0	0	0	0	0	0	0	4	2	2	B7ZDF3	
ENSMUST00000140963						30	15	31	11	0	0	352	426	364	0	345		
ENSMUST00000140964	ENSMUSG00000074165	7	41633203	41651530	1	0	0	1	0	0	0	3	25	3	6	0	Q9CRL6	
ENSMUST00000140965						5	6	2	0	6	3	0	0	0	0	0		
ENSMUST00000140966	ENSMUSG00000030259	6	145746748	145821079	1	2	6	2	0	5	2	0	0	0	1	0	E9QA00	
ENSMUST00000140969						14	11	17	25	17	11	3	9	12	0	21		
ENSMUST00000140970						0	1	4	0	0	0	0	0	0	4	0		
ENSMUST00000140971						0	0	1	0	0	0	0	0	2	0	1		
ENSMUST00000140972						3	1	5	2	1	4	0	5	0	0	10		
ENSMUST00000140973						0	0	9	2	2	0	0	426	16	13	40		
ENSMUST00000140974						0	0	0	0	9	0	1163	2122	1765	57	1859		
ENSMUST00000140975	ENSMUSG00000020652	12	4196004	4234294	-1	19	10	28	39	19	10	17	102	28	26	43		Q8K015
ENSMUST00000140976						4	3	2	4	2	0	26	39	18	15	23		
ENSMUST00000140977						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000140979	ENSMUSG00000023927	17	51736187	51833290	-1	9	0	0	0	0	0	331	502	593	31	328	E9PVB7	
ENSMUST00000140981						5	5	14	114	2	1	0	0	0	0	0		
ENSMUST00000140982	ENSMUSG00000028803	4	135445420	135495038	-1	2	1	0	0	0	0	64	0	18	2	38	F6V4P1	
ENSMUST00000140983	ENSMUSG00000026811	2	32599709	32620806	1	0	0	23	24	0	1	0	2	0	1	0	Z4YLN2	
ENSMUST00000140984						3	0	0	0	5	0	0	15	4	0	7		
ENSMUST00000140985						2	5	3	2	8	1	0	7	1	2	4		
ENSMUST00000140986	ENSMUSG00000020739	11	115564434	115583985	1	0	0	0	0	3	0	0	10	0	2	0	Z4YM95	
ENSMUST00000140988						4	3	36	6	5	4	0	0	3	0	0		
ENSMUST00000140990						11	3	11	2	9	3	5	11	11	0	15		
ENSMUST00000140991	ENSMUSG00000020755	11	115933282	115966725	1	55	59	156	65	68	24	370	658	345	276	254		Q02614
ENSMUST00000140992						0	2	0	4	0	1	0	0	0	1	1		
ENSMUST00000140993	ENSMUSG00000026932	2	26055535	26123220	-1	0	0	0	0	0	0	1	0	0	0	0	A2ARL3	
ENSMUST00000140994						50	35	70	31	60	18	2	10	14	0	15		
ENSMUST00000140995						3	3	28	1	3	1	0	0	0	0	0		
ENSMUST00000140996	ENSMUSG00000029458	5	121660563	121687256	1	0	0	0	0	5	0	34	0	72	32	109	D6RG84	
ENSMUST00000140997						2	4	0	1	6	2	0	0	0	7	4		
ENSMUST00000140998						0	0	0	4	1	0	1	0	0	2	2		
ENSMUST00000140999	ENSMUSG00000009563	2	32757234	32762244	1	0	0	0	0	0	0	0	0	0	4	0	H3BK73	
ENSMUST00000141001						0	4	0	15	0	0	0	37	7	0	0		
ENSMUST00000141002						5	2	0	0	3	1	36	223	57	7	55		
ENSMUST00000141003	ENSMUSG00000038705	2	181251449	181288035	-1	5	0	7	1	2	0	0	0	8	0	0	D6RGU7	
ENSMUST00000141006						323	309	805	285	275	106	3	21	6	1	10		
ENSMUST00000141007	ENSMUSG00000028744	4	139294029	139310708	-1	0	0	0	0	0	0	0	0	0	0	0	F6QNQ2	
ENSMUST00000141009						10	7	7	3	10	3	0	14	4	2	10		
ENSMUST00000141010						1	3	2	4	0	3	0	0	0	0	0		
ENSMUST00000141012						0	0	2	0	1	0	18	8	73	0	23		
ENSMUST00000141013						5	1	0	34	0	0	305	546	569	424	585		
ENSMUST00000141014						1	0	0	0	0	0	0	0	4	0	8		
ENSMUST00000141015						5	1	0	0	2	2	0	0	0	0	0		
ENSMUST00000141016						0	0	0	3	1	0	12	26	17	8	28		
ENSMUST00000141017	ENSMUSG00000029192	5	36490604	36593276	-1	2	0	5	0	6	0	4	1	17	2	13	D6RHS3	
ENSMUST00000141018						0	4	7	3	4	1	17	40	28	2	52		
ENSMUST00000141019						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141020	ENSMUSG00000041849	15	5095981	5108539	-1	0	0	2	3	1	2	28	28	48	0	31	D3YYK3	
ENSMUST00000141021	ENSMUSG00000031604	8	64718139	64733792	-1	0	0	0	0	0	0	0	0	11	65	14	D3YTN3	
ENSMUST00000141022	ENSMUSG00000029017	5	21737141	21757152	1	0	0	0	0	0	0	0	8	0	0	1	F7BPA5	
ENSMUST00000141024	ENSMUSG00000022545	16	13109684	13150617	1	7	0	3	3	2	0	0	6	0	0	2	D6RHP2	
ENSMUST00000141025						0	0	0	5	2	2	0	0	0	0	0		
ENSMUST00000141026						1	0	0	2	0	0	2	0	0	0	0		
ENSMUST00000141029						15	11	11	109	17	12	0	8	3	0	11		
ENSMUST00000141031						46	49	91	60	72	30	5	12	12	2	19		
ENSMUST00000141033	ENSMUSG00000028712	4	115563649	115579015	1	0	0	0	0	0	0	0	0	0	0	0	A2A8S8	
ENSMUST00000141034	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	0	2	0	0	0	D3YWM1	
ENSMUST00000141036						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141037						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000141038						2	3	3	0	4	4	0	0	4	0	2		
ENSMUST00000141039	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0		Q3UTJ2
ENSMUST00000141040	ENSMUSG00000061894	4	128583539	128610098	-1	0	1	6	0	2	0	0	0	0	0	0	B1AS95	
ENSMUST00000141041						5	4	0	0	2	0	0	0	0	0	0		
ENSMUST00000141042						4	1	2	3	2	0	0	2	1	0	5		
ENSMUST00000141043						0	0	0	7	0	0	779	81	1345	0	427		
ENSMUST00000141044						2	1	4	0	1	2	0	3	2	0	2		
ENSMUST00000141045						0	0	0	0	0	0	71	350	74	57	14		
ENSMUST00000141046	ENSMUSG00000041064	9	65587160	65595967	1	2	6	0	180	11	1	0	0	0	0	0	D3YZ87	
ENSMUST00000141047	ENSMUSG00000096764	2	112266314	112406319	1	5	0	0	0	2	2	104	138	181	9	147	Q6P6P5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141048						374	505	1677	406	325	142	4	9	31	6	20		
ENSMUST00000141049						21	25	78	27	22	10	15	88	20	18	72		
ENSMUST00000141050						1	0	0	5	0	0	2	0	0	0	2		
ENSMUST00000141051						21	29	64	19	27	12	8	52	10	4	22		
ENSMUST00000141052	ENSMUSG00000034998	17	88440711	88490533	1	3	4	3	16	5	6	0	0	217	0	187	E9PYQ6	
ENSMUST00000141053						0	3	13	2	7	0	0	0	0	0	3		
ENSMUST00000141054						16	13	35	13	21	6	16	18	16	0	22		
ENSMUST00000141055						6	0	29	6	18	11	11	26	17	0	16		
ENSMUST00000141056						6	0	0	1	3	1	0	0	0	0	0		
ENSMUST00000141057						0	0	0	0	0	0	1	17	0	0	0		
ENSMUST00000141058	ENSMUSG00000036452	18	38601534	39376284	1	1	2	1	0	2	0	5	7	2	0	6	F6Q7M1	
ENSMUST00000141059						168	156	221	156	222	88	15	6	4	3	20		
ENSMUST00000141060						17	16	32	65	28	12	0	1	1	0	1		
ENSMUST00000141061						11	11	14	19	14	9	3	13	25	1	41		
ENSMUST00000141062	ENSMUSG00000006345	10	75561604	75586200	1	2	1	37	2	5	4	772	797	754	50	324	D3YWZ7	
ENSMUST00000141063	ENSMUSG00000057596	7	104470014	104507849	-1	0	0	0	0	0	0	0	0	2	2	3	F6SX36	
ENSMUST00000141064						10	12	10	8	12	5	0	0	0	0	0		
ENSMUST00000141065						0	0	2	1	4	0	2	0	0	0	2		
ENSMUST00000141066	ENSMUSG00000064247	5	110099969	110105953	1	1	0	0	90	0	0	0	0	0	0	0	D3Z2L0	
ENSMUST00000141067						1	4	7	3	3	3	0	0	0	0	0		
ENSMUST00000141068						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141069						7	2	3	54	5	0	0	0	0	0	0		
ENSMUST00000141070						2	4	14	14	8	2	1	6	9	0	0		
ENSMUST00000141071						1	2	2	2	5	1	19	20	15	0	38		
ENSMUST00000141072						14	6	11	4	5	0	17	37	31	0	23		
ENSMUST00000141073						1	0	1	1	5	0	0	0	0	0	0		
ENSMUST00000141075						2	4	3	0	0	2	0	18	9	7	9		
ENSMUST00000141077						38	50	38	79	47	18	19	45	15	7	16		
ENSMUST00000141078	ENSMUSG00000056215	6	34029448	34134034	1	0	2	0	0	2	0	0	0	0	0	0	F6Z1G4	
ENSMUST00000141079						0	2	3	0	5	0	15	171	27	8	62		
ENSMUST00000141080						0	0	1	0	3	0	0	0	0	0	0		
ENSMUST00000141081						1	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000141083	ENSMUSG00000032812	7	101348067	101412586	1	1	0	6	1	2	0	0	0	0	0	4		
ENSMUST00000141084	ENSMUSG00000031099	X	47809368	47892974	-1	0	4	0	0	0	0	0	0	0	0	0	Q8BS67	
ENSMUST00000141085						9	8	37	8	15	4	0	0	0	0	0		
ENSMUST00000141086						0	0	0	1	1	1	0	0	0	0	0		
ENSMUST00000141087						0	0	0	0	0	0	2	0	4	13	0		
ENSMUST00000141089	ENSMUSG00000032493	9	110813994	110824523	1	4	0	0	4	4	7	0	0	0	0	0	K7E6F0	
ENSMUST00000141091						0	1	3	1	3	0	0	0	0	0	0		
ENSMUST00000141092						3	5	9	4	2	4	14	50	41	3	74		
ENSMUST00000141093						5	0	2	0	3	0	0	2	0	0	2		
ENSMUST00000141094						6	3	1	5	7	2	1	24	4	4	21		
ENSMUST00000141095						0	0	1	0	0	0	0	2	0	0	0		
ENSMUST00000141098						6	3	6	6	10	1	0	2	0	0	2		
ENSMUST00000141099	ENSMUSG00000070953	2	34777556	34799912	-1	0	0	0	22	1	0	0	0	2	10	0	D6RHN6	
ENSMUST00000141100	ENSMUSG00000016257	2	174465067	174473081	-1	0	0	0	22	5	4	0	15	0	3	9	B0QZU3	
ENSMUST00000141101	ENSMUSG00000029516	5	115845278	116008947	1	4	0	0	0	0	0	0	0	18	0	15	F6SBR5	
ENSMUST00000141102						5	7	17	112	12	10	0	1	0	0	0		
ENSMUST00000141103						0	5	6	2	0	2	0	0	0	0	0		
ENSMUST00000141104						2	2	3	0	2	0	17	24	6	2	0		
ENSMUST00000141105						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000141106						13	5	31	26	16	2	1	1	1	0	5		
ENSMUST00000141107						5	2	4	9	6	5	0	0	0	0	0		
ENSMUST00000141108	ENSMUSG00000029060	4	155654677	155669198	-1	6	6	13	0	1	0	83	58	30	0	53	A2A9P8	
ENSMUST00000141109						0	0	0	43	0	0	0	0	0	0	0		
ENSMUST00000141110	ENSMUSG00000038705	2	181251449	181288035	-1	0	0	3	0	2	5	0	0	0	0	28	D6RG43	
ENSMUST00000141111						8	3	5	53	0	0	0	0	0	0	0		
ENSMUST00000141112	ENSMUSG00000078584	4	119203570	119232712	-1	89	86	171	129	104	73	63	88	84	14	86		Q5EBG8
ENSMUST00000141113						0	0	0	1	0	0	20	0	3	0	8		
ENSMUST00000141114	ENSMUSG00000052423	1	171270328	171276896	1	1	0	0	0	0	1	0	0	0	0	0	D3YVA5	
ENSMUST00000141115						69	66	87	76	114	73	50	96	95	9	122		
ENSMUST00000141116	ENSMUSG00000043866	7	105739393	105744361	-1	14	18	20	43	12	10	51	463	112	20	95		Q8K0H5
ENSMUST00000141117						1	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000141118	ENSMUSG00000032786	9	106233455	106248126	-1	4	3	14	77	10	8	55	61	36	9	59	Q3V0B2	Q8VC19
ENSMUST00000141119	ENSMUSG00000033257	1	74661745	74703730	1	0	0	0	24	0	0	7	3	10	0	5	D3Z402	
ENSMUST00000141121						0	0	0	0	0	0	11	2	10	1	4		
ENSMUST00000141122	ENSMUSG00000078879	2	176670522	176719085	1	16	12	4	10	8	7	1	1	2	0	1	D6RGN8	
ENSMUST00000141123	ENSMUSG00000023328	5	137287519	137294466	1	0	0	10	19	0	0	0	0	0	0	1	D3Z064	
ENSMUST00000141124	ENSMUSG00000033021	1	75435930	75443179	1	2	0	0	1	2	0	0	6	6	1	7	D3Z3L0	
ENSMUST00000141125						5	4	0	0	0	0	14	38	9	16	25		
ENSMUST00000141126	ENSMUSG00000030846	7	128439777	128461717	-1	0	0	0	13	0	0	0	0	0	32	0		
ENSMUST00000141127						2	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000141128						0	0	19	0	5	1	89	0	0	0	0		
ENSMUST00000141129						2	5	2	2	0	0	2	8	8	0	4		
ENSMUST00000141130	ENSMUSG00000051855	6	30723547	30748465	1	0	0	3	2	0	0	0	0	0	0	0		
ENSMUST00000141131	ENSMUSG00000060371	5	130369455	130847412	1	2	5	4	4	3	6	0	0	0	0	0		
ENSMUST00000141132	ENSMUSG00000024426	17	35897595	35910075	-1	0	0	5	3	1	2	0	2	5	0	0	B8JJ72	
ENSMUST00000141134	ENSMUSG00000054406	11	74346624	74352621	-1	1	0	0	0	12	0	0	0	0	0	0		
ENSMUST00000141135	ENSMUSG00000028125	3	122044443	122180123	1	27	11	46	12	23	4	2	4	1	2	0	A0A0G2JGG8	
ENSMUST00000141137	ENSMUSG00000038011	5	124725085	124834308	1	13	48	33	0	41	0	2	1	1	0	4	F7ABZ6	
ENSMUST00000141138						2	0	0	1	0	0	53	117	44	26	26		
ENSMUST00000141139						0	0	5	2	3	0	2	19	11	3	15		
ENSMUST00000141140	ENSMUSG00000056824	2	165351297	165368729	-1	0	0	0	0	0	0	0	0	0	0	0	A2A4U4	
ENSMUST00000141141						0	0	0	0	0	0	0	4	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141142						4	2	4	3	2	2	0	0	0	0	0		
ENSMUST00000141143						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000141144	ENSMUSG00000020083	10	62107655	62143920	-1	3	5	70	14	12	6	0	1	0	0	2	D3Z7G3	
ENSMUST00000141146	ENSMUSG00000001029	11	106377656	106388075	-1	0	3	0	0	0	3	12	16	9	13	0	B1ARJ2	
ENSMUST00000141147						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000141148	ENSMUSG00000015222	1	66175273	66442583	1	0	0	0	0	0	0	0	0	0	0	0	F7ALC8	
ENSMUST00000141150						17	20	26	17	29	11	3	22	9	3	22		
ENSMUST00000141151						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000141152						48	46	25	21	36	13	7	5	10	5	8		
ENSMUST00000141153						4	1	16	33	6	5	0	1	0	0	0		
ENSMUST00000141154						5	0	0	1	4	0	0	0	1	0	0		
ENSMUST00000141155						6	5	7	9	8	2	0	0	0	0	0		
ENSMUST00000141156	ENSMUSG00000037161	3	51388412	51396738	-1	5	0	20	8	0	0	0	0	0	0	0	D3Z134	
ENSMUST00000141158	ENSMUSG00000013033	8	83900105	83941954	1	46	38	121	110	55	25	10	26	19	4	64		Q80TR1
ENSMUST00000141159	ENSMUSG00000068373	2	104143073	104410334	-1	134	43	92	55	76	23	0	0	0	0	0	F6ZGR6	
ENSMUST00000141161						15	10	14	5	9	4	4	50	4	3	13		
ENSMUST00000141163						2	0	0	0	0	4	0	0	0	0	0		
ENSMUST00000141164						0	0	0	115	0	0	0	0	0	0	0		
ENSMUST00000141165	ENSMUSG00000028619	4	107134155	107179116	-1	0	1	0	20	0	0	0	55	4	8	0	D3YXQ1	
ENSMUST00000141166						4	2	6	10	5	1	7	26	14	0	15		
ENSMUST00000141167	ENSMUSG00000022151	15	5185525	5218336	1	0	0	1	0	1	0	0	0	27	118	21	D3Z1T8	
ENSMUST00000141169	ENSMUSG00000020485	11	87737552	87743623	1	14	8	24	10	10	8	15	40	18	5	15	G3UVU8	
ENSMUST00000141170						0	0	2	2	0	0	0	56	14	10	33		
ENSMUST00000141171	ENSMUSG00000020232	10	81346048	81350480	-1	0	0	0	40	6	0	157	118	84	0	35	F7AVN4	
ENSMUST00000141173						0	6	10	3	14	0	0	1	0	0	26		
ENSMUST00000141175						34	56	70	8	65	0	175	767	297	48	356		
ENSMUST00000141176	ENSMUSG00000040785	16	94370618	94469222	1	1	0	2	0	0	0	1	0	0	0	0	F6XYB0	
ENSMUST00000141177						2	3	2	0	1	0	2	19	7	0	8		
ENSMUST00000141178						0	0	0	0	0	0	0	19	0	0	24		
ENSMUST00000141179						0	0	0	0	0	0	0	99	0	3	0		
ENSMUST00000141180						8	5	7	3	2	3	0	3	0	0	6		
ENSMUST00000141181						3	0	9	5	4	0	0	0	0	0	0		
ENSMUST00000141182						0	0	54	40	27	14	0	0	0	0	0		
ENSMUST00000141183						0	3	4	3	6	0	3	14	0	0	6		
ENSMUST00000141184						479	409	601	285	548	273	4	33	23	6	13		
ENSMUST00000141185	ENSMUSG00000038775	9	119052778	119071525	1	0	0	1	0	7	0	7	39	11	0	2		Q91YD6
ENSMUST00000141186						3	4	38	9	3	4	11	13	9	0	7		
ENSMUST00000141187						576	419	2441	734	786	351	2	32	10	4	35		
ENSMUST00000141188	ENSMUSG00000044811	11	114996721	115001880	-1	3	7	20	0	14	0	282	1862	391	1238	384	E0CYN3	
ENSMUST00000141189						1	2	0	0	1	3	0	0	0	0	0		
ENSMUST00000141190						5	9	10	6	6	5	1	4	2	0	8		
ENSMUST00000141191	ENSMUSG00000036632	3	54735539	54751318	1	65	53	372	121	77	40	2	2	0	0	6	D6RCG2	
ENSMUST00000141192	ENSMUSG00000040785	16	94370618	94469222	1	10	0	6	0	4	0	1	4	0	0	0	F6ZS17	
ENSMUST00000141193						1	0	13	3	6	2	2	2	0	0	0		
ENSMUST00000141194						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141195						4	0	2	0	2	0	0	16	5	5	0		
ENSMUST00000141196	ENSMUSG00000044681	5	28200819	28245792	-1	0	0	0	11	0	0	0	0	0	0	0		
ENSMUST00000141198						1	3	0	2	0	0	0	0	0	0	0		
ENSMUST00000141200	ENSMUSG00000069893	11	48946150	48979398	-1	2	0	3	2	1	1	0	3	7	7	22	Q5SVN9	
ENSMUST00000141201						33	0	139	28	45	12	0	0	0	0	3		
ENSMUST00000141202	ENSMUSG00000031617	8	77595982	77610698	-1	0	1	2	5	5	6	0	0	2	5	0	D3YWM0	
ENSMUST00000141203	ENSMUSG00000038126	5	124250959	124327972	-1	0	0	7	0	0	3	0	0	2	6	0	D6RDQ9	
ENSMUST00000141204	ENSMUSG00000023930	17	40764734	40807003	-1	0	0	0	0	0	0	0	0	0	0	0	D6RDB4	
ENSMUST00000141205						8	4	27	3	7	0	17	0	5	5	15		
ENSMUST00000141206	ENSMUSG00000020225	10	120201590	120224917	1	0	0	0	0	0	0	8	99	17	86	10	D6RIR2	
ENSMUST00000141207						3	2	3	10	4	3	0	0	0	0	0		
ENSMUST00000141208						99	110	620	97	80	51	19	80	30	19	60		
ENSMUST00000141210						0	0	2	76	6	2	0	0	0	0	0		
ENSMUST00000141211						0	1	0	0	0	0	50	41	24	8	17		
ENSMUST00000141212						39	38	114	61	34	12	0	3	9	3	5		
ENSMUST00000141213						4	3	3	12	3	4	2	24	10	0	23		
ENSMUST00000141214						5	3	15	0	8	0	0	0	0	0	0		
ENSMUST00000141215	ENSMUSG00000026784	2	22895522	22940266	1	1	0	0	19	2	0	0	0	0	1	0	B8JJX0	
ENSMUST00000141217						8	13	29	18	4	7	11	33	16	38	32		
ENSMUST00000141218						1	0	4	0	0	1	4	9	36	2	15		
ENSMUST00000141219						5	0	0	4	0	0	0	0	0	0	3		
ENSMUST00000141220						0	0	0	0	0	0	12	24	8	3	35		
ENSMUST00000141221						1	0	2	0	1	0	0	0	0	0	2		
ENSMUST00000141223						0	2	1	0	2	1	2	4	10	0	8		
ENSMUST00000141224						0	0	0	0	5	1	0	0	0	0	5		
ENSMUST00000141225						0	0	3	36	0	1	3	17	0	0	5		
ENSMUST00000141226						17	26	39	28	27	22	11	15	25	23	48		
ENSMUST00000141227	ENSMUSG00000028644	4	119175457	119190011	-1	0	0	0	0	0	0	0	0	0	0	0	D6RFS7	
ENSMUST00000141228	ENSMUSG00000020265	10	77606097	77641543	1	0	0	0	0	0	0	97	68	102	90	84	G3UWX9	
ENSMUST00000141229						14	14	16	30	13	8	0	4	2	0	5		
ENSMUST00000141230						7	2	5	19	8	2	17	47	19	0	26		
ENSMUST00000141231						9	8	10	14	6	4	8	27	13	3	19		
ENSMUST00000141232						0	0	0	64	0	0	0	3	0	16	10		
ENSMUST00000141233						15	24	40	15	17	9	7	28	13	1	5		
ENSMUST00000141234						6	0	8	3	4	2	27	341	84	13	109		
ENSMUST00000141235	ENSMUSG00000057572	4	129335695	129354547	1	1647	1841	3529	1367	1923	934	106	477	209	93	240	B2KGA7	
ENSMUST00000141236						1	3	19	0	7	0	2	0	0	146	16		
ENSMUST00000141237						12	8	36	24	18	13	59	255	105	12	138		
ENSMUST00000141238						0	3	7	1	1	0	0	0	0	0	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141240	ENSMUSG00000024187	17	26211822	26244223	-1	0	0	6	2	0	1	0	6	0	0	14	F6SQM4	
ENSMUST00000141241	ENSMUSG00000036099	10	93939165	94035817	-1	0	0	0	0	0	0	0	3	1	2	0	F6W383	
ENSMUST00000141243						3	4	11	1	2	2	0	0	0	0	0		
ENSMUST00000141244	ENSMUSG00000039842	8	18595131	18803189	1	1	1	6	1	0	1	0	0	0	0	0	F6QJ89	
ENSMUST00000141245	ENSMUSG00000030492	7	35448796	35466036	1	3	6	5	4	2	3	0	0	0	0	0	F7AUJ6	
ENSMUST00000141246						0	4	1	0	0	0	10	22	8	1	11		
ENSMUST00000141247						7	3	9	9	4	3	0	1	1	0	3		
ENSMUST00000141248						8	9	19	0	9	0	0	12	2	0	2		
ENSMUST00000141249	ENSMUSG00000042641	1	153779381	153844142	-1	3	7	2	0	8	3	2	26	3	17	6	V9GXL8	
ENSMUST00000141250	ENSMUSG00000032845	18	65265529	65393888	-1	29	9	27	32	39	18	0	0	0	0	0	F6ZZL0	
ENSMUST00000141251						10	4	11	5	10	0	6	16	9	11	11		
ENSMUST00000141252						0	3	3	85	6	1	0	0	0	3	0		
ENSMUST00000141253	ENSMUSG00000038696	2	34406771	34624950	1	1	1	10	40	2	1	0	6	0	0	2	A0A0A6YVX6	
ENSMUST00000141254	ENSMUSG00000025140	11	120635712	120643769	-1	0	0	0	0	0	0	0	0	0	0	0	A2ABZ2	
ENSMUST00000141255						8	2	15	130	21	9	1	0	0	0	0		
ENSMUST00000141257						0	2	0	0	1	0	3	0	4	0	6		
ENSMUST00000141258	ENSMUSG00000018906	11	54100095	54131665	1	4	2	5	1	16	5	0	0	1	0	0	F6ULE1	
ENSMUST00000141260						0	3	9	7	10	0	0	0	0	0	13		
ENSMUST00000141261						2	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000141262						0	5	0	0	4	2	0	0	1	0	0		
ENSMUST00000141263	ENSMUSG00000029012	5	22486485	22550429	-1	0	2	0	0	2	0	0	0	0	0	0	D3Z0X3	
ENSMUST00000141264	ENSMUSG00000075284	2	73429610	73529734	-1	0	0	5	0	1	1	81	46	179	4	121	F6QWW7	
ENSMUST00000141266						4	2	34	34	7	2	4	7	9	2	11		
ENSMUST00000141268	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	0	0	0	103	207	83	116	65	D3YZT9	
ENSMUST00000141269						2	0	8	0	2	1	0	0	0	0	0		
ENSMUST00000141270						0	0	8	0	0	0	21	7	13	0	13		
ENSMUST00000141272						7	5	8	3	9	7	0	0	0	0	0		
ENSMUST00000141273						3	9	3	0	5	3	0	35	0	2	0		
ENSMUST00000141274						0	0	3	37	1	0	17	76	27	245	32		
ENSMUST00000141276						0	0	0	2	2	0	0	0	2	14	0		
ENSMUST00000141277						0	0	1	44	2	0	4	15	7	0	3		
ENSMUST00000141278						41	47	95	47	47	39	13	52	27	3	37		
ENSMUST00000141279						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000141280	ENSMUSG00000044378	6	137983586	138079916	-1	0	1	0	0	0	0	0	1	0	0	0		
ENSMUST00000141281	ENSMUSG00000038593	5	122237848	122264460	-1	0	9	0	114	0	0	86	282	116	53	217	D6RDQ2	
ENSMUST00000141282						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000141283	ENSMUSG00000029009	4	148039077	148059551	1	9	0	5	17	11	6	27	11	11	0	17	A2A7F9	
ENSMUST00000141284						3	3	2	4	5	2	3	20	8	3	6		
ENSMUST00000141285						4	11	5	5	4	4	35	158	89	4	110		
ENSMUST00000141286						796	644	340	227	505	119	7	3	6	3	10		
ENSMUST00000141287						63	62	155	73	57	19	0	3	2	0	12		
ENSMUST00000141288						1	3	1	3	2	2	0	0	0	0	0		
ENSMUST00000141290	ENSMUSG00000044367	11	70216789	70221064	-1	0	0	34	37	0	0	1	0	0	0	0	A2CF71	
ENSMUST00000141291	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	8	44	7	0	0	0	0	0	13	A2AD32	
ENSMUST00000141292	ENSMUSG00000038651	13	41114307	41171684	1	5	2	0	0	3	0	0	0	0	0	0	F6RWL8	
ENSMUST00000141293	ENSMUSG00000028990	4	149485229	149496668	1	0	0	0	7	0	0	3	0	8	0	0	B1AS04	
ENSMUST00000141294						0	0	0	0	0	4	0	0	0	0	0		
ENSMUST00000141295	ENSMUSG00000090231	17	34856374	34862518	-1	0	0	0	0	0	0	10	3	0	52	16	F6W2T4	
ENSMUST00000141296						9	8	9	9	5	11	0	0	1	2	4		
ENSMUST00000141297	ENSMUSG00000025743	4	130792537	130826319	1	0	5	21	0	0	2	0	0	0	0	0	B1ASF6	
ENSMUST00000141298	ENSMUSG00000036591	2	20847919	20968881	-1	47	44	119	46	51	25	7	59	104	10	93	B7ZCJ1	
ENSMUST00000141301						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141302	ENSMUSG00000033763	8	110721476	110741400	1	0	0	0	0	0	0	0	0	0	0	5	F7D291	
ENSMUST00000141304						5	4	3	0	0	2	0	2	0	0	3		
ENSMUST00000141305	ENSMUSG00000030323	6	115853470	115926699	1	7	0	15	0	22	3	0	5	0	0	3	S4R282	
ENSMUST00000141306	ENSMUSG00000041351	4	137664726	137729861	1	5	7	5	15	9	9	0	1	0	0	12	A2ALS7	
ENSMUST00000141308						0	0	0	0	0	0	35	834	65	35	84		
ENSMUST00000141309	ENSMUSG00000005378	5	135052957	135064959	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1S2	
ENSMUST00000141310	ENSMUSG00000031410	X	135579555	135598777	-1	0	0	1	0	1	0	0	0	0	0	0	A2AEI5	
ENSMUST00000141311	ENSMUSG00000011096	7	44848991	44855421	1	0	0	5	106	0	1	0	13	13	4	6	D3YWZ1	
ENSMUST00000141313						4	6	2	1	5	1	0	0	0	0	0		
ENSMUST00000141314	ENSMUSG00000041119	17	31386234	31476310	1	0	0	0	0	4	0	0	0	0	0	0	F7APE3	
ENSMUST00000141315						0	0	1	98	0	0	0	1	0	0	0		
ENSMUST00000141316						0	2	5	3	4	4	6	20	10	1	13		
ENSMUST00000141317						1	1	4	1	0	2	1	1	1	0	1		
ENSMUST00000141318						0	0	0	0	0	0	46	274	69	14	27		
ENSMUST00000141319						2	1	4	3	2	1	3	11	3	0	5		
ENSMUST00000141320						1	2	1	7	3	0	3	14	4	9	1		
ENSMUST00000141321	ENSMUSG00000072640	11	78826584	78846870	1	0	0	0	0	0	2	7	12	8	31	0	E9PX24	
ENSMUST00000141322						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000141323						4	8	11	1	7	0	2	16	3	0	4		
ENSMUST00000141324						2	0	3	4	1	1	6	18	7	0	9		
ENSMUST00000141325	ENSMUSG00000024055	17	32924688	32947402	-1	2	0	1	8	7	3	6	3	7	0	5	G3UVU3	
ENSMUST00000141326						6	1	9	11	8	5	3	2	4	0	0		
ENSMUST00000141327						9	0	10	2	7	4	8	49	16	1	13		
ENSMUST00000141328						5	6	14	11	9	7	0	13	3	0	1		
ENSMUST00000141330						2	0	5	1	2	0	5	10	36	0	15		
ENSMUST00000141331						4	2	9	8	1	0	1	0	1	0	0		
ENSMUST00000141332						4	0	2	2	0	0	3	1	0	0	6		
ENSMUST00000141333						6	3	6	15	4	4	0	0	0	0	0		
ENSMUST00000141334						3	0	3	3	0	0	9	35	7	24	17		
ENSMUST00000141335						0	0	7	0	0	0	0	0	0	0	0		
ENSMUST00000141336						29	34	229	11	36	33	2	5	0	2	3		
ENSMUST00000141337						0	3	0	0	0	0	19	187	38	0	36		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141339	ENSMUSG00000057715	1	11414105	11975901	1	0	0	0	0	0	0	0	0	0	0	0	F6RV71	
ENSMUST00000141340						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141342						23	20	53	243	37	19	9	4	7	0	13		
ENSMUST00000141343						7	6	9	0	2	0	5	17	59	0	13		
ENSMUST00000141345						0	0	7	64	0	0	0	0	0	0	0		
ENSMUST00000141346	ENSMUSG00000068250	6	149157147	149188712	-1	0	1	1	0	0	0	0	3	0	5	0	B8JKU9	
ENSMUST00000141348						1	2	13	5	3	0	0	0	1	0	0		
ENSMUST00000141349						5	3	13	4	6	2	0	11	3	0	3		
ENSMUST00000141350						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000141351						2	4	2	118	6	7	1	2	0	0	1		
ENSMUST00000141352	ENSMUSG00000019731	8	72480641	72492614	-1	0	0	0	4	0	0	0	4	14	0	16	F7BUQ6	
ENSMUST00000141353	ENSMUSG00000042208	11	23564961	23633639	-1	0	0	0	0	0	0	0	0	0	0	0	Z4YN22	
ENSMUST00000141354	ENSMUSG00000040990	X	159627272	159978069	1	0	0	2	0	1	0	0	22	0	0	0	E9Q0C1	
ENSMUST00000141355	ENSMUSG00000030695	7	126795234	126800751	-1	3	0	6	2	3	0	3	13	11	3	8	D3Z510	
ENSMUST00000141356						1	2	1	21	2	0	0	0	0	0	0		
ENSMUST00000141357						4	7	5	16	7	0	30	281	64	9	61		
ENSMUST00000141358						0	3	0	0	1	0	0	0	0	0	0		
ENSMUST00000141359	ENSMUSG00000015189	6	4600839	4643355	1	0	0	0	0	0	0	0	0	0	0	4	F6TUA2	
ENSMUST00000141360	ENSMUSG00000020634	12	4879032	4907705	-1	0	0	0	4	0	0	27	20	63	11	13	D6RGU9	
ENSMUST00000141361						1	1	3	0	0	0	0	31	6	0	8		
ENSMUST00000141362	ENSMUSG00000024818	19	5877808	5885766	1	0	0	0	1	0	0	0	7	6	0	17	F6ZZX2	
ENSMUST00000141363						2	5	5	94	15	2	0	3	3	0	7		
ENSMUST00000141364	ENSMUSG00000022487	15	103402405	103430470	-1	0	4	0	0	0	0	0	0	0	9	0		Q9DAN6
ENSMUST00000141365	ENSMUSG00000026728	2	13573927	13582826	1	0	0	1	30	0	0	2	8	4	3	17	A2AKJ2	
ENSMUST00000141366	ENSMUSG00000000167	9	50617321	50625000	1	16	17	24	26	20	11	4	6	1	4	1	D3Z3T0	
ENSMUST00000141367	ENSMUSG00000040624	10	3740364	3967303	1	6	4	1	0	3	2	0	0	0	0	0	F7CES2	
ENSMUST00000141368						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141369						6	2	9	9	3	6	8	73	20	3	44		
ENSMUST00000141370	ENSMUSG00000038112	9	39587396	39604403	-1	0	0	2	5	0	4	0	0	0	0	0	D3Z518	
ENSMUST00000141371						0	0	4	4	2	0	0	2	0	1	0		
ENSMUST00000141372						0	5	0	0	2	1	4	287	208	230	156		
ENSMUST00000141373						5	3	6	7	5	1	2	18	6	0	29		
ENSMUST00000141374						41	66	92	42	57	31	10	9	10	0	10		
ENSMUST00000141376						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000141377	ENSMUSG00000028099	3	96711490	96727628	-1	5	4	0	0	0	0	0	0	0	0	0		Q9D483
ENSMUST00000141378	ENSMUSG00000061479	7	27187005	27196271	-1	5	0	8	0	0	3	0	0	0	0	0	D6RI83	
ENSMUST00000141379						7	4	8	6	8	1	0	1	0	0	2		
ENSMUST00000141380	ENSMUSG00000085601	7	19099046	19118368	-1	2	1	1	53	4	0	0	0	0	0	0	D3YZT1	
ENSMUST00000141381						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141382	ENSMUSG00000042254	9	65265180	65280605	1	21	15	0	0	48	25	0	0	0	0	1	D6RD06	
ENSMUST00000141383	ENSMUSG00000034724	5	96070333	96164171	-1	0	1	0	0	0	0	0	0	0	0	10	D3YVH6	
ENSMUST00000141384						71	70	108	112	116	59	60	412	84	0	57		
ENSMUST00000141385	ENSMUSG00000070371	7	127932638	127946725	-1	0	1	0	0	0	0	0	0	0	0	0	D3YY92	
ENSMUST00000141386						9	3	12	31	8	3	0	0	0	0	0		
ENSMUST00000141387	ENSMUSG00000027887	3	108211472	108226648	-1	5	5	51	37	14	7	0	0	0	0	0	A2AE45	O89104
ENSMUST00000141388						50	53	99	28	34	11	0	0	3	0	2		
ENSMUST00000141389						7	4	85	5	5	4	0	1	0	0	0		
ENSMUST00000141391						4	1	28	1	1	0	0	1	0	6	0		
ENSMUST00000141392						8	12	0	0	15	21	16	0	14	26	14		
ENSMUST00000141393						0	0	3	28	4	0	0	0	0	0	0		
ENSMUST00000141395						9	4	11	7	5	1	0	1	8	1	20		
ENSMUST00000141396						10	3	32	23	24	1	0	10	25	0	48		
ENSMUST00000141397						3	0	19	7	6	2	0	0	0	0	0		
ENSMUST00000141398	ENSMUSG00000074895	13	54783998	54788459	1	18	13	23	1	21	8	0	0	0	0	0	Q27ZI7	
ENSMUST00000141400						0	0	0	0	0	0	2	0	12	0	0		
ENSMUST00000141401						2	1	1	60	4	0	0	0	0	0	2		
ENSMUST00000141403						0	0	0	24	5	0	0	0	0	0	0		
ENSMUST00000141404	ENSMUSG00000022757	16	56690332	56717450	-1	0	0	0	5	0	0	0	0	0	0	0	B8JJG9	
ENSMUST00000141406						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000141408						0	0	0	0	1	0	0	6	2	0	2		
ENSMUST00000141409	ENSMUSG00000018334	11	79013440	79146407	-1	2	2	23	112	10	0	0	0	7	0	8	Q5SXE2	
ENSMUST00000141410	ENSMUSG00000024959	19	6941861	6951898	1	5	4	9	5	6	4	51	74	54	73	40	F7ABX5	
ENSMUST00000141411						2	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000141412	ENSMUSG00000026173	1	74542888	74567794	1	0	0	30	0	0	4	0	0	0	0	0	D6RGN2	
ENSMUST00000141413						1	3	4	0	9	0	0	4	0	2	3		
ENSMUST00000141414						72	49	681	135	53	52	10	23	28	13	14		
ENSMUST00000141415	ENSMUSG00000019373	11	59817795	59839838	-1	0	1	0	0	0	1	0	0	0	0	0	D3Z036	
ENSMUST00000141416	ENSMUSG00000057406	5	33820725	33897975	1	6	0	0	0	0	0	0	0	18	11	0	F6Y765	
ENSMUST00000141417	ENSMUSG00000026019	1	60069785	60098645	-1	5	0	0	1	1	2	1	10	1	0	8	D3Z369	
ENSMUST00000141418						3	1	8	0	2	2	0	4	9	0	11		
ENSMUST00000141419						212	231	321	211	233	145	8	43	33	16	48		
ENSMUST00000141421						4	2	7	3	7	0	0	0	0	0	1		
ENSMUST00000141422						35	20	38	41	32	13	2	0	4	0	20		
ENSMUST00000141423						0	0	0	10	0	0	0	2	2	4	2		
ENSMUST00000141424	ENSMUSG00000037712	14	45458792	45530118	-1	3	3	0	1	3	4	0	0	0	0	4	A6X941	
ENSMUST00000141425						5	7	17	6	12	2	0	0	0	0	1		
ENSMUST00000141426	ENSMUSG00000043411	4	137593755	137658537	1	0	0	0	0	0	0	13	41	8	1	4	F6VSP0	
ENSMUST00000141427						2	1	8	20	9	4	0	0	0	0	0		
ENSMUST00000141429	ENSMUSG00000061533	12	90998492	91384409	-1	0	11	15	0	16	0	170	320	529	138	274	B7ZNX8	Q8BI22
ENSMUST00000141430						3	1	0	0	2	0	0	4	4	0	0		
ENSMUST00000141431						0	0	0	3	0	0	36	111	76	0	140		
ENSMUST00000141432						3	1	9	3	5	0	0	0	0	0	0		
ENSMUST00000141434						2	0	0	0	3	0	75	37	76	3	52		
ENSMUST00000141435						4	3	15	0	3	4	4	20	16	0	24		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141436	ENSMUSG00000018654	11	11685003	11772926	1	0	0	0	0	0	0	4	0	0	0	5	Q5SWT6	
ENSMUST00000141437	ENSMUSG00000074646	2	155973279	156007977	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZCN8	
ENSMUST00000141438	ENSMUSG00000050174	3	37404910	37420211	-1	6	4	0	9	3	0	0	0	0	0	0	A0A0G2JE11	
ENSMUST00000141439						4	3	2	0	3	0	0	0	0	0	0		
ENSMUST00000141441						0	0	11	7	5	0	6	2	0	2	5		
ENSMUST00000141442						11	10	12	18	10	8	14	49	18	0	43		
ENSMUST00000141443	ENSMUSG00000037685	5	67618140	67847434	-1	3	3	15	4	5	1	0	4	0	10	2	F6Q8P7	
ENSMUST00000141444						3	3	10	5	6	2	0	1	1	0	4		
ENSMUST00000141446	ENSMUSG00000022194	14	54892500	54898169	1	0	0	0	4	2	0	48	69	58	12	146	D3Z055	
ENSMUST00000141447	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	4	18	1	0	13	3	35	5	70	E0CYX5	
ENSMUST00000141448						0	6	0	0	0	0	1	0	71	0	11		
ENSMUST00000141449	ENSMUSG00000068551	6	48427697	48445825	-1	0	0	0	0	0	0	4	0	0	0	0	S4R1N3	
ENSMUST00000141451						10	4	16	11	11	5	0	0	0	0	0		
ENSMUST00000141453	ENSMUSG00000022185	14	54642161	54686931	-1	18	0	0	14	0	11	0	0	0	52	0	Q52KR6	
ENSMUST00000141456						1	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000141457						2	2	1	0	2	1	0	27	4	5	14		
ENSMUST00000141458						6	3	2	0	1	3	5	29	14	0	10		
ENSMUST00000141459						8	4	13	3	10	6	2	0	0	0	0		
ENSMUST00000141460						203	129	739	192	78	56	8	80	14	4	14		
ENSMUST00000141461						15	20	15	5	6	1	0	10	3	0	3		
ENSMUST00000141462						0	0	0	0	1	0	0	7	0	0	0		
ENSMUST00000141463	ENSMUSG00000027281	2	136891218	137071950	1	0	0	7	0	0	0	1	0	1	1	0	A2AHF0	
ENSMUST00000141464						0	0	3	2	0	0	0	0	3	0	0		
ENSMUST00000141465	ENSMUSG00000046897	15	102203648	102215606	1	0	0	0	2	0	0	23	18	29	0	26	D3Z4A3	
ENSMUST00000141466						15	0	4	12	12	3	2	5	1	0	0		
ENSMUST00000141467						1	0	0	0	0	0	0	184	10	0	0		
ENSMUST00000141470						0	2	0	94	4	9	70	232	61	197	56		
ENSMUST00000141471	ENSMUSG00000028064	3	88435959	88461182	-1	0	0	5	3	6	0	5	0	0	0	0	D3YVM6	
ENSMUST00000141472						4	0	46	11	6	4	2	0	4	2	0		
ENSMUST00000141474						3	1	5	1	3	1	0	18	0	0	0		
ENSMUST00000141475	ENSMUSG00000055762	15	75894796	75909556	-1	0	3	4	87	4	2	0	0	0	0	0	E9PUM6	
ENSMUST00000141477						4	0	2	96	3	2	0	2	0	0	1		
ENSMUST00000141478						2	1	0	10	2	2	0	0	0	0	0		
ENSMUST00000141479						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141480						8	5	18	14	14	9	0	39	6	16	12		
ENSMUST00000141481						3	3	3	30	10	6	0	0	0	0	0		
ENSMUST00000141482	ENSMUSG00000027359	2	126552407	126588243	1	4	4	3	0	0	1	2	0	0	4	0	A2ANX6	
ENSMUST00000141483	ENSMUSG00000029661	6	4504814	4541544	1	7	2	8	16	7	1	0	0	0	0	2	E0CXI2	
ENSMUST00000141486						1	0	0	0	0	0	34	14	77	5	86		
ENSMUST00000141487	ENSMUSG00000037697	14	45593174	45658143	-1	0	0	0	0	0	0	43	262	231	31	116	G3UWN4	
ENSMUST00000141489	ENSMUSG00000047989	18	24104757	24121953	-1	0	9	3	21	0	4	0	45	0	7	0	D3Z6F3	
ENSMUST00000141490	ENSMUSG00000037159	6	40439088	40466813	1	5	0	9	1	4	3	0	2	0	0	1	D3Z4B4	
ENSMUST00000141491	ENSMUSG00000070828	7	11397915	11402741	1	0	0	6	3	9	0	0	0	0	0	0	L7N266	
ENSMUST00000141492						0	0	0	0	0	0	0	0	31	2	14		
ENSMUST00000141493	ENSMUSG00000047613	4	153957237	153961925	1	3	0	2	0	0	1	0	0	0	3	0	A0A0A0MQL2	
ENSMUST00000141495						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000141496						5	8	11	4	4	7	28	71	24	6	14		
ENSMUST00000141497	ENSMUSG00000027652	2	158409848	158499253	1	0	15	40	0	0	29	113	1031	311	64	36	A2ACC7	
ENSMUST00000141498						4	1	11	8	3	0	0	35	11	5	12		
ENSMUST00000141499						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141500						0	0	4	31	0	0	0	0	0	0	0		
ENSMUST00000141501						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000141502						0	0	0	0	3	3	1	0	0	0	0		
ENSMUST00000141503						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141504	ENSMUSG00000030243	6	142350342	142387087	-1	14	23	13	15	17	17	2	13	4	0	11	F6S4D9	
ENSMUST00000141505	ENSMUSG00000031596	8	40862396	40922308	1	1	1	3	80	8	5	0	0	0	0	0		
ENSMUST00000141506						16	8	136	356	21	13	0	5	0	0	5		
ENSMUST00000141507	ENSMUSG00000024201	17	56326062	56402870	1	1	11	0	10	21	14	65	263	78	30	63	F7BTY2	
ENSMUST00000141508						2	7	4	1	5	0	0	1	0	0	0		
ENSMUST00000141509						2	0	10	2	0	3	0	7	0	0	0		
ENSMUST00000141510	ENSMUSG00000029408	5	124061530	124095798	-1	6	0	0	0	0	0	0	0	0	0	0	D6RFD9	
ENSMUST00000141512	ENSMUSG00000057715	1	11414105	11975901	1	0	2	1	2	2	0	0	0	0	0	0		Q8BZJ8
ENSMUST00000141513						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000141514						0	0	0	0	0	0	1	5	0	0	0		
ENSMUST00000141515						16	16	40	17	23	12	0	3	4	1	4		
ENSMUST00000141516	ENSMUSG00000059995	11	102289300	102296631	-1	0	0	9	0	0	20	161	632	235	103	123	F6RCN9	
ENSMUST00000141517						11	10	7	8	9	4	2	6	5	2	2		
ENSMUST00000141518	ENSMUSG00000006219	4	141576062	141606096	-1	3	1	0	28	3	0	0	0	0	0	0	A2ADE7	
ENSMUST00000141519						0	2	6	4	8	0	0	1	12	26	0		
ENSMUST00000141520						2	1	3	4	3	0	8	4	3	0	8		
ENSMUST00000141521						26	19	25	42	25	18	0	0	0	0	0		
ENSMUST00000141522						0	0	0	0	0	0	0	0	2	1	0		
ENSMUST00000141523						0	0	0	0	0	0	26	28	21	0	15		
ENSMUST00000141525	ENSMUSG00000040774	3	106502260	106547802	-1	2	1	0	189	10	4	3	6	17	29	15	D3Z5Y5	
ENSMUST00000141526						28	27	26	17	36	14	0	1	5	0	3		
ENSMUST00000141527						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000141528						4	3	4	6	5	0	208	1217	376	22	596		
ENSMUST00000141529						0	3	3	1	2	0	4	7	3	3	3		
ENSMUST00000141530	ENSMUSG00000018593	11	55394500	55420080	-1	0	4	31	59	5	0	0	0	0	0	0	Q5NCU3	
ENSMUST00000141531						7	0	10	2	11	0	11	0	0	16	30		
ENSMUST00000141533						15	11	29	45	25	6	0	1	0	0	0		
ENSMUST00000141534						0	0	5	17	3	0	29	68	12	3	33		
ENSMUST00000141535						1	0	2	1	9	0	0	0	18	0	0		
ENSMUST00000141536						4	0	0	109	5	0	0	0	9	4	66		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141537						1	2	0	3	3	0	0	14	3	0	0		
ENSMUST00000141539						12	0	14	169	19	4	125	194	33	8	87		
ENSMUST00000141540						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000141542						2	2	0	31	0	0	0	0	0	0	0		
ENSMUST00000141544						0	0	3	0	0	0	14	105	17	9	10		
ENSMUST00000141545						3	3	0	1	1	0	0	0	0	1	0		
ENSMUST00000141546						6	0	4	3	3	2	15	11	12	0	28		
ENSMUST00000141548						16	12	51	0	0	0	1	6	2	2	4		
ENSMUST00000141550						0	0	0	2	0	0	0	0	2	0	0		
ENSMUST00000141552						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141553	ENSMUSG00000051674	5	73481000	73560794	1	0	0	0	22	2	0	0	0	0	0	0	F7A063	
ENSMUST00000141555						0	3	4	0	0	3	0	0	1	2	0		
ENSMUST00000141556						2	0	4	0	4	0	11	14	23	7	4		
ENSMUST00000141557	ENSMUSG00000021711	13	104142149	104178469	-1	0	72	102	38	0	30	39	142	68	84	125		Q3TIR1
ENSMUST00000141558						1	0	1	81	5	0	0	0	0	0	0		
ENSMUST00000141560	ENSMUSG00000006301	1	74288247	74305622	-1	0	0	0	124	0	0	0	0	0	0	0	D3Z0A5	
ENSMUST00000141561						3	6	5	2	3	0	0	0	0	0	1		
ENSMUST00000141562						1	5	18	2	2	1	0	0	1	0	0		
ENSMUST00000141563						0	0	3	2	1	0	0	0	0	0	1		
ENSMUST00000141565						32	21	52	34	26	24	22	6	16	2	34		
ENSMUST00000141566						0	0	0	1	4	3	0	0	0	0	0		
ENSMUST00000141567	ENSMUSG00000015094	2	25399351	25409494	1	0	0	0	0	0	0	0	0	0	0	0	A2AJ20	
ENSMUST00000141568						1	4	4	6	1	2	49	797	184	48	300		
ENSMUST00000141569						2	0	4	0	0	1	10	167	52	56	69		
ENSMUST00000141570						1	0	1	2	6	0	11	195	15	12	13		
ENSMUST00000141572	ENSMUSG00000006711	13	24845135	24901270	1	0	24	0	109	0	0	0	0	0	0	0	F2Z497	
ENSMUST00000141573	ENSMUSG00000046709	5	102907948	103211334	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JEJ8	
ENSMUST00000141574						9	4	30	7	8	4	0	0	2	0	0		
ENSMUST00000141576						0	1	0	0	8	1	0	0	0	0	0		
ENSMUST00000141577	ENSMUSG00000054874	19	5664635	5688908	-1	0	1	0	0	0	0	0	0	5	0	0	F7AXS1	
ENSMUST00000141578						1	1	0	58	0	1	0	0	0	0	0		
ENSMUST00000141579						6	3	25	8	7	5	22	112	16	9	39		
ENSMUST00000141581	ENSMUSG00000000416	6	18366478	18514843	-1	0	0	0	0	0	3	0	0	0	0	0	F6XSM7	
ENSMUST00000141583						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000141584						6	3	16	7	2	2	24	302	49	13	94		
ENSMUST00000141585	ENSMUSG00000018239	11	53324679	53333301	1	2	4	9	6	3	1	0	0	0	0	1	F6QZB1	
ENSMUST00000141586						10	2	8	3	7	1	0	0	4	0	0		
ENSMUST00000141587						6	9	55	13	17	2	0	0	0	0	0		
ENSMUST00000141588	ENSMUSG00000028116	3	123006206	123035015	-1	4	2	0	0	2	3	0	0	0	0	0	D6RGM5	
ENSMUST00000141589						0	2	4	43	2	2	24	113	144	0	144		
ENSMUST00000141590						0	2	0	4	2	3	5	13	13	2	14		
ENSMUST00000141592						0	0	0	2	0	0	0	35	13	6	14		
ENSMUST00000141594						0	1	13	3	6	0	0	0	0	0	0		
ENSMUST00000141595						0	0	0	0	0	0	1	5	0	0	7		
ENSMUST00000141596						0	8	9	72	13	4	18	32	8	1	8		
ENSMUST00000141597						19	14	11	15	13	8	1	3	7	1	3		
ENSMUST00000141598						2	1	4	35	3	0	4	17	9	1	13		
ENSMUST00000141599						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000141600	ENSMUSG00000029804	6	58831465	58920398	1	0	0	0	20	0	0	2	1	0	0	3	D3Z3U0	
ENSMUST00000141601	ENSMUSG00000044681	5	28200819	28245792	-1	12	12	12	8	7	6	0	1	3	0	0	F7C041	Q4VAB4
ENSMUST00000141602	ENSMUSG00000029622	5	145114215	145130705	1	1	1	0	103	7	0	45	26	18	0	38	D3Z6S0	
ENSMUST00000141603						14	31	45	53	19	9	0	2	0	0	0		
ENSMUST00000141604	ENSMUSG00000031399	X	74384719	74393272	-1	0	0	0	0	0	0	0	5	2	0	0	D6RJK2	
ENSMUST00000141605						12	7	15	4	15	2	4	11	1	2	3		
ENSMUST00000141606	ENSMUSG00000002279	17	25579174	25662826	1	8	3	9	23	6	1	0	0	0	0	2	F6YC79	
ENSMUST00000141607						0	5	9	0	5	0	0	0	0	0	0		
ENSMUST00000141608						0	0	0	0	0	0	49	101	39	16	36		
ENSMUST00000141609						1	0	0	0	0	0	0	12	0	0	2		
ENSMUST00000141610	ENSMUSG00000024829	19	3282901	3292837	1	0	0	1	0	0	0	0	4	0	29	0	D6RJ32	
ENSMUST00000141611						0	0	4	1	1	0	0	5	0	0	0		
ENSMUST00000141612						0	0	3	0	1	1	6	5	13	0	12		
ENSMUST00000141613						2	0	0	0	0	0	25	150	10	0	36		
ENSMUST00000141614	ENSMUSG00000020744	11	115614178	115628295	-1	1	0	0	0	0	0	5	3	0	0	9	A2A9V4	
ENSMUST00000141615						0	8	14	2	5	1	0	49	0	32	4		
ENSMUST00000141616						0	2	15	3	3	2	6	127	7	12	31		
ENSMUST00000141617						26	18	27	61	18	11	5	8	5	12	3		
ENSMUST00000141618						2	0	24	13	5	0	2	27	11	2	11		
ENSMUST00000141619						0	1	5	0	1	1	0	0	12	0	0		
ENSMUST00000141620						3	0	0	4	5	0	24	67	43	4	58		
ENSMUST00000141621						0	0	0	1	0	1	9	14	16	3	13		
ENSMUST00000141622	ENSMUSG00000021062	12	76797960	76822908	-1	3	1	0	0	0	0	0	0	0	1	0	D3YYX5	
ENSMUST00000141623	ENSMUSG00000018559	11	69981156	69990601	1	2	1	0	0	0	0	380	407	192	31	157	J3QPC9	
ENSMUST00000141624						4	3	4	4	1	2	0	0	0	0	1		
ENSMUST00000141625	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	2	0	0	0	0	0	0	0	F6TCC6	
ENSMUST00000141626						2	0	5	26	1	1	1	0	3	0	8		
ENSMUST00000141628	ENSMUSG00000043411	4	137593755	137658537	1	0	0	0	0	0	0	27	243	93	30	77	A2ALR5	
ENSMUST00000141629	ENSMUSG00000031167	X	8138975	8145880	-1	0	4	0	0	0	2	11	215	82	41	39	S4R2M6	
ENSMUST00000141630	ENSMUSG00000025747	5	30058202	30073617	-1	186	160	80	179	239	142	0	34	11	3	20	D6RCW9	
ENSMUST00000141631	ENSMUSG00000023990	17	47737030	47792419	1	0	0	0	1	0	0	0	4	0	0	4	D3YZM7	
ENSMUST00000141632						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000141633						2	0	3	42	3	1	0	0	0	0	0		
ENSMUST00000141634						0	8	38	46	36	11	0	0	0	0	0		
ENSMUST00000141635	ENSMUSG00000003526	16	18060357	18090203	-1	13	6	23	0	8	0	4	0	0	0	0	F6YFQ5	
ENSMUST00000141636						1	0	1	4	1	1	0	3	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141638						4	1	0	3	7	8	0	0	0	0	0		
ENSMUST00000141640						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000141641						1	1	3	0	0	0	0	0	1	0	0		
ENSMUST00000141642	ENSMUSG00000037108	5	137787798	137822621	1	4	2	0	2	0	2	2	4	0	17	11	F6VAP9	
ENSMUST00000141643						0	0	3	10	4	0	0	0	0	0	0		
ENSMUST00000141644						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000141645						65	64	246	61	68	43	8	12	27	4	49		
ENSMUST00000141646						2	2	6	0	3	1	0	0	2	0	2		
ENSMUST00000141647						30	27	91	10	40	12	0	44	5	7	9		
ENSMUST00000141648						4	3	0	1	5	3	1	4	2	0	1		
ENSMUST00000141650	ENSMUSG00000027074	2	84936579	84958509	1	2	0	1	89	0	2	4	0	2	2	4	Z4YM12	
ENSMUST00000141651						3	2	26	0	6	3	0	1	0	0	0		
ENSMUST00000141653	ENSMUSG00000038718	2	34171457	34373142	-1	1	0	1	41	4	3	0	0	0	0	0	B2FDH3	
ENSMUST00000141654						0	0	0	0	0	0	9	34	16	24	9		
ENSMUST00000141655						4	0	0	3	0	2	0	0	0	0	0		
ENSMUST00000141657						4	8	3	3	4	0	1	0	0	0	3		
ENSMUST00000141658						0	0	2	3	0	3	15	9	10	0	0		
ENSMUST00000141659						5	1	9	0	6	3	2	0	7	0	6		
ENSMUST00000141660	ENSMUSG00000042425	X	140367494	140394540	1	2	3	0	3	0	2	0	0	0	0	0	B1AVD7	
ENSMUST00000141661						4	2	9	2	2	0	1	0	5	1	0		
ENSMUST00000141662	ENSMUSG00000024426	17	35897595	35910075	-1	0	5	14	0	0	3	19	17	25	0	38		Q8K341
ENSMUST00000141663						3	3	14	4	0	1	0	0	1	0	1		
ENSMUST00000141664						1	0	0	2	5	1	0	0	0	3	0		
ENSMUST00000141665						2	4	0	0	0	0	0	25	27	3	12		
ENSMUST00000141666						4	4	3	32	2	5	0	1	0	0	1		
ENSMUST00000141667						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000141668						0	0	0	0	0	0	33	71	25	35	63		
ENSMUST00000141669						0	2	10	1	0	4	0	0	2	0	5		
ENSMUST00000141670						11	4	16	50	10	4	13	79	31	6	79		
ENSMUST00000141671						4	3	1	6	0	0	0	0	0	0	2		
ENSMUST00000141672						0	4	0	1	0	0	44	165	63	15	113		
ENSMUST00000141673						0	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000141674						1	0	2	2	2	2	1	20	9	0	11		
ENSMUST00000141675						2	3	10	4	2	0	0	0	0	0	0		
ENSMUST00000141676						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000141677						2	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000141680	ENSMUSG00000031865	6	83165920	83200117	1	0	0	4	0	5	0	0	0	0	0	0	D3Z2M9	
ENSMUST00000141682	ENSMUSG00000014303	16	4594713	4624924	1	0	0	1	0	0	0	0	0	1	1	1	D3YYX4	
ENSMUST00000141683						0	1	28	21	8	0	9	0	5	8	0		
ENSMUST00000141685						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141687	ENSMUSG00000029247	5	76951307	76967509	1	1	0	4	0	0	0	0	0	0	0	0	D3Z6P1	
ENSMUST00000141689						0	0	2	1	4	1	0	2	0	1	2		
ENSMUST00000141690						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000141691						7	8	53	41	13	14	0	73	0	0	17		
ENSMUST00000141692						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141693						4	6	15	5	12	2	0	0	0	0	2		
ENSMUST00000141694						15	22	54	41	26	17	0	0	0	1	0		
ENSMUST00000141695	ENSMUSG00000040746	11	70647235	70651421	1	1	3	9	9	14	10	80	214	80	27	107	D6RCH3	
ENSMUST00000141698						4	3	1	0	1	1	5	16	4	0	1		
ENSMUST00000141699						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141701						2	1	28	4	3	1	0	4	9	0	6		
ENSMUST00000141702						4	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000141703	ENSMUSG00000020268	11	54826866	54860916	-1	14	19	83	22	15	19	0	6	0	3	3	D6RD13	
ENSMUST00000141704	ENSMUSG00000023072	7	35397035	35438689	1	6	7	11	14	0	0	13	0	0	14	0	E9Q9S2	
ENSMUST00000141705						45	23	84	41	43	29	3	0	0	0	2		
ENSMUST00000141706						13	0	0	0	10	2	0	0	0	0	0		
ENSMUST00000141707						0	0	1	0	1	0	0	3	2	0	0		
ENSMUST00000141708						14	10	30	14	10	12	0	0	0	0	0		
ENSMUST00000141709	ENSMUSG00000026222	1	85649988	85709998	1	1	1	4	4	5	3	70	86	95	7	102	F6Q968	
ENSMUST00000141711	ENSMUSG00000029836	6	51470360	51483704	1	0	0	0	0	7	2	0	0	0	0	4	D3Z313	
ENSMUST00000141712						4	2	13	1	5	0	0	0	1	0	0		
ENSMUST00000141713	ENSMUSG00000074224	7	29519205	29538057	1	55	60	142	219	88	48	0	0	0	0	0	E9Q1N0	
ENSMUST00000141714						3	1	9	1	3	1	0	63	0	7	7		
ENSMUST00000141715						0	2	0	0	0	1	2	3	3	0	0		
ENSMUST00000141716						3	6	11	5	7	3	4	10	19	2	15		
ENSMUST00000141717						0	2	0	0	2	6	0	0	0	0	0		
ENSMUST00000141718	ENSMUSG00000040811	7	19176421	19206482	1	0	0	4	5	3	0	10	10	17	3	15		
ENSMUST00000141719						0	0	0	0	0	0	60	0	0	0	0		
ENSMUST00000141720	ENSMUSG00000028347	4	48585174	48663131	1	0	0	0	1	0	0	0	0	0	0	0	A2AML9	
ENSMUST00000141721						9	0	11	54	10	6	6	72	15	0	0		
ENSMUST00000141722	ENSMUSG00000019790	10	9755547	9901079	-1	5	1	0	115	11	0	493	759	1492	17	569	D3Z079	
ENSMUST00000141724	ENSMUSG00000020083	10	62107655	62143920	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2E9	
ENSMUST00000141725	ENSMUSG00000027087	2	83724397	83806916	1	0	0	0	44	0	0	3	1	8	0	12	B7ZCI9	
ENSMUST00000141726	ENSMUSG00000038563	7	82648614	82777852	1	0	5	0	6	0	0	0	0	0	0	0	D3Z1V3	
ENSMUST00000141727						2	2	5	2	6	1	2	4	7	0	27		
ENSMUST00000141728						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000141730						1	0	0	15	2	0	3	0	7	3	0		
ENSMUST00000141732						3	0	11	8	0	0	0	0	0	0	0		
ENSMUST00000141733	ENSMUSG00000029723	5	137745730	137768450	1	0	0	0	0	0	1	786	1365	860	98	630	F6VXN4	
ENSMUST00000141734						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000141735						0	0	0	0	0	0	9	14	28	11	37		
ENSMUST00000141736						1	3	3	48	4	1	0	0	0	0	0		
ENSMUST00000141737						2	0	1	60	1	1	0	0	0	0	0		
ENSMUST00000141738						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141739						0	1	0	3	1	1	0	3	0	0	1		
ENSMUST00000141740	ENSMUSG00000037270	3	36863104	37053033	1	0	0	0	0	0	0	0	60	0	0	0	F6YAT5	
ENSMUST00000141742						0	1	0	0	0	0	0	0	0	5	5		
ENSMUST00000141743						0	4	11	8	8	0	0	0	0	0	0		
ENSMUST00000141744						4	2	3	3	6	0	0	0	0	0	0		
ENSMUST00000141745						3	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000141746						33	25	133	25	20	9	0	0	0	0	0		
ENSMUST00000141747						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141748						0	0	0	103	4	2	0	5	0	0	0		
ENSMUST00000141749						26	10	25	327	26	0	0	20	32	6	45		
ENSMUST00000141750						1	0	0	0	0	0	0	0	80	0	22		
ENSMUST00000141751						1	1	6	0	2	0	0	0	0	0	0		
ENSMUST00000141753						1	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000141754						0	3	0	9	0	1	179	196	0	2	0		
ENSMUST00000141755	ENSMUSG00000010554	11	74770830	74828525	1	80	88	301	149	114	55	20	50	30	13	37		Q9CQG2
ENSMUST00000141756						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141757						1	3	3	0	2	0	0	0	0	1	1		
ENSMUST00000141759						6	0	3	4	2	2	2	4	8	0	0		
ENSMUST00000141760	ENSMUSG00000060985	1	156255296	156303664	-1	0	0	0	0	0	0	0	0	0	0	0	J3QP93	
ENSMUST00000141761	ENSMUSG00000003868	7	45421852	45438096	-1	3	3	6	5	3	1	10	0	27	0	35	D3YXQ8	
ENSMUST00000141762	ENSMUSG00000034706	11	114727408	114757889	1	0	0	0	0	1	0	0	0	0	0	0	R4GML5	
ENSMUST00000141763						4	0	6	0	2	5	2	24	16	0	10		
ENSMUST00000141764						3	0	0	3	4	5	0	6	9	0	4		
ENSMUST00000141765						0	2	0	0	1	1	4	10	2	0	8		
ENSMUST00000141766						5	3	0	5	5	7	0	2	0	0	0		
ENSMUST00000141767						0	0	0	67	1	1	0	0	0	0	2		
ENSMUST00000141768						0	1	3	5	0	0	2	0	1	0	2		
ENSMUST00000141770						21	12	37	125	14	6	4	0	0	0	3		
ENSMUST00000141771						67	64	178	88	50	27	0	0	1	0	4		
ENSMUST00000141772						2	0	2	3	0	1	0	0	0	0	0		
ENSMUST00000141773						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141774						6	1	12	12	7	0	3	4	9	1	13		
ENSMUST00000141775	ENSMUSG00000032224	9	70089310	70142560	-1	783	377	2048	4317	730	450	0	10	1	1	6	D3YVT3	
ENSMUST00000141776						5	6	6	0	9	1	0	0	0	0	2		
ENSMUST00000141778						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141779						2	3	8	0	9	5	0	8	5	13	12		
ENSMUST00000141780						3	2	6	0	1	0	0	4	0	0	0		
ENSMUST00000141781						9	8	6	0	13	5	57	258	47	18	98		
ENSMUST00000141782						0	0	3	1	0	3	6	2	0	0	2		
ENSMUST00000141783	ENSMUSG00000026188	1	72284369	72303104	1	0	1	4	1	3	0	0	0	0	0	0	D3YUR6	
ENSMUST00000141784	ENSMUSG00000031543	8	22974844	23150497	1	0	0	0	0	0	0	2	0	0	0	5	G8JL84	
ENSMUST00000141785						5	3	11	84	5	3	0	0	0	0	0		
ENSMUST00000141788						4	1	9	8	2	2	0	0	1	0	2		
ENSMUST00000141789						0	0	2	0	0	0	4	0	0	0	0		
ENSMUST00000141790						0	0	4	0	2	0	0	0	0	0	0		
ENSMUST00000141791						0	0	1	0	2	0	0	0	10	0	4		
ENSMUST00000141792						0	1	4	3	4	6	2	1	2	0	5		
ENSMUST00000141793						12	12	32	25	18	18	30	108	61	7	88		
ENSMUST00000141794						3	4	1	8	1	3	1	2	1	3	1		
ENSMUST00000141795						0	0	0	0	0	2	0	0	0	1	0		
ENSMUST00000141796						0	0	0	8	0	0	0	0	0	0	1		
ENSMUST00000141798	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	0	0	0	0	0	0	0	0		Q8CI15
ENSMUST00000141799						1	0	0	0	0	0	22	9	19	0	0		
ENSMUST00000141800						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141801						1	4	2	1	3	4	1	1	0	0	0		
ENSMUST00000141802						10	14	16	43	25	10	0	1	0	0	0		
ENSMUST00000141803						5	6	0	0	0	3	16	0	0	11	3		
ENSMUST00000141804	ENSMUSG00000038618	7	141215860	141218658	1	2	0	0	1	0	0	8	0	2	0	0	D3YXM9	
ENSMUST00000141805	ENSMUSG00000052301	7	126847416	126852705	1	8	0	5	60	5	2	0	0	0	0	0	D3YZ51	
ENSMUST00000141806	ENSMUSG00000062859	17	28066747	28080639	-1	0	2	0	185	7	0	0	0	0	0	0	B2KF23	
ENSMUST00000141807						0	4	0	0	0	0	257	152	364	2484	347		
ENSMUST00000141808	ENSMUSG00000006471	2	25244821	25256022	-1	0	0	0	0	0	0	0	0	0	0	0	F6XCS1	
ENSMUST00000141812						0	1	0	0	1	0	0	0	2	0	0		
ENSMUST00000141813						2	0	3	15	0	0	2	9	5	8	6		
ENSMUST00000141814	ENSMUSG00000032841	2	101714285	101883027	-1	0	0	0	0	0	0	0	0	0	0	0	F6VRG5	
ENSMUST00000141815						0	0	0	14	15	0	17	70	15	17	0		
ENSMUST00000141816	ENSMUSG00000085473	4	88755195	88755590	-1	0	2	0	0	0	0	0	0	0	0	0	Q3UMN9	
ENSMUST00000141817						2	0	0	45	1	2	0	0	0	0	0		
ENSMUST00000141818	ENSMUSG00000015401	X	164088830	164118860	1	3	2	0	0	1	0	0	0	0	0	0	A2AHZ5	
ENSMUST00000141820						1	0	26	11	1	7	16	35	0	3	0		
ENSMUST00000141821	ENSMUSG00000032245	9	62838785	62852006	1	6	3	0	14	2	6	1	2	0	0	3	D6RE34	
ENSMUST00000141823						0	0	0	0	0	0	19	0	0	0	9		
ENSMUST00000141824	ENSMUSG00000029094	5	35893319	36003923	1	0	4	5	0	3	0	0	0	1	0	8	E9Q8X9	
ENSMUST00000141825	ENSMUSG00000000827	2	181497142	181517966	1	0	0	0	0	0	1	0	0	0	0	0	F6VQ81	
ENSMUST00000141826						2	0	0	33	0	0	0	7	10	0	7		
ENSMUST00000141827						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000141828						6	0	6	12	12	1	0	0	0	0	0		
ENSMUST00000141830	ENSMUSG00000042032	11	40679314	40695203	-1	0	0	0	38	0	3	67	189	338	280	173	E0CYU5	
ENSMUST00000141831						3	3	1	11	4	2	0	0	1	0	0		
ENSMUST00000141832						3	0	5	3	2	2	0	0	0	0	0		
ENSMUST00000141833	ENSMUSG00000056698	6	72565922	72598413	-1	8	28	47	23	34	24	16	31	18	0	26		
ENSMUST00000141834	ENSMUSG00000028919	4	141239499	141257564	1	5	0	4	60	4	4	0	0	0	0	0	A2A828	
ENSMUST00000141835						2	0	4	1	0	3	0	1	0	0	0		
ENSMUST00000141836						4	4	18	7	1	1	4	12	25	2	22		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141837	ENSMUSG00000018566	11	69942539	69948188	-1	2	0	2	7	2	0	1	0	0	0	0	J3QK17	
ENSMUST00000141838						2	5	3	5	0	1	2	17	4	1	6		
ENSMUST00000141839						2	1	2	16	0	1	1	48	22	44	19		
ENSMUST00000141840	ENSMUSG00000006931	11	100408456	100414836	-1	0	0	0	0	1	0	2	0	0	2	0	H3BK18	
ENSMUST00000141841						1	0	2	4	2	0	0	0	0	0	0		
ENSMUST00000141842						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000141844						1	4	13	5	2	4	0	0	0	0	0		
ENSMUST00000141845						0	0	10	2	3	1	0	0	0	2	0		
ENSMUST00000141847						6	4	4	9	8	7	0	0	0	0	0		
ENSMUST00000141848						6	1	4	3	3	0	2	9	4	0	3		
ENSMUST00000141849						18	19	167	0	17	5	12	29	40	13	31		
ENSMUST00000141851						0	0	0	0	0	2	0	75	17	0	28		
ENSMUST00000141852	ENSMUSG00000018651	11	84078920	84129600	-1	0	2	0	7	1	0	0	2	0	0	9	B1AT25	
ENSMUST00000141853						10	4	17	43	12	3	0	0	0	4	11		
ENSMUST00000141854						2	0	3	2	3	3	1	2	0	0	2		
ENSMUST00000141855						1	1	2	2	5	0	3	3	6	0	0		
ENSMUST00000141856	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	1	0	0	0	0	1	D3Z502	
ENSMUST00000141857	ENSMUSG00000029655	5	150608007	150666183	-1	4	1	3	28	5	2	2	3	8	11	3	D3YTM6	
ENSMUST00000141858						2	6	11	9	0	0	0	0	0	0	0		
ENSMUST00000141859	ENSMUSG00000020289	11	32225628	32267707	-1	0	0	10	1	0	4	24	11	0	0	3	F2Z3Y4	
ENSMUST00000141860						3	2	1	0	2	0	0	0	0	0	5		
ENSMUST00000141861						21	9	57	18	22	7	5	1	3	1	9		
ENSMUST00000141862						0	0	1	52	1	2	1	0	0	4	23		
ENSMUST00000141863						2	0	3	0	1	0	0	0	0	0	2		
ENSMUST00000141864						1	1	1	0	0	1	0	0	0	0	0		
ENSMUST00000141865						4	0	9	8	9	4	0	0	0	0	0		
ENSMUST00000141866						6	5	29	40	17	6	6	21	11	2	29		
ENSMUST00000141867						14	14	23	12	5	4	2	12	3	0	4		
ENSMUST00000141868						9	5	41	8	9	7	0	1	0	0	0		
ENSMUST00000141870						0	0	0	0	0	0	0	0	1	0	1		
ENSMUST00000141871	ENSMUSG00000020747	11	115765433	115799366	1	0	0	0	0	0	0	0	0	0	0	0	B1AT97	
ENSMUST00000141872	ENSMUSG00000027405	2	130274430	130279313	1	0	0	0	16	0	0	9	0	1	0	16	F7CHP9	
ENSMUST00000141873						34	45	91	23	47	15	11	39	31	17	56		
ENSMUST00000141874						12	7	14	20	15	7	50	126	167	27	46		
ENSMUST00000141876						29	25	246	36	35	17	38	84	83	0	56		
ENSMUST00000141877						0	0	1	129	0	0	0	0	0	0	0		
ENSMUST00000141878	ENSMUSG00000026466	1	156004599	156036480	-1	6	0	2	0	0	0	0	25	6	0	7	D3YZP0	
ENSMUST00000141879						0	0	0	0	0	0	0	3	0	0	2		
ENSMUST00000141880	ENSMUSG00000093989	11	70238124	70239842	-1	1	2	0	6	4	0	0	0	0	0	0	H3BJV0	
ENSMUST00000141881						23	20	29	6	22	6	2	25	19	4	11		
ENSMUST00000141882						3	2	2	4	3	1	1	8	3	2	10		
ENSMUST00000141883	ENSMUSG00000029070	4	155839680	155844088	1	0	4	5	83	12	0	0	0	1	0	1	A2AD97	
ENSMUST00000141884						4	2	4	7	0	0	0	2	0	0	29		
ENSMUST00000141885	ENSMUSG00000022964	16	91574503	91597800	-1	1	0	2	14	0	1	3	1	0	0	14	D6RH99	
ENSMUST00000141886						2	3	6	1	3	0	0	0	4	0	3		
ENSMUST00000141887	ENSMUSG00000060675	19	7557459	7588545	1	9	5	23	79	5	1	12	25	11	86	32	D3YYG1	
ENSMUST00000141888						4	2	5	6	7	2	0	0	0	0	0		
ENSMUST00000141889	ENSMUSG00000066113	4	86053915	86428385	1	0	0	0	16	0	1	0	0	0	0	0		Q8BLI0
ENSMUST00000141890						8	6	21	3	12	4	0	0	0	0	0		
ENSMUST00000141894						0	3	0	0	1	0	5	16	10	0	5		
ENSMUST00000141895						2	0	15	7	7	0	4	25	12	0	11		
ENSMUST00000141896						2	0	6	2	0	2	0	0	0	0	0		
ENSMUST00000141897						0	1	0	0	5	0	0	0	0	0	0		
ENSMUST00000141898	ENSMUSG00000020774	11	73304992	73329596	-1	0	1	2	1	2	2	0	0	0	2	4	D6RJ20	
ENSMUST00000141899	ENSMUSG00000032046	2	150832493	150904741	-1	0	0	3	0	0	0	0	52	0	0	0	D6RFU2	
ENSMUST00000141900						0	0	1	0	0	1	0	0	2	0	0		
ENSMUST00000141901						1	1	1	4	1	0	0	7	0	0	0		
ENSMUST00000141902	ENSMUSG00000039753	5	43744615	43821638	-1	8	0	5	0	0	0	1077	6654	1222	2210	1444	F6W6I1	
ENSMUST00000141903	ENSMUSG00000032604	9	108507713	108515941	1	0	0	0	0	0	0	6	0	13	8	0	F6TDS3	
ENSMUST00000141904	ENSMUSG00000059430	6	83512905	83536265	-1	0	0	0	3	3	0	0	0	0	0	0	D3YZY0	
ENSMUST00000141905						0	3	0	1	2	2	0	0	0	0	0		
ENSMUST00000141906						0	1	0	0	0	0	0	0	4	0	0		
ENSMUST00000141907						1	0	16	0	4	0	0	3	0	1	0		
ENSMUST00000141908						3	1	1	5	2	1	41	59	41	24	40		
ENSMUST00000141910						0	0	0	0	1	0	0	5	0	1	0		
ENSMUST00000141911						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141913						1	0	0	38	0	0	0	0	0	2	0		
ENSMUST00000141914						0	0	0	95	4	1	1	0	2	0	2		
ENSMUST00000141915						7	1	5	5	7	0	2	8	3	0	6		
ENSMUST00000141916	ENSMUSG00000058454	7	143823145	143848410	1	19	0	36	15	0	0	0	0	0	0	0		O88455
ENSMUST00000141917						20	20	255	10	10	5	5	38	3	13	13		
ENSMUST00000141918						5	0	2	3	5	0	0	0	0	0	0		
ENSMUST00000141919						40	29	56	242	50	39	0	0	0	0	0		
ENSMUST00000141920	ENSMUSG00000030960	7	132827457	132852673	-1	0	2	0	0	0	0	0	0	0	0	0	A0A087WQN6	
ENSMUST00000141921						0	0	0	129	8	0	0	1	7	0	0		
ENSMUST00000141924						1	3	20	0	0	4	0	0	0	0	0		
ENSMUST00000141925						3	4	15	9	15	0	40	285	109	83	171		
ENSMUST00000141927						0	0	0	2	0	0	9	85	36	3	22		
ENSMUST00000141928						0	0	21	3	0	1	0	1	3	0	0		
ENSMUST00000141931	ENSMUSG00000063524	4	150236721	150248879	1	1	2	4	0	3	0	25	16	36	14	16	B1ARR6	
ENSMUST00000141932						3	2	4	15	9	0	0	5	3	0	9		
ENSMUST00000141933	ENSMUSG00000028718	4	115000159	115043196	1	10	15	52	0	25	18	0	0	0	0	0	D6RH61	
ENSMUST00000141934						2	3	2	8	4	5	2	3	2	0	0		
ENSMUST00000141936	ENSMUSG00000031131	X	57088106	57106540	1	2	2	2	2	1	0	0	0	0	0	0	A2AFK0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000141938						3	5	11	17	4	0	0	38	19	0	0		
ENSMUST00000141939						7	7	16	0	13	0	12	10	7	17	19		
ENSMUST00000141941						0	3	0	0	2	2	0	0	1	0	0		
ENSMUST00000141942						18	27	27	63	63	18	0	7	18	5	27		
ENSMUST00000141943	ENSMUSG00000041592	11	113776374	114067046	-1	2	2	8	11	23	3	0	0	0	0	0	B1ASR7	
ENSMUST00000141944						2	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000141945						0	0	11	0	0	0	0	0	0	0	0		
ENSMUST00000141947						2	2	2	2	2	1	0	1	0	0	0		
ENSMUST00000141948						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000141950	ENSMUSG00000041609	5	115648175	115731621	-1	5	0	0	0	0	0	4	0	12	0	8	F6RQR3	
ENSMUST00000141951						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000141952						1	0	0	0	3	0	7	9	12	0	38		
ENSMUST00000141953						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000141954						2	3	2	1	2	0	10	0	8	0	23		
ENSMUST00000141955						0	5	0	33	7	3	0	0	0	0	0		
ENSMUST00000141956						2	2	0	1	1	2	0	0	0	0	0		
ENSMUST00000141957	ENSMUSG00000031889	8	105225145	105253053	1	4	13	36	0	8	4	144	193	110	0	0	D6RCI5	
ENSMUST00000141959	ENSMUSG00000022773	16	17069696	17087045	1	0	0	0	6	0	0	0	0	0	0	0	D3Z104	
ENSMUST00000141960						102	88	374	141	103	50	7	22	26	3	50		
ENSMUST00000141961						0	0	0	0	0	2	61	95	111	513	148		
ENSMUST00000141962						3	0	0	0	10	0	21	11	20	0	10		
ENSMUST00000141963						1	0	1	1	0	0	0	0	12	0	0		
ENSMUST00000141965						4	2	1	0	2	0	1	3	1	0	2		
ENSMUST00000141966	ENSMUSG00000028962	5	24423837	24440950	1	0	1	21	17	7	6	66	24	56	15	45	D3Z5G3	
ENSMUST00000141967						10	3	7	4	4	4	0	6	5	1	6		
ENSMUST00000141968	ENSMUSG00000028883	5	13125414	13602565	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4Q3	
ENSMUST00000141969						3	7	22	9	4	3	2	1	2	0	0		
ENSMUST00000141970						4	2	6	5	3	2	0	0	0	0	2		
ENSMUST00000141971	ENSMUSG00000022679	16	13903161	13949619	1	1	0	0	10	1	0	0	0	0	0	0	E9Q4P9	
ENSMUST00000141972	ENSMUSG00000046679	6	86438374	86473500	1	0	0	0	0	0	0	0	0	0	14	14		Q8R3C1
ENSMUST00000141973						0	5	13	0	2	0	7	23	11	2	22		
ENSMUST00000141974	ENSMUSG00000059005	2	75659261	75669407	1	13	5	288	53	0	0	10	135	14	80	61	A2AL13	
ENSMUST00000141975						0	0	0	16	0	0	6	5	3	0	0		
ENSMUST00000141976	ENSMUSG00000041609	5	115648175	115731621	-1	0	1	9	1	2	0	2	0	0	0	0	D6RJL4	
ENSMUST00000141977	ENSMUSG00000052748	1	151367699	151428455	-1	0	0	0	0	1	0	0	0	0	0	0	F7ABE5	
ENSMUST00000141978						39	29	272	103	35	29	1	10	5	0	11		
ENSMUST00000141979						0	2	3	4	2	0	17	1571	95	293	391		
ENSMUST00000141980						0	0	2	0	0	0	0	5	0	4	0		
ENSMUST00000141981						7	4	11	11	11	3	0	2	0	0	3		
ENSMUST00000141982						2	2	0	2	0	0	0	0	0	3	0		
ENSMUST00000141983						2	2	3	0	2	1	4	0	3	0	17		
ENSMUST00000141984	ENSMUSG00000060733	10	71347763	71433327	1	1	2	2	0	2	0	0	0	0	0	0	F6X767	
ENSMUST00000141985	ENSMUSG00000025855	5	139017306	139150001	-1	3	1	3	0	0	0	0	0	0	0	0	D3Z4L4	
ENSMUST00000141986						1	2	0	0	1	0	0	0	0	0	2		
ENSMUST00000141987						3	2	16	2	2	1	0	0	0	0	0		
ENSMUST00000141988	ENSMUSG00000000154	7	143473721	143499334	1	7	5	2	10	3	0	0	0	0	0	3	D6RDC9	
ENSMUST00000141990	ENSMUSG00000028845	4	126322121	126325688	-1	3	0	1	0	2	0	0	0	0	0	0	A3KFX9	
ENSMUST00000141991						0	4	0	7	4	0	3	0	4	2	3		
ENSMUST00000141992						1	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000141993						4	1	0	6	3	3	0	4	10	0	3		
ENSMUST00000141994						5	7	5	43	6	2	0	0	0	0	0		
ENSMUST00000141995	ENSMUSG00000028402	4	81278500	81442815	-1	0	5	3	1	3	0	0	0	0	0	2	I7HJS5	
ENSMUST00000141996						0	0	1	0	0	0	29	18	37	3	11		
ENSMUST00000141997	ENSMUSG00000030795	7	127967457	127985701	1	0	0	5	0	3	0	9	177	27	18	31	G3UZD2	
ENSMUST00000141998						2	5	3	5	5	0	0	6	0	0	4		
ENSMUST00000141999	ENSMUSG00000052423	1	171270328	171276896	1	0	1	0	0	0	0	0	3	3	0	0	D3YUU0	
ENSMUST00000142000						21	13	59	25	40	24	3	9	12	3	19		
ENSMUST00000142001	ENSMUSG00000028152	3	138742195	138907905	1	0	0	0	0	0	0	0	0	7	0	0	D6REF5	
ENSMUST00000142002						0	0	0	0	0	0	3	4	5	10	16		
ENSMUST00000142003	ENSMUSG00000045038	17	86167785	86657919	1	3	4	5	395	11	6	0	5	0	0	2	Q8C944	
ENSMUST00000142004						0	0	0	3	0	0	7	12	8	2	9		
ENSMUST00000142005	ENSMUSG00000045205	4	11261315	11322137	-1	23	19	117	16	22	10	2	4	7	0	0	D6RI72	
ENSMUST00000142006						0	0	14	10	11	0	4	21	7	1	27		
ENSMUST00000142007						3	2	0	0	2	3	0	50	19	4	21		
ENSMUST00000142010	ENSMUSG00000014504	18	34330847	34336599	1	0	0	0	0	0	0	4	9	7	8	0	D6RHP8	
ENSMUST00000142011	ENSMUSG00000032531	9	102716672	102733418	1	35	26	89	334	60	16	53	81	102	0	45	Q3TP05	
ENSMUST00000142012	ENSMUSG00000037904	12	110975353	110979040	-1	0	0	0	178	0	0	39	19	0	0	0	D3Z2N1	
ENSMUST00000142013						60	30	71	74	52	34	1	7	4	0	5		
ENSMUST00000142014						0	0	9	21	4	0	0	2	2	2	0		
ENSMUST00000142015						0	0	1	0	3	0	7	24	7	3	10		
ENSMUST00000142016						15	15	27	53	26	8	1	2	1	0	2		
ENSMUST00000142017	ENSMUSG00000020340	11	46193850	46312859	-1	1	0	14	5	9	0	539	0	667	0	705	F6QD74	
ENSMUST00000142018						2	3	11	14	6	4	0	8	0	0	7		
ENSMUST00000142020						21	11	39	86	22	13	0	57	21	14	9		
ENSMUST00000142021						7	7	14	6	0	0	0	0	0	0	0		
ENSMUST00000142022						0	0	0	0	0	0	0	0	0	0	5		
ENSMUST00000142023						6	1	8	1	2	0	4	3	5	0	5		
ENSMUST00000142024						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142026						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000142027						16	0	57	12	27	0	12	3	10	0	2		
ENSMUST00000142028	ENSMUSG00000026933	2	25926838	25983282	-1	0	0	0	0	0	0	0	0	0	0	0	F6QF29	
ENSMUST00000142029	ENSMUSG00000042380	4	127243784	127247809	1	8	6	30	54	19	8	504	581	251	106	202		Q78RX3
ENSMUST00000142030	ENSMUSG00000034377	17	6106437	6251128	1	0	0	0	5	0	0	0	0	0	0	4	D3Z003	
ENSMUST00000142031						1	0	1	2	0	0	0	0	33	0	12		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142033						0	0	0	0	0	0	51	242	43	82	0		
ENSMUST00000142034						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000142035						0	5	0	0	3	3	0	6	0	0	4		
ENSMUST00000142036						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000142038						2	2	2	1	3	0	0	0	0	0	4		
ENSMUST00000142039						9	3	25	78	16	6	36	78	13	0	35		
ENSMUST00000142040						10	13	31	21	16	10	0	0	0	0	1		
ENSMUST00000142041						91	44	307	126	67	41	15	35	31	3	35		
ENSMUST00000142042						25	23	54	18	11	10	1	18	11	5	17		
ENSMUST00000142043						2	0	1	7	4	0	3	68	7	0	19		
ENSMUST00000142045						1	3	1	0	7	0	0	14	0	0	0		
ENSMUST00000142046	ENSMUSG00000020672	12	30174482	30373375	-1	0	0	2	0	0	0	0	0	0	0	0	D6RFR4	
ENSMUST00000142048						21	16	25	33	27	16	0	0	0	0	0		
ENSMUST00000142049						3	0	10	3	0	0	0	0	1	0	1		
ENSMUST00000142050						0	2	0	1	0	0	0	1	1	0	1		
ENSMUST00000142051	ENSMUSG00000028047	3	89215180	89226837	1	0	0	0	0	0	0	0	0	0	0	2	D3Z6N1	
ENSMUST00000142052						0	0	0	0	0	0	0	0	19	0	0		
ENSMUST00000142054						2	7	17	1	9	2	2	0	0	0	0		
ENSMUST00000142055	ENSMUSG00000040296	4	40203773	40239828	-1	0	5	0	0	8	4	24	0	36	0	16	A2AP29	
ENSMUST00000142056						8	5	12	36	11	11	1	0	9	11	9		
ENSMUST00000142057						3	3	5	8	6	5	3	3	5	2	7		
ENSMUST00000142058	ENSMUSG00000038429	6	124815019	124829484	-1	0	0	0	0	0	0	0	0	6	0	0	D3Z4K7	
ENSMUST00000142059						3	8	17	0	7	3	1	33	9	4	4		
ENSMUST00000142060	ENSMUSG00000028268	3	142560026	142573209	1	1	2	0	0	0	0	0	0	0	4	15	D3YUH5	
ENSMUST00000142061	ENSMUSG00000060126	14	75845093	75848525	1	10	14	0	5	17	0	0	69	25	36	10	D3YU75	
ENSMUST00000142062	ENSMUSG00000025967	1	63176825	63180486	1	0	0	0	46	0	2	116	0	166	1583	285	M0QWK5	
ENSMUST00000142063	ENSMUSG00000013973	1	171329145	171342331	1	0	0	0	49	1	0	27	0	24	0	19	D3Z0F7	
ENSMUST00000142064	ENSMUSG00000043067	9	24411776	24503140	-1	0	0	0	0	1	0	37	137	58	35	117		A6X919
ENSMUST00000142065	ENSMUSG00000038615	11	96817414	96829968	-1	0	0	0	12	0	0	0	0	0	0	0	A2A6D1	
ENSMUST00000142066	ENSMUSG00000057766	18	12252362	12305720	-1	0	0	0	6	1	0	0	0	0	0	0	D3Z2G0	
ENSMUST00000142069	ENSMUSG00000018661	11	113649169	113667054	1	0	0	0	0	0	0	16	0	0	0	2	F6QQB5	
ENSMUST00000142070						208	127	353	78	140	48	8	6	22	10	30		
ENSMUST00000142071	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	3	0	0	0	23	0	0	18	0	E9Q8F0	
ENSMUST00000142072						14	5	9	6	14	4	0	0	0	0	0		
ENSMUST00000142075						0	2	7	0	10	3	23	159	91	2	77		
ENSMUST00000142078						13	2	18	0	2	6	0	0	0	0	0		
ENSMUST00000142079	ENSMUSG00000030254	6	112619850	112696686	-1	0	0	0	0	0	0	0	3	0	0	12	F6ZKR0	
ENSMUST00000142080	ENSMUSG00000057406	5	33820725	33897975	1	19	10	35	18	20	5	0	59	55	16	65	F6S6G6	
ENSMUST00000142081	ENSMUSG00000036555	5	140661827	140702378	-1	0	1	0	58	0	1	4	0	7	0	0	D3YXD4	
ENSMUST00000142082						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000142083						5	0	12	0	2	0	0	0	0	0	0		
ENSMUST00000142084						20	13	28	25	14	5	42	184	60	20	111		
ENSMUST00000142085	ENSMUSG00000024767	19	7198202	7206316	-1	1	0	0	8	0	1	0	7	0	0	8	D3Z7K0	
ENSMUST00000142086	ENSMUSG00000017146	11	101488764	101551955	-1	0	0	0	6	1	0	0	0	4	0	0	A0A087WPK5	
ENSMUST00000142087	ENSMUSG00000026939	2	25620067	25622005	-1	0	0	0	5	0	0	26	39	0	119	19		A2AJB2
ENSMUST00000142088	ENSMUSG00000020051	10	87521795	87584136	1	1	2	0	0	0	0	0	0	0	0	0	D3YZ73	
ENSMUST00000142089	ENSMUSG00000048442	11	115899966	115906269	1	0	0	3	0	2	0	2	0	0	0	0		Q8BT42
ENSMUST00000142090	ENSMUSG00000040479	2	91932824	91975864	-1	0	0	0	0	0	4	33	0	50	0	32	D6RIP2	
ENSMUST00000142092	ENSMUSG00000052593	12	21323509	21373632	-1	2	0	0	27	1	2	0	0	0	0	37	J3QMF2	
ENSMUST00000142093	ENSMUSG00000026981	2	24336853	24351494	1	0	0	0	0	0	0	0	0	3	2	3	A0A0A6YVU4	
ENSMUST00000142094	ENSMUSG00000038224	11	75431732	75439591	-1	5	0	0	0	6	4	1	0	0	0	0	E9PXE0	
ENSMUST00000142095						4	5	4	7	1	2	0	0	0	0	0		
ENSMUST00000142096	ENSMUSG00000026853	2	30400471	30415813	-1	4	0	4	2	3	1	9	11	5	2	4	B7ZDD9	
ENSMUST00000142097	ENSMUSG00000018677	11	102402985	102407946	-1	0	0	0	0	0	0	0	0	0	0	0	D6RE23	
ENSMUST00000142098						1	0	8	0	1	3	0	0	0	0	3		
ENSMUST00000142101						8	13	31	25	22	4	25	70	51	6	112		
ENSMUST00000142102						1	0	0	0	0	0	0	2	2	0	3		
ENSMUST00000142103	ENSMUSG00000061859	4	98395785	98719603	1	5	7	74	2	3	2	2	13	6	1	0	F6RSZ8	
ENSMUST00000142105	ENSMUSG00000025466	7	140096770	140102441	-1	0	0	0	0	0	0	0	0	0	14	5	F6SJM7	
ENSMUST00000142106						0	0	0	0	0	5	25	0	0	1	15		
ENSMUST00000142110						4	5	12	8	10	6	0	0	0	0	0		
ENSMUST00000142111						2	1	0	5	0	1	34	527	71	10	145		
ENSMUST00000142112						4	2	7	17	3	1	1	1	1	1	0		
ENSMUST00000142113	ENSMUSG00000063972	2	38723370	38927688	-1	0	0	0	0	2	0	0	0	0	0	0	Z4YMW4	
ENSMUST00000142114	ENSMUSG00000023051	15	102518192	102523676	1	0	0	0	0	0	0	0	0	0	3	0	D3YUS9	
ENSMUST00000142115						0	0	5	0	8	1	2	2	0	0	0		
ENSMUST00000142116	ENSMUSG00000035245	6	97110024	97149182	-1	0	0	0	14	5	1	0	0	0	0	0	D3Z5Q3	
ENSMUST00000142117						101	90	213	158	146	67	4	92	25	16	30		
ENSMUST00000142118						16	14	43	23	15	10	0	0	1	0	1		
ENSMUST00000142119	ENSMUSG00000028042	3	89377644	89394776	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z0B5	
ENSMUST00000142120	ENSMUSG00000048787	7	119853163	119896291	-1	3	3	0	0	7	0	0	5	9	8	19	D3YWG7	
ENSMUST00000142121						0	0	12	4	0	1	4	1	0	0	0		
ENSMUST00000142122						18	10	12	14	23	17	0	0	0	0	0		
ENSMUST00000142123						0	0	0	32	0	0	0	0	0	0	0		
ENSMUST00000142124						4	2	0	3	2	1	6	18	12	1	9		
ENSMUST00000142125	ENSMUSG00000043962	4	126164082	126202760	-1	0	0	13	6	4	2	3	3	2	0	2	A2AJI7	
ENSMUST00000142126						0	0	0	0	0	2	0	0	0	2	0		
ENSMUST00000142127	ENSMUSG00000051730	2	69871198	69885615	-1	0	0	0	0	0	1	0	0	12	50	21	D6RCI3	
ENSMUST00000142128						1	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000142129	ENSMUSG00000036510	8	99024471	99416471	-1	0	1	0	0	0	0	0	0	0	0	0	E9PYB2	
ENSMUST00000142130	ENSMUSG00000063972	2	38723370	38927688	-1	0	0	0	31	0	0	0	0	1	0	0	A0A0A0MQG4	
ENSMUST00000142131						1	1	5	11	7	1	0	0	0	3	14		
ENSMUST00000142132						0	1	0	10	0	1	0	0	0	0	0		
ENSMUST00000142134						0	1	2	17	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142135						98	116	366	179	144	108	8	20	6	10	28		
ENSMUST00000142136						9	5	18	2	5	4	0	1	0	0	0		
ENSMUST00000142138						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142139						6	8	4	4	9	3	2	2	13	0	14		
ENSMUST00000142140						92	90	247	84	108	58	4	2	9	2	9		
ENSMUST00000142141						5	0	21	2	2	1	2	4	1	1	4		
ENSMUST00000142142						0	2	3	1	0	0	25	177	53	26	69		
ENSMUST00000142143						13	9	31	7	10	9	0	1	0	0	0		
ENSMUST00000142144						2	3	5	8	7	3	0	0	0	0	0		
ENSMUST00000142145						2	2	4	0	0	2	0	0	0	0	0		
ENSMUST00000142146						0	3	0	0	1	2	0	0	0	0	0		
ENSMUST00000142147						7	10	15	16	2	4	17	20	280	4	95		
ENSMUST00000142148						4	0	13	10	4	4	46	89	39	14	79		
ENSMUST00000142149						4	3	1	8	2	0	0	0	0	0	0		
ENSMUST00000142150						3	0	1	2	6	4	0	5	2	1	3		
ENSMUST00000142152	ENSMUSG00000025059	X	85701937	85776819	-1	6	8	6	0	9	0	175	519	70	58	52	B1ASZ3	
ENSMUST00000142153						0	0	7	0	7	6	184	984	256	33	268		
ENSMUST00000142154						1	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000142155	ENSMUSG00000021643	13	100107997	100114571	1	0	0	0	12	0	0	9	0	5	0	7		O88892
ENSMUST00000142156						1	0	2	0	0	0	0	0	0	0	3		
ENSMUST00000142157						1	0	15	43	3	0	0	0	0	0	0		
ENSMUST00000142158	ENSMUSG00000074895	13	54783998	54788459	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0M0	
ENSMUST00000142159						0	2	6	0	10	3	0	0	0	0	0		
ENSMUST00000142160	ENSMUSG00000036959	X	48341358	48408049	1	0	1	0	0	0	0	0	1	1	0	0	F6ZBD9	
ENSMUST00000142161	ENSMUSG00000032925	14	123659971	123975618	1	8	4	18	7	6	0	0	0	0	0	1		Q8VDV0
ENSMUST00000142162						30	20	69	79	30	23	0	1	1	1	4		
ENSMUST00000142164						9	9	30	10	9	6	1	0	1	0	4		
ENSMUST00000142166	ENSMUSG00000020839	11	76902159	76916587	1	1	0	5	0	3	0	0	0	2	1	0	Q5NCR1	
ENSMUST00000142169						3	0	1	32	6	1	21	22	16	18	21		
ENSMUST00000142170						3	3	8	38	11	0	0	0	0	0	0		
ENSMUST00000142171						8	6	26	7	18	0	0	0	0	0	0		
ENSMUST00000142172						0	1	2	5	1	0	0	0	0	0	0		
ENSMUST00000142173						22	29	33	24	33	13	11	78	8	3	13		
ENSMUST00000142174	ENSMUSG00000019970	10	21882184	21999903	1	2	2	0	0	0	0	0	0	0	0	0	D3Z0E8	
ENSMUST00000142175						1	1	5	3	11	1	0	0	0	0	0		
ENSMUST00000142176						0	2	5	0	0	0	0	4	3	3	1		
ENSMUST00000142177						32	28	352	56	31	25	0	0	0	0	1		
ENSMUST00000142179						1	7	15	44	5	3	0	1	0	0	1		
ENSMUST00000142180						2	4	9	2	5	6	0	2	0	1	3		
ENSMUST00000142181						3	0	7	0	2	0	0	0	0	0	0		
ENSMUST00000142182						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142183						7	11	29	20	8	5	1	14	5	1	4		
ENSMUST00000142184	ENSMUSG00000020564	12	33147693	33375659	1	16	8	43	167	18	10	37	266	86	12	69	F6RLA6	
ENSMUST00000142185	ENSMUSG00000037017	5	138116903	138134265	1	0	0	0	0	1	0	0	0	0	0	0	F6QX94	
ENSMUST00000142186						1	2	1	0	0	0	0	0	0	1	0		
ENSMUST00000142187						0	0	6	0	0	0	24	102	5	68	10		
ENSMUST00000142189						3	8	3	4	7	0	0	0	0	0	0		
ENSMUST00000142190						7	4	10	7	6	1	0	0	0	0	0		
ENSMUST00000142191						1	0	0	0	0	0	29	76	50	171	46		
ENSMUST00000142192						21	26	42	29	23	16	0	10	2	0	15		
ENSMUST00000142193	ENSMUSG00000024905	19	3388857	3407823	1	2	8	0	3	12	4	0	5	0	0	0		Q9WTJ6
ENSMUST00000142194	ENSMUSG00000023051	15	102518192	102523676	1	0	0	3	0	5	8	0	0	0	0	9	D3YZS5	
ENSMUST00000142196						0	0	4	2	4	0	0	0	0	0	0		
ENSMUST00000142197						2	4	13	3	1	0	0	0	1	0	1		
ENSMUST00000142198						5	1	0	4	4	3	0	2	0	0	3		
ENSMUST00000142199						1	0	0	0	1	0	1	0	0	0	0		
ENSMUST00000142200						0	0	0	1	0	0	0	1	1	0	0		
ENSMUST00000142201	ENSMUSG00000005150	8	85075035	85081306	-1	0	0	0	0	0	0	0	0	0	0	0	F7C259	
ENSMUST00000142202						8	2	10	1	5	5	0	0	0	0	0		
ENSMUST00000142203						10	9	0	0	1	10	32	122	41	10	138		
ENSMUST00000142205						2	0	0	3	6	0	0	0	0	0	0		
ENSMUST00000142206						4	0	4	4	4	0	4	17	1	2	7		
ENSMUST00000142208						5	8	5	6	10	9	0	0	0	0	0		
ENSMUST00000142210						2	5	6	1	3	2	0	0	0	0	0		
ENSMUST00000142211	ENSMUSG00000029571	6	13069759	13089269	1	0	0	0	89	1	0	2	7	16	23	11	D3Z6E0	
ENSMUST00000142213						0	0	0	15	0	0	22	20	17	0	0		
ENSMUST00000142214						0	0	0	5	0	0	0	0	0	0	4		
ENSMUST00000142215						0	4	6	0	0	0	106	17	440	7	224		
ENSMUST00000142216						0	3	0	0	1	3	0	0	2	1	0		
ENSMUST00000142217						0	0	0	0	0	1	0	0	2	0	1		
ENSMUST00000142218						9	10	20	9	10	5	0	0	0	0	0		
ENSMUST00000142219						6	5	21	6	7	3	0	0	0	0	0		
ENSMUST00000142220						3	12	5	7	7	0	0	5	0	0	5		
ENSMUST00000142221	ENSMUSG00000018899	11	53770014	53778374	1	0	0	0	0	0	0	0	18	7	10	30	D6RH71	
ENSMUST00000142222						2	4	12	3	8	2	4	10	9	0	8		
ENSMUST00000142223						0	3	0	5	0	4	0	0	0	0	0		
ENSMUST00000142224						3	1	6	2	0	0	0	0	0	0	0		
ENSMUST00000142225						21	11	17	36	14	8	1	1	3	0	8		
ENSMUST00000142226						8	0	30	30	10	6	72	24	59	0	147		
ENSMUST00000142227	ENSMUSG00000028312	4	52439243	52488260	1	10	0	0	31	5	3	0	0	19	0	0	B1AWH6	
ENSMUST00000142228	ENSMUSG00000011118	9	37659902	37669222	-1	7	0	0	2	5	0	0	0	0	1	1	D6RDS8	
ENSMUST00000142229	ENSMUSG00000018012	11	120721470	120723969	1	0	2	0	0	3	0	0	3	2	0	5	A2AC13	
ENSMUST00000142230	ENSMUSG00000060863	12	105146014	105155225	1	0	5	2	8	0	0	0	0	0	0	0	D3YZN1	
ENSMUST00000142231	ENSMUSG00000040479	2	91932824	91975864	-1	0	0	0	11	10	0	1014	764	406	79	501	D6RDR3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142232	ENSMUSG00000026854	2	30982279	31023586	1	0	0	0	0	0	0	0	0	0	0	0	B0R093	
ENSMUST00000142233						2	1	1	4	5	0	0	13	3	2	1		
ENSMUST00000142234	ENSMUSG00000044768	1	97606318	97662074	-1	0	0	0	0	0	0	219	564	621	532	470	M0QWF6	
ENSMUST00000142235						0	1	0	0	0	0	7	10	3	4	13		
ENSMUST00000142236						0	2	9	2	6	2	1	0	0	0	0		
ENSMUST00000142237						0	0	2	2	2	0	2	19	3	0	1		
ENSMUST00000142238						4	3	7	221	11	6	0	0	1	0	3		
ENSMUST00000142239						1	0	0	0	0	6	0	0	0	0	0		
ENSMUST00000142240						5	2	6	4	5	2	0	5	0	0	1		
ENSMUST00000142241	ENSMUSG00000024742	19	10199132	10204169	-1	0	0	0	0	23	8	14	59	57	0	101	Q91Z50	
ENSMUST00000142243						0	4	3	0	1	0	1	1	1	0	0		
ENSMUST00000142244						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000142245						0	1	0	2	2	3	0	0	0	0	0		
ENSMUST00000142246	ENSMUSG00000025870	13	54575015	54581128	1	6	0	3	3	7	1	3	10	0	0	3	F6ZTU1	
ENSMUST00000142247	ENSMUSG00000024695	19	12763660	12796126	-1	0	0	0	101	0	0	0	0	54	34	32	E0CY81	
ENSMUST00000142248						0	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000142250						15	8	26	15	16	6	0	10	1	5	6		
ENSMUST00000142251	ENSMUSG00000051747	2	76703980	76982547	-1	5	6	3	4	1	0	0	0	0	0	0	F6Q6Z0	
ENSMUST00000142252						5	3	7	4	5	0	259	1428	281	16	474		
ENSMUST00000142253						2	0	7	6	0	5	6	10	2	0	2		
ENSMUST00000142254						11	3	22	5	4	0	0	0	0	0	0		
ENSMUST00000142255						0	1	6	0	0	0	0	19	4	0	5		
ENSMUST00000142256						1	1	2	8	1	4	0	19	3	0	3		
ENSMUST00000142257						1	2	4	0	3	4	0	0	0	0	0		
ENSMUST00000142258	ENSMUSG00000026014	1	60482292	60567104	-1	0	2	0	6	0	0	0	0	1	2	0	F2Z3X7	
ENSMUST00000142259	ENSMUSG00000022761	16	17508688	17526333	1	15	2	12	2	6	0	44	121	26	12	30	F6VJI5	
ENSMUST00000142261						3	4	0	0	1	1	0	0	0	0	0		
ENSMUST00000142262	ENSMUSG00000051043	11	114851152	114872617	1	0	2	8	16	0	0	0	0	0	0	1	B7FAT7	
ENSMUST00000142263						1	0	0	0	0	1	2	0	5	16	0		
ENSMUST00000142264						68	59	316	101	60	29	0	5	2	1	5		
ENSMUST00000142265						11	0	15	1	7	0	0	0	0	0	0		
ENSMUST00000142266						2	2	3	50	0	3	0	0	0	0	3		
ENSMUST00000142267	ENSMUSG00000031214	X	98554277	98891025	-1	0	0	0	45	0	0	0	0	0	0	0	B1AV64	
ENSMUST00000142269						74	40	135	80	88	36	15	78	28	16	45		
ENSMUST00000142271	ENSMUSG00000032966	2	151542483	151561692	1	2	10	16	0	0	0	0	7	0	0	0	F6X9I3	
ENSMUST00000142272						12	11	49	30	22	10	9	74	18	3	37		
ENSMUST00000142273						18	9	17	17	14	5	0	0	0	0	0		
ENSMUST00000142274						0	0	8	0	12	0	0	0	0	0	0		
ENSMUST00000142275						3	1	3	2	0	0	0	5	6	0	2		
ENSMUST00000142276						1	4	13	8	6	3	5	80	21	7	52		
ENSMUST00000142277	ENSMUSG00000067365	5	38260185	38269634	1	0	1	4	0	2	2	0	0	0	0	2	F6YUB1	
ENSMUST00000142278	ENSMUSG00000027287	2	120567671	120601255	1	0	0	0	1	2	0	79	232	267	375	366	B0R030	
ENSMUST00000142281						0	4	0	3	13	4	37	52	24	15	56		
ENSMUST00000142283	ENSMUSG00000057156	14	54852736	54870961	-1	8	0	58	146	26	7	96	261	134	18	92		
ENSMUST00000142284						11	0	3	4	8	4	0	209	0	0	0		
ENSMUST00000142285						2	0	0	0	0	0	12	36	0	3	5		
ENSMUST00000142287						3	0	2	0	3	0	0	19	4	12	7		
ENSMUST00000142288						5	2	18	0	13	3	8	26	2	4	3		
ENSMUST00000142290	ENSMUSG00000022801	16	32914100	33015647	1	0	3	0	0	0	0	0	0	3	0	7	F6Y466	
ENSMUST00000142291	ENSMUSG00000024985	19	55741810	55933654	1	0	0	0	2	2	3	2	0	0	0	0	D3Z002	
ENSMUST00000142293	ENSMUSG00000040690	4	130047840	130099283	1	3	0	1	0	0	0	1	0	0	0	2	A3KFV2	
ENSMUST00000142294						9	9	8	1	7	6	0	0	0	0	0		
ENSMUST00000142295	ENSMUSG00000014039	16	97791467	97851850	-1	0	12	22	4	17	0	3	14	20	0	87	D6RIL7	
ENSMUST00000142296						7	11	4	7	8	5	20	81	39	12	74		
ENSMUST00000142298						5	2	6	12	4	3	25	91	23	4	48		
ENSMUST00000142299						1	0	1	2	2	1	0	14	5	2	12		
ENSMUST00000142300	ENSMUSG00000044350	14	77024200	77036904	-1	34	17	20	379	59	39	2	11	8	2	7	H3BL27	
ENSMUST00000142301						0	0	0	0	0	2	0	0	0	0	14		
ENSMUST00000142302						5	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142303						4	2	3	7	6	0	0	0	0	2	1		
ENSMUST00000142304						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000142305						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000142306						0	0	8	41	7	1	0	1	0	0	0		
ENSMUST00000142307						0	0	33	0	0	0	0	1	23	0	0		
ENSMUST00000142308						26	32	134	54	40	17	1	13	8	1	6		
ENSMUST00000142311	ENSMUSG00000005774	3	94954075	94961561	1	0	0	0	0	0	0	0	0	3	0	0	K4DI79	
ENSMUST00000142312	ENSMUSG00000042499	2	74679557	74687016	1	0	0	2	135	2	1	0	0	0	0	0	A2ASM7	
ENSMUST00000142313	ENSMUSG00000035919	9	22475715	22888280	1	9	2	42	6	5	2	0	0	9	0	4	D3Z6T1	
ENSMUST00000142315	ENSMUSG00000023764	11	3131850	3193463	-1	21	33	7	16	13	6	9	13	6	5	10	A8Y5K4	
ENSMUST00000142316	ENSMUSG00000022945	16	93883901	93906115	1	4	1	3	114	10	9	0	0	0	0	0	D3YTP6	
ENSMUST00000142317	ENSMUSG00000057246	17	34398820	34460734	1	2	1	0	0	0	0	0	0	0	0	0	A6X8K9	
ENSMUST00000142318						2	2	0	0	1	0	82	209	101	17	94		
ENSMUST00000142319	ENSMUSG00000037447	1	36307733	36324029	1	0	0	0	0	0	0	0	0	0	0	0	D3Z7U1	
ENSMUST00000142320						0	0	0	0	0	0	17	30	12	26	9		
ENSMUST00000142321						4	3	0	0	0	4	16	27	8	0	0		
ENSMUST00000142324	ENSMUSG00000026879	2	35256380	35307892	1	4	0	6	4	5	0	1371	487	1229	84	657	A6PWS5	
ENSMUST00000142325						3	2	18	6	7	3	0	41	0	0	16		
ENSMUST00000142326	ENSMUSG00000035469	14	59201209	59237265	1	0	2	4	0	0	3	0	0	0	0	0	G3UZL2	
ENSMUST00000142327						53	56	112	39	68	40	14	20	51	3	105		
ENSMUST00000142328						20	9	72	9	18	12	0	0	0	0	2		
ENSMUST00000142329	ENSMUSG00000034156	11	87760541	87785928	1	0	0	0	0	0	0	0	34	0	0	13	F6WV49	
ENSMUST00000142331	ENSMUSG00000021252	12	85815448	85824550	-1	18	7	31	24	11	5	4	6	3	3	4	D3YUR8	
ENSMUST00000142332						33	15	73	55	53	38	19	45	56	0	67		
ENSMUST00000142333	ENSMUSG00000037325	3	36573142	36613477	-1	0	0	0	22	2	0	0	0	0	0	0	D3YXR1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142334						6	2	0	2	7	0	0	0	4	0	3		
ENSMUST00000142336						6	0	12	5	0	0	0	0	0	0	0		
ENSMUST00000142337	ENSMUSG00000059772	7	126689468	126695784	-1	0	0	0	0	0	0	5	8	31	0	0	D6RE55	
ENSMUST00000142339						0	2	7	8	4	4	0	0	0	0	0		
ENSMUST00000142340	ENSMUSG00000022972	16	90925809	90934927	-1	3	1	2	122	11	1	0	3	0	0	0	D3YUI6	
ENSMUST00000142341						0	5	2	1	2	0	0	20	4	7	8		
ENSMUST00000142342						7	0	0	26	6	3	0	0	0	0	0		
ENSMUST00000142343	ENSMUSG00000019178	5	135747220	135778385	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNW1	
ENSMUST00000142344	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	12	0	0	38	0	53	0	101	E9Q770	
ENSMUST00000142345						9	9	12	12	9	6	9	47	27	11	31		
ENSMUST00000142346	ENSMUSG00000078440	10	81384428	81391560	1	0	0	2	3	0	0	37	10	0	13	5	D3Z7J7	
ENSMUST00000142347						1	2	2	0	0	1	0	0	0	0	0		
ENSMUST00000142348						0	0	5	0	0	4	0	0	0	0	0		
ENSMUST00000142349	ENSMUSG00000040167	7	131388652	131410521	-1	0	0	1	0	0	0	3	1	1	0	0	D3YVZ8	
ENSMUST00000142350						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000142351	ENSMUSG00000023951	17	46016993	46032377	-1	0	0	0	252	0	0	0	0	40	0	12	F8WH81	
ENSMUST00000142352	ENSMUSG00000002992	7	19671579	19681423	-1	0	0	11	0	0	0	0	0	0	0	0	Q3UJG0	Q05020
ENSMUST00000142355						240	176	3689	293	219	83	0	1	0	0	0		
ENSMUST00000142356	ENSMUSG00000000486	7	127214447	127233130	-1	0	0	3	4	0	0	56	0	13	23	28	D3YVG1	
ENSMUST00000142357						0	0	1	1	2	0	0	119	12	2	4		
ENSMUST00000142358						4	3	2	7	3	8	5	5	4	2	0		
ENSMUST00000142359						2	2	3	6	4	2	0	0	0	0	4		
ENSMUST00000142360						2	1	2	2	0	0	0	0	0	0	0		
ENSMUST00000142361						1	1	1	0	0	0	0	0	0	0	1		
ENSMUST00000142362						43	50	135	55	38	13	34	183	67	14	87		
ENSMUST00000142363						72	53	46	50	58	31	77	188	102	12	151		
ENSMUST00000142364						1	2	2	0	2	0	0	0	0	0	0		
ENSMUST00000142365	ENSMUSG00000004056	7	27591552	27640826	1	4	3	1	1	4	4	3	0	0	0	0	D3YZJ5	
ENSMUST00000142366						0	0	0	0	0	0	7	23	15	0	10		
ENSMUST00000142367						26	12	20	30	26	7	1	2	2	2	12		
ENSMUST00000142368	ENSMUSG00000005611	7	110868266	110982461	-1	0	0	0	21	0	0	0	0	0	0	0	D3YVX3	
ENSMUST00000142369						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000142370						0	8	2	2	7	0	3	9	4	0	2		
ENSMUST00000142371						4	0	7	7	0	0	0	1	0	23	26		
ENSMUST00000142372						10	5	5	5	3	1	0	16	3	1	13		
ENSMUST00000142375						166	161	78	146	196	81	24	79	54	107	55		
ENSMUST00000142376						6	9	10	6	9	0	43	6	206	11	173		
ENSMUST00000142377						3	1	5	5	2	1	2	6	2	0	6		
ENSMUST00000142378	ENSMUSG00000021708	13	91880400	92131656	-1	38	33	48	71	51	31	1	3	5	0	3	F6TYF8	
ENSMUST00000142379						3	1	3	15	5	1	13	11	39	1	29		
ENSMUST00000142380	ENSMUSG00000028329	4	46155347	46196311	-1	0	2	4	0	3	0	0	23	5	0	6		Q64267
ENSMUST00000142381						21	13	32	65	28	14	30	90	40	51	53		
ENSMUST00000142382						0	1	0	2	0	0	16	53	22	8	33		
ENSMUST00000142384	ENSMUSG00000028573	4	95557507	95926939	1	0	5	0	2	0	0	6	21	5	19	0	F6WQK7	
ENSMUST00000142385	ENSMUSG00000005373	5	135089890	135138382	1	7	5	11	26	15	12	0	0	0	0	28		
ENSMUST00000142386						2	2	6	1	6	2	0	6	2	0	0		
ENSMUST00000142387	ENSMUSG00000001228	17	56303321	56323486	1	3	2	0	53	2	0	0	0	0	0	0	E9Q5Y5	
ENSMUST00000142388	ENSMUSG00000000248	6	128934381	128984707	1	68	55	41	45	89	55	0	0	3	3	1	F5CSM6	Q9D676
ENSMUST00000142389	ENSMUSG00000037965	16	11136592	11176393	-1	1	0	0	92	2	0	0	0	2	0	2	D3YVH9	
ENSMUST00000142390						1	1	2	3	4	2	0	0	0	0	0		
ENSMUST00000142391						25	24	45	130	24	9	7	23	2	0	8		
ENSMUST00000142392	ENSMUSG00000020893	11	69095217	69109960	1	0	0	0	0	5	1	5	45	25	4	221	E9Q8V5	
ENSMUST00000142393						96	151	141	110	124	77	42	164	88	56	81		
ENSMUST00000142394						0	0	1	0	0	0	6	25	10	25	0		
ENSMUST00000142395	ENSMUSG00000054823	8	25601601	25719667	1	0	16	41	62	58	0	39	229	1301	159	1394	D3Z357	
ENSMUST00000142396	ENSMUSG00000020279	11	32187541	32200279	-1	7	0	14	23	9	0	4	0	1	0	9	B7ZD65	
ENSMUST00000142398						0	0	9	0	4	0	34	256	76	1	21		
ENSMUST00000142399						2	4	3	6	6	3	4	0	0	0	0		
ENSMUST00000142400	ENSMUSG00000043909	2	121193281	121271407	-1	4	6	8	0	2	0	0	0	1	0	0	F6S5E4	
ENSMUST00000142401	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	0	1	21	0	D3Z1S1	
ENSMUST00000142402						3	5	28	38	23	4	1	0	1	0	13		
ENSMUST00000142403						3	3	2	2	6	2	0	1	0	0	1		
ENSMUST00000142404						0	2	2	0	0	1	0	0	0	1	0		
ENSMUST00000142405	ENSMUSG00000033576	15	77044729	77057107	1	7	7	4	3	8	4	0	0	0	0	1	D6RFC1	
ENSMUST00000142406						80	70	218	96	85	28	10	23	17	1	19		
ENSMUST00000142407	ENSMUSG00000029203	5	65537233	65598988	1	26	29	102	59	19	17	29	90	33	25	33	Q6ZWQ6	P61087
ENSMUST00000142408						0	0	4	11	3	3	1829	9590	1595	3066	1979		
ENSMUST00000142409	ENSMUSG00000023805	17	5941280	6044290	1	3	9	9	4	15	0	0	0	0	1	0	D3YWM9	
ENSMUST00000142410	ENSMUSG00000024184	17	26195999	26199087	-1	1	1	1	2	0	0	0	0	0	0	0	F6S5U2	
ENSMUST00000142411	ENSMUSG00000012609	12	85824659	86061893	1	1	0	0	127	2	0	0	0	0	0	0	D3Z5H9	
ENSMUST00000142412						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000142414	ENSMUSG00000038013	11	98863638	98905040	1	0	0	0	0	0	0	5	4	6	0	10	D3Z0K7	
ENSMUST00000142415						0	0	6	0	1	0	0	0	0	0	0		
ENSMUST00000142416	ENSMUSG00000042554	1	130576713	130629621	-1	0	7	0	0	8	0	0	0	0	0	0	E9PVX4	
ENSMUST00000142418						10	7	14	6	8	7	15	83	32	6	62		
ENSMUST00000142419	ENSMUSG00000030108	6	121300227	121337733	1	2	0	0	1	2	1	0	0	0	0	0	D3YWZ5	
ENSMUST00000142420						0	1	13	17	1	2	3	6	5	0	5		
ENSMUST00000142421						1	1	3	0	0	0	80	83	71	0	49		
ENSMUST00000142422						5	3	17	0	0	2	73	167	70	6	22		
ENSMUST00000142424	ENSMUSG00000032563	9	105053239	105079888	1	0	0	0	0	0	0	64	194	90	73	92	D6RI16	
ENSMUST00000142426						1	0	0	0	0	1	0	399	0	0	0		
ENSMUST00000142427						2	14	20	91	5	0	0	0	0	0	0		
ENSMUST00000142428	ENSMUSG00000032959	5	117282654	117287625	-1	0	1	2	0	2	2	0	0	0	0	0	D6RHS6	
ENSMUST00000142430						593	695	436	909	741	333	1040	4237	2359	1692	1494		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142431	ENSMUSG00000004630	8	3623371	3625545	-1	0	0	2	2	3	1	1	1	0	0	0		
ENSMUST00000142432						0	3	5	0	5	2	0	0	1	1	6		
ENSMUST00000142433						20	10	107	33	18	7	3	11	9	4	11		
ENSMUST00000142434	ENSMUSG00000028226	4	17852893	18119145	1	68	70	511	208	48	38	3	0	1	0	1	B1AVG8	
ENSMUST00000142435						3	7	4	12	9	8	0	0	0	0	0		
ENSMUST00000142436	ENSMUSG00000026867	2	34674594	34755232	-1	0	0	1	18	3	0	0	0	24	3	7	E9Q0D1	
ENSMUST00000142437	ENSMUSG00000054312	3	95862634	95871519	-1	0	1	0	1	1	0	11	51	0	46	12	D3YVZ9	
ENSMUST00000142438						7	8	29	10	18	9	0	13	0	0	6		
ENSMUST00000142439						4	3	3	170	7	3	0	2	0	0	0		
ENSMUST00000142440						11	1	54	11	15	7	4	26	6	3	9		
ENSMUST00000142441						1	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000142442						19	7	29	22	35	13	38	291	94	4	99		
ENSMUST00000142443						7	4	11	3	2	0	0	0	0	0	0		
ENSMUST00000142444						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000142446						0	5	3	0	0	0	5	126	14	10	15		
ENSMUST00000142447						0	0	0	0	0	0	0	5	0	0	1		
ENSMUST00000142448						2	4	3	54	2	0	0	0	1	0	0		
ENSMUST00000142449	ENSMUSG00000038777	3	95160457	95174024	1	0	0	0	0	0	0	0	1	0	0	0	E9Q4N1	
ENSMUST00000142450	ENSMUSG00000055923	5	76873659	76905514	-1	0	0	0	0	0	0	1	0	0	0	0	D3Z2L6	
ENSMUST00000142451						2	3	21	12	6	0	4	8	0	0	6		
ENSMUST00000142452						16	14	123	29	14	17	1	10	0	0	7		
ENSMUST00000142453						0	4	2	1	0	0	0	0	0	0	0		
ENSMUST00000142454	ENSMUSG00000028496	4	87769925	88033364	-1	3	0	3	25	3	0	0	0	4	1	2	E9Q3B8	
ENSMUST00000142455						0	4	0	0	0	0	13	27	53	3	32		
ENSMUST00000142456	ENSMUSG00000025421	18	76930126	76972902	1	2	2	0	32	2	0	0	13	0	10	8	D6RI20	
ENSMUST00000142457						6	0	20	5	11	0	0	0	0	0	0		
ENSMUST00000142459						0	5	5	0	4	0	0	0	0	0	0		
ENSMUST00000142460						4	3	2	1	10	3	0	0	0	0	0		
ENSMUST00000142461						27	23	85	71	33	16	9	13	5	2	4		
ENSMUST00000142463						0	0	0	96	2	0	2	0	0	0	0		
ENSMUST00000142464						0	2	0	1	3	0	2	6	4	1	0		
ENSMUST00000142465	ENSMUSG00000049807	11	97415533	97502402	1	0	0	0	0	0	0	40	385	81	6	28	D6RDB5	
ENSMUST00000142466	ENSMUSG00000031748	8	93809966	93969388	1	0	0	0	0	0	1	0	0	0	0	0	F6WC15	
ENSMUST00000142467						0	0	0	26	2	0	0	0	0	0	0		
ENSMUST00000142468						2	0	0	9	4	1	0	21	12	3	16		
ENSMUST00000142469						0	0	0	0	1	0	7	85	18	101	32		
ENSMUST00000142470						64	86	227	48	48	25	13	51	12	5	23		
ENSMUST00000142471						12	19	21	13	25	7	0	0	0	0	0		
ENSMUST00000142472	ENSMUSG00000020712	11	106276672	106288745	1	18	10	23	26	31	7	1	0	0	0	0	Q9D4R6	
ENSMUST00000142473						14	15	31	21	16	0	3	9	19	0	24		
ENSMUST00000142474						1	0	0	0	5	0	0	3	0	51	0		
ENSMUST00000142475	ENSMUSG00000036510	8	99024471	99416471	-1	7	11	20	15	15	11	0	0	0	0	0	E9PZC1	
ENSMUST00000142476	ENSMUSG00000001020	3	90603771	90606045	1	0	1	2	1	3	1	6	0	0	18	7	A0A0G2JGD2	
ENSMUST00000142477						0	0	1	3	1	1	0	0	0	0	0		
ENSMUST00000142478						0	1	3	5	2	6	0	0	0	0	0		
ENSMUST00000142479						6	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000142480						4	2	10	8	8	2	3	6	0	0	0		
ENSMUST00000142481						5	11	50	15	17	7	42	197	52	15	72		
ENSMUST00000142482						1	1	0	2	0	0	21	187	30	169	42		
ENSMUST00000142483						6	0	21	9	10	3	3	13	1	0	5		
ENSMUST00000142484						8	3	9	9	9	0	3	17	8	4	2		
ENSMUST00000142485	ENSMUSG00000026977	2	60209887	60250676	1	1	0	0	0	0	0	13	173	16	0	2	F7B2M7	
ENSMUST00000142488	ENSMUSG00000026307	1	91298338	91321075	1	0	2	1	0	0	0	0	2	0	0	0	D3Z7G6	
ENSMUST00000142489						0	1	2	21	1	4	1	0	1	0	0		
ENSMUST00000142490						0	0	0	13	0	0	0	0	0	0	0		
ENSMUST00000142491						5	4	0	2	3	0	22	54	49	3	68		
ENSMUST00000142493						0	0	0	0	0	1	10	0	23	0	17		
ENSMUST00000142494	ENSMUSG00000031922	9	13807792	13827107	-1	0	0	0	0	0	0	0	0	0	0	0	D6RDR1	
ENSMUST00000142495	ENSMUSG00000056962	11	116837432	116843449	-1	6	0	0	152	7	0	0	16	22	14	56	G3UVU9	
ENSMUST00000142496	ENSMUSG00000024948	19	6341135	6355615	1	0	0	0	0	0	0	788	79	332	0	255	D6RCZ7	
ENSMUST00000142497						2	1	0	0	1	1	0	16	0	0	0		
ENSMUST00000142498						8	0	2	2	4	1	1	0	0	0	1		
ENSMUST00000142499	ENSMUSG00000020490	11	58917908	58927158	1	0	0	7	2	3	1	0	0	0	0	1		Q9JK39
ENSMUST00000142500	ENSMUSG00000018566	11	69942539	69948188	-1	5	1	3	29	1	5	0	0	0	0	0	A0A0G2JDD0	
ENSMUST00000142501	ENSMUSG00000047642	10	121641588	121692892	1	0	0	0	0	0	0	0	0	0	0	0	D3YXS3	
ENSMUST00000142502						0	0	0	27	0	1	24	12	17	0	20		
ENSMUST00000142503						0	0	4	0	0	0	0	0	0	6	2		
ENSMUST00000142504						2	2	8	3	3	2	0	1	0	0	0		
ENSMUST00000142505	ENSMUSG00000074264	3	113555710	113606699	-1	0	3	1	0	2	0	3	1	3	3	0	D3YYQ5	
ENSMUST00000142506						0	0	0	5	0	0	0	0	0	3	0		
ENSMUST00000142507						23	14	56	56	32	16	1	4	3	0	2		
ENSMUST00000142508						1	1	2	0	3	0	11	79	44	16	127		
ENSMUST00000142510	ENSMUSG00000070858	5	33983433	33985013	1	2	4	0	0	0	0	9	0	0	6	0	F6RNB2	
ENSMUST00000142512	ENSMUSG00000029761	6	34598500	34775473	1	1	0	1	2	4	0	1	2	0	5	4	E9Q9F3	
ENSMUST00000142513						1	1	0	0	0	0	0	4	0	0	0		
ENSMUST00000142514						12	15	42	28	37	12	2	1	2	2	4		
ENSMUST00000142515						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142516	ENSMUSG00000005907	5	3596066	3637232	1	0	1	0	0	1	0	0	0	0	0	1	D3Z5A7	
ENSMUST00000142517						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142518						22	21	97	28	31	18	1	1	0	2	6		
ENSMUST00000142519						5	2	8	4	3	2	53	0	3	10	16		
ENSMUST00000142522	ENSMUSG00000026979	2	24367580	24414954	1	1	0	48	0	8	0	58	32	43	0	35	A0A0A6YXA6	
ENSMUST00000142523	ENSMUSG00000020248	10	82748701	82764144	-1	0	0	0	0	0	1	0	20	15	0	7	D3Z723	
ENSMUST00000142524						0	2	0	28	0	0	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142525						0	0	0	2	0	2	0	0	1	3	8		
ENSMUST00000142526						6	5	15	8	6	1	1	11	3	1	5		
ENSMUST00000142527						23	30	61	28	25	14	1	0	2	0	2		
ENSMUST00000142528						1	0	0	0	0	1	0	0	0	0	3		
ENSMUST00000142529						0	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000142530	ENSMUSG00000020807	11	72153929	72207459	-1	5	14	0	44	0	0	47	62	77	0	49	F2Z3W1	
ENSMUST00000142531						9	6	31	10	29	9	54	105	40	0	122		
ENSMUST00000142532						1	0	7	2	7	0	55	18	37	0	61		
ENSMUST00000142534						0	0	0	62	0	0	0	0	2	0	9		
ENSMUST00000142535						2	2	9	15	2	1	0	0	0	2	0		
ENSMUST00000142536						0	0	0	0	0	4	13	20	0	0	0		
ENSMUST00000142537						2	1	3	0	4	0	0	0	0	0	0		
ENSMUST00000142538						0	0	0	11	1	0	0	0	0	0	0		
ENSMUST00000142539	ENSMUSG00000048249	17	26715650	26776635	1	3	0	6	10	0	3	27	29	199	40	173	B8JJI2	
ENSMUST00000142540	ENSMUSG00000033688	9	103250521	103305082	-1	3	3	0	62	7	0	0	0	0	0	0	D3Z4X8	
ENSMUST00000142541	ENSMUSG00000000738	8	123062942	123097760	1	2	3	13	0	4	0	0	0	1	7	26	D3Z342	
ENSMUST00000142542						28	15	44	46	43	0	0	0	0	0	0		
ENSMUST00000142543	ENSMUSG00000034274	11	4895320	4928867	1	0	0	0	0	0	0	0	0	4	0	0	Q5SVF8	
ENSMUST00000142545	ENSMUSG00000019303	11	101091823	101095436	-1	2	0	0	0	0	0	4	0	1	0	1	D6RFC4	
ENSMUST00000142546	ENSMUSG00000049252	2	40595246	42653624	-1	3	0	0	0	0	0	0	0	0	0	0	F6YDG9	
ENSMUST00000142547						3	3	21	3	5	2	0	0	0	0	0		
ENSMUST00000142548						5	0	0	0	5	5	0	0	0	0	0		
ENSMUST00000142549						1	2	4	3	0	0	1	0	0	1	0		
ENSMUST00000142550						7	6	19	125	9	8	0	0	0	0	0		
ENSMUST00000142551						4	5	15	9	7	4	0	0	0	0	0		
ENSMUST00000142553	ENSMUSG00000035245	6	97110024	97149182	-1	0	7	8	1	7	0	0	0	0	0	0	D3YWW8	
ENSMUST00000142554	ENSMUSG00000026842	2	31688376	31804227	1	0	0	0	0	0	2	0	0	0	0	0	A0A0A6YXS9	
ENSMUST00000142555						119	23	6	54	401	58	3596	0	48	1397	67		
ENSMUST00000142556	ENSMUSG00000090053	4	57434247	57712016	1	0	3	0	0	0	0	0	0	0	0	0	G3X9P1	
ENSMUST00000142557						0	0	0	0	0	0	12	1	4	76	6		
ENSMUST00000142558	ENSMUSG00000006728	10	127063534	127067920	1	0	0	0	0	0	0	84	0	31	40	50	D6RHS5	
ENSMUST00000142559						2	8	0	3	5	2	46	294	53	0	78		
ENSMUST00000142560						1	0	0	3	1	0	0	0	0	0	2		
ENSMUST00000142561						3	0	20	108	11	6	2	1	2	0	5		
ENSMUST00000142562						2	2	5	9	0	1	7	70	36	1	46		
ENSMUST00000142563						0	0	0	2	0	0	3	3	0	0	0		
ENSMUST00000142564						0	0	0	1	1	0	0	1	0	0	0		
ENSMUST00000142565						0	0	0	3	1	2	0	6	14	9	16		
ENSMUST00000142566						0	0	0	10	0	0	0	0	0	0	0		
ENSMUST00000142568						8	10	11	6	9	6	3	0	0	0	3		
ENSMUST00000142570						9	2	9	0	3	3	29	508	24	27	79		
ENSMUST00000142571						8	8	19	10	4	2	0	7	6	0	2		
ENSMUST00000142572	ENSMUSG00000038611	7	141228784	141262750	1	10	0	12	2	12	0	107	222	115	19	63	F7ANA1	
ENSMUST00000142573						94	53	683	109	61	35	0	2	0	0	2		
ENSMUST00000142574						0	0	1	81	3	7	0	0	0	0	0		
ENSMUST00000142575	ENSMUSG00000036892	7	30493622	30513402	1	2	0	4	15	6	0	0	0	0	0	0	D3YV12	
ENSMUST00000142576						5	5	28	255	15	5	4	9	0	0	0		
ENSMUST00000142577						21	26	58	42	36	14	106	435	252	27	271		
ENSMUST00000142578						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000142580						0	0	4	0	3	0	0	1	0	0	0		
ENSMUST00000142582	ENSMUSG00000029564	5	114853664	114883880	1	2	0	28	0	0	0	0	0	0	0	1	F7BGB3	
ENSMUST00000142583						5	4	4	4	7	4	0	0	0	0	0		
ENSMUST00000142584						0	0	0	1	0	1	4	0	16	0	5		
ENSMUST00000142585	ENSMUSG00000028675	4	135870918	135873850	-1	0	0	3	11	5	3	49	210	225	645	219	Z4YMU7	
ENSMUST00000142586						2	2	6	5	0	2	0	4	3	0	7		
ENSMUST00000142587						1	1	4	60	4	2	0	0	0	7	0		
ENSMUST00000142588						0	4	6	2	0	1	0	0	0	0	17		
ENSMUST00000142589						18	28	22	74	18	11	0	0	0	0	0		
ENSMUST00000142590						1	0	0	0	3	0	0	11	0	3	10		
ENSMUST00000142591						1	0	0	17	0	0	0	0	0	0	0		
ENSMUST00000142592						1	0	3	0	3	0	14	24	4	4	0		
ENSMUST00000142593						2	0	0	0	0	0	0	5	0	98	24		
ENSMUST00000142594	ENSMUSG00000023861	17	8282904	8297661	1	3	3	17	106	4	5	9	19	11	0	30	E9Q0V4	
ENSMUST00000142595	ENSMUSG00000039048	9	35204206	35211055	-1	0	0	0	0	2	0	4	13	0	0	12	D3Z5V7	
ENSMUST00000142596	ENSMUSG00000059439	11	85353167	85826058	1	0	0	0	7	0	2	0	0	0	0	0	F7CPM1	
ENSMUST00000142597	ENSMUSG00000003099	7	17004640	17027924	-1	4	0	0	10	0	0	62	121	56	29	29	F7BX26	
ENSMUST00000142598						1	1	3	13	5	1	0	1	0	0	0		
ENSMUST00000142599						2	3	0	36	7	3	4	31	18	31	16		
ENSMUST00000142600						12	10	25	14	13	8	0	2	1	2	4		
ENSMUST00000142601	ENSMUSG00000031644	8	60993195	61131346	1	3	0	0	0	2	1	0	0	4	0	5	F6R259	
ENSMUST00000142602						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142603						3	0	20	5	5	2	0	0	0	0	4		
ENSMUST00000142604						9	5	2	11	7	4	828	2751	634	3731	320		
ENSMUST00000142605						0	5	0	0	2	0	0	5	0	0	11		
ENSMUST00000142606						1	0	0	62	2	0	0	0	1	0	0		
ENSMUST00000142607						28	22	65	53	53	22	1	0	1	0	3		
ENSMUST00000142608						109	107	279	143	113	67	9	19	22	10	32		
ENSMUST00000142609	ENSMUSG00000042066	1	132356315	132391281	-1	2	0	0	0	0	0	30	11	2	6	0	Q3T9T1	
ENSMUST00000142610	ENSMUSG00000033728	15	76710623	76717699	1	0	0	0	0	0	0	0	46	12	8	3	D6REG8	
ENSMUST00000142611						0	0	20	0	0	0	0	0	0	0	0		
ENSMUST00000142612						10	6	22	20	4	2	0	0	0	0	0		
ENSMUST00000142613	ENSMUSG00000050732	6	72385223	72390703	-1	10	18	75	17	21	12	96	331	115	39	142		
ENSMUST00000142615	ENSMUSG00000001518	6	128409444	128424931	-1	17	24	49	23	23	13	0	10	0	0	8	Q3TWL5	
ENSMUST00000142616	ENSMUSG00000031921	8	107069400	107096547	-1	9	6	3	0	9	11	40	58	20	7	8	F6VIR4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142617						86	66	276	422	103	41	2	6	3	0	7		
ENSMUST00000142618	ENSMUSG00000040451	19	32122727	32389714	-1	26	21	159	13	26	21	9	21	43	0	25		Q8VCQ6
ENSMUST00000142619						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000142620						10	8	23	14	6	4	0	0	0	0	0		
ENSMUST00000142622						0	0	0	0	0	0	0	61	7	13	11		
ENSMUST00000142623	ENSMUSG00000016626	7	107166990	107198102	1	0	7	2	0	4	0	0	0	0	0	0		
ENSMUST00000142624	ENSMUSG00000035967	X	56454857	56507843	1	0	0	0	0	0	0	32	1089	86	86	72	F6RIR5	
ENSMUST00000142626						3	2	0	0	0	2	0	0	0	0	0		
ENSMUST00000142628						1	0	0	0	1	0	0	0	0	0	5		
ENSMUST00000142629	ENSMUSG00000099481	7	102065511	102083765	1	11	10	19	18	10	6	7	47	0	2	25	F6R278	
ENSMUST00000142630						1	5	4	9	10	6	2	8	0	2	3		
ENSMUST00000142631						1	0	2	0	1	0	18	55	22	0	34		
ENSMUST00000142632						36	27	103	51	73	36	1	1	1	2	2		
ENSMUST00000142633						1	12	41	9	2	3	0	0	0	0	0		
ENSMUST00000142635	ENSMUSG00000029755	6	6877805	6882085	-1	6	0	0	173	0	0	0	0	0	0	0		P70396
ENSMUST00000142636	ENSMUSG00000027157	2	111162061	111229602	-1	5	1	31	11	8	4	0	0	0	0	0	A2AJ40	
ENSMUST00000142637						0	1	2	11	1	0	58	53	67	13	62		
ENSMUST00000142638	ENSMUSG00000025040	X	17556564	17572325	-1	0	0	3	2	0	0	0	0	19	0	0	H3BJ77	
ENSMUST00000142639						17	12	19	28	6	7	0	0	0	0	0		
ENSMUST00000142640	ENSMUSG00000078652	11	101316213	101323537	1	0	0	0	147	9	2	0	0	11	0	14	A2A4J3	
ENSMUST00000142641						2	2	1	2	0	0	0	1	0	0	0		
ENSMUST00000142643						4	1	0	4	4	2	35	208	16	10	15		
ENSMUST00000142644						1	2	2	6	1	0	0	0	0	0	0		
ENSMUST00000142645						123	157	199	145	125	90	10	60	42	24	55		
ENSMUST00000142646						0	1	0	0	4	0	0	0	0	0	6		
ENSMUST00000142647	ENSMUSG00000049878	4	121145373	121215084	-1	0	0	0	0	0	0	1	0	2	0	2	A2A7F3	
ENSMUST00000142648						2	18	7	4	3	6	0	1	0	0	0		
ENSMUST00000142649						4	0	6	11	6	2	4	10	8	0	2		
ENSMUST00000142650						12	12	25	6	26	7	13	22	7	0	31		
ENSMUST00000142651						0	2	1	2	1	1	1	0	1	0	3		
ENSMUST00000142652						0	5	1	2	1	0	0	0	0	0	0		
ENSMUST00000142653						13	8	31	13	18	7	1	0	0	0	0		
ENSMUST00000142654						2	1	8	9	7	1	19	26	12	0	23		
ENSMUST00000142655	ENSMUSG00000005882	2	155846894	155930310	-1	0	0	0	0	1	0	0	0	0	0	0	D6RJ23	
ENSMUST00000142656						0	0	0	0	3	0	10	74	2	0	10		
ENSMUST00000142657						0	0	5	2	2	0	0	0	0	4	0		
ENSMUST00000142658						1	1	3	0	1	1	2	8	4	0	0		
ENSMUST00000142659	ENSMUSG00000036246	8	69808679	69821870	1	65	53	128	74	56	38	22	97	32	11	29	F7AIU6	
ENSMUST00000142660						0	0	0	8	0	0	0	1	0	0	0		
ENSMUST00000142661						4	5	3	0	2	1	2	7	2	0	0		
ENSMUST00000142662						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142663	ENSMUSG00000014418	7	46760466	46796064	-1	0	0	0	0	0	0	70	102	0	0	0		P59438
ENSMUST00000142664	ENSMUSG00000029470	5	122707544	122729738	1	0	0	0	1	0	0	46	34	46	20	51	D3Z5U5	
ENSMUST00000142665						21	12	51	30	51	7	14	26	38	5	33		
ENSMUST00000142666	ENSMUSG00000022760	16	17527982	17531136	-1	0	2	2	12	0	5	4	4	14	0	2	D3YV14	
ENSMUST00000142667						0	4	6	1	1	2	0	0	0	0	0		
ENSMUST00000142668						0	0	2	0	0	0	0	3	0	17	19		
ENSMUST00000142669						0	0	3	0	0	0	5	7	0	0	0		
ENSMUST00000142670	ENSMUSG00000037216	1	37871738	37876228	1	0	0	3	2	1	0	0	9	0	0	0	D3Z7N1	
ENSMUST00000142671						1	3	1	6	2	3	0	0	0	0	0		
ENSMUST00000142672						0	5	0	0	0	0	0	0	164	25	208		
ENSMUST00000142673						1	3	0	3	0	1	17	0	6	3	12		
ENSMUST00000142674						7	10	25	21	11	4	0	0	0	0	0		
ENSMUST00000142675	ENSMUSG00000029718	5	137605103	137613784	-1	0	1	1	2	8	2	3	18	8	8	33	D3YZE3	
ENSMUST00000142676	ENSMUSG00000032527	9	100982032	101034898	-1	0	4	0	0	2	0	0	0	0	0	0	D3YZC1	
ENSMUST00000142677						66	86	84	69	89	44	6	42	18	2	23		
ENSMUST00000142679	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	19	84	248	91	95	F6UV57	
ENSMUST00000142680	ENSMUSG00000035152	11	83299024	83405035	1	9	3	7	99	6	1	0	3	0	0	0	Q5SWR0	
ENSMUST00000142681	ENSMUSG00000048939	16	29231851	29378732	-1	0	13	16	21	0	0	0	0	0	0	0	D6RHM2	
ENSMUST00000142682	ENSMUSG00000032965	16	49699233	49765126	1	2	0	3	48	2	0	88	240	161	47	76		
ENSMUST00000142683	ENSMUSG00000022010	14	76414961	76507765	1	2	4	2	3	4	1	0	0	0	13	20	H3BLI9	
ENSMUST00000142684						7	4	14	31	8	12	31	67	60	2	49		
ENSMUST00000142685						11	6	9	51	9	8	11	50	10	7	14		
ENSMUST00000142686						2	3	8	4	1	2	0	0	0	0	0		
ENSMUST00000142687						3	2	15	4	4	1	0	7	0	3	8		
ENSMUST00000142688	ENSMUSG00000049252	2	40595246	42653624	-1	11	12	16	25	16	12	0	0	0	0	0		
ENSMUST00000142689						0	3	5	10	5	1	0	14	0	0	15		
ENSMUST00000142690	ENSMUSG00000063889	18	3266048	3337748	-1	0	5	0	0	0	1	6	34	13	15	5	Q3TTH6	
ENSMUST00000142691						1	0	0	44	0	0	0	6	0	0	0		
ENSMUST00000142692	ENSMUSG00000027243	2	91710852	91721545	1	66	81	151	59	85	49	8	53	23	6	16		Q8BR93
ENSMUST00000142693						4	10	23	12	12	13	4	24	14	4	0		
ENSMUST00000142694						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000142695						0	1	8	0	3	3	0	0	0	0	0		
ENSMUST00000142696						7	4	25	12	9	2	0	0	0	0	0		
ENSMUST00000142697	ENSMUSG00000033149	16	45746243	45953598	-1	3	0	2	2	5	0	1	1	0	0	0	D3Z1R8	
ENSMUST00000142698	ENSMUSG00000025432	10	127000709	127020994	1	0	0	0	0	1	1	1	1	4	0	2	D3Z3N6	
ENSMUST00000142699						1	0	0	7	5	0	0	0	0	3	0		
ENSMUST00000142700						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000142701	ENSMUSG00000029458	5	121660563	121687256	1	112	229	69	33	135	75	87	379	136	56	149	A0A0G2JF68	
ENSMUST00000142702						7	5	10	94	6	7	0	2	0	2	1		
ENSMUST00000142703						5	2	16	1	0	0	2	1	0	1	8		
ENSMUST00000142704	ENSMUSG00000032883	1	78657825	78707743	1	0	0	0	0	0	0	0	0	0	0	0		Q9CZW4
ENSMUST00000142705						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142706	ENSMUSG00000067148	17	46243920	46248054	-1	0	0	0	1	0	0	6	0	0	0	0	D3Z7Q8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142707						0	0	0	0	3	0	0	6	1	4	3		
ENSMUST00000142708						5	2	9	3	4	4	0	5	0	0	2		
ENSMUST00000142710						0	0	0	7	0	0	0	0	0	0	0		
ENSMUST00000142711						8	0	2	2	0	7	0	0	0	0	0		
ENSMUST00000142713	ENSMUSG00000035585	7	3692863	3701024	1	3	2	8	4	6	1	6	6	14	6	12	D3YWG5	
ENSMUST00000142714	ENSMUSG00000035649	4	44755877	44932215	1	3	1	2	0	0	4	0	5	3	0	13	E0CY20	
ENSMUST00000142716	ENSMUSG00000029761	6	34598500	34775473	1	6	0	7	1	17	1	0	0	0	5	7	F6QLP8	
ENSMUST00000142717						4	6	6	14	0	3	0	0	4	2	12		
ENSMUST00000142718	ENSMUSG00000027201	2	125084628	125123661	-1	0	0	22	0	0	0	0	0	0	31	26	A2ATP6	
ENSMUST00000142719						7	4	4	0	4	3	4	9	0	0	0		
ENSMUST00000142720						2	0	0	0	7	0	0	6	5	0	0		
ENSMUST00000142721	ENSMUSG00000001053	11	51643063	51650842	-1	4	0	5	0	3	2	0	0	0	0	0	A2AA65	
ENSMUST00000142722	ENSMUSG00000028546	4	110203722	110351909	-1	0	0	3	5	2	4	0	0	0	0	0	A2A9S1	
ENSMUST00000142724						0	3	1	184	9	9	2	13	3	2	5		
ENSMUST00000142725						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000142726						0	3	6	2	2	0	0	64	20	6	74		
ENSMUST00000142727						0	0	0	20	0	0	0	0	0	0	0		
ENSMUST00000142729	ENSMUSG00000017861	2	163054687	163084688	1	20	22	17	8	23	7	14	18	9	5	13	A2A5P3	
ENSMUST00000142730						0	1	1	4	4	0	0	0	0	0	0		
ENSMUST00000142731						7	0	0	3	5	3	0	0	0	0	0		
ENSMUST00000142732						1	2	2	3	2	0	0	0	0	0	0		
ENSMUST00000142733						0	4	5	5	11	5	20	30	22	4	49		
ENSMUST00000142734	ENSMUSG00000050335	14	47367751	47386160	1	2	4	0	59	9	0	414	448	345	390	228	Q8C253	
ENSMUST00000142735						1	3	5	42	3	3	50	95	66	298	20		
ENSMUST00000142736						0	7	0	0	6	0	9	181	34	0	68		
ENSMUST00000142737	ENSMUSG00000001999	2	127070665	127097084	1	3	0	2	0	3	0	5	23	10	74	0	A2ASB1	
ENSMUST00000142738						12	12	15	36	14	2	0	0	0	0	0		
ENSMUST00000142739	ENSMUSG00000017376	11	78567168	78697373	-1	43	41	120	280	51	23	105	329	226	63	187		O54949
ENSMUST00000142740	ENSMUSG00000001998	2	127008717	127067909	1	0	0	1	0	0	0	0	0	0	2	3	H3BK54	
ENSMUST00000142741						11	8	9	9	6	2	0	0	2	1	0		
ENSMUST00000142742	ENSMUSG00000029361	5	117781032	117958840	1	128	99	375	422	167	82	1	0	1	0	4		Q9Z0J4
ENSMUST00000142743						10	6	16	11	14	6	4	9	0	4	5		
ENSMUST00000142745						2	2	2	2	0	3	0	0	0	27	4		
ENSMUST00000142746						7	0	7	1	2	1	6	0	19	15	33		
ENSMUST00000142747						3	1	3	120	7	1	0	0	0	3	4		
ENSMUST00000142748	ENSMUSG00000003809	8	84886393	84893921	-1	0	0	0	12	0	0	0	0	0	0	0	D3Z4I2	
ENSMUST00000142749						3	3	0	6	2	3	0	4	2	0	5		
ENSMUST00000142750						1	2	2	2	1	0	0	0	0	0	4		
ENSMUST00000142752	ENSMUSG00000042625	17	56560965	56584585	-1	3	1	0	0	0	1	0	9	0	3	6	F6R703	
ENSMUST00000142754						1	0	1	0	1	0	0	0	0	1	0		
ENSMUST00000142755						2	0	2	2	0	0	0	8	2	0	4		
ENSMUST00000142756						0	2	1	31	0	0	0	0	7	27	5		
ENSMUST00000142757						0	0	0	0	0	0	61	601	215	155	172		
ENSMUST00000142758						2	2	5	0	3	1	2	0	0	0	0		
ENSMUST00000142759						5	0	8	2	6	5	0	0	0	0	0		
ENSMUST00000142760	ENSMUSG00000066438	12	80692591	80724214	1	4	1	7	2	2	2	0	0	0	0	0		
ENSMUST00000142761						11	12	28	4	14	7	0	10	0	0	0		
ENSMUST00000142762	ENSMUSG00000059921	3	141465216	141834924	1	0	0	0	0	0	0	0	0	0	0	0	Q3UQ08	O08747
ENSMUST00000142763						6	2	16	9	7	3	6	40	16	4	27		
ENSMUST00000142764						25	28	141	63	41	11	1	11	7	0	14		
ENSMUST00000142765						3	0	0	0	1	1	0	3	3	0	3		
ENSMUST00000142766	ENSMUSG00000050558	2	132337733	132385447	-1	51	61	394	116	48	38	6	2	2	1	7	E0CY28	
ENSMUST00000142767	ENSMUSG00000033213	2	122636986	122641191	1	3	0	1	3	1	0	0	0	0	0	0	A2AK37	
ENSMUST00000142768						2	7	3	8	2	3	14	120	20	14	41		
ENSMUST00000142769						99	67	291	144	131	44	12	7	16	2	30		
ENSMUST00000142770						19	15	33	24	29	12	2	2	4	0	6		
ENSMUST00000142771						10	0	42	2	7	8	10	8	13	0	25		
ENSMUST00000142772	ENSMUSG00000027168	2	105668900	105697364	1	11	2	34	4	10	5	0	0	0	0	0	V9GXI6	
ENSMUST00000142773						0	3	4	8	0	0	21	73	40	52	51		
ENSMUST00000142775						5	10	29	5	11	3	0	0	3	0	3		
ENSMUST00000142776						55	67	43	125	61	43	1	13	3	1	8		
ENSMUST00000142778						7	0	7	7	4	4	11	60	64	5	53		
ENSMUST00000142779	ENSMUSG00000023452	5	32736301	32785646	-1	0	0	0	0	0	0	0	0	0	0	0	F7C386	
ENSMUST00000142780						0	0	0	0	0	0	0	10	0	0	0		
ENSMUST00000142781						0	0	2	1	2	1	3	2	0	0	2		
ENSMUST00000142783	ENSMUSG00000079235	9	121797627	121839461	-1	9	4	7	4	9	3	0	0	0	0	0	Q8BYN7	
ENSMUST00000142784						1	2	4	35	9	2	2	0	5	0	8		
ENSMUST00000142785						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000142786						61	80	81	41	78	32	8	58	60	17	95		
ENSMUST00000142788	ENSMUSG00000018565	11	69968222	69982517	-1	0	0	0	0	1	0	28	82	31	132	19	J3QJV1	
ENSMUST00000142790						0	0	1	0	3	0	0	0	0	0	0		
ENSMUST00000142791						0	1	6	1	1	3	51	197	171	23	76		
ENSMUST00000142792						3	1	2	1	0	0	0	0	5	24	0		
ENSMUST00000142793						6	7	5	8	8	7	1	4	0	0	6		
ENSMUST00000142794						1	0	2	5	4	4	0	0	6	0	0		
ENSMUST00000142796	ENSMUSG00000020083	10	62107655	62143920	-1	0	0	0	47	0	0	0	0	0	0	0		Q9D882
ENSMUST00000142797						7	3	15	1	10	2	0	14	11	3	9		
ENSMUST00000142798						17	19	135	25	21	11	2	2	3	0	0		
ENSMUST00000142799						9	4	11	18	11	2	0	0	5	0	5		
ENSMUST00000142800	ENSMUSG00000018398	11	53519257	53549565	1	3	6	0	1	6	1	0	0	0	0	0	E0CYM4	
ENSMUST00000142801	ENSMUSG00000026858	2	30364233	30385521	1	0	0	2	58	2	2	0	0	1	2	0	A2AWJ1	
ENSMUST00000142802						0	2	1	30	3	1	0	0	0	0	0		
ENSMUST00000142803						7	6	10	13	10	5	0	0	0	0	0		
ENSMUST00000142805						0	1	5	9	0	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142806						33	28	39	22	29	17	1	16	0	4	12		
ENSMUST00000142807	ENSMUSG00000038957	9	57708540	57752499	1	0	0	1	49	2	4	0	5	0	0	3	D3YYS4	
ENSMUST00000142808	ENSMUSG00000066026	4	144892827	144928209	1	0	0	0	13	0	0	11	70	27	6	42	B1ARS9	
ENSMUST00000142809						382	292	635	544	394	189	21	68	40	7	58		
ENSMUST00000142811						3	0	7	1	0	0	0	0	3	0	4		
ENSMUST00000142812						23	20	94	32	35	13	12	19	0	2	8		
ENSMUST00000142813	ENSMUSG00000035392	2	37798991	38287390	-1	0	1	0	4	0	0	0	0	0	0	0	D6RHP6	
ENSMUST00000142816						2	2	0	2	0	0	8	17	0	0	30		
ENSMUST00000142817	ENSMUSG00000061751	16	33974258	34573532	-1	0	0	0	0	0	0	0	0	0	0	0	F6QYT9	
ENSMUST00000142818						5	3	8	10	10	4	2	1	1	0	1		
ENSMUST00000142819	ENSMUSG00000020109	10	59879556	59899302	1	9	3	21	35	11	2	6	29	7	14	8		Q9QYI4
ENSMUST00000142820	ENSMUSG00000027519	2	173659760	173707343	1	0	22	36	52	0	25	0	36	47	7	0	D6RFT6	
ENSMUST00000142821	ENSMUSG00000020083	10	62107655	62143920	-1	0	0	0	0	2	0	0	0	0	0	0		Q9D882
ENSMUST00000142822	ENSMUSG00000079042	8	65012976	65037336	-1	0	0	6	0	1	1	0	0	0	0	0		P0DMC4
ENSMUST00000142823						2	4	9	2	6	2	5	0	10	2	0		
ENSMUST00000142824						84	105	416	218	82	32	5	23	16	0	15		
ENSMUST00000142825						126	110	49	134	159	68	6	17	12	1	14		
ENSMUST00000142826						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000142827	ENSMUSG00000021470	13	63815240	63900302	1	0	0	0	0	1	0	0	0	0	2	0	F6SJP9	
ENSMUST00000142829						1	0	0	0	0	0	1	22	4	9	16		
ENSMUST00000142830						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000142831						2	2	4	0	2	0	0	6	0	0	0		
ENSMUST00000142834	ENSMUSG00000020812	11	116671660	116675799	1	0	0	0	0	0	0	0	6	0	22	0	F2Z424	
ENSMUST00000142836						8	10	5	76	9	0	0	0	0	0	0		
ENSMUST00000142837	ENSMUSG00000038024	4	86748555	86850603	1	2	0	4	0	0	0	32	0	256	22	122		A6H8H2
ENSMUST00000142838	ENSMUSG00000034118	5	130073326	130135729	1	0	0	0	0	0	0	0	0	0	0	0	D3Z1F4	
ENSMUST00000142839						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000142840						0	5	18	51	6	5	0	0	2	0	2		
ENSMUST00000142841	ENSMUSG00000030781	7	128265657	128272430	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0A1	
ENSMUST00000142842						88	64	633	125	71	37	3	9	5	1	13		
ENSMUST00000142843	ENSMUSG00000050010	5	67607882	67623552	1	1	7	14	130	6	1	4	5	5	1	8	S4R2D4	
ENSMUST00000142844						0	0	0	0	1	0	9	5	38	0	47		
ENSMUST00000142847	ENSMUSG00000001768	2	145784734	145887616	1	0	2	0	4	2	0	0	0	0	0	0	E0CZD2	
ENSMUST00000142848						0	0	1	0	1	2	0	2	0	0	1		
ENSMUST00000142849						0	0	0	2	0	0	10	117	30	15	27		
ENSMUST00000142850	ENSMUSG00000041607	18	82475146	82585637	1	0	0	0	0	0	5	4	29	0	0	0	F6VME3	
ENSMUST00000142851	ENSMUSG00000026761	2	48902824	48950277	-1	0	0	5	0	0	1	8	9	15	4	7	A2AI40	
ENSMUST00000142852						1	0	5	4	0	0	1	7	1	0	3		
ENSMUST00000142853	ENSMUSG00000035640	10	80130451	80140835	-1	0	1	1	9	4	1	0	1	1	0	0	D3YXP8	
ENSMUST00000142854	ENSMUSG00000042190	5	113612354	113650426	-1	0	2	11	5	1	0	0	2	0	0	0		
ENSMUST00000142856	ENSMUSG00000054074	2	18040676	18049051	-1	3	0	6	0	5	0	0	0	0	0	0	Z4YN47	
ENSMUST00000142857	ENSMUSG00000059555	2	25192966	25196886	-1	0	0	0	0	0	0	0	0	4	0	0	A0A0A6YXM0	
ENSMUST00000142859	ENSMUSG00000005881	2	156008045	156018279	1	5	0	15	0	0	1	14	7	10	0	0	F6UIS1	
ENSMUST00000142860						4	3	2	2	5	0	0	0	0	0	0		
ENSMUST00000142861						32	28	27	22	25	28	0	2	3	4	3		
ENSMUST00000142862						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000142863	ENSMUSG00000038347	17	13482553	13761825	-1	2	2	1	3	4	1	0	0	0	0	0	D3Z6U2	
ENSMUST00000142864	ENSMUSG00000063450	12	75818134	76110926	1	0	0	2	0	1	0	0	0	0	0	0	D3Z2J8	
ENSMUST00000142865						1	3	11	14	6	1	0	8	2	2	1		
ENSMUST00000142866						0	4	2	4	0	5	0	0	0	0	0		
ENSMUST00000142867	ENSMUSG00000020634	12	4879032	4907705	-1	0	0	0	65	11	4	61	0	11	0	21		Q99KJ0
ENSMUST00000142868	ENSMUSG00000026946	2	51948487	51973494	-1	0	0	0	1	0	2	4	36	6	27	5	B7ZD12	
ENSMUST00000142869						2	0	9	1	2	1	0	0	0	0	0		
ENSMUST00000142870						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000142872	ENSMUSG00000035236	2	39066214	39190734	-1	0	1	0	16	1	0	0	0	1	0	0	B0R0E3	
ENSMUST00000142873	ENSMUSG00000030990	7	102210208	102238567	1	0	0	3	0	0	0	4	0	0	0	2	D3Z1R5	
ENSMUST00000142874						2	0	0	0	2	0	15	80	20	8	23		
ENSMUST00000142876	ENSMUSG00000041720	16	17280351	17406314	-1	7	5	15	9	13	7	3	14	7	0	8	D6RJ66	
ENSMUST00000142877						12	14	19	18	12	11	0	0	1	0	0		
ENSMUST00000142878						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000142880						0	0	0	9	0	0	1	1	9	0	5		
ENSMUST00000142881						6	3	15	7	7	0	1	5	0	2	0		
ENSMUST00000142882						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000142883	ENSMUSG00000000386	16	97447035	97462907	-1	0	0	0	0	0	0	0	0	0	0	0	D3YV39	
ENSMUST00000142884						2	0	0	0	0	0	0	13	6	0	0		
ENSMUST00000142885	ENSMUSG00000008318	7	100845848	100863446	-1	0	0	0	73	3	0	3	32	21	5	13	D3YTN8	
ENSMUST00000142887	ENSMUSG00000026972	2	24925352	24935252	-1	0	0	0	0	0	0	0	0	0	0	0	F7ANZ2	
ENSMUST00000142888	ENSMUSG00000029015	5	21810655	21865604	-1	0	8	0	0	6	4	0	0	0	0	1	D6RIK0	
ENSMUST00000142889						2	4	1	0	3	0	0	0	0	0	0		
ENSMUST00000142890	ENSMUSG00000028152	3	138742195	138907905	1	9	15	33	5	7	9	609	791	597	86	341	Q05BH2	
ENSMUST00000142891						6	6	115	25	11	0	0	8	0	0	0		
ENSMUST00000142892	ENSMUSG00000045503	2	164456964	164479638	1	4	0	0	73	0	0	0	10	2	0	2	D6RE24	
ENSMUST00000142893	ENSMUSG00000045382	1	128588199	128592293	-1	0	0	0	5	0	0	280	471	393	207	568	E9Q2D4	
ENSMUST00000142894						7	2	9	5	5	0	0	0	0	0	0		
ENSMUST00000142896	ENSMUSG00000030116	6	122505845	122529290	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3L7	
ENSMUST00000142898	ENSMUSG00000031901	8	105991337	106053840	1	2	2	14	3	3	1	4	3	3	2	1		
ENSMUST00000142899	ENSMUSG00000039345	16	8470788	8490684	1	0	1	5	3	7	2	1	0	0	2	8	D3Z0D7	
ENSMUST00000142900						1	4	0	24	5	1	0	2	0	0	0		
ENSMUST00000142901	ENSMUSG00000028356	4	63143275	63154799	-1	1	0	3	1	2	0	2	9	3	1	0	I7HIQ9	
ENSMUST00000142902						3	0	32	0	11	2	2	19	2	0	10		
ENSMUST00000142904						0	0	5	0	0	0	10	70	6	0	8		
ENSMUST00000142905						6	5	4	4	16	7	0	0	0	0	0		
ENSMUST00000142906						0	0	11	10	11	4	5	2	6	0	0		
ENSMUST00000142908						4	2	0	2	4	4	3	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000142909						3	1	5	0	5	3	1	0	0	4	28		
ENSMUST00000142910						6	0	15	10	9	0	3	122	0	0	19		
ENSMUST00000142912						2	3	3	2	4	1	0	0	0	0	0		
ENSMUST00000142913	ENSMUSG00000017978	6	23262773	23839421	-1	0	0	9	0	0	0	0	0	0	4	2	S4R1C6	
ENSMUST00000142915						3	2	0	0	5	3	26	16	0	0	24		
ENSMUST00000142917	ENSMUSG00000021745	14	11553532	12242041	1	16	6	53	74	21	17	0	0	0	0	0	D6RD11	
ENSMUST00000142918						0	0	4	0	2	1	0	0	1	0	2		
ENSMUST00000142920	ENSMUSG00000026005	1	66700831	66719805	1	0	0	0	0	0	0	0	0	0	0	0	M0QWQ0	
ENSMUST00000142921						42	42	338	109	28	24	6	70	3	5	42		
ENSMUST00000142922						0	2	5	11	0	3	0	0	0	2	0		
ENSMUST00000142923						0	0	0	0	0	0	0	39	9	0	0		
ENSMUST00000142924						4	6	6	9	14	5	0	2	0	1	2		
ENSMUST00000142925						0	1	0	0	0	0	13	87	19	0	39		
ENSMUST00000142926						5	5	12	3	16	6	20	45	56	11	71		
ENSMUST00000142927						2	0	12	16	5	0	0	0	4	0	7		
ENSMUST00000142928						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000142929						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000142930						0	7	0	0	0	0	9	48	11	0	9		
ENSMUST00000142931	ENSMUSG00000021694	13	108158731	108195364	1	0	4	0	0	0	0	10	0	0	0	0	D6RIM0	
ENSMUST00000142932						1040	907	3772	1045	1045	467	21	73	43	9	58		
ENSMUST00000142934	ENSMUSG00000070844	7	8183265	8200320	-1	22	25	29	29	25	9	0	0	0	0	0	D3YZ97	
ENSMUST00000142935						2	5	5	2	4	0	4	9	7	0	5		
ENSMUST00000142936						3	2	0	1	0	2	36	45	359	244	185		
ENSMUST00000142938	ENSMUSG00000030269	6	113237843	113281392	1	7	3	15	166	15	4	42	23	20	0	42	D6RFN8	
ENSMUST00000142939						0	0	1	2	2	2	13	8	65	44	72		
ENSMUST00000142940	ENSMUSG00000042625	17	56560965	56584585	-1	1	1	5	2	0	0	33	54	0	20	0	F6XJ79	
ENSMUST00000142941	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	3	0	0	0	25	31	30	0	40		Q9Z0H4
ENSMUST00000142942						6	7	16	8	7	4	34	66	25	40	25		
ENSMUST00000142943						1	3	20	3	3	2	2	4	0	2	4		
ENSMUST00000142944						2	1	3	6	2	4	0	0	0	0	0		
ENSMUST00000142945	ENSMUSG00000004451	1	119470305	119504794	-1	0	0	2	0	0	2	5	10	10	2	6	F6QC68	
ENSMUST00000142946						44	34	81	35	25	18	7	10	42	2	54		
ENSMUST00000142947	ENSMUSG00000030722	7	126382854	126396737	-1	0	0	0	0	0	0	0	0	8	0	1		
ENSMUST00000142948	ENSMUSG00000034758	10	81590904	81601073	-1	0	0	7	0	0	0	0	0	0	0	0	D3Z5E1	
ENSMUST00000142949						94	98	616	117	100	45	30	58	37	9	43		
ENSMUST00000142950						1	1	1	0	1	2	0	0	1	0	0		
ENSMUST00000142951	ENSMUSG00000030091	6	91013068	91116829	-1	5	4	2	4	6	0	57	0	37	8	34	F6XGN0	
ENSMUST00000142952	ENSMUSG00000044702	7	122107262	122132985	-1	0	0	0	0	10	13	0	0	8	0	0	D6RDD1	
ENSMUST00000142954						0	0	3	3	0	1	0	0	0	0	0		
ENSMUST00000142955						4	10	10	5	6	2	2	0	0	0	0		
ENSMUST00000142956						1	2	2	0	0	0	4	0	4	0	6		
ENSMUST00000142957	ENSMUSG00000023452	5	32736301	32785646	-1	6	7	0	8	9	5	154	394	95	3	75	D6RIN9	
ENSMUST00000142958	ENSMUSG00000030584	7	29303951	29317588	1	2	0	0	0	3	0	0	0	0	0	0	F6YKQ9	
ENSMUST00000142959						37	6	104	0	31	2	269	1316	311	17	419		
ENSMUST00000142960	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZCP6	
ENSMUST00000142961						0	0	0	0	0	0	0	7	22	3	0		
ENSMUST00000142963	ENSMUSG00000000416	6	18366478	18514843	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z551	
ENSMUST00000142964	ENSMUSG00000020287	11	32226505	32232700	1	2	5	5	0	1	0	27	58	24	7	7	F2Z3Y1	
ENSMUST00000142966						2	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000142967						0	0	0	2	0	0	5	49	14	16	19		
ENSMUST00000142969						1	0	1	2	0	1	0	0	0	0	2		
ENSMUST00000142970						3	1	8	6	10	0	0	0	0	0	0		
ENSMUST00000142971						9	7	19	5	13	10	0	0	0	0	0		
ENSMUST00000142972	ENSMUSG00000021196	13	6579768	6648777	-1	4	0	0	0	0	1	0	77	6	1	7	F6YL81	
ENSMUST00000142973	ENSMUSG00000039652	19	37021291	37208601	-1	3	0	2	3	1	0	0	1	0	0	0	D3Z5F3	
ENSMUST00000142974						99	99	192	91	71	50	2	14	10	3	12		
ENSMUST00000142975						0	0	0	5	0	0	0	150	243	35	111		
ENSMUST00000142976						0	0	0	25	0	0	0	0	0	0	0		
ENSMUST00000142977	ENSMUSG00000024483	18	36559987	36665917	1	25	0	34	0	18	0	409	1136	1333	62	1030	E9Q1M6	
ENSMUST00000142978						2	5	2	0	2	1	4	0	1	0	0		
ENSMUST00000142979						0	1	4	3	2	0	0	0	0	0	0		
ENSMUST00000142980						7	4	8	5	3	4	3	69	16	32	8		
ENSMUST00000142981						9	4	17	6	6	4	0	4	0	3	0		
ENSMUST00000142982						4	0	5	37	2	2	0	0	1	0	0		
ENSMUST00000142983						0	0	2	23	1	0	0	0	0	0	0		
ENSMUST00000142984						3	7	12	2	3	0	0	34	22	0	43		
ENSMUST00000142985						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000142987						0	2	0	0	0	1	0	0	1	0	1		
ENSMUST00000142988						1	1	9	7	0	0	0	0	0	0	2		
ENSMUST00000142989						0	0	6	0	0	0	15	20	33	3	34		
ENSMUST00000142991						4	0	31	9	4	0	0	5	0	0	8		
ENSMUST00000142992						3	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000142993	ENSMUSG00000017837	11	100619244	100627607	1	1	0	10	33	4	7	5	4	0	0	15	F6XZA4	
ENSMUST00000142994	ENSMUSG00000025227	19	46341121	46375252	1	0	0	4	0	0	0	115	0	13	0	24	D6RFE3	
ENSMUST00000142995						4	0	4	5	3	5	6	9	12	0	3		
ENSMUST00000142997	ENSMUSG00000035478	10	80392539	80399550	-1	3	7	11	4	13	1	99	175	55	29	75	F6WZH1	
ENSMUST00000142998						8	0	1	2	4	1	0	2	0	0	3		
ENSMUST00000142999						1	1	0	0	0	3	0	1	0	4	0		
ENSMUST00000143000						2	8	0	0	4	4	0	18	0	13	0		
ENSMUST00000143002						1	3	6	0	1	1	0	0	0	0	0		
ENSMUST00000143003						1	0	0	0	0	0	0	15	0	0	0		
ENSMUST00000143004	ENSMUSG00000030353	6	128224288	128300823	-1	0	0	0	48	0	0	1	0	0	0	0	F6ULG6	
ENSMUST00000143005	ENSMUSG00000002428	3	20057811	20118490	1	0	0	0	10	0	0	0	0	39	0	0	G3UVU1	
ENSMUST00000143006						2	0	0	0	0	0	3	7	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143007						0	0	1	0	1	0	0	7	2	0	3		
ENSMUST00000143008						0	3	0	0	4	3	28	134	69	4	91		
ENSMUST00000143010	ENSMUSG00000021340	13	24943152	24990753	1	0	2	4	5	0	1	0	66	10	0	7	Q5NCE6	
ENSMUST00000143011						0	0	0	0	0	0	0	11	0	0	5		
ENSMUST00000143012						0	2	3	108	1	3	0	0	0	1	0		
ENSMUST00000143013						0	0	0	0	0	0	2	0	0	0	1		
ENSMUST00000143014						4	0	3	0	8	4	6	56	0	24	14		
ENSMUST00000143015						2	6	9	0	1	7	4	12	10	2	8		
ENSMUST00000143017						0	0	0	0	0	0	0	8	0	4	48		
ENSMUST00000143018						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000143019						16	10	43	39	29	11	27	45	41	0	42		
ENSMUST00000143021	ENSMUSG00000009350	11	87793581	87804413	1	3	2	2	0	1	0	34	0	15	0	18	A0A0A0MQL9	
ENSMUST00000143022						0	0	0	0	0	0	1	3	0	0	0		
ENSMUST00000143023	ENSMUSG00000022957	16	91729281	91920597	1	3	2	3	15	5	1	6	7	7	4	13	F6R6C8	
ENSMUST00000143024						0	1	0	61	2	0	0	0	114	0	29		
ENSMUST00000143026	ENSMUSG00000032076	9	47530173	47857637	1	10	4	0	31	0	7	0	0	0	0	0	E0CY16	
ENSMUST00000143027	ENSMUSG00000040367	5	3845173	3866596	1	1	0	0	1	0	0	0	0	0	0	1	D3Z4M8	
ENSMUST00000143028						0	2	0	0	0	0	3	2	0	0	0		
ENSMUST00000143029						46	41	66	85	48	27	5	52	21	6	27		
ENSMUST00000143030	ENSMUSG00000015365	15	88982909	89055152	1	3	0	0	8	0	0	0	0	0	0	0	G3UYS5	
ENSMUST00000143031	ENSMUSG00000063450	12	75818134	76110926	1	34	27	44	47	49	29	698	271	2290	28	1439	E9QP46	
ENSMUST00000143032						1	0	2	13	2	0	0	0	0	0	0		
ENSMUST00000143033	ENSMUSG00000075023	2	93855361	93869157	-1	0	0	0	0	0	0	0	0	0	0	0	A2AIH1	
ENSMUST00000143034						1	4	0	0	4	1	6	31	13	5	12		
ENSMUST00000143035	ENSMUSG00000038178	11	75531694	75577575	1	7	5	5	255	9	12	7	4	8	0	11	Q5ND24	
ENSMUST00000143036						44	35	128	91	74	41	0	0	0	0	4		
ENSMUST00000143037						1675	1899	3414	1436	2359	1084	25	137	88	50	106		
ENSMUST00000143038						0	2	0	0	0	3	2	0	0	0	0		
ENSMUST00000143039						9	4	6	18	18	15	13	71	23	5	48		
ENSMUST00000143040	ENSMUSG00000038451	6	124808661	124810619	1	0	0	0	36	14	0	77	49	64	0	45	D3YX10	
ENSMUST00000143041	ENSMUSG00000027787	3	69721985	69756373	1	0	0	2	9	1	0	1	5	5	11	7	D6RHT4	
ENSMUST00000143042						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000143043	ENSMUSG00000016458	2	105126529	105173616	1	0	0	0	144	8	0	0	0	0	0	0	F6Y2T6	
ENSMUST00000143044						5	6	0	84	1	4	0	11	0	3	0		
ENSMUST00000143045						4	5	25	15	17	4	0	2	3	0	5		
ENSMUST00000143046						8	5	2	4	8	1	0	0	0	0	0		
ENSMUST00000143047	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	0	0	0	0	0	0	0	3		P0C8K7
ENSMUST00000143048						12	21	47	9	8	3	0	1	1	0	3		
ENSMUST00000143049						0	0	0	0	0	0	15	36	28	0	48		
ENSMUST00000143050						1	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000143051	ENSMUSG00000090100	2	120732816	120850604	-1	0	0	0	0	0	0	0	0	73	0	39	A2AW13	
ENSMUST00000143052	ENSMUSG00000018377	11	88068279	88084729	1	4	1	4	0	0	6	0	277	4	3	7	Q5SXC3	
ENSMUST00000143053						4	2	19	4	1	1	0	25	9	3	7		
ENSMUST00000143054	ENSMUSG00000048100	3	108571698	108583222	1	26	24	27	20	39	5	29	142	48	281	60		P61216
ENSMUST00000143055	ENSMUSG00000028599	4	145213463	145246870	-1	0	0	0	28	0	0	4	1	0	0	6	D6RG55	
ENSMUST00000143056						12	0	25	144	17	0	0	0	0	1	1		
ENSMUST00000143057	ENSMUSG00000031591	8	41340197	41374773	-1	3	0	2	231	10	3	0	0	0	0	0	D3Z505	
ENSMUST00000143058	ENSMUSG00000039763	16	91614257	91619026	-1	0	0	0	2	0	0	0	0	0	0	0	D3Z032	
ENSMUST00000143059						4	0	10	0	0	0	0	0	2	2	1		
ENSMUST00000143061						0	0	1	24	1	0	0	0	0	0	0		
ENSMUST00000143063						1	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000143066						7	3	28	5	3	2	1	0	0	0	0		
ENSMUST00000143067						7	5	15	13	7	4	0	0	1	1	0		
ENSMUST00000143069						1	0	25	36	5	4	3	7	34	11	10		
ENSMUST00000143071						4	2	4	3	2	3	0	0	0	0	0		
ENSMUST00000143072						2	4	11	1	0	0	5	32	13	0	29		
ENSMUST00000143073						5	7	6	38	11	8	1	3	8	72	3		
ENSMUST00000143074	ENSMUSG00000106631	5	107507621	107580596	1	31259	28324	194833	65551	29306	12988	208	615	521	89	481	F7CG54	
ENSMUST00000143075						0	0	3	0	6	1	0	3	6	0	0		
ENSMUST00000143076						10	7	3	10	9	1	2	42	9	0	7		
ENSMUST00000143077	ENSMUSG00000044252	18	12755314	12941841	-1	0	0	0	0	1	1	1	0	0	0	0	D3Z7I9	
ENSMUST00000143078						1	0	6	7	4	3	21	165	37	6	62		
ENSMUST00000143079						4	4	9	0	7	1	0	0	0	0	0		
ENSMUST00000143080						3	3	2	158	0	1	0	0	0	0	0		
ENSMUST00000143081						0	0	2	0	0	0	3	0	9	1	7		
ENSMUST00000143082	ENSMUSG00000006763	7	46686108	46710680	-1	16	20	38	42	35	4	23	42	35	4	23	G1UCX4	Q9D2C2
ENSMUST00000143083	ENSMUSG00000096519	9	3013140	3014344	1	9039	6970	26448	20754	10254	8012	0	0	9	0	0	J3QPJ9	
ENSMUST00000143084						0	1	5	0	5	5	0	0	0	0	0		
ENSMUST00000143085						8	0	6	232	23	14	224	317	371	22	357		
ENSMUST00000143087						2	1	5	3	0	1	0	3	0	0	0		
ENSMUST00000143088						6	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000143089						38	21	104	42	24	21	0	3	2	0	0		
ENSMUST00000143090						5	0	1	0	1	0	2	4	5	0	4		
ENSMUST00000143091	ENSMUSG00000029772	6	29768011	29912310	1	0	0	0	0	0	0	2	0	16	1	12		
ENSMUST00000143092						2	1	2	3	3	0	1	0	2	0	2		
ENSMUST00000143093						4	3	0	0	2	1	0	0	0	0	0		
ENSMUST00000143094						56	35	37	33	75	46	4	23	6	7	6		
ENSMUST00000143095	ENSMUSG00000035392	2	37798991	38287390	-1	0	0	0	33	0	0	3	3	0	0	0	D6RI65	
ENSMUST00000143096						2	1	1	0	3	0	2	10	0	2	2		
ENSMUST00000143097						0	1	28	0	5	0	6	0	7	1	2		
ENSMUST00000143098						0	0	0	0	0	0	0	3	5	22	8		
ENSMUST00000143099						4	2	0	62	2	3	0	1	3	1	4		
ENSMUST00000143100						0	2	0	64	3	0	4	5	0	0	3		
ENSMUST00000143101	ENSMUSG00000004285	6	29467718	29470512	1	0	2	10	4	9	6	0	0	0	0	0	F7B2B4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143102						1	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000143104	ENSMUSG00000039740	4	47465067	47474333	-1	3	1	2	0	0	1	3	0	5	1	0	F6RBY3	
ENSMUST00000143105	ENSMUSG00000040569	4	14502430	14621805	-1	0	0	0	0	1	2	0	0	0	0	0	A2AJZ6	
ENSMUST00000143106						3	8	14	0	2	0	0	19	0	7	0		
ENSMUST00000143107	ENSMUSG00000046364	7	109519147	109522367	1	2	7	14	33	9	9	129	671	200	600	145		P14115
ENSMUST00000143108	ENSMUSG00000060002	10	88452745	88504073	-1	2	2	2	2	6	2	0	9	0	2	0	F6ZDL8	
ENSMUST00000143111						0	0	0	0	0	0	0	38	12	0	0		
ENSMUST00000143113						1	0	0	5	0	1	0	0	0	0	0		
ENSMUST00000143114						3	2	4	4	2	1	0	34	10	0	16		
ENSMUST00000143115						6	0	5	14	10	6	1	16	10	3	21		
ENSMUST00000143116	ENSMUSG00000028563	4	98355370	98383306	-1	0	0	0	39	0	0	0	0	0	18	0	F6R2M8	
ENSMUST00000143117	ENSMUSG00000020280	11	23665674	23732876	1	0	0	2	0	2	0	0	0	0	0	0	B0QZU5	
ENSMUST00000143118	ENSMUSG00000031840	8	70754679	70758677	1	0	1	0	26	0	3	0	0	0	0	1	D3YZP5	
ENSMUST00000143119	ENSMUSG00000098794	2	30281043	30301078	1	2	0	0	0	0	0	0	0	0	0	0	F7BCN9	
ENSMUST00000143120						0	0	0	19	0	1	0	0	0	0	1		
ENSMUST00000143121						0	0	0	2	1	0	4	9	0	0	5		
ENSMUST00000143123	ENSMUSG00000040170	1	162874317	162898726	-1	0	0	0	0	1	0	0	0	0	0	0	D3YVR1	
ENSMUST00000143124	ENSMUSG00000000538	11	60226714	60352905	-1	1	0	0	0	0	1	0	0	0	0	0	F6RBX1	
ENSMUST00000143125	ENSMUSG00000032786	9	106233455	106248126	-1	0	1	4	2	4	4	34	34	30	17	38	F6RYA6	
ENSMUST00000143126	ENSMUSG00000020311	11	30930774	30954335	-1	0	1	0	0	2	0	0	0	0	0	0	F7AQQ2	
ENSMUST00000143128						2	0	3	0	3	1	0	0	0	0	0		
ENSMUST00000143130						0	0	6	2	0	0	0	0	0	0	0		
ENSMUST00000143131	ENSMUSG00000020566	12	17284721	17329359	-1	4	2	10	2	11	3	0	0	0	0	0	D3YVW5	
ENSMUST00000143132	ENSMUSG00000005907	5	3596066	3637232	1	4	0	0	1	0	0	0	0	0	0	0	F7CF88	
ENSMUST00000143134						2	8	18	5	9	2	0	0	0	0	0		
ENSMUST00000143136						2	2	0	1	2	1	0	0	1	0	0		
ENSMUST00000143137	ENSMUSG00000023961	17	44096308	44105809	-1	40	25	161	0	0	0	39	147	67	53	79		Q8BTJ4
ENSMUST00000143138						0	1	0	0	0	0	0	1	0	0	3		
ENSMUST00000143139	ENSMUSG00000025155	11	120789201	120796403	-1	3	0	0	0	0	0	0	0	10	0	0	B1ATU6	
ENSMUST00000143140						2	2	11	3	3	0	11	60	20	3	33		
ENSMUST00000143141						20	15	36	16	43	16	1	0	0	0	0		
ENSMUST00000143142	ENSMUSG00000035967	X	56454857	56507843	1	0	0	0	0	0	0	79	2646	238	74	46	F6WNG1	
ENSMUST00000143143	ENSMUSG00000021792	14	40993740	41013788	-1	0	0	3	6	0	0	0	0	0	0	0	D3YYG8	
ENSMUST00000143144	ENSMUSG00000025871	13	54551218	54565435	-1	4	0	10	0	0	0	0	0	0	0	0	D3YXF2	
ENSMUST00000143145	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	1	0	0	0	0	0	Q05BF2	
ENSMUST00000143146						3	3	16	5	6	0	32	40	26	25	66		
ENSMUST00000143147	ENSMUSG00000042303	15	80977765	81012289	1	0	0	0	8	0	3	0	0	2	0	0	D6RFR6	
ENSMUST00000143148						13	6	47	8	8	1	9	10	14	0	19		
ENSMUST00000143149						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000143150						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000143151						3	1	0	23	3	1	3	0	0	0	3		
ENSMUST00000143152						0	1	0	3	2	0	0	0	0	0	0		
ENSMUST00000143153	ENSMUSG00000022094	14	70303469	70351425	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z3C5	
ENSMUST00000143154	ENSMUSG00000043085	4	141613376	141618633	-1	77	107	201	138	109	51	8	22	4	2	18	F2Z3W9	
ENSMUST00000143155	ENSMUSG00000030838	7	46195350	46238503	-1	0	0	0	0	0	11	3	0	5	0	0	D6RIM8	
ENSMUST00000143156						6	0	0	54	0	0	2	29	13	0	7		
ENSMUST00000143157						0	2	2	0	1	0	0	0	0	0	0		
ENSMUST00000143158	ENSMUSG00000057789	17	27019810	27029009	-1	0	0	0	0	0	0	4	0	0	0	0	F7CUQ1	
ENSMUST00000143159						0	0	0	0	0	0	3	0	0	0	5		
ENSMUST00000143160						0	1	5	1	5	2	0	0	0	0	0		
ENSMUST00000143161						57	42	182	113	86	32	4	1	1	0	5		
ENSMUST00000143162	ENSMUSG00000038347	17	13482553	13761825	-1	0	0	0	0	0	0	0	0	0	0	0	E9PY37	
ENSMUST00000143163						27	34	40	23	31	16	4	31	13	2	15		
ENSMUST00000143164						17	24	204	40	16	5	1	1	3	0	0		
ENSMUST00000143165						0	0	0	0	0	0	0	3	0	0	1		
ENSMUST00000143168						1	2	3	2	1	0	27	81	60	3	93		
ENSMUST00000143169						0	0	5	0	0	0	0	2	2	0	2		
ENSMUST00000143170	ENSMUSG00000022538	16	30560494	30587592	-1	0	0	0	5	0	0	72	257	146	129	157	D6RFS1	
ENSMUST00000143171						4	2	0	5	3	3	0	0	0	0	0		
ENSMUST00000143172	ENSMUSG00000032359	9	90054152	90076089	1	1	0	0	3	0	2	0	0	0	0	0	D3YVI3	
ENSMUST00000143173						0	1	4	0	0	2	2	8	13	0	22		
ENSMUST00000143174						17	12	17	45	32	7	23	40	59	3	51		
ENSMUST00000143175	ENSMUSG00000018565	11	69968222	69982517	-1	4	1	7	7	2	1	2	4	2	3	0	J3QMW4	
ENSMUST00000143176	ENSMUSG00000026490	1	179960472	180165603	1	22	16	28	17	45	24	3	18	4	6	16	F6S5Z6	
ENSMUST00000143177	ENSMUSG00000003518	11	101971143	101987013	-1	0	0	0	13	0	0	5	0	6	7	1	H3BLK2	
ENSMUST00000143178						799	728	922	797	812	420	596	1128	464	118	372		
ENSMUST00000143179	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	1	0	0	0	0	0	0	0	0	D3Z105	
ENSMUST00000143180	ENSMUSG00000032507	9	113963637	114046191	-1	1	0	41	5	6	6	31	68	95	0	7	D6RFC8	
ENSMUST00000143181						5	0	8	41	6	4	0	0	0	0	0		
ENSMUST00000143182						58	64	90	60	63	41	15	25	21	3	45		
ENSMUST00000143184	ENSMUSG00000090266	11	116843278	116854263	1	0	0	0	0	0	0	0	15	1	0	0	B7ZC87	
ENSMUST00000143185						3	0	5	3	2	0	2	0	0	0	5		
ENSMUST00000143186	ENSMUSG00000055963	4	12906838	12983553	1	1	1	2	16	0	0	0	2	0	5	0		B2B9E1
ENSMUST00000143187						0	2	10	0	4	0	0	3	6	0	0		
ENSMUST00000143188	ENSMUSG00000027184	2	103762941	103797649	-1	0	0	0	0	1	1	7	0	157	9	187	F6YLI0	
ENSMUST00000143189	ENSMUSG00000041594	14	122918971	122984035	-1	0	1	0	1	0	2	9	0	4	0	0	D6RHA9	
ENSMUST00000143190						1	3	0	0	2	0	1	0	13	6	8		
ENSMUST00000143192						2	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000143193						0	0	0	1	0	0	0	0	6	0	2		
ENSMUST00000143194						0	0	0	12	5	0	6	40	24	0	68		
ENSMUST00000143195						3	0	0	0	7	0	0	0	0	0	0		
ENSMUST00000143196						0	0	0	2	1	1	3	27	2	0	8		
ENSMUST00000143197						0	3	0	0	1	0	0	0	0	0	0		
ENSMUST00000143198						11	12	14	7	9	7	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143199						2	4	2	20	4	2	16	39	21	0	23		
ENSMUST00000143200						1	0	0	23	8	3	0	0	0	0	0		
ENSMUST00000143201						0	0	0	1	0	0	0	2	7	0	0		
ENSMUST00000143203	ENSMUSG00000020546	11	90476492	90638084	-1	104	124	355	140	112	56	13	43	13	3	38		Q9WV89
ENSMUST00000143204						0	0	0	3	2	2	0	5	0	4	0		
ENSMUST00000143205						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000143206						1	3	0	0	1	1	0	42	0	0	0		
ENSMUST00000143207						21	14	193	0	25	14	0	0	0	0	0		
ENSMUST00000143210						0	0	0	0	2	2	3	6	4	0	0		
ENSMUST00000143212						2	1	2	2	0	0	0	0	0	2	2		
ENSMUST00000143213	ENSMUSG00000073771	4	117119219	117125725	-1	3	1	4	2	0	0	0	0	0	0	0	S4R1J4	
ENSMUST00000143214	ENSMUSG00000015757	10	7792891	7823135	1	195	217	145	232	160	53	9	50	48	8	72	D6RJ77	
ENSMUST00000143215						4	3	5	4	9	3	0	0	0	0	0		
ENSMUST00000143216						68	71	142	83	92	42	0	2	1	0	6		
ENSMUST00000143217						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000143218						3	0	8	4	0	0	0	4	8	0	19		
ENSMUST00000143219	ENSMUSG00000017781	11	75588097	75628804	1	0	0	0	41	0	0	424	1582	946	165	705	Q5ND42	P53810
ENSMUST00000143220						0	0	0	0	0	0	0	0	3	0	3		
ENSMUST00000143221						3	3	5	2	6	0	0	0	0	0	0		
ENSMUST00000143222						0	2	1	3	0	0	3	2	0	0	2		
ENSMUST00000143223	ENSMUSG00000031168	X	8185329	8193512	-1	0	0	0	0	0	0	59	104	52	24	44	A2AC29	
ENSMUST00000143224						18	23	52	48	24	12	8	40	18	0	23		
ENSMUST00000143225						2	1	4	0	0	4	4	15	11	0	16		
ENSMUST00000143226	ENSMUSG00000006345	10	75561604	75586200	1	3	0	0	0	0	0	0	0	0	0	17	D3YWW4	
ENSMUST00000143228	ENSMUSG00000020389	11	52004221	52089784	1	5	1	9	64	13	2	4	81	18	3	18	F2Z3Z6	
ENSMUST00000143229	ENSMUSG00000039754	5	136136146	136141615	1	5	0	5	4	2	1	2	0	0	0	6	F7B4H2	
ENSMUST00000143230						0	0	0	0	0	0	8	0	6	0	10		
ENSMUST00000143231						3	1	1	8	2	2	10	56	20	57	16		
ENSMUST00000143232						0	1	0	0	3	1	990	604	1053	183	407		
ENSMUST00000143233						25	24	58	45	23	20	23	100	41	22	35		
ENSMUST00000143234						4	5	7	13	3	3	0	3	1	0	1		
ENSMUST00000143235	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ71	
ENSMUST00000143236	ENSMUSG00000037012	10	62268855	62379908	-1	0	4	0	0	0	0	0	0	0	0	0	B4YB29	
ENSMUST00000143237						6	2	6	4	0	0	0	0	0	0	0		
ENSMUST00000143238	ENSMUSG00000068099	15	82252397	82260753	1	13	10	11	30	8	4	0	0	0	0	0	D3YWK9	
ENSMUST00000143239						5	1	6	6	3	4	63	150	6	11	48		
ENSMUST00000143240						2	0	1	0	2	0	0	0	3	0	5		
ENSMUST00000143241	ENSMUSG00000019518	5	138172002	138180429	1	0	0	0	0	0	0	10	65	15	0	29	E9Q416	
ENSMUST00000143243						10	4	29	12	9	2	26	106	39	2	60		
ENSMUST00000143246						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143248						0	0	0	0	0	0	44	82	36	20	42		
ENSMUST00000143249	ENSMUSG00000027787	3	69721985	69756373	1	1	2	6	40	2	1	0	0	0	0	0	D3YYX2	
ENSMUST00000143251	ENSMUSG00000019590	11	105933702	105953336	-1	9	3	10	11	10	3	0	0	2	0	0	A2A685	
ENSMUST00000143252						19	15	49	39	28	10	0	0	1	0	6		
ENSMUST00000143253	ENSMUSG00000026975	2	24962400	24972163	1	3	0	0	4	8	0	0	0	0	0	1	A0A0A6YY79	
ENSMUST00000143254	ENSMUSG00000024236	18	4920540	5119299	1	0	9	11	94	13	15	4125	5480	9172	262	6685	E9Q983	
ENSMUST00000143256						1	0	0	0	0	0	0	0	0	6	0		
ENSMUST00000143257						9	2	4	25	4	3	0	0	0	0	0		
ENSMUST00000143258	ENSMUSG00000027750	3	54361109	54391037	1	0	0	0	0	0	0	0	0	0	0	0	F7C9H0	
ENSMUST00000143262						6	0	0	15	11	3	1	0	3	0	0		
ENSMUST00000143263	ENSMUSG00000031342	X	166238911	166388988	1	4	0	3	0	15	2	1	0	0	0	0		P35803
ENSMUST00000143265	ENSMUSG00000031751	8	93971588	94012663	-1	1	1	12	12	3	1	6	2	2	2	4	H3BJC0	
ENSMUST00000143267						44	45	211	55	42	24	1	0	1	0	3		
ENSMUST00000143268	ENSMUSG00000037979	5	124834418	124862424	-1	0	0	2	1	3	0	7	0	13	2	8	D3YUR9	
ENSMUST00000143269						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143270						1	0	2	1	1	0	1	0	1	0	1		
ENSMUST00000143271						2	2	1	7	0	0	1	0	0	0	0		
ENSMUST00000143273						0	1	0	1	0	0	0	0	0	0	2		
ENSMUST00000143274						1	3	9	2	1	1	6	2	0	0	0		
ENSMUST00000143275	ENSMUSG00000043079	18	60593973	60660142	-1	20	0	0	26	35	27	3	0	0	0	15		Q8CC35
ENSMUST00000143276						14	22	21	33	27	7	28	26	11	0	10		
ENSMUST00000143277	ENSMUSG00000028580	4	130663321	130781564	1	0	0	0	2	0	0	0	2	10	0	0	A8WHM8	
ENSMUST00000143278	ENSMUSG00000029861	6	42315312	42324643	-1	0	0	0	54	0	0	0	0	0	0	0	E9Q8P8	
ENSMUST00000143279	ENSMUSG00000035064	7	120842831	120907219	1	2	3	11	14	3	0	0	0	0	0	0	D3Z1Y3	
ENSMUST00000143280	ENSMUSG00000020495	11	87077732	87086774	-1	0	1	0	0	0	0	0	34	0	3	0	Q99LS6	
ENSMUST00000143281						2	3	2	5	2	0	18	38	25	0	50		
ENSMUST00000143282	ENSMUSG00000030304	6	148179079	148212374	-1	0	0	0	0	3	0	0	197	24	0	22		
ENSMUST00000143283						4	2	0	3	3	1	1	0	0	0	0		
ENSMUST00000143284	ENSMUSG00000031618	8	76899442	77245012	1	0	0	2	33	0	0	0	0	0	0	0	D3Z7J4	
ENSMUST00000143285	ENSMUSG00000034771	10	81574561	81590845	1	0	0	0	0	0	0	0	1	0	0	1	D3Z1A4	
ENSMUST00000143286	ENSMUSG00000068457	Y	1096861	1245759	-1	0	0	2	0	0	0	0	0	0	0	0	E9Q504	
ENSMUST00000143288	ENSMUSG00000025579	11	119267887	119285454	1	6	4	12	0	16	5	2	5	0	0	6	F6R5R5	
ENSMUST00000143289						0	0	0	11	0	0	0	0	0	0	7		
ENSMUST00000143290	ENSMUSG00000020271	11	32642724	32746816	1	5	2	3	0	0	3	0	0	35	0	7	F7BGU3	
ENSMUST00000143292						0	0	0	0	0	0	8	0	13	2	7		
ENSMUST00000143293						0	0	0	0	0	0	0	51	36	0	0		
ENSMUST00000143294						5	3	7	64	9	6	0	1	0	0	0		
ENSMUST00000143295						0	0	3	0	0	0	2	1	1	0	0		
ENSMUST00000143296						0	1	2	0	0	0	0	1	0	0	0		
ENSMUST00000143297						4	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000143298						0	1	2	3	1	2	1	0	0	0	0		
ENSMUST00000143299						3	5	7	9	5	0	0	0	0	0	0		
ENSMUST00000143300						1	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000143301						2	1	0	0	0	0	0	23	6	6	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143303	ENSMUSG00000047733	19	6080033	6080788	1	0	1	2	3	3	0	0	1	0	0	1	D3Z338	
ENSMUST00000143304	ENSMUSG00000028671	4	135963727	135968178	1	2	2	17	240	8	3	1	10	4	1	0	B1AV53	
ENSMUST00000143305						4	4	4	0	2	1	10	36	29	4	29		
ENSMUST00000143306						0	0	0	0	1	2	2	2	4	15	2		
ENSMUST00000143307						1	2	1	1	3	2	1	3	12	0	5		
ENSMUST00000143308						8	8	17	39	12	9	2	4	0	4	9		
ENSMUST00000143309						11	1	3	10	4	7	2	0	0	0	0		
ENSMUST00000143310	ENSMUSG00000031134	X	57383530	57393036	-1	6	0	0	0	4	3	0	0	44	13	45	S4R1F6	
ENSMUST00000143312						3	4	7	5	5	4	0	0	0	0	1		
ENSMUST00000143313						0	0	0	0	2	0	0	0	1	0	0		
ENSMUST00000143314	ENSMUSG00000050312	16	62732444	62786818	-1	70	18	219	100	16	29	47	67	95	29	31	D6RDT7	
ENSMUST00000143316						2	1	4	5	3	0	291	227	235	148	280		
ENSMUST00000143318						4	3	4	0	12	2	0	0	0	0	0		
ENSMUST00000143319						5	2	19	4	6	4	0	0	2	0	0		
ENSMUST00000143320						2	0	4	3	0	2	1	0	3	1	3		
ENSMUST00000143321	ENSMUSG00000051727	7	97451323	97459557	1	0	0	3	13	0	1	0	0	0	0	0		
ENSMUST00000143322	ENSMUSG00000035064	7	120842831	120907219	1	0	0	0	0	0	0	4	1	10	0	9	D3Z088	
ENSMUST00000143323						7	3	17	5	9	3	0	2	0	0	4		
ENSMUST00000143325	ENSMUSG00000030452	7	55931287	55962476	-1	3	1	13	29	5	3	0	1	0	0	2		
ENSMUST00000143326						3	0	1	0	1	0	2	0	12	4	0		
ENSMUST00000143327	ENSMUSG00000026049	1	44086613	44102441	-1	3	3	12	0	0	0	3	0	0	0	0	D3YUH0	
ENSMUST00000143329						6	3	5	1	3	4	0	0	0	0	0		
ENSMUST00000143330						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000143331						0	2	0	0	0	0	7	183	105	78	44		
ENSMUST00000143333						3	3	0	1	3	1	1	6	4	1	3		
ENSMUST00000143334						0	3	0	1	0	0	0	0	0	0	0		
ENSMUST00000143335						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143336						2	2	0	0	3	1	10	111	14	8	6		
ENSMUST00000143337	ENSMUSG00000035696	4	44126210	44233789	-1	0	0	0	44	5	0	29	9	62	3	31	B1AWE7	
ENSMUST00000143338	ENSMUSG00000058454	7	143823145	143848410	1	0	2	2	0	6	0	0	0	5	0	5	D3Z7G1	
ENSMUST00000143339	ENSMUSG00000078716	4	43668971	43692668	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7V8	
ENSMUST00000143340						5	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000143341						10	11	12	59	21	3	5	0	19	0	8		
ENSMUST00000143342	ENSMUSG00000026019	1	60069785	60098645	-1	0	1	0	0	0	0	4	0	1	39	0	D3Z369	
ENSMUST00000143343	ENSMUSG00000003531	16	18052860	18071632	1	6	1	0	0	0	0	0	0	0	0	0	Q3TV71	
ENSMUST00000143344						1	3	0	0	0	0	54	91	9	50	37		
ENSMUST00000143345						6	0	20	11	4	3	0	0	0	0	0		
ENSMUST00000143347						8	0	11	11	7	4	2	6	0	0	5		
ENSMUST00000143348						4	0	0	2	6	1	0	0	0	0	0		
ENSMUST00000143349	ENSMUSG00000027184	2	103762941	103797649	-1	0	0	0	0	1	0	22	44	12	8	26	F6YP03	
ENSMUST00000143350						12	5	43	278	11	9	2	5	0	0	0		
ENSMUST00000143351						2	0	1	2	9	4	0	17	2	9	17		
ENSMUST00000143352	ENSMUSG00000063652	11	53949965	53980332	-1	2	3	0	0	7	1	0	1	2	0	0	F6YI98	
ENSMUST00000143353						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143354	ENSMUSG00000024330	17	34039437	34066685	1	0	0	16	3	2	0	4	3	9	1	17	Q3UUU1	
ENSMUST00000143355						1	1	0	6	2	0	0	10	2	0	5		
ENSMUST00000143356						0	0	0	0	2	0	8	4	18	0	24		
ENSMUST00000143357						4	2	9	4	6	7	0	2	4	0	0		
ENSMUST00000143358	ENSMUSG00000070565	1	157135182	157412595	-1	3	4	1	0	0	0	0	0	0	0	0	D3Z7S1	
ENSMUST00000143359	ENSMUSG00000031441	8	12757014	12868728	1	0	0	0	2	0	4	88	178	159	37	158	F6Z063	
ENSMUST00000143360						0	2	10	0	3	4	0	22	1	0	15		
ENSMUST00000143361						0	0	0	0	0	0	4	12	16	12	11		
ENSMUST00000143362						3	0	7	1	2	4	0	49	32	17	15		
ENSMUST00000143363						87	88	195	210	96	50	5	11	7	4	10		
ENSMUST00000143364						8	9	8	7	5	3	0	0	0	0	1		
ENSMUST00000143365	ENSMUSG00000040407	5	3928054	4081310	1	0	0	7	0	2	0	0	1	13	1	9		
ENSMUST00000143366	ENSMUSG00000031090	7	143795584	143822849	-1	0	2	2	0	0	2	0	0	2	0	0	D6RDE7	
ENSMUST00000143367						11	14	36	18	12	9	0	0	0	0	0		
ENSMUST00000143368	ENSMUSG00000073643	1	79702262	79776143	-1	0	0	0	21	0	0	0	0	0	0	0	D3Z057	
ENSMUST00000143369						2	2	0	0	0	2	39	12	7	2	16		
ENSMUST00000143370						29	33	80	201	41	14	1	7	7	1	1		
ENSMUST00000143371						0	4	0	1	2	0	0	2	2	0	2		
ENSMUST00000143372						7	7	14	0	10	7	2	2	13	2	8		
ENSMUST00000143373	ENSMUSG00000048939	16	29231851	29378732	-1	0	0	0	0	21	14	0	0	0	0	0	D3YU82	
ENSMUST00000143374						4	2	18	5	4	4	4	3	0	1	3		
ENSMUST00000143375	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	0	0	0	0	56	D6RCG5	
ENSMUST00000143376	ENSMUSG00000046314	12	44852488	45074493	-1	0	0	0	6	0	0	0	0	0	0	0	B8JJ84	
ENSMUST00000143377						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000143379	ENSMUSG00000015837	11	50199366	50210827	-1	0	0	0	0	0	0	0	0	0	13	0	D3YZJ1	
ENSMUST00000143380	ENSMUSG00000075296	19	3972328	3981645	1	14	15	23	17	20	10	2	4	5	0	4	E9Q3E1	
ENSMUST00000143381						9	3	1	27	4	3	0	0	0	0	0		
ENSMUST00000143383						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000143384						18	16	56	64	26	12	0	21	5	1	19		
ENSMUST00000143385	ENSMUSG00000035649	4	44755877	44932215	1	0	0	0	11	0	1	0	0	6	1	4	E9Q193	
ENSMUST00000143386	ENSMUSG00000020176	11	11930508	12038683	-1	2	1	0	1	2	1	0	0	0	0	3	Q5SUW0	
ENSMUST00000143387						4	4	1	0	3	0	0	0	0	0	2		
ENSMUST00000143388						7	0	2	2	0	2	0	3	0	27	3		
ENSMUST00000143389						6	5	6	9	5	3	0	0	0	0	2		
ENSMUST00000143390						0	3	6	0	5	0	0	3	3	3	1		
ENSMUST00000143393	ENSMUSG00000022090	14	70164218	70177681	-1	0	0	2	0	0	0	354	216	301	37	143	E9Q996	
ENSMUST00000143394						2	4	3	7	7	6	14	10	2	0	5		
ENSMUST00000143395						0	0	0	0	0	2	45	2	31	3	25		
ENSMUST00000143396						3	3	1	5	0	1	0	0	0	0	2		
ENSMUST00000143397						1	2	0	3	0	0	0	0	14	0	16		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143398						0	0	13	0	2	1	0	15	17	5	17		
ENSMUST00000143399						0	0	6	0	3	0	0	0	3	0	0		
ENSMUST00000143400	ENSMUSG00000048175	15	98134637	98165625	-1	27	33	210	49	41	24	419	1169	409	102	279		
ENSMUST00000143401						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143402						8	9	8	10	7	3	11	81	39	108	32		
ENSMUST00000143403						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000143404						0	2	1	4	2	1	23	32	20	0	8		
ENSMUST00000143405	ENSMUSG00000005674	1	171216011	171222514	-1	0	0	0	0	0	0	23	43	19	13	18	M0QWR6	
ENSMUST00000143406	ENSMUSG00000025572	11	117765988	117782198	-1	2	2	2	22	2	3	4	0	0	0	0	B1ATB5	
ENSMUST00000143407						1	3	13	9	1	0	1	1	1	0	3		
ENSMUST00000143408						0	1	0	0	0	0	26	82	29	8	40		
ENSMUST00000143409						7	1	3	1	2	4	2	3	2	2	0		
ENSMUST00000143410	ENSMUSG00000040086	3	154786291	155055407	-1	0	0	0	13	0	0	0	0	0	0	0		Q5GIG6
ENSMUST00000143411	ENSMUSG00000031516	8	34090420	34108796	-1	1	1	1	0	0	0	19	42	0	12	8	D3Z6A1	
ENSMUST00000143412	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	0	0	4	5	67	0	0	0	E9PZE8	
ENSMUST00000143413	ENSMUSG00000014402	7	46888949	46919969	-1	0	0	0	38	0	0	0	0	0	0	0	D3Z2V5	
ENSMUST00000143414	ENSMUSG00000056144	7	104244457	104340693	1	9	5	5	14	8	5	31	242	97	5	106		Q99PP6
ENSMUST00000143415	ENSMUSG00000061533	12	90998492	91384409	-1	14	4	26	3	17	8	0	181	0	0	0	F7CIB0	
ENSMUST00000143416						0	1	0	85	2	2	0	0	2	0	0		
ENSMUST00000143417	ENSMUSG00000028522	4	103114390	103165754	1	0	0	0	10	1	2	0	0	1	1	2	B1AY30	
ENSMUST00000143418						8	8	81	33	18	2	5	11	13	32	24		
ENSMUST00000143419	ENSMUSG00000034159	1	93151349	93160948	-1	0	7	24	52	11	0	0	0	0	0	0		Q8CEZ4
ENSMUST00000143420						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000143421	ENSMUSG00000032400	9	64137144	64173104	-1	0	0	0	0	0	0	0	0	0	0	0	H3BL96	
ENSMUST00000143422						1	2	12	26	10	2	0	0	0	0	0		
ENSMUST00000143423						0	2	0	4	1	0	5	45	10	15	11		
ENSMUST00000143424	ENSMUSG00000034748	10	81621785	81627797	-1	7	0	13	18	11	1	4	2	6	0	10	D3YY89	
ENSMUST00000143425	ENSMUSG00000000339	3	116488963	116508208	-1	0	0	0	57	1	0	0	0	0	2	0	D6RD00	
ENSMUST00000143426	ENSMUSG00000028699	4	116161869	116167601	-1	0	0	0	0	4	2	0	0	0	0	0	A0A0A0MQL3	
ENSMUST00000143427	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	0	0	0	0	0	D6RFC0	
ENSMUST00000143430						2	0	0	10	1	0	7	30	9	38	15		
ENSMUST00000143431	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	4	3	8	0	6	D3YZ04	
ENSMUST00000143432	ENSMUSG00000040690	4	130047840	130099283	1	17	9	54	24	38	22	0	0	0	5	0	E9Q0X4	
ENSMUST00000143433	ENSMUSG00000028344	4	48279760	48431954	1	11	3	4	7	4	0	0	0	13	0	7	S4R2B7	
ENSMUST00000143434						0	2	1	1	2	3	0	0	0	0	0		
ENSMUST00000143436	ENSMUSG00000029127	5	38189735	38220457	-1	9	0	0	0	4	5	18	36	18	3	2	D6RGL5	
ENSMUST00000143438						23	11	29	12	16	8	16	67	29	0	50		
ENSMUST00000143439						1	0	22	2	3	1	53	91	18	7	19		
ENSMUST00000143441	ENSMUSG00000031807	8	71592176	71601092	1	2	0	0	133	5	0	8	17	0	6	9	D3Z4X1	
ENSMUST00000143442						32	26	29	25	15	23	0	4	2	0	0		
ENSMUST00000143443						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143444						1	0	0	0	13	0	0	0	0	0	2		
ENSMUST00000143445						3	3	3	77	6	0	86	356	379	16	115		
ENSMUST00000143446						6	2	29	9	11	6	8	0	0	0	12		
ENSMUST00000143447						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000143449	ENSMUSG00000021470	13	63815240	63900302	1	0	0	0	0	0	0	0	0	7	0	6	A0A0A0MQM1	
ENSMUST00000143450						1	1	3	0	3	0	0	0	0	0	1		
ENSMUST00000143451						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143452						1	0	8	3	3	3	0	0	0	0	0		
ENSMUST00000143455	ENSMUSG00000029591	5	114130386	114139323	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDS8	
ENSMUST00000143456						7	11	2	9	12	7	0	7	2	2	2		
ENSMUST00000143457						0	5	0	0	0	6	78	445	238	31	277		
ENSMUST00000143459						3	0	2	1	0	0	0	0	0	0	11		
ENSMUST00000143460						3	0	6	58	8	0	0	0	0	0	0		
ENSMUST00000143462						0	0	1	2	2	5	0	0	0	0	0		
ENSMUST00000143463	ENSMUSG00000004707	1	171588624	171607410	-1	0	5	4	5	4	0	16	84	45	24	62	M0QWN5	
ENSMUST00000143464						0	2	5	0	2	0	0	0	0	0	0		
ENSMUST00000143465						0	0	0	11	0	0	8	90	0	0	36		
ENSMUST00000143466						3	6	28	16	18	13	8	19	19	3	9		
ENSMUST00000143467	ENSMUSG00000016495	19	29348599	29367390	-1	2	0	0	0	0	0	43	104	66	412	81		Q9D3P8
ENSMUST00000143468						2	1	1	0	1	1	0	35	10	11	20		
ENSMUST00000143470						0	0	55	15	16	0	12	45	9	0	17		
ENSMUST00000143471						3	1	0	0	2	0	5	13	3	4	0		
ENSMUST00000143472	ENSMUSG00000021893	14	31336638	31371986	1	14	14	0	14	0	13	97	599	167	63	215	F2Z3X0	
ENSMUST00000143474						0	0	2	31	0	2	0	0	0	1	0		
ENSMUST00000143475						3	4	2	4	5	1	0	0	0	0	0		
ENSMUST00000143476						1	2	1	0	1	0	0	3	0	0	0		
ENSMUST00000143477						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000143478						3	6	21	8	9	9	11	12	6	0	17		
ENSMUST00000143480						4	3	13	7	10	1	0	0	0	1	0		
ENSMUST00000143481						6	0	4	0	1	0	4	117	6	17	7		
ENSMUST00000143482						4	3	3	2	0	2	12	13	9	2	15		
ENSMUST00000143483						0	0	2	1	4	1	0	0	0	0	0		
ENSMUST00000143484	ENSMUSG00000033256	2	122348892	122369162	-1	0	0	0	0	0	0	0	0	0	1	0	F6WJR3	
ENSMUST00000143485	ENSMUSG00000015745	3	95988429	95996001	-1	0	0	0	0	0	0	0	4	6	4	0	D3YVD1	
ENSMUST00000143486	ENSMUSG00000026708	1	161070713	161086724	1	0	0	8	6	0	0	0	0	0	0	0	M0QWX6	
ENSMUST00000143487						11	8	49	12	25	6	9	33	31	0	26		
ENSMUST00000143489						2	0	0	0	0	0	4	106	13	9	0		
ENSMUST00000143490	ENSMUSG00000078896	2	175469985	175482171	1	0	0	0	0	0	0	0	0	0	0	0	L7N468	
ENSMUST00000143491						4	5	2	3	6	5	0	0	0	0	0		
ENSMUST00000143492						0	0	0	2	0	0	2	3	8	0	0		
ENSMUST00000143493						15	9	14	7	12	0	0	0	9	0	0		
ENSMUST00000143494	ENSMUSG00000028637	4	119322893	119415521	-1	0	0	0	0	0	0	0	0	0	0	0	A8WHU2	
ENSMUST00000143495	ENSMUSG00000029713	5	137528127	137533510	-1	0	0	0	0	0	0	486	1122	139	0	0	E9PWM7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143496						17	13	23	50	9	5	7	5	0	0	6		
ENSMUST00000143497						2	0	13	2	1	3	0	0	0	0	0		
ENSMUST00000143498	ENSMUSG00000038712	3	95281345	95296166	1	0	2	2	0	0	0	33	74	49	0	41	A0A0G2JDK1	
ENSMUST00000143499	ENSMUSG00000004056	7	27591552	27640826	1	2	0	0	0	1	0	3	0	2	0	4	D3Z5X2	
ENSMUST00000143501						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143502						0	2	24	21	7	7	6	11	7	1	9		
ENSMUST00000143503						1	3	0	18	2	3	40	331	54	0	19		
ENSMUST00000143504	ENSMUSG00000031851	8	125729963	125748235	1	2	0	0	2	0	1	0	15	7	0	9	D3Z2W9	
ENSMUST00000143505						4	1	5	1	4	1	0	0	0	0	0		
ENSMUST00000143506	ENSMUSG00000041607	18	82475146	82585637	1	0	0	0	0	0	0	0	1	0	0	3		P04370
ENSMUST00000143507						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000143508	ENSMUSG00000078681	7	65691169	65701913	1	0	0	0	0	0	0	3	0	0	0	3	D3Z3H7	
ENSMUST00000143509						0	0	0	0	4	9	42	150	79	0	136		
ENSMUST00000143510						3	0	8	0	5	0	132	314	208	62	198		
ENSMUST00000143511						0	0	7	2	0	0	0	0	0	0	2		
ENSMUST00000143512	ENSMUSG00000000244	7	143005046	143019644	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0S2	
ENSMUST00000143513						2	0	10	6	0	0	10	14	43	0	15		
ENSMUST00000143514	ENSMUSG00000074513	3	84496093	84582625	-1	0	1	7	105	8	0	149	326	514	371	317	G5E8V9	
ENSMUST00000143515						0	0	0	0	0	0	0	8	0	0	0		
ENSMUST00000143516						8	6	7	7	6	1	6	14	21	0	13		
ENSMUST00000143517	ENSMUSG00000035027	10	81105915	81124697	1	27	4	32	51	24	10	201	420	190	56	190		Q63932
ENSMUST00000143518	ENSMUSG00000038080	13	47043499	47084613	1	0	0	0	0	2	3	6	23	0	0	0	F6V3V2	
ENSMUST00000143519						3	0	2	4	17	9	2	2	2	0	9		
ENSMUST00000143520						2	3	5	0	3	0	0	1	1	0	0		
ENSMUST00000143521	ENSMUSG00000031400	X	74409483	74429194	-1	0	0	0	0	0	0	2259	119	2919	72	1398	A3KG36	
ENSMUST00000143522	ENSMUSG00000079344	19	33498037	33517780	-1	4	10	1	0	9	2	0	0	0	0	0	F6RR30	
ENSMUST00000143523						180	165	773	179	120	65	0	7	4	1	8		
ENSMUST00000143524						1	0	3	3	1	0	83	35	46	0	61		
ENSMUST00000143526						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000143528						3	0	0	2	0	8	22	1	24	9	24		
ENSMUST00000143529						10	8	66	24	10	4	0	9	1	0	1		
ENSMUST00000143531	ENSMUSG00000029669	6	21771395	21852515	-1	0	0	5	34	0	1	0	0	0	0	0		
ENSMUST00000143532						0	1	7	7	2	1	0	0	0	0	1		
ENSMUST00000143533	ENSMUSG00000028483	4	83417724	83467676	1	4	0	2	6	6	3	24	177	55	21	35		Q9D2C9
ENSMUST00000143534						23	26	49	22	16	12	8	22	17	9	32		
ENSMUST00000143535						0	0	0	0	1	0	1	0	0	0	0		
ENSMUST00000143536						2	5	1	7	1	0	3	83	25	2	51		
ENSMUST00000143537	ENSMUSG00000005982	16	3872375	3904780	1	0	2	0	0	0	0	60	47	63	0	28	H3BJZ6	
ENSMUST00000143538						2	3	0	1	3	3	3	8	1	2	0		
ENSMUST00000143539	ENSMUSG00000021998	14	75131101	75230842	1	1	0	1	8	1	0	9	19	34	0	46	D3YZ25	
ENSMUST00000143540	ENSMUSG00000020143	11	34226815	34783892	-1	4	10	14	27	15	3	0	4	0	7	0	D6RGU3	
ENSMUST00000143541	ENSMUSG00000030990	7	102210208	102238567	1	0	1	0	0	0	0	12	0	0	0	0	D3Z4K4	
ENSMUST00000143542	ENSMUSG00000028533	4	92144329	92147234	-1	0	1	5	1	2	0	0	0	0	0	0	F6T8K1	
ENSMUST00000143543						2	0	0	21	0	0	0	8	0	0	11		
ENSMUST00000143544						1	0	0	1	0	1	1	0	9	19	0		
ENSMUST00000143545						5	2	0	0	4	2	0	21	0	11	12		
ENSMUST00000143546						1	0	1	4	0	0	0	0	0	0	0		
ENSMUST00000143547	ENSMUSG00000027405	2	130274430	130279313	1	2	1	0	0	1	2	0	4	0	0	10	F6TLG3	
ENSMUST00000143548						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143549	ENSMUSG00000041119	17	31386234	31476310	1	0	5	0	0	4	0	0	0	0	4	0	D6REE8	
ENSMUST00000143551						6	9	2	25	8	1	0	6	6	1	6		
ENSMUST00000143552						0	1	6	19	2	2	0	0	0	1	0		
ENSMUST00000143553						6	0	4	1	2	2	0	0	0	0	0		
ENSMUST00000143554						4	2	1	3	3	3	0	1	10	0	62		
ENSMUST00000143556						1	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000143557	ENSMUSG00000037475	X	41794991	41920674	-1	1	0	0	0	0	0	0	14	20	2	0	F6VK25	
ENSMUST00000143558						0	3	1	5	2	1	0	0	0	0	0		
ENSMUST00000143560	ENSMUSG00000064267	5	122206804	122242297	1	4	5	13	36	7	0	2	0	0	0	0	D3Z019	
ENSMUST00000143561	ENSMUSG00000025512	7	141493136	141539857	-1	0	2	3	4	4	2	66	105	51	23	42	D3YWG2	
ENSMUST00000143562	ENSMUSG00000036817	5	139200637	139249840	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5Q2	
ENSMUST00000143563	ENSMUSG00000071226	6	120666369	120771190	1	2	14	42	0	7	3	0	0	0	1	4	F7B218	
ENSMUST00000143565						0	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000143566						2	5	22	0	9	2	15	15	27	7	22		
ENSMUST00000143567	ENSMUSG00000026463	1	133699457	133801041	-1	177	181	493	1084	245	113	49	89	57	9	70	Q6Q477	
ENSMUST00000143570						1	11	7	0	19	0	0	3025	870	2247	659		
ENSMUST00000143571	ENSMUSG00000038366	11	97799000	97838764	1	2	2	4	53	1	0	0	0	0	0	0	A2A6G0	
ENSMUST00000143573	ENSMUSG00000027429	2	144556229	144590749	1	1	0	0	11	2	2	25	20	63	0	41	A2ANA0	
ENSMUST00000143575						28	16	213	43	44	16	77	93	67	45	66		
ENSMUST00000143576						11	1	0	5	0	0	15	0	9	0	24		
ENSMUST00000143577	ENSMUSG00000040690	4	130047840	130099283	1	0	0	0	0	0	0	2	0	0	9	20	A3KFV7	
ENSMUST00000143578	ENSMUSG00000020617	11	109787651	109828046	-1	3	2	0	5	2	2	0	0	0	0	1	A2AGP8	
ENSMUST00000143579						4	2	15	8	5	1	24	20	71	5	65		
ENSMUST00000143580						0	0	0	0	1	0	0	0	37	12	64		
ENSMUST00000143581	ENSMUSG00000031023	7	109703690	109712189	1	2	4	4	198	8	0	0	0	0	0	0	D3YXP0	
ENSMUST00000143582	ENSMUSG00000019817	10	13060504	13131694	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143583						4	1	6	41	5	2	0	0	0	0	0		
ENSMUST00000143584						10	3	2	5	13	6	3	46	16	2	12		
ENSMUST00000143586						0	0	6	0	1	0	0	0	0	0	0		
ENSMUST00000143587						4	3	32	1	1	4	0	79	5	4	25		
ENSMUST00000143588						24	23	52	20	28	12	0	0	1	1	2		
ENSMUST00000143589						0	2	0	41	3	3	0	0	0	0	0		
ENSMUST00000143590	ENSMUSG00000043671	7	35685165	35754454	-1	0	1	0	0	0	2	3	3	12	0	1	F6WY75	
ENSMUST00000143592						0	0	16	0	0	0	0	0	0	0	0		
ENSMUST00000143594	ENSMUSG00000020070	10	62980223	63017210	1	12	8	15	0	15	0	5	53	20	3	28	Q8BR30	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143596						3	2	6	0	8	0	0	2	0	9	2		
ENSMUST00000143597						13	6	38	10	19	5	2	14	7	2	8		
ENSMUST00000143598						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000143599						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000143600	ENSMUSG00000021963	14	57798180	57804980	1	0	0	0	29	4	0	89	436	170	96	0	D3Z2N9	
ENSMUST00000143601	ENSMUSG00000028613	4	107802261	107876840	1	0	0	0	0	0	0	0	0	0	0	0		Q924X6
ENSMUST00000143602						0	0	0	0	0	0	1	0	0	0	3		
ENSMUST00000143603						76	74	204	63	62	27	14	29	33	0	40		
ENSMUST00000143604						10	18	75	24	21	10	7	14	17	0	23		
ENSMUST00000143606						9	9	17	9	9	6	2	0	0	1	9		
ENSMUST00000143607						0	0	0	0	0	0	0	14	0	0	0		
ENSMUST00000143608						5	1	0	0	4	1	0	7	0	8	1		
ENSMUST00000143609	ENSMUSG00000021830	14	45134448	45220328	-1	0	1	0	0	0	0	0	2	0	0	0	D3Z7P6	
ENSMUST00000143610	ENSMUSG00000041688	X	145446425	145505181	-1	0	4	4	21	6	4	0	0	1	0	2	B1AXE9	
ENSMUST00000143611	ENSMUSG00000033377	3	116918258	116968987	-1	0	0	0	0	0	0	0	0	1	2	0	D3Z486	
ENSMUST00000143612						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000143613						0	0	2	0	1	0	4	6	10	1	30		
ENSMUST00000143614	ENSMUSG00000040964	4	140514485	140666012	-1	2	2	13	13	8	2	0	0	0	0	0	A2AWP7	
ENSMUST00000143615						6	17	4	3	8	7	7	0	13	0	21		
ENSMUST00000143616	ENSMUSG00000026798	2	29787493	29797935	1	106	64	116	77	83	25	4	39	15	6	40	D6RJJ8	
ENSMUST00000143617						0	0	0	0	0	0	8	8	0	2	0		
ENSMUST00000143620	ENSMUSG00000075610	11	94777217	94782703	-1	0	0	0	0	0	0	3	14	8	0	2	H9KV20	
ENSMUST00000143621	ENSMUSG00000034245	6	91156665	91174692	1	0	1	0	0	0	2	0	0	1	0	0	D3Z2G7	
ENSMUST00000143623	ENSMUSG00000026649	1	171113918	171126967	1	3	0	0	2	8	4	10	14	0	0	0	M0QW89	
ENSMUST00000143624	ENSMUSG00000020051	10	87521795	87584136	1	0	1	0	0	0	0	0	0	0	0	0	F6YTR5	
ENSMUST00000143625	ENSMUSG00000026811	2	32599709	32620806	1	0	1	1	10	13	1	0	1	1	0	0	A0A0A6YW84	
ENSMUST00000143626						7	8	36	8	10	4	0	0	0	0	0		
ENSMUST00000143627						3	2	0	0	5	2	2	3	0	0	0		
ENSMUST00000143628						3	1	0	34	0	1	0	2	5	0	2		
ENSMUST00000143629						4	36	36	0	35	7	0	0	0	0	0		
ENSMUST00000143630	ENSMUSG00000047767	7	101289392	101302251	-1	8	2	0	3	0	0	36	108	40	0	76		Q6KAU8
ENSMUST00000143631						2	5	3	13	6	0	199	470	410	48	300		
ENSMUST00000143632	ENSMUSG00000028796	4	128654702	128752881	1	0	15	0	5	0	1	53	141	37	0	80	D6REH8	
ENSMUST00000143633	ENSMUSG00000025504	7	141338880	141363020	1	0	0	2	2	0	2	0	0	0	0	0	D3YWI5	
ENSMUST00000143634						1	3	6	0	1	3	0	2	2	0	0		
ENSMUST00000143635						1	3	1	0	1	3	0	0	0	0	2		
ENSMUST00000143636	ENSMUSG00000026110	1	37439340	37541016	-1	2	0	2	0	0	2	0	9	0	13	7	D3Z166	
ENSMUST00000143637	ENSMUSG00000042766	3	89234177	89246309	-1	0	6	50	63	24	5	0	0	13	0	3	E9PUI3	
ENSMUST00000143639	ENSMUSG00000066613	5	109996521	110010411	1	0	0	0	0	0	0	0	0	12	3	2	K7N6R7	
ENSMUST00000143640						170	143	623	196	248	87	1	4	2	0	3		
ENSMUST00000143641	ENSMUSG00000068270	X	6399854	6637448	1	0	0	0	0	4	2	1	0	0	0	1	E9PUX3	
ENSMUST00000143642						2	1	5	10	0	0	0	0	0	0	3		
ENSMUST00000143644	ENSMUSG00000028519	4	103619359	104744844	1	0	0	0	92	6	0	0	0	0	0	0	A0A0A0MQI4	
ENSMUST00000143646						1	3	4	1	1	1	0	0	0	0	0		
ENSMUST00000143647						1	0	0	0	0	1	0	0	0	8	0		
ENSMUST00000143648						3	0	0	1	1	3	2	6	0	1	3		
ENSMUST00000143650	ENSMUSG00000035992	11	54438199	54518235	1	8	5	7	5	3	2	6	2	0	0	17	F6RJ64	
ENSMUST00000143653						2	7	17	7	7	4	0	0	0	1	0		
ENSMUST00000143654						0	0	0	0	0	0	17	26	18	38	17		
ENSMUST00000143656						2	3	0	10	2	2	0	4	11	13	0		
ENSMUST00000143657						0	0	0	0	0	3	0	0	0	5	0		
ENSMUST00000143659						0	1	1	237	3	0	0	0	0	0	0		
ENSMUST00000143660						17	12	15	21	11	9	2	18	0	0	2		
ENSMUST00000143661	ENSMUSG00000037887	7	142079490	142095843	-1	1	0	7	9	4	0	0	0	0	0	0	B7ZC52	
ENSMUST00000143662	ENSMUSG00000043243	8	71597648	71607936	1	0	0	11	14	9	8	0	19	0	2	7	D3YZB0	
ENSMUST00000143663	ENSMUSG00000074627	2	157208550	157279549	-1	15	14	18	23	22	15	0	1	0	0	0	E9PYI4	
ENSMUST00000143664	ENSMUSG00000030359	6	128483567	128526720	-1	0	0	0	0	0	0	0	0	0	0	0	D3YUI3	
ENSMUST00000143665						0	0	1	2	0	3	0	0	0	0	0		
ENSMUST00000143666						1	4	3	106	3	2	0	0	0	0	0		
ENSMUST00000143667						0	0	0	0	0	0	0	8	2	0	1		
ENSMUST00000143668						0	0	0	0	1	0	0	0	14	0	0		
ENSMUST00000143670						8	6	8	26	6	2	3	0	4	2	0		
ENSMUST00000143672	ENSMUSG00000039176	7	79446231	79466362	-1	0	0	0	0	0	0	30	13	16	0	7	F7BP45	
ENSMUST00000143674	ENSMUSG00000026239	1	86542994	86582629	-1	0	0	17	38	0	0	0	6	6	0	5	M0QWR1	
ENSMUST00000143675						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143676						5	0	23	40	5	0	0	0	0	0	0		
ENSMUST00000143677						0	3	15	24	9	6	0	0	0	0	0		
ENSMUST00000143678						0	0	5	0	0	0	0	0	0	0	22		
ENSMUST00000143679						6	2	0	3	10	1	0	0	0	0	0		
ENSMUST00000143680						31	17	82	66	32	13	33	358	130	9	196		
ENSMUST00000143681	ENSMUSG00000031353	X	162760402	162779092	1	1	1	0	0	2	0	0	2	0	0	0	F6U539	
ENSMUST00000143682	ENSMUSG00000052384	16	32142785	32165594	-1	106	1	187	139	109	1	1	5	5	0	5		Q8BMT4
ENSMUST00000143683						6	2	5	4	5	0	4	4	4	0	7		
ENSMUST00000143684						4	1	0	4	10	4	0	0	0	0	0		
ENSMUST00000143685						4	0	0	0	3	0	227	81	408	0	252		
ENSMUST00000143686						0	4	2	0	3	1	8	23	9	0	13		
ENSMUST00000143688						0	0	1	28	0	1	6	0	6	4	3		
ENSMUST00000143689						2	0	3	0	0	4	15	55	8	0	29		
ENSMUST00000143690	ENSMUSG00000017734	2	164486106	164493319	1	0	0	0	37	0	0	0	0	0	0	0	A2A5G0	
ENSMUST00000143691						7	8	3	237	16	2	0	0	0	1	0		
ENSMUST00000143692	ENSMUSG00000052889	7	122288751	122634402	1	15	15	46	159	18	15	148	499	358	49	223		P68404
ENSMUST00000143693	ENSMUSG00000057554	13	12439415	12464944	-1	0	0	0	0	0	0	62	416	2	223	112	Q8C6H0	
ENSMUST00000143694						2	4	7	7	6	5	0	17	4	0	5		
ENSMUST00000143696	ENSMUSG00000031389	X	73891442	73921870	-1	0	0	2	2	0	0	28	104	25	0	63	F6YWG4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143697	ENSMUSG00000022679	16	13903161	13949619	1	0	2	2	20	0	0	0	0	0	1	0	D3Z6M3	
ENSMUST00000143698						21	18	30	0	13	8	11	4	16	0	20		
ENSMUST00000143699						0	0	24	0	0	6	0	90	0	0	90		
ENSMUST00000143700	ENSMUSG00000027366	2	126890391	126933235	-1	0	0	0	2	1	1	95	438	184	79	58	F6RJQ8	
ENSMUST00000143701						1	7	0	0	0	0	0	0	0	0	0		
ENSMUST00000143702	ENSMUSG00000029826	6	38305286	38354603	-1	3	1	9	0	8	5	40	33	92	3	130		Q3UPF5
ENSMUST00000143703	ENSMUSG00000002265	7	6703892	6730421	-1	3	0	0	0	4	2	0	0	0	0	0	D6RGA4	
ENSMUST00000143704						5	4	0	63	11	8	0	0	0	0	0		
ENSMUST00000143707						17	4	16	31	14	13	0	0	0	0	0		
ENSMUST00000143708						2	4	6	7	4	2	3	23	0	0	4		
ENSMUST00000143709	ENSMUSG00000073684	4	155249802	155256687	1	0	0	0	0	0	0	75	45	35	0	10	F6QQ55	
ENSMUST00000143711						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143712						0	0	0	0	0	0	13	70	18	16	21		
ENSMUST00000143713	ENSMUSG00000051457	7	127132232	127137823	-1	7	8	22	9	6	4	40	63	53	2	53	Q544C5	P15702
ENSMUST00000143714						53	61	253	71	64	39	21	34	42	2	55		
ENSMUST00000143716	ENSMUSG00000021595	13	69533746	69635780	1	0	0	0	33	0	2	0	0	0	0	0	H3BJF3	
ENSMUST00000143718						0	0	0	1	3	0	0	10	0	2	11		
ENSMUST00000143720	ENSMUSG00000018428	11	88830792	88864586	-1	13	8	6	9	22	6	23	28	0	0	0		O08715
ENSMUST00000143721	ENSMUSG00000028019	3	81036416	81214040	1	23	17	31	185	38	22	0	1	0	0	0	D6RGS6	
ENSMUST00000143722						3	1	9	3	1	0	4	14	0	0	0		
ENSMUST00000143723						4	2	9	0	2	0	30	18	20	3	37		
ENSMUST00000143724						12	19	3	27	22	13	8	0	19	0	18		
ENSMUST00000143725						0	0	0	0	0	0	3	0	2	0	1		
ENSMUST00000143726						3	1	3	4	3	0	2	4	7	1	10		
ENSMUST00000143727						2	0	4	5	3	3	0	1	2	0	2		
ENSMUST00000143728	ENSMUSG00000036737	9	119238432	119322427	-1	0	0	0	0	0	0	5	0	0	0	0	F7AVI9	
ENSMUST00000143729						309	424	1035	247	253	130	0	7	4	0	9		
ENSMUST00000143730	ENSMUSG00000033021	1	75435930	75443179	1	0	0	0	0	0	0	9	9	8	0	0	D3YVK2	
ENSMUST00000143731						0	0	0	35	0	0	1	3	0	2	1		
ENSMUST00000143733						0	3	0	1	6	0	63	247	142	144	48		
ENSMUST00000143734						1	1	5	1	2	0	0	10	7	0	24		
ENSMUST00000143735	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	2	0	1	0	0	0	0	0	E9Q441	
ENSMUST00000143736						3	3	3	0	5	1	26	382	27	57	98		
ENSMUST00000143737						0	0	0	2	2	3	13	81	11	20	14		
ENSMUST00000143739	ENSMUSG00000020622	12	10369973	10390173	1	5	2	61	7	5	3	0	0	0	0	0	D3Z145	
ENSMUST00000143740						1	1	3	0	0	0	0	0	0	3	0		
ENSMUST00000143741	ENSMUSG00000001670	8	109990437	109999803	1	0	1	0	0	2	0	0	0	0	0	0	D3Z307	
ENSMUST00000143742	ENSMUSG00000028573	4	95557507	95926939	1	0	0	2	0	1	0	0	0	0	0	0	F7ANG8	
ENSMUST00000143743	ENSMUSG00000009566	2	32682609	32704145	-1	2	0	3	0	0	2	0	0	1	0	1	A0A0A6YWU6	
ENSMUST00000143744						2	0	2	3	2	3	27	24	42	0	52		
ENSMUST00000143745						1	3	2	4	0	2	1	4	0	0	0		
ENSMUST00000143746	ENSMUSG00000041961	11	5276324	5444847	-1	1	2	0	15	5	5	0	0	0	0	0	F7D553	
ENSMUST00000143747						2	0	7	6	0	2	225	294	185	59	174		
ENSMUST00000143749						19	14	44	26	13	9	10	37	11	9	7		
ENSMUST00000143750	ENSMUSG00000108605	11	73925002	73928945	1	3	5	5	3	7	0	0	0	0	0	0		
ENSMUST00000143751						3	1	1	0	2	0	4	28	2	2	19		
ENSMUST00000143752	ENSMUSG00000029802	6	58584523	58695676	1	2	3	3	0	3	0	0	0	0	0	0	S4R2E1	
ENSMUST00000143753						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000143756	ENSMUSG00000038544	4	59769637	59801589	-1	0	0	0	6	0	0	0	0	0	4	0	Z4YLT1	
ENSMUST00000143757						4	0	4	3	4	1	0	0	0	0	0		
ENSMUST00000143758	ENSMUSG00000005107	5	38349273	38503143	-1	0	0	0	0	0	0	0	0	17	0	1	Q7TSK9	
ENSMUST00000143759						0	0	0	0	1	0	0	0	0	0	7		
ENSMUST00000143762	ENSMUSG00000040599	11	71019611	71027371	1	0	0	2	0	0	0	0	0	0	0	3		
ENSMUST00000143763						0	0	2	2	1	0	7	0	0	0	0		
ENSMUST00000143764	ENSMUSG00000075249	2	82943634	83008937	1	43	28	72	35	41	13	0	0	0	0	0		A2ARZ3
ENSMUST00000143766						0	0	0	72	0	0	0	0	0	0	0		
ENSMUST00000143768						42	37	99	33	36	19	3	10	9	1	13		
ENSMUST00000143769						2	3	4	5	0	2	0	6	6	9	10		
ENSMUST00000143770						1	3	0	0	0	3	0	23	20	0	12		
ENSMUST00000143771	ENSMUSG00000036257	12	44221370	44312343	1	0	4	0	1	2	0	233	33	16	35	0	E9QAC9	
ENSMUST00000143772	ENSMUSG00000040963	11	70092644	70106187	1	0	0	6	0	0	0	0	0	0	0	0	J3QMY0	
ENSMUST00000143773						0	0	0	0	0	0	0	15	2	0	0		
ENSMUST00000143774						0	2	1	0	1	0	0	0	0	1	3		
ENSMUST00000143775						0	3	0	0	1	0	0	17	3	0	3		
ENSMUST00000143776	ENSMUSG00000038718	2	34171457	34373142	-1	0	0	0	27	0	0	0	0	0	2	0	D6RCU6	
ENSMUST00000143777						6	2	6	113	9	2	0	0	0	0	0		
ENSMUST00000143778						7	4	11	13	5	3	0	0	0	0	0		
ENSMUST00000143780	ENSMUSG00000017760	2	164832873	164841032	1	0	0	0	0	0	0	597	662	781	129	699	A2A5J9	
ENSMUST00000143782						0	0	0	18	1	1	2	4	0	4	4		
ENSMUST00000143783	ENSMUSG00000000247	2	38339281	38369733	1	0	1	5	183	10	2	0	0	0	0	0	F6Z9H5	
ENSMUST00000143784						2	0	0	0	0	3	18	0	0	42	39		
ENSMUST00000143785	ENSMUSG00000031834	8	70768176	70776713	-1	0	0	2	21	1	0	0	33	0	0	0	F7CB91	
ENSMUST00000143786	ENSMUSG00000005686	7	110768206	110812405	1	0	1	10	3	5	1	50	40	92	5	92	F6XQD0	
ENSMUST00000143788						3	1	9	4	2	2	0	0	0	0	0		
ENSMUST00000143789	ENSMUSG00000079444	17	47686739	47694455	-1	13	13	61	74	16	12	0	3	0	2	1	D3Z6Q6	
ENSMUST00000143790						0	0	0	0	3	0	1	0	0	0	0		
ENSMUST00000143791	ENSMUSG00000014329	10	70922832	71159700	-1	9	11	11	22	14	16	0	1	0	6	23		Q99MQ1
ENSMUST00000143792	ENSMUSG00000006345	10	75561604	75586200	1	0	0	0	0	0	0	0	0	0	0	17	D3YVY4	
ENSMUST00000143793						8	4	1	0	0	3	0	0	0	0	0		
ENSMUST00000143794						47	22	87	62	38	31	1	0	0	0	18		
ENSMUST00000143795						0	0	0	134	4	2	0	0	0	0	0		
ENSMUST00000143797						0	1	1	3	3	2	0	0	0	0	0		
ENSMUST00000143798						0	0	1	3	3	0	18	56	17	6	17		
ENSMUST00000143799						0	0	0	2	3	0	126	296	224	220	145		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143800						0	0	2	1	1	0	0	0	0	0	0		
ENSMUST00000143802						5	4	6	7	10	2	2	5	1	1	5		
ENSMUST00000143803						9	5	9	2	9	4	3	9	0	2	11		
ENSMUST00000143804						2	1	0	0	3	0	3	4	7	13	9		
ENSMUST00000143805						0	0	18	14	0	0	15	24	0	0	11		
ENSMUST00000143806						57	44	101	69	63	17	130	353	293	50	360		
ENSMUST00000143807						2	4	4	1	0	2	14	246	43	13	49		
ENSMUST00000143808						2	0	4	3	4	0	7	20	10	2	29		
ENSMUST00000143809						0	4	6	20	4	1	0	2	0	3	8		
ENSMUST00000143810						5	1	3	2	4	1	2	4	0	0	3		
ENSMUST00000143813	ENSMUSG00000043644	11	120348678	120351190	1	1	4	11	21	5	2	19	43	12	4	9	F6YD18	
ENSMUST00000143814	ENSMUSG00000030034	6	83121765	83125431	-1	0	4	5	97	4	0	0	0	0	1	0	D6RES5	
ENSMUST00000143815						1	4	6	3	5	1	0	0	0	0	0		
ENSMUST00000143816						150	85	830	184	68	31	8	15	15	4	19		
ENSMUST00000143817	ENSMUSG00000039850	11	119491347	119511437	1	0	0	0	0	0	0	40	20	23	2	18	E9PXN2	
ENSMUST00000143818						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143820	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0	D3Z203	
ENSMUST00000143822	ENSMUSG00000049396	11	76210571	76217664	-1	0	2	1	10	3	1	0	0	0	1	1	E9Q6V6	
ENSMUST00000143823	ENSMUSG00000038127	16	27388869	27452218	1	0	1	5	0	2	0	0	3	0	21	21	F6UK66	
ENSMUST00000143824						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143825	ENSMUSG00000063838	7	4151260	4164860	-1	4	0	6	14	3	4	0	2	0	3	0	D3Z5F0	
ENSMUST00000143826						6	11	29	8	8	3	12	3	10	2	8		
ENSMUST00000143827	ENSMUSG00000044005	10	128194457	128210004	1	0	0	0	0	29	0	0	0	0	0	0	D6RI88	
ENSMUST00000143829	ENSMUSG00000036087	5	72914304	72978829	1	10	13	12	0	10	3	452	919	323	53	115		Q8CI08
ENSMUST00000143830						15	11	57	29	19	11	0	0	0	0	0		
ENSMUST00000143831						3	3	0	33	1	0	17	25	0	0	8		
ENSMUST00000143832	ENSMUSG00000062345	1	107511423	107535478	1	0	0	0	0	0	2	3	1	2	1	0	F6ZFV0	
ENSMUST00000143833	ENSMUSG00000008129	8	84148025	84172590	1	0	0	6	4	2	0	0	0	0	0	0	D3YVH8	
ENSMUST00000143834						2	4	8	5	3	4	16	49	37	2	36		
ENSMUST00000143835	ENSMUSG00000030649	7	101881325	101901845	1	0	0	6	1	1	1	13	31	18	14	7	E9Q0Y1	
ENSMUST00000143837						46	37	58	41	67	18	1	10	0	2	17		
ENSMUST00000143839						0	3	7	4	7	0	2	0	0	0	3		
ENSMUST00000143840	ENSMUSG00000029063	4	155562378	155591001	1	0	0	0	11	0	2	0	3	3	0	0	A2A9N8	
ENSMUST00000143841	ENSMUSG00000025766	3	41742611	41803320	1	5	5	0	0	0	0	0	0	0	0	0	D6RH74	
ENSMUST00000143842	ENSMUSG00000034621	11	102475915	102556392	-1	19	12	66	65	23	19	219	879	646	69	378		A2A6A1
ENSMUST00000143843	ENSMUSG00000025268	X	150806370	150814345	-1	0	4	0	1	5	0	0	0	0	2	0	A2AG46	
ENSMUST00000143844	ENSMUSG00000025142	11	120672973	120709447	1	0	0	2	5	1	2	6	17	0	0	7	E9PWZ4	
ENSMUST00000143846						0	0	3	1	2	0	3	0	1	0	0		
ENSMUST00000143848						0	0	0	2	0	0	11	13	0	0	19		
ENSMUST00000143849						1	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000143850	ENSMUSG00000018442	11	71007164	71019841	-1	8	11	12	7	12	0	107	406	134	15	139		Q8BNI4
ENSMUST00000143851						6	2	25	7	9	4	0	0	0	0	0		
ENSMUST00000143852	ENSMUSG00000048277	11	117809668	117814283	1	0	0	3	1	3	0	6	8	4	0	13	H3BKU5	
ENSMUST00000143853	ENSMUSG00000045636	8	40990914	41133726	-1	0	1	0	0	1	0	10	25	22	15	12	F6Q593	
ENSMUST00000143854						3	0	4	14	0	1	8	53	34	3	27		
ENSMUST00000143855						3	1	5	1	2	0	0	6	2	0	12		
ENSMUST00000143856						3	1	6	46	9	2	2	4	4	0	1		
ENSMUST00000143858						1	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000143861						0	1	7	0	0	0	15	9	15	3	6		
ENSMUST00000143862						0	0	0	0	0	0	1	2	4	0	5		
ENSMUST00000143863						4	2	2	5	7	0	0	0	0	0	0		
ENSMUST00000143864						0	0	0	0	0	0	0	0	1	4	0		
ENSMUST00000143865	ENSMUSG00000025340	5	130171798	130214342	1	0	0	5	0	2	0	0	0	0	2	0	F6VIJ0	
ENSMUST00000143866						5	7	8	111	14	3	0	0	0	0	5		
ENSMUST00000143867	ENSMUSG00000029175	5	30647933	30659729	1	0	0	0	0	0	0	154	0	23	20	60	D6RFU7	
ENSMUST00000143868	ENSMUSG00000038080	13	47043499	47084613	1	5	0	8	15	9	0	0	0	0	1	0	D3Z353	
ENSMUST00000143871						94	0	46	109	75	42	3	0	11	3	0		
ENSMUST00000143872						0	0	0	0	4	0	0	0	0	3	0		
ENSMUST00000143873						57	46	251	355	71	48	26	95	39	4	80		
ENSMUST00000143874						0	0	0	81	0	8	0	0	0	0	0		
ENSMUST00000143875	ENSMUSG00000000766	10	6758506	7038198	1	0	2	4	4	1	2	0	0	0	0	0	Q4U2P9	
ENSMUST00000143876						2	0	0	0	0	0	0	9	0	0	0		
ENSMUST00000143878						24	9	59	20	22	8	26	111	35	10	55		
ENSMUST00000143879						0	0	0	0	2	0	0	38	0	0	0		
ENSMUST00000143880	ENSMUSG00000041649	X	153237466	153396132	1	0	0	0	5	3	1	0	0	0	0	0	A6PWN1	
ENSMUST00000143881						0	5	3	5	1	1	0	0	0	1	0		
ENSMUST00000143883						3	4	11	187	21	2	0	0	0	0	0		
ENSMUST00000143884						5	1	2	1	6	5	0	0	2	0	0		
ENSMUST00000143885	ENSMUSG00000065999	4	147553277	147585198	1	3	3	3	1	1	1	0	0	1	0	0	A2A7A3	
ENSMUST00000143886						10	3	21	44	8	3	0	1	1	0	4		
ENSMUST00000143887						1	1	10	3	7	2	0	0	0	0	0		
ENSMUST00000143889						2	4	0	19	1	0	5	2	0	0	4		
ENSMUST00000143890						2	0	0	0	2	1	0	11	2	0	6		
ENSMUST00000143891	ENSMUSG00000019803	10	42561963	42583632	-1	4	2	3	0	3	4	0	0	0	0	0	D3YZ24	
ENSMUST00000143892						3	4	15	1	1	0	0	0	0	0	0		
ENSMUST00000143894	ENSMUSG00000062044	7	45783738	45804144	1	0	0	2	0	0	2	0	0	0	0	0	F6S534	
ENSMUST00000143895						1	2	0	1	7	0	1	2	0	0	0		
ENSMUST00000143896						4	3	0	1	0	0	0	0	0	0	0		
ENSMUST00000143897						2	1	5	1	1	3	0	0	0	1	0		
ENSMUST00000143899						2	0	0	16	0	6	82	252	74	47	101		
ENSMUST00000143900	ENSMUSG00000031730	8	109591343	109608673	-1	1	2	0	26	0	0	0	0	0	0	3	E9Q1V3	
ENSMUST00000143901						2	2	21	9	3	4	6	23	5	0	14		
ENSMUST00000143902						7	5	67	12	11	4	0	5	1	0	0		
ENSMUST00000143903						0	0	1	0	1	0	1	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143905						0	0	14	0	5	0	13	4	14	5	9		
ENSMUST00000143906						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000143907	ENSMUSG00000036026	17	45660171	45686905	-1	0	2	0	74	2	2	0	0	0	0	0	D3YXV7	
ENSMUST00000143908	ENSMUSG00000031314	X	101532734	101601789	1	0	0	0	5	0	4	41	0	153	0	185	S4R1B9	
ENSMUST00000143909						17	16	50	27	24	11	9	119	17	8	19		
ENSMUST00000143910	ENSMUSG00000025421	18	76930126	76972902	1	0	0	0	4	0	1	2	0	0	2	6	D3YZI3	
ENSMUST00000143911	ENSMUSG00000017950	2	163506808	163572910	1	2	1	12	25	3	0	0	0	0	0	0	A2A5I4	
ENSMUST00000143912						7	10	16	28	7	5	5	0	0	0	2		
ENSMUST00000143913	ENSMUSG00000039814	8	18932729	18950975	-1	6	0	0	0	0	0	5	0	10	2	3	D6RIN5	
ENSMUST00000143914	ENSMUSG00000064310	16	55225175	55297986	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BGZ8
ENSMUST00000143915	ENSMUSG00000020176	11	11930508	12038683	-1	0	0	0	13	1	1	0	0	0	0	1	B1ATS8	
ENSMUST00000143916	ENSMUSG00000032297	9	59577917	59607292	1	17	19	21	485	44	20	0	0	0	0	0	D6RHP1	
ENSMUST00000143917						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000143918						44	68	88	57	48	29	13	13	47	2	53		
ENSMUST00000143919						1	0	15	17	13	5	0	0	0	0	0		
ENSMUST00000143920	ENSMUSG00000020886	11	70017085	70045532	1	23	26	303	50	41	11	1	2	0	0	3	J3QMR8	
ENSMUST00000143921						2	0	7	47	3	3	0	0	0	2	4		
ENSMUST00000143922	ENSMUSG00000086056	1	166483613	166497588	-1	6	9	15	9	5	2	0	0	0	0	0	B2RWH8	
ENSMUST00000143923						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000143924	ENSMUSG00000014767	17	15499888	15528379	1	2	0	0	0	0	0	0	0	0	0	9	E9Q9Z7	
ENSMUST00000143925						0	0	0	1	1	4	3	1	0	1	10		
ENSMUST00000143926						1	0	0	0	2	0	2	38	13	0	25		
ENSMUST00000143927	ENSMUSG00000038205	3	97658193	97673812	1	2	0	0	119	0	0	4	0	0	0	0	D6RG50	
ENSMUST00000143928	ENSMUSG00000022415	15	80091334	80119501	1	5	4	1	3	2	3	0	0	0	2	0	D3YWY9	
ENSMUST00000143929						1	4	4	113	4	1	0	0	0	0	0		
ENSMUST00000143930						1	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000143931						9	4	18	147	12	0	1	0	0	0	0		
ENSMUST00000143932						0	0	1	0	2	2	5	0	0	0	0		
ENSMUST00000143933						0	1	0	1	2	0	0	0	0	0	0		
ENSMUST00000143934						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000143935						6	0	1	2	5	2	0	0	0	0	0		
ENSMUST00000143936	ENSMUSG00000038936	1	179668210	179687189	1	1	0	0	0	0	0	4	0	0	0	0	F6SP57	
ENSMUST00000143937	ENSMUSG00000021645	13	100124852	100137690	1	2	0	0	0	2	0	0	31	0	0	0	B8JJX7	
ENSMUST00000143938						9	6	26	60	13	10	0	0	0	0	0		
ENSMUST00000143939	ENSMUSG00000045983	16	20668313	20692884	1	5	12	5	4	6	0	0	818	0	102	1		
ENSMUST00000143940						3	2	4	1	2	0	0	0	0	0	0		
ENSMUST00000143941	ENSMUSG00000029686	6	47453398	47526139	1	1	0	0	1	0	1	4	3	0	0	1		
ENSMUST00000143942	ENSMUSG00000001604	4	136247729	136274898	1	2	5	5	71	2	4	0	0	0	0	0	A2AW45	
ENSMUST00000143943	ENSMUSG00000030209	6	135713233	136173511	-1	0	0	0	0	0	0	0	0	0	0	0	Q8CG69	
ENSMUST00000143944						4	2	6	4	4	0	4	5	21	0	26		
ENSMUST00000143946						1	3	0	11	2	2	1	3	0	0	2		
ENSMUST00000143947						0	0	0	0	0	0	0	3	4	2	0		
ENSMUST00000143948						2	4	18	8	6	2	4	14	4	3	19		
ENSMUST00000143950						1	0	3	0	6	2	1	2	1	1	0		
ENSMUST00000143951	ENSMUSG00000042308	7	127776670	127800122	1	0	2	0	15	0	0	0	0	0	0	2	D3YXL2	
ENSMUST00000143952						1	0	0	32	0	1	0	0	0	0	0		
ENSMUST00000143953						5	1	14	27	0	2	0	0	0	1	3		
ENSMUST00000143954						0	1	8	0	3	0	44	236	156	140	113		
ENSMUST00000143955	ENSMUSG00000037286	9	100597798	100959375	1	0	0	0	0	4	3	3	0	0	3	0	F6TNY1	
ENSMUST00000143957						0	6	2	8	6	7	0	0	0	0	0		
ENSMUST00000143958	ENSMUSG00000068457	Y	1096861	1245759	-1	9	4	1	11	8	5	0	1	39	0	19	D6RJL0	
ENSMUST00000143959						161	135	450	150	189	83	1	2	6	4	22		
ENSMUST00000143960	ENSMUSG00000021098	12	72881109	72940774	-1	0	0	0	0	0	0	0	0	0	0	0	F7BAS9	
ENSMUST00000143961	ENSMUSG00000068039	17	12915701	12925067	1	0	0	0	13	0	0	9	2	6	38	12	F2Z483	
ENSMUST00000143963						69	89	109	44	53	42	6	8	1	0	18		
ENSMUST00000143965						7	4	0	2	5	0	30	138	14	544	138		
ENSMUST00000143966						27	29	41	21	24	8	1	2	7	2	5		
ENSMUST00000143968						0	0	0	29	0	1	0	0	0	0	0		
ENSMUST00000143969						10	7	28	5	7	3	0	0	0	0	0		
ENSMUST00000143970	ENSMUSG00000026857	2	30807826	30823033	1	1	4	3	8	1	0	0	0	0	0	0	A0A0A6YX97	
ENSMUST00000143971	ENSMUSG00000050608	4	139101814	139131113	-1	15	14	20	33	23	8	172	472	143	526	145		Q7TNS2
ENSMUST00000143972						739	751	1305	546	776	377	20	83	40	17	72		
ENSMUST00000143973						0	1	1	0	1	0	1	0	0	0	0		
ENSMUST00000143974	ENSMUSG00000075256	2	79330543	79456785	-1	0	0	0	0	0	0	0	0	0	0	0	A2AQH1	
ENSMUST00000143975	ENSMUSG00000073007	X	107792590	107872909	1	0	0	0	2	1	0	0	0	0	0	0	B1ATX5	
ENSMUST00000143976	ENSMUSG00000070374	11	74283736	74289646	1	3	4	0	2	0	1	0	0	0	0	0	B1ARL2	
ENSMUST00000143977	ENSMUSG00000026933	2	25926838	25983282	-1	0	0	0	0	0	4	35	33	66	8	114	V9GXD7	
ENSMUST00000143978	ENSMUSG00000066030	4	144190719	144196934	1	0	3	0	0	0	0	0	0	0	0	0	A2A961	
ENSMUST00000143979						3	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000143980						121	146	105	22	97	25	23	69	22	8	69		
ENSMUST00000143981						1	0	3	1	8	0	0	0	0	0	0		
ENSMUST00000143982						5	2	11	3	11	4	0	0	0	0	0		
ENSMUST00000143983						2	3	0	0	1	0	0	4	1	0	0		
ENSMUST00000143984	ENSMUSG00000039201	X	8154472	8176181	-1	0	0	0	0	0	0	42	90	34	6	0	S4R2S6	
ENSMUST00000143985						0	1	3	3	2	0	3	6	10	0	9		
ENSMUST00000143986						5	6	24	6	12	2	0	1	2	0	0		
ENSMUST00000143987	ENSMUSG00000024099	17	66078795	66101559	-1	5	0	1	13	2	2	56	195	145	555	86		Q9D6J6
ENSMUST00000143988	ENSMUSG00000020282	11	32209585	32222300	-1	1	0	0	0	0	0	0	1	0	1	2	A7M7T5	
ENSMUST00000143989						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000143990	ENSMUSG00000041891	18	65980754	66022580	-1	2	0	2	1	10	3	0	0	0	0	0	D3Z5B9	
ENSMUST00000143991	ENSMUSG00000018171	11	86583865	86683836	-1	1	4	2	2	4	3	2	2	0	0	0	Q5SXR2	
ENSMUST00000143992						0	0	0	0	0	0	14	40	16	59	11		
ENSMUST00000143994	ENSMUSG00000073791	4	99829198	99912788	1	10	4	2	2	6	0	1	1	0	0	0	S4R277	
ENSMUST00000143996						6	4	5	6	12	8	0	5	1	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000143997	ENSMUSG00000016933	2	160731300	160775760	1	10	6	19	7	14	2	4	12	7	1	14	F6SLL0	
ENSMUST00000143998						15	12	89	45	11	8	24	48	9	0	23		
ENSMUST00000144000						0	0	2	10	0	0	42	57	14	0	25		
ENSMUST00000144001	ENSMUSG00000022537	16	30511855	30550842	-1	0	0	0	0	0	0	0	0	0	0	0	F6Q8S3	
ENSMUST00000144003						12	10	0	0	6	0	0	0	0	0	0		
ENSMUST00000144004						5	4	3	3	10	3	0	5	3	0	3		
ENSMUST00000144005						1	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000144007						2	0	2	2	7	3	1	0	0	0	0		
ENSMUST00000144008						2	3	0	1	1	0	0	0	0	0	0		
ENSMUST00000144009	ENSMUSG00000042323	14	31019138	31121592	1	0	2	1	1	0	0	0	0	0	0	7	D3YYG4	
ENSMUST00000144010						0	1	3	2	2	2	0	0	2	0	1		
ENSMUST00000144011	ENSMUSG00000026925	2	26396249	26409203	-1	2	0	0	0	2	2	0	0	7	0	0	F6XC48	
ENSMUST00000144012						13	4	12	8	7	4	14	0	8	0	9		
ENSMUST00000144013						0	0	0	0	0	0	1	1	0	3	11		
ENSMUST00000144014						2	2	1	5	6	7	0	0	2	0	3		
ENSMUST00000144015						37	22	183	43	37	13	2	2	0	0	2		
ENSMUST00000144016						12	2	11	9	16	4	0	0	0	0	0		
ENSMUST00000144019						2	0	1	3	2	1	0	0	0	0	0		
ENSMUST00000144021						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144022						1	3	7	6	9	2	0	3	0	0	4		
ENSMUST00000144025						4	0	3	4	1	0	0	28	6	0	18		
ENSMUST00000144027						0	0	2	0	0	1	0	2	0	1	3		
ENSMUST00000144028	ENSMUSG00000020834	11	78032280	78037866	1	0	0	3	0	0	5	97	129	89	8	41	D6RDR9	
ENSMUST00000144030	ENSMUSG00000035310	5	100441918	100500639	-1	3	4	0	4	0	0	0	67	0	0	30	D6RJL6	
ENSMUST00000144032	ENSMUSG00000034427	11	115858406	115892603	1	0	0	12	9	8	3	0	0	0	0	0	F6YB52	
ENSMUST00000144034	ENSMUSG00000058454	7	143823145	143848410	1	0	0	0	0	0	0	1	0	0	0	0	D3YXR4	
ENSMUST00000144035						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144037						4	6	10	17	8	3	20	106	42	49	61		
ENSMUST00000144040						0	0	0	7	0	3	0	0	0	1	0		
ENSMUST00000144041	ENSMUSG00000033763	8	110721476	110741400	1	14	8	51	330	30	8	0	0	0	0	5	D3YWC9	
ENSMUST00000144044						28	24	111	30	44	18	0	5	0	2	7		
ENSMUST00000144046	ENSMUSG00000020653	12	24651371	24662774	1	6	3	6	0	3	5	0	6	0	0	6	D3Z293	
ENSMUST00000144047	ENSMUSG00000026289	1	87755870	87792428	1	1	0	2	33	5	0	0	5	0	0	4	D3YZW7	
ENSMUST00000144048						2	0	3	3	3	2	0	0	3	0	0		
ENSMUST00000144049	ENSMUSG00000020812	11	116671660	116675799	1	5	4	10	10	3	2	3	0	3	2	3	E9PZV8	
ENSMUST00000144050	ENSMUSG00000042002	5	114254164	114273807	-1	2	2	9	7	2	2	0	0	0	0	0	E9PZL8	
ENSMUST00000144051						0	0	0	0	0	8	16	4	6	5	25		
ENSMUST00000144052						0	0	0	5	0	0	3	0	0	0	0		
ENSMUST00000144053						3	1	0	0	0	4	1	3	0	0	2		
ENSMUST00000144054	ENSMUSG00000040811	7	19176421	19206482	1	0	0	0	0	0	0	15	8	3	0	0		
ENSMUST00000144055						0	0	0	35	0	1	0	2	0	3	5		
ENSMUST00000144056						0	0	0	15	0	0	16	5	0	0	5		
ENSMUST00000144057						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144058						4	1	2	6	7	3	27	127	44	8	43		
ENSMUST00000144059						0	1	0	72	0	0	0	2	2	2	0		
ENSMUST00000144060	ENSMUSG00000021711	13	104142149	104178469	-1	55	0	0	0	48	0	14	237	92	41	0		Q3TIR1
ENSMUST00000144061	ENSMUSG00000021770	14	21750531	21798725	1	0	0	1	151	0	0	31	73	128	0	83	D6REI9	
ENSMUST00000144062						6	0	9	1	2	1	0	0	0	0	0		
ENSMUST00000144063						3	1	0	0	3	1	0	0	5	0	5		
ENSMUST00000144064	ENSMUSG00000029561	5	114896936	114912234	1	0	6	16	8	15	0	38	913	57	43	236	F6Y3A6	
ENSMUST00000144065						2	4	0	0	0	0	0	0	0	4	0		
ENSMUST00000144066						7	4	0	4	5	5	0	0	0	0	0		
ENSMUST00000144067	ENSMUSG00000064284	15	85806972	85811697	-1	7	2	3	58	2	2	0	0	0	0	0		Q8R3A2
ENSMUST00000144068	ENSMUSG00000060681	X	56609757	56664230	1	0	0	2	22	4	3	63	52	95	15	44	D3Z0Q9	
ENSMUST00000144069						2	0	5	4	3	0	0	0	0	0	0		
ENSMUST00000144070	ENSMUSG00000023723	11	88204388	88211507	1	0	0	0	1	0	0	32	87	48	44	25	F7ARZ1	
ENSMUST00000144071						5	0	12	3	3	3	0	2	3	0	4		
ENSMUST00000144072						1	4	6	5	5	2	0	5	6	6	8		
ENSMUST00000144073	ENSMUSG00000054405	4	132535550	132553742	1	0	0	0	13	0	0	1	10	4	0	3	E9PZT4	
ENSMUST00000144074						2	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000144075						0	0	5	0	0	0	34	12	35	9	74		
ENSMUST00000144076						0	0	0	0	0	2	1	0	3	0	26		
ENSMUST00000144077	ENSMUSG00000025980	1	55077835	55088243	-1	0	0	0	0	0	0	0	0	4	0	0	D3Z7J9	
ENSMUST00000144079	ENSMUSG00000029847	6	34945278	34988404	-1	6	2	0	4	3	3	0	0	0	0	0	D3Z3R5	
ENSMUST00000144080						6	2	10	3	5	3	16	49	37	12	54		
ENSMUST00000144081						0	0	0	0	8	0	12	0	0	0	0		
ENSMUST00000144082						216	212	174	299	250	104	2	22	2	0	7		
ENSMUST00000144083						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144085						0	1	1	0	1	0	2	6	0	3	2		
ENSMUST00000144086	ENSMUSG00000015950	5	134220053	134229625	-1	0	18	20	147	34	0	260	714	802	64	579	S4R293	
ENSMUST00000144087	ENSMUSG00000034949	10	81233155	81252123	1	3	1	27	31	0	2	0	6	0	0	0	D3YXQ2	
ENSMUST00000144088	ENSMUSG00000026781	2	23068168	23114510	1	5	3	7	22	5	12	0	0	0	4	0	Z4YN06	
ENSMUST00000144089						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144090						6	0	23	108	26	5	0	0	0	0	0		
ENSMUST00000144091						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144093						0	0	0	17	0	4	6	0	12	0	9		
ENSMUST00000144097						3	4	9	12	12	4	25	167	31	3	42		
ENSMUST00000144098	ENSMUSG00000096867	X	154043986	154055039	-1	5	5	0	2	5	0	1	0	0	0	0	A2BED8	
ENSMUST00000144099	ENSMUSG00000039298	4	70216856	70410443	-1	85	95	228	190	83	38	29	63	81	0	72		Q8K389
ENSMUST00000144100	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	0	0	1	0	0	0	2	7	F6ZRF0	
ENSMUST00000144101						5	4	6	6	5	6	0	0	0	0	3		
ENSMUST00000144102						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000144103						4	2	2	2	7	3	11	0	10	0	5		
ENSMUST00000144104						1	0	0	4	4	1	0	4	1	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144106						7	13	16	22	9	3	9	41	9	2	13		
ENSMUST00000144108						10	3	18	8	6	0	21	64	20	4	28		
ENSMUST00000144110	ENSMUSG00000027189	2	102300119	102407828	-1	0	1	0	0	0	0	0	0	3	0	0	A2AGP1	
ENSMUST00000144111	ENSMUSG00000004085	2	72285637	72442610	1	1	0	6	2	1	1	0	0	0	1	0	A2ASW6	
ENSMUST00000144112						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000144113						0	0	0	0	0	0	22	0	14	44	10		
ENSMUST00000144114	ENSMUSG00000028629	4	120921196	120925017	-1	0	0	0	3	0	0	0	4	4	4	0	Z4YLZ9	
ENSMUST00000144115	ENSMUSG00000037997	6	127446840	127494261	1	0	0	0	0	0	0	0	0	3	13	10		
ENSMUST00000144116						13	12	21	5	17	15	0	2	2	3	2		
ENSMUST00000144117						3	0	0	0	0	0	242	971	715	1453	661		
ENSMUST00000144119						0	0	0	0	7	0	316	274	121	10	141		
ENSMUST00000144120	ENSMUSG00000027394	2	129065942	129096283	1	12	11	13	18	18	6	0	0	0	0	0	F6ZXS5	
ENSMUST00000144121	ENSMUSG00000049550	5	123577795	123684618	-1	4	0	1	6	0	0	0	0	7	0	0	F6RAY2	
ENSMUST00000144122	ENSMUSG00000051900	7	120409647	120544813	1	4	0	3	6	7	0	0	0	0	0	0	D6RDD8	
ENSMUST00000144123						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144124						87	53	363	14	62	32	0	3	4	0	0		
ENSMUST00000144125						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144127						0	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000144128						1	4	5	4	7	0	0	0	9	0	6		
ENSMUST00000144129						6	6	20	7	6	5	7	129	51	0	49		
ENSMUST00000144130						6	0	47	13	6	6	0	0	0	0	0		
ENSMUST00000144131	ENSMUSG00000030177	6	120324323	120364374	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q516	
ENSMUST00000144132	ENSMUSG00000005774	3	94954075	94961561	1	0	0	0	0	0	0	0	80	23	21	23	D6RDE5	
ENSMUST00000144133						1	3	6	0	0	2	0	0	0	0	0		
ENSMUST00000144135						0	0	0	2	1	2	2	3	0	7	0		
ENSMUST00000144136						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144137						1	3	3	0	3	1	3	0	0	0	4		
ENSMUST00000144138	ENSMUSG00000025920	1	16228674	16520112	-1	1	0	0	0	0	1	0	0	3	0	0		Q8CJ67
ENSMUST00000144139						8991	12790	20125	5732	10139	4356	75	474	155	89	205		
ENSMUST00000144140						3	0	0	5	0	2	1	0	0	0	0		
ENSMUST00000144141	ENSMUSG00000022124	14	103080239	103099566	-1	0	0	0	76	8	7	3	13	171	18	102	D3YWZ0	
ENSMUST00000144142	ENSMUSG00000052525	17	71552061	71589533	1	0	2	1	0	0	0	0	0	0	0	0		Q5IBH7
ENSMUST00000144143	ENSMUSG00000026766	2	50279881	50296801	-1	0	0	6	66	5	0	10	51	50	21	23	A2AQT7	
ENSMUST00000144144	ENSMUSG00000029268	5	87459490	87482260	-1	9	0	4	0	1	4	0	0	0	0	0	D3YUX6	
ENSMUST00000144145						19	21	57	20	24	14	0	1	0	0	0		
ENSMUST00000144146						0	0	0	0	0	0	0	10	5	0	0		
ENSMUST00000144148	ENSMUSG00000039382	X	7721973	7728201	1	0	0	0	0	2	0	0	0	0	0	0	A0A0A0MQH0	
ENSMUST00000144149						0	0	6	3	5	0	5	62	13	13	15		
ENSMUST00000144150	ENSMUSG00000002475	18	10644411	10706771	-1	0	1	9	0	0	1	0	0	0	1	1	F6RSE8	
ENSMUST00000144151	ENSMUSG00000033088	15	78947724	79005867	1	2	0	6	1	1	2	0	4	7	0	7	J9JI90	
ENSMUST00000144152						2	0	2	1	5	1	14	27	7	4	11		
ENSMUST00000144153	ENSMUSG00000033909	11	118259651	118290244	-1	0	12	36	194	36	12	0	0	4	0	10	B0QZF8	
ENSMUST00000144154						3	2	4	17	7	8	0	0	0	0	1		
ENSMUST00000144155	ENSMUSG00000016386	2	106693269	106868356	1	0	0	2	2	0	1	0	0	0	0	0	B1AX06	
ENSMUST00000144156	ENSMUSG00000061877	7	81494275	81498281	-1	0	0	0	5	15	4	0	0	0	0	0	D3YXE9	
ENSMUST00000144157						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000144158	ENSMUSG00000046727	18	36345619	36402980	1	0	0	2	0	0	0	0	0	0	0	0	D3YVS7	
ENSMUST00000144159						0	3	0	0	0	2	0	0	0	0	0		
ENSMUST00000144160						0	0	0	38	25	0	0	0	0	0	0		
ENSMUST00000144161						82	87	362	108	96	49	18	61	28	8	40		
ENSMUST00000144162						5	4	19	138	10	2	0	50	10	0	17		
ENSMUST00000144164	ENSMUSG00000020268	11	54826866	54860916	-1	0	0	0	1	2	0	1	0	0	1	5		Q9DA03
ENSMUST00000144165						1	0	11	236	5	3	8	37	8	3	28		
ENSMUST00000144167	ENSMUSG00000028420	4	53826045	53862019	1	3	0	1	1	0	0	66	19	47	0	33	X1WI17	
ENSMUST00000144168						3	2	6	0	10	4	8	4	6	0	6		
ENSMUST00000144169						14	2	20	57	5	0	0	0	0	0	0		
ENSMUST00000144170						0	1	4	52	3	0	0	0	0	0	0		
ENSMUST00000144171						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000144172						3	5	33	2	6	0	0	0	0	107	20		
ENSMUST00000144173	ENSMUSG00000042759	7	126584942	126589112	1	0	0	8	4	7	2	10	59	30	2	32		
ENSMUST00000144174						0	0	11	2	0	3	0	0	0	0	0		
ENSMUST00000144175	ENSMUSG00000041658	X	153139981	153171943	1	1	0	4	15	7	0	2	0	1	3	0	G3UYP1	
ENSMUST00000144176	ENSMUSG00000028617	4	107233514	107253532	-1	0	0	0	0	3	0	0	0	0	1	3	F6UPZ3	
ENSMUST00000144177	ENSMUSG00000025911	1	9547948	9580673	1	11	7	20	6	13	8	0	0	0	0	0		Q8R0N6
ENSMUST00000144179	ENSMUSG00000074736	2	149829211	150004392	1	0	0	3	0	2	0	0	0	0	0	0	B1AYD3	
ENSMUST00000144181						1	0	2	8	1	0	0	0	0	0	0		
ENSMUST00000144182	ENSMUSG00000024457	17	36837134	36859398	1	0	0	0	18	2	0	0	0	0	3	0	B8JJ56	
ENSMUST00000144183	ENSMUSG00000058331	13	67747800	67755228	-1	8	0	6	5	9	2	0	0	0	0	0	B8JJY3	
ENSMUST00000144184						1	4	5	4	0	0	0	0	0	0	0		
ENSMUST00000144185						2	0	5	0	5	1	0	5	0	0	6		
ENSMUST00000144186						1	0	1	2	0	0	17	36	25	7	48		
ENSMUST00000144187	ENSMUSG00000002012	X	73655994	73660117	-1	4	1	9	4	1	5	0	0	0	0	1	A2ALM3	
ENSMUST00000144188	ENSMUSG00000017548	11	79993106	80034123	1	0	2	0	0	0	0	0	21	13	8	24	F7B7H9	
ENSMUST00000144189	ENSMUSG00000036862	7	105752989	105787654	-1	0	0	0	381	0	39	0	0	0	0	0	F6TP58	
ENSMUST00000144190						2	0	2	0	2	0	9	4	0	0	27		
ENSMUST00000144191						1	2	0	2	0	0	4	3	0	0	3		
ENSMUST00000144192						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000144194						4	2	6	18	0	0	2	0	0	0	3		
ENSMUST00000144195	ENSMUSG00000032557	9	104046599	104063134	-1	0	0	4	0	0	0	29	49	63	8	52	F6VRI6	
ENSMUST00000144196	ENSMUSG00000040860	4	141016637	141060550	-1	0	2	3	5	2	0	3	0	5	2	3	B7ZC90	
ENSMUST00000144197						5	1	0	7	3	1	0	2	0	1	3		
ENSMUST00000144198						5	0	8	22	2	5	0	0	4	0	0		
ENSMUST00000144199						27	22	49	102	38	15	30	91	57	7	62		
ENSMUST00000144200						2	0	5	1	3	2	0	0	2	1	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144201						1	0	0	1	4	0	0	0	0	0	0		
ENSMUST00000144203						0	0	0	0	0	0	0	5	0	0	2		
ENSMUST00000144204	ENSMUSG00000036918	17	87282886	87381769	1	0	0	0	0	0	9	7	0	8	0	7	D6RG81	
ENSMUST00000144205						0	0	0	0	0	0	8	0	0	2	3		
ENSMUST00000144206						12	11	72	50	10	4	2	0	2	0	3		
ENSMUST00000144207	ENSMUSG00000030649	7	101881325	101901845	1	0	0	0	0	0	0	0	43	20	2	10		P60007
ENSMUST00000144209						0	3	5	28	3	2	0	0	0	0	0		
ENSMUST00000144210						4	1	31	6	6	3	18	39	13	5	20		
ENSMUST00000144211	ENSMUSG00000039860	5	135806890	135874772	1	17	17	61	112	25	12	0	0	0	0	0		Q80WV7
ENSMUST00000144213						0	0	9	53	4	0	0	0	0	0	0		
ENSMUST00000144214						12	14	20	16	17	13	1	8	4	1	8		
ENSMUST00000144215	ENSMUSG00000022969	16	91406164	91425834	1	0	0	0	0	0	0	0	0	22	0	12	E9Q083	
ENSMUST00000144216	ENSMUSG00000023791	16	32084418	32099738	-1	5	6	9	185	12	10	3	22	17	1	34	F7CUX5	
ENSMUST00000144217	ENSMUSG00000051351	4	136284683	136293942	1	0	0	0	6	0	2	0	0	0	0	0	A2AW49	
ENSMUST00000144218						3	1	0	4	6	0	0	7	0	0	0		
ENSMUST00000144219						9	8	17	20	10	7	3	2	0	0	2		
ENSMUST00000144220						0	5	12	48	6	5	0	5	0	0	9		
ENSMUST00000144221	ENSMUSG00000048249	17	26715650	26776635	1	1	0	0	12	8	0	14	6	392	162	207	B8JJI0	
ENSMUST00000144223						0	2	6	2	0	1	0	0	0	0	0		
ENSMUST00000144225						2	2	5	24	2	0	0	4	5	2	4		
ENSMUST00000144226						2	2	7	8	4	0	11	22	31	0	43		
ENSMUST00000144228						9	5	25	4	2	5	5	9	0	2	3		
ENSMUST00000144229	ENSMUSG00000000530	15	101128522	101145336	1	4	2	2	25	2	0	1	1	6	0	5		
ENSMUST00000144231						34	38	189	76	33	22	13	61	27	5	54		
ENSMUST00000144233	ENSMUSG00000075704	16	18426384	18479073	1	0	2	6	1	1	0	1	0	0	0	0		
ENSMUST00000144234	ENSMUSG00000001436	10	77032241	77061002	1	17	0	15	33	0	0	32	0	14	5	46	Q542F3	P41438
ENSMUST00000144235						6	0	16	19	0	0	0	293	46	0	230		
ENSMUST00000144236	ENSMUSG00000024150	17	87254658	87265935	-1	0	8	10	7	18	0	30	84	72	0	129	D0EW11	Q8K5B2
ENSMUST00000144237	ENSMUSG00000021221	12	83213745	83487716	-1	0	0	0	4	4	0	0	0	0	0	0	F7CL41	
ENSMUST00000144238						5	6	15	8	5	0	29	104	51	3	90		
ENSMUST00000144239						3	1	2	5	4	2	29	214	106	6	157		
ENSMUST00000144240						0	0	0	0	1	1	1	0	0	0	0		
ENSMUST00000144241	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1S5	
ENSMUST00000144242						4	3	4	0	2	1	10	3	6	1	20		
ENSMUST00000144243	ENSMUSG00000023930	17	40764734	40807003	-1	2	0	2	0	4	1	0	0	0	0	0	D3YVR2	
ENSMUST00000144244						0	0	0	0	1	0	0	0	5	0	11		
ENSMUST00000144245						30	17	25	17	21	14	0	0	0	0	0		
ENSMUST00000144246						1	1	1	3	4	0	12	9	15	0	25		
ENSMUST00000144247	ENSMUSG00000037486	12	3426857	3506852	1	0	1	0	56	0	0	11	17	84	2	29	D6RI62	
ENSMUST00000144248	ENSMUSG00000035545	7	4137039	4148177	1	3	0	0	0	0	1	186	0	186	0	181	D3YXV8	
ENSMUST00000144249						40	36	40	87	45	30	5	13	12	1	36		
ENSMUST00000144250						0	0	3	0	6	4	0	13	0	14	11		
ENSMUST00000144251	ENSMUSG00000048537	9	44686304	44735198	-1	0	0	0	0	0	0	0	0	0	0	0	E9PWW4	
ENSMUST00000144252	ENSMUSG00000027465	2	152293828	152313996	1	0	0	0	16	0	0	1	2	1	0	0	B0R080	
ENSMUST00000144253						743	584	508	473	922	224	16	87	63	20	143		
ENSMUST00000144254	ENSMUSG00000075318	2	65620771	65767447	1	0	0	0	0	0	0	0	0	0	0	0	F7AMU5	
ENSMUST00000144255	ENSMUSG00000042625	17	56560965	56584585	-1	0	0	0	0	0	0	0	201	79	13	51	D6RJ78	
ENSMUST00000144257						0	0	0	114	7	4	0	0	1	0	0		
ENSMUST00000144258	ENSMUSG00000057672	8	83669762	83699179	-1	3	0	24	0	6	12	6058	4599	4488	301	3656		P70268
ENSMUST00000144259						0	4	7	6	14	2	3	11	1	0	12		
ENSMUST00000144262						42	35	61	96	69	40	2	6	1	1	6		
ENSMUST00000144263						4	0	5	15	5	3	0	0	0	0	0		
ENSMUST00000144264	ENSMUSG00000000766	10	6758506	7038198	1	3	0	9	0	0	2	0	0	0	0	0		P42866
ENSMUST00000144265						0	2	4	2	1	5	445	167	620	937	344		
ENSMUST00000144267	ENSMUSG00000030562	7	87246096	87398710	1	5	0	0	0	5	3	0	0	0	0	0	S4R1R3	
ENSMUST00000144268	ENSMUSG00000038569	5	122323223	122354233	-1	1	2	1	0	1	0	0	2	0	0	0	D3Z515	
ENSMUST00000144269	ENSMUSG00000047671	4	117126794	117128738	1	3	3	12	0	9	1	3	6	0	0	0	A0A0A0MQL6	
ENSMUST00000144270	ENSMUSG00000005672	5	75574916	75656722	1	0	0	0	142	0	13	737	1037	693	98	482	F7DD14	P05532
ENSMUST00000144271						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000144272	ENSMUSG00000029775	6	30401868	30455179	1	0	0	0	0	0	0	8	49	33	7	0		
ENSMUST00000144273						2	2	2	5	0	0	0	0	0	0	0		
ENSMUST00000144274						7	5	4	14	9	12	1	0	2	0	3		
ENSMUST00000144275	ENSMUSG00000027274	2	136873780	136891389	-1	0	0	1	7	0	3	30	174	50	172	30		
ENSMUST00000144276	ENSMUSG00000059439	11	85353167	85826058	1	3	5	6	10	11	5	0	12	4	0	13	Q5SWI1	
ENSMUST00000144278						0	0	0	0	2	0	0	2	37	6	16		
ENSMUST00000144280						19	17	15	78	21	20	34	209	58	20	28		
ENSMUST00000144281	ENSMUSG00000003810	4	116306762	116464183	-1	3	2	9	2	4	4	0	0	0	0	0	B1AST6	
ENSMUST00000144282						1	0	4	0	8	4	0	1	0	4	0		
ENSMUST00000144283	ENSMUSG00000057554	13	12439415	12464944	-1	2	2	0	0	1	0	66	121	114	66	56	A8DIL0	
ENSMUST00000144284						5	2	1	3	1	0	3	2	1	0	4		
ENSMUST00000144285						0	0	0	0	0	0	18	131	8	0	0		
ENSMUST00000144286						0	1	0	0	2	0	9	41	0	0	22		
ENSMUST00000144287						402	449	600	25	252	148	0	2	21	10	26		
ENSMUST00000144288	ENSMUSG00000021493	13	55495795	55513676	-1	0	0	1	17	1	2	0	0	0	0	0	B8JJB2	
ENSMUST00000144289	ENSMUSG00000041540	6	143828425	144781977	-1	0	0	0	0	2	0	0	0	0	0	2	B2KFM7	
ENSMUST00000144290						6	4	1	5	5	6	0	0	4	0	2		
ENSMUST00000144292						23	26	34	21	27	20	3	4	1	0	1		
ENSMUST00000144293						11	7	50	15	16	6	12	19	18	10	57		
ENSMUST00000144295						8	8	10	65	15	2	20	50	26	7	29		
ENSMUST00000144296	ENSMUSG00000029710	5	137350109	137378669	1	28	7	11	0	28	25	0	0	0	0	0		P54761
ENSMUST00000144297						23	17	56	11	21	17	0	0	0	0	0		
ENSMUST00000144298						0	0	0	4	8	0	0	0	0	0	0		
ENSMUST00000144299						4	3	17	5	3	4	135	297	206	10	153		
ENSMUST00000144300						2	0	0	0	0	2	91	69	78	0	179		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144301						86	71	432	349	59	38	0	5	0	0	1		
ENSMUST00000144302	ENSMUSG00000052613	10	73099342	74649737	1	9	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000144303	ENSMUSG00000004849	5	137034993	137046135	-1	0	1	0	0	0	0	58	13	51	24	39	D3Z0D6	
ENSMUST00000144304						3	7	6	10	3	0	67	441	115	29	166		
ENSMUST00000144305						0	0	0	28	1	4	0	0	0	0	0		
ENSMUST00000144306	ENSMUSG00000078656	11	101253707	101259549	1	0	2	0	0	0	0	15	5	15	16	8	E9PXS9	
ENSMUST00000144307						17	15	11	9	10	5	8	8	9	5	4		
ENSMUST00000144308						3	1	21	9	10	2	0	30	33	3	11		
ENSMUST00000144309						0	0	0	0	0	0	2	4	4	3	0		
ENSMUST00000144310						0	0	1	14	0	0	140	92	31	7	81		
ENSMUST00000144311						8	3	6	2	2	2	2	4	2	5	2		
ENSMUST00000144314						5	5	8	1	3	2	23	7	29	0	28		
ENSMUST00000144315						2	0	8	13	4	0	0	2	2	0	0		
ENSMUST00000144316						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000144317						2	0	0	0	0	1	34	47	25	6	64		
ENSMUST00000144318						7	14	11	10	12	4	0	2	7	0	4		
ENSMUST00000144319						2	0	8	94	4	2	0	5	12	3	17		
ENSMUST00000144320						5	5	4	29	0	6	0	0	9	0	0		
ENSMUST00000144321	ENSMUSG00000020459	11	29526408	29545279	1	0	0	0	0	0	0	1	0	6	0	0	Q5M6W7	
ENSMUST00000144322	ENSMUSG00000040415	10	127190378	127195728	-1	1	1	3	3	2	0	0	5	0	0	0	D3Z4X6	
ENSMUST00000144323						5	2	4	2	2	5	3	0	0	0	0		
ENSMUST00000144324						3	0	11	2	0	1	0	37	11	10	0		
ENSMUST00000144325						0	0	0	1	0	0	0	0	1	0	0		
ENSMUST00000144326	ENSMUSG00000038546	13	43402673	43480973	-1	7	6	20	87	16	12	707	2771	1306	170	732	E9Q5D6	
ENSMUST00000144327	ENSMUSG00000027556	3	14766216	14808368	-1	4	2	2	2	1	0	0	0	0	0	0	D3YYQ4	
ENSMUST00000144328						0	0	25	1	4	6	4	5	0	0	8		
ENSMUST00000144329	ENSMUSG00000028645	4	119108711	119137983	1	0	0	9	3	3	0	3	4	0	0	15	G3UYL0	
ENSMUST00000144330						31	21	26	52	37	30	11	11	18	0	16		
ENSMUST00000144331	ENSMUSG00000023927	17	51736187	51833290	-1	0	0	0	58	0	0	123	162	165	0	0		Q60611
ENSMUST00000144332						2	0	9	2	3	1	0	0	0	0	0		
ENSMUST00000144333						7	2	2	1	4	0	0	0	0	0	0		
ENSMUST00000144334						3	2	8	0	4	1	0	0	0	0	0		
ENSMUST00000144335						0	4	12	11	2	0	0	0	0	0	0		
ENSMUST00000144336						0	0	0	0	0	0	6	4	5	0	0		
ENSMUST00000144337	ENSMUSG00000079523	6	72957347	72958748	-1	6	2	14	46	4	2	7	38	15	4	26		
ENSMUST00000144338						8	15	14	4	6	4	0	0	0	0	1		
ENSMUST00000144340						155	129	657	242	185	108	4	17	5	1	18		
ENSMUST00000144341						0	0	12	2	5	0	0	0	1	0	0		
ENSMUST00000144342						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144343						3	0	0	0	1	0	0	0	0	0	4		
ENSMUST00000144344	ENSMUSG00000027971	3	125404076	125728899	1	0	0	0	0	1	0	0	0	0	0	0	D3YWZ6	
ENSMUST00000144345	ENSMUSG00000052384	16	32142785	32165594	-1	0	0	0	23	0	0	0	3	0	0	0	D3Z2Y0	
ENSMUST00000144346						51	35	50	37	38	21	3	9	2	0	3		
ENSMUST00000144348	ENSMUSG00000037410	9	90202027	90270804	-1	0	0	0	15	0	0	0	0	0	24	2	F6W2R3	
ENSMUST00000144349						0	5	6	1	2	1	22	50	7	6	25		
ENSMUST00000144352						0	2	13	3	0	2	0	0	0	0	0		
ENSMUST00000144353						2	1	0	0	1	0	0	3	2	1	3		
ENSMUST00000144354						3	2	4	3	5	1	3	0	2	0	0		
ENSMUST00000144355	ENSMUSG00000026201	1	75210838	75215606	1	0	0	0	9	0	0	0	0	5	7	9	D3YXM1	
ENSMUST00000144356	ENSMUSG00000008035	X	10715013	10719690	1	0	0	0	0	0	0	25	0	0	0	0	F7D5Q6	
ENSMUST00000144357						0	0	0	0	0	1	0	0	12	0	0		
ENSMUST00000144358	ENSMUSG00000045106	2	104867805	105017904	1	1	0	0	1	0	2	0	1	0	1	0	F6YTE1	
ENSMUST00000144359						0	0	0	0	0	0	0	8	70	20	18		
ENSMUST00000144360						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000144361						1	5	7	4	4	3	4	0	6	0	11		
ENSMUST00000144363	ENSMUSG00000029208	5	69556923	69575973	1	0	0	0	0	0	0	1	0	0	0	0	F6ZM03	
ENSMUST00000144364	ENSMUSG00000038271	6	125145241	125161782	1	0	0	0	0	0	0	1	0	42	0	84	D6RH90	
ENSMUST00000144365						5	7	5	4	6	0	1	0	1	1	1		
ENSMUST00000144367						5	5	4	2	1	3	0	0	0	5	0		
ENSMUST00000144369						3	5	3	0	0	0	0	0	6	0	13		
ENSMUST00000144370						10	11	62	32	28	12	0	0	0	0	0		
ENSMUST00000144371						0	1	1	4	0	0	0	0	2	0	0		
ENSMUST00000144372						3	3	0	0	3	1	0	0	0	0	0		
ENSMUST00000144373	ENSMUSG00000033423	4	117550365	117674297	1	2	1	0	2	0	1	0	0	2	0	5	A0A0A0MQH3	
ENSMUST00000144374						0	1	0	0	4	0	11	28	13	2	37		
ENSMUST00000144375						5	3	4	8	0	0	670	3356	772	307	611		
ENSMUST00000144376						17	16	19	7	20	10	0	9	8	0	10		
ENSMUST00000144377	ENSMUSG00000033624	8	111094630	111137074	1	2	4	8	3	6	0	16	5	42	3	40	D6RD07	
ENSMUST00000144378						49	61	184	64	62	38	113	594	216	227	135		
ENSMUST00000144379						3	0	5	0	9	0	2	3	2	0	0		
ENSMUST00000144380						1	0	9	1	2	0	80	65	70	178	35		
ENSMUST00000144381						0	3	3	1	4	0	0	3	15	0	12		
ENSMUST00000144382	ENSMUSG00000034595	17	35865593	35875596	1	0	1	0	0	0	0	1629	1016	1906	225	1129		Q8BQ30
ENSMUST00000144383						61	39	151	510	75	55	3	15	10	1	9		
ENSMUST00000144384						9	7	5	12	9	4	0	8	4	2	6		
ENSMUST00000144385						16	16	38	30	12	8	3	9	5	0	6		
ENSMUST00000144386	ENSMUSG00000070643	1	133382303	133424377	-1	13	12	64	2	16	11	40	26	30	5	15	D3Z7I3	
ENSMUST00000144387						0	2	1	6	2	0	0	1	0	0	1		
ENSMUST00000144388						6095	5301	2883	82974	13987	1913	4	13	19	9	34		
ENSMUST00000144389	ENSMUSG00000028959	5	24438440	24445287	-1	6	0	10	0	8	0	21	30	0	0	0	D6RCW0	
ENSMUST00000144390						0	0	0	0	0	6	33	0	412	15	153		
ENSMUST00000144391						2	6	16	6	8	9	0	0	0	0	0		
ENSMUST00000144392	ENSMUSG00000010051	9	107576927	107581710	1	0	0	0	9	6	0	0	0	0	0	0	D3YXU8	
ENSMUST00000144393						3	0	0	5	5	0	11	80	5	0	22		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144394	ENSMUSG00000027257	2	91255954	91264679	1	0	0	0	0	0	0	0	0	0	0	0	B1AW92	
ENSMUST00000144395						1	0	0	0	0	0	98	0	13	0	0		
ENSMUST00000144396						0	0	0	0	0	0	20	14	12	0	8		
ENSMUST00000144397						2	1	2	9	6	3	17	7	64	3	49		
ENSMUST00000144398						20	5	21	28	19	17	0	0	0	0	0		
ENSMUST00000144399	ENSMUSG00000020542	11	65176561	65269989	-1	5	5	24	0	0	0	0	0	0	0	0	F6TBX6	
ENSMUST00000144400						0	1	0	2	6	2	0	0	0	0	0		
ENSMUST00000144401						49	40	287	49	26	14	7	30	14	3	6		
ENSMUST00000144402						31	27	77	69	50	24	0	2	4	1	0		
ENSMUST00000144403	ENSMUSG00000027270	2	136052239	136069917	1	8	3	36	13	5	2	0	0	1	0	0	A2AT95	
ENSMUST00000144404						68	58	225	136	77	37	13	47	37	4	44		
ENSMUST00000144405						0	0	2	2	3	0	3	4	3	0	3		
ENSMUST00000144406	ENSMUSG00000042308	7	127776670	127800122	1	0	0	0	11	0	3	0	0	16	0	8	D3YUD4	
ENSMUST00000144408	ENSMUSG00000043017	7	16906490	16910905	1	31	22	77	159	45	11	135	215	283	17	152		P43252
ENSMUST00000144409	ENSMUSG00000024949	19	6363690	6378030	1	0	0	0	55	0	0	9	11	21	5	25	D6RDB7	
ENSMUST00000144410						1	3	2	0	2	0	0	0	0	0	0		
ENSMUST00000144413						6	5	7	32	7	8	0	0	0	0	4		
ENSMUST00000144414						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144415						4	8	5	0	3	0	0	0	0	0	0		
ENSMUST00000144416	ENSMUSG00000043671	7	35685165	35754454	-1	1	1	0	0	1	0	0	0	0	0	0	F7D0Q0	
ENSMUST00000144417	ENSMUSG00000043687	8	120608602	120647632	-1	0	4	2	22	1	0	0	0	0	0	0	D6RIP9	
ENSMUST00000144418						1	2	4	8	6	2	0	0	0	0	0		
ENSMUST00000144422						7	3	3	8	5	3	0	0	2	0	0		
ENSMUST00000144423						1	2	2	3	0	3	0	0	0	0	1		
ENSMUST00000144425						0	2	3	1	0	0	0	0	2	0	0		
ENSMUST00000144426						0	3	0	1	0	2	0	0	0	0	1		
ENSMUST00000144427	ENSMUSG00000028708	4	115839198	115879250	1	0	0	0	0	1	0	0	0	0	0	0	F6Y5U1	
ENSMUST00000144428						3	2	7	8	3	2	0	2	1	0	0		
ENSMUST00000144429	ENSMUSG00000031328	X	74223461	74249820	-1	35	0	47	0	0	28	2661	14226	2448	808	4403	F6XC15	
ENSMUST00000144430	ENSMUSG00000024160	17	24886643	24892152	1	0	0	0	0	0	0	0	0	4	0	3	F6Y7L3	
ENSMUST00000144431	ENSMUSG00000018570	11	69897352	69900987	-1	13	7	0	15	17	0	0	0	0	3	0	J3QNJ8	
ENSMUST00000144432						0	0	1	4	2	0	0	0	0	0	0		
ENSMUST00000144433						0	0	0	2	1	0	0	0	1	0	0		
ENSMUST00000144434						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000144435						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000144436						5	0	0	0	3	3	0	0	0	0	0		
ENSMUST00000144437						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144438						3	1	2	25	1	3	0	0	0	0	0		
ENSMUST00000144440	ENSMUSG00000037216	1	37871738	37876228	1	0	0	0	3	0	1	0	6	0	1	0	D3Z093	
ENSMUST00000144441						6	0	8	74	7	1	0	0	0	0	3		
ENSMUST00000144442						0	4	0	0	4	0	0	0	0	0	0		
ENSMUST00000144443						8	0	17	9	4	5	2624	7837	1340	2232	1158		
ENSMUST00000144444	ENSMUSG00000057880	16	8513429	8621568	1	4	4	6	0	7	0	0	0	0	0	0	F6RN86	
ENSMUST00000144445						2	1	1	2	1	1	0	1	1	0	1		
ENSMUST00000144446						0	1	1	0	2	0	17	29	10	5	4		
ENSMUST00000144447						1130	775	2760	1465	1152	512	41	156	118	20	249		
ENSMUST00000144448						1	0	3	5	5	4	0	0	0	0	0		
ENSMUST00000144449						8	5	22	10	7	5	0	1	0	0	1		
ENSMUST00000144450						0	1	0	1	0	0	0	0	0	4	2		
ENSMUST00000144451						3	1	7	9	0	0	0	0	0	0	1		
ENSMUST00000144452						13	17	66	32	20	12	0	4	0	0	4		
ENSMUST00000144454						3	1	0	0	7	0	717	1326	596	183	372		
ENSMUST00000144455	ENSMUSG00000072244	7	104218793	104235152	1	1	1	2	0	0	0	0	0	0	0	0	D3Z676	
ENSMUST00000144456						0	0	0	0	0	0	0	0	0	0	35		
ENSMUST00000144457						0	0	4	0	0	2	5	0	0	23	5		
ENSMUST00000144458	ENSMUSG00000031826	8	119910360	119957560	1	5	0	0	89	5	8	0	0	0	8	0		P52479
ENSMUST00000144459	ENSMUSG00000071253	10	62920633	62946498	1	0	0	0	2	0	0	0	14	60	11	54	D3YVC9	
ENSMUST00000144461	ENSMUSG00000022960	16	91677268	91688765	-1	0	0	0	0	0	0	0	0	0	0	0	D6RJM0	
ENSMUST00000144462						0	0	0	0	0	3	0	2	0	0	0		
ENSMUST00000144463	ENSMUSG00000000384	11	6615598	6626067	-1	0	1	0	0	1	0	4	0	2	0	4	Q5SWP0	
ENSMUST00000144464	ENSMUSG00000041605	1	136213531	136234264	-1	1	0	2	7	0	0	0	0	0	0	0	D3YZT8	
ENSMUST00000144465	ENSMUSG00000021848	14	48657679	48667644	-1	3	0	5	1	3	4	0	0	0	0	0	D3Z4G2	
ENSMUST00000144466						4	2	1	219	6	2	0	2	0	0	0		
ENSMUST00000144467	ENSMUSG00000034110	5	130144861	130155806	1	0	0	0	4	4	1	0	0	0	0	0	F6QXA3	
ENSMUST00000144468	ENSMUSG00000034006	18	80253292	80292725	1	7	0	5	13	8	3	12	15	34	8	44	D3Z2D5	
ENSMUST00000144469						0	3	3	0	4	3	6	39	3	2	28		
ENSMUST00000144470	ENSMUSG00000070814	7	13258967	13278721	-1	0	0	2	2	0	3	0	0	0	0	0	D3Z6U3	
ENSMUST00000144471						0	0	1	3	7	7	25	108	23	3	33		
ENSMUST00000144472	ENSMUSG00000058240	16	91689322	91728975	-1	4	0	0	4	0	0	34	50	53	91	41	F7BGV1	
ENSMUST00000144473	ENSMUSG00000020739	11	115564434	115583985	1	4	4	0	0	0	2	9	0	0	11	11	Z4YLV0	
ENSMUST00000144474						1	1	9	6	2	2	3	0	0	0	0		
ENSMUST00000144475						1	0	1	0	0	0	1	0	1	0	1		
ENSMUST00000144476	ENSMUSG00000002458	2	181688419	181693977	-1	0	0	2	1	0	0	7	1112	158	35	49	F6WK59	
ENSMUST00000144477	ENSMUSG00000020388	11	54054928	54069014	-1	6	0	5	0	0	0	1	0	0	0	0	A8Y5C3	
ENSMUST00000144478						0	0	4	1	0	0	3	35	4	0	24		
ENSMUST00000144479	ENSMUSG00000045761	17	71673261	71729669	1	25	12	63	48	38	22	1	0	1	0	0	F6YU21	
ENSMUST00000144480	ENSMUSG00000038936	1	179668210	179687189	1	1	0	0	0	0	0	1	0	2	1	0	F6S0R8	
ENSMUST00000144481						0	0	0	0	0	17	0	0	0	0	0		
ENSMUST00000144482	ENSMUSG00000039375	8	54629055	54887184	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJE2	
ENSMUST00000144483	ENSMUSG00000031256	X	134059187	134086819	1	0	0	0	5	0	0	1	0	15	3	16	A2AEJ8	
ENSMUST00000144484	ENSMUSG00000031922	9	13807792	13827107	-1	13	2	2	184	10	5	5	7	15	9	9	D6RDE1	
ENSMUST00000144485	ENSMUSG00000067571	19	10978307	10993250	-1	0	3	2	0	3	3	0	0	0	0	0	D3YZF5	
ENSMUST00000144486						4	0	5	1	0	2	17	26	7	2	32		
ENSMUST00000144488	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	5	6	0	0	0	0	0	0	D6RGP5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144489						0	0	0	0	0	0	30	0	0	0	0		
ENSMUST00000144490						0	1	3	3	4	3	16	17	17	0	19		
ENSMUST00000144491						34	22	66	0	23	19	0	0	0	0	0		
ENSMUST00000144492						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000144493						2	0	0	0	2	0	19	107	70	105	50		
ENSMUST00000144494						0	0	0	107	0	1	0	0	0	0	0		
ENSMUST00000144495	ENSMUSG00000035495	4	46114746	46138694	-1	0	0	0	0	0	0	0	3	3	0	2	B1AWH2	
ENSMUST00000144496	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z011	
ENSMUST00000144497						1	3	9	17	0	1	0	0	0	0	0		
ENSMUST00000144498	ENSMUSG00000022292	15	37923952	37961318	-1	0	0	0	0	1	0	3	24	38	32	20	D6RFP5	
ENSMUST00000144499						0	3	10	5	5	1	0	5	0	0	0		
ENSMUST00000144500						4	4	10	4	10	5	1	3	2	0	3		
ENSMUST00000144502	ENSMUSG00000034156	11	87760541	87785928	1	0	4	0	0	1	0	4	1	1	1	0	F7CD74	
ENSMUST00000144503						3	0	0	1	3	0	0	0	0	0	0		
ENSMUST00000144504						0	9	22	0	0	0	0	1	0	0	0		
ENSMUST00000144505						13	20	40	19	24	11	0	0	0	0	0		
ENSMUST00000144506						3	1	1	0	0	0	22	192	48	6	37		
ENSMUST00000144507						7	2	11	7	8	7	0	0	0	0	0		
ENSMUST00000144508	ENSMUSG00000013921	7	30291672	30308367	1	0	3	8	32	4	4	0	0	0	0	0	D3Z2W8	
ENSMUST00000144509	ENSMUSG00000038244	7	112225856	112355194	1	0	0	0	0	0	3	0	0	0	0	0	F6WY65	
ENSMUST00000144511	ENSMUSG00000000142	11	108920349	108950783	1	3	1	10	98	6	0	0	0	0	0	0	A2ABQ7	
ENSMUST00000144512	ENSMUSG00000050812	4	58798911	58912749	-1	0	0	0	0	0	0	0	1	7	0	0	A2ALV8	
ENSMUST00000144513	ENSMUSG00000022779	16	16870736	16892990	1	0	0	0	0	2	0	0	0	0	4	0	D3Z2F4	
ENSMUST00000144514	ENSMUSG00000063015	5	93181933	93206495	-1	0	2	1	222	0	2	1	3	9	0	5	D3Z602	
ENSMUST00000144515	ENSMUSG00000002205	7	44748413	44777515	1	0	0	0	0	1	0	0	9	7	0	18	D3Z2U5	
ENSMUST00000144516						2	0	8	5	4	1	124	137	263	23	313		
ENSMUST00000144517						0	1	1	2	2	0	0	0	0	0	0		
ENSMUST00000144518						2	2	0	1	0	1	0	0	1	0	2		
ENSMUST00000144519						3	1	12	6	5	0	2	1	3	0	4		
ENSMUST00000144520	ENSMUSG00000006476	2	25054355	25062881	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWK2	
ENSMUST00000144521	ENSMUSG00000063663	X	108737016	108834372	-1	8	3	9	6	0	3	8	142	170	46	0	G3UXF9	
ENSMUST00000144522						13	5	10	16	17	7	0	0	0	0	0		
ENSMUST00000144523						9	0	0	0	0	5	16	103	28	21	0		
ENSMUST00000144524	ENSMUSG00000030341	6	125349362	125362484	1	0	0	4	8	0	4	26	185	36	0	66	F7A4X5	
ENSMUST00000144525						0	2	0	2	0	0	14	89	12	32	28		
ENSMUST00000144526	ENSMUSG00000035621	10	80148272	80158368	1	0	2	0	0	0	0	10	22	5	0	3	D3YZI7	
ENSMUST00000144527						3	0	21	1	0	4	5	6	3	0	3		
ENSMUST00000144528	ENSMUSG00000024810	19	29925114	29960718	1	2	1	0	0	1	0	0	0	0	2	0	D3Z6T7	
ENSMUST00000144529	ENSMUSG00000033880	11	118392751	118402092	-1	4	6	12	2	0	0	0	24	0	37	0	F6VRP8	
ENSMUST00000144530	ENSMUSG00000039671	2	165784152	165899016	-1	0	0	0	1	0	0	0	0	0	0	0	A2A479	
ENSMUST00000144531	ENSMUSG00000059278	11	69395487	69396680	1	0	1	0	24	0	0	104	130	69	368	40		Q9D2U5
ENSMUST00000144532						5	4	48	6	5	1	0	0	1	1	0		
ENSMUST00000144533	ENSMUSG00000024122	17	24073680	24150924	-1	0	0	2	0	0	0	0	0	0	0	0	F2Z4A5	
ENSMUST00000144534						3	5	4	15	5	0	20	189	12	0	27		
ENSMUST00000144535						1	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000144536						2	1	5	1	2	1	0	2	1	3	1		
ENSMUST00000144537	ENSMUSG00000054693	9	70678997	70780229	1	1	0	0	73	3	0	3	0	4	0	6	D3Z1E6	
ENSMUST00000144538						60	66	196	51	57	25	1	8	3	0	8		
ENSMUST00000144540						6	6	9	0	5	2	95	970	181	39	189		
ENSMUST00000144543						0	0	4	2	0	0	0	0	3	1	2		
ENSMUST00000144544	ENSMUSG00000079277	2	74711927	74748442	1	0	0	0	18	1	0	0	0	0	0	0	G3UZU1	
ENSMUST00000144547	ENSMUSG00000020262	10	77290726	77418270	-1	0	0	0	0	0	0	0	0	0	0	0	D6RGS1	
ENSMUST00000144548	ENSMUSG00000059149	1	132022806	132068062	-1	0	0	0	0	0	0	0	0	0	0	0		Q6PDC8
ENSMUST00000144549	ENSMUSG00000032841	2	101714285	101883027	-1	0	1	0	1	4	0	0	0	0	0	0	B0R103	
ENSMUST00000144550	ENSMUSG00000001729	12	112653821	112674884	-1	10	9	22	8	13	6	44	15	50	3	42	D3YXX3	
ENSMUST00000144551						0	0	18	0	0	2	0	0	0	9	0		
ENSMUST00000144552						2	0	6	5	5	0	5	19	1	18	0		
ENSMUST00000144553						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000144554						2	1	5	0	3	0	0	0	0	0	0		
ENSMUST00000144555						30	23	41	31	48	23	5	11	0	0	14		
ENSMUST00000144557						7	5	12	20	8	4	0	0	0	0	3		
ENSMUST00000144558	ENSMUSG00000061535	5	43515538	43618803	1	1	0	1	0	2	0	0	0	0	0	1	D3YZZ1	
ENSMUST00000144559	ENSMUSG00000074812	2	128591209	128598464	1	8	7	24	5	10	3	0	0	0	0	0	I6XKQ3	
ENSMUST00000144560						7	2	6	0	6	4	0	5	0	0	6		
ENSMUST00000144561						0	0	0	0	0	0	0	0	0	15	0		
ENSMUST00000144562						0	0	2	31	2	0	0	0	0	2	0		
ENSMUST00000144563						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144565						5	1	5	4	0	3	3	2	5	0	2		
ENSMUST00000144566						1	0	0	47	0	4	0	0	0	0	0		
ENSMUST00000144569						8	3	12	2	7	0	139	836	255	55	234		
ENSMUST00000144571						5	0	4	300	8	3	110	93	44	53	21		
ENSMUST00000144572						15	16	31	75	22	6	0	0	0	0	13		
ENSMUST00000144573						7	8	17	30	10	7	0	0	0	0	3		
ENSMUST00000144574	ENSMUSG00000029176	5	52834012	52867797	1	2	2	0	0	0	0	150	617	283	223	185	D6RDT6	
ENSMUST00000144576	ENSMUSG00000062963	1	171288563	171295024	-1	0	2	3	6	0	4	71	99	23	14	6	M0QWS4	
ENSMUST00000144577	ENSMUSG00000006392	4	118409337	118415782	1	1	0	1	117	0	2	29	39	33	27	25	A2A9C6	
ENSMUST00000144578	ENSMUSG00000060397	7	12881177	12893422	1	15	21	15	21	11	14	9	20	14	6	9	Q8BGV5	
ENSMUST00000144580						5	2	11	3	3	3	13	43	6	2	13		
ENSMUST00000144581						0	3	2	1	3	1	0	18	6	2	12		
ENSMUST00000144582	ENSMUSG00000032044	9	35267865	35277731	1	3	2	3	2	5	0	0	0	0	0	0	F6W6X9	
ENSMUST00000144583						1	3	66	13	0	1	8	18	30	3	27		
ENSMUST00000144584	ENSMUSG00000026650	2	3409043	3422648	-1	0	2	1	0	0	0	0	0	0	0	1	A2AJG4	
ENSMUST00000144585	ENSMUSG00000036529	15	89288236	89315311	-1	0	16	11	10	41	0	2266	1084	1691	64	1374		Q6ZPE2
ENSMUST00000144586						11	20	40	0	31	0	2	17	23	10	45		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144587						45	32	250	49	45	23	0	1	2	1	1		
ENSMUST00000144588						7	3	10	224	9	5	21	43	41	0	53		
ENSMUST00000144589						1	3	7	5	1	1	0	2	0	0	4		
ENSMUST00000144590						8	0	0	0	0	11	0	0	3	0	0		
ENSMUST00000144592						5	6	14	11	6	0	0	0	0	0	0		
ENSMUST00000144593	ENSMUSG00000025909	1	8361475	9299878	-1	15	0	85	12	9	6	0	1	0	0	0	D6RJM3	
ENSMUST00000144595						1	0	1	0	1	0	0	0	6	0	12		
ENSMUST00000144596	ENSMUSG00000001946	9	37528078	37538319	1	3	0	12	43	0	0	0	0	0	0	0	D3YV70	
ENSMUST00000144597						0	0	0	0	1	0	16	5	7	7	6		
ENSMUST00000144598	ENSMUSG00000044150	X	159526688	159593081	1	2	2	1	1	3	3	0	0	0	0	0	A2AG55	
ENSMUST00000144599						6	2	2	4	1	1	0	1	0	0	2		
ENSMUST00000144600	ENSMUSG00000023092	X	56731787	56793346	1	0	1	1	1	3	1	0	0	0	0	0	A2AEY1	
ENSMUST00000144601						2	1	0	0	0	0	9	20	7	0	10		
ENSMUST00000144602	ENSMUSG00000026156	1	23761753	23849158	1	3	0	5	210	6	3	0	0	0	0	0	D3YY32	
ENSMUST00000144603	ENSMUSG00000029416	5	127595664	127632897	-1	0	5	0	0	2	1	39	0	13	3	21	F7AZ26	
ENSMUST00000144605						29	32	13	19	29	20	0	0	0	0	2		
ENSMUST00000144608						0	0	0	0	0	1	16	73	13	5	5		
ENSMUST00000144609						6	5	2	14	2	1	4	0	2	3	5		
ENSMUST00000144611						1	0	7	4	5	2	0	0	0	0	0		
ENSMUST00000144613						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000144614	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	10	0	0	0	8	0	0	25	D3YUQ9	
ENSMUST00000144615						4	1	7	1	0	3	0	1	3	0	0		
ENSMUST00000144616						1	1	13	5	3	1	2	7	2	0	11		
ENSMUST00000144617	ENSMUSG00000026111	1	37430139	37439124	1	0	0	4	0	0	0	0	23	0	79	0	D3YXX4	
ENSMUST00000144618	ENSMUSG00000032204	9	71110659	71168682	-1	5	3	7	3	2	0	0	0	0	0	0	E9Q8P3	
ENSMUST00000144619	ENSMUSG00000022037	14	65968483	65981548	1	2	1	4	1	4	4	0	0	0	0	0	E9Q2G2	
ENSMUST00000144620	ENSMUSG00000028681	4	117096075	117116101	1	0	21	0	0	39	23	3	7	0	0	4	D6RG83	
ENSMUST00000144621						2	1	3	0	1	1	5	6	7	0	11		
ENSMUST00000144622						0	12	35	0	13	14	0	0	11	0	0		
ENSMUST00000144623	ENSMUSG00000029314	5	100845713	100899102	1	1	0	5	21	0	0	1	0	0	0	4		
ENSMUST00000144624						0	0	6	0	0	0	60	113	0	0	109		
ENSMUST00000144625						18	15	20	9	22	13	0	0	0	0	0		
ENSMUST00000144626						3	1	15	2	3	1	0	0	0	0	1		
ENSMUST00000144627						2	1	1	0	0	0	6	1	0	3	2		
ENSMUST00000144628						2	5	16	6	3	0	3	19	10	0	5		
ENSMUST00000144629	ENSMUSG00000027719	3	37063527	37121930	1	2	0	3	54	11	0	0	0	0	0	0		Q5SUE7
ENSMUST00000144630						0	3	148	26	0	0	6	14	6	0	11		
ENSMUST00000144631						0	0	0	0	0	0	0	17	1	0	0		
ENSMUST00000144632						1	8	9	3	1	3	0	0	0	0	0		
ENSMUST00000144633						3	3	10	3	4	3	4	9	12	0	4		
ENSMUST00000144635						2	0	1	4	3	1	3	0	2	0	5		
ENSMUST00000144636						4	2	2	0	0	1	6	77	11	8	37		
ENSMUST00000144638						2	2	3	3	4	0	119	164	109	19	151		
ENSMUST00000144639						4	3	3	3	3	6	0	0	0	155	0		
ENSMUST00000144640	ENSMUSG00000043670	10	81019589	81025662	-1	1	0	0	10	6	1	0	0	0	0	0	D3Z0Z5	
ENSMUST00000144641						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144642	ENSMUSG00000021156	13	9684836	9765321	-1	2	0	0	2	0	0	0	0	0	0	0	D3Z500	
ENSMUST00000144643						0	0	8	5	0	3	6	47	0	3	11		
ENSMUST00000144644						4	0	5	18	2	0	1	3	1	0	3		
ENSMUST00000144645	ENSMUSG00000026767	2	12347263	12419470	-1	0	5	0	0	0	2	30	0	13	5	6	D6RGU8	
ENSMUST00000144646						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000144647	ENSMUSG00000078440	10	81384428	81391560	1	5	6	13	8	2	2	19	29	17	0	38		Q99LN9
ENSMUST00000144648						4	2	4	6	7	0	0	2	2	0	4		
ENSMUST00000144650						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144652	ENSMUSG00000042133	2	69722545	69754012	1	0	0	2	0	0	0	0	37	0	0	8	A2AR01	
ENSMUST00000144653	ENSMUSG00000022151	15	5185525	5218336	1	5	1	0	9	2	4	0	0	0	0	0	D3Z767	
ENSMUST00000144654						24	15	39	74	32	7	0	0	4	2	5		
ENSMUST00000144656						2	4	3	15	3	3	0	0	0	0	0		
ENSMUST00000144658						4	4	0	2	0	0	0	15	13	1	11		
ENSMUST00000144659						2	2	0	4	1	2	0	0	2	0	2		
ENSMUST00000144660	ENSMUSG00000099913	1	53325507	53352667	-1	3	0	10	5	0	0	3	3	3	0	0		Q8BFS9
ENSMUST00000144662	ENSMUSG00000024691	19	12545740	12589768	1	0	0	0	0	14	6	0	14	0	0	0		Q9D2L9
ENSMUST00000144663						22	30	48	17	28	16	8	38	28	7	33		
ENSMUST00000144664						11	12	17	21	12	4	0	3	1	1	6		
ENSMUST00000144665						9	5	10	6	8	4	0	0	0	0	0		
ENSMUST00000144666						26	25	49	34	35	14	13	21	14	0	25		
ENSMUST00000144667						2	0	0	0	1	2	473	881	209	77	344		
ENSMUST00000144668	ENSMUSG00000012117	4	133969028	134000918	-1	11	0	0	12	7	0	913	1769	1015	92	446		Q99KU1
ENSMUST00000144669						0	1	0	2	1	3	10	31	3	0	4		
ENSMUST00000144670						3	4	4	5	10	2	0	0	0	0	0		
ENSMUST00000144671						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144672						3	2	2	3	2	7	2	3	2	0	0		
ENSMUST00000144673	ENSMUSG00000093574	5	32737230	32827109	-1	0	0	0	0	0	0	0	0	0	19	17	F6TVX7	
ENSMUST00000144674						15	9	63	15	14	3	0	83	17	3	27		
ENSMUST00000144675	ENSMUSG00000003813	8	84834019	84840665	-1	4	1	6	1	0	1	29	14	0	5	10	F6YL88	
ENSMUST00000144676	ENSMUSG00000023088	16	14361558	14475737	1	4	0	7	0	1	0	0	0	0	0	0	D3Z407	
ENSMUST00000144677						20	24	16	12	22	22	0	0	0	0	0		
ENSMUST00000144678						392	274	2337	535	473	225	12	30	26	5	27		
ENSMUST00000144679	ENSMUSG00000029445	5	123171807	123182727	-1	1	0	3	5	0	1	0	0	0	3	0	F6X9Z6	
ENSMUST00000144681	ENSMUSG00000034659	19	10870660	10882001	-1	0	0	2	5	3	2	3	0	0	0	0	D3Z3Z2	
ENSMUST00000144682						1	0	2	7	3	1	0	7	3	0	2		
ENSMUST00000144683						4	5	7	35	6	5	0	7	2	0	2		
ENSMUST00000144684						3	1	2	91	7	7	0	0	0	0	0		
ENSMUST00000144685						2	3	0	0	0	1	0	6	4	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144686	ENSMUSG00000074646	2	155973279	156007977	-1	0	0	0	0	0	0	0	0	0	0	0	A3KGK0	
ENSMUST00000144687						7	4	13	5	4	5	12	29	24	0	33		
ENSMUST00000144688						4	1	3	0	0	1	0	0	0	0	1		
ENSMUST00000144691	ENSMUSG00000002489	16	89787111	89980080	-1	0	0	0	0	0	0	0	0	0	0	0	J3QMH1	
ENSMUST00000144692						11	1	6	2	7	4	0	0	2	0	1		
ENSMUST00000144693						0	0	0	0	4	0	81	451	129	70	170		
ENSMUST00000144694	ENSMUSG00000018417	1	51749765	51916071	-1	1	4	10	3	6	5	0	0	0	0	0	D3YV80	
ENSMUST00000144695	ENSMUSG00000073007	X	107792590	107872909	1	0	0	0	0	0	0	0	0	0	0	0	B1ATX4	
ENSMUST00000144696						49	35	48	25	46	22	5	29	18	11	21		
ENSMUST00000144697						5	5	2	2	2	0	0	2	0	0	0		
ENSMUST00000144698						8	6	5	12	2	0	2	0	0	8	0		
ENSMUST00000144699	ENSMUSG00000069769	11	88339382	88718513	-1	0	0	0	17	0	0	0	5	6	2	0	B1AT10	
ENSMUST00000144700	ENSMUSG00000037552	7	28359604	28372599	-1	10	0	0	340	14	3	34	0	33	0	58		
ENSMUST00000144701	ENSMUSG00000018474	11	69343273	69369406	-1	0	0	2	0	1	1	4	0	0	1	4	B0QZH8	
ENSMUST00000144706						2	2	11	7	8	5	0	11	0	0	0		
ENSMUST00000144707						3	2	2	36	5	2	8	0	0	0	0		
ENSMUST00000144708						0	0	0	0	0	0	0	7	2	0	4		
ENSMUST00000144709						0	0	0	0	0	0	1	0	2	0	0		
ENSMUST00000144710	ENSMUSG00000042894	2	89974709	89978712	1	4	0	0	1	3	0	0	0	0	0	0	A2AWB5	
ENSMUST00000144711	ENSMUSG00000039375	8	54629055	54887184	-1	2	2	0	0	0	0	0	0	0	0	0	G3UVU7	
ENSMUST00000144712						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000144713	ENSMUSG00000060961	5	88886818	89239653	1	1	0	2	1	2	0	0	0	0	0	0	D3Z7I7	
ENSMUST00000144714						0	2	8	10	6	6	158	513	348	10	515		
ENSMUST00000144715						3	0	4	8	4	3	4	2	7	1	11		
ENSMUST00000144716						9	7	21	44	4	0	9	31	4	8	0		
ENSMUST00000144717						2	1	1	1	3	1	0	0	0	0	0		
ENSMUST00000144720						0	0	0	1	10	1	0	3	4	0	3		
ENSMUST00000144721	ENSMUSG00000049728	7	127863047	127876828	-1	0	1	9	7	1	0	0	0	0	0	0	D3Z404	
ENSMUST00000144722						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000144723						6	8	10	8	11	8	3	8	0	0	4		
ENSMUST00000144724	ENSMUSG00000061984	11	73814118	73816880	-1	1	4	0	4	1	1	0	0	0	0	0	A7DTG5	
ENSMUST00000144725	ENSMUSG00000020437	11	6506548	6520965	-1	5	0	5	6	14	10	375	503	320	0	312	D6RHL4	
ENSMUST00000144726						3	5	8	3	2	1	7	12	9	0	28		
ENSMUST00000144727						5	4	3	6	6	4	0	0	0	0	0		
ENSMUST00000144729						6	8	4	20	10	11	3	15	13	5	4		
ENSMUST00000144730						8	3	3	36	6	2	0	0	0	0	0		
ENSMUST00000144731	ENSMUSG00000018669	11	96907426	96916496	-1	0	1	0	0	2	0	1	20	9	0	0	A2A6E1	
ENSMUST00000144732						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000144733						2	0	34	7	5	3	0	0	1	0	0		
ENSMUST00000144736						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144737						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000144739	ENSMUSG00000030450	7	56239760	56536518	1	0	17	14	14	5	0	0	0	0	0	0	D6RIQ8	
ENSMUST00000144740						25	21	102	24	18	15	0	0	2	0	0		
ENSMUST00000144741						0	0	2	0	0	0	0	6	3	10	6		
ENSMUST00000144742	ENSMUSG00000029177	5	30666777	30674830	1	2	0	0	2	2	0	68	246	64	24	58		O35216
ENSMUST00000144743						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144744						11	8	16	58	9	7	0	8	5	0	5		
ENSMUST00000144746	ENSMUSG00000027900	3	106547798	106575890	1	0	1	0	0	0	0	0	0	0	29	7	D3YYJ9	
ENSMUST00000144748						21	13	16	0	23	12	5	63	38	22	68		
ENSMUST00000144749						2	2	2	49	8	1	0	7	8	0	20		
ENSMUST00000144751						0	5	23	10	16	19	30	69	62	3	144		
ENSMUST00000144752						4	0	13	2	6	4	0	0	0	0	0		
ENSMUST00000144753	ENSMUSG00000079481	X	101849385	102092055	1	2	0	2	4	0	0	0	0	0	0	0	A0A0G2JFH6	
ENSMUST00000144754						25	19	0	0	13	12	0	0	0	0	0		
ENSMUST00000144755						10	2	3	10	10	1	0	0	0	0	0		
ENSMUST00000144756						10	5	21	9	13	9	0	1	1	0	4		
ENSMUST00000144758						2	3	1	7	3	0	0	3	8	0	2		
ENSMUST00000144759	ENSMUSG00000025616	16	87454703	87483517	1	0	0	0	0	0	0	17	451	124	132	135	D6RHQ6	
ENSMUST00000144760	ENSMUSG00000100846	1	65100619	65119558	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR76	
ENSMUST00000144762	ENSMUSG00000031887	8	105258286	105264609	-1	1	0	3	54	0	2	17	0	0	6	8	D6RCI0	
ENSMUST00000144763						2	1	3	0	3	0	0	0	0	0	0		
ENSMUST00000144764	ENSMUSG00000028199	3	154596711	154623182	1	0	0	0	0	0	0	0	0	0	0	0	D3Z2X0	
ENSMUST00000144766						47	36	264	85	35	14	99	669	159	36	264		
ENSMUST00000144767						0	0	3	0	1	3	0	10	9	0	4		
ENSMUST00000144768	ENSMUSG00000032519	9	120110374	120124504	1	1	0	0	0	0	0	76	50	55	6	32	D6RCI6	
ENSMUST00000144769						3	3	7	9	7	4	0	0	0	0	0		
ENSMUST00000144771						3	7	19	0	3	0	0	2	0	0	10		
ENSMUST00000144772	ENSMUSG00000042345	17	31207873	31242202	1	1	2	8	0	2	0	3	0	0	0	0	D6RCF9	
ENSMUST00000144773						9	9	23	13	35	7	0	0	0	0	0		
ENSMUST00000144775						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000144776	ENSMUSG00000029993	6	87009236	87028461	1	2	3	0	2	2	2	19	25	13	26	7	D3Z285	
ENSMUST00000144777						4	0	12	39	4	2	24	86	27	0	30		
ENSMUST00000144778						0	0	0	0	0	0	7	45	0	0	41		
ENSMUST00000144779						2	8	8	5	5	7	34	52	32	4	42		
ENSMUST00000144780	ENSMUSG00000027198	2	93661028	93822568	-1	1	1	2	2	1	0	0	0	0	0	0	B0QZZ7	
ENSMUST00000144781	ENSMUSG00000035601	4	45297127	45316131	1	1	4	8	0	3	2	3	6	12	27	11	Z4YLM5	
ENSMUST00000144782						0	0	101	66	0	20	0	20	0	0	0		
ENSMUST00000144784						40	41	63	46	45	31	45	116	56	17	101		
ENSMUST00000144786						0	0	1	8	0	0	0	0	0	2	0		
ENSMUST00000144787						5	5	10	3	12	4	0	0	0	0	0		
ENSMUST00000144788	ENSMUSG00000024663	19	10001669	10038380	1	6	5	8	7	3	3	0	7	0	0	0		Q8VDV3
ENSMUST00000144789						6	4	3	0	0	0	0	0	0	0	0		
ENSMUST00000144790	ENSMUSG00000022433	15	79417856	79443919	-1	0	0	6	2	2	1	8	5	4	0	15	A8Y2Z9	
ENSMUST00000144791						2	7	3	28	6	5	16	226	92	23	172		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144792						14	11	32	21	25	3	2	3	2	0	11		
ENSMUST00000144793						23	11	16	14	28	6	1	1	0	0	0		
ENSMUST00000144794	ENSMUSG00000050335	14	47367751	47386160	1	0	0	2	0	1	3	11	42	7	2	15	D3YVT4	
ENSMUST00000144795	ENSMUSG00000030590	7	29152511	29156234	-1	0	2	0	0	0	3	0	0	3	0	0	F6S0H0	
ENSMUST00000144797	ENSMUSG00000039543	14	20394190	20452226	-1	0	9	0	0	4	18	0	0	0	0	0	D3Z4F0	
ENSMUST00000144798						0	0	4	4	0	3	0	0	0	0	0		
ENSMUST00000144799						0	0	0	2	0	3	0	20	3	4	3		
ENSMUST00000144800						4	6	13	0	0	7	0	0	0	0	0		
ENSMUST00000144801						4	4	0	3	9	2	0	0	0	0	0		
ENSMUST00000144802						0	0	0	3	3	3	0	0	0	0	0		
ENSMUST00000144804						10	5	10	48	11	17	0	2	0	0	0		
ENSMUST00000144805						16	7	45	14	12	7	1	0	2	2	0		
ENSMUST00000144806	ENSMUSG00000038280	10	42583822	42702459	1	0	1	0	0	0	1	0	0	46	9	25	D3Z4W7	
ENSMUST00000144807						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000144808	ENSMUSG00000030732	7	100006404	100034728	1	0	0	0	0	0	1	1	0	0	0	0	F6WCT1	
ENSMUST00000144809						0	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000144810	ENSMUSG00000027829	3	65946151	65958249	-1	0	2	0	0	0	1	17	55	46	3	33	F7BER3	
ENSMUST00000144811						0	4	0	107	5	5	0	5	10	7	10		
ENSMUST00000144812						8	4	14	13	6	3	13	69	35	8	48		
ENSMUST00000144813						4	0	0	33	2	3	10	12	9	3	18		
ENSMUST00000144814						3	2	9	7	0	0	0	0	0	0	0		
ENSMUST00000144815						0	2	0	0	0	4	2	3	0	0	1		
ENSMUST00000144816						0	2	14	0	4	0	86	362	169	17	184		
ENSMUST00000144817	ENSMUSG00000075267	2	76648476	76658556	1	0	0	0	2	4	4	0	2	0	0	0	B0R0L9	
ENSMUST00000144819						11	1	12	10	9	8	26	95	50	13	56		
ENSMUST00000144820						0	0	1	0	1	0	0	0	1	0	0		
ENSMUST00000144821						0	0	0	0	0	0	0	0	0	0	7		
ENSMUST00000144823						1	0	3	0	5	0	0	3	2	0	6		
ENSMUST00000144824						22	12	41	20	16	8	3	15	25	0	22		
ENSMUST00000144825	ENSMUSG00000034813	10	119454034	120087261	1	0	0	0	0	0	0	0	0	0	0	0		Q925T6
ENSMUST00000144826	ENSMUSG00000023087	3	51224447	51251644	1	9369	9605	5376	6102	8031	3455	4217	13675	8253	2846	5786		O35710
ENSMUST00000144827	ENSMUSG00000044083	2	153780879	153844752	1	14	13	21	17	23	7	0	4	5	0	6		Q8C9R9
ENSMUST00000144829						5	1	12	6	10	2	0	1	0	0	0		
ENSMUST00000144830						4	2	5	0	4	1	0	0	2	4	4		
ENSMUST00000144832						1	4	3	0	5	1	0	0	0	0	0		
ENSMUST00000144833						8	1	22	6	5	2	0	0	0	0	0		
ENSMUST00000144834	ENSMUSG00000018362	11	106988629	106999541	-1	11	6	54	26	7	3	5	3	4	7	0	A2A600	
ENSMUST00000144835						0	1	0	0	0	1	38	217	36	42	60		
ENSMUST00000144836						0	0	3	1	2	3	0	0	0	0	0		
ENSMUST00000144837						9	6	20	147	15	3	0	0	0	0	0		
ENSMUST00000144838						33	31	64	50	35	11	0	0	1	1	1		
ENSMUST00000144839						0	0	0	13	0	0	0	0	0	0	0		
ENSMUST00000144840						0	0	1	4	1	0	2	3	0	17	6		
ENSMUST00000144841						6	5	5	6	2	2	0	0	0	0	0		
ENSMUST00000144842						2	1	10	8	2	7	0	0	0	0	0		
ENSMUST00000144843	ENSMUSG00000036087	5	72914304	72978829	1	0	0	0	10	0	0	13	388	489	56	370		Q8CI08
ENSMUST00000144845	ENSMUSG00000027447	2	148871722	148875692	-1	0	3	4	0	0	0	0	18	229	706	129	A2APX3	
ENSMUST00000144846						6	3	8	8	7	1	4	11	13	1	16		
ENSMUST00000144847	ENSMUSG00000074582	2	166805588	166898052	1	2	0	16	0	3	5	3	0	23	0	22	F6YCJ0	
ENSMUST00000144848						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144850	ENSMUSG00000043510	5	110829070	110839777	-1	0	0	0	0	0	0	0	14	0	0	0	F6WN43	
ENSMUST00000144851	ENSMUSG00000028889	4	124850679	124855242	1	3	5	15	29	8	2	6	19	12	6	6	G8JL83	
ENSMUST00000144856	ENSMUSG00000089917	2	181569149	181584892	-1	0	0	0	0	0	0	46	0	0	0	0	F6V4H6	
ENSMUST00000144857						4	3	1	32	9	2	9	16	11	1	15		
ENSMUST00000144858	ENSMUSG00000035642	7	97550331	97579497	-1	2	0	2	7	2	0	0	0	0	1	0	Q8CF11	
ENSMUST00000144859						2	0	2	0	0	0	421	1457	657	1545	390		
ENSMUST00000144860						1	1	0	0	1	0	0	1	0	0	0		
ENSMUST00000144861	ENSMUSG00000071322	17	7324646	7345974	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3T8	
ENSMUST00000144862						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144863	ENSMUSG00000085272	7	4965260	4971168	-1	22	17	42	21	30	13	0	1	0	1	0		P0C5K0
ENSMUST00000144864						4	4	10	0	6	0	0	2	0	0	74		
ENSMUST00000144865	ENSMUSG00000027466	2	152316334	152332653	-1	2	1	3	5	2	0	6	6	11	0	20	F6VII1	
ENSMUST00000144866						0	1	2	2	1	0	0	16	0	0	4		
ENSMUST00000144868						0	0	0	116	5	4	5	302	39	3	74		
ENSMUST00000144869						1	0	0	75	0	0	0	0	0	0	0		
ENSMUST00000144871						5	3	2	1	3	0	1	2	0	0	7		
ENSMUST00000144872						16	8	33	10	13	7	0	0	0	1	0		
ENSMUST00000144873						93	40	246	123	48	20	0	6	1	0	0		
ENSMUST00000144874	ENSMUSG00000033021	1	75435930	75443179	1	0	0	2	0	6	4	0	6	7	6	11	D3Z2T0	
ENSMUST00000144877						6	0	6	3	1	1	33	160	61	56	82		
ENSMUST00000144878	ENSMUSG00000034110	5	130144861	130155806	1	2	1	12	46	4	4	0	3	1	1	0		
ENSMUST00000144879						10	6	10	2	2	3	1	0	0	0	2		
ENSMUST00000144880						1	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000144881						16	18	74	22	17	18	4	21	11	0	14		
ENSMUST00000144882						0	0	6	2	4	3	0	0	0	0	0		
ENSMUST00000144883	ENSMUSG00000003068	10	80115803	80130682	1	18	16	50	63	15	11	454	1025	379	35	465		Q9WTK7
ENSMUST00000144884						0	0	2	2	3	0	0	0	0	0	0		
ENSMUST00000144885						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000144886						16	28	60	37	22	14	3	1	5	1	9		
ENSMUST00000144887						10	1	10	6	3	3	0	0	0	0	0		
ENSMUST00000144888						2	1	5	0	2	2	0	0	0	0	1		
ENSMUST00000144889						2	1	10	17	0	6	0	0	0	0	0		
ENSMUST00000144890						5	0	0	17	13	4	72	104	0	0	57		
ENSMUST00000144891						3	2	13	3	5	5	0	0	9	0	8		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144892	ENSMUSG00000075270	2	75989141	76338774	-1	26	14	69	299	19	14	0	14	1	1	0	F6SXR7	
ENSMUST00000144893						0	4	2	32	7	6	5	7	22	6	7		
ENSMUST00000144894						5	2	9	2	7	2	0	0	0	0	0		
ENSMUST00000144895						28	27	85	28	26	13	3	4	11	0	23		
ENSMUST00000144897	ENSMUSG00000059772	7	126689468	126695784	-1	288	240	649	167	225	103	32	82	36	20	38		Q8BX32
ENSMUST00000144898						0	1	0	1	0	0	0	0	2	0	4		
ENSMUST00000144899						2	0	1	3	2	3	1	0	0	0	0		
ENSMUST00000144900	ENSMUSG00000000134	X	7762560	7775202	1	0	0	0	0	2	0	14	2	9	0	17	A2AEW2	
ENSMUST00000144901						3	2	9	0	2	2	4	26	14	10	22		
ENSMUST00000144902	ENSMUSG00000020282	11	32209585	32222300	-1	0	0	0	0	0	0	0	0	0	0	0	A2AVE5	
ENSMUST00000144903						4	3	2	10	1	2	2	6	11	2	11		
ENSMUST00000144904						3	2	5	2	9	5	3	0	3	2	1		
ENSMUST00000144905						0	0	2	12	0	1	0	0	11	0	4		
ENSMUST00000144906						1	3	15	4	7	0	0	0	0	0	0		
ENSMUST00000144907						1	3	1	5	2	1	0	0	0	0	0		
ENSMUST00000144908						0	0	0	0	2	5	0	0	0	0	0		
ENSMUST00000144909						23	17	68	0	21	9	778	423	874	65	593		
ENSMUST00000144910	ENSMUSG00000047446	12	40005447	40038025	-1	0	0	0	0	0	0	0	5	0	22	0	G3UVX1	
ENSMUST00000144911	ENSMUSG00000035969	4	43381979	43427088	1	0	0	0	11	0	1	0	0	0	0	0	B0R001	
ENSMUST00000144912						0	0	8	2	1	3	0	0	0	0	0		
ENSMUST00000144913						3	0	5	0	1	1	6	28	17	0	30		
ENSMUST00000144914	ENSMUSG00000084902	14	13814949	13914478	-1	6	6	14	6	8	2	0	0	0	0	0	D3Z1Y0	
ENSMUST00000144916	ENSMUSG00000026692	1	162793188	162813972	-1	3	5	0	0	0	2	0	0	0	0	0	D3Z2C5	
ENSMUST00000144917						2	0	0	0	0	3	30	19193	36	13	42		
ENSMUST00000144918						8	2	9	6	7	7	15	63	16	3	16		
ENSMUST00000144919						0	5	0	0	0	0	0	7	0	0	0		
ENSMUST00000144920	ENSMUSG00000030282	6	142756686	142775714	1	4	0	15	20	7	5	7	25	38	10	28		
ENSMUST00000144921						2	4	8	10	4	5	8	5	5	0	17		
ENSMUST00000144923						3	0	4	0	0	0	1	12	6	10	2		
ENSMUST00000144924						0	0	5	0	0	0	0	0	5	18	0		
ENSMUST00000144925						1	0	3	4	2	0	0	0	0	0	0		
ENSMUST00000144927						5	0	13	44	4	0	10	23	9	5	6		
ENSMUST00000144929						8	6	13	0	16	22	0	0	0	0	0		
ENSMUST00000144930						0	0	0	0	0	0	0	19	0	0	0		
ENSMUST00000144931						1	2	3	38	2	5	0	0	0	0	0		
ENSMUST00000144934						10	0	0	42	3	2	0	2	0	2	0		
ENSMUST00000144935	ENSMUSG00000000318	11	70156197	70170834	1	0	0	0	0	0	0	0	8	0	0	7	A2CF65	
ENSMUST00000144936	ENSMUSG00000079020	15	73577424	73645762	-1	0	0	11	8	8	0	101	308	108	44	40	F7BEQ1	
ENSMUST00000144938						4	0	0	1	2	3	0	0	0	2	0		
ENSMUST00000144939						3	0	1	0	2	0	0	0	0	9	0		
ENSMUST00000144940	ENSMUSG00000040447	11	72451638	72489904	-1	1	0	0	0	0	0	0	0	0	0	3	F6WK70	
ENSMUST00000144941						0	0	0	0	0	0	2	0	1	1	3		
ENSMUST00000144942	ENSMUSG00000020538	11	60199089	60222581	-1	3	2	0	69	0	4	397	0	377	0	144	A0A0A0MQK3	
ENSMUST00000144943						0	4	9	1	4	1	0	0	0	0	0		
ENSMUST00000144944						0	0	0	0	2	0	0	10	2	0	14		
ENSMUST00000144945						25	17	46	12	25	12	0	3	6	1	0		
ENSMUST00000144946						0	3	3	4	0	0	51	1126	91	16	263		
ENSMUST00000144947	ENSMUSG00000004221	X	74393290	74453854	1	2	0	0	2	0	1	0	0	0	0	2	A3KG39	
ENSMUST00000144948						2	1	4	0	0	1	0	1	2	1	0		
ENSMUST00000144949						6	3	3	0	12	3	0	0	0	0	0		
ENSMUST00000144950	ENSMUSG00000028035	3	152178511	152210302	-1	0	0	0	3	2	0	0	0	0	8	0		Q9D832
ENSMUST00000144951						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144953						2	1	9	5	1	2	0	13	7	2	7		
ENSMUST00000144954	ENSMUSG00000030346	6	126923050	126939587	-1	0	0	0	1	0	0	0	0	6	1	0	D3Z7I5	
ENSMUST00000144955	ENSMUSG00000023987	17	47726842	47734482	1	0	2	8	1	2	1	0	0	0	0	0	D3YZ92	
ENSMUST00000144956	ENSMUSG00000074364	7	15946977	15967567	-1	0	0	0	0	0	0	0	0	1	1	15	D3Z7U7	
ENSMUST00000144957	ENSMUSG00000026723	2	13509014	13544668	-1	0	0	0	0	0	0	3	3	10	22	0	A0A0A6YWY7	
ENSMUST00000144958						2	2	2	5	6	1	3	42	10	34	26		
ENSMUST00000144959	ENSMUSG00000034813	10	119454034	120087261	1	0	0	0	0	0	0	0	0	0	0	0	D3Z6T4	
ENSMUST00000144960	ENSMUSG00000087279	11	70615848	70616890	1	0	1	0	0	0	2	0	0	0	0	1	J3QJW4	
ENSMUST00000144961						2	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000144962						4	3	8	10	0	0	36	114	42	0	34		
ENSMUST00000144963	ENSMUSG00000026972	2	24925352	24935252	-1	0	0	0	8	6	0	29	40	0	0	0	D6RDR8	
ENSMUST00000144964						22	16	68	72	36	24	90	416	91	37	189		
ENSMUST00000144965	ENSMUSG00000039137	4	63414910	63495991	-1	3	0	3	3	6	5	0	0	0	0	0	F6RBK9	
ENSMUST00000144966						0	0	2	0	0	0	0	0	2	0	0		
ENSMUST00000144967	ENSMUSG00000048271	5	28317121	28419239	1	2	0	0	0	2	2	0	2	37	0	31	F6RNF9	
ENSMUST00000144968						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000144969						31	18	72	24	47	18	1	1	1	1	3		
ENSMUST00000144970						5	4	14	12	12	6	8	12	9	0	13		
ENSMUST00000144971	ENSMUSG00000038072	5	25221904	25265918	1	1	1	3	2	4	0	0	0	1	0	0	D3YUC2	
ENSMUST00000144972						3	3	0	0	3	2	0	1	0	0	5		
ENSMUST00000144973						0	37	472	34	5	12	1	4	0	1	1		
ENSMUST00000144976	ENSMUSG00000030269	6	113237843	113281392	1	0	0	0	0	0	0	29	29	14	4	0	F6YA17	
ENSMUST00000144977						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144978						2	0	3	0	0	3	0	36	76	169	45		
ENSMUST00000144980						2	0	1	2	1	1	0	6	4	0	2		
ENSMUST00000144982						0	0	5	2	0	2	0	2	0	6	2		
ENSMUST00000144983						0	3	1	1	1	0	0	0	0	0	0		
ENSMUST00000144985	ENSMUSG00000028479	4	44034075	44084177	-1	0	0	0	0	2	2	0	0	0	0	0	F6WD11	
ENSMUST00000144986						2	0	18	2	5	0	0	0	0	0	0		
ENSMUST00000144987						19	24	74	19	23	20	0	0	0	0	0		
ENSMUST00000144988	ENSMUSG00000020160	11	18879817	19018985	-1	27	12	31	41	35	17	0	8	0	0	4		Q60954
ENSMUST00000144989						0	0	0	7	1	0	2	0	5	0	11		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000144991						2	5	7	15	3	2	0	0	0	0	0		
ENSMUST00000144992						1	0	2	1	2	0	1	24	5	2	17		
ENSMUST00000144994						1	1	0	0	2	0	0	0	0	0	12		
ENSMUST00000144995						8	7	32	96	26	0	6	27	3	0	15		
ENSMUST00000144996						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000144997	ENSMUSG00000029192	5	36490604	36593276	-1	6	1	15	2	5	2	0	0	0	0	2	D3YWM7	
ENSMUST00000144998	ENSMUSG00000028654	4	122995652	123002485	1	1	1	0	121	0	1	0	0	0	0	0	B1ARS4	
ENSMUST00000144999	ENSMUSG00000036002	4	43032414	43046220	-1	1	0	2	1	4	2	0	3	0	0	6	A0A0G2JDA3	
ENSMUST00000145000						4	0	2	9	5	3	0	9	0	0	3		
ENSMUST00000145001	ENSMUSG00000028104	3	96577872	96594181	-1	0	0	1	0	0	1	27	43	43	8	15	D3YXS1	
ENSMUST00000145002						0	2	4	5	2	3	3	1	0	0	3		
ENSMUST00000145003	ENSMUSG00000047022	12	57230427	57497199	1	0	0	0	0	0	0	0	0	0	4	6	E9Q8Z7	
ENSMUST00000145004						45	26	91	39	35	16	1	3	0	0	4		
ENSMUST00000145005						2	2	5	2	3	0	0	0	0	0	0		
ENSMUST00000145006	ENSMUSG00000050890	4	134275002	134287895	-1	0	0	1	0	3	0	1	4	11	1	6	F6VDY0	
ENSMUST00000145007	ENSMUSG00000051906	8	4102787	4105835	-1	6	0	6	19	0	0	0	0	0	0	0	G3UVT9	
ENSMUST00000145008						37	55	197	86	47	33	28	71	52	3	82		
ENSMUST00000145009						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145010						1	1	3	8	2	0	10	8	0	2	9		
ENSMUST00000145011						1	0	8	0	2	0	0	0	0	0	0		
ENSMUST00000145013	ENSMUSG00000020273	11	23862646	23895253	-1	440	424	991	469	595	286	21	79	68	27	87	F6THF3	
ENSMUST00000145014						2	0	0	0	0	2	0	4	0	0	0		
ENSMUST00000145015						0	0	0	2	0	0	25	104	25	38	23		
ENSMUST00000145016	ENSMUSG00000054814	5	73998453	74068431	-1	1	1	5	0	0	0	0	0	0	0	2	D3YVJ5	
ENSMUST00000145019						0	0	0	2	0	0	8	0	0	0	0		
ENSMUST00000145020	ENSMUSG00000028803	4	135445420	135495038	-1	4	0	3	95	2	1	0	3	14	0	6	A2ADH7	
ENSMUST00000145022						0	2	4	1	3	0	1	1	3	4	4		
ENSMUST00000145023						0	2	0	2	2	0	15	0	57	17	18		
ENSMUST00000145024	ENSMUSG00000057722	4	101717404	101815352	1	0	0	0	14	0	0	0	0	1	0	0	A2AV66	
ENSMUST00000145025						2	4	12	59	3	2	22	139	31	5	40		
ENSMUST00000145026						4	4	3	2	5	4	25	5	29	0	56		
ENSMUST00000145027	ENSMUSG00000037020	7	30240138	30280419	-1	0	0	48	0	50	0	0	0	0	0	0	E9PUI7	
ENSMUST00000145029						0	3	6	0	0	0	4	7	11	0	12		
ENSMUST00000145031	ENSMUSG00000005774	3	94954075	94961561	1	0	0	0	0	0	0	0	0	0	0	0	D3YZK7	
ENSMUST00000145032						1	3	1	0	3	3	0	0	0	1	0		
ENSMUST00000145033						2	5	13	3	3	0	0	0	0	1	0		
ENSMUST00000145034	ENSMUSG00000019734	7	3665790	3677553	-1	4	2	13	2	8	0	18	180	22	16	49		
ENSMUST00000145035	ENSMUSG00000053852	X	56870163	57001558	1	0	0	0	0	0	0	0	0	0	0	0	F6Y0G3	
ENSMUST00000145036						10	10	9	2	6	7	0	0	0	0	0		
ENSMUST00000145037						0	2	0	0	2	0	10	4	38	12	9		
ENSMUST00000145038	ENSMUSG00000038267	13	34179158	34345182	-1	2	5	17	106	7	2	0	0	0	0	0	F7AWS1	
ENSMUST00000145039						2	0	3	2	2	0	0	3	0	0	0		
ENSMUST00000145040						34	14	38	459	45	10	0	0	0	0	7		
ENSMUST00000145041	ENSMUSG00000074156	8	93351843	93363676	-1	6	3	4	1	2	1	0	0	0	0	0	D3Z298	
ENSMUST00000145042						117	148	134	109	152	82	6	7	6	0	16		
ENSMUST00000145043						0	4	10	16	3	0	2	19	11	6	9		
ENSMUST00000145044	ENSMUSG00000047502	4	106680417	106730925	-1	1	3	0	0	2	1	0	0	0	0	0	A2AVR3	
ENSMUST00000145045						0	0	0	0	1	0	0	6	0	0	16		
ENSMUST00000145047						0	1	0	0	2	0	1	1	1	0	0		
ENSMUST00000145048	ENSMUSG00000020694	11	105178807	105283959	1	7	0	7	4	5	0	21	26	18	0	22	B7ZC85	
ENSMUST00000145049	ENSMUSG00000030498	7	51862015	51994975	1	4	1	4	3	1	0	0	0	0	0	0	D3Z503	
ENSMUST00000145051	ENSMUSG00000025001	19	38930915	38971051	1	0	0	0	0	0	0	0	0	5	3	3	D3Z414	
ENSMUST00000145052						18	10	21	43	20	13	0	0	0	0	0		
ENSMUST00000145053	ENSMUSG00000061046	17	25779843	25785673	-1	3	0	8	4	6	0	11	12	16	5	24	D3YUS7	
ENSMUST00000145054						0	0	0	0	0	0	0	0	4	14	13		
ENSMUST00000145055	ENSMUSG00000021754	13	111746428	111808993	-1	0	0	0	43	0	3	0	0	0	0	12	D3YVX9	
ENSMUST00000145057						4	4	4	2	3	2	8	8	4	8	0		
ENSMUST00000145058						0	0	16	122	8	0	222	218	277	39	180		
ENSMUST00000145059						6	8	0	2	5	2	3	8	3	0	1		
ENSMUST00000145060						2	2	6	10	4	6	5	12	13	0	41		
ENSMUST00000145061	ENSMUSG00000034853	4	106744555	106804998	-1	0	2	15	10	3	0	0	0	0	0	0	E0CXP8	
ENSMUST00000145062	ENSMUSG00000029630	5	145977194	146009618	-1	4	2	2	6	4	0	0	0	0	9	0	D6RJM4	
ENSMUST00000145063						110	85	22	30	84	30	3	18	0	7	4		
ENSMUST00000145065						0	0	3	0	0	0	0	822	0	37	0		
ENSMUST00000145066						0	0	4	0	1	0	0	21	0	0	0		
ENSMUST00000145067	ENSMUSG00000031442	8	12873806	13020905	1	10	6	38	7	13	14	0	22	37	0	0	G3UX72	
ENSMUST00000145069	ENSMUSG00000040666	16	96200470	96228933	1	0	0	0	0	1	0	0	0	0	1	0	F6QLU8	
ENSMUST00000145070	ENSMUSG00000067795	1	16065979	16093325	-1	28	25	75	451	51	20	0	20	3	2	5	F6QJK4	
ENSMUST00000145071	ENSMUSG00000021983	14	59647531	60197179	-1	11	7	21	31	10	6	0	0	0	0	0	D6RG72	
ENSMUST00000145072	ENSMUSG00000034842	5	92331827	92414628	1	0	0	0	0	0	0	0	0	0	0	0	E9Q630	
ENSMUST00000145073	ENSMUSG00000037754	2	158665398	158766334	1	94	112	303	0	96	78	19	456	0	23	0	A2AC90	
ENSMUST00000145074						4	2	0	4	9	1	3	56	2	0	24		
ENSMUST00000145075	ENSMUSG00000027238	2	121545529	121807087	-1	0	0	0	32	1	0	0	0	0	0	0	F2Z448	
ENSMUST00000145077						1	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000145078	ENSMUSG00000036054	8	70234226	70279915	1	3	2	0	3	4	1	0	0	1	0	0	D3YVJ0	
ENSMUST00000145079	ENSMUSG00000006345	10	75561604	75586200	1	0	0	8	0	2	0	50	69	108	2	48	D3YYH6	
ENSMUST00000145080						0	0	2	0	7	0	0	0	0	0	3		
ENSMUST00000145082	ENSMUSG00000029475	5	122870665	122989823	-1	2	0	0	125	13	3	0	0	0	0	0	D3YV31	
ENSMUST00000145083						4	2	0	147	10	4	2	1	3	0	12		
ENSMUST00000145084	ENSMUSG00000029304	5	104435118	104441050	1	0	0	0	1	0	0	0	0	0	0	0	D3Z513	
ENSMUST00000145086						0	2	0	2	0	0	0	1	11	0	0		
ENSMUST00000145087						3	7	3	13	2	3	0	0	0	0	1		
ENSMUST00000145088						72	50	280	139	60	22	1	12	0	1	25		
ENSMUST00000145089						15	5	12	50	19	7	1360	7324	2014	333	3162		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145090						35	32	76	70	47	25	0	5	1	0	1		
ENSMUST00000145091						21	27	51	22	26	10	8	23	16	7	19		
ENSMUST00000145092	ENSMUSG00000025920	1	16228674	16520112	-1	2	0	0	0	0	0	0	0	0	2	0	D3YXB2	
ENSMUST00000145093	ENSMUSG00000006932	9	120929216	120960507	1	5	2	5	22	0	0	3	3	5	0	0	D3YUH4	
ENSMUST00000145094						5	0	3	0	10	3	0	5	2	0	0		
ENSMUST00000145096						2	3	2	0	6	0	0	0	0	0	0		
ENSMUST00000145097						2	0	0	0	0	0	0	82	5	3	15		
ENSMUST00000145098						9	0	0	15	15	0	0	0	3	0	1		
ENSMUST00000145099						1	0	0	0	0	1	0	0	0	0	1		
ENSMUST00000145100	ENSMUSG00000034429	15	75969123	75975868	1	0	0	0	0	0	0	0	3	4	0	0	F6XU31	
ENSMUST00000145101	ENSMUSG00000009108	3	108092789	108101432	1	0	0	3	0	5	0	0	0	0	0	0	A2AE31	
ENSMUST00000145102						2	2	3	4	5	2	0	0	0	0	0		
ENSMUST00000145103	ENSMUSG00000019817	10	13060504	13131694	1	2	3	0	1	4	0	0	0	0	0	0	B0QZX5	
ENSMUST00000145104						0	0	0	0	0	0	34	0	41	15	43		
ENSMUST00000145106						3	8	2	3	6	3	6	11	4	4	2		
ENSMUST00000145107						18	19	27	64	37	15	0	0	0	0	0		
ENSMUST00000145108						5	1	7	2	1	0	0	0	0	0	0		
ENSMUST00000145109						1	1	0	12	2	1	0	0	0	0	0		
ENSMUST00000145110	ENSMUSG00000067571	19	10978307	10993250	-1	0	0	2	2	2	0	0	0	0	0	0	D3Z471	
ENSMUST00000145112	ENSMUSG00000022721	16	18248679	18254772	1	0	0	0	0	0	0	0	0	0	4	2	F6ZHN3	
ENSMUST00000145113						13	10	26	11	9	1	1	3	1	0	1		
ENSMUST00000145114	ENSMUSG00000063179	7	131371141	131387839	1	0	0	0	0	2	0	0	0	0	9	13		Q8BP74
ENSMUST00000145115						9	8	13	9	12	5	1	0	3	0	2		
ENSMUST00000145116						2	5	2	1	6	3	21	77	17	6	19		
ENSMUST00000145117						0	0	1	4	5	2	1	0	0	2	2		
ENSMUST00000145118	ENSMUSG00000052593	12	21323509	21373632	-1	0	4	0	0	0	0	0	0	0	0	0		Q9Z0F8
ENSMUST00000145119						0	0	0	0	1	0	3	10	7	4	6		
ENSMUST00000145120	ENSMUSG00000056153	18	88665224	88927481	-1	1	0	0	0	0	0	0	0	4	4	11	D3Z776	
ENSMUST00000145121						11	9	48	23	23	13	3	17	6	0	37		
ENSMUST00000145122						2	0	1	2	5	0	5	4	3	1	8		
ENSMUST00000145123						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145124						0	2	0	0	0	0	2	2	2	1	0		
ENSMUST00000145125						0	1	3	4	10	5	0	30	7	22	37		
ENSMUST00000145126						199	223	212	153	260	128	18	30	39	12	47		
ENSMUST00000145128						19	11	43	14	29	12	154	1242	279	61	309		
ENSMUST00000145130						0	3	6	1	4	1	0	0	0	0	0		
ENSMUST00000145131	ENSMUSG00000050605	7	24291039	24301232	-1	0	4	0	0	0	0	0	0	0	0	0	D3Z6B8	
ENSMUST00000145132						2	8	0	7	7	0	35	219	91	20	121		
ENSMUST00000145133						9	9	45	0	26	16	0	0	0	0	0		
ENSMUST00000145134						0	0	0	0	0	0	0	5	0	0	4		
ENSMUST00000145136	ENSMUSG00000022974	16	91014037	91044543	-1	0	0	0	0	0	0	0	0	0	0	0	F6YS88	
ENSMUST00000145137						0	1	0	3	4	5	0	0	0	0	0		
ENSMUST00000145138						0	14	0	22	0	4	6	158	39	4	13		
ENSMUST00000145139	ENSMUSG00000059820	9	50605240	50617464	-1	27	35	154	59	42	19	9	12	14	0	20	D3YWF5	
ENSMUST00000145140						212	192	222	205	205	126	7	15	6	2	18		
ENSMUST00000145141						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145142	ENSMUSG00000041020	X	159414572	159498757	1	1	0	1	0	3	0	0	0	0	0	0	A2AG51	
ENSMUST00000145144						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000145145	ENSMUSG00000010277	11	78261752	78290623	1	5	0	4	12	2	1	0	0	0	0	5	F6RD13	
ENSMUST00000145146						0	0	0	27	0	0	0	0	0	0	12		
ENSMUST00000145147						8	4	2	0	9	2	0	0	0	0	0		
ENSMUST00000145148						0	0	2	8	8	0	0	4	2	0	0		
ENSMUST00000145150	ENSMUSG00000014232	16	3908801	3941147	1	0	2	0	1	0	1	3	10	0	0	0	D3Z1F2	
ENSMUST00000145151						0	0	3	0	0	4	0	0	1	0	2		
ENSMUST00000145152	ENSMUSG00000029433	5	123509765	123525488	-1	21	8	28	14	14	3	15	73	42	7	57	Q8R1D8	
ENSMUST00000145153						6	6	19	30	11	9	0	2	0	0	0		
ENSMUST00000145154						4	5	4	2	2	5	3	22	6	0	18		
ENSMUST00000145155	ENSMUSG00000022292	15	37923952	37961318	-1	0	0	3	16	0	1	0	0	7	0	0	D3Z0X2	
ENSMUST00000145156	ENSMUSG00000064065	10	6885796	7052478	-1	0	0	0	0	0	0	33	32	144	21	85	D3YVQ1	
ENSMUST00000145157	ENSMUSG00000033099	15	78934933	78943634	1	4	0	2	27	0	2	31	50	20	17	7	B7ZBY4	
ENSMUST00000145158						10	4	6	5	10	2	0	0	0	0	0		
ENSMUST00000145159						0	0	0	0	0	0	990	3241	1339	96	1308		
ENSMUST00000145160						8	1	1	2	3	4	0	9	9	38	46		
ENSMUST00000145161	ENSMUSG00000029802	6	58584523	58695676	1	0	0	0	0	0	0	0	0	0	0	4	D3Z150	
ENSMUST00000145162						1	3	0	1	0	0	2	4	0	0	0		
ENSMUST00000145164						3	5	6	6	5	4	23	81	22	3	77		
ENSMUST00000145165	ENSMUSG00000002948	8	4238740	4251423	1	12	12	0	20	9	5	12	87	17	2	28		Q8CE90
ENSMUST00000145166	ENSMUSG00000033021	1	75435930	75443179	1	2	2	4	0	9	3	8	10	9	0	13	D3Z3M0	
ENSMUST00000145167	ENSMUSG00000075703	5	30232581	30272427	1	29	18	51	28	27	16	60	294	137	45	150		Q80TA1
ENSMUST00000145168						1	0	10	11	5	3	0	0	23	0	5		
ENSMUST00000145169						10	12	24	7	9	1	0	0	0	0	0		
ENSMUST00000145171						14	8	21	8	6	4	0	0	0	0	0		
ENSMUST00000145172						3	2	3	4	1	0	0	2	9	21	7		
ENSMUST00000145173						1	1	15	0	2	2	0	0	0	0	1		
ENSMUST00000145174						13	10	14	47	17	3	15	9	6	3	16		
ENSMUST00000145175	ENSMUSG00000022292	15	37923952	37961318	-1	5	3	14	58	10	3	0	5	0	4	5	D3YVM0	
ENSMUST00000145177						0	1	2	9	0	0	0	0	0	0	0		
ENSMUST00000145179						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145180						0	0	0	0	0	1	3	44	0	0	7		
ENSMUST00000145181	ENSMUSG00000026490	1	179960472	180165603	1	0	0	0	0	0	0	0	0	0	0	0	F6W0C2	
ENSMUST00000145183						4	2	6	143	8	4	2	11	5	0	9		
ENSMUST00000145184	ENSMUSG00000025505	7	141327739	141337156	1	3	0	3	5	0	6	0	0	0	0	8		Q9D3H0
ENSMUST00000145186	ENSMUSG00000027829	3	65946151	65958249	-1	0	0	0	1	0	0	0	4	0	0	29	F7BI63	
ENSMUST00000145187						0	0	0	0	0	0	0	0	2	15	11		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145188	ENSMUSG00000026312	1	109982431	110140157	1	0	1	0	0	0	0	0	0	0	0	0	D3Z0J7	
ENSMUST00000145189						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145190						1	2	0	0	0	0	2	0	0	1	0		
ENSMUST00000145192						2	4	3	1	0	0	9	8	18	3	18		
ENSMUST00000145193						444	361	1191	501	628	298	14	92	38	2	67		
ENSMUST00000145194						4	2	9	2	5	0	0	3	0	0	4		
ENSMUST00000145195	ENSMUSG00000037994	3	135307700	135345387	1	6	5	23	8	12	7	0	0	0	0	0	D6RDC5	
ENSMUST00000145197	ENSMUSG00000029544	5	115168689	115194381	-1	0	0	0	0	0	0	0	0	0	0	0	Q812F6	
ENSMUST00000145198						5	2	7	42	5	1	0	1	0	0	0		
ENSMUST00000145199						0	0	2	2	0	0	0	0	1	0	0		
ENSMUST00000145200	ENSMUSG00000024818	19	5877808	5885766	1	0	0	0	0	3	0	16	7	0	0	0	D3Z5G2	
ENSMUST00000145201						4	0	0	0	6	1	2	0	8	0	10		
ENSMUST00000145202						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000145203						1	2	1	1	0	0	0	1	0	0	0		
ENSMUST00000145205						5	0	16	11	3	2	0	37	3	0	5		
ENSMUST00000145209						2	4	0	1	0	0	0	0	0	0	0		
ENSMUST00000145210	ENSMUSG00000024667	19	10533865	10556238	-1	0	0	0	0	0	0	0	0	0	0	0		Q9CQC4
ENSMUST00000145211	ENSMUSG00000031022	7	109712181	109723850	-1	23	25	30	30	26	14	0	0	0	0	0	D3YXQ0	
ENSMUST00000145212	ENSMUSG00000000244	7	143005046	143019644	1	0	0	6	5	7	6	20	6	5	5	34	D6RHS4	
ENSMUST00000145213	ENSMUSG00000003033	8	72240018	72257385	1	5	3	5	5	6	1	15	9	18	0	24	S4R1Q4	
ENSMUST00000145214						0	0	0	0	0	0	20	26	9	7	9		
ENSMUST00000145215						7	1	6	1	3	0	0	14	3	0	22		
ENSMUST00000145216						3	5	1	10	1	1	85	371	86	79	2		
ENSMUST00000145217						5	0	13	21	9	0	0	0	0	0	0		
ENSMUST00000145218						7	12	20	20	5	8	1	3	1	0	5		
ENSMUST00000145219						0	6	0	152	9	0	0	0	1	0	0		
ENSMUST00000145220						0	1	0	0	0	0	0	74	6	31	22		
ENSMUST00000145221	ENSMUSG00000069248	13	33832345	33843408	-1	0	0	1	1	0	0	0	0	0	0	0	I7HM39	
ENSMUST00000145222						1	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000145223						1	1	2	52	0	4	0	2	6	0	0		
ENSMUST00000145224						24	21	31	68	24	17	0	4	5	2	8		
ENSMUST00000145225	ENSMUSG00000022498	16	11074911	11134650	-1	0	3	0	0	0	0	2	3	11	0	0	D6RHA0	
ENSMUST00000145226						12	0	0	0	3	0	0	10	12	15	10		
ENSMUST00000145227	ENSMUSG00000018411	11	104231390	104332090	1	0	2	0	0	0	1	0	0	0	0	0	B1AQW4	
ENSMUST00000145228						0	1	6	1	4	1	0	0	0	0	0		
ENSMUST00000145229	ENSMUSG00000031631	8	46151771	46195590	1	2	0	0	38	0	0	0	2	9	7	0	E9Q0S9	
ENSMUST00000145230						0	0	0	0	0	0	0	7	0	3	0		
ENSMUST00000145231						4	0	3	2	3	0	0	8	2	1	0		
ENSMUST00000145232						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000145233						5	0	29	28	0	3	0	0	0	0	26		
ENSMUST00000145234						1	2	0	2	1	1	0	0	1	0	0		
ENSMUST00000145235						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145237	ENSMUSG00000070828	7	11397915	11402741	1	21	9	24	13	15	0	0	0	0	0	0		Q3URS2
ENSMUST00000145238						0	0	2	0	0	0	39	34	30	7	0		
ENSMUST00000145239	ENSMUSG00000029270	5	107908053	107987085	-1	2	2	0	1	1	1	15	141	66	13	38	D3YW04	
ENSMUST00000145241						3	1	37	5	1	0	0	0	0	0	0		
ENSMUST00000145242						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145243						3	7	10	8	8	5	0	0	0	0	0		
ENSMUST00000145245						0	0	2	58	0	0	0	0	0	0	0		
ENSMUST00000145246						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000145247						14	5	38	11	7	2	0	2	2	2	0		
ENSMUST00000145248						1	0	0	25	0	0	5	27	18	23	18		
ENSMUST00000145249						0	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000145251						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000145252						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145253						1	1	14	23	2	2	0	0	0	0	0		
ENSMUST00000145254						0	0	2	58	0	1	0	0	0	0	0		
ENSMUST00000145255						3	0	0	7	0	0	0	0	18	0	0		
ENSMUST00000145256						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000145257	ENSMUSG00000029477	5	123035769	123047016	-1	0	0	12	4	0	4	0	0	3	0	0	D6RGA7	
ENSMUST00000145258	ENSMUSG00000006576	1	75546266	75562172	1	3	0	8	0	0	0	0	0	0	0	0	F6Q7T0	
ENSMUST00000145259	ENSMUSG00000008690	15	89355719	89372826	1	0	0	0	0	0	0	110	18	59	112	70	D6RGR7	
ENSMUST00000145260						14	10	46	31	29	15	0	1	1	0	0		
ENSMUST00000145261	ENSMUSG00000050390	4	129219578	129261404	-1	2	0	1	0	5	0	0	0	0	0	4	D3Z0K5	
ENSMUST00000145264						1	0	1	1	2	2	23	80	13	43	32		
ENSMUST00000145265						0	1	0	0	0	0	175	26	259	349	186		
ENSMUST00000145266	ENSMUSG00000021639	13	100460218	100492579	-1	2	1	3	0	0	0	6	70	12	33	5	Q91YN8	
ENSMUST00000145267						3	1	1	0	0	0	0	0	0	0	7		
ENSMUST00000145270	ENSMUSG00000054874	19	5664635	5688908	-1	0	0	0	0	0	12	26	0	29	0	2	F7DCB1	
ENSMUST00000145271						2	1	4	1	0	0	14	24	14	46	26		
ENSMUST00000145272						3	1	2	7	1	1	0	0	1	2	1		
ENSMUST00000145273						1	3	0	2	0	2	57	292	172	8	106		
ENSMUST00000145274						3	5	0	0	5	0	0	0	0	0	0		
ENSMUST00000145275						0	0	44	14	24	0	55	235	108	0	141		
ENSMUST00000145276	ENSMUSG00000073468	17	8311102	8396852	1	0	0	0	0	0	0	0	0	0	14	0	D6RFQ7	
ENSMUST00000145277						53	59	89	75	71	41	0	2	4	1	11		
ENSMUST00000145278						1	0	4	3	5	3	6	9	18	2	13		
ENSMUST00000145280	ENSMUSG00000005886	1	13139105	13374083	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z4F6	
ENSMUST00000145281						0	0	4	4	2	0	0	0	8	0	10		
ENSMUST00000145282	ENSMUSG00000066037	4	136310942	136359447	1	0	0	0	6	0	3	0	34	11	5	13	V9GWW3	
ENSMUST00000145283						4	0	0	5	0	0	0	0	1	0	0		
ENSMUST00000145284	ENSMUSG00000044583	X	167304929	167330558	-1	0	0	0	0	0	0	2	2	6	7	3	A2AHJ1	
ENSMUST00000145285						0	0	2	5	0	0	0	0	0	0	0		
ENSMUST00000145287	ENSMUSG00000031097	7	142441808	142444410	1	0	0	0	1	0	0	0	0	0	0	0	A2A6K0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145288						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000145289						2	0	0	0	2	0	0	12	15	3	14		
ENSMUST00000145290						0	0	0	6	2	0	0	14	6	2	4		
ENSMUST00000145291						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000145292	ENSMUSG00000003812	8	84908560	84922915	1	2	0	0	1	1	0	0	8	0	0	0	S4R1G0	
ENSMUST00000145293						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145294	ENSMUSG00000004952	5	136083916	136111860	1	5	0	5	1	2	0	0	0	0	0	0	F6WTE9	
ENSMUST00000145295	ENSMUSG00000031503	8	11312805	11449287	1	2	0	0	0	0	0	0	3	0	0	8	D3YV27	
ENSMUST00000145296						0	0	0	4	2	5	0	0	0	0	0		
ENSMUST00000145298						140	171	414	199	126	63	17	88	52	6	105		
ENSMUST00000145299						2	3	4	13	0	0	0	0	0	0	0		
ENSMUST00000145300						7	3	37	33	15	10	74	493	107	53	149		
ENSMUST00000145301	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYZ1	
ENSMUST00000145302	ENSMUSG00000062393	X	6779306	6948363	1	1	0	0	0	0	4	0	1	0	0	0	F6UUZ3	
ENSMUST00000145303	ENSMUSG00000021998	14	75131101	75230842	1	43	0	76	74	20	35	12393	25588	29820	5075	21688		Q61233
ENSMUST00000145304						0	0	2	21	13	7	0	0	1	1	0		
ENSMUST00000145305						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000145306						3	0	11	351	11	0	0	0	0	0	0		
ENSMUST00000145307						22	36	75	33	18	12	21	17	11	5	28		
ENSMUST00000145308						4	2	2	4	5	2	0	15	7	13	8		
ENSMUST00000145309						7	6	7	73	3	5	0	3	2	0	2		
ENSMUST00000145310	ENSMUSG00000029769	6	29396309	29426994	1	2	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000145311						38	43	182	31	7	20	0	2	4	0	4		
ENSMUST00000145312						7	3	13	2	14	2	0	0	0	0	0		
ENSMUST00000145313						10	14	33	46	24	12	17	151	42	5	72		
ENSMUST00000145314	ENSMUSG00000090115	17	47630690	47686738	1	0	2	0	0	2	2	0	0	0	0	0	D3YZI5	
ENSMUST00000145315						7	9	17	7	5	6	0	115	0	24	0		
ENSMUST00000145316						10	5	11	12	7	9	0	0	0	0	2		
ENSMUST00000145317						3	0	5	3	2	0	0	11	2	2	4		
ENSMUST00000145318	ENSMUSG00000043510	5	110829070	110839777	-1	1	3	2	0	2	0	11	4	0	0	0	F6UL52	
ENSMUST00000145319						2	1	0	0	0	0	0	10	9	4	10		
ENSMUST00000145320						0	0	0	0	0	0	32	72	37	0	0		
ENSMUST00000145321						15	25	29	18	9	9	0	0	0	0	0		
ENSMUST00000145322						0	0	10	0	15	0	0	0	0	0	0		
ENSMUST00000145323						40	19	62	40	29	22	0	0	0	0	0		
ENSMUST00000145324	ENSMUSG00000028621	4	107066988	107088268	1	0	0	0	3	0	0	0	0	0	0	2	B1AS39	
ENSMUST00000145325						2	4	15	58	4	0	2	4	5	2	4		
ENSMUST00000145326						2	1	8	0	7	0	0	0	0	0	0		
ENSMUST00000145327						0	0	0	85	0	0	50	123	33	95	37		
ENSMUST00000145328						1	4	2	216	8	1	0	0	0	0	2		
ENSMUST00000145329						46	40	54	46	65	31	7	25	24	7	25		
ENSMUST00000145330						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000145331	ENSMUSG00000018362	11	106988629	106999541	-1	0	0	0	2	3	0	0	13	0	0	0	F2Z431	
ENSMUST00000145332						2	1	1	3	7	4	0	0	0	0	0		
ENSMUST00000145333						8	6	7	1	3	3	0	0	0	0	0		
ENSMUST00000145335						0	0	6	0	0	0	10	76	2	44	27		
ENSMUST00000145336						0	0	0	0	0	1	0	0	2	0	0		
ENSMUST00000145337						1	1	0	1	1	0	7	7	0	11	0		
ENSMUST00000145339						57	42	198	54	59	27	5	33	20	5	20		
ENSMUST00000145340						40	31	38	26	28	32	8	17	16	0	29		
ENSMUST00000145341						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000145342						5	4	0	3	0	0	0	0	0	0	0		
ENSMUST00000145344						5	0	2	4	0	3	0	0	0	0	0		
ENSMUST00000145345	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	100	96	73	9	75	F6YFM0	
ENSMUST00000145347	ENSMUSG00000052105	17	66336982	66449750	-1	5	10	23	2	0	17	0	0	0	0	0	B8JJI7	
ENSMUST00000145348						0	1	4	1	5	0	0	0	0	0	0		
ENSMUST00000145349						0	2	3	0	10	0	5	24	7	0	8		
ENSMUST00000145350						2	0	4	1	0	0	173	127	64	0	95		
ENSMUST00000145351						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145352	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	4	4	0	42	38	40	5	43	D6RCV1	
ENSMUST00000145353	ENSMUSG00000020362	11	49671503	49712723	-1	6	7	25	14	10	5	460	1288	454	115	354		Q8K3P5
ENSMUST00000145354						0	0	0	0	0	0	0	4	3	4	0		
ENSMUST00000145355						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145356						6	3	12	12	12	2	4	9	5	3	2		
ENSMUST00000145357						0	5	5	3	6	1	1	8	3	0	5		
ENSMUST00000145358						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000145359						5	0	0	1	0	0	2	0	0	2	2		
ENSMUST00000145360						0	0	11	148	13	5	0	0	5	5	26		
ENSMUST00000145361	ENSMUSG00000038668	4	58435255	58553898	-1	0	1	0	26	0	1	0	0	0	0	1	A2AMJ1	
ENSMUST00000145362	ENSMUSG00000035045	X	95711678	95932637	1	39	26	65	29	39	15	1	3	4	4	3	S4R1K0	
ENSMUST00000145363						18	8	12	31	21	10	8	0	0	0	7		
ENSMUST00000145364						1	0	0	4	4	0	761	12744	2550	673	2176		
ENSMUST00000145365						0	1	6	1	3	0	0	1	0	0	1		
ENSMUST00000145366						2	2	0	5	4	3	0	0	0	0	2		
ENSMUST00000145367						0	1	2	0	4	0	0	0	0	0	0		
ENSMUST00000145368	ENSMUSG00000028745	4	139192899	139291818	1	0	1	0	0	3	0	10	0	24	62	33	A0A0A0MQI9	
ENSMUST00000145369						1	6	0	2	2	2	0	0	0	0	1		
ENSMUST00000145370	ENSMUSG00000034674	10	82629828	82650799	1	2	6	0	11	4	7	0	0	0	0	0	D3Z417	
ENSMUST00000145371						85	47	33	8203	138	26	6	35	12	4	16		
ENSMUST00000145373						3	1	8	2	4	3	0	0	0	0	0		
ENSMUST00000145374						0	6	6	0	4	4	0	0	0	0	0		
ENSMUST00000145375						3	0	0	18	0	2	0	0	0	0	0		
ENSMUST00000145377						0	1	0	0	1	3	0	2	0	0	0		
ENSMUST00000145378						0	0	0	0	0	0	88	240	246	21	227		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145379	ENSMUSG00000028444	4	41657498	41697089	-1	0	0	0	67	6	2	1	2	3	0	0	A2AMR7	
ENSMUST00000145380						1	2	4	0	5	2	0	0	0	0	0		
ENSMUST00000145381	ENSMUSG00000030737	7	99657804	99711340	-1	0	0	4	8	0	0	0	0	0	0	0	D3YZA9	
ENSMUST00000145382						9	5	5	3	6	7	0	1	0	0	0		
ENSMUST00000145384						0	0	14	74	4	0	8	5	0	0	0		
ENSMUST00000145385						58	61	84	73	55	32	1	14	13	6	14		
ENSMUST00000145386						20	18	54	17	20	9	0	0	0	0	0		
ENSMUST00000145387						0	0	0	76	1	2	0	1	0	0	0		
ENSMUST00000145388	ENSMUSG00000042459	2	154008265	154016079	1	3	7	6	1	0	5	0	0	0	0	0	B7ZCG3	
ENSMUST00000145390						594	731	954	488	600	318	13	68	32	4	18		
ENSMUST00000145391	ENSMUSG00000074818	19	45026906	45046614	-1	22	21	22	131	22	0	0	0	0	0	0	E9Q9W7	
ENSMUST00000145393						14	18	234	63	18	14	0	4	12	0	2		
ENSMUST00000145394	ENSMUSG00000004568	8	3393006	3456601	1	1	0	4	43	6	0	46	12	35	1	21	D3YWI3	
ENSMUST00000145396						2	2	28	13	14	3	14	24	94	0	64		
ENSMUST00000145397	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	0	2	0	0	0	0	0	0	D3YYQ1	
ENSMUST00000145398						0	0	0	18	2	0	0	0	0	0	0		
ENSMUST00000145399						0	2	2	0	1	1	0	0	0	0	0		
ENSMUST00000145401	ENSMUSG00000020279	11	32187541	32200279	-1	29	27	59	27	39	26	0	12	5	0	4	Q78PA5	Q01114
ENSMUST00000145402	ENSMUSG00000023861	17	8282904	8297661	1	2	0	0	0	3	2	0	0	11	0	0	D3Z786	
ENSMUST00000145403						3	2	12	1	0	2	13	13	0	0	0		
ENSMUST00000145404						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145405						0	0	3	15	5	1	0	0	0	0	0		
ENSMUST00000145406						0	0	0	39	0	1	0	0	0	0	0		
ENSMUST00000145407	ENSMUSG00000052581	6	80018877	80810143	1	0	0	1	1	3	4	0	0	0	0	0	D3YVG2	
ENSMUST00000145408						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000145409						0	0	3	0	1	0	84	203	168	32	81		
ENSMUST00000145412	ENSMUSG00000031379	X	164269371	164373011	1	1	2	0	1	1	0	1	2	6	8	1	A2AIH8	
ENSMUST00000145414						8	6	7	85	13	6	10	40	28	5	72		
ENSMUST00000145416						1	0	4	9	2	1	2	0	2	2	0		
ENSMUST00000145417						1	2	3	1	3	3	0	0	0	0	0		
ENSMUST00000145418						19	22	59	156	23	12	11	11	11	5	19		
ENSMUST00000145419	ENSMUSG00000015222	1	66175273	66442583	1	4	0	15	2	2	2	0	0	0	0	0	G3UZK9	
ENSMUST00000145421						21	26	282	16	27	11	15	61	27	4	47		
ENSMUST00000145422	ENSMUSG00000043535	2	29124181	29182471	1	3	1	14	3	6	0	0	18	27	3	73	F6R186	
ENSMUST00000145423	ENSMUSG00000026837	2	27886425	28039514	1	0	4	2	3	0	4	8	13	0	3	0	A3KGE7	
ENSMUST00000145424						1	0	0	0	0	0	3	3	0	0	4		
ENSMUST00000145425						2	1	0	0	4	2	0	0	0	0	5		
ENSMUST00000145426						0	1	3	1	1	0	0	0	0	0	0		
ENSMUST00000145427						0	0	6	2	0	1	0	1	0	0	0		
ENSMUST00000145428						7	0	9	0	0	0	0	0	0	0	0		
ENSMUST00000145429						1	0	0	2	2	0	0	0	0	0	2		
ENSMUST00000145430						2	1	15	55	4	1	0	0	0	0	3		
ENSMUST00000145431						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145432	ENSMUSG00000040785	16	94370618	94469222	1	15	4	0	4	4	10	0	0	0	1	1	Q05BF2	
ENSMUST00000145433						3	2	3	1	1	0	0	0	0	0	0		
ENSMUST00000145434						2	1	1	7	0	1	0	0	0	0	0		
ENSMUST00000145439						4	5	34	17	5	8	4	0	1	0	0		
ENSMUST00000145440	ENSMUSG00000026222	1	85649988	85709998	1	60	53	299	73	67	35	20	86	52	37	217	D6RIJ4	
ENSMUST00000145441						4	3	32	43	3	5	0	0	0	0	0		
ENSMUST00000145443						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000145444	ENSMUSG00000041911	2	71528113	71533981	1	0	0	0	0	0	0	0	0	0	0	0	G3V009	
ENSMUST00000145445						17	7	14	23	30	7	0	16	0	0	3		
ENSMUST00000145446						0	2	1	63	4	0	0	0	0	0	0		
ENSMUST00000145447						12	9	18	11	7	7	26	114	49	10	50		
ENSMUST00000145449						2	1	3	62	0	0	0	1	0	0	1		
ENSMUST00000145450						0	1	1	7	1	1	0	19	11	3	8		
ENSMUST00000145451	ENSMUSG00000046351	13	23353103	23369208	-1	5	5	7	52	3	4	0	0	0	0	0	B7ZCB1	
ENSMUST00000145452						3	2	7	0	8	0	2	7	2	4	0		
ENSMUST00000145453						6	0	1	0	3	0	0	0	0	1	0		
ENSMUST00000145454	ENSMUSG00000053819	3	126596302	126846326	1	6	9	11	2	5	2	16	169	85	9	70	E9QAJ4	
ENSMUST00000145455	ENSMUSG00000014554	6	83480217	83506969	-1	10	7	9	9	15	2	4	48	9	0	20	S4R1F5	
ENSMUST00000145456						4	1	0	17	1	1	3	4	3	11	18		
ENSMUST00000145457						91	79	327	114	74	39	25	121	77	12	108		
ENSMUST00000145458	ENSMUSG00000031626	8	45507788	45827906	1	0	0	1	4	0	0	0	0	0	0	0	D3Z4W6	
ENSMUST00000145459	ENSMUSG00000026199	1	75192151	75199387	1	0	0	43	0	0	0	37	252	63	0	1	J3KMQ5	
ENSMUST00000145462	ENSMUSG00000023979	17	47385393	47392967	1	31	27	151	38	38	13	0	0	0	0	3	E9PWU1	
ENSMUST00000145463	ENSMUSG00000024959	19	6941861	6951898	1	1	0	5	1	6	5	34	33	23	48	45	F6S493	
ENSMUST00000145465	ENSMUSG00000019767	10	4482502	4562231	1	1	1	1	1	3	1	0	0	0	0	0	D3Z4M1	
ENSMUST00000145466						5	3	17	12	5	0	0	58	7	25	57		
ENSMUST00000145467	ENSMUSG00000062234	5	108569411	108629755	-1	0	13	50	25	18	0	80	222	133	36	175	D6RHK5	
ENSMUST00000145468	ENSMUSG00000028688	4	116794310	116807640	-1	0	0	0	0	0	0	0	0	0	0	0	F6ZMT3	
ENSMUST00000145469	ENSMUSG00000058806	10	61838236	61979108	-1	0	0	2	0	4	0	0	0	0	0	0	F6Y6J7	
ENSMUST00000145470						7	2	3	2	2	0	34	194	59	58	175		
ENSMUST00000145471						5	1	2	0	4	0	0	3	0	0	5		
ENSMUST00000145472	ENSMUSG00000005774	3	94954075	94961561	1	0	0	0	2	0	0	0	0	0	0	0	D6RDE5	
ENSMUST00000145473						7	2	8	0	3	8	0	0	0	0	0		
ENSMUST00000145474						0	0	0	0	0	0	0	0	0	3	2		
ENSMUST00000145475						0	0	0	0	0	1	0	46	14	0	36		
ENSMUST00000145476						2	0	3	74	1	4	7	10	3	0	3		
ENSMUST00000145477	ENSMUSG00000071708	X	157443855	157492287	-1	7	3	23	0	14	0	16	58	15	34	27	E9PZ58	
ENSMUST00000145478						1	0	8	47	5	10	0	0	3	0	0		
ENSMUST00000145479						5	3	9	154	8	0	0	0	0	0	0		
ENSMUST00000145480	ENSMUSG00000024077	17	78649913	78737196	-1	0	0	0	0	0	0	5	0	43	4	18	F6Z700	
ENSMUST00000145481	ENSMUSG00000026946	2	51948487	51973494	-1	0	0	4	11	4	0	41	271	76	416	59	Q3UJ82	O35309

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145482	ENSMUSG00000023007	15	99295087	99317018	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145483						6	8	16	179	9	6	0	0	0	0	0		
ENSMUST00000145484						0	9	0	34	0	0	44	111	29	0	16		
ENSMUST00000145490						5	0	34	6	11	4	0	0	0	0	0		
ENSMUST00000145491						33	29	101	32	30	8	0	0	0	0	5		
ENSMUST00000145492	ENSMUSG00000053702	2	17343909	17731464	-1	0	0	0	0	0	0	0	0	0	0	1	Q8BWC6	
ENSMUST00000145493						9	9	22	6	5	8	0	1	0	0	0		
ENSMUST00000145494	ENSMUSG00000055313	13	21421275	21441058	-1	0	1	4	0	0	0	1	0	0	0	0	Q3V0V1	
ENSMUST00000145495						2	11	2	11	10	9	0	0	0	0	0		
ENSMUST00000145496						22	17	58	34	27	21	0	4	1	0	13		
ENSMUST00000145497						9	11	10	17	23	7	2	7	0	1	6		
ENSMUST00000145498						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000145499	ENSMUSG00000025478	7	139086001	139102704	1	0	0	0	0	0	0	0	0	0	0	0	D3Z360	
ENSMUST00000145500						1	2	4	0	3	2	0	0	0	0	0		
ENSMUST00000145501						0	0	0	0	3	3	0	0	0	32	14		
ENSMUST00000145503						5	0	12	14	4	4	3	28	7	5	11		
ENSMUST00000145505						35	33	65	53	38	18	1	7	6	1	6		
ENSMUST00000145506						16	16	12	20	19	3	2	23	9	18	4		
ENSMUST00000145507						0	0	0	0	0	0	0	6	0	0	0		
ENSMUST00000145508						44	35	371	54	26	12	3	15	18	0	42		
ENSMUST00000145509						1	0	0	21	1	1	0	1	1	0	4		
ENSMUST00000145511						2	1	3	6	1	4	0	0	0	0	0		
ENSMUST00000145512						3	2	2	81	6	0	0	0	0	0	0		
ENSMUST00000145513						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000145514						3	6	3	1	4	5	31	9	21	6	43		
ENSMUST00000145516						3	4	4	0	8	2	0	0	0	0	0		
ENSMUST00000145518	ENSMUSG00000041133	X	152016428	152062694	1	4	1	0	6	0	4	52	6	163	47	187	S4R179	
ENSMUST00000145519	ENSMUSG00000041375	7	16274042	16286795	-1	1	0	5	1	0	2	17	46	42	4	14	D3Z1Q6	
ENSMUST00000145521						133	134	1175	244	178	94	3	7	2	2	3		
ENSMUST00000145522	ENSMUSG00000021235	12	84361657	84373796	1	0	0	0	0	0	0	0	0	5	0	0	F6ZE40	
ENSMUST00000145523						4	3	11	28	10	0	0	0	0	0	0		
ENSMUST00000145524	ENSMUSG00000038807	11	74383356	74590186	-1	1	2	0	26	4	0	8	3	12	1	5	Q5SUE5	
ENSMUST00000145526						20	0	33	18	23	20	0	0	0	0	0		
ENSMUST00000145527	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	0	1	0	0	0	0	0	0		P0C8K7
ENSMUST00000145528						0	0	0	0	1	0	0	0	10	0	36		
ENSMUST00000145529						89	79	418	2047	208	114	7	32	6	4	19		
ENSMUST00000145530	ENSMUSG00000025781	2	10056016	10080510	-1	0	4	14	29	3	0	0	0	0	2	0	A2AKV3	
ENSMUST00000145531						5	0	0	2	6	3	0	0	0	0	0		
ENSMUST00000145532	ENSMUSG00000042709	11	60400626	60418457	-1	0	0	0	1	0	0	7	0	0	1	0	H3BLF0	
ENSMUST00000145535						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000145537						0	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000145538	ENSMUSG00000032235	9	69397906	69433122	1	0	0	0	0	0	0	0	0	0	0	0	B0V2N9	
ENSMUST00000145539	ENSMUSG00000001901	11	106008124	106034549	1	7	0	0	14	25	0	0	0	0	0	0	M0QW64	
ENSMUST00000145540						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145541						32	29	23	17	37	14	0	6	6	0	7		
ENSMUST00000145542	ENSMUSG00000034327	14	67715937	67742310	1	0	0	0	0	0	0	0	0	0	0	0	D3Z7J5	
ENSMUST00000145543						2	4	3	3	4	0	3	4	9	0	4		
ENSMUST00000145544						13	8	42	25	0	6	0	1	0	0	0		
ENSMUST00000145545						5	2	4	8	3	4	0	0	0	0	0		
ENSMUST00000145546						0	0	4	2	1	4	0	0	0	0	2		
ENSMUST00000145547						0	0	3	0	0	0	31	151	27	11	66		
ENSMUST00000145548						2	3	0	0	2	1	2	5	3	0	2		
ENSMUST00000145550	ENSMUSG00000009894	11	59407134	59451186	-1	3	2	3	1	0	1	0	0	0	0	0	I7HIK2	
ENSMUST00000145551						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000145553	ENSMUSG00000027215	2	93419111	93463140	-1	0	0	10	4	2	0	0	0	0	0	0	A2AIJ2	
ENSMUST00000145554						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000145555	ENSMUSG00000030313	6	148988071	149101680	-1	0	3	5	7	6	5	0	0	0	0	0	E9Q0R9	
ENSMUST00000145556						2	0	0	0	3	2	1	0	0	3	19		
ENSMUST00000145558	ENSMUSG00000027883	3	108678638	108722309	-1	0	2	0	0	3	2	0	0	0	0	2	A2AEL5	
ENSMUST00000145559						4	3	4	26	5	0	0	0	0	0	0		
ENSMUST00000145561						0	0	0	0	0	0	0	21	0	0	2		
ENSMUST00000145564						1	1	0	3	1	3	0	0	0	0	0		
ENSMUST00000145565						1	0	1	54	2	1	0	0	0	0	0		
ENSMUST00000145566						0	5	13	41	0	0	40	36	46	0	41		
ENSMUST00000145567	ENSMUSG00000038545	17	46650337	46664364	1	0	0	43	0	0	0	29	40	26	0	79	E9Q6H4	
ENSMUST00000145569	ENSMUSG00000055609	11	32276400	32278116	1	7	0	1	2	6	2	0	0	0	0	0	A7M7S6	
ENSMUST00000145571	ENSMUSG00000018196	1	143716338	143749676	1	0	0	22	0	0	0	0	7	0	6	5	B7ZC40	
ENSMUST00000145572						0	0	0	0	0	0	17	67	10	20	3		
ENSMUST00000145573						6	1	5	2	5	2	0	0	0	0	0		
ENSMUST00000145574	ENSMUSG00000025875	13	54789377	54796776	1	0	0	0	0	0	0	10	28	10	1	8	F6R550	
ENSMUST00000145575	ENSMUSG00000026921	2	26580014	26593120	1	0	0	0	5	0	0	0	0	0	0	0	F6W8P4	
ENSMUST00000145578	ENSMUSG00000026792	2	32925216	32961614	-1	0	0	0	0	0	0	0	2	0	0	0	A2AHX2	
ENSMUST00000145580						0	2	0	0	0	1	0	0	0	0	52		
ENSMUST00000145582	ENSMUSG00000075040	2	91643669	91649791	-1	0	0	0	0	0	0	6	0	0	0	13	D6RCZ0	
ENSMUST00000145583						25	13	16	7	40	13	0	22	9	0	14		
ENSMUST00000145586	ENSMUSG00000037475	X	41794991	41920674	-1	0	0	0	0	0	1	0	45	7	6	0	F6W2C7	
ENSMUST00000145587						4	0	3	16	7	2	0	0	0	0	0		
ENSMUST00000145588						2	3	6	30	2	2	38	284	101	19	129		
ENSMUST00000145589						0	0	3	2	0	0	18	0	8	3	0		
ENSMUST00000145590						4	4	9	6	2	9	3	5	2	5	6		
ENSMUST00000145591						1	0	0	0	0	2	0	0	0	1	0		
ENSMUST00000145592	ENSMUSG00000025825	5	113772748	113778288	1	0	0	2	1	1	1	3	18	7	0	26	D3Z0K9	
ENSMUST00000145593						1	2	0	2	2	0	3	0	1	4	0		
ENSMUST00000145594						0	0	0	0	0	0	3	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145595						1	2	1	2	1	1	0	0	0	0	0		
ENSMUST00000145597	ENSMUSG00000031637	8	45999303	46029477	1	2	8	1	2	5	0	0	0	0	0	0	H3BK12	
ENSMUST00000145598	ENSMUSG00000044647	2	65845767	66031546	1	14	4	4	0	16	0	0	0	0	0	0		P59055
ENSMUST00000145599						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000145600	ENSMUSG00000024773	19	6241668	6262335	1	4	6	52	12	12	13	999	1531	597	109	573	F6V3Y9	
ENSMUST00000145601	ENSMUSG00000036510	8	99024471	99416471	-1	0	0	0	0	0	4	0	0	0	0	0	D6RG94	
ENSMUST00000145602						2	2	2	2	1	0	0	0	2	19	7		
ENSMUST00000145603						9	9	7	3	6	1	0	0	0	0	0		
ENSMUST00000145604						3	16	68	23	13	4	12	26	17	0	31		
ENSMUST00000145605						11	4	30	49	10	9	0	7	2	0	1		
ENSMUST00000145606	ENSMUSG00000027184	2	103762941	103797649	-1	0	0	3	5	0	0	0	0	9	0	11	A2BH47	
ENSMUST00000145607						2	2	25	62	10	10	17	95	20	1	37		
ENSMUST00000145608	ENSMUSG00000037788	6	57727807	57825159	-1	61	70	129	136	65	32	1	1	3	0	11		
ENSMUST00000145609						0	0	0	2	3	0	0	19	0	34	0		
ENSMUST00000145610						0	9	0	4	1	8	5045	8398	5490	2769	4379		
ENSMUST00000145611						4	0	4	0	0	0	0	1	0	6	0		
ENSMUST00000145612	ENSMUSG00000029314	5	100845713	100899102	1	0	1	0	15	5	0	8	0	11	0	15	D3YUY8	
ENSMUST00000145614	ENSMUSG00000037740	2	130563742	130568695	1	103	96	135	120	126	68	37	98	62	60	58		Q80ZS3
ENSMUST00000145615						4	5	7	53	13	5	0	0	0	0	0		
ENSMUST00000145616	ENSMUSG00000025350	10	128913593	128922888	-1	0	0	0	0	2	0	5	22	3	0	5	D3YZQ7	
ENSMUST00000145617	ENSMUSG00000070704	5	87065927	87092555	-1	0	0	0	0	0	0	0	0	0	0	0	D3YWN0	
ENSMUST00000145618	ENSMUSG00000036270	8	105880881	105894908	1	0	1	0	2	0	0	0	2	21	0	13	F6V5I7	
ENSMUST00000145619						2	2	1	0	0	3	13	58	18	11	10		
ENSMUST00000145621						1	1	7	5	3	0	13	12	11	0	18		
ENSMUST00000145622	ENSMUSG00000012640	7	43296197	43313294	-1	14	10	26	0	16	8	75	157	34	36	29	S4R1I9	
ENSMUST00000145623						0	4	5	3	2	3	0	1	0	0	0		
ENSMUST00000145624						2	0	11	46	9	2	0	0	0	0	0		
ENSMUST00000145625						0	0	1	0	0	0	0	0	0	0	11		
ENSMUST00000145626						0	0	2	6	1	0	0	0	0	0	6		
ENSMUST00000145627						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000145628						5	3	11	4	6	4	0	36	5	6	14		
ENSMUST00000145629						19	15	37	16	10	7	43	63	64	4	50		
ENSMUST00000145630	ENSMUSG00000039137	4	63414910	63495991	-1	0	0	0	1	0	0	0	0	0	0	0	F7BB17	
ENSMUST00000145631	ENSMUSG00000021327	13	21387013	21402755	-1	0	0	0	0	0	0	4	24	12	3	4	F6VSC7	
ENSMUST00000145632						0	0	0	3	1	0	2	6	3	15	0		
ENSMUST00000145633	ENSMUSG00000018672	11	96849870	96861203	1	4	0	15	6	2	2	1	0	0	0	0	F2Z4A2	
ENSMUST00000145634	ENSMUSG00000025421	18	76930126	76972902	1	0	0	0	0	0	0	46	113	76	150	46		Q3UGR5
ENSMUST00000145636						0	2	6	3	0	0	1	0	0	0	0		
ENSMUST00000145639						19	11	54	25	23	4	0	0	0	0	0		
ENSMUST00000145640	ENSMUSG00000061288	5	117120129	117275219	1	0	0	0	0	0	0	79	0	141	0	102		
ENSMUST00000145641						2	3	2	1	0	0	1	9	4	1	1		
ENSMUST00000145642						3	1	7	1	0	0	0	0	0	0	0		
ENSMUST00000145643						6	5	12	47	10	4	5	8	14	3	11		
ENSMUST00000145645	ENSMUSG00000051674	5	73481000	73560794	1	0	3	10	23	5	0	0	0	0	0	0	D3Z4A7	
ENSMUST00000145647						5	3	0	0	0	2	0	0	0	0	0		
ENSMUST00000145648	ENSMUSG00000044550	X	136590842	136668378	1	0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000145649						3	7	12	11	9	0	0	0	0	1	0		
ENSMUST00000145650	ENSMUSG00000004233	3	99141068	99239186	1	4	8	15	22	11	4	0	0	0	2	0	Q8BZQ9	
ENSMUST00000145651						18	0	44	0	0	0	153	366	76	7	50		
ENSMUST00000145653	ENSMUSG00000045411	7	44246722	44252319	1	0	0	2	0	0	1	0	0	2	1	0	D3Z7R5	
ENSMUST00000145654						1	0	12	3	1	0	7	11	4	2	0		
ENSMUST00000145655						2	0	0	0	4	2	0	0	0	0	1		
ENSMUST00000145656	ENSMUSG00000026946	2	51948487	51973494	-1	3	5	5	5	3	5	0	16	7	7	5	B7ZD13	
ENSMUST00000145657	ENSMUSG00000059890	9	44923131	44965600	-1	12	0	0	0	1	8	19	0	36	11	16	D6RGN7	
ENSMUST00000145658	ENSMUSG00000032897	4	120757438	120831572	-1	2	1	0	68	1	0	2	2	0	2	2	A2A764	
ENSMUST00000145659						0	0	0	0	0	2	54	144	88	17	64		
ENSMUST00000145660						0	0	0	29	2	2	0	0	13	0	0		
ENSMUST00000145661						5	1	0	0	3	0	12	78	0	19	3		
ENSMUST00000145662	ENSMUSG00000029055	4	154983115	155056784	-1	18	10	13	3	23	16	0	0	1	0	1		A2AP18
ENSMUST00000145663						5	3	1	0	0	0	0	0	0	0	2		
ENSMUST00000145664	ENSMUSG00000007880	4	133679008	133756769	-1	9	3	40	70	32	6	1270	3308	2047	0	1445	E9QAQ7	
ENSMUST00000145665	ENSMUSG00000020227	10	120141648	120202130	-1	9	10	15	0	0	0	505	1543	476	33	260	D3Z007	
ENSMUST00000145666						0	0	0	16	1	2	0	0	0	0	0		
ENSMUST00000145667	ENSMUSG00000029404	5	124116089	124118196	1	1	0	7	17	4	3	21	18	10	4	18	D3Z6F1	
ENSMUST00000145668						0	0	0	0	0	0	0	0	75	0	55		
ENSMUST00000145669						1	1	2	0	3	1	1	0	4	0	0		
ENSMUST00000145670						0	0	0	0	2	0	29	0	0	0	0		
ENSMUST00000145671	ENSMUSG00000001507	11	95044474	95076801	-1	2	2	0	0	0	3	0	0	0	0	0	F6UD16	
ENSMUST00000145672	ENSMUSG00000032081	9	46232933	46235636	-1	3	0	5	7	5	0	0	0	0	0	0	D3YXN8	
ENSMUST00000145673						18	5	45	35	17	0	0	0	0	0	8		
ENSMUST00000145674						11	12	12	14	9	5	0	0	3	0	3		
ENSMUST00000145675	ENSMUSG00000031161	X	7930120	7947889	-1	3	0	0	82	4	0	53	0	0	0	0	Q3UG37	
ENSMUST00000145676	ENSMUSG00000000686	11	77515121	77538607	1	3	0	2	7	2	0	0	2	2	0	2	F6YMW3	
ENSMUST00000145677						0	0	0	0	0	0	0	0	0	0	7		
ENSMUST00000145678	ENSMUSG00000031570	8	25720061	25724887	1	0	0	0	17	2	0	0	0	0	0	0	D6RCW4	
ENSMUST00000145679						0	0	0	2	2	0	278	2598	404	2352	511		
ENSMUST00000145680						36	45	82	62	46	18	68	575	78	16	150		
ENSMUST00000145681						1	2	0	1	5	1	0	0	0	0	0		
ENSMUST00000145682						0	0	6	118	5	0	0	1	4	1	2		
ENSMUST00000145683	ENSMUSG00000024055	17	32924688	32947402	-1	2	0	2	3	0	1	21	10	10	3	10	D6RH52	
ENSMUST00000145684						0	0	0	0	0	0	84	138	155	7	60		
ENSMUST00000145685	ENSMUSG00000029802	6	58584523	58695676	1	0	0	0	0	0	0	0	6	0	0	0	S4R2M4	
ENSMUST00000145687						0	2	3	0	2	1	1	5	2	2	3		
ENSMUST00000145688						0	0	0	17	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145689						15	12	21	21	15	6	19	67	19	5	54		
ENSMUST00000145690						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000145691						0	3	2	1	0	0	0	0	0	0	0		
ENSMUST00000145692						0	6	13	2	0	15	0	0	42	0	64		
ENSMUST00000145693	ENSMUSG00000022124	14	103080239	103099566	-1	0	0	0	14	0	0	651	1820	703	192	605	Q5PRF6	Q8C4V4
ENSMUST00000145694	ENSMUSG00000027346	2	132529082	132587729	-1	0	0	0	0	0	0	0	0	0	98	0	D6RHB5	
ENSMUST00000145695	ENSMUSG00000050052	8	13952009	13975032	-1	2	0	4	58	2	0	0	0	0	1	0	D3YVM3	
ENSMUST00000145696						2	2	2	1	8	4	7	23	21	120	23		
ENSMUST00000145697						3	2	19	21	8	3	0	0	1	0	7		
ENSMUST00000145698	ENSMUSG00000026883	2	35558266	35730994	1	4	8	22	284	39	0	0	0	0	0	0	D6RDE3	
ENSMUST00000145699						0	0	0	2	1	0	0	0	2	0	4		
ENSMUST00000145700						8	9	28	11	11	7	0	1	0	0	0		
ENSMUST00000145701	ENSMUSG00000026925	2	26396249	26409203	-1	0	0	19	0	0	0	36	454	199	16	150		Q9JII1
ENSMUST00000145702						4	0	16	8	12	0	0	7	4	2	10		
ENSMUST00000145703						0	0	0	17	0	3	0	0	0	0	0		
ENSMUST00000145704						3	2	8	1	15	6	0	0	0	0	0		
ENSMUST00000145705	ENSMUSG00000003581	11	4135202	4141172	1	0	3	0	81	0	0	0	0	0	0	0	Z4YMC8	
ENSMUST00000145706						1	4	10	8	6	0	5	36	6	1	16		
ENSMUST00000145707						0	0	0	19	5	0	0	0	0	0	0		
ENSMUST00000145708						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145709						0	0	12	4	12	3	1179	3114	1382	249	995		
ENSMUST00000145710						15	9	8	9	0	0	0	0	0	0	0		
ENSMUST00000145712						1	3	3	24	6	0	0	0	0	0	0		
ENSMUST00000145713						5	3	8	5	11	4	0	2	0	0	2		
ENSMUST00000145714						6	0	0	25	11	3	0	0	0	0	0		
ENSMUST00000145715						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000145716						5	2	4	0	3	0	0	0	0	7	8		
ENSMUST00000145717						4	2	4	0	3	7	0	2	3	0	0		
ENSMUST00000145718						0	0	0	0	0	1	3	44	12	4	1		
ENSMUST00000145719	ENSMUSG00000044224	15	10446756	10470516	-1	0	0	0	1	1	0	0	50	0	5	0	F6QYD2	
ENSMUST00000145720						12	12	89	82	17	8	76	240	142	11	153		
ENSMUST00000145721						2	8	10	12	5	5	7	53	6	5	0		
ENSMUST00000145723						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000145724	ENSMUSG00000041718	X	144317804	144374450	1	0	0	2	0	0	0	0	0	0	0	0	E9Q2P6	
ENSMUST00000145725						5	6	11	2	4	4	0	0	0	0	1		
ENSMUST00000145726	ENSMUSG00000062210	18	49979427	50107173	1	0	0	0	0	0	2	0	0	21	85	23	J3QNA5	
ENSMUST00000145727	ENSMUSG00000058388	3	103968110	104024598	1	18	14	8	19	16	12	0	4	5	0	2	Q5IBN5	Q9QZ09
ENSMUST00000145728						6	4	20	13	4	3	15	18	5	2	28		
ENSMUST00000145729	ENSMUSG00000029452	5	121451893	121524183	1	0	0	2	15	0	0	0	2	0	1	0		
ENSMUST00000145730						52	82	49	113	99	68	4	1	6	0	8		
ENSMUST00000145731	ENSMUSG00000038116	2	156196466	156309952	1	2	0	0	2	0	1	0	0	0	2	0	A2AV92	
ENSMUST00000145732						10	14	39	13	12	6	1	1	3	0	3		
ENSMUST00000145733						3	3	0	110	0	0	0	1	0	4	0		
ENSMUST00000145734						3	1	9	3	12	2	20	105	39	7	52		
ENSMUST00000145735	ENSMUSG00000087260	3	107278858	107284082	1	10	9	11	65	13	11	446	1269	372	1263	196	G3UW70	
ENSMUST00000145736						7	6	1	15	10	6	0	0	1	1	1		
ENSMUST00000145737	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	0	0	0	0	0	0	0	0	B1AT88	
ENSMUST00000145738	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	0	348	5	0	21	F6YCM8	
ENSMUST00000145739	ENSMUSG00000030844	7	128373621	128418758	-1	0	1	0	5	4	0	1	0	0	0	0		
ENSMUST00000145740						2	5	0	0	8	4	38	86	30	8	11		
ENSMUST00000145741						0	5	3	0	0	0	0	130	47	11	39		
ENSMUST00000145742						0	0	0	0	18	0	247	900	137	25	456		
ENSMUST00000145743						13	8	8	9	1	9	0	1	6	0	4		
ENSMUST00000145744						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145745	ENSMUSG00000025728	17	25926427	25944510	-1	0	0	0	0	0	0	0	0	6	0	5	D3Z1K3	
ENSMUST00000145746						2	2	5	0	2	1	0	0	0	0	1		
ENSMUST00000145747						1	1	6	3	2	1	18	50	55	7	105		
ENSMUST00000145748	ENSMUSG00000034324	5	127241808	127565793	1	0	0	0	0	0	0	0	0	0	0	0	F6S419	
ENSMUST00000145749						3	3	3	10	10	3	39	235	55	14	64		
ENSMUST00000145750						6	5	8	12	9	2	0	0	0	0	0		
ENSMUST00000145752						1	1	0	4	1	0	3	10	1	0	0		
ENSMUST00000145753	ENSMUSG00000042613	3	89436706	89450952	1	0	0	0	0	7	0	0	0	0	0	0	D3Z2F0	
ENSMUST00000145754	ENSMUSG00000037868	10	67535475	67542188	1	2	1	0	40	0	0	0	0	0	0	0	D3Z4G7	
ENSMUST00000145755						0	0	6	4	0	0	0	0	0	0	1		
ENSMUST00000145756						2	2	8	2	0	2	0	6	1	0	2		
ENSMUST00000145757						8	4	8	5	13	8	1	3	0	1	2		
ENSMUST00000145758						2	3	3	3	3	1	0	1	5	0	7		
ENSMUST00000145759						2	1	0	4	3	3	0	0	0	0	0		
ENSMUST00000145760	ENSMUSG00000035696	4	44126210	44233789	-1	0	0	0	0	0	0	41	23	23	0	34	B1AWE9	
ENSMUST00000145762	ENSMUSG00000042675	7	126776955	126780514	1	0	0	0	21	0	0	0	0	0	0	0	D3YZG6	
ENSMUST00000145763						7	5	19	2	2	4	0	0	0	0	0		
ENSMUST00000145764	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	39	0	0	0	0	0	0	0	D3Z356	
ENSMUST00000145765						0	0	0	6	3	1	5	7	4	0	0		
ENSMUST00000145766						3	1	7	5	2	3	0	0	0	0	0		
ENSMUST00000145767	ENSMUSG00000031137	X	59062145	59568071	-1	0	0	1	18	0	0	0	0	0	0	0	B1AU22	
ENSMUST00000145768						1	3	1	6	1	3	0	0	0	0	0		
ENSMUST00000145770						2	1	1	12	2	0	1	0	0	0	0		
ENSMUST00000145771						0	2	1	2	2	1	0	0	0	0	0		
ENSMUST00000145772	ENSMUSG00000017677	11	79239372	79254671	-1	4	4	12	94	8	1	50	49	126	57	183	M0QWT9	
ENSMUST00000145774						3	0	0	2	7	0	0	0	0	0	9		
ENSMUST00000145775						0	0	0	0	0	0	0	0	6	0	0		
ENSMUST00000145776						60	64	200	36	72	24	44	126	143	11	214		
ENSMUST00000145777						0	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000145778	ENSMUSG00000025825	5	113772748	113778288	1	0	4	4	36	6	0	5	41	30	18	29	F6ZBG7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145779						2	2	0	4	1	1	4	4	7	0	6		
ENSMUST00000145780	ENSMUSG00000033152	6	88842558	88875044	-1	0	0	2	33	2	0	0	0	0	0	0	D3YZ50	
ENSMUST00000145781	ENSMUSG00000025145	11	120713925	120721128	1	14	0	35	0	18	0	1	71	0	0	0	E9PVE2	
ENSMUST00000145783						32	21	90	77	38	20	745	4156	1184	83	2379		
ENSMUST00000145784	ENSMUSG00000032311	9	55220222	55326844	-1	0	0	2	0	0	0	0	0	0	0	0	I6L9B2	
ENSMUST00000145785	ENSMUSG00000029522	5	115466262	115474722	1	0	0	1	2	0	0	0	0	0	0	0	S4R2K6	
ENSMUST00000145786						2	0	3	9	3	0	1	0	0	0	1		
ENSMUST00000145787						48	33	32	66	47	27	6	23	20	3	26		
ENSMUST00000145788	ENSMUSG00000046947	6	39573873	39588769	1	0	0	0	0	2	0	9	96	27	7	16		
ENSMUST00000145791	ENSMUSG00000001750	19	3896050	3907133	-1	2	2	3	2	4	5	22	208	23	0	112	Q9JHF5	
ENSMUST00000145792						0	0	0	0	0	0	0	4	1	1	2		
ENSMUST00000145793						2	3	2	11	18	4	164	159	92	0	84		
ENSMUST00000145795						13	6	11	28	13	8	17	24	19	0	24		
ENSMUST00000145796						0	0	9	43	6	7	0	0	0	0	0		
ENSMUST00000145797	ENSMUSG00000057977	4	114163384	114245028	1	0	0	0	0	0	0	0	0	0	0	0	A6PWC1	
ENSMUST00000145798	ENSMUSG00000079051	2	129038145	129048172	-1	17	8	9	203	26	6	0	0	1	0	2	A2AP89	
ENSMUST00000145802						8	14	26	22	15	15	3	4	4	1	0		
ENSMUST00000145805						2	1	0	4	4	0	0	30	39	4	45		
ENSMUST00000145806						3	4	0	0	1	0	43	153	68	20	100		
ENSMUST00000145807						1	1	0	0	0	1	1	0	0	0	0		
ENSMUST00000145808	ENSMUSG00000026915	2	37483228	37703859	-1	2	0	0	0	1	0	0	0	0	0	0	A2BH82	
ENSMUST00000145809						0	0	0	4	0	0	0	0	3	0	0		
ENSMUST00000145810	ENSMUSG00000038651	13	41114307	41171684	1	0	1	1	1	3	2	0	0	0	0	0	F6ZC70	
ENSMUST00000145811						0	1	2	3	6	3	1	0	0	0	0		
ENSMUST00000145812						1	1	2	0	3	1	0	0	0	0	0		
ENSMUST00000145813						0	0	0	30	0	0	0	0	0	0	0		
ENSMUST00000145814						1	1	13	0	4	0	13	0	18	62	5		
ENSMUST00000145816						0	0	0	0	0	0	12	31	23	5	18		
ENSMUST00000145817						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000145818						0	0	0	0	5	0	1	0	8	0	0		
ENSMUST00000145819						3	3	4	1	0	1	0	54	5	35	24		
ENSMUST00000145820						0	1	10	3	0	3	6	0	4	1	0		
ENSMUST00000145821	ENSMUSG00000029462	5	122354369	122364984	1	0	0	0	33	0	0	0	0	0	221	0	D3YYD5	
ENSMUST00000145822						0	0	0	0	2	0	14	165	18	57	0		
ENSMUST00000145823	ENSMUSG00000040712	11	70669463	70688105	-1	4	0	0	0	6	6	294	303	209	1	123	D6RCU2	
ENSMUST00000145825						16	10	44	9	12	6	11	23	12	1	21		
ENSMUST00000145826	ENSMUSG00000032046	2	150832493	150904741	-1	3	1	5	0	2	2	3	23	0	0	5	F7BHM8	
ENSMUST00000145827	ENSMUSG00000071064	8	79028437	79193766	1	7	0	0	0	14	0	0	0	0	0	0	F6ZJ37	
ENSMUST00000145828						2	1	8	9	0	3	16	53	20	2	43		
ENSMUST00000145829						0	1	3	1	2	0	0	0	0	0	0		
ENSMUST00000145830	ENSMUSG00000022568	15	76047158	76069784	-1	0	0	0	0	0	0	0	22	0	0	7	D3YU97	
ENSMUST00000145832						40	12	40	164	61	23	1	2	0	0	1		
ENSMUST00000145833	ENSMUSG00000022960	16	91677268	91688765	-1	0	3	0	0	0	2	0	0	0	0	17	F7CV24	
ENSMUST00000145834	ENSMUSG00000020785	11	73019008	73042073	1	0	4	10	0	10	1	2	0	0	0	10	B1AUD3	
ENSMUST00000145836						10	3	9	7	12	4	0	3	2	0	0		
ENSMUST00000145837						0	0	2	1	0	3	0	0	0	0	1		
ENSMUST00000145838	ENSMUSG00000027198	2	93661028	93822568	-1	0	0	0	0	1	0	0	0	2	0	0	A2AIG3	
ENSMUST00000145839						0	1	0	47	2	3	1	0	4	0	2		
ENSMUST00000145840						6	5	48	7	5	1	0	0	0	0	0		
ENSMUST00000145841	ENSMUSG00000028713	4	115624725	115647723	-1	0	0	6	2	0	7	0	0	0	0	0	F6X6A4	
ENSMUST00000145842						56	70	287	96	92	33	4	20	19	5	23		
ENSMUST00000145843	ENSMUSG00000026307	1	91298338	91321075	1	1	0	0	0	0	1	0	0	0	0	0	D3Z3I6	
ENSMUST00000145844						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000145846						2	6	16	0	6	1	381	1843	796	1265	1121		
ENSMUST00000145847						1	0	0	107	1	1	0	0	0	0	0		
ENSMUST00000145849						45	20	190	211	54	18	0	1	0	0	2		
ENSMUST00000145850						3	0	1	0	0	0	430	2059	640	15	728		
ENSMUST00000145851	ENSMUSG00000027309	2	130706200	130906406	-1	0	1	2	1	0	0	8	0	0	0	0	F6W2S3	
ENSMUST00000145853	ENSMUSG00000002428	3	20057811	20118490	1	3	1	3	3	2	3	32	400	95	99	103	E9PVX5	
ENSMUST00000145854	ENSMUSG00000064267	5	122206804	122242297	1	1	3	2	4	3	5	1	1	0	0	0	D3YZ46	
ENSMUST00000145855						30	27	241	55	40	16	0	5	0	0	7		
ENSMUST00000145857						44	50	174	60	42	40	7	17	19	3	17		
ENSMUST00000145858	ENSMUSG00000075703	5	30232581	30272427	1	0	0	4	19	0	0	6	0	9	0	8	D6RE20	
ENSMUST00000145859						27	38	47	68	47	35	11	78	27	23	35		
ENSMUST00000145860	ENSMUSG00000045636	8	40990914	41133726	-1	13	14	12	173	14	15	0	0	0	0	0	E9Q8N4	
ENSMUST00000145861						20	21	63	35	33	16	1	4	3	0	1		
ENSMUST00000145862	ENSMUSG00000012519	8	111311797	111338177	-1	4	0	3	1	2	0	3	0	0	10	0	D3YV42	
ENSMUST00000145863						4	1	2	6	4	0	0	8	3	1	2		
ENSMUST00000145864						30	18	37	33	29	11	1	21	2	1	11		
ENSMUST00000145866						5	2	6	1	2	0	0	0	0	0	0		
ENSMUST00000145867						20	26	172	13	0	15	55	128	105	0	71		
ENSMUST00000145868	ENSMUSG00000039354	1	72583251	72633134	1	0	1	0	1	0	4	0	0	0	0	0	D3Z0J8	
ENSMUST00000145869						0	0	5	5	4	0	0	0	0	0	0		
ENSMUST00000145870						0	3	7	0	5	2	0	0	0	0	2		
ENSMUST00000145872	ENSMUSG00000040363	X	12036740	12160355	-1	1	2	3	14	7	0	0	0	0	0	0	F7BEN2	
ENSMUST00000145873	ENSMUSG00000036026	17	45660171	45686905	-1	3	2	0	0	4	0	0	0	0	0	0	D3Z2D8	
ENSMUST00000145874						0	0	2	0	2	0	0	0	0	6	16		
ENSMUST00000145875	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	0	18	0	0	0	0	0	0	0	G3UX68	
ENSMUST00000145876						5	0	0	2	0	4	2	25	6	0	15		
ENSMUST00000145877						23	37	28	78	31	9	14	117	22	8	52		
ENSMUST00000145878						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145879						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000145880						1	0	0	2	0	0	0	0	0	0	7		
ENSMUST00000145881						3	6	24	32	9	7	0	7	7	14	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145882						0	2	8	5	2	2	4	0	0	0	8		
ENSMUST00000145883	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	D3YZA6	
ENSMUST00000145884	ENSMUSG00000026930	2	26315515	26348237	1	0	0	0	0	0	0	0	27	11	1	0	F6SX81	
ENSMUST00000145885						7	4	8	7	8	6	2	0	2	1	0		
ENSMUST00000145886						11	1	21	22	17	14	0	0	0	0	0		
ENSMUST00000145887	ENSMUSG00000046774	X	101794656	101798642	1	0	1	0	0	0	2	0	0	0	0	0	F6QFT7	
ENSMUST00000145888						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000145889						0	0	0	0	0	0	29	54	0	5	5		
ENSMUST00000145890	ENSMUSG00000033416	10	75351111	75517972	-1	9	5	10	11	18	3	3	3	1	1	0		
ENSMUST00000145891						0	0	0	0	0	0	0	4	0	3	2		
ENSMUST00000145892	ENSMUSG00000031442	8	12873806	13020905	1	2	0	0	0	0	0	0	0	0	0	0	F6ZFQ8	
ENSMUST00000145895	ENSMUSG00000024150	17	87254658	87265935	-1	8	5	12	16	11	3	3	6	3	0	5	D3Z6A4	
ENSMUST00000145896	ENSMUSG00000048583	7	142650766	142666816	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z4N4	
ENSMUST00000145898						45	37	37	45	45	37	6	22	14	4	13		
ENSMUST00000145899	ENSMUSG00000028456	4	43058953	43264871	1	0	0	0	0	0	0	0	0	0	0	0	F7CEK4	
ENSMUST00000145900	ENSMUSG00000003534	17	35681567	35704621	-1	0	0	2	6	0	0	0	0	0	0	0	B0V2I0	
ENSMUST00000145901						10	13	52	27	20	4	16	19	16	2	23		
ENSMUST00000145903	ENSMUSG00000070953	2	34777556	34799912	-1	33	20	29	43	20	6	8	54	24	17	20		Q8VCH5
ENSMUST00000145904	ENSMUSG00000037514	2	131262495	131299188	1	0	0	0	0	0	0	45	78	81	23	48	F6VV40	
ENSMUST00000145905	ENSMUSG00000027506	3	8925593	9004723	-1	9	4	21	7	10	6	0	0	17	0	18	D3Z125	
ENSMUST00000145906						4	5	7	8	4	6	0	35	16	2	0		
ENSMUST00000145908						0	1	1	3	9	0	1	0	0	0	0		
ENSMUST00000145909						3	3	8	9	5	4	0	0	0	0	0		
ENSMUST00000145910	ENSMUSG00000024077	17	78649913	78737196	-1	97	69	385	341	109	39	636	1630	1143	77	617		O55106
ENSMUST00000145911						3	0	0	4	0	2	0	0	0	0	0		
ENSMUST00000145912						1	0	5	3	1	0	5	24	5	9	7		
ENSMUST00000145913	ENSMUSG00000032531	9	102716672	102733418	1	2	0	1	5	2	2	0	0	19	0	0	B8JK82	
ENSMUST00000145915						2	1	6	2	2	2	10	30	14	2	23		
ENSMUST00000145917						3	2	8	5	3	8	8	80	12	8	11		
ENSMUST00000145918	ENSMUSG00000053477	18	69343356	69689079	1	3	5	3	2	2	0	1	0	0	0	0		
ENSMUST00000145919	ENSMUSG00000034518	8	74993356	75031978	1	26	44	101	6	50	19	132	255	234	132	136	G3UX81	
ENSMUST00000145920						4	0	2	55	10	0	0	0	0	0	0		
ENSMUST00000145921						0	0	1	5	1	0	0	0	0	0	0		
ENSMUST00000145922						5	1	18	15	4	3	4	0	0	0	2		
ENSMUST00000145923						0	2	0	79	6	0	0	0	2	0	1		
ENSMUST00000145925						4	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000145927						0	0	0	0	0	0	0	0	0	1	6		
ENSMUST00000145928	ENSMUSG00000006345	10	75561604	75586200	1	2	0	0	0	2	0	0	0	5	0	6	D3YY79	
ENSMUST00000145929						6	9	42	4	7	1	1	2	0	0	1		
ENSMUST00000145930						66	38	230	146	33	30	1	4	2	2	4		
ENSMUST00000145933						0	0	0	0	0	0	1	3	0	0	0		
ENSMUST00000145934	ENSMUSG00000037907	11	77470485	77489678	-1	0	6	61	162	23	16	2	18	0	5	8	Q5F260	
ENSMUST00000145935						2	1	0	71	2	2	0	2	3	0	0		
ENSMUST00000145936	ENSMUSG00000037868	10	67535475	67542188	1	2	0	14	22	4	0	0	0	0	0	0	D3YYY2	
ENSMUST00000145937	ENSMUSG00000032531	9	102716672	102733418	1	0	0	0	0	2	0	0	0	0	0	0	B8JK83	
ENSMUST00000145938						3	1	5	61	3	0	0	0	0	0	0		
ENSMUST00000145939						4	0	7	5	9	0	94	60	272	17	133		
ENSMUST00000145940	ENSMUSG00000030352	6	127961396	128143594	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000145942	ENSMUSG00000032643	4	124700701	124708611	1	0	0	0	0	0	0	0	0	0	0	0	D6RJ68	
ENSMUST00000145943	ENSMUSG00000000154	7	143473721	143499334	1	7	0	0	9	4	0	2	0	0	5	0	D6RGN1	
ENSMUST00000145944	ENSMUSG00000033152	6	88842558	88875044	-1	0	0	10	3	3	0	0	1	0	0	0	D3YW47	
ENSMUST00000145945						0	2	0	8	0	3	0	3	4	0	0		
ENSMUST00000145946						3	5	2	14	4	0	0	0	0	0	0		
ENSMUST00000145947						2	3	5	3	7	1	4	35	7	0	13		
ENSMUST00000145948	ENSMUSG00000004446	6	120891930	120916853	-1	4	0	11	4	5	1	3	7	4	6	6	D3Z463	
ENSMUST00000145949						2	0	0	2	0	4	0	0	3	12	13		
ENSMUST00000145951	ENSMUSG00000061080	16	39984361	42181679	1	0	0	0	0	0	0	0	0	0	0	0	F6SB80	
ENSMUST00000145952						10	0	8	8	0	6	6	13	0	8	0		
ENSMUST00000145953						100	72	281	100	94	50	0	4	1	0	3		
ENSMUST00000145954	ENSMUSG00000015133	7	66226912	66388350	-1	7	8	5	4	0	0	6	17	8	2	3	F6YIW9	
ENSMUST00000145955						0	0	5	1	0	1	0	0	0	0	0		
ENSMUST00000145956	ENSMUSG00000038644	7	44532746	44548849	-1	7	1	6	53	3	1	0	0	0	0	3	D3YVY8	
ENSMUST00000145957						3	1	0	3	5	3	12	32	20	0	24		
ENSMUST00000145958	ENSMUSG00000062014	14	46808149	46822242	-1	2	2	0	0	1	1	14	20	36	108	42	D3YY93	
ENSMUST00000145959	ENSMUSG00000038520	7	44840901	44849079	-1	0	0	0	0	0	0	58	32	42	0	0	I6L974	
ENSMUST00000145960	ENSMUSG00000040029	6	148770683	148831467	-1	2	0	3	51	9	0	0	0	0	0	0	B2KGD7	
ENSMUST00000145962						0	0	0	1	0	0	1	3	0	0	2		
ENSMUST00000145963	ENSMUSG00000057130	18	80206795	80223533	1	9	0	11	13	15	8	71	160	93	98	62		P83877
ENSMUST00000145964						0	2	8	3	5	0	7	29	9	0	11		
ENSMUST00000145965						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000145967						0	2	0	0	0	0	0	202	0	0	0		
ENSMUST00000145968	ENSMUSG00000026491	1	179744894	179803680	-1	5	0	2	0	1	0	5	15	0	0	0	F6SJR1	
ENSMUST00000145969	ENSMUSG00000018196	1	143716338	143749676	1	1	1	2	7	5	2	0	0	0	0	0	Q3UQ95	Q923X4
ENSMUST00000145970						1	2	8	1	4	1	4	2	1	0	11		
ENSMUST00000145974						13	15	12	47	13	9	0	1	0	0	0		
ENSMUST00000145975	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000145976						3	2	48	0	17	4	15	81	17	0	6		
ENSMUST00000145977						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000145978						0	0	0	5	2	0	0	0	0	0	0		
ENSMUST00000145979						0	0	1	3	0	0	0	0	0	2	1		
ENSMUST00000145980	ENSMUSG00000028557	4	109451098	109484728	-1	3	1	5	39	4	4	19	81	311	187	246	Z4YLT8	
ENSMUST00000145981						1	3	4	5	0	0	0	0	0	0	0		
ENSMUST00000145982						16	3	17	10	15	0	102	2139	657	143	643		
ENSMUST00000145983						0	0	0	0	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000145984	ENSMUSG00000052736	6	129647496	129660689	-1	3	2	2	9	3	2	0	2	2	0	0	Q8CB89	
ENSMUST00000145986						1	4	0	2	1	0	13	4	25	0	22		
ENSMUST00000145988	ENSMUSG00000030882	7	105640562	105721799	1	98	89	157	114	128	55	121	413	246	12	483	D3Z2X2	
ENSMUST00000145989						2	3	0	4	6	0	0	0	0	0	0		
ENSMUST00000145990						2	6	11	7	9	7	0	1	0	0	2		
ENSMUST00000145991						2	2	1	1	2	1	5	21	5	13	4		
ENSMUST00000145992	ENSMUSG00000027955	3	79884533	79946280	1	0	0	0	0	0	0	0	0	0	0	0	D3YXF7	
ENSMUST00000145993						0	0	0	0	0	12	0	19	3	11	0		
ENSMUST00000145995	ENSMUSG00000050558	2	132337733	132385447	-1	0	0	0	11	0	0	0	0	0	0	0	A2AMQ9	
ENSMUST00000145996						47	38	34	42	66	30	0	6	2	1	1		
ENSMUST00000145997						0	1	2	13	2	3	0	0	0	0	0		
ENSMUST00000145998						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000145999						0	0	0	2	0	0	1	0	0	0	0		
ENSMUST00000146000						16	17	67	16	16	15	4	4	21	3	25		
ENSMUST00000146001						52	33	61	64	65	18	7	10	1	0	7		
ENSMUST00000146002						0	1	0	2	0	1	0	0	3	0	2		
ENSMUST00000146003						0	0	0	142	8	2	0	6	10	21	0		
ENSMUST00000146004						3	1	14	0	4	2	0	6	0	0	0		
ENSMUST00000146006						24	22	70	0	26	0	4	8	0	0	2		
ENSMUST00000146007	ENSMUSG00000000739	8	123142847	123158315	-1	3	0	0	5	3	3	0	0	0	0	0	D6RH78	
ENSMUST00000146008						23	11	43	60	17	17	23	79	24	9	41		
ENSMUST00000146009	ENSMUSG00000023805	17	5941280	6044290	1	0	0	0	288	0	2	0	0	0	0	0	D3Z6E7	
ENSMUST00000146011						5	1	4	1	8	3	0	2	0	0	0		
ENSMUST00000146012						0	0	0	0	0	0	30	0	18	0	0		
ENSMUST00000146013						0	0	8	14	12	1	31	772	257	0	427		
ENSMUST00000146015						0	0	0	0	0	0	0	3	8	0	6		
ENSMUST00000146017	ENSMUSG00000030683	7	126950563	126970606	1	0	0	0	24	0	0	0	3	4	0	8	D3YY14	
ENSMUST00000146018						2	2	1	0	2	2	0	0	0	0	0		
ENSMUST00000146019						0	3	0	12	1	1	0	0	0	0	1		
ENSMUST00000146020						0	0	3	0	4	0	4	0	5	17	15		
ENSMUST00000146021						0	0	0	0	0	8	280	629	2666	276	2111		
ENSMUST00000146022						1	1	15	22	4	0	0	8	8	12	9		
ENSMUST00000146023						0	1	0	79	4	9	0	19	2	0	9		
ENSMUST00000146024						2	1	3	0	2	4	7	0	27	0	16		
ENSMUST00000146025						4	3	0	0	0	2	0	0	6	0	7		
ENSMUST00000146026						0	0	0	0	0	0	0	4	0	1	0		
ENSMUST00000146027						0	0	0	0	0	0	0	7	6	0	4		
ENSMUST00000146028	ENSMUSG00000020063	10	63319005	63381704	-1	0	0	0	0	0	0	120	295	89	9	44	F6YAQ3	
ENSMUST00000146029						50	59	125	59	58	28	16	26	8	0	31		
ENSMUST00000146030	ENSMUSG00000034958	10	81204508	81230833	-1	25	25	73	63	46	16	3	1	2	0	4	D6RIJ5	
ENSMUST00000146031	ENSMUSG00000041654	11	113244853	113650079	-1	0	0	0	36	2	0	0	0	0	0	4	B1ARC4	
ENSMUST00000146032						9	11	25	6	13	0	0	11	6	11	23		
ENSMUST00000146033	ENSMUSG00000010142	11	61126755	61149372	1	0	0	0	0	0	0	0	0	0	0	0	B1ATI3	
ENSMUST00000146035						20	11	23	18	16	4	5	20	10	11	5		
ENSMUST00000146036						2	0	0	1	2	0	0	0	0	0	9		
ENSMUST00000146037						1	0	0	128	8	0	6	31	14	0	18		
ENSMUST00000146038						137	92	493	427	152	65	5	9	5	3	14		
ENSMUST00000146039	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z662	
ENSMUST00000146040	ENSMUSG00000020564	12	33147693	33375659	1	0	0	0	0	0	0	154	87	199	0	244	F7C0E4	
ENSMUST00000146042						1	4	16	5	7	0	0	0	0	0	0		
ENSMUST00000146044	ENSMUSG00000041890	5	114727407	114775517	-1	36	39	108	65	66	30	0	581	0	10	0	F6U8T2	
ENSMUST00000146045						1	0	0	0	0	0	0	0	0	1	2		
ENSMUST00000146046						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146047	ENSMUSG00000039851	16	91053935	91095122	-1	2	5	4	0	5	0	1	0	0	0	0	D3Z4P0	
ENSMUST00000146048						0	0	0	0	0	4	2	2	3	0	2		
ENSMUST00000146050	ENSMUSG00000000049	11	108343354	108414396	1	2	0	5	0	4	1	0	0	0	0	0	J3JS85	
ENSMUST00000146051						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000146052	ENSMUSG00000030505	7	49778346	49858265	1	2	0	0	0	0	1	0	0	0	0	0	F6Y6T5	
ENSMUST00000146053	ENSMUSG00000018841	11	82876434	82890614	-1	0	10	0	0	13	0	33	134	29	0	50	Q9EP65	
ENSMUST00000146054	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	38	0	0	0	0	0	0	0		P0C8K7
ENSMUST00000146055						0	5	8	0	3	3	0	0	0	17	0		
ENSMUST00000146056						4	1	0	1	0	0	0	0	1	0	0		
ENSMUST00000146057						1	1	0	0	0	0	38	112	72	2	48		
ENSMUST00000146059	ENSMUSG00000021156	13	9684836	9765321	-1	0	1	0	0	1	0	3	0	0	4	6	D3Z7P1	
ENSMUST00000146061						0	0	22	110	6	12	50	0	45	14	0		
ENSMUST00000146062						3	5	5	27	4	3	3	3	12	1	16		
ENSMUST00000146063	ENSMUSG00000035476	X	85574022	85634469	1	1	1	1	0	0	0	0	2	3	0	0	F6XIV6	
ENSMUST00000146064						0	0	1	0	0	0	4	0	0	0	3		
ENSMUST00000146065						2	4	3	0	2	0	0	0	0	0	0		
ENSMUST00000146066						0	0	0	0	0	0	0	18	0	12	0		
ENSMUST00000146067	ENSMUSG00000020173	11	12236608	12464960	-1	0	7	10	2	4	4	0	0	0	0	0	F6RR81	
ENSMUST00000146068						7	7	13	8	3	0	0	2	7	0	0		
ENSMUST00000146069						31	40	113	91	32	18	5	11	14	1	7		
ENSMUST00000146070						0	1	2	26	2	0	0	5	6	0	10		
ENSMUST00000146071	ENSMUSG00000027843	3	103859795	103912247	1	0	0	0	9	6	0	120	87	144	138	135	E9QAS3	
ENSMUST00000146072	ENSMUSG00000029561	5	114896936	114912234	1	0	3	1	3	3	0	0	0	0	0	0	D3Z352	
ENSMUST00000146073						1	0	0	0	2	3	0	0	0	0	0		
ENSMUST00000146074	ENSMUSG00000074221	7	29983955	30028282	1	51	43	98	29	50	30	86	136	136	22	103	Q0VGV0	
ENSMUST00000146075						19	10	73	52	26	11	0	0	0	0	0		
ENSMUST00000146076						0	2	23	7	3	3	0	0	0	0	0		
ENSMUST00000146077						0	2	0	3	8	4	43	4994	502	91	1789		
ENSMUST00000146078	ENSMUSG00000028519	4	103619359	104744844	1	7	2	40	78	4	0	0	1	0	0	0	F2Z465	
ENSMUST00000146079						0	0	3	0	1	0	0	430	0	58	0		
ENSMUST00000146080	ENSMUSG00000029063	4	155562378	155591001	1	0	0	0	0	0	0	0	0	0	3	0	A2A9P0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146081						0	0	1	2	2	1	1	0	0	0	7		
ENSMUST00000146082						1	3	4	4	1	0	0	0	0	0	0		
ENSMUST00000146083						2	0	11	8	10	9	1	0	0	0	0		
ENSMUST00000146084						4	5	2	0	0	0	0	2	0	0	0		
ENSMUST00000146085	ENSMUSG00000041375	7	16274042	16286795	-1	0	0	0	0	0	0	68	266	56	18	74	G3UYE3	
ENSMUST00000146086						0	4	6	11	6	3	18	13	3	7	0		
ENSMUST00000146087						46	36	23	23	46	26	24	101	26	109	35		
ENSMUST00000146088	ENSMUSG00000035944	15	85832306	85858822	1	75	69	413	95	99	47	82	209	161	36	124		A3KMP2
ENSMUST00000146089						0	0	0	0	0	1	0	10	0	0	0		
ENSMUST00000146090						16	16	65	15	18	9	2	46	4	2	15		
ENSMUST00000146092	ENSMUSG00000016477	13	29906575	29985668	-1	2	0	4	16	3	0	1	2	2	0	0	I7HFT6	
ENSMUST00000146093						2	2	7	31	11	4	0	0	0	0	2		
ENSMUST00000146095						0	1	0	1	8	4	0	60	18	0	6		
ENSMUST00000146096						0	2	0	39	2	1	0	0	0	0	0		
ENSMUST00000146097						4	0	16	3	3	5	0	2	0	0	8		
ENSMUST00000146098						4	2	10	1	3	3	3	4	2	1	6		
ENSMUST00000146099						5	4	5	5	2	2	0	0	0	0	0		
ENSMUST00000146100	ENSMUSG00000070000	8	71708387	71725716	-1	0	10	0	43	0	0	51	0	14	0	0		Q8K285
ENSMUST00000146101	ENSMUSG00000032690	5	120730333	120749853	-1	4	4	0	3	2	2	7	47	17	3	55	F7CFL3	
ENSMUST00000146102						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146103						3	0	0	0	0	2	189	1409	326	243	54		
ENSMUST00000146104	ENSMUSG00000007570	17	28313530	28326568	1	21	11	21	9	8	9	9	0	15	2	18	B8JJD1	
ENSMUST00000146105						0	0	0	2	0	0	0	4	0	10	2		
ENSMUST00000146106						0	0	0	3	2	0	2	2	1	0	0		
ENSMUST00000146107	ENSMUSG00000012211	12	113074502	113088917	1	0	0	0	0	0	0	0	0	0	0	0		Q9D9U4
ENSMUST00000146108						3865	3690	1736	3243	3102	1809	202	403	386	110	343		
ENSMUST00000146109	ENSMUSG00000036580	3	55112108	55137322	1	4	3	0	0	0	0	0	0	0	0	0	D3Z2D6	
ENSMUST00000146111						0	3	0	0	4	1	1	0	3	1	5		
ENSMUST00000146112	ENSMUSG00000087230	1	136181474	136207097	-1	3	3	0	0	0	0	0	0	0	0	0	F6U3L2	
ENSMUST00000146113						0	0	7	0	17	0	0	0	0	0	0		
ENSMUST00000146114	ENSMUSG00000004633	6	54039554	54301810	1	3	2	0	3	2	0	0	14	2	0	4		Q80XD1
ENSMUST00000146115						27	15	62	16	11	6	3	3	4	0	6		
ENSMUST00000146117						0	2	0	0	0	0	79	103	54	25	56		
ENSMUST00000146118						0	0	2	161	4	1	0	0	0	0	0		
ENSMUST00000146120						4	0	4	1	5	1	0	10	7	7	6		
ENSMUST00000146122	ENSMUSG00000067299	1	65061872	65063452	-1	5	0	5	0	0	1	0	0	0	0	0	F7CUK9	
ENSMUST00000146125	ENSMUSG00000059834	3	41626720	41742514	-1	0	0	0	0	0	0	10	65	24	26	3	D6REI8	
ENSMUST00000146126						8	6	6	8	8	6	0	0	0	0	0		
ENSMUST00000146127						5	1	1	3	1	1	0	0	0	2	0		
ENSMUST00000146128	ENSMUSG00000038704	7	44465391	44467758	1	0	0	4	0	0	0	0	0	0	0	0	D3Z253	
ENSMUST00000146129						3	0	0	3	1	2	8	33	1	0	0		
ENSMUST00000146130						2	2	0	0	3	2	0	7	0	0	0		
ENSMUST00000146131	ENSMUSG00000027374	2	127587222	127606829	1	0	3	3	0	0	0	6	8	3	26	11	B2FDG7	
ENSMUST00000146133						2	1	2	0	3	0	0	0	0	0	0		
ENSMUST00000146135						4	1	4	2	1	0	0	0	0	0	3		
ENSMUST00000146136						15	4	10	25	16	7	22	75	30	8	78		
ENSMUST00000146137	ENSMUSG00000003458	1	172066013	172082795	-1	0	10	0	6	0	0	0	0	0	23	0	D6RCJ2	
ENSMUST00000146138						2	0	0	2	4	0	0	6	0	0	0		
ENSMUST00000146139						4	1	1	3	3	0	0	3	4	0	7		
ENSMUST00000146140						24	14	157	32	21	6	7	12	4	0	15		
ENSMUST00000146141						568	494	1107	532	502	277	3	60	36	9	39		
ENSMUST00000146142						3	3	1	2	3	0	0	7	7	0	0		
ENSMUST00000146143						0	2	0	0	2	3	0	0	4	0	10		
ENSMUST00000146144						0	0	1	2	0	3	0	0	0	0	0		
ENSMUST00000146146						0	4	0	2	6	0	0	0	0	0	4		
ENSMUST00000146147						2	0	3	4	4	3	116	1679	222	84	355		
ENSMUST00000146148						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146149						0	1	4	2	0	0	3	15	22	0	16		
ENSMUST00000146150	ENSMUSG00000049092	14	45219719	45281230	1	7	4	5	25	6	3	8	8	8	8	6	E9Q343	
ENSMUST00000146151						9	3	17	9	6	5	4	29	13	24	17		
ENSMUST00000146153	ENSMUSG00000036833	2	24976033	25054057	1	0	0	0	1	0	0	0	0	0	0	0	B0R011	
ENSMUST00000146155	ENSMUSG00000045411	7	44246722	44252319	1	0	0	9	0	0	0	0	0	0	0	0	D3Z520	
ENSMUST00000146156						19	5	8	6	7	5	4	5	6	0	5		
ENSMUST00000146157	ENSMUSG00000044361	15	76119517	76126596	-1	34	0	90	42	29	0	0	0	0	0	0	E9Q3A6	
ENSMUST00000146158						4	3	0	9	3	6	41	102	43	0	36		
ENSMUST00000146159						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000146160						0	2	0	0	4	2	0	0	0	0	0		
ENSMUST00000146162	ENSMUSG00000053580	11	105589986	105929304	1	0	0	0	0	0	0	0	0	0	0	14	F6VP19	
ENSMUST00000146163						0	2	3	4	5	1	7	49	7	0	26		
ENSMUST00000146164						14	6	7	20	5	8	0	0	0	0	0		
ENSMUST00000146165	ENSMUSG00000025766	3	41742611	41803320	1	0	0	0	0	0	0	0	0	6	0	0		Q8BGN2
ENSMUST00000146166						9	6	13	5	11	8	5	17	3	3	22		
ENSMUST00000146167						0	3	0	1	0	2	11	64	12	1	15		
ENSMUST00000146168						1	2	0	3	0	1	0	0	0	13	5		
ENSMUST00000146169						35	9	70	0	27	13	0	37	0	0	9		
ENSMUST00000146171						1	0	0	0	0	2	9	7	0	0	0		
ENSMUST00000146172	ENSMUSG00000027457	2	151590549	151632593	-1	4	4	5	98	8	3	0	0	0	0	0	S4R180	
ENSMUST00000146173						1	0	0	13	0	3	0	0	0	0	0		
ENSMUST00000146174	ENSMUSG00000060863	12	105146014	105155225	1	6	14	30	18	11	6	0	0	0	0	0	Q4FZI4	P56841
ENSMUST00000146175	ENSMUSG00000005893	6	92091390	92174294	1	0	0	18	8	0	9	88	0	270	20	260	Q3ZAR9	
ENSMUST00000146176						0	1	9	0	0	0	0	2	0	0	1		
ENSMUST00000146177						3	0	0	0	0	3	9	2	5	0	10		
ENSMUST00000146179	ENSMUSG00000020282	11	32209585	32222300	-1	0	0	0	0	0	0	0	0	3	0	16	F2Z3W3	
ENSMUST00000146180						4	4	11	24	7	4	1	0	0	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146181						33	27	126	119	37	18	2	9	6	0	12		
ENSMUST00000146182						18	11	35	36	28	16	14	87	26	7	49		
ENSMUST00000146183						5	3	2	0	2	1	0	0	0	0	0		
ENSMUST00000146184	ENSMUSG00000028964	4	150897133	150914437	-1	0	0	1	4	0	1	5	34	4	15	3	A2A817	
ENSMUST00000146185	ENSMUSG00000042726	5	121371725	121385632	-1	0	2	0	10	1	0	0	0	0	0	0	D3Z5F4	
ENSMUST00000146186						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000146187						7	7	10	7	0	1	0	0	0	0	0		
ENSMUST00000146188						0	0	0	13	2	0	6	0	3	0	0		
ENSMUST00000146189						89	62	488	223	90	66	1	10	6	2	12		
ENSMUST00000146190	ENSMUSG00000021470	13	63815240	63900302	1	0	4	4	0	0	0	0	0	0	0	0	F7BXZ2	
ENSMUST00000146191						21	18	53	23	22	12	0	0	0	0	0		
ENSMUST00000146192						0	2	1	4	0	0	0	0	0	0	0		
ENSMUST00000146193						0	1	1	0	0	0	4	22	35	12	47		
ENSMUST00000146194						0	0	0	21	0	0	3	4	4	0	3		
ENSMUST00000146196	ENSMUSG00000062410	3	98741523	98763127	-1	0	0	0	0	2	1	0	0	0	0	0	B1ARP0	
ENSMUST00000146197	ENSMUSG00000020840	11	76924809	76987379	1	2	1	2	4	2	0	0	0	0	0	0	E9PZH4	
ENSMUST00000146198						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000146200	ENSMUSG00000029686	6	47453398	47526139	1	8	0	0	0	0	0	57	18	0	0	0	Q3TPM3	
ENSMUST00000146201	ENSMUSG00000032309	9	55208925	55224433	1	4	0	12	160	5	6	0	58	27	0	41	Q3V492	
ENSMUST00000146202						9	18	14	121	23	14	0	2	1	0	5		
ENSMUST00000146203	ENSMUSG00000040620	11	70984091	71004437	-1	0	2	0	0	0	0	0	0	1	0	11	J3QNQ9	
ENSMUST00000146204						5	0	14	5	4	2	0	0	1	0	1		
ENSMUST00000146205	ENSMUSG00000075520	2	15526479	16255555	1	22	24	31	20	25	12	0	0	0	0	0	A2AJX4	
ENSMUST00000146206						1	2	1	0	2	4	2	0	0	0	0		
ENSMUST00000146207	ENSMUSG00000013495	5	108629770	108648782	1	3	1	15	20	10	2	2	18	3	3	9	Q8BHJ8	
ENSMUST00000146209						0	0	1	5	9	3	0	10	0	28	0		
ENSMUST00000146210						0	0	10	4	0	3	5	17	10	0	31		
ENSMUST00000146211						3	2	0	2	4	1	0	0	0	0	0		
ENSMUST00000146212						29	29	53	23	31	16	88	246	238	15	360		
ENSMUST00000146213	ENSMUSG00000015214	X	71364760	71419196	1	0	0	1	27	0	0	5	5	6	0	5	I7HPV7	
ENSMUST00000146214						1	0	0	0	3	6	0	0	0	0	0		
ENSMUST00000146215						19	23	47	126	25	16	3	35	9	5	9		
ENSMUST00000146216						0	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000146217						4	2	6	3	6	7	0	0	0	0	0		
ENSMUST00000146219						1	2	0	1	2	2	0	0	0	0	0		
ENSMUST00000146220	ENSMUSG00000026239	1	86542994	86582629	-1	3	11	21	94	17	8	0	6	0	0	10	M0QWG6	
ENSMUST00000146221						0	0	0	5	0	0	23	94	4	14	0		
ENSMUST00000146223						2	4	4	1	7	2	0	1	1	0	0		
ENSMUST00000146225						0	1	2	3	1	5	9	54	21	26	29		
ENSMUST00000146226						0	0	1	0	0	0	99	65	31	7	15		
ENSMUST00000146228						5	6	2	0	12	3	5	8	6	0	9		
ENSMUST00000146229						0	1	21	20	0	2	0	90	0	0	9		
ENSMUST00000146230						1	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000146233	ENSMUSG00000040483	11	72301629	72313733	1	18	19	20	19	21	10	0	21	4	74	23		Q5NBU8
ENSMUST00000146234						0	0	0	3	0	1	33	0	74	5	10		
ENSMUST00000146235						20	28	51	17	29	12	0	11	3	7	11		
ENSMUST00000146236	ENSMUSG00000044813	4	45423278	45532470	-1	0	0	3	0	3	0	0	0	1	0	0	A2AKW1	
ENSMUST00000146237						0	0	0	0	0	0	0	12	0	2	0		
ENSMUST00000146238						2	6	25	8	6	2	2	1	3	0	3		
ENSMUST00000146239						2	1	3	2	2	0	0	0	0	0	0		
ENSMUST00000146240						0	0	0	0	1	1	0	2	0	0	0		
ENSMUST00000146241						9	12	25	10	17	5	101	117	49	26	131		
ENSMUST00000146242						6	7	9	125	4	1	0	0	0	0	0		
ENSMUST00000146243	ENSMUSG00000050619	2	121158273	121171125	-1	10	9	16	274	23	7	94	288	128	35	87	B7ZCX1	
ENSMUST00000146244						1	0	12	0	6	0	7	5	7	0	15		
ENSMUST00000146245						0	0	0	0	0	0	13	1	8	0	3		
ENSMUST00000146246						4	3	4	3	7	0	3	0	0	0	2		
ENSMUST00000146247	ENSMUSG00000026764	2	49619298	49774778	1	0	0	0	0	1	0	0	0	0	0	2	A2ARD4	
ENSMUST00000146248						0	0	0	0	0	0	2	2	5	0	4		
ENSMUST00000146249						47	32	216	46	32	17	0	1	1	0	2		
ENSMUST00000146252						3	3	23	9	2	2	6	24	19	0	18		
ENSMUST00000146253						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000146254						105	55	203	269	134	60	3172	11453	6180	749	9423		
ENSMUST00000146255						3	3	11	10	1	3	3	0	0	2	4		
ENSMUST00000146256						8	10	54	21	9	4	0	0	0	0	0		
ENSMUST00000146257						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000146258	ENSMUSG00000028549	4	99765402	99929813	-1	1	5	1	4	4	0	2	0	0	7	0		Q9CQ82
ENSMUST00000146259						2	3	15	6	9	0	27	99	53	0	73		
ENSMUST00000146260						1	0	0	1	0	0	0	7	6	1	1		
ENSMUST00000146261	ENSMUSG00000020652	12	4196004	4234294	-1	7	8	10	9	14	6	4	3	7	2	7	F7D1K8	
ENSMUST00000146262						3	0	2	10	4	0	7	84	41	0	45		
ENSMUST00000146263						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146264						0	4	5	1	2	0	0	0	0	7	0		
ENSMUST00000146265	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	6	F6RB97	
ENSMUST00000146266						42	39	77	34	34	32	5	5	3	0	4		
ENSMUST00000146267	ENSMUSG00000059149	1	132022806	132068062	-1	3	0	0	73	11	0	0	0	0	0	0	H7BXC0	
ENSMUST00000146268	ENSMUSG00000030352	6	127961396	128143594	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z6M6	
ENSMUST00000146270						3	0	4	50	7	0	0	0	0	0	0		
ENSMUST00000146271	ENSMUSG00000022194	14	54892500	54898169	1	6	6	12	11	5	1	2	12	1	0	13	G3UWY6	
ENSMUST00000146272						3	0	2	20	2	3	0	0	0	2	0		
ENSMUST00000146273						15	6	44	22	3	9	6	0	6	0	6		
ENSMUST00000146274	ENSMUSG00000040649	6	122447296	122498761	-1	12	10	2	5	8	4	0	0	0	0	0		Q80WS1
ENSMUST00000146275						0	1	0	27	6	0	0	0	0	0	1		
ENSMUST00000146276						2	1	6	64	5	2	4	5	6	0	13		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146277						4	4	15	2	4	4	0	1	0	0	0		
ENSMUST00000146278	ENSMUSG00000070844	7	8183265	8200320	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1K8	
ENSMUST00000146279						2	1	4	35	4	0	0	0	0	0	5		
ENSMUST00000146280						0	0	0	17	0	0	62	255	131	16	21		
ENSMUST00000146281						0	0	4	2	7	2	7	88	31	17	41		
ENSMUST00000146282	ENSMUSG00000026312	1	109982431	110140157	1	14	2	10	5	10	7	0	0	0	0	0	Q8BLT5	
ENSMUST00000146283						4	3	8	0	7	1	0	0	0	0	1		
ENSMUST00000146284						0	0	0	1	0	2	3	21	13	7	27		
ENSMUST00000146285						0	2	1	0	0	0	139	1234	331	65	275		
ENSMUST00000146286						3	1	2	2	4	0	0	8	0	0	5		
ENSMUST00000146287	ENSMUSG00000019843	10	39368855	39565381	1	0	0	0	0	0	9	0	0	0	0	0		P39688
ENSMUST00000146288	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	0	0	0	0	0	0	0	0	7	B7ZD63	
ENSMUST00000146289						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146290						1	0	0	0	3	1	48	219	111	7	174		
ENSMUST00000146291						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000146292	ENSMUSG00000034145	12	87021340	87090043	1	13	6	40	16	0	5	0	0	0	0	0		Q8CBX0
ENSMUST00000146293						8	5	11	21	6	7	91	423	215	18	281		
ENSMUST00000146295	ENSMUSG00000029106	5	34573664	34632308	1	0	0	1	0	0	0	0	0	7	0	7	D3Z0T1	
ENSMUST00000146296						6	3	6	0	4	0	0	0	0	0	0		
ENSMUST00000146297	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	8	64	3	2	428	3995	1	0	45	Q3U313	Q8VH51
ENSMUST00000146298						2	2	1	3	3	3	20	59	47	4	120		
ENSMUST00000146299	ENSMUSG00000092511	17	34856412	34882042	-1	0	0	0	0	5	0	0	0	0	8	0	B8JJN0	
ENSMUST00000146300						18	11	50	28	11	4	0	1	1	0	1		
ENSMUST00000146301						16	17	37	31	29	17	0	12	7	1	7		
ENSMUST00000146302						5	1	1	2	6	1	0	0	0	0	0		
ENSMUST00000146303						7	5	11	23	12	7	87	466	69	21	155		
ENSMUST00000146305	ENSMUSG00000025511	7	141475240	141493427	1	4	6	0	55	3	2	0	0	0	0	0	D3Z0T3	
ENSMUST00000146306						0	3	8	3	16	0	0	0	20	0	11		
ENSMUST00000146307	ENSMUSG00000037110	2	146239879	146512026	-1	0	0	2	3	2	2	10	5	0	3	17	F7AI67	
ENSMUST00000146308						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000146309						14	10	67	90	37	15	3	3	2	0	20		
ENSMUST00000146310						1	0	0	0	0	0	110	502	69	0	0		
ENSMUST00000146311						7	0	7	0	0	2	0	0	0	0	0		
ENSMUST00000146312	ENSMUSG00000037286	9	100597798	100959375	1	0	0	0	12	0	0	0	0	19	0	0	Q8C918	
ENSMUST00000146313						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146315						1	3	0	2	0	0	6	22	7	6	2		
ENSMUST00000146316						1	0	0	0	0	0	0	2	2	4	0		
ENSMUST00000146317	ENSMUSG00000035203	7	5080235	5098178	1	0	0	0	0	1	0	64	31	22	0	29	D3Z4V3	
ENSMUST00000146318						1	0	0	1	1	1	27	941	202	293	172		
ENSMUST00000146319						0	1	4	0	4	1	0	0	0	0	0		
ENSMUST00000146321						3	0	4	40	6	1	5	0	4	0	2		
ENSMUST00000146322						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146323						3	6	2	0	0	3	3	0	5	0	0		
ENSMUST00000146324	ENSMUSG00000050174	3	37404910	37420211	-1	0	0	0	0	0	0	0	0	0	3	0	Q8CH41	
ENSMUST00000146325	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	0	0	27	0	0	0	0	D3Z3R4	
ENSMUST00000146327						28	34	68	49	44	15	13	30	4	6	28		
ENSMUST00000146328	ENSMUSG00000030035	6	83119044	83121559	-1	3	0	0	0	1	2	106	125	19	11	36	D3Z168	
ENSMUST00000146329						23	16	68	218	26	18	0	2	0	0	1		
ENSMUST00000146330						6	5	17	75	18	6	6	0	7	5	7		
ENSMUST00000146331						0	0	9	0	0	4	0	0	0	0	0		
ENSMUST00000146332						35	28	91	184	67	29	5	0	0	0	10		
ENSMUST00000146335	ENSMUSG00000014030	4	44524757	44710487	-1	1	1	4	242	6	1	0	0	0	0	0	V9GXS5	
ENSMUST00000146338	ENSMUSG00000020910	11	67037905	67052594	-1	7	6	16	22	14	6	52	200	82	48	26		Q99KS6
ENSMUST00000146339						15	23	32	22	46	7	18	65	32	4	54		
ENSMUST00000146340	ENSMUSG00000027994	3	129914960	129970206	-1	1	4	2	0	2	2	0	17	0	0	6	F6SD17	
ENSMUST00000146341	ENSMUSG00000029822	6	50293330	50456201	-1	0	0	0	0	0	0	0	2	5	0	0	D3YVF7	
ENSMUST00000146342						0	0	1	0	0	0	0	0	3	0	0		
ENSMUST00000146343						37	24	37	32	48	19	2	6	4	2	17		
ENSMUST00000146344						2	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000146347						0	1	0	1	0	0	3	25	9	16	16		
ENSMUST00000146348	ENSMUSG00000030216	6	136813654	136828233	-1	0	0	6	14	1	0	0	1	0	0	2		
ENSMUST00000146350						6	4	7	5	6	3	0	2	1	0	0		
ENSMUST00000146351						0	0	20	1	7	0	0	0	0	0	3		
ENSMUST00000146352						28	33	54	21	26	14	8	34	32	9	43		
ENSMUST00000146353						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146354	ENSMUSG00000015950	5	134220053	134229625	-1	0	0	0	0	1	1	207	142	650	29	322		Q09014
ENSMUST00000146355						3	0	7	8	3	0	39	107	28	8	48		
ENSMUST00000146356	ENSMUSG00000028152	3	138742195	138907905	1	6	5	6	0	0	0	0	0	0	3	0	D3YV61	
ENSMUST00000146358	ENSMUSG00000034771	10	81574561	81590845	1	6	11	23	24	16	15	0	0	0	0	0		Q9WVB2
ENSMUST00000146359						71	73	437	87	63	24	4	12	4	0	6		
ENSMUST00000146360						3	0	7	2	3	0	0	0	0	0	0		
ENSMUST00000146361						9	11	12	42	16	3	3	2	0	0	5		
ENSMUST00000146362						0	0	2	0	0	2	167	452	78	7	91		
ENSMUST00000146363	ENSMUSG00000036352	2	25998543	26021747	-1	0	0	0	0	0	0	0	5	0	0	0	F6Z1E7	
ENSMUST00000146365						68	63	292	88	76	27	5	14	11	0	16		
ENSMUST00000146367						7	3	2	11	14	4	0	1	0	0	6		
ENSMUST00000146368						0	0	0	3	3	0	1	2	4	0	3		
ENSMUST00000146370						1	4	0	0	0	0	6	46	17	0	0		
ENSMUST00000146371						0	0	5	0	2	3	3	8	2	0	0		
ENSMUST00000146373						1	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000146374	ENSMUSG00000038517	11	97136171	97151495	-1	0	0	0	2	0	1	16	0	9	0	8	A2A9T1	
ENSMUST00000146375	ENSMUSG00000029004	5	23434441	23504235	1	3	3	1	0	0	0	46	89	113	0	53	A0A0G2JDX7	
ENSMUST00000146376	ENSMUSG00000050390	4	129219578	129261404	-1	0	2	2	2	2	0	0	0	0	0	0	D3Z770	
ENSMUST00000146377	ENSMUSG00000072946	12	84285232	84315832	1	5	0	5	4	0	4	13	0	12	9	0		Q8VDQ1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146378						8	4	3	3	8	5	4	8	3	5	11		
ENSMUST00000146380	ENSMUSG00000007659	2	152780668	152831728	-1	0	0	3	0	0	0	27	13	0	0	8	A2AHX8	
ENSMUST00000146381						54	46	129	102	40	21	5	23	30	0	39		
ENSMUST00000146382						4	9	13	21	10	10	0	3	0	3	5		
ENSMUST00000146383	ENSMUSG00000030815	7	127573340	127583307	1	0	0	0	0	0	0	40	29	29	27	14	D6RG71	
ENSMUST00000146384						0	2	3	0	0	0	0	45	7	16	0		
ENSMUST00000146385	ENSMUSG00000032878	11	28385685	28584324	-1	4	2	5	0	0	0	0	0	0	0	0	E0CX32	
ENSMUST00000146386						0	0	0	0	0	0	8	15	1	1	17		
ENSMUST00000146387						0	0	0	3	12	0	0	0	0	0	0		
ENSMUST00000146388	ENSMUSG00000019850	10	19000910	19015657	-1	4	0	17	4	5	2	0	0	3	0	3	D3YXE1	
ENSMUST00000146389						0	1	2	2	0	1	0	0	0	0	0		
ENSMUST00000146390	ENSMUSG00000047904	11	113619342	113626028	1	3	10	24	82	14	6	0	1	0	0	1		P30875
ENSMUST00000146391						5	7	23	53	5	7	0	0	0	0	0		
ENSMUST00000146392						10	10	24	26	16	8	12	20	20	8	19		
ENSMUST00000146394						2	0	1	1	2	1	1	1	2	0	3		
ENSMUST00000146395	ENSMUSG00000021693	13	106958996	107022126	-1	0	0	0	0	0	0	0	0	0	0	0	F6RLL5	
ENSMUST00000146396	ENSMUSG00000089809	5	99297244	99729065	-1	24	26	65	48	27	13	0	0	0	0	1	F5H8M5	
ENSMUST00000146399						0	0	0	1	0	0	7	9	13	0	4		
ENSMUST00000146400						4	7	6	8	7	6	8	13	0	0	6		
ENSMUST00000146401	ENSMUSG00000067367	5	38220470	38234306	1	0	0	1	0	0	0	2	0	0	0	0	D6RDT2	
ENSMUST00000146402	ENSMUSG00000025722	7	80890723	80901269	-1	0	0	0	0	0	0	0	12	2	0	3	F6RXX6	
ENSMUST00000146403						15	7	21	31	13	6	0	0	0	0	0		
ENSMUST00000146405						2	0	3	0	2	0	0	0	0	0	2		
ENSMUST00000146406	ENSMUSG00000031158	X	7899357	7908351	1	1	0	0	6	0	2	152	161	81	39	61	A2AES1	
ENSMUST00000146408						6	6	10	4	8	2	0	0	0	2	7		
ENSMUST00000146409	ENSMUSG00000034320	18	61192919	61211612	-1	93	92	251	133	87	49	191	577	487	47	415		Q62273
ENSMUST00000146410						5	0	2	2	2	3	3	0	0	3	0		
ENSMUST00000146411	ENSMUSG00000020884	11	70054085	70057894	1	0	0	0	2	9	0	0	0	0	17	0		P34927
ENSMUST00000146412	ENSMUSG00000061689	2	156613705	156764363	1	0	1	0	0	0	0	58	77	49	1	65	H3BJW9	
ENSMUST00000146413	ENSMUSG00000027635	2	156995265	157007154	-1	0	0	0	0	0	0	0	2	0	0	0	A2ACV5	
ENSMUST00000146414						12	7	29	10	8	8	0	0	0	0	4		
ENSMUST00000146415	ENSMUSG00000043621	4	138709837	138737167	-1	14	4	25	14	9	8	1	0	0	0	1		Q8BG34
ENSMUST00000146416						5	2	20	299	15	0	0	0	0	3	0		
ENSMUST00000146417	ENSMUSG00000057068	5	92555069	92591279	1	9	8	16	11	9	5	0	0	0	0	0	D3YWC7	
ENSMUST00000146418						22	16	54	47	17	8	4	12	3	3	7		
ENSMUST00000146419						7	2	2	2	4	0	5	0	18	1	0		
ENSMUST00000146420						1	1	3	4	2	2	0	4	2	0	0		
ENSMUST00000146421						3	2	4	0	0	1	0	0	0	1	4		
ENSMUST00000146423	ENSMUSG00000039195	2	32377097	32381938	-1	50	50	410	127	61	38	21	38	15	3	28	A0A0A6YXJ8	
ENSMUST00000146425	ENSMUSG00000029651	5	147957320	148316065	1	0	2	5	18	1	3	0	0	0	0	0	D6RI77	
ENSMUST00000146426	ENSMUSG00000078350	4	154020470	154026230	-1	0	0	0	0	0	0	0	0	0	3	0	S4R1P3	
ENSMUST00000146427						0	0	0	19	4	2	0	0	0	0	0		
ENSMUST00000146428						10	0	19	16	14	6	11	25	3	4	9		
ENSMUST00000146429						23	11	68	14	22	16	6	1	2	0	21		
ENSMUST00000146430	ENSMUSG00000029192	5	36490604	36593276	-1	10	0	5	0	0	0	381	2642	46	0	302	E9Q8K4	
ENSMUST00000146431	ENSMUSG00000020829	11	78465697	78472059	1	0	1	2	83	1	1	1	1	0	0	1	F6QD87	
ENSMUST00000146432	ENSMUSG00000026436	1	132007607	132032612	1	3	0	10	33	2	1	2	7	32	0	12	Q8C6Q0	
ENSMUST00000146433	ENSMUSG00000069785	11	85846790	85850333	-1	6	4	12	12	11	2	0	0	0	2	3	F6QMA6	
ENSMUST00000146434						4	3	6	4	7	0	4	3	15	0	46		
ENSMUST00000146435						3	2	12	1	4	1	3	0	2	0	0		
ENSMUST00000146436						39	25	64	28	45	18	1	14	3	0	13		
ENSMUST00000146437						0	0	0	0	0	0	1	0	3	0	2		
ENSMUST00000146438	ENSMUSG00000021870	14	26413168	26534931	-1	0	0	0	0	0	0	13	21	53	5	15	F6WY34	
ENSMUST00000146439	ENSMUSG00000078922	11	48985327	48994172	-1	4	1	20	8	11	4	0	0	2	28	5	Q5SVP4	
ENSMUST00000146440	ENSMUSG00000020175	10	75037058	75054748	1	0	3	0	0	0	0	0	6	0	0	0		Q8CAM5
ENSMUST00000146441	ENSMUSG00000028207	4	9448069	9669344	-1	5	5	12	2	2	4	1	1	0	0	3	Q6P8S1	
ENSMUST00000146442	ENSMUSG00000015766	6	137477245	137654876	-1	0	1	0	0	0	0	0	20	22	0	14	D3Z7F4	
ENSMUST00000146443	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	0	14	0	0	264	0	60	0	F7BUB8	
ENSMUST00000146444	ENSMUSG00000015755	10	7905653	7956230	-1	15	19	13	41	16	9	1670	6911	3655	584	3295		Q99K90
ENSMUST00000146445						1	0	1	0	0	0	0	0	3	0	0		
ENSMUST00000146446						28	36	91	32	35	12	0	0	6	0	11		
ENSMUST00000146447	ENSMUSG00000048747	4	97568133	97778078	-1	7	4	1	0	4	5	0	0	0	0	0	F6S0S7	
ENSMUST00000146448						27	28	37	48	58	17	0	0	0	0	0		
ENSMUST00000146449						1	0	0	9	2	0	7	15	11	0	9		
ENSMUST00000146450	ENSMUSG00000099481	7	102065511	102083765	1	2	0	2	0	3	2	0	3	8	1	0	D3Z526	
ENSMUST00000146451	ENSMUSG00000050705	17	35892677	35897431	-1	9	5	33	108	8	12	14	15	13	0	11	B8JJ66	
ENSMUST00000146452						0	5	2	3	5	2	0	2	0	0	2		
ENSMUST00000146453						45	22	124	59	45	29	1	4	5	0	18		
ENSMUST00000146454	ENSMUSG00000027405	2	130274430	130279313	1	0	0	0	0	0	0	5	3	5	2	0	F7CHQ7	
ENSMUST00000146455	ENSMUSG00000001036	11	61517249	61579687	-1	4	2	0	2	0	0	0	0	0	0	6	A8Y5D5	
ENSMUST00000146457	ENSMUSG00000039985	6	148921035	148946467	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVY1	
ENSMUST00000146458	ENSMUSG00000029505	5	110664373	110770717	-1	7	0	27	4	33	7	0	0	0	0	0	Q641K9	
ENSMUST00000146459						14	8	34	26	20	12	34	92	70	8	41		
ENSMUST00000146460						1	3	12	7	1	0	0	0	0	0	0		
ENSMUST00000146461						3	2	4	3	8	1	0	0	0	0	0		
ENSMUST00000146462						0	0	0	0	0	0	0	48	6	1	1		
ENSMUST00000146463						2	1	6	3	3	0	4	3	8	0	6		
ENSMUST00000146464						3	2	3	0	3	3	0	1	1	0	1		
ENSMUST00000146466						14	4	8	2	25	8	0	25	0	0	0		
ENSMUST00000146467						3	0	42	0	2	0	0	0	0	0	0		
ENSMUST00000146468	ENSMUSG00000050335	14	47367751	47386160	1	10	0	16	24	5	3	22	64	91	0	87	Q8C253	
ENSMUST00000146469						5	2	0	18	2	3	6	4	11	4	17		
ENSMUST00000146470	ENSMUSG00000034826	5	92415540	92435219	-1	12	18	41	40	16	5	0	2	7	0	8	D6RFN7	
ENSMUST00000146471						4	7	12	48	10	4	11	24	19	3	41		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146472	ENSMUSG00000003534	17	35681567	35704621	-1	6	4	13	4	5	3	2	0	0	0	2	B0V2H9	
ENSMUST00000146473						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000146474						0	0	0	0	2	1	0	0	1	0	0		
ENSMUST00000146475						12	11	13	91	11	12	0	0	0	0	0		
ENSMUST00000146476	ENSMUSG00000035297	5	100518309	100547803	1	9	0	3	19	7	2	0	0	0	0	5	D3Z1R9	
ENSMUST00000146477						2	3	7	2	1	6	1	5	5	0	7		
ENSMUST00000146478	ENSMUSG00000023232	4	130253495	130279205	-1	5	1	6	13	6	0	0	0	0	3	3	B2KFY1	
ENSMUST00000146479						3	0	7	16	5	2	0	20	0	0	7		
ENSMUST00000146480						6	7	5	1	3	2	0	0	0	0	0		
ENSMUST00000146482	ENSMUSG00000035064	7	120842831	120907219	1	0	2	1	1	1	1	1	4	0	2	2	F6ZEU2	
ENSMUST00000146483						7	10	15	11	15	5	0	0	0	0	0		
ENSMUST00000146484						113	62	455	130	157	64	2	28	18	0	32		
ENSMUST00000146485	ENSMUSG00000039254	2	32236590	32255005	1	2	5	0	2	3	0	0	0	0	0	0	B0R070	
ENSMUST00000146486						3	6	1	0	6	0	0	4	4	0	0		
ENSMUST00000146487						20	11	29	12	13	10	3	9	2	2	14		
ENSMUST00000146488						10	6	58	8	13	4	0	0	2	0	4		
ENSMUST00000146489						1	2	2	1	2	3	0	0	0	0	0		
ENSMUST00000146490						60	94	321	59	95	35	1	32	8	0	35		
ENSMUST00000146491						0	0	0	10	4	0	0	0	0	0	0		
ENSMUST00000146492	ENSMUSG00000021708	13	91880400	92131656	-1	5	5	4	152	11	6	0	0	0	0	0	D3Z685	
ENSMUST00000146493						1	0	1	86	2	3	0	1	0	0	0		
ENSMUST00000146494	ENSMUSG00000067229	19	39113898	39187072	1	4	0	0	0	0	0	0	0	0	0	0	D6RJ25	
ENSMUST00000146496						0	0	0	21	0	0	0	0	0	0	0		
ENSMUST00000146497						6	7	0	0	2	8	99	153	69	17	60		
ENSMUST00000146498	ENSMUSG00000009566	2	32682609	32704145	-1	0	2	3	0	7	0	0	0	0	0	2	A0A0A6YX96	
ENSMUST00000146499						11	14	21	7	17	11	4	0	0	2	0		
ENSMUST00000146500						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146502	ENSMUSG00000051373	2	32095528	32110820	1	9	0	11	2	10	4	0	1	0	1	0	A0A0A6YX24	
ENSMUST00000146503						0	2	0	22	0	1	0	0	0	0	0		
ENSMUST00000146505						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000146506	ENSMUSG00000002102	2	91054009	91066369	1	0	0	0	4	2	0	0	26	21	0	0	F6Q2E3	
ENSMUST00000146507						0	3	4	1	5	0	13	40	18	2	12		
ENSMUST00000146508						0	0	1	13	0	1	10	6	1	2	0		
ENSMUST00000146509						6	3	2	24	9	1	0	0	0	0	0		
ENSMUST00000146510	ENSMUSG00000029346	5	112337392	112343040	-1	0	0	0	0	0	0	43	71	11	5	12	F6Q7H5	
ENSMUST00000146511	ENSMUSG00000016503	5	146948657	146955614	1	4	0	0	67	3	0	44	108	42	4	42	F6RCF6	
ENSMUST00000146512	ENSMUSG00000015852	3	87250758	87263738	-1	4	0	1	0	2	5	0	0	0	0	1	D3YYJ5	
ENSMUST00000146513	ENSMUSG00000096914	8	57774052	58912640	-1	2	3	0	0	1	0	0	0	0	0	0	D6RIJ0	
ENSMUST00000146514						11	6	8	3	3	0	101	156	171	24	95		
ENSMUST00000146516	ENSMUSG00000035621	10	80148272	80158368	1	10	2	7	73	12	11	17	24	29	0	78	D3Z7H2	
ENSMUST00000146517						6	1	0	12	4	1	0	2	0	0	0		
ENSMUST00000146518						1	0	11	4	0	1	0	0	0	0	0		
ENSMUST00000146519						3	1	1	0	1	0	5	16	13	0	4		
ENSMUST00000146520	ENSMUSG00000025747	5	30058202	30073617	-1	0	0	0	0	0	0	22	22	0	90	0	A0A0G2JGF0	
ENSMUST00000146521						6	3	11	1	5	1	0	3	0	0	0		
ENSMUST00000146522						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000146523						11	8	9	7	8	2	0	24	0	0	0		
ENSMUST00000146525						7	0	4	33	2	0	64	66	20	31	68		
ENSMUST00000146526						7	8	22	55	15	0	227	401	126	1	169		
ENSMUST00000146527						6	0	22	183	7	2	0	0	14	2	20		
ENSMUST00000146528						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146530						0	2	15	2	10	3	0	0	4	0	7		
ENSMUST00000146533						1	1	1	144	7	1	0	0	0	0	1		
ENSMUST00000146534						2	3	0	0	6	2	0	0	0	0	0		
ENSMUST00000146536	ENSMUSG00000020437	11	6506548	6520965	-1	3	0	0	0	3	0	0	8	5	0	3	D6RGA2	
ENSMUST00000146537						174	137	736	407	169	78	14	29	25	5	31		
ENSMUST00000146538						0	0	0	0	0	0	14	29	10	7	37		
ENSMUST00000146539						30	23	163	56	34	18	3	2	0	0	0		
ENSMUST00000146540						0	0	1	0	2	0	0	0	2	0	0		
ENSMUST00000146541						0	2	0	0	4	2	5	11	8	1	24		
ENSMUST00000146543	ENSMUSG00000078350	4	154020470	154026230	-1	0	4	1	0	3	0	0	0	0	0	0	S4R2T3	
ENSMUST00000146544						2	1	4	3	5	0	5	13	9	1	15		
ENSMUST00000146545						2	6	15	3	12	0	54	108	214	427	250		
ENSMUST00000146547	ENSMUSG00000028309	4	49632006	49656887	1	0	0	2	35	5	0	0	0	0	0	0	A2AIR1	
ENSMUST00000146548						2	0	2	3	0	2	6	52	3	6	5		
ENSMUST00000146549	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	0	0	0	0	6	2	12	4	22	D6RCZ8	
ENSMUST00000146551						0	0	0	0	0	0	28	2	11	0	8		
ENSMUST00000146552						17	0	143	0	5	14	0	0	4	0	5		
ENSMUST00000146555	ENSMUSG00000000902	10	75896769	75921617	-1	0	0	0	0	0	0	0	0	0	1	0	F6U415	
ENSMUST00000146556	ENSMUSG00000020873	11	95384692	95391776	1	2	0	2	9	0	0	0	0	0	2	0	E0CZ89	
ENSMUST00000146557	ENSMUSG00000079442	2	32587095	32599698	1	0	0	0	0	0	0	1	0	8	0	11	A0A0A6YVT0	
ENSMUST00000146558						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000146559	ENSMUSG00000030990	7	102210208	102238567	1	2	2	0	43	4	0	0	0	2	2	0	D3YZA4	
ENSMUST00000146561						28	26	88	36	30	12	0	0	0	0	0		
ENSMUST00000146562						0	2	11	4	2	5	0	0	0	0	0		
ENSMUST00000146563						10	5	5	11	6	0	0	0	1	1	0		
ENSMUST00000146564						35	23	51	18	23	18	1	9	3	2	8		
ENSMUST00000146565						20	7	18	55	13	9	0	0	0	0	0		
ENSMUST00000146566						0	0	1	40	1	0	0	0	0	0	0		
ENSMUST00000146567						0	2	0	9	0	0	1	0	6	0	4		
ENSMUST00000146568	ENSMUSG00000029122	5	37289098	37336894	-1	1	9	5	0	6	1	0	0	0	0	0	F6Z2D6	
ENSMUST00000146569	ENSMUSG00000039738	16	3979105	4003770	-1	2	8	35	4	8	0	11	16	33	7	33	F6XZI3	
ENSMUST00000146570	ENSMUSG00000055923	5	76873659	76905514	-1	0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000146571						2	1	3	2	5	1	0	0	3	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146572	ENSMUSG00000038366	11	97799000	97838764	1	0	0	0	15	0	0	2	0	0	0	0	A2A6G6	
ENSMUST00000146573	ENSMUSG00000036781	9	66946086	66949516	1	0	0	1	0	0	0	0	4	0	0	0	F6S6Q3	
ENSMUST00000146574						0	1	7	7	3	3	0	0	11	0	0		
ENSMUST00000146575						3	0	0	5	2	3	4	0	0	3	6		
ENSMUST00000146577						3	0	0	0	0	3	45	1549	266	276	437		
ENSMUST00000146578						7	0	0	13	6	3	0	0	0	0	0		
ENSMUST00000146579						4	0	5	10	3	0	0	9	3	8	0		
ENSMUST00000146580						0	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000146583	ENSMUSG00000051579	X	136168984	136172342	-1	0	0	9	4	0	0	0	3	0	18	7	A2AJR8	
ENSMUST00000146584						7	4	14	7	6	0	10	131	17	20	48		
ENSMUST00000146585						11	2	19	5	18	6	31	58	20	9	12		
ENSMUST00000146586						0	5	1	14	0	3	0	0	0	0	0		
ENSMUST00000146588						0	0	1	0	0	0	9	0	7	8	16		
ENSMUST00000146589						0	2	3	0	0	3	0	0	0	0	7		
ENSMUST00000146590	ENSMUSG00000020109	10	59879556	59899302	1	0	0	11	0	0	0	172	375	270	38	217		Q9QYI4
ENSMUST00000146591						0	0	0	187	9	0	0	0	0	1	1		
ENSMUST00000146592	ENSMUSG00000033569	1	25067476	25829707	-1	5	11	0	0	0	0	0	0	0	0	0	Q68FL1	
ENSMUST00000146593						6	3	14	4	10	5	0	0	0	3	0		
ENSMUST00000146595						39	26	67	120	39	41	3	5	7	3	14		
ENSMUST00000146596						5	8	11	8	11	3	8	4	10	7	42		
ENSMUST00000146597	ENSMUSG00000062345	1	107511423	107535478	1	1	0	0	0	0	0	6	34	11	30	28	F6QN99	
ENSMUST00000146598	ENSMUSG00000027746	3	53853376	53863830	-1	17	16	18	37	18	16	169	634	270	442	188		P61961
ENSMUST00000146599						1	0	3	123	3	0	0	2	0	0	0		
ENSMUST00000146600						5	8	3	14	8	2	16	25	45	2	40		
ENSMUST00000146601	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	4	0	0	23	36	49	26	35	D3Z3N3	
ENSMUST00000146602						3	0	2	1	1	2	0	2	2	3	3		
ENSMUST00000146603						20	0	10	1	25	5	10	92	0	22	0		
ENSMUST00000146604						73	50	544	168	59	50	4	6	4	0	5		
ENSMUST00000146605	ENSMUSG00000035642	7	97550331	97579497	-1	4	0	15	10	0	2	3	0	5	0	0	D3Z442	
ENSMUST00000146606						4	0	6	7	0	6	0	0	0	0	0		
ENSMUST00000146607						5	3	13	8	7	0	0	0	0	0	0		
ENSMUST00000146608						1	1	7	0	0	0	0	0	1	0	0		
ENSMUST00000146609	ENSMUSG00000041375	7	16274042	16286795	-1	1	0	3	21	3	0	0	0	5	0	0	A0A0G2JDC5	
ENSMUST00000146610						20	18	98	33	25	17	0	0	0	0	0		
ENSMUST00000146611	ENSMUSG00000078771	11	79526560	79530609	-1	0	1	1	0	0	0	3	23	0	2	4	Q5SYH8	
ENSMUST00000146612	ENSMUSG00000039936	4	149649168	149702571	-1	5	0	0	1	0	0	0	64	0	4	0	B1AS26	
ENSMUST00000146613						18	19	48	16	14	1	0	1	0	0	1		
ENSMUST00000146615						0	4	0	6	6	3	0	3	0	1	2		
ENSMUST00000146616						5	3	0	0	2	0	0	0	0	0	3		
ENSMUST00000146617	ENSMUSG00000028803	4	135445420	135495038	-1	0	0	0	0	0	0	4	0	0	0	0	A2ADH8	
ENSMUST00000146618						12	0	24	40	6	1	0	0	0	0	0		
ENSMUST00000146619						6	0	4	5	7	3	3	0	0	0	0		
ENSMUST00000146620	ENSMUSG00000022469	15	97744770	97767972	-1	0	0	7	26	6	3	0	0	0	0	0	D3Z4E9	
ENSMUST00000146621						6	10	11	7	11	5	0	6	5	3	7		
ENSMUST00000146623	ENSMUSG00000050627	9	114899341	114933987	-1	23	16	26	102	37	11	1065	1808	1904	401	661	B2RSR7	Q3ULJ0
ENSMUST00000146625	ENSMUSG00000063049	8	47667178	47675556	-1	9	2	0	35	8	0	0	0	0	0	0	B6ZI39	
ENSMUST00000146626	ENSMUSG00000074673	2	152962485	153008482	1	0	7	0	3	11	0	0	0	0	0	0	D6RCJ6	
ENSMUST00000146627	ENSMUSG00000031626	8	45507788	45827906	1	2	0	0	5	0	0	0	0	0	0	0	F6V513	
ENSMUST00000146628	ENSMUSG00000022472	15	81992523	82033862	-1	10	16	0	21	13	19	30	0	0	0	21	D6RDE8	
ENSMUST00000146629	ENSMUSG00000015759	14	46775582	46788411	-1	0	6	13	0	0	0	0	0	0	0	0	D6RGU4	
ENSMUST00000146630	ENSMUSG00000042613	3	89436706	89450952	1	3	3	7	0	0	0	134	58	168	4	172	D3YY15	
ENSMUST00000146631						0	4	0	23	3	4	32	118	67	216	93		
ENSMUST00000146634	ENSMUSG00000049482	8	122476143	122484138	1	0	1	0	17	0	0	0	0	0	0	0	D3Z7U9	
ENSMUST00000146635	ENSMUSG00000041828	11	110025634	110095978	-1	1	0	0	1	0	2	0	0	0	0	0	F6YSZ8	
ENSMUST00000146636						4	1	12	7	5	3	0	3	2	0	0		
ENSMUST00000146637	ENSMUSG00000036529	15	89288236	89315311	-1	0	0	9	0	0	3	0	0	0	0	0	F7AWK3	
ENSMUST00000146638						8	1	0	5	29	13	57	488	71	41	85		
ENSMUST00000146639						0	1	0	0	0	0	2	0	0	0	0		
ENSMUST00000146640	ENSMUSG00000020256	10	83487450	83534140	-1	6	8	0	0	0	3	1	0	0	0	0	D3Z6B9	
ENSMUST00000146641						13	3	2	14	9	7	53	47	22	3	29		
ENSMUST00000146642	ENSMUSG00000057156	14	54852736	54870961	-1	2	0	0	0	0	0	0	0	4	0	1	D3YV74	
ENSMUST00000146643						4	1	2	7	3	3	6	33	11	0	27		
ENSMUST00000146645						3	0	0	4	0	0	25	0	9	0	0		
ENSMUST00000146646						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000146647	ENSMUSG00000032702	19	25236975	25434496	1	21	13	31	142	37	5	0	0	0	0	0	E9Q944	
ENSMUST00000146648						1	0	2	0	1	4	0	0	0	0	0		
ENSMUST00000146650	ENSMUSG00000009350	11	87793581	87804413	1	2	0	7	5	4	2	63	334	27	18	12	F7DC05	
ENSMUST00000146651						3	1	4	1	1	0	0	0	0	0	0		
ENSMUST00000146652						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000146653						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146655						0	0	2	58	0	0	0	0	0	0	0		
ENSMUST00000146656						2	0	3	0	4	0	0	0	0	1	0		
ENSMUST00000146659						0	0	0	35	0	0	18	0	0	0	8		
ENSMUST00000146660						0	0	0	99	5	0	0	0	0	0	0		
ENSMUST00000146661						6	0	10	4	8	0	13	17	0	13	0		
ENSMUST00000146662						0	0	0	0	0	0	8	0	0	0	0		
ENSMUST00000146664						0	1	2	0	2	1	0	0	0	0	0		
ENSMUST00000146665	ENSMUSG00000033845	1	4773206	4785739	-1	0	0	39	0	0	0	13	29	4	23	21	A0A0A6YVP4	
ENSMUST00000146666						10	4	6	6	9	5	0	25	4	8	7		
ENSMUST00000146667	ENSMUSG00000030177	6	120324323	120364374	-1	0	1	3	12	0	1	0	0	4	0	0	D3YV60	
ENSMUST00000146668						2	0	10	1	6	3	0	0	0	0	0		
ENSMUST00000146669	ENSMUSG00000049537	5	83278145	83355195	-1	4	1	0	0	1	0	0	0	0	0	0	F6V7S2	
ENSMUST00000146672	ENSMUSG00000002771	7	45831883	45870928	-1	2	0	5	87	3	2	4	2	7	2	9	D3Z2M4	
ENSMUST00000146673	ENSMUSG00000086965	16	18498901	18501658	1	11	6	5	8	4	5	1	3	0	2	6	D3YWW5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146674						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000146675	ENSMUSG00000022487	15	103402405	103430470	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DAN6
ENSMUST00000146676						0	0	0	79	0	0	0	1	2	0	3		
ENSMUST00000146677						9	5	44	0	16	14	0	68	106	0	0		
ENSMUST00000146680						0	0	0	0	0	1	2	0	0	0	0		
ENSMUST00000146682	ENSMUSG00000052613	10	73099342	74649737	1	3	0	2	0	0	1	0	0	0	0	0		Q99PJ1
ENSMUST00000146683						1	0	4	23	0	0	0	0	0	0	0		
ENSMUST00000146684						0	1	3	6	2	1	0	147	42	62	16		
ENSMUST00000146685						1	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000146686						58	41	204	81	49	16	18	93	21	3	20		
ENSMUST00000146687						6	3	5	6	7	4	0	2	0	0	0		
ENSMUST00000146688	ENSMUSG00000086147	4	146971976	146990755	1	2	5	8	0	0	2	0	0	0	0	0	H3BLB0	
ENSMUST00000146689						1	6	1	11	3	4	0	0	0	0	0		
ENSMUST00000146691						2	10	0	0	10	0	107	142	1874	90838	8044		
ENSMUST00000146692	ENSMUSG00000010751	7	143634806	143649661	-1	18	0	46	35	23	0	0	9	0	0	0		Q9ER62
ENSMUST00000146693	ENSMUSG00000020868	11	94663851	94677515	-1	0	0	2	0	0	0	7	0	0	0	0	F2Z434	
ENSMUST00000146694	ENSMUSG00000036890	2	44564412	44927657	-1	0	0	0	0	0	0	0	0	0	0	0	B1AY88	
ENSMUST00000146695						0	0	0	1	2	0	8	51	41	58	56		
ENSMUST00000146696						3	4	0	1	2	0	36	194	37	11	68		
ENSMUST00000146697						4	3	3	2	3	0	3	6	6	0	4		
ENSMUST00000146698	ENSMUSG00000029464	5	122371876	122382902	1	2	2	2	8	10	5	0	0	0	0	0	F6WTD8	
ENSMUST00000146699						17	21	78	16	26	8	14	10	23	8	3		
ENSMUST00000146703						1	3	3	3	1	0	3	5	6	0	3		
ENSMUST00000146705						1	1	27	2	5	0	1	0	1	0	2		
ENSMUST00000146706	ENSMUSG00000024163	17	24892153	24936977	-1	0	0	0	0	1	0	0	0	0	0	0	D3YWH6	
ENSMUST00000146707						1	2	7	21	0	3	4	12	3	0	7		
ENSMUST00000146708	ENSMUSG00000022708	16	42875881	43642602	1	1	2	1	0	5	0	0	0	0	0	0	E0CXK1	
ENSMUST00000146709						0	3	5	1	1	4	0	0	3	0	0		
ENSMUST00000146710						3	0	8	22	1	0	0	2	2	0	0		
ENSMUST00000146711						3	8	22	14	11	8	52	205	66	9	42		
ENSMUST00000146712						0	0	4	0	0	0	0	0	1	0	0		
ENSMUST00000146713						1	2	0	2	1	0	2	22	16	0	10		
ENSMUST00000146714						1	0	1	17	0	0	0	0	1	0	0		
ENSMUST00000146715	ENSMUSG00000036817	5	139200637	139249840	1	0	0	8	0	1	1	0	0	3	0	0	D3Z3N5	
ENSMUST00000146716						4	0	0	4	5	0	0	0	2	0	0		
ENSMUST00000146718						11	12	31	13	15	2	12	23	53	4	62		
ENSMUST00000146719	ENSMUSG00000053411	15	79915807	79971119	-1	0	0	0	3	0	0	0	0	0	0	0	F6WJA6	
ENSMUST00000146720						52	24	126	238	61	40	2	0	2	3	3		
ENSMUST00000146721						3	2	4	63	4	4	12	40	3	22	6		
ENSMUST00000146722	ENSMUSG00000049659	11	20685084	20741589	-1	8	0	11	0	0	9	381	1952	191	59	80		Q80WT5
ENSMUST00000146723	ENSMUSG00000024236	18	4920540	5119299	1	0	0	0	0	0	0	15	53	25	29	24	F6TBK9	
ENSMUST00000146724						2	1	19	9	10	1	6	8	8	1	9		
ENSMUST00000146725						1	2	29	7	0	0	0	0	1	0	1		
ENSMUST00000146726						2	1	0	3	2	1	4	3	0	0	3		
ENSMUST00000146727						15	3	19	100	19	15	0	0	0	0	0		
ENSMUST00000146729						0	2	2	3	0	2	4	4	5	0	11		
ENSMUST00000146730	ENSMUSG00000003279	17	69969073	70821413	1	0	0	0	0	0	0	0	0	0	0	0	D3Z709	
ENSMUST00000146731						0	0	1	6	0	0	0	0	0	0	0		
ENSMUST00000146732						0	0	5	1	2	0	1	0	0	0	2		
ENSMUST00000146733	ENSMUSG00000013936	5	122100951	122113472	1	1	0	0	0	4	0	0	4	0	3	0	A0A0G2JE15	
ENSMUST00000146734	ENSMUSG00000029029	4	154142372	154167420	1	0	0	0	0	0	0	0	0	0	3	1	F6VR19	
ENSMUST00000146735						2	4	14	3	0	1	0	0	0	0	0		
ENSMUST00000146736	ENSMUSG00000022487	15	103402405	103430470	-1	0	0	0	0	0	0	3	9	0	0	0	F6SXE5	
ENSMUST00000146737						2	0	0	2	3	6	0	0	0	0	0		
ENSMUST00000146738	ENSMUSG00000062044	7	45783738	45804144	1	4	1	3	1	9	0	0	0	0	0	0	F6TC98	
ENSMUST00000146739						2	0	1	3	1	1	0	0	0	0	0		
ENSMUST00000146740	ENSMUSG00000001017	3	90498956	90509498	-1	2	2	1	69	6	0	0	0	47	5	46	D3Z7T7	
ENSMUST00000146741						6	3	11	9	3	5	0	0	0	0	0		
ENSMUST00000146742						0	1	6	0	1	1	0	0	0	0	0		
ENSMUST00000146743						8	5	5	0	2	8	0	7	0	2	2		
ENSMUST00000146747						0	0	0	0	0	0	3	31	0	0	0		
ENSMUST00000146748						3	1	10	7	8	0	0	0	1	0	0		
ENSMUST00000146749	ENSMUSG00000069170	13	81095068	81633154	-1	0	4	3	65	0	2	0	0	0	0	0	Q8BPQ5	
ENSMUST00000146750						27	13	16	0	0	0	0	2	0	1	1		
ENSMUST00000146752						1	7	0	19	3	2	3	14	7	0	29		
ENSMUST00000146753						57	80	56	57	62	10	3	26	10	2	18		
ENSMUST00000146756	ENSMUSG00000023051	15	102518192	102523676	1	8	7	19	21	10	4	16	16	16	5	22	D3Z282	
ENSMUST00000146757						12	3	13	4	6	3	5	16	0	0	6		
ENSMUST00000146758						19	6	40	27	21	15	4	29	2	3	8		
ENSMUST00000146759						0	0	12	0	0	1	0	5	3	0	0		
ENSMUST00000146760	ENSMUSG00000089989	7	45131189	45136432	-1	0	2	2	16	3	0	37	28	30	0	0	A9QW46	P49772
ENSMUST00000146761						2	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000146762						1	3	3	3	5	1	9	29	15	7	28		
ENSMUST00000146763	ENSMUSG00000025938	1	12866549	12992650	-1	8	0	0	0	10	5	0	0	0	0	0	A0A087WP15	
ENSMUST00000146764	ENSMUSG00000004934	10	81153266	81167923	-1	51	42	77	31	75	14	68	117	59	8	87	D6RGB7	
ENSMUST00000146765						0	6	4	4	5	3	0	4	0	0	3		
ENSMUST00000146767	ENSMUSG00000057572	4	129335695	129354547	1	6	0	8	1	2	0	0	6	4	12	0		Q505B7
ENSMUST00000146768						0	0	4	55	4	1	0	0	0	2	0		
ENSMUST00000146770						3	2	0	0	9	3	0	5	7	0	6		
ENSMUST00000146771						47	48	186	189	81	39	138	265	205	12	375		
ENSMUST00000146772						3	0	0	0	3	5	1	0	1	0	1		
ENSMUST00000146773						2	1	5	3	0	2	0	0	0	1	0		
ENSMUST00000146774						1	0	4	0	2	0	0	0	0	0	0		
ENSMUST00000146775	ENSMUSG00000000416	6	18366478	18514843	-1	0	15	0	0	0	0	0	0	0	0	0	F6Q1W8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146776						0	0	3	0	0	2	0	22	0	52	33		
ENSMUST00000146777						5	2	14	86	6	3	0	4	0	0	2		
ENSMUST00000146780	ENSMUSG00000036687	5	139802485	139819917	-1	2	0	2	56	1	0	0	0	0	0	0	D3Z382	
ENSMUST00000146781						0	2	0	0	0	1	0	5	0	0	3		
ENSMUST00000146782	ENSMUSG00000023990	17	47737030	47792419	1	0	1	0	0	0	0	203	600	214	50	154	F6W7D6	
ENSMUST00000146784						3	5	6	1	14	2	0	13	4	2	20		
ENSMUST00000146785	ENSMUSG00000029922	6	39397804	39420462	-1	2	0	0	2	0	0	25	0	83	0	15	F6WPC3	
ENSMUST00000146786	ENSMUSG00000020679	11	83850063	83905819	1	0	0	17	7	0	2	0	0	0	0	0	F6XBL0	
ENSMUST00000146787						0	0	0	0	0	0	0	0	16	0	0		
ENSMUST00000146788						1	0	1	1	0	0	0	9	4	3	1		
ENSMUST00000146789						2	0	0	20	3	0	0	0	0	0	0		
ENSMUST00000146790	ENSMUSG00000031391	X	73853778	73896105	-1	0	0	0	0	0	1	3	1	0	0	3	B7ZCD3	
ENSMUST00000146791						10	8	15	6	17	4	0	0	0	0	0		
ENSMUST00000146792						1	1	3	0	1	0	9	166	43	9	8		
ENSMUST00000146793						1	2	3	0	6	3	0	3	8	3	5		
ENSMUST00000146794	ENSMUSG00000047257	9	110834588	110841313	1	0	4	0	10	12	10	0	0	0	0	1		Q8K4I7
ENSMUST00000146795						1	0	0	0	4	1	35	4	13	5	17		
ENSMUST00000146796						0	0	0	6	4	0	0	0	0	0	0		
ENSMUST00000146797						29	21	46	22	19	22	2	6	4	0	7		
ENSMUST00000146799						2	5	0	3	0	2	0	0	0	0	0		
ENSMUST00000146800						12	0	29	9	9	5	2	10	6	1	60		
ENSMUST00000146802						13	18	64	28	27	1	7	70	23	6	125		
ENSMUST00000146803						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000146804	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	9	0	4	0	5	0	6	F6RL36	
ENSMUST00000146805	ENSMUSG00000031298	X	160390690	160498070	1	0	0	0	0	0	0	0	0	0	0	0	A2AHP7	
ENSMUST00000146807						11	10	9	19	7	4	1	0	2	0	1		
ENSMUST00000146808	ENSMUSG00000046671	4	134525550	134535387	-1	0	0	0	14	0	0	15	0	0	29	8	D3Z0X8	
ENSMUST00000146809	ENSMUSG00000025138	11	120618372	120625240	-1	6	0	0	0	0	3	199	288	110	20	67	A2ABY6	
ENSMUST00000146811						0	1	5	0	2	2	0	0	0	0	0		
ENSMUST00000146812						7	0	8	12	0	0	0	15	3	2	8		
ENSMUST00000146813						0	1	0	0	1	0	0	3	3	0	1		
ENSMUST00000146814						7	8	12	16	6	5	0	1	0	0	2		
ENSMUST00000146815	ENSMUSG00000037996	4	86983124	87230477	-1	0	0	0	0	1	0	0	0	0	0	1	F6RT95	
ENSMUST00000146816	ENSMUSG00000027075	2	84838850	84863594	1	0	2	0	0	0	1	0	0	0	0	0	B0R0N4	
ENSMUST00000146817						3	0	7	5	10	0	0	0	0	0	1		
ENSMUST00000146818						0	0	0	71	2	0	0	0	0	1	0		
ENSMUST00000146819	ENSMUSG00000039842	8	18595131	18803189	1	0	1	0	0	0	3	0	3	5	0	13	E9PX19	
ENSMUST00000146820						208	219	870	326	294	153	0	0	2	0	1		
ENSMUST00000146821	ENSMUSG00000022292	15	37923952	37961318	-1	0	1	0	1	0	0	0	0	2	0	0	D3YXX2	
ENSMUST00000146822						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000146823						1	0	0	15	0	0	0	0	0	0	10		
ENSMUST00000146824						7	2	2	2	3	1	69	213	64	240	49		
ENSMUST00000146826						4	1	25	10	8	0	0	0	0	0	0		
ENSMUST00000146827						0	2	0	4	4	1	0	0	0	0	0		
ENSMUST00000146828	ENSMUSG00000029686	6	47453398	47526139	1	1	3	1	6	5	0	8	8	8	5	18	D3Z2H3	
ENSMUST00000146829						2	0	3	0	0	4	0	28	0	0	8		
ENSMUST00000146830						0	1	0	0	1	0	0	0	0	12	0		
ENSMUST00000146831	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	46	21	19	9	0	D3YXD6	
ENSMUST00000146832	ENSMUSG00000038145	9	122117283	122169702	1	0	1	0	5	0	0	9	49	70	6	40	D3YVW4	
ENSMUST00000146833						3	2	1	4	2	0	0	0	11	0	7		
ENSMUST00000146835						0	2	0	0	7	0	0	0	3	0	0		
ENSMUST00000146836	ENSMUSG00000046262	4	144206775	144213318	-1	0	1	4	1	3	2	0	0	0	0	0	A6PWB2	
ENSMUST00000146837	ENSMUSG00000025162	11	120961749	120991330	-1	0	0	0	0	0	0	11	0	22	0	0	F6VU53	
ENSMUST00000146838						10	6	17	61	5	4	0	0	0	3	2		
ENSMUST00000146839						1404	1382	3278	1555	1708	897	21	184	72	26	126		
ENSMUST00000146840	ENSMUSG00000014195	11	100582818	100620168	-1	2	2	6	3	1	0	0	0	0	0	0	A2A5E1	
ENSMUST00000146841	ENSMUSG00000042010	5	114146535	114250761	1	3	5	10	73	1	4	0	1	3	0	1	D3Z0B3	
ENSMUST00000146842	ENSMUSG00000016458	2	105126529	105173616	1	0	0	0	45	0	0	0	0	0	0	0	A2A401	
ENSMUST00000146843						7	7	1	7	8	7	0	0	0	0	1		
ENSMUST00000146844						0	0	2	1	0	2	2	22	0	0	0		
ENSMUST00000146847						2	0	2	1	3	3	3	24	9	0	52		
ENSMUST00000146848						4	0	7	3	3	1	0	0	0	1	0		
ENSMUST00000146850						72	50	395	134	58	31	1	1	1	0	4		
ENSMUST00000146851	ENSMUSG00000028600	4	108014791	108096445	-1	0	0	0	0	0	0	0	0	0	0	0	Q6P3D8	
ENSMUST00000146852						2	3	0	35	0	5	1	14	3	2	10		
ENSMUST00000146853						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000146855						0	3	2	2	0	0	0	0	0	0	0		
ENSMUST00000146856						13	15	21	10	25	7	0	0	0	2	0		
ENSMUST00000146858						0	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000146859	ENSMUSG00000029127	5	38189735	38220457	-1	1	1	6	42	1	2	1	1	0	2	4	F6YIG8	
ENSMUST00000146860	ENSMUSG00000001946	9	37528078	37538319	1	3	0	2	1	8	1	0	2	0	0	0	D3Z5Y0	
ENSMUST00000146861						1	1	5	37	2	5	0	0	27	0	0		
ENSMUST00000146862						2	0	0	30	1	0	0	0	0	0	0		
ENSMUST00000146863	ENSMUSG00000038005	8	60890418	60907580	1	0	0	0	40	0	1	0	34	0	17	10	D6RFB7	
ENSMUST00000146864	ENSMUSG00000029125	5	38038742	38137765	1	1	1	0	0	0	0	35	15	63	0	36		
ENSMUST00000146865	ENSMUSG00000002997	12	31958476	32061296	-1	6	5	18	30	12	0	274	614	284	39	130	H3BK84	
ENSMUST00000146866						2	2	15	5	11	4	0	0	0	0	0		
ENSMUST00000146867	ENSMUSG00000044533	17	24718116	24721929	1	6	0	0	0	6	0	0	14	0	3	6	D3YWJ3	
ENSMUST00000146869						0	0	0	0	0	2	4	342	78	55	143		
ENSMUST00000146870						40	56	108	49	60	22	4	28	15	5	24		
ENSMUST00000146871	ENSMUSG00000018401	11	87592162	87616302	1	0	0	0	0	0	0	0	0	0	0	0	A7M7R1	
ENSMUST00000146872	ENSMUSG00000004263	6	124742544	124756524	-1	0	2	0	55	5	0	14	0	9	0	7	D3YYE6	
ENSMUST00000146873	ENSMUSG00000026589	1	157506728	157568425	1	3	4	9	13	9	8	0	5	0	0	0	F6Q2Y9	
ENSMUST00000146874						1	0	0	0	0	1	3	1	3	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146875						1	2	1	2	4	2	0	1	1	0	0		
ENSMUST00000146876	ENSMUSG00000020263	10	83600033	83648738	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z340	
ENSMUST00000146877						0	2	2	1	0	0	0	0	1	0	0		
ENSMUST00000146878	ENSMUSG00000006930	11	100347327	100356128	-1	2	0	1	11	0	0	0	0	0	0	0	G3UZT4	
ENSMUST00000146879						0	0	2	8	0	0	5	0	0	0	5		
ENSMUST00000146880						0	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000146881	ENSMUSG00000036617	2	19909780	20810713	1	0	0	0	0	0	0	0	0	0	0	0	B1AY49	
ENSMUST00000146882						1	1	11	6	4	0	0	4	0	2	0		
ENSMUST00000146884						11	13	18	8	21	6	0	3	0	5	13		
ENSMUST00000146885						3	5	6	4	4	1	0	0	0	0	0		
ENSMUST00000146886						4	5	0	0	1	5	17	116	27	4	45		
ENSMUST00000146888						155	138	237	106	104	68	7	13	7	1	22		
ENSMUST00000146889						2	3	1	1	3	1	11	196	67	64	77		
ENSMUST00000146890						0	0	0	0	1	1	0	0	0	0	8		
ENSMUST00000146891						71	80	92	63	65	39	1	6	5	0	3		
ENSMUST00000146892						0	0	2	5	1	0	30	34	10	26	4		
ENSMUST00000146893						0	0	3	3	0	0	3	17	15	4	1		
ENSMUST00000146894	ENSMUSG00000020653	12	24651371	24662774	1	0	0	0	0	0	0	0	0	3	0	0	D3Z0S4	
ENSMUST00000146895	ENSMUSG00000035011	10	81135220	81152995	1	0	0	2	27	0	0	0	1	3	0	0	D3YZI8	
ENSMUST00000146896	ENSMUSG00000020923	11	102304560	102319742	-1	0	2	0	0	1	0	0	0	0	0	0	G3UZW9	
ENSMUST00000146897						3	0	0	0	1	0	0	0	3	0	0		
ENSMUST00000146898						0	0	0	33	0	0	2	7	6	0	7		
ENSMUST00000146899	ENSMUSG00000001211	10	78269178	78352489	-1	0	0	0	0	0	0	3	0	0	0	0	D3YV65	
ENSMUST00000146900						3	0	3	0	5	1	2	14	4	6	7		
ENSMUST00000146901						9	8	4	2	14	12	0	9	5	17	17		
ENSMUST00000146903	ENSMUSG00000023118	7	19024377	19054618	1	35	29	65	40	41	27	102	349	177	14	325	S4R2Q3	
ENSMUST00000146904						6	2	3	3	6	5	3	7	5	2	8		
ENSMUST00000146905	ENSMUSG00000047446	12	40005447	40038025	-1	9	16	14	23	9	9	6	15	7	26	7		P61213
ENSMUST00000146907	ENSMUSG00000040601	7	26435113	26476142	1	4	3	0	2	9	0	0	0	0	0	0		
ENSMUST00000146908						55	33	120	68	52	42	2	35	12	4	29		
ENSMUST00000146910						1	0	0	1	4	3	2	9	6	1	8		
ENSMUST00000146911						16	24	16	24	27	14	77	261	280	89	250		
ENSMUST00000146912	ENSMUSG00000020728	11	108425192	108860615	1	3	2	14	3	2	0	0	0	0	0	0	I7HPW3	
ENSMUST00000146913						0	0	2	0	1	2	24	224	70	25	70		
ENSMUST00000146914						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000146916	ENSMUSG00000034771	10	81574561	81590845	1	0	0	0	0	0	0	0	0	0	0	12	E9PV07	
ENSMUST00000146917						3	0	3	7	2	0	0	0	0	0	4		
ENSMUST00000146919	ENSMUSG00000054823	8	25601601	25719667	1	3	0	0	33	0	8	467	2109	1060	87	635		Q6P2L6
ENSMUST00000146920						6	6	9	6	9	0	0	2	0	0	6		
ENSMUST00000146921						0	11	14	13	0	7	5	55	8	0	10		
ENSMUST00000146922						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000146923	ENSMUSG00000024163	17	24892153	24936977	-1	19	3	37	94	32	9	39	34	62	9	38	Q3UHB5	Q9ESN9
ENSMUST00000146924						1	1	0	0	1	4	5	4	2	0	0		
ENSMUST00000146925						2	0	2	1	2	1	3	4	11	1	12		
ENSMUST00000146927	ENSMUSG00000006333	7	3703993	3706897	1	7	0	0	0	0	0	955	2080	860	640	521	F7CJS8	
ENSMUST00000146930						3	3	11	54	8	3	2	21	6	0	13		
ENSMUST00000146931	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	101	0	1	5	2	0	0	6		
ENSMUST00000146932						0	4	19	52	0	0	0	0	0	0	0		
ENSMUST00000146933						1	0	0	0	0	0	2	13	6	0	4		
ENSMUST00000146934	ENSMUSG00000037286	9	100597798	100959375	1	3	11	0	2	0	4	34	224	202	96	71	F6XQW1	
ENSMUST00000146935						0	0	0	0	0	0	3	28	21	2	17		
ENSMUST00000146936						3	1	1	4	4	0	0	0	0	0	0		
ENSMUST00000146937						2	2	1	2	3	0	5	16	0	0	2		
ENSMUST00000146939						0	0	0	0	0	0	1	3	0	0	0		
ENSMUST00000146940	ENSMUSG00000084128	8	106130319	106136974	-1	2	0	0	0	7	4	2	0	0	0	0	D3Z139	
ENSMUST00000146941	ENSMUSG00000020483	11	87979525	87987533	-1	0	0	0	4	3	0	18	35	23	3	18	D6RIN4	
ENSMUST00000146942						0	2	2	2	0	2	2	12	3	4	1		
ENSMUST00000146943	ENSMUSG00000063600	3	29082023	29691209	1	4	1	4	3	1	0	0	0	0	0	0	D3YYS1	
ENSMUST00000146944						0	0	0	2	0	0	0	1	0	0	0		
ENSMUST00000146945						78	87	454	96	64	36	0	8	7	3	12		
ENSMUST00000146946						5	1	1	2	0	0	0	1	0	0	0		
ENSMUST00000146947						1	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000146948	ENSMUSG00000037270	3	36863104	37053033	1	3	0	0	0	2	0	0	238	200	102	454	F6RPM4	
ENSMUST00000146950						3	0	3	0	2	2	0	0	0	0	0		
ENSMUST00000146951						3	1	4	2	3	3	0	0	1	0	0		
ENSMUST00000146952						2	1	3	3	2	0	0	0	0	0	0		
ENSMUST00000146953						0	0	8	0	0	0	43	248	3	23	0		
ENSMUST00000146955	ENSMUSG00000030824	7	45492874	45510406	-1	0	0	8	0	1	1	147	253	250	0	194	H3BK79	
ENSMUST00000146956						0	2	1	3	0	2	18	59	22	12	30		
ENSMUST00000146958						0	0	0	0	1	0	0	0	0	5	0		
ENSMUST00000146959	ENSMUSG00000030495	7	35186385	35201114	1	0	5	0	2	5	0	0	0	0	0	0	F6U9B9	
ENSMUST00000146960						0	0	0	1	3	2	0	0	0	0	0		
ENSMUST00000146961						4	1	2	58	2	3	7	26	9	9	14		
ENSMUST00000146962						2	0	6	3	3	0	0	0	0	0	0		
ENSMUST00000146964						0	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000146965						3	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000146966						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000146967	ENSMUSG00000028339	4	47208161	47313167	1	1	1	0	2	1	0	0	0	0	0	0	A2AJY6	
ENSMUST00000146968	ENSMUSG00000058486	6	34880426	34910876	-1	0	11	0	0	0	0	0	119	0	14	0	S4R1X1	
ENSMUST00000146969						0	0	0	0	0	0	2	0	0	1	0		
ENSMUST00000146970						5	1	0	0	0	0	1	2	2	0	2		
ENSMUST00000146971						21	29	76	69	40	21	5	41	28	4	60		
ENSMUST00000146972	ENSMUSG00000031848	8	70673248	70678752	1	1	0	0	0	1	0	4	6	0	2	4	D3YTP8	
ENSMUST00000146973	ENSMUSG00000030730	7	126445858	126463108	-1	0	0	6	0	5	3	0	7	0	1	0	F6RQN3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000146974						8	2	29	21	16	15	24	56	31	8	36		
ENSMUST00000146975	ENSMUSG00000027309	2	130706200	130906406	-1	2	3	2	25	0	1	0	1	0	0	1	B0R039	
ENSMUST00000146977						1	0	5	1	1	0	151	62	301	1	232		
ENSMUST00000146979						0	0	0	0	1	1	49	270	148	192	208		
ENSMUST00000146983						2	3	5	3	3	2	0	1	0	0	0		
ENSMUST00000146984						22	8	30	13	25	10	3	40	17	2	21		
ENSMUST00000146986	ENSMUSG00000037868	10	67535475	67542188	1	0	0	0	0	0	0	0	1	0	1	0	D3YXS2	
ENSMUST00000146987						0	0	8	0	0	1	4	0	0	0	20		
ENSMUST00000146988						8	9	20	12	19	6	0	0	5	0	5		
ENSMUST00000146989						21	22	28	31	23	8	4	21	6	10	27		
ENSMUST00000146990						2	2	25	10	11	4	0	0	0	0	0		
ENSMUST00000146991						1	0	1	3	3	1	0	0	0	0	0		
ENSMUST00000146993	ENSMUSG00000015365	15	88982909	89055152	1	0	21	70	20	8	0	0	0	0	0	0	D3YWG8	
ENSMUST00000146995						0	1	5	1	1	0	0	8	7	0	0		
ENSMUST00000146996	ENSMUSG00000030990	7	102210208	102238567	1	0	0	0	0	0	0	0	8	9	0	5	D3YZI4	
ENSMUST00000146997						6	7	22	0	2	0	0	0	0	0	0		
ENSMUST00000146998	ENSMUSG00000056394	7	13277283	13311433	1	7	0	2	49	4	0	0	0	17	0	0	E9PV36	
ENSMUST00000146999						15	19	19	27	20	13	116	409	144	132	112		
ENSMUST00000147000	ENSMUSG00000025916	1	9968624	10009136	-1	3	1	0	0	0	1	24	216	18	18	2	H3BKX2	
ENSMUST00000147001						0	0	0	0	0	1	92	232	81	50	70		
ENSMUST00000147002						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147003	ENSMUSG00000023791	16	32084418	32099738	-1	0	0	0	0	0	0	14	112	33	15	0	F6WL03	
ENSMUST00000147004						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000147005						59	1	2	184	2	1	4921	2364	8614	238	8102		
ENSMUST00000147007						0	1	0	0	0	0	1	10	3	1	6		
ENSMUST00000147008						1	1	3	0	0	0	8	0	0	0	0		
ENSMUST00000147009	ENSMUSG00000001054	11	51623671	51635896	-1	0	0	14	0	0	0	33	51	9	0	8	F6VIG0	
ENSMUST00000147010						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147011						0	0	0	88	5	4	0	0	12	0	9		
ENSMUST00000147013						3	4	15	17	7	2	1	0	1	18	1		
ENSMUST00000147014						31	32	0	2	56	37	1	8	6	4	8		
ENSMUST00000147015						5	7	12	38	9	4	3	5	0	0	4		
ENSMUST00000147016						188	121	927	243	223	101	3	11	18	6	22		
ENSMUST00000147017						1	0	5	8	0	0	0	1	0	2	0		
ENSMUST00000147018	ENSMUSG00000041650	14	122534324	122891100	1	0	0	2	1	0	1	1	0	0	0	0	H3BKW6	
ENSMUST00000147020						5	3	12	0	4	2	9	22	23	0	23		
ENSMUST00000147021	ENSMUSG00000026095	1	53344617	53352752	-1	0	5	3	90	4	2	0	14	14	25	11	M0QW65	
ENSMUST00000147022						0	0	0	17	0	0	84	25	23	0	2		
ENSMUST00000147023						0	0	0	0	1	0	1	4	0	1	1		
ENSMUST00000147024	ENSMUSG00000075395	16	14562316	14621300	1	111	103	77	63	114	47	1	19	9	4	14	A9C473	
ENSMUST00000147025	ENSMUSG00000052459	16	44085402	44139705	-1	0	0	0	0	0	0	2	0	4	0	4	D3YZ23	
ENSMUST00000147026						10	4	17	12	9	7	0	0	0	0	0		
ENSMUST00000147027						0	0	3	55	1	0	0	4	2	0	0		
ENSMUST00000147028						7	0	7	7	5	4	67	53	37	171	65		
ENSMUST00000147030	ENSMUSG00000028649	4	123349633	123684360	-1	0	7	4	58	0	6	0	0	66	0	56	F6XCT0	
ENSMUST00000147032	ENSMUSG00000022696	16	44240180	44333196	-1	0	0	0	1	2	0	0	0	0	0	2	F6YLH2	
ENSMUST00000147033						1	2	5	0	1	0	3	0	0	0	0		
ENSMUST00000147035						11	15	6	13	10	10	3	0	2	0	2		
ENSMUST00000147036						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000147037						1	1	0	16	0	0	0	0	0	0	0		
ENSMUST00000147038	ENSMUSG00000027522	2	174076308	174099771	1	0	0	0	6	0	0	0	0	10	7	16	B7ZCB8	
ENSMUST00000147039						4	7	16	14	6	3	0	0	0	0	0		
ENSMUST00000147040						6	0	0	0	0	0	143	0	0	0	58		
ENSMUST00000147041	ENSMUSG00000040969	3	133112278	133234949	-1	23	17	26	11	29	10	2	1	1	1	0		Q80VK6
ENSMUST00000147042						0	1	0	35	3	2	1	0	0	2	0		
ENSMUST00000147043						2	2	3	1	3	1	0	0	5	0	3		
ENSMUST00000147044	ENSMUSG00000036989	7	105604463	105633571	-1	1	1	8	81	4	2	0	0	0	0	0	D3YUY7	
ENSMUST00000147046	ENSMUSG00000040785	16	94370618	94469222	1	0	3	0	0	0	1	0	0	2	0	0	D3Z2K0	
ENSMUST00000147047						0	0	9	5	0	4	3	3	0	24	11		
ENSMUST00000147048						9	6	9	2	11	2	0	0	0	0	0		
ENSMUST00000147049						65	67	146	172	60	54	5	17	6	10	11		
ENSMUST00000147050						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000147051						5	2	13	5	7	7	0	3	0	0	0		
ENSMUST00000147052						12	9	26	34	21	8	0	0	1	0	0		
ENSMUST00000147053						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000147054						0	2	12	35	6	6	3	2	1	17	6		
ENSMUST00000147055						3	1	0	1	1	0	6	14	22	2	0		
ENSMUST00000147056						6	2	11	12	0	2	0	0	5	0	0		
ENSMUST00000147057						0	0	0	0	0	0	0	0	5	0	0		
ENSMUST00000147058						1	2	2	3	3	0	21	49	25	13	8		
ENSMUST00000147059						0	0	0	0	0	0	187	565	39	108	13		
ENSMUST00000147060						0	1	2	30	3	1	2	9	0	0	8		
ENSMUST00000147061						0	5	11	4	0	0	0	21	0	2	0		
ENSMUST00000147062						0	0	0	0	0	0	26	114	46	4	65		
ENSMUST00000147063						12	3	46	15	12	6	0	0	0	0	0		
ENSMUST00000147064						0	1	0	0	0	0	10	57	10	12	5		
ENSMUST00000147065						0	0	2	1	0	1	14	2	28	0	41		
ENSMUST00000147068						3	0	4	14	5	0	0	7	0	0	4		
ENSMUST00000147069						0	2	0	35	3	2	0	0	0	0	0		
ENSMUST00000147070						4	4	5	27	10	5	7	80	24	0	24		
ENSMUST00000147071						1	0	6	0	4	0	0	0	0	1	0		
ENSMUST00000147072	ENSMUSG00000031864	8	68793929	68829410	1	0	0	0	2	0	0	11	25	18	12	9	F6WSW2	
ENSMUST00000147074						40	19	69	37	28	13	0	12	4	0	5		
ENSMUST00000147075						1	1	14	5	1	0	0	0	0	2	18		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147076						35	22	157	2	49	0	84	94	113	1	128		
ENSMUST00000147077	ENSMUSG00000060288	4	119300010	119320546	-1	0	0	2	7	4	0	0	17	0	0	0	A2BGI8	
ENSMUST00000147078						0	3	2	2	7	0	0	0	0	0	0		
ENSMUST00000147079	ENSMUSG00000005124	15	66891320	66923201	1	4	0	0	21	7	0	1	0	0	0	7		
ENSMUST00000147080	ENSMUSG00000020019	10	93640681	93747207	1	2	3	6	18	0	0	0	0	0	0	0	D3Z053	
ENSMUST00000147081	ENSMUSG00000014767	17	15499888	15528379	1	0	0	0	10	0	2	0	0	0	0	0	E9Q084	
ENSMUST00000147083						301	205	1115	924	389	172	29	60	35	2	87		
ENSMUST00000147084						1	0	11	4	2	0	0	0	0	2	7		
ENSMUST00000147085						12	8	9	9	19	7	6	13	3	0	18		
ENSMUST00000147086	ENSMUSG00000030720	7	126571207	126585817	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVA8	
ENSMUST00000147087						4	6	33	12	8	3	18	10	27	13	37		
ENSMUST00000147089						3	1	6	6	1	5	0	0	0	0	0		
ENSMUST00000147091						21	0	47	1	19	14	4	8	0	7	11		
ENSMUST00000147092						1	1	5	1	0	0	0	0	0	0	0		
ENSMUST00000147093						1	3	0	0	0	9	21	1	0	5	0		
ENSMUST00000147094						1	0	5	1	3	1	2	2	2	0	4		
ENSMUST00000147095						4	12	21	6	12	3	0	0	0	0	0		
ENSMUST00000147096						7	5	8	5	18	4	32	36	20	70	19		
ENSMUST00000147097	ENSMUSG00000028494	4	86648386	86670060	-1	1	0	3	0	0	2	223	598	226	367	153	B1AXR3	
ENSMUST00000147098	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	0	0	0	0	5	43	24	0	4	E9PZF9	
ENSMUST00000147099						8	11	25	17	16	7	0	11	2	1	9		
ENSMUST00000147101	ENSMUSG00000001930	6	125546774	125686679	1	4	4	0	0	16	1	25	58	50	31	29	S4R195	
ENSMUST00000147102						1	1	16	91	4	5	12	12	5	1	6		
ENSMUST00000147103	ENSMUSG00000031220	X	100402221	100442717	-1	57	60	270	95	97	51	1	6	1	0	6		Q6E1M8
ENSMUST00000147104						0	2	5	0	2	2	0	29	17	0	18		
ENSMUST00000147105	ENSMUSG00000027201	2	125084628	125123661	-1	0	10	0	132	18	0	0	0	7	0	0	A2ATP5	
ENSMUST00000147106						0	0	0	1	1	1	16	23	12	5	3		
ENSMUST00000147107						11	3	25	18	13	10	0	0	0	0	0		
ENSMUST00000147109						0	6	5	8	0	0	0	49	8	5	38		
ENSMUST00000147110	ENSMUSG00000015790	2	26913381	26916530	-1	0	0	0	0	0	0	58	325	93	91	0	A0A0A6YVR9	
ENSMUST00000147111						0	0	0	0	0	0	0	48	0	18	14		
ENSMUST00000147112						0	0	12	14	0	2	5	11	0	7	6		
ENSMUST00000147113	ENSMUSG00000048652	3	146645195	146685592	-1	3	0	0	0	0	0	0	1	0	0	0		D3YUG0
ENSMUST00000147114	ENSMUSG00000002043	7	19508670	19516145	1	0	0	0	0	0	0	0	14	0	0	0	D6RD01	
ENSMUST00000147115	ENSMUSG00000031922	9	13807792	13827107	-1	0	0	0	0	2	0	0	105	20	66	46	B8JJE7	
ENSMUST00000147116						4	10	6	4	10	0	4	22	0	9	9		
ENSMUST00000147117	ENSMUSG00000022884	16	23107444	23114136	1	0	0	0	0	0	0	0	0	0	0	0	D6RJ60	
ENSMUST00000147118						1	0	0	2	0	0	1	0	0	0	0		
ENSMUST00000147120						2	3	2	12	2	1	17	17	39	0	34		
ENSMUST00000147121	ENSMUSG00000012405	14	18267823	18271391	-1	0	2	0	34	6	3	0	0	3	0	0	B8JKK2	
ENSMUST00000147122						3	0	5	3	2	0	0	0	0	0	0		
ENSMUST00000147123						21	14	75	16	13	9	8	48	23	6	44		
ENSMUST00000147124						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000147125	ENSMUSG00000038797	7	80860920	80876537	1	0	1	0	0	0	4	21	19	15	1	8	D3YTK9	
ENSMUST00000147126						1	0	1	4	3	1	0	0	0	0	0		
ENSMUST00000147127						6	7	6	0	17	0	0	0	0	0	0		
ENSMUST00000147129	ENSMUSG00000031095	X	38533274	38576196	-1	4	9	0	14	7	0	0	9	13	11	18	J3QJX0	
ENSMUST00000147131						0	0	1	0	0	0	0	2	0	3	0		
ENSMUST00000147132						0	0	0	28	0	0	0	0	0	0	6		
ENSMUST00000147133						1	3	4	9	2	0	0	0	0	0	0		
ENSMUST00000147134	ENSMUSG00000032327	9	58063788	58153996	1	0	0	0	1	0	0	0	0	0	0	3	E9Q3G2	
ENSMUST00000147135						0	0	0	0	0	0	6	0	0	0	0		
ENSMUST00000147136						0	1	0	0	0	0	1	1	0	2	1		
ENSMUST00000147137						0	0	0	30	0	0	0	0	0	0	0		
ENSMUST00000147138	ENSMUSG00000063889	18	3266048	3337748	-1	0	2	1	1	0	0	0	0	0	13	2	D3YVP3	
ENSMUST00000147139	ENSMUSG00000048332	3	53041528	53261679	1	0	10	25	0	0	6	1	0	2	7	35		Q8BM86
ENSMUST00000147143						0	0	0	2	0	1	0	0	0	0	0		
ENSMUST00000147145						0	0	6	0	0	1	70	219	29	0	0		
ENSMUST00000147146	ENSMUSG00000008496	7	25087344	25159922	-1	3	2	14	101	4	1	0	0	0	0	0	F6X6U7	
ENSMUST00000147147	ENSMUSG00000036893	2	24789928	24919614	-1	0	0	0	0	0	7	0	0	13	4	0		Q5DW34
ENSMUST00000147148	ENSMUSG00000061461	5	53267083	53278540	1	0	0	0	0	0	0	293	530	191	360	153	D3Z7Q2	
ENSMUST00000147149						1	0	13	0	2	4	0	0	3	0	0		
ENSMUST00000147150	ENSMUSG00000030530	7	80388585	80405436	-1	0	2	2	36	4	6	4	2	2	0	14	D3YTP7	
ENSMUST00000147151						51	54	175	74	80	34	9	10	11	2	35		
ENSMUST00000147152	ENSMUSG00000025268	X	150806370	150814345	-1	4	0	3	14	1	2	0	0	0	1	4	A2AG47	
ENSMUST00000147153	ENSMUSG00000087303	19	33719670	33769142	-1	13	6	19	78	10	7	0	1	0	0	0	D3YY49	
ENSMUST00000147154						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000147155	ENSMUSG00000001520	6	128399296	128416427	1	3	1	2	2	0	4	0	0	0	0	0	F7BIJ5	
ENSMUST00000147156						7	7	6	8	10	7	0	0	0	0	0		
ENSMUST00000147157	ENSMUSG00000020288	11	23487882	23498030	-1	1	0	0	36	2	0	5	53	78	71	55	A2AF81	
ENSMUST00000147158	ENSMUSG00000002459	1	4909576	5070285	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z4Z8	
ENSMUST00000147159						1	3	4	2	2	1	0	0	0	0	0		
ENSMUST00000147160						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147161						2	1	2	6	4	1	1	0	0	0	0		
ENSMUST00000147162						6	7	34	38	26	4	23	35	13	9	36		
ENSMUST00000147163	ENSMUSG00000036819	11	59450045	59458567	1	19	0	0	0	56	0	17	0	0	0	0		Q8BFT6
ENSMUST00000147164						0	1	2	4	0	2	14	17	32	3	38		
ENSMUST00000147165						4	7	9	53	0	8	0	35	41	0	9		
ENSMUST00000147167						0	0	13	0	0	0	0	0	0	0	0		
ENSMUST00000147168	ENSMUSG00000001786	10	86021972	86051873	1	0	0	1	9	0	0	0	18	5	7	4	D6RJ76	
ENSMUST00000147169	ENSMUSG00000029847	6	34945278	34988404	-1	2	2	17	43	6	0	0	0	0	0	0	F6S2M6	
ENSMUST00000147170						4	1	6	0	3	2	0	0	0	0	0		
ENSMUST00000147171	ENSMUSG00000000766	10	6758506	7038198	1	0	3	0	0	0	0	0	0	0	0	0		P42866
ENSMUST00000147172						0	1	1	0	0	0	0	0	5	0	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147175						21	19	19	71	31	13	5	8	3	3	19		
ENSMUST00000147176						6	0	0	0	4	0	5	0	10	0	0		
ENSMUST00000147178						1	1	8	0	3	3	0	0	0	0	0		
ENSMUST00000147179						5	1	3	86	8	3	0	1	0	0	0		
ENSMUST00000147180						0	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000147182						14	11	67	6	31	0	21	22	0	0	0		
ENSMUST00000147183						76	71	187	326	116	71	34	67	49	13	62		
ENSMUST00000147184						5	4	10	2	5	1	2	0	0	0	1		
ENSMUST00000147185	ENSMUSG00000086228	9	65361060	65380377	1	13	10	35	85	22	11	2	4	6	0	3	G3UW59	
ENSMUST00000147188						3	0	5	1	1	1	2	15	5	2	0		
ENSMUST00000147189	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	7	0	0	0	0	0		Q99PJ1
ENSMUST00000147190						2	2	3	44	1	1	16	88	23	11	45		
ENSMUST00000147191						3	7	6	96	3	1	0	0	4	1	0		
ENSMUST00000147192						3	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000147193	ENSMUSG00000047193	9	6928503	7184446	-1	0	10	0	0	0	15	0	109	53	0	5		Q45VK7
ENSMUST00000147195						5	3	4	4	12	1	0	10	5	0	22		
ENSMUST00000147196	ENSMUSG00000019797	10	43525121	43540994	-1	7	7	6	0	8	2	0	0	0	0	0	D3Z316	
ENSMUST00000147197	ENSMUSG00000044252	18	12755314	12941841	-1	0	0	0	0	0	1	0	0	1	1	1	D6RDE4	
ENSMUST00000147199						0	0	0	0	1	0	1	0	0	0	16		
ENSMUST00000147200	ENSMUSG00000028064	3	88435959	88461182	-1	2	2	9	0	1	0	61	0	31	0	0	D3YUM4	
ENSMUST00000147201						0	0	0	134	0	0	0	0	0	0	5		
ENSMUST00000147202						0	2	12	0	0	0	0	11	0	0	0		
ENSMUST00000147203						6	5	31	8	14	1	7	35	21	14	46		
ENSMUST00000147204	ENSMUSG00000079484	2	30266203	30282149	1	0	1	0	0	0	0	1	7	1	0	0	F7CAL7	
ENSMUST00000147205						1	0	1	3	0	0	1	4	2	2	5		
ENSMUST00000147207						0	0	0	0	0	0	30	0	0	0	5		
ENSMUST00000147209						1	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000147210						2	1	0	19	0	0	0	123	42	0	10		
ENSMUST00000147211						15	8	47	34	25	13	0	1	5	1	6		
ENSMUST00000147213	ENSMUSG00000029802	6	58584523	58695676	1	7	10	12	2	6	6	0	0	0	0	0	D3YZX5	
ENSMUST00000147214						2	0	1	40	4	4	0	0	3	0	3		
ENSMUST00000147215						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147216						8	1	2	5	5	2	0	0	0	1	0		
ENSMUST00000147217	ENSMUSG00000028108	3	95734147	95739569	-1	3	5	1	0	0	1	75	26	51	1	47	D3YZV0	
ENSMUST00000147218	ENSMUSG00000026436	1	132007607	132032612	1	8	10	51	5	5	7	181	804	372	139	391	F6ZCI1	
ENSMUST00000147219						4	0	18	21	9	10	520	1013	614	269	568		
ENSMUST00000147220						0	5	6	0	0	4	0	4	0	0	13		
ENSMUST00000147223						62	45	113	80	74	29	15	38	15	4	55		
ENSMUST00000147224						3	8	4	10	12	5	0	5	0	0	4		
ENSMUST00000147225	ENSMUSG00000004071	16	4750348	4790292	-1	318	362	70	75	235	69	2	1	4	0	7	F6X7Q6	
ENSMUST00000147226						16	22	57	210	30	6	3	8	5	0	0		
ENSMUST00000147227						0	1	0	5	1	0	0	45	0	0	0		
ENSMUST00000147228	ENSMUSG00000028649	4	123349633	123684360	-1	22	18	39	21	33	13	2	0	19	0	0	F6SHS0	
ENSMUST00000147229						13	13	65	61	15	9	1	6	2	1	1		
ENSMUST00000147232						0	1	6	1	1	0	22	88	17	6	42		
ENSMUST00000147233						0	0	2	18	10	0	78	1786	209	38	949		
ENSMUST00000147234						0	0	1	0	0	0	0	0	10	0	0		
ENSMUST00000147236						0	1	2	0	1	0	4	0	9	3	10		
ENSMUST00000147237	ENSMUSG00000005774	3	94954075	94961561	1	0	0	1	20	0	0	0	0	0	1	0	D3Z0D4	
ENSMUST00000147238						1	0	5	0	0	1	12	51	12	0	0		
ENSMUST00000147239	ENSMUSG00000017119	11	101552149	101581951	1	3	2	0	1	0	1	0	0	0	0	0	A2A4R0	
ENSMUST00000147241	ENSMUSG00000037336	12	4862440	4874359	-1	0	3	0	20	0	0	0	0	4	0	0	D6RDD7	
ENSMUST00000147242						2	2	3	0	0	2	0	0	2	0	0		
ENSMUST00000147243						12	5	12	20	6	5	0	0	0	0	0		
ENSMUST00000147244	ENSMUSG00000040464	5	5537454	5559538	-1	3	1	9	2	0	0	0	0	0	0	0	D6RCG6	
ENSMUST00000147245						13	15	45	24	25	17	6	9	9	6	10		
ENSMUST00000147246	ENSMUSG00000005674	1	171216011	171222514	-1	0	0	0	0	0	0	4	0	1	1	0	D3Z346	
ENSMUST00000147247						35	20	84	365	59	32	26	53	23	1	52		
ENSMUST00000147248						1	2	1	4	1	0	0	1	0	0	0		
ENSMUST00000147249	ENSMUSG00000101152	9	104040662	104075879	1	1	0	0	1	2	1	0	1	0	0	0	F6U473	
ENSMUST00000147250	ENSMUSG00000032363	9	90163069	90208071	1	0	0	0	0	0	0	0	0	0	1	0	F6UD05	
ENSMUST00000147251	ENSMUSG00000068740	3	108390851	108415552	-1	10	4	0	3	0	0	2	0	0	0	3	F7BHW1	
ENSMUST00000147252						12	10	22	8	19	4	0	0	0	1	0		
ENSMUST00000147253						0	2	8	5	3	0	0	0	0	0	0		
ENSMUST00000147254						8	2	9	7	5	3	0	0	3	1	4		
ENSMUST00000147255						38	42	37	411	64	40	11	45	35	6	27		
ENSMUST00000147256						30	28	256	65	47	28	3	2	6	2	20		
ENSMUST00000147257	ENSMUSG00000052301	7	126847416	126852705	1	0	0	0	0	0	0	0	0	0	0	0	D3Z126	
ENSMUST00000147258						0	2	4	12	4	5	2	4	6	19	10		
ENSMUST00000147259						0	0	0	0	2	0	3	0	0	0	1		
ENSMUST00000147261						1	0	5	1	8	1	0	1	0	0	0		
ENSMUST00000147262						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000147263						4	14	9	11	8	2	1	0	2	0	2		
ENSMUST00000147264						0	0	0	0	0	0	23	43	0	0	8		
ENSMUST00000147265						35	39	69	24	34	21	72	481	75	67	166		
ENSMUST00000147266						1	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000147267						3	0	13	177	5	2	30	29	41	0	14		
ENSMUST00000147268						0	0	0	0	5	3	0	33	0	0	0		
ENSMUST00000147269	ENSMUSG00000033416	10	75351111	75517972	-1	0	0	4	1	0	0	0	4	2	0	2	D3YY66	
ENSMUST00000147270	ENSMUSG00000028977	4	148804429	148954889	1	0	0	0	13	0	0	0	0	0	0	0	B1AS47	
ENSMUST00000147271						0	0	0	32	0	0	0	0	0	0	0		
ENSMUST00000147272	ENSMUSG00000035649	4	44755877	44932215	1	22	24	32	21	13	6	44	209	136	53	149		B1AX39
ENSMUST00000147273						7	7	13	9	7	8	9	60	11	4	25		
ENSMUST00000147274						1	0	0	2	0	0	51	110	52	5	55		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147275	ENSMUSG00000019087	X	74297097	74304721	1	0	0	1	0	5	0	0	0	11	0	0	B7FAU7	
ENSMUST00000147276						3	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000147277	ENSMUSG00000060733	10	71347763	71433327	1	0	3	0	0	0	0	29	0	103	14	124		Q7TT16
ENSMUST00000147278						21	9	15	10	35	16	11	0	0	0	0		
ENSMUST00000147279	ENSMUSG00000015357	9	65294260	65330658	1	2	0	0	0	0	0	0	0	0	0	2	F7BB92	
ENSMUST00000147280						4	1	4	2	2	1	0	0	0	0	1		
ENSMUST00000147281	ENSMUSG00000071477	6	48024188	48048911	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z5F8	
ENSMUST00000147282	ENSMUSG00000030322	6	115840697	115853371	-1	10	11	6	9	12	6	0	5	8	4	20	Q3TU27	
ENSMUST00000147283	ENSMUSG00000041476	X	157698910	157752591	1	0	2	0	0	1	0	0	0	0	0	0	D6RJ22	
ENSMUST00000147284						1	0	1	10	2	0	0	0	0	0	0		
ENSMUST00000147285						7	7	23	65	6	5	0	0	0	0	0		
ENSMUST00000147286						0	2	3	5	1	2	0	0	1	0	1		
ENSMUST00000147287						9	7	10	28	16	15	7	8	7	1	15		
ENSMUST00000147288	ENSMUSG00000035585	7	3692863	3701024	1	1	1	0	1	2	0	3	19	26	9	16		
ENSMUST00000147289	ENSMUSG00000040829	11	70459433	70466202	1	0	0	0	0	0	0	0	0	0	0	1	J3QK22	
ENSMUST00000147290						1	0	0	0	0	0	3	0	2	0	0		
ENSMUST00000147291						0	0	0	0	2	3	0	2	8	0	8		
ENSMUST00000147292	ENSMUSG00000028698	4	116221618	116303056	1	1	0	13	23	8	0	0	0	0	0	1	B1AUF8	
ENSMUST00000147293						18	33	36	13	20	17	1	9	7	2	11		
ENSMUST00000147295						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147296						1	0	17	0	0	1	2	0	0	0	0		
ENSMUST00000147297						1	0	0	3	2	2	0	4	0	0	0		
ENSMUST00000147298						7	2	14	94	11	10	0	0	0	0	0		
ENSMUST00000147299						0	9	11	18	11	3	0	0	0	0	0		
ENSMUST00000147301	ENSMUSG00000020686	11	83421902	83429455	-1	0	0	59	0	0	19	1	0	1	0	0	F2Z4A6	
ENSMUST00000147302						0	0	0	23	0	0	1	0	3	0	2		
ENSMUST00000147303						3	3	5	4	7	0	71	539	143	21	278		
ENSMUST00000147304	ENSMUSG00000055436	3	158010473	158036639	-1	0	0	0	0	0	0	5	29	17	0	7	F6TN80	
ENSMUST00000147305	ENSMUSG00000031928	9	14784654	14837123	1	0	0	12	10	3	0	3	0	5	2	4	B2KF76	
ENSMUST00000147306						1	0	1	1	4	0	0	0	0	11	0		
ENSMUST00000147307						22	12	73	29	26	10	0	0	0	0	0		
ENSMUST00000147308	ENSMUSG00000025995	1	45795166	45823619	1	0	0	0	11	0	0	1	0	0	0	0	D3Z504	
ENSMUST00000147309						21	25	47	26	35	16	17	41	28	6	30		
ENSMUST00000147310						0	0	2	1	3	1	7	4	5	7	0		
ENSMUST00000147311						1	1	2	2	1	1	212	801	248	1450	181		
ENSMUST00000147312						0	0	0	0	0	0	25	4	11	8	4		
ENSMUST00000147313	ENSMUSG00000056153	18	88665224	88927481	-1	0	1	2	2	1	0	0	0	7	0	0		
ENSMUST00000147314						2	2	4	1	3	2	0	0	0	0	0		
ENSMUST00000147315						1	0	0	0	2	0	0	33	6	0	11		
ENSMUST00000147316						5	3	5	0	0	4	0	1	0	0	0		
ENSMUST00000147318						0	0	0	3	0	4	3	2	3	0	10		
ENSMUST00000147319						5	4	24	172	14	2	0	2	0	0	4		
ENSMUST00000147321						2	0	0	0	0	0	0	5	2	0	0		
ENSMUST00000147322						6	4	1	4	4	1	0	0	0	0	0		
ENSMUST00000147323	ENSMUSG00000020622	12	10369973	10390173	1	0	9	12	0	0	9	0	0	0	0	0	D6REF4	
ENSMUST00000147325						0	0	0	0	0	0	37	38	44	15	27		
ENSMUST00000147326	ENSMUSG00000040528	11	106751226	106768794	1	3	0	2	0	0	0	78	421	191	212	10		Q3TB92
ENSMUST00000147327						2	6	12	6	7	5	17	8	7	0	15		
ENSMUST00000147328	ENSMUSG00000036687	5	139802485	139819917	-1	0	0	4	7	3	0	0	0	0	0	0	D3Z295	
ENSMUST00000147329						17	15	24	14	25	12	0	0	0	1	0		
ENSMUST00000147330						4	7	6	29	8	5	0	0	0	0	2		
ENSMUST00000147331	ENSMUSG00000025486	7	140863670	140882309	-1	0	0	0	7	0	0	16	0	5	1	4	D3YTK6	
ENSMUST00000147332	ENSMUSG00000025421	18	76930126	76972902	1	6	5	47	0	18	3	1	0	0	0	1		Q3UGR5
ENSMUST00000147333	ENSMUSG00000027318	2	131050591	131063814	-1	2	2	5	3	3	2	0	0	0	0	1	F6Z4C4	
ENSMUST00000147334						0	3	0	6	0	0	0	0	0	0	0		
ENSMUST00000147335						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000147336						0	0	0	20	0	0	0	0	0	0	0		
ENSMUST00000147337	ENSMUSG00000038696	2	34406771	34624950	1	24	0	0	34	0	0	146	241	163	69	194		Q8BKH7
ENSMUST00000147338						7	4	32	9	11	9	7	7	13	0	10		
ENSMUST00000147339	ENSMUSG00000075028	2	92965151	93046167	-1	0	0	0	9	0	0	0	0	0	0	0	A0A0A0MQL7	
ENSMUST00000147340						0	0	0	3	1	0	8	11	12	55	6		
ENSMUST00000147341						0	7	0	0	0	0	0	0	2	0	2		
ENSMUST00000147342	ENSMUSG00000040728	4	11331933	11386783	-1	4	0	3	0	0	0	0	0	0	0	0	Z4YMV4	
ENSMUST00000147343						5	2	6	6	2	1	17	21	41	0	31		
ENSMUST00000147344						0	0	8	18	0	0	0	0	0	5	0		
ENSMUST00000147345						4	0	0	0	0	0	32	114	80	11	29		
ENSMUST00000147346						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147347						2	0	0	1	0	0	0	5	0	1	0		
ENSMUST00000147348	ENSMUSG00000029174	5	64156305	64351486	1	3	0	0	0	0	2	0	0	8	0	124	F6QUA9	
ENSMUST00000147349	ENSMUSG00000031196	X	75172715	75382615	-1	1	0	10	0	3	0	0	0	0	0	0	B1AW26	
ENSMUST00000147350	ENSMUSG00000027668	3	32529465	32579239	1	0	0	0	0	0	0	0	0	10	0	0	D3Z5P8	
ENSMUST00000147351						2	5	5	5	4	2	0	0	0	0	0		
ENSMUST00000147352	ENSMUSG00000040785	16	94370618	94469222	1	4	0	0	0	0	0	0	0	0	0	0	D6RHT6	
ENSMUST00000147353						0	0	0	0	0	0	3	0	20	0	9		
ENSMUST00000147354	ENSMUSG00000038668	4	58435255	58553898	-1	1	0	8	21	2	1	0	0	0	0	0	A2AMJ0	
ENSMUST00000147355						0	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000147356	ENSMUSG00000034813	10	119454034	120087261	1	0	5	0	137	21	2	0	0	0	0	0	Q6GQT7	
ENSMUST00000147358						0	0	0	0	0	0	6	41	0	0	15		
ENSMUST00000147360						0	0	33	0	0	7	270	478	140	0	651		
ENSMUST00000147361						0	0	0	0	0	0	7	19	0	4	17		
ENSMUST00000147362	ENSMUSG00000037552	7	28359604	28372599	-1	0	0	0	0	4	0	0	2	0	0	0	D3YY99	
ENSMUST00000147363	ENSMUSG00000072946	12	84285232	84315832	1	9	15	29	6	10	10	9	3	17	0	3		Q8VDQ1
ENSMUST00000147364						0	2	12	0	3	2	2	0	7	0	9		
ENSMUST00000147365	ENSMUSG00000026739	2	18677018	18686629	1	1	4	3	39	1	0	4	0	0	0	0	A2ASR5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147366						0	3	10	0	7	0	0	4	6	0	9		
ENSMUST00000147367						5	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000147368						1	2	6	1	2	1	0	2	0	0	0		
ENSMUST00000147369						1	3	6	12	10	2	103	399	30	29	29		
ENSMUST00000147371						5	1	1	4	1	0	1	0	2	0	0		
ENSMUST00000147372						35	29	194	80	39	33	4	31	2	2	6		
ENSMUST00000147373	ENSMUSG00000028729	4	118620799	118627776	1	0	0	0	0	0	0	25	0	0	0	3	A2ACZ1	
ENSMUST00000147374						0	2	0	16	6	0	0	0	0	0	0		
ENSMUST00000147375						6	4	1	7	4	3	2	9	5	8	4		
ENSMUST00000147376						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000147377						2	0	21	0	5	3	0	0	0	0	6		
ENSMUST00000147380	ENSMUSG00000027715	3	36564865	36572150	-1	5	2	0	0	0	0	33	66	124	39	67	D6RIK7	
ENSMUST00000147381						0	2	2	1	1	0	0	1	0	0	1		
ENSMUST00000147382						44	74	103	51	44	28	0	15	10	7	21		
ENSMUST00000147383						31	0	142	122	33	32	14	94	24	0	79		
ENSMUST00000147384						0	4	12	182	2	3	0	2	0	0	0		
ENSMUST00000147385						26	19	20	31	22	10	7	5	8	0	5		
ENSMUST00000147386	ENSMUSG00000000686	11	77515121	77538607	1	0	4	0	0	0	0	0	0	0	1	7	F7C9J3	
ENSMUST00000147387						5	1	1	5	2	2	12	22	0	0	12		
ENSMUST00000147388						1	0	2	1	2	1	0	0	0	0	0		
ENSMUST00000147389	ENSMUSG00000022487	15	103402405	103430470	-1	0	0	0	3	0	1	0	0	0	0	0	D3YUE6	
ENSMUST00000147390						3	6	4	3	3	2	0	3	0	0	2		
ENSMUST00000147391	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	43	0	0	0	0	A0A087WQT4	
ENSMUST00000147392						0	1	0	1	2	0	0	0	0	0	0		
ENSMUST00000147393	ENSMUSG00000044783	1	88262471	88277633	-1	6	6	0	74	0	1	267	0	353	23	440	D6RI36	
ENSMUST00000147394	ENSMUSG00000036781	9	66946086	66949516	1	0	0	0	0	0	0	0	0	0	0	0	D6RH49	
ENSMUST00000147395						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000147396						2	0	0	1	5	2	0	0	0	0	0		
ENSMUST00000147397						20	13	240	37	16	0	5	15	7	0	1		
ENSMUST00000147399	ENSMUSG00000086564	3	100993529	101029556	-1	0	0	26	0	0	0	312	3144	1239	234	1687		A8E0Y8
ENSMUST00000147400	ENSMUSG00000051855	6	30723547	30748465	1	2	2	1	2	4	4	0	0	0	0	0	D3YZ83	
ENSMUST00000147401	ENSMUSG00000030505	7	49778346	49858265	1	0	0	5	0	0	0	0	0	0	0	0	D6RGQ1	
ENSMUST00000147402						0	0	0	2	0	0	0	16	0	0	1		
ENSMUST00000147403						6	8	24	9	3	6	0	13	12	7	44		
ENSMUST00000147404						1	1	14	0	1	2	16	55	33	0	8		
ENSMUST00000147405	ENSMUSG00000035919	9	22475715	22888280	1	0	0	0	0	0	0	1	25	8	34	0		Q811G0
ENSMUST00000147406						0	4	4	5	0	3	0	8	9	0	8		
ENSMUST00000147407	ENSMUSG00000021606	13	73319874	73328542	-1	4	0	4	29	6	0	38	66	39	139	14	D6RJ54	
ENSMUST00000147408						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147409	ENSMUSG00000028186	3	146570426	146632305	1	2	2	1	2	0	0	0	0	0	5	0	A0A0G2JFT6	
ENSMUST00000147413						6	8	10	8	10	5	0	6	2	0	3		
ENSMUST00000147414						1	6	7	6	3	0	7	17	9	0	17		
ENSMUST00000147415						0	0	4	1	0	2	0	0	0	0	0		
ENSMUST00000147416						5	9	30	4	14	5	10	69	31	1	45		
ENSMUST00000147418						3	0	1	3	2	0	0	3	0	0	0		
ENSMUST00000147419	ENSMUSG00000031604	8	64718139	64733792	-1	0	1	4	1	1	0	2	6	5	3	7	D3Z458	
ENSMUST00000147421						8	2	15	7	10	3	7	57	53	2	39		
ENSMUST00000147422	ENSMUSG00000000301	11	59970614	60046489	-1	1	0	2	0	3	0	0	1	1	0	0	B1ARC9	
ENSMUST00000147423						0	6	5	47	5	4	29	49	54	4	101		
ENSMUST00000147424						84	94	222	93	85	38	6	22	3	0	5		
ENSMUST00000147426	ENSMUSG00000040964	4	140514485	140666012	-1	2	6	17	12	6	5	18	9	8	0	17	A2AWP4	
ENSMUST00000147427						4	4	4	29	4	0	7	2	8	0	10		
ENSMUST00000147428	ENSMUSG00000030670	7	114550166	114562972	-1	0	7	1	52	2	0	0	0	0	0	2	D6RCU9	
ENSMUST00000147430						6	3	17	86	0	0	1055	495	1676	396	1160		
ENSMUST00000147431	ENSMUSG00000001247	7	30957770	30973464	-1	2	0	0	99	4	0	0	0	8	0	0	D3YYU9	
ENSMUST00000147432						3	4	4	3	3	1	3	82	3	6	2		
ENSMUST00000147433	ENSMUSG00000035236	2	39066214	39190734	-1	2	0	2	0	0	2	0	49	27	9	22	D6RHQ0	
ENSMUST00000147434	ENSMUSG00000066137	4	73401032	73405072	-1	2	0	0	2	0	0	0	2	0	0	1	F6QJY6	
ENSMUST00000147435	ENSMUSG00000012848	7	12922290	12926686	1	3	3	10	16	0	0	0	13	17	0	0	D3YYM6	
ENSMUST00000147436						0	3	3	0	1	1	131	0	40	0	15		
ENSMUST00000147437	ENSMUSG00000018565	11	69968222	69982517	-1	0	1	3	11	2	0	3	2	3	0	0	B1AR48	
ENSMUST00000147439	ENSMUSG00000001829	7	101663633	101790168	1	0	0	1	0	0	0	4	0	0	0	10	D3YZF1	
ENSMUST00000147440	ENSMUSG00000020211	10	80798198	80804924	1	4	0	2	33	1	1	4	7	0	0	0	D3Z5A6	
ENSMUST00000147441						30	35	72	44	38	28	94	420	238	43	216		
ENSMUST00000147442						3	3	2	6	10	3	0	0	0	0	0		
ENSMUST00000147443						20	14	103	36	14	13	0	0	0	0	1		
ENSMUST00000147444						15	18	37	12	36	10	0	6	2	0	4		
ENSMUST00000147447						2	2	0	0	0	1	0	3	0	3	1		
ENSMUST00000147448	ENSMUSG00000044813	4	45423278	45532470	-1	2	0	3	2	0	1	0	0	0	0	0	A2AKW4	
ENSMUST00000147450						0	0	0	19	1	0	0	0	0	0	0		
ENSMUST00000147451						0	6	5	0	3	3	0	0	0	0	0		
ENSMUST00000147452						1	2	3	2	0	0	30	144	43	102	31		
ENSMUST00000147453						2	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000147454	ENSMUSG00000034813	10	119454034	120087261	1	0	0	8	0	6	0	0	0	0	0	0	D3YZL8	
ENSMUST00000147455						7	4	5	2	6	12	0	0	0	0	0		
ENSMUST00000147456	ENSMUSG00000058793	2	132263148	132312050	1	0	0	0	55	0	0	0	0	4	4	0	H3BKR7	
ENSMUST00000147457						2	1	0	5	1	1	0	3	2	1	5		
ENSMUST00000147458	ENSMUSG00000028669	4	135975460	135987264	-1	0	0	5	1	0	0	1	8	0	0	0	B1AV57	
ENSMUST00000147459						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147460						0	2	5	5	6	4	0	0	0	6	0		
ENSMUST00000147461						0	0	0	0	1	0	0	0	15	3	34		
ENSMUST00000147462						0	0	0	0	0	0	6	0	34	8	25		
ENSMUST00000147464						0	1	0	0	0	0	0	23	7	0	2		
ENSMUST00000147466	ENSMUSG00000056770	12	108106431	108179314	-1	0	3	17	26	0	1	0	0	0	3	25	D6RCY6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147467						3	3	47	2	4	0	0	13	2	0	4		
ENSMUST00000147468	ENSMUSG00000036620	11	50210890	50235103	1	2	2	6	39	5	0	0	3	5	0	2	A8Y5H5	
ENSMUST00000147469	ENSMUSG00000021221	12	83213745	83487716	-1	0	0	2	0	0	15	2	0	0	0	0	F7CPB1	
ENSMUST00000147470						4	0	3	2	3	0	0	0	0	0	0		
ENSMUST00000147471						2	4	3	66	10	2	0	9	9	4	21		
ENSMUST00000147472						0	0	0	0	0	2	2	0	5	0	6		
ENSMUST00000147473	ENSMUSG00000106892	5	148893775	148995147	-1	0	0	4	1	0	0	2	0	0	0	2	D3YYB5	
ENSMUST00000147475	ENSMUSG00000005803	2	122765237	122809569	1	0	0	0	0	0	0	4	7	4	14	4	H3BJM5	
ENSMUST00000147476						50	53	91	33	38	20	0	4	2	1	11		
ENSMUST00000147477						2	1	2	0	2	0	1	0	1	0	0		
ENSMUST00000147479						0	0	0	20	0	0	0	0	0	0	0		
ENSMUST00000147480						3	7	8	5	6	2	0	0	0	0	0		
ENSMUST00000147481						0	0	4	3	0	0	0	2	0	0	0		
ENSMUST00000147482	ENSMUSG00000042671	1	153653025	153700323	1	0	0	2	6	0	0	0	0	0	0	0	D3YX00	
ENSMUST00000147483	ENSMUSG00000058831	6	29376671	29388468	-1	0	1	0	0	0	0	0	0	0	0	0	G3UXM0	
ENSMUST00000147484	ENSMUSG00000024099	17	66078795	66101559	-1	0	3	0	10	0	0	5	4	6	240	30	D6RGN4	
ENSMUST00000147485						0	0	0	71	0	0	0	0	0	0	0		
ENSMUST00000147486	ENSMUSG00000005917	11	21994764	22002897	-1	0	3	0	55	3	0	0	0	0	0	0	G3V000	
ENSMUST00000147488	ENSMUSG00000039844	2	29619720	29740978	1	4	1	0	0	3	0	525	842	485	110	462	F6ZDE5	
ENSMUST00000147489						0	2	1	2	1	1	1	1	0	0	1		
ENSMUST00000147490	ENSMUSG00000039294	11	121222588	121229322	-1	0	0	0	10	0	2	40	19	39	3	7	X1WI15	
ENSMUST00000147491						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000147492						5	0	1	1	2	2	9	12	6	2	5		
ENSMUST00000147493						3	4	18	16	7	5	14	6	11	0	18		
ENSMUST00000147495	ENSMUSG00000048537	9	44686304	44735198	-1	6	0	18	19	0	0	0	0	0	0	0	D3Z4N0	
ENSMUST00000147496	ENSMUSG00000032754	5	120511168	120534024	1	5	2	12	81	7	1	1	1	3	0	2		
ENSMUST00000147497						2	3	2	1	7	0	0	0	0	0	0		
ENSMUST00000147498						2	3	0	1	2	5	7	45	30	16	36		
ENSMUST00000147500						9	8	10	4	6	1	0	12	3	0	3		
ENSMUST00000147501	ENSMUSG00000001036	11	61517249	61579687	-1	0	2	2	0	3	0	1	0	0	0	2	A8Y5D4	
ENSMUST00000147502						8	1	5	4	2	1	2	0	0	0	0		
ENSMUST00000147503						3	0	6	4	1	0	0	3	0	0	0		
ENSMUST00000147505	ENSMUSG00000025855	5	139017306	139150001	-1	0	0	1	1	0	2	0	0	0	0	0	D3Z406	
ENSMUST00000147506	ENSMUSG00000020261	11	55204350	55236330	1	0	0	0	0	0	0	0	0	0	0	0	Q5F228	
ENSMUST00000147507						0	4	0	0	0	0	4	17	0	0	10		
ENSMUST00000147510						2	0	7	0	0	0	141	855	219	0	293		
ENSMUST00000147511						0	0	2	0	1	0	62	379	65	94	82		
ENSMUST00000147512						49	56	123	75	52	30	12	60	14	7	60		
ENSMUST00000147513						0	2	1	0	3	0	0	2	2	0	3		
ENSMUST00000147514						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000147515						3	5	2	0	6	1	52	71	43	0	102		
ENSMUST00000147516						1	0	10	8	6	3	4	8	4	0	14		
ENSMUST00000147517	ENSMUSG00000060131	2	126320973	126500674	-1	0	2	2	2	1	0	0	13	66	0	0	F2Z411	
ENSMUST00000147518						5	12	43	5	7	12	0	0	7	3	5		
ENSMUST00000147519	ENSMUSG00000028718	4	115000159	115043196	1	1	0	0	1	0	0	0	0	0	0	0	F6VXM5	
ENSMUST00000147520						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000147521	ENSMUSG00000054293	X	107148927	107173661	1	0	0	0	0	0	0	3	16	8	0	3	A2ASC3	
ENSMUST00000147523	ENSMUSG00000026307	1	91298338	91321075	1	0	0	0	0	0	0	0	0	0	0	0	F6ZFP8	
ENSMUST00000147524	ENSMUSG00000034818	10	81459227	81482709	-1	0	0	2	19	1	1	0	0	0	0	0	D3Z4K9	
ENSMUST00000147525	ENSMUSG00000039620	8	36457548	36514320	1	11	12	16	0	5	0	0	0	0	0	0		Q80WQ4
ENSMUST00000147526	ENSMUSG00000015766	6	137477245	137654876	-1	0	0	0	6	0	1	0	0	0	0	37	Q3UGL1	
ENSMUST00000147527						0	1	0	2	0	1	0	0	0	0	0		
ENSMUST00000147528	ENSMUSG00000026792	2	32925216	32961614	-1	1	0	3	0	0	1	5	0	0	0	0	A2AHX4	
ENSMUST00000147529	ENSMUSG00000031214	X	98554277	98891025	-1	0	0	6	0	0	0	0	0	0	0	2	B1AXS4	
ENSMUST00000147530						0	0	18	4	0	4	0	7	11	0	0		
ENSMUST00000147531						0	0	0	5	5	0	6	18	11	2	18		
ENSMUST00000147532	ENSMUSG00000051977	17	15543079	15564354	-1	0	1	1	2	0	0	0	5	0	7	0		Q96EQ9
ENSMUST00000147533						0	1	0	1	0	0	0	0	0	3	0		
ENSMUST00000147534						2	0	0	1	0	0	0	0	9	0	15		
ENSMUST00000147535	ENSMUSG00000063229	7	46841475	46855627	1	6	9	14	2	4	4	55	39	97	94	35	D3YZQ9	
ENSMUST00000147536						1	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000147537						26	31	95	98	38	26	2	12	3	2	16		
ENSMUST00000147539						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000147540	ENSMUSG00000043909	2	121193281	121271407	-1	0	0	20	11	7	2	22	117	60	17	79	F6QNC8	
ENSMUST00000147543						0	1	1	15	2	0	0	1	0	1	4		
ENSMUST00000147544						2	3	7	118	3	0	0	0	0	0	0		
ENSMUST00000147545	ENSMUSG00000048701	10	70097121	70193200	1	26	18	55	244	46	22	104	239	185	14	165		D3YZP9
ENSMUST00000147546						0	1	0	0	1	0	0	6	11	7	7		
ENSMUST00000147547						5	3	20	0	6	3	0	0	0	4	0		
ENSMUST00000147549						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000147550						0	4	0	2	2	1	0	32	7	14	9		
ENSMUST00000147551						1	0	0	65	0	1	4	14	12	0	4		
ENSMUST00000147552	ENSMUSG00000026222	1	85649988	85709998	1	0	1	0	0	0	0	133	371	300	29	267	Q6NTA3	O35892
ENSMUST00000147553						1	0	1	0	0	0	27	0	90	46	59		
ENSMUST00000147554						0	0	0	0	0	0	0	1	0	0	3		
ENSMUST00000147556	ENSMUSG00000037846	10	67979570	68059740	1	7	13	22	0	13	0	0	0	0	0	0		Q14B46
ENSMUST00000147557						3	0	0	3	0	4	0	21	6	0	11		
ENSMUST00000147558						1	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000147559	ENSMUSG00000002031	9	44767908	44792714	1	0	0	0	0	0	0	18	23	30	37	16	D3YWI2	
ENSMUST00000147560						1	0	0	2	0	0	5	12	0	0	0		
ENSMUST00000147561						4	4	9	5	6	0	18	103	44	6	46		
ENSMUST00000147563	ENSMUSG00000025786	9	123066160	123113205	-1	19	21	57	72	41	17	963	3137	1342	162	630		Q8R173
ENSMUST00000147564						10	17	50	20	18	6	12	28	13	5	23		
ENSMUST00000147565						0	0	0	22	6	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147566	ENSMUSG00000021608	13	73467197	73516422	1	0	0	10	45	3	0	38	0	36	0	0	D6RFA8	
ENSMUST00000147567	ENSMUSG00000023143	16	5195289	5204012	-1	16	0	0	276	15	0	0	23	35	15	48	D3Z6C9	
ENSMUST00000147570	ENSMUSG00000027404	2	130171414	130179403	-1	13	1	11	24	4	6	7	30	0	0	0	A0A0G2JGN4	
ENSMUST00000147571	ENSMUSG00000026049	1	44086613	44102441	-1	0	1	0	142	0	0	0	26	0	0	0		Q3TUU5
ENSMUST00000147572	ENSMUSG00000028796	4	128654702	128752881	1	7	0	21	31	0	0	30	13	26	0	12	B1ASA3	
ENSMUST00000147573	ENSMUSG00000018669	11	96907426	96916496	-1	0	1	0	31	1	2	6	0	5	5	3	D6RII4	
ENSMUST00000147574	ENSMUSG00000029106	5	34573664	34632308	1	0	2	0	0	1	1	143	124	183	10	80	D3Z0T1	
ENSMUST00000147575						4195	4736	7430	3579	4110	2040	85	391	179	41	206		
ENSMUST00000147576						2	3	1	0	0	0	0	0	0	0	0		
ENSMUST00000147577						2	3	3	0	6	3	0	0	0	0	0		
ENSMUST00000147578						31	23	36	59	32	9	0	0	0	0	0		
ENSMUST00000147579						3	2	0	2	4	2	0	0	0	0	0		
ENSMUST00000147580	ENSMUSG00000048330	7	109034312	109083331	-1	18	17	11	4	25	12	1	1	0	0	1	F7CE80	
ENSMUST00000147581						0	5	0	1	10	2	2	4	2	6	10		
ENSMUST00000147582						50	36	252	72	43	30	43	108	99	12	122		
ENSMUST00000147583						3	1	4	5	1	0	0	0	0	0	0		
ENSMUST00000147584						8	5	20	1	3	1	0	59	11	8	0		
ENSMUST00000147585	ENSMUSG00000038776	1	180976210	181020904	-1	5	4	6	2	11	2	0	0	0	0	0	D3Z4M3	
ENSMUST00000147586						3	1	1	0	4	1	15	0	19	7	7		
ENSMUST00000147587	ENSMUSG00000005686	7	110768206	110812405	1	0	4	3	0	1	1	0	0	0	0	3	D3YU73	
ENSMUST00000147588	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	0	0	0	40	14	128	0	0	Q80TR0	
ENSMUST00000147589						0	0	0	0	0	0	0	1	5	0	0		
ENSMUST00000147590						0	0	0	0	0	0	70	341	123	103	101		
ENSMUST00000147591	ENSMUSG00000027465	2	152293828	152313996	1	2	0	8	40	2	2	0	0	8	0	2	B0R081	
ENSMUST00000147592						0	0	0	0	0	0	26	0	1	2	64		
ENSMUST00000147593						0	2	3	0	5	3	0	0	0	0	0		
ENSMUST00000147595	ENSMUSG00000038203	6	52257694	52260880	-1	6	7	6	6	20	6	0	0	0	0	0	E0CXK7	
ENSMUST00000147596						0	0	7	14	4	0	0	0	0	0	0		
ENSMUST00000147597						4	3	7	14	5	0	0	0	0	0	0		
ENSMUST00000147598						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000147599						61	46	197	126	56	26	2	6	9	1	16		
ENSMUST00000147600	ENSMUSG00000035403	2	37776249	37799103	1	0	0	4	60	0	2	0	0	0	0	0		
ENSMUST00000147601	ENSMUSG00000027603	2	155490379	155518237	-1	0	0	2	102	7	0	0	0	0	0	0	A2AQN2	
ENSMUST00000147602						2	3	0	0	4	4	0	0	0	0	0		
ENSMUST00000147603	ENSMUSG00000029192	5	36490604	36593276	-1	2	1	0	3	0	2	0	0	0	0	0	D3Z2A1	
ENSMUST00000147604	ENSMUSG00000037860	1	173350879	173466040	1	17	20	4	0	7	11	30	158	28	47	23		Q91VJ1
ENSMUST00000147605	ENSMUSG00000031767	8	114133557	114154739	1	0	1	0	0	2	0	50	228	40	94	17		Q99P30
ENSMUST00000147606	ENSMUSG00000025938	1	12866549	12992650	-1	0	0	0	0	0	0	0	0	0	0	0	Q148W2	
ENSMUST00000147607						0	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000147609						0	0	41	6	0	0	0	0	0	0	0		
ENSMUST00000147610						39	29	65	61	53	26	13	13	13	0	19		
ENSMUST00000147611	ENSMUSG00000008489	4	91250763	91400785	-1	3	0	0	2	2	1	0	0	0	0	0	B1AXZ3	
ENSMUST00000147612						0	1	4	3	0	4	0	3	0	0	3		
ENSMUST00000147613	ENSMUSG00000037234	8	26021421	26119224	-1	0	1	0	0	0	0	23	125	63	30	38	F6W1A2	
ENSMUST00000147614						4	0	0	0	0	1	0	87	15	0	0		
ENSMUST00000147615	ENSMUSG00000085079	1	21383556	21386373	1	21	17	21	13	22	15	0	0	0	0	0		P0C7A0
ENSMUST00000147616						0	0	0	16	0	9	0	0	0	0	0		
ENSMUST00000147617						3	0	6	1	1	3	0	0	0	0	0		
ENSMUST00000147619	ENSMUSG00000056310	5	130255619	130341563	1	0	2	0	0	0	0	4	0	7	0	0	F6VNP0	
ENSMUST00000147621						0	0	0	61	0	3	0	0	0	0	0		
ENSMUST00000147624						7	9	17	5	17	5	0	0	0	0	0		
ENSMUST00000147625	ENSMUSG00000039768	4	151933691	151982137	1	1	0	5	1	5	0	6	0	0	0	0	A2A8D1	
ENSMUST00000147626	ENSMUSG00000024124	17	23972126	23975230	-1	0	0	0	0	0	0	0	0	0	0	0	D3YZM1	
ENSMUST00000147627	ENSMUSG00000074643	2	156071842	156111965	-1	9	5	0	0	0	4	23	13	45	15	94	E9Q806	
ENSMUST00000147628						2	0	4	16	6	1	5	6	4	4	5		
ENSMUST00000147629	ENSMUSG00000040407	5	3928054	4081310	1	0	0	0	1	0	1	0	27	0	12	2	G3UX24	
ENSMUST00000147630	ENSMUSG00000095990	17	17121415	17146831	1	19	18	134	25	31	9	47	156	46	77	35	E9PZP6	
ENSMUST00000147631	ENSMUSG00000023284	5	110110092	110129794	1	1	0	0	0	4	0	0	0	2	1	0	D3Z778	
ENSMUST00000147632	ENSMUSG00000071451	13	34162964	34178172	1	3	0	0	26	7	2	16	74	22	31	29		P0C7N9
ENSMUST00000147635						2	0	3	9	11	7	400	4137	1349	206	1614		
ENSMUST00000147636						2	0	10	19	3	4	0	0	0	0	0		
ENSMUST00000147637						8	8	3	5	10	3	21	24	31	1	28		
ENSMUST00000147639	ENSMUSG00000030315	6	114860628	114969994	-1	0	0	0	102	2	0	0	0	0	0	0	D3Z130	
ENSMUST00000147640	ENSMUSG00000055491	19	46044886	46072915	1	3	0	8	6	6	2	0	0	0	0	0	D3Z1F1	
ENSMUST00000147641	ENSMUSG00000034429	15	75969123	75975868	1	10	0	0	0	0	0	0	0	0	4	0	F6QUN2	
ENSMUST00000147642	ENSMUSG00000074247	8	71469199	71476098	1	0	0	0	0	0	0	11	0	0	0	0	D3YXY5	
ENSMUST00000147643						7	0	18	0	0	8	0	2	14	4	14		
ENSMUST00000147644						5	0	0	0	0	0	0	33	0	0	0		
ENSMUST00000147645						3	1	4	12	2	3	0	5	5	0	0		
ENSMUST00000147647						0	8	26	65	3	2	8	3	0	2	0		
ENSMUST00000147648						8	6	32	61	14	1	0	17	9	4	9		
ENSMUST00000147650						22	8	67	0	23	9	0	32	8	2	0		
ENSMUST00000147651						3	1	8	1	2	1	0	6	0	5	0		
ENSMUST00000147652	ENSMUSG00000028898	4	132311763	132329538	-1	0	0	0	0	0	0	31	37	13	36	22	E9Q3V7	
ENSMUST00000147655						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000147656	ENSMUSG00000002342	8	70172356	70183681	1	0	0	0	11	12	0	67	49	25	0	23	M0QWV0	
ENSMUST00000147657						21	13	42	37	13	5	0	1	2	0	2		
ENSMUST00000147659						0	2	2	8	8	4	0	0	2	0	0		
ENSMUST00000147660						0	0	0	0	0	0	0	37	11	2	15		
ENSMUST00000147661	ENSMUSG00000026049	1	44086613	44102441	-1	0	0	0	0	0	0	0	1	0	9	0	D3Z1S9	
ENSMUST00000147662	ENSMUSG00000023039	15	101411043	101430313	1	0	2	1	3	1	0	0	0	2	0	10	D3Z6N5	
ENSMUST00000147663	ENSMUSG00000052581	6	80018877	80810143	1	5	6	11	0	0	0	0	0	0	0	0		
ENSMUST00000147664	ENSMUSG00000005107	5	38349273	38503143	-1	0	0	18	0	0	0	0	0	6	0	0	D3Z1X2	
ENSMUST00000147665						3	0	0	48	1	1	3	12	6	0	8		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147666						43	67	234	82	59	22	2	16	8	1	11		
ENSMUST00000147667						1	0	0	1	2	2	6	5	2	0	8		
ENSMUST00000147668	ENSMUSG00000053730	4	129676355	129696838	-1	6	0	4	1	1	2	0	0	0	0	0	D6RJL2	
ENSMUST00000147669	ENSMUSG00000030125	6	124769863	124779727	-1	3	0	6	6	4	0	1	0	0	0	0	D3Z182	
ENSMUST00000147670	ENSMUSG00000031887	8	105258286	105264609	-1	6	4	3	2	4	0	4	38	9	2	0	D6RGL2	
ENSMUST00000147671	ENSMUSG00000059820	9	50605240	50617464	-1	0	0	0	233	0	0	0	15	0	0	20	D3Z5E5	
ENSMUST00000147672						12	8	16	13	20	6	9	11	10	1	10		
ENSMUST00000147673						1	2	9	4	5	0	0	0	0	0	0		
ENSMUST00000147674						11	4	32	21	11	5	0	0	0	0	0		
ENSMUST00000147675	ENSMUSG00000042489	4	126556935	126593903	1	0	0	0	10	0	1	0	0	8	0	0	B1ARX5	
ENSMUST00000147676	ENSMUSG00000031928	9	14784654	14837123	1	0	0	0	1	0	0	0	0	4	5	11	F6RX99	
ENSMUST00000147677						7	3	2	2	3	3	0	0	0	0	0		
ENSMUST00000147679						0	2	13	5	2	0	26	110	68	2	99		
ENSMUST00000147680						0	3	4	4	2	1	0	0	0	0	0		
ENSMUST00000147682						5	3	17	3	8	6	0	20	0	2	15		
ENSMUST00000147683						12	2	10	7	8	2	2	0	2	0	3		
ENSMUST00000147684	ENSMUSG00000036309	11	52231995	52246858	1	0	0	7	11	4	0	18	12	43	101	41	E9Q3Q7	
ENSMUST00000147686						0	0	0	0	0	2	1	0	0	1	0		
ENSMUST00000147687						0	0	0	11	1	0	0	0	0	0	0		
ENSMUST00000147688	ENSMUSG00000023791	16	32084418	32099738	-1	0	0	0	0	0	0	23	56	13	14	2	F6RUP6	
ENSMUST00000147692						5	0	18	5	0	0	0	3	4	0	6		
ENSMUST00000147693						1	3	11	45	5	0	0	0	0	0	0		
ENSMUST00000147694	ENSMUSG00000048895	11	80477023	80481184	1	0	1	3	95	0	0	0	0	0	0	0	B1AQH0	
ENSMUST00000147695	ENSMUSG00000048814	1	38793645	38836711	-1	82	52	54	510	87	30	0	2	1	1	1	B2RT44	
ENSMUST00000147696	ENSMUSG00000032657	3	89183143	89189295	1	0	0	16	151	0	4	0	19	0	0	17	D6RFB2	
ENSMUST00000147697	ENSMUSG00000037661	3	30855950	30897192	1	0	0	5	2	0	2	0	17	13	6	9	D3Z2M1	
ENSMUST00000147698						1	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000147699	ENSMUSG00000034659	19	10870660	10882001	-1	13	3	11	6	15	3	0	3	2	0	7	D3YX08	
ENSMUST00000147700	ENSMUSG00000042671	1	153653025	153700323	1	2	0	4	0	0	0	0	0	0	0	0	D3YYE5	
ENSMUST00000147701						0	0	0	0	0	0	0	0	2	0	1		
ENSMUST00000147702						1	4	3	1	0	0	0	0	0	0	0		
ENSMUST00000147703	ENSMUSG00000009030	2	37350074	37359332	-1	0	3	0	0	3	0	6	8	105	224	78	A2AVP3	
ENSMUST00000147705						0	2	0	0	0	0	196	543	417	124	239		
ENSMUST00000147706						0	0	2	2	1	1	0	0	0	0	0		
ENSMUST00000147707	ENSMUSG00000002546	2	32287384	32307921	1	1	0	0	2	0	0	0	0	0	0	0	A2AN45	
ENSMUST00000147708	ENSMUSG00000031311	X	101429318	101448591	1	1	0	0	0	0	5	0	0	0	0	0	B1AXT0	
ENSMUST00000147709	ENSMUSG00000034785	4	107291465	107307169	-1	2	0	0	1	1	0	0	0	0	0	0	D6RCH6	
ENSMUST00000147710	ENSMUSG00000018672	11	96849870	96861203	1	2	3	4	0	0	5	0	0	0	0	0	F6WZN3	
ENSMUST00000147712	ENSMUSG00000035919	9	22475715	22888280	1	0	0	32	0	6	0	38	18	0	15	43		Q811G0
ENSMUST00000147713						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000147714	ENSMUSG00000022185	14	54642161	54686931	-1	5	10	57	37	20	3	1201	1963	2205	102	2084	F6RJ39	
ENSMUST00000147715						2	0	4	2	0	0	0	0	0	0	7		
ENSMUST00000147716						40	36	136	46	33	16	1	8	2	0	7		
ENSMUST00000147718	ENSMUSG00000017776	11	75679259	75706908	1	6	13	7	0	15	2	37	31	69	37	125	F7D232	
ENSMUST00000147719						0	0	6	3	1	2	0	30	3	0	25		
ENSMUST00000147720	ENSMUSG00000000326	16	18406886	18426852	-1	0	0	0	0	0	0	0	0	2	0	0	D3Z227	
ENSMUST00000147721	ENSMUSG00000084845	4	155734800	155740564	1	0	0	0	92	2	0	0	1	2	0	1		B2RWJ3
ENSMUST00000147723						0	0	2	1	2	0	0	0	0	0	6		
ENSMUST00000147724						1	0	2	0	0	0	0	0	4	0	0		
ENSMUST00000147725						0	1	0	0	0	0	0	2	4	6	0		
ENSMUST00000147726	ENSMUSG00000051169	6	113415319	113419340	-1	2	0	0	0	0	0	0	0	5	3	0	F6WLR1	
ENSMUST00000147727						15	13	41	11	15	3	0	0	0	0	4		
ENSMUST00000147728						2	3	15	6	2	0	0	0	0	0	0		
ENSMUST00000147729						11	12	20	12	17	12	1	13	5	1	15		
ENSMUST00000147730	ENSMUSG00000028680	4	117128655	117133963	-1	0	0	0	0	1	0	130	220	81	15	85	F6V5S5	
ENSMUST00000147731	ENSMUSG00000028789	4	128930233	128962442	-1	0	0	0	0	0	0	5	0	0	0	0	A2A821	
ENSMUST00000147732	ENSMUSG00000040652	9	65668001	65690300	1	1	21	105	0	0	0	395	1002	410	118	310	J3QND2	
ENSMUST00000147733						3	2	0	3	17	2	0	27	8	0	12		
ENSMUST00000147734						0	3	8	7	2	0	0	7	3	3	6		
ENSMUST00000147735						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147736	ENSMUSG00000026918	2	27445579	27507662	-1	0	2	0	5	2	1	0	0	6	0	3	A2AKB0	
ENSMUST00000147737	ENSMUSG00000038126	5	124250959	124327972	-1	0	0	0	0	0	17	0	0	23	0	0	D6RDQ9	
ENSMUST00000147738						5	0	6	185	7	5	17	8	14	2	12		
ENSMUST00000147739	ENSMUSG00000000884	16	18498768	18566679	1	0	2	0	0	2	1	1	0	0	0	0	D3Z0M5	
ENSMUST00000147740						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000147741	ENSMUSG00000035112	11	101260567	101277409	1	14	24	9	14	0	20	0	9	8	0	0	E9PZ38	
ENSMUST00000147743						14	12	23	27	1	9	3	10	2	0	13		
ENSMUST00000147744	ENSMUSG00000039943	2	135659011	136014593	1	57	25	95	360	87	37	8	46	17	16	28	A2AT93	
ENSMUST00000147745						1	0	0	0	0	0	0	19	0	0	0		
ENSMUST00000147746						0	0	0	3	0	0	0	0	0	1	0		
ENSMUST00000147747	ENSMUSG00000027425	2	144368983	144407676	1	0	0	0	1	0	0	14	11	16	0	23	E9QA90	
ENSMUST00000147748						5	0	7	11	7	4	63	110	30	17	70		
ENSMUST00000147749						2	2	1	0	1	1	0	0	2	1	0		
ENSMUST00000147750						1	2	5	0	2	0	7	0	0	2	0		
ENSMUST00000147751	ENSMUSG00000040594	11	33211795	33513746	-1	1	3	0	3	0	0	0	0	0	0	0	Q5SSA8	
ENSMUST00000147752						1	2	4	1	2	4	1	3	3	0	6		
ENSMUST00000147753						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000147755	ENSMUSG00000039844	2	29619720	29740978	1	0	10	0	0	9	0	194	0	244	0	134	E0CXV1	
ENSMUST00000147756						4	3	4	8	6	0	0	10	4	0	17		
ENSMUST00000147757						4	0	9	7	8	4	0	0	1	0	0		
ENSMUST00000147758	ENSMUSG00000041439	1	52656286	52727462	-1	37	42	201	0	35	9	328	1755	1291	167	796	F6U3S2	
ENSMUST00000147759	ENSMUSG00000023088	16	14361558	14475737	1	0	0	0	28	0	0	52	0	44	0	0	E9Q1I5	
ENSMUST00000147760	ENSMUSG00000040613	6	122577792	122602444	-1	1	0	2	0	0	0	0	0	2	0	0	D3Z675	
ENSMUST00000147761						27	11	68	18	32	20	0	0	2	2	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147763	ENSMUSG00000038827	4	56802345	56809601	1	0	0	0	0	3	1	6	0	5	0	0	F6ZCU9	
ENSMUST00000147764	ENSMUSG00000006219	4	141576062	141606096	-1	0	0	0	0	0	0	0	0	0	0	0	A2ADE5	
ENSMUST00000147765						0	0	0	5	0	0	1	0	2	0	9		
ENSMUST00000147766						0	1	18	3	0	0	3	8	3	0	0		
ENSMUST00000147767						6	4	0	2	3	3	8	22	13	0	13		
ENSMUST00000147768	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZP2	
ENSMUST00000147769						0	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000147770	ENSMUSG00000057234	2	109092297	109280748	-1	0	0	0	21	0	0	0	5	3	16	11	A2AGM2	
ENSMUST00000147772						11	10	10	91	16	9	0	0	6	0	2		
ENSMUST00000147773	ENSMUSG00000027719	3	37063527	37121930	1	3	0	0	0	0	0	0	0	0	0	0	F6TQG5	
ENSMUST00000147775	ENSMUSG00000032900	18	56588350	56594782	1	0	0	0	2	0	0	0	0	0	0	0	F6VMD1	
ENSMUST00000147776	ENSMUSG00000015001	15	65876053	65912397	-1	0	0	0	0	0	0	0	0	0	0	0	F6W8F5	
ENSMUST00000147778	ENSMUSG00000035640	10	80130451	80140835	-1	0	0	0	84	0	0	0	0	0	0	0	E9Q6U0	
ENSMUST00000147779						8	3	12	210	12	5	0	0	2	0	0		
ENSMUST00000147780						5	0	4	0	0	7	0	0	0	11	0		
ENSMUST00000147781	ENSMUSG00000025583	11	119602905	119899576	1	24	10	38	0	25	13	932	228	1169	234	274	E9PXZ5	
ENSMUST00000147782						2	9	0	5	7	0	9	61	25	38	8		
ENSMUST00000147783						0	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000147784						5	3	0	3	2	4	0	0	0	0	0		
ENSMUST00000147785	ENSMUSG00000006219	4	141576062	141606096	-1	0	0	0	13	0	0	0	0	0	0	0	A2ADE9	
ENSMUST00000147786	ENSMUSG00000030965	7	132859225	132885111	1	0	0	0	78	0	0	0	0	30	0	0	D6RHR6	
ENSMUST00000147787						1	1	3	81	2	1	0	0	2	0	0		
ENSMUST00000147788	ENSMUSG00000027224	2	122302191	122313730	-1	0	0	0	0	2	0	0	0	0	0	0	A2AQ94	
ENSMUST00000147789						3	1	7	55	5	3	2	7	5	0	9		
ENSMUST00000147790						15	9	13	16	13	3	4	12	10	6	7		
ENSMUST00000147791						0	0	0	0	0	1	0	0	0	0	4		
ENSMUST00000147792	ENSMUSG00000019102	11	61207537	61218421	1	2	0	1	9	0	0	0	0	0	0	0	B1ATI6	
ENSMUST00000147793						0	0	0	3	0	2	1	0	4	0	0		
ENSMUST00000147794						7	5	29	5	5	2	0	0	0	0	0		
ENSMUST00000147796						5	1	3	4	6	2	8	24	10	8	7		
ENSMUST00000147797						14	11	25	56	14	5	0	2	0	0	10		
ENSMUST00000147798						11	9	31	4	8	9	0	3	4	0	4		
ENSMUST00000147799						1	0	0	1	0	0	0	14	20	5	15		
ENSMUST00000147800	ENSMUSG00000042268	1	131744022	131771504	1	3	3	4	1	7	5	0	0	0	0	0	D3Z1A3	
ENSMUST00000147801	ENSMUSG00000008307	5	3571566	3584356	1	3	4	0	0	7	0	0	0	3	0	0	D6RH70	
ENSMUST00000147802	ENSMUSG00000020175	10	75037058	75054748	1	24	10	59	34	39	11	0	41	7	0	10		Q8CAM5
ENSMUST00000147803	ENSMUSG00000071322	17	7324646	7345974	1	1	5	4	1	2	0	0	0	0	0	0		
ENSMUST00000147804	ENSMUSG00000036208	16	44724301	44737284	1	0	0	0	0	1	0	0	0	0	0	4	D6RFS8	
ENSMUST00000147805						0	0	0	0	0	1	0	1	4	0	5		
ENSMUST00000147806						7	0	13	48	12	0	6	17	5	0	0		
ENSMUST00000147807						1	0	0	23	3	0	0	0	0	0	0		
ENSMUST00000147808						10	9	35	4	12	4	0	0	0	0	1		
ENSMUST00000147809						0	3	0	0	3	0	3	25	0	3	0		
ENSMUST00000147810						1	3	7	3	2	1	0	0	0	0	0		
ENSMUST00000147812	ENSMUSG00000052926	8	84956610	84969767	-1	0	0	0	0	0	0	26	0	0	12	14		Q9CWY8
ENSMUST00000147813						0	0	0	5	0	0	15	4	0	0	0		
ENSMUST00000147814						2	4	6	1	3	1	2	4	4	0	3		
ENSMUST00000147815						4	0	21	0	4	0	17	40	37	9	56		
ENSMUST00000147816						2	0	0	0	0	1	22	267	42	10	32		
ENSMUST00000147817						3	11	0	0	0	0	0	7	13	2	8		
ENSMUST00000147818						32	17	50	35	50	15	0	0	0	0	0		
ENSMUST00000147819	ENSMUSG00000019437	11	78176711	78181909	1	0	0	2	4	0	0	0	14	7	1	1	E9PY70	
ENSMUST00000147820						0	1	4	2	0	0	0	2	0	0	1		
ENSMUST00000147821						1	1	0	1	2	0	0	8	0	0	0		
ENSMUST00000147822						54	57	66	70	52	32	45	232	96	20	113		
ENSMUST00000147823						0	4	5	137	4	2	0	0	2	2	4		
ENSMUST00000147824						138	119	627	375	206	91	3	12	13	3	33		
ENSMUST00000147825						0	0	0	0	0	0	23	33	19	3	18		
ENSMUST00000147826	ENSMUSG00000047613	4	153957237	153961925	1	0	2	0	7	6	0	73	25	4	62	16	D6RH81	
ENSMUST00000147827						3	0	6	0	9	0	39	395	19	73	50		
ENSMUST00000147828						96	82	201	262	104	45	9	39	12	4	25		
ENSMUST00000147830						18	14	63	26	10	5	14	16	7	1	9		
ENSMUST00000147831						5	0	15	4	0	0	2	0	0	0	0		
ENSMUST00000147832						2	6	1	1	6	1	0	0	0	0	0		
ENSMUST00000147833						0	1	1	12	0	0	0	0	0	0	0		
ENSMUST00000147835	ENSMUSG00000083649	7	5124938	5125950	-1	6	3	1	53	9	3	0	2	1	5	1	A6H622	Q61820
ENSMUST00000147836	ENSMUSG00000032135	9	44134469	44142727	1	0	4	4	0	0	0	0	0	0	0	0	F7ATH5	
ENSMUST00000147837	ENSMUSG00000035495	4	46114746	46138694	-1	0	2	0	31	0	0	12	3	26	2	10	B1AWH1	
ENSMUST00000147838						96	77	123	56	64	36	5	19	11	2	21		
ENSMUST00000147839						0	0	0	2	0	0	56	80	72	4	89		
ENSMUST00000147840	ENSMUSG00000030844	7	128373621	128418758	-1	6	2	7	38	3	3	0	0	0	0	0	D3Z1B6	
ENSMUST00000147841						0	0	0	0	0	0	6	0	4	0	2		
ENSMUST00000147842	ENSMUSG00000032320	9	56041845	56061882	1	7	2	14	53	9	0	0	13	8	0	0	D6RHL9	
ENSMUST00000147843						0	1	4	37	1	1	1	0	2	0	4		
ENSMUST00000147844						0	0	3	2	0	0	3	5	2	0	13		
ENSMUST00000147845	ENSMUSG00000033379	4	117884326	117887333	-1	0	0	14	160	11	4	86	675	153	31	211		
ENSMUST00000147846						5	0	8	4	4	3	0	41	0	0	102		
ENSMUST00000147849	ENSMUSG00000022842	16	20611593	20646485	1	0	0	0	0	0	1	0	0	0	0	0	F6T2B3	
ENSMUST00000147851						4	0	4	2	8	5	0	0	1	0	0		
ENSMUST00000147852	ENSMUSG00000041000	4	128883580	128911328	1	16	12	26	353	25	9	0	2	0	0	3	D6RJM1	
ENSMUST00000147853						4	10	7	18	9	5	0	4	0	1	6		
ENSMUST00000147854	ENSMUSG00000106677	5	87459490	87490871	-1	3	7	3	2	4	0	0	0	0	0	0		Q80X89
ENSMUST00000147855	ENSMUSG00000046262	4	144206775	144213318	-1	0	0	0	0	0	0	0	0	0	0	0	A6PWB3	
ENSMUST00000147856						122	106	351	107	109	44	2	6	5	0	13		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147857						1	5	5	2	8	1	0	0	0	0	0		
ENSMUST00000147858						0	3	11	3	8	1	3	38	18	3	33		
ENSMUST00000147859						2	0	0	0	2	3	0	0	0	0	0		
ENSMUST00000147860						0	0	9	10	6	2	0	0	0	0	0		
ENSMUST00000147861						5	2	5	8	4	3	0	0	1	0	2		
ENSMUST00000147862						63	47	110	65	50	32	26	37	30	6	57		
ENSMUST00000147863						0	0	12	6	0	0	0	0	0	0	2		
ENSMUST00000147864						33	37	33	34	28	20	17	49	38	3	36		
ENSMUST00000147865						4	3	17	9	5	0	0	0	0	0	0		
ENSMUST00000147866	ENSMUSG00000006471	2	25244821	25256022	-1	0	0	0	0	0	2	0	0	0	3	0	E0CXI9	
ENSMUST00000147867						0	2	4	8	1	1	0	0	0	0	0		
ENSMUST00000147869						5	5	4	76	7	2	0	0	0	1	0		
ENSMUST00000147872						3	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000147873						2	0	4	2	3	0	0	0	0	0	4		
ENSMUST00000147874	ENSMUSG00000020389	11	52004221	52089784	1	0	1	0	0	1	0	0	3	5	0	0	F6RUB4	
ENSMUST00000147875	ENSMUSG00000072640	11	78826584	78846870	1	147	142	289	168	145	94	25	142	74	16	73		Q3UN90
ENSMUST00000147876	ENSMUSG00000061894	4	128583539	128610098	-1	1	0	0	64	4	2	0	0	0	0	1	B1AS94	
ENSMUST00000147877						6	0	0	1	4	4	0	0	0	0	0		
ENSMUST00000147878						11	15	15	8	13	8	9	22	9	3	17		
ENSMUST00000147879						2	1	6	4	2	1	0	0	0	0	0		
ENSMUST00000147880						0	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000147881						0	0	0	0	0	0	125	518	179	133	76		
ENSMUST00000147882						18	16	7	34	20	21	7	32	10	6	34		
ENSMUST00000147883						0	0	0	19	1	2	1	0	0	0	1		
ENSMUST00000147884	ENSMUSG00000022498	16	11074911	11134650	-1	83	104	100	325	183	91	31	64	30	19	46	D6REU4	
ENSMUST00000147885	ENSMUSG00000026983	2	24276954	24283426	1	0	0	0	0	5	0	0	0	0	0	0	A0A0A6YWE1	
ENSMUST00000147886						1	0	0	2	0	0	0	15	7	0	0		
ENSMUST00000147887	ENSMUSG00000037552	7	28359604	28372599	-1	4	2	15	34	0	1	2	0	1	0	4	D3Z1B1	
ENSMUST00000147888						10	13	12	7	21	6	15	42	43	8	62		
ENSMUST00000147889	ENSMUSG00000023267	4	33062999	33095865	1	0	4	0	3	2	0	0	0	0	0	1	F6YZH6	
ENSMUST00000147890						2	3	11	2	2	2	7	15	24	0	6		
ENSMUST00000147891	ENSMUSG00000022961	16	91647506	91679221	1	16	6	11	12	11	4	460	2237	802	106	1204	F7CU80	
ENSMUST00000147892						0	0	0	0	6	3	0	0	0	0	0		
ENSMUST00000147893	ENSMUSG00000029119	5	36806921	36830653	-1	3	0	15	2	5	5	0	25	0	0	6	F6Z025	
ENSMUST00000147894						18	22	37	31	28	14	37	147	64	22	76		
ENSMUST00000147895						2	4	5	0	6	1	0	9	0	1	4		
ENSMUST00000147897						3	3	17	6	5	4	19	51	31	0	109		
ENSMUST00000147898						5	12	19	8	0	4	7	92	31	15	43		
ENSMUST00000147899						2	1	10	173	12	3	0	0	0	0	0		
ENSMUST00000147900	ENSMUSG00000019087	X	74297097	74304721	1	2	1	2	50	0	2	6	2	5	5	10	B7FAU3	
ENSMUST00000147901	ENSMUSG00000027993	3	84160439	84306877	-1	0	0	0	0	0	0	0	0	0	0	0	D3YTN5	
ENSMUST00000147902						4	0	5	3	1	2	0	0	0	0	0		
ENSMUST00000147903	ENSMUSG00000028919	4	141239499	141257564	1	0	0	0	63	0	0	0	0	0	0	0	A2A832	
ENSMUST00000147904						0	0	11	29	4	2	0	5	10	12	12		
ENSMUST00000147905	ENSMUSG00000022149	15	6445327	6498751	1	4	0	0	0	1	4	0	0	0	2	0	H3BKN4	
ENSMUST00000147906						1	3	0	2	1	1	0	0	0	0	0		
ENSMUST00000147907						0	5	5	16	14	4	0	0	0	0	0		
ENSMUST00000147908						4	1	0	26	8	0	0	49	19	10	12		
ENSMUST00000147909						9	9	22	45	33	4	0	0	0	0	0		
ENSMUST00000147910						0	0	0	0	0	0	2	4	0	0	0		
ENSMUST00000147911						0	0	0	0	0	0	0	0	0	7	0		
ENSMUST00000147912	ENSMUSG00000018398	11	53519257	53549565	1	0	1	0	0	0	0	0	0	0	5	0	B1AQY9	
ENSMUST00000147913						0	1	6	2	2	0	1	1	1	0	0		
ENSMUST00000147914	ENSMUSG00000020109	10	59879556	59899302	1	7	6	2	49	12	7	111	111	133	16	54	Q8C4C9	
ENSMUST00000147915						8	0	4	135	23	1	0	8	0	0	5		
ENSMUST00000147916						4	0	0	3	2	0	0	0	0	0	0		
ENSMUST00000147917						3	8	2	0	2	2	0	0	0	0	0		
ENSMUST00000147918						4	1	13	1	2	2	3	2	16	0	2		
ENSMUST00000147920	ENSMUSG00000029730	5	138164583	138172422	-1	3	1	7	72	5	5	2	1	0	3	3		
ENSMUST00000147921						2	2	12	1	7	0	2	4	6	3	8		
ENSMUST00000147922						10	9	2	11	11	10	1	2	3	0	2		
ENSMUST00000147923						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147924						0	4	2	9	5	5	0	0	1	0	3		
ENSMUST00000147925						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000147926						5	8	7	2	9	5	3	26	3	3	1		
ENSMUST00000147927						3	6	1	12	2	2	0	9	12	0	11		
ENSMUST00000147928	ENSMUSG00000031370	X	163935443	163958661	-1	0	0	0	0	0	0	3	1	6	9	11	B1B0F0	
ENSMUST00000147930						78	119	139	63	117	74	19	67	25	60	53		
ENSMUST00000147931						23	22	47	23	32	14	8	24	31	1	37		
ENSMUST00000147932						3	2	7	11	5	0	0	2	0	0	0		
ENSMUST00000147933						4	0	1	0	0	0	9	3	25	0	16		
ENSMUST00000147934	ENSMUSG00000039958	6	149139849	149151171	1	5	1	0	0	0	2	0	53	0	0	5	Q80VP4	
ENSMUST00000147935						1	2	2	3	2	0	0	0	7	0	6		
ENSMUST00000147936	ENSMUSG00000051124	6	48676129	48679114	1	0	0	0	2	0	1	16	102	16	50	31	F7BEI3	
ENSMUST00000147938	ENSMUSG00000015755	10	7905653	7956230	-1	0	0	18	17	6	9	114	12	476	0	314	D3Z216	
ENSMUST00000147940						6	1	8	0	4	1	7	8	20	0	11		
ENSMUST00000147941						6	2	22	12	18	0	17	1482	17	53	106		
ENSMUST00000147942						10	3	54	9	7	5	9	0	12	2	3		
ENSMUST00000147943						8	2	3	6	3	3	0	0	0	0	0		
ENSMUST00000147944						0	2	1	0	0	1	0	8	3	0	18		
ENSMUST00000147945						0	1	0	0	3	0	0	5	5	0	0		
ENSMUST00000147946						2	6	4	4	6	2	0	0	0	0	0		
ENSMUST00000147947						6	3	6	6	7	6	0	0	0	0	0		
ENSMUST00000147948	ENSMUSG00000041423	3	88364584	88368541	1	0	0	0	1	0	0	0	0	0	0	0	D3Z1S5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000147949	ENSMUSG00000005982	16	3872375	3904780	1	0	0	9	0	0	0	14	0	21	25	18	D6RDS3	
ENSMUST00000147950						4	1	1	0	0	0	0	78	97	23	24		
ENSMUST00000147952	ENSMUSG00000002205	7	44748413	44777515	1	2	6	25	0	13	6	137	153	139	0	19	E9Q754	
ENSMUST00000147953						2	0	4	18	4	0	0	0	0	0	0		
ENSMUST00000147954						42	25	515	131	58	43	2226	11786	1901	4261	1714		
ENSMUST00000147955						1	0	1	3	2	1	0	0	0	0	0		
ENSMUST00000147956						2	1	9	2	1	2	4	21	6	0	11		
ENSMUST00000147957						1	1	0	103	7	0	4	5	3	0	6		
ENSMUST00000147958						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147960						2	3	4	3	4	0	3	0	15	0	0		
ENSMUST00000147961						10	0	11	8	11	3	21	24	7	11	15		
ENSMUST00000147962	ENSMUSG00000038526	3	95897768	95904691	-1	1	3	6	3	3	2	0	0	0	0	2	D3Z4J8	
ENSMUST00000147963						0	0	0	14	0	0	0	0	0	0	0		
ENSMUST00000147964	ENSMUSG00000031832	8	119597975	119605222	-1	31	16	76	137	50	28	65	143	116	0	252	D6RI25	
ENSMUST00000147966						0	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000147967						5	0	16	9	5	0	0	0	0	0	0		
ENSMUST00000147968						9	6	40	8	15	5	0	0	0	0	0		
ENSMUST00000147969						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147970						17	16	28	12	27	14	2	3	3	4	5		
ENSMUST00000147971	ENSMUSG00000020883	11	98082556	98150403	-1	0	0	0	0	0	0	12	20	0	1	0	A2A550	
ENSMUST00000147972						1	0	6	0	0	0	5	22	12	28	23		
ENSMUST00000147973						1116	931	4517	1149	1261	590	23	88	50	8	80		
ENSMUST00000147974	ENSMUSG00000004264	6	124712336	124716950	1	1	0	0	0	0	0	0	0	0	0	0	F6Q8V7	
ENSMUST00000147975						13	18	22	11	19	10	1	11	5	5	6		
ENSMUST00000147976	ENSMUSG00000001768	2	145784734	145887616	1	0	0	25	0	0	0	173	875	360	94	129	E0CYG9	
ENSMUST00000147977						22	15	64	22	26	12	33	46	93	4	96		
ENSMUST00000147978						11	6	8	12	7	1	5	3	8	0	3		
ENSMUST00000147979	ENSMUSG00000000441	6	115618067	115676635	-1	2	0	15	0	1	1	6	7	19	0	24	F6TUC4	
ENSMUST00000147980						7	6	1	6	7	3	0	0	0	0	0		
ENSMUST00000147981	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	3	3	0	0	0	D3YZ95	
ENSMUST00000147982						65	53	96	126	76	35	8	13	5	0	13		
ENSMUST00000147983	ENSMUSG00000007564	17	20945311	20965916	1	1	8	0	0	3	0	32	0	0	0	0	G3UWL2	
ENSMUST00000147984						5	3	0	9	4	0	0	0	8	46	1		
ENSMUST00000147985						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000147987						2	4	1	0	0	0	0	8	0	2	2		
ENSMUST00000147988						2	2	3	4	5	5	0	0	0	0	0		
ENSMUST00000147990	ENSMUSG00000039130	6	30366380	30391028	-1	1	0	6	0	0	0	0	0	0	0	0	D3Z5A4	
ENSMUST00000147991	ENSMUSG00000041423	3	88364584	88368541	1	0	0	28	0	0	0	0	0	0	0	0	Q0VBT6	Q6TCG5
ENSMUST00000147992						8	3	20	7	5	0	12	5	12	0	5		
ENSMUST00000147994						0	0	0	0	0	0	0	4	0	1	5		
ENSMUST00000147995	ENSMUSG00000045752	7	143069249	143071093	1	0	0	0	0	0	0	1	0	0	0	0	D3Z6S3	
ENSMUST00000147996						3	0	27	49	19	7	0	0	0	0	0		
ENSMUST00000147997						0	3	5	2	1	0	0	0	0	0	0		
ENSMUST00000147998						1	0	0	1	1	0	0	0	8	45	1		
ENSMUST00000147999	ENSMUSG00000066036	4	139352609	139489588	1	0	4	0	8	0	5	533	796	1372	30	753	Z4YMA7	
ENSMUST00000148000						1	2	0	6	3	5	18	24	14	12	11		
ENSMUST00000148001						13	7	20	53	13	5	0	0	0	0	6		
ENSMUST00000148002	ENSMUSG00000025855	5	139017306	139150001	-1	0	0	0	0	2	2	0	0	0	0	0	D3Z068	
ENSMUST00000148003						0	0	0	0	0	0	1	18	4	1	0		
ENSMUST00000148005						1614	1977	1778	1224	1484	702	22	138	52	37	56		
ENSMUST00000148006						1	0	0	0	0	0	0	0	9	0	19		
ENSMUST00000148007	ENSMUSG00000040838	11	104685707	104753962	1	13	5	113	50	11	6	0	0	0	0	0	F6RS26	
ENSMUST00000148008	ENSMUSG00000029802	6	58584523	58695676	1	1	0	0	0	1	0	0	0	0	0	0	D3YVG8	
ENSMUST00000148009						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148011	ENSMUSG00000079109	5	143909964	143933968	1	13	42	258	10	6	11	3	3	0	0	0	B9EJ22	
ENSMUST00000148012	ENSMUSG00000054594	7	3609813	3616157	-1	0	5	10	9	15	4	1	3	0	0	0	D3YXX9	
ENSMUST00000148013						9	14	23	18	18	4	0	0	4	0	4		
ENSMUST00000148014						0	1	0	2	0	0	4	107	0	7	0		
ENSMUST00000148015						1	2	5	5	5	8	1	1	0	0	0		
ENSMUST00000148016						4	0	6	29	9	16	20	39	31	9	12		
ENSMUST00000148018						2	5	19	6	8	1	2	3	2	2	2		
ENSMUST00000148020	ENSMUSG00000044816	1	65105285	65123214	-1	0	2	0	1	2	0	1	2	0	2	0	D3YUK5	
ENSMUST00000148021	ENSMUSG00000037098	17	25989036	26069409	-1	0	0	1	2	0	1	0	0	0	0	0	D3Z1T5	
ENSMUST00000148022						3	7	13	0	8	5	1	1	1	4	3		
ENSMUST00000148023						0	2	7	3	3	4	0	0	2	0	2		
ENSMUST00000148024						4	0	6	5	5	3	1	3	1	0	2		
ENSMUST00000148025						1	0	1	7	2	0	21	52	34	26	20		
ENSMUST00000148026						1	2	0	0	0	0	0	0	0	2	1		
ENSMUST00000148029						11	8	9	11	12	2	0	0	0	0	0		
ENSMUST00000148030						18	12	64	16	6	8	1	1	0	0	0		
ENSMUST00000148031	ENSMUSG00000027778	3	68892499	69004570	-1	0	0	0	0	0	0	0	15	15	0	13	D3Z157	
ENSMUST00000148032						0	0	0	0	0	0	15	0	0	0	0		
ENSMUST00000148033						4	3	1	1	2	1	0	0	0	0	0		
ENSMUST00000148034						1	0	3	24	4	1	0	0	0	0	0		
ENSMUST00000148035						1	2	1	0	0	2	2	11	5	0	5		
ENSMUST00000148036						11	21	42	3	46	17	548	556	365	66	268		
ENSMUST00000148037						4	7	24	8	8	5	50	216	103	3	156		
ENSMUST00000148038	ENSMUSG00000061298	4	110397661	111664324	1	41	19	87	35	26	26	0	3	1	0	2	F6VQN0	
ENSMUST00000148039	ENSMUSG00000061576	5	26817203	27727505	1	0	1	1	11	0	1	0	0	0	0	0	D6RFR3	
ENSMUST00000148040						28	0	24	28	22	17	0	14	11	0	0		
ENSMUST00000148041						3	2	3	9	5	0	0	0	5	3	10		
ENSMUST00000148042	ENSMUSG00000026974	2	24949792	24962075	1	9	7	19	52	12	3	13	14	15	14	28		Q9CQG3
ENSMUST00000148043						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000148044						0	0	3	0	0	0	25	2	30	0	23		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148045						7	22	19	4	0	6	0	35	17	0	12		
ENSMUST00000148046						2	4	4	0	2	1	0	0	0	0	0		
ENSMUST00000148047	ENSMUSG00000026110	1	37439340	37541016	-1	0	0	1	0	0	0	0	0	0	0	0	D3YZH7	
ENSMUST00000148048						0	0	0	0	0	0	0	0	12	2	4		
ENSMUST00000148049	ENSMUSG00000025083	19	56912361	57008228	-1	8	5	24	32	10	8	0	0	0	0	2	D3YYQ6	
ENSMUST00000148050						104	93	330	133	113	53	1	12	6	4	16		
ENSMUST00000148051						0	1	1	85	0	1	0	0	0	0	0		
ENSMUST00000148052						0	0	0	0	0	0	0	1	0	2	0		
ENSMUST00000148053	ENSMUSG00000020385	11	51261730	51281766	1	5	0	0	0	0	0	22	167	92	74	87	F2Z3V2	
ENSMUST00000148054						12	6	21	79	14	6	0	0	0	2	7		
ENSMUST00000148055	ENSMUSG00000026768	2	12106632	12301922	-1	2	0	1	2	0	0	0	0	0	0	1	G3UYV5	
ENSMUST00000148056	ENSMUSG00000001864	2	31950139	31973442	1	0	0	0	3	0	0	0	0	0	4	0	A0A0A6YWH2	
ENSMUST00000148059	ENSMUSG00000028496	4	87769925	88033364	-1	0	0	0	0	0	0	0	7	0	0	0	E9PXP8	
ENSMUST00000148060						10	13	30	114	17	9	3	12	1	0	8		
ENSMUST00000148061						1	6	0	1	1	1	22	125	62	151	108		
ENSMUST00000148062	ENSMUSG00000023902	17	23600856	23611019	1	0	0	0	0	0	0	0	0	0	0	0	E9PXB1	
ENSMUST00000148065	ENSMUSG00000003534	17	35681567	35704621	-1	0	0	0	0	0	0	0	0	0	0	0	D6RII6	
ENSMUST00000148067						3	4	19	12	6	0	0	0	0	0	0		
ENSMUST00000148068						1	0	4	0	4	1	34	650	15	12	20		
ENSMUST00000148069						6	8	15	4	5	3	0	0	0	0	0		
ENSMUST00000148070	ENSMUSG00000020268	11	54826866	54860916	-1	4	9	14	11	8	5	0	0	0	0	0		Q9DA03
ENSMUST00000148071	ENSMUSG00000055313	13	21421275	21441058	-1	8	10	4	3	3	0	0	2	0	0	4	D3YUW1	
ENSMUST00000148072						0	0	1	37	0	2	0	0	3	0	0		
ENSMUST00000148073						4	0	5	100	2	0	0	0	0	1	11		
ENSMUST00000148074						4	3	8	6	6	2	3	68	2	0	20		
ENSMUST00000148075						0	0	0	71	0	1	0	0	0	0	0		
ENSMUST00000148076						0	1	5	1	1	0	0	1	0	0	0		
ENSMUST00000148077						5	1	23	15	8	4	0	0	0	0	0		
ENSMUST00000148079						13	12	28	122	4	10	3	4	0	0	4		
ENSMUST00000148080						0	1	3	5	2	0	0	0	0	0	2		
ENSMUST00000148081						0	0	0	0	0	0	0	11	3	0	4		
ENSMUST00000148083						0	1	0	2	0	0	77	293	198	111	93		
ENSMUST00000148084						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000148085						2	1	62	6	2	4	41	336	32	69	99		
ENSMUST00000148086	ENSMUSG00000031922	9	13807792	13827107	-1	0	0	0	0	0	0	55	0	0	0	0		Q8CEE0
ENSMUST00000148088	ENSMUSG00000010607	9	22156846	22158358	1	3	2	5	72	8	1	0	0	0	0	0		P0C1P0
ENSMUST00000148090						3	1	0	0	1	2	0	5	3	0	12		
ENSMUST00000148091						2	3	1	2	2	1	0	0	0	0	2		
ENSMUST00000148093						33	26	59	8	32	17	4	13	2	3	2		
ENSMUST00000148094	ENSMUSG00000029730	5	138164583	138172422	-1	0	6	0	3	0	1	0	6	0	0	4	D3Z335	
ENSMUST00000148095						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000148096						0	0	0	0	0	0	0	9	0	0	0		
ENSMUST00000148097						5	4	4	1	3	2	0	0	0	0	1		
ENSMUST00000148098						15	6	11	9	7	5	49	242	73	9	105		
ENSMUST00000148099						6	1	16	0	8	1	0	0	0	0	0		
ENSMUST00000148100						0	0	3	7	1	0	3	11	0	0	9		
ENSMUST00000148101						0	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000148102						2	0	11	12	5	0	6	22	6	30	0		
ENSMUST00000148103						0	2	3	1	0	2	0	0	0	0	0		
ENSMUST00000148104						16	6	38	13	11	1	16	37	25	11	96		
ENSMUST00000148105						0	0	0	40	0	0	4	12	26	14	24		
ENSMUST00000148106	ENSMUSG00000031618	8	76899442	77245012	1	0	14	21	36	0	0	0	0	0	0	8	D6RIL1	
ENSMUST00000148107						4	0	9	1	2	1	5	10	5	0	2		
ENSMUST00000148108	ENSMUSG00000056698	6	72565922	72598413	-1	0	0	0	0	0	0	0	0	9	0	0		
ENSMUST00000148109	ENSMUSG00000021850	14	49226358	49245428	-1	0	0	0	0	0	0	0	0	0	0	0	D6RDQ1	
ENSMUST00000148110						2	0	4	3	4	2	4	149	11	8	27		
ENSMUST00000148111						2	2	4	0	1	0	0	0	0	3	0		
ENSMUST00000148112						0	0	0	0	0	0	0	5	16	11	21		
ENSMUST00000148113						20	14	23	175	35	7	0	0	0	0	0		
ENSMUST00000148114						50	46	142	72	52	32	21	53	57	6	68		
ENSMUST00000148115						1	1	0	7	1	0	0	1	0	0	0		
ENSMUST00000148116						2	0	0	0	0	0	0	20	14	21	9		
ENSMUST00000148117						3	0	9	2	0	0	0	0	0	0	0		
ENSMUST00000148118						3	4	10	5	2	1	0	4	0	0	3		
ENSMUST00000148119						15	11	15	4	13	11	21	69	38	0	72		
ENSMUST00000148120						7	3	8	5	6	0	6	10	2	0	11		
ENSMUST00000148121	ENSMUSG00000021786	14	16238656	16249808	-1	0	0	0	0	0	0	0	0	0	0	6	D3Z6F9	
ENSMUST00000148123						7	9	12	10	15	4	0	0	0	0	0		
ENSMUST00000148124	ENSMUSG00000022863	16	78359860	78377192	-1	0	1	4	11	2	2	10	19	5	0	6	D3Z1M9	
ENSMUST00000148125						0	0	0	39	0	0	0	18	14	23	0		
ENSMUST00000148126						21	15	39	22	28	19	204	2333	87	111	75		
ENSMUST00000148127						1	1	0	62	0	0	0	0	0	0	0		
ENSMUST00000148128						3	1	13	17	2	3	60	344	128	43	107		
ENSMUST00000148129						3	6	7	0	11	1	0	0	0	0	0		
ENSMUST00000148130						0	0	1	0	1	1	0	0	0	0	4		
ENSMUST00000148131						16	7	17	7	34	11	0	0	0	0	0		
ENSMUST00000148133						3	8	4	27	11	3	0	1	0	1	8		
ENSMUST00000148134	ENSMUSG00000024184	17	26195999	26199087	-1	1	0	4	0	0	1	0	0	0	0	0	F6Q519	
ENSMUST00000148135						0	0	4	39	0	0	0	0	0	0	0		
ENSMUST00000148137	ENSMUSG00000079342	19	33775521	33787462	-1	5	2	6	2	0	3	0	0	0	0	0	F6WYC8	
ENSMUST00000148138						16	17	49	45	19	14	0	0	0	0	0		
ENSMUST00000148139						0	0	0	2	3	0	0	0	6	0	6		
ENSMUST00000148140						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148141						0	0	0	3	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148142						5	5	8	5	13	2	1	2	1	3	12		
ENSMUST00000148143						0	0	5	0	3	0	0	38	16	2	9		
ENSMUST00000148144	ENSMUSG00000034593	9	75071015	75223688	1	0	0	0	0	0	0	42	0	61	0	151	F6TDE5	
ENSMUST00000148145						8	5	3	7	6	0	1	0	0	0	0		
ENSMUST00000148146						2	0	2	4	2	1	0	0	2	0	0		
ENSMUST00000148147						0	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000148148						9	11	12	28	8	4	0	0	0	0	0		
ENSMUST00000148149						2	0	1	2	1	1	0	0	0	1	0		
ENSMUST00000148150	ENSMUSG00000005447	7	25295049	25297986	-1	0	0	0	161	2	0	3	7	0	6	0	D3Z2X5	
ENSMUST00000148151						0	19	137	28	20	13	54	175	100	27	135		
ENSMUST00000148152	ENSMUSG00000019843	10	39368855	39565381	1	0	0	16	1	0	1	0	0	0	0	2	D3YZA2	
ENSMUST00000148153						0	3	5	6	3	0	12	48	21	6	41		
ENSMUST00000148154	ENSMUSG00000017405	11	78166106	78176675	-1	1	1	0	2	0	0	0	0	0	1	0	E9Q258	
ENSMUST00000148155	ENSMUSG00000031933	9	14885814	14903949	-1	1	0	11	1	0	0	0	4	0	0	0	D3YZI1	
ENSMUST00000148156						6	8	18	25	15	6	3	17	12	2	28		
ENSMUST00000148157						0	1	5	0	0	6	0	0	0	0	0		
ENSMUST00000148158						10	0	0	2	16	0	0	0	0	1	0		
ENSMUST00000148159	ENSMUSG00000062210	18	49979427	50107173	1	7	5	2	8	8	6	864	3567	914	693	302	D3Z325	
ENSMUST00000148160						3	2	2	0	1	3	0	0	0	0	0		
ENSMUST00000148161						4	2	5	2	7	1	0	0	0	0	0		
ENSMUST00000148162	ENSMUSG00000061981	11	78037931	78060434	1	0	0	0	0	0	0	0	0	0	0	0	E9PV09	
ENSMUST00000148163						0	2	0	0	0	1	0	2	3	0	3		
ENSMUST00000148164						2	2	1	0	2	0	0	2	0	0	1		
ENSMUST00000148165						1	1	12	12	8	3	0	44	0	16	18		
ENSMUST00000148166						21	12	8	11	14	10	0	0	6	0	0		
ENSMUST00000148167						2	0	0	11	1	4	0	0	0	0	2		
ENSMUST00000148168						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000148169						1	1	0	1	2	1	0	5	0	0	0		
ENSMUST00000148170						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000148172						1	3	2	45	5	0	0	0	0	0	0		
ENSMUST00000148173						0	3	4	31	4	3	0	0	0	11	4		
ENSMUST00000148174						3	3	5	2	3	2	0	0	0	0	0		
ENSMUST00000148175						0	0	0	17	0	0	0	3	0	0	0		
ENSMUST00000148176						0	3	2	4	5	0	0	29	10	3	0		
ENSMUST00000148177						0	0	0	1	1	0	0	2	0	0	0		
ENSMUST00000148178	ENSMUSG00000059208	17	33646233	33686860	-1	2	4	10	120	12	8	9	39	17	7	22		Q9D0E1
ENSMUST00000148179						3	4	8	6	2	0	4	8	8	2	22		
ENSMUST00000148181						3	0	1	0	6	0	0	0	0	0	0		
ENSMUST00000148182						2	3	0	63	5	0	0	0	0	0	0		
ENSMUST00000148183						2	3	3	6	2	2	5	5	2	0	5		
ENSMUST00000148184						0	0	1	0	2	1	0	0	0	0	0		
ENSMUST00000148185						0	2	1	0	1	0	0	0	0	0	0		
ENSMUST00000148186						2	2	0	3	3	1	0	0	0	1	0		
ENSMUST00000148187						0	2	5	5	1	4	1	3	0	0	0		
ENSMUST00000148188	ENSMUSG00000037446	17	28351515	28365182	-1	1	0	0	52	4	0	0	0	1	0	0	F7BGL3	
ENSMUST00000148189						1	0	9	5	2	2	31	153	40	10	54		
ENSMUST00000148190						52	47	165	42	60	30	5	17	2	0	1		
ENSMUST00000148191						47	50	185	71	70	43	521	730	837	119	704		
ENSMUST00000148192						0	0	0	81	0	0	0	2	0	0	1		
ENSMUST00000148193	ENSMUSG00000040473	5	5579278	5664239	-1	4	2	1	1	1	0	0	0	0	0	0	D3YV72	
ENSMUST00000148194	ENSMUSG00000074677	3	15795145	15848528	-1	0	1	0	0	0	0	14	98	17	34	14	F6UP26	
ENSMUST00000148195						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148196	ENSMUSG00000054808	7	28893248	28962340	-1	1	0	1	1	0	0	0	0	0	0	0	D3Z761	
ENSMUST00000148197						2	3	7	5	7	0	0	0	0	0	0		
ENSMUST00000148198						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000148199						1	0	0	0	0	0	4	13	0	0	3		
ENSMUST00000148200						1	0	9	1	1	0	0	0	0	0	0		
ENSMUST00000148201	ENSMUSG00000026418	1	135779434	135810989	1	10	3	4	0	4	4	0	0	0	0	0		Q9WUZ5
ENSMUST00000148203						1	1	2	3	4	2	3	1	3	2	4		
ENSMUST00000148204	ENSMUSG00000040842	4	141113001	141139775	-1	9	4	17	0	10	0	83	107	105	20	43	A2AA85	
ENSMUST00000148205						2	0	0	0	3	0	0	0	0	0	1		
ENSMUST00000148206						0	5	4	0	0	1	0	0	0	0	0		
ENSMUST00000148208	ENSMUSG00000029513	5	116013586	116024508	-1	0	0	0	0	0	0	0	28	14	12	27	S4R2R1	
ENSMUST00000148209						2	3	1	5	5	1	0	0	1	0	1		
ENSMUST00000148210	ENSMUSG00000070880	2	70553072	70602014	1	0	0	0	29	0	2	0	0	0	0	0	D3Z1L8	
ENSMUST00000148211	ENSMUSG00000022568	15	76047158	76069784	-1	0	1	5	7	0	0	0	0	0	0	0	D3YVA3	
ENSMUST00000148212						0	0	0	1	3	0	0	0	0	0	0		
ENSMUST00000148213						1	0	4	2	2	0	0	1	0	0	3		
ENSMUST00000148214						30	11	68	0	31	12	0	4	0	0	0		
ENSMUST00000148216						0	0	1	0	0	2	0	0	2	0	0		
ENSMUST00000148218						0	4	11	28	0	1	3	7	0	0	0		
ENSMUST00000148219	ENSMUSG00000024914	19	5422805	5424979	-1	0	0	0	0	0	0	359	214	335	139	122	F6T9K1	
ENSMUST00000148220						8	2	16	9	8	4	30	244	33	13	49		
ENSMUST00000148221	ENSMUSG00000025877	13	55005985	55021385	-1	0	0	0	0	0	0	10	13	11	3	20	D3Z2E4	
ENSMUST00000148222	ENSMUSG00000025869	13	54584185	54590090	-1	0	0	0	0	0	0	0	0	0	15	0	D3Z7M5	
ENSMUST00000148223						3	6	4	3	7	0	28	0	24	0	0		
ENSMUST00000148225						26	24	90	24	36	16	1	0	0	0	0		
ENSMUST00000148227						40	25	164	81	87	38	67	159	124	11	233		
ENSMUST00000148228						3	2	4	38	6	3	1	10	4	3	13		
ENSMUST00000148229						0	0	0	2	1	0	7	5	7	0	4		
ENSMUST00000148232	ENSMUSG00000025371	11	119913441	119919548	1	2	1	3	32	8	1	0	0	2	0	0	B1AZ41	
ENSMUST00000148233						4	2	4	54	6	0	0	0	1	0	0		
ENSMUST00000148234	ENSMUSG00000056018	8	129067134	129183732	1	39	53	29	44	45	17	9	6	15	0	18	D6RD02	
ENSMUST00000148235	ENSMUSG00000014633	8	116888685	116921455	-1	0	0	0	7	0	0	52	124	41	95	26		Q8K199

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148236						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148237						1	0	4	1	1	0	0	0	0	0	0		
ENSMUST00000148238	ENSMUSG00000032342	9	78448208	78475348	1	0	0	0	6	0	0	0	22	19	13	0	D6RCK0	
ENSMUST00000148239						1	1	4	0	0	0	65	279	19	0	0		
ENSMUST00000148240						5	7	4	3	4	0	0	0	0	0	0		
ENSMUST00000148241						3	6	12	6	7	2	7	64	40	21	73		
ENSMUST00000148242	ENSMUSG00000018761	11	69656697	69662642	-1	0	0	0	0	0	0	127	68	53	13	56	E9PVP3	
ENSMUST00000148243	ENSMUSG00000040596	1	166384622	166409863	-1	0	0	0	0	0	0	3	0	0	0	0	D6RH56	
ENSMUST00000148245	ENSMUSG00000029516	5	115845278	116008947	1	0	0	0	0	0	0	0	0	0	0	0	D3Z1K6	
ENSMUST00000148246	ENSMUSG00000040811	7	19176421	19206482	1	3	5	0	0	0	0	189	284	193	0	186	D6RGM3	
ENSMUST00000148247						17	29	28	37	41	19	0	0	0	0	0		
ENSMUST00000148248						0	0	7	3	6	0	3185	8381	4388	1517	4399		
ENSMUST00000148249						14	15	30	142	23	13	2	0	2	0	1		
ENSMUST00000148250	ENSMUSG00000031391	X	73853778	73896105	-1	2	0	0	0	0	0	0	0	0	0	0	F7A5H7	
ENSMUST00000148251						52	77	101	27	63	21	6	36	16	1	19		
ENSMUST00000148252	ENSMUSG00000038685	2	181319739	181356616	1	8	0	10	0	0	0	0	30	0	0	0	Z4YLW7	
ENSMUST00000148253						0	0	0	1	0	0	0	0	0	0	2		
ENSMUST00000148254						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000148255	ENSMUSG00000024269	18	25127223	25169007	-1	186	149	465	188	212	99	3	11	11	0	15	E9PUD7	
ENSMUST00000148256						2	3	1	110	0	0	2	0	0	0	0		
ENSMUST00000148257	ENSMUSG00000005268	15	10177238	10349180	1	1	0	1	0	0	0	0	0	0	0	0		Q08501
ENSMUST00000148258	ENSMUSG00000059208	17	33646233	33686860	-1	0	0	0	0	0	0	16	274	74	0	46	F6W322	
ENSMUST00000148259						48	47	195	78	45	17	7	4	18	1	21		
ENSMUST00000148260						1	0	3	2	2	2	2	13	3	3	6		
ENSMUST00000148261	ENSMUSG00000029310	5	104046306	104065379	1	1	1	2	1	2	0	0	3	9	0	0	A2AH30	
ENSMUST00000148262						0	0	0	4	0	7	1946	1006	1163	200	873		
ENSMUST00000148263	ENSMUSG00000018425	11	86768846	86807746	-1	0	1	0	0	0	0	30	0	36	47	71	Q5SXR4	
ENSMUST00000148264	ENSMUSG00000025340	5	130171798	130214342	1	0	1	0	0	0	0	12	41	54	0	32	D3Z2L2	
ENSMUST00000148265	ENSMUSG00000068917	3	89164795	89176921	1	0	0	0	0	0	0	5	0	53	5	47	D3Z4P7	
ENSMUST00000148266						0	2	0	1	2	0	5	11	7	0	0		
ENSMUST00000148267						6	11	9	18	9	6	0	0	0	0	0		
ENSMUST00000148268						8	7	4	73	9	4	0	0	0	0	0		
ENSMUST00000148269	ENSMUSG00000040774	3	106502260	106547802	-1	0	0	5	59	0	0	1	0	171	464	155	D3YX12	
ENSMUST00000148270						2	0	0	0	0	0	169	119	159	2	106		
ENSMUST00000148271	ENSMUSG00000044991	2	132686931	132751055	1	2	0	0	0	2	0	10	0	24	0	14	Z4YMI8	
ENSMUST00000148272						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000148274						0	1	6	5	1	0	8	14	2	5	20		
ENSMUST00000148275						2	2	5	0	5	5	0	0	0	0	0		
ENSMUST00000148276	ENSMUSG00000041609	5	115648175	115731621	-1	3	0	18	0	0	2	0	11	21	0	4	F6R5X6	
ENSMUST00000148277						6	10	21	9	11	4	0	0	0	0	0		
ENSMUST00000148278						0	0	5	4	0	3	37	330	4	48	38		
ENSMUST00000148279	ENSMUSG00000036890	2	44564412	44927657	-1	1	0	0	8	3	0	0	0	0	0	0	A0A0A0MQK2	
ENSMUST00000148280	ENSMUSG00000038366	11	97799000	97838764	1	0	0	5	0	4	2	0	0	0	0	0	A2A6H0	
ENSMUST00000148281	ENSMUSG00000047502	4	106680417	106730925	-1	3	0	7	4	0	1	0	0	0	0	0	A8Y5T7	
ENSMUST00000148282						1	1	2	2	1	1	212	801	248	1450	181		
ENSMUST00000148283						8	7	11	0	3	3	2	12	0	0	5		
ENSMUST00000148285						0	0	0	0	0	0	118	138	192	18	113		
ENSMUST00000148286	ENSMUSG00000040557	5	134932368	134942637	1	0	3	12	0	0	0	0	0	2	0	1	F6RCZ2	
ENSMUST00000148288						7	4	3	10	8	2	15	18	5	3	27		
ENSMUST00000148289						6	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000148290	ENSMUSG00000087610	3	96576984	96580663	1	2	6	36	7	6	0	1	2	1	3	5	D3Z167	
ENSMUST00000148291						2	1	2	0	3	0	1	3	14	3	4		
ENSMUST00000148292	ENSMUSG00000005686	7	110768206	110812405	1	3	0	0	0	3	2	200	108	423	9	330	D3Z4N3	
ENSMUST00000148294						1	1	5	0	0	0	0	28	6	5	24		
ENSMUST00000148295						3	2	1	5	3	0	0	0	0	5	12		
ENSMUST00000148296						2	1	10	8	6	6	0	0	0	0	0		
ENSMUST00000148297						2	0	7	3	0	0	0	0	10	0	0		
ENSMUST00000148298						10	4	5	2	12	2	7	12	28	0	35		
ENSMUST00000148299						3	2	4	2	4	2	7	12	9	6	9		
ENSMUST00000148300						0	0	9	24	0	0	0	2	0	0	0		
ENSMUST00000148301	ENSMUSG00000036986	9	58218076	58249786	-1	0	0	0	0	0	0	0	0	2	0	0	D6RII9	
ENSMUST00000148302						1	0	0	4	1	0	0	0	0	0	0		
ENSMUST00000148303						1	1	3	1	1	0	0	0	0	0	0		
ENSMUST00000148304	ENSMUSG00000040455	4	21767156	21837872	1	0	0	0	0	0	0	0	0	7	0	9	E9Q4D8	
ENSMUST00000148305	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	4	D6RFR5	
ENSMUST00000148306						2	4	0	2	4	1	0	15	20	0	43		
ENSMUST00000148307	ENSMUSG00000025728	17	25926427	25944510	-1	0	1	0	0	0	0	0	0	0	0	0	D3YZX1	
ENSMUST00000148311	ENSMUSG00000102439	3	93273523	93293686	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXI5	
ENSMUST00000148312						0	2	0	0	0	2	3	17	4	48	8		
ENSMUST00000148313						82	92	171	66	93	16	37	156	43	6	90		
ENSMUST00000148314	ENSMUSG00000087006	2	93955810	93957201	-1	7	0	12	6	0	7	0	0	1	0	0	A0A087WSH6	
ENSMUST00000148315						10	11	24	8	16	11	41	56	103	11	131		
ENSMUST00000148317	ENSMUSG00000031392	X	74013914	74023918	-1	0	0	0	0	0	0	0	0	0	0	0	F7CUT1	
ENSMUST00000148319						0	0	0	0	0	0	0	154	6	0	605		
ENSMUST00000148321						2	1	4	0	0	2	2	0	0	0	0		
ENSMUST00000148322						0	0	0	77	5	1	0	0	0	0	0		
ENSMUST00000148323						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000148324	ENSMUSG00000063450	12	75818134	76110926	1	3	1	11	3	4	1	0	0	0	0	0	D3Z2P5	
ENSMUST00000148325						0	0	0	0	0	1	1	5	7	1	6		
ENSMUST00000148328	ENSMUSG00000031837	8	119446719	119472640	1	2	2	3	0	0	6	0	0	0	0	0	D3Z103	
ENSMUST00000148330	ENSMUSG00000026034	1	58410189	58424066	-1	0	0	0	0	0	0	103	4223	25	0	0		P22518
ENSMUST00000148331	ENSMUSG00000028382	4	59471868	59549364	-1	0	0	0	0	0	0	265	841	2617	470	1124		Q8BHD7
ENSMUST00000148333	ENSMUSG00000015653	5	5664829	5694578	-1	0	0	0	21	0	0	0	0	0	0	11	D3Z1C4	
ENSMUST00000148334	ENSMUSG00000027584	2	181715016	181720985	1	0	0	4	1	2	2	0	0	0	0	1	B0R0B7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148336						0	1	0	0	1	1	1	0	0	4	0		
ENSMUST00000148337						0	0	0	21	0	0	4	0	10	0	6		
ENSMUST00000148338						0	0	2	14	0	1	61	155	79	57	22		
ENSMUST00000148339	ENSMUSG00000013997	1	171338008	171345646	-1	0	1	0	0	0	0	0	0	4	0	12	D3Z2Y2	
ENSMUST00000148340						1	0	0	0	2	0	0	0	0	3	0		
ENSMUST00000148341	ENSMUSG00000032818	18	77281958	77442341	1	14	9	22	18	28	12	0	0	0	0	0	D3YUR7	
ENSMUST00000148342						1	7	46	2	15	9	0	0	0	0	0		
ENSMUST00000148343						0	2	0	23	4	2	1	0	0	0	0		
ENSMUST00000148344	ENSMUSG00000048537	9	44686304	44735198	-1	0	0	42	18	37	0	0	3	0	0	0	F6RUK9	
ENSMUST00000148345						449	441	987	426	467	202	9	115	51	13	31		
ENSMUST00000148346						71	57	214	64	49	30	3	6	6	0	11		
ENSMUST00000148347	ENSMUSG00000040473	5	5579278	5664239	-1	0	0	0	0	0	0	0	0	0	0	0	F6S241	
ENSMUST00000148348						1	0	3	7	5	2	9	21	36	0	11		
ENSMUST00000148349	ENSMUSG00000029752	6	7675169	7693254	-1	7	0	3	0	0	0	0	0	0	0	0	D3Z028	
ENSMUST00000148350						8	6	10	79	5	3	0	3	0	0	8		
ENSMUST00000148351	ENSMUSG00000002319	14	55625400	55637895	-1	5	0	15	0	5	0	40	49	0	14	0	D6RES6	
ENSMUST00000148352	ENSMUSG00000040434	2	92365046	92374869	-1	0	0	0	0	0	0	0	0	0	0	0	H3BKM6	
ENSMUST00000148354						12	3	20	1	3	2	2	17	7	2	2		
ENSMUST00000148355						10	12	11	9	10	1	0	0	1	0	0		
ENSMUST00000148356	ENSMUSG00000026950	2	52136647	52338798	-1	0	0	0	0	1	0	0	0	1	1	5	G3UWS1	
ENSMUST00000148358	ENSMUSG00000089715	15	79823896	79834688	-1	0	0	0	5	0	0	0	0	0	0	0	D3Z329	
ENSMUST00000148359						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000148360						13	14	12	145	16	7	3	1	1	0	4		
ENSMUST00000148361	ENSMUSG00000028042	3	89377644	89394776	-1	0	0	0	0	0	0	73	29	58	0	41	D3Z2X8	
ENSMUST00000148362	ENSMUSG00000071477	6	48024188	48048911	-1	2	0	0	0	0	0	0	0	8	0	2	F6QAV8	
ENSMUST00000148363						0	5	2	4	5	1	0	0	0	0	0		
ENSMUST00000148365						1	0	4	0	2	0	10	6	2	2	0		
ENSMUST00000148366	ENSMUSG00000070972	4	58995062	59025573	1	0	0	3	0	0	0	0	0	2	0	0	Z4YLX5	
ENSMUST00000148367						4	3	9	6	11	2	9	47	20	4	45		
ENSMUST00000148368	ENSMUSG00000042744	5	121220219	121368577	1	6	0	2	0	2	0	0	0	1	0	8	F6XXX5	
ENSMUST00000148369						0	0	0	0	18	0	0	0	0	0	0		
ENSMUST00000148370						0	0	0	0	0	0	7	6	0	18	21		
ENSMUST00000148371	ENSMUSG00000021203	12	103388682	103406350	1	6	0	7	21	4	0	0	0	0	0	0	F6SXD2	
ENSMUST00000148372						7	0	4	38	6	2	0	0	0	0	0		
ENSMUST00000148373						0	0	0	0	0	0	0	6	48	0	28		
ENSMUST00000148374	ENSMUSG00000072964	X	135885851	135891081	1	2	0	4	32	3	4	0	2	0	9	1	A2AGB8	
ENSMUST00000148376						0	0	5	9	10	4	0	0	0	0	0		
ENSMUST00000148378						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148379						0	0	0	0	1	0	14	31	17	53	25		
ENSMUST00000148380						0	0	0	41	1	0	0	0	0	0	0		
ENSMUST00000148381	ENSMUSG00000002635	7	34184499	34196661	-1	0	0	0	0	2	0	0	6	0	0	0	F6SGV3	
ENSMUST00000148382	ENSMUSG00000025728	17	25926427	25944510	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1F8	
ENSMUST00000148384						159	164	126	130	191	92	13	42	36	4	48		
ENSMUST00000148385	ENSMUSG00000034349	3	69004738	69034623	1	0	0	5	29	3	4	0	328	237	133	165	D6RCX2	
ENSMUST00000148386						7	0	5	22	6	0	2	7	0	0	1		
ENSMUST00000148387						8	3	1	2	5	5	0	0	0	0	2		
ENSMUST00000148388						1	0	6	0	1	0	1	0	1	1	0		
ENSMUST00000148389						0	0	0	7	0	0	8	5	14	16	19		
ENSMUST00000148390	ENSMUSG00000038267	13	34179158	34345182	-1	29	31	94	0	42	24	1	1	0	0	19	F7BP73	
ENSMUST00000148391						0	0	0	34	5	0	0	0	0	1	1		
ENSMUST00000148392						0	3	6	2	10	0	0	0	0	0	0		
ENSMUST00000148393						2	0	0	29	0	0	0	4	0	0	6		
ENSMUST00000148394						20	10	23	165	27	19	6	6	6	0	5		
ENSMUST00000148395						2	3	4	13	12	0	0	0	0	1	0		
ENSMUST00000148396	ENSMUSG00000021553	13	58545399	58610877	-1	8	5	11	19	10	7	1	4	5	0	0	D6RFS6	
ENSMUST00000148397						1	0	0	4	5	0	0	0	0	0	0		
ENSMUST00000148398						3	6	14	12	11	3	0	0	0	0	0		
ENSMUST00000148399						0	3	8	3	6	1	18	75	17	3	16		
ENSMUST00000148400						4	2	4	3	7	3	0	4	0	7	8		
ENSMUST00000148401	ENSMUSG00000026740	2	18195654	18392830	-1	0	1	4	0	0	0	0	0	0	0	0	F6WEH1	
ENSMUST00000148402	ENSMUSG00000027596	2	154791402	155051012	1	5	1	5	4	1	0	0	0	1	0	0	A2ALT2	
ENSMUST00000148403	ENSMUSG00000035674	7	3617373	3620327	1	0	0	0	5	1	0	12	14	11	45	0	D6RGT3	
ENSMUST00000148404						11	7	5	87	6	1	0	0	0	0	0		
ENSMUST00000148406	ENSMUSG00000073684	4	155249802	155256687	1	2	0	0	0	0	0	0	0	0	0	0	F2Z421	
ENSMUST00000148407						102	71	503	125	97	46	8	23	16	0	24		
ENSMUST00000148408	ENSMUSG00000039375	8	54629055	54887184	-1	13	24	36	13	10	5	1	1	4	0	9	H3BKT9	
ENSMUST00000148409	ENSMUSG00000028709	4	115828092	115836185	1	1	1	0	3	3	0	0	0	0	0	2	A2A8T5	
ENSMUST00000148410						0	0	5	6	0	0	10	41	44	0	88		
ENSMUST00000148411	ENSMUSG00000084927	6	141708118	141773810	-1	9	5	5	5	2	1	0	1	0	0	0	L7N264	
ENSMUST00000148414						0	0	0	3	5	0	0	0	0	3	0		
ENSMUST00000148415						1	0	0	1	4	0	0	0	0	2	0		
ENSMUST00000148416						7	2	9	5	5	3	0	0	0	0	0		
ENSMUST00000148417	ENSMUSG00000027224	2	122302191	122313730	-1	4	0	0	5	0	0	0	0	0	0	0	A2AQ95	
ENSMUST00000148418						3	4	0	19	11	2	0	0	0	0	0		
ENSMUST00000148419						2	0	0	3	1	0	10	54	12	0	19		
ENSMUST00000148421						3	7	9	8	0	0	0	0	0	0	0		
ENSMUST00000148422						1	0	1	23	2	1	2	0	0	0	0		
ENSMUST00000148423						0	1	1	0	0	2	2	0	1	0	4		
ENSMUST00000148424						0	0	5	0	3	0	0	0	0	0	0		
ENSMUST00000148425	ENSMUSG00000058446	6	54816916	54893500	1	0	0	0	24	0	0	0	0	0	0	0		
ENSMUST00000148426						0	0	0	0	0	0	0	175	0	11	0		
ENSMUST00000148428						3	7	5	4	15	2	1	0	5	0	6		
ENSMUST00000148430	ENSMUSG00000038347	17	13482553	13761825	-1	10	0	0	167	0	0	2	3	0	0	0	Q9Z1F3	
ENSMUST00000148431	ENSMUSG00000024371	17	34862604	34898265	-1	0	0	0	0	0	3	0	0	0	6	0	B8JJM9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148432						7	2	15	22	6	10	1	0	1	0	1		
ENSMUST00000148433						7	14	44	14	6	6	25	14	17	1	14		
ENSMUST00000148434						7	8	32	46	5	10	4	4	11	0	7		
ENSMUST00000148436						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148437						2	0	2	0	0	0	6	0	8	0	9		
ENSMUST00000148438						84	75	87	68	91	51	4	13	11	3	5		
ENSMUST00000148439						0	0	14	0	0	0	0	0	0	0	0		
ENSMUST00000148440	ENSMUSG00000036091	9	107580818	107587359	1	0	0	0	0	0	0	0	1	0	0	0		Q8VEI3
ENSMUST00000148441						15	19	132	178	17	18	0	0	0	1	8		
ENSMUST00000148442	ENSMUSG00000074221	7	29983955	30028282	1	8	0	5	148	18	12	6	0	36	0	25	E9PYI1	
ENSMUST00000148443	ENSMUSG00000049439	1	60343323	60388060	1	341	315	279	143	207	67	21	89	21	3	10	J3QPT8	
ENSMUST00000148444						3	0	0	1	3	0	0	0	2	0	2		
ENSMUST00000148446						9	4	25	8	20	13	0	0	0	0	0		
ENSMUST00000148447						0	0	2	0	0	0	3	0	2	0	0		
ENSMUST00000148449						17	11	16	27	13	4	0	0	0	0	0		
ENSMUST00000148450	ENSMUSG00000036099	10	93939165	94035817	-1	0	1	3	3	7	1	0	3	2	0	1	F6TIK3	
ENSMUST00000148451	ENSMUSG00000005299	5	33739673	33782817	-1	62	59	225	163	65	37	6	17	7	3	15		
ENSMUST00000148452						0	0	6	0	1	0	0	0	0	0	0		
ENSMUST00000148453	ENSMUSG00000041769	7	138846079	138883057	1	1	1	1	4	0	1	0	8	2	0	2	D6RCH9	
ENSMUST00000148454						1	20	37	0	35	13	54	122	80	0	95		
ENSMUST00000148455						0	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000148456	ENSMUSG00000033276	1	74601445	74636894	1	0	0	0	0	0	0	0	0	6	0	22	E9Q341	
ENSMUST00000148459	ENSMUSG00000030518	7	64756091	65156570	-1	0	0	5	65	2	0	0	0	0	0	0	D3Z6Z5	
ENSMUST00000148460						4	0	46	68	1	8	320	809	299	103	155		
ENSMUST00000148461						2	1	3	1	0	1	6	19	6	1	9		
ENSMUST00000148462						1	5	3	2	8	3	0	0	0	0	5		
ENSMUST00000148463						0	1	10	4	0	3	0	0	0	0	0		
ENSMUST00000148465	ENSMUSG00000027708	3	35892105	35937445	-1	1	0	0	0	5	0	35	119	72	83	41		
ENSMUST00000148467						18	24	27	33	35	14	100	290	137	178	173		
ENSMUST00000148468						6	5	9	1	8	2	0	0	5	1	0		
ENSMUST00000148469	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000148470	ENSMUSG00000035437	2	37443279	37566454	1	0	0	0	46	5	2	0	0	4	0	0	A2AWB0	
ENSMUST00000148471						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148472						10	8	19	18	16	3	0	4	1	2	1		
ENSMUST00000148473						4	1	4	4	2	0	0	0	0	0	1		
ENSMUST00000148474						10	9	71	2	12	9	0	0	0	0	0		
ENSMUST00000148475						109	64	400	452	99	42	7	55	49	3	89		
ENSMUST00000148476	ENSMUSG00000027170	2	104999656	105017080	-1	0	0	0	0	0	0	0	0	0	0	2	A2A701	
ENSMUST00000148477						5	3	15	0	11	0	0	0	0	0	0		
ENSMUST00000148479						4	0	0	3	8	4	127	61	79	11	81		
ENSMUST00000148480	ENSMUSG00000035505	5	90214724	90224001	-1	0	0	6	40	0	1	3	4	7	0	0	D6RHB9	
ENSMUST00000148481						1	4	1	1	6	3	0	2	0	0	0		
ENSMUST00000148482	ENSMUSG00000050705	17	35892677	35897431	-1	0	4	0	7	0	0	56	11	0	11	0	B8JJ66	
ENSMUST00000148483	ENSMUSG00000045251	7	127418967	127422068	-1	0	0	0	0	0	0	135	240	103	15	61		
ENSMUST00000148484	ENSMUSG00000075410	11	116653534	116668389	1	2	0	2	105	8	0	0	0	0	0	0	D6RIM9	
ENSMUST00000148485	ENSMUSG00000030127	6	124958413	124965538	-1	0	0	1	41	0	2	0	0	0	0	0	D3Z0S0	
ENSMUST00000148486	ENSMUSG00000003279	17	69969073	70821413	1	17	8	9	0	19	16	0	0	0	0	0	E9QAR5	
ENSMUST00000148487						1	2	0	114	9	4	0	0	0	0	0		
ENSMUST00000148488	ENSMUSG00000053398	3	98313170	98339990	-1	0	0	0	0	0	0	0	0	0	0	0	F6ZSB7	
ENSMUST00000148489						5	8	95	13	13	4	0	0	0	0	0		
ENSMUST00000148490						3	6	3	10	4	3	0	2	2	0	0		
ENSMUST00000148491						0	0	27	4	6	0	0	0	0	0	11		
ENSMUST00000148493						0	1	10	5	8	0	0	0	0	0	0		
ENSMUST00000148494						3	1	15	1	8	2	0	0	1	1	3		
ENSMUST00000148495	ENSMUSG00000043410	5	106840192	106926321	-1	0	2	5	0	0	0	0	0	0	0	0	F7C082	
ENSMUST00000148497	ENSMUSG00000014444	8	122481698	122551329	-1	5	6	46	0	0	12	17	7	17	0	0	F6PYU5	
ENSMUST00000148498						0	1	0	0	2	2	35	184	19	13	38		
ENSMUST00000148499						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000148500						6	4	0	4	6	0	0	61	0	6	0		
ENSMUST00000148502						1	0	0	3	4	5	0	0	0	0	0		
ENSMUST00000148503						0	0	14	2	10	0	35	3	9	0	15		
ENSMUST00000148505						0	4	0	0	0	0	1	0	1	0	0		
ENSMUST00000148506						3	1	3	0	3	0	0	0	0	0	0		
ENSMUST00000148507						0	0	0	4	2	0	1	15	0	6	22		
ENSMUST00000148508	ENSMUSG00000073616	1	92637145	92641985	-1	2	0	1	74	7	2	12	31	15	15	5	F6VAI7	
ENSMUST00000148509						0	1	3	0	2	0	2	0	0	0	0		
ENSMUST00000148510						0	4	2	0	10	4	9	50	9	3	23		
ENSMUST00000148512	ENSMUSG00000000301	11	59970614	60046489	-1	0	0	7	10	2	1	0	2	0	2	1	B1ARD1	
ENSMUST00000148513						58	64	173	51	64	21	11	23	18	2	18		
ENSMUST00000148514						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148515	ENSMUSG00000026207	1	75375297	75432320	1	0	0	0	9	0	0	0	0	0	0	0	D3Z7T0	
ENSMUST00000148516						50	77	89	30	78	37	7	98	46	11	51		
ENSMUST00000148517	ENSMUSG00000030116	6	122505845	122529290	1	11	16	9	14	14	11	0	1	1	8	0		Q9QZJ6
ENSMUST00000148518						2	1	3	4	6	2	0	0	1	1	1		
ENSMUST00000148519	ENSMUSG00000028292	4	34614957	34660167	1	0	0	4	0	0	0	0	0	0	0	0	A2AT41	
ENSMUST00000148520						7	1	10	5	11	5	4	5	3	0	7		
ENSMUST00000148521						8	12	23	12	11	6	2	1	2	0	3		
ENSMUST00000148523	ENSMUSG00000030269	6	113237843	113281392	1	0	1	8	2	0	0	0	9	0	0	19	F6SBM1	
ENSMUST00000148524						1	0	9	104	3	1	0	0	0	0	0		
ENSMUST00000148525	ENSMUSG00000051469	18	24009702	24020810	-1	5	6	5	43	7	4	20	22	17	6	10	D3YVP1	
ENSMUST00000148527						1	2	1	1	4	3	0	0	0	0	0		
ENSMUST00000148531						1	0	0	7	9	0	0	2	1	0	1		
ENSMUST00000148532	ENSMUSG00000042918	7	45639977	45646521	1	2	0	0	0	3	0	1	0	0	0	0		Q0ZCJ7
ENSMUST00000148533						0	0	2	0	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148535						0	2	3	10	3	4	14	81	16	7	26		
ENSMUST00000148536						3	0	7	3	5	0	5	1	5	1	1		
ENSMUST00000148537						6	4	17	7	5	3	36	171	20	26	33		
ENSMUST00000148538						6	4	12	25	1	2	0	0	0	0	0		
ENSMUST00000148539						0	4	2	0	0	0	14	140	24	12	13		
ENSMUST00000148541	ENSMUSG00000024121	17	24163866	24169702	-1	1	0	3	83	6	3	6	7	2	2	4	E9Q9C5	
ENSMUST00000148543						0	0	0	10	1	0	0	4	18	0	16		
ENSMUST00000148544						26	20	22	201	29	18	1	0	3	2	1		
ENSMUST00000148545						3	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000148547						5	7	6	2	0	1	254	183	118	33	145		
ENSMUST00000148549	ENSMUSG00000005378	5	135052957	135064959	-1	2	0	5	2	1	0	0	0	0	0	2	D3YWZ3	
ENSMUST00000148550	ENSMUSG00000026567	1	165485183	165576774	1	31	25	30	42	29	5	0	0	0	0	0		Q8C0T9
ENSMUST00000148551						13	8	43	29	15	4	2	3	4	0	5		
ENSMUST00000148553						0	1	0	51	0	0	6	0	0	5	0		
ENSMUST00000148554						3	0	5	2	3	0	0	0	5	0	11		
ENSMUST00000148555						2	1	0	2	10	0	8	22	0	0	0		
ENSMUST00000148556	ENSMUSG00000024063	17	72918305	72941942	1	2	3	4	1	0	0	0	0	2	0	1	F6UVG6	
ENSMUST00000148557						7	5	20	0	18	2	0	0	0	0	15		
ENSMUST00000148558	ENSMUSG00000024973	19	7612541	7639642	1	6	1	8	3	2	0	0	0	0	0	0	D3YZK9	
ENSMUST00000148559	ENSMUSG00000023927	17	51736187	51833290	-1	3	1	0	3	0	1	0	0	0	0	2	D3YU76	
ENSMUST00000148560						0	0	0	34	0	0	0	0	0	0	0		
ENSMUST00000148561						2	1	4	1	0	0	42	82	71	65	99		
ENSMUST00000148562	ENSMUSG00000022832	16	34649921	34678618	1	2	3	9	7	10	0	0	0	0	0	0	D3Z184	
ENSMUST00000148563						19	18	3	11	25	9	0	0	0	0	2		
ENSMUST00000148564						7	3	0	6	12	1	0	2	5	1	4		
ENSMUST00000148565	ENSMUSG00000030851	7	46861203	46878142	1	0	0	0	0	0	0	0	0	0	0	1	D3YVR7	
ENSMUST00000148566						2	1	4	2	3	0	0	0	1	0	1		
ENSMUST00000148570	ENSMUSG00000031309	X	159210307	159368244	1	0	0	0	0	0	0	1	0	0	0	0	B1AXN5	
ENSMUST00000148571						14	12	22	4	19	12	37	172	41	0	78		
ENSMUST00000148572						1	1	7	7	3	2	0	0	0	0	0		
ENSMUST00000148573						5	1	10	10	6	4	10	29	23	19	7		
ENSMUST00000148574	ENSMUSG00000020743	11	115607918	115612969	-1	0	2	2	0	0	2	0	0	0	0	0	A2A9W1	
ENSMUST00000148575	ENSMUSG00000074884	2	121449195	121458313	1	0	0	0	0	0	0	304	638	278	1859	253	D6RIP7	
ENSMUST00000148577	ENSMUSG00000024993	19	60811585	60836227	1	0	0	0	0	0	0	0	0	11	23	7	D6RIQ6	
ENSMUST00000148578						4	3	6	0	0	0	0	0	0	0	0		
ENSMUST00000148580						3	3	3	0	0	2	9	18	0	0	0		
ENSMUST00000148581	ENSMUSG00000023966	17	46122035	46144216	-1	4	4	2	3	2	3	0	0	0	0	0	F7B7Q8	
ENSMUST00000148582						3	7	3	3	4	4	0	1	0	0	0		
ENSMUST00000148583	ENSMUSG00000026737	2	18842255	18998126	-1	1	0	0	0	1	0	21	37	36	0	27	A2ASS3	
ENSMUST00000148584	ENSMUSG00000042371	11	61672781	61720826	-1	0	0	0	0	0	9	0	0	0	0	0		Q5SWY8
ENSMUST00000148586						15	11	33	16	16	5	1	0	0	0	3		
ENSMUST00000148588	ENSMUSG00000052783	5	34660379	34755305	1	0	0	2	0	0	1	1	12	2	0	0	F7BEP0	
ENSMUST00000148589	ENSMUSG00000006471	2	25244821	25256022	-1	0	8	0	5	6	0	47	46	54	0	82	E0CYR1	
ENSMUST00000148590						9	4	13	8	3	3	11	40	20	6	39		
ENSMUST00000148591						0	0	0	0	3	1	14	11	9	3	16		
ENSMUST00000148592						22	7	13	3	33	0	121	158	112	41	59		
ENSMUST00000148593						2	3	4	4	4	0	0	0	0	0	0		
ENSMUST00000148594						5	1	9	6	3	3	0	0	0	0	0		
ENSMUST00000148595	ENSMUSG00000028826	4	134802759	134853345	-1	1	0	1	6	2	0	2	9	2	0	2	E0CZE6	
ENSMUST00000148596	ENSMUSG00000028996	4	149449687	149454978	-1	5	9	17	12	9	5	0	0	0	1	2	F6R1Y3	
ENSMUST00000148599	ENSMUSG00000074607	2	163203125	163324170	1	0	0	0	78	0	3	0	0	0	0	0	F6XVL5	
ENSMUST00000148600						1	3	3	5	6	3	3	9	7	4	0		
ENSMUST00000148601	ENSMUSG00000020777	11	116171888	116199045	-1	0	0	21	0	0	0	330	977	526	63	385	A2A848	
ENSMUST00000148602	ENSMUSG00000000416	6	18366478	18514843	-1	20	0	44	0	0	8	0	0	0	0	0	R7RU63	B9EJA2
ENSMUST00000148603						0	0	1	28	2	2	0	1	0	0	0		
ENSMUST00000148604	ENSMUSG00000025272	X	150645304	150657583	-1	4	12	96	12	12	7	0	0	0	0	0	A2AFN3	
ENSMUST00000148605						1	4	8	6	11	0	0	3	0	2	2		
ENSMUST00000148606						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000148608						0	3	1	2	4	3	0	0	0	3	0		
ENSMUST00000148609						5	9	61	9	12	5	6	240	20	1	15		
ENSMUST00000148611						0	2	0	5	1	2	0	0	0	1	0		
ENSMUST00000148612						9	3	13	3	13	6	22	0	6	21	35		
ENSMUST00000148613						3	1	3	0	5	2	11	672	20	17	220		
ENSMUST00000148614						2	8	1	3	4	0	0	0	1	0	0		
ENSMUST00000148615						0	6	7	5	11	2	0	0	1	0	0		
ENSMUST00000148616						1	2	3	3	0	2	0	1	1	0	0		
ENSMUST00000148618	ENSMUSG00000057541	5	23740648	23783711	-1	40	33	118	0	0	12	9	16	16	12	58	B7ZNL8	
ENSMUST00000148619						560	746	1442	507	742	418	28	101	42	15	55		
ENSMUST00000148620						6	3	8	1	7	5	0	0	0	0	0		
ENSMUST00000148621						1	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000148622	ENSMUSG00000041229	X	151520672	151633859	1	1	1	0	0	1	0	0	0	0	0	0	A2ABU9	
ENSMUST00000148623						2	0	0	16	5	2	0	0	4	1	0		
ENSMUST00000148624	ENSMUSG00000039382	X	7721973	7728201	1	0	0	0	0	0	0	8	2	10	0	7	F7CAT9	
ENSMUST00000148625						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148626						8	9	13	13	7	1	0	6	9	0	3		
ENSMUST00000148627						19	6	20	20	16	8	1	4	0	1	4		
ENSMUST00000148628						7	5	17	1	14	8	60	73	34	7	89		
ENSMUST00000148629						1	0	0	7	3	0	0	6	6	14	0		
ENSMUST00000148630						1	1	8	5	9	1	0	0	0	0	0		
ENSMUST00000148631	ENSMUSG00000066892	9	20618118	20644767	-1	21	8	20	17	1	0	42	224	148	3	73		Q9EPX5
ENSMUST00000148632						7	5	17	64	5	2	0	1	3	0	6		
ENSMUST00000148633	ENSMUSG00000003161	5	8046078	8069379	1	15	13	45	440	59	31	1762	6190	1749	1112	1041		Q6P069
ENSMUST00000148634						2	2	3	4	7	1	0	0	0	0	4		
ENSMUST00000148636						4	2	16	3	10	3	4	7	4	3	6		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148638	ENSMUSG00000029782	6	30479053	30509783	-1	0	0	0	0	0	0	0	2	0	4	0	D3YZT2	
ENSMUST00000148639	ENSMUSG00000029671	6	22288227	22298522	1	3	0	0	5	3	0	0	0	3	0	0	Q8BRT3	
ENSMUST00000148640						2	1	0	36	2	2	0	0	0	0	0		
ENSMUST00000148642						2	1	0	4	4	0	2	0	0	0	0		
ENSMUST00000148643	ENSMUSG00000017670	2	165288031	165326479	-1	2	0	0	0	9	3	1	377	0	14	39	F6YXR3	
ENSMUST00000148644						1	4	2	3	6	6	0	0	1	0	0		
ENSMUST00000148645						0	1	4	0	2	0	0	0	0	0	0		
ENSMUST00000148646						0	0	4	3	0	0	404	2368	501	209	735		
ENSMUST00000148647	ENSMUSG00000040455	4	21767156	21837872	1	0	0	0	0	0	0	2	0	4	0	4	F7BAC1	
ENSMUST00000148648						1	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000148649	ENSMUSG00000026592	1	157099139	157108680	-1	6	0	1	0	0	1	0	0	0	0	0	D6RGU0	
ENSMUST00000148650						1	0	9	9	17	0	0	19	0	0	0		
ENSMUST00000148652	ENSMUSG00000051359	15	37366175	37792570	-1	2	0	0	54	2	0	0	0	0	0	0	D3Z2Z8	
ENSMUST00000148653						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000148656						4	3	14	3	6	1	8	57	11	3	18		
ENSMUST00000148658						0	0	0	0	0	0	0	0	2	1	0		
ENSMUST00000148659						0	4	1	2	6	2	15	14	7	2	22		
ENSMUST00000148660	ENSMUSG00000038740	2	33729953	33887946	-1	0	1	0	3	3	1	0	0	0	0	24	A2ARF0	
ENSMUST00000148661	ENSMUSG00000041594	14	122918971	122984035	-1	0	0	0	0	0	0	0	0	0	6	0		Q8BG19
ENSMUST00000148662						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000148663						5	0	6	0	0	0	3	45	9	14	24		
ENSMUST00000148664						1	1	17	19	3	2	0	0	0	0	0		
ENSMUST00000148665	ENSMUSG00000020211	10	80798198	80804924	1	12	11	35	421	30	12	531	752	373	35	329	G3UVU2	
ENSMUST00000148666	ENSMUSG00000024985	19	55741810	55933654	1	1	1	18	4	0	0	2	0	0	0	0	D3Z1L0	
ENSMUST00000148667	ENSMUSG00000028878	4	132899213	132922558	-1	0	0	0	1	3	0	0	0	0	0	0	A2ADS1	
ENSMUST00000148669						0	0	1	58	3	2	0	0	0	0	0		
ENSMUST00000148670	ENSMUSG00000025473	7	139978932	139992562	-1	0	3	8	0	2	0	0	0	166	0	437	E9Q359	
ENSMUST00000148671	ENSMUSG00000010122	11	61343401	61378345	-1	0	2	3	23	1	0	0	0	0	0	0	F6XMB0	
ENSMUST00000148672						0	4	14	8	5	3	3	12	0	0	9		
ENSMUST00000148673	ENSMUSG00000035126	4	103038065	103114555	-1	1	3	11	2	7	2	0	1	1	0	0	F6QPI2	
ENSMUST00000148674						2	0	0	0	3	3	0	0	0	0	0		
ENSMUST00000148675						0	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000148676						9	15	7	4	5	2	0	0	0	0	0		
ENSMUST00000148677	ENSMUSG00000026560	1	166662055	166681845	-1	10	0	0	0	0	10	0	0	0	0	0	Q14DT3	
ENSMUST00000148678						2	3	0	2	1	1	2	21	2	2	7		
ENSMUST00000148679						2	1	10	4	4	0	1	142	14	32	18		
ENSMUST00000148680						0	0	0	0	0	0	3	12	6	15	2		
ENSMUST00000148681	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	0	0	0	0	0	102	14	24	A2AM65	
ENSMUST00000148682						0	0	5	9	1	0	0	0	0	0	0		
ENSMUST00000148683						2	1	0	8	5	1	1	4	1	2	6		
ENSMUST00000148684						0	3	3	0	4	1	0	0	0	0	0		
ENSMUST00000148686	ENSMUSG00000043410	5	106840192	106926321	-1	45	32	37	52	33	19	0	0	0	0	10	D6RJK3	
ENSMUST00000148688	ENSMUSG00000034853	4	106744555	106804998	-1	0	0	0	0	0	1	0	0	0	0	0	E0CYA0	
ENSMUST00000148689						0	0	5	3	6	4	0	0	2	0	0		
ENSMUST00000148691						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148692						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000148693						0	0	0	60	1	0	0	0	2	0	0		
ENSMUST00000148694						0	0	0	1	0	0	0	0	0	4	0		
ENSMUST00000148695						0	0	16	9	3	0	0	0	0	0	0		
ENSMUST00000148696						0	1	0	0	2	0	0	2	0	0	1		
ENSMUST00000148697						5	3	1	0	0	0	1	0	0	0	0		
ENSMUST00000148698						17	13	12	12	12	13	11	7	26	11	44		
ENSMUST00000148701	ENSMUSG00000032743	7	125707888	125874793	1	3	0	1	45	0	0	2	0	0	0	5	D3Z212	
ENSMUST00000148702	ENSMUSG00000025878	13	55027880	55100300	-1	0	0	5	0	14	2	48	393	198	147	140	E9PWM5	
ENSMUST00000148703						1	2	5	4	2	2	2	2	3	0	2		
ENSMUST00000148706						0	0	0	86	0	4	21	0	42	33	25		
ENSMUST00000148707						34	42	45	55	37	17	2	8	8	0	1		
ENSMUST00000148708	ENSMUSG00000046550	X	153832225	153834243	1	0	0	1	0	0	2	0	0	0	2	1	B1AXT4	
ENSMUST00000148710						2	1	0	0	0	0	37	11	38	1	113		
ENSMUST00000148711						4	2	0	0	1	3	0	0	38	0	76		
ENSMUST00000148712						30	40	124	59	32	21	2	13	2	0	3		
ENSMUST00000148713	ENSMUSG00000071064	8	79028437	79193766	1	18	13	113	87	11	7	2	5	5	0	5	F6ULU2	
ENSMUST00000148714	ENSMUSG00000003235	16	20498817	20509955	1	0	2	0	0	3	0	15	133	34	18	20	F6T9C3	
ENSMUST00000148715	ENSMUSG00000009246	7	143069153	143094642	-1	3	0	13	9	3	0	1	0	2	0	0	F6RUN7	
ENSMUST00000148716	ENSMUSG00000025466	7	140096770	140102441	-1	12	3	34	19	20	13	0	0	0	0	1		Q8R2K1
ENSMUST00000148717						15	14	16	8	22	7	18	57	14	6	14		
ENSMUST00000148719						0	1	0	124	0	0	0	1	0	0	0		
ENSMUST00000148720	ENSMUSG00000036923	10	62659043	62726128	-1	0	0	0	0	0	1	0	0	0	0	1	F6QZ35	
ENSMUST00000148721	ENSMUSG00000050705	17	35892677	35897431	-1	0	0	0	40	4	0	38	166	55	0	56	B8JJ69	
ENSMUST00000148722						2	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000148723						8	4	0	2	7	6	1	0	0	0	0		
ENSMUST00000148725						2	1	16	5	6	4	4	15	6	0	4		
ENSMUST00000148726						0	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000148727						0	2	0	2	0	0	0	0	0	1	0		
ENSMUST00000148728	ENSMUSG00000071337	6	86404219	86433405	1	0	0	0	0	0	0	1	0	20	0	25		
ENSMUST00000148731	ENSMUSG00000020151	10	116018213	116274932	1	0	0	0	0	0	0	6	36	0	0	0		Q62132
ENSMUST00000148732						2	1	0	7	2	0	0	0	0	0	0		
ENSMUST00000148733						2	0	6	1	2	2	3	15	13	3	14		
ENSMUST00000148734						1	1	8	2	3	0	0	0	0	0	0		
ENSMUST00000148735						11	6	34	17	11	0	17	21	12	0	13		
ENSMUST00000148736	ENSMUSG00000018661	11	113649169	113667054	1	3	0	11	3	7	4	6	59	9	8	13	A2A6N9	
ENSMUST00000148738						3	3	4	7	9	3	27	103	24	1	65		
ENSMUST00000148739	ENSMUSG00000054966	6	145365134	145614319	-1	22	23	31	29	34	13	0	0	1	0	0	E9PY33	
ENSMUST00000148741	ENSMUSG00000041375	7	16274042	16286795	-1	0	0	1	3	1	1	10	4	22	0	15	D6RFU6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148742						6	5	24	4	11	3	0	6	0	0	1		
ENSMUST00000148744						0	0	0	106	0	0	2	3	4	0	0		
ENSMUST00000148745						5	2	3	0	5	1	0	0	6	0	3		
ENSMUST00000148746						0	0	0	0	0	0	3	1	0	0	0		
ENSMUST00000148747	ENSMUSG00000051747	2	76703980	76982547	-1	3	0	7	0	11	0	0	0	0	0	0	A2AT70	
ENSMUST00000148748	ENSMUSG00000023206	2	11705290	11734317	1	0	0	0	0	0	1	21	99	0	34	2	Q810T6	
ENSMUST00000148749						0	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000148750	ENSMUSG00000060961	5	88886818	89239653	1	52	43	182	108	60	30	0	2	2	4	4		O88343
ENSMUST00000148751						76	47	202	210	106	35	12	52	39	11	50		
ENSMUST00000148752	ENSMUSG00000042055	7	129591863	129635738	1	5	0	4	5	0	2	0	0	27	0	0		
ENSMUST00000148753						2	0	1	0	0	0	0	1	0	0	0		
ENSMUST00000148754	ENSMUSG00000022185	14	54642161	54686931	-1	0	0	0	0	0	0	0	260	0	0	4		Q9JIX8
ENSMUST00000148755	ENSMUSG00000027457	2	151590549	151632593	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148756						2	4	13	13	5	5	0	0	0	0	0		
ENSMUST00000148757						0	0	0	0	1	1	0	26	11	1	11		
ENSMUST00000148758						4	4	17	8	12	7	3	8	3	6	17		
ENSMUST00000148759	ENSMUSG00000020463	11	29172890	29220797	1	0	0	1	0	0	1	0	188	105	114	103	M0QW93	
ENSMUST00000148760						0	0	0	38	0	0	0	0	0	0	0		
ENSMUST00000148761	ENSMUSG00000034175	11	5098926	5106093	1	0	0	0	0	0	0	5	0	0	0	0	Z4YMS1	
ENSMUST00000148762	ENSMUSG00000078498	4	147305674	147333734	1	8	7	7	6	10	2	0	0	0	0	0	F6VKC7	
ENSMUST00000148763						6	8	5	14	19	3	1	2	3	1	0		
ENSMUST00000148764						0	0	0	0	1	0	626	581	1077	1588	1103		
ENSMUST00000148765	ENSMUSG00000037904	12	110975353	110979040	-1	2	2	5	10	6	0	0	20	0	10	25		Q8BH83
ENSMUST00000148766						8	0	2	8	4	1	0	2	1	0	0		
ENSMUST00000148767						1	3	4	3	4	0	0	2	1	0	3		
ENSMUST00000148768						1	3	8	3	6	0	0	1	0	7	0		
ENSMUST00000148769	ENSMUSG00000059834	3	41626720	41742514	-1	0	0	0	0	0	0	0	0	14	0	17		G5E861
ENSMUST00000148770						91	68	478	117	50	46	1	7	4	2	2		
ENSMUST00000148771						6	5	7	5	9	3	36	66	47	4	67		
ENSMUST00000148772	ENSMUSG00000036817	5	139200637	139249840	1	1	0	3	2	1	1	0	0	0	0	0	D3YUW9	
ENSMUST00000148773	ENSMUSG00000029504	5	110653451	110660496	1	5	0	3	0	0	1	4	10	6	2	16	F6R1R9	
ENSMUST00000148774						6	5	7	3	1	5	0	5	1	0	6		
ENSMUST00000148775	ENSMUSG00000022708	16	42875881	43642602	1	4	0	0	0	0	0	0	0	0	0	0	E0CXT9	
ENSMUST00000148777						26	42	19	19	22	7	10	33	6	7	12		
ENSMUST00000148778						0	2	4	1	7	2	0	0	0	0	0		
ENSMUST00000148779						0	3	0	2	0	0	18	434	270	169	227		
ENSMUST00000148780						0	2	2	9	0	0	32	18	56	4	64		
ENSMUST00000148781						2	3	1	2	3	4	0	2	2	0	3		
ENSMUST00000148782						3	6	8	4	5	3	0	0	0	0	0		
ENSMUST00000148784						3	7	7	10	11	6	1	1	4	0	4		
ENSMUST00000148786						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000148787						4	1	11	84	10	7	6	10	10	13	10		
ENSMUST00000148788						3	0	8	7	8	1	0	1	1	0	1		
ENSMUST00000148789						8	13	31	46	35	10	0	0	0	0	0		
ENSMUST00000148790						1	0	13	0	3	0	0	2	0	0	6		
ENSMUST00000148791	ENSMUSG00000026798	2	29787493	29797935	1	0	0	0	5	0	0	0	0	18	0	17	B7ZCV4	
ENSMUST00000148792						8	4	9	7	3	5	0	0	0	0	0		
ENSMUST00000148793						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000148794	ENSMUSG00000027620	2	156147239	156180238	-1	0	2	0	3	0	2	68	839	405	134	266	F7AA45	
ENSMUST00000148795						0	0	0	0	0	0	144	91	219	162	154		
ENSMUST00000148796						1	4	12	2	4	0	4	12	12	4	10		
ENSMUST00000148797						5	0	6	2	5	3	0	0	0	1	4		
ENSMUST00000148798	ENSMUSG00000027185	2	103721256	103761270	-1	6	2	14	6	4	6	0	0	2	0	2	E9Q498	
ENSMUST00000148799						1	4	1	2	1	0	2	0	0	0	0		
ENSMUST00000148800						0	0	14	0	1	0	334	839	802	47	763		
ENSMUST00000148801						1	0	0	5	4	2	0	0	0	4	1		
ENSMUST00000148802						1	6	0	1	4	4	0	20	2	0	0		
ENSMUST00000148803						0	3	24	6	18	0	0	0	0	0	0		
ENSMUST00000148805						7	11	43	18	7	5	10	22	23	26	39		
ENSMUST00000148806						0	0	1	29	1	0	0	0	0	0	0		
ENSMUST00000148808						4	3	0	0	0	0	5	1	0	22	2		
ENSMUST00000148809						7	6	28	1	9	1	0	21	0	0	0		
ENSMUST00000148810	ENSMUSG00000026483	1	151571186	151721939	1	18	25	71	127	30	9	3455	9992	6469	915	4277		Q3UW53
ENSMUST00000148811	ENSMUSG00000038172	4	83220300	83324255	-1	5	2	15	0	4	1	0	0	0	0	7	E0CY48	
ENSMUST00000148812						98	86	292	75	112	61	5	12	6	1	22		
ENSMUST00000148814						6	2	9	11	3	7	0	8	0	0	0		
ENSMUST00000148815						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000148816	ENSMUSG00000050994	10	10335703	10472326	-1	2	0	0	0	4	6	1	26	3	7	20	G3UXD9	
ENSMUST00000148817						0	0	1	0	0	0	0	7	0	0	0		
ENSMUST00000148818						3	3	3	4	8	0	3	7	8	1	15		
ENSMUST00000148819						12	9	21	12	15	9	6	10	8	1	11		
ENSMUST00000148820	ENSMUSG00000024136	17	24440081	24443105	-1	0	0	0	2	2	0	0	0	1	0	0	D6RJ55	
ENSMUST00000148821	ENSMUSG00000024770	19	34067358	34084918	1	6	4	4	0	5	4	0	0	0	0	0	D6RJJ5	
ENSMUST00000148822						13	7	26	14	17	8	118	400	231	22	479		
ENSMUST00000148823	ENSMUSG00000020023	10	94311949	94590956	1	4	3	12	3	1	0	0	0	0	0	0	F6S041	
ENSMUST00000148824						2	2	0	0	2	2	2	76	24	4	23		
ENSMUST00000148825	ENSMUSG00000063450	12	75818134	76110926	1	2	4	0	0	3	1	13	19	41	0	19	F6VTU3	
ENSMUST00000148827	ENSMUSG00000027695	3	27938695	28133362	1	0	0	7	2	0	0	15	410	14	2	0	F6WKY8	
ENSMUST00000148828						11	9	20	39	15	9	0	6	0	0	2		
ENSMUST00000148829	ENSMUSG00000034320	18	61192919	61211612	-1	0	3	0	27	0	4	0	0	0	0	8	E9PZ06	
ENSMUST00000148830						1	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000148831	ENSMUSG00000040532	5	135009152	135012175	1	0	0	1	0	0	0	0	120	0	20	0		
ENSMUST00000148833	ENSMUSG00000027346	2	132529082	132587729	-1	0	3	9	0	1	0	0	696	101	7	189	D6RHS8	
ENSMUST00000148834	ENSMUSG00000038836	6	34780432	34859459	1	7	10	7	8	9	3	0	0	0	0	2	D6RI59	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148835	ENSMUSG00000038271	6	125145241	125161782	1	0	0	0	0	0	0	58	66	20	0	0	F6VMG1	
ENSMUST00000148836						11	23	35	12	20	10	0	0	0	0	0		
ENSMUST00000148837						0	0	0	22	0	0	0	0	0	0	0		
ENSMUST00000148839						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148840						0	2	4	57	7	2	0	5	6	0	0		
ENSMUST00000148841						3	3	6	2	0	1	2	3	6	2	16		
ENSMUST00000148842						1	0	4	0	0	0	0	0	0	0	7		
ENSMUST00000148843	ENSMUSG00000066037	4	136310942	136359447	1	19	12	12	7	7	2	6	7	15	6	11	Q8VHM5	
ENSMUST00000148845						3	2	18	4	3	1	14	20	17	0	17		
ENSMUST00000148846						5	0	32	2	9	0	14	321	36	12	79		
ENSMUST00000148848						2	2	3	1	4	0	0	5	1	0	1		
ENSMUST00000148849						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000148850	ENSMUSG00000036452	18	38601534	39376284	1	0	0	1	0	0	0	0	0	0	0	0	D3Z1X5	
ENSMUST00000148851	ENSMUSG00000057895	9	122923072	122931028	1	9	4	0	81	6	5	0	0	0	0	0	D3Z140	
ENSMUST00000148852	ENSMUSG00000026890	2	36081953	36105408	-1	0	0	0	19	5	1	0	0	0	0	0		Q9R1R0
ENSMUST00000148853						5	4	3	1	3	3	0	0	1	0	0		
ENSMUST00000148854	ENSMUSG00000015850	3	95676201	95687917	-1	1	0	4	4	5	2	4	0	0	0	0	D3Z0T6	
ENSMUST00000148855						0	0	0	0	0	0	0	0	0	5	0		
ENSMUST00000148856						4	4	6	2	3	0	0	0	0	0	2		
ENSMUST00000148857						33	32	154	76	51	21	2	26	3	1	6		
ENSMUST00000148858						3	0	10	4	5	0	1	14	0	0	4		
ENSMUST00000148859						24	9	10	10	0	3	0	0	0	0	0		
ENSMUST00000148860						3	0	1	8	3	2	1	0	0	0	1		
ENSMUST00000148861						3	0	14	34	15	3	4	254	11	33	27		
ENSMUST00000148862						0	3	2	0	0	0	0	0	0	0	0		
ENSMUST00000148863						0	1	6	5	4	2	1	1	1	0	1		
ENSMUST00000148864						15	13	10	7	11	9	0	0	0	0	0		
ENSMUST00000148866						0	0	0	0	0	0	21	0	19	0	8		
ENSMUST00000148867						1	0	0	0	0	0	4	4	0	0	0		
ENSMUST00000148868	ENSMUSG00000041708	15	83779467	83858494	1	0	0	3	1	0	6	0	0	0	0	0	E9PWC1	
ENSMUST00000148869						0	0	2	0	1	0	70	55	89	11	63		
ENSMUST00000148870						5	3	4	3	6	0	1	0	0	0	0		
ENSMUST00000148871						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000148872						0	0	0	1	3	3	0	0	0	0	6		
ENSMUST00000148873	ENSMUSG00000038525	5	21645813	21662694	1	3	9	7	132	3	5	0	0	0	0	0		Q9D0L7
ENSMUST00000148874						3	5	20	5	9	3	6	31	4	0	13		
ENSMUST00000148875						7	0	0	10	4	10	4	4	0	0	0		
ENSMUST00000148876	ENSMUSG00000041975	2	70964561	71055583	-1	9	0	11	3	0	3	0	0	0	0	0		A2AUU0
ENSMUST00000148877	ENSMUSG00000027331	2	118814003	118853957	1	3	1	4	0	3	3	0	2	1	0	0	H3BJJ3	
ENSMUST00000148878						2	3	7	10	1	3	2	15	4	2	5		
ENSMUST00000148879	ENSMUSG00000029730	5	138164583	138172422	-1	0	0	0	0	0	0	7	30	0	0	0	D3Z6N3	
ENSMUST00000148880	ENSMUSG00000030779	7	122965686	123002557	1	2	1	1	5	3	0	2	0	2	0	0	D3YZU8	
ENSMUST00000148881						3	1	0	0	0	0	7	0	0	0	0		
ENSMUST00000148882						0	0	0	0	0	0	5	28	15	7	3		
ENSMUST00000148883						1	0	0	2	1	1	0	0	1	0	2		
ENSMUST00000148884						3	2	15	13	2	1	2	5	5	0	2		
ENSMUST00000148886						0	2	0	0	1	0	0	6	6	16	9		
ENSMUST00000148887						0	0	0	0	3	2	0	4	3	0	10		
ENSMUST00000148888						0	0	0	0	0	0	0	0	0	0	1		
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ENSMUST00000148890						0	0	0	0	2	0	9	39	6	7	11		
ENSMUST00000148891	ENSMUSG00000054728	13	42680623	43138526	1	45	12	57	54	20	11	0	0	0	3	22		Q2M3X8
ENSMUST00000148893	ENSMUSG00000022436	15	78899667	78919517	1	1	0	5	6	5	0	0	0	1	0	0	A2A5V1	
ENSMUST00000148894	ENSMUSG00000024188	17	26252910	26285504	1	6	5	10	0	0	0	11	132	57	29	16	D6RGP6	
ENSMUST00000148895	ENSMUSG00000017428	11	80428615	80473248	1	0	0	4	0	0	1	53	237	34	128	15	G3UYH2	
ENSMUST00000148896						7	0	9	2	6	0	5	11	4	0	20		
ENSMUST00000148897	ENSMUSG00000020214	10	112083354	112108098	1	12	4	13	515	24	15	0	1	1	0	0		Q9CQ35
ENSMUST00000148899	ENSMUSG00000060002	10	88452745	88504073	-1	4	0	15	5	6	8	1	0	0	0	0	F6X1K1	
ENSMUST00000148900						0	6	21	0	4	9	1377	5147	3671	735	4548		
ENSMUST00000148901						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000148902	ENSMUSG00000032812	7	101348067	101412586	1	0	3	1	0	2	4	6	0	0	0	17	D3YYF5	
ENSMUST00000148903	ENSMUSG00000009376	6	17463800	17573980	1	0	0	0	0	0	0	0	0	1	0	0	F6RCC5	
ENSMUST00000148904						1	1	0	0	2	0	2	1	0	2	3		
ENSMUST00000148905	ENSMUSG00000027574	2	180934772	180954699	-1	0	0	0	13	5	0	0	0	0	0	0	F6S2R0	
ENSMUST00000148906						0	0	3	0	5	6	27	28	10	0	32		
ENSMUST00000148908						1	0	3	2	2	2	0	0	5	0	0		
ENSMUST00000148909						1	0	4	125	8	0	0	0	0	0	0		
ENSMUST00000148910	ENSMUSG00000020023	10	94311949	94590956	1	3	6	7	3	4	0	0	0	0	0	0	F6R793	
ENSMUST00000148911						36	24	99	54	30	13	0	0	0	1	0		
ENSMUST00000148912						0	2	2	10	3	1	0	0	0	0	4		
ENSMUST00000148913						3	4	14	11	7	3	3	34	14	2	27		
ENSMUST00000148914						5	7	8	1	3	2	23	48	20	8	21		
ENSMUST00000148917						6	1	9	4	4	3	4	0	7	0	4		
ENSMUST00000148918						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000148920						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000148921						6	2	7	1	6	2	1	2	2	0	2		
ENSMUST00000148923						88	62	337	192	89	60	0	1	4	0	4		
ENSMUST00000148924						0	3	3	3	1	0	0	0	0	0	0		
ENSMUST00000148925						32	21	56	23	23	15	0	0	0	0	0		
ENSMUST00000148926	ENSMUSG00000030203	6	134715468	134792625	-1	0	0	4	0	1	0	4	7	0	0	16		
ENSMUST00000148927						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000148928	ENSMUSG00000087444	15	100422147	100428150	1	12	8	26	17	13	2	1	0	0	0	1	Q3TR11	
ENSMUST00000148929	ENSMUSG00000048537	9	44686304	44735198	-1	0	2	2	12	5	0	0	0	1	0	0	D3YVB9	
ENSMUST00000148930	ENSMUSG00000028565	4	97772734	98118874	1	0	0	0	2	0	0	1	7	12	0	7	F7CDR2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000148932						6	4	0	4	6	4	0	0	0	0	3		
ENSMUST00000148933						15	8	10	6	0	2	0	222	0	13	21		
ENSMUST00000148934	ENSMUSG00000029056	4	154964123	154980938	1	5	0	0	0	0	6	0	63	37	12	42	F7B6K4	
ENSMUST00000148935	ENSMUSG00000028830	4	126753544	126870070	1	0	0	0	7	0	0	0	2	0	0	3	A2A786	
ENSMUST00000148936						2	5	5	123	6	4	0	1	0	0	1		
ENSMUST00000148937						20	11	16	16	11	3	0	8	0	0	8		
ENSMUST00000148938						0	0	1	2	0	1	10	50	15	0	10		
ENSMUST00000148939	ENSMUSG00000034570	11	3494375	3504821	-1	0	0	20	42	6	0	0	65	0	0	12	V9GXL7	
ENSMUST00000148940						0	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000148941						33	35	37	43	36	26	6	40	30	4	40		
ENSMUST00000148942						0	5	0	0	0	2	2	0	1	0	4		
ENSMUST00000148943						0	0	4	0	1	0	0	5	0	0	2		
ENSMUST00000148944						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000148945	ENSMUSG00000075595	11	95712673	95835115	1	12	0	0	32	3	3	79	738	195	54	274	F2Z3V9	
ENSMUST00000148946						2	9	53	104	0	0	0	0	0	0	0		
ENSMUST00000148947						2	1	0	5	1	0	0	0	0	0	0		
ENSMUST00000148948						0	0	0	3	1	1	1	8	4	0	1		
ENSMUST00000148949						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000148950	ENSMUSG00000052485	13	98686235	98694834	-1	8	1	9	19	6	7	1	0	0	0	0	D3Z2U9	
ENSMUST00000148951						0	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000148952						1101	1251	1124	695	1120	548	40	130	94	37	109		
ENSMUST00000148953						2	0	2	74	7	0	0	0	0	0	0		
ENSMUST00000148954	ENSMUSG00000034813	10	119454034	120087261	1	0	0	0	0	0	0	0	0	0	0	0	D3YWY4	
ENSMUST00000148955	ENSMUSG00000025421	18	76930126	76972902	1	16	13	18	0	24	7	8	0	13	3	26		Q3UGR5
ENSMUST00000148956	ENSMUSG00000001036	11	61517249	61579687	-1	1	0	0	8	0	2	2	0	0	0	0	F7CUV7	
ENSMUST00000148957						3	1	4	4	6	2	0	1	0	0	1		
ENSMUST00000148958						0	1	0	0	0	0	36	236	25	293	30		
ENSMUST00000148959						5	6	5	4	6	1	0	2	3	0	4		
ENSMUST00000148960	ENSMUSG00000024048	17	70993656	71002878	-1	4	3	2	132	11	3	399	503	448	378	276	Q6ZWQ9	
ENSMUST00000148961						11	4	24	7	9	4	93	2	139	73	237		
ENSMUST00000148962						1	3	0	4	1	1	1	1	2	1	13		
ENSMUST00000148963						3	1	2	1	0	1	0	0	0	0	0		
ENSMUST00000148964						4	0	14	0	2	7	0	0	0	0	0		
ENSMUST00000148965						1	0	0	0	0	0	1	0	1	0	0		
ENSMUST00000148966	ENSMUSG00000022679	16	13903161	13949619	1	0	0	0	0	0	0	0	0	0	0	0	D6RHR1	
ENSMUST00000148968						0	0	0	0	0	0	24	93	17	29	6		
ENSMUST00000148969	ENSMUSG00000052533	2	30286397	30344266	1	0	0	3	14	0	1	0	0	1	0	0	F2Z4A7	
ENSMUST00000148970						6	2	9	2	1	0	2	3	2	0	6		
ENSMUST00000148971						0	0	0	0	4	0	15	0	54	0	48		
ENSMUST00000148973						2	5	0	0	1	7	0	65	0	0	61		
ENSMUST00000148974						3	0	4	0	2	2	0	0	0	0	0		
ENSMUST00000148975	ENSMUSG00000038618	7	141215860	141218658	1	0	0	0	0	0	2	0	0	1	0	0	D3YZL5	
ENSMUST00000148976						5	3	0	2	0	0	49	486	88	56	62		
ENSMUST00000148978						0	0	0	33	1	0	6	0	7	0	14		
ENSMUST00000148979	ENSMUSG00000028786	4	129105548	129111626	1	0	4	5	2	3	4	0	0	0	0	0	D3YUQ8	
ENSMUST00000148980	ENSMUSG00000051703	1	75479532	75485705	1	0	0	0	71	0	2	0	0	0	0	0	D3Z7R8	
ENSMUST00000148982						1	0	0	32	1	1	0	0	0	0	0		
ENSMUST00000148983						6	0	1	5	3	0	0	6	0	0	17		
ENSMUST00000148984						73	59	24	66	132	52	0	1	3	0	2		
ENSMUST00000148985						5	5	22	19	22	10	0	13	4	3	5		
ENSMUST00000148986						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000148987	ENSMUSG00000032469	9	99575799	99584501	1	0	0	0	64	2	2	0	0	0	0	0	D3YXA2	
ENSMUST00000148988	ENSMUSG00000027397	2	129198764	129211616	1	0	0	0	36	0	1	0	1	0	0	6	B0R035	
ENSMUST00000148989	ENSMUSG00000062210	18	49979427	50107173	1	1	2	0	27	0	0	88	106	407	464	235	D3YWJ5	
ENSMUST00000148990	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	15	0	0	0	0	0	0	0		
ENSMUST00000148991						2	0	6	0	0	0	6	0	12	0	17		
ENSMUST00000148993						5	4	0	0	4	1	0	7	19	5	13		
ENSMUST00000148994	ENSMUSG00000062110	5	74204816	74531759	-1	3	6	1	0	2	3	0	0	0	0	1		
ENSMUST00000148995						0	0	0	0	1	0	10	19	8	0	0		
ENSMUST00000148996						0	0	1	17	1	0	0	0	0	0	0		
ENSMUST00000148998						0	0	5	0	0	0	0	4	10	0	18		
ENSMUST00000148999						4	2	0	3	3	3	0	0	0	0	28		
ENSMUST00000149001						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000149002						45	42	48	41	33	27	5	5	3	7	14		
ENSMUST00000149003						4	2	3	3	0	0	362	2050	508	0	217		
ENSMUST00000149004						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000149006						3	4	10	40	4	1	0	0	0	0	0		
ENSMUST00000149007						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000149008						130	73	647	247	91	57	4	10	6	0	10		
ENSMUST00000149009	ENSMUSG00000029761	6	34598500	34775473	1	10	8	9	0	0	0	0	0	0	0	0	S4R1T7	
ENSMUST00000149010						3	2	2	0	5	0	14	172	21	11	49		
ENSMUST00000149011	ENSMUSG00000048012	7	44731481	44751050	-1	226	185	520	246	230	158	16	77	29	10	20	E9QAY2	
ENSMUST00000149012						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000149013						1	0	0	5	3	11	50	21	102	0	50		
ENSMUST00000149015						0	1	0	0	3	0	11	48	9	0	0		
ENSMUST00000149016						0	2	0	174	0	7	0	0	0	0	6		
ENSMUST00000149017						31	31	30	28	45	24	6	7	7	7	6		
ENSMUST00000149018						2	0	3	2	3	0	0	5	2	0	0		
ENSMUST00000149019	ENSMUSG00000017119	11	101552149	101581951	1	0	3	12	2	16	0	105	1346	63	173	82	F6S397	
ENSMUST00000149020						2	1	10	4	3	5	2	27	0	0	7		
ENSMUST00000149021	ENSMUSG00000031010	X	13071498	13173328	1	0	0	0	0	1	0	13	2	34	0	6	G3UY52	
ENSMUST00000149022	ENSMUSG00000028649	4	123349633	123684360	-1	0	4	0	16	0	1	3	76	7	7	31	F6RL59	
ENSMUST00000149023	ENSMUSG00000035104	6	82041043	82093099	1	3	2	15	17	5	3	0	0	0	0	0	D3Z511	
ENSMUST00000149024	ENSMUSG00000038301	6	51523901	51590679	1	1	0	0	0	0	0	0	104	168	438	147	S4R1A0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149026	ENSMUSG00000054226	6	85911865	85930284	1	2	3	15	154	10	0	0	3	4	2	0	D3Z5E8	
ENSMUST00000149027						71	76	76	43	82	43	43	113	120	14	139		
ENSMUST00000149028						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149029						2	3	4	0	3	4	0	0	7	0	9		
ENSMUST00000149030						49	46	304	66	51	30	0	0	1	0	1		
ENSMUST00000149031						0	0	7	0	0	0	0	0	0	0	0		
ENSMUST00000149032						0	0	0	0	0	0	0	0	64	0	56		
ENSMUST00000149033						8	8	12	13	11	5	5	34	16	1	19		
ENSMUST00000149034	ENSMUSG00000041654	11	113244853	113650079	-1	4	3	16	86	4	3	4	3	9	0	9	B1ARC5	
ENSMUST00000149035	ENSMUSG00000000884	16	18498768	18566679	1	0	0	0	0	0	0	0	0	0	0	0	D3YUW3	
ENSMUST00000149036						5	0	3	9	1	1	0	1	0	0	0		
ENSMUST00000149037						11	2	7	5	11	5	0	0	0	0	0		
ENSMUST00000149038						3	6	11	0	5	3	10	17	29	2	36		
ENSMUST00000149039	ENSMUSG00000046598	16	31422280	31458901	1	0	0	0	0	1	2	7	0	2	2	5	D3Z2Y8	
ENSMUST00000149040						0	0	0	1	7	1	2	3	2	0	4		
ENSMUST00000149041						0	0	0	0	1	0	0	3	0	0	0		
ENSMUST00000149042						7	5	14	43	10	6	0	0	0	0	0		
ENSMUST00000149043	ENSMUSG00000040767	11	32205415	32208984	1	0	0	0	0	0	0	0	0	5	13	3	A7M7T3	
ENSMUST00000149045	ENSMUSG00000005233	2	69193895	69206194	-1	0	0	0	0	0	0	0	0	3	0	9	A2AUT1	
ENSMUST00000149046	ENSMUSG00000085925	12	109589194	109600330	-1	26	21	79	109	44	17	4	6	6	0	2	B4YB44	Q7M732
ENSMUST00000149047	ENSMUSG00000028528	4	101496648	101642799	1	0	3	2	0	4	1	0	0	1	0	0	B1B0B8	
ENSMUST00000149049	ENSMUSG00000040350	11	48826140	48852209	1	4	2	3	2	3	6	0	0	0	0	0	B7ZC92	
ENSMUST00000149050	ENSMUSG00000005150	8	85075035	85081306	-1	0	0	0	0	0	0	0	0	1	6	0		Q9DAJ4
ENSMUST00000149051						16	17	4	10	19	5	15	36	35	4	44		
ENSMUST00000149052	ENSMUSG00000040428	7	45526330	45554229	1	14	10	18	13	13	4	0	0	0	0	0	E9PUJ9	
ENSMUST00000149053						2	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000149054						1	1	0	0	0	0	3	58	7	4	7		
ENSMUST00000149055						14	7	26	15	13	9	16	32	37	0	37		
ENSMUST00000149056						0	0	3	0	2	4	0	32	0	0	0		
ENSMUST00000149057						48	44	97	52	43	23	84	199	168	25	100		
ENSMUST00000149058						0	0	0	0	0	0	0	0	3	0	1		
ENSMUST00000149059						9	8	11	3	11	8	0	0	1	0	1		
ENSMUST00000149060						2	0	0	8	0	0	0	0	1	0	1		
ENSMUST00000149061						0	0	0	0	1	0	10	21	30	7	38		
ENSMUST00000149062						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000149063	ENSMUSG00000031171	X	8238668	8252406	-1	0	0	0	0	0	0	0	1	2	0	1	F6Q475	
ENSMUST00000149064	ENSMUSG00000054469	17	73107985	73243368	1	0	0	0	11	0	0	0	0	4	0	0	B0V2Q9	
ENSMUST00000149066	ENSMUSG00000022913	16	95979933	95990960	-1	6	0	11	0	4	1	11	52	7	0	0	D6RG59	
ENSMUST00000149067						2	4	1	3	5	1	0	2	0	1	1		
ENSMUST00000149068	ENSMUSG00000028063	3	88480147	88509956	-1	8	2	7	227	12	4	0	0	0	0	6	D3YUF7	
ENSMUST00000149069	ENSMUSG00000028224	4	15957925	15992589	1	0	0	0	0	0	0	0	0	1	0	5	A2AMG5	
ENSMUST00000149071	ENSMUSG00000028010	3	129824912	129831396	-1	1	1	2	161	1	2	0	36	4	5	2	D3YZ09	
ENSMUST00000149073						0	0	0	0	0	2	1	0	0	0	0		
ENSMUST00000149074						0	0	0	0	0	0	31	20	25	10	18		
ENSMUST00000149075						2	2	12	2	6	3	0	4	0	0	0		
ENSMUST00000149076						0	2	5	87	7	0	72	108	70	11	39		
ENSMUST00000149077						1	0	0	2	3	0	0	0	0	0	0		
ENSMUST00000149079						73	29	0	1250	206	77	0	0	0	0	2		
ENSMUST00000149080						0	0	0	1	0	4	0	0	0	0	3		
ENSMUST00000149081	ENSMUSG00000069094	3	19223108	19311322	-1	0	0	0	0	0	0	0	0	0	0	0	F6VJY9	
ENSMUST00000149082						2	2	2	0	0	2	5	14	11	3	11		
ENSMUST00000149083						4	0	9	0	0	3	0	1	1	1	0		
ENSMUST00000149085						0	0	0	293	9	9	36	145	48	6	102		
ENSMUST00000149086	ENSMUSG00000006649	7	30458315	30487223	1	0	0	4	1	1	0	0	0	0	0	0	F6RCI4	
ENSMUST00000149087						21	20	59	192	37	31	38	106	56	4	112		
ENSMUST00000149088						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149089	ENSMUSG00000056724	9	110624789	110654161	-1	7	0	8	37	5	1	244	25	230	0	220	D3Z2K6	
ENSMUST00000149091						6	0	4	1	7	1	8	69	36	5	28		
ENSMUST00000149093						28	14	55	113	41	11	2	44	12	3	23		
ENSMUST00000149094						5	2	3	9	8	2	4	2	4	1	10		
ENSMUST00000149096						34	26	124	42	55	11	59	51	45	3	50		
ENSMUST00000149097						0	3	0	86	0	4	0	0	0	0	0		
ENSMUST00000149099						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149100	ENSMUSG00000030222	6	137054825	137170497	-1	5	3	2	77	4	3	0	1	0	0	0		
ENSMUST00000149101	ENSMUSG00000033308	3	118562129	119432924	1	1	0	0	12	1	1	0	0	0	0	0	A0A0G2JF48	
ENSMUST00000149103						0	0	0	0	0	0	0	10	0	3	5		
ENSMUST00000149104						1	0	0	0	0	0	5	8	0	0	3		
ENSMUST00000149105	ENSMUSG00000002342	8	70172356	70183681	1	0	0	0	0	0	1	8	0	9	0	0	F6UNW2	
ENSMUST00000149106	ENSMUSG00000028603	4	108043839	108144998	-1	1	3	0	6	0	0	0	28	46	32	18	A2APS4	
ENSMUST00000149107						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000149108						5	3	22	7	6	1	1	4	1	1	1		
ENSMUST00000149109						0	0	0	0	0	0	1	0	0	0	1		
ENSMUST00000149110	ENSMUSG00000022537	16	30511855	30550842	-1	7	5	7	3	8	2	1	0	0	0	0	F7D1Q2	
ENSMUST00000149111	ENSMUSG00000058794	15	103248212	103258403	-1	13	14	9	11	11	9	30	117	74	43	106		
ENSMUST00000149112						0	4	1	0	2	0	0	0	2	0	3		
ENSMUST00000149113						6	5	30	6	5	1	0	0	0	0	2		
ENSMUST00000149114						9	9	6	10	16	3	0	0	0	0	0		
ENSMUST00000149115						1	2	0	1	0	0	0	0	0	0	11		
ENSMUST00000149116	ENSMUSG00000025809	8	128685654	128733200	1	0	1	0	0	0	0	0	47	0	1	0	A0A0A0MQJ3	
ENSMUST00000149117						13	13	29	60	15	6	0	0	1	3	4		
ENSMUST00000149118						0	0	1	3	3	0	0	0	0	0	0		
ENSMUST00000149119	ENSMUSG00000026427	1	131153181	131187658	1	10	8	18	6	6	4	21	16	27	0	25	M0QWK9	
ENSMUST00000149121						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000149122	ENSMUSG00000030647	7	97400003	97407802	1	7	3	0	34	0	0	0	41	39	272	38		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149123	ENSMUSG00000029569	6	13580687	13608100	-1	5	3	0	23	11	4	9	188	43	70	15		
ENSMUST00000149125	ENSMUSG00000068614	2	114047282	114053548	-1	3	7	3	26	7	4	0	0	0	0	0	F6WX90	
ENSMUST00000149126	ENSMUSG00000032691	11	59541568	59566956	1	0	0	0	0	0	0	9	0	3	0	0	Q5SXI6	
ENSMUST00000149127						0	0	2	0	3	0	0	53	20	11	27		
ENSMUST00000149129	ENSMUSG00000019055	4	147909753	147936767	-1	4	5	0	0	4	0	7	11	0	3	0	F6WNR1	
ENSMUST00000149130						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149131	ENSMUSG00000038871	6	34476207	34505613	1	0	0	0	0	0	0	18	3	2	6	55	D3Z223	
ENSMUST00000149132						2	1	6	1	0	0	1	6	0	2	1		
ENSMUST00000149134						1	3	3	1	3	0	20	229	37	5	108		
ENSMUST00000149135						1	1	2	7	3	0	3	13	16	0	23		
ENSMUST00000149138						3	2	3	0	3	1	2	0	9	3	1		
ENSMUST00000149139						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000149140	ENSMUSG00000041245	X	151198078	151320152	1	0	0	7	6	1	0	0	0	0	0	0	V9GXP7	
ENSMUST00000149141						1	1	3	6	2	0	0	3	1	0	11		
ENSMUST00000149142						4	5	0	3	2	3	0	0	0	0	0		
ENSMUST00000149143						0	0	2	0	0	0	0	19	15	419	34		
ENSMUST00000149144	ENSMUSG00000024750	19	21272278	21282289	1	0	0	0	0	0	0	67	189	237	57	139	D6RFT9	
ENSMUST00000149145						0	3	5	16	9	0	48	2262	153	144	386		
ENSMUST00000149146	ENSMUSG00000028876	4	124880899	124917800	1	35	26	90	118	53	26	1	0	0	0	0	F6WVB0	
ENSMUST00000149147	ENSMUSG00000052949	11	116336353	116413032	-1	3	3	65	0	24	27	13	10	1	5	39	F7D0T8	
ENSMUST00000149148	ENSMUSG00000035745	10	79970715	79977190	1	0	0	0	0	0	2	2	4	5	1	10	F7BA29	
ENSMUST00000149149						0	0	0	0	0	0	2	7	3	5	0		
ENSMUST00000149150	ENSMUSG00000039115	9	118606690	118901003	1	18	17	24	23	24	9	2	5	3	0	0	F7DB81	
ENSMUST00000149151	ENSMUSG00000039737	5	136178127	136198963	-1	0	0	0	16	0	0	19	11	9	40	13	D3YXD3	
ENSMUST00000149152						29	26	9	60	45	16	0	4	1	0	3		
ENSMUST00000149154	ENSMUSG00000051323	X	133582860	133688987	-1	9	5	16	232	16	11	0	0	0	0	0		Q80TF3
ENSMUST00000149155						4	0	6	1	2	0	32	54	34	3	35		
ENSMUST00000149157						3	5	4	5	2	4	5	29	28	1	16		
ENSMUST00000149158	ENSMUSG00000027965	3	114904078	115125722	1	3	1	5	1	5	2	0	0	0	0	0	D3YTM3	
ENSMUST00000149159	ENSMUSG00000020484	11	5520659	5525893	1	4	1	20	5	5	3	112	299	259	48	205	G3UYH6	
ENSMUST00000149160						6	2	4	3	0	0	30	46	17	12	73		
ENSMUST00000149161						0	0	0	18	9	5	0	0	9	0	0		
ENSMUST00000149162						9	9	3	3	11	2	5	0	0	0	0		
ENSMUST00000149163	ENSMUSG00000000827	2	181497142	181517966	1	0	0	0	0	0	8	0	0	0	0	15		Q9CYZ2
ENSMUST00000149164						1	1	2	9	3	0	0	0	0	0	0		
ENSMUST00000149165						15	11	63	13	11	13	0	0	0	0	0		
ENSMUST00000149166						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000149167	ENSMUSG00000037822	5	65446844	65537184	-1	3	0	0	48	0	0	0	0	0	0	0	D3YYP6	
ENSMUST00000149168	ENSMUSG00000028542	4	117834506	117875198	1	33	22	216	110	48	16	0	0	3	3	0	E9PWC4	
ENSMUST00000149169	ENSMUSG00000041298	5	148871584	148929320	-1	0	0	0	0	0	0	0	0	0	0	0	D3YWJ8	
ENSMUST00000149170						0	1	0	3	3	1	0	0	0	0	0		
ENSMUST00000149171						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149174	ENSMUSG00000034349	3	69004738	69034623	1	0	0	0	0	1	0	0	0	14	30	19	A0A0A6YXY3	
ENSMUST00000149175						0	1	1	0	0	0	0	2	11	33	65		
ENSMUST00000149176	ENSMUSG00000030527	7	80586627	80688877	-1	0	0	0	2	1	0	0	0	0	0	5	F6UMS9	
ENSMUST00000149177	ENSMUSG00000039546	4	153373221	153482811	-1	3	0	0	5	1	0	0	0	0	0	0	D6RH95	
ENSMUST00000149178						6	0	0	0	1	5	39	0	30	7	117		
ENSMUST00000149179	ENSMUSG00000016356	2	180986535	181017540	1	41	21	18	0	8	0	27	0	0	0	4	F6UFI2	
ENSMUST00000149180						0	0	5	0	0	0	0	0	0	3	0		
ENSMUST00000149181	ENSMUSG00000041975	2	70964561	71055583	-1	0	0	0	0	0	0	0	0	0	1	0	F6Q7P7	
ENSMUST00000149182	ENSMUSG00000075044	19	8160165	8218900	-1	0	0	11	0	0	0	0	0	0	0	0	A0JNU1	
ENSMUST00000149183						0	0	0	0	2	1	0	6	29	57	0		
ENSMUST00000149184						0	0	0	0	0	0	2	20	4	4	28		
ENSMUST00000149185						3	1	0	5	2	0	0	0	0	0	0		
ENSMUST00000149187	ENSMUSG00000053483	1	171281945	171287991	-1	0	0	0	27	3	0	0	0	0	0	0	D6RJJ7	
ENSMUST00000149188						5	0	14	6	16	7	1	0	0	0	0		
ENSMUST00000149189	ENSMUSG00000021270	12	110690605	110702728	-1	0	0	0	13	0	0	0	0	0	0	0	A2A6A2	
ENSMUST00000149191						14	16	20	74	28	6	6	33	16	9	15		
ENSMUST00000149193	ENSMUSG00000026888	2	64912476	65024987	-1	0	0	0	1	1	0	0	0	0	0	0	A2ASX4	
ENSMUST00000149194	ENSMUSG00000018554	11	69935796	69941605	1	17	0	15	0	0	3	0	2	0	0	0	J3QNB9	
ENSMUST00000149195						7	8	2	9	4	5	2	0	0	0	0		
ENSMUST00000149196	ENSMUSG00000075415	2	31026206	31142008	-1	3	0	2	1	1	0	0	0	17	0	0	A2AQ39	
ENSMUST00000149197						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000149198						1	0	0	0	0	0	0	10	0	3	0		
ENSMUST00000149200	ENSMUSG00000023051	15	102518192	102523676	1	0	0	0	2	1	0	0	0	8	0	0	D6RCY4	
ENSMUST00000149201						3	0	0	11	1	2	0	1	1	0	4		
ENSMUST00000149202						0	6	9	6	8	2	0	3	1	0	0		
ENSMUST00000149203						11	23	28	17	22	12	0	0	0	0	1		
ENSMUST00000149204						0	1	0	14	0	0	29	0	58	62	59		
ENSMUST00000149205						0	0	4	0	0	0	0	385	38	0	0		
ENSMUST00000149207						10	4	38	6	11	7	2	17	2	3	9		
ENSMUST00000149208	ENSMUSG00000029507	5	110773667	110780659	-1	0	2	0	0	0	0	0	0	0	1	3	D3Z092	
ENSMUST00000149210						1	0	0	0	0	0	3	14	32	0	57		
ENSMUST00000149211						23	37	23	3	2	0	4	11	8	1	12		
ENSMUST00000149212						7	1	3	2	1	3	0	0	0	1	4		
ENSMUST00000149214	ENSMUSG00000056763	1	10037987	10136768	1	0	0	0	0	0	0	0	0	0	0	0	F6QJJ3	
ENSMUST00000149215						0	3	0	0	3	2	0	0	0	0	0		
ENSMUST00000149216						2	0	4	0	3	0	0	1	0	0	0		
ENSMUST00000149217						0	0	6	1	0	0	0	0	0	0	0		
ENSMUST00000149218	ENSMUSG00000031399	X	74384719	74393272	-1	3	0	4	0	3	0	0	0	0	0	14	D6RJ75	
ENSMUST00000149219						181	152	706	283	240	85	2	2	6	6	7		
ENSMUST00000149220						20	50	51	101	31	16	12	22	8	0	11		
ENSMUST00000149221	ENSMUSG00000035969	4	43381979	43427088	1	3	3	40	9	3	3	0	0	0	0	0	G3UYW4	
ENSMUST00000149222						0	0	0	37	3	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149225	ENSMUSG00000027901	3	106482405	106503030	1	3	0	4	64	2	5	21	56	61	8	79	A0A0A6YWK8	
ENSMUST00000149227						0	0	1	54	3	1	0	0	0	0	0		
ENSMUST00000149228	ENSMUSG00000005267	11	62700356	62731905	-1	11	0	0	0	0	0	0	0	0	0	0		Q9EQB9
ENSMUST00000149229	ENSMUSG00000026784	2	22895522	22940266	1	0	0	0	0	0	0	0	0	0	0	0	F6ZCX7	
ENSMUST00000149230						2	3	1	2	4	0	1	0	0	0	0		
ENSMUST00000149232	ENSMUSG00000022678	16	14163275	14192928	1	0	0	0	1	0	2	11	19	21	6	22	F6Q325	
ENSMUST00000149233						3	6	5	12	7	1	5	9	9	0	14		
ENSMUST00000149234						30	13	34	28	36	16	0	0	0	0	1		
ENSMUST00000149235	ENSMUSG00000054728	13	42680623	43138526	1	0	0	2	0	4	5	0	0	0	0	0		Q2M3X8
ENSMUST00000149236	ENSMUSG00000046613	16	20589471	20605377	1	0	0	5	0	0	8	0	0	0	0	0	F2Z3U9	
ENSMUST00000149238						0	0	2	0	4	0	0	8	17	10	13		
ENSMUST00000149240						0	0	0	0	2	1	0	0	0	101	39		
ENSMUST00000149241	ENSMUSG00000032135	9	44134469	44142727	1	5	4	2	119	4	3	0	2	0	0	0	D6RFP0	
ENSMUST00000149242						0	0	0	4	2	2	0	0	1	0	0		
ENSMUST00000149243	ENSMUSG00000032563	9	105053239	105079888	1	5	5	12	32	11	5	5	18	5	8	6	D3Z456	
ENSMUST00000149244						16	3	8	2	5	3	50	181	102	3	199		
ENSMUST00000149245						3	3	9	3	3	2	0	0	0	0	0		
ENSMUST00000149248	ENSMUSG00000000738	8	123062942	123097760	1	0	7	17	49	4	0	0	0	0	0	14	D3Z1Z1	
ENSMUST00000149249	ENSMUSG00000046873	X	157535371	157598715	-1	1	0	0	18	0	0	0	5	14	0	0	A2AC84	
ENSMUST00000149250						1	3	2	2	2	0	0	0	0	0	0		
ENSMUST00000149253						0	0	3	32	6	0	0	0	0	2	0		
ENSMUST00000149254						39	52	37	77	45	30	6	24	9	15	18		
ENSMUST00000149255						0	0	1	0	0	0	1	0	0	0	0		
ENSMUST00000149256						0	2	2	1	5	0	1	0	0	0	0		
ENSMUST00000149257						7	7	21	16	13	9	2	6	9	3	20		
ENSMUST00000149258						8	9	33	8	1	5	0	0	0	0	1		
ENSMUST00000149259						0	0	0	0	0	0	0	0	130	14	28		
ENSMUST00000149260						3	0	5	0	1	1	0	0	0	0	0		
ENSMUST00000149261	ENSMUSG00000024953	19	6906697	6910106	-1	3	5	12	7	0	6	11392	15747	5672	8656	3089	H3BJQ7	
ENSMUST00000149262	ENSMUSG00000036825	3	146404642	146440144	1	0	0	4	0	0	0	0	0	0	0	0	D3Z6T5	
ENSMUST00000149263						0	0	1	2	0	0	0	0	0	3	0		
ENSMUST00000149266						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000149267	ENSMUSG00000038005	8	60890418	60907580	1	0	0	0	4	1	0	0	4	0	26	0	D6RIJ8	
ENSMUST00000149268						4	2	0	4	3	0	0	0	0	0	0		
ENSMUST00000149269						0	1	2	2	0	0	1	0	0	0	0		
ENSMUST00000149270						0	1	0	0	0	0	2	1	3	0	0		
ENSMUST00000149271						4	0	17	2	13	4	0	3	0	0	0		
ENSMUST00000149272						24	11	27	78	38	10	0	0	0	0	0		
ENSMUST00000149273	ENSMUSG00000033763	8	110721476	110741400	1	2	0	4	12	0	0	0	0	0	0	0	F6S054	
ENSMUST00000149274	ENSMUSG00000031314	X	101532734	101601789	1	1	0	0	0	1	0	0	0	10	0	42	A0A067XG50	
ENSMUST00000149276						40	32	57	65	55	30	3	9	10	6	14		
ENSMUST00000149277	ENSMUSG00000024426	17	35897595	35910075	-1	3	0	3	10	0	0	8	20	7	0	22		Q8K341
ENSMUST00000149279						2	3	4	4	3	4	2	72	7	0	10		
ENSMUST00000149280						2	0	0	0	0	5	0	0	0	0	0		
ENSMUST00000149281						5	1	6	2	5	2	0	0	0	0	0		
ENSMUST00000149282						6	5	6	13	4	6	1	0	0	0	0		
ENSMUST00000149284						0	2	0	6	5	4	1	0	0	0	0		
ENSMUST00000149286	ENSMUSG00000037697	14	45593174	45658143	-1	0	0	0	0	0	0	0	0	67	25	0	D6RH62	
ENSMUST00000149287	ENSMUSG00000017734	2	164486106	164493319	1	2	0	0	45	1	2	0	6	5	19	4	Q330P7	Q9CRD4
ENSMUST00000149288						9	8	6	8	13	5	0	0	2	2	4		
ENSMUST00000149289						4	2	1	1	5	1	4	10	11	3	2		
ENSMUST00000149290						0	0	4	1	0	0	0	0	1	2	0		
ENSMUST00000149291						234	227	200	224	267	97	5	11	16	6	35		
ENSMUST00000149292	ENSMUSG00000029712	5	137553517	137569582	1	0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000149293						2	2	24	0	3	1	14	70	14	5	36		
ENSMUST00000149294	ENSMUSG00000026976	2	24420560	24475599	-1	0	0	3	0	6	0	0	0	0	0	0	A2AIU6	
ENSMUST00000149295	ENSMUSG00000028397	4	74242497	74405860	1	0	0	0	0	0	0	0	0	0	0	0	I7HLQ5	
ENSMUST00000149296	ENSMUSG00000055850	6	72359714	72366956	-1	0	0	0	0	1	1	0	3	6	0	2	S4R201	
ENSMUST00000149297	ENSMUSG00000028530	4	101152367	101265282	-1	0	0	0	57	3	1	0	0	0	0	7	B1ASP3	
ENSMUST00000149298						2	0	1	31	1	2	0	0	0	0	0		
ENSMUST00000149299						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000149301	ENSMUSG00000050812	4	58798911	58912749	-1	0	2	12	11	0	0	147	0	314	0	127	A2ALV7	
ENSMUST00000149302						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149303	ENSMUSG00000044349	2	158375638	158386145	1	0	0	0	0	0	0	0	0	0	0	0	D6RHR4	
ENSMUST00000149304	ENSMUSG00000046947	6	39573873	39588769	1	0	0	3	4	0	0	2	23	9	0	8	F6QFE9	
ENSMUST00000149305						0	2	0	0	4	2	0	0	0	0	0		
ENSMUST00000149306						0	0	0	18	2	3	0	0	0	0	0		
ENSMUST00000149309	ENSMUSG00000041720	16	17280351	17406314	-1	0	0	4	0	0	0	6	0	0	0	0	F6Y9T6	
ENSMUST00000149310	ENSMUSG00000025950	1	65158616	65186500	-1	0	0	0	0	0	0	0	0	0	0	0	D3YVY3	
ENSMUST00000149311						10	4	2	23	9	6	7	12	14	0	10		
ENSMUST00000149312						1	0	4	0	2	1	2	14	7	1	7		
ENSMUST00000149313						2	4	7	8	4	8	157	515	214	108	328		
ENSMUST00000149314						24	22	66	10	23	9	7	4	6	0	5		
ENSMUST00000149315	ENSMUSG00000079316	X	166457253	166479867	-1	0	1	0	0	1	1	0	0	0	0	0	A2AFP4	
ENSMUST00000149316						0	0	1	1	0	0	0	0	0	0	4		
ENSMUST00000149317						0	0	9	1	1	1	0	0	0	0	0		
ENSMUST00000149318						0	2	3	3	4	4	1	0	0	0	0		
ENSMUST00000149320	ENSMUSG00000025920	1	16228674	16520112	-1	0	1	0	1	1	1	0	0	0	0	0	D3Z6D2	
ENSMUST00000149321						2	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000149322	ENSMUSG00000032527	9	100982032	101034898	-1	0	0	8	5	11	7	0	0	0	1	18	E9Q1J7	
ENSMUST00000149323	ENSMUSG00000015214	X	71364760	71419196	1	1	1	0	0	0	1	0	3	0	0	6	Q8CIU6	
ENSMUST00000149324	ENSMUSG00000018339	11	54902453	54910377	1	4	1	0	10	9	2	6	5	0	0	0	D3Z7Y0	
ENSMUST00000149326						2	0	1	0	6	0	0	0	0	2	0		
ENSMUST00000149327	ENSMUSG00000020883	11	98082556	98150403	-1	0	0	0	0	0	1	0	0	0	0	0	A2A533	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149328						0	0	3	0	0	0	7	27	0	10	5		
ENSMUST00000149329						0	1	3	0	0	0	26	42	172	18	63		
ENSMUST00000149330	ENSMUSG00000041718	X	144317804	144374450	1	0	0	0	2	0	0	0	0	2	12	0	E9Q161	
ENSMUST00000149331	ENSMUSG00000033737	X	106420041	106485401	-1	0	0	0	0	0	0	0	0	0	0	0	A2AMR1	
ENSMUST00000149332						0	1	0	0	0	0	32	71	14	11	25		
ENSMUST00000149333	ENSMUSG00000028454	4	43017635	43025819	-1	0	0	0	0	0	0	10	43	16	13	8	F6YPG3	
ENSMUST00000149334						6	9	17	5	4	11	0	5	0	0	2		
ENSMUST00000149335						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149336						21	12	57	31	41	28	0	0	0	0	2		
ENSMUST00000149337						0	0	0	0	0	0	0	4	0	2	3		
ENSMUST00000149339						0	0	2	2	1	0	2	15	4	12	6		
ENSMUST00000149340						0	1	2	0	1	0	0	14	0	4	4		
ENSMUST00000149341						2	2	7	7	6	0	12	21	8	3	15		
ENSMUST00000149342	ENSMUSG00000053161	1	83159752	83210574	1	0	0	0	0	5	0	0	0	0	0	0	D6REG5	
ENSMUST00000149344						0	0	0	0	0	0	3	0	0	0	2		
ENSMUST00000149345						0	1	7	3	8	0	4	10	7	4	0		
ENSMUST00000149346						0	0	5	24	0	1	5	1	6	7	1		
ENSMUST00000149347	ENSMUSG00000047733	19	6080033	6080788	1	1	0	0	0	0	0	0	0	1	0	0	D3Z5B7	
ENSMUST00000149349	ENSMUSG00000003123	7	25379527	25398710	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4M2	
ENSMUST00000149350	ENSMUSG00000037426	5	32863701	32994236	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5Y4	
ENSMUST00000149351						1	0	2	0	2	0	8	34	28	11	56		
ENSMUST00000149352						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000149353	ENSMUSG00000028226	4	17852893	18119145	1	8	11	15	4	8	1	0	0	1	0	1	B1AVH0	
ENSMUST00000149354						0	3	2	1	2	0	5	31	8	4	23		
ENSMUST00000149355						2	1	0	0	2	0	12	0	4	0	4		
ENSMUST00000149356						1	1	2	5	0	1	0	0	0	0	0		
ENSMUST00000149357	ENSMUSG00000028496	4	87769925	88033364	-1	7	1	2	0	3	3	0	0	2	14	5	Q3UIA3	
ENSMUST00000149358						1	0	0	0	0	0	191	812	162	78	79		
ENSMUST00000149359	ENSMUSG00000009569	16	13256481	13417529	1	95	115	193	72	130	59	79	104	178	11	114	Q5DTZ3	
ENSMUST00000149360	ENSMUSG00000039911	4	149896283	149955043	-1	3	0	0	0	0	0	1	0	0	0	0	A2A7B2	
ENSMUST00000149361						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149362						2	3	1	2	6	1	15	27	29	12	35		
ENSMUST00000149363						1	0	9	33	7	0	5	0	0	0	0		
ENSMUST00000149364	ENSMUSG00000086112	14	60087071	60096093	1	0	0	0	1	0	0	0	0	0	0	0	D3YWV1	
ENSMUST00000149365						2	0	0	15	0	4	0	0	0	0	0		
ENSMUST00000149366	ENSMUSG00000028614	4	107367784	107416346	1	0	0	0	0	0	4	35	0	0	25	0	J3QPB5	
ENSMUST00000149368	ENSMUSG00000002885	8	83723251	83741326	-1	0	2	0	0	1	0	41	10	54	2	73	S4R1V8	
ENSMUST00000149369						1	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000149370	ENSMUSG00000017004	2	164332740	164334396	1	5	2	0	0	0	1	0	0	0	0	0	F6RYE9	
ENSMUST00000149371						2	3	5	119	1	4	7	7	81	0	77		
ENSMUST00000149372						18	21	43	21	23	8	1	1	7	1	8		
ENSMUST00000149375						2	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000149376						0	2	0	0	0	0	0	2	0	0	0		
ENSMUST00000149379						0	2	5	2	5	0	6	6	0	0	0		
ENSMUST00000149380	ENSMUSG00000010311	1	133897199	133907999	-1	0	0	0	0	0	0	0	0	0	0	0	E9PUR1	
ENSMUST00000149381						0	0	1	1	1	1	4	14	4	0	4		
ENSMUST00000149383	ENSMUSG00000038696	2	34406771	34624950	1	0	0	0	24	0	0	15	7	26	0	37	A0A0A6YW60	
ENSMUST00000149384	ENSMUSG00000029328	5	100033577	100039664	-1	0	0	8	83	4	0	85	482	245	350	327	F6ZKM7	
ENSMUST00000149385						0	2	9	19	0	2	3	6	0	0	14		
ENSMUST00000149388						3	0	9	14	4	3	0	3	4	0	8		
ENSMUST00000149389	ENSMUSG00000025142	11	120672973	120709447	1	2	2	0	2	6	0	19	40	14	4	11	A2ABZ8	
ENSMUST00000149390						4	4	12	19	5	10	0	2	0	0	0		
ENSMUST00000149391						0	28	65	0	10	0	641	4976	1124	249	1933		
ENSMUST00000149392						1	3	2	1	2	0	5	27	13	20	43		
ENSMUST00000149393						15	12	4	15	13	7	4	52	1	7	18		
ENSMUST00000149394	ENSMUSG00000061589	10	80755206	80795461	1	7	0	46	269	22	6	12	17	11	0	21	F6SJX8	
ENSMUST00000149395	ENSMUSG00000055541	7	4003402	4063204	-1	0	0	0	2	0	0	42	206	30	234	30	D6RGS7	Q8BG84
ENSMUST00000149396						0	0	0	0	0	0	8	45	5	0	28		
ENSMUST00000149397						4	0	10	0	7	4	5	4	13	3	19		
ENSMUST00000149399	ENSMUSG00000009628	8	33516738	33585582	1	4	0	7	10	2	3	0	0	1	0	4	D3YVF5	
ENSMUST00000149400						7	0	7	1	3	2	50	75	4	26	19		
ENSMUST00000149401						0	0	0	0	0	0	0	11	3	0	1		
ENSMUST00000149402						0	0	0	1	0	2	0	9	3	2	3		
ENSMUST00000149403	ENSMUSG00000020333	11	54303798	54364756	1	0	0	12	3	1	2	0	0	2	0	0	B1ARG5	
ENSMUST00000149404						0	3	0	0	0	4	0	0	0	0	0		
ENSMUST00000149405	ENSMUSG00000052712	17	29268788	29302881	1	2	0	2	0	5	3	401	635	465	465	258		Q99KU6
ENSMUST00000149406						0	2	1	19	2	3	17	17	25	2	15		
ENSMUST00000149407	ENSMUSG00000022580	15	75704280	75714410	1	13	0	6	17	23	0	0	3	0	0	0	Q80WU2	
ENSMUST00000149408						1	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000149409						1	0	5	7	5	2	11	4	14	7	32		
ENSMUST00000149410	ENSMUSG00000049550	5	123577795	123684618	-1	15	16	27	0	11	2	15	0	121	0	32	Q8C0S5	
ENSMUST00000149411						1	0	0	0	2	0	126	105	129	78	54		
ENSMUST00000149412						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149414	ENSMUSG00000021983	14	59647531	60197179	-1	1	0	5	18	1	0	0	0	0	0	0	D3Z1A2	
ENSMUST00000149415	ENSMUSG00000002222	6	71388634	71440637	-1	8	1	28	0	2	3	378	1899	865	168	555	F6V8A7	
ENSMUST00000149416						1	0	0	0	0	1	13	8	19	3	30		
ENSMUST00000149417						30	30	106	60	34	18	45	901	113	30	305		
ENSMUST00000149418	ENSMUSG00000044339	5	114123926	114128218	-1	0	0	0	37	0	4	0	0	0	0	0	A0A0G2JER8	
ENSMUST00000149419	ENSMUSG00000022469	15	97744770	97767972	-1	0	0	0	26	0	0	0	0	0	0	0	D6RGA9	
ENSMUST00000149420						0	5	6	6	4	1	121	947	315	126	347		
ENSMUST00000149421						4	2	3	5	5	1	0	0	0	0	0		
ENSMUST00000149422						3	0	18	7	0	4	28	148	56	0	36		
ENSMUST00000149423						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149424						1	1	8	0	4	2	1	0	0	3	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149425						7	0	22	5	7	0	0	2	1	0	0		
ENSMUST00000149426						6	5	20	0	3	8	3	23	17	0	33		
ENSMUST00000149427						5	0	0	5	0	0	1	0	0	0	0		
ENSMUST00000149430						2	3	7	25	12	4	1	4	1	0	7		
ENSMUST00000149431	ENSMUSG00000021200	12	103321142	103356001	-1	2	5	0	159	7	0	9	8	11	0	28		Q8K0L0
ENSMUST00000149432	ENSMUSG00000027940	3	90072649	90100902	1	0	0	0	50	3	0	0	0	3	0	2	D3YVR0	
ENSMUST00000149433						5	2	58	30	3	0	1	3	0	1	0		
ENSMUST00000149436	ENSMUSG00000026280	1	93751500	93790610	1	0	2	1	0	0	3	14	9	23	8	19	D3YZP6	
ENSMUST00000149437						33	23	23	32	31	6	8	16	6	0	13		
ENSMUST00000149439						3	0	1	2	0	6	0	0	0	0	0		
ENSMUST00000149440	ENSMUSG00000023868	17	8525372	8986648	1	0	0	0	3	0	4	0	0	0	0	1		Q8CA95
ENSMUST00000149441	ENSMUSG00000003199	17	56005711	56016790	1	0	0	3	34	0	2	332	314	65	0	155		Q3TV65
ENSMUST00000149442						7	16	36	54	10	5	6	11	4	3	6		
ENSMUST00000149443						0	0	1	0	1	1	0	0	0	0	0		
ENSMUST00000149444	ENSMUSG00000039176	7	79446231	79466362	-1	0	0	0	14	0	0	388	444	418	46	304	D6RIP1	
ENSMUST00000149445						151	141	94	123	163	96	9	25	13	4	21		
ENSMUST00000149446	ENSMUSG00000055799	6	72626378	72789254	-1	0	0	6	0	0	0	0	0	0	0	0	F6VNH1	
ENSMUST00000149447						1	0	5	0	1	0	0	0	0	0	0		
ENSMUST00000149448	ENSMUSG00000058486	6	34880426	34910876	-1	0	1	11	9	0	2	4	0	7	0	0	D3Z101	
ENSMUST00000149449	ENSMUSG00000050174	3	37404910	37420211	-1	0	0	0	55	0	1	0	10	0	1	0	A2ACT8	
ENSMUST00000149450						8	0	16	6	10	7	0	2	0	0	0		
ENSMUST00000149451						8	8	8	18	8	5	0	0	0	0	1		
ENSMUST00000149453	ENSMUSG00000028621	4	107066988	107088268	1	39	30	45	50	27	0	0	0	9	0	0	F2Z4B1	
ENSMUST00000149454						3	3	49	6	8	1	0	20	7	3	14		
ENSMUST00000149455						0	0	0	0	0	0	3	0	1	0	0		
ENSMUST00000149456						0	0	0	13	0	1	0	0	0	0	0		
ENSMUST00000149457						2	1	0	7	3	1	0	0	0	0	0		
ENSMUST00000149458						0	0	5	119	4	1	0	0	0	0	0		
ENSMUST00000149459	ENSMUSG00000020694	11	105178807	105283959	1	0	0	0	81	3	3	0	2	0	0	0	B7ZC84	
ENSMUST00000149460						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149461	ENSMUSG00000002728	2	145902099	145916425	1	0	0	0	0	0	0	0	0	0	0	0	E9PZX8	
ENSMUST00000149462	ENSMUSG00000025869	13	54584185	54590090	-1	4	2	0	1	3	5	1	11	0	0	8	D6RDE0	
ENSMUST00000149464						10	2	49	17	17	4	7	7	19	0	17		
ENSMUST00000149465						2	0	0	0	0	0	5	12	7	0	0		
ENSMUST00000149466	ENSMUSG00000068373	2	104143073	104410334	-1	0	0	16	0	0	0	0	0	0	0	0	F6TUM7	
ENSMUST00000149467						0	0	0	0	0	1	0	3	1	0	0		
ENSMUST00000149468						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149469						1	0	7	39	4	3	0	0	0	0	0		
ENSMUST00000149470						16	0	37	18	13	3	0	3	0	0	0		
ENSMUST00000149471						0	2	0	3	0	1	0	3	0	0	0		
ENSMUST00000149473						5	3	10	60	0	4	2	13	4	0	14		
ENSMUST00000149474						4	1	0	0	0	1	2	0	0	0	0		
ENSMUST00000149475						0	4	3	8	0	5	68	265	239	12	141		
ENSMUST00000149476	ENSMUSG00000025007	19	40550257	40588463	-1	0	0	0	36	0	0	0	0	0	0	0	D3Z0B4	
ENSMUST00000149477						5	1	0	1	5	1	0	2	3	0	0		
ENSMUST00000149478						12	0	25	17	0	0	0	0	0	0	0		
ENSMUST00000149479						0	2	2	0	3	0	6	7	3	0	0		
ENSMUST00000149480						0	2	3	3	1	0	0	0	0	0	0		
ENSMUST00000149482						4	2	4	9	6	0	0	0	0	0	0		
ENSMUST00000149483	ENSMUSG00000036769	X	23693051	23806025	1	0	0	2	10	2	2	0	3	9	0	15	D6RHR5	
ENSMUST00000149485	ENSMUSG00000019868	10	14654755	14705560	-1	0	0	0	0	0	0	51	168	64	92	41	F6W5Q8	
ENSMUST00000149486	ENSMUSG00000040481	11	107033081	107132127	-1	3	1	2	2	3	0	11	8	60	0	47	A2A653	
ENSMUST00000149487	ENSMUSG00000036091	9	107580818	107587359	1	0	0	0	0	0	0	0	0	0	0	0	D3YVY7	
ENSMUST00000149489						20	16	34	56	20	10	21	35	24	4	27		
ENSMUST00000149490						5	11	31	34	13	9	63	311	105	24	179		
ENSMUST00000149491						4	7	3	6	5	3	0	0	0	0	2		
ENSMUST00000149492						11	3	10	73	8	5	0	0	0	0	0		
ENSMUST00000149493						1	0	2	46	5	1	1	0	5	0	6		
ENSMUST00000149494						3	6	2	0	3	5	0	1	1	0	0		
ENSMUST00000149495						0	0	4	13	0	0	24	0	0	0	0		
ENSMUST00000149496						0	0	0	0	0	3	0	2	0	1	2		
ENSMUST00000149497						0	0	0	0	0	0	0	21	0	21	0		
ENSMUST00000149498						0	0	0	0	0	1	11	0	0	0	0		
ENSMUST00000149499	ENSMUSG00000037110	2	146239879	146512026	-1	0	0	0	0	0	0	33	0	167	0	107	F7CGP0	
ENSMUST00000149501						4	1	6	0	2	4	0	2	0	0	0		
ENSMUST00000149502	ENSMUSG00000026049	1	44086613	44102441	-1	0	0	0	0	0	0	0	0	0	4	0	D3YXN3	
ENSMUST00000149503						0	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000149504						3	6	0	0	0	2	6	12	0	0	0		
ENSMUST00000149505						2	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000149507						0	0	0	0	0	0	3	10	2	4	0		
ENSMUST00000149508						1	0	0	5	3	0	0	0	0	0	0		
ENSMUST00000149509						5	0	0	1	4	0	0	0	0	0	1		
ENSMUST00000149510	ENSMUSG00000029538	5	115327177	115333080	1	0	0	0	0	0	2	64	124	14	0	35	F6RTE1	
ENSMUST00000149511						683	642	1895	714	849	419	27	130	75	32	108		
ENSMUST00000149512	ENSMUSG00000045348	5	137729899	137741607	-1	0	7	26	0	0	4	7	4	1	1	0	E9PXJ0	
ENSMUST00000149513						3	1	0	0	1	0	7	83	34	0	0		
ENSMUST00000149516						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149517						0	1	3	1	3	2	0	1	0	0	0		
ENSMUST00000149518						0	0	0	0	0	0	3	25	0	2	7		
ENSMUST00000149519						32	16	69	36	40	17	5	5	6	0	41		
ENSMUST00000149520						0	1	0	1	0	0	0	0	0	0	2		
ENSMUST00000149521						2	2	10	6	6	3	13	15	21	0	50		
ENSMUST00000149522						71	36	275	88	67	38	4	1	5	0	4		
ENSMUST00000149523						1	1	1	0	1	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149524						2	0	8	3	2	1	0	0	0	0	0		
ENSMUST00000149525	ENSMUSG00000004221	X	74393290	74453854	1	2	0	0	0	0	0	23	7	32	28	52	A3KG38	
ENSMUST00000149526	ENSMUSG00000020289	11	32225628	32267707	-1	0	0	0	6	0	0	0	0	0	0	0	D6RGB2	
ENSMUST00000149527						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000149528						5	1	0	0	0	0	119	0	410	70	232		
ENSMUST00000149529	ENSMUSG00000031097	7	142441808	142444410	1	1	2	5	6	3	2	51	48	13	140	24		P13412
ENSMUST00000149530	ENSMUSG00000031748	8	93809966	93969388	1	0	0	0	0	0	0	0	0	0	0	1	F6W1B2	
ENSMUST00000149531						7	1	1	0	3	2	0	95	11	67	26		
ENSMUST00000149532	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	7	27	7	6	D3YZU7	
ENSMUST00000149533	ENSMUSG00000029217	5	72755716	72868483	-1	6	4	3	6	6	3	0	2	0	0	0		
ENSMUST00000149534	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	0	0	0	0	0	0	0	0	0	F6QD41	
ENSMUST00000149535	ENSMUSG00000030877	7	120982509	121014787	1	1	0	2	0	2	2	0	0	0	0	0	D3Z0S3	
ENSMUST00000149536	ENSMUSG00000026482	1	152516760	152766351	-1	1	1	0	0	2	0	0	0	0	0	0	A0A087WSF9	
ENSMUST00000149537						0	0	11	51	11	8	0	19	0	0	0		
ENSMUST00000149539						5	3	6	6	8	9	4	16	10	4	24		
ENSMUST00000149540						1	3	3	28	4	1	2	3	0	0	0		
ENSMUST00000149541						45	40	255	68	46	21	2	51	14	0	24		
ENSMUST00000149542	ENSMUSG00000026240	1	86582904	86609375	1	5	1	9	63	2	2	1	6	0	1	2	D3Z6T8	
ENSMUST00000149543	ENSMUSG00000050821	16	20693282	20703048	1	0	0	1	67	1	1	0	0	1	0	0	D3YVN0	
ENSMUST00000149544	ENSMUSG00000042198	4	3938888	3951046	1	0	0	0	0	0	0	0	2	8	5	0	B1AXC8	
ENSMUST00000149545	ENSMUSG00000081044	X	93968659	93975470	1	6	0	0	11	7	0	0	0	0	0	0	B1ASY6	
ENSMUST00000149546						0	0	0	5	0	0	0	2	0	0	0		
ENSMUST00000149547	ENSMUSG00000028524	4	102741297	102973628	1	2	0	6	0	6	2	0	3	12	0	0	F7CPX0	
ENSMUST00000149548						1	0	0	4	0	0	12	0	0	0	0		
ENSMUST00000149549						8	0	0	4	3	6	0	6	0	3	10		
ENSMUST00000149550						2	3	0	0	4	1	0	0	0	0	0		
ENSMUST00000149551						0	4	0	1	0	0	11	12	6	0	18		
ENSMUST00000149553						0	0	10	5	8	0	11	78	31	6	54		
ENSMUST00000149555						64	62	456	110	53	35	0	14	5	1	11		
ENSMUST00000149556						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000149557						59	48	138	85	59	52	5	11	6	1	9		
ENSMUST00000149558						2	0	0	1	0	3	6	17	3	0	4		
ENSMUST00000149559						0	1	4	173	7	3	0	6	4	0	5		
ENSMUST00000149560						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149561						2	0	0	2	2	1	0	0	0	0	0		
ENSMUST00000149563						7	3	15	9	5	1	0	0	0	0	0		
ENSMUST00000149564	ENSMUSG00000034601	12	71136848	71243303	1	0	0	0	22	16	0	17	169	88	18	39		E9PV87
ENSMUST00000149565	ENSMUSG00000031467	8	18846277	18891361	1	44	38	114	191	48	32	11	105	20	4	27		Q9D1E8
ENSMUST00000149566	ENSMUSG00000043716	1	16101295	16104662	-1	4	0	0	0	0	0	2338	10037	3971	18637	2734	F6XI62	
ENSMUST00000149567						0	0	0	7	0	2	0	0	0	0	0		
ENSMUST00000149568						0	0	0	26	0	0	0	2	3	4	4		
ENSMUST00000149569	ENSMUSG00000033576	15	77044729	77057107	1	8	3	41	12	10	4	0	0	0	0	0	B7ZC54	
ENSMUST00000149570						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000149571						8	10	9	11	8	0	0	0	0	0	0		
ENSMUST00000149573						34	38	189	112	33	24	0	1	1	0	0		
ENSMUST00000149575	ENSMUSG00000066196	4	43651335	43653594	-1	2	0	0	0	0	1	0	0	0	0	0	F6ZRZ4	
ENSMUST00000149578	ENSMUSG00000054766	2	30057378	30072577	1	3	3	1	181	16	0	0	0	0	0	0	A2BE92	
ENSMUST00000149579	ENSMUSG00000039219	13	14063232	14199603	1	6	3	28	11	11	7	58	151	173	59	142	F6R6U0	
ENSMUST00000149580	ENSMUSG00000033099	15	78934933	78943634	1	0	0	0	4	0	0	41	48	25	110	66	B7ZBX7	
ENSMUST00000149581						0	0	0	0	1	1	0	5	1	2	0		
ENSMUST00000149582	ENSMUSG00000042292	15	81012281	81190757	-1	0	0	5	41	12	21	436	348	541	0	352		Q8K4J6
ENSMUST00000149583						0	0	5	1	4	0	0	0	0	0	2		
ENSMUST00000149584						10	0	0	0	11	12	0	0	9	0	21		
ENSMUST00000149585	ENSMUSG00000001240	11	101246028	101259546	1	0	0	0	0	1	0	0	0	0	0	0	D6RHQ4	
ENSMUST00000149586						8	4	14	14	9	3	7	35	8	3	39		
ENSMUST00000149587						0	0	0	0	0	0	2	1	4	0	2		
ENSMUST00000149588	ENSMUSG00000004535	6	52713729	52766780	1	0	0	0	92	2	1	0	0	0	2	7	D3Z715	
ENSMUST00000149589	ENSMUSG00000025572	11	117765988	117782198	-1	5	2	20	7	9	6	31	60	27	5	74	F7D254	
ENSMUST00000149590						16	9	43	14	13	10	4	40	30	0	48		
ENSMUST00000149591						2	2	5	39	4	4	0	1	0	0	2		
ENSMUST00000149593	ENSMUSG00000038173	8	46986925	47094895	1	0	1	1	0	1	0	0	0	0	1	0	F6R291	
ENSMUST00000149595						0	0	0	0	0	0	13	34	35	13	34		
ENSMUST00000149596	ENSMUSG00000046312	4	41495604	41503076	-1	4	1	16	2	6	4	0	0	0	0	0	A2ANN7	
ENSMUST00000149597	ENSMUSG00000017801	11	101087277	101092207	1	0	0	1	58	2	0	0	4	8	6	5	A2BFA9	
ENSMUST00000149598						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000149599						0	0	0	1	0	1	0	0	1	0	0		
ENSMUST00000149600	ENSMUSG00000038569	5	122323223	122354233	-1	5	3	0	0	0	1	0	0	0	0	10	F6VRS2	
ENSMUST00000149602	ENSMUSG00000055923	5	76873659	76905514	-1	1	0	8	0	0	2	0	6	0	0	0	F7A4F9	
ENSMUST00000149603						4	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000149604	ENSMUSG00000085957	5	134558146	134560171	-1	20	24	57	33	35	20	0	3	1	0	1	Q5G5D5	
ENSMUST00000149605						0	0	0	5	3	0	0	0	0	0	0		
ENSMUST00000149607						0	0	0	0	0	0	4	3	0	0	0		
ENSMUST00000149610	ENSMUSG00000023456	6	124810586	124814296	-1	15	3	5	6	0	3	442	20	115	79	89	H7BXC3	
ENSMUST00000149611						3	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000149612						0	0	0	0	0	0	0	7	9	0	0		
ENSMUST00000149614						39	36	80	60	39	27	0	5	3	5	1		
ENSMUST00000149615						2	1	5	0	3	3	0	40	0	0	0		
ENSMUST00000149616	ENSMUSG00000051747	2	76703980	76982547	-1	0	5	0	0	3	0	0	0	0	0	0	A2AT64	
ENSMUST00000149617	ENSMUSG00000057068	5	92555069	92591279	1	2	0	0	0	0	0	0	0	0	0	0	D3Z2U0	
ENSMUST00000149620						0	0	0	0	0	2	1	1	1	0	0		
ENSMUST00000149621						0	1	1	60	4	7	0	0	0	0	0		
ENSMUST00000149622						1	2	5	5	2	0	0	0	0	0	2		
ENSMUST00000149623	ENSMUSG00000020484	11	5520659	5525893	1	4	2	1	2	8	4	50	45	58	4	117	H3BLF6	
ENSMUST00000149624						1	0	0	16	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149625						0	5	3	0	2	1	0	0	0	0	0		
ENSMUST00000149627						1	4	1	16	0	0	0	0	4	0	2		
ENSMUST00000149628						0	1	3	0	2	0	3	0	6	0	11		
ENSMUST00000149629						437	421	1364	658	573	378	3	32	18	110	44		
ENSMUST00000149630	ENSMUSG00000021708	13	91880400	92131656	-1	1	0	0	0	0	1	0	1	0	0	1	F6TCD3	
ENSMUST00000149631						0	0	0	2	0	0	0	0	0	0	5		
ENSMUST00000149632						0	0	2	3	1	0	1	10	0	0	0		
ENSMUST00000149633	ENSMUSG00000040569	4	14502430	14621805	-1	4	3	7	10	7	4	0	0	0	0	0	A2AJZ5	
ENSMUST00000149634						1	0	8	34	2	0	0	0	0	0	0		
ENSMUST00000149635						8	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149636	ENSMUSG00000028671	4	135963727	135968178	1	1	0	0	3	0	0	0	2	0	0	0	B1AV54	
ENSMUST00000149637						5	2	0	82	5	0	0	0	0	0	0		
ENSMUST00000149638	ENSMUSG00000079334	9	107578887	107584050	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149639						0	1	0	1	0	0	14	104	187	53	127		
ENSMUST00000149640						8	0	0	57	5	3	0	1	0	0	0		
ENSMUST00000149642	ENSMUSG00000034187	11	103821782	103954056	-1	0	0	0	1	0	0	0	0	0	0	0	G3UX98	
ENSMUST00000149643	ENSMUSG00000005233	2	69193895	69206194	-1	0	0	0	0	0	0	0	5	25	31	0	A2AUT3	
ENSMUST00000149644	ENSMUSG00000025877	13	55005985	55021385	-1	2	0	4	0	0	0	34	78	50	38	74	D6RCV7	
ENSMUST00000149645						15	12	45	16	29	14	35	154	32	10	75		
ENSMUST00000149646	ENSMUSG00000004285	6	29467718	29470512	1	3	2	3	2	0	1	0	8	2	0	7		
ENSMUST00000149647						2	0	0	65	3	0	0	0	0	0	0		
ENSMUST00000149648	ENSMUSG00000029017	5	21737141	21757152	1	4	4	10	5	9	3	0	0	0	0	2	D3Z1T9	
ENSMUST00000149649						0	4	0	1	4	2	0	22	0	11	11		
ENSMUST00000149650						6	4	13	3	12	5	0	0	0	0	0		
ENSMUST00000149651						30	23	30	14	26	15	6	15	3	7	15		
ENSMUST00000149652	ENSMUSG00000004267	6	124760053	124769673	-1	5	3	17	70	10	3	0	0	0	0	0	D3Z2S4	
ENSMUST00000149653						17	9	16	38	19	9	1	0	0	0	1		
ENSMUST00000149654	ENSMUSG00000019738	7	30231948	30233390	1	0	0	1	0	0	0	0	15	5	9	0	D3Z3Z8	
ENSMUST00000149655	ENSMUSG00000037994	3	135307700	135345387	1	2	1	2	0	3	1	0	0	0	0	0	A0A0G2JEX4	
ENSMUST00000149656						2	0	0	2	0	0	2	27	2	0	0		
ENSMUST00000149657	ENSMUSG00000001082	5	34633642	34637212	-1	4	0	0	32	0	0	6	0	0	0	0	D3YYM9	
ENSMUST00000149658						25	15	95	32	22	15	3	10	5	2	5		
ENSMUST00000149659						1	0	2	9	0	0	0	0	0	0	0		
ENSMUST00000149660						34	14	22	15	30	14	2	2	1	1	3		
ENSMUST00000149662	ENSMUSG00000059439	11	85353167	85826058	1	0	0	0	0	4	0	9	5	11	3	9	F6VJ09	
ENSMUST00000149663	ENSMUSG00000063193	11	114922781	114934386	-1	10	9	33	29	18	11	1278	4779	1108	1228	1322	Q3TEQ8	
ENSMUST00000149664						5	1	6	53	3	2	0	0	0	0	0		
ENSMUST00000149665						2	4	0	2	3	0	0	0	0	0	0		
ENSMUST00000149666	ENSMUSG00000054966	6	145365134	145614319	-1	2	1	5	2	1	2	0	0	0	0	0	B2KFR3	
ENSMUST00000149668	ENSMUSG00000017718	11	117825924	117839908	1	19	18	91	0	17	0	0	0	0	0	20	B1AQL0	
ENSMUST00000149669						1	2	5	2	1	4	0	49	0	0	0		
ENSMUST00000149670						0	0	0	4	0	0	0	0	1	0	2		
ENSMUST00000149671	ENSMUSG00000011154	7	83774101	83794880	-1	4	0	3	0	0	0	0	0	0	0	0	D3YUC3	
ENSMUST00000149672	ENSMUSG00000028519	4	103619359	104744844	1	4	2	0	2	0	0	0	0	0	0	0	F6VRL0	
ENSMUST00000149673						0	0	5	0	0	0	0	8	0	0	3		
ENSMUST00000149674						37	37	99	38	44	15	3	10	4	1	5		
ENSMUST00000149675						7	9	4	18	10	1	2	18	16	5	36		
ENSMUST00000149676	ENSMUSG00000042788	4	43427019	43429134	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ27	
ENSMUST00000149678						8	16	17	110	23	10	1	1	2	0	1		
ENSMUST00000149679	ENSMUSG00000026761	2	48902824	48950277	-1	1	0	1	26	1	0	0	0	5	10	0	A2AI43	
ENSMUST00000149680						0	0	0	0	0	0	0	0	0	23	0		
ENSMUST00000149682						20	7	21	10	12	3	0	3	4	0	3		
ENSMUST00000149683	ENSMUSG00000020728	11	108425192	108860615	1	3	7	2	38	5	3	0	0	0	0	0	I7HJR4	
ENSMUST00000149684						1	5	0	0	1	4	175	119	135	16	273		
ENSMUST00000149685						0	0	0	0	0	0	0	9	72	0	12		
ENSMUST00000149686						9	8	13	9	20	7	3	9	5	1	7		
ENSMUST00000149688						2	0	1	0	1	0	1	1	0	0	1		
ENSMUST00000149689						9	3	0	0	4	0	0	8	0	2	4		
ENSMUST00000149690						14	7	22	105	18	7	0	0	0	0	0		
ENSMUST00000149691						4	2	6	12	2	0	11	78	29	19	18		
ENSMUST00000149692	ENSMUSG00000089865	9	72958852	73016319	1	0	0	0	4	4	0	0	26	0	0	4	E9PYU5	
ENSMUST00000149694						0	2	0	1	0	0	6	4	17	0	0		
ENSMUST00000149695						0	0	0	0	11	1	0	0	0	0	17		
ENSMUST00000149697	ENSMUSG00000027429	2	144556229	144590749	1	1	6	0	0	0	0	0	0	5	0	0	A2AN98	
ENSMUST00000149698	ENSMUSG00000017929	2	167298444	167349183	-1	0	0	0	1	0	0	0	3	9	3	25	F6XV02	
ENSMUST00000149699	ENSMUSG00000044501	17	22361453	22377281	1	0	6	0	3	0	0	40	0	0	10	0	E9QAA1	
ENSMUST00000149700	ENSMUSG00000028494	4	86648386	86670060	-1	6	0	21	4	2	0	59	61	52	201	103	B1AXR5	
ENSMUST00000149701						1	0	0	3	3	3	3	3	3	0	0		
ENSMUST00000149703	ENSMUSG00000020899	11	68985697	69008460	-1	1	0	0	0	0	1	2	0	0	2	2	G3UY86	
ENSMUST00000149704						62	40	238	52	39	18	0	5	3	0	4		
ENSMUST00000149705	ENSMUSG00000074736	2	149829211	150004392	1	0	0	2	0	0	0	0	0	0	0	0	B1AYD6	
ENSMUST00000149706	ENSMUSG00000097487	11	101418812	101425333	-1	48	49	349	53	43	37	6	8	5	3	9	F7BAN7	
ENSMUST00000149708						1	0	2	0	2	0	0	0	2	0	4		
ENSMUST00000149709						8	2	3	18	3	0	1	17	1	0	0		
ENSMUST00000149710	ENSMUSG00000020672	12	30174482	30373375	-1	9	0	5	0	0	0	0	0	0	0	0	D6RCX3	
ENSMUST00000149711						53	41	53	28	39	39	1	12	9	16	26		
ENSMUST00000149712	ENSMUSG00000074771	2	136501910	136562091	1	0	4	27	5	12	3	0	0	0	0	0	D6RDT8	
ENSMUST00000149713						0	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000149714	ENSMUSG00000035310	5	100441918	100500639	-1	0	0	0	0	0	0	14	17	0	0	0	E9PV28	
ENSMUST00000149716	ENSMUSG00000024158	17	24840143	24864450	1	5	3	2	104	1	8	0	0	0	0	0	D3YUX8	
ENSMUST00000149717						0	4	4	0	0	0	0	0	0	0	0		
ENSMUST00000149718						19	15	29	24	36	12	0	4	2	0	5		
ENSMUST00000149719	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	7	0	0	164	46	37	24	72	Q3TPY5	Q8CBW3
ENSMUST00000149720						50	74	246	263	94	44	89	244	101	16	129		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149721						0	0	0	0	0	1	0	0	0	2	0		
ENSMUST00000149722						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149723						0	0	4	64	1	1	0	0	0	0	0		
ENSMUST00000149724						7	0	5	20	3	1	3	1	0	1	2		
ENSMUST00000149725						2	4	56	14	8	0	0	0	0	0	0		
ENSMUST00000149726	ENSMUSG00000002320	14	55635965	55643806	-1	0	0	0	0	0	0	0	0	26	25	0	D6RGM8	
ENSMUST00000149727	ENSMUSG00000038178	11	75531694	75577575	1	1	0	8	113	4	4	3	5	8	0	11	Q5ND25	
ENSMUST00000149728	ENSMUSG00000029670	6	21949571	21976038	1	0	0	0	3	0	0	0	0	17	0	14		
ENSMUST00000149729						0	0	1	1	1	1	0	226	10	56	34		
ENSMUST00000149730						8	13	14	14	12	4	4	3	3	0	10		
ENSMUST00000149732	ENSMUSG00000012187	1	78510991	78538173	1	8	7	2	1	8	1	0	0	0	4	0	D3YW64	
ENSMUST00000149733	ENSMUSG00000009614	2	27188393	27248337	-1	0	0	0	0	0	0	0	0	0	0	0	A2AH53	
ENSMUST00000149734						3	6	14	8	3	2	26	241	23	8	99		
ENSMUST00000149735						124	127	535	122	126	62	8	41	23	10	38		
ENSMUST00000149736						1	4	5	0	5	0	0	0	0	0	0		
ENSMUST00000149737						0	1	7	0	10	0	0	0	0	0	0		
ENSMUST00000149738						34	3	9	0	3	2	0	0	0	0	0		
ENSMUST00000149739	ENSMUSG00000066031	4	143789352	143795575	1	4	1	0	0	0	3	0	0	0	0	0	A6PWA4	
ENSMUST00000149740						1	0	1	0	0	0	6	4	2	0	7		
ENSMUST00000149743	ENSMUSG00000039911	4	149896283	149955043	-1	6	0	7	1	3	1	0	0	0	0	0	A2A7B0	
ENSMUST00000149744	ENSMUSG00000001435	10	77052178	77166548	-1	10	6	11	70	29	10	0	0	0	0	0	D3Z5C2	
ENSMUST00000149745	ENSMUSG00000039087	13	37778400	37952002	1	0	0	8	41	0	0	13	4	103	0	22		Q3UH06
ENSMUST00000149746						13	18	60	13	15	7	5	9	7	9	16		
ENSMUST00000149747	ENSMUSG00000019338	3	95006590	95015448	-1	0	1	17	0	11	0	0	0	0	0	0	D3Z717	
ENSMUST00000149748						0	1	6	16	3	0	1	2	2	2	2		
ENSMUST00000149749	ENSMUSG00000030982	7	118740226	118842966	1	0	0	0	0	0	0	15	95	27	0	7	F6RR19	
ENSMUST00000149750						3	0	0	6	3	0	57	23	65	1	28		
ENSMUST00000149751						0	0	0	0	0	0	0	0	0	4	0		
ENSMUST00000149752	ENSMUSG00000031626	8	45507788	45827906	1	0	1	5	1	1	0	0	0	0	0	0	D3YTN2	
ENSMUST00000149753						1	2	2	2	4	1	0	0	0	0	0		
ENSMUST00000149754						0	2	0	0	0	2	0	0	0	0	0		
ENSMUST00000149755						3	0	5	3	0	0	24	108	35	64	28		
ENSMUST00000149756	ENSMUSG00000034377	17	6106437	6251128	1	198	177	472	305	200	99	42	69	52	11	108	Q3UH13	
ENSMUST00000149757						13	18	77	12	19	6	0	1	0	0	0		
ENSMUST00000149758						11	6	8	7	7	2	0	0	0	0	0		
ENSMUST00000149759	ENSMUSG00000029177	5	30666777	30674830	1	1	1	4	14	0	0	3	3	3	0	5	A0A0G2JEV0	
ENSMUST00000149760						0	0	0	1	0	0	14	11	7	0	17		
ENSMUST00000149761						0	2	23	9	0	0	0	0	0	0	0		
ENSMUST00000149762						0	1	1	1	0	0	0	0	0	0	1		
ENSMUST00000149763	ENSMUSG00000028785	4	129111570	129122036	-1	0	0	0	0	0	0	16	18	1	0	8	A2A7R5	
ENSMUST00000149764						3	5	4	4	3	0	20	127	34	1	61		
ENSMUST00000149765						4	0	2	3	7	8	8	6	12	2	12		
ENSMUST00000149766						2	3	4	0	2	2	0	2	0	0	0		
ENSMUST00000149767	ENSMUSG00000036580	3	55112108	55137322	1	0	0	1	11	2	0	0	0	3	0	0	D3Z1M5	
ENSMUST00000149768						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149769	ENSMUSG00000030268	6	144993835	145076184	-1	3	0	0	0	2	3	0	0	0	0	0	B2KFA9	
ENSMUST00000149770						6	2	0	119	7	2	7	61	0	12	21		
ENSMUST00000149771						0	0	0	0	0	0	41	212	73	10	89		
ENSMUST00000149773						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000149774	ENSMUSG00000031389	X	73891442	73921870	-1	0	0	0	0	0	0	0	0	0	0	0	F6SL55	
ENSMUST00000149775						2	6	4	5	2	2	0	0	0	0	0		
ENSMUST00000149776	ENSMUSG00000030203	6	134715468	134792625	-1	24	24	31	18	31	11	6	9	14	1	19	Q8BZE4	
ENSMUST00000149777	ENSMUSG00000018677	11	102402985	102407946	-1	0	0	0	0	0	0	4	0	0	0	0	B0QZI4	
ENSMUST00000149778	ENSMUSG00000040532	5	135009152	135012175	1	9	0	11	3	6	0	15	114	36	35	99		
ENSMUST00000149779						0	1	0	2	3	1	0	0	1	0	0		
ENSMUST00000149780						4	7	57	25	6	5	9	26	9	0	49		
ENSMUST00000149781						26	15	34	6	30	9	6	29	11	8	24		
ENSMUST00000149782	ENSMUSG00000092544	8	69742862	69774886	-1	0	0	0	19	0	0	0	0	2	4	0	E9PUR3	
ENSMUST00000149783						0	2	3	0	2	3	0	0	0	0	0		
ENSMUST00000149784						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000149785						0	1	0	90	4	3	0	0	0	0	0		
ENSMUST00000149786						0	0	1	1	1	1	0	5	2	0	1		
ENSMUST00000149787						3	7	24	11	9	5	0	0	0	0	0		
ENSMUST00000149788						11	7	10	6	9	9	1	3	2	2	2		
ENSMUST00000149789	ENSMUSG00000026921	2	26580014	26593120	1	0	0	8	0	0	0	0	0	0	0	1	G3UWX8	
ENSMUST00000149790						5	4	2	0	0	0	0	0	0	0	0		
ENSMUST00000149791	ENSMUSG00000026110	1	37439340	37541016	-1	0	0	0	0	0	0	0	0	3	0	0	D6RG46	
ENSMUST00000149792						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149793						0	0	0	107	0	0	0	0	0	0	0		
ENSMUST00000149794	ENSMUSG00000028410	4	40722150	40737149	1	0	0	2	33	8	0	0	0	0	0	0	B1AXX9	
ENSMUST00000149795						17	13	39	24	10	11	1	0	1	0	0		
ENSMUST00000149796						7	2	13	0	10	5	273	743	378	441	317		
ENSMUST00000149797	ENSMUSG00000022722	16	59612949	59639391	-1	0	0	0	0	3	0	2	0	0	7	2	D3Z067	
ENSMUST00000149798						18	35	98	24	25	5	0	0	2	0	5		
ENSMUST00000149799						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149800	ENSMUSG00000032537	9	101922128	102354693	-1	39	46	171	153	41	14	0	0	0	0	1	Q8CA63	
ENSMUST00000149801						0	2	6	21	5	1	0	0	0	0	0		
ENSMUST00000149802						38	36	71	75	45	30	30	45	39	6	66		
ENSMUST00000149803	ENSMUSG00000063889	18	3266048	3337748	-1	2	0	0	0	2	0	2	0	0	0	0	Q9CQ87	
ENSMUST00000149804						0	1	2	11	5	3	3	88	10	3	15		
ENSMUST00000149805						126	97	802	370	157	62	1	7	9	1	12		
ENSMUST00000149806						6	2	8	4	9	4	3	17	7	3	22		
ENSMUST00000149807	ENSMUSG00000037600	4	133518963	133530790	1	0	0	0	80	0	0	0	0	0	0	1	A2A9F3	
ENSMUST00000149808						3	0	2	0	7	1	2173	1731	1085	170	810		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149809						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149810	ENSMUSG00000026754	2	39016155	39065541	-1	0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000149811						0	0	5	10	4	0	0	0	0	0	1		
ENSMUST00000149812						0	0	0	0	0	0	0	11	0	3	0		
ENSMUST00000149814						0	0	0	51	0	0	0	0	2	0	0		
ENSMUST00000149816						25	0	0	8	0	11	41	474	24	0	19		
ENSMUST00000149818						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149819	ENSMUSG00000089847	7	105640056	105655748	1	0	0	0	0	0	0	6	33	4	8	0	D6RG99	
ENSMUST00000149821						5	2	6	116	7	5	0	1	0	0	0		
ENSMUST00000149823						1	3	2	121	5	3	0	2	0	0	1		
ENSMUST00000149824						1	5	7	8	4	2	0	1	0	0	0		
ENSMUST00000149825	ENSMUSG00000090202	3	146645193	146651317	-1	5	0	15	8	5	1	0	0	0	0	0	G5E8V6	
ENSMUST00000149827						15	4	14	16	21	2	4	61	29	4	54		
ENSMUST00000149828						6	7	5	3	1	1	5	3	5	0	3		
ENSMUST00000149829	ENSMUSG00000045932	19	34550694	34576419	1	5	4	4	0	6	2	0	5	1	0	1	D3YZ80	
ENSMUST00000149831						1	0	0	0	0	0	0	0	3	1	3		
ENSMUST00000149832	ENSMUSG00000038302	10	42312585	42478565	-1	0	0	0	2	0	0	0	1	0	0	0	F6RBS7	
ENSMUST00000149833	ENSMUSG00000022972	16	90925809	90934927	-1	0	0	0	24	3	1	0	0	0	7	10	D3YZC4	
ENSMUST00000149834						0	0	0	0	0	1	21	153	91	19	36		
ENSMUST00000149835	ENSMUSG00000029404	5	124116089	124118196	1	0	3	0	27	6	3	4	3	0	5	6	D3Z668	
ENSMUST00000149836	ENSMUSG00000040809	3	106147554	106167564	-1	0	1	1	0	0	0	2	7	7	19	0	F6RU51	
ENSMUST00000149837						4	5	6	23	5	4	0	0	0	9	0		
ENSMUST00000149838						4	8	12	12	9	1	4	7	16	0	0		
ENSMUST00000149841						0	0	0	0	0	0	59	271	130	85	70		
ENSMUST00000149842						0	7	9	2	1	4	5	26	9	2	15		
ENSMUST00000149843						28	22	103	36	33	20	3	20	10	2	20		
ENSMUST00000149844						3	0	3	3	0	0	0	0	2	0	4		
ENSMUST00000149845	ENSMUSG00000020827	11	70562881	70614483	1	0	0	0	2	0	0	0	0	0	1	0	J3QP32	
ENSMUST00000149846						5	4	8	3	11	2	0	2	0	0	5		
ENSMUST00000149847						8	14	47	53	15	14	18	134	75	4	111		
ENSMUST00000149849						2	4	0	0	6	0	0	0	0	0	0		
ENSMUST00000149850						12	10	0	0	12	10	0	49	0	0	0		
ENSMUST00000149851	ENSMUSG00000030518	7	64756091	65156570	-1	7	8	1	0	1	3	0	0	0	0	0	D3YX96	
ENSMUST00000149852						65	70	200	62	61	30	1	0	3	1	1		
ENSMUST00000149853						0	2	0	1	2	0	0	17	0	0	13		
ENSMUST00000149854	ENSMUSG00000027346	2	132529082	132587729	-1	0	0	13	0	0	0	257	903	552	0	83	D6RGT7	
ENSMUST00000149855	ENSMUSG00000052133	16	35541145	35664732	1	3	2	1	39	3	2	0	0	0	0	0	F6UDD7	
ENSMUST00000149856						24	16	85	42	51	16	0	0	0	0	4		
ENSMUST00000149857						2	0	4	0	6	0	0	0	0	10	0		
ENSMUST00000149858	ENSMUSG00000052087	13	55369732	55384687	1	1	2	7	40	6	3	0	0	6	0	0	D6RCH4	
ENSMUST00000149859						0	0	1	0	0	0	39	377	118	83	25		
ENSMUST00000149860						0	1	0	0	2	2	1	0	0	0	3		
ENSMUST00000149861						0	0	0	4	0	1	0	0	1	0	0		
ENSMUST00000149862						3	2	0	0	6	0	10	2	3	0	17		
ENSMUST00000149863	ENSMUSG00000090110	X	75404846	75416584	-1	0	0	0	0	0	0	2	0	4	3	0	A3KGA5	Q61908
ENSMUST00000149864	ENSMUSG00000029695	6	23072173	23132986	-1	1	2	4	0	0	0	0	0	0	0	0	F6VMP2	
ENSMUST00000149866						1	0	1	2	0	0	0	0	1	0	0		
ENSMUST00000149867	ENSMUSG00000020864	11	94328001	94341841	1	10	13	20	11	6	8	6	37	4	0	17	B7ZC98	
ENSMUST00000149868	ENSMUSG00000033379	4	117884326	117887333	-1	0	0	8	3	1	1	44	189	84	14	117	M0QWE4	
ENSMUST00000149869						1	0	0	0	0	0	3	18	0	9	0		
ENSMUST00000149870						2	0	0	2	6	2	0	0	0	0	0		
ENSMUST00000149871						0	0	0	0	27	0	119	0	95	0	173		
ENSMUST00000149872						1	1	1	19	3	0	0	0	0	0	0		
ENSMUST00000149874						2	0	12	45	9	2	56	54	77	75	94		
ENSMUST00000149875						3	2	3	36	6	2	0	0	0	0	0		
ENSMUST00000149876	ENSMUSG00000030986	7	133720942	133782726	-1	6	3	0	0	0	0	0	0	5	0	0	D3Z255	
ENSMUST00000149877	ENSMUSG00000029428	5	128984557	129008574	-1	2	0	4	0	0	0	0	6	0	0	9	D3YY94	
ENSMUST00000149878						0	0	0	0	4	0	4	44	48	63	72		
ENSMUST00000149880						0	1	0	0	0	2	0	1	0	0	2		
ENSMUST00000149881						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000149882						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000149883						3	4	8	4	6	2	2	12	2	2	3		
ENSMUST00000149884	ENSMUSG00000001018	3	90488026	90491033	-1	0	0	0	62	5	5	0	42	65	86	29		Q9Z266
ENSMUST00000149885	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	D3Z3E5	
ENSMUST00000149886						80	72	332	72	65	45	37	156	35	18	64		
ENSMUST00000149887						0	1	5	3	0	0	0	0	13	0	23		
ENSMUST00000149888						3	4	3	7	11	4	0	1	0	0	0		
ENSMUST00000149890						9	9	14	17	12	7	0	0	0	0	0		
ENSMUST00000149891	ENSMUSG00000041153	4	15997121	16013888	-1	0	0	0	14	0	0	0	9	0	0	0	A2AMG8	
ENSMUST00000149892	ENSMUSG00000022848	16	35694062	35769356	-1	0	0	0	15	0	0	306	484	252	52	186	D6RI31	
ENSMUST00000149893						19	18	123	34	22	9	6	3	9	2	7		
ENSMUST00000149895						2	0	3	6	1	4	0	0	0	0	1		
ENSMUST00000149896						0	0	0	1	1	2	0	0	0	0	0		
ENSMUST00000149897						1	0	3	3	5	1	11	0	16	0	51		
ENSMUST00000149898						1	1	2	7	1	0	0	3	0	4	0		
ENSMUST00000149899						8	6	0	150	15	0	0	0	0	2	17		
ENSMUST00000149900						6	6	19	9	5	3	0	3	2	0	3		
ENSMUST00000149901	ENSMUSG00000022656	16	46387706	46498525	-1	0	1	0	0	0	0	0	0	0	2	1	F7A4R2	
ENSMUST00000149902						1	0	6	0	2	0	0	0	0	0	0		
ENSMUST00000149903	ENSMUSG00000035539	4	45890303	45950774	1	0	5	19	30	10	12	4	27	5	15	7	F6QNN0	
ENSMUST00000149904						3	4	38	3	3	2	0	0	0	0	0		
ENSMUST00000149905						23	20	33	77	31	20	0	21	4	11	4		
ENSMUST00000149907						29	37	53	33	42	23	26	79	36	17	46		
ENSMUST00000149908						0	3	0	1	7	0	2	22	13	2	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000149910						411	327	2219	1022	523	204	0	0	14	0	0		
ENSMUST00000149911						0	1	3	0	4	2	0	0	6	2	2		
ENSMUST00000149912						8	8	27	210	26	14	2	21	0	0	4		
ENSMUST00000149913	ENSMUSG00000055932	8	91313532	91668439	1	2	5	0	0	9	0	0	0	0	0	0	D3Z127	
ENSMUST00000149915						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149916						2	0	0	0	3	0	0	0	0	0	5		
ENSMUST00000149917						0	2	0	0	0	0	0	1	0	0	1		
ENSMUST00000149918	ENSMUSG00000068335	6	83030934	83033471	-1	18	0	39	71	12	12	26	128	23	0	50		
ENSMUST00000149919						0	0	0	0	0	0	0	5	0	10	8		
ENSMUST00000149920						0	0	0	0	0	0	1	0	0	1	0		
ENSMUST00000149921						3	2	7	6	2	3	0	8	5	3	6		
ENSMUST00000149922						2	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000149923						9	4	7	35	7	3	0	0	0	0	0		
ENSMUST00000149924						5	9	2	0	6	2	0	0	0	0	0		
ENSMUST00000149925						0	0	1	135	6	0	0	0	0	0	2		
ENSMUST00000149926	ENSMUSG00000061887	4	106910701	107049694	1	0	0	0	42	0	0	0	0	0	0	0	B1AS34	
ENSMUST00000149927	ENSMUSG00000044768	1	97606318	97662074	-1	0	0	0	4	0	0	1733	6968	1785	1176	1186		Q8VEB3
ENSMUST00000149928						3	0	0	0	2	0	0	0	0	0	5		
ENSMUST00000149929						35	35	52	67	46	29	17	70	17	0	17		
ENSMUST00000149930						5	2	4	0	2	1	9	2	10	0	15		
ENSMUST00000149931	ENSMUSG00000030230	6	139989673	140041457	-1	0	0	0	1	0	0	0	0	0	0	0	D6RCJ4	
ENSMUST00000149933						2	0	0	3	7	1	0	0	0	0	2		
ENSMUST00000149934						1	3	7	2	1	0	3	8	9	3	3		
ENSMUST00000149936						16	14	39	29	9	18	36	547	103	76	111		
ENSMUST00000149937						0	1	3	0	2	3	0	0	0	0	0		
ENSMUST00000149939						3	1	0	2	1	0	0	0	14	10	75		
ENSMUST00000149941						0	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000149943						5	7	15	8	13	2	0	0	0	0	0		
ENSMUST00000149944						3	6	13	9	0	7	4976	24444	4326	5107	1250		
ENSMUST00000149945						15	18	26	15	17	12	1	0	0	0	1		
ENSMUST00000149946						5	4	12	4	11	0	0	6	0	0	0		
ENSMUST00000149947						0	0	0	0	0	0	0	0	0	4	0		
ENSMUST00000149948						0	0	0	22	0	1	0	0	1	0	0		
ENSMUST00000149949	ENSMUSG00000051736	10	39118804	39133914	-1	0	0	0	1	0	0	0	0	0	0	0	B2RVF6	Q8CF36
ENSMUST00000149953						2	0	3	0	3	1	0	18	3	0	0		
ENSMUST00000149954						0	3	0	2	3	0	3	2	9	0	2		
ENSMUST00000149955	ENSMUSG00000027405	2	130274430	130279313	1	0	0	0	0	0	0	6	31	2	5	0	F6USW7	
ENSMUST00000149956	ENSMUSG00000012123	4	134065912	134092504	1	0	0	0	33	1	0	0	5	5	1	13	I7HM00	
ENSMUST00000149957						0	1	4	2	0	6	0	1	0	0	0		
ENSMUST00000149959						0	1	0	29	3	0	0	0	1	0	0		
ENSMUST00000149960						0	5	0	0	0	4	8	60	9	0	28		
ENSMUST00000149961	ENSMUSG00000025350	10	128913593	128922888	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z0N7	
ENSMUST00000149962	ENSMUSG00000026127	1	34439851	34449356	1	0	2	0	0	6	0	3	2	23	15	39	D6RCI8	
ENSMUST00000149963						4	2	0	2	0	1	0	0	0	1	0		
ENSMUST00000149964	ENSMUSG00000016346	2	181075579	181135300	-1	64	38	171	234	84	37	0	2	0	0	1	B7ZBV9	
ENSMUST00000149966	ENSMUSG00000029452	5	121451893	121524183	1	1	1	0	22	1	0	0	0	0	0	0	D3Z5R2	
ENSMUST00000149967	ENSMUSG00000024663	19	10001669	10038380	1	3	2	12	3	2	1	0	0	0	2	2	D3YZ86	
ENSMUST00000149968						4	4	11	9	8	0	0	15	0	2	14		
ENSMUST00000149969						8	0	41	0	0	0	6	11	5	5	26		
ENSMUST00000149970						0	1	37	2	1	1	0	0	0	0	0		
ENSMUST00000149971						9	1	7	4	5	0	9	46	9	12	26		
ENSMUST00000149972						0	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000149973						0	1	0	0	1	0	0	0	3	0	1		
ENSMUST00000149975	ENSMUSG00000053754	14	52198151	52257723	-1	20	7	0	0	0	0	206	555	563	38	273	F7AL76	
ENSMUST00000149976						48	35	260	118	51	33	0	2	3	0	2		
ENSMUST00000149977	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000149979						0	0	0	29	0	0	0	0	0	0	0		
ENSMUST00000149980						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000149981						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000149982						158	165	814	404	249	134	8	43	10	4	25		
ENSMUST00000149983	ENSMUSG00000028124	3	122245557	122270732	1	1	0	1	0	0	0	388	954	513	69	153	F6VNW5	
ENSMUST00000149984						0	2	1	0	1	0	0	0	0	0	0		
ENSMUST00000149985						14	16	114	28	23	7	67	175	102	11	162		
ENSMUST00000149986						2	0	0	0	1	0	2	0	0	0	0		
ENSMUST00000149987						4	3	8	1	9	0	10	24	4	2	14		
ENSMUST00000149988						48	39	77	53	53	34	2	2	0	0	2		
ENSMUST00000149989						1	0	12	0	3	0	64	146	0	25	0		
ENSMUST00000149991						6	9	19	14	17	4	0	0	0	0	3		
ENSMUST00000149992	ENSMUSG00000031601	8	40492540	40515847	-1	11	7	21	34	7	3	42	96	96	32	59	Q543X5	Q60809
ENSMUST00000149993						4	0	11	4	8	3	0	0	0	0	0		
ENSMUST00000149995						3	5	7	4	3	1	0	0	1	0	1		
ENSMUST00000149996	ENSMUSG00000026000	1	67000517	67038872	-1	0	0	0	0	0	0	14	0	0	0	1	B2KGR2	
ENSMUST00000149997						41	30	172	41	36	29	1	0	0	0	1		
ENSMUST00000149998						5	4	3	3	0	3	0	0	0	3	3		
ENSMUST00000149999	ENSMUSG00000031216	X	99003248	99074728	1	2	1	4	3	6	2	0	0	0	0	0	B1AZJ1	
ENSMUST00000150000	ENSMUSG00000024294	18	10725548	10818704	1	0	0	0	0	0	0	14	198	0	10	0	F6YFW9	
ENSMUST00000150001						0	1	3	1	8	1	37	231	102	28	49		
ENSMUST00000150002						1	0	23	4	3	1	0	0	0	0	0		
ENSMUST00000150004						6	2	13	8	4	1	17	12	25	1	13		
ENSMUST00000150006	ENSMUSG00000048922	14	67676331	67715841	-1	15	8	10	0	0	13	35	59	29	7	48		Q14B71
ENSMUST00000150007						4	0	7	8	0	4	7	6	0	0	5		
ENSMUST00000150008						34	42	33	31	45	21	2	13	6	0	9		
ENSMUST00000150009						2	1	4	0	1	2	0	0	1	0	0		
ENSMUST00000150010						2	0	15	5	5	4	4	58	22	0	33		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150011						7	4	0	1	1	0	0	0	0	0	0		
ENSMUST00000150012						3	2	0	3	4	0	0	0	0	0	0		
ENSMUST00000150013	ENSMUSG00000069805	13	62864753	62888282	-1	1	0	0	0	0	0	0	0	1	15	0	F6YS63	
ENSMUST00000150014						808	636	2808	929	1074	539	7	62	29	4	34		
ENSMUST00000150015	ENSMUSG00000020814	11	116803062	116828046	-1	2	0	0	40	3	2	0	0	0	0	0	Q9D1T2	
ENSMUST00000150016						1	5	3	2	3	4	5	2	0	2	2		
ENSMUST00000150017						4	2	26	5	4	0	0	0	0	0	0		
ENSMUST00000150018						0	4	12	0	1	2	4	14	4	15	5		
ENSMUST00000150019	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	181	106	184	88	0	D6REI5	
ENSMUST00000150020						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150021						0	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000150022						6	0	9	20	9	0	799	7944	1247	378	1668		
ENSMUST00000150023	ENSMUSG00000033855	17	88597684	88662586	1	0	2	1	0	0	0	0	0	0	0	0		Q8CDJ8
ENSMUST00000150026	ENSMUSG00000019082	7	141429744	141437892	-1	2	0	1	1	0	0	0	0	0	0	0	G3UY41	
ENSMUST00000150027						9	4	21	14	14	1	2	9	8	6	16		
ENSMUST00000150028						4	0	3	1	3	2	119	178	117	1	108		
ENSMUST00000150029	ENSMUSG00000019854	10	18055861	18125155	1	0	0	0	0	0	0	109	201	52	0	65	F6R6F1	
ENSMUST00000150030						6	4	19	61	11	3	1	0	0	0	1		
ENSMUST00000150031						31	22	51	21	31	22	2	17	10	0	13		
ENSMUST00000150032						1	0	0	0	0	0	0	8	0	0	4		
ENSMUST00000150033	ENSMUSG00000037339	5	33600347	33629635	-1	0	0	0	0	0	0	13	31	3	0	5	D6REV4	
ENSMUST00000150034						2	6	6	0	1	1	0	0	0	0	2		
ENSMUST00000150035						9	12	12	150	17	9	0	0	0	0	2		
ENSMUST00000150036						1	0	0	1	0	0	0	0	1	1	0		
ENSMUST00000150039						2	1	6	0	3	3	2	29	21	3	22		
ENSMUST00000150040	ENSMUSG00000026696	1	162570515	162599084	1	1	2	0	224	2	3	0	12	0	10	0		O70480
ENSMUST00000150041	ENSMUSG00000038236	6	52214491	52221854	-1	3	5	8	186	10	5	0	0	0	0	0	A0A087WR88	
ENSMUST00000150042	ENSMUSG00000030706	7	100545751	100608297	-1	64	54	351	105	60	39	29	93	47	91	34	E9QPQ8	
ENSMUST00000150043						5	8	2	3	8	3	0	0	0	0	0		
ENSMUST00000150044	ENSMUSG00000050854	4	118540941	118544044	-1	3	0	4	9	5	0	0	0	0	0	0	A8WIT2	
ENSMUST00000150045						38	26	76	132	49	18	0	4	1	2	2		
ENSMUST00000150046						0	0	5	0	0	4	361	2386	702	996	1011		
ENSMUST00000150047						0	6	0	0	3	2	0	580	12	28	20		
ENSMUST00000150048						19	19	18	50	23	14	12	26	14	3	10		
ENSMUST00000150049						0	0	0	0	0	1	57	256	2	8	0		
ENSMUST00000150050	ENSMUSG00000074365	7	15882617	15904020	1	27	0	52	0	23	16	0	0	0	0	0	B6ZND8	
ENSMUST00000150051						53	30	24	22	47	26	7	5	5	5	5		
ENSMUST00000150052						28	20	161	49	20	7	1	4	0	0	2		
ENSMUST00000150053						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000150054	ENSMUSG00000057606	14	31523082	31591343	-1	5	10	8	2	2	6	0	0	0	0	0	E9PVR3	
ENSMUST00000150056	ENSMUSG00000050705	17	35892677	35897431	-1	2	1	2	0	1	0	7	32	5	0	0	B8JJ67	
ENSMUST00000150057	ENSMUSG00000020083	10	62107655	62143920	-1	4	7	0	12	0	0	0	0	0	0	0	D3YVG9	
ENSMUST00000150058						0	0	4	3	3	2	0	0	0	0	1		
ENSMUST00000150059	ENSMUSG00000062590	1	86154780	86278284	1	1	1	1	2	2	0	0	4	4	3	0	F7B303	
ENSMUST00000150060	ENSMUSG00000047766	9	60568859	60688158	-1	9	17	22	0	15	2	0	0	8	3	2	D6RIL3	
ENSMUST00000150061	ENSMUSG00000027699	3	27097222	27153878	-1	0	3	0	0	0	0	1	27	1	7	0	H3BL18	
ENSMUST00000150062						1	1	1	0	4	0	0	0	0	0	0		
ENSMUST00000150063	ENSMUSG00000029713	5	137528127	137533510	-1	7	3	20	117	7	4	323	642	283	28	323	Q3U9V4	P62880
ENSMUST00000150065	ENSMUSG00000074358	7	18890883	18910415	-1	5	0	5	0	0	2	0	0	0	0	0	D3Z7J8	
ENSMUST00000150066						5	0	4	18	4	0	0	0	0	1	0		
ENSMUST00000150067						6	2	12	4	1	1	5	6	0	2	17		
ENSMUST00000150068	ENSMUSG00000092470	16	17835277	17891671	-1	21	24	104	53	36	16	12	17	5	0	44	E9Q548	
ENSMUST00000150069						5	2	8	4	7	3	0	6	6	1	5		
ENSMUST00000150070	ENSMUSG00000062908	3	153922357	153944632	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2A5	
ENSMUST00000150071	ENSMUSG00000053091	7	66689889	66717256	1	2	0	5	2	5	1	0	0	0	0	6	D3YU94	
ENSMUST00000150072						1	3	4	2	0	0	1	0	0	0	0		
ENSMUST00000150074	ENSMUSG00000033773	5	107597373	107661838	1	2	6	5	5	8	4	0	0	0	1	1	D3Z2V7	
ENSMUST00000150075						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000150076	ENSMUSG00000060216	11	70432635	70440828	1	0	1	5	0	3	0	72	74	95	5	90	J3QN53	
ENSMUST00000150077						2	0	9	0	10	0	18	12	0	0	0		
ENSMUST00000150078	ENSMUSG00000062175	2	156840007	156855570	1	1	2	9	40	6	3	0	2	1	0	5	H3BJF0	
ENSMUST00000150080						3	1	2	36	3	2	0	0	0	0	0		
ENSMUST00000150081						0	1	1	4	4	2	4	0	0	0	0		
ENSMUST00000150082						43	36	216	72	40	20	0	7	0	0	2		
ENSMUST00000150083						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000150085						0	0	0	0	0	0	0	1	0	0	6		
ENSMUST00000150086						0	0	0	0	0	2	45	43	102	0	62		
ENSMUST00000150087						4	0	3	75	2	11	0	0	0	0	0		
ENSMUST00000150088						2	2	0	3	0	2	0	0	0	0	0		
ENSMUST00000150089	ENSMUSG00000019970	10	21882184	21999903	1	2	1	3	2	1	1	0	0	0	0	19	D3YXA3	
ENSMUST00000150090						9	10	15	5	10	0	3	30	12	4	9		
ENSMUST00000150091						4	3	0	0	0	3	8	12	0	0	0		
ENSMUST00000150092	ENSMUSG00000059142	17	22846697	22867134	-1	1	0	0	0	0	0	0	5	5	0	1	Q8BNS8	
ENSMUST00000150093	ENSMUSG00000032519	9	120110374	120124504	1	0	0	0	0	3	0	0	4	0	0	0	D6RCX1	
ENSMUST00000150094						6	11	38	15	24	4	0	0	17	3	26		
ENSMUST00000150095						0	0	0	6	0	0	18	105	91	0	74		
ENSMUST00000150096	ENSMUSG00000033295	4	118208213	118291405	-1	17	0	0	4	19	0	0	0	0	0	0	F6Y3V0	
ENSMUST00000150097	ENSMUSG00000040785	16	94370618	94469222	1	0	0	2	0	2	2	0	0	0	0	0	D3Z330	
ENSMUST00000150098						1	1	10	1	2	1	0	0	0	0	0		
ENSMUST00000150100						0	0	2	0	0	0	4	0	8	2	13		
ENSMUST00000150101						18	2	33	4	8	4	19	145	32	7	29		
ENSMUST00000150102	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0	D3YUT0	
ENSMUST00000150103						2	0	4	25	0	0	3	19	0	19	7		
ENSMUST00000150104						0	0	0	0	0	0	0	4	4	4	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150105						35	30	75	46	41	9	18	41	20	6	36		
ENSMUST00000150106	ENSMUSG00000042078	5	114026910	114091570	-1	3	5	10	19	3	6	0	0	0	0	0	D3Z379	
ENSMUST00000150107						1	8	6	3	3	0	6	4	10	2	56		
ENSMUST00000150108						0	0	0	0	0	0	0	222	0	0	0		
ENSMUST00000150109						1	0	0	0	0	1	1	0	0	0	2		
ENSMUST00000150110	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	0	47	20	0	0	D6RG88	
ENSMUST00000150113						0	0	0	1	0	0	0	2	0	0	0		
ENSMUST00000150114						33	22	11	14	30	14	0	3	3	0	9		
ENSMUST00000150115						0	1	0	0	3	0	0	31	0	0	0		
ENSMUST00000150116						0	1	0	0	0	0	0	0	8	0	0		
ENSMUST00000150117						1	2	5	0	0	0	6	12	17	19	34		
ENSMUST00000150118						1	0	11	1	0	0	3	4	7	0	4		
ENSMUST00000150120	ENSMUSG00000023505	6	124829547	124833701	1	0	0	0	7	2	0	122	66	91	113	32	D3Z3H6	
ENSMUST00000150121						0	0	0	0	0	0	0	6	7	0	5		
ENSMUST00000150122						6	2	7	60	15	5	2	42	13	0	25		
ENSMUST00000150123						5	2	10	66	10	0	0	0	0	0	0		
ENSMUST00000150124						851	707	774	695	928	366	63	200	101	23	168		
ENSMUST00000150125						1	0	12	47	7	1	0	0	0	0	0		
ENSMUST00000150126						3	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000150127						7	28	27	59	16	0	0	0	0	0	0		
ENSMUST00000150128	ENSMUSG00000014633	8	116888685	116921455	-1	1365	1066	217	288	975	231	78	109	2	83	26	D6RJ47	
ENSMUST00000150129						11	5	14	14	8	2	0	0	4	1	7		
ENSMUST00000150130	ENSMUSG00000037426	5	32863701	32994236	1	0	0	0	0	0	0	4	0	6	0	3	D3Z419	
ENSMUST00000150132						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150133						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000150134	ENSMUSG00000050860	11	95824499	95832140	1	0	3	2	133	4	4	761	1369	1119	114	883	F6Y6Q2	
ENSMUST00000150135	ENSMUSG00000028944	5	24862744	25100642	-1	0	0	0	13	1	0	8	0	11	0	8	D3YUS1	
ENSMUST00000150137						2	2	3	2	2	2	0	137	693	5242	851		
ENSMUST00000150139	ENSMUSG00000029101	5	34949445	35039644	1	3	3	7	5	9	5	0	0	0	0	0	F6YRR2	
ENSMUST00000150140						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000150141						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150142	ENSMUSG00000006576	1	75546266	75562172	1	0	0	0	43	0	0	0	0	0	0	0	D3YWK8	
ENSMUST00000150143						4	3	1	3	5	5	0	0	0	0	0		
ENSMUST00000150144						2	4	2	2	6	8	0	0	0	0	0		
ENSMUST00000150146	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000150147						39	30	78	55	33	33	8	14	11	2	20		
ENSMUST00000150148						8	5	12	6	4	1	0	0	0	0	0		
ENSMUST00000150150	ENSMUSG00000073705	4	149127121	149137629	-1	0	1	4	1	0	1	0	0	0	0	3	A6PWQ1	
ENSMUST00000150151						5	1	11	6	9	2	1	3	0	0	2		
ENSMUST00000150152						3	0	2	1	3	0	1	4	2	0	1		
ENSMUST00000150153						0	0	0	0	0	0	48	376	150	70	143		
ENSMUST00000150155	ENSMUSG00000029442	5	123252102	123327484	1	37	31	48	15	18	11	0	0	2	0	0	F6W2U4	
ENSMUST00000150156						3	6	0	0	4	7	0	0	0	1	0		
ENSMUST00000150157						0	0	0	0	0	0	144	652	36	32	19		
ENSMUST00000150158	ENSMUSG00000055491	19	46044886	46072915	1	0	0	0	0	3	0	0	0	0	0	0	D3YYR7	
ENSMUST00000150160						37	24	52	28	33	23	16	16	19	1	25		
ENSMUST00000150161						9	12	19	3	3	6	445	976	1034	47	1437		
ENSMUST00000150162						0	3	0	0	2	0	28	0	12	5	7		
ENSMUST00000150163	ENSMUSG00000041605	1	136213531	136234264	-1	0	4	0	0	3	0	0	0	0	0	0	D3YZL7	
ENSMUST00000150165						5	4	17	0	0	0	31	41	8	151	18		
ENSMUST00000150166						6	1	7	8	11	4	2	4	3	0	3		
ENSMUST00000150167	ENSMUSG00000049723	9	7344381	7369499	1	0	0	0	0	1	1	0	0	0	0	0	D3Z705	
ENSMUST00000150168						0	0	0	0	0	0	0	151	0	0	0		
ENSMUST00000150169						0	12	25	41	6	3	0	0	0	2	0		
ENSMUST00000150170						32	9	37	482	53	37	1	0	0	0	0		
ENSMUST00000150172						11	14	114	15	17	8	2	3	9	0	6		
ENSMUST00000150174						1	2	2	5	7	1	28	29	69	52	61		
ENSMUST00000150175	ENSMUSG00000063524	4	150236721	150248879	1	0	0	2	20	2	0	6	6	3	4	5	B1ARR7	
ENSMUST00000150176						1	3	4	0	0	0	7	0	0	8	4		
ENSMUST00000150177						0	0	0	0	0	1	0	26	8	0	2		
ENSMUST00000150179						3	5	5	4	4	1	0	0	4	0	1		
ENSMUST00000150180	ENSMUSG00000033174	6	88724412	88828360	1	4	0	5	122	4	1	4	2	0	0	0		
ENSMUST00000150182	ENSMUSG00000002265	7	6703892	6730421	-1	0	0	0	37	0	6	0	0	0	0	0	D6RGA4	
ENSMUST00000150183	ENSMUSG00000027160	2	110017817	110173360	1	18	10	9	3	16	3	0	1	0	0	0	F6U3Z3	
ENSMUST00000150184	ENSMUSG00000001827	7	101858331	101870788	-1	9	1	34	4	3	1	0	0	0	0	0	Q9R223	
ENSMUST00000150187						1	3	1	5	2	0	12	3	1	3	6		
ENSMUST00000150188	ENSMUSG00000053801	7	45825227	45830944	-1	0	16	30	0	18	2	0	15	0	13	21	F7CPC6	
ENSMUST00000150189						1	1	0	2	0	2	0	0	0	0	0		
ENSMUST00000150190						0	0	3	3	1	0	3	2	9	0	7		
ENSMUST00000150191						1	1	1	2	0	0	0	16	0	59	17		
ENSMUST00000150192						0	1	3	0	0	0	0	8	4	0	2		
ENSMUST00000150193						2	0	2	0	0	4	0	2	0	0	0		
ENSMUST00000150194						0	2	0	0	0	0	0	3	0	0	1		
ENSMUST00000150196						2	2	2	67	7	2	0	0	0	0	0		
ENSMUST00000150197						0	0	6	0	0	4	0	0	0	0	0		
ENSMUST00000150199						0	1	23	0	7	3	0	4	0	0	9		
ENSMUST00000150200						2	0	4	3	0	0	0	0	0	1	0		
ENSMUST00000150201						0	0	0	0	0	0	84	87	157	6	98		
ENSMUST00000150204	ENSMUSG00000033379	4	117884326	117887333	-1	3	0	0	0	0	0	0	0	0	0	0	A0A0A0MQJ5	
ENSMUST00000150205						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000150206						41	38	108	26	31	19	12	27	34	0	45		
ENSMUST00000150207	ENSMUSG00000054405	4	132535550	132553742	1	0	0	0	0	0	0	66	20	0	7	8	F6TQL3	
ENSMUST00000150208						4	1	14	8	2	6	30	149	59	0	98		
ENSMUST00000150209						2	3	1	3	0	0	0	9	3	1	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150210						2	0	1	3	1	1	8	57	17	37	11		
ENSMUST00000150211						4	8	12	3	5	0	3	2	0	0	0		
ENSMUST00000150212	ENSMUSG00000027628	2	156547584	156568972	1	0	0	0	0	0	0	0	0	0	0	0	B7ZD25	
ENSMUST00000150213						0	0	52	30	15	0	0	597	256	33	398		
ENSMUST00000150214						0	1	0	0	2	0	74	131	37	108	35		
ENSMUST00000150215						26	12	26	442	29	10	2	1	2	1	1		
ENSMUST00000150217	ENSMUSG00000068329	6	83051266	83055273	-1	0	0	0	0	0	0	52	9	0	0	9	F6XUR8	
ENSMUST00000150218						16	12	46	22	17	10	0	0	0	0	7		
ENSMUST00000150219						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000150221						1	0	1	0	2	0	0	0	1	0	0		
ENSMUST00000150222						14	15	62	6	16	6	0	0	0	0	0		
ENSMUST00000150223						1	2	0	50	0	4	1	1	2	0	1		
ENSMUST00000150224						2	3	9	15	3	1	2	12	2	0	15		
ENSMUST00000150225						11	8	14	5	16	4	16	53	26	3	35		
ENSMUST00000150226	ENSMUSG00000029310	5	104046306	104065379	1	0	0	8	0	4	0	9	17	21	24	0	A2AH27	
ENSMUST00000150227						18	14	22	6	18	7	0	0	1	0	4		
ENSMUST00000150228						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000150229						2	2	4	2	4	0	0	0	1	0	6		
ENSMUST00000150230						25	23	38	48	28	18	6	7	9	0	10		
ENSMUST00000150232	ENSMUSG00000027282	2	90847155	90866810	1	0	0	0	0	0	6	71	0	0	298	77	Q9D050	
ENSMUST00000150234						1	3	0	15	9	5	0	0	0	0	0		
ENSMUST00000150235	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	8	0	1	0	9	0	19	0		P27699
ENSMUST00000150236	ENSMUSG00000002871	6	88902251	88912238	1	0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000150237						2	0	3	0	0	0	0	4	3	0	5		
ENSMUST00000150238						8	8	7	4	11	12	0	0	0	0	0		
ENSMUST00000150240						4	5	6	1	6	5	3	0	18	0	0		
ENSMUST00000150241						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000150242						48	40	120	71	48	26	6	29	9	12	23		
ENSMUST00000150243						1	1	2	3	3	1	15	118	69	93	178		
ENSMUST00000150244	ENSMUSG00000034218	9	53439149	53536740	-1	1	0	0	2	1	0	0	0	0	0	0	D3Z0Q2	
ENSMUST00000150245						1	0	0	2	3	1	2	0	0	0	2		
ENSMUST00000150247	ENSMUSG00000047495	8	14095865	14847680	1	8	0	23	0	4	0	0	0	0	0	0		Q8BJ42
ENSMUST00000150248						0	0	0	0	2	0	1	0	0	0	0		
ENSMUST00000150249						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150250						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150253	ENSMUSG00000000325	16	18348182	18407076	1	0	0	0	18	0	1	0	7	0	2	1	D6RI19	
ENSMUST00000150254	ENSMUSG00000028556	4	98936671	99120915	-1	0	0	0	0	0	0	0	0	0	0	0	F6ZJ55	
ENSMUST00000150257						4	7	20	4	7	6	0	5	9	0	18		
ENSMUST00000150258	ENSMUSG00000020097	10	61098642	61147703	-1	15	0	45	33	36	0	0	183	27	0	161	D6REF7	
ENSMUST00000150259						111	82	770	162	94	62	7	25	14	5	17		
ENSMUST00000150260						31	25	52	244	42	18	0	0	0	0	2		
ENSMUST00000150261	ENSMUSG00000027082	2	84432855	84476775	-1	0	0	0	0	0	0	0	0	0	4	0	A2ARA4	
ENSMUST00000150262						1	6	6	4	11	0	0	0	0	0	0		
ENSMUST00000150264						9	5	7	1	6	1	0	0	0	9	7		
ENSMUST00000150266						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000150267	ENSMUSG00000024581	18	62977836	62999450	1	3	0	0	0	0	0	8	8	37	56	36	D3Z4B2	
ENSMUST00000150268	ENSMUSG00000027998	3	83055522	83072355	1	0	0	17	13	5	0	104	607	291	457	246		Q922V4
ENSMUST00000150269	ENSMUSG00000020251	10	82650433	82690650	-1	1	1	0	3	1	0	0	0	0	0	0	F6U4D1	
ENSMUST00000150271	ENSMUSG00000000308	2	121357714	121363737	1	5	0	3	0	0	0	0	0	0	0	0	A2ARP5	
ENSMUST00000150272						6	15	17	12	13	6	7	25	33	19	42		
ENSMUST00000150274						2	0	0	2	1	0	0	0	1	0	0		
ENSMUST00000150275	ENSMUSG00000043372	11	103132429	103139876	1	1	2	4	84	4	4	1	2	8	1	7	A2AB66	
ENSMUST00000150277						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150278	ENSMUSG00000044378	6	137983586	138079916	-1	1	1	1	3	1	1	0	0	0	0	0		
ENSMUST00000150279	ENSMUSG00000030094	6	91489305	91515888	-1	23	19	38	43	28	14	18	63	42	4	113		
ENSMUST00000150280						2	7	14	15	11	5	0	0	2	0	3		
ENSMUST00000150281	ENSMUSG00000029534	6	17692933	17943025	1	0	0	0	0	0	0	0	9	0	8	0	D6RHR0	
ENSMUST00000150282	ENSMUSG00000015202	10	7119063	7212237	-1	5	3	0	1	3	0	3	16	0	5	0		Q8BMA3
ENSMUST00000150283						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000150284	ENSMUSG00000046311	11	49203292	49218816	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDA7	
ENSMUST00000150285	ENSMUSG00000028521	4	103170649	103215164	-1	38	19	20	258	38	0	0	10	27	0	10	Q8BX24	
ENSMUST00000150286						0	2	0	0	1	0	0	0	0	1	0		
ENSMUST00000150288						18	20	23	29	26	14	6	52	0	3	18		
ENSMUST00000150289						8	0	0	12	0	0	0	0	2	0	0		
ENSMUST00000150290	ENSMUSG00000050335	14	47367751	47386160	1	0	5	0	18	0	0	12280	20699	8226	7918	4746	Q8C253	
ENSMUST00000150291						0	3	0	0	0	0	1	0	10	0	9		
ENSMUST00000150292						6	10	60	27	7	6	0	4	0	1	0		
ENSMUST00000150293						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150295						22	9	13	22	26	7	0	0	0	0	0		
ENSMUST00000150296	ENSMUSG00000040040	14	57424062	57517936	1	2	0	0	19	2	0	0	0	4	0	2	D6RJ41	
ENSMUST00000150297	ENSMUSG00000009894	11	59407134	59451186	-1	0	4	2	10	0	0	0	4	0	1	0	B2FDF7	
ENSMUST00000150298						0	0	0	0	0	0	0	0	0	0	10		
ENSMUST00000150299						7	0	5	17	4	2	0	0	0	0	0		
ENSMUST00000150300	ENSMUSG00000038665	6	36846022	37300184	-1	13	5	12	0	23	6	0	0	0	0	0	S4R215	
ENSMUST00000150301						3	0	0	0	1	0	5	0	7	4	1		
ENSMUST00000150302	ENSMUSG00000080316	17	17830719	17843009	1	0	0	0	0	0	0	0	0	0	0	0	J3QMI7	
ENSMUST00000150303	ENSMUSG00000064068	3	89209081	89227088	-1	1	1	13	18	1	1	2	3	2	0	4	G3UZR5	
ENSMUST00000150304						0	0	0	0	1	0	0	0	0	3	0		
ENSMUST00000150305						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150306						21	12	60	9	18	17	0	17	3	0	12		
ENSMUST00000150307	ENSMUSG00000031778	8	94772009	94782423	1	4	2	0	0	2	0	0	0	0	0	0	D6RCV0	
ENSMUST00000150308						2	1	5	0	0	1	0	0	4	0	0		
ENSMUST00000150309	ENSMUSG00000070972	4	58995062	59025573	1	0	0	0	0	0	0	0	0	0	0	0	F2Z3Z8	
ENSMUST00000150310						41	30	31	33	48	18	53	156	87	21	107		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150311	ENSMUSG00000030720	7	126571207	126585817	-1	1	1	1	2	4	0	113	242	187	14	133	D3Z6L5	
ENSMUST00000150313						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150315						0	0	0	0	0	0	4	2	4	0	4		
ENSMUST00000150316	ENSMUSG00000002728	2	145902099	145916425	1	1	0	1	0	1	0	0	3	0	0	0	E9Q023	
ENSMUST00000150317	ENSMUSG00000063450	12	75818134	76110926	1	8	0	0	43	8	0	0	0	0	0	0	Q6ZWN0	
ENSMUST00000150318						2	2	25	3	1	1	0	0	0	0	0		
ENSMUST00000150319						1	0	4	2	7	1	5	21	6	6	2		
ENSMUST00000150320						5	9	5	5	8	8	26	50	75	4	70		
ENSMUST00000150321						1	4	5	16	2	3	0	0	0	0	0		
ENSMUST00000150322						9	6	18	86	11	8	6	16	0	0	4		
ENSMUST00000150324	ENSMUSG00000061046	17	25779843	25785673	-1	0	0	0	0	0	0	47	0	45	0	4		Q9DB32
ENSMUST00000150325	ENSMUSG00000027078	2	84798828	84810335	1	0	0	0	0	0	0	0	0	0	3	2	A2ATR9	
ENSMUST00000150326						10	8	37	21	20	5	3	8	4	2	3		
ENSMUST00000150327						0	0	0	0	0	0	8	0	13	0	14		
ENSMUST00000150328						11	0	7	1	2	0	143	81	140	0	129		
ENSMUST00000150330						0	0	0	15	0	0	52	15	0	0	0		
ENSMUST00000150331						6	1	4	1	6	2	0	0	0	0	0		
ENSMUST00000150332						8	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000150333	ENSMUSG00000045983	16	20668313	20692884	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150334						5	2	9	1	10	0	0	0	0	0	0		
ENSMUST00000150335	ENSMUSG00000011096	7	44848991	44855421	1	0	0	0	0	0	0	0	0	0	0	0	D3Z4R0	
ENSMUST00000150336	ENSMUSG00000005267	11	62700356	62731905	-1	37	33	76	82	51	28	4	6	8	0	14	Q3UZW0	
ENSMUST00000150338	ENSMUSG00000061589	10	80755206	80795461	1	0	0	25	0	0	2	0	0	27	0	0	F7CVL0	
ENSMUST00000150339						0	1	0	1	0	4	0	0	0	0	0		
ENSMUST00000150340						2	3	17	2	8	2	0	2	0	0	7		
ENSMUST00000150341						3	1	8	6	3	4	0	0	0	0	0		
ENSMUST00000150342						3	2	19	40	3	4	3	16	7	0	5		
ENSMUST00000150344	ENSMUSG00000036099	10	93939165	94035817	-1	0	0	0	0	0	0	0	0	0	0	0	F7CPT8	
ENSMUST00000150346	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	D3Z485	
ENSMUST00000150347						8	4	16	52	3	1	0	0	0	0	0		
ENSMUST00000150348						6	4	7	4	3	2	2	4	0	0	2		
ENSMUST00000150349						1	0	1	76	3	0	3	1	0	0	0		
ENSMUST00000150350	ENSMUSG00000074129	7	45125565	45128745	-1	9	7	8	29	16	0	778	1261	560	766	409	Q5M9M0	P19253
ENSMUST00000150351						0	0	0	0	0	0	3	2	0	5	5		
ENSMUST00000150352	ENSMUSG00000021661	13	98263158	98274750	1	11	3	8	20	8	13	0	34	8	9	13	Q6AXE4	
ENSMUST00000150353						2	3	0	2	1	0	5	0	1	0	5		
ENSMUST00000150354	ENSMUSG00000005981	16	4039971	4077827	-1	0	0	0	0	0	0	1	0	0	0	0	S4R1P4	
ENSMUST00000150355						8	4	19	4	18	0	0	0	0	0	6		
ENSMUST00000150356						8	3	13	258	19	10	0	4	10	0	3		
ENSMUST00000150357	ENSMUSG00000028795	4	129619274	129623947	-1	0	0	0	0	0	0	0	0	0	0	0	A2AE01	
ENSMUST00000150358						0	0	0	12	5	3	0	0	0	0	0		
ENSMUST00000150359	ENSMUSG00000050050	5	92607954	92675271	-1	8	9	55	13	19	6	0	2	1	0	1		Q8CDI6
ENSMUST00000150360	ENSMUSG00000045917	4	63558781	63586357	1	0	0	0	0	0	0	57	7	19	0	8	Z4YLK8	
ENSMUST00000150361	ENSMUSG00000029561	5	114896936	114912234	1	0	2	0	0	0	0	7	12	3	0	36	D3Z324	
ENSMUST00000150362						2	0	4	0	2	2	0	0	0	0	0		
ENSMUST00000150363						2	0	11	2	5	1	3	3	4	0	3		
ENSMUST00000150365	ENSMUSG00000029772	6	29768011	29912310	1	6	5	12	120	13	10	2	4	0	0	2	E9PX77	
ENSMUST00000150368						0	0	0	0	0	0	0	0	60	23	68		
ENSMUST00000150369						10	4	2	0	3	4	3	178	3	2	14		
ENSMUST00000150370						0	1	1	1	3	0	38	111	65	41	40		
ENSMUST00000150371	ENSMUSG00000022185	14	54642161	54686931	-1	0	0	0	0	24	0	10	0	0	0	31	B8JJ91	
ENSMUST00000150372						0	1	4	12	0	0	7	4	0	10	4		
ENSMUST00000150373						1	1	0	1	4	2	1	0	0	0	0		
ENSMUST00000150374	ENSMUSG00000000766	10	6758506	7038198	1	0	1	0	1	0	0	0	0	0	0	0	Q4U2P1	
ENSMUST00000150376						0	2	0	0	0	0	11	14	8	0	8		
ENSMUST00000150377	ENSMUSG00000020868	11	94663851	94677515	-1	0	1	9	1	2	0	1	5	0	0	0	G3UZH1	
ENSMUST00000150378	ENSMUSG00000020883	11	98082556	98150403	-1	5	3	11	112	7	2	5	4	5	1	2	A2A536	
ENSMUST00000150379	ENSMUSG00000036893	2	24789928	24919614	-1	2	4	3	0	0	0	0	0	0	0	14	Q8BRN2	
ENSMUST00000150380						4	2	6	25	3	5	0	0	0	0	1		
ENSMUST00000150381	ENSMUSG00000020282	11	32209585	32222300	-1	0	1	0	0	0	0	0	0	0	0	0	A2AVE4	
ENSMUST00000150383						5	1	12	3	2	0	0	2	0	0	0		
ENSMUST00000150384	ENSMUSG00000087075	12	111406809	111412077	1	4	4	14	32	12	2	0	0	0	0	0	G3UW55	
ENSMUST00000150386						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000150387	ENSMUSG00000030357	6	128429735	128438677	-1	2	0	0	54	7	0	46	22	46	0	22	F6S2D5	
ENSMUST00000150390						11	14	30	11	21	10	78	175	120	22	215		
ENSMUST00000150391						3	0	21	0	0	0	4	10	0	4	16		
ENSMUST00000150392						41	36	20	154	48	26	1	3	1	0	1		
ENSMUST00000150393	ENSMUSG00000023051	15	102518192	102523676	1	0	0	2	24	3	0	0	6	8	0	0	D3Z033	
ENSMUST00000150394						0	0	2	0	0	0	0	0	0	0	6		
ENSMUST00000150395	ENSMUSG00000035919	9	22475715	22888280	1	0	0	0	0	0	0	0	139	83	0	0		Q811G0
ENSMUST00000150396	ENSMUSG00000017858	2	163017354	163046141	1	0	2	3	29	0	4	8	30	35	11	23	F6RBL8	
ENSMUST00000150397						0	0	0	0	1	0	0	13	1	0	0		
ENSMUST00000150398						1	0	0	0	0	1	0	0	1	3	6		
ENSMUST00000150399	ENSMUSG00000033819	15	76671615	76694919	1	0	0	16	0	0	0	52	37	51	8	52	Q8CFW6	
ENSMUST00000150400						125	130	264	222	112	59	9	23	24	0	34		
ENSMUST00000150401	ENSMUSG00000027405	2	130274430	130279313	1	0	1	0	0	10	0	0	33	0	5	0	F6V095	
ENSMUST00000150402						2	2	1	30	2	2	0	0	0	0	0		
ENSMUST00000150403	ENSMUSG00000002103	2	91202885	91214098	1	2	0	0	3	2	0	7	0	4	14	17	B7ZCF5	
ENSMUST00000150404	ENSMUSG00000026921	2	26580014	26593120	1	0	0	0	0	0	0	4	6	5	0	0	Q3UTJ7	
ENSMUST00000150405						3	1	0	1	7	0	0	0	0	1	0		
ENSMUST00000150406	ENSMUSG00000029703	5	136122772	136136074	-1	0	0	1	4	4	0	11	0	39	0	0	H9KV12	
ENSMUST00000150407						49	47	89	86	71	22	7	51	17	10	24		
ENSMUST00000150408						1	0	2	4	2	0	0	1	0	0	0		
ENSMUST00000150409						5	2	10	103	10	2	3	2	2	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150410						0	0	0	32	0	0	3	0	0	0	0		
ENSMUST00000150411						7	3	3	13	2	4	0	3	1	0	1		
ENSMUST00000150412	ENSMUSG00000089945	4	57568179	57896984	1	5	0	3	95	23	11	0	0	0	0	36	F7AA26	
ENSMUST00000150413						0	0	2	12	1	0	0	0	0	0	0		
ENSMUST00000150414						14	5	36	5	10	10	9	5	0	0	0		
ENSMUST00000150416						4	0	0	2	0	0	178	333	130	60	98		
ENSMUST00000150417						1	0	5	2	7	1	2	9	9	0	10		
ENSMUST00000150419						3	1	2	4	0	5	46	110	44	11	94		
ENSMUST00000150420						1	0	0	0	0	0	0	0	3	0	0		
ENSMUST00000150421	ENSMUSG00000023072	7	35397035	35438689	1	4	0	8	0	4	1	0	5	0	52	8	F6RCX2	
ENSMUST00000150422						0	0	0	25	0	0	0	0	0	0	0		
ENSMUST00000150423						14	10	20	12	23	0	0	0	0	0	0		
ENSMUST00000150424						0	0	0	0	0	0	101	475	240	42	145		
ENSMUST00000150425						8	4	10	8	12	4	0	0	0	0	1		
ENSMUST00000150426						1	5	2	2	0	1	2	1	5	0	3		
ENSMUST00000150427						0	3	0	8	0	2	0	0	0	0	0		
ENSMUST00000150428						27	14	22	19	29	11	0	0	0	0	0		
ENSMUST00000150429						2	3	0	2	1	0	0	0	0	0	0		
ENSMUST00000150430						4	4	3	5	10	1	0	18	7	0	15		
ENSMUST00000150431						5	4	21	143	10	11	12	64	45	4	63		
ENSMUST00000150432	ENSMUSG00000020027	10	95385362	95417180	-1	6	0	2	5	4	3	0	0	0	0	5	D3Z355	
ENSMUST00000150433						1	5	2	0	2	1	2	0	0	2	0		
ENSMUST00000150434	ENSMUSG00000063663	X	108737016	108834372	-1	2	7	9	0	13	4	254	170	81	52	141		A2AHJ4
ENSMUST00000150435						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150436						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150437						0	0	3	68	7	0	3	5	5	6	0		
ENSMUST00000150438	ENSMUSG00000044221	5	88659448	88676171	-1	0	0	5	6	2	0	0	0	0	0	0	D3YZS7	
ENSMUST00000150439						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000150440	ENSMUSG00000029290	5	105876565	105915818	1	0	0	0	1	0	0	11	25	41	3	42	D3YXQ7	
ENSMUST00000150441						1	4	5	12	3	3	1	10	0	0	5		
ENSMUST00000150443						0	1	2	0	0	2	13	11	30	0	10		
ENSMUST00000150444						4	0	3	0	0	3	83	25	88	0	63		
ENSMUST00000150445						6	2	22	94	5	0	0	0	0	0	0		
ENSMUST00000150446						0	0	0	66	0	0	0	0	0	4	0		
ENSMUST00000150447						17	7	23	81	16	14	8	1	0	0	5		
ENSMUST00000150448						0	1	0	37	1	2	0	0	1	0	0		
ENSMUST00000150449	ENSMUSG00000001768	2	145784734	145887616	1	3	5	5	3	3	4	0	0	0	0	0	E0CYG9	
ENSMUST00000150451						41	55	105	46	42	28	4	21	6	9	13		
ENSMUST00000150452						3	5	1	6	2	3	1	1	2	0	2		
ENSMUST00000150453	ENSMUSG00000051359	15	37366175	37792570	-1	0	3	3	43	3	1	0	0	0	0	0	D3Z1M0	
ENSMUST00000150454						2	1	10	5	10	1	0	0	0	0	0		
ENSMUST00000150456	ENSMUSG00000024048	17	70993656	71002878	-1	0	0	1	1	3	4	27	56	19	0	61	D3YV37	
ENSMUST00000150457						9	10	16	15	7	2	0	0	0	0	0		
ENSMUST00000150458	ENSMUSG00000042988	11	120653788	120661175	-1	4	0	8	72	6	1	0	0	0	0	0	B7ZCA6	
ENSMUST00000150459	ENSMUSG00000087651	10	83722865	83762761	1	8	6	5	23	10	5	0	1	0	2	2		P0C913
ENSMUST00000150460						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000150461						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150462	ENSMUSG00000068735	2	93187548	93201759	1	0	0	0	39	0	0	0	0	0	0	0	A2AGS6	
ENSMUST00000150463						5	2	14	62	8	4	0	2	0	0	0		
ENSMUST00000150464						4	1	0	37	4	3	0	0	0	0	0		
ENSMUST00000150465						1	0	0	0	0	2	0	2	1	0	0		
ENSMUST00000150467						0	2	1	2	3	0	0	0	0	0	0		
ENSMUST00000150468						6	8	14	5	8	2	16	42	25	9	13		
ENSMUST00000150469	ENSMUSG00000058392	17	32036100	32062865	1	1	0	2	2	5	2	0	6	9	1	12	F7AGW8	
ENSMUST00000150470	ENSMUSG00000079173	5	137378637	137477064	-1	1	3	5	4	6	3	0	0	0	0	0	F7ACV3	
ENSMUST00000150473	ENSMUSG00000026843	2	31572651	31617526	1	5	2	44	0	0	0	8	0	2	9	4	F6W2V3	
ENSMUST00000150474						0	0	0	0	0	0	0	2	0	0	8		
ENSMUST00000150476	ENSMUSG00000030741	7	126370060	126377450	-1	0	0	0	6	0	0	0	0	0	0	3	D3YWU4	
ENSMUST00000150477						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150479	ENSMUSG00000089847	7	105640056	105655748	1	0	1	3	10	0	0	3	92	21	39	14	D6RJ48	
ENSMUST00000150480						23	18	77	38	27	17	1	9	1	4	3		
ENSMUST00000150481	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	0	0	0	0	0	D3Z2V1	
ENSMUST00000150483	ENSMUSG00000024431	18	39410545	39491301	-1	1	0	0	0	2	1	0	0	2	1	1	D3Z280	
ENSMUST00000150484						0	0	3	0	0	0	1	0	0	0	1		
ENSMUST00000150485						2	3	3	3	5	3	7	7	2	11	0		
ENSMUST00000150486						6	1	14	4	2	0	0	0	0	1	0		
ENSMUST00000150487						3	1	5	0	4	0	0	0	0	0	0		
ENSMUST00000150488	ENSMUSG00000039375	8	54629055	54887184	-1	0	0	4	0	0	1	0	0	0	0	0	Q8C8Y2	
ENSMUST00000150489	ENSMUSG00000041708	15	83779467	83858494	1	2	4	4	4	7	0	0	0	0	0	0	F7BTE7	
ENSMUST00000150490						73	50	458	152	68	45	0	2	0	0	3		
ENSMUST00000150491						0	1	5	6	10	2	7	6	5	6	8		
ENSMUST00000150492						0	0	0	2	0	0	0	0	0	0	2		
ENSMUST00000150493						11	3	4	2	9	3	0	0	0	0	9		
ENSMUST00000150494	ENSMUSG00000050921	X	107088492	107104974	1	5	0	0	0	5	0	0	8	0	19	18	F6SDQ0	
ENSMUST00000150495						8	2	25	5	3	6	0	0	0	0	0		
ENSMUST00000150496						2	2	6	49	3	3	0	1	0	1	3		
ENSMUST00000150497						4	0	10	5	8	3	28	57	19	70	34		
ENSMUST00000150498	ENSMUSG00000069171	13	78188973	78199757	-1	9	5	50	17	15	4	0	0	0	4	6	B8JJI9	
ENSMUST00000150499						2	3	17	3	8	0	0	93	27	13	37		
ENSMUST00000150500						0	0	0	0	0	0	16	0	7	8	6		
ENSMUST00000150501						4	3	11	27	3	2	0	0	0	2	2		
ENSMUST00000150502						0	0	0	4	0	0	2	1	2	0	0		
ENSMUST00000150503						0	0	45	63	1	2	0	0	4	0	6		
ENSMUST00000150504						5	3	5	4	2	0	16	22	2	2	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150505						4	3	2	57	3	6	0	0	0	0	0		
ENSMUST00000150506						8	6	16	4	2	0	7	27	18	20	13		
ENSMUST00000150507						13	12	54	11	18	6	1	13	4	0	10		
ENSMUST00000150508	ENSMUSG00000027215	2	93419111	93463140	-1	5	2	2	2	3	3	64	84	20	15	64	A2AIJ2	
ENSMUST00000150509						3	6	3	16	4	1	2	7	10	0	15		
ENSMUST00000150510						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000150511	ENSMUSG00000038822	10	45577829	45712345	1	0	0	0	0	0	4	6	16	4	4	0	H9KV09	
ENSMUST00000150512						3	0	11	13	5	4	0	0	0	0	0		
ENSMUST00000150513	ENSMUSG00000056260	3	106684987	106736577	1	0	0	0	0	0	0	0	2	0	0	0	D3Z1H3	
ENSMUST00000150515						0	0	1	2	2	0	0	1	0	0	0		
ENSMUST00000150516						3	1	0	2	2	2	0	0	3	0	0		
ENSMUST00000150517						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150519						1	1	0	18	4	3	4	0	0	0	0		
ENSMUST00000150520						1	2	0	4	2	0	0	0	0	0	0		
ENSMUST00000150521						3	3	2	3	1	1	0	1	1	0	1		
ENSMUST00000150522	ENSMUSG00000038172	4	83220300	83324255	-1	0	1	3	2	2	0	0	0	0	0	9	E0CX38	
ENSMUST00000150523						0	0	2	4	3	2	19	28	13	9	11		
ENSMUST00000150524						64	56	264	78	62	40	0	2	2	0	2		
ENSMUST00000150525	ENSMUSG00000063052	3	158036662	158068487	1	5	0	0	0	0	0	11	38	46	16	57	D6RHB1	
ENSMUST00000150526						1	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000150527						1	0	19	4	3	0	0	0	0	0	5		
ENSMUST00000150528	ENSMUSG00000041375	7	16274042	16286795	-1	0	1	0	0	0	0	0	0	0	0	0	G3UXX6	
ENSMUST00000150530	ENSMUSG00000030727	7	126428759	126449245	1	3	2	0	2	4	2	0	0	0	0	2	D6RGR2	
ENSMUST00000150531	ENSMUSG00000020811	11	71749920	71789647	1	1	2	14	11	0	2	0	0	0	0	0	B1AUZ4	
ENSMUST00000150532						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000150533						0	7	4	0	4	2	1	2	1	1	1		
ENSMUST00000150534						1	2	3	0	1	1	0	0	0	0	0		
ENSMUST00000150535	ENSMUSG00000013936	5	122100951	122113472	1	0	0	0	0	2	1	0	0	0	0	0	D3Z0I3	
ENSMUST00000150537						0	0	0	0	0	0	8	38	3	0	0		
ENSMUST00000150538						0	6	0	0	0	0	0	1	0	0	0		
ENSMUST00000150539						0	0	4	1	6	2	0	0	0	0	0		
ENSMUST00000150541						0	0	1	1	1	0	200	181	70	36	45		
ENSMUST00000150542						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000150543						2	0	8	1	0	1	2	0	0	0	0		
ENSMUST00000150545	ENSMUSG00000027472	2	153008890	153015427	-1	0	0	17	53	18	0	0	0	0	0	0	D6RFC3	
ENSMUST00000150546						0	0	0	56	1	0	1	0	0	0	2		
ENSMUST00000150547						2	2	4	105	8	4	28	83	69	57	27		
ENSMUST00000150548						5	5	19	26	13	0	0	0	0	3	0		
ENSMUST00000150549						4	6	13	6	13	9	13	12	43	4	0		
ENSMUST00000150550						0	0	6	0	0	0	1	0	2	0	12		
ENSMUST00000150551						8	9	0	192	6	2	0	0	0	0	0		
ENSMUST00000150552						11	13	51	18	9	4	1	1	1	0	14		
ENSMUST00000150553						3	7	16	11	5	5	8	43	13	3	25		
ENSMUST00000150554	ENSMUSG00000031328	X	74223461	74249820	-1	0	0	0	0	0	0	0	1978	153	181	108	J3JS91	
ENSMUST00000150555						0	0	2	50	2	2	0	4	0	0	6		
ENSMUST00000150557	ENSMUSG00000060519	1	156653617	156674356	-1	17	0	11	32	12	0	0	0	0	0	35	M0QWH2	
ENSMUST00000150558						6	0	9	87	8	1	13	19	24	0	24		
ENSMUST00000150560						2	0	6	1	7	2	2	13	3	0	16		
ENSMUST00000150561						7	12	14	21	5	7	0	0	0	0	0		
ENSMUST00000150562	ENSMUSG00000025579	11	119267887	119285454	1	1	4	10	4	4	2	0	0	0	0	1	F6VEG4	
ENSMUST00000150563	ENSMUSG00000019590	11	105933702	105953336	-1	4	4	3	95	13	0	0	0	0	0	4	V9GWU6	
ENSMUST00000150564						5	0	0	1	1	0	0	0	1	0	0		
ENSMUST00000150565						9	0	87	14	9	6	4	9	2	10	9		
ENSMUST00000150566						5	3	3	9	3	1	0	0	0	0	0		
ENSMUST00000150568	ENSMUSG00000000869	11	53602982	53618669	-1	1	2	3	0	3	3	3	0	2	2	2	G3UXB0	
ENSMUST00000150569	ENSMUSG00000002992	7	19671579	19681423	-1	0	1	0	5	0	0	0	0	0	0	0	Q3UJG0	Q05020
ENSMUST00000150570						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150571	ENSMUSG00000017999	2	167015193	167034947	1	63	62	146	98	42	24	10	27	19	1	31		Q921N6
ENSMUST00000150572						0	0	8	1	0	0	0	0	0	0	0		
ENSMUST00000150573						2	4	8	19	5	2	0	3	3	4	0		
ENSMUST00000150574						6	7	29	18	4	8	0	0	0	0	0		
ENSMUST00000150575	ENSMUSG00000029922	6	39397804	39420462	-1	4	0	13	0	6	0	152	8	224	90	332	F6QJX8	
ENSMUST00000150576	ENSMUSG00000048758	9	106429454	106431568	1	47	32	187	71	34	14	734	1252	790	4184	539	Q5M8M8	P47915
ENSMUST00000150577						0	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000150578						53	44	233	67	57	19	3	6	10	2	10		
ENSMUST00000150580						5	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000150582						26	24	31	28	22	14	45	72	87	42	58		
ENSMUST00000150583						6	0	4	21	5	0	0	0	0	0	0		
ENSMUST00000150584						0	1	0	31	4	0	2	6	0	0	0		
ENSMUST00000150585	ENSMUSG00000030534	7	80269649	80291754	1	7	0	36	15	0	0	11	200	0	0	35	S4R1H4	
ENSMUST00000150586						3	3	5	0	2	2	1	0	0	0	10		
ENSMUST00000150587	ENSMUSG00000030720	7	126571207	126585817	-1	1	0	0	0	0	1	85	114	71	7	72	D3YZN0	
ENSMUST00000150588	ENSMUSG00000027547	2	168748332	168767943	-1	2	0	19	0	0	4	0	0	0	0	0	A2AUZ6	
ENSMUST00000150589						9	0	12	3	10	0	0	0	0	0	0		
ENSMUST00000150590						0	0	1	0	0	0	3	0	0	0	0		
ENSMUST00000150591						0	0	0	90	0	0	2	3	0	0	0		
ENSMUST00000150592	ENSMUSG00000028464	4	43514711	43523765	-1	0	1	6	48	2	4	0	0	2	0	1	A2AIM5	
ENSMUST00000150593						9	5	5	0	1	0	11	369	142	48	74		
ENSMUST00000150594	ENSMUSG00000074139	9	92309377	92357876	1	0	0	0	1	2	0	0	0	0	0	0	B1B193	
ENSMUST00000150595	ENSMUSG00000068115	2	150934519	151039382	-1	5	1	0	0	0	1	0	0	0	0	0	A2ANB7	
ENSMUST00000150596	ENSMUSG00000000805	11	84957786	84966044	1	0	2	0	0	0	0	0	0	3	0	0	D6RCZ3	
ENSMUST00000150597						2	0	5	1	8	0	0	110	5	22	34		
ENSMUST00000150598						4	1	0	2	3	0	17	37	23	3	47		
ENSMUST00000150599						3	3	2	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150602	ENSMUSG00000047459	2	155236533	155250277	1	0	0	0	86	0	3	0	3	3	0	3	A2AVR9	
ENSMUST00000150603	ENSMUSG00000004849	5	137034993	137046135	-1	3	2	15	61	9	4	4	0	0	0	2	D3YXN0	
ENSMUST00000150605						6	4	31	20	13	5	9	17	0	0	5		
ENSMUST00000150606						0	4	5	86	11	0	2	4	0	0	0		
ENSMUST00000150607						4	2	5	3	1	0	0	0	1	0	0		
ENSMUST00000150608						7	0	7	12	13	2	4	12	5	5	13		
ENSMUST00000150609						4	0	3	8	2	2	26	21	0	19	18		
ENSMUST00000150610						4	0	16	2	1	1	16	30	0	0	17		
ENSMUST00000150611	ENSMUSG00000027287	2	120567671	120601255	1	0	0	0	0	0	0	84	307	731	1345	754	E9Q8A1	
ENSMUST00000150612						1	1	0	6	0	0	0	0	0	0	0		
ENSMUST00000150614						0	0	0	87	2	0	0	0	0	0	0		
ENSMUST00000150615						2	1	3	1	0	1	0	4	7	0	0		
ENSMUST00000150617						4	4	9	3	6	5	1	0	0	1	0		
ENSMUST00000150618	ENSMUSG00000042198	4	3938888	3951046	1	5	5	9	5	13	9	1	1	3	0	0		Q8K2Q5
ENSMUST00000150619						0	2	0	4	0	0	32	8	21	0	17		
ENSMUST00000150620						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000150622						0	0	3	1	0	2	0	0	0	0	0		
ENSMUST00000150624	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	433	831	197	17	80		Q9Z0H4
ENSMUST00000150625	ENSMUSG00000036813	2	25080304	25085716	1	1	2	8	0	0	1	0	0	0	0	0	A0A0A6YY80	
ENSMUST00000150626	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	0	0	0	0	0	0	0	0	17	D3Z261	
ENSMUST00000150629						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150630						5	5	0	12	3	3	14	8	24	0	33		
ENSMUST00000150632	ENSMUSG00000034175	11	5098926	5106093	1	1	0	0	0	0	0	0	0	6	0	0	Q5SUU0	
ENSMUST00000150633	ENSMUSG00000032446	9	118478212	118486132	1	8	1	3	4	0	1	0	0	0	0	0	F6VSW9	
ENSMUST00000150634	ENSMUSG00000090124	1	88095062	88220002	1	0	0	0	0	2	0	218	82	423	71	306	D3YZ96	
ENSMUST00000150635						1	0	0	6	0	0	0	0	78	0	2		
ENSMUST00000150636	ENSMUSG00000023007	15	99295087	99317018	1	0	5	0	0	0	0	0	1	0	0	0	F6QF44	
ENSMUST00000150637						0	0	6	4	4	1	10	42	54	0	77		
ENSMUST00000150638						3	4	3	5	9	1	1	0	0	0	0		
ENSMUST00000150639	ENSMUSG00000044548	12	71309884	71320107	1	0	8	11	300	16	7	0	0	0	0	0	D3Z5V0	
ENSMUST00000150640						7	4	19	2	0	0	0	109	3	2	5		
ENSMUST00000150641						31	14	67	98	59	15	0	0	0	0	5		
ENSMUST00000150642						2	0	0	2	6	1	0	0	0	0	9		
ENSMUST00000150643	ENSMUSG00000026888	2	64912476	65024987	-1	4	2	5	0	0	0	0	0	0	0	0	A2ASX3	
ENSMUST00000150644						1	0	16	0	4	0	614	2493	537	172	538		
ENSMUST00000150645						3	2	4	3	6	1	0	0	0	0	2		
ENSMUST00000150646						0	0	1	0	3	0	0	0	0	0	0		
ENSMUST00000150647	ENSMUSG00000024121	17	24163866	24169702	-1	0	0	3	96	4	4	0	0	0	0	0	D3Z3B2	
ENSMUST00000150648						1	1	3	0	1	0	0	2	2	0	6		
ENSMUST00000150649	ENSMUSG00000073491	1	173566284	173599274	-1	8	7	31	5	7	3	1	0	0	0	1	D3Z5G0	
ENSMUST00000150650	ENSMUSG00000095362	2	177831791	177840336	-1	2	0	6	0	0	1	8	13	0	12	2	K7N6R3	
ENSMUST00000150652						3	0	6	68	1	0	0	1	0	0	0		
ENSMUST00000150653						0	0	0	0	0	1	0	0	3	0	0		
ENSMUST00000150654						10	0	11	3	7	3	0	0	0	0	0		
ENSMUST00000150655	ENSMUSG00000005982	16	3872375	3904780	1	0	4	7	6	4	2	53	100	67	4	52		Q9DBU2
ENSMUST00000150656						1	4	17	17	7	8	0	2	3	1	6		
ENSMUST00000150657						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150658						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000150659						0	0	0	0	0	0	0	5	9	20	7		
ENSMUST00000150660	ENSMUSG00000037712	14	45458792	45530118	-1	3	0	0	2	0	0	0	2	0	0	0	A6X940	
ENSMUST00000150661						2	2	1	44	1	1	0	0	0	0	9		
ENSMUST00000150662						1	1	8	6	0	0	0	0	0	0	3		
ENSMUST00000150663						5	1	17	2	4	0	0	4	4	0	0		
ENSMUST00000150664	ENSMUSG00000039611	4	49584506	49597876	-1	1	0	1	183	4	2	0	0	0	0	0	A2AKL2	
ENSMUST00000150665						4	4	16	5	0	1	1	2	0	0	0		
ENSMUST00000150666	ENSMUSG00000040272	2	93833467	93849943	-1	0	0	0	0	0	0	0	5	0	0	0	F6RIQ1	
ENSMUST00000150667						8	6	26	19	13	9	0	4	3	0	6		
ENSMUST00000150668						14	11	19	15	13	5	12	2	7	0	17		
ENSMUST00000150669						6	6	4	5	3	4	0	0	0	0	0		
ENSMUST00000150670	ENSMUSG00000062661	2	31245823	31295989	1	0	2	0	15	2	0	0	0	0	0	0	A0A0A6YY43	
ENSMUST00000150672						9	8	33	24	17	9	19	22	35	4	94		
ENSMUST00000150673						5	2	5	7	7	1	4	26	19	2	12		
ENSMUST00000150674						6	7	29	0	9	2	0	0	0	1	0		
ENSMUST00000150675						7	5	12	93	4	0	0	3	3	0	0		
ENSMUST00000150676						0	2	2	36	1	0	0	2	7	4	8		
ENSMUST00000150677						0	3	0	0	0	2	3	1	1	2	2		
ENSMUST00000150679	ENSMUSG00000025786	9	123066160	123113205	-1	0	0	1	13	0	0	0	12	0	0	0	D6RHA3	
ENSMUST00000150680	ENSMUSG00000031750	8	110741829	110805924	-1	0	12	22	20	21	9	0	0	0	0	0		Q8R1R4
ENSMUST00000150681	ENSMUSG00000018995	7	96951505	97064758	1	0	0	2	3	1	0	28	40	41	27	21		
ENSMUST00000150682	ENSMUSG00000029176	5	52834012	52867797	1	2	2	0	1	1	0	0	0	0	0	0	A0A0G2JGY2	
ENSMUST00000150683						2	6	11	100	9	0	17	17	21	5	15		
ENSMUST00000150684						1	3	24	1	0	0	11	32	31	0	46		
ENSMUST00000150685	ENSMUSG00000020263	10	83600033	83648738	-1	1	0	2	0	2	0	0	0	7	1	0	D6RFR7	
ENSMUST00000150687						2	3	2	2	1	3	0	4	0	1	4		
ENSMUST00000150688						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000150689						3	1	5	4	3	4	0	2	0	0	6		
ENSMUST00000150691						2	4	11	34	6	4	0	0	0	0	0		
ENSMUST00000150692						4	0	2	0	4	1	1	3	2	0	0		
ENSMUST00000150693						3	2	23	9	3	5	0	0	0	0	0		
ENSMUST00000150695	ENSMUSG00000079484	2	30266203	30282149	1	0	0	0	0	0	0	0	0	0	0	0	A2AQZ5	
ENSMUST00000150697	ENSMUSG00000000384	11	6615598	6626067	-1	0	0	0	0	0	0	18	0	0	43	0	E9PUT1	
ENSMUST00000150699						3	1	3	3	4	2	0	0	0	0	0		
ENSMUST00000150700						0	0	0	4	0	0	5	1	0	0	0		
ENSMUST00000150701						0	0	9	39	8	4	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150703						2	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000150704	ENSMUSG00000036099	10	93939165	94035817	-1	273	254	466	276	265	112	5	33	28	13	22		Q3ZK22
ENSMUST00000150706						17	13	24	5	15	6	3	0	0	0	4		
ENSMUST00000150707						1	4	2	1	2	2	0	0	0	0	0		
ENSMUST00000150708						0	1	2	9	0	0	2	0	1	0	2		
ENSMUST00000150709	ENSMUSG00000029173	5	52640087	52669708	-1	0	0	37	0	22	0	23	86	42	17	0	D6RGM2	
ENSMUST00000150711						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150713	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	10	31	3	15	9	D3YZX2	
ENSMUST00000150714	ENSMUSG00000035455	11	11787431	11808962	-1	0	0	0	0	0	0	0	0	0	0	0	Q5SWU3	
ENSMUST00000150715	ENSMUSG00000068457	Y	1096861	1245759	-1	0	0	0	0	0	0	1	0	0	0	0	F7BBC1	
ENSMUST00000150717						8	7	4	181	7	0	0	0	0	0	0		
ENSMUST00000150718						0	0	5	26	4	4	0	0	2	0	0		
ENSMUST00000150719						8	3	0	3	7	0	57	167	27	123	14		
ENSMUST00000150720						1	0	0	0	0	1	3	6	18	5	8		
ENSMUST00000150721	ENSMUSG00000044835	1	161142691	161170498	1	0	0	3	0	0	2	0	0	0	0	0	A0A0A6YY30	
ENSMUST00000150722						43	62	70	271	52	30	3	15	3	7	15		
ENSMUST00000150723	ENSMUSG00000017264	4	148558429	148582401	1	1	0	0	2	1	1	1	3	4	0	5	G3UWL4	
ENSMUST00000150724						5	1	15	8	6	3	3	8	3	0	0		
ENSMUST00000150725						43	53	50	33	57	31	3	15	3	5	6		
ENSMUST00000150726						3	1	1	42	5	0	0	3	0	1	0		
ENSMUST00000150727	ENSMUSG00000058317	14	18573575	18894267	-1	0	0	0	5	3	0	0	0	0	0	0		Q91W82
ENSMUST00000150728						19	16	34	15	20	9	16	151	57	15	87		
ENSMUST00000150729						3	11	21	12	9	7	6	5	7	0	21		
ENSMUST00000150730						6	25	95	221	46	45	13	0	10	0	37		
ENSMUST00000150731						6	7	16	12	6	2	55	287	100	9	118		
ENSMUST00000150732						0	1	12	1	4	0	0	11	3	0	3		
ENSMUST00000150733						4	0	4	4	7	5	2	0	2	0	2		
ENSMUST00000150734						17	12	42	24	40	16	0	0	0	0	0		
ENSMUST00000150736	ENSMUSG00000020389	11	52004221	52089784	1	2	1	0	0	0	0	0	4	1	0	0	F6ULF3	
ENSMUST00000150737	ENSMUSG00000039419	6	45060061	47304213	1	4	5	4	0	2	0	0	0	0	0	0	A0A0G2JE70	
ENSMUST00000150738						0	4	3	2	9	5	0	0	0	0	0		
ENSMUST00000150739						6	5	0	0	0	0	26	349	47	124	60		
ENSMUST00000150740						3	2	1	3	2	1	0	0	0	0	0		
ENSMUST00000150741	ENSMUSG00000051747	2	76703980	76982547	-1	8	1	7	9	4	5	0	0	0	0	0	F6ZRX7	
ENSMUST00000150742						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150744						2	4	9	54	5	2	0	0	0	0	0		
ENSMUST00000150745						23	21	64	32	41	19	0	76	12	19	42		
ENSMUST00000150746						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150747						0	0	2	0	1	1	6	27	8	0	22		
ENSMUST00000150748						1	1	5	4	2	0	6	12	0	0	9		
ENSMUST00000150750	ENSMUSG00000020290	11	23256041	23298249	1	0	0	0	0	0	0	4	0	0	0	0	F6YA11	
ENSMUST00000150752						2	4	15	1	0	0	0	0	0	0	0		
ENSMUST00000150753						2	4	6	8	1	5	6	15	7	0	10		
ENSMUST00000150755						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000150756	ENSMUSG00000027868	3	99240381	99354259	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDG4	
ENSMUST00000150757						0	2	0	0	0	0	32	250	106	45	131		
ENSMUST00000150758	ENSMUSG00000024430	18	12741324	12755146	1	0	0	0	0	0	0	0	0	0	0	0		Q9D424
ENSMUST00000150759						23	15	79	6	0	0	158	0	0	17	0		
ENSMUST00000150760						1	0	0	0	0	0	124	357	107	30	170		
ENSMUST00000150761	ENSMUSG00000033740	1	6487231	6860940	1	0	0	0	0	0	0	0	0	0	0	0	Q148A0	Q80TY4
ENSMUST00000150762	ENSMUSG00000061718	11	98348404	98357796	1	19	15	86	17	41	11	0	0	0	0	0		Q60829
ENSMUST00000150763						3	3	11	5	11	4	6	21	6	0	18		
ENSMUST00000150764						24	3	35	33	40	20	3	20	6	4	3		
ENSMUST00000150765						1	0	0	0	1	3	5	36	0	0	2		
ENSMUST00000150766	ENSMUSG00000034647	17	65967501	66077089	-1	0	0	0	1	0	0	21	0	59	0	53	Q3U569	
ENSMUST00000150767						8	10	14	0	11	8	128	605	161	60	294		
ENSMUST00000150768	ENSMUSG00000034327	14	67715937	67742310	1	0	0	0	0	0	3	30	0	52	5	24	E9PUA6	
ENSMUST00000150769						3	2	4	6	1	0	0	0	0	1	0		
ENSMUST00000150770	ENSMUSG00000026785	2	30077684	30091022	1	0	0	4	4	1	0	0	0	0	0	0	A2BE97	
ENSMUST00000150771						2	2	1	1	2	2	0	0	0	0	0		
ENSMUST00000150773						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150774	ENSMUSG00000008153	6	124430759	124464794	-1	6	0	1	2	3	4	0	0	0	0	0		
ENSMUST00000150775	ENSMUSG00000052949	11	116336353	116413032	-1	0	0	0	0	0	0	3	6	0	0	4	F6XBS7	
ENSMUST00000150776						1	1	18	9	5	1	5	63	23	7	27		
ENSMUST00000150778						0	0	0	0	0	0	8	13	8	2	0		
ENSMUST00000150779	ENSMUSG00000054256	5	115429599	115455698	1	7	18	56	47	15	10	0	3	0	1	1		Q61474
ENSMUST00000150780						6	0	12	3	8	6	114	147	64	22	61		
ENSMUST00000150781						0	1	1	7	1	0	0	0	0	1	3		
ENSMUST00000150783						6	6	6	0	4	2	0	0	0	0	0		
ENSMUST00000150784						8	4	0	1	0	0	34	1396	25	60	17		
ENSMUST00000150785						27	7	64	58	43	18	6	17	23	4	59		
ENSMUST00000150786						4	8	7	12	13	5	2	2	3	0	0		
ENSMUST00000150787	ENSMUSG00000039556	X	7557296	7574283	-1	19	11	116	49	21	3	0	16	0	3	3		Q9JIG4
ENSMUST00000150788						1	4	3	49	2	3	0	0	0	0	0		
ENSMUST00000150789						37	44	208	96	37	13	4	8	8	0	14		
ENSMUST00000150790	ENSMUSG00000039345	16	8470788	8490684	1	0	0	8	0	0	0	5	1	0	7	0	D3YVA4	
ENSMUST00000150791	ENSMUSG00000000154	7	143473721	143499334	1	0	0	0	2	0	0	0	0	0	0	0	D6RDC9	
ENSMUST00000150792						13	10	34	21	24	7	0	0	0	0	0		
ENSMUST00000150793						0	1	0	0	1	1	0	3	0	0	0		
ENSMUST00000150795	ENSMUSG00000044456	12	102283048	102390855	1	1	9	3	7	6	4	25	46	20	2	26	D3Z076	
ENSMUST00000150796						1	0	0	0	0	0	3	92	3	0	15		
ENSMUST00000150797						1	0	0	10	2	0	0	1	0	0	0		
ENSMUST00000150798						4	2	6	83	2	3	0	0	0	0	0		
ENSMUST00000150799						2	1	6	3	2	2	6	6	5	2	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150800						3	3	3	0	6	0	0	2	0	1	0		
ENSMUST00000150802						6	6	4	7	0	3	16	4	81	7	41		
ENSMUST00000150803						36	59	215	89	59	40	3	9	8	0	3		
ENSMUST00000150804	ENSMUSG00000031730	8	109591343	109608673	-1	0	0	0	0	0	0	0	0	0	0	0	F6TCT7	
ENSMUST00000150805	ENSMUSG00000029452	5	121451893	121524183	1	0	0	0	8	0	0	0	0	0	0	0	A0A0G2JGD3	
ENSMUST00000150806	ENSMUSG00000034928	13	54679399	54693907	-1	14	13	0	0	0	0	1656	1034	707	0	546		Q3UHJ8
ENSMUST00000150807	ENSMUSG00000057110	2	35109492	35178822	1	1	2	3	1	0	0	2	0	10	2	12	A0A0G2JE96	
ENSMUST00000150808						0	3	21	12	2	0	0	0	0	0	0		
ENSMUST00000150809	ENSMUSG00000066224	4	41723836	41731142	-1	0	0	7	70	0	3	0	0	0	0	0	B7ZP08	
ENSMUST00000150810						4	4	3	5	6	3	13	22	33	24	14		
ENSMUST00000150811						2	1	4	1	3	0	0	0	0	0	0		
ENSMUST00000150812						2	2	20	9	5	1	3	9	14	0	3		
ENSMUST00000150813	ENSMUSG00000029192	5	36490604	36593276	-1	11	8	9	15	14	10	43	31	145	0	207	E9PZY7	
ENSMUST00000150814						1	0	16	6	7	5	0	0	0	0	1		
ENSMUST00000150815	ENSMUSG00000047215	5	65388364	65391444	-1	0	0	0	0	2	0	0	0	0	0	2	A0A0G2JFQ3	
ENSMUST00000150816						3	5	3	5	5	3	3	3	1	0	3		
ENSMUST00000150817						9	7	35	76	25	20	1	1	2	0	0		
ENSMUST00000150819	ENSMUSG00000034382	17	47436615	47470638	1	52	17	204	202	64	23	5	1	11	1	20		Q91Z58
ENSMUST00000150820	ENSMUSG00000032327	9	58063788	58153996	1	0	0	0	0	0	0	0	0	0	0	0	E9QAQ2	
ENSMUST00000150821	ENSMUSG00000026667	1	170193420	170215397	-1	0	31	56	5	0	0	715	1677	271	135	262	Q8C0N6	
ENSMUST00000150822	ENSMUSG00000032098	9	44673233	44686305	1	1	3	0	0	3	3	0	0	0	0	0	F6XTD2	
ENSMUST00000150823						0	1	0	4	0	0	0	0	0	0	0		
ENSMUST00000150824						9	3	10	5	8	3	3	8	0	0	4		
ENSMUST00000150825						1	3	6	2	3	0	0	10	2	1	2		
ENSMUST00000150826	ENSMUSG00000034563	9	72985429	73016340	1	0	0	0	0	0	0	2242	1378	3984	2559	1540		Q640L3
ENSMUST00000150827						0	0	0	52	0	0	0	0	0	0	0		
ENSMUST00000150828	ENSMUSG00000001211	10	78269178	78352489	-1	2	0	4	4	1	2	0	0	0	0	0	D3YUW0	
ENSMUST00000150829						23	18	55	30	30	14	0	5	9	2	3		
ENSMUST00000150830	ENSMUSG00000028573	4	95557507	95926939	1	3	1	0	1	1	2	0	1	0	0	0	B1AY71	
ENSMUST00000150831						1	0	2	1	2	2	0	0	0	0	0		
ENSMUST00000150832						4	2	6	0	3	6	0	2	3	0	0		
ENSMUST00000150833	ENSMUSG00000074457	3	90537254	90543151	1	4	2	4	0	1	2	0	1	0	0	0	D3Z2Y6	
ENSMUST00000150834	ENSMUSG00000026739	2	18677018	18686629	1	0	0	0	0	0	0	0	7	11	2	0	A2ASR7	
ENSMUST00000150835						4	4	2	24	12	2	0	3	0	0	0		
ENSMUST00000150836	ENSMUSG00000036893	2	24789928	24919614	-1	0	0	0	1	0	0	0	0	0	0	0	A0A0A6YXA8	
ENSMUST00000150837						11	15	20	7	16	0	113	380	200	35	341		
ENSMUST00000150838	ENSMUSG00000007207	5	135023482	135051100	1	19	1	25	0	8	0	0	0	0	0	15	D6RFB9	
ENSMUST00000150839						1	2	2	4	6	2	0	0	0	0	0		
ENSMUST00000150840						1	0	1	0	1	0	0	42	27	62	29		
ENSMUST00000150841						1	0	3	14	1	5	0	3	4	0	3		
ENSMUST00000150842						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000150843	ENSMUSG00000037514	2	131262495	131299188	1	0	7	0	0	18	0	107	381	265	0	61	Q3U4S0	
ENSMUST00000150844	ENSMUSG00000030929	7	119768679	119794058	-1	0	2	0	37	0	0	0	0	8	0	7		Q5BKS4
ENSMUST00000150845	ENSMUSG00000020100	10	60712072	60752794	-1	0	1	6	0	2	0	0	0	0	0	0	D6RI95	
ENSMUST00000150846						5	0	0	0	1	0	2	3	7	0	0		
ENSMUST00000150847						0	1	1	112	6	0	1	0	3	0	4		
ENSMUST00000150848	ENSMUSG00000068036	17	13760539	13906150	1	0	0	0	0	0	0	0	0	361	0	123		Q9QZQ1
ENSMUST00000150849	ENSMUSG00000058388	3	103968110	104024598	1	3	4	1	1	0	0	11	0	2	0	0	D6RIJ6	
ENSMUST00000150850						59	62	225	93	63	36	3	15	16	1	11		
ENSMUST00000150852						0	0	0	0	7	0	38	47	18	0	9		
ENSMUST00000150853						3	7	31	42	12	7	108	255	202	15	70		
ENSMUST00000150854						14	24	59	19	12	13	9	15	17	3	26		
ENSMUST00000150855						2	2	3	7	1	1	1	0	0	0	0		
ENSMUST00000150856						1	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000150857	ENSMUSG00000006127	11	75630988	75648871	1	0	0	0	0	0	1	140	2034	79	47	0	D6RI67	
ENSMUST00000150858						0	0	0	23	0	0	41	10	163	0	90		
ENSMUST00000150859						0	0	1	0	1	0	0	0	0	0	12		
ENSMUST00000150860						0	0	0	0	0	0	7	0	0	0	0		
ENSMUST00000150861						0	1	0	0	0	0	0	28	10	0	6		
ENSMUST00000150862						4	0	6	3	1	4	0	0	0	0	6		
ENSMUST00000150863	ENSMUSG00000020728	11	108425192	108860615	1	0	5	0	32	6	0	0	0	0	8	0	J3JS86	
ENSMUST00000150864	ENSMUSG00000028644	4	119175457	119190011	-1	0	0	2	0	3	0	0	0	0	0	0	D6RCV8	
ENSMUST00000150865						0	0	1	0	0	0	0	8	2	1	0		
ENSMUST00000150866						1	1	6	5	5	0	0	1	2	0	0		
ENSMUST00000150867	ENSMUSG00000009246	7	143069153	143094642	-1	10	7	24	0	39	11	0	0	0	0	0		Q9JJH7
ENSMUST00000150868						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000150869						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000150870						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150871						0	0	9	0	0	0	0	1	0	0	2		
ENSMUST00000150872						0	0	15	0	0	0	24	5	16	1	11		
ENSMUST00000150873						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150874						5	2	14	7	4	0	2	9	0	0	9		
ENSMUST00000150875						0	2	3	2	0	2	9	0	0	0	0		
ENSMUST00000150876						0	1	0	1	1	0	12	8	2	14	2		
ENSMUST00000150877	ENSMUSG00000024354	18	35614604	35627244	-1	0	0	0	0	0	0	0	0	0	0	0	D6RDS7	
ENSMUST00000150878						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000150879						4	1	5	6	2	2	0	0	0	0	5		
ENSMUST00000150880						0	0	0	0	0	0	14	6	13	0	0		
ENSMUST00000150881	ENSMUSG00000029020	4	147873599	147904704	-1	2	1	0	44	7	0	0	0	0	0	0	A2A7Y8	
ENSMUST00000150882						0	0	0	0	0	1	0	0	0	0	6		
ENSMUST00000150883	ENSMUSG00000061702	7	25669139	25675166	-1	0	0	0	0	0	0	0	0	0	0	0	F6VMA8	
ENSMUST00000150884	ENSMUSG00000057522	11	95414080	95493406	1	0	0	0	0	0	0	0	0	13	6	4	B1ATK6	
ENSMUST00000150885						8	0	19	1	2	5	20	8	39	0	22		
ENSMUST00000150886	ENSMUSG00000008028	7	44360043	44385820	-1	3	2	5	0	6	3	0	0	0	0	0	H3BIU9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150887						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000150888						1	0	2	0	0	0	2	0	0	0	0		
ENSMUST00000150890	ENSMUSG00000026770	2	11642807	11693193	1	2	3	1	1	1	3	0	0	0	0	0	Q3THW2	
ENSMUST00000150891						0	0	0	0	0	0	42	373	0	0	33		
ENSMUST00000150892	ENSMUSG00000013921	7	30291672	30308367	1	1	2	0	0	0	0	0	0	0	0	0	D3Z115	
ENSMUST00000150893	ENSMUSG00000031922	9	13807792	13827107	-1	4	1	5	0	5	3	0	0	4	0	0	B8JJF0	
ENSMUST00000150894	ENSMUSG00000068663	16	10545339	10744878	1	0	1	2	103	1	0	0	0	0	0	0	D3YVA1	
ENSMUST00000150896	ENSMUSG00000035392	2	37798991	38287390	-1	0	0	0	0	0	0	0	0	0	0	0	D6RH88	
ENSMUST00000150897	ENSMUSG00000061356	14	65598546	65648531	1	21	14	31	26	10	8	0	0	0	0	0	D3YWJ0	
ENSMUST00000150898						35	27	386	22	30	10	5	11	6	0	9		
ENSMUST00000150899						2	2	16	1	0	4	8	14	29	1	34		
ENSMUST00000150900	ENSMUSG00000031410	X	135579555	135598777	-1	2	3	2	2	0	0	0	0	0	0	0	A2AEI4	
ENSMUST00000150901	ENSMUSG00000007655	6	17306335	17341452	1	1	0	0	5	3	0	0	0	0	0	0	H3BKG0	
ENSMUST00000150902	ENSMUSG00000051497	11	110968033	111027968	1	0	0	0	0	0	0	0	0	0	0	0	A2A5W7	
ENSMUST00000150903						0	0	3	0	0	0	0	0	0	0	1		
ENSMUST00000150904	ENSMUSG00000034109	3	75875084	75956949	-1	0	0	0	0	0	3	7	6	14	10	14	F6RUD1	
ENSMUST00000150905						1	0	4	0	0	0	1	0	0	8	0		
ENSMUST00000150907						2	3	6	0	5	3	0	6	5	0	6		
ENSMUST00000150908						0	0	0	0	0	2	21	11	9	2	1		
ENSMUST00000150909						1	0	0	1	4	2	1	0	0	0	0		
ENSMUST00000150910						3	2	5	0	0	0	0	0	0	0	0		
ENSMUST00000150911	ENSMUSG00000026049	1	44086613	44102441	-1	0	0	0	10	0	0	7	64	11	25	0		Q3TUU5
ENSMUST00000150912	ENSMUSG00000033705	2	120629126	120731895	1	8	11	20	77	4	1	0	0	24	3	42	A2AKI2	
ENSMUST00000150913	ENSMUSG00000000359	2	152626951	152635198	1	1	2	11	14	0	0	2	1	0	0	0	A3KGR6	
ENSMUST00000150914	ENSMUSG00000031229	X	105797615	105929403	-1	0	0	0	0	0	0	3	0	18	0	5	Q8C2S3	
ENSMUST00000150915						0	0	0	11	1	3	0	0	6	0	1		
ENSMUST00000150916	ENSMUSG00000021661	13	98263158	98274750	1	2	0	7	160	16	9	7	91	74	65	64	D3Z4I1	
ENSMUST00000150917	ENSMUSG00000030720	7	126571207	126585817	-1	0	0	0	0	0	0	22	37	0	0	0	S4R2L1	
ENSMUST00000150918						2	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000150919						0	4	3	8	3	3	20	103	81	10	125		
ENSMUST00000150920	ENSMUSG00000040387	4	24612554	24851124	-1	2	4	0	1	4	0	0	0	0	0	0	J3KML3	
ENSMUST00000150921						44	35	95	63	46	24	28	87	80	7	104		
ENSMUST00000150922						1	0	2	3	0	0	0	16	0	7	55		
ENSMUST00000150923						0	5	0	0	8	0	7	13	4	7	7		
ENSMUST00000150924	ENSMUSG00000034786	17	34589806	34591754	1	0	0	11	0	0	0	1806	3632	1223	190	810	G3UZQ1	
ENSMUST00000150925						2	0	22	180	6	1	2	2	0	0	0		
ENSMUST00000150926						1	1	1	10	0	0	14	7	18	0	20		
ENSMUST00000150927						0	0	0	0	0	0	0	10	1	1	0		
ENSMUST00000150928	ENSMUSG00000041351	4	137664726	137729861	1	7	6	0	20	9	7	1	0	0	0	0	A2ALS3	
ENSMUST00000150929						8	9	2	8	8	12	1	0	1	0	0		
ENSMUST00000150930						3	3	4	1	0	0	0	0	1	0	3		
ENSMUST00000150931	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	0	5	0	0	D3Z3C0	
ENSMUST00000150932						4	2	2	1	2	0	0	5	4	2	0		
ENSMUST00000150933	ENSMUSG00000030727	7	126428759	126449245	1	2	4	14	16	4	0	2	11	3	0	6	D6RCU7	
ENSMUST00000150934						0	2	2	0	0	3	0	0	0	0	0		
ENSMUST00000150935						3	1	4	59	0	1	0	0	8	2	0		
ENSMUST00000150936						4	0	5	12	3	5	0	0	0	0	0		
ENSMUST00000150938						0	0	0	2	6	0	0	0	0	4	0		
ENSMUST00000150939						23	22	57	30	39	10	1	5	7	1	10		
ENSMUST00000150940						0	0	0	0	0	0	0	5	4	4	0		
ENSMUST00000150941	ENSMUSG00000002059	11	78188430	78192193	1	3	0	0	0	0	0	0	1	0	0	0	B1AQD4	
ENSMUST00000150942						7	5	23	6	6	3	20	60	28	3	25		
ENSMUST00000150943						1	1	0	1	2	4	0	5	4	17	4		
ENSMUST00000150944						1	0	0	0	0	2	0	0	0	1	0		
ENSMUST00000150945						51	64	219	77	61	24	4	6	12	0	16		
ENSMUST00000150946						124	126	167	191	126	67	30	229	47	123	79		
ENSMUST00000150947						4	4	5	1	4	1	0	0	0	0	0		
ENSMUST00000150948	ENSMUSG00000078776	7	28129466	28164811	1	58	45	116	65	92	40	0	0	0	0	0	E9PVG8	
ENSMUST00000150949						0	0	0	0	0	0	85	328	267	366	151		
ENSMUST00000150950						3	3	4	3	1	2	0	0	0	0	0		
ENSMUST00000150951						2	2	4	2	6	6	0	0	0	0	0		
ENSMUST00000150952						2	0	8	19	6	6	0	0	4	0	5		
ENSMUST00000150954						3	1	2	7	7	2	0	0	0	2	0		
ENSMUST00000150955						4	5	1	2	6	2	8	21	4	7	0		
ENSMUST00000150956						5	6	12	3	4	4	3	1	2	4	5		
ENSMUST00000150957						0	0	1	0	1	0	0	2	0	0	0		
ENSMUST00000150958						7	3	12	522	18	3	0	0	0	0	1		
ENSMUST00000150959						0	1	0	4	0	0	4	37	18	4	5		
ENSMUST00000150960						0	0	22	14	10	5	3	52	4	14	20		
ENSMUST00000150961						6	0	0	4	0	0	0	0	1	0	1		
ENSMUST00000150962						31	12	37	36	23	12	7	3	0	0	11		
ENSMUST00000150963	ENSMUSG00000046844	8	114205612	114374071	1	2	2	2	46	5	2	0	0	0	0	0	D3Z434	
ENSMUST00000150964	ENSMUSG00000003363	7	27532000	27553218	-1	0	2	6	16	1	0	0	0	2	0	6	D3Z179	
ENSMUST00000150965						4	0	0	0	0	0	11	158	28	23	35		
ENSMUST00000150966						4	2	0	6	6	0	0	0	0	0	0		
ENSMUST00000150967	ENSMUSG00000026222	1	85649988	85709998	1	0	0	0	0	0	0	86	83	192	23	122	Q3U5P2	
ENSMUST00000150968	ENSMUSG00000055681	8	70302518	70312993	1	2	0	0	0	0	0	473	342	314	115	201	D3Z315	
ENSMUST00000150969	ENSMUSG00000007610	8	71488103	71499583	1	1	2	3	2	1	3	0	0	0	0	11	B2RRS4	Q923K4
ENSMUST00000150970						4	1	1	0	0	0	0	63	0	5	0		
ENSMUST00000150971	ENSMUSG00000025903	1	4807788	4848410	1	0	0	0	0	0	0	6	2	0	0	0		P97823
ENSMUST00000150972	ENSMUSG00000020176	11	11930508	12038683	-1	3	5	8	218	4	4	0	0	0	0	0	B1ATS7	
ENSMUST00000150974	ENSMUSG00000034785	4	107291465	107307169	-1	0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000150975	ENSMUSG00000022194	14	54892500	54898169	1	0	6	0	0	15	0	46	404	63	0	223	G3UY42	
ENSMUST00000150976	ENSMUSG00000035104	6	82041043	82093099	1	3	1	4	5	0	3	0	0	0	0	0	D3Z4B6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000150977						0	0	0	2	1	0	0	1	0	0	3		
ENSMUST00000150978						4	1	5	9	8	4	2	5	3	0	3		
ENSMUST00000150979						1	1	2	1	1	1	1	0	1	0	4		
ENSMUST00000150980						1	1	0	1	0	0	3	7	0	0	0		
ENSMUST00000150981	ENSMUSG00000054720	5	105519388	105613018	1	1	2	0	75	0	2	0	0	2	0	0	D3Z557	
ENSMUST00000150982						1	0	4	3	0	2	0	0	0	0	0		
ENSMUST00000150983						36	25	114	502	68	35	5	10	20	1	7		
ENSMUST00000150984						0	4	5	0	6	0	3	7	0	0	0		
ENSMUST00000150986						176	139	1577	280	135	103	3	47	13	1	32		
ENSMUST00000150987						4	1	1	3	2	0	0	3	1	0	3		
ENSMUST00000150988						3	0	1	0	0	1	0	0	0	16	4		
ENSMUST00000150989	ENSMUSG00000090173	11	62847069	62877465	1	0	0	0	0	0	0	0	0	0	0	5	B7ZC91	
ENSMUST00000150990	ENSMUSG00000025421	18	76930126	76972902	1	0	0	0	26	0	0	0	18	0	0	0		Q3UGR5
ENSMUST00000150991						4	10	0	14	19	8	0	0	0	0	0		
ENSMUST00000150992	ENSMUSG00000053581	5	139471211	139484549	-1	0	0	0	5	0	0	0	0	0	0	0	D3YUL0	
ENSMUST00000150993	ENSMUSG00000071669	16	11322908	11755472	1	41	33	77	45	38	19	1	8	6	0	13		
ENSMUST00000150995	ENSMUSG00000064284	15	85806972	85811697	-1	0	0	0	17	1	0	9	7	0	0	0		Q8R3A2
ENSMUST00000150996						35	33	268	53	49	23	3	2	0	0	2		
ENSMUST00000150997						1	2	7	2	3	4	13	140	52	42	166		
ENSMUST00000150998						44	30	97	48	49	21	0	4	0	1	5		
ENSMUST00000150999						1	5	4	18	2	2	2	1	5	0	2		
ENSMUST00000151001						0	4	3	76	8	0	0	0	0	4	0		
ENSMUST00000151002						18	14	15	11	20	17	0	1	5	0	0		
ENSMUST00000151003						0	0	0	0	1	0	3	1	0	0	0		
ENSMUST00000151004	ENSMUSG00000067795	1	16065979	16093325	-1	0	0	0	0	0	0	0	0	0	0	0	F6QJK4	
ENSMUST00000151005						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151006						0	0	0	50	1	0	0	0	0	0	0		
ENSMUST00000151007						1	3	1	17	3	3	0	0	0	0	0		
ENSMUST00000151008						2	1	12	0	2	0	5	9	4	0	2		
ENSMUST00000151009						3	0	5	6	3	3	0	11	0	0	8		
ENSMUST00000151010						4	1	5	0	6	1	0	1	0	0	0		
ENSMUST00000151011	ENSMUSG00000022094	14	70303469	70351425	-1	2	2	1	0	2	2	0	0	3	0	0	D3YXD7	
ENSMUST00000151012	ENSMUSG00000040550	4	14809498	14826587	-1	12	14	16	0	26	0	63	339	104	267	92	F6VDQ9	
ENSMUST00000151013	ENSMUSG00000018923	11	70451919	70453727	1	0	0	0	16	0	0	0	2	0	6	5	G3UZ31	
ENSMUST00000151015						0	2	0	3	0	0	0	0	0	1	0		
ENSMUST00000151016	ENSMUSG00000026005	1	66700831	66719805	1	3	3	3	154	19	2	8	12	32	10	11	M0QWJ2	
ENSMUST00000151017						3	4	2	6	2	1	0	37	7	4	11		
ENSMUST00000151018						6	2	9	1	3	1	0	0	0	0	0		
ENSMUST00000151019						21	28	47	37	40	17	0	0	0	0	2		
ENSMUST00000151020						0	0	0	10	0	2	0	11	9	15	18		
ENSMUST00000151021						2	4	1	7	5	5	0	0	0	0	0		
ENSMUST00000151022	ENSMUSG00000067916	4	147132038	147180579	1	4	8	11	4	5	2	0	2	2	2	3	B1AVX1	
ENSMUST00000151023						8	17	6	9	12	0	0	0	0	0	0		
ENSMUST00000151024	ENSMUSG00000035539	4	45890303	45950774	1	4	0	0	19	2	4	0	0	0	0	0	F7BHM1	
ENSMUST00000151025	ENSMUSG00000049649	4	133209340	133212536	-1	0	0	9	0	0	0	0	1	0	0	0	B1AUM8	
ENSMUST00000151026						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151027						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151029	ENSMUSG00000047462	13	19727417	19732951	-1	69	59	719	98	56	25	77	59	44	16	36	B9EKH0	
ENSMUST00000151030						30	26	142	105	45	20	126	157	26	7	93		
ENSMUST00000151031	ENSMUSG00000053111	7	133776861	133881532	1	4	0	4	11	1	2	0	0	0	0	0	D3Z7V1	
ENSMUST00000151033	ENSMUSG00000023092	X	56731787	56793346	1	0	0	1	0	0	0	0	0	0	0	0	A2AEY0	
ENSMUST00000151034						0	0	1	0	0	0	62	595	21	0	204		
ENSMUST00000151035						4	3	1	0	2	1	0	0	0	0	0		
ENSMUST00000151036						15	9	73	22	24	13	4	542	66	21	222		
ENSMUST00000151037						0	0	0	0	0	0	0	62	18	16	0		
ENSMUST00000151039	ENSMUSG00000042918	7	45639977	45646521	1	0	0	0	0	0	2	2	0	0	0	0	F6XRP9	
ENSMUST00000151041						1	3	0	1	2	1	4	7	0	2	21		
ENSMUST00000151042						0	0	0	0	0	0	4	0	20	0	0		
ENSMUST00000151044						1	0	1	1	1	0	0	10	8	0	33		
ENSMUST00000151045	ENSMUSG00000020524	11	57011387	57330244	1	10	19	0	37	20	20	0	0	0	0	0	F6YNQ1	
ENSMUST00000151046						0	0	1	26	0	1	0	28	5	0	2		
ENSMUST00000151047						160	90	870	231	75	48	64	292	63	33	143		
ENSMUST00000151048						14	17	44	26	26	6	0	0	0	0	0		
ENSMUST00000151049						20	12	20	10	13	2	3	8	5	6	7		
ENSMUST00000151050						5	3	7	2	1	3	0	0	0	0	0		
ENSMUST00000151052						18	9	30	22	21	4	5	3	5	0	3		
ENSMUST00000151053						0	0	1	4	0	0	0	1	0	0	0		
ENSMUST00000151054						2	0	0	1	2	0	7	7	0	1	5		
ENSMUST00000151055	ENSMUSG00000042197	1	33761545	33814595	-1	3	3	1	0	0	1	0	0	0	0	0	A0A0A6YWV3	
ENSMUST00000151056						0	1	0	0	0	0	26	12	1	4	18		
ENSMUST00000151057						2	2	0	0	5	2	3	32	20	51	18		
ENSMUST00000151058						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000151059						0	9	0	0	10	0	0	25	0	86	1		
ENSMUST00000151060						3	4	3	5	3	0	0	0	0	0	0		
ENSMUST00000151061						17	13	32	21	25	19	117	710	176	15	270		
ENSMUST00000151062						0	0	1	6	1	0	2	0	1	2	0		
ENSMUST00000151063	ENSMUSG00000055850	6	72359714	72366956	-1	0	0	0	4	1	2	3	2	3	0	10	S4R2J5	
ENSMUST00000151065						13	11	43	55	4	7	1	35	23	0	28		
ENSMUST00000151066	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	0	0	0	0	81	21	0	0	D3YY68	
ENSMUST00000151067						0	0	0	0	1	0	29	85	8	36	10		
ENSMUST00000151068						15	8	22	12	13	4	324	1013	378	87	475		
ENSMUST00000151071	ENSMUSG00000030207	6	135197977	135244955	1	2	0	6	40	5	2	0	0	0	0	2	E0CXF7	
ENSMUST00000151072	ENSMUSG00000022439	15	84324026	84342978	1	0	0	2	0	0	0	0	2	0	0	3	F2Z489	
ENSMUST00000151073						1	0	28	1	5	5	0	1	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151074						0	0	0	0	2	0	0	0	0	6	6		
ENSMUST00000151075						4	7	4	4	3	0	15	73	20	24	14		
ENSMUST00000151077	ENSMUSG00000039543	14	20394190	20452226	-1	0	0	0	0	6	0	0	0	0	0	0	D3Z337	
ENSMUST00000151078	ENSMUSG00000005882	2	155846894	155930310	-1	18	13	0	0	0	0	16	0	0	0	38	D6RDC3	
ENSMUST00000151079						7	0	4	10	5	2	7	51	24	11	44		
ENSMUST00000151080						7	3	0	18	8	5	0	0	0	0	0		
ENSMUST00000151081	ENSMUSG00000004642	5	33634952	33652574	-1	0	0	0	55	0	0	0	0	0	0	0	D3Z1S0	
ENSMUST00000151082						1	0	0	0	1	0	12	13	0	0	0		
ENSMUST00000151083	ENSMUSG00000078490	4	155409190	155466823	1	76	52	331	115	66	46	0	4	0	1	4		Q3UY96
ENSMUST00000151084	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	10	0	12	0	F6VJ22	
ENSMUST00000151085						0	0	0	3	5	0	10	9	17	3	21		
ENSMUST00000151086	ENSMUSG00000037072	3	144570304	144597680	1	1	0	6	0	2	2	0	0	3	4	3	A0A0G2JEF3	
ENSMUST00000151087						0	2	4	3	0	1	0	0	0	0	0		
ENSMUST00000151088						2	1	1	2	6	2	3	1	4	0	2		
ENSMUST00000151089						0	0	0	0	0	0	0	0	0	12	0		
ENSMUST00000151090						20	10	20	21	17	9	0	10	5	0	6		
ENSMUST00000151092						0	0	7	15	0	8	0	0	0	0	0		
ENSMUST00000151093						6	5	6	22	6	3	0	0	1	1	0		
ENSMUST00000151095						1	0	2	2	3	0	1	5	0	0	1		
ENSMUST00000151097	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	0	0	0	0	0	0	0	0	A2AT61	
ENSMUST00000151098	ENSMUSG00000063564	11	51289920	51583918	1	0	1	3	0	6	3	0	0	0	0	1	B1ATK5	
ENSMUST00000151100						0	0	0	48	0	3	0	0	0	0	0		
ENSMUST00000151102						4	3	11	9	6	5	0	0	0	0	3		
ENSMUST00000151103						3	0	6	146	10	2	1	1	0	2	0		
ENSMUST00000151104	ENSMUSG00000029167	5	51454250	51567726	-1	0	0	2	0	0	2	0	0	0	0	0	D3Z4V5	O70343
ENSMUST00000151105						147	147	1584	193	108	55	4	24	10	7	8		
ENSMUST00000151106						8	3	0	2	4	3	7	171	29	7	63		
ENSMUST00000151107	ENSMUSG00000045639	7	127607031	127615797	-1	0	2	0	21	2	0	1	0	0	2	0	A0A087WSE9	
ENSMUST00000151108						0	2	0	0	1	0	0	174	0	0	0		
ENSMUST00000151109						0	0	1	13	1	0	0	0	0	1	0		
ENSMUST00000151110	ENSMUSG00000057530	4	137862237	137965229	1	0	0	0	83	1	2	0	1	2	0	0	B1AXF8	
ENSMUST00000151111						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000151113	ENSMUSG00000012126	4	134102570	134127593	1	0	0	0	0	0	0	7	30	4	0	5	I7HM02	
ENSMUST00000151114	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	0	0	0	0	0	313	0	406		Q9WV30
ENSMUST00000151115						1	0	0	2	0	8	1	0	1	0	0		
ENSMUST00000151116	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000151117						1	1	3	0	0	3	1	2	7	0	10		
ENSMUST00000151118						3	0	0	17	0	0	1532	6805	2317	13477	1851		
ENSMUST00000151119	ENSMUSG00000040268	7	130865756	130913312	1	0	4	4	2	3	0	3	19	8	0	12	D6RCU3	
ENSMUST00000151120	ENSMUSG00000007891	7	142371148	142388038	-1	0	22	46	118	24	5	28875	23577	16443	7872	9694	Q3UCD9	P18242
ENSMUST00000151121	ENSMUSG00000040940	7	24902912	24926594	1	0	1	5	8	6	1	9	10	18	0	36	D3YVJ9	
ENSMUST00000151123	ENSMUSG00000030701	7	100642892	100662414	-1	1	1	19	3	0	2	0	0	0	0	0	D3YZT7	
ENSMUST00000151124						3	5	5	7	8	0	0	0	1	0	0		
ENSMUST00000151125						0	0	0	0	0	0	50	0	112	14	95		
ENSMUST00000151126						2	2	2	0	3	3	5	25	16	0	10		
ENSMUST00000151127	ENSMUSG00000029001	4	148152800	148160482	-1	11	12	28	24	14	4	0	0	0	0	1	G3UYF5	
ENSMUST00000151128						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000151129	ENSMUSG00000028691	4	116685544	116700822	1	1	0	0	16	2	0	120	553	114	0	0	B1AXW5	
ENSMUST00000151130	ENSMUSG00000033256	2	122348892	122369162	-1	0	0	0	0	4	0	0	0	0	0	0	F7AIV2	
ENSMUST00000151131						12	2	28	12	8	2	8	72	21	9	33		
ENSMUST00000151132						3	0	0	16	0	1	0	0	0	0	0		
ENSMUST00000151133						0	0	0	1	1	0	5	10	4	5	7		
ENSMUST00000151134						31	24	33	45	17	17	1	2	0	0	0		
ENSMUST00000151135						4	4	10	4	3	2	0	0	0	0	1		
ENSMUST00000151137	ENSMUSG00000030695	7	126795234	126800751	-1	0	0	4	7	3	0	2045	522	1557	122	938	D3YWI1	
ENSMUST00000151139						1	0	0	1	0	1	0	0	0	1	3		
ENSMUST00000151140						0	3	1	0	1	7	0	0	0	0	0		
ENSMUST00000151142						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000151143						2	0	6	1	5	0	12	330	17	15	75		
ENSMUST00000151144	ENSMUSG00000055360	13	13182715	13191923	1	2	2	4	0	0	4	0	0	0	0	0	F2Z418	
ENSMUST00000151145						3	1	0	2	8	2	0	4	6	0	7		
ENSMUST00000151146	ENSMUSG00000022436	15	78899667	78919517	1	0	0	0	2	0	0	0	0	0	0	0	S4R2T6	
ENSMUST00000151147						0	0	4	3	3	0	1	0	0	0	0		
ENSMUST00000151148	ENSMUSG00000035637	4	44981395	44990734	1	0	0	2	0	0	0	18	0	0	0	0	B1AXQ0	
ENSMUST00000151149	ENSMUSG00000030269	6	113237843	113281392	1	0	1	7	0	8	2	0	9	10	22	27	F7BA73	
ENSMUST00000151150						20	18	75	29	34	8	0	0	0	0	0		
ENSMUST00000151151						2	3	0	2	3	1	12	185	68	48	67		
ENSMUST00000151152	ENSMUSG00000058248	1	192190774	192510159	1	18	10	28	0	14	5	0	0	0	0	0	A0A0A6YVS8	
ENSMUST00000151153	ENSMUSG00000008398	10	93247414	93311135	-1	5	0	1	2	0	0	7	62	13	26	10	G3UVW8	
ENSMUST00000151154						50	56	36	41	45	32	0	6	4	0	4		
ENSMUST00000151155	ENSMUSG00000024150	17	87254658	87265935	-1	0	0	3	0	0	0	42	26	53	17	49	D3Z1G3	
ENSMUST00000151156						3	1	2	6	8	0	0	0	7	0	11		
ENSMUST00000151158						5	3	0	2	0	0	25	23	12	0	18		
ENSMUST00000151160	ENSMUSG00000025142	11	120672973	120709447	1	0	5	6	2	2	1	6	4	0	0	10	A2AC05	
ENSMUST00000151161						4	0	0	0	3	0	0	0	2	0	4		
ENSMUST00000151162	ENSMUSG00000040007	2	118900377	118924528	1	8	2	6	99	3	0	0	0	0	0	0	Z4YMJ8	
ENSMUST00000151163						22	29	75	29	25	22	12	42	113	212	118		
ENSMUST00000151165	ENSMUSG00000017132	11	118132019	118248592	-1	0	1	1	2	3	3	29	15	67	0	35	B1AQE4	
ENSMUST00000151167						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151168						22	22	87	37	49	26	0	2	0	0	0		
ENSMUST00000151169						4	1	3	1	2	0	0	1	0	0	3		
ENSMUST00000151171						1	0	3	0	1	0	4	75	18	1	16		
ENSMUST00000151172						0	0	0	1	0	0	0	0	0	3	1		
ENSMUST00000151173	ENSMUSG00000029464	5	122371876	122382902	1	1	5	7	2	1	0	5	12	8	6	10	F7CWA0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151174						55	46	65	26	58	32	56	37	95	12	103		
ENSMUST00000151175						1	3	1	8	2	2	0	0	0	0	0		
ENSMUST00000151176	ENSMUSG00000037860	1	173350879	173466040	1	0	0	0	0	0	0	2	27	10	8	15	D3Z341	
ENSMUST00000151177	ENSMUSG00000041328	7	92643712	92669933	-1	11	9	141	6	14	5	100	1445	400	94	306	F6UFZ5	
ENSMUST00000151178						0	0	0	77	0	0	0	0	0	0	0		
ENSMUST00000151179						1	1	0	2	2	0	0	0	0	0	0		
ENSMUST00000151180	ENSMUSG00000050050	5	92607954	92675271	-1	10	12	75	21	0	8	1	3	2	0	2		Q8CDI6
ENSMUST00000151181						0	0	1	1	1	1	0	0	0	1	0		
ENSMUST00000151182						0	0	0	178	2	1	0	0	0	0	0		
ENSMUST00000151183	ENSMUSG00000022701	16	43889800	43964314	1	0	0	2	0	2	2	2	5	0	6	0	A9C444	
ENSMUST00000151184	ENSMUSG00000004455	5	122158278	122175273	1	0	0	0	0	0	3	306	1106	115	78	107	A0A0G2JE42	
ENSMUST00000151186						43	53	409	54	60	24	0	6	2	0	0		
ENSMUST00000151187	ENSMUSG00000029782	6	30479053	30509783	-1	16	7	20	18	11	7	2	5	4	0	6	Q8C214	
ENSMUST00000151189	ENSMUSG00000033184	18	46560235	46597535	-1	0	0	0	18	0	0	324	610	456	109	359	D3YZZ5	
ENSMUST00000151191						0	0	0	31	0	3	0	0	0	0	6		
ENSMUST00000151192						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151193						0	0	0	0	0	0	121	546	117	111	88		
ENSMUST00000151194						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151195						14	5	20	17	19	5	87	146	134	25	143		
ENSMUST00000151196	ENSMUSG00000038770	5	144983519	145084030	-1	4	6	2	28	4	4	0	0	0	0	0	D3Z0I2	
ENSMUST00000151197	ENSMUSG00000000167	9	50617321	50625000	1	0	0	0	39	0	0	0	0	1	0	3	D3Z2K7	
ENSMUST00000151199						1	2	2	1	3	0	0	0	0	0	0		
ENSMUST00000151200						0	0	2	5	0	0	0	0	12	0	0		
ENSMUST00000151201	ENSMUSG00000035266	5	100762145	100798598	-1	7	6	20	120	10	3	4	0	2	0	0	Q8BKT5	
ENSMUST00000151202	ENSMUSG00000035621	10	80148272	80158368	1	3	0	5	233	0	2	0	7	4	3	12	D3YYX7	
ENSMUST00000151203	ENSMUSG00000028708	4	115839198	115879250	1	0	0	1	0	0	0	43	0	33	7	0	F6YIU3	
ENSMUST00000151204						0	8	2	7	6	8	4	4	1	0	2		
ENSMUST00000151205						5	3	10	7	2	0	4	0	0	0	0		
ENSMUST00000151206						0	1	1	3	0	0	8	24	10	6	22		
ENSMUST00000151208						0	0	1	3	3	2	1	0	3	0	0		
ENSMUST00000151210						4	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000151211						4	0	3	0	3	0	0	0	0	0	7		
ENSMUST00000151212	ENSMUSG00000006345	10	75561604	75586200	1	5	0	3	6	4	0	3	1	3	0	3	D3Z2C6	
ENSMUST00000151213						7	3	8	11	4	0	0	0	2	0	0		
ENSMUST00000151214	ENSMUSG00000004267	6	124760053	124769673	-1	1	0	2	0	0	3	0	0	0	0	0		
ENSMUST00000151218	ENSMUSG00000018906	11	54100095	54131665	1	6	0	7	1	1	0	0	0	0	0	2	B0QZH2	
ENSMUST00000151219						0	1	0	0	1	1	0	36	18	0	17		
ENSMUST00000151221						5	1	2	0	0	5	4009	1995	2578	333	2278		
ENSMUST00000151222						0	1	10	21	13	3	9	55	15	14	32		
ENSMUST00000151223						4	1	1	0	2	3	0	17	4	0	18		
ENSMUST00000151224	ENSMUSG00000009216	2	27110380	27142491	-1	26	9	52	187	31	14	0	0	0	0	0	B2RVN8	Q8BUM6
ENSMUST00000151225						12	6	8	10	9	6	10	14	10	1	6		
ENSMUST00000151226						40	32	99	37	30	27	3	0	0	0	1		
ENSMUST00000151227	ENSMUSG00000037463	7	28692849	28699338	1	1	0	0	41	2	0	0	0	0	0	2	D3Z3I2	
ENSMUST00000151228	ENSMUSG00000046311	11	49203292	49218816	1	0	0	0	0	0	0	5	0	0	0	0	J3JS22	
ENSMUST00000151230						0	1	0	0	0	0	1	7	0	2	0		
ENSMUST00000151231	ENSMUSG00000046774	X	101794656	101798642	1	4	2	21	0	15	7	0	0	0	0	0	E9Q4Y8	
ENSMUST00000151232						2	0	0	0	3	0	1	0	0	0	2		
ENSMUST00000151233						7	1	4	4	3	7	0	3	0	0	0		
ENSMUST00000151234						6	1	9	4	7	2	0	0	0	0	0		
ENSMUST00000151235						1	3	0	0	5	3	6	69	16	5	27		
ENSMUST00000151236						5	3	2	7	3	4	1	1	0	0	0		
ENSMUST00000151237	ENSMUSG00000042105	7	128611328	128696425	1	0	0	0	0	0	0	27	231	0	43	19		
ENSMUST00000151238						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151239	ENSMUSG00000047617	2	25455141	25461094	-1	0	0	0	0	0	0	0	36	0	0	0	A2AJ30	
ENSMUST00000151240						478	427	637	370	490	280	32	22	87	9	114		
ENSMUST00000151241						2	1	7	1	4	0	0	0	0	0	0		
ENSMUST00000151242	ENSMUSG00000000730	10	78041947	78063622	1	0	9	0	0	0	6	0	4	0	0	0	A3EWM2	Q9CWR8
ENSMUST00000151243	ENSMUSG00000006611	13	23702034	23710854	-1	297	248	270	213	273	117	25	102	36	12	47	F7CW53	
ENSMUST00000151244	ENSMUSG00000022708	16	42875881	43642602	1	1	2	0	4	2	3	0	0	4	0	0	E0CX28	
ENSMUST00000151245						0	0	0	28	0	0	0	7	8	2	0		
ENSMUST00000151246	ENSMUSG00000029001	4	148152800	148160482	-1	0	1	0	12	0	0	0	0	0	0	0	A2A7H4	
ENSMUST00000151247						0	0	0	0	0	0	0	0	3	0	0		
ENSMUST00000151248						3	0	1	1	3	0	0	5	3	2	0		
ENSMUST00000151249	ENSMUSG00000028261	4	24898083	24905001	1	0	0	1	0	0	0	1	7	0	20	5	A2AJX3	
ENSMUST00000151250						2	3	3	0	7	2	156	327	73	0	44		
ENSMUST00000151251						7	3	2	1	5	4	11	16	34	2	32		
ENSMUST00000151252						456	496	2120	377	416	159	8	10	11	0	12		
ENSMUST00000151253						3	5	12	0	0	3	0	0	0	0	0		
ENSMUST00000151254	ENSMUSG00000030663	7	116039397	116105210	1	0	0	0	0	0	8	19	0	24	0	0	D6RI64	
ENSMUST00000151255						13	11	38	25	15	9	0	0	0	3	4		
ENSMUST00000151256						3	0	3	0	2	0	0	0	0	0	0		
ENSMUST00000151257						0	7	2	11	4	1	0	1	0	0	0		
ENSMUST00000151258	ENSMUSG00000030760	7	98206389	98321208	-1	0	0	27	0	23	0	0	63	0	0	54	Q8CIG2	
ENSMUST00000151261						0	2	0	2	0	2	0	0	0	0	0		
ENSMUST00000151262						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151263						0	0	17	2	1	0	8	83	15	3	21		
ENSMUST00000151264	ENSMUSG00000038406	7	45002948	45016363	-1	3	2	7	19	1	2	28	35	36	1	56	D3YYM8	
ENSMUST00000151265	ENSMUSG00000012350	2	103263433	103303278	-1	3	3	7	2	1	0	0	0	0	0	0	A2BIB6	
ENSMUST00000151266	ENSMUSG00000003531	16	18052860	18071632	1	0	0	0	3	7	0	0	40	16	0	8	D3Z558	
ENSMUST00000151268						0	0	31	0	3	1	601	579	289	36	216		
ENSMUST00000151269						10	9	15	7	17	12	0	0	0	0	0		
ENSMUST00000151270						0	3	8	11	5	3	0	0	0	0	0		
ENSMUST00000151271						0	0	0	3	0	1	0	3	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151272	ENSMUSG00000026036	1	58445151	58481816	1	3	5	6	2	5	0	0	0	0	0	7	D3YYF0	
ENSMUST00000151273	ENSMUSG00000035311	10	88379132	88447329	1	26	25	50	0	33	21	0	336	0	51	0	D6RJ30	
ENSMUST00000151274						0	0	5	0	0	0	0	2	0	0	0		
ENSMUST00000151276	ENSMUSG00000001864	2	31950139	31973442	1	0	0	0	22	0	0	0	0	0	0	0	A0A0A6YW96	
ENSMUST00000151277						152	105	288	472	199	92	3	5	10	1	11		
ENSMUST00000151278						7	8	0	3	10	0	0	4	3	1	0		
ENSMUST00000151279						1	2	0	0	0	0	0	0	0	0	3		
ENSMUST00000151280	ENSMUSG00000028497	4	88396144	88438928	-1	13	19	6	22	16	11	1227	7340	2469	1284	1427	F7CPS1	
ENSMUST00000151281	ENSMUSG00000033740	1	6487231	6860940	1	2	0	0	0	0	0	0	0	0	0	0	Q148A0	Q80TY4
ENSMUST00000151283						3	2	0	0	6	0	1	12	4	33	19		
ENSMUST00000151284						0	3	0	5	9	1	4	2	0	0	5		
ENSMUST00000151285	ENSMUSG00000041408	14	34673928	34747983	1	3	3	0	0	1	0	97	574	94	13	1	F6YCH1	
ENSMUST00000151286						7	1	2	5	0	0	0	5	0	0	16		
ENSMUST00000151287	ENSMUSG00000068039	17	12915701	12925067	1	6	6	5	2	14	1	152	310	203	160	176		P11983
ENSMUST00000151288	ENSMUSG00000079020	15	73577424	73645762	-1	50	45	117	66	68	37	48	57	27	17	62		Q0P5V9
ENSMUST00000151289	ENSMUSG00000040451	19	32122727	32389714	-1	4	0	4	50	8	0	550	1742	967	620	619		Q8VCQ6
ENSMUST00000151290						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000151291						0	1	0	0	0	1	0	0	0	0	2		
ENSMUST00000151292						61	43	222	0	49	15	46	121	14	16	130		
ENSMUST00000151293	ENSMUSG00000024187	17	26211822	26244223	-1	0	3	2	3	0	0	0	0	5	0	8	D3Z6P3	
ENSMUST00000151294						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151295						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000151296	ENSMUSG00000026096	1	53313624	53326343	1	0	0	0	0	0	0	0	36	0	91	0	M0QWD2	
ENSMUST00000151297						4	2	10	1	0	8	0	0	4	0	0		
ENSMUST00000151298	ENSMUSG00000027088	2	69789623	69800005	1	0	1	0	25	0	2	6	17	15	21	0	B0R0D2	
ENSMUST00000151300						0	0	31	0	1	0	0	0	2	1	2		
ENSMUST00000151301						4	0	0	0	9	0	0	0	0	0	0		
ENSMUST00000151302						2	3	4	0	2	0	0	0	0	1	0		
ENSMUST00000151304						16	4	20	143	26	16	46	73	57	8	82		
ENSMUST00000151305	ENSMUSG00000078627	11	105360798	105456735	-1	0	0	0	0	3	0	0	0	0	0	0	F6WKB0	
ENSMUST00000151306						2	0	5	71	7	2	0	0	0	0	3		
ENSMUST00000151307	ENSMUSG00000024691	19	12545740	12589768	1	13	0	65	23	0	0	0	27	9	11	6	D3YYD2	
ENSMUST00000151308	ENSMUSG00000059486	6	56777524	56797813	-1	3	0	0	4	0	0	4	0	0	0	1		
ENSMUST00000151309	ENSMUSG00000033569	1	25067476	25829707	-1	7	0	10	4	16	0	0	0	0	0	0		Q80ZF8
ENSMUST00000151311	ENSMUSG00000063889	18	3266048	3337748	-1	5	0	0	0	5	0	0	0	0	7	4	D3YXV5	
ENSMUST00000151312						7	6	10	3	5	6	1	0	1	0	1		
ENSMUST00000151313						7	3	3	3	2	1	0	2	0	0	4		
ENSMUST00000151314	ENSMUSG00000040701	14	55098578	55106593	-1	4	3	11	7	10	5	48	138	67	10	64	D6RFT7	
ENSMUST00000151315						3	2	2	2	0	0	2	0	0	0	0		
ENSMUST00000151316	ENSMUSG00000028542	4	117834506	117875198	1	0	0	1	2	2	1	0	0	0	0	0		
ENSMUST00000151317						0	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000151318	ENSMUSG00000019518	5	138172002	138180429	1	0	0	0	0	0	0	0	0	0	0	0	E9Q9U6	
ENSMUST00000151319	ENSMUSG00000037458	15	38487430	38519266	-1	0	1	0	0	0	1	133	256	608	172	381	D3Z2P3	
ENSMUST00000151320	ENSMUSG00000027668	3	32529465	32579239	1	5	1	10	4	7	3	0	9	2	0	6	F6XRI9	
ENSMUST00000151321						1	3	7	12	7	4	3	58	20	3	41		
ENSMUST00000151322	ENSMUSG00000029095	5	35757880	35884973	1	7	0	0	2	6	4	0	0	0	0	0	F7A5C5	
ENSMUST00000151323						2	0	1	4	1	0	15	16	30	33	44		
ENSMUST00000151324						1	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000151325						7	1	0	8	7	0	3	6	2	0	7		
ENSMUST00000151326	ENSMUSG00000009108	3	108092789	108101432	1	0	2	6	13	0	4	0	2	0	1	5	A2AE32	
ENSMUST00000151327						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000151328						1	1	0	3	3	0	0	0	0	0	0		
ENSMUST00000151329						2	0	8	2	3	4	2	0	0	0	0		
ENSMUST00000151330	ENSMUSG00000067081	1	89950220	90014666	-1	0	0	0	0	0	0	0	0	0	0	0	D6REF8	
ENSMUST00000151332	ENSMUSG00000025887	9	5345430	5373032	1	0	0	0	2	3	3	0	8	5	24	12	E9Q575	
ENSMUST00000151333						5	4	9	5	8	7	5	22	9	0	33		
ENSMUST00000151334						12	15	36	10	10	2	0	82	26	7	24		
ENSMUST00000151335						3	0	0	10	0	5	0	1	0	0	1		
ENSMUST00000151336						3	2	14	4	8	3	2	25	4	2	4		
ENSMUST00000151338	ENSMUSG00000026034	1	58410189	58424066	-1	0	0	0	0	0	0	32	1432	515	604	379		P22518
ENSMUST00000151339						4	8	16	14	9	5	2	0	0	85	3		
ENSMUST00000151340	ENSMUSG00000026649	1	171113918	171126967	1	0	0	0	0	0	0	0	0	0	0	0	D3Z0N5	
ENSMUST00000151341	ENSMUSG00000024905	19	3388857	3407823	1	9	8	17	50	10	5	1	3	0	0	0	Q9D571	
ENSMUST00000151342						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000151343						138	78	1887	225	83	32	1	10	1	0	2		
ENSMUST00000151345						0	0	0	0	1	0	3	0	5	0	0		
ENSMUST00000151346	ENSMUSG00000028649	4	123349633	123684360	-1	0	0	0	0	0	0	442	157	1352	83	2009	F7ACR9	
ENSMUST00000151347						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151348	ENSMUSG00000030979	7	133686243	133710072	-1	71	79	138	19	19	8	4	8	4	1	1	E9Q8N3	
ENSMUST00000151349						0	0	0	0	0	0	0	0	2	1	0		
ENSMUST00000151350	ENSMUSG00000058626	17	45630204	45659325	-1	2	0	2	0	0	2	0	0	0	0	0	A0A0A0MQJ1	
ENSMUST00000151351						3	1	3	6	7	4	6	19	26	4	29		
ENSMUST00000151352	ENSMUSG00000029454	5	121525038	121545905	-1	4	1	1	3	2	0	0	15	1	0	3	A0A0G2JGA5	
ENSMUST00000151353	ENSMUSG00000047694	X	98936316	98949017	1	0	0	3	9	0	0	3	0	10	22	0	B1AV66	
ENSMUST00000151354						8	4	70	16	10	0	4	27	0	5	43		
ENSMUST00000151355						4	1	2	3	7	3	0	0	0	0	0		
ENSMUST00000151357						3	1	1	0	3	0	0	0	0	0	0		
ENSMUST00000151358						0	0	0	0	0	0	13	5	16	0	8		
ENSMUST00000151359						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000151360	ENSMUSG00000022272	15	25622525	25813673	1	1	3	6	5	3	3	0	0	0	0	0	D3Z2E0	
ENSMUST00000151361						0	0	0	40	0	3	70	0	60	0	25		
ENSMUST00000151362						0	0	5	0	0	0	0	0	0	0	9		
ENSMUST00000151364						93	77	191	106	124	61	4	58	28	18	32		
ENSMUST00000151365	ENSMUSG00000078923	2	167607638	167632095	-1	0	3	9	3	1	0	243	307	153	0	122	B7ZBY7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151366						4	1	11	0	2	0	9	104	9	17	23		
ENSMUST00000151368						1	0	6	123	10	0	100	145	244	10	248		
ENSMUST00000151370						14	0	34	17	14	11	55	266	127	33	237		
ENSMUST00000151371						1	3	2	3	0	1	0	2	0	0	0		
ENSMUST00000151372	ENSMUSG00000039662	4	152297227	152307121	1	32	6	26	0	59	0	541	538	429	0	357	Q6PGA6	
ENSMUST00000151373	ENSMUSG00000000631	11	77763246	77865980	1	3	2	42	11	9	5	11	1	6	1	7	E9PUR2	
ENSMUST00000151375						0	3	11	1	2	3	0	11	2	0	0		
ENSMUST00000151376	ENSMUSG00000091028	9	3000922	3002330	1	13916	13830	14336	12058	14213	10932	3	3	4	7	4	F6VLK5	
ENSMUST00000151377						0	4	6	0	1	8	0	24	0	0	4		
ENSMUST00000151378						0	2	3	1	2	0	0	0	2	0	2		
ENSMUST00000151379						0	0	1	0	1	0	0	3	3	0	5		
ENSMUST00000151380	ENSMUSG00000027102	2	74704615	74707933	1	0	0	1	11	2	1	0	0	0	0	0	F6W963	
ENSMUST00000151382						0	0	0	34	0	0	0	0	0	0	0		
ENSMUST00000151383						4	8	1	4	2	3	0	0	0	0	0		
ENSMUST00000151384						7	0	8	188	0	3	13	114	35	8	93		
ENSMUST00000151385	ENSMUSG00000078652	11	101316213	101323537	1	0	0	3	0	1	0	33	0	86	5	32	A2A4J1	
ENSMUST00000151386						1	0	0	0	4	2	20	0	0	3	17		
ENSMUST00000151387	ENSMUSG00000079636	X	37458585	37473964	1	4	0	0	0	0	0	0	0	0	0	0	G3UX41	
ENSMUST00000151388						9	16	33	10	14	7	0	0	0	0	0		
ENSMUST00000151389						1	3	2	1	0	1	2	2	0	1	0		
ENSMUST00000151390	ENSMUSG00000034674	10	82629828	82650799	1	24	9	45	26	36	25	21	101	25	21	16		P56581
ENSMUST00000151392						3	0	0	2	0	1	0	57	7	0	4		
ENSMUST00000151393	ENSMUSG00000030035	6	83119044	83121559	-1	6	0	17	0	16	4	0	87	0	4	0		
ENSMUST00000151394						3	0	0	69	3	0	39	110	78	287	89		
ENSMUST00000151395						0	0	7	2	3	2	0	0	0	0	0		
ENSMUST00000151396						4	1	11	3	4	5	1	0	1	1	3		
ENSMUST00000151397	ENSMUSG00000040797	6	121372933	121473678	-1	44	54	117	210	56	45	0	0	0	0	0		
ENSMUST00000151399						9	6	22	0	11	4	0	0	0	0	0		
ENSMUST00000151400	ENSMUSG00000031452	8	13550733	13562461	-1	0	0	0	0	0	0	2	0	0	0	0	E9PY36	
ENSMUST00000151402						1	0	0	4	0	0	2	16	26	2	23		
ENSMUST00000151403	ENSMUSG00000025272	X	150645304	150657583	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q098	
ENSMUST00000151404						4	10	13	8	19	9	0	0	0	0	0		
ENSMUST00000151405	ENSMUSG00000050335	14	47367751	47386160	1	2	3	3	0	2	2	0	0	0	0	0	D3YZJ2	
ENSMUST00000151406	ENSMUSG00000027323	2	119112793	119147445	1	2	0	1	4	3	0	11	0	6	3	8	F7AT35	
ENSMUST00000151407						0	1	1	4	2	0	12	91	15	3	21		
ENSMUST00000151408	ENSMUSG00000021708	13	91880400	92131656	-1	23	24	39	25	36	12	0	7	5	1	13	F7B9R2	
ENSMUST00000151409						2	2	2	129	6	0	0	0	0	0	0		
ENSMUST00000151410						16	21	12	5	9	10	9	12	31	2	22		
ENSMUST00000151411						0	0	0	0	2	0	0	0	0	1	0		
ENSMUST00000151412						1	1	5	7	1	2	1	0	0	0	0		
ENSMUST00000151413	ENSMUSG00000061451	19	5070859	5085531	-1	2	3	4	0	0	1	0	0	0	1	0	D3YTM7	
ENSMUST00000151414	ENSMUSG00000035297	5	100518309	100547803	1	0	0	0	0	0	0	24	17	25	123	18	D3YV99	
ENSMUST00000151415						3	4	0	0	2	2	0	0	0	0	1		
ENSMUST00000151416						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000151418						1	3	2	1	6	0	0	19	0	0	0		
ENSMUST00000151419						5	0	0	0	0	2	3	17	0	0	5		
ENSMUST00000151420						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151421	ENSMUSG00000066129	7	139894696	139941537	1	37	27	41	90	45	24	0	0	0	0	0	D3Z5B8	
ENSMUST00000151422						0	0	1	33	0	0	0	0	0	0	0		
ENSMUST00000151423						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000151424						1	0	2	32	2	1	10	21	6	5	17		
ENSMUST00000151425						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151428						1	5	10	0	11	4	0	1	1	0	0		
ENSMUST00000151429						2	1	0	0	2	3	0	0	2	0	0		
ENSMUST00000151430	ENSMUSG00000037475	X	41794991	41920674	-1	0	0	0	0	0	1	8	130	54	124	113	F6SBF2	
ENSMUST00000151431						0	0	2	0	0	0	4	0	81	10	45		
ENSMUST00000151432						4	0	0	0	5	2	0	0	0	0	0		
ENSMUST00000151433						41	42	104	80	47	36	5	15	5	2	23		
ENSMUST00000151435						6	0	3	2	10	0	34	584	4	49	42		
ENSMUST00000151436	ENSMUSG00000018474	11	69343273	69369406	-1	2	8	0	2	3	1	0	0	0	2	0	F6V4V3	
ENSMUST00000151437						1	2	7	2	5	0	0	0	0	0	0		
ENSMUST00000151439						7	0	13	42	6	6	4	23	6	0	18		
ENSMUST00000151440	ENSMUSG00000040483	11	72301629	72313733	1	3	2	6	4	8	1	0	4	2	0	0	Z4YN17	
ENSMUST00000151441						6	4	4	12	6	2	7	17	10	7	8		
ENSMUST00000151442						4	4	22	0	4	0	10	0	33	0	74		
ENSMUST00000151444						22	19	34	49	28	22	0	0	0	0	1		
ENSMUST00000151445						0	5	0	7	0	0	26	0	46	0	19		
ENSMUST00000151446	ENSMUSG00000004393	11	6258919	6267772	-1	2	2	0	0	0	1	15	0	0	0	0	Q5SVX2	
ENSMUST00000151447	ENSMUSG00000002617	17	23173869	23193252	-1	4	0	0	57	6	0	0	0	0	0	0	B1B1D4	
ENSMUST00000151448	ENSMUSG00000024124	17	23972126	23975230	-1	3	2	2	1	3	0	0	0	0	0	0	D6REI2	
ENSMUST00000151449	ENSMUSG00000057541	5	23740648	23783711	-1	1	3	0	4	0	1	4	0	0	0	5	F6XMS4	
ENSMUST00000151450						3	7	37	4	24	10	717	925	342	60	371		
ENSMUST00000151451	ENSMUSG00000030802	7	127904082	127910221	1	2	2	1	2	1	0	110	42	78	10	62	D3Z7R0	
ENSMUST00000151452						0	5	0	0	0	4	0	20	5	31	22		
ENSMUST00000151453						2	2	13	6	4	6	2	2	1	0	0		
ENSMUST00000151454						4	4	3	2	4	0	0	0	0	0	0		
ENSMUST00000151455						16	5	7	100	34	8	7	9	0	0	0		
ENSMUST00000151456						4	4	3	3	4	2	0	0	1	0	1		
ENSMUST00000151457						4	3	3	0	3	2	2	0	0	0	2		
ENSMUST00000151458	ENSMUSG00000042719	5	121397936	121444378	1	6	4	0	0	0	0	0	34	0	6	9	F6XQZ4	
ENSMUST00000151459						0	0	5	0	2	0	0	0	0	0	0		
ENSMUST00000151460						8	3	23	7	11	4	1	0	0	1	5		
ENSMUST00000151461						6	3	9	18	4	1	0	19	25	4	8		
ENSMUST00000151462						1	0	7	0	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151463						4	2	8	5	3	5	0	0	0	0	1		
ENSMUST00000151464	ENSMUSG00000048782	7	114743694	114850383	1	1	1	2	1	0	5	0	0	0	0	0	D3Z5D7	
ENSMUST00000151465	ENSMUSG00000027900	3	106547798	106575890	1	0	0	0	0	0	0	11	21	12	7	3	D3Z6B7	
ENSMUST00000151466	ENSMUSG00000038375	2	155381059	155389850	1	0	0	2	0	4	4	0	0	0	0	0	A2ARD1	
ENSMUST00000151467						4	1	8	56	1	2	3	16	6	0	9		
ENSMUST00000151468						19	20	12	7	15	14	0	0	5	0	1		
ENSMUST00000151469						2	3	6	17	8	5	0	2	0	1	8		
ENSMUST00000151470						0	2	1	0	7	3	0	0	0	0	1		
ENSMUST00000151473	ENSMUSG00000029670	6	21949571	21976038	1	0	0	0	0	0	0	0	43	0	0	29	D3YX13	
ENSMUST00000151474	ENSMUSG00000062110	5	74204816	74531759	-1	7	2	11	11	9	0	2	14	9	0	4	Q3TR67	Q8BTY8
ENSMUST00000151475						18	26	33	60	31	20	0	13	5	1	5		
ENSMUST00000151476						0	0	0	0	0	0	0	2	0	0	4		
ENSMUST00000151477	ENSMUSG00000039477	5	142724661	142817662	-1	10	0	0	1155	9	0	79	52	75	32	184	D3YV17	
ENSMUST00000151478						5	1	2	6	8	2	0	1	0	0	0		
ENSMUST00000151479						4	1	14	9	6	3	0	0	0	0	0		
ENSMUST00000151480						0	0	0	113	2	0	0	0	0	0	0		
ENSMUST00000151481						5	12	0	4	14	4	0	0	0	0	0		
ENSMUST00000151482						6	3	5	6	0	1	5	30	53	1	28		
ENSMUST00000151483						16	14	31	9	12	7	0	1	1	0	0		
ENSMUST00000151484	ENSMUSG00000005362	6	106780201	106800077	-1	0	1	3	0	3	0	0	0	31	232	24		
ENSMUST00000151485	ENSMUSG00000032020	9	41011098	41161697	-1	0	0	0	1	8	1	124	30	155	9	152		Q8BGG7
ENSMUST00000151486	ENSMUSG00000019823	10	41476314	41487032	1	1	1	13	8	8	3	3	4	5	0	4	D3Z5P6	
ENSMUST00000151487						0	0	0	0	0	0	0	10	0	0	4		
ENSMUST00000151488						2	3	11	5	7	4	775	680	736	150	646		
ENSMUST00000151489						5	8	0	3	13	3	82	67	17	17	53		
ENSMUST00000151490						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151491	ENSMUSG00000061751	16	33974258	34573532	-1	0	0	0	0	2	1	0	0	0	0	2	B1B1A7	
ENSMUST00000151492						0	0	9	0	0	0	17	0	2	0	18		
ENSMUST00000151493	ENSMUSG00000017760	2	164832873	164841032	1	0	0	0	7	0	0	0	0	0	0	0	A2A5J7	
ENSMUST00000151494	ENSMUSG00000027574	2	180934772	180954699	-1	0	0	0	0	3	1	0	0	0	0	0	F6YW57	
ENSMUST00000151495	ENSMUSG00000039307	11	121204433	121222655	1	0	0	0	0	0	0	0	0	0	0	0	F6UV46	
ENSMUST00000151496	ENSMUSG00000034449	11	84820856	84828994	-1	9	2	16	83	8	3	25	52	22	0	28	F2Z445	
ENSMUST00000151497						0	0	1	0	1	0	0	0	0	0	3		
ENSMUST00000151498	ENSMUSG00000018501	11	62316426	62458541	-1	2	4	6	1	3	4	133	49	253	2	219	Q3UV08	
ENSMUST00000151499						1	5	2	7	11	5	0	16	8	0	0		
ENSMUST00000151500						0	16	21	58	6	7	331	338	398	36	109		
ENSMUST00000151502						2	0	0	0	1	1	0	0	0	0	2		
ENSMUST00000151503						0	0	0	0	0	0	46	303	89	19	169		
ENSMUST00000151504						5	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000151505						34	27	50	52	47	29	2	26	0	0	0		
ENSMUST00000151506	ENSMUSG00000023467	7	45486262	45523632	1	0	0	3	22	3	0	0	0	0	0	0	D3Z489	
ENSMUST00000151507						9	3	11	17	9	0	0	0	0	0	1		
ENSMUST00000151508						2	2	0	27	3	0	0	0	1	3	0		
ENSMUST00000151509	ENSMUSG00000021376	13	47025170	47044737	-1	0	0	0	0	2	0	0	0	0	0	0	D6RIK3	
ENSMUST00000151510						0	2	0	8	2	0	0	0	0	0	0		
ENSMUST00000151511	ENSMUSG00000027498	2	172370681	172382448	1	0	0	0	11	0	2	28	2	29	3	18	A2APA3	
ENSMUST00000151513	ENSMUSG00000035530	11	100319885	100322096	1	1	1	1	71	2	3	7	133	21	7	39	J3QPZ8	
ENSMUST00000151514						0	2	10	11	1	3	0	0	0	0	0		
ENSMUST00000151515	ENSMUSG00000018569	11	69964779	69967885	1	5	1	6	17	0	1	0	1	0	0	0	J3QQ48	
ENSMUST00000151516	ENSMUSG00000045973	4	45395923	45408766	-1	0	0	0	0	0	0	0	0	26	5	10	G3UYJ3	
ENSMUST00000151517						13	6	73	193	42	21	251	826	261	45	363		
ENSMUST00000151518						38	24	47	43	35	20	4	26	22	1	21		
ENSMUST00000151519						0	3	0	0	1	0	0	0	0	0	1		
ENSMUST00000151520						5	3	5	6	3	2	0	0	0	0	0		
ENSMUST00000151522	ENSMUSG00000004668	11	9191942	9684259	1	0	1	1	5	0	3	0	0	0	0	0	A2AAW4	
ENSMUST00000151523						0	0	0	0	1	0	10	3	23	9	31		
ENSMUST00000151524	ENSMUSG00000021597	13	77043088	77135473	-1	4	9	5	38	8	0	21	46	35	38	15		Q8R3P9
ENSMUST00000151525						332	256	1218	384	357	160	6	11	6	4	12		
ENSMUST00000151526	ENSMUSG00000017631	11	76416734	76622314	-1	0	0	11	0	0	0	0	0	0	0	0	H3BKV6	
ENSMUST00000151527						1	0	3	3	3	1	2	5	4	0	7		
ENSMUST00000151528	ENSMUSG00000031302	X	101299168	101325963	1	16	0	141	107	0	0	0	0	0	0	0	A2AGI2	
ENSMUST00000151529	ENSMUSG00000026767	2	12347263	12419470	-1	1	1	0	0	1	0	0	9	4	0	7	F7BWU4	
ENSMUST00000151530						32	38	81	28	32	28	0	3	5	0	10		
ENSMUST00000151531						2	1	7	3	0	0	7	44	0	2	26		
ENSMUST00000151532						56	58	492	79	62	9	14	56	17	3	34		
ENSMUST00000151533						1	2	0	8	0	3	0	0	0	0	0		
ENSMUST00000151534						6	1	3	28	2	4	1	0	0	0	0		
ENSMUST00000151535	ENSMUSG00000028973	5	24393663	24410054	1	0	0	6	0	0	0	3	32	7	3	6	F6ZFC5	
ENSMUST00000151536						2	2	7	5	6	1	1	0	9	0	10		
ENSMUST00000151537						3	1	0	1	0	2	12	127	0	4	11		
ENSMUST00000151539						0	1	0	5	1	1	0	0	0	0	0		
ENSMUST00000151540						1	1	1	22	6	3	0	0	0	0	0		
ENSMUST00000151541						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151542	ENSMUSG00000039611	4	49584506	49597876	-1	0	0	0	0	0	0	0	0	0	0	0	A2AKL3	
ENSMUST00000151543	ENSMUSG00000003282	4	3900996	3938423	-1	0	0	0	0	0	0	0	0	1	0	0	D6RES7	
ENSMUST00000151544						0	0	0	0	0	0	9	18	22	0	33		
ENSMUST00000151545						1	11	5	2	6	4	0	0	1	0	7		
ENSMUST00000151546						9	4	11	4	7	4	64	176	56	9	119		
ENSMUST00000151547	ENSMUSG00000053964	7	28833854	28841708	1	1	0	0	0	0	0	2	0	8	2	12	A0A087WSD9	
ENSMUST00000151548						0	0	0	7	2	0	0	0	0	0	0		
ENSMUST00000151549						0	0	0	0	0	0	0	0	1	3	0		
ENSMUST00000151551						0	0	0	0	0	1	1	0	0	0	1		
ENSMUST00000151553						4	3	0	0	1	0	0	0	0	0	0		
ENSMUST00000151554						0	1	0	0	0	0	43	118	169	6	124		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151555						35	11	42	150	44	22	0	5	4	0	4		
ENSMUST00000151556						22	18	34	44	5	0	9	42	18	9	27		
ENSMUST00000151557						0	0	0	0	0	0	1	0	0	0	2		
ENSMUST00000151559						0	0	0	4	0	0	3	4	9	14	3		
ENSMUST00000151560						5	4	10	9	11	7	11	6	16	2	23		
ENSMUST00000151561						5	5	31	73	8	3	0	0	0	0	0		
ENSMUST00000151562						1	0	3	0	3	0	0	0	0	0	0		
ENSMUST00000151563	ENSMUSG00000006005	1	150392838	150449935	1	0	0	0	0	9	0	77	743	169	150	169	F6RX08	
ENSMUST00000151565						0	2	0	0	8	2	4	1	24	2	53		
ENSMUST00000151566	ENSMUSG00000021338	13	24012344	24280795	-1	1	3	0	3	1	5	1	2	2	0	3	F6XQY1	
ENSMUST00000151567	ENSMUSG00000036377	5	76656512	76873554	1	0	4	0	2	1	2	0	3	0	0	1	F7BFN2	
ENSMUST00000151568	ENSMUSG00000063015	5	93181933	93206495	-1	0	0	8	0	0	0	112	301	194	3	68	D3Z680	
ENSMUST00000151569	ENSMUSG00000038241	2	155956458	155998900	1	0	0	0	25	0	0	0	0	0	0	0	B7ZCN3	
ENSMUST00000151571						4	8	6	98	8	4	1	18	15	0	15		
ENSMUST00000151572						6	3	10	5	7	2	0	1	0	2	3		
ENSMUST00000151573	ENSMUSG00000047248	7	100372233	100470152	1	9	11	70	13	12	2	7	70	0	9	10	F6WK98	
ENSMUST00000151574						3	4	2	3	1	0	1	0	0	0	0		
ENSMUST00000151576						4	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000151577						1	2	1	81	3	0	0	1	1	0	3		
ENSMUST00000151578						0	0	0	12	0	0	0	6	0	0	0		
ENSMUST00000151579						0	1	3	0	2	0	0	0	0	0	0		
ENSMUST00000151580						0	2	3	0	5	0	0	0	0	0	0		
ENSMUST00000151581						0	0	0	20	0	0	5	0	0	36	0		
ENSMUST00000151582						100	104	214	205	94	56	21	48	35	5	75		
ENSMUST00000151583						4	0	4	7	0	0	0	0	8	0	4		
ENSMUST00000151584						2	2	1	0	0	0	6	11	0	7	40		
ENSMUST00000151585						8	6	11	27	8	4	3	4	1	0	0		
ENSMUST00000151586						4	0	1	8	0	2	4	3	5	2	13		
ENSMUST00000151587						13	11	67	16	16	9	6	20	17	0	40		
ENSMUST00000151588						15	27	25	40	33	9	9	13	22	4	26		
ENSMUST00000151589	ENSMUSG00000014198	11	100627543	100692455	-1	5	0	10	17	3	0	0	0	0	0	0	F6QJI2	
ENSMUST00000151590	ENSMUSG00000016933	2	160731300	160775760	1	4	2	8	15	13	5	0	0	0	0	0	G3UXP4	
ENSMUST00000151591						0	2	0	1	1	0	0	0	0	0	0		
ENSMUST00000151592	ENSMUSG00000054034	X	136200948	136203876	-1	1	1	0	4	0	0	0	0	0	0	0	A2AJS1	
ENSMUST00000151593	ENSMUSG00000026933	2	25926838	25983282	-1	0	1	0	0	2	0	0	0	0	0	0	F6W3X2	
ENSMUST00000151594						4	3	5	3	2	2	0	0	0	5	4		
ENSMUST00000151595						5	0	5	1	1	1	7	0	2	0	5		
ENSMUST00000151596						7	2	2	0	6	2	0	0	0	0	0		
ENSMUST00000151597						10	2	12	8	7	5	0	0	0	0	0		
ENSMUST00000151598						9	2	9	5	4	3	2	1	1	1	0		
ENSMUST00000151600						0	0	0	0	0	0	0	420	0	65	68		
ENSMUST00000151601						2	0	4	4	0	0	1	0	0	0	0		
ENSMUST00000151602						0	0	0	4	0	0	6	0	0	0	0		
ENSMUST00000151603						0	1	0	1	3	2	0	0	0	0	0		
ENSMUST00000151604						5	5	31	4	3	2	0	0	0	0	0		
ENSMUST00000151605						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151606	ENSMUSG00000027868	3	99240381	99354259	1	0	0	1	7	1	0	0	0	0	0	0	A0A0G2JG43	
ENSMUST00000151607						4	2	4	0	8	2	0	3	0	0	0		
ENSMUST00000151608						5	1	8	5	0	0	40	280	77	50	111		
ENSMUST00000151609	ENSMUSG00000023873	17	8988333	9008319	1	2	0	6	14	2	4	61	204	61	90	66	Q3TTN6	
ENSMUST00000151610	ENSMUSG00000027546	2	168634438	168742409	-1	0	1	0	65	0	0	0	0	0	0	0	B2FDH4	
ENSMUST00000151611						6	3	1	3	0	3	0	0	1	0	0		
ENSMUST00000151612						4	10	4	17	0	0	24	78	31	0	71		
ENSMUST00000151613						2	2	9	6	4	1	32	113	142	2	147		
ENSMUST00000151614						0	0	0	8	0	0	0	1	0	0	0		
ENSMUST00000151615						0	5	2	1	0	0	0	9	0	7	82		
ENSMUST00000151618	ENSMUSG00000051169	6	113415319	113419340	-1	0	0	0	0	0	0	0	0	0	1	0	F6UDW0	
ENSMUST00000151619						0	0	0	31	2	1	2	25	8	6	13		
ENSMUST00000151620						29	23	22	19	43	20	40	67	19	13	59		
ENSMUST00000151621						4	0	2	0	3	1	0	1	0	1	1		
ENSMUST00000151622	ENSMUSG00000079470	1	78658038	78671512	1	8	0	4	69	0	6	12	0	10	4	1	E9Q9S3	
ENSMUST00000151623	ENSMUSG00000019872	10	57794335	57811830	1	0	5	3	0	1	0	12	2	24	11	5	D3Z1B4	
ENSMUST00000151624						0	0	0	0	0	0	0	0	1	0	3		
ENSMUST00000151625						3	0	9	3	1	0	0	19	5	20	0		
ENSMUST00000151626						40	48	303	113	48	32	3	5	4	0	7		
ENSMUST00000151627						0	0	25	6	0	7	35	21	31	0	90		
ENSMUST00000151628						0	2	0	0	0	0	18	38	14	13	11		
ENSMUST00000151629						2	0	7	3	4	0	45	8	52	2	34		
ENSMUST00000151630	ENSMUSG00000041040	1	59913006	59985346	1	1	0	0	0	0	0	0	0	0	0	0	M0QWW4	
ENSMUST00000151631	ENSMUSG00000035637	4	44981395	44990734	1	0	0	9	2	6	0	0	5	0	0	0	D6REG4	
ENSMUST00000151632						10	7	6	2	5	2	1	3	3	0	1		
ENSMUST00000151633	ENSMUSG00000065952	8	3567990	3584939	1	4	7	20	14	4	7	0	0	0	0	0	D3Z250	
ENSMUST00000151635	ENSMUSG00000022285	15	36770770	36794547	-1	0	0	0	5	0	0	0	1	4	4	3	D3YXF4	
ENSMUST00000151636	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	0	0	0	0	0	0	0	2	F6VVW4	
ENSMUST00000151638						0	0	0	3	2	2	0	0	0	0	0		
ENSMUST00000151640						0	1	0	0	0	0	0	0	0	0	3		
ENSMUST00000151641						1	2	3	4	5	2	0	0	0	0	0		
ENSMUST00000151642						0	0	0	0	0	0	247	206	73	11	126		
ENSMUST00000151644						0	0	0	0	0	0	27	80	42	0	7		
ENSMUST00000151645						16	10	60	12	11	4	1	1	0	0	0		
ENSMUST00000151646	ENSMUSG00000044709	7	19564946	19573823	-1	1	1	6	14	0	4	2	5	5	0	10	D3Z684	
ENSMUST00000151647						24	5	56	63	18	13	0	2	0	0	0		
ENSMUST00000151648	ENSMUSG00000042404	3	90265185	90280669	1	0	3	0	15	2	0	13	2	14	0	6	F6RPS8	
ENSMUST00000151649						852	898	724	1032	825	405	57	254	145	13	140		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151654	ENSMUSG00000015468	17	34564268	34588503	1	0	0	0	0	0	0	0	0	0	0	0	G3UZH3	
ENSMUST00000151655						0	1	36	0	0	0	0	0	0	0	0		
ENSMUST00000151656						0	1	15	22	3	3	0	0	0	0	0		
ENSMUST00000151657						0	3	0	0	0	0	0	0	0	1	0		
ENSMUST00000151658	ENSMUSG00000039048	9	35204206	35211055	-1	0	0	0	0	0	0	27	33	4	0	0	D6RJ42	
ENSMUST00000151659						4	3	11	49	5	2	0	0	15	16	18		
ENSMUST00000151660						1	0	0	0	0	0	0	34	19	5	44		
ENSMUST00000151661						0	3	0	1	0	0	0	0	0	1	0		
ENSMUST00000151662						17	19	19	12	15	7	0	2	0	0	2		
ENSMUST00000151664	ENSMUSG00000039220	17	35916434	35932283	1	2	0	1	0	0	0	1	5	8	9	8	S4R164	
ENSMUST00000151666						0	0	0	0	0	0	0	88	0	0	0		
ENSMUST00000151667						3	2	0	3	5	2	0	0	0	0	2		
ENSMUST00000151668						6	0	7	3	0	2	0	0	0	0	0		
ENSMUST00000151671	ENSMUSG00000053063	6	129342691	129365303	1	11	15	26	15	10	5	220	300	348	425	164	D3YXD8	
ENSMUST00000151672						3	2	2	3	6	4	0	2	0	0	0		
ENSMUST00000151673						0	0	0	0	2	0	0	0	0	0	2		
ENSMUST00000151674	ENSMUSG00000023505	6	124829547	124833701	1	0	0	0	0	0	0	0	0	0	0	1	D3YXE3	
ENSMUST00000151675						23	23	75	30	39	19	0	1	5	1	5		
ENSMUST00000151677						7	10	46	16	25	10	12	7	7	0	15		
ENSMUST00000151678	ENSMUSG00000003518	11	101971143	101987013	-1	43	20	67	13	43	36	0	110	0	0	77	Q3V2Y9	
ENSMUST00000151679	ENSMUSG00000045983	16	20668313	20692884	1	1	1	5	3	2	0	0	0	3	0	0	D3YWY7	
ENSMUST00000151680						0	0	0	101	8	1	0	2	2	0	0		
ENSMUST00000151681	ENSMUSG00000048249	17	26715650	26776635	1	0	0	0	0	1	0	36	1	163	121	124	B8JJI3	
ENSMUST00000151682	ENSMUSG00000038119	9	35421128	35507652	1	0	0	0	10	0	0	0	0	0	0	0	D3Z2P1	
ENSMUST00000151683	ENSMUSG00000026749	2	38511643	38594606	1	0	3	2	2	0	0	1	0	0	1	3	A2ATP0	
ENSMUST00000151684						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000151686						0	1	6	3	4	9	3	26	9	1	2		
ENSMUST00000151689	ENSMUSG00000031232	X	105968084	106011906	-1	11	0	32	32	0	0	49	209	140	54	108	A2ADH1	
ENSMUST00000151690						9	0	0	6	0	17	13	31	14	36	17		
ENSMUST00000151691						8	13	10	13	18	0	0	0	0	0	11		
ENSMUST00000151692						1	4	0	0	5	2	0	0	0	0	0		
ENSMUST00000151693						1	0	0	1	0	3	0	0	0	0	0		
ENSMUST00000151694						0	0	0	0	0	0	4	0	0	0	0		
ENSMUST00000151695						3	0	6	5	3	0	7	0	5	0	12		
ENSMUST00000151697	ENSMUSG00000033222	3	100938860	100969663	-1	0	0	0	11	0	2	0	0	0	0	2	F6RQ10	
ENSMUST00000151698	ENSMUSG00000028581	4	130913125	130936141	1	18	18	81	42	43	15	22755	29838	16705	1886	15302	Q544S4	Q61168
ENSMUST00000151699						1	1	6	31	0	2	0	0	0	1	0		
ENSMUST00000151700						19	18	34	9	29	7	0	0	0	0	0		
ENSMUST00000151701						0	2	12	0	4	1	37	280	0	0	57		
ENSMUST00000151702	ENSMUSG00000008682	X	74270812	74273135	1	0	0	12	0	0	4	2950	2220	2593	6055	1370	I7HLV2	
ENSMUST00000151704						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000151705						0	0	0	52	0	0	5	5	52	0	31		
ENSMUST00000151706	ENSMUSG00000001827	7	101858331	101870788	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q543	
ENSMUST00000151707						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151708	ENSMUSG00000026385	1	120113280	120121078	-1	3	3	2	6	1	2	8	8	0	8	0	Q4VWZ5	
ENSMUST00000151709	ENSMUSG00000063232	12	103980243	103989957	-1	0	0	9	9	0	0	0	0	0	0	0	D3Z0P3	
ENSMUST00000151710						3	1	13	7	8	2	0	0	0	0	0		
ENSMUST00000151711						0	0	5	0	4	5	1	160	0	40	7		
ENSMUST00000151712						2	6	0	0	5	1	5	48	14	3	44		
ENSMUST00000151713						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000151714	ENSMUSG00000023349	6	123229843	123247021	1	10	5	12	4	5	3	16	34	6	11	0	D6RJL3	
ENSMUST00000151715						0	0	0	0	0	0	0	0	12	96	15		
ENSMUST00000151718	ENSMUSG00000024039	17	31612623	31637199	-1	0	2	10	23	5	4	0	0	0	0	0	D3Z4K2	
ENSMUST00000151720						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151721	ENSMUSG00000055409	7	49974864	50865255	1	0	0	0	93	2	2	0	0	0	0	0	D3YV40	
ENSMUST00000151722						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000151723						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151724						3	2	13	5	13	11	0	0	0	4	5		
ENSMUST00000151725						1	0	6	44	2	0	2	4	5	0	17		
ENSMUST00000151726						0	1	1	2	0	0	0	7	1	0	5		
ENSMUST00000151727						0	0	1	1	0	1	1	1	1	0	3		
ENSMUST00000151728						2	3	8	16	14	7	36	36	33	0	46		
ENSMUST00000151729						1	3	8	10	6	0	1	0	0	0	0		
ENSMUST00000151730						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151731						0	0	0	0	2	1	0	3	0	0	0		
ENSMUST00000151732						0	12	0	0	0	0	2	10	0	0	58		
ENSMUST00000151733						24	19	19	29	43	19	3	1	1	1	3		
ENSMUST00000151734						9	8	16	6	9	6	39	439	72	145	161		
ENSMUST00000151735	ENSMUSG00000060771	1	37754776	37866429	-1	0	1	10	3	5	0	10	55	15	18	23	D6RIK6	
ENSMUST00000151736						0	1	0	0	1	3	0	0	2	0	0		
ENSMUST00000151737						5	17	8	9	5	8	0	0	0	0	0		
ENSMUST00000151738	ENSMUSG00000039629	6	29917012	29959681	1	10	0	21	0	11	5	0	16	0	2	5	F6RUA3	
ENSMUST00000151739						18	20	55	16	20	7	12	22	38	2	26		
ENSMUST00000151740						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151741						5	15	28	21	16	4	13	149	69	13	82		
ENSMUST00000151742						86	95	350	75	112	48	25	88	37	13	54		
ENSMUST00000151743	ENSMUSG00000055313	13	21421275	21441058	-1	0	0	1	0	6	0	0	0	0	0	0	E9Q492	
ENSMUST00000151745						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151746						7	4	20	23	14	5	3	17	28	0	27		
ENSMUST00000151747	ENSMUSG00000038302	10	42312585	42478565	-1	0	0	0	0	0	0	0	10	0	12	0	F6VT60	
ENSMUST00000151748						2	1	5	0	0	3	5	24	7	17	6		
ENSMUST00000151749						2	2	2	4	2	8	2	0	1	3	0		
ENSMUST00000151750						2	1	5	3	1	0	6	0	6	1	3		
ENSMUST00000151751						0	3	22	21	7	6	5	77	4	15	32		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151752						37	10	182	17	0	17	0	62	67	21	140		
ENSMUST00000151755						1	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000151756						2	0	11	7	5	6	9	54	8	9	13		
ENSMUST00000151757	ENSMUSG00000036452	18	38601534	39376284	1	0	0	0	0	0	0	0	0	2	0	0	F7D661	
ENSMUST00000151758	ENSMUSG00000062995	6	8630527	8778488	-1	0	0	0	2	1	0	0	0	1	0	0	D3Z699	
ENSMUST00000151759						0	2	10	76	7	3	4	3	1	0	0		
ENSMUST00000151760						2	1	12	0	0	0	0	0	0	3	0		
ENSMUST00000151762						37	23	105	699	45	31	1	10	0	0	3		
ENSMUST00000151763						29	21	83	30	46	17	26	97	66	16	98		
ENSMUST00000151764	ENSMUSG00000045106	2	104867805	105017904	1	0	0	0	0	0	0	0	1	0	0	0	A2A6Z8	
ENSMUST00000151766						2	0	20	5	0	2	0	0	0	0	0		
ENSMUST00000151767						4	4	0	3	6	0	5	55	8	16	19		
ENSMUST00000151768						5	5	19	13	3	2	77	901	26	26	29		
ENSMUST00000151769	ENSMUSG00000026617	1	185332149	185357777	1	0	0	1	8	3	1	0	0	0	0	0	D3Z5X0	
ENSMUST00000151770	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	D6RD03	
ENSMUST00000151771						5	0	9	4	0	5	84	3	61	0	34		
ENSMUST00000151772	ENSMUSG00000031196	X	75172715	75382615	-1	0	0	0	0	0	0	0	0	1	0	0	D3YW61	
ENSMUST00000151773						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151774						0	0	0	0	0	0	0	4	0	0	0		
ENSMUST00000151775						11	18	167	21	12	10	0	3	1	1	1		
ENSMUST00000151776						0	2	1	12	0	4	0	0	0	0	0		
ENSMUST00000151777	ENSMUSG00000051855	6	30723547	30748465	1	0	3	1	2	2	0	0	0	0	0	0	D3YZU2	
ENSMUST00000151780	ENSMUSG00000042371	11	61672781	61720826	-1	0	5	11	18	0	0	0	1	0	0	0	F6UXY4	
ENSMUST00000151781	ENSMUSG00000027605	2	155517948	155585724	1	0	0	0	0	0	2	0	3	0	1	18	F7CU63	
ENSMUST00000151783						2	0	1	62	2	0	0	0	0	0	0		
ENSMUST00000151784						0	2	4	1	0	2	0	0	0	0	0		
ENSMUST00000151785						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000151786	ENSMUSG00000039737	5	136178127	136198963	-1	79	70	222	116	78	55	70	116	61	46	53		Q9CWV6
ENSMUST00000151788	ENSMUSG00000025887	9	5345430	5373032	1	2	0	4	2	0	0	1	11	0	20	8	D6RCG7	
ENSMUST00000151789	ENSMUSG00000057265	12	84409071	84433780	1	0	0	0	0	0	0	0	0	1	1	0	F6SSU6	
ENSMUST00000151790						3	1	1	7	4	4	3	3	7	2	13		
ENSMUST00000151791						2	0	7	5	4	1	0	0	0	0	0		
ENSMUST00000151792						4	3	7	6	10	1	13	4	0	0	5		
ENSMUST00000151793	ENSMUSG00000038644	7	44532746	44548849	-1	0	20	9	0	0	25	0	0	3	0	17	D6RFB8	
ENSMUST00000151794						4	2	8	0	0	1	0	5	17	1	8		
ENSMUST00000151795						8	2	4	0	12	4	13	7	14	0	0		
ENSMUST00000151796	ENSMUSG00000030357	6	128429735	128438677	-1	0	3	2	1	2	0	0	0	0	5	25	F7CAT1	
ENSMUST00000151797	ENSMUSG00000024114	17	23836785	23844172	-1	9	4	34	16	10	4	5	13	3	0	1		Q920S2
ENSMUST00000151798						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151799	ENSMUSG00000050896	2	84871924	84886710	-1	14	0	0	149	12	4	8	7	7	0	0	A2ATS6	
ENSMUST00000151801						8	15	31	10	18	4	0	4	0	0	2		
ENSMUST00000151802						6	11	1	18	9	9	0	12	0	0	4		
ENSMUST00000151803	ENSMUSG00000036620	11	50210890	50235103	1	4	4	0	0	0	0	27	72	17	0	46	F7BME0	
ENSMUST00000151804						2	0	0	15	5	4	0	0	0	0	0		
ENSMUST00000151805						2	2	0	24	2	0	0	0	0	0	0		
ENSMUST00000151806	ENSMUSG00000039205	2	32352327	32380970	1	2	0	10	0	0	0	11	7	16	0	22	F6S5B6	
ENSMUST00000151807	ENSMUSG00000043411	4	137593755	137658537	1	0	2	5	0	0	1	0	2	2	0	2	F6TH61	
ENSMUST00000151808	ENSMUSG00000058392	17	32036100	32062865	1	5	1	2	2	2	1	2	7	3	0	5	D6RDD0	
ENSMUST00000151809	ENSMUSG00000029577	5	114380607	114421169	1	1	0	0	23	0	0	0	2	31	0	18	A0A0G2JEX8	
ENSMUST00000151810	ENSMUSG00000057977	4	114163384	114245028	1	2	0	0	0	2	1	0	0	0	0	0	A6PWC2	
ENSMUST00000151811						11	2	6	9	12	4	1	1	0	1	0		
ENSMUST00000151813	ENSMUSG00000028771	5	20986645	21055911	-1	0	0	0	23	1	0	20	1	79	0	17	D6RGT2	
ENSMUST00000151815						5	0	6	0	0	0	0	34	21	9	4		
ENSMUST00000151818						5	1	0	2	3	0	0	0	0	0	0		
ENSMUST00000151819						3	0	9	25	4	1	0	0	0	0	0		
ENSMUST00000151821	ENSMUSG00000021643	13	100107997	100114571	1	0	0	0	45	6	0	0	0	0	0	0	B2KF73	
ENSMUST00000151822	ENSMUSG00000040451	19	32122727	32389714	-1	0	4	6	0	3	0	0	7	9	4	0	D3YV54	
ENSMUST00000151823						26	22	52	55	35	18	1	5	7	0	1		
ENSMUST00000151824						0	1	0	4	4	0	0	0	0	0	0		
ENSMUST00000151826	ENSMUSG00000042854	2	166792531	166799505	1	71	54	97	107	79	31	11	26	24	4	20	Q543M9	
ENSMUST00000151827						19	24	83	39	39	15	6	30	26	6	24		
ENSMUST00000151829						3	0	24	14	3	3	13	22	23	0	28		
ENSMUST00000151830	ENSMUSG00000001240	11	101246028	101259546	1	1	2	4	62	4	2	0	0	0	0	0	A2A4K2	
ENSMUST00000151831	ENSMUSG00000050188	4	126096623	126098584	1	0	0	0	0	3	3	0	0	0	0	0	A8Y5G9	
ENSMUST00000151832						1	0	0	0	0	0	0	25	72	0	141		
ENSMUST00000151833						12	13	107	8	21	3	12	10	11	17	18		
ENSMUST00000151834						1	0	2	4	4	1	0	0	0	0	0		
ENSMUST00000151837						3	0	7	79	8	4	6	8	9	0	15		
ENSMUST00000151838	ENSMUSG00000028795	4	129619274	129623947	-1	0	0	0	0	0	0	0	20	8	25	0	E9Q567	
ENSMUST00000151839	ENSMUSG00000029722	5	137650463	137684726	-1	2	4	0	355	10	14	0	2	0	0	0	Q3TBU7	
ENSMUST00000151840	ENSMUSG00000035642	7	97550331	97579497	-1	0	0	3	0	1	0	0	0	0	3	0	D3YY39	
ENSMUST00000151842						0	2	9	3	6	0	0	0	0	0	0		
ENSMUST00000151843						10	12	16	69	28	10	112	170	95	24	134		
ENSMUST00000151844						1	0	1	3	0	0	0	1	2	0	0		
ENSMUST00000151845						2	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000151846						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000151847						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151849						2	3	34	9	4	7	11	55	22	0	24		
ENSMUST00000151850						5	9	9	5	18	5	0	0	2	0	1		
ENSMUST00000151852	ENSMUSG00000025145	11	120713925	120721128	1	9	2	8	7	10	2	0	0	0	2	7	A2AC11	
ENSMUST00000151853	ENSMUSG00000070323	9	7571396	7581885	1	5	0	8	3	4	0	0	0	17	4	6	D3YV89	
ENSMUST00000151854						10	6	11	62	7	11	118	140	155	0	103		
ENSMUST00000151855	ENSMUSG00000049482	8	122476143	122484138	1	0	11	39	0	7	8	0	50	9	0	0	G3UXB4	
ENSMUST00000151856	ENSMUSG00000031575	8	25816191	25847694	-1	4	10	17	20	7	6	11	37	15	7	18	D6RET1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151857						3	2	12	93	15	4	0	0	0	0	0		
ENSMUST00000151858	ENSMUSG00000034758	10	81590904	81601073	-1	0	2	0	3	2	1	0	0	0	0	0	D6RI70	
ENSMUST00000151859						1	6	6	1	3	2	0	0	1	0	1		
ENSMUST00000151860						11	11	48	52	14	9	0	5	0	0	5		
ENSMUST00000151861	ENSMUSG00000066892	9	20618118	20644767	-1	0	0	0	0	0	0	0	3	0	8	0		
ENSMUST00000151863	ENSMUSG00000052423	1	171270328	171276896	1	0	0	0	0	0	0	118	43	34	0	41	A0A0A6YXS2	
ENSMUST00000151864						15	6	37	9	17	5	7	10	5	1	12		
ENSMUST00000151866						10	12	17	20	15	6	0	9	2	0	12		
ENSMUST00000151867	ENSMUSG00000015468	17	34564268	34588503	1	0	0	0	0	0	0	0	0	0	0	0	G3UZH3	
ENSMUST00000151868						4	6	34	6	7	0	3	0	0	0	0		
ENSMUST00000151869						11	7	130	8	0	1	0	0	4	0	4		
ENSMUST00000151870						8	2	11	23	2	2	0	0	0	0	0		
ENSMUST00000151871						2	2	2	3	2	4	0	27	6	4	4		
ENSMUST00000151872						1	0	0	1	4	2	0	9	5	6	6		
ENSMUST00000151874	ENSMUSG00000026427	1	131153181	131187658	1	0	0	0	0	0	0	31	0	58	8	87		Q61211
ENSMUST00000151875						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151876	ENSMUSG00000025140	11	120635712	120643769	-1	0	0	0	0	0	0	0	0	0	0	0	A2ABZ0	
ENSMUST00000151877	ENSMUSG00000049811	11	23007531	23030788	1	5	2	2	18	5	2	1	3	4	3	0	B1AVK2	
ENSMUST00000151878	ENSMUSG00000031922	9	13807792	13827107	-1	0	0	0	0	0	0	0	0	0	0	0	F7BGJ9	
ENSMUST00000151879						7	0	9	5	9	2	129	305	145	31	270		
ENSMUST00000151880	ENSMUSG00000020409	11	43433744	43447981	1	0	3	16	55	7	6	224	481	677	1151	509	Z4YM25	
ENSMUST00000151882						8	12	20	101	20	4	62	157	107	10	53		
ENSMUST00000151885						2	4	10	1	2	2	0	4	0	0	0		
ENSMUST00000151886						0	8	0	30	0	7	0	2	0	0	1		
ENSMUST00000151887						11	8	16	14	9	4	18	56	30	2	38		
ENSMUST00000151888	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	0	3	0	0	2	0	0	0	0	E0CZD3	
ENSMUST00000151889	ENSMUSG00000033055	15	79053094	79062893	-1	1	0	1	1	2	0	0	1	4	0	0	B7ZBY0	
ENSMUST00000151890	ENSMUSG00000025139	7	141874813	141918507	-1	2	0	14	1	2	0	0	0	0	0	19	A9JEI5	
ENSMUST00000151891						0	0	0	1	5	0	2	0	0	0	4		
ENSMUST00000151892						0	0	4	4	2	5	3	47	9	2	13		
ENSMUST00000151893						2	0	3	4	0	0	0	0	1	0	2		
ENSMUST00000151894						26	15	117	41	29	14	76	52	104	9	182		
ENSMUST00000151895						6	4	4	0	1	0	0	0	0	0	0		
ENSMUST00000151897						7	4	41	11	5	5	0	19	4	0	4		
ENSMUST00000151898						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000151899						17	18	86	26	29	9	1	4	3	2	2		
ENSMUST00000151900						0	0	0	0	2	3	2	19	0	12	3		
ENSMUST00000151903	ENSMUSG00000028331	4	46376505	46389437	-1	40	25	99	27	26	18	5	0	0	0	0	F6QNL9	
ENSMUST00000151905	ENSMUSG00000002031	9	44767908	44792714	1	0	0	0	0	0	0	4	7	4	0	3	D3Z405	
ENSMUST00000151906	ENSMUSG00000034164	11	5106265	5152257	-1	0	8	0	10	3	2	0	7	0	0	0	F6U7K9	
ENSMUST00000151907						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151908						56	66	158	66	74	40	30	230	87	5	195		
ENSMUST00000151909						5	10	16	9	11	3	0	0	0	0	0		
ENSMUST00000151910						2	1	9	6	7	8	0	0	0	0	0		
ENSMUST00000151911	ENSMUSG00000031381	X	164419793	164433916	1	11	0	11	0	0	0	0	11	12	0	25	M0QWY7	
ENSMUST00000151912	ENSMUSG00000046491	11	43474276	43491525	1	2	0	4	5	1	2	0	0	0	0	0	G3UXA9	
ENSMUST00000151913	ENSMUSG00000057173	1	39665301	39720997	-1	14	10	21	37	14	7	0	0	0	0	0		D3YU81
ENSMUST00000151914	ENSMUSG00000047045	X	142681406	142843494	1	1	0	2	0	4	0	0	5	2	0	4	F7AY95	
ENSMUST00000151915						22	14	32	18	21	5	1	16	7	1	5		
ENSMUST00000151916						2	0	0	0	0	0	3	0	0	0	1		
ENSMUST00000151917						0	0	4	0	0	0	0	20	5	4	0		
ENSMUST00000151918	ENSMUSG00000021541	13	56773113	56895789	-1	70	46	247	81	54	28	0	0	0	0	0	D6RI84	
ENSMUST00000151919						5	7	38	17	9	5	0	0	0	0	0		
ENSMUST00000151920						126	85	778	180	90	44	12	32	19	0	21		
ENSMUST00000151922						0	2	1	3	4	0	1	2	0	0	0		
ENSMUST00000151923						0	1	4	0	0	1	0	0	0	0	0		
ENSMUST00000151924						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000151925						0	0	8	60	4	2	9	33	19	6	36		
ENSMUST00000151926	ENSMUSG00000058317	14	18573575	18894267	-1	0	0	2	5	1	1	0	0	0	0	2	D3YXD1	
ENSMUST00000151927	ENSMUSG00000044098	3	103914120	103966636	1	9	9	12	0	0	7	28	119	137	17	104	D6RG56	
ENSMUST00000151928	ENSMUSG00000020211	10	80798198	80804924	1	0	1	0	0	0	0	126	6	138	6	137	D3YW09	
ENSMUST00000151929						0	0	0	6	4	1	0	0	0	0	0		
ENSMUST00000151930						2	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000151932						0	0	8	4	0	0	0	7	10	0	5		
ENSMUST00000151933	ENSMUSG00000030386	7	12478293	12496235	1	0	0	0	0	0	0	5	10	5	0	11	Q69Z88	
ENSMUST00000151934						0	1	0	2	7	4	4	0	2	0	0		
ENSMUST00000151935						5	0	7	4	0	1	5	2	5	0	6		
ENSMUST00000151936						2	2	5	96	18	0	25	25	18	4	33		
ENSMUST00000151937	ENSMUSG00000027010	2	71271063	71367749	-1	82	53	252	131	83	32	133	303	167	41	145		Q8BH59
ENSMUST00000151938						41	35	89	30	39	19	39	309	108	307	125		
ENSMUST00000151939	ENSMUSG00000075284	2	73429610	73529734	-1	1	0	2	1	3	2	0	0	7	1	3	F6RQI2	
ENSMUST00000151940						0	1	4	6	1	0	0	27	25	0	16		
ENSMUST00000151941	ENSMUSG00000041229	X	151520672	151633859	1	0	0	0	0	0	0	0	2	2	0	0	F7BTQ5	
ENSMUST00000151942						4	3	3	2	3	0	3	6	6	0	4		
ENSMUST00000151943						0	0	0	0	0	0	289	643	306	79	319		
ENSMUST00000151944						0	0	0	0	0	0	6	0	8	0	0		
ENSMUST00000151946						9	2	16	7	9	0	0	0	1	0	2		
ENSMUST00000151947	ENSMUSG00000029344	5	112276691	112315361	1	2	0	16	12	0	2	0	0	0	0	0	D3YV96	
ENSMUST00000151948						3	5	5	3	7	4	0	0	0	0	0		
ENSMUST00000151950	ENSMUSG00000064061	16	48924232	48994165	-1	2	0	1	1	0	0	0	11	0	0	2	F6Z1P8	
ENSMUST00000151951						0	0	4	1	4	0	9	17	24	7	33		
ENSMUST00000151952	ENSMUSG00000026110	1	37439340	37541016	-1	29	0	33	0	0	11	65	33	196	33	98		Q812G0
ENSMUST00000151953						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000151956	ENSMUSG00000060787	11	87913920	87916685	-1	1	2	0	9	0	0	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000151957						12	11	23	41	24	10	152	611	240	20	583		
ENSMUST00000151958						2	2	0	27	0	0	12	1261	519	110	426		
ENSMUST00000151959						0	0	0	1	5	2	0	0	0	0	0		
ENSMUST00000151960	ENSMUSG00000064065	10	6885796	7052478	-1	0	1	0	1	0	0	19	42	46	2	39	D3Z0U6	
ENSMUST00000151961	ENSMUSG00000029073	4	155864723	155869440	-1	0	0	0	2	2	0	28	26	40	3	19	Z4YLU2	
ENSMUST00000151962						5	4	8	6	3	0	0	2	0	0	2		
ENSMUST00000151963						3	0	0	0	1	0	0	0	0	1	2		
ENSMUST00000151964	ENSMUSG00000038764	4	57190841	57301837	-1	0	1	0	0	1	1	1	0	1	0	0	A2ALL1	
ENSMUST00000151965						0	2	2	267	5	4	2	5	0	2	0		
ENSMUST00000151966						5	9	21	0	0	6	66	167	103	43	48		
ENSMUST00000151968						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000151969	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	101	67	68	14	29	D6RDC0	
ENSMUST00000151970						2	7	12	111	14	0	1	2	0	0	4		
ENSMUST00000151971						27	26	73	33	28	14	31	100	33	10	52		
ENSMUST00000151972						0	0	2	34	3	0	0	0	0	0	0		
ENSMUST00000151973						2	1	2	6	0	1	1	0	1	0	0		
ENSMUST00000151974						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000151975						1	0	3	11	4	1	0	0	0	0	0		
ENSMUST00000151976						7	5	12	8	11	0	7	13	13	19	11		
ENSMUST00000151977						27	17	60	355	23	14	0	0	0	0	0		
ENSMUST00000151978	ENSMUSG00000020393	11	5191552	5261558	-1	25	19	73	23	26	15	20	11	31	1	40	F6S1T7	
ENSMUST00000151980						174	155	469	370	234	128	258	1917	612	229	1133		
ENSMUST00000151981						0	0	6	3	0	0	115	18	118	208	40		
ENSMUST00000151982	ENSMUSG00000000632	11	77930800	77979048	1	0	4	0	0	12	10	0	0	0	0	0	F6XNR8	
ENSMUST00000151983						0	0	4	0	3	2	3	35	10	6	7		
ENSMUST00000151985	ENSMUSG00000027849	3	103575231	103645569	1	3	2	5	22	2	0	0	0	0	0	0	D6RIM4	
ENSMUST00000151986	ENSMUSG00000024335	17	34112023	34122634	-1	24	4	33	611	12	12	50	33	50	2	29	I7HPW1	
ENSMUST00000151987						1	0	2	0	0	0	1	0	0	0	1		
ENSMUST00000151988	ENSMUSG00000005982	16	3872375	3904780	1	8	3	17	38	3	2	10	0	13	5	6	D3YYN1	
ENSMUST00000151989						0	0	0	6	0	0	0	0	0	0	2		
ENSMUST00000151990						0	1	0	0	3	6	0	0	0	4	5		
ENSMUST00000151991						0	3	2	4	0	0	0	29	13	0	7		
ENSMUST00000151992						0	4	6	6	8	10	1	6	2	2	12		
ENSMUST00000151993						6	3	0	0	3	5	0	0	0	0	0		
ENSMUST00000151995						1	0	0	0	0	1	0	0	17	0	0		
ENSMUST00000151996	ENSMUSG00000031179	X	64173548	64178778	1	0	1	4	0	1	0	0	0	0	0	0	A2AMW6	
ENSMUST00000151997						1	6	11	2	2	3	0	4	0	0	0		
ENSMUST00000151999	ENSMUSG00000072487	15	73761410	73839699	-1	19	18	66	24	35	17	0	0	0	0	0	E9PUJ8	
ENSMUST00000152000						4	0	27	15	7	3	5	12	8	2	16		
ENSMUST00000152004						13	6	5	4	9	3	0	0	0	0	0		
ENSMUST00000152005	ENSMUSG00000015733	6	17636234	17666972	1	0	0	0	0	0	0	0	0	0	54	53		
ENSMUST00000152006	ENSMUSG00000041977	3	87617559	87738034	1	9	22	22	0	9	0	194	433	332	33	341	D6RGQ8	
ENSMUST00000152007						11	4	13	4	5	9	57	265	108	60	158		
ENSMUST00000152008	ENSMUSG00000069631	11	106163330	106202168	-1	0	0	0	0	2	0	0	0	0	0	0	B1AR92	
ENSMUST00000152009						3	3	5	57	2	1	0	0	0	0	0		
ENSMUST00000152010						19	14	38	15	31	13	0	6	0	0	3		
ENSMUST00000152011						2	5	1	6	2	3	0	0	0	0	0		
ENSMUST00000152012	ENSMUSG00000030209	6	135713233	136173511	-1	3	11	4	0	7	5	0	0	0	0	0	A0A0G2JEA7	
ENSMUST00000152013	ENSMUSG00000005374	5	135149657	135165760	1	1	0	12	0	2	0	4	4	3	0	5	D3YZH8	
ENSMUST00000152015						0	0	0	0	0	0	0	0	0	1	1		
ENSMUST00000152016						0	0	0	0	0	0	0	52	0	0	13		
ENSMUST00000152017						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000152018	ENSMUSG00000021848	14	48657679	48667644	-1	0	0	3	4	4	3	0	0	0	0	0	D3YZ94	
ENSMUST00000152019						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152020						4	5	6	19	9	12	0	4	0	0	3		
ENSMUST00000152021						0	0	5	6	1	0	14	47	7	1	20		
ENSMUST00000152022						160	103	399	277	160	87	140	576	218	19	468		
ENSMUST00000152023	ENSMUSG00000028565	4	97772734	98118874	1	0	0	0	11	0	2	3	6	14	3	13	B1AUB6	
ENSMUST00000152026						2	2	15	6	2	3	3	23	38	4	24		
ENSMUST00000152028						6	6	17	51	4	0	0	3	4	0	0		
ENSMUST00000152029	ENSMUSG00000059430	6	83512905	83536265	-1	0	4	6	3	0	0	0	0	0	0	0	D3Z2K3	
ENSMUST00000152032						0	0	9	5	0	1	0	9	0	2	4		
ENSMUST00000152033						4	1	2	0	2	0	0	12	0	0	2		
ENSMUST00000152034	ENSMUSG00000031444	8	13037308	13056676	1	0	0	0	0	0	0	206	250	52	133	50	D3Z521	
ENSMUST00000152035	ENSMUSG00000020847	11	75830999	75938429	-1	0	2	2	1	3	0	0	0	0	0	0	B7FAU1	
ENSMUST00000152036						0	1	0	0	3	3	0	0	3	1	3		
ENSMUST00000152037	ENSMUSG00000052997	7	34140688	34169599	-1	0	2	3	1	2	0	0	68	15	41	20	H3BJQ2	
ENSMUST00000152038						21	22	107	29	23	14	4	11	4	1	8		
ENSMUST00000152039	ENSMUSG00000039620	8	36457548	36514320	1	0	0	0	0	5	2	0	0	0	0	0		Q80WQ4
ENSMUST00000152040	ENSMUSG00000048939	16	29231851	29378732	-1	1	1	0	0	3	0	0	0	0	0	0	D3YV41	
ENSMUST00000152041	ENSMUSG00000034842	5	92331827	92414628	1	2	2	2	0	0	0	1	0	1	0	1	F6Z2C7	
ENSMUST00000152042	ENSMUSG00000001508	11	94962791	94976327	-1	0	0	4	0	5	1	0	0	0	0	0	Q5SWB4	
ENSMUST00000152044						0	2	0	46	0	0	0	0	1	0	0		
ENSMUST00000152045						4	0	11	0	5	1	3	17	12	0	9		
ENSMUST00000152046						1	1	0	6	2	1	0	0	0	0	0		
ENSMUST00000152048						2	2	4	1	1	0	2	6	2	0	10		
ENSMUST00000152049						1	0	0	29	0	0	0	0	4	12	3		
ENSMUST00000152050						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000152051	ENSMUSG00000052301	7	126847416	126852705	1	0	0	0	0	0	1	0	0	0	0	0	D3YYV2	
ENSMUST00000152053						0	1	5	1	4	2	4	26	2	0	18		
ENSMUST00000152054	ENSMUSG00000040521	10	127011572	127030840	-1	2	3	1	14	10	4	0	0	0	0	6	D3Z4M7	
ENSMUST00000152055						1	6	0	13	6	3	0	0	0	0	0		
ENSMUST00000152056	ENSMUSG00000028322	4	45316613	45342732	-1	0	0	2	11	1	0	10	52	31	3	4	F6TGV1	
ENSMUST00000152057	ENSMUSG00000051022	5	39613935	39755475	-1	0	0	4	64	3	2	0	0	0	1	2	D3YZM3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152058						0	3	0	0	1	1	0	0	4	0	0		
ENSMUST00000152059						3	7	0	0	0	4	49	183	68	0	22		
ENSMUST00000152060	ENSMUSG00000024483	18	36559987	36665917	1	0	1	0	0	0	0	8	0	0	0	0	F6RRY0	
ENSMUST00000152061	ENSMUSG00000070280	9	119169455	119365553	-1	0	3	0	5	5	3	0	1	0	0	0	F7AMC9	
ENSMUST00000152062						0	0	0	0	0	0	18	55	35	47	21		
ENSMUST00000152063						15	11	68	26	29	10	66	112	122	5	242		
ENSMUST00000152064						3	3	12	0	2	4	3	0	0	6	12		
ENSMUST00000152065	ENSMUSG00000020654	12	4133103	4213525	1	0	0	0	0	0	0	0	0	0	0	0	B8JK56	
ENSMUST00000152066	ENSMUSG00000067367	5	38220470	38234306	1	3	3	0	0	3	2	0	0	0	0	0	D3Z009	
ENSMUST00000152067	ENSMUSG00000022094	14	70303469	70351425	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152068						11	7	3	5	6	2	4	13	14	0	28		
ENSMUST00000152071	ENSMUSG00000041607	18	82475146	82585637	1	0	0	31	0	35	0	0	42	7	11	23	F6TYB7	
ENSMUST00000152072						0	6	3	0	1	0	0	2	0	0	5		
ENSMUST00000152075	ENSMUSG00000026418	1	135779434	135810989	1	0	5	12	0	0	3	0	0	0	0	0		Q9WUZ5
ENSMUST00000152076						3	0	0	3	6	3	6	3	13	0	21		
ENSMUST00000152077						2	0	7	3	0	0	11	0	0	0	0		
ENSMUST00000152080	ENSMUSG00000019731	8	72480641	72492614	-1	55	41	105	78	44	24	4716	5521	4048	320	2620		Q8CD26
ENSMUST00000152081						3	4	7	7	4	2	30	40	91	2	53		
ENSMUST00000152082						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000152083						0	0	4	0	0	0	41	4	80	0	36		
ENSMUST00000152084	ENSMUSG00000018900	11	53864542	53891660	-1	0	1	0	0	0	2	0	0	3	0	9	F6TNN8	
ENSMUST00000152085						3	2	2	0	4	0	2	5	0	0	0		
ENSMUST00000152087						6	4	6	16	5	5	1	2	0	0	2		
ENSMUST00000152088	ENSMUSG00000001143	1	36419871	36445271	-1	2	1	10	4	7	0	4	9	6	0	12	F6QN75	
ENSMUST00000152090						2	0	6	0	1	1	0	0	0	0	0		
ENSMUST00000152091						12	8	5	17	13	4	16	17	13	16	15		
ENSMUST00000152092						2	0	5	1	5	1	0	0	0	0	0		
ENSMUST00000152093	ENSMUSG00000022044	14	66344296	66361680	1	3	0	3	3	1	2	0	0	0	0	0	D3Z6P6	
ENSMUST00000152094						1	0	1	32	1	2	0	0	0	0	1		
ENSMUST00000152095	ENSMUSG00000056004	5	9266118	9481825	1	12	10	0	2	9	2	0	1	0	0	3	D6RHB7	
ENSMUST00000152096	ENSMUSG00000033352	11	65688243	65788297	-1	0	0	0	0	0	0	1	0	0	0	0	B1ATL6	
ENSMUST00000152097						0	1	2	77	3	2	0	3	3	0	7		
ENSMUST00000152098	ENSMUSG00000055401	4	148145716	148152140	-1	0	1	0	7	4	0	108	72	80	66	26	Z4YN00	
ENSMUST00000152099						3	3	4	3	3	7	0	0	0	0	0		
ENSMUST00000152100						4	0	0	2	0	0	1	0	0	0	9		
ENSMUST00000152101						165	158	695	168	163	65	10	16	18	8	23		
ENSMUST00000152102						48	42	75	76	47	13	9	72	28	5	42		
ENSMUST00000152103	ENSMUSG00000040797	6	121372933	121473678	-1	9	58	55	0	28	0	1	1	0	1	4	D6RHQ8	
ENSMUST00000152104						0	2	0	30	1	1	0	1	0	0	0		
ENSMUST00000152105	ENSMUSG00000029651	5	147957320	148316065	1	1	4	0	4	0	0	2	8	0	19	1	D3YUM9	
ENSMUST00000152106						2	5	9	1	5	3	0	0	0	0	2		
ENSMUST00000152107	ENSMUSG00000024188	17	26252910	26285504	1	0	0	0	0	0	0	0	0	0	0	0	F6QU81	
ENSMUST00000152108	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	1	0	0	2	0	D3Z773	
ENSMUST00000152110						14	0	61	0	2	2	29	42	51	13	11		
ENSMUST00000152111	ENSMUSG00000012187	1	78510991	78538173	1	3	2	5	24	1	0	0	0	0	0	0	D3YZB8	
ENSMUST00000152113						9	5	43	15	22	4	0	0	0	0	0		
ENSMUST00000152114	ENSMUSG00000042671	1	153653025	153700323	1	1	0	0	3	0	0	0	0	0	0	0	D3Z1V2	
ENSMUST00000152115	ENSMUSG00000020415	11	43420250	43426251	-1	0	0	0	0	0	0	0	0	0	0	0	D6RIQ0	
ENSMUST00000152117	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	1	0	0	3	0	4		
ENSMUST00000152119	ENSMUSG00000020397	11	46436925	46442721	1	0	0	0	26	0	0	0	0	3	0	3	F2Z449	
ENSMUST00000152120						5	1	2	3	4	4	0	0	0	0	0		
ENSMUST00000152121						1	0	2	4	4	0	0	0	0	0	0		
ENSMUST00000152122	ENSMUSG00000006476	2	25054355	25062881	1	0	0	0	12	0	4	6	0	0	0	0	A2AJ91	
ENSMUST00000152123						0	0	0	8	0	0	0	0	0	0	0		
ENSMUST00000152124						0	2	2	4	0	0	0	0	0	0	0		
ENSMUST00000152126	ENSMUSG00000028797	4	129600668	129624059	1	6	0	0	0	0	0	448	1565	579	96	537	D6RDC0	
ENSMUST00000152127						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152129						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000152130						0	0	1	45	1	1	0	0	0	2	0		
ENSMUST00000152131						1	0	0	0	1	1	0	0	0	0	1		
ENSMUST00000152132						6	6	10	9	15	8	0	0	0	0	3		
ENSMUST00000152133						0	0	4	2	0	0	0	0	0	0	1		
ENSMUST00000152134	ENSMUSG00000051517	4	43496142	43499695	-1	0	0	0	0	0	0	0	21	0	5	0	F6S324	
ENSMUST00000152135	ENSMUSG00000017679	2	163602314	163619013	1	9	10	8	20	12	4	2	2	4	1	7	A6PW50	
ENSMUST00000152136	ENSMUSG00000073856	7	118855760	118972652	1	0	0	0	0	0	0	0	1	0	0	0	D6RI33	
ENSMUST00000152137						2	0	12	1	0	6	0	0	0	0	0		
ENSMUST00000152138						0	12	17	6	15	16	1	0	0	0	0		
ENSMUST00000152139						7	5	13	12	6	4	0	0	0	0	0		
ENSMUST00000152140						0	0	0	2	1	2	0	11	0	2	4		
ENSMUST00000152141						0	0	0	30	0	0	0	0	0	1	1		
ENSMUST00000152142						2	0	0	28	0	0	0	0	3	0	0		
ENSMUST00000152144						0	0	0	2	0	0	0	0	0	2	1		
ENSMUST00000152145						24	12	130	35	16	8	1	0	0	0	0		
ENSMUST00000152146						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152148						1	0	2	0	0	0	0	0	5	3	3		
ENSMUST00000152149	ENSMUSG00000050043	2	84671316	84679140	-1	3	0	3	0	2	0	0	0	0	2	0	D3YYX0	
ENSMUST00000152150	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	0	0	0	0	33	0	0	A2AEB8	
ENSMUST00000152151						0	0	0	0	0	0	27	42	0	0	31		
ENSMUST00000152152						0	2	1	1	0	1	11	12	0	0	2		
ENSMUST00000152153						5	1	4	87	7	1	5	3	3	3	9		
ENSMUST00000152155						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000152156						0	0	3	57	0	0	0	76	0	0	151		
ENSMUST00000152158	ENSMUSG00000074673	2	152962485	153008482	1	0	0	0	0	0	0	0	0	0	0	0	D6RG93	
ENSMUST00000152159	ENSMUSG00000057751	4	154170730	154275713	1	9	16	44	41	23	9	0	0	0	1	1	B1ASH4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152160	ENSMUSG00000040746	11	70647235	70651421	1	0	0	0	0	0	0	1	0	42	0	9	D6RH35	
ENSMUST00000152161	ENSMUSG00000036893	2	24789928	24919614	-1	0	0	0	0	0	0	0	9	7	0	0	A2AIS5	
ENSMUST00000152162						2	1	1	3	0	1	2	5	3	3	6		
ENSMUST00000152163						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152164						7	6	6	0	2	0	0	0	0	0	0		
ENSMUST00000152165	ENSMUSG00000039515	2	30416039	30447806	1	0	1	0	27	0	2	0	0	0	0	0	D6RFC2	
ENSMUST00000152167						0	1	0	4	0	0	0	7	37	0	171		
ENSMUST00000152168	ENSMUSG00000031617	8	77595982	77610698	-1	0	5	0	1	1	0	2	0	12	0	5	D3YVG4	
ENSMUST00000152169						0	0	0	0	1	0	3	4	0	0	12		
ENSMUST00000152170	ENSMUSG00000026784	2	22895522	22940266	1	3	1	3	0	1	0	0	3	0	2	0	Q9CZQ1	
ENSMUST00000152171	ENSMUSG00000048442	11	115899966	115906269	1	4	7	32	5	11	6	17	21	14	11	13		Q8BT42
ENSMUST00000152173						2	2	3	3	1	1	0	0	0	0	0		
ENSMUST00000152174						1	1	6	100	5	1	4	24	21	3	12		
ENSMUST00000152175						1	7	12	6	3	2	0	16	18	2	21		
ENSMUST00000152176						0	3	2	1	2	1	0	0	0	0	0		
ENSMUST00000152177						1	0	0	49	1	0	0	0	0	0	0		
ENSMUST00000152178						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000152180						6	3	8	3	5	0	0	5	0	0	0		
ENSMUST00000152181						0	0	0	1	0	0	0	4	0	0	0		
ENSMUST00000152182	ENSMUSG00000021893	14	31336638	31371986	1	0	0	0	0	16	0	0	149	82	0	43	F2Z3X0	
ENSMUST00000152183	ENSMUSG00000020843	11	76406952	76416292	1	1	0	0	0	1	0	21	7	9	11	10	Z4YN86	
ENSMUST00000152184						2	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000152185	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	0	0	0	0	0	0	0	0	A2AT65	
ENSMUST00000152186						10	13	20	22	19	3	2	66	11	0	19		
ENSMUST00000152187						7	4	19	12	3	1	0	0	3	0	2		
ENSMUST00000152189	ENSMUSG00000031851	8	125729963	125748235	1	0	0	6	1	5	3	152	0	20	63	53	D3YXL1	
ENSMUST00000152191						0	2	11	0	0	5	115	166	51	36	37		
ENSMUST00000152193	ENSMUSG00000038121	18	68260187	68300333	-1	2	0	4	97	4	2	2	3	3	16	5	D3Z4B5	
ENSMUST00000152194	ENSMUSG00000046093	4	123183227	123194701	1	4	0	1	1	3	0	0	0	0	0	0	F2Z3Z1	
ENSMUST00000152195						7	3	13	14	7	4	0	4	3	0	1		
ENSMUST00000152196						0	0	0	0	13	10	52	26	231	10	195		
ENSMUST00000152197	ENSMUSG00000022914	16	95992092	96082526	-1	0	0	0	0	0	0	0	0	0	0	0	F7D5W0	
ENSMUST00000152198						0	0	0	0	0	0	0	0	0	10	0		
ENSMUST00000152199	ENSMUSG00000070972	4	58995062	59025573	1	1	0	0	0	0	0	22	31	29	1	21		A2ALW5
ENSMUST00000152200	ENSMUSG00000031347	X	72913532	72918411	-1	0	0	1	5	4	0	0	0	0	0	0	B1AUQ7	
ENSMUST00000152201						0	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000152202						8	0	6	1	11	5	0	0	2	0	8		
ENSMUST00000152204	ENSMUSG00000074895	13	54783998	54788459	1	0	0	0	0	0	0	0	0	0	0	0		Q3UTA9
ENSMUST00000152205	ENSMUSG00000068917	3	89164795	89176921	1	3	0	0	28	3	2	1	8	2	0	9	D3Z7L4	
ENSMUST00000152206						0	1	1	2	2	0	0	0	0	0	0		
ENSMUST00000152207	ENSMUSG00000043279	5	137105644	137116209	-1	0	0	0	21	0	0	23	3	22	0	18	D3YVX5	
ENSMUST00000152208	ENSMUSG00000026418	1	135779434	135810989	1	6	0	0	9	5	0	0	0	0	0	0		Q9WUZ5
ENSMUST00000152209	ENSMUSG00000050424	X	73033981	73037103	-1	0	0	10	2	13	4	0	0	0	0	0	F6ZWH4	
ENSMUST00000152210	ENSMUSG00000014353	2	128818118	128854261	1	0	0	0	0	0	0	16	0	23	0	26	Z4YML9	
ENSMUST00000152211						4	2	0	1	2	1	0	5	2	2	2		
ENSMUST00000152212						0	0	0	0	0	0	12	0	46	9	0		
ENSMUST00000152213						6	7	9	104	4	4	69	34	36	5	20		
ENSMUST00000152214	ENSMUSG00000096549	17	47688517	47694736	-1	5	0	2	6	1	1	0	0	0	0	1	F6R2T0	
ENSMUST00000152215	ENSMUSG00000067206	5	73606642	73632526	-1	3	1	0	0	0	8	0	0	0	0	0	D3Z0I0	
ENSMUST00000152216						300	318	384	272	277	125	26	73	51	8	96		
ENSMUST00000152217						5	1	24	3	8	4	0	0	0	0	0		
ENSMUST00000152218						0	0	8	19	3	1	0	2	6	2	3		
ENSMUST00000152219						0	0	0	0	0	0	0	0	5	4	0		
ENSMUST00000152221						0	1	1	0	0	0	6	30	12	20	14		
ENSMUST00000152222	ENSMUSG00000000901	10	75923222	75932502	-1	1	0	9	0	0	0	0	0	0	0	0	F6QGW1	
ENSMUST00000152223	ENSMUSG00000039903	16	90826719	90905109	1	0	0	0	54	10	7	0	0	0	0	0	D6RCJ7	
ENSMUST00000152224						0	4	0	0	3	0	13	0	17	0	20		
ENSMUST00000152225	ENSMUSG00000039354	1	72583251	72633134	1	8	6	9	14	7	4	0	0	0	0	0		Q8BJL0
ENSMUST00000152226						0	0	1	0	0	0	301	273	168	33	107		
ENSMUST00000152227	ENSMUSG00000022472	15	81992523	82033862	-1	0	0	35	0	0	0	163	400	221	30	139		Q9CQT7
ENSMUST00000152228	ENSMUSG00000031201	X	75416628	75454001	1	0	0	0	0	0	0	1	0	0	0	0	E9Q0P6	
ENSMUST00000152231						0	2	8	3	0	4	5	18	12	0	6		
ENSMUST00000152232						29	27	175	61	24	15	0	0	0	0	0		
ENSMUST00000152233	ENSMUSG00000026199	1	75192151	75199387	1	0	0	0	0	0	1	212	453	347	106	337	J3QM81	
ENSMUST00000152234						2	1	3	4	2	3	0	1	0	0	1		
ENSMUST00000152235						3	0	3	5	1	0	0	0	0	0	12		
ENSMUST00000152236						61	63	231	53	59	28	11	33	9	3	23		
ENSMUST00000152237	ENSMUSG00000026941	2	25563115	25574845	-1	0	4	32	0	0	0	2	3	4	2	6	F6QNH6	
ENSMUST00000152238						2	0	25	3	6	0	2	2	4	0	2		
ENSMUST00000152239	ENSMUSG00000026049	1	44086613	44102441	-1	0	1	2	0	0	0	0	0	0	0	0		Q3TUU5
ENSMUST00000152240						2	0	5	4	4	0	11	101	15	8	36		
ENSMUST00000152241	ENSMUSG00000002028	9	44803355	44881296	-1	9	3	0	0	0	0	0	0	0	0	0	S4R2S5	
ENSMUST00000152242						4	4	12	0	3	2	0	24	4	9	1		
ENSMUST00000152243	ENSMUSG00000034327	14	67715937	67742310	1	0	5	5	14	6	0	0	1	3	1	2	D3YZ64	
ENSMUST00000152245						0	0	0	50	0	0	0	0	11	0	0		
ENSMUST00000152246						11	2	20	15	17	2	0	0	0	0	0		
ENSMUST00000152247	ENSMUSG00000039477	5	142724661	142817662	-1	0	10	51	104	30	0	1288	711	2187	34	2079	F6Z7L1	
ENSMUST00000152248	ENSMUSG00000040621	X	166170454	166190512	1	0	0	1	0	0	0	0	0	0	0	0	E9PZ44	
ENSMUST00000152251						2	0	10	0	0	7	60	187	137	26	252		
ENSMUST00000152252						0	0	0	0	0	0	7	0	21	0	0		
ENSMUST00000152253						20	7	63	138	32	12	0	0	1	0	0		
ENSMUST00000152255						3	5	5	5	7	2	0	0	0	0	0		
ENSMUST00000152256						0	0	2	1	2	0	0	2	0	0	0		
ENSMUST00000152257	ENSMUSG00000034201	11	5054132	5065327	-1	0	0	0	0	0	0	0	0	27	0	0	Z4YN41	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152258	ENSMUSG00000006720	13	21945094	21960779	1	0	1	0	0	0	1	0	0	1	0	0	H3BJS2	
ENSMUST00000152259						5	2	16	8	0	10	213	81	66	14	169		
ENSMUST00000152260						10	8	20	8	13	2	1	2	0	0	3		
ENSMUST00000152261						52	62	55	39	58	27	3	57	19	8	22		
ENSMUST00000152262						1	2	3	6	3	3	1	1	0	1	0		
ENSMUST00000152263						2	2	6	3	5	3	0	0	0	0	0		
ENSMUST00000152265	ENSMUSG00000042726	5	121371725	121385632	-1	0	0	2	12	1	0	11	48	39	8	47	D3YWU1	
ENSMUST00000152266						5	6	1	0	2	0	0	4	0	0	0		
ENSMUST00000152267	ENSMUSG00000000486	7	127214447	127233130	-1	4	0	0	0	0	0	37	67	0	0	84		
ENSMUST00000152269						0	3	3	33	7	0	0	0	0	0	0		
ENSMUST00000152270	ENSMUSG00000029454	5	121525038	121545905	-1	0	0	0	0	0	0	0	0	0	0	0	F7DD22	
ENSMUST00000152271	ENSMUSG00000066043	4	132355923	132422489	-1	0	0	3	14	1	1	0	0	0	0	0	A0A0A0MQJ4	
ENSMUST00000152272						0	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000152273	ENSMUSG00000031441	8	12757014	12868728	1	1	0	0	0	8	2	0	21	10	0	17	F6R5M4	
ENSMUST00000152274						0	0	4	0	0	2	91	223	29	6	32		
ENSMUST00000152275						8	14	35	16	12	5	1	1	1	0	3		
ENSMUST00000152276						0	2	3	2	1	0	96	935	151	167	480		
ENSMUST00000152277						7	5	29	5	6	8	8	49	13	5	21		
ENSMUST00000152280						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000152281	ENSMUSG00000037552	7	28359604	28372599	-1	2	0	3	0	0	1	10	0	0	0	7	D6RFC7	
ENSMUST00000152282						4	5	0	2	8	0	0	0	0	0	0		
ENSMUST00000152283						2	2	6	6	8	3	0	0	0	0	0		
ENSMUST00000152285						5	0	1	4	8	5	14	37	23	3	37		
ENSMUST00000152286	ENSMUSG00000021643	13	100107997	100114571	1	2	0	0	0	0	0	3	0	2	0	0	B2KF73	
ENSMUST00000152287						1	7	6	1	6	1	28	126	31	6	55		
ENSMUST00000152288	ENSMUSG00000001964	X	74254687	74261548	1	0	0	0	0	0	0	263	380	180	0	142	D6RFS0	
ENSMUST00000152289						0	0	1	0	1	0	0	2	5	0	2		
ENSMUST00000152290						0	3	1	6	0	1	1	2	0	1	2		
ENSMUST00000152291	ENSMUSG00000050379	X	36911326	36991794	-1	0	0	0	6	0	0	0	0	0	0	0	A2A3W1	
ENSMUST00000152293						3	0	2	204	13	7	0	3	2	0	2		
ENSMUST00000152294	ENSMUSG00000061759	10	4432467	4455141	1	0	0	0	0	0	0	14	0	3	0	0	D6RG65	
ENSMUST00000152295						0	0	3	2	0	0	4	0	5	30	6		
ENSMUST00000152296						5	5	4	8	7	5	0	0	0	0	0		
ENSMUST00000152297						1	2	3	0	5	4	69	5	30	107	194		
ENSMUST00000152298						7	0	2	81	6	0	30	42	13	12	16		
ENSMUST00000152299						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000152300						18	12	68	38	19	12	1	5	7	1	14		
ENSMUST00000152301	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	0	0	0	0	0	D3Z413	
ENSMUST00000152303						0	3	2	0	6	2	11	0	3	0	4		
ENSMUST00000152304	ENSMUSG00000025572	11	117765988	117782198	-1	0	0	0	0	0	0	4	1	2	0	3	B1ATB7	
ENSMUST00000152305	ENSMUSG00000042581	1	129273302	130219278	1	88	98	526	299	116	88	0	0	2	0	6	D3Z366	
ENSMUST00000152307						6	4	8	5	2	4	1	7	3	5	9		
ENSMUST00000152308						0	0	0	0	0	9	0	0	0	0	0		
ENSMUST00000152309	ENSMUSG00000030980	7	118842222	118856254	-1	1	3	0	0	0	0	0	0	2	0	0	D3Z5V3	
ENSMUST00000152310						4	5	32	0	4	0	0	0	0	0	6		
ENSMUST00000152311						1	0	5	0	2	1	0	0	0	0	3		
ENSMUST00000152312						144	136	265	117	115	57	3	75	14	8	21		
ENSMUST00000152314	ENSMUSG00000051043	11	114851152	114872617	1	0	0	0	0	0	0	0	0	0	0	0	B7FAT9	
ENSMUST00000152315	ENSMUSG00000045639	7	127607031	127615797	-1	3	0	6	3	3	4	0	0	0	0	0	D3YV15	
ENSMUST00000152316						18	17	8	8	10	7	0	11	10	0	8		
ENSMUST00000152317						0	0	0	0	0	4	0	0	0	1	0		
ENSMUST00000152318	ENSMUSG00000026027	1	58973522	58995715	1	0	0	0	0	0	0	50	127	136	18	75	M0QWE6	
ENSMUST00000152319						3	4	8	16	7	0	0	0	0	0	0		
ENSMUST00000152320						0	0	21	54	6	0	0	0	0	0	0		
ENSMUST00000152321						0	0	7	3	3	2	0	0	10	8	4		
ENSMUST00000152322	ENSMUSG00000035969	4	43381979	43427088	1	0	0	22	5	2	0	0	0	0	0	0	B0R000	
ENSMUST00000152323						5	5	18	5	3	4	39	5	0	0	12		
ENSMUST00000152324	ENSMUSG00000061171	2	65316430	65364034	-1	0	0	0	0	0	0	0	0	0	0	1	A2ASI2	
ENSMUST00000152325	ENSMUSG00000036893	2	24789928	24919614	-1	0	4	0	0	0	0	0	0	0	1	5	F6WWY8	
ENSMUST00000152326						0	10	0	7	12	5	0	0	0	1	0		
ENSMUST00000152327	ENSMUSG00000027323	2	119112793	119147445	1	16	5	23	0	0	1	33	21	18	0	10	D6RCK1	
ENSMUST00000152328						0	0	0	1	0	0	2	28	2	3	4		
ENSMUST00000152329						10	6	16	28	8	8	4	35	6	1	45		
ENSMUST00000152330						11	11	39	19	14	4	0	0	0	0	0		
ENSMUST00000152331						0	0	0	49	0	0	0	0	0	0	0		
ENSMUST00000152332						5	6	7	0	9	6	0	0	3	0	0		
ENSMUST00000152333						25	19	19	23	21	16	11	37	14	6	29		
ENSMUST00000152334						5	2	15	11	5	0	32	125	34	5	33		
ENSMUST00000152336						1	1	1	55	3	0	0	0	0	0	0		
ENSMUST00000152337						2	1	26	46	1	2	0	6	2	0	8		
ENSMUST00000152338	ENSMUSG00000024750	19	21272278	21282289	1	0	1	0	1	0	0	0	19	12	0	0	D3YYE8	
ENSMUST00000152339						0	0	2	2	5	0	5	14	7	0	28		
ENSMUST00000152340	ENSMUSG00000040451	19	32122727	32389714	-1	2	0	0	2	4	6	150	102	272	233	373		Q8VCQ6
ENSMUST00000152341						4	3	5	8	5	6	3	8	5	0	4		
ENSMUST00000152342						2	3	8	2	1	0	5	5	4	0	2		
ENSMUST00000152343	ENSMUSG00000079460	X	112239049	112243852	1	0	0	1	0	1	1	0	0	0	0	0	F6UK53	
ENSMUST00000152344						1	2	4	0	1	1	0	0	0	0	2		
ENSMUST00000152345						84	70	418	49	53	39	2	2	3	0	12		
ENSMUST00000152346						0	0	0	41	0	0	0	0	0	0	0		
ENSMUST00000152347	ENSMUSG00000027288	2	120506820	120563843	-1	0	0	0	0	0	0	18	0	43	0	83	F6UL00	
ENSMUST00000152348						0	3	11	61	4	5	27	31	29	47	21		
ENSMUST00000152349	ENSMUSG00000024948	19	6341135	6355615	1	0	0	0	0	0	0	0	0	0	0	0	D6RG51	
ENSMUST00000152350						1	2	1	0	2	0	0	0	0	0	0		
ENSMUST00000152353						3	2	4	3	0	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152354						20	22	50	44	15	8	0	5	3	1	3		
ENSMUST00000152355						46	24	81	70	38	25	2	5	5	0	1		
ENSMUST00000152356						2	3	17	3	3	0	0	0	0	9	0		
ENSMUST00000152357	ENSMUSG00000037652	3	30899371	30969415	-1	0	0	0	0	0	0	0	7	41	0	28	D6REI6	
ENSMUST00000152358						0	0	1	20	0	0	12	14	85	15	32		
ENSMUST00000152359						1	2	1	4	7	0	0	1	0	0	0		
ENSMUST00000152360						97	72	197	166	95	53	4	18	3	3	8		
ENSMUST00000152361	ENSMUSG00000022791	16	32643874	32683493	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5M1	
ENSMUST00000152362	ENSMUSG00000039449	2	4622058	4652113	-1	1	0	1	4	1	0	73	103	384	390	263		Q8BM39
ENSMUST00000152363	ENSMUSG00000015519	10	28972288	28986303	-1	2	1	0	0	0	0	0	0	0	0	0	D3Z001	
ENSMUST00000152364						3	0	0	1	2	1	65	398	255	189	167		
ENSMUST00000152366						2	0	3	0	1	0	0	3	11	4	15		
ENSMUST00000152367	ENSMUSG00000027201	2	125084628	125123661	-1	0	0	0	9	0	0	0	4	0	14	12		Q8C854
ENSMUST00000152369						0	3	0	1	0	2	0	55	4	0	3		
ENSMUST00000152370						0	0	0	0	0	0	3	38	0	5	4		
ENSMUST00000152371						2	5	6	1	2	2	25	182	32	42	47		
ENSMUST00000152372						3	0	1	0	1	0	0	0	3	0	0		
ENSMUST00000152373						6	4	8	4	7	1	0	0	5	0	2		
ENSMUST00000152374	ENSMUSG00000026857	2	30807826	30823033	1	0	0	0	0	0	0	14	13	3	0	0	A2APZ3	
ENSMUST00000152376						2	0	2	0	4	1	0	0	0	0	0		
ENSMUST00000152377	ENSMUSG00000039977	9	15559864	15627933	-1	0	0	0	0	0	1	0	0	0	0	1	D3Z2N8	
ENSMUST00000152378	ENSMUSG00000048617	8	84946991	84956603	1	88	70	529	127	66	39	6	21	8	3	12	E9PXB4	
ENSMUST00000152380	ENSMUSG00000027326	2	119047119	119105501	1	0	0	2	13	1	0	0	0	2	0	0	A3KGI5	
ENSMUST00000152381						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152382						2	1	1	0	2	1	12	18	14	0	13		
ENSMUST00000152383	ENSMUSG00000041650	14	122534324	122891100	1	3	3	15	5	7	5	0	0	0	0	0	H3BK61	
ENSMUST00000152385						2	0	5	0	0	3	0	0	0	0	0		
ENSMUST00000152386	ENSMUSG00000056752	11	65831282	66168551	-1	4	9	11	23	20	10	1	0	3	0	7	F7DC70	
ENSMUST00000152387	ENSMUSG00000035310	5	100441918	100500639	-1	0	0	12	0	3	9	20	0	95	39	114	E9Q8B7	
ENSMUST00000152388						1	2	3	59	1	2	0	0	0	0	0		
ENSMUST00000152389	ENSMUSG00000043036	5	122108040	122140823	-1	0	2	0	0	0	0	27	135	34	136	37	D6RE42	
ENSMUST00000152390	ENSMUSG00000046020	2	153241533	153270247	1	0	0	14	0	0	0	5	3	15	0	12	E9Q686	
ENSMUST00000152391	ENSMUSG00000039130	6	30366380	30391028	-1	0	0	0	0	0	0	0	0	0	1	0	H3BKM2	
ENSMUST00000152392	ENSMUSG00000021411	13	34627840	34652681	-1	9	1	3	0	2	0	1	0	0	0	1	D3Z5D8	
ENSMUST00000152393						0	1	1	0	0	0	0	6	0	0	0		
ENSMUST00000152394						4	2	4	0	3	0	0	0	0	0	0		
ENSMUST00000152395	ENSMUSG00000018541	11	97745481	97766556	-1	3	1	3	7	4	0	7	7	0	0	2	F7BY36	
ENSMUST00000152396	ENSMUSG00000025786	9	123066160	123113205	-1	0	0	0	0	0	0	0	0	0	0	0	D6RHS2	
ENSMUST00000152397						0	0	1	0	1	0	14	115	75	5	84		
ENSMUST00000152398						2	4	5	1	3	1	17	59	55	295	41		
ENSMUST00000152399						0	5	0	0	0	0	0	0	4	0	4		
ENSMUST00000152400						15	18	40	92	23	13	0	0	0	0	1		
ENSMUST00000152402						7	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000152403	ENSMUSG00000026553	1	172082529	172122330	1	0	0	0	0	0	0	0	0	0	0	0	F6XJN3	
ENSMUST00000152404	ENSMUSG00000020694	11	105178807	105283959	1	1	0	2	0	0	0	17	0	36	8	35	F6XSD0	
ENSMUST00000152405						0	0	0	0	2	0	0	0	0	0	1		
ENSMUST00000152406						0	0	0	18	0	0	0	0	0	0	0		
ENSMUST00000152407	ENSMUSG00000044533	17	24718116	24721929	1	4	0	0	97	0	4	0	0	5	0	5	D3YVC1	
ENSMUST00000152408	ENSMUSG00000054814	5	73998453	74068431	-1	2	3	22	5	13	2	3	11	4	5	4		
ENSMUST00000152410	ENSMUSG00000030960	7	132827457	132852673	-1	0	0	0	0	0	0	5	1	3	14	0	A0A087WQ96	
ENSMUST00000152411						116	68	109	791	135	83	0	1	2	0	4		
ENSMUST00000152413						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000152414						3	3	1	5	2	1	0	6	1	0	7		
ENSMUST00000152415						1	3	3	75	0	0	9	11	3	0	0		
ENSMUST00000152416						4	1	4	0	2	2	0	0	0	0	0		
ENSMUST00000152417	ENSMUSG00000024371	17	34862604	34898265	-1	15	5	0	0	14	0	0	0	0	0	13	B8JJN2	
ENSMUST00000152418	ENSMUSG00000035268	2	163658386	163726158	1	0	0	0	29	0	4	1	0	3	0	0	B7ZC20	
ENSMUST00000152419						5	6	0	3	0	2	0	0	0	0	0		
ENSMUST00000152420	ENSMUSG00000074063	8	119434124	119446256	1	10	0	4	10	17	7	2082	2407	1089	128	883	Q8VC10	
ENSMUST00000152421						0	1	6	2	2	1	0	0	0	0	0		
ENSMUST00000152422	ENSMUSG00000031516	8	34090420	34108796	-1	2	0	0	0	3	0	122	419	170	410	45	F6XWI6	
ENSMUST00000152423	ENSMUSG00000018796	8	46471041	46536051	1	0	0	0	2	0	0	0	0	0	0	0	F6WNZ2	
ENSMUST00000152424	ENSMUSG00000035298	7	99466004	99474022	1	0	3	0	7	2	1	0	0	1	0	1	F6W0Q8	
ENSMUST00000152425						3	0	0	2	0	0	0	0	0	1	0		
ENSMUST00000152426	ENSMUSG00000040990	X	159627272	159978069	1	0	0	0	0	0	0	35	17	25	30	32	B0R0Y8	
ENSMUST00000152427						45	30	66	69	43	32	0	0	1	0	7		
ENSMUST00000152428						2	4	0	0	5	0	0	0	11	0	0		
ENSMUST00000152430						1	3	0	35	0	0	2	0	0	2	1		
ENSMUST00000152431						0	0	0	0	0	0	4	0	0	0	0		
ENSMUST00000152432						7	1	1	42	8	6	1	1	6	0	12		
ENSMUST00000152433						0	1	4	9	0	0	1	0	3	0	3		
ENSMUST00000152434	ENSMUSG00000025736	17	25828867	25831842	1	0	0	0	0	0	0	0	0	0	0	0	F6Q269	
ENSMUST00000152435						0	0	0	0	0	0	0	0	0	2	1		
ENSMUST00000152436						0	3	5	0	0	0	0	0	0	0	0		
ENSMUST00000152437						0	0	0	0	0	0	10	17	38	9	37		
ENSMUST00000152438	ENSMUSG00000036872	8	86482260	86580686	-1	14	4	13	28	18	10	0	0	0	0	1		Q80WJ6
ENSMUST00000152440						0	2	2	0	2	0	3	18	0	0	4		
ENSMUST00000152441						0	3	2	63	7	1	849	874	785	4705	475		
ENSMUST00000152442	ENSMUSG00000022094	14	70303469	70351425	-1	7	0	3	2	7	2	0	1	0	0	0	D3Z6P5	
ENSMUST00000152444						6	2	46	43	2	2	4	4	2	2	11		
ENSMUST00000152445						26	17	58	61	15	0	0	0	0	0	0		
ENSMUST00000152447	ENSMUSG00000029780	6	56882400	56923932	-1	0	0	2	0	0	0	59	130	135	14	34	S4R2D9	
ENSMUST00000152448	ENSMUSG00000019942	10	69336635	69352938	-1	1	0	8	3	8	6	0	9	0	0	0	D3Z2T9	
ENSMUST00000152449						2	2	7	7	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152450						2	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000152451						0	0	5	0	4	4	8	2	2	0	2		
ENSMUST00000152452	ENSMUSG00000027651	2	158028497	158132297	1	7	7	17	21	12	8	0	0	2	0	7		Q9CSU0
ENSMUST00000152453						7	7	2	8	8	3	0	10	4	0	15		
ENSMUST00000152454						9	0	4	87	9	0	0	5	4	5	13		
ENSMUST00000152455	ENSMUSG00000032717	17	47815328	47834691	-1	1	4	6	122	6	0	1	0	0	0	0	D3Z3N7	
ENSMUST00000152456						0	0	0	11	1	0	0	0	0	1	1		
ENSMUST00000152457	ENSMUSG00000031271	X	139079257	139085236	-1	1	1	0	0	0	0	0	0	0	0	0	B1AW62	
ENSMUST00000152458						0	0	0	0	0	0	0	13	0	1	0		
ENSMUST00000152459	ENSMUSG00000032076	9	47530173	47857637	1	0	0	19	66	0	0	0	0	0	0	0	E9PYN1	
ENSMUST00000152460						0	0	0	0	0	0	0	12	1	0	0		
ENSMUST00000152461						3	0	2	0	0	0	0	0	1	0	0		
ENSMUST00000152463	ENSMUSG00000025283	X	155213132	155216449	-1	0	0	0	7	0	8	102	2052	70	273	126	S4R2T2	
ENSMUST00000152464						6	0	24	11	11	2	0	0	0	0	0		
ENSMUST00000152465						0	3	5	0	0	0	0	0	0	0	0		
ENSMUST00000152466						0	0	0	0	0	1	2	0	2	0	2		
ENSMUST00000152468						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000152469						5	5	6	4	13	3	25	0	11	0	5		
ENSMUST00000152471	ENSMUSG00000050373	2	164785823	164793816	1	5	4	18	12	10	5	1	4	4	0	4	G3UY23	
ENSMUST00000152472	ENSMUSG00000015597	17	46383731	46420920	1	0	0	0	0	0	0	0	0	2	0	0	F6R9J2	
ENSMUST00000152473	ENSMUSG00000016356	2	180986535	181017540	1	2	1	0	3	5	0	0	0	2	0	0	F6ZXI1	
ENSMUST00000152474	ENSMUSG00000044060	5	107497378	107512556	1	4	0	2	4	4	0	0	0	0	0	10	D3YUW2	
ENSMUST00000152475						9	0	0	2	5	0	34	56	52	3	93		
ENSMUST00000152476						2	0	2	2	3	2	2	13	10	4	13		
ENSMUST00000152477						9	11	6	5	11	5	0	0	0	0	0		
ENSMUST00000152478						4	1	1	4	2	3	0	1	1	1	1		
ENSMUST00000152479						1	8	11	13	2	5	6	7	2	0	5		
ENSMUST00000152480						6	8	30	6	8	2	0	18	0	9	54		
ENSMUST00000152481						6	5	11	10	5	2	14	69	70	15	128		
ENSMUST00000152482						4	0	0	0	3	3	0	0	0	0	0		
ENSMUST00000152484						3	0	3	0	0	0	0	5	8	0	8		
ENSMUST00000152485	ENSMUSG00000069495	2	49451486	49551948	1	0	0	0	0	1	0	24	54	31	0	14	A2AQV0	
ENSMUST00000152486						7	3	7	7	8	7	7	6	9	2	21		
ENSMUST00000152487	ENSMUSG00000018566	11	69942539	69948188	-1	0	0	0	0	0	1	0	0	0	0	0	J3QMX9	
ENSMUST00000152488	ENSMUSG00000058486	6	34880426	34910876	-1	0	0	0	0	0	0	0	0	7	0	0	D3Z4Z6	
ENSMUST00000152489						3	6	3	0	1	0	0	0	0	0	0		
ENSMUST00000152490						3	0	0	0	2	0	0	9	7	0	6		
ENSMUST00000152491						8	1	22	4	13	0	0	0	0	0	0		
ENSMUST00000152492						0	4	12	0	1	2	23	15	16	36	9		
ENSMUST00000152493						10	7	6	14	12	6	41	40	17	0	47		
ENSMUST00000152495						3	1	0	2	0	0	0	22	9	0	0		
ENSMUST00000152496	ENSMUSG00000015869	11	116470845	116494202	-1	0	2	5	3	3	0	0	0	0	0	0	B1AT84	
ENSMUST00000152497						59	41	114	49	58	28	0	6	5	0	9		
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ENSMUST00000152499						0	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000152500						6	5	0	5	8	0	5	24	13	0	32		
ENSMUST00000152501	ENSMUSG00000026226	1	86016816	86029958	1	0	0	0	0	0	0	0	0	0	0	0		Q9D9T6
ENSMUST00000152502						11	14	7	8	15	6	3	6	19	0	21		
ENSMUST00000152503						62	57	136	60	86	31	9	21	24	1	35		
ENSMUST00000152504	ENSMUSG00000024270	18	24579881	24603817	-1	0	2	6	52	3	0	0	0	0	0	0	D3Z0J4	
ENSMUST00000152505	ENSMUSG00000003923	10	71225464	71238280	-1	0	0	0	0	0	0	11	0	22	8	5	D3Z0F3	
ENSMUST00000152506						4	1	10	4	0	0	0	7	0	0	9		
ENSMUST00000152507	ENSMUSG00000025089	19	58235604	58455909	-1	0	0	0	0	0	0	0	0	1	0	0		P97785
ENSMUST00000152508						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000152509						5	4	11	3	7	4	0	2	0	1	0		
ENSMUST00000152510						4	4	15	4	5	5	3	3	2	0	0		
ENSMUST00000152511	ENSMUSG00000031543	8	22974844	23150497	1	22	9	40	0	0	0	4	1	0	0	3	F7D1P5	
ENSMUST00000152512						2	0	0	0	5	0	1	18	4	0	11		
ENSMUST00000152513						8	8	14	11	9	4	0	0	0	0	0		
ENSMUST00000152515	ENSMUSG00000037143	2	145934784	146215039	1	0	0	0	0	0	0	0	0	0	0	0	B7ZCD4	
ENSMUST00000152516						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152517	ENSMUSG00000060807	12	103646630	103657212	-1	2	3	0	1	1	3	0	0	0	0	0	D3Z2I9	
ENSMUST00000152518						7	21	30	33	15	11	0	0	0	13	0		
ENSMUST00000152519						0	0	0	1	2	1	36	96	78	396	68		
ENSMUST00000152520						357	373	551	278	335	186	20	75	42	15	55		
ENSMUST00000152521	ENSMUSG00000035530	11	100319885	100322096	1	0	3	34	2	7	8	39	1332	96	19	86	J3QN87	
ENSMUST00000152522	ENSMUSG00000017721	2	164497520	164508301	1	0	6	18	8	7	0	0	0	0	0	0	F6U4X6	
ENSMUST00000152523						8	1	1	8	3	0	0	0	0	0	0		
ENSMUST00000152525						1	0	1	1	0	2	0	0	0	0	0		
ENSMUST00000152526	ENSMUSG00000028207	4	9448069	9669344	-1	0	0	0	0	0	0	0	0	0	0	0	A2AL77	
ENSMUST00000152527						1	0	0	6	2	8	0	0	0	0	0		
ENSMUST00000152528						0	0	6	0	4	11	51	93	40	1	0		
ENSMUST00000152529						16	0	0	0	18	0	0	0	0	0	0		
ENSMUST00000152531	ENSMUSG00000031075	7	144588549	144751974	-1	1	3	0	3	3	5	0	0	0	0	4	F6R6E1	
ENSMUST00000152532	ENSMUSG00000031918	9	13748410	13806481	1	0	2	0	0	2	0	0	0	0	0	1	B8JJF3	
ENSMUST00000152533	ENSMUSG00000071369	10	19934472	20142753	1	70	48	58	36	70	32	0	6	15	0	14	D3Z5H1	
ENSMUST00000152534						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152535						2	3	2	1	5	1	0	0	59	34	64		
ENSMUST00000152536	ENSMUSG00000023286	4	155943831	155959604	1	0	0	0	0	0	0	0	7	0	0	0	B0QZM2	
ENSMUST00000152537						4	0	0	90	4	1	9	35	21	12	31		
ENSMUST00000152539						6	0	9	80	7	0	40	40	29	6	28		
ENSMUST00000152540						5	4	0	0	11	0	24	36	16	0	59		
ENSMUST00000152541						6	9	15	16	6	7	30	22	41	0	36		
ENSMUST00000152543						5	0	0	3	7	4	4	12	3	2	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152544						2	6	25	76	13	6	0	0	0	0	0		
ENSMUST00000152545						1	6	5	7	2	6	6	8	9	0	13		
ENSMUST00000152546	ENSMUSG00000001441	11	97205842	97280638	-1	0	0	4	0	0	0	0	10	0	0	0	F6Z7Y0	
ENSMUST00000152547	ENSMUSG00000029686	6	47453398	47526139	1	0	0	0	24	0	0	0	0	0	0	0	D3YUS8	
ENSMUST00000152548						28	8	42	29	27	14	43	158	132	10	226		
ENSMUST00000152549						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152550						3	1	17	0	5	1	0	0	0	0	0		
ENSMUST00000152551						2	1	2	16	0	0	9	49	11	49	14		
ENSMUST00000152553	ENSMUSG00000050312	16	62732444	62786818	-1	2	0	2	7	0	0	0	0	3	4	15	D3YXZ6	
ENSMUST00000152554						2	4	10	0	2	0	0	0	0	0	6		
ENSMUST00000152555	ENSMUSG00000021687	13	94201310	94285857	-1	0	0	0	10	4	0	162	15	66	0	19	Q3TSA8	
ENSMUST00000152556						0	2	1	4	6	1	4	0	0	0	1		
ENSMUST00000152557	ENSMUSG00000046351	13	23353103	23369208	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZCB1	
ENSMUST00000152558	ENSMUSG00000079020	15	73577424	73645762	-1	2	3	0	0	0	0	0	2	0	0	5	F6Z9M3	
ENSMUST00000152559						0	2	10	11	3	5	37	10	20	0	15		
ENSMUST00000152560						38	27	132	54	39	22	7	10	11	2	14		
ENSMUST00000152562	ENSMUSG00000021771	14	21831269	21845879	1	1	4	7	48	0	4	0	2	0	0	0	D3YUN8	
ENSMUST00000152563						7	0	37	2	7	3	0	0	0	0	0		
ENSMUST00000152564	ENSMUSG00000037270	3	36863104	37053033	1	34	32	0	0	0	0	738	621	1142	0	752		A2AAE1
ENSMUST00000152565	ENSMUSG00000028793	4	129058271	129085886	1	0	5	3	76	0	0	304	235	444	2	241	A2A7Q8	
ENSMUST00000152566	ENSMUSG00000019461	11	69846376	69852058	1	0	0	12	15	0	0	124	59	124	7	74	Q5F284	
ENSMUST00000152567	ENSMUSG00000041351	4	137664726	137729861	1	1	1	6	172	7	5	0	0	0	0	0	A2ALS2	
ENSMUST00000152568						0	2	2	0	0	1	0	3	7	0	5		
ENSMUST00000152571	ENSMUSG00000030263	6	145115653	145174934	1	3	0	3	2	4	1	44	40	38	19	23	E9Q2C8	
ENSMUST00000152572	ENSMUSG00000011751	7	27356383	27447686	-1	0	0	5	0	0	0	0	0	0	0	0	D3YWH8	
ENSMUST00000152573						4	4	0	0	2	2	0	0	0	0	0		
ENSMUST00000152574						4	2	0	12	0	2	8	41	14	2	38		
ENSMUST00000152575						29	30	1341	56	40	0	0	8	0	3	7		
ENSMUST00000152577						81	55	261	19	67	25	22	29	18	4	25		
ENSMUST00000152578	ENSMUSG00000000826	2	181520485	181555133	1	0	0	0	62	0	0	0	0	0	0	0	A2AUE1	
ENSMUST00000152579						1015	983	724	1239	1458	807	140	521	314	73	564		
ENSMUST00000152580						13	11	10	150	18	3	10	64	12	0	50		
ENSMUST00000152581	ENSMUSG00000029772	6	29768011	29912310	1	0	0	0	4	0	0	0	0	0	0	2	H3BKG8	
ENSMUST00000152582						48	35	171	50	32	26	1	4	1	0	3		
ENSMUST00000152583						5	9	9	38	6	1	0	0	5	0	7		
ENSMUST00000152584						6	0	3	1	0	1	0	0	0	0	2		
ENSMUST00000152585	ENSMUSG00000002871	6	88902251	88912238	1	0	0	0	0	0	0	31	0	16	0	0		
ENSMUST00000152586						4	5	7	3	0	2	0	0	0	0	0		
ENSMUST00000152587	ENSMUSG00000015942	5	134184019	134224355	1	0	0	1	0	1	0	2	48	22	0	27	F7BET1	
ENSMUST00000152588						14	8	59	7	12	4	0	0	0	0	0		
ENSMUST00000152589	ENSMUSG00000078812	11	69916714	69921958	-1	0	0	0	5	0	0	0	0	0	0	0	A0A0A0MQM0	
ENSMUST00000152590	ENSMUSG00000022451	15	94577951	94589889	-1	3	0	2	33	3	0	0	2	0	0	4	D3Z2H0	
ENSMUST00000152591	ENSMUSG00000025743	4	130792537	130826319	1	3	0	14	5	5	0	0	0	0	0	0	B1ASF6	
ENSMUST00000152592	ENSMUSG00000003068	10	80115803	80130682	1	0	0	0	0	2	0	43	269	31	24	15	F6WNS2	
ENSMUST00000152593	ENSMUSG00000042185	9	31386192	31421333	1	0	0	0	0	0	15	0	0	0	0	0	D6RD05	
ENSMUST00000152594	ENSMUSG00000040433	9	96682770	96752831	-1	46	28	33	32	32	8	125	282	199	59	126	Q3LR78	
ENSMUST00000152596						1	2	15	0	4	2	0	2	0	1	14		
ENSMUST00000152598						5	3	5	1	2	0	0	1	0	0	7		
ENSMUST00000152601						1	0	7	3	0	2	10	30	16	0	47		
ENSMUST00000152602						0	1	7	0	0	0	0	0	0	0	0		
ENSMUST00000152603						10	5	19	16	17	9	3	20	3	0	0		
ENSMUST00000152604						0	0	0	0	1	0	0	1	0	0	0		
ENSMUST00000152605						5	0	20	90	0	4	4	14	6	0	10		
ENSMUST00000152606						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000152607						0	0	0	0	0	1	0	13	0	0	0		
ENSMUST00000152608						0	0	0	9	0	0	41	233	47	118	62		
ENSMUST00000152609						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000152610	ENSMUSG00000044308	2	69897246	70024013	1	1	0	3	0	0	0	0	57	13	0	28	A2AV05	
ENSMUST00000152611						0	0	4	21	0	0	20	13	0	0	0		
ENSMUST00000152612						33	43	480	76	29	22	59	195	68	17	134		
ENSMUST00000152613						1	1	7	0	4	2	17	0	23	0	0		
ENSMUST00000152614						12	16	61	113	24	11	0	1	0	0	0		
ENSMUST00000152615						6	0	0	3	0	1	2	1	1	0	0		
ENSMUST00000152616	ENSMUSG00000049470	11	53350833	53421830	1	0	0	0	0	0	0	0	2	0	0	0	F6WNE9	
ENSMUST00000152617						31	3	29	13	44	17	0	213	0	0	0		
ENSMUST00000152618	ENSMUSG00000020821	11	70700548	70731964	1	13	8	1	15	20	14	61	27	59	2	22	Q3V3Y9	
ENSMUST00000152620	ENSMUSG00000025102	7	81782182	81789478	-1	0	4	9	30	2	1	3	4	5	14	7	D6RIL2	
ENSMUST00000152621						0	0	0	6	6	3	0	0	0	0	0		
ENSMUST00000152622						0	7	6	0	5	1	141	491	553	1465	174		
ENSMUST00000152623						4	5	7	3	3	1	0	6	13	2	45		
ENSMUST00000152624						2	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000152626						3	1	2	1	3	0	0	72	0	0	5		
ENSMUST00000152628						1	2	4	0	0	2	0	0	0	0	0		
ENSMUST00000152629						6	3	0	6	5	1	1	0	0	0	0		
ENSMUST00000152630						1	3	2	4	4	3	0	0	0	0	0		
ENSMUST00000152631	ENSMUSG00000070733	5	73019987	73256619	-1	0	0	2	0	1	0	0	0	0	0	0	F6SDM9	
ENSMUST00000152632						5	9	14	26	12	4	0	1	3	2	7		
ENSMUST00000152633						5	6	3	1	3	0	7	48	16	5	30		
ENSMUST00000152634	ENSMUSG00000021694	13	108158731	108195364	1	0	0	0	0	0	0	0	34	0	0	7	D6RET0	
ENSMUST00000152635	ENSMUSG00000000318	11	70156197	70170834	1	0	0	0	0	0	0	0	0	0	2	0	B1AU01	
ENSMUST00000152636	ENSMUSG00000036893	2	24789928	24919614	-1	0	0	1	0	0	0	2	8	3	0	3	A0A0A6YWA0	
ENSMUST00000152637						67	64	306	236	73	38	9	25	16	0	17		
ENSMUST00000152638						7	6	4	128	13	2	5	1	6	0	3		
ENSMUST00000152639						9	8	21	11	9	4	35	39	51	6	115		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152640						17	19	32	99	41	32	60	179	128	10	204		
ENSMUST00000152641						0	0	0	0	0	0	3	0	6	4	0		
ENSMUST00000152642	ENSMUSG00000029233	5	76140271	76155504	1	1	3	0	3	2	2	4	1	0	0	3		
ENSMUST00000152643	ENSMUSG00000026047	1	44106546	44118808	-1	3	7	12	2	14	2	0	5	9	1	3	D6RE32	
ENSMUST00000152644						4	1	2	18	2	0	2	4	18	21	10		
ENSMUST00000152646						16	9	42	20	24	5	0	0	0	0	0		
ENSMUST00000152647						1	1	5	1	1	1	0	0	0	0	0		
ENSMUST00000152649	ENSMUSG00000030452	7	55931287	55962476	-1	1	0	0	53	0	0	0	0	0	22	0	D3YUE5	
ENSMUST00000152650						5	1	18	2	2	1	2	3	5	0	11		
ENSMUST00000152651						427	434	779	345	393	165	48	188	71	18	84		
ENSMUST00000152652	ENSMUSG00000047495	8	14095865	14847680	1	0	0	0	128	0	0	0	0	0	0	0	Q0VF59	
ENSMUST00000152653	ENSMUSG00000018661	11	113649169	113667054	1	0	0	0	0	0	0	0	1	1	0	0	F6YD49	
ENSMUST00000152654	ENSMUSG00000026123	1	34849976	34879580	1	0	2	4	2	5	2	0	0	0	5	0	D3Z3L2	
ENSMUST00000152655	ENSMUSG00000052613	10	73099342	74649737	1	0	7	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000152656	ENSMUSG00000009073	11	4765845	4849536	-1	2	0	0	0	1	0	0	0	0	0	0	F7DBY2	
ENSMUST00000152657	ENSMUSG00000006345	10	75561604	75586200	1	0	0	0	0	0	0	2	0	0	0	0	D3YYH6	
ENSMUST00000152658						3	4	5	4	2	6	30	47	9	0	11		
ENSMUST00000152659	ENSMUSG00000026176	1	74391509	74397285	1	3	0	0	67	2	0	43	18	60	100	53	F7AIT6	
ENSMUST00000152660						7	1	0	2	0	2	0	0	0	0	0		
ENSMUST00000152661						7	4	4	1	6	1	0	0	0	1	0		
ENSMUST00000152662						1	1	5	75	7	1	7	0	98	137	227		
ENSMUST00000152664	ENSMUSG00000079465	1	82586921	82722059	1	0	1	2	4	1	2	0	0	0	0	2	F6RIS8	
ENSMUST00000152665						0	0	0	102	3	2	1	4	1	0	0		
ENSMUST00000152666						19	19	17	19	13	16	56	54	50	11	98		
ENSMUST00000152667						0	0	1	16	1	1	0	0	0	0	0		
ENSMUST00000152668						99	91	537	150	99	46	3	12	10	3	24		
ENSMUST00000152670						0	0	1	0	0	1	0	7	0	0	0		
ENSMUST00000152671	ENSMUSG00000066760	7	17074040	17133450	1	1	2	3	2	1	3	0	0	0	0	0	D3YXQ6	
ENSMUST00000152672						0	0	0	0	0	0	2	0	2	4	20		
ENSMUST00000152674	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	5	0	1	0	1	0	0	0	E9Q270	
ENSMUST00000152675						1	2	3	5	2	2	0	15	3	2	8		
ENSMUST00000152676						4	0	0	28	4	2	0	0	0	0	0		
ENSMUST00000152677						1	1	0	1	5	1	2	0	0	0	0		
ENSMUST00000152678						77	78	358	120	96	53	3	17	20	1	21		
ENSMUST00000152679						2	0	0	4	3	0	0	0	0	0	0		
ENSMUST00000152680						3	0	1	0	1	0	0	0	0	9	0		
ENSMUST00000152681	ENSMUSG00000022214	14	55560006	55570065	1	0	0	0	0	0	0	61	0	10	0	58	D6REI5	
ENSMUST00000152682						0	0	0	0	0	0	0	17	158	0	40		
ENSMUST00000152683						3	5	3	29	1	3	0	0	4	0	1		
ENSMUST00000152684						2	1	1	3	5	2	0	3	1	0	1		
ENSMUST00000152685						3	3	0	0	0	0	0	0	0	0	4		
ENSMUST00000152686						3	1	10	2	0	1	0	0	0	0	0		
ENSMUST00000152687	ENSMUSG00000042333	4	154922210	154928563	-1	0	0	0	0	0	0	0	5	0	0	0	F6Y2U8	
ENSMUST00000152688						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000152689						7	0	0	0	0	1	102	1003	252	20	447		
ENSMUST00000152690						2	1	1	2	2	3	0	0	0	0	0		
ENSMUST00000152692						4	0	0	0	0	0	1	1	0	0	0		
ENSMUST00000152693	ENSMUSG00000030450	7	56239760	56536518	1	11	0	42	9	19	3	0	0	0	0	0	D6RCY7	
ENSMUST00000152694						11	6	47	13	22	9	0	20	0	0	4		
ENSMUST00000152695						0	0	0	189	3	2	0	36	10	0	14		
ENSMUST00000152696						0	0	0	96	1	0	0	0	0	0	3		
ENSMUST00000152697						0	0	5	0	1	0	0	11	3	0	0		
ENSMUST00000152698	ENSMUSG00000001300	8	8617434	8660773	-1	2	0	1	0	1	0	0	0	1	1	0	F6RSU6	
ENSMUST00000152699						0	0	0	8	0	0	1	0	0	31	0		
ENSMUST00000152700	ENSMUSG00000020485	11	87737552	87743623	1	7	5	0	6	12	0	176	376	143	674	117	D6RHM5	
ENSMUST00000152701						0	2	0	40	0	0	28	0	15	5	16		
ENSMUST00000152702						6	6	13	349	13	6	0	1	0	0	0		
ENSMUST00000152703	ENSMUSG00000037613	7	143665809	143685872	-1	16	17	21	0	4	5	65	83	96	76	84	Q3U3F7	Q9ER63
ENSMUST00000152704	ENSMUSG00000021660	13	98309896	98317006	-1	0	3	10	0	0	3	1359	5901	1381	5356	1077	Q3UJR8	Q64152
ENSMUST00000152705	ENSMUSG00000056698	6	72565922	72598413	-1	0	0	0	2	1	1	0	2	3	0	6	D3Z5B5	
ENSMUST00000152706						0	0	0	0	0	0	32	74	27	286	44		
ENSMUST00000152707	ENSMUSG00000026173	1	74542888	74567794	1	0	0	24	0	0	0	0	0	0	0	0	D6RGN2	
ENSMUST00000152708						3	4	0	2	4	4	1	3	0	0	5		
ENSMUST00000152710						3	5	10	20	16	4	610	937	605	111	637		
ENSMUST00000152711	ENSMUSG00000041911	2	71528113	71533981	1	0	0	0	0	0	0	0	0	0	0	0	G3XA72	
ENSMUST00000152712						1	1	0	5	2	3	0	0	2	0	2		
ENSMUST00000152713	ENSMUSG00000026921	2	26580014	26593120	1	2	2	3	0	1	0	0	0	0	0	0	F6RMR6	
ENSMUST00000152714						3	2	5	6	7	1	0	0	0	0	0		
ENSMUST00000152715						6	3	28	6	11	3	0	14	4	0	33		
ENSMUST00000152716						8	1	17	3	3	0	0	31	0	0	12		
ENSMUST00000152717	ENSMUSG00000063172	4	107253593	107279938	1	2	0	0	23	2	1	0	0	0	0	7		Q9D6H2
ENSMUST00000152718	ENSMUSG00000040919	11	30426006	30471827	-1	0	0	0	0	0	0	0	0	0	0	0	F2Z426	
ENSMUST00000152719						28	37	46	28	36	22	0	5	0	0	6		
ENSMUST00000152720						7	5	3	6	6	3	0	0	0	0	0		
ENSMUST00000152721	ENSMUSG00000017760	2	164832873	164841032	1	0	0	0	0	0	0	37	74	53	0	0	A2A5J6	
ENSMUST00000152722						1	3	9	1	1	0	0	0	0	0	0		
ENSMUST00000152723						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000152724	ENSMUSG00000090115	17	47630690	47686738	1	3	0	0	0	0	3	7	6	16	6	13	Q8BUQ6	
ENSMUST00000152725	ENSMUSG00000021156	13	9684836	9765321	-1	2	3	4	4	1	0	0	9	0	0	0	D3Z029	
ENSMUST00000152727	ENSMUSG00000029416	5	127595664	127632897	-1	3	2	11	0	0	0	0	0	7	0	0	D3Z4X0	
ENSMUST00000152728						0	0	0	0	0	0	0	19	5	3	2		
ENSMUST00000152729						6	2	14	2	7	2	9	81	32	14	100		
ENSMUST00000152730	ENSMUSG00000050197	X	38121219	38129967	1	3	0	4	76	4	2	0	0	0	0	0	F6YCR7	
ENSMUST00000152731						0	2	0	3	0	0	40	13	15	0	17		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152732						7	9	16	6	6	5	0	20	4	0	10		
ENSMUST00000152733						0	0	3	69	0	2	0	0	1	0	1		
ENSMUST00000152735						98	143	54	46	56	27	6	16	17	2	24		
ENSMUST00000152738						0	2	2	3	3	0	2	3	2	0	0		
ENSMUST00000152739						4	0	4	7	1	0	0	35	6	9	7		
ENSMUST00000152741						0	0	0	0	0	0	0	2	0	2	1		
ENSMUST00000152742						4	2	4	0	3	1	0	0	0	0	0		
ENSMUST00000152743	ENSMUSG00000023074	X	53344598	53370502	-1	0	3	0	6	0	0	127	84	33	134	40		Q8VEL0
ENSMUST00000152744						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000152746						1	8	10	2	0	7	0	0	0	0	0		
ENSMUST00000152747						11	1	13	13	19	9	64	315	81	2	155		
ENSMUST00000152748						1	5	22	7	7	2	0	2	0	0	1		
ENSMUST00000152749						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000152751						125	133	201	73	116	41	7	8	9	1	12		
ENSMUST00000152752	ENSMUSG00000038346	6	125009145	125037870	1	0	0	3	0	0	1	0	0	2	0	2	D3Z517	
ENSMUST00000152753						4	3	2	34	3	1	20	63	52	10	37		
ENSMUST00000152755						0	0	0	0	0	0	60	31	61	18	181		
ENSMUST00000152756						35	24	73	383	54	24	4	9	6	0	8		
ENSMUST00000152757						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152759	ENSMUSG00000014418	7	46760466	46796064	-1	2	0	1	21	0	0	5	3	9	0	0	D3YYJ4	
ENSMUST00000152760						0	0	0	0	0	0	15	6	15	6	0		
ENSMUST00000152761	ENSMUSG00000037012	10	62268855	62379908	-1	7	2	9	0	3	1	0	3	0	0	0	D3Z365	
ENSMUST00000152762	ENSMUSG00000028792	4	128991958	129011529	1	0	3	5	6	2	5	0	0	19	0	23	F7BP55	
ENSMUST00000152763						2	0	5	3	4	1	1	0	0	0	0		
ENSMUST00000152766	ENSMUSG00000005882	2	155846894	155930310	-1	0	0	0	0	0	0	0	0	7	14	14	A6PWX8	
ENSMUST00000152768						2	2	0	9	2	1	6	20	5	0	5		
ENSMUST00000152769						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000152770						20	13	46	1191	53	13	3	7	4	8	6		
ENSMUST00000152772	ENSMUSG00000000276	11	89035179	89066850	-1	0	0	0	107	0	0	4	5	0	0	0	F2Z490	
ENSMUST00000152773						5	2	4	6	2	2	0	7	8	0	23		
ENSMUST00000152774						66	57	409	113	35	27	0	2	3	0	0		
ENSMUST00000152775						1	0	0	1	4	0	0	0	0	0	0		
ENSMUST00000152776						1	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000152777	ENSMUSG00000036833	2	24976033	25054057	1	2	0	0	0	0	0	0	0	7	0	8	B0R010	
ENSMUST00000152778						0	0	2	2	4	0	24	30	29	54	31		
ENSMUST00000152779						14	6	7	6	6	6	0	0	0	0	0		
ENSMUST00000152782	ENSMUSG00000075254	16	33684466	33771576	1	48	39	298	142	49	26	24	41	58	35	174	E9Q440	
ENSMUST00000152783	ENSMUSG00000036873	3	145938014	145944829	1	0	0	5	19	0	0	2	0	29	27	40	F6XV67	
ENSMUST00000152785	ENSMUSG00000005150	8	85075035	85081306	-1	2	0	0	0	0	4	0	0	0	0	0	D6RGR4	
ENSMUST00000152786						46	27	97	186	42	19	1	11	1	2	11		
ENSMUST00000152788						16	22	50	25	17	11	1	1	0	1	1		
ENSMUST00000152789	ENSMUSG00000064068	3	89209081	89227088	-1	0	0	0	2	1	1	5	38	6	1	2	G3UXB5	
ENSMUST00000152791	ENSMUSG00000001855	2	31974436	32053975	1	0	0	0	0	0	0	5	15	0	6	0	A0A0A6YY32	
ENSMUST00000152792						35	17	55	212	23	9	24	22	6	0	20		
ENSMUST00000152794						0	2	0	1	2	0	0	2	0	0	0		
ENSMUST00000152795						0	0	0	0	0	1	0	0	0	0	3		
ENSMUST00000152796	ENSMUSG00000040025	4	132184912	132212303	-1	23	8	34	42	21	13	147	224	99	15	48		Q91YT7
ENSMUST00000152797						1	1	21	0	7	1	1	0	3	0	0		
ENSMUST00000152798	ENSMUSG00000038732	13	30136498	30246717	1	2	5	0	32	2	2	1	0	0	0	0	Q5T1H3	
ENSMUST00000152800						26	30	145	40	22	7	9	0	10	0	5		
ENSMUST00000152801						36	38	75	51	58	22	12	49	6	12	39		
ENSMUST00000152802	ENSMUSG00000009376	6	17463800	17573980	1	2	0	0	0	0	2	0	0	1	0	0	F6X333	
ENSMUST00000152804	ENSMUSG00000046727	18	36345619	36402980	1	1	0	2	1	4	0	14	11	0	3	0	F5H8M7	
ENSMUST00000152805	ENSMUSG00000029106	5	34573664	34632308	1	4	0	4	0	13	4	0	2123	22	97	31	F6RDR0	
ENSMUST00000152806						14	19	36	11	18	6	2	5	0	5	3		
ENSMUST00000152807						13	7	16	10	10	0	13	37	18	0	22		
ENSMUST00000152808						6	3	13	6	3	0	0	2	2	0	5		
ENSMUST00000152809	ENSMUSG00000026678	1	169655501	169695813	1	2	2	0	0	1	0	0	0	0	0	0	A0A0A6YWD0	
ENSMUST00000152810						2	3	3	3	2	2	0	0	2	0	0		
ENSMUST00000152811						12	20	55	16	23	22	0	0	0	0	0		
ENSMUST00000152812						5	0	10	0	4	0	78	488	78	30	94		
ENSMUST00000152814						0	3	3	7	6	2	5	4	0	0	4		
ENSMUST00000152816						2	0	2	2	0	0	5	12	9	0	12		
ENSMUST00000152817						2	0	4	7	6	2	0	0	0	0	0		
ENSMUST00000152818						0	0	9	4	4	7	0	0	0	0	0		
ENSMUST00000152819	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	22	2	0	0	0	0	0		Q99PJ1
ENSMUST00000152820						2	2	4	2	1	0	6	5	16	0	11		
ENSMUST00000152824	ENSMUSG00000032400	9	64137144	64173104	-1	2	0	0	0	0	0	0	4	0	0	0	F6TCM4	
ENSMUST00000152826						180	217	129	125	117	71	0	0	9	4	10		
ENSMUST00000152828						29	21	248	43	57	19	14	12	5	0	23		
ENSMUST00000152829	ENSMUSG00000034552	2	83915079	83941228	-1	1	4	14	6	10	1	0	0	0	0	0	B2FDH1	
ENSMUST00000152830	ENSMUSG00000023927	17	51736187	51833290	-1	21	13	13	286	29	16	27	50	122	7	62		Q60611
ENSMUST00000152831	ENSMUSG00000030302	6	113743831	114042613	-1	49	48	50	17	16	13	0	0	0	0	0	S4R1C4	
ENSMUST00000152832						2	1	0	5	0	6	0	0	0	0	0		
ENSMUST00000152833						4	1	2	58	7	0	0	0	90	122	166		
ENSMUST00000152834						2	1	0	0	4	0	0	0	3	0	3		
ENSMUST00000152835						4	2	6	0	3	1	0	0	0	0	0		
ENSMUST00000152836						21	13	55	22	20	7	0	10	8	2	4		
ENSMUST00000152837	ENSMUSG00000021792	14	40993740	41013788	-1	0	1	1	2	1	0	0	0	0	0	0	D3Z143	
ENSMUST00000152838	ENSMUSG00000031290	X	147470375	147554081	-1	0	0	0	0	0	0	0	0	0	0	0	A2AMP0	
ENSMUST00000152841	ENSMUSG00000022269	15	26309048	26409576	1	3	0	0	144	0	0	0	0	0	0	0	D3YXE6	
ENSMUST00000152842						0	4	1	1	4	3	0	0	0	0	0		
ENSMUST00000152843						0	0	0	0	0	0	46	59	35	0	0		
ENSMUST00000152844	ENSMUSG00000055567	1	66468367	66699866	1	2	0	0	0	0	1	0	0	0	0	0	F6ZAB0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152845						3	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000152846	ENSMUSG00000036002	4	43032414	43046220	-1	0	1	4	25	4	1	0	0	0	0	9	S4R159	
ENSMUST00000152847	ENSMUSG00000037313	5	33658128	33678995	1	0	0	0	22	0	0	0	0	4	0	0	D3Z1Y4	
ENSMUST00000152848						4	9	31	213	27	7	0	0	0	0	0		
ENSMUST00000152850						0	0	0	0	0	0	2	18	3	0	0		
ENSMUST00000152851						0	0	1	1	3	0	0	0	0	0	0		
ENSMUST00000152852						0	4	2	0	0	0	1	7	2	0	0		
ENSMUST00000152853	ENSMUSG00000024431	18	39410545	39491301	-1	2	0	0	87	4	0	16	10	198	3	121	E9Q310	
ENSMUST00000152855	ENSMUSG00000026162	1	74967139	75125200	-1	2	6	12	7	7	3	120	224	108	138	79	F7BTP0	
ENSMUST00000152857						5	5	6	113	16	8	0	2	0	0	0		
ENSMUST00000152859						4	1	3	3	4	3	0	0	0	0	0		
ENSMUST00000152860						1	2	0	2	3	0	2	7	7	0	2		
ENSMUST00000152861						0	0	0	0	0	1	6	4	0	0	0		
ENSMUST00000152864						3	2	3	7	5	0	0	23	0	8	0		
ENSMUST00000152865						5	1	0	13	6	0	0	0	0	0	0		
ENSMUST00000152866						0	2	0	0	2	0	6	54	10	0	21		
ENSMUST00000152868						1	1	0	67	1	0	0	0	0	1	0		
ENSMUST00000152869	ENSMUSG00000005774	3	94954075	94961561	1	0	0	1	5	0	0	0	0	0	0	0	D3YTK4	
ENSMUST00000152870						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000152871	ENSMUSG00000060038	8	85071757	85075162	1	0	0	0	0	0	0	10	34	15	9	22	F6W7I2	
ENSMUST00000152872	ENSMUSG00000029475	5	122870665	122989823	-1	0	1	0	0	0	3	13	0	11	0	19	F6QTG9	
ENSMUST00000152874						9	8	9	0	0	2	0	0	0	0	0		
ENSMUST00000152876	ENSMUSG00000030706	7	100545751	100608297	-1	0	0	0	0	1	0	21	94	30	94	27	D3Z6C8	
ENSMUST00000152877	ENSMUSG00000029670	6	21949571	21976038	1	0	0	6	0	0	0	22	31	26	325	169	S4R1J3	
ENSMUST00000152878	ENSMUSG00000070323	9	7571396	7581885	1	11	7	3	0	8	1	0	62	30	33	22	F6QKX8	
ENSMUST00000152879						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152880						0	0	0	50	1	1	0	0	0	0	3		
ENSMUST00000152881	ENSMUSG00000037270	3	36863104	37053033	1	0	1	0	0	0	1	10	0	0	0	0	D6RI50	
ENSMUST00000152882						7	8	7	8	2	3	5	25	32	9	27		
ENSMUST00000152883						1	0	4	1	0	0	8	16	17	48	5		
ENSMUST00000152884						11	13	18	11	9	4	0	0	0	0	0		
ENSMUST00000152885						2	3	21	66	5	3	0	1	0	1	3		
ENSMUST00000152886						0	0	3	5	1	1	0	0	0	0	0		
ENSMUST00000152887						0	2	4	1	0	3	0	0	0	0	0		
ENSMUST00000152888						0	2	3	0	10	0	82	29	260	0	199		
ENSMUST00000152889	ENSMUSG00000087166	4	98726734	98738480	1	3	5	10	20	4	1	0	0	0	0	0	E9PZU6	
ENSMUST00000152890						14	6	15	110	19	11	0	2	6	0	10		
ENSMUST00000152892	ENSMUSG00000054708	10	81628540	81647610	1	1	3	4	60	3	2	0	0	0	0	0	D3YXX7	
ENSMUST00000152893						0	0	0	1	1	0	0	2	6	0	0		
ENSMUST00000152894						18	8	0	60	24	16	0	0	25	0	0		
ENSMUST00000152895						0	0	5	1	3	2	0	0	0	0	4		
ENSMUST00000152896						3	0	0	7	1	0	0	0	0	0	1		
ENSMUST00000152897						0	0	0	9	4	4	0	0	0	0	1		
ENSMUST00000152898						2	4	0	3	0	0	0	0	2	0	0		
ENSMUST00000152899						0	0	1	8	0	0	5	10	12	5	13		
ENSMUST00000152900	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	5	0	0	0	F6W4F5	
ENSMUST00000152901						1	0	3	0	4	1	6	0	0	1	0		
ENSMUST00000152902	ENSMUSG00000038704	7	44465391	44467758	1	0	0	0	0	0	0	0	0	0	0	0	D6RE19	
ENSMUST00000152903						3	3	3	4	7	4	0	0	0	0	0		
ENSMUST00000152904						22	23	43	30	42	24	1	0	0	0	0		
ENSMUST00000152905						4	3	3	27	0	0	25	17	2	0	14		
ENSMUST00000152906						0	0	0	0	0	0	6	0	6	0	0		
ENSMUST00000152907						9	2	17	7	6	9	3	1	2	0	1		
ENSMUST00000152908	ENSMUSG00000054074	2	18040676	18049051	-1	0	2	1	9	4	1	0	0	0	0	0	Z4YLL5	
ENSMUST00000152909	ENSMUSG00000000142	11	108920349	108950783	1	0	0	0	0	0	0	0	0	0	0	0	A2ABQ9	
ENSMUST00000152910	ENSMUSG00000031085	7	143866871	143897506	1	9	7	5	8	6	0	0	0	0	0	0	D3YYH9	
ENSMUST00000152911						6	2	5	3	5	0	0	0	0	0	0		
ENSMUST00000152912						0	0	10	9	0	0	45	152	85	0	130		
ENSMUST00000152913	ENSMUSG00000021235	12	84361657	84373796	1	0	0	0	0	0	1	35	22	0	0	10	D6RG57	
ENSMUST00000152914						5	5	14	4	4	4	0	2	2	5	9		
ENSMUST00000152915						0	0	0	11	0	0	0	25	44	0	0		
ENSMUST00000152917						35	31	76	18	38	21	2	2	11	0	9		
ENSMUST00000152918						5	0	22	3	12	4	14	92	33	13	84		
ENSMUST00000152919	ENSMUSG00000027620	2	156147239	156180238	-1	0	5	0	6	4	0	20	30	37	120	121	D6RCZ8	
ENSMUST00000152920						8	5	3	7	9	4	0	0	0	0	3		
ENSMUST00000152921	ENSMUSG00000037475	X	41794991	41920674	-1	0	0	1	0	0	0	0	0	0	0	0	B1AZI7	
ENSMUST00000152922						7	10	4	7	10	6	2	0	9	1	2		
ENSMUST00000152924						2	1	2	62	2	0	0	0	0	0	0		
ENSMUST00000152926						0	1	2	4	2	0	2	12	2	0	4		
ENSMUST00000152927						26	28	319	35	32	21	0	34	9	0	20		
ENSMUST00000152928						0	3	2	2	3	3	0	0	0	0	0		
ENSMUST00000152929	ENSMUSG00000027189	2	102300119	102407828	-1	1	1	0	0	0	0	0	0	7	0	5	F7B7X2	
ENSMUST00000152930						5	11	25	13	10	8	1	0	0	1	0		
ENSMUST00000152931						1	0	0	0	5	0	23	18	38	0	11		
ENSMUST00000152932						0	0	7	0	0	0	0	0	0	1	0		
ENSMUST00000152933						40	39	146	28	57	20	2	7	2	0	5		
ENSMUST00000152934						1	2	0	1	4	1	0	8	0	3	0		
ENSMUST00000152935	ENSMUSG00000045098	19	3767421	3818303	1	0	0	0	0	0	0	5	0	4	1	0	D3YXL6	
ENSMUST00000152936	ENSMUSG00000016495	19	29348599	29367390	-1	0	0	0	0	0	0	0	43	5	13	0	D3YV19	
ENSMUST00000152938	ENSMUSG00000048967	8	69887788	69902712	-1	4	1	3	172	11	6	0	7	7	0	3	A0A0A0MQI6	
ENSMUST00000152939						4	8	8	10	6	0	1	22	8	0	7		
ENSMUST00000152940						0	2	1	1	1	1	0	9	0	0	2		
ENSMUST00000152941	ENSMUSG00000078897	2	175422300	175435807	-1	0	0	0	0	0	0	4	17	0	0	0	Q8BHI0	
ENSMUST00000152942						12	18	51	28	14	5	20	78	46	6	63		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000152945	ENSMUSG00000029455	5	121566027	121593824	-1	1	0	0	107	3	0	0	20	7	0	8	D3YYF3	
ENSMUST00000152946	ENSMUSG00000025223	19	46032593	46045214	-1	0	2	0	78	0	0	209	485	216	65	212	D3Z1C5	
ENSMUST00000152947	ENSMUSG00000029032	4	154278486	154301676	-1	6	0	6	12	10	2	0	1	0	0	2	B1ASH8	
ENSMUST00000152948						0	0	0	0	0	0	3	3	0	0	0		
ENSMUST00000152949	ENSMUSG00000033576	15	77044729	77057107	1	0	0	0	0	0	0	0	0	0	0	0	B7ZC57	
ENSMUST00000152950						2	3	4	0	6	3	0	0	0	2	0		
ENSMUST00000152952						2	0	2	0	4	0	3	1	0	0	0		
ENSMUST00000152953						1	7	2	1	4	3	0	0	0	0	0		
ENSMUST00000152954	ENSMUSG00000019143	18	36783008	36792562	1	12	8	29	38	11	3	117	374	101	41	124		Q99KK9
ENSMUST00000152955						46	27	76	39	29	21	38	193	94	16	130		
ENSMUST00000152956	ENSMUSG00000079592	9	44107245	44109187	1	0	0	0	35	0	2	0	0	1	0	0	D3YUN6	
ENSMUST00000152958	ENSMUSG00000000049	11	108343354	108414396	1	0	0	0	2	0	1	0	0	0	0	0	I7HJR3	
ENSMUST00000152959						100	100	598	171	120	48	2	22	7	1	35		
ENSMUST00000152960	ENSMUSG00000006732	10	127041414	127046365	1	3	4	12	68	10	3	0	0	0	0	0	D3YXU6	
ENSMUST00000152961						0	0	0	0	0	0	0	2	0	0	3		
ENSMUST00000152962	ENSMUSG00000038366	11	97799000	97838764	1	3	0	7	41	5	1	0	0	0	0	6	A2A6G7	
ENSMUST00000152964	ENSMUSG00000020899	11	68985697	69008460	-1	1	1	3	60	1	1	0	0	0	2	0	F6RUL9	
ENSMUST00000152965						0	0	2	0	0	1	68	183	47	6	21		
ENSMUST00000152966	ENSMUSG00000047090	10	128800036	128804370	-1	26	20	56	34	18	17	68	201	74	4	167	D6RES3	
ENSMUST00000152967						5	5	7	4	15	8	14	85	9	86	58		
ENSMUST00000152969						2	0	5	8	10	0	0	3	5	7	0		
ENSMUST00000152970						9	7	20	12	8	22	16	53	17	34	19		
ENSMUST00000152971	ENSMUSG00000056938	11	103101682	103112200	1	1	3	0	0	0	0	25	4	0	7	20	B0QZY3	
ENSMUST00000152972						0	4	0	0	0	0	0	10	0	0	0		
ENSMUST00000152973	ENSMUSG00000066756	7	18176494	18181862	1	7	6	0	8	10	0	0	0	0	0	0		Q6B9Z0
ENSMUST00000152974	ENSMUSG00000039814	8	18932729	18950975	-1	0	0	0	0	0	0	11	0	0	0	0	D6RJ59	
ENSMUST00000152975						7	4	10	2	5	3	2	0	0	0	3		
ENSMUST00000152976	ENSMUSG00000067274	5	115559467	115563727	1	0	0	0	125	6	0	0	13	0	0	0	D3YVM5	
ENSMUST00000152977						1	1	7	3	0	0	0	0	0	0	0		
ENSMUST00000152978	ENSMUSG00000013033	8	83900105	83941954	1	0	0	0	1	0	0	0	0	0	0	0	E9Q3V9	
ENSMUST00000152979	ENSMUSG00000020898	11	69015911	69036473	1	12	9	43	15	1	9	0	2	0	24	68	E0CXT1	
ENSMUST00000152980						6	2	2	2	2	1	0	0	0	0	0		
ENSMUST00000152981	ENSMUSG00000026737	2	18842255	18998126	-1	2	2	0	0	0	0	13	0	170	0	123	F6RJE8	
ENSMUST00000152982						3	2	5	262	11	7	3	17	1	4	5		
ENSMUST00000152983	ENSMUSG00000026270	1	92934376	92947941	1	19	10	17	0	12	0	95	69	48	14	53	D6RGR0	
ENSMUST00000152984						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000152985						17	5	13	0	14	11	0	45	0	0	18		
ENSMUST00000152988	ENSMUSG00000026921	2	26580014	26593120	1	0	0	0	0	0	0	0	0	0	0	0	G3UY71	
ENSMUST00000152989	ENSMUSG00000042251	1	131797381	131821473	1	0	0	0	0	0	0	0	0	0	0	0	F7B8J4	
ENSMUST00000152990						0	0	7	0	0	3	12	40	0	5	12		
ENSMUST00000152991						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000152992						0	0	0	0	1	2	0	3	3	0	2		
ENSMUST00000152993	ENSMUSG00000054428	4	132530555	132533659	-1	4	2	3	29	5	1	0	38	0	0	8	E9PV44	
ENSMUST00000152994						1	1	6	0	0	0	0	0	0	7	0		
ENSMUST00000152995	ENSMUSG00000005649	7	13398132	13408887	1	0	0	0	0	0	0	0	0	0	0	0	Q812F5	
ENSMUST00000152996	ENSMUSG00000035125	6	81923669	81959915	1	3	0	0	0	0	0	6	8	7	3	0	S4R198	
ENSMUST00000152997						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000152998						1	0	2	0	0	0	1	0	0	0	4		
ENSMUST00000152999						26	30	23	82	18	10	4	8	2	1	6		
ENSMUST00000153000						106	104	419	298	101	58	20	21	43	7	23		
ENSMUST00000153001	ENSMUSG00000058740	2	25863734	25918273	1	2	5	0	2	5	4	0	0	0	0	1	A0A0G2JDW4	
ENSMUST00000153002	ENSMUSG00000025716	2	22227503	22618252	1	4	0	6	0	0	0	0	0	0	1	0	B1AYY3	
ENSMUST00000153003	ENSMUSG00000033055	15	79053094	79062893	-1	0	0	0	34	0	0	0	2	0	0	0	D6REF6	
ENSMUST00000153004						1029	1127	1097	1086	837	353	31	72	56	5	145		
ENSMUST00000153005	ENSMUSG00000000339	3	116488963	116508208	-1	1	2	8	0	0	0	4	0	0	4	0	D3Z263	
ENSMUST00000153006						2	0	1	1	6	5	3	3	0	0	5		
ENSMUST00000153007	ENSMUSG00000053091	7	66689889	66717256	1	0	0	0	50	4	0	4	7	12	4	3	D3YTN6	
ENSMUST00000153008						0	0	10	0	5	1	19	55	15	3	7		
ENSMUST00000153009	ENSMUSG00000048655	3	55137339	55172935	1	4	3	23	5	4	5	0	0	0	0	0	D3Z7W2	
ENSMUST00000153011						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000153014						0	0	1	2	0	0	0	0	4	0	0		
ENSMUST00000153015						0	0	0	0	0	0	4	0	0	1	0		
ENSMUST00000153016	ENSMUSG00000024236	18	4920540	5119299	1	1	1	0	0	2	0	0	0	4	0	3	D3Z2X9	
ENSMUST00000153017						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000153018						1	4	15	51	5	2	51	151	99	9	102		
ENSMUST00000153020	ENSMUSG00000030990	7	102210208	102238567	1	2	0	0	1	0	0	0	5	0	0	0	D3YYE3	
ENSMUST00000153021						0	0	0	20	5	4	0	1	1	0	2		
ENSMUST00000153024	ENSMUSG00000031266	X	134588149	134601125	-1	0	0	0	2	0	0	0	3	0	34	6	A2BDV6	
ENSMUST00000153025						50	30	160	43	58	23	0	2	0	0	0		
ENSMUST00000153026	ENSMUSG00000028108	3	95734147	95739569	-1	0	4	0	0	0	0	0	0	0	0	0	D3YV22	
ENSMUST00000153027						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153029						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153031	ENSMUSG00000037990	10	58813359	59138916	1	223	118	898	361	129	67	5	16	7	0	10		Q8C120
ENSMUST00000153032						0	0	2	10	1	0	0	0	0	2	3		
ENSMUST00000153033						3	0	5	1	2	0	4	32	0	4	14		
ENSMUST00000153034						3	0	0	6	0	0	0	0	0	0	1		
ENSMUST00000153036						0	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000153037	ENSMUSG00000026388	1	120121187	120188189	1	4	3	3	2	2	1	0	0	0	0	0	F6SAX2	
ENSMUST00000153038						3	0	0	0	5	3	33	169	703	67	261		
ENSMUST00000153039						3	2	2	2	5	3	2	1	4	0	4		
ENSMUST00000153040						0	2	1	0	3	0	0	0	0	0	0		
ENSMUST00000153041						4	0	2	5	1	2	5	8	6	0	9		
ENSMUST00000153042						4	2	13	0	0	4	0	16	7	0	3		
ENSMUST00000153043	ENSMUSG00000058756	11	98740638	98769006	1	0	0	0	22	0	0	0	0	0	0	0	A3KFN7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153044						36	27	36	24	29	18	0	3	3	1	6		
ENSMUST00000153045						4	0	8	8	8	4	0	0	0	4	0		
ENSMUST00000153046						3	0	0	115	0	1	3	0	0	0	0		
ENSMUST00000153047						0	0	0	0	0	0	8	27	16	16	0		
ENSMUST00000153048						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000153050						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153052						0	0	0	0	0	0	0	0	0	40	0		
ENSMUST00000153053						2	0	8	0	2	1	0	21	31	25	8		
ENSMUST00000153054						10	1	13	6	8	3	5	46	24	5	52		
ENSMUST00000153055						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153056						0	0	0	0	0	0	448	676	769	532	793		
ENSMUST00000153058	ENSMUSG00000020649	12	24708241	24714146	1	6	5	4	2	11	1	0	3	0	0	10	D3Z0D8	
ENSMUST00000153059						0	3	0	68	4	0	3	0	2	0	7		
ENSMUST00000153060	ENSMUSG00000057455	18	30973489	31317290	-1	4	3	0	3	9	3	0	0	0	0	0		P70425
ENSMUST00000153061						4	4	0	0	4	2	0	2	0	2	0		
ENSMUST00000153062	ENSMUSG00000040785	16	94370618	94469222	1	0	0	3	0	0	0	0	0	0	0	0	Q05BF2	
ENSMUST00000153063						0	0	0	0	0	0	0	0	0	3	10		
ENSMUST00000153064						4	5	15	5	4	0	0	0	0	0	0		
ENSMUST00000153065	ENSMUSG00000025871	13	54551218	54565435	-1	17	7	17	0	16	0	404	1197	183	18	140	D3Z1F7	
ENSMUST00000153066						0	2	5	0	0	0	0	2	0	7	4		
ENSMUST00000153067						0	4	3	6	4	6	12	62	9	10	6		
ENSMUST00000153068						0	0	14	0	0	0	0	0	0	0	0		
ENSMUST00000153069						0	3	10	2	0	0	14	60	12	0	23		
ENSMUST00000153070	ENSMUSG00000032449	9	97074961	97111157	-1	0	0	14	0	0	2	0	15	49	0	59	D6RH79	
ENSMUST00000153071	ENSMUSG00000021768	14	21733394	21751181	-1	0	0	1	0	0	0	0	0	0	1	0	V9GXG6	
ENSMUST00000153072	ENSMUSG00000067424	17	33089310	33106203	1	1	0	5	5	3	0	1	0	0	0	0	F6R6Y7	
ENSMUST00000153073	ENSMUSG00000007646	11	87376645	87404954	-1	0	1	0	0	0	1	2	73	20	40	4	F2Z433	
ENSMUST00000153074						2	0	2	0	2	2	0	0	0	0	0		
ENSMUST00000153075						0	2	25	11	9	0	0	5	0	0	8		
ENSMUST00000153076	ENSMUSG00000020859	11	93996091	94126085	1	18	16	0	9	0	0	71	716	100	65	221	Z4YMB8	
ENSMUST00000153077						5	5	14	11	6	0	28	54	3	6	39		
ENSMUST00000153079						17	15	25	45	23	15	14	59	51	10	51		
ENSMUST00000153080						3	2	11	8	4	1	1	13	0	0	1		
ENSMUST00000153081	ENSMUSG00000038618	7	141215860	141218658	1	0	0	5	27	0	0	0	0	4	3	2	D3Z133	
ENSMUST00000153084	ENSMUSG00000020818	11	116852440	116875635	1	0	0	0	0	0	0	42	17	5	0	22		Q8BJ51
ENSMUST00000153085						2	0	7	39	3	2	187	342	164	14	92		
ENSMUST00000153086						9	17	25	11	22	5	0	0	3	0	0		
ENSMUST00000153088						96	137	124	61	108	71	35	156	40	64	46		
ENSMUST00000153090	ENSMUSG00000020566	12	17284721	17329359	-1	2	0	0	5	0	0	0	0	0	0	0	D3Z1Q7	
ENSMUST00000153091						7	4	20	8	11	8	0	0	3	1	1		
ENSMUST00000153092						0	3	0	1	0	1	9	0	9	0	0		
ENSMUST00000153093						0	2	0	1	1	0	0	0	0	0	0		
ENSMUST00000153094	ENSMUSG00000028914	4	141793612	141815976	1	0	0	0	51	0	0	6	4	12	0	22	A2AS92	
ENSMUST00000153096						9	7	5	7	6	5	5	6	3	0	0		
ENSMUST00000153097	ENSMUSG00000068264	2	131207078	131213514	1	1	0	0	0	0	1	0	0	0	0	0	A2ANC4	
ENSMUST00000153098						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000153099						85	67	418	121	112	42	2	11	18	5	23		
ENSMUST00000153100	ENSMUSG00000043411	4	137593755	137658537	1	2	0	0	57	7	4	0	0	3	0	0	A2BDP2	
ENSMUST00000153101						0	2	17	8	11	2	0	752	0	43	163		
ENSMUST00000153102	ENSMUSG00000037486	12	3426857	3506852	1	0	0	0	0	0	0	96	176	235	29	199	D6REV1	
ENSMUST00000153103						0	0	0	0	0	0	0	0	10	0	19		
ENSMUST00000153104						4	7	12	11	14	3	0	0	0	1	7		
ENSMUST00000153105						1	1	0	2	0	0	0	0	0	0	6		
ENSMUST00000153107						0	2	8	3	4	5	0	0	4	0	0		
ENSMUST00000153108	ENSMUSG00000027957	3	116669470	116712831	-1	4	2	1	41	8	2	0	0	0	0	0	D3YXZ7	
ENSMUST00000153109						9	12	7	15	12	7	7	70	20	5	28		
ENSMUST00000153110						1	1	0	1	0	1	0	10	4	3	3		
ENSMUST00000153111						28	27	41	8	31	27	4	20	5	0	24		
ENSMUST00000153112	ENSMUSG00000038685	2	181319739	181356616	1	2	0	10	1	2	0	0	0	0	0	0	A2AU08	
ENSMUST00000153114	ENSMUSG00000014599	3	107741048	107760469	-1	0	0	0	47	0	0	69	84	133	2	60	D3Z090	
ENSMUST00000153115	ENSMUSG00000044768	1	97606318	97662074	-1	4	0	8	295	10	5	128	373	285	33	247		Q8VEB3
ENSMUST00000153116						0	0	0	7	0	0	7	5	11	0	14		
ENSMUST00000153117	ENSMUSG00000036980	5	138178617	138187451	-1	17	4	33	18	16	6	0	0	0	0	0	S4R1R2	
ENSMUST00000153118	ENSMUSG00000024173	17	25343245	25345562	-1	0	0	9	5	10	2	0	0	0	12	5	E9PY32	
ENSMUST00000153119						0	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000153120						13	3	7	1	11	2	0	0	0	0	0		
ENSMUST00000153121	ENSMUSG00000075302	2	70508819	70540884	1	0	0	0	0	0	0	0	0	0	0	0	F6WLA9	
ENSMUST00000153123	ENSMUSG00000003531	16	18052860	18071632	1	0	0	0	0	0	4	0	0	0	0	0	Q80ZS8	
ENSMUST00000153124						33	29	210	33	20	16	25	65	41	4	100		
ENSMUST00000153125	ENSMUSG00000033416	10	75351111	75517972	-1	1034	1008	3273	1126	1150	504	9	58	35	106	64	F6ZAY0	
ENSMUST00000153126						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153127						0	0	16	115	10	3	0	0	0	0	0		
ENSMUST00000153128	ENSMUSG00000037408	1	36471620	36508764	1	50	31	95	105	54	23	471	784	597	30	571		Q69ZF7
ENSMUST00000153129						0	0	7	0	0	0	2	13	8	5	0		
ENSMUST00000153131						0	3	12	8	2	0	3	9	4	0	7		
ENSMUST00000153132						0	0	0	38	0	0	0	0	2	0	0		
ENSMUST00000153133						2	8	10	2	3	1	0	0	0	0	0		
ENSMUST00000153134						3	1	4	2	2	0	0	18	9	0	0		
ENSMUST00000153136	ENSMUSG00000026987	2	59899363	60209839	-1	0	1	0	0	2	0	11	37	85	1	67	A2AUY3	
ENSMUST00000153137	ENSMUSG00000047022	12	57230427	57497199	1	8	4	11	5	6	1	0	3	0	0	0	E9PZ24	
ENSMUST00000153138						2	2	6	1	1	1	1	11	1	0	5		
ENSMUST00000153139						0	3	0	3	4	2	0	0	1	0	0		
ENSMUST00000153140						3	3	4	2	0	3	1	5	2	9	0		
ENSMUST00000153141	ENSMUSG00000015291	X	74304998	74311862	1	1	1	0	0	1	2	0	2	3	0	5	D6RI86	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153142						2	1	3	4	5	2	0	0	0	0	0		
ENSMUST00000153143	ENSMUSG00000006335	7	3620324	3629929	-1	0	1	0	0	1	0	9	0	0	0	7	D6RHM4	
ENSMUST00000153145						7	6	22	12	7	0	2	4	6	0	8		
ENSMUST00000153146	ENSMUSG00000014856	8	105326354	105335219	1	0	0	0	0	0	0	20	0	15	18	0	S4R1H6	
ENSMUST00000153147	ENSMUSG00000010803	11	42130939	42182930	-1	3	0	0	3	4	1	0	0	0	0	0	E9Q2L8	
ENSMUST00000153148	ENSMUSG00000030032	6	83149361	83156397	-1	41	9	60	67	44	17	0	12	2	0	10		Q9R0D8
ENSMUST00000153149						11	7	29	30	10	0	0	0	0	0	0		
ENSMUST00000153150						0	0	0	3	0	0	2	0	2	1	2		
ENSMUST00000153151						1	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000153152						2	0	31	0	12	0	0	476	3	26	16		
ENSMUST00000153154						3	1	79	28	1	2	19	67	14	4	58		
ENSMUST00000153155						5	3	11	5	5	10	8	13	7	0	4		
ENSMUST00000153157						7	7	2	34	11	1	0	6	2	5	3		
ENSMUST00000153159						12	12	23	17	16	15	17	135	32	37	47		
ENSMUST00000153160						4	10	14	8	6	2	0	0	0	0	0		
ENSMUST00000153161						16	16	68	27	21	20	9	15	13	0	19		
ENSMUST00000153162						17	13	111	135	36	13	29	199	80	0	98		
ENSMUST00000153163						1	2	8	3	2	1	0	0	0	0	0		
ENSMUST00000153164						18	12	26	90	26	19	23	57	27	2	32		
ENSMUST00000153165	ENSMUSG00000029313	5	103692374	103855322	1	0	4	3	114	16	0	16	0	43	0	167	B1AVP1	
ENSMUST00000153166	ENSMUSG00000030849	7	130162451	133123350	-1	0	0	0	0	5	13	0	0	0	0	4	D6RJK5	
ENSMUST00000153167						6	7	2	6	7	6	0	1	0	0	1		
ENSMUST00000153168						4	2	3	8	6	0	0	1	0	1	0		
ENSMUST00000153169	ENSMUSG00000035203	7	5080235	5098178	1	3	2	10	62	2	3	16	16	18	0	18	D3Z550	
ENSMUST00000153171						5	0	0	5	2	3	2	11	4	3	2		
ENSMUST00000153172	ENSMUSG00000029270	5	107908053	107987085	-1	1	2	7	1	2	1	0	0	4	2	6	D3YUV7	
ENSMUST00000153173						61	114	103	38	63	49	4	17	3	39	17		
ENSMUST00000153174	ENSMUSG00000037736	5	66745827	67057158	1	0	0	0	0	0	0	0	0	0	0	0	F6W1Y9	
ENSMUST00000153176						9	5	14	9	12	3	5	11	0	0	20		
ENSMUST00000153177						1	0	3	1	0	2	0	1	0	0	0		
ENSMUST00000153178						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000153179						5	0	6	0	3	1	11	27	34	0	48		
ENSMUST00000153182						69	38	400	99	77	20	1	4	2	0	11		
ENSMUST00000153183	ENSMUSG00000005374	5	135149657	135165760	1	36	32	88	57	51	22	113	226	110	16	167		Q9R099
ENSMUST00000153184						3	3	0	0	2	5	0	0	0	0	0		
ENSMUST00000153185						0	0	24	5	6	14	0	0	0	0	0		
ENSMUST00000153186						78	95	251	134	92	46	8	24	0	9	13		
ENSMUST00000153187						10	0	0	0	0	0	0	81	13	0	62		
ENSMUST00000153189	ENSMUSG00000006219	4	141576062	141606096	-1	1	0	3	1	1	1	0	0	0	0	0	A2ADE6	
ENSMUST00000153190	ENSMUSG00000019082	7	141429744	141437892	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153191	ENSMUSG00000025512	7	141493136	141539857	-1	5	0	0	0	0	0	139	174	32	0	130		Q922Q9
ENSMUST00000153192						15	12	28	9	4	11	0	0	0	0	0		
ENSMUST00000153193	ENSMUSG00000024516	18	65800549	65817665	1	0	0	1	18	0	0	0	0	0	124	23	D3Z5H3	
ENSMUST00000153194	ENSMUSG00000039987	5	20758663	20882124	-1	4	4	21	0	0	6	3	0	0	0	0	F6X6S4	
ENSMUST00000153195						5	2	50	8	8	3	4	12	2	0	5		
ENSMUST00000153196						2	2	0	0	0	3	0	0	0	0	0		
ENSMUST00000153197	ENSMUSG00000003199	17	56005711	56016790	1	5	0	4	1	8	0	151	138	72	0	48	F7BQ76	
ENSMUST00000153198						2	4	11	2	1	0	0	0	0	0	0		
ENSMUST00000153199						6	0	11	9	6	3	66	276	152	353	215		
ENSMUST00000153200						5	4	0	1	0	2	0	0	0	0	0		
ENSMUST00000153201						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153203						0	0	2	0	0	0	52	44	39	67	35		
ENSMUST00000153204	ENSMUSG00000039850	11	119491347	119511437	1	0	0	2	9	0	1	24	0	0	5	6	E9PXA0	
ENSMUST00000153205						0	0	5	1	4	1	9	27	23	0	17		
ENSMUST00000153206						0	0	0	0	4	2	0	0	0	0	1		
ENSMUST00000153207						2	3	0	1	3	0	0	0	0	0	0		
ENSMUST00000153209	ENSMUSG00000052298	11	54717456	54787675	-1	0	0	7	15	1	0	0	0	0	0	8	B1AZK1	
ENSMUST00000153210						0	0	0	0	0	0	0	0	0	8	0		
ENSMUST00000153211						18	18	25	34	26	10	12	14	17	0	23		
ENSMUST00000153214						1	0	0	0	0	0	4	0	9	75	8		
ENSMUST00000153215						1	0	1	3	3	0	7	3	0	2	2		
ENSMUST00000153216						4	5	24	3	10	0	6	0	4	0	2		
ENSMUST00000153217						2	1	4	2	11	3	6	34	19	1	15		
ENSMUST00000153218	ENSMUSG00000052305	7	103826534	103828096	-1	0	10	26	0	8	0	12	0	12	82	25	E9Q223	
ENSMUST00000153219						45	36	66	58	68	23	7	61	15	8	36		
ENSMUST00000153220						1	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000153221	ENSMUSG00000025271	X	150588229	150643878	1	0	0	1	1	0	0	0	8	4	0	5	A2AFM8	
ENSMUST00000153222	ENSMUSG00000073096	6	48554796	48570722	1	0	0	1	8	1	0	26	11	36	3	28	D3Z0E0	
ENSMUST00000153223						2	2	4	2	6	0	0	0	1	1	0		
ENSMUST00000153224	ENSMUSG00000027752	3	54728678	54735393	-1	0	0	0	0	0	0	0	26	17	86	18	D3YYN3	
ENSMUST00000153225						5	9	16	1	2	7	1	1	2	0	11		
ENSMUST00000153226						1	3	15	3	4	3	0	3	0	0	3		
ENSMUST00000153227						0	6	3	5	7	1	0	6	0	0	4		
ENSMUST00000153229						1	2	0	0	0	1	0	0	2	0	7		
ENSMUST00000153230						16	15	39	33	25	8	276	1100	263	22	369		
ENSMUST00000153231						0	0	1	0	1	0	3	1	1	2	5		
ENSMUST00000153233						0	1	0	4	0	0	11	168	29	22	31		
ENSMUST00000153234	ENSMUSG00000021699	13	108449948	109953461	1	6	3	24	12	7	2	3	0	0	0	0	F6QFD1	
ENSMUST00000153236						98	77	87	484	122	85	26	73	41	5	36		
ENSMUST00000153237						0	3	1	0	0	2	0	0	0	0	0		
ENSMUST00000153238	ENSMUSG00000004815	5	108646693	108669672	-1	0	0	0	23	0	4	0	0	12	0	0	D6RI30	
ENSMUST00000153240						2	3	1	1	0	1	1	0	0	0	0		
ENSMUST00000153241						0	0	4	3	0	0	0	0	0	0	3		
ENSMUST00000153242						2	2	1	69	3	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153243						5	5	67	6	2	4	5	18	10	1	23		
ENSMUST00000153244						6	2	5	2	1	0	40	56	35	15	51		
ENSMUST00000153245						0	0	0	4	2	0	92	106	79	21	47		
ENSMUST00000153246						6	10	4	3	4	3	6	129	14	50	74		
ENSMUST00000153247	ENSMUSG00000026226	1	86016816	86029958	1	0	0	12	0	5	0	0	0	0	0	0	A5HNY3	
ENSMUST00000153248	ENSMUSG00000032900	18	56588350	56594782	1	3	1	7	0	3	2	0	0	0	0	0	F7C987	
ENSMUST00000153249						0	0	0	16	0	0	0	0	0	1	0		
ENSMUST00000153250	ENSMUSG00000001497	12	56691767	56712822	1	0	25	53	49	40	17	0	0	0	0	0	Q3V1K1	P47242
ENSMUST00000153251	ENSMUSG00000030590	7	29152511	29156234	-1	0	0	0	0	0	0	0	13	0	0	10	F6ZXW2	
ENSMUST00000153252						0	0	0	2	0	0	0	26	0	0	4		
ENSMUST00000153254						2	1	0	4	0	0	0	2	0	0	0		
ENSMUST00000153255						12	13	63	8	11	7	21	140	35	10	40		
ENSMUST00000153256	ENSMUSG00000038298	3	96829284	96870926	1	0	14	25	0	13	0	0	0	0	0	0		
ENSMUST00000153257	ENSMUSG00000073771	4	117119219	117125725	-1	0	4	0	0	3	1	0	2	0	0	3	A9JD57	
ENSMUST00000153258						0	0	0	0	0	0	0	33	0	0	0		
ENSMUST00000153259						0	0	1	52	0	2	0	0	0	0	0		
ENSMUST00000153260						1	0	0	0	1	2	13	51	25	15	32		
ENSMUST00000153262						0	0	5	0	0	7	2	7	7	0	6		
ENSMUST00000153263	ENSMUSG00000068876	3	94760069	94786492	-1	0	7	0	0	0	0	1	6	1	0	2	A0A0G2JFG0	
ENSMUST00000153264						0	0	0	36	0	0	0	0	0	0	0		
ENSMUST00000153265						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000153266						0	0	0	0	0	0	0	6	0	0	0		
ENSMUST00000153267	ENSMUSG00000039396	8	53586867	53639065	-1	1	2	64	5	3	0	0	0	0	0	0	D3Z756	
ENSMUST00000153268	ENSMUSG00000063975	6	142234227	142322981	-1	3	8	0	0	2	5	0	0	0	4	1	E0CX90	
ENSMUST00000153269						16	7	7	50	16	13	5	4	8	0	5		
ENSMUST00000153271						0	2	2	0	4	0	0	0	0	0	0		
ENSMUST00000153272						1	2	2	3	10	0	1	0	2	0	0		
ENSMUST00000153273	ENSMUSG00000078632	11	103451955	103504597	-1	93	63	323	104	84	40	0	0	0	0	0	B1AWG4	
ENSMUST00000153274	ENSMUSG00000028962	5	24423837	24440950	1	0	3	0	0	2	2	0	8	14	1	9		
ENSMUST00000153275						0	0	7	77	1	2	0	0	4	0	0		
ENSMUST00000153276						0	1	3	27	0	0	0	0	0	4	9		
ENSMUST00000153277	ENSMUSG00000030814	7	127661456	127708933	-1	3	7	10	10	13	3	0	0	5	0	0		
ENSMUST00000153278	ENSMUSG00000038718	2	34171457	34373142	-1	2	4	0	6	0	0	1	4	4	3	6	D6RCU6	
ENSMUST00000153279						0	1	0	1	0	0	11	11	18	4	18		
ENSMUST00000153280	ENSMUSG00000038236	6	52214491	52221854	-1	7	6	47	14	16	6	3	10	3	2	7	G3UZU9	
ENSMUST00000153281	ENSMUSG00000071660	19	8809075	8819333	-1	36	31	131	21	37	13	5	49	40	0	39	Q6P3Y6	
ENSMUST00000153282						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153284						0	0	0	2	0	0	0	0	0	0	4		
ENSMUST00000153285	ENSMUSG00000000738	8	123062942	123097760	1	0	0	0	0	7	4	0	0	0	0	17	D3YXB7	
ENSMUST00000153286						65	54	244	115	76	37	13	18	17	2	13		
ENSMUST00000153287	ENSMUSG00000033685	7	100493337	100502020	1	1	2	0	3	5	4	6862	2587	3761	298	3086	D3YXM5	
ENSMUST00000153289						0	2	0	3	4	2	4	0	3	0	0		
ENSMUST00000153290						7	14	9	2	9	0	0	4	3	51	73		
ENSMUST00000153291						0	2	4	0	0	2	0	0	0	0	0		
ENSMUST00000153292						0	0	0	0	0	0	0	0	7	10	0		
ENSMUST00000153293						0	0	0	0	1	0	1	0	0	0	0		
ENSMUST00000153294						3	3	1	0	4	1	2	8	4	3	3		
ENSMUST00000153295	ENSMUSG00000025193	19	43752996	43768638	1	0	0	0	0	2	0	0	0	20	8	12	D3YY50	
ENSMUST00000153298						6	0	43	4	0	0	0	0	0	0	2		
ENSMUST00000153299	ENSMUSG00000006958	16	20733127	20742384	1	3	0	0	19	0	0	0	0	0	0	0	S4R1K6	
ENSMUST00000153300	ENSMUSG00000027326	2	119047119	119105501	1	0	0	0	0	0	0	2	0	0	0	0	A3KGI6	
ENSMUST00000153301						2	3	7	136	4	1	0	0	0	0	2		
ENSMUST00000153302	ENSMUSG00000035234	5	100805192	100820965	-1	0	1	0	0	0	1	10	1	6	0	0	D6RHB0	
ENSMUST00000153303						0	0	0	108	0	0	0	0	0	1	0		
ENSMUST00000153305	ENSMUSG00000018669	11	96907426	96916496	-1	0	0	0	0	0	0	0	0	0	0	0	F2Z486	
ENSMUST00000153306	ENSMUSG00000038429	6	124815019	124829484	-1	3	0	3	2	3	2	5	2	2	0	3	D3YYA5	
ENSMUST00000153307						7	3	7	21	13	3	0	0	3	0	0		
ENSMUST00000153308	ENSMUSG00000034164	11	5106265	5152257	-1	2	2	4	2	6	0	0	0	0	0	0	F7BCQ7	
ENSMUST00000153309						4	6	10	57	3	6	30	59	11	3	13		
ENSMUST00000153310						3	5	4	2	1	7	0	43	19	77	20		
ENSMUST00000153312						0	2	0	321	30	13	2	2	3	2	2		
ENSMUST00000153314	ENSMUSG00000058135	3	108012255	108017973	-1	9	2	7	0	8	6	0	18	0	0	0	F6WHQ7	
ENSMUST00000153315	ENSMUSG00000028555	4	109406623	109444745	1	1	0	7	0	3	1	0	0	0	0	0	X1WI14	
ENSMUST00000153316	ENSMUSG00000038335	11	74898071	74909342	1	1	2	0	0	2	0	3	0	0	0	0	F6ZVN6	
ENSMUST00000153317	ENSMUSG00000057363	1	43746966	43827800	-1	0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000153318	ENSMUSG00000031402	X	75109733	75131016	-1	1	0	0	0	0	0	46	83	116	0	12	B7ZCM0	
ENSMUST00000153319						3	0	2	0	0	0	5	9	30	5	58		
ENSMUST00000153320	ENSMUSG00000021771	14	21831269	21845879	1	1	3	0	11	0	0	0	7	176	400	287	D3YZT5	
ENSMUST00000153321						0	0	0	14	0	1	1	0	0	1	0		
ENSMUST00000153322						7	9	10	9	7	11	0	3	2	1	0		
ENSMUST00000153323						6	1	4	3	3	0	1	16	0	0	10		
ENSMUST00000153324	ENSMUSG00000072244	7	104218793	104235152	1	0	0	0	1	0	2	0	0	0	0	0	D3Z7U8	
ENSMUST00000153325						0	0	0	0	0	0	2	11	0	1	0		
ENSMUST00000153326						0	1	3	0	0	0	4	29	6	0	12		
ENSMUST00000153327						6	1	0	0	3	0	0	0	0	0	2		
ENSMUST00000153329						88	80	719	139	63	30	0	7	12	0	10		
ENSMUST00000153330	ENSMUSG00000044816	1	65105285	65123214	-1	0	0	1	0	0	0	0	0	0	0	0	D6RG74	
ENSMUST00000153331						12	17	28	6	13	13	0	0	0	0	0		
ENSMUST00000153333						8	15	5	20	12	7	0	2	6	0	2		
ENSMUST00000153334						12	13	84	45	29	8	32	80	60	5	77		
ENSMUST00000153335						0	0	0	1	1	0	1	0	0	0	0		
ENSMUST00000153336	ENSMUSG00000028152	3	138742195	138907905	1	0	0	5	29	1	0	0	0	0	0	0	F7C5E2	
ENSMUST00000153337	ENSMUSG00000051469	18	24009702	24020810	-1	1	0	3	1	0	2	46	131	137	159	105		Q91VN1
ENSMUST00000153338	ENSMUSG00000061809	2	24071721	24096595	-1	2	3	5	2	2	1	0	1	0	1	1	Z4YMT0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153339						7	0	0	0	0	0	16	81	12	7	16		
ENSMUST00000153340						2	3	0	0	1	4	2	0	0	0	4		
ENSMUST00000153341						20	15	33	19	30	15	1	7	6	0	3		
ENSMUST00000153342						4	0	3	74	1	0	2	1	3	0	4		
ENSMUST00000153343	ENSMUSG00000024843	19	3851773	3894369	1	0	0	3	0	0	0	1	0	9	2	0	D6RG40	
ENSMUST00000153345						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153346	ENSMUSG00000025142	11	120672973	120709447	1	0	1	0	0	0	0	0	0	0	0	0	A2AC01	
ENSMUST00000153348	ENSMUSG00000038576	1	182763860	182896591	1	0	1	5	55	8	6	0	0	0	0	0		Q8BH32
ENSMUST00000153349						0	2	0	2	1	0	1	3	1	2	2		
ENSMUST00000153350						1	2	9	0	8	0	0	6	0	0	10		
ENSMUST00000153351						4	1	1	0	3	5	0	1	2	3	0		
ENSMUST00000153353						1	0	41	0	0	3	0	45	0	16	21		
ENSMUST00000153355						0	2	0	0	0	0	2	0	0	0	0		
ENSMUST00000153356						1	0	1	0	2	1	2	0	3	0	0		
ENSMUST00000153358	ENSMUSG00000028541	4	117869260	117883487	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQK1	
ENSMUST00000153359						33	25	114	21	35	19	121	391	195	25	219		
ENSMUST00000153360	ENSMUSG00000047989	18	24104757	24121953	-1	9	0	22	0	15	2	289	1099	475	450	387		Q8BHA0
ENSMUST00000153362						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000153363						2	0	1	2	0	0	0	0	0	0	2		
ENSMUST00000153364	ENSMUSG00000064080	6	91212455	91272540	1	2	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000153365						4	11	23	173	26	9	0	19	10	0	18		
ENSMUST00000153366						7	4	3	6	14	6	1	0	0	0	0		
ENSMUST00000153367	ENSMUSG00000002105	2	91061791	91070417	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZCF3	
ENSMUST00000153368						107	87	241	132	138	64	18	38	18	4	35		
ENSMUST00000153369	ENSMUSG00000028341	4	48045153	48086447	1	0	0	30	0	0	0	2	0	0	2	7	F6R7A2	
ENSMUST00000153370						2	8	6	87	8	8	58	945	189	37	242		
ENSMUST00000153371	ENSMUSG00000036989	7	105604463	105633571	-1	0	0	3	1	1	0	0	0	0	0	0	D3Z7V9	
ENSMUST00000153372						0	1	6	21	0	1	0	1	0	0	5		
ENSMUST00000153373						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153374						0	0	5	15	2	0	0	5	0	0	0		
ENSMUST00000153375	ENSMUSG00000026975	2	24962400	24972163	1	1	0	1	0	0	0	0	0	0	0	0	A0A0A6YY05	
ENSMUST00000153377	ENSMUSG00000038503	7	83884466	83901532	1	9	5	13	19	10	4	7	11	12	9	0	F6SWV4	
ENSMUST00000153378						0	0	0	80	1	0	0	0	0	0	0		
ENSMUST00000153379						0	0	6	3	0	0	0	6	0	0	0		
ENSMUST00000153380						1	7	7	16	9	3	0	5	1	3	4		
ENSMUST00000153381						13	5	72	23	13	2	5	40	27	1	42		
ENSMUST00000153382						1	0	7	0	0	0	0	0	0	0	0		
ENSMUST00000153383						789	807	484	460	646	315	3	26	33	4	52		
ENSMUST00000153384						4	4	5	4	3	4	16	8	22	1	32		
ENSMUST00000153385						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000153386						5	0	47	0	5	0	0	61	0	0	67		
ENSMUST00000153387						2	6	8	51	4	3	0	9	0	0	0		
ENSMUST00000153388	ENSMUSG00000036067	2	27021363	27027998	-1	0	0	0	1	0	0	2	0	2	0	5	A2AR27	
ENSMUST00000153389						1	0	8	8	1	1	1	2	0	0	0		
ENSMUST00000153390	ENSMUSG00000062995	6	8630527	8778488	-1	0	0	0	0	0	0	0	0	0	0	6	D3Z376	
ENSMUST00000153391						5	0	0	0	1	0	5	0	0	0	3		
ENSMUST00000153392						0	0	0	0	0	0	0	4	0	0	0		
ENSMUST00000153393						0	2	2	30	0	0	0	4	0	0	3		
ENSMUST00000153394	ENSMUSG00000028980	4	149979475	150009023	-1	0	1	2	5	4	0	36	6	23	6	23	A2A7A8	
ENSMUST00000153395						3	2	9	19	6	4	5	321	174	98	79		
ENSMUST00000153397	ENSMUSG00000022702	16	18877037	18970309	1	0	0	0	0	0	0	17	5	27	0	16	D6RE52	
ENSMUST00000153398	ENSMUSG00000022914	16	95992092	96082526	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q2N1	
ENSMUST00000153399	ENSMUSG00000039886	5	135735485	135744448	-1	0	0	0	14	1	0	0	0	0	0	0	D3Z0U3	
ENSMUST00000153400	ENSMUSG00000090231	17	34856374	34862518	-1	2	1	9	6	1	4	0	4	0	0	9	B8JJM3	
ENSMUST00000153401						0	2	5	0	3	2	0	0	0	0	0		
ENSMUST00000153403						17	5	230	75	11	7	0	3	7	0	6		
ENSMUST00000153404						2	1	0	0	3	2	3	15	2	0	0		
ENSMUST00000153405						0	1	10	7	2	1	2	1	1	2	4		
ENSMUST00000153406						1	0	1	2	1	0	0	149	23	0	0		
ENSMUST00000153407						2	0	2	0	2	2	1	0	0	0	1		
ENSMUST00000153408	ENSMUSG00000057948	11	116062095	116077961	-1	1	0	0	2	4	1	7	1	2	0	3	A2A855	
ENSMUST00000153409						0	0	0	1	0	1	3	29	7	0	3		
ENSMUST00000153410						4	1	0	3	6	1	9	6	13	0	15		
ENSMUST00000153411						0	0	4	0	3	0	16	89	29	42	43		
ENSMUST00000153412						5	1	2	5	3	3	2	3	6	0	13		
ENSMUST00000153413						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000153414	ENSMUSG00000020385	11	51261730	51281766	1	0	5	0	0	5	0	0	0	0	0	0	F2Z3V2	
ENSMUST00000153415						2	0	0	1	0	0	0	1	0	0	4		
ENSMUST00000153416						27	16	60	48	40	14	0	1	3	0	2		
ENSMUST00000153417						2	0	3	3	1	1	0	16	49	0	11		
ENSMUST00000153418	ENSMUSG00000030781	7	128265657	128272430	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153419						2	2	0	4	2	1	1	0	0	0	0		
ENSMUST00000153420	ENSMUSG00000051682	17	48264295	48275360	1	0	0	4	0	0	2	0	0	0	0	0		
ENSMUST00000153421						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000153422						0	1	3	3	0	0	0	1	0	0	2		
ENSMUST00000153423						2	2	8	7	2	1	6	4	0	0	0		
ENSMUST00000153424	ENSMUSG00000000223	X	134404551	134456573	1	52	15	25	567	59	21	2	0	0	0	8		Q05AA6
ENSMUST00000153425	ENSMUSG00000023764	11	3131850	3193463	-1	45	0	12	22	0	0	0	38	0	0	0	E9Q8V3	
ENSMUST00000153426	ENSMUSG00000021493	13	55495795	55513676	-1	2	1	14	40	4	1	0	1	0	0	3	B8JJB1	
ENSMUST00000153427	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	2	0	0	0	0	0	0	F6XIT3	
ENSMUST00000153428	ENSMUSG00000037791	11	77982754	78030539	1	0	5	0	0	0	3	66	125	33	1	37	Q5SS87	
ENSMUST00000153430						5	7	4	7	3	5	2	23	6	1	14		
ENSMUST00000153432	ENSMUSG00000062209	1	68032186	69108059	-1	1	2	0	0	0	3	0	0	0	0	0	B2KGF7	
ENSMUST00000153433						9	9	19	5	11	6	3	2	1	0	12		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153435						2	3	4	2	8	3	1	5	3	0	1		
ENSMUST00000153436						1	3	0	0	0	2	0	0	7	3	9		
ENSMUST00000153437						3	1	2	0	9	1	11	34	43	0	35		
ENSMUST00000153438						22	28	55	17	41	19	4	17	18	3	22		
ENSMUST00000153439						12	11	50	10	15	8	0	1	0	0	0		
ENSMUST00000153440	ENSMUSG00000000148	5	140705011	140719379	1	4	0	0	0	1	0	240	0	0	39	111	D6RE40	
ENSMUST00000153441	ENSMUSG00000001034	11	61488812	61494406	-1	0	0	1	0	0	0	20	23	38	0	15	Z4YLV8	
ENSMUST00000153442	ENSMUSG00000029328	5	100033577	100039664	-1	1	4	6	3	3	0	223	2154	413	273	425	F6VQH5	
ENSMUST00000153445	ENSMUSG00000045761	17	71673261	71729669	1	0	0	0	0	9	2	0	0	0	0	0		Q3TYG6
ENSMUST00000153446						45	40	114	73	90	28	19	43	53	7	92		
ENSMUST00000153447						3	5	0	0	5	3	0	0	0	0	0		
ENSMUST00000153448	ENSMUSG00000061577	8	94923694	94943290	1	3	0	6	2	6	0	1	0	0	0	0	D3Z3T1	
ENSMUST00000153449	ENSMUSG00000000317	11	70224128	70229798	-1	0	0	0	2	0	2	0	0	0	0	0	A2CF73	
ENSMUST00000153450						4	3	1	47	3	0	2	0	0	0	0		
ENSMUST00000153451	ENSMUSG00000040952	7	24884371	24889806	1	0	0	0	42	0	0	0	5	0	9	0	D3YUT3	
ENSMUST00000153452	ENSMUSG00000054102	7	26535023	26575615	1	0	0	0	0	0	0	0	0	0	0	0	D3YYQ3	
ENSMUST00000153453	ENSMUSG00000041598	11	113726850	113751881	-1	0	0	0	9	1	0	0	2	0	0	0	A2A6Q3	
ENSMUST00000153454						32	3	56	30	27	16	0	3	2	0	2		
ENSMUST00000153455						6	2	9	4	8	1	0	0	0	0	0		
ENSMUST00000153457						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153459						0	0	8	0	2	2	0	65	12	3	32		
ENSMUST00000153460	ENSMUSG00000022037	14	65968483	65981548	1	1	0	0	3	4	0	4	0	7	5	20	E9Q8Y5	
ENSMUST00000153462	ENSMUSG00000005936	17	28951950	28969549	1	3	0	5	2	3	0	31	2	66	6	37	B2KF10	
ENSMUST00000153464						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000153465						2	2	6	5	0	0	0	0	0	0	0		
ENSMUST00000153466	ENSMUSG00000045775	11	115462474	115474398	1	3	0	0	0	0	6	0	0	0	0	0	A0A0A0MQH7	
ENSMUST00000153467	ENSMUSG00000070972	4	58995062	59025573	1	0	0	0	0	0	0	0	0	0	5	0	F2Z410	
ENSMUST00000153468						1	1	3	0	0	0	0	0	0	0	0		
ENSMUST00000153469						1	0	1	0	1	0	5	0	2	0	15		
ENSMUST00000153470	ENSMUSG00000062797	7	89917529	89941199	-1	10	6	5	0	6	9	5	14	0	5	5		Q9DD02
ENSMUST00000153471	ENSMUSG00000075267	2	76648476	76658556	1	3	0	0	0	0	0	0	2	0	1	0	B0R0L8	
ENSMUST00000153472						1	1	0	56	3	0	6	48	40	7	34		
ENSMUST00000153473	ENSMUSG00000001829	7	101663633	101790168	1	0	0	0	0	0	1	3	7	4	0	0	D3Z7V2	
ENSMUST00000153475						5	5	6	6	1	5	0	0	3	0	3		
ENSMUST00000153476	ENSMUSG00000020804	11	116586432	116597680	1	5	0	31	26	9	0	0	4	2	0	0	Q14A64	O88816
ENSMUST00000153477	ENSMUSG00000035621	10	80148272	80158368	1	1	0	0	64	0	2	8	8	3	2	13	D3Z1J8	
ENSMUST00000153478	ENSMUSG00000041607	18	82475146	82585637	1	0	10	0	0	0	0	0	0	7	0	0	F7A0B0	
ENSMUST00000153480	ENSMUSG00000014767	17	15499888	15528379	1	2	0	18	4	0	0	21	89	35	12	9	F6XYI9	
ENSMUST00000153481	ENSMUSG00000022292	15	37923952	37961318	-1	0	0	0	0	0	0	0	0	0	0	0	D6RFN4	
ENSMUST00000153482	ENSMUSG00000020877	11	97029938	97033958	1	3	1	6	8	1	5	0	0	0	0	0	A2A709	
ENSMUST00000153484	ENSMUSG00000026791	2	32972990	32982083	-1	3	0	0	0	0	0	0	0	0	0	0	Q2TK26	
ENSMUST00000153485	ENSMUSG00000020868	11	94663851	94677515	-1	0	0	0	169	9	8	0	0	1	0	0	F2Z436	
ENSMUST00000153486						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153487						0	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000153488	ENSMUSG00000036282	14	49172226	49191031	1	3	0	6	0	5	8	111	223	80	17	67		Q8CES0
ENSMUST00000153489						2	0	0	0	0	1	3	7	7	1	14		
ENSMUST00000153491	ENSMUSG00000037902	2	129592835	129632228	1	0	0	0	0	0	0	2	0	6	5	0	A2ANC1	
ENSMUST00000153492	ENSMUSG00000000738	8	123062942	123097760	1	0	0	0	0	0	0	20	0	7	0	21	G3UX97	
ENSMUST00000153494	ENSMUSG00000014198	11	100627543	100692455	-1	0	5	4	15	3	0	0	0	0	0	1	A2A5E8	
ENSMUST00000153495						1	1	2	2	0	0	2	1	0	0	0		
ENSMUST00000153496						0	0	0	67	4	3	0	0	0	0	0		
ENSMUST00000153498						0	0	0	0	2	0	78	10	184	0	75		
ENSMUST00000153499	ENSMUSG00000068739	3	108424865	108445209	-1	2	0	1	10	2	0	51	30	80	14	33	A2AFS1	
ENSMUST00000153500	ENSMUSG00000005514	5	135670033	135735326	1	5	2	0	0	4	0	123	15	274	0	222	E9Q997	
ENSMUST00000153501						0	3	6	0	2	0	59	115	173	130	65		
ENSMUST00000153502	ENSMUSG00000061455	4	48124915	48186507	1	0	0	0	50	4	1	5	7	17	10	22	B1AVI2	
ENSMUST00000153503						4	9	18	2	9	3	4	6	2	0	5		
ENSMUST00000153504						1	2	10	4	4	0	10	16	11	0	21		
ENSMUST00000153505						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000153506	ENSMUSG00000027994	3	129914960	129970206	-1	7	0	1	0	0	0	15	73	0	79	68	D6RIL8	
ENSMUST00000153507						0	4	3	0	0	3	4	0	3	0	3		
ENSMUST00000153508						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000153509						4	0	4	83	5	5	0	0	1	0	0		
ENSMUST00000153510	ENSMUSG00000037243	11	58307069	58314627	1	0	0	6	102	30	0	0	404	118	32	117		Q3U381
ENSMUST00000153511	ENSMUSG00000053291	7	27168424	27178896	-1	0	0	0	0	0	2	0	0	0	0	0	S4R232	
ENSMUST00000153512	ENSMUSG00000014313	15	35925886	35938246	-1	0	0	11	0	0	2	2	5	5	0	9		Q9CPQ1
ENSMUST00000153513						0	0	0	0	0	0	24	0	0	5	47		
ENSMUST00000153514	ENSMUSG00000027620	2	156147239	156180238	-1	0	0	0	0	0	0	116	1441	230	270	462	E9Q999	
ENSMUST00000153515	ENSMUSG00000005514	5	135670033	135735326	1	0	0	0	0	0	0	0	0	0	0	7	E9PVT9	
ENSMUST00000153516						1	0	4	0	2	0	35	401	67	16	41		
ENSMUST00000153517						0	1	0	1	6	3	0	0	0	0	0		
ENSMUST00000153518						12	7	38	22	11	1	0	0	0	0	0		
ENSMUST00000153519	ENSMUSG00000005373	5	135089890	135138382	1	0	0	0	0	0	0	0	0	0	0	0		Q99MZ3
ENSMUST00000153520	ENSMUSG00000038366	11	97799000	97838764	1	1	4	14	5	3	2	0	0	1	0	3	A2A6G4	
ENSMUST00000153524						0	5	1	33	5	1	206	302	1799	6180	1357		
ENSMUST00000153525						8	0	0	54	13	5	0	13	27	0	5		
ENSMUST00000153526						10	0	43	0	13	14	0	32	0	2	93		
ENSMUST00000153527	ENSMUSG00000026360	1	143999338	144004161	-1	0	1	8	1	1	0	77	875	203	412	199	A0A087WRB0	
ENSMUST00000153528	ENSMUSG00000013878	8	26119368	26143871	1	0	0	0	0	0	0	0	9	17	0	5		Q8CBG9
ENSMUST00000153529	ENSMUSG00000029095	5	35757880	35884973	1	0	0	0	0	0	0	0	0	0	0	0	F6W6N3	
ENSMUST00000153530						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000153531						2	3	9	3	1	5	4	41	16	1	44		
ENSMUST00000153532						0	0	0	5	0	0	0	149	0	0	4		
ENSMUST00000153534						19	18	24	2	9	5	0	0	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153535	ENSMUSG00000026976	2	24420560	24475599	-1	4	0	7	2	3	0	0	0	0	0	0	A2AIU8	
ENSMUST00000153536	ENSMUSG00000029209	5	69573108	69592340	-1	0	1	2	52	0	0	0	0	0	0	0	D6RCJ1	
ENSMUST00000153537						0	1	0	2	0	1	52	122	48	161	46		
ENSMUST00000153538						2	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000153539	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	0	0	0	0	0	0	0	0	0	D6RHT1	
ENSMUST00000153540	ENSMUSG00000057265	12	84409071	84433780	1	0	0	0	0	0	1	0	0	0	0	0	F7A549	
ENSMUST00000153541	ENSMUSG00000000290	10	77530252	77565708	1	0	3	13	14	1	16	724	3925	800	395	1030	M0QWA7	
ENSMUST00000153542						0	0	2	1	2	0	0	2	3	0	3		
ENSMUST00000153543	ENSMUSG00000029228	5	74592447	74702912	-1	4	0	7	1	10	1	0	2	6	0	5	D3YTM4	
ENSMUST00000153545						0	1	3	5	3	3	1	2	0	1	1		
ENSMUST00000153546	ENSMUSG00000024675	19	11404770	11427246	1	0	0	0	0	2	0	10	112	14	138	66	D3YZH6	
ENSMUST00000153547						8	1	0	0	5	0	0	3	10	0	22		
ENSMUST00000153548	ENSMUSG00000031099	X	47809368	47892974	-1	0	1	0	0	0	2	0	0	1	0	0	F6Z6F4	
ENSMUST00000153549						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000153550						4	2	5	2	4	2	2	0	0	0	0		
ENSMUST00000153551						2	1	11	37	6	0	0	0	0	0	0		
ENSMUST00000153553						6	8	21	8	4	2	8	49	7	11	12		
ENSMUST00000153554	ENSMUSG00000025781	2	10056016	10080510	-1	0	0	2	0	2	0	0	0	8	0	0	A2AKV2	
ENSMUST00000153555						4	3	3	0	2	2	0	34	25	0	0		
ENSMUST00000153556						6	3	2	4	3	3	0	0	0	0	2		
ENSMUST00000153557						0	0	2	1	0	0	6	9	0	1	7		
ENSMUST00000153558	ENSMUSG00000021687	13	94201310	94285857	-1	0	0	4	1	0	0	67	0	344	194	179	Q3TSA8	
ENSMUST00000153560	ENSMUSG00000001741	7	83642848	83745726	-1	16	10	20	20	9	3	0	0	0	0	0	D6RI15	
ENSMUST00000153561	ENSMUSG00000026872	2	44983632	45117395	-1	11	7	14	9	7	5	4	14	7	4	10	H3BKR1	
ENSMUST00000153563						5	2	3	0	2	0	0	0	4	2	8		
ENSMUST00000153564						4	0	0	2	2	1	7	25	7	69	16		
ENSMUST00000153565	ENSMUSG00000044221	5	88659448	88676171	-1	1	0	1	5	0	0	0	0	0	5	50	D3YUN1	
ENSMUST00000153566	ENSMUSG00000030753	7	98703103	98718062	1	1	2	0	19	1	0	1	0	0	0	0	D6RH75	
ENSMUST00000153568						10	7	10	20	6	0	0	0	0	0	0		
ENSMUST00000153569						18	13	24	20	21	4	1	9	12	4	26		
ENSMUST00000153570	ENSMUSG00000012609	12	85824659	86061893	1	0	0	0	0	0	0	0	4	0	0	0	H3BJV4	
ENSMUST00000153571						0	4	0	4	13	0	1	2	0	0	1		
ENSMUST00000153573	ENSMUSG00000054708	10	81628540	81647610	1	0	1	9	3	6	0	0	0	0	0	0	D3YYK5	
ENSMUST00000153574	ENSMUSG00000026222	1	85649988	85709998	1	0	0	0	0	0	0	134	201	166	38	139	E9QA05	
ENSMUST00000153576						0	0	2	0	0	0	0	6	0	0	0		
ENSMUST00000153578						14	4	10	101	15	22	7	39	23	0	26		
ENSMUST00000153579						0	0	0	0	2	0	5	6	5	0	0		
ENSMUST00000153580	ENSMUSG00000027287	2	120567671	120601255	1	1	0	2	4	0	2	7	41	16	14	11	B0R029	
ENSMUST00000153582						25	16	83	19	19	4	7	10	5	0	11		
ENSMUST00000153583						1	1	0	2	0	2	0	0	0	0	0		
ENSMUST00000153584						4	6	0	1	2	0	4	18	3	0	5		
ENSMUST00000153585						0	0	0	0	2	0	0	0	0	0	12		
ENSMUST00000153586						2	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000153587	ENSMUSG00000031099	X	47809368	47892974	-1	0	0	3	19	1	3	0	0	0	0	0	F6QS43	
ENSMUST00000153588	ENSMUSG00000028766	4	137741733	137796384	-1	0	3	2	0	0	1	0	1	0	0	3	B1AXF5	
ENSMUST00000153590	ENSMUSG00000058558	5	107900502	107909005	1	5	0	7	73	11	3	0	11	3	0	3	D3YYV8	
ENSMUST00000153591						0	0	0	0	2	0	0	0	0	1	0		
ENSMUST00000153592						0	0	0	0	0	0	376	703	362	95	257		
ENSMUST00000153593						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153594	ENSMUSG00000036864	7	30539134	30552296	-1	0	0	0	0	0	0	2	2	0	0	3	D3YUL1	
ENSMUST00000153596						2	2	3	1	2	2	102	189	157	21	105		
ENSMUST00000153597	ENSMUSG00000054823	8	25601601	25719667	1	0	0	0	0	0	0	0	0	0	0	11	D3YUP2	
ENSMUST00000153598						2	3	0	2	2	0	0	0	0	0	0		
ENSMUST00000153601	ENSMUSG00000026976	2	24420560	24475599	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ49	
ENSMUST00000153602						0	1	0	24	2	0	0	0	2	0	0		
ENSMUST00000153603						2	4	4	5	3	3	3	2	4	0	2		
ENSMUST00000153604						9	1	7	5	12	0	18	61	12	47	29		
ENSMUST00000153606						0	4	0	0	0	0	0	3	1	4	0		
ENSMUST00000153607						4	2	1	0	5	1	0	0	0	2	0		
ENSMUST00000153608						1	2	1	2	0	0	7	14	19	0	11		
ENSMUST00000153609	ENSMUSG00000030512	7	66059003	66074587	1	8	0	3	74	4	0	37	132	39	118	75		P57784
ENSMUST00000153611						0	0	5	2	0	0	6	0	468	327	344		
ENSMUST00000153612	ENSMUSG00000024483	18	36559987	36665917	1	0	0	0	0	0	0	0	0	0	0	0	F7DD37	
ENSMUST00000153613						1	0	0	5	6	1	0	0	1	0	0		
ENSMUST00000153614						0	2	3	0	0	0	3	0	4	0	0		
ENSMUST00000153615						6	1	3	2	7	2	0	0	0	0	0		
ENSMUST00000153617	ENSMUSG00000010311	1	133897199	133907999	-1	0	3	33	17	3	0	0	0	0	0	0	E9PUR1	
ENSMUST00000153618	ENSMUSG00000036833	2	24976033	25054057	1	1	0	0	2	5	0	2	6	3	0	10	B0R009	
ENSMUST00000153619						10	1	18	1	8	4	0	4	1	0	2		
ENSMUST00000153620	ENSMUSG00000031156	X	7884041	7894492	1	0	0	0	0	2	0	0	0	0	0	0	F6WZ30	
ENSMUST00000153621						3	10	36	14	12	11	4	9	4	3	5		
ENSMUST00000153622						5	0	33	0	6	0	0	0	0	24	0		
ENSMUST00000153623	ENSMUSG00000027893	3	107663118	107696560	-1	5	3	10	22	4	2	4	4	85	3	82	D3Z2Q0	
ENSMUST00000153624						0	3	0	0	0	2	0	0	0	0	0		
ENSMUST00000153625						5	9	14	3	9	8	7	11	12	0	16		
ENSMUST00000153626						11	12	50	21	12	3	0	4	18	0	14		
ENSMUST00000153627	ENSMUSG00000021177	12	99884517	99955219	1	0	0	10	0	0	0	55	56	0	13	71	B8JJC1	
ENSMUST00000153628						0	5	13	2	3	2	0	0	0	21	0		
ENSMUST00000153629						0	0	0	0	0	0	0	3	0	1	1		
ENSMUST00000153630	ENSMUSG00000038775	9	119052778	119071525	1	0	5	0	0	1	1	3	0	0	0	0	D6RJK4	
ENSMUST00000153631						2	0	7	0	0	0	0	4	4	0	3		
ENSMUST00000153632						2	0	3	3	3	0	0	0	0	1	0		
ENSMUST00000153633						0	0	0	0	0	1	80	223	175	66	66		
ENSMUST00000153634	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	0	2	81	4	31	37	0	B7ZCP5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153635						16	14	21	11	16	2	1	0	0	0	0		
ENSMUST00000153636						3	2	0	4	5	2	0	0	0	0	0		
ENSMUST00000153638						25	24	30	29	26	16	25	116	48	8	91		
ENSMUST00000153639						1	1	4	30	5	2	0	0	0	0	0		
ENSMUST00000153640	ENSMUSG00000030870	7	122067175	122082194	1	0	8	1	1	5	2	1	0	8	1	11		
ENSMUST00000153641	ENSMUSG00000014867	2	26920040	26933928	-1	2	6	1	0	0	0	144	20	165	0	127	E0CXD9	
ENSMUST00000153643						0	0	0	0	0	0	17	71	8	0	12		
ENSMUST00000153644						0	0	6	0	2	0	0	0	0	0	0		
ENSMUST00000153645						3	5	11	4	6	1	2	2	2	0	5		
ENSMUST00000153648	ENSMUSG00000029247	5	76951307	76967509	1	3	11	10	0	15	9	0	0	4	0	12	D6RCU8	
ENSMUST00000153649						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153650	ENSMUSG00000002578	10	128630843	128645991	-1	1	0	1	4	0	1	0	0	0	0	0	D6RG62	
ENSMUST00000153651						0	2	1	0	1	0	7	36	7	3	15		
ENSMUST00000153652	ENSMUSG00000078812	11	69916714	69921958	-1	0	1	0	7	3	0	2	38	6	2	12	J3QPS8	
ENSMUST00000153653						5	3	5	15	5	1	0	7	5	0	4		
ENSMUST00000153655	ENSMUSG00000039671	2	165784152	165899016	-1	46	0	54	38	67	56	165	573	159	0	155	A2A480	
ENSMUST00000153656						0	0	5	20	0	0	0	0	0	1	5		
ENSMUST00000153657						0	1	5	2	2	0	0	0	0	0	0		
ENSMUST00000153658	ENSMUSG00000024012	17	29332072	29347904	-1	1	0	0	1	1	3	75	26	33	0	29	D3YXC2	
ENSMUST00000153660						79	99	301	107	75	22	0	26	8	0	16		
ENSMUST00000153661	ENSMUSG00000056952	6	113697050	113711069	1	1	3	3	0	0	0	97	211	84	42	54	F6W3K2	
ENSMUST00000153662	ENSMUSG00000026556	1	172000960	172028444	-1	2	1	13	37	4	4	0	0	0	0	0	D3Z4X2	
ENSMUST00000153663						0	1	8	0	22	27	35	149	68	10	28		
ENSMUST00000153664	ENSMUSG00000029103	5	35091501	35105766	-1	6	0	8	0	0	0	53	92	38	144	38	F6WMD1	
ENSMUST00000153665	ENSMUSG00000025877	13	55005985	55021385	-1	0	9	0	7	45	5	1580	5539	1507	66	1569	E9Q3Z4	
ENSMUST00000153666						6	1	7	7	4	1	6	19	3	8	11		
ENSMUST00000153668	ENSMUSG00000059248	11	117199661	117362325	1	2	0	0	0	2	2	8	6	10	2	12	A8Y5D3	
ENSMUST00000153670						2	0	6	5	4	2	19	172	0	0	42		
ENSMUST00000153671						0	12	0	66	22	0	170	716	483	91	593		
ENSMUST00000153673	ENSMUSG00000030428	7	4119408	4136708	1	0	0	0	0	0	0	0	0	0	0	0	D6RG66	
ENSMUST00000153674						0	2	0	29	0	4	0	43	10	20	9		
ENSMUST00000153676						0	1	7	0	5	0	0	0	0	0	0		
ENSMUST00000153677						27	24	46	26	36	15	0	0	0	4	1		
ENSMUST00000153678	ENSMUSG00000025156	11	120784272	120789102	1	0	0	0	0	0	0	27	0	8	0	18	D6RCV3	
ENSMUST00000153679						3	0	10	6	2	5	12	78	75	2	47		
ENSMUST00000153680						0	0	2	0	1	0	4	11	7	0	30		
ENSMUST00000153681						4	4	14	5	3	4	7	89	11	16	27		
ENSMUST00000153682						3	0	0	6	4	0	0	0	3	0	0		
ENSMUST00000153683						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000153684	ENSMUSG00000018572	11	69995777	70000009	1	0	0	0	22	0	0	152	1561	0	66	98		Q8BSN5
ENSMUST00000153687	ENSMUSG00000025261	X	151800807	151935417	1	118	92	213	941	103	44	13	0	0	0	0	D6RDF2	
ENSMUST00000153688						0	0	0	0	22	0	0	118	0	0	5		
ENSMUST00000153689						1	0	4	0	5	5	29	29	15	0	34		
ENSMUST00000153690						4	1	0	0	0	1	14	20	10	0	17		
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ENSMUST00000153692						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153693	ENSMUSG00000042104	14	118985039	119099430	-1	0	1	4	0	1	0	0	0	0	0	0	F6X3X7	
ENSMUST00000153694						5	8	8	9	2	4	0	0	0	0	0		
ENSMUST00000153695	ENSMUSG00000042501	1	10324720	10719945	-1	8	6	7	1	6	7	2	6	4	1	1	D6RI56	
ENSMUST00000153696	ENSMUSG00000037339	5	33600347	33629635	-1	1	0	1	0	0	0	0	0	0	0	0	D3YZ55	
ENSMUST00000153697	ENSMUSG00000030771	7	112368308	112413104	1	0	0	0	0	0	0	0	2	0	0	0	F6VUN6	
ENSMUST00000153698	ENSMUSG00000030979	7	133686243	133710072	-1	0	3	0	0	1	2	0	0	0	0	0	E9PYC9	
ENSMUST00000153699						1	2	4	0	10	5	0	2	3	0	2		
ENSMUST00000153700	ENSMUSG00000040652	9	65668001	65690300	1	3	0	0	13	7	3	2813	1548	1332	97	1542		O08608
ENSMUST00000153702						0	3	3	1	2	0	0	6	2	0	7		
ENSMUST00000153703	ENSMUSG00000029001	4	148152800	148160482	-1	0	0	3	0	3	0	0	0	0	1	0	F6UI76	
ENSMUST00000153704						0	0	3	0	2	0	0	0	0	0	0		
ENSMUST00000153706						0	0	30	0	0	0	0	0	0	0	0		
ENSMUST00000153707	ENSMUSG00000026447	1	133045667	133108687	1	1	1	0	11	0	0	0	0	0	0	0	D3Z091	
ENSMUST00000153708						3	7	24	2	13	2	46	7	48	14	87		
ENSMUST00000153709						16	22	19	18	24	6	4	14	4	1	9		
ENSMUST00000153710	ENSMUSG00000087153	8	19682268	19698275	1	0	0	0	0	0	0	0	0	35	81	14	D3Z1Y8	
ENSMUST00000153711						11	4	5	1	10	7	0	1	4	1	2		
ENSMUST00000153712						0	0	0	3	1	0	55	29	0	4	0		
ENSMUST00000153713	ENSMUSG00000032680	2	152415587	152444330	1	1	3	13	6	5	4	0	0	0	0	0	D6RI41	
ENSMUST00000153714						1	0	2	0	0	0	0	0	6	0	0		
ENSMUST00000153716						0	0	0	0	0	0	151	62	139	30	109		
ENSMUST00000153717						45	25	109	43	30	25	0	3	2	2	6		
ENSMUST00000153720						0	0	10	11	0	0	0	0	0	0	0		
ENSMUST00000153721	ENSMUSG00000028923	4	141066512	141078357	-1	0	0	0	0	0	0	0	0	1	5	0	F6RCM5	
ENSMUST00000153723	ENSMUSG00000029998	6	86386006	86397154	-1	1	2	11	64	0	0	14	2	28	0	36	D3Z275	
ENSMUST00000153725	ENSMUSG00000031824	8	120114152	120165306	1	0	3	3	0	5	2	160	0	0	0	0	D3YUS2	
ENSMUST00000153727						1	4	12	2	3	1	13	32	15	3	30		
ENSMUST00000153729						7	10	13	4	10	0	0	3	3	0	4		
ENSMUST00000153730						9	5	14	26	12	0	0	2	7	0	9		
ENSMUST00000153731	ENSMUSG00000090247	10	128917882	128924035	-1	0	1	0	9	2	0	0	5	0	0	0	D3Z4L7	
ENSMUST00000153732	ENSMUSG00000041623	11	113684412	113694647	1	2	2	11	3	5	0	14	38	21	0	12	A2A6P5	
ENSMUST00000153733						10	11	29	184	19	11	29	13	43	6	51		
ENSMUST00000153734						6	3	1	0	7	5	0	0	0	0	0		
ENSMUST00000153735	ENSMUSG00000022090	14	70164218	70177681	-1	3	0	0	14	5	0	1132	1657	804	205	834		Q8R1G6
ENSMUST00000153736	ENSMUSG00000035298	7	99466004	99474022	1	2	0	0	8	1	0	1	0	0	0	0	F6Z4V4	
ENSMUST00000153737						2	0	0	3	2	0	0	0	0	1	0		
ENSMUST00000153738						1	1	0	30	1	0	0	0	0	0	0		
ENSMUST00000153739	ENSMUSG00000067786	2	157560078	157562522	1	0	7	7	32	0	2	20	4	15	0	8	Q548P9	Q61979

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153740						3	3	71	247	29	0	0	1	0	0	0		
ENSMUST00000153741	ENSMUSG00000022957	16	91729281	91920597	1	0	0	0	0	0	0	0	0	0	0	0	Q6J1S9	
ENSMUST00000153742						0	0	0	0	0	0	1	3	2	0	0		
ENSMUST00000153744	ENSMUSG00000024222	17	28399095	28517524	-1	0	0	5	0	2	3	0	0	0	0	3	B8JJC2	
ENSMUST00000153745	ENSMUSG00000024168	17	25057702	25081181	-1	3	3	0	3	12	0	0	0	0	0	2	D3Z204	
ENSMUST00000153746	ENSMUSG00000034401	4	111719984	111829184	1	3	3	5	0	4	1	0	7	2	0	2		Q3U6K5
ENSMUST00000153747	ENSMUSG00000037791	11	77982754	78030539	1	0	3	0	0	0	0	0	0	0	2	0	F7AXU7	
ENSMUST00000153748						290	303	810	239	329	149	248	1365	588	584	632		
ENSMUST00000153749						1	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000153750						6	3	27	25	12	3	6	26	24	0	15		
ENSMUST00000153751						9	19	61	16	14	14	0	0	0	0	3		
ENSMUST00000153752						0	5	2	64	1	4	0	0	0	0	0		
ENSMUST00000153754	ENSMUSG00000054720	5	105519388	105613018	1	2	0	7	0	7	1	8	0	7	0	10	D3YUV5	
ENSMUST00000153755						3	1	2	14	0	2	0	4	0	0	0		
ENSMUST00000153756						2	5	2	7	9	2	2	4	3	2	11		
ENSMUST00000153757						1	4	14	3	5	2	0	6	1	0	2		
ENSMUST00000153758	ENSMUSG00000029616	5	121428590	121452506	-1	47	53	173	66	56	24	10	71	25	4	51	D6RG87	
ENSMUST00000153759						14	9	40	15	9	2	0	0	0	0	0		
ENSMUST00000153760						4	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000153761	ENSMUSG00000061086	11	104550663	104595753	1	0	0	0	0	0	2	0	0	0	3	0	A2A6Q8	
ENSMUST00000153762						6	6	7	6	12	11	2	3	1	0	4		
ENSMUST00000153763						0	0	0	0	0	1	50	291	79	0	60		
ENSMUST00000153764						0	0	0	0	0	0	93	99	48	15	51		
ENSMUST00000153765	ENSMUSG00000036339	14	48446128	48515135	1	0	0	0	0	0	0	21	0	37	2	46	D6RHS9	
ENSMUST00000153766						1	6	1	12	7	2	116	362	302	30	382		
ENSMUST00000153768						2	2	1	1	5	1	0	2	0	0	0		
ENSMUST00000153769						4	2	87	4	3	3	0	0	0	0	1		
ENSMUST00000153770						0	0	3	5	0	0	0	0	0	0	0		
ENSMUST00000153771	ENSMUSG00000049897	2	26934047	26953496	1	0	0	0	4	3	3	0	0	0	0	1	B0R044	
ENSMUST00000153772						6	0	8	56	6	1	0	0	1	0	1		
ENSMUST00000153773	ENSMUSG00000053091	7	66689889	66717256	1	0	0	0	0	0	0	0	8	6	0	0	F6QWY7	
ENSMUST00000153775	ENSMUSG00000051359	15	37366175	37792570	-1	0	0	31	3	0	0	0	0	0	0	0	D3YVA2	
ENSMUST00000153776						4	1	4	35	8	6	0	0	0	0	0		
ENSMUST00000153777	ENSMUSG00000062190	6	57702540	57739439	1	0	0	3	0	0	0	16	89	38	26	22	F6RJV6	
ENSMUST00000153778						0	2	17	23	3	2	0	0	2	0	0		
ENSMUST00000153779						2	0	0	1	6	4	0	45	21	0	9		
ENSMUST00000153780						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000153781						23	7	83	17	27	11	0	18	0	0	0		
ENSMUST00000153782						0	0	0	0	0	0	3	0	0	0	2		
ENSMUST00000153783	ENSMUSG00000053093	14	54970688	54994634	-1	0	0	0	2	1	0	0	0	0	0	0	B8JJH1	
ENSMUST00000153784	ENSMUSG00000053852	X	56870163	57001558	1	4	14	0	0	0	0	0	0	0	0	0		B7ZCC9
ENSMUST00000153787	ENSMUSG00000018428	11	88830792	88864586	-1	4	0	4	3	1	0	0	0	0	0	0	F6V317	
ENSMUST00000153788						3	0	9	3	0	4	0	53	0	0	15		
ENSMUST00000153789	ENSMUSG00000014418	7	46760466	46796064	-1	0	0	2	0	0	0	10	60	50	0	50	F6Q7C7	
ENSMUST00000153790						5	8	10	9	14	5	67	265	142	7	274		
ENSMUST00000153792	ENSMUSG00000074220	7	30121942	30134665	1	3	1	0	26	3	1	0	1	0	0	1	D3YYS3	
ENSMUST00000153793						3	3	16	4	9	3	3	49	11	3	26		
ENSMUST00000153796						5	3	0	10	0	0	5	38	14	4	14		
ENSMUST00000153798	ENSMUSG00000031626	8	45507788	45827906	1	7	11	12	3	5	7	0	1	0	0	0		Q3UTJ2
ENSMUST00000153799	ENSMUSG00000070643	1	133382303	133424377	-1	11	6	0	81	27	7	0	7	0	0	0		Q04891
ENSMUST00000153800	ENSMUSG00000070000	8	71708387	71725716	-1	0	0	0	0	0	0	9	0	10	0	0	D3Z6N2	
ENSMUST00000153801						98	106	216	137	98	53	0	0	0	0	0		
ENSMUST00000153802						107	60	286	357	108	103	0	0	3	0	0		
ENSMUST00000153803	ENSMUSG00000035572	4	45342101	45379759	1	0	0	0	0	0	1	8	24	10	0	28	Z4YN28	
ENSMUST00000153804						1	1	0	0	1	1	3	5	3	0	1		
ENSMUST00000153806						1	0	2	0	0	2	1	0	2	5	0		
ENSMUST00000153807						0	0	6	0	0	0	3	0	0	0	0		
ENSMUST00000153808						0	0	1	1	0	0	0	0	0	2	0		
ENSMUST00000153809						1	0	1	3	0	0	4	13	11	0	24		
ENSMUST00000153811	ENSMUSG00000037600	4	133518963	133530790	1	0	0	0	96	0	4	0	0	0	0	0	A2A9F2	
ENSMUST00000153812						12	4	19	4	13	1	0	0	2	1	1		
ENSMUST00000153813	ENSMUSG00000040520	4	26324506	26346891	-1	0	0	0	27	0	0	0	0	1	0	0	A8Y5Q7	
ENSMUST00000153815						15	19	33	38	26	16	32	114	134	15	154		
ENSMUST00000153816	ENSMUSG00000013936	5	122100951	122113472	1	1	0	2	2	0	0	0	0	0	0	0	F6RBQ5	
ENSMUST00000153819						1	5	19	0	4	6	790	270	58	109	130		
ENSMUST00000153820	ENSMUSG00000036986	9	58218076	58249786	-1	38	24	78	30	56	15	40	12	30	4	56	D3YXR5	
ENSMUST00000153821	ENSMUSG00000049470	11	53350833	53421830	1	0	0	0	0	0	0	4	3	14	0	0	B7ZC42	
ENSMUST00000153822						1	1	2	1	1	1	0	3	1	0	1		
ENSMUST00000153823	ENSMUSG00000029699	5	135960211	135974531	-1	0	0	5	78	3	0	0	0	0	0	0	F7AS28	
ENSMUST00000153824	ENSMUSG00000017421	11	80383279	80405733	1	0	0	0	0	0	0	0	0	0	0	3	B1AQG7	
ENSMUST00000153826	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	7	7	4	1	5	D3YV76	
ENSMUST00000153828						1	3	4	0	5	2	0	0	0	0	6		
ENSMUST00000153829						1	0	5	1	0	1	0	0	0	0	0		
ENSMUST00000153830	ENSMUSG00000021792	14	40993740	41013788	-1	3	0	4	1	6	3	0	0	0	0	0	Q3U125	
ENSMUST00000153831	ENSMUSG00000005936	17	28951950	28969549	1	0	0	0	0	0	0	12	7	85	0	14	B2KF11	
ENSMUST00000153832	ENSMUSG00000029416	5	127595664	127632897	-1	0	0	0	48	0	0	0	147	0	0	0	D6RDC2	
ENSMUST00000153833	ENSMUSG00000004328	7	17031507	17062427	-1	2	1	2	38	2	0	0	0	0	0	0	D3Z377	
ENSMUST00000153834						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000153835						5	1	2	6	6	3	8	15	3	0	2		
ENSMUST00000153836						90	50	117	253	110	48	2	0	6	0	0		
ENSMUST00000153837	ENSMUSG00000028894	4	124741850	124801511	1	0	1	6	6	3	6	0	0	0	0	0	F2Z437	
ENSMUST00000153838	ENSMUSG00000044791	9	110532597	110618633	1	29	28	54	70	43	18	971	2751	2448	342	1702		E9Q5F9
ENSMUST00000153839	ENSMUSG00000031166	X	8123301	8132892	-1	0	0	0	0	0	0	0	0	0	0	0	A2AC24	
ENSMUST00000153840						2	1	2	3	2	1	2	0	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153841						197	160	669	207	177	95	6	33	17	9	37		
ENSMUST00000153842						42	57	59	50	50	35	25	668	21	27	193		
ENSMUST00000153843	ENSMUSG00000048794	6	90403479	90428797	-1	17	11	32	31	18	13	2	8	1	1	3		
ENSMUST00000153844	ENSMUSG00000031403	X	75095854	75109777	1	0	1	1	0	0	0	1	40	11	33	0	F6S1S5	
ENSMUST00000153845						2	8	0	0	1	6	0	0	0	0	0		
ENSMUST00000153846	ENSMUSG00000074419	7	3816781	3825687	-1	0	0	0	0	0	0	0	0	0	0	0	F6PZL4	
ENSMUST00000153847						0	0	0	0	5	1	492	1620	898	1431	910		
ENSMUST00000153848						0	1	5	1	3	0	30	467	123	7	127		
ENSMUST00000153849						2	0	10	27	4	8	0	0	1	0	0		
ENSMUST00000153850						0	1	3	1	0	1	0	1	0	0	0		
ENSMUST00000153851						1	3	0	2	2	2	0	0	0	0	0		
ENSMUST00000153852						2	6	6	5	3	0	0	0	0	0	0		
ENSMUST00000153853	ENSMUSG00000027981	3	113605067	113630149	-1	3	0	9	4	0	0	6	0	2	0	4	F6TN13	
ENSMUST00000153854						9	3	33	6	5	6	2	23	14	16	16		
ENSMUST00000153855						3	3	14	81	10	1	8	6	14	0	21		
ENSMUST00000153856	ENSMUSG00000064246	1	134182176	134190181	1	0	0	0	0	0	0	0	63	15	0	12		Q61362
ENSMUST00000153857						3	0	2	0	6	0	122	80	132	7	95		
ENSMUST00000153858						14	2	12	7	5	8	14	97	20	12	33		
ENSMUST00000153859						7	1	15	5	11	3	21	13	21	4	12		
ENSMUST00000153860	ENSMUSG00000033788	6	84008590	84211060	1	0	0	0	6	13	7	0	0	0	0	0		
ENSMUST00000153861	ENSMUSG00000028249	4	6365650	6408423	1	0	0	0	1	2	0	0	0	104	1897	238	A2AKJ6	
ENSMUST00000153862						21	8	23	22	15	10	0	0	0	0	0		
ENSMUST00000153863						1	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000153864						47	22	31	445	105	52	0	1	0	0	1		
ENSMUST00000153866						0	0	0	0	3	1	0	0	1	1	0		
ENSMUST00000153867	ENSMUSG00000029730	5	138164583	138172422	-1	0	0	0	16	0	2	41	9	36	6	37	D3Z2K9	
ENSMUST00000153868						1	4	12	0	1	1	0	60	27	11	74		
ENSMUST00000153869	ENSMUSG00000043411	4	137593755	137658537	1	3	3	0	1	6	1	0	4	4	2	10	F7ALR2	
ENSMUST00000153870	ENSMUSG00000040548	11	106502147	106613423	-1	1	1	6	2	3	1	0	0	0	0	2	B1ATR4	
ENSMUST00000153871	ENSMUSG00000044551	14	70154405	70159502	-1	6	4	5	61	12	6	75	83	39	0	66		Q66JV7
ENSMUST00000153872						2	1	16	2	3	5	18	3	12	0	19		
ENSMUST00000153873	ENSMUSG00000062210	18	49979427	50107173	1	0	0	0	0	0	0	0	0	10	24	22	D3Z0Q1	
ENSMUST00000153874	ENSMUSG00000002871	6	88902251	88912238	1	0	3	2	4	7	2	7	16	19	0	8	D3Z018	
ENSMUST00000153875	ENSMUSG00000059810	4	62559847	62704001	1	16	6	36	16	13	11	5	9	17	8	7	F6X4A2	
ENSMUST00000153877						2	4	28	2	2	0	0	31	8	2	11		
ENSMUST00000153880	ENSMUSG00000040697	4	141760189	141790931	-1	0	0	2	2	0	3	0	0	0	1	0	A2AS91	
ENSMUST00000153881						47	28	167	68	59	26	47	69	78	6	105		
ENSMUST00000153882						5	2	16	2	6	2	1	0	0	0	0		
ENSMUST00000153885						4	0	3	0	5	0	4	4	0	0	0		
ENSMUST00000153886	ENSMUSG00000026819	2	32414487	32451445	-1	2	0	0	2	3	0	0	0	0	0	0	A0A0A6YWC1	
ENSMUST00000153887						0	3	6	4	0	0	0	0	1	6	13		
ENSMUST00000153888	ENSMUSG00000024985	19	55741810	55933654	1	0	3	0	0	0	0	0	0	20	0	19	F6XQR1	
ENSMUST00000153889	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	0	0	0	0	0	0	F6XRZ6	
ENSMUST00000153890						4	1	4	10	9	2	21	22	17	2	23		
ENSMUST00000153891						2	1	6	39	2	2	0	0	0	0	2		
ENSMUST00000153892	ENSMUSG00000020738	11	115523102	115536276	-1	20	12	10	53	33	11	766	1378	458	1346	368		P61957
ENSMUST00000153894	ENSMUSG00000025873	13	54621784	54664068	1	0	0	0	0	1	0	0	0	37	13	0	F6XLD9	
ENSMUST00000153895						0	0	0	0	0	6	0	146	0	18	2		
ENSMUST00000153896						16	17	13	12	33	10	7	44	12	0	13		
ENSMUST00000153897						2	3	4	1	3	2	3	19	5	0	7		
ENSMUST00000153900	ENSMUSG00000043929	X	94234599	94277724	1	0	0	0	0	0	0	0	0	0	0	0	A2AAX0	
ENSMUST00000153901						0	0	4	0	0	4	0	0	0	0	0		
ENSMUST00000153902						3	4	11	6	2	3	9	0	4	1	12		
ENSMUST00000153903	ENSMUSG00000070733	5	73019987	73256619	-1	0	0	0	0	0	0	2	1	0	0	0	F6Q1V8	
ENSMUST00000153904	ENSMUSG00000045973	4	45395923	45408766	-1	3	0	0	41	5	2	8	0	0	0	0	A2AKV9	
ENSMUST00000153905	ENSMUSG00000039804	2	165000357	165034867	-1	0	0	0	10	0	0	0	0	0	0	0	A2A5L3	
ENSMUST00000153906	ENSMUSG00000028546	4	110203722	110351909	-1	2	0	3	0	0	0	0	0	0	0	0	A2A9R5	
ENSMUST00000153907						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000153908						3	1	2	8	4	2	0	1	0	2	0		
ENSMUST00000153910	ENSMUSG00000041605	1	136213531	136234264	-1	0	0	0	0	0	0	0	0	0	0	0	D6RJ44	
ENSMUST00000153911	ENSMUSG00000032531	9	102716672	102733418	1	3	0	7	58	6	0	15	0	0	0	0	B8JK86	
ENSMUST00000153912						9	0	2	4	3	4	0	4	1	0	6		
ENSMUST00000153914	ENSMUSG00000026754	2	39016155	39065541	-1	0	0	0	0	0	0	43	99	80	75	52		
ENSMUST00000153915						64	0	95	29	94	35	15	94	38	10	60		
ENSMUST00000153916						1	0	0	0	0	0	0	1	2	0	0		
ENSMUST00000153917						1	0	0	0	1	1	0	1	0	0	0		
ENSMUST00000153918						0	0	0	1	0	0	0	7	0	0	5		
ENSMUST00000153920						31	25	86	9	26	2	58	201	57	36	145		
ENSMUST00000153922	ENSMUSG00000062980	6	21985916	22256404	1	3	0	4	16	7	3	0	0	0	1	0	S4R2A1	
ENSMUST00000153923						10	4	18	20	22	3	0	0	3	0	0		
ENSMUST00000153924						123	155	243	86	128	59	58	132	58	6	45		
ENSMUST00000153925						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000153926	ENSMUSG00000038764	4	57190841	57301837	-1	2	0	0	41	4	0	0	0	15	0	2	A2ALK9	
ENSMUST00000153927						0	0	0	0	2	0	2	6	8	2	12		
ENSMUST00000153928						3	0	13	2	1	1	52	123	15	0	24		
ENSMUST00000153929						1	1	1	0	0	0	0	0	2	0	3		
ENSMUST00000153930	ENSMUSG00000022487	15	103402405	103430470	-1	0	0	0	10	2	2	0	0	0	0	0		Q9DAN6
ENSMUST00000153931	ENSMUSG00000058835	2	22940073	23040241	-1	0	0	0	0	12	0	0	0	0	0	0	B7ZCU2	
ENSMUST00000153932						3	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000153933						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000153934						1	0	7	0	3	2	0	1	0	0	4		
ENSMUST00000153935						8	3	10	10	4	0	5	5	9	0	12		
ENSMUST00000153936						26	31	48	103	24	20	50	143	64	5	138		
ENSMUST00000153938	ENSMUSG00000014592	4	150917322	151861876	-1	12	9	1	9	14	3	13	81	21	11	43	Q3TYE0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000153939						14	7	5	5	11	11	17	27	22	14	21		
ENSMUST00000153940						0	0	0	176	0	0	0	0	7	0	17		
ENSMUST00000153941	ENSMUSG00000044712	12	73286779	73354049	1	16330	20130	6246	8903	12714	5527	4523	17371	7512	2335	5251	D3YUW5	
ENSMUST00000153942	ENSMUSG00000029757	6	5725639	6028039	1	1	1	1	7	3	1	0	0	0	0	0	D3Z258	
ENSMUST00000153943	ENSMUSG00000018750	11	69765912	69784023	1	7	4	2	21	0	3	0	0	0	0	0	Q5F296	
ENSMUST00000153944						11	13	71	29	20	17	0	8	1	1	5		
ENSMUST00000153945						0	0	0	0	0	0	0	206	0	2	0		
ENSMUST00000153946						39	36	16	21	38	18	0	0	0	1	1		
ENSMUST00000153947						2	0	1	5	0	0	3	54	8	0	11		
ENSMUST00000153948	ENSMUSG00000005696	X	42502453	42529330	1	0	0	0	0	0	0	0	0	0	5	1	S4R2F6	
ENSMUST00000153949						0	1	0	3	6	1	0	0	0	23	0		
ENSMUST00000153952						1	3	7	12	2	1	0	0	0	0	0		
ENSMUST00000153953	ENSMUSG00000028678	4	117159639	117182639	-1	1	0	0	1	0	0	0	0	0	0	0	A2AE72	
ENSMUST00000153954	ENSMUSG00000056296	14	13284780	13615459	1	0	0	3	0	1	0	0	0	0	0	0	D3Z5Q8	
ENSMUST00000153955						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000153956						7	1	7	7	9	3	0	3	2	0	9		
ENSMUST00000153957						12	12	20	3	9	0	58	175	37	28	150		
ENSMUST00000153959	ENSMUSG00000000318	11	70156197	70170834	1	2	4	9	6	7	2	5	0	4	0	0	B1AU03	
ENSMUST00000153960						1	0	2	1	0	0	12	22	8	0	26		
ENSMUST00000153961						6	5	22	7	4	11	0	0	0	0	0		
ENSMUST00000153962						6	0	0	8	3	3	2	13	12	1	35		
ENSMUST00000153963	ENSMUSG00000015189	6	4600839	4643355	1	0	0	1	31	6	0	0	0	0	0	0		
ENSMUST00000153964	ENSMUSG00000020061	10	88518279	88605152	-1	8	2	9	3	0	0	0	0	0	0	0	F7D574	
ENSMUST00000153965	ENSMUSG00000032531	9	102716672	102733418	1	0	0	3	4	0	2	351	0	0	34	0	B8JK87	
ENSMUST00000153966	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	0	10	0	1	0	4	1	5	0	D3Z461	
ENSMUST00000153967						2	2	15	39	5	0	0	0	3	0	15		
ENSMUST00000153968						2	1	0	4	3	0	2747	1943	2620	171	3632		
ENSMUST00000153970	ENSMUSG00000032309	9	55208925	55224433	1	0	0	12	0	0	0	108	362	65	4	0	D6RFT2	
ENSMUST00000153971						0	0	0	0	0	0	4	8	0	25	11		
ENSMUST00000153972						3	0	0	0	4	0	2	0	0	0	0		
ENSMUST00000153973						0	0	15	2	3	3	17	56	60	17	48		
ENSMUST00000153974						34	32	60	85	40	26	0	1	2	0	0		
ENSMUST00000153975						1	0	0	0	1	3	1	2	0	1	1		
ENSMUST00000153976	ENSMUSG00000023118	7	19024377	19054618	1	3	0	1	7	6	1	0	0	0	0	0	D3Z2M2	
ENSMUST00000153977						4	0	2	8	5	2	0	1	2	0	0		
ENSMUST00000153978						0	0	8	1	8	6	0	2	3	0	2		
ENSMUST00000153979						0	0	0	0	0	0	0	0	15	8	38		
ENSMUST00000153980						20	10	17	220	32	11	15	8	58	0	57		
ENSMUST00000153981						1	0	6	2	0	0	0	0	0	0	0		
ENSMUST00000153982						41	28	111	35	19	33	3	67	5	0	10		
ENSMUST00000153983	ENSMUSG00000018858	11	115403752	115412674	1	0	0	0	22	0	0	2	2	2	0	0		Q8R035
ENSMUST00000153984	ENSMUSG00000001036	11	61517249	61579687	-1	0	0	0	27	0	0	0	0	0	0	0	F7CD65	
ENSMUST00000153985	ENSMUSG00000053347	17	21962552	22071168	1	27	21	101	51	38	23	13	20	27	29	32	D3YYH7	
ENSMUST00000153986						1	2	0	2	0	0	0	16	0	0	5		
ENSMUST00000153987						1	1	3	129	4	0	5	18	15	0	16		
ENSMUST00000153988	ENSMUSG00000040785	16	94370618	94469222	1	3	0	0	0	0	0	2	0	0	0	0	D3YZ03	
ENSMUST00000153989						23	21	44	38	40	16	10	40	21	7	35		
ENSMUST00000153990	ENSMUSG00000026027	1	58973522	58995715	1	0	0	0	0	0	3	215	320	53	0	81	M0QW98	
ENSMUST00000153991						0	0	0	21	2	1	0	0	0	0	0		
ENSMUST00000153992	ENSMUSG00000040865	1	62958418	63114667	-1	0	0	40	0	4	0	0	0	26	0	2	B1AT34	
ENSMUST00000153993	ENSMUSG00000040938	11	70212752	70216417	1	0	0	0	0	0	0	0	0	0	0	0	E0CZ25	
ENSMUST00000153994						0	0	0	0	0	1	1	22	5	0	12		
ENSMUST00000153995	ENSMUSG00000020471	11	5872180	5878292	-1	5	0	2	0	0	0	0	0	0	0	2	A8Y5G7	
ENSMUST00000153996	ENSMUSG00000026924	2	26409431	26445216	-1	0	3	4	0	0	0	44	34	43	2	45	F6T8X6	
ENSMUST00000153997	ENSMUSG00000078747	4	41941572	41943124	1	15	8	22	32	11	9	0	3	0	0	3	A2APU9	
ENSMUST00000153998	ENSMUSG00000000823	2	181582103	181592803	-1	0	0	0	32	0	0	0	0	5	0	0	B7ZCR8	
ENSMUST00000153999	ENSMUSG00000040283	11	49165585	49187159	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQJ9	
ENSMUST00000154001	ENSMUSG00000018677	11	102402985	102407946	-1	3	1	12	27	3	3	0	0	0	0	0	B0QZI7	
ENSMUST00000154002						73	75	260	108	89	47	23	48	34	2	48		
ENSMUST00000154003						11	16	22	27	25	16	2	22	2	0	12		
ENSMUST00000154004	ENSMUSG00000068457	Y	1096861	1245759	-1	0	0	0	0	0	0	18	0	62	1	19	Q3UQE8	
ENSMUST00000154005						2	0	0	2	2	0	5	6	0	0	19		
ENSMUST00000154007	ENSMUSG00000028618	4	107178399	107200996	1	0	0	7	0	3	5	390	1952	647	140	177	D6RI96	
ENSMUST00000154008						0	4	4	5	7	1	23	68	20	9	7		
ENSMUST00000154009						2	3	5	4	5	3	0	2	0	0	0		
ENSMUST00000154010	ENSMUSG00000052751	6	48593883	48599082	1	0	0	1	327	1	2	0	0	1	1	0	E9Q8A0	
ENSMUST00000154011						3	0	0	16	0	1	0	0	0	0	0		
ENSMUST00000154012						0	0	0	0	7	0	0	0	0	0	0		
ENSMUST00000154013						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000154014						0	0	0	0	0	0	64	54	63	16	39		
ENSMUST00000154017						2	0	3	2	2	4	2	1	4	0	1		
ENSMUST00000154018						36	27	100	22	28	34	5	23	22	21	15		
ENSMUST00000154019						1	2	3	35	2	2	0	4	0	0	6		
ENSMUST00000154020						1	0	1	10	1	0	0	0	0	1	0		
ENSMUST00000154021	ENSMUSG00000074825	2	127138772	127143442	-1	5	7	12	8	9	10	0	19	0	0	0		A2ASA8
ENSMUST00000154022						0	3	27	0	0	0	2	0	0	0	0		
ENSMUST00000154023						9	11	12	6	3	5	2	7	2	0	14		
ENSMUST00000154024						1	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000154025						0	2	1	0	0	1	0	0	0	0	0		
ENSMUST00000154026						1	1	0	0	2	1	1	1	0	2	2		
ENSMUST00000154028						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154029						7	0	3	2	4	8	0	84	11	4	10		
ENSMUST00000154031						3	0	6	0	0	0	28	83	134	9	70		
ENSMUST00000154032	ENSMUSG00000036966	15	102116528	102136234	-1	7	0	0	40	16	0	1855	2216	1410	239	1064	E9Q9B3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154033						0	0	0	10	0	0	2	0	0	0	0		
ENSMUST00000154034	ENSMUSG00000061878	11	116530925	116536674	1	0	0	0	0	0	0	0	0	0	4	0	B1AT89	
ENSMUST00000154035						0	1	7	0	0	3	0	0	1	1	3		
ENSMUST00000154036						37	25	199	36	23	13	1	1	0	0	5		
ENSMUST00000154039						2	2	0	0	0	2	5	15	0	0	6		
ENSMUST00000154040	ENSMUSG00000031631	8	46151771	46195590	1	0	0	0	24	0	0	0	0	0	0	0	E9PZJ3	
ENSMUST00000154041						0	0	0	42	1	0	3	4	7	0	0		
ENSMUST00000154042	ENSMUSG00000036231	12	35925620	35949736	1	1	2	2	1	0	1	0	0	0	0	0	A7NSI2	
ENSMUST00000154043	ENSMUSG00000021224	12	83794034	83921934	-1	7	0	0	6	9	0	197	0	571	0	350		Q9QZS3
ENSMUST00000154045	ENSMUSG00000026307	1	91298338	91321075	1	0	0	0	0	0	0	0	0	0	0	0	M0QWF1	
ENSMUST00000154046	ENSMUSG00000018474	11	69343273	69369406	-1	4	0	0	2	0	0	0	0	0	0	3	B0QZH7	
ENSMUST00000154047						0	0	0	6	0	0	0	4	9	0	8		
ENSMUST00000154048						77	65	441	140	81	42	14	58	43	6	75		
ENSMUST00000154049						16	14	27	52	0	0	5	0	15	0	20		
ENSMUST00000154050	ENSMUSG00000026843	2	31572651	31617526	1	0	0	0	0	0	0	0	0	0	0	5	A0A0A6YX76	
ENSMUST00000154051	ENSMUSG00000062949	X	60223290	60592698	-1	2	3	0	0	10	0	135	0	0	0	0	F6Q8D3	
ENSMUST00000154052						1	0	0	0	0	0	0	0	1	0	2		
ENSMUST00000154053						5	3	7	3	7	1	0	0	0	0	1		
ENSMUST00000154054						8	4	10	5	14	6	0	0	4	1	3		
ENSMUST00000154055						0	0	0	0	0	0	23	0	0	0	150		
ENSMUST00000154056						0	0	0	0	1	0	0	1	3	2	0		
ENSMUST00000154057						4	0	14	2	6	2	4	3	2	0	0		
ENSMUST00000154059						16	1	13	0	0	13	0	0	0	0	0		
ENSMUST00000154061						48	43	110	93	37	28	0	0	0	0	0		
ENSMUST00000154062						0	0	0	0	0	5	0	6	0	0	4		
ENSMUST00000154063	ENSMUSG00000092260	8	69741639	69749970	-1	0	0	0	61	0	1	0	0	0	0	0	D3YVX8	
ENSMUST00000154064						2	0	0	0	0	2	6	13	5	8	1		
ENSMUST00000154071						1	0	8	4	1	1	0	0	0	0	0		
ENSMUST00000154073						4	1	3	0	3	6	4	5	0	0	4		
ENSMUST00000154074	ENSMUSG00000029466	5	122421693	122444912	1	0	0	0	0	0	0	0	0	0	0	0	F6WXH0	
ENSMUST00000154075						1	1	0	1	3	2	11	15	31	0	36		
ENSMUST00000154076	ENSMUSG00000032396	9	64306756	64341288	-1	2	0	0	1	1	1	0	0	0	0	0	D3YUD6	
ENSMUST00000154077						2	5	5	1	0	4	76	7	47	3	77		
ENSMUST00000154078	ENSMUSG00000021057	12	76324891	76334153	1	48	52	263	106	63	32	7	25	18	5	13		D3YVF0
ENSMUST00000154079	ENSMUSG00000029772	6	29768011	29912310	1	0	0	0	0	0	0	0	0	0	0	0	D3YX97	
ENSMUST00000154080						0	6	0	2	0	0	28	210	18	48	22		
ENSMUST00000154081						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154083						2	1	6	6	4	2	0	0	0	0	0		
ENSMUST00000154084						1	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000154086	ENSMUSG00000072814	5	95742014	95746617	1	3	2	0	0	0	0	0	0	0	0	0	D3YXK9	
ENSMUST00000154087						53	37	137	323	64	34	34	61	44	2	75		
ENSMUST00000154088						2	3	17	0	0	2	0	4	1	0	5		
ENSMUST00000154089	ENSMUSG00000062421	11	103966739	103985337	1	4	0	14	2	3	4	1	0	3	0	1	A2A6T9	
ENSMUST00000154090						74	59	216	101	95	53	0	26	7	0	8		
ENSMUST00000154091						0	3	0	3	2	0	3	0	25	50	30		
ENSMUST00000154092						34	40	65	60	31	21	518	3558	1086	348	1385		
ENSMUST00000154093						0	2	0	0	0	4	1	0	0	0	0		
ENSMUST00000154094						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000154095						1	0	0	0	2	6	8	20	5	2	9		
ENSMUST00000154096	ENSMUSG00000029320	5	103648039	103656010	-1	0	0	0	0	0	0	0	0	0	0	0	Q810Q2	
ENSMUST00000154097						4	1	3	0	1	0	0	1	0	0	0		
ENSMUST00000154098	ENSMUSG00000055850	6	72359714	72366956	-1	2	1	2	1	2	0	0	0	0	2	0		Q9CY62
ENSMUST00000154099						16	8	32	89	4	3	0	62	5	0	30		
ENSMUST00000154100	ENSMUSG00000021196	13	6579768	6648777	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JD99	
ENSMUST00000154101	ENSMUSG00000006576	1	75546266	75562172	1	7	0	11	9	8	5	0	0	0	0	0	D3Z5A2	
ENSMUST00000154102						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154103	ENSMUSG00000058145	7	66839735	67152625	1	0	0	0	0	0	0	0	0	0	0	1	F6RTQ0	
ENSMUST00000154104						9	8	10	6	12	2	5	12	8	2	4		
ENSMUST00000154105	ENSMUSG00000053841	4	129626078	129641065	-1	0	0	0	0	0	0	0	0	29	6	60	A2ADZ4	
ENSMUST00000154106						1	2	4	11	7	2	2	4	0	0	5		
ENSMUST00000154107						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154108						0	2	0	66	5	2	0	0	0	0	0		
ENSMUST00000154111	ENSMUSG00000078919	2	168209048	168230591	-1	7	1	5	9	4	1	2	19	7	21	10		O70152
ENSMUST00000154112						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000154114	ENSMUSG00000023805	17	5941280	6044290	1	0	0	0	0	0	5	0	0	0	0	0	F7BI35	
ENSMUST00000154115	ENSMUSG00000036779	8	88199213	88259722	1	1	0	0	0	0	1	19	58	94	23	91	F6UPY1	
ENSMUST00000154117	ENSMUSG00000004070	16	4726361	4766742	1	0	0	3	51	1	2	25	8	15	25	8	D3Z4A2	
ENSMUST00000154118						1	0	10	4	8	1	12	0	2	0	0		
ENSMUST00000154119						4	6	1	6	3	0	0	0	0	0	0		
ENSMUST00000154120	ENSMUSG00000028528	4	101496648	101642799	1	2	3	0	29	0	0	0	0	0	0	0	B1B0B7	
ENSMUST00000154121	ENSMUSG00000035649	4	44755877	44932215	1	0	0	3	2	2	0	0	0	0	0	0	E9PUW4	
ENSMUST00000154122						0	0	0	2	0	0	0	7	1	0	0		
ENSMUST00000154123						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000154124						3	0	0	0	0	0	13	269	0	86	18		
ENSMUST00000154125						13	7	5	8	8	5	0	0	0	0	0		
ENSMUST00000154126						2	0	1	6	4	3	60	118	23	9	9		
ENSMUST00000154127						0	1	1	18	3	2	0	0	3	0	0		
ENSMUST00000154129						4	1	4	2	0	0	0	8	0	0	0		
ENSMUST00000154130						2	1	5	1	4	0	0	0	0	0	0		
ENSMUST00000154131	ENSMUSG00000009555	2	32705784	32713076	-1	1	1	3	59	6	3	66	295	80	10	147	D6RHP4	
ENSMUST00000154132	ENSMUSG00000019868	10	14654755	14705560	-1	4	0	0	42	4	0	26	52	8	0	6		Q9CR26
ENSMUST00000154133	ENSMUSG00000038776	1	180976210	181020904	-1	0	3	3	4	2	0	5	0	0	0	15	F6YTS6	
ENSMUST00000154134						7	4	14	4	8	1	0	0	0	0	0		
ENSMUST00000154135	ENSMUSG00000063889	18	3266048	3337748	-1	0	1	0	0	0	0	0	0	4	7	0		P27699

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154136						2	0	0	56	0	0	0	0	0	0	0		
ENSMUST00000154138	ENSMUSG00000018548	11	87127077	87220683	1	0	0	0	0	0	0	0	16	3	2	3	F6XMH5	
ENSMUST00000154139	ENSMUSG00000042589	5	121856366	122050102	-1	0	2	0	0	0	0	0	0	0	0	0	F6YIR2	
ENSMUST00000154141						0	4	3	0	3	0	2	16	2	17	11		
ENSMUST00000154142						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154143						1	4	2	3	4	4	7	7	0	0	22		
ENSMUST00000154144						2	0	1	125	5	0	0	0	0	0	0		
ENSMUST00000154145						28	25	6	38	37	14	15	49	29	9	36		
ENSMUST00000154146	ENSMUSG00000043587	9	96823336	96892669	-1	4	1	0	0	1	1	0	0	0	0	0	D3YUT4	
ENSMUST00000154148	ENSMUSG00000102805	3	84496426	85887518	-1	5	2	0	19	0	0	0	31	30	17	2	E9QAY5	
ENSMUST00000154149	ENSMUSG00000038456	6	39462378	39557867	-1	13	4	36	76	6	11	0	1	0	0	5	D3Z1C6	
ENSMUST00000154150						6	8	4	7	1	2	287	694	483	175	382		
ENSMUST00000154151						6	4	7	2	4	1	3	85	4	36	10		
ENSMUST00000154152	ENSMUSG00000027993	3	84160439	84306877	-1	0	0	0	0	0	0	0	0	0	0	0	D3YY12	
ENSMUST00000154153	ENSMUSG00000046634	11	8826708	8973266	-1	50	22	94	32	64	21	0	0	0	0	0	A0A0A0MQK4	
ENSMUST00000154154	ENSMUSG00000078497	4	147361303	147391004	1	2	4	4	0	3	0	0	0	0	0	0	A2A7I1	
ENSMUST00000154155						0	3	0	8	3	2	0	0	0	0	0		
ENSMUST00000154156						0	0	0	0	0	0	0	51	16	13	0		
ENSMUST00000154157						0	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000154158						0	0	0	0	2	0	0	0	5	15	15		
ENSMUST00000154160	ENSMUSG00000027357	2	132846666	132866785	1	1	0	0	0	0	5	0	3	12	0	0	E9PYF8	
ENSMUST00000154161	ENSMUSG00000032540	9	122351608	122381524	1	5	2	3	4	0	2	0	0	0	0	0	D3Z7K3	
ENSMUST00000154162						1	0	0	0	0	1	4	0	68	122	85		
ENSMUST00000154163	ENSMUSG00000030067	6	98925338	99522721	-1	2	2	0	77	2	0	18	6	49	2	13	D3Z2T4	
ENSMUST00000154164						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154165	ENSMUSG00000021715	13	104631140	104817142	-1	0	2	0	0	0	0	3	0	0	0	0	D3Z2U3	
ENSMUST00000154166	ENSMUSG00000023960	17	44078813	44086567	1	0	0	2	12	4	0	0	0	0	60	9		Q9EQG7
ENSMUST00000154168						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000154169	ENSMUSG00000047881	5	63908897	63968897	-1	9	0	0	40	14	3	258	1440	396	99	289		Q8K2J7
ENSMUST00000154170						0	1	0	0	1	0	0	0	15	0	0		
ENSMUST00000154171						0	0	0	34	0	0	0	0	0	0	0		
ENSMUST00000154172						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000154174	ENSMUSG00000060538	7	126886171	126922917	-1	1	0	0	2	0	0	11	15	2	0	4	F6VVM1	
ENSMUST00000154175						5	1	1	2	0	0	0	4	0	3	1		
ENSMUST00000154176						7	2	6	2	2	4	0	0	0	0	0		
ENSMUST00000154178						0	0	0	0	0	0	0	0	12	1	14		
ENSMUST00000154179						0	0	3	89	0	2	0	0	8	0	0		
ENSMUST00000154180	ENSMUSG00000039903	16	90826719	90905109	1	8	4	11	0	4	3	0	1	0	0	0	D3Z1H0	
ENSMUST00000154181	ENSMUSG00000029699	5	135960211	135974531	-1	0	2	6	3	6	4	0	0	0	0	0	D3YUQ6	
ENSMUST00000154182						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000154183						4	0	8	1	3	5	0	0	0	0	18		
ENSMUST00000154184	ENSMUSG00000025647	9	109038565	109057777	1	0	5	17	0	6	0	93	1328	10	0	32		Q9D7I0
ENSMUST00000154185						3	3	4	3	6	0	13	14	12	1	6		
ENSMUST00000154186						9	3	30	291	13	6	0	1	0	0	0		
ENSMUST00000154187	ENSMUSG00000025161	11	120948480	120960868	1	0	0	0	13	3	0	666	40	405	4	254	B1ATM1	
ENSMUST00000154189						4	3	16	3	3	1	6	0	0	0	7		
ENSMUST00000154191						5	1	13	7	2	0	0	0	0	0	0		
ENSMUST00000154193	ENSMUSG00000033705	2	120629126	120731895	1	16	15	27	172	29	16	8	35	29	9	37	F7B335	
ENSMUST00000154195						0	1	5	0	4	7	0	11	0	3	0		
ENSMUST00000154196						0	6	4	0	3	2	0	0	2	5	0		
ENSMUST00000154197						0	4	0	1	9	0	0	0	0	0	0		
ENSMUST00000154198						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154199	ENSMUSG00000030409	7	19083849	19093821	1	0	0	0	0	0	0	0	0	0	0	0	D6RI32	
ENSMUST00000154200						0	1	8	3	2	1	0	2	0	0	3		
ENSMUST00000154201						1	0	0	0	0	0	4	11	0	1	0		
ENSMUST00000154202						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154203						1	2	13	2	5	1	0	0	0	0	0		
ENSMUST00000154204						19	12	79	29	25	8	4	2	2	0	1		
ENSMUST00000154205	ENSMUSG00000024270	18	24579881	24603817	-1	3	0	32	29	10	0	0	0	0	0	9	D3Z7N4	
ENSMUST00000154206	ENSMUSG00000041650	14	122534324	122891100	1	0	0	1	8	0	1	0	0	0	0	6	D3YWM4	
ENSMUST00000154207	ENSMUSG00000037742	9	78478449	78489151	-1	31	0	24	20	0	7	411	0	3291	1660	2262	D3YZ68	
ENSMUST00000154208	ENSMUSG00000066026	4	144892827	144928209	1	3	6	26	29	19	12	17	160	10	9	31		O88876
ENSMUST00000154209	ENSMUSG00000006191	13	29191746	29855674	-1	0	0	0	0	0	1	0	0	0	0	0	F6S0I8	
ENSMUST00000154210	ENSMUSG00000026754	2	39016155	39065541	-1	0	0	0	0	0	0	0	12	3	0	2		
ENSMUST00000154211						13	19	27	26	31	10	1	13	10	0	9		
ENSMUST00000154212	ENSMUSG00000020135	10	80295977	80318263	1	1	0	2	30	1	0	0	0	0	0	0	D3YYQ9	
ENSMUST00000154213	ENSMUSG00000027635	2	156995265	157007154	-1	10	4	23	16	3	2	0	18	7	5	12	B0QZT5	
ENSMUST00000154214						7	5	0	2	10	4	0	0	0	0	5		
ENSMUST00000154215						2	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000154216						3	2	2	145	8	4	2	0	0	0	0		
ENSMUST00000154218						4	4	0	3	2	2	10	84	25	3	41		
ENSMUST00000154219	ENSMUSG00000027810	3	58525821	58557501	1	0	0	0	0	0	0	41	247	8	132	0	D6RFN2	
ENSMUST00000154220						4	3	9	2	3	1	16	48	11	17	29		
ENSMUST00000154221	ENSMUSG00000016487	6	146888487	147032025	1	0	1	0	0	4	0	0	0	0	0	9	F7CUU8	
ENSMUST00000154222						19	18	117	186	24	0	0	0	0	0	0		
ENSMUST00000154224						4	4	5	6	6	6	0	0	0	0	0		
ENSMUST00000154225						1	0	4	3	4	2	5	9	9	0	13		
ENSMUST00000154226	ENSMUSG00000045268	4	119169513	119174195	-1	2	0	0	2	0	0	0	0	6	0	7	A8Y5E1	
ENSMUST00000154227						6	0	2	5	2	5	3	25	7	5	9		
ENSMUST00000154228	ENSMUSG00000067081	1	89950220	90014666	-1	0	0	0	0	0	0	0	0	0	0	0		Q8VHA6
ENSMUST00000154229	ENSMUSG00000028894	4	124741850	124801511	1	4	0	7	2	2	0	0	0	0	0	0	A0A0A0MQG5	
ENSMUST00000154230	ENSMUSG00000036591	2	20847919	20968881	-1	0	0	0	0	0	0	0	0	0	0	12	B7ZCJ1	
ENSMUST00000154231						0	0	12	102	32	14	28	76	76	0	103		
ENSMUST00000154232	ENSMUSG00000024335	17	34112023	34122634	-1	5	0	14	3	14	0	841	1384	1321	106	907	Q3TH63	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154233						0	0	0	30	0	1	0	2	3	0	5		
ENSMUST00000154234						2	0	0	6	0	4	0	0	0	0	0		
ENSMUST00000154235	ENSMUSG00000024188	17	26252910	26285504	1	3	7	8	192	18	4	10	32	26	0	49	D6REI1	
ENSMUST00000154236	ENSMUSG00000038880	17	24895116	24897502	1	4	0	7	56	1	4	2	0	3	2	0		Q9JIK9
ENSMUST00000154237	ENSMUSG00000026456	1	134405559	134411740	1	21	4	22	39	26	7	209	2708	492	81	768		Q9DB73
ENSMUST00000154238	ENSMUSG00000034813	10	119454034	120087261	1	12	19	149	19	18	1	0	4	0	0	0	D3Z6R6	
ENSMUST00000154239	ENSMUSG00000032812	7	101348067	101412586	1	0	0	0	9	0	0	1	1	1	0	339	F6XBJ8	
ENSMUST00000154240						5	6	26	16	8	0	0	0	0	0	0		
ENSMUST00000154241	ENSMUSG00000107283	5	31140654	31154251	-1	0	0	43	43	0	20	53	227	122	75	128		P19258
ENSMUST00000154243	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	E9QAH3	
ENSMUST00000154244	ENSMUSG00000031161	X	7930120	7947889	-1	2	0	4	25	2	2	0	3	0	0	6	B1AUA9	
ENSMUST00000154245	ENSMUSG00000034842	5	92331827	92414628	1	0	2	0	0	3	0	0	0	0	0	0	E9Q984	
ENSMUST00000154247						3	0	2	2	3	0	0	0	0	2	0		
ENSMUST00000154248	ENSMUSG00000042216	5	113243220	113310786	-1	4	0	10	6	0	4	0	0	0	0	0	D3YUT7	
ENSMUST00000154249						58	29	163	32	54	32	21	46	20	0	39		
ENSMUST00000154251						3	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000154253	ENSMUSG00000039382	X	7721973	7728201	1	0	3	0	0	2	2	7	28	29	2	25	S4R186	
ENSMUST00000154254						2	0	0	0	0	0	28	70	41	27	21		
ENSMUST00000154255	ENSMUSG00000036918	17	87282886	87381769	1	5	7	8	0	22	0	577	57	203	0	317	F6ZVR4	
ENSMUST00000154256	ENSMUSG00000085795	8	26977336	26981461	1	0	0	0	223	0	0	281	650	304	36	355	F6M3K1	P0CL69
ENSMUST00000154257	ENSMUSG00000027673	3	32736990	32751566	1	2	5	13	8	8	6	2	4	0	2	6	F6Y6V5	
ENSMUST00000154258	ENSMUSG00000056486	2	73610660	73775346	-1	0	0	0	0	0	0	0	0	0	0	0	B2FDI0	
ENSMUST00000154259						0	0	0	0	0	0	0	9	5	0	4		
ENSMUST00000154260						1	2	0	0	2	0	20	56	47	0	64		
ENSMUST00000154261						16	14	29	5	9	6	0	0	0	1	1		
ENSMUST00000154262						26	19	173	96	20	9	0	0	0	0	0		
ENSMUST00000154263						1	3	1	0	2	0	0	0	0	0	0		
ENSMUST00000154264						1	0	3	6	2	3	5	0	0	0	2		
ENSMUST00000154265						58	65	89	49	49	34	3	53	6	3	5		
ENSMUST00000154266	ENSMUSG00000029552	6	17065149	17105828	1	0	1	1	35	0	0	0	0	37	62	59	D6RH72	
ENSMUST00000154267						1	1	1	23	1	1	0	0	0	0	0		
ENSMUST00000154268						0	1	0	0	2	3	0	19	0	11	0		
ENSMUST00000154269	ENSMUSG00000026730	2	12924041	13003455	1	0	1	1	7	2	0	2	2	3	27	7	A2AUR3	
ENSMUST00000154270	ENSMUSG00000030208	6	135362545	135383173	1	20	18	37	18	30	11	0	0	11	0	33	S4R2U4	
ENSMUST00000154271	ENSMUSG00000078931	8	107044698	107048614	-1	4	1	2	2	3	3	5	30	10	3	6	S4R2R8	
ENSMUST00000154272						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154273						36	19	80	35	41	15	2	1	1	0	0		
ENSMUST00000154274						11	16	38	130	21	4	13	36	17	31	0		
ENSMUST00000154275						0	0	0	0	0	0	0	0	0	4	4		
ENSMUST00000154276	ENSMUSG00000022973	16	90936092	91011308	-1	4	0	54	0	4	0	170	1539	488	78	501	F7CD11	
ENSMUST00000154277						12	15	14	130	21	4	1	0	0	1	1		
ENSMUST00000154278						34	50	95	252	58	24	9	20	9	0	20		
ENSMUST00000154279	ENSMUSG00000087166	4	98726734	98738480	1	11	0	4	5	9	5	0	0	0	0	0		Q587J6
ENSMUST00000154280	ENSMUSG00000057637	4	143107391	143212995	-1	0	0	0	0	0	0	0	0	0	0	0	A2A7B7	
ENSMUST00000154281						5	0	11	156	16	2	0	0	0	0	0		
ENSMUST00000154282						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000154283	ENSMUSG00000028621	4	107066988	107088268	1	1	0	1	0	2	0	0	0	0	0	0	B1AS40	
ENSMUST00000154286						13	10	24	16	15	7	6	31	5	2	20		
ENSMUST00000154287	ENSMUSG00000059890	9	44923131	44965600	-1	0	6	0	0	2	0	46	58	56	3	47	E9Q442	
ENSMUST00000154288	ENSMUSG00000035960	14	50924968	50927139	1	1	5	0	62	5	4	0	6	0	0	4	D3Z6R9	
ENSMUST00000154289						10	3	8	5	11	1	3	42	19	7	17		
ENSMUST00000154290						2	2	0	0	0	0	0	0	0	1	0		
ENSMUST00000154291						2	4	8	5	4	4	0	4	0	0	2		
ENSMUST00000154292	ENSMUSG00000030838	7	46195350	46238503	-1	0	12	14	8	16	0	0	3	0	0	0	E9PYX1	
ENSMUST00000154293	ENSMUSG00000014771	17	15519208	15527301	-1	0	0	0	0	0	0	0	0	0	0	7	A2T4N6	
ENSMUST00000154294	ENSMUSG00000045915	11	68587021	68597966	1	0	3	18	11	7	3	0	0	0	0	0		Q5SV66
ENSMUST00000154295	ENSMUSG00000030737	7	99657804	99711340	-1	0	0	6	0	7	0	0	0	0	0	0	F6TQP9	
ENSMUST00000154299						2	7	13	0	3	2	0	0	0	0	0		
ENSMUST00000154300						1	1	0	5	1	0	0	0	0	0	0		
ENSMUST00000154301	ENSMUSG00000080316	17	17830719	17843009	1	0	0	0	0	0	0	0	0	1	0	1	F7ANW7	
ENSMUST00000154302						100	67	340	1195	95	63	0	14	5	0	4		
ENSMUST00000154303						3	2	24	8	4	2	19	26	12	0	40		
ENSMUST00000154304	ENSMUSG00000020781	11	115814724	115823094	1	2	3	6	0	5	3	8	13	0	0	11	B0QZP4	
ENSMUST00000154306						1	0	0	2	2	0	125	252	185	44	86		
ENSMUST00000154307						3	3	6	0	10	5	12	63	42	0	47		
ENSMUST00000154308						3	5	4	5	4	0	0	0	10	0	4		
ENSMUST00000154309						4	6	16	11	1	0	0	0	0	0	2		
ENSMUST00000154310						10	4	0	10	3	2	0	0	0	0	0		
ENSMUST00000154311						0	0	0	1	2	0	7	66	10	0	0		
ENSMUST00000154312						0	3	10	0	0	2	0	0	0	0	0		
ENSMUST00000154313						33	27	27	223	43	20	0	0	0	0	0		
ENSMUST00000154315						0	2	0	0	3	1	0	0	0	0	0		
ENSMUST00000154316	ENSMUSG00000026918	2	27445579	27507662	-1	7	2	6	5	5	2	0	0	0	0	16	A2AKA9	
ENSMUST00000154317						3	7	6	96	3	1	0	0	4	1	0		
ENSMUST00000154318						6	1	5	5	1	0	0	9	0	5	3		
ENSMUST00000154319	ENSMUSG00000020453	11	3288874	3309083	1	1	4	5	1	7	1	0	1	3	0	0	Q5NBY8	
ENSMUST00000154320						1	3	0	0	0	0	0	3	0	4	3		
ENSMUST00000154321						0	1	1	5	4	2	0	5	2	0	0		
ENSMUST00000154322						22	14	101	84	19	15	21	53	19	0	88		
ENSMUST00000154323	ENSMUSG00000032402	9	63646767	63757994	-1	6	0	3	0	9	3	10	0	5	0	0	A2CG44	
ENSMUST00000154324						1	2	1	4	5	3	2	10	8	0	26		
ENSMUST00000154325						16	14	55	38	16	9	1	0	5	0	1		
ENSMUST00000154327						0	0	0	0	1	0	2	0	0	0	0		
ENSMUST00000154328						0	0	0	1	4	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154330	ENSMUSG00000020477	11	5703983	5715680	-1	24	15	104	27	17	6	3	59	9	0	9		Q9CQV5
ENSMUST00000154331	ENSMUSG00000023030	15	100387898	100425072	-1	0	0	0	0	0	0	4	0	0	0	0	D3Z0R6	
ENSMUST00000154332						0	5	2	0	3	1	22	92	59	211	46		
ENSMUST00000154333						4	5	4	89	9	2	0	0	0	0	0		
ENSMUST00000154335	ENSMUSG00000051682	17	48264295	48275360	1	0	0	0	3	1	0	0	9	6	0	5	D3YYN5	
ENSMUST00000154336						6	0	4	0	13	7	20	2	30	3	17		
ENSMUST00000154337						3	5	6	1	3	2	0	0	0	0	0		
ENSMUST00000154339						6	0	3	6	6	0	3	23	0	25	37		
ENSMUST00000154340						1	4	0	14	9	4	13	52	7	27	48		
ENSMUST00000154341						0	4	0	2	9	3	6	0	4	0	7		
ENSMUST00000154342	ENSMUSG00000035984	18	34562634	34579115	-1	4	3	2	2	6	0	0	0	0	0	0		Q99MH5
ENSMUST00000154343						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000154347	ENSMUSG00000048992	17	23843855	23859776	1	1	2	0	0	15	2	0	0	0	0	0	D6RGT5	
ENSMUST00000154348						1	1	8	6	5	3	0	0	0	0	0		
ENSMUST00000154349						16	16	147	0	16	15	0	0	0	0	0		
ENSMUST00000154350						0	0	0	1	0	0	0	4	4	2	0		
ENSMUST00000154351						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000154353						3	3	3	0	3	0	2	3	0	0	0		
ENSMUST00000154355						1	1	1	116	7	2	0	0	2	0	0		
ENSMUST00000154356	ENSMUSG00000006932	9	120929216	120960507	1	0	0	0	0	0	0	48	469	30	216	729	E9Q6A9	
ENSMUST00000154357	ENSMUSG00000033688	9	103250521	103305082	-1	0	3	0	7	0	0	0	0	0	1	0	F6W4D3	
ENSMUST00000154358	ENSMUSG00000034211	5	129715497	129722556	1	0	0	0	0	0	0	0	0	0	17	4	D3YWF8	
ENSMUST00000154359						0	3	9	1	2	0	2	18	4	0	14		
ENSMUST00000154362						18	14	47	66	21	16	9	13	12	0	10		
ENSMUST00000154363	ENSMUSG00000024158	17	24840143	24864450	1	0	1	6	8	4	1	0	6	0	0	0	D3YV58	
ENSMUST00000154364	ENSMUSG00000041720	16	17280351	17406314	-1	0	0	0	46	9	7	397	286	887	0	489	E9Q3L2	
ENSMUST00000154365						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000154366						3	5	4	7	10	3	0	0	0	0	0		
ENSMUST00000154368						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154369						3	1	7	23	5	5	3	0	0	0	3		
ENSMUST00000154370	ENSMUSG00000039850	11	119491347	119511437	1	1	0	1	53	0	0	0	0	0	0	0	E9PXA0	
ENSMUST00000154371	ENSMUSG00000050912	9	7764041	7794333	1	0	0	16	0	0	10	182	101	86	133	166	D6RI40	
ENSMUST00000154372	ENSMUSG00000001441	11	97205842	97280638	-1	0	0	7	0	0	0	0	0	0	0	4	F6RAU6	
ENSMUST00000154373						37	36	119	151	64	23	0	3	2	0	7		
ENSMUST00000154374	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0	Q3ZB71	Q9Z0E3
ENSMUST00000154375	ENSMUSG00000030352	6	127961396	128143594	-1	1	0	4	0	1	2	0	0	0	0	0	D3YV18	
ENSMUST00000154376	ENSMUSG00000039652	19	37021291	37208601	-1	5	5	12	6	14	10	0	5	0	0	0		
ENSMUST00000154378						106	50	455	114	48	13	1	10	3	1	4		
ENSMUST00000154381	ENSMUSG00000001418	3	88325023	88331313	1	0	0	0	0	0	0	240	339	159	74	149	H3BJ16	
ENSMUST00000154382						4	8	35	17	11	2	0	2	4	0	5		
ENSMUST00000154383	ENSMUSG00000024667	19	10533865	10556238	-1	5	0	13	0	0	0	82	73	12	52	25		Q9CQC4
ENSMUST00000154385	ENSMUSG00000072944	X	140006805	140062712	-1	0	3	0	8	0	0	0	0	0	0	0	A2AG11	
ENSMUST00000154386						2	1	4	5	5	1	3	3	1	1	1		
ENSMUST00000154387						0	1	0	2	2	0	0	6	0	2	11		
ENSMUST00000154389						2	3	15	5	9	4	0	0	0	0	0		
ENSMUST00000154391						0	3	0	0	0	0	0	0	0	9	4		
ENSMUST00000154392	ENSMUSG00000041119	17	31386234	31476310	1	0	0	0	0	5	0	0	3	0	1	0	F6ZAU1	
ENSMUST00000154393	ENSMUSG00000025266	X	150983141	151017322	-1	0	1	0	1	0	0	15	0	13	0	0	S4R2Q1	
ENSMUST00000154394						4	2	4	4	6	2	0	0	0	0	0		
ENSMUST00000154395						1	1	2	1	1	0	0	8	0	0	0		
ENSMUST00000154396	ENSMUSG00000059439	11	85353167	85826058	1	19	0	7	0	0	5	107	146	52	10	95	F7C0F2	
ENSMUST00000154398	ENSMUSG00000037921	8	61928087	62037701	1	2	0	0	9	3	3	0	6	0	2	8	D3Z3B3	
ENSMUST00000154399						3	1	0	4	6	1	2	0	0	2	0		
ENSMUST00000154400						0	0	0	0	0	0	19	3	15	0	10		
ENSMUST00000154401	ENSMUSG00000022442	15	83483772	83510893	-1	0	0	2	1	0	1	0	0	0	0	0	A6PW19	
ENSMUST00000154402	ENSMUSG00000026095	1	53344617	53352752	-1	17	14	24	18	14	10	16	15	12	0	18	D3Z0F1	
ENSMUST00000154403						0	0	0	0	2	10	91	614	87	44	100		
ENSMUST00000154404						0	0	0	0	0	0	5	0	0	4	0		
ENSMUST00000154405						7	6	8	22	2	3	0	2	4	3	10		
ENSMUST00000154406						9	3	12	16	10	2	8	6	11	0	172		
ENSMUST00000154408	ENSMUSG00000029320	5	103648039	103656010	-1	0	0	0	0	0	0	0	0	0	0	0	Q810Q2	
ENSMUST00000154410						3	2	1	1	4	1	0	0	0	0	0		
ENSMUST00000154411						37	29	54	25	36	15	2	6	3	0	10		
ENSMUST00000154412	ENSMUSG00000027224	2	122302191	122313730	-1	5	4	23	4	9	3	0	0	0	0	0	A2AQ93	
ENSMUST00000154413						0	0	1	0	0	0	0	1	1	0	0		
ENSMUST00000154415	ENSMUSG00000078771	11	79526560	79530609	-1	0	3	1	0	0	3	36	318	198	901	119	J3QP09	
ENSMUST00000154416	ENSMUSG00000028218	4	12153409	12172015	-1	0	0	0	0	0	0	0	4	0	0	0	F6VZK2	
ENSMUST00000154418	ENSMUSG00000074884	2	121449195	121458313	1	0	0	0	0	0	0	1	17	5	0	0	D6RCY2	
ENSMUST00000154419						0	0	0	0	0	0	2	1	0	4	0		
ENSMUST00000154420						0	0	0	0	0	1	8	20	10	1	13		
ENSMUST00000154421						10	4	19	20	14	4	0	8	9	3	3		
ENSMUST00000154422						1	0	1	0	0	0	0	0	1	0	0		
ENSMUST00000154423						3	1	3	6	4	3	0	1	1	0	2		
ENSMUST00000154424	ENSMUSG00000040855	X	162411954	162643649	-1	15	25	130	0	5	0	2	8	0	1	2	B1AV20	
ENSMUST00000154425						9	10	17	4	16	7	3	12	20	1	0		
ENSMUST00000154426	ENSMUSG00000043909	2	121193281	121271407	-1	3	0	4	3	1	0	0	3	6	1	12	F6ZRL3	
ENSMUST00000154428	ENSMUSG00000030533	7	80325292	80341005	-1	18	10	25	0	26	16	100	85	0	0	37	D6RIN1	
ENSMUST00000154429						0	5	0	6	16	9	49	193	108	39	132		
ENSMUST00000154430	ENSMUSG00000018449	11	70970213	70977833	1	5	0	3	3	5	2	0	0	2	0	2	J3QP63	
ENSMUST00000154431						5	4	0	0	0	1	0	0	0	0	0		
ENSMUST00000154432						7	18	25	11	11	8	5	17	15	1	14		
ENSMUST00000154433						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000154434						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154435						1	4	1	0	2	0	0	0	2	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154436						2	15	4	8	9	0	0	9	0	0	17		
ENSMUST00000154437						0	1	0	3	1	0	31	160	36	20	38		
ENSMUST00000154438	ENSMUSG00000071337	6	86404219	86433405	1	0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000154439						3	0	14	5	8	4	0	5	0	0	0		
ENSMUST00000154440	ENSMUSG00000030220	6	136923655	136941899	-1	1	0	0	0	1	0	57	145	60	134	61	D3YWL7	
ENSMUST00000154441						7	3	4	6	9	6	0	0	0	1	0		
ENSMUST00000154442						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000154443	ENSMUSG00000017652	2	165055627	165072948	1	4	0	0	5	0	3	0	0	0	0	0	S4R2M8	
ENSMUST00000154444						0	0	0	34	0	0	0	0	0	0	0		
ENSMUST00000154445						60	47	305	74	35	28	0	0	1	0	3		
ENSMUST00000154446	ENSMUSG00000005089	2	102658659	102790784	1	1	0	0	0	0	0	0	0	0	0	0	F6ZRK3	
ENSMUST00000154447						0	0	0	18	1	0	0	3	0	0	0		
ENSMUST00000154448	ENSMUSG00000029563	6	14901349	15441977	1	90	64	179	1006	179	94	0	4	4	1	11	D3Z7E9	
ENSMUST00000154449						1	0	5	3	3	0	0	0	0	0	0		
ENSMUST00000154450	ENSMUSG00000001065	8	123254195	123269745	1	1	0	0	14	0	0	0	0	0	0	0	D3Z1K4	
ENSMUST00000154451						3	2	2	10	5	2	3	7	0	0	6		
ENSMUST00000154453	ENSMUSG00000026834	2	58267453	58357895	-1	0	0	0	0	0	1	0	0	0	0	0	D3Z1K2	
ENSMUST00000154454	ENSMUSG00000031453	8	13566950	13677603	-1	0	1	1	1	1	0	6	2	17	0	6	D6RFE0	
ENSMUST00000154455						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000154456	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	0	0	39	0	0	A2AQF1	
ENSMUST00000154458						4	1	3	62	11	0	0	0	2	0	0		
ENSMUST00000154460	ENSMUSG00000021824	14	21031442	21052508	-1	17	8	13	5	12	3	389	2085	439	780	385		Q9JKC8
ENSMUST00000154461						3	3	3	4	5	4	0	0	0	0	0		
ENSMUST00000154463	ENSMUSG00000026418	1	135779434	135810989	1	0	0	0	2	0	2	0	0	0	0	0		Q9WUZ5
ENSMUST00000154464	ENSMUSG00000039787	2	29869164	29882840	1	2	3	7	53	7	6	1	0	0	0	1	A3KGW4	
ENSMUST00000154465						3	3	5	2	6	4	20	88	51	6	81		
ENSMUST00000154466	ENSMUSG00000005611	7	110868266	110982461	-1	3	0	0	0	0	4	0	0	0	0	1	D3YUG8	
ENSMUST00000154467						153	156	355	189	111	69	19	20	25	4	32		
ENSMUST00000154468						35	30	49	28	26	24	112	66	114	6	94		
ENSMUST00000154469	ENSMUSG00000040532	5	135009152	135012175	1	0	1	0	90	2	4	62	214	48	91	46		
ENSMUST00000154470	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	1	43	2	2	0	0	0	0	0		P27699
ENSMUST00000154473	ENSMUSG00000062753	17	27563575	27565749	-1	0	0	3	0	3	0	144	179	100	171	38	Q3V2N7	
ENSMUST00000154474	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	0	0	0	0	0	157	0	184	D6RH40	
ENSMUST00000154475						10	2	16	22	7	7	0	0	0	31	21		
ENSMUST00000154476						1	1	2	0	0	0	2	0	0	0	2		
ENSMUST00000154477						5	0	0	43	9	0	16	170	53	0	87		
ENSMUST00000154478						0	2	0	3	1	0	0	41	1	0	8		
ENSMUST00000154479						6	6	5	9	17	9	0	0	0	6	13		
ENSMUST00000154481						2	1	4	0	3	0	0	0	0	0	0		
ENSMUST00000154482						2	0	0	42	4	0	0	0	0	0	0		
ENSMUST00000154483	ENSMUSG00000025162	11	120961749	120991330	-1	0	0	0	2	0	2	152	164	132	0	117	F7A4U8	
ENSMUST00000154484						11	6	0	15	6	19	0	0	0	0	0		
ENSMUST00000154485						2	2	0	1	0	2	0	42	4	0	0		
ENSMUST00000154486						0	0	0	0	4	0	0	17	7	0	12		
ENSMUST00000154487						2	0	2	0	1	0	0	0	2	2	3		
ENSMUST00000154489	ENSMUSG00000037012	10	62268855	62379908	-1	0	0	0	0	0	0	0	0	0	0	0	B4YB29	
ENSMUST00000154490						1	0	0	32	3	6	0	0	0	1	8		
ENSMUST00000154492						35	25	45	24	33	23	0	29	18	7	23		
ENSMUST00000154494						8	4	12	0	11	8	35	293	43	15	101		
ENSMUST00000154495						16	13	105	18	38	12	7	7	6	0	12		
ENSMUST00000154496	ENSMUSG00000045751	4	24496451	24602950	1	0	0	0	0	0	0	0	0	0	0	0	G3UYM2	
ENSMUST00000154497						0	0	0	0	0	0	0	4	0	0	0		
ENSMUST00000154498	ENSMUSG00000044628	2	25242255	25244262	1	0	5	6	136	5	5	0	1	0	0	0	Z4YMD3	
ENSMUST00000154499						0	3	2	0	0	0	0	8	0	0	0		
ENSMUST00000154500	ENSMUSG00000034724	5	96070333	96164171	-1	0	2	0	53	3	0	0	0	0	0	0	D3Z5R3	
ENSMUST00000154501	ENSMUSG00000020228	10	120083608	120112987	-1	0	0	0	0	0	0	46	0	48	7	16	D6RGT6	
ENSMUST00000154502						0	0	0	0	0	2	237	189	169	30	82		
ENSMUST00000154503						1	0	0	0	0	0	4	3	2	0	8		
ENSMUST00000154505						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000154506						4	0	0	2	3	2	0	9	2	0	5		
ENSMUST00000154507	ENSMUSG00000024052	17	71182560	71249817	1	0	0	1	4	4	0	0	0	0	0	0	F6VTY5	
ENSMUST00000154508						14	6	69	4	12	14	0	0	0	0	2		
ENSMUST00000154509	ENSMUSG00000063450	12	75818134	76110926	1	3	1	3	24	6	0	0	0	0	0	0	D3Z412	
ENSMUST00000154510	ENSMUSG00000058794	15	103248212	103258403	-1	0	3	3	0	6	1	114	323	182	41	85	D3Z4E8	
ENSMUST00000154511						0	0	0	0	0	0	0	0	0	4	0		
ENSMUST00000154512						0	0	2	84	8	2	0	0	0	0	0		
ENSMUST00000154513						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154514						3	3	9	17	5	1	0	0	0	0	0		
ENSMUST00000154516						0	0	0	0	0	0	0	0	4	3	0		
ENSMUST00000154517						0	0	2	0	1	0	0	0	0	4	3		
ENSMUST00000154518	ENSMUSG00000043924	4	135369576	135398227	-1	1	0	2	105	7	4	0	1	0	0	0	A2A991	
ENSMUST00000154519						1	0	0	4	0	0	0	0	0	10	8		
ENSMUST00000154520	ENSMUSG00000086361	15	73834561	73839908	1	2	4	5	42	7	3	0	0	0	0	0	D3YTM9	
ENSMUST00000154521						0	2	4	4	0	1	0	0	0	1	0		
ENSMUST00000154523						22	26	57	36	26	15	7	36	34	4	56		
ENSMUST00000154525	ENSMUSG00000032841	2	101714285	101883027	-1	0	0	0	0	0	0	0	0	0	0	0	B0R105	
ENSMUST00000154526	ENSMUSG00000090231	17	34856374	34862518	-1	0	0	0	0	0	0	28	86	28	87	430	F6XQ00	
ENSMUST00000154527						0	0	0	0	1	0	0	0	0	0	2		
ENSMUST00000154528						0	0	0	0	0	0	0	5	0	4	0		
ENSMUST00000154529						2	0	24	0	0	1	32	51	52	3	44		
ENSMUST00000154531						1	0	7	0	8	0	0	16	18	4	8		
ENSMUST00000154532						0	1	9	0	0	1	0	0	22	4	14		
ENSMUST00000154533						6	6	0	0	0	3	1065	1675	228	6936	1232		
ENSMUST00000154534						8	6	13	10	2	6	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154535	ENSMUSG00000028438	4	41390745	41464887	-1	0	0	0	6	0	0	0	0	0	0	0	A2BGK7	
ENSMUST00000154536						26	14	31	9	13	4	2	0	0	0	0		
ENSMUST00000154537	ENSMUSG00000024831	19	3260924	3283017	-1	5	0	30	88	0	4	2	0	0	0	0	D6RFT3	
ENSMUST00000154538	ENSMUSG00000067001	1	107399655	107452689	1	1	0	0	1	0	0	0	0	0	0	0	D3Z2N5	
ENSMUST00000154540						3	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000154541						5	4	1	4	2	0	0	12	0	0	0		
ENSMUST00000154542						123	170	267	76	104	47	9	34	13	10	10		
ENSMUST00000154543						4	8	16	39	3	7	0	0	0	0	0		
ENSMUST00000154544						49	34	57	68	60	31	0	0	0	0	0		
ENSMUST00000154545	ENSMUSG00000017144	2	51130438	51149111	-1	12	23	57	24	22	8	2	5	9	0	4	E9Q8D7	
ENSMUST00000154546						0	0	3	19	0	3	18	0	23	2	24		
ENSMUST00000154547	ENSMUSG00000029782	6	30479053	30509783	-1	0	0	1	1	0	0	0	0	0	0	6		
ENSMUST00000154548						4	0	3	0	0	0	0	0	0	6	0		
ENSMUST00000154549						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154550						6	0	0	4	0	0	128	240	70	213	113		
ENSMUST00000154551	ENSMUSG00000036452	18	38601534	39376284	1	0	0	4	0	0	0	78	0	113	0	96	F6XTB7	
ENSMUST00000154552	ENSMUSG00000031157	X	7894519	7899269	-1	0	0	0	0	0	0	4	0	0	0	0	A2AER9	
ENSMUST00000154553	ENSMUSG00000073468	17	8311102	8396852	1	0	0	0	36	0	0	484	725	319	401	191		Q5SSN7
ENSMUST00000154555	ENSMUSG00000044265	7	104153013	104164831	-1	0	2	15	3	0	3	0	0	0	1	0	D3YW75	
ENSMUST00000154556						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154557	ENSMUSG00000069378	18	53464546	53575907	1	5	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154558	ENSMUSG00000030204	6	135011612	135023776	1	0	0	0	0	0	0	0	0	0	0	0	F6QKD2	
ENSMUST00000154559						4	2	7	7	3	3	0	0	0	0	0		
ENSMUST00000154562	ENSMUSG00000031148	X	7697131	7710262	1	0	0	0	0	0	0	0	0	30	2	2	F6XU64	
ENSMUST00000154563						1	0	0	1	0	0	3	2	4	0	6		
ENSMUST00000154564						0	0	6	84	1	1	0	2	0	0	4		
ENSMUST00000154565	ENSMUSG00000025150	11	120729489	120732114	-1	0	0	3	0	5	0	0	0	0	12	3	F6YNX9	
ENSMUST00000154567						8	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000154568						61	63	43	109	79	101	2	6	7	0	8		
ENSMUST00000154569						2	5	4	0	3	3	0	0	0	0	0		
ENSMUST00000154571	ENSMUSG00000035545	7	4137039	4148177	1	0	0	0	7	0	0	0	3	10	0	10	D3Z042	
ENSMUST00000154572						0	1	20	4	1	2	1	2	0	0	8		
ENSMUST00000154573						16	6	12	11	18	4	5	33	15	12	17		
ENSMUST00000154574						12	0	54	17	9	13	12	53	35	19	45		
ENSMUST00000154575						0	2	16	5	8	8	3	5	4	4	16		
ENSMUST00000154576						0	2	3	1	4	2	5	25	14	0	25		
ENSMUST00000154578						3	5	6	8	15	7	0	0	0	0	0		
ENSMUST00000154580						0	0	13	0	1	0	1	0	0	0	0		
ENSMUST00000154581						94	95	70	57	86	54	6	19	21	1	18		
ENSMUST00000154583	ENSMUSG00000039285	9	118040499	118069794	1	10	6	5	33	21	6	53	241	167	44	112		Q9QYP6
ENSMUST00000154584	ENSMUSG00000055762	15	75894796	75909556	-1	0	0	0	9	2	0	8	36	0	3	8	Q80T06	
ENSMUST00000154585	ENSMUSG00000027829	3	65946151	65958249	-1	0	0	0	0	0	0	8	49	47	59	0	F6WYR6	
ENSMUST00000154586	ENSMUSG00000092541	9	88407432	88456616	-1	18	13	55	19	19	0	0	2	0	0	4	G3UY67	
ENSMUST00000154588	ENSMUSG00000020649	12	24708241	24714146	1	0	0	0	0	0	0	15	40	69	0	0	F6RUC3	
ENSMUST00000154589	ENSMUSG00000032384	9	65908924	66045015	1	0	0	0	7	0	0	0	2	9	1	1	D3Z2A2	
ENSMUST00000154590						18	17	17	24	18	11	0	35	9	0	10		
ENSMUST00000154591						7	6	9	10	5	9	33	351	69	11	96		
ENSMUST00000154593						4	3	8	0	0	2	3	22	5	6	22		
ENSMUST00000154594	ENSMUSG00000045983	16	20668313	20692884	1	0	5	0	0	0	1	0	0	0	0	0		
ENSMUST00000154595	ENSMUSG00000026853	2	30400471	30415813	-1	0	0	0	0	0	0	0	13	0	0	0	A2AWJ5	
ENSMUST00000154596						0	0	13	22	4	2	341	360	145	120	125		
ENSMUST00000154597	ENSMUSG00000030493	7	35392152	35396836	-1	0	0	0	0	0	0	11	21	0	2	0		Q8BHL6
ENSMUST00000154598						0	0	0	0	0	0	0	26	0	0	0		
ENSMUST00000154599	ENSMUSG00000020541	11	90643465	90688366	-1	0	0	2	10	0	2	0	0	3	1	0	A6PWP3	
ENSMUST00000154600						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154601	ENSMUSG00000024787	19	6119399	6128304	-1	0	0	4	7	2	0	0	0	0	0	0	D3Z479	
ENSMUST00000154602	ENSMUSG00000040167	7	131388652	131410521	-1	1	1	2	68	4	2	0	12	0	11	24	D3YYG0	
ENSMUST00000154603	ENSMUSG00000021185	12	100779057	100896981	1	0	2	0	0	0	0	2	0	0	0	0	D6RI81	
ENSMUST00000154604	ENSMUSG00000033486	2	121392631	121413792	-1	10	11	30	9	20	7	0	17	0	3	12	D6RCY8	
ENSMUST00000154605						2	1	0	2	1	1	0	4	1	0	7		
ENSMUST00000154606						36	34	107	33	57	22	2	3	5	0	3		
ENSMUST00000154607						0	32	150	70	36	27	0	4	1	0	2		
ENSMUST00000154608						3	1	12	0	8	3	0	17	1	0	0		
ENSMUST00000154609	ENSMUSG00000020232	10	81346048	81350480	-1	0	0	0	0	0	0	18	45	57	0	54	E9Q2W1	
ENSMUST00000154610						3	0	2	0	4	0	0	0	0	0	0		
ENSMUST00000154611						1	2	18	2	4	1	0	0	0	0	0		
ENSMUST00000154612						0	2	2	0	2	2	0	0	0	0	0		
ENSMUST00000154613	ENSMUSG00000089917	2	181569149	181584892	-1	0	0	0	0	1	1	4	6	0	0	0	F6W7K4	
ENSMUST00000154614						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154617	ENSMUSG00000020516	11	86498871	86544805	-1	12	13	19	10	14	10	96	330	104	62	98		Q8BSK8
ENSMUST00000154619	ENSMUSG00000029769	6	29396309	29426994	1	1	0	18	19	23	9	0	0	1	2	0	F6VCV9	
ENSMUST00000154620						0	3	0	1	6	0	59	20	66	0	18		
ENSMUST00000154621	ENSMUSG00000030316	6	115004381	115037876	-1	0	2	12	5	7	0	0	3	0	4	4	D6RGT1	
ENSMUST00000154622						4	0	0	2	6	3	0	0	0	0	0		
ENSMUST00000154623	ENSMUSG00000020744	11	115614178	115628295	-1	0	0	25	27	5	4	2	4	7	2	0	A2A9V3	
ENSMUST00000154624						15	5	14	27	13	6	0	0	0	0	0		
ENSMUST00000154625						33	21	30	387	63	36	2	5	2	1	0		
ENSMUST00000154626						0	0	0	0	0	0	69	0	105	0	87		
ENSMUST00000154627						1	0	0	0	0	0	16	0	4	0	0		
ENSMUST00000154628						27	27	189	62	40	13	15	58	11	4	25		
ENSMUST00000154629	ENSMUSG00000060402	7	34674468	34812711	-1	14	14	17	48	11	7	0	0	0	0	0	D6RCV4	
ENSMUST00000154630	ENSMUSG00000019087	X	74297097	74304721	1	0	0	3	2	0	0	0	6	0	0	0	F7AYP0	
ENSMUST00000154633						30	24	49	58	33	20	23	33	24	2	35		
ENSMUST00000154634						12	2	39	17	13	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154635						3	1	0	2	5	1	0	0	0	5	0		
ENSMUST00000154636						3	2	2	25	6	5	0	0	0	0	0		
ENSMUST00000154638	ENSMUSG00000031352	X	169250193	169320372	-1	3	2	6	18	2	0	0	1	0	3	2	G3UXK7	
ENSMUST00000154639						4	1	3	6	3	1	0	0	0	0	1		
ENSMUST00000154640	ENSMUSG00000028830	4	126753544	126870070	1	0	0	0	112	4	1	0	4	0	0	4	A2A788	
ENSMUST00000154641						5	2	28	1	2	0	0	5	2	0	3		
ENSMUST00000154642						0	0	3	64	0	0	61	99	62	239	23		
ENSMUST00000154643						5	39	59	26	35	0	0	0	0	0	0		
ENSMUST00000154644	ENSMUSG00000043659	9	24097996	24316398	1	2	0	0	0	0	0	0	0	0	0	0	A6X922	
ENSMUST00000154645						0	0	0	0	0	0	28	0	6	0	83		
ENSMUST00000154646						3	4	0	56	2	1	0	0	3	0	0		
ENSMUST00000154647	ENSMUSG00000079484	2	30266203	30282149	1	11	0	7	11	9	3	0	0	3	0	7		Q9DB26
ENSMUST00000154648						0	3	0	1	0	2	12	7	0	5	9		
ENSMUST00000154649						5	3	8	8	0	1	34	689	38	123	118		
ENSMUST00000154650	ENSMUSG00000013523	2	170346991	170427845	-1	0	0	0	0	3	0	0	6	0	1	0	F7BNZ5	
ENSMUST00000154651	ENSMUSG00000014867	2	26920040	26933928	-1	0	0	5	0	2	0	23	0	0	0	21	F7CH13	
ENSMUST00000154652	ENSMUSG00000038119	9	35421128	35507652	1	1	9	7	0	3	7	0	0	2	0	0	Q3TZM7	
ENSMUST00000154653						0	0	0	0	0	1	0	15	4	4	3		
ENSMUST00000154655	ENSMUSG00000001642	6	34302434	34317478	-1	4	0	0	17	0	0	0	0	0	0	0	D3YVJ7	
ENSMUST00000154656						6	1	27	6	9	6	2	0	2	0	1		
ENSMUST00000154657						1	0	2	0	2	2	0	4	0	0	0		
ENSMUST00000154658						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000154659	ENSMUSG00000036862	7	105752989	105787654	-1	9	1	20	0	11	6	0	0	0	0	1	F6PYJ6	
ENSMUST00000154660						5	4	7	5	13	2	60	81	30	34	55		
ENSMUST00000154661						0	0	1	35	3	0	0	0	0	0	3		
ENSMUST00000154662	ENSMUSG00000056004	5	9266118	9481825	1	0	7	5	0	0	0	0	0	0	0	0		Q3UZV7
ENSMUST00000154664						10	7	8	4	10	7	0	0	0	0	0		
ENSMUST00000154665	ENSMUSG00000025420	18	76977148	77047308	-1	16	29	81	45	35	8	0	0	0	0	0		Q9D3R6
ENSMUST00000154666	ENSMUSG00000068457	Y	1096861	1245759	-1	33	32	63	24	51	19	6	0	18	9	28	D6RFT4	
ENSMUST00000154667						56	61	68	70	56	24	15	136	34	10	50		
ENSMUST00000154668	ENSMUSG00000027977	3	123526166	123690853	-1	6	5	0	0	0	0	0	0	0	0	0	E9PZJ4	
ENSMUST00000154669						2	0	6	0	5	0	0	39	25	8	36		
ENSMUST00000154670	ENSMUSG00000050705	17	35892677	35897431	-1	5	0	0	0	3	0	0	48	10	9	23	F6W3U3	
ENSMUST00000154671						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000154672	ENSMUSG00000049550	5	123577795	123684618	-1	16	7	43	37	22	17	0	17	29	2	23	F7CB97	
ENSMUST00000154674						0	1	2	0	3	2	0	0	0	0	0		
ENSMUST00000154675	ENSMUSG00000024136	17	24440081	24443105	-1	2	1	3	0	2	0	0	0	0	0	0	D3Z3Z7	
ENSMUST00000154676	ENSMUSG00000023030	15	100387898	100425072	-1	0	0	0	0	0	0	0	0	0	0	0	D3YXP3	
ENSMUST00000154677	ENSMUSG00000027620	2	156147239	156180238	-1	0	2	0	0	0	0	45	147	61	7	69	D6RJ85	
ENSMUST00000154679	ENSMUSG00000028099	3	96711490	96727628	-1	14	24	30	17	0	6	52	259	121	0	56	B2RX77	Q9D483
ENSMUST00000154680						1	2	1	62	3	0	0	0	0	0	0		
ENSMUST00000154681						2	1	2	0	0	0	0	1	2	0	0		
ENSMUST00000154683						2	2	1	1	5	1	0	0	0	3	0		
ENSMUST00000154684						13	9	49	17	35	12	0	6	2	0	8		
ENSMUST00000154685	ENSMUSG00000031834	8	70768176	70776713	-1	0	0	0	0	0	0	1	2	6	0	1	F6R2V5	
ENSMUST00000154686	ENSMUSG00000029462	5	122354369	122364984	1	0	1	0	0	0	0	83	94	103	357	84	D6RH43	
ENSMUST00000154687						0	5	10	18	7	5	9	70	36	4	117		
ENSMUST00000154688						3	2	5	0	1	3	6	5	0	0	3		
ENSMUST00000154689	ENSMUSG00000028863	4	125085134	125113238	1	86	87	525	170	94	41	56	156	107	21	129		Q2VPQ9
ENSMUST00000154690	ENSMUSG00000032285	9	54698873	54716315	1	0	2	0	37	2	1	0	0	2	0	0	D3Z1U5	
ENSMUST00000154691	ENSMUSG00000039048	9	35204206	35211055	-1	20	12	15	10	15	9	15	126	35	0	44	D6RCV5	
ENSMUST00000154692						3	6	1	4	4	0	0	0	0	0	0		
ENSMUST00000154693						0	0	0	0	1	2	7	0	4	17	11		
ENSMUST00000154694						0	1	0	0	0	0	0	12	3	1	3		
ENSMUST00000154695	ENSMUSG00000031169	X	8193848	8206525	-1	0	4	0	0	0	0	0	2	2	0	0	S4R2I7	
ENSMUST00000154696	ENSMUSG00000029699	5	135960211	135974531	-1	0	1	5	0	0	0	0	0	0	0	0	F6ZA92	
ENSMUST00000154697						4	3	4	3	6	2	0	0	0	0	0		
ENSMUST00000154698						5	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000154699						16	15	34	50	23	18	0	2	4	1	4		
ENSMUST00000154700						0	0	7	98	8	3	4	30	13	1	16		
ENSMUST00000154701	ENSMUSG00000020389	11	52004221	52089784	1	0	1	0	0	0	0	0	5	0	0	0	F6RX76	
ENSMUST00000154702						3	2	3	6	1	5	5	54	8	0	22		
ENSMUST00000154704	ENSMUSG00000041966	2	71055328	71099142	1	79	76	229	150	83	47	61	181	115	28	148		Q3TUL7
ENSMUST00000154705	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	49	3	F6QWT6	
ENSMUST00000154706						36	53	50	25	39	15	1	6	2	1	4		
ENSMUST00000154707						8	3	23	38	32	0	4	0	0	0	3		
ENSMUST00000154708	ENSMUSG00000037221	5	137596645	137601058	-1	0	0	0	0	0	0	4	0	12	0	4	D3Z1F3	
ENSMUST00000154709						1	0	4	2	2	0	0	0	0	180	0		
ENSMUST00000154710						4	3	9	7	9	1	35	231	93	7	134		
ENSMUST00000154711						0	0	0	5	0	1	0	3	3	0	9		
ENSMUST00000154712						2	5	6	8	6	4	0	8	6	0	0		
ENSMUST00000154713	ENSMUSG00000029445	5	123171807	123182727	-1	2	0	2	3	0	0	0	0	0	0	0	D3Z1U3	
ENSMUST00000154714						0	1	0	0	0	0	0	0	16	0	0		
ENSMUST00000154715	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	4	0	0	D3Z7M6	
ENSMUST00000154716						0	0	0	0	0	0	5	2	0	52	13		
ENSMUST00000154717						0	1	0	0	0	0	0	30	0	6	1		
ENSMUST00000154718	ENSMUSG00000019854	10	18055861	18125155	1	0	0	0	9	6	0	0	12	0	0	0	D3Z2E3	
ENSMUST00000154721						1	0	0	135	0	3	0	0	14	0	23		
ENSMUST00000154722						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154723	ENSMUSG00000048537	9	44686304	44735198	-1	0	2	0	41	2	0	1	0	0	0	0	F7B296	
ENSMUST00000154724	ENSMUSG00000095538	7	27168430	27181086	-1	0	0	0	0	6	0	0	4	4	0	4	D6RFS9	
ENSMUST00000154725	ENSMUSG00000061410	8	121598703	121652901	-1	2	1	0	0	0	3	0	5	0	1	14	F6XMW0	
ENSMUST00000154726	ENSMUSG00000045193	10	80165985	80172786	1	0	0	4	0	0	0	0	6	9	0	7	D3YU80	
ENSMUST00000154727	ENSMUSG00000040624	10	3740364	3967303	1	1	12	46	0	3	0	0	18	0	0	0	F7C583	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154728	ENSMUSG00000029208	5	69556923	69575973	1	0	0	0	14	0	0	8	46	10	14	11		
ENSMUST00000154729						3	2	6	6	6	3	16	88	12	8	14		
ENSMUST00000154730	ENSMUSG00000034591	10	83230848	83337882	-1	6	1	2	0	0	0	0	0	0	0	0	D3YYW2	
ENSMUST00000154731						4	0	2	0	5	1	0	4	0	0	1		
ENSMUST00000154732	ENSMUSG00000001173	X	47912387	47965868	1	30	27	19	26	46	15	10	17	11	2	12	F7CAV3	
ENSMUST00000154733						3	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000154734						0	2	0	1	3	1	0	0	0	0	0		
ENSMUST00000154737						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000154738						0	1	3	6	6	4	0	0	0	0	0		
ENSMUST00000154740						0	0	0	0	0	0	11	1	10	0	5		
ENSMUST00000154741	ENSMUSG00000027778	3	68892499	69004570	-1	0	0	0	0	0	0	5	0	15	1	0	D3YWI8	
ENSMUST00000154742	ENSMUSG00000020564	12	33147693	33375659	1	7	14	10	6	12	10	70	188	182	6	268	D3Z7I2	
ENSMUST00000154743						0	3	10	6	2	1	2	0	4	0	7		
ENSMUST00000154744	ENSMUSG00000036890	2	44564412	44927657	-1	457	721	494	175	711	351	26	69	74	24	115	A0A0A0MQI8	
ENSMUST00000154745						0	0	0	1	0	0	0	3	3	8	0		
ENSMUST00000154746	ENSMUSG00000025576	11	118489762	118911597	-1	2	0	3	0	5	3	0	0	0	0	0	B7ZC11	
ENSMUST00000154747						6	6	5	1	0	1	4	0	0	1	0		
ENSMUST00000154748	ENSMUSG00000023088	16	14361558	14475737	1	0	1	8	21	6	2	0	0	0	0	0	D3YYJ6	
ENSMUST00000154749						4	1	9	2	1	5	0	4	0	0	3		
ENSMUST00000154750	ENSMUSG00000028096	3	96868281	96905346	-1	5	5	0	31	5	3	8	9	4	11	5	D6RI66	
ENSMUST00000154751						12	13	21	13	15	4	0	2	2	0	1		
ENSMUST00000154752						0	5	5	0	1	0	0	0	0	0	0		
ENSMUST00000154753	ENSMUSG00000026922	2	26593057	26604417	-1	1	0	1	84	4	0	4	3	9	2	9	A2AI22	
ENSMUST00000154754						0	0	0	0	0	0	0	2	1	0	0		
ENSMUST00000154755						578	605	1340	626	668	366	15	69	41	6	53		
ENSMUST00000154756	ENSMUSG00000034570	11	3494375	3504821	-1	17	8	0	0	14	0	0	0	6	3	14	A0A075B6D7	
ENSMUST00000154757	ENSMUSG00000040850	11	30771726	30880361	1	3	4	34	71	7	2	0	1	1	0	0	F6R7K9	
ENSMUST00000154758						3	1	0	0	4	4	0	0	0	0	0		
ENSMUST00000154759						2	1	0	0	2	0	0	2	2	0	0		
ENSMUST00000154760						57	35	235	90	54	25	2	3	0	0	4		
ENSMUST00000154761						1	0	1	2	0	0	0	2	0	0	5		
ENSMUST00000154762						0	0	0	1	0	3	0	0	7	0	16		
ENSMUST00000154763						1	2	1	26	1	2	0	4	0	0	1		
ENSMUST00000154764	ENSMUSG00000026971	2	60598292	60722643	-1	0	0	0	0	0	0	0	0	0	0	0	B1AYG7	
ENSMUST00000154765	ENSMUSG00000021062	12	76797960	76822908	-1	0	0	0	6	0	1	0	0	0	0	0	D3Z1A7	
ENSMUST00000154767						7	10	71	5	8	0	0	0	2	0	5		
ENSMUST00000154768						6	4	11	0	9	2	423	1859	610	3345	484		
ENSMUST00000154769	ENSMUSG00000046671	4	134525550	134535387	-1	0	0	0	0	0	0	0	0	0	0	0	D3YW54	
ENSMUST00000154770						28	55	48	41	108	33	3	7	15	5	3		
ENSMUST00000154771						3	1	3	3	1	0	0	0	0	0	0		
ENSMUST00000154772	ENSMUSG00000011958	9	69989466	70008317	1	0	0	0	24	0	0	2	5	0	8	19	D6RE50	
ENSMUST00000154773	ENSMUSG00000059834	3	41626720	41742514	-1	0	1	0	0	1	0	0	0	0	0	0	F6X8R3	
ENSMUST00000154774						3	3	6	0	10	1	342	1286	558	243	859		
ENSMUST00000154776						3	4	7	2	5	2	0	0	0	0	1		
ENSMUST00000154777						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154778						3	3	4	18	8	4	0	0	0	0	0		
ENSMUST00000154779	ENSMUSG00000035642	7	97550331	97579497	-1	2	0	0	0	3	0	0	0	0	20	0	D6RJJ4	
ENSMUST00000154780	ENSMUSG00000073130	X	71928816	71940870	1	0	0	5	0	0	4	0	0	0	0	0	I7HLZ6	
ENSMUST00000154781						2	2	0	3	5	0	0	0	3	0	2		
ENSMUST00000154782	ENSMUSG00000066129	7	139894696	139941537	1	9	16	0	0	0	0	1	0	2	0	0	F6SPU5	
ENSMUST00000154783						5	1	8	14	4	0	4	10	0	3	6		
ENSMUST00000154784						0	0	0	0	0	0	30	128	23	53	28		
ENSMUST00000154785						0	0	7	0	9	1	0	20	0	0	0		
ENSMUST00000154786	ENSMUSG00000032850	5	118190736	118245116	-1	0	0	0	23	0	3	0	0	0	0	0	D3Z0I9	
ENSMUST00000154787	ENSMUSG00000027752	3	54728678	54735393	-1	0	0	0	0	0	0	0	8	2	14	0	F6SGT4	
ENSMUST00000154788						4	2	3	2	4	4	4	0	3	0	3		
ENSMUST00000154790						0	3	0	6	5	8	4	1	11	0	6		
ENSMUST00000154791	ENSMUSG00000042626	3	89418443	89430027	1	0	0	0	0	0	0	0	0	0	0	0	D3YXZ9	
ENSMUST00000154793						0	2	0	0	0	0	1	4	2	2	12		
ENSMUST00000154794						0	2	0	2	0	0	0	0	0	0	0		
ENSMUST00000154795						3	2	0	3	1	0	0	1	0	0	0		
ENSMUST00000154796						0	0	3	3	7	4	32	53	49	8	92		
ENSMUST00000154797						3	2	2	2	5	1	5	16	20	1	25		
ENSMUST00000154799						1	1	12	1	4	0	13	27	10	21	5		
ENSMUST00000154800						0	0	0	97	5	1	0	0	2	0	0		
ENSMUST00000154801	ENSMUSG00000034145	12	87021340	87090043	1	19	11	22	11	28	9	0	0	1	0	0	D6RI74	
ENSMUST00000154802	ENSMUSG00000021376	13	47025170	47044737	-1	0	0	4	30	7	1	0	0	0	0	0	D3Z217	
ENSMUST00000154803						0	0	7	0	0	0	0	0	0	0	1		
ENSMUST00000154804						6	3	8	1	3	3	0	0	0	0	0		
ENSMUST00000154805						21	22	20	29	34	14	2	5	9	0	11		
ENSMUST00000154806						0	2	0	3	2	1	108	683	581	18	249		
ENSMUST00000154807	ENSMUSG00000046079	5	105699969	105832436	1	0	0	0	48	0	0	0	0	0	0	0	D3YV62	
ENSMUST00000154808						0	2	0	0	1	0	1	0	1	0	0		
ENSMUST00000154809	ENSMUSG00000015094	2	25399351	25409494	1	0	0	0	13	0	0	0	1	0	0	0	A2AJ19	
ENSMUST00000154811						0	1	0	6	2	0	6	0	7	3	0		
ENSMUST00000154812	ENSMUSG00000018378	11	88098058	88194140	1	6	2	33	167	11	5	0	0	11	6	30	F2Z3X3	
ENSMUST00000154814	ENSMUSG00000064284	15	85806972	85811697	-1	0	1	0	1	6	0	0	5	0	3	3	D3Z3I7	
ENSMUST00000154815						0	0	0	0	0	0	43	0	60	11	81		
ENSMUST00000154816						13	12	80	29	16	2	4	0	2	0	3		
ENSMUST00000154817						4	3	4	9	14	4	0	21	8	4	6		
ENSMUST00000154818	ENSMUSG00000053852	X	56870163	57001558	1	5	0	24	0	24	0	0	0	0	0	0		B7ZCC9
ENSMUST00000154819	ENSMUSG00000026110	1	37439340	37541016	-1	0	0	0	0	0	1	0	0	0	0	0		Q812G0
ENSMUST00000154821						0	0	0	2	0	0	1	0	1	0	0		
ENSMUST00000154822	ENSMUSG00000024694	19	12695786	12719902	1	0	0	0	0	0	0	0	0	0	0	0	D3Z1F5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154823						4	1	6	6	7	4	2	6	4	0	13		
ENSMUST00000154824	ENSMUSG00000028649	4	123349633	123684360	-1	2	0	15	0	0	0	0	534	0	65	0	F6YKN8	
ENSMUST00000154826						16	2	36	31	27	12	0	0	0	0	13		
ENSMUST00000154827	ENSMUSG00000041718	X	144317804	144374450	1	0	5	10	0	3	0	12	40	29	3	20	E9PX10	
ENSMUST00000154828						0	0	0	2	0	1	0	0	0	1	0		
ENSMUST00000154829						19	5	48	412	32	7	29	88	51	7	48		
ENSMUST00000154830						0	1	4	4	3	0	0	0	3	2	2		
ENSMUST00000154831	ENSMUSG00000047554	7	109972187	109986929	-1	0	0	0	43	2	2	0	0	5	7	6	D6RDC1	
ENSMUST00000154832						314	304	304	228	288	155	97	529	227	34	441		
ENSMUST00000154833						6	10	0	2	6	1	0	0	0	0	0		
ENSMUST00000154835	ENSMUSG00000086112	14	60087071	60096093	1	13	10	10	14	11	11	0	0	0	0	1	D3YXY1	
ENSMUST00000154836						0	0	0	0	0	0	0	32	0	9	0		
ENSMUST00000154837						0	0	0	0	0	0	802	10751	975	0	114		
ENSMUST00000154838						9	3	2	0	4	2	0	0	0	0	0		
ENSMUST00000154839						8	6	16	6	9	5	4	13	18	6	3		
ENSMUST00000154840	ENSMUSG00000005373	5	135089890	135138382	1	1	0	20	8	4	0	0	0	0	0	11	F6Q3B6	
ENSMUST00000154841	ENSMUSG00000027613	2	155819832	155826925	-1	0	6	9	0	0	0	53	176	49	25	46	D6RG53	
ENSMUST00000154842	ENSMUSG00000002279	17	25579174	25662826	1	2	0	20	4	4	1	0	0	8	0	5	F6RND1	
ENSMUST00000154843						0	0	0	5	0	0	13	68	36	8	43		
ENSMUST00000154844						3	2	2	3	2	4	0	0	0	0	0		
ENSMUST00000154845						1	0	21	9	3	2	0	0	0	0	0		
ENSMUST00000154846	ENSMUSG00000023232	4	130253495	130279205	-1	0	2	0	13	0	0	0	0	0	0	0	B2KFY2	
ENSMUST00000154847						3	0	7	0	0	3	0	6	0	0	0		
ENSMUST00000154849						3	0	0	3	3	1	0	0	0	0	0		
ENSMUST00000154850						3	0	3	0	1	0	1	1	3	0	11		
ENSMUST00000154851	ENSMUSG00000025409	10	127281956	127289018	-1	1	0	0	0	5	0	36	14	38	5	50	G3UXV1	
ENSMUST00000154852						3	0	4	0	3	0	3	4	0	3	0		
ENSMUST00000154853	ENSMUSG00000035642	7	97550331	97579497	-1	0	0	0	0	0	0	0	17	3	0	0	D3YZD8	
ENSMUST00000154855						1	1	3	0	4	0	0	0	0	0	0		
ENSMUST00000154856						0	2	0	7	0	1	8	0	5	0	0		
ENSMUST00000154857						0	3	0	2	0	0	1	0	0	0	0		
ENSMUST00000154858						3	5	3	0	3	1	7	8	19	6	4		
ENSMUST00000154859						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000154860						7	2	7	9	5	3	0	5	1	0	1		
ENSMUST00000154861						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154862						1	4	4	0	2	1	0	5	0	2	0		
ENSMUST00000154863						68	65	271	182	64	49	6	38	13	5	52		
ENSMUST00000154864	ENSMUSG00000025626	X	52912266	52956943	1	3	0	0	0	0	1	0	0	25	12	0		Q9D4J7
ENSMUST00000154865	ENSMUSG00000059456	14	66153257	66281052	-1	0	5	12	3	4	0	98	1881	60	80	107	F7CCX1	
ENSMUST00000154866	ENSMUSG00000031229	X	105797615	105929403	-1	0	0	0	0	0	0	0	0	3	0	3	A6PWK7	
ENSMUST00000154867						0	5	10	33	11	2	0	4	0	2	3		
ENSMUST00000154869						12	2	0	6	3	0	0	0	0	1	0		
ENSMUST00000154870						1431	1871	4423	1086	2244	874	26	105	72	36	128		
ENSMUST00000154871						7	3	5	1	7	0	123	261	208	4	295		
ENSMUST00000154872	ENSMUSG00000067567	X	102284639	102505359	-1	0	0	0	0	0	0	5	14	0	9	1	S4R2V6	
ENSMUST00000154873	ENSMUSG00000002249	17	28331671	28350805	-1	5	0	3	201	14	6	0	0	0	0	0	F6TTJ9	
ENSMUST00000154874	ENSMUSG00000026171	1	74593748	74601397	-1	3	0	0	0	0	0	0	3	0	0	3	D3YXC4	
ENSMUST00000154875						0	5	28	50	3	5	0	0	3	2	10		
ENSMUST00000154876	ENSMUSG00000033032	18	61730261	61786702	-1	0	0	7	0	0	12	0	5	0	11	0	D6RD10	
ENSMUST00000154877						0	0	4	0	0	0	5	0	4	0	2		
ENSMUST00000154879						0	2	0	0	4	0	4	11	7	0	0		
ENSMUST00000154880						0	0	4	2	3	2	0	3	5	0	0		
ENSMUST00000154881						21	20	25	21	16	9	11	13	12	1	11		
ENSMUST00000154882						1	0	5	3	1	3	28	34	49	2	29		
ENSMUST00000154883						3	4	9	6	9	8	10	21	5	0	22		
ENSMUST00000154884						8	1	13	5	10	2	0	0	1	0	0		
ENSMUST00000154885						0	0	0	2	1	0	0	0	0	0	1		
ENSMUST00000154886	ENSMUSG00000024979	19	55180733	55196313	1	3	1	8	4	0	3	0	0	0	0	0	D3Z273	
ENSMUST00000154887						0	7	2	1	0	2	0	7	0	0	14		
ENSMUST00000154888						0	1	5	6	8	5	3	9	10	0	17		
ENSMUST00000154889	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZCP8	
ENSMUST00000154890						4	0	23	18	14	7	25	15	12	0	21		
ENSMUST00000154891	ENSMUSG00000030815	7	127573340	127583307	1	0	0	0	0	0	0	102	327	0	0	0	D6RGU6	
ENSMUST00000154892						0	0	7	0	0	1	0	0	0	0	0		
ENSMUST00000154893						30	18	61	268	43	28	0	1	1	2	4		
ENSMUST00000154894						3	0	0	4	0	1	7	0	2	5	0		
ENSMUST00000154895	ENSMUSG00000029032	4	154278486	154301676	-1	0	2	8	9	0	4	0	0	0	0	0	B1ASH7	
ENSMUST00000154896						4	8	25	41	12	8	134	533	536	16	685		
ENSMUST00000154898						5	3	27	7	20	5	0	0	0	0	0		
ENSMUST00000154899	ENSMUSG00000026767	2	12347263	12419470	-1	1	0	0	2	0	0	42	47	17	0	29	D6RCI2	
ENSMUST00000154900						0	1	6	0	0	0	0	28	5	0	0		
ENSMUST00000154901						3	3	8	0	8	2	0	0	0	0	0		
ENSMUST00000154902	ENSMUSG00000022793	16	38742264	38769049	1	12	3	7	0	0	8	2	19	4	9	11	F2Z3X1	
ENSMUST00000154903						11	8	19	20	20	11	36	214	94	18	168		
ENSMUST00000154904	ENSMUSG00000042303	15	80977765	81012289	1	0	0	0	0	0	0	0	0	1	0	0	F6VZH1	
ENSMUST00000154905						2	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000154906	ENSMUSG00000000766	10	6758506	7038198	1	5	2	21	5	3	0	0	0	0	0	0		P42866
ENSMUST00000154907						0	0	3	124	1	3	0	0	0	0	0		
ENSMUST00000154908						3	7	6	11	2	2	4	13	16	0	14		
ENSMUST00000154909						18	19	24	22	22	8	8	16	15	9	22		
ENSMUST00000154910						0	0	0	0	0	0	5	2	11	0	7		
ENSMUST00000154911						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154912						0	0	2	0	0	1	4	47	4	21	9		
ENSMUST00000154913	ENSMUSG00000035458	7	4518305	4524229	-1	0	0	0	0	0	0	0	0	0	1	0	D3Z160	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000154914						16	13	30	46	26	7	6	29	23	12	19		
ENSMUST00000154915	ENSMUSG00000020530	11	84832361	84870817	-1	0	0	0	64	6	4	341	1585	818	369	683		Q5SV77
ENSMUST00000154916						0	0	0	109	4	0	0	0	0	0	0		
ENSMUST00000154917	ENSMUSG00000001441	11	97205842	97280638	-1	0	1	0	68	0	0	4	4	34	0	21	F2Z3V5	
ENSMUST00000154918						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154920						0	0	0	3	3	0	1	0	0	0	0		
ENSMUST00000154921	ENSMUSG00000035310	5	100441918	100500639	-1	0	0	0	15	0	4	29	0	144	62	59	E9PV28	
ENSMUST00000154922	ENSMUSG00000028232	4	3549041	3574853	-1	0	0	0	1	0	0	0	16	10	0	0		Q9D850
ENSMUST00000154923						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154924						6	8	7	11	8	0	7	38	9	13	5		
ENSMUST00000154925						4	0	1	12	2	0	0	19	5	0	3		
ENSMUST00000154926	ENSMUSG00000034591	10	83230848	83337882	-1	0	0	0	2	0	0	0	0	0	0	0	D3Z5A5	
ENSMUST00000154927						4	2	8	62	5	6	0	0	1	0	0		
ENSMUST00000154928						6	0	12	0	2	3	0	0	0	0	0		
ENSMUST00000154929	ENSMUSG00000029125	5	38038742	38137765	1	0	0	0	28	3	0	20	163	29	33	25	D3YY98	
ENSMUST00000154930						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154932	ENSMUSG00000025537	5	129863421	129898549	-1	1	2	66	5	4	3	0	0	0	0	0	D3Z1B5	
ENSMUST00000154933	ENSMUSG00000051504	7	55768178	55778925	1	2	18	46	66	7	23	0	11	3	4	0	D6RFU8	
ENSMUST00000154935	ENSMUSG00000040537	5	8072352	8368160	-1	0	0	0	0	0	0	0	0	0	0	0	F6PZ09	
ENSMUST00000154936						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000154937						0	2	0	0	1	0	0	3	0	3	3		
ENSMUST00000154938						7	3	0	31	4	0	0	4	0	0	0		
ENSMUST00000154939						8	8	0	5	0	0	0	0	0	0	0		
ENSMUST00000154940						31	21	58	54	29	20	0	3	0	0	2		
ENSMUST00000154941	ENSMUSG00000000766	10	6758506	7038198	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2X5	
ENSMUST00000154942	ENSMUSG00000074165	7	41633203	41651530	1	7	1	3	2	3	2	0	0	3	0	1	D3Z1H2	
ENSMUST00000154944						0	2	2	14	1	0	0	0	1	0	1		
ENSMUST00000154945						0	0	0	0	0	0	0	0	5	0	0		
ENSMUST00000154948						0	0	0	2	0	1	12	23	0	4	18		
ENSMUST00000154949						3	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000154950	ENSMUSG00000045983	16	20668313	20692884	1	0	0	1	6	0	0	0	0	0	0	0	D3YWC6	
ENSMUST00000154951						914	1024	782	943	1081	603	191	947	415	157	543		
ENSMUST00000154952						2	0	38	1	3	2	2	8	12	1	13		
ENSMUST00000154954						0	0	0	0	0	0	69	92	49	79	32		
ENSMUST00000154955						10	0	14	0	11	0	0	19	0	0	0		
ENSMUST00000154956	ENSMUSG00000026526	1	175600374	175625635	-1	0	0	0	35	2	0	9	37	5	0	2	H3BJV5	
ENSMUST00000154957						1	1	0	2	3	1	7	18	11	2	24		
ENSMUST00000154959	ENSMUSG00000027257	2	91255954	91264679	1	0	0	0	0	0	0	0	0	0	0	0	B1AW95	
ENSMUST00000154960						0	0	0	7	0	0	50	82	22	0	59		
ENSMUST00000154961						0	1	1	0	0	0	16	7	72	5	38		
ENSMUST00000154962	ENSMUSG00000015806	5	45434021	45450236	-1	2	2	5	0	3	0	0	0	0	0	0	D3Z1A1	
ENSMUST00000154963						0	0	0	0	0	0	4	0	0	9	10		
ENSMUST00000154964						21	21	12	23	16	8	1	2	3	0	1		
ENSMUST00000154965						2	2	0	0	1	0	2	0	0	0	0		
ENSMUST00000154967						2	1	0	5	0	0	8	14	18	10	27		
ENSMUST00000154968	ENSMUSG00000002963	7	44857139	44862992	1	0	0	0	0	0	0	0	0	0	0	0	D3YZV7	
ENSMUST00000154969						0	3	9	3	8	7	12	18	10	0	11		
ENSMUST00000154970	ENSMUSG00000041064	9	65587160	65595967	1	0	0	33	1	20	18	0	0	0	0	9	D6RFC6	
ENSMUST00000154971						269	373	199	142	279	108	6	5	8	0	3		
ENSMUST00000154972						17	23	38	44	24	13	90	193	92	50	128		
ENSMUST00000154973	ENSMUSG00000056260	3	106684987	106736577	1	0	2	0	0	0	0	2	0	0	0	0	D3Z005	
ENSMUST00000154974						10	3	43	53	14	2	24	47	49	8	37		
ENSMUST00000154975	ENSMUSG00000067367	5	38220470	38234306	1	7	3	40	0	1	1	4	0	0	43	16	D6RDT2	
ENSMUST00000154976						13	21	26	9	20	9	2	14	8	0	12		
ENSMUST00000154977						0	0	0	33	0	0	0	0	0	0	0		
ENSMUST00000154978	ENSMUSG00000061536	9	121680047	121705490	-1	1	2	9	39	9	1	5	1	4	2	3	D3Z110	
ENSMUST00000154979	ENSMUSG00000040964	4	140514485	140666012	-1	2	0	2	0	0	2	0	0	0	0	0	A8Y5U3	
ENSMUST00000154980						1	0	0	0	0	0	22	67	19	28	22		
ENSMUST00000154981						1063	643	1110	1245	1101	375	47	341	142	31	276		
ENSMUST00000154982	ENSMUSG00000024122	17	24073680	24150924	-1	3	3	1	1	4	0	0	1	0	0	2	F2Z3V6	
ENSMUST00000154983						1	2	1	26	2	3	0	1	0	0	2		
ENSMUST00000154984						0	0	0	5	3	0	0	0	0	0	0		
ENSMUST00000154985						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000154986						8	7	8	2	9	5	0	0	0	2	2		
ENSMUST00000154987	ENSMUSG00000108815	7	127785608	127803802	1	0	0	0	0	0	0	20	144	158	28	96		
ENSMUST00000154988						6	4	11	2	8	4	2	0	0	0	3		
ENSMUST00000154989						3	1	4	3	2	2	0	1	0	0	1		
ENSMUST00000154991	ENSMUSG00000042625	17	56560965	56584585	-1	9	2	7	47	10	0	17	197	69	1	89	F6Z0Y5	
ENSMUST00000154992						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000154994	ENSMUSG00000021156	13	9684836	9765321	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z4G1	
ENSMUST00000154995						0	2	1	1	6	2	15	28	45	8	33		
ENSMUST00000154996						2	0	4	3	4	1	8	40	26	9	84		
ENSMUST00000154998						19	0	45	21	0	0	10	11	11	3	38		
ENSMUST00000154999						2	0	1	4	0	0	194	991	186	297	104		
ENSMUST00000155000	ENSMUSG00000027522	2	174076308	174099771	1	2	0	4	74	6	1	9	8	13	3	19	B7ZCB9	
ENSMUST00000155001						3	0	8	0	0	0	5	5	0	0	2		
ENSMUST00000155002	ENSMUSG00000054252	5	33721674	33737068	1	0	0	0	57	6	0	0	0	0	0	0	D3Z7U5	
ENSMUST00000155003	ENSMUSG00000026696	1	162570515	162599084	1	1	3	1	18	0	1	18	77	5	4	0		O70480
ENSMUST00000155004						4	3	2	0	0	0	0	0	0	0	0		
ENSMUST00000155005	ENSMUSG00000042289	7	127800604	127803802	1	3	2	1	3	2	2	0	5	7	0	0		
ENSMUST00000155006						1	0	0	0	0	1	0	1	0	0	0		
ENSMUST00000155007	ENSMUSG00000034245	6	91156665	91174692	1	2	2	0	0	0	0	1	0	0	0	0	F6UL83	
ENSMUST00000155008						0	6	0	1	13	4	1956	6940	2608	15747	2139		
ENSMUST00000155009	ENSMUSG00000000753	11	75409769	75422701	-1	5	2	13	7	3	3	0	1	0	0	0	E9PZX2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155012						4	0	0	0	3	1	6	0	0	0	7		
ENSMUST00000155014	ENSMUSG00000044037	9	110879870	110900530	1	52	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155015						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000155016	ENSMUSG00000003279	17	69969073	70821413	1	0	3	28	0	5	6	0	0	0	0	2		Q9D415
ENSMUST00000155017						0	0	0	0	0	0	0	1	0	1	0		
ENSMUST00000155019						1	1	0	0	2	0	0	1	0	0	0		
ENSMUST00000155020	ENSMUSG00000104217	1	4807892	4886770	1	0	0	0	0	0	0	13	138	180	49	33	J3QM41	
ENSMUST00000155021	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000155022	ENSMUSG00000030204	6	135011612	135023776	1	20	18	116	29	12	8	3	25	0	0	4		
ENSMUST00000155023	ENSMUSG00000040606	4	142102390	142239401	-1	47	21	48	42	56	27	0	0	0	0	0	F6RLJ7	
ENSMUST00000155024						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155025						5	10	32	44	13	5	3	6	7	1	9		
ENSMUST00000155026						4	0	0	7	4	2	2	4	6	1	13		
ENSMUST00000155027						5	5	13	7	7	3	0	5	2	0	10		
ENSMUST00000155028						0	4	0	0	0	0	0	0	0	4	0		
ENSMUST00000155029						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000155030	ENSMUSG00000024220	17	28177207	28205886	1	4	1	0	1	0	0	17	7	16	9	14	B2KF18	
ENSMUST00000155031	ENSMUSG00000043284	11	60864452	60879272	-1	0	3	5	3	2	0	7	0	21	0	2	Z4YN74	
ENSMUST00000155033						0	0	0	0	0	0	1	12	8	15	4		
ENSMUST00000155034	ENSMUSG00000070385	3	103074014	103099720	1	11	10	8	16	10	5	0	0	0	0	0	A0A0G2JFD4	
ENSMUST00000155035	ENSMUSG00000017631	11	76416734	76622314	-1	0	5	1	52	6	2	12	6	10	0	6	Z4YN68	
ENSMUST00000155036						0	2	2	0	1	1	2	4	2	0	0		
ENSMUST00000155037	ENSMUSG00000029629	6	11907809	12081205	1	3	1	1	8	0	1	0	1	7	7	4		
ENSMUST00000155038	ENSMUSG00000013150	8	105713854	105758664	-1	0	0	14	8	4	0	3	2	0	0	2	D3Z3T3	
ENSMUST00000155039						4	3	10	6	3	3	0	14	4	1	13		
ENSMUST00000155040						2	1	0	0	2	0	0	0	2	2	0		
ENSMUST00000155041						0	0	2	98	1	0	0	2	2	0	0		
ENSMUST00000155042						12	10	25	19	16	7	0	0	0	0	0		
ENSMUST00000155043						0	2	3	0	1	0	0	0	0	0	0		
ENSMUST00000155044	ENSMUSG00000040620	11	70984091	71004437	-1	0	0	0	0	0	0	0	0	0	0	4	J3QJZ5	
ENSMUST00000155045						4	1	0	5	2	2	7	12	12	0	4		
ENSMUST00000155047	ENSMUSG00000038074	6	54577604	54597308	-1	10	0	0	0	0	0	0	0	0	0	0	D6RDT0	
ENSMUST00000155048	ENSMUSG00000040473	5	5579278	5664239	-1	0	0	0	0	0	3	0	0	0	0	2	F6WCD2	
ENSMUST00000155049						20	9	26	5	17	15	0	3	5	0	0		
ENSMUST00000155050	ENSMUSG00000002963	7	44857139	44862992	1	5	9	5	55	7	1	14	25	19	7	23		
ENSMUST00000155051	ENSMUSG00000014767	17	15499888	15528379	1	0	1	5	4	2	0	0	0	0	2	3	D3Z453	
ENSMUST00000155052						0	0	2	47	0	0	0	0	0	1	0		
ENSMUST00000155053	ENSMUSG00000020840	11	76924809	76987379	1	0	0	0	5	0	2	6	0	0	0	0	E9QA53	
ENSMUST00000155054	ENSMUSG00000022201	15	12117831	12185683	1	1	0	3	0	0	0	3	0	23	10	25	F6V459	
ENSMUST00000155055	ENSMUSG00000045636	8	40990914	41133726	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2Y9	
ENSMUST00000155056	ENSMUSG00000035547	7	98121559	98178274	-1	6	1	13	6	3	5	0	0	1	0	0	D3Z432	
ENSMUST00000155057						2	1	0	0	2	2	4	30	4	0	4		
ENSMUST00000155058						4	2	0	6	3	0	0	0	0	0	0		
ENSMUST00000155059						4	0	10	7	10	3	3	2	2	0	0		
ENSMUST00000155060	ENSMUSG00000035585	7	3692863	3701024	1	0	0	0	90	0	0	0	0	0	0	0	D6RH65	
ENSMUST00000155061						0	3	26	154	11	7	17	38	12	7	23		
ENSMUST00000155062						0	1	0	1	2	1	10	90	61	93	24		
ENSMUST00000155063						0	0	10	26	0	1	0	0	9	0	10		
ENSMUST00000155065						5	6	8	8	3	4	7	23	7	2	11		
ENSMUST00000155066						0	0	0	2	0	3	0	0	0	2	0		
ENSMUST00000155067						4	0	12	9	0	0	0	0	0	0	0		
ENSMUST00000155068	ENSMUSG00000034610	4	108459426	108559421	1	0	5	31	2	8	9	0	0	17	0	0	A0A0A0MQJ6	
ENSMUST00000155070						6	2	1	7	6	5	0	0	3	0	6		
ENSMUST00000155071						4	3	15	6	0	0	15	28	19	5	17		
ENSMUST00000155072						8	5	14	12	9	9	0	6	0	0	5		
ENSMUST00000155073						0	2	10	0	1	2	0	0	0	0	2		
ENSMUST00000155075	ENSMUSG00000049571	7	139600951	139683817	-1	22	21	68	446	31	9	0	14	4	0	1	D6RJ10	
ENSMUST00000155076						7	3	13	2	4	3	0	1	0	1	1		
ENSMUST00000155077	ENSMUSG00000026228	1	86099026	86111970	-1	2	1	0	6	3	3	0	0	0	1	0	G3UVT8	
ENSMUST00000155078	ENSMUSG00000070425	7	102065713	102096864	1	0	0	0	6	0	0	4	0	0	0	0	F6WIA6	
ENSMUST00000155079						0	1	1	2	3	1	0	0	2	0	0		
ENSMUST00000155080	ENSMUSG00000042788	4	43427019	43429134	-1	1	3	0	0	2	0	0	0	0	0	0	G3UXM7	
ENSMUST00000155081						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155082	ENSMUSG00000034903	2	65088339	65239403	-1	0	0	0	3	0	1	0	0	0	0	0	B1AZ20	
ENSMUST00000155083						20	21	21	26	37	15	98	728	122	19	128		
ENSMUST00000155084	ENSMUSG00000026211	1	75479310	75506452	-1	27	15	16	9	14	7	0	0	0	0	0	A0A0A0MQG1	
ENSMUST00000155085						0	0	0	0	0	0	0	2	0	0	2		
ENSMUST00000155086						0	0	1	0	2	0	0	50	2	5	8		
ENSMUST00000155087						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155088						1	3	0	4	3	3	0	7	0	0	4		
ENSMUST00000155089						23	27	57	27	25	16	3	2	0	3	2		
ENSMUST00000155090	ENSMUSG00000031142	X	7607083	7635196	1	18	13	14	0	0	0	0	0	0	0	0	S4R182	
ENSMUST00000155092						10	8	38	8	5	2	0	0	0	9	0		
ENSMUST00000155093						1	1	0	38	4	1	0	0	0	0	0		
ENSMUST00000155094	ENSMUSG00000026222	1	85649988	85709998	1	1	0	0	0	0	0	46	11	138	356	41		O35892
ENSMUST00000155095						2	2	24	6	6	0	0	0	0	0	0		
ENSMUST00000155096						1	0	4	0	0	8	2	0	5	0	0		
ENSMUST00000155097						19	11	41	32	38	12	0	0	0	0	0		
ENSMUST00000155098	ENSMUSG00000021493	13	55495795	55513676	-1	2	3	7	8	0	0	0	0	0	0	0		Q3TJD7
ENSMUST00000155099						22	11	50	153	35	16	225	470	204	50	189		
ENSMUST00000155100						3	3	13	7	6	0	3	8	0	0	6		
ENSMUST00000155102	ENSMUSG00000061878	11	116530925	116536674	1	0	0	1	0	0	0	0	0	0	1	0	B1AT85	
ENSMUST00000155104	ENSMUSG00000018677	11	102402985	102407946	-1	0	0	4	0	0	0	0	0	0	0	0	B0QZI3	
ENSMUST00000155105						11	8	23	173	22	14	10	15	17	2	30		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155107	ENSMUSG00000020718	11	106768253	106779537	-1	22	14	25	11	13	6	26	93	65	11	37	D6RFU3	
ENSMUST00000155108	ENSMUSG00000037286	9	100597798	100959375	1	0	0	2	0	0	0	0	31	32	11	0	D6RH50	
ENSMUST00000155109	ENSMUSG00000013698	1	172196728	172206804	-1	5	4	3	14	5	0	2	0	2	2	0	D3Z375	
ENSMUST00000155110						5	0	0	0	0	0	0	12	6	0	7		
ENSMUST00000155112	ENSMUSG00000021224	12	83794034	83921934	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1E8	
ENSMUST00000155113						2	0	3	0	0	0	0	0	1	0	0		
ENSMUST00000155114	ENSMUSG00000035984	18	34562634	34579115	-1	0	0	1	0	0	0	0	0	0	3	0	D6RHT7	
ENSMUST00000155115						85	96	270	96	99	62	23	160	64	16	93		
ENSMUST00000155116	ENSMUSG00000022283	15	36595661	36608973	-1	0	0	0	0	0	0	39	339	22	37	15	F6ZAX1	
ENSMUST00000155117						3	1	1	1	3	0	1	0	0	0	0		
ENSMUST00000155118	ENSMUSG00000005447	7	25295049	25297986	-1	0	1	0	2	2	2	0	0	0	0	0	Q8CA83	
ENSMUST00000155119						8	4	10	4	2	3	6	7	2	0	9		
ENSMUST00000155120						101	104	199	174	148	93	87	225	65	102	74		
ENSMUST00000155121						12	31	215	29	17	24	17	31	16	3	40		
ENSMUST00000155122						5	1	0	21	3	0	0	0	0	0	0		
ENSMUST00000155123	ENSMUSG00000038611	7	141228784	141262750	1	0	0	0	129	7	1	0	96	187	0	137	D6RI35	
ENSMUST00000155124						0	0	1	3	2	1	0	0	0	0	0		
ENSMUST00000155126	ENSMUSG00000005677	1	171213970	171220701	1	9	4	18	24	16	6	0	10	0	9	5	Q3UEP1	
ENSMUST00000155127						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000155128	ENSMUSG00000038797	7	80860920	80876537	1	120	214	527	51	154	52	6	0	4	6	0	D3YW76	
ENSMUST00000155129	ENSMUSG00000028896	4	132331919	132353605	-1	0	0	0	0	0	0	0	0	0	0	0	A2CER2	
ENSMUST00000155130						4	9	0	7	0	7	0	18	0	0	0		
ENSMUST00000155131						0	10	18	17	7	0	96	603	260	117	646		
ENSMUST00000155132						1	4	0	87	7	1	0	0	0	0	0		
ENSMUST00000155133						5	3	1	34	9	1	0	2	0	1	2		
ENSMUST00000155134						0	0	2	0	0	0	0	19	8	0	0		
ENSMUST00000155135						0	0	0	108	0	3	0	3	5	0	0		
ENSMUST00000155137						1	0	0	1	1	0	0	2	0	0	0		
ENSMUST00000155138	ENSMUSG00000030683	7	126950563	126970606	1	0	0	0	0	1	0	1	5	0	1	0		
ENSMUST00000155139	ENSMUSG00000032040	9	35124408	35176061	-1	0	3	0	7	6	0	0	33	1	8	22	D6RFQ0	
ENSMUST00000155140						4	3	4	3	8	4	0	0	0	0	0		
ENSMUST00000155141						1	0	3	3	1	1	0	0	0	0	0		
ENSMUST00000155142	ENSMUSG00000028760	4	137993022	138208508	1	3	1	6	1	2	5	0	0	2	0	2	A2AMI3	
ENSMUST00000155143						3	1	2	0	0	0	0	3	51	0	20		
ENSMUST00000155144						0	0	4	0	2	0	2	0	0	0	2		
ENSMUST00000155145	ENSMUSG00000030265	6	145216699	145250239	-1	0	0	1	1	0	0	0	4	0	0	2	B2KGV5	
ENSMUST00000155146						3	6	20	4	12	2	16	36	38	2	60		
ENSMUST00000155147						0	3	11	0	2	2	0	0	0	0	0		
ENSMUST00000155148						49	63	171	35	66	30	0	21	10	0	14		
ENSMUST00000155149						2	0	2	0	1	0	0	12	5	6	0		
ENSMUST00000155151	ENSMUSG00000024188	17	26252910	26285504	1	0	0	4	65	3	0	0	0	0	0	6	D3YZ82	
ENSMUST00000155152	ENSMUSG00000014195	11	100582818	100620168	-1	0	0	0	0	0	0	50	443	124	112	80	F7BTP8	
ENSMUST00000155153						6	3	25	6	4	6	1	5	2	0	9		
ENSMUST00000155154						1	9	40	97	4	2	0	0	0	2	0		
ENSMUST00000155155						2	2	5	4	2	1	2	24	5	23	2		
ENSMUST00000155157	ENSMUSG00000046862	4	143412426	143421091	1	0	0	0	0	0	0	0	0	7	0	10	A6PW91	
ENSMUST00000155158	ENSMUSG00000033768	19	6418731	6544169	1	0	0	0	0	2	0	0	0	0	0	0	F6WN33	
ENSMUST00000155160						4	2	1	1	2	1	39	30	61	5	19		
ENSMUST00000155161						16	8	0	12	11	5	12	10	4	2	12		
ENSMUST00000155162						5	3	1	3	8	0	0	1	0	0	0		
ENSMUST00000155163						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155164						2	5	14	241	11	0	0	0	0	0	1		
ENSMUST00000155167						5	3	50	24	9	4	4	18	25	0	25		
ENSMUST00000155168						5	6	8	3	4	1	0	0	0	0	0		
ENSMUST00000155169						13	9	40	6	31	15	12	53	15	19	13		
ENSMUST00000155170	ENSMUSG00000038668	4	58435255	58553898	-1	1	0	0	0	1	0	0	0	0	0	0	A2AMI9	
ENSMUST00000155171	ENSMUSG00000043410	5	106840192	106926321	-1	4	6	0	0	0	0	0	0	0	0	0	F6XQ35	
ENSMUST00000155172	ENSMUSG00000019763	10	4401915	4432388	-1	1	1	0	48	1	0	10	13	3	4	10	D3Z331	
ENSMUST00000155174						0	0	1	7	2	2	7	9	15	9	5		
ENSMUST00000155175	ENSMUSG00000031075	7	144588549	144751974	-1	3	0	6	2	5	0	0	0	0	0	0	D3Z035	
ENSMUST00000155176						0	0	5	0	5	0	0	2	0	5	2		
ENSMUST00000155177						0	0	0	50	0	0	0	0	0	0	4		
ENSMUST00000155179						1	0	0	43	1	1	0	0	0	0	0		
ENSMUST00000155181						16	15	19	8	13	11	2	4	4	1	3		
ENSMUST00000155182						3	1	2	2	0	0	0	68	11	9	14		
ENSMUST00000155183						0	0	4	0	0	0	15	3	3	0	6		
ENSMUST00000155186	ENSMUSG00000006345	10	75561604	75586200	1	0	0	0	10	0	0	108	546	89	26	121	F6V328	
ENSMUST00000155187						2	5	7	8	3	2	0	10	0	0	2		
ENSMUST00000155188	ENSMUSG00000056737	6	72544391	72562983	1	0	0	0	0	2	0	0	0	8	0	0	D3YZN3	
ENSMUST00000155189						0	0	5	114	1	0	13	1	9	0	22		
ENSMUST00000155190						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000155192						0	2	0	2	2	1	0	0	0	0	1		
ENSMUST00000155193						0	0	2	5	9	6	0	0	0	0	0		
ENSMUST00000155194						0	5	3	0	8	3	0	4	0	0	0		
ENSMUST00000155195	ENSMUSG00000043079	18	60593973	60660142	-1	6	0	0	0	0	0	1	0	0	0	0	Q3URF1	Q8CC35
ENSMUST00000155196	ENSMUSG00000026856	2	30392254	30400529	1	0	0	0	0	0	0	0	0	0	0	0	F6T220	
ENSMUST00000155197	ENSMUSG00000020435	11	3703731	3863903	-1	1	0	0	43	1	0	0	0	0	0	0	Q5F210	
ENSMUST00000155198	ENSMUSG00000026788	2	33450287	33468559	-1	0	0	0	0	2	0	0	8	0	0	0	A2AUS1	
ENSMUST00000155200	ENSMUSG00000018761	11	69656697	69662642	-1	0	0	0	0	0	0	0	0	0	0	0	Q5F2B1	
ENSMUST00000155201						171	155	260	106	164	87	0	11	0	1	6		
ENSMUST00000155202	ENSMUSG00000038533	2	154436481	154539356	1	5	4	23	58	15	1	0	0	0	0	0	F6QMQ3	
ENSMUST00000155203	ENSMUSG00000069114	3	9250602	9285333	1	49	40	223	500	50	42	4	14	5	3	10	E9Q8X5	
ENSMUST00000155204						1	1	0	0	0	0	14	164	14	0	3		
ENSMUST00000155205	ENSMUSG00000009555	2	32705784	32713076	-1	4	0	7	50	5	1	21	47	27	4	16	B0R021	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155207	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	0	0	0	0	53	132	26	A2AEB3	
ENSMUST00000155209						1	0	1	1	0	0	0	26	6	2	0		
ENSMUST00000155210						1	0	0	3	0	0	3	0	0	0	2		
ENSMUST00000155211	ENSMUSG00000084945	8	14745329	14747427	-1	2	3	3	2	3	1	0	0	0	0	0	D3Z6T9	
ENSMUST00000155212						1	1	1	2	5	1	2	3	5	0	4		
ENSMUST00000155213						8	4	16	50	0	4	7	6	17	0	16		
ENSMUST00000155214						9	3	9	7	4	2	0	0	0	0	0		
ENSMUST00000155215	ENSMUSG00000031284	X	143518591	143797796	1	0	0	10	0	0	0	0	0	0	0	0	A3KGC4	
ENSMUST00000155216	ENSMUSG00000026567	1	165485183	165576774	1	21	0	3	0	6	7	1	0	1	0	0	M0QWB5	
ENSMUST00000155218	ENSMUSG00000020428	11	42306437	42321072	-1	0	0	0	0	0	0	0	0	0	0	0		P16305
ENSMUST00000155219						8	5	17	5	7	6	0	0	0	0	0		
ENSMUST00000155220						8	9	21	18	8	5	0	0	0	0	0		
ENSMUST00000155221	ENSMUSG00000022498	16	11074911	11134650	-1	0	1	0	22	0	0	0	0	0	0	0	D6RDR0	
ENSMUST00000155222						2	3	7	2	0	0	0	10	6	5	6		
ENSMUST00000155223	ENSMUSG00000034755	X	120290259	120910619	1	0	0	0	0	0	0	0	0	0	0	0	Q2TJH9	
ENSMUST00000155225	ENSMUSG00000033728	15	76710623	76717699	1	0	0	1	59	0	0	0	0	0	0	0		
ENSMUST00000155226	ENSMUSG00000022895	16	95702075	95721051	1	2	1	0	1	0	0	1	0	46	0	182	D3Z4F9	
ENSMUST00000155227	ENSMUSG00000024816	19	5849702	5875274	-1	0	0	0	36	0	2	20	2	33	0	35	D3Z5B2	
ENSMUST00000155228						2	1	0	1	1	2	0	0	0	0	6		
ENSMUST00000155229	ENSMUSG00000038576	1	182763860	182896591	1	0	0	0	20	1	0	0	0	0	0	0	A0A0A6YY90	
ENSMUST00000155230	ENSMUSG00000070044	8	45336717	45382291	-1	0	0	0	82	1	2	0	0	1	7	17	Q8CBZ9	
ENSMUST00000155231						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155232	ENSMUSG00000028199	3	154596711	154623182	1	0	2	0	0	2	0	0	0	0	0	0	D3YUG9	
ENSMUST00000155233	ENSMUSG00000000386	16	97447035	97462907	-1	0	0	0	0	0	0	0	12	0	0	2	S4R279	
ENSMUST00000155235						4	0	0	2	0	0	0	0	0	11	14		
ENSMUST00000155236	ENSMUSG00000040599	11	71019611	71027371	1	1	0	2	0	0	0	2	0	3	0	0	A0A0G2JDA2	
ENSMUST00000155237	ENSMUSG00000026915	2	37483228	37703859	-1	4	0	2	40	7	2	0	0	6	0	0	A2BH83	
ENSMUST00000155238						1	0	0	41	2	1	0	0	0	0	0		
ENSMUST00000155239						5	4	22	85	17	2	0	0	0	0	1		
ENSMUST00000155240						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155242	ENSMUSG00000021270	12	110690605	110702728	-1	3	3	0	2	2	4	0	0	21	654	168	B7ZC50	
ENSMUST00000155243						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155244	ENSMUSG00000002980	7	19756131	19771016	-1	3	5	27	28	6	4	0	0	0	0	0	D3YTK7	
ENSMUST00000155245						4	2	5	5	8	2	0	0	0	0	0		
ENSMUST00000155246						2	0	1	4	1	0	8	9	15	0	14		
ENSMUST00000155247						37	29	22	37	42	18	2	6	10	1	14		
ENSMUST00000155248	ENSMUSG00000053367	7	6252710	6282066	1	0	0	0	1	7	2	0	0	0	0	0	F6QS57	
ENSMUST00000155249	ENSMUSG00000027111	2	71745616	71858416	1	9	5	52	14	16	9	0	0	0	0	6	F6VSK8	
ENSMUST00000155250						0	0	2	59	2	4	0	6	0	0	0		
ENSMUST00000155251	ENSMUSG00000029718	5	137605103	137613784	-1	0	0	0	0	0	0	0	0	0	0	0	D3YWH0	
ENSMUST00000155252						2	2	4	75	7	1	0	0	1	0	0		
ENSMUST00000155253						8	6	26	7	9	6	0	0	0	0	0		
ENSMUST00000155255						44	33	87	709	44	48	8	14	10	1	26		
ENSMUST00000155256	ENSMUSG00000066568	7	34344646	34393315	-1	0	0	0	0	1	0	128	230	341	62	250	F6X2V9	
ENSMUST00000155257	ENSMUSG00000028741	4	139347435	139352576	-1	2	1	7	0	0	1	8	42	13	0	13	D6RCI7	
ENSMUST00000155258	ENSMUSG00000027429	2	144556229	144590749	1	0	0	0	0	2	0	0	0	0	0	0	A2AN97	
ENSMUST00000155259						2	4	1	64	4	2	0	0	0	0	0		
ENSMUST00000155260						8	7	12	5	9	7	4	9	5	8	7		
ENSMUST00000155261	ENSMUSG00000063870	6	125095981	125130591	1	3	4	6	292	15	4	2	5	3	1	4	G5E8V7	
ENSMUST00000155262						1	3	3	3	1	1	0	0	0	0	0		
ENSMUST00000155263	ENSMUSG00000020673	12	30054659	30132624	-1	3	1	0	0	0	1	0	0	0	0	0	G3UXW8	
ENSMUST00000155264						3	2	0	12	0	0	0	0	0	0	0		
ENSMUST00000155265						0	0	0	3	2	1	5	7	0	0	13		
ENSMUST00000155266	ENSMUSG00000029499	5	110274282	110286186	-1	0	0	0	0	0	0	0	15	6	2	0	D6REH1	
ENSMUST00000155267						6	0	9	4	3	1	7	14	8	0	12		
ENSMUST00000155268						35	30	26	47	38	20	0	11	1	0	3		
ENSMUST00000155269	ENSMUSG00000026825	2	32308471	32353338	-1	0	0	0	4	0	0	0	0	0	0	0	F6RRH9	
ENSMUST00000155271						29	25	40	31	36	20	1	1	0	0	0		
ENSMUST00000155272	ENSMUSG00000029246	5	76913249	76951578	-1	13	9	25	207	32	0	10	0	24	0	0	D6RHB8	
ENSMUST00000155273	ENSMUSG00000036632	3	54735539	54751318	1	0	1	1	4	1	0	5	9	4	6	4	D6RCG2	
ENSMUST00000155274						0	0	0	1	0	0	0	183	0	10	8		
ENSMUST00000155275						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000155276						8	1	0	7	8	0	6	14	0	6	17		
ENSMUST00000155277						21	23	21	37	41	8	35	141	47	17	99		
ENSMUST00000155278	ENSMUSG00000020300	11	31872211	31935634	1	6	0	0	0	0	0	243	544	283	2	204	Q5SU47	
ENSMUST00000155279						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155280						3	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000155281	ENSMUSG00000039501	2	167035793	167063015	-1	0	4	8	2	5	0	338	116	199	0	19	A2A5R5	
ENSMUST00000155282	ENSMUSG00000034593	9	75071015	75223688	1	0	0	0	0	0	0	386	333	894	0	361	D3Z4J3	
ENSMUST00000155283	ENSMUSG00000023443	X	137115397	137122083	-1	1	0	0	2	1	2	0	0	0	0	0	G3UXJ1	
ENSMUST00000155284	ENSMUSG00000019854	10	18055861	18125155	1	2	2	5	37	0	2	0	69	50	0	0	D6RIN6	
ENSMUST00000155285	ENSMUSG00000020184	10	117688888	117710758	-1	43	41	258	0	37	28	362	2164	188	82	290	J3QP04	
ENSMUST00000155286						0	0	18	3	0	0	8	32	6	0	7		
ENSMUST00000155287						5	1	21	2	9	5	32	57	7	12	14		
ENSMUST00000155288						4	1	12	4	10	8	0	125	31	34	44		
ENSMUST00000155289	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	12	0	0	0	0	Q5GMH1	
ENSMUST00000155290						4	2	4	0	1	0	0	0	0	0	0		
ENSMUST00000155291						0	2	0	0	0	1	6	17	10	1	12		
ENSMUST00000155293						0	0	1	0	0	0	0	0	0	2	3		
ENSMUST00000155294	ENSMUSG00000073006	X	107945735	107948465	-1	0	1	0	0	0	0	0	0	0	0	0	B1ATX8	
ENSMUST00000155295						0	2	13	10	4	5	6	2	5	0	0		
ENSMUST00000155296						0	0	0	3	0	0	86	281	47	210	21		
ENSMUST00000155297						0	0	6	0	0	0	0	0	0	0	0		
ENSMUST00000155298						43	38	176	614	49	23	1	11	1	0	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155299						1	1	1	0	4	0	0	0	0	1	0		
ENSMUST00000155300	ENSMUSG00000067367	5	38220470	38234306	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5X8	
ENSMUST00000155301	ENSMUSG00000066892	9	20618118	20644767	-1	2	1	1	3	4	0	1	1	1	0	0	D3YWZ8	
ENSMUST00000155303						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155304						1	1	1	2	0	3	2	15	10	0	0		
ENSMUST00000155305						3	1	15	7	7	3	11	8	1	0	0		
ENSMUST00000155306						0	0	0	0	6	0	0	0	0	0	0		
ENSMUST00000155307						3	4	25	2	3	2	0	0	0	0	0		
ENSMUST00000155308	ENSMUSG00000059974	9	28994750	29963141	-1	0	3	0	1	0	0	0	0	0	0	0	F6RQ26	
ENSMUST00000155309	ENSMUSG00000028132	3	121201761	121283098	-1	6	4	19	4	13	2	0	5	4	0	6		Q8CGF5
ENSMUST00000155310						0	0	2	212	12	0	0	3	0	0	0		
ENSMUST00000155311	ENSMUSG00000001827	7	101858331	101870788	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q3D3	
ENSMUST00000155312						17	9	61	30	20	4	0	0	2	0	4		
ENSMUST00000155313	ENSMUSG00000030796	7	45215753	45233635	1	0	2	0	9	0	0	0	0	1	0	2	E9Q9U3	
ENSMUST00000155314	ENSMUSG00000058028	7	6222278	6239423	1	3	0	0	0	1	0	0	0	0	0	0	D3Z0V0	
ENSMUST00000155315						0	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000155316	ENSMUSG00000020400	11	54910785	54962917	-1	0	0	0	45	4	1	0	2	2	0	2	D3Z410	
ENSMUST00000155318						11	9	9	16	16	0	0	0	0	0	0		
ENSMUST00000155320	ENSMUSG00000031074	7	144838083	144844436	1	0	0	0	35	0	0	1	0	0	0	0	D3YWD4	
ENSMUST00000155321	ENSMUSG00000029416	5	127595664	127632897	-1	0	0	0	5	2	0	0	0	0	0	0	D3Z5E9	
ENSMUST00000155322						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155324						49	48	82	87	52	27	2	2	4	0	6		
ENSMUST00000155325						3	3	20	8	7	5	178	195	115	85	110		
ENSMUST00000155326						2	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000155327						8	4	12	35	11	9	35	125	105	5	146		
ENSMUST00000155328						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000155329	ENSMUSG00000024483	18	36559987	36665917	1	0	21	0	8	1	7	207	18	555	10	372	E9PUR0	
ENSMUST00000155330						1	1	4	21	2	2	0	2	0	2	0		
ENSMUST00000155331						28	14	71	36	29	19	60	138	38	5	73		
ENSMUST00000155333						1	0	0	57	0	0	0	0	2	0	0		
ENSMUST00000155335						3	0	0	1	1	0	0	1	0	0	0		
ENSMUST00000155336						6	0	24	8	12	7	3	35	3	3	9		
ENSMUST00000155338						0	8	0	9	5	5	0	0	0	4	0		
ENSMUST00000155339						3	0	0	3	4	0	0	7	0	0	14		
ENSMUST00000155340						0	4	1	3	2	1	30	113	50	8	47		
ENSMUST00000155341						5	8	7	5	9	1	7	3	11	0	27		
ENSMUST00000155342	ENSMUSG00000029217	5	72755716	72868483	-1	8	8	27	0	0	0	0	131	0	79	71	F6W1T9	
ENSMUST00000155343						2	2	7	4	5	4	0	9	6	0	5		
ENSMUST00000155344						4	2	0	0	0	1	0	5	3	0	7		
ENSMUST00000155346	ENSMUSG00000028687	4	116807723	116819440	1	0	0	0	0	0	0	4	2	5	1	0	E9Q9J3	
ENSMUST00000155347	ENSMUSG00000027610	2	155563181	155592810	-1	7	4	5	39	6	1	0	0	0	0	0	A2AQN9	
ENSMUST00000155348	ENSMUSG00000024011	17	29318877	29329413	1	42	42	121	103	53	23	399	1373	469	25	434	F6QYZ5	
ENSMUST00000155351						5	9	14	5	17	9	19	40	50	10	68		
ENSMUST00000155352						2	1	0	32	2	1	0	2	2	1	4		
ENSMUST00000155354	ENSMUSG00000036940	4	136550540	136602723	-1	0	0	1	0	1	0	10	5	4	0	0	F6ZC60	
ENSMUST00000155355						4	2	4	3	3	1	0	0	0	1	1		
ENSMUST00000155356	ENSMUSG00000004113	2	24603887	24763152	-1	0	0	0	0	2	2	0	0	0	0	1	F7C9S8	
ENSMUST00000155357						0	0	0	0	0	0	0	0	2	0	16		
ENSMUST00000155358	ENSMUSG00000049583	7	87602544	88134907	1	0	5	2	128	12	5	0	0	0	0	0	F6YJ89	
ENSMUST00000155359						0	0	0	0	0	0	1	0	1	0	0		
ENSMUST00000155360						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155361						2	4	3	8	4	5	0	0	0	0	0		
ENSMUST00000155362	ENSMUSG00000035266	5	100762145	100798598	-1	4	0	9	2	2	1	0	3	2	0	5	F6VYI2	
ENSMUST00000155363						9	16	11	18	11	12	1	0	1	0	0		
ENSMUST00000155364	ENSMUSG00000023861	17	8282904	8297661	1	0	0	2	28	0	0	411	335	264	1115	225	Q3UX28	P63030
ENSMUST00000155365	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	0	0	0	0	0	0	0	0	A2AT66	
ENSMUST00000155366						3	2	12	5	10	3	0	0	0	0	0		
ENSMUST00000155367	ENSMUSG00000016495	19	29348599	29367390	-1	2	2	5	8	3	2	4	79	26	22	30	D3YY76	
ENSMUST00000155368						215	267	984	365	227	120	9	40	23	3	32		
ENSMUST00000155369	ENSMUSG00000037475	X	41794991	41920674	-1	0	1	0	0	0	0	0	0	0	0	0	B8A4C2	
ENSMUST00000155370	ENSMUSG00000005881	2	156008045	156018279	1	0	5	0	0	0	0	70	110	0	0	0	F6RK81	
ENSMUST00000155371						4	6	4	0	9	2	18	116	4	8	16		
ENSMUST00000155372						2	5	2	0	0	0	7	17	11	16	10		
ENSMUST00000155373						2	0	0	2	0	1	0	0	0	0	0		
ENSMUST00000155375						51	26	66	315	57	47	0	1	1	0	3		
ENSMUST00000155376						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000155377						4	4	16	7	2	3	46	347	38	0	48		
ENSMUST00000155378	ENSMUSG00000030264	6	113046225	113068273	1	0	0	3	16	0	0	19	24	13	68	19	D3YYB2	
ENSMUST00000155379	ENSMUSG00000042726	5	121371725	121385632	-1	2	0	7	0	3	0	2	0	0	0	0	D3YX05	
ENSMUST00000155380						0	2	0	2	0	0	1	1	1	0	4		
ENSMUST00000155381	ENSMUSG00000017639	11	79591212	79698023	1	0	0	0	111	4	0	9	7	23	1	40	F6YI06	
ENSMUST00000155383						7	9	11	8	7	3	0	4	1	0	3		
ENSMUST00000155385	ENSMUSG00000028199	3	154596711	154623182	1	2	3	17	5	12	5	0	0	0	0	0	D3Z4Q4	
ENSMUST00000155386	ENSMUSG00000020564	12	33147693	33375659	1	3	0	0	1	5	1	1	1	4	1	8	D3Z095	
ENSMUST00000155387	ENSMUSG00000003531	16	18052860	18071632	1	4	6	9	45	6	6	6	14	3	0	5	D3YUN0	
ENSMUST00000155389	ENSMUSG00000028952	4	152019774	152027671	-1	0	3	0	41	0	3	7	0	5	0	8		Q1H9T6
ENSMUST00000155391	ENSMUSG00000028689	4	116708509	116751206	1	0	0	0	0	7	0	10	46	8	23	12	I6L983	
ENSMUST00000155392	ENSMUSG00000054280	5	32789820	32854256	-1	2	0	12	15	12	0	3	0	27	0	100	F6RN94	
ENSMUST00000155393						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155394						0	0	0	0	0	5	0	0	0	2	0		
ENSMUST00000155395						5	1	2	1	1	2	0	0	0	0	0		
ENSMUST00000155396						0	2	0	2	2	0	0	0	0	0	0		
ENSMUST00000155397						0	0	0	0	0	0	16	0	19	0	0		
ENSMUST00000155398						3	2	7	0	0	2	2	0	2	0	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155399						2	2	3	3	0	0	4	4	9	12	29		
ENSMUST00000155400						5	6	4	3	4	3	0	4	8	0	6		
ENSMUST00000155401						0	4	0	0	7	4	0	0	0	0	0		
ENSMUST00000155403						6	6	6	51	15	10	0	1	1	0	1		
ENSMUST00000155404						8	13	40	11	12	5	0	0	0	0	0		
ENSMUST00000155405	ENSMUSG00000024869	19	4000580	4005816	1	30	31	65	80	52	30	12	54	13	0	27		Q9CR24
ENSMUST00000155406						0	2	2	0	2	0	5	0	23	97	22		
ENSMUST00000155407	ENSMUSG00000024331	18	20030633	20059554	-1	1	3	3	0	0	5	0	0	0	0	0	F6RM34	
ENSMUST00000155408						2	5	4	0	10	9	0	1	22	0	0		
ENSMUST00000155409	ENSMUSG00000048038	2	26271646	26294557	-1	0	3	8	5	8	1	0	0	0	0	0	F6VE79	
ENSMUST00000155410						0	0	0	0	0	0	47	31	61	55	38		
ENSMUST00000155411	ENSMUSG00000019822	10	41485642	41490369	-1	1	0	1	1	1	0	5	31	12	0	9	D6RGM4	
ENSMUST00000155412						1	2	0	10	5	0	0	3	6	0	9		
ENSMUST00000155413	ENSMUSG00000008318	7	100845848	100863446	-1	20	7	34	18	21	9	1170	1404	831	174	810	D6RIM1	
ENSMUST00000155414						1	0	2	0	0	0	0	0	0	0	4		
ENSMUST00000155415	ENSMUSG00000016487	6	146888487	147032025	1	2	0	4	1	4	0	1	0	0	0	3	F6S1C4	
ENSMUST00000155416						41	37	265	91	31	23	1	5	1	0	1		
ENSMUST00000155417						1	3	0	2	2	2	9	0	4	0	16		
ENSMUST00000155418	ENSMUSG00000002103	2	91202885	91214098	1	0	0	0	0	0	0	0	0	19	0	0	B7ZCF4	
ENSMUST00000155419	ENSMUSG00000030711	7	126672865	126676432	-1	2	1	8	3	3	1	3	0	1	0	0	D3Z2P8	
ENSMUST00000155420						2	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000155421						33	28	120	44	45	25	6	14	3	0	6		
ENSMUST00000155422						0	10	21	34	8	0	1	0	0	0	0		
ENSMUST00000155423						7	1	11	12	8	4	0	0	0	0	0		
ENSMUST00000155424						2	0	2	2	2	2	0	1	0	0	0		
ENSMUST00000155425	ENSMUSG00000016356	2	180986535	181017540	1	0	0	0	5	0	0	0	14	2	0	9	F6ZZM4	
ENSMUST00000155426						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000155428						5	0	5	29	0	0	0	4	0	0	0		
ENSMUST00000155429						3	0	6	1	7	2	0	0	3	0	3		
ENSMUST00000155430	ENSMUSG00000074812	2	128591209	128598464	1	6	3	0	5	8	3	0	0	0	0	0	A2AQG6	
ENSMUST00000155431						6	0	5	25	0	0	41	12	59	19	5		
ENSMUST00000155433	ENSMUSG00000047866	8	86624043	86723873	1	35	27	96	54	20	10	28	42	39	4	37		Q9DBN5
ENSMUST00000155434						1	2	2	2	2	0	4	286	31	20	67		
ENSMUST00000155435	ENSMUSG00000059820	9	50605240	50617464	-1	0	0	0	0	0	0	13	24	26	17	14	D3YU88	
ENSMUST00000155436						1	1	5	0	2	4	14	0	62	0	44		
ENSMUST00000155437						3	1	5	0	6	4	0	0	0	0	0		
ENSMUST00000155438						2	1	5	3	2	0	0	0	5	0	0		
ENSMUST00000155439						0	3	0	0	2	0	5	22	4	29	3		
ENSMUST00000155440						3	4	10	3	3	1	3	57	25	11	29		
ENSMUST00000155441						0	3	2	3	0	1	4	2	2	1	4		
ENSMUST00000155442						0	0	0	0	0	0	8	25	0	2	0		
ENSMUST00000155443						0	0	2	3	0	0	0	0	0	0	0		
ENSMUST00000155445						0	0	0	2	0	0	0	1	2	0	1		
ENSMUST00000155446						164	285	154	81	122	90	28	153	77	275	107		
ENSMUST00000155447						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155448	ENSMUSG00000012609	12	85824659	86061893	1	0	3	0	0	0	0	0	23	24	0	0		Q8CHB8
ENSMUST00000155449						1	2	1	60	1	1	1	0	0	0	0		
ENSMUST00000155450	ENSMUSG00000027506	3	8925593	9004723	-1	0	0	5	0	1	1	3	3	2	0	4	D6RJ37	
ENSMUST00000155451						0	0	0	0	0	1	2	0	4	0	0		
ENSMUST00000155452	ENSMUSG00000022956	16	91684398	91931687	-1	0	4	0	0	0	0	46	145	0	200	29	F6XVM5	
ENSMUST00000155453						0	1	0	0	1	0	12	56	8	6	5		
ENSMUST00000155454						0	1	10	0	0	0	0	0	0	0	1		
ENSMUST00000155456	ENSMUSG00000029994	6	86736840	86793584	-1	0	0	0	0	0	0	0	27	4	85	14	F7ANV6	
ENSMUST00000155457						13	12	13	205	12	10	0	0	0	0	0		
ENSMUST00000155458						11	7	25	24	22	14	0	0	0	0	0		
ENSMUST00000155459	ENSMUSG00000021699	13	108449948	109953461	1	0	1	1	0	1	0	0	0	0	0	0	F6YIS2	
ENSMUST00000155460						23	17	53	4	17	11	13	62	20	10	28		
ENSMUST00000155461						4	5	9	23	5	0	120	0	165	0	94		
ENSMUST00000155463						4	2	26	29	2	0	2	2	1	0	5		
ENSMUST00000155464						0	0	0	0	0	0	0	3	0	4	0		
ENSMUST00000155465						0	0	0	0	2	0	0	0	0	2	0		
ENSMUST00000155466	ENSMUSG00000030068	6	99257484	99666797	-1	14	16	27	11	17	11	0	1	1	0	0	H3BJN7	
ENSMUST00000155467						0	0	6	5	10	0	0	0	0	0	0		
ENSMUST00000155468						2	0	12	3	3	7	0	12	0	1	2		
ENSMUST00000155469						0	3	3	0	0	6	0	0	0	0	0		
ENSMUST00000155470	ENSMUSG00000027355	2	116878691	116892494	1	0	6	0	5	0	2	0	0	0	0	0		
ENSMUST00000155471						3	2	24	11	4	3	16	21	0	0	5		
ENSMUST00000155473						2	6	3	0	0	5	5	0	1	1	21		
ENSMUST00000155474						1	1	0	3	4	0	0	12	1	2	1		
ENSMUST00000155476						8	4	5	4	3	0	0	0	0	2	3		
ENSMUST00000155477						0	0	0	0	1	2	31	4	90	0	34		
ENSMUST00000155478	ENSMUSG00000040350	11	48826140	48852209	1	62	45	15	943	95	57	1	2	2	0	8	B2RR25	
ENSMUST00000155479						1	0	2	1	3	0	0	11	14	6	16		
ENSMUST00000155480	ENSMUSG00000076432	12	21390071	21417637	-1	0	2	0	0	0	0	252	1075	181	238	95	F6YY69	
ENSMUST00000155483						1	5	0	1	2	2	5	27	15	4	25		
ENSMUST00000155484						5	1	13	11	3	7	0	0	2	0	0		
ENSMUST00000155485	ENSMUSG00000068876	3	94760069	94786492	-1	29	16	41	59	37	14	0	0	0	0	0	A0A0G2JEK8	
ENSMUST00000155486	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	0	0	0	0	204	107	563	0	273	Q5RIN0	
ENSMUST00000155487	ENSMUSG00000038212	13	65064663	65112982	-1	0	0	0	143	7	0	40	309	452	286	309		Q8CIA9
ENSMUST00000155488						7	0	0	2	5	6	0	0	0	0	0		
ENSMUST00000155490	ENSMUSG00000020935	11	102994047	103028333	-1	4	0	0	0	5	3	75	63	25	1	10	B0QZX9	
ENSMUST00000155491	ENSMUSG00000047843	5	144244437	144446757	1	2	2	4	0	1	1	0	0	0	0	0	Q8C7X8	
ENSMUST00000155492	ENSMUSG00000012211	12	113074502	113088917	1	0	0	0	0	0	0	0	0	0	0	0	D3YZ63	
ENSMUST00000155493	ENSMUSG00000020745	11	74673949	74724670	-1	0	3	0	2	2	0	123	108	13	4	0	Q5SW16	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155494	ENSMUSG00000039841	6	28239927	28398005	-1	0	0	2	35	0	0	5	5	0	7	4	D3YZL3	
ENSMUST00000155495	ENSMUSG00000049606	5	106616739	106697287	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z1E4	
ENSMUST00000155497						15	17	30	118	20	7	197	1644	370	276	685		
ENSMUST00000155500	ENSMUSG00000019173	11	100715009	100738215	-1	1	1	0	4	1	0	1	1	3	1	8	A2A5F6	
ENSMUST00000155501						0	0	0	77	0	0	0	0	0	0	0		
ENSMUST00000155502						3	0	2	3	3	0	0	0	1	0	6		
ENSMUST00000155503	ENSMUSG00000016262	1	192844488	192855756	-1	2	1	0	1	0	0	0	0	0	0	0	A0A0A6YXT5	
ENSMUST00000155506						0	1	0	56	4	0	2	0	0	0	0		
ENSMUST00000155507						24	11	67	18	27	17	296	677	431	68	885		
ENSMUST00000155509						8	14	38	26	19	9	1	2	0	0	6		
ENSMUST00000155510	ENSMUSG00000032815	8	123268300	123318576	-1	4	0	0	0	0	0	3	0	0	1	0	D3YZ28	
ENSMUST00000155511	ENSMUSG00000079235	9	121797627	121839461	-1	0	0	0	0	0	1	0	2	0	0	0	F6RL14	
ENSMUST00000155512						9	2	17	59	12	8	67	253	123	15	122		
ENSMUST00000155513						2	4	17	2	2	1	0	2	0	0	0		
ENSMUST00000155514						4	0	4	0	0	0	7	70	38	0	48		
ENSMUST00000155515	ENSMUSG00000022772	16	31962506	32003287	-1	2	0	0	0	2	0	0	8	0	0	0	F7A4L2	
ENSMUST00000155516	ENSMUSG00000055371	2	52691664	52742281	-1	2	1	0	4	0	0	0	0	0	0	0	Q3YEC8	
ENSMUST00000155517						2	2	0	62	1	2	50	246	100	5	23		
ENSMUST00000155518						7	7	11	3	13	11	1	0	3	0	0		
ENSMUST00000155519	ENSMUSG00000040728	4	11331933	11386783	-1	11	5	10	8	14	11	0	0	0	0	0	Z4YMQ5	
ENSMUST00000155520	ENSMUSG00000005687	3	103171655	103179166	1	0	0	0	0	0	0	49	256	95	48	56	D6RHR7	
ENSMUST00000155521						9	6	15	10	12	10	1	9	5	0	2		
ENSMUST00000155522	ENSMUSG00000028391	4	62448653	62470896	-1	0	0	0	17	2	0	0	0	0	0	0	B7ZCH5	
ENSMUST00000155523						69	36	378	82	46	37	6	20	6	0	9		
ENSMUST00000155524						1	1	5	2	0	1	3	32	2	4	6		
ENSMUST00000155525						3	2	3	1	2	0	0	9	0	9	11		
ENSMUST00000155526						5	0	6	1	2	0	0	4	0	4	0		
ENSMUST00000155527	ENSMUSG00000036510	8	99024471	99416471	-1	8	0	0	0	4	7	0	0	0	0	0	E9Q451	
ENSMUST00000155529	ENSMUSG00000020251	10	82650433	82690650	-1	0	0	0	0	0	4	0	0	0	0	0	H3BJ56	
ENSMUST00000155530	ENSMUSG00000026767	2	12347263	12419470	-1	0	0	0	0	0	0	86	85	0	20	32	D6RGT9	
ENSMUST00000155532						1	3	7	0	2	1	0	7	2	3	15		
ENSMUST00000155533	ENSMUSG00000030450	7	56239760	56536518	1	4	4	0	4	7	3	0	0	0	0	0		
ENSMUST00000155534	ENSMUSG00000037974	7	141788972	141819231	1	187	118	951	269	264	98	0	0	0	0	0	E9QAQ8	
ENSMUST00000155535	ENSMUSG00000027583	2	181387762	181459426	-1	1	1	4	2	1	1	0	0	0	0	0	E0CZ94	
ENSMUST00000155537						13	5	45	13	14	3	3	9	7	0	7		
ENSMUST00000155538						3	4	13	0	0	0	0	8	0	0	4		
ENSMUST00000155539						3	4	2	2	8	3	3	8	6	0	9		
ENSMUST00000155543	ENSMUSG00000030272	6	113334124	113343984	-1	0	0	0	5	4	1	0	0	0	0	0	D3Z368	
ENSMUST00000155544						25	22	63	32	38	14	0	5	0	0	0		
ENSMUST00000155546						3	0	12	72	13	0	0	0	0	0	0		
ENSMUST00000155547						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000155548						0	2	0	67	0	0	0	1	0	0	0		
ENSMUST00000155551	ENSMUSG00000035572	4	45342101	45379759	1	62	56	110	47	79	32	165	546	256	32	190		A2AKB9
ENSMUST00000155552						0	0	0	0	0	0	0	54	38	27	50		
ENSMUST00000155553						0	0	3	15	0	0	0	3	0	2	0		
ENSMUST00000155554						3	5	22	4	3	5	6	4	7	0	11		
ENSMUST00000155555						158	124	766	235	117	54	31	20	48	2	77		
ENSMUST00000155556						2	7	16	3	6	5	0	0	0	0	1		
ENSMUST00000155557						0	3	6	2	6	2	14	35	21	3	36		
ENSMUST00000155558						34	36	135	41	42	28	0	7	7	0	11		
ENSMUST00000155559	ENSMUSG00000020614	11	109669749	109722279	-1	22	13	39	62	26	11	0	0	0	11	17		Q8CID3
ENSMUST00000155560						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155561						16	14	45	23	24	7	0	0	0	0	0		
ENSMUST00000155563						0	0	2	2	1	0	0	0	0	0	0		
ENSMUST00000155564	ENSMUSG00000031565	8	25513654	25575714	1	3	1	0	1	3	0	0	0	0	0	0	D3YW77	
ENSMUST00000155565						24	28	48	26	40	18	2	3	0	0	2		
ENSMUST00000155566						18	20	128	32	21	19	77	554	160	58	295		
ENSMUST00000155567						0	0	0	0	0	0	0	4	0	0	0		
ENSMUST00000155568	ENSMUSG00000033526	2	121310561	121355396	-1	0	0	0	0	0	0	0	0	0	0	0	F6Q5C6	
ENSMUST00000155569						0	4	8	0	0	0	66	0	101	0	58		
ENSMUST00000155570	ENSMUSG00000027238	2	121545529	121807087	-1	0	0	0	0	0	0	0	2	0	0	0	B0R0D5	
ENSMUST00000155571	ENSMUSG00000037750	11	78094660	78156700	1	15	15	24	138	24	15	140	247	228	0	244		Q6P539
ENSMUST00000155572	ENSMUSG00000030650	7	118597297	118675086	1	624	788	258	383	754	384	19	33	32	4	24	D3Z0S8	
ENSMUST00000155573	ENSMUSG00000048668	6	128357000	128362911	-1	10	11	23	12	12	10	8	21	7	0	5	D3YUX9	
ENSMUST00000155575	ENSMUSG00000019132	13	24801657	24814013	1	0	0	0	0	0	0	72	611	439	51	190	B7FAT3	
ENSMUST00000155576	ENSMUSG00000036452	18	38601534	39376284	1	2	1	13	15	0	2	486	442	815	23	636	E9QAQ3	
ENSMUST00000155577	ENSMUSG00000001082	5	34633642	34637212	-1	0	0	0	0	0	6	5	5	17	0	0	D3YWD5	
ENSMUST00000155579	ENSMUSG00000016262	1	192844488	192855756	-1	0	0	0	84	13	13	0	0	0	0	0		A7DTG3
ENSMUST00000155580	ENSMUSG00000043131	6	83326016	83343776	1	2	0	0	12	4	1	0	0	3	0	0		
ENSMUST00000155581						4	6	2	71	4	2	0	0	0	0	0		
ENSMUST00000155582						12	4	6	31	7	2	27	168	67	14	113		
ENSMUST00000155583						4	0	5	0	4	0	0	0	0	0	0		
ENSMUST00000155584						1	0	0	0	0	0	4	4	7	0	0		
ENSMUST00000155585						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155586	ENSMUSG00000036053	2	52857860	53134202	1	0	0	0	0	0	0	6	8	5	1	0	A2AQW2	
ENSMUST00000155587	ENSMUSG00000026103	1	52163448	52233232	-1	1	1	0	0	0	0	136	417	119	63	149	F6U529	
ENSMUST00000155589						1	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000155590						25	20	54	25	40	17	1	0	1	0	2		
ENSMUST00000155592	ENSMUSG00000006335	7	3620324	3629929	-1	0	1	16	0	0	3	71	71	119	28	27		Q3U1J1
ENSMUST00000155593						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000155594	ENSMUSG00000041180	19	36554639	36621135	1	0	0	0	0	0	0	0	0	0	0	0	D6RI27	
ENSMUST00000155595						0	2	5	0	0	2	0	23	0	0	0		
ENSMUST00000155596						4	3	2	4	3	4	0	0	1	2	0		
ENSMUST00000155597	ENSMUSG00000031387	X	73922121	73930850	-1	0	0	0	0	0	0	0	0	35	0	4	D6RHA2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155598	ENSMUSG00000028962	5	24423837	24440950	1	0	0	0	0	0	0	0	0	0	0	0	D3YUF1	
ENSMUST00000155599						0	0	14	16	2	3	19	6	0	12	5		
ENSMUST00000155600						0	1	2	1	0	0	0	0	0	0	0		
ENSMUST00000155601	ENSMUSG00000036833	2	24976033	25054057	1	0	0	4	1	0	0	61	467	133	33	111	F6UDU9	
ENSMUST00000155602	ENSMUSG00000026781	2	23068168	23114510	1	4	3	13	19	6	1	0	0	23	3	0	Z4YM84	
ENSMUST00000155603						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155604						0	0	11	2	3	0	18	211	31	9	36		
ENSMUST00000155605						0	5	0	110	11	1	34	246	660	200	2084		
ENSMUST00000155606	ENSMUSG00000020151	10	116018213	116274932	1	5	0	5	0	5	3	0	14	9	7	5		Q62132
ENSMUST00000155607						8	0	10	39	4	5	14	0	0	4	0		
ENSMUST00000155608						54	38	83	45	60	25	5	46	12	1	36		
ENSMUST00000155609						4	3	0	0	0	2	0	0	0	43	0		
ENSMUST00000155611						1	1	0	55	2	3	18	2	12	5	11		
ENSMUST00000155612	ENSMUSG00000013936	5	122100951	122113472	1	0	0	0	2	0	0	0	0	0	0	0	D3YUI7	
ENSMUST00000155613						5	3	3	0	2	2	0	0	3	2	8		
ENSMUST00000155614						12	19	73	34	29	13	2	8	9	0	10		
ENSMUST00000155615						0	2	2	0	0	0	0	0	0	0	0		
ENSMUST00000155616						3	2	6	37	10	6	17	428	57	0	63		
ENSMUST00000155618						0	1	1	16	1	1	1	2	6	0	4		
ENSMUST00000155620						6	7	7	6	2	4	0	3	4	0	2		
ENSMUST00000155623						1	1	3	2	1	0	9	0	4	0	0		
ENSMUST00000155624						2	2	0	2	7	0	0	0	0	0	0		
ENSMUST00000155625						10	5	3	11	3	8	0	0	5	0	4		
ENSMUST00000155626						1	3	0	4	6	3	53	298	145	70	154		
ENSMUST00000155627						27	15	58	181	32	27	0	0	0	0	0		
ENSMUST00000155628	ENSMUSG00000003534	17	35681567	35704621	-1	2	0	31	15	2	0	0	0	0	0	0	G3UXE5	
ENSMUST00000155629						4	0	3	1	0	2	1	10	4	3	3		
ENSMUST00000155630	ENSMUSG00000020774	11	73304992	73329596	-1	2	1	0	2	0	0	0	0	0	0	0	V9GXG0	
ENSMUST00000155631	ENSMUSG00000074673	2	152962485	153008482	1	0	0	0	1	0	1	0	0	0	0	0	Z4YLM0	
ENSMUST00000155632						3	2	0	3	3	0	2	0	0	0	0		
ENSMUST00000155633	ENSMUSG00000068663	16	10545339	10744878	1	36	13	0	0	38	6	577	828	735	72	598		Q80U30
ENSMUST00000155634	ENSMUSG00000005107	5	38349273	38503143	-1	6	12	16	0	8	0	23	60	45	0	56	B9EHN5	
ENSMUST00000155635						12	13	45	8	13	6	40	230	0	47	51		
ENSMUST00000155636						3	2	40	15	10	4	0	0	0	0	1		
ENSMUST00000155637						190	105	527	685	122	94	0	0	0	0	0		
ENSMUST00000155638	ENSMUSG00000014313	15	35925886	35938246	-1	1	1	15	2	2	0	2	12	0	7	4	A0A0G2JDA6	
ENSMUST00000155639						0	0	0	0	0	0	26	118	50	0	22		
ENSMUST00000155640	ENSMUSG00000034998	17	88440711	88490533	1	2	0	0	9	2	0	4	2	9	3	19	D3Z6Z3	
ENSMUST00000155642	ENSMUSG00000029026	4	154056253	154140208	-1	4	6	13	34	6	1	0	0	0	0	0	H3BK76	
ENSMUST00000155643						2	2	3	10	2	2	0	0	0	2	1		
ENSMUST00000155644						2	0	10	16	3	0	0	0	0	0	0		
ENSMUST00000155645						2	0	0	0	1	1	0	0	3	0	3		
ENSMUST00000155646						0	0	0	22	1	1	0	0	0	0	0		
ENSMUST00000155647						8	13	11	8	12	7	1	5	3	0	3		
ENSMUST00000155648						2	0	0	2	0	1	0	0	0	5	0		
ENSMUST00000155649	ENSMUSG00000014074	16	32277459	32301434	1	2	0	0	214	0	0	0	0	6	5	4	E9Q0M6	
ENSMUST00000155650	ENSMUSG00000044252	18	12755314	12941841	-1	0	0	0	2	0	0	0	0	0	0	0	D3YZ66	
ENSMUST00000155651						20	12	12	90	13	6	0	0	0	0	0		
ENSMUST00000155652						0	2	0	1	1	0	0	0	0	0	1		
ENSMUST00000155653						29	18	58	52	39	15	0	0	0	0	2		
ENSMUST00000155654						0	0	0	0	0	0	25	0	27	5	38		
ENSMUST00000155655						11	8	0	6	8	15	14	1429	32	0	92		
ENSMUST00000155656						0	0	22	23	0	3	0	0	0	0	0		
ENSMUST00000155657						0	2	0	46	2	0	12	20	13	2	4		
ENSMUST00000155659						3	2	1	60	1	3	0	7	2	0	3		
ENSMUST00000155660						172	179	237	174	272	141	35	93	68	17	82		
ENSMUST00000155661						2	0	0	36	1	1	0	4	12	2	9		
ENSMUST00000155662	ENSMUSG00000049755	11	58315114	58330339	-1	0	0	0	3	0	0	2	0	0	0	0	A8Y5R7	
ENSMUST00000155663						2	4	3	0	3	2	0	0	0	0	0		
ENSMUST00000155664						2	3	2	0	0	0	0	0	0	0	0		
ENSMUST00000155665						3	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000155666						37	23	83	37	38	18	0	4	1	0	5		
ENSMUST00000155667						1	2	5	1	0	1	4	3	0	0	0		
ENSMUST00000155668						0	1	2	3	1	1	14	34	10	4	8		
ENSMUST00000155669						4015	4289	8627	15981	3088	891	2	9	40	4	41		
ENSMUST00000155670						0	0	1	3	0	0	0	0	0	0	0		
ENSMUST00000155671	ENSMUSG00000029462	5	122354369	122364984	1	39	33	44	52	24	12	35	167	82	49	80		Q9QZ88
ENSMUST00000155672	ENSMUSG00000041769	7	138846079	138883057	1	11	8	10	0	14	6	259	1103	423	99	248	F6RV17	
ENSMUST00000155673						6	1	3	23	4	3	5	7	6	4	5		
ENSMUST00000155675						0	0	0	0	0	0	6	237	56	4	0		
ENSMUST00000155676	ENSMUSG00000015290	X	74365718	74373218	-1	0	0	5	13	11	3	104	328	120	10	85	Q3UK94	P21126
ENSMUST00000155677	ENSMUSG00000055553	8	70508272	70527956	-1	3	5	10	21	8	3	22	20	21	5	8	D3YWA5	
ENSMUST00000155679	ENSMUSG00000031918	9	13748410	13806481	1	7	0	0	0	10	0	0	124	60	69	60	Q6P572	
ENSMUST00000155680						37	37	33	27	31	15	0	5	0	0	2		
ENSMUST00000155682						1	1	4	0	1	2	0	0	0	0	0		
ENSMUST00000155683						4	0	4	2	2	0	0	0	0	0	0		
ENSMUST00000155685						13	7	18	11	10	6	0	0	0	0	0		
ENSMUST00000155686						0	1	0	1	5	0	0	0	0	1	0		
ENSMUST00000155687						4	3	8	1	1	0	0	0	0	0	0		
ENSMUST00000155689	ENSMUSG00000052395	14	30654360	30691317	1	34	12	115	0	35	3	0	110	0	0	0	D6RFD6	
ENSMUST00000155690	ENSMUSG00000020182	11	11814101	11898144	-1	0	0	0	0	0	0	0	0	0	3	0	Q5SUV9	
ENSMUST00000155692	ENSMUSG00000040785	16	94370618	94469222	1	0	0	0	0	0	0	0	0	0	0	0	D6RFU5	
ENSMUST00000155693						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155694	ENSMUSG00000039329	11	121146143	121148319	1	1	1	1	3	2	0	0	0	0	0	1	B7ZCA2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155695						0	0	15	4	0	2	0	0	0	0	0		
ENSMUST00000155696						7	7	18	31	11	3	0	0	0	0	0		
ENSMUST00000155697	ENSMUSG00000024818	19	5877808	5885766	1	0	4	23	0	0	0	508	1507	457	157	355		Q8CFJ7
ENSMUST00000155698						1	0	4	7	3	2	0	3	0	0	2		
ENSMUST00000155699						2	2	6	9	2	3	1	3	2	0	0		
ENSMUST00000155700						0	4	43	2	7	6	28	2	37	0	57		
ENSMUST00000155701	ENSMUSG00000052613	10	73099342	74649737	1	3	0	20	13	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000155702	ENSMUSG00000038335	11	74898071	74909342	1	9	0	5	38	4	3	0	5	5	0	4	D6RI76	
ENSMUST00000155703						8	5	12	5	4	3	0	0	0	0	0		
ENSMUST00000155704						3	1	2	2	4	2	0	3	2	0	2		
ENSMUST00000155705	ENSMUSG00000056737	6	72544391	72562983	1	0	0	0	0	0	0	38	20	0	9	14	D3Z4K5	
ENSMUST00000155706						10	1	4	8	8	3	0	0	0	0	0		
ENSMUST00000155707	ENSMUSG00000017466	11	118301069	118355740	-1	1	0	11	67	6	2	511	847	315	149	400	B1AQJ3	
ENSMUST00000155708	ENSMUSG00000024277	18	23752333	23893861	1	0	0	0	17	0	0	0	2	24	2	13	D3YYK8	
ENSMUST00000155709	ENSMUSG00000020744	11	115614178	115628295	-1	0	4	6	12	6	0	0	3	0	0	0	A2A9V2	
ENSMUST00000155710	ENSMUSG00000028411	4	40682382	40703194	-1	4	2	1	2	3	2	2	0	4	0	4	E0CXB7	
ENSMUST00000155711						6	0	8	3	4	1	9	0	6	1	10		
ENSMUST00000155712	ENSMUSG00000018501	11	62316426	62458541	-1	18	0	0	29	16	5	653	1904	888	57	870	Q8CHB6	
ENSMUST00000155713						3	0	0	0	0	0	0	0	34	0	0		
ENSMUST00000155714						3	4	21	2	8	2	0	0	0	0	0		
ENSMUST00000155715						23	19	24	148	33	10	0	0	0	0	0		
ENSMUST00000155716	ENSMUSG00000026200	1	75198236	75210813	-1	0	0	4	0	15	0	57	238	68	16	82		Q8VC60
ENSMUST00000155718						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000155719						1	2	9	0	0	1	1	0	4	0	4		
ENSMUST00000155720						16	0	38	75	0	16	32	58	63	0	21		
ENSMUST00000155721	ENSMUSG00000048703	5	27495639	27501438	-1	52	41	21	61	40	24	0	0	0	0	0	K7N6S0	
ENSMUST00000155723						8	1	14	4	0	3	0	0	0	0	7		
ENSMUST00000155724						39	30	236	55	17	17	13	12	19	0	34		
ENSMUST00000155725						2	0	2	8	3	0	2	0	8	0	9		
ENSMUST00000155726						2	6	13	4	8	5	1	6	0	0	2		
ENSMUST00000155727	ENSMUSG00000021745	14	11553532	12242041	1	0	0	1	0	0	0	0	0	0	0	0	D3Z2S6	
ENSMUST00000155728						22	16	69	24	21	11	0	7	0	1	1		
ENSMUST00000155729						2	0	3	7	4	2	1	1	2	0	0		
ENSMUST00000155730						3	0	1	2	2	1	0	0	1	0	1		
ENSMUST00000155731						4	6	11	9	7	7	1	4	4	0	9		
ENSMUST00000155732	ENSMUSG00000021514	13	65278814	65304221	1	3	1	1	8	4	1	0	0	15	6	8	D3Z1J4	
ENSMUST00000155733						0	0	0	0	0	1	0	4	0	0	0		
ENSMUST00000155734						6	7	4	2	9	5	0	5	0	0	0		
ENSMUST00000155735	ENSMUSG00000033728	15	76710623	76717699	1	0	0	0	0	0	0	60	0	14	4	22		Q8VC16
ENSMUST00000155736						0	0	1	6	3	0	0	0	0	0	0		
ENSMUST00000155737	ENSMUSG00000027669	3	32580332	32616585	-1	21	19	11	14	31	12	3	19	13	2	13		P29387
ENSMUST00000155738						3	1	1	1	3	0	4	0	4	1	9		
ENSMUST00000155739	ENSMUSG00000069456	10	127801152	127846565	1	7	9	2	7	6	7	0	10	1	0	4	D6RFQ4	
ENSMUST00000155740						11	10	33	9	12	5	14	16	16	2	29		
ENSMUST00000155741						1	0	3	0	3	0	2	2	0	2	1		
ENSMUST00000155742	ENSMUSG00000031402	X	75109733	75131016	-1	0	0	0	0	0	0	8	0	0	0	4	B7ZCM1	
ENSMUST00000155743						7	2	6	0	3	0	0	0	2	0	2		
ENSMUST00000155744						0	0	3	0	5	0	156	1102	51	0	507		
ENSMUST00000155745						1	0	0	0	0	0	0	2	7	2	3		
ENSMUST00000155746						2	4	0	47	5	0	0	5	14	2	9		
ENSMUST00000155747						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000155748						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000155749	ENSMUSG00000028527	4	101419277	101466995	1	0	9	0	0	1	0	0	0	0	0	0	F6TEU8	
ENSMUST00000155750						1	0	0	0	2	2	1	11	0	0	0		
ENSMUST00000155751						5	1	9	5	6	1	0	0	0	0	0		
ENSMUST00000155752						1	2	0	170	4	0	0	2	3	0	4		
ENSMUST00000155753						2	3	12	7	3	4	3	2	3	0	0		
ENSMUST00000155754						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000155755						40	25	86	58	25	20	0	3	0	0	0		
ENSMUST00000155756						0	0	0	0	0	0	38	101	34	14	23		
ENSMUST00000155757	ENSMUSG00000028646	4	123917446	123936997	1	11	0	12	7	16	14	47	115	84	24	66		Q99K70
ENSMUST00000155759	ENSMUSG00000048497	11	62648664	62666354	1	5	2	0	1	0	1	14	11	16	31	16		Q8R3L0
ENSMUST00000155760						7	0	0	84	7	9	0	0	0	0	0		
ENSMUST00000155761						49	26	184	48	37	15	1	4	6	0	9		
ENSMUST00000155762	ENSMUSG00000038366	11	97799000	97838764	1	5	0	11	0	0	0	0	1	2	0	0	A2A6H1	
ENSMUST00000155763	ENSMUSG00000023764	11	3131850	3193463	-1	0	0	3	0	0	0	0	0	0	0	0	Q5NC01	
ENSMUST00000155764	ENSMUSG00000056004	5	9266118	9481825	1	4	5	0	22	2	5	0	0	5	0	0	E9PUJ3	
ENSMUST00000155765						7	15	6	3	17	10	0	0	0	0	0		
ENSMUST00000155767						0	0	0	0	0	0	0	0	0	6	0		
ENSMUST00000155768						0	0	0	0	4	1	1	0	0	0	1		
ENSMUST00000155769						6	8	8	5	8	7	11	4	0	0	12		
ENSMUST00000155770						0	0	0	13	0	2	0	0	7	4	6		
ENSMUST00000155771	ENSMUSG00000036054	8	70234226	70279915	1	3	1	4	0	5	1	0	0	0	0	2	D3Z0I4	
ENSMUST00000155772						0	0	21	72	0	0	0	0	3	0	0		
ENSMUST00000155773						2	3	2	0	2	1	0	0	1	0	0		
ENSMUST00000155774						85	62	256	114	81	46	4	18	8	0	21		
ENSMUST00000155775	ENSMUSG00000029049	4	155086577	155145505	1	0	0	0	1	0	0	1	0	0	0	0	B1AUE7	
ENSMUST00000155777						1	0	0	1	2	0	3	0	3	0	0		
ENSMUST00000155778	ENSMUSG00000025786	9	123066160	123113205	-1	0	0	0	0	0	0	93	4	57	0	0	Q05D46	
ENSMUST00000155779						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155780						0	0	0	0	0	1	0	0	0	1	2		
ENSMUST00000155781	ENSMUSG00000022474	15	81951108	81960930	-1	0	0	0	0	0	0	0	0	0	0	0	D6RG76	
ENSMUST00000155782	ENSMUSG00000050947	3	108186335	108192286	1	0	0	0	0	0	0	3	1	0	0	0	A0A0G2JEP5	
ENSMUST00000155785						5	3	9	2	12	3	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155787						2	0	1	0	1	2	0	0	0	0	0		
ENSMUST00000155788						1	0	1	2	3	4	0	0	1	0	0		
ENSMUST00000155790	ENSMUSG00000026853	2	30400471	30415813	-1	0	2	0	0	0	0	29	3	15	0	0	F7BF80	
ENSMUST00000155791	ENSMUSG00000022897	16	94570010	94695517	1	0	1	0	0	0	0	0	0	0	0	0	A9C478	
ENSMUST00000155792						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155793	ENSMUSG00000025332	X	152233020	152274535	1	4	0	0	0	4	1	0	127	13	14	21	F6WXI0	
ENSMUST00000155794						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000155795						6	3	12	11	8	5	0	0	0	0	0		
ENSMUST00000155797	ENSMUSG00000023235	8	4325210	4360020	1	3	0	0	5	0	0	0	0	4	12	0	A0A087WRS0	
ENSMUST00000155798	ENSMUSG00000058076	1	171127165	171150603	-1	2	0	2	29	0	2	80	104	57	26	48	D3Z1A8	
ENSMUST00000155800						0	0	21	0	3	3	0	0	0	0	0		
ENSMUST00000155801						6	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000155802	ENSMUSG00000038147	1	171839697	171890718	1	510	443	582	473	579	285	1960	13046	4211	5902	3498		
ENSMUST00000155803						0	0	4	0	3	1	0	9	0	0	0		
ENSMUST00000155804						1	3	10	4	9	2	0	0	0	0	0		
ENSMUST00000155805						0	0	0	48	4	0	0	0	6	0	6		
ENSMUST00000155806						2	0	2	0	0	3	0	0	0	0	9		
ENSMUST00000155807	ENSMUSG00000096201	9	3036877	3038316	1	4899	4641	7052	4749	4723	3611	0	2	1	0	3	J3QMT9	
ENSMUST00000155808						1	0	0	0	2	0	0	41	17	0	2		
ENSMUST00000155809	ENSMUSG00000037254	2	10094593	10131396	-1	0	0	4	0	3	0	0	0	0	0	0	Q3UEG7	
ENSMUST00000155810						6	0	11	5	2	2	0	1	0	0	0		
ENSMUST00000155811	ENSMUSG00000027166	2	105966709	106003549	-1	0	0	0	0	2	0	12	14	0	14	0	F7CGC9	
ENSMUST00000155813						0	0	0	68	0	0	0	0	0	0	0		
ENSMUST00000155814	ENSMUSG00000024039	17	31612623	31637199	-1	2	8	12	22	4	0	0	0	0	0	0	D3YUF2	
ENSMUST00000155815						4	4	12	7	6	5	10	11	19	0	15		
ENSMUST00000155818						0	0	0	0	0	0	26	28	35	15	16		
ENSMUST00000155819						0	2	0	0	5	0	0	0	0	2	0		
ENSMUST00000155820						7	4	5	8	12	9	0	0	0	0	0		
ENSMUST00000155821	ENSMUSG00000008575	4	82290173	82705750	-1	2	2	3	0	3	3	0	0	0	0	0	A2ADI3	
ENSMUST00000155823						7	5	0	8	8	1	0	0	0	0	0		
ENSMUST00000155824						62	50	76	172	62	11	10	65	36	0	46		
ENSMUST00000155825						0	1	7	0	7	0	0	1	3	6	9		
ENSMUST00000155826						2	5	7	6	3	3	0	0	0	0	0		
ENSMUST00000155827						5	5	15	15	10	0	1	0	0	2	0		
ENSMUST00000155829						292	244	813	338	345	202	102	266	186	26	262		
ENSMUST00000155830						2	0	0	8	3	6	129	541	221	120	196		
ENSMUST00000155832						2	2	6	1	4	2	0	8	0	0	2		
ENSMUST00000155833	ENSMUSG00000025855	5	139017306	139150001	-1	4	1	2	11	0	0	0	0	0	0	0	D3Z4A5	
ENSMUST00000155834						2	0	0	4	2	0	0	0	0	0	2		
ENSMUST00000155835						0	0	0	175	0	0	0	0	0	0	0		
ENSMUST00000155837	ENSMUSG00000027620	2	156147239	156180238	-1	0	1	0	0	3	0	159	2551	1249	360	412	D6RCZ8	
ENSMUST00000155838						14	15	10	5	16	10	1	2	3	0	5		
ENSMUST00000155839						6	13	21	11	8	11	3	1	0	0	2		
ENSMUST00000155840						0	2	0	1	1	0	0	3	0	0	0		
ENSMUST00000155841						37	26	91	9	16	19	4	17	10	5	14		
ENSMUST00000155842						3	0	2	0	3	0	9	19	5	0	8		
ENSMUST00000155843	ENSMUSG00000019173	11	100715009	100738215	-1	1	0	3	0	3	0	6	2	6	0	0	A2A5F5	
ENSMUST00000155844						0	0	0	42	0	1	12	45	29	24	11		
ENSMUST00000155846						0	0	2	1	2	1	0	0	0	0	0		
ENSMUST00000155847						1	0	0	0	1	1	0	3	4	0	2		
ENSMUST00000155848						8	0	0	0	10	9	0	1	0	0	0		
ENSMUST00000155849						4	1	15	4	5	2	27	38	58	6	48		
ENSMUST00000155850						2	2	5	0	4	2	0	0	0	8	4		
ENSMUST00000155851						2	0	4	2	2	1	1	0	0	0	0		
ENSMUST00000155852	ENSMUSG00000060771	1	37754776	37866429	-1	0	0	0	0	0	0	0	0	0	14	7	Q3TR21	
ENSMUST00000155853						0	0	0	0	1	0	0	0	0	4	0		
ENSMUST00000155854	ENSMUSG00000032740	11	29373658	29510808	1	0	2	0	0	2	2	3	0	12	0	0	Z4YLP6	
ENSMUST00000155856	ENSMUSG00000052419	6	13867735	13871518	-1	0	0	0	0	0	0	182	601	169	325	74	F2Z3Y9	
ENSMUST00000155857						5	3	9	4	6	4	0	0	0	0	0		
ENSMUST00000155858	ENSMUSG00000031626	8	45507788	45827906	1	0	0	1	3	1	0	0	0	0	0	0	F7BEU1	
ENSMUST00000155859	ENSMUSG00000022304	15	39768485	39857470	-1	0	0	1	1	0	0	0	0	0	0	0	F6ZLZ4	
ENSMUST00000155860						4	0	0	12	10	0	8	28	23	0	14		
ENSMUST00000155861	ENSMUSG00000054823	8	25601601	25719667	1	5	0	28	112	16	7	368	564	813	53	544		Q6P2L6
ENSMUST00000155862						0	0	11	0	1	3	0	2	3	0	0		
ENSMUST00000155863						0	1	0	0	0	3	0	0	0	0	1		
ENSMUST00000155865						2	1	3	1	1	2	5	1	2	0	14		
ENSMUST00000155866	ENSMUSG00000027714	3	36552606	36565727	1	0	2	0	5	0	0	0	0	5	41	9	D6RGB5	
ENSMUST00000155867						1	2	2	11	2	0	0	0	0	0	0		
ENSMUST00000155868						10	3	6	5	6	1	19	125	32	0	46		
ENSMUST00000155869	ENSMUSG00000001062	8	123242356	123254348	-1	0	0	0	0	0	0	118	182	146	0	18	D6RGB6	
ENSMUST00000155870						5	2	19	8	9	1	0	1	1	0	1		
ENSMUST00000155871						3	6	3	3	3	1	18	31	41	12	55		
ENSMUST00000155872						3	1	6	2	0	1	0	0	0	0	0		
ENSMUST00000155873	ENSMUSG00000059291	4	136028265	136053428	-1	0	0	0	45	0	3	643	450	671	6444	783	A2BH06	
ENSMUST00000155874						7	7	10	5	10	0	1	0	0	0	0		
ENSMUST00000155875						59	17	0	34	0	0	28	34	27	0	33		
ENSMUST00000155876	ENSMUSG00000027429	2	144556229	144590749	1	0	0	0	0	0	0	0	0	0	0	0	A2AN99	
ENSMUST00000155878	ENSMUSG00000020782	11	115824049	115855780	1	4	1	0	4	3	0	0	0	0	0	0	B1ATA7	
ENSMUST00000155879						1	0	2	0	0	0	0	0	0	2	0		
ENSMUST00000155880	ENSMUSG00000057406	5	33820725	33897975	1	0	4	0	0	1	0	0	0	7	0	3	D3Z229	
ENSMUST00000155881						1	2	2	2	5	0	7	3	0	0	2		
ENSMUST00000155882	ENSMUSG00000023092	X	56731787	56793346	1	1	3	0	0	1	0	0	0	0	0	0	A2AEX9	
ENSMUST00000155886						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155887						8	1	1	4	6	4	40	75	77	2	145		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155888						2	1	1	6	3	1	0	2	1	0	1		
ENSMUST00000155889						0	0	0	12	0	0	0	0	0	0	0		
ENSMUST00000155890						209	154	1224	229	299	99	1	13	6	9	12		
ENSMUST00000155891						3	0	5	0	3	0	64	170	45	13	55		
ENSMUST00000155892	ENSMUSG00000019854	10	18055861	18125155	1	0	0	0	0	0	0	0	0	23	0	0	F7AB82	
ENSMUST00000155893						0	2	0	3	7	6	0	0	0	9	0		
ENSMUST00000155894						0	5	9	7	9	0	24	55	10	17	23		
ENSMUST00000155895						2	2	2	0	1	0	1	0	13	0	18		
ENSMUST00000155896						0	0	21	40	0	1	0	1	0	0	0		
ENSMUST00000155897						7	0	8	0	1	1	12	0	19	4	3		
ENSMUST00000155898						0	1	1	0	2	0	0	12	5	3	13		
ENSMUST00000155899						16	13	24	20	18	9	0	2	1	0	4		
ENSMUST00000155901	ENSMUSG00000034724	5	96070333	96164171	-1	16	8	28	9	18	8	327	949	345	68	274		Q8VEG6
ENSMUST00000155902	ENSMUSG00000029730	5	138164583	138172422	-1	0	0	0	0	0	0	0	0	0	0	2	D3Z0J6	
ENSMUST00000155903	ENSMUSG00000042208	11	23564961	23633639	-1	0	2	6	0	2	0	0	23	32	20	13	M0QWF3	
ENSMUST00000155904	ENSMUSG00000024150	17	87254658	87265935	-1	0	0	0	49	0	1	2	4	5	0	7	D3YVL4	
ENSMUST00000155905	ENSMUSG00000028345	4	48430858	48473459	-1	5	0	6	0	11	3	10	205	94	54	46	F6ZZ61	
ENSMUST00000155907	ENSMUSG00000022449	15	94270163	94465418	-1	15	19	19	24	21	6	0	0	0	0	0		P59511
ENSMUST00000155908	ENSMUSG00000041890	5	114727407	114775517	-1	0	0	0	0	0	0	337	514	173	19	142	F7BIK4	
ENSMUST00000155909						0	0	2	53	0	2	0	0	0	0	0		
ENSMUST00000155910						24	27	84	46	32	16	1	0	0	0	1		
ENSMUST00000155911						11	11	24	11	7	11	25	30	69	8	93		
ENSMUST00000155913						2	0	0	0	0	0	18	30	10	0	0		
ENSMUST00000155914						2	2	0	2	0	0	0	4	9	0	11		
ENSMUST00000155915						0	0	1	4	1	0	0	0	0	0	0		
ENSMUST00000155916	ENSMUSG00000034903	2	65088339	65239403	-1	0	0	0	0	0	1	3	1	0	0	0	B1AZ26	
ENSMUST00000155917	ENSMUSG00000041684	1	44118957	44144770	1	0	2	0	0	2	0	0	0	0	0	1	A0A087WRD0	
ENSMUST00000155918						20	8	26	22	19	17	0	0	0	0	0		
ENSMUST00000155919	ENSMUSG00000020097	10	61098642	61147703	-1	0	0	1	2	0	0	6	0	0	0	0	D3YZT4	
ENSMUST00000155920						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000155924						0	0	4	0	0	1	0	4	0	0	2		
ENSMUST00000155925						2	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000155926	ENSMUSG00000068762	3	107938847	107943749	-1	0	0	1	5	0	0	0	0	0	0	0	A0A087WNU8	
ENSMUST00000155927						0	0	2	135	4	2	2	1	2	0	1		
ENSMUST00000155928	ENSMUSG00000041720	16	17280351	17406314	-1	0	0	0	0	0	1	0	0	0	3	3	F6XSW4	
ENSMUST00000155929						1	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000155930						9	9	18	38	8	5	1	3	1	0	0		
ENSMUST00000155931	ENSMUSG00000078786	7	27195781	27210186	1	0	0	0	0	0	0	0	0	1	0	0	F6XBP4	
ENSMUST00000155932						2	1	4	103	6	5	0	0	2	0	0		
ENSMUST00000155933						4	5	0	0	4	5	0	0	0	0	0		
ENSMUST00000155934						0	0	0	0	0	0	3	15	7	0	0		
ENSMUST00000155935						2	0	0	0	0	1	0	3	5	0	3		
ENSMUST00000155936						2	0	0	0	0	0	0	49	0	9	0		
ENSMUST00000155937						4	3	6	12	4	5	4	1	3	2	1		
ENSMUST00000155938						4	1	0	1	4	1	0	1	0	2	3		
ENSMUST00000155939	ENSMUSG00000032869	2	151715812	151744186	-1	21	0	0	17	0	0	84	145	101	34	31	D6REH2	
ENSMUST00000155940						1	2	2	0	0	0	0	0	1	0	0		
ENSMUST00000155941						0	0	0	0	0	0	27	266	30	0	49		
ENSMUST00000155942						1	2	4	5	1	0	0	0	3	0	2		
ENSMUST00000155943						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000155945						5	6	0	6	11	1	5	6	8	0	6		
ENSMUST00000155946						2	0	16	3	0	4	132	284	96	14	173		
ENSMUST00000155947						2	0	6	0	3	4	0	3	0	3	17		
ENSMUST00000155948						5	4	9	0	1	4	23	59	33	16	58		
ENSMUST00000155950						5	2	6	0	2	1	0	0	0	0	1		
ENSMUST00000155951						5	3	20	83	8	5	14	9	0	0	64		
ENSMUST00000155953						0	0	17	0	0	0	14	303	138	1	98		
ENSMUST00000155954						18	19	60	32	32	15	0	0	0	0	1		
ENSMUST00000155955	ENSMUSG00000011831	5	107744795	107875107	-1	3	0	0	5	0	0	0	3	1	2	7	E9Q7X9	
ENSMUST00000155956						0	0	0	0	0	0	4	10	4	66	0		
ENSMUST00000155957	ENSMUSG00000003534	17	35681567	35704621	-1	0	0	6	0	11	5	0	0	1	0	0	E9PW79	
ENSMUST00000155958						2	3	8	4	4	3	1	1	0	1	1		
ENSMUST00000155959	ENSMUSG00000019854	10	18055861	18125155	1	0	0	0	0	0	0	11	0	0	0	0	F6YT69	
ENSMUST00000155960	ENSMUSG00000071064	8	79028437	79193766	1	0	0	0	0	8	7	0	0	0	0	0	F6XU43	
ENSMUST00000155961						4	6	11	2	5	3	61	1040	184	101	317		
ENSMUST00000155962	ENSMUSG00000061171	2	65316430	65364034	-1	0	0	0	0	0	0	0	0	0	0	0	F6WP73	
ENSMUST00000155963						1	0	2	6	2	0	5	8	0	3	0		
ENSMUST00000155964	ENSMUSG00000000247	2	38339281	38369733	1	0	0	2	0	0	0	0	0	0	0	0	A0A0A0MQK9	
ENSMUST00000155966	ENSMUSG00000023791	16	32084418	32099738	-1	0	0	0	0	0	0	6	395	29	38	0	F6YX19	
ENSMUST00000155967						0	0	0	0	0	0	0	0	0	2	3		
ENSMUST00000155968						2	1	0	2	6	5	0	18	8	5	9		
ENSMUST00000155969						0	0	0	2	4	2	9	176	8	2	31		
ENSMUST00000155970						0	0	4	1	0	0	6	46	98	30	77		
ENSMUST00000155972						5	0	8	2	2	2	9	28	28	0	82		
ENSMUST00000155973	ENSMUSG00000024949	19	6363690	6378030	1	2	3	3	3	8	0	151	116	291	0	355	D3YVH4	
ENSMUST00000155974	ENSMUSG00000056763	1	10037987	10136768	1	0	0	0	7	0	0	0	0	0	0	0	D3Z378	
ENSMUST00000155975						2	2	3	0	1	0	0	0	0	0	0		
ENSMUST00000155977						0	3	9	3	0	0	0	0	0	0	0		
ENSMUST00000155978	ENSMUSG00000051675	4	65604986	65616238	1	0	0	0	0	0	0	3	0	0	0	1	A2AGS0	
ENSMUST00000155979						11	15	34	27	17	8	0	0	0	0	1		
ENSMUST00000155980	ENSMUSG00000037339	5	33600347	33629635	-1	1	0	4	0	3	0	5	0	0	1	0	D3YUF6	
ENSMUST00000155981						0	0	0	0	0	0	1	0	0	0	1		
ENSMUST00000155983	ENSMUSG00000042625	17	56560965	56584585	-1	0	0	0	0	0	0	0	8	0	0	9	D6RHP9	
ENSMUST00000155984						115	117	259	116	124	71	7	18	13	3	23		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000155985						1	5	0	4	3	2	1	12	4	0	2		
ENSMUST00000155986						8	2	5	13	11	3	0	0	37	159	125		
ENSMUST00000155988						1	2	14	0	3	0	1	1	1	1	4		
ENSMUST00000155989						0	0	0	18	0	0	0	2	4	1	4		
ENSMUST00000155990	ENSMUSG00000028906	4	131923413	132075321	-1	0	0	0	2	1	0	0	154	0	51	0	F7CR30	
ENSMUST00000155991						7	17	15	18	19	10	0	15	2	1	7		
ENSMUST00000155993						0	0	0	41	0	0	0	0	0	0	0		
ENSMUST00000155994						3	4	8	7	8	0	2	375	51	35	254		
ENSMUST00000155995						5	10	8	7	6	3	1	6	0	2	6		
ENSMUST00000155996	ENSMUSG00000030970	7	132987563	133124354	-1	0	2	0	0	0	0	0	0	0	0	0	E9PZG2	
ENSMUST00000155998	ENSMUSG00000020790	11	72690006	72772146	1	46	56	80	67	68	37	189	1540	547	461	755		Q810B6
ENSMUST00000155999						4	2	0	5	5	2	0	2	0	0	0		
ENSMUST00000156000	ENSMUSG00000039382	X	7721973	7728201	1	0	0	5	1	10	0	2	7	0	3	0	F6Q8K5	
ENSMUST00000156001	ENSMUSG00000048701	10	70097121	70193200	1	20	27	29	35	18	22	7	13	12	3	25	F6SXB0	
ENSMUST00000156002						4	3	19	10	7	1	0	0	0	0	0		
ENSMUST00000156003						13	0	37	45	28	6	277	952	398	17	1072		
ENSMUST00000156004						5	6	5	2	9	3	0	0	2	0	0		
ENSMUST00000156006						1	0	1	126	8	4	3	4	3	0	4		
ENSMUST00000156007						97	89	115	80	89	70	25	107	60	35	76		
ENSMUST00000156008						1	4	1	3	3	4	8	6	0	0	0		
ENSMUST00000156009	ENSMUSG00000001435	10	77052178	77166548	-1	8	17	18	22	10	10	0	3	3	0	12	D3Z556	
ENSMUST00000156010						1	6	10	56	9	3	0	0	0	0	0		
ENSMUST00000156012						5	0	4	0	8	3	11	152	24	10	46		
ENSMUST00000156013						2	3	0	8	0	0	0	0	3	0	0		
ENSMUST00000156014						1	2	11	4	0	2	0	0	2	0	0		
ENSMUST00000156015	ENSMUSG00000028102	3	96635376	96645366	1	0	0	0	42	0	0	0	0	0	1	8	D6RFR1	
ENSMUST00000156016						2	0	0	1	0	0	9	16	3	3	15		
ENSMUST00000156017						1	0	3	0	0	0	0	2	0	0	0		
ENSMUST00000156019	ENSMUSG00000020859	11	93996091	94126085	1	0	0	0	0	0	0	79	34	414	13	315	F6SH61	
ENSMUST00000156021	ENSMUSG00000035495	4	46114746	46138694	-1	2	0	1	15	0	3	2	0	1	0	3	B1AWH3	
ENSMUST00000156023						0	0	0	0	0	0	5	3	0	0	2		
ENSMUST00000156024	ENSMUSG00000025870	13	54575015	54581128	1	2	2	8	50	5	0	0	0	3	1	0	D3Z4X7	
ENSMUST00000156025	ENSMUSG00000060568	1	167001417	167091302	1	0	0	0	9	0	0	0	0	0	0	6		Q8BQN5
ENSMUST00000156026						0	0	0	0	0	0	1	1	0	1	0		
ENSMUST00000156027						4	2	11	8	1	1	1	0	0	0	0		
ENSMUST00000156028						1	2	0	0	2	0	0	0	0	1	1		
ENSMUST00000156029						19	21	67	30	25	17	22	178	67	0	108		
ENSMUST00000156030						1	3	2	4	5	0	0	0	0	0	0		
ENSMUST00000156031						7	3	2	0	6	2	0	0	2	1	0		
ENSMUST00000156032	ENSMUSG00000022577	15	75551268	75567255	-1	0	0	0	0	0	0	0	0	0	0	0	Q8K356	
ENSMUST00000156033	ENSMUSG00000004267	6	124760053	124769673	-1	0	2	0	4	0	2	1	0	0	0	0		
ENSMUST00000156034						0	0	0	4	0	5	0	0	0	0	1		
ENSMUST00000156035	ENSMUSG00000032469	9	99575799	99584501	1	1	0	0	0	0	0	0	0	0	0	0	F6UCV1	
ENSMUST00000156036						0	0	0	0	0	0	53	37	96	48	102		
ENSMUST00000156037						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000156038	ENSMUSG00000044864	3	38449259	38484844	-1	33	38	47	25	41	15	80	112	177	29	136	F7BE84	
ENSMUST00000156039						1	1	0	0	4	4	0	23	25	13	2		
ENSMUST00000156040						0	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000156041						3	4	0	0	4	2	0	0	0	0	8		
ENSMUST00000156042	ENSMUSG00000036959	X	48341358	48408049	1	0	0	10	0	2	0	20	1	16	0	12	D6REH6	
ENSMUST00000156043	ENSMUSG00000022433	15	79417856	79443919	-1	66	42	458	116	75	42	0	2	2	0	8	A9J9D8	
ENSMUST00000156044	ENSMUSG00000039987	5	20758663	20882124	-1	1	0	0	3	0	0	0	0	0	0	0	D6RJJ1	
ENSMUST00000156045	ENSMUSG00000022475	15	97792664	97844502	-1	8	4	5	18	7	8	0	5	0	0	28	E9PZG4	
ENSMUST00000156046						87	64	57	75	77	36	1	3	8	1	4		
ENSMUST00000156047	ENSMUSG00000031142	X	7607083	7635196	1	0	0	0	0	4	0	0	0	0	0	0	B1AVA6	
ENSMUST00000156048						0	3	9	1	1	0	0	1	3	2	2		
ENSMUST00000156049						1	3	0	5	0	2	0	0	0	0	0		
ENSMUST00000156050						2	3	2	0	0	0	0	41	17	0	20		
ENSMUST00000156051						9	14	24	18	15	5	3	0	1	0	2		
ENSMUST00000156052	ENSMUSG00000002578	10	128630843	128645991	-1	0	0	0	0	0	0	0	0	0	0	0	F6U9E6	
ENSMUST00000156053						11	0	54	87	29	15	0	0	0	0	0		
ENSMUST00000156054	ENSMUSG00000027522	2	174076308	174099771	1	0	0	0	0	0	0	0	0	16	2	0	F7CJY7	
ENSMUST00000156055	ENSMUSG00000028403	4	82798738	82859958	-1	1	1	1	1	1	1	0	0	0	0	0	Q5SRP0	
ENSMUST00000156056						0	0	0	30	0	0	7	4	0	0	6		
ENSMUST00000156057						0	0	0	0	1	0	6	66	30	0	5		
ENSMUST00000156058						0	1	0	41	0	0	4	0	0	0	1		
ENSMUST00000156059						1	0	1	2	3	1	0	3	7	3	3		
ENSMUST00000156060						9	12	5	5	9	3	186	534	596	296	438		
ENSMUST00000156061						1	3	11	99	4	1	11	11	16	2	17		
ENSMUST00000156062	ENSMUSG00000038330	4	88627320	88634411	-1	1	3	0	0	0	0	0	0	0	0	0	S4R2Q0	
ENSMUST00000156063	ENSMUSG00000030254	6	112619850	112696686	-1	2	0	0	0	0	2	8	8	6	0	2	W4VSP9	
ENSMUST00000156064						16	3	36	20	14	5	0	3	0	0	8		
ENSMUST00000156065						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000156066	ENSMUSG00000036872	8	86482260	86580686	-1	5	0	0	0	3	0	0	0	0	0	0	F6WKU5	
ENSMUST00000156067	ENSMUSG00000047909	2	11777876	11790329	1	0	0	0	0	0	0	0	0	0	7	0	D6RGL4	
ENSMUST00000156069						2	0	0	39	1	2	0	0	0	0	0		
ENSMUST00000156070	ENSMUSG00000053801	7	45825227	45830944	-1	2	0	5	55	3	1	0	0	0	3	0	D6REU5	
ENSMUST00000156071	ENSMUSG00000045312	13	94057796	94195409	1	3	8	14	44	0	4	0	0	0	0	0	D3Z698	
ENSMUST00000156072						2	0	9	0	5	0	6	18	13	0	23		
ENSMUST00000156073						4	0	3	159	8	6	5	14	16	3	23		
ENSMUST00000156074						0	0	0	0	0	0	0	0	14	0	8		
ENSMUST00000156075						4	2	7	47	6	3	0	6	0	3	15		
ENSMUST00000156076						2	0	4	3	3	3	0	0	0	1	0		
ENSMUST00000156077						1	0	4	5	4	1	6	27	32	2	26		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156078						49	39	154	53	64	24	4	5	9	3	41		
ENSMUST00000156079						0	0	0	0	0	0	0	0	12	5	3		
ENSMUST00000156080	ENSMUSG00000029452	5	121451893	121524183	1	0	0	1	0	0	0	0	0	0	0	0	D3Z2K1	
ENSMUST00000156082	ENSMUSG00000036257	12	44221370	44312343	1	0	0	0	0	0	0	0	268	14	38	5	F7B2N8	
ENSMUST00000156083						0	0	3	7	3	2	40	12	18	0	11		
ENSMUST00000156085						33	25	112	100	39	27	5	76	36	29	48		
ENSMUST00000156087						2	0	6	3	4	2	0	0	0	0	0		
ENSMUST00000156088						4	2	5	3	5	2	0	0	0	0	0		
ENSMUST00000156089						420	380	2092	411	447	228	9	74	26	6	42		
ENSMUST00000156091						0	1	0	0	0	0	27	299	101	14	168		
ENSMUST00000156092						3	10	13	3	9	4	2	6	0	11	0		
ENSMUST00000156093	ENSMUSG00000047085	7	44429018	44463351	1	4	5	0	72	13	0	0	0	0	0	0	D3Z2D1	
ENSMUST00000156094						0	0	14	15	6	11	30	15	32	2	44		
ENSMUST00000156096	ENSMUSG00000031012	X	13517080	13851367	-1	9	0	192	0	2	19	55	142	68	0	59	A0A067XG53	
ENSMUST00000156097	ENSMUSG00000020057	10	88322804	88379080	-1	0	9	39	5	4	12	0	0	16	0	0	D6RJL8	
ENSMUST00000156098						2	2	4	4	1	2	5	17	4	1	17		
ENSMUST00000156100	ENSMUSG00000027714	3	36552606	36565727	1	0	0	0	0	2	0	3	0	7	0	2	A0A0G2JFV9	
ENSMUST00000156101	ENSMUSG00000020120	11	16971206	17052381	-1	0	0	1	0	0	1	0	4	2	2	2	Q5F270	
ENSMUST00000156102						0	1	2	44	6	0	2	1	2	0	3		
ENSMUST00000156103						5	4	27	5	7	7	2	0	1	0	0		
ENSMUST00000156105	ENSMUSG00000021716	13	104792484	104839274	1	3	5	0	9	9	0	6	0	14	0	0		Q4V9W2
ENSMUST00000156106	ENSMUSG00000030301	6	147475828	147632612	1	0	0	6	8	0	1	0	0	0	0	0	D6RFV3	
ENSMUST00000156107						2	4	0	0	3	0	0	0	0	0	0		
ENSMUST00000156108						5	4	5	72	16	0	29	469	46	40	54		
ENSMUST00000156110	ENSMUSG00000062234	5	108569411	108629755	-1	11	0	14	0	0	0	225	784	179	99	165	F6SLK1	
ENSMUST00000156111	ENSMUSG00000005417	11	59661305	59780860	1	0	2	0	0	1	0	0	66	0	4	11	F6XZM9	
ENSMUST00000156112						0	0	0	67	2	0	0	0	0	0	0		
ENSMUST00000156113	ENSMUSG00000029009	4	148039077	148059551	1	0	0	0	0	3	0	15	101	5	11	18	F7BGN3	
ENSMUST00000156114	ENSMUSG00000025332	X	152233020	152274535	1	1	0	0	1	1	1	11	32	24	0	0	F7BXT3	
ENSMUST00000156116						8	0	52	11	14	8	0	0	0	0	0		
ENSMUST00000156117	ENSMUSG00000014529	5	3651181	3680325	1	1	1	0	0	0	0	0	0	0	0	0	F7AB47	
ENSMUST00000156118	ENSMUSG00000023266	17	47689030	47704286	1	2	0	4	18	5	1	0	0	0	0	3	D3Z2C8	
ENSMUST00000156119						0	4	0	13	0	0	0	1	0	0	0		
ENSMUST00000156120						0	4	6	37	10	1	72	89	118	12	140		
ENSMUST00000156121	ENSMUSG00000046699	X	64264885	64276996	-1	4	1	7	14	3	0	0	0	0	0	0	B1AU89	
ENSMUST00000156122						4	4	4	79	13	5	2	14	6	2	32		
ENSMUST00000156123						3	6	13	9	12	7	0	7	0	1	0		
ENSMUST00000156124						0	0	0	0	2	0	0	0	5	21	9		
ENSMUST00000156125	ENSMUSG00000029098	5	35583040	35615352	1	0	0	0	2	0	0	36	15	47	3	30	D3Z2N6	
ENSMUST00000156126						6	1	12	4	11	4	0	0	1	0	0		
ENSMUST00000156127						0	0	1	0	0	0	0	0	4	0	1		
ENSMUST00000156128						60	65	179	91	64	37	7	44	21	5	35		
ENSMUST00000156129						11	11	11	17	20	11	2	11	3	1	8		
ENSMUST00000156130						13	1	9	8	12	3	59	132	56	30	56		
ENSMUST00000156131						2	0	0	0	1	0	6	16	6	0	43		
ENSMUST00000156132						2	0	3	0	3	0	0	0	0	0	0		
ENSMUST00000156133	ENSMUSG00000022969	16	91406164	91425834	1	68	55	397	182	50	34	43	154	71	8	129	E9Q294	
ENSMUST00000156134	ENSMUSG00000017664	2	165276554	165287869	-1	0	0	0	0	0	0	0	0	0	0	0	Q5GMG8	
ENSMUST00000156135	ENSMUSG00000030806	7	127803900	127824549	-1	37	29	48	376	76	50	0	0	0	1	0		
ENSMUST00000156136						1	0	5	0	0	0	0	0	15	0	0		
ENSMUST00000156137						0	2	2	0	0	0	0	0	0	2	0		
ENSMUST00000156138	ENSMUSG00000042523	12	84114366	84147498	1	20	0	0	0	0	0	0	0	0	0	0	D6RHN1	
ENSMUST00000156139						11	4	0	2	6	2	0	0	0	0	2		
ENSMUST00000156140						4	4	16	15	5	2	2	53	1	5	1		
ENSMUST00000156141	ENSMUSG00000030269	6	113237843	113281392	1	2	0	0	1	3	3	0	0	0	0	10	D3Z1C1	
ENSMUST00000156142						1	0	0	0	4	0	0	0	0	0	1		
ENSMUST00000156143	ENSMUSG00000022679	16	13903161	13949619	1	2	0	1	24	2	0	0	0	0	0	0	D3YXY8	
ENSMUST00000156145						8	11	11	15	9	13	10	39	22	58	1		
ENSMUST00000156146	ENSMUSG00000009894	11	59407134	59451186	-1	0	0	0	5	0	1	0	0	3	0	0	I7HFU4	
ENSMUST00000156147						8	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000156148						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000156151						0	0	0	0	0	1	0	2	0	1	0		
ENSMUST00000156152	ENSMUSG00000070371	7	127932638	127946725	-1	4	0	4	5	4	1	3	0	0	1	0	D3Z2A9	
ENSMUST00000156153						4	2	1	0	4	0	6	6	20	2	7		
ENSMUST00000156154						7	12	27	17	22	6	35	51	35	0	19		
ENSMUST00000156155						4	1	27	3	6	0	0	2	0	0	0		
ENSMUST00000156157						10	5	6	5	14	6	0	0	1	0	0		
ENSMUST00000156158	ENSMUSG00000042726	5	121371725	121385632	-1	14	9	44	17	30	14	58	469	152	6	339	A0A0G2JG49	
ENSMUST00000156159	ENSMUSG00000074899	2	120046157	120085772	-1	48	37	65	40	71	31	0	1	0	0	1	F6UCX4	
ENSMUST00000156160						12	5	10	0	14	4	0	49	30	339	71		
ENSMUST00000156161						5	8	9	8	8	7	4	24	16	2	13		
ENSMUST00000156162	ENSMUSG00000034145	12	87021340	87090043	1	0	1	1	7	0	1	1	0	0	0	0	D3Z6R7	
ENSMUST00000156163	ENSMUSG00000029767	6	29348069	29377110	1	176	173	390	70	94	45	7	18	0	0	20	G3UXA8	
ENSMUST00000156164						0	0	6	37	5	0	1	0	0	0	8		
ENSMUST00000156166	ENSMUSG00000025754	7	76229887	77124698	1	4	5	12	3	2	3	0	0	0	0	0	D3Z1M2	
ENSMUST00000156167						2	0	0	5	2	1	0	5	2	0	1		
ENSMUST00000156168						3	0	1	5	4	0	2	12	3	2	7		
ENSMUST00000156170						0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000156172	ENSMUSG00000041020	X	159414572	159498757	1	0	1	0	0	1	0	0	0	0	0	0	Q8C0A6	
ENSMUST00000156173	ENSMUSG00000020740	11	115584255	115604051	-1	0	0	0	26	0	0	0	172	0	0	0	S4R2D2	
ENSMUST00000156174	ENSMUSG00000027673	3	32736990	32751566	1	0	0	0	0	0	0	3	0	0	7	0	F6VXF9	
ENSMUST00000156175						11	14	24	21	20	12	0	3	3	2	2		
ENSMUST00000156176	ENSMUSG00000041669	12	103196908	103242150	-1	0	0	0	1	0	0	0	0	0	0	0	D6RCX4	
ENSMUST00000156177	ENSMUSG00000059857	3	109780040	110144011	-1	6	0	0	0	0	7	0	0	0	0	0		Q8R4G0

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156178						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000156179						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156180	ENSMUSG00000029655	5	150608007	150666183	-1	0	0	0	0	0	0	26	191	61	120	41	F6WBP1	
ENSMUST00000156181						5	3	11	5	1	4	0	0	0	0	0		
ENSMUST00000156182						1	3	0	0	1	1	2	8	3	0	0		
ENSMUST00000156184						42	25	129	44	16	21	0	4	2	0	7		
ENSMUST00000156186						11	20	7	5	9	6	0	3	0	0	0		
ENSMUST00000156187	ENSMUSG00000022441	15	83866712	84065379	-1	26	17	29	28	28	14	0	0	0	0	0		Q6P1E8
ENSMUST00000156188	ENSMUSG00000067768	X	73214333	73222453	1	0	0	0	0	0	0	0	0	0	14	0	B1B0R5	
ENSMUST00000156189						1	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000156190						4	3	0	0	4	2	0	0	0	0	0		
ENSMUST00000156191	ENSMUSG00000050854	4	118540941	118544044	-1	2	0	4	9	7	0	1	0	0	0	0	A8WIT3	
ENSMUST00000156192						10	14	0	0	0	0	0	0	0	0	0		
ENSMUST00000156194						0	0	6	14	0	0	0	0	0	13	11		
ENSMUST00000156195						3	3	5	3	4	1	0	0	0	0	0		
ENSMUST00000156196						10	9	44	819	40	13	56	16	8	0	41		
ENSMUST00000156197						4	0	10	14	2	0	0	0	0	0	5		
ENSMUST00000156198	ENSMUSG00000010067	9	107551555	107562267	1	0	0	0	0	3	0	0	0	0	0	0	D6REH3	
ENSMUST00000156199						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000156200	ENSMUSG00000028328	4	46038935	46116032	1	0	0	0	0	0	0	0	0	0	1	0	G3UYG4	
ENSMUST00000156201	ENSMUSG00000020439	11	3517523	3540612	-1	4	0	0	27	2	6	0	0	0	0	0	D3YZ10	
ENSMUST00000156202						0	2	0	39	1	1	0	0	11	0	0		
ENSMUST00000156203	ENSMUSG00000042104	14	118985039	119099430	-1	0	0	0	22	3	0	0	0	0	0	0	E9Q4X2	
ENSMUST00000156204						0	1	0	0	4	0	0	2	14	0	15		
ENSMUST00000156206	ENSMUSG00000028689	4	116708509	116751206	1	1	0	0	2	1	0	8	22	0	11	0	F6VPT0	
ENSMUST00000156207						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000156208	ENSMUSG00000025409	10	127281956	127289018	-1	3	1	19	6	10	6	7	18	24	0	33	D3YV97	
ENSMUST00000156212						0	6	10	7	0	2	47	588	159	0	263		
ENSMUST00000156213						53	36	236	165	51	36	0	6	3	0	7		
ENSMUST00000156214						1	3	6	5	5	1	10	23	26	2	28		
ENSMUST00000156215						40	19	95	35	33	24	3	15	15	5	38		
ENSMUST00000156216	ENSMUSG00000027168	2	105668900	105697364	1	15	5	39	12	11	5	0	0	0	0	0	A2A409	
ENSMUST00000156217						0	0	0	0	0	0	123	1009	377	0	18		
ENSMUST00000156218	ENSMUSG00000062931	10	82224850	82241280	-1	0	4	13	16	0	2	0	0	0	32	0	D6RJ82	
ENSMUST00000156221						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000156222						0	0	0	1	1	0	4	0	1	4	5		
ENSMUST00000156223	ENSMUSG00000028573	4	95557507	95926939	1	0	0	0	0	2	1	3	0	0	2	2	F6V664	
ENSMUST00000156225	ENSMUSG00000028581	4	130913125	130936141	1	0	0	0	2	0	0	4	0	26	0	15	B1ASF7	
ENSMUST00000156226	ENSMUSG00000045983	16	20668313	20692884	1	6	0	14	131	13	0	0	252	13	52	10	D6RCH1	
ENSMUST00000156227						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000156229						0	2	0	44	6	1	0	0	0	0	0		
ENSMUST00000156230						0	9	2	0	6	0	580	225	436	23	327		
ENSMUST00000156231						4	2	3	9	3	1	47	208	97	8	183		
ENSMUST00000156232	ENSMUSG00000074749	2	146855864	146970097	1	0	0	12	4	1	0	0	3	12	0	0	Z4YN37	
ENSMUST00000156233	ENSMUSG00000025266	X	150983141	151017322	-1	0	0	0	0	0	0	0	0	0	0	3	A2ALP3	
ENSMUST00000156234	ENSMUSG00000063889	18	3266048	3337748	-1	0	0	0	0	0	0	0	0	0	0	0	D3Z2U7	
ENSMUST00000156237						0	3	22	0	4	3	0	8	0	0	0		
ENSMUST00000156238	ENSMUSG00000060961	5	88886818	89239653	1	0	0	0	1	0	0	0	0	0	0	0	E9Q8N8	
ENSMUST00000156241	ENSMUSG00000036845	7	30555441	30559838	-1	7	0	8	1	3	3	12	21	16	0	13	D3Z769	
ENSMUST00000156244	ENSMUSG00000020167	10	80409514	80433647	-1	0	1	1	1	1	0	0	0	0	0	1	D3Z037	
ENSMUST00000156246						9	10	31	18	13	7	0	3	0	0	0		
ENSMUST00000156247						8	1	0	44	7	2	7	27	16	11	10		
ENSMUST00000156248						5	0	2	2	3	0	0	0	0	0	0		
ENSMUST00000156249	ENSMUSG00000008348	5	125385965	125390202	-1	0	1	0	5	0	0	0	19	3	0	3		P0CG50
ENSMUST00000156250						0	0	28	0	0	0	0	52	36	35	6		
ENSMUST00000156251						14	6	53	13	9	2	0	3	0	0	0		
ENSMUST00000156252	ENSMUSG00000020333	11	54303798	54364756	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7Y2	
ENSMUST00000156253	ENSMUSG00000052997	7	34140688	34169599	-1	1	0	1	1	0	1	0	0	0	0	0	A2BH29	
ENSMUST00000156254	ENSMUSG00000036026	17	45660171	45686905	-1	4	0	27	10	8	5	3	3	11	0	4	D3YY83	
ENSMUST00000156255	ENSMUSG00000017754	2	164839518	164857711	-1	9	0	5	61	0	1	5	0	0	0	5	A2A5K4	
ENSMUST00000156256	ENSMUSG00000035032	9	105162156	105395524	-1	1	1	2	4	4	1	0	0	0	0	0	D6RH85	
ENSMUST00000156257	ENSMUSG00000051747	2	76703980	76982547	-1	0	0	0	0	0	1	0	0	0	0	0	F6ZZ75	
ENSMUST00000156258	ENSMUSG00000027582	2	181364928	181383628	1	0	0	0	0	0	3	0	7	0	2	6	F7C2Y9	
ENSMUST00000156259	ENSMUSG00000066037	4	136310942	136359447	1	0	1	0	0	0	0	0	3	0	0	2	A2AW40	
ENSMUST00000156261						4	4	0	0	4	0	52	6	0	0	0		
ENSMUST00000156262	ENSMUSG00000058388	3	103968110	104024598	1	4	4	5	23	2	2	0	0	0	0	0	D3YTP5	
ENSMUST00000156263						0	0	2	0	0	0	59	47	127	43	103		
ENSMUST00000156264	ENSMUSG00000064090	11	26471322	26593999	-1	1	0	0	0	2	0	0	0	7	0	0	Q5SP86	
ENSMUST00000156266						0	0	0	0	1	3	0	3	0	0	10		
ENSMUST00000156267						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156268						2	4	0	3	3	0	0	34	5	0	21		
ENSMUST00000156269						29	0	16	38	34	14	0	0	0	3	0		
ENSMUST00000156270						1	0	0	0	2	0	13	3	7	1	5		
ENSMUST00000156272	ENSMUSG00000005107	5	38349273	38503143	-1	0	0	11	1	3	2	4	0	3	0	3		
ENSMUST00000156273						36	21	171	54	33	16	1	9	7	0	8		
ENSMUST00000156274						11	13	48	25	15	9	0	0	1	0	0		
ENSMUST00000156276						0	7	7	0	9	4	0	0	0	0	0		
ENSMUST00000156277	ENSMUSG00000021210	13	4434306	4457530	1	0	0	4	1	4	0	0	0	0	0	0	D3Z3P8	
ENSMUST00000156278						10	5	8	1	17	2	0	0	0	0	0		
ENSMUST00000156279						124	79	607	156	120	65	0	2	3	0	5		
ENSMUST00000156280	ENSMUSG00000020463	11	29172890	29220797	1	0	2	2	0	0	0	0	0	44	0	0	Q5RJB9	
ENSMUST00000156281	ENSMUSG00000027652	2	158409848	158499253	1	1	0	1	152	4	0	0	0	2	0	2	A2APV5	
ENSMUST00000156282	ENSMUSG00000079666	5	5437827	5479143	-1	3	2	4	0	10	5	0	0	0	0	0	D6RFV2	
ENSMUST00000156283						3	0	11	19	1	0	0	5	0	5	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156284	ENSMUSG00000026739	2	18677018	18686629	1	0	0	0	1	1	3	1	8	3	0	7	A2ASR8	
ENSMUST00000156287						3	1	3	0	11	0	0	0	0	0	1		
ENSMUST00000156288						14	3	10	1	9	5	0	0	4	1	4		
ENSMUST00000156289						5	4	7	17	9	3	1	0	0	0	0		
ENSMUST00000156290	ENSMUSG00000033209	5	110879803	111289780	1	72	54	239	284	53	25	11	14	13	3	68		Q80XJ3
ENSMUST00000156291	ENSMUSG00000024742	19	10199132	10204169	-1	0	0	0	0	0	0	0	0	0	0	0	Q91Z50	
ENSMUST00000156294	ENSMUSG00000057778	11	72777232	72796142	-1	22	49	38	12	10	26	76	240	74	41	56		Q5SSH8
ENSMUST00000156295						2	3	0	65	0	0	0	0	0	5	0		
ENSMUST00000156296						3	0	0	0	0	0	0	0	3	0	0		
ENSMUST00000156298						4	2	5	56	0	2	0	0	0	3	0		
ENSMUST00000156299						7	6	20	16	15	4	21	97	39	10	77		
ENSMUST00000156300						6	1	10	3	5	2	12	48	33	9	15		
ENSMUST00000156301						4	1	16	0	2	2	0	0	0	0	1		
ENSMUST00000156302	ENSMUSG00000020070	10	62980223	63017210	1	1	0	0	0	0	1	0	0	0	0	0	D3Z7T9	
ENSMUST00000156303						0	0	0	2	1	0	0	5	5	0	2		
ENSMUST00000156304						4	3	44	10	8	0	7	9	5	0	9		
ENSMUST00000156306	ENSMUSG00000026814	2	32646595	32682669	1	6	0	10	3	13	6	2	0	1	0	0	F7BZW0	
ENSMUST00000156307						0	3	1	1	1	0	0	0	0	0	0		
ENSMUST00000156308						0	2	0	0	0	1	9	200	5	17	40		
ENSMUST00000156309	ENSMUSG00000039936	4	149649168	149702571	-1	0	2	0	2	0	0	2	3	3	0	3	B1AS28	
ENSMUST00000156310	ENSMUSG00000062908	3	153922357	153944632	-1	0	0	0	0	0	3	3	0	0	0	13	D6RFD7	
ENSMUST00000156312						58	44	114	119	71	30	1	1	2	2	4		
ENSMUST00000156313	ENSMUSG00000039262	2	32151082	32234537	1	4	0	1	2	0	2	0	0	20	0	6	F6V431	
ENSMUST00000156314	ENSMUSG00000028309	4	49632006	49656887	1	5	3	5	152	9	22	0	0	116	0	109	A2AIR2	
ENSMUST00000156315	ENSMUSG00000018669	11	96907426	96916496	-1	0	0	0	0	0	0	7	15	14	0	0	A2A6D9	
ENSMUST00000156316						3	6	13	30	7	3	2	4	1	0	23		
ENSMUST00000156317						2	6	10	0	0	0	0	0	0	7	9		
ENSMUST00000156318						2	3	0	0	0	0	0	0	0	2	5		
ENSMUST00000156319	ENSMUSG00000031860	8	69832491	69872292	1	0	1	0	0	0	0	0	0	2	0	0	D6RIQ9	
ENSMUST00000156320						4	0	7	91	9	3	0	0	0	0	0		
ENSMUST00000156321	ENSMUSG00000008035	X	10715013	10719690	1	0	0	0	0	2	0	32	5	52	0	28	F6XIS3	
ENSMUST00000156322						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000156323						0	0	0	0	0	0	16	36	0	22	0		
ENSMUST00000156324	ENSMUSG00000073724	4	144059126	144069327	1	0	1	0	0	14	0	0	7	5	4	3	E0CZ59	
ENSMUST00000156325						3	3	1	30	2	1	9	42	14	2	28		
ENSMUST00000156326	ENSMUSG00000034757	11	102284931	102289237	1	11	0	14	83	14	2	290	369	255	38	269		Q3V209
ENSMUST00000156328						0	0	0	19	0	0	0	0	1	0	0		
ENSMUST00000156329						0	7	11	4	8	7	0	0	0	0	0		
ENSMUST00000156330						98	117	285	140	140	60	52	67	43	8	59		
ENSMUST00000156332						2	0	3	6	4	1	3	1	5	2	2		
ENSMUST00000156333	ENSMUSG00000014444	8	122481698	122551329	-1	13	0	0	0	0	0	1	154	0	22	171	F7AC58	
ENSMUST00000156334						2	0	1	52	6	2	12	105	32	32	71		
ENSMUST00000156335	ENSMUSG00000014402	7	46888949	46919969	-1	12	18	24	7	15	11	0	16	0	0	11	D3Z0S9	
ENSMUST00000156336						9	8	33	15	13	12	0	0	0	1	0		
ENSMUST00000156337	ENSMUSG00000008855	11	102194432	102230166	-1	0	0	0	0	0	0	7	0	16	0	0	B7ZDF4	
ENSMUST00000156338						1	0	0	22	0	0	0	1	0	0	0		
ENSMUST00000156339	ENSMUSG00000029101	5	34949445	35039644	1	0	1	0	3	5	0	2	0	0	0	0	D3YXA5	
ENSMUST00000156340						1	3	14	3	4	1	0	0	0	0	0		
ENSMUST00000156341						4	3	6	3	9	1	0	3	0	0	0		
ENSMUST00000156343						7	5	33	16	13	0	76	1449	146	26	221		
ENSMUST00000156344						0	4	0	3	0	0	99	208	285	143	229		
ENSMUST00000156346						6	0	66	1	12	2	3	5	5	3	11		
ENSMUST00000156347						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000156348						17	5	54	17	10	9	0	0	10	0	6		
ENSMUST00000156349						5	5	34	70	9	4	0	0	2	0	0		
ENSMUST00000156351						1	5	29	11	5	0	203	540	174	22	239		
ENSMUST00000156352						0	3	7	24	3	0	0	0	3	5	0		
ENSMUST00000156353						4	0	33	27	0	0	59	82	44	0	81		
ENSMUST00000156354						33	42	113	11	16	10	5	8	7	0	12		
ENSMUST00000156355	ENSMUSG00000038241	2	155956458	155998900	1	0	0	0	0	0	0	0	0	0	0	9	F7BUJ0	
ENSMUST00000156356	ENSMUSG00000029600	5	120594305	120612589	-1	4	0	0	0	0	0	0	0	0	2	4	F6Y0D0	
ENSMUST00000156357						0	0	1	1	0	1	4	63	27	1	31		
ENSMUST00000156358	ENSMUSG00000042404	3	90265185	90280669	1	0	2	7	0	2	0	0	0	0	0	0	F6W646	
ENSMUST00000156359	ENSMUSG00000067274	5	115559467	115563727	1	7	9	4	0	12	0	1298	1549	0	51	0	S4R1N1	
ENSMUST00000156360	ENSMUSG00000045679	12	16988648	17000408	-1	15	11	44	59	24	10	34	77	72	4	91	Q3UU83	
ENSMUST00000156361						0	3	0	4	3	3	0	1	0	0	0		
ENSMUST00000156363	ENSMUSG00000035851	5	86804221	86836659	1	0	0	4	0	2	0	91	593	266	37	238	D6RG95	
ENSMUST00000156365						0	1	6	2	2	2	4	17	7	0	17		
ENSMUST00000156366						0	0	8	32	6	0	0	4	0	0	0		
ENSMUST00000156367	ENSMUSG00000022708	16	42875881	43642602	1	0	0	0	0	0	0	0	0	0	0	3	E0CYJ9	
ENSMUST00000156368						3	1	3	3	4	1	5	24	4	1	9		
ENSMUST00000156369						4	0	1	0	4	0	0	2	2	0	18		
ENSMUST00000156370						2	0	3	8	2	3	5	4	2	2	4		
ENSMUST00000156371						2	2	3	75	2	1	0	0	0	0	0		
ENSMUST00000156372	ENSMUSG00000040952	7	24884371	24889806	1	0	0	0	0	0	0	2000	2266	1520	6584	978	D3YUG3	
ENSMUST00000156373						0	0	0	0	0	2	0	0	8	0	5		
ENSMUST00000156374						2	0	6	0	7	2	336	1382	402	91	571		
ENSMUST00000156375						3	2	0	53	3	0	0	0	0	0	0		
ENSMUST00000156377						3	4	14	0	3	3	271	172	186	19	169		
ENSMUST00000156378						4	4	14	16	12	6	0	18	0	0	3		
ENSMUST00000156379						0	3	0	0	0	0	2	5	0	0	0		
ENSMUST00000156380	ENSMUSG00000087687	8	3621551	3624231	1	4	1	5	8	2	3	483	1385	291	1889	190		P0DJE0
ENSMUST00000156381						0	1	6	3	4	0	0	0	0	0	1		
ENSMUST00000156382						4	4	10	1	0	0	2	0	0	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156383						3	3	9	12	6	1	4	5	1	2	7		
ENSMUST00000156384						5	5	38	17	4	3	0	0	0	0	0		
ENSMUST00000156385	ENSMUSG00000054405	4	132535550	132553742	1	0	1	1	3	1	1	16	26	3	24	7	F7CXJ2	
ENSMUST00000156386						0	0	0	15	1	2	0	0	0	0	1		
ENSMUST00000156389	ENSMUSG00000005575	7	13035120	13038275	-1	0	0	0	40	5	0	49	39	69	17	38	F6YXS3	
ENSMUST00000156390	ENSMUSG00000025059	X	85701937	85776819	-1	0	0	0	0	0	0	369	1012	655	85	295		Q64516
ENSMUST00000156392	ENSMUSG00000026049	1	44086613	44102441	-1	1	0	0	0	0	0	13	0	0	12	4		Q3TUU5
ENSMUST00000156393						1	2	0	1	2	1	1	1	1	1	0		
ENSMUST00000156394						1	4	3	1	5	2	0	0	1	0	5		
ENSMUST00000156396						1	0	4	13	2	3	0	0	0	0	0		
ENSMUST00000156397	ENSMUSG00000027546	2	168634438	168742409	-1	0	0	1	7	0	0	0	0	0	0	0	A2AQC9	
ENSMUST00000156398						0	0	0	0	3	0	0	4	0	62	35		
ENSMUST00000156399						0	3	1	0	2	0	0	0	0	2	0		
ENSMUST00000156400						0	0	0	24	1	0	0	0	0	0	0		
ENSMUST00000156402						0	1	0	1	2	0	0	11	4	5	2		
ENSMUST00000156404						3	2	7	2	3	2	36	70	33	1	0		
ENSMUST00000156405						3	6	13	6	7	1	0	0	0	0	1		
ENSMUST00000156406						21	15	13	20	30	5	6	6	5	1	6		
ENSMUST00000156407						9	11	27	3	9	4	0	1	4	0	4		
ENSMUST00000156408	ENSMUSG00000046750	7	28284652	28291186	-1	7	8	15	3	17	9	1	4	2	0	2	F6TYD6	
ENSMUST00000156410	ENSMUSG00000027425	2	144368983	144407676	1	0	0	0	0	0	0	0	0	0	0	0	F6S6Z2	
ENSMUST00000156411	ENSMUSG00000033055	15	79053094	79062893	-1	0	0	3	0	3	2	45	19	5	6	0	F6QTQ3	
ENSMUST00000156412	ENSMUSG00000026874	2	34983331	35061438	-1	0	0	0	0	0	0	6	67	5	15	5		
ENSMUST00000156413						5	9	5	0	2	0	0	0	0	0	1		
ENSMUST00000156414						2	3	0	1	4	2	0	2	0	4	0		
ENSMUST00000156415						7	0	0	1	4	3	0	3	0	0	16		
ENSMUST00000156417	ENSMUSG00000000731	10	78030022	78043610	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0E3
ENSMUST00000156420						14	0	18	0	0	0	0	27	0	0	0		
ENSMUST00000156421						3	0	1	0	7	2	0	0	4	4	0		
ENSMUST00000156422	ENSMUSG00000019647	18	47235598	47368870	-1	1	0	0	0	4	0	0	0	0	0	0		O35464
ENSMUST00000156423						25	19	22	60	14	7	1	0	1	1	4		
ENSMUST00000156424						2	3	0	1	0	2	1	5	5	0	14		
ENSMUST00000156425						0	0	0	0	0	0	4	2	7	0	6		
ENSMUST00000156426	ENSMUSG00000023249	9	106470322	106476949	-1	0	0	0	0	0	0	14	0	1	0	7	E9PX17	
ENSMUST00000156427						2	5	3	0	3	0	0	0	0	0	0		
ENSMUST00000156428	ENSMUSG00000032306	9	57544256	57552763	-1	0	2	0	0	0	0	0	0	0	0	0	F6Q3K8	
ENSMUST00000156429						0	0	1	1	2	0	69	80	38	21	41		
ENSMUST00000156430						0	3	8	1	4	2	0	0	0	0	0		
ENSMUST00000156431	ENSMUSG00000021884	14	31552905	31641286	-1	202	209	631	240	221	86	22	77	21	15	42		Q9QXE0
ENSMUST00000156432						2	4	8	0	3	2	0	0	0	0	0		
ENSMUST00000156433						0	0	0	97	0	1	0	9	2	3	2		
ENSMUST00000156434						0	0	0	0	0	4	0	0	0	0	1		
ENSMUST00000156435	ENSMUSG00000002059	11	78188430	78192193	1	1	0	0	0	0	0	0	0	0	3	8	F7BE32	
ENSMUST00000156436						11	9	124	11	14	3	16	66	48	26	61		
ENSMUST00000156437	ENSMUSG00000044017	5	129096750	129204599	1	0	0	0	0	0	0	0	0	0	0	1	B2RXV6	
ENSMUST00000156439						0	2	0	1	2	2	0	0	0	0	0		
ENSMUST00000156440	ENSMUSG00000032078	9	46273064	46282643	1	20	11	25	131	34	11	27	176	55	56	91		Q62384
ENSMUST00000156441						1	4	0	0	1	0	0	0	0	0	0		
ENSMUST00000156442	ENSMUSG00000026924	2	26409431	26445216	-1	0	0	0	0	0	0	252	1229	334	53	279	F7BPW6	
ENSMUST00000156444						16	10	11	10	4	0	3	10	4	0	7		
ENSMUST00000156445						0	0	0	0	0	0	0	10	8	7	4		
ENSMUST00000156447						13	0	10	19	9	4	0	0	0	0	11		
ENSMUST00000156448						3	0	0	3	0	1	0	0	0	0	0		
ENSMUST00000156449	ENSMUSG00000031284	X	143518591	143797796	1	0	0	0	5	4	0	0	0	0	0	0	A3KGC3	
ENSMUST00000156450						0	2	17	0	0	0	41	124	0	0	39		
ENSMUST00000156451						0	0	0	127	3	1	0	0	0	0	0		
ENSMUST00000156452						3	5	0	0	7	2	3	10	8	2	8		
ENSMUST00000156453	ENSMUSG00000062563	12	24665838	24681813	-1	0	0	0	0	0	5	0	0	0	0	0		
ENSMUST00000156454	ENSMUSG00000025421	18	76930126	76972902	1	0	0	0	12	0	0	0	0	1	0	0	D3YUN7	
ENSMUST00000156455						0	0	0	0	0	0	0	0	53	90	0		
ENSMUST00000156456						0	0	0	0	2	0	0	0	1	0	0		
ENSMUST00000156458						4	3	2	3	3	2	0	31	13	0	14		
ENSMUST00000156459						10	4	8	18	10	3	2	6	4	0	9		
ENSMUST00000156460	ENSMUSG00000029034	4	155869546	155889103	1	8	4	13	3	2	0	0	9	6	3	22	D6RH69	
ENSMUST00000156461	ENSMUSG00000032249	9	62341293	62378812	1	0	2	0	6	2	0	160	743	208	144	53	F6UFG6	
ENSMUST00000156462						2	0	5	0	1	1	0	0	0	0	0		
ENSMUST00000156463						2	3	3	230	1	5	0	1	2	1	1		
ENSMUST00000156464						5	8	68	19	6	6	0	0	2	0	5		
ENSMUST00000156465						0	0	0	55	0	0	0	4	17	0	9		
ENSMUST00000156468						0	0	3	0	0	0	0	1	0	0	2		
ENSMUST00000156469	ENSMUSG00000037197	2	11585437	11604153	-1	5	4	2	0	5	0	0	0	0	0	0	A2AP40	
ENSMUST00000156470						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156471						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156472						2	4	0	5	5	2	2	0	0	0	0		
ENSMUST00000156473	ENSMUSG00000046032	X	101097786	101222563	-1	0	0	0	4	2	1	14	15	8	5	10	Q3V2H3	
ENSMUST00000156474	ENSMUSG00000029475	5	122870665	122989823	-1	0	0	4	43	3	0	0	0	0	0	0	D3YUE3	
ENSMUST00000156475						0	4	3	3	7	5	4	6	8	3	21		
ENSMUST00000156478						2	1	1	9	1	1	0	0	0	0	1		
ENSMUST00000156479						0	0	1	4	0	2	0	0	0	0	0		
ENSMUST00000156480						4	8	0	4	10	4	3	0	3	0	5		
ENSMUST00000156481	ENSMUSG00000015804	5	45520229	45529276	1	17	12	58	46	20	15	24	68	21	6	15		Q920D3
ENSMUST00000156482						2	6	5	78	5	0	0	0	0	0	0		
ENSMUST00000156483	ENSMUSG00000010342	11	87405065	87555823	1	6	5	12	6	11	2	0	7	1	0	2	B2KGK9	
ENSMUST00000156484	ENSMUSG00000047407	17	70844205	70853546	-1	5	1	2	0	0	1	0	0	0	0	0	F6TUU5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156485	ENSMUSG00000032531	9	102716672	102733418	1	0	1	1	13	0	2	0	0	0	0	0	B8JK84	
ENSMUST00000156486	ENSMUSG00000030265	6	145216699	145250239	-1	0	0	0	0	0	0	64	182	138	7	59	E9Q8V2	
ENSMUST00000156487						7	5	0	1	5	0	114	1234	279	83	198		
ENSMUST00000156488	ENSMUSG00000037926	11	77216287	77460220	1	0	1	0	136	0	1	0	0	3	0	3	A0A0A0MQJ2	
ENSMUST00000156489						6	4	7	113	20	2	0	10	0	0	0		
ENSMUST00000156490						1	1	2	2	4	0	0	0	0	0	0		
ENSMUST00000156491						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156492	ENSMUSG00000034164	11	5106265	5152257	-1	4	6	4	6	3	2	0	1	0	1	0	E0CY77	
ENSMUST00000156493						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156495						3	0	0	6	0	0	0	2	0	0	0		
ENSMUST00000156496						10	8	32	0	14	2	3	0	0	0	0		
ENSMUST00000156497						1	0	4	0	0	1	0	0	0	0	0		
ENSMUST00000156499						5	1	8	47	5	0	0	0	0	0	1		
ENSMUST00000156500						4	7	2	6	9	0	0	0	0	1	0		
ENSMUST00000156501						8	1	17	19	10	4	2	7	3	0	3		
ENSMUST00000156502	ENSMUSG00000022779	16	16870736	16892990	1	0	0	0	0	0	0	22	0	44	0	19	D3Z084	
ENSMUST00000156503						0	0	2	35	1	0	130	303	82	315	58		
ENSMUST00000156504						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156505	ENSMUSG00000007570	17	28313530	28326568	1	0	0	0	0	1	0	2	16	5	0	1	B8JJD2	
ENSMUST00000156506						3	3	9	0	4	0	0	0	0	0	0		
ENSMUST00000156507	ENSMUSG00000001583	11	69851005	69858730	-1	3	0	0	6	2	0	0	0	0	0	0	Q5F2B6	
ENSMUST00000156509						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156510	ENSMUSG00000033943	2	119897228	119969581	1	0	0	0	0	0	0	0	0	188	0	17		A2AWL7
ENSMUST00000156512						34	31	51	34	31	23	10	56	24	10	62		
ENSMUST00000156513						5	3	17	8	3	3	16	87	50	2	37		
ENSMUST00000156514						36	21	131	30	38	27	0	1	1	0	2		
ENSMUST00000156517						6	4	12	10	6	4	0	0	0	0	1		
ENSMUST00000156518						48	39	84	45	39	15	9	30	4	5	23		
ENSMUST00000156520	ENSMUSG00000032540	9	122351608	122381524	1	0	10	7	26	5	11	329	867	456	81	155		Q9DBL9
ENSMUST00000156521						0	0	2	0	0	0	11	5	0	0	0		
ENSMUST00000156522	ENSMUSG00000022757	16	56690332	56717450	-1	4	2	0	0	0	4	10	87	43	41	32	B8JJG3	
ENSMUST00000156524						3	4	12	4	6	1	12	50	20	6	24		
ENSMUST00000156525						0	0	0	0	13	1	0	0	0	30	0		
ENSMUST00000156527						0	0	3	12	1	0	0	0	0	0	3		
ENSMUST00000156528						0	0	2	0	1	0	1	0	0	0	1		
ENSMUST00000156529	ENSMUSG00000030990	7	102210208	102238567	1	0	0	4	32	0	4	201	275	274	41	134		Q3TQR0
ENSMUST00000156530	ENSMUSG00000006143	5	136054492	136064326	1	0	1	10	0	0	0	0	0	0	0	1	F6X493	
ENSMUST00000156531						3	1	0	1	0	0	3	13	0	0	8		
ENSMUST00000156532						2	1	9	3	1	2	0	0	0	0	0		
ENSMUST00000156533						7	0	4	4	5	1	1	0	1	0	2		
ENSMUST00000156534						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000156535						0	2	2	2	2	1	0	2	0	0	4		
ENSMUST00000156536						1	0	4	0	0	1	0	0	0	0	0		
ENSMUST00000156537	ENSMUSG00000030805	7	127824294	127849019	1	0	1	0	7	0	1	79	51	131	59	110	D6RJ29	
ENSMUST00000156539						9	6	9	3	9	3	0	0	0	0	0		
ENSMUST00000156540						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000156542	ENSMUSG00000039738	16	3979105	4003770	-1	48	26	98	65	63	45	42	92	83	0	63	F6R0R3	
ENSMUST00000156543						0	0	3	2	1	0	2	1	2	0	0		
ENSMUST00000156544						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000156545	ENSMUSG00000057948	11	116062095	116077961	-1	0	0	0	0	0	0	4	1	2	0	0	A2A858	
ENSMUST00000156546	ENSMUSG00000035891	15	86139128	86186141	-1	0	0	0	0	0	0	59	0	21	0	41	D3Z254	
ENSMUST00000156547						1	0	4	45	3	3	15	1	9	4	6		
ENSMUST00000156549						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156550	ENSMUSG00000024807	19	6046576	6053712	1	0	0	8	5	0	0	86	1	70	5	136	D3Z1Y1	
ENSMUST00000156551						1	2	0	0	3	0	5	35	4	2	2		
ENSMUST00000156552						0	0	29	0	2	0	0	389	201	14	73		
ENSMUST00000156553	ENSMUSG00000001741	7	83642848	83745726	-1	3	0	2	2	1	0	0	0	0	0	0	D3Z3C7	
ENSMUST00000156554						0	1	3	0	1	0	0	0	1	0	1		
ENSMUST00000156555	ENSMUSG00000027546	2	168634438	168742409	-1	1	2	2	0	2	2	0	0	0	0	0	A2AUZ1	
ENSMUST00000156556						1	0	1	7	2	0	12	55	19	27	5		
ENSMUST00000156558	ENSMUSG00000028664	4	136647539	136835988	-1	0	0	0	0	0	0	0	0	0	0	5	F6Q4H2	
ENSMUST00000156559						3	5	0	4	0	0	5	7	0	0	0		
ENSMUST00000156560	ENSMUSG00000031442	8	12873806	13020905	1	6	3	1	21	1	1	0	0	0	0	0	D3Z3S7	
ENSMUST00000156561						8	3	6	33	13	8	10	62	40	6	54		
ENSMUST00000156562						3	4	36	2	6	1	64	60	22	12	86		
ENSMUST00000156563						15	17	18	26	16	7	7	6	9	3	16		
ENSMUST00000156564						1	1	1	0	1	2	0	2	0	0	2		
ENSMUST00000156565						12	6	9	18	12	5	4	23	5	0	17		
ENSMUST00000156567	ENSMUSG00000034853	4	106744555	106804998	-1	2	0	0	9	0	3	0	0	0	0	0	E0CYS0	
ENSMUST00000156568						18	6	36	17	12	8	0	13	7	0	8		
ENSMUST00000156569						0	2	0	1	2	0	16	21	0	7	8		
ENSMUST00000156570	ENSMUSG00000024052	17	71182560	71249817	1	4	6	14	18	3	2	7	10	14	5	33		Q99PI5
ENSMUST00000156571						0	4	19	5	2	4	0	0	0	0	0		
ENSMUST00000156572	ENSMUSG00000051853	15	98737621	98763214	-1	1	0	0	117	3	2	0	0	0	0	2	D3YV25	
ENSMUST00000156573	ENSMUSG00000020061	10	88518279	88605152	-1	2	0	0	0	4	0	0	0	0	0	0	F6RQD1	
ENSMUST00000156574						6	1	23	8	5	2	0	0	0	0	3		
ENSMUST00000156575						3	1	0	1	1	3	0	0	0	0	0		
ENSMUST00000156577						3	2	9	5	6	2	0	0	0	0	3		
ENSMUST00000156578	ENSMUSG00000026817	2	32621758	32635058	1	1	1	5	3	4	4	0	0	0	1	1	Z4YN97	
ENSMUST00000156580	ENSMUSG00000033653	16	21423118	21644680	1	0	0	0	0	0	0	0	0	0	0	0	F7A250	
ENSMUST00000156581						4	1	0	6	4	3	7	84	15	2	35		
ENSMUST00000156582	ENSMUSG00000049119	4	5644090	6108223	1	5	0	10	41	0	0	0	0	0	0	0	B1AWG6	
ENSMUST00000156583						2	1	0	1	1	0	0	0	0	0	1		
ENSMUST00000156584						4	4	3	15	2	4	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156585	ENSMUSG00000025223	19	46032593	46045214	-1	3	0	13	0	10	0	0	0	0	0	0		P70662
ENSMUST00000156586						0	2	0	0	0	3	27	120	4	46	21		
ENSMUST00000156587						31	23	271	19	40	18	1	0	0	0	0		
ENSMUST00000156588						1	3	8	5	7	6	0	0	4	0	0		
ENSMUST00000156589						2	0	2	4	1	2	0	0	0	0	0		
ENSMUST00000156590	ENSMUSG00000051455	11	102663716	102682237	1	0	0	3	7	2	0	0	0	0	0	0		
ENSMUST00000156591	ENSMUSG00000068036	17	13760539	13906150	1	0	0	0	6	0	0	0	0	0	0	0	D3Z7L2	
ENSMUST00000156592						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000156593	ENSMUSG00000030786	7	128062640	128118491	1	0	3	5	2	1	0	38	31	32	7	60	D6RJ73	
ENSMUST00000156594						0	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000156595						1	1	4	16	6	2	0	0	1	0	0		
ENSMUST00000156596	ENSMUSG00000028524	4	102741297	102973628	1	0	0	0	0	0	0	0	0	3	0	0	F6VMS8	
ENSMUST00000156597	ENSMUSG00000063052	3	158036662	158068487	1	0	0	8	0	1	1	39	95	20	129	0	D6RFC5	
ENSMUST00000156598	ENSMUSG00000048120	19	40612366	40741602	1	0	0	3	2	0	0	187	149	577	233	551	D6RHQ2	
ENSMUST00000156600						89	83	762	132	93	36	2	22	10	2	15		
ENSMUST00000156602						162	134	367	194	183	96	7	35	24	10	58		
ENSMUST00000156603						0	0	0	0	0	0	6	114	17	8	12		
ENSMUST00000156604						1	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000156605	ENSMUSG00000085111	10	85927681	85946206	1	0	0	0	0	1	0	0	0	0	0	0	M0QWE9	
ENSMUST00000156606						5	0	15	2	0	2	5	0	0	0	0		
ENSMUST00000156607						2	0	3	0	0	0	63	92	38	0	24		
ENSMUST00000156608						81	63	249	385	93	69	2	4	11	0	7		
ENSMUST00000156610	ENSMUSG00000036872	8	86482260	86580686	-1	0	0	28	0	10	6	0	0	0	0	0	D6RCU5	
ENSMUST00000156611						1	3	8	3	2	0	0	0	0	0	11		
ENSMUST00000156613	ENSMUSG00000026135	1	74565127	74588246	-1	23	10	31	45	33	12	26	20	33	0	0	M0QWZ4	
ENSMUST00000156614						0	1	5	14	0	0	0	0	0	0	0		
ENSMUST00000156616	ENSMUSG00000025261	X	151800807	151935417	1	1	2	0	7	1	1	3	0	9	3	0	A0A0G2JD97	
ENSMUST00000156617	ENSMUSG00000009563	2	32757234	32762244	1	0	0	0	0	0	0	21	34	25	12	13	E9QAU3	
ENSMUST00000156618						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000156619	ENSMUSG00000068205	2	140395309	142392966	1	2	0	0	0	0	0	0	0	0	0	0	F6TQH7	
ENSMUST00000156620						0	0	0	0	0	0	31	12	32	16	72		
ENSMUST00000156621						0	1	0	2	1	0	0	0	0	0	0		
ENSMUST00000156622						0	0	7	1	0	0	14	54	66	33	96		
ENSMUST00000156623						2	0	0	0	0	0	30	9	145	160	669		
ENSMUST00000156624						6	4	9	1	4	0	0	0	0	0	0		
ENSMUST00000156625						0	0	1	1	0	2	0	0	0	0	0		
ENSMUST00000156626						0	0	20	1	18	11	1	12	0	2	0		
ENSMUST00000156627						11	23	10	10	18	10	0	0	0	0	0		
ENSMUST00000156628	ENSMUSG00000042323	14	31019138	31121592	1	0	0	0	0	0	0	0	0	0	0	0	D3YYF2	
ENSMUST00000156629	ENSMUSG00000020286	11	23516203	23521155	-1	8	9	12	13	16	12	0	0	0	0	0	A2AF85	
ENSMUST00000156630	ENSMUSG00000046079	5	105699969	105832436	1	0	0	0	0	0	0	0	0	0	0	0	D3Z5Q6	
ENSMUST00000156631						0	0	4	0	5	0	0	0	0	0	0		
ENSMUST00000156634						6	7	17	5	6	0	0	0	0	0	0		
ENSMUST00000156635	ENSMUSG00000059713	4	135412308	135433853	-1	0	0	0	59	0	0	2	0	2	2	0	A2A994	
ENSMUST00000156636	ENSMUSG00000015222	1	66175273	66442583	1	1	0	0	9	0	0	0	0	0	0	0	G3UXY3	
ENSMUST00000156637	ENSMUSG00000030774	7	97788541	97912381	1	8	0	38	18	20	2	0	0	0	0	0	S4R2K7	
ENSMUST00000156638	ENSMUSG00000031090	7	143795584	143822849	-1	14	0	0	2	0	0	20	97	41	17	30	D6RDE7	
ENSMUST00000156639	ENSMUSG00000025665	X	111388192	111537959	-1	0	0	6	10	0	2	0	0	0	0	1	B1B0X4	
ENSMUST00000156640						0	0	12	1	0	0	0	24	8	4	3		
ENSMUST00000156641						12	6	5	0	2	2	92	219	78	121	78		
ENSMUST00000156642						0	0	0	0	0	0	28	657	69	95	77		
ENSMUST00000156643	ENSMUSG00000034903	2	65088339	65239403	-1	0	0	0	24	0	0	0	0	6	0	0	B1AZ25	
ENSMUST00000156644	ENSMUSG00000000290	10	77530252	77565708	1	5	0	0	6	16	0	338	954	244	75	484	M0QWJ6	
ENSMUST00000156645						2	1	0	1	3	2	9	19	123	0	77		
ENSMUST00000156646	ENSMUSG00000037344	5	137314558	137333597	-1	1	0	3	1	0	0	2	0	0	1	2	D3Z362	
ENSMUST00000156647						23	10	61	28	36	7	804	2894	819	134	2260		
ENSMUST00000156648	ENSMUSG00000031309	X	159210307	159368244	1	0	0	0	0	0	0	0	0	4	0	8	F6UG16	
ENSMUST00000156649						1	0	0	4	2	0	2	0	3	0	5		
ENSMUST00000156651						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156652	ENSMUSG00000069094	3	19223108	19311322	-1	3	2	1	4	0	1	0	2	0	0	0	D6RIM5	
ENSMUST00000156653						1	0	4	0	0	2	44	5	21	0	39		
ENSMUST00000156654						0	0	5	0	2	1	0	0	0	0	0		
ENSMUST00000156655						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156656						20	32	52	50	36	30	0	3	4	2	9		
ENSMUST00000156657						0	0	0	0	4	1	0	0	0	0	0		
ENSMUST00000156658						40	29	63	257	40	19	18	38	59	13	126		
ENSMUST00000156659						7	0	0	62	5	6	2	0	0	0	0		
ENSMUST00000156660						3	0	2	3	1	0	2	0	0	1	0		
ENSMUST00000156661						17	9	43	11	16	18	0	7	151	12	212		
ENSMUST00000156662	ENSMUSG00000048473	6	142785204	142804502	-1	7	3	3	5	8	5	15	132	31	35	33	Q3UN63	
ENSMUST00000156663						7	2	5	2	9	3	2	6	4	0	4		
ENSMUST00000156665						0	1	0	5	0	2	0	0	0	0	0		
ENSMUST00000156667						0	0	2	0	0	0	0	0	0	7	3		
ENSMUST00000156668						1	0	2	0	2	1	0	0	0	0	0		
ENSMUST00000156669	ENSMUSG00000026883	2	35558266	35730994	1	0	0	0	4	0	0	18	219	39	15	60	F6QQP6	
ENSMUST00000156671						0	2	5	3	0	2	0	3	0	0	0		
ENSMUST00000156672						0	2	2	0	0	0	5	66	19	7	6		
ENSMUST00000156673						12	33	33	0	22	25	30	92	26	5	39		
ENSMUST00000156674	ENSMUSG00000063894	13	21513222	21531120	-1	0	1	1	0	0	0	3	0	10	0	1	D3Z716	
ENSMUST00000156675	ENSMUSG00000062590	1	86154780	86278284	1	0	0	0	0	1	1	0	0	0	0	0	F6QPP0	
ENSMUST00000156676						0	4	2	0	0	0	0	7	8	5	4		
ENSMUST00000156677						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156678						0	0	0	0	0	1	534	349	458	192	315		
ENSMUST00000156679	ENSMUSG00000022237	15	31291479	31367759	-1	3	8	10	0	7	0	209	4	113	0	186		Q3U0L2

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156680	ENSMUSG00000037808	9	13827716	13846541	1	0	0	0	0	0	0	38	110	0	24	57	D6RG49	
ENSMUST00000156681						4	0	0	0	3	0	8	37	27	7	11		
ENSMUST00000156683						2	3	2	16	5	0	0	0	0	0	0		
ENSMUST00000156684						18	19	40	433	40	10	10	11	67	3	53		
ENSMUST00000156685						7	5	18	24	6	1	68	62	44	35	32		
ENSMUST00000156686						0	0	0	79	1	0	8	6	4	0	2		
ENSMUST00000156687	ENSMUSG00000026123	1	34849976	34879580	1	38	42	69	93	40	19	25	28	37	3	40	Q3UFC9	Q9QZC7
ENSMUST00000156688	ENSMUSG00000007659	2	152780668	152831728	-1	1	2	0	13	2	0	13	5	9	0	0	A2AHX7	
ENSMUST00000156689						21	15	49	45	25	7	0	0	0	0	0		
ENSMUST00000156690	ENSMUSG00000030557	7	67231163	67372858	-1	0	7	28	6	21	16	615	1897	739	207	617		Q60929
ENSMUST00000156694	ENSMUSG00000051615	14	120478461	120507194	1	19	19	73	0	17	13	38	1027	250	48	97	F6W8Q2	
ENSMUST00000156695	ENSMUSG00000062995	6	8630527	8778488	-1	3	2	0	0	0	3	33	46	20	16	26	S4R217	
ENSMUST00000156696						0	0	0	0	0	6	0	5	12	0	5		
ENSMUST00000156697	ENSMUSG00000041380	X	146962513	147197277	1	10	0	12	1	0	2	0	0	0	0	0	S4R2T0	
ENSMUST00000156698						69	65	246	163	103	52	5	24	10	3	13		
ENSMUST00000156700	ENSMUSG00000034327	14	67715937	67742310	1	0	0	2	0	0	0	75	229	58	35	63	D6RH42	
ENSMUST00000156701						10	23	13	19	30	12	27	32	26	30	38		
ENSMUST00000156702	ENSMUSG00000026853	2	30400471	30415813	-1	2	0	0	49	0	8	0	0	27	3	8	D6REV7	
ENSMUST00000156703						3	2	3	9	5	1	0	1	0	0	1		
ENSMUST00000156704						2	4	3	0	3	2	0	0	1	0	0		
ENSMUST00000156705						8	0	0	25	2	0	0	0	0	0	0		
ENSMUST00000156706						1	0	1	1	3	1	5	9	0	0	12		
ENSMUST00000156707	ENSMUSG00000004221	X	74393290	74453854	1	0	0	0	0	0	0	9	0	36	8	0	A3KG44	
ENSMUST00000156708						0	1	1	12	0	0	0	0	0	1	8		
ENSMUST00000156709						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156710						4	3	20	7	6	3	0	2	0	0	0		
ENSMUST00000156711	ENSMUSG00000026848	2	30952959	30959015	1	0	0	0	0	0	0	157	486	74	47	114	F6VK94	
ENSMUST00000156712						2	3	3	0	1	2	0	0	0	2	1		
ENSMUST00000156713	ENSMUSG00000022962	16	91621186	91646952	-1	0	16	31	0	0	0	117	244	107	21	146	D6RCG1	
ENSMUST00000156714	ENSMUSG00000040703	7	25802475	25816913	-1	9	7	5	6	12	2	2	2	0	0	0	D3Z762	
ENSMUST00000156715						0	0	20	0	0	0	0	0	10	5	9		
ENSMUST00000156716						3	3	4	35	11	2	2	2	12	17	7		
ENSMUST00000156717	ENSMUSG00000024862	19	5107746	5118560	-1	1	3	5	82	7	1	0	2	0	0	4	D3Z5Y7	
ENSMUST00000156719						1	2	0	0	6	2	0	0	0	0	0		
ENSMUST00000156720						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000156721						0	5	5	0	0	1	0	0	5	0	0		
ENSMUST00000156722	ENSMUSG00000029602	5	120648812	120679597	1	33	0	74	196	45	23	0	0	0	0	0		Q9Z268
ENSMUST00000156723						0	0	4	0	4	1	4	38	6	0	13		
ENSMUST00000156724						0	1	3	99	1	0	0	2	4	2	1		
ENSMUST00000156725						120	109	366	380	184	91	26	49	74	7	84		
ENSMUST00000156726	ENSMUSG00000026749	2	38511643	38594606	1	1	0	0	0	0	0	10	30	38	11	18	A2ATP1	
ENSMUST00000156727	ENSMUSG00000020566	12	17284721	17329359	-1	0	5	11	3	10	0	0	0	0	0	0	D3Z5W3	
ENSMUST00000156728						4	2	2	63	4	0	0	0	0	0	0		
ENSMUST00000156729						3	1	4	41	4	2	0	2	20	20	15		
ENSMUST00000156731	ENSMUSG00000075256	2	79330543	79456785	-1	1	0	0	0	0	0	0	0	0	0	0	A2AQH0	
ENSMUST00000156732						0	0	0	0	1	4	83	2299	152	87	206		
ENSMUST00000156733						4	6	0	0	6	0	0	3	15	0	0		
ENSMUST00000156735						10	6	58	26	14	1	24	187	47	2	80		
ENSMUST00000156736						1	4	0	11	1	0	6	10	0	0	2		
ENSMUST00000156737						0	0	2	1	0	2	0	0	0	1	0		
ENSMUST00000156738						0	0	0	0	3	2	0	0	3	0	1		
ENSMUST00000156739						9	5	22	26	12	11	41	31	17	4	9		
ENSMUST00000156740	ENSMUSG00000018501	11	62316426	62458541	-1	5	16	22	0	0	6	196	158	109	120	1246	F7C134	
ENSMUST00000156741	ENSMUSG00000031157	X	7894519	7899269	-1	0	0	0	0	0	0	109	257	48	94	132	A2AER8	
ENSMUST00000156742	ENSMUSG00000028581	4	130913125	130936141	1	0	0	0	0	0	0	712	22	707	0	576	F6WX18	
ENSMUST00000156743						2	4	2	9	3	0	0	0	0	0	0		
ENSMUST00000156745						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000156746	ENSMUSG00000028644	4	119175457	119190011	-1	0	0	13	0	3	0	0	0	0	0	0	A2A7P6	
ENSMUST00000156747	ENSMUSG00000050468	2	127338639	127357651	1	0	0	23	0	8	1	0	0	0	0	0	A2ARG6	
ENSMUST00000156748	ENSMUSG00000028952	4	152019774	152027671	-1	1	0	0	0	0	0	0	2	5	0	6	F6ZA56	
ENSMUST00000156749						0	1	0	0	1	0	1	3	0	0	5		
ENSMUST00000156750	ENSMUSG00000012126	4	134102570	134127593	1	0	2	0	0	0	0	11	24	19	0	0	I7HPX9	
ENSMUST00000156751	ENSMUSG00000019888	10	101681487	102391469	1	0	0	0	0	0	0	0	0	0	0	0	D3Z683	
ENSMUST00000156752	ENSMUSG00000022201	15	12117831	12185683	1	0	0	1	0	0	0	27	211	85	59	114	F6QJP7	
ENSMUST00000156753						108	143	1559	218	84	78	1	3	0	0	1		
ENSMUST00000156754						0	5	2	0	3	0	0	5	3	0	7		
ENSMUST00000156755						0	0	0	0	0	0	0	1	0	0	9		
ENSMUST00000156756	ENSMUSG00000015214	X	71364760	71419196	1	0	0	0	0	0	0	0	0	9	0	0	Q8CIU3	
ENSMUST00000156757						10	7	0	3	5	4	0	0	0	0	0		
ENSMUST00000156758	ENSMUSG00000037697	14	45593174	45658143	-1	0	0	0	0	2	0	0	0	0	16	0	G3UVX0	
ENSMUST00000156759						72	62	25	39	48	32	0	0	0	0	9		
ENSMUST00000156760						3	0	0	0	0	2	0	0	0	1	2		
ENSMUST00000156761						1	3	0	0	0	2	0	0	0	3	0		
ENSMUST00000156762						0	0	0	0	0	0	4	1	0	0	3		
ENSMUST00000156763						4	3	0	3	6	1	0	3	1	0	5		
ENSMUST00000156764						5	2	7	9	7	5	0	0	1	0	4		
ENSMUST00000156765	ENSMUSG00000026888	2	64912476	65024987	-1	3	1	0	2	4	0	0	3	0	0	0	A2ASX1	
ENSMUST00000156766						0	0	0	0	0	0	476	4578	513	364	304		
ENSMUST00000156767						0	0	0	0	0	0	3	0	0	0	1		
ENSMUST00000156768	ENSMUSG00000015980	7	139212988	139242979	1	2	0	6	24	0	1	0	0	0	0	0	D3Z4G6	
ENSMUST00000156769	ENSMUSG00000056900	3	32817546	32938071	1	0	0	3	0	2	0	0	0	0	0	0	F6ZE47	
ENSMUST00000156770	ENSMUSG00000054435	6	48684549	48692060	1	0	0	0	0	0	0	0	20	12	0	0	D6RGS2	
ENSMUST00000156771	ENSMUSG00000028617	4	107233514	107253532	-1	0	1	1	13	2	1	0	0	10	0	0	D3Z416	
ENSMUST00000156772						77	85	170	71	77	62	2	8	5	3	15		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156773						6	3	5	8	4	0	0	0	0	0	0		
ENSMUST00000156775						3	2	12	16	9	1	0	0	0	0	0		
ENSMUST00000156776						0	0	1	0	1	0	0	2	3	0	4		
ENSMUST00000156777						4	2	2	3	4	2	3	8	0	0	0		
ENSMUST00000156778	ENSMUSG00000031256	X	134059187	134086819	1	0	0	0	0	0	0	0	0	5	0	0	F6ZKC7	
ENSMUST00000156779	ENSMUSG00000031090	7	143795584	143822849	-1	0	0	0	0	0	0	0	0	0	1	0	D3Z0K2	
ENSMUST00000156782	ENSMUSG00000021944	14	63198922	63271692	-1	0	5	23	0	14	3	1	0	2	1	1	A4K4Z6	
ENSMUST00000156783						7	0	14	6	9	1	0	0	0	0	0		
ENSMUST00000156784	ENSMUSG00000000581	11	17257579	17269176	1	1	3	1	25	2	0	59	420	137	460	77	A0A0A0MQK7	
ENSMUST00000156785						4	2	6	4	10	0	0	0	1	0	0		
ENSMUST00000156786						2	0	3	0	2	1	0	0	0	0	0		
ENSMUST00000156787						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000156788						0	0	0	3	0	0	19	170	18	9	49		
ENSMUST00000156789	ENSMUSG00000026649	1	171113918	171126967	1	4	0	0	1	1	0	0	4	0	0	1	A0A087WNZ4	
ENSMUST00000156791						0	0	0	52	1	0	0	0	0	0	0		
ENSMUST00000156792						11	4	32	5	9	0	0	0	0	0	0		
ENSMUST00000156793						4	9	1	0	11	6	317	1500	889	161	757		
ENSMUST00000156794						0	0	0	0	11	0	94	633	232	47	289		
ENSMUST00000156795						0	4	2	0	0	0	0	98	10	0	0		
ENSMUST00000156796						26	29	41	36	34	11	3	17	10	2	16		
ENSMUST00000156797						6	0	6	10	3	3	0	0	0	0	0		
ENSMUST00000156798	ENSMUSG00000020083	10	62107655	62143920	-1	3	0	0	2	0	0	0	0	0	0	0	D3YYX8	
ENSMUST00000156799						1	0	0	1	1	1	0	0	0	0	0		
ENSMUST00000156800						1	1	0	57	5	2	0	7	50	434	59		
ENSMUST00000156801	ENSMUSG00000031918	9	13748410	13806481	1	0	0	0	0	0	0	0	0	0	0	0	B8JJF6	
ENSMUST00000156802						1	0	3	0	0	1	19	29	15	3	13		
ENSMUST00000156805	ENSMUSG00000033852	2	120027493	120043033	1	0	0	11	0	2	0	0	0	0	0	0	B7ZCN0	
ENSMUST00000156806	ENSMUSG00000051674	5	73481000	73560794	1	2	0	0	0	0	0	0	0	0	0	0	D3Z664	
ENSMUST00000156807						2	1	1	1	1	2	0	0	0	0	0		
ENSMUST00000156808						0	0	0	0	0	0	10	16	13	2	15		
ENSMUST00000156810						1	1	13	0	7	6	0	0	0	0	0		
ENSMUST00000156811						3	0	0	0	0	0	0	3	6	0	0		
ENSMUST00000156812	ENSMUSG00000034471	11	115799183	115813639	-1	0	4	0	16	3	0	0	0	0	0	0	A0A0A0MQF9	
ENSMUST00000156813	ENSMUSG00000032698	2	103957986	103981878	1	0	0	0	0	0	0	0	0	0	0	0	A2BHP2	
ENSMUST00000156814						10	10	30	28	13	9	0	4	0	0	7		
ENSMUST00000156815						0	2	6	4	3	3	12	10	0	0	18		
ENSMUST00000156816	ENSMUSG00000033845	1	4773206	4785739	-1	52	38	73	46	41	27	9	30	13	5	16		Q9CPR5
ENSMUST00000156817	ENSMUSG00000050705	17	35892677	35897431	-1	0	0	0	0	5	0	0	0	0	0	0	B8JJ68	
ENSMUST00000156818	ENSMUSG00000086875	19	33459609	33473191	-1	5	4	3	3	1	2	0	0	0	0	0	F6QKH6	
ENSMUST00000156819	ENSMUSG00000029101	5	34949445	35039644	1	0	5	0	3	7	1	3	0	0	1	0	F7B2U5	
ENSMUST00000156820	ENSMUSG00000014599	3	107741048	107760469	-1	0	0	3	0	0	0	33	98	39	0	35	F6RNW8	
ENSMUST00000156821						0	2	2	0	1	0	40	327	91	239	98		
ENSMUST00000156824						3	5	36	61	9	4	0	0	0	0	0		
ENSMUST00000156826						0	0	0	11	1	2	0	0	0	0	0		
ENSMUST00000156828	ENSMUSG00000032921	11	68921835	68927081	-1	0	2	16	0	8	0	0	0	0	0	0	G3UX65	
ENSMUST00000156829	ENSMUSG00000029863	6	42264985	42282508	1	0	0	0	0	0	0	17	0	17	0	34	D6RFN6	
ENSMUST00000156830						0	0	0	0	0	0	0	2	0	0	2		
ENSMUST00000156832						0	3	0	0	5	3	0	0	0	0	1		
ENSMUST00000156833						2	2	3	96	8	0	0	0	0	0	0		
ENSMUST00000156834	ENSMUSG00000034312	6	90656088	90810123	-1	7	0	30	21	13	4	0	3	12	0	8		
ENSMUST00000156835	ENSMUSG00000001053	11	51643063	51650842	-1	2	0	6	95	0	6	0	0	0	0	0	A2AA66	
ENSMUST00000156836	ENSMUSG00000028629	4	120921196	120925017	-1	0	8	18	126	4	1	2	0	12	10	10	A0A0A0MQI0	
ENSMUST00000156837	ENSMUSG00000019373	11	59817795	59839838	-1	0	0	0	0	0	0	0	0	0	0	0	F6YCA7	
ENSMUST00000156838						8	10	33	8	12	0	65	796	122	58	183		
ENSMUST00000156839	ENSMUSG00000017679	2	163602314	163619013	1	1	3	4	26	4	3	0	0	0	0	3	A2A5I7	
ENSMUST00000156840						6	3	9	16	4	4	4	3	4	0	4		
ENSMUST00000156841						2	0	2	1	1	1	0	0	0	0	2		
ENSMUST00000156842						0	1	2	0	0	0	0	0	0	0	2		
ENSMUST00000156843						11	7	38	16	10	4	0	3	2	0	0		
ENSMUST00000156844	ENSMUSG00000078875	2	177000956	177012787	1	0	0	0	1	0	0	4	0	0	3	2	A2BG90	
ENSMUST00000156845						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156846	ENSMUSG00000039826	2	29761224	29788502	-1	19	13	59	20	25	22	76	199	56	20	103	H3BLS1	
ENSMUST00000156847						3	3	18	5	4	4	19	55	62	8	52		
ENSMUST00000156848						0	1	1	2	9	2	0	2	0	10	0		
ENSMUST00000156849	ENSMUSG00000030263	6	145115653	145174934	1	0	3	0	0	0	0	0	0	0	0	0	F6VUK8	
ENSMUST00000156850						2	1	2	0	6	0	0	4	4	1	0		
ENSMUST00000156851						0	0	4	23	0	0	0	1	0	0	0		
ENSMUST00000156852						117	105	482	121	117	57	6	33	16	7	36		
ENSMUST00000156853						6	13	24	22	11	5	2	32	8	2	19		
ENSMUST00000156854						18	13	59	30	18	13	13	50	15	21	37		
ENSMUST00000156855	ENSMUSG00000008318	7	100845848	100863446	-1	5	3	14	5	2	0	106	85	103	10	56	D3YWL9	
ENSMUST00000156856	ENSMUSG00000013997	1	171338008	171345646	-1	3	0	1	19	0	0	9	0	4	0	15	D3Z3I3	
ENSMUST00000156857	ENSMUSG00000026812	2	28641228	28691167	1	6	4	0	17	5	1	3	0	5	3	2	F2Z3W0	
ENSMUST00000156858						4	8	21	7	4	4	1	32	17	0	33		
ENSMUST00000156859	ENSMUSG00000025745	5	30118304	30155162	-1	24	19	36	39	49	16	143	294	189	97	159		Q8BMS1
ENSMUST00000156860						4	4	0	3	1	1	0	0	0	1	0		
ENSMUST00000156861	ENSMUSG00000060519	1	156653617	156674356	-1	0	21	29	0	13	0	12	25	10	0	12	A0A087WRX4	
ENSMUST00000156862	ENSMUSG00000002249	17	28331671	28350805	-1	0	0	0	31	0	0	0	0	0	0	0	F6TTJ9	
ENSMUST00000156863						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000156864	ENSMUSG00000068250	6	149157147	149188712	-1	0	0	0	0	0	0	0	58	4	0	0		
ENSMUST00000156865	ENSMUSG00000064329	2	66270778	66440840	-1	0	4	0	0	7	3	0	0	0	0	0		
ENSMUST00000156866						0	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000156867						1	0	4	1	3	0	0	9	4	0	2		
ENSMUST00000156868						1	0	0	0	1	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156869						6	10	10	13	7	5	2	1	4	0	2		
ENSMUST00000156870						0	0	0	0	0	3	0	0	12	0	0		
ENSMUST00000156871						5	2	1	1	0	1	1	1	1	0	3		
ENSMUST00000156872						18	11	32	32	22	10	33	813	38	22	124		
ENSMUST00000156873	ENSMUSG00000064246	1	134182176	134190181	1	11	0	5	10	0	4	241	6362	38	0	0		Q61362
ENSMUST00000156874						2	4	0	5	0	1	0	0	0	0	0		
ENSMUST00000156876	ENSMUSG00000041439	1	52656286	52727462	-1	0	0	34	255	14	18	828	2251	1221	82	1106	D3Z183	
ENSMUST00000156877	ENSMUSG00000020225	10	120201590	120224917	1	0	0	0	4	0	0	24	0	12	27	25	D3YZA0	
ENSMUST00000156878						40	32	160	165	59	28	96	303	193	7	212		
ENSMUST00000156879	ENSMUSG00000034563	9	72985429	73016340	1	0	0	0	33	0	0	3	12	18	3	17	D3Z5G5	
ENSMUST00000156880						0	0	5	8	0	0	0	0	0	0	0		
ENSMUST00000156881						12	6	8	7	12	6	0	0	0	0	0		
ENSMUST00000156883						0	0	1	1	4	0	0	0	0	0	0		
ENSMUST00000156884						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156885						0	1	2	1	4	4	0	0	0	0	0		
ENSMUST00000156886	ENSMUSG00000030450	7	56239760	56536518	1	0	0	0	0	0	1	0	0	0	0	0	D3Z251	
ENSMUST00000156887	ENSMUSG00000026103	1	52163448	52233232	-1	0	0	0	0	0	0	0	0	0	5	13	F7B327	
ENSMUST00000156888						1	4	23	10	12	3	4	3	4	0	5		
ENSMUST00000156889	ENSMUSG00000014301	16	4616464	4624988	-1	0	0	0	0	0	2	0	0	0	0	0	D6RI93	
ENSMUST00000156890						11	3	8	137	9	2	7	5	5	0	3		
ENSMUST00000156891						0	2	0	11	0	0	20	115	64	0	83		
ENSMUST00000156893	ENSMUSG00000027655	2	158794807	158858214	1	0	0	0	0	0	0	0	0	0	0	0	A2ACP9	
ENSMUST00000156894						0	2	7	10	3	2	13	37	29	0	30		
ENSMUST00000156895	ENSMUSG00000039997	1	173920407	173942672	-1	1	0	0	0	0	0	0	0	0	18	0		
ENSMUST00000156896						0	0	60	0	3	0	48	196	123	15	176		
ENSMUST00000156897	ENSMUSG00000039911	4	149896283	149955043	-1	0	0	3	0	0	0	0	0	0	0	0	A2A7B3	
ENSMUST00000156898	ENSMUSG00000079426	6	113378113	113390448	1	0	10	0	4	28	10	1123	1092	1179	116	914		P59999
ENSMUST00000156899						13	9	21	1	8	5	1	2	2	0	3		
ENSMUST00000156900						1	0	0	11	0	0	0	162	22	0	0		
ENSMUST00000156901						0	0	0	134	2	2	12	7	22	11	13		
ENSMUST00000156902						4	2	13	43	5	2	5	7	4	2	5		
ENSMUST00000156904	ENSMUSG00000020573	12	32173473	32208659	-1	23	10	8	22	21	3	404	1542	1209	345	929		Q9JHG7
ENSMUST00000156905						0	0	0	90	0	0	0	0	0	0	0		
ENSMUST00000156906						7	4	24	10	16	5	1	5	1	2	0		
ENSMUST00000156907						10	0	10	100	12	10	8	17	22	0	35		
ENSMUST00000156908						10	8	19	16	12	5	287	1293	647	171	716		
ENSMUST00000156909						0	0	2	7	2	0	0	0	0	0	0		
ENSMUST00000156910						11	5	9	0	0	3	10	55	0	14	9		
ENSMUST00000156911						0	0	8	2	0	0	0	8	35	0	39		
ENSMUST00000156913						1	0	3	1	8	4	10	9	10	0	10		
ENSMUST00000156914						0	0	0	25	3	1	0	0	0	0	0		
ENSMUST00000156915	ENSMUSG00000014313	15	35925886	35938246	-1	0	0	0	52	0	0	0	0	0	0	3	D3Z6E1	
ENSMUST00000156916						0	1	4	5	4	3	0	0	0	0	0		
ENSMUST00000156917						3	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000156918	ENSMUSG00000048537	9	44686304	44735198	-1	0	0	0	3	0	5	2	0	6	0	0	E9Q307	
ENSMUST00000156919	ENSMUSG00000027257	2	91255954	91264679	1	0	1	3	0	2	0	0	1	0	0	0	B1AW93	
ENSMUST00000156920	ENSMUSG00000033819	15	76671615	76694919	1	0	0	0	0	0	0	0	0	0	3	0	F6TBE5	
ENSMUST00000156921	ENSMUSG00000046364	7	109519147	109522367	1	3	0	6	102	5	0	0	7	3	0	9	G3UZV5	
ENSMUST00000156922	ENSMUSG00000051675	4	65604986	65616238	1	7	0	8	47	2	3	0	0	0	0	0	A2AGS1	
ENSMUST00000156923						2	0	28	61	2	11	1	5	2	0	0		
ENSMUST00000156924						4	2	3	7	9	0	1	10	3	0	2		
ENSMUST00000156927	ENSMUSG00000058794	15	103248212	103258403	-1	0	0	0	0	0	0	48	574	0	0	0		
ENSMUST00000156928						1	5	11	1	8	0	6	7	18	0	13		
ENSMUST00000156929						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156931						9	5	7	5	10	7	4	52	25	14	28		
ENSMUST00000156932	ENSMUSG00000018750	11	69765912	69784023	1	0	3	0	10	0	0	2	0	0	0	8	B0QZJ2	
ENSMUST00000156933	ENSMUSG00000057110	2	35109492	35178822	1	0	0	18	0	0	0	288	0	1530	202	1511	R4GML6	A2AL36
ENSMUST00000156934						1044	972	3018	800	1251	546	16	78	46	14	81		
ENSMUST00000156935	ENSMUSG00000069565	10	80261486	80288408	1	0	2	2	0	2	0	70	13	0	16	0	D3Z4J1	
ENSMUST00000156936						2	0	0	0	1	0	0	22	0	0	0		
ENSMUST00000156938						4	5	28	12	4	10	14	51	0	3	37		
ENSMUST00000156939						0	1	1	1	6	0	0	0	0	0	0		
ENSMUST00000156940						2	2	12	16	3	3	2	7	0	0	2		
ENSMUST00000156941						18	0	37	12	35	18	0	0	0	0	0		
ENSMUST00000156942						0	2	2	83	4	1	0	0	0	0	0		
ENSMUST00000156944						2	2	8	3	2	0	10	14	14	7	18		
ENSMUST00000156945	ENSMUSG00000024169	17	25016091	25099495	1	0	1	0	0	2	0	2	9	2	0	7	E9Q925	
ENSMUST00000156946						23	12	14	46	11	16	2	8	3	2	13		
ENSMUST00000156948						2	0	4	8	3	0	31	158	78	8	73		
ENSMUST00000156949						2	1	0	46	5	0	0	0	0	0	0		
ENSMUST00000156951	ENSMUSG00000022779	16	16870736	16892990	1	8	8	14	13	13	0	3	25	20	0	19	F6SDD7	
ENSMUST00000156952						23	17	46	1113	40	25	3	6	0	0	4		
ENSMUST00000156953						0	0	0	0	2	0	0	1	0	0	0		
ENSMUST00000156954	ENSMUSG00000035576	2	162943472	162974522	1	0	1	0	0	0	0	0	0	0	0	0	Q3V558	
ENSMUST00000156955						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000156956						2	5	0	0	0	0	0	23	6	0	5		
ENSMUST00000156957	ENSMUSG00000038704	7	44465391	44467758	1	0	0	4	28	0	0	0	0	0	0	1	F6S4J6	
ENSMUST00000156958						0	6	9	0	9	0	75	5	847	52	610		
ENSMUST00000156959	ENSMUSG00000031397	X	74177259	74208500	1	0	0	0	2	0	0	0	0	0	0	0	D6REV0	
ENSMUST00000156960						2	0	1	0	0	2	0	0	6	4	0		
ENSMUST00000156961						6	5	0	1	0	0	0	0	0	0	0		
ENSMUST00000156962						15	9	26	13	15	8	0	0	0	0	0		
ENSMUST00000156963	ENSMUSG00000059518	5	136982164	136988021	-1	4	1	6	169	10	8	10	31	31	15	19		
ENSMUST00000156964						3	3	7	5	5	0	0	0	0	0	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000156966						0	1	2	37	2	0	0	0	6	0	0		
ENSMUST00000156967						1	0	0	100	2	0	4	0	0	0	0		
ENSMUST00000156968	ENSMUSG00000028884	4	132768332	132778752	1	57	49	411	99	41	33	2	8	5	0	5	F6V8R7	
ENSMUST00000156969	ENSMUSG00000000384	11	6615598	6626067	-1	7	8	22	0	0	6	150	306	124	31	37		Q91YM4
ENSMUST00000156970	ENSMUSG00000003808	8	84856989	84869257	1	8	0	23	0	0	0	63	0	0	0	30	D6RIJ2	
ENSMUST00000156971						0	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000156972						0	6	0	0	7	0	0	0	0	0	0		
ENSMUST00000156973	ENSMUSG00000008307	5	3571566	3584356	1	0	0	0	1	0	0	0	2	0	0	0	F6QJ46	
ENSMUST00000156975						13	2	19	8	6	5	29	46	34	1	61		
ENSMUST00000156978						1	0	1	0	1	2	1	2	0	3	10		
ENSMUST00000156979	ENSMUSG00000035864	10	108497650	109010982	-1	0	2	0	3	6	0	0	0	0	0	0	D3Z7R4	
ENSMUST00000156980	ENSMUSG00000037921	8	61928087	62037701	1	5	4	14	4	2	2	1	1	2	2	8	D3YZ76	
ENSMUST00000156981	ENSMUSG00000022708	16	42875881	43642602	1	0	0	0	12	1	0	1	0	0	0	0	E0CYH3	
ENSMUST00000156982						3	4	7	3	3	5	4	38	10	1	9		
ENSMUST00000156983	ENSMUSG00000037174	3	51252720	51340663	-1	0	4	0	55	8	1	0	0	0	0	0	A0A0A6YWF3	
ENSMUST00000156984						2	1	0	11	0	0	0	0	0	0	0		
ENSMUST00000156985						0	0	0	0	0	0	1	3	0	0	9		
ENSMUST00000156986						8	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000156987						5	4	1	4	0	2	20	38	25	12	28		
ENSMUST00000156988	ENSMUSG00000037742	9	78478449	78489151	-1	0	10	34	41	10	6	94	208	141	0	194	D3Z3I8	
ENSMUST00000156989						2	0	2	4	0	0	0	0	0	0	0		
ENSMUST00000156990	ENSMUSG00000020167	10	80409514	80433647	-1	0	0	17	23	0	12	0	0	46	0	0	F6T941	
ENSMUST00000156992	ENSMUSG00000030761	7	98051060	98119524	-1	8	11	15	9	0	3	23	44	19	15	62		
ENSMUST00000156993	ENSMUSG00000074646	2	155973279	156007977	-1	0	0	0	0	0	3	0	0	1	0	0	B7ZCN7	
ENSMUST00000156995						0	0	0	0	0	0	0	4	0	0	7		
ENSMUST00000156996	ENSMUSG00000015001	15	65876053	65912397	-1	0	2	0	9	13	2	0	0	0	0	0	F6T2M1	
ENSMUST00000156997						22	7	70	20	25	14	36	73	59	0	38		
ENSMUST00000156998						0	0	0	0	0	1	0	0	0	5	0		
ENSMUST00000156999						0	1	0	162	10	2	0	1	0	0	0		
ENSMUST00000157000						2	0	4	0	3	3	0	0	0	0	0		
ENSMUST00000157001						0	4	3	41	2	0	0	12	7	106	90		
ENSMUST00000157002						16	16	33	116	24	12	0	0	0	0	0		
ENSMUST00000157003						0	0	1	5	0	3	0	2	0	4	0		
ENSMUST00000157004						0	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000157005	ENSMUSG00000001521	6	128321161	128355851	-1	82	78	547	148	81	43	1	3	6	0	10		
ENSMUST00000157006	ENSMUSG00000032564	9	104547286	105034544	1	2	0	0	0	1	2	0	0	0	0	0	D3Z5V2	
ENSMUST00000157007						7	4	16	2	4	5	0	0	0	0	3		
ENSMUST00000157008						4	1	7	1	3	2	4	2	5	0	4		
ENSMUST00000157009	ENSMUSG00000019843	10	39368855	39565381	1	0	1	17	1	3	0	0	0	0	0	0	D3YVZ0	
ENSMUST00000157012	ENSMUSG00000043411	4	137593755	137658537	1	0	0	0	0	0	0	12	100	4	13	0	F6VSQ9	
ENSMUST00000157013						0	0	0	0	0	0	7	111	0	0	0		
ENSMUST00000157014						2	1	16	5	2	0	0	0	0	0	0		
ENSMUST00000157015	ENSMUSG00000013973	1	171329145	171342331	1	0	0	0	0	2	0	6	6	2	1	4		
ENSMUST00000157016						1	5	16	5	9	4	0	0	0	0	0		
ENSMUST00000157017	ENSMUSG00000053390	17	32993129	33005457	1	3	4	0	0	2	0	0	13	0	3	2	B0V2W3	
ENSMUST00000157019	ENSMUSG00000055612	2	72476159	72486893	1	15	2	5	17	7	0	0	0	0	0	0	A2AR39	
ENSMUST00000157020	ENSMUSG00000094814	15	10325380	10373749	1	0	0	0	0	0	0	0	0	0	0	0	F6WEZ7	
ENSMUST00000157021	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	1	1	0	0	2	G3UYQ0	
ENSMUST00000157023						8	7	9	10	7	6	3	6	5	3	5		
ENSMUST00000157024						388	342	1354	437	494	233	15	77	45	11	34		
ENSMUST00000157025						20	20	37	16	32	9	4	11	3	1	14		
ENSMUST00000157026						0	0	3	0	0	0	5	2	4	0	4		
ENSMUST00000157027	ENSMUSG00000060600	11	70657202	70662513	1	2	0	3	0	0	3	3	6	16	0	14	Q5SX59	
ENSMUST00000157028	ENSMUSG00000030881	7	105634203	105640416	-1	0	0	0	0	0	3	0	0	1	4	19	D6RI79	
ENSMUST00000157029						0	0	0	0	0	0	70	38	132	49	59		
ENSMUST00000157030						0	2	1	4	1	0	0	0	0	0	0		
ENSMUST00000157031						84	69	85	43	83	44	1	37	19	4	21		
ENSMUST00000157032						16	11	28	43	26	15	0	2	0	0	0		
ENSMUST00000157033						5	0	4	3	6	2	2	0	2	0	0		
ENSMUST00000157034	ENSMUSG00000022201	15	12117831	12185683	1	1	0	0	0	0	0	29	146	38	49	0	F6RTK9	
ENSMUST00000157035						0	0	0	0	1	0	0	4	2	0	8		
ENSMUST00000157036						13	17	16	13	17	7	1	19	6	6	14		
ENSMUST00000157037						85	102	115	99	77	49	23	111	61	12	83		
ENSMUST00000157038						2	1	5	32	3	1	4	0	0	7	4		
ENSMUST00000157039						0	0	0	0	0	0	0	0	0	4	3		
ENSMUST00000157040	ENSMUSG00000051855	6	30723547	30748465	1	0	0	0	0	0	0	0	0	2	0	0	D3Z328	Q07646
ENSMUST00000157041						1	2	2	0	2	2	0	16	0	2	21		
ENSMUST00000157043						0	4	7	62	1	0	0	0	0	0	2		
ENSMUST00000157044	ENSMUSG00000005980	16	4036942	4040024	1	0	1	1	0	0	0	1	0	0	2	0	D3YXC7	
ENSMUST00000157045						0	0	0	74	8	5	0	24	9	25	24		
ENSMUST00000157046						2	1	10	0	9	0	0	0	0	0	0		
ENSMUST00000157047						2	0	0	121	4	2	0	0	0	0	2		
ENSMUST00000157048	ENSMUSG00000079502	2	28926949	29055066	-1	2	0	4	101	5	3	0	0	0	0	0	B2RWG1	
ENSMUST00000157049						0	3	0	1	2	2	0	0	0	3	4		
ENSMUST00000157050	ENSMUSG00000029528	5	115506676	115555987	1	3	1	6	0	2	1	131	19	70	3	41		
ENSMUST00000157051						1	0	0	1	1	0	0	0	0	2	3		
ENSMUST00000157052						0	1	0	3	1	0	0	0	0	2	2		
ENSMUST00000157053						0	0	0	0	0	0	0	18	0	0	0		
ENSMUST00000157054						8	6	7	11	13	6	0	1	1	0	1		
ENSMUST00000157055						2	5	10	10	5	1	1	7	0	1	2		
ENSMUST00000157056	ENSMUSG00000034006	18	80253292	80292725	1	0	0	0	0	0	0	0	0	0	0	0	D3YYH5	
ENSMUST00000157060	ENSMUSG00000040666	16	96200470	96228933	1	0	0	0	33	0	0	0	0	0	0	0	F7CKA6	
ENSMUST00000157061	ENSMUSG00000020781	11	115814724	115823094	1	4	3	2	3	4	0	3	5	0	0	0	F6X5E8	
ENSMUST00000157062						3	3	2	0	1	2	0	0	0	1	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000157063						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000157064						2	3	8	7	2	3	0	0	0	0	1		
ENSMUST00000157065	ENSMUSG00000005360	15	8634124	8710764	-1	1	1	0	1	0	2	0	0	0	0	0	D3YY51	
ENSMUST00000157066						0	0	0	0	0	0	1	21	8	0	1		
ENSMUST00000157067	ENSMUSG00000003644	4	133847290	133887797	-1	13	6	51	4	28	9	17	33	32	0	58	F6RQA2	
ENSMUST00000157068						3	3	3	7	6	2	0	0	0	0	0		
ENSMUST00000157069						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000157070						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000157071	ENSMUSG00000044770	10	42860370	42960780	1	0	0	0	0	0	0	0	0	0	0	0	D3Z554	
ENSMUST00000157072						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000157073						47	32	66	67	102	29	2	3	0	2	3		
ENSMUST00000157074						34	15	50	25	24	13	6	9	16	1	16		
ENSMUST00000157075	ENSMUSG00000020828	11	70540064	70558110	1	0	0	0	0	0	0	2	1	0	0	0	J3QK47	
ENSMUST00000157076						2	5	3	22	0	0	0	3	2	0	2		
ENSMUST00000157077						5	3	10	10	4	7	2	18	10	0	12		
ENSMUST00000157078						2	1	2	5	1	1	3	14	0	3	10		
ENSMUST00000157079						10	2	14	4	11	3	0	0	0	0	0		
ENSMUST00000159002	ENSMUSG00000075000	10	67266689	67285305	-1	0	2	9	0	6	2	5	3	42	19	27	E0CZ57	
ENSMUST00000159003						4	2	2	1	2	2	0	0	0	0	0		
ENSMUST00000159004	ENSMUSG00000093973	7	47426328	47452139	-1	0	4	45	15	11	0	625	2635	545	361	446		
ENSMUST00000159005						3	0	6	11	2	0	0	0	0	0	3		
ENSMUST00000159007	ENSMUSG00000000378	11	6546887	6596744	1	0	0	0	4	0	0	0	0	3	6	0	E0CZ84	
ENSMUST00000159008						2	0	0	6	2	0	0	3	2	0	0		
ENSMUST00000159009	ENSMUSG00000050410	17	35512734	35516824	-1	0	0	2	0	0	0	23	4	19	0	8	E0CY69	
ENSMUST00000159010						4	5	6	9	9	3	0	0	0	0	4		
ENSMUST00000159012						0	0	0	2	0	12	0	0	0	0	0		
ENSMUST00000159013						0	0	0	4	2	3	1	0	4	0	0		
ENSMUST00000159014						10	7	11	5	9	12	3	0	20	0	0		
ENSMUST00000159016	ENSMUSG00000020329	10	79736123	79746581	-1	6	3	0	27	0	3	45	38	1	5	91	E9PWD9	
ENSMUST00000159017						0	2	0	0	0	0	4	0	12	0	0		
ENSMUST00000159018	ENSMUSG00000038722	5	145140362	145148078	1	7	0	0	0	0	0	56	273	153	1195	121	E0CX20	
ENSMUST00000159019						0	1	0	2	0	0	0	13	1	12	0		
ENSMUST00000159020	ENSMUSG00000020077	10	62493833	62527451	-1	3	0	0	1	1	0	9	30	42	114	16	E0CZH1	
ENSMUST00000159021	ENSMUSG00000037509	1	34678188	34813309	1	0	0	0	48	0	0	0	2	0	0	0	E0CY60	
ENSMUST00000159022						0	0	0	0	4	0	0	0	0	0	2		
ENSMUST00000159023						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000159024	ENSMUSG00000021461	13	63304709	63497278	-1	3	0	6	5	3	0	0	0	1	0	0	E0CYC3	
ENSMUST00000159025						0	0	3	0	2	1	0	0	0	0	0		
ENSMUST00000159026	ENSMUSG00000033060	14	101729957	101934710	1	0	0	6	0	1	6	0	0	0	0	0	Q3UPW3	
ENSMUST00000159027	ENSMUSG00000021816	14	20499364	20546573	-1	0	0	7	23	0	0	7	37	0	0	9		P48453
ENSMUST00000159028	ENSMUSG00000043004	14	19872559	19977627	-1	0	0	0	0	0	0	50	86	62	243	31		P63213
ENSMUST00000159029						10	2	17	6	5	8	86	64	41	15	19		
ENSMUST00000159033	ENSMUSG00000034908	9	45937857	45955247	-1	1	1	1	9	0	3	6	0	3	0	0	F7CNB6	
ENSMUST00000159034	ENSMUSG00000026799	2	29346819	29524793	1	0	0	0	0	0	0	0	0	0	0	0	E0CYF9	
ENSMUST00000159035	ENSMUSG00000006014	1	150449412	150466165	-1	0	0	0	0	0	1	0	0	0	0	0	E0CY90	
ENSMUST00000159036						0	0	0	40	0	4	0	0	0	0	0		
ENSMUST00000159038	ENSMUSG00000059149	1	132022806	132068062	-1	0	0	0	0	0	0	0	0	0	0	0		Q6PDC8
ENSMUST00000159039	ENSMUSG00000031876	8	104281347	104310145	-1	3	2	28	39	0	2	0	0	10	3	1	B7ZP21	
ENSMUST00000159041	ENSMUSG00000026335	1	97795114	98095646	-1	2	2	6	0	5	1	0	0	0	0	0	F6TGI4	
ENSMUST00000159042						15	14	29	14	14	15	0	0	9	2	0		
ENSMUST00000159043	ENSMUSG00000019952	10	99107036	99198074	1	4	1	0	0	0	0	4	0	0	0	6	F6VAH7	
ENSMUST00000159044						3	0	6	0	12	3	0	0	0	0	0		
ENSMUST00000159045						0	1	0	0	0	0	1	0	1	11	0		
ENSMUST00000159046	ENSMUSG00000022150	15	6299788	6440712	1	0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000159047						0	0	0	4	0	0	20	2	14	0	7		
ENSMUST00000159048	ENSMUSG00000024112	17	25374285	25433783	-1	0	35	43	59	70	0	0	0	1	0	1	E0CYZ3	
ENSMUST00000159049						0	1	0	2	3	0	0	1	0	0	5		
ENSMUST00000159050	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	30	0	177	0	0	E0CXS9	
ENSMUST00000159051						3	2	9	8	6	4	0	0	0	0	0		
ENSMUST00000159052						16	8	51	134	11	6	0	1	0	0	0		
ENSMUST00000159054	ENSMUSG00000022452	15	82338959	82349091	1	1	0	0	0	2	2	13	34	4	4	15	E0CZF0	
ENSMUST00000159055	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	10	251	14	8	1	0	0	0	0	E0CYU3	
ENSMUST00000159056						8	1	8	7	4	6	0	0	0	0	0		
ENSMUST00000159057						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000159058						448	349	2354	509	526	271	13	37	39	16	51		
ENSMUST00000159059						0	0	0	88	4	4	2	8	3	0	2		
ENSMUST00000159060						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159061						1	0	7	2	1	0	0	0	0	0	1		
ENSMUST00000159062	ENSMUSG00000047013	6	85469574	85502994	-1	0	0	0	458	85	15	0	0	0	0	0	Q3UGY7	Q6NS60
ENSMUST00000159063	ENSMUSG00000023994	17	48386885	48409906	-1	0	0	0	0	0	0	42	0	124	4	59		
ENSMUST00000159064	ENSMUSG00000027942	3	90051636	90068347	1	1	0	0	3	2	0	0	0	56	172	70		Q8R092
ENSMUST00000159065	ENSMUSG00000055692	16	17276300	17283229	1	0	0	22	0	11	0	0	0	0	0	0		Q9JJB1
ENSMUST00000159066	ENSMUSG00000089872	1	190700202	190911770	-1	0	0	0	35	4	0	4	0	0	0	4	E0CY13	
ENSMUST00000159067	ENSMUSG00000106247	5	138264952	138279958	-1	51	26	187	104	65	29	0	3	0	3	0	E0CXM8	
ENSMUST00000159068	ENSMUSG00000045875	14	66635251	66733462	1	32	16	39	48	24	22	1	0	1	0	0		P97718
ENSMUST00000159069						2	4	6	1	3	4	133	49	253	2	219		
ENSMUST00000159070						5	3	5	4	4	1	0	0	0	0	5		
ENSMUST00000159073	ENSMUSG00000043004	14	19872559	19977627	-1	5	1	14	6	3	6	0	10	16	444	0		P63213
ENSMUST00000159074	ENSMUSG00000029634	5	146209192	146221555	-1	0	0	0	0	0	0	6	15	0	0	0	E0CYS7	
ENSMUST00000159075						1	1	5	0	0	0	0	0	0	0	0		
ENSMUST00000159076	ENSMUSG00000040340	8	3470862	3487181	1	0	9	0	0	0	6	0	0	19	0	0	Q80YS7	
ENSMUST00000159077						1	1	4	2	0	0	0	6	0	5	4		
ENSMUST00000159078	ENSMUSG00000026163	1	83254139	83408200	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159079	ENSMUSG00000079036	12	87425840	87444017	-1	0	0	0	0	0	0	0	0	0	0	0	E0CY72	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159080						12	11	13	6	14	9	4	28	10	6	27		
ENSMUST00000159081	ENSMUSG00000051355	11	22896136	22982382	-1	19	21	38	74	29	22	20	26	3	26	12	A2RSF1	Q8K4M5
ENSMUST00000159082						0	0	0	0	0	0	13	25	19	0	0		
ENSMUST00000159083						8	6	11	8	7	3	0	0	0	0	0		
ENSMUST00000159084	ENSMUSG00000024799	19	6062821	6068373	-1	0	0	0	4	2	0	0	0	0	0	0	E0CX74	
ENSMUST00000159085	ENSMUSG00000003721	1	121304353	121332589	-1	3	0	7	8	10	0	0	0	0	0	0		Q91WG1
ENSMUST00000159086	ENSMUSG00000024298	17	32771236	32788287	-1	28	34	79	48	56	21	272	317	640	51	527	G5E905	
ENSMUST00000159088						1	0	0	84	5	0	0	0	0	0	0		
ENSMUST00000159089						1	0	7	0	0	0	0	5	0	2	4		
ENSMUST00000159090						0	3	2	1	1	2	5	26	8	8	46		
ENSMUST00000159091						0	0	7	0	10	0	42	238	78	0	93		
ENSMUST00000159092						9	0	5	0	4	5	19	54	131	48	160		
ENSMUST00000159093	ENSMUSG00000072663	15	9578193	9748868	-1	0	0	0	0	0	0	0	0	0	0	0	E0CX63	
ENSMUST00000159094						5	0	15	10	5	5	0	0	0	0	0		
ENSMUST00000159095						0	2	0	0	0	2	1	0	0	0	0		
ENSMUST00000159096	ENSMUSG00000025533	5	130011258	130029247	-1	0	2	0	1	3	0	167	279	155	14	92	F7D439	
ENSMUST00000159098						4	4	5	1	3	1	0	0	0	0	0		
ENSMUST00000159099	ENSMUSG00000001366	9	78081499	78109065	-1	7	1	8	0	2	2	22	68	28	0	44		Q8BK06
ENSMUST00000159100	ENSMUSG00000032534	9	102584598	102626534	-1	0	0	0	10	0	0	0	0	3	0	0	E0CX88	
ENSMUST00000159101	ENSMUSG00000032295	9	57130690	57142722	1	0	0	0	0	0	0	0	31	0	0	0	F6TFL1	
ENSMUST00000159102						7	3	14	8	0	0	9	13	27	2	43		
ENSMUST00000159103						3	0	0	0	0	0	0	1	0	1	0		
ENSMUST00000159104	ENSMUSG00000060475	17	12966796	12992546	-1	0	0	0	0	0	0	19	12	47	41	4	F7CCI4	
ENSMUST00000159105						4	0	4	0	1	6	3	52	20	6	13		
ENSMUST00000159106						3	1	13	0	4	5	1	0	2	2	4		
ENSMUST00000159107						1	2	4	7	0	0	0	1	2	2	0		
ENSMUST00000159109	ENSMUSG00000040524	9	65692391	65827564	-1	46	38	185	70	82	41	298	389	597	32	505		Q8BZ47
ENSMUST00000159110	ENSMUSG00000019979	10	90989311	91082770	-1	0	15	0	9	0	0	837	2180	954	63	569		O88879
ENSMUST00000159111						19	9	40	16	20	9	0	0	1	0	2		
ENSMUST00000159112						0	0	2	1	0	1	0	0	0	0	0		
ENSMUST00000159114						10	16	9	30	35	10	0	2	3	1	3		
ENSMUST00000159115						1	0	3	3	4	3	0	0	0	0	0		
ENSMUST00000159116						5	1	3	58	2	0	6	7	5	0	14		
ENSMUST00000159118						0	0	0	3	1	1	0	0	0	0	0		
ENSMUST00000159120	ENSMUSG00000036523	12	16670615	16800886	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXG4	
ENSMUST00000159121						1	0	11	0	7	2	0	8	9	0	10		
ENSMUST00000159122	ENSMUSG00000052760	1	85717083	85778643	-1	28	21	36	29	43	14	0	0	16	0	0	Q3UTB2	
ENSMUST00000159123	ENSMUSG00000036948	5	138259656	138264033	-1	0	0	0	0	0	0	50	546	62	0	115	E9Q6X8	
ENSMUST00000159124	ENSMUSG00000003500	6	29200434	29216364	-1	10	0	0	66	30	11	0	0	0	0	69		P50096
ENSMUST00000159125	ENSMUSG00000003721	1	121304353	121332589	-1	0	0	1	0	0	0	1	0	0	1	0	E0CZ00	
ENSMUST00000159126						0	0	4	0	0	13	0	0	0	0	6		
ENSMUST00000159127	ENSMUSG00000023830	17	12682406	12769664	-1	0	2	6	3	1	0	0	0	0	0	0		
ENSMUST00000159128						0	0	13	9	0	7	0	3	0	1	4		
ENSMUST00000159129						0	1	0	0	3	2	0	0	0	0	0		
ENSMUST00000159130	ENSMUSG00000032295	9	57130690	57142722	1	4	1	8	6	2	5	49	19	11	0	45	E0CZB0	
ENSMUST00000159131						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000159132	ENSMUSG00000022558	15	76380261	76453038	1	0	0	0	0	0	0	6	88	4	0	0		
ENSMUST00000159135						0	1	0	5	1	0	3	0	0	0	0		
ENSMUST00000159136						8	0	39	3	10	14	30	0	76	0	65		
ENSMUST00000159137						3	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000159139	ENSMUSG00000038240	10	43221486	43464882	1	3	6	3	22	3	0	0	0	0	0	0		Q33DR3
ENSMUST00000159140						46	38	119	74	70	32	174	259	208	10	476		
ENSMUST00000159141	ENSMUSG00000025812	8	127063893	127612286	1	2	2	12	20	5	2	0	0	0	0	0	E0CXD3	
ENSMUST00000159143						2	5	6	7	2	0	2	0	0	0	0		
ENSMUST00000159144						0	0	1	0	0	0	0	2	0	0	3		
ENSMUST00000159145	ENSMUSG00000056832	6	38381469	38427647	1	0	77	36	25	20	0	0	0	0	0	0	E0CX73	
ENSMUST00000159146	ENSMUSG00000036948	5	138259656	138264033	-1	0	0	0	0	0	0	0	0	0	0	0	F6VAB1	
ENSMUST00000159147	ENSMUSG00000021481	13	55105311	55134825	1	0	0	0	0	0	0	0	0	0	6	0	E9PYN2	
ENSMUST00000159148	ENSMUSG00000024857	19	4081578	4087340	1	5	4	14	3	6	3	0	0	0	0	0	G5E8W3	
ENSMUST00000159149	ENSMUSG00000038421	1	170917576	170927583	-1	7	0	2	6	3	0	0	10	0	16	2	F7DEW9	
ENSMUST00000159150						0	0	0	1	1	0	0	0	55	156	34		
ENSMUST00000159151						1	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000159152	ENSMUSG00000021458	13	63014934	63326096	1	23	24	97	26	18	11	0	3	3	1	0	F6SS74	
ENSMUST00000159154						20	28	47	33	27	7	1	0	0	0	4		
ENSMUST00000159156	ENSMUSG00000046111	9	15316915	15357788	-1	0	1	0	0	0	0	0	0	0	0	0	F6URK1	
ENSMUST00000159158	ENSMUSG00000064373	15	3268547	3280508	1	3	0	2	2	2	0	3	0	0	2	0	E0CZ76	
ENSMUST00000159159	ENSMUSG00000074207	3	138260991	138290698	1	10	0	16	8	9	6	0	1	0	19	3	E0CXV3	
ENSMUST00000159160	ENSMUSG00000022906	16	35938470	35972605	1	8	6	12	8	5	0	9	6	11	3	13	F6U1Y8	
ENSMUST00000159161						136	88	540	162	160	72	1	4	2	1	11		
ENSMUST00000159162	ENSMUSG00000024558	18	73928486	74065359	-1	7	0	0	10	0	0	0	0	0	0	0	E9Q3I6	
ENSMUST00000159163	ENSMUSG00000037542	10	21377291	21396585	1	1	0	0	0	0	1	0	0	0	0	0	F6T4U0	
ENSMUST00000159164	ENSMUSG00000029275	5	107716657	107726036	-1	0	0	0	6	0	0	1	0	1	0	0		
ENSMUST00000159165						0	0	0	0	0	0	1	0	0	1	0		
ENSMUST00000159166						53	37	90	34	59	24	20	36	16	3	21		
ENSMUST00000159167						23	19	78	44	28	15	0	0	1	0	1		
ENSMUST00000159168	ENSMUSG00000089862	6	8259288	8459470	1	2	0	0	0	2	0	80	153	0	0	0	E0CXP6	
ENSMUST00000159169	ENSMUSG00000021990	14	60634001	60764556	1	5	6	0	6	5	0	0	0	0	0	0	E0CXN6	
ENSMUST00000159170						3	2	3	22	7	8	0	2	2	0	2		
ENSMUST00000159171	ENSMUSG00000038421	1	170917576	170927583	-1	0	0	5	5	0	5	15	0	19	23	64		Q920A9
ENSMUST00000159172						6	2	6	79	3	2	2	0	0	0	0		
ENSMUST00000159173	ENSMUSG00000041879	1	135382312	135430499	-1	0	0	2	8	0	0	0	0	3	0	0	F6UT58	
ENSMUST00000159174						1	2	0	5	0	1	0	0	0	0	0		
ENSMUST00000159175	ENSMUSG00000090166	14	43922720	43923559	-1	10	1	6	0	2	0	0	0	0	0	0	Q923L6	
ENSMUST00000159176						0	3	0	0	0	0	299	41	89	0	38		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159177						15	17	9	10	17	13	0	0	0	0	0		
ENSMUST00000159178	ENSMUSG00000052942	19	28258851	28680077	-1	4	3	6	5	1	4	0	0	0	0	0	E0CX93	
ENSMUST00000159179						2	2	5	4	3	3	0	0	0	0	0		
ENSMUST00000159180	ENSMUSG00000003469	14	70457476	70468832	1	5	2	0	0	2	0	0	0	0	0	0	E0CXJ1	
ENSMUST00000159181						5	4	18	20	8	2	0	0	0	5	0		
ENSMUST00000159182						1	0	0	0	1	1	0	1	1	2	1		
ENSMUST00000159183						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159184						7	5	5	9	5	5	9	16	2	0	2		
ENSMUST00000159185						0	0	0	26	0	0	0	0	0	0	0		
ENSMUST00000159186	ENSMUSG00000028931	4	152390742	152477871	-1	4	1	0	0	9	0	29	0	13	0	13	E0CXZ9	
ENSMUST00000159187						0	1	6	1	0	3	0	0	0	0	0		
ENSMUST00000159188	ENSMUSG00000036834	3	63696234	63899472	-1	2	3	32	8	3	0	0	0	0	0	0	E0CY47	
ENSMUST00000159189	ENSMUSG00000036928	5	138280240	138312393	1	0	0	1	0	0	2	0	8	1	0	0	F6TV98	
ENSMUST00000159192						0	0	0	1	0	0	0	0	0	0	4		
ENSMUST00000159193	ENSMUSG00000020177	10	117232237	117238703	-1	3	2	6	4	5	0	0	0	0	0	0	Q8BM26	
ENSMUST00000159194	ENSMUSG00000000295	10	31313382	31328204	1	0	0	2	0	3	0	13	0	0	13	14	E0CYK6	
ENSMUST00000159195	ENSMUSG00000042349	1	131254343	131279606	-1	3	1	8	3	4	0	0	0	7	0	3	E0CY50	
ENSMUST00000159196	ENSMUSG00000037989	13	49036303	49148014	-1	20	18	30	13	30	13	0	0	0	0	0	F6SRP4	
ENSMUST00000159197	ENSMUSG00000014767	17	15499888	15528379	1	0	0	38	13	0	0	0	0	4	0	0	E9Q6D9	
ENSMUST00000159198						1	2	3	0	4	1	42	1863	297	1309	260		
ENSMUST00000159199	ENSMUSG00000021615	13	89774027	90089608	-1	450	345	1762	628	549	311	20	85	32	6	55		
ENSMUST00000159200	ENSMUSG00000079654	6	29169232	29179584	-1	28	13	80	668	46	17	1	0	0	0	0		B2RU40
ENSMUST00000159202						0	0	0	0	0	0	21	0	0	9	0		
ENSMUST00000159203						2	1	24	4	9	5	10	22	6	0	19		
ENSMUST00000159204						2	2	2	40	3	3	0	1	1	0	0		
ENSMUST00000159205						7	6	8	3	10	3	1	0	0	0	1		
ENSMUST00000159206						0	1	0	0	0	0	4	63	5	3	8		
ENSMUST00000159207	ENSMUSG00000026641	1	171411313	171419142	1	2	0	1	38	3	1	79	81	64	7	65	E0CYP7	
ENSMUST00000159208						0	0	0	0	0	0	0	6	0	14	0		
ENSMUST00000159209	ENSMUSG00000023010	15	99392882	99410049	1	0	0	6	55	8	0	177	98	144	7	150		Q9D2C7
ENSMUST00000159210	ENSMUSG00000025221	19	45791839	45816061	-1	0	1	3	1	0	1	0	0	0	0	0	E0CXC0	
ENSMUST00000159211						9	2	27	193	0	7	8	12	17	0	45		
ENSMUST00000159212	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQM6	
ENSMUST00000159214						1	0	1	0	2	0	0	2	0	0	0		
ENSMUST00000159215						18	9	9	18	17	6	0	6	0	0	1		
ENSMUST00000159216	ENSMUSG00000064373	15	3268547	3280508	1	15	0	16	0	0	0	0	0	25	0	0		P70274
ENSMUST00000159217						0	0	4	16	0	0	0	0	34	95	19		
ENSMUST00000159218	ENSMUSG00000022558	15	76380261	76453038	1	0	3	0	2	0	0	529	285	7	0	2	G3XA21	
ENSMUST00000159219						0	20	22	32	31	16	4	8	0	0	10		
ENSMUST00000159220						0	0	0	0	0	1	0	1	0	0	0		
ENSMUST00000159221	ENSMUSG00000022286	15	37233036	37363569	1	4	7	9	2	6	2	0	0	0	0	0	F6UT30	
ENSMUST00000159222						0	0	3	2	0	1	0	0	2	0	2		
ENSMUST00000159223	ENSMUSG00000068037	17	12841079	12868143	-1	0	2	0	0	8	1	0	0	0	0	0	E0CYD1	
ENSMUST00000159224						3	0	0	3	0	0	3	1	0	0	19		
ENSMUST00000159226						8	3	5	9	9	3	0	4	4	0	13		
ENSMUST00000159227						50	31	192	0	0	15	0	0	0	20	0		
ENSMUST00000159228	ENSMUSG00000019952	10	99107036	99198074	1	0	0	0	2	0	0	0	6	18	0	0	A6H699	
ENSMUST00000159229	ENSMUSG00000095577	6	131486400	131491493	1	2	5	44	2	5	4	0	0	0	0	0	F6URP1	
ENSMUST00000159230	ENSMUSG00000040918	1	164249046	164265385	1	0	0	0	109	0	0	13	27	75	0	74	Q8R4Y1	
ENSMUST00000159231	ENSMUSG00000031257	X	134086421	134221956	-1	2	0	4	2	0	1	0	0	0	0	0		
ENSMUST00000159232	ENSMUSG00000055197	1	74881509	74885419	-1	0	0	2	42	0	0	0	0	0	0	0	E0CXR7	
ENSMUST00000159233						1	6	12	6	6	2	0	0	0	0	0		
ENSMUST00000159234						28	23	31	68	34	16	26	251	68	75	70		
ENSMUST00000159235	ENSMUSG00000019470	8	3608421	3621316	-1	0	0	4	0	10	2	9	0	6	0	6	E0CYF8	
ENSMUST00000159236	ENSMUSG00000027692	3	28263214	28675858	1	34	46	73	24	54	29	12	9	2	0	21		P83510
ENSMUST00000159237	ENSMUSG00000023994	17	48386885	48409906	-1	0	1	2	0	0	0	0	24	0	0	6	F6TWX0	
ENSMUST00000159238	ENSMUSG00000005882	2	155846894	155930310	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXL8	
ENSMUST00000159239						131	70	287	141	155	69	13	81	52	43	109		
ENSMUST00000159240						9	5	57	26	6	8	0	0	0	0	0		
ENSMUST00000159241	ENSMUSG00000009093	10	75814943	75822543	-1	0	3	0	3	3	0	0	0	0	0	0	E9PVU4	
ENSMUST00000159242	ENSMUSG00000055692	16	17276300	17283229	1	4	8	12	0	8	0	0	3	0	0	0		Q9JJB1
ENSMUST00000159243						0	0	2	3	3	0	0	0	0	0	9		
ENSMUST00000159245	ENSMUSG00000025221	19	45791839	45816061	-1	0	0	0	0	0	0	1	0	0	0	2	F6TBA6	
ENSMUST00000159246	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZ08	
ENSMUST00000159247						44	34	314	78	39	14	23	33	70	188	118		
ENSMUST00000159249	ENSMUSG00000042286	14	31139013	31168641	-1	0	0	0	0	3	0	4	3	0	0	0	F7BK35	
ENSMUST00000159250	ENSMUSG00000043467	1	161002922	161034849	-1	0	0	0	0	2	0	0	0	70	0	17	Q8C3U9	
ENSMUST00000159251						4	0	0	1	4	2	0	0	0	0	0		
ENSMUST00000159252	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	0	15	0	0	0	9	0	0	0	E0CXV8	
ENSMUST00000159253						2	0	3	9	0	2	0	0	4	0	0		
ENSMUST00000159254						1	4	0	0	2	5	0	0	0	0	0		
ENSMUST00000159255						32	41	64	58	64	41	0	0	5	5	17		
ENSMUST00000159258	ENSMUSG00000033060	14	101729957	101934710	1	2	0	10	3	0	0	0	0	0	0	0	E0CZD8	
ENSMUST00000159259	ENSMUSG00000031257	X	134086421	134221956	-1	3	3	0	0	0	2	0	0	0	0	0	E0CYB0	
ENSMUST00000159261						7	5	24	60	18	12	1	2	2	4	5		
ENSMUST00000159263	ENSMUSG00000029275	5	107716657	107726036	-1	2	2	5	63	8	2	3	0	2	2	0	H3BLQ9	
ENSMUST00000159264						0	1	0	3	4	0	0	0	0	0	0		
ENSMUST00000159265						6	3	0	3	8	4	0	0	0	0	0		
ENSMUST00000159266						0	0	0	0	0	1	0	0	0	0	1		
ENSMUST00000159267						0	0	5	3	0	1	0	0	0	0	0		
ENSMUST00000159269	ENSMUSG00000024672	19	11321039	11336146	-1	0	0	0	0	0	0	2	3	0	0	0	F6TW47	
ENSMUST00000159270						0	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000159272	ENSMUSG00000029130	5	29195992	29228457	1	0	0	0	0	0	0	0	0	1	0	0	E0CY22	
ENSMUST00000159274						0	0	1	3	1	0	2	0	6	1	13		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159276						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000159278	ENSMUSG00000021481	13	55105311	55134825	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7N8	
ENSMUST00000159279	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	0	0	0	0	0	12	24	14	F6VAL0	
ENSMUST00000159280	ENSMUSG00000026799	2	29346819	29524793	1	0	0	0	0	0	0	0	9	0	0	0	E0CZG8	
ENSMUST00000159281						4	4	15	10	5	0	2	12	6	0	19		
ENSMUST00000159282						0	0	0	0	0	0	0	29	17	6	13		
ENSMUST00000159283	ENSMUSG00000032575	9	106838312	106891979	-1	10	5	22	80	12	9	8	15	21	29	21	Q3TMX5	
ENSMUST00000159284	ENSMUSG00000026502	1	178187417	178257301	1	1	1	1	23	3	0	0	0	0	2	0	E0CYV4	
ENSMUST00000159285	ENSMUSG00000021614	13	89655312	89742509	-1	0	0	1	0	0	0	0	14	0	17	2	F7B6F7	
ENSMUST00000159286	ENSMUSG00000014782	8	105373274	105382862	1	35	22	48	96	51	22	3	0	0	1	0	E0CZA7	
ENSMUST00000159287						0	0	0	1	0	0	0	0	3	0	3		
ENSMUST00000159289						0	0	2	4	1	0	0	0	0	0	0		
ENSMUST00000159290	ENSMUSG00000038733	1	181173228	181211552	-1	1	1	2	0	3	0	74	117	191	36	81	F6UT94	
ENSMUST00000159291						1	0	20	0	20	0	0	0	7	0	14		
ENSMUST00000159292	ENSMUSG00000006289	14	50906478	50924893	-1	445	413	298	347	374	157	381	838	409	147	584		
ENSMUST00000159293						0	0	0	26	0	0	46	92	62	71	60		
ENSMUST00000159294	ENSMUSG00000031925	9	13619990	13709533	1	68	56	279	63	60	35	16	8	24	0	42	F6U238	
ENSMUST00000159295	ENSMUSG00000022956	16	91684398	91931687	-1	0	0	1	0	0	0	0	0	0	0	8	F7D3P8	
ENSMUST00000159297						0	2	0	0	0	0	0	49	16	34	34		
ENSMUST00000159298						3	2	9	8	5	3	0	0	0	0	4		
ENSMUST00000159299	ENSMUSG00000039835	10	18390322	18533892	1	1	4	3	5	0	1	0	0	0	1	0	E0CXY4	
ENSMUST00000159300	ENSMUSG00000021597	13	77043088	77135473	-1	0	0	0	0	0	0	0	0	0	0	3	E0CX75	
ENSMUST00000159301						9	7	7	13	3	4	0	0	0	0	0		
ENSMUST00000159302	ENSMUSG00000017485	14	16365179	16430787	1	0	0	0	0	0	0	0	21	3	0	0	F6V2E8	
ENSMUST00000159303						1	5	13	7	6	3	0	0	0	0	0		
ENSMUST00000159304	ENSMUSG00000020457	11	3187360	3266415	-1	2	0	0	0	0	0	0	0	0	0	0	F7BQ65	
ENSMUST00000159305	ENSMUSG00000005610	7	111070568	111083030	-1	4	2	6	75	2	3	0	0	0	0	4	F7DAB1	
ENSMUST00000159306	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	2	2	0	0	13	0	0	14	F7B5Z3	
ENSMUST00000159307						3	2	0	2	1	0	0	0	2	0	0		
ENSMUST00000159308	ENSMUSG00000027692	3	28263214	28675858	1	0	0	0	0	0	0	0	0	0	0	0	E0CZD7	
ENSMUST00000159310						61	33	343	123	36	21	0	0	2	2	1		
ENSMUST00000159311	ENSMUSG00000025979	1	55131231	55154899	1	0	0	0	0	0	0	0	0	4	13	4	E0CXA9	
ENSMUST00000159312	ENSMUSG00000054702	1	79606876	79671972	-1	0	0	1	0	0	0	2	0	0	0	0	E0CXQ0	
ENSMUST00000159314	ENSMUSG00000033060	14	101729957	101934710	1	2	4	0	0	8	11	0	0	0	0	0	E9PYI7	
ENSMUST00000159315	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	0	0	3	1	27	407	181	70	107	F6TRR6	
ENSMUST00000159316	ENSMUSG00000026694	1	162532127	162548551	-1	0	0	0	0	0	0	0	0	0	1	6	H3BLK3	
ENSMUST00000159317						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000159318						1	1	0	2	1	3	0	2	0	0	0		
ENSMUST00000159319						14	11	23	73	19	5	0	1	2	0	0		
ENSMUST00000159320						0	0	0	0	0	0	14	115	25	25	8		
ENSMUST00000159321						10	12	9	3	8	6	17	128	31	13	37		
ENSMUST00000159322						3	0	2	0	0	0	6	16	27	0	32		
ENSMUST00000159323	ENSMUSG00000032000	9	7848699	7873186	-1	0	0	0	0	0	0	18	13	15	29	15	E0CZ68	
ENSMUST00000159325						26	31	183	30	27	17	4	6	12	6	22		
ENSMUST00000159327	ENSMUSG00000022346	15	61985341	61990374	1	0	0	0	0	0	0	0	0	0	5	0		P01108
ENSMUST00000159328	ENSMUSG00000035845	15	88805244	88819318	-1	2	2	12	20	2	3	0	0	7	0	4	E0CZB5	
ENSMUST00000159329	ENSMUSG00000041771	12	102128733	102267091	1	40	37	39	291	61	44	0	3	2	0	0	E9PUL6	
ENSMUST00000159330						0	0	0	0	1	0	0	1	0	1	7		
ENSMUST00000159331						0	0	2	3	0	0	0	0	0	0	1		
ENSMUST00000159332						1	2	20	5	0	0	0	0	0	0	1		
ENSMUST00000159333	ENSMUSG00000061207	17	34823993	34836945	-1	0	0	0	0	0	0	0	0	0	4	0	F7CHD9	
ENSMUST00000159334	ENSMUSG00000004151	12	38779380	38868215	1	0	0	0	2	0	0	0	0	0	8	1	Q8CCR6	
ENSMUST00000159335	ENSMUSG00000089862	6	8259288	8459470	1	7	8	16	39	6	6	1	10	1	3	8	E0CYZ5	
ENSMUST00000159336						14	8	14	0	0	0	0	0	0	0	0		
ENSMUST00000159337	ENSMUSG00000021614	13	89655312	89742509	-1	4	1	9	22	8	5	0	0	2	0	2	Q8BS97	
ENSMUST00000159338	ENSMUSG00000022346	15	61985341	61990374	1	1	0	9	58	7	5	0	1	0	0	0	E0CZD1	
ENSMUST00000159339						4	2	8	2	9	3	0	1	0	2	0		
ENSMUST00000159340	ENSMUSG00000003199	17	56005711	56016790	1	0	1	2	0	4	0	486	476	292	66	198	F7BJW2	
ENSMUST00000159341						8	3	12	7	5	2	0	0	0	0	0		
ENSMUST00000159342	ENSMUSG00000038368	4	88094629	88411011	1	0	0	0	0	0	0	21	34	0	0	26	E9PYJ6	
ENSMUST00000159343						5	1	12	7	6	0	0	1	4	12	5		
ENSMUST00000159344	ENSMUSG00000073664	1	60180599	60338328	1	0	0	0	0	0	0	0	0	0	0	0	F6U6E8	
ENSMUST00000159345	ENSMUSG00000029413	5	92257659	92278170	-1	0	0	0	43	0	3	547	1483	811	238	733	G3XA18	
ENSMUST00000159346	ENSMUSG00000053080	19	7417625	7425904	1	0	0	0	135	0	0	0	0	0	0	0	F6T4X0	
ENSMUST00000159347						5	3	0	1	3	4	0	0	0	0	0		
ENSMUST00000159348	ENSMUSG00000053080	19	7417625	7425904	1	16	8	23	120	39	29	0	6	2	5	44		Q4VA45
ENSMUST00000159349						0	0	0	0	0	0	0	3	3	11	4		
ENSMUST00000159350						0	0	0	0	0	0	4	0	2	0	0		
ENSMUST00000159351	ENSMUSG00000030589	7	29134851	29153961	1	0	0	0	0	0	0	644	24	592	0	658		Q8BTM9
ENSMUST00000159352	ENSMUSG00000041426	1	52844929	52920986	1	0	0	0	0	0	0	0	26	0	71	0	E0CX19	
ENSMUST00000159354						15	22	36	22	19	9	0	0	0	0	0		
ENSMUST00000159355						4	0	4	4	0	3	0	0	0	0	0		
ENSMUST00000159356						0	0	1	18	1	0	0	0	2	0	2		
ENSMUST00000159357	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYJ8	
ENSMUST00000159358						2	0	2	0	0	0	0	0	9	0	19		
ENSMUST00000159359						1	1	0	3	1	0	0	0	0	1	0		
ENSMUST00000159362						10	6	11	4	11	3	0	6	3	1	11		
ENSMUST00000159365	ENSMUSG00000045875	14	66635251	66733462	1	0	0	0	0	16	5	0	0	0	0	0	Q8BUE5	
ENSMUST00000159366	ENSMUSG00000058318	2	92093117	92364666	1	0	0	2	8	0	0	0	0	24	0	6	F6TL54	
ENSMUST00000159367	ENSMUSG00000089872	1	190700202	190911770	-1	23	0	0	0	30	8	22	0	22	0	47	E0CYA1	
ENSMUST00000159368	ENSMUSG00000072663	15	9578193	9748868	-1	0	0	0	0	0	0	0	0	0	1	1		Q8C9J3
ENSMUST00000159369						9	8	9	4	5	7	0	0	0	0	0		
ENSMUST00000159370						0	0	0	1	0	0	0	6	0	3	0		
ENSMUST00000159371						9	5	0	0	8	0	233	338	176	32	135		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159372	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	0	0	0	0	0	2	0	0	E0CYS5	
ENSMUST00000159373	ENSMUSG00000027405	2	130274430	130279313	1	0	0	0	0	0	0	0	0	0	0	0	F6U250	
ENSMUST00000159374						13	1	0	0	0	2	0	0	0	1	0		
ENSMUST00000159375	ENSMUSG00000054065	7	141078218	141090510	1	0	1	4	16	0	0	0	0	0	0	1	E0CY06	
ENSMUST00000159376						11	1	14	18	4	5	6	12	5	0	6		
ENSMUST00000159377						2	3	8	43	8	2	0	0	2	0	0		
ENSMUST00000159378	ENSMUSG00000089862	6	8259288	8459470	1	0	0	0	0	0	0	12	6	17	12	15	E0CZ61	
ENSMUST00000159381						2	2	7	16	0	0	0	0	0	0	0		
ENSMUST00000159382						1	1	11	4	1	0	0	0	0	0	0		
ENSMUST00000159383						4	4	2	81	5	3	0	0	0	0	0		
ENSMUST00000159384	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXC9	
ENSMUST00000159385						13	12	29	4	29	5	1	5	0	0	1		
ENSMUST00000159386	ENSMUSG00000032280	9	61372366	61418497	1	0	7	28	554	0	21	1064	935	1659	43	1499	E0CXS2	
ENSMUST00000159387						4	6	8	11	1	4	6	19	20	1	29		
ENSMUST00000159388	ENSMUSG00000027860	3	102153583	102204693	-1	13	16	15	14	20	7	0	0	1	3	21	A0A0H2UH25	
ENSMUST00000159389	ENSMUSG00000038425	18	70508680	70530620	-1	0	0	0	0	0	0	35	41	19	0	0	E9Q3H9	
ENSMUST00000159390	ENSMUSG00000024238	18	5591860	5775467	1	0	0	0	0	0	0	0	0	24	0	11	E9PXY5	
ENSMUST00000159391	ENSMUSG00000030329	6	124996694	125003096	1	6	0	7	97	2	0	0	0	0	0	0	E0CYN7	
ENSMUST00000159392						13	14	21	18	21	10	7	8	0	0	0		
ENSMUST00000159393						30	30	36	25	30	17	24	38	23	10	65		
ENSMUST00000159394	ENSMUSG00000041831	17	6673458	6738042	1	5	4	0	11	12	10	0	0	0	0	0	E0CYJ1	
ENSMUST00000159395	ENSMUSG00000026546	1	172520801	172545870	1	5	6	5	1	7	7	0	0	0	0	0	E0CXK6	
ENSMUST00000159396						4	0	2	5	0	1	0	0	0	0	0		
ENSMUST00000159397						10	14	17	623	22	11	0	0	0	0	0		
ENSMUST00000159398	ENSMUSG00000025977	1	55248658	55363469	-1	0	0	0	49	2	3	0	0	0	0	0		Q924M5
ENSMUST00000159400						158	151	202	114	170	92	15	34	22	32	22		
ENSMUST00000159401						20	7	16	11	23	11	13	15	45	0	19		
ENSMUST00000159402						0	1	0	0	2	1	5	0	0	3	0		
ENSMUST00000159403	ENSMUSG00000030145	6	118427319	118455528	-1	0	0	4	0	0	1	0	0	0	0	2	E0CZG2	
ENSMUST00000159405	ENSMUSG00000051375	18	38185914	38212053	-1	0	0	0	0	0	0	8	2	13	0	21	Q8CFX3	
ENSMUST00000159406						0	0	0	0	0	0	83	109	85	6	35		
ENSMUST00000159409						2	1	10	1	1	0	0	0	0	0	0		
ENSMUST00000159410	ENSMUSG00000079022	15	71795795	72034227	-1	1	0	0	0	0	3	0	0	0	0	0	E0CYH5	
ENSMUST00000159413						1	0	3	3	2	1	0	0	4	0	7		
ENSMUST00000159414	ENSMUSG00000043336	16	57353093	57573126	1	0	16	55	39	0	2	55	551	157	163	233	E0CYM1	
ENSMUST00000159415	ENSMUSG00000054752	4	53631471	53707009	1	0	0	1	0	0	0	0	0	0	0	0	F8WGT4	
ENSMUST00000159416	ENSMUSG00000031883	8	104534700	104550343	1	5	7	19	10	9	6	0	2	0	0	0	G3XA26	
ENSMUST00000159417	ENSMUSG00000026344	1	125867622	125913101	-1	60	71	204	163	80	50	4	8	6	2	9		Q8BLC3
ENSMUST00000159418						2	0	7	70	15	0	0	0	0	0	0		
ENSMUST00000159419						3	2	0	270	0	1	0	0	0	0	0		
ENSMUST00000159420						0	2	0	0	0	0	72	94	42	21	35		
ENSMUST00000159421						6	0	7	3	0	0	5	7	2	5	11		
ENSMUST00000159423						17	6	26	13	22	2	6	21	24	0	38		
ENSMUST00000159424						0	0	0	6	2	0	0	0	12	0	0		
ENSMUST00000159425						16	0	0	30	22	20	14	105	114	20	69		
ENSMUST00000159426						197	99	185	1268	217	146	5	46	19	4	28		
ENSMUST00000159427						0	0	0	0	0	0	11	125	9	17	23		
ENSMUST00000159428						0	2	1	1	3	3	2	10	2	1	1		
ENSMUST00000159429	ENSMUSG00000022552	15	76347040	76351111	-1	0	2	0	1	0	0	21	140	10	35	26	F6UHH8	
ENSMUST00000159430	ENSMUSG00000022335	15	68083766	68258856	-1	8	0	27	11	2	0	0	0	0	0	0	E0CY83	
ENSMUST00000159431						0	0	2	0	2	0	0	7	14	26	10		
ENSMUST00000159432						46	52	197	54	44	19	1	8	0	0	4		
ENSMUST00000159433	ENSMUSG00000089862	6	8259288	8459470	1	0	0	0	0	0	0	0	142	120	95	55	E0CXP6	
ENSMUST00000159434						2	1	5	3	1	1	2	3	2	2	5		
ENSMUST00000159435						0	0	0	0	3	1	4	0	3	0	7		
ENSMUST00000159436	ENSMUSG00000026519	1	180942344	180975112	1	0	0	11	103	2	0	0	0	0	0	0	E0CXM3	
ENSMUST00000159439						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159440	ENSMUSG00000044005	10	128194457	128210004	1	0	5	23	2	0	0	0	0	0	0	0	E0CYF7	
ENSMUST00000159441						21	43	67	23	45	33	19	80	66	56	88		
ENSMUST00000159442						7	4	8	3	3	1	0	0	0	0	0		
ENSMUST00000159443						0	2	4	0	1	2	4	41	14	20	9		
ENSMUST00000159444						2	8	10	9	2	3	1	2	1	0	0		
ENSMUST00000159446	ENSMUSG00000025221	19	45791839	45816061	-1	0	0	0	0	0	0	0	0	0	0	0	F7BWB2	
ENSMUST00000159447	ENSMUSG00000038538	6	38433950	38524825	1	21	16	36	22	27	8	3	53	0	11	0	F6UTU1	
ENSMUST00000159448	ENSMUSG00000037351	1	36698114	36714422	-1	0	2	2	53	1	2	0	0	0	0	17	E0CYB4	
ENSMUST00000159449						5	0	6	6	8	0	4	18	4	0	3		
ENSMUST00000159450						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000159451	ENSMUSG00000032503	9	112065091	112235938	-1	9	7	6	4	11	1	0	0	0	0	0	E9Q4A0	
ENSMUST00000159453						2	2	3	2	2	2	11	96	9	10	14		
ENSMUST00000159454						2	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000159455	ENSMUSG00000089840	14	57112506	57115883	-1	7	7	7	5	10	1	0	0	0	0	0	E0CX42	
ENSMUST00000159456	ENSMUSG00000055717	14	103650228	103704907	1	10	8	13	1	0	0	5	25	5	0	9	F7B673	
ENSMUST00000159457						0	2	4	3	1	3	6	7	11	0	7		
ENSMUST00000159458						2	5	8	4	9	2	0	4	0	0	0		
ENSMUST00000159459	ENSMUSG00000021638	13	100496507	100552718	-1	0	7	20	0	0	2	0	9	3	1	0	E0CZ73	
ENSMUST00000159461	ENSMUSG00000033538	9	5308828	5336783	1	0	1	0	0	0	0	10	858	147	1457	302	F6SUE5	
ENSMUST00000159462	ENSMUSG00000021597	13	77043088	77135473	-1	3	1	6	152	12	0	0	0	0	0	0		
ENSMUST00000159463	ENSMUSG00000038521	6	124530345	124542359	-1	0	0	10	2	0	0	0	0	0	0	0	E0CZE7	
ENSMUST00000159464						1	0	0	0	0	0	3	0	0	0	5		
ENSMUST00000159465						0	2	2	0	1	2	0	18	0	0	3		
ENSMUST00000159466						0	0	0	0	0	0	0	51	14	5	17		
ENSMUST00000159467	ENSMUSG00000029635	5	146231230	146302874	1	0	1	0	17	0	1	2	2	5	0	4	E0CY29	
ENSMUST00000159469						1	0	0	71	0	0	5	0	176	44	142		
ENSMUST00000159470	ENSMUSG00000037999	5	62602445	62766159	-1	1	4	19	0	4	1	0	0	0	0	0	E0CXD0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159473	ENSMUSG00000032115	9	44379490	44392369	1	0	0	0	0	0	0	0	0	0	0	0	F6TRP3	
ENSMUST00000159474						2	1	11	2	4	1	0	0	0	0	0		
ENSMUST00000159475	ENSMUSG00000024797	19	6067842	6080324	-1	2	1	0	0	5	1	18	38	9	0	10	F6TKZ2	
ENSMUST00000159476						2	1	2	4	0	2	0	0	0	0	0		
ENSMUST00000159477						76	55	451	72	54	27	2	16	2	8	6		
ENSMUST00000159478						21	28	72	54	48	17	1	5	5	1	5		
ENSMUST00000159479	ENSMUSG00000059022	6	29473162	29507952	-1	0	0	1	11	28	0	0	0	0	0	0	F6UH68	
ENSMUST00000159480						0	0	0	0	0	0	10	24	6	24	39		
ENSMUST00000159481	ENSMUSG00000004127	3	138143448	138159821	1	0	2	5	0	0	0	0	9	5	6	3	E0CY61	
ENSMUST00000159482						71	47	298	216	68	33	0	0	1	0	2		
ENSMUST00000159483						6	5	4	8	8	0	0	8	23	0	13		
ENSMUST00000159484						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159485						1	1	3	8	2	2	0	0	3	0	9		
ENSMUST00000159486						4	1	11	10	14	4	1	0	25	3	2		
ENSMUST00000159487						4	6	7	2	4	2	0	0	1	0	0		
ENSMUST00000159489						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159490	ENSMUSG00000022150	15	6299788	6440712	1	0	0	1	3	0	0	0	0	0	6	11	E0CYJ2	
ENSMUST00000159491						18	14	91	11	20	5	0	0	0	0	0		
ENSMUST00000159492	ENSMUSG00000004897	3	87906321	87916132	1	10	0	23	91	9	4	5	0	0	0	0	E0CXA0	
ENSMUST00000159493						3	2	8	16	8	1	0	0	0	0	0		
ENSMUST00000159494	ENSMUSG00000055692	16	17276300	17283229	1	1	0	0	0	0	0	0	0	0	0	0	E0CZ44	
ENSMUST00000159496						3	1	5	4	5	0	3	31	16	0	20		
ENSMUST00000159497						2	1	5	86	5	6	7	30	11	1	11		
ENSMUST00000159498						20	9	43	6	19	22	0	2	0	0	0		
ENSMUST00000159499	ENSMUSG00000032086	9	45838580	45864399	1	2	0	0	0	0	0	0	0	0	0	0	F6UH57	
ENSMUST00000159500	ENSMUSG00000066441	12	79174337	79192293	-1	3	2	0	0	0	0	9	0	9	43	34	E0CYX0	
ENSMUST00000159502						2	1	1	0	0	0	0	0	1	0	0		
ENSMUST00000159503						0	0	0	0	0	2	2	0	0	0	0		
ENSMUST00000159504						62	75	85	78	72	31	2	4	5	0	5		
ENSMUST00000159505	ENSMUSG00000027804	3	79591342	79603650	1	0	0	0	0	0	0	0	0	0	4	0	A0A0A6YW70	
ENSMUST00000159506						6	8	12	9	11	7	0	0	0	0	0		
ENSMUST00000159507						19	12	36	32	14	14	1	5	0	0	1		
ENSMUST00000159508						2	0	0	54	1	0	0	0	0	0	2		
ENSMUST00000159509						1	1	1	0	1	1	6	2	7	0	6		
ENSMUST00000159510	ENSMUSG00000042121	5	113937094	113993894	-1	0	0	0	6	0	0	0	0	0	0	0	E0CXT3	
ENSMUST00000159511	ENSMUSG00000025812	8	127063893	127612286	1	3	2	1	0	1	0	0	0	0	0	0	F6T4Y3	
ENSMUST00000159512	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	0	7	0	0	0	0	0	0	E9PWH3	
ENSMUST00000159514	ENSMUSG00000022698	16	44139830	44163366	1	0	0	0	138	0	0	0	76	65	7	135		Q6PGB6
ENSMUST00000159515	ENSMUSG00000021638	13	100496507	100552718	-1	0	0	0	0	0	1	0	0	0	0	0	E0CZ91	
ENSMUST00000159516	ENSMUSG00000026584	1	163929100	163955126	1	0	1	0	0	0	0	0	0	0	0	0	F6TFM1	
ENSMUST00000159517	ENSMUSG00000089696	3	94264036	94266784	1	8	16	7	2	8	5	0	0	0	0	0	K7N6S3	
ENSMUST00000159518						0	0	0	0	0	0	6	19	4	0	7		
ENSMUST00000159519						2	0	3	1	0	0	2	92	0	0	3		
ENSMUST00000159520						28	13	23	12	23	15	0	0	4	0	0		
ENSMUST00000159521						5	0	5	4	3	1	0	0	0	0	0		
ENSMUST00000159522						1	1	0	14	1	3	0	0	0	0	0		
ENSMUST00000159523						0	0	0	0	0	0	6	12	0	0	0		
ENSMUST00000159524	ENSMUSG00000090268	3	94196714	94199802	1	27	23	21	25	16	12	0	0	0	0	0	E0CXI6	
ENSMUST00000159525						11	9	19	4	19	8	0	0	0	0	1		
ENSMUST00000159526						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000159527	ENSMUSG00000045994	9	26733728	26763101	1	7	0	11	15	11	2	0	0	0	0	0	Q8R1V2	
ENSMUST00000159528						0	0	0	0	0	0	6	30	7	0	4		
ENSMUST00000159529	ENSMUSG00000026344	1	125867622	125913101	-1	8	4	3	6	12	0	0	0	0	0	0	E0CXP0	
ENSMUST00000159530	ENSMUSG00000025907	1	6206197	6276648	1	13	8	19	1	6	5	14	240	51	78	109	F6TLJ4	
ENSMUST00000159531	ENSMUSG00000023010	15	99392882	99410049	1	0	3	0	0	0	0	0	0	0	0	0		Q9D2C7
ENSMUST00000159532						28	19	43	48	29	22	13	27	10	39	43		
ENSMUST00000159533						1	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000159534						29	19	119	223	36	22	40	318	131	9	134		
ENSMUST00000159535	ENSMUSG00000023994	17	48386885	48409906	-1	0	0	0	4	0	0	0	4	15	0	13	E0CY40	
ENSMUST00000159536						3	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000159537	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0	E0CX45	
ENSMUST00000159538						3	0	47	4	12	3	3	5	3	0	0		
ENSMUST00000159540						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159541	ENSMUSG00000090112	10	11149427	11217595	1	4	0	4	0	0	2	12	10	10	0	0		Q7TPQ3
ENSMUST00000159542	ENSMUSG00000022788	16	16416917	16600549	-1	1	1	1	0	0	0	0	0	0	0	8	E0CZ69	
ENSMUST00000159545	ENSMUSG00000028559	4	109061145	109202272	-1	0	0	0	0	0	0	1048	2605	1177	674	161	F8VQE8	
ENSMUST00000159546	ENSMUSG00000040514	5	7304119	7311491	1	2	2	4	0	3	0	0	0	0	0	0		Q9D5W8
ENSMUST00000159547						126	81	618	139	106	71	38	131	73	9	106		
ENSMUST00000159548	ENSMUSG00000019470	8	3608421	3621316	-1	0	1	0	0	0	0	0	0	0	0	0	F6TM12	
ENSMUST00000159549						0	0	1	0	0	1	4	0	0	0	0		
ENSMUST00000159550						0	1	1	0	0	1	19	113	36	42	24		
ENSMUST00000159551	ENSMUSG00000060475	17	12966796	12992546	-1	0	1	44	105	31	0	124	612	285	90	203	E0CYH0	
ENSMUST00000159552						1	1	2	0	0	0	0	0	0	0	18		
ENSMUST00000159553						0	0	0	0	0	3	9	17	67	25	31		
ENSMUST00000159554	ENSMUSG00000074604	3	51660360	51682677	1	0	0	0	0	0	0	17	49	23	70	0	A0A0A6YWX7	
ENSMUST00000159555	ENSMUSG00000056870	1	44551511	44796838	1	0	0	0	0	0	0	0	0	0	0	0	E0CX89	
ENSMUST00000159556	ENSMUSG00000024857	19	4081578	4087340	1	0	0	2	1	0	3	0	1	0	0	0	G3XA16	
ENSMUST00000159557	ENSMUSG00000037787	12	111713261	111754980	1	0	0	1	0	3	0	2	0	3	0	0	E9PUI9	
ENSMUST00000159558	ENSMUSG00000025920	1	16228674	16520112	-1	0	3	0	0	11	7	0	0	0	0	0		Q8CJ67
ENSMUST00000159559	ENSMUSG00000037989	13	49036303	49148014	-1	0	0	35	0	66	0	0	0	0	0	0	E0CYT1	
ENSMUST00000159560						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159561						10	6	32	21	2	3	0	0	0	0	0		
ENSMUST00000159563	ENSMUSG00000016493	1	195036826	195092249	-1	1	0	0	3	2	0	0	0	0	0	9		
ENSMUST00000159564	ENSMUSG00000025977	1	55248658	55363469	-1	2	0	0	0	0	0	0	0	0	0	1	F6TV20	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159565	ENSMUSG00000056617	9	46303361	46319986	-1	48	28	66	19	39	14	1	3	2	0	3	E9PVU2	
ENSMUST00000159566	ENSMUSG00000025955	1	65012689	65032759	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYR9	
ENSMUST00000159567	ENSMUSG00000035142	12	52097737	52312744	1	22	29	19	30	33	17	4	20	13	3	7	F7D3P0	
ENSMUST00000159569	ENSMUSG00000063108	9	20432972	20460162	-1	17	12	10	21	24	10	99	328	108	81	75	G3XA08	
ENSMUST00000159570	ENSMUSG00000068263	6	87730869	87755908	1	0	0	0	47	0	0	0	0	0	0	2		Q9JJF6
ENSMUST00000159571						18	16	16	22	25	9	0	43	2	2	18		
ENSMUST00000159572	ENSMUSG00000037847	19	18631950	18652194	1	83	117	352	120	77	60	29	167	64	38	80		Q91W63
ENSMUST00000159573						4	0	0	2	1	3	0	0	0	0	0		
ENSMUST00000159574	ENSMUSG00000042743	13	104109741	104141735	1	1	0	0	0	0	3	0	0	0	1	0	E0CX61	
ENSMUST00000159575						37	21	219	31	38	25	0	0	0	0	0		
ENSMUST00000159576	ENSMUSG00000032059	9	50775019	50843542	1	155	112	209	148	221	134	2	3	3	0	11	E0CZ10	
ENSMUST00000159577						2	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000159578	ENSMUSG00000070686	5	93634993	93671551	-1	0	0	37	4	17	0	4	8	7	1	13	E0CYF0	
ENSMUST00000159579						8	10	21	13	21	4	0	0	0	0	0		
ENSMUST00000159580						2	5	6	2	5	1	0	0	0	0	0		
ENSMUST00000159581						0	0	15	2	9	3	0	0	2	0	0		
ENSMUST00000159582	ENSMUSG00000052477	1	84992690	85270566	-1	0	0	0	0	0	0	0	3	8	25	5	E0CXN9	
ENSMUST00000159583						0	0	0	0	0	0	0	1	2	0	2		
ENSMUST00000159584	ENSMUSG00000090061	5	63649102	63810546	1	32	36	51	40	74	26	0	5	2	0	4		Q6P5U7
ENSMUST00000159585						1	0	2	5	0	0	0	14	0	0	0		
ENSMUST00000159586	ENSMUSG00000027860	3	102153583	102204693	-1	0	0	0	0	2	0	0	0	0	0	4	E0CX72	
ENSMUST00000159587						2	1	0	3	6	6	36	81	74	446	125		
ENSMUST00000159588						1	1	2	4	2	2	0	0	0	0	0		
ENSMUST00000159590	ENSMUSG00000040913	19	45578254	45660312	-1	3	4	8	0	9	0	75	0	4	0	2	E0CYL5	
ENSMUST00000159591						6	0	3	7	8	3	2	3	9	1	2		
ENSMUST00000159592	ENSMUSG00000042121	5	113937094	113993894	-1	53	35	158	76	70	38	353	868	798	47	614		Q76I79
ENSMUST00000159593	ENSMUSG00000024857	19	4081578	4087340	1	0	0	6	0	1	0	0	0	0	0	0	E0CXZ2	
ENSMUST00000159594						7	2	4	17	6	6	3	5	0	2	5		
ENSMUST00000159596	ENSMUSG00000074500	9	18455575	18478268	-1	13	15	34	238	24	7	0	3	4	0	0	Q9D4E2	
ENSMUST00000159597	ENSMUSG00000033060	14	101729957	101934710	1	8	0	0	0	5	0	0	0	0	2	0	F6VG99	
ENSMUST00000159598	ENSMUSG00000021684	13	95024454	95250336	-1	1	0	0	0	0	0	0	0	0	0	0	E0CY70	
ENSMUST00000159600						5	12	0	40	13	8	0	0	0	0	0		
ENSMUST00000159603						5	2	9	0	3	2	0	0	1	0	0		
ENSMUST00000159604						0	1	1	1	1	1	56	459	62	24	102		
ENSMUST00000159605	ENSMUSG00000033632	18	25168999	25467321	1	0	0	0	3	0	0	0	0	0	1	5	E0CYF6	
ENSMUST00000159606	ENSMUSG00000051506	14	32959547	33185508	-1	0	0	0	1	3	0	48	13	90	3	71	E0CXD5	
ENSMUST00000159607						1	1	0	2	3	1	5	37	10	9	18		
ENSMUST00000159608	ENSMUSG00000021684	13	95024454	95250336	-1	5	4	30	20	10	4	0	0	0	0	0	E9PUL4	
ENSMUST00000159610	ENSMUSG00000024112	17	25374285	25433783	-1	15	0	23	95	9	7	0	0	0	0	0	E9Q6P9	
ENSMUST00000159611	ENSMUSG00000070448	14	51451962	51461293	1	6	0	0	0	0	0	0	0	0	0	0	O35199	
ENSMUST00000159612						0	2	13	7	4	3	0	1	0	0	0		
ENSMUST00000159614	ENSMUSG00000025646	9	109059747	109074124	-1	0	0	0	0	0	0	5	1	1	0	0	F6U6D4	
ENSMUST00000159615						3	0	39	0	1	0	30	111	14	14	19		
ENSMUST00000159616	ENSMUSG00000060780	6	77242689	77257791	1	0	0	0	98	1	0	0	0	0	0	0		Q8K377
ENSMUST00000159617	ENSMUSG00000041406	1	163945993	163994796	-1	0	0	0	0	0	0	1	0	0	1	0	F7DEW2	
ENSMUST00000159619	ENSMUSG00000025533	5	130011258	130029247	-1	6	2	0	0	8	0	43	0	63	39	5		Q91YI0
ENSMUST00000159620	ENSMUSG00000032575	9	106838312	106891979	-1	1	0	0	0	0	2	0	0	0	0	0	F6USD5	
ENSMUST00000159622	ENSMUSG00000004127	3	138143448	138159821	1	3	0	0	19	5	0	0	0	0	2	0	E9Q663	
ENSMUST00000159623	ENSMUSG00000024112	17	25374285	25433783	-1	0	0	0	44	5	0	0	0	0	0	0	E9Q6E4	
ENSMUST00000159624	ENSMUSG00000089872	1	190700202	190911770	-1	23	14	46	35	14	9	0	1	0	0	1		Q8BLK9
ENSMUST00000159625						2	1	6	4	2	1	6	13	0	2	4		
ENSMUST00000159626	ENSMUSG00000063063	6	76881637	77979699	-1	0	0	6	0	0	0	0	0	0	0	0		Q61301
ENSMUST00000159628						12	2	37	33	29	5	2	2	0	0	0		
ENSMUST00000159629						6	5	1	3	6	1	0	0	0	0	0		
ENSMUST00000159630	ENSMUSG00000032280	9	61372366	61418497	1	0	0	3	102	0	0	108	109	156	0	33	Q3TY99	
ENSMUST00000159631	ENSMUSG00000005413	8	75093591	75100596	1	3	1	1	3	3	1	0	0	0	0	3	H3BKP1	
ENSMUST00000159632						5	1	9	5	4	0	0	0	0	0	0		
ENSMUST00000159633	ENSMUSG00000037989	13	49036303	49148014	-1	1	2	0	0	0	0	0	0	0	0	0	F7BQG5	
ENSMUST00000159634	ENSMUSG00000071657	19	8837467	8848683	1	0	0	0	0	0	0	66	13	35	0	36		Q9Z2E9
ENSMUST00000159636						3	3	4	157	8	3	13	50	29	2	61		
ENSMUST00000159638						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159639						0	2	0	5	9	3	0	0	0	1	0		
ENSMUST00000159640						2	3	8	0	0	6	2	19	4	4	5		
ENSMUST00000159641	ENSMUSG00000023990	17	47737030	47792419	1	1	3	6	3	8	3	0	0	0	0	0	E9PXZ1	
ENSMUST00000159642						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159643						3	2	3	0	6	3	0	0	0	0	0		
ENSMUST00000159644	ENSMUSG00000016194	1	193221634	193264075	-1	0	0	0	13	0	1	0	9	24	204	99	F2Z3U6	
ENSMUST00000159645	ENSMUSG00000040325	9	106821874	106880992	1	26	29	93	104	30	5	42	0	22	0	20		Q80TR8
ENSMUST00000159646	ENSMUSG00000061950	17	65782573	65841926	1	0	0	0	6	5	0	55	59	88	5	115	F6V294	
ENSMUST00000159647	ENSMUSG00000042015	13	94976344	95023314	1	0	0	0	0	0	0	1	0	0	0	0	B2RQV3	
ENSMUST00000159648	ENSMUSG00000026698	1	161969186	161973435	1	0	0	0	18	0	0	4	0	2	0	0	E0CZA4	
ENSMUST00000159649	ENSMUSG00000036948	5	138259656	138264033	-1	0	0	0	0	0	0	645	1360	468	38	408	A0A0G2JDC3	
ENSMUST00000159650						17	23	68	57	23	18	2	0	3	2	1		
ENSMUST00000159651	ENSMUSG00000061244	14	49012146	49066653	-1	3	1	0	0	2	3	1	0	0	1	0	F6SMI5	
ENSMUST00000159652						0	0	7	5	0	0	18	155	23	5	40		
ENSMUST00000159653	ENSMUSG00000071657	19	8837467	8848683	1	0	0	0	0	0	0	0	0	0	7	11	F6US45	
ENSMUST00000159654	ENSMUSG00000044337	1	90203980	90216751	1	1	5	4	4	3	0	0	0	0	1	4		
ENSMUST00000159655						0	0	6	3	5	0	0	0	0	0	1		
ENSMUST00000159656						0	2	0	0	1	7	0	13	0	5	5		
ENSMUST00000159657	ENSMUSG00000040669	6	122317731	122340561	-1	0	1	2	1	2	0	0	0	0	0	0	E0CYR2	
ENSMUST00000159658	ENSMUSG00000050150	3	135348029	135397827	1	2	3	3	1	1	0	0	0	0	1	0	E0CY67	
ENSMUST00000159659						0	1	1	0	0	0	0	0	0	3	3		
ENSMUST00000159660	ENSMUSG00000042524	15	79724070	79742536	-1	0	0	2	9	0	0	7	7	16	0	4	E0CY39	
ENSMUST00000159661						5	0	0	0	2	0	12	100	46	26	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159662						3	1	10	4	1	2	0	0	0	0	0		
ENSMUST00000159664	ENSMUSG00000033083	14	101442360	101609191	-1	1	0	0	0	2	0	6	0	8	0	1	F6S7E8	
ENSMUST00000159665						10	6	22	15	14	15	1	0	3	0	3		
ENSMUST00000159666	ENSMUSG00000037318	1	193175453	193201703	-1	0	0	1	0	1	0	0	21	10	7	16	A0A0A6YXD0	
ENSMUST00000159667						11	9	73	14	14	9	0	0	1	0	0		
ENSMUST00000159668						0	5	4	4	0	0	0	2	0	0	0		
ENSMUST00000159670	ENSMUSG00000033400	3	116739999	116808166	-1	0	0	0	0	0	0	0	0	0	0	0	E0CX86	
ENSMUST00000159671						2	2	16	4	0	4	0	0	0	0	0		
ENSMUST00000159672						3	3	0	4	2	0	30	34	41	9	41		
ENSMUST00000159673	ENSMUSG00000038733	1	181173228	181211552	-1	0	0	0	0	0	0	16	375	13	0	0	F7DFQ2	
ENSMUST00000159674	ENSMUSG00000000606	14	51411001	51419527	1	0	0	0	0	0	0	0	0	0	0	0	F7D4U1	
ENSMUST00000159675						2	2	2	2	5	0	2	12	13	0	12		
ENSMUST00000159676	ENSMUSG00000036834	3	63696234	63899472	-1	0	1	0	0	0	0	0	0	0	0	0		Q4KWH5
ENSMUST00000159677	ENSMUSG00000029406	5	124118690	124249760	-1	6	3	2	2	8	2	0	3	1	0	3	A0A0G2JFQ8	
ENSMUST00000159678						0	2	10	2	3	3	0	0	0	0	0		
ENSMUST00000159679	ENSMUSG00000040113	1	163702256	163725232	-1	9	7	0	5	7	3	0	0	0	0	0		B2RXM4
ENSMUST00000159680	ENSMUSG00000027692	3	28263214	28675858	1	0	0	0	0	0	0	0	0	0	0	10	B9EKN8	
ENSMUST00000159681						3	2	1	5	4	1	0	0	0	0	0		
ENSMUST00000159682						15	7	10	0	6	8	0	0	1	0	0		
ENSMUST00000159683	ENSMUSG00000022792	16	16302965	16309640	1	0	0	0	0	0	0	8	0	0	0	0	E9PX65	
ENSMUST00000159684	ENSMUSG00000030098	6	91761509	91827250	-1	2	0	0	4	3	0	0	0	0	0	0	E0CXS4	
ENSMUST00000159685	ENSMUSG00000060743	1	180800832	180813943	-1	2	0	0	0	0	0	2	237	598	2574	296	E0CYN1	
ENSMUST00000159686						2	5	9	6	9	2	0	0	0	0	0		
ENSMUST00000159687	ENSMUSG00000079197	14	55587441	55591113	-1	0	0	0	0	0	0	89	0	178	90	117	E0CZ90	
ENSMUST00000159688	ENSMUSG00000026656	1	170958617	170976547	-1	0	0	0	0	0	0	382	120	780	3472	934	E9Q415	
ENSMUST00000159689						0	0	0	0	0	0	6	57	16	0	11		
ENSMUST00000159690	ENSMUSG00000074794	13	80883384	80896035	1	0	0	0	0	13	0	71	372	309	134	363	E0CY84	
ENSMUST00000159691						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159692	ENSMUSG00000046324	19	29608214	29648415	-1	778	641	3929	1225	987	415	151	592	371	142	446		Q3UVK0
ENSMUST00000159693	ENSMUSG00000079478	19	5728088	5731732	-1	0	0	8	7	0	2	6	0	7	0	0	E0CYU9	
ENSMUST00000159694	ENSMUSG00000040331	7	130532523	130573118	-1	2	2	16	3	1	2	70	547	60	0	0	E0CY57	
ENSMUST00000159695						9	11	1	5	7	8	0	0	0	0	2		
ENSMUST00000159696						11	11	35	24	17	6	0	1	4	3	2		
ENSMUST00000159697	ENSMUSG00000023832	17	12942890	12960747	-1	17	8	21	57	10	3	0	0	1	13	0	G3XA25	
ENSMUST00000159698						7	2	6	2	2	3	22	47	77	10	91		
ENSMUST00000159699	ENSMUSG00000056758	10	120361275	120476469	-1	14	21	13	0	0	0	0	0	0	0	0	Q6NSP9	
ENSMUST00000159702						0	0	0	33	0	0	0	0	1	1	1		
ENSMUST00000159703						8	5	16	10	14	0	2	8	4	0	2		
ENSMUST00000159704	ENSMUSG00000036955	10	62538626	62578457	-1	24	22	66	70	24	17	62	154	72	21	55	H3BIY2	
ENSMUST00000159705						1	2	0	2	0	2	0	0	0	0	0		
ENSMUST00000159708						37	15	14	40	32	18	8	7	5	3	22		
ENSMUST00000159710	ENSMUSG00000038045	17	78883938	78906992	-1	0	0	0	0	1	0	0	0	0	0	0	E0CYC7	
ENSMUST00000159711						0	0	0	0	0	0	16	63	13	0	22		
ENSMUST00000159713	ENSMUSG00000052616	8	104446719	104509910	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXE5	
ENSMUST00000159714						11	8	75	36	24	15	10	18	7	6	26		
ENSMUST00000159715	ENSMUSG00000037280	15	100691813	100729376	-1	0	11	15	7	0	8	870	2429	1288	223	1028		Q8C7U7
ENSMUST00000159716						2	0	0	28	1	0	2	0	0	2	2		
ENSMUST00000159717						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159718						7	6	44	8	3	2	11	33	8	3	43		
ENSMUST00000159719						58	31	39	55	44	33	23	76	73	7	86		
ENSMUST00000159720	ENSMUSG00000028028	3	127670310	127780527	-1	0	0	1	0	0	0	0	0	0	2	0	F6V0L2	
ENSMUST00000159721	ENSMUSG00000043183	13	54503779	54551290	1	0	0	0	48	0	0	0	0	0	0	0	E0CX51	
ENSMUST00000159722						3	3	7	55	3	1	0	0	2	0	0		
ENSMUST00000159723						3	0	0	0	0	1	21	60	23	0	6		
ENSMUST00000159724						230	173	1334	316	214	133	75	72	219	15	326		
ENSMUST00000159725	ENSMUSG00000026102	1	52785427	52817688	-1	16	12	27	203	47	16	2	4	5	0	12	E0CYQ4	
ENSMUST00000159726						4	0	0	138	3	1	0	0	0	0	0		
ENSMUST00000159727	ENSMUSG00000058318	2	92093117	92364666	1	2	0	0	0	0	0	33	0	12	0	28	F6U6L3	
ENSMUST00000159728	ENSMUSG00000006542	1	74738922	74749221	-1	3	3	20	22	5	1	0	0	0	0	0	E0CX18	
ENSMUST00000159729	ENSMUSG00000021990	14	60634001	60764556	1	0	0	6	39	0	3	0	0	0	0	0	E0CZ51	
ENSMUST00000159730						19	9	34	23	17	11	6	6	0	0	8		
ENSMUST00000159732						239	226	646	268	291	151	4	126	21	4	11		
ENSMUST00000159733						2	0	0	2	5	0	0	3	0	0	5		
ENSMUST00000159734	ENSMUSG00000070448	14	51451962	51461293	1	0	0	4	2	3	7	0	0	0	0	0	O35198	
ENSMUST00000159735						2	0	0	0	3	0	0	5	0	0	0		
ENSMUST00000159736						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159737						1	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000159739	ENSMUSG00000038550	3	95878503	95882251	-1	10	9	33	77	20	6	0	4	2	0	7	A2RTE4	Q3TQ03
ENSMUST00000159741						1	1	4	1	1	1	0	0	0	0	0		
ENSMUST00000159742	ENSMUSG00000033400	3	116739999	116808166	-1	5	4	1	1	3	2	53	14	212	7	112	A0A0G2JGI9	
ENSMUST00000159743						0	1	0	0	0	0	15	16	23	46	13		
ENSMUST00000159745						13	7	18	16	18	9	44	392	72	13	110		
ENSMUST00000159746						1	0	4	2	1	2	0	0	0	0	0		
ENSMUST00000159747	ENSMUSG00000037509	1	34678188	34813309	1	41	30	102	77	68	9	0	0	0	0	0	E9PYK8	
ENSMUST00000159748	ENSMUSG00000039210	1	187215508	187351704	1	2	0	0	7	7	3	7	0	15	0	0	M0QWJ1	
ENSMUST00000159749	ENSMUSG00000026175	1	74409376	74435559	1	4	0	3	0	0	5	0	0	0	0	1	F6V2H5	
ENSMUST00000159750						4	1	5	0	6	3	0	0	0	1	1		
ENSMUST00000159753	ENSMUSG00000009687	7	31032722	31042481	-1	1	0	6	3	4	0	157	47	191	650	207	E0CYX7	
ENSMUST00000159754						19	15	33	28	24	10	1	3	0	0	1		
ENSMUST00000159755	ENSMUSG00000068299	6	85899051	85904884	-1	1	2	10	4	2	0	3	5	0	1	1	E0CYM0	
ENSMUST00000159756	ENSMUSG00000040061	2	118707517	118728438	-1	0	0	0	0	0	2	306	279	576	41	496	E9PYI3	
ENSMUST00000159757						6	3	19	13	5	6	0	0	0	16	3		
ENSMUST00000159758						90	82	293	94	70	34	5	29	12	0	20		
ENSMUST00000159759	ENSMUSG00000047423	19	5425157	5427313	1	10	10	0	68	17	7	1433	1575	778	175	553	E9QNR6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159761						2	1	2	6	1	0	0	1	1	0	0		
ENSMUST00000159762						24	15	33	16	17	2	59	150	90	4	160		
ENSMUST00000159763	ENSMUSG00000040265	1	161982453	162478034	-1	0	0	0	0	0	0	0	1	0	0	0	F2Z460	
ENSMUST00000159764						0	0	0	0	2	0	0	191	222	27	105		
ENSMUST00000159765						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159766						18	16	40	82	30	16	0	5	8	0	23		
ENSMUST00000159768						8	7	18	0	16	5	0	0	1	0	2		
ENSMUST00000159769						1	2	1	0	3	0	0	0	0	0	0		
ENSMUST00000159770						4	4	9	3	6	0	2	5	4	0	2		
ENSMUST00000159771	ENSMUSG00000033287	15	78428564	78438909	1	0	6	3	20	0	6	0	9	2	0	0	E0CZ97	
ENSMUST00000159772	ENSMUSG00000021693	13	106958996	107022126	-1	0	0	0	6	0	0	223	439	360	91	210	E0CZ72	
ENSMUST00000159773	ENSMUSG00000036636	17	25133391	25162104	1	0	0	0	0	0	0	1	0	0	0	0	F7BK14	
ENSMUST00000159774	ENSMUSG00000037818	3	40846970	40938138	1	2	14	14	123	43	0	0	183	68	6	61		Q8C1A9
ENSMUST00000159775	ENSMUSG00000022364	15	57912199	57970067	1	2	0	0	64	8	0	0	0	0	0	0	E0CYF4	
ENSMUST00000159776						0	0	0	5	0	0	6	29	9	1	35		
ENSMUST00000159777	ENSMUSG00000063458	14	22019712	23056085	1	1	0	0	0	9	2	0	7	0	0	7	E0CZ28	
ENSMUST00000159778	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZA5	
ENSMUST00000159780	ENSMUSG00000046613	16	20589471	20605377	1	16	21	49	41	44	14	1	1	0	0	0	E0CZ01	
ENSMUST00000159781	ENSMUSG00000029586	5	143181017	143205075	1	10	3	13	2	9	7	0	0	0	0	0	Q8CDE8	
ENSMUST00000159782						0	0	4	6	0	0	0	0	0	0	0		
ENSMUST00000159783						5	0	5	16	14	5	0	0	0	0	0		
ENSMUST00000159784						3	0	0	0	5	0	285	617	432	0	238		
ENSMUST00000159785	ENSMUSG00000045962	6	119923969	120038672	-1	1	4	11	0	0	5	2	0	0	0	4	F6TW99	
ENSMUST00000159786	ENSMUSG00000029207	5	66298703	66618784	-1	20	18	62	41	34	18	0	2	1	4	9		Q9DBR4
ENSMUST00000159787						0	0	0	0	7	6	0	0	0	9	2		
ENSMUST00000159788						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159789	ENSMUSG00000060743	1	180800832	180813943	-1	0	0	8	8	0	0	3536	2304	1719	5887	1889	E0CZ27	
ENSMUST00000159792	ENSMUSG00000026546	1	172520801	172545870	1	0	1	7	1	3	0	0	0	0	1	0	E0CXK6	
ENSMUST00000159794	ENSMUSG00000026361	1	143598800	143702893	-1	1	1	8	1	6	0	17	32	31	2	23	A0A087WPQ2	
ENSMUST00000159797						6	4	9	3	3	0	0	0	0	0	0		
ENSMUST00000159798	ENSMUSG00000047592	5	138225898	138253363	1	0	0	0	0	0	0	0	0	0	37	0	E9PXC9	
ENSMUST00000159799	ENSMUSG00000045994	9	26733728	26763101	1	7	5	0	0	0	0	0	0	0	0	0	Q8R531	
ENSMUST00000159800						1	2	2	2	0	0	0	0	0	0	0		
ENSMUST00000159801						13	0	0	5	8	0	0	0	0	0	0		
ENSMUST00000159802						14	7	12	23	18	6	10	7	2	4	15		
ENSMUST00000159803						23	10	41	36	27	18	0	5	1	0	1		
ENSMUST00000159804	ENSMUSG00000030165	6	129591782	129598775	1	0	0	0	1	0	0	0	5	1	4	1	E0CZ14	
ENSMUST00000159805						1	0	5	2	5	5	14	14	38	0	15		
ENSMUST00000159806	ENSMUSG00000033060	14	101729957	101934710	1	0	0	0	0	0	0	0	3	3	0	36	F6TFN2	
ENSMUST00000159807						10	20	30	0	27	13	9	145	0	10	30		
ENSMUST00000159808						5	0	0	3	4	2	5	63	22	4	26		
ENSMUST00000159809	ENSMUSG00000020258	9	106152857	106158138	-1	2	0	0	0	0	0	1	0	0	0	0	E0CXF4	
ENSMUST00000159810	ENSMUSG00000090112	10	11149427	11217595	1	0	0	0	22	0	5	13	0	103	0	78		Q7TPQ3
ENSMUST00000159811	ENSMUSG00000055692	16	17276300	17283229	1	0	0	0	0	0	0	0	0	6	0	0		Q9JJB1
ENSMUST00000159812						4	0	5	0	0	2	0	0	0	1	2		
ENSMUST00000159813	ENSMUSG00000001844	5	143316489	143329256	-1	4	0	0	0	0	2	176	260	25	65	30	M0QWP4	
ENSMUST00000159814	ENSMUSG00000049866	1	88673125	88702221	-1	21	18	69	206	23	20	512	740	606	145	553		P61208
ENSMUST00000159815						7	4	15	8	9	7	28	76	29	1	34		
ENSMUST00000159816	ENSMUSG00000043336	16	57353093	57573126	1	18	0	35	18	20	5	0	0	0	0	0	E0CYH7	
ENSMUST00000159817	ENSMUSG00000026694	1	162532127	162548551	-1	0	0	0	0	0	0	15	13	20	0	16	E9PYK1	
ENSMUST00000159818	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0	E0CYB6	
ENSMUST00000159819						0	0	0	28	0	0	0	0	34	19	66		
ENSMUST00000159821						0	1	2	188	2	0	0	0	0	0	2		
ENSMUST00000159823						30	27	41	23	27	4	21	108	45	5	60		
ENSMUST00000159824						3	0	0	5	4	0	19	0	21	5	6		
ENSMUST00000159825						4	1	7	3	4	0	171	0	1	7	128		
ENSMUST00000159826	ENSMUSG00000054770	1	57955101	58018956	-1	0	0	0	0	0	0	0	0	7	0	3	E0CXJ5	
ENSMUST00000159828						0	2	2	0	6	0	0	0	0	0	3		
ENSMUST00000159829						0	0	1	8	2	0	10	12	36	16	15		
ENSMUST00000159830						9	9	9	308	15	4	0	0	0	0	0		
ENSMUST00000159831						3	5	15	9	14	2	4	12	9	7	9		
ENSMUST00000159832	ENSMUSG00000024797	19	6067842	6080324	-1	5	6	9	9	38	0	0	9	13	0	27		Q3UVL4
ENSMUST00000159833						0	0	4	1	0	0	0	0	0	0	0		
ENSMUST00000159834	ENSMUSG00000020930	11	102881204	102885216	1	2	4	8	7	6	3	1	0	1	0	2	E0CXL2	
ENSMUST00000159835	ENSMUSG00000019795	10	7629373	7681136	-1	8	8	14	6	13	8	3	0	6	3	2	E0CYT8	
ENSMUST00000159836						2	2	7	34	6	5	0	6	3	1	2		
ENSMUST00000159837						0	5	3	0	0	0	0	17	4	0	3		
ENSMUST00000159839	ENSMUSG00000048402	1	118834132	119053619	-1	0	0	0	0	0	0	0	0	0	0	0	A5A9W5	
ENSMUST00000159840	ENSMUSG00000028931	4	152390742	152477871	-1	10	0	32	0	15	0	3169	1496	2117	142	1287	Q3UPV6	
ENSMUST00000159841	ENSMUSG00000026335	1	97795114	98095646	-1	0	0	1	0	0	2	4	7	0	0	0	F6T0D3	
ENSMUST00000159842						0	1	0	0	0	0	1	4	0	0	0		
ENSMUST00000159843						0	1	2	1	5	0	2	22	2	1	9		
ENSMUST00000159844						0	0	0	0	0	0	0	0	0	0	5		
ENSMUST00000159845						3	1	8	0	3	0	5	2	0	12	0		
ENSMUST00000159846						7	2	18	4	4	4	2	7	2	0	7		
ENSMUST00000159847						72	86	239	75	76	40	1	10	5	3	12		
ENSMUST00000159849						23	15	45	78	18	10	0	0	0	0	0		
ENSMUST00000159850						6	6	5	3	0	0	0	0	0	0	0		
ENSMUST00000159851						0	0	0	4	6	4	0	0	0	0	1		
ENSMUST00000159852	ENSMUSG00000001524	17	35667730	35673739	-1	3	1	7	0	4	2	0	0	0	0	0	E0CYM3	
ENSMUST00000159853						2	2	11	0	2	0	0	0	0	0	0		
ENSMUST00000159854						2	0	2	5	4	4	0	0	0	0	0		
ENSMUST00000159855	ENSMUSG00000033004	14	103113411	103346814	-1	0	11	25	0	0	28	32	0	182	0	147	E9PUJ6	
ENSMUST00000159856						2	2	0	1	0	0	8	12	38	54	99		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159858	ENSMUSG00000021977	14	59133040	59142893	-1	6	6	5	3	4	2	0	0	0	0	0	E0CXF5	
ENSMUST00000159859	ENSMUSG00000024792	19	6080762	6084944	-1	0	1	0	23	2	0	0	4	1	0	0	E0CX79	
ENSMUST00000159860						2	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000159861	ENSMUSG00000073530	1	158711727	158980490	-1	169	103	761	474	135	82	1	6	5	2	10	E9PZ87	
ENSMUST00000159863	ENSMUSG00000038550	3	95878503	95882251	-1	0	0	3	0	0	0	0	2	2	0	0	H3BKT8	
ENSMUST00000159864						2	1	0	1	1	0	4	7	4	3	13		
ENSMUST00000159865	ENSMUSG00000068037	17	12841079	12868143	-1	4	2	0	4	0	0	0	0	0	0	0	E0CX57	
ENSMUST00000159866	ENSMUSG00000030365	6	128887588	128898167	1	2	3	8	5	5	0	17	81	8	44	4	B7ZP15	Q9WVF9
ENSMUST00000159867	ENSMUSG00000044367	11	70216789	70221064	-1	0	0	0	0	1	0	0	0	0	0	0	E0CXV4	
ENSMUST00000159868						2	2	16	10	5	0	0	0	0	1	0		
ENSMUST00000159869						0	0	0	6	0	0	0	17	10	7	9		
ENSMUST00000159870						3	6	5	5	8	4	0	0	0	0	0		
ENSMUST00000159871	ENSMUSG00000031782	8	94838321	94854895	1	0	0	0	0	0	0	0	13	0	0	12	F6SFF5	
ENSMUST00000159872						2	2	5	4	6	2	8	51	28	0	44		
ENSMUST00000159873						7	3	4	2	4	3	0	0	0	0	0		
ENSMUST00000159876	ENSMUSG00000026226	1	86016816	86029958	1	0	0	5	0	0	0	0	0	0	0	0		Q9D9T6
ENSMUST00000159877	ENSMUSG00000052631	6	72513644	72521634	-1	11	0	0	13	5	5	0	0	0	0	0	E0CYY5	
ENSMUST00000159878						1	3	1	3	0	5	0	0	4	0	2		
ENSMUST00000159879	ENSMUSG00000018199	1	143750790	143777068	-1	40	37	60	60	44	10	65	83	72	32	67	Q3TJ75	O08848
ENSMUST00000159880	ENSMUSG00000041831	17	6673458	6738042	1	3	3	28	0	22	8	0	0	0	0	0	E9PUK9	
ENSMUST00000159881						27	19	13	12	15	14	2	1	0	0	0		
ENSMUST00000159882						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000159883	ENSMUSG00000021189	12	101918901	101958246	-1	2	0	0	0	0	1	16	0	26	0	18	F6T5L3	
ENSMUST00000159885						4	3	7	4	3	1	0	3	0	0	0		
ENSMUST00000159886						0	1	39	0	0	0	7	12	22	13	5		
ENSMUST00000159887						10	8	6	10	8	2	114	1402	155	120	16		
ENSMUST00000159888						3	0	3	31	3	4	160	31	92	13	76		
ENSMUST00000159889						10	8	3	3	10	2	0	0	0	0	0		
ENSMUST00000159891	ENSMUSG00000030148	6	123106428	123143999	1	74	57	274	142	86	29	2	10	16	4	24	E0CY25	
ENSMUST00000159892						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000159893	ENSMUSG00000039233	13	13997949	14039638	-1	0	0	0	0	0	0	41	258	67	68	57	E0CXJ6	
ENSMUST00000159894						2	2	4	1	2	1	0	5	0	0	0		
ENSMUST00000159895						5	2	10	13	8	5	40	65	67	3	99		
ENSMUST00000159896						42	44	145	23	21	20	0	3	0	0	0		
ENSMUST00000159898						30	20	71	46	46	24	578	4125	1326	82	1960		
ENSMUST00000159899	ENSMUSG00000039047	3	152714100	152980408	1	23	9	45	69	24	18	80	236	170	94	255		Q9CXY9
ENSMUST00000159901	ENSMUSG00000015748	3	95830124	95855885	-1	0	0	0	0	0	0	6	65	0	9	3	F6T4V0	
ENSMUST00000159902	ENSMUSG00000089798	5	107534709	107551542	1	0	0	0	0	0	0	0	0	0	0	0	E3W998	
ENSMUST00000159903						0	2	20	0	0	0	211	2505	48	220	165		
ENSMUST00000159904	ENSMUSG00000048655	3	55137339	55172935	1	0	1	0	0	0	0	0	0	0	0	0	E9Q3J3	
ENSMUST00000159905						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000159906	ENSMUSG00000025907	1	6206197	6276648	1	2	2	0	2	0	0	0	0	4	0	0	E0CZG6	
ENSMUST00000159907						2	1	1	2	2	0	10	19	7	6	8		
ENSMUST00000159908						4	0	9	0	0	1	107	102	38	17	39		
ENSMUST00000159909						16	0	29	22	20	12	77	191	92	8	194		
ENSMUST00000159910	ENSMUSG00000021614	13	89655312	89742509	-1	3	0	1	0	13	0	441	559	1058	292	1010	G3XA35	
ENSMUST00000159911						0	1	2	2	1	1	8	8	6	0	4		
ENSMUST00000159912						2	5	6	15	9	2	0	0	1	0	2		
ENSMUST00000159914	ENSMUSG00000026489	1	180165238	180199602	-1	4	0	0	0	1	2	0	0	0	0	0	E0CZ05	
ENSMUST00000159915						4	3	4	1	4	0	0	0	0	0	0		
ENSMUST00000159916	ENSMUSG00000045114	7	127017531	127021211	-1	0	3	11	97	3	7	0	0	1	0	0		E9PUL5
ENSMUST00000159917	ENSMUSG00000019795	10	7629373	7681136	-1	0	3	0	0	0	0	295	1054	271	218	139	E9PWE0	
ENSMUST00000159918						6	20	17	0	6	0	0	0	0	0	4		
ENSMUST00000159919						15	9	25	6	19	3	0	0	2	0	5		
ENSMUST00000159920	ENSMUSG00000062040	7	29893333	29906572	-1	0	0	8	9	0	4	8	11	0	0	4		P10077
ENSMUST00000159922						0	0	0	0	0	0	4	0	0	2	0		
ENSMUST00000159923						2	0	0	3	3	0	6	54	0	29	23		
ENSMUST00000159924	ENSMUSG00000009687	7	31032722	31042481	-1	0	0	0	0	0	0	0	514	0	0	0	Q3TDW1	P97808
ENSMUST00000159925						29	21	53	19	42	20	18	2	44	0	70		
ENSMUST00000159926	ENSMUSG00000027880	3	109080469	109116687	1	0	4	1	7	5	1	0	2	0	0	0	E0CY52	
ENSMUST00000159927	ENSMUSG00000049109	10	28668360	28883818	1	0	4	0	0	0	0	9	0	0	0	0	E0CY68	
ENSMUST00000159928						2	4	6	2	4	1	4	16	5	0	0		
ENSMUST00000159929						4	0	5	2	2	0	12	72	25	3	40		
ENSMUST00000159930	ENSMUSG00000066224	4	41723836	41731142	-1	2	0	0	26	0	0	0	0	0	0	0	E0CY10	
ENSMUST00000159931	ENSMUSG00000021578	13	74350309	74365783	1	0	0	0	0	0	1	4	0	1	9	20	E0CYP1	
ENSMUST00000159932						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000159934						1	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000159935						10	10	28	272	26	12	1446	1803	1786	117	1427		
ENSMUST00000159936	ENSMUSG00000029823	6	38551334	38609470	1	14	12	16	7	21	0	94	264	88	13	63	E0CYQ8	
ENSMUST00000159938						0	0	0	5	1	0	0	0	0	1	0		
ENSMUST00000159939	ENSMUSG00000016624	15	84785381	84856049	-1	5	10	27	184	14	10	0	0	6	0	0		Q8C966
ENSMUST00000159940						4	4	0	3	9	1	0	0	0	0	0		
ENSMUST00000159941	ENSMUSG00000001844	5	143316489	143329256	-1	0	0	0	26	0	0	6	19	27	15	0	E0CYN6	
ENSMUST00000159942						0	0	2	35	2	0	0	0	0	0	0		
ENSMUST00000159943	ENSMUSG00000039153	17	44495987	44814797	-1	2	0	0	3	0	0	0	0	0	0	0		Q08775
ENSMUST00000159944	ENSMUSG00000022744	16	58727910	58734251	1	4	0	0	0	2	1	0	0	120	35	49	E0CY66	
ENSMUST00000159945	ENSMUSG00000033210	16	45535309	45607001	1	10	14	0	10	12	9	0	0	0	0	0		Q6UJY2
ENSMUST00000159946						0	0	0	0	0	0	2	0	0	0	1		
ENSMUST00000159948						8	9	7	4	7	1	0	0	0	1	0		
ENSMUST00000159949						16	6	28	27	11	5	0	8	5	0	9		
ENSMUST00000159951	ENSMUSG00000033083	14	101442360	101609191	-1	0	0	5	0	0	0	0	8	0	2	29	F6SUV7	
ENSMUST00000159952	ENSMUSG00000098950	2	156071845	156127092	-1	0	0	0	0	0	0	0	0	0	0	0	F6TXD3	
ENSMUST00000159954						3	1	0	0	2	0	6	22	0	0	2		
ENSMUST00000159955	ENSMUSG00000026639	1	193207699	193343878	1	0	0	10	11	50	23	0	0	0	0	0		Q61087

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000159956						0	0	11	0	0	2	0	0	0	0	1		
ENSMUST00000159957	ENSMUSG00000021470	13	63815240	63900302	1	0	3	0	0	0	1	4	2	0	9	16	F6TW36	
ENSMUST00000159958	ENSMUSG00000025776	1	17727045	17766344	1	0	6	0	0	1	0	0	3	0	1	0		Q8CGD2
ENSMUST00000159959						1	0	3	98	2	0	0	0	0	0	0		
ENSMUST00000159960	ENSMUSG00000058441	15	89059734	89073567	1	3	1	11	1	5	0	0	0	0	0	0	F6TVW7	
ENSMUST00000159961	ENSMUSG00000058318	2	92093117	92364666	1	0	0	0	0	0	0	141	23	189	17	287	F6URE6	
ENSMUST00000159962	ENSMUSG00000022792	16	16302965	16309640	1	6	10	5	27	10	5	0	3	0	0	2	E9PX65	
ENSMUST00000159963	ENSMUSG00000026450	1	134111242	134151540	1	21	0	8	21	28	8	0	0	0	0	0	B2RS82	Q9D7Q1
ENSMUST00000159964	ENSMUSG00000047592	5	138225898	138253363	1	89	85	325	131	86	59	7	48	34	38	106	E0CYW5	
ENSMUST00000159966						0	0	0	0	0	2	12	68	22	28	64		
ENSMUST00000159967						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000159968	ENSMUSG00000033805	5	107402736	107430035	1	0	1	0	0	0	4	0	0	0	0	0	E0CXI7	
ENSMUST00000159969	ENSMUSG00000026656	1	170958617	170976547	-1	0	1	0	2	4	0	26	0	89	184	12	A0A0B4J1E6	
ENSMUST00000159970						3	6	4	2	12	0	17	76	99	0	113		
ENSMUST00000159973	ENSMUSG00000091255	5	14933221	14938429	-1	42	59	34	50	61	24	0	0	0	0	0	K7N6S8	
ENSMUST00000159974						35	24	115	28	46	9	41	166	64	3	68		
ENSMUST00000159975	ENSMUSG00000030589	7	29134851	29153961	1	0	0	0	0	0	0	1633	0	481	0	594		Q8BTM9
ENSMUST00000159976	ENSMUSG00000041734	3	87078593	87174747	-1	0	34	2	15	0	25	1	0	0	10	119		Q80W68
ENSMUST00000159977	ENSMUSG00000019795	10	7629373	7681136	-1	2	7	6	47	6	2	2	5	5	1	8	E0CYJ5	
ENSMUST00000159978						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000159979						4	1	3	3	7	0	19	106	27	7	16		
ENSMUST00000159980						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000159982						0	10	8	0	0	3	0	0	0	0	0		
ENSMUST00000159983	ENSMUSG00000024972	19	7596660	7607193	-1	13	6	93	0	0	6	0	2	0	0	2		Q91VD1
ENSMUST00000159984	ENSMUSG00000038115	6	125690419	126040126	1	13	3	18	0	10	0	23	258	41	37	12	F6UR69	
ENSMUST00000159985	ENSMUSG00000031936	9	15051841	15112108	-1	27	21	26	37	46	24	0	0	0	1	0		Q3V1H3
ENSMUST00000159986	ENSMUSG00000060475	17	12966796	12992546	-1	8	0	16	0	3	0	42	62	46	20	38		Q9ER69
ENSMUST00000159987						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000159988	ENSMUSG00000023995	17	48447956	48451522	-1	0	0	0	0	0	0	0	0	0	0	0	E0CX84	
ENSMUST00000159989	ENSMUSG00000037033	3	144822623	144849357	-1	17	12	20	19	24	10	0	0	0	0	0	E9PUL3	
ENSMUST00000159990	ENSMUSG00000019952	10	99107036	99198074	1	0	7	6	242	34	11	70	322	163	31	179	Q9D3W6	
ENSMUST00000159991	ENSMUSG00000040009	10	74967177	75016907	1	270	279	683	99	130	113	5	7	5	6	13	Q542R8	O70443
ENSMUST00000159993	ENSMUSG00000079022	15	71795795	72034227	-1	525	472	1220	490	616	313	8	59	25	5	46	E9Q7P1	
ENSMUST00000159994	ENSMUSG00000009070	10	74957477	75032586	-1	11	11	45	17	29	3	0	0	1	0	0	E9Q6E1	
ENSMUST00000159995	ENSMUSG00000033400	3	116739999	116808166	-1	5	1	1	4	2	1	2	3	2	0	6	F7CSZ6	
ENSMUST00000159996	ENSMUSG00000003199	17	56005711	56016790	1	0	0	4	0	6	0	0	0	0	0	0	E0CXX6	
ENSMUST00000159997						0	2	0	0	0	0	2	0	0	1	0		
ENSMUST00000159998	ENSMUSG00000050103	12	37241641	37582202	1	0	1	1	2	2	0	0	0	0	0	0		Q8BS35
ENSMUST00000159999						4	1	2	3	0	0	0	0	0	0	0		
ENSMUST00000160000						0	0	0	0	1	0	50	121	63	5	39		
ENSMUST00000160002						11	15	18	8	17	8	0	0	0	1	4		
ENSMUST00000160003	ENSMUSG00000040913	19	45578254	45660312	-1	0	0	4	3	5	0	0	15	0	0	11	E0CXZ3	
ENSMUST00000160004						2	1	1	10	0	1	4	9	4	4	8		
ENSMUST00000160005						34	18	151	208	40	31	14	70	27	13	28		
ENSMUST00000160006						5	1	3	0	4	2	69	386	170	31	336		
ENSMUST00000160007						0	0	0	0	0	0	0	4	0	0	3		
ENSMUST00000160008						2	1	0	0	5	3	0	10	2	0	7		
ENSMUST00000160009	ENSMUSG00000022346	15	61985341	61990374	1	7	4	47	17	10	0	31	103	20	30	18		P01108
ENSMUST00000160010						13	18	19	25	8	10	3	38	5	6	2		
ENSMUST00000160011	ENSMUSG00000024120	17	84705247	84790789	-1	0	0	0	0	0	1	1	2	1	0	0	F6V2A3	
ENSMUST00000160012						0	0	0	0	1	2	93	293	134	26	123		
ENSMUST00000160013	ENSMUSG00000043004	14	19872559	19977627	-1	51	37	178	179	43	24	522	2040	780	1075	632		P63213
ENSMUST00000160014	ENSMUSG00000006463	19	4878668	4885397	1	0	0	2	60	0	0	0	0	0	0	0	E0CZ11	
ENSMUST00000160015						2	1	2	0	2	2	0	0	2	4	2		
ENSMUST00000160016	ENSMUSG00000032878	11	28385685	28584324	-1	0	2	0	4	0	0	0	0	0	0	0	F7B6W4	
ENSMUST00000160018	ENSMUSG00000040913	19	45578254	45660312	-1	3	0	3	2	5	0	14	0	12	12	25	E0CZ74	
ENSMUST00000160019	ENSMUSG00000040287	10	127501686	127508823	1	3	9	0	10	12	4	0	33	17	6	24		Q8BZ71
ENSMUST00000160020						2	0	1	46	2	0	0	4	3	0	3		
ENSMUST00000160021	ENSMUSG00000021578	13	74350309	74365783	1	0	0	0	0	0	0	0	0	0	0	0		Q3TC33
ENSMUST00000160022						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160023	ENSMUSG00000026090	1	37611677	37720085	-1	10	9	257	0	5	0	0	2	0	3	3	F7B0R9	
ENSMUST00000160024	ENSMUSG00000042286	14	31139013	31168641	-1	0	0	0	0	0	0	2	6	0	8	1	F7CT68	
ENSMUST00000160025						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000160026						1	0	0	0	1	0	0	9	3	0	3		
ENSMUST00000160027	ENSMUSG00000060073	12	70974621	70996347	1	89	59	140	115	82	52	14	89	43	81	47	Q58EV4	O70435
ENSMUST00000160028	ENSMUSG00000024799	19	6062821	6068373	-1	5	1	1	37	0	0	2	5	0	2	0	E0CX82	
ENSMUST00000160029						3	8	1	0	2	3	1	0	0	1	0		
ENSMUST00000160031						4510	5377	7481	4303	4300	1938	68	423	99	44	141		
ENSMUST00000160032						1	4	0	0	3	2	50	495	95	43	57		
ENSMUST00000160033						0	3	3	0	0	5	33	31	0	7	0		
ENSMUST00000160034						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160035						2	0	8	78	0	2	0	11	0	0	0		
ENSMUST00000160036						20	19	25	16	27	6	1	12	6	3	1		
ENSMUST00000160037	ENSMUSG00000027165	2	101560781	101649532	-1	0	0	0	0	0	0	0	0	0	0	0		Q9CQI4
ENSMUST00000160038						1	2	0	0	2	6	0	1	0	0	0		
ENSMUST00000160039	ENSMUSG00000001524	17	35667730	35673739	-1	0	0	3	0	0	0	0	0	0	0	0	E0CXV5	
ENSMUST00000160041	ENSMUSG00000032118	9	36821939	36878924	1	3	2	2	0	0	2	0	0	0	0	0	F6SG45	
ENSMUST00000160042						6	1	0	3	0	6	0	5	0	0	7		
ENSMUST00000160043						2	4	1	1	6	2	0	0	0	0	5		
ENSMUST00000160044	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	0	4	0	96	430	200	318	125	F7B1A4	
ENSMUST00000160045	ENSMUSG00000079424	5	95305911	95343917	1	0	0	0	0	5	0	0	0	0	0	0	L7N469	
ENSMUST00000160046						23	17	16	8	26	5	0	4	3	0	11		
ENSMUST00000160047						0	3	1	0	1	1	0	0	0	0	0		
ENSMUST00000160048	ENSMUSG00000020231	10	76259429	76345291	-1	0	0	0	0	0	0	21	0	0	0	0		Q8BWT5

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160049						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000160050	ENSMUSG00000030226	6	138362918	138581968	-1	0	0	0	3	0	0	0	0	0	0	0	E0CXD7	
ENSMUST00000160051						2	3	0	38	3	2	0	0	0	0	0		
ENSMUST00000160052						0	0	2	0	0	0	255	1188	222	1897	172		
ENSMUST00000160053						2	2	1	5	4	0	0	0	0	0	0		
ENSMUST00000160054						0	0	0	2	4	0	0	0	0	0	0		
ENSMUST00000160055	ENSMUSG00000049946	8	58911755	58914298	1	3	0	4	33	5	2	0	0	0	0	0	E9Q6W0	
ENSMUST00000160056	ENSMUSG00000043467	1	161002922	161034849	-1	0	0	0	0	0	0	0	19	12	24	23	Q8C3U9	
ENSMUST00000160057						0	1	8	2	1	0	31	215	43	2	36		
ENSMUST00000160058						58	46	124	81	64	33	5	2	8	0	24		
ENSMUST00000160059						4	7	1	6	7	3	1	1	4	1	4		
ENSMUST00000160060	ENSMUSG00000026450	1	134111242	134151540	1	0	15	5	0	0	3	0	0	0	0	0		Q9D7Q1
ENSMUST00000160061						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000160062	ENSMUSG00000025907	1	6206197	6276648	1	0	1	1	74	2	0	0	0	2	0	0	E0CYU7	
ENSMUST00000160063	ENSMUSG00000029207	5	66298703	66618784	-1	1	2	12	0	2	3	0	0	0	0	1	F6V8Y6	
ENSMUST00000160064	ENSMUSG00000033538	9	5308828	5336783	1	0	4	5	2	5	1	5	21	6	15	13	C6L648	
ENSMUST00000160066						12	8	18	59	11	6	0	0	0	0	0		
ENSMUST00000160067						0	0	0	0	4	0	0	0	0	0	1		
ENSMUST00000160068						0	0	0	0	0	0	0	0	4	2	4		
ENSMUST00000160069						3	2	11	5	3	6	53	148	65	2	81		
ENSMUST00000160070						3	1	1	2	0	1	0	0	0	0	3		
ENSMUST00000160071						0	4	12	7	2	0	0	0	0	0	0		
ENSMUST00000160072	ENSMUSG00000009070	10	74957477	75032586	-1	0	0	0	0	0	0	0	0	1	1	1	E0CYZ0	
ENSMUST00000160074	ENSMUSG00000004896	3	87922601	87930717	-1	0	2	0	0	0	5	19	9	28	1	10	E9PUL0	
ENSMUST00000160075	ENSMUSG00000038722	5	145140362	145148078	1	4	0	14	3	9	8	51	151	70	337	62	E0CX20	
ENSMUST00000160077	ENSMUSG00000079144	1	193168046	193177832	1	0	0	0	4	0	0	0	0	0	0	0	A0A0A6YXC6	
ENSMUST00000160078						9	3	8	2	5	3	0	0	0	0	1		
ENSMUST00000160079						3	0	3	4	3	5	1	26	9	19	16		
ENSMUST00000160081						16	0	48	0	9	0	0	6	0	0	4		
ENSMUST00000160082	ENSMUSG00000026087	1	37890477	37898535	1	12	11	9	20	16	12	5	15	5	7	10		
ENSMUST00000160084	ENSMUSG00000037351	1	36698114	36714422	-1	15	17	12	6	9	5	0	0	0	4	0	E0CZD4	
ENSMUST00000160085	ENSMUSG00000054302	12	54670340	54695897	-1	0	0	0	4	4	0	0	4	0	0	0	E0CXF0	
ENSMUST00000160086						6	1	6	0	5	3	0	0	0	0	0		
ENSMUST00000160087	ENSMUSG00000037989	13	49036303	49148014	-1	8	0	36	0	8	0	0	0	0	0	0		
ENSMUST00000160090						0	7	0	0	0	0	0	0	0	0	0		
ENSMUST00000160092						10	2	10	340	17	15	0	0	0	0	0		
ENSMUST00000160093						0	0	1	2	2	0	0	0	0	0	0		
ENSMUST00000160094						0	0	0	1	0	0	1	3	4	0	2		
ENSMUST00000160095	ENSMUSG00000021990	14	60634001	60764556	1	3	0	19	0	1	0	0	0	0	0	0	F6V9S1	
ENSMUST00000160097						0	2	0	0	0	0	5	10	15	0	14		
ENSMUST00000160098						0	0	0	0	0	0	5	0	0	0	0		
ENSMUST00000160100	ENSMUSG00000061816	1	66924295	66945404	-1	3	0	2	0	0	0	0	0	0	0	0	E0CZ30	
ENSMUST00000160101						5	3	4	1	1	2	0	3	0	0	2		
ENSMUST00000160102	ENSMUSG00000026489	1	180165238	180199602	-1	1	0	1	8	3	1	0	0	0	0	0	E0CYD3	
ENSMUST00000160103	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYY8	
ENSMUST00000160104	ENSMUSG00000035946	5	75075601	75077893	1	9	5	15	170	8	8	0	0	0	0	0	E0CZ09	
ENSMUST00000160106						2	7	7	6	6	3	73	110	131	12	185		
ENSMUST00000160107	ENSMUSG00000025184	19	42518759	42592343	1	0	0	0	0	0	0	48	244	79	218	82	E0CYN2	
ENSMUST00000160108						0	0	0	10	6	0	0	2	8	0	4		
ENSMUST00000160109	ENSMUSG00000015748	3	95830124	95855885	-1	0	0	0	0	0	0	0	8	13	5	8	E0CYD0	
ENSMUST00000160111						1	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000160112						9	12	16	13	8	13	0	4	0	2	5		
ENSMUST00000160113	ENSMUSG00000079036	12	87425840	87444017	-1	0	0	13	0	0	0	0	3	5	6	0	E0CX46	
ENSMUST00000160114						42	43	219	6	29	7	10	98	37	0	24		
ENSMUST00000160115	ENSMUSG00000042015	13	94976344	95023314	1	10	7	61	141	22	10	0	0	0	0	0	S4R290	
ENSMUST00000160116	ENSMUSG00000035270	16	56204313	56273756	1	0	0	0	0	1	0	4	1	21	1	4		Q80XH2
ENSMUST00000160118	ENSMUSG00000048495	1	57388237	57407101	-1	0	0	0	1	0	1	0	5	0	3	2	E0CZH0	
ENSMUST00000160119						40	22	92	55	43	12	18	417	55	50	53		
ENSMUST00000160120	ENSMUSG00000032023	9	40894849	40964118	-1	1	0	6	4	0	0	0	0	0	1	0	E0CX29	
ENSMUST00000160121	ENSMUSG00000026489	1	180165238	180199602	-1	2	0	0	10	0	0	0	0	0	0	0	E0CYG7	
ENSMUST00000160122						0	0	1	59	3	0	1	2	1	5	4		
ENSMUST00000160123						0	4	2	8	2	2	0	2	0	0	1		
ENSMUST00000160124	ENSMUSG00000084786	9	20642878	20647140	1	6	4	1	5	4	7	10	28	7	14	18		Q9EPV8
ENSMUST00000160125						0	0	3	1	3	0	0	2	5	0	3		
ENSMUST00000160126						15	21	38	29	14	8	0	5	5	0	6		
ENSMUST00000160127						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000160128						3	2	7	6	5	6	0	3	2	0	3		
ENSMUST00000160129	ENSMUSG00000025533	5	130011258	130029247	-1	9	4	32	8	3	10	0	0	4	0	8		Q91YI0
ENSMUST00000160130						14	15	16	19	21	8	13	71	54	4	48		
ENSMUST00000160131						3	0	0	11	2	2	0	107	22	0	17		
ENSMUST00000160132	ENSMUSG00000005610	7	111070568	111083030	-1	4	0	0	40	0	0	22	0	218	37	206	F6TW20	
ENSMUST00000160133	ENSMUSG00000029832	6	51432670	51458768	1	2	0	5	56	0	0	0	0	0	0	0	E9PWE6	
ENSMUST00000160134	ENSMUSG00000022150	15	6299788	6440712	1	3	0	9	2	8	4	1	0	0	23	12	E0CXT5	
ENSMUST00000160135	ENSMUSG00000029673	5	131437333	132543344	-1	2	0	4	0	2	0	0	0	0	0	0	E0CZ47	
ENSMUST00000160136						0	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000160138	ENSMUSG00000034908	9	45937857	45955247	-1	0	0	2	3	0	2	160	51	132	7	80	F6TVH9	
ENSMUST00000160139	ENSMUSG00000021666	13	97137937	97181195	1	1	0	3	2	0	0	0	0	0	0	0	E0CY79	
ENSMUST00000160140						13	8	8	8	8	8	0	0	0	0	0		
ENSMUST00000160141						8	3	7	77	10	3	4	0	0	0	3		
ENSMUST00000160142						11	5	4	2	7	3	0	0	0	0	0		
ENSMUST00000160143	ENSMUSG00000004896	3	87922601	87930717	-1	4	4	28	95	5	2	0	0	0	0	8	E0CYK3	
ENSMUST00000160144	ENSMUSG00000038876	10	29344178	29362442	-1	0	0	9	28	5	3	15	24	14	39	4		Q9CZW6
ENSMUST00000160145						1	0	1	0	0	0	169	200	63	7	15		
ENSMUST00000160146						33	43	51	67	48	21	17	37	23	8	48		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160147	ENSMUSG00000032295	9	57130690	57142722	1	13	4	18	13	10	0	0	0	34	0	0	Q3ZCX9	Q91W89
ENSMUST00000160148						17	13	12	13	17	4	4	27	17	11	19		
ENSMUST00000160150	ENSMUSG00000004894	3	88021750	88027583	-1	0	0	2	0	7	0	0	0	0	0	0	E0CXI3	
ENSMUST00000160151						12	14	26	30	12	8	0	2	2	0	7		
ENSMUST00000160153						2	6	7	5	3	4	0	29	14	0	8		
ENSMUST00000160155						3	2	17	8	5	7	16	111	23	31	18		
ENSMUST00000160157						7	7	25	13	10	4	176	416	131	277	143		
ENSMUST00000160158						6	2	0	2	8	2	0	0	0	0	0		
ENSMUST00000160159						29	13	48	82	26	5	1	0	3	0	0		
ENSMUST00000160160	ENSMUSG00000106631	5	107507621	107580596	1	0	8	30	0	1	10	0	1	0	0	2	A0A0G2JDB2	
ENSMUST00000160161						0	2	13	184	9	0	0	1	0	0	0		
ENSMUST00000160162						0	1	0	2	1	1	0	0	0	0	3		
ENSMUST00000160163	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	0	0	1	0	0	0	27	0	0	E0CYV8	
ENSMUST00000160165	ENSMUSG00000098950	2	156071845	156127092	-1	0	0	0	0	0	0	0	0	0	0	0	F6U693	
ENSMUST00000160166						1	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000160167						2	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000160168						67	60	182	43	65	27	15	15	64	3	26		
ENSMUST00000160169	ENSMUSG00000026489	1	180165238	180199602	-1	0	0	0	2	0	0	0	0	0	6	10	E0CXR1	
ENSMUST00000160170						2	2	2	4	5	3	0	0	0	0	0		
ENSMUST00000160171						3	0	0	2	2	1	0	0	5	0	1		
ENSMUST00000160172	ENSMUSG00000022553	15	76351294	76354380	1	0	3	5	0	1	0	0	59	25	0	0	E0CYF5	
ENSMUST00000160173						7	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000160174						10	5	46	7	11	8	0	46	0	13	9		
ENSMUST00000160175	ENSMUSG00000022416	15	80287238	80398279	1	4	5	0	0	6	0	0	0	0	0	1	F6V0N5	
ENSMUST00000160179						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000160180	ENSMUSG00000024646	18	84851338	84880401	1	0	3	8	18	11	10	22	7	19	88	3	Q544Z9	P56395
ENSMUST00000160181	ENSMUSG00000059022	6	29473162	29507952	-1	7	4	0	4	10	0	0	0	0	0	0	F7B5X1	
ENSMUST00000160183						2	1	5	1	1	0	0	0	0	0	2		
ENSMUST00000160184	ENSMUSG00000032591	9	108080436	108085003	1	0	0	0	0	0	0	1	0	0	0	3	F7C0X2	
ENSMUST00000160185						0	0	0	0	0	0	0	0	0	0	5		
ENSMUST00000160186	ENSMUSG00000021189	12	101918901	101958246	-1	3	0	0	0	0	1	3	1	13	20	22	F6TRN1	
ENSMUST00000160189						23	12	34	36	37	12	56	85	88	2	110		
ENSMUST00000160190						0	0	0	60	3	2	7	5	12	0	5		
ENSMUST00000160191	ENSMUSG00000014782	8	105373274	105382862	1	10	5	0	3	0	4	0	0	0	0	0	E9Q7C3	
ENSMUST00000160192						0	1	6	0	0	0	0	0	0	0	0		
ENSMUST00000160193						0	0	7	0	1	0	11	5	9	2	20		
ENSMUST00000160194	ENSMUSG00000030589	7	29134851	29153961	1	0	0	4	12	1	0	25	31	57	0	132	E0CX54	
ENSMUST00000160195						0	0	0	0	3	0	0	0	2	0	4		
ENSMUST00000160196						3	2	2	0	0	1	13	37	18	21	26		
ENSMUST00000160197	ENSMUSG00000033769	6	84618487	85069513	-1	29	26	87	68	34	14	102	291	206	28	146		A6H5Z3
ENSMUST00000160198						0	0	0	0	0	0	15	0	0	0	0		
ENSMUST00000160199	ENSMUSG00000039153	17	44495987	44814797	-1	0	0	0	32	2	0	6	0	19	0	11	F7CZB5	
ENSMUST00000160200	ENSMUSG00000035632	7	3645268	3661109	1	0	0	0	0	0	0	0	0	0	0	0	F6UAW9	
ENSMUST00000160201	ENSMUSG00000028138	3	138443093	138455499	1	0	0	0	0	0	0	0	0	2	0	2	A0A0G2JDX2	
ENSMUST00000160202						3	3	6	4	6	0	0	2	3	0	0		
ENSMUST00000160204						8	4	3	0	2	0	100	436	0	0	46		
ENSMUST00000160205						0	1	9	1	6	1	0	2	0	0	1		
ENSMUST00000160206						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160207	ENSMUSG00000042961	15	7206120	7398395	-1	0	0	0	209	16	15	0	0	0	0	0	E0CXM4	
ENSMUST00000160208						3	2	0	0	3	0	0	43	2	21	0		
ENSMUST00000160209						0	2	0	4	0	1	0	0	0	0	0		
ENSMUST00000160210						1657	1628	6934	985	2755	933	17	240	63	43	75		
ENSMUST00000160211	ENSMUSG00000009093	10	75814943	75822543	-1	5	0	11	0	10	2	0	0	0	0	0		Q9D4P7
ENSMUST00000160212	ENSMUSG00000053004	6	114397936	114483296	1	1	2	2	63	8	2	0	0	0	0	0	E0CXH0	
ENSMUST00000160213						0	0	2	1	1	0	283	6218	955	1038	593		
ENSMUST00000160214	ENSMUSG00000067604	1	38939149	38950276	1	4	7	0	0	4	0	0	0	0	0	0	E0CXN4	
ENSMUST00000160215	ENSMUSG00000056832	6	38381469	38427647	1	0	0	0	0	0	0	0	0	0	0	0	E0CXQ7	
ENSMUST00000160216	ENSMUSG00000039488	9	9660891	10904775	-1	7	8	14	37	24	0	0	0	0	0	0		P68500
ENSMUST00000160217	ENSMUSG00000105383	9	109057933	109074120	-1	35	4	39	41	43	19	41	71	17	8	62	I6L9G2	
ENSMUST00000160218	ENSMUSG00000093536	7	6398715	6432093	1	6	6	21	6	12	6	0	0	0	0	0	A0A504	
ENSMUST00000160219	ENSMUSG00000032998	4	119537004	119629119	1	0	0	1	3	0	0	0	0	3	0	10	E0CYS8	
ENSMUST00000160220	ENSMUSG00000042605	5	121711337	121816493	1	2	1	0	0	0	0	1	7	1	0	2	F6U2Q5	
ENSMUST00000160221						3	1	5	9	5	5	4	2	19	1	12		
ENSMUST00000160222						9	12	37	4	17	0	0	25	0	0	0		
ENSMUST00000160223	ENSMUSG00000072598	14	44001664	44006418	-1	3	0	2	0	0	0	0	0	0	0	0	Q5GAN0	
ENSMUST00000160225						5	3	12	13	3	2	9	28	0	1	6		
ENSMUST00000160226						2	1	5	6	6	1	1	0	0	2	2		
ENSMUST00000160228						1	1	2	1	0	0	0	3	0	0	2		
ENSMUST00000160229	ENSMUSG00000007817	14	25459185	25666743	1	0	2	0	78	3	0	4	5	21	0	6	E0CX95	
ENSMUST00000160230	ENSMUSG00000021712	13	104178797	104203372	1	1	1	1	18	1	0	0	0	4	16	9	E0CY80	
ENSMUST00000160232	ENSMUSG00000021615	13	89774027	90089608	-1	0	1	0	0	1	2	0	0	0	0	2	E0CZC8	
ENSMUST00000160233	ENSMUSG00000024797	19	6067842	6080324	-1	0	1	0	0	0	0	0	0	0	0	3	E0CX85	
ENSMUST00000160234						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000160235						1	3	2	0	1	2	0	0	0	0	0		
ENSMUST00000160236	ENSMUSG00000072663	15	9578193	9748868	-1	17	22	82	6	24	15	1	16	22	16	8	E0CYG3	
ENSMUST00000160237						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000160238						2	0	0	0	0	2	0	3	1	2	1		
ENSMUST00000160240	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	0	0	0	0	0	0	0	F7D425	
ENSMUST00000160243	ENSMUSG00000060459	16	22985854	23029101	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYI5	
ENSMUST00000160244	ENSMUSG00000004151	12	38779380	38868215	1	8	3	0	3	8	5	0	6	10	5	11	E0CZ37	
ENSMUST00000160245						1	1	13	5	5	3	4	29	10	7	10		
ENSMUST00000160246	ENSMUSG00000029130	5	29195992	29228457	1	0	0	0	0	0	0	0	0	0	0	0		Q9JIT1
ENSMUST00000160247	ENSMUSG00000044948	19	47737561	47919299	-1	17	24	12	28	28	13	0	4	0	0	4	E9Q7R9	
ENSMUST00000160248	ENSMUSG00000022335	15	68083766	68258856	-1	11	7	7	0	0	0	56	17	49	0	56		Q7TS63

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160249	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	0	0	0	192	165	65	4	0		Q5XPI3
ENSMUST00000160250						18	7	7	227	12	0	6	9	18	5	31		
ENSMUST00000160251	ENSMUSG00000021189	12	101918901	101958246	-1	0	0	0	14	0	0	7	0	0	0	12	Q5M8S1	
ENSMUST00000160252						5	2	1	15	1	1	0	0	0	0	0		
ENSMUST00000160253						11	5	3	2	11	5	0	117	68	0	20		
ENSMUST00000160256						0	0	0	19	2	0	1	0	0	0	2		
ENSMUST00000160259						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160260	ENSMUSG00000026565	1	165865154	166002678	-1	32	25	0	44	30	16	186	265	274	35	238		
ENSMUST00000160261	ENSMUSG00000034098	3	76074270	76710019	1	3	2	0	0	0	0	0	0	0	0	0		Q8BFR2
ENSMUST00000160262	ENSMUSG00000071324	10	41914990	42018442	-1	92	0	3	34	0	35	2	0	0	1	5		Q3URY6
ENSMUST00000160265						1	3	2	1	6	3	0	8	0	8	0		
ENSMUST00000160266						0	1	13	0	2	2	2	6	0	13	14		
ENSMUST00000160267	ENSMUSG00000036661	15	73512560	73572242	1	1	0	0	1	3	0	0	0	4	0	0	F6SUD2	
ENSMUST00000160269	ENSMUSG00000024146	17	87025550	87035810	1	0	0	0	0	0	0	134	845	128	37	10	F6TQQ9	
ENSMUST00000160270						3	4	15	14	7	2	2	16	5	6	5		
ENSMUST00000160271	ENSMUSG00000028559	4	109061145	109202272	-1	0	0	0	39	4	6	2004	9440	3261	3219	1822	Q5FWX7	
ENSMUST00000160272	ENSMUSG00000025812	8	127063893	127612286	1	8	0	7	4	8	0	0	0	0	0	5	A5D6P2	
ENSMUST00000160273						9	0	11	0	10	0	0	0	0	0	0		
ENSMUST00000160274						1	1	3	16	4	2	1	1	2	0	0		
ENSMUST00000160275						3	0	5	5	4	0	5	4	0	0	4		
ENSMUST00000160276	ENSMUSG00000037902	2	129592835	129632228	1	0	0	0	0	0	0	0	0	0	31	0		
ENSMUST00000160277						3	9	55	9	7	5	0	0	0	0	0		
ENSMUST00000160279	ENSMUSG00000021415	13	34924409	34955875	1	0	7	6	8	0	3	0	0	0	0	0		Q497N7
ENSMUST00000160280						1	4	0	3	9	3	7	43	9	0	25		
ENSMUST00000160281	ENSMUSG00000030042	6	82618992	82705365	-1	2	0	0	39	0	1	17	8	21	64	25	E0CYA9	
ENSMUST00000160282						0	0	0	7	2	0	1	132	28	0	63		
ENSMUST00000160283						6	3	20	5	10	2	0	0	0	0	0		
ENSMUST00000160284						0	2	0	0	0	0	1	1	1	0	0		
ENSMUST00000160285	ENSMUSG00000043020	3	146040526	146108130	-1	13	21	15	13	18	5	0	0	0	0	0	B2RY71	
ENSMUST00000160286						2	0	4	0	0	0	0	5	0	0	0		
ENSMUST00000160287						18	6	11	14	10	3	5	2	9	12	10		
ENSMUST00000160289	ENSMUSG00000040331	7	130532523	130573118	-1	4	4	0	69	7	0	295	776	433	461	295	G3XA30	
ENSMUST00000160290	ENSMUSG00000090164	6	128849090	128891126	-1	15	9	11	10	19	5	17	174	31	96	23	E0CXF8	
ENSMUST00000160291	ENSMUSG00000034902	10	81292963	81319973	1	0	0	0	15	2	0	9	0	21	0	16	E0CZ71	
ENSMUST00000160292	ENSMUSG00000059336	18	78100091	78142119	-1	2	0	3	2	15	1	0	0	0	0	0		Q8VHL0
ENSMUST00000160293	ENSMUSG00000022555	15	76502015	76511951	-1	0	0	0	0	0	0	78	0	9	2	0	F6V8W6	
ENSMUST00000160294						3	5	10	2	7	2	60	540	61	20	132		
ENSMUST00000160295						6	1	24	5	9	6	2	1	0	3	0		
ENSMUST00000160296						5	0	6	9	12	6	3	0	0	0	0		
ENSMUST00000160297						0	8	0	0	0	0	0	0	0	0	0		
ENSMUST00000160298	ENSMUSG00000089901	14	43925390	43933411	1	507	442	390	517	598	259	41	468	84	96	122	E0CXS8	
ENSMUST00000160299	ENSMUSG00000019785	10	33512286	33624769	-1	5	2	2	0	1	0	0	0	0	0	0		Q8BG92
ENSMUST00000160300	ENSMUSG00000046178	6	8948431	9249032	1	5	0	0	0	9	0	0	0	0	0	0		Q61200
ENSMUST00000160301						2	0	1	0	2	0	0	0	0	0	8		
ENSMUST00000160302	ENSMUSG00000037318	1	193175453	193201703	-1	6	0	6	10	4	0	87	572	192	158	186	A0A0A6YY84	
ENSMUST00000160303	ENSMUSG00000026546	1	172520801	172545870	1	0	0	1	0	1	1	2	18	6	4	8	E0CXX5	
ENSMUST00000160304						1	3	12	1	4	1	4	14	6	4	16		
ENSMUST00000160305	ENSMUSG00000025776	1	17727045	17766344	1	0	0	0	0	0	0	0	0	0	0	0	E0CYY0	
ENSMUST00000160307	ENSMUSG00000027692	3	28263214	28675858	1	0	0	0	0	0	0	0	0	0	0	0	B2RQ80	
ENSMUST00000160308						2	4	4	2	3	0	1	0	0	1	0		
ENSMUST00000160310						0	0	19	2	4	1	2	6	4	0	3		
ENSMUST00000160311	ENSMUSG00000064373	15	3268547	3280508	1	0	0	0	0	1	0	0	0	0	0	2	E0CY03	
ENSMUST00000160312						0	2	2	1	6	4	0	4	8	0	0		
ENSMUST00000160314						0	0	4	7	7	0	0	0	0	0	0		
ENSMUST00000160315						1	0	0	5	0	0	4	0	0	2	4		
ENSMUST00000160316						1	2	1	5	2	4	0	1	0	1	1		
ENSMUST00000160317						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160318						0	1	5	1	0	0	0	0	11	0	0		
ENSMUST00000160319	ENSMUSG00000023994	17	48386885	48409906	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYF3	
ENSMUST00000160320						6	2	11	0	7	6	0	0	0	0	0		
ENSMUST00000160322	ENSMUSG00000042743	13	104109741	104141735	1	2	0	0	65	0	0	2	0	0	0	0	E0CZ99	
ENSMUST00000160323						5	1	0	8	2	0	0	0	0	0	0		
ENSMUST00000160324						1	0	13	0	0	0	0	0	0	0	0		
ENSMUST00000160325						4	1	4	6	7	5	0	16	7	0	8		
ENSMUST00000160326	ENSMUSG00000022710	16	8689595	8792308	-1	0	0	0	47	3	5	515	4844	1571	144	1060	E0CY04	
ENSMUST00000160327						19	17	21	15	14	8	0	0	0	0	0		
ENSMUST00000160328						112	96	658	274	167	124	6	4	6	1	7		
ENSMUST00000160329	ENSMUSG00000066643	12	8973892	9028847	1	24	16	11	90	27	0	6	1	10	0	0	E0CYD5	
ENSMUST00000160330						0	3	0	0	2	3	0	0	0	0	0		
ENSMUST00000160331						3	6	9	33	4	3	0	0	0	0	2		
ENSMUST00000160332						0	0	0	0	0	0	11	84	21	0	0		
ENSMUST00000160333						7	7	6	8	16	3	0	0	3	0	3		
ENSMUST00000160335						0	0	0	0	0	1	33	46	32	0	50		
ENSMUST00000160336						3	1	11	0	5	0	2	0	1	0	1		
ENSMUST00000160337	ENSMUSG00000019923	10	72654845	72674964	1	10	9	4	4	2	8	52	86	92	517	91		Q9CQU5
ENSMUST00000160338	ENSMUSG00000004567	8	3500457	3515232	1	0	2	5	8	0	1	0	0	0	0	0	E0CZ07	
ENSMUST00000160339	ENSMUSG00000025905	1	5588466	5606131	1	0	5	0	0	0	0	0	0	0	0	0	Q14AL5	P33534
ENSMUST00000160340	ENSMUSG00000060579	14	9550092	11162035	-1	4	0	4	2	0	0	0	0	0	0	0	E9PZ91	
ENSMUST00000160341						3	4	12	17	11	2	0	57	7	0	17		
ENSMUST00000160342	ENSMUSG00000021917	14	30999826	31001672	-1	0	0	4	4	6	0	15	20	3	51	8	E0CZF9	
ENSMUST00000160343						0	0	0	0	1	0	1	2	0	0	2		
ENSMUST00000160344	ENSMUSG00000054434	5	123068415	123117749	1	0	0	0	11	0	0	0	0	0	0	0	E0CX33	
ENSMUST00000160345	ENSMUSG00000047369	1	181738988	181769674	1	8	10	2	7	7	4	0	0	0	0	0	Q8CAE5	
ENSMUST00000160346						2	2	3	2	3	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160347	ENSMUSG00000036523	12	16670615	16800886	-1	0	0	0	0	0	0	0	0	0	0	0	F6U5E3	
ENSMUST00000160348						0	0	0	108	2	2	1	0	0	0	0		
ENSMUST00000160349						14	21	21	23	23	13	48	166	71	0	87		
ENSMUST00000160350						0	2	0	3	1	1	0	0	0	0	0		
ENSMUST00000160352	ENSMUSG00000037720	5	67260565	67291461	1	1	0	0	0	0	0	51	43	76	62	14		
ENSMUST00000160353						0	0	5	0	0	0	0	0	0	2	0		
ENSMUST00000160354						0	2	0	0	5	0	0	7	4	0	0		
ENSMUST00000160355	ENSMUSG00000042524	15	79724070	79742536	-1	2	2	3	19	3	3	1	3	4	0	2	E0CY44	
ENSMUST00000160356	ENSMUSG00000054065	7	141078218	141090510	1	0	1	0	0	0	0	6	19	8	0	0	F6V8P6	
ENSMUST00000160357						0	0	6	1	0	0	0	18	4	0	14		
ENSMUST00000160358						0	0	0	2	1	2	0	0	0	0	0		
ENSMUST00000160359	ENSMUSG00000032374	9	92542223	92608428	1	11	0	0	0	0	0	0	0	0	30	16	E9Q718	
ENSMUST00000160360	ENSMUSG00000061436	6	38694390	38876165	-1	0	0	0	125	0	0	0	0	0	0	0		
ENSMUST00000160362						8	4	52	5	4	1	0	1	1	0	0		
ENSMUST00000160363						2	0	3	0	7	0	0	0	0	0	0		
ENSMUST00000160364						5	0	6	0	7	3	6	14	3	0	19		
ENSMUST00000160365	ENSMUSG00000031876	8	104281347	104310145	-1	0	0	0	0	0	0	0	0	0	0	0	F6T5N6	
ENSMUST00000160366	ENSMUSG00000037787	12	111713261	111754980	1	1	0	0	2	0	0	7	8	0	0	0	E9Q3I2	
ENSMUST00000160367						0	0	77	0	0	0	0	0	1	0	0		
ENSMUST00000160369	ENSMUSG00000003549	7	19344778	19356524	1	8	8	8	4	1	3	0	5	5	0	7	E9PUM0	
ENSMUST00000160370						0	0	0	0	0	1	3	14	9	9	12		
ENSMUST00000160371	ENSMUSG00000002949	8	4259731	4275913	-1	0	0	3	0	5	0	12	84	0	0	0	F7C189	
ENSMUST00000160372	ENSMUSG00000038876	10	29344178	29362442	-1	0	0	0	0	0	0	119	152	84	122	85		Q9CZW6
ENSMUST00000160373	ENSMUSG00000023990	17	47737030	47792419	1	0	0	0	0	0	0	0	0	0	0	0	E9PWJ9	
ENSMUST00000160374	ENSMUSG00000054675	5	113793729	113800516	-1	0	1	2	1	2	0	0	1	0	0	0	E0CYG1	
ENSMUST00000160375	ENSMUSG00000006289	14	50906478	50924893	-1	0	1	0	0	0	0	0	3	0	0	0	E0CYK9	
ENSMUST00000160376	ENSMUSG00000052942	19	28258851	28680077	-1	0	1	5	9	2	2	0	0	6	0	0	E0CYJ3	
ENSMUST00000160377	ENSMUSG00000033200	17	25369273	25374442	1	4	0	14	15	8	11	0	0	0	0	0	G3XA07	
ENSMUST00000160378	ENSMUSG00000062480	17	12923833	12940402	-1	0	2	6	0	1	0	0	0	0	0	0	F2Z459	
ENSMUST00000160379	ENSMUSG00000090071	1	74854934	74857732	1	12	14	13	521	16	6	0	0	0	0	0		O35926
ENSMUST00000160381						2	2	3	0	0	5	0	0	0	0	0		
ENSMUST00000160382	ENSMUSG00000070686	5	93634993	93671551	-1	25	0	6	0	0	0	0	0	0	0	0	E0CZF1	
ENSMUST00000160383	ENSMUSG00000029130	5	29195992	29228457	1	0	0	0	0	0	0	0	5	0	2	0	E0CZC4	
ENSMUST00000160384	ENSMUSG00000032131	9	44273188	44288615	-1	1	2	1	58	2	2	0	0	0	0	0	E0CY02	
ENSMUST00000160386	ENSMUSG00000061244	14	49012146	49066653	-1	0	1	1	2	1	0	0	0	0	7	11	E0CYX2	
ENSMUST00000160387						4	7	4	1	3	1	0	0	0	0	0		
ENSMUST00000160388						4	6	11	42	4	0	6	0	0	2	5		
ENSMUST00000160389						4	1	3	4	7	5	0	1	0	1	1		
ENSMUST00000160390	ENSMUSG00000050103	12	37241641	37582202	1	54	34	129	74	67	29	1	8	1	4	10		Q8BS35
ENSMUST00000160392	ENSMUSG00000037335	11	57828705	57832818	-1	12	0	21	127	2	8	0	0	0	0	0	Q5SQG1	Q64279
ENSMUST00000160393	ENSMUSG00000006289	14	50906478	50924893	-1	31	31	193	55	21	17	1	11	0	6	13		
ENSMUST00000160394						3	5	11	10	4	1	0	0	0	2	0		
ENSMUST00000160395						0	0	0	37	0	0	1	0	0	1	3		
ENSMUST00000160396	ENSMUSG00000030589	7	29134851	29153961	1	0	0	4	1	0	0	0	116	22	7	70	F7BK25	
ENSMUST00000160399	ENSMUSG00000019883	10	29313166	29346661	1	2	3	0	29	0	3	8	70	64	58	27		Q9D9V3
ENSMUST00000160400						1	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000160401	ENSMUSG00000041625	14	122816223	122913757	-1	0	5	0	5	1	0	0	0	1	0	0	E0CX39	
ENSMUST00000160402						3	4	2	2	2	1	0	0	0	0	0		
ENSMUST00000160403						3	3	12	6	15	0	276	123	196	39	71		
ENSMUST00000160405	ENSMUSG00000022710	16	8689595	8792308	-1	16	6	31	2	18	0	382	2089	769	477	729	E9PXY8	
ENSMUST00000160406						5	6	15	2	3	8	12	116	14	0	19		
ENSMUST00000160407						0	1	2	2	0	0	12	120	27	23	35		
ENSMUST00000160408						3	0	1	21	4	0	0	0	0	0	0		
ENSMUST00000160409	ENSMUSG00000042015	13	94976344	95023314	1	0	0	0	0	0	0	0	0	0	0	0	S4R2A7	
ENSMUST00000160410						0	0	0	0	0	0	3	0	0	0	0		
ENSMUST00000160411						3	2	72	6	9	0	0	0	0	0	0		
ENSMUST00000160412						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160413	ENSMUSG00000045404	12	99964499	100062682	1	0	11	0	12	7	0	26	29	29	25	35	Q3TYG8	Q8R1P5
ENSMUST00000160414						1	0	4	2	7	1	0	0	0	0	0		
ENSMUST00000160415						0	2	3	0	0	2	0	0	19	0	0		
ENSMUST00000160416	ENSMUSG00000038039	10	58255497	58305599	1	0	0	0	0	0	2	6	12	25	0	0	F6UT01	
ENSMUST00000160417						0	0	0	0	0	0	0	13	0	0	0		
ENSMUST00000160418						0	19	14	18	0	15	0	0	0	0	0		
ENSMUST00000160419						1	1	1	2	1	0	0	1	0	0	1		
ENSMUST00000160421						0	0	0	76	0	0	0	0	0	0	0		
ENSMUST00000160422	ENSMUSG00000029625	5	145167213	145182041	1	0	0	0	0	0	0	184	689	172	113	85	E0CXT7	
ENSMUST00000160424	ENSMUSG00000022416	15	80287238	80398279	1	48	35	148	217	97	44	23	6	16	1	76	E9Q7P2	
ENSMUST00000160425	ENSMUSG00000068245	14	59347407	59365470	-1	0	0	7	9	6	2	0	18	5	123	18		A6H5X4
ENSMUST00000160426	ENSMUSG00000032295	9	57130690	57142722	1	3	0	0	2	0	2	0	0	6	0	3	F6U7S0	
ENSMUST00000160427	ENSMUSG00000038039	10	58255497	58305599	1	2	2	8	19	1	0	0	0	3	0	0	E0CY89	
ENSMUST00000160428						1	6	9	15	3	1	0	0	1	0	1		
ENSMUST00000160430						0	0	13	0	0	0	154	506	107	16	291		
ENSMUST00000160433	ENSMUSG00000058975	7	46396497	46438375	1	4	6	5	8	7	5	0	0	0	0	0	E9PVV3	
ENSMUST00000160434						3	0	3	1	0	4	0	0	0	0	0		
ENSMUST00000160435						0	0	0	0	1	4	0	0	3	0	0		
ENSMUST00000160436	ENSMUSG00000091002	7	138208974	138397730	-1	7	2	6	26	8	1	0	1	0	0	1		Q3B807
ENSMUST00000160437						27	15	44	8	18	16	112	258	108	9	216		
ENSMUST00000160438	ENSMUSG00000040913	19	45578254	45660312	-1	3	1	2	4	2	1	0	2	6	0	6	E0CXP5	
ENSMUST00000160439	ENSMUSG00000026197	1	75168646	75171629	1	0	5	0	0	8	5	901	1211	550	321	343		Q91X58
ENSMUST00000160440						8	4	3	6	5	5	0	0	0	0	0		
ENSMUST00000160441						111	35	219	914	118	76	1	4	0	0	2		
ENSMUST00000160442	ENSMUSG00000020231	10	76259429	76345291	-1	4	2	13	0	0	0	0	0	6	0	0	F7DDW0	
ENSMUST00000160443	ENSMUSG00000048148	8	72646711	72714746	1	5	3	16	10	9	0	0	0	0	0	0	E0CY71	
ENSMUST00000160444						0	3	0	0	0	3	10	0	0	0	19		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160447						10	6	9	163	21	12	1	4	4	6	0		
ENSMUST00000160448	ENSMUSG00000024792	19	6080762	6084944	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXA3	
ENSMUST00000160449						6	4	18	11	8	3	2	0	1	1	0		
ENSMUST00000160450	ENSMUSG00000009070	10	74957477	75032586	-1	0	0	0	0	3	0	0	0	0	0	0	E0CXH7	
ENSMUST00000160451						3	3	17	1	3	1	0	0	0	0	0		
ENSMUST00000160452	ENSMUSG00000038658	19	29522282	29606829	1	8	4	16	0	11	0	62	102	49	17	111	F7CN51	
ENSMUST00000160453						0	1	2	0	0	0	3	0	0	0	3		
ENSMUST00000160454						3	0	16	2	2	0	2	57	0	2	22		
ENSMUST00000160455	ENSMUSG00000025188	19	42755105	42779978	-1	0	2	2	101	6	5	57	60	67	13	69	Q3U309	
ENSMUST00000160456	ENSMUSG00000038473	1	170302668	170589861	-1	9	0	17	34	12	0	0	3	34	0	35		Q9D3A8
ENSMUST00000160457	ENSMUSG00000059142	17	22846697	22867134	-1	34	27	234	19	29	24	3	11	3	26	14	E9PYM8	
ENSMUST00000160458						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000160459						5	3	4	6	9	2	4	2	4	2	10		
ENSMUST00000160460						0	3	6	1	4	2	0	0	0	0	0		
ENSMUST00000160461	ENSMUSG00000090112	10	11149427	11217595	1	0	1	0	0	0	0	6	0	0	0	7	F7D4T4	
ENSMUST00000160462	ENSMUSG00000042605	5	121711337	121816493	1	0	0	2	0	0	1	2	5	8	0	7	F6U209	
ENSMUST00000160464						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000160465	ENSMUSG00000023045	15	102150526	102163474	1	0	0	4	3	0	0	91	16	78	3	226	F6SMH4	
ENSMUST00000160466	ENSMUSG00000038473	1	170302668	170589861	-1	3	8	5	5	6	5	4	0	0	0	3	Q3TRB6	
ENSMUST00000160467						2	3	0	0	7	1	0	0	0	0	0		
ENSMUST00000160468						0	5	0	2	2	2	50	142	193	26	297		
ENSMUST00000160469						2	2	1	2	5	3	0	0	0	0	0		
ENSMUST00000160470						14	16	19	34	13	13	1	4	10	0	3		
ENSMUST00000160471	ENSMUSG00000039210	1	187215508	187351704	1	15	8	0	35	9	0	0	12	8	0	5		Q7TQC7
ENSMUST00000160472	ENSMUSG00000025983	1	54250683	54368727	1	6	0	5	15	5	4	0	0	0	6	1	E9Q7E1	
ENSMUST00000160473						1	4	2	0	1	0	0	0	0	0	0		
ENSMUST00000160474						10	8	6	10	8	2	114	1402	155	120	16		
ENSMUST00000160475	ENSMUSG00000038084	16	29579334	29654884	1	4	0	0	8	3	0	0	9	0	10	41	E0CXD1	
ENSMUST00000160476	ENSMUSG00000025004	19	39767071	39812814	-1	0	0	0	11	0	0	0	0	0	0	0	E9Q7C8	
ENSMUST00000160477	ENSMUSG00000021266	12	108860030	108894174	-1	0	0	15	0	0	0	0	0	0	0	0	E0CXX4	
ENSMUST00000160478	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	1	0	0	0	0	0	0	E0CY19	
ENSMUST00000160479	ENSMUSG00000029449	5	123103044	123132692	-1	0	0	0	31	0	0	0	0	0	0	0	Q4VA10	Q8BYP3
ENSMUST00000160480	ENSMUSG00000059851	7	4740115	4747514	1	0	0	0	0	0	0	3	0	0	0	0	E0CXW4	
ENSMUST00000160481	ENSMUSG00000039210	1	187215508	187351704	1	8	0	3	0	0	0	0	0	15	0	10	M0QWF5	
ENSMUST00000160482	ENSMUSG00000026489	1	180165238	180199602	-1	0	0	0	0	0	0	15	0	21	0	0	E0CYC1	
ENSMUST00000160483	ENSMUSG00000041831	17	6673458	6738042	1	11	8	38	12	10	3	7	14	2	4	22		Q99N48
ENSMUST00000160484	ENSMUSG00000033400	3	116739999	116808166	-1	18	27	42	23	45	24	16	129	98	12	84	F6XXE6	
ENSMUST00000160485	ENSMUSG00000033200	17	25369273	25374442	1	1	0	0	7	0	0	0	0	0	0	0	E0CXD8	
ENSMUST00000160486	ENSMUSG00000026641	1	171411313	171419142	1	1	0	23	2	15	0	491	1128	345	67	220	E9Q722	
ENSMUST00000160487						0	0	0	4	0	0	7	0	1	0	0		
ENSMUST00000160488	ENSMUSG00000021040	12	87443896	87452206	1	7	4	8	2	2	1	29	67	31	243	22		Q9D8T7
ENSMUST00000160489						0	2	6	0	1	2	0	2	0	0	2		
ENSMUST00000160491						4	4	8	5	7	7	0	0	0	0	0		
ENSMUST00000160493	ENSMUSG00000045962	6	119923969	120038672	-1	3	3	4	0	2	0	0	0	7	3	69	F6TAR7	
ENSMUST00000160494						4	10	11	8	7	0	0	0	0	0	0		
ENSMUST00000160495	ENSMUSG00000040113	1	163702256	163725232	-1	4	1	9	2	3	1	0	0	0	0	0	E0CXE9	
ENSMUST00000160496	ENSMUSG00000038115	6	125690419	126040126	1	0	17	6	25	9	18	0	0	0	0	1		Q8CFW1
ENSMUST00000160498						74	65	225	99	94	54	9	54	37	2	36		
ENSMUST00000160499						6	5	14	3	5	0	0	0	0	0	0		
ENSMUST00000160500						0	4	3	1	1	2	0	0	0	0	0		
ENSMUST00000160501	ENSMUSG00000017485	14	16365179	16430787	1	0	0	0	0	0	0	8	10	52	0	11	F6U5K2	
ENSMUST00000160502	ENSMUSG00000039296	5	143216316	143226890	-1	4	5	0	2	5	0	0	0	0	0	0	B9EIX3	
ENSMUST00000160503	ENSMUSG00000032575	9	106838312	106891979	-1	0	0	1	1	0	2	45	33	41	100	5	F6T4L3	
ENSMUST00000160504	ENSMUSG00000034544	3	66981390	67358396	1	1	1	3	72	2	0	0	0	0	0	0	E0CX50	
ENSMUST00000160505	ENSMUSG00000038521	6	124530345	124542359	-1	4	0	0	0	0	0	0	0	0	67	49	E9Q6C2	
ENSMUST00000160506						7	7	0	6	0	8	21	60	35	0	55		
ENSMUST00000160507	ENSMUSG00000022110	14	73525319	73596142	1	3	2	6	0	0	0	38	272	42	54	6		Q9Z2I9
ENSMUST00000160508	ENSMUSG00000026519	1	180942344	180975112	1	2	0	2	0	0	4	0	2	0	0	1	E0CX31	
ENSMUST00000160509						8	7	7	9	15	4	0	0	0	0	0		
ENSMUST00000160510						10	14	12	19	7	4	8	90	10	0	16		
ENSMUST00000160511	ENSMUSG00000029823	6	38551334	38609470	1	0	0	0	0	1	1	196	1298	766	92	689	E0CZB9	
ENSMUST00000160512						0	0	0	1	0	0	2	3	0	0	0		
ENSMUST00000160513	ENSMUSG00000079022	15	71795795	72034227	-1	2	1	0	1	1	1	0	0	0	0	0	F6TGL6	
ENSMUST00000160514						0	2	0	0	1	4	0	0	0	0	0		
ENSMUST00000160515						0	5	0	0	2	1	0	0	1	0	0		
ENSMUST00000160517						0	0	0	21	0	1	0	0	0	0	0		
ENSMUST00000160518	ENSMUSG00000027692	3	28263214	28675858	1	2	0	0	0	1	0	0	0	7	0	0	E9PUL9	
ENSMUST00000160519						4	3	9	13	2	3	2	1	0	0	2		
ENSMUST00000160520						23	19	28	24	31	15	3	2	2	0	2		
ENSMUST00000160521						1	0	0	0	0	0	3	31	15	13	17		
ENSMUST00000160522						1	8	10	3	3	2	0	0	0	1	2		
ENSMUST00000160523						202	170	176	190	239	127	16	74	29	13	56		
ENSMUST00000160525						5	0	3	5	1	1	6	31	4	3	17		
ENSMUST00000160526						3	7	3	1	3	0	0	0	0	0	0		
ENSMUST00000160527	ENSMUSG00000074491	8	3707064	3720651	-1	3	2	15	10	3	2	0	0	0	0	0	F6T066	
ENSMUST00000160529						3	0	0	1	0	4	30	107	47	23	24		
ENSMUST00000160530	ENSMUSG00000033632	18	25168999	25467321	1	0	0	0	0	0	0	0	0	6	0	0	E0CYF6	
ENSMUST00000160531						3	0	9	8	0	0	0	0	0	0	0		
ENSMUST00000160532						3	2	11	9	5	2	0	0	0	1	0		
ENSMUST00000160533						7	0	0	7	5	0	0	0	0	0	0		
ENSMUST00000160534	ENSMUSG00000089694	6	85706727	85713205	-1	38	8	23	24	37	28	0	0	0	0	0	E0CYR6	
ENSMUST00000160535						4	1	2	7	2	2	0	0	0	0	3		
ENSMUST00000160536	ENSMUSG00000026519	1	180942344	180975112	1	7	2	22	4	9	1	4	6	5	0	4	E0CX77	
ENSMUST00000160538	ENSMUSG00000035953	14	50926070	50930856	-1	0	0	0	0	0	0	10	0	3	0	16	E0CYE6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160539	ENSMUSG00000038624	10	52388972	52404607	1	2	0	2	0	2	4	0	0	0	0	0	E0CYE7	
ENSMUST00000160541	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	4	0	0	0	0	E0CYI6	
ENSMUST00000160542	ENSMUSG00000064202	19	28893042	28967800	-1	0	4	0	0	0	0	0	6	0	0	0	B7ZWC9	
ENSMUST00000160546						1	1	0	4	0	4	0	0	0	0	0		
ENSMUST00000160547						10	1	6	14	4	2	0	0	0	0	0		
ENSMUST00000160548	ENSMUSG00000034212	1	92870129	92902906	-1	10	6	13	8	12	7	0	0	1	0	0	E0CYY3	
ENSMUST00000160549						0	4	2	5	0	0	10	12	6	0	0		
ENSMUST00000160550						8	0	3	31	6	3	0	0	0	0	0		
ENSMUST00000160552						1	3	0	0	4	1	0	52	4	0	6		
ENSMUST00000160553						1	0	0	3	1	0	0	328	29	1	45		
ENSMUST00000160554						1167	1584	3597	11781	5089	970	1225	11709	2915	4683	1269		
ENSMUST00000160556	ENSMUSG00000071657	19	8837467	8848683	1	0	0	1	5	2	0	0	0	0	0	0		Q9Z2E9
ENSMUST00000160557						0	0	0	3	0	0	0	11	11	0	8		
ENSMUST00000160558						0	0	6	1	0	0	1	8	4	0	4		
ENSMUST00000160560	ENSMUSG00000022552	15	76347040	76351111	-1	0	0	0	16	0	0	0	0	0	0	0	E0CZH2	
ENSMUST00000160561						9	15	11	669	26	0	1	7	1	4	0		
ENSMUST00000160563						0	0	0	4	0	0	0	0	1	0	4		
ENSMUST00000160565	ENSMUSG00000037849	1	173468509	173491041	-1	14	8	67	13	13	8	0	6	2	1	6	G3UZV2	
ENSMUST00000160566						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000160567						1	1	3	2	3	0	0	0	0	0	0		
ENSMUST00000160570	ENSMUSG00000039210	1	187215508	187351704	1	4	8	18	0	0	0	0	0	0	13	0	E0CZ29	
ENSMUST00000160571	ENSMUSG00000022724	16	59471775	59492461	1	8	0	9	63	16	4	0	0	0	0	19		Q8CD15
ENSMUST00000160572						23	7	28	25	25	8	2	3	2	2	0		
ENSMUST00000160574	ENSMUSG00000029625	5	145167213	145182041	1	7	2	8	22	2	4	0	6	9	0	0	M0QWM8	
ENSMUST00000160575						2	2	3	8	3	0	0	0	0	0	0		
ENSMUST00000160576	ENSMUSG00000049792	12	111709488	111713257	-1	0	11	16	23	9	3	18	0	68	72	38		Q8CI32
ENSMUST00000160578						4	6	5	2	9	3	0	0	0	0	0		
ENSMUST00000160579						5	0	4	74	7	0	13	9	9	11	9		
ENSMUST00000160580						4	4	0	0	4	2	0	0	0	0	0		
ENSMUST00000160581	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0	F6TSJ9	
ENSMUST00000160582						0	0	0	2	0	0	0	0	0	0	2		
ENSMUST00000160583	ENSMUSG00000038538	6	38433950	38524825	1	69	62	116	333	78	56	416	929	747	69	629		Q80WC1
ENSMUST00000160584	ENSMUSG00000032295	9	57130690	57142722	1	0	0	0	0	0	0	0	0	0	0	0	E0CYW2	
ENSMUST00000160585	ENSMUSG00000031480	8	22227313	22261334	1	0	9	0	0	2	0	3	50	19	0	42	G3XA27	
ENSMUST00000160586						104	65	395	160	82	36	121	1228	294	120	323		
ENSMUST00000160587						16	4	36	0	13	0	0	4	0	0	0		
ENSMUST00000160589	ENSMUSG00000026090	1	37611677	37720085	-1	3	3	7	17	6	2	0	0	0	0	0	E0CXB3	
ENSMUST00000160590	ENSMUSG00000024797	19	6067842	6080324	-1	1	2	3	6	6	4	59	172	38	51	34		Q3UVL4
ENSMUST00000160591						0	0	0	0	0	0	42	137	42	54	50		
ENSMUST00000160592						3	2	0	31	3	1	0	0	0	0	0		
ENSMUST00000160593						8	14	8	7	13	7	1	0	0	0	0		
ENSMUST00000160594						7	2	1	45	3	3	2	4	2	0	13		
ENSMUST00000160595						0	0	0	0	0	0	0	5	0	2	0		
ENSMUST00000160596	ENSMUSG00000031876	8	104281347	104310145	-1	18	10	38	20	34	13	0	9	0	0	0	E0CXA2	
ENSMUST00000160597	ENSMUSG00000038084	16	29579334	29654884	1	29	29	33	34	32	23	95	333	168	66	167		P58281
ENSMUST00000160598						7	0	1	8	6	1	0	22	28	0	74		
ENSMUST00000160599						0	1	0	0	0	0	1	0	0	0	2		
ENSMUST00000160600						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000160601						2	0	0	23	2	0	0	0	0	0	0		
ENSMUST00000160602						0	5	4	4	5	5	0	0	0	0	0		
ENSMUST00000160606						7	0	3	0	1	0	2	3	0	1	0		
ENSMUST00000160607						2	1	0	2	2	2	0	0	0	0	0		
ENSMUST00000160609	ENSMUSG00000034040	5	130872082	131308497	-1	0	0	1	7	2	0	0	0	0	0	0	E9Q714	
ENSMUST00000160610	ENSMUSG00000040287	10	127501686	127508823	1	0	0	0	2	2	0	0	0	0	0	0	E0CXX9	
ENSMUST00000160611	ENSMUSG00000036879	8	85840959	86061376	1	4	5	9	4	3	2	1	7	11	0	12	E0CZ55	
ENSMUST00000160612	ENSMUSG00000022148	15	6579871	6663313	1	0	0	5	1	3	1	0	2	2	3	5	E0CY17	
ENSMUST00000160613						8	3	25	8	3	1	0	0	0	0	2		
ENSMUST00000160614						0	0	0	0	0	0	8	7	0	0	3		
ENSMUST00000160615						6	5	6	23	4	2	0	0	2	0	0		
ENSMUST00000160616	ENSMUSG00000026347	1	127486546	127679548	-1	9	7	15	0	13	5	0	3	0	0	0		Q8C996
ENSMUST00000160617	ENSMUSG00000021461	13	63304709	63497278	-1	0	0	2	3	1	0	0	0	0	0	0	E0CYY7	
ENSMUST00000160618	ENSMUSG00000034908	9	45937857	45955247	-1	0	0	0	5	3	2	6	8	0	0	7	F7DFH5	
ENSMUST00000160619						26	24	73	42	33	19	0	0	0	0	0		
ENSMUST00000160620						6	3	13	1	6	3	5	4	0	3	0		
ENSMUST00000160621						0	0	0	1	3	1	26	57	17	0	36		
ENSMUST00000160622						0	0	2	2	5	0	0	0	0	0	0		
ENSMUST00000160623						2	3	1	2	6	2	0	0	0	0	0		
ENSMUST00000160625						2	0	0	94	2	0	0	1	0	0	0		
ENSMUST00000160627	ENSMUSG00000036523	12	16670615	16800886	-1	0	0	0	0	0	3	0	0	0	0	0	F6TVY7	
ENSMUST00000160628						275	248	700	328	380	212	13	61	35	15	61		
ENSMUST00000160629	ENSMUSG00000029625	5	145167213	145182041	1	0	0	0	46	5	0	222	137	241	89	99	B2LVG5	
ENSMUST00000160630						4	4	5	2	5	3	0	0	0	0	0		
ENSMUST00000160631	ENSMUSG00000022558	15	76380261	76453038	1	3	0	3	0	1	0	19	0	0	0	0	F6UUF6	
ENSMUST00000160632						2	2	1	1	3	0	5	2	13	4	4		
ENSMUST00000160633	ENSMUSG00000000378	11	6546887	6596744	1	0	0	0	0	3	2	382	338	225	41	201	E0CXR5	
ENSMUST00000160634	ENSMUSG00000040514	5	7304119	7311491	1	6	2	5	0	5	5	0	0	0	0	0		Q9D5W8
ENSMUST00000160635	ENSMUSG00000023010	15	99392882	99410049	1	0	0	0	0	0	0	874	227	156	0	129		Q9D2C7
ENSMUST00000160636						1	0	5	0	0	0	1	82	37	28	54		
ENSMUST00000160637						9	6	6	118	18	0	0	0	0	0	1		
ENSMUST00000160638	ENSMUSG00000036834	3	63696234	63899472	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQM2	
ENSMUST00000160639	ENSMUSG00000059336	18	78100091	78142119	-1	4	3	7	7	4	3	7	3	7	2	6		Q8VHL0
ENSMUST00000160640	ENSMUSG00000027942	3	90051636	90068347	1	6	4	4	2	8	3	39	210	87	36	83		Q8R092
ENSMUST00000160641	ENSMUSG00000026407	1	136052750	136119822	1	0	0	32	35	0	27	0	0	0	0	0	E9Q7B5	
ENSMUST00000160643	ENSMUSG00000020077	10	62493833	62527451	-1	3	3	8	0	0	0	0	2	0	196	5	E0CYA5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160645	ENSMUSG00000025854	5	138754514	138810077	1	7	6	3	61	6	0	173	68	466	12	200	E0CY01	
ENSMUST00000160646	ENSMUSG00000019791	10	30608141	30618479	-1	5	0	0	0	0	0	14	27	6	10	0	E9Q7F8	
ENSMUST00000160647						50	51	45	49	65	51	0	1	0	0	0		
ENSMUST00000160648	ENSMUSG00000004896	3	87922601	87930717	-1	12	5	14	17	0	8	20	65	0	39	0	E9PZV3	
ENSMUST00000160649	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	17	0	0	15	0	0	0	13	Q05CH9	
ENSMUST00000160650	ENSMUSG00000014782	8	105373274	105382862	1	1	1	3	2	6	2	0	0	0	0	0	E0CYM2	
ENSMUST00000160651						5	5	19	14	6	2	3	7	1	2	6		
ENSMUST00000160652	ENSMUSG00000032425	9	88548020	88571061	1	0	0	0	0	0	0	0	4	0	7	0	E0CY31	
ENSMUST00000160653	ENSMUSG00000038991	13	38500273	38528824	-1	13	5	18	39	9	20	69	0	58	8	0	E9PXX7	
ENSMUST00000160654						1	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000160655						61	38	45	205	51	37	1	5	9	1	7		
ENSMUST00000160656	ENSMUSG00000059149	1	132022806	132068062	-1	4	9	28	0	0	1	110	195	329	24	242	F7D4J0	
ENSMUST00000160658	ENSMUSG00000022311	15	47580637	48792063	-1	0	0	0	0	0	0	0	0	0	0	0	E9PWJ0	
ENSMUST00000160660	ENSMUSG00000021481	13	55105311	55134825	1	0	0	0	0	0	0	0	0	0	0	0	E0CYN4	
ENSMUST00000160662	ENSMUSG00000026023	1	59256906	59352993	1	66	61	214	404	99	73	12	38	11	1	4	E3W997	
ENSMUST00000160663						0	0	8	0	0	3	2	0	2	4	6		
ENSMUST00000160664	ENSMUSG00000061950	17	65782573	65841926	1	19	9	9	21	0	0	933	902	1686	16	1176	E9PX53	
ENSMUST00000160665	ENSMUSG00000040265	1	161982453	162478034	-1	5	0	15	0	8	2	0	0	3	0	4	E0CXZ8	
ENSMUST00000160666	ENSMUSG00000030329	6	124996694	125003096	1	0	2	1	0	5	0	0	0	0	0	0	F7CH06	
ENSMUST00000160667						0	0	0	0	0	0	8	0	4	11	4		
ENSMUST00000160668						34	30	126	41	64	24	0	13	2	2	4		
ENSMUST00000160669						0	0	0	0	0	0	33	170	123	363	111		
ENSMUST00000160670						5	2	10	9	2	4	21	74	53	0	146		
ENSMUST00000160671						13	17	61	32	18	15	0	12	9	3	7		
ENSMUST00000160672	ENSMUSG00000039153	17	44495987	44814797	-1	0	0	0	0	0	0	0	1	0	4	0	F7CN98	
ENSMUST00000160673	ENSMUSG00000039153	17	44495987	44814797	-1	0	0	0	0	0	0	0	0	0	0	0		Q08775
ENSMUST00000160674						0	0	0	0	1	0	0	13	4	0	0		
ENSMUST00000160675						3	0	7	1	0	0	1	0	0	0	0		
ENSMUST00000160676						3	0	3	3	1	0	5	1	0	5	0		
ENSMUST00000160677						4	6	8	3	6	1	0	0	2	0	0		
ENSMUST00000160678						0	0	0	44	0	0	0	0	0	0	0		
ENSMUST00000160680						1	0	3	4	1	0	0	0	0	0	3		
ENSMUST00000160681	ENSMUSG00000020246	10	82696160	82742428	1	7	3	5	4	9	3	80	250	99	33	76	F6T088	
ENSMUST00000160682	ENSMUSG00000084786	9	20642878	20647140	1	0	0	0	0	0	0	1418	3052	785	2773	564		Q9EPV8
ENSMUST00000160683						0	0	0	0	0	0	129	548	244	812	125		
ENSMUST00000160684	ENSMUSG00000004446	6	120891930	120916853	-1	0	4	28	0	0	0	120	677	167	37	165		P70444
ENSMUST00000160685	ENSMUSG00000040627	6	122553801	122564180	1	17	4	89	15	18	6	0	10	5	4	17	E0CXQ9	
ENSMUST00000160686	ENSMUSG00000045962	6	119923969	120038672	-1	0	1	0	0	0	0	0	0	0	0	0	J3QPK0	
ENSMUST00000160687	ENSMUSG00000079036	12	87425840	87444017	-1	0	0	0	0	0	0	0	0	0	4	1	F6U5G1	
ENSMUST00000160688	ENSMUSG00000003721	1	121304353	121332589	-1	0	0	0	23	0	0	0	0	0	4	0	E0CZ15	
ENSMUST00000160689	ENSMUSG00000009687	7	31032722	31042481	-1	0	0	0	0	0	0	407	551	394	1969	312	E0CXM5	
ENSMUST00000160690	ENSMUSG00000040151	3	144429706	144570181	-1	4	1	4	20	5	0	1	0	2	0	2	E0CYX6	
ENSMUST00000160692						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160693	ENSMUSG00000049690	1	125913620	126830799	-1	0	0	1	0	0	0	0	0	0	0	0	E0CYQ5	
ENSMUST00000160694	ENSMUSG00000004891	3	87971078	87980451	1	50	34	95	104	61	38	0	32	0	7	65		Q6P5H2
ENSMUST00000160695						3	1	10	0	2	6	0	0	0	0	0		
ENSMUST00000160696	ENSMUSG00000040669	6	122317731	122340561	-1	3	9	18	0	19	5	0	0	0	0	0	Q7TT35	
ENSMUST00000160697						0	0	0	0	2	0	33	122	159	56	118		
ENSMUST00000160699	ENSMUSG00000042790	9	45863425	45906894	-1	0	0	0	0	0	0	95	171	162	16	108		Q8BFU3
ENSMUST00000160700						1	2	4	7	5	4	0	0	0	0	0		
ENSMUST00000160701	ENSMUSG00000004151	12	38779380	38868215	1	0	0	0	0	0	0	0	0	0	0	6	E0CYN8	
ENSMUST00000160702						5	13	34	19	13	7	0	2	0	0	0		
ENSMUST00000160703	ENSMUSG00000040055	14	57123303	57133611	-1	8	5	0	2	4	12	0	0	0	0	0	E0CX48	
ENSMUST00000160704	ENSMUSG00000030329	6	124996694	125003096	1	3	0	1	0	4	0	0	0	0	0	5		Q6P1B3
ENSMUST00000160705	ENSMUSG00000089862	6	8259288	8459470	1	2	3	0	7	0	0	6	3	16	19	9	E0CX23	
ENSMUST00000160706	ENSMUSG00000054702	1	79606876	79671972	-1	0	0	0	0	0	0	0	0	8	0	0	E0CZ77	
ENSMUST00000160707						86	52	55	301	116	88	2	0	1	0	5		
ENSMUST00000160708	ENSMUSG00000004626	8	3630955	3643644	1	68	61	139	108	85	39	644	2268	1008	229	730	Q548T0	Q64324
ENSMUST00000160709						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000160710	ENSMUSG00000038925	14	24293214	24309966	1	0	4	0	5	4	0	0	0	0	0	0	E0CZ60	
ENSMUST00000160711						1	1	2	0	1	1	0	0	0	0	0		
ENSMUST00000160712	ENSMUSG00000024792	19	6080762	6084944	-1	0	2	2	0	0	0	24	0	15	5	8	E0CXR3	
ENSMUST00000160713	ENSMUSG00000038425	18	70508680	70530620	-1	37	37	23	146	49	19	8	44	33	0	48	E0CZD6	
ENSMUST00000160715	ENSMUSG00000021187	12	101645443	101718523	-1	0	0	1	0	0	0	0	0	0	0	0	E0CXQ6	
ENSMUST00000160716						26	12	51	129	61	27	1	0	0	0	0		
ENSMUST00000160717	ENSMUSG00000025812	8	127063893	127612286	1	22	27	41	72	20	30	0	0	2	0	3		Q99NH2
ENSMUST00000160718						2	2	0	0	5	0	0	0	0	0	0		
ENSMUST00000160719	ENSMUSG00000031647	8	60632827	60676729	1	27	22	6	14	13	3	3	9	5	9	0		Q9D3X9
ENSMUST00000160720						15	18	41	42	27	7	8	11	17	3	31		
ENSMUST00000160721	ENSMUSG00000051375	18	38185914	38212053	-1	24	28	66	265	45	37	6	0	1	0	1	E0CXD4	
ENSMUST00000160722	ENSMUSG00000027165	2	101560781	101649532	-1	0	0	0	0	0	0	0	22	0	32	12		Q9CQI4
ENSMUST00000160723						44	30	86	34	33	22	12	25	14	3	24		
ENSMUST00000160724	ENSMUSG00000032280	9	61372366	61418497	1	1	0	0	0	0	0	12	0	13	0	26	E0CYM5	
ENSMUST00000160725						0	0	0	0	0	0	8	71	26	6	15		
ENSMUST00000160726	ENSMUSG00000051062	11	35797382	35798884	-1	16	14	38	265	18	8	0	0	0	0	0		Q80WS3
ENSMUST00000160727						7	2	8	4	2	0	6	46	7	6	47		
ENSMUST00000160728	ENSMUSG00000022558	15	76380261	76453038	1	0	1	0	0	0	0	9	0	12	0	7	E0CYC5	
ENSMUST00000160729	ENSMUSG00000036928	5	138280240	138312393	1	4	1	4	79	4	2	0	0	1	0	4	E0CYH8	
ENSMUST00000160730						15	4	13	32	12	5	0	2	1	2	0		
ENSMUST00000160731	ENSMUSG00000036879	8	85840959	86061376	1	5	2	10	0	1	1	0	24	0	0	9	F7DF70	
ENSMUST00000160732	ENSMUSG00000006542	1	74738922	74749221	-1	17	12	44	161	30	16	0	3	0	0	3		Q8BGM7
ENSMUST00000160733	ENSMUSG00000022386	15	85879312	85897394	1	0	0	0	4	2	0	0	0	0	0	0	F7CCK8	
ENSMUST00000160734	ENSMUSG00000001524	17	35667730	35673739	-1	0	0	0	0	0	0	0	0	0	0	0	Q542U3	O70422
ENSMUST00000160735	ENSMUSG00000021461	13	63304709	63497278	-1	1	0	0	0	0	0	0	1	0	0	0	F7DEE2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160736						0	0	4	0	2	0	0	0	0	0	0		
ENSMUST00000160737						12	14	30	154	11	11	0	0	0	0	0		
ENSMUST00000160739						4	5	3	4	3	0	0	11	7	14	4		
ENSMUST00000160740	ENSMUSG00000021614	13	89655312	89742509	-1	0	1	0	0	1	0	4	183	22	59	35	F7B603	
ENSMUST00000160741						4	0	9	0	1	0	0	0	0	0	0		
ENSMUST00000160742						0	0	0	0	0	0	0	10	4	0	5		
ENSMUST00000160743						15	4	9	195	18	6	0	0	0	0	1		
ENSMUST00000160744	ENSMUSG00000026150	1	82724890	82752394	1	1	0	0	1	2	0	0	25	0	8	5	F7BC60	
ENSMUST00000160745						0	1	0	2	2	1	0	0	0	0	0		
ENSMUST00000160747	ENSMUSG00000040524	9	65692391	65827564	-1	0	4	0	6	4	1	0	0	0	0	0	E0CYU4	
ENSMUST00000160748						0	2	0	7	1	0	8	20	5	0	7		
ENSMUST00000160749	ENSMUSG00000003500	6	29200434	29216364	-1	2	2	0	34	5	2	0	0	0	1	0	E0CZC7	
ENSMUST00000160750	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	0	1	0	0	0	24	50	13	F7CTF8	
ENSMUST00000160751						1	2	3	5	3	3	2	0	0	0	0		
ENSMUST00000160752	ENSMUSG00000001524	17	35667730	35673739	-1	0	0	0	0	0	0	0	0	10	0	0	E0CY64	
ENSMUST00000160753						4	0	2	2	0	2	5	10	0	4	0		
ENSMUST00000160755						4	1	5	7	5	0	0	0	0	0	0		
ENSMUST00000160757						3	0	31	5	9	2	4	4	0	0	0		
ENSMUST00000160758	ENSMUSG00000033004	14	103113411	103346814	-1	48	34	43	24	43	0	558	457	1602	38	1550	F6SMY7	
ENSMUST00000160759						0	0	0	0	0	0	0	0	20	26	0		
ENSMUST00000160760						5	3	3	3	9	2	2	9	0	0	3		
ENSMUST00000160761						2	1	8	7	9	1	0	0	0	0	0		
ENSMUST00000160762	ENSMUSG00000029625	5	145167213	145182041	1	0	0	0	0	0	0	0	0	0	0	0	F7B6Z5	
ENSMUST00000160764	ENSMUSG00000093701	16	91391721	91419451	1	0	0	0	0	0	0	61	0	40	0	0	F6XX07	
ENSMUST00000160765						1	0	2	0	1	3	0	0	0	0	0		
ENSMUST00000160766	ENSMUSG00000025812	8	127063893	127612286	1	4	10	17	0	9	6	0	0	0	0	2	E0CY24	
ENSMUST00000160767						5	5	14	31	5	0	0	0	1	0	0		
ENSMUST00000160768	ENSMUSG00000050103	12	37241641	37582202	1	0	0	0	0	0	0	0	0	0	0	0	E0CYN0	
ENSMUST00000160769						0	0	0	0	0	0	4	0	13	0	8		
ENSMUST00000160770	ENSMUSG00000013076	9	14541966	14615483	-1	58	47	258	325	58	37	1	4	2	8	59		Q9D4H4
ENSMUST00000160771						30	31	47	28	30	16	0	3	1	0	2		
ENSMUST00000160772						2	1	3	5	3	1	0	3	1	0	1		
ENSMUST00000160773						1	0	0	2	0	3	0	0	0	0	0		
ENSMUST00000160774	ENSMUSG00000028559	4	109061145	109202272	-1	0	0	0	0	0	0	190	1831	1	0	0	F6UHR6	
ENSMUST00000160775						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160776						7	15	6	8	7	4	6	31	21	0	15		
ENSMUST00000160777	ENSMUSG00000025905	1	5588466	5606131	1	4	4	4	9	3	3	0	0	0	0	0	Q14AL5	P33534
ENSMUST00000160779						7	9	26	11	16	4	7	31	12	2	21		
ENSMUST00000160780	ENSMUSG00000053004	6	114397936	114483296	1	7	7	14	2	0	0	0	0	0	3	0	B3Y5T0	P70174
ENSMUST00000160781	ENSMUSG00000060475	17	12966796	12992546	-1	12	18	10	100	13	15	164	805	186	124	95		Q9ER69
ENSMUST00000160782						1	0	7	65	3	0	0	0	0	0	1		
ENSMUST00000160783						2	3	3	0	2	1	0	0	0	0	0		
ENSMUST00000160784	ENSMUSG00000022550	15	76576358	76595816	1	0	0	0	0	0	0	0	0	0	0	0	E0CXW2	
ENSMUST00000160785	ENSMUSG00000015127	17	25188397	25234443	1	5	4	0	3	0	2	0	0	0	0	0	F6TWQ1	
ENSMUST00000160786	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	0	0	0	263	885	438	663	271		Q6PCP5
ENSMUST00000160787	ENSMUSG00000064373	15	3268547	3280508	1	2	0	0	0	2	2	0	0	0	0	0	E0CX80	
ENSMUST00000160788	ENSMUSG00000019979	10	90989311	91082770	-1	0	0	0	130	1	3	0	0	0	0	0	Q80VR5	
ENSMUST00000160789	ENSMUSG00000026494	1	178529125	178939200	1	14	7	62	119	14	13	4	0	7	0	12	E9PX64	
ENSMUST00000160790						11	12	22	48	32	11	0	1	2	1	0		
ENSMUST00000160791						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000160792	ENSMUSG00000089844	1	85083069	85109853	-1	47	37	108	62	57	22	36	339	58	174	55	E9PV05	
ENSMUST00000160793						3	3	2	5	5	0	0	0	0	0	0		
ENSMUST00000160794						1	0	2	25	3	2	0	0	0	0	0		
ENSMUST00000160795	ENSMUSG00000056617	9	46303361	46319986	-1	1	2	2	2	0	0	0	0	0	0	0	E0CYQ9	
ENSMUST00000160796	ENSMUSG00000026336	1	98421124	98516991	1	2	3	6	0	0	0	0	0	0	0	0	Q14DL2	
ENSMUST00000160798						1	1	3	1	2	1	0	0	0	0	0		
ENSMUST00000160799						0	0	0	0	0	0	2	28	15	0	0		
ENSMUST00000160800	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	0	0	0	0	0	0	0	0	E0CY11	
ENSMUST00000160801	ENSMUSG00000042015	13	94976344	95023314	1	7	9	13	7	0	5	80	306	151	29	115		Q3UDP0
ENSMUST00000160802						792	1012	554	242	859	423	17	128	60	39	93		
ENSMUST00000160803						26	20	148	35	18	14	0	0	0	0	0		
ENSMUST00000160804						3	2	2	3	0	0	6	1	4	0	4		
ENSMUST00000160805	ENSMUSG00000055717	14	103650228	103704907	1	6	2	0	9	12	5	8	0	12	4	12	F7D4S5	
ENSMUST00000160806						5	9	11	6	19	10	12	45	13	3	35		
ENSMUST00000160807						12	9	24	6	19	7	0	0	0	0	0		
ENSMUST00000160808						0	0	6	3	0	0	0	15	0	0	3		
ENSMUST00000160810	ENSMUSG00000026247	1	87147655	87156521	-1	0	0	0	241	14	0	0	0	0	0	0		Q9JMI0
ENSMUST00000160811	ENSMUSG00000042790	9	45863425	45906894	-1	0	0	0	0	0	0	6	0	15	0	3	E0CZF4	
ENSMUST00000160812						0	0	1	0	0	0	0	0	0	0	1		
ENSMUST00000160813						0	1	2	16	0	0	4	0	13	0	9		
ENSMUST00000160814						8	0	4	0	8	0	0	0	0	0	0		
ENSMUST00000160815						0	1	2	2	1	0	0	0	0	0	0		
ENSMUST00000160816						1	0	0	2	0	0	4	3	0	2	0		
ENSMUST00000160818						8	8	16	0	0	0	0	0	0	0	0		
ENSMUST00000160819						4	2	20	1	9	1	0	0	1	0	4		
ENSMUST00000160820						0	4	0	1	0	0	2	4	13	0	7		
ENSMUST00000160821	ENSMUSG00000042605	5	121711337	121816493	1	2	5	1	0	1	3	0	0	5	0	0	F7B6X4	
ENSMUST00000160822	ENSMUSG00000079144	1	193168046	193177832	1	79	0	7	0	0	4	1	54	1	0	0		Q9DAE8
ENSMUST00000160823	ENSMUSG00000038240	10	43221486	43464882	1	35	24	77	146	52	32	6	13	6	1	16	E0CYM9	
ENSMUST00000160824						13	9	36	23	16	4	4	24	7	2	10		
ENSMUST00000160825	ENSMUSG00000049792	12	111709488	111713257	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYW3	
ENSMUST00000160826	ENSMUSG00000098650	11	22834744	22982090	-1	2	0	0	0	2	0	500	1659	363	51	250	F7BCN0	
ENSMUST00000160827						0	0	3	0	2	0	0	43	8	0	0		
ENSMUST00000160828						2	3	0	7	0	0	0	0	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160829						2	0	1	5	7	1	0	1	0	0	0		
ENSMUST00000160830	ENSMUSG00000021187	12	101645443	101718523	-1	0	0	0	0	0	0	0	0	0	0	0		Q91XT6
ENSMUST00000160831						2	2	0	3	1	0	3	20	3	3	17		
ENSMUST00000160832						9	7	9	12	9	5	0	2	0	0	1		
ENSMUST00000160833						0	0	1	0	0	0	4	0	0	1	3		
ENSMUST00000160834	ENSMUSG00000073664	1	60180599	60338328	1	18	24	21	22	25	11	88	165	134	79	139	E9PYP2	
ENSMUST00000160835	ENSMUSG00000035953	14	50926070	50930856	-1	0	1	3	0	7	0	7	105	24	0	7		Q3TWL2
ENSMUST00000160836	ENSMUSG00000030232	6	140622663	140678472	1	2	2	4	37	3	2	10	0	0	0	0		Q9Z248
ENSMUST00000160837	ENSMUSG00000048495	1	57388237	57407101	-1	0	0	0	0	0	0	0	16	0	0	0	G3UW53	
ENSMUST00000160838						0	0	0	0	0	0	2	6	0	0	0		
ENSMUST00000160839						6	3	4	2	4	3	0	0	0	0	0		
ENSMUST00000160840						0	0	0	3	0	0	6	64	7	0	33		
ENSMUST00000160841						2	1	0	1	0	2	0	0	0	0	0		
ENSMUST00000160843	ENSMUSG00000040669	6	122317731	122340561	-1	4	0	6	9	8	6	0	0	0	0	0	E0CXT0	
ENSMUST00000160844	ENSMUSG00000024109	17	90033631	91093071	-1	25	38	157	29	31	27	0	0	1	0	0		Q9CS84
ENSMUST00000160845						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000160847	ENSMUSG00000022821	16	37580153	37632020	1	7	7	16	9	0	0	0	0	0	0	0		O09173
ENSMUST00000160848						1	0	0	0	2	2	0	2	0	0	2		
ENSMUST00000160849	ENSMUSG00000036928	5	138280240	138312393	1	0	0	13	1	0	1	0	5	0	0	5	F7CBN2	
ENSMUST00000160850						0	2	9	0	0	0	0	0	0	0	6		
ENSMUST00000160851						9	2	9	1	4	0	0	0	0	0	0		
ENSMUST00000160852	ENSMUSG00000079478	19	5728088	5731732	-1	11	3	24	75	3	4	51	33	44	0	22	Q545N1	P56873
ENSMUST00000160853	ENSMUSG00000022553	15	76351294	76354380	1	0	0	0	50	0	0	565	643	423	96	244		Q9D0U6
ENSMUST00000160854	ENSMUSG00000056870	1	44551511	44796838	1	18	18	26	217	29	20	0	1	0	0	4		Q8K2A1
ENSMUST00000160855	ENSMUSG00000037509	1	34678188	34813309	1	25	10	28	24	20	15	32	37	13	8	24	E0CYG8	
ENSMUST00000160856	ENSMUSG00000004151	12	38779380	38868215	1	0	0	0	0	0	0	0	0	0	17	0	E0CZ54	
ENSMUST00000160857						1	0	0	81	3	0	0	0	0	0	0		
ENSMUST00000160858						1	1	2	3	3	0	0	38	11	0	3		
ENSMUST00000160859	ENSMUSG00000021638	13	100496507	100552718	-1	0	8	0	34	0	0	0	0	0	0	4	B2RS24	Q61146
ENSMUST00000160860	ENSMUSG00000014164	13	58004221	58113592	-1	39	35	75	56	50	26	1	2	0	1	10	J3KMI2	
ENSMUST00000160862	ENSMUSG00000004637	8	114439655	115352708	1	4	2	6	12	3	1	10	11	0	0	0		Q91WL8
ENSMUST00000160863						0	0	0	0	0	0	0	0	7	0	3		
ENSMUST00000160864	ENSMUSG00000060073	12	70974621	70996347	1	0	0	0	4	0	0	0	0	0	13	0	E0CX62	
ENSMUST00000160865						1	1	4	2	1	0	7	28	12	4	11		
ENSMUST00000160866						3	4	0	4	5	1	9	30	31	12	35		
ENSMUST00000160867	ENSMUSG00000030365	6	128887588	128898167	1	0	2	0	4	0	0	0	0	3	0	0		
ENSMUST00000160868						4	0	0	0	1	0	1	0	0	0	2		
ENSMUST00000160869	ENSMUSG00000054065	7	141078218	141090510	1	5	1	0	26	7	4	0	0	0	0	0	E0CYP0	
ENSMUST00000160870	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160871	ENSMUSG00000025907	1	6206197	6276648	1	0	1	0	0	0	0	10	23	63	16	68	E0CYY6	
ENSMUST00000160872	ENSMUSG00000045962	6	119923969	120038672	-1	0	0	1	0	1	0	1	0	0	0	1	F6V9V5	
ENSMUST00000160873						1	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000160874	ENSMUSG00000084786	9	20642878	20647140	1	0	0	0	0	0	0	28	128	0	13	0	E0CY91	
ENSMUST00000160875						1	1	0	0	3	0	44	48	9	6	0		
ENSMUST00000160876						0	5	0	2	0	0	0	1	0	0	5		
ENSMUST00000160877						12	2	3	4	8	3	0	10	11	4	17		
ENSMUST00000160878	ENSMUSG00000003500	6	29200434	29216364	-1	0	0	6	0	22	3	0	0	0	0	0	E0CYE2	
ENSMUST00000160879	ENSMUSG00000026489	1	180165238	180199602	-1	0	1	0	0	0	0	65	117	68	12	17	A0A0A6YXD9	
ENSMUST00000160880	ENSMUSG00000021040	12	87443896	87452206	1	0	0	0	0	0	0	0	31	0	13	8	F7DE82	
ENSMUST00000160881	ENSMUSG00000026698	1	161969186	161973435	1	2	2	25	0	2	0	29	37	70	39	67	E0CXG9	
ENSMUST00000160882	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	766	440	198	49	8		Q08122
ENSMUST00000160883	ENSMUSG00000027822	3	63933507	63964768	-1	3	0	2	0	0	0	14	143	90	43	58		Q99J27
ENSMUST00000160884	ENSMUSG00000028931	4	152390742	152477871	-1	11	10	12	155	15	23	14	0	0	0	30		P62482
ENSMUST00000160885	ENSMUSG00000050410	17	35512734	35516824	-1	12	6	0	46	6	4	0	18	0	0	0	G3XA31	
ENSMUST00000160886	ENSMUSG00000002033	9	44969572	44980431	-1	0	1	1	0	1	0	0	0	0	0	0	E0CXP3	
ENSMUST00000160887						3	8	1	1	2	0	0	0	0	0	1		
ENSMUST00000160888	ENSMUSG00000029130	5	29195992	29228457	1	1	0	0	22	5	0	0	0	0	0	0	E0CY41	
ENSMUST00000160889	ENSMUSG00000089872	1	190700202	190911770	-1	0	0	0	0	14	5	43	202	5	46	11	F6VA16	
ENSMUST00000160890	ENSMUSG00000006289	14	50906478	50924893	-1	3	0	2	2	5	2	0	6	0	0	7	E0CXW7	
ENSMUST00000160891						1	0	0	1	0	0	0	0	1	0	0		
ENSMUST00000160892						1	4	6	4	3	3	0	0	0	0	0		
ENSMUST00000160893	ENSMUSG00000025184	19	42518759	42592343	1	0	1	0	5	0	0	10	0	23	79	41	E0CZA8	
ENSMUST00000160894	ENSMUSG00000063063	6	76881637	77979699	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXB9	
ENSMUST00000160895						11	9	35	10	12	6	1	6	20	1	28		
ENSMUST00000160896	ENSMUSG00000015127	17	25188397	25234443	1	9	6	39	112	38	9	11	16	0	0	0	E0CYD7	
ENSMUST00000160897	ENSMUSG00000071657	19	8837467	8848683	1	0	0	0	0	0	0	0	0	0	0	0	E0CXJ2	
ENSMUST00000160898						3	1	18	6	7	2	6	22	7	3	12		
ENSMUST00000160899	ENSMUSG00000045994	9	26733728	26763101	1	0	0	0	33	0	20	0	0	0	0	0	Q8R531	
ENSMUST00000160900						0	1	0	0	0	0	0	21	0	0	0		
ENSMUST00000160901						3	1	3	2	5	0	3	3	0	4	2		
ENSMUST00000160902	ENSMUSG00000032115	9	44379490	44392369	1	2	0	0	136	5	0	20	12	84	0	107		Q9JKR6
ENSMUST00000160903						4	0	4	0	5	0	8	45	20	0	18		
ENSMUST00000160904						1	0	0	68	0	0	1	0	0	0	0		
ENSMUST00000160905	ENSMUSG00000021415	13	34924409	34955875	1	6	0	9	0	10	0	0	0	0	0	0		Q497N7
ENSMUST00000160906	ENSMUSG00000026885	2	35751241	35979913	-1	0	0	14	0	0	0	0	3	9	0	0	F7BQM5	
ENSMUST00000160907						5	1	18	6	4	1	0	17	0	0	4		
ENSMUST00000160908	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	0	0	10	E9Q6Z8	
ENSMUST00000160909						6	4	14	1	9	6	0	3	0	0	2		
ENSMUST00000160910	ENSMUSG00000024238	18	5591860	5775467	1	0	3	0	0	0	1	0	0	0	0	0	E0CX96	
ENSMUST00000160911						0	0	0	184	10	4	0	0	2	0	13		
ENSMUST00000160912	ENSMUSG00000048148	8	72646711	72714746	1	0	0	0	0	0	0	0	0	0	0	0	F6U6S4	
ENSMUST00000160913						6	8	44	13	11	5	5	20	15	4	8		
ENSMUST00000160914	ENSMUSG00000022553	15	76351294	76354380	1	0	0	4	0	2	0	63	64	37	0	44	E0CYK4	
ENSMUST00000160915						6	0	0	0	2	0	0	0	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000160916						3	2	6	230	5	2	17	19	13	0	31		
ENSMUST00000160918	ENSMUSG00000054474	6	71128166	71144439	-1	18	22	152	54	30	20	0	2	0	0	6		Q80W22
ENSMUST00000160919						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160920	ENSMUSG00000033200	17	25369273	25374442	1	0	7	0	15	0	0	0	0	0	0	0	E9Q3M4	
ENSMUST00000160921						7	4	8	3	3	0	0	1	0	0	1		
ENSMUST00000160922						0	2	0	14	0	0	117	0	196	13	216		
ENSMUST00000160923						0	0	0	8	0	0	0	0	0	8	22		
ENSMUST00000160924						0	4	10	6	3	3	0	4	4	0	4		
ENSMUST00000160926	ENSMUSG00000041406	1	163945993	163994796	-1	0	1	0	53	1	0	0	0	0	0	0	E0CX91	
ENSMUST00000160927						7	7	22	13	6	6	30	39	24	0	48		
ENSMUST00000160928						9	5	4	0	9	0	0	0	0	13	0		
ENSMUST00000160929	ENSMUSG00000016194	1	193221634	193264075	-1	0	0	0	0	0	0	0	0	0	0	12	Q3TJI8	
ENSMUST00000160930	ENSMUSG00000064373	15	3268547	3280508	1	0	0	0	0	0	0	0	0	17	2	0	E0CZC5	
ENSMUST00000160931	ENSMUSG00000021461	13	63304709	63497278	-1	0	0	0	11	0	0	0	0	0	0	0	E0CYI2	
ENSMUST00000160934	ENSMUSG00000027692	3	28263214	28675858	1	0	19	7	9	5	0	5	25	8	4	4	E0CYV5	
ENSMUST00000160936	ENSMUSG00000013611	15	36504062	36555573	-1	2	1	0	0	1	3	0	0	0	0	0	E0CXB6	
ENSMUST00000160937	ENSMUSG00000029754	6	6863334	6868568	1	531	299	1485	8608	774	419	0	45	20	10	24		P70397
ENSMUST00000160939						6	6	1	0	6	2	0	0	0	2	0		
ENSMUST00000160940	ENSMUSG00000037705	9	42329619	42399929	-1	21	15	0	5	0	25	1	0	1	1	2		O08523
ENSMUST00000160941						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160942	ENSMUSG00000051225	15	57985419	58011009	1	27	26	66	70	52	29	3	5	5	10	17		Q8K2P2
ENSMUST00000160943	ENSMUSG00000041515	8	120736358	120756694	1	6	0	0	0	2	2	14	0	0	0	17	F7C1A3	
ENSMUST00000160945	ENSMUSG00000026024	1	59162926	59237231	-1	0	0	0	38	0	0	0	1	0	0	0	A0A087WSC7	
ENSMUST00000160946	ENSMUSG00000046111	9	15316915	15357788	-1	0	0	0	3	0	2	0	1	0	0	0	F7BWD7	
ENSMUST00000160948						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000160949						6	0	0	11	0	0	0	0	0	0	4		
ENSMUST00000160952						1	0	0	40	0	3	0	0	0	0	17		
ENSMUST00000160953	ENSMUSG00000026163	1	83254139	83408200	-1	33	22	72	48	43	21	0	0	0	0	0	E9PUC4	
ENSMUST00000160955						8	5	1	3	7	3	0	0	0	0	0		
ENSMUST00000160956	ENSMUSG00000060579	14	9550092	11162035	-1	0	0	5	6	0	1	0	0	0	0	0	E9Q3M6	
ENSMUST00000160957	ENSMUSG00000021684	13	95024454	95250336	-1	0	0	0	5	0	0	0	0	0	0	0	E0CXQ1	
ENSMUST00000160959	ENSMUSG00000036513	3	57644349	57651715	-1	16	11	12	18	11	6	62	139	60	130	31	Q497T6	Q8BXC6
ENSMUST00000160961	ENSMUSG00000036636	17	25133391	25162104	1	17	19	67	11	10	21	156	472	60	4	44	E9PYL4	
ENSMUST00000160962	ENSMUSG00000061436	6	38694390	38876165	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160963	ENSMUSG00000029925	6	38875404	39084585	1	0	0	0	2	1	1	0	0	0	0	10	F6SG79	
ENSMUST00000160964	ENSMUSG00000036564	8	95676980	95715119	1	0	4	3	44	5	4	0	0	0	0	0	E0CZ50	
ENSMUST00000160966	ENSMUSG00000005610	7	111070568	111083030	-1	1	0	0	0	2	1	0	1	4	0	1	F7CHS2	
ENSMUST00000160968	ENSMUSG00000003721	1	121304353	121332589	-1	0	0	0	0	0	0	44	0	0	0	0		Q91WG1
ENSMUST00000160969						1	3	22	4	3	1	0	0	0	0	1		
ENSMUST00000160970						2	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000160972	ENSMUSG00000026150	1	82724890	82752394	1	0	4	0	0	0	0	251	1403	269	152	93		Q6PCP5
ENSMUST00000160973	ENSMUSG00000021990	14	60634001	60764556	1	28	27	94	29	0	31	0	0	0	0	0	E9Q3I3	
ENSMUST00000160974						5	2	8	7	3	0	0	1	2	0	0		
ENSMUST00000160975						2	0	8	9	6	2	0	4	0	0	0		
ENSMUST00000160976						4	3	3	1	0	2	0	3	0	5	0		
ENSMUST00000160977	ENSMUSG00000024792	19	6080762	6084944	-1	2	0	0	0	2	0	63	79	50	0	45	E0CXM9	
ENSMUST00000160978						1	1	1	30	1	3	3	86	57	128	72		
ENSMUST00000160980	ENSMUSG00000073664	1	60180599	60338328	1	5	0	0	2	0	1	0	0	9	0	0	F7D418	
ENSMUST00000160981	ENSMUSG00000021666	13	97137937	97181195	1	0	2	3	0	2	2	0	9	5	2	6	F7B693	
ENSMUST00000160982						41	36	107	62	46	25	5	1	3	0	10		
ENSMUST00000160983						0	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000160985	ENSMUSG00000053128	9	44066327	44113517	-1	1	0	0	0	0	0	0	0	0	0	2	H9KV16	
ENSMUST00000160986						141	110	494	152	123	51	85	237	121	4	226		
ENSMUST00000160987	ENSMUSG00000020077	10	62493833	62527451	-1	18	25	142	45	34	30	186	1205	239	428	291		P13609
ENSMUST00000160988						12	3	16	74	15	9	6	0	8	0	15		
ENSMUST00000160989						13	4	14	16	10	0	0	12	11	0	26		
ENSMUST00000160990						0	0	0	13	0	0	0	1	0	0	0		
ENSMUST00000160991	ENSMUSG00000048402	1	118834132	119053619	-1	3	5	0	1	2	0	0	0	0	0	0	A5AA26	
ENSMUST00000160993						6	3	7	26	14	5	38	43	37	3	63		
ENSMUST00000160994						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000160995						82	138	15	26	46	30	0	1	0	0	0		
ENSMUST00000160996	ENSMUSG00000004151	12	38779380	38868215	1	0	1	9	0	0	0	0	0	5	0	2	E0CXE6	
ENSMUST00000160998						2	2	6	41	4	3	0	0	0	0	1		
ENSMUST00000160999						2	0	4	3	3	5	1	7	1	3	0		
ENSMUST00000161000	ENSMUSG00000038174	1	58522806	58586323	-1	0	0	0	0	0	2	0	0	0	0	0	E0CZ67	
ENSMUST00000161002	ENSMUSG00000026247	1	87147655	87156521	-1	0	15	42	91	22	20	0	0	0	0	0		Q9JMI0
ENSMUST00000161003	ENSMUSG00000033323	18	80407959	80469695	-1	0	0	0	0	0	0	17	220	11	15	15	E0CZ13	
ENSMUST00000161004	ENSMUSG00000023009	15	99422035	99457748	-1	1	0	4	0	0	0	0	1	0	0	0	F7DEN0	
ENSMUST00000161008	ENSMUSG00000033004	14	103113411	103346814	-1	0	7	2	0	0	6	151	1171	321	164	327	F6T4V9	
ENSMUST00000161009						3	5	4	37	4	0	57	68	102	9	30		
ENSMUST00000161010						3	3	16	3	4	3	0	0	0	0	1		
ENSMUST00000161011	ENSMUSG00000021189	12	101918901	101958246	-1	0	0	0	2	0	0	0	25	40	53	4	E9Q717	
ENSMUST00000161012	ENSMUSG00000050410	17	35512734	35516824	-1	0	0	19	34	0	0	91	113	73	44	58	G3XA31	
ENSMUST00000161013						2	0	8	1	1	0	0	8	0	0	3		
ENSMUST00000161014						45	41	80	92	52	26	18	57	27	6	39		
ENSMUST00000161015	ENSMUSG00000027718	3	37222759	37232636	-1	3	1	0	0	0	0	0	0	0	0	0	E9PX58	
ENSMUST00000161016						1	0	8	12	4	0	0	2	0	0	4		
ENSMUST00000161017	ENSMUSG00000026494	1	178529125	178939200	1	112	109	211	190	161	84	13	9	27	3	8		Q7TNC6
ENSMUST00000161018	ENSMUSG00000021481	13	55105311	55134825	1	1	0	0	26	0	0	0	0	0	0	4	E0CXP1	
ENSMUST00000161019						5	0	6	2	6	3	0	0	0	0	0		
ENSMUST00000161020						5	0	0	10	2	0	240	1641	318	83	99		
ENSMUST00000161021	ENSMUSG00000027860	3	102153583	102204693	-1	0	0	0	0	0	0	0	0	0	0	0	F7BWJ0	
ENSMUST00000161022	ENSMUSG00000040969	3	133112278	133234949	-1	7	2	5	2	8	4	0	0	0	1	0		Q80VK6
ENSMUST00000161023	ENSMUSG00000021040	12	87443896	87452206	1	10	2	14	6	5	5	11	33	11	38	10	Q14AR0	Q9D8T7

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161025						0	0	0	0	0	0	2	0	0	2	0		
ENSMUST00000161026						0	0	0	0	0	0	0	0	6	0	0		
ENSMUST00000161027						0	1	2	2	2	5	97	663	177	772	139		
ENSMUST00000161028	ENSMUSG00000037106	15	58510048	58665092	1	42	17	64	37	54	14	1	0	0	1	1	E0CZ42	
ENSMUST00000161029	ENSMUSG00000090206	8	95310566	95326323	1	0	0	0	0	4	3	0	0	0	0	0		Q6IMH0
ENSMUST00000161030						0	0	1	0	0	0	12	18	4	4	0		
ENSMUST00000161031	ENSMUSG00000068245	14	59347407	59365470	-1	3	2	0	0	0	0	2	0	0	38	27		A6H5X4
ENSMUST00000161032	ENSMUSG00000041879	1	135382312	135430499	-1	0	5	0	11	3	0	47	48	98	0	51	E0CXB2	
ENSMUST00000161033						1	0	1	5	4	0	0	0	0	0	0		
ENSMUST00000161034	ENSMUSG00000022766	16	17331371	17343575	1	14	5	3	0	10	6	0	1	0	5	0		P49182
ENSMUST00000161035	ENSMUSG00000024112	17	25374285	25433783	-1	0	0	0	6	2	1	0	0	0	0	0	F6USE5	
ENSMUST00000161036						24	3	13	29	18	7	0	0	0	0	0		
ENSMUST00000161037						232	210	182	246	323	182	32	102	81	4	64		
ENSMUST00000161038						3	10	28	5	2	4	13	62	11	14	3		
ENSMUST00000161039						1	0	8	2	1	2	9	0	0	0	13		
ENSMUST00000161040	ENSMUSG00000022150	15	6299788	6440712	1	0	0	0	0	0	0	0	6	0	0	0	Q9DCE6	
ENSMUST00000161041						18	17	36	25	16	10	4	4	10	7	10		
ENSMUST00000161042	ENSMUSG00000034908	9	45937857	45955247	-1	0	0	0	0	0	0	0	0	0	0	7	F6SS13	
ENSMUST00000161044						7	2	3	4	1	2	17	47	29	2	49		
ENSMUST00000161045	ENSMUSG00000030166	6	119902698	119922828	1	5	8	9	0	0	5	0	60	0	0	0	E0CZA6	
ENSMUST00000161046	ENSMUSG00000022710	16	8689595	8792308	-1	0	0	0	0	7	0	455	0	1538	0	686	F8VPX1	
ENSMUST00000161047	ENSMUSG00000047592	5	138225898	138253363	1	2	0	1	9	2	0	15	41	17	73	185	E0CX47	
ENSMUST00000161048	ENSMUSG00000045962	6	119923969	120038672	-1	0	0	0	0	0	0	8	0	13	0	0	F7CC62	
ENSMUST00000161049						5	4	11	1	5	1	2	2	0	0	1		
ENSMUST00000161050						0	3	1	0	2	0	0	0	0	0	2		
ENSMUST00000161051	ENSMUSG00000005610	7	111070568	111083030	-1	0	0	2	0	0	0	2829	6821	5026	1050	2415	F7CBP1	
ENSMUST00000161052	ENSMUSG00000036834	3	63696234	63899472	-1	5	5	7	5	3	4	0	0	0	0	0	E0CZ95	
ENSMUST00000161053	ENSMUSG00000038148	16	26463135	26482765	1	5	4	11	4	8	3	0	0	0	0	0	Q14BW2	Q925N4
ENSMUST00000161054	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	0	0	0	0	5	2	133	26	0	Q3V116	
ENSMUST00000161055						3	7	8	31	0	2	6	0	3	0	9		
ENSMUST00000161056	ENSMUSG00000048402	1	118834132	119053619	-1	0	0	0	0	0	0	0	0	0	0	0	A5AA25	
ENSMUST00000161057	ENSMUSG00000036885	3	62338344	62462221	1	3	3	0	0	3	4	0	0	2	0	1	F6TAL7	
ENSMUST00000161058						5	0	0	1	5	0	0	0	0	0	0		
ENSMUST00000161059	ENSMUSG00000054434	5	123068415	123117749	1	0	1	17	17	2	4	0	0	0	0	0	E0CYA8	
ENSMUST00000161060						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161061	ENSMUSG00000039065	15	31601852	31621227	1	6	3	9	3	4	3	0	3	0	4	18	E0CXY7	
ENSMUST00000161062						2	0	3	4	4	1	0	0	0	0	0		
ENSMUST00000161063	ENSMUSG00000005958	16	21204755	21223305	1	23	11	33	91	30	13	0	0	0	0	0	E0CYA3	
ENSMUST00000161064	ENSMUSG00000042605	5	121711337	121816493	1	0	0	10	0	1	2	87	204	153	0	121	F6U2C2	
ENSMUST00000161065						0	0	0	0	0	0	25	0	13	3	9		
ENSMUST00000161066	ENSMUSG00000056870	1	44551511	44796838	1	2	0	2	0	1	0	0	0	0	0	0	E0CXG2	
ENSMUST00000161067	ENSMUSG00000058318	2	92093117	92364666	1	0	0	0	0	0	0	0	109	0	5	0	F6TKP4	
ENSMUST00000161068	ENSMUSG00000003721	1	121304353	121332589	-1	0	0	0	2	0	0	0	0	0	0	0	E0CXL0	
ENSMUST00000161069	ENSMUSG00000022096	14	70552212	70573548	1	0	9	11	399	45	18	0	0	0	0	0		Q61645
ENSMUST00000161070	ENSMUSG00000030092	6	104492790	104863406	1	0	6	0	10	6	6	0	0	0	0	0	E0CXE3	
ENSMUST00000161071						0	3	0	0	0	0	0	2	0	0	0		
ENSMUST00000161072	ENSMUSG00000022553	15	76351294	76354380	1	1	0	0	1	0	0	11	14	17	41	0	F7CCK2	
ENSMUST00000161073						0	1	0	1	0	0	3	3	0	0	2		
ENSMUST00000161074	ENSMUSG00000019791	10	30608141	30618479	-1	2	0	5	50	5	0	44	78	52	117	30		Q9CPS6
ENSMUST00000161075	ENSMUSG00000026502	1	178187417	178257301	1	4	1	0	35	5	3	67	107	81	6	64	Q8BIB9	
ENSMUST00000161076	ENSMUSG00000040331	7	130532523	130573118	-1	0	0	3	0	0	0	6	14	19	7	20	F6UGP0	
ENSMUST00000161077	ENSMUSG00000021481	13	55105311	55134825	1	0	0	2	0	2	3	12	3	13	0	8	F7CTY2	
ENSMUST00000161078	ENSMUSG00000047013	6	85469574	85502994	-1	0	0	0	20	0	14	0	0	0	0	0	Q3UGY7	Q6NS60
ENSMUST00000161079						0	0	0	0	0	0	0	31	0	0	0		
ENSMUST00000161080	ENSMUSG00000037847	19	18631950	18652194	1	0	2	6	4	4	5	1	1	3	0	4	E0CZA2	
ENSMUST00000161081	ENSMUSG00000071324	10	41914990	42018442	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZ41	
ENSMUST00000161082						3	4	9	47	8	3	0	2	2	0	3		
ENSMUST00000161083	ENSMUSG00000021069	12	70190811	70231488	-1	6	7	3	9	17	5	0	19	7	0	25	Q3UEJ6	
ENSMUST00000161084	ENSMUSG00000030549	7	79593363	79617657	-1	4	3	0	0	2	0	0	0	0	0	1	G3UYA4	
ENSMUST00000161085						0	0	0	0	0	0	133	0	113	34	176		
ENSMUST00000161086						0	0	0	0	0	0	0	0	0	0	26		
ENSMUST00000161087						2	1	6	2	2	0	0	0	0	0	0		
ENSMUST00000161088	ENSMUSG00000022235	15	31568791	31590119	1	0	0	1	1	0	1	0	0	0	4	3	E0CXT6	
ENSMUST00000161089	ENSMUSG00000039021	2	32757026	32775633	-1	0	11	110	0	20	0	0	0	0	0	1	Q3V0B6	
ENSMUST00000161090	ENSMUSG00000024799	19	6062821	6068373	-1	0	0	0	0	0	0	0	18	8	5	0	E0CZB2	
ENSMUST00000161092						5	1	0	0	0	0	0	0	0	1	0		
ENSMUST00000161093	ENSMUSG00000035834	13	81673843	81711013	-1	0	0	0	0	0	0	2	2	2	1	10	E0CX67	
ENSMUST00000161094	ENSMUSG00000025533	5	130011258	130029247	-1	0	0	13	6	0	2	175	137	42	84	109		Q91YI0
ENSMUST00000161095						1	4	3	9	4	2	1	4	6	0	2		
ENSMUST00000161097	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	1	1	0	0	0	0	0	E0CYS3	
ENSMUST00000161098						1	0	3	3	2	0	3	14	0	0	0		
ENSMUST00000161099						1	0	4	3	3	0	28	44	66	6	53		
ENSMUST00000161100						0	5	16	0	0	0	0	0	0	0	4		
ENSMUST00000161102						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161103						6	4	29	123	15	6	0	2	2	0	2		
ENSMUST00000161104						0	3	8	2	0	1	0	0	0	0	0		
ENSMUST00000161105						9	11	2	5	3	1	0	0	0	0	0		
ENSMUST00000161106						7	0	10	15	0	0	80	198	74	21	39		
ENSMUST00000161107						8	4	22	7	16	7	0	0	0	2	0		
ENSMUST00000161108						8	11	30	32	24	10	0	0	0	0	0		
ENSMUST00000161109						7	4	6	6	4	1	0	0	0	0	0		
ENSMUST00000161110	ENSMUSG00000073396	17	40727120	40731782	1	12	3	8	1	10	1	0	0	0	0	0		Q3LHH8
ENSMUST00000161111						0	0	0	0	0	0	31	69	48	12	30		
ENSMUST00000161112						2	6	6	0	7	0	0	1	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161113						33	26	83	35	31	13	6	6	31	0	26		
ENSMUST00000161114	ENSMUSG00000032122	9	37229149	37255738	-1	0	0	18	0	0	7	172	321	184	44	170		Q9WU81
ENSMUST00000161115	ENSMUSG00000045994	9	26733728	26763101	1	8	14	110	0	26	0	0	1	0	0	0	Q6PIG8	
ENSMUST00000161116						5	10	9	3	10	3	0	2	0	0	4		
ENSMUST00000161117	ENSMUSG00000023994	17	48386885	48409906	-1	0	0	0	0	0	0	0	0	0	1	0	F6TUY8	
ENSMUST00000161118	ENSMUSG00000041831	17	6673458	6738042	1	8	0	0	15	0	0	0	2	0	0	0	E0CYH1	
ENSMUST00000161119						6	5	3	1	7	3	0	0	0	0	0		
ENSMUST00000161120	ENSMUSG00000048655	3	55137339	55172935	1	0	0	0	0	0	2	0	0	0	0	0	E9Q3J3	
ENSMUST00000161122	ENSMUSG00000025979	1	55131231	55154899	1	0	0	0	0	0	0	20	0	0	5	11	E0CX17	
ENSMUST00000161123	ENSMUSG00000019795	10	7629373	7681136	-1	1	3	2	0	0	0	0	149	117	37	75	F6TXE3	
ENSMUST00000161124						41	46	37	22	55	17	0	4	14	0	18		
ENSMUST00000161125						0	2	2	0	0	0	0	0	0	9	0		
ENSMUST00000161127	ENSMUSG00000061950	17	65782573	65841926	1	0	0	0	54	0	0	3	11	3	0	7	E0CYV2	
ENSMUST00000161128						5	5	18	2	8	3	0	0	0	0	0		
ENSMUST00000161129						0	3	9	0	3	0	41	50	15	15	79		
ENSMUST00000161130						0	10	4	0	0	0	0	0	0	0	0		
ENSMUST00000161131						73	60	259	118	59	33	1	14	12	0	1		
ENSMUST00000161132	ENSMUSG00000046111	9	15316915	15357788	-1	0	0	0	0	0	0	38	0	73	0	0		Q8BQ48
ENSMUST00000161134						9	9	26	14	11	4	0	5	0	0	6		
ENSMUST00000161135						0	0	0	0	0	0	0	0	22	0	7		
ENSMUST00000161137	ENSMUSG00000027835	3	75516490	75556856	-1	5	0	2	12	1	0	336	418	111	269	107		Q8VE70
ENSMUST00000161138						17	13	48	32	14	7	0	0	0	0	0		
ENSMUST00000161139						24	11	47	20	28	17	0	0	3	1	2		
ENSMUST00000161140	ENSMUSG00000026546	1	172520801	172545870	1	0	0	0	0	0	0	0	0	0	0	0	E0CXK5	
ENSMUST00000161141	ENSMUSG00000004127	3	138143448	138159821	1	0	0	0	0	0	0	0	0	0	10	4	E0CZ56	
ENSMUST00000161142						6	1	9	2	8	0	0	0	0	0	4		
ENSMUST00000161143						1	0	0	1	1	0	2	0	0	0	0		
ENSMUST00000161144	ENSMUSG00000026572	1	165137855	165160773	-1	0	0	0	0	0	0	0	1	0	0	0	F6USC6	
ENSMUST00000161145						0	0	2	0	0	0	0	0	4	0	4		
ENSMUST00000161147						0	0	9	0	0	1	0	6	0	0	0		
ENSMUST00000161148	ENSMUSG00000089809	5	99297244	99729065	-1	14	13	16	37	22	6	0	0	0	0	0	E0CXU2	
ENSMUST00000161149	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	0	2	0	0	0	0	0	0	0	E0CYR2	
ENSMUST00000161151						4	3	0	6	3	1	4	4	0	2	5		
ENSMUST00000161152	ENSMUSG00000026580	1	164115264	164150026	1	0	0	6	1	0	1	79	140	130	36	55	F6TL88	
ENSMUST00000161153						3	0	0	0	0	0	6	0	0	0	0		
ENSMUST00000161154	ENSMUSG00000021266	12	108860030	108894174	-1	3	0	0	0	0	0	53	42	78	12	53		P32921
ENSMUST00000161155						12	9	4	49	11	10	0	0	0	0	0		
ENSMUST00000161156	ENSMUSG00000020121	10	121780991	122047315	-1	2	4	4	3	4	5	0	0	1	0	0	F7D9F7	
ENSMUST00000161157	ENSMUSG00000024677	19	11516512	11531256	1	14	18	40	5	14	3	55	336	96	131	228	E0CZC1	
ENSMUST00000161158						1	2	0	4	2	0	3	517	21	19	10		
ENSMUST00000161159	ENSMUSG00000042605	5	121711337	121816493	1	0	0	0	3	0	0	0	67	4	2	15	F6UTV7	
ENSMUST00000161160						3	4	0	2	4	0	0	0	0	0	5		
ENSMUST00000161162	ENSMUSG00000071176	8	14911663	15001085	1	2	8	0	0	0	3	0	0	0	0	0	F7BCP8	
ENSMUST00000161163						2	3	13	5	7	0	5	5	5	6	3		
ENSMUST00000161164	ENSMUSG00000004151	12	38779380	38868215	1	5	4	5	3	1	0	0	0	0	0	0	E0CXX3	
ENSMUST00000161165	ENSMUSG00000009291	10	77581720	77598732	1	1	2	2	6	1	1	0	0	0	0	0	E0CXB5	
ENSMUST00000161166	ENSMUSG00000035953	14	50926070	50930856	-1	1	0	0	0	0	0	0	7	0	0	0	E0CZF6	
ENSMUST00000161167	ENSMUSG00000071324	10	41914990	42018442	-1	0	1	1	1	2	0	0	0	0	0	0	F7B746	
ENSMUST00000161168						3	2	9	1	5	6	2	2	3	0	0		
ENSMUST00000161169						123	103	175	270	167	95	63	154	104	18	100		
ENSMUST00000161170	ENSMUSG00000072623	6	118461950	118479320	-1	52	56	92	85	49	27	2	5	4	3	11	Q8BIS1	
ENSMUST00000161171						1	1	3	1	0	1	0	0	1	0	0		
ENSMUST00000161172	ENSMUSG00000074656	2	154871410	154892935	-1	12	12	25	265	25	10	3	7	3	51	14	E0CXJ3	
ENSMUST00000161173						22	21	55	62	35	11	0	6	1	0	3		
ENSMUST00000161175						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000161176						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161177						5	4	10	2	5	0	0	0	0	0	0		
ENSMUST00000161178	ENSMUSG00000049687	15	82338942	82345743	1	16	0	52	51	8	11	0	0	0	0	0		
ENSMUST00000161179						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000161180						8	6	7	72	8	7	0	0	0	0	0		
ENSMUST00000161181	ENSMUSG00000029635	5	146231230	146302874	1	0	7	1	0	0	17	69	328	151	25	85	E9Q6E2	
ENSMUST00000161182	ENSMUSG00000032295	9	57130690	57142722	1	0	0	0	0	0	5	50	5	77	21	46	E9PZ88	
ENSMUST00000161183						0	0	0	0	0	0	4	13	2	1	3		
ENSMUST00000161184						0	0	0	1	11	4	0	1	0	0	0		
ENSMUST00000161185						1	0	0	1	0	0	5	0	0	0	6		
ENSMUST00000161186	ENSMUSG00000038084	16	29579334	29654884	1	0	0	0	0	0	0	73	57	189	0	74		P58281
ENSMUST00000161187	ENSMUSG00000042790	9	45863425	45906894	-1	0	0	0	0	0	0	14	62	24	0	76		Q8BFU3
ENSMUST00000161188	ENSMUSG00000022788	16	16416917	16600549	-1	1	0	0	1	0	0	11	5	8	4	12		Q91ZT5
ENSMUST00000161189	ENSMUSG00000041879	1	135382312	135430499	-1	3	0	0	0	3	0	177	38	129	0	200	E0CY46	
ENSMUST00000161190						4	4	3	4	4	2	1	2	1	2	1		
ENSMUST00000161191						0	1	3	150	6	2	0	0	19	0	26		
ENSMUST00000161193						7	6	46	3	7	4	0	0	0	0	0		
ENSMUST00000161194	ENSMUSG00000032280	9	61372366	61418497	1	9	2	5	57	5	4	11	9	5	0	14	E0CZB4	
ENSMUST00000161195						4	0	4	0	8	3	0	0	0	0	0		
ENSMUST00000161196						44	38	79	84	41	26	6	28	2	4	2		
ENSMUST00000161198	ENSMUSG00000057103	6	85910154	85915687	-1	3	7	12	13	8	2	18	44	10	24	8	E9PUL7	
ENSMUST00000161199						3	0	16	108	11	1	3	3	5	0	9		
ENSMUST00000161200						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161201						0	2	0	0	0	0	0	0	0	1	0		
ENSMUST00000161202	ENSMUSG00000013611	15	36504062	36555573	-1	6	1	16	0	10	0	0	2	0	1	1		Q6P8Y7
ENSMUST00000161203	ENSMUSG00000042790	9	45863425	45906894	-1	0	0	0	0	0	0	41	193	89	23	34		Q8BFU3
ENSMUST00000161204	ENSMUSG00000066441	12	79174337	79192293	-1	7	17	8	16	19	3	90	254	110	120	112		Q9QYF1
ENSMUST00000161205						7	6	13	5	6	3	0	0	0	0	1		
ENSMUST00000161206						4	5	6	6	12	4	0	0	0	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161207	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	2	0	0	584	0	1021	0	567	E0CY14	
ENSMUST00000161208						0	3	4	0	4	1	0	13	0	0	0		
ENSMUST00000161209						0	0	0	101	0	0	0	0	20	0	0		
ENSMUST00000161210	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	1	0	0	0	0	0	0	0	0	E0CXA6	
ENSMUST00000161211	ENSMUSG00000002679	12	81573557	81595008	-1	0	0	0	5	0	0	18	18	18	116	36		Q921D4
ENSMUST00000161212						8	3	7	11	6	4	3	8	7	0	2		
ENSMUST00000161213						4	2	4	0	6	0	0	0	0	1	1		
ENSMUST00000161214						5	6	8	1	6	3	0	0	0	0	0		
ENSMUST00000161215	ENSMUSG00000026198	1	75171717	75180392	-1	0	1	6	0	2	0	0	5	0	2	0	F6SGP4	
ENSMUST00000161217	ENSMUSG00000029638	6	8509600	8597548	1	0	0	0	0	0	0	0	0	7	0	7		Q8K3I9
ENSMUST00000161218						4	3	11	27	8	2	0	6	0	2	0		
ENSMUST00000161219	ENSMUSG00000021917	14	30999826	31001672	-1	2	2	3	4	1	2	4	9	0	0	1	F6UR10	
ENSMUST00000161220	ENSMUSG00000053004	6	114397936	114483296	1	11	11	0	0	0	0	0	0	0	0	0	B3Y5T0	P70174
ENSMUST00000161221						1	0	0	11	0	0	51	23	51	1	27		
ENSMUST00000161222						3	0	5	7	2	1	14	39	15	4	11		
ENSMUST00000161223						1	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000161224	ENSMUSG00000057037	1	139547053	139560272	-1	0	0	0	0	0	2	0	0	0	0	0	A0A0A6YXP6	
ENSMUST00000161225						3	15	14	11	11	14	0	0	0	0	0		
ENSMUST00000161226						26	24	118	355	40	35	0	7	3	0	4		
ENSMUST00000161227	ENSMUSG00000029823	6	38551334	38609470	1	37	43	317	0	51	36	179	1182	174	163	222	Q05CX5	
ENSMUST00000161228						5	1	2	182	3	1	0	0	0	0	0		
ENSMUST00000161230						66	62	76	66	98	35	42	219	61	13	67		
ENSMUST00000161231						0	0	12	98	8	0	0	1	0	2	7		
ENSMUST00000161232	ENSMUSG00000032425	9	88548020	88571061	1	0	1	4	0	3	0	4	16	0	21	4		
ENSMUST00000161233	ENSMUSG00000037720	5	67260565	67291461	1	1	0	0	22	2	0	32	105	45	62	30	E0CXY5	
ENSMUST00000161234						0	0	0	55	5	1	0	0	0	0	4		
ENSMUST00000161235	ENSMUSG00000079144	1	193168046	193177832	1	0	0	2	1	0	0	0	0	0	2	0		Q9DAE8
ENSMUST00000161236	ENSMUSG00000028931	4	152390742	152477871	-1	0	2	0	3	0	1	0	0	0	0	0	E0CXI4	
ENSMUST00000161237	ENSMUSG00000059022	6	29473162	29507952	-1	3	6	7	4	9	2	0	0	0	0	0	E0CYL0	
ENSMUST00000161238						1	0	4	104	5	4	0	3	5	0	1		
ENSMUST00000161239						1	2	13	3	2	1	3	5	0	2	0		
ENSMUST00000161240	ENSMUSG00000090035	10	99108159	99113247	1	24	32	83	136	58	23	239	747	368	35	272		O08832
ENSMUST00000161241	ENSMUSG00000026641	1	171411313	171419142	1	7	11	45	9	6	16	134	647	128	41	363	Q3UQH7	Q61069
ENSMUST00000161242						5	3	0	3	5	0	70	136	41	28	0		
ENSMUST00000161243	ENSMUSG00000045962	6	119923969	120038672	-1	0	0	0	2	5	1	64	215	85	26	140	F6U2S8	
ENSMUST00000161245						0	2	4	0	3	2	0	0	0	0	0		
ENSMUST00000161246	ENSMUSG00000033805	5	107402736	107430035	1	3	1	0	39	4	0	0	0	0	0	0	F6URA2	
ENSMUST00000161247	ENSMUSG00000043004	14	19872559	19977627	-1	0	2	0	0	2	1	0	0	0	4	4		P63213
ENSMUST00000161248						15	12	13	10	16	7	2	10	19	12	12		
ENSMUST00000161249	ENSMUSG00000063458	14	22019712	23056085	1	0	0	4	0	0	0	3	12	14	0	4	E0CYG4	
ENSMUST00000161250	ENSMUSG00000023010	15	99392882	99410049	1	0	2	6	2	0	0	94	123	90	0	85		Q9D2C7
ENSMUST00000161252	ENSMUSG00000025188	19	42755105	42779978	-1	0	0	0	33	0	1	0	15	0	0	2	F7BWJ7	
ENSMUST00000161253	ENSMUSG00000032591	9	108080436	108085003	1	0	1	0	0	0	0	0	2	0	1	0	A0A0A6YWW4	
ENSMUST00000161254	ENSMUSG00000048148	8	72646711	72714746	1	19	19	0	0	46	29	3	3	3	1	3	E0CX99	
ENSMUST00000161256	ENSMUSG00000023994	17	48386885	48409906	-1	0	0	0	0	0	0	0	0	0	0	15	F7DFJ2	
ENSMUST00000161257						3	3	5	129	7	0	0	0	0	0	0		
ENSMUST00000161258						0	4	0	1	2	0	0	0	0	0	0		
ENSMUST00000161259						2	4	14	3	9	6	56	168	95	20	206		
ENSMUST00000161260						3	4	7	11	8	3	0	2	3	0	3		
ENSMUST00000161261						2	0	3	4	0	0	0	0	0	0	0		
ENSMUST00000161262						0	2	8	8	7	3	2	17	11	4	2		
ENSMUST00000161263	ENSMUSG00000051111	13	95954594	96132577	-1	29	21	52	147	62	19	0	0	0	0	0		Q69ZS6
ENSMUST00000161264						0	0	8	1	2	0	2	0	0	8	3		
ENSMUST00000161265	ENSMUSG00000022558	15	76380261	76453038	1	0	0	0	0	0	0	3	16	0	12	0	F6TUR0	
ENSMUST00000161266	ENSMUSG00000022234	15	31590800	31601847	-1	0	3	5	60	0	4	0	0	4	5	5	E0CZA1	
ENSMUST00000161267	ENSMUSG00000052477	1	84992690	85270566	-1	11	6	42	44	9	3	114	511	185	146	135	E0CY74	
ENSMUST00000161268						0	0	1	0	1	4	0	0	0	0	0		
ENSMUST00000161269						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000161270						2	0	6	1	2	2	1	0	0	0	1		
ENSMUST00000161271						0	0	0	0	0	1	70	187	54	21	51		
ENSMUST00000161272	ENSMUSG00000032575	9	106838312	106891979	-1	0	3	0	0	1	0	0	0	0	8	2	F7C1S6	
ENSMUST00000161273	ENSMUSG00000029406	5	124118690	124249760	-1	0	0	0	30	23	0	0	0	0	0	0	E9PYJ7	
ENSMUST00000161275						2	0	2	0	0	0	0	0	0	0	3		
ENSMUST00000161276	ENSMUSG00000059022	6	29473162	29507952	-1	0	0	0	0	0	0	0	2	0	1	0	F7DED4	
ENSMUST00000161277	ENSMUSG00000025812	8	127063893	127612286	1	0	2	4	1	0	0	0	0	0	0	0	F6UGU7	
ENSMUST00000161278	ENSMUSG00000033004	14	103113411	103346814	-1	8	7	41	12	15	3	37	99	72	8	123	F7CZG3	
ENSMUST00000161279	ENSMUSG00000075593	5	138264921	138272840	-1	0	0	0	0	0	0	0	0	0	0	0	Q3V1B8	
ENSMUST00000161280						6	5	0	1	3	3	2	1	0	0	5		
ENSMUST00000161281						3	0	0	0	0	0	17	108	70	9	59		
ENSMUST00000161283	ENSMUSG00000024677	19	11516512	11531256	1	0	0	0	0	0	0	0	0	0	0	9	F6TGK4	
ENSMUST00000161284	ENSMUSG00000021090	12	72441866	72514334	1	0	9	20	0	5	0	0	1	0	0	0	E9PUL2	
ENSMUST00000161285						23	26	29	258	34	14	2	12	2	0	1		
ENSMUST00000161286	ENSMUSG00000022858	16	22244549	22266005	-1	22	8	15	53	16	4	239	739	168	468	177		P62996
ENSMUST00000161287						2	1	0	1	2	3	0	0	0	0	0		
ENSMUST00000161288	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	0	0	0	1	0	0	0	0	0	F6U338	
ENSMUST00000161289	ENSMUSG00000060560	8	105131800	105150109	1	17	16	35	24	24	13	0	0	0	0	0		Q8R0W5
ENSMUST00000161290	ENSMUSG00000040669	6	122317731	122340561	-1	0	1	0	0	1	0	0	0	0	0	0	F7D980	
ENSMUST00000161292	ENSMUSG00000030329	6	124996694	125003096	1	0	0	0	0	0	0	0	0	1	0	0	E0CZ88	
ENSMUST00000161293						2	6	5	1	11	2	0	0	0	0	0		
ENSMUST00000161294	ENSMUSG00000022525	16	29209695	29230531	1	2	2	0	0	0	0	0	0	0	0	0	E0CYE9	
ENSMUST00000161295	ENSMUSG00000024238	18	5591860	5775467	1	0	0	0	5	0	0	13	0	12	8	28	E0CY37	
ENSMUST00000161296						0	0	0	3	4	3	5	8	14	0	13		
ENSMUST00000161297						2	0	0	7	0	0	24	5	0	0	0		
ENSMUST00000161299						3	10	11	11	12	5	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161300	ENSMUSG00000026489	1	180165238	180199602	-1	9	0	3	0	1	4	250	328	252	73	64	F7B1B6	
ENSMUST00000161301	ENSMUSG00000048402	1	118834132	119053619	-1	0	0	2	1	6	4	0	0	0	0	0	A5AA27	
ENSMUST00000161302	ENSMUSG00000060579	14	9550092	11162035	-1	2	0	4	2	3	5	3	0	0	2	0		O89106
ENSMUST00000161303						12	13	51	17	11	4	0	0	1	0	0		
ENSMUST00000161304						0	15	0	8	5	9	29	63	35	9	13		
ENSMUST00000161305						0	0	63	0	0	0	0	0	0	0	0		
ENSMUST00000161306	ENSMUSG00000054537	5	86705186	86745815	-1	12	12	7	11	15	5	0	0	0	1	1		Q5S248
ENSMUST00000161308	ENSMUSG00000060743	1	180800832	180813943	-1	20	22	6	20	21	10	1510	423	115	431	185		P84244
ENSMUST00000161309						2	5	21	2	6	5	0	4	1	2	0		
ENSMUST00000161310						3	1	2	0	4	2	0	0	0	0	0		
ENSMUST00000161311						0	2	16	0	0	0	0	0	0	3	10		
ENSMUST00000161312	ENSMUSG00000037797	3	138415466	138430892	1	0	0	0	0	8	0	0	0	0	0	0	E0CYI4	
ENSMUST00000161313						39	38	38	30	41	25	0	15	3	3	2		
ENSMUST00000161314						6	2	15	4	12	2	0	1	0	0	1		
ENSMUST00000161315	ENSMUSG00000021481	13	55105311	55134825	1	0	1	0	49	2	0	0	0	0	0	1	E0CY94	
ENSMUST00000161316						1	0	0	0	1	0	0	11	3	0	0		
ENSMUST00000161317	ENSMUSG00000024231	18	3382988	3436377	1	0	2	0	0	0	0	8	68	13	0	0	E0CYT5	
ENSMUST00000161318	ENSMUSG00000032115	9	44379490	44392369	1	0	0	15	41	24	10	130	255	0	74	434		Q9JKR6
ENSMUST00000161320	ENSMUSG00000006014	1	150449412	150466165	-1	0	0	0	0	0	0	1	0	0	0	37	E0CXA1	
ENSMUST00000161321						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161322	ENSMUSG00000041625	14	122816223	122913757	-1	0	0	0	0	0	0	0	0	0	0	0	H3BKQ5	
ENSMUST00000161324	ENSMUSG00000061950	17	65782573	65841926	1	3	0	4	31	3	2	9	15	8	0	8	E0CX37	
ENSMUST00000161325	ENSMUSG00000041771	12	102128733	102267091	1	0	0	8	0	0	0	0	0	0	0	0	F7B0S9	
ENSMUST00000161326	ENSMUSG00000022698	16	44139830	44163366	1	0	0	5	0	5	0	16	84	15	10	14		Q6PGB6
ENSMUST00000161327	ENSMUSG00000025907	1	6206197	6276648	1	0	0	0	0	0	0	359	1073	544	121	222	F7CC56	
ENSMUST00000161328	ENSMUSG00000052942	19	28258851	28680077	-1	3	0	0	0	0	0	3	0	0	0	0	E0CX93	
ENSMUST00000161329	ENSMUSG00000022364	15	57912199	57970067	1	4	4	4	1	8	2	0	22	2	14	7	F6T4B0	
ENSMUST00000161330	ENSMUSG00000038658	19	29522282	29606829	1	0	1	0	0	0	0	6	125	19	7	4	F7DEJ0	
ENSMUST00000161331	ENSMUSG00000029634	5	146209192	146221555	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZ82	
ENSMUST00000161332						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000161333						2	0	0	1	3	1	0	0	3	0	26		
ENSMUST00000161334	ENSMUSG00000074569	2	172450313	172458596	-1	0	0	61	0	0	0	0	0	0	1	0	F7CBR4	
ENSMUST00000161335	ENSMUSG00000030232	6	140622663	140678472	1	3	6	7	0	5	4	77	187	78	15	55		Q9Z248
ENSMUST00000161336	ENSMUSG00000033400	3	116739999	116808166	-1	1	0	0	3	0	0	114	0	358	0	135	E0CYU6	
ENSMUST00000161337						3	0	4	26	4	0	0	0	0	0	0		
ENSMUST00000161338	ENSMUSG00000032295	9	57130690	57142722	1	1	1	8	1	5	0	0	1	1	0	6	F6TAQ6	
ENSMUST00000161339	ENSMUSG00000045875	14	66635251	66733462	1	0	4	17	0	0	0	0	1	0	0	0		P97718
ENSMUST00000161340						0	1	5	103	0	4	0	0	0	0	0		
ENSMUST00000161341						28	10	56	1233	52	39	3	9	7	3	13		
ENSMUST00000161342	ENSMUSG00000041957	16	16213318	16272712	1	9	3	8	0	19	5	0	0	1	0	0	E0CXK9	
ENSMUST00000161343						0	7	0	0	4	3	0	37	4	16	5		
ENSMUST00000161345	ENSMUSG00000049109	10	28668360	28883818	1	0	2	0	0	0	0	0	0	0	0	0	E0CYT7	
ENSMUST00000161347	ENSMUSG00000022659	16	45610380	45622867	1	3	0	7	4	0	2	1	2	0	2	0		Q6RFH4
ENSMUST00000161348	ENSMUSG00000025812	8	127063893	127612286	1	4	6	2	2	1	0	1	0	0	1	0	F6URI7	
ENSMUST00000161350						1	3	0	0	0	2	0	28	0	2	1		
ENSMUST00000161351	ENSMUSG00000035329	12	59200655	59219725	-1	0	2	2	12	5	1	21	39	153	12	63	E0CZ63	
ENSMUST00000161352						5	0	7	1	12	0	7	10	7	0	15		
ENSMUST00000161353						14	19	68	8	15	6	0	0	0	0	0		
ENSMUST00000161354	ENSMUSG00000032131	9	44273188	44288615	-1	13	7	27	54	29	13	0	0	3	0	0	Q91WA9	
ENSMUST00000161355	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0	E0CXR8	
ENSMUST00000161356	ENSMUSG00000042453	5	21884454	22344702	-1	0	14	42	17	29	0	0	0	0	1	0		Q60841
ENSMUST00000161357						17	22	66	53	36	21	0	0	0	0	0		
ENSMUST00000161358	ENSMUSG00000055540	16	59653483	60605531	-1	4	4	5	1	5	0	0	0	0	0	0	E9PUK8	
ENSMUST00000161359						0	4	0	1	1	1	26	58	21	26	37		
ENSMUST00000161360						35	24	105	36	40	14	4	8	10	3	26		
ENSMUST00000161361	ENSMUSG00000026344	1	125867622	125913101	-1	1	0	0	1	0	0	0	0	0	0	0	F6TKE8	
ENSMUST00000161363	ENSMUSG00000028559	4	109061145	109202272	-1	10	4	3	0	7	0	0	105	0	0	0	E9Q6C1	
ENSMUST00000161365	ENSMUSG00000030148	6	123106428	123143999	1	0	0	0	0	0	0	580	3517	872	2443	546		Q9QZ15
ENSMUST00000161367	ENSMUSG00000037318	1	193175453	193201703	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW19	
ENSMUST00000161368	ENSMUSG00000024939	19	5728087	5729653	-1	0	0	0	0	0	1	175	151	100	0	71	Q7TMI7	Q9QUI1
ENSMUST00000161369	ENSMUSG00000037720	5	67260565	67291461	1	4	5	0	136	4	0	205	481	69	118	74		Q9CR67
ENSMUST00000161371						0	1	1	1	3	0	0	0	0	0	0		
ENSMUST00000161372	ENSMUSG00000058441	15	89059734	89073567	1	0	4	19	63	0	0	0	1	0	0	1		Q6IMP4
ENSMUST00000161373						0	0	2	0	3	0	75	147	31	10	39		
ENSMUST00000161374	ENSMUSG00000029673	5	131437333	132543344	-1	6	1	6	440	16	10	0	0	0	0	0	E9PWJ4	
ENSMUST00000161375						1	0	2	4	0	0	1	1	2	0	0		
ENSMUST00000161376						1	3	0	0	4	1	0	2	2	0	8		
ENSMUST00000161377						0	1	0	12	1	0	0	0	0	0	0		
ENSMUST00000161378	ENSMUSG00000003549	7	19344778	19356524	1	3	3	0	1	1	0	5	0	0	0	0	H3BJK4	
ENSMUST00000161379	ENSMUSG00000026489	1	180165238	180199602	-1	0	0	1	0	0	0	0	2	0	6	0	A0A0A6YVT9	
ENSMUST00000161381	ENSMUSG00000034739	9	44101729	44109187	1	21	0	0	44	0	0	0	0	0	0	0		Q8K480
ENSMUST00000161384						4	0	3	2	0	3	0	2	0	0	0		
ENSMUST00000161385	ENSMUSG00000094113	6	131486400	131553763	1	0	0	0	0	0	0	0	0	0	0	0	F7D4R8	
ENSMUST00000161386	ENSMUSG00000048148	8	72646711	72714746	1	51	30	262	38	40	18	0	2	0	1	0	E0CYZ6	
ENSMUST00000161387						3	1	6	5	2	2	0	0	0	0	0		
ENSMUST00000161388						1	1	0	0	1	0	2	0	2	2	5		
ENSMUST00000161389	ENSMUSG00000089773	4	112006269	112029538	1	0	0	0	0	0	0	0	0	0	0	0		A7TZE6
ENSMUST00000161390	ENSMUSG00000029624	5	145147514	145167108	-1	1	2	1	7	1	0	0	0	0	0	0	E0CXI1	
ENSMUST00000161391						0	0	3	1	0	0	187	264	66	10	111		
ENSMUST00000161392						0	0	0	0	0	0	5	0	0	0	0		
ENSMUST00000161393	ENSMUSG00000032295	9	57130690	57142722	1	0	2	0	43	0	0	2	12	4	0	11	E0CXI0	
ENSMUST00000161396	ENSMUSG00000021615	13	89774027	90089608	-1	0	2	0	0	0	0	0	0	0	0	2	E0CY05	
ENSMUST00000161398	ENSMUSG00000029130	5	29195992	29228457	1	0	0	6	1	0	0	0	0	0	0	0	E0CZ33	
ENSMUST00000161399						99	53	146	1206	171	68	1	9	5	7	14		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161400						0	1	4	0	1	0	2	8	0	2	0		
ENSMUST00000161401	ENSMUSG00000063694	6	50562563	50566538	-1	59	63	101	110	81	23	84	133	35	185	49	Q56A15	P62897
ENSMUST00000161402	ENSMUSG00000024109	17	90033631	91093071	-1	0	2	0	0	0	0	0	0	0	0	0		Q9CS84
ENSMUST00000161403						142	82	449	544	157	76	64	299	134	12	252		
ENSMUST00000161404						0	1	2	4	3	0	0	0	0	0	0		
ENSMUST00000161405	ENSMUSG00000022286	15	37233036	37363569	1	20	15	25	67	33	8	0	1	0	0	0	Q9DCN4	
ENSMUST00000161406	ENSMUSG00000016194	1	193221634	193264075	-1	2	0	5	1	0	2	0	0	0	0	0	F6TSI8	
ENSMUST00000161408	ENSMUSG00000032131	9	44273188	44288615	-1	3	2	7	143	6	2	0	0	0	0	0	E0CYI8	
ENSMUST00000161409	ENSMUSG00000022635	15	93386097	93398334	-1	1	0	0	15	4	0	0	44	17	14	20	E0CZE5	
ENSMUST00000161410	ENSMUSG00000021266	12	108860030	108894174	-1	17	17	0	0	0	5	64	39	0	40	284	Q3U6U7	P32921
ENSMUST00000161411						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000161412	ENSMUSG00000032503	9	112065091	112235938	-1	2	2	0	1	3	0	0	0	0	0	0		Q9DCB4
ENSMUST00000161413						5	4	6	0	6	2	0	0	0	0	0		
ENSMUST00000161414						0	0	0	0	0	2	2	0	2	0	0		
ENSMUST00000161415						4	4	18	0	8	8	129	1488	348	31	395		
ENSMUST00000161417	ENSMUSG00000050150	3	135348029	135397827	1	1	1	3	2	0	0	1	2	0	0	1	F7CTY9	
ENSMUST00000161418	ENSMUSG00000043592	17	48454901	48539714	1	0	0	0	0	0	0	0	0	2	0	0	F7CT06	
ENSMUST00000161419						5	3	1	9	3	0	1	0	0	0	0		
ENSMUST00000161420						5	1	5	5	4	2	0	0	0	0	4		
ENSMUST00000161421	ENSMUSG00000031647	8	60632827	60676729	1	19	16	244	159	50	18	2	6	3	0	13		Q9D3X9
ENSMUST00000161422						0	1	1	2	0	0	0	0	0	0	0		
ENSMUST00000161423						0	0	11	4	0	0	1	0	0	0	0		
ENSMUST00000161424						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000161425	ENSMUSG00000038932	2	180621956	180642708	-1	0	0	0	28	0	1	0	0	0	0	0	E9Q5K1	
ENSMUST00000161426						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000161427						2	3	8	3	7	6	0	0	0	0	0		
ENSMUST00000161428	ENSMUSG00000019795	10	7629373	7681136	-1	2	6	3	1	2	1	2	85	43	14	31	F6V9F1	
ENSMUST00000161429	ENSMUSG00000047992	18	84720019	84740436	1	2	0	0	28	0	2	0	0	0	0	0	E0CXZ4	
ENSMUST00000161430	ENSMUSG00000039021	2	32757026	32775633	-1	0	0	0	0	0	0	0	0	0	0	0	E9PZ84	
ENSMUST00000161431	ENSMUSG00000045994	9	26733728	26763101	1	0	0	0	115	0	0	0	0	0	0	0		
ENSMUST00000161432						3	0	23	1	2	2	8	0	141	0	65		
ENSMUST00000161433						2	3	27	7	7	2	5	10	8	0	7		
ENSMUST00000161434						5	4	9	2	1	3	3	160	5	5	25		
ENSMUST00000161435	ENSMUSG00000009647	10	59446984	59616692	-1	18	13	25	28	28	14	5	1	7	1	3	E0CYL3	
ENSMUST00000161436	ENSMUSG00000022668	16	44736768	44746363	-1	0	0	0	0	0	0	6	0	0	5	0	F6XXP5	
ENSMUST00000161437						1	0	5	0	5	0	0	0	0	0	0		
ENSMUST00000161438						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000161440						2	0	5	0	3	0	1	6	5	5	6		
ENSMUST00000161441	ENSMUSG00000074794	13	80883384	80896035	1	0	0	69	13	6	0	60	0	398	149	428	E0CZE1	
ENSMUST00000161442						2	2	5	3	10	1	0	1	0	1	1		
ENSMUST00000161443						7	8	19	7	20	8	0	2	1	0	2		
ENSMUST00000161445	ENSMUSG00000021816	14	20499364	20546573	-1	0	0	8	0	0	0	172	302	216	72	149	E0CZ78	
ENSMUST00000161446	ENSMUSG00000030092	6	104492790	104863406	1	0	2	0	2	4	0	0	0	0	0	0	E0CY26	
ENSMUST00000161448	ENSMUSG00000046658	5	143249697	143270022	-1	120	132	231	317	153	71	12	35	6	0	38	G3XA34	
ENSMUST00000161450	ENSMUSG00000030226	6	138362918	138581968	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BZL8
ENSMUST00000161451	ENSMUSG00000048402	1	118834132	119053619	-1	0	0	0	0	0	0	0	0	0	0	0	A5A9W3	
ENSMUST00000161452	ENSMUSG00000033805	5	107402736	107430035	1	1	0	0	0	0	0	0	0	0	0	0	E0CXW5	
ENSMUST00000161453						0	0	0	0	0	0	19	33	28	56	43		
ENSMUST00000161454						0	0	0	16	0	0	0	0	0	0	1		
ENSMUST00000161455	ENSMUSG00000020898	11	69015911	69036473	1	1	0	0	1	31	0	0	0	0	0	16	E0CXE7	
ENSMUST00000161456						1	0	0	11	3	0	0	0	0	0	0		
ENSMUST00000161457	ENSMUSG00000012422	13	90089123	90143907	1	4	1	6	4	5	1	11	17	23	202	7	E0CY07	
ENSMUST00000161458	ENSMUSG00000032425	9	88548020	88571061	1	2	9	84	36	0	18	54	618	85	0	0	E9Q732	
ENSMUST00000161459	ENSMUSG00000071350	14	59402009	59440884	-1	5	10	5	8	9	6	21	78	56	22	49	B2RXP3	
ENSMUST00000161460						11	8	10	27	17	6	36	120	56	61	96		
ENSMUST00000161462						0	4	0	0	0	0	0	8	0	0	0		
ENSMUST00000161464						0	2	3	2	6	0	0	0	0	2	0		
ENSMUST00000161465						25	3	145	21	23	2	0	0	0	0	14		
ENSMUST00000161466						4	4	2	1	4	3	0	0	0	0	0		
ENSMUST00000161467						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000161468						0	3	2	0	3	3	0	0	0	1	0		
ENSMUST00000161469						3	1	12	47	4	3	0	0	2	0	2		
ENSMUST00000161470						0	3	0	0	0	4	5	5	2	2	4		
ENSMUST00000161471						0	0	0	0	0	0	0	0	0	0	13		
ENSMUST00000161472						0	1	3	0	5	0	0	0	2	0	0		
ENSMUST00000161474						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161475	ENSMUSG00000074424	3	94174412	94178193	-1	27	26	12	23	23	12	0	0	0	0	0	Q3UTC4	
ENSMUST00000161476	ENSMUSG00000015748	3	95830124	95855885	-1	8	2	11	112	6	2	51	133	129	131	31		Q922U1
ENSMUST00000161478						3	2	2	0	2	0	0	0	0	0	0		
ENSMUST00000161479						1	0	3	116	0	1	0	0	0	1	6		
ENSMUST00000161481	ENSMUSG00000024154	17	88668660	88715152	1	0	0	1	0	2	2	0	0	0	0	0	E0CYD4	
ENSMUST00000161482						0	0	0	0	0	0	3	16	7	5	11		
ENSMUST00000161484						0	0	11	1	0	2	0	0	0	0	2		
ENSMUST00000161485	ENSMUSG00000038473	1	170302668	170589861	-1	0	0	0	0	0	0	51	39	51	2	41	E0CYH9	
ENSMUST00000161486	ENSMUSG00000084786	9	20642878	20647140	1	4	2	0	2	0	4	0	13	6	0	0	E0CY38	
ENSMUST00000161487	ENSMUSG00000034613	10	122678762	122945795	1	6	8	8	49	11	9	4	5	18	2	21		Q3UYC0
ENSMUST00000161488						6	3	9	4	9	0	79	867	84	5	124		
ENSMUST00000161489						0	3	0	0	4	0	0	0	0	0	0		
ENSMUST00000161490	ENSMUSG00000029334	5	98929773	99037351	-1	24	26	75	77	17	16	1	0	0	40	7	Q8CAH8	
ENSMUST00000161492						3	3	0	2	0	3	0	1	0	0	0		
ENSMUST00000161493						32	23	87	34	35	24	0	1	2	0	2		
ENSMUST00000161494	ENSMUSG00000029638	6	8509600	8597548	1	5	7	13	5	16	8	2	25	9	2	5		
ENSMUST00000161495	ENSMUSG00000026377	1	118321839	118333822	1	1	0	1	9	0	0	4	0	1	0	1	E0CXU3	
ENSMUST00000161496						1	3	2	2	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161497	ENSMUSG00000070031	1	85600378	85645037	1	0	0	0	0	0	0	0	0	0	0	0	F7DFN7	
ENSMUST00000161498						4	3	16	3	4	2	0	0	0	1	1		
ENSMUST00000161499						8	8	26	9	10	4	21	126	15	3	89		
ENSMUST00000161500	ENSMUSG00000032118	9	36821939	36878924	1	0	0	1	3	0	0	0	0	0	0	0	E0CYY9	
ENSMUST00000161501	ENSMUSG00000000378	11	6546887	6596744	1	2	4	8	3	0	0	41	88	83	29	71	E0CYY2	
ENSMUST00000161502	ENSMUSG00000046152	8	31187331	31261738	1	0	10	4	12	10	0	0	0	0	0	0		Q5F2L2
ENSMUST00000161503						1	1	2	27	9	5	19	87	59	26	87		
ENSMUST00000161504	ENSMUSG00000061244	14	49012146	49066653	-1	0	0	2	29	0	1	77	250	187	41	0	E9PZ92	
ENSMUST00000161506						1	2	1	1	6	1	0	0	0	0	0		
ENSMUST00000161507						1	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000161508	ENSMUSG00000038876	10	29344178	29362442	-1	0	0	0	0	0	0	0	20	14	8	12	H9KV17	
ENSMUST00000161510						21	17	294	20	25	10	0	3	0	0	2		
ENSMUST00000161512	ENSMUSG00000045962	6	119923969	120038672	-1	1	4	13	4	2	2	0	0	0	0	0		
ENSMUST00000161513	ENSMUSG00000004151	12	38779380	38868215	1	0	1	13	0	0	0	0	0	0	0	0	E0CYI1	
ENSMUST00000161514	ENSMUSG00000037280	15	100691813	100729376	-1	0	5	21	0	6	7	0	0	0	0	0		Q8C7U7
ENSMUST00000161515	ENSMUSG00000003135	1	39534992	39546889	1	20	0	0	234	21	0	0	11	43	22	11		Q9CWN7
ENSMUST00000161516	ENSMUSG00000089809	5	99297244	99729065	-1	14	14	14	25	16	10	0	0	0	0	0	E0CXS0	
ENSMUST00000161517	ENSMUSG00000093701	16	91391721	91419451	1	0	0	0	0	0	0	42	220	36	0	0	F7BJH9	
ENSMUST00000161518						4	2	43	11	8	2	0	1	0	0	1		
ENSMUST00000161519	ENSMUSG00000030145	6	118427319	118455528	-1	0	0	0	0	0	0	0	0	0	1	1	Q9CZ86	
ENSMUST00000161520	ENSMUSG00000052616	8	104446719	104509910	-1	341	368	147	431	270	135	5	20	21	8	23	E0CZE9	
ENSMUST00000161521	ENSMUSG00000025646	9	109059747	109074124	-1	0	0	0	0	0	0	0	0	20	0	0	E9Q6L5	
ENSMUST00000161522	ENSMUSG00000030589	7	29134851	29153961	1	0	5	0	0	0	0	0	0	0	0	0	E0CZ06	
ENSMUST00000161523	ENSMUSG00000026519	1	180942344	180975112	1	0	0	4	18	7	0	1530	1327	1168	65	602		Q91YT8
ENSMUST00000161524						2	3	0	3	1	3	0	0	0	0	1		
ENSMUST00000161525	ENSMUSG00000018909	7	99535466	99606771	1	9	3	19	6	16	8	0	0	0	0	0	E0CY53	
ENSMUST00000161526						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161527	ENSMUSG00000022553	15	76351294	76354380	1	0	0	0	0	0	1	350	460	394	62	202		Q9D0U6
ENSMUST00000161528	ENSMUSG00000024799	19	6062821	6068373	-1	0	0	0	6	0	0	0	0	0	0	0	Q3V3I6	
ENSMUST00000161530						47	29	218	70	71	28	0	2	0	0	2		
ENSMUST00000161531						1	1	1	2	1	0	5	6	13	7	72		
ENSMUST00000161532	ENSMUSG00000022286	15	37233036	37363569	1	0	2	0	0	0	0	0	0	0	0	0	F6TZV3	
ENSMUST00000161533						1	2	0	3	0	2	0	0	0	0	0		
ENSMUST00000161534						5	2	4	60	0	2	0	0	0	0	1		
ENSMUST00000161536						7	2	1	6	3	1	2	2	2	0	4		
ENSMUST00000161537						74	50	127	110	93	30	13	36	23	8	22		
ENSMUST00000161538	ENSMUSG00000029823	6	38551334	38609470	1	27	33	113	19	29	26	88	564	133	116	179		Q7TNC4
ENSMUST00000161539						15	23	13	3	13	10	0	0	1	0	0		
ENSMUST00000161541						1	1	0	1	1	0	4	28	5	3	4		
ENSMUST00000161542	ENSMUSG00000038425	18	70508680	70530620	-1	0	0	0	0	0	0	0	0	0	18	0		
ENSMUST00000161543						0	0	0	0	0	0	4	0	4	0	17		
ENSMUST00000161544						17	21	51	21	39	15	22	51	33	7	77		
ENSMUST00000161545	ENSMUSG00000030098	6	91761509	91827250	-1	3	0	4	7	6	0	0	0	0	0	0	F7BQ55	
ENSMUST00000161546	ENSMUSG00000047013	6	85469574	85502994	-1	47	36	86	0	0	0	2	0	0	1	3	Q3UGY7	Q6NS60
ENSMUST00000161547						4	3	20	13	5	0	0	0	0	0	0		
ENSMUST00000161548	ENSMUSG00000024792	19	6080762	6084944	-1	0	0	4	3	0	0	0	28	8	3	0	E0CZD9	
ENSMUST00000161549						1	1	2	0	0	2	0	0	0	1	0		
ENSMUST00000161550	ENSMUSG00000033487	14	72537946	72710003	-1	0	0	3	0	0	0	2	0	0	1	0	F7BWH4	
ENSMUST00000161551	ENSMUSG00000021481	13	55105311	55134825	1	0	0	0	0	0	0	0	0	0	0	0	E0CYH6	
ENSMUST00000161552						0	2	0	2	0	0	2	0	0	2	0		
ENSMUST00000161553	ENSMUSG00000054509	14	56575619	56659794	1	30	23	46	87	46	22	922	1843	1918	58	1243	E9PYK3	
ENSMUST00000161554						0	0	0	0	1	0	2	6	6	0	5		
ENSMUST00000161555						3	1	1	1	8	0	0	0	0	0	0		
ENSMUST00000161556						2	2	10	4	0	5	5	1	4	1	13		
ENSMUST00000161557	ENSMUSG00000048148	8	72646711	72714746	1	0	0	0	0	0	0	0	0	0	0	0	E0CY71	
ENSMUST00000161558						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161559	ENSMUSG00000005763	1	165788681	165877277	1	0	0	0	0	1	0	0	18	1	0	14	A2MZG6	
ENSMUST00000161560	ENSMUSG00000035459	10	86841198	87008025	-1	14	18	54	0	19	0	0	1	0	1	1	F7CNH8	
ENSMUST00000161561	ENSMUSG00000055737	15	3317760	3583492	-1	4	0	17	2	1	4	0	1	0	5	0	Q3UP14	
ENSMUST00000161562						16	15	23	14	14	9	1	10	2	12	1		
ENSMUST00000161563						9	6	15	16	10	15	0	0	0	0	0		
ENSMUST00000161564	ENSMUSG00000023032	15	100761747	100823968	1	1	0	0	8	0	0	0	0	0	1	0	E0CYV1	
ENSMUST00000161566	ENSMUSG00000030098	6	91761509	91827250	-1	2	1	0	45	6	3	0	0	0	0	0	E0CYS1	
ENSMUST00000161567	ENSMUSG00000026335	1	97795114	98095646	-1	14	35	233	0	26	20	861	2812	1449	186	664	E9Q704	
ENSMUST00000161568	ENSMUSG00000012422	13	90089123	90143907	1	45	68	53	73	63	41	304	927	315	433	205		Q9CR64
ENSMUST00000161569						2	4	8	2	3	0	6	22	12	0	2		
ENSMUST00000161570						0	0	1	2	0	0	0	1	0	0	0		
ENSMUST00000161572						0	0	0	26	0	0	0	65	96	225	61		
ENSMUST00000161573						0	0	0	3	2	0	0	105	5	17	5		
ENSMUST00000161574	ENSMUSG00000029634	5	146209192	146221555	-1	2	0	3	12	1	1	0	0	52	13	46	E0CYZ9	
ENSMUST00000161575						1	1	4	0	1	1	0	0	0	0	0		
ENSMUST00000161576	ENSMUSG00000031770	8	94386438	94395377	1	0	9	0	149	12	0	828	1298	799	195	536	Q3TMN9	Q9JJK5
ENSMUST00000161577						2	3	0	2	5	2	0	2	0	0	0		
ENSMUST00000161580						42	35	83	129	34	19	0	6	5	0	10		
ENSMUST00000161582	ENSMUSG00000020181	10	109682660	110456204	-1	0	7	0	0	0	0	0	0	0	1	5	F6SRT8	
ENSMUST00000161584						2	2	7	0	0	1	0	0	0	0	0		
ENSMUST00000161586	ENSMUSG00000034902	10	81292963	81319973	1	1	2	5	26	4	0	34	36	27	0	46	F6SMP3	
ENSMUST00000161587	ENSMUSG00000043592	17	48454901	48539714	1	0	0	0	0	0	0	2	13	0	0	17	F6TUJ1	
ENSMUST00000161589	ENSMUSG00000073530	1	158711727	158980490	-1	1	2	0	0	1	1	0	0	0	0	0	F6TFC9	
ENSMUST00000161590	ENSMUSG00000074604	3	51660360	51682677	1	0	0	0	0	0	0	25	22	17	47	22	E0CZ62	
ENSMUST00000161591						0	0	5	1	0	0	2	0	4	0	0		
ENSMUST00000161592	ENSMUSG00000054302	12	54670340	54695897	-1	121	84	228	124	86	68	73	478	61	128	100		Q5BU09
ENSMUST00000161593						0	1	0	0	2	0	8	81	43	5	16		
ENSMUST00000161594						0	0	9	2	2	2	0	6	6	0	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161595						86	102	259	121	93	65	24	159	48	18	54		
ENSMUST00000161596	ENSMUSG00000039047	3	152714100	152980408	1	7	2	3	5	3	3	0	6	0	3	0	E9Q421	
ENSMUST00000161598	ENSMUSG00000002679	12	81573557	81595008	-1	3	0	0	0	0	0	0	0	0	67	9	E0CYA6	
ENSMUST00000161600	ENSMUSG00000038174	1	58522806	58586323	-1	22	14	46	24	28	11	54	38	33	33	16		Q8C729
ENSMUST00000161601	ENSMUSG00000028717	4	115056426	115071755	1	0	0	0	77	0	0	11	0	8	1	1	Q3TZH7	P22091
ENSMUST00000161602						3	3	3	0	0	0	0	0	0	0	0		
ENSMUST00000161603						1	2	3	7	5	3	7	5	1	0	6		
ENSMUST00000161604						0	0	0	17	1	1	55	173	66	0	49		
ENSMUST00000161605	ENSMUSG00000019883	10	29313166	29346661	1	4	0	1	17	0	3	0	0	0	0	2	E0CXS3	
ENSMUST00000161606	ENSMUSG00000034908	9	45937857	45955247	-1	0	0	0	0	0	0	0	0	0	0	0	F7B6N2	
ENSMUST00000161608	ENSMUSG00000054770	1	57955101	58018956	-1	0	0	0	6	3	9	50	1	118	31	102	E9PYP3	
ENSMUST00000161609	ENSMUSG00000040423	1	160906418	160974978	1	28	23	32	131	32	19	481	1321	692	162	564		Q4VGL6
ENSMUST00000161610	ENSMUSG00000042096	5	114003703	114025682	1	0	0	0	0	12	0	0	0	0	0	0		
ENSMUST00000161611	ENSMUSG00000006014	1	150449412	150466165	-1	38	34	592	76	60	25	0	0	0	367	1931	E0CZ58	
ENSMUST00000161612	ENSMUSG00000022550	15	76576358	76595816	1	0	0	0	0	0	3	0	14	2	0	0	E0CXE8	
ENSMUST00000161613						3	6	14	1	10	4	0	0	0	0	0		
ENSMUST00000161615						0	0	0	0	0	0	1	2	0	0	0		
ENSMUST00000161616						0	0	1	0	2	0	0	0	0	0	18		
ENSMUST00000161617	ENSMUSG00000042279	6	115944938	115950236	1	0	0	0	0	0	0	0	0	0	0	0	E0CZ52	
ENSMUST00000161618						3	5	3	9	4	4	0	6	7	3	1		
ENSMUST00000161619	ENSMUSG00000038115	6	125690419	126040126	1	0	0	0	0	1	0	0	0	0	0	0	E0CZF2	
ENSMUST00000161620	ENSMUSG00000037902	2	129592835	129632228	1	1	0	0	0	0	1	0	0	0	0	0	E0CYM8	
ENSMUST00000161621						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161624						12702	14238	32298	12085	13042	6154	186	1035	388	89	344		
ENSMUST00000161625						3	5	4	5	2	1	0	0	0	0	0		
ENSMUST00000161627						4	4	7	3	3	2	4	27	4	12	0		
ENSMUST00000161628						1	0	0	0	0	0	11	125	12	1	15		
ENSMUST00000161629						0	0	0	0	0	0	0	0	0	12	0		
ENSMUST00000161630	ENSMUSG00000022529	16	3744093	3750790	1	0	18	39	0	0	0	45	2	14	0	17	E0CZ03	
ENSMUST00000161631						9	1	9	0	4	0	2	0	0	0	4		
ENSMUST00000161632	ENSMUSG00000026489	1	180165238	180199602	-1	3	3	0	0	1	1	93	46	152	4	47	F6T0A8	
ENSMUST00000161633						0	3	38	0	5	6	0	0	0	1	0		
ENSMUST00000161634						0	3	0	3	6	5	6	47	9	0	19		
ENSMUST00000161635						6	4	24	5	10	5	0	0	0	0	0		
ENSMUST00000161636	ENSMUSG00000030148	6	123106428	123143999	1	0	0	0	0	0	0	5	28	0	8	8	E0CYQ6	
ENSMUST00000161637						6	0	0	3	6	0	0	0	0	0	0		
ENSMUST00000161638	ENSMUSG00000034362	16	36119946	36131241	-1	0	0	3	0	0	0	0	0	0	0	0	E0CZ96	
ENSMUST00000161639	ENSMUSG00000021666	13	97137937	97181195	1	0	0	0	0	0	0	0	122	119	0	0		Q8R2Q4
ENSMUST00000161640	ENSMUSG00000025533	5	130011258	130029247	-1	0	0	0	0	0	0	158	168	160	0	84	E0CY49	
ENSMUST00000161641						2	0	3	1	0	2	349	258	206	13	157		
ENSMUST00000161642	ENSMUSG00000032000	9	7848699	7873186	-1	0	2	2	0	0	1	51	438	143	70	78	F7BQL8	
ENSMUST00000161644	ENSMUSG00000029406	5	124118690	124249760	-1	3	0	7	0	2	0	0	1	0	0	0	E0CXR4	
ENSMUST00000161645	ENSMUSG00000032534	9	102584598	102626534	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYR4	
ENSMUST00000161646						3	5	5	0	4	5	0	0	0	0	0		
ENSMUST00000161647	ENSMUSG00000075593	5	138264921	138272840	-1	2	0	0	0	0	0	0	13	13	0	11	E9Q7N6	
ENSMUST00000161648	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	0	3	0	0	0	0	0	0	E0CYI3	
ENSMUST00000161649	ENSMUSG00000071262	14	79212353	79247369	-1	0	0	27	0	0	0	0	0	0	0	0	Q3UT76	
ENSMUST00000161650	ENSMUSG00000053004	6	114397936	114483296	1	0	0	12	4	15	7	0	0	0	0	0	B3Y5T0	P70174
ENSMUST00000161651	ENSMUSG00000022313	15	51877429	51884614	1	0	0	0	0	0	0	9	0	0	16	0	E0CYI7	
ENSMUST00000161652	ENSMUSG00000029635	5	146231230	146302874	1	1	0	0	59	0	0	0	3	5	0	0	E0CYC4	
ENSMUST00000161653	ENSMUSG00000022311	15	47580637	48792063	-1	1	8	2	4	8	4	0	1	0	0	0	F6TRD7	
ENSMUST00000161654						2	3	2	0	9	0	0	0	5	4	0		
ENSMUST00000161655						9	5	4	14	4	4	0	0	0	0	0		
ENSMUST00000161656						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161657						0	0	0	71	0	0	0	0	0	0	0		
ENSMUST00000161658	ENSMUSG00000024112	17	25374285	25433783	-1	0	0	5	0	3	0	0	0	0	0	0	F6U5P7	
ENSMUST00000161659	ENSMUSG00000027822	3	63933507	63964768	-1	4	15	20	210	29	7	0	11	32	0	14		Q99J27
ENSMUST00000161660						0	0	0	0	2	0	0	0	2	0	0		
ENSMUST00000161662	ENSMUSG00000020329	10	79736123	79746581	-1	0	4	2	0	0	0	0	4	19	4	0	F6TLB0	
ENSMUST00000161663	ENSMUSG00000032295	9	57130690	57142722	1	0	0	13	0	4	0	0	65	49	0	53	E9PYM7	
ENSMUST00000161665	ENSMUSG00000075593	5	138264921	138272840	-1	0	0	0	0	0	2	1	0	0	0	0	E0CXV6	
ENSMUST00000161667						8	3	0	8	7	5	6	67	21	9	40		
ENSMUST00000161668						2	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000161669	ENSMUSG00000035953	14	50926070	50930856	-1	0	0	6	0	0	0	40	96	22	7	30	F7CNA9	
ENSMUST00000161670	ENSMUSG00000070448	14	51451962	51461293	1	1	2	0	2	0	0	0	0	0	0	0	L7N268	
ENSMUST00000161671						8	3	7	139	0	3	4	14	6	3	5		
ENSMUST00000161672						5	6	25	6	14	4	0	1	0	0	0		
ENSMUST00000161673						11	16	13	11	20	18	10	52	8	0	82		
ENSMUST00000161674						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161675	ENSMUSG00000089844	1	85083069	85109853	-1	0	0	0	0	0	0	9	0	22	44	13	E9Q3M7	
ENSMUST00000161676						7	1	3	21	4	0	0	0	1	0	0		
ENSMUST00000161677	ENSMUSG00000060780	6	77242689	77257791	1	6	0	0	0	0	0	0	0	0	0	0		Q8K377
ENSMUST00000161678	ENSMUSG00000023068	10	52417547	52440192	1	1	0	1	2	0	0	0	42	22	22	10	E0CXB8	
ENSMUST00000161679	ENSMUSG00000015127	17	25188397	25234443	1	3	1	7	11	3	3	0	0	0	0	13		Q5FWH2
ENSMUST00000161680	ENSMUSG00000040340	8	3470862	3487181	1	0	0	2	25	23	0	10	11	4	3	0	G3XA23	
ENSMUST00000161682						1	0	5	3	2	2	0	11	150	0	148		
ENSMUST00000161683						11	7	25	20	14	8	54	200	81	6	149		
ENSMUST00000161684	ENSMUSG00000009687	7	31032722	31042481	-1	0	2	7	89	14	3	156	335	183	280	236	Q3TDW1	P97808
ENSMUST00000161685	ENSMUSG00000052477	1	84992690	85270566	-1	63	50	57	51	58	20	14	187	37	17	48	F7D3Q7	
ENSMUST00000161686						12	12	16	12	23	7	10	7	6	1	12		
ENSMUST00000161687						29	38	105	43	39	5	4	8	6	6	5		
ENSMUST00000161689	ENSMUSG00000032280	9	61372366	61418497	1	0	2	0	123	8	4	0	0	0	0	0	E0CXU1	
ENSMUST00000161691	ENSMUSG00000036928	5	138280240	138312393	1	0	6	8	6	4	0	2	4	2	0	0	E0CXH6	
ENSMUST00000161692						39	29	50	104	59	29	1	0	1	1	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161693	ENSMUSG00000017485	14	16365179	16430787	1	0	0	0	0	0	1	17	287	7	14	26	F6XX57	
ENSMUST00000161694						2	0	5	3	1	0	0	7	0	0	3		
ENSMUST00000161695						5	10	26	4	7	5	0	0	0	1	0		
ENSMUST00000161696						101	107	224	116	101	46	15	55	25	2	43		
ENSMUST00000161698						0	0	0	0	0	0	99	193	68	328	26		
ENSMUST00000161699	ENSMUSG00000018501	11	62316426	62458541	-1	0	0	0	0	0	0	3	3	0	0	0	F6TWR1	
ENSMUST00000161700						0	0	11	30	8	0	0	0	0	0	0		
ENSMUST00000161701	ENSMUSG00000051375	18	38185914	38212053	-1	16	10	37	189	33	4	0	0	0	1	3	F7BJK1	
ENSMUST00000161702	ENSMUSG00000031647	8	60632827	60676729	1	5	2	2	6	2	2	0	0	0	0	0		Q9D3X9
ENSMUST00000161703	ENSMUSG00000034739	9	44101729	44109187	1	1	1	24	3	5	8	0	0	0	0	0	E0CXS1	
ENSMUST00000161704						5	3	2	5	5	1	0	0	0	0	3		
ENSMUST00000161705						1	4	7	3	2	4	13	106	17	20	42		
ENSMUST00000161707						6	2	11	1	10	9	0	46	2	0	0		
ENSMUST00000161708						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000161709						6	2	10	9	3	3	0	0	0	0	0		
ENSMUST00000161710						4	1	5	4	3	3	0	0	0	0	0		
ENSMUST00000161711	ENSMUSG00000052214	7	19228334	19256543	1	5	0	20	24	8	3	16	60	21	1	35		
ENSMUST00000161712	ENSMUSG00000079036	12	87425840	87444017	-1	6	10	29	0	5	0	21	25	11	0	49	E0CX46	
ENSMUST00000161713	ENSMUSG00000039661	8	31089471	31097047	1	11	5	7	3	11	0	0	0	0	0	0		Q9D700
ENSMUST00000161714						2	3	3	0	2	2	0	0	0	0	0		
ENSMUST00000161715						1	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000161716	ENSMUSG00000029207	5	66298703	66618784	-1	1	1	8	1	7	2	0	0	0	0	0	E0CYB2	
ENSMUST00000161717						6	1	1	0	3	0	10	13	3	3	4		
ENSMUST00000161718	ENSMUSG00000024799	19	6062821	6068373	-1	1	0	9	2	5	2	10	24	6	0	5	E0CYD6	
ENSMUST00000161719	ENSMUSG00000034902	10	81292963	81319973	1	1	0	6	3	0	1	0	0	0	0	0	F7C0X9	
ENSMUST00000161720						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000161722	ENSMUSG00000027860	3	102153583	102204693	-1	1	2	2	9	2	2	0	0	0	0	0		
ENSMUST00000161723						12	8	6	10	12	5	0	0	0	0	0		
ENSMUST00000161724	ENSMUSG00000089844	1	85083069	85109853	-1	3	14	4	0	2	1	9	85	23	57	44	E9Q422	
ENSMUST00000161725						2	1	11	6	8	4	0	1	3	0	9		
ENSMUST00000161726	ENSMUSG00000034544	3	66981390	67358396	1	0	0	0	13	0	0	0	0	0	0	0		Q9DBU6
ENSMUST00000161727						0	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000161728						1	1	0	15	2	0	0	0	0	1	0		
ENSMUST00000161729						53	44	115	66	73	28	3	14	5	1	19		
ENSMUST00000161730						6	3	5	3	9	4	1	4	4	1	14		
ENSMUST00000161731	ENSMUSG00000044042	2	113327736	113716767	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7P6	
ENSMUST00000161732	ENSMUSG00000022550	15	76576358	76595816	1	9	0	0	0	0	0	0	5	0	4	0	E0CXE8	
ENSMUST00000161734						2	0	2	1	1	0	0	0	0	0	0		
ENSMUST00000161736						0	7	0	2	1	0	11	24	153	30	333		
ENSMUST00000161737	ENSMUSG00000016194	1	193221634	193264075	-1	7	4	8	3	4	3	599	1788	604	1313	284	Q4JHD9	P50172
ENSMUST00000161738	ENSMUSG00000023830	17	12682406	12769664	-1	12	3	10	3	12	2	0	0	3	0	4	F6SFP4	
ENSMUST00000161739	ENSMUSG00000040669	6	122317731	122340561	-1	0	0	0	0	0	0	57	45	104	0	0	Q7TT35	
ENSMUST00000161740	ENSMUSG00000038925	14	24293214	24309966	1	14	5	0	0	0	0	0	0	0	0	0	E9PWE7	
ENSMUST00000161741	ENSMUSG00000038690	5	145183698	145192062	-1	0	4	7	10	3	2	251	427	270	1623	196		P56135
ENSMUST00000161743	ENSMUSG00000026489	1	180165238	180199602	-1	5	0	0	0	0	2	0	0	0	0	0	E0CYT4	
ENSMUST00000161744	ENSMUSG00000026478	1	153218922	153332786	-1	4	2	0	0	0	0	0	27	0	0	0	F6SFQ3	
ENSMUST00000161745	ENSMUSG00000069920	8	105252638	105255153	-1	0	0	0	134	3	0	0	0	0	0	0	F8WI62	
ENSMUST00000161746	ENSMUSG00000026489	1	180165238	180199602	-1	0	0	0	0	2	0	0	0	0	0	0	E0CXI5	
ENSMUST00000161747	ENSMUSG00000068037	17	12841079	12868143	-1	0	0	0	0	0	0	0	0	0	0	0	Q0VB49	P30554
ENSMUST00000161748						0	2	2	0	2	0	32	128	0	30	33		
ENSMUST00000161749						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161750						2	1	4	4	3	2	2	3	3	3	2		
ENSMUST00000161751	ENSMUSG00000056832	6	38381469	38427647	1	0	0	0	0	0	0	0	0	0	1	0	E0CYE0	
ENSMUST00000161752	ENSMUSG00000047003	15	75616679	75625300	1	0	0	6	72	6	2	0	1	3	0	2	E0CX66	
ENSMUST00000161753						5	7	5	5	9	2	2	7	1	0	6		
ENSMUST00000161754						12	9	7	7	14	2	0	1	0	3	1		
ENSMUST00000161755						1	3	1	2	2	2	2	2	5	0	4		
ENSMUST00000161756	ENSMUSG00000037434	1	191906767	191913247	1	3	4	0	15	0	0	0	0	22	8	2	F6TRQ3	
ENSMUST00000161757						1	4	3	73	8	2	0	0	0	0	0		
ENSMUST00000161758	ENSMUSG00000040325	9	106821874	106880992	1	18	0	60	14	0	10	54	155	88	29	87		Q80TR8
ENSMUST00000161760						24	34	101	94	33	10	4	12	0	2	4		
ENSMUST00000161761						2	2	8	7	0	2	0	0	0	0	0		
ENSMUST00000161762	ENSMUSG00000031781	8	94819818	94838358	-1	0	0	2	26	0	2	194	94	83	77	55	E0CYY1	
ENSMUST00000161764	ENSMUSG00000042349	1	131254343	131279606	-1	0	3	3	0	14	0	73	391	85	62	98	E9PYL6	
ENSMUST00000161765						31	11	178	146	31	8	0	13	0	0	6		
ENSMUST00000161766						9	2	13	59	12	5	0	0	2	0	6		
ENSMUST00000161767						0	0	0	0	1	0	45	258	71	23	84		
ENSMUST00000161768						2	2	6	2	7	4	0	0	0	0	0		
ENSMUST00000161769	ENSMUSG00000100725	1	178323074	178337728	-1	0	3	2	301	17	6	1300	8112	4362	766	2995	G3XA10	
ENSMUST00000161770	ENSMUSG00000055737	15	3317760	3583492	-1	4	1	11	9	8	0	0	1	0	0	0	E0CXS6	
ENSMUST00000161771						0	1	2	4	0	0	0	0	0	0	0		
ENSMUST00000161772						37	39	45	26	25	15	5	11	7	0	9		
ENSMUST00000161773	ENSMUSG00000050217	1	31176401	31204725	1	4	0	0	0	0	0	0	0	0	0	0	A0A087WQ68	
ENSMUST00000161774						0	0	0	2	0	4	0	36	0	17	4		
ENSMUST00000161775	ENSMUSG00000055692	16	17276300	17283229	1	0	0	0	0	0	0	0	0	0	0	0		Q9JJB1
ENSMUST00000161776	ENSMUSG00000027834	3	75557547	75643495	1	0	0	0	0	0	0	2	11	2	8	2	E0CYW0	
ENSMUST00000161777						6	4	8	4	8	4	0	0	0	1	0		
ENSMUST00000161778	ENSMUSG00000023010	15	99392882	99410049	1	0	0	16	4	0	4	66	48	64	8	86	E0CX98	
ENSMUST00000161779	ENSMUSG00000061436	6	38694390	38876165	-1	48	38	113	106	53	36	179	104	449	13	404		Q9QZR5
ENSMUST00000161780						2	0	0	0	0	0	0	0	5	23	0		
ENSMUST00000161781						87	91	82	83	101	44	13	50	19	9	115		
ENSMUST00000161782						9	11	7	33	9	7	0	0	0	0	0		
ENSMUST00000161783						0	0	0	8	14	0	0	0	0	0	7		
ENSMUST00000161784						3	6	8	5	4	2	0	9	1	0	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161785	ENSMUSG00000047003	15	75616679	75625300	1	0	0	54	6	24	0	22	22	38	4	19		Q02526
ENSMUST00000161786						0	0	0	31	2	0	0	0	0	0	0		
ENSMUST00000161787						5	3	6	5	12	0	0	0	1	1	0		
ENSMUST00000161788	ENSMUSG00000046152	8	31187331	31261738	1	13	14	17	9	16	13	5	6	6	0	0		Q5F2L2
ENSMUST00000161789	ENSMUSG00000009291	10	77581720	77598732	1	0	0	0	0	0	0	0	0	0	0	0	E0CXQ8	
ENSMUST00000161790						2	4	15	0	1	6	5	0	12	81	53		
ENSMUST00000161791						192	124	598	166	204	86	18	39	15	27	36		
ENSMUST00000161792	ENSMUSG00000031781	8	94819818	94838358	-1	0	0	0	0	0	0	92	75	59	40	39	F7BWP1	
ENSMUST00000161793						0	0	0	0	0	1	0	0	0	1	0		
ENSMUST00000161794						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161795	ENSMUSG00000046111	9	15316915	15357788	-1	2	0	9	0	0	0	0	65	28	1	0		Q8BQ48
ENSMUST00000161796	ENSMUSG00000066456	9	83109948	83146685	-1	0	0	0	0	0	0	8	0	3	43	7		Q9DCB1
ENSMUST00000161798						4	2	0	2	0	1	0	0	0	0	0		
ENSMUST00000161799						2	1	3	5	2	3	1	0	0	0	0		
ENSMUST00000161800	ENSMUSG00000048782	7	114743694	114850383	1	4	6	2	0	10	1	0	0	0	0	0	E0CXR9	
ENSMUST00000161801	ENSMUSG00000021219	12	82588292	83162056	1	15	4	9	120	7	7	0	0	0	0	0	Q3UTM5	
ENSMUST00000161802	ENSMUSG00000045962	6	119923969	120038672	-1	0	0	0	0	1	0	73	173	223	23	139	F6S7V4	
ENSMUST00000161803	ENSMUSG00000019848	10	45178098	45318452	1	6	3	0	0	6	3	0	0	0	0	0	E0CZB6	
ENSMUST00000161804	ENSMUSG00000029673	5	131437333	132543344	-1	39	23	95	259	73	30	2	0	0	0	0	E9PZ86	
ENSMUST00000161805	ENSMUSG00000009687	7	31032722	31042481	-1	6	5	13	20	15	3	1881	2239	1631	2180	1196	Q3TDW1	P97808
ENSMUST00000161806						7	4	3	0	4	2	0	0	1	1	1		
ENSMUST00000161807	ENSMUSG00000079197	14	55587441	55591113	-1	0	0	0	12	3	0	332	560	256	1460	279	Q5SVP3	P97372
ENSMUST00000161808						14	6	27	140	21	8	3	48	41	2	32		
ENSMUST00000161809						5	5	6	8	2	5	8	218	6	2	34		
ENSMUST00000161810	ENSMUSG00000025977	1	55248658	55363469	-1	2	0	0	0	0	1	0	0	0	0	0	M0QWZ3	
ENSMUST00000161811	ENSMUSG00000060780	6	77242689	77257791	1	1	5	0	24	4	4	0	0	0	0	0	E0CX41	
ENSMUST00000161812	ENSMUSG00000022150	15	6299788	6440712	1	0	0	0	0	0	0	0	0	4	18	0	E9PX84	
ENSMUST00000161813	ENSMUSG00000064202	19	28893042	28967800	-1	2	4	3	5	3	1	0	0	0	0	0	E0CYX4	
ENSMUST00000161814	ENSMUSG00000026489	1	180165238	180199602	-1	0	0	0	12	0	1	0	0	0	0	0	E0CXR6	
ENSMUST00000161816						5	8	32	0	0	0	20	139	24	28	22		
ENSMUST00000161817	ENSMUSG00000044164	13	43615710	43670945	1	0	0	0	0	0	0	0	0	0	0	0	E0CZ87	
ENSMUST00000161818	ENSMUSG00000003721	1	121304353	121332589	-1	0	2	0	47	0	4	3	0	0	5	0	E0CYQ1	
ENSMUST00000161821	ENSMUSG00000073481	1	184813068	184846451	-1	0	1	0	3	2	0	65	152	50	60	69	E0CZH6	
ENSMUST00000161824						0	1	14	2	1	0	0	0	0	0	0		
ENSMUST00000161825	ENSMUSG00000021666	13	97137937	97181195	1	15	8	21	23	15	11	23	113	51	11	84	E9Q7N5	
ENSMUST00000161827	ENSMUSG00000029510	5	138273655	138280005	-1	0	0	0	22	0	0	11	31	8	0	5		Q8BKV1
ENSMUST00000161828	ENSMUSG00000041528	9	108051534	108083346	-1	1	0	4	4	4	0	5	9	2	0	23	E0CXL3	
ENSMUST00000161829						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000161830						0	0	0	0	0	0	0	28	0	7	3		
ENSMUST00000161831						3	8	4	6	10	0	12	0	0	0	0		
ENSMUST00000161832						0	0	0	0	0	0	0	1	3	8	1		
ENSMUST00000161833						0	0	0	31	4	0	0	0	0	0	2		
ENSMUST00000161834	ENSMUSG00000084786	9	20642878	20647140	1	0	0	0	0	0	0	6	37	0	34	6	G3UWR6	
ENSMUST00000161836						8	2	15	5	2	2	3	2	0	0	8		
ENSMUST00000161837	ENSMUSG00000021790	14	41072911	41092197	1	4	0	0	2	0	3	0	0	0	0	0	E0CXB0	
ENSMUST00000161838	ENSMUSG00000041879	1	135382312	135430499	-1	3	1	0	63	0	0	0	0	1	0	0	E0CY46	
ENSMUST00000161839						4	3	13	104	8	0	0	0	0	0	3		
ENSMUST00000161840						3	0	11	61	3	2	13	28	61	0	78		
ENSMUST00000161842						0	0	10	6	3	2	6	37	2	2	15		
ENSMUST00000161843						11	8	5	13	19	13	30	63	36	8	31		
ENSMUST00000161844						1	0	0	32	1	1	0	0	0	0	0		
ENSMUST00000161845	ENSMUSG00000038690	5	145183698	145192062	-1	2	1	4	0	0	0	0	10	3	2	5	F6USF4	
ENSMUST00000161846	ENSMUSG00000063063	6	76881637	77979699	-1	9	11	0	25	16	2	0	0	0	0	0		Q61301
ENSMUST00000161847	ENSMUSG00000026519	1	180942344	180975112	1	2	1	0	39	1	0	2	4	7	0	11	E0CX44	
ENSMUST00000161849						10	6	22	6	16	8	6	18	11	70	2		
ENSMUST00000161850	ENSMUSG00000036879	8	85840959	86061376	1	3	1	0	4	3	0	6	0	0	4	8	E0CX43	
ENSMUST00000161851						4	2	1	0	1	3	0	0	0	0	0		
ENSMUST00000161852						0	2	8	0	1	5	0	0	5	0	0		
ENSMUST00000161853						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000161854	ENSMUSG00000034902	10	81292963	81319973	1	0	0	0	0	24	27	564	496	666	75	353	E0CYP4	
ENSMUST00000161855	ENSMUSG00000093536	7	6398715	6432093	1	2	0	7	0	6	0	0	0	0	0	0	A0A504	
ENSMUST00000161856	ENSMUSG00000043639	19	53677306	53867080	1	31	0	71	0	48	4	0	0	0	0	1	F6TAZ4	
ENSMUST00000161858						113	110	427	179	139	85	1	2	10	3	8		
ENSMUST00000161859	ENSMUSG00000029634	5	146209192	146221555	-1	0	5	0	52	5	5	228	400	412	56	193		Q9DBU5
ENSMUST00000161860						11	17	30	11	16	6	6	3	0	0	0		
ENSMUST00000161861	ENSMUSG00000022788	16	16416917	16600549	-1	46	42	93	41	33	23	1072	1630	1051	920	848		Q91ZT5
ENSMUST00000161863	ENSMUSG00000022416	15	80287238	80398279	1	0	0	0	55	2	0	0	0	0	0	0	F6TAX9	
ENSMUST00000161864	ENSMUSG00000059149	1	132022806	132068062	-1	0	0	0	0	0	0	0	0	0	0	0	E0CX35	
ENSMUST00000161865	ENSMUSG00000026407	1	136052750	136119822	1	0	3	0	0	3	0	0	0	0	0	0	F7CNJ1	
ENSMUST00000161866	ENSMUSG00000038550	3	95878503	95882251	-1	0	0	3	9	0	2	0	4	5	1	1	H3BJP8	
ENSMUST00000161867	ENSMUSG00000038550	3	95878503	95882251	-1	3	2	0	1	2	0	0	2	0	1	0	F6U6T6	
ENSMUST00000161869	ENSMUSG00000034902	10	81292963	81319973	1	0	0	0	0	2	0	54	24	18	5	28	F6TL71	
ENSMUST00000161870	ENSMUSG00000056888	10	111985448	112002631	-1	0	0	0	0	0	0	24	395	11	37	4	G3UYI2	
ENSMUST00000161871						7	3	3	7	3	3	0	0	0	0	0		
ENSMUST00000161872						3	0	1	1	1	0	0	0	6	0	0		
ENSMUST00000161873	ENSMUSG00000018821	19	42123273	42129059	-1	7	2	8	6	4	2	3	0	0	0	0	E0CXY9	
ENSMUST00000161874						0	0	0	1	0	0	12	127	0	25	8		
ENSMUST00000161875						3	0	1	0	4	4	3	26	5	0	7		
ENSMUST00000161876						1	1	0	1	1	2	0	13	7	5	21		
ENSMUST00000161877						21	14	57	9	14	15	0	0	12	0	9		
ENSMUST00000161878						0	4	0	0	1	0	0	0	0	0	0		
ENSMUST00000161879	ENSMUSG00000029207	5	66298703	66618784	-1	0	1	55	8	0	0	0	0	0	0	2	E0CZA9	
ENSMUST00000161880	ENSMUSG00000026514	1	181352628	181460641	1	4	1	3	49	12	0	0	0	0	0	0	Q9D6E1	
ENSMUST00000161881	ENSMUSG00000055991	5	145204562	145221750	1	0	0	0	0	0	0	1	0	1	0	0	F6SSC9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161882	ENSMUSG00000084786	9	20642878	20647140	1	1	0	0	0	1	0	3	90	11	14	20	E0CZB3	
ENSMUST00000161883	ENSMUSG00000020592	12	8771323	8793715	1	0	4	16	51	5	2	0	0	0	0	1	E0CYT6	
ENSMUST00000161884	ENSMUSG00000025533	5	130011258	130029247	-1	0	0	1	0	0	0	4	0	3	0	5	E0CYV3	
ENSMUST00000161885	ENSMUSG00000061207	17	34823993	34836945	-1	0	2	0	18	0	0	0	2	0	0	0	F6SFN2	
ENSMUST00000161886	ENSMUSG00000025221	19	45791839	45816061	-1	0	0	0	0	0	0	0	0	0	0	0	Q3YAB1	
ENSMUST00000161887	ENSMUSG00000084786	9	20642878	20647140	1	0	0	0	0	0	0	751	241	397	1276	241	E0CYW1	
ENSMUST00000161888	ENSMUSG00000072572	14	51892889	51896745	1	0	0	0	0	0	0	0	0	0	0	0	E0CY93	
ENSMUST00000161889						6	1	26	4	5	10	0	2	0	0	15		
ENSMUST00000161891						1	1	0	0	2	0	4	12	4	0	9		
ENSMUST00000161892	ENSMUSG00000022452	15	82338959	82349091	1	0	0	4	0	0	5	58	117	94	35	31	E0CXP9	
ENSMUST00000161894						36	28	32	28	41	25	1	2	2	5	6		
ENSMUST00000161895	ENSMUSG00000060579	14	9550092	11162035	-1	0	2	0	0	1	1	0	0	0	0	0	E9PVU9	
ENSMUST00000161896	ENSMUSG00000055991	5	145204562	145221750	1	3	0	0	0	0	0	0	0	0	0	0	E0CX87	
ENSMUST00000161897						0	0	0	53	6	0	0	6	0	0	3		
ENSMUST00000161898	ENSMUSG00000069135	17	8165501	8196804	1	0	0	0	0	0	0	7	17	16	16	16	F6UTB8	
ENSMUST00000161899						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161900	ENSMUSG00000063931	7	34912379	35044708	1	0	3	0	0	0	0	3	0	2	0	0	G3UXC5	
ENSMUST00000161901						3	4	3	0	3	1	0	0	1	0	3		
ENSMUST00000161902	ENSMUSG00000002679	12	81573557	81595008	-1	0	0	0	0	2	0	0	0	0	0	0	E0CXQ3	
ENSMUST00000161904	ENSMUSG00000062040	7	29893333	29906572	-1	14	14	8	14	7	5	0	2	0	0	0		P10077
ENSMUST00000161905						0	2	6	0	6	4	10	45	13	3	8		
ENSMUST00000161906						0	1	4	0	1	0	0	1	0	0	0		
ENSMUST00000161907	ENSMUSG00000053080	19	7417625	7425904	1	0	0	0	208	2	0	0	0	0	0	0	A0A087WPN4	
ENSMUST00000161908	ENSMUSG00000026584	1	163929100	163955126	1	0	9	0	0	4	0	178	581	247	41	153		Q9DBQ7
ENSMUST00000161909	ENSMUSG00000037254	2	10094593	10131396	-1	0	2	0	0	0	0	0	0	0	0	0	E0CX69	
ENSMUST00000161910						10	3	3	6	5	5	0	0	0	0	0		
ENSMUST00000161911						0	0	1	2	0	1	0	0	0	0	0		
ENSMUST00000161912						29	27	77	253	55	21	8	28	21	3	20		
ENSMUST00000161913	ENSMUSG00000021666	13	97137937	97181195	1	0	2	12	0	0	0	4	0	0	0	4	Q8C1C2	
ENSMUST00000161915	ENSMUSG00000001844	5	143316489	143329256	-1	0	6	19	1	12	2	13	62	63	0	9		Q9D6H5
ENSMUST00000161918	ENSMUSG00000027942	3	90051636	90068347	1	0	2	3	3	0	3	21	120	0	43	0	E0CYZ4	
ENSMUST00000161919						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000161920	ENSMUSG00000035834	13	81673843	81711013	-1	0	0	0	0	0	0	0	0	0	0	0		Q6NXY9
ENSMUST00000161922						17	26	6	23	19	13	1	0	0	0	0		
ENSMUST00000161926						1	2	1	2	0	1	0	0	0	0	0		
ENSMUST00000161927	ENSMUSG00000071324	10	41914990	42018442	-1	0	0	0	2	0	0	0	0	0	0	0	Q8BTB2	
ENSMUST00000161928						10	7	6	60	10	4	0	1	0	0	0		
ENSMUST00000161929	ENSMUSG00000021666	13	97137937	97181195	1	5	2	7	29	5	1	1	8	1	0	1	E0CXH2	
ENSMUST00000161930						1	0	10	1	2	0	0	0	1	0	2		
ENSMUST00000161931	ENSMUSG00000045114	7	127017531	127021211	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161932	ENSMUSG00000040969	3	133112278	133234949	-1	3	4	0	2	2	2	0	0	0	0	0	E0CXB4	
ENSMUST00000161933						11	5	37	10	28	14	0	0	0	0	0		
ENSMUST00000161934	ENSMUSG00000041879	1	135382312	135430499	-1	0	0	2	0	0	0	0	31	5	6	15	F6TLX3	
ENSMUST00000161935						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000161936						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161937	ENSMUSG00000045648	1	70725715	70885397	1	9	0	19	0	0	0	0	0	0	0	0		Q505H4
ENSMUST00000161938	ENSMUSG00000029406	5	124118690	124249760	-1	16	7	71	196	35	9	7	2	8	0	25		Q6ZPQ6
ENSMUST00000161941						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000161942						0	0	4	2	4	1	17	21	24	0	29		
ENSMUST00000161944						12	4	12	7	6	2	41	110	11	114	27		
ENSMUST00000161945						1	4	4	19	4	1	0	0	0	0	0		
ENSMUST00000161946						4	7	19	7	7	9	0	0	0	1	0		
ENSMUST00000161947						1	0	4	2	1	0	2	49	12	2	20		
ENSMUST00000161948	ENSMUSG00000023009	15	99422035	99457748	-1	0	0	0	0	0	0	0	0	2	0	0	E0CYV6	
ENSMUST00000161949	ENSMUSG00000027508	3	9687479	9833679	-1	79	60	407	345	102	74	4570	9054	7207	356	5197	A6H659	Q3U1F9
ENSMUST00000161950	ENSMUSG00000039021	2	32757026	32775633	-1	1	0	18	0	0	0	0	0	0	0	0	Q3V0B6	
ENSMUST00000161951						4	4	4	1	6	3	0	0	1	1	3		
ENSMUST00000161952						0	0	1	37	0	0	0	2	2	0	3		
ENSMUST00000161953						2	0	4	6	8	0	0	0	1	0	0		
ENSMUST00000161954	ENSMUSG00000049690	1	125913620	126830799	-1	31	0	47	129	41	0	0	0	0	0	0	Q6NZK2	
ENSMUST00000161955						0	0	0	0	0	0	15	23	13	0	0		
ENSMUST00000161956						38	38	41	37	44	36	0	0	3	1	3		
ENSMUST00000161957						2	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000161958	ENSMUSG00000039021	2	32757026	32775633	-1	0	0	0	20	0	0	0	0	0	0	0	E0CYM6	
ENSMUST00000161959						1	1	2	2	6	1	0	0	0	0	0		
ENSMUST00000161960	ENSMUSG00000070870	1	65048554	65051149	-1	2	2	3	3	4	5	0	0	0	0	0	E0CXE4	
ENSMUST00000161961						2	0	1	0	2	1	0	0	0	0	0		
ENSMUST00000161962						11	11	45	22	22	12	14	52	37	6	79		
ENSMUST00000161963						0	3	0	0	5	0	0	0	0	0	0		
ENSMUST00000161964	ENSMUSG00000027692	3	28263214	28675858	1	2	0	0	0	14	0	0	0	0	0	0	E0CZF8	
ENSMUST00000161966	ENSMUSG00000038473	1	170302668	170589861	-1	0	0	0	219	4	0	13	33	48	0	12	E9PYK5	
ENSMUST00000161967						4	5	4	0	14	6	0	0	3	0	2		
ENSMUST00000161968						3	3	0	4	7	0	0	0	0	0	0		
ENSMUST00000161969	ENSMUSG00000042279	6	115944938	115950236	1	0	2	0	0	14	0	0	0	0	0	0		Q8VIK3
ENSMUST00000161970	ENSMUSG00000026885	2	35751241	35979913	-1	0	0	0	0	26	0	0	7	0	0	5	E0CZ80	
ENSMUST00000161971	ENSMUSG00000005763	1	165788681	165877277	1	0	0	0	0	0	0	0	0	5	2	0	Q3UU54	
ENSMUST00000161972	ENSMUSG00000062200	3	64690660	64844765	-1	0	21	3	14	0	0	0	0	0	0	0	E9PYL5	
ENSMUST00000161973						31	18	60	44	10	7	0	0	0	0	0		
ENSMUST00000161974						3	1	10	6	2	1	3	40	3	16	17		
ENSMUST00000161976	ENSMUSG00000022346	15	61985341	61990374	1	0	0	0	31	2	6	16	14	17	0	21		P01108
ENSMUST00000161977	ENSMUSG00000021461	13	63304709	63497278	-1	6	6	7	9	17	0	11	8	0	0	6	Q8CBR3	
ENSMUST00000161978	ENSMUSG00000032118	9	36821939	36878924	1	8	12	38	4	8	4	0	0	0	0	0	F7BWM9	
ENSMUST00000161979						15	17	71	14	12	8	0	1	0	1	0		
ENSMUST00000161980	ENSMUSG00000004151	12	38779380	38868215	1	8	2	10	0	0	0	0	0	0	0	3	E0CXD2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000161982						5	2	0	2	4	1	8	6	8	0	16		
ENSMUST00000161983						30	23	40	11	25	11	0	3	0	0	0		
ENSMUST00000161984	ENSMUSG00000029510	5	138273655	138280005	-1	0	0	0	0	0	0	0	0	30	0	25	M0QWK4	
ENSMUST00000161986	ENSMUSG00000031985	8	124863033	124890057	1	1	0	0	37	8	0	0	4	42	0	31	Q05DV2	
ENSMUST00000161987	ENSMUSG00000019979	10	90989311	91082770	-1	64	73	163	71	79	48	6	24	25	10	30	Q80VR5	
ENSMUST00000161988						3	6	8	18	7	2	0	0	3	0	0		
ENSMUST00000161989	ENSMUSG00000021816	14	20499364	20546573	-1	5	5	1	7	0	1	56	68	36	8	13	E9Q6P2	
ENSMUST00000161990						4	2	2	3	10	1	0	0	0	0	0		
ENSMUST00000161991	ENSMUSG00000033083	14	101442360	101609191	-1	22	0	15	0	0	0	0	0	11	0	0	E9Q6Q8	
ENSMUST00000161992						3	3	3	1	3	0	0	0	0	0	0		
ENSMUST00000161993	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	38	0	142	0	86	E0CY76	
ENSMUST00000161994	ENSMUSG00000038550	3	95878503	95882251	-1	0	0	8	0	7	0	0	0	0	0	0	E0CYK0	
ENSMUST00000161995	ENSMUSG00000032502	9	111561437	111690348	-1	14	0	7	14	1	9	1	2	0	0	0	F2Z462	
ENSMUST00000161996						6	0	12	0	4	3	0	0	0	0	0		
ENSMUST00000161997	ENSMUSG00000022181	15	4727175	4815456	1	0	0	0	0	0	0	0	0	0	0	4	Q8BRY4	
ENSMUST00000161998	ENSMUSG00000036523	12	16670615	16800886	-1	0	0	0	56	3	3	0	0	0	0	0	E0CYD8	
ENSMUST00000162000	ENSMUSG00000030329	6	124996694	125003096	1	4	5	7	6	5	3	2	4	3	0	3		
ENSMUST00000162001	ENSMUSG00000041515	8	120736358	120756694	1	3	3	35	7	18	2	0	0	4	0	4	Q544J7	P23611
ENSMUST00000162002						10	5	7	280	11	8	1	0	0	0	0		
ENSMUST00000162003	ENSMUSG00000026150	1	82724890	82752394	1	0	0	0	0	0	5	20	99	47	10	20	E0CYB9	
ENSMUST00000162004	ENSMUSG00000025188	19	42755105	42779978	-1	1	3	2	13	16	0	477	196	372	21	218		
ENSMUST00000162005						3	2	6	0	0	1	0	1	2	13	8		
ENSMUST00000162006						10	18	0	19	11	5	0	2	0	0	0		
ENSMUST00000162007	ENSMUSG00000025920	1	16228674	16520112	-1	0	0	0	0	0	0	12	25	30	12	19		Q8CJ67
ENSMUST00000162008	ENSMUSG00000038240	10	43221486	43464882	1	0	0	0	0	0	0	4	23	0	0	0	F6T4Z4	
ENSMUST00000162009						6	5	0	0	2	2	6	22	0	5	0		
ENSMUST00000162010						0	0	0	0	0	0	1	0	0	7	4		
ENSMUST00000162011	ENSMUSG00000064294	1	58113130	58200698	1	4	2	18	8	5	2	0	0	1	0	0	A0A087WQC8	
ENSMUST00000162012						1	0	0	0	1	0	1	1	1	0	0		
ENSMUST00000162013						38	46	154	81	67	29	11	6	0	0	4		
ENSMUST00000162014	ENSMUSG00000052616	8	104446719	104509910	-1	1	0	0	59	2	1	0	0	0	0	0		Q8C0V1
ENSMUST00000162015						4	3	5	3	4	4	0	0	0	0	0		
ENSMUST00000162017	ENSMUSG00000028931	4	152390742	152477871	-1	0	2	2	0	0	0	3	1	0	0	3	E0CYS2	
ENSMUST00000162018						3	0	9	12	8	4	0	41	0	0	9		
ENSMUST00000162019						3	2	0	3	0	1	2	1	3	0	0		
ENSMUST00000162020	ENSMUSG00000063605	8	94902869	94918098	-1	2	4	1	64	8	1	0	0	0	0	0	E0CYE3	
ENSMUST00000162021	ENSMUSG00000033200	17	25369273	25374442	1	4	0	0	5	3	0	0	0	0	0	0	E9Q7E3	
ENSMUST00000162022	ENSMUSG00000052942	19	28258851	28680077	-1	80	54	196	577	131	55	66	127	127	5	109	Q0GE24	
ENSMUST00000162023	ENSMUSG00000020079	10	62429209	62449738	-1	15	13	101	0	26	0	33	99	22	0	20	M0QWM4	
ENSMUST00000162024						3	2	3	9	7	3	0	6	8	5	12		
ENSMUST00000162025	ENSMUSG00000022416	15	80287238	80398279	1	0	0	0	0	0	0	0	0	0	0	0	F7BQ85	
ENSMUST00000162026						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000162028						2	0	0	0	1	0	0	0	0	2	0		
ENSMUST00000162029	ENSMUSG00000023999	17	49615136	49909847	1	2	6	0	38	2	4	0	0	0	0	1	E0CXK4	
ENSMUST00000162030						10	7	6	2	3	5	0	11	4	4	0		
ENSMUST00000162031	ENSMUSG00000058407	1	37985189	37997893	-1	15	6	33	27	15	14	115	339	129	194	121		Q9CQ79
ENSMUST00000162032						1	6	5	15	3	3	0	0	0	0	0		
ENSMUST00000162033	ENSMUSG00000022613	15	89334398	89337015	1	0	0	2	0	5	0	0	0	0	0	0	F6VA44	
ENSMUST00000162034	ENSMUSG00000089862	6	8259288	8459470	1	0	0	0	22	0	0	32	60	20	22	25	E0CYC9	
ENSMUST00000162035						12	8	6	5	9	7	0	0	0	0	0		
ENSMUST00000162036	ENSMUSG00000034544	3	66981390	67358396	1	0	0	19	0	0	0	17	4	18	80	18		Q9DBU6
ENSMUST00000162037						8	10	0	6	0	5	0	0	0	0	0		
ENSMUST00000162038	ENSMUSG00000052760	1	85717083	85778643	-1	1	0	3	3	8	2	38	179	102	36	97	Q8C9T1	
ENSMUST00000162039						3	2	6	1	1	1	2	11	6	4	6		
ENSMUST00000162040						8	5	19	59	2	3	2	2	2	0	2		
ENSMUST00000162041	ENSMUSG00000038039	10	58255497	58305599	1	12	0	0	0	5	6	74	190	26	43	40	E9PWI6	
ENSMUST00000162043						1	1	0	0	3	0	27	0	19	0	13		
ENSMUST00000162044	ENSMUSG00000016624	15	84785381	84856049	-1	9	7	0	0	0	2	3	0	0	1	2	E9PVV0	
ENSMUST00000162045						26	17	47	47	29	12	6	54	37	19	30		
ENSMUST00000162046	ENSMUSG00000094672	6	123822814	123853190	-1	9	7	10	6	14	7	0	0	0	0	0	W4VSP2	
ENSMUST00000162047						0	0	0	0	0	0	148	516	165	9	147		
ENSMUST00000162048						21	18	23	30	22	12	0	0	46	0	26		
ENSMUST00000162049	ENSMUSG00000023032	15	100761747	100823968	1	8	10	6	0	9	7	5	0	10	1	25		Q8JZR6
ENSMUST00000162050						12	7	6	6	21	7	0	0	0	0	0		
ENSMUST00000162052						0	4	17	0	6	4	0	0	2	0	0		
ENSMUST00000162053	ENSMUSG00000024640	19	15904678	15947337	-1	24	14	19	73	19	13	1	0	26	0	16	Q3U6K9	
ENSMUST00000162054	ENSMUSG00000022335	15	68083766	68258856	-1	16	9	21	34	42	24	165	347	251	30	208		Q7TS63
ENSMUST00000162055	ENSMUSG00000061207	17	34823993	34836945	-1	0	0	0	0	1	0	6	24	12	0	5	F6XXB9	
ENSMUST00000162056						6	3	9	3	1	1	10	3	13	0	18		
ENSMUST00000162057	ENSMUSG00000022744	16	58727910	58734251	1	0	0	0	28	2	2	26	0	37	0	6		Q9CQX5
ENSMUST00000162059						6	2	20	3	3	0	0	1	2	0	3		
ENSMUST00000162060	ENSMUSG00000027833	3	66971727	66981771	-1	0	0	4	0	2	0	0	1	0	0	0		
ENSMUST00000162061	ENSMUSG00000025188	19	42755105	42779978	-1	0	4	1	0	0	0	7	0	23	0	3	E9PYL0	
ENSMUST00000162063						0	0	0	0	0	0	0	0	3	0	0		
ENSMUST00000162064						0	1	7	1	2	0	17	7	41	0	28		
ENSMUST00000162065	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DCB4
ENSMUST00000162066	ENSMUSG00000001844	5	143316489	143329256	-1	0	0	0	0	0	0	14	15	3	2	12	E0CXP7	
ENSMUST00000162067						0	2	3	0	3	1	0	1	0	0	1		
ENSMUST00000162069	ENSMUSG00000030680	7	127015033	127017352	-1	3	0	0	0	8	0	58	271	165	61	146	F6V0H0	
ENSMUST00000162070						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000162071						0	0	0	13	0	0	0	36	0	0	5		
ENSMUST00000162072	ENSMUSG00000034908	9	45937857	45955247	-1	0	0	0	0	0	0	8	2	12	0	13	E0CXC7	
ENSMUST00000162073	ENSMUSG00000032059	9	50775019	50843542	1	0	7	1	0	10	0	2	45	33	0	20	E0CZF3	
ENSMUST00000162074	ENSMUSG00000037720	5	67260565	67291461	1	2	0	1	0	4	0	0	4	0	2	4	E0CYW6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162075	ENSMUSG00000038991	13	38500273	38528824	-1	9	5	12	43	11	6	0	0	0	0	35		
ENSMUST00000162076						0	5	7	0	1	0	0	0	0	0	2		
ENSMUST00000162077						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000162078						0	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000162079						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000162080						10	5	18	4	13	0	7	3	5	0	0		
ENSMUST00000162081						0	2	1	2	2	0	0	0	0	0	0		
ENSMUST00000162082						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000162084	ENSMUSG00000042279	6	115944938	115950236	1	13	7	33	0	0	8	0	0	0	0	0	E0CYL2	
ENSMUST00000162085	ENSMUSG00000055692	16	17276300	17283229	1	0	0	0	0	0	0	0	8	4	4	11	E0CYG5	
ENSMUST00000162086	ENSMUSG00000021470	13	63815240	63900302	1	12	16	28	5	11	6	8	86	31	41	45	F7DFI4	
ENSMUST00000162087	ENSMUSG00000009687	7	31032722	31042481	-1	0	0	0	0	0	0	5499	10342	3919	21009	4348	Q3TDW1	P97808
ENSMUST00000162088						18	1	81	7	0	11	17	199	0	0	28		
ENSMUST00000162090						4	3	11	7	1	3	5	0	2	0	0		
ENSMUST00000162091						10	10	8	5	8	8	0	0	0	0	0		
ENSMUST00000162092	ENSMUSG00000021917	14	30999826	31001672	-1	7	0	0	0	0	0	0	0	0	0	9		Q9D958
ENSMUST00000162093	ENSMUSG00000006542	1	74738922	74749221	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXJ7	
ENSMUST00000162094	ENSMUSG00000022150	15	6299788	6440712	1	4	1	0	1	2	0	0	0	0	0	0	E0CZ53	
ENSMUST00000162096	ENSMUSG00000066861	5	120876142	120887613	-1	11	0	6	0	6	5	58	394	27	16	89	Q05BJ7	
ENSMUST00000162097	ENSMUSG00000032503	9	112065091	112235938	-1	8	0	0	0	0	0	0	0	0	0	0		Q9DCB4
ENSMUST00000162098	ENSMUSG00000027833	3	66971727	66981771	-1	0	0	3	0	4	1	0	2	0	0	0	F6UTR6	
ENSMUST00000162099	ENSMUSG00000003500	6	29200434	29216364	-1	0	0	0	0	0	0	18	39	46	0	47		P50096
ENSMUST00000162100						0	3	3	0	1	0	12	0	0	0	2		
ENSMUST00000162101	ENSMUSG00000029673	5	131437333	132543344	-1	4	1	0	0	0	0	0	0	0	0	2	S4R200	
ENSMUST00000162102						3	1	0	2	1	1	2	37	9	0	14		
ENSMUST00000162103						3	6	0	3	6	2	0	0	0	0	0		
ENSMUST00000162104						3	3	16	10	12	1	0	0	0	0	0		
ENSMUST00000162105						2	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000162106	ENSMUSG00000054302	12	54670340	54695897	-1	0	0	0	10	0	0	5	11	32	176	32	E0CYG0	
ENSMUST00000162107						1	0	1	3	1	0	0	0	0	0	0		
ENSMUST00000162108	ENSMUSG00000030729	7	100227394	100278868	1	0	0	19	0	2	0	7	2	19	1	10	E0CX81	
ENSMUST00000162109	ENSMUSG00000061950	17	65782573	65841926	1	0	0	0	0	12	0	1	946	0	0	0	E0CXK8	
ENSMUST00000162110	ENSMUSG00000064202	19	28893042	28967800	-1	2	4	5	0	0	0	0	0	2	0	0	F6UU42	
ENSMUST00000162111						42	45	100	93	95	47	7	25	9	3	9		
ENSMUST00000162112	ENSMUSG00000036523	12	16670615	16800886	-1	0	0	68	0	72	0	0	0	0	0	0		Q3UHK3
ENSMUST00000162114	ENSMUSG00000027942	3	90051636	90068347	1	99	138	274	166	96	60	86	219	96	36	155		Q8R092
ENSMUST00000162116	ENSMUSG00000009687	7	31032722	31042481	-1	0	0	0	0	0	0	0	0	31	279	34	Q3TDW1	P97808
ENSMUST00000162117	ENSMUSG00000037577	17	32183770	32189549	-1	3	0	0	3	8	1	0	0	0	0	0	G3XA19	
ENSMUST00000162118	ENSMUSG00000060743	1	180800832	180813943	-1	0	0	0	42	0	2	0	19	14	14	57	E0CYR7	
ENSMUST00000162119	ENSMUSG00000068037	17	12841079	12868143	-1	0	0	0	0	0	0	0	0	0	0	0	E0CX40	
ENSMUST00000162120						4	5	12	1	6	4	0	2	0	1	3		
ENSMUST00000162122						3	5	12	3	5	2	0	4	0	1	0		
ENSMUST00000162123						3	1	1	0	5	2	0	0	0	0	0		
ENSMUST00000162124						0	0	0	0	0	0	4	0	12	0	0		
ENSMUST00000162125						8	6	41	12	6	4	6	19	11	0	12		
ENSMUST00000162126	ENSMUSG00000053128	9	44066327	44113517	-1	5	2	3	77	2	1	0	0	0	0	0		Q8BUH7
ENSMUST00000162127	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	128	0	3	4	542	F6TS96	
ENSMUST00000162128						1	3	8	7	2	0	0	0	0	1	1		
ENSMUST00000162129						0	0	0	17	0	1	0	0	0	0	0		
ENSMUST00000162130	ENSMUSG00000039153	17	44495987	44814797	-1	0	0	0	0	0	0	2	0	6	0	7	F6TRA6	
ENSMUST00000162131	ENSMUSG00000021990	14	60634001	60764556	1	6	6	7	6	8	1	2	0	2	0	13	F6SRZ4	
ENSMUST00000162132	ENSMUSG00000043592	17	48454901	48539714	1	0	0	0	0	0	0	2	1	0	2	4	F6TRC7	
ENSMUST00000162134						0	0	0	0	0	0	150	84	62	20	0		
ENSMUST00000162135						0	0	2	0	0	1	0	2	4	0	0		
ENSMUST00000162136	ENSMUSG00000038421	1	170917576	170927583	-1	0	0	0	0	0	0	0	0	0	8	0	E0CX78	
ENSMUST00000162137						5	2	4	85	3	5	0	0	0	0	1		
ENSMUST00000162138	ENSMUSG00000027835	3	75516490	75556856	-1	0	2	6	20	1	0	0	144	58	0	0	E0CY82	
ENSMUST00000162139						7	2	17	5	9	4	0	0	2	0	0		
ENSMUST00000162140						1	5	7	3	1	1	0	0	0	0	0		
ENSMUST00000162141						0	0	1	0	1	0	6	1	2	0	2		
ENSMUST00000162142						176	192	997	731	325	178	2	5	12	7	29		
ENSMUST00000162143						8	28	22	21	27	17	1	0	0	0	1		
ENSMUST00000162144	ENSMUSG00000037747	10	70557682	70655965	-1	0	0	0	0	0	0	0	0	0	0	0	F6U6Z2	
ENSMUST00000162145						856	830	1446	968	910	436	140	855	249	38	243		
ENSMUST00000162146	ENSMUSG00000058318	2	92093117	92364666	1	0	0	0	7	1	0	0	5	0	0	19	E0CYN5	
ENSMUST00000162147	ENSMUSG00000029334	5	98929773	99037351	-1	2	8	0	4	13	10	0	0	0	61	17	Q3TMJ2	
ENSMUST00000162149						0	1	9	7	3	0	0	0	0	0	5		
ENSMUST00000162150	ENSMUSG00000041957	16	16213318	16272712	1	11	17	10	199	9	6	0	0	1	0	2	E0CX59	
ENSMUST00000162151	ENSMUSG00000033210	16	45535309	45607001	1	0	0	5	0	6	0	0	0	0	0	0	M0QW97	
ENSMUST00000162152						0	0	5	76	0	1	0	0	0	0	0		
ENSMUST00000162153	ENSMUSG00000021684	13	95024454	95250336	-1	0	7	6	0	0	1	0	0	0	0	0	E9PX38	
ENSMUST00000162154						0	2	0	97	0	3	24	99	20	66	46		
ENSMUST00000162155	ENSMUSG00000022416	15	80287238	80398279	1	14	8	0	417	23	7	0	0	0	0	0	E0CXK2	
ENSMUST00000162156	ENSMUSG00000028101	3	96696384	96706070	1	12	5	63	9	12	3	35	118	37	5	70	H3BLM4	
ENSMUST00000162157						16	18	33	10	15	7	0	7	9	0	10		
ENSMUST00000162158	ENSMUSG00000089773	4	112006269	112029538	1	0	0	2	0	4	0	0	0	0	0	0		A7TZE6
ENSMUST00000162159	ENSMUSG00000021090	12	72441866	72514334	1	6	10	0	13	13	4	0	0	0	0	0		Q8CDN9
ENSMUST00000162160	ENSMUSG00000022635	15	93386097	93398334	-1	0	0	0	0	2	0	0	0	0	0	0		Q9CZ96
ENSMUST00000162161	ENSMUSG00000020077	10	62493833	62527451	-1	2	0	0	0	0	0	711	19940	8063	38928	8013		P13609
ENSMUST00000162162						7	3	4	11	6	2	0	5	0	1	5		
ENSMUST00000162164	ENSMUSG00000041625	14	122816223	122913757	-1	0	0	2	42	2	2	2	1	0	0	0	E0CZ04	
ENSMUST00000162165						2	0	2	2	0	0	0	0	0	0	2		
ENSMUST00000162166	ENSMUSG00000090061	5	63649102	63810546	1	1	0	2	162	4	0	0	0	0	0	0	E0CY00	
ENSMUST00000162167						2	0	0	6	2	3	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162168	ENSMUSG00000055991	5	145204562	145221750	1	0	0	6	5	4	0	0	0	5	0	3	F6TRS7	
ENSMUST00000162169						0	0	0	0	0	0	0	22	0	0	4		
ENSMUST00000162170	ENSMUSG00000030329	6	124996694	125003096	1	16	11	15	2	27	10	35	32	19	11	35		Q6P1B3
ENSMUST00000162172	ENSMUSG00000026885	2	35751241	35979913	-1	3	0	6	1	0	5	0	0	1	0	0	E0CXL9	
ENSMUST00000162173	ENSMUSG00000022335	15	68083766	68258856	-1	8	17	16	0	2	3	0	0	0	0	0	E0CX30	
ENSMUST00000162174						4	4	7	2	2	0	0	4	2	0	11		
ENSMUST00000162175	ENSMUSG00000061244	14	49012146	49066653	-1	14	3	0	128	15	0	272	808	365	160	318		Q3TPX4
ENSMUST00000162176	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	1	Q4JJC0	
ENSMUST00000162177	ENSMUSG00000006289	14	50906478	50924893	-1	1	0	6	16	6	2	0	0	0	0	3	E0CYN9	
ENSMUST00000162178	ENSMUSG00000018042	15	83153494	83172592	-1	25	17	75	40	26	15	5	4	9	1	16	F2Z456	
ENSMUST00000162179						5	0	8	0	3	2	0	0	0	0	0		
ENSMUST00000162180						2	0	6	0	4	0	0	0	0	0	0		
ENSMUST00000162181	ENSMUSG00000022949	16	92485736	92541243	1	0	1	0	1	5	2	0	0	0	0	0	E0CY42	
ENSMUST00000162182	ENSMUSG00000045648	1	70725715	70885397	1	0	0	0	0	0	0	0	0	0	0	0		Q505H4
ENSMUST00000162183	ENSMUSG00000035845	15	88805244	88819318	-1	12	0	0	65	11	11	84	107	93	0	109		Q8VDB2
ENSMUST00000162184	ENSMUSG00000038658	19	29522282	29606829	1	12	12	74	75	15	7	0	3	0	0	1		Q69ZJ7
ENSMUST00000162185	ENSMUSG00000030226	6	138362918	138581968	-1	3	0	1	9	0	1	0	0	0	1	0	E0CYK7	
ENSMUST00000162187	ENSMUSG00000050526	1	134385940	134390981	1	11	5	4	16	8	6	0	1	4	1	3	G3XA12	
ENSMUST00000162188	ENSMUSG00000058318	2	92093117	92364666	1	0	0	4	0	0	0	11	0	9	0	26	E0CZ79	
ENSMUST00000162189						6	3	9	3	2	4	0	0	0	0	0		
ENSMUST00000162190	ENSMUSG00000045962	6	119923969	120038672	-1	2	1	0	5	0	0	0	0	0	0	0	F7B663	
ENSMUST00000162191	ENSMUSG00000022744	16	58727910	58734251	1	0	0	1	0	0	0	0	23	0	0	22	E0CY63	
ENSMUST00000162192						0	0	1	3	3	1	2	0	0	0	5		
ENSMUST00000162193						5	3	4	12	7	4	29	55	103	5	102		
ENSMUST00000162194	ENSMUSG00000023019	15	99717515	99725005	1	1	0	7	0	0	0	0	0	1	2	0	E0CXN5	
ENSMUST00000162196						0	0	0	0	3	3	0	1	0	0	0		
ENSMUST00000162197						7	5	21	7	15	4	1	2	2	0	4		
ENSMUST00000162199						8	2	10	8	0	1	0	0	0	0	1		
ENSMUST00000162200						3	0	0	15	3	0	0	0	0	0	0		
ENSMUST00000162201	ENSMUSG00000056306	3	54897068	54915887	-1	8	0	13	1	0	0	0	0	0	0	0		Q8CD78
ENSMUST00000162202	ENSMUSG00000049109	10	28668360	28883818	1	17	23	20	15	13	5	3	3	0	0	4	E0CY68	
ENSMUST00000162204						5	2	10	18	7	7	2	8	12	0	29		
ENSMUST00000162205						0	0	0	40	0	2	0	0	0	0	0		
ENSMUST00000162206						225	277	210	96	176	66	0	0	5	0	38		
ENSMUST00000162207	ENSMUSG00000022529	16	3744093	3750790	1	7	11	43	11	12	5	46	813	55	31	81	E9PXW0	
ENSMUST00000162208						0	2	0	28	0	0	0	2	0	2	0		
ENSMUST00000162210						4	4	3	125	3	2	0	0	22	2	13		
ENSMUST00000162211						6	3	3	7	10	4	0	0	0	0	0		
ENSMUST00000162214						42	43	213	44	44	13	1	6	0	0	2		
ENSMUST00000162215	ENSMUSG00000003500	6	29200434	29216364	-1	0	0	0	88	0	0	0	0	3	6	0	E0CXK0	
ENSMUST00000162216						0	0	2	2	2	0	0	0	0	0	0		
ENSMUST00000162217						2	1	6	1	1	4	5	10	5	2	2		
ENSMUST00000162219	ENSMUSG00000029634	5	146209192	146221555	-1	0	0	0	0	0	1	0	0	39	6	29	F6VG71	
ENSMUST00000162220	ENSMUSG00000029627	5	145194946	145201868	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYH2	
ENSMUST00000162221	ENSMUSG00000045404	12	99964499	100062682	1	7	0	37	277	3	0	0	0	0	0	0	E0CX83	
ENSMUST00000162222						13	11	5	13	16	8	0	1	0	0	0		
ENSMUST00000162223						3	4	10	2	10	4	7	30	13	22	18		
ENSMUST00000162224	ENSMUSG00000038925	14	24293214	24309966	1	2	9	9	7	1	7	2	1	0	0	0	E0CX49	
ENSMUST00000162225						5	2	6	1	0	1	0	0	0	0	0		
ENSMUST00000162226	ENSMUSG00000043467	1	161002922	161034849	-1	323	300	1487	350	353	182	206	403	268	35	335	Q8C3U9	
ENSMUST00000162227						35	29	211	45	45	14	1	3	1	0	5		
ENSMUST00000162228	ENSMUSG00000058239	7	30945248	30956803	-1	0	0	0	0	0	0	4	6	7	0	0	F8WI12	
ENSMUST00000162230						30	23	117	25	28	21	4	17	11	0	15		
ENSMUST00000162232						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000162233						1	7	0	4	3	4	0	0	0	0	0		
ENSMUST00000162234	ENSMUSG00000026584	1	163929100	163955126	1	12	0	0	5	17	5	88	97	201	77	286		Q9DBQ7
ENSMUST00000162235	ENSMUSG00000032118	9	36821939	36878924	1	0	0	0	0	0	1	0	0	0	0	0	F6TRI8	
ENSMUST00000162236	ENSMUSG00000018501	11	62316426	62458541	-1	5	1	0	0	0	0	18	0	0	0	0	F6SFD2	
ENSMUST00000162237	ENSMUSG00000024949	19	6363690	6378030	1	0	1	0	28	0	0	22	7	45	5	25	F6SRV1	
ENSMUST00000162238						5	10	48	9	13	4	2	21	9	4	10		
ENSMUST00000162240	ENSMUSG00000038084	16	29579334	29654884	1	0	0	0	0	2	0	0	0	0	0	2	F6U775	
ENSMUST00000162241						2	2	5	1	1	0	3	70	24	8	34		
ENSMUST00000162242	ENSMUSG00000003500	6	29200434	29216364	-1	3	8	27	0	0	0	0	8	0	19	0	F6XXH9	
ENSMUST00000162243						10	10	4	11	16	9	3	17	9	2	8		
ENSMUST00000162244	ENSMUSG00000029625	5	145167213	145182041	1	0	0	4	3	4	2	122	92	46	43	93	B2LVG6	
ENSMUST00000162245	ENSMUSG00000036928	5	138280240	138312393	1	0	0	0	0	0	7	42	24	0	2	2		O70576
ENSMUST00000162246	ENSMUSG00000066456	9	83109948	83146685	-1	0	0	0	80	5	3	0	0	0	13	0		Q9DCB1
ENSMUST00000162247	ENSMUSG00000079036	12	87425840	87444017	-1	0	9	0	17	0	2	0	88	24	0	0	E0CYA7	
ENSMUST00000162248						7	2	8	4	5	4	2	0	0	0	0		
ENSMUST00000162249						3	0	14	1	9	4	2	14	8	2	9		
ENSMUST00000162250	ENSMUSG00000009687	7	31032722	31042481	-1	0	0	0	3	0	0	616	3059	244	1152	348	F6TWM7	
ENSMUST00000162251	ENSMUSG00000037747	10	70557682	70655965	-1	4	5	10	3	1	0	0	0	0	0	0	F7D3N3	
ENSMUST00000162252	ENSMUSG00000036395	9	26763044	26806468	-1	11	13	43	7	16	9	0	0	0	0	0	E0CY86	
ENSMUST00000162253						3	5	5	1	4	7	0	0	0	0	0		
ENSMUST00000162254						2	0	0	0	0	0	0	0	0	0	5		
ENSMUST00000162255						2	0	0	14	0	2	11	7	0	0	0		
ENSMUST00000162256						4	2	23	4	9	5	6	42	4	3	7		
ENSMUST00000162257	ENSMUSG00000025907	1	6206197	6276648	1	4	0	6	0	0	0	195	1201	465	121	171	F7CCJ3	
ENSMUST00000162258						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000162260						0	0	1	2	1	1	0	0	0	0	0		
ENSMUST00000162261						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000162263						1	0	0	2	0	0	0	0	5	4	0		
ENSMUST00000162264	ENSMUSG00000046111	9	15316915	15357788	-1	0	1	0	0	0	0	0	12	0	0	4	F6V9M5	
ENSMUST00000162265	ENSMUSG00000051050	18	44027869	44032208	1	1	0	0	1	0	1	0	0	0	0	0	B9EJP9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162266	ENSMUSG00000001524	17	35667730	35673739	-1	3	3	2	7	6	3	0	0	0	0	2	E0CYK8	
ENSMUST00000162267	ENSMUSG00000032998	4	119537004	119629119	1	1	0	0	0	2	1	0	0	0	0	3	Q3TAY5	
ENSMUST00000162269	ENSMUSG00000036834	3	63696234	63899472	-1	7	13	0	0	0	0	0	0	0	0	0		Q4KWH5
ENSMUST00000162270						0	0	0	13	1	0	0	0	0	0	0		
ENSMUST00000162271	ENSMUSG00000021977	14	59133040	59142893	-1	5	6	36	8	4	3	0	0	0	0	0	E0CXJ8	
ENSMUST00000162272	ENSMUSG00000061950	17	65782573	65841926	1	0	3	5	7	2	1	27	22	71	0	16	F6TLH3	
ENSMUST00000162273	ENSMUSG00000063063	6	76881637	77979699	-1	50	43	315	87	52	26	0	1	2	0	4	Q8BS72	
ENSMUST00000162274	ENSMUSG00000023010	15	99392882	99410049	1	2	0	5	3	2	4	8	14	9	0	10	E0CZE8	
ENSMUST00000162275						0	0	7	2	0	0	0	0	0	0	0		
ENSMUST00000162276						17	14	44	25	21	7	3	17	18	15	28		
ENSMUST00000162277	ENSMUSG00000021072	12	70453095	70468040	1	1	0	0	0	0	0	8	203	144	74	57	F6V084	
ENSMUST00000162278	ENSMUSG00000060579	14	9550092	11162035	-1	0	0	0	0	0	0	0	0	0	0	0		O89106
ENSMUST00000162279						4	1	6	29	4	1	3	0	0	0	0		
ENSMUST00000162280	ENSMUSG00000042873	6	113168090	113195384	-1	203	141	905	757	236	103	0	16	5	0	3		Q5U4E0
ENSMUST00000162281						0	0	0	0	0	3	5	0	5	4	0		
ENSMUST00000162282						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000162283	ENSMUSG00000026519	1	180942344	180975112	1	0	0	0	55	0	0	0	0	0	0	0	E0CXH8	
ENSMUST00000162284						1	0	6	0	2	0	8	10	6	0	0		
ENSMUST00000162285						3	0	21	11	0	4	2	10	15	0	12		
ENSMUST00000162286						11	8	11	13	16	5	0	0	0	0	0		
ENSMUST00000162287						0	0	0	0	0	0	64	36	39	12	22		
ENSMUST00000162288						7	2	1	0	4	1	3	0	2	0	4		
ENSMUST00000162290	ENSMUSG00000018909	7	99535466	99606771	1	2	0	0	1	1	3	0	9	9	0	17	F7DF62	
ENSMUST00000162291	ENSMUSG00000073664	1	60180599	60338328	1	5	7	3	2	0	1	6	9	37	3	9	F7BJ98	
ENSMUST00000162292	ENSMUSG00000021684	13	95024454	95250336	-1	0	0	0	0	0	0	0	0	0	0	0	E9PYP0	
ENSMUST00000162293	ENSMUSG00000030098	6	91761509	91827250	-1	65	64	118	153	102	38	6	26	8	4	9	E0CXE0	
ENSMUST00000162294	ENSMUSG00000090206	8	95310566	95326323	1	1	1	4	0	6	2	28	25	16	5	16	F6TW27	
ENSMUST00000162295	ENSMUSG00000032452	9	97444395	98033181	-1	57	50	244	100	78	33	1	0	0	0	4		Q9ER65
ENSMUST00000162296						0	2	0	0	1	2	0	0	0	0	0		
ENSMUST00000162297	ENSMUSG00000032534	9	102584598	102626534	-1	0	0	0	22	0	0	0	1	0	0	5	E0CZ48	
ENSMUST00000162298						3	3	11	1	5	0	0	0	0	1	0		
ENSMUST00000162300	ENSMUSG00000030098	6	91761509	91827250	-1	0	0	0	49	7	0	0	0	0	0	0	G3XA20	
ENSMUST00000162301	ENSMUSG00000024231	18	3382988	3436377	1	0	0	0	0	0	0	2	33	0	0	0		Q9D4H8
ENSMUST00000162302						9	7	26	9	7	4	2	19	4	0	10		
ENSMUST00000162303	ENSMUSG00000084786	9	20642878	20647140	1	3	7	5	5	8	3	49	82	49	110	33		Q9EPV8
ENSMUST00000162305						0	6	7	10	7	1	11	290	25	40	22		
ENSMUST00000162307						9	13	19	1	9	1	0	4	0	1	0		
ENSMUST00000162308	ENSMUSG00000038722	5	145140362	145148078	1	0	0	0	0	0	0	0	36	0	16	7		Q6PGH1
ENSMUST00000162309	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	64	0	0	0	0	0	0	0	G3XA13	
ENSMUST00000162310						14	10	90	8	5	2	1	13	5	0	4		
ENSMUST00000162312						18	9	12	0	2	4	0	283	0	17	0		
ENSMUST00000162313	ENSMUSG00000043592	17	48454901	48539714	1	5	5	0	17	0	3	0	0	0	0	0	E0CXQ5	
ENSMUST00000162314						2	2	3	5	6	0	0	0	0	0	0		
ENSMUST00000162316	ENSMUSG00000037787	12	111713261	111754980	1	39	41	71	47	50	30	9	57	33	2	34	E9Q6C3	
ENSMUST00000162317	ENSMUSG00000000215	7	142678656	142699510	-1	3	0	1	2	0	0	0	0	0	0	0	E0CXX7	
ENSMUST00000162319	ENSMUSG00000022558	15	76380261	76453038	1	0	0	0	0	0	0	5	0	0	0	0	E9PYI5	
ENSMUST00000162320						0	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000162321	ENSMUSG00000033287	15	78428564	78438909	1	0	0	0	0	5	0	0	0	4	2	0	F7B6A4	
ENSMUST00000162322						0	0	3	0	1	3	0	0	0	0	0		
ENSMUST00000162323	ENSMUSG00000022500	16	10959275	11066157	-1	2	1	8	29	3	3	0	0	0	2	0	E0CYR5	
ENSMUST00000162324						0	2	14	1	4	1	1	0	0	1	1		
ENSMUST00000162326	ENSMUSG00000039233	13	13997949	14039638	-1	0	0	0	0	0	0	11	0	0	96	0	E0CZ81	
ENSMUST00000162327	ENSMUSG00000042605	5	121711337	121816493	1	0	1	0	0	0	0	0	8	27	0	42	F6V8M6	
ENSMUST00000162328						1	1	0	116	5	4	0	0	0	0	0		
ENSMUST00000162329						7	10	3	10	5	1	0	0	0	0	0		
ENSMUST00000162330						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000162331						169	124	700	153	200	115	2	9	10	1	16		
ENSMUST00000162332						2	2	2	43	2	2	0	0	0	0	0		
ENSMUST00000162333	ENSMUSG00000068037	17	12841079	12868143	-1	0	0	0	0	0	0	0	0	0	0	0	Q0VB49	P30554
ENSMUST00000162335	ENSMUSG00000038876	10	29344178	29362442	-1	15	16	3	3	4	12	147	1072	481	498	306		Q9CZW6
ENSMUST00000162336						25	18	23	31	19	12	1	7	14	3	8		
ENSMUST00000162337						4	0	8	13	8	4	6	27	13	6	10		
ENSMUST00000162338						1	0	6	8	3	1	2	0	0	1	0		
ENSMUST00000162339	ENSMUSG00000022386	15	85879312	85897394	1	0	0	0	0	0	0	0	0	0	0	2	F7CNH0	
ENSMUST00000162340						4	2	2	2	2	1	0	4	1	3	4		
ENSMUST00000162341						9	11	25	17	14	11	0	7	2	2	2		
ENSMUST00000162342	ENSMUSG00000054702	1	79606876	79671972	-1	7422	9963	5769	6279	5029	1745	185	570	217	67	219		Q7TN05
ENSMUST00000162343						1	2	2	2	4	2	0	0	0	0	0		
ENSMUST00000162344						0	0	0	36	0	2	0	0	0	0	0		
ENSMUST00000162345						1	0	0	43	0	0	0	0	0	0	0		
ENSMUST00000162346						3	1	5	8	0	0	0	0	0	0	3		
ENSMUST00000162349	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	0	0	0	0	0	0	1	0	Q3TIZ5	Q9DBR4
ENSMUST00000162350	ENSMUSG00000022181	15	4727175	4815456	1	8	2	6	6	4	2	0	0	0	0	0	E9Q6D8	
ENSMUST00000162351						0	0	0	0	0	0	25	0	47	5	19		
ENSMUST00000162352						4	0	2	219	0	2	0	1	0	0	0		
ENSMUST00000162354	ENSMUSG00000022555	15	76502015	76511951	-1	1	0	1	0	0	0	85	332	48	13	94	F6UUI9	
ENSMUST00000162355	ENSMUSG00000041528	9	108051534	108083346	-1	4	2	5	140	7	1	59	93	152	3	100		Q5XPI3
ENSMUST00000162356	ENSMUSG00000021957	14	30548359	30574722	1	0	0	0	28	1	1	0	0	27	0	0	E0CY51	
ENSMUST00000162357						0	0	0	0	0	0	4	0	0	0	0		
ENSMUST00000162358	ENSMUSG00000001844	5	143316489	143329256	-1	0	0	0	0	0	0	0	0	4	0	0	E0CY85	
ENSMUST00000162359	ENSMUSG00000061436	6	38694390	38876165	-1	0	0	16	0	0	1	32	16	41	1	42	Q5D0E9	Q9QZR5
ENSMUST00000162360	ENSMUSG00000038690	5	145183698	145192062	-1	0	0	0	3	0	0	25	138	48	72	55	M0QWW1	
ENSMUST00000162361						6	2	16	5	4	1	0	0	1	3	2		
ENSMUST00000162362	ENSMUSG00000034544	3	66981390	67358396	1	0	2	0	44	4	2	0	0	0	2	0	E0CZ17	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162363						2	4	1	148	8	2	0	0	0	0	1		
ENSMUST00000162364	ENSMUSG00000025979	1	55131231	55154899	1	62	71	181	84	55	33	167	802	173	395	137		Q6PEB6
ENSMUST00000162365	ENSMUSG00000044176	18	62548911	62661366	1	0	0	0	0	0	3	0	1	0	1	0	E0CXN2	
ENSMUST00000162366	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TDW6	
ENSMUST00000162367	ENSMUSG00000006014	1	150449412	150466165	-1	0	0	0	0	0	0	0	0	0	74	4		
ENSMUST00000162368	ENSMUSG00000045962	6	119923969	120038672	-1	0	0	0	0	0	0	34	67	175	3	152	F7CBK9	
ENSMUST00000162369						29	29	62	203	34	24	12	46	25	5	45		
ENSMUST00000162371	ENSMUSG00000014980	1	152370735	152386688	-1	0	0	0	1	0	0	0	0	0	0	0	E0CY96	
ENSMUST00000162372	ENSMUSG00000029221	5	67306955	67358443	1	20	25	29	41	23	14	122	388	187	100	181		Q5IRJ6
ENSMUST00000162373	ENSMUSG00000039153	17	44495987	44814797	-1	2	0	0	0	0	0	10	2	0	0	19	E0CY45	
ENSMUST00000162374	ENSMUSG00000100621	19	6076945	6082256	-1	7	10	21	63	9	8	0	0	0	1	0	F6SG70	
ENSMUST00000162375	ENSMUSG00000021461	13	63304709	63497278	-1	1	0	4	1	1	2	0	0	0	0	0	E0CXC4	
ENSMUST00000162376	ENSMUSG00000021578	13	74350309	74365783	1	0	0	0	0	0	2	17	79	47	111	31	E0CYX9	
ENSMUST00000162378	ENSMUSG00000036395	9	26763044	26806468	-1	3	1	2	8	2	0	0	0	0	0	0	E0CYW9	
ENSMUST00000162379	ENSMUSG00000034908	9	45937857	45955247	-1	5	4	12	0	2	0	0	3	0	0	76	F6SV01	
ENSMUST00000162382	ENSMUSG00000029207	5	66298703	66618784	-1	0	1	0	0	0	0	0	0	0	0	0	E0CYJ4	
ENSMUST00000162383	ENSMUSG00000029638	6	8509600	8597548	1	0	0	0	0	2	1	0	4	0	0	4	E0CXI8	
ENSMUST00000162384	ENSMUSG00000003360	15	98645134	98662889	-1	0	0	5	45	9	3	0	2	5	2	6	E0CXN3	
ENSMUST00000162385	ENSMUSG00000042298	11	62281473	62328451	1	0	0	0	0	0	0	0	0	0	0	3	F7BCD5	
ENSMUST00000162386	ENSMUSG00000029823	6	38551334	38609470	1	0	0	4	0	0	0	0	0	0	0	0	E0CYQ8	
ENSMUST00000162387	ENSMUSG00000095550	5	25948253	25954417	-1	12	3	13	9	7	6	0	0	0	0	0	G3UY31	
ENSMUST00000162388	ENSMUSG00000042184	5	113692422	113724772	-1	3	9	29	6	3	2	0	0	0	0	0	E0CYD9	
ENSMUST00000162389	ENSMUSG00000068037	17	12841079	12868143	-1	1	0	3	0	0	0	0	0	0	0	0	E0CX70	
ENSMUST00000162390						11	3	7	12	6	7	57	151	24	0	15		
ENSMUST00000162392						26	12	49	49	26	12	487	1656	829	43	1216		
ENSMUST00000162393	ENSMUSG00000033852	2	120027493	120043033	1	0	24	0	0	42	0	0	19	13	0	0	E0CXG8	
ENSMUST00000162394						1	5	16	4	0	1	1	9	6	3	18		
ENSMUST00000162395	ENSMUSG00000060475	17	12966796	12992546	-1	0	1	2	0	1	3	0	0	0	0	1	E0CZF5	
ENSMUST00000162396	ENSMUSG00000042121	5	113937094	113993894	-1	0	1	6	3	0	3	0	2	4	0	1	F7CBJ9	
ENSMUST00000162397						2	0	0	0	0	0	50	169	43	10	20		
ENSMUST00000162398						0	0	0	3	1	1	0	0	0	0	0		
ENSMUST00000162399						4	3	24	8	3	3	0	0	0	0	0		
ENSMUST00000162401						0	2	12	9	6	5	0	0	0	0	0		
ENSMUST00000162402						0	4	2	5	4	2	0	0	0	0	1		
ENSMUST00000162403	ENSMUSG00000037989	13	49036303	49148014	-1	0	0	0	10	0	0	0	1	0	0	2	E9Q6Q2	
ENSMUST00000162404	ENSMUSG00000018909	7	99535466	99606771	1	0	0	0	5	0	0	2	0	0	0	0	E0CYB1	
ENSMUST00000162405	ENSMUSG00000071324	10	41914990	42018442	-1	1	3	4	5	3	0	0	0	0	1	0	Q8BTB2	
ENSMUST00000162406						3	2	0	0	0	0	0	0	1	0	0		
ENSMUST00000162408						12	20	115	11	11	11	0	1	0	0	3		
ENSMUST00000162409	ENSMUSG00000039735	3	122538719	122619715	-1	20	17	29	88	23	8	21	65	18	21	34	E9PUK3	
ENSMUST00000162410						0	0	0	0	7	0	17	0	6	0	0		
ENSMUST00000162411						4	3	5	3	3	1	1	0	0	0	9		
ENSMUST00000162412	ENSMUSG00000021684	13	95024454	95250336	-1	3	6	5	4	17	8	0	0	0	0	0	E9PXX4	
ENSMUST00000162413	ENSMUSG00000022858	16	22244549	22266005	-1	0	6	0	0	0	11	117	338	140	481	168		
ENSMUST00000162414						1	3	6	186	15	0	0	4	0	0	4		
ENSMUST00000162415	ENSMUSG00000005610	7	111070568	111083030	-1	15	10	25	67	15	10	1089	3791	1920	629	1273	G3XA17	
ENSMUST00000162416	ENSMUSG00000024640	19	15904678	15947337	-1	0	1	0	0	0	0	2	0	0	0	11	E9Q6P1	
ENSMUST00000162417						1	1	9	1	6	6	3	7	3	0	7		
ENSMUST00000162418						5	10	8	9	8	6	16	151	40	40	61		
ENSMUST00000162419						2	0	7	1	4	2	0	0	0	0	0		
ENSMUST00000162420	ENSMUSG00000044542	11	50950806	50953765	-1	70	56	587	140	59	33	1	0	0	1	6	E0CZF7	
ENSMUST00000162421	ENSMUSG00000052477	1	84992690	85270566	-1	18	10	14	22	14	7	3	32	11	0	22	E0CXL1	
ENSMUST00000162422	ENSMUSG00000020246	10	82696160	82742428	1	0	0	0	0	0	0	21	13	47	8	39	F6T0G2	
ENSMUST00000162423						8	0	7	1	3	5	1	2	0	0	1		
ENSMUST00000162424	ENSMUSG00000058441	15	89059734	89073567	1	20	6	58	194	32	12	0	0	0	0	0		Q6IMP4
ENSMUST00000162425	ENSMUSG00000043004	14	19872559	19977627	-1	0	0	0	0	0	0	268	412	300	958	203		P63213
ENSMUST00000162426						1	1	1	70	3	0	0	1	0	0	0		
ENSMUST00000162427						17	9	10	5	9	7	0	0	0	0	0		
ENSMUST00000162428	ENSMUSG00000021481	13	55105311	55134825	1	0	0	0	0	0	0	0	0	0	0	0	E0CZ32	
ENSMUST00000162429	ENSMUSG00000009291	10	77581720	77598732	1	0	0	0	0	0	0	0	0	0	0	0	E0CY65	
ENSMUST00000162430						0	0	0	0	0	0	5	5	5	0	0		
ENSMUST00000162431	ENSMUSG00000025727	17	25946387	25952565	-1	24	17	54	90	30	20	1	0	0	0	0	E0CXQ2	
ENSMUST00000162433	ENSMUSG00000040913	19	45578254	45660312	-1	0	0	0	0	0	0	26	0	0	2	0	E0CX21	
ENSMUST00000162434						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162435	ENSMUSG00000025920	1	16228674	16520112	-1	10	0	0	15	3	3	0	0	0	0	2		Q8CJ67
ENSMUST00000162437						34	27	85	75	56	31	14	77	21	7	49		
ENSMUST00000162438	ENSMUSG00000063108	9	20432972	20460162	-1	6	0	7	41	4	0	0	0	13	19	5	E0CYR0	
ENSMUST00000162439	ENSMUSG00000027833	3	66971727	66981771	-1	3	0	2	81	0	0	0	0	1	0	0		
ENSMUST00000162440						0	0	0	0	0	0	3	8	0	0	0		
ENSMUST00000162441						1	0	1	0	0	0	0	0	1	0	1		
ENSMUST00000162442						59	45	68	512	133	68	4	0	4	0	7		
ENSMUST00000162443	ENSMUSG00000038521	6	124530345	124542359	-1	9	10	16	25	21	4	0	1	1	40	0	E9Q6C2	
ENSMUST00000162444						4	1	9	5	4	2	0	0	0	0	0		
ENSMUST00000162445						13	11	3	3	5	14	229	117	625	7	386		
ENSMUST00000162446						6	4	11	3	3	6	2	0	4	0	6		
ENSMUST00000162447						0	0	0	0	9	0	9	4	6	5	21		
ENSMUST00000162448						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000162449	ENSMUSG00000050122	1	37026596	37187613	1	0	0	0	0	0	0	1	0	0	5	0	Q8BH17	
ENSMUST00000162451						1	3	12	2	6	3	12	51	24	2	11		
ENSMUST00000162455						1	0	2	0	1	1	10	67	51	4	30		
ENSMUST00000162456	ENSMUSG00000025812	8	127063893	127612286	1	9	0	0	0	24	7	0	0	0	0	0		
ENSMUST00000162459						1	1	1	0	0	4	0	4	7	2	2		
ENSMUST00000162460	ENSMUSG00000023994	17	48386885	48409906	-1	0	0	0	53	0	0	166	316	18	10	185	Q3UP82	P23708
ENSMUST00000162461	ENSMUSG00000030166	6	119902698	119922828	1	0	0	0	0	0	0	98	336	160	76	79		P43352

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162462						2	1	5	2	5	3	0	0	0	0	0		
ENSMUST00000162463						14	9	7	77	13	6	0	0	0	0	0		
ENSMUST00000162464	ENSMUSG00000036879	8	85840959	86061376	1	0	0	2	0	0	0	0	0	3	0	0	E0CXM1	
ENSMUST00000162465						5	10	28	5	7	2	0	0	0	0	0		
ENSMUST00000162466	ENSMUSG00000031878	8	104511028	104534637	-1	0	0	0	0	0	0	14	137	0	86	76	E0CZE0	
ENSMUST00000162467	ENSMUSG00000043592	17	48454901	48539714	1	0	0	10	3	4	0	0	0	0	0	0	F7BJ90	
ENSMUST00000162468	ENSMUSG00000026336	1	98421124	98516991	1	7	0	6	6	13	3	0	0	0	0	0	E0CXJ0	
ENSMUST00000162469						3	5	3	6	3	3	0	0	0	0	0		
ENSMUST00000162470						6	4	6	5	7	2	0	0	0	0	0		
ENSMUST00000162471	ENSMUSG00000034098	3	76074270	76710019	1	0	0	0	0	1	1	0	0	0	0	0	F7B641	
ENSMUST00000162473						6	6	7	9	5	6	0	1	0	0	0		
ENSMUST00000162475						25	15	54	48	36	14	0	0	2	0	3		
ENSMUST00000162476	ENSMUSG00000021481	13	55105311	55134825	1	0	0	0	0	0	0	0	0	4	0	0	E0CZ32	
ENSMUST00000162478	ENSMUSG00000033487	14	72537946	72710003	-1	2	0	0	17	3	0	0	0	0	0	0	E0CXY0	
ENSMUST00000162479	ENSMUSG00000022668	16	44736768	44746363	-1	2	0	0	130	10	9	0	0	0	19	0	F6SMJ7	
ENSMUST00000162480	ENSMUSG00000037318	1	193175453	193201703	-1	0	0	0	5	0	0	7	39	22	6	27	A0A0A6YWS1	
ENSMUST00000162481	ENSMUSG00000023995	17	48447956	48451522	-1	2	0	0	0	0	0	0	0	0	0	0	E0CYC8	
ENSMUST00000162483						2	7	9	4	8	8	0	5	3	0	0		
ENSMUST00000162484	ENSMUSG00000039488	9	9660891	10904775	-1	18	7	0	0	0	4	0	0	0	0	0	E9PYK7	
ENSMUST00000162485	ENSMUSG00000027692	3	28263214	28675858	1	0	0	0	0	0	0	0	0	0	0	0	E0CY98	
ENSMUST00000162486						0	1	2	1	5	0	0	0	0	0	0		
ENSMUST00000162487						1	1	1	0	3	2	0	0	0	0	0		
ENSMUST00000162488	ENSMUSG00000036661	15	73512560	73572242	1	0	16	17	0	0	0	0	0	0	0	0	F7B6S5	
ENSMUST00000162489	ENSMUSG00000028717	4	115056426	115071755	1	7	6	15	0	15	6	10	0	0	0	23	Q3TZH7	P22091
ENSMUST00000162490						2	0	0	0	0	0	1	6	3	3	0		
ENSMUST00000162491	ENSMUSG00000022386	15	85879312	85897394	1	0	0	1	7	1	2	0	0	0	0	8	E0CZ49	
ENSMUST00000162492	ENSMUSG00000038658	19	29522282	29606829	1	12	0	8	0	8	20	69	89	344	25	300	F6S7U1	
ENSMUST00000162493						5	5	4	0	2	0	0	0	3	0	1		
ENSMUST00000162494	ENSMUSG00000029635	5	146231230	146302874	1	23	0	12	84	21	0	0	0	0	0	99	E0CZC3	
ENSMUST00000162495	ENSMUSG00000028294	4	34688559	34730206	-1	2	1	0	27	0	2	0	0	0	0	0	E0CXC1	
ENSMUST00000162496						0	0	0	3	3	2	7	37	3	0	19		
ENSMUST00000162497	ENSMUSG00000058318	2	92093117	92364666	1	1	1	0	0	0	1	8	4	23	4	0		
ENSMUST00000162498	ENSMUSG00000015127	17	25188397	25234443	1	2	3	9	84	6	4	2	2	8	0	2	E0CY27	
ENSMUST00000162499	ENSMUSG00000042524	15	79724070	79742536	-1	0	0	0	0	0	0	0	0	0	0	0	E0CY32	
ENSMUST00000162500						0	0	0	0	2	7	11	0	0	1	0		
ENSMUST00000162501						6	0	6	1	6	2	0	0	0	0	9		
ENSMUST00000162502	ENSMUSG00000051550	7	4983483	4996158	-1	0	0	1	113	2	0	0	0	0	0	0	E0CYL8	
ENSMUST00000162503	ENSMUSG00000022550	15	76576358	76595816	1	0	0	0	27	4	0	20	0	0	0	5	E9PUK2	
ENSMUST00000162504						5	4	7	6	6	5	44	173	127	68	118		
ENSMUST00000162505	ENSMUSG00000014767	17	15499888	15528379	1	195	195	291	240	234	117	28	149	50	26	65	Q6RI65	P29037
ENSMUST00000162507	ENSMUSG00000025004	19	39767071	39812814	-1	0	1	3	0	0	0	0	0	0	0	0	E0CXY8	
ENSMUST00000162508	ENSMUSG00000056888	10	111985448	112002631	-1	6	4	7	0	3	0	25	266	72	285	127	Q4QQK5	Q9CWG1
ENSMUST00000162509						1	2	2	0	1	0	0	0	0	0	0		
ENSMUST00000162510						1	6	3	1	7	0	8	20	3	5	8		
ENSMUST00000162511	ENSMUSG00000044176	18	62548911	62661366	1	0	0	10	0	1	3	0	0	0	0	0	E0CXG7	
ENSMUST00000162512	ENSMUSG00000022668	16	44736768	44746363	-1	22	31	30	24	16	16	84	206	117	29	81		Q9CY28
ENSMUST00000162513						1	0	0	0	3	1	0	2	0	0	1		
ENSMUST00000162514	ENSMUSG00000081362	4	96195197	96236659	-1	7	8	8	7	10	5	0	0	0	0	0		
ENSMUST00000162515						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162516	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	15	2	0	0	0	0	0	0	E0CX26	
ENSMUST00000162517	ENSMUSG00000033287	15	78428564	78438909	1	0	0	0	0	6	0	0	0	0	0	0	E0CYD2	
ENSMUST00000162518						1	0	3	2	0	0	0	0	0	0	2		
ENSMUST00000162519	ENSMUSG00000047592	5	138225898	138253363	1	22	28	77	10	25	7	0	0	0	0	0	Q3TBA1	
ENSMUST00000162521	ENSMUSG00000029925	6	38875404	39084585	1	6	7	15	16	9	4	0	1	0	0	1	Q3TRY5	
ENSMUST00000162522						6	5	6	28	5	6	1	6	0	0	2		
ENSMUST00000162523						2	5	5	6	6	2	0	0	0	0	0		
ENSMUST00000162524	ENSMUSG00000020231	10	76259429	76345291	-1	1	2	20	34	8	6	0	0	1	0	1	F7BCF6	
ENSMUST00000162525	ENSMUSG00000036955	10	62538626	62578457	-1	0	0	0	0	0	0	0	0	0	0	0	E0CXN7	
ENSMUST00000162527						2	2	4	4	9	2	0	1	4	0	2		
ENSMUST00000162528	ENSMUSG00000025221	19	45791839	45816061	-1	0	0	2	29	7	5	0	0	0	0	0	Q3YAB3	
ENSMUST00000162529	ENSMUSG00000034908	9	45937857	45955247	-1	1	0	0	0	0	1	85	12	101	0	51	F7DF36	
ENSMUST00000162530						3	1	1	2	2	0	55	60	36	7	76		
ENSMUST00000162531	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	3	0	0	0	0	0	0	E0CZ83	
ENSMUST00000162532	ENSMUSG00000022235	15	31568791	31590119	1	3	2	3	3	4	1	0	0	0	0	3	E0CXH4	
ENSMUST00000162533						1	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000162534	ENSMUSG00000046324	19	29608214	29648415	-1	0	1	0	0	0	0	45	8	137	3	62	F6TQS9	
ENSMUST00000162535						10	4	0	0	0	0	0	0	15	0	18		
ENSMUST00000162536	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0	E0CXL4	
ENSMUST00000162537						381	281	2765	941	428	239	4	5	14	2	23		
ENSMUST00000162538	ENSMUSG00000031781	8	94819818	94838358	-1	27	33	80	62	39	7	103	240	101	48	109		Q8WTY4
ENSMUST00000162539						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162540	ENSMUSG00000063458	14	22019712	23056085	1	14	6	10	1	10	10	4	32	9	34	17	E0CY73	
ENSMUST00000162541	ENSMUSG00000045962	6	119923969	120038672	-1	1	0	3	0	0	2	75	278	183	6	228	F7CZC4	
ENSMUST00000162542						5	2	3	0	1	2	9	10	11	33	5		
ENSMUST00000162543	ENSMUSG00000037720	5	67260565	67291461	1	0	0	0	2	0	0	17	14	59	180	53	Q9CZM3	
ENSMUST00000162544						5	4	15	4	13	5	0	0	0	0	0		
ENSMUST00000162546						5	5	10	2	2	3	0	0	6	0	8		
ENSMUST00000162548						5	7	2	2	9	2	0	0	0	12	2		
ENSMUST00000162549						31	18	183	75	21	17	3	23	2	0	10		
ENSMUST00000162550						2	0	0	2	0	0	6	11	4	3	0		
ENSMUST00000162551						5	2	7	3	2	3	0	0	0	0	0		
ENSMUST00000162552	ENSMUSG00000048402	1	118834132	119053619	-1	0	0	0	0	0	0	0	0	0	0	0	A5A9W5	
ENSMUST00000162553	ENSMUSG00000025979	1	55131231	55154899	1	0	1	1	67	2	0	24	169	62	0	0	E0CYJ0	
ENSMUST00000162554	ENSMUSG00000056832	6	38381469	38427647	1	85	3	58	29	25	38	11	26	20	4	36		Q8BS45

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162555	ENSMUSG00000090206	8	95310566	95326323	1	1	0	0	8	0	0	0	0	0	0	0	F2Z458	
ENSMUST00000162557						0	0	2	0	0	0	48	187	52	110	66		
ENSMUST00000162559						0	1	22	2	0	0	0	0	1	0	0		
ENSMUST00000162560	ENSMUSG00000032115	9	44379490	44392369	1	0	0	0	0	0	0	0	0	0	0	15	E0CYZ2	
ENSMUST00000162561	ENSMUSG00000052631	6	72513644	72521634	-1	1	0	14	0	6	0	0	0	0	0	0	E2QRQ0	
ENSMUST00000162562	ENSMUSG00000020258	9	106152857	106158138	-1	0	3	2	4	1	0	0	0	0	0	0	E0CZG7	
ENSMUST00000162563	ENSMUSG00000004151	12	38779380	38868215	1	0	0	0	0	4	0	0	0	0	0	5	Q549J8	P41164
ENSMUST00000162564	ENSMUSG00000107705	6	8259450	8597480	1	18	0	3	0	0	0	63	116	46	2	90	E0CZ38	
ENSMUST00000162567	ENSMUSG00000029638	6	8509600	8597548	1	0	0	0	0	1	0	0	3	10	0	0		
ENSMUST00000162568						5	3	8	3	4	2	0	0	0	0	0		
ENSMUST00000162569	ENSMUSG00000021124	12	79156017	79172667	-1	0	0	0	0	0	0	134	438	106	192	55	F6UHS3	
ENSMUST00000162570						28	23	34	37	35	10	3	12	8	4	15		
ENSMUST00000162571						0	0	0	0	6	11	0	0	0	0	0		
ENSMUST00000162572						3	0	2	1	0	4	0	0	0	0	0		
ENSMUST00000162573						1	1	2	0	12	2	7	41	4	7	23		
ENSMUST00000162574						4	8	0	1	0	1	3	2	0	4	0		
ENSMUST00000162575	ENSMUSG00000024799	19	6062821	6068373	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZ93	
ENSMUST00000162576	ENSMUSG00000026102	1	52785427	52817688	-1	0	0	0	0	0	0	0	0	0	0	0	E0CX64	
ENSMUST00000162578						0	0	0	0	3	1	0	0	0	0	1		
ENSMUST00000162580						82	84	111	219	78	42	16	29	31	2	40		
ENSMUST00000162581	ENSMUSG00000037989	13	49036303	49148014	-1	8	13	13	0	17	14	0	0	0	0	0	E0CZE3	
ENSMUST00000162582	ENSMUSG00000003721	1	121304353	121332589	-1	0	0	0	0	0	0	16	0	21	9	24	E0CXS5	
ENSMUST00000162583	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	136	1195	0	0	0		Q08122
ENSMUST00000162584						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162585	ENSMUSG00000022181	15	4727175	4815456	1	49	42	55	31	54	35	0	1	1	46	23	Q91X70	
ENSMUST00000162586						10	7	2	9	3	3	2	0	7	0	18		
ENSMUST00000162587	ENSMUSG00000032086	9	45838580	45864399	1	0	0	0	0	0	0	5	13	9	5	0	F6TV37	
ENSMUST00000162588	ENSMUSG00000090083	17	29614790	29641664	1	0	0	0	21	0	0	0	0	0	0	0	E0CY08	
ENSMUST00000162589						2	0	0	0	0	1	0	12	0	0	0		
ENSMUST00000162590						0	0	0	0	0	0	0	11	0	8	6		
ENSMUST00000162591						25	26	37	17	26	6	0	0	0	0	0		
ENSMUST00000162592	ENSMUSG00000062040	7	29893333	29906572	-1	14	4	0	16	10	0	0	0	0	5	0		P10077
ENSMUST00000162593	ENSMUSG00000038538	6	38433950	38524825	1	0	0	4	0	0	0	17	0	70	0	86	F6TB64	
ENSMUST00000162594	ENSMUSG00000038722	5	145140362	145148078	1	0	7	1	2	2	0	404	2074	518	1494	296	E0CX20	
ENSMUST00000162595						0	0	0	0	3	1	0	0	0	0	0		
ENSMUST00000162596						1	3	5	0	0	1	0	0	5	0	0		
ENSMUST00000162597	ENSMUSG00000026799	2	29346819	29524793	1	0	0	0	0	0	0	0	0	0	0	0	E0CXF6	
ENSMUST00000162598	ENSMUSG00000009291	10	77581720	77598732	1	0	0	0	4	0	0	0	3	3	0	0	E0CXX2	
ENSMUST00000162599	ENSMUSG00000037509	1	34678188	34813309	1	1	7	0	0	0	6	0	0	0	0	5	E0CX56	
ENSMUST00000162600	ENSMUSG00000056870	1	44551511	44796838	1	0	0	0	0	0	0	0	0	0	0	0	E0CXC5	
ENSMUST00000162601						2	0	4	0	0	0	5	4	0	0	0		
ENSMUST00000162602	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	6	E0CZE2	
ENSMUST00000162603	ENSMUSG00000026799	2	29346819	29524793	1	7	0	0	0	2	0	0	0	0	0	0	F7B179	
ENSMUST00000162604						9	4	6	6	3	5	0	0	0	0	0		
ENSMUST00000162605						1	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000162606	ENSMUSG00000019795	10	7629373	7681136	-1	0	0	0	9	11	6	44	109	19	110	23	E0CYV0	
ENSMUST00000162607	ENSMUSG00000048402	1	118834132	119053619	-1	0	0	0	0	0	0	0	0	0	0	0	F6UUE3	
ENSMUST00000162609						1	2	4	3	2	2	0	13	0	0	0		
ENSMUST00000162610	ENSMUSG00000019806	10	13647054	13868980	-1	2	2	1	5	1	3	12	52	12	27	18	Q3TS32	Q9D8B1
ENSMUST00000162611						1	0	0	57	5	3	0	0	0	0	0		
ENSMUST00000162612	ENSMUSG00000098950	2	156071845	156127092	-1	0	0	0	0	0	0	0	0	0	0	7	F7CZD1	
ENSMUST00000162613						3	1	1	3	0	0	27	253	56	15	123		
ENSMUST00000162616	ENSMUSG00000031876	8	104281347	104310145	-1	0	0	0	0	0	0	0	9	0	0	0	E0CXA2	
ENSMUST00000162617	ENSMUSG00000033083	14	101442360	101609191	-1	0	0	0	0	14	0	0	0	0	6	26	E0CX53	
ENSMUST00000162618	ENSMUSG00000019979	10	90989311	91082770	-1	2	6	11	18	3	0	56	0	592	0	221	G3XA09	
ENSMUST00000162619	ENSMUSG00000029334	5	98929773	99037351	-1	0	0	16	0	0	0	0	1	0	0	0	A0A0G2JEE8	
ENSMUST00000162620						4	7	2	4	3	1	1	1	1	0	1		
ENSMUST00000162621						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000162622						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162623	ENSMUSG00000026799	2	29346819	29524793	1	2	2	0	2	0	2	0	0	0	0	0	E0CXS7	
ENSMUST00000162624	ENSMUSG00000023010	15	99392882	99410049	1	2	0	3	4	3	0	181	43	209	24	136	E0CXR0	
ENSMUST00000162625	ENSMUSG00000001366	9	78081499	78109065	-1	0	0	0	117	0	1	0	0	0	0	0	E0CYX8	
ENSMUST00000162626	ENSMUSG00000060073	12	70974621	70996347	1	0	0	0	0	0	0	18	24	0	0	9	E0CZ34	
ENSMUST00000162627	ENSMUSG00000025920	1	16228674	16520112	-1	0	5	0	6	4	0	0	0	0	0	0		Q8CJ67
ENSMUST00000162628	ENSMUSG00000059149	1	132022806	132068062	-1	0	0	0	1	0	0	0	0	0	0	0	F6UGV8	
ENSMUST00000162629	ENSMUSG00000039153	17	44495987	44814797	-1	0	0	0	0	0	0	0	0	0	0	0	E9PUK7	
ENSMUST00000162630	ENSMUSG00000025004	19	39767071	39812814	-1	0	12	0	0	5	0	0	0	0	2	0	E0CYU2	
ENSMUST00000162631	ENSMUSG00000004897	3	87906321	87916132	1	0	0	0	1	0	0	13	2	11	9	5	E0CYW7	
ENSMUST00000162632						1	0	2	3	3	0	0	10	3	0	10		
ENSMUST00000162633	ENSMUSG00000032118	9	36821939	36878924	1	0	5	0	3	3	3	0	0	0	0	0	E0CXY1	
ENSMUST00000162634						1	0	11	5	5	3	0	25	21	13	13		
ENSMUST00000162635	ENSMUSG00000041831	17	6673458	6738042	1	0	0	0	0	0	0	0	0	14	0	0	E9PXV1	
ENSMUST00000162636						4	0	2	5	12	0	2	12	6	3	9		
ENSMUST00000162637						0	2	0	1	4	1	0	0	0	0	0		
ENSMUST00000162638						0	0	0	0	0	0	72	199	63	14	51		
ENSMUST00000162640						20	31	49	85	32	18	0	4	1	0	7		
ENSMUST00000162642	ENSMUSG00000039047	3	152714100	152980408	1	18	11	36	14	17	10	0	2	0	2	0	Q8BXX3	
ENSMUST00000162643	ENSMUSG00000009646	10	59403660	59421976	1	0	1	3	0	0	0	0	0	0	1	0	F6UTM6	
ENSMUST00000162644						2	0	1	52	2	3	0	2	1	0	0		
ENSMUST00000162645	ENSMUSG00000007817	14	25459185	25666743	1	25	18	68	60	50	32	2591	2217	3680	128	2415		Q6P1E1
ENSMUST00000162646	ENSMUSG00000049690	1	125913620	126830799	-1	14	6	11	4	15	4	0	0	0	0	0	E0CYS4	
ENSMUST00000162647						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162648	ENSMUSG00000036955	10	62538626	62578457	-1	3	5	12	0	9	1	23	199	0	33	59	F7DEX6	
ENSMUST00000162650	ENSMUSG00000016493	1	195036826	195092249	-1	1	2	8	0	3	0	10	39	21	11	26		O88174

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162652						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162653						2	3	10	1	4	0	0	0	3	2	6		
ENSMUST00000162654						8	0	10	3	11	2	3	39	7	3	16		
ENSMUST00000162655	ENSMUSG00000032534	9	102584598	102626534	-1	0	0	0	0	0	0	52	427	176	77	147		Q3UPP8
ENSMUST00000162656						28	20	52	17	32	18	1	1	5	2	1		
ENSMUST00000162657						4	0	8	0	8	5	0	0	0	0	0		
ENSMUST00000162658	ENSMUSG00000041515	8	120736358	120756694	1	1	0	1	0	0	0	5	0	0	0	0	E0CZE4	
ENSMUST00000162659	ENSMUSG00000062743	17	21383748	21399265	1	1	0	1	1	1	0	0	1	1	11	18	Q6PEP4	
ENSMUST00000162660						5	4	7	1	10	1	0	0	0	0	0		
ENSMUST00000162661	ENSMUSG00000025221	19	45791839	45816061	-1	0	0	0	0	0	0	0	0	0	0	0	E0CX94	
ENSMUST00000162662						1	0	0	7	0	3	2	0	3	0	0		
ENSMUST00000162663						0	0	0	0	0	1	2	39	12	27	13		
ENSMUST00000162664						226	173	1800	338	317	145	1	12	12	0	13		
ENSMUST00000162665	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0	F6S7Z1	
ENSMUST00000162666	ENSMUSG00000030365	6	128887588	128898167	1	2	0	1	0	2	0	0	0	0	0	0	E0CX52	
ENSMUST00000162669						0	0	0	0	0	0	0	7	5	0	0		
ENSMUST00000162670	ENSMUSG00000021684	13	95024454	95250336	-1	8	2	0	5	4	1	5	7	4	7	10	F7CT85	
ENSMUST00000162671	ENSMUSG00000022788	16	16416917	16600549	-1	0	0	0	0	0	0	0	695	278	722	270		Q91ZT5
ENSMUST00000162672	ENSMUSG00000021578	13	74350309	74365783	1	0	0	0	3	0	0	5	0	4	1	0	E0CXT2	
ENSMUST00000162673						1	1	0	11	1	1	0	0	0	0	0		
ENSMUST00000162674	ENSMUSG00000021977	14	59133040	59142893	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZH4	
ENSMUST00000162675						3	1	0	1	3	1	0	0	0	0	1		
ENSMUST00000162676	ENSMUSG00000086277	1	161942086	161979636	-1	0	4	0	5	3	0	0	1	0	0	0	E0CXC6	
ENSMUST00000162678						7	2	5	11	3	2	3	5	4	8	7		
ENSMUST00000162679						0	0	0	0	0	0	0	7	0	0	0		
ENSMUST00000162680	ENSMUSG00000006471	2	25244821	25256022	-1	0	10	4	0	28	0	19	39	0	0	31	E0CX27	
ENSMUST00000162681	ENSMUSG00000026335	1	97795114	98095646	-1	0	0	0	0	0	0	25	212	68	67	60	F7D4K4	
ENSMUST00000162682	ENSMUSG00000019795	10	7629373	7681136	-1	0	0	1	25	0	2	2	1	1	0	0	E0CYF2	
ENSMUST00000162683	ENSMUSG00000050410	17	35512734	35516824	-1	0	1	0	0	6	4	0	0	0	0	0	E0CZ64	
ENSMUST00000162684						0	1	3	50	8	0	14	67	44	2	46		
ENSMUST00000162685	ENSMUSG00000026514	1	181352628	181460641	1	0	0	0	0	0	0	0	0	0	0	0	G3XA11	
ENSMUST00000162686	ENSMUSG00000048495	1	57388237	57407101	-1	0	0	1	227	5	0	0	0	8	27	0		A2RSX7
ENSMUST00000162687						0	0	26	0	3	0	0	7	0	0	0		
ENSMUST00000162688						2	0	6	3	0	0	15	116	37	18	30		
ENSMUST00000162689						47	41	251	41	55	30	0	1	5	1	5		
ENSMUST00000162690						0	1	7	0	0	0	0	0	0	0	0		
ENSMUST00000162691	ENSMUSG00000022110	14	73525319	73596142	1	2	1	4	1	6	0	0	0	0	0	1		
ENSMUST00000162692						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000162693	ENSMUSG00000034544	3	66981390	67358396	1	0	0	0	0	0	5	0	14	17	24	7	E9Q6P8	
ENSMUST00000162694	ENSMUSG00000020329	10	79736123	79746581	-1	0	0	0	64	22	10	0	0	0	0	26	E0CY15	
ENSMUST00000162695	ENSMUSG00000038805	17	85613608	85629302	1	52	29	217	105	37	23	0	0	0	0	0	Q52KB8	
ENSMUST00000162696						2	3	9	3	2	1	0	3	0	2	2		
ENSMUST00000162698						5	4	9	1	5	3	0	7	3	3	3		
ENSMUST00000162699	ENSMUSG00000042790	9	45863425	45906894	-1	0	0	6	0	0	0	14	43	39	0	22	E0CXG0	
ENSMUST00000162700						2	7	4	3	6	2	4	51	9	2	18		
ENSMUST00000162701	ENSMUSG00000042642	3	89401004	89411870	-1	0	0	1	0	1	0	10	9	6	0	10	E0CZ66	
ENSMUST00000162702	ENSMUSG00000036395	9	26763044	26806468	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BZW3	
ENSMUST00000162703	ENSMUSG00000061950	17	65782573	65841926	1	0	0	1	0	0	0	12	10	18	9	26	F6U5N5	
ENSMUST00000162704						3	2	5	0	0	3	0	0	4	3	7		
ENSMUST00000162705						0	0	3	15	0	0	21	0	0	0	0		
ENSMUST00000162707						0	0	6	0	0	0	3	4	14	0	11		
ENSMUST00000162708	ENSMUSG00000036908	19	3935186	3949340	1	0	0	34	32	17	6	5124	6001	4669	966	3865	E9PYK0	
ENSMUST00000162709						7	10	15	4	4	5	6	2	0	0	0		
ENSMUST00000162710						4	6	4	30	4	0	0	0	0	0	0		
ENSMUST00000162711	ENSMUSG00000021024	12	55384222	55418454	1	4	5	11	33	7	4	0	0	0	5	4	E0CYT2	
ENSMUST00000162713						0	1	6	54	4	0	4	10	2	2	7		
ENSMUST00000162715	ENSMUSG00000021614	13	89655312	89742509	-1	0	1	4	3	0	1	0	1	2	0	0	E0CZC0	
ENSMUST00000162716						0	0	10	3	0	0	0	0	0	0	0		
ENSMUST00000162717						0	0	0	3	2	0	6	11	0	0	6		
ENSMUST00000162718						0	4	10	13	5	12	21	90	76	0	225		
ENSMUST00000162719						0	0	1	2	0	2	0	0	8	0	4		
ENSMUST00000162720	ENSMUSG00000006463	19	4878668	4885397	1	0	10	0	0	0	0	0	0	13	15	0	E0CYB8	
ENSMUST00000162721						2	0	1	2	1	0	2	0	0	2	0		
ENSMUST00000162722						0	4	0	17	1	3	7	0	7	0	9		
ENSMUST00000162723						9	7	16	44	10	3	0	2	2	2	2		
ENSMUST00000162725	ENSMUSG00000026489	1	180165238	180199602	-1	1	6	17	7	14	2	0	0	0	0	0	E0CXT4	
ENSMUST00000162726	ENSMUSG00000075227	19	6061192	6062472	1	3	7	13	434	32	2	331	501	246	80	166		Q9QY66
ENSMUST00000162727	ENSMUSG00000025812	8	127063893	127612286	1	0	0	5	0	0	1	0	0	0	0	0	F6TB42	
ENSMUST00000162728						1	3	10	8	6	1	0	0	0	0	0		
ENSMUST00000162729						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162730						2	10	2	9	2	0	0	18	2	0	11		
ENSMUST00000162731	ENSMUSG00000051550	7	4983483	4996158	-1	6	7	10	377	0	10	27	79	47	0	58		Q80VM4
ENSMUST00000162732						1	0	0	7	1	0	20	188	24	0	4		
ENSMUST00000162733	ENSMUSG00000009687	7	31032722	31042481	-1	59	48	380	77	66	29	291	2597	592	100	1579	E0CXN1	
ENSMUST00000162734	ENSMUSG00000022792	16	16302965	16309640	1	0	0	0	0	0	0	0	5	0	0	0	F7BWC1	
ENSMUST00000162735	ENSMUSG00000021187	12	101645443	101718523	-1	61	55	322	139	57	49	5	42	6	1	17		Q91XT6
ENSMUST00000162737						1	0	0	0	0	1	69	256	154	0	146		
ENSMUST00000162739	ENSMUSG00000003500	6	29200434	29216364	-1	0	0	0	0	0	0	0	31	1	0	0	F7DEU6	
ENSMUST00000162740						2	0	2	6	1	1	0	0	0	0	0		
ENSMUST00000162743						0	0	0	0	0	0	0	0	0	8	2		
ENSMUST00000162744						3	2	1	0	1	0	2	1	0	0	0		
ENSMUST00000162745						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162746	ENSMUSG00000026580	1	164115264	164150026	1	20	21	31	21	26	16	405	832	561	97	741		Q01102
ENSMUST00000162747	ENSMUSG00000022525	16	29209695	29230531	1	0	0	0	24	6	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162748	ENSMUSG00000021266	12	108860030	108894174	-1	0	0	0	0	2	5	0	0	0	0	0	E0CXQ4	
ENSMUST00000162749						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000162750						2	4	0	0	1	0	0	0	0	0	0		
ENSMUST00000162751	ENSMUSG00000025920	1	16228674	16520112	-1	5	0	8	0	2	0	0	0	0	0	0		Q8CJ67
ENSMUST00000162752	ENSMUSG00000073494	1	170232749	170253608	1	13	17	28	22	19	6	0	3	0	0	2	Q45HK4	
ENSMUST00000162753	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	0	0	0	0	6	4	0	0	F6U715	
ENSMUST00000162754						9	8	19	5	18	5	12	17	23	3	22		
ENSMUST00000162755						2	0	1	0	0	0	1	0	0	0	3		
ENSMUST00000162756	ENSMUSG00000022613	15	89334398	89337015	1	0	0	0	0	0	0	0	0	0	1	0	F7CHR4	
ENSMUST00000162757	ENSMUSG00000090061	5	63649102	63810546	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JGP2	
ENSMUST00000162758						3	2	30	19	0	6	0	0	2	0	0		
ENSMUST00000162759	ENSMUSG00000036955	10	62538626	62578457	-1	35	39	297	79	53	28	29	80	30	6	58	E0CXJ9	
ENSMUST00000162760						19	17	5	15	18	14	8	76	36	4	28		
ENSMUST00000162761	ENSMUSG00000031883	8	104534700	104550343	1	9	3	19	30	6	8	6	0	4	0	2	G3XA26	
ENSMUST00000162762						5	5	8	3	10	7	0	3	3	0	9		
ENSMUST00000162763						24	11	22	11	15	10	0	3	6	0	10		
ENSMUST00000162764						3	2	2	6	8	2	128	476	261	21	375		
ENSMUST00000162765						5	3	15	0	0	3	0	0	0	1	0		
ENSMUST00000162766						12	12	19	16	14	11	0	0	2	0	3		
ENSMUST00000162767						23	22	116	28	24	11	1	1	1	0	5		
ENSMUST00000162768	ENSMUSG00000026197	1	75168646	75171629	1	0	0	0	0	0	0	13	0	0	0	0	E0CY18	
ENSMUST00000162769	ENSMUSG00000026489	1	180165238	180199602	-1	0	0	0	15	0	2	0	0	0	0	0	A0A0A6YXI0	
ENSMUST00000162772	ENSMUSG00000030226	6	138362918	138581968	-1	8	11	22	8	16	11	0	0	0	0	0		Q8BZL8
ENSMUST00000162773						2	1	0	5	2	4	0	0	0	0	0		
ENSMUST00000162774	ENSMUSG00000033210	16	45535309	45607001	1	0	0	0	0	0	0	0	0	0	0	0	M0QWN6	
ENSMUST00000162775						29	16	28	27	31	3	4	2	2	0	7		
ENSMUST00000162776						0	0	3	143	4	2	0	0	0	0	3		
ENSMUST00000162777	ENSMUSG00000027692	3	28263214	28675858	1	0	0	17	0	0	0	0	0	0	0	12	E0CXD6	
ENSMUST00000162778	ENSMUSG00000028101	3	96696384	96706070	1	1	0	0	59	1	1	0	0	0	0	7	E0CZH5	
ENSMUST00000162779	ENSMUSG00000041559	1	134037254	134048277	1	0	5	3	1	4	6	0	0	0	0	0	E0CX60	
ENSMUST00000162780	ENSMUSG00000072663	15	9578193	9748868	-1	0	0	0	0	2	0	0	2	5	0	0	E0CY95	
ENSMUST00000162781						0	0	0	0	0	0	6	0	6	63	0		
ENSMUST00000162782						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000162783	ENSMUSG00000032131	9	44273188	44288615	-1	1	0	0	1	1	0	0	3	0	0	0	F6XWY6	
ENSMUST00000162785						229	134	438	848	248	159	0	16	6	3	18		
ENSMUST00000162786						0	0	0	41	4	2	0	0	4	0	0		
ENSMUST00000162787	ENSMUSG00000028559	4	109061145	109202272	-1	0	0	0	12	0	0	438	1896	2718	5943	2562	E9PXZ2	
ENSMUST00000162788						0	0	0	0	0	0	0	0	8	0	20		
ENSMUST00000162789	ENSMUSG00000021124	12	79156017	79172667	-1	0	3	0	0	0	0	43	663	228	324	131	E0CYE5	
ENSMUST00000162790	ENSMUSG00000003721	1	121304353	121332589	-1	0	0	0	0	2	1	0	0	20	28	11	E0CXF1	
ENSMUST00000162792	ENSMUSG00000033400	3	116739999	116808166	-1	0	0	0	0	0	0	338	1350	822	95	470	F8VPN4	
ENSMUST00000162793	ENSMUSG00000037747	10	70557682	70655965	-1	2	3	0	1	0	1	0	0	0	0	0	E0CXW9	
ENSMUST00000162794						0	1	1	0	0	0	5	30	13	4	12		
ENSMUST00000162795	ENSMUSG00000025907	1	6206197	6276648	1	4	1	1	0	1	1	231	455	720	78	310	E9PX56	
ENSMUST00000162796	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	2	0	0	0	0	0	0	0	E0CXW0	
ENSMUST00000162797						14	12	67	36	12	6	3	44	11	4	28		
ENSMUST00000162798						40	36	83	75	69	36	16	46	15	3	20		
ENSMUST00000162799						4	8	17	12	6	5	0	4	8	3	5		
ENSMUST00000162800	ENSMUSG00000025955	1	65012689	65032759	-1	5	6	12	4	9	4	0	0	0	0	0	G3XA14	
ENSMUST00000162801						2	1	4	4	6	2	0	7	0	4	0		
ENSMUST00000162802	ENSMUSG00000013076	9	14541966	14615483	-1	1	0	2	24	4	1	1	0	0	0	0	E0CY12	
ENSMUST00000162803						1	0	0	1	2	0	27	109	193	38	83		
ENSMUST00000162804						10	1	3	0	0	0	0	3	2	3	0		
ENSMUST00000162805						7	9	12	6	5	4	0	0	1	0	3		
ENSMUST00000162806						7	1	0	1	2	0	2	4	6	0	0		
ENSMUST00000162807	ENSMUSG00000050587	2	96318169	97631666	1	5	0	10	0	4	6	0	0	0	1	0		Q8C031
ENSMUST00000162808	ENSMUSG00000033287	15	78428564	78438909	1	0	0	0	0	0	0	0	2	0	1	0	F7C1U0	
ENSMUST00000162809	ENSMUSG00000075610	11	94777217	94782703	-1	0	6	0	12	0	2	0	0	0	0	0		B7ZWI3
ENSMUST00000162810	ENSMUSG00000024799	19	6062821	6068373	-1	0	2	0	0	0	0	8	0	0	0	7	E0CX92	
ENSMUST00000162811	ENSMUSG00000044066	11	20227037	20249429	-1	12	12	24	33	12	6	0	15	4	4	4	Q3TRP8	
ENSMUST00000162812	ENSMUSG00000029406	5	124118690	124249760	-1	0	0	0	42	0	0	0	0	0	0	21		Q6ZPQ6
ENSMUST00000162813						0	0	3	0	0	0	0	2	10	2	6		
ENSMUST00000162814	ENSMUSG00000060743	1	180800832	180813943	-1	0	0	0	22	0	0	0	8639	8256	31151	5023		P84244
ENSMUST00000162815	ENSMUSG00000030162	6	129485244	129507165	-1	3	0	0	2	2	0	3	0	6	2	0	E0CXW6	
ENSMUST00000162816	ENSMUSG00000039153	17	44495987	44814797	-1	19	10	51	177	25	16	4	4	3	1	0	E0CZC6	
ENSMUST00000162817	ENSMUSG00000060579	14	9550092	11162035	-1	0	0	0	0	1	0	0	0	0	0	0	F6SV10	
ENSMUST00000162818	ENSMUSG00000055717	14	103650228	103704907	1	5	0	15	0	0	0	7	0	3	2	4	F6V9T4	
ENSMUST00000162819	ENSMUSG00000038733	1	181173228	181211552	-1	39	0	79	472	39	0	1308	2849	2491	284	1090		Q8C6G8
ENSMUST00000162820						3	2	8	5	3	1	0	0	0	0	0		
ENSMUST00000162821	ENSMUSG00000033769	6	84618487	85069513	-1	1	0	0	12	0	0	0	0	5	0	0	E0CY34	
ENSMUST00000162824						0	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000162825	ENSMUSG00000033487	14	72537946	72710003	-1	0	0	0	0	13	0	37	341	525	34	407	F6TLV3	
ENSMUST00000162827	ENSMUSG00000032425	9	88548020	88571061	1	22	14	0	0	33	0	34	75	124	102	154	E9Q732	
ENSMUST00000162830	ENSMUSG00000022311	15	47580637	48792063	-1	18	15	18	3	22	10	0	0	0	0	0		Q80T79
ENSMUST00000162831						2	0	0	127	4	2	0	0	0	0	0		
ENSMUST00000162832						0	2	13	0	4	0	174	246	102	73	92		
ENSMUST00000162833	ENSMUSG00000031257	X	134086421	134221956	-1	3	1	0	3	2	0	0	2	0	0	2		
ENSMUST00000162834	ENSMUSG00000018042	15	83153494	83172592	-1	0	2	0	0	1	3	32	0	34	0	22	A0A0A0MQM3	
ENSMUST00000162835						51	31	331	91	44	15	4	6	5	0	7		
ENSMUST00000162836						9	9	4	10	9	2	0	0	0	0	1		
ENSMUST00000162838						4	3	6	6	4	2	1	0	1	0	3		
ENSMUST00000162839	ENSMUSG00000038384	5	123142193	123168629	1	3	0	0	0	0	1	2	5	1	0	16	G3UZ56	
ENSMUST00000162840						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000162842						0	0	0	0	0	3	0	1	0	10	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162843						1	6	1	1	3	0	0	0	0	0	1		
ENSMUST00000162844	ENSMUSG00000038521	6	124530345	124542359	-1	13	2	58	26	28	13	0	2	0	1	0	E0CYK5	
ENSMUST00000162845	ENSMUSG00000021693	13	106958996	107022126	-1	0	0	0	0	0	0	0	9	27	75	63	F6SUU5	
ENSMUST00000162846	ENSMUSG00000033538	9	5308828	5336783	1	0	0	2	0	0	0	8	32	0	199	13	E0CY92	
ENSMUST00000162847						0	0	3	0	0	0	2	4	0	1	3		
ENSMUST00000162848						264	221	891	263	316	142	24	90	64	20	70		
ENSMUST00000162849	ENSMUSG00000039087	13	37778400	37952002	1	3	6	31	25	9	10	11	0	56	0	49	F6UB40	
ENSMUST00000162850						0	0	0	0	0	0	0	1	0	4	0		
ENSMUST00000162851	ENSMUSG00000060073	12	70974621	70996347	1	0	0	0	3	1	0	0	11	17	10	6	E0CYL6	
ENSMUST00000162852						2	0	1	0	0	0	0	4	1	0	6		
ENSMUST00000162853						42	26	221	277	45	20	1	12	2	2	5		
ENSMUST00000162854	ENSMUSG00000023999	17	49615136	49909847	1	9	0	24	5	0	9	0	0	0	0	0	E9PX57	
ENSMUST00000162855	ENSMUSG00000035329	12	59200655	59219725	-1	0	0	2	0	0	1	0	34	48	0	3	F7CTA1	
ENSMUST00000162856						16	11	19	13	15	9	0	0	0	0	0		
ENSMUST00000162857						315	300	1011	268	368	130	3	14	7	3	17		
ENSMUST00000162858						4	1	0	0	5	0	2	13	9	0	8		
ENSMUST00000162859						0	5	3	1	2	0	1	2	2	4	3		
ENSMUST00000162860	ENSMUSG00000038039	10	58255497	58305599	1	0	9	0	0	0	0	0	0	0	0	0	E0CYI9	
ENSMUST00000162861	ENSMUSG00000029587	5	143235163	143248834	1	5	3	8	14	5	8	1	0	0	0	0	E0CYZ8	
ENSMUST00000162862	ENSMUSG00000036636	17	25133391	25162104	1	5	3	8	0	5	0	11	9	11	0	27	F6SUM2	
ENSMUST00000162863	ENSMUSG00000024558	18	73928486	74065359	-1	28	0	91	170	44	25	10	0	0	0	0	E9PXX5	
ENSMUST00000162864	ENSMUSG00000004127	3	138143448	138159821	1	0	0	103	171	87	45	0	0	0	0	0		
ENSMUST00000162865						2	0	1	0	0	0	41	85	44	3	92		
ENSMUST00000162866						0	0	0	0	0	0	34	83	11	49	11		
ENSMUST00000162867						0	0	0	0	0	0	11	2	10	0	4		
ENSMUST00000162869						1	0	3	0	1	1	0	0	0	0	0		
ENSMUST00000162870						5	7	5	2	4	4	0	0	6	0	9		
ENSMUST00000162871						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162872	ENSMUSG00000030092	6	104492790	104863406	1	7	0	7	0	0	0	0	0	0	0	0		Q9JMB8
ENSMUST00000162873						3	0	0	2	3	0	0	0	0	0	1		
ENSMUST00000162874						71	41	114	473	101	87	22	3	84	3	104		
ENSMUST00000162875	ENSMUSG00000026090	1	37611677	37720085	-1	30	13	66	90	57	20	0	0	0	0	2	E9Q3M9	
ENSMUST00000162876	ENSMUSG00000042453	5	21884454	22344702	-1	1	0	0	0	0	1	0	0	0	0	0	F6U2B2	
ENSMUST00000162877	ENSMUSG00000049690	1	125913620	126830799	-1	0	7	0	0	0	6	0	0	0	0	0	Q8C6S8	
ENSMUST00000162878	ENSMUSG00000039153	17	44495987	44814797	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZ12	
ENSMUST00000162879	ENSMUSG00000040913	19	45578254	45660312	-1	0	0	0	0	0	0	38	16	0	0	0	E0CXV9	
ENSMUST00000162880						1	0	0	26	0	0	0	0	0	0	0		
ENSMUST00000162882						5	0	13	0	5	0	0	0	0	0	7		
ENSMUST00000162883	ENSMUSG00000003199	17	56005711	56016790	1	0	0	0	0	0	0	1	202	139	30	0	E0CYJ7	
ENSMUST00000162884						0	0	0	0	1	0	2	0	2	0	0		
ENSMUST00000162885	ENSMUSG00000089773	4	112006269	112029538	1	0	0	0	0	1	1	0	0	0	0	0		A7TZE6
ENSMUST00000162886	ENSMUSG00000032591	9	108080436	108085003	1	0	0	0	0	0	11	3	0	0	1	2	E0CXN0	
ENSMUST00000162887	ENSMUSG00000038421	1	170917576	170927583	-1	0	0	0	0	0	0	0	0	0	0	0	E0CY58	
ENSMUST00000162888						1	1	7	5	2	0	0	0	0	0	0		
ENSMUST00000162889						76	82	52	61	81	39	1	2	3	0	3		
ENSMUST00000162891	ENSMUSG00000039835	10	18390322	18533892	1	8	0	0	2	5	0	0	0	0	0	2	E0CYL9	
ENSMUST00000162892						2	2	0	5	0	0	0	0	0	0	0		
ENSMUST00000162893	ENSMUSG00000023047	15	102445367	102454630	1	0	0	0	0	0	0	0	3	0	0	0	F6V9X7	
ENSMUST00000162894						5	0	4	4	5	2	0	0	0	0	0		
ENSMUST00000162895						6	2	7	5	13	3	6	12	9	0	20		
ENSMUST00000162896						19	22	22	16	40	15	3	19	14	0	2		
ENSMUST00000162897						0	10	0	0	7	0	0	0	0	0	0		
ENSMUST00000162898	ENSMUSG00000060073	12	70974621	70996347	1	1	0	0	0	0	0	0	0	0	0	0	F7BWF9	
ENSMUST00000162899	ENSMUSG00000026344	1	125867622	125913101	-1	3	1	2	0	6	0	0	0	0	0	0	E0CXP0	
ENSMUST00000162901	ENSMUSG00000013076	9	14541966	14615483	-1	1	1	4	8	7	3	0	0	0	0	0	E0CYQ3	
ENSMUST00000162902						32	31	57	35	33	24	11	13	8	4	12		
ENSMUST00000162903	ENSMUSG00000030232	6	140622663	140678472	1	2	2	0	0	1	0	11	49	12	1	1	F6V059	
ENSMUST00000162904						0	0	0	0	3	0	15	0	160	249	313		
ENSMUST00000162905						0	0	0	2	0	2	0	0	0	0	0		
ENSMUST00000162906						0	1	3	0	1	0	0	0	0	0	0		
ENSMUST00000162907	ENSMUSG00000025812	8	127063893	127612286	1	0	0	0	0	0	0	0	0	0	0	0	E9PYJ2	
ENSMUST00000162908	ENSMUSG00000024857	19	4081578	4087340	1	2	0	5	6	2	0	0	0	0	0	0	G3XA29	
ENSMUST00000162909						22	10	45	34	44	13	5	83	18	0	38		
ENSMUST00000162910						0	2	5	8	0	1	0	0	0	0	0		
ENSMUST00000162912						0	1	8	3	1	1	4	16	16	4	14		
ENSMUST00000162913	ENSMUSG00000022416	15	80287238	80398279	1	0	0	0	0	0	0	0	0	0	0	0	F7BCE6	
ENSMUST00000162914						3	1	11	0	4	4	4	10	9	1	16		
ENSMUST00000162915	ENSMUSG00000032295	9	57130690	57142722	1	0	0	0	0	0	0	0	0	30	0	8	E0CXM6	
ENSMUST00000162916						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162918						2	1	1	3	2	0	0	0	0	0	0		
ENSMUST00000162919						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162920						65	60	50	22	70	37	31	302	99	61	160		
ENSMUST00000162921	ENSMUSG00000021597	13	77043088	77135473	-1	0	0	0	0	0	0	0	0	0	4	0	Q8C211	
ENSMUST00000162922						18	9	30	119	26	5	0	5	0	0	10		
ENSMUST00000162923						0	0	0	0	0	0	19	73	49	35	0		
ENSMUST00000162924						5	1	0	0	1	1	15	40	73	103	43		
ENSMUST00000162925	ENSMUSG00000070031	1	85600378	85645037	1	6	5	0	0	0	0	0	91	30	45	17	F6V9G0	
ENSMUST00000162926						11	4	42	35	10	6	0	0	0	0	0		
ENSMUST00000162927						6	3	21	47	6	2	2	3	0	0	0		
ENSMUST00000162928						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162929						4	3	6	12	3	0	10	60	46	0	68		
ENSMUST00000162930						0	10	15	17	10	5	4	39	14	9	28		
ENSMUST00000162931						1	0	1	1	1	1	0	0	0	0	0		
ENSMUST00000162932	ENSMUSG00000030226	6	138362918	138581968	-1	2	2	3	1	2	2	0	0	0	0	0	E0CY33	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000162933						201	169	609	212	134	77	3	25	22	7	61		
ENSMUST00000162934	ENSMUSG00000028101	3	96696384	96706070	1	5	6	0	0	8	4	68	48	48	10	157	E0CZ31	
ENSMUST00000162935						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162936						5	3	6	19	4	3	4	21	12	0	18		
ENSMUST00000162937						7	2	2	4	5	6	0	0	0	0	0		
ENSMUST00000162938						2	0	3	66	5	4	0	0	0	0	0		
ENSMUST00000162939						28	3	74	14	33	12	473	155	1104	18	894		
ENSMUST00000162940	ENSMUSG00000073457	17	13230257	13237184	1	27	24	159	35	32	10	0	1	0	0	0		Q9QYZ3
ENSMUST00000162941	ENSMUSG00000001844	5	143316489	143329256	-1	0	0	0	3	0	0	0	0	11	0	0	E0CX22	
ENSMUST00000162942						8	6	19	143	25	13	0	1	0	0	0		
ENSMUST00000162943	ENSMUSG00000009291	10	77581720	77598732	1	0	0	12	1	2	0	8	0	0	0	0	F6TFF2	
ENSMUST00000162944	ENSMUSG00000021597	13	77043088	77135473	-1	9	4	53	23	10	5	1	5	5	0	2	Q8C211	
ENSMUST00000162945	ENSMUSG00000021990	14	60634001	60764556	1	21	16	18	5	23	10	3104	7626	5413	646	3974	E0CYU0	
ENSMUST00000162946						0	0	0	0	0	0	43	0	336	0	111		
ENSMUST00000162947	ENSMUSG00000039735	3	122538719	122619715	-1	2	2	0	1	2	0	0	0	8	0	12	E9PUI5	
ENSMUST00000162948	ENSMUSG00000029811	6	48872896	48909188	1	15	0	35	16	12	0	0	0	0	0	0	E9PYN9	
ENSMUST00000162949						7	2	6	15	2	3	0	0	0	0	1		
ENSMUST00000162950	ENSMUSG00000031668	6	70844515	70905245	1	2	4	0	60	3	3	5	8	6	3	2		
ENSMUST00000162951						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000162952						4	5	8	2	1	2	6	5	9	0	8		
ENSMUST00000162953	ENSMUSG00000049792	12	111709488	111713257	-1	0	0	0	47	0	2	0	0	0	0	0	E0CX76	
ENSMUST00000162954						43	33	65	31	40	22	64	346	119	8	130		
ENSMUST00000162955						10	8	11	15	6	2	0	0	0	0	0		
ENSMUST00000162956						0	1	0	4	2	0	0	0	0	0	0		
ENSMUST00000162957	ENSMUSG00000035953	14	50926070	50930856	-1	0	0	0	0	0	0	76	300	77	0	72	E0CZ18	
ENSMUST00000162959						0	4	10	6	4	2	0	0	0	0	0		
ENSMUST00000162960						24	28	67	20	31	12	18	15	14	1	18		
ENSMUST00000162961	ENSMUSG00000079036	12	87425840	87444017	-1	0	0	7	0	8	0	6	60	0	9	17		P0CB42
ENSMUST00000162962						0	0	10	0	0	0	53	4	0	0	36		
ENSMUST00000162963	ENSMUSG00000038733	1	181173228	181211552	-1	113	99	698	113	104	99	1548	8142	3199	404	2110	E0CYH4	
ENSMUST00000162964	ENSMUSG00000070686	5	93634993	93671551	-1	9	12	19	23	14	6	0	0	0	0	0	E9PWI7	
ENSMUST00000162965						7	3	8	1	7	3	0	224	0	37	46		
ENSMUST00000162966						0	0	2	141	4	0	0	0	0	0	0		
ENSMUST00000162967						4	2	16	4	3	0	0	0	0	0	0		
ENSMUST00000162968						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000162969	ENSMUSG00000034613	10	122678762	122945795	1	7	6	10	4	2	0	0	0	7	0	8	E0CYP3	
ENSMUST00000162970						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000162971	ENSMUSG00000021461	13	63304709	63497278	-1	0	0	0	23	1	0	0	0	0	0	0	E0CYQ7	
ENSMUST00000162972						4	7	18	5	10	4	60	43	122	551	87		
ENSMUST00000162973	ENSMUSG00000032280	9	61372366	61418497	1	0	0	0	0	0	0	1438	3553	682	139	976		Q08122
ENSMUST00000162974						1	0	1	0	0	1	42	157	69	0	73		
ENSMUST00000162975	ENSMUSG00000029130	5	29195992	29228457	1	0	0	0	0	1	1	0	0	0	0	0	F6URG7	
ENSMUST00000162976	ENSMUSG00000079478	19	5728088	5731732	-1	0	1	0	0	0	0	0	2	0	0	0	F7B6D3	
ENSMUST00000162977						40	40	0	0	19	16	0	0	1	3	0		
ENSMUST00000162978						4	0	0	1	1	0	0	2	0	0	24		
ENSMUST00000162979						2	0	1	3	1	0	0	0	0	0	0		
ENSMUST00000162981	ENSMUSG00000036879	8	85840959	86061376	1	0	0	0	0	1	1	0	0	0	0	0	E0CY30	
ENSMUST00000162982	ENSMUSG00000023830	17	12682406	12769664	-1	2	0	2	2	1	0	0	0	0	0	0	E0CXV7	
ENSMUST00000162983						0	2	2	1	3	2	0	0	0	0	0		
ENSMUST00000162984	ENSMUSG00000038039	10	58255497	58305599	1	0	0	2	0	0	0	0	0	0	0	0	E0CX24	
ENSMUST00000162985						14	14	40	13	22	16	47	239	91	22	57		
ENSMUST00000162986	ENSMUSG00000079036	12	87425840	87444017	-1	26	16	55	22	23	20	1	9	8	1	0	E0CZH7	
ENSMUST00000162987						4	2	2	5	9	3	0	0	0	0	0		
ENSMUST00000162988	ENSMUSG00000026546	1	172520801	172545870	1	0	0	0	0	0	0	0	0	0	0	0	E0CXX0	
ENSMUST00000162991						0	0	2	3	6	1	0	0	0	0	0		
ENSMUST00000162992						0	0	1	3	1	3	0	0	0	0	0		
ENSMUST00000162993						2	8	23	7	10	7	0	0	0	0	0		
ENSMUST00000162994	ENSMUSG00000029207	5	66298703	66618784	-1	0	0	0	22	0	0	0	0	0	0	0	E0CZ85	
ENSMUST00000162995						1	0	0	0	0	0	5	0	0	3	0		
ENSMUST00000162996						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000162997	ENSMUSG00000052557	8	117158135	117215997	1	15	20	5	14	10	15	71	48	136	0	45	F6TZU3	
ENSMUST00000162998	ENSMUSG00000068399	14	51361756	51569982	1	23	30	15	27	29	14	0	0	0	0	0	Q6UY52	
ENSMUST00000162999						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000163000						4	6	0	2	3	2	0	6	4	2	2		
ENSMUST00000163001						1	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000163002						0	0	2	0	0	2	0	0	0	0	0		
ENSMUST00000163003						11	16	16	15	15	4	143	75	63	23	32		
ENSMUST00000163004						0	3	0	0	1	0	0	0	0	0	0		
ENSMUST00000163006						0	0	0	0	0	0	1	7	2	0	6		
ENSMUST00000163007						2	5	2	28	3	3	13	24	19	8	12		
ENSMUST00000163008						11	6	6	388	18	7	0	0	0	0	0		
ENSMUST00000163010						5	4	6	5	8	10	0	8	1	1	5		
ENSMUST00000163011	ENSMUSG00000026478	1	153218922	153332786	-1	0	0	0	0	2	0	4	0	0	0	16	F6TLW1	
ENSMUST00000163012						11	14	54	57	19	10	12	11	8	1	16		
ENSMUST00000163013						13	12	20	18	21	13	3	0	6	0	0		
ENSMUST00000163014	ENSMUSG00000005610	7	111070568	111083030	-1	2	1	5	0	0	3	9	28	0	7	2	F6UU81	
ENSMUST00000163015						4	0	8	0	3	1	0	0	1	0	0		
ENSMUST00000163016						4	3	7	4	4	0	59	85	150	11	131		
ENSMUST00000163017	ENSMUSG00000049641	10	52022502	52028471	1	6	3	0	82	0	0	0	0	0	0	0		Q8BGW8
ENSMUST00000163018						4	5	5	3	10	4	0	0	1	0	0		
ENSMUST00000163019	ENSMUSG00000000606	14	51411001	51419527	1	21	15	120	19	14	4	0	0	0	0	0	F6U6R2	
ENSMUST00000163020						8	6	9	21	9	1	0	0	0	0	0		
ENSMUST00000163021						0	0	20	0	4	0	0	0	0	0	0		
ENSMUST00000163022						1	0	1	10	5	2	4	7	9	1	13		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000163023						8	9	13	12	13	10	0	0	6	1	3		
ENSMUST00000163024	ENSMUSG00000030226	6	138362918	138581968	-1	0	11	5	3	8	3	0	0	0	0	0		Q8BZL8
ENSMUST00000163025						0	1	0	2	1	1	0	0	0	0	0		
ENSMUST00000163026	ENSMUSG00000048148	8	72646711	72714746	1	0	0	0	0	0	0	0	0	0	0	0	F7DAC7	
ENSMUST00000163027						0	0	0	73	4	0	0	0	0	0	0		
ENSMUST00000163028						2	2	0	14	5	1	0	0	0	0	0		
ENSMUST00000163029						3	0	5	11	5	4	4	38	21	0	23		
ENSMUST00000163030	ENSMUSG00000038384	5	123142193	123168629	1	0	0	0	258	0	0	67	22	178	0	228		Q8CFT2
ENSMUST00000163031	ENSMUSG00000021124	12	79156017	79172667	-1	8	3	6	10	5	3	79	204	92	188	111	F6T4B9	
ENSMUST00000163032						1	0	1	0	0	0	2	8	3	0	2		
ENSMUST00000163033						3	4	1	4	3	3	5	19	14	7	18		
ENSMUST00000163034	ENSMUSG00000037902	2	129592835	129632228	1	0	0	0	0	0	1	118	0	301	0	235	E0CX65	
ENSMUST00000163035						1	0	0	0	1	1	0	5	0	0	0		
ENSMUST00000163036						2	1	3	1	3	0	0	0	0	3	0		
ENSMUST00000163037	ENSMUSG00000031994	9	30942562	30963838	1	27	23	39	18	22	16	0	0	0	0	0	F6U6K2	
ENSMUST00000163038						17	14	29	22	23	11	3	0	3	0	3		
ENSMUST00000163039						1	2	0	0	0	0	0	12	2	0	3		
ENSMUST00000163040						9	6	5	6	9	5	0	3	0	0	0		
ENSMUST00000163041	ENSMUSG00000054065	7	141078218	141090510	1	0	0	23	60	2	0	0	0	0	0	0	E0CY75	
ENSMUST00000163042	ENSMUSG00000050097	8	104831572	104840093	1	0	0	0	0	0	0	0	0	0	0	0	E0CXA5	
ENSMUST00000163043						0	0	6	9	0	0	0	0	2	0	0		
ENSMUST00000163044						1	0	0	2	2	0	11	7	6	2	12		
ENSMUST00000163045						0	1	1	0	2	0	0	0	0	2	0		
ENSMUST00000163046						0	0	15	4	17	0	0	2	5	0	0		
ENSMUST00000163047	ENSMUSG00000029823	6	38551334	38609470	1	0	0	0	28	0	0	0	49	170	23	0	E9Q715	
ENSMUST00000163048	ENSMUSG00000063334	10	111972664	111988432	1	66	73	117	45	80	34	184	862	200	82	359		Q8BGA5
ENSMUST00000163049	ENSMUSG00000033105	10	76531588	76557138	1	0	2	1	4	1	0	0	0	0	0	0	F7BJL0	
ENSMUST00000163050						1	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000163054						27	19	33	264	40	24	0	0	1	0	0		
ENSMUST00000163055	ENSMUSG00000038925	14	24293214	24309966	1	0	1	3	1	5	0	0	0	0	0	0	E9Q3J0	
ENSMUST00000163057						0	0	0	0	1	0	59	24	55	3	48		
ENSMUST00000163058	ENSMUSG00000026024	1	59162926	59237231	-1	25	4	0	106	12	0	0	0	0	0	0		Q920R0
ENSMUST00000163059						3	3	0	0	6	2	0	31	0	13	7		
ENSMUST00000163060	ENSMUSG00000022096	14	70552212	70573548	1	46	14	95	11	47	23	8	2	2	0	8	E9PZ81	
ENSMUST00000163061	ENSMUSG00000054770	1	57955101	58018956	-1	13	0	4	1	0	8	0	0	0	0	0	E9PYP3	
ENSMUST00000163062	ENSMUSG00000071176	8	14911663	15001085	1	2	19	56	0	3	2	4	4	0	0	2	F7BQE4	
ENSMUST00000163063	ENSMUSG00000004151	12	38779380	38868215	1	1	0	1	2	0	0	0	0	0	0	0	F6TUZ8	
ENSMUST00000163064						11	12	84	58	12	0	0	0	0	0	0		
ENSMUST00000163065	ENSMUSG00000030226	6	138362918	138581968	-1	13	5	1	9	4	0	0	0	0	0	0	E9PWI9	
ENSMUST00000163066						1	1	3	2	1	0	0	1	0	0	2		
ENSMUST00000163067	ENSMUSG00000054752	4	53631471	53707009	1	0	0	0	0	0	0	0	1	0	0	0	E0CXZ1	
ENSMUST00000163068						130	121	271	221	132	75	0	3	0	0	2		
ENSMUST00000163070	ENSMUSG00000021024	12	55384222	55418454	1	1	0	2	3	0	0	0	0	0	5	0	E0CXB1	
ENSMUST00000163071	ENSMUSG00000020181	10	109682660	110456204	-1	0	1	0	0	5	4	0	0	0	0	0	F6U6A7	
ENSMUST00000163072						5	4	2	0	10	0	0	2	0	0	0		
ENSMUST00000163073	ENSMUSG00000022148	15	6579871	6663313	1	0	0	0	0	2	2	69	1005	145	64	111	F6V072	
ENSMUST00000163075	ENSMUSG00000034902	10	81292963	81319973	1	0	0	0	55	0	0	3842	3270	3067	256	3133		O70161
ENSMUST00000163078	ENSMUSG00000024677	19	11516512	11531256	1	5	3	2	0	3	0	0	20	7	13	3		Q99N09
ENSMUST00000163079	ENSMUSG00000043467	1	161002922	161034849	-1	0	0	0	0	0	0	56	209	72	16	65	Q8C3U9	
ENSMUST00000163080	ENSMUSG00000090066	3	138065052	138081506	1	94	77	169	180	101	41	0	0	0	1	0	E0CYV9	
ENSMUST00000163082	ENSMUSG00000022150	15	6299788	6440712	1	2	0	16	0	0	3	0	0	7	34	116	F6TQN9	
ENSMUST00000163083	ENSMUSG00000024646	18	84851338	84880401	1	0	2	6	2	7	5	123	418	117	455	116	E0CY88	
ENSMUST00000163084						5	3	3	6	4	4	0	0	0	0	0		
ENSMUST00000163085	ENSMUSG00000019795	10	7629373	7681136	-1	3	0	0	0	0	0	156	278	299	380	140	F7D432	
ENSMUST00000163086						0	0	0	0	0	1	50	243	14	58	65		
ENSMUST00000163087						7	2	12	49	4	1	4	9	4	6	1		
ENSMUST00000163088						0	0	0	10	2	0	16	65	30	0	37		
ENSMUST00000163089	ENSMUSG00000055874	6	70956531	70961066	1	0	0	0	189	6	0	0	0	0	0	0	E0CZH3	
ENSMUST00000163090						2	3	0	3	0	0	0	0	0	0	0		
ENSMUST00000163091	ENSMUSG00000021461	13	63304709	63497278	-1	0	0	9	3	2	0	0	22	9	0	2		P50652
ENSMUST00000163092	ENSMUSG00000029442	5	123252102	123327484	1	9	0	0	0	0	18	0	0	0	0	0	E9PVE7	
ENSMUST00000163093	ENSMUSG00000071573	19	33137747	33392295	-1	0	0	0	71	0	1	3	0	11	0	0	E9Q243	
ENSMUST00000163094	ENSMUSG00000062031	7	140941391	140947664	1	4	1	7	0	8	4	0	10	8	0	18	E9QA85	
ENSMUST00000163095	ENSMUSG00000041846	12	101039409	101083702	-1	0	0	0	0	22	0	176	337	289	113	147	E9Q481	
ENSMUST00000163096	ENSMUSG00000094981	7	22200341	22201264	-1	2	0	4	2	2	0	0	0	0	0	0	K9J7G2	
ENSMUST00000163097	ENSMUSG00000049658	13	100017994	100104070	-1	1	3	4	71	3	4	0	0	0	0	0	E9PYY8	
ENSMUST00000163100	ENSMUSG00000048922	14	67676331	67715841	-1	1	0	14	25	17	0	14	14	52	14	7		Q14B71
ENSMUST00000163102	ENSMUSG00000095113	14	42636467	42641917	-1	0	0	1	0	0	4	0	0	0	0	0	F6YU13	
ENSMUST00000163106						0	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000163107	ENSMUSG00000024050	17	32354055	32389401	-1	12	18	0	0	0	4	76	49	88	8	147	E9PZC6	
ENSMUST00000163110						7	5	10	4	7	7	0	0	0	0	0		
ENSMUST00000163111						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000163113	ENSMUSG00000090854	10	104194042	104196522	1	0	0	0	0	0	0	0	0	0	0	0	L7N2C4	
ENSMUST00000163114						10	12	57	9	16	5	0	0	0	0	0		
ENSMUST00000163116	ENSMUSG00000022577	15	75551268	75567255	-1	157	136	700	161	173	71	3	5	9	1	6	Q544M1	Q9WUC3
ENSMUST00000163118	ENSMUSG00000006529	14	30929180	30943289	-1	12	4	25	27	17	8	4	5	6	6	0		Q61702
ENSMUST00000163119	ENSMUSG00000004364	1	80264923	80340480	-1	0	5	2	24	2	0	166	233	116	25	99		Q9JLV5
ENSMUST00000163121	ENSMUSG00000026829	2	28496891	28505415	1	5	5	0	9	6	10	0	0	0	0	10		Q8VI38
ENSMUST00000163123	ENSMUSG00000054640	17	81388691	81649607	-1	19	17	38	16	30	15	21	88	62	4	81	Q68FL0	
ENSMUST00000163125						52	52	178	144	87	26	14	30	15	3	26		
ENSMUST00000163127						1	4	11	4	7	0	3	5	4	0	4		
ENSMUST00000163128	ENSMUSG00000044024	18	37955079	37959179	1	0	5	5	487	18	13	0	0	2	2	0	E9Q3X7	
ENSMUST00000163130	ENSMUSG00000026740	2	18195654	18392830	-1	0	0	0	0	0	0	0	2	2	0	2	F6YK70	
ENSMUST00000163131	ENSMUSG00000038524	18	37957431	37969774	-1	0	0	0	0	0	0	12	0	8	0	0	E9PVQ1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000163132						4	0	8	3	13	1	0	0	0	0	0		
ENSMUST00000163133	ENSMUSG00000002845	16	38558698	38592162	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7W3	
ENSMUST00000163134	ENSMUSG00000066392	12	88722876	90334935	1	5	6	6	7	6	0	0	0	0	0	0		Q6P9K9
ENSMUST00000163135						9	4	3	7	12	4	4	2	1	0	0		
ENSMUST00000163137	ENSMUSG00000006154	7	4460674	4480487	1	17	8	20	94	16	11	0	0	1	0	3	E9Q2P3	
ENSMUST00000163139	ENSMUSG00000030084	6	89316314	89362620	-1	92	48	126	101	157	68	25	6	8	14	148		P70206
ENSMUST00000163140						9	7	2	169	13	10	48	62	0	26	30		
ENSMUST00000163141	ENSMUSG00000002297	5	8396973	8422716	-1	0	0	1	0	0	0	0	0	0	0	0	F7AV51	
ENSMUST00000163147	ENSMUSG00000026383	1	119545037	119649000	-1	0	0	0	0	0	0	1	0	0	0	0		Q8BGS1
ENSMUST00000163148						69	52	569	10	51	43	0	2	0	0	3		
ENSMUST00000163149	ENSMUSG00000021557	13	59449537	59585227	-1	5	5	4	0	0	0	0	0	0	0	0	F6ZCF0	
ENSMUST00000163152						3	4	7	2	0	0	6	0	3	0	0		
ENSMUST00000163153	ENSMUSG00000032050	9	52047150	52088737	1	11	16	43	0	23	11	493	1114	763	171	577		P26043
ENSMUST00000163159	ENSMUSG00000043635	5	89677087	89883334	-1	0	16	18	61	22	32	1	7	1	0	3	E9Q287	
ENSMUST00000163161						2	0	4	2	3	0	0	3	2	0	2		
ENSMUST00000163163	ENSMUSG00000021636	13	100595957	100616971	-1	0	0	6	51	0	0	1	4	0	2	0	E9Q1T5	
ENSMUST00000163164	ENSMUSG00000001441	11	97205842	97280638	-1	0	0	2	0	1	0	0	3	5	0	0	F7ANF4	
ENSMUST00000163167						0	7	0	0	0	0	0	0	0	0	0		
ENSMUST00000163168	ENSMUSG00000042079	6	117900324	117925622	1	0	0	11	153	7	0	273	842	1007	189	852		Q9Z2X1
ENSMUST00000163172	ENSMUSG00000090840	19	8740718	8741225	1	2	2	0	0	8	3	0	1	1	0	0	G3UW99	
ENSMUST00000163176	ENSMUSG00000043962	4	126164082	126202760	-1	0	1	0	0	2	0	4	35	21	0	13	F7AB07	
ENSMUST00000163179	ENSMUSG00000026384	1	119652467	119837613	-1	2	0	0	0	1	2	0	0	0	0	0	F7CWQ9	
ENSMUST00000163180						2	2	30	0	0	0	0	116	14	1	10		
ENSMUST00000163183	ENSMUSG00000066306	7	101969843	102014959	1	1	4	13	11	2	1	169	1053	297	83	330	F6ZQA3	
ENSMUST00000163185						14	13	23	13	10	7	0	0	2	0	0		
ENSMUST00000163186						1	0	1	0	1	6	0	0	0	0	0		
ENSMUST00000163188						2	1	2	81	10	0	4	21	24	0	0		
ENSMUST00000163189	ENSMUSG00000002020	12	84783212	84876532	-1	0	0	55	0	39	0	0	0	0	0	0	E9Q1D6	
ENSMUST00000163190	ENSMUSG00000032479	9	109931460	110083955	1	24	12	42	29	33	9	0	0	3	0	4	A0A0G2JFH2	
ENSMUST00000163192	ENSMUSG00000062762	9	36779159	36797361	-1	0	0	0	95	0	0	0	0	15	15	28		
ENSMUST00000163193	ENSMUSG00000040820	16	94129195	94313563	-1	0	0	0	199	22	22	22	66	22	0	66	Q3TZ03	Q920N2
ENSMUST00000163195						4	5	24	6	4	4	0	1	8	0	5		
ENSMUST00000163199						4	3	9	2	4	2	0	0	0	0	0		
ENSMUST00000163200	ENSMUSG00000051243	9	58196298	58204319	-1	4	2	8	9	3	11	0	0	0	0	0	E9Q9N7	
ENSMUST00000163201						2	5	4	7	7	1	0	3	0	0	6		
ENSMUST00000163202	ENSMUSG00000016179	1	193346346	193370298	-1	0	1	0	0	0	0	0	0	0	0	0	F6YRI7	
ENSMUST00000163205	ENSMUSG00000024576	18	61555274	61590061	1	7	7	14	6	5	4	48	84	61	8	81	E9Q4G7	
ENSMUST00000163207						1	0	3	0	0	0	10	20	9	20	2		
ENSMUST00000163209	ENSMUSG00000020014	10	92775619	93081618	-1	5	19	14	10	16	8	0	0	0	2	3	F6SXY8	
ENSMUST00000163210	ENSMUSG00000006740	18	6201002	6242174	-1	0	0	0	0	0	0	37	0	510	0	0	E9QAK5	
ENSMUST00000163213						5	3	14	4	8	4	11	0	10	0	9		
ENSMUST00000163214	ENSMUSG00000002020	12	84783212	84876532	-1	4	0	7	0	3	0	0	0	1	0	3	F6XGT5	
ENSMUST00000163215	ENSMUSG00000039059	2	180099465	180104488	-1	1	0	0	0	0	0	0	0	0	0	0	E9Q540	
ENSMUST00000163216	ENSMUSG00000092166	5	95106938	95111158	1	0	0	31	0	0	0	0	0	0	0	0	L7N277	
ENSMUST00000163220	ENSMUSG00000037787	12	111713261	111754980	1	0	0	0	0	0	0	0	0	0	6	0		Q9CQW7
ENSMUST00000163222						13	7	0	3	15	6	9	0	9	0	0		
ENSMUST00000163226	ENSMUSG00000053819	3	126596302	126846326	1	9	5	13	11	12	9	5	46	21	9	26	Q8CCM0	
ENSMUST00000163227	ENSMUSG00000055602	17	13061104	13082481	1	0	0	8	2	6	0	0	2	0	0	1	D3Z452	
ENSMUST00000163229	ENSMUSG00000039742	6	29319140	29336019	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0U4	
ENSMUST00000163230	ENSMUSG00000022661	16	45382135	45409053	-1	16	9	21	0	12	0	0	0	0	0	6	Q80VX2	
ENSMUST00000163231	ENSMUSG00000042350	12	84918148	84970900	-1	30	5	45	21	23	8	75	784	70	72	0	E9PZX5	
ENSMUST00000163233	ENSMUSG00000041353	X	150397773	150459154	-1	0	0	2	0	0	0	0	0	0	0	0	E9PZH0	
ENSMUST00000163235	ENSMUSG00000029862	6	42286685	42315756	1	0	2	1	2	0	1	0	0	1	0	0	F6VSA8	
ENSMUST00000163237						0	5	0	0	6	0	0	0	0	0	0		
ENSMUST00000163238	ENSMUSG00000020212	10	118141787	118168997	1	0	0	0	0	0	0	167	302	199	46	264	B2RPU6	
ENSMUST00000163239	ENSMUSG00000038305	1	57774162	57948394	1	0	4	3	0	0	0	0	0	0	0	0	E9Q7S4	
ENSMUST00000163240						7	7	43	4	15	6	0	0	0	0	0		
ENSMUST00000163241	ENSMUSG00000091721	3	132630191	132645350	1	3	5	5	3	3	5	0	0	0	0	0		E9PW74
ENSMUST00000163242	ENSMUSG00000016541	15	85336381	85463836	1	22	12	30	115	24	11	6125	24815	8473	2729	4304		P28658
ENSMUST00000163246	ENSMUSG00000061904	10	91116574	91124059	-1	0	0	0	0	0	0	69	963	54	0	0	E9PX16	
ENSMUST00000163248						3	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000163250						0	0	0	2	0	0	1	1	0	0	0		
ENSMUST00000163252	ENSMUSG00000026659	1	170873498	170885540	-1	6	3	10	7	7	2	2	10	8	0	2	F6ZTK6	
ENSMUST00000163255	ENSMUSG00000067399	9	88839164	88848190	1	25	43	45	0	17	13	1	7	0	0	0		P86449
ENSMUST00000163257	ENSMUSG00000064138	13	77708690	78166238	1	0	0	0	0	0	0	0	85	0	8	25		Q3TNH5
ENSMUST00000163259	ENSMUSG00000091744	18	62662108	62662928	1	6	5	4	6	6	3	0	0	0	0	0	E9Q5I2	
ENSMUST00000163260	ENSMUSG00000026413	1	135871395	135919207	-1	18	5	32	0	0	5	0	0	0	0	0		P97350
ENSMUST00000163263	ENSMUSG00000082639	X	26200678	26231355	-1	0	0	0	0	0	0	0	0	0	0	0	B1B0R1	
ENSMUST00000163264	ENSMUSG00000004530	5	113842436	113908758	-1	6	3	6	0	5	2	0	1	0	0	5	E9PVJ1	
ENSMUST00000163265	ENSMUSG00000025154	19	41766588	41802084	-1	0	0	82	68	30	13	0	0	0	1	0	E9Q4T1	
ENSMUST00000163268						0	0	0	17	1	1	55	173	66	0	49		
ENSMUST00000163271	ENSMUSG00000033174	6	88724412	88828360	1	24	16	63	51	38	16	20	7	0	0	0	E9Q3B9	
ENSMUST00000163272	ENSMUSG00000017548	11	79993106	80034123	1	11	13	26	157	0	3	0	1000	593	108	297	E9PW15	
ENSMUST00000163275						0	0	0	0	0	0	5	18	10	2	3		
ENSMUST00000163276	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	E9PWX6	
ENSMUST00000163277	ENSMUSG00000103766	3	88243380	88287210	-1	0	3	0	0	4	2	0	1	1	0	0	A0A0A6YVY1	
ENSMUST00000163279	ENSMUSG00000037062	3	144683678	144720335	-1	12	12	12	29	17	8	2218	10948	4213	2556	2341		Q9JK48
ENSMUST00000163280	ENSMUSG00000021417	13	34977748	35027094	-1	0	3	0	1	5	0	0	0	0	0	0	E9PYA9	
ENSMUST00000163281	ENSMUSG00000049214	4	111972923	111988223	1	0	2	8	0	1	0	0	0	0	0	0		A7XV04
ENSMUST00000163282						4	0	11	1	4	0	0	0	0	1	0		
ENSMUST00000163284						26	24	33	36	24	11	3	2	3	0	5		
ENSMUST00000163287	ENSMUSG00000025159	19	41941086	41981157	-1	0	0	0	0	0	0	103	354	8	44	1	F7C9N6	
ENSMUST00000163288	ENSMUSG00000028542	4	117834506	117875198	1	0	0	0	0	0	0	0	9	0	0	6	E9Q3V0	
ENSMUST00000163289	ENSMUSG00000033458	7	64346758	64374095	-1	0	0	0	0	16	0	11	5	23	0	17		Q69ZT1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000163290	ENSMUSG00000051786	15	89098357	89123087	-1	0	0	0	0	0	0	0	0	0	0	3	F6ZAT3	
ENSMUST00000163295	ENSMUSG00000005871	18	34220924	34322189	1	1	0	2	0	0	1	0	2	3	0	0	F6Z405	
ENSMUST00000163296						0	1	3	0	1	2	0	0	0	2	5		
ENSMUST00000163297						9	16	50	28	16	4	0	0	0	1	0		
ENSMUST00000163299	ENSMUSG00000034164	11	5106265	5152257	-1	0	3	0	0	0	0	4	0	4	0	0		Q91VF5
ENSMUST00000163300	ENSMUSG00000048076	11	59211412	59228270	-1	0	10	0	121	20	10	61	163	62	49	74		P84078
ENSMUST00000163301	ENSMUSG00000048728	11	50872720	50887651	-1	0	0	32	0	0	0	0	0	0	0	0	Q80Y34	
ENSMUST00000163304						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000163305	ENSMUSG00000094817	14	26082297	26235744	1	1	1	1	0	0	0	0	0	0	0	0	Q8BX39	
ENSMUST00000163306	ENSMUSG00000043962	4	126164082	126202760	-1	0	0	2	0	1	0	0	0	6	0	0	F6YSQ2	
ENSMUST00000163307	ENSMUSG00000021697	13	108316332	108407782	1	5	0	0	0	8	2	0	0	18	0	37		Q8BH88
ENSMUST00000163309	ENSMUSG00000025892	9	4417899	4796234	-1	0	0	0	43	0	0	0	0	0	0	0	E9PX01	
ENSMUST00000163311	ENSMUSG00000061479	7	27187005	27196271	-1	9	4	0	0	5	0	0	57	0	0	0		Q62189
ENSMUST00000163312						5	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000163313	ENSMUSG00000022296	15	38933142	38949405	1	6	6	22	4	5	3	0	0	0	2	0		Q8VHV1
ENSMUST00000163316						1	1	4	0	2	2	0	0	0	0	0		
ENSMUST00000163319	ENSMUSG00000038583	10	53337686	53345999	1	12	14	8	11	0	5	1	0	0	0	4		P61014
ENSMUST00000163320	ENSMUSG00000005442	7	25267704	25294159	1	0	3	0	45	0	11	939	1076	1137	47	898		Q924A2
ENSMUST00000163321	ENSMUSG00000037974	7	141788972	141819231	1	0	0	0	0	0	0	0	0	0	0	0	E9PWB6	
ENSMUST00000163322	ENSMUSG00000063142	14	23289431	24004859	-1	2	0	3	1	0	0	0	0	0	0	0	E9Q9P4	
ENSMUST00000163324	ENSMUSG00000037536	14	47472561	47531962	1	0	20	0	0	0	0	58	60	182	0	144		Q80XI1
ENSMUST00000163325	ENSMUSG00000090539	14	4776337	4785002	1	0	2	3	5	0	3	0	0	0	0	0	L7N276	
ENSMUST00000163326	ENSMUSG00000020788	11	72961169	72993044	1	0	0	0	0	4	33	224	0	150	66	195	E9Q559	
ENSMUST00000163328	ENSMUSG00000046959	5	108669878	108675569	-1	6	11	0	5	0	4	3	2	0	0	2	Q3UPH6	P58735
ENSMUST00000163329	ENSMUSG00000055720	9	57910986	57929968	1	8	5	21	21	13	3	1320	1399	853	181	654		Q91W67
ENSMUST00000163330	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	13	3	12	0	0	E9PWA1	
ENSMUST00000163333	ENSMUSG00000022255	15	34082694	34142386	1	0	0	0	0	0	0	24	35	60	7	68	F6QHD1	
ENSMUST00000163336	ENSMUSG00000056234	14	32159865	32179855	1	0	29	23	14	33	18	82	244	77	70	82	Q5U4H9	
ENSMUST00000163337						4	2	5	4	2	4	1	2	3	1	3		
ENSMUST00000163338	ENSMUSG00000079387	X	148857640	148924139	1	0	0	0	0	0	0	0	0	0	0	0	L7N278	
ENSMUST00000163339	ENSMUSG00000022106	14	73123037	73207843	1	1	2	0	3	1	2	2	0	0	0	4		
ENSMUST00000163344	ENSMUSG00000040147	X	16709282	16817366	-1	0	0	0	0	0	0	0	0	1	1	3	E9PVL9	
ENSMUST00000163345	ENSMUSG00000024969	19	7275396	7341860	-1	1	0	0	5	0	1	11	9	3	0	3	F7CRG8	
ENSMUST00000163347	ENSMUSG00000036377	5	76656512	76873554	1	5	3	0	121	2	0	4	0	0	0	0	E9Q3Y7	
ENSMUST00000163348	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	0	0	0	0	41	31	72	45	G5E8Y1	
ENSMUST00000163350	ENSMUSG00000021911	14	32201949	32297550	1	4	13	0	68	25	4	0	38	182	47	118		O88622
ENSMUST00000163352	ENSMUSG00000075229	16	36071660	36092118	1	0	3	2	26	0	0	13	6	0	0	0	E9Q4B5	
ENSMUST00000163354						8	5	51	4	12	13	0	103	0	32	20		
ENSMUST00000163356	ENSMUSG00000025731	17	25875464	25886007	1	0	0	4	87	5	0	5	5	11	0	4	E9Q7K5	
ENSMUST00000163358						3	4	0	0	3	2	0	30	11	5	2		
ENSMUST00000163361	ENSMUSG00000040420	15	22549022	23474418	1	4	4	1	5	6	0	0	0	0	0	0	Q8BLB5	
ENSMUST00000163367	ENSMUSG00000024552	18	78146940	78209094	-1	3	5	21	12	6	6	0	0	0	0	0		
ENSMUST00000163370	ENSMUSG00000002489	16	89787111	89980080	-1	30	0	0	0	0	0	260	0	30	16	4	G3UWG2	
ENSMUST00000163371	ENSMUSG00000029672	6	22306520	22356243	-1	1	0	0	1	0	2	0	0	0	0	0	E9Q8C5	
ENSMUST00000163372	ENSMUSG00000042350	12	84918148	84970900	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7I2	
ENSMUST00000163375	ENSMUSG00000040505	17	84658234	84683011	-1	0	10	3	4	7	2	0	0	0	2	0	E9QA91	
ENSMUST00000163376						4	5	7	7	7	4	0	0	0	0	2		
ENSMUST00000163377	ENSMUSG00000064030	10	128747879	128766568	1	10	7	17	60	18	0	304	443	214	178	204		Q8CHP5
ENSMUST00000163379	ENSMUSG00000013701	14	32180162	32201898	-1	0	0	0	0	0	0	0	14	0	0	0	E9Q3T4	
ENSMUST00000163382	ENSMUSG00000022403	15	81363669	81400077	-1	0	0	1	90	6	4	0	0	8	20	21	E9Q1X9	
ENSMUST00000163384	ENSMUSG00000027288	2	120506820	120563843	-1	1	0	0	0	0	0	0	0	0	0	18	F6QFS1	
ENSMUST00000163388						4	0	4	5	1	0	0	0	0	0	0		
ENSMUST00000163389	ENSMUSG00000030890	7	105736592	105742925	1	0	0	0	27	0	0	273	1518	254	0	0		O55222
ENSMUST00000163392	ENSMUSG00000033111	14	12284209	12303231	1	12	11	7	18	8	0	35	221	43	90	44		Q8BGD0
ENSMUST00000163393						6	8	8	5	15	10	0	0	0	4	4		
ENSMUST00000163394	ENSMUSG00000073460	17	12888902	12910000	-1	13	5	24	46	19	7	0	4	3	0	2	B2RXZ1	
ENSMUST00000163395						10	3	16	10	6	2	7	21	11	4	15		
ENSMUST00000163397	ENSMUSG00000025243	9	123593820	123632565	-1	2	1	5	0	1	0	0	0	0	0	0	F6TTF6	
ENSMUST00000163398	ENSMUSG00000025159	19	41941086	41981157	-1	1	0	0	0	1	0	224	401	337	0	153	E9PUY8	
ENSMUST00000163399	ENSMUSG00000046774	X	101794656	101798642	1	0	0	0	10	0	0	0	0	0	0	0	F6R3T1	
ENSMUST00000163400	ENSMUSG00000042557	9	57072040	57128366	1	0	1	0	0	0	0	0	0	0	0	0	E9PXF9	
ENSMUST00000163401	ENSMUSG00000037674	9	72532240	72622937	1	34	27	39	324	43	17	120	306	214	39	144	F8VPJ6	
ENSMUST00000163402	ENSMUSG00000090935	12	81497941	81532911	-1	17	21	21	25	24	0	16	18	20	12	24		Q9D6K5
ENSMUST00000163406						0	10	0	0	9	0	0	0	0	0	0		
ENSMUST00000163408						3	1	3	16	3	6	0	0	0	0	0		
ENSMUST00000163409	ENSMUSG00000028986	5	24100605	24160792	1	17	0	0	90	17	11	0	0	0	0	0	G3UW75	
ENSMUST00000163410						10	4	39	5	1	2	0	0	0	0	0		
ENSMUST00000163416						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000163418						4	2	1	10	5	1	4	22	34	1	41		
ENSMUST00000163419	ENSMUSG00000022983	16	90228957	90284425	-1	0	0	20	0	11	4	129	335	175	18	159	Q7TSH6	
ENSMUST00000163421	ENSMUSG00000024182	17	26138688	26195811	1	0	12	7	0	0	0	293	230	337	21	27	Q14DJ8	
ENSMUST00000163425	ENSMUSG00000039232	10	12939983	12964259	-1	8	9	12	213	16	4	976	2830	1149	609	879	Q3U5V8	
ENSMUST00000163427	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	0	0	0	2	0	5	5	0	E9Q9D9	
ENSMUST00000163428	ENSMUSG00000022801	16	32914100	33015647	1	0	0	5	0	0	0	24	5	28	0	28	F6TPH7	
ENSMUST00000163433	ENSMUSG00000054302	12	54670340	54695897	-1	0	0	157	0	0	0	144	782	334	1004	257		Q5BU09
ENSMUST00000163435	ENSMUSG00000026384	1	119652467	119837613	-1	0	6	3	48	4	1	0	0	12	0	6	E9Q0S8	
ENSMUST00000163437	ENSMUSG00000002718	2	166906040	166946389	1	0	0	0	0	0	0	2	49	0	0	0	F6ZEW4	
ENSMUST00000163439	ENSMUSG00000090314	3	92868359	92870216	-1	10	7	22	15	15	13	0	1	0	0	0	G5E8Z3	
ENSMUST00000163441	ENSMUSG00000040813	9	106658746	106685927	-1	0	3	0	253	34	9	17	9	0	25	22	E9Q137	
ENSMUST00000163442	ENSMUSG00000046329	17	57043711	57059863	-1	0	1	0	0	0	0	0	1	0	0	0	F6XQ75	
ENSMUST00000163445						0	0	21	0	0	0	0	5	0	0	0		
ENSMUST00000163446	ENSMUSG00000024613	18	60813755	60848971	-1	23	8	50	35	32	0	50	0	0	0	113	Q05CS0	
ENSMUST00000163448	ENSMUSG00000019929	10	97479500	97518162	1	5	4	10	3	6	5	0	0	0	225	20	Q3UKR1	P28654
ENSMUST00000163450	ENSMUSG00000025272	X	150645304	150657583	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q1E1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000163452	ENSMUSG00000052751	6	48593883	48599082	1	17	13	60	0	0	0	14	58	0	5	1		Q5U4E2
ENSMUST00000163454						0	10	7	0	3	2	0	0	0	0	0		
ENSMUST00000163455	ENSMUSG00000022324	15	34306680	34436242	1	18	0	0	141	29	0	0	0	0	0	0	A0A0A0MQM7	
ENSMUST00000163458	ENSMUSG00000081044	X	93968659	93975470	1	1	0	3	5	1	0	0	0	0	0	0	B2RUM3	
ENSMUST00000163459	ENSMUSG00000043962	4	126164082	126202760	-1	0	0	0	0	0	0	16	89	68	7	62	F6YH92	
ENSMUST00000163461	ENSMUSG00000096663	7	20509617	20510534	-1	1	0	0	0	0	0	0	0	0	0	0	K7N6X7	
ENSMUST00000163462						6	2	17	11	5	2	0	0	0	0	0		
ENSMUST00000163464	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5J3	
ENSMUST00000163465						4	7	4	2	10	3	0	0	1	0	0		
ENSMUST00000163467	ENSMUSG00000096078	12	115446409	115446869	-1	6	5	10	1	4	4	0	0	0	0	0	A0A075B680	
ENSMUST00000163468						4	5	3	4	6	5	0	0	0	0	0		
ENSMUST00000163469	ENSMUSG00000090874	14	50298337	50299330	-1	3	2	3	1	2	2	0	0	0	0	0	Q14AK5	
ENSMUST00000163471						0	5	0	0	0	1	0	0	0	0	0		
ENSMUST00000163472	ENSMUSG00000091604	15	99702176	99705490	-1	0	0	0	75	0	0	0	4	0	0	1	F7BGH6	
ENSMUST00000163473	ENSMUSG00000021111	12	105784694	105838944	1	0	0	0	0	0	0	0	0	0	0	0	E9PWC8	
ENSMUST00000163474	ENSMUSG00000013353	7	43492044	43505940	-1	0	0	0	0	0	0	0	13	6	2	4	E9PXL1	
ENSMUST00000163475	ENSMUSG00000091474	7	41599230	41628533	1	21	17	56	47	18	8	10	46	27	26	10	E9Q0Q3	
ENSMUST00000163476	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	0	129	45	0	0		Q6ZPR5
ENSMUST00000163478						15	14	38	11	24	10	0	0	1	2	5		
ENSMUST00000163480						3	1	8	0	5	0	0	0	0	0	0		
ENSMUST00000163481	ENSMUSG00000004371	7	4772373	4782857	-1	1	1	2	0	5	2	0	0	0	0	0	F7A7F2	
ENSMUST00000163482	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5D0	
ENSMUST00000163483	ENSMUSG00000020149	11	20201432	20226856	1	0	0	0	0	0	0	738	734	0	0	0	Q0PD67	P62821
ENSMUST00000163486	ENSMUSG00000022020	14	79334204	79390778	-1	1	0	0	0	2	1	7	44	36	8	20	E9PZ53	
ENSMUST00000163489						0	1	0	16	2	0	1006	4693	896	752	935		
ENSMUST00000163492	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	3	0	0	2	0	0	0	0	0	Q3TCZ2	Q9JIM1
ENSMUST00000163494	ENSMUSG00000068227	15	78480553	78495066	-1	10	0	5	3	15	1	0	0	0	0	0		P16297
ENSMUST00000163495	ENSMUSG00000053469	15	66670753	66850721	1	1	0	22	5	19	0	119	14	69	0	86	F6Y2X8	
ENSMUST00000163496	ENSMUSG00000005125	15	66929321	66969640	-1	13	0	6	3	2	2	0	0	0	0	2	E9Q5I8	
ENSMUST00000163497	ENSMUSG00000019944	10	69151434	69291791	1	0	0	0	70	2	0	0	0	0	0	0	E9PYH9	
ENSMUST00000163499	ENSMUSG00000022119	14	105106751	105177327	-1	0	4	0	3	18	4	28	52	108	25	64	E9Q640	
ENSMUST00000163501						3	3	5	0	2	3	0	0	0	0	0		
ENSMUST00000163502	ENSMUSG00000025075	19	56287137	56320822	1	0	0	0	0	0	0	0	0	0	0	0	F7B276	
ENSMUST00000163504	ENSMUSG00000051314	7	30818348	30823775	-1	3	0	32	0	7	0	156	1073	272	43	132		Q8VCK6
ENSMUST00000163505	ENSMUSG00000019986	10	20952547	21080428	1	7	0	7	0	9	3	0	26	0	0	0	E9Q552	
ENSMUST00000163506	ENSMUSG00000037570	15	99242818	99251961	-1	9	14	0	0	0	2	59	286	34	68	0	Q3TJY1	
ENSMUST00000163507	ENSMUSG00000033065	15	98092589	98132447	1	0	25	27	0	0	0	0	61	0	13	0		P47857
ENSMUST00000163511	ENSMUSG00000029771	6	29526625	29541871	1	24	9	23	5	26	8	89	174	99	22	156	Q3U169	P56477
ENSMUST00000163514	ENSMUSG00000062563	12	24665838	24681813	-1	0	0	0	42	0	0	1	0	0	1	1		
ENSMUST00000163516	ENSMUSG00000024589	18	64887756	65217826	1	46	26	2	393	38	31	202	519	242	20	236	E9PXB7	
ENSMUST00000163521						1	4	1	2	0	3	1	0	4	1	14		
ENSMUST00000163523						4	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000163524	ENSMUSG00000049336	11	36006656	37235964	-1	0	0	30	41	21	0	0	0	0	0	0	A0A0A0MQB7	
ENSMUST00000163525	ENSMUSG00000090872	14	4664192	4670850	1	0	7	0	0	0	5	0	0	0	0	0	L7N2D9	
ENSMUST00000163526						3	2	3	4	8	5	0	0	0	0	3		
ENSMUST00000163528	ENSMUSG00000046836	1	183276352	183297269	-1	0	0	16	14	21	11	0	3	26	60	21		Q8K2Q7
ENSMUST00000163530	ENSMUSG00000028107	3	95739976	95760206	-1	8	0	19	31	10	10	0	67	0	0	0	E9Q7H6	
ENSMUST00000163531						32	44	154	104	72	31	0	3	1	0	1		
ENSMUST00000163533	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	2	0	0	0	3	1	3	0	E9QA48	
ENSMUST00000163534	ENSMUSG00000071291	13	67490167	67500555	-1	0	2	0	0	2	0	2	0	4	13	8	E9Q218	
ENSMUST00000163536	ENSMUSG00000027690	3	28697903	28731359	1	2	5	2	0	10	3	0	0	0	0	0	E9PXR7	
ENSMUST00000163538	ENSMUSG00000064179	7	4504570	4516382	-1	0	0	2	3	4	4	0	0	0	0	0	E9PZB4	
ENSMUST00000163544	ENSMUSG00000095710	5	10947805	11044948	1	0	0	0	0	0	0	0	0	0	0	0	F7AXK2	
ENSMUST00000163545	ENSMUSG00000022119	14	105106751	105177327	-1	4	0	0	0	0	3	43	106	45	3	20	E9PYZ7	
ENSMUST00000163546						5	0	7	100	6	2	0	1	0	0	0		
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ENSMUST00000163553						0	0	0	0	0	0	0	4	0	0	0		
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ENSMUST00000163559	ENSMUSG00000029530	9	123678439	123783457	1	8	3	17	129	7	0	0	0	0	0	0		Q9WUT7
ENSMUST00000163560	ENSMUSG00000064179	7	4504570	4516382	-1	0	1	2	3	1	0	0	0	0	0	0	E9Q334	
ENSMUST00000163566	ENSMUSG00000095044	14	41962708	41967927	-1	2	1	6	8	1	8	0	0	0	0	0	L7N2C0	
ENSMUST00000163567						29	30	95	87	51	14	16	25	52	0	71		
ENSMUST00000163568	ENSMUSG00000024134	17	85684277	85688274	-1	190	82	174	2490	306	175	0	1	2	0	0		Q62232
ENSMUST00000163569	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	0	0	0	240	0	495	51	680		Q80U58
ENSMUST00000163570						0	9	0	0	0	1	0	0	0	0	0		
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ENSMUST00000163574	ENSMUSG00000092518	7	4753226	4771302	-1	0	16	0	0	37	0	0	0	0	0	0	M0QW72	
ENSMUST00000163575						7	5	8	2	5	3	3	1	2	0	5		
ENSMUST00000163576	ENSMUSG00000026288	1	87620312	87720507	1	3	5	4	3	8	2	0	0	0	0	4	E9Q752	
ENSMUST00000163579						2	2	1	1	1	0	0	0	0	0	0		
ENSMUST00000163582	ENSMUSG00000059895	15	73723145	73758766	1	46	16	85	123	37	14	0	13	0	0	0		Q9D658
ENSMUST00000163584	ENSMUSG00000051579	X	136168984	136172342	-1	11	9	19	16	20	12	0	7	0	4	2		Q9CZY2
ENSMUST00000163586	ENSMUSG00000051705	9	59734259	59750649	-1	0	0	0	0	0	0	0	0	0	12	0		
ENSMUST00000163588	ENSMUSG00000033855	17	88597684	88662586	1	30	13	57	19	24	7	0	0	2	4	25		Q8CDJ8
ENSMUST00000163589	ENSMUSG00000030200	6	134396318	134438736	1	2	8	7	9	0	16	0	0	0	4	4		Q9CPT0
ENSMUST00000163590	ENSMUSG00000024505	18	49696145	49755601	-1	127	146	423	227	165	72	3	23	11	6	18	B7ZP35	
ENSMUST00000163591	ENSMUSG00000044024	18	37955079	37959179	1	0	0	0	0	0	0	0	0	0	0	5	E9PX33	
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ENSMUST00000163593						2	3	3	10	2	1	0	0	0	0	0		
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ENSMUST00000163599	ENSMUSG00000091584	14	43779488	43784745	-1	4	8	3	5	0	0	0	0	0	0	0	E9PXN0	
ENSMUST00000163600	ENSMUSG00000021548	13	85189408	85223469	1	0	0	0	0	0	2	13	69	28	60	17	E9PWD3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000163601	ENSMUSG00000030970	7	132987563	133124354	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q815	
ENSMUST00000163602						0	7	27	0	0	0	0	2	10	32	41		
ENSMUST00000163603						0	0	0	0	0	0	8	0	0	0	0		
ENSMUST00000163605	ENSMUSG00000035842	17	66123520	66152167	1	59	56	170	109	72	34	22	50	43	8	61		Q6AXC6
ENSMUST00000163606	ENSMUSG00000079434	1	87509889	87597845	1	1	0	0	0	0	0	0	0	0	0	0	E9Q0P5	
ENSMUST00000163607	ENSMUSG00000093820	6	123492508	123533406	-1	6	8	1	11	0	3	0	0	0	0	0	K7N6Y7	
ENSMUST00000163608						6	8	8	74	8	3	0	0	0	0	0		
ENSMUST00000163609	ENSMUSG00000108631	7	128248895	128253365	1	0	0	0	0	0	0	0	0	0	0	6		Q62219
ENSMUST00000163610	ENSMUSG00000025487	7	140881968	140898643	1	6	0	2	0	1	0	134	161	109	0	15	E9Q5I9	
ENSMUST00000163614						3	0	7	2	2	0	0	0	2	0	0		
ENSMUST00000163617	ENSMUSG00000030103	6	108660629	108666925	1	0	4	0	0	1	2	12	10	39	0	10	E9Q2C3	
ENSMUST00000163619	ENSMUSG00000013353	7	43492044	43505940	-1	13	10	31	16	15	8	12	83	26	8	46	A0A0B4J1M4	
ENSMUST00000163620	ENSMUSG00000019232	3	130617448	130637521	1	3	0	0	0	0	0	0	0	0	0	0	E9PYH3	
ENSMUST00000163621	ENSMUSG00000026384	1	119652467	119837613	-1	0	0	0	0	1	0	4	0	0	0	0	E9QA59	
ENSMUST00000163623	ENSMUSG00000021365	13	41309916	41487320	-1	4	0	17	30	20	3	38	8	14	13	13		
ENSMUST00000163624	ENSMUSG00000037801	9	63421455	63602493	-1	0	0	0	0	24	5	0	0	0	0	0	B7ZNG8	
ENSMUST00000163625						1	3	16	7	0	2	1	1	1	0	0		
ENSMUST00000163626	ENSMUSG00000074340	3	105973711	105987423	1	5	5	30	4	5	1	0	5	8	0	4	E9Q099	
ENSMUST00000163628	ENSMUSG00000044279	17	57059105	57065918	1	4	2	2	8	0	0	0	0	0	0	0	E9PZ04	
ENSMUST00000163636	ENSMUSG00000090627	14	6528612	6537290	-1	23	11	16	20	22	9	0	0	0	0	0	L7N297	
ENSMUST00000163640	ENSMUSG00000047515	6	136827626	136840662	1	0	0	2	0	0	0	0	0	0	0	0		Q810N5
ENSMUST00000163643	ENSMUSG00000006276	8	72341001	72421474	-1	22	14	48	45	40	15	556	988	745	118	669		Q60902
ENSMUST00000163646						3	2	5	4	1	2	0	1	0	0	0		
ENSMUST00000163647						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000163648						1	0	0	1	0	0	2	0	0	8	0		
ENSMUST00000163650						2	0	12	5	0	0	0	13	5	0	6		
ENSMUST00000163651	ENSMUSG00000094881	Y	2599099	2599434	1	0	0	1	1	3	0	0	0	0	0	0	A9Z055	
ENSMUST00000163652	ENSMUSG00000090166	14	43922720	43923559	-1	0	0	2	1	0	0	0	0	0	0	0	Q923L6	
ENSMUST00000163653	ENSMUSG00000028456	4	43058953	43264871	1	0	0	0	0	4	0	0	0	0	0	0		Q9Z1N9
ENSMUST00000163654	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	14	0	15	0		Q8BGJ9
ENSMUST00000163655	ENSMUSG00000090713	14	43288312	43293813	-1	10	12	27	9	14	3	0	0	0	1	0	E9Q0P0	
ENSMUST00000163657	ENSMUSG00000040325	9	106821874	106880992	1	0	0	0	0	0	0	0	1	0	1	3	F7A803	
ENSMUST00000163658	ENSMUSG00000091662	7	10579756	10613576	-1	7	5	4	2	0	1	0	0	0	0	0	Q8VIC1	
ENSMUST00000163659	ENSMUSG00000034829	8	71560556	71566649	-1	35	16	73	111	35	7	4	10	4	1	1		Q8VC33
ENSMUST00000163660	ENSMUSG00000027550	3	14533788	14572658	1	0	0	9	50	3	1	4	0	0	0	0	E9Q8Q7	
ENSMUST00000163661	ENSMUSG00000059994	3	87376387	87402934	1	0	12	8	2	8	6	64	534	141	272	168	E9Q958	
ENSMUST00000163663	ENSMUSG00000031523	8	36567751	36953143	-1	0	0	0	0	0	2	0	0	0	0	0	E9PXD2	
ENSMUST00000163665						1	0	0	0	1	1	1	6	1	0	0		
ENSMUST00000163666	ENSMUSG00000059796	11	69666936	69672423	-1	0	0	0	3	0	0	1166	5576	1464	4472	1429	Q5F2A7	P60843
ENSMUST00000163667	ENSMUSG00000022439	15	84324026	84342978	1	0	0	36	8	20	10	19	0	35	0	16	E9PYG5	
ENSMUST00000163668	ENSMUSG00000026860	2	30344809	30359337	-1	0	0	0	0	0	0	0	0	0	0	0		Q8R3V5
ENSMUST00000163670	ENSMUSG00000096326	12	115868773	115869227	-1	0	0	0	0	2	0	0	0	0	0	0	A0A075B674	
ENSMUST00000163672	ENSMUSG00000029028	4	154011731	154021513	1	1	0	0	0	2	0	10	25	12	0	8	F6YT33	
ENSMUST00000163677	ENSMUSG00000020590	12	35047189	35147469	1	2	0	9	19	6	5	14	3	22	3	17	E9Q7T4	
ENSMUST00000163678	ENSMUSG00000030237	6	141805440	141856199	-1	0	2	1	0	0	0	0	0	0	0	0	E9PWV5	
ENSMUST00000163680	ENSMUSG00000054640	17	81388691	81649607	-1	0	0	0	0	0	0	0	0	0	0	0	G5E8Y0	
ENSMUST00000163688	ENSMUSG00000047793	1	93235841	93301065	1	2	1	0	0	0	0	0	0	3	0	3	F6V5H4	
ENSMUST00000163691	ENSMUSG00000042622	15	79347541	79359072	1	13	7	20	135	10	6	42	49	44	17	21	Q3U0G5	O54791
ENSMUST00000163693						0	0	0	0	0	1	3	0	0	0	1		
ENSMUST00000163694	ENSMUSG00000032294	9	59656368	59679375	1	21	0	6	9	26	0	1076	2508	1317	202	1998		P52480
ENSMUST00000163695	ENSMUSG00000005262	16	18811779	18835261	1	0	0	3	1	1	0	0	13	14	70	29	E9Q0Y6	
ENSMUST00000163696						0	3	0	0	0	0	3	11	5	0	19		
ENSMUST00000163697						76	71	310	246	84	57	6	33	10	4	24		
ENSMUST00000163699						0	0	3	1	1	0	0	0	0	0	0		
ENSMUST00000163701	ENSMUSG00000037259	2	144470557	144527414	-1	84	48	106	0	58	46	3	11	11	0	10	E9Q4Z6	
ENSMUST00000163705	ENSMUSG00000038522	10	40001575	40025268	-1	22	7	30	84	22	4	0	0	0	0	0		Q8VCV9
ENSMUST00000163708						63	48	176	143	81	32	2	9	1	4	6		
ENSMUST00000163709	ENSMUSG00000001280	15	102406143	102436404	1	0	0	0	0	0	5	16	0	0	0	0		O89090
ENSMUST00000163710	ENSMUSG00000064179	7	4504570	4516382	-1	0	0	0	0	0	0	29	39	23	89	8		O88346
ENSMUST00000163713	ENSMUSG00000021548	13	85189408	85223469	1	2	1	1	0	0	1	0	19	6	9	10	F7D1U6	
ENSMUST00000163714	ENSMUSG00000022019	14	87416639	87545373	1	0	0	0	0	0	0	0	0	0	0	0	E9Q6T6	
ENSMUST00000163716	ENSMUSG00000071847	18	62922327	62953195	1	13	13	6	0	13	12	0	0	0	1	0		Q3U128
ENSMUST00000163717	ENSMUSG00000034681	17	24414675	24425895	1	0	5	15	28	0	0	71	136	105	6	86		Q99M28
ENSMUST00000163718	ENSMUSG00000068113	X	23882553	23907607	1	2	1	9	5	4	1	0	0	1	1	0	B1AXB9	
ENSMUST00000163719	ENSMUSG00000095681	14	5071040	5093318	1	3	0	2	19	9	0	0	0	0	0	0	L7N2D5	
ENSMUST00000163721						6	9	11	7	6	4	0	0	0	0	0		
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ENSMUST00000163723	ENSMUSG00000041708	15	83779467	83858494	1	0	0	5	0	0	0	0	0	0	0	0	E9Q0C0	
ENSMUST00000163724	ENSMUSG00000090485	2	152569338	152569538	1	0	2	0	0	2	0	0	0	0	0	0	Q30KP4	
ENSMUST00000163725	ENSMUSG00000094804	14	42847980	42853477	-1	8	3	0	0	0	1	0	0	0	0	0	F6U3N7	
ENSMUST00000163727	ENSMUSG00000033740	1	6487231	6860940	1	0	0	115	8	20	0	0	0	0	0	0	Q148A0	Q80TY4
ENSMUST00000163729						0	1	0	39	0	2	0	0	0	0	0		
ENSMUST00000163730	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	15	0	0	4	0	9	0	3	E9Q4Q6	
ENSMUST00000163732	ENSMUSG00000058183	4	154869585	154895528	1	0	0	0	3	1	0	0	0	0	0	0	E9PVK7	
ENSMUST00000163734	ENSMUSG00000033249	8	105269801	105275845	1	0	0	0	101	0	0	0	0	5	0	0	Q3UG93	
ENSMUST00000163735	ENSMUSG00000001416	3	88297116	88321767	1	0	0	0	0	0	0	23	0	0	0	0	F6Q609	
ENSMUST00000163736						2	1	4	3	6	0	0	6	4	0	6		
ENSMUST00000163738	ENSMUSG00000094258	14	4632352	4640802	1	2	0	3	0	0	0	0	0	0	0	0	K7N6Y0	
ENSMUST00000163739	ENSMUSG00000031539	8	22787354	22805654	-1	26	15	56	92	41	16	139	322	204	47	179		Q8R2R9
ENSMUST00000163742	ENSMUSG00000024534	18	52767709	52915935	1	0	0	0	0	3	0	0	5	0	0	0	E9Q4E2	
ENSMUST00000163745						1	0	0	6	1	0	3	9	8	17	4		
ENSMUST00000163746	ENSMUSG00000086040	6	54429603	54503768	1	39	11	64	0	0	0	1	0	0	0	3	D3Z5R4	
ENSMUST00000163747	ENSMUSG00000021285	12	111828458	111908055	-1	0	0	0	3	0	2	0	6	1	0	0	Q3UW51	
ENSMUST00000163748	ENSMUSG00000037174	3	51252720	51340663	-1	0	0	0	0	0	0	135	149	424	0	257		Q9JHC9

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000163749	ENSMUSG00000091695	18	67562387	67562851	1	15	4	47	9	3	2	2	0	4	2	1	F6QL70	
ENSMUST00000163750	ENSMUSG00000010376	14	55662265	55671906	-1	1	4	0	0	1	0	0	28	0	187	29	Q3UI46	P29595
ENSMUST00000163751	ENSMUSG00000030653	7	101421691	101512829	1	2	1	4	52	42	0	837	619	1161	139	551	Q3TXZ6	
ENSMUST00000163753	ENSMUSG00000019888	10	101681487	102391469	1	0	0	0	0	15	0	0	0	0	0	0		Q9D306
ENSMUST00000163754	ENSMUSG00000022401	15	81400138	81456807	1	100	57	442	76	85	39	97	209	172	24	148		B7ZMP1
ENSMUST00000163755						24	14	13	169	33	25	14	167	62	6	91		
ENSMUST00000163756	ENSMUSG00000002345	8	70139499	70167488	1	0	0	0	0	0	3	0	0	0	0	7	K7N7F1	
ENSMUST00000163757						1	3	0	82	6	1	0	0	0	0	0		
ENSMUST00000163760	ENSMUSG00000019944	10	69151434	69291791	1	0	0	0	0	0	1	0	1	0	0	0	F6UIH6	
ENSMUST00000163761	ENSMUSG00000019856	10	53633145	53750909	-1	10	5	0	0	0	0	0	0	0	1	0	F6TU77	
ENSMUST00000163762	ENSMUSG00000032841	2	101714285	101883027	-1	40	16	0	22	0	2	0	648	0	0	0		A2AVJ5
ENSMUST00000163763	ENSMUSG00000044279	17	57059105	57065918	1	5	1	12	122	6	2	1	0	0	0	0		Q8QZT4
ENSMUST00000163764	ENSMUSG00000025764	3	41555731	41616864	1	0	0	0	6	14	0	54	0	0	0	0		Q6ZPI0
ENSMUST00000163765	ENSMUSG00000022142	15	8109313	8159857	1	32	31	65	40	33	14	135	358	229	85	242		Q99P88
ENSMUST00000163766	ENSMUSG00000050619	2	121158273	121171125	-1	0	0	7	0	0	7	101	0	394	0	316	E9Q5B4	
ENSMUST00000163767	ENSMUSG00000022212	14	55510445	55517431	1	0	0	0	0	0	0	0	0	0	0	0		Q9Z140
ENSMUST00000163770	ENSMUSG00000026442	1	132564690	132741797	-1	0	0	0	0	0	0	0	0	0	0	0	E9PW06	
ENSMUST00000163771	ENSMUSG00000030109	6	121343076	121365775	1	0	0	5	0	4	0	0	0	0	0	2	F6SJH4	
ENSMUST00000163772						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000163773	ENSMUSG00000022441	15	83866712	84065379	-1	0	1	0	0	2	0	0	0	0	0	0	F6RST1	
ENSMUST00000163774	ENSMUSG00000031534	8	22462615	22476879	-1	0	0	0	24	0	0	0	0	0	0	0	E9PUT6	
ENSMUST00000163775	ENSMUSG00000046688	3	127789805	127832164	1	0	0	0	0	0	0	10	37	10	7	38	I3PQW8	Q793I8
ENSMUST00000163776	ENSMUSG00000054988	3	20314473	20367177	-1	0	0	0	0	0	0	0	0	0	0	0		P29755
ENSMUST00000163779	ENSMUSG00000025889	6	60731575	60829855	-1	4	0	0	0	0	0	0	8	0	22	0		O55042
ENSMUST00000163782	ENSMUSG00000049676	7	29181321	29214035	-1	4	0	0	2	0	0	0	16	0	0	0	F6TU54	
ENSMUST00000163783	ENSMUSG00000031881	8	104614141	104624396	-1	30	20	56	38	32	11	0	0	0	0	0	Q546A8	O88338
ENSMUST00000163785	ENSMUSG00000032773	19	8663789	8683587	1	50	29	131	82	73	29	0	4	2	1	4		P12657
ENSMUST00000163787	ENSMUSG00000091903	5	11594913	11599784	1	12	2	1	0	2	2	0	0	0	0	0	Q2TB45	
ENSMUST00000163788						0	0	0	1	0	0	0	2	2	5	2		
ENSMUST00000163790	ENSMUSG00000079364	14	7545151	7568566	-1	35	3	3	210	20	17	0	0	0	0	0	Q5FWC9	
ENSMUST00000163794						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000163796	ENSMUSG00000025875	13	54789377	54796776	1	0	0	0	0	0	0	0	5	6	0	0	E9PWC3	
ENSMUST00000163797	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	0	0	0	21	0	0	0	0	F6X7I4	
ENSMUST00000163798						3	4	7	15	7	2	8	75	42	4	32		
ENSMUST00000163799	ENSMUSG00000030688	7	101317086	101346626	1	11	0	15	23	4	4	5	0	0	0	4	E9PVP0	
ENSMUST00000163800	ENSMUSG00000095024	14	19594139	19602581	-1	18	14	0	0	4	2	0	0	0	0	0	E9Q6Y1	
ENSMUST00000163801	ENSMUSG00000071665	X	153118786	153132861	1	0	3	0	0	6	8	0	0	0	0	0		Q3UM89
ENSMUST00000163803	ENSMUSG00000090751	7	42903251	42933789	-1	12	6	4	4	7	5	0	0	0	0	0	E9Q0K5	
ENSMUST00000163804	ENSMUSG00000006154	7	4460674	4480487	1	0	0	2	2	4	0	0	0	0	0	0	E9PV32	
ENSMUST00000163805						2	3	3	0	3	2	30	31	5	7	14		
ENSMUST00000163808	ENSMUSG00000090461	10	118289629	118295038	-1	1	0	0	0	0	0	0	0	0	0	0		Q9JJY8
ENSMUST00000163810	ENSMUSG00000035299	X	169685199	170005736	1	0	0	0	0	0	0	0	0	0	0	0		O70583
ENSMUST00000163812	ENSMUSG00000038943	7	80294450	80316259	1	0	0	9	84	5	0	0	76	91	55	30	G3UW86	
ENSMUST00000163816	ENSMUSG00000032118	9	36821939	36878924	1	3	0	0	0	0	7	0	0	0	0	0		Q8K0X8
ENSMUST00000163819						5	1	9	9	8	4	7	12	6	0	9		
ENSMUST00000163820	ENSMUSG00000032246	9	62858104	62875918	1	3	3	0	0	4	0	0	2	0	78	10	E9Q1L1	
ENSMUST00000163821	ENSMUSG00000041362	19	58973358	59076069	-1	20	1	68	178	17	11	33	0	0	0	0		Q8K2Q9
ENSMUST00000163823						0	2	2	0	0	0	0	0	7	8	0		
ENSMUST00000163826	ENSMUSG00000091676	14	7362097	7365134	-1	8	5	1	3	7	0	0	0	0	0	0	L7N2A9	
ENSMUST00000163827	ENSMUSG00000030177	6	120324323	120364374	-1	0	0	0	0	0	0	0	7	0	0	0	E9Q478	
ENSMUST00000163829	ENSMUSG00000029580	5	142903115	142906754	-1	0	0	0	0	0	0	6	2	16	7	0	E9Q2D1	
ENSMUST00000163830						15	8	23	16	14	7	2	7	1	0	5		
ENSMUST00000163832	ENSMUSG00000022707	16	70313949	70569716	1	0	0	0	61	0	0	127	297	152	57	176		Q9D6Y9
ENSMUST00000163833						3	0	6	4	3	0	0	0	1	0	0		
ENSMUST00000163837	ENSMUSG00000031708	8	83571700	83594491	-1	0	2	0	5	8	0	34	111	31	0	72	Q52L67	
ENSMUST00000163839	ENSMUSG00000094992	9	109645122	109664652	-1	11	6	12	10	7	5	2	14	16	2	8	F7C9P2	
ENSMUST00000163843						0	0	0	1	3	0	0	0	13	11	1		
ENSMUST00000163844	ENSMUSG00000006932	9	120929216	120960507	1	0	0	0	0	0	0	0	0	596	176	1037	E9PW26	
ENSMUST00000163845	ENSMUSG00000030447	7	55841745	55932602	1	1	0	0	13	0	0	823	2710	1765	252	763		Q7TMB8
ENSMUST00000163846						0	3	4	2	8	0	35	167	90	12	155		
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ENSMUST00000163850	ENSMUSG00000091754	14	6735685	6742332	-1	6	8	0	0	8	5	0	0	0	0	0	E9Q5P1	
ENSMUST00000163852	ENSMUSG00000090762	7	12693998	12733105	-1	19	8	23	14	4	2	0	0	0	0	0	E9Q4U5	
ENSMUST00000163854	ENSMUSG00000026074	1	39900913	40026310	1	0	0	1	13	17	0	0	478	200	37	179	E9PVG7	
ENSMUST00000163855	ENSMUSG00000023027	15	100227819	100261244	1	0	0	0	14	0	0	0	0	81	30	28	E9PYW2	
ENSMUST00000163856	ENSMUSG00000051147	8	67494867	67502580	1	7	3	3	4	9	3	0	8	7	6	11	Q78ZC4	P50295
ENSMUST00000163858	ENSMUSG00000005986	19	4270180	4283137	-1	6	6	22	22	34	0	45	22	37	10	0	E9Q821	
ENSMUST00000163864						12	9	23	10	17	4	12	14	9	21	6		
ENSMUST00000163865	ENSMUSG00000024043	17	67842713	68004120	-1	0	0	0	0	0	7	2	0	0	0	0		Q8BN58
ENSMUST00000163867	ENSMUSG00000020312	10	79617940	79637918	-1	30	31	68	52	52	21	0	3	2	0	0		Q8BMC3
ENSMUST00000163869	ENSMUSG00000091490	8	43183119	43193881	1	7	5	15	9	18	4	0	0	0	0	0	E9PW10	
ENSMUST00000163871	ENSMUSG00000017978	6	23262773	23839421	-1	0	0	0	34	8	0	0	0	0	0	0	E9Q835	
ENSMUST00000163878	ENSMUSG00000017288	11	76046226	76179647	-1	0	1	0	0	0	0	2	0	0	0	0	E9Q8C4	
ENSMUST00000163879	ENSMUSG00000032570	9	105403539	105527319	-1	4	7	0	11	1	0	62	116	275	18	297	Q8BMS7	
ENSMUST00000163881	ENSMUSG00000090853	13	41273803	41273977	-1	0	0	0	0	0	0	0	0	0	0	0	F6QIW7	
ENSMUST00000163884	ENSMUSG00000002845	16	38558698	38592162	1	0	0	0	0	0	0	95	224	80	37	69		Q9CYC3
ENSMUST00000163885	ENSMUSG00000091275	14	5939225	5961745	-1	7	6	15	51	8	4	0	0	0	0	0	K7N721	
ENSMUST00000163887	ENSMUSG00000055945	17	8340406	8344112	1	0	15	0	262	12	12	0	37	9	0	12		Q6PAN7
ENSMUST00000163888	ENSMUSG00000005583	13	83504034	83667080	1	0	0	12	17	15	0	28	124	23	8	39	A0A0H2UH28	
ENSMUST00000163889	ENSMUSG00000040472	14	55715873	55722257	-1	0	0	0	24	0	0	287	312	247	32	172		Q9JHK4
ENSMUST00000163892						20	18	33	31	34	15	176	588	336	56	411		
ENSMUST00000163893	ENSMUSG00000006154	7	4460674	4480487	1	0	0	19	0	0	0	0	0	0	0	0		Q8R5F8
ENSMUST00000163895	ENSMUSG00000033392	9	113812586	113919697	1	6	9	20	0	5	3	0	0	61	9	56	F7DCH5	
ENSMUST00000163897	ENSMUSG00000051243	9	58196298	58204319	-1	2	7	9	12	12	0	0	0	0	0	0		Q5RKR3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000163898	ENSMUSG00000036256	5	77349240	77408041	-1	0	0	4	17	9	0	0	4	3	0	13	E9Q5D9	
ENSMUST00000163901	ENSMUSG00000005442	7	25267704	25294159	1	0	0	0	0	0	0	0	173	0	2	0	F6SAZ4	
ENSMUST00000163902						0	0	9	9	1	0	93	1881	181	270	206		
ENSMUST00000163903	ENSMUSG00000064307	7	101912984	101933895	-1	0	0	12	0	2	0	8	3	10	1	16		Q9DAK8
ENSMUST00000163905	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	0	5	5	0	0	0	0	0	0	E9PZV0	
ENSMUST00000163906						5	0	10	24	4	0	0	0	0	0	0		
ENSMUST00000163907						2	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000163909						0	4	0	0	2	3	0	0	0	0	0		
ENSMUST00000163912	ENSMUSG00000090440	14	43298872	43306004	1	3	10	13	9	6	0	0	0	0	1	1	F6QVC4	
ENSMUST00000163913	ENSMUSG00000015957	7	98835112	98855195	1	0	0	6	27	9	3	0	0	0	0	0	E9PYZ1	
ENSMUST00000163914						0	0	0	17	45	0	0	0	0	0	0		
ENSMUST00000163915	ENSMUSG00000025875	13	54789377	54796776	1	4	2	2	0	5	3	0	7	0	0	3	E9QAJ5	
ENSMUST00000163917						0	2	2	1	2	1	0	1	1	0	0		
ENSMUST00000163922						3	11	3	5	4	1	0	0	0	0	0		
ENSMUST00000163924	ENSMUSG00000021938	14	56722441	56778316	-1	8	3	7	6	11	2	3	50	27	7	19		Q8R326
ENSMUST00000163925	ENSMUSG00000031559	8	49370886	49521095	1	0	1	0	2	0	0	0	0	0	0	0	Q9D4V1	
ENSMUST00000163928						2	2	3	1	1	1	0	0	0	0	0		
ENSMUST00000163929	ENSMUSG00000025019	19	41482645	41562246	1	7	10	8	5	10	8	4	0	6	0	6	A4FTY7	Q6ZPI3
ENSMUST00000163931	ENSMUSG00000078687	4	60218621	60222599	-1	0	0	0	0	0	2	0	0	0	0	0	E9PVW0	
ENSMUST00000163932						1	0	0	1	0	0	0	0	0	0	3		
ENSMUST00000163936	ENSMUSG00000029862	6	42286685	42315756	1	7	0	6	0	0	0	0	0	0	0	0	F6QI82	
ENSMUST00000163937	ENSMUSG00000045201	14	15357519	15438987	-1	1	2	5	1	0	0	0	0	0	0	0	Q543Z7	Q8VCH9
ENSMUST00000163940	ENSMUSG00000044092	5	139405280	139415623	1	6	9	7	4	25	3	939	1533	661	195	784	Q497Y9	
ENSMUST00000163941						3	0	7	5	0	0	6	49	14	0	19		
ENSMUST00000163943						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000163944						0	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000163945						4	0	3	5	0	0	0	0	0	0	0		
ENSMUST00000163946	ENSMUSG00000078570	4	124849080	124851196	-1	0	0	0	0	0	0	38	73	38	19	6	E9Q9M4	
ENSMUST00000163948	ENSMUSG00000002845	16	38558698	38592162	1	0	1	0	12	5	0	19	34	16	17	28	E9QA83	
ENSMUST00000163949	ENSMUSG00000051855	6	30723547	30748465	1	7	3	6	5	7	4	4	7	7	3	14		Q07646
ENSMUST00000163950						2	1	0	24	4	0	0	0	1	0	5		
ENSMUST00000163954	ENSMUSG00000023403	6	49395604	49469501	1	0	0	0	35	0	0	0	0	0	0	0	E9Q260	
ENSMUST00000163955	ENSMUSG00000021794	14	34310727	34345144	1	0	0	4	0	0	0	6	32	27	11	25	F7CFA5	
ENSMUST00000163957						0	1	2	0	0	0	4	29	20	0	0		
ENSMUST00000163959	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	0	249	0	0	0	0	2	0	2	E9Q6V5	
ENSMUST00000163960						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000163961	ENSMUSG00000082101	11	83275110	83286726	-1	23	18	20	45	21	8	2	0	1	0	2	V9GXG1	
ENSMUST00000163963	ENSMUSG00000029672	6	22306520	22356243	-1	2	1	0	1	0	0	0	0	0	0	23	G5E911	
ENSMUST00000163964						2	7	2	4	6	4	0	2	0	0	0		
ENSMUST00000163966	ENSMUSG00000023944	17	45567775	45573271	-1	0	0	0	2	0	0	0	0	0	0	0	E9PX27	
ENSMUST00000163967	ENSMUSG00000009214	2	27061636	27072179	-1	4	7	0	10	8	0	0	0	0	0	0	E9QA72	
ENSMUST00000163968	ENSMUSG00000006019	7	16197147	16222037	-1	0	0	0	0	0	0	243	384	241	1	277		
ENSMUST00000163969	ENSMUSG00000025272	X	150645304	150657583	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q160	
ENSMUST00000163970	ENSMUSG00000095528	14	43602627	43608065	-1	5	6	0	0	10	0	0	0	0	0	0	L7N286	
ENSMUST00000163972	ENSMUSG00000032199	9	71478437	71485935	-1	5	11	17	6	0	7	28	0	21	23	18		Q6P6I6
ENSMUST00000163973						18	15	41	25	27	5	0	3	7	2	6		
ENSMUST00000163974						0	0	0	0	0	4	0	0	1	0	0		
ENSMUST00000163975						5	3	9	8	1	1	0	0	0	0	0		
ENSMUST00000163977						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000163979	ENSMUSG00000032479	9	109931460	110083955	1	25	13	114	0	0	3	256	0	478	0	328		
ENSMUST00000163981	ENSMUSG00000032523	9	121784016	121792507	-1	0	0	0	0	7	14	0	1	0	0	0		Q9D1G3
ENSMUST00000163982	ENSMUSG00000037801	9	63421455	63602493	-1	0	0	0	0	0	0	0	0	0	0	0	B2RUB3	
ENSMUST00000163985						0	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000163987	ENSMUSG00000047866	8	86624043	86723873	1	3	0	8	0	0	0	0	3	0	1	0	Q8BK80	
ENSMUST00000163990						4	0	1	1	0	0	0	3	0	0	3		
ENSMUST00000163991	ENSMUSG00000071724	15	76294434	76296896	1	13	3	60	193	24	18	309	484	182	19	184	D6MZJ6	
ENSMUST00000163992						43	51	216	76	80	37	2	12	5	13	9		
ENSMUST00000163993	ENSMUSG00000004994	8	84257795	84270380	-1	0	0	0	0	0	0	4	5	0	4	6	E9Q5P3	
ENSMUST00000163994						4	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000163995						0	0	6	0	0	0	30	15	73	0	0		
ENSMUST00000163997	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	0	0	1	0	0	E9Q9L1	
ENSMUST00000163998	ENSMUSG00000092137	9	71479325	71592265	-1	0	0	0	0	2	2	0	0	0	0	0	E9PZ54	
ENSMUST00000164000						5	1	5	9	3	0	0	0	0	0	3		
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ENSMUST00000164004						2	3	3	4	6	2	6	28	12	3	13		
ENSMUST00000164006	ENSMUSG00000029687	6	47530139	47595341	-1	0	0	0	1	0	0	3	0	0	7	11	F6T3Z0	
ENSMUST00000164007	ENSMUSG00000036172	16	44943678	44981380	1	0	0	0	0	0	0	11	34	0	0	0		Q5UKY4
ENSMUST00000164009						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164010	ENSMUSG00000004661	9	57790353	57836793	-1	2	0	0	53	0	1	0	8	15	0	21	E9PW42	
ENSMUST00000164011	ENSMUSG00000021555	13	59585259	59634798	1	0	2	0	0	0	1	0	0	0	0	0	F6UFC8	
ENSMUST00000164012	ENSMUSG00000003476	6	55090049	55133016	-1	4	2	5	1	4	4	0	0	0	0	0	E9PXI8	
ENSMUST00000164014						7	3	4	0	13	2	0	0	0	0	0		
ENSMUST00000164016	ENSMUSG00000025509	7	141455198	141460743	1	22	9	44	126	27	14	78	127	63	0	56		Q8BJ56
ENSMUST00000164018	ENSMUSG00000039607	9	116572746	117629913	-1	3	3	2	0	1	1	0	0	0	0	0		Q8BWL5
ENSMUST00000164019						0	1	0	3	2	2	3	40	9	0	8		
ENSMUST00000164020						68	54	147	41	53	37	0	2	0	0	4		
ENSMUST00000164022	ENSMUSG00000017286	11	76120987	76243725	-1	0	0	0	0	0	0	58	257	144	402	0	F6ZTG3	
ENSMUST00000164023	ENSMUSG00000058260	12	103994743	104013755	-1	0	3	3	0	1	1	0	0	0	0	0	E9Q865	
ENSMUST00000164026	ENSMUSG00000068349	15	74813452	74818815	-1	7	9	10	5	1	7	0	0	0	0	0	E9PX31	
ENSMUST00000164027						0	0	0	23	0	0	31	24	88	0	59		
ENSMUST00000164034	ENSMUSG00000019944	10	69151434	69291791	1	0	0	0	2	3	0	0	0	0	0	0		Q9DAK3
ENSMUST00000164035	ENSMUSG00000004661	9	57790353	57836793	-1	17	12	32	23	18	5	51	89	69	4	144		Q9Z1N7
ENSMUST00000164036						1	0	0	9	1	0	0	0	0	0	0		
ENSMUST00000164037	ENSMUSG00000004347	6	56069804	56569103	-1	0	0	23	29	47	15	0	0	0	0	0	E9Q7V6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000164038	ENSMUSG00000095056	14	4397526	4406347	1	0	3	0	0	0	3	0	0	0	0	0	K7N6T3	
ENSMUST00000164039	ENSMUSG00000043531	19	50143301	50678646	-1	20	11	17	7	19	10	0	1	1	0	0	E9PYT6	
ENSMUST00000164041	ENSMUSG00000076733	12	115765333	115765635	-1	1	0	4	2	1	1	1	1	0	0	0	A0A075B678	
ENSMUST00000164042	ENSMUSG00000090353	2	126215100	126216212	1	2197	2190	12835	3192	1836	930	10	48	29	1	46	F6U8B9	
ENSMUST00000164044	ENSMUSG00000059498	1	171051174	171064935	-1	0	0	0	0	0	0	6419	19551	8625	30148	7310	A0A0B4J1M6	
ENSMUST00000164045	ENSMUSG00000096073	7	23250762	23251682	-1	0	0	0	1	0	0	0	0	0	0	0	D3YTY2	
ENSMUST00000164047	ENSMUSG00000001627	12	40201567	40248504	-1	0	0	0	0	0	0	79	174	16	3	4	F6TBT6	
ENSMUST00000164048						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000164050	ENSMUSG00000022831	16	36934983	36963212	1	1	0	0	0	1	0	1095	1046	1307	57	986	E9Q4E5	
ENSMUST00000164052	ENSMUSG00000001376	6	3498382	3603531	1	26	26	46	22	22	12	12	43	15	10	15		Q8CI71
ENSMUST00000164053						3	0	6	5	0	0	0	0	0	59	16		
ENSMUST00000164055						13	8	5	6	12	6	7	15	23	4	33		
ENSMUST00000164056	ENSMUSG00000048897	7	80024814	80094173	1	34	10	57	16	0	35	880	1440	551	88	622		Q3U288
ENSMUST00000164061						3	4	17	9	6	2	0	0	0	0	0		
ENSMUST00000164064	ENSMUSG00000090451	18	78349754	78350701	1	0	4	9	2	3	1	0	1	0	0	0	B2RY53	
ENSMUST00000164066	ENSMUSG00000000420	18	24205344	24286818	1	0	0	0	0	5	0	8	0	119	40	90	F6PYE1	
ENSMUST00000164067	ENSMUSG00000050087	11	50354462	50359699	1	0	0	0	0	9	0	0	0	0	0	0		Q9CVN6
ENSMUST00000164068						0	0	0	0	0	0	0	0	0	0	18		
ENSMUST00000164069	ENSMUSG00000090472	14	4555405	4562747	1	0	2	0	2	0	0	0	0	0	0	0	L7N2D6	
ENSMUST00000164070	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	0	21	0	0	0	0	0	0	0	E9Q147	
ENSMUST00000164071	ENSMUSG00000025272	X	150645304	150657583	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q1Q4	
ENSMUST00000164072						0	0	3	0	2	0	0	0	0	0	0		
ENSMUST00000164073						2	3	1	4	5	0	0	0	0	25	7		
ENSMUST00000164076	ENSMUSG00000031872	8	104170513	104219092	1	22	0	0	0	0	13	0	1	0	0	0	E9Q314	
ENSMUST00000164077	ENSMUSG00000020212	10	118141787	118168997	1	0	0	0	0	14	11	74	54	141	52	117	E9PW14	
ENSMUST00000164078	ENSMUSG00000044092	5	139405280	139415623	1	14	9	29	18	16	19	296	485	423	53	602	F7AVJ9	
ENSMUST00000164079	ENSMUSG00000031939	9	15306214	15312104	1	1	0	0	1	8	0	19	149	37	59	37		Q9D4V4
ENSMUST00000164081	ENSMUSG00000043943	9	18321951	18402995	-1	0	0	0	0	11	0	0	0	0	0	0	E9PY80	
ENSMUST00000164082	ENSMUSG00000034913	14	75582834	75593116	-1	0	0	0	0	0	0	0	0	0	0	0		Q32MG2
ENSMUST00000164083	ENSMUSG00000044475	10	60002805	60099990	1	0	7	17	4	10	3	0	44	32	45	84		Q9D8Z1
ENSMUST00000164086	ENSMUSG00000026384	1	119652467	119837613	-1	0	0	0	0	0	0	2	2	2	1	1	F6U7Q0	
ENSMUST00000164088	ENSMUSG00000020166	10	116485161	116581511	-1	0	0	0	0	0	6	0	382	0	42	0	E9Q027	
ENSMUST00000164091	ENSMUSG00000029862	6	42286685	42315756	1	0	0	10	0	15	0	0	0	0	0	0	E9Q2N3	
ENSMUST00000164093	ENSMUSG00000078787	7	27153714	27158668	1	11	3	0	2	0	6	2	0	6	1	0	E9PWV0	
ENSMUST00000164095	ENSMUSG00000030451	7	56050196	56231800	1	0	71	118	30	94	0	474	697	988	37	1057		Q4U2R1
ENSMUST00000164096	ENSMUSG00000090553	1	133603871	133610291	-1	2	4	0	1	0	0	2	4	0	0	5	E9Q4F4	
ENSMUST00000164097	ENSMUSG00000006538	1	74945315	74951672	-1	20	7	34	129	33	5	2	4	4	0	4	Q80XI9	
ENSMUST00000164098						0	2	0	1	0	0	0	0	0	0	2		
ENSMUST00000164099	ENSMUSG00000031993	9	30427329	30466726	1	53	32	61	81	54	27	194	427	310	33	282	Q6P4T1	
ENSMUST00000164100	ENSMUSG00000032186	9	75565621	75611325	-1	2	0	9	2	2	3	0	0	0	0	1		Q9JKK7
ENSMUST00000164101	ENSMUSG00000004221	X	74393290	74453854	1	9	0	0	0	0	0	90	0	0	0	0		O88522
ENSMUST00000164102	ENSMUSG00000020843	11	76406952	76416292	1	0	0	0	14	1	1	0	0	0	0	0	E9PXB9	
ENSMUST00000164106						33	33	86	33	34	30	1	10	13	2	28		
ENSMUST00000164107	ENSMUSG00000009681	10	75060896	75184923	1	47	43	97	404	82	37	458	617	659	49	602		Q6PAJ1
ENSMUST00000164108	ENSMUSG00000004364	1	80264923	80340480	-1	4	0	8	5	7	0	612	2698	1245	133	650	E9Q4T8	
ENSMUST00000164110						22	40	240	88	48	6	2	0	0	0	10		
ENSMUST00000164111	ENSMUSG00000034751	13	102732486	103334497	-1	7	8	30	24	12	12	0	1	2	0	1	Q8BGU6	
ENSMUST00000164113	ENSMUSG00000036466	9	64385626	64709205	1	0	0	0	3	0	0	0	0	0	2	0	E9Q918	
ENSMUST00000164114	ENSMUSG00000044033	2	77009902	77170636	-1	0	0	0	0	0	0	1	0	0	0	0	E9Q8Q6	
ENSMUST00000164119	ENSMUSG00000040212	7	45918023	45921426	-1	6	3	18	13	14	3	49	67	39	24	34		O35912
ENSMUST00000164120	ENSMUSG00000027469	2	152847964	152895321	1	21	0	106	124	0	0	38	39	31	0	112		A2APB8
ENSMUST00000164121	ENSMUSG00000035365	10	88091432	88146941	-1	0	1	0	0	0	0	0	2	0	0	0	E9QAI0	
ENSMUST00000164122						1	3	0	1	0	4	0	0	0	4	0		
ENSMUST00000164123	ENSMUSG00000027861	3	102086415	102146514	1	0	2	0	0	3	1	0	0	0	0	0	E9PZ67	
ENSMUST00000164127	ENSMUSG00000021548	13	85189408	85223469	1	3	0	0	6	2	0	7	35	8	0	8	Q3UUW5	
ENSMUST00000164128	ENSMUSG00000079434	1	87509889	87597845	1	9	7	6	0	3	4	0	0	0	0	0		
ENSMUST00000164129	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	36	0	0	3	4	7	0	3	F6Z4Q6	
ENSMUST00000164132						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164134						4	0	8	102	8	7	6	12	4	7	18		
ENSMUST00000164137						6	3	3	124	6	8	9	39	0	0	4		
ENSMUST00000164138						3	3	8	10	4	1	0	0	0	0	0		
ENSMUST00000164139	ENSMUSG00000091568	14	6016759	6038209	-1	0	13	4	55	18	8	0	0	0	0	0	E9Q5Q3	
ENSMUST00000164140						5	0	11	22	12	5	0	0	0	0	0		
ENSMUST00000164143	ENSMUSG00000023827	17	12118704	12219645	1	1	0	3	14	3	1	0	0	0	0	0	E9Q6S5	
ENSMUST00000164144						0	0	0	0	0	0	0	2	3	0	2		
ENSMUST00000164146	ENSMUSG00000063163	16	69856874	69863744	-1	0	0	4	2	0	0	0	0	0	0	0	F7A9A8	
ENSMUST00000164147	ENSMUSG00000026970	2	60750193	60963192	-1	0	1	2	0	8	6	252	412	197	0	264	E9PZ21	
ENSMUST00000164148	ENSMUSG00000071179	12	103668808	103676139	-1	5	5	28	9	5	6	0	0	0	0	0	D3Z660	
ENSMUST00000164155	ENSMUSG00000021416	13	34946614	34963810	-1	0	0	0	4	0	0	3	34	11	27	10	E9PY42	
ENSMUST00000164157	ENSMUSG00000093825	14	49928563	49931787	-1	4	7	0	0	6	1	0	0	0	0	0	E9PZU2	
ENSMUST00000164161	ENSMUSG00000025404	10	127380327	127499384	1	5	2	16	5	14	3	218	105	326	18	180	E9Q0F6	
ENSMUST00000164163	ENSMUSG00000022372	15	66780819	66831829	-1	8	8	24	9	12	9	1769	2171	3324	911	2582	Q4FJX0	Q60898
ENSMUST00000164166	ENSMUSG00000001416	3	88297116	88321767	1	0	0	0	0	0	0	18	20	0	2	0	E9Q133	
ENSMUST00000164167	ENSMUSG00000090957	17	17911039	17911947	-1	3	4	19	10	9	3	1	0	4	0	6	F7CXE4	
ENSMUST00000164169						5	3	0	5	5	2	4	32	7	5	5		
ENSMUST00000164172	ENSMUSG00000027186	2	103411688	103450989	1	0	3	5	0	5	3	0	0	0	0	0	Q3V1F7	Q8VDK3
ENSMUST00000164175	ENSMUSG00000031876	8	104281347	104310145	-1	2	0	11	2	5	2	21	19	15	0	4	E9PXC5	
ENSMUST00000164176						2	5	5	2	5	2	2	1	1	0	0		
ENSMUST00000164178	ENSMUSG00000079173	5	137378637	137477064	-1	86	67	261	145	125	66	2	0	2	1	14	E9PWQ7	
ENSMUST00000164179	ENSMUSG00000059498	1	171051174	171064935	-1	13	4	8	730	20	14	2	5	6	9	4	E9PVR4	
ENSMUST00000164180						6	5	16	9	6	3	0	0	0	0	0		
ENSMUST00000164181	ENSMUSG00000090841	10	128490860	128493875	-1	22	14	38	29	28	14	11046	21186	7980	41410	5775	Q642K0	Q60605
ENSMUST00000164182	ENSMUSG00000055730	8	104734003	104741634	1	6	0	6	0	17	10	0	0	0	6	1		Q8QZR3
ENSMUST00000164183	ENSMUSG00000021147	13	8802968	8871909	-1	3	7	15	99	1	7	5	0	27	17	23	Q05BF4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000164184						1	2	6	11	3	0	197	302	145	87	125		
ENSMUST00000164186	ENSMUSG00000041923	18	22693181	23041653	-1	0	0	5	0	4	0	0	0	0	0	0	E9Q947	
ENSMUST00000164189	ENSMUSG00000022562	15	76296597	76328015	-1	0	7	56	71	26	0	0	4	4	1	0	E9Q484	
ENSMUST00000164190	ENSMUSG00000009073	11	4765845	4849536	-1	0	0	0	0	0	0	0	0	4	0	4	E9PW99	
ENSMUST00000164192	ENSMUSG00000071042	17	75435905	75529043	1	26	6	24	9	37	4	0	1	2	3	3	Q6NZH9	
ENSMUST00000164195	ENSMUSG00000019990	10	20398004	20725078	-1	10	0	15	7	6	0	0	0	0	0	0	E9PW23	
ENSMUST00000164199	ENSMUSG00000025374	10	128401395	128411492	-1	6	10	11	10	11	6	45	44	36	14	31		Q8R2Y9
ENSMUST00000164202	ENSMUSG00000043639	19	53677306	53867080	1	9	40	0	76	0	28	0	0	0	0	0		Q3UQS8
ENSMUST00000164203						0	0	0	0	0	0	0	0	0	72	0		
ENSMUST00000164204	ENSMUSG00000024909	19	5473973	5481853	1	0	0	0	0	0	0	0	0	0	0	0	F7AYH6	
ENSMUST00000164205	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164207	ENSMUSG00000054252	5	33721674	33737068	1	0	0	0	0	0	0	0	0	0	0	0	F6TK14	
ENSMUST00000164208	ENSMUSG00000021903	14	32028989	32062197	1	10	8	0	0	23	6	2	2	4	0	4	G3UWF7	
ENSMUST00000164209	ENSMUSG00000094936	19	4784293	4793901	-1	0	0	0	4	0	0	42	68	30	23	17	Q5CZX8	
ENSMUST00000164211						32	38	194	69	49	25	1	1	0	0	4		
ENSMUST00000164212	ENSMUSG00000019944	10	69151434	69291791	1	0	0	0	0	0	0	0	0	0	0	0	E9QAZ7	
ENSMUST00000164213	ENSMUSG00000042787	9	119444923	119465517	1	8	0	0	81	6	0	5	32	19	4	13	E9PZS5	
ENSMUST00000164215	ENSMUSG00000021557	13	59449537	59585227	-1	7	7	17	6	3	13	25	41	51	16	141		Q641K1
ENSMUST00000164216	ENSMUSG00000091685	3	79336661	79464129	1	5	3	1	4	2	7	1	0	1	0	0	E9QAV2	
ENSMUST00000164217	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	0	39	0	0	0	0	0	7	5	E9PWY7	
ENSMUST00000164219	ENSMUSG00000015653	5	5664829	5694578	-1	23	11	31	24	27	0	0	0	0	5	0	B2RX33	Q8BWB6
ENSMUST00000164220	ENSMUSG00000040599	11	71019611	71027371	1	0	0	0	0	0	0	10	10	44	15	1		Q9CY25
ENSMUST00000164222	ENSMUSG00000038524	18	37957431	37969774	-1	0	0	1	0	2	0	0	0	0	0	0	E9QA76	
ENSMUST00000164223	ENSMUSG00000079608	18	70472454	70501066	1	0	0	0	0	0	0	0	0	0	0	0	Q9CPT8	P59096
ENSMUST00000164225	ENSMUSG00000056476	3	59005825	59318682	1	47	39	71	0	60	23	0	0	0	0	0		Q8BQM9
ENSMUST00000164226						4	4	2	0	0	0	0	0	0	0	0		
ENSMUST00000164227	ENSMUSG00000091511	10	130471332	130497379	-1	6	9	8	9	9	3	0	0	0	0	0	E9PZX4	
ENSMUST00000164228						13	8	11	12	18	5	0	0	0	0	0		
ENSMUST00000164232	ENSMUSG00000095044	14	41962708	41967927	-1	6	4	10	1	0	7	0	0	0	0	0	F6T8D7	
ENSMUST00000164233	ENSMUSG00000028410	4	40722150	40737149	1	28	31	28	27	35	19	9	52	13	7	21	Q5NTY0	P63037
ENSMUST00000164235	ENSMUSG00000021840	14	47298314	47323204	1	0	81	1	0	42	52	31	54	0	0	43		Q8BH93
ENSMUST00000164236						2	2	10	1	3	1	0	0	0	0	0		
ENSMUST00000164241						0	0	1	0	2	6	0	0	0	0	0		
ENSMUST00000164242	ENSMUSG00000040312	17	35517100	35531015	1	0	2	12	77	17	3	0	38	43	4	32		Q8K2I2
ENSMUST00000164243	ENSMUSG00000079108	12	55155104	55263020	1	2	1	0	2	1	2	132	623	177	176	120	E9PXC0	
ENSMUST00000164245	ENSMUSG00000094545	7	20441670	20442593	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q365	
ENSMUST00000164246	ENSMUSG00000041729	9	62419492	62537044	-1	2	0	3	0	2	0	0	1	0	0	0	G3UW48	
ENSMUST00000164248						10	6	18	15	17	7	0	0	0	0	0		
ENSMUST00000164250	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	21	0	1	3	0	0	0	0	E9PYE0	
ENSMUST00000164251	ENSMUSG00000024158	17	24840143	24864450	1	8	3	3	2	2	2	1	0	0	0	0	E9Q2H8	
ENSMUST00000164252	ENSMUSG00000004561	14	51884842	51893039	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0X9	
ENSMUST00000164253	ENSMUSG00000024576	18	61555274	61590061	1	0	0	3	0	0	0	6	62	0	0	14	F6YBC9	
ENSMUST00000164259	ENSMUSG00000040462	10	127094259	127121160	-1	12	18	13	14	44	0	2205	3480	2746	554	2352		Q8K2C7
ENSMUST00000164260	ENSMUSG00000037851	13	49682100	49734267	1	0	0	0	0	0	0	21	0	0	19	92		Q8BU30
ENSMUST00000164262	ENSMUSG00000096846	5	11256033	11260494	1	0	0	0	0	0	0	0	0	0	0	0	L7N284	
ENSMUST00000164263	ENSMUSG00000002489	16	89787111	89980080	-1	2	6	30	30	3	0	0	0	0	0	0	E9Q1R7	
ENSMUST00000164264						1	0	0	1	0	0	0	0	5	0	0		
ENSMUST00000164267	ENSMUSG00000049241	5	123876736	123880020	-1	29	14	58	25	48	16	0	0	0	0	0	E9PZR8	
ENSMUST00000164269	ENSMUSG00000026384	1	119652467	119837613	-1	0	0	0	0	0	0	0	0	0	0	1	F6ZWR8	
ENSMUST00000164271	ENSMUSG00000054934	10	116417861	116473878	-1	0	2	0	16	2	1	0	0	0	0	1	F6TJT3	
ENSMUST00000164272	ENSMUSG00000079460	X	112239049	112243852	1	3	2	4	0	4	3	0	0	0	0	0	F6UK53	
ENSMUST00000164273	ENSMUSG00000031934	9	15005161	15045478	-1	16	11	11	15	21	10	0	25	8	0	0		Q9JIP4
ENSMUST00000164275						3	5	13	8	12	7	0	0	0	0	0		
ENSMUST00000164277	ENSMUSG00000091569	14	44433635	44439086	1	6	1	3	0	0	2	0	0	0	0	0	F7CFJ3	
ENSMUST00000164280	ENSMUSG00000020335	11	50921823	50931633	-1	8	12	0	0	1	0	0	0	0	0	0		Q9QXT9
ENSMUST00000164283	ENSMUSG00000003316	8	111154421	111259216	-1	0	0	0	134	0	0	0	0	0	0	0	E9PWD8	
ENSMUST00000164288	ENSMUSG00000095973	7	20872256	20873179	1	0	0	0	0	0	0	0	0	0	0	0	L7N2A6	
ENSMUST00000164290	ENSMUSG00000026815	2	28609450	28621982	-1	17	13	38	68	24	16	0	0	0	0	0	B7ZNH2	
ENSMUST00000164292						8	2	4	3	4	1	2	0	0	0	0		
ENSMUST00000164294						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164295						2	2	7	27	3	1	0	0	4	2	0		
ENSMUST00000164296	ENSMUSG00000026918	2	27445579	27507662	-1	0	0	0	0	0	0	176	231	313	6	157	Q3TUI3	Q8K2F0
ENSMUST00000164297	ENSMUSG00000057977	4	114163384	114245028	1	0	0	0	0	0	0	0	0	0	0	0		A7XV14
ENSMUST00000164298	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	0	1	5	5	212	61	48	21	F6ZTZ2	
ENSMUST00000164300						4	0	35	10	7	0	0	0	0	0	5		
ENSMUST00000164302	ENSMUSG00000038305	1	57774162	57948394	1	0	0	0	0	0	0	0	1	1	0	0	E9PZE9	
ENSMUST00000164303						0	0	0	0	0	0	5	0	0	0	0		
ENSMUST00000164304	ENSMUSG00000056917	19	5651185	5663707	-1	0	0	11	0	10	0	3074	3439	2542	390	1362	E9Q0Y4	
ENSMUST00000164307	ENSMUSG00000090346	6	56985295	56986350	1	1	2	3	0	3	1	0	0	0	0	0	B2RQT2	
ENSMUST00000164309	ENSMUSG00000005410	8	75109528	75128439	1	43	33	138	124	59	23	731	455	486	99	367	Q52KC3	
ENSMUST00000164311	ENSMUSG00000036131	X	50895180	50942710	-1	7	8	6	0	5	0	0	0	2	1	1	E9PXK8	
ENSMUST00000164315	ENSMUSG00000000631	11	77763246	77865980	1	1	0	1	1	2	1	0	0	0	0	0	E9Q0K8	
ENSMUST00000164322						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000164325						26	27	37	23	32	16	2	5	7	1	15		
ENSMUST00000164326	ENSMUSG00000021111	12	105784694	105838944	1	0	0	4	96	1	9	0	3	54	92	51	E9Q5Z1	
ENSMUST00000164332						0	1	0	3	1	0	19	97	42	57	29		
ENSMUST00000164334	ENSMUSG00000000631	11	77763246	77865980	1	0	3	0	0	0	0	99	0	0	0	0		Q9JMH9
ENSMUST00000164336						17	15	37	47	21	9	0	0	6	0	3		
ENSMUST00000164337	ENSMUSG00000062031	7	140941391	140947664	1	6	7	8	0	19	5	10	94	34	0	43	E9Q4H7	
ENSMUST00000164338						0	0	0	15	0	0	0	0	0	0	0		
ENSMUST00000164340						2	6	10	11	13	0	0	0	0	0	0		
ENSMUST00000164341	ENSMUSG00000056234	14	32159865	32179855	1	2	3	0	0	0	0	0	0	5	12	5	E9PWU9	
ENSMUST00000164342	ENSMUSG00000012296	17	46257851	46283026	-1	0	5	0	20	0	7	59	103	58	0	46		Q9DCD5
ENSMUST00000164343						61	56	167	38	63	28	1	11	3	0	5		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000164344	ENSMUSG00000091768	13	55132962	55133548	-1	0	0	0	0	0	0	0	0	0	0	0	F6TMR5	
ENSMUST00000164345	ENSMUSG00000030823	7	127382260	127387166	-1	0	0	3	0	0	0	46	99	60	18	48	E9PX22	
ENSMUST00000164351						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000164353						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000164354	ENSMUSG00000001627	12	40201567	40248504	-1	2	2	7	3	0	1	0	0	0	3	0	E9QA38	
ENSMUST00000164358						2	0	0	4	3	2	0	0	2	1	0		
ENSMUST00000164359	ENSMUSG00000078812	11	69916714	69921958	-1	4	0	0	19	0	0	321	697	108	95	70		P63242
ENSMUST00000164362	ENSMUSG00000073755	4	126609818	126614371	1	89	39	137	0	147	11	8	18	4	14	24		Q8BP99
ENSMUST00000164363	ENSMUSG00000055320	7	112679318	112906807	1	2	0	0	1	0	0	0	0	0	0	0	Q3USK5	
ENSMUST00000164364						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000164365	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	F7A6Z4	
ENSMUST00000164366	ENSMUSG00000091617	14	7466362	7483762	-1	0	4	0	0	0	0	1	0	0	0	0	A6NAT4	
ENSMUST00000164371						2	0	0	3	3	0	0	0	0	0	0		
ENSMUST00000164372	ENSMUSG00000092036	14	19532896	19549958	-1	34	19	0	80	5	0	0	0	0	0	0	L7N2A3	
ENSMUST00000164373	ENSMUSG00000032318	9	55538672	55546180	1	8	0	18	103	0	1	0	0	0	0	0	Q0VAX2	
ENSMUST00000164374						7	14	15	16	14	5	6	46	16	5	15		
ENSMUST00000164375	ENSMUSG00000029860	6	42349630	42360213	1	19	10	33	18	24	14	1490	2139	1372	99	1348		Q62523
ENSMUST00000164376	ENSMUSG00000094936	19	4784293	4793901	-1	0	0	2	0	0	0	0	0	24	5	0	F6TBN8	
ENSMUST00000164377	ENSMUSG00000032554	9	103204001	103230444	-1	0	0	0	0	0	0	0	0	11	0	0	E9Q939	
ENSMUST00000164378	ENSMUSG00000029405	5	92052146	92083719	-1	0	10	16	14	9	5	95	353	52	0	0	Q3U541	P97379
ENSMUST00000164382	ENSMUSG00000045246	8	119623854	119635680	-1	0	0	0	152	2	2	0	0	0	0	0		Q80XM3
ENSMUST00000164383						0	0	0	0	0	0	4	4	8	10	40		
ENSMUST00000164384	ENSMUSG00000075316	2	66480080	66634962	-1	0	0	0	0	0	0	0	0	0	0	0		Q62205
ENSMUST00000164385						6	0	0	1	3	2	17	30	15	2	17		
ENSMUST00000164386	ENSMUSG00000021139	12	81358860	81532905	-1	0	0	2	0	2	0	0	0	0	0	0		Q9D6K5
ENSMUST00000164387	ENSMUSG00000060240	7	141426446	141429491	-1	0	0	56	0	0	0	1	0	0	0	1		Q9JKC6
ENSMUST00000164388	ENSMUSG00000024909	19	5473973	5481853	1	2	2	8	0	8	3	0	0	7	0	0	F6Z1C2	
ENSMUST00000164390	ENSMUSG00000000708	17	53566861	53672720	1	0	0	2	0	2	0	0	0	10	0	37	E9Q1F7	
ENSMUST00000164391	ENSMUSG00000057770	7	104924806	104925762	-1	5	5	8	2	2	4	0	0	0	0	0	Q8VGW3	
ENSMUST00000164393	ENSMUSG00000019856	10	53633145	53750909	-1	0	1	1	0	0	1	0	0	0	0	0	F6ZCT9	
ENSMUST00000164394	ENSMUSG00000094314	10	100335676	100336591	1	1	0	71	1	1	0	0	0	0	0	0	K9J7E2	
ENSMUST00000164395	ENSMUSG00000032594	9	108002501	108048782	1	0	0	0	0	0	0	6	0	0	0	7	F7CWH3	
ENSMUST00000164396						3	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000164397	ENSMUSG00000022686	16	19760208	19772753	1	0	4	3	0	0	0	0	0	0	6	0		Q8BGY6
ENSMUST00000164399	ENSMUSG00000035268	2	163658386	163726158	1	0	0	0	1	0	5	50	44	21	33	20	Q3TP50	O70139
ENSMUST00000164400						0	0	0	0	0	0	0	0	2	2	0		
ENSMUST00000164403	ENSMUSG00000036054	8	70234226	70279915	1	0	0	0	0	0	2	46	0	0	6	0		Q8CH09
ENSMUST00000164404	ENSMUSG00000038838	17	35655634	35667592	-1	0	0	0	0	0	0	0	0	0	1	0	F7A8L1	
ENSMUST00000164406	ENSMUSG00000015702	3	95296096	95307176	-1	3	0	0	9	0	0	0	0	0	0	0		Q9JHQ0
ENSMUST00000164407	ENSMUSG00000091682	13	19260884	19263528	1	2	0	0	0	0	0	0	0	0	0	0	L7N479	
ENSMUST00000164408	ENSMUSG00000096904	14	6405827	6412482	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6X2	
ENSMUST00000164409	ENSMUSG00000094001	7	21133211	21134128	-1	0	0	0	0	0	0	0	0	0	0	0	K7N726	
ENSMUST00000164410	ENSMUSG00000052749	7	104355382	104369884	-1	0	10	7	10	7	9	450	1549	879	142	2001	E9PVL6	
ENSMUST00000164411	ENSMUSG00000040899	17	8236043	8257127	1	8	0	8	0	0	0	0	0	0	0	18	Q542B6	O54689
ENSMUST00000164412						1	2	0	4	6	6	0	0	8	1	0		
ENSMUST00000164415	ENSMUSG00000090799	14	50891389	50893255	-1	12	10	35	31	13	7	0	0	0	1	3	G3UW92	
ENSMUST00000164416	ENSMUSG00000038542	8	13077189	13105459	-1	0	7	16	31	16	27	358	636	364	31	308		Q8BFV2
ENSMUST00000164420						75347	107441	174791	70887	66088	32235	629	3767	1347	386	1244		
ENSMUST00000164421						0	0	0	0	0	0	13	106	24	42	15		
ENSMUST00000164422	ENSMUSG00000048312	7	41032719	41045302	1	33	32	256	40	39	25	0	0	0	0	0	E9PVP9	
ENSMUST00000164425	ENSMUSG00000020684	11	83409137	83421039	1	28	31	80	117	42	16	0	0	0	0	0		Q5SSG5
ENSMUST00000164426						0	2	0	1	1	0	0	24	0	4	9		
ENSMUST00000164427						11	14	8	38	21	4	156	673	175	35	398		
ENSMUST00000164428	ENSMUSG00000090439	10	60399726	60403556	1	4	3	17	40	8	0	55	164	48	17	83	G3UW87	
ENSMUST00000164429	ENSMUSG00000090666	10	33994989	33995054	-1	0	0	0	0	0	0	0	0	0	0	0	Q3USA7	
ENSMUST00000164430	ENSMUSG00000028163	3	135584655	135691547	-1	0	1	12	0	0	3	894	1598	1782	57	1161		P25799
ENSMUST00000164431	ENSMUSG00000090935	12	81497941	81532911	-1	17	12	10	0	10	15	92	373	178	185	87	E9PVQ9	
ENSMUST00000164434						1	1	6	0	3	0	0	0	0	0	0		
ENSMUST00000164438						2	0	5	0	0	0	0	0	10	0	16		
ENSMUST00000164439	ENSMUSG00000004896	3	87922601	87930717	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q693	
ENSMUST00000164440						0	0	1	31	2	0	0	0	1	0	1		
ENSMUST00000164441	ENSMUSG00000074502	9	18404418	18411502	1	2	4	25	0	0	2	0	0	0	0	0		Q3USZ2
ENSMUST00000164442	ENSMUSG00000039059	2	180099465	180104488	-1	0	4	0	0	0	0	0	0	0	0	0	E9Q5S3	
ENSMUST00000164443						3	5	5	1	1	0	0	0	0	1	0		
ENSMUST00000164446	ENSMUSG00000095864	7	12041299	12042219	1	3	3	0	4	3	0	0	0	0	0	0	E9PY60	
ENSMUST00000164447	ENSMUSG00000046688	3	127789805	127832164	1	0	1	1	6	0	0	7	151	50	0	0	I3PQW8	Q793I8
ENSMUST00000164449	ENSMUSG00000019558	X	73673150	73682502	1	0	0	0	0	0	0	0	0	0	0	0	E9Q151	
ENSMUST00000164454	ENSMUSG00000071178	12	103728156	103830373	-1	19	19	46	16	39	11	0	0	0	0	0		P22599
ENSMUST00000164455						0	1	35	8	2	0	0	3	1	0	4		
ENSMUST00000164458	ENSMUSG00000022771	16	17086555	17111257	-1	0	0	0	0	0	0	2	241	5	382	101		Q9D787
ENSMUST00000164459	ENSMUSG00000091185	14	4892416	4902431	1	4	4	16	0	0	12	0	0	0	0	0	L7N2D2	
ENSMUST00000164460						1	4	4	8	5	5	44	107	48	7	91		
ENSMUST00000164462	ENSMUSG00000090362	7	86996465	87037968	1	5	5	2	7	3	0	0	0	0	0	0	E9Q067	
ENSMUST00000164465	ENSMUSG00000049612	11	79500982	79504084	-1	7	5	50	13	8	4	7	35	6	18	14	G3XA53	
ENSMUST00000164467	ENSMUSG00000007656	9	75037614	75060313	1	0	0	6	0	0	0	98	177	133	397	81		P56212
ENSMUST00000164469						8	7	24	15	10	1	0	4	2	0	15		
ENSMUST00000164470	ENSMUSG00000031948	8	111993440	112011323	-1	0	0	0	0	0	0	0	17	0	0	0	Q8R2P8	
ENSMUST00000164471	ENSMUSG00000091034	5	104070064	104077608	-1	0	4	1	0	0	2	0	0	0	0	0	B9UIU9	
ENSMUST00000164472	ENSMUSG00000059689	6	117841180	117845956	1	0	2	0	0	4	0	58	125	28	63	23		Q80V23
ENSMUST00000164473	ENSMUSG00000038496	1	83012523	83038448	-1	3	7	5	3	9	2	0	0	0	0	0		Q99PL8
ENSMUST00000164474	ENSMUSG00000035172	11	101162679	101171351	-1	11	0	0	0	0	13	0	0	2	4	16		Q8VCE9
ENSMUST00000164476						0	0	22	0	3	0	29	104	17	50	40		
ENSMUST00000164479	ENSMUSG00000030688	7	101317086	101346626	1	0	0	0	0	0	0	11	10	0	0	0	Q0VG22	Q9JMD3
ENSMUST00000164481	ENSMUSG00000042306	3	90526856	90528837	1	0	0	9	6	5	0	1	0	2	0	2	E9Q2K8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000164482	ENSMUSG00000006526	14	30825590	30876986	1	0	0	0	45	0	0	0	0	0	0	0	E9Q626	
ENSMUST00000164484	ENSMUSG00000090707	14	5857918	5880382	-1	5	3	9	51	12	1	0	0	0	0	0	E9Q257	
ENSMUST00000164486	ENSMUSG00000022801	16	32914100	33015647	1	0	0	0	186	7	3	0	0	3	0	0	E9Q0H5	
ENSMUST00000164487						24	21	38	34	36	8	0	6	0	2	1		
ENSMUST00000164489	ENSMUSG00000094337	GL456354.1	82993	86051	-1	0	0	9	0	0	2	0	0	0	0	0	E9PVT6	
ENSMUST00000164490	ENSMUSG00000022756	16	17572018	17576998	-1	0	0	0	0	0	0	0	0	0	0	0	E9PZW6	
ENSMUST00000164491	ENSMUSG00000090667	6	98235708	98342754	-1	6	4	12	5	5	0	0	0	0	0	0	B2RVL9	
ENSMUST00000164495	ENSMUSG00000043673	12	11090202	11150842	-1	14	1	9	5	8	6	0	0	0	0	0		Q8BQZ8
ENSMUST00000164499						1	0	1	4	4	0	0	4	0	0	0		
ENSMUST00000164501						2	2	6	0	0	0	0	0	0	0	2		
ENSMUST00000164502	ENSMUSG00000090588	17	35617923	35626637	-1	54	30	220	95	57	23	0	0	0	0	0	F7C950	
ENSMUST00000164504	ENSMUSG00000031631	8	46151771	46195590	1	16	14	3	0	7	0	63	405	144	219	9		Q6ZPR1
ENSMUST00000164505	ENSMUSG00000061904	10	91116574	91124059	-1	3	0	8	171	14	9	741	1613	665	169	874		Q8VEM8
ENSMUST00000164506	ENSMUSG00000020925	11	102684686	102697782	-1	10	8	20	0	0	2	0	0	33	22	0	E9Q2S9	
ENSMUST00000164508	ENSMUSG00000045744	17	24473884	24475469	1	0	0	0	0	0	0	0	0	0	0	0	Q8BV89	
ENSMUST00000164509						16	9	24	66	13	12	0	0	0	0	0		
ENSMUST00000164510						2	0	0	0	1	0	4	4	0	0	3		
ENSMUST00000164511						0	0	0	4	1	0	0	0	0	0	0		
ENSMUST00000164512	ENSMUSG00000079391	14	4182576	4204895	1	0	3	0	93	14	2	0	0	0	0	0	L7N2C2	
ENSMUST00000164513	ENSMUSG00000046080	6	129408862	129424763	1	10	3	36	20	9	7	1	30	0	0	0		Q8BRU4
ENSMUST00000164517	ENSMUSG00000095724	12	87772425	87775755	-1	53	41	100	164	85	39	3	19	9	0	17	F6YNI8	
ENSMUST00000164518	ENSMUSG00000090369	19	42052248	42053627	1	23	9	125	24	27	10	0	1	0	0	0		Q80Y39
ENSMUST00000164519	ENSMUSG00000029706	6	28442334	28449353	-1	0	0	7	0	0	0	0	0	0	0	0		P32115
ENSMUST00000164521						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164523	ENSMUSG00000090602	9	17030045	17030899	1	2	6	23	9	6	5	0	0	1	2	0	E9Q5T3	
ENSMUST00000164524	ENSMUSG00000023918	17	42656891	42692284	-1	0	0	1	0	0	0	0	0	0	0	0	E9PY10	
ENSMUST00000164525	ENSMUSG00000038371	7	110308013	110614922	-1	0	0	0	0	0	0	0	0	0	0	0	F7BBM8	
ENSMUST00000164526	ENSMUSG00000094011	7	20167460	20168377	-1	1	0	1	2	1	0	0	0	0	0	0	K7N6X3	
ENSMUST00000164527	ENSMUSG00000090715	7	23504642	23505589	-1	6	3	3	3	4	1	0	0	0	0	0	G3UW71	
ENSMUST00000164528	ENSMUSG00000090808	16	14502100	14509199	1	8	2	7	5	5	4	0	0	0	0	0	F6VZZ1	
ENSMUST00000164529	ENSMUSG00000054263	15	7129559	7197489	1	20	14	21	77	30	16	18	75	55	30	67		P42703
ENSMUST00000164532	ENSMUSG00000022378	15	63929097	64060448	-1	0	4	0	0	4	0	2327	11280	3915	1278	2470		Q921M7
ENSMUST00000164536						17	6	37	12	20	3	0	0	1	0	0		
ENSMUST00000164537	ENSMUSG00000094934	7	23055540	23056463	1	0	0	0	0	0	0	0	0	0	0	0	K9J7G0	
ENSMUST00000164538	ENSMUSG00000009487	7	46240987	46311434	1	200	149	899	300	209	111	0	2	0	0	4	G3UWC8	
ENSMUST00000164539	ENSMUSG00000027867	3	99885406	100143322	1	38	24	38	26	23	15	0	0	0	0	0		Q5S003
ENSMUST00000164541						0	0	0	0	8	0	0	18	7	0	0		
ENSMUST00000164542	ENSMUSG00000022370	15	55534094	55557748	-1	0	0	0	0	0	0	15	142	35	404	62	G5E909	
ENSMUST00000164543						0	4	18	0	4	0	0	59	0	0	0		
ENSMUST00000164544	ENSMUSG00000094929	14	5253907	5260580	-1	0	0	9	3	0	0	0	0	0	0	0	E9PZM0	
ENSMUST00000164545	ENSMUSG00000022756	16	17572018	17576998	-1	2	4	23	26	1	0	0	0	0	0	0	E9Q6V0	
ENSMUST00000164547	ENSMUSG00000025701	6	116410077	116461178	-1	0	0	0	0	0	0	347	188	1130	19	635	E9QA93	
ENSMUST00000164551	ENSMUSG00000034800	2	127574662	127587094	-1	0	0	0	0	0	0	0	0	1	0	5		Q8BIQ3
ENSMUST00000164553	ENSMUSG00000068566	7	3289080	3300442	1	0	0	0	65	0	3	392	934	1371	256	988	Q0VE46	O35682
ENSMUST00000164556	ENSMUSG00000019854	10	18055861	18125155	1	0	0	0	0	0	0	0	0	0	0	0	E9Q632	
ENSMUST00000164558	ENSMUSG00000021244	12	84996321	85070515	1	0	0	0	0	0	0	4	226	1	13	26	F6YTL8	
ENSMUST00000164559	ENSMUSG00000038371	7	110308013	110614922	-1	0	0	0	0	0	0	0	0	0	0	0	F6QG63	
ENSMUST00000164560	ENSMUSG00000039742	6	29319140	29336019	1	12	0	0	0	0	0	0	0	0	0	0	B7ZWJ6	
ENSMUST00000164562						0	0	0	0	0	1	20	39	29	0	0		
ENSMUST00000164563	ENSMUSG00000029701	6	29123576	29165006	-1	0	0	0	0	0	0	3	2	10	1	0	F6SB18	
ENSMUST00000164565						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164566	ENSMUSG00000038528	10	39958061	39986646	-1	157	135	197	3570	186	107	7	35	8	1	5	Q8C3P4	
ENSMUST00000164567	ENSMUSG00000018211	2	164214454	164221660	-1	0	0	2	3	5	3	0	0	0	0	0		Q9JHY4
ENSMUST00000164573	ENSMUSG00000028133	3	121155398	121171695	-1	0	0	0	0	0	0	1	7	2	0	0	F7AYC4	
ENSMUST00000164574	ENSMUSG00000090553	1	133603871	133610291	-1	3	0	7	187	6	2	0	2	0	0	1	E9PXQ9	
ENSMUST00000164575						5	3	5	1	8	0	11	13	49	0	21		
ENSMUST00000164578	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	0	12	0	0		O70585
ENSMUST00000164579	ENSMUSG00000022899	16	36750178	36784962	-1	0	5	0	0	2	0	0	0	0	0	0	E9Q329	
ENSMUST00000164580	ENSMUSG00000062031	7	140941391	140947664	1	0	0	0	11	0	0	102	500	119	0	41	F6QM56	
ENSMUST00000164582	ENSMUSG00000039988	3	157947239	158008034	1	0	0	1	183	2	0	44	252	236	10	104		Q3UX43
ENSMUST00000164583	ENSMUSG00000054672	7	140247301	140299791	1	9	15	45	19	19	14	0	0	0	0	9	B3F5L4	
ENSMUST00000164584						3	6	20	9	8	0	0	0	0	0	0		
ENSMUST00000164585	ENSMUSG00000090512	14	5821934	5830329	-1	0	0	15	0	0	0	0	0	0	0	0	L7N298	
ENSMUST00000164587						0	7	0	22	15	2	3438	17056	11034	24414	5437		
ENSMUST00000164589	ENSMUSG00000030590	7	29152511	29156234	-1	0	0	0	0	0	0	16	25	0	7	0	E9PYD1	
ENSMUST00000164591	ENSMUSG00000020009	10	19591949	19610229	1	2	0	0	14	0	0	17	32	54	0	4	E9PX11	
ENSMUST00000164592						24	23	64	21	18	5	37	92	47	10	48		
ENSMUST00000164598	ENSMUSG00000021751	14	8225511	8259353	-1	14	12	25	20	31	10	11	11	12	0	6		Q9QXD1
ENSMUST00000164599	ENSMUSG00000038371	7	110308013	110614922	-1	2	0	0	0	0	0	0	0	0	0	0	F6ZDC5	
ENSMUST00000164600	ENSMUSG00000006014	1	150449412	150466165	-1	0	0	0	0	0	0	0	0	0	0	0	E0CZ58	
ENSMUST00000164603	ENSMUSG00000079386	14	4430992	4519452	1	0	0	0	0	0	0	0	0	0	0	0	A6NAS3	
ENSMUST00000164604						0	0	0	1	0	0	1	2	0	0	0		
ENSMUST00000164606						778	654	1943	571	968	449	7	35	32	7	42		
ENSMUST00000164607	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	83	0	30	0	13	Q8C8Z9	
ENSMUST00000164609	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	4	0	0	0	0	0	0		Q9R0Q4
ENSMUST00000164610						3	1	15	0	3	0	1	6	2	0	3		
ENSMUST00000164611						0	0	4	0	0	0	6	0	17	12	63		
ENSMUST00000164613	ENSMUSG00000094925	14	41348609	41356839	1	8	0	6	10	0	9	0	0	0	0	0	F7BTS7	
ENSMUST00000164614	ENSMUSG00000047878	15	83226726	83251774	-1	21	0	0	69	27	0	0	0	0	0	0	Q3UF00	Q67BJ4
ENSMUST00000164617						25	6	21	19	11	17	9	32	9	4	24		
ENSMUST00000164618	ENSMUSG00000023942	17	45585200	45599606	-1	0	3	1	28	1	0	0	0	0	0	0	E9PVH9	
ENSMUST00000164621						0	0	8	0	1	2	0	0	0	0	0		
ENSMUST00000164622						7	8	16	6	5	8	0	0	1	0	2		
ENSMUST00000164623	ENSMUSG00000022756	16	17572018	17576998	-1	0	2	0	0	0	3	0	0	0	0	0	E9Q4Z9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000164624	ENSMUSG00000022105	14	73183673	73325822	-1	1	0	0	5	0	0	0	0	0	0	3	E9Q5C5	
ENSMUST00000164626	ENSMUSG00000029771	6	29526625	29541871	1	0	1	2	2	2	0	0	0	0	0	0	E9Q5T2	
ENSMUST00000164627	ENSMUSG00000060147	13	33917918	34002794	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q3Y1	
ENSMUST00000164628						0	3	4	3	7	0	0	3	6	0	0		
ENSMUST00000164632	ENSMUSG00000021872	14	51007751	51010758	1	2	9	21	12	30	0	0	0	0	1	0	G3UWD1	
ENSMUST00000164636						3	0	0	4	5	2	63	272	46	19	48		
ENSMUST00000164638						3	4	3	7	0	2	0	0	0	0	0		
ENSMUST00000164639	ENSMUSG00000024798	19	35958734	36057507	-1	9	0	4	4	9	0	1	30	7	4	0		P32304
ENSMUST00000164643	ENSMUSG00000020366	11	49846751	49886421	1	0	0	0	0	0	2	0	0	0	0	0		Q9WTU6
ENSMUST00000164647	ENSMUSG00000024043	17	67842713	68004120	-1	12	4	0	0	5	0	0	0	0	0	0	E9Q642	
ENSMUST00000164648	ENSMUSG00000030199	6	134035700	134270158	1	2	0	3	17	3	1	0	0	2	0	18	E9QAJ7	
ENSMUST00000164649	ENSMUSG00000028785	4	129111570	129122036	-1	7	10	107	89	18	0	0	0	0	0	0		P84075
ENSMUST00000164650						0	3	0	15	0	3	0	0	0	0	0		
ENSMUST00000164651	ENSMUSG00000095296	5	11502685	11507417	1	0	0	12	4	0	0	0	0	0	0	0	L7N2A2	
ENSMUST00000164653	ENSMUSG00000049676	7	29181321	29214035	-1	2	0	0	2	4	0	0	0	3	2	0		E9Q355
ENSMUST00000164655	ENSMUSG00000060373	14	52073380	52104028	-1	14	0	72	47	43	15	0	0	0	0	0		Q9Z204
ENSMUST00000164656						0	0	0	1	6	0	0	0	0	0	0		
ENSMUST00000164658						1	1	2	3	3	1	0	0	0	0	0		
ENSMUST00000164659	ENSMUSG00000019970	10	21882184	21999903	1	0	0	6	0	10	0	0	0	0	0	0	E9Q8C1	
ENSMUST00000164660	ENSMUSG00000051354	10	26229707	26272172	1	3	3	6	6	8	5	0	0	0	0	0		Q8C4H2
ENSMUST00000164661	ENSMUSG00000090693	9	88580891	88588819	1	15	8	34	6	8	10	0	3	0	3	0		Q3TL54
ENSMUST00000164662	ENSMUSG00000005045	4	152338651	152390194	1	2	0	49	171	74	54	0	0	0	0	0	E9PYU4	
ENSMUST00000164663	ENSMUSG00000091725	14	44285580	44291068	1	4	5	4	0	3	0	0	0	0	0	0	F6YKI2	
ENSMUST00000164664	ENSMUSG00000025374	10	128401395	128411492	-1	1	0	3	0	4	0	3	3	8	0	9	E9Q1I2	
ENSMUST00000164665	ENSMUSG00000024811	19	36834232	36893477	1	1	0	0	0	0	1	38	17	174	5	25	F6V619	
ENSMUST00000164666	ENSMUSG00000071856	18	44425060	44812182	-1	24	43	97	241	51	13	4	13	5	0	9	G3UW40	
ENSMUST00000164667	ENSMUSG00000092124	18	31609512	31610751	1	5	7	1	78	10	7	1	1	0	0	0	Q8C4T2	
ENSMUST00000164669						0	0	2	0	6	0	0	4	0	0	7		
ENSMUST00000164671						7	4	9	3	8	2	0	2	0	1	0		
ENSMUST00000164673						17	14	145	24	26	10	1	0	2	0	9		
ENSMUST00000164674						0	0	1	0	52	0	0	0	0	0	0		
ENSMUST00000164675	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7V2	
ENSMUST00000164677	ENSMUSG00000090744	7	41545674	41573662	-1	0	2	0	0	1	0	0	0	0	0	0	E9PZ63	
ENSMUST00000164679						2	1	4	2	1	1	3	9	5	0	5		
ENSMUST00000164680						3	0	2	7	3	1	37	56	49	0	27		
ENSMUST00000164681	ENSMUSG00000025487	7	140881968	140898643	1	0	0	0	0	0	0	0	161	0	0	0	E9Q0U1	
ENSMUST00000164683	ENSMUSG00000094010	7	21011532	21012455	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4H3	
ENSMUST00000164685	ENSMUSG00000015340	X	9435252	9487771	-1	0	0	0	0	0	1	0	0	241	0	0	E9Q802	
ENSMUST00000164688	ENSMUSG00000023048	15	102459028	102462806	1	0	2	9	44	2	0	1380	9350	1193	185	931		Q9CQJ5
ENSMUST00000164691						1	0	2	2	2	6	3	15	4	0	5		
ENSMUST00000164693	ENSMUSG00000045802	X	96306178	96456294	-1	2	3	4	1	3	0	0	0	0	0	0		
ENSMUST00000164694						23	15	13	9	26	17	0	1	1	1	6		
ENSMUST00000164696	ENSMUSG00000091756	14	3963547	3970207	1	6	6	0	0	3	0	0	0	0	0	0	E9Q058	
ENSMUST00000164697	ENSMUSG00000022176	14	54476100	54480431	1	3	3	10	78	5	7	0	0	0	0	0	E9PVZ0	
ENSMUST00000164699						3	1	0	2	4	1	1	0	0	0	0		
ENSMUST00000164700						0	2	4	0	1	0	0	0	0	0	0		
ENSMUST00000164702						1	1	4	0	0	2	0	0	0	0	0		
ENSMUST00000164703	ENSMUSG00000048385	15	76516203	76522129	-1	0	0	0	0	0	7	0	0	0	0	0		Q99M85
ENSMUST00000164705	ENSMUSG00000013833	10	79894708	79908923	-1	0	0	0	0	0	0	0	0	0	0	0	E9PZW4	
ENSMUST00000164710	ENSMUSG00000030782	7	128246812	128255699	1	0	0	0	8	0	0	0	0	0	0	0		Q62219
ENSMUST00000164712						0	0	0	0	1	0	1	3	0	0	0		
ENSMUST00000164713	ENSMUSG00000020961	12	91638542	91788387	-1	21	13	0	19	17	0	0	0	5	0	65	E9PXP7	
ENSMUST00000164717						7	1	9	2	16	10	47	104	0	8	50		
ENSMUST00000164721	ENSMUSG00000032311	9	55220222	55326844	-1	15	0	74	0	10	0	0	0	12	0	0		Q9WTX4
ENSMUST00000164723						0	0	6	4	4	3	0	0	0	0	5		
ENSMUST00000164725	ENSMUSG00000036560	7	31059342	31070935	1	0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000164726	ENSMUSG00000049580	7	98350668	98361328	-1	0	0	0	0	0	0	0	0	0	0	0	Q08EE6	Q8CBR6
ENSMUST00000164727	ENSMUSG00000039109	13	36867178	37050244	-1	20	0	0	0	0	13	0	129	61	0	45		Q8BH61
ENSMUST00000164728	ENSMUSG00000022636	16	52248996	52454074	-1	1	2	0	3	3	2	8	102	56	0	44	E9Q4G8	
ENSMUST00000164729	ENSMUSG00000095445	X	11324659	11324976	1	0	2	0	0	0	0	0	0	0	0	0	Q5M8Q2	
ENSMUST00000164730	ENSMUSG00000000562	3	105870858	105908926	1	0	2	2	0	1	0	124	1431	211	38	0	Q497R5	
ENSMUST00000164732	ENSMUSG00000091382	6	57389580	57390666	-1	2	4	2	0	4	1	0	0	0	0	0	Q8R2C8	
ENSMUST00000164733	ENSMUSG00000029810	6	48833818	48841496	-1	9	0	73	23	21	8	15	100	42	23	46		Q9R1Q6
ENSMUST00000164737	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	0	4	0	0	E9PVP5	
ENSMUST00000164738	ENSMUSG00000025730	17	25882114	25919727	-1	0	1	0	25	0	0	0	0	0	0	0	E9Q7Y6	
ENSMUST00000164739						1	4	2	0	7	0	1	0	4	0	0		
ENSMUST00000164741	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	0	0	6	1	12	0	27	0	31	F6WSY2	
ENSMUST00000164744	ENSMUSG00000030061	6	97183670	97205647	-1	0	0	0	0	0	0	0	70	43	61	0	Q3TL72	
ENSMUST00000164745	ENSMUSG00000030759	7	113513834	113571511	1	0	0	0	0	0	0	335	644	540	521	343		Q922J9
ENSMUST00000164746	ENSMUSG00000024924	19	27216484	27254231	1	0	0	0	38	0	0	0	0	0	0	0	E9Q643	
ENSMUST00000164748	ENSMUSG00000037992	11	98927818	98974942	1	13	6	165	0	0	0	211	2773	139	1	179	Q3U3R3	P11416
ENSMUST00000164750	ENSMUSG00000017724	11	101769742	101785371	-1	0	0	13	0	8	2	0	0	0	0	1		P28322
ENSMUST00000164751	ENSMUSG00000019971	10	100488289	100573655	1	24	23	29	12	18	8	2	15	12	22	21	E9Q9M0	
ENSMUST00000164752	ENSMUSG00000004347	6	56069804	56569103	-1	27	0	0	0	0	0	0	0	0	0	0	Q5D0E7	Q64338
ENSMUST00000164753						205	165	207	149	248	115	2	8	10	5	13		
ENSMUST00000164754	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	0	0	0	0	0	0	0	0		Q9DCB4
ENSMUST00000164756	ENSMUSG00000091337	2	125673095	125674785	1	5	2	3	36	4	1	677	2129	696	317	483		Q9DCR4
ENSMUST00000164758						0	0	0	0	2	4	13	63	87	26	114		
ENSMUST00000164759	ENSMUSG00000038371	7	110308013	110614922	-1	18	13	54	19	28	0	122	158	157	53	193	E9Q305	
ENSMUST00000164761	ENSMUSG00000034456	6	90333284	90364551	1	25	0	43	35	39	0	0	0	0	0	0	Q3UEL5	
ENSMUST00000164763	ENSMUSG00000019841	10	39732118	39875211	1	20	0	0	0	0	13	152	202	426	29	190		Q61493
ENSMUST00000164764	ENSMUSG00000091863	X	152563334	152563969	1	0	1	0	0	1	3	0	0	0	0	0	G3UW52	
ENSMUST00000164765						0	0	14	20	5	0	55	696	191	10	287		
ENSMUST00000164766	ENSMUSG00000022176	14	54476100	54480431	1	10	4	12	51	8	0	1	8	3	5	15	E9Q4D5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000164769	ENSMUSG00000023942	17	45585200	45599606	-1	3	1	11	3	3	2	0	0	0	0	0	E9PXM6	
ENSMUST00000164770						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000164772	ENSMUSG00000045083	4	35706647	36951747	-1	0	11	23	0	6	5	0	0	0	0	0	B2RQD4	Q3URE9
ENSMUST00000164773	ENSMUSG00000020205	10	111506286	111508645	1	17	18	35	592	25	9	61	147	67	17	86		Q62392
ENSMUST00000164774	ENSMUSG00000000759	8	12614277	12672248	-1	0	0	0	0	0	0	57	144	141	0	58	E9Q0R3	
ENSMUST00000164775						0	0	4	0	0	0	0	0	4	0	2		
ENSMUST00000164776	ENSMUSG00000025159	19	41941086	41981157	-1	0	0	0	12	0	0	141	19	166	85	310	E9PUY8	
ENSMUST00000164777	ENSMUSG00000064202	19	28893042	28967800	-1	0	0	17	0	3	0	0	0	0	0	0	B7ZWD0	
ENSMUST00000164779	ENSMUSG00000022471	15	81987835	82040085	1	0	0	0	0	0	0	0	0	0	0	0	E9PZD4	
ENSMUST00000164781	ENSMUSG00000024798	19	35958734	36057507	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4Q7	
ENSMUST00000164782	ENSMUSG00000020953	12	51593341	51605773	1	11	0	0	128	20	7	0	0	0	0	0		Q62507
ENSMUST00000164783						19	15	15	34	18	12	0	0	0	0	2		
ENSMUST00000164784	ENSMUSG00000092094	5	6769010	7344756	-1	22	10	17	15	20	8	0	0	0	0	0	F6QGP8	
ENSMUST00000164786	ENSMUSG00000025185	19	42593982	42612813	-1	0	0	23	22	19	1	0	0	0	0	0	E9Q600	
ENSMUST00000164787	ENSMUSG00000040420	15	22549022	23474418	1	6	7	13	17	15	8	0	0	0	0	0	E9Q9Q6	
ENSMUST00000164791	ENSMUSG00000020407	11	9118103	9136170	1	0	0	8	27	0	0	1852	731	786	1401	641	Q5SUC8	P52624
ENSMUST00000164792	ENSMUSG00000024680	19	11615523	11623719	-1	1	0	0	0	1	0	8	30	7	0	19	B2RTF7	P20490
ENSMUST00000164794						10	4	16	2	11	11	0	0	0	1	2		
ENSMUST00000164795						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164798	ENSMUSG00000021111	12	105784694	105838944	1	0	0	0	0	0	0	20	7	14	7	43	F7CXD5	
ENSMUST00000164799	ENSMUSG00000059475	9	20468549	20492746	-1	0	1	0	0	0	0	5	19	15	0	7	E9Q7W5	
ENSMUST00000164800	ENSMUSG00000031351	X	72987339	73031543	1	0	0	0	31	7	0	0	0	0	0	0	G5E8W8	
ENSMUST00000164801						0	0	0	0	0	0	0	0	0	0	5		
ENSMUST00000164803	ENSMUSG00000035365	10	88091432	88146941	-1	0	0	2	0	0	0	0	0	0	0	1	E9Q6W8	
ENSMUST00000164806	ENSMUSG00000022407	15	80948490	80970947	1	0	1	0	0	1	0	34	18	26	0	22	E9Q3T7	
ENSMUST00000164807	ENSMUSG00000005161	8	84969587	84974834	1	1	0	0	0	0	0	151	211	53	368	125		Q61171
ENSMUST00000164809	ENSMUSG00000007591	14	55650182	55652539	1	22	11	12	12	12	11	0	21	6	0	6	A9P6P9	
ENSMUST00000164812	ENSMUSG00000003308	9	21229730	21239332	-1	24	12	59	290	27	13	39	79	63	9	76		Q9Z2X8
ENSMUST00000164817						56	47	82	126	85	56	3	9	8	1	18		
ENSMUST00000164818	ENSMUSG00000020594	12	8674134	8752581	1	2	3	0	1	0	0	0	0	0	0	0	F6YD01	
ENSMUST00000164820	ENSMUSG00000005442	7	25267704	25294159	1	0	0	0	0	0	0	0	22	0	0	2	F6QIA9	
ENSMUST00000164821						9	1	3	9	9	3	0	15	15	0	17		
ENSMUST00000164822	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	0	0	0	0	27	0	0	0	G1EE51	Q99LJ7
ENSMUST00000164825	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	3	0	0	0	0	0	18	6	5	E9PZX9	
ENSMUST00000164826	ENSMUSG00000033170	15	78775138	78803042	-1	34	6	31	205	54	22	1797	2878	1554	146	1721	E9PUV9	
ENSMUST00000164828	ENSMUSG00000040374	3	5560188	5576239	-1	6	0	0	0	0	0	31	143	85	181	33	Q91YZ5	
ENSMUST00000164831	ENSMUSG00000025404	10	127380327	127499384	1	0	0	0	0	0	0	0	0	167	0	110	E9Q9D6	
ENSMUST00000164832	ENSMUSG00000024067	17	74299474	74323944	-1	2	0	0	1	0	0	0	0	0	0	0		Q99LT0
ENSMUST00000164833	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	0	0	0	47	304	124	58	174	F7A465	
ENSMUST00000164834	ENSMUSG00000091735	9	106463962	106465938	-1	4	2	26	321	23	6	0	1	1	2	1		Q80UC6
ENSMUST00000164835	ENSMUSG00000026740	2	18195654	18392830	-1	0	0	0	0	0	0	0	0	0	17	14	F7C8U2	
ENSMUST00000164837	ENSMUSG00000050088	17	14943184	14959570	1	9	0	7	90	11	7	83	666	131	63	130		Q9DAY5
ENSMUST00000164838	ENSMUSG00000092019	12	87618869	87622955	1	22	16	18	26	17	10	0	0	0	0	1	Q3UT53	
ENSMUST00000164843	ENSMUSG00000024942	19	5988546	6015825	-1	0	0	0	82	27	0	3838	5002	3328	259	2045	Q3TI07	O35350
ENSMUST00000164845	ENSMUSG00000090662	7	8470525	8489075	-1	27	24	66	10	39	11	0	0	0	0	0	L7N2B5	
ENSMUST00000164848	ENSMUSG00000091722	14	75455982	75526141	1	14	9	27	15	11	9	0	0	0	0	2	B2RWG3	
ENSMUST00000164853	ENSMUSG00000078588	4	117866524	117872557	-1	20	17	34	41	24	15	0	2	0	0	0	Q3V0I8	
ENSMUST00000164855	ENSMUSG00000090551	4	108847399	108848619	-1	3	0	2	196	5	3	0	5	2	0	5	Q8C992	
ENSMUST00000164856	ENSMUSG00000090966	17	23384803	23401864	1	10	16	8	8	11	11	0	0	0	0	0		E9Q6I0
ENSMUST00000164859	ENSMUSG00000034252	9	80066903	80144953	1	0	0	0	18	10	0	7	119	37	75	30		Q6P7W0
ENSMUST00000164861						2	2	5	5	3	2	0	0	0	0	0		
ENSMUST00000164863	ENSMUSG00000090996	2	164460967	164490760	1	0	0	0	3	0	0	0	24	0	31	0	E9PXJ7	
ENSMUST00000164864						9	4	17	12	7	9	1	0	0	0	4		
ENSMUST00000164866	ENSMUSG00000028345	4	48430858	48473459	-1	0	0	0	0	7	0	0	0	0	0	0		Q3URQ0
ENSMUST00000164868	ENSMUSG00000021906	14	32085374	32103202	1	4	8	0	0	0	3	0	38	0	0	0	E9Q690	
ENSMUST00000164869						6	0	18	1	2	0	0	0	0	0	0		
ENSMUST00000164870						2	0	0	7	2	0	0	0	0	0	4		
ENSMUST00000164871	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	0	0	0	0	E9PUX1	
ENSMUST00000164875	ENSMUSG00000091450	5	109046873	109059452	-1	8	7	13	4	7	3	0	0	0	0	0	E9Q4X4	
ENSMUST00000164876						7	4	25	15	4	5	0	0	0	0	0		
ENSMUST00000164877	ENSMUSG00000041670	1	22286251	22805724	-1	0	10	25	37	4	2	0	1	0	0	0	Q7TPL9	
ENSMUST00000164880	ENSMUSG00000094313	7	5610411	5611313	-1	1	1	3	0	3	0	0	0	0	0	0	W4VSP5	
ENSMUST00000164882						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164884	ENSMUSG00000031879	8	104639839	104641965	-1	5	7	15	119	11	0	13	0	38	14	22		Q9D187
ENSMUST00000164886	ENSMUSG00000066682	5	137865827	137871815	-1	14	10	22	24	21	16	1384	4661	1528	3760	1477		Q2YFS1
ENSMUST00000164887	ENSMUSG00000028778	4	130130217	130139359	-1	0	0	11	0	0	0	0	0	0	0	0		P58307
ENSMUST00000164888						2	1	0	0	1	0	4	30	8	0	19		
ENSMUST00000164889	ENSMUSG00000035778	2	35400179	35463231	-1	4	0	0	0	2	2	0	0	5	0	0	Q3TXW0	P23336
ENSMUST00000164890	ENSMUSG00000031861	8	69822429	69831102	1	0	27	87	223	0	0	58	395	0	0	155	Q6P290	
ENSMUST00000164891	ENSMUSG00000018648	11	84048041	84069261	-1	0	0	0	0	0	0	0	0	0	0	0	Q542U4	Q9JLY7
ENSMUST00000164893	ENSMUSG00000041923	18	22693181	23041653	-1	0	0	0	0	0	1	0	0	0	0	0	G3UW35	
ENSMUST00000164895	ENSMUSG00000042570	10	79540245	79555199	-1	0	0	0	79	0	0	0	0	0	0	0	E9Q269	
ENSMUST00000164896						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000164900						0	2	0	0	0	0	28	13	49	24	57		
ENSMUST00000164902	ENSMUSG00000004561	14	51884842	51893039	1	0	2	0	0	0	1	40	26	10	16	0	E9Q7K9	
ENSMUST00000164904	ENSMUSG00000001687	5	148504635	148552789	-1	2	4	10	27	9	4	362	887	1572	786	969		Q9Z2M6
ENSMUST00000164907	ENSMUSG00000054723	17	56713932	56717699	-1	14	12	43	16	29	0	65	87	57	20	14	G3XA49	
ENSMUST00000164915	ENSMUSG00000001424	6	28475139	28935162	1	15	15	75	80	37	14	0	4	9	0	5	E9Q3E9	
ENSMUST00000164916	ENSMUSG00000075229	16	36071660	36092118	1	7	0	0	0	14	5	0	49	27	51	21		Q8R3Q6
ENSMUST00000164917	ENSMUSG00000090627	14	6528612	6537290	-1	0	0	0	0	0	0	0	0	0	0	0	K7N759	
ENSMUST00000164918	ENSMUSG00000091930	7	10158652	10176286	-1	5	4	8	1	4	4	0	0	0	0	0	L7N2B2	
ENSMUST00000164919	ENSMUSG00000002900	12	31265234	31329644	1	0	0	0	0	0	0	0	1	0	1	0	E9PYT5	
ENSMUST00000164920						1	2	0	1	0	0	1	19	0	0	0		
ENSMUST00000164922	ENSMUSG00000029771	6	29526625	29541871	1	1	0	7	0	0	2	0	2	0	0	5		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000164923						5	2	5	8	0	2	0	1	0	1	0		
ENSMUST00000164924	ENSMUSG00000025509	7	141455198	141460743	1	0	0	6	0	4	2	21	160	0	0	20	H3BIT5	
ENSMUST00000164925	ENSMUSG00000028133	3	121155398	121171695	-1	0	2	0	19	7	4	0	0	0	1	7	E9PVR5	
ENSMUST00000164927	ENSMUSG00000025575	11	118406289	118419086	-1	0	2	7	2	9	0	0	13	55	0	51		Q8VCF1
ENSMUST00000164929	ENSMUSG00000001249	7	31098725	31115290	-1	10	9	22	17	18	5	0	0	0	0	0	E9Q3X9	
ENSMUST00000164930	ENSMUSG00000032479	9	109931460	110083955	1	24	23	101	30	33	20	23	106	53	19	29	E9PZ43	
ENSMUST00000164931	ENSMUSG00000020513	11	86544991	86567360	1	0	0	0	0	0	0	1	0	0	6	0	F6Q5J9	
ENSMUST00000164932	ENSMUSG00000050463	15	101946004	101954287	-1	37	24	59	33	31	11	0	0	1	0	0	E9Q0F0	
ENSMUST00000164933						1	1	5	4	0	0	0	0	0	0	0		
ENSMUST00000164934						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000164935	ENSMUSG00000090843	12	83954499	83984852	-1	26	20	44	41	32	16	0	7	1	0	0	E9Q357	
ENSMUST00000164936	ENSMUSG00000090659	13	67779754	67792512	1	0	0	0	0	0	0	0	0	0	2	0	E9Q1L8	
ENSMUST00000164938	ENSMUSG00000023048	15	102459028	102462806	1	0	0	0	0	0	0	3	0	0	0	0	E9PZX3	
ENSMUST00000164939						36	29	50	44	33	14	101	186	288	31	358		
ENSMUST00000164940	ENSMUSG00000060890	X	100605497	100618493	1	0	0	0	1	0	0	0	0	0	0	0	E9PXD3	
ENSMUST00000164944	ENSMUSG00000038540	7	83584927	83625614	1	0	1	5	0	7	0	0	0	0	0	0	E9Q6Y0	
ENSMUST00000164945	ENSMUSG00000018845	11	82910550	82943403	1	0	1	0	1	27	0	0	0	0	0	0		Q8CGY6
ENSMUST00000164947	ENSMUSG00000059005	2	75659261	75669407	1	0	0	0	0	0	0	80	445	290	727	219	Q0VG47	Q8BG05
ENSMUST00000164948	ENSMUSG00000091131	14	41381628	41386379	-1	22	15	52	37	17	13	0	0	0	0	0	F6QI24	
ENSMUST00000164950	ENSMUSG00000055692	16	17276300	17283229	1	0	0	0	252	9	12	0	0	0	0	0		Q9JJB1
ENSMUST00000164954	ENSMUSG00000091091	3	32471588	32492231	-1	17	14	27	14	25	14	0	1	0	0	1	E9Q7U0	
ENSMUST00000164955						6	7	21	36	8	0	0	1	0	0	0		
ENSMUST00000164956						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164957	ENSMUSG00000023048	15	102459028	102462806	1	0	2	0	0	0	0	9729	16230	5722	1910	3844		Q9CQJ5
ENSMUST00000164960	ENSMUSG00000030134	6	118011438	118091546	1	18	21	43	44	39	18	1	4	0	0	2	A6H650	
ENSMUST00000164961						2	2	0	1	10	6	63	152	26	31	56		
ENSMUST00000164962	ENSMUSG00000092137	9	71479325	71592265	-1	0	2	1	0	0	0	0	0	0	0	0	E9Q2N5	
ENSMUST00000164963	ENSMUSG00000054770	1	57955101	58018956	-1	3	8	34	0	4	0	0	0	9	0	0	E9Q945	
ENSMUST00000164964	ENSMUSG00000062737	13	27121701	27127546	1	3	0	6	1	0	0	0	0	0	0	0	Q8CGZ8	
ENSMUST00000164965	ENSMUSG00000066383	9	106499967	106502249	1	0	0	3	1	0	0	0	0	0	0	0		Q9D9K8
ENSMUST00000164967	ENSMUSG00000093863	14	41448203	41453518	-1	13	3	7	12	0	2	0	0	0	0	0	F7BAX1	
ENSMUST00000164968						0	0	4	0	3	0	0	5	0	0	0		
ENSMUST00000164969						1	0	3	5	3	0	0	0	0	0	0		
ENSMUST00000164971						8	6	16	7	7	7	8	6	45	0	53		
ENSMUST00000164972	ENSMUSG00000022561	15	76331231	76334907	1	0	0	0	12	0	0	22	28	0	0	0	E9Q4I5	
ENSMUST00000164974	ENSMUSG00000002718	2	166906040	166946389	1	0	0	0	0	0	0	0	0	0	24	7	F7D1H9	
ENSMUST00000164975						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000164978						0	2	3	0	2	0	4	1	2	0	0		
ENSMUST00000164979	ENSMUSG00000020014	10	92775619	93081618	-1	0	0	0	0	0	0	0	0	2	0	0	F6Z1L4	
ENSMUST00000164980	ENSMUSG00000004530	5	113842436	113908758	-1	27	0	91	159	34	18	54	951	7	119	123	E9PX03	
ENSMUST00000164982	ENSMUSG00000025730	17	25882114	25919727	-1	0	0	4	0	3	0	62	0	6	0	11	E9Q016	
ENSMUST00000164983	ENSMUSG00000023015	15	99620496	99651656	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q071	
ENSMUST00000164985	ENSMUSG00000099820	2	86074742	86075674	1	2	5	7	0	0	2	0	0	0	0	0	Q7TR85	
ENSMUST00000164987	ENSMUSG00000006154	7	4460674	4480487	1	0	0	0	0	2	1	0	1	0	0	0	F7BBD2	
ENSMUST00000164988	ENSMUSG00000010066	9	107399612	107529343	1	0	0	0	5	0	0	0	0	0	0	0	E9Q683	
ENSMUST00000164989	ENSMUSG00000021910	14	31170930	31216946	-1	0	0	2	0	0	2	0	45	60	0	121		Q80TM9
ENSMUST00000164992	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	0	0	0	0	16	0	0	46	E9Q2M5	
ENSMUST00000164993	ENSMUSG00000041324	13	16011851	16027211	1	0	0	0	0	0	1	89	74	210	26	115	Q3UY39	Q04998
ENSMUST00000164996	ENSMUSG00000090949	7	86795141	86812032	1	1	5	2	4	4	0	0	0	0	0	0	L7N2B7	
ENSMUST00000164998	ENSMUSG00000000420	18	24205344	24286818	1	2	0	4	13	2	0	0	0	3	1	3	E9Q0U0	
ENSMUST00000164999	ENSMUSG00000079109	5	143909964	143933968	1	0	0	0	0	0	0	1	0	2	0	0	F6TK25	
ENSMUST00000165000	ENSMUSG00000078487	4	155790439	155799503	1	13	9	8	15	13	4	0	0	0	0	0	F6YK91	
ENSMUST00000165001						6	7	7	7	8	2	0	0	0	0	0		
ENSMUST00000165003	ENSMUSG00000091923	14	44716838	44724987	-1	10	0	0	0	5	0	0	0	0	0	0	E9Q207	
ENSMUST00000165004	ENSMUSG00000045948	7	28739641	28741820	-1	2	1	0	26	2	0	2	12	0	0	0	E9PUY1	
ENSMUST00000165006						5	0	5	7	7	2	1	0	0	0	1		
ENSMUST00000165007	ENSMUSG00000063576	17	46674550	46680930	-1	0	0	40	101	23	13	374	483	95	42	55		
ENSMUST00000165009						0	0	0	0	0	0	18	33	4	3	0		
ENSMUST00000165012	ENSMUSG00000090581	3	64537561	64565298	-1	0	3	0	0	6	14	0	0	0	0	0	L7N478	
ENSMUST00000165013	ENSMUSG00000019874	10	57784881	57788450	1	2	3	1	1	5	0	0	6	0	7	3	E9Q0H6	
ENSMUST00000165015	ENSMUSG00000035235	14	61598226	61605946	1	0	8	9	2	9	0	28	0	0	0	0		Q9CYB0
ENSMUST00000165017	ENSMUSG00000015176	19	46075863	46085528	1	25	21	89	90	32	21	122	256	137	235	272	E9Q5C9	
ENSMUST00000165020	ENSMUSG00000068037	17	12841079	12868143	-1	0	0	0	0	0	0	0	0	0	0	0	Q0VB49	P30554
ENSMUST00000165021						7	5	3	24	0	1	0	0	2	0	0		
ENSMUST00000165022	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	0	0	16	0	F6ZGI7	
ENSMUST00000165023	ENSMUSG00000030846	7	128439777	128461717	-1	0	0	0	0	0	0	0	42	20	17	37	Q921W2	
ENSMUST00000165024	ENSMUSG00000058297	10	60106219	60135198	1	104	86	425	450	131	75	0	20	8	0	9	F6SLR4	
ENSMUST00000165025						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000165027	ENSMUSG00000001627	12	40201567	40248504	-1	0	0	0	0	0	0	0	0	34	0	14	E9PVS0	
ENSMUST00000165028	ENSMUSG00000042570	10	79540245	79555199	-1	0	0	2	115	0	0	0	0	19	0	57		Q3U3N0
ENSMUST00000165029	ENSMUSG00000066537	7	41399732	41448641	-1	6	1	1	2	1	0	0	0	0	0	0	L7N269	
ENSMUST00000165031	ENSMUSG00000006599	7	46796103	46823800	1	0	1	2	25	0	0	3	9	8	3	7	E9PWY2	
ENSMUST00000165032	ENSMUSG00000024535	18	53245662	53390823	1	8	8	5	19	8	5	57	426	119	72	114		Q9CRB0
ENSMUST00000165033	ENSMUSG00000038418	18	34859823	34864984	1	4	5	7	0	7	6	13	3723	21	10	161	Q544D6	P08046
ENSMUST00000165036	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	0	0	0	0	0	0	0	0	E9PZ73	
ENSMUST00000165043						5	1	6	6	6	3	6	21	3	1	10		
ENSMUST00000165044	ENSMUSG00000061393	9	119402444	119433501	1	7	9	31	98	20	14	2	3	5	2	6		P27040
ENSMUST00000165045	ENSMUSG00000051504	7	55768178	55778925	1	0	0	0	0	0	0	0	0	0	21	17	B7ZMQ6	
ENSMUST00000165046	ENSMUSG00000078599	4	111919392	111950358	1	2	3	0	2	0	0	0	0	0	0	0		A7XV07
ENSMUST00000165052	ENSMUSG00000032737	7	101822632	101838076	-1	39	0	0	105	0	26	266	390	251	36	274		Q6P549
ENSMUST00000165055	ENSMUSG00000030889	7	120739557	120805742	1	0	0	0	0	0	0	0	0	0	0	0	F6Z0V3	
ENSMUST00000165058						33	31	413	44	46	26	0	0	0	0	0		
ENSMUST00000165061	ENSMUSG00000090700	17	32659410	32676687	1	24	13	21	28	21	5	0	0	0	0	0	G3UW81	
ENSMUST00000165062	ENSMUSG00000006007	1	150319417	150333906	1	0	0	0	0	0	0	0	0	0	0	0		Q9QW08

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000165063						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000165066	ENSMUSG00000040865	1	62958418	63114667	-1	0	1	0	0	0	0	0	0	411	0	243	E9Q9Q0	
ENSMUST00000165067	ENSMUSG00000035948	10	106936164	107123668	-1	4	0	3	4	2	2	0	0	0	0	0		Q14DH7
ENSMUST00000165071						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000165072	ENSMUSG00000040025	4	132184912	132212303	-1	0	0	0	0	0	0	0	4	3	0	0	F6Y6H7	
ENSMUST00000165075	ENSMUSG00000039716	9	106892825	107231909	-1	2	0	0	0	2	0	0	0	0	0	0	F7CVM6	
ENSMUST00000165077	ENSMUSG00000021548	13	85189408	85223469	1	0	1	0	50	0	0	2	0	6	9	0	E9QA43	
ENSMUST00000165079	ENSMUSG00000002803	12	112976482	112978930	1	16	5	33	5	0	8	88	79	54	16	71		Q8K2J9
ENSMUST00000165080	ENSMUSG00000073094	X	75146056	75163770	-1	0	0	0	0	0	2	0	0	0	0	0		Q3V0X1
ENSMUST00000165083						6	0	0	1	6	1	0	0	0	0	4		
ENSMUST00000165084	ENSMUSG00000024563	18	76241580	76305731	1	0	0	0	0	0	0	0	9	3	0	0	E9PXA8	
ENSMUST00000165086	ENSMUSG00000063889	18	3266048	3337748	-1	0	1	0	0	0	0	3	0	0	0	10		P27699
ENSMUST00000165087	ENSMUSG00000021363	13	41025120	41079706	-1	0	20	32	28	0	12	0	0	0	0	6		Q04859
ENSMUST00000165088	ENSMUSG00000032268	9	49081260	49117587	1	9	8	24	18	24	6	0	0	0	0	0		Q9ER04
ENSMUST00000165090						1	2	0	2	2	1	0	5	3	1	2		
ENSMUST00000165092	ENSMUSG00000005899	16	17619354	17644828	1	0	0	2	19	2	3	0	0	0	0	0	E9QAA5	
ENSMUST00000165093	ENSMUSG00000042350	12	84918148	84970900	-1	2	1	0	8	0	1	0	0	0	0	0	E9PYE5	
ENSMUST00000165095	ENSMUSG00000016664	15	83375607	83464606	-1	67	46	0	15	29	29	0	0	24	0	0	Q3TDA7	Q9WVE8
ENSMUST00000165096	ENSMUSG00000030681	7	126986860	127014621	-1	19	15	50	41	30	15	7278	6983	6342	987	4231	E9Q3X0	
ENSMUST00000165097						0	0	1	1	0	0	6	9	10	0	10		
ENSMUST00000165099	ENSMUSG00000029821	6	50188888	50263862	-1	75	45	104	69	61	48	44	127	78	8	93	E9Q5V3	
ENSMUST00000165100	ENSMUSG00000004561	14	51884842	51893039	1	0	0	0	0	0	0	2	31	18	5	18	E9Q0X9	
ENSMUST00000165102	ENSMUSG00000060613	19	40153353	40187333	-1	0	1	1	0	0	0	0	0	0	0	0	E9Q8U5	
ENSMUST00000165104	ENSMUSG00000040111	9	40293233	40531383	-1	0	0	0	0	0	0	70	160	23	11	86		Q80TI0
ENSMUST00000165105	ENSMUSG00000025899	9	3335478	3387050	1	0	0	0	0	0	0	0	0	0	4	0		Q80Y20
ENSMUST00000165109	ENSMUSG00000079434	1	87509889	87597845	1	12	4	8	3	5	7	0	0	0	0	2	Q0VGI4	Q9JMH3
ENSMUST00000165111	ENSMUSG00000020917	11	100476353	100528000	-1	0	0	0	0	0	0	1419	2584	1379	187	1011		Q91V92
ENSMUST00000165113	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	465	0	1	0	Q8BLD4	
ENSMUST00000165114	ENSMUSG00000021127	12	80107760	80113013	-1	6	1	42	296	12	11	0	0	2443	108	1449	Q543H2	P23950
ENSMUST00000165117	ENSMUSG00000040274	5	3341485	3531008	1	42	51	116	259	57	39	59	60	122	13	121	Q0VBK8	Q64261
ENSMUST00000165120	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	17	0	0	0	0	0	0	0	E9PWL5	
ENSMUST00000165122	ENSMUSG00000015957	7	98835112	98855195	1	4	0	0	84	3	0	0	0	0	0	0	E9Q692	
ENSMUST00000165123	ENSMUSG00000024576	18	61555274	61590061	1	5	4	6	49	17	2	491	2064	573	102	368	Q6PJ87	Q8BK63
ENSMUST00000165124	ENSMUSG00000001249	7	31098725	31115290	-1	12	4	12	30	8	10	0	0	0	0	0		
ENSMUST00000165125	ENSMUSG00000026411	1	136008150	136035342	1	0	2	2	1	0	0	0	0	0	0	0		Q9CR23
ENSMUST00000165126	ENSMUSG00000090137	8	70508263	70510801	-1	0	1	0	0	0	0	646	1367	732	3281	317	Q66JP1	P62984
ENSMUST00000165127	ENSMUSG00000023944	17	45567775	45573271	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q0C3	
ENSMUST00000165128	ENSMUSG00000060268	4	117213333	117252125	-1	7	4	6	10	20	0	0	3	1	1	0	E9Q963	
ENSMUST00000165129						1	1	0	0	1	0	1	7	0	25	23		
ENSMUST00000165131	ENSMUSG00000091561	18	31819862	31820413	-1	0	2	1	3	1	1	0	0	0	0	0	F6Y363	
ENSMUST00000165133	ENSMUSG00000091311	13	59712284	59719289	1	26	24	132	51	46	19	0	0	0	0	0	E9QA57	
ENSMUST00000165134	ENSMUSG00000020986	12	58958383	59012017	-1	0	0	0	0	1	3	54	168	257	297	189	E9Q1S3	
ENSMUST00000165135						3	4	27	5	7	4	4	10	20	2	17		
ENSMUST00000165136	ENSMUSG00000091733	14	43071142	43076643	-1	4	9	7	19	6	4	0	0	0	0	0	K7N6U8	
ENSMUST00000165139						0	2	6	0	3	1	0	0	0	0	4		
ENSMUST00000165140						2	1	0	0	0	0	8	16	4	0	5		
ENSMUST00000165141	ENSMUSG00000002020	12	84783212	84876532	-1	4	1	6	4	4	0	0	0	0	0	0	F6WSP3	
ENSMUST00000165143	ENSMUSG00000024833	19	5940543	5964206	-1	41	20	75	50	51	27	79	79	35	9	80	Q8C2T6	
ENSMUST00000165144	ENSMUSG00000038838	17	35655634	35667592	-1	0	0	6	74	3	3	0	0	0	0	0	E9PWQ5	
ENSMUST00000165147	ENSMUSG00000066108	7	141839070	141873084	1	201	140	717	257	236	118	3	7	7	1	7	E9Q5I3	
ENSMUST00000165148	ENSMUSG00000061882	5	123930679	123969895	1	12	12	18	16	11	13	0	0	4	0	4		E9PVD1
ENSMUST00000165149	ENSMUSG00000024036	17	31295483	31350696	1	22	21	60	395	37	19	94	190	162	15	140	Q8R070	
ENSMUST00000165150						4	1	7	13	6	0	0	0	0	0	2		
ENSMUST00000165151						5	3	0	8	10	2	0	0	0	0	0		
ENSMUST00000165153						1	0	0	0	0	0	484	13	446	46	331		
ENSMUST00000165154						1	4	0	2	1	0	7	42	2	0	6		
ENSMUST00000165161						7	9	0	3	6	1	0	0	0	0	0		
ENSMUST00000165163	ENSMUSG00000059323	15	76622088	76639958	-1	5	5	18	43	8	3	12	39	17	39	18	F7A0T4	
ENSMUST00000165164	ENSMUSG00000069678	6	83077869	83080855	1	0	0	7	16	0	0	0	34	26	51	14		Q8R023
ENSMUST00000165165	ENSMUSG00000091345	9	105856070	105960643	-1	20	12	0	25	23	17	0	0	0	0	10		
ENSMUST00000165167	ENSMUSG00000074377	7	13909677	13989607	-1	7	4	6	2	0	3	0	0	0	0	0	D3Z6M7	
ENSMUST00000165169						0	1	5	1	3	3	0	0	0	1	0		
ENSMUST00000165170	ENSMUSG00000062154	15	78378400	78395912	-1	0	0	0	0	8	5	0	1	0	0	0	Q3KNN2	Q9D9J2
ENSMUST00000165173	ENSMUSG00000090816	10	86539883	86541334	-1	16	11	27	26	21	5	0	0	0	0	0	E9Q4Z5	
ENSMUST00000165174	ENSMUSG00000023050	15	102497649	102517064	-1	0	0	0	0	0	0	0	0	0	0	0	E9QA89	
ENSMUST00000165175	ENSMUSG00000053025	7	75114894	75309262	-1	0	0	4	45	9	13	0	0	0	0	0		Q8BG39
ENSMUST00000165177	ENSMUSG00000032215	9	73113426	73123333	1	1	0	8	0	2	0	0	6	5	0	0	E9PY85	
ENSMUST00000165179						0	0	0	2	1	1	0	87	27	0	29		
ENSMUST00000165180	ENSMUSG00000092080	5	109330381	109364481	1	8	16	7	15	20	2	0	0	0	0	0	E9Q025	
ENSMUST00000165182						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000165183	ENSMUSG00000050824	17	25489875	25497288	-1	0	0	29	0	0	8	0	0	0	0	0		O08858
ENSMUST00000165184						0	0	0	0	0	0	1	3	0	0	0		
ENSMUST00000165185						11	8	22	9	16	5	0	0	0	0	0		
ENSMUST00000165187						85	98	191	220	127	44	0	22	7	4	25		
ENSMUST00000165190	ENSMUSG00000059323	15	76622088	76639958	-1	13	5	22	4	0	0	0	0	0	0	0	E9Q2M2	
ENSMUST00000165192						2	1	9	2	3	1	0	0	0	0	0		
ENSMUST00000165193	ENSMUSG00000094634	14	6020654	6108665	-1	3	0	0	37	0	0	0	0	2	0	0	E9QAJ8	
ENSMUST00000165194	ENSMUSG00000048200	7	141461094	141466613	1	2	2	1	41	3	0	0	7	0	1	4	E9Q196	
ENSMUST00000165196	ENSMUSG00000103766	3	88243380	88287210	-1	5	5	32	0	6	7	0	0	0	0	0	E9Q2A2	
ENSMUST00000165198						9	8	2	6	4	4	1	0	2	15	0		
ENSMUST00000165199	ENSMUSG00000022620	15	89472476	89477425	-1	21	6	60	169	41	11	133	241	151	26	103		P50428
ENSMUST00000165201	ENSMUSG00000038679	15	50654752	50890463	-1	23	15	56	23	40	8	191	991	244	79	251	G3UW90	
ENSMUST00000165204						0	3	0	0	0	0	0	0	0	1	0		
ENSMUST00000165205	ENSMUSG00000090958	7	98489283	98502181	1	62	37	168	91	74	28	5	3	6	1	32	G3XA59	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000165208	ENSMUSG00000038670	7	44501699	44524656	-1	28	25	57	48	47	29	0	2	1	0	4		Q5XKE0
ENSMUST00000165210	ENSMUSG00000022565	15	76170974	76232574	-1	5	1	10	0	0	0	170	0	59	0	105	F6R059	
ENSMUST00000165211	ENSMUSG00000043557	17	29827956	29970087	-1	1	0	0	0	3	0	0	0	0	0	1	F6XL33	
ENSMUST00000165212	ENSMUSG00000025006	19	40295049	40402267	-1	0	0	0	0	0	0	11	67	104	0	38	E9PYX6	
ENSMUST00000165215	ENSMUSG00000024798	19	35958734	36057507	-1	0	0	0	0	0	0	0	0	0	0	12	E9Q4Q7	
ENSMUST00000165216	ENSMUSG00000001441	11	97205842	97280638	-1	0	0	0	0	0	0	60	15	300	0	0	F6QYF8	
ENSMUST00000165217						10	13	37	16	13	5	0	0	0	0	0		
ENSMUST00000165219	ENSMUSG00000027079	2	84722104	84727350	-1	41	40	90	26	40	26	20	82	15	0	42		Q99LI9
ENSMUST00000165220	ENSMUSG00000091053	13	8029828	8038106	-1	55	57	748	699	100	31	0	2	2	0	3	E9Q1C0	
ENSMUST00000165221	ENSMUSG00000020908	11	67078300	67102291	1	22	0	29	0	59	7	0	1	0	0	0		P13541
ENSMUST00000165223	ENSMUSG00000064302	1	118389058	118612678	1	0	6	0	8	0	0	589	925	952	0	689	E9Q6L0	
ENSMUST00000165224						3	5	5	4	11	0	0	5	2	1	2		
ENSMUST00000165225	ENSMUSG00000045034	13	92425896	92441658	1	0	0	0	53	0	0	0	0	0	0	0	E9Q655	
ENSMUST00000165229	ENSMUSG00000091449	18	20682592	20682963	-1	0	0	11	1	2	0	0	0	0	0	0	G3UWD7	
ENSMUST00000165230	ENSMUSG00000023882	17	21423227	21435640	1	5	0	14	0	7	4	0	5	0	0	0	E9PW05	
ENSMUST00000165231	ENSMUSG00000038060	9	119102478	119148246	1	0	4	8	18	8	5	0	0	0	0	0	E9Q8C0	
ENSMUST00000165232	ENSMUSG00000002944	5	17781690	17888801	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UAI3	Q08857
ENSMUST00000165233	ENSMUSG00000052151	10	79526430	79533787	-1	0	0	2	85	3	0	0	0	0	0	6	E9PV78	
ENSMUST00000165234	ENSMUSG00000038383	2	155278243	155357430	-1	4	0	0	0	0	2	0	0	0	64	0		Q8K358
ENSMUST00000165235						1	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000165239	ENSMUSG00000005442	7	25267704	25294159	1	0	3	7	0	1	0	1381	0	1147	0	933	E9Q6T8	
ENSMUST00000165240	ENSMUSG00000015957	7	98835112	98855195	1	0	1	5	0	0	0	0	0	0	0	0	E9PVI8	
ENSMUST00000165241	ENSMUSG00000050605	7	24291039	24301232	-1	4	4	0	1	13	0	7	4	6	11	10	Q923D1	
ENSMUST00000165242	ENSMUSG00000033216	6	88257334	88446539	-1	22	20	62	143	30	11	47	57	60	20	62		Q9JHW4
ENSMUST00000165245						5	5	3	8	5	0	0	0	0	0	0		
ENSMUST00000165246						0	0	0	3	2	0	0	8	0	0	0		
ENSMUST00000165248	ENSMUSG00000039059	2	180099465	180104488	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7T5	
ENSMUST00000165250	ENSMUSG00000054598	5	65979358	66004285	-1	0	0	10	0	0	0	0	0	2	1	0	Q8CC80	
ENSMUST00000165252	ENSMUSG00000063543	9	48450400	48450786	1	5	0	15	0	5	6	41	0	29	188	63		Q9D0T1
ENSMUST00000165253	ENSMUSG00000021555	13	59585259	59634798	1	0	0	0	0	0	0	7	0	7	0	0	F6ZAJ8	
ENSMUST00000165255	ENSMUSG00000091539	18	3122492	3123412	-1	12	10	15	0	7	3	0	0	0	0	0	E9Q373	
ENSMUST00000165257	ENSMUSG00000049580	7	98350668	98361328	-1	0	0	0	22	0	0	0	0	0	0	0	Q08EE6	Q8CBR6
ENSMUST00000165258	ENSMUSG00000022401	15	81400138	81456807	1	0	0	0	0	0	0	5	0	6	0	12	E9Q7I3	
ENSMUST00000165262	ENSMUSG00000022212	14	55510445	55517431	1	0	0	9	20	5	2	0	0	0	0	0	Q3UYN2	
ENSMUST00000165263	ENSMUSG00000032091	9	45172726	45204092	-1	4	5	0	0	5	3	0	0	0	1	0	E9Q4T9	
ENSMUST00000165265						3	0	0	0	0	0	1	0	0	1	0		
ENSMUST00000165266	ENSMUSG00000003848	8	107412486	107425051	-1	0	0	0	0	0	0	0	0	0	0	0	F6YBB8	
ENSMUST00000165269	ENSMUSG00000021879	14	26693274	26891703	1	15	17	17	8	22	13	0	3	3	0	2	F6QA95	
ENSMUST00000165270						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000165271						3	8	2	7	3	7	0	3	7	1	0		
ENSMUST00000165274	ENSMUSG00000031434	X	139821632	139871677	-1	1	0	0	4	0	0	0	0	0	0	0	E9Q112	
ENSMUST00000165276	ENSMUSG00000051243	9	58196298	58204319	-1	41	33	240	545	63	20	2	3	0	0	1		Q5RKR3
ENSMUST00000165279	ENSMUSG00000022562	15	76296597	76328015	-1	5	5	2	74	5	0	5	8	8	0	10	E9PZB8	
ENSMUST00000165280	ENSMUSG00000021796	14	34410734	34503341	-1	0	1	0	2	4	0	64	98	232	47	91	Q60607	
ENSMUST00000165281	ENSMUSG00000028873	4	124918465	124939311	-1	4	2	4	5	7	3	2	6	0	6	2	E9Q2C7	
ENSMUST00000165282						0	0	1	0	0	0	0	7	0	0	0		
ENSMUST00000165286	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	44	0	0	0	0	0	0	0	E9PYX3	
ENSMUST00000165288	ENSMUSG00000001986	X	41400854	41678601	1	0	0	0	0	0	0	0	11	0	0	0	B0QZW1	
ENSMUST00000165289	ENSMUSG00000079383	14	5015891	5019119	1	50	56	202	1	66	47	0	0	0	0	0	L7N281	
ENSMUST00000165291	ENSMUSG00000091809	14	14407102	14408198	1	3	6	21	3	8	3	0	0	0	0	0		
ENSMUST00000165293	ENSMUSG00000020594	12	8674134	8752581	1	0	7	21	0	0	0	25	0	0	0	51	E9Q0P1	
ENSMUST00000165296	ENSMUSG00000032554	9	103204001	103230444	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q2Q7	
ENSMUST00000165299						0	0	5	4	1	1	0	0	1	1	1		
ENSMUST00000165302						0	1	0	54	4	0	0	0	0	0	0		
ENSMUST00000165305	ENSMUSG00000021898	14	26894557	26915258	1	0	5	3	5	0	4	1	3	4	0	3	E9PWC7	
ENSMUST00000165306	ENSMUSG00000092417	17	35121455	35124814	1	4	0	28	100	13	9	152	188	149	12	54	Q6PES3	
ENSMUST00000165307	ENSMUSG00000015749	3	95929246	95947390	1	12	0	31	20	11	0	190	403	247	94	161		P97822
ENSMUST00000165308	ENSMUSG00000054676	7	38183217	38197568	1	6	18	29	5	15	9	129	62	147	42	85		Q8WUR0
ENSMUST00000165309	ENSMUSG00000040374	3	5560188	5576239	-1	0	0	0	5	0	2	0	6	28	35	5	Q91YZ5	
ENSMUST00000165310	ENSMUSG00000079419	19	11469366	11482192	1	253	295	800	239	358	139	319	2770	496	1655	691		Q99N08
ENSMUST00000165311	ENSMUSG00000025189	19	43440436	43497212	1	22	21	56	269	40	22	0	0	0	0	1		Q0GA42
ENSMUST00000165313	ENSMUSG00000036249	2	51924448	51935163	-1	0	6	0	0	0	0	148	1509	218	182	112		Q99J64
ENSMUST00000165315	ENSMUSG00000032422	9	88376750	88438958	-1	0	0	0	0	0	0	287	1315	597	35	170		Q8BHY8
ENSMUST00000165316	ENSMUSG00000037851	13	49682100	49734267	1	39	0	0	79	37	0	0	0	0	0	0		Q8BU30
ENSMUST00000165318	ENSMUSG00000061898	5	143172186	143180775	-1	9	15	29	131	21	0	0	13	0	0	0		Q8BQC8
ENSMUST00000165320	ENSMUSG00000061374	7	5007057	5014697	-1	6	14	54	392	19	5	185	99	103	21	124	Q3TRV0	Q9WTJ4
ENSMUST00000165321	ENSMUSG00000000759	8	12614277	12672248	-1	0	0	0	0	0	0	7	3	0	3	10	F7AJZ3	
ENSMUST00000165322	ENSMUSG00000025234	9	59388258	59486618	-1	0	0	3	0	0	0	245	637	714	37	242	H9KV21	
ENSMUST00000165323	ENSMUSG00000041923	18	22693181	23041653	-1	0	0	0	2	0	2	0	0	0	0	0	E9Q5X0	
ENSMUST00000165324	ENSMUSG00000062007	8	72189668	72200995	1	7	7	0	0	0	0	60	297	32	54	92		Q6VYH9
ENSMUST00000165329						5	0	3	72	2	0	64	288	94	18	69		
ENSMUST00000165330	ENSMUSG00000095201	7	20101158	20102081	1	2	0	4	0	1	0	0	0	0	0	0	E9PZR7	
ENSMUST00000165331	ENSMUSG00000052337	6	71831331	71877388	1	0	0	0	0	0	0	2	0	37	0	0	Q3TZK4	
ENSMUST00000165332						0	0	0	1	2	2	0	0	0	0	0		
ENSMUST00000165333						4	0	0	0	0	1	8	11	21	0	34		
ENSMUST00000165334						0	0	0	0	0	0	0	9	1	0	5		
ENSMUST00000165335	ENSMUSG00000029064	4	155491361	155559269	1	0	0	0	18	0	0	310	2	590	137	490	Q3TQ70	P62874
ENSMUST00000165337						0	0	0	47	4	0	0	0	0	0	3		
ENSMUST00000165341	ENSMUSG00000091455	10	107762223	107912134	-1	22	34	22	24	33	15	0	0	0	0	0		F7A4A7
ENSMUST00000165343	ENSMUSG00000074673	2	152962485	153008482	1	0	0	0	0	0	2	0	0	0	0	0	F6ZRM1	
ENSMUST00000165344	ENSMUSG00000029275	5	107716657	107726036	-1	14	7	2	109	24	5	0	4	5	0	0	A1L3P3	
ENSMUST00000165345	ENSMUSG00000094864	X	123029202	123029669	-1	13	17	26	35	19	7	0	0	0	0	0	F6QAC8	
ENSMUST00000165349	ENSMUSG00000094349	14	42988342	42993624	-1	0	0	5	10	0	3	0	0	0	0	0	F6ZAP6	
ENSMUST00000165356	ENSMUSG00000022370	15	55534094	55557748	-1	3	1	2	2	2	0	0	0	0	3	0	F7CXG9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000165358	ENSMUSG00000091109	13	96490733	96491120	1	0	0	0	0	0	0	0	0	0	0	0	E9Q955	
ENSMUST00000165359	ENSMUSG00000031387	X	73922121	73930850	-1	0	0	1	0	0	0	11	0	0	11	1	G3XA46	
ENSMUST00000165363	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	30	8	22	17	39		Q6ZPR5
ENSMUST00000165365	ENSMUSG00000035914	9	58524300	58555132	-1	0	0	0	71	30	0	0	0	0	0	0	A6MDC5	Q8VE98
ENSMUST00000165370	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	0	0	0	0	0	0	0	0	3	E9PX07	
ENSMUST00000165371						5	3	3	11	16	8	0	7	3	0	0		
ENSMUST00000165375	ENSMUSG00000075394	15	103018934	103036852	1	10	12	110	62	27	8	0	0	0	0	0	G3UX59	
ENSMUST00000165379	ENSMUSG00000075427	15	98186013	98195542	-1	3	2	4	1	1	8	0	0	0	0	0	E9Q1P2	
ENSMUST00000165380	ENSMUSG00000022899	16	36750178	36784962	-1	2	2	0	0	1	0	0	0	0	0	0	E9Q0L2	
ENSMUST00000165381						1	5	36	11	18	7	2	14	0	1	4		
ENSMUST00000165386	ENSMUSG00000091119	15	3280627	3303526	-1	1	4	0	4	3	4	0	1	1	0	0	E9PX14	
ENSMUST00000165387	ENSMUSG00000024277	18	23752333	23893861	1	0	5	4	4	5	0	71	0	65	2	85	E9Q1B7	
ENSMUST00000165388						13	13	103	12	12	5	0	2	1	0	1		
ENSMUST00000165389	ENSMUSG00000011958	9	69989466	70008317	1	0	0	0	0	0	0	198	433	366	54	137	Q91VL0	
ENSMUST00000165390	ENSMUSG00000064120	17	49428362	49455435	1	72	95	55	207	96	38	9	20	13	3	19	G3UWH1	
ENSMUST00000165392	ENSMUSG00000032641	6	134869093	134898578	-1	6	0	2	12	10	0	0	0	0	0	0		Q61121
ENSMUST00000165394	ENSMUSG00000005575	7	13035120	13038275	-1	0	2	5	11	0	2	36	100	31	0	0	G5E919	
ENSMUST00000165395						0	0	0	0	2	4	0	0	0	0	0		
ENSMUST00000165398	ENSMUSG00000074625	2	158512796	158550762	1	8	0	0	0	0	10	0	0	0	0	0		E9Q6X9
ENSMUST00000165399	ENSMUSG00000030435	7	5062143	5079945	1	0	7	13	0	0	15	535	1036	405	54	474	Q3KQM4	
ENSMUST00000165400	ENSMUSG00000033632	18	25168999	25467321	1	11	8	15	15	0	0	10	78	29	0	18	E9QAK8	
ENSMUST00000165401						13	4	65	19	22	15	3	0	1	0	5		
ENSMUST00000165405						2	1	7	8	5	1	1	14	2	1	2		
ENSMUST00000165407						2	2	4	3	3	0	0	0	0	0	0		
ENSMUST00000165408	ENSMUSG00000018126	15	79258195	79285537	-1	6	6	39	17	17	7	0	0	0	0	0		Q80Y61
ENSMUST00000165409						13	13	23	5	19	3	0	0	0	0	0		
ENSMUST00000165410						2	0	17	7	10	0	1	1	0	0	1		
ENSMUST00000165413	ENSMUSG00000037885	2	129800517	129832287	1	9	13	25	397	14	8	116	123	144	5	151		Q80ZW0
ENSMUST00000165414						2	6	0	3	4	0	0	0	0	0	0		
ENSMUST00000165416	ENSMUSG00000002458	2	181688419	181693977	-1	4	2	5	1	3	2	669	1676	785	171	342	Q78NN4	Q9CX84
ENSMUST00000165417	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	1	0	0	G3UW65	
ENSMUST00000165418	ENSMUSG00000022811	16	33380775	33503903	1	19	37	63	110	36	15	144	489	223	94	217	Q548L0	Q61624
ENSMUST00000165419						1	1	4	2	5	2	0	0	0	0	0		
ENSMUST00000165420	ENSMUSG00000048911	2	131298064	131352892	-1	0	0	0	0	0	0	157	328	186	18	156	Q4VA59	Q8BGI1
ENSMUST00000165424	ENSMUSG00000092073	5	94648382	94686353	1	0	0	0	0	0	0	0	0	0	0	0	E9PZS2	
ENSMUST00000165425						6	0	0	3	4	0	0	0	0	0	0		
ENSMUST00000165429	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	0	0	0	3	8	4	3	0	E9Q3W8	
ENSMUST00000165430	ENSMUSG00000000326	16	18406886	18426852	-1	35	38	113	50	50	21	26	150	25	100	80		O88587
ENSMUST00000165431	ENSMUSG00000091114	14	4249631	4258006	1	2	7	0	0	6	0	0	0	0	0	0	K7N754	
ENSMUST00000165432	ENSMUSG00000022209	14	55222007	55241435	1	0	0	0	0	0	4	0	0	0	0	0	Q149L0	
ENSMUST00000165436	ENSMUSG00000027550	3	14533788	14572658	1	0	0	0	0	0	0	0	0	0	0	0	E9PVL4	
ENSMUST00000165437						3	0	11	4	3	0	0	0	0	0	0		
ENSMUST00000165438						0	0	0	42	0	0	0	0	0	0	0		
ENSMUST00000165440	ENSMUSG00000025404	10	127380327	127499384	1	0	0	0	0	0	0	0	0	0	0	2	F6TDX7	
ENSMUST00000165443	ENSMUSG00000016619	15	84923428	84942955	1	26	24	71	61	54	22	533	1112	708	92	461		Q9JIH2
ENSMUST00000165445	ENSMUSG00000058028	7	6222278	6239423	1	0	0	0	0	0	0	0	0	0	0	0	B2RTN3	
ENSMUST00000165448						11	0	4	11	5	3	0	0	0	0	0		
ENSMUST00000165449						0	0	0	0	3	0	0	0	0	1	0		
ENSMUST00000165453	ENSMUSG00000022565	15	76170974	76232574	-1	2	2	15	30	5	5	0	0	0	0	0		
ENSMUST00000165454	ENSMUSG00000091585	JH584299.1	716296	720517	1	5	0	8	0	5	10	0	0	0	0	0		
ENSMUST00000165455	ENSMUSG00000029708	6	28416091	28428390	-1	0	0	0	4	1	0	5	0	0	0	0	F6VDD7	
ENSMUST00000165456	ENSMUSG00000030109	6	121343076	121365775	1	0	0	0	0	0	0	0	0	0	0	0	F7AYZ6	
ENSMUST00000165457	ENSMUSG00000030970	7	132987563	133124354	-1	0	4	0	11	13	6	4	2	0	0	0	E9Q123	
ENSMUST00000165459						0	1	0	0	1	0	0	20	10	0	8		
ENSMUST00000165460	ENSMUSG00000045795	7	81571292	81596836	1	17	16	26	162	18	19	209	753	388	57	415		Q571B6
ENSMUST00000165465						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000165466	ENSMUSG00000079388	14	4334763	4354688	1	11	6	10	9	7	6	0	0	0	0	2	Q9D073	
ENSMUST00000165469	ENSMUSG00000025006	19	40295049	40402267	-1	0	0	8	4	3	0	110	80	259	20	16	E9Q6A3	
ENSMUST00000165470	ENSMUSG00000055368	8	92960079	93001667	1	0	0	9	11	3	0	0	0	0	0	0		O55192
ENSMUST00000165475						0	0	0	0	0	0	0	10	0	0	0		
ENSMUST00000165477	ENSMUSG00000021557	13	59449537	59585227	-1	20	6	56	21	25	3	5	11	4	0	13	E9PXA7	
ENSMUST00000165478						116	107	529	141	131	57	2	4	1	0	8		
ENSMUST00000165480						0	1	0	23	5	2	0	0	0	0	0		
ENSMUST00000165485	ENSMUSG00000024909	19	5473973	5481853	1	0	0	0	18	6	0	41	124	44	11	83	Q542X5	Q9WVJ9
ENSMUST00000165486						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000165487	ENSMUSG00000025509	7	141455198	141460743	1	2	0	8	3	1	0	0	11	0	3	20	E9Q323	
ENSMUST00000165488						3	2	1	3	0	1	0	0	0	0	3		
ENSMUST00000165489						0	0	0	0	0	0	217	89	981	6	320		
ENSMUST00000165490						8	5	3	3	3	5	0	0	0	0	0		
ENSMUST00000165492						14	18	14	5	15	6	3	27	8	6	3		
ENSMUST00000165493	ENSMUSG00000028706	4	116032842	116053876	-1	30	26	101	56	29	25	0	0	1	0	0		C4P6S0
ENSMUST00000165495	ENSMUSG00000078580	7	127389673	127393629	-1	279	220	1703	796	321	169	14	61	49	13	52	E9PZQ8	
ENSMUST00000165496						0	0	1	1	2	0	0	4	3	2	0		
ENSMUST00000165499	ENSMUSG00000090317	9	78447865	78448786	-1	7	4	3	190	4	4	0	0	0	0	0	Q8C6J8	
ENSMUST00000165504	ENSMUSG00000073423	17	33629090	33631779	1	1	2	4	10	2	2	117	201	116	11	62	E9Q9N0	
ENSMUST00000165506						4	0	0	35	4	0	0	0	0	0	0		
ENSMUST00000165508						0	0	0	21	0	0	0	0	0	0	0		
ENSMUST00000165512	ENSMUSG00000001566	5	29473034	29478470	-1	7	9	27	0	19	8	0	0	0	0	0	A2RSX2	
ENSMUST00000165515	ENSMUSG00000048440	17	32536558	32551798	1	22	24	33	20	30	23	0	289	0	25	0	E9PW68	
ENSMUST00000165518						0	3	3	0	0	0	19	57	27	20	66		
ENSMUST00000165519	ENSMUSG00000035164	9	52111985	52168111	-1	33	26	40	62	23	17	14	22	24	4	29	E9Q1I3	
ENSMUST00000165520						53	43	1045	105	38	24	0	5	0	0	2		
ENSMUST00000165522	ENSMUSG00000025075	19	56287137	56320822	1	6	0	2	0	0	3	0	0	0	0	0	F7D2A6	
ENSMUST00000165523	ENSMUSG00000021906	14	32085374	32103202	1	3	0	0	0	1	4	13	0	9	4	4	E9Q4W0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000165524						0	0	0	0	0	0	0	0	8	18	18		
ENSMUST00000165525	ENSMUSG00000091775	17	47016696	47016956	-1	0	1	23	2	4	2	0	0	3	0	0	E9Q2Z4	
ENSMUST00000165526	ENSMUSG00000021974	14	58070547	58112337	1	46	53	121	202	28	49	0	2	2	4	2	E9Q2N2	
ENSMUST00000165527						0	0	0	0	0	1	0	1	0	0	0		
ENSMUST00000165528						0	1	5	46	5	2	2	0	0	2	2		
ENSMUST00000165530	ENSMUSG00000043008	16	19946499	19983037	-1	2	0	0	0	0	0	3	12	11	0	0	F6T3Y1	
ENSMUST00000165531	ENSMUSG00000022899	16	36750178	36784962	-1	0	0	0	0	0	0	0	0	0	0	0	E9PYQ9	
ENSMUST00000165532	ENSMUSG00000025794	9	120571517	120574653	1	12	18	6	11	15	7	1715	2859	1541	5853	1589		Q9CR57
ENSMUST00000165534						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000165535						3	3	2	3	1	3	0	0	0	0	0		
ENSMUST00000165536	ENSMUSG00000029178	5	64803388	64832901	1	12	9	22	118	17	12	1529	2080	2395	191	2547	Q545J5	Q60980
ENSMUST00000165537	ENSMUSG00000009585	15	79891659	79915906	1	0	0	0	0	0	0	0	0	49	0	9	Q3U5C5	Q99J72
ENSMUST00000165538	ENSMUSG00000043301	16	94749266	94997696	-1	19	19	43	26	34	17	0	0	0	0	0		
ENSMUST00000165539	ENSMUSG00000025487	7	140881968	140898643	1	1	0	2	0	0	0	0	3	0	0	0	F6PXS6	
ENSMUST00000165540	ENSMUSG00000027861	3	102086415	102146514	1	0	0	0	12	12	0	0	0	0	0	0	F6QYE1	
ENSMUST00000165541	ENSMUSG00000059895	15	73723145	73758766	1	0	0	0	13	5	6	247	204	154	29	241		Q9D658
ENSMUST00000165542						29	20	46	34	32	21	0	0	0	0	0		
ENSMUST00000165543						0	0	0	3	0	0	0	24	0	0	0		
ENSMUST00000165548						0	0	0	8	0	0	0	0	0	0	0		
ENSMUST00000165549	ENSMUSG00000026029	1	58795374	58847503	1	6	2	51	7	10	7	139	456	56	344	217	Q3U607	O89110
ENSMUST00000165553	ENSMUSG00000091718	14	43722253	43727485	-1	4	2	14	3	5	0	0	0	0	0	0	F7ANP4	
ENSMUST00000165554	ENSMUSG00000026288	1	87620312	87720507	1	2	3	4	0	0	4	11	20	9	0	3	F7BZA7	
ENSMUST00000165555	ENSMUSG00000024294	18	10725548	10818704	1	0	0	0	0	0	0	83	82	407	25	269		Q80SY4
ENSMUST00000165559	ENSMUSG00000052928	18	75431224	75697696	-1	179	133	1012	415	143	66	24	23	16	9	38	E9Q1U6	
ENSMUST00000165561	ENSMUSG00000091264	13	41249860	41276574	1	44	30	43	160	51	24	180	586	267	38	127		E9Q942
ENSMUST00000165562						3	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000165563	ENSMUSG00000020111	10	59702477	59864132	1	0	11	21	86	9	0	1031	902	555	190	519		Q8VCX5
ENSMUST00000165565	ENSMUSG00000017421	11	80383279	80405733	1	0	0	0	0	0	0	0	0	9	0	0		Q9JMD0
ENSMUST00000165566	ENSMUSG00000040929	19	27761721	28011166	-1	59	50	62	113	51	31	61	227	98	30	127		P48381
ENSMUST00000165567	ENSMUSG00000022106	14	73123037	73207843	1	3	0	0	0	0	0	0	0	13	0	9	E9Q7J4	
ENSMUST00000165568	ENSMUSG00000004561	14	51884842	51893039	1	0	1	0	2	0	0	0	14	8	3	8	F7AGB5	
ENSMUST00000165569	ENSMUSG00000034913	14	75582834	75593116	-1	5	6	0	0	13	0	0	0	0	0	0		Q32MG2
ENSMUST00000165571						0	2	12	0	5	2	0	0	0	1	0		
ENSMUST00000165572						0	1	0	86	5	4	0	0	70	13	60		
ENSMUST00000165576	ENSMUSG00000029672	6	22306520	22356243	-1	8	6	34	9	17	5	33	112	28	41	39		Q91VU0
ENSMUST00000165577						4	1	3	3	4	1	0	1	0	0	0		
ENSMUST00000165580	ENSMUSG00000090515	16	88671026	88671671	-1	5	2	3	0	2	1	0	0	0	0	0	E9PX37	
ENSMUST00000165582	ENSMUSG00000022403	15	81363669	81400077	-1	2	1	6	35	3	0	12	60	40	39	37	E9Q1V0	
ENSMUST00000165584						0	0	0	6	0	0	0	0	5	0	0		
ENSMUST00000165590	ENSMUSG00000005871	18	34220924	34322189	1	0	0	0	0	0	0	0	0	0	0	0	F6Q4R2	
ENSMUST00000165591	ENSMUSG00000090710	9	36475638	36477212	1	1	0	0	0	2	0	0	0	0	0	0	B3GLJ6	
ENSMUST00000165593	ENSMUSG00000049985	13	112288451	112384002	1	13	0	55	0	24	0	0	0	0	0	0	E9Q0E9	
ENSMUST00000165594	ENSMUSG00000001833	9	25252439	25308571	1	3	2	0	10	2	0	664	2589	956	1647	621	E9Q1G8	
ENSMUST00000165596	ENSMUSG00000032480	9	110084320	110117830	-1	31	0	26	4	21	14	225	326	227	53	246		Q99PU8
ENSMUST00000165598	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	0	0	0	5	0	0	0	3	0	E9Q352	
ENSMUST00000165599	ENSMUSG00000020340	11	46193850	46312859	-1	0	0	11	53	0	0	48	71	189	0	90		Q5SQX6
ENSMUST00000165601	ENSMUSG00000035835	10	79860475	79874634	-1	0	0	0	0	0	0	0	3	9	0	5	E9Q8U7	
ENSMUST00000165602	ENSMUSG00000026463	1	133699457	133801041	-1	0	0	0	0	0	0	17	40	20	0	43	Q6Q477	
ENSMUST00000165605	ENSMUSG00000038515	8	13176869	13200624	-1	8	7	19	38	15	7	0	1	1	1	0		Q9D3N8
ENSMUST00000165607	ENSMUSG00000034252	9	80066903	80144953	1	0	7	0	0	0	0	348	1100	586	0	217	F6Z9A1	
ENSMUST00000165608	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	1	0	0	0	187	1172	326	40	279	F7B8F0	
ENSMUST00000165609						11	0	12	21	19	3	0	0	0	0	0		
ENSMUST00000165611	ENSMUSG00000095914	7	9927624	9953585	-1	0	5	0	0	0	0	0	0	0	0	0	E9Q5D8	
ENSMUST00000165613	ENSMUSG00000038500	17	35972541	35980236	-1	1	4	0	18	1	1	2	5	4	0	1	E9Q601	
ENSMUST00000165614	ENSMUSG00000040420	15	22549022	23474418	1	0	0	0	0	0	0	0	0	0	0	0	E9Q941	
ENSMUST00000165616	ENSMUSG00000022801	16	32914100	33015647	1	0	0	0	0	0	1	0	0	0	0	0	E9Q892	
ENSMUST00000165617	ENSMUSG00000024975	19	53892231	53929861	1	0	0	0	15	0	0	23	0	192	17	196		Q61823
ENSMUST00000165619	ENSMUSG00000094628	14	4726775	4747493	1	4	0	0	22	12	0	0	0	0	0	0	E9PUT9	
ENSMUST00000165620						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000165623						18	19	52	123	29	11	26	360	73	5	121		
ENSMUST00000165626	ENSMUSG00000091195	11	31182376	31182462	-1	0	0	0	0	0	0	0	0	0	0	0	F7BTU1	
ENSMUST00000165628	ENSMUSG00000038697	8	123996318	124021309	-1	15	9	33	13	0	13	248	356	300	66	220		Q91WQ5
ENSMUST00000165629						4	0	4	0	0	3	107	781	212	7	157		
ENSMUST00000165630	ENSMUSG00000042870	8	75033686	75070121	1	0	0	0	1	29	0	0	0	46	0	0	Q561M4	O88746
ENSMUST00000165631	ENSMUSG00000002845	16	38558698	38592162	1	0	0	0	0	0	0	0	2	0	0	0	F6QHF9	
ENSMUST00000165635	ENSMUSG00000002728	2	145902099	145916425	1	0	0	0	22	0	0	0	0	0	0	0	E9PYH1	
ENSMUST00000165640	ENSMUSG00000037007	5	138139702	138155744	-1	0	0	0	0	0	0	2	0	3	5	0	Q8C689	
ENSMUST00000165641						3	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000165643						29	29	122	186	79	32	0	104	6	0	11		
ENSMUST00000165645	ENSMUSG00000036718	5	139706696	139736336	-1	4	2	8	5	9	4	0	0	0	0	2	F6UYB3	
ENSMUST00000165646						0	0	0	0	0	0	8	17	9	22	0		
ENSMUST00000165648	ENSMUSG00000036304	16	43969078	43979093	-1	0	6	15	27	2	0	4	11	0	0	4		Q5Y5T3
ENSMUST00000165649	ENSMUSG00000041028	14	37120444	37135322	-1	0	19	32	33	10	9	1038	3399	1382	2051	859		Q91VC9
ENSMUST00000165651	ENSMUSG00000021933	14	62392676	62456289	-1	0	2	0	0	4	7	0	0	0	0	0	E9Q6H0	
ENSMUST00000165654						9	3	26	3	6	1	14	17	3	4	13		
ENSMUST00000165656						0	4	0	0	2	2	0	0	0	2	1		
ENSMUST00000165657	ENSMUSG00000020600	12	8528483	8599066	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BZV2	
ENSMUST00000165660	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	4	0	0	0	5	59	6	0	10	F6XQN1	
ENSMUST00000165663	ENSMUSG00000026605	1	189640606	189688086	-1	1	2	0	0	2	3	0	0	0	0	0	E9Q776	
ENSMUST00000165664						44	31	169	40	29	27	38	67	52	3	49		
ENSMUST00000165665	ENSMUSG00000059495	9	42963842	43105718	-1	25	0	16	210	69	74	0	0	0	0	49	F8VQN6	
ENSMUST00000165666	ENSMUSG00000050875	18	59062248	59076962	1	5	0	0	0	0	0	0	0	0	0	0	E9Q5J6	
ENSMUST00000165667	ENSMUSG00000030782	7	128246812	128255699	1	0	0	0	0	0	0	0	0	0	2	0	E9Q1D5	
ENSMUST00000165669						0	0	0	0	0	0	2	0	0	0	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000165671	ENSMUSG00000001289	15	102326116	102331873	1	0	0	2	0	0	0	0	0	0	0	0	E9PVG3	
ENSMUST00000165672						0	0	2	0	0	0	0	0	0	1	0		
ENSMUST00000165673	ENSMUSG00000048794	6	90403479	90428797	-1	8	0	8	0	8	0	0	0	0	0	0	E9PYA2	
ENSMUST00000165677						5	16	34	10	11	0	6	33	0	1	2		
ENSMUST00000165679	ENSMUSG00000034177	11	87662722	87735539	1	0	13	0	0	0	0	0	0	0	0	16		Q5NCP0
ENSMUST00000165680	ENSMUSG00000091423	13	117218701	117221075	-1	36	45	61	324	60	40	5	30	14	3	18	Q9CZ61	
ENSMUST00000165682	ENSMUSG00000041696	9	65398488	65414853	1	34	35	97	183	33	23	1	1	4	0	6	E9PUV1	
ENSMUST00000165684	ENSMUSG00000013833	10	79894708	79908923	-1	10	0	0	96	15	0	320	0	428	0	220	G3UW74	
ENSMUST00000165686						4	2	6	8	6	1	19	68	33	7	64		
ENSMUST00000165687	ENSMUSG00000091972	16	26503793	26526771	-1	16	12	28	13	26	7	0	1	0	0	0		P86045
ENSMUST00000165690	ENSMUSG00000015363	15	89075124	89087077	1	8	0	23	164	13	5	91	112	125	19	124		Q99JY4
ENSMUST00000165691						4	3	6	8	8	4	0	0	0	0	0		
ENSMUST00000165692	ENSMUSG00000091679	17	18581727	18598157	1	0	0	0	0	0	0	0	0	0	0	0	E9PZU5	
ENSMUST00000165693	ENSMUSG00000027606	3	19508595	19610862	1	0	0	0	0	2	0	0	0	0	0	0		Q9CQ94
ENSMUST00000165700	ENSMUSG00000091041	8	110082803	110102753	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDB8	
ENSMUST00000165702						3	4	2	2	5	2	0	0	0	0	0		
ENSMUST00000165704	ENSMUSG00000006498	10	79854427	79864771	1	15	11	20	6	15	24	14	33	0	0	0	Q8BGJ5	
ENSMUST00000165705	ENSMUSG00000030443	7	6315660	6331285	-1	0	0	0	0	0	0	0	0	0	0	1		Q3V080
ENSMUST00000165706						8	2	5	2	7	0	81	248	204	137	418		
ENSMUST00000165709	ENSMUSG00000028514	4	106316213	106441322	1	0	33	52	66	10	3	0	14	0	9	0	E9PV45	
ENSMUST00000165710	ENSMUSG00000052099	14	64086234	64097670	1	2	2	10	0	4	8	0	0	0	0	0	E9PXD1	
ENSMUST00000165711	ENSMUSG00000036908	19	3935186	3949340	1	7	6	0	30	0	3	0	197	27	0	36	E9Q8P6	
ENSMUST00000165713	ENSMUSG00000079378	14	5131519	5139959	1	1	13	0	21	6	6	0	0	0	0	0	L7N2C6	
ENSMUST00000165714	ENSMUSG00000037536	14	47472561	47531962	1	0	4	14	0	9	0	56	0	0	21	0		Q80XI1
ENSMUST00000165717	ENSMUSG00000001289	15	102326116	102331873	1	1	0	0	0	0	0	649	1997	518	3190	468	E9Q093	
ENSMUST00000165718						4	2	1	5	3	0	0	0	0	0	0		
ENSMUST00000165720	ENSMUSG00000033813	1	4857814	4897909	1	18	7	14	119	14	5	0	0	0	0	4	E9PYD5	
ENSMUST00000165721	ENSMUSG00000024576	18	61555274	61590061	1	0	0	0	6	0	0	476	809	460	126	443		Q8BK63
ENSMUST00000165722	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	F7D8X7	
ENSMUST00000165724	ENSMUSG00000006498	10	79854427	79864771	1	6	0	13	0	11	2	0	0	0	0	0	F7AXP1	
ENSMUST00000165725	ENSMUSG00000022212	14	55510445	55517431	1	4	0	10	2	5	0	0	0	0	0	0	E9QA77	
ENSMUST00000165727	ENSMUSG00000022106	14	73123037	73207843	1	1	2	4	3	0	0	0	0	0	4	5	E9QA84	
ENSMUST00000165729						0	0	0	2	1	0	1	2	0	0	0		
ENSMUST00000165730	ENSMUSG00000023015	15	99620496	99651656	-1	0	0	0	0	0	0	1	0	0	0	0	E9Q071	
ENSMUST00000165733						107	82	107	192	163	67	26	20	32	2	36		
ENSMUST00000165735	ENSMUSG00000001348	9	22126731	22135746	-1	0	3	12	2	8	0	0	0	0	0	11		Q05117
ENSMUST00000165738	ENSMUSG00000063268	15	76231174	76243441	-1	6	15	29	24	0	0	149	222	185	78	328	Q8CIE4	
ENSMUST00000165740	ENSMUSG00000031708	8	83571700	83594491	-1	0	6	0	43	0	0	305	1759	210	531	72	G3UWE1	
ENSMUST00000165742						1	3	5	0	3	0	0	5	3	0	5		
ENSMUST00000165743	ENSMUSG00000036046	15	84943936	84988551	-1	0	0	46	62	0	0	3346	0	2463	0	1924	B1APX2	
ENSMUST00000165744	ENSMUSG00000091472	14	7293648	7315049	-1	4	7	7	22	9	3	0	0	1	0	0	L7N296	
ENSMUST00000165745						7	8	4	3	6	4	0	0	5	0	8		
ENSMUST00000165747						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000165748						1	1	11	3	5	6	0	0	0	0	0		
ENSMUST00000165750						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000165754						19	16	9	36	17	14	7	66	26	18	17		
ENSMUST00000165756	ENSMUSG00000095172	Y	15882421	15884771	-1	0	0	2	0	0	1	0	0	0	0	0	J3KMI7	
ENSMUST00000165758	ENSMUSG00000051984	19	44516957	44545864	-1	1	0	0	0	2	3	0	1	0	0	1	F6QFX0	
ENSMUST00000165761	ENSMUSG00000024924	19	27216484	27254231	1	3	3	0	1	2	0	0	0	0	0	0	F6RKS4	
ENSMUST00000165762	ENSMUSG00000039059	2	180099465	180104488	-1	2	0	0	19	0	5	0	0	0	0	0	E9Q292	
ENSMUST00000165764	ENSMUSG00000006724	10	127048250	127053006	1	14	0	25	0	0	9	0	0	1	0	1		O35084
ENSMUST00000165765						2	0	2	1	3	1	0	0	0	0	0		
ENSMUST00000165766	ENSMUSG00000033335	9	21424908	21507759	1	0	0	0	24	9	0	0	8	0	0	25	Q3T9X3	
ENSMUST00000165768	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	1	0	0	0	0	6	23	7	F6QG91	
ENSMUST00000165769	ENSMUSG00000092165	14	44556795	44562827	-1	8	4	8	5	6	4	0	0	0	0	0	F6ZZG8	
ENSMUST00000165770	ENSMUSG00000045333	8	87661810	87959595	-1	0	1	120	28	19	0	0	0	0	0	0	G3UW89	
ENSMUST00000165771	ENSMUSG00000091239	7	86225206	86246201	-1	1	3	3	1	4	2	0	0	0	0	0	E9Q3F5	
ENSMUST00000165773						0	0	0	0	0	0	0	0	0	0	10		
ENSMUST00000165774	ENSMUSG00000028270	3	142620602	142638008	1	11	14	22	3	11	13	335	3291	651	3116	1660		Q9Z0E6
ENSMUST00000165776	ENSMUSG00000021953	14	63492347	63509092	-1	0	0	0	0	0	0	0	0	0	0	0	F6Y7H0	
ENSMUST00000165777	ENSMUSG00000022471	15	81987835	82040085	1	1	1	1	3	7	4	0	0	3	0	0	E9Q163	
ENSMUST00000165778	ENSMUSG00000042570	10	79540245	79555199	-1	0	0	0	0	0	0	2	0	1	0	0	E9Q500	
ENSMUST00000165780	ENSMUSG00000029862	6	42286685	42315756	1	0	0	0	0	0	0	0	0	0	0	0	F6QL23	
ENSMUST00000165781	ENSMUSG00000090655	17	57508783	57545314	-1	14	18	21	10	9	7	0	0	0	0	0	E9PX34	
ENSMUST00000165783						4	7	16	10	2	4	38	56	65	3	86		
ENSMUST00000165784						1	4	2	6	2	2	0	0	0	0	0		
ENSMUST00000165786	ENSMUSG00000029778	6	55451978	55501451	1	0	0	0	0	0	0	0	0	0	0	0	E9Q968	
ENSMUST00000165787						25	4	52	7	33	12	13	0	6	0	7		
ENSMUST00000165790	ENSMUSG00000022750	16	17759618	17793382	1	0	0	0	0	0	0	0	0	0	0	0		Q99JN2
ENSMUST00000165792						1	3	2	6	6	1	0	0	0	0	0		
ENSMUST00000165793						0	0	0	114	0	0	0	0	0	0	0		
ENSMUST00000165797						1	1	0	159	5	3	3	0	8	0	0		
ENSMUST00000165798	ENSMUSG00000026605	1	189640606	189688086	-1	2	0	4	0	1	0	0	2	4	16	1	F6V6F0	
ENSMUST00000165799						0	1	1	0	2	1	0	0	4	4	0		
ENSMUST00000165802						22	5	62	23	24	10	9	22	10	0	34		
ENSMUST00000165803						0	2	0	0	0	0	0	6	0	1	0		
ENSMUST00000165804	ENSMUSG00000023027	15	100227819	100261244	1	1	0	1	1	0	0	4	6	2	0	15	E9PZB1	
ENSMUST00000165806	ENSMUSG00000019794	10	7726000	7763150	1	2	2	4	4	4	1	107	506	181	157	97	E9PZI6	
ENSMUST00000165810	ENSMUSG00000091712	16	5147109	5183934	1	23	13	37	54	42	14	0	0	0	0	0	B2RXM5	
ENSMUST00000165811						0	2	0	3	3	1	0	0	0	0	1		
ENSMUST00000165813	ENSMUSG00000095232	7	33287291	33288611	1	4	0	0	1	1	2	0	0	0	0	0	F6WYW0	
ENSMUST00000165814	ENSMUSG00000096470	14	5678784	5687457	-1	4	5	3	6	5	9	0	0	0	0	0	K7N6U2	
ENSMUST00000165816						32	25	151	33	52	20	1	0	1	0	0		
ENSMUST00000165817						0	3	16	0	3	1	3	2	2	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000165819	ENSMUSG00000087408	8	70315775	70331592	1	0	0	0	231	0	7	0	0	0	0	0		P20863
ENSMUST00000165820	ENSMUSG00000032661	5	120753098	120777661	-1	7	5	10	2	2	2	3	34	9	6	18	F7CXR7	
ENSMUST00000165821						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000165824	ENSMUSG00000026227	1	86045863	86055456	1	40	20	58	23	41	11	0	0	0	0	0	B7ZMV2	Q9CYS6
ENSMUST00000165826	ENSMUSG00000022801	16	32914100	33015647	1	0	0	0	0	0	0	0	0	5	0	0	F6YZL6	
ENSMUST00000165829	ENSMUSG00000085584	X	143099594	143104297	1	20	8	83	24	12	14	0	0	0	1	0		Q32KG4
ENSMUST00000165830	ENSMUSG00000039738	16	3979105	4003770	-1	7	6	34	9	8	5	0	17	15	1	21	F7A9G8	
ENSMUST00000165831						8	3	11	5	6	1	0	0	0	0	0		
ENSMUST00000165834	ENSMUSG00000091888	10	79148797	79195012	1	10	7	2	3	3	7	0	0	0	0	0	E9Q1L0	
ENSMUST00000165835	ENSMUSG00000022025	14	79637690	79662170	-1	5	0	0	0	0	0	1	0	0	0	0	G5E8Z6	
ENSMUST00000165837	ENSMUSG00000001280	15	102406143	102436404	1	0	0	2	5	0	0	0	0	0	0	0	E9Q113	
ENSMUST00000165838	ENSMUSG00000002274	17	25794571	25797136	-1	7	4	25	23	4	4	21	35	11	7	7	A2RSN4	Q8C1Q4
ENSMUST00000165839	ENSMUSG00000032114	9	44398176	44402963	1	13	5	32	25	18	9	300	410	229	67	125	Q9D1F9	
ENSMUST00000165841						2	1	0	0	0	3	0	113	0	0	0		
ENSMUST00000165842	ENSMUSG00000028102	3	96635376	96645366	1	3	0	4	0	0	0	0	0	14	0	0	E9PXK7	
ENSMUST00000165843						2	2	4	4	5	0	2	0	0	0	0		
ENSMUST00000165845	ENSMUSG00000046818	3	137621612	137628333	1	2	2	7	13	3	1	0	0	0	0	0	E9Q253	
ENSMUST00000165846						0	0	0	0	0	1	2	6	5	2	2		
ENSMUST00000165848	ENSMUSG00000090714	7	11161374	11166182	-1	0	0	0	0	0	0	0	0	0	0	0		A7KBS4
ENSMUST00000165849						8	3	2	4	5	4	1	14	15	4	27		
ENSMUST00000165851						0	0	2	0	2	0	6	5	0	0	3		
ENSMUST00000165853	ENSMUSG00000028788	4	129811219	129850003	1	18	12	34	4	25	13	826	4756	1492	1092	1019		O70274
ENSMUST00000165854	ENSMUSG00000024283	18	7868832	7973547	1	0	0	6	0	0	0	0	0	140	29	7	F6Z247	
ENSMUST00000165855	ENSMUSG00000034353	1	91179822	91225196	1	3	0	25	137	12	5	0	0	0	4	0	E9Q915	
ENSMUST00000165856	ENSMUSG00000033316	5	110544355	110621380	1	6	0	22	0	14	3	85	124	68	13	45	Q3TB05	
ENSMUST00000165857	ENSMUSG00000029778	6	55451978	55501451	1	0	5	0	3	6	0	0	0	0	0	0	E9Q4B3	
ENSMUST00000165858						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000165859	ENSMUSG00000043015	1	52630703	52651919	1	0	9	0	37	0	5	102	406	134	0	49		Q8CB65
ENSMUST00000165860	ENSMUSG00000066036	4	139352609	139489588	1	0	0	95	51	0	0	32	338	36	104	0		A2AN08
ENSMUST00000165861	ENSMUSG00000028759	4	138216296	138244683	1	0	0	0	2	0	0	44	64	144	24	0		Q3TEA8
ENSMUST00000165862						0	3	8	0	0	1	0	0	0	0	0		
ENSMUST00000165866	ENSMUSG00000042570	10	79540245	79555199	-1	17	6	33	9	11	5	0	0	0	0	0	E9Q3D9	
ENSMUST00000165867	ENSMUSG00000031753	8	110846600	110882227	1	7	13	4	26	13	6	0	0	0	0	22	Q7TSQ9	
ENSMUST00000165868						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000165870	ENSMUSG00000015981	7	139103638	139213307	-1	14	14	28	6	26	0	1	7	0	0	3	E9PXK4	
ENSMUST00000165873	ENSMUSG00000001052	3	129982759	130061553	-1	1	6	1	0	6	1	190	464	442	20	282	F6VJC5	
ENSMUST00000165874	ENSMUSG00000060568	1	167001417	167091302	1	0	30	16	0	19	13	0	3	0	0	0		Q8BQN5
ENSMUST00000165876	ENSMUSG00000032479	9	109931460	110083955	1	0	11	0	122	0	14	0	224	57	0	211	A0A0B4J1M9	P27546
ENSMUST00000165878	ENSMUSG00000004207	10	60277627	60302597	1	0	22	58	8	27	32	12842	32554	15007	3273	18022	E9PZ00	
ENSMUST00000165879						5	3	33	11	6	2	0	0	0	0	3		
ENSMUST00000165881	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	0	0	0	2	0	F6ZEX4	
ENSMUST00000165883						0	0	3	0	0	2	1	7	0	1	0		
ENSMUST00000165884	ENSMUSG00000003153	6	122727809	122801640	-1	1	2	0	16	1	0	0	0	0	0	5	E9Q2G7	
ENSMUST00000165886	ENSMUSG00000042350	12	84918148	84970900	-1	0	0	7	19	4	0	0	0	0	0	0	E9PYA6	
ENSMUST00000165887	ENSMUSG00000060962	7	30763756	30781063	1	0	0	22	21	0	7	0	0	0	0	0	E9Q2P1	
ENSMUST00000165889						2	2	12	0	0	0	0	0	0	9	15		
ENSMUST00000165890						0	3	4	6	5	0	8	68	8	0	13		
ENSMUST00000165892	ENSMUSG00000078903	2	175191065	175206917	-1	1	0	0	0	2	0	0	0	0	0	0	A2ART0	
ENSMUST00000165898	ENSMUSG00000028064	3	88435959	88461182	-1	0	0	0	0	0	0	0	44	12	0	0		Q62178
ENSMUST00000165901	ENSMUSG00000049580	7	98350668	98361328	-1	22	12	0	0	0	0	0	0	0	0	0	Q08EE6	Q8CBR6
ENSMUST00000165903						24	27	286	28	33	14	0	0	0	0	0		
ENSMUST00000165904	ENSMUSG00000090298	10	33766424	33782115	-1	2	0	0	2	0	0	0	0	0	0	0	G5E904	
ENSMUST00000165906	ENSMUSG00000073427	10	82378593	82381237	1	59	53	176	88	55	29	3	24	4	7	9	Q3UF22	
ENSMUST00000165907						6	7	13	5	10	5	0	0	0	0	0		
ENSMUST00000165909	ENSMUSG00000029086	5	43993620	44102032	-1	20	8	71	25	16	5	0	0	0	0	0	Q8CDK8	
ENSMUST00000165910						0	0	0	0	0	0	0	0	1	0	3		
ENSMUST00000165912	ENSMUSG00000024050	17	32354055	32389401	-1	2	1	0	19	0	3	0	0	0	0	2	E9Q1G2	
ENSMUST00000165913	ENSMUSG00000050428	7	19119859	19140172	1	0	0	8	80	15	4	141	0	60	15	1		Q8BG80
ENSMUST00000165914						6	8	0	2	0	6	0	0	4	0	0		
ENSMUST00000165915						0	3	1	6	6	3	0	0	0	0	0		
ENSMUST00000165916	ENSMUSG00000094542	7	22437306	22438229	-1	0	0	0	0	0	0	0	0	0	0	0	E9PWL6	
ENSMUST00000165917						11	5	6	16	7	3	0	0	0	0	0		
ENSMUST00000165921	ENSMUSG00000096691	7	7550967	7566786	-1	7	17	0	7	0	4	0	0	0	0	0	K7N705	
ENSMUST00000165922	ENSMUSG00000027552	3	14578641	14606309	1	9	9	4	0	6	5	2	0	7	37	15	E9Q011	
ENSMUST00000165923						0	0	0	42	0	0	2	8	10	1	5		
ENSMUST00000165924	ENSMUSG00000001280	15	102406143	102436404	1	3	0	28	0	1	0	40	0	498	0	459	G3X8Q0	
ENSMUST00000165927						0	0	18	5	1	0	0	0	0	0	13		
ENSMUST00000165928	ENSMUSG00000091794	5	151561661	151586906	-1	15	18	14	6	17	14	0	0	0	0	5	E9Q280	
ENSMUST00000165929	ENSMUSG00000021898	14	26894557	26915258	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000165935	ENSMUSG00000036167	15	93398350	93491913	1	0	15	29	190	37	10	0	0	22	0	16	G3UWD4	
ENSMUST00000165936	ENSMUSG00000092137	9	71479325	71592265	-1	3	0	0	0	0	0	0	0	0	0	0	E9Q3C8	
ENSMUST00000165937	ENSMUSG00000074607	2	163203125	163324170	1	10	9	31	24	26	6	0	0	0	0	2	E9Q0B9	
ENSMUST00000165944						5	4	49	1	15	5	0	0	0	0	0		
ENSMUST00000165947						0	4	7	3	2	0	0	0	0	0	0		
ENSMUST00000165949	ENSMUSG00000029788	6	30611010	30631745	1	0	0	0	0	4	0	0	0	0	0	0	E9PYY7	
ENSMUST00000165950						6	2	3	4	5	2	0	0	0	0	0		
ENSMUST00000165951	ENSMUSG00000040950	11	70130329	70137550	1	33	35	47	42	77	29	0	0	0	11	16	A9XX86	
ENSMUST00000165952	ENSMUSG00000040021	10	7681209	7716458	1	23	26	72	72	33	16	321	890	430	59	333		Q8BYR2
ENSMUST00000165953	ENSMUSG00000024369	17	34850391	34856372	1	4	0	8	7	4	0	142	260	139	47	93	Q3UIA1	P19426
ENSMUST00000165954	ENSMUSG00000024858	19	4286001	4306222	-1	3	0	5	0	0	3	423	143	223	21	155	F6QY34	
ENSMUST00000165955	ENSMUSG00000021884	14	31552905	31641286	-1	0	0	0	0	0	0	2	44	16	30	0	E9Q0K0	
ENSMUST00000165956	ENSMUSG00000033883	3	36151017	36170342	1	56	44	82	70	60	34	14	34	15	21	19	F7A4H5	
ENSMUST00000165957	ENSMUSG00000002205	7	44748413	44777515	1	2	0	15	29	0	3	73	25	100	0	59	E9PW85	
ENSMUST00000165961	ENSMUSG00000094879	7	21360368	21361291	-1	0	0	0	0	0	0	0	0	0	0	0	E9QA94	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000165962	ENSMUSG00000026605	1	189640606	189688086	-1	0	0	0	0	1	0	0	0	0	0	4	E9PY14	
ENSMUST00000165963	ENSMUSG00000069911	11	34314822	34422640	1	17	22	70	16	31	0	0	0	14	3	0		Q6GQV1
ENSMUST00000165964	ENSMUSG00000056394	7	13277283	13311433	1	19	0	0	0	25	0	0	0	12	0	30	Q3U4X8	
ENSMUST00000165965	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	0	0	0	0	0	E9QMP6	
ENSMUST00000165966						25	33	32	123	63	43	1	1	2	0	2		
ENSMUST00000165968						10	3	13	2	13	3	0	0	0	1	0		
ENSMUST00000165969						4	3	18	1	1	7	0	0	0	0	0		
ENSMUST00000165970						0	1	14	3	0	2	0	0	0	0	0		
ENSMUST00000165971	ENSMUSG00000019917	10	59164113	59221847	-1	6	4	11	113	9	4	44	169	42	140	44		
ENSMUST00000165978	ENSMUSG00000021275	12	110889264	110972394	1	53	49	161	109	87	0	188	411	416	34	327	Q3UH45	
ENSMUST00000165980	ENSMUSG00000017002	2	164354070	164389095	-1	4	0	4	5	9	2	1285	2603	841	3889	1420	E9Q748	
ENSMUST00000165981	ENSMUSG00000021910	14	31170930	31216946	-1	2	7	21	48	14	0	222	429	278	17	378		Q80TM9
ENSMUST00000165982						0	0	0	3	0	0	391	640	290	338	227		
ENSMUST00000165984	ENSMUSG00000049103	9	124101950	124113557	1	0	0	0	0	0	0	483	4845	421	1229	429	Q543S8	P51683
ENSMUST00000165985						7	4	7	1	3	2	0	0	0	0	0		
ENSMUST00000165986	ENSMUSG00000019856	10	53633145	53750909	-1	3	3	2	0	0	1	0	0	0	0	0	F6R487	
ENSMUST00000165988	ENSMUSG00000094784	14	43229832	43235304	-1	5	6	0	5	4	2	0	0	0	0	0	L7N2C7	
ENSMUST00000165989	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	4	0	0	0	0	2	0	0	E9Q2G8	
ENSMUST00000165990	ENSMUSG00000030237	6	141805440	141856199	-1	11	6	5	5	4	6	0	0	0	0	0		Q9EP96
ENSMUST00000165991	ENSMUSG00000038304	3	96798763	96829351	-1	0	0	14	11	0	4	3	14	4	1	1	E9Q0X3	
ENSMUST00000165992						3	0	3	3	1	3	0	1	3	0	0		
ENSMUST00000165993	ENSMUSG00000023968	17	46428926	46431776	1	2	0	0	0	0	0	0	0	0	0	0	E9Q860	
ENSMUST00000165999	ENSMUSG00000091586	17	32506462	32528894	1	12	9	23	45	20	7	56	135	82	36	62	G3UW78	
ENSMUST00000166001	ENSMUSG00000027684	3	29951296	30548008	-1	0	0	0	0	0	0	0	0	0	0	0	O35700	
ENSMUST00000166004	ENSMUSG00000031833	8	70778117	70792433	-1	44	46	256	452	66	41	1255	2251	1509	113	1662	E9Q8S5	
ENSMUST00000166005	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	0	0	0	33	15	1	0	8		Q8R1D1
ENSMUST00000166007	ENSMUSG00000021782	14	24133953	24245920	-1	9	4	7	0	0	4	1	1	1	2	2	F6VMK9	
ENSMUST00000166008						7	3	8	6	0	1	0	0	0	0	0		
ENSMUST00000166010	ENSMUSG00000025264	X	151087094	151096543	-1	1	0	1	11	9	0	14	37	3	11	14	G3UWF3	
ENSMUST00000166015						1	0	11	1	6	1	13	4	0	0	4		
ENSMUST00000166016						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000166018	ENSMUSG00000031965	9	24720812	24774303	-1	2	3	0	103	4	3	0	0	0	0	0		Q9ES03
ENSMUST00000166019	ENSMUSG00000018040	15	83113433	83122801	-1	2	0	7	4	9	0	57	14	28	5	0	E9PYF0	
ENSMUST00000166020	ENSMUSG00000038371	7	110308013	110614922	-1	0	7	0	0	0	5	0	0	46	0	0	E9Q0D4	
ENSMUST00000166021	ENSMUSG00000028069	3	88043108	88055993	1	0	0	20	12	12	0	0	0	0	9	5		Q3TFK5
ENSMUST00000166022	ENSMUSG00000022996	15	98771753	98778150	-1	7	8	23	15	2	0	0	0	0	0	0		P48614
ENSMUST00000166023	ENSMUSG00000035835	10	79860475	79874634	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4F1	
ENSMUST00000166025	ENSMUSG00000091494	14	4838106	4846867	1	12	8	0	20	16	4	0	0	0	0	0	K7N735	
ENSMUST00000166030	ENSMUSG00000022412	15	80234080	80253366	1	19	21	99	168	18	15	22	8	41	0	39	B2RPW2	Q8BGV8
ENSMUST00000166031	ENSMUSG00000005986	19	4270180	4283137	-1	0	0	6	2	0	1	10	22	5	4	6	F6QRW3	
ENSMUST00000166032	ENSMUSG00000041912	3	94413273	94434668	1	15	22	2	29	5	7	4	3	2	0	4		Q80VL1
ENSMUST00000166033	ENSMUSG00000078578	3	135438149	135468198	1	11	2	11	57	11	7	740	1302	354	461	357	Q4QQL2	P61079
ENSMUST00000166034						0	3	15	0	8	6	0	0	0	0	0		
ENSMUST00000166036	ENSMUSG00000039653	4	49489422	49506557	-1	1	0	0	6	2	0	1	0	1	0	0		Q91X34
ENSMUST00000166039	ENSMUSG00000022249	15	10500102	10558668	-1	2	0	2	2	1	0	0	0	0	0	0	E9Q190	
ENSMUST00000166040	ENSMUSG00000015474	17	34616662	34628510	-1	0	0	3	6	2	3	45	16	32	0	0		O35448
ENSMUST00000166043						9	16	40	21	16	3	2	0	0	1	2		
ENSMUST00000166044	ENSMUSG00000003779	18	34624624	34633265	1	21	5	27	21	14	4	60	83	290	87	235		P97329
ENSMUST00000166049	ENSMUSG00000025075	19	56287137	56320822	1	0	0	0	0	0	0	0	0	0	0	0	E9Q092	
ENSMUST00000166052						11	11	26	3	4	0	0	0	0	0	0		
ENSMUST00000166053						0	0	0	8	6	3	0	0	0	0	0		
ENSMUST00000166055	ENSMUSG00000079434	1	87509889	87597845	1	0	0	2	132	6	2	0	0	0	0	0	E9Q2Z0	
ENSMUST00000166056	ENSMUSG00000066463	9	78311972	78314797	-1	11	15	30	13	9	4	0	0	0	0	0	G5E8X8	
ENSMUST00000166057						16	0	0	95	0	0	0	0	0	0	0		
ENSMUST00000166060						0	1	0	0	0	0	0	0	14	0	0		
ENSMUST00000166062	ENSMUSG00000024283	18	7868832	7973547	1	0	0	0	3	0	0	0	0	20	7	0	E9PZH6	
ENSMUST00000166063						0	0	0	0	0	0	0	4	24	0	5		
ENSMUST00000166071						0	0	3	0	0	2	0	8	3	4	9		
ENSMUST00000166074	ENSMUSG00000024798	19	35958734	36057507	-1	0	13	0	0	0	0	0	0	0	0	0	B6VJS2	
ENSMUST00000166075	ENSMUSG00000021877	14	26638074	26665084	1	0	0	0	19	0	0	382	710	317	131	395	E9Q2C2	
ENSMUST00000166076						1	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000166078	ENSMUSG00000031575	8	25816191	25847694	-1	0	0	0	0	0	0	64	233	113	49	18	E9PU93	
ENSMUST00000166079	ENSMUSG00000093853	7	22498761	22499678	-1	1	0	0	0	0	0	0	0	0	0	0	L7N288	
ENSMUST00000166080	ENSMUSG00000098692	13	67345246	67375733	-1	1	3	12	2	1	3	6	10	0	2	0	F2Z406	
ENSMUST00000166081	ENSMUSG00000091859	17	19504811	19532060	1	6	9	8	5	4	3	0	0	0	0	0	E9QAZ9	
ENSMUST00000166082	ENSMUSG00000025512	7	141493136	141539857	-1	0	0	0	0	0	32	0	54	103	58	0		
ENSMUST00000166083	ENSMUSG00000030889	7	120739557	120805742	1	3	3	14	1	4	2	0	0	0	0	0	F6YMQ0	
ENSMUST00000166084						2	2	2	1	2	2	0	4	0	0	0		
ENSMUST00000166086	ENSMUSG00000091827	5	17373180	17378028	1	3	1	19	9	5	4	0	0	0	0	0	E9Q366	
ENSMUST00000166088	ENSMUSG00000009070	10	74957477	75032586	-1	0	9	13	0	0	0	0	0	0	0	0	E9PWZ8	
ENSMUST00000166090	ENSMUSG00000025159	19	41941086	41981157	-1	0	0	0	0	0	0	41	0	0	0	9	F7A0X7	
ENSMUST00000166091						0	5	4	3	0	3	26	2	0	0	3		
ENSMUST00000166095						2	4	3	5	0	0	1	4	1	0	4		
ENSMUST00000166096						0	0	0	34	1	0	0	0	0	0	0		
ENSMUST00000166097	ENSMUSG00000025245	9	123694416	123717625	-1	0	0	0	0	0	0	0	0	0	7	0	E9Q9P1	
ENSMUST00000166098	ENSMUSG00000073842	4	60066469	60070475	-1	10	0	18	4	0	0	0	0	0	0	0	E9QA79	
ENSMUST00000166099	ENSMUSG00000079165	5	137641334	137642902	1	0	0	0	0	7	0	165	1317	264	42	541	E9Q529	
ENSMUST00000166100	ENSMUSG00000073602	1	107153940	107278361	-1	2	4	3	2	7	4	0	0	0	0	0	Q9D1Q5	
ENSMUST00000166101	ENSMUSG00000021061	12	76580488	76710547	-1	100	87	330	139	129	53	2	6	6	4	6	E9Q397	
ENSMUST00000166102	ENSMUSG00000004347	6	56069804	56569103	-1	0	0	0	1	0	0	0	0	0	0	0	Q5D0E7	Q64338
ENSMUST00000166103	ENSMUSG00000006676	9	108490602	108502337	1	3	2	8	53	15	10	89	132	79	0	56	E9Q9M5	
ENSMUST00000166104	ENSMUSG00000015536	13	114818236	114832275	1	2	0	0	3	1	0	23	112	31	336	75	F6ZGI7	
ENSMUST00000166105	ENSMUSG00000090286	14	124005355	124007629	1	1395	1119	11467	3408	1814	941	8	32	36	9	33	E9Q9P2	
ENSMUST00000166109						4	5	10	2	2	0	8	50	35	16	55		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000166110	ENSMUSG00000095743	14	43573843	43579146	-1	10	9	4	2	0	2	0	0	0	0	0	F7AXR3	
ENSMUST00000166112	ENSMUSG00000041361	9	71504347	71592360	-1	0	0	0	16	0	0	0	0	0	0	0	E9PWY8	
ENSMUST00000166114						6	7	7	4	6	3	0	0	0	0	0		
ENSMUST00000166115	ENSMUSG00000024958	19	6938069	6942450	-1	5	1	4	0	0	0	59	271	57	2	25		Q80ZU9
ENSMUST00000166117	ENSMUSG00000051235	12	11240926	11265787	-1	12	15	39	37	18	7	34	26	45	10	20		Q8BMI4
ENSMUST00000166118						0	2	3	2	0	2	0	0	0	0	0		
ENSMUST00000166119	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	5	0	0	0	0	0	9	0	0		Q9JIM1
ENSMUST00000166120	ENSMUSG00000021079	12	71123173	71136675	-1	4	4	4	2	4	4	8	26	12	44	12		Q9WV98
ENSMUST00000166121	ENSMUSG00000091649	14	59320964	59341351	-1	4	10	4	5	5	2	2	71	11	225	97	B4XVQ1	
ENSMUST00000166122						4	3	0	3	4	2	0	1	1	0	7		
ENSMUST00000166123	ENSMUSG00000021282	12	111538101	111546753	1	21	41	32	99	45	22	1118	5436	1326	441	853	Q3TQR3	P59325
ENSMUST00000166126	ENSMUSG00000049100	3	45378398	45435623	1	52	45	182	188	67	26	1	3	3	1	1	E9PXQ7	
ENSMUST00000166128	ENSMUSG00000025185	19	42593982	42612813	-1	0	2	6	2	0	0	0	0	0	0	0	E9PY86	
ENSMUST00000166129	ENSMUSG00000105875	5	123927418	123938388	1	2	3	12	2	4	0	2	0	0	0	1	A0A0G2JGB6	
ENSMUST00000166131	ENSMUSG00000090967	7	42260053	42300755	1	6	6	4	0	10	0	0	0	0	0	0	L7N2B8	
ENSMUST00000166135	ENSMUSG00000003153	6	122727809	122801640	-1	0	0	0	0	0	0	260	0	935	0	728	E9PZF2	
ENSMUST00000166136						1	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000166137	ENSMUSG00000037860	1	173350879	173466040	1	144	149	340	181	209	104	61	800	157	135	126		Q91VJ1
ENSMUST00000166139	ENSMUSG00000037568	1	190947646	190979296	-1	29	0	14	26	7	0	3	2	0	4	5		Q8C5G2
ENSMUST00000166140	ENSMUSG00000074628	2	157087055	157096482	1	2	0	0	0	3	0	0	0	0	0	0	E9PZS3	
ENSMUST00000166141	ENSMUSG00000095632	7	23808286	23809200	-1	6	0	0	8	2	0	0	0	0	0	0	K7N6T9	
ENSMUST00000166142	ENSMUSG00000033287	15	78428564	78438909	1	1	0	0	113	0	0	0	0	0	0	0	F6SYN4	
ENSMUST00000166143						5	0	5	4	0	7	0	0	0	1	0		
ENSMUST00000166146	ENSMUSG00000025730	17	25882114	25919727	-1	13	11	19	11	6	5	13	14	23	0	15	E9Q0X8	
ENSMUST00000166147						6	10	8	14	6	6	0	1	0	0	2		
ENSMUST00000166148	ENSMUSG00000038524	18	37957431	37969774	-1	0	0	0	0	0	0	0	0	1	0	0	E9Q363	
ENSMUST00000166151						11	0	5	15	32	10	61	139	79	0	63		
ENSMUST00000166152	ENSMUSG00000039716	9	106892825	107231909	-1	3	0	0	4	2	2	0	0	0	0	0	F7AGL4	
ENSMUST00000166155	ENSMUSG00000068206	15	79229173	79256674	1	0	0	0	9	3	0	17	20	0	7	0	E9PUZ5	
ENSMUST00000166156	ENSMUSG00000014503	18	34409423	34442789	1	7	6	0	8	10	0	22	59	36	20	59		Q9JLG4
ENSMUST00000166159	ENSMUSG00000000544	1	166130238	166166510	1	3	1	2	2	0	0	0	0	0	2	0	E9PY15	
ENSMUST00000166161	ENSMUSG00000064179	7	4504570	4516382	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q688	
ENSMUST00000166162						0	0	0	4	0	0	0	0	0	0	5		
ENSMUST00000166163	ENSMUSG00000056856	7	138940730	139083976	1	14	9	13	11	0	0	0	0	0	0	0	E9Q7K7	
ENSMUST00000166166						0	0	0	3	0	0	0	0	0	6	0		
ENSMUST00000166168	ENSMUSG00000047766	9	60568859	60688158	-1	0	7	0	0	0	0	0	28	1	42	28	E9Q8C9	
ENSMUST00000166169	ENSMUSG00000049295	14	52006077	52020733	-1	4	4	31	77	0	7	0	29	0	0	0	Q6IQX8	
ENSMUST00000166170	ENSMUSG00000022454	15	95219451	95528706	-1	19	18	27	130	10	0	0	0	0	0	0		Q61220
ENSMUST00000166171	ENSMUSG00000074656	2	154871410	154892935	-1	9	12	0	0	0	0	126	1091	157	124	129	Q3ULL5	Q99L45
ENSMUST00000166172	ENSMUSG00000026596	1	156558786	156649568	1	102	73	175	91	107	59	119	195	244	36	321	B2RQ57	
ENSMUST00000166173	ENSMUSG00000091175	3	91088137	91090803	-1	3	2	1	1	2	1	0	0	0	0	0	G3UWB8	
ENSMUST00000166176	ENSMUSG00000015536	13	114818236	114832275	1	45	36	29	33	60	19	15	75	19	13	35		
ENSMUST00000166178						2	1	0	1	2	1	0	0	0	0	0		
ENSMUST00000166179	ENSMUSG00000018893	15	77015489	77050670	-1	2	0	4	5	2	0	0	0	0	0	0	Q3UVB1	P04247
ENSMUST00000166184						0	0	0	2	0	1	0	0	0	1	0		
ENSMUST00000166185						2	0	3	4	4	1	0	0	0	0	0		
ENSMUST00000166187	ENSMUSG00000019232	3	130617448	130637521	1	0	0	8	5	0	0	0	1	0	0	0		Q8BWU8
ENSMUST00000166191	ENSMUSG00000049303	19	4445908	4477447	-1	0	0	0	30	2	0	0	0	0	0	1	E9Q6I4	
ENSMUST00000166192	ENSMUSG00000025607	6	30747554	30896794	-1	0	0	0	0	0	0	21	5	9	23	40		
ENSMUST00000166193	ENSMUSG00000051985	1	135953578	136006342	-1	69	59	129	110	113	62	0	0	0	0	0		Q3KNY0
ENSMUST00000166197						1	3	0	0	1	0	0	0	0	0	0		
ENSMUST00000166199	ENSMUSG00000056486	2	73610660	73775346	-1	4	4	11	11	5	0	0	0	0	0	0	A7VK13	
ENSMUST00000166200						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000166201	ENSMUSG00000057729	10	79874476	79883174	1	0	0	1	0	1	0	5	28	0	0	0	F6ZK01	
ENSMUST00000166202						1	0	1	0	1	3	0	0	0	0	0		
ENSMUST00000166203	ENSMUSG00000049134	19	56320035	56390037	-1	20	0	0	0	1	0	0	0	0	4	11	E9PZF4	
ENSMUST00000166206	ENSMUSG00000079156	5	138021429	138050636	1	1	0	0	2	0	1	0	0	0	0	0		Q9QYZ5
ENSMUST00000166207	ENSMUSG00000051910	7	115470872	116038796	-1	7	0	25	0	14	7	0	0	0	1	6	Q3V1J7	P40645
ENSMUST00000166214	ENSMUSG00000038299	18	32837225	32866420	1	0	20	18	91	0	0	17	104	81	48	123	Q3TA68	
ENSMUST00000166215						0	0	1	4	4	0	34	725	68	102	129		
ENSMUST00000166219	ENSMUSG00000078963	18	80229758	80247102	-1	9	8	41	63	18	14	3	49	14	6	24		B2RXB2
ENSMUST00000166223	ENSMUSG00000022464	15	96994823	97055956	-1	11	6	0	3	5	8	0	0	0	5	1		Q8R1S9
ENSMUST00000166224	ENSMUSG00000033122	13	64058274	64089201	-1	0	0	14	11	13	0	0	0	0	0	0		P70385
ENSMUST00000166227	ENSMUSG00000090441	3	97673031	97674694	-1	0	0	0	0	0	0	0	0	0	0	0	F6SP27	
ENSMUST00000166232	ENSMUSG00000031955	8	111710485	111743849	-1	32	13	117	262	46	15	0	0	0	12	46		Q61140
ENSMUST00000166233	ENSMUSG00000023106	5	123907175	123928835	1	7	5	32	81	6	4	52	331	98	166	60	E9Q0G1	
ENSMUST00000166234						23	0	17	9	0	8	25	251	75	0	25		
ENSMUST00000166235						3	2	10	50	5	0	0	0	8	0	0		
ENSMUST00000166236	ENSMUSG00000029530	9	123678439	123783457	1	8	0	90	0	0	0	0	15	3	21	0		Q9WUT7
ENSMUST00000166237	ENSMUSG00000028064	3	88435959	88461182	-1	0	0	3	0	0	0	7784	12391	6932	509	5201		Q62178
ENSMUST00000166239	ENSMUSG00000029710	5	137350109	137378669	1	5	0	30	0	1	0	2	1	0	0	41		P54761
ENSMUST00000166240	ENSMUSG00000019892	10	103063198	103236322	-1	10	14	38	2	12	4	0	0	0	0	0		Q0P5X1
ENSMUST00000166241	ENSMUSG00000036790	X	66649318	66661393	1	31	43	132	21	45	23	2	15	2	1	3	Q14DT0	Q810C0
ENSMUST00000166247	ENSMUSG00000029810	6	48833818	48841496	-1	9	7	30	6	6	9	11	71	0	71	91		Q9R1Q6
ENSMUST00000166249						0	0	0	0	0	0	0	5	3	0	3		
ENSMUST00000166250	ENSMUSG00000048897	7	80024814	80094173	1	0	0	46	136	36	0	78	181	152	46	120		Q3U288
ENSMUST00000166252	ENSMUSG00000023952	17	46161032	46169370	1	1	0	0	2	2	0	0	16	6	0	13	F6RLV6	
ENSMUST00000166253	ENSMUSG00000024909	19	5473973	5481853	1	4	4	0	0	0	0	23	0	9	3	2	E9Q3F3	
ENSMUST00000166254	ENSMUSG00000059900	6	115729131	115762410	-1	0	6	0	5	6	3	0	0	0	0	0		Q4FJU9
ENSMUST00000166255	ENSMUSG00000090395	12	113654967	113655244	1	6	4	0	3	0	1	0	0	0	0	0	A0A075B676	
ENSMUST00000166256	ENSMUSG00000063163	16	69856874	69863744	-1	0	0	0	0	0	0	0	0	0	0	0	F6PXD2	
ENSMUST00000166257	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5Y2	
ENSMUST00000166258	ENSMUSG00000000915	5	123973628	124005558	1	0	0	3	24	3	1	4	2	0	0	0	F7DCR9	
ENSMUST00000166259	ENSMUSG00000079434	1	87509889	87597845	1	0	3	15	18	0	6	0	0	0	0	0	Q0VGI4	Q9JMH3

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000166267						0	0	0	0	0	0	61	30	30	0	12		
ENSMUST00000166268	ENSMUSG00000064179	7	4504570	4516382	-1	0	0	0	0	0	0	0	0	0	0	0	E9QA86	
ENSMUST00000166272	ENSMUSG00000032268	9	49081260	49117587	1	0	0	0	0	2	0	0	0	0	0	0	E9Q862	
ENSMUST00000166273	ENSMUSG00000032816	9	65101486	65137940	1	0	0	4	0	1	0	0	0	0	0	0	A0JNS2	
ENSMUST00000166275	ENSMUSG00000079409	14	3188255	3196681	1	0	0	0	0	0	0	0	0	0	0	0	Q497R9	
ENSMUST00000166276						1	0	0	0	0	0	0	5	1	0	0		
ENSMUST00000166277	ENSMUSG00000090336	8	13705889	13743066	1	5	5	11	4	8	4	0	0	0	3	2	G3UW36	
ENSMUST00000166278	ENSMUSG00000037661	3	30855950	30897192	1	2	6	0	0	0	4	53	155	1	15	9		Q3U3F9
ENSMUST00000166280	ENSMUSG00000047428	17	46297421	46303271	1	1	6	0	5	9	0	0	0	0	4	0		Q8K1E3
ENSMUST00000166281	ENSMUSG00000090550	1	90953108	90954027	1	2	3	3	8	3	0	0	0	0	0	0	G3UWC3	
ENSMUST00000166282	ENSMUSG00000037885	2	129800517	129832287	1	29	17	108	83	49	19	300	624	429	42	386	E9PXA2	
ENSMUST00000166285						6	1	3	2	8	0	3	6	5	1	5		
ENSMUST00000166287						18	13	28	96	14	2	18	48	33	2	110		
ENSMUST00000166288	ENSMUSG00000044365	3	134236484	134262161	1	2	1	2	81	4	2	0	0	0	0	0		Q6NXI8
ENSMUST00000166291	ENSMUSG00000090553	1	133603871	133610291	-1	0	0	0	0	0	0	4	0	6	6	0	E9Q0W8	
ENSMUST00000166294	ENSMUSG00000022514	16	26581704	26730117	1	5	0	0	0	1	10	10	15	13	20	45	E9Q6I2	
ENSMUST00000166297	ENSMUSG00000048031	3	87435773	87500678	1	0	0	0	0	0	0	0	0	0	0	0		Q68SN8
ENSMUST00000166298	ENSMUSG00000029209	5	69573108	69592340	-1	0	0	0	0	0	0	0	0	0	0	8		Q9CRC9
ENSMUST00000166299	ENSMUSG00000048264	13	9276528	9668928	1	14	23	38	0	2	16	0	0	35	0	5	E9PWR4	
ENSMUST00000166302						0	1	2	4	0	0	0	0	0	0	0		
ENSMUST00000166303	ENSMUSG00000024909	19	5473973	5481853	1	0	0	6	3	1	0	2	7	7	1	0	E9Q8E0	
ENSMUST00000166306	ENSMUSG00000096525	6	40995830	40999479	-1	3	5	9	3	6	0	0	0	0	0	0	F6R7E8	
ENSMUST00000166311						2	6	4	0	1	0	4	0	0	0	0		
ENSMUST00000166312	ENSMUSG00000020863	11	94287890	94321988	-1	35	21	98	83	30	21	37	217	64	26	100		Q5SUF2
ENSMUST00000166315	ENSMUSG00000066406	7	75455534	75754609	1	0	51	179	22	101	67	1361	9821	6304	461	5584	E9Q394	
ENSMUST00000166318	ENSMUSG00000038388	6	50110241	50198939	1	0	0	0	0	0	0	0	8	0	0	0	Q3UN60	Q9JLB0
ENSMUST00000166320	ENSMUSG00000001508	11	94962791	94976327	-1	0	0	0	0	0	0	0	0	0	0	0		P82350
ENSMUST00000166322						100	86	108	134	95	74	8	30	8	0	17		
ENSMUST00000166323						3	5	2	5	6	8	6	100	0	4	37		
ENSMUST00000166325	ENSMUSG00000078588	4	117866524	117872557	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q214	
ENSMUST00000166327	ENSMUSG00000091631	17	18424104	18452324	1	4	1	1	2	5	5	0	0	0	0	0	L7N274	
ENSMUST00000166328	ENSMUSG00000091272	3	68867917	68870266	-1	9	6	6	192	17	6	0	0	0	0	0	Q8CCI1	
ENSMUST00000166329	ENSMUSG00000021111	12	105784694	105838944	1	0	0	0	0	0	0	0	0	253	0	46	E9PVN7	
ENSMUST00000166330						2	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000166335	ENSMUSG00000013822	9	22112989	22117148	-1	0	6	5	7	11	0	12	12	12	4	4	Q545S6	P60003
ENSMUST00000166336	ENSMUSG00000034751	13	102732486	103334497	-1	0	0	0	0	0	0	0	0	0	0	0	F7AIF3	
ENSMUST00000166339	ENSMUSG00000039474	5	36966104	36989205	-1	56	27	203	0	36	40	8	22	11	6	0	Q3UN10	
ENSMUST00000166340	ENSMUSG00000058239	7	30945248	30956803	-1	0	0	0	13	2	0	0	4	10	0	5	F6WLF9	
ENSMUST00000166341	ENSMUSG00000038256	3	97203662	97297917	-1	25	14	55	45	16	25	32	0	96	0	60		Q9D219
ENSMUST00000166343	ENSMUSG00000091043	17	40904741	40914350	-1	5	4	4	9	1	3	0	1	1	0	1	E9Q5L8	
ENSMUST00000166346						2	3	2	9	5	3	0	3	2	0	6		
ENSMUST00000166347						7	5	18	0	0	0	0	0	9	0	61		
ENSMUST00000166348	ENSMUSG00000040899	17	8236043	8257127	1	0	0	0	0	0	2	0	0	0	0	0	Q542B6	O54689
ENSMUST00000166350	ENSMUSG00000094543	14	44197661	44203133	1	4	2	7	4	2	0	0	0	0	0	0	F6ZMY5	
ENSMUST00000166352						8	3	22	7	6	3	22	170	46	14	85		
ENSMUST00000166353	ENSMUSG00000090408	3	67365461	67375163	-1	58	52	79	3837	151	54	2	0	1	1	2	F6Z0L5	
ENSMUST00000166354	ENSMUSG00000060147	13	33917918	34002794	-1	0	0	0	107	2	0	0	2	0	0	0	E9PZQ9	
ENSMUST00000166355	ENSMUSG00000090774	7	85951867	85961482	-1	6	5	0	5	3	2	0	0	0	0	0	E9PW21	
ENSMUST00000166358	ENSMUSG00000036564	8	95676980	95715119	1	7	0	3	0	0	0	0	1	0	0	0	E9Q168	
ENSMUST00000166360	ENSMUSG00000001211	10	78269178	78352489	-1	0	0	0	0	0	0	2	1	8	0	43		Q9D517
ENSMUST00000166362						2	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000166364						0	1	5	0	3	2	0	11	7	0	4		
ENSMUST00000166367	ENSMUSG00000032030	9	53614582	53670014	-1	0	0	0	0	16	5	41	59	42	89	89	E9PV12	
ENSMUST00000166368						2	1	2	7	0	2	0	4	7	0	4		
ENSMUST00000166373	ENSMUSG00000079183	10	97724874	97726755	-1	3	7	7	11	11	9	0	1	1	0	0	Q8BQN9	
ENSMUST00000166376	ENSMUSG00000060572	4	141010418	141015984	1	9	2	29	19	6	2	1	0	2	0	0	Q99PM0	
ENSMUST00000166378	ENSMUSG00000024283	18	7868832	7973547	1	0	0	0	72	1	0	0	0	0	0	4	E9Q6U6	
ENSMUST00000166380	ENSMUSG00000095753	6	69648824	69649363	-1	0	1	0	0	2	2	1	0	2	17	12	A0A075B677	
ENSMUST00000166381	ENSMUSG00000090546	X	61183246	61185558	-1	0	1	4	3	1	1	0	0	0	0	0	E9Q0B4	
ENSMUST00000166382						74	29	110	2	27	0	19	103	58	7	0		
ENSMUST00000166383	ENSMUSG00000002020	12	84783212	84876532	-1	11	5	0	5	1	1	0	0	0	0	2	F6UFW9	
ENSMUST00000166384	ENSMUSG00000025915	1	9798107	9900845	1	0	0	0	2	0	0	151	1332	419	453	243		Q9ERE3
ENSMUST00000166388	ENSMUSG00000026979	2	24367580	24414954	1	0	4	0	0	0	1	1042	474	1381	45	1169		Q8BLR5
ENSMUST00000166390	ENSMUSG00000030109	6	121343076	121365775	1	0	0	9	7	6	2	1	0	0	0	1	E9Q5U8	
ENSMUST00000166392						4	3	12	4	5	3	0	0	0	0	0		
ENSMUST00000166393	ENSMUSG00000026659	1	170873498	170885540	-1	0	0	4	0	0	0	4	4	5	0	6	F6QRT3	
ENSMUST00000166395	ENSMUSG00000047407	17	70844205	70853546	-1	15	7	13	29	11	7	4	18	3	5	8	G3UWC5	
ENSMUST00000166396						7	7	21	3	21	14	40	169	62	7	84		
ENSMUST00000166397	ENSMUSG00000066900	5	117091680	117116113	-1	0	8	0	38	0	0	316	387	143	0	154		
ENSMUST00000166399						6	3	5	3	4	0	0	0	0	0	0		
ENSMUST00000166400						0	0	2	17	0	1	0	0	0	0	0		
ENSMUST00000166403						0	0	2	3	1	1	21	18	16	23	8		
ENSMUST00000166404						9	5	23	12	19	3	0	0	0	0	0		
ENSMUST00000166406	ENSMUSG00000031283	X	143285674	143394262	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TP73	Q920C1
ENSMUST00000166407	ENSMUSG00000071655	19	8871559	8875663	1	5	10	13	0	10	3	1082	1425	913	556	408		Q922Y1
ENSMUST00000166408						53	70	211	78	83	25	12	136	18	12	55		
ENSMUST00000166409	ENSMUSG00000029178	5	64803388	64832901	1	0	3	11	5	13	0	227	427	158	0	0	Q545J5	Q60980
ENSMUST00000166410	ENSMUSG00000094132	14	4855576	4875851	1	0	0	0	0	0	0	0	0	0	0	0	A6NAU0	
ENSMUST00000166411	ENSMUSG00000068882	2	69861562	69871846	1	0	0	0	18	0	0	23	0	30	37	62	Q564E6	P32067
ENSMUST00000166412	ENSMUSG00000036372	19	10204014	10207824	1	0	0	0	0	0	0	141	266	108	287	26	E9Q853	
ENSMUST00000166414						3	6	14	3	6	4	0	0	0	1	0		
ENSMUST00000166415						12	3	14	6	14	1	9	17	18	2	27		
ENSMUST00000166416	ENSMUSG00000039958	6	149139849	149151171	1	0	0	2	0	0	0	0	0	0	24	11	E9PY99	
ENSMUST00000166417						46	52	107	706	66	21	0	7	3	1	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000166418						0	2	2	7	2	3	0	0	0	0	0		
ENSMUST00000166419						25	12	13	39	34	19	4	31	0	0	27		
ENSMUST00000166420	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q514	
ENSMUST00000166422	ENSMUSG00000026384	1	119652467	119837613	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q210	
ENSMUST00000166425	ENSMUSG00000020530	11	84832361	84870817	-1	0	0	0	26	0	0	0	0	2	0	0	E9Q389	
ENSMUST00000166426	ENSMUSG00000024392	17	35135178	35147322	1	0	0	0	79	20	0	0	0	0	1	0	Q3UF95	
ENSMUST00000166427	ENSMUSG00000058586	15	83089506	83116674	1	10	8	18	20	16	7	10	15	16	0	16	Q3U3G8	
ENSMUST00000166428	ENSMUSG00000022565	15	76170974	76232574	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q9J6	
ENSMUST00000166429	ENSMUSG00000042700	12	82170016	82451782	1	37	34	108	208	30	26	566	423	1029	41	922		Q8C0T5
ENSMUST00000166431	ENSMUSG00000043719	9	105687809	105828160	-1	0	0	0	0	0	0	0	0	0	0	8	E9Q6A6	
ENSMUST00000166435	ENSMUSG00000023027	15	100227819	100261244	1	0	1	0	0	0	0	0	0	17	4	0	F6U840	
ENSMUST00000166436	ENSMUSG00000017288	11	76046226	76179647	-1	0	0	0	0	0	0	12	0	0	0	6	F6Z4G7	
ENSMUST00000166437						1	0	3	6	1	0	0	0	0	0	0		
ENSMUST00000166438						5	0	5	6	6	5	0	0	0	0	0		
ENSMUST00000166439	ENSMUSG00000030970	7	132987563	133124354	-1	0	0	0	0	0	0	163	407	253	31	154	Q91YZ2	
ENSMUST00000166440	ENSMUSG00000040621	X	166170454	166190512	1	0	0	0	0	0	0	0	0	0	0	0	E9QA54	
ENSMUST00000166442	ENSMUSG00000079491	17	36115876	36121465	-1	0	0	0	0	0	0	0	44	3	22	0	F6T1I5	
ENSMUST00000166444	ENSMUSG00000042515	X	139210042	139238335	1	0	0	6	0	1	1	0	0	0	0	1	E9PXL9	
ENSMUST00000166445	ENSMUSG00000029676	6	25743737	25809246	-1	0	0	0	0	0	0	38	39	93	74	79		Q91WC1
ENSMUST00000166447	ENSMUSG00000090619	7	42116471	42195776	1	8	11	13	4	6	1	0	0	0	0	0	L7N2A1	
ENSMUST00000166449						1	0	5	2	1	0	0	0	0	0	0		
ENSMUST00000166450						0	2	10	26	10	4	0	0	0	0	0		
ENSMUST00000166453						12	6	3	6	9	3	1	1	4	0	6		
ENSMUST00000166455	ENSMUSG00000020407	11	9118103	9136170	1	0	0	0	0	0	0	0	0	0	5	0	F6YBT6	
ENSMUST00000166457	ENSMUSG00000030109	6	121343076	121365775	1	4	0	0	4	0	0	0	0	0	0	0	G5E8Z4	
ENSMUST00000166458	ENSMUSG00000017978	6	23262773	23839421	-1	0	14	0	0	0	0	0	0	0	0	0	E9Q5C0	
ENSMUST00000166459						3	3	1	2	2	4	0	0	0	0	0		
ENSMUST00000166461	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	0	0	4	0	0	F7CVZ7	
ENSMUST00000166462	ENSMUSG00000039742	6	29319140	29336019	1	0	0	0	1	14	5	0	1	0	0	0	B7XG46	
ENSMUST00000166463						5	5	9	4	3	5	0	0	0	0	0		
ENSMUST00000166464	ENSMUSG00000078894	2	176226569	176240328	1	0	0	0	0	0	0	0	0	0	0	0	F7ACM4	
ENSMUST00000166465						1	3	2	2	7	1	0	3	0	6	0		
ENSMUST00000166466						0	0	0	0	0	0	86	503	83	39	14		
ENSMUST00000166467	ENSMUSG00000036083	13	23839434	23860714	1	0	0	22	0	0	9	0	0	0	0	0	G3UWD9	
ENSMUST00000166468	ENSMUSG00000019889	10	28074820	28597397	1	30	22	35	136	33	19	7	3	5	29	65		P35822
ENSMUST00000166469	ENSMUSG00000023944	17	45567775	45573271	-1	0	0	1	0	5	3	0	0	0	0	8	E9Q3D6	
ENSMUST00000166471	ENSMUSG00000021111	12	105784694	105838944	1	0	0	3	0	0	0	0	0	207	7	154	F6VTN8	
ENSMUST00000166472	ENSMUSG00000040282	2	115581716	115778768	1	0	14	40	161	28	0	0	12	0	0	24	E9PWV4	
ENSMUST00000166474	ENSMUSG00000091987	Y	2900989	2912206	1	0	0	3	0	0	0	0	0	0	0	0	B2RWR6	
ENSMUST00000166478	ENSMUSG00000031422	X	136732942	136743690	-1	11	5	0	0	0	3	79	0	0	0	14		Q9R0Q4
ENSMUST00000166480	ENSMUSG00000051786	15	89098357	89123087	-1	0	0	0	2	0	2	0	9	3	0	4	F6X8A1	
ENSMUST00000166484	ENSMUSG00000029333	5	99217426	99252927	-1	0	0	5	0	0	0	4	0	8	0	1	E9Q813	
ENSMUST00000166487	ENSMUSG00000004460	16	22857845	22879634	1	66	78	134	120	92	36	13	58	17	4	19		Q99KV1
ENSMUST00000166489	ENSMUSG00000023286	4	155943831	155959604	1	30	25	0	25	32	23	0	0	0	0	0		Q6P073
ENSMUST00000166493	ENSMUSG00000096869	14	7116798	7125412	-1	3	0	11	3	12	4	0	0	0	0	0	K7N6G4	
ENSMUST00000166494	ENSMUSG00000079410	14	3049285	3076840	1	35	45	7	23	28	6	0	0	0	0	0	K7N6T7	
ENSMUST00000166495	ENSMUSG00000026740	2	18195654	18392830	-1	28	17	32	36	36	17	59	232	149	30	116		Q61712
ENSMUST00000166496	ENSMUSG00000025020	19	41600257	41743665	-1	0	0	0	0	0	0	0	0	0	0	0	E9QAW9	
ENSMUST00000166497	ENSMUSG00000025277	14	8002902	8056555	1	19	10	22	27	16	0	2	7	0	3	10		Q8R2Y0
ENSMUST00000166498						3	5	0	4	2	1	5	42	11	2	13		
ENSMUST00000166499	ENSMUSG00000094098	7	8367460	8383238	-1	15	17	20	11	15	5	0	0	0	0	0	L7N2E1	
ENSMUST00000166502	ENSMUSG00000060671	3	89939481	89963508	-1	3	3	0	0	0	1	1	0	2	0	0	F6WT01	
ENSMUST00000166503						3	0	16	0	2	3	0	0	1	0	0		
ENSMUST00000166505	ENSMUSG00000090919	3	46442197	46448219	-1	4	0	19	0	14	6	0	0	0	0	0	G5E8X2	
ENSMUST00000166510	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	12	0	0	0	E9Q1I7	
ENSMUST00000166511	ENSMUSG00000020003	10	19859929	19907689	-1	0	1	0	17	0	0	0	0	0	0	0	B7ZNK8	
ENSMUST00000166512	ENSMUSG00000022661	16	45382135	45409053	-1	0	0	0	0	0	0	0	0	0	0	0	Q05D16	
ENSMUST00000166517						9	6	34	16	9	3	1	5	7	0	10		
ENSMUST00000166518	ENSMUSG00000002014	X	73787028	73790830	1	0	0	0	18	0	0	339	427	167	1262	115	Q9D8L3	
ENSMUST00000166524	ENSMUSG00000048424	15	8968426	9066551	1	0	0	0	0	1	0	0	0	0	0	0		Q6PDH4
ENSMUST00000166525	ENSMUSG00000000708	17	53566861	53672720	1	0	6	3	0	4	2	0	19	0	0	0	F6ZCH1	
ENSMUST00000166526	ENSMUSG00000061613	17	31647082	31658754	-1	0	3	6	10	0	0	37	153	36	58	26	G3UW94	
ENSMUST00000166527	ENSMUSG00000093948	14	42655938	42663605	1	0	0	0	0	0	0	0	0	0	0	0	F6XQQ1	
ENSMUST00000166528						6	3	8	5	7	5	0	0	0	0	0		
ENSMUST00000166531						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000166537	ENSMUSG00000036309	11	52231995	52246858	1	0	0	0	0	0	0	17	10	42	182	45	E9PUV4	
ENSMUST00000166538	ENSMUSG00000000131	7	126101715	126200501	-1	0	4	2	0	1	0	0	54	7	3	0	F6U927	
ENSMUST00000166539						6	5	4	5	18	16	55	73	33	26	26		
ENSMUST00000166540	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	0	0	0	0	124	304	123	0	28	F6ZII1	
ENSMUST00000166542	ENSMUSG00000028634	4	119733784	120138045	1	18	32	245	297	44	30	6	0	7	0	0		A2A884
ENSMUST00000166543	ENSMUSG00000024096	17	65848433	65885755	-1	41	20	83	35	62	24	24	47	44	32	42		Q62172
ENSMUST00000166545	ENSMUSG00000052955	6	53873279	53978671	-1	15	10	15	7	18	14	0	0	0	1	0		Q9D3S9
ENSMUST00000166546	ENSMUSG00000095406	12	34290274	34291092	-1	13	9	19	11	13	10	0	0	0	0	0	E9Q1N8	
ENSMUST00000166548	ENSMUSG00000055932	8	91313532	91668439	1	1	0	3	3	0	0	10	0	10	0	0	E9Q1E4	
ENSMUST00000166549	ENSMUSG00000007656	9	75037614	75060313	1	2	0	0	0	3	5	0	4	0	0	5		P56212
ENSMUST00000166552						0	0	0	0	0	0	25	0	0	0	0		
ENSMUST00000166554	ENSMUSG00000043384	X	135742733	135803474	1	20	17	0	0	0	0	8	119	4	0	1		Q5U4C1
ENSMUST00000166557						0	2	0	7	4	0	2	0	0	2	0		
ENSMUST00000166558						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000166562	ENSMUSG00000079583	X	60436052	60539249	-1	0	0	0	0	0	0	0	0	0	0	0	E9QAS1	
ENSMUST00000166563	ENSMUSG00000023952	17	46161032	46169370	1	0	0	0	11	2	0	2	6	3	0	9	E9Q004	
ENSMUST00000166565						1	0	9	0	4	0	0	0	0	0	3		
ENSMUST00000166577	ENSMUSG00000014498	10	128377115	128408704	1	0	0	1	5	0	0	0	0	0	0	0	F7BT68	
ENSMUST00000166578	ENSMUSG00000063480	15	82041319	82047598	-1	16	20	51	72	27	7	5	30	22	4	19	E9PZS4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000166580	ENSMUSG00000041986	9	53911460	53975301	-1	3	9	2	0	0	7	0	0	0	0	0	E9Q0K9	
ENSMUST00000166581	ENSMUSG00000028001	3	83026076	83033627	1	9	12	16	16	21	23	0	0	0	10	0		E9PV24
ENSMUST00000166582						7	0	3	2	5	0	0	7	8	4	17		
ENSMUST00000166583						12	3	7	5	13	3	0	3	0	0	4		
ENSMUST00000166585	ENSMUSG00000021557	13	59449537	59585227	-1	3	0	9	7	2	0	0	0	6	0	0	E9Q3T5	
ENSMUST00000166586						0	0	9	0	4	0	0	0	0	0	0		
ENSMUST00000166589	ENSMUSG00000092123	2	155735810	155735866	-1	1	0	1	0	0	0	0	0	0	0	0	F6Y7E7	
ENSMUST00000166590						0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000166591	ENSMUSG00000042992	6	134639510	134711187	1	2	10	6	0	0	0	70	68	35	20	10	E9Q2W8	
ENSMUST00000166592	ENSMUSG00000031691	8	85036915	85057583	1	14	0	11	185	20	1	0	1	0	0	0	E9PV58	
ENSMUST00000166597						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000166599	ENSMUSG00000033794	5	107431549	107435039	1	28	30	25	32	50	22	0	1	0	1	0	B2RT16	Q9D5U0
ENSMUST00000166601						8	8	7	14	6	0	0	0	0	24	0		
ENSMUST00000166603	ENSMUSG00000020307	10	79682195	79688394	1	5	5	23	0	13	3	1731	1813	899	237	498		Q8CFI2
ENSMUST00000166605						0	1	4	1	2	0	5	8	2	8	4		
ENSMUST00000166608	ENSMUSG00000025374	10	128401395	128411492	-1	0	0	24	0	0	0	261	326	21	21	33	E9Q199	
ENSMUST00000166609						1	0	2	2	0	1	19	64	35	20	95		
ENSMUST00000166610	ENSMUSG00000033565	15	77078990	77307053	-1	0	0	87	0	7	0	21	5	28	0	46		Q8BP71
ENSMUST00000166613						0	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000166615	ENSMUSG00000031930	8	107436398	107558594	1	54	26	83	61	60	23	2882	3971	2793	406	2212	I3RSH5	Q9DBH0
ENSMUST00000166617	ENSMUSG00000047428	17	46297421	46303271	1	0	0	0	45	0	4	0	0	0	0	4		Q8K1E3
ENSMUST00000166618	ENSMUSG00000091400	14	6965449	6973818	-1	5	4	0	1	7	0	0	0	0	0	0	L7N2A7	
ENSMUST00000166619						2	2	0	0	16	0	269	213	86	54	173		
ENSMUST00000166620						0	0	0	0	0	0	0	0	0	36	0		
ENSMUST00000166622	ENSMUSG00000006522	14	30908573	30923760	-1	0	0	0	0	0	1	0	0	0	0	0	F6ZXJ7	
ENSMUST00000166623	ENSMUSG00000091694	15	77633951	77643286	-1	0	0	0	0	0	13	0	0	0	0	0	E9PUZ0	
ENSMUST00000166624	ENSMUSG00000026384	1	119652467	119837613	-1	3	0	0	0	0	0	0	0	15	0	4	F6ZHZ9	
ENSMUST00000166626	ENSMUSG00000024037	17	31494323	31519974	-1	0	0	0	0	0	0	3	4	6	2	1	F7CM37	
ENSMUST00000166627	ENSMUSG00000073423	17	33629090	33631779	1	0	0	0	0	0	0	362	153	214	61	105		Q9DCK4
ENSMUST00000166629	ENSMUSG00000078500	4	145868794	145899975	1	0	0	0	0	0	0	0	0	0	0	0	O88231	
ENSMUST00000166630						3	1	8	3	9	0	0	0	0	0	0		
ENSMUST00000166632						3	1	5	3	4	0	0	0	2	0	0		
ENSMUST00000166633	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	0	0	0	0	0	0	0	0	0	E9PXQ6	
ENSMUST00000166638	ENSMUSG00000031512	8	11840474	11855761	1	0	0	19	0	0	0	0	0	2	0	1		Q9DA77
ENSMUST00000166644	ENSMUSG00000047696	3	36007244	36053547	-1	8	7	7	4	7	2	0	0	0	0	0	E9PVZ3	
ENSMUST00000166645	ENSMUSG00000096577	12	115742205	115742647	-1	6	5	10	1	4	4	0	0	0	0	0	A0A075B680	
ENSMUST00000166646	ENSMUSG00000032849	14	118482692	118706219	-1	5	24	59	130	35	0	13	365	68	26	24	E9Q467	
ENSMUST00000166647						3	0	2	4	0	3	0	0	0	0	0		
ENSMUST00000166650	ENSMUSG00000035429	7	4548612	4604041	-1	23	37	45	48	29	15	0	0	0	0	0	E9Q0N2	
ENSMUST00000166652	ENSMUSG00000030653	7	101421691	101512829	1	0	0	0	11	0	12	44	0	1273	0	348	Q5PR72	
ENSMUST00000166654						4	8	5	25	10	2	5	9	2	0	0		
ENSMUST00000166658	ENSMUSG00000001289	15	102326116	102331873	1	3	3	32	44	10	9	19	37	39	65	14		Q9WU28
ENSMUST00000166663						3	2	2	7	3	0	16	26	17	0	21		
ENSMUST00000166664	ENSMUSG00000021139	12	81358860	81532905	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVN6	
ENSMUST00000166666						10	3	25	5	2	1	0	0	0	1	0		
ENSMUST00000166668	ENSMUSG00000030889	7	120739557	120805742	1	46	27	205	52	43	14	0	0	0	0	0		Q3UVV9
ENSMUST00000166673						2	5	2	3	7	3	0	0	0	0	0		
ENSMUST00000166674	ENSMUSG00000092152	14	42254659	42260048	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6Z0	
ENSMUST00000166677						37	41	97	35	39	11	4	12	18	6	19		
ENSMUST00000166678	ENSMUSG00000092035	6	4747306	4760517	1	0	0	0	0	0	0	0	0	0	0	0	E9Q3F7	
ENSMUST00000166681	ENSMUSG00000092004	6	115227343	115259294	1	0	0	0	0	0	0	0	0	0	0	0	F6ZF64	
ENSMUST00000166682	ENSMUSG00000032637	7	126491708	126503437	-1	13	5	10	35	4	4	865	70	802	0	800	E9Q5Q0	
ENSMUST00000166684						14	0	34	17	0	6	0	23	15	0	7		
ENSMUST00000166687	ENSMUSG00000041263	3	89083981	89093311	-1	9	0	19	0	0	0	1205	1289	810	113	442	Q3TDG5	Q8BG26
ENSMUST00000166688						0	1	1	3	3	0	0	0	0	0	0		
ENSMUST00000166689						0	0	9	15	0	1	4	0	0	8	0		
ENSMUST00000166690						1	2	5	0	0	0	0	0	0	0	0		
ENSMUST00000166691						10	3	4	25	10	4	21	34	28	0	83		
ENSMUST00000166692	ENSMUSG00000026931	19	58785803	58794461	-1	7	4	5	7	3	2	0	0	0	0	0		Q9CQT6
ENSMUST00000166693	ENSMUSG00000067288	17	33819027	33824562	-1	0	0	0	0	0	0	0	0	0	0	0	Q059I1	P62858
ENSMUST00000166694	ENSMUSG00000022586	15	74979534	74983430	-1	0	0	0	0	0	0	0	1	0	0	0		Q9WU67
ENSMUST00000166696	ENSMUSG00000020037	10	84756062	84906538	1	0	0	0	4	9	0	0	0	0	0	0		Q7TNK1
ENSMUST00000166700	ENSMUSG00000091095	11	69364019	69369408	1	0	0	0	36	0	1	0	0	0	0	0	F6Z984	
ENSMUST00000166701	ENSMUSG00000023952	17	46161032	46169370	1	0	0	9	8	4	3	38	61	56	3	67	F7A4M1	
ENSMUST00000166703						0	0	5	0	0	1	0	14	14	0	29		
ENSMUST00000166705						2	2	5	5	6	0	0	0	0	0	2		
ENSMUST00000166707	ENSMUSG00000039639	16	92346001	92359468	-1	8	3	3	0	6	2	0	0	0	0	0	Q545H6	P23299
ENSMUST00000166708	ENSMUSG00000087230	1	136181474	136207097	-1	6	0	4	2	3	4	0	0	0	0	0	F7DD52	
ENSMUST00000166710						2	2	1	3	1	2	0	0	0	0	0		
ENSMUST00000166711	ENSMUSG00000022407	15	80948490	80970947	1	23	28	69	81	47	29	52	176	65	32	131	E9Q0A0	
ENSMUST00000166712	ENSMUSG00000033417	19	60524696	60581023	-1	0	26	43	0	0	16	0	0	55	110	309	E9PV69	
ENSMUST00000166713	ENSMUSG00000039782	5	43233170	43289724	1	0	0	0	206	0	0	0	0	3	0	0	E9Q969	
ENSMUST00000166714	ENSMUSG00000094978	7	33373234	33374559	1	2	1	0	5	0	2	0	0	0	0	0	E9PWZ2	
ENSMUST00000166716	ENSMUSG00000032492	9	110722085	110747145	-1	12	14	0	111	24	7	0	3	1	1	2		P41593
ENSMUST00000166719	ENSMUSG00000000131	7	126101715	126200501	-1	6	2	13	2	3	0	16	186	37	1	78	F6ZUE3	
ENSMUST00000166723	ENSMUSG00000091803	12	81359026	81485127	-1	1	0	4	0	0	0	11	0	0	0	2	G3UWC6	
ENSMUST00000166724	ENSMUSG00000039059	2	180099465	180104488	-1	0	2	0	0	0	0	0	0	0	0	0	E9PZM9	
ENSMUST00000166726	ENSMUSG00000034751	13	102732486	103334497	-1	0	0	5	0	11	0	11	2	0	0	2	E9Q1M8	
ENSMUST00000166727						5	0	5	3	1	2	0	4	2	0	4		
ENSMUST00000166728						1	3	2	1	3	3	0	0	6	0	0		
ENSMUST00000166729	ENSMUSG00000026828	2	57997884	58045860	1	0	0	0	0	0	0	0	0	0	0	0		Q8C102
ENSMUST00000166731	ENSMUSG00000036172	16	44943678	44981380	1	248	331	353	252	446	187	12	56	24	8	14	E9Q7T2	
ENSMUST00000166734	ENSMUSG00000033392	9	113812586	113919697	1	8	4	7	5	8	4	113	228	184	10	151	Q08EB6	
ENSMUST00000166735	ENSMUSG00000021111	12	105784694	105838944	1	0	0	0	0	0	0	48	78	1	17	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000166736						0	0	0	45	2	0	0	0	0	0	0		
ENSMUST00000166737	ENSMUSG00000044519	14	33967070	33978764	-1	44395	71458	54155	22972	42088	16952	218	2251	595	437	739		Q5HZG9
ENSMUST00000166743	ENSMUSG00000021840	14	47298314	47323204	1	73	0	155	129	53	0	919	1783	1316	133	812		Q8BH93
ENSMUST00000166744						0	0	0	3	0	0	19	0	91	0	0		
ENSMUST00000166746	ENSMUSG00000091174	9	35741049	35742252	1	1	0	0	0	0	0	0	0	0	0	0	B3GLJ5	
ENSMUST00000166748	ENSMUSG00000020893	11	69095217	69109960	1	0	0	34	0	0	0	3	0	49	86	0		O35973
ENSMUST00000166749	ENSMUSG00000039555	4	51216678	51230272	1	3	2	20	7	1	0	0	0	0	0	0	B1AWN8	
ENSMUST00000166750	ENSMUSG00000034390	8	117257019	117461503	1	13	9	64	148	22	10	3647	3110	7688	344	5711		Q9D486
ENSMUST00000166752	ENSMUSG00000017288	11	76046226	76179647	-1	0	0	0	1	0	0	0	0	0	0	0	E9PYD3	
ENSMUST00000166753						15	9	9	7	7	3	0	0	0	0	0		
ENSMUST00000166755						3	0	3	7	0	0	0	0	0	0	0		
ENSMUST00000166758	ENSMUSG00000025468	7	140069880	140082548	-1	5	4	7	10	7	2	0	0	0	0	0		Q9DCA7
ENSMUST00000166759						2	2	0	0	4	0	0	0	0	0	0		
ENSMUST00000166764	ENSMUSG00000078498	4	147305674	147333734	1	0	0	0	0	0	0	0	0	0	0	0	O88231	
ENSMUST00000166765						0	0	0	3	3	0	0	0	0	0	0		
ENSMUST00000166766	ENSMUSG00000018040	15	83113433	83122801	-1	6	3	12	0	0	0	110	84	87	21	44	F6VVA3	
ENSMUST00000166768	ENSMUSG00000033594	8	123232255	123236209	-1	20	14	50	155	27	18	57	35	70	0	34	B2RTE8	Q8BNN1
ENSMUST00000166769	ENSMUSG00000029145	5	31187558	31193430	-1	0	0	0	0	0	0	23	162	1	0	45		Q61749
ENSMUST00000166770	ENSMUSG00000021974	14	58070547	58112337	1	0	0	1	26	1	0	0	0	0	0	1	E9Q864	
ENSMUST00000166771						64	49	165	965	75	58	0	2	1	0	0		
ENSMUST00000166772	ENSMUSG00000071235	12	84641019	84651455	1	12	10	31	28	18	0	0	0	0	0	0		Q3SYK4
ENSMUST00000166773	ENSMUSG00000028738	4	139653538	139670280	1	12	2	15	48	24	11	1	0	0	0	1	E9Q0R6	
ENSMUST00000166774	ENSMUSG00000060332	2	130195194	130264445	1	0	0	0	0	0	0	0	0	0	0	0		Q8R4P4
ENSMUST00000166775	ENSMUSG00000015846	2	27676440	27762957	1	0	0	22	0	12	1	60	0	28	0	111	A2AJP1	P28700
ENSMUST00000166776	ENSMUSG00000094132	14	4855576	4875851	1	0	0	0	31	0	0	0	0	0	0	0	L7N2C5	
ENSMUST00000166777						2	5	7	0	1	1	0	0	0	0	0		
ENSMUST00000166778						0	0	0	50	0	0	0	0	0	1	3		
ENSMUST00000166779	ENSMUSG00000091312	2	11625606	11626264	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q206	
ENSMUST00000166783	ENSMUSG00000032735	18	61799395	61911852	-1	15	10	33	9	12	0	0	0	0	2	1		Q69ZX8
ENSMUST00000166788						21	27	69	31	30	16	1	7	18	3	21		
ENSMUST00000166791	ENSMUSG00000042502	7	127191660	127196050	-1	27	13	64	35	27	15	610	1567	612	78	490		Q9CWK3
ENSMUST00000166792						19	14	82	24	26	14	1	2	2	0	0		
ENSMUST00000166793	ENSMUSG00000037236	18	35562146	35593835	1	45	66	65	55	66	41	46	142	58	86	89	Q5BL18	Q8K310
ENSMUST00000166799	ENSMUSG00000010066	9	107399612	107529343	1	0	0	0	0	0	0	1	0	5	0	0		Q6PHS9
ENSMUST00000166800						35	35	68	49	67	22	0	0	0	0	2		
ENSMUST00000166801	ENSMUSG00000043008	16	19946499	19983037	-1	0	3	0	1	3	0	0	0	38	9	0	E9QAK3	
ENSMUST00000166802	ENSMUSG00000061577	8	94923694	94943290	1	21	0	0	0	18	17	96	238	52	24	153	A6H6A1	
ENSMUST00000166804	ENSMUSG00000052151	10	79526430	79533787	-1	0	0	0	0	0	0	0	0	0	0	0	G3XA61	
ENSMUST00000166808	ENSMUSG00000091471	19	44543722	44552831	-1	0	0	0	0	0	0	0	0	2	2	0	F6Z9R1	
ENSMUST00000166809						0	0	0	3	2	0	0	0	0	2	2		
ENSMUST00000166810	ENSMUSG00000021906	14	32085374	32103202	1	0	1	0	22	3	1	0	5	0	0	5	E9Q7K0	
ENSMUST00000166811	ENSMUSG00000039542	9	49502136	49798925	-1	0	6	93	0	0	0	0	0	1	0	15	E9QB01	
ENSMUST00000166814	ENSMUSG00000035131	1	146494760	146902472	1	6	0	5	0	0	0	0	0	0	0	0		Q499E0
ENSMUST00000166820	ENSMUSG00000025404	10	127380327	127499384	1	0	0	0	57	0	0	59	34	25	0	0		Q80TM6
ENSMUST00000166821	ENSMUSG00000021245	12	85234529	85270591	-1	0	39	0	40	51	12	13	40	48	8	20	Q68FG1	
ENSMUST00000166823	ENSMUSG00000029152	5	73292784	73314069	1	11	8	18	19	14	7	39	158	79	21	64		Q9CRD0
ENSMUST00000166825	ENSMUSG00000043943	9	18321951	18402995	-1	4	1	5	7	0	4	0	0	1	0	0	Q3UZV6	Q9CZR2
ENSMUST00000166831						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000166834						0	3	2	1	2	1	0	0	0	0	0		
ENSMUST00000166836	ENSMUSG00000090639	9	103190208	103230307	-1	0	0	1	142	0	0	168	105	98	1	132	E9Q035	
ENSMUST00000166837	ENSMUSG00000091594	7	42705469	42727017	-1	22	23	24	13	23	18	1	0	0	1	0	E9Q6S4	
ENSMUST00000166838	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	0	0	0	0	0	0	0	0	F6S7C9	
ENSMUST00000166839						53	43	155	198	83	49	27	90	65	13	85		
ENSMUST00000166843	ENSMUSG00000092137	9	71479325	71592265	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q8U3	
ENSMUST00000166844						0	0	1	54	0	0	0	1	0	2	0		
ENSMUST00000166847	ENSMUSG00000075569	5	143933035	143985719	1	18	12	30	15	8	11	2	1	2	0	6	E9PYQ0	
ENSMUST00000166848	ENSMUSG00000079386	14	4430992	4519452	1	0	0	0	0	1	0	0	0	0	0	1	K7N6X4	
ENSMUST00000166849						2	0	1	0	0	0	0	1	0	0	0		
ENSMUST00000166852	ENSMUSG00000091742	17	46439578	46440099	-1	9	6	4	4	9	5	0	5	3	12	6	E9PZB3	
ENSMUST00000166853						0	9	51	39	34	16	24	170	35	6	125		
ENSMUST00000166854	ENSMUSG00000002845	16	38558698	38592162	1	0	1	0	0	0	0	0	0	0	2	10	F6VN87	
ENSMUST00000166855	ENSMUSG00000050164	15	81235499	81238963	1	25	16	46	91	27	15	1	0	1	0	4	Q3UY93	
ENSMUST00000166857						0	0	0	0	0	0	171	960	262	187	108		
ENSMUST00000166859	ENSMUSG00000033545	8	111536097	111626030	1	0	0	0	0	0	0	0	0	0	0	0	E9PWL2	
ENSMUST00000166860	ENSMUSG00000000544	1	166130238	166166510	1	5	0	0	0	0	0	0	0	0	31	16		
ENSMUST00000166864						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000166866						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000166867						6	3	0	2	3	4	0	0	0	0	0		
ENSMUST00000166871						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000166873	ENSMUSG00000022321	15	18818947	19014236	1	0	3	3	0	0	2	0	0	0	0	0		P70408
ENSMUST00000166875	ENSMUSG00000022106	14	73123037	73207843	1	2	0	0	0	1	1	0	0	0	2	0	F6QHR6	
ENSMUST00000166877	ENSMUSG00000051910	7	115470872	116038796	-1	21	8	60	3	12	0	0	5	1	0	0	E9PUW0	
ENSMUST00000166879	ENSMUSG00000021932	14	62292589	62372992	1	0	0	0	0	0	0	0	0	0	14	4	E9PYC5	
ENSMUST00000166880	ENSMUSG00000036744	7	106814144	106820709	1	3	0	2	0	2	0	0	0	0	1	0	Q9D3U9	
ENSMUST00000166881						0	0	0	0	0	0	8	0	0	0	10		
ENSMUST00000166883						0	6	25	17	3	5	0	0	0	0	0		
ENSMUST00000166885	ENSMUSG00000038371	7	110308013	110614922	-1	0	0	0	0	0	0	0	0	3	0	0	F6QZ02	
ENSMUST00000166886						2	5	4	15	4	1	0	0	0	0	0		
ENSMUST00000166889	ENSMUSG00000025487	7	140881968	140898643	1	0	0	0	2	0	1	690	954	590	298	318	E9PY93	
ENSMUST00000166890	ENSMUSG00000004347	6	56069804	56569103	-1	0	19	0	0	0	0	2	0	0	2	0	Q8CDV2	
ENSMUST00000166892	ENSMUSG00000027894	3	107467543	107518018	-1	0	0	0	2	0	0	0	0	0	0	0	E9Q4S9	
ENSMUST00000166895	ENSMUSG00000096685	14	6832231	6840311	-1	4	2	0	0	2	0	0	0	0	0	0	K7N6V4	
ENSMUST00000166897	ENSMUSG00000022752	16	57121714	57154530	1	4	8	8	240	17	2	187	707	301	142	180		Q9CZW5
ENSMUST00000166898	ENSMUSG00000091938	4	42629719	42631714	1	4	4	3	4	4	4	0	0	0	0	0	F6Z9S8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000166899	ENSMUSG00000094856	3	137671524	137672540	1	10016	11863	49586	11009	9094	4332	72	198	157	23	104	L7N280	
ENSMUST00000166902						1	1	3	17	3	1	0	0	0	0	0		
ENSMUST00000166905	ENSMUSG00000039952	9	108204634	108263958	-1	16	10	58	0	14	12	92	0	28	0	0	Q544G5	Q62165
ENSMUST00000166906						0	2	8	0	0	0	0	0	0	0	4		
ENSMUST00000166909	ENSMUSG00000024947	19	6334979	6340891	1	1	1	4	10	0	0	0	0	0	0	0	E9PV51	
ENSMUST00000166912	ENSMUSG00000091144	14	59380833	59395381	-1	67	52	197	60	49	18	14	35	27	15	21	B4XVP9	
ENSMUST00000166913						0	1	1	5	4	0	0	0	0	0	0		
ENSMUST00000166914	ENSMUSG00000091528	7	43018798	43048106	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0M3	
ENSMUST00000166915	ENSMUSG00000090553	1	133603871	133610291	-1	5	2	3	24	0	0	271	656	188	648	100		P62305
ENSMUST00000166917	ENSMUSG00000022307	15	41447482	41861048	1	0	0	2	0	0	0	10	94	5	48	8	B1H3M0	
ENSMUST00000166919	ENSMUSG00000019945	10	68430953	68541896	-1	0	0	2	0	0	0	0	0	0	0	1	E9Q849	
ENSMUST00000166920	ENSMUSG00000026921	2	26580014	26593120	1	5	2	9	6	4	0	0	0	0	0	0	Q3UTJ7	
ENSMUST00000166923	ENSMUSG00000021555	13	59585259	59634798	1	0	0	2	4	0	0	0	0	0	0	0	E9Q6K7	
ENSMUST00000166924	ENSMUSG00000029088	5	48389502	49524907	-1	1	2	21	4	2	0	0	0	0	0	0	Q3YAA5	
ENSMUST00000166926	ENSMUSG00000091680	15	89386827	89388867	1	15	11	63	43	37	9	0	0	0	0	0	E9Q9M9	
ENSMUST00000166927						4	0	5	0	3	5	0	0	0	0	0		
ENSMUST00000166928	ENSMUSG00000091022	14	4084120	4099306	1	17	9	10	11	15	5	0	0	0	0	0	L7N285	
ENSMUST00000166930	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	5	0	0	0	15	247	92	52	90		Q9R0Q4
ENSMUST00000166931	ENSMUSG00000021131	12	80634022	80644341	-1	3	0	2	2	2	0	10	21	33	330	18	G3UW85	
ENSMUST00000166932						3	0	0	0	1	0	0	16	0	2	2		
ENSMUST00000166933						5	0	4	7	9	5	2	14	11	2	13		
ENSMUST00000166936						2	0	0	0	2	0	0	1	0	0	0		
ENSMUST00000166937	ENSMUSG00000096737	7	20883198	20884121	-1	0	0	0	0	0	0	0	0	0	0	0	L7N2C9	
ENSMUST00000166938	ENSMUSG00000052337	6	71831331	71877388	1	11	0	0	0	0	2	117	355	28	37	72	E9Q800	
ENSMUST00000166939	ENSMUSG00000002885	8	83723251	83741326	-1	0	0	0	88	14	13	0	0	0	0	0	Q9DC42	
ENSMUST00000166940	ENSMUSG00000021044	12	88360554	88461719	1	17	13	47	31	21	9	52	35	25	0	24		Q9D0L4
ENSMUST00000166943						8	5	4	8	3	1	27	36	21	5	55		
ENSMUST00000166948	ENSMUSG00000094385	7	21162185	21163108	1	0	0	0	0	0	0	0	0	0	0	0	L7N270	
ENSMUST00000166950	ENSMUSG00000078974	11	16500530	16508484	-1	4	4	0	13	12	7	19	54	22	201	22	G3UWH0	
ENSMUST00000166952	ENSMUSG00000040666	16	96200470	96228933	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2Q9	
ENSMUST00000166954						23	22	42	19	42	12	0	0	0	0	0		
ENSMUST00000166956	ENSMUSG00000091519	18	76856405	76900342	1	17	8	15	563	33	11	0	0	0	0	0		A7M7C7
ENSMUST00000166957	ENSMUSG00000038725	15	44457553	44597143	1	12	0	13	8	26	8	0	0	0	3	8	E9PUU8	
ENSMUST00000166958						25	19	163	32	31	7	0	0	1	0	0		
ENSMUST00000166959	ENSMUSG00000064179	7	4504570	4516382	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q0G9	
ENSMUST00000166960						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000166962	ENSMUSG00000029778	6	55451978	55501451	1	0	0	0	14	0	0	0	0	0	0	0	E9QAL0	
ENSMUST00000166964	ENSMUSG00000013833	10	79894708	79908923	-1	5	2	20	6	3	5	3	2	11	0	4	E9QAH8	
ENSMUST00000166965	ENSMUSG00000020594	12	8674134	8752581	1	0	1	3	0	0	2	0	0	5	0	0	E9Q765	
ENSMUST00000166967	ENSMUSG00000020961	12	91638542	91788387	-1	2	0	1	4	0	1	0	2	0	3	0	E9Q9N5	
ENSMUST00000166968	ENSMUSG00000041014	14	38368952	39473088	-1	33	43	290	139	55	30	0	3	0	0	3		O35181
ENSMUST00000166972	ENSMUSG00000060279	7	44900374	44929490	-1	2	1	3	0	4	0	0	0	0	0	1		P17426
ENSMUST00000166973						5	0	15	7	7	6	0	0	0	0	6		
ENSMUST00000166974	ENSMUSG00000059323	15	76622088	76639958	-1	3	1	3	28	3	1	0	0	0	0	0	E9PZL7	
ENSMUST00000166975	ENSMUSG00000052337	6	71831331	71877388	1	0	0	23	4	0	3	0	0	45	14	0	E9QAY6	
ENSMUST00000166976	ENSMUSG00000055707	8	70450228	70476943	-1	9	0	20	344	0	0	88	153	0	11	70	E9Q4C1	
ENSMUST00000166977	ENSMUSG00000042632	15	79286228	79328390	-1	41	15	41	23	41	0	32	43	44	8	55	Q3UN31	P97819
ENSMUST00000166979	ENSMUSG00000002227	3	104794836	104818563	-1	0	0	10	5	45	1	601	738	630	29	716	E9PW39	
ENSMUST00000166980	ENSMUSG00000003534	17	35681567	35704621	-1	0	0	0	0	0	0	0	8	4	0	0		Q03146
ENSMUST00000166983						2	0	3	31	0	2	3	2	0	3	0		
ENSMUST00000166984	ENSMUSG00000028034	3	152210422	152236826	1	34	20	44	138	34	18	49	80	20	25	52	Q3TUE1	
ENSMUST00000166986						0	0	0	0	0	2	0	0	0	34	2		
ENSMUST00000166987						9	0	9	8	10	3	0	0	0	0	0		
ENSMUST00000166990	ENSMUSG00000024576	18	61555274	61590061	1	0	0	0	12	1	0	0	35	75	16	39	E9PWB2	
ENSMUST00000166992						4	5	17	9	5	5	0	3	3	1	6		
ENSMUST00000166994						2	0	3	0	6	0	0	0	0	0	3		
ENSMUST00000166995	ENSMUSG00000033857	11	118476829	118489209	1	5	0	3	4	2	4	1	0	4	0	1	E9Q017	
ENSMUST00000166996						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000166997						46	35	87	49	39	24	18	49	31	12	44		
ENSMUST00000167000						28	27	98	30	27	21	2	8	4	2	4		
ENSMUST00000167002	ENSMUSG00000030223	6	137252319	137463233	1	4	8	9	1	3	0	98	394	96	119	147	E9PVJ6	
ENSMUST00000167004	ENSMUSG00000031545	8	23172946	23208453	-1	24	20	62	52	45	26	470	764	520	115	449		Q8K2C8
ENSMUST00000167006						2	3	12	6	4	2	5	19	14	3	12		
ENSMUST00000167008	ENSMUSG00000038861	3	94974731	95006843	1	0	0	0	41	0	0	13	48	55	1	25		Q8BKC8
ENSMUST00000167011	ENSMUSG00000056459	12	76347782	76369602	-1	0	0	0	0	0	0	0	0	0	0	15	G3UW50	
ENSMUST00000167012						15	10	8	10	10	2	0	0	1	0	0		
ENSMUST00000167014						6	10	10	49	17	3	0	0	0	0	0		
ENSMUST00000167015	ENSMUSG00000022185	14	54642161	54686931	-1	0	0	0	61	0	0	0	0	0	0	0		Q9JIX8
ENSMUST00000167016						4	0	1	3	1	1	0	0	0	0	0		
ENSMUST00000167018	ENSMUSG00000025730	17	25882114	25919727	-1	0	0	0	0	0	0	0	0	0	0	22	E9PXR4	
ENSMUST00000167020	ENSMUSG00000024283	18	7868832	7973547	1	8	5	7	9	5	3	18	111	8	22	15		Q924H7
ENSMUST00000167021	ENSMUSG00000022106	14	73123037	73207843	1	4	1	8	95	6	3	0	2	2	0	3	E9Q213	
ENSMUST00000167023	ENSMUSG00000025155	11	120789201	120796403	-1	0	0	0	0	0	0	107	291	167	23	109		Q8C2P3
ENSMUST00000167024						0	0	3	4	5	0	0	3	3	2	7		
ENSMUST00000167025	ENSMUSG00000062203	16	11219292	11254270	-1	1	0	0	0	3	2	23	132	0	0	2	F7CE88	
ENSMUST00000167027	ENSMUSG00000025204	19	44548572	44555440	-1	2	2	7	78	0	1	3	0	4	0	0	E9Q9J5	
ENSMUST00000167028						0	3	0	3	4	1	0	0	0	0	0		
ENSMUST00000167032	ENSMUSG00000026288	1	87620312	87720507	1	24	0	22	22	13	11	451	1627	1298	137	990		Q9ES52
ENSMUST00000167033						2	2	4	0	6	1	0	0	0	0	0		
ENSMUST00000167035						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000167036	ENSMUSG00000021417	13	34977748	35027094	-1	0	0	0	0	0	0	14	117	57	103	18	E9Q858	
ENSMUST00000167041	ENSMUSG00000096732	5	11416418	11421235	1	0	0	0	0	0	0	0	0	0	0	0	L7N294	
ENSMUST00000167042	ENSMUSG00000078765	7	30563301	30567960	1	21	0	23	27	21	10	31	283	20	0	112		Q8BGJ9
ENSMUST00000167049	ENSMUSG00000066363	12	104214544	104221129	1	7	12	0	0	7	2	25	35	20	27	20		Q80X76

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000167053						13	12	20	9	9	2	0	0	0	0	0		
ENSMUST00000167055	ENSMUSG00000075289	19	4164324	4175479	-1	12	8	31	96	22	8	120	454	184	26	465	E9PX09	
ENSMUST00000167056						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000167057						0	0	0	0	0	0	6	0	0	0	0		
ENSMUST00000167058	ENSMUSG00000034751	13	102732486	103334497	-1	42	28	172	67	25	16	5	14	54	2	27		Q811L6
ENSMUST00000167059	ENSMUSG00000023905	17	23675447	23677449	-1	0	0	0	0	8	2	0	17	0	0	0	E9PZT5	
ENSMUST00000167060	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	0	0	0	0	0	0	0	0	F6QH05	
ENSMUST00000167061	ENSMUSG00000090777	16	18218170	18219313	1	11	6	20	25	19	7	0	0	0	0	0	F6WEU2	
ENSMUST00000167063						0	0	2	1	3	4	0	29	17	12	8		
ENSMUST00000167064						12	11	25	14	11	4	2	2	0	0	2		
ENSMUST00000167066	ENSMUSG00000021884	14	31552905	31641286	-1	0	0	1	0	0	1	2	0	0	45	0	E9PWM4	
ENSMUST00000167067	ENSMUSG00000001504	13	72628820	72634198	1	2	2	11	3	3	2	0	0	0	0	0	E9PZB5	
ENSMUST00000167068						4	0	7	2	3	0	0	0	0	0	0		
ENSMUST00000167070	ENSMUSG00000001576	17	26561489	26656931	1	0	0	0	2	2	0	0	18	0	14	13	F6SLP4	
ENSMUST00000167071	ENSMUSG00000038457	8	13435459	13461452	1	0	0	0	0	0	13	0	0	0	0	0	G5E908	
ENSMUST00000167072	ENSMUSG00000032578	9	107296026	107302784	1	0	0	0	5	0	0	3	1	0	0	5	E9Q2F4	
ENSMUST00000167073						10	8	7	7	9	0	1	4	2	2	5		
ENSMUST00000167074	ENSMUSG00000031990	9	27097385	27155421	-1	9	10	23	41	9	4	0	8	5	0	3	E9Q769	
ENSMUST00000167075						6	2	0	10	2	4	0	0	0	0	0		
ENSMUST00000167078	ENSMUSG00000034109	3	75875084	75956949	-1	0	0	0	0	0	0	175	625	534	103	278		Q8BXA1
ENSMUST00000167079						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000167080	ENSMUSG00000031506	1	135132700	135145317	1	0	29	87	0	39	0	179	70	212	21	197		Q8BUM3
ENSMUST00000167082	ENSMUSG00000029869	6	41605482	41620509	1	6	0	11	0	4	1	0	1	0	0	3	F6TDC5	
ENSMUST00000167084	ENSMUSG00000023079	5	134357656	134456716	-1	0	0	0	9	0	0	0	0	28	5	47		Q9JI57
ENSMUST00000167085	ENSMUSG00000038305	1	57774162	57948394	1	4	4	3	73	7	3	0	0	0	2	0	E9PVQ3	
ENSMUST00000167086	ENSMUSG00000086564	3	100993529	101029556	-1	29	17	0	24	39	18	324	0	73	1	306	A0A0B4J1L8	
ENSMUST00000167087	ENSMUSG00000020091	10	61432497	61452669	-1	0	0	0	11	0	0	0	0	313	0	0	Q3UFP6	P70445
ENSMUST00000167089						11	8	10	7	20	2	0	0	0	0	0		
ENSMUST00000167091	ENSMUSG00000025237	9	59617284	59650290	1	0	0	20	0	7	4	53	379	78	20	61	Q05BZ2	
ENSMUST00000167092						3	0	0	0	0	0	0	9	15	0	0		
ENSMUST00000167093	ENSMUSG00000090572	17	20540517	20564756	-1	7	0	9	12	5	1	0	0	0	0	0	K7N747	
ENSMUST00000167095	ENSMUSG00000032268	9	49081260	49117587	1	0	0	5	0	0	0	0	0	0	0	0	E9PWX9	
ENSMUST00000167096	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	0	0	0	0	8	13	0	0	0	Q8C1R2	
ENSMUST00000167097	ENSMUSG00000015474	17	34616662	34628510	-1	5	0	3	20	4	0	21	75	24	9	12	G5E8W7	
ENSMUST00000167099	ENSMUSG00000095318	14	42518878	42524282	-1	0	4	0	4	11	3	0	0	0	0	0	L7N2E0	
ENSMUST00000167100	ENSMUSG00000021982	14	59560896	59597836	-1	0	0	0	0	0	0	0	0	0	0	0	G3UW39	
ENSMUST00000167102						3	0	0	14	1	2	1	2	0	0	0		
ENSMUST00000167103	ENSMUSG00000066392	12	88722876	90334935	1	51	7	0	0	53	9	0	0	0	0	0	E9Q2X2	
ENSMUST00000167106	ENSMUSG00000031639	8	45395665	45410608	-1	18	13	0	7	9	8	1	10	3	13	15		Q99MB1
ENSMUST00000167107	ENSMUSG00000055240	17	33360507	33394641	-1	15	10	8	2	8	6	21	115	45	26	13	Q8BP18	
ENSMUST00000167110	ENSMUSG00000038615	11	96817414	96829968	-1	0	0	0	29	33	8	0	1	0	0	0		Q61985
ENSMUST00000167111	ENSMUSG00000038975	3	153907287	153913009	-1	7	0	0	5	0	6	0	27	17	14	18		P53612
ENSMUST00000167113	ENSMUSG00000079162	9	89084624	89092835	-1	46	46	65	38	54	40	10	49	11	0	11		P86448
ENSMUST00000167114	ENSMUSG00000017288	11	76046226	76179647	-1	0	0	0	0	0	0	0	0	8	0	0	E9PWD1	
ENSMUST00000167115	ENSMUSG00000022636	16	52248996	52454074	-1	0	0	0	0	0	0	25	154	0	2	10	F6QH25	
ENSMUST00000167116	ENSMUSG00000022159	14	52261759	52279545	-1	0	0	0	0	0	0	0	0	0	3	0	Q0PD64	P59279
ENSMUST00000167118	ENSMUSG00000030598	7	28716804	28738144	1	0	0	0	2	0	0	0	0	0	0	0	Q3V064	Q9QZM8
ENSMUST00000167119	ENSMUSG00000025931	1	20890606	20939650	1	0	0	0	0	0	0	0	0	0	0	0		Q80ZE5
ENSMUST00000167122	ENSMUSG00000032363	9	90163069	90208071	1	0	0	26	21	44	11	0	5	4	0	12	E9PX36	
ENSMUST00000167127						2	0	2	3	0	0	0	0	0	0	0		
ENSMUST00000167130						0	0	0	7	0	0	0	0	0	0	0		
ENSMUST00000167131	ENSMUSG00000079652	6	29279593	29290680	1	1	1	4	3	5	0	0	0	0	2	1	E9Q318	
ENSMUST00000167133	ENSMUSG00000091375	5	109286269	109297556	-1	15	3	9	8	7	4	0	0	0	0	0	L7N2A0	
ENSMUST00000167136						1	0	1	0	0	0	5	0	14	0	2		
ENSMUST00000167138						0	0	0	0	0	1	2	0	1	0	1		
ENSMUST00000167139						7	4	8	3	9	4	0	0	0	0	0		
ENSMUST00000167140	ENSMUSG00000071711	15	78406712	78414002	1	0	0	8	197	3	6	392	511	291	36	153	Q3UW66	
ENSMUST00000167143	ENSMUSG00000040592	11	106311341	106314762	-1	0	0	0	5	5	0	74	66	75	567	277		P15530
ENSMUST00000167144	ENSMUSG00000021624	13	102693558	102739629	1	0	0	0	0	1	0	0	3	4	0	0	E9PVS6	
ENSMUST00000167145						1	2	4	0	2	4	12	49	18	6	9		
ENSMUST00000167147	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	0	0	0	0	4	0	2	0	0	E9Q081	
ENSMUST00000167149	ENSMUSG00000038615	11	96817414	96829968	-1	0	0	0	33	20	0	751	529	712	0	287	Q6GTN8	Q61985
ENSMUST00000167150						8	4	10	3	9	1	0	2	0	2	0		
ENSMUST00000167151						14	19	48	51	30	10	0	0	0	0	0		
ENSMUST00000167152	ENSMUSG00000068037	17	12841079	12868143	-1	2	0	0	4	0	2	0	0	0	0	0	Q0VB49	P30554
ENSMUST00000167153	ENSMUSG00000078716	4	43668971	43692668	1	64	70	167	456	144	86	4	11	7	1	0		B1AWJ5
ENSMUST00000167154	ENSMUSG00000073007	X	107792590	107872909	1	0	0	0	0	0	0	0	0	0	0	0	B1ATX6	
ENSMUST00000167155	ENSMUSG00000042015	13	94976344	95023314	1	0	0	0	0	0	0	1	0	0	0	0	B2RQV3	
ENSMUST00000167156	ENSMUSG00000036602	10	103007846	103029054	-1	12	5	0	63	20	13	0	0	0	0	0		Q8C8B0
ENSMUST00000167159						5	5	46	28	12	4	379	488	481	48	945		
ENSMUST00000167160	ENSMUSG00000029001	4	148152800	148160482	-1	4	0	0	0	0	0	3	3	0	0	9	A2A7H5	
ENSMUST00000167161	ENSMUSG00000003779	18	34624624	34633265	1	0	2	0	0	0	6	118	183	9	166	1		P97329
ENSMUST00000167162						0	1	1	5	0	0	26	93	66	0	86		
ENSMUST00000167163	ENSMUSG00000060147	13	33917918	34002794	-1	2	0	6	0	0	0	0	0	0	0	0	Q4FJQ6	Q60854
ENSMUST00000167164	ENSMUSG00000049583	7	87602544	88134907	1	14	10	0	26	9	7	0	0	0	0	0	B2BH30	Q3UVX5
ENSMUST00000167169						1	1	0	0	0	0	0	0	2	0	0		
ENSMUST00000167172						0	0	4	0	1	1	50	65	167	0	196		
ENSMUST00000167173	ENSMUSG00000022623	15	89499623	89560261	1	5	4	1	52	10	3	0	0	0	0	0	E9Q1P5	
ENSMUST00000167174						3	2	4	1	5	0	36	113	38	0	25		
ENSMUST00000167175	ENSMUSG00000021884	14	31552905	31641286	-1	0	0	0	0	0	0	0	0	10	0	0	E9Q9L4	
ENSMUST00000167178	ENSMUSG00000020513	11	86544991	86567360	1	0	7	0	0	12	10	0	10	0	13	0	Q5SWF8	Q9R1K7
ENSMUST00000167179	ENSMUSG00000037143	2	145934784	146215039	1	0	0	0	0	0	0	0	0	0	0	0	Q80ZP9	
ENSMUST00000167180	ENSMUSG00000040771	17	48410014	48417266	1	8	0	17	13	8	0	66	191	118	188	102		Q8R5F3
ENSMUST00000167182	ENSMUSG00000042079	6	117900324	117925622	1	0	19	18	0	9	0	187	400	251	218	104		Q9Z2X1

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000167183	ENSMUSG00000042570	10	79540245	79555199	-1	0	0	5	3	6	0	0	1	0	0	0	E9Q119	
ENSMUST00000167187	ENSMUSG00000024576	18	61555274	61590061	1	0	4	0	0	0	0	36	0	282	19	178	E9Q2U6	
ENSMUST00000167190	ENSMUSG00000043557	17	29827956	29970087	-1	5	5	2	112	17	10	0	0	0	1	0	E9Q6S8	
ENSMUST00000167191	ENSMUSG00000044499	10	36506814	36834397	1	0	4	13	117	0	2	0	0	0	0	0	B2RXW6	Q8BSL4
ENSMUST00000167195	ENSMUSG00000023942	17	45585200	45599606	-1	1	1	3	27	0	0	0	0	0	0	0	E9Q503	
ENSMUST00000167196	ENSMUSG00000020692	11	82900768	82908411	-1	0	0	0	0	0	0	0	5	0	0	3	F7BBL8	
ENSMUST00000167197	ENSMUSG00000060601	7	44549616	44553951	-1	0	0	6	0	0	0	0	49	0	0	0		Q60644
ENSMUST00000167198	ENSMUSG00000038542	8	13077189	13105459	-1	0	0	0	0	0	0	6	0	19	0	6	F6QZZ3	
ENSMUST00000167199	ENSMUSG00000024683	19	11770415	11774944	1	8	7	10	12	9	5	30	116	43	97	31		Q99N93
ENSMUST00000167200	ENSMUSG00000059994	3	87376387	87402934	1	0	0	0	0	0	0	16	227	4	20	49	E9Q5S9	
ENSMUST00000167201	ENSMUSG00000001424	6	28475139	28935162	1	133	115	569	188	162	50	6	15	7	2	24	Q3TJ56	
ENSMUST00000167202						0	0	0	0	0	0	0	4	0	6	0		
ENSMUST00000167203	ENSMUSG00000049658	13	100017994	100104070	-1	0	0	0	0	0	1	0	0	2	0	0	F6Y5R2	
ENSMUST00000167204	ENSMUSG00000027797	3	55242364	55539068	1	15	16	12	24	16	10	0	0	0	1	4	Q80VB6	
ENSMUST00000167210						0	2	0	1	2	3	0	0	0	0	0		
ENSMUST00000167211	ENSMUSG00000027168	2	105668900	105697364	1	0	0	0	0	0	0	0	0	0	0	0		P63015
ENSMUST00000167213	ENSMUSG00000030889	7	120739557	120805742	1	0	0	0	0	0	0	0	0	0	0	0		Q3UVV9
ENSMUST00000167214	ENSMUSG00000023913	17	43568098	43612201	1	0	0	4	2	0	2	0	0	0	13	0	E9Q6J0	
ENSMUST00000167215	ENSMUSG00000005986	19	4270180	4283137	-1	2	2	15	0	0	3	3	0	5	0	5	E9Q6X4	
ENSMUST00000167216						0	3	6	6	3	2	0	0	0	0	1		
ENSMUST00000167217	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	0	0	0	1	0	E9Q5R0	
ENSMUST00000167218	ENSMUSG00000030970	7	132987563	133124354	-1	0	0	0	40	1	0	0	0	0	0	0	E9QA96	
ENSMUST00000167220	ENSMUSG00000053470	6	71588972	71632990	-1	19	0	0	86	15	21	93	0	88	0	207		Q6PCM1
ENSMUST00000167221						0	1	0	0	0	1	0	0	1	0	0		
ENSMUST00000167222						3	1	20	3	2	0	0	0	0	0	0		
ENSMUST00000167223						0	0	1	8	2	4	70	142	122	5	168		
ENSMUST00000167225						0	0	6	0	3	4	3065	4533	1738	330	988		
ENSMUST00000167227	ENSMUSG00000071235	12	84641019	84651455	1	6	5	16	23	0	8	0	0	0	0	0		Q3SYK4
ENSMUST00000167231	ENSMUSG00000090740	14	51690308	51695448	-1	1	2	3	0	0	0	0	0	0	0	0	F7D8Y4	
ENSMUST00000167232	ENSMUSG00000033847	7	13324655	13360672	1	11	0	18	5	4	4	0	0	2	3	5	Q08EC7	
ENSMUST00000167234	ENSMUSG00000029778	6	55451978	55501451	1	6	0	10	0	0	3	0	0	0	0	0	E9PVE8	
ENSMUST00000167237	ENSMUSG00000060147	13	33917918	34002794	-1	0	3	0	1	0	5	0	0	0	0	0	E9Q5Q5	
ENSMUST00000167239	ENSMUSG00000049134	19	56320035	56390037	-1	18	0	7	24	0	0	5	0	0	0	0	E9Q641	
ENSMUST00000167240	ENSMUSG00000032946	19	6399340	6415216	1	0	0	0	0	0	0	1407	1706	773	2	930		Q9QUG9
ENSMUST00000167241	ENSMUSG00000027288	2	120506820	120563843	-1	0	0	0	0	0	0	0	2	15	0	6	F6SID8	
ENSMUST00000167242	ENSMUSG00000022100	14	70654246	70766628	-1	253	257	459	296	290	144	0	0	0	36	0	E9PUW7	
ENSMUST00000167243	ENSMUSG00000090665	10	99443730	99447007	1	29	29	221	42	53	21	369	2847	747	130	1407		
ENSMUST00000167244						69	67	329	94	73	37	23	54	32	5	60		
ENSMUST00000167245	ENSMUSG00000095056	14	4397526	4406347	1	6	9	2	0	7	0	0	0	0	0	0	K7N760	
ENSMUST00000167246	ENSMUSG00000034403	X	99465734	99471273	-1	0	0	0	0	0	0	31	44	70	37	48	Q05CG5	O55176
ENSMUST00000167248	ENSMUSG00000095187	11	49551749	49552684	1	0	8	18	7	21	4	0	0	0	0	0	Q7TQT4	
ENSMUST00000167250	ENSMUSG00000035835	10	79860475	79874634	-1	18	4	59	51	19	14	36	58	31	6	47	E9QAX3	
ENSMUST00000167251						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000167252	ENSMUSG00000029771	6	29526625	29541871	1	0	0	1	0	0	5	19	16	0	7	24	F6Z6C6	
ENSMUST00000167253	ENSMUSG00000094149	7	22228564	22229484	-1	3	2	0	0	0	0	0	0	0	0	0	K9J7G4	
ENSMUST00000167256	ENSMUSG00000052293	13	100651579	100656060	1	0	0	0	2	0	0	0	0	0	0	0		Q8VI33
ENSMUST00000167257						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000167258	ENSMUSG00000038756	11	96133786	96165451	1	31	15	35	29	22	15	0	0	0	0	0		A4Q9E8
ENSMUST00000167260	ENSMUSG00000060147	13	33917918	34002794	-1	0	0	0	27	5	0	0	0	0	0	0	E9Q0P9	
ENSMUST00000167261	ENSMUSG00000031738	8	92674288	92680956	1	12	13	9	2	21	12	0	0	0	0	0		Q9ER75
ENSMUST00000167262	ENSMUSG00000034239	11	103534577	103621140	-1	6	0	0	0	4	2	0	0	0	0	0	E9Q472	
ENSMUST00000167263	ENSMUSG00000025497	7	141269085	141276786	-1	24	17	216	139	63	21	0	0	0	0	0	A0PJK7	
ENSMUST00000167264	ENSMUSG00000031585	8	33731833	33777173	1	0	1	2	18	0	1	168	594	219	194	111		Q9D902
ENSMUST00000167268						13	5	6	9	9	15	10	18	20	0	40		
ENSMUST00000167270	ENSMUSG00000049252	2	40595246	42653624	-1	12	5	17	0	12	8	0	0	0	0	0	E9Q202	
ENSMUST00000167271	ENSMUSG00000043190	13	76001535	76018712	-1	0	0	0	0	0	0	0	28	4	3	0		Q8K2P6
ENSMUST00000167272						2	0	1	0	0	3	0	0	0	0	0		
ENSMUST00000167273	ENSMUSG00000040435	7	45522916	45526268	-1	7	8	53	41	13	14	0	73	0	0	17	B2RRL7	P17564
ENSMUST00000167275	ENSMUSG00000076439	17	37010743	37023398	-1	1	5	2	2	1	2	1	0	0	0	0	Q29ZQ5	
ENSMUST00000167278	ENSMUSG00000029687	6	47530139	47595341	-1	0	0	2	0	1	0	0	0	0	0	0	F7CW38	
ENSMUST00000167280	ENSMUSG00000041538	17	34238903	34245907	1	0	0	0	0	2	4	0	0	0	0	0	E9Q479	
ENSMUST00000167281	ENSMUSG00000000753	11	75409769	75422701	-1	0	0	0	0	0	2	0	0	4	4	5	F6S1M4	
ENSMUST00000167284						3	2	0	12	2	0	0	0	0	0	0		
ENSMUST00000167285						24	16	61	25	28	15	611	1536	538	117	555		
ENSMUST00000167286	ENSMUSG00000019944	10	69151434	69291791	1	1	0	1	1	0	0	0	0	0	0	0	E9PZ17	
ENSMUST00000167287	ENSMUSG00000078588	4	117866524	117872557	-1	0	0	1	1	0	0	0	0	0	0	0	F6ZQN5	
ENSMUST00000167288	ENSMUSG00000000409	4	129548344	129573641	-1	0	0	0	0	0	3	0	0	27	51	1	E9Q696	
ENSMUST00000167290	ENSMUSG00000044600	8	72565188	72571088	-1	19	14	58	27	22	5	404	949	373	278	247		Q5RKS2
ENSMUST00000167293	ENSMUSG00000004364	1	80264923	80340480	-1	1	1	0	0	0	1	45	68	39	1	10	F6ZZK0	
ENSMUST00000167294	ENSMUSG00000051648	8	105382807	105413502	-1	29	0	87	16	32	11	0	1	0	0	0		Q562E2
ENSMUST00000167298	ENSMUSG00000006154	7	4460674	4480487	1	0	0	0	0	0	2	0	0	0	0	0	E9PV13	
ENSMUST00000167299	ENSMUSG00000030769	7	123214780	123273253	1	0	0	45	0	10	0	1	5	3	0	7		Q8K0E3
ENSMUST00000167303	ENSMUSG00000015957	7	98835112	98855195	1	0	0	0	159	13	5	0	0	0	0	4	Q059Y4	P48615
ENSMUST00000167304	ENSMUSG00000024909	19	5473973	5481853	1	6	3	8	17	1	1	23	49	23	4	9	E9Q1U0	
ENSMUST00000167305	ENSMUSG00000048978	13	25252040	25270502	-1	2	0	15	0	0	1	0	0	0	0	0		P97799
ENSMUST00000167309	ENSMUSG00000030766	7	123279218	123369915	-1	0	0	0	0	0	0	190	332	302	36	341	E9QAJ9	
ENSMUST00000167314	ENSMUSG00000091805	17	20462373	20481236	-1	7	10	4	4	6	3	0	0	0	0	0	E9PYS0	
ENSMUST00000167315						9	3	20	14	9	4	14	155	44	3	64		
ENSMUST00000167316	ENSMUSG00000007812	5	145231715	145247302	1	9	8	8	22	12	2	178	610	312	118	119	Q9CZP3	
ENSMUST00000167317	ENSMUSG00000026358	1	144242296	144249242	-1	1	0	0	0	1	1	0	0	0	0	0	E9PZR4	
ENSMUST00000167319						0	2	5	0	4	0	1	17	0	11	4		
ENSMUST00000167320	ENSMUSG00000056724	9	110624789	110654161	-1	2	28	118	369	6	4	5303	3155	4429	5	4266	E9Q9L6	
ENSMUST00000167322	ENSMUSG00000021185	12	100779057	100896981	1	19	14	36	0	0	0	0	36	15	0	0		Q8BH86
ENSMUST00000167323	ENSMUSG00000090698	6	134981718	134986836	1	40	41	202	315	60	34	4	2	6	0	1	E9Q0X2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000167325						0	7	5	8	11	0	8	1	3	4	9		
ENSMUST00000167326	ENSMUSG00000092148	14	42434156	42439673	-1	0	2	12	3	0	0	0	0	0	0	0	F6YKY3	
ENSMUST00000167327	ENSMUSG00000015143	12	80167542	80260371	-1	5	12	29	0	34	12	2611	1407	5467	146	3795	A1BN54	
ENSMUST00000167328						2	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000167332	ENSMUSG00000023942	17	45585200	45599606	-1	5	1	3	0	0	0	0	0	0	0	0	E9Q221	
ENSMUST00000167334	ENSMUSG00000027790	3	72888557	72967863	-1	0	0	0	6	4	0	0	0	0	0	0	F8VQM5	
ENSMUST00000167338	ENSMUSG00000030101	6	108107028	108185582	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q265	
ENSMUST00000167340						4	0	3	3	10	7	0	0	0	0	1		
ENSMUST00000167342	ENSMUSG00000039911	4	149896283	149955043	-1	2	0	2	6	2	1	0	0	0	0	0	E9Q768	
ENSMUST00000167343						7	4	3	7	11	1	0	0	0	0	0		
ENSMUST00000167344						1	2	1	6	0	3	0	0	1	0	3		
ENSMUST00000167346	ENSMUSG00000047412	9	31030644	31075879	1	1	0	0	0	0	0	49	172	116	18	96		Q8R0A2
ENSMUST00000167348	ENSMUSG00000026463	1	133699457	133801041	-1	288	177	626	5522	263	173	2	46	2	0	0	F6V4K0	
ENSMUST00000167352	ENSMUSG00000015575	17	26676396	26699644	1	124	153	143	99	87	64	41	204	77	19	169		Q9CQD8
ENSMUST00000167353	ENSMUSG00000019467	10	127182521	127190054	-1	9	14	69	25	13	0	7	2	0	3	24		
ENSMUST00000167354	ENSMUSG00000027680	3	34019943	34070322	1	1	0	0	17	14	2	128	883	353	978	185	A0A0H2UH27	
ENSMUST00000167355	ENSMUSG00000022661	16	45382135	45409053	-1	0	0	0	0	0	0	0	0	0	0	2	E9PZI9	
ENSMUST00000167358	ENSMUSG00000096481	10	77781850	77782542	-1	11	8	51	87	34	12	0	0	0	0	0	E9Q1M3	
ENSMUST00000167360	ENSMUSG00000032842	17	46303221	46328352	-1	2	0	0	87	0	0	57	56	89	0	58		Q8R4P9
ENSMUST00000167361						0	0	0	0	0	0	31	71	0	48	0		
ENSMUST00000167362						0	0	0	3	0	2	0	0	2	0	0		
ENSMUST00000167363						7	8	42	14	12	13	1	1	2	0	2		
ENSMUST00000167364	ENSMUSG00000033949	18	46165302	46212607	-1	35	34	39	160	66	23	1	2	3	0	5	E9Q3A0	
ENSMUST00000167365						1	3	0	1	3	2	0	0	0	0	0		
ENSMUST00000167366	ENSMUSG00000025515	7	141690340	141754693	1	6	0	10	0	0	0	0	0	0	0	0	F6QGV1	
ENSMUST00000167369	ENSMUSG00000057092	7	31068172	31076704	-1	12	11	11	7	15	7	2	0	0	0	1	Q3TLM3	Q61835
ENSMUST00000167370	ENSMUSG00000031845	8	117095854	117133720	1	0	0	2	0	0	0	0	0	0	1	0	E9Q321	
ENSMUST00000167371	ENSMUSG00000024909	19	5473973	5481853	1	0	0	3	0	0	0	0	0	0	1	14	E9Q3N9	
ENSMUST00000167374	ENSMUSG00000021408	13	34002363	34035170	1	15	16	19	29	11	14	336	1659	667	111	485		Q60855
ENSMUST00000167376	ENSMUSG00000021877	14	26638074	26665084	1	0	0	0	0	0	0	0	7	0	3	0	F6UFB9	
ENSMUST00000167377	ENSMUSG00000030536	7	80711583	80825974	-1	40	34	67	110	68	51	21345	39303	44891	3923	32437		Q9JKF1
ENSMUST00000167379						8	10	0	0	11	0	1957	2817	1445	168	1559		
ENSMUST00000167381						0	0	1	0	0	0	1	0	0	1	0		
ENSMUST00000167382	ENSMUSG00000091670	17	20208230	20234872	-1	8	6	2	4	5	5	0	0	0	0	0	E9Q3A5	
ENSMUST00000167383						6	5	6	6	6	1	0	0	0	0	0		
ENSMUST00000167384	ENSMUSG00000019944	10	69151434	69291791	1	2	1	0	0	0	0	0	0	0	0	9	E9PZ72	
ENSMUST00000167386						0	0	0	0	0	0	101	5	1006	0	1374		
ENSMUST00000167387	ENSMUSG00000004032	3	107895821	107898686	1	0	0	0	0	0	0	0	10	0	0	7	E9PV63	
ENSMUST00000167388	ENSMUSG00000050761	16	18620319	18622403	-1	13	9	16	98	2	5	13	32	33	57	35		P56400
ENSMUST00000167389	ENSMUSG00000058586	15	83089506	83116674	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5R2	
ENSMUST00000167390	ENSMUSG00000053897	3	135825279	135888572	1	7	0	7	29	11	7	0	0	0	4	0		Q91W10
ENSMUST00000167391	ENSMUSG00000030022	6	92772699	92943492	-1	47	47	331	25	33	9	1	5	0	3	19	E9PYV8	
ENSMUST00000167395	ENSMUSG00000018707	12	110601452	110666945	1	0	0	1	0	0	3	7	35	0	0	20	F6ZX84	
ENSMUST00000167397	ENSMUSG00000091563	14	4110526	4132784	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7T1	
ENSMUST00000167399	ENSMUSG00000022871	16	22918382	22939766	1	6	0	0	27	0	5	0	0	0	0	0		Q9QXC1
ENSMUST00000167400	ENSMUSG00000020346	11	49244191	49263030	1	10	0	0	61	0	0	60	42	560	42	60	Q544F0	P27808
ENSMUST00000167401	ENSMUSG00000022106	14	73123037	73207843	1	6	3	44	1	0	4	0	16	5	2	3	E9Q5U1	
ENSMUST00000167403	ENSMUSG00000081058	3	96238108	96239127	-1	0	4	5	161	5	2	12	27	20	4	21	B9EI85	P84228
ENSMUST00000167404						0	3	33	0	0	5	16	58	31	4	34		
ENSMUST00000167405	ENSMUSG00000049580	7	98350668	98361328	-1	0	0	0	31	6	0	0	0	0	0	0	Q08EE6	Q8CBR6
ENSMUST00000167406	ENSMUSG00000091896	18	35771559	35807172	1	0	0	5	0	7	6	0	15	0	0	0	Q3UT95	P62838
ENSMUST00000167409	ENSMUSG00000090868	14	52983201	52983860	1	5	0	0	0	0	1	0	0	0	0	0	A0A075B685	
ENSMUST00000167413						0	0	1	0	3	0	0	0	0	0	0		
ENSMUST00000167414	ENSMUSG00000090497	13	49976258	49976488	-1	0	1	0	4	3	1	0	0	0	0	0	F6ZAF2	
ENSMUST00000167417						0	0	0	0	0	0	0	0	0	21	0		
ENSMUST00000167418	ENSMUSG00000023913	17	43568098	43612201	1	1	0	1	2	0	0	0	11	3	30	5	E9Q4T5	
ENSMUST00000167419	ENSMUSG00000024037	17	31494323	31519974	-1	1	0	5	69	5	4	2	5	0	0	0	E9Q1H7	
ENSMUST00000167421	ENSMUSG00000090805	GL456233.1	25190	25788	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000167423	ENSMUSG00000091922	2	58470116	58471077	1	9	14	24	4	10	5	0	0	0	0	0	Q3V2J7	
ENSMUST00000167426						17	0	25	15	10	0	0	0	0	0	0		
ENSMUST00000167427	ENSMUSG00000017002	2	164354070	164389095	-1	4	2	14	5	16	1	0	0	0	0	0	E9Q4A3	
ENSMUST00000167429						2	2	14	139	6	6	9	31	14	2	9		
ENSMUST00000167430	ENSMUSG00000079402	14	3652030	3673215	1	13	7	2	57	5	8	0	0	0	0	0	Q9CZI1	
ENSMUST00000167431	ENSMUSG00000031553	8	24677225	24725852	-1	0	0	0	0	2	0	0	1	0	0	0	F6TMV4	
ENSMUST00000167432	ENSMUSG00000001225	12	31390871	31473917	1	3	0	0	5	2	4	0	3	0	0	0	E9QAZ3	
ENSMUST00000167433						1	0	2	1	0	2	20	56	11	0	22		
ENSMUST00000167435	ENSMUSG00000004056	7	27591552	27640826	1	0	0	0	20	0	0	845	396	846	99	519	Q3TY95	Q60823
ENSMUST00000167436	ENSMUSG00000060938	11	68901583	68906989	1	0	0	0	0	0	0	0	0	0	5	0	Q4FZH2	P61255
ENSMUST00000167438	ENSMUSG00000080725	X	26912743	26935697	-1	0	0	0	0	0	0	0	0	0	0	0	L7MUF1	
ENSMUST00000167439	ENSMUSG00000025318	8	121729623	121794276	1	10	7	20	307	41	0	4	9	18	4	2		Q9ET77
ENSMUST00000167440	ENSMUSG00000095518	14	41696393	41701885	-1	0	0	0	13	6	0	0	0	0	0	0	F6U3N7	
ENSMUST00000167441	ENSMUSG00000030495	7	35186385	35201114	1	1	1	3	1	0	0	0	0	1	0	0	E9Q1V6	
ENSMUST00000167442						3	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000167443	ENSMUSG00000028541	4	117869260	117883487	-1	0	0	3	16	2	0	0	0	4	0	0	E9Q8H8	
ENSMUST00000167446	ENSMUSG00000047757	X	164980592	164997272	1	4	5	11	20	0	6	14	31	17	13	12	Q3TEX6	
ENSMUST00000167447						19	11	47	48	41	18	150	819	284	39	677		
ENSMUST00000167448	ENSMUSG00000042350	12	84918148	84970900	-1	0	0	8	0	0	0	18	12	29	0	6	E9Q2W2	
ENSMUST00000167449	ENSMUSG00000021910	14	31170930	31216946	-1	5	1	4	3	5	5	4	28	17	4	22	F7AFP3	
ENSMUST00000167455						8	2	10	0	3	4	530	1208	296	24	152		
ENSMUST00000167456						9	8	14	4	14	0	0	20	3	0	10		
ENSMUST00000167457	ENSMUSG00000059475	9	20468549	20492746	-1	41	44	59	53	49	30	12	99	72	4	31	E9Q951	
ENSMUST00000167458	ENSMUSG00000002996	12	31926254	31950535	-1	15	24	29	12	24	10	37	150	78	44	59	E9Q469	
ENSMUST00000167459	ENSMUSG00000022139	14	120275669	120431697	1	10	0	18	40	24	18	971	1273	1063	178	859		Q8C181
ENSMUST00000167460	ENSMUSG00000005220	5	72300025	72504473	-1	11	8	8	8	0	6	0	4	3	0	3		Q9Z319

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000167462	ENSMUSG00000034751	13	102732486	103334497	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q4Q9	
ENSMUST00000167464	ENSMUSG00000091656	17	20267547	20285430	-1	8	3	8	0	3	2	0	0	0	0	0	E9PY92	
ENSMUST00000167466	ENSMUSG00000020964	12	91806043	91849157	-1	0	0	26	0	0	17	255	252	1550	65	925	Q6GTY4	Q9Z2G6
ENSMUST00000167475						8	7	1	2	2	4	0	0	0	0	0		
ENSMUST00000167479	ENSMUSG00000032327	9	58063788	58153996	1	0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000167480						3	0	4	0	0	1	0	2	0	0	0		
ENSMUST00000167481	ENSMUSG00000020232	10	81346048	81350480	-1	0	0	0	0	0	0	0	0	26	22	0	Q3U1L0	Q9Z104
ENSMUST00000167483	ENSMUSG00000018040	15	83113433	83122801	-1	0	8	13	29	7	3	21	41	29	0	26	E9QAX0	
ENSMUST00000167484	ENSMUSG00000029778	6	55451978	55501451	1	2	2	1	119	10	1	0	0	0	0	0		
ENSMUST00000167487	ENSMUSG00000024924	19	27216484	27254231	1	27	26	49	39	28	10	3	32	7	0	3		P98156
ENSMUST00000167488	ENSMUSG00000038214	10	43479140	43515396	1	22	0	22	35	0	0	0	22	14	0	0		Q6PAL0
ENSMUST00000167489	ENSMUSG00000024215	17	27714352	27728951	-1	0	0	0	0	0	0	0	0	0	0	0		Q9WTP3
ENSMUST00000167491	ENSMUSG00000048200	7	141461094	141466613	1	4	2	0	19	0	6	0	0	2	2	4	E9PZB6	
ENSMUST00000167492	ENSMUSG00000068341	6	78375874	78378865	-1	0	1	0	0	0	2	0	0	0	0	0	G3UWG6	
ENSMUST00000167493	ENSMUSG00000038650	7	141160328	141172851	-1	20	0	18	24	19	14	4041	3936	2731	720	1379		Q91VI7
ENSMUST00000167495						3	4	16	7	8	10	79	169	154	9	290		
ENSMUST00000167496	ENSMUSG00000028309	4	49632006	49656887	1	8	0	14	5	9	11	34	269	308	24	75		Q5DTM8
ENSMUST00000167497	ENSMUSG00000029869	6	41605482	41620509	1	4	2	8	0	4	0	0	0	0	0	0	F6W657	
ENSMUST00000167498						10	8	10	9	20	3	7	39	9	13	24		
ENSMUST00000167499						16	10	31	31	20	11	0	0	0	0	3		
ENSMUST00000167501	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	18	22	4	11	2	E9PWX6	
ENSMUST00000167504	ENSMUSG00000091537	9	109074568	109082587	-1	13	6	17	53	11	14	167	444	113	527	86	Q14A47	Q8K003
ENSMUST00000167505	ENSMUSG00000038457	8	13435459	13461452	1	22	7	29	33	21	0	0	0	0	0	0	G3UWB7	
ENSMUST00000167507	ENSMUSG00000034427	11	115858406	115892603	1	7	0	13	7	3	0	2	1	3	1	0	F6Y6G7	
ENSMUST00000167509	ENSMUSG00000018449	11	70970213	70977833	1	0	0	0	0	0	0	3	0	0	26	0	Q0PL81	
ENSMUST00000167511	ENSMUSG00000024858	19	4286001	4306222	-1	0	0	0	0	2	0	6	7	15	0	12	F6Y9P3	
ENSMUST00000167512						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000167513	ENSMUSG00000021432	13	38932140	38960875	-1	0	3	0	83	6	2	71	442	111	194	137		Q922Q5
ENSMUST00000167514	ENSMUSG00000092622	9	73101836	73104438	1	1	1	0	85	1	0	0	0	0	8	0		Q9CWU5
ENSMUST00000167515						1	2	1	22	1	0	0	5	0	0	0		
ENSMUST00000167516	ENSMUSG00000091183	13	62772200	62785808	-1	7	2	4	2	0	1	4	8	6	4	3	F7A0E9	
ENSMUST00000167518	ENSMUSG00000037503	1	34813219	34843065	-1	0	14	193	0	0	0	322	369	617	0	158	G3UWF0	
ENSMUST00000167522						3	0	1	3	0	0	0	0	0	0	0		
ENSMUST00000167523	ENSMUSG00000004032	3	107895821	107898686	1	0	7	2	7	0	0	0	0	7	0	0	E9Q024	
ENSMUST00000167524						2	7	1	2	3	2	0	0	0	0	0		
ENSMUST00000167525	ENSMUSG00000063253	8	83434493	83458391	-1	0	0	0	27	6	0	0	117	27	77	26		Q78YZ6
ENSMUST00000167528	ENSMUSG00000060985	1	156255296	156303664	-1	3	0	52	0	0	10	1	7	5	1	1	J3QPB7	
ENSMUST00000167529	ENSMUSG00000029811	6	48872896	48909188	1	0	22	0	0	0	0	0	0	0	0	0	E9PYN9	
ENSMUST00000167533						1	4	0	5	0	2	3	0	0	0	0		
ENSMUST00000167536	ENSMUSG00000091526	10	58703995	58704279	1	1	0	0	0	0	0	0	0	0	0	0	Q3V0L9	
ENSMUST00000167541	ENSMUSG00000022425	15	54838898	54920146	-1	0	8	0	5	8	7	1	0	2	0	19		Q9R1E6
ENSMUST00000167542	ENSMUSG00000024283	18	7868832	7973547	1	3	0	11	0	0	0	0	0	73	23	13	F7CLA8	
ENSMUST00000167545	ENSMUSG00000001227	17	56123085	56140343	-1	0	0	57	0	46	18	4373	5618	3702	447	3458	Q3UTK5	O54951
ENSMUST00000167546	ENSMUSG00000026641	1	171411313	171419142	1	0	0	12	79	0	0	297	140	336	77	236	Q3UQH7	Q61069
ENSMUST00000167547						55	37	85	81	59	41	83	231	144	12	190		
ENSMUST00000167549	ENSMUSG00000037419	9	14353990	14381242	-1	34	19	43	234	42	13	45	119	60	24	126		Q8C522
ENSMUST00000167550	ENSMUSG00000049694	6	90301219	90305449	1	5	4	51	19	9	7	0	0	0	0	5		Q8C5S3
ENSMUST00000167551	ENSMUSG00000090411	7	23753911	23754852	1	4	3	0	3	2	1	0	0	0	0	0	E9PYW5	
ENSMUST00000167552						3	2	2	1	2	1	0	0	0	0	0		
ENSMUST00000167556	ENSMUSG00000025758	3	40800019	40816883	1	9	8	10	0	9	4	24	54	39	4	37	E9PVH4	Q64702
ENSMUST00000167564						0	0	4	1	0	0	0	0	0	0	0		
ENSMUST00000167565	ENSMUSG00000090641	13	67038594	67061170	-1	9	10	11	34	11	3	14	53	15	12	9	E9PXJ4	
ENSMUST00000167566	ENSMUSG00000094205	5	11770548	11775300	1	0	0	0	0	0	0	0	0	0	0	0	L7MUE8	
ENSMUST00000167567	ENSMUSG00000028926	5	4803391	5420312	-1	5	3	4	0	9	4	0	1	2	6	1	E9Q9M2	
ENSMUST00000167568						5	5	19	6	11	1	0	0	0	0	0		
ENSMUST00000167569	ENSMUSG00000004771	9	64715299	64737758	-1	0	0	0	0	1	0	96	302	44	5	13	E9Q6B3	
ENSMUST00000167571	ENSMUSG00000062203	16	11219292	11254270	-1	9	14	9	135	12	4	34	109	81	9	49		Q8R050
ENSMUST00000167572						4	0	16	110	6	2	4	7	4	0	5		
ENSMUST00000167574	ENSMUSG00000050541	11	43774606	43901210	-1	5	2	59	120	0	0	0	1	1	0	2	Q9DBL0	
ENSMUST00000167577						19	20	0	0	19	1	0	0	0	0	0		
ENSMUST00000167579						2	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000167580	ENSMUSG00000071984	17	7738569	7827302	-1	0	0	0	91	0	0	0	0	0	0	3	E9Q8V0	
ENSMUST00000167582	ENSMUSG00000059895	15	73723145	73758766	1	88	80	174	14	75	30	0	3	0	4	3	E9PXS4	
ENSMUST00000167585						0	0	2	0	0	0	1	0	5	18	0		
ENSMUST00000167588	ENSMUSG00000036913	8	124793019	124834713	1	68	40	169	394	116	65	3	11	3	0	5		Q505D9
ENSMUST00000167589						6	6	10	28	8	4	9	7	19	0	13		
ENSMUST00000167591	ENSMUSG00000063651	7	25367620	25369724	-1	3	4	3	0	4	6	0	0	0	0	0	G3UWC9	
ENSMUST00000167592						4	2	8	2	4	3	0	0	0	0	0		
ENSMUST00000167593	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	0	0	0	0	0	0	7	0	0	E9PYF9	
ENSMUST00000167594						0	0	2	0	0	0	43	0	182	0	194		
ENSMUST00000167595	ENSMUSG00000025241	9	123789510	123851899	-1	0	0	0	297	43	0	149	647	400	30	408		Q8VDC1
ENSMUST00000167596	ENSMUSG00000000204	11	83175186	83190221	1	44	43	295	351	29	13	6382	57473	15417	7797	20904	Q3UV66	
ENSMUST00000167597						1	0	0	0	0	0	0	4	2	2	2		
ENSMUST00000167598	ENSMUSG00000042306	3	90526856	90528837	1	7	3	0	6	4	5	0	6	1	3	0		Q9D2Q8
ENSMUST00000167599						2	0	1	1	0	2	0	0	0	0	0		
ENSMUST00000167602						2	4	8	4	3	4	0	0	1	0	1		
ENSMUST00000167607	ENSMUSG00000026668	2	4976122	4985748	1	3	0	21	8	5	0	0	0	0	0	0		Q14BU0
ENSMUST00000167608	ENSMUSG00000079652	6	29279593	29290680	1	2	0	0	7	0	0	0	3	0	0	0	E9Q5P2	
ENSMUST00000167610	ENSMUSG00000024610	18	60803848	60812646	1	0	0	0	0	0	0	0	0	0	0	0	Q3U4Q8	P04441
ENSMUST00000167611	ENSMUSG00000079557	17	33685692	33718670	-1	7	8	23	0	0	0	6	0	5	0	0	Q8CA25	
ENSMUST00000167612	ENSMUSG00000020111	10	59702477	59864132	1	0	1	4	5	0	0	2	1	1	0	2	F6Z1Z9	
ENSMUST00000167615	ENSMUSG00000093833	14	41550120	41555583	-1	0	2	0	12	2	0	0	0	0	0	0	L7N271	
ENSMUST00000167617	ENSMUSG00000094715	14	51606066	51611310	-1	3	3	0	6	3	0	0	0	0	0	0	M0QW51	
ENSMUST00000167618	ENSMUSG00000091096	5	106609098	106609201	1	2	2	2	2	0	1	0	1	1	0	0	F6VDB5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000167619	ENSMUSG00000034480	X	129749742	130465834	1	19	0	0	231	109	0	0	113	75	28	88	E9Q4U7	
ENSMUST00000167622						7	3	14	14	6	5	0	0	0	0	0		
ENSMUST00000167623	ENSMUSG00000040420	15	22549022	23474418	1	0	0	0	0	0	0	0	0	0	0	0	F6RSC2	
ENSMUST00000167624	ENSMUSG00000024026	17	30592866	30612659	-1	0	0	14	45	3	5	32	57	63	244	13	A5GZX3	Q9CPU0
ENSMUST00000167626	ENSMUSG00000025730	17	25882114	25919727	-1	0	0	0	24	0	0	0	44	0	0	0	Q0PD11	Q8VHQ4
ENSMUST00000167628	ENSMUSG00000038388	6	50110241	50198939	1	5	0	14	22	1	4	0	0	0	0	0	E9PWC5	
ENSMUST00000167629						1	2	2	0	3	0	0	0	0	0	0		
ENSMUST00000167633	ENSMUSG00000031872	8	104170513	104219092	1	0	0	74	0	0	0	0	0	0	0	0		Q9EQG5
ENSMUST00000167634	ENSMUSG00000022589	15	74851010	74856318	-1	10	13	34	8	24	4	0	0	0	0	0	G3UWE4	
ENSMUST00000167635						5	0	0	1	1	2	0	20	0	0	12		
ENSMUST00000167636	ENSMUSG00000006390	4	118428093	118432953	1	0	0	0	0	0	4	1550	1967	1178	222	570	Q548M4	Q9JLJ5
ENSMUST00000167638	ENSMUSG00000091008	6	42980690	42981150	1	0	3	0	0	0	1	0	0	0	0	0	A0A075B683	
ENSMUST00000167639						7	9	17	29	22	0	0	0	0	0	0		
ENSMUST00000167641	ENSMUSG00000052525	17	71552061	71589533	1	0	0	0	0	0	0	0	0	0	0	0		Q5IBH7
ENSMUST00000167642						0	0	0	0	5	0	21	0	67	28	28		
ENSMUST00000167643	ENSMUSG00000091780	15	89371639	89373818	-1	4	0	0	5	6	2	14	11	4	10	9		Q8VCL2
ENSMUST00000167644						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000167645						0	0	4	0	0	0	0	0	12	7	14		
ENSMUST00000167646	ENSMUSG00000002985	7	19696109	19699166	-1	0	0	0	0	0	0	1179	1158	643	1513	2731	E9Q327	
ENSMUST00000167648						16	3	33	3	5	6	0	0	0	0	0		
ENSMUST00000167650						0	4	1	1	6	3	0	0	0	0	0		
ENSMUST00000167652	ENSMUSG00000038371	7	110308013	110614922	-1	1	0	0	0	0	0	0	0	0	0	0	E9Q4I8	
ENSMUST00000167655						8	0	21	7	4	2	55	59	70	4	72		
ENSMUST00000167656						212	169	1067	213	315	116	70	276	80	22	92		
ENSMUST00000167658						16	9	94	39	26	11	0	0	0	0	6		
ENSMUST00000167659	ENSMUSG00000031109	X	49009707	49288259	-1	7	3	7	1	5	0	0	6	0	10	0		Q8R0Z2
ENSMUST00000167661	ENSMUSG00000015790	2	26913381	26916530	-1	0	0	0	0	0	0	62	115	28	87	19		
ENSMUST00000167662	ENSMUSG00000001576	17	26561489	26656931	1	19	4	41	44	22	14	360	339	282	64	375	Q4FK22	Q9DC16
ENSMUST00000167664	ENSMUSG00000031434	X	139821632	139871677	-1	1	1	0	0	1	0	0	0	0	1	0	F6WL51	
ENSMUST00000167667	ENSMUSG00000035086	11	101285952	101302286	-1	0	0	0	0	0	0	0	156	37	0	15	E9PX06	
ENSMUST00000167668						0	0	0	0	0	0	3	30	10	12	9		
ENSMUST00000167669	ENSMUSG00000095593	10	77776252	77776944	-1	19	6	56	64	19	0	0	0	0	0	0	L7N2C3	
ENSMUST00000167670						13	10	36	22	13	13	2	1	3	2	4		
ENSMUST00000167671	ENSMUSG00000046841	10	84526305	84534036	-1	6	9	39	125	10	0	1642	0	2580	65	1112		Q8BMK4
ENSMUST00000167673	ENSMUSG00000054293	X	107148927	107173661	1	0	0	0	0	0	0	18	0	48	65	41	Q8BY68	
ENSMUST00000167674	ENSMUSG00000032567	9	105395392	105412229	1	0	0	0	0	0	3	0	0	0	0	5	E9Q1A4	
ENSMUST00000167675						3	1	0	1	2	3	0	0	1	0	0		
ENSMUST00000167676						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000167677						1	0	1	124	4	4	1	0	0	0	0		
ENSMUST00000167678	ENSMUSG00000025142	11	120672973	120709447	1	13	5	8	0	13	3	12	23	18	0	14	F7B7K7	
ENSMUST00000167679	ENSMUSG00000030223	6	137252319	137463233	1	32	24	70	162	42	0	5	19	15	13	13	E9Q4I1	
ENSMUST00000167681						0	3	0	0	0	0	0	0	4	0	0		
ENSMUST00000167682	ENSMUSG00000050954	13	48487647	48513451	-1	0	0	0	0	0	0	0	0	0	0	0	G5E912	
ENSMUST00000167683	ENSMUSG00000082211	8	21315546	21316481	1	0	0	0	0	0	0	0	0	0	0	0	F2Z403	
ENSMUST00000167685						3	1	1	1	4	0	0	0	0	0	0		
ENSMUST00000167686	ENSMUSG00000082976	8	20900606	20902444	-1	1	2	0	1	2	0	0	0	0	0	2	E9Q8Z3	
ENSMUST00000167688	ENSMUSG00000000303	8	106603351	106670246	1	0	0	0	0	9	0	0	0	0	0	9		
ENSMUST00000167689	ENSMUSG00000042570	10	79540245	79555199	-1	5	2	8	6	0	0	0	0	1	0	2	E9QAB1	
ENSMUST00000167690						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000167691	ENSMUSG00000030325	6	128778485	128789215	-1	15	8	16	14	16	7	0	21	2	3	9	E9Q3U6	
ENSMUST00000167692	ENSMUSG00000023942	17	45585200	45599606	-1	4	0	0	0	0	0	28	0	7	0	20		Q9JIM1
ENSMUST00000167694	ENSMUSG00000078940	2	164662894	164674087	-1	0	0	0	0	0	0	0	0	0	0	0		A2A5H7
ENSMUST00000167695	ENSMUSG00000053580	11	105589986	105929304	1	0	0	0	0	3	0	0	0	0	0	0	F6ZIH9	
ENSMUST00000167699	ENSMUSG00000021911	14	32201949	32297550	1	2	4	0	0	0	0	0	4	0	0	2	E9Q7T9	
ENSMUST00000167703	ENSMUSG00000031553	8	24677225	24725852	-1	0	0	0	0	0	0	0	0	0	0	0	E9PYS3	
ENSMUST00000167705						0	2	6	0	2	0	1	5	4	0	7		
ENSMUST00000167706	ENSMUSG00000020166	10	116485161	116581511	-1	0	1	0	0	0	0	0	0	78	0	0	E9Q8D5	
ENSMUST00000167707	ENSMUSG00000035835	10	79860475	79874634	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVZ4	
ENSMUST00000167708	ENSMUSG00000046876	13	45549758	45964991	-1	85	0	395	263	0	54	0	225	0	3	262		P54254
ENSMUST00000167709						1	1	5	2	0	0	0	0	0	0	0		
ENSMUST00000167711	ENSMUSG00000025316	8	121949750	122029258	1	0	0	9	0	3	0	0	35	0	5	0	F6V6B6	
ENSMUST00000167712	ENSMUSG00000091657	14	41619286	41624612	-1	0	0	0	2	28	0	0	0	0	0	0	F6SKY8	
ENSMUST00000167713	ENSMUSG00000090897	17	40561507	40579549	1	2	5	1	1	4	1	0	0	0	0	0	A8R0T9	
ENSMUST00000167715	ENSMUSG00000042557	9	57072040	57128366	1	0	22	0	0	15	0	250	395	794	0	427		Q60520
ENSMUST00000167717						20	0	0	14	0	1	59	0	0	0	0		
ENSMUST00000167718						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000167719						1	0	9	3	4	1	0	0	0	0	1		
ENSMUST00000167721	ENSMUSG00000029580	5	142903115	142906754	-1	6	0	0	0	0	6	14678	0	10269	0	6563	E9Q1F2	
ENSMUST00000167723	ENSMUSG00000026070	1	40465552	40500854	1	5	0	19	12	6	3	4	15	18	7	6	Q8C257	
ENSMUST00000167724	ENSMUSG00000024811	19	36834232	36893477	1	0	0	0	0	0	0	0	0	96	3	59	F6YVU7	
ENSMUST00000167731	ENSMUSG00000022346	15	61985341	61990374	1	11	9	26	93	15	0	28	35	44	0	48	F6PX41	
ENSMUST00000167732						0	0	3	1	1	0	0	30	41	7	25		
ENSMUST00000167734						16	12	10	30	25	5	0	0	0	0	0		
ENSMUST00000167740	ENSMUSG00000071266	17	22424222	22456689	1	5	0	1	3	4	0	2	20	1	0	1	Q8K3B4	
ENSMUST00000167741	ENSMUSG00000024248	17	83501919	83514333	-1	0	0	19	11	8	0	0	35	0	7	0	E9PZS8	
ENSMUST00000167744						0	0	0	70	0	0	0	0	0	0	0		
ENSMUST00000167746	ENSMUSG00000016756	13	24327420	24477285	1	7	88	206	112	112	88	1025	1255	34	319	14		Q61419
ENSMUST00000167748						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000167749	ENSMUSG00000023882	17	21423227	21435640	1	0	0	2	1	0	2	3	2	6	0	1	E9Q520	
ENSMUST00000167750						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000167751	ENSMUSG00000028466	4	43562332	43567060	1	0	0	0	3	0	4	309	537	234	442	203	E9PW77	
ENSMUST00000167753	ENSMUSG00000090817	3	98445675	98457126	-1	15	14	0	0	0	17	0	0	0	0	0	E9Q007	
ENSMUST00000167754	ENSMUSG00000022565	15	76170974	76232574	-1	2	0	6	40	5	2	6	0	4	0	7		
ENSMUST00000167755	ENSMUSG00000021071	12	70244539	70347614	-1	69	78	79	351	75	42	0	0	0	1	2	E9Q524	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000167759	ENSMUSG00000032637	7	126491708	126503437	-1	9	3	64	145	19	8	944	3853	1287	82	1708	Q3TGG2	
ENSMUST00000167760						7	7	25	14	8	10	3	8	1	0	8		
ENSMUST00000167761						0	15	23	54	16	1	0	2	0	0	1		
ENSMUST00000167764	ENSMUSG00000031565	8	25513654	25575714	1	0	0	0	0	0	0	0	0	5	0	19		P16092
ENSMUST00000167766	ENSMUSG00000039470	8	40423815	40510268	1	0	0	0	0	0	0	0	10	3	5	0		P59267
ENSMUST00000167767	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	29	11	48	0	0	F6UY70	
ENSMUST00000167771	ENSMUSG00000091045	7	12651706	12684991	-1	533	397	8815	780	352	160	1	4	8	0	6	E9PXC1	
ENSMUST00000167772						8	1	1	23	35	0	0	0	0	0	0		
ENSMUST00000167773	ENSMUSG00000032393	9	65032458	65082650	1	4	0	7	56	8	2	76	106	558	0	329		Q80YA7
ENSMUST00000167776	ENSMUSG00000024642	19	14448072	14598051	-1	13	7	25	19	13	0	50	84	195	52	216	F6ZBY9	
ENSMUST00000167778	ENSMUSG00000000884	16	18498768	18566679	1	0	0	0	79	0	0	0	0	0	0	0		Q9EQ15
ENSMUST00000167780	ENSMUSG00000023087	3	51224447	51251644	1	0	3	0	0	0	3	4	13	6	1	7	B2RTJ8	O35710
ENSMUST00000167781						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000167786	ENSMUSG00000030470	7	48830398	48848051	-1	0	10	0	0	0	0	0	0	0	0	0	Q545C7	P50462
ENSMUST00000167787	ENSMUSG00000018363	11	106820066	106920715	-1	0	0	8	0	5	0	65	100	254	17	146		A2A5Z6
ENSMUST00000167789						3	0	14	5	0	0	0	0	0	0	0		
ENSMUST00000167790	ENSMUSG00000038580	7	141278331	141279133	-1	0	0	3	0	1	2	0	0	0	0	0	Q3UKU8	Q08535
ENSMUST00000167791	ENSMUSG00000036473	17	24175431	24209387	-1	10	0	0	0	0	0	0	0	0	0	0		Q3UUG6
ENSMUST00000167792	ENSMUSG00000023827	17	12118704	12219645	1	0	1	5	0	3	2	13	0	1	0	0	E9Q2T9	
ENSMUST00000167794						0	1	6	0	2	1	40	450	164	44	74		
ENSMUST00000167796						0	0	0	1	0	0	84	250	93	229	39		
ENSMUST00000167797	ENSMUSG00000020359	11	51584757	51604489	1	19	11	70	67	15	6	7	35	8	13	26		Q8R1K4
ENSMUST00000167799	ENSMUSG00000022401	15	81400138	81456807	1	0	0	0	0	0	0	0	0	0	0	0	E9Q1R1	
ENSMUST00000167804	ENSMUSG00000061374	7	5007057	5014697	-1	0	8	0	8	0	0	94	0	47	23	23	Q3TRV0	Q9WTJ4
ENSMUST00000167805						0	0	0	1	0	0	0	6	0	1	0		
ENSMUST00000167806	ENSMUSG00000001441	11	97205842	97280638	-1	0	0	0	0	0	0	7	3	5	0	0	E9Q6F4	
ENSMUST00000167810	ENSMUSG00000006154	7	4460674	4480487	1	0	4	2	3	2	0	0	0	0	0	0	E9PWX4	
ENSMUST00000167812	ENSMUSG00000026358	1	144242296	144249242	-1	0	0	3	3	0	0	0	3	0	2	0	A0A087WQQ4	
ENSMUST00000167813						0	3	3	0	0	1	0	0	0	2	0		
ENSMUST00000167815						0	1	4	4	0	2	0	0	3	0	0		
ENSMUST00000167816	ENSMUSG00000040877	12	108894272	109028452	1	43	21	185	38	61	14	43	66	31	8	31		E9Q349
ENSMUST00000167817	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	0	0	0	0	0	0	0	0	0	F6VLR8	
ENSMUST00000167818	ENSMUSG00000035086	11	101285952	101302286	-1	0	0	0	0	0	0	196	213	304	90	279	E9PX06	
ENSMUST00000167819						0	0	0	11	0	0	0	0	0	0	0		
ENSMUST00000167820	ENSMUSG00000025159	19	41941086	41981157	-1	0	0	0	0	0	0	0	0	0	0	0	F6RGK4	
ENSMUST00000167824	ENSMUSG00000021700	13	110054187	110280206	-1	275	182	1518	862	241	137	3	35	3	1	11	Q542T7	P62823
ENSMUST00000167827	ENSMUSG00000024909	19	5473973	5481853	1	1	0	12	6	0	0	0	6	0	0	0	E9Q2T8	
ENSMUST00000167828						0	1	0	0	1	0	0	1	0	0	0		
ENSMUST00000167829						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000167830	ENSMUSG00000090436	7	86148042	86171724	-1	6	8	5	3	5	3	0	0	0	0	0	G5E8Z7	
ENSMUST00000167833	ENSMUSG00000091617	14	7466362	7483762	-1	0	0	0	0	0	0	0	0	0	0	0	E9PZQ5	
ENSMUST00000167838						0	0	0	0	1	0	0	49	0	4	9		
ENSMUST00000167839	ENSMUSG00000090764	14	4165030	4173503	1	0	0	0	0	0	0	0	0	0	0	0	K7N6U7	
ENSMUST00000167840						0	0	0	0	0	0	645	1360	468	38	408		
ENSMUST00000167841	ENSMUSG00000026814	2	32646595	32682669	1	0	0	0	28	0	0	0	26	0	38	26	Q3UAM9	
ENSMUST00000167842	ENSMUSG00000022249	15	10500102	10558668	-1	0	3	0	0	0	0	0	0	0	0	0	F6SJC5	
ENSMUST00000167843						162	135	162	909	216	107	0	4	0	0	5		
ENSMUST00000167845						3	7	9	9	10	8	0	0	0	0	0		
ENSMUST00000167846	ENSMUSG00000023403	6	49395604	49469501	1	0	2	0	0	0	0	0	0	0	0	0	F6QH34	
ENSMUST00000167847						0	2	15	6	8	0	0	0	0	0	0		
ENSMUST00000167849						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000167850	ENSMUSG00000055681	8	70302518	70312993	1	0	1	0	0	0	0	13	24	0	2	12	F6XIG5	
ENSMUST00000167855	ENSMUSG00000024909	19	5473973	5481853	1	0	0	0	0	0	0	14	0	3	0	0	E9Q2A0	
ENSMUST00000167856	ENSMUSG00000000631	11	77763246	77865980	1	13	9	25	12	21	8	0	13	10	45	99	E9QA74	
ENSMUST00000167858	ENSMUSG00000027550	3	14533788	14572658	1	9	2	1	3	3	3	0	9	2	5	3	F7ANC5	
ENSMUST00000167859	ENSMUSG00000039878	10	128395934	128401224	-1	0	0	60	26	16	9	0	0	0	0	0		Q9D856
ENSMUST00000167860	ENSMUSG00000023951	17	46016993	46032377	-1	24	9	12	142	8	0	7	194	122	25	86	F6ZE01	
ENSMUST00000167861	ENSMUSG00000036748	19	46329812	46338660	-1	20	4	40	35	26	7	835	1380	730	231	518		Q9CXX9
ENSMUST00000167862	ENSMUSG00000058586	15	83089506	83116674	1	10	12	13	3	6	2	0	0	0	0	0	E9Q2Z9	
ENSMUST00000167863						0	0	0	0	0	2	0	2	0	0	0		
ENSMUST00000167866	ENSMUSG00000032279	9	54586511	54604661	1	19	4	19	29	17	7	107	302	164	107	126		Q9D6R2
ENSMUST00000167868	ENSMUSG00000010064	9	107650634	107669530	-1	7	17	16	9	19	10	0	0	0	0	0		Q9DCP2
ENSMUST00000167869						3	5	2	8	3	0	0	4	0	0	2		
ENSMUST00000167871	ENSMUSG00000095931	7	22842688	22843605	-1	0	0	0	0	0	0	0	0	0	0	0	K7N701	
ENSMUST00000167872						61	62	158	64	84	41	0	3	7	1	5		
ENSMUST00000167875	ENSMUSG00000005233	2	69193895	69206194	-1	0	0	0	0	0	0	0	0	0	0	0		Q3UA16
ENSMUST00000167876	ENSMUSG00000015749	3	95929246	95947390	1	0	0	0	0	0	1	39	175	109	139	79	E9PZF5	
ENSMUST00000167877	ENSMUSG00000028007	3	117781647	117868936	-1	7	2	3	0	0	2	0	22	6	10	11	F7D3B8	
ENSMUST00000167879	ENSMUSG00000000915	5	123973628	124005558	1	0	1	3	0	2	2	0	0	0	0	0	E9Q3C5	
ENSMUST00000167880						343	326	638	270	414	203	3	17	15	1	13		
ENSMUST00000167882	ENSMUSG00000096839	14	6613967	6622418	-1	0	12	11	4	6	0	0	0	0	0	0	E9QAI8	
ENSMUST00000167883						2	3	0	1	1	0	0	0	0	3	0		
ENSMUST00000167885	ENSMUSG00000007656	9	75037614	75060313	1	2	0	3	0	2	2	8	20	0	3	15		P56212
ENSMUST00000167887	ENSMUSG00000066392	12	88722876	90334935	1	0	0	0	0	0	3	0	0	0	0	0		Q6P9K9
ENSMUST00000167888	ENSMUSG00000030688	7	101317086	101346626	1	0	0	0	0	0	0	0	15	0	6	23	G3UW37	
ENSMUST00000167891	ENSMUSG00000021255	12	86361117	86521628	1	0	0	3	19	2	0	0	0	0	0	0		Q61539
ENSMUST00000167893	ENSMUSG00000029821	6	50188888	50263862	-1	3	6	9	64	4	2	49	69	84	26	60	E9Q308	
ENSMUST00000167895						6	0	0	0	3	2	0	0	0	0	0		
ENSMUST00000167897	ENSMUSG00000035835	10	79860475	79874634	-1	0	0	0	0	0	0	0	0	0	0	0	E9PZA9	
ENSMUST00000167898						19	13	28	25	20	10	0	0	0	0	0		
ENSMUST00000167899	ENSMUSG00000091514	8	25754509	25769704	1	11	14	33	47	24	11	0	16	5	3	5	E9Q7H2	
ENSMUST00000167902	ENSMUSG00000091148	14	4481745	4490177	1	26	26	5	3	8	7	0	0	0	0	0	K7N6T8	
ENSMUST00000167903						2	0	1	0	3	4	0	33	0	0	2		
ENSMUST00000167905						3	0	4	0	6	4	2	0	0	4	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000167906	ENSMUSG00000090592	9	13444034	13446753	-1	996	666	11891	1447	340	148	0	1	0	0	0	F6T7Q8	
ENSMUST00000167908	ENSMUSG00000091897	5	15028950	15032998	-1	6	8	27	20	7	20	0	0	0	0	0	K7N6W5	
ENSMUST00000167909						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000167911						0	0	0	32	3	0	171	751	511	157	227		
ENSMUST00000167912	ENSMUSG00000037664	7	143458350	143461050	-1	0	0	11	619	0	0	0	0	0	0	0		P49919
ENSMUST00000167913	ENSMUSG00000079371	14	6105321	6125807	-1	18	14	0	6	10	0	0	0	0	0	0	K7N6V0	
ENSMUST00000167914	ENSMUSG00000097565	13	67491152	67526151	-1	0	0	0	0	0	0	0	0	4	0	0	M0QWH4	
ENSMUST00000167915	ENSMUSG00000057337	10	60181532	60219260	-1	0	0	0	11	0	0	0	0	0	0	0		O88199
ENSMUST00000167916	ENSMUSG00000074424	3	94174412	94178193	-1	7	9	12	9	0	7	0	0	0	0	1	Q3UTC4	
ENSMUST00000167918	ENSMUSG00000029405	5	92052146	92083719	-1	0	5	0	142	0	5	0	0	0	9	0	Q542W3	P97379
ENSMUST00000167920						3	0	7	108	0	2	0	0	0	0	7		
ENSMUST00000167921	ENSMUSG00000044646	18	75820178	76148561	1	7	3	6	368	18	4	0	0	0	1	3		Q8VCZ7
ENSMUST00000167923	ENSMUSG00000092167	14	7083208	7100621	-1	0	0	0	0	0	2	0	0	0	0	0	K7N751	
ENSMUST00000167924	ENSMUSG00000024401	17	35199381	35202007	-1	2	0	27	0	0	0	9	0	59	0	0		
ENSMUST00000167925	ENSMUSG00000005364	6	106710357	106749037	-1	15	11	50	9	16	6	0	1	0	3	6	Q05A81	P21183
ENSMUST00000167926	ENSMUSG00000028937	4	152178134	152271855	1	8	8	20	8	13	7	0	12	0	0	18	E9PYH2	
ENSMUST00000167927	ENSMUSG00000025159	19	41941086	41981157	-1	106	99	499	150	122	58	76	521	169	15	205	E9PW47	
ENSMUST00000167929	ENSMUSG00000021898	14	26894557	26915258	1	2	1	2	2	0	0	0	0	0	0	0	E9Q6H3	
ENSMUST00000167930	ENSMUSG00000060279	7	44900374	44929490	-1	0	0	0	118	0	0	0	409	50	44	252		P17426
ENSMUST00000167935	ENSMUSG00000030945	7	119554469	119600694	1	0	48	118	238	111	55	0	0	0	0	0		Q8K0L3
ENSMUST00000167936						0	3	0	3	0	0	0	0	0	0	0		
ENSMUST00000167937	ENSMUSG00000039474	5	36966104	36989205	-1	0	3	0	0	0	0	0	0	0	0	2	F7D926	
ENSMUST00000167940	ENSMUSG00000019214	17	25718926	25727419	-1	0	0	0	0	0	0	0	2	0	2	5	F6ZBE7	
ENSMUST00000167941						4	3	0	0	7	1	0	0	0	0	0		
ENSMUST00000167943	ENSMUSG00000052798	10	117750624	117792705	-1	0	1	0	0	0	0	0	0	0	0	0	E9Q4V9	
ENSMUST00000167944	ENSMUSG00000051323	X	133582860	133688987	-1	0	2	8	0	5	1	0	0	0	0	0	E9Q5E1	
ENSMUST00000167946	ENSMUSG00000040118	5	15934691	16374511	1	1	20	0	1	1	0	0	0	0	0	0	E9Q1X8	
ENSMUST00000167947	ENSMUSG00000029028	4	154011731	154021513	1	0	0	0	0	0	0	33	9	17	0	0	F6Z4L9	
ENSMUST00000167950	ENSMUSG00000070780	5	66016549	66173118	-1	0	6	149	1	37	0	550	938	525	95	603		Q91WT8
ENSMUST00000167951	ENSMUSG00000090470	9	98864767	98866583	1	6	3	15	148	13	7	0	0	0	0	1		Q9CWP9
ENSMUST00000167955	ENSMUSG00000037640	7	27731389	27753702	1	0	0	0	0	0	0	5	0	0	0	9	Q8K0D9	
ENSMUST00000167956	ENSMUSG00000040899	17	8236043	8257127	1	0	9	0	8	13	0	3	0	2	2	21	Q542B6	O54689
ENSMUST00000167959	ENSMUSG00000078938	15	89390174	89410503	-1	0	0	5	12	0	1	0	0	0	0	0	E7D6R1	B5KM66
ENSMUST00000167962	ENSMUSG00000023460	17	66494512	66519717	-1	7	6	2	0	0	0	77	311	148	41	123		P35283
ENSMUST00000167963						0	2	9	0	3	1	6	50	8	7	13		
ENSMUST00000167964						12	16	26	30	23	14	4	4	11	0	25		
ENSMUST00000167965	ENSMUSG00000030782	7	128246812	128255699	1	0	0	0	0	0	0	0	8	0	0	0		Q62219
ENSMUST00000167967						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000167968	ENSMUSG00000022382	15	85535439	85581821	-1	6	15	29	187	23	11	0	0	0	0	0	E9Q5E3	
ENSMUST00000167969	ENSMUSG00000090963	5	110046232	110046486	-1	0	1	0	2	1	0	1	6	3	0	1	F7BFU5	
ENSMUST00000167970						0	0	0	54	3	1	0	0	0	0	0		
ENSMUST00000167971	ENSMUSG00000038305	1	57774162	57948394	1	0	0	0	88	3	0	0	0	0	0	0	E9Q8P1	
ENSMUST00000167972	ENSMUSG00000058440	6	30047988	30153458	1	0	0	0	0	0	0	25	0	111	2	26		Q9WU00
ENSMUST00000167974	ENSMUSG00000094295	10	129965736	129966698	-1	10	0	5	8	7	10	0	0	0	0	0	K7N727	
ENSMUST00000167975						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000167976	ENSMUSG00000091381	10	79468943	79492154	1	7	7	8	3	8	4	0	0	0	0	0	E9Q0G7	
ENSMUST00000167977	ENSMUSG00000033016	18	80606205	80713071	-1	20	0	74	0	2	10	1745	2071	2145	138	1724	B5B2N7	
ENSMUST00000167978	ENSMUSG00000021263	12	108686792	108702306	-1	17	18	32	22	37	7	4	41	4	5	45		Q8R2F2
ENSMUST00000167979						6	8	21	5	7	9	11	8	19	1	80		
ENSMUST00000167981	ENSMUSG00000091347	13	66227319	66227573	-1	4	2	0	4	6	0	0	0	0	0	0	F7AIG4	
ENSMUST00000167984	ENSMUSG00000004561	14	51884842	51893039	1	0	0	0	2	0	0	0	0	2	0	0	E9PYZ3	
ENSMUST00000167985						0	0	2	0	0	0	0	0	4	0	0		
ENSMUST00000167986	ENSMUSG00000078945	13	100144063	100202092	-1	0	0	0	0	0	0	268	201	382	137	180	A9C471	
ENSMUST00000167987	ENSMUSG00000020323	10	79781474	79790961	-1	0	0	0	0	2	0	10	7	0	0	5	F6R4F9	
ENSMUST00000167990						18	25	63	27	30	13	21	20	45	5	78		
ENSMUST00000167992	ENSMUSG00000039530	8	39005867	39165112	1	4	2	6	137	6	0	33	98	27	152	67		Q8BTV1
ENSMUST00000167993	ENSMUSG00000023918	17	42656891	42692284	-1	0	9	0	14	0	0	0	0	0	0	0	A0A0D9SEG9	
ENSMUST00000167994	ENSMUSG00000051977	17	15543079	15564354	-1	85	65	126	95	92	31	17	158	52	13	68	E9Q4V2	
ENSMUST00000167995	ENSMUSG00000090987	10	100396287	100397072	-1	4	5	28	9	4	5	0	0	0	0	0	L7N2D7	
ENSMUST00000167998	ENSMUSG00000028048	3	89202928	89208966	1	11	0	26	12	22	12	119	228	127	47	130		P17439
ENSMUST00000168002	ENSMUSG00000079655	X	26028214	26051041	-1	0	0	0	0	0	0	0	0	0	0	0	Q4KL04	
ENSMUST00000168003	ENSMUSG00000063415	6	84571414	84593908	-1	15	29	71	55	43	0	0	2	0	2	17		Q811W2
ENSMUST00000168005	ENSMUSG00000031024	7	109523911	109617147	-1	1	5	0	1	2	0	0	5	1	2	4		Q924W7
ENSMUST00000168007	ENSMUSG00000043366	7	102740721	102759471	-1	11	0	13	12	1	9	0	0	0	0	0		Q8VBV9
ENSMUST00000168010						1	0	22	8	4	5	0	0	0	0	0		
ENSMUST00000168012						3	2	48	55	0	0	0	168	41	22	23		
ENSMUST00000168013	ENSMUSG00000031858	8	70016123	70042734	-1	0	82	0	52	84	41	715	1537	865	173	959	Z4YNA3	
ENSMUST00000168015	ENSMUSG00000002227	3	104794836	104818563	-1	0	0	0	0	1	0	1240	2923	874	129	1317		P23249
ENSMUST00000168016						6	11	7	9	9	7	0	0	0	0	0		
ENSMUST00000168018	ENSMUSG00000055681	8	70302518	70312993	1	0	0	0	0	0	0	446	362	156	101	212	E9Q6I5	
ENSMUST00000168019						0	0	25	0	0	3	142	934	471	1330	500		
ENSMUST00000168020						0	0	0	0	0	0	65	110	57	119	73		
ENSMUST00000168029	ENSMUSG00000058586	15	83089506	83116674	1	0	1	0	2	0	1	0	0	0	0	0	E9Q8E7	
ENSMUST00000168031						7	1	9	9	5	2	3	273	396	138	362		
ENSMUST00000168032	ENSMUSG00000028456	4	43058953	43264871	1	0	0	0	0	0	0	0	0	0	0	0	F6X605	
ENSMUST00000168033	ENSMUSG00000091945	17	23290934	23312313	-1	13	14	3	0	7	6	0	0	0	0	0	E9Q281	
ENSMUST00000168034	ENSMUSG00000056234	14	32159865	32179855	1	0	0	0	0	0	1	0	0	0	9	0	E9PVM8	
ENSMUST00000168036	ENSMUSG00000020166	10	116485161	116581511	-1	0	0	0	0	0	0	0	0	148	36	73	E9Q027	
ENSMUST00000168037						3	4	7	20	9	1	0	0	0	0	0		
ENSMUST00000168038	ENSMUSG00000027956	3	79812564	79852773	-1	5	3	0	0	10	0	2	0	0	0	1		Q8VEH0
ENSMUST00000168039	ENSMUSG00000032006	9	6168612	6378843	1	3	4	4	4	3	2	0	0	0	0	0		Q925I7
ENSMUST00000168043	ENSMUSG00000056648	11	96281905	96285315	1	0	0	2	79	0	0	0	0	0	0	0	A2A9Z8	P09632
ENSMUST00000168044	ENSMUSG00000043557	17	29827956	29970087	-1	0	0	0	0	0	0	4	0	0	0	4	F7ABV5	
ENSMUST00000168045	ENSMUSG00000073794	4	98818475	98823840	-1	0	0	0	0	0	0	0	0	0	0	0	A6PWL3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000168047	ENSMUSG00000036622	4	140986873	141007330	1	8	10	11	21	13	12	60	30	36	0	62	E9PYX5	
ENSMUST00000168049	ENSMUSG00000090471	7	142165024	142165737	-1	25	17	238	236	32	17	0	0	0	0	0	A7MAW9	
ENSMUST00000168050	ENSMUSG00000090315	17	20029425	20048205	-1	4	9	8	2	6	3	0	0	0	0	0	E9Q2J5	
ENSMUST00000168052						0	0	2	0	0	0	0	0	0	0	4		
ENSMUST00000168053	ENSMUSG00000095683	7	23131854	23144480	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UT86	
ENSMUST00000168055	ENSMUSG00000017286	11	76120987	76243725	-1	0	0	0	0	0	2	8	0	14	125	35	F7BB55	
ENSMUST00000168056	ENSMUSG00000044024	18	37955079	37959179	1	0	0	0	0	0	0	0	0	0	0	0	E9Q872	
ENSMUST00000168057						0	0	0	0	4	0	0	0	0	1	0		
ENSMUST00000168058	ENSMUSG00000055204	5	90227166	90366577	-1	0	0	0	147	0	0	51	0	174	0	134	E9Q804	
ENSMUST00000168060						5	2	7	14	2	1	0	0	0	0	1		
ENSMUST00000168062	ENSMUSG00000001416	3	88297116	88321767	1	4	0	0	1	4	0	0	47	0	0	0	Q3U0I3	
ENSMUST00000168064	ENSMUSG00000091243	16	65815633	65863057	1	6	5	30	72	12	9	0	0	0	0	0	E9Q1Y1	
ENSMUST00000168065	ENSMUSG00000023015	15	99620496	99651656	-1	0	0	0	0	0	0	0	0	0	0	20	F6WD40	
ENSMUST00000168069						0	0	17	5	5	6	0	0	0	0	0		
ENSMUST00000168070						5	5	13	8	11	8	21	66	43	7	47		
ENSMUST00000168071	ENSMUSG00000022636	16	52248996	52454074	-1	3	0	12	46	6	5	0	0	0	0	0	Q5MPX5	
ENSMUST00000168072	ENSMUSG00000062200	3	64690660	64844765	-1	0	0	11	0	0	0	0	0	0	0	0	E9PZ74	
ENSMUST00000168073	ENSMUSG00000040140	17	43615335	43630299	-1	51	9	15	85	22	10	0	0	0	0	0	E9PZ50	
ENSMUST00000168074						1	1	0	0	0	4	36	201	45	4	41		
ENSMUST00000168076	ENSMUSG00000046822	10	81028538	81037426	-1	12	0	0	0	10	20	22	111	0	0	37		Q99K24
ENSMUST00000168078						8	0	3	10	0	2	0	0	0	1	0		
ENSMUST00000168079	ENSMUSG00000025404	10	127380327	127499384	1	0	2	0	0	0	0	0	0	0	0	0	F6QRV2	
ENSMUST00000168080						40	33	67	82	39	26	0	29	12	6	15		
ENSMUST00000168081	ENSMUSG00000025932	1	14168954	14310235	-1	11	0	0	14	0	0	0	0	0	0	0	F6YST4	
ENSMUST00000168082						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168083	ENSMUSG00000025204	19	44548572	44555440	-1	0	0	0	0	0	0	0	155	0	11	8	E9PY23	
ENSMUST00000168084						2	2	1	0	0	2	0	0	0	0	0		
ENSMUST00000168085						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168086	ENSMUSG00000025764	3	41555731	41616864	1	0	0	0	16	1	13	0	16	147	22	55		Q6ZPI0
ENSMUST00000168088	ENSMUSG00000091882	14	6049469	6058267	-1	11	18	0	4	13	5	0	0	0	0	0	K7N6X9	
ENSMUST00000168089	ENSMUSG00000017188	11	101277968	101279114	-1	0	2	0	32	0	0	0	0	0	0	0	E9Q6W2	
ENSMUST00000168090	ENSMUSG00000076525	6	68541644	68542422	1	1	2	1	1	2	2	0	0	0	0	2	F6XWB2	
ENSMUST00000168092	ENSMUSG00000029333	5	99217426	99252927	-1	0	0	0	80	18	5	24	19	11	8	45		Q8JZL7
ENSMUST00000168093	ENSMUSG00000041187	7	16842902	16870464	1	7	4	21	68	0	5	793	1406	938	93	628		Q8BZ03
ENSMUST00000168095	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	0	0	0	0	127	0	46	0	E9Q775	
ENSMUST00000168097	ENSMUSG00000025142	11	120672973	120709447	1	2	4	5	9	4	0	0	0	0	0	19	E9Q779	
ENSMUST00000168098	ENSMUSG00000063972	2	38723370	38927688	-1	21	2	8	0	0	22	39	0	0	10	0		Q64249
ENSMUST00000168099	ENSMUSG00000025968	1	63143596	63176833	-1	0	0	0	0	0	3	102	730	350	428	305		Q91VD9
ENSMUST00000168100	ENSMUSG00000076433	11	118332360	118342500	-1	7	2	36	4	13	0	1	6	0	0	12		Q497N6
ENSMUST00000168101	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	0	0	0	0	0	E9Q1T4	
ENSMUST00000168103						0	0	0	0	0	0	139	342	195	154	170		
ENSMUST00000168106	ENSMUSG00000015749	3	95929246	95947390	1	2	8	0	0	10	10	9	0	0	0	43	E9Q0X5	
ENSMUST00000168107	ENSMUSG00000095551	14	41901813	41907290	-1	6	2	23	0	2	3	0	0	0	0	0	L7N471	
ENSMUST00000168110	ENSMUSG00000020014	10	92775619	93081618	-1	36	24	24	23	32	4	10	52	19	0	21		Q8C6S9
ENSMUST00000168111						2	0	5	2	0	0	14	100	27	60	9		
ENSMUST00000168112	ENSMUSG00000023055	15	102706779	102722178	-1	8	2	0	1	0	0	6	222	0	7	27	F6Q5V4	
ENSMUST00000168114	ENSMUSG00000056234	14	32159865	32179855	1	3	0	0	3	2	0	0	0	0	0	0	E9PZ59	
ENSMUST00000168115	ENSMUSG00000020528	11	61729650	61762088	-1	0	0	0	13	0	0	54	248	77	113	89	Q5SWZ0	Q8R574
ENSMUST00000168116						30	23	65	36	36	22	0	0	0	0	2		
ENSMUST00000168117	ENSMUSG00000019944	10	69151434	69291791	1	2	0	2	0	6	0	0	0	0	0	0	E9Q1X7	
ENSMUST00000168118						2	7	5	0	0	0	0	5	0	0	2		
ENSMUST00000168119	ENSMUSG00000041698	6	141907282	141946962	-1	15	14	47	38	21	9	1	2	1	1	0	E9Q0W2	
ENSMUST00000168120	ENSMUSG00000072949	12	84009502	84017670	1	9	6	8	135	13	1	22	292	26	5	19		O55137
ENSMUST00000168121						3	4	8	4	9	3	3	8	3	3	2		
ENSMUST00000168122						2	3	5	0	0	6	3	7	0	0	11		
ENSMUST00000168124	ENSMUSG00000020840	11	76924809	76987379	1	0	0	0	0	0	0	24	112	89	36	29	E9Q6V3	
ENSMUST00000168126	ENSMUSG00000026398	1	136842571	136960448	-1	8	9	3	105	13	4	0	0	0	1	0	Q1WLP7	
ENSMUST00000168128	ENSMUSG00000092142	14	41402885	41408281	-1	16	15	31	7	7	0	0	0	0	0	0	F6YHC1	
ENSMUST00000168129	ENSMUSG00000020628	12	28690629	28750453	-1	17	4	0	0	0	0	176	314	194	48	161		Q8K2L8
ENSMUST00000168130	ENSMUSG00000018820	19	42163951	42194590	1	0	1	0	7	6	0	0	0	10	0	0	E9Q4U6	
ENSMUST00000168134	ENSMUSG00000037519	7	144476758	144553729	-1	34	26	6	47	20	0	0	136	203	0	93	B2RXW8	
ENSMUST00000168135						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168136						1	1	0	3	1	0	0	0	0	0	0		
ENSMUST00000168137						113	133	272	92	96	44	9	31	27	1	34		
ENSMUST00000168139						6	16	6	0	8	2	0	0	0	0	0		
ENSMUST00000168141						0	1	5	1	1	1	0	0	6	0	0		
ENSMUST00000168142	ENSMUSG00000032554	9	103204001	103230444	-1	0	0	0	0	0	0	0	642	0	98	0	F7CJN9	
ENSMUST00000168144	ENSMUSG00000051361	X	38772671	38962686	1	0	5	7	1	2	2	1	0	0	0	0	B1AX85	
ENSMUST00000168148	ENSMUSG00000040065	19	12427905	12432110	1	15	9	6	21	18	5	0	1	0	0	1	Q5RKV8	
ENSMUST00000168149	ENSMUSG00000098463	14	26081516	26096127	1	0	0	0	0	0	11	0	0	0	0	0	Q8BX39	
ENSMUST00000168150						2	1	0	4	2	0	0	0	0	0	0		
ENSMUST00000168154	ENSMUSG00000094036	5	11845539	11850352	1	0	0	0	0	0	0	0	0	0	0	0	F7A7Y6	
ENSMUST00000168156	ENSMUSG00000090527	3	59729790	59752333	1	8	1	2	2	3	1	0	0	0	0	0	W4VSP6	
ENSMUST00000168157	ENSMUSG00000040860	4	141016637	141060550	-1	0	23	0	1	30	0	0	51	0	4	64		Q8CJ40
ENSMUST00000168158	ENSMUSG00000095339	7	10900740	10905050	-1	6	0	15	0	5	0	0	0	0	0	0	E9Q3G0	
ENSMUST00000168161	ENSMUSG00000090379	14	44365357	44370841	1	4	5	11	7	4	5	0	0	0	0	0	K7N749	
ENSMUST00000168162	ENSMUSG00000029231	5	75152292	75198215	1	53	27	77	62	44	29	0	0	0	0	0		P26618
ENSMUST00000168163	ENSMUSG00000035365	10	88091432	88146941	-1	2	0	0	2	2	2	0	0	1	4	0	E9QA71	
ENSMUST00000168164	ENSMUSG00000038542	8	13077189	13105459	-1	26	13	31	445	27	0	19	0	0	10	20	E9Q5V9	
ENSMUST00000168165	ENSMUSG00000096446	14	43100601	43115190	1	10	12	42	4	4	4	0	0	0	0	0	K7N744	
ENSMUST00000168166	ENSMUSG00000007656	9	75037614	75060313	1	9	8	7	18	6	9	57	31	37	51	45		P56212
ENSMUST00000168168						3	4	0	18	7	3	0	0	0	0	0		
ENSMUST00000168169	ENSMUSG00000075111	2	88972954	88980257	-1	0	0	0	0	0	0	0	0	0	0	0	A2ATG2	
ENSMUST00000168171	ENSMUSG00000073424	17	32685627	32703352	1	5	9	8	58	0	0	0	0	0	0	0	Q99N18	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000168172	ENSMUSG00000038058	6	54923949	54972612	-1	22	21	39	0	6	0	519	1231	518	306	265	Q540J8	Q8BHB0
ENSMUST00000168174	ENSMUSG00000031241	X	107667964	107688978	1	7	2	0	0	0	0	0	0	0	0	0	E9Q5R8	
ENSMUST00000168175	ENSMUSG00000091076	17	23343977	23360128	1	9	14	14	8	12	7	0	0	0	0	0	E9Q0E7	
ENSMUST00000168176	ENSMUSG00000032679	2	104095801	104115354	1	44	0	77	0	0	0	0	0	0	0	0	A2BI31	O55186
ENSMUST00000168177	ENSMUSG00000042557	9	57072040	57128366	1	0	0	27	34	0	0	77	0	217	19	196		Q60520
ENSMUST00000168178						24	11	38	21	5	0	6	0	0	0	8		
ENSMUST00000168179	ENSMUSG00000079227	9	124121543	124147699	1	1	0	2	2	0	0	0	17	3	2	0	E9Q351	
ENSMUST00000168184	ENSMUSG00000038209	1	171518122	171535294	-1	6	4	6	12	12	6	0	0	1	0	0	F6YSS8	
ENSMUST00000168185	ENSMUSG00000059323	15	76622088	76639958	-1	22	20	49	107	44	18	58	53	47	2	75	G3UW83	
ENSMUST00000168186	ENSMUSG00000021111	12	105784694	105838944	1	0	2	0	0	0	0	0	6	24	16	23	E9QAN2	
ENSMUST00000168189	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	0	60	9	0	3038	2058	4206	192	3593		Q924Z6
ENSMUST00000168191	ENSMUSG00000047921	15	72589621	73061204	-1	18	9	53	40	19	4	0	0	0	0	0	E9PZ41	
ENSMUST00000168193	ENSMUSG00000052374	13	12269426	12340760	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JI91
ENSMUST00000168194	ENSMUSG00000025470	7	140036391	140040605	1	2	7	8	110	16	5	105	314	132	46	103		Q6P0X2
ENSMUST00000168195	ENSMUSG00000022952	16	92601466	92826149	-1	0	0	0	303	2	5	46	100	100	0	139	G3UWD2	
ENSMUST00000168196	ENSMUSG00000051648	8	105382807	105413502	-1	0	0	0	0	0	0	0	0	0	0	0	F7CJT5	
ENSMUST00000168200	ENSMUSG00000022389	15	81802421	81826861	1	0	0	1	19	3	0	0	0	0	0	0	E9Q331	
ENSMUST00000168203	ENSMUSG00000010476	7	137193673	137314445	-1	0	0	0	0	0	0	0	0	0	0	0	Q6NXL3	
ENSMUST00000168206	ENSMUSG00000021910	14	31170930	31216946	-1	22	14	47	132	30	9	1681	3001	2147	108	2559		Q80TM9
ENSMUST00000168207						0	0	0	0	0	0	17	0	0	0	0		
ENSMUST00000168209						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168211	ENSMUSG00000027894	3	107467543	107518018	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168213	ENSMUSG00000013353	7	43492044	43505940	-1	5	2	7	1	1	0	4	7	0	0	17	E9Q2G4	
ENSMUST00000168216						4	1	5	0	0	3	3	0	10	0	8		
ENSMUST00000168217	ENSMUSG00000004561	14	51884842	51893039	1	0	1	1	3	0	1	0	0	0	0	0	E9Q5R5	
ENSMUST00000168218	ENSMUSG00000043284	11	60864452	60879272	-1	13	0	0	0	0	3	18	73	0	0	31	E9Q933	
ENSMUST00000168222						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000168223	ENSMUSG00000038712	3	95281345	95296166	1	5	0	38	0	7	0	881	1837	710	328	709		Q76LS9
ENSMUST00000168226						17	20	45	28	16	7	0	1	0	0	0		
ENSMUST00000168229	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	E9PWM2	
ENSMUST00000168230	ENSMUSG00000090806	7	85558703	85569088	-1	5	7	8	0	6	2	0	0	0	0	0	K7N702	
ENSMUST00000168235	ENSMUSG00000026259	1	87476834	87573870	-1	5	1	8	1	8	1	0	0	0	0	0	F6SWQ9	
ENSMUST00000168236						2	3	27	2	2	2	0	66	42	23	25		
ENSMUST00000168237	ENSMUSG00000053333	1	86703808	87050095	1	6	0	0	30	0	5	0	12	58	0	0		Q8CI75
ENSMUST00000168238						2	1	2	2	0	1	0	0	0	0	1		
ENSMUST00000168240						0	4	5	9	0	0	3	0	0	0	0		
ENSMUST00000168242						2	0	0	0	0	0	0	0	6	0	0		
ENSMUST00000168247	ENSMUSG00000058638	7	12834761	12850577	1	0	0	0	0	0	3	120	382	267	397	199		
ENSMUST00000168249	ENSMUSG00000079608	18	70472454	70501066	1	0	2	2	8	0	0	2	2	0	0	0	Q9CPT8	P59096
ENSMUST00000168250						2	0	0	21	2	0	2	0	0	0	0		
ENSMUST00000168252	ENSMUSG00000030378	7	14410686	14446769	-1	3	5	3	0	0	2	0	0	0	0	0	Q8BGL3	
ENSMUST00000168254	ENSMUSG00000079339	19	34592888	34601968	-1	0	4	9	15	10	6	0	0	0	34	0	E9PXF7	
ENSMUST00000168255						0	1	7	0	0	0	0	0	0	13	3		
ENSMUST00000168256						2	3	15	0	3	1	0	0	0	0	6		
ENSMUST00000168260	ENSMUSG00000032578	9	107296026	107302784	1	4	9	2	22	15	8	15	25	0	0	0	E9Q273	
ENSMUST00000168264	ENSMUSG00000033436	X	134804145	134809221	-1	0	10	30	0	19	0	0	8	0	0	0		Q6A058
ENSMUST00000168265	ENSMUSG00000024160	17	24886643	24892152	1	0	0	0	155	0	0	0	0	0	0	0	E9PW49	
ENSMUST00000168266	ENSMUSG00000027067	2	85037234	85047109	1	8	13	15	16	1	6	59	272	0	15	0		Q08943
ENSMUST00000168267						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168268						3	0	12	4	6	2	4	4	6	0	6		
ENSMUST00000168269	ENSMUSG00000040329	3	7569994	7613760	-1	0	2	11	5	0	0	1	2	1	0	4	Q3UT18	
ENSMUST00000168270	ENSMUSG00000022620	15	89472476	89477425	-1	3	1	0	2	4	6	11	11	5	0	22	F6QGM0	
ENSMUST00000168271						8	4	7	24	1	6	18	56	14	3	45		
ENSMUST00000168272	ENSMUSG00000096278	17	23880880	23900787	1	6	0	4	7	4	0	0	0	0	0	0	E9PYC2	
ENSMUST00000168274	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	5	0	1	0	0	0	0	0	0	E9Q0Q5	
ENSMUST00000168275	ENSMUSG00000022019	14	87416639	87545373	1	3	5	24	44	10	0	0	0	28	32	36		Q91W18
ENSMUST00000168276	ENSMUSG00000060671	3	89939481	89963508	-1	1	2	0	40	5	4	0	0	0	0	0	E9QAL4	
ENSMUST00000168278						0	3	5	0	0	2	0	0	0	0	0		
ENSMUST00000168279	ENSMUSG00000022899	16	36750178	36784962	-1	0	1	6	1	0	1	0	0	0	0	0	G3XA51	
ENSMUST00000168280	ENSMUSG00000078853	11	58199556	58207591	1	0	0	0	0	0	0	57	204	0	174	209	E9Q9N8	
ENSMUST00000168281						3	7	8	6	3	0	0	0	0	0	0		
ENSMUST00000168282	ENSMUSG00000024182	17	26138688	26195811	1	0	0	0	0	0	0	0	0	0	0	0	F6SKQ8	
ENSMUST00000168285						3	1	1	8	3	2	0	6	3	3	9		
ENSMUST00000168287						0	6	0	0	0	0	0	0	0	0	0		
ENSMUST00000168288	ENSMUSG00000042589	5	121856366	122050102	-1	0	0	71	329	43	14	0	0	0	0	0		P70298
ENSMUST00000168292	ENSMUSG00000090625	2	174330319	174346712	-1	0	1	6	0	6	0	144	1648	103	169	63	E9Q2U8	
ENSMUST00000168295	ENSMUSG00000030109	6	121343076	121365775	1	10	2	15	3	5	2	0	0	1	0	0	E9PW98	
ENSMUST00000168298	ENSMUSG00000095817	10	77770633	77771325	-1	13	9	43	71	18	4	0	0	0	0	0	W4VSP7	
ENSMUST00000168299						1	2	8	2	5	1	0	1	0	0	0		
ENSMUST00000168301	ENSMUSG00000007656	9	75037614	75060313	1	0	0	0	24	0	0	0	14	7	6	0	E9PXD7	
ENSMUST00000168302	ENSMUSG00000062939	1	51987148	52107189	1	2	6	1	9	3	0	26	146	31	124	25	Q3V157	
ENSMUST00000168303	ENSMUSG00000026384	1	119652467	119837613	-1	0	0	0	14	0	0	0	0	0	0	0	E9PUU9	
ENSMUST00000168306	ENSMUSG00000096901	14	3931756	3940185	1	2	0	0	4	0	0	0	0	0	0	0	K7N6Y0	
ENSMUST00000168308						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000168309	ENSMUSG00000032375	9	66775202	66795490	-1	0	6	0	2	0	0	0	73	19	21	38	Q3TRQ2	Q8C7N7
ENSMUST00000168310						2	2	1	0	1	1	0	0	0	0	0		
ENSMUST00000168311	ENSMUSG00000034990	7	121083322	121163097	1	2	0	5	0	0	1	0	1	1	0	1	E9PWK6	
ENSMUST00000168312	ENSMUSG00000027860	3	102153583	102204693	-1	3	0	4	36	6	0	0	0	0	0	0	Q3UXU7	
ENSMUST00000168315	ENSMUSG00000073952	7	103320401	103321360	1	0	0	2	5	0	4	0	0	0	0	0	E9QAV0	
ENSMUST00000168318	ENSMUSG00000090894	17	37492468	37499674	1	7	2	7	8	3	4	0	0	0	0	0	A2RT31	
ENSMUST00000168320	ENSMUSG00000091140	14	42594502	42599882	-1	9	5	20	6	3	5	0	0	0	0	0	F6ZIG1	
ENSMUST00000168321	ENSMUSG00000038777	3	95160457	95174024	1	0	0	0	0	0	0	0	0	1	0	0	E9Q613	
ENSMUST00000168322						2	2	5	0	0	1	0	0	0	0	0		
ENSMUST00000168324	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	22	0	0	0	0	0	0	0	E9PZ55	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000168326	ENSMUSG00000095383	7	22522967	22523890	1	0	0	0	0	0	0	0	0	0	0	0	E9Q9N3	
ENSMUST00000168327						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000168328						1	1	14	0	0	2	0	0	0	0	0		
ENSMUST00000168329	ENSMUSG00000067848	5	11918043	11922821	1	0	0	0	0	0	0	0	0	0	0	0	F7D1B3	
ENSMUST00000168330	ENSMUSG00000024909	19	5473973	5481853	1	0	0	0	0	1	0	6	9	0	7	0	F6R0V7	
ENSMUST00000168331	ENSMUSG00000074434	8	21583027	21583961	1	0	0	0	0	0	0	0	0	0	0	0	L7N2A5	
ENSMUST00000168332	ENSMUSG00000091159	9	22454290	22462062	1	7	13	35	5	10	5	0	1	1	0	0	F7A3L5	
ENSMUST00000168333	ENSMUSG00000078765	7	30563301	30567960	1	0	2	0	0	0	0	0	0	0	0	0	E9Q809	
ENSMUST00000168334	ENSMUSG00000056234	14	32159865	32179855	1	42	0	28	53	19	0	0	16	24	17	12	E9Q8Q4	
ENSMUST00000168335	ENSMUSG00000040046	7	46647130	46672537	-1	0	0	2	0	0	0	0	0	0	0	0	Q3TZH2	
ENSMUST00000168337						0	0	0	24	0	0	0	0	24	0	0		
ENSMUST00000168338	ENSMUSG00000060950	12	111678105	111683902	1	0	0	0	0	0	5	0	18	5	4	2		Q80XC2
ENSMUST00000168339	ENSMUSG00000079580	17	29526033	29549593	-1	3	9	0	7	6	0	3	0	0	2	1	Q14AF1	
ENSMUST00000168340	ENSMUSG00000082211	8	21315546	21316481	1	0	0	0	0	0	0	0	0	0	0	0	K7N7D8	
ENSMUST00000168341	ENSMUSG00000090824	7	6439836	6440896	1	0	2	0	41	0	5	0	0	0	0	0	Q7TQV3	
ENSMUST00000168343						1	1	1	8	4	3	1	0	1	0	3		
ENSMUST00000168345	ENSMUSG00000091512	3	137918506	137928900	1	8	2	8	51	2	2	194	845	338	324	351	Q542I7	O88653
ENSMUST00000168346						8	0	5	9	6	3	3	51	21	5	24		
ENSMUST00000168348	ENSMUSG00000000631	11	77763246	77865980	1	15	5	19	10	10	13	0	0	0	0	26	E9QAX2	
ENSMUST00000168350	ENSMUSG00000060147	13	33917918	34002794	-1	0	0	0	0	0	0	24	0	23	450	51	E9Q6X2	
ENSMUST00000168351						9	0	1	0	1	13	60	279	100	17	222		
ENSMUST00000168352	ENSMUSG00000028184	3	148815583	148990555	-1	3	0	32	0	0	0	0	1	0	11	7	Q0P6A0	
ENSMUST00000168353	ENSMUSG00000015467	17	34613349	34615971	-1	2	2	12	4	3	0	0	0	3	3	4	E9QAK9	
ENSMUST00000168355						1	2	5	2	1	0	11	26	12	5	4		
ENSMUST00000168357	ENSMUSG00000043531	19	50143301	50678646	-1	0	0	0	1	0	0	0	0	0	0	0	E9Q203	
ENSMUST00000168360	ENSMUSG00000025130	11	120560298	120573253	-1	0	0	0	0	0	1	58	372	138	61	142	E9Q8G8	
ENSMUST00000168361	ENSMUSG00000020594	12	8674134	8752581	1	18	7	0	29	0	15	0	237	0	46	0		Q80U58
ENSMUST00000168362	ENSMUSG00000001424	6	28475139	28935162	1	0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000168363						27	26	47	70	47	18	11	17	2	5	9		
ENSMUST00000168364						4	6	7	4	7	6	12	14	28	2	46		
ENSMUST00000168366	ENSMUSG00000004771	9	64715299	64737758	-1	2	2	0	0	0	2	113	263	46	68	24	F6R2Z5	
ENSMUST00000168367	ENSMUSG00000021555	13	59585259	59634798	1	0	0	0	2	4	0	0	3	8	2	5	E9Q2U4	
ENSMUST00000168370						246	232	301	230	300	177	4	30	12	3	24		
ENSMUST00000168372	ENSMUSG00000004364	1	80264923	80340480	-1	1	0	0	0	0	1	0	117	0	0	0	F6UY44	
ENSMUST00000168374						2	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000168376	ENSMUSG00000078937	15	89416405	89425863	-1	3	1	4	45	6	1	2	3	2	0	5	E9Q393	
ENSMUST00000168378	ENSMUSG00000036473	17	24175431	24209387	-1	0	57	274	10	122	16	169	206	259	9	175		Q3UUG6
ENSMUST00000168379						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168381	ENSMUSG00000073557	1	134754658	134955942	-1	0	0	0	0	0	0	0	0	0	0	0	A6H644	
ENSMUST00000168382	ENSMUSG00000057561	18	46597704	46610225	1	0	3	0	0	1	0	163	449	246	646	219	Q4FJR7	Q60872
ENSMUST00000168383	ENSMUSG00000022758	16	17561885	17577800	1	25	13	63	117	28	16	0	0	0	0	0	E9Q857	
ENSMUST00000168385	ENSMUSG00000056234	14	32159865	32179855	1	4	0	0	0	0	0	0	0	0	36	0	E9Q0D2	
ENSMUST00000168386	ENSMUSG00000064125	8	4209543	4217459	-1	50	34	79	161	59	30	1	4	3	0	1	E9PV26	
ENSMUST00000168387	ENSMUSG00000033788	6	84008590	84211060	1	14	8	19	0	0	0	0	0	0	0	0		Q9ESD7
ENSMUST00000168388						33	22	39	19	30	20	0	0	0	0	0		
ENSMUST00000168389						0	0	0	0	0	0	2	0	12	0	2		
ENSMUST00000168391	ENSMUSG00000015474	17	34616662	34628510	-1	0	0	0	0	0	0	0	0	0	0	0		O35448
ENSMUST00000168392	ENSMUSG00000096601	7	23066533	23067456	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7F4	
ENSMUST00000168396	ENSMUSG00000000568	5	99955935	99978938	-1	0	1	0	3	3	2	30	68	47	0	59	E9Q4W5	
ENSMUST00000168398	ENSMUSG00000096813	7	21300502	21301467	-1	0	0	0	0	0	0	0	0	0	0	0	L7N2C8	
ENSMUST00000168399	ENSMUSG00000004530	5	113842436	113908758	-1	3	4	4	0	1	0	0	0	0	0	0	E9PZJ0	
ENSMUST00000168400	ENSMUSG00000060147	13	33917918	34002794	-1	0	0	0	0	0	0	7	3	9	3	0	E9PYY0	
ENSMUST00000168401	ENSMUSG00000015568	8	68880491	68907448	1	1	1	0	1	0	0	0	0	0	2	14		P11152
ENSMUST00000168403	ENSMUSG00000031241	X	107667964	107688978	1	4	3	0	0	3	1	0	0	0	0	0	Q8BKE4	
ENSMUST00000168404	ENSMUSG00000006389	4	118442415	118457513	-1	0	0	0	0	11	3	1	1	0	5	1	E9Q7U5	
ENSMUST00000168406	ENSMUSG00000023367	6	48840919	48847071	1	6	0	7	0	0	0	25	0	0	18	0		Q9DCS1
ENSMUST00000168407	ENSMUSG00000095918	5	11183072	11187810	1	0	0	0	0	3	0	0	0	0	0	0	L7N474	
ENSMUST00000168408	ENSMUSG00000022248	15	10486018	10499063	1	0	0	0	0	0	0	0	9	4	12	0	E9PY19	
ENSMUST00000168409						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000168410	ENSMUSG00000036473	17	24175431	24209387	-1	93	5	0	0	0	0	1	57	37	0	49		Q3UUG6
ENSMUST00000168412	ENSMUSG00000049300	3	110246109	110250998	-1	1	11	1	29	25	1	0	1	1	0	34		Q6NZB1
ENSMUST00000168413						0	0	0	0	0	0	0	57	18	0	26		
ENSMUST00000168414						4	3	2	5	12	2	0	0	0	0	1		
ENSMUST00000168416	ENSMUSG00000091734	6	58307268	58308290	1	2	4	0	1	3	5	0	0	0	0	0	Q9EQ41	
ENSMUST00000168419	ENSMUSG00000024644	18	84667470	84685633	-1	0	0	0	0	18	13	613	485	464	248	544		Q9D1A2
ENSMUST00000168422						0	2	3	0	1	0	0	0	0	0	1		
ENSMUST00000168423	ENSMUSG00000024563	18	76241580	76305731	1	5	0	16	12	11	4	118	278	78	48	66		Q62432
ENSMUST00000168425						3	3	4	4	4	2	0	0	0	0	0		
ENSMUST00000168428	ENSMUSG00000033545	8	111536097	111626030	1	0	0	0	0	0	0	0	0	0	0	0		Q91V17
ENSMUST00000168429	ENSMUSG00000026384	1	119652467	119837613	-1	0	0	0	0	0	0	0	0	0	0	0	F6PWT7	
ENSMUST00000168430						0	1	0	1	1	0	0	0	0	0	0		
ENSMUST00000168431	ENSMUSG00000026074	1	39900913	40026310	1	13	13	6	25	4	12	580	2496	1390	215	913	F8VPL5	
ENSMUST00000168432						5	4	1	6	4	3	0	0	0	0	0		
ENSMUST00000168434	ENSMUSG00000020530	11	84832361	84870817	-1	0	0	0	35	11	0	0	0	0	0	0		Q5SV77
ENSMUST00000168435	ENSMUSG00000035713	7	97309380	97332020	-1	0	0	0	0	0	0	0	14	0	4	0	M0QWN7	
ENSMUST00000168436						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168438	ENSMUSG00000038170	3	97689824	97888707	-1	39	0	98	39	25	28	0	0	3	4	6	E9Q1A0	
ENSMUST00000168439						5	1	7	3	2	2	0	0	0	0	0		
ENSMUST00000168440	ENSMUSG00000091504	17	55592341	55624672	-1	4	0	2	2	1	2	0	0	0	0	0	E9Q1C1	
ENSMUST00000168443	ENSMUSG00000027443	2	148789361	148793546	1	6	2	1	3	0	2	0	0	0	0	0	E9Q1S9	
ENSMUST00000168444	ENSMUSG00000021799	14	34590618	34600142	-1	11	3	6	28	10	5	0	0	0	0	0		Q9QXZ9
ENSMUST00000168445	ENSMUSG00000034445	19	10577454	10588548	1	19	9	55	20	19	8	1000	932	811	91	462		Q6P1H1
ENSMUST00000168446	ENSMUSG00000024283	18	7868832	7973547	1	6	3	0	0	0	0	9	0	20	0	10	E9PXS5	
ENSMUST00000168451	ENSMUSG00000021910	14	31170930	31216946	-1	0	0	0	0	0	0	0	0	0	0	0	F6UKP3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000168452	ENSMUSG00000091411	9	36119934	36128779	-1	1	2	5	2	2	1	0	0	0	0	0	G5E8W5	
ENSMUST00000168454						3	2	1	1	0	2	0	0	0	1	0		
ENSMUST00000168456						2	4	0	0	0	0	4	21	4	5	39		
ENSMUST00000168457	ENSMUSG00000047751	7	139943789	139945112	1	9	7	36	520	13	11	0	1	0	0	1	B2RSF1	Q6J1H4
ENSMUST00000168458	ENSMUSG00000096183	14	7255889	7264714	-1	3	0	0	0	6	3	0	0	0	0	0	L7N299	
ENSMUST00000168459	ENSMUSG00000039364	11	121053458	121063569	-1	0	0	0	0	0	0	0	0	0	0	0	Q9D966	
ENSMUST00000168460	ENSMUSG00000029130	5	29195992	29228457	1	3	4	2	1	0	4	0	0	0	0	0		Q9JIT1
ENSMUST00000168461	ENSMUSG00000028793	4	129058271	129085886	1	0	0	0	12	0	0	36	200	42	71	176	E9Q2L7	
ENSMUST00000168462						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168463	ENSMUSG00000091803	12	81359026	81485127	-1	0	0	0	64	0	1	40	34	50	253	25	E9Q3U7	
ENSMUST00000168465	ENSMUSG00000001120	10	76761857	76961887	-1	0	0	0	0	4	0	0	13	0	0	0		P57722
ENSMUST00000168471						0	0	6	4	0	0	0	4	0	0	0		
ENSMUST00000168472						0	0	0	0	0	0	2	1	0	2	0		
ENSMUST00000168474						3	0	16	20	4	2	0	2	2	0	3		
ENSMUST00000168479	ENSMUSG00000075592	14	55854036	55874735	1	66	35	35	0	70	35	17	16	0	0	0		Q5DTZ0
ENSMUST00000168480	ENSMUSG00000094460	14	6210617	6219292	-1	20	15	10	7	0	0	0	0	0	0	0	D3Z7A4	
ENSMUST00000168483	ENSMUSG00000066007	4	146156824	146198755	1	0	0	0	8	0	0	0	0	0	0	0	A2A7V0	
ENSMUST00000168484	ENSMUSG00000025159	19	41941086	41981157	-1	11	6	10	6	7	3	0	9	0	0	0	E9PW47	
ENSMUST00000168485	ENSMUSG00000053093	14	54970688	54994634	-1	31	0	79	36	31	8	0	0	0	0	0	B2RXX9	Q91Z83
ENSMUST00000168488	ENSMUSG00000021953	14	63492347	63509092	-1	0	0	7	0	0	0	0	0	0	0	0	F7AJL7	
ENSMUST00000168489	ENSMUSG00000092032	7	42011792	42058981	-1	6	3	4	3	13	6	0	0	0	0	0	E9PUT5	
ENSMUST00000168490	ENSMUSG00000032842	17	46303221	46328352	-1	0	4	0	0	0	0	4	0	1	0	8	E9PY11	
ENSMUST00000168493						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168495						4	2	14	2	7	0	4	34	21	6	26		
ENSMUST00000168497						2	1	8	0	0	0	0	2	3	0	3		
ENSMUST00000168498	ENSMUSG00000031448	8	13221663	13254162	-1	3	4	4	0	2	4	0	0	0	0	0	E9Q4C0	
ENSMUST00000168499	ENSMUSG00000032109	9	44252713	44268599	-1	0	4	0	2	14	8	3173	2650	1942	184	1588		Q3TL44
ENSMUST00000168500	ENSMUSG00000002297	5	8396973	8422716	-1	6	9	7	0	7	6	26	85	51	86	51	E9PW04	
ENSMUST00000168501	ENSMUSG00000041229	X	151520672	151633859	1	0	0	19	0	0	0	29	19	40	0	36		Q80TJ7
ENSMUST00000168502	ENSMUSG00000042557	9	57072040	57128366	1	0	0	28	0	18	19	21	239	0	61	0		Q60520
ENSMUST00000168503	ENSMUSG00000055401	4	148145716	148152140	-1	0	0	0	0	0	0	0	40	14	0	45		Q9QZN4
ENSMUST00000168505						5	0	9	0	0	0	3	0	2	4	0		
ENSMUST00000168506						5	2	10	2	5	1	2	3	0	0	2		
ENSMUST00000168507	ENSMUSG00000005936	17	28951950	28969549	1	0	0	5	0	10	0	0	12	108	0	42		Q8CDD8
ENSMUST00000168508						3	4	5	0	0	0	0	2	0	0	0		
ENSMUST00000168509	ENSMUSG00000001785	10	85871831	85889096	1	0	0	0	7	0	0	0	0	0	0	28	E9QAL6	
ENSMUST00000168510	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	0	0	0	0	0	0	0	0	F7CRQ2	
ENSMUST00000168513						0	0	0	1	0	0	0	0	0	2	0		
ENSMUST00000168514	ENSMUSG00000038599	1	182565007	182632352	1	6	5	19	6	12	6	0	0	0	0	0		Q91VA3
ENSMUST00000168515	ENSMUSG00000026458	1	134296783	134332928	-1	47	27	157	123	43	0	0	0	0	0	0	B8QI36	
ENSMUST00000168517						0	2	3	3	7	2	0	0	0	0	0		
ENSMUST00000168520	ENSMUSG00000025436	10	126868430	126901371	-1	2	2	3	6	0	2	25	34	11	15	14	G3UW46	
ENSMUST00000168522	ENSMUSG00000022372	15	66780819	66831829	-1	0	3	2	0	4	2	5	4	8	5	11		
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ENSMUST00000168527	ENSMUSG00000056268	1	138963435	139178960	1	0	0	0	0	0	0	303	366	305	61	458	E9Q246	
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ENSMUST00000168529	ENSMUSG00000032872	9	87022014	87077774	1	1	0	9	60	4	0	620	2130	1172	830	650		Q3TDX8
ENSMUST00000168531	ENSMUSG00000051262	6	85732513	85765754	-1	10	0	0	9	7	13	0	10	3	1	2		
ENSMUST00000168532	ENSMUSG00000010066	9	107399612	107529343	1	0	0	0	58	0	0	0	0	0	0	0		Q6PHS9
ENSMUST00000168533	ENSMUSG00000033327	17	34670535	34719815	1	31	0	10	684	52	27	1	0	0	0	29	E9Q2T3	
ENSMUST00000168536	ENSMUSG00000025041	19	46886831	47015153	-1	0	0	0	12	0	0	643	1496	1070	174	847		Q3V1L4
ENSMUST00000168538						0	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000168542	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	0	0	0	1	0	0	0	0	0	E9PZC7	
ENSMUST00000168545	ENSMUSG00000031659	8	88272403	88329962	1	0	0	0	0	0	0	4	651	0	1	65		P51829
ENSMUST00000168546	ENSMUSG00000026113	1	37299865	37410736	1	6	8	0	20	0	2	35	75	23	1	58	F6R4N2	
ENSMUST00000168547						0	2	0	0	0	0	0	20	0	0	0		
ENSMUST00000168549						4	7	7	7	7	3	0	0	0	0	0		
ENSMUST00000168550	ENSMUSG00000025499	7	141189105	141194005	-1	0	0	0	0	0	0	6	4	2	0	0		Q61411
ENSMUST00000168551	ENSMUSG00000095573	Y	2720339	2720674	-1	0	0	1	1	3	0	0	0	0	0	0	A9Z055	
ENSMUST00000168552	ENSMUSG00000029071	4	155847402	155859303	1	0	0	0	0	0	0	143	0	153	0	154		P51141
ENSMUST00000168553	ENSMUSG00000028901	4	132221025	132261602	-1	197	150	653	211	164	77	23	204	69	88	89		Q9JL60
ENSMUST00000168554	ENSMUSG00000056219	10	53474964	53475467	1	4	2	22	0	5	8	0	0	0	0	0	F2Z3Z2	
ENSMUST00000168555	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	7	2	5	24	E9PWX6	
ENSMUST00000168560	ENSMUSG00000091530	17	3532554	3533213	1	5	4	2	0	5	3	0	7	0	4	1	G5E8X0	
ENSMUST00000168561	ENSMUSG00000087230	1	136181474	136207097	-1	17	14	37	14	25	12	0	0	1	0	1	E9QAI4	
ENSMUST00000168564	ENSMUSG00000000131	7	126101715	126200501	-1	0	1	0	0	2	0	40	150	52	8	53	F6Y2I6	
ENSMUST00000168565	ENSMUSG00000038534	11	97050628	97068904	1	0	0	0	4	6	0	3	143	25	30	83	F8VQM4	
ENSMUST00000168566	ENSMUSG00000027663	3	32334792	32366014	-1	3	0	4	3	0	0	1	0	101	10	0	B9EI21	
ENSMUST00000168568						1	0	0	1	0	0	20	23	37	0	23		
ENSMUST00000168572	ENSMUSG00000044499	10	36506814	36834397	1	2	0	0	0	11	0	0	0	0	0	0	B2RXW6	Q8BSL4
ENSMUST00000168574	ENSMUSG00000045658	1	84036296	84364180	-1	28	24	119	37	13	6	27	157	17	51	48		Q3UBG2
ENSMUST00000168575	ENSMUSG00000021938	14	56722441	56778316	-1	0	0	0	0	0	5	7	69	28	13	34	F7D909	
ENSMUST00000168578	ENSMUSG00000030431	7	4784557	4789656	-1	11	7	18	139	18	4	4	3	1	23	8		A9JSM3
ENSMUST00000168579	ENSMUSG00000025161	11	120948480	120960868	1	14	17	27	107	22	18	717	1841	338	99	627	Q3UDP9	P57787
ENSMUST00000168580	ENSMUSG00000094757	7	20232908	20233828	-1	3	2	0	0	0	0	0	0	0	0	0	K9J7G4	
ENSMUST00000168581	ENSMUSG00000022471	15	81987835	82040085	1	0	0	0	0	0	0	0	0	0	0	0	E9Q4A4	
ENSMUST00000168582						0	2	13	3	0	0	0	1	4	0	0		
ENSMUST00000168584	ENSMUSG00000021916	14	31001393	31012441	1	45	62	102	0	39	23	49	406	108	81	72		Q6NSU3
ENSMUST00000168587	ENSMUSG00000075486	14	101633766	101640686	-1	1	3	0	2	0	0	45	360	94	129	21	B7ZNP3	
ENSMUST00000168589	ENSMUSG00000022372	15	66780819	66831829	-1	0	0	0	0	0	0	174	1	834	0	643	Q4FJX0	Q60898
ENSMUST00000168592	ENSMUSG00000023964	6	3685680	3764714	-1	0	2	0	0	0	0	0	0	0	0	0		Q60755
ENSMUST00000168593	ENSMUSG00000023826	17	10840384	12063361	1	1	0	0	0	0	0	0	0	0	0	0	F6TNF2	
ENSMUST00000168594	ENSMUSG00000024858	19	4286001	4306222	-1	0	0	0	0	0	0	0	24	0	0	0	F7AEX1	
ENSMUST00000168598	ENSMUSG00000053580	11	105589986	105929304	1	1	0	0	24	0	0	0	0	0	0	1	E9Q2K2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000168599	ENSMUSG00000002718	2	166906040	166946389	1	0	4	0	0	0	0	13	0	42	0	0	E9Q1T9	
ENSMUST00000168600	ENSMUSG00000030889	7	120739557	120805742	1	53	50	105	59	60	26	1	5	2	0	8	E9Q0W9	
ENSMUST00000168601						0	1	18	22	5	0	0	3	0	0	2		
ENSMUST00000168602						2	2	0	0	4	2	0	0	0	0	0		
ENSMUST00000168612	ENSMUSG00000033044	11	67798187	67816002	1	9	5	4	8	4	0	0	0	0	0	0		Q8CHS7
ENSMUST00000168613	ENSMUSG00000040147	X	16709282	16817366	-1	0	0	0	0	2	3	0	0	0	3	1	E9Q3X6	
ENSMUST00000168615	ENSMUSG00000049878	4	121145373	121215084	-1	29	23	18	0	17	0	0	33	0	0	0	E9Q532	
ENSMUST00000168617	ENSMUSG00000020014	10	92775619	93081618	-1	0	3	0	0	0	8	0	0	0	0	14	E9PZY5	
ENSMUST00000168619	ENSMUSG00000094151	14	43179867	43187988	1	5	3	2	1	2	0	0	0	0	0	1	E9PZI8	
ENSMUST00000168621	ENSMUSG00000025314	2	90429754	90580647	-1	0	0	15	138	15	0	89	179	302	15	328	E9Q4S7	
ENSMUST00000168622	ENSMUSG00000072494	14	54872669	54877550	-1	2	0	7	137	1	0	0	0	0	0	0	H3BJB2	
ENSMUST00000168623						2	1	9	1	4	0	0	0	0	0	0		
ENSMUST00000168629	ENSMUSG00000048996	13	21536974	21542775	-1	6	6	6	3	13	0	0	0	0	0	0	Q7TQT9	
ENSMUST00000168630	ENSMUSG00000063626	8	28646717	29219338	-1	68	80	352	124	75	59	0	9	2	0	4		Q8K1S2
ENSMUST00000168631	ENSMUSG00000026991	2	59160850	59355208	1	0	0	0	0	0	0	0	0	0	0	0		Q68FH0
ENSMUST00000168632						8	3	6	1	4	6	0	2	5	0	2		
ENSMUST00000168633						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000168634						0	0	1	1	5	2	3	7	16	5	18		
ENSMUST00000168636						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000168637						0	0	0	2	0	0	0	3	0	0	0		
ENSMUST00000168641	ENSMUSG00000091844	1	44055952	44061936	-1	15	19	34	19	19	15	1	8	2	2	2	F6VUT6	
ENSMUST00000168644	ENSMUSG00000001052	3	129982759	130061553	-1	2	3	5	0	1	0	30	0	10	0	19	F6YIN5	
ENSMUST00000168645	ENSMUSG00000037652	3	30899371	30969415	-1	40	35	89	45	54	21	337	691	544	56	704		Q8CHP6
ENSMUST00000168646	ENSMUSG00000079242	15	89429589	89430868	1	40	36	57	139	44	32	10	49	32	12	48	Q8BGL5	
ENSMUST00000168649						0	0	0	0	0	0	9	12	0	0	18		
ENSMUST00000168651	ENSMUSG00000038095	5	124368702	124426001	-1	0	3	10	113	9	6	309	322	1119	23	657	F7CVW0	
ENSMUST00000168653						3	0	0	5	0	2	0	0	0	0	0		
ENSMUST00000168654						39	44	86	31	35	22	0	51	46	27	36		
ENSMUST00000168656						0	0	0	23	0	0	0	6	0	0	3		
ENSMUST00000168657						11	5	5	0	7	5	53	461	54	52	47		
ENSMUST00000168659	ENSMUSG00000096477	17	37111042	37111980	-1	6	3	13	9	4	2	0	0	0	0	0	L7N475	
ENSMUST00000168660	ENSMUSG00000029862	6	42286685	42315756	1	0	3	20	0	0	0	0	0	0	0	0	F7A9J6	
ENSMUST00000168662						0	0	0	0	0	0	2	0	0	8	0		
ENSMUST00000168664	ENSMUSG00000028520	4	103230445	103290863	-1	7	0	7	4	3	1	0	0	0	0	0		Q9D5Q8
ENSMUST00000168665	ENSMUSG00000032403	9	63394447	63399246	-1	0	0	0	12	1	0	25	59	23	24	7		Q0VG49
ENSMUST00000168666	ENSMUSG00000090273	17	56770250	56772208	1	0	0	0	122	0	0	2	7	5	0	4	F6TNE3	
ENSMUST00000168667						0	2	5	0	19	0	0	0	0	0	0		
ENSMUST00000168668						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168669	ENSMUSG00000021953	14	63492347	63509092	-1	0	0	0	0	0	0	0	0	0	0	0	F6X7T7	
ENSMUST00000168672						0	1	0	14	0	0	0	2	0	0	0		
ENSMUST00000168673	ENSMUSG00000091792	14	42185391	42190791	-1	4	5	0	0	6	0	0	0	0	0	0	L7N292	
ENSMUST00000168675						2	1	0	7	0	2	0	0	0	0	0		
ENSMUST00000168678	ENSMUSG00000042557	9	57072040	57128366	1	0	0	0	20	0	0	85	140	155	0	164		Q60520
ENSMUST00000168680	ENSMUSG00000092009	16	49057486	49199104	1	38	37	43	28	44	24	0	1	0	0	0	E9Q264	
ENSMUST00000168683	ENSMUSG00000006498	10	79854427	79864771	1	1	0	0	41	1	2	0	0	0	9	0	E9Q0W3	
ENSMUST00000168684	ENSMUSG00000049985	13	112288451	112384002	1	2	0	0	0	0	0	0	0	0	24	2	Q8BV14	
ENSMUST00000168689	ENSMUSG00000033857	11	118476829	118489209	1	3	1	0	0	1	0	4	18	0	5	9	F7CXI4	
ENSMUST00000168690	ENSMUSG00000022247	15	10474779	10485947	-1	0	0	0	0	0	0	1	3	0	0	0	F6WEP7	
ENSMUST00000168691	ENSMUSG00000025602	9	40192316	40213604	1	45	50	54	86	42	33	3	33	0	12	19	Q99PG8	
ENSMUST00000168693	ENSMUSG00000030376	7	16130300	16160509	1	42	35	46	330	72	18	3	4	2	0	7	Q8K596	
ENSMUST00000168697						5	8	0	0	0	0	151	875	130	1	0		
ENSMUST00000168698	ENSMUSG00000031827	8	119809225	119840579	-1	12	6	0	0	0	0	139	72	0	0	0	Q544F6	Q9CQI6
ENSMUST00000168699						42	36	124	130	44	24	0	2	6	2	7		
ENSMUST00000168700	ENSMUSG00000053012	6	71271677	71285319	1	0	5	0	12	0	0	100	448	166	93	100		Q99JT5
ENSMUST00000168702	ENSMUSG00000090881	14	59244441	59260216	-1	7	10	20	13	12	5	1	1	0	1	1	E9PVF1	
ENSMUST00000168704						78	70	244	96	99	46	449	971	1005	135	1588		
ENSMUST00000168705						31	22	61	52	0	13	0	0	0	0	1		
ENSMUST00000168707	ENSMUSG00000014932	5	32611171	32687057	1	0	0	0	0	0	0	8	7	35	13	22	Q3TJI7	Q04736
ENSMUST00000168708	ENSMUSG00000024734	19	10914287	10920632	-1	2	0	0	2	2	0	0	0	0	0	0	F7CW32	
ENSMUST00000168710	ENSMUSG00000091491	17	18914322	18948071	1	8	7	5	1	10	2	0	0	0	0	0	K7N6Z2	
ENSMUST00000168712						0	0	0	38	3	0	0	0	0	1	0		
ENSMUST00000168713						5	9	7	4	3	1	0	1	1	0	0		
ENSMUST00000168714	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	0	0	0	0	0	0	0	17	E9PVI1	
ENSMUST00000168716	ENSMUSG00000022221	14	55784996	55788857	-1	15	10	44	50	20	12	10	126	20	0	46	E9PZP3	
ENSMUST00000168718	ENSMUSG00000024811	19	36834232	36893477	1	3	0	2	0	0	0	0	0	7	2	5	F6S169	
ENSMUST00000168720	ENSMUSG00000033159	1	75134554	75142711	-1	22	6	36	66	18	9	73	242	99	11	115		Q8K158
ENSMUST00000168722	ENSMUSG00000059586	15	59374198	59601683	1	16	16	20	4	15	4	4	25	10	9	6		Q91VT1
ENSMUST00000168723	ENSMUSG00000026740	2	18195654	18392830	-1	0	0	0	0	0	0	16	41	16	0	19	F6ZL86	
ENSMUST00000168724	ENSMUSG00000053852	X	56870163	57001558	1	0	1	0	2	0	1	0	0	0	0	0	Q80T58	
ENSMUST00000168725						14	15	109	5	7	4	0	123	0	5	0		
ENSMUST00000168726						0	0	3	12	3	2	0	0	0	0	0		
ENSMUST00000168727	ENSMUSG00000021943	14	33923587	33935280	1	20	13	28	207	30	14	0	0	0	0	0		P97737
ENSMUST00000168729	ENSMUSG00000022218	14	55700009	55713492	-1	0	0	27	76	23	22	503	455	438	0	434		
ENSMUST00000168730	ENSMUSG00000095664	7	85136240	85155902	-1	5	4	0	2	3	3	0	0	0	0	0	K7N6T2	
ENSMUST00000168731						0	0	0	25	0	0	0	1	0	0	0		
ENSMUST00000168733	ENSMUSG00000094634	14	6020654	6108665	-1	25	0	1	69	0	0	0	0	1	0	1	A6NAS8	
ENSMUST00000168736						6	5	5	3	4	1	0	0	0	0	0		
ENSMUST00000168737						0	0	2	1	0	0	1	0	0	0	0		
ENSMUST00000168738						6	6	13	2	11	2	0	0	0	0	0		
ENSMUST00000168739						2	3	6	1	5	3	0	0	0	0	0		
ENSMUST00000168740	ENSMUSG00000041920	11	109450855	109473598	-1	8	1	9	40	9	2	34	27	27	4	66	H9KV19	
ENSMUST00000168741	ENSMUSG00000003316	8	111154421	111259216	-1	0	3	0	5	5	0	108	31	52	11	106	F6RSH1	
ENSMUST00000168743	ENSMUSG00000001441	11	97205842	97280638	-1	0	0	0	0	0	0	0	2	0	0	0	F6V7K3	
ENSMUST00000168746	ENSMUSG00000029713	5	137528127	137533510	-1	0	2	2	3	0	0	1438	949	738	18	293	E9PWM7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000168747	ENSMUSG00000025324	7	58658202	58829426	1	54	23	53	278	53	21	49	73	55	9	83	Q3V1Y7	O54827
ENSMUST00000168751						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168753						5	5	16	5	0	7	0	0	0	0	0		
ENSMUST00000168755	ENSMUSG00000050144	3	88410498	88425139	-1	0	23	17	4	39	12	217	579	116	61	0	Q3TNN4	
ENSMUST00000168756	ENSMUSG00000022407	15	80948490	80970947	1	0	0	0	0	0	0	12	0	0	9	0	E9Q242	
ENSMUST00000168757	ENSMUSG00000019302	11	101009452	101063719	1	13	0	0	0	0	0	332	926	2010	206	1476	K3W4T3	
ENSMUST00000168759	ENSMUSG00000039716	9	106892825	107231909	-1	0	1	12	0	2	0	0	0	0	0	0	F6YXW9	
ENSMUST00000168761	ENSMUSG00000022247	15	10474779	10485947	-1	0	0	0	0	0	0	4	2	3	24	1	F6QAG4	
ENSMUST00000168762						1	0	4	81	0	4	0	0	0	0	0		
ENSMUST00000168764						0	0	2	0	2	1	0	0	0	0	0		
ENSMUST00000168767	ENSMUSG00000074826	13	66904914	66909236	1	14	2	37	13	17	9	0	5	0	1	2	Q3TQP0	
ENSMUST00000168769	ENSMUSG00000091101	10	100340836	100341762	1	29	20	64	10	30	16	0	0	0	0	0	E9PX25	
ENSMUST00000168771						6	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168772	ENSMUSG00000021636	13	100595957	100616971	-1	0	6	8	15	0	7	0	0	5	0	0	A1BQX3	Q3UZP0
ENSMUST00000168774	ENSMUSG00000013089	16	22381309	22439719	-1	38	21	20	0	54	16	0	78	28	0	93	Q8BJR1	
ENSMUST00000168776	ENSMUSG00000026276	1	93478964	93510260	1	0	0	0	0	0	0	0	73	113	179	162		P42208
ENSMUST00000168779	ENSMUSG00000071252	13	77135540	77613291	1	20	13	16	19	12	14	3	6	10	8	3		Q3UPC7
ENSMUST00000168780	ENSMUSG00000025404	10	127380327	127499384	1	0	2	0	0	0	1	0	0	0	0	0	E9Q013	
ENSMUST00000168782	ENSMUSG00000021922	14	30886476	30901981	1	11	1	0	0	0	15	5	0	5	0	8	E9Q5L2	
ENSMUST00000168783	ENSMUSG00000026288	1	87620312	87720507	1	0	13	35	12	0	0	1243	0	1911	0	1307		Q9ES52
ENSMUST00000168785						0	0	35	0	7	3	10	0	9	4	27		
ENSMUST00000168786	ENSMUSG00000041115	X	152144268	152225236	1	15	0	0	200	0	0	0	0	0	0	0	A4GZ26	
ENSMUST00000168787	ENSMUSG00000062202	17	30215524	30576287	-1	34	36	177	68	109	47	363	375	424	51	237		Q8C726
ENSMUST00000168790	ENSMUSG00000090404	14	6765962	6774411	-1	4	0	0	0	0	0	0	0	0	0	0	K7N6Y6	
ENSMUST00000168793	ENSMUSG00000055003	6	119315133	119330766	-1	0	7	0	0	4	6	1	0	0	0	2		Q8BGX3
ENSMUST00000168794	ENSMUSG00000091638	7	20787285	20788208	1	0	0	0	0	0	0	0	0	0	0	0	E9Q1Q5	
ENSMUST00000168795						6	3	24	81	0	0	0	0	0	0	13		
ENSMUST00000168797	ENSMUSG00000079012	12	104338486	104394257	1	14	3	6	4	4	2	0	0	0	14	0		Q03734
ENSMUST00000168798						8	3	9	57	4	0	157	317	207	20	85		
ENSMUST00000168799						0	0	0	10	0	0	0	0	1	0	0		
ENSMUST00000168801	ENSMUSG00000003153	6	122727809	122801640	-1	0	0	1	0	0	0	4	0	0	0	0	E9Q4C4	
ENSMUST00000168802	ENSMUSG00000001280	15	102406143	102436404	1	1	0	0	3	0	2	2	0	0	0	0	E9Q2V3	
ENSMUST00000168805						0	3	8	8	6	0	35	114	64	61	69		
ENSMUST00000168806						34	36	82	46	39	12	1	9	7	2	17		
ENSMUST00000168807	ENSMUSG00000090892	7	8136950	8161654	-1	26	31	93	33	26	21	0	0	0	0	0	E9Q5C7	
ENSMUST00000168808						0	0	0	0	0	0	0	1	1	0	1		
ENSMUST00000168810	ENSMUSG00000041014	14	38368952	39473088	-1	3	1	0	0	0	0	0	0	0	0	0	E9Q396	
ENSMUST00000168811	ENSMUSG00000078954	15	84720052	84772207	1	5	0	10	0	0	2	1	0	0	1	2		Q9CXP4
ENSMUST00000168813						0	0	2	53	3	0	0	0	2	0	0		
ENSMUST00000168815	ENSMUSG00000044678	15	74796874	74799986	-1	0	2	0	0	0	3	0	0	0	1	0		Q9CWP4
ENSMUST00000168816						3	2	9	3	2	0	0	0	0	0	0		
ENSMUST00000168817						7	7	9	27	0	10	59	789	72	53	131		
ENSMUST00000168818	ENSMUSG00000049130	7	16246743	16259540	-1	19	0	24	0	26	20	254	551	509	127	636		P30993
ENSMUST00000168821	ENSMUSG00000021557	13	59449537	59585227	-1	4	1	15	1	1	0	0	0	2	0	0	Q8C1R2	
ENSMUST00000168822	ENSMUSG00000005262	16	18811779	18835261	1	0	0	1	0	0	0	0	0	0	0	0	E9Q6S9	
ENSMUST00000168824	ENSMUSG00000025243	9	123593820	123632565	-1	0	0	0	0	0	0	0	0	0	0	0	F7AVF9	
ENSMUST00000168825	ENSMUSG00000030782	7	128246812	128255699	1	8	8	34	19	16	8	0	0	0	0	0	E9PYQ1	
ENSMUST00000168828	ENSMUSG00000000552	15	103313895	103340086	-1	17	3	35	312	20	10	545	568	471	35	318		Q8VD12
ENSMUST00000168831	ENSMUSG00000019558	X	73673150	73682502	1	0	0	0	0	0	0	0	0	0	0	0	F6UKB4	
ENSMUST00000168832	ENSMUSG00000025602	9	40192316	40213604	1	0	0	5	0	0	0	0	0	13	0	0	E9Q2D3	
ENSMUST00000168833	ENSMUSG00000037536	14	47472561	47531962	1	37	0	25	0	23	7	95	217	144	71	106		Q80XI1
ENSMUST00000168834						0	0	0	0	0	0	0	0	3	0	0		
ENSMUST00000168837	ENSMUSG00000055403	6	88950683	89110031	1	21	28	32	20	32	13	1	14	4	1	6	Q8CDD1	
ENSMUST00000168838	ENSMUSG00000092008	19	39842660	39886769	-1	10	3	3	1	13	2	0	0	0	0	0	E9PXC3	
ENSMUST00000168839	ENSMUSG00000004677	8	71272714	71360712	1	0	0	0	0	0	0	1012	1	782	0	1054	E9PWZ6	
ENSMUST00000168841	ENSMUSG00000049103	9	124101950	124113557	1	69	45	88	545	100	71	128	733	190	230	193	Q543S8	P51683
ENSMUST00000168843						31	30	62	35	35	12	1	8	5	0	7		
ENSMUST00000168844	ENSMUSG00000032396	9	64306756	64341288	-1	26	22	48	0	0	17	39	123	68	20	84		Q8C0S1
ENSMUST00000168846	ENSMUSG00000067713	15	98812798	98831508	-1	11	7	19	19	16	13	1934	4187	1835	496	1334	Q3TWR3	O54950
ENSMUST00000168847	ENSMUSG00000007610	8	71488103	71499583	1	6	3	10	26	5	3	0	0	0	1	0	E9PWV7	
ENSMUST00000168852						4	2	11	9	3	0	16	65	47	2	51		
ENSMUST00000168855	ENSMUSG00000021670	13	96648967	96670936	-1	3	3	7	0	0	0	0	22	0	32	44	E9Q149	
ENSMUST00000168856						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000168858	ENSMUSG00000079333	17	81441763	81441923	1	0	0	0	0	0	0	0	0	0	0	0	F6ZF91	
ENSMUST00000168862						1	2	5	37	0	3	0	2	0	0	4		
ENSMUST00000168863	ENSMUSG00000015363	15	89075124	89087077	1	0	0	0	2	0	0	107	15	48	12	42	E9Q7A5	
ENSMUST00000168864	ENSMUSG00000037206	9	58156265	58159221	-1	7	0	33	31	16	10	3	1	1	0	2		Q6GU68
ENSMUST00000168866	ENSMUSG00000091418	14	4415448	4443839	1	9	2	0	4	2	2	0	0	0	0	0	L7N2B9	
ENSMUST00000168869	ENSMUSG00000005547	7	26835305	26843548	1	0	0	14	13	6	0	0	0	0	0	0	E9Q5D4	
ENSMUST00000168871	ENSMUSG00000045034	13	92425896	92441658	1	16	10	30	115	25	15	1	1	0	0	0		Q3UUF8
ENSMUST00000168872	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	341	0	115	0	73	E9Q9N6	
ENSMUST00000168875	ENSMUSG00000091049	5	25999022	26004798	-1	2	20	9	21	14	9	0	0	0	0	0	E9QAN3	
ENSMUST00000168877	ENSMUSG00000091614	17	29519281	29519790	-1	6	5	4	9	5	3	0	0	1	0	0	E9PWY5	
ENSMUST00000168878	ENSMUSG00000029381	5	92683435	92965318	1	0	0	0	0	0	0	0	0	0	1	0	E9Q6I3	
ENSMUST00000168879	ENSMUSG00000078937	15	89416405	89425863	-1	0	3	0	0	5	1	0	0	4	0	3	F6QXT4	
ENSMUST00000168880	ENSMUSG00000060671	3	89939481	89963508	-1	3	2	1	81	6	3	0	0	0	0	0	E9Q8R2	
ENSMUST00000168882	ENSMUSG00000025423	18	77065208	77155708	1	20	1	22	0	1	9	0	0	0	1	0	G3UWE3	
ENSMUST00000168883	ENSMUSG00000013353	7	43492044	43505940	-1	0	0	0	1	0	0	0	2	1	1	11	E9Q1U5	
ENSMUST00000168884	ENSMUSG00000001249	7	31098725	31115290	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWE8	
ENSMUST00000168885						5	2	8	7	4	2	0	0	0	0	1		
ENSMUST00000168887	ENSMUSG00000024070	17	78949405	79020816	-1	0	0	0	13	0	8	23	0	3	0	26		Q8K1Y2
ENSMUST00000168888	ENSMUSG00000051648	8	105382807	105413502	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVN1	
ENSMUST00000168889	ENSMUSG00000022021	14	86655367	87141224	-1	0	2	0	0	0	0	17	9	28	8	23		Q9Z207
ENSMUST00000168890	ENSMUSG00000042834	18	33437019	33464029	-1	0	0	0	15	0	0	0	0	0	0	0	Q542Q5	Q07475

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000168891	ENSMUSG00000022884	16	23107444	23114136	1	0	0	0	0	7	0	0	0	0	12	0	E9Q561	
ENSMUST00000168892	ENSMUSG00000057842	13	67312998	67332560	-1	3	0	2	4	2	1	15	33	4	11	7	Q8BIN6	
ENSMUST00000168894						11	0	22	7	9	8	3	0	0	0	1		
ENSMUST00000168895						0	0	8	12	0	1	0	0	0	0	0		
ENSMUST00000168899						0	2	0	43	1	0	0	0	4	29	7		
ENSMUST00000168900	ENSMUSG00000042747	3	89245966	89249906	1	3	0	6	46	5	0	121	246	111	163	105	A0A0A0MQN1	
ENSMUST00000168902	ENSMUSG00000000753	11	75409769	75422701	-1	6	7	5	3	1	0	3	8	0	6	0	E9PXR9	
ENSMUST00000168905						0	3	0	0	2	0	0	0	0	0	0		
ENSMUST00000168906	ENSMUSG00000090594	14	44123851	44129043	1	4	2	13	4	8	1	0	0	0	0	0	F7C9A1	
ENSMUST00000168907	ENSMUSG00000025915	1	9798107	9900845	1	0	0	0	0	0	0	116	313	75	131	65		Q9ERE3
ENSMUST00000168908						5	3	10	7	6	7	2	6	0	1	12		
ENSMUST00000168910	ENSMUSG00000029530	9	123678439	123783457	1	0	0	0	0	0	0	0	0	0	0	17		Q9WUT7
ENSMUST00000168914						20	23	75	60	39	9	0	4	4	0	5		
ENSMUST00000168916	ENSMUSG00000027257	2	91255954	91264679	1	0	0	0	0	0	0	2	0	0	3	0	Q543N7	Q99JB8
ENSMUST00000168918	ENSMUSG00000025880	18	75367529	75395935	1	7	1	0	0	3	2	0	32	34	0	36	B2RPW6	O35253
ENSMUST00000168919	ENSMUSG00000030149	6	129610323	129623864	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TCW7	
ENSMUST00000168920						1	3	1	2	7	3	0	0	0	0	0		
ENSMUST00000168921	ENSMUSG00000025245	9	123694416	123717625	-1	1	0	0	0	0	0	14	73	23	76	8	F6VTH5	
ENSMUST00000168922	ENSMUSG00000038838	17	35655634	35667592	-1	0	0	8	34	12	0	13	0	0	0	7	F6YJY2	
ENSMUST00000168923						8	15	16	8	6	3	0	6	4	4	5		
ENSMUST00000168924						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168926	ENSMUSG00000094532	7	23019006	23019923	-1	0	0	0	0	0	0	0	0	0	0	0	D3YTX5	
ENSMUST00000168928	ENSMUSG00000011960	15	98538689	98570923	-1	13	3	44	12	6	0	36	0	28	0	76	E9Q7A7	
ENSMUST00000168930	ENSMUSG00000022176	14	54476100	54480431	1	0	0	0	0	0	0	0	0	0	0	1	F6Z0Z5	
ENSMUST00000168931	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	6	0	0	4	E9Q3S9	
ENSMUST00000168933						1	0	0	5	3	5	7	396	11	0	19		
ENSMUST00000168934						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000168936	ENSMUSG00000001089	4	136469761	136554780	1	1	1	2	0	2	1	0	4	0	0	3	F6XG76	
ENSMUST00000168937	ENSMUSG00000042688	9	75369062	75410005	-1	0	26	58	0	28	13	397	531	238	0	193		Q61532
ENSMUST00000168938	ENSMUSG00000023883	17	14945009	14961273	-1	6	7	13	15	14	5	41	104	68	12	84	E9Q5L7	
ENSMUST00000168941	ENSMUSG00000026983	2	24276954	24283426	1	0	4	2	1	0	0	0	0	0	0	0		Q9QYY1
ENSMUST00000168943						0	0	0	19	5	0	0	0	0	0	0		
ENSMUST00000168944	ENSMUSG00000004347	6	56069804	56569103	-1	1	0	0	0	0	0	0	0	0	0	0		Q64338
ENSMUST00000168945	ENSMUSG00000095710	5	10947805	11044948	1	0	2	0	0	0	0	0	0	0	0	0	K7N7D7	
ENSMUST00000168947	ENSMUSG00000025142	11	120672973	120709447	1	0	0	0	0	0	0	2	2	0	3	0	F7D2E0	
ENSMUST00000168948	ENSMUSG00000022561	15	76331231	76334907	1	0	0	0	0	3	0	3	8	3	0	2	F6YZ21	
ENSMUST00000168949						146	147	173	74	154	60	1	12	5	3	10		
ENSMUST00000168952						9	4	7	10	7	4	0	0	0	0	0		
ENSMUST00000168953	ENSMUSG00000094383	JH584299.1	90482	93220	1	31	46	0	50	37	22	0	0	0	0	0		
ENSMUST00000168954	ENSMUSG00000041444	9	32116136	32268446	1	12	16	8	15	24	16	8	15	11	0	23		Q811P8
ENSMUST00000168956						1	3	26	1	4	1	36	37	27	0	36		
ENSMUST00000168958	ENSMUSG00000030970	7	132987563	133124354	-1	5	0	13	1	1	4	0	0	0	0	0	E9PWQ9	
ENSMUST00000168959						0	0	0	100	0	2	0	1	0	0	0		
ENSMUST00000168960	ENSMUSG00000078648	15	95824459	95830072	-1	7	1	36	2	8	5	1	0	1	2	0	E9Q4A1	
ENSMUST00000168961						10	5	26	11	7	3	0	0	2	0	0		
ENSMUST00000168963						1	5	3	3	0	0	0	0	0	0	0		
ENSMUST00000168965	ENSMUSG00000029672	6	22306520	22356243	-1	6	1	4	1	5	0	0	0	4	2	3	E9Q6F0	
ENSMUST00000168967	ENSMUSG00000028273	3	142239590	142395696	-1	20	0	16	25	16	0	33	0	36	7	35	D9J303	
ENSMUST00000168971	ENSMUSG00000001416	3	88297116	88321767	1	0	0	0	0	0	0	0	0	0	0	0	F6ZVG8	
ENSMUST00000168972	ENSMUSG00000052334	14	41943995	42003821	1	0	0	0	0	0	0	0	0	0	3	0	E9PZD6	
ENSMUST00000168973						0	0	1	0	0	1	0	0	8	0	15		
ENSMUST00000168974	ENSMUSG00000003644	4	133847290	133887797	-1	6	0	14	0	27	4	5212	5204	5265	239	2711	E9PWV3	
ENSMUST00000168976						4	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000168977	ENSMUSG00000021244	12	84996321	85070515	1	0	1	0	223	9	0	9	169	7	0	43	E9Q803	
ENSMUST00000168979	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVF3	
ENSMUST00000168981	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	0	0	0	0	0	0	0	3	E9PVS2	
ENSMUST00000168982						0	0	0	0	0	0	0	0	1	0	6		
ENSMUST00000168984	ENSMUSG00000094735	7	20193710	20194633	1	0	0	0	0	7	0	0	0	0	0	0	E9PUW9	
ENSMUST00000168986	ENSMUSG00000021906	14	32085374	32103202	1	0	1	0	0	0	0	0	0	0	0	6	E9PZL5	
ENSMUST00000168988						4	0	7	17	7	0	0	0	0	0	4		
ENSMUST00000168989	ENSMUSG00000036225	18	14968685	15151446	-1	20	22	43	838	48	22	14	18	22	2	12	E9Q6T9	
ENSMUST00000168991	ENSMUSG00000022255	15	34082694	34142386	1	0	0	0	16	0	0	0	0	25	15	58	E9PUX0	
ENSMUST00000168992	ENSMUSG00000051359	15	37366175	37792570	-1	0	0	0	0	0	0	0	0	0	0	0		Q91X97
ENSMUST00000168993						2	2	17	4	3	1	0	0	0	0	0		
ENSMUST00000168997	ENSMUSG00000094120	10	77758990	77759682	-1	12	18	41	139	42	12	0	0	0	0	0	E9Q2H5	
ENSMUST00000168998	ENSMUSG00000032827	6	4902917	5165661	1	2	2	5	0	4	2	0	0	0	0	0	Q3UXW4	
ENSMUST00000169002						0	0	5	0	2	0	0	0	1	0	1		
ENSMUST00000169003	ENSMUSG00000032387	9	65629648	65660528	1	8	6	0	26	6	9	2	9	5	3	4	Q9CWY6	
ENSMUST00000169004						1	1	0	21	5	0	0	0	0	0	0		
ENSMUST00000169006	ENSMUSG00000094714	X	54622211	54639019	1	0	0	0	1	0	0	0	0	0	0	0	A6X8J1	
ENSMUST00000169007	ENSMUSG00000005547	7	26835305	26843548	1	3	5	2	0	4	0	0	0	0	0	0	F7B9W9	
ENSMUST00000169008						0	0	0	0	0	1	0	0	7	0	0		
ENSMUST00000169009	ENSMUSG00000002603	7	25687002	25705077	1	0	0	3	15	6	7	58	0	18	6	21	E9Q6I6	
ENSMUST00000169010	ENSMUSG00000024283	18	7868832	7973547	1	2	3	7	26	1	2	0	0	0	0	0	E9PVK9	
ENSMUST00000169012	ENSMUSG00000011486	17	57032773	57041654	-1	0	9	7	0	9	7	0	0	0	0	0		Q8BVN7
ENSMUST00000169013						7	4	7	1	0	2	0	0	0	0	0		
ENSMUST00000169014						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000169016	ENSMUSG00000019990	10	20398004	20725078	-1	8	9	6	9	10	6	7	0	0	0	91	E9Q5I0	
ENSMUST00000169017	ENSMUSG00000059498	1	171051174	171064935	-1	0	2	3	0	10	0	1186	8647	1989	6605	1234	E9PUV2	
ENSMUST00000169019						0	0	0	0	0	0	4	0	0	0	0		
ENSMUST00000169020	ENSMUSG00000003316	8	111154421	111259216	-1	50	52	186	112	85	42	1565	3366	4048	199	2900	Q53WR6	Q61543
ENSMUST00000169023	ENSMUSG00000091477	14	43543576	43551213	1	7	11	6	7	14	6	0	0	0	0	0	E9Q2M1	
ENSMUST00000169024	ENSMUSG00000029862	6	42286685	42315756	1	7	7	0	5	0	16	0	0	0	0	0	F7C9S1	
ENSMUST00000169025						0	3	0	0	0	2	141	416	1582	541	873		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000169028						2	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000169031						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000169032	ENSMUSG00000025950	1	65158616	65186500	-1	0	0	0	0	0	0	0	0	0	0	0		O88844
ENSMUST00000169033	ENSMUSG00000099083	15	102525946	102625464	-1	0	0	0	0	0	0	4	3	0	0	0	Q3U2X8	Q8R0S1
ENSMUST00000169034	ENSMUSG00000039530	8	39005867	39165112	1	0	0	0	0	1	2	0	0	0	5	3	Q99J74	
ENSMUST00000169035	ENSMUSG00000039782	5	43233170	43289724	1	8	14	15	225	17	5	21	86	65	5	130	E9Q5X2	
ENSMUST00000169036	ENSMUSG00000041180	19	36554639	36621135	1	1	0	25	0	0	0	0	0	2	2	4	B2RPZ5	
ENSMUST00000169037	ENSMUSG00000031659	8	88272403	88329962	1	21	0	0	151	34	22	0	0	0	0	0		P51829
ENSMUST00000169040	ENSMUSG00000002250	17	28232754	28301469	1	0	5	0	13	0	2	10	0	1	0	38	E9PV57	
ENSMUST00000169041	ENSMUSG00000035852	10	79821021	79830452	1	0	0	0	9	0	0	0	0	8	0	27		Q9D279
ENSMUST00000169042						2	1	0	0	0	0	1	3	1	2	5		
ENSMUST00000169043						4	5	6	0	5	1	0	0	0	0	0		
ENSMUST00000169047						5	2	0	4	12	2	0	0	0	0	0		
ENSMUST00000169050	ENSMUSG00000022247	15	10474779	10485947	-1	1	0	0	15	0	0	0	0	0	28	9	E9Q2V8	
ENSMUST00000169051						0	1	0	208	0	0	10	29	69	23	36		
ENSMUST00000169053	ENSMUSG00000028560	4	98923810	98935543	1	0	0	0	60	0	0	0	1	0	0	2	E9Q778	
ENSMUST00000169056	ENSMUSG00000070616	4	143535954	143542471	1	0	0	10	0	20	11	0	0	0	0	0	A2A8C4	
ENSMUST00000169057	ENSMUSG00000050122	1	37026596	37187613	1	14	6	7	8	8	8	0	0	0	0	0	Q9D5X0	
ENSMUST00000169058	ENSMUSG00000004771	9	64715299	64737758	-1	0	0	0	0	0	0	359	1271	344	94	155	E9Q3P9	
ENSMUST00000169059						0	7	4	0	0	0	0	3	0	0	0		
ENSMUST00000169061	ENSMUSG00000022191	15	12824815	12935290	1	15	18	22	55	0	18	0	0	0	0	0		Q5HZJ0
ENSMUST00000169062	ENSMUSG00000091923	14	44716838	44724987	-1	0	10	1	5	0	5	0	0	0	0	0	E9PW76	
ENSMUST00000169064	ENSMUSG00000027778	3	68892499	69004570	-1	0	0	0	0	0	1	52	19	0	16	0		Q8K057
ENSMUST00000169065						93	72	273	82	99	41	0	4	2	1	8		
ENSMUST00000169067	ENSMUSG00000015474	17	34616662	34628510	-1	9	5	11	44	9	3	0	14	0	0	13		O35448
ENSMUST00000169068	ENSMUSG00000040813	9	106658746	106685927	-1	3	8	0	0	0	0	152	169	0	51	15	E9Q137	
ENSMUST00000169069	ENSMUSG00000051786	15	89098357	89123087	-1	3	0	0	0	0	0	0	0	11	0	5	F6W5U8	
ENSMUST00000169070	ENSMUSG00000062148	14	51853699	51854643	1	13	8	15	5	16	7	0	3	0	0	0	Q923L7	
ENSMUST00000169071						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000169074	ENSMUSG00000021068	12	70011435	70111925	-1	0	0	0	9	0	0	0	143	462	0	0		Q61043
ENSMUST00000169075						1	0	4	0	0	0	1	0	0	0	0		
ENSMUST00000169078						25	10	30	23	26	8	5	6	6	2	9		
ENSMUST00000169079	ENSMUSG00000027550	3	14533788	14572658	1	11	13	8	6	12	7	2	14	5	15	5	G5E8Y2	
ENSMUST00000169082	ENSMUSG00000044217	15	99590849	99594829	1	0	9	18	7	5	0	0	0	0	9	14		Q9WTY4
ENSMUST00000169083	ENSMUSG00000021709	13	103818787	103920514	-1	0	6	0	4	13	9	2	44	0	0	0	B7ZNX6	
ENSMUST00000169085	ENSMUSG00000025731	17	25875464	25886007	1	0	0	0	8	0	0	0	0	0	0	0	E9Q5B2	
ENSMUST00000169087	ENSMUSG00000094370	14	5718336	5741577	-1	0	5	3	0	7	0	0	0	0	0	0	A6NAS9	
ENSMUST00000169088	ENSMUSG00000002900	12	31265234	31329644	1	46	24	10	39	19	18	0	0	1	0	125		P02469
ENSMUST00000169089	ENSMUSG00000020594	12	8674134	8752581	1	0	4	0	0	0	0	0	0	1364	23	272		Q80U58
ENSMUST00000169090						10	9	11	235	6	6	0	0	0	0	0		
ENSMUST00000169091	ENSMUSG00000006498	10	79854427	79864771	1	0	0	0	0	0	0	0	0	0	0	0	F7DCW4	
ENSMUST00000169092	ENSMUSG00000025198	19	44034944	44069785	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVM2	
ENSMUST00000169093	ENSMUSG00000038838	17	35655634	35667592	-1	1	1	0	0	0	0	0	0	3	1	0	F6Z939	
ENSMUST00000169094	ENSMUSG00000029405	5	92052146	92083719	-1	15	0	0	0	11	0	0	147	96	143	138	Q3U541	P97379
ENSMUST00000169095	ENSMUSG00000002944	5	17781690	17888801	-1	10	7	5	2	8	2	0	0	0	3	0	Q3UAI3	Q08857
ENSMUST00000169099	ENSMUSG00000049134	19	56320035	56390037	-1	0	9	9	0	7	0	0	0	0	0	0	F7CXG1	
ENSMUST00000169104	ENSMUSG00000037669	12	8208107	8285758	1	26	34	29	51	42	41	111	171	216	174	261	A0A0F6AIX6	
ENSMUST00000169105	ENSMUSG00000000631	11	77763246	77865980	1	0	0	0	0	0	0	26	0	0	0	0	B2RRE2	
ENSMUST00000169106						2	3	0	0	10	0	7	0	25	0	0		
ENSMUST00000169108	ENSMUSG00000022565	15	76170974	76232574	-1	0	0	0	0	0	0	9	241	7	0	5		Q9QXS1
ENSMUST00000169109	ENSMUSG00000047507	17	25242659	25256364	-1	0	0	0	12	0	3	1	0	0	0	1	E9Q350	
ENSMUST00000169113						48	51	574	103	75	34	0	3	2	0	2		
ENSMUST00000169114	ENSMUSG00000021583	13	74639872	74691875	1	14	17	15	6	23	9	128	509	351	562	283		Q9EQH2
ENSMUST00000169116	ENSMUSG00000037940	8	81342556	82125036	1	11	0	0	17	7	0	0	0	0	0	0	Q3URI3	
ENSMUST00000169120						17	7	11	26	22	4	0	0	0	0	0		
ENSMUST00000169121	ENSMUSG00000024743	19	10389090	10453181	1	12	14	41	401	110	55	0	0	0	0	0	E9PZA8	
ENSMUST00000169122	ENSMUSG00000019877	10	57515774	57532530	-1	0	0	0	0	1	0	8	5	88	0	20	E9PY81	
ENSMUST00000169123	ENSMUSG00000091013	1	182157144	182158319	-1	6	18	17	140	11	10	1	0	0	0	0	E9PVR6	
ENSMUST00000169124	ENSMUSG00000091803	12	81359026	81485127	-1	0	0	0	0	4	0	0	0	0	0	0	E9Q5H8	
ENSMUST00000169125	ENSMUSG00000091764	8	69654479	69666982	1	7	3	2	1	2	1	0	2	1	0	0	F6Y9Y8	
ENSMUST00000169126	ENSMUSG00000071984	17	7738569	7827302	-1	2	2	1	9	5	4	0	0	0	0	0	E9PXG4	
ENSMUST00000169128						26	21	47	28	25	13	1	5	2	1	6		
ENSMUST00000169129	ENSMUSG00000051910	7	115470872	116038796	-1	7	10	9	3	21	5	0	0	0	0	0	E9PUW0	
ENSMUST00000169130	ENSMUSG00000091926	7	42764438	42793496	-1	12	9	7	0	7	5	0	0	0	0	0	K7N712	
ENSMUST00000169133	ENSMUSG00000071711	15	78406712	78414002	1	11	3	8	30	6	0	34	104	0	0	16	Q3UW66	
ENSMUST00000169134						0	4	0	0	0	0	23	136	54	7	44		
ENSMUST00000169137	ENSMUSG00000079471	17	45600967	45602102	-1	0	2	4	25	0	4	0	0	0	0	0	E9PXI1	
ENSMUST00000169139						0	0	15	22	0	0	441	5	325	27	353		
ENSMUST00000169141	ENSMUSG00000025020	19	41600257	41743665	-1	41	46	58	115	56	18	1	1	0	0	1	E9Q2P0	
ENSMUST00000169142	ENSMUSG00000057842	13	67312998	67332560	-1	2	0	0	0	0	0	0	84	33	0	0	Q8BIN6	
ENSMUST00000169143	ENSMUSG00000049676	7	29181321	29214035	-1	0	0	0	0	0	0	0	0	9	0	0		E9Q355
ENSMUST00000169144						2	2	2	4	2	1	0	0	0	0	0		
ENSMUST00000169145						7	6	0	0	3	3	0	0	0	0	0		
ENSMUST00000169148	ENSMUSG00000096279	12	24251846	24252181	-1	0	2	1	186	7	0	0	0	0	0	0	L7N2D1	
ENSMUST00000169149	ENSMUSG00000021910	14	31170930	31216946	-1	0	0	0	0	0	0	0	0	4	0	0	F7AVB2	
ENSMUST00000169150						5	7	6	3	4	1	18	33	5	0	20		
ENSMUST00000169152	ENSMUSG00000095360	14	6435796	6444611	-1	0	0	0	0	2	0	0	0	0	0	0	K7N711	
ENSMUST00000169154	ENSMUSG00000090302	5	88268919	88282835	1	2	0	2	1	2	3	0	0	0	0	0	E9Q079	
ENSMUST00000169155	ENSMUSG00000093896	12	115847881	115848331	-1	1	2	0	1	2	1	0	0	0	1	0	A0A0B4J1N0	
ENSMUST00000169156	ENSMUSG00000090121	12	70154142	70183887	1	0	0	0	0	0	0	0	0	0	0	0	G3UZN6	
ENSMUST00000169158	ENSMUSG00000090935	12	81497941	81532911	-1	0	0	0	0	0	0	4	2	0	0	0		Q9D6K5
ENSMUST00000169159	ENSMUSG00000024673	19	11249675	11266241	-1	6	4	1	5	6	1	32	22	34	140	103	Q542S5	P19437
ENSMUST00000169161	ENSMUSG00000042350	12	84918148	84970900	-1	19	15	17	10	22	15	12	6	20	2	5	E9PY98	
ENSMUST00000169162	ENSMUSG00000023050	15	102497649	102517064	-1	0	1	0	0	0	0	0	0	0	0	0	E9PZU4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000169164						0	0	0	74	1	0	0	0	0	0	0		
ENSMUST00000169165	ENSMUSG00000095758	7	21349373	21350296	1	0	0	0	0	0	0	0	0	0	0	0	L7N2B4	
ENSMUST00000169168	ENSMUSG00000033470	14	73029128	73049114	-1	0	5	6	6	6	2	1	5	1	3	9		Q920A1
ENSMUST00000169169	ENSMUSG00000091898	14	31208312	31211729	1	0	1	0	5	2	0	1	2	3	0	0		P19123
ENSMUST00000169172	ENSMUSG00000028030	3	132684144	132841688	1	11	10	18	30	11	0	79	153	180	13	88	E9Q1W7	
ENSMUST00000169176						0	3	4	2	2	1	1	0	0	0	1		
ENSMUST00000169177						0	0	0	26	1	1	0	0	0	0	0		
ENSMUST00000169178						12	4	28	23	25	7	0	0	0	0	0		
ENSMUST00000169179	ENSMUSG00000031661	8	88521344	88594887	1	0	19	35	0	28	5	1	2	2	0	4	E9Q5K6	
ENSMUST00000169181						1	0	3	0	2	0	2	7	0	0	0		
ENSMUST00000169182						6	0	4	0	4	0	0	0	0	0	1		
ENSMUST00000169184						4	0	13	4	4	5	0	0	0	0	0		
ENSMUST00000169186	ENSMUSG00000035790	16	32099800	32108069	1	0	1	0	0	0	0	608	3308	950	2220	478		Q9CQA8
ENSMUST00000169187						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000169188	ENSMUSG00000007656	9	75037614	75060313	1	2	1	0	0	1	1	7	0	5	23	0	E9Q4B9	
ENSMUST00000169189	ENSMUSG00000024459	17	36984061	36989537	-1	3	5	0	11	3	5	0	0	0	0	0	A7VMS3	
ENSMUST00000169190	ENSMUSG00000092060	5	67392147	67428310	-1	122	111	758	267	123	78	1739	4087	3846	286	2483		P86174
ENSMUST00000169192	ENSMUSG00000005986	19	4270180	4283137	-1	1	0	11	0	0	0	0	6	0	0	0	F7C8Z0	
ENSMUST00000169194						4	2	10	1	3	1	318	208	651	5	688		
ENSMUST00000169195						2	2	6	112	4	3	5	1	4	0	2		
ENSMUST00000169196	ENSMUSG00000021670	13	96648967	96670936	-1	1	0	1	120	6	1	0	0	8	0	2	E9PY17	
ENSMUST00000169197						0	0	1	0	0	0	0	9	0	1	0		
ENSMUST00000169198	ENSMUSG00000026271	1	92950865	92986391	1	21	11	44	44	29	10	9	182	31	6	71	Q3TBY9	Q9ES90
ENSMUST00000169200	ENSMUSG00000024158	17	24840143	24864450	1	0	5	6	0	0	4	63	43	19	44	17	E9PYA3	
ENSMUST00000169201	ENSMUSG00000047773	11	89420987	89639631	-1	0	9	9	11	0	0	0	0	0	0	0	F6X7B3	
ENSMUST00000169202	ENSMUSG00000021670	13	96648967	96670936	-1	3	6	2	0	3	0	7	6	6	6	28	F6X166	
ENSMUST00000169204	ENSMUSG00000022403	15	81363669	81400077	-1	2	0	1	0	0	1	0	0	0	1	1	E9Q5V1	
ENSMUST00000169206	ENSMUSG00000090864	7	8907173	8931504	-1	0	0	0	0	0	0	0	0	0	0	0	K7N728	
ENSMUST00000169207						5	7	3	3	6	3	0	3	3	0	0		
ENSMUST00000169208						0	1	5	3	0	1	4	0	0	0	0		
ENSMUST00000169211	ENSMUSG00000028523	4	102986379	103005594	1	6	0	2	0	0	1	0	0	0	0	0	G3UW44	
ENSMUST00000169212	ENSMUSG00000054252	5	33721674	33737068	1	10	6	0	235	32	19	0	0	0	0	0	Q7TSI8	
ENSMUST00000169213						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169214						2	0	2	0	1	0	6	0	11	53	61		
ENSMUST00000169215	ENSMUSG00000094021	14	7036535	7044970	-1	5	3	0	0	3	0	0	2	0	0	0	K7N6U3	
ENSMUST00000169220	ENSMUSG00000034116	17	57279100	57328031	1	0	0	0	0	0	0	1555	5079	2092	389	1649	E9PXI0	
ENSMUST00000169222	ENSMUSG00000028064	3	88435959	88461182	-1	0	0	7	0	0	0	0	398	3	0	561		Q62178
ENSMUST00000169224						9	2	19	5	7	6	4	0	0	0	0		
ENSMUST00000169226	ENSMUSG00000018893	15	77015489	77050670	-1	11	3	6	3	10	6	0	0	0	0	0	Q3UVB1	P04247
ENSMUST00000169228						4	1	1	1	0	0	10	3	0	14	10		
ENSMUST00000169230	ENSMUSG00000007034	17	34914466	34930436	1	0	0	0	4	0	0	2	0	4	2	0	E9PWK0	
ENSMUST00000169232	ENSMUSG00000050447	2	50066429	50193569	1	19	12	0	0	9	2	0	0	0	0	0		Q8BPP5
ENSMUST00000169234	ENSMUSG00000012705	8	3655770	3660110	1	7	5	24	9	11	10	4	15	9	2	15	Q5BMX4	Q99P87
ENSMUST00000169235						11	6	5	5	9	2	0	4	0	0	0		
ENSMUST00000169237	ENSMUSG00000040472	14	55715873	55722257	-1	6	0	30	172	41	0	15	107	15	0	39		Q9JHK4
ENSMUST00000169238	ENSMUSG00000022407	15	80948490	80970947	1	0	0	0	0	0	2	0	3	0	0	5	E9Q0A0	
ENSMUST00000169239						0	0	1	0	0	1	0	0	0	0	4		
ENSMUST00000169240	ENSMUSG00000028024	3	129269175	129332720	-1	0	0	1	0	0	0	1	0	0	0	0	F6YHW2	
ENSMUST00000169241	ENSMUSG00000026466	1	156004599	156036480	-1	0	6	0	0	0	0	712	2265	808	69	660	E9PWW2	
ENSMUST00000169247	ENSMUSG00000096468	X	54531208	54548016	1	0	0	0	0	0	0	0	0	0	0	0	A6X8J1	
ENSMUST00000169252	ENSMUSG00000048440	17	32536558	32551798	1	0	1	1	3	4	0	0	0	5	0	0	E9QB04	
ENSMUST00000169255						0	0	6	0	0	0	22	84	0	6	29		
ENSMUST00000169256	ENSMUSG00000063455	6	38123174	38254009	-1	50	30	60	66	81	52	0	0	2	0	14		Q68FD9
ENSMUST00000169259						1	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000169264	ENSMUSG00000020286	11	23516203	23521155	-1	0	1	0	0	0	0	0	0	0	0	0		Q810S2
ENSMUST00000169266	ENSMUSG00000005442	7	25267704	25294159	1	41	18	157	942	73	37	2190	763	1961	49	1732		Q924A2
ENSMUST00000169268						5	1	0	0	0	2	0	33	0	4	0		
ENSMUST00000169269	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	4	2	0	0	0	9	11	8	E9Q8C8	
ENSMUST00000169270	ENSMUSG00000000628	6	82725025	82774454	-1	1	2	7	6	5	1	0	0	0	0	0	E9Q9M6	
ENSMUST00000169273	ENSMUSG00000054008	18	60685978	60713389	-1	46	36	122	73	72	32	6748	4472	7893	491	5536		Q3UHN9
ENSMUST00000169280	ENSMUSG00000024050	17	32354055	32389401	-1	0	0	0	60	0	0	0	0	1	0	0	E9PZC6	
ENSMUST00000169282	ENSMUSG00000053040	9	66814994	66834726	-1	40	38	148	182	55	37	297	930	402	132	343		Q9DCZ9
ENSMUST00000169283						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169287	ENSMUSG00000015474	17	34616662	34628510	-1	0	0	1	0	0	1	0	0	0	0	0	E9PVM9	
ENSMUST00000169288	ENSMUSG00000031934	9	15005161	15045478	-1	0	0	1	0	2	2	6	4	8	0	7	E9PY07	
ENSMUST00000169289	ENSMUSG00000022565	15	76170974	76232574	-1	3	2	32	6	5	5	0	0	0	0	0	E9PW24	
ENSMUST00000169290	ENSMUSG00000002718	2	166906040	166946389	1	9	0	0	0	7	8	63	82	23	100	34	E9QAX7	
ENSMUST00000169295	ENSMUSG00000051998	1	133679091	133690108	-1	24	8	31	31	23	14	19	34	16	12	84		Q8BHB3
ENSMUST00000169299	ENSMUSG00000061723	7	142498836	142516009	1	7	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169302						0	0	1	3	2	0	0	0	0	0	4		
ENSMUST00000169303	ENSMUSG00000053825	10	106470310	106933467	1	24	31	54	14	14	18	0	0	0	0	1		
ENSMUST00000169304	ENSMUSG00000025204	19	44548572	44555440	-1	1	1	1	2	5	4	0	0	0	0	22	F6VCY0	
ENSMUST00000169305						0	0	0	12	1	1	0	0	0	0	0		
ENSMUST00000169307	ENSMUSG00000047352	9	39954257	39957069	-1	13	8	21	13	12	11	0	0	0	0	1	Q8VF15	
ENSMUST00000169308	ENSMUSG00000025731	17	25875464	25886007	1	4	15	88	0	0	0	20	74	0	17	29	G5E8X1	
ENSMUST00000169309	ENSMUSG00000035351	10	88146992	88178388	1	7	0	15	24	0	7	0	0	0	17	0		Q9CWU9
ENSMUST00000169310	ENSMUSG00000030314	6	114643097	114860614	1	24	20	0	0	8	0	0	0	0	0	0	A0A0A0MQN4	
ENSMUST00000169311	ENSMUSG00000003848	8	107412486	107425051	-1	0	2	0	1	0	0	4	0	0	3	0	E9PW56	
ENSMUST00000169312	ENSMUSG00000046691	8	106883863	106893601	-1	22	23	39	0	0	0	751	1228	443	122	184		P0CG14
ENSMUST00000169313						0	0	0	4	0	1	0	0	0	0	0		
ENSMUST00000169314	ENSMUSG00000058258	13	8885501	8892451	1	83	43	89	667	90	45	132	483	286	557	181	G3XA48	
ENSMUST00000169317						0	0	0	0	0	0	0	26	8	27	5		
ENSMUST00000169319	ENSMUSG00000001627	12	40201567	40248504	-1	0	0	0	0	0	1	0	0	0	0	0	E9QA50	
ENSMUST00000169321						0	1	0	3	1	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000169322	ENSMUSG00000095206	13	66851343	66851513	-1	0	0	0	0	0	0	0	0	0	0	0	L7N2C1	
ENSMUST00000169324	ENSMUSG00000040596	1	166384622	166409863	-1	8	19	33	0	25	31	16	25	18	0	59	E9Q3B2	
ENSMUST00000169329	ENSMUSG00000083012	5	143548706	143564531	1	0	0	0	0	0	0	0	0	0	0	0		Q3ZN08
ENSMUST00000169333						6	1	8	1	6	1	0	39	8	27	0		
ENSMUST00000169335	ENSMUSG00000037813	2	158182533	158229222	-1	0	0	0	0	0	0	0	0	0	0	0	A2AC60	
ENSMUST00000169339						0	0	0	0	0	0	0	13	0	0	5		
ENSMUST00000169343	ENSMUSG00000022587	15	74955051	74959905	1	0	18	27	10	18	0	4	73	18	0	33	Q99JA5	
ENSMUST00000169345	ENSMUSG00000009394	6	115134902	115282006	1	18	19	74	20	31	13	0	0	0	0	0		Q64332
ENSMUST00000169347	ENSMUSG00000066952	5	114289166	114365357	1	0	8	0	16	0	9	0	2	0	0	0	E9PWM9	
ENSMUST00000169350	ENSMUSG00000029797	6	48448229	48501250	1	111	32	127	249	119	46	0	0	0	0	0	E9Q0I4	
ENSMUST00000169353	ENSMUSG00000031788	8	95099832	95142540	-1	11	0	13	0	15	0	16	151	81	27	70		
ENSMUST00000169354						0	0	5	2	0	0	0	0	0	0	0		
ENSMUST00000169357	ENSMUSG00000092118	7	51860577	51862267	-1	9	4	6	117	4	6	9	11	12	3	12	E9Q5Z5	
ENSMUST00000169358						4	4	0	0	0	0	0	4	5	0	0		
ENSMUST00000169360	ENSMUSG00000044024	18	37955079	37959179	1	1	0	0	0	0	2	0	0	0	0	0	E9Q2K0	
ENSMUST00000169361	ENSMUSG00000090505	14	41484232	41489485	-1	3	3	7	8	2	0	0	0	0	0	0	L7N2D0	
ENSMUST00000169362	ENSMUSG00000096023	14	5326255	5334928	-1	4	5	3	6	5	9	0	0	0	0	0	K7N6U2	
ENSMUST00000169364	ENSMUSG00000091148	14	4481745	4490177	1	0	0	0	0	0	0	0	0	0	0	0	K7N6V6	
ENSMUST00000169365	ENSMUSG00000004032	3	107895821	107898686	1	2	1	0	6	1	2	0	0	0	0	0	E9PV63	
ENSMUST00000169367	ENSMUSG00000023050	15	102497649	102517064	-1	3	0	6	85	5	6	0	0	0	0	0	E9PUZ1	
ENSMUST00000169371	ENSMUSG00000038070	4	84884309	85131921	1	21	14	0	0	0	7	14	56	49	6	29		A2AM05
ENSMUST00000169373	ENSMUSG00000091531	17	37313411	37314437	-1	9	7	5	5	7	2	0	0	0	0	1	B2RT33	
ENSMUST00000169374	ENSMUSG00000091435	7	20844098	20844985	-1	0	0	0	0	0	0	0	0	0	0	0	K7N6Y3	
ENSMUST00000169377	ENSMUSG00000023050	15	102497649	102517064	-1	0	0	28	85	6	0	11	0	9	4	22		Q60700
ENSMUST00000169378	ENSMUSG00000022561	15	76331231	76334907	1	3	3	16	23	12	6	4	18	9	0	12	E9QA52	
ENSMUST00000169381	ENSMUSG00000048003	4	134211970	134227383	-1	13	7	58	0	2	2	0	0	0	0	0	B3VNK5	
ENSMUST00000169382	ENSMUSG00000093987	Y	3367147	3410167	-1	0	24	0	0	11	2	0	0	0	0	0		O35698
ENSMUST00000169383	ENSMUSG00000023952	17	46161032	46169370	1	8	0	0	0	16	10	0	26	46	0	0	E9PVQ4	
ENSMUST00000169384	ENSMUSG00000095466	14	42763525	42768821	-1	7	9	5	7	16	3	0	0	0	0	0	F6ZAP6	
ENSMUST00000169385	ENSMUSG00000022246	15	10568979	10714631	-1	0	0	0	85	19	15	9	28	16	110	244		Q9EP71
ENSMUST00000169387	ENSMUSG00000037940	8	81342556	82125036	1	0	0	0	0	0	0	0	9	1	0	14	E9Q7X1	
ENSMUST00000169389	ENSMUSG00000091550	17	21093172	21094704	1	10	7	36	16	10	3	0	0	0	0	0	E9Q3Y8	
ENSMUST00000169390	ENSMUSG00000029326	5	100039985	100068760	1	12	13	0	0	10	5	25	75	35	0	45		Q8BGB7
ENSMUST00000169391	ENSMUSG00000047109	16	93919031	94008837	-1	0	1	0	30	0	0	0	0	0	0	0	A2RSP0	Q9Z0S3
ENSMUST00000169392	ENSMUSG00000005442	7	25267704	25294159	1	0	0	0	31	4	1	13	0	37	2	25	E9PWB7	
ENSMUST00000169393	ENSMUSG00000039294	11	121222588	121229322	-1	0	0	0	0	0	0	0	2	0	0	0	E9Q3W5	
ENSMUST00000169394	ENSMUSG00000040918	1	164249046	164265385	1	0	0	3	6	4	3	0	0	0	0	0	E9Q2R3	
ENSMUST00000169396	ENSMUSG00000073245	X	35404183	35427093	1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000169397	ENSMUSG00000024327	17	34028267	34031690	-1	0	2	0	13	5	0	405	468	102	89	228	A0A068BIT0	Q31125
ENSMUST00000169398	ENSMUSG00000074502	9	18404418	18411502	1	35	30	38	46	39	19	0	1	2	0	3		Q3USZ2
ENSMUST00000169399	ENSMUSG00000032215	9	73113426	73123333	1	1	0	0	17	0	0	45	29	43	3	0	G3UW80	
ENSMUST00000169401	ENSMUSG00000024424	18	12599926	12737050	1	7	8	13	6	7	8	38	97	27	45	56	E9PV21	
ENSMUST00000169403	ENSMUSG00000043962	4	126164082	126202760	-1	0	0	0	0	0	0	8	9	0	3	0	E9Q5X3	
ENSMUST00000169404	ENSMUSG00000019990	10	20398004	20725078	-1	1	10	9	0	16	7	0	0	0	0	0	E9Q0W7	
ENSMUST00000169406	ENSMUSG00000091277	12	48554182	48559971	-1	107	71	28	57	33	24	5	12	4	4	3	E9Q4A5	
ENSMUST00000169407	ENSMUSG00000029634	5	146209192	146221555	-1	5	2	19	0	0	0	67	960	31	0	25		Q9DBU5
ENSMUST00000169408	ENSMUSG00000023027	15	100227819	100261244	1	0	0	0	0	0	0	3	0	142	0	71	E9Q356	
ENSMUST00000169409	ENSMUSG00000026358	1	144242296	144249242	-1	0	0	0	0	0	0	4	44	2	25	43	E9PZR4	
ENSMUST00000169411						1	1	4	1	2	0	0	0	0	0	0		
ENSMUST00000169413						0	0	4	117	3	6	0	0	0	0	0		
ENSMUST00000169415	ENSMUSG00000092074	17	6310547	6317474	-1	1	0	27	15	0	0	104	515	168	644	66		P51807
ENSMUST00000169416						6	5	4	1	8	3	0	0	0	0	0		
ENSMUST00000169418	ENSMUSG00000031422	X	136732942	136743690	-1	0	0	0	0	0	0	13	16	0	0	0		Q9R0Q4
ENSMUST00000169421						0	0	5	9	0	0	0	1	0	0	0		
ENSMUST00000169422	ENSMUSG00000029790	6	30653457	30693749	-1	0	0	2	0	0	1	0	0	0	0	0	E9Q8S3	
ENSMUST00000169423	ENSMUSG00000014592	4	150917322	151861876	-1	54	37	227	259	73	34	0	0	0	0	0		A2A891
ENSMUST00000169424						1	0	0	0	3	3	0	0	0	0	0		
ENSMUST00000169426	ENSMUSG00000015749	3	95929246	95947390	1	0	0	0	5	0	0	0	0	0	0	0	A0A0G2JEK9	
ENSMUST00000169428	ENSMUSG00000060765	11	58577822	58581877	1	4	6	0	5	12	4	0	0	0	0	0	Q5NCD2	
ENSMUST00000169432						2	1	0	0	3	3	1	0	0	12	0		
ENSMUST00000169433	ENSMUSG00000091648	3	94362438	94364566	1	2	2	5	183	7	5	0	0	0	0	0		P0CG09
ENSMUST00000169434	ENSMUSG00000021557	13	59449537	59585227	-1	0	2	0	35	0	0	0	0	0	0	1	E9Q2R5	
ENSMUST00000169437	ENSMUSG00000070436	7	99345375	99353230	-1	9	18	30	141	10	13	0	0	0	0	11		P19324
ENSMUST00000169438	ENSMUSG00000022565	15	76170974	76232574	-1	8	6	50	12	12	15	74	2754	49	0	552	E9Q3W4	
ENSMUST00000169439	ENSMUSG00000091060	1	162647193	162658219	-1	3	3	2	3	0	0	0	2	0	0	0	Q3UWS6	
ENSMUST00000169441						1	7	4	0	7	5	0	1	0	0	0		
ENSMUST00000169445	ENSMUSG00000079450	X	123103495	123188795	1	0	0	0	0	0	0	0	0	0	0	0	Q8K193	
ENSMUST00000169446	ENSMUSG00000030101	6	108107028	108185582	-1	2	3	0	4	3	4	0	1	0	0	3	F6QZU1	
ENSMUST00000169447						12	0	0	0	11	3	0	0	0	0	0		
ENSMUST00000169448						6	1	25	144	8	1	2	4	0	0	2		
ENSMUST00000169449	ENSMUSG00000027894	3	107467543	107518018	-1	129	11	57	218	106	65	0	1	0	0	0		Q8BJI1
ENSMUST00000169450						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169453	ENSMUSG00000003847	8	107293470	107379517	1	0	0	0	556	0	0	99	0	0	0	0		Q9WV30
ENSMUST00000169454						3	0	33	2	12	2	25	37	27	14	28		
ENSMUST00000169457						23	22	49	19	15	8	7	20	10	3	11		
ENSMUST00000169459	ENSMUSG00000074818	19	45026906	45046614	-1	3	0	41	40	43	12	0	4	0	0	2	E9Q9W7	
ENSMUST00000169461						0	0	6	0	3	1	48	76	40	0	28		
ENSMUST00000169462	ENSMUSG00000018126	15	79258195	79285537	-1	0	0	3	123	3	0	0	0	0	0	0	E9QAX1	
ENSMUST00000169464	ENSMUSG00000061689	2	156613705	156764363	1	24	22	5	28	27	0	0	0	0	0	0		B1AZP2
ENSMUST00000169465	ENSMUSG00000091700	14	4709238	4717678	1	0	0	0	0	0	0	0	0	0	0	0	K7N6V6	
ENSMUST00000169466	ENSMUSG00000022621	15	89582533	89591923	-1	0	0	0	2	0	0	0	0	0	1	2	E9Q473	
ENSMUST00000169470	ENSMUSG00000024647	18	86711110	86718283	1	2	0	0	0	0	2	0	0	0	0	0		Q8BGU2
ENSMUST00000169472						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000169473	ENSMUSG00000096372	14	43410827	43416350	-1	0	3	9	10	10	4	0	0	0	0	0	F7BY56	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000169474						0	5	8	3	9	0	9	39	15	4	18		
ENSMUST00000169476						69	64	76	174	69	35	4	14	10	1	18		
ENSMUST00000169477						6	12	3	2	7	3	4	4	3	4	1		
ENSMUST00000169478	ENSMUSG00000024283	18	7868832	7973547	1	2	3	0	0	3	2	9	0	0	16	1	F6R357	
ENSMUST00000169479	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	7	0	0	0	12	0	0	0	G1EE51	Q99LJ7
ENSMUST00000169480	ENSMUSG00000023927	17	51736187	51833290	-1	14	14	131	0	17	5	38	283	0	25	167		Q60611
ENSMUST00000169483	ENSMUSG00000006498	10	79854427	79864771	1	0	2	0	0	0	1	0	0	0	0	0	E9Q279	
ENSMUST00000169485	ENSMUSG00000029480	5	125413858	125434121	-1	64	58	123	101	94	48	136	180	122	10	135	Q6NZL1	
ENSMUST00000169486	ENSMUSG00000010476	7	137193673	137314445	-1	0	43	46	231	61	0	0	0	0	0	0	Q6NXL3	
ENSMUST00000169488	ENSMUSG00000024050	17	32354055	32389401	-1	13	0	20	176	27	7	87	46	97	6	63	F6ZBR8	
ENSMUST00000169489	ENSMUSG00000031375	X	73483602	73495933	1	0	0	0	0	0	0	0	0	0	0	0	Q3TNY9	P28653
ENSMUST00000169492	ENSMUSG00000007656	9	75037614	75060313	1	0	0	0	0	0	0	0	187	0	0	0	E9Q827	
ENSMUST00000169496						1	0	0	1	3	0	653	990	456	49	383		
ENSMUST00000169498	ENSMUSG00000044024	18	37955079	37959179	1	0	0	0	0	0	0	0	0	0	0	0	E9Q812	
ENSMUST00000169499	ENSMUSG00000091556	X	36423601	36491830	-1	11	11	21	11	10	4	0	0	0	0	0	E9Q0C6	
ENSMUST00000169500	ENSMUSG00000022020	14	79334204	79390778	-1	1	0	0	0	2	2	0	0	4	3	4	E9Q3U5	
ENSMUST00000169503	ENSMUSG00000020954	12	51608541	51691914	-1	0	14	15	61	14	7	177	708	371	61	139	B2RQS1	
ENSMUST00000169504	ENSMUSG00000022019	14	87416639	87545373	1	13	15	6	9	4	4	3	10	10	0	2		Q91W18
ENSMUST00000169505	ENSMUSG00000059201	6	29060220	29073877	1	1	4	0	0	5	0	0	0	0	0	0	E9Q7Z0	
ENSMUST00000169507	ENSMUSG00000020166	10	116485161	116581511	-1	0	0	0	0	0	0	12	8	35	30	39	E9Q8R6	
ENSMUST00000169513	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	0	0	0	0	0	0	0	0		Q99LJ7
ENSMUST00000169517	ENSMUSG00000022369	15	55557408	55626423	1	0	0	0	0	0	2	0	0	1	0	0	F6ZKA0	
ENSMUST00000169518						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000169519	ENSMUSG00000022248	15	10486018	10499063	1	0	0	0	41	0	0	0	3	0	0	0	E9PXK0	
ENSMUST00000169520						5	2	9	10	2	2	0	0	0	0	0		
ENSMUST00000169524	ENSMUSG00000021111	12	105784694	105838944	1	0	2	0	0	0	2	0	6	8	2	0	F7DC29	
ENSMUST00000169525						4	3	8	3	8	5	0	0	0	0	0		
ENSMUST00000169527						2	0	3	2	1	0	0	0	0	0	2		
ENSMUST00000169529						4	8	13	0	9	3	48	6	16	5	10		
ENSMUST00000169530	ENSMUSG00000027957	3	116669470	116712831	-1	1	0	0	70	0	0	0	0	0	0	0	E9Q3V2	
ENSMUST00000169531	ENSMUSG00000091193	16	77846693	77853020	1	72	57	766	287	94	41	2	4	2	1	7	C6EQI3	
ENSMUST00000169532						6	3	4	7	5	0	0	0	0	0	0		
ENSMUST00000169533						2	4	1	0	2	1	2	0	0	0	0		
ENSMUST00000169534	ENSMUSG00000054892	5	72695978	72752777	-1	11	12	14	13	19	9	0	0	0	0	0	B2RQ20	
ENSMUST00000169535						5	1	0	3	0	0	7	12	6	0	15		
ENSMUST00000169536	ENSMUSG00000018820	19	42163951	42194590	1	53	32	231	170	69	48	668	2321	903	134	997		Q3TXX3
ENSMUST00000169540	ENSMUSG00000079349	X	155053061	155063145	-1	0	0	0	0	0	0	0	0	0	0	0	O89009	
ENSMUST00000169541	ENSMUSG00000024969	19	7275396	7341860	-1	0	1	0	53	0	6	0	0	0	0	0	E9Q8H5	
ENSMUST00000169542	ENSMUSG00000015652	5	5736317	5749326	-1	7	2	5	0	0	0	0	0	0	0	0	F7AFI0	
ENSMUST00000169543	ENSMUSG00000044279	17	57059105	57065918	1	0	0	0	0	0	0	0	0	0	0	1		Q8QZT4
ENSMUST00000169544	ENSMUSG00000038045	17	78883938	78906992	-1	13	9	8	5	0	8	2	0	0	0	3		P0CC03
ENSMUST00000169545	ENSMUSG00000030167	6	129666015	129678973	-1	0	0	0	1	2	0	0	0	2	0	0	E9QAJ6	
ENSMUST00000169546	ENSMUSG00000035640	10	80130451	80140835	-1	0	0	2	0	0	0	0	0	0	0	0	E9PW07	
ENSMUST00000169547	ENSMUSG00000038178	11	75531694	75577575	1	0	0	181	0	113	7	805	283	947	56	628		Q8CGA3
ENSMUST00000169548						0	11	0	0	0	0	10	20	3	0	11		
ENSMUST00000169550	ENSMUSG00000059939	4	156109982	156127265	1	0	8	25	56	11	0	20	0	0	12	31	A2ASP7	
ENSMUST00000169552						54	48	160	93	67	29	7	25	16	0	53		
ENSMUST00000169553						0	1	0	0	0	0	0	6	3	49	18		
ENSMUST00000169554	ENSMUSG00000002845	16	38558698	38592162	1	0	0	0	0	0	0	2	0	0	0	0	F6V6S1	
ENSMUST00000169555	ENSMUSG00000091227	14	7440924	7450917	-1	149	197	327	3296	168	111	0	18	2	0	2	K7N743	
ENSMUST00000169556	ENSMUSG00000091874	7	5194916	5196747	-1	10	8	16	10	11	4	0	0	0	0	0	Q9EPS9	
ENSMUST00000169557						24	15	12	13	25	16	9	47	14	5	9		
ENSMUST00000169558	ENSMUSG00000059475	9	20468549	20492746	-1	0	0	0	0	0	0	24	544	23	180	31	G5E8Z9	
ENSMUST00000169559	ENSMUSG00000091259	17	20573829	20596259	-1	0	7	0	0	11	3	0	0	0	0	0	E9PWD5	
ENSMUST00000169560	ENSMUSG00000069808	11	76179671	76214827	1	6	0	5	0	7	4	0	6	2	5	12	E9Q1B2	
ENSMUST00000169563						0	0	0	0	0	0	14	34	4	5	7		
ENSMUST00000169566						0	0	0	11	1	0	0	0	0	1	0		
ENSMUST00000169569						0	0	2	0	2	2	0	0	0	0	0		
ENSMUST00000169570	ENSMUSG00000030970	7	132987563	133124354	-1	22	10	50	36	25	10	0	0	0	0	0		P56546
ENSMUST00000169571						0	2	0	0	5	2	17	85	31	59	20		
ENSMUST00000169572	ENSMUSG00000028270	3	142620602	142638008	1	0	0	0	5	7	0	19	0	93	144	247	E9Q2N7	
ENSMUST00000169573	ENSMUSG00000041361	9	71504347	71592360	-1	0	0	0	0	0	0	0	0	0	1	0	E9Q565	
ENSMUST00000169575	ENSMUSG00000062154	15	78378400	78395912	-1	4	0	30	8	6	0	0	0	0	1	0	E9QA37	
ENSMUST00000169576	ENSMUSG00000020166	10	116485161	116581511	-1	0	3	10	0	7	0	16	191	82	33	61	E9Q7M5	
ENSMUST00000169578						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169579						0	2	0	0	3	0	8	0	0	2	6		
ENSMUST00000169580						37	19	56	8	25	0	35	169	73	31	100		
ENSMUST00000169582	ENSMUSG00000068284	16	44173246	44227465	1	107	85	265	0	1	51	447	946	243	116	244	B2RUQ2	
ENSMUST00000169583	ENSMUSG00000079265	14	44649204	44706456	-1	5	0	6	4	3	0	0	0	0	0	0	E9Q8R3	
ENSMUST00000169584	ENSMUSG00000040413	11	46668960	46707061	-1	38	37	172	47	36	23	0	1	3	0	5	A8C1R4	
ENSMUST00000169587	ENSMUSG00000090634	14	43258649	43266799	1	5	15	54	9	12	2	0	0	0	0	0	E9Q1N7	
ENSMUST00000169588	ENSMUSG00000090538	14	106100753	106101157	-1	2	2	4	1	6	6	0	0	0	0	0	F7ANJ3	
ENSMUST00000169591	ENSMUSG00000048440	17	32536558	32551798	1	13	0	0	0	0	0	125	104	174	33	152	Q99N17	
ENSMUST00000169593	ENSMUSG00000037638	12	112678828	112682747	1	0	11	62	205	22	0	1493	1428	1102	74	622		Q811H0
ENSMUST00000169594	ENSMUSG00000031010	X	13071498	13173328	1	1	0	2	55	1	1	41	4	129	0	54	E9PWA9	
ENSMUST00000169595						0	0	1	2	1	0	0	0	0	0	1		
ENSMUST00000169597	ENSMUSG00000021275	12	110889264	110972394	1	0	0	0	0	0	46	0	0	0	0	0	Q3UH45	
ENSMUST00000169598	ENSMUSG00000031553	8	24677225	24725852	-1	0	1	0	0	0	0	0	0	0	0	0	E9QA56	
ENSMUST00000169599						2	2	2	6	2	2	0	0	0	0	0		
ENSMUST00000169601	ENSMUSG00000091725	14	44285580	44291068	1	0	0	0	0	0	0	0	0	0	0	0	L7N2B0	
ENSMUST00000169603	ENSMUSG00000028780	5	17574281	17730268	1	0	0	2	0	0	0	0	0	0	0	0	E9Q0Z0	
ENSMUST00000169604	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	0	0	0	0	0	0	0	17	11	Q14AC9	Q9D9S1
ENSMUST00000169605						9	7	24	4	14	8	0	1	0	0	0		
ENSMUST00000169609	ENSMUSG00000032018	9	42254177	42264300	-1	0	0	0	11	0	6	45	391	124	78	87		O88822

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000169610						3	3	0	0	4	0	0	0	0	0	0		
ENSMUST00000169611	ENSMUSG00000023921	17	40934685	40961989	1	13	16	29	11	15	7	108	314	243	211	128		P16332
ENSMUST00000169612	ENSMUSG00000091811	7	16272014	16273692	-1	10	9	46	277	25	18	71	256	94	21	84	E9PV59	
ENSMUST00000169613	ENSMUSG00000060803	19	4035407	4037921	-1	7	1	13	13	4	1	156	224	76	71	157		P19157
ENSMUST00000169619	ENSMUSG00000001280	15	102406143	102436404	1	0	2	0	3	3	0	0	0	1	0	0	E9Q0S7	
ENSMUST00000169620						0	1	4	5	6	3	0	0	0	0	0		
ENSMUST00000169621						0	0	0	0	1	0	5	0	10	10	7		
ENSMUST00000169622	ENSMUSG00000029028	4	154011731	154021513	1	0	0	0	47	0	0	0	47	0	0	0	E9PV22	
ENSMUST00000169623	ENSMUSG00000029032	4	154278486	154301676	-1	0	0	0	0	0	0	0	0	2	0	1		Q3U5C8
ENSMUST00000169624						2	3	3	2	1	1	0	1	0	1	0		
ENSMUST00000169625						1	5	0	3	7	0	23	244	48	49	175		
ENSMUST00000169627	ENSMUSG00000037003	15	102102988	102116401	1	27	26	0	5	40	34	84	139	123	18	104		Q8CGB6
ENSMUST00000169628	ENSMUSG00000021910	14	31170930	31216946	-1	1	0	0	0	7	0	129	464	43	15	79	F6YR29	
ENSMUST00000169630	ENSMUSG00000027569	2	180581304	180586304	1	1	0	1	53	5	2	3	3	0	0	0		Q9DAT2
ENSMUST00000169631	ENSMUSG00000078598	4	113477891	113999503	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q072	
ENSMUST00000169632						0	0	12	0	1	1	0	1	0	5	10		
ENSMUST00000169637	ENSMUSG00000001289	15	102326116	102331873	1	2	1	8	6	1	0	4	18	5	5	0	E9Q5Q8	
ENSMUST00000169638	ENSMUSG00000061079	7	110061702	110095392	1	6	0	0	0	0	3	0	213	0	0	0		O70230
ENSMUST00000169644						4	0	8	0	2	0	0	0	0	0	0		
ENSMUST00000169647						1	0	2	0	2	0	0	0	0	2	0		
ENSMUST00000169649	ENSMUSG00000021906	14	32085374	32103202	1	4	0	8	6	2	0	0	0	0	0	4	E9PWW7	
ENSMUST00000169651	ENSMUSG00000032109	9	44252713	44268599	-1	0	0	0	167	4	14	172	341	536	26	362		Q3TL44
ENSMUST00000169652	ENSMUSG00000049625	13	56173703	56178885	-1	43	30	250	74	51	27	1198	2390	875	243	929		Q8JZM6
ENSMUST00000169653						4	3	0	85	0	0	10	12	12	0	15		
ENSMUST00000169656	ENSMUSG00000034532	14	65266701	65321501	1	11	11	17	6	9	10	0	1	0	1	0	Q14BG9	Q9QZM9
ENSMUST00000169657	ENSMUSG00000067356	12	17924294	17925668	1	146	114	395	623	209	138	5	21	11	1	7	Q8BL23	
ENSMUST00000169658	ENSMUSG00000034913	14	75582834	75593116	-1	11	7	13	0	0	10	0	0	0	0	0	E9Q4B1	
ENSMUST00000169659	ENSMUSG00000026409	1	130689182	130729253	-1	103	69	314	59	52	27	72	164	199	19	156	Q6GTL7	
ENSMUST00000169661						12	3	4	0	5	2	0	0	0	0	0		
ENSMUST00000169662	ENSMUSG00000005899	16	17619354	17644828	1	0	0	1	14	1	0	2	0	0	0	0	E9Q5Z0	
ENSMUST00000169664						4	5	6	4	5	0	0	7	0	0	0		
ENSMUST00000169665	ENSMUSG00000025509	7	141455198	141460743	1	0	0	0	26	5	2	292	22	600	31	383	E9PZA4	
ENSMUST00000169666						6	9	0	2	10	0	2	0	3	0	3		
ENSMUST00000169667	ENSMUSG00000022369	15	55557408	55626423	1	9	7	9	7	14	6	0	0	0	15	0		Q8BJS8
ENSMUST00000169668	ENSMUSG00000024085	17	64600736	64755110	1	2	1	0	0	0	0	25	0	170	26	116	F6QMB7	
ENSMUST00000169669	ENSMUSG00000090812	12	87199723	87213541	1	4	6	77	11	6	0	0	2	3	0	5	H9H9T8	
ENSMUST00000169670	ENSMUSG00000039552	10	33905111	33916021	1	18	21	121	23	32	22	0	0	0	0	0		Q8BYM7
ENSMUST00000169671						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000169673	ENSMUSG00000024989	19	38055025	38074425	1	8	12	10	78	8	4	22	45	48	51	14		Q8BT07
ENSMUST00000169674						3	4	8	4	3	0	2	2	0	0	6		
ENSMUST00000169675	ENSMUSG00000090872	14	4664192	4670850	1	0	0	0	1	0	0	0	0	0	0	0	E9PZ99	
ENSMUST00000169678	ENSMUSG00000090544	15	27025386	27026207	1	15	16	5	61	10	5	0	0	2	2	0	F6YTZ4	
ENSMUST00000169679	ENSMUSG00000042439	18	65580230	65689443	1	0	7	16	0	0	0	1	9	3	2	0		Q6NXK2
ENSMUST00000169681	ENSMUSG00000058655	15	102073773	102097172	1	23	33	76	82	49	32	2479	5807	3783	1028	2439		Q8BGD9
ENSMUST00000169683	ENSMUSG00000096399	7	7786151	7819867	-1	0	0	1	0	0	0	0	0	0	0	0	E9Q7U8	
ENSMUST00000169684	ENSMUSG00000020323	10	79781474	79790961	-1	15	19	33	19	16	0	95	74	0	19	38		Q14B24
ENSMUST00000169686	ENSMUSG00000091350	17	18151930	18185178	1	8	4	5	4	0	0	0	0	0	0	0	L7N2A4	
ENSMUST00000169687	ENSMUSG00000026827	2	57237635	57370719	1	0	0	13	0	0	0	0	103	0	3	0		Q64521
ENSMUST00000169689	ENSMUSG00000096903	7	20533837	20534760	1	0	0	0	0	0	0	0	0	0	0	0	L7N293	
ENSMUST00000169692	ENSMUSG00000091230	19	47170469	47171134	-1	4	2	15	3	6	3	0	0	0	0	0	F7DCP6	
ENSMUST00000169693	ENSMUSG00000031654	8	87468854	87472592	-1	11	4	18	0	9	0	0	0	0	0	0	Q7TNF5	Q9R171
ENSMUST00000169694	ENSMUSG00000023913	17	43568098	43612201	1	2	3	9	0	7	0	603	401	777	429	644	E9Q330	
ENSMUST00000169695	ENSMUSG00000078676	11	98804905	98833814	1	22	17	47	0	26	20	1344	2893	1516	113	1578		Q8K3W3
ENSMUST00000169697	ENSMUSG00000095273	7	22163118	22164035	-1	1	0	1	2	1	0	0	0	0	0	0	K7N6U0	
ENSMUST00000169698	ENSMUSG00000042250	3	90726906	90741517	1	3	11	18	16	16	6	53	128	27	24	12	B7ZMZ4	
ENSMUST00000169699						10	10	12	7	14	0	0	0	0	0	0		
ENSMUST00000169700						1	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000169701	ENSMUSG00000017286	11	76120987	76243725	-1	0	0	0	0	0	0	43	69	39	21	77	E9Q197	
ENSMUST00000169702						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169707	ENSMUSG00000011960	15	98538689	98570923	-1	25	23	50	48	27	15	429	1126	618	138	429		Q9QWV9
ENSMUST00000169712	ENSMUSG00000019992	10	20347819	20361669	1	21	12	40	48	22	13	31	85	32	29	20		Q8VED8
ENSMUST00000169713	ENSMUSG00000024998	19	38481109	38785030	1	35	13	32	10	8	12	0	0	0	0	9		Q8K4S1
ENSMUST00000169714	ENSMUSG00000022565	15	76170974	76232574	-1	0	0	0	0	0	0	163	0	72	0	230		Q9QXS1
ENSMUST00000169721	ENSMUSG00000022987	15	98285588	98296130	-1	42	15	126	7	37	22	0	2	0	0	0		Q8BZ34
ENSMUST00000169722	ENSMUSG00000056234	14	32159865	32179855	1	0	0	0	1	0	0	61	46	289	460	244	E9Q2H3	
ENSMUST00000169723	ENSMUSG00000025509	7	141455198	141460743	1	0	1	6	7	4	3	37	70	68	6	35	E9Q144	
ENSMUST00000169728	ENSMUSG00000021932	14	62292589	62372992	1	4	2	2	0	0	0	12	41	46	109	23	F6WF94	
ENSMUST00000169729	ENSMUSG00000023942	17	45585200	45599606	-1	1	0	0	16	0	2	0	0	0	0	0	E9Q3D1	
ENSMUST00000169730	ENSMUSG00000074311	7	22069057	22097907	1	0	0	0	0	0	0	0	0	0	0	0	E9Q8L6	
ENSMUST00000169732	ENSMUSG00000002728	2	145902099	145916425	1	0	0	0	0	0	0	0	0	0	0	0	E9PXA4	
ENSMUST00000169734	ENSMUSG00000017288	11	76046226	76179647	-1	0	0	0	0	0	0	3	0	55	0	28	E9Q648	
ENSMUST00000169735						4	0	10	52	6	3	0	0	0	0	0		
ENSMUST00000169736						20	3	35	13	23	8	143	401	121	0	358		
ENSMUST00000169740						18	11	10	12	18	14	0	0	0	0	3		
ENSMUST00000169741						3	2	13	2	2	7	2	0	7	0	8		
ENSMUST00000169743						3	0	0	47	1	0	0	0	0	0	0		
ENSMUST00000169744	ENSMUSG00000030168	6	119353150	119417704	-1	9	0	9	36	0	0	753	466	1466	63	617	Q53YY3	Q8BQS5
ENSMUST00000169745	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	4	0	0	0	0	74	16	0	0	E9PXA7	
ENSMUST00000169748	ENSMUSG00000031788	8	95099832	95142540	-1	10	12	57	70	28	0	126	142	125	5	60	E9PWU7	
ENSMUST00000169749						1	1	1	0	2	2	0	0	0	0	0		
ENSMUST00000169750	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	2	2	0	0	5	0	0	0	E9PW51	
ENSMUST00000169751						5	1	7	4	0	2	0	0	0	0	0		
ENSMUST00000169754	ENSMUSG00000026288	1	87620312	87720507	1	7	0	0	15	11	0	772	745	915	86	957		Q9ES52
ENSMUST00000169756	ENSMUSG00000072605	14	43010188	43015628	-1	7	0	0	0	0	0	0	0	0	0	0	D3YXI8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000169758	ENSMUSG00000075569	5	143933035	143985719	1	0	1	3	7	2	0	0	2	0	0	0	Q9CUJ3	
ENSMUST00000169759	ENSMUSG00000021417	13	34977748	35027094	-1	49	43	224	40	39	20	17	23	14	9	27	E9Q7A8	
ENSMUST00000169765	ENSMUSG00000025159	19	41941086	41981157	-1	0	0	0	0	0	0	0	0	4	0	0	F6TJQ8	
ENSMUST00000169767	ENSMUSG00000019214	17	25718926	25727419	-1	2	0	3	0	0	0	0	7	2	2	0	F6YVH6	
ENSMUST00000169772	ENSMUSG00000038305	1	57774162	57948394	1	8	8	7	1	9	0	0	0	0	0	1		Q91WJ7
ENSMUST00000169774	ENSMUSG00000094298	7	20204684	20205607	-1	2	0	4	2	2	0	0	0	0	0	0	K9J7G2	
ENSMUST00000169775	ENSMUSG00000025159	19	41941086	41981157	-1	4	3	11	5	3	4	20	33	28	0	25	E9Q5T0	
ENSMUST00000169776	ENSMUSG00000002100	2	91118144	91136516	1	3	0	74	6	0	0	0	0	0	37	84	Q3UIK0	
ENSMUST00000169777						1	0	6	87	6	0	0	0	0	0	0		
ENSMUST00000169778						0	0	2	1	0	0	24	33	33	1	57		
ENSMUST00000169779						1	0	0	3	1	2	3	68	4	12	34		
ENSMUST00000169781						0	0	1	3	5	3	3	7	3	0	7		
ENSMUST00000169782	ENSMUSG00000031508	8	11611583	11635754	-1	9	7	31	22	7	4	11	20	14	4	21	Q8BG46	
ENSMUST00000169783	ENSMUSG00000054477	18	45268860	45686024	1	0	0	5	0	0	0	0	0	0	0	0	B4YDY0	
ENSMUST00000169785	ENSMUSG00000036560	7	31059342	31070935	1	5	4	3	1	0	2	0	0	0	0	0		
ENSMUST00000169786	ENSMUSG00000055322	1	73910231	74124449	-1	0	27	38	0	0	0	0	0	0	0	0	E9Q0S6	
ENSMUST00000169787						69	48	174	76	81	37	0	0	0	0	0		
ENSMUST00000169794	ENSMUSG00000091376	3	60006743	60025420	1	3	3	5	4	3	1	0	0	0	0	0	B2RWD2	
ENSMUST00000169795						4	0	9	0	0	0	0	0	0	0	1		
ENSMUST00000169796	ENSMUSG00000079685	10	7444873	7473477	-1	0	1	0	0	0	0	15	0	32	2	13	J3KMI5	
ENSMUST00000169797	ENSMUSG00000037849	1	173468509	173491041	-1	0	0	0	1	0	0	0	0	3	0	0	G3UXS8	
ENSMUST00000169798						0	0	9	4	3	3	17	52	30	2	29		
ENSMUST00000169799	ENSMUSG00000027550	3	14533788	14572658	1	0	0	0	0	0	0	3	2	2	3	2	F7ABL5	
ENSMUST00000169800	ENSMUSG00000107662	10	129174084	129175019	-1	9	7	0	0	10	0	0	0	0	0	0	Q8VGC5	
ENSMUST00000169803	ENSMUSG00000071636	16	17208135	17213921	1	50	32	132	698	72	36	0	0	0	0	0	E9PZY2	
ENSMUST00000169804	ENSMUSG00000032199	9	71478437	71485935	-1	0	0	9	32	8	0	0	0	23	0	0	E9PZ03	
ENSMUST00000169805	ENSMUSG00000092120	17	17703941	17734167	1	9	4	5	5	8	3	0	0	0	0	0	E9PXJ8	
ENSMUST00000169807	ENSMUSG00000018537	11	97688823	97700497	-1	13	0	74	20	4	14	3	6	0	5	5		P23798
ENSMUST00000169810	ENSMUSG00000023015	15	99620496	99651656	-1	0	0	0	0	0	0	5	0	0	0	0	E9Q9N9	
ENSMUST00000169811						2	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000169812	ENSMUSG00000028007	3	117781647	117868936	-1	3	0	0	13	2	2	5	37	6	13	3	F6RSR4	
ENSMUST00000169814	ENSMUSG00000058586	15	83089506	83116674	1	0	3	7	4	2	4	0	0	0	0	0	F6TMN2	
ENSMUST00000169817	ENSMUSG00000020212	10	118141787	118168997	1	13	12	0	32	7	0	90	318	236	102	280	E9Q0B1	
ENSMUST00000169818	ENSMUSG00000091306	14	54640952	54648293	1	0	3	4	7	0	0	0	0	0	0	0	F6ZL36	
ENSMUST00000169819	ENSMUSG00000039315	5	38706462	38876812	-1	0	0	7	0	5	4	2	4	2	3	2		Q9QZE2
ENSMUST00000169820	ENSMUSG00000006154	7	4460674	4480487	1	0	0	0	0	0	0	0	0	0	0	0	E9PVI7	
ENSMUST00000169823						2	1	1	0	0	1	0	0	0	0	1		
ENSMUST00000169825	ENSMUSG00000055022	15	92051165	92341967	1	0	2	0	7	0	0	0	0	0	0	0		P12960
ENSMUST00000169826	ENSMUSG00000025290	14	24490681	24496146	1	10	12	6	31	16	6	1044	5364	1374	9260	1039	Q5M9M7	P62849
ENSMUST00000169828	ENSMUSG00000038615	11	96817414	96829968	-1	8	7	58	0	0	0	25	874	0	21	139	Q3V3M1	
ENSMUST00000169833	ENSMUSG00000017832	11	100713850	100714575	1	13	0	24	84	10	4	20	9	17	0	11	G3UWB9	
ENSMUST00000169834	ENSMUSG00000037738	8	22073616	22125053	-1	11	13	17	3	17	14	0	0	0	0	0		Q7TSC3
ENSMUST00000169838	ENSMUSG00000023800	17	3326573	3519397	1	34	21	4	156	32	2	16	34	31	35	1		Q6ZPF3
ENSMUST00000169841	ENSMUSG00000020440	6	28423560	28426602	1	3	0	0	0	0	0	592	0	166	139	174		P84084
ENSMUST00000169842						4	9	14	11	5	2	0	7	7	1	4		
ENSMUST00000169843						0	3	3	67	0	1	0	0	0	0	0		
ENSMUST00000169844						9	10	9	7	9	0	0	0	0	0	0		
ENSMUST00000169845						10	8	0	7	6	6	30	134	70	137	125		
ENSMUST00000169849	ENSMUSG00000047129	10	87058045	87230589	1	2	0	0	2	2	3	0	0	0	0	1	E9Q9Q5	
ENSMUST00000169850	ENSMUSG00000025089	19	58235604	58455909	-1	5	4	0	0	27	6	0	1	0	0	0		P97785
ENSMUST00000169851	ENSMUSG00000032479	9	109931460	110083955	1	14	8	36	17	15	11	2	3	2	1	6	Q78TF3	
ENSMUST00000169852	ENSMUSG00000002111	2	91082390	91115756	1	2	2	10	0	2	3	4190	3461	2431	446	1730	E9Q6W1	
ENSMUST00000169854	ENSMUSG00000056917	19	5651185	5663707	-1	23	8	42	603	31	27	969	2048	2258	0	1746	E9Q0Y4	
ENSMUST00000169855						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169857	ENSMUSG00000066677	1	173673675	173698392	1	0	0	0	0	0	0	0	0	0	0	0		Q3V3Q4
ENSMUST00000169859	ENSMUSG00000091731	10	58713606	58718210	-1	0	4	0	0	2	0	0	0	0	0	0	F6SK43	
ENSMUST00000169860	ENSMUSG00000062270	9	90091665	90114774	-1	0	0	0	7	0	0	1954	5685	946	1093	617	Q569V4	P60762
ENSMUST00000169861	ENSMUSG00000024976	19	53944306	54033268	1	24	16	34	0	0	12	207	1005	208	124	0		O88520
ENSMUST00000169862	ENSMUSG00000054321	18	14783245	14900359	1	18	20	23	217	31	14	15	52	19	10	25		G5E8Z2
ENSMUST00000169863	ENSMUSG00000041817	13	97067287	97129521	1	0	12	0	10	18	6	4	4	3	5	0		Q5XG69
ENSMUST00000169866	ENSMUSG00000019856	10	53633145	53750909	-1	0	0	0	0	0	0	0	0	0	0	0	E9QAL2	
ENSMUST00000169869						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169870	ENSMUSG00000015363	15	89075124	89087077	1	0	2	2	4	0	3	462	456	243	0	171	E9PXM1	
ENSMUST00000169878	ENSMUSG00000002699	11	34046920	34092295	1	0	0	0	0	0	0	1345	4549	1205	1106	1456		Q60787
ENSMUST00000169879	ENSMUSG00000042557	9	57072040	57128366	1	1	3	0	0	0	1	4	0	12	0	4	E9Q2L1	
ENSMUST00000169880	ENSMUSG00000021782	14	24133953	24245920	-1	5	2	20	8	5	5	1	0	0	0	4	F6Z115	
ENSMUST00000169885	ENSMUSG00000028542	4	117834506	117875198	1	1	0	0	3	0	0	0	6	0	0	0	E9Q517	
ENSMUST00000169886	ENSMUSG00000042515	X	139210042	139238335	1	0	0	0	14	0	0	0	0	0	0	0	E9Q6B0	
ENSMUST00000169888	ENSMUSG00000025404	10	127380327	127499384	1	4	0	0	0	12	4	0	62	0	50	0	F6Z9T5	
ENSMUST00000169889	ENSMUSG00000029687	6	47530139	47595341	-1	3	4	0	0	0	0	0	0	0	0	0	F7AQX0	
ENSMUST00000169891	ENSMUSG00000015363	15	89075124	89087077	1	3	0	12	0	6	0	83	25	57	23	26	E9Q8R5	
ENSMUST00000169893	ENSMUSG00000036915	7	30447534	30457690	-1	5	0	18	14	0	0	0	0	0	0	0		Q7TSU7
ENSMUST00000169895	ENSMUSG00000021876	14	51091077	51106151	1	9	10	13	7	5	8	0	40	29	24	0	Q8C7E4	
ENSMUST00000169897	ENSMUSG00000038843	19	17326141	17356667	-1	15	16	21	13	15	5	601	4053	1265	150	1097		Q09324
ENSMUST00000169898						1	0	0	0	0	3	0	1	0	0	0		
ENSMUST00000169900	ENSMUSG00000075316	2	66480080	66634962	-1	0	12	0	0	0	0	0	0	0	0	0	E9PW82	
ENSMUST00000169901	ENSMUSG00000030173	6	129898996	129917650	-1	0	0	0	0	0	0	0	0	0	0	0	F7CLL3	
ENSMUST00000169902						4	2	3	2	7	2	0	0	1	1	2		
ENSMUST00000169905	ENSMUSG00000022255	15	34082694	34142386	1	0	0	4	0	4	2	31	143	66	35	107	F6ZSG0	
ENSMUST00000169906	ENSMUSG00000021910	14	31170930	31216946	-1	3	0	7	15	9	7	85	161	121	7	200	E9PZT1	
ENSMUST00000169907	ENSMUSG00000016179	1	193346346	193370298	-1	17	0	0	0	1	2	0	0	0	0	0	E9Q679	
ENSMUST00000169909	ENSMUSG00000027777	3	68064802	68626481	1	4	0	0	0	0	0	64	422	163	523	123		Q3TI53
ENSMUST00000169910	ENSMUSG00000041408	14	34673928	34747983	1	0	0	0	0	0	0	0	0	656	0	178		Q65Z40
ENSMUST00000169911						2	0	0	0	0	0	0	0	0	0	0		

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ENSMUST00000169912						2	4	1	0	0	1	0	0	0	0	0		
ENSMUST00000169913	ENSMUSG00000048782	7	114743694	114850383	1	7	2	5	0	0	0	0	0	0	0	0	G3UW77	
ENSMUST00000169918						4	2	8	13	10	6	25	92	41	4	91		
ENSMUST00000169919	ENSMUSG00000030782	7	128246812	128255699	1	0	0	0	0	0	0	0	0	0	0	5		Q62219
ENSMUST00000169921	ENSMUSG00000020166	10	116485161	116581511	-1	0	2	1	0	5	0	143	428	237	190	172		Q8C5L3
ENSMUST00000169922	ENSMUSG00000078671	7	73426638	73541830	-1	44	32	132	72	52	33	632	2249	1846	251	1905		E9PZM4
ENSMUST00000169926	ENSMUSG00000001627	12	40201567	40248504	-1	2	1	2	1	0	0	30	164	41	64	32	E9Q1E6	
ENSMUST00000169927	ENSMUSG00000042429	1	134199223	134235431	-1	0	3	0	0	0	6	0	14	0	2	0		Q60612
ENSMUST00000169928	ENSMUSG00000020758	11	115974709	116008412	1	1	13	0	0	43	0	0	0	0	0	0	A2A864	
ENSMUST00000169931	ENSMUSG00000006932	9	120929216	120960507	1	0	0	0	0	0	0	0	3	0	0	0	F7BAC9	
ENSMUST00000169933						1	0	0	1	3	0	0	0	0	0	0		
ENSMUST00000169934	ENSMUSG00000021239	12	84569762	84595457	1	0	42	0	0	0	0	1	3	0	0	6	Q6PDC1	
ENSMUST00000169935	ENSMUSG00000091636	17	69439326	69489233	1	7	8	7	59	7	10	4	36	2	1	1		G3UWD5
ENSMUST00000169937						0	0	0	0	0	0	0	15	26	0	5		
ENSMUST00000169938	ENSMUSG00000021111	12	105784694	105838944	1	14	0	9	0	0	0	76	581	136	0	109	E9QAY4	
ENSMUST00000169940						3	2	3	5	2	1	1	0	4	0	12		
ENSMUST00000169941	ENSMUSG00000025013	19	41083981	41206774	-1	12	0	0	40	33	0	0	0	0	0	0	E9Q5B9	
ENSMUST00000169942	ENSMUSG00000036218	15	92396915	92771819	1	8	11	6	233	26	4	0	0	0	0	0	E9PUZ9	
ENSMUST00000169943	ENSMUSG00000024909	19	5473973	5481853	1	2	1	0	0	5	0	0	0	8	6	13	E9PYW6	
ENSMUST00000169945	ENSMUSG00000021670	13	96648967	96670936	-1	1	3	0	0	3	1	9	24	16	3	0	F7CA39	
ENSMUST00000169948	ENSMUSG00000029397	5	91948904	91963068	-1	72	42	59	259	82	53	331	1710	212	290	93	G3UWD8	
ENSMUST00000169950	ENSMUSG00000048231	17	36458917	36462334	-1	3	6	11	9	14	1	0	0	0	0	0	Q85ZW8	
ENSMUST00000169951						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169952						0	0	2	3	2	0	0	0	0	0	0		
ENSMUST00000169954	ENSMUSG00000091039	16	89205861	89206388	1	3	3	20	2	2	1	0	0	0	0	0	E9Q0A8	
ENSMUST00000169955						3	0	4	3	0	1	0	0	32	3	12		
ENSMUST00000169960	ENSMUSG00000048264	13	9276528	9668928	1	8	0	25	28	22	0	6	2	16	4	43	B7ZMZ7	
ENSMUST00000169961	ENSMUSG00000079084	9	13246982	13289409	1	0	0	0	0	5	0	18	28	103	61	61	Q9D6Z7	
ENSMUST00000169962						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000169964						0	0	0	21	0	0	0	0	0	0	0		
ENSMUST00000169965	ENSMUSG00000018449	11	70970213	70977833	1	0	0	0	0	0	0	10	0	6	43	0	Q0PL79	
ENSMUST00000169966	ENSMUSG00000021670	13	96648967	96670936	-1	1	5	4	4	0	1	0	7	4	0	6	E9Q5H3	
ENSMUST00000169967						10	5	19	15	17	9	0	0	0	0	0		
ENSMUST00000169968						43	28	66	39	35	18	1	2	2	0	6		
ENSMUST00000169969	ENSMUSG00000015474	17	34616662	34628510	-1	0	0	0	0	0	0	25	12	3	0	19	F6SPQ1	
ENSMUST00000169972	ENSMUSG00000095371	14	42291907	42297358	-1	0	2	0	0	9	6	0	0	0	0	0	L7N476	
ENSMUST00000169976						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000169978	ENSMUSG00000022014	14	77904239	78002656	1	2	6	7	7	8	2	7	29	9	34	12	Q9D3Q7	
ENSMUST00000169979						1	2	0	0	2	1	24	55	58	3	86		
ENSMUST00000169980						2	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000169982	ENSMUSG00000039763	16	91614257	91619026	-1	28	18	45	36	30	13	44	191	124	138	86	E9Q1L7	
ENSMUST00000169984						1	4	2	1	2	0	0	0	0	0	2		
ENSMUST00000169990	ENSMUSG00000028542	4	117834506	117875198	1	0	2	9	11	15	4	0	0	0	0	0	E9Q3Z2	
ENSMUST00000169991						2	1	12	1	2	1	0	5	4	0	16		
ENSMUST00000169993						3	2	3	4	2	0	0	2	0	6	2		
ENSMUST00000169995						4	5	0	3	3	2	11	20	9	0	6		
ENSMUST00000169997	ENSMUSG00000067220	5	72603696	72644275	-1	4	0	3	2	0	0	1	0	0	0	3		P29974
ENSMUST00000170000	ENSMUSG00000042396	9	48488709	48495330	-1	10	5	10	58	12	4	305	1282	513	1528	482	Q14A95	Q9CQT2
ENSMUST00000170002	ENSMUSG00000021111	12	105784694	105838944	1	3	0	0	0	0	0	52	10	103	0	19	E9PZR3	
ENSMUST00000170007	ENSMUSG00000025544	14	122107038	122159604	1	0	1	0	170	4	6	0	0	62	6	19	E9Q850	
ENSMUST00000170010	ENSMUSG00000024844	19	5364641	5366645	-1	0	5	11	19	2	0	8	0	0	0	0		O54962
ENSMUST00000170013	ENSMUSG00000035694	10	112163621	112216555	1	0	0	0	0	3	0	0	2	0	0	0	E9Q2J8	
ENSMUST00000170015	ENSMUSG00000046329	17	57043711	57059863	-1	0	0	0	0	0	0	5	0	1	0	4	F6X0P2	
ENSMUST00000170017	ENSMUSG00000017286	11	76120987	76243725	-1	0	0	0	0	0	1	9	212	91	21	0	E9Q055	
ENSMUST00000170018	ENSMUSG00000042570	10	79540245	79555199	-1	0	0	0	17	2	0	0	0	0	0	0	E9Q674	
ENSMUST00000170019	ENSMUSG00000035983	12	40222758	40229184	1	1	0	0	0	0	0	0	0	0	0	0	F6U8E6	
ENSMUST00000170021	ENSMUSG00000091215	9	35685079	35687390	-1	3	0	1	3	0	2	0	0	0	0	0	E9Q658	
ENSMUST00000170023						0	2	0	1	3	0	3	1	3	0	2		
ENSMUST00000170024						0	0	1	4	4	2	0	11	2	0	12		
ENSMUST00000170027						7	1	1	4	1	4	0	0	0	0	0		
ENSMUST00000170028	ENSMUSG00000029862	6	42286685	42315756	1	0	0	0	3	0	0	0	0	0	0	0	F6X177	
ENSMUST00000170030	ENSMUSG00000091248	9	36581278	36582635	-1	4	2	1	0	0	2	0	0	0	0	0	B3GLJ4	
ENSMUST00000170033	ENSMUSG00000049717	8	9970020	9977686	-1	16	1	8	3	9	17	0	0	29	10	27		Q8BTF7
ENSMUST00000170035	ENSMUSG00000022636	16	52248996	52454074	-1	0	0	0	0	0	0	42	274	144	22	168	E9Q3Q6	
ENSMUST00000170036	ENSMUSG00000003382	3	87525407	87540156	1	0	2	18	0	8	0	335	604	365	52	392		Q8R4Z4
ENSMUST00000170037	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	0	0	0	0	2	41	0	0	E9Q0P1	
ENSMUST00000170040	ENSMUSG00000079378	14	5131519	5139959	1	0	0	0	0	0	0	0	0	0	0	0	Q497R9	
ENSMUST00000170041						0	0	0	4	1	0	0	0	0	0	0		
ENSMUST00000170042						0	0	0	0	0	0	0	0	0	3	13		
ENSMUST00000170045						1	0	1	0	3	2	0	0	0	0	0		
ENSMUST00000170046	ENSMUSG00000022369	15	55557408	55626423	1	11	15	16	15	13	3	2	0	5	0	4		Q8BJS8
ENSMUST00000170048	ENSMUSG00000090622	10	69209762	69213098	-1	25	26	56	264	24	19	0	0	1	3	2	G5E8X6	
ENSMUST00000170049	ENSMUSG00000035582	7	97919955	98049663	1	3	0	0	0	0	0	0	0	0	0	0		Q3TT99
ENSMUST00000170050	ENSMUSG00000022255	15	34082694	34142386	1	0	0	0	0	0	0	16	205	243	0	9	F6QFT1	
ENSMUST00000170051	ENSMUSG00000002944	5	17781690	17888801	-1	3	5	4	6	4	4	0	3	0	50	29	Q3UAI3	Q08857
ENSMUST00000170054	ENSMUSG00000040054	10	128092783	128129303	1	23	19	0	0	29	15	534	1706	855	95	1271	E9Q374	
ENSMUST00000170055	ENSMUSG00000036745	3	146852367	146984009	1	16	0	14	6	26	19	3	4	0	5	4	E9PWB8	
ENSMUST00000170056	ENSMUSG00000035112	11	101260567	101277409	1	0	0	0	0	5	2	0	0	0	0	0	F6X7K7	
ENSMUST00000170057	ENSMUSG00000094105	5	11681959	11686856	1	0	0	2	0	0	0	0	0	0	0	0	F6XVS9	
ENSMUST00000170058	ENSMUSG00000004032	3	107895821	107898686	1	7	2	3	9	3	0	0	0	0	0	0	E9Q5L9	
ENSMUST00000170060	ENSMUSG00000021271	12	110850279	110869998	1	133	89	301	421	114	60	91	257	135	20	142	E9PUU5	
ENSMUST00000170062	ENSMUSG00000019877	10	57515774	57532530	-1	0	0	0	0	0	0	0	0	5	4	0	E9Q553	
ENSMUST00000170063						1	2	2	5	3	1	0	2	2	0	2		
ENSMUST00000170064	ENSMUSG00000091933	5	10947807	10952592	1	7	4	13	6	3	0	0	0	0	0	0	L7N291	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000170065	ENSMUSG00000020014	10	92775619	93081618	-1	9	4	0	3	4	5	3	11	7	0	15	F6V4L0	
ENSMUST00000170068	ENSMUSG00000015149	7	28766735	28788665	1	0	4	36	0	0	0	73	685	74	0	0		Q8VDQ8
ENSMUST00000170069	ENSMUSG00000032091	9	45172726	45204092	-1	0	0	32	16	0	0	0	1	0	0	0	E9Q4A7	
ENSMUST00000170070	ENSMUSG00000019214	17	25718926	25727419	-1	0	0	0	2	3	0	5	0	0	0	0	E9PVJ3	
ENSMUST00000170075	ENSMUSG00000002307	17	33909414	33915589	1	3	7	14	119	10	8	11	85	0	10	53	Q3UKR0	
ENSMUST00000170076	ENSMUSG00000091151	17	20419163	20420059	1	1	2	2	0	4	1	0	0	0	0	0	E9PWK2	
ENSMUST00000170077	ENSMUSG00000020961	12	91638542	91788387	-1	0	0	0	93	2	1	9	8	14	1	14	E9PYZ0	
ENSMUST00000170078						0	0	0	56	0	0	0	0	12	0	0		
ENSMUST00000170083						31	0	670	24	13	26	8	12	0	0	0		
ENSMUST00000170086	ENSMUSG00000037321	17	34187553	34197225	1	9	4	0	96	5	0	678	953	924	124	1038		P21958
ENSMUST00000170089	ENSMUSG00000015053	6	88193891	88207032	1	24	17	25	108	0	15	175	134	107	9	74	Q3U320	O09100
ENSMUST00000170091	ENSMUSG00000025044	8	39581700	39642678	-1	13	7	12	4	8	1	36	294	46	1109	288	Q8CED7	P30204
ENSMUST00000170092	ENSMUSG00000037503	1	34813219	34843065	-1	0	0	0	4	1	0	42	15	52	3	19	E9Q917	
ENSMUST00000170094	ENSMUSG00000091122	14	44583153	44588402	1	4	2	9	0	0	2	0	0	0	0	0	F6VRJ8	
ENSMUST00000170096	ENSMUSG00000033361	X	71962624	71972722	1	4	0	163	0	8	0	0	0	0	1	3		Q6PAQ9
ENSMUST00000170097						1	0	0	4	8	0	0	43	9	9	11		
ENSMUST00000170100	ENSMUSG00000022248	15	10486018	10499063	1	46	59	87	0	16	14	26	71	18	6	24	F7CJR1	
ENSMUST00000170101	ENSMUSG00000091388	8	71042645	71043040	-1	0	0	0	0	0	0	0	6	4	2	1	F7CLK7	
ENSMUST00000170102	ENSMUSG00000001089	4	136469761	136554780	1	0	25	0	0	45	28	0	0	18	0	0		Q8R4U7
ENSMUST00000170104	ENSMUSG00000079396	14	6259747	6287250	-1	23	42	25	40	42	18	0	0	0	0	0	Q8C7R2	
ENSMUST00000170105	ENSMUSG00000078598	4	113477891	113999503	-1	1	0	2	1	2	1	0	0	0	1	0	E9Q4T3	
ENSMUST00000170106	ENSMUSG00000034990	7	121083322	121163097	1	2	0	0	0	1	0	0	0	0	0	0	E9PVT3	
ENSMUST00000170109	ENSMUSG00000031558	5	47983138	48307733	1	3	0	6	4	9	4	0	0	0	2	0	G3UZ88	
ENSMUST00000170110						1	7	0	0	0	0	52	168	80	50	73		
ENSMUST00000170111	ENSMUSG00000021752	14	8214148	8223567	1	13	11	43	61	26	4	6	19	43	2	28	A2RS47	Q8BNL5
ENSMUST00000170112	ENSMUSG00000021782	14	24133953	24245920	-1	0	0	2	0	5	2	1	0	0	2	0	F7BYL0	
ENSMUST00000170113	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	2	22	3	0	0	0	1	0	0	E9Q5E9	
ENSMUST00000170115	ENSMUSG00000030782	7	128246812	128255699	1	0	0	0	0	0	0	0	0	2	0	0	E9Q1V4	
ENSMUST00000170116	ENSMUSG00000049680	11	5713417	5762376	-1	0	0	0	15	15	0	6	0	0	0	0		Q5NCI0
ENSMUST00000170117	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	2	0	0	0	0	2	E9Q1M2	
ENSMUST00000170118						1	2	0	1	1	0	0	0	0	0	0		
ENSMUST00000170119						0	0	0	4	0	0	5	135	8	0	4		
ENSMUST00000170121	ENSMUSG00000022561	15	76331231	76334907	1	0	0	0	0	0	0	8	0	9	0	7	F6T7Y8	
ENSMUST00000170122	ENSMUSG00000090733	3	90212522	90213651	-1	0	0	0	9	2	2	0	0	0	0	0		Q6ZWU9
ENSMUST00000170123	ENSMUSG00000096488	14	3412614	3433800	1	13	7	2	57	5	8	0	0	0	0	0	Q9CZI1	
ENSMUST00000170124	ENSMUSG00000090891	6	87104746	87112997	1	30	13	206	36	37	11	4	6	4	3	4	F7D6F6	
ENSMUST00000170125	ENSMUSG00000015749	3	95929246	95947390	1	2	0	0	2	3	0	4	24	19	41	26	E9Q2G1	
ENSMUST00000170126	ENSMUSG00000022621	15	89582533	89591923	-1	0	0	0	0	2	5	0	0	0	2	3	E9Q0F8	
ENSMUST00000170127	ENSMUSG00000022307	15	41447482	41861048	1	0	0	2	70	0	0	89	222	618	132	484	E9Q0A7	
ENSMUST00000170129	ENSMUSG00000021911	14	32201949	32297550	1	0	0	0	59	1	3	0	0	0	0	0	E9Q3C4	
ENSMUST00000170131	ENSMUSG00000094107	7	9816782	9841325	-1	0	0	0	0	0	0	0	0	0	0	0	K7N709	
ENSMUST00000170132	ENSMUSG00000024947	19	6334979	6340891	1	0	0	0	0	0	0	3	0	0	0	0	F6ZTV9	
ENSMUST00000170133						0	1	4	0	5	0	2	0	0	0	0		
ENSMUST00000170134	ENSMUSG00000022391	15	81704248	81729919	-1	0	12	115	154	42	0	0	0	33	0	0		P46061
ENSMUST00000170135						457	426	1979	565	491	226	21	88	25	4	39		
ENSMUST00000170137	ENSMUSG00000060904	10	88730858	88744094	1	0	0	0	98	0	0	0	0	0	0	5	E9Q006	
ENSMUST00000170139	ENSMUSG00000038305	1	57774162	57948394	1	0	0	1	0	0	0	0	0	0	0	0		Q91WJ7
ENSMUST00000170141	ENSMUSG00000031697	8	85299632	85308278	1	0	0	0	25	4	1	0	34	0	0	7	Q3TQX1	
ENSMUST00000170142	ENSMUSG00000029821	6	50188888	50263862	-1	1	0	0	0	0	3	1312	4178	1956	828	1365		Q9Z2D3
ENSMUST00000170143						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000170144	ENSMUSG00000050587	2	96318169	97631666	1	0	0	2	0	1	0	0	0	0	0	0	E9QA73	
ENSMUST00000170146	ENSMUSG00000092083	1	15287254	15723750	1	59	58	100	83	66	41	4	1	4	0	2		A6H8H5
ENSMUST00000170148	ENSMUSG00000033027	6	129639064	129643337	-1	0	0	0	0	0	0	0	0	0	0	0	L7N477	
ENSMUST00000170149	ENSMUSG00000053819	3	126596302	126846326	1	0	0	0	0	0	0	0	25	0	8	40	F6RWZ9	
ENSMUST00000170152	ENSMUSG00000036915	7	30447534	30457690	-1	3	0	0	0	0	0	0	0	0	0	0	F6WZB3	
ENSMUST00000170153	ENSMUSG00000046761	15	76001093	76014336	-1	0	19	0	518	57	13	0	0	0	0	22		Q148V8
ENSMUST00000170155						33	36	63	91	44	17	0	1	0	0	0		
ENSMUST00000170156	ENSMUSG00000021313	13	11553103	12106945	-1	0	52	90	455	94	41	1	1	1	0	3	F6U7V1	
ENSMUST00000170157	ENSMUSG00000010095	19	8706882	8723369	-1	0	40	7	30	32	17	30	40	12	7	43		P10852
ENSMUST00000170159	ENSMUSG00000033196	11	67171027	67197517	1	0	0	0	0	0	0	0	0	0	0	0	G3UW82	
ENSMUST00000170160	ENSMUSG00000037940	8	81342556	82125036	1	0	4	0	0	0	3	6	3	7	7	15	E9Q2C4	
ENSMUST00000170161						0	0	0	0	0	0	0	0	24	1	0		
ENSMUST00000170163						4	4	0	1	0	0	49	275	46	24	78		
ENSMUST00000170164	ENSMUSG00000025404	10	127380327	127499384	1	3	0	0	15	0	0	0	0	0	0	0	E9PX98	
ENSMUST00000170166	ENSMUSG00000094187	7	23606175	23607089	1	5	5	4	7	4	0	0	0	0	0	0	K7N6W9	
ENSMUST00000170167	ENSMUSG00000052033	2	170496428	170519123	1	2	1	0	94	7	10	0	0	3	3	3	E9Q4Q8	
ENSMUST00000170168						3	0	2	2	1	0	0	0	0	0	0		
ENSMUST00000170173						0	0	6	0	5	4	0	0	0	0	0		
ENSMUST00000170174	ENSMUSG00000090690	14	42496884	42502349	-1	3	6	7	9	6	0	0	0	0	0	0	F6WLE9	
ENSMUST00000170176	ENSMUSG00000024037	17	31494323	31519974	-1	0	0	0	18	0	11	0	0	0	0	0	F6VLT8	
ENSMUST00000170181	ENSMUSG00000028780	5	17574281	17730268	1	1	0	0	14	0	2	0	0	0	1	2	E9PXL2	
ENSMUST00000170184						0	0	0	0	0	0	0	0	0	8	0		
ENSMUST00000170186	ENSMUSG00000025701	6	116410077	116461178	-1	0	0	0	0	0	0	965	0	1063	0	740	E9Q6H6	
ENSMUST00000170188	ENSMUSG00000021009	12	98676741	98737405	-1	2	0	45	9	0	32	0	17	22	6	50	G5E8J4	
ENSMUST00000170189						0	1	1	0	0	0	2	3	1	1	0		
ENSMUST00000170190	ENSMUSG00000038671	2	181357690	181365404	-1	0	8	0	34	7	3	0	34	0	10	0	E9PZK7	
ENSMUST00000170191						4	5	2	0	0	2	5	4	3	0	0		
ENSMUST00000170193						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000170195						8	4	4	5	7	1	1	0	5	0	7		
ENSMUST00000170196	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	0	0	0	0	0	A7UAK8	
ENSMUST00000170200						0	1	1	0	1	1	1	0	1	10	0		
ENSMUST00000170201	ENSMUSG00000022801	16	32914100	33015647	1	0	0	0	0	0	0	0	0	0	0	0	B2RXP1	
ENSMUST00000170202	ENSMUSG00000020444	11	59183875	59192212	-1	1	2	5	51	9	2	65	236	52	93	42	Q564G0	
ENSMUST00000170204	ENSMUSG00000039661	8	31089471	31097047	1	0	0	0	0	0	2	0	0	0	0	0		Q9D700

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000170205	ENSMUSG00000092116	13	98489348	98492001	-1	5	0	0	7	6	5	0	0	0	0	0	E9PW43	
ENSMUST00000170206						2	3	1	2	2	0	0	2	0	0	1		
ENSMUST00000170207	ENSMUSG00000091563	14	4110526	4132784	1	11	6	6	44	20	6	0	0	0	0	0	K7N734	
ENSMUST00000170208						0	2	0	1	0	0	2	23	4	9	14		
ENSMUST00000170209						13	7	29	11	8	6	0	17	41	6	33		
ENSMUST00000170212						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000170213	ENSMUSG00000015749	3	95929246	95947390	1	0	0	0	0	0	0	0	0	0	0	0	E9PVI5	
ENSMUST00000170217	ENSMUSG00000026245	1	78417975	78488897	-1	0	0	0	0	0	0	0	0	12	149	109		Q9WUA2
ENSMUST00000170219	ENSMUSG00000035640	10	80130451	80140835	-1	21	0	28	0	19	0	17	11	0	3	9	E9QP85	
ENSMUST00000170221						4	2	3	0	2	5	0	0	0	0	0		
ENSMUST00000170223	ENSMUSG00000022220	14	55769058	55784042	-1	0	19	33	55	44	22	0	66	28	0	62		Q91WF3
ENSMUST00000170224	ENSMUSG00000091049	5	25999022	26004798	-1	3	0	0	0	0	3	0	0	0	0	0	D3Z7H5	
ENSMUST00000170225	ENSMUSG00000073423	17	33629090	33631779	1	5	1	4	4	2	0	203	236	159	28	116	E9Q4H9	
ENSMUST00000170226	ENSMUSG00000063268	15	76231174	76243441	-1	5	3	5	107	3	9	20	170	12	0	41	F6Z9X8	
ENSMUST00000170227	ENSMUSG00000091867	7	26931631	26939384	-1	14	6	19	27	25	8	0	1	0	0	0	B2RXZ2	
ENSMUST00000170229						3	7	12	10	5	1	11	33	8	6	27		
ENSMUST00000170232						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000170233						2	4	10	4	5	3	0	0	0	0	3		
ENSMUST00000170234	ENSMUSG00000038759	6	35177421	35247596	1	0	0	0	0	0	1	2	10	6	3	10	E9Q880	
ENSMUST00000170236	ENSMUSG00000041552	X	155573455	155623814	-1	1	4	0	3	2	0	0	0	0	0	0	F6WEC8	
ENSMUST00000170237	ENSMUSG00000040936	9	120960268	121277197	-1	1	0	3	1	10	0	0	1	0	0	3	E9Q220	
ENSMUST00000170239	ENSMUSG00000002500	17	24727820	24736143	1	9	0	21	28	3	5	0	0	0	0	0	E9PWZ3	
ENSMUST00000170241	ENSMUSG00000028478	4	44004452	44032846	1	0	0	0	33	0	0	1335	3366	1819	697	1255	Q6PFA2	
ENSMUST00000170242	ENSMUSG00000004677	8	71272714	71360712	1	47	31	107	173	74	0	989	2124	1625	74	1429	E9PZW8	
ENSMUST00000170243	ENSMUSG00000000420	18	24205344	24286818	1	0	0	0	0	0	0	0	13	26	0	0		O08912
ENSMUST00000170244	ENSMUSG00000091572	3	64258961	64287495	-1	0	7	11	4	6	3	0	0	0	0	0	E9Q107	
ENSMUST00000170246	ENSMUSG00000032268	9	49081260	49117587	1	0	0	0	1	0	0	0	0	0	0	0	B7ZN60	
ENSMUST00000170248	ENSMUSG00000059049	4	82897920	83052339	-1	16	22	0	0	0	0	0	0	0	0	0	E9Q5Z7	
ENSMUST00000170249	ENSMUSG00000091296	14	51630273	51635666	-1	3	4	4	2	0	0	0	0	0	0	0	E9Q7X3	
ENSMUST00000170251	ENSMUSG00000040046	7	46647130	46672537	-1	0	0	0	0	0	0	0	0	1	0	0	E9Q060	
ENSMUST00000170252						1	0	2	0	0	0	0	0	0	2	1		
ENSMUST00000170253	ENSMUSG00000021910	14	31170930	31216946	-1	0	0	0	0	0	0	17	24	0	5	0	F6ZL69	
ENSMUST00000170254						0	0	31	12	2	0	0	0	0	0	0		
ENSMUST00000170255	ENSMUSG00000068085	15	82389154	82394022	-1	5	4	9	9	12	3	0	0	0	0	0		P24457
ENSMUST00000170257	ENSMUSG00000092162	10	130445707	130455894	-1	4	7	12	17	5	4	0	0	0	0	0	G5E8Y4	
ENSMUST00000170259	ENSMUSG00000075604	15	74834125	74841643	-1	101	66	176	583	145	89	0	1	1	1	3	Q3TG86	
ENSMUST00000170260	ENSMUSG00000094025	5	11127634	11132487	1	4	0	0	0	0	0	0	0	0	0	0	F6R3J9	
ENSMUST00000170261						0	0	4	10	6	0	2	20	0	0	3		
ENSMUST00000170263	ENSMUSG00000031562	8	48099092	48153233	1	0	0	0	85	24	0	0	0	0	0	0	G3X908	
ENSMUST00000170265	ENSMUSG00000019990	10	20398004	20725078	-1	0	0	11	8	0	2	36	1	103	15	166	E9PZN2	
ENSMUST00000170266	ENSMUSG00000023964	6	3685680	3764714	-1	0	0	9	0	1	0	0	0	0	0	0		Q60755
ENSMUST00000170267	ENSMUSG00000100004	10	24100878	24101912	-1	6	0	25	6	10	9	0	0	0	0	0		Q5QD05
ENSMUST00000170268	ENSMUSG00000091898	14	31208312	31211729	1	0	0	2	0	0	1	0	0	0	4	0	E9Q8P0	
ENSMUST00000170269	ENSMUSG00000002881	1	52457294	52500679	-1	0	0	0	0	2	0	57	0	267	37	213	E9PZ64	
ENSMUST00000170270	ENSMUSG00000068999	3	64490821	64509735	-1	0	1	11	0	16	1	0	0	0	0	1	L7N2D3	
ENSMUST00000170271	ENSMUSG00000047428	17	46297421	46303271	1	18	5	20	431	25	6	0	0	0	0	0	E9Q0Y2	
ENSMUST00000170272	ENSMUSG00000039671	2	165784152	165899016	-1	0	0	3	0	0	0	0	0	8	0	56	Q3UH28	
ENSMUST00000170273	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	0	0	0	6	0	E9Q1V5	
ENSMUST00000170275	ENSMUSG00000096295	8	21378560	21379402	1	0	0	0	0	0	1	0	0	0	0	0	Q8C1N9	
ENSMUST00000170278						12	10	6	19	17	6	1	9	0	2	10		
ENSMUST00000170279						1	0	7	2	0	4	0	2	2	0	0		
ENSMUST00000170280	ENSMUSG00000092049	3	64388621	64415296	-1	10	6	6	12	6	5	0	0	0	0	0	E9Q277	
ENSMUST00000170281						3	5	9	19	5	1	9	40	14	8	27		
ENSMUST00000170283	ENSMUSG00000005986	19	4270180	4283137	-1	0	0	0	0	0	0	5	12	0	0	9	F6YTJ4	
ENSMUST00000170285	ENSMUSG00000040701	14	55098578	55106593	-1	0	0	0	0	0	0	132	269	13	0	2		O88512
ENSMUST00000170286						47	43	545	71	50	33	0	3	8	0	11		
ENSMUST00000170287	ENSMUSG00000021670	13	96648967	96670936	-1	5	7	9	8	18	0	13	44	143	9	70	F2Z470	
ENSMUST00000170288						0	0	3	0	0	2	2	3	0	0	13		
ENSMUST00000170289						7	4	4	6	2	3	3	6	0	4	9		
ENSMUST00000170290	ENSMUSG00000094602	7	23577185	23578099	1	1	3	2	0	4	2	0	0	0	0	0	L7N275	
ENSMUST00000170292	ENSMUSG00000024947	19	6334979	6340891	1	0	0	5	0	0	2	21	38	0	6	20	F7CJP6	
ENSMUST00000170293	ENSMUSG00000029713	5	137528127	137533510	-1	0	0	0	0	0	0	3272	1189	1335	62	646	D3YZX3	
ENSMUST00000170295	ENSMUSG00000046337	1	36562692	36683183	-1	11	9	0	4	21	0	0	0	0	0	0	E9PXB2	
ENSMUST00000170296	ENSMUSG00000003824	8	84872111	84888221	1	0	0	2	8	0	0	5	15	11	23	6	E9PYH4	
ENSMUST00000170297	ENSMUSG00000046020	2	153241533	153270247	1	0	0	0	5	0	0	0	0	13	0	4	E9Q154	
ENSMUST00000170299						0	0	0	9	0	0	0	0	6	0	0		
ENSMUST00000170300	ENSMUSG00000026288	1	87620312	87720507	1	0	9	16	0	7	0	10	1482	0	0	0		Q9ES52
ENSMUST00000170301	ENSMUSG00000067848	5	11918043	11922821	1	0	0	10	0	3	0	0	0	0	0	0	A3KN63	
ENSMUST00000170303	ENSMUSG00000091228	11	93949819	93968293	-1	0	0	15	0	0	0	481	656	338	2204	328	E9PZF0	
ENSMUST00000170304	ENSMUSG00000006241	9	21927471	21935872	1	0	0	21	29	0	3	0	0	0	0	0		Q8C963
ENSMUST00000170308	ENSMUSG00000007656	9	75037614	75060313	1	0	1	3	0	5	1	282	862	330	1443	199		P56212
ENSMUST00000170309	ENSMUSG00000053644	18	56509687	56572951	-1	0	0	0	0	0	0	2	0	4	0	0	E9Q1H3	
ENSMUST00000170310	ENSMUSG00000007656	9	75037614	75060313	1	0	0	0	0	0	0	4	28	12	3	8		P56212
ENSMUST00000170311						3	0	5	1	3	0	0	9	0	0	3		
ENSMUST00000170315	ENSMUSG00000030528	7	80454733	80535119	-1	16	23	31	79	22	20	0	0	0	0	0	E9PZ97	
ENSMUST00000170317						0	0	0	70	8	0	0	12	3	7	2		
ENSMUST00000170318	ENSMUSG00000031553	8	24677225	24725852	-1	0	0	0	0	0	0	0	64	0	0	0	E9PYS9	
ENSMUST00000170319	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	0	0	0	0	0	0	0	0	E9Q5U4	
ENSMUST00000170320	ENSMUSG00000040812	2	90782727	90834437	1	139	100	187	81	144	74	5	44	20	8	23		Q8CDK2
ENSMUST00000170322	ENSMUSG00000092111	17	22943184	22958814	1	0	9	3	1	6	0	0	0	0	0	0	E9PZA6	
ENSMUST00000170323	ENSMUSG00000022542	16	4986858	4997852	-1	13	8	41	26	19	13	0	1	0	0	0	Q9D451	
ENSMUST00000170324						5	2	4	3	1	0	0	0	0	0	1		
ENSMUST00000170325						1	0	2	3	0	1	12	25	21	2	18		
ENSMUST00000170327						10	8	24	6	21	8	3	3	2	0	6		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000170329						29	13	23	0	0	0	0	0	0	0	0		
ENSMUST00000170331	ENSMUSG00000013701	14	32180162	32201898	-1	7	4	10	7	0	1	19	0	0	40	28	E9PVF9	
ENSMUST00000170334						0	0	0	0	0	0	5	0	0	0	0		
ENSMUST00000170335						13	64	142	370	138	43	1258	4171	2870	803	1926		
ENSMUST00000170336	ENSMUSG00000025404	10	127380327	127499384	1	0	0	12	0	16	0	0	0	0	0	0	Q148X5	
ENSMUST00000170337						0	0	1	0	0	1	0	0	0	0	5		
ENSMUST00000170338						3	2	0	3	7	4	0	4	0	5	0		
ENSMUST00000170339						10	0	7	0	3	2	0	0	0	1	0		
ENSMUST00000170341	ENSMUSG00000091059	5	109215502	109224622	-1	8	5	8	0	4	5	0	0	0	0	0	E9Q759	
ENSMUST00000170342	ENSMUSG00000000916	5	135369953	135376805	1	0	0	0	31	5	0	0	0	2	0	3	E9QAY1	
ENSMUST00000170343	ENSMUSG00000021910	14	31170930	31216946	-1	0	0	0	0	0	0	8	0	0	0	0	F6PY46	
ENSMUST00000170345	ENSMUSG00000015474	17	34616662	34628510	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q0T0	
ENSMUST00000170347	ENSMUSG00000048924	13	100669481	100697240	1	1	0	5	65	0	15	11	9	0	0	12	G3UWA1	
ENSMUST00000170348						25	19	242	58	21	10	2	4	0	1	0		
ENSMUST00000170349	ENSMUSG00000091080	9	98842503	98843385	1	2	1	12	208	9	7	0	0	0	0	0	G3UW32	
ENSMUST00000170350	ENSMUSG00000012535	6	29540827	29609887	-1	11	0	16	3	7	0	24	20	73	25	76	E9Q0H8	
ENSMUST00000170352	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	0	0	0	0	0	0	0	0	E9Q387	
ENSMUST00000170354	ENSMUSG00000022407	15	80948490	80970947	1	4	2	1	22	4	1	0	0	0	0	0	E9PZI0	
ENSMUST00000170356	ENSMUSG00000043067	9	24411776	24503140	-1	0	0	0	34	0	0	53	57	49	0	27		A6X919
ENSMUST00000170359	ENSMUSG00000026584	1	163929100	163955126	1	0	0	0	0	0	5	0	0	0	0	0		Q9DBQ7
ENSMUST00000170360	ENSMUSG00000024798	19	35958734	36057507	-1	0	0	0	76	2	0	0	0	0	0	5	E9Q1X2	
ENSMUST00000170361	ENSMUSG00000028273	3	142239590	142395696	-1	0	0	155	0	0	9	0	93	0	0	0	E9Q8P5	
ENSMUST00000170366	ENSMUSG00000005899	16	17619354	17644828	1	0	0	3	0	2	0	0	0	0	0	0	E9Q914	
ENSMUST00000170367	ENSMUSG00000041540	6	143828425	144781977	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVR0	
ENSMUST00000170368	ENSMUSG00000022106	14	73123037	73207843	1	0	0	0	0	0	0	0	0	0	0	0	E9PZR2	
ENSMUST00000170369						37	12	37	26	34	37	2	10	11	0	16		
ENSMUST00000170370	ENSMUSG00000022106	14	73123037	73207843	1	0	0	1	0	0	1	3	0	0	0	0	E9QAL7	
ENSMUST00000170371	ENSMUSG00000005553	7	30712209	30725535	1	26	0	0	0	0	12	0	0	0	0	0	Q91WH7	
ENSMUST00000170372	ENSMUSG00000035112	11	101260567	101277409	1	0	0	0	0	0	0	0	0	0	1	1	F6Z709	
ENSMUST00000170373	ENSMUSG00000024759	19	7494040	7538608	1	0	8	37	129	17	18	31	43	71	0	34	E9PYT3	
ENSMUST00000170374	ENSMUSG00000005686	7	110768206	110812405	1	29	16	68	58	34	21	1155	603	4311	272	3540		O08739
ENSMUST00000170375						1	1	36	32	6	1	3	10	0	0	7		
ENSMUST00000170376	ENSMUSG00000019809	10	13523842	13553142	-1	0	0	6	8	3	0	0	0	15	49	6	E9QA46	
ENSMUST00000170377	ENSMUSG00000028057	3	88716838	88731049	1	0	9	0	0	8	0	175	453	229	43	210	G5E8W6	
ENSMUST00000170378	ENSMUSG00000021557	13	59449537	59585227	-1	4	0	11	30	3	4	0	0	0	0	0	Q8C1R2	
ENSMUST00000170379						0	0	0	1	0	1	5	0	2	0	5		
ENSMUST00000170380						2	2	5	13	7	0	0	0	0	0	0		
ENSMUST00000170381	ENSMUSG00000039364	11	121053458	121063569	-1	0	0	0	6	0	0	0	0	0	2	0	Q9D966	
ENSMUST00000170382	ENSMUSG00000091625	6	56701063	56704710	-1	3	0	2	3	0	1	78	164	41	124	45		P62322
ENSMUST00000170385						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000170386	ENSMUSG00000046991	17	14829331	14934653	-1	17	11	24	15	14	4	0	2	0	1	1		Q8C5V5
ENSMUST00000170388	ENSMUSG00000036353	3	59216272	59262871	-1	0	0	0	8	0	3	144	464	316	537	166	Q546L4	Q9CPV9
ENSMUST00000170390	ENSMUSG00000091191	11	53772281	53773187	-1	6	2	5	4	5	4	7	32	19	9	63	Q8C6U3	
ENSMUST00000170391	ENSMUSG00000041235	4	8690406	8867659	1	0	0	0	19	0	0	0	43	0	22	0	E9PV74	
ENSMUST00000170392	ENSMUSG00000079563	17	32413100	32424167	-1	10	15	31	27	20	9	21	24	4	3	29		Q8VCS0
ENSMUST00000170393	ENSMUSG00000013089	16	22381309	22439719	-1	0	0	0	0	0	0	0	2	3	0	0	E9Q288	
ENSMUST00000170394	ENSMUSG00000017376	11	78567168	78697373	-1	0	0	0	0	0	0	0	10	1	3	0	F6QKY6	
ENSMUST00000170396	ENSMUSG00000085111	10	85927681	85946206	1	65	64	473	210	51	51	2	9	2	0	9	M0QW46	
ENSMUST00000170397	ENSMUSG00000032327	9	58063788	58153996	1	13	4	26	8	15	13	0	0	0	0	0		
ENSMUST00000170400	ENSMUSG00000070280	9	119169455	119365553	-1	11	0	0	0	10	0	0	0	0	0	0	Q497L9	
ENSMUST00000170401						29	25	32	25	32	29	0	17	21	0	32		
ENSMUST00000170402	ENSMUSG00000091651	7	7876651	7902462	-1	9	5	2	0	7	6	0	0	0	0	0	K7N741	
ENSMUST00000170403						0	5	0	0	2	0	0	0	0	0	0		
ENSMUST00000170405						3	1	3	0	6	1	0	0	0	0	0		
ENSMUST00000170406						14	11	17	13	16	5	2	0	1	0	0		
ENSMUST00000170409	ENSMUSG00000013833	10	79894708	79908923	-1	0	0	0	18	0	0	0	0	0	0	0	E9PWX0	
ENSMUST00000170412	ENSMUSG00000096002	7	12581470	12606544	-1	10	6	18	11	12	11	0	0	0	0	0	L7N473	
ENSMUST00000170414						5	4	2	7	3	3	0	0	0	0	0		
ENSMUST00000170415	ENSMUSG00000006522	14	30908573	30923760	-1	0	1	1	5	0	2	0	2	0	0	0	E9PVS1	
ENSMUST00000170416	ENSMUSG00000038291	8	46033261	46152159	-1	0	11	16	0	0	0	69	127	144	54	85		Q3ZT31
ENSMUST00000170419	ENSMUSG00000091624	5	108842947	108852510	-1	3	15	0	2	9	5	0	0	0	0	0	K7N6Z8	
ENSMUST00000170420	ENSMUSG00000026659	1	170873498	170885540	-1	1	5	0	2	3	0	3	9	4	2	2	G3UW79	
ENSMUST00000170421	ENSMUSG00000051243	9	58196298	58204319	-1	7	0	3	24	3	2	0	0	0	0	0		Q5RKR3
ENSMUST00000170422	ENSMUSG00000070354	11	79513385	79530589	-1	0	0	0	0	0	0	0	9	22	0	0		Q8VD58
ENSMUST00000170423						2	1	3	3	2	2	0	0	0	0	0		
ENSMUST00000170424	ENSMUSG00000096717	17	19053493	19081311	1	10	6	4	9	7	5	0	0	0	0	0	E9PZ56	
ENSMUST00000170425						0	0	0	0	0	0	0	0	0	0	4		
ENSMUST00000170426	ENSMUSG00000032268	9	49081260	49117587	1	9	0	8	8	10	0	0	0	0	0	0	F7C9D1	
ENSMUST00000170427	ENSMUSG00000091429	14	44518276	44523444	1	8	5	10	15	4	1	0	0	0	0	0	F6XGJ4	
ENSMUST00000170428	ENSMUSG00000100549	4	88819959	88820531	1	0	1	2	0	2	3	0	0	0	0	0		Q61716
ENSMUST00000170429						12	15	22	12	18	11	0	0	0	0	0		
ENSMUST00000170430	ENSMUSG00000030660	7	116337265	116443449	-1	52	48	54	104	56	29	311	907	657	434	448	F8VPL2	
ENSMUST00000170436	ENSMUSG00000021910	14	31170930	31216946	-1	3	0	0	0	0	0	27	16	46	0	41	F6ZL22	
ENSMUST00000170438	ENSMUSG00000002107	2	6539694	7509563	-1	7	29	32	42	35	5	163	877	383	40	474	E9QA47	
ENSMUST00000170441						3	2	0	1	3	0	0	0	0	0	0		
ENSMUST00000170442	ENSMUSG00000058239	7	30945248	30956803	-1	0	0	0	61	0	2	0	15	8	0	18	F6PWU6	
ENSMUST00000170444	ENSMUSG00000020407	11	9118103	9136170	1	0	0	0	0	0	0	919	2345	577	293	373	E9Q5K7	
ENSMUST00000170445						0	0	1	0	3	4	0	0	0	0	0		
ENSMUST00000170447						0	1	2	0	2	3	0	0	0	0	0		
ENSMUST00000170448	ENSMUSG00000027568	2	180499976	180544980	1	5	0	40	0	12	0	0	0	0	0	0	A2ACT4	O88319
ENSMUST00000170449						23	26	54	371	78	28	0	0	0	0	0		
ENSMUST00000170452						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000170453						0	0	2	4	7	0	0	0	0	0	0		
ENSMUST00000170455						0	0	0	0	0	0	0	0	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000170456						4	8	7	45	10	4	0	0	0	0	0		
ENSMUST00000170457						27	18	70	57	47	22	1	14	13	3	9		
ENSMUST00000170459	ENSMUSG00000030970	7	132987563	133124354	-1	0	0	0	10	1	0	0	0	5	0	3	E9Q4S8	
ENSMUST00000170460	ENSMUSG00000022617	15	89416405	89429908	-1	0	0	0	0	0	0	0	0	0	0	0	F6RRT7	
ENSMUST00000170461	ENSMUSG00000047583	3	154576431	154597104	-1	41	34	31	225	43	29	0	0	0	0	0	E9PYE2	
ENSMUST00000170463						10	7	9	5	8	9	0	1	1	0	2		
ENSMUST00000170464	ENSMUSG00000022707	16	70313949	70569716	1	0	0	0	0	4	0	48	233	126	0	11	F6ZHD8	
ENSMUST00000170468	ENSMUSG00000029507	5	110773667	110780659	-1	0	0	0	0	0	0	48	48	3	10	31		Q9WU56
ENSMUST00000170469	ENSMUSG00000090547	14	5630281	5633028	-1	6	2	17	11	5	2	0	0	0	0	0	K7N6Y8	
ENSMUST00000170472	ENSMUSG00000026489	1	180165238	180199602	-1	10	15	51	0	0	9	331	570	104	132	50		Q60936
ENSMUST00000170473						7	12	39	18	12	8	9	19	16	0	18		
ENSMUST00000170476	ENSMUSG00000026854	2	30982279	31023586	1	0	25	34	0	43	0	68	39	36	9	81		Q8C6M1
ENSMUST00000170477	ENSMUSG00000004661	9	57790353	57836793	-1	0	0	1	0	5	2	2	1	0	0	0	E9Q9J9	
ENSMUST00000170479						29	19	119	223	36	22	40	318	131	9	134		
ENSMUST00000170480	ENSMUSG00000096793	14	3810074	3966518	1	14	0	0	30	0	0	0	0	0	0	0	E9PW72	
ENSMUST00000170481	ENSMUSG00000031393	X	74026592	74135363	-1	18	27	49	0	46	17	340	685	699	57	606		Q9Z2D6
ENSMUST00000170482						10	4	2	5	5	8	36	135	57	16	47		
ENSMUST00000170486						20	12	53	19	27	0	0	0	0	0	0		
ENSMUST00000170488	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	0	0	0	0	2	1	0	0	0	E9Q7R8	
ENSMUST00000170489	ENSMUSG00000032097	9	44604892	44640731	1	35	26	71	134	60	39	5424	13458	11238	1737	9415		P54823
ENSMUST00000170491						12	5	35	88	18	11	446	540	343	73	401		
ENSMUST00000170495	ENSMUSG00000002900	12	31265234	31329644	1	2	0	0	42	4	1	0	0	0	0	0	E9Q339	
ENSMUST00000170496	ENSMUSG00000054099	5	8422850	8454797	1	3	3	2	4	2	0	11	3	3	0	16		Q8BGP6
ENSMUST00000170500						1	0	4	3	9	2	10	70	23	2	23		
ENSMUST00000170501	ENSMUSG00000058807	11	58501598	58502572	-1	0	0	8	0	0	0	0	0	0	0	0	F6WSM5	
ENSMUST00000170502	ENSMUSG00000035086	11	101285952	101302286	-1	0	0	0	0	0	0	0	0	0	0	0	E9QAM0	
ENSMUST00000170504	ENSMUSG00000091983	6	42471162	42476335	-1	5	6	14	15	11	1	0	0	0	0	5	Q8VGP5	
ENSMUST00000170505	ENSMUSG00000038528	10	39958061	39986646	-1	3	2	12	3	13	8	0	0	0	0	0	F6YK23	
ENSMUST00000170506						0	0	10	3	8	2	25	134	92	6	95		
ENSMUST00000170507	ENSMUSG00000020101	10	60346851	60372684	1	0	0	0	4	5	5	138	14	57	0	35	E9Q251	
ENSMUST00000170511	ENSMUSG00000090486	1	78497026	78512158	-1	47	0	209	163	36	20	0	0	0	0	0	B2RQY6	
ENSMUST00000170512						8	27	63	36	23	15	0	0	0	0	0		
ENSMUST00000170513	ENSMUSG00000004296	11	44400063	44414033	1	0	7	23	0	5	9	0	0	0	0	0	Q3ZAX5	P43432
ENSMUST00000170514						3	0	4	3	2	0	0	0	0	0	0		
ENSMUST00000170516	ENSMUSG00000024952	19	6829085	6840601	-1	14	8	30	151	20	6	712	690	487	56	376		Q9Z2B9
ENSMUST00000170517	ENSMUSG00000034263	9	64960832	64986974	1	0	8	3	16	0	2	150	434	221	159	153		Q8R3P6
ENSMUST00000170518	ENSMUSG00000090290	8	126426652	126475065	-1	36	22	52	120	46	14	7	11	13	1	32	E9Q368	
ENSMUST00000170519	ENSMUSG00000021906	14	32085374	32103202	1	0	0	2	0	2	0	0	21	13	0	0	F6XLU3	
ENSMUST00000170520	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q878	
ENSMUST00000170521	ENSMUSG00000090487	14	3030002	3038762	1	2	0	5	9	4	0	0	0	0	0	0	K7N746	
ENSMUST00000170523	ENSMUSG00000029188	5	53038081	53071664	1	1	2	4	6	2	0	0	0	0	0	0	E9QAX5	
ENSMUST00000170525	ENSMUSG00000091402	12	111979111	111981317	-1	0	0	8	2	0	0	0	0	0	0	0	B2RV38	
ENSMUST00000170531						33	33	109	42	27	14	1	3	1	0	0		
ENSMUST00000170532						6	0	0	1	0	0	4	6	6	1	9		
ENSMUST00000170533						2	0	3	7	3	1	0	0	0	0	0		
ENSMUST00000170534	ENSMUSG00000021751	14	8225511	8259353	-1	0	0	0	4	0	0	2	0	17	0	3	E9Q5T5	
ENSMUST00000170535	ENSMUSG00000058440	6	30047988	30153458	1	3	0	0	0	0	2	0	24	0	14	13	G3XA39	
ENSMUST00000170536	ENSMUSG00000029442	5	123252102	123327484	1	39	19	131	56	16	0	1	7	2	0	11	B2RR19	
ENSMUST00000170538	ENSMUSG00000021417	13	34977748	35027094	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVM6	
ENSMUST00000170540	ENSMUSG00000021111	12	105784694	105838944	1	0	0	0	0	0	0	0	0	0	0	0	E9QAN5	
ENSMUST00000170543						0	0	0	2	0	1	0	0	0	0	5		
ENSMUST00000170546	ENSMUSG00000094258	14	4632352	4640802	1	4	0	0	12	0	0	0	0	0	0	0	E9Q0R1	
ENSMUST00000170551	ENSMUSG00000096452	12	115861867	115862355	-1	5	7	14	1	0	2	0	0	0	1	3	A0A0B4J1M0	
ENSMUST00000170552	ENSMUSG00000027751	3	54692807	54728766	1	6	4	14	14	4	3	249	942	545	162	517		Q7TT00
ENSMUST00000170553	ENSMUSG00000022255	15	34082694	34142386	1	0	0	0	0	0	0	0	0	0	0	25	F6ZQL0	
ENSMUST00000170554	ENSMUSG00000017316	11	102099930	102101319	-1	0	0	0	1	0	1	0	0	0	0	0	Q496X5	P10601
ENSMUST00000170555	ENSMUSG00000021557	13	59449537	59585227	-1	5	0	0	4	7	4	5	13	0	9	16		Q641K1
ENSMUST00000170556	ENSMUSG00000025140	11	120635712	120643769	-1	41	31	202	82	55	33	7	5	11	3	17	Q3UTR5	Q922W5
ENSMUST00000170566	ENSMUSG00000002459	1	4909576	5070285	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q1A3	
ENSMUST00000170572						11	11	27	28	16	5	0	0	0	0	0		
ENSMUST00000170573	ENSMUSG00000090863	13	31556134	31559333	-1	15	11	46	256	28	13	0	0	0	0	0	Q3UTW2	
ENSMUST00000170574						1	0	12	3	0	1	0	0	0	0	0		
ENSMUST00000170575	ENSMUSG00000019214	17	25718926	25727419	-1	8	8	29	21	17	12	0	6	15	0	0	E9Q2M3	
ENSMUST00000170577						9	5	12	189	13	9	0	2	6	1	1		
ENSMUST00000170578	ENSMUSG00000048027	17	15806253	15826586	-1	17	13	22	183	22	10	16	25	15	8	15		Q7TQ33
ENSMUST00000170579	ENSMUSG00000038528	10	39958061	39986646	-1	3	3	14	4	10	3	0	0	0	0	0	E9PYY6	
ENSMUST00000170580	ENSMUSG00000051726	12	17172100	17176888	-1	38	31	68	345	65	28	1	1	1	0	0	E9PYC0	
ENSMUST00000170581	ENSMUSG00000024043	17	67842713	68004120	-1	2	0	0	0	0	1	0	0	0	0	0	F6ZDY5	
ENSMUST00000170582						4	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000170584	ENSMUSG00000033170	15	78775138	78803042	-1	0	11	37	76	0	4	0	15	64	0	168		P58660
ENSMUST00000170585						0	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000170588	ENSMUSG00000020439	11	3517523	3540612	-1	0	0	0	0	0	0	0	0	0	0	0		Q921U8
ENSMUST00000170590	ENSMUSG00000017286	11	76120987	76243725	-1	0	0	1	28	1	0	0	0	0	17	6	E9Q2R6	
ENSMUST00000170591	ENSMUSG00000036814	9	123636122	123678885	-1	7	0	0	12	0	1	0	0	0	0	0	F6WK13	
ENSMUST00000170592	ENSMUSG00000063881	11	73371246	73375704	1	0	0	7	0	0	0	0	0	0	0	0	Q8VGI2	
ENSMUST00000170594	ENSMUSG00000043929	X	94234599	94277724	1	0	0	0	0	0	0	5	24	36	0	9	A2AAX3	
ENSMUST00000170596	ENSMUSG00000091468	10	79356576	79397198	1	11	9	13	8	11	4	0	0	0	0	0	G3UWA2	
ENSMUST00000170597						9	0	8	5	7	4	0	0	0	0	0		
ENSMUST00000170600	ENSMUSG00000021906	14	32085374	32103202	1	0	0	5	0	0	0	0	0	0	5	0	E9Q8U8	
ENSMUST00000170603	ENSMUSG00000024050	17	32354055	32389401	-1	0	1	1	84	5	3	0	1	2	1	2	E9Q5R9	
ENSMUST00000170608	ENSMUSG00000029917	6	65381105	65458150	1	7	23	17	1	14	4	0	0	0	0	0	G3UWA8	
ENSMUST00000170612	ENSMUSG00000041959	3	93555080	93564643	1	0	0	0	0	2	0	0	0	0	0	0	Q3TC45	P08207
ENSMUST00000170613	ENSMUSG00000091882	14	6049469	6058267	-1	0	0	0	0	0	0	0	0	0	0	0	K7N745	
ENSMUST00000170614						3	1	3	1	9	3	0	0	0	0	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000170617	ENSMUSG00000024050	17	32354055	32389401	-1	3	0	9	3	7	10	41	37	24	3	7	E9Q5W4	
ENSMUST00000170618	ENSMUSG00000090129	15	98206971	98221056	-1	59	47	192	83	65	37	0	1	0	0	0	E9PZS7	
ENSMUST00000170620						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000170624						0	1	6	0	7	1	0	0	1	0	1		
ENSMUST00000170625	ENSMUSG00000059900	6	115729131	115762410	-1	5	0	17	0	1	0	87	96	56	36	18	E9Q6I9	
ENSMUST00000170626						2	2	1	14	3	5	0	0	0	0	0		
ENSMUST00000170627	ENSMUSG00000001289	15	102326116	102331873	1	0	0	0	0	0	0	3	13	0	3	3	E9PZ62	
ENSMUST00000170628	ENSMUSG00000041481	12	104236245	104241939	1	0	4	8	0	5	0	19	18	14	12	13		
ENSMUST00000170629	ENSMUSG00000022385	15	85859707	85876572	1	25	14	75	69	40	16	83	53	86	5	37	Q542Q3	Q8R080
ENSMUST00000170630	ENSMUSG00000022471	15	81987835	82040085	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0B8	
ENSMUST00000170631	ENSMUSG00000005547	7	26835305	26843548	1	0	1	0	0	0	2	0	0	0	3	0	F6SHL3	
ENSMUST00000170633	ENSMUSG00000047921	15	72589621	73061204	-1	23	21	15	31	26	12	5	10	16	2	45	E9Q3T8	
ENSMUST00000170634						61	37	176	76	39	24	3	5	7	1	3		
ENSMUST00000170635	ENSMUSG00000006154	7	4460674	4480487	1	2	2	4	10	2	2	0	0	0	0	0	E9PZ95	
ENSMUST00000170637						1	0	2	0	0	0	0	0	0	6	8		
ENSMUST00000170638						3	2	5	8	3	0	0	2	1	1	1		
ENSMUST00000170639	ENSMUSG00000090364	14	3688783	3698000	1	0	0	0	0	0	0	0	0	0	0	0	K7N693	
ENSMUST00000170640	ENSMUSG00000001576	17	26561489	26656931	1	2	1	0	1	1	0	7	6	5	1	33	F6Z6A5	
ENSMUST00000170643	ENSMUSG00000068048	X	37899097	37901770	-1	4	4	5	2	6	2	0	0	0	0	0	A4FTZ4	
ENSMUST00000170644						0	5	21	178	13	0	0	59	10	9	38		
ENSMUST00000170647	ENSMUSG00000012535	6	29540827	29609887	-1	0	2	0	0	0	0	0	630	40	240	150	F6TDZ2	
ENSMUST00000170650	ENSMUSG00000092164	6	139492973	139501976	-1	2	1	0	2	3	3	0	0	0	0	0	B2RVE2	
ENSMUST00000170651	ENSMUSG00000033826	17	30624354	30875264	1	84	77	95	125	103	46	609	997	1393	41	935		Q91XQ0
ENSMUST00000170653	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	380	814	443	4	215		Q60875
ENSMUST00000170654						0	0	0	0	0	0	2	0	2	0	0		
ENSMUST00000170656						1	0	0	2	0	7	0	0	0	0	0		
ENSMUST00000170661						0	0	0	4	1	0	0	0	1	0	0		
ENSMUST00000170662	ENSMUSG00000061517	14	118233232	118237030	-1	15	9	49	895	24	11	0	0	0	0	0		Q811W0
ENSMUST00000170664	ENSMUSG00000019232	3	130617448	130637521	1	0	1	0	0	0	2	0	0	0	0	0	F7AY26	
ENSMUST00000170665	ENSMUSG00000090356	16	21152655	21154000	-1	27	22	49	30	44	11	40	377	94	114	38	Q9CQH1	
ENSMUST00000170667	ENSMUSG00000035378	6	100568256	100671157	-1	3	3	0	18	7	0	7	21	10	14	4		Q7TMX5
ENSMUST00000170669						0	0	0	0	0	0	0	0	18	0	10		
ENSMUST00000170671	ENSMUSG00000042515	X	139210042	139238335	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2F3	
ENSMUST00000170672	ENSMUSG00000022494	16	11984113	12270902	1	13	13	91	21	8	16	0	0	0	0	0		Q9CZN4
ENSMUST00000170673	ENSMUSG00000090404	14	6765962	6774411	-1	0	7	0	0	0	3	0	0	0	0	0	K7N714	
ENSMUST00000170674						0	3	3	3	6	2	0	0	0	0	0		
ENSMUST00000170675						18	16	23	15	28	13	263	526	356	13	770		
ENSMUST00000170676	ENSMUSG00000086848	3	92620081	92621660	-1	1	2	0	0	0	0	0	0	0	0	0	D3YV94	
ENSMUST00000170677	ENSMUSG00000022106	14	73123037	73207843	1	0	6	19	0	8	0	0	0	8	0	0		Q99LJ7
ENSMUST00000170680	ENSMUSG00000064065	10	6885796	7052478	-1	1	0	5	3	0	0	2	4	9	0	3	Q3UX69	
ENSMUST00000170683						1	0	0	8	2	0	0	0	0	0	0		
ENSMUST00000170684						7	5	9	15	12	0	0	0	0	0	0		
ENSMUST00000170686	ENSMUSG00000090643	14	5970744	5979137	-1	0	7	5	0	0	7	0	0	0	0	0	K7N724	
ENSMUST00000170690	ENSMUSG00000020027	10	95385362	95417180	-1	0	10	0	0	0	0	0	0	0	0	0	Q548Q7	O35717
ENSMUST00000170693	ENSMUSG00000091896	18	35771559	35807172	1	7	8	0	128	0	0	1004	3971	1161	230	674	Q3UT95	P62838
ENSMUST00000170694	ENSMUSG00000093979	14	19563801	19585135	-1	0	9	0	0	3	0	0	7	0	2	1	E9Q501	
ENSMUST00000170695	ENSMUSG00000049100	3	45378398	45435623	1	7	6	7	8	7	5	0	0	0	0	0	Q925I8	
ENSMUST00000170696	ENSMUSG00000060671	3	89939481	89963508	-1	0	0	5	0	0	5	2	0	0	0	0	E9Q114	
ENSMUST00000170699	ENSMUSG00000058239	7	30945248	30956803	-1	1	0	0	0	0	0	190	0	101	15	71	E9PZY3	
ENSMUST00000170700	ENSMUSG00000007122	1	172209894	172219868	-1	0	1	0	0	0	0	0	0	0	0	0	E9Q489	
ENSMUST00000170701						0	0	5	0	0	0	0	5	0	0	0		
ENSMUST00000170703						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000170704	ENSMUSG00000090326	5	62813823	62888308	1	9	7	12	8	7	4	0	0	0	0	0	E9PZX1	
ENSMUST00000170705	ENSMUSG00000031585	8	33731833	33777173	1	0	0	0	2	0	0	19	280	64	229	65		Q9D902
ENSMUST00000170706						2	2	0	8	3	0	0	0	0	0	0		
ENSMUST00000170709	ENSMUSG00000052099	14	64086234	64097670	1	3	3	10	2	3	0	0	0	0	0	0	E9PWV1	
ENSMUST00000170710	ENSMUSG00000017286	11	76120987	76243725	-1	4	1	3	58	3	4	0	0	5	0	0		Q9CPV4
ENSMUST00000170711	ENSMUSG00000025764	3	41555731	41616864	1	8	3	5	43	8	9	0	3	58	0	65		Q6ZPI0
ENSMUST00000170712	ENSMUSG00000022019	14	87416639	87545373	1	0	1	0	0	0	0	0	0	0	0	1	F6ZI20	
ENSMUST00000170713						6	1	11	4	1	3	14	50	16	1	25		
ENSMUST00000170715	ENSMUSG00000044533	17	24718116	24721929	1	4	13	0	0	0	0	5	0	0	3	0	Q58EU3	P25444
ENSMUST00000170716	ENSMUSG00000060600	11	70657202	70662513	1	0	0	0	0	0	0	0	81	0	0	41		P21550
ENSMUST00000170718	ENSMUSG00000026587	1	158362273	158691781	1	0	0	0	11	0	0	0	0	0	0	0	Q3TPU9	
ENSMUST00000170719	ENSMUSG00000021789	14	41131782	41136452	1	8	12	4	14	9	4	0	0	0	0	0	Q9CQI1	
ENSMUST00000170720						0	3	5	2	4	1	210	1251	415	280	401		
ENSMUST00000170723	ENSMUSG00000023918	17	42656891	42692284	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0D9SEG9	
ENSMUST00000170724	ENSMUSG00000003153	6	122727809	122801640	-1	5	4	23	12	5	7	2	3	5	1	13	E9Q6T5	
ENSMUST00000170725	ENSMUSG00000024254	17	84676302	84700333	1	0	0	0	1	0	0	0	0	0	0	0	E9Q0P2	
ENSMUST00000170728	ENSMUSG00000022565	15	76170974	76232574	-1	1	2	1	12	0	0	0	0	0	0	0	A0A0B4J1M3	
ENSMUST00000170729	ENSMUSG00000006932	9	120929216	120960507	1	0	0	0	0	0	0	0	0	0	0	0	F6QZ47	
ENSMUST00000170730	ENSMUSG00000017288	11	76046226	76179647	-1	0	0	10	16	0	0	0	0	0	0	0	E9Q3C3	
ENSMUST00000170731	ENSMUSG00000020458	11	29692947	29744331	1	0	0	0	0	0	0	89	164	224	38	186	Q8BH78	
ENSMUST00000170733						3	3	7	11	5	4	0	1	0	0	0		
ENSMUST00000170737	ENSMUSG00000010066	9	107399612	107529343	1	68	0	59	0	20	35	0	5	0	0	12		Q6PHS9
ENSMUST00000170738	ENSMUSG00000093985	14	7006115	7027449	-1	6	3	7	64	4	0	0	0	1	0	0	A6NAS4	
ENSMUST00000170739	ENSMUSG00000060671	3	89939481	89963508	-1	0	0	0	0	0	0	0	0	0	0	3	F6SPT4	
ENSMUST00000170740						0	0	0	0	0	0	0	3	0	0	0		
ENSMUST00000170741	ENSMUSG00000020530	11	84832361	84870817	-1	0	0	0	0	0	0	8	190	0	0	0	E9Q6H9	
ENSMUST00000170744	ENSMUSG00000028640	2	172549593	172558622	1	0	0	0	0	0	0	0	0	0	0	0	Q3ULB3	
ENSMUST00000170750						6	10	29	13	7	4	8	11	6	0	2		
ENSMUST00000170752						3	5	5	7	2	5	0	0	2	0	2		
ENSMUST00000170753	ENSMUSG00000054474	6	71128166	71144439	-1	0	0	0	0	0	0	0	0	0	0	1	F7AFM3	
ENSMUST00000170754						39	29	84	73	50	29	16	79	27	3	64		
ENSMUST00000170757	ENSMUSG00000045975	16	97855210	97922633	-1	141	102	373	515	191	75	44	97	95	28	97	E9Q3C1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000170758	ENSMUSG00000024247	17	83215292	83225070	1	0	0	11	0	1	2	0	0	0	0	0	F6YRX3	
ENSMUST00000170759	ENSMUSG00000050668	17	78835516	78848299	1	21	19	39	77	39	20	173	935	342	1121	340		
ENSMUST00000170760	ENSMUSG00000091055	18	78043614	78057395	-1	7	1	7	159	7	3	0	0	1	0	0	A7E1W8	
ENSMUST00000170767	ENSMUSG00000029708	6	28416091	28428390	-1	1	2	3	95	5	2	8	18	8	1	10	E9Q6U7	
ENSMUST00000170768						1	2	6	1	2	0	4	43	27	0	49		
ENSMUST00000170770	ENSMUSG00000074165	7	41633203	41651530	1	0	0	0	0	0	0	0	43	4	0	0	Q8BUQ3	
ENSMUST00000170771	ENSMUSG00000019779	10	34483400	34611226	1	31	31	31	32	0	21	0	0	0	15	0		Q922K9
ENSMUST00000170772						2	1	5	2	1	2	0	0	0	0	0		
ENSMUST00000170773	ENSMUSG00000036718	5	139706696	139736336	-1	26	16	33	9	14	14	0	1	42	4	9	E9PZD2	
ENSMUST00000170774	ENSMUSG00000004347	6	56069804	56569103	-1	5	7	0	7	7	0	0	0	0	0	2	Q9D5W0	
ENSMUST00000170776	ENSMUSG00000054893	7	6286579	6307883	1	0	8	8	11	18	0	0	0	0	0	0		Q2TL60
ENSMUST00000170777						1	0	10	2	1	3	0	0	0	0	0		
ENSMUST00000170780	ENSMUSG00000091652	7	5220478	5221410	1	4	1	0	4	2	2	0	0	0	0	0	K7N731	
ENSMUST00000170781	ENSMUSG00000028133	3	121155398	121171695	-1	0	0	3	0	6	6	0	10	0	0	0	E9PZT2	
ENSMUST00000170786						4	2	2	2	8	3	0	0	0	0	0		
ENSMUST00000170787						12	3	3	11	5	2	0	0	0	0	0		
ENSMUST00000170788	ENSMUSG00000027777	3	68064802	68626481	1	4	0	5	67	5	5	0	0	0	0	0	A0A097PIJ2	Q3TI53
ENSMUST00000170790	ENSMUSG00000071613	14	3133997	3141609	1	13	5	0	0	0	0	0	0	0	0	0	K7N708	
ENSMUST00000170792	ENSMUSG00000046709	5	102907948	103211334	-1	83	49	280	91	70	41	0	6	3	0	4	Q80W82	
ENSMUST00000170794	ENSMUSG00000024247	17	83215292	83225070	1	6	7	2	80	19	3	12	6	2	7	22		Q5RJI4
ENSMUST00000170795	ENSMUSG00000001150	10	76468971	76515856	1	30	31	100	55	56	34	1010	1601	1572	125	1158		Q9WUU9
ENSMUST00000170796						12	6	37	13	27	3	7	23	8	5	11		
ENSMUST00000170797						0	0	2	32	2	0	0	3	3	0	8		
ENSMUST00000170799	ENSMUSG00000078771	11	79526560	79530609	-1	19	9	15	8	13	10	81	799	145	295	141		P20934
ENSMUST00000170800	ENSMUSG00000026674	1	169972307	170110762	-1	0	0	0	73	0	0	1	3	0	34	14		Q62371
ENSMUST00000170801	ENSMUSG00000025198	19	44034944	44069785	-1	11	0	0	0	19	7	0	0	180	0	0		
ENSMUST00000170802	ENSMUSG00000024277	18	23752333	23893861	1	14	15	0	0	0	11	0	0	0	0	0	E9Q6X0	
ENSMUST00000170803	ENSMUSG00000013089	16	22381309	22439719	-1	0	1	0	0	2	0	0	0	0	0	3	F6Q487	
ENSMUST00000170805	ENSMUSG00000022871	16	22918382	22939766	1	0	2	0	5	6	0	0	0	0	0	0		Q9QXC1
ENSMUST00000170806						0	0	0	0	0	1	0	1	0	2	0		
ENSMUST00000170808	ENSMUSG00000095486	6	123609758	123650635	-1	11	10	21	0	4	3	0	0	0	0	0	E9Q7S8	
ENSMUST00000170810	ENSMUSG00000061904	10	91116574	91124059	-1	0	7	0	0	0	0	166	953	361	27	402	G5E902	
ENSMUST00000170811	ENSMUSG00000060450	18	38296635	38317847	1	6	0	0	48	0	0	101	410	166	126	130	G3XA54	
ENSMUST00000170813	ENSMUSG00000024043	17	67842713	68004120	-1	0	0	0	0	0	0	0	0	0	1	0	F6XG99	
ENSMUST00000170815						4	2	9	1	4	2	1	0	0	0	4		
ENSMUST00000170816	ENSMUSG00000091619	12	4592826	4592927	-1	0	0	0	111	1	2	1	1	2	0	1	Q3T9W8	
ENSMUST00000170817	ENSMUSG00000063796	19	8591254	8611834	1	0	36	1	0	0	0	0	3	2	0	5		O88909
ENSMUST00000170819	ENSMUSG00000040022	19	59902884	59943654	-1	11	1	0	0	0	3	7	3	24	3	6		G3XA57
ENSMUST00000170820	ENSMUSG00000058498	4	152307019	152318993	-1	0	0	0	1	0	3	0	0	0	0	0	E9PW78	
ENSMUST00000170825						0	0	0	27	4	2	0	0	5	0	3		
ENSMUST00000170826	ENSMUSG00000090015	5	109923400	109943936	1	0	0	0	0	0	0	0	1	0	3	1	K7N6W1	
ENSMUST00000170827	ENSMUSG00000068036	17	13760539	13906150	1	0	0	0	0	0	0	150	349	500	0	250	E9Q852	
ENSMUST00000170828	ENSMUSG00000079435	X	134585654	134588062	1	5	8	11	0	0	0	5	0	0	0	0	E9Q131	
ENSMUST00000170831						0	0	0	0	0	0	0	9	0	0	2		
ENSMUST00000170832	ENSMUSG00000064156	5	88317312	88328814	1	47	25	83	25	20	1	0	0	0	0	0	E9PYQ4	
ENSMUST00000170833	ENSMUSG00000000628	6	82725025	82774454	-1	3	5	63	40	9	9	0	0	2	0	0	E9Q5B5	
ENSMUST00000170835	ENSMUSG00000091962	7	86915300	86955177	1	2	0	4	4	8	4	0	0	0	0	0	K7N6U5	
ENSMUST00000170836	ENSMUSG00000015671	13	14613242	14625671	1	1	6	6	20	7	3	802	2945	929	4434	670		P49722
ENSMUST00000170837	ENSMUSG00000091955	7	24862213	24862697	1	6	3	0	0	7	2	0	0	0	0	0	J3QK33	Q6ZWY8
ENSMUST00000170839						12	8	13	27	11	6	0	0	1	0	2		
ENSMUST00000170840	ENSMUSG00000021911	14	32201949	32297550	1	4	0	11	0	0	4	62	455	72	47	122	E9Q088	
ENSMUST00000170841	ENSMUSG00000025500	7	141210043	141214082	-1	15	22	0	9	0	0	0	0	8	0	0	B7ZMW1	
ENSMUST00000170845	ENSMUSG00000034730	15	74516195	74589465	1	0	0	0	0	0	0	0	32	0	1	0	E9Q4H5	
ENSMUST00000170846	ENSMUSG00000034858	9	74953053	75032468	1	8	7	0	116	17	3	65	123	119	25	81		Q69ZK7
ENSMUST00000170847	ENSMUSG00000027869	3	98805504	98814443	-1	0	0	0	0	0	0	0	0	0	0	0		O35469
ENSMUST00000170850						8	0	16	16	13	0	4	27	2	0	0		
ENSMUST00000170851						0	0	0	1	2	0	7	40	8	0	13		
ENSMUST00000170853	ENSMUSG00000022973	16	90936092	91011308	-1	10	20	0	7	11	7	325	0	220	0	44	E9Q7S0	
ENSMUST00000170854	ENSMUSG00000024283	18	7868832	7973547	1	0	0	0	7	0	0	12	4	0	8	58	F7A7S5	
ENSMUST00000170855	ENSMUSG00000091089	14	50895942	50897456	-1	4	11	19	46	16	10	0	2	0	1	0	B7ZMY3	
ENSMUST00000170856	ENSMUSG00000027857	3	102775465	102782718	-1	2	2	3	2	1	0	1	0	1	0	3	E9Q4F3	
ENSMUST00000170857	ENSMUSG00000025316	8	121949750	122029258	1	19	13	34	16	39	13	25	108	32	9	45		Q8VBU8
ENSMUST00000170858	ENSMUSG00000023827	17	12118704	12219645	1	0	0	0	0	0	0	11	0	0	0	0	E9Q2W7	
ENSMUST00000170861	ENSMUSG00000030775	16	48734690	48771956	-1	4	2	0	1	5	1	4	14	6	27	15		
ENSMUST00000170862	ENSMUSG00000024576	18	61555274	61590061	1	0	0	1	0	0	0	0	396	81	0	0	E9Q3W1	
ENSMUST00000170863						0	0	5	0	0	1	119	0	37	0	0		
ENSMUST00000170865	ENSMUSG00000022019	14	87416639	87545373	1	0	0	0	0	0	0	20	96	20	0	0		Q91W18
ENSMUST00000170870						7	11	0	3	10	3	0	4	0	0	1		
ENSMUST00000170872	ENSMUSG00000023885	17	14665500	14694262	-1	44	28	64	39	56	18	0	0	0	10	21		Q03350
ENSMUST00000170873	ENSMUSG00000001376	6	3498382	3603531	1	5	1	2	2	4	4	0	0	0	0	0		Q8CI71
ENSMUST00000170877	ENSMUSG00000051786	15	89098357	89123087	-1	0	0	0	0	0	1	1	5	0	0	0	F6YBF3	
ENSMUST00000170878	ENSMUSG00000021624	13	102693558	102739629	1	4	0	0	0	4	0	0	0	0	0	0	E9Q009	
ENSMUST00000170879	ENSMUSG00000048200	7	141461094	141466613	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2F1	
ENSMUST00000170882	ENSMUSG00000042675	7	126776955	126780514	1	0	0	0	0	0	0	0	165	0	0	0		P61237
ENSMUST00000170883	ENSMUSG00000034088	1	93405940	93478815	-1	34	27	94	44	58	38	363	1492	678	282	824	Q3U4Z7	Q8VDJ3
ENSMUST00000170884	ENSMUSG00000001280	15	102406143	102436404	1	0	0	0	0	0	0	0	0	0	0	0	E9Q0S7	
ENSMUST00000170885	ENSMUSG00000015340	X	9435252	9487771	-1	3	1	1	5	2	1	0	0	0	0	0	E9Q7S3	
ENSMUST00000170887						3	0	1	0	1	1	0	2	0	0	0		
ENSMUST00000170889	ENSMUSG00000094838	Y	11197024	11199374	-1	0	0	2	0	0	1	0	0	0	0	0	J3KMI7	
ENSMUST00000170891						0	0	0	0	0	0	0	14	0	0	0		
ENSMUST00000170892	ENSMUSG00000091441	7	141029131	141029620	1	1	1	1	0	1	0	1	0	0	0	1	F6Y3H4	
ENSMUST00000170893	ENSMUSG00000091618	10	3256208	3267771	-1	31	21	27	32	23	9	19	29	17	1	8	B1B213	
ENSMUST00000170895	ENSMUSG00000020444	11	59183875	59192212	-1	0	3	0	0	0	0	118	153	78	62	73	E9Q7K1	
ENSMUST00000170897	ENSMUSG00000004364	1	80264923	80340480	-1	0	0	0	0	0	0	7	0	36	0	22	F6R0N8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000170898						25	26	34	20	25	12	5	21	2	9	11		
ENSMUST00000170899	ENSMUSG00000022801	16	32914100	33015647	1	0	0	0	0	0	1	0	0	0	0	0	B7ZWM8	
ENSMUST00000170901	ENSMUSG00000028212	4	11191351	11204779	1	0	8	0	0	0	0	0	0	0	0	0	Q544H6	Q9Z238
ENSMUST00000170903	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	2	5	0	0	0	0	0	0	0	E9Q3F9	
ENSMUST00000170904	ENSMUSG00000032554	9	103204001	103230444	-1	0	0	0	0	2	0	24	1270	102	156	198	F7BAE9	
ENSMUST00000170905	ENSMUSG00000033016	18	80606205	80713071	-1	0	15	0	383	8	0	0	0	0	0	0	B5B2N2	
ENSMUST00000170907						2	3	4	4	2	4	0	0	0	0	3		
ENSMUST00000170908	ENSMUSG00000023330	2	126152141	126165279	1	0	0	0	12	0	4	0	41	18	20	20		Q9D8U7
ENSMUST00000170909	ENSMUSG00000038482	8	13339674	13377702	1	35	32	32	48	31	14	1684	3301	2711	951	1597	Q3V3X3	Q08639
ENSMUST00000170910						3	0	0	5	5	4	0	0	5	0	0		
ENSMUST00000170912	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	65	4	1	0	0	0	20	14	A0A0G2JFL4	
ENSMUST00000170915	ENSMUSG00000022565	15	76170974	76232574	-1	1	2	5	7	2	2	0	0	0	0	0	A0A0B4J1M7	
ENSMUST00000170918	ENSMUSG00000028024	3	129269175	129332720	-1	5	4	0	9	3	0	0	2	0	0	0	F7B9G4	
ENSMUST00000170919	ENSMUSG00000091779	10	104142987	104153674	1	3	2	21	8	5	2	0	0	0	0	0	E9Q4G9	
ENSMUST00000170920	ENSMUSG00000095608	10	129974605	129975567	-1	5	8	15	8	7	0	0	0	0	0	0	E9PVJ7	
ENSMUST00000170921	ENSMUSG00000021492	13	55417958	55426793	-1	0	4	0	0	6	0	0	8	4	2	0	E9Q698	
ENSMUST00000170922	ENSMUSG00000095730	7	7231327	7247328	-1	14	10	15	9	11	4	0	0	0	0	0	L7N2D4	
ENSMUST00000170923	ENSMUSG00000094811	14	6296365	6304843	-1	0	0	0	0	7	14	0	0	0	0	0	E9Q2Q1	
ENSMUST00000170926	ENSMUSG00000032698	2	103957986	103981878	1	3	9	14	0	3	0	135	506	143	26	100	Q544Z2	P25801
ENSMUST00000170927						465	534	590	365	295	126	7	9	11	2	5		
ENSMUST00000170928	ENSMUSG00000020397	11	46436925	46442721	1	0	3	0	0	5	0	5	0	0	2	5		Q9CZB6
ENSMUST00000170931	ENSMUSG00000095064	7	21832351	21833274	1	0	0	0	0	0	0	0	0	0	0	0	K9J7G0	
ENSMUST00000170932	ENSMUSG00000024283	18	7868832	7973547	1	0	0	0	156	7	2	0	14	13	3	14		
ENSMUST00000170934	ENSMUSG00000028799	4	128773088	128806045	-1	2	4	0	63	7	2	0	0	0	0	14	E9QA68	
ENSMUST00000170935	ENSMUSG00000034602	10	122992061	123076505	-1	12	13	13	29	43	8	282	454	0	0	443	B9EKJ3	
ENSMUST00000170939	ENSMUSG00000022607	15	73205105	73423191	-1	9	4	3	2	20	6	5	0	7	0	4		P34152
ENSMUST00000170941	ENSMUSG00000071068	17	48300038	48312534	1	29	26	121	227	45	25	2808	7840	4625	671	2795		Q2LA85
ENSMUST00000170942	ENSMUSG00000057003	11	67238029	67260446	1	0	0	0	39	0	0	0	0	0	0	0		Q5SX39
ENSMUST00000170943						4	3	7	4	2	8	2	4	2	4	0		
ENSMUST00000170945	ENSMUSG00000070868	4	112232245	112300468	1	0	0	0	0	0	0	0	0	0	0	0		A7TZF0
ENSMUST00000170946						4	2	6	2	0	5	0	0	0	0	0		
ENSMUST00000170947	ENSMUSG00000032057	9	51081313	51102078	-1	7	3	9	7	8	4	0	0	0	0	0		Q80Y73
ENSMUST00000170950						3	2	14	1	7	0	0	0	1	0	0		
ENSMUST00000170951						4	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000170952						1	0	3	0	1	1	0	0	0	0	0		
ENSMUST00000170953	ENSMUSG00000090862	7	116331505	116334195	-1	0	7	20	74	14	5	1099	3692	1473	3432	1162	Q5BLJ7	P62301
ENSMUST00000170954	ENSMUSG00000035165	7	100176670	100184869	1	0	0	2	4	4	2	0	10	0	7	0	Q545H9	Q9WTW2
ENSMUST00000170955	ENSMUSG00000018126	15	79258195	79285537	-1	3	4	7	21	0	8	0	0	0	0	0		Q80Y61
ENSMUST00000170956						0	1	0	2	2	0	0	33	8	0	0		
ENSMUST00000170957	ENSMUSG00000021302	13	14052449	14063401	-1	29	33	44	50	31	30	105	395	178	217	113	Q3V0T8	Q9WTN0
ENSMUST00000170958						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000170959						2	1	1	59	4	1	1	1	1	2	2		
ENSMUST00000170960						62	47	212	61	71	45	3	6	4	2	0		
ENSMUST00000170962	ENSMUSG00000031917	8	107056877	107060926	1	2	63	156	209	75	28	0	0	0	0	0	E9Q109	
ENSMUST00000170967						0	0	0	0	4	0	4	45	0	2	6		
ENSMUST00000170971	ENSMUSG00000030830	7	127296260	127335138	1	0	0	0	0	0	0	2395	0	3488	141	3321		P24063
ENSMUST00000170972	ENSMUSG00000011008	3	146149833	146195513	1	0	0	1	2	1	0	0	0	0	0	0	F7B2J7	
ENSMUST00000170979	ENSMUSG00000036940	4	136550540	136602723	-1	3	6	0	0	0	2	18	0	25	0	0	F6Z4I3	
ENSMUST00000170983						13	16	4	8	10	7	0	0	0	0	0		
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ENSMUST00000170985						2	0	0	0	0	1	2	13	4	18	4		
ENSMUST00000170988	ENSMUSG00000023963	17	43667425	43751431	1	14	12	15	8	16	9	12	58	22	28	13	Q544S6	Q9JKJ9
ENSMUST00000170989	ENSMUSG00000021417	13	34977748	35027094	-1	1	0	2	85	5	5	11	49	29	52	21	E9PUY9	
ENSMUST00000170991	ENSMUSG00000060147	13	33917918	34002794	-1	0	0	0	3	0	0	0	0	0	3	0	E9Q4R2	
ENSMUST00000170992	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	61	0	0	0	43	E9PY90	
ENSMUST00000170994	ENSMUSG00000020628	12	28690629	28750453	-1	8	6	14	34	15	5	0	0	4	0	8	Q8C0C3	
ENSMUST00000170996	ENSMUSG00000005899	16	17619354	17644828	1	1	0	0	0	2	0	0	0	0	0	10	E9Q0L7	
ENSMUST00000170998	ENSMUSG00000070304	9	45117876	45130070	1	30	37	67	52	52	22	7	7	22	0	7	Q1MXF8	Q56A07
ENSMUST00000171000	ENSMUSG00000035258	16	56477846	56690128	1	6	0	0	4	0	8	0	0	0	0	1	E9Q8E3	
ENSMUST00000171001	ENSMUSG00000066026	4	144892827	144928209	1	0	0	0	0	0	0	191	571	113	89	225	G5E8W9	
ENSMUST00000171002	ENSMUSG00000022758	16	17561885	17577800	1	0	0	0	0	0	0	0	0	0	0	3	E9PY29	
ENSMUST00000171003						7	7	10	11	10	3	2	9	7	6	7		
ENSMUST00000171004						2	3	2	1	3	1	0	0	0	0	0		
ENSMUST00000171005						0	0	0	0	0	0	53	0	0	0	3		
ENSMUST00000171007	ENSMUSG00000091007	12	36381242	36382181	-1	2	0	6	234	8	3	0	0	0	0	0	Q3UQD6	
ENSMUST00000171008	ENSMUSG00000030109	6	121343076	121365775	1	0	0	0	0	0	0	0	0	0	0	0	E9PXG1	
ENSMUST00000171009						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000171010	ENSMUSG00000031585	8	33731833	33777173	1	0	0	0	0	2	0	0	27	0	0	0		Q9D902
ENSMUST00000171014	ENSMUSG00000005553	7	30712209	30725535	1	2	5	5	2	4	3	0	0	0	0	0	F6S7B0	
ENSMUST00000171017						1	2	5	0	4	1	3	4	0	0	0		
ENSMUST00000171018	ENSMUSG00000031872	8	104170513	104219092	1	0	20	0	57	15	0	0	0	0	0	0	E9PVP2	
ENSMUST00000171020						9	3	11	6	7	3	0	0	0	0	0		
ENSMUST00000171022	ENSMUSG00000030970	7	132987563	133124354	-1	1	0	1	0	0	3	0	0	0	0	1	E9Q0V8	
ENSMUST00000171023	ENSMUSG00000000600	5	3803184	3845564	1	21	19	20	84	0	12	9	36	42	52	33		Q6S5J6
ENSMUST00000171024	ENSMUSG00000048647	2	119516505	119547627	-1	174	135	199	184	153	117	31	121	65	21	31		Q8CDF7
ENSMUST00000171026						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000171029						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171030	ENSMUSG00000061689	2	156613705	156764363	1	0	0	0	0	0	0	142	38	144	77	159	F6YMR0	
ENSMUST00000171031	ENSMUSG00000034165	17	47505051	47599691	1	16	11	36	0	15	13	263	180	201	51	280	Q3TSW4	P30282
ENSMUST00000171032	ENSMUSG00000040938	11	70212752	70216417	1	4	9	17	47	4	2	0	0	0	0	0		Q5NC32
ENSMUST00000171033						1	1	0	0	1	1	0	2	0	0	0		
ENSMUST00000171034	ENSMUSG00000060147	13	33917918	34002794	-1	0	0	0	10	0	0	0	0	9	0	22	K7E6F1	
ENSMUST00000171035	ENSMUSG00000015749	3	95929246	95947390	1	0	0	2	3	3	0	0	7	0	0	0	E9Q5H2	
ENSMUST00000171036						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000171039	ENSMUSG00000091924	7	26611021	26612164	-1	7	7	3	2	2	0	0	0	0	0	0	Q8R299	
ENSMUST00000171040	ENSMUSG00000021243	12	84970897	84983303	1	0	3	15	0	0	0	0	31	0	52	0	E9Q186	
ENSMUST00000171041	ENSMUSG00000018442	11	71007164	71019841	-1	9	2	0	53	4	2	217	474	202	226	136	Q3U957	
ENSMUST00000171042	ENSMUSG00000024283	18	7868832	7973547	1	2	1	0	26	11	0	0	0	0	0	19	E9Q4Y9	
ENSMUST00000171044						5	0	2	0	0	0	0	29	27	8	56		
ENSMUST00000171045	ENSMUSG00000053469	15	66670753	66850721	1	0	0	0	0	0	0	0	11	51	7	84	F6XYF6	
ENSMUST00000171052	ENSMUSG00000078588	4	117866524	117872557	-1	0	0	0	0	0	0	0	0	0	0	1	E9PUW8	
ENSMUST00000171053	ENSMUSG00000079380	14	5185793	5193743	1	0	0	0	0	1	0	0	0	0	0	0	L7N2E2	
ENSMUST00000171054						16	22	18	56	24	14	0	0	0	0	0		
ENSMUST00000171055	ENSMUSG00000029361	5	117781032	117958840	1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0J4
ENSMUST00000171057	ENSMUSG00000052337	6	71831331	71877388	1	0	0	0	0	0	0	6	9	12	0	9	E9PVS5	
ENSMUST00000171058	ENSMUSG00000079426	6	113378113	113390448	1	16	0	38	35	0	5	5	10	2	0	0	E9PWA7	
ENSMUST00000171059	ENSMUSG00000090744	7	41545674	41573662	-1	12	11	12	19	10	2	0	1	0	0	0	E9Q1W9	
ENSMUST00000171061	ENSMUSG00000040936	9	120960268	121277197	-1	0	0	0	0	0	0	0	0	0	3	0		Q3V129
ENSMUST00000171063	ENSMUSG00000027016	2	77410634	77819639	-1	12	0	0	0	2	0	0	0	0	0	0	G5E8Y8	
ENSMUST00000171064						0	4	0	2	1	1	4	0	7	0	0		
ENSMUST00000171065						6	5	0	1	8	0	0	2	0	3	0		
ENSMUST00000171066	ENSMUSG00000010751	7	143634806	143649661	-1	3703	3904	1704	2860	2281	917	67	237	238	41	315	Q78QS6	
ENSMUST00000171070	ENSMUSG00000022106	14	73123037	73207843	1	21	17	344	34	30	13	9	33	14	14	9	E9PY30	
ENSMUST00000171071	ENSMUSG00000041258	18	82593593	82692883	-1	37	43	54	25	76	30	201	640	516	57	554	B2RR24	
ENSMUST00000171072	ENSMUSG00000000708	17	53566861	53672720	1	0	3	0	0	0	0	0	9	32	2	21	F6SIC5	
ENSMUST00000171073	ENSMUSG00000096859	7	23834812	23835726	-1	6	4	4	6	0	3	0	0	0	0	0	G3UW31	
ENSMUST00000171075	ENSMUSG00000039717	3	13946393	14182287	1	0	0	4	0	0	0	0	0	0	0	1	E9Q5X7	
ENSMUST00000171076						2	0	0	0	3	0	0	0	0	0	8		
ENSMUST00000171077	ENSMUSG00000051504	7	55768178	55778925	1	0	0	0	0	19	6	0	0	1	0	2	Q4QQK7	
ENSMUST00000171080	ENSMUSG00000035455	11	11787431	11808962	-1	8	0	0	15	15	0	0	40	0	0	0		Q8BPY9
ENSMUST00000171081	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	0	0	0	0	0	0	0	0	0	E9PWY7	
ENSMUST00000171083						0	0	2	0	2	0	0	15	0	2	0		
ENSMUST00000171088	ENSMUSG00000032841	2	101714285	101883027	-1	0	32	78	50	58	31	223	1534	435	60	660		A2AVJ5
ENSMUST00000171089	ENSMUSG00000029706	6	28442334	28449353	-1	0	0	0	0	11	0	0	0	0	0	0	B7ZNC8	
ENSMUST00000171091	ENSMUSG00000091129	9	106626582	106627675	1	4	4	5	9	6	0	0	0	0	0	0	G3UWF2	
ENSMUST00000171093	ENSMUSG00000095918	5	11183072	11187810	1	0	0	0	0	0	0	0	0	0	0	0	F6VCN9	
ENSMUST00000171095	ENSMUSG00000039716	9	106892825	107231909	-1	2	0	17	11	4	9	3	3	0	2	0	F6VMI1	
ENSMUST00000171100	ENSMUSG00000004771	9	64715299	64737758	-1	0	0	0	34	0	0	95	529	76	4	6	E9PZB2	
ENSMUST00000171102						0	0	2	3	0	0	0	0	0	0	0		
ENSMUST00000171105	ENSMUSG00000022518	16	4835416	4867691	1	7	0	0	0	0	13	0	0	0	0	0	A6H692	
ENSMUST00000171106	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	0	0	0	6	0	38	0	0	F6ZV59	
ENSMUST00000171107	ENSMUSG00000092109	14	118266960	118267688	1	4	3	1	2	3	3	0	0	0	0	0	G3UW68	
ENSMUST00000171108	ENSMUSG00000062115	11	60105013	60199197	1	0	0	0	200	0	0	116	0	0	0	0		Q61818
ENSMUST00000171109	ENSMUSG00000040957	18	11839220	11945627	1	21	16	32	311	25	0	0	9	0	0	8	Q3U148	
ENSMUST00000171112	ENSMUSG00000034343	1	91250304	91290337	1	0	0	0	15	0	0	0	0	5	0	0		Q9CY34
ENSMUST00000171115	ENSMUSG00000022391	15	81704248	81729919	-1	19	22	33	8	29	10	0	0	16	0	0		P46061
ENSMUST00000171118						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000171119						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000171120	ENSMUSG00000091086	10	111125851	111126738	1	4	0	10	5	22	0	4	27	23	33	24	E9PUX4	
ENSMUST00000171121	ENSMUSG00000015474	17	34616662	34628510	-1	0	1	4	1	0	7	354	361	164	29	79		O35448
ENSMUST00000171122						0	6	3	0	0	0	0	0	0	0	0		
ENSMUST00000171123	ENSMUSG00000024858	19	4286001	4306222	-1	0	0	0	24	1	0	0	0	0	0	0	E9PW16	
ENSMUST00000171127	ENSMUSG00000069270	13	23683449	23683924	-1	2	0	2	45	7	5	2	24	6	3	5	B2RVF0	P22752
ENSMUST00000171128	ENSMUSG00000046329	17	57043711	57059863	-1	0	0	0	2	1	1	0	0	0	0	0	F7ANR8	
ENSMUST00000171129	ENSMUSG00000040648	1	97706048	97770411	-1	4	0	0	0	0	0	35	208	197	56	83		Q6ZQB6
ENSMUST00000171131	ENSMUSG00000090308	10	86655939	86657381	1	15	13	33	29	27	11	0	0	0	0	0	E9Q1V8	
ENSMUST00000171132	ENSMUSG00000022707	16	70313949	70569716	1	0	8	0	0	0	12	3	0	7	0	0	G3UW30	
ENSMUST00000171134	ENSMUSG00000042788	4	43427019	43429134	-1	0	0	5	0	6	0	0	0	0	0	0	E9Q4G6	
ENSMUST00000171137	ENSMUSG00000021408	13	34002363	34035170	1	3	0	0	0	0	0	96	0	296	0	252	F7D1J2	
ENSMUST00000171139	ENSMUSG00000016283	17	37480851	37483552	-1	0	0	0	0	0	0	0	0	0	0	0	Q6W9L1	
ENSMUST00000171140						0	0	0	0	0	0	108	634	45	47	101		
ENSMUST00000171142						6	3	9	12	6	2	0	0	0	4	0		
ENSMUST00000171143	ENSMUSG00000040339	3	108970997	109027607	-1	0	0	0	56	17	0	17	17	34	0	17	E9Q4R1	
ENSMUST00000171146						0	0	7	0	0	0	0	1	4	12	5		
ENSMUST00000171148	ENSMUSG00000037321	17	34187553	34197225	1	0	0	0	0	0	0	94	63	74	11	56	F6QHF1	
ENSMUST00000171150	ENSMUSG00000079409	14	3188255	3196681	1	17	8	10	6	30	6	0	0	0	0	0	E9PZN8	
ENSMUST00000171151	ENSMUSG00000020056	10	88201093	88246158	1	3	1	0	0	0	1	7	30	0	26	0	G3UWG7	
ENSMUST00000171153	ENSMUSG00000095329	12	23968510	23968845	-1	2	2	7	392	16	5	0	0	0	0	0	L7N290	
ENSMUST00000171155	ENSMUSG00000055652	7	75848310	75874131	1	37	12	42	0	51	0	237	75	186	34	0		Q8R2P1
ENSMUST00000171158	ENSMUSG00000020592	12	8771323	8793715	1	20	11	20	3	9	7	0	5	5	19	84	Q3V1F2	P18828
ENSMUST00000171163						17	11	16	17	14	7	0	0	3	0	5		
ENSMUST00000171164	ENSMUSG00000025958	1	64532645	64604548	1	0	0	0	0	0	0	20	49	47	28	0	Q62347	
ENSMUST00000171165	ENSMUSG00000034343	1	91250304	91290337	1	30	21	56	44	34	14	42	176	114	76	68		Q9CY34
ENSMUST00000171166	ENSMUSG00000090509	17	35601549	35650571	1	4	2	10	5	9	2	0	0	0	0	1	E9PXB6	
ENSMUST00000171169						14	10	14	15	17	12	7	10	8	2	13		
ENSMUST00000171170						3	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000171171	ENSMUSG00000024037	17	31494323	31519974	-1	27	21	23	28	29	0	9	181	41	0	90	E9Q156	
ENSMUST00000171172	ENSMUSG00000034509	17	46147390	46153553	-1	12	13	14	3	24	7	227	361	144	71	132		Q9DCX1
ENSMUST00000171174	ENSMUSG00000013353	7	43492044	43505940	-1	7	3	10	5	4	2	2	2	3	0	14	A2RSL7	
ENSMUST00000171175						1	1	1	0	4	0	0	0	0	0	0		
ENSMUST00000171176	ENSMUSG00000036251	1	88277661	88389293	1	17	0	0	18	0	0	0	0	0	0	0		Q8R4D5
ENSMUST00000171178	ENSMUSG00000021697	13	108316332	108407782	1	0	0	0	0	0	0	4	0	12	0	19	E9PW09	
ENSMUST00000171180						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000171181	ENSMUSG00000040666	16	96200470	96228933	1	0	4	16	0	0	0	0	0	0	0	0		Q9WUZ7
ENSMUST00000171182	ENSMUSG00000033545	8	111536097	111626030	1	9	0	57	0	37	7	64	528	175	25	268	E9PZB7	
ENSMUST00000171183	ENSMUSG00000045948	7	28739641	28741820	-1	6	2	24	12	5	2	15	26	5	0	10		O35680
ENSMUST00000171185						4	4	15	11	5	2	0	0	0	0	0		
ENSMUST00000171186	ENSMUSG00000091541	6	57070895	57071945	1	0	2	0	0	3	1	0	0	0	0	0	A2RST7	

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ENSMUST00000171187	ENSMUSG00000005871	18	34220924	34322189	1	0	0	0	58	4	0	0	1	10	1	22	E9Q4H1	
ENSMUST00000171188	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	0	0	0	0	0	A7UAK5	
ENSMUST00000171189	ENSMUSG00000036473	17	24175431	24209387	-1	0	46	0	46	0	46	0	32	0	0	0		Q3UUG6
ENSMUST00000171191	ENSMUSG00000028109	3	95559677	95587671	1	0	0	0	0	0	0	0	0	0	0	0		Q9D5T7
ENSMUST00000171192	ENSMUSG00000071724	15	76294434	76296896	1	0	4	11	3	9	0	88	246	65	10	74	G3UXH6	
ENSMUST00000171194						35	23	56	45	50	23	0	0	1	0	1		
ENSMUST00000171195						4	4	5	2	0	1	0	0	0	0	0		
ENSMUST00000171197	ENSMUSG00000055320	7	112679318	112906807	1	0	0	0	1	0	0	0	0	0	0	7	E9QAK6	
ENSMUST00000171202	ENSMUSG00000093926	14	42157290	42162622	-1	0	0	9	0	13	0	0	0	0	0	0	F7BAX1	
ENSMUST00000171203						10	2	10	5	6	5	523	46	294	23	255		
ENSMUST00000171204						2	1	2	0	1	4	0	0	0	0	0		
ENSMUST00000171205	ENSMUSG00000037617	15	36179368	36235610	1	5	11	30	57	12	12	26	87	60	27	35		Q80ZX8
ENSMUST00000171207						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000171210	ENSMUSG00000059060	12	79297351	79508656	1	0	0	4	0	0	0	0	0	2	4	0	E9QAZ6	
ENSMUST00000171211	ENSMUSG00000034761	12	69803750	69893200	-1	0	0	0	24	7	0	0	0	0	45	0	E9Q1T3	
ENSMUST00000171212						2	1	7	8	0	0	0	2	2	0	6		
ENSMUST00000171213	ENSMUSG00000091006	7	85406376	85415676	-1	9	10	3	2	4	2	0	0	0	0	0	G3XA45	
ENSMUST00000171214						0	0	3	0	0	0	0	0	9	0	0		
ENSMUST00000171215	ENSMUSG00000027288	2	120506820	120563843	-1	3	7	11	22	11	8	107	8	690	0	193	E9Q7S1	
ENSMUST00000171216						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000171217						1	1	6	3	3	3	0	0	0	0	0		
ENSMUST00000171218	ENSMUSG00000038371	7	110308013	110614922	-1	1	2	0	0	1	0	0	0	0	0	0	E9Q372	
ENSMUST00000171223	ENSMUSG00000028874	4	132974095	133001910	1	7	6	8	1	6	4	2955	434	2147	356	2211		P14234
ENSMUST00000171224	ENSMUSG00000087194	4	112804616	113286973	-1	2	1	0	3	0	0	0	0	0	0	0		A7XUZ6
ENSMUST00000171225	ENSMUSG00000001249	7	31098725	31115290	-1	0	0	0	0	4	2	0	0	0	3	2	F7C9T6	
ENSMUST00000171229	ENSMUSG00000021417	13	34977748	35027094	-1	0	0	0	0	6	1	59	350	104	580	59		Q9WUR2
ENSMUST00000171231	ENSMUSG00000037548	17	34143307	34151553	1	0	10	0	9	20	16	19	36	23	30	104	F7AD18	
ENSMUST00000171233	ENSMUSG00000024036	17	31295483	31350696	1	6	7	37	3	11	5	81	189	46	24	59	Q8R070	
ENSMUST00000171234						1	10	11	3	4	11	0	0	0	0	1		
ENSMUST00000171235						7	9	54	7	15	2	0	3	0	4	3		
ENSMUST00000171237						0	0	0	0	0	0	32	124	25	91	26		
ENSMUST00000171238	ENSMUSG00000058881	18	82910879	83005314	1	3	3	7	192	96	47	516	668	1961	112	1414		Q7TSH3
ENSMUST00000171239	ENSMUSG00000020609	12	7977648	8016835	1	0	1	0	0	0	0	0	0	0	30	0	F7A3M3	
ENSMUST00000171243	ENSMUSG00000037801	9	63421455	63602493	-1	20	4	9	0	0	0	0	0	0	0	0	E9PUW2	
ENSMUST00000171244	ENSMUSG00000001285	15	102331709	102338139	1	0	0	2	0	0	0	94	90	25	46	15	F7A3N3	
ENSMUST00000171245	ENSMUSG00000023048	15	102459028	102462806	1	7	0	22	21	8	0	351	1462	328	53	409		Q9CQJ5
ENSMUST00000171247	ENSMUSG00000059552	11	69580359	69591873	1	0	0	0	14	0	0	0	0	0	0	0	Q80ZA1	
ENSMUST00000171249	ENSMUSG00000028100	3	96706067	96708562	-1	13	6	0	64	0	0	5	0	5	7	5		Q9CWD3
ENSMUST00000171251	ENSMUSG00000066224	4	41723836	41731142	-1	5	6	47	18	21	5	0	1	0	0	0		A6PWV5
ENSMUST00000171252	ENSMUSG00000060147	13	33917918	34002794	-1	1	0	0	7	0	0	0	0	0	14	7	E9Q108	
ENSMUST00000171253						4	2	1	10	3	4	0	0	0	0	0		
ENSMUST00000171254	ENSMUSG00000018449	11	70970213	70977833	1	0	0	0	0	0	0	25	59	55	74	0	Q0PL80	
ENSMUST00000171256	ENSMUSG00000024563	18	76241580	76305731	1	4	0	1	8	4	0	15	6	19	30	36	E9Q5P9	
ENSMUST00000171257	ENSMUSG00000052909	13	67763798	67773629	-1	0	0	0	0	3	1	0	0	0	0	0	F7D8Z3	
ENSMUST00000171258	ENSMUSG00000021417	13	34977748	35027094	-1	0	0	0	0	0	0	34	35	12	63	9	E9PYC6	
ENSMUST00000171259	ENSMUSG00000001249	7	31098725	31115290	-1	0	0	0	0	0	0	0	1	0	2	1	F6W6S4	
ENSMUST00000171260	ENSMUSG00000023572	2	121008403	121016904	1	1	0	0	0	0	2	29	4	18	0	45		Q3TVC7
ENSMUST00000171261						1	0	3	10	0	0	0	0	0	0	0		
ENSMUST00000171262						3	6	1	2	2	1	0	0	0	0	0		
ENSMUST00000171263	ENSMUSG00000040253	3	142530342	142550149	1	34	33	86	19	33	25	166	1076	523	482	1231	Q91Z40	
ENSMUST00000171264	ENSMUSG00000090553	1	133603871	133610291	-1	0	0	0	0	0	0	0	0	0	0	0	E9PZG9	
ENSMUST00000171265	ENSMUSG00000025915	1	9798107	9900845	1	7	0	0	16	6	2	0	0	0	0	0		Q9ERE3
ENSMUST00000171266	ENSMUSG00000005125	15	6929321	66969640	-1	2	3	1	5	2	0	0	1	0	0	0	E9Q0J8	
ENSMUST00000171267	ENSMUSG00000021624	13	102693558	102739629	1	2	4	3	7	6	3	1	0	3	0	1	F2Z425	
ENSMUST00000171268	ENSMUSG00000058740	2	25863734	25918273	1	0	0	0	38	0	0	0	0	0	0	0	C0KTP6	
ENSMUST00000171270	ENSMUSG00000102313	12	115386697	115387128	-1	0	0	1	0	1	0	0	0	0	1	1	A0A075B684	
ENSMUST00000171271	ENSMUSG00000020609	12	7977648	8016835	1	4	3	6	14	1	1	0	0	0	0	0	E9Q4G4	
ENSMUST00000171273						3	0	0	4	0	0	0	2	0	0	0		
ENSMUST00000171277						6	11	35	19	9	7	0	1	1	0	0		
ENSMUST00000171279	ENSMUSG00000021911	14	32201949	32297550	1	0	0	0	24	0	0	9	0	5	2	25	E9Q954	
ENSMUST00000171280	ENSMUSG00000074365	7	15882617	15904020	1	6	0	3	3	9	0	0	0	0	0	0	B6ZND9	
ENSMUST00000171282						5	2	0	0	0	0	21	0	0	55	0		
ENSMUST00000171284	ENSMUSG00000055660	17	94727080	94749892	-1	5	13	12	3	16	6	14	70	29	5	15		Q3U034
ENSMUST00000171289	ENSMUSG00000053819	3	126596302	126846326	1	0	0	0	0	0	0	0	13	84	0	50	E9Q1T1	
ENSMUST00000171291	ENSMUSG00000024037	17	31494323	31519974	-1	0	0	0	0	0	0	5	10	15	0	9	E9Q1L4	
ENSMUST00000171292	ENSMUSG00000026594	1	156804166	156939626	-1	0	0	0	4	0	0	0	0	0	0	0		Q9ERD6
ENSMUST00000171293						2	0	8	0	6	0	0	0	0	0	2		
ENSMUST00000171297	ENSMUSG00000090942	18	60293380	60303016	1	1331	980	9344	2046	1786	901	9	24	26	11	44	G3UWE2	
ENSMUST00000171300	ENSMUSG00000025538	5	129846986	129864050	1	27	0	24	55	30	13	0	27	13	21	27		Q8BPG6
ENSMUST00000171305	ENSMUSG00000091700	14	4709238	4717678	1	2	2	0	0	1	1	0	0	0	0	0	K7N6T8	
ENSMUST00000171306	ENSMUSG00000030361	6	128609227	128623533	-1	0	2	0	4	2	0	0	12	0	2	0	E9Q0W1	
ENSMUST00000171307	ENSMUSG00000071494	6	42538067	42539020	-1	14	3	21	4	11	6	1	1	5	0	8	A0A0B4J1M2	
ENSMUST00000171309	ENSMUSG00000022878	16	23146536	23158028	1	3	2	0	5	0	0	0	1	0	1	0	E9PWU4	
ENSMUST00000171311	ENSMUSG00000029754	6	6863334	6868568	1	0	0	0	0	0	0	0	0	0	0	0		P70397
ENSMUST00000171313	ENSMUSG00000028012	3	129804408	129822587	-1	9	3	22	10	10	5	0	0	0	0	0	Q543W9	O35214
ENSMUST00000171314						5	4	20	10	13	2	0	0	0	0	0		
ENSMUST00000171317	ENSMUSG00000090685	6	29471437	29473465	1	4	3	19	5	6	2	0	1	0	0	0	B9EJX3	
ENSMUST00000171318	ENSMUSG00000025544	14	122107038	122159604	1	4	5	12	0	0	0	102	861	569	114	372	E9PZ69	
ENSMUST00000171319	ENSMUSG00000091937	1	39804148	39805332	-1	4	4	0	0	1	2	0	0	0	0	0	F6S692	
ENSMUST00000171320						0	5	18	0	2	1	9	52	33	3	85		
ENSMUST00000171321	ENSMUSG00000096727	17	34181988	34187764	-1	1	0	3	0	0	0	119	639	74	72	53	F6QXK7	
ENSMUST00000171322	ENSMUSG00000091318	1	32543686	32547294	-1	48	31	294	72	45	28	1	1	1	0	1	E9PXF3	
ENSMUST00000171324	ENSMUSG00000091387	13	96924689	96950912	1	36	28	146	229	34	17	3	10	5	0	2		E9Q649
ENSMUST00000171325	ENSMUSG00000022800	16	32877500	32908963	1	4	6	8	0	0	0	0	0	0	0	0		Q91Z49

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000171328						0	0	0	0	0	0	1	1	0	1	0		
ENSMUST00000171330	ENSMUSG00000015314	1	171917515	171953170	1	9	6	5	8	4	3	24	93	34	62	92	Q18PG5	Q9ET39
ENSMUST00000171332	ENSMUSG00000028763	4	137468769	137570630	1	90	56	201	46	149	73	1	0	1	11	411	E9PZ16	
ENSMUST00000171334						5	7	10	3	1	3	0	0	0	4	1		
ENSMUST00000171335						8	6	18	8	4	4	0	0	0	0	0		
ENSMUST00000171337	ENSMUSG00000031626	8	45507788	45827906	1	0	0	0	0	0	0	0	0	0	0	0	B9EKP8	
ENSMUST00000171338						0	0	0	20	0	0	0	12	12	27	59		
ENSMUST00000171339	ENSMUSG00000091285	18	9726197	9726670	-1	4	6	6	2	5	1	0	0	0	1	0	F6RSK3	
ENSMUST00000171340	ENSMUSG00000022562	15	76296597	76328015	-1	33	10	0	15	28	20	0	0	0	0	0		Q8K010
ENSMUST00000171341	ENSMUSG00000025075	19	56287137	56320822	1	0	4	0	0	3	0	0	0	0	0	0	E9Q0C5	
ENSMUST00000171342	ENSMUSG00000025373	10	128411616	128441438	1	2	5	23	23	10	5	0	0	0	18	66		Q8BH75
ENSMUST00000171343	ENSMUSG00000021796	14	34410734	34503341	-1	0	1	0	86	7	0	22	44	49	3	25	E9PW65	
ENSMUST00000171346						0	3	3	0	2	1	0	0	0	0	0		
ENSMUST00000171347	ENSMUSG00000074874	13	60895351	60897447	-1	7	0	4	0	4	4	4	32	3	104	42		
ENSMUST00000171348	ENSMUSG00000095048	4	73668354	73672396	1	0	24	16	0	0	0	0	0	0	0	0	E9Q5Z9	
ENSMUST00000171349	ENSMUSG00000030279	6	143010920	143100141	-1	0	15	66	0	21	0	143	427	147	38	205	E9Q026	
ENSMUST00000171352	ENSMUSG00000024969	19	7275396	7341860	-1	22	15	111	30	41	14	117	190	182	9	243	F7A3Q3	
ENSMUST00000171353	ENSMUSG00000049939	6	28661831	28831747	-1	2	0	4	4	5	2	0	0	0	1	0	E9PUX8	
ENSMUST00000171355						6	8	13	6	13	8	2	0	1	0	2		
ENSMUST00000171356	ENSMUSG00000035983	12	40222758	40229184	1	0	3	2	0	0	0	3	0	1	0	0	F6TJN7	
ENSMUST00000171358						0	0	0	80	0	0	0	0	0	4	0		
ENSMUST00000171359	ENSMUSG00000057092	7	31068172	31076704	-1	0	0	3	1	0	0	0	0	0	0	0	E9Q966	
ENSMUST00000171360	ENSMUSG00000063277	14	7640895	7643972	-1	0	0	0	0	0	0	0	0	0	0	0	L7N2B6	
ENSMUST00000171362	ENSMUSG00000103711	1	171418872	171420352	1	5	0	1	1	0	3	2	26	3	0	14	E9PY03	
ENSMUST00000171363	ENSMUSG00000032890	4	120854816	120896579	1	0	0	0	0	0	0	2	0	0	2	0	Q14BY7	Q80U57
ENSMUST00000171364						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000171366	ENSMUSG00000030768	1	183086266	183221522	-1	0	27	37	0	0	9	0	0	0	16	26		Q3TDN0
ENSMUST00000171368	ENSMUSG00000015749	3	95929246	95947390	1	5	3	0	12	0	0	21	102	86	227	63	E9Q5H9	
ENSMUST00000171370	ENSMUSG00000025374	10	128401395	128411492	-1	0	0	0	66	0	0	0	0	6	0	0	E9Q2V9	
ENSMUST00000171373	ENSMUSG00000055320	7	112679318	112906807	1	5	5	27	11	7	2	0	0	0	0	0	E9PVJ5	
ENSMUST00000171376	ENSMUSG00000015474	17	34616662	34628510	-1	8	1	23	14	11	0	0	51	0	0	18		O35448
ENSMUST00000171378						5	0	34	5	4	3	2	3	3	0	3		
ENSMUST00000171381	ENSMUSG00000041642	1	136131389	136177998	1	2	0	3	0	2	1	22	2	18	0	21	F6ZSF2	
ENSMUST00000171382						3	0	4	1	0	0	0	0	0	0	0		
ENSMUST00000171384	ENSMUSG00000027800	3	57285611	57301988	-1	23	14	18	17	21	6	2	3	0	66	12		Q64302
ENSMUST00000171385	ENSMUSG00000029192	5	36490604	36593276	-1	0	0	0	0	0	0	1850	8626	1508	940	1625	E9PYB1	
ENSMUST00000171388	ENSMUSG00000095490	14	42111963	42117369	-1	2	0	0	0	8	0	0	0	0	0	0	E9Q0A2	
ENSMUST00000171391						0	0	6	0	0	0	0	0	0	0	0		
ENSMUST00000171393	ENSMUSG00000024969	19	7275396	7341860	-1	2	0	1	3	0	0	48	12	90	0	38	E9Q2J6	
ENSMUST00000171394	ENSMUSG00000073805	7	134881926	134938430	-1	23	15	46	68	47	12	0	0	0	0	0	E9PZW7	
ENSMUST00000171395						9	2	22	10	6	3	3	0	0	1	3		
ENSMUST00000171396						3	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000171397						5	1	2	4	4	0	0	0	0	0	0		
ENSMUST00000171398	ENSMUSG00000019558	X	73673150	73682502	1	2	3	2	0	5	0	0	0	0	0	0	E9Q6T2	
ENSMUST00000171400	ENSMUSG00000090291	19	10455371	10457447	-1	70	42	522	355	85	43	0	7	3	0	5	G3XA50	
ENSMUST00000171401	ENSMUSG00000044581	10	82282116	82285278	-1	16	18	80	36	22	14	0	0	0	0	0	E9Q0G0	
ENSMUST00000171403	ENSMUSG00000049119	4	5644090	6108223	1	3	0	37	26	11	4	0	1	2	1	0		Q8C739
ENSMUST00000171404	ENSMUSG00000035666	2	28822299	28840360	-1	6	0	0	38	0	0	0	35	60	0	38	E9Q2B0	
ENSMUST00000171405	ENSMUSG00000036155	1	127205015	127488336	1	0	0	0	0	0	0	7	0	76	0	44	Q059T5	Q8R4G6
ENSMUST00000171407						0	0	0	5	4	0	0	7	0	0	0		
ENSMUST00000171409	ENSMUSG00000020111	10	59702477	59864132	1	0	0	0	0	0	0	8	199	49	0	35	E9Q9E0	
ENSMUST00000171410						0	0	0	6	0	0	0	25	0	0	0		
ENSMUST00000171411						0	3	0	0	0	2	498	1155	335	747	204		
ENSMUST00000171412	ENSMUSG00000039952	9	108204634	108263958	-1	0	0	0	67	26	0	0	5	160	0	39	Q544G5	Q62165
ENSMUST00000171413						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171414	ENSMUSG00000021884	14	31552905	31641286	-1	0	0	0	0	0	1	0	0	23	8	0	E9Q7H7	
ENSMUST00000171415	ENSMUSG00000025204	19	44548572	44555440	-1	15	8	13	13	8	9	27	248	69	18	38	Q3V406	
ENSMUST00000171416	ENSMUSG00000035781	10	79910053	79917006	-1	46	47	352	169	68	38	0	0	34	0	0	B2RRK4	Q4VBF2
ENSMUST00000171418	ENSMUSG00000020594	12	8674134	8752581	1	0	0	0	0	0	0	0	0	10	3	26	F7A034	
ENSMUST00000171419	ENSMUSG00000029580	5	142903115	142906754	-1	0	17	0	47	0	0	249	129	6724	28	5147	E9Q5F4	
ENSMUST00000171422	ENSMUSG00000060671	3	89939481	89963508	-1	1	0	7	12	2	2	0	0	0	1	0	E9Q491	
ENSMUST00000171423						0	0	12	0	0	0	11	15	7	12	2		
ENSMUST00000171424						2	8	4	4	5	3	0	15	3	0	0		
ENSMUST00000171425	ENSMUSG00000074361	7	16234585	16244154	-1	37	37	75	58	37	37	187	225	75	37	490	E9PVQ2	
ENSMUST00000171426	ENSMUSG00000025404	10	127380327	127499384	1	0	0	0	0	0	0	0	215	0	0	0	F6WY86	
ENSMUST00000171427	ENSMUSG00000000617	11	50850685	50866208	1	5	0	41	0	0	0	7	0	0	0	9		Q5NCH9
ENSMUST00000171428	ENSMUSG00000091568	14	6016759	6038209	-1	9	0	0	0	0	0	0	2	0	0	1	L7N295	
ENSMUST00000171432	ENSMUSG00000025185	19	42593982	42612813	-1	0	0	0	0	6	9	0	0	0	0	2		Q924C6
ENSMUST00000171433	ENSMUSG00000035299	X	169685199	170005736	1	5197	2359	116785	12798	5602	3110	13	71	49	10	159		O70583
ENSMUST00000171434	ENSMUSG00000025404	10	127380327	127499384	1	0	1	0	1	1	0	0	0	0	0	0	E9PZ57	
ENSMUST00000171435	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	2	1	1	0	0	0	0	0	E9PZU7	
ENSMUST00000171436	ENSMUSG00000016664	15	83375607	83464606	-1	0	0	213	88	34	0	615	1325	945	147	884	Q3TDA7	Q9WVE8
ENSMUST00000171437						0	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000171438	ENSMUSG00000031553	8	24677225	24725852	-1	0	8	22	0	0	0	0	0	26	0	37	F8VQ03	
ENSMUST00000171444	ENSMUSG00000004661	9	57790353	57836793	-1	14	21	21	45	19	21	0	67	71	0	18		Q9Z1N7
ENSMUST00000171445	ENSMUSG00000006154	7	4460674	4480487	1	7	0	0	7	10	5	0	0	0	0	2	E9Q4X5	
ENSMUST00000171447	ENSMUSG00000026659	1	170873498	170885540	-1	0	0	0	0	0	0	4	19	3	1	4	F7BAT9	
ENSMUST00000171450						32	39	68	67	34	14	3	3	0	0	2		
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ENSMUST00000171455						1	0	2	5	4	1	0	0	0	0	0		
ENSMUST00000171456	ENSMUSG00000031659	8	88272403	88329962	1	0	13	93	9	29	0	105	187	0	0	243		P51829
ENSMUST00000171458	ENSMUSG00000067616	7	43774604	43779263	1	9	7	12	10	0	4	0	0	0	0	0		Q9QYN3
ENSMUST00000171459	ENSMUSG00000021139	12	81358860	81532905	-1	0	0	0	0	0	0	0	6	0	50	6	E9PVQ9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000171460	ENSMUSG00000036106	15	84669620	84703673	1	57	54	258	0	18	19	17	5	0	1	26		Q812A5
ENSMUST00000171461	ENSMUSG00000060450	18	38296635	38317847	1	11	15	10	127	11	13	88	222	204	31	149		Q9JI90
ENSMUST00000171462	ENSMUSG00000059820	9	50605240	50617464	-1	0	0	0	0	0	0	0	0	0	0	0	E9PUQ3	
ENSMUST00000171465						1	0	4	2	3	1	2	4	17	0	26		
ENSMUST00000171466	ENSMUSG00000057842	13	67312998	67332560	-1	2	5	10	2	4	1	6	9	0	6	9	B9EIT6	
ENSMUST00000171467						11	21	67	29	23	11	1	0	0	0	0		
ENSMUST00000171469	ENSMUSG00000092097	18	8694077	8694541	1	3	0	0	1	3	1	6	8	15	2	10	E9PZ96	
ENSMUST00000171470	ENSMUSG00000024529	18	52516069	52529867	-1	4	10	13	6	6	4	0	0	0	0	0	Q3TXH3	P28301
ENSMUST00000171473	ENSMUSG00000091405	3	96261682	96263311	-1	17	9	41	44	10	7	9	36	21	1	42	B2RTM0	P62806
ENSMUST00000171474	ENSMUSG00000014074	16	32277459	32301434	1	0	0	17	25	8	0	25	0	8	0	0	E9PYW4	
ENSMUST00000171478	ENSMUSG00000059323	15	76622088	76639958	-1	0	0	12	0	0	2	0	0	4	1	0	F7A431	
ENSMUST00000171479	ENSMUSG00000026409	1	130689182	130729253	-1	0	0	0	0	0	0	0	44	0	0	0	B2Z893	
ENSMUST00000171481						1	2	8	44	7	4	0	0	0	0	0		
ENSMUST00000171482	ENSMUSG00000091297	4	120588745	120609673	1	2	5	9	7	2	8	2	8	2	8	0	G3UWA7	
ENSMUST00000171484						0	2	0	11	2	1	0	0	0	0	0		
ENSMUST00000171486	ENSMUSG00000024283	18	7868832	7973547	1	0	0	0	0	0	0	12	2	47	0	1	E9Q020	
ENSMUST00000171488						0	0	0	0	0	0	1	0	3	0	0		
ENSMUST00000171489						4	3	7	14	2	1	2	18	2	3	4		
ENSMUST00000171492						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171494	ENSMUSG00000025374	10	128401395	128411492	-1	7	5	10	69	9	2	1	4	4	1	0	E9PW70	
ENSMUST00000171496	ENSMUSG00000016763	15	83602583	83725021	-1	89	50	133	111	78	52	0	3	0	0	2		Q6NZL8
ENSMUST00000171498	ENSMUSG00000075599	5	138021261	138034664	1	1	0	0	2	0	1	0	0	0	0	0		Q9QYZ5
ENSMUST00000171499	ENSMUSG00000079227	9	124121543	124147699	1	0	0	0	6	8	0	8	4	2	30	16	E9Q3E5	
ENSMUST00000171502						6	8	12	8	11	13	0	0	0	0	0		
ENSMUST00000171503	ENSMUSG00000034623	14	64075438	64090162	-1	0	5	0	0	0	0	0	0	0	0	0	E9QA75	
ENSMUST00000171504						16	8	11	20	9	7	0	5	5	0	3		
ENSMUST00000171509	ENSMUSG00000054252	5	33721674	33737068	1	0	0	41	0	0	0	0	0	0	0	3	E9QNJ9	
ENSMUST00000171510	ENSMUSG00000037851	13	49682100	49734267	1	1	0	0	0	0	0	0	0	4	0	3	F6Q6R1	
ENSMUST00000171515	ENSMUSG00000092157	11	82028224	82038562	-1	0	1	2	2	0	0	0	0	0	0	0	F7AKR5	
ENSMUST00000171518	ENSMUSG00000071291	13	67490167	67500555	-1	0	0	0	3	4	0	15	135	0	18	12		P16372
ENSMUST00000171519	ENSMUSG00000038543	3	95883954	95892005	-1	0	0	0	0	0	0	5	111	7	137	13		Q8R2K8
ENSMUST00000171521						5	0	6	8	6	1	0	0	0	0	0		
ENSMUST00000171523	ENSMUSG00000090342	7	9754636	9770571	-1	0	0	0	0	0	0	0	0	0	0	0	L7N282	
ENSMUST00000171526						1	1	0	0	0	0	0	138	3	0	0		
ENSMUST00000171527						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171528	ENSMUSG00000046329	17	57043711	57059863	-1	2	0	3	0	6	3	0	0	1	0	2	F7BBH5	
ENSMUST00000171529	ENSMUSG00000043461	3	69819542	69859940	-1	2	5	3	0	3	4	0	0	0	0	0		Q925E8
ENSMUST00000171530	ENSMUSG00000001627	12	40201567	40248504	-1	0	0	0	0	0	0	163	1022	336	124	172	E9Q949	
ENSMUST00000171531	ENSMUSG00000090455	7	142257647	142258354	-1	6	7	48	8	8	4	0	0	0	0	0	E9Q8S1	
ENSMUST00000171532						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000171533	ENSMUSG00000042834	18	33437019	33464029	-1	25	29	97	508	67	33	0	0	2	1	0	Q542Q5	Q07475
ENSMUST00000171534	ENSMUSG00000094658	Y	2830680	2841854	1	6	5	0	0	0	2	0	0	0	0	0		O35698
ENSMUST00000171535						14	3	5	34	8	9	7	23	6	4	6		
ENSMUST00000171536						2	0	7	14	4	0	0	0	0	0	0		
ENSMUST00000171537	ENSMUSG00000021670	13	96648967	96670936	-1	1	0	0	2	0	1	0	0	0	0	0	E9PVG9	
ENSMUST00000171538						5	0	0	0	2	2	2	5	0	3	6		
ENSMUST00000171541	ENSMUSG00000003153	6	122727809	122801640	-1	0	1	1	0	1	0	0	0	0	0	0	E9PX20	
ENSMUST00000171542	ENSMUSG00000091212	16	89570176	89571183	-1	12	5	24	7	16	3	0	0	0	0	0	E9Q2E9	
ENSMUST00000171543	ENSMUSG00000029086	5	43993620	44102032	-1	0	0	0	0	0	0	0	0	0	0	0	Q8R056	
ENSMUST00000171544						3	0	0	3	2	0	0	0	0	0	1		
ENSMUST00000171545	ENSMUSG00000022425	15	54838898	54920146	-1	17	9	5	0	13	7	0	0	0	28	0		Q9R1E6
ENSMUST00000171546						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171547						0	3	3	8	8	2	0	2	2	2	2		
ENSMUST00000171548	ENSMUSG00000028541	4	117869260	117883487	-1	11	4	51	5	4	8	0	3	0	0	0	E9PY89	
ENSMUST00000171549	ENSMUSG00000004266	6	124720707	124738714	-1	9	6	0	7	8	9	148	46	43	0	33	Q3UCJ0	P29351
ENSMUST00000171551	ENSMUSG00000021796	14	34410734	34503341	-1	4	3	0	2	0	4	0	0	0	0	0	E9Q2G5	
ENSMUST00000171553	ENSMUSG00000001627	12	40201567	40248504	-1	0	0	1	0	2	0	4	0	21	21	35	E9PZB9	
ENSMUST00000171554	ENSMUSG00000049100	3	45378398	45435623	1	7	5	5	7	5	7	0	0	0	0	0	E9PX28	
ENSMUST00000171556	ENSMUSG00000014602	1	93015464	93101951	-1	0	0	0	0	0	0	0	0	0	0	0	E9QAN4	
ENSMUST00000171557						0	0	0	0	0	0	50	546	62	0	115		
ENSMUST00000171560	ENSMUSG00000041708	15	83779467	83858494	1	0	0	0	0	0	0	0	0	0	0	0	F7D2T2	
ENSMUST00000171561	ENSMUSG00000025159	19	41941086	41981157	-1	3	0	3	28	0	0	0	0	0	0	0		Q9D071
ENSMUST00000171562	ENSMUSG00000022565	15	76170974	76232574	-1	15	0	94	35	40	7	0	0	0	0	108	E9Q3W4	
ENSMUST00000171564	ENSMUSG00000040354	10	127296221	127311786	-1	0	0	0	0	0	0	0	0	0	38	80	E9QB02	
ENSMUST00000171565	ENSMUSG00000023050	15	102497649	102517064	-1	7	0	1	0	0	0	0	0	0	0	0		Q60700
ENSMUST00000171567						6	4	5	0	14	2	0	0	0	0	0		
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ENSMUST00000171569						16	25	20	35	42	13	2	7	3	0	22		
ENSMUST00000171572	ENSMUSG00000003233	16	20516982	20532520	1	3	6	15	46	15	6	157	134	186	6	130	E9Q967	
ENSMUST00000171578						6	4	3	1	0	2	0	0	2	3	3		
ENSMUST00000171579						0	0	0	0	0	0	0	0	0	1	2		
ENSMUST00000171580	ENSMUSG00000022621	15	89582533	89591923	-1	0	0	0	0	0	1	0	0	3	0	0	E9Q8G6	
ENSMUST00000171581						16	10	53	17	24	5	0	31	8	0	8		
ENSMUST00000171583	ENSMUSG00000000420	18	24205344	24286818	1	1	0	1	0	0	2	38	5	40	3	8	E9PVK6	
ENSMUST00000171584	ENSMUSG00000032842	17	46303221	46328352	-1	5	3	7	7	10	8	0	4	0	0	0	E9PZG1	
ENSMUST00000171586	ENSMUSG00000025020	19	41600257	41743665	-1	3	0	10	52	3	1	0	0	1	0	1	E9Q117	
ENSMUST00000171587	ENSMUSG00000092021	5	105323042	105346472	-1	5	3	0	0	13	5	1	0	1	3	0	A9YVJ5	
ENSMUST00000171588	ENSMUSG00000054263	15	7129559	7197489	1	50	33	46	14	54	21	59	153	89	33	181		P42703
ENSMUST00000171592						2	3	6	3	1	0	4	7	3	0	3		
ENSMUST00000171597	ENSMUSG00000026036	1	58445151	58481816	1	10	14	0	0	8	0	87	222	87	232	76		Q9EQ80
ENSMUST00000171598	ENSMUSG00000021906	14	32085374	32103202	1	2	0	0	0	0	0	1	0	0	0	0	E9Q2B7	
ENSMUST00000171599	ENSMUSG00000006498	10	79854427	79864771	1	3	0	11	15	4	0	4	0	2	0	2	E9PZ39	
ENSMUST00000171600	ENSMUSG00000040270	4	32238804	32586108	1	72	57	156	0	97	0	26	33	14	8	60		P97303
ENSMUST00000171601	ENSMUSG00000038388	6	50110241	50198939	1	0	2	1	0	0	0	0	0	0	0	0	E9Q2R8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000171604	ENSMUSG00000060613	19	40153353	40187333	-1	0	0	1	0	0	0	0	0	0	0	0	E9Q2L0	
ENSMUST00000171606	ENSMUSG00000021557	13	59449537	59585227	-1	0	0	0	20	0	0	0	0	0	9	10		Q641K1
ENSMUST00000171608						0	0	0	0	1	1	2	6	4	4	18		
ENSMUST00000171611	ENSMUSG00000031553	8	24677225	24725852	-1	3	0	0	2	1	2	3	0	0	0	0	Q6P907	
ENSMUST00000171613	ENSMUSG00000023964	6	3685680	3764714	-1	0	0	0	10	0	0	0	0	0	0	0		Q60755
ENSMUST00000171614						8	3	24	10	8	5	1	6	1	1	4		
ENSMUST00000171616	ENSMUSG00000001225	12	31390871	31473917	1	3	7	0	0	7	1	1	0	0	1	0	E9PY22	
ENSMUST00000171619	ENSMUSG00000031448	8	13221663	13254162	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q333	
ENSMUST00000171620	ENSMUSG00000027550	3	14533788	14572658	1	3	0	0	3	0	0	0	0	0	3	0	F6QGT9	
ENSMUST00000171621	ENSMUSG00000046688	3	127789805	127832164	1	27	1	148	0	13	0	62	241	28	71	79	I3PQW8	Q793I8
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ENSMUST00000171627	ENSMUSG00000078598	4	113477891	113999503	-1	0	0	0	0	0	0	0	0	0	0	0	K4DID5	
ENSMUST00000171629	ENSMUSG00000045094	18	61493794	61536536	-1	29	21	77	97	49	15	151	292	154	40	318	E9Q5R6	
ENSMUST00000171630						69	39	129	72	89	48	1	2	10	1	7		
ENSMUST00000171632						4	5	7	0	3	3	1	2	4	0	3		
ENSMUST00000171633	ENSMUSG00000039315	5	38706462	38876812	-1	4	8	19	10	4	4	0	0	0	0	0	E9PXZ8	
ENSMUST00000171634	ENSMUSG00000022565	15	76170974	76232574	-1	12	10	29	17	9	10	0	0	0	0	0		
ENSMUST00000171635	ENSMUSG00000065987	8	3917655	3926844	-1	0	0	0	0	0	0	0	0	0	0	0		Q8CJ91
ENSMUST00000171636	ENSMUSG00000090827	14	4983935	4992409	1	8	3	0	8	0	7	0	0	0	0	0	K7N723	
ENSMUST00000171637	ENSMUSG00000035722	10	79996494	80015572	1	0	31	64	13	73	44	2318	3107	2475	59	1907	E9Q6G4	
ENSMUST00000171639						1	0	51	3	3	4	0	0	0	0	3		
ENSMUST00000171640	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	0	0	0	136	825	271	25	73	F6SHF3	
ENSMUST00000171641	ENSMUSG00000028447	4	41714798	41723170	-1	3	0	0	0	0	0	0	0	13	0	0	E9Q919	
ENSMUST00000171642	ENSMUSG00000026405	1	130634773	130661632	-1	2	0	0	0	2	0	0	0	0	0	0	F6QLW4	
ENSMUST00000171643	ENSMUSG00000022212	14	55510445	55517431	1	9	0	25	7	3	4	0	0	0	0	0		Q9Z140
ENSMUST00000171644	ENSMUSG00000000440	6	115360951	115490399	1	14	4	23	35	10	4	0	11	7	7	0	M1VPI1	
ENSMUST00000171645	ENSMUSG00000028057	3	88716838	88731049	1	0	0	2	8	0	0	30	17	16	50	35	E9Q3Z0	
ENSMUST00000171646	ENSMUSG00000040732	16	95359169	95586593	-1	0	0	0	0	3	0	14	0	0	9	7	E9PY05	
ENSMUST00000171647	ENSMUSG00000036814	9	123636122	123678885	-1	7	0	0	0	0	0	0	0	0	0	0	E9Q0H0	
ENSMUST00000171649	ENSMUSG00000071657	19	8837467	8848683	1	1	0	0	8	0	0	32	20	13	9	13		
ENSMUST00000171651						2	1	5	2	3	3	0	0	0	0	0		
ENSMUST00000171652	ENSMUSG00000091956	9	67759437	67760930	1	1	0	0	199	1	0	0	0	0	0	0	Q80XU5	
ENSMUST00000171653						0	0	3	1	0	1	0	0	0	0	0		
ENSMUST00000171654	ENSMUSG00000032289	9	59966931	60522046	-1	0	37	169	0	4	11	0	5	1	0	7		Q3UTY6
ENSMUST00000171656	ENSMUSG00000090629	16	58914285	58929392	-1	5	4	3	0	3	3	0	0	0	0	0	F8VQ90	
ENSMUST00000171658	ENSMUSG00000039738	16	3979105	4003770	-1	3	5	4	71	9	1	8	5	9	0	8	E9PYE7	
ENSMUST00000171662						3	2	7	2	6	1	1	0	0	0	0		
ENSMUST00000171664	ENSMUSG00000091692	7	40987543	40995435	1	28	19	74	30	25	16	0	0	0	0	0	B2RX47	
ENSMUST00000171666	ENSMUSG00000022617	15	89416405	89429908	-1	0	0	0	0	0	0	70	798	88	10	67	F6SKI6	
ENSMUST00000171671	ENSMUSG00000090383	7	41836881	41872670	-1	11	12	5	10	4	6	0	0	0	0	0	K7N6V2	
ENSMUST00000171678	ENSMUSG00000042210	9	106440051	106447678	-1	0	3	0	0	0	0	0	0	0	0	0	E9Q136	
ENSMUST00000171679	ENSMUSG00000091601	17	37151007	37152051	-1	2	4	2	13	6	1	0	0	0	0	0	Q6UAH1	
ENSMUST00000171681	ENSMUSG00000020323	10	79781474	79790961	-1	2	1	0	0	0	0	10	19	0	3	2	F7AUN8	
ENSMUST00000171682	ENSMUSG00000040040	14	57424062	57517936	1	0	0	0	1	0	1	0	0	0	0	0	F6QZ23	
ENSMUST00000171683	ENSMUSG00000021982	14	59560896	59597836	-1	8	6	18	0	15	6	36	196	77	73	58		Q8BMD5
ENSMUST00000171686	ENSMUSG00000021418	13	35893472	35906359	-1	95	45	352	198	137	70	5	19	10	6	10		Q8R1F9
ENSMUST00000171687	ENSMUSG00000002845	16	38558698	38592162	1	12	1	45	32	18	12	0	0	18	0	15		Q9CYC3
ENSMUST00000171688	ENSMUSG00000072115	14	51091077	51102007	1	5	4	16	6	0	4	5	49	22	48	12	Q3TBG7	P21570
ENSMUST00000171689	ENSMUSG00000027544	2	168476410	168601657	-1	0	0	0	16	18	0	0	0	0	0	0	Q8C443	
ENSMUST00000171690	ENSMUSG00000057715	1	11414105	11975901	1	48	1	191	57	41	0	6	5	6	1	6		Q8BZJ8
ENSMUST00000171691	ENSMUSG00000043557	17	29827956	29970087	-1	0	11	69	581	86	11	0	0	11	0	11	E9PY95	
ENSMUST00000171692	ENSMUSG00000091155	14	62663667	62692243	1	7	6	7	8	8	5	0	2	0	2	3	E9Q6A2	
ENSMUST00000171693	ENSMUSG00000027186	2	103411688	103450989	1	0	1	0	0	3	0	0	0	0	0	0	Q3V1F7	Q8VDK3
ENSMUST00000171696	ENSMUSG00000017679	2	163602314	163619013	1	0	9	0	24	0	0	298	323	378	49	203		Q9D3D0
ENSMUST00000171697						3	1	0	2	1	0	3	5	6	0	1		
ENSMUST00000171699	ENSMUSG00000038305	1	57774162	57948394	1	2	0	0	0	0	0	0	0	0	0	0	E9Q5S6	
ENSMUST00000171700						34	35	35	35	23	28	16	25	22	1	22		
ENSMUST00000171702	ENSMUSG00000023015	15	99620496	99651656	-1	11	20	24	0	32	0	85	45	238	0	93		Q9WVM1
ENSMUST00000171706	ENSMUSG00000093898	14	6583959	6590613	-1	13	7	6	1	7	6	0	0	0	0	0	K7N6Y2	
ENSMUST00000171707						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171708	ENSMUSG00000087166	4	98726734	98738480	1	0	0	0	0	0	0	0	0	0	0	0	E9PXD6	
ENSMUST00000171711						2	7	2	5	5	0	61	295	105	31	87		
ENSMUST00000171712						9	6	26	5	14	0	0	0	0	0	0		
ENSMUST00000171714	ENSMUSG00000091821	X	123221399	123222481	-1	12	7	8	58	18	6	0	0	0	0	0	B2RZI1	
ENSMUST00000171719	ENSMUSG00000049103	9	124101950	124113557	1	2	3	11	4	4	2	88	1253	180	288	127	Q543S8	P51683
ENSMUST00000171721	ENSMUSG00000024969	19	7275396	7341860	-1	0	0	0	0	0	0	0	0	0	0	0	F6ZS70	
ENSMUST00000171727						2	0	4	0	7	3	0	0	0	0	0		
ENSMUST00000171728	ENSMUSG00000024050	17	32354055	32389401	-1	0	0	0	0	0	0	9	0	4	0	0	E9Q869	
ENSMUST00000171733						1	2	9	5	4	2	14	7	7	21	16		
ENSMUST00000171735	ENSMUSG00000021910	14	31170930	31216946	-1	19	35	115	25	34	20	3	20	16	7	11		Q80TM9
ENSMUST00000171736	ENSMUSG00000039059	2	180099465	180104488	-1	0	0	0	24	0	0	0	0	0	0	0	E9Q522	
ENSMUST00000171737	ENSMUSG00000011179	12	17544873	17551502	1	31	31	79	191	65	26	280	673	255	295	679		P00860
ENSMUST00000171738	ENSMUSG00000044348	X	136981116	137038302	-1	2	6	1	6	0	7	0	11	0	0	0	E9PZF7	
ENSMUST00000171741	ENSMUSG00000095961	17	19660399	19694748	1	5	7	5	2	4	4	0	0	0	0	0	L7N279	
ENSMUST00000171742						3	4	4	0	0	0	0	0	0	0	0		
ENSMUST00000171745	ENSMUSG00000094931	7	22871224	22872147	1	0	0	0	0	0	0	0	0	0	0	0	E9Q346	
ENSMUST00000171748	ENSMUSG00000043467	1	161002922	161034849	-1	0	0	0	0	2	0	3	0	0	0	35	F7ALN1	
ENSMUST00000171749	ENSMUSG00000054753	7	3154658	3169203	-1	43	28	64	279	52	53	1	5	3	2	5	E9PWS4	
ENSMUST00000171751	ENSMUSG00000033565	15	77078990	77307053	-1	34	0	0	0	43	0	0	0	0	0	0		Q8BP71
ENSMUST00000171752	ENSMUSG00000079423	5	95510758	95522953	1	7	1	0	10	9	0	0	0	0	0	0	E9PVT6	
ENSMUST00000171754	ENSMUSG00000034271	12	85599105	85639878	1	12	10	38	6	20	4	1359	1328	909	151	763		P97875
ENSMUST00000171755						0	0	0	0	0	0	19	0	66	5	46		
ENSMUST00000171757						4	0	11	4	2	3	0	56	0	0	24		
ENSMUST00000171762	ENSMUSG00000039738	16	3979105	4003770	-1	0	0	0	5	0	0	0	2	8	0	0	E9Q0M1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000171765	ENSMUSG00000024386	18	32123129	32139570	-1	10	10	32	39	24	8	0	0	0	12	0		P33587
ENSMUST00000171767	ENSMUSG00000022106	14	73123037	73207843	1	0	2	0	19	0	0	0	7	0	9	9	E9Q3B1	
ENSMUST00000171769	ENSMUSG00000033857	11	118476829	118489209	1	0	0	0	0	0	0	16	43	15	0	0	E9PY27	
ENSMUST00000171770	ENSMUSG00000021065	12	77238104	77476338	1	17	0	14	87	30	8	174	523	260	162	206		Q9WTS2
ENSMUST00000171772	ENSMUSG00000020009	10	19591949	19610229	1	0	0	4	0	0	0	59	111	105	18	82	E9Q3Y5	
ENSMUST00000171774	ENSMUSG00000003233	16	20516982	20532520	1	0	0	0	71	0	0	4	30	0	4	73	E9Q150	
ENSMUST00000171775						0	2	6	1	0	0	0	0	0	0	0		
ENSMUST00000171777	ENSMUSG00000039620	8	36457548	36514320	1	2	4	8	3	4	5	0	0	0	0	0		Q80WQ4
ENSMUST00000171779	ENSMUSG00000036172	16	44943678	44981380	1	3	1	0	2	3	1	13	17	7	4	6		Q5UKY4
ENSMUST00000171781						0	1	0	0	4	2	1	2	0	0	0		
ENSMUST00000171783	ENSMUSG00000095902	7	13177719	13178669	1	2	3	1	0	7	3	0	0	0	0	0	E9Q235	
ENSMUST00000171784	ENSMUSG00000095360	14	6435796	6444611	-1	5	0	0	0	0	4	0	0	0	0	0	E9Q2A7	
ENSMUST00000171785						2	2	11	1	0	1	0	0	0	0	0		
ENSMUST00000171786	ENSMUSG00000000568	5	99955935	99978938	-1	0	0	0	0	0	0	207	683	351	14	167	E9Q5B6	
ENSMUST00000171788	ENSMUSG00000014837	8	105280410	105289528	-1	27	18	18	124	53	0	9	0	0	0	9		Q810A5
ENSMUST00000171789	ENSMUSG00000005262	16	18811779	18835261	1	0	0	0	0	0	0	39	144	73	336	70	E9Q475	
ENSMUST00000171791	ENSMUSG00000034751	13	102732486	103334497	-1	0	2	26	0	10	0	0	0	0	0	46	E9PWX8	
ENSMUST00000171792						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171794	ENSMUSG00000023079	5	134357656	134456716	-1	0	0	0	0	0	0	0	0	11	0	0	Q6PD35	
ENSMUST00000171795	ENSMUSG00000024127	17	85063477	85090267	-1	0	21	17	12	19	0	61	325	126	58	106		Q8C167
ENSMUST00000171796	ENSMUSG00000014602	1	93015464	93101951	-1	73	59	348	49	83	41	0	8	0	0	6	G3UW47	
ENSMUST00000171797	ENSMUSG00000058799	10	111473192	111498142	1	389	413	934	329	492	199	153	705	160	150	249	E9PW66	
ENSMUST00000171798	ENSMUSG00000091017	1	191162584	191164817	-1	19	13	54	23	28	9	0	1	0	0	0	B7XG49	
ENSMUST00000171799	ENSMUSG00000091996	9	45182007	45250020	1	7	6	16	8	14	0	2	41	4	2	22	E9Q2Z6	
ENSMUST00000171802	ENSMUSG00000046101	1	9908638	9942085	1	0	0	0	2	0	0	0	17	7	4	5		E9Q956
ENSMUST00000171804	ENSMUSG00000044378	6	137983586	138079916	-1	10	4	11	7	0	5	0	0	0	0	0		Q8CBB2
ENSMUST00000171805						0	0	0	119	0	0	0	0	0	0	0		
ENSMUST00000171807	ENSMUSG00000019856	10	53633145	53750909	-1	0	0	3	0	7	0	1	0	0	0	0	F6RSY8	
ENSMUST00000171808	ENSMUSG00000002297	5	8396973	8422716	-1	0	0	0	14	0	0	2	114	38	0	0	B2RS44	Q9QZ41
ENSMUST00000171809						3	3	3	6	8	0	0	0	0	0	0		
ENSMUST00000171810	ENSMUSG00000079389	14	4317283	4325721	1	0	4	0	4	3	3	0	0	0	0	0	E9PW52	
ENSMUST00000171811	ENSMUSG00000092048	10	130417772	130429612	-1	10	5	11	8	7	4	0	0	0	0	0	G3UW56	
ENSMUST00000171813	ENSMUSG00000090747	17	40520022	40530702	1	0	0	0	0	3	0	0	0	0	0	0	F7AMQ8	
ENSMUST00000171818						6	1	8	7	3	3	0	0	0	0	1		
ENSMUST00000171820	ENSMUSG00000001168	5	120861421	120873506	1	0	0	0	3	0	0	0	0	2	0	0	E9Q326	
ENSMUST00000171821	ENSMUSG00000002205	7	44748413	44777515	1	0	0	0	0	0	0	0	0	0	0	0	E9PY18	
ENSMUST00000171823						2	6	35	14	9	3	3	0	4	3	13		
ENSMUST00000171826	ENSMUSG00000022621	15	89582533	89591923	-1	0	0	0	0	0	0	0	0	0	0	0	F6Y6I9	
ENSMUST00000171830	ENSMUSG00000052749	7	104355382	104369884	-1	2	4	8	2	8	7	163	3209	249	152	478	Q8BY96	
ENSMUST00000171835	ENSMUSG00000049281	9	40269216	40291618	1	24	19	163	9	32	8	2	4	0	0	3	Q0P666	Q8BHK2
ENSMUST00000171837						2	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000171838	ENSMUSG00000023055	15	102706779	102722178	-1	11	8	18	17	22	23	39	150	86	18	128	E9Q7U2	
ENSMUST00000171841	ENSMUSG00000091879	5	109420013	109453387	1	5	8	2	7	8	5	0	0	0	0	0	E9PYF5	
ENSMUST00000171843	ENSMUSG00000056856	7	138940730	139083976	1	26	21	36	21	24	10	0	0	0	0	0	F6TN46	
ENSMUST00000171844	ENSMUSG00000053644	18	56509687	56572951	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q1G1	
ENSMUST00000171845	ENSMUSG00000051154	2	18672384	18676231	1	0	0	0	0	0	0	2	0	0	0	1		Q63829
ENSMUST00000171847	ENSMUSG00000023942	17	45585200	45599606	-1	6	0	15	0	12	0	0	0	0	0	0	Q3TCZ2	Q9JIM1
ENSMUST00000171849	ENSMUSG00000021906	14	32085374	32103202	1	0	2	2	0	0	2	0	0	0	0	6	F6SAD4	
ENSMUST00000171850	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	0	0	0	0	0	0	0	0	E9PUZ3	
ENSMUST00000171851						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171852						1	1	0	0	3	1	0	1	0	2	0		
ENSMUST00000171853	ENSMUSG00000092130	12	84875769	84878132	1	12	8	57	417	23	13	1	0	0	0	4	Q8BQF7	
ENSMUST00000171855						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171856	ENSMUSG00000025234	9	59388258	59486618	-1	0	0	0	0	2	0	0	36	0	11	0	F7A7T5	
ENSMUST00000171859	ENSMUSG00000025875	13	54789377	54796776	1	1	4	8	2	0	0	0	14	8	2	0	F7CRB7	
ENSMUST00000171861	ENSMUSG00000000131	7	126101715	126200501	-1	0	0	0	0	0	2	42	1212	0	112	67	F6YJ47	
ENSMUST00000171864						2	2	2	9	6	3	14	12	13	0	11		
ENSMUST00000171865						1	2	0	0	4	3	4	21	8	2	3		
ENSMUST00000171866	ENSMUSG00000090764	14	4165030	4173503	1	3	4	6	8	3	3	0	2	0	0	0	E9Q9P5	
ENSMUST00000171867						7	3	5	6	5	2	0	0	0	0	0		
ENSMUST00000171868						3	4	5	2	12	4	0	0	0	0	0		
ENSMUST00000171869	ENSMUSG00000023027	15	100227819	100261244	1	2	0	4	79	0	2	1	2	3	0	5	E9PZ49	
ENSMUST00000171871						1	1	6	0	0	0	0	0	5	7	8		
ENSMUST00000171872	ENSMUSG00000024327	17	34028267	34031690	-1	0	0	4	0	0	0	0	0	52	0	0	E9PV10	
ENSMUST00000171874						0	0	11	3	4	3	0	2	0	0	0		
ENSMUST00000171876						4	7	19	17	16	5	0	0	1	0	5		
ENSMUST00000171877	ENSMUSG00000028716	4	115088708	115093899	1	0	0	0	0	0	0	0	0	0	0	0	G3UW41	
ENSMUST00000171880	ENSMUSG00000034990	7	121083322	121163097	1	0	3	0	2	5	0	0	0	0	0	0	E9Q5L1	
ENSMUST00000171881						5	1	4	2	2	0	1	0	0	0	3		
ENSMUST00000171882	ENSMUSG00000030970	7	132987563	133124354	-1	0	0	0	25	1	2	0	0	0	0	0	E9PX05	
ENSMUST00000171887	ENSMUSG00000104445	3	88242874	88254709	-1	6	6	2	75	14	5	0	0	0	1	1		Q8BUX5
ENSMUST00000171888						0	4	9	2	8	2	0	0	0	0	0		
ENSMUST00000171896	ENSMUSG00000031434	X	139821632	139871677	-1	0	0	0	0	0	0	0	0	0	0	0	E9PWS0	
ENSMUST00000171897						3	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000171898	ENSMUSG00000090738	9	35776524	35778109	-1	0	3	0	0	1	0	0	0	0	0	0	E9Q4V7	
ENSMUST00000171900	ENSMUSG00000032301	9	54950790	54958030	1	2	6	6	95	7	2	3	6	3	0	3	E9Q0X0	
ENSMUST00000171901						1	0	0	0	0	0	6	26	12	1	25		
ENSMUST00000171904	ENSMUSG00000054342	7	24370263	24386690	1	21	7	42	266	22	12	61	36	26	27	105		O89109
ENSMUST00000171906	ENSMUSG00000090691	14	6868502	6889962	-1	11	0	4	167	17	11	0	0	0	0	0	K7N757	
ENSMUST00000171908	ENSMUSG00000023015	15	99620496	99651656	-1	0	0	0	0	0	1	0	0	0	0	0	E9Q851	
ENSMUST00000171910						0	0	11	6	0	0	0	0	0	2	21		
ENSMUST00000171912	ENSMUSG00000078765	7	30563301	30567960	1	0	0	0	5	4	0	0	117	0	12	43		Q8BGJ9
ENSMUST00000171913						2	0	1	5	6	1	0	0	0	0	0		
ENSMUST00000171914	ENSMUSG00000094892	17	19577231	19612317	1	3	3	0	2	2	2	0	0	0	0	0	E9PZS9	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000171915	ENSMUSG00000024254	17	84676302	84700333	1	4	7	10	10	11	13	0	0	0	0	0	Q7TSR6	
ENSMUST00000171916	ENSMUSG00000041481	12	104236245	104241939	1	0	0	7	0	0	0	0	0	0	0	0	E9Q499	
ENSMUST00000171920						0	2	9	2	0	0	23	69	41	8	51		
ENSMUST00000171922						7	7	4	7	11	5	2	18	16	0	8		
ENSMUST00000171923	ENSMUSG00000040936	9	120960268	121277197	-1	0	0	1	10	0	0	0	0	0	0	0	E9Q2P5	
ENSMUST00000171924						0	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000171925	ENSMUSG00000042210	9	106440051	106447678	-1	0	3	20	28	5	0	0	0	0	0	0	E9PW22	
ENSMUST00000171928						36	28	77	11	39	17	3	17	2	2	5		
ENSMUST00000171929	ENSMUSG00000026605	1	189640606	189688086	-1	54	62	87	59	62	34	97	168	261	175	148	E9Q3P4	
ENSMUST00000171933	ENSMUSG00000031337	X	71210767	71315691	1	0	0	3	0	0	0	0	0	0	0	0		Q9Z2C5
ENSMUST00000171937	ENSMUSG00000058230	7	16493719	16614993	-1	0	0	6	0	0	5	2	0	13	0	22	B2RTN5	Q91YM2
ENSMUST00000171938	ENSMUSG00000035455	11	11787431	11808962	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BPY9
ENSMUST00000171939	ENSMUSG00000026523	1	175698593	175815734	1	0	1	9	14	2	11	0	0	0	0	0		Q9D565
ENSMUST00000171941	ENSMUSG00000060671	3	89939481	89963508	-1	0	0	0	0	0	0	0	0	0	0	0	F6QLG1	
ENSMUST00000171942	ENSMUSG00000090864	7	8907173	8931504	-1	9	8	0	20	2	0	0	0	0	0	0	F6W043	
ENSMUST00000171944						0	0	1	3	0	0	0	2	0	0	0		
ENSMUST00000171945	ENSMUSG00000030345	6	126876020	126921839	-1	2	0	8	0	3	0	0	2	0	2	1	K3W4S9	
ENSMUST00000171947	ENSMUSG00000091077	Y	9130999	9133924	-1	200	168	149	196	208	137	0	0	0	0	0	Q78EE2	
ENSMUST00000171949	ENSMUSG00000004661	9	57790353	57836793	-1	1	0	0	0	3	0	2	0	50	0	18	F6TCR9	
ENSMUST00000171950						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000171951						1	2	3	0	1	0	3	0	5	0	0		
ENSMUST00000171952	ENSMUSG00000025198	19	44034944	44069785	-1	0	0	5	0	0	1	0	0	0	0	0	E9PZB0	
ENSMUST00000171953	ENSMUSG00000025666	X	81070698	81097872	1	1	0	0	47	4	0	0	0	0	0	1		Q9JJG6
ENSMUST00000171959						4	3	5	0	3	2	10	0	11	0	4		
ENSMUST00000171960						1	0	1	0	0	0	120	861	167	0	121		
ENSMUST00000171962	ENSMUSG00000044433	8	3587450	3609074	1	32	9	110	104	22	9	0	2	0	1	2	E9Q5B0	
ENSMUST00000171964	ENSMUSG00000090827	14	4983935	4992409	1	0	0	4	0	25	0	0	0	0	0	0	L7N287	
ENSMUST00000171965						5	1	0	69	3	0	0	0	0	0	0		
ENSMUST00000171967	ENSMUSG00000094157	14	42310210	42325394	1	0	0	0	0	0	0	0	0	0	0	0	L7N2E4	
ENSMUST00000171968	ENSMUSG00000030970	7	132987563	133124354	-1	0	0	0	0	1	0	2	0	3	0	2		
ENSMUST00000171970	ENSMUSG00000039004	13	38345716	38499728	1	12	13	19	252	27	7	1	0	0	0	0		P20722
ENSMUST00000171974						0	0	0	0	0	2	0	1	0	0	0		
ENSMUST00000171975	ENSMUSG00000025234	9	59388258	59486618	-1	20	17	34	24	21	10	1026	3976	1416	231	894		Q9Z1K5
ENSMUST00000171976						2	3	18	103	1	3	1	7	4	0	22		
ENSMUST00000171977	ENSMUSG00000041361	9	71504347	71592360	-1	0	1	1	0	2	0	0	0	0	0	0	E9Q4R0	
ENSMUST00000171978						5	3	0	5	0	0	2	0	0	0	0		
ENSMUST00000171980	ENSMUSG00000092047	6	129862649	129864393	1	1	1	3	3	3	0	0	2	0	0	0	F7CVU0	
ENSMUST00000171982						11	7	10	6	0	1	0	0	0	0	0		
ENSMUST00000171985						11	13	7	4	12	2	1	3	6	0	4		
ENSMUST00000171986	ENSMUSG00000040022	19	59902884	59943654	-1	13	19	4	22	18	8	24	86	27	16	40	G3UW57	
ENSMUST00000171987	ENSMUSG00000091814	14	6712183	6720251	-1	49	29	43	90	54	17	0	0	0	0	0	L7N2E3	
ENSMUST00000171989	ENSMUSG00000067714	6	125067920	125082472	1	0	0	13	12	13	0	0	18	7	0	15	G3X9K0	
ENSMUST00000171994						0	0	0	3	0	0	0	0	0	3	0		
ENSMUST00000171996	ENSMUSG00000091407	17	23459675	23479597	-1	15	23	7	2	17	5	0	0	0	0	0	K7N6V1	
ENSMUST00000171999	ENSMUSG00000006378	15	79030874	79043558	1	11	5	10	31	0	4	16	0	4	15	25	E9PWY6	
ENSMUST00000172000	ENSMUSG00000096370	19	4742913	4811612	-1	0	0	0	0	0	0	0	0	0	7	13	F7BGR7	
ENSMUST00000172001	ENSMUSG00000036560	7	31059342	31070935	1	2	2	2	2	3	0	0	1	0	0	0	F7CXY1	
ENSMUST00000172002	ENSMUSG00000025739	17	25717171	25719406	1	2	8	30	21	12	7	0	0	0	0	0		Q9JMF3
ENSMUST00000172004						20	13	42	27	15	4	0	1	0	0	0		
ENSMUST00000172005	ENSMUSG00000026312	1	109982431	110140157	1	0	0	0	0	0	0	0	0	0	0	0		Q8BM92
ENSMUST00000172006						0	3	0	0	2	0	0	0	0	0	0		
ENSMUST00000172013	ENSMUSG00000005262	16	18811779	18835261	1	2	0	0	7	1	0	0	43	41	120	24	E9Q646	
ENSMUST00000172015	ENSMUSG00000041248	9	32372418	32399192	1	13	20	0	30	37	17	0	2	0	1	0	G3UWE7	
ENSMUST00000172016						0	0	0	0	0	0	3	10	0	2	5		
ENSMUST00000172017						183	170	110	140	166	101	65	128	48	17	72		
ENSMUST00000172018	ENSMUSG00000024283	18	7868832	7973547	1	0	0	0	0	0	0	0	55	139	0	217	E9Q5D5	
ENSMUST00000172020	ENSMUSG00000039201	X	8154472	8176181	-1	7	0	0	0	5	0	181	187	96	9	93	E9PWX7	
ENSMUST00000172023						0	0	0	0	0	5	6	13	4	21	10		
ENSMUST00000172025	ENSMUSG00000089951	2	176423594	176435761	1	0	0	0	0	0	0	0	0	0	0	0	F7CJN1	
ENSMUST00000172026	ENSMUSG00000027857	3	102775465	102782718	-1	0	0	0	0	0	0	0	2	0	0	0	E9Q4F3	
ENSMUST00000172028						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172029						0	0	0	0	0	0	0	10	2	0	0		
ENSMUST00000172031	ENSMUSG00000037940	8	81342556	82125036	1	4	17	18	2	4	8	37	27	30	14	49	E9PVM1	
ENSMUST00000172032	ENSMUSG00000091813	8	105000853	105020410	1	12	5	23	16	20	7	0	0	0	0	0	F6Z9B9	
ENSMUST00000172034						1	1	4	7	2	0	0	3	3	0	4		
ENSMUST00000172035	ENSMUSG00000037275	11	58120002	58168539	-1	14	5	19	43	24	25	24	67	57	10	51	E9PUU4	
ENSMUST00000172038	ENSMUSG00000072675	14	26118349	26129763	1	0	5	20	8	7	0	0	0	0	0	0	Q3UY88	
ENSMUST00000172040						0	0	0	5	1	0	0	0	4	5	6		
ENSMUST00000172041	ENSMUSG00000025198	19	44034944	44069785	-1	0	0	0	16	0	2	0	0	0	0	0	E9PUH5	
ENSMUST00000172042	ENSMUSG00000026659	1	170873498	170885540	-1	0	0	1	9	5	0	0	0	0	0	2	E9PUU1	
ENSMUST00000172044	ENSMUSG00000043467	1	161002922	161034849	-1	0	0	0	0	0	0	0	0	0	0	0	Q8C3U9	
ENSMUST00000172045	ENSMUSG00000029267	5	108065674	108109004	1	0	0	0	102	2	0	0	0	0	4	0	E9PYX9	
ENSMUST00000172046	ENSMUSG00000086040	6	54429603	54503768	1	0	0	0	0	0	0	0	0	0	0	0	E9Q2D0	
ENSMUST00000172052						2	0	0	0	2	0	0	0	0	0	5		
ENSMUST00000172053	ENSMUSG00000022621	15	89582533	89591923	-1	0	0	0	0	0	0	4	0	0	0	5	E9PZU3	
ENSMUST00000172054						0	3	7	0	0	0	2	75	0	26	16		
ENSMUST00000172056	ENSMUSG00000000759	8	12614277	12672248	-1	0	0	0	0	0	0	0	0	0	0	5	F6QMZ4	
ENSMUST00000172057	ENSMUSG00000026594	1	156804166	156939626	-1	25	16	20	5	23	8	2	8	2	4	51		Q9ERD6
ENSMUST00000172065						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000172067						0	0	1	4	2	3	0	0	0	0	0		
ENSMUST00000172068	ENSMUSG00000038305	1	57774162	57948394	1	0	0	2	0	0	0	0	0	0	0	0	E9Q106	
ENSMUST00000172069	ENSMUSG00000006724	10	127048250	127053006	1	0	16	0	44	22	0	0	0	0	0	0	E9Q3C2	
ENSMUST00000172070	ENSMUSG00000020027	10	95385362	95417180	-1	0	0	34	0	3	4	3	22	0	7	14	Q548Q7	O35717
ENSMUST00000172073	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	1	0	0	1	Q6VYI4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172074						7	5	23	15	4	3	0	6	0	0	0		
ENSMUST00000172079	ENSMUSG00000090553	1	133603871	133610291	-1	0	2	0	0	3	0	6	8	4	8	0	E9PXQ9	
ENSMUST00000172081						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000172082						134	153	371	212	107	64	3	19	8	10	21		
ENSMUST00000172083						1	1	1	1	0	2	0	4	0	0	0		
ENSMUST00000172084	ENSMUSG00000029778	6	55451978	55501451	1	0	0	0	0	0	0	0	0	0	0	0	E9Q3E8	
ENSMUST00000172088	ENSMUSG00000042097	6	117862100	117873291	1	16	0	7	22	13	0	0	4	4	10	7		P24399
ENSMUST00000172089	ENSMUSG00000021111	12	105784694	105838944	1	2	3	14	0	4	0	18	42	21	8	13	F7AB38	
ENSMUST00000172091						0	1	0	1	3	1	0	2	0	8	1		
ENSMUST00000172095	ENSMUSG00000048612	19	37899036	38043577	-1	15	14	21	26	28	18	0	0	0	0	0	E9Q390	
ENSMUST00000172097	ENSMUSG00000080316	17	17830719	17843009	1	4	2	8	4	0	4	0	0	0	0	2	E9Q8Q8	E9Q8Q8
ENSMUST00000172098	ENSMUSG00000025328	4	140785365	140810648	-1	58	38	248	103	53	19	13	179	66	0	59	E9QAM4	
ENSMUST00000172099	ENSMUSG00000063142	14	23289431	24004859	-1	9	0	0	0	4	0	0	0	0	0	0	F6WSZ3	
ENSMUST00000172101						7	1	4	2	7	0	0	2	0	0	0		
ENSMUST00000172103	ENSMUSG00000090716	14	44402671	44410688	-1	2	9	4	11	4	4	0	0	0	0	0	F7CQW8	
ENSMUST00000172104	ENSMUSG00000021684	13	95024454	95250336	-1	0	0	0	0	6	0	0	0	0	0	0	E9Q7S6	
ENSMUST00000172106	ENSMUSG00000095829	5	11341516	11346286	1	0	0	0	0	0	0	0	0	0	0	0	F6X687	
ENSMUST00000172107	ENSMUSG00000022403	15	81363669	81400077	-1	5	3	4	28	4	2	164	386	125	145	183		Q99L47
ENSMUST00000172108	ENSMUSG00000001441	11	97205842	97280638	-1	0	0	0	12	0	0	0	0	0	0	0	E9Q039	
ENSMUST00000172109	ENSMUSG00000078816	7	3289179	3331099	1	0	1	1	1	0	0	14	3	9	0	17	Q2NKI4	
ENSMUST00000172110	ENSMUSG00000079383	14	5015891	5019119	1	0	0	0	0	0	0	0	0	0	0	0	E9PW80	
ENSMUST00000172111	ENSMUSG00000090794	7	5544197	5545129	-1	5	3	1	3	0	0	0	0	0	0	0	K7N758	
ENSMUST00000172115	ENSMUSG00000041708	15	83779467	83858494	1	0	0	0	23	0	0	0	0	0	0	0	E9PZI5	
ENSMUST00000172116	ENSMUSG00000043943	9	18321951	18402995	-1	2	0	0	0	0	0	0	0	1	0	0	E9PV01	
ENSMUST00000172117	ENSMUSG00000091142	14	51568892	51574063	-1	0	2	4	0	0	0	0	0	0	0	0	E9Q528	
ENSMUST00000172118						2	3	2	0	1	3	0	8	6	0	0		
ENSMUST00000172119						3	1	10	1	4	3	0	0	0	0	1		
ENSMUST00000172122	ENSMUSG00000022119	14	105106751	105177327	-1	11	3	2	0	7	1	41	177	43	25	70		
ENSMUST00000172123						4	2	3	2	7	2	0	0	0	0	0		
ENSMUST00000172126	ENSMUSG00000027530	3	10244209	10301183	-1	6	9	42	2	4	1	0	0	0	0	0		Q9DAK4
ENSMUST00000172132	ENSMUSG00000023456	6	124810586	124814296	-1	33	30	49	33	40	23	5298	5104	2609	4375	1750		P17751
ENSMUST00000172134						2	0	2	0	7	2	0	0	1	7	0		
ENSMUST00000172136	ENSMUSG00000060260	7	139248482	139267253	1	0	12	26	9	50	9	6	56	0	0	9	E9Q9M8	
ENSMUST00000172138	ENSMUSG00000021624	13	102693558	102739629	1	0	1	5	2	0	1	0	0	0	3	0	E9Q0I3	
ENSMUST00000172140	ENSMUSG00000090961	5	108797193	108808754	-1	6	11	3	7	11	2	0	0	0	0	0	L7N472	
ENSMUST00000172142	ENSMUSG00000021910	14	31170930	31216946	-1	12	7	11	11	6	6	744	1913	1052	137	1076		Q80TM9
ENSMUST00000172146						0	0	0	0	0	0	0	0	0	62	1		
ENSMUST00000172148	ENSMUSG00000007480	18	68337603	68339711	1	7	5	5	12	12	4	3	2	4	1	6	G3UWB6	
ENSMUST00000172151						0	0	0	8	1	0	0	0	0	0	0		
ENSMUST00000172153	ENSMUSG00000053469	15	66670753	66850721	1	0	0	0	0	0	0	61	19	38	17	0	F7AYJ4	
ENSMUST00000172154	ENSMUSG00000023027	15	100227819	100261244	1	0	2	2	0	2	1	7	7	166	13	162	E9PWM8	
ENSMUST00000172155	ENSMUSG00000091497	X	90892142	90893134	1	3	7	3	4	2	0	0	0	0	0	0	G3UW88	
ENSMUST00000172158	ENSMUSG00000042570	10	79540245	79555199	-1	0	4	7	74	5	0	0	1	1	1	0	Q9CZI4	
ENSMUST00000172159	ENSMUSG00000026875	2	34941750	34961772	-1	50	28	99	811	92	19	8	8	8	3	8		P39428
ENSMUST00000172160						0	0	0	0	5	1	0	2	0	0	6		
ENSMUST00000172162						12	4	14	15	5	9	0	3	3	1	3		
ENSMUST00000172163	ENSMUSG00000094954	14	42463881	42472122	1	8	9	0	0	7	0	0	0	0	0	0	K7N6Y5	
ENSMUST00000172164	ENSMUSG00000022756	16	17572018	17576998	-1	14	9	27	16	9	10	0	0	0	0	2		Q8BLQ7
ENSMUST00000172165	ENSMUSG00000026276	1	93478964	93510260	1	8	0	36	0	5	6	421	1301	586	840	39	E9Q3V6	
ENSMUST00000172166	ENSMUSG00000021555	13	59585259	59634798	1	0	2	0	0	0	0	0	8	2	0	0	F6WYJ5	
ENSMUST00000172167	ENSMUSG00000037940	8	81342556	82125036	1	2	0	3	59	6	1	0	1	0	0	0	E9PZR9	
ENSMUST00000172168						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172170	ENSMUSG00000023952	17	46161032	46169370	1	0	15	0	0	11	0	0	235	0	27	0	E9QA45	
ENSMUST00000172171	ENSMUSG00000043943	9	18321951	18402995	-1	6	7	5	0	18	0	0	0	0	1	0	G3UWC2	
ENSMUST00000172175	ENSMUSG00000071661	19	8802530	8804854	1	11	9	53	22	33	13	22	25	9	9	9		Q91X45
ENSMUST00000172177	ENSMUSG00000002617	17	23173869	23193252	-1	6	1	0	1	0	1	9	18	0	7	1	B1B1D3	
ENSMUST00000172178	ENSMUSG00000092071	7	89632097	89633124	-1	6	3	9	73	7	5	0	0	0	0	0	Q8CAG4	
ENSMUST00000172181						0	0	0	0	0	0	1	0	1	0	1		
ENSMUST00000172182	ENSMUSG00000005899	16	17619354	17644828	1	0	0	0	0	0	0	0	0	0	0	0	E9Q146	
ENSMUST00000172184	ENSMUSG00000052180	13	33879816	33905708	-1	1	7	5	16	13	3	0	0	0	0	0	W4VSP4	
ENSMUST00000172186	ENSMUSG00000018379	11	88047373	88053755	1	0	0	0	0	0	0	0	0	0	0	0	F6QXN3	
ENSMUST00000172187						0	0	0	1	4	1	3	0	0	3	3		
ENSMUST00000172188	ENSMUSG00000030101	6	108107028	108185582	-1	0	0	0	32	1	0	0	0	0	0	0	E9Q0Z7	
ENSMUST00000172190	ENSMUSG00000090417	17	18243570	18277508	-1	4	3	3	1	5	1	0	0	0	0	0	E9PZK8	
ENSMUST00000172191	ENSMUSG00000091650	15	77508271	77517319	1	0	0	0	0	3	0	0	0	2	0	0	E9PZG0	
ENSMUST00000172198	ENSMUSG00000024563	18	76241580	76305731	1	0	0	0	0	0	0	0	0	0	0	0	E9PZV6	
ENSMUST00000172199	ENSMUSG00000094145	6	123385262	123418061	-1	8	9	12	0	16	9	0	0	0	0	0	L7N2B1	
ENSMUST00000172200						10	0	10	6	0	0	0	0	0	0	0		
ENSMUST00000172203	ENSMUSG00000091771	17	19773363	19812536	1	9	3	4	3	2	3	0	0	0	0	0	E9PWW0	
ENSMUST00000172205						5	11	36	69	17	9	0	0	0	0	0		
ENSMUST00000172206						3	2	6	5	1	1	0	1	1	0	2		
ENSMUST00000172207	ENSMUSG00000006998	16	20651652	20663414	1	0	0	40	0	0	0	0	0	2	0	10	E9Q2S8	
ENSMUST00000172208	ENSMUSG00000022389	15	81802421	81826861	1	0	1	5	6	3	1	0	0	0	0	0	E9Q3N8	
ENSMUST00000172209						2	1	10	3	2	2	0	0	2	0	3		
ENSMUST00000172210						9	0	0	0	0	0	2	11	5	0	6		
ENSMUST00000172214						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000172215	ENSMUSG00000048200	7	141461094	141466613	1	4	2	5	2	6	0	0	0	2	0	0	E9PXF1	
ENSMUST00000172216						5	1	6	6	3	1	7	18	18	4	3		
ENSMUST00000172218						1	6	2	0	12	2	0	0	0	0	2		
ENSMUST00000172220	ENSMUSG00000055670	11	72796226	72927120	1	0	34	0	48	61	30	1666	1671	3482	65	3447	E9Q5W5	
ENSMUST00000172222	ENSMUSG00000079434	1	87509889	87597845	1	0	0	0	0	13	0	0	0	0	0	0	E9Q0I0	
ENSMUST00000172225						4	0	5	3	5	0	0	0	0	0	0		
ENSMUST00000172226						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172229	ENSMUSG00000047407	17	70844205	70853546	-1	0	0	0	0	0	0	0	5	0	0	0	Q3TVD4	P70284

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172230	ENSMUSG00000062782	7	140335843	140336820	1	7	3	18	8	9	7	0	0	0	0	0	Q7TRT9	
ENSMUST00000172233	ENSMUSG00000035086	11	101285952	101302286	-1	0	0	0	0	0	0	28	0	0	0	13	E9PYD6	
ENSMUST00000172235	ENSMUSG00000070327	11	119393100	119487418	1	3	2	3	0	0	2	23	794	89	85	137	Q3U0U2	
ENSMUST00000172237	ENSMUSG00000022122	14	103814625	103844173	-1	0	23	34	82	30	0	0	0	0	519	426		P48302
ENSMUST00000172238	ENSMUSG00000025374	10	128401395	128411492	-1	2	0	0	2	0	0	0	13	0	0	5	E9Q5F7	
ENSMUST00000172239	ENSMUSG00000025041	19	46886831	47015153	-1	0	4	57	18	0	0	380	2390	990	765	291	E9Q9M1	
ENSMUST00000172240	ENSMUSG00000049600	7	13004936	13009822	-1	14	5	32	221	36	9	23	28	37	9	47	Q52KG4	
ENSMUST00000172241						3	2	5	1	0	1	12	59	9	7	10		
ENSMUST00000172244	ENSMUSG00000025176	19	42045610	42070953	1	1	0	9	1	0	2	0	1	1	0	0	E9Q1R2	
ENSMUST00000172246						2	5	4	4	5	1	0	9	9	0	7		
ENSMUST00000172247	ENSMUSG00000004032	3	107895821	107898686	1	1	2	1	0	0	1	0	1	0	11	0	E9PVM7	
ENSMUST00000172251	ENSMUSG00000036826	7	30565427	30567962	1	5	0	5	0	0	0	3	0	0	0	0	E9Q0U5	
ENSMUST00000172252	ENSMUSG00000028057	3	88716838	88731049	1	0	0	0	0	0	0	71	664	52	172	58	E9Q672	
ENSMUST00000172253	ENSMUSG00000020009	10	19591949	19610229	1	0	1	0	20	0	1	0	0	0	0	5	E9Q2T5	
ENSMUST00000172254	ENSMUSG00000037851	13	49682100	49734267	1	0	0	6	17	5	3	0	0	0	0	0	E9Q866	
ENSMUST00000172256						0	0	0	3	6	5	0	0	0	0	0		
ENSMUST00000172257	ENSMUSG00000070983	4	52970623	52971567	1	5	4	7	8	4	0	0	0	0	0	0	Q8VFN0	
ENSMUST00000172259						3	7	8	4	12	3	0	0	0	0	1		
ENSMUST00000172261	ENSMUSG00000019944	10	69151434	69291791	1	2	2	1	0	0	0	0	0	0	0	0	E9Q922	
ENSMUST00000172262	ENSMUSG00000025198	19	44034944	44069785	-1	0	0	0	0	0	0	0	0	0	0	0	F6Z6D6	
ENSMUST00000172264	ENSMUSG00000034751	13	102732486	103334497	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q6G0	
ENSMUST00000172266	ENSMUSG00000078995	13	67362113	67375810	-1	0	2	7	4	4	0	1	0	0	1	2	F2Z406	
ENSMUST00000172269	ENSMUSG00000011751	7	27356383	27447686	-1	0	16	51	343	36	17	0	0	3	0	2	Q91ZE6	
ENSMUST00000172270	ENSMUSG00000091198	15	81499084	81499548	-1	6	2	84	11	20	5	0	1	0	1	0	F6YH22	
ENSMUST00000172271	ENSMUSG00000023411	14	55824795	55833943	1	46	38	216	346	89	33	0	2	2	0	2		Q8K120
ENSMUST00000172272	ENSMUSG00000021500	13	55635027	55681256	1	3	3	34	11	0	3	413	1723	1316	428	909		Q569Z5
ENSMUST00000172274						0	1	3	0	0	0	0	0	0	0	0		
ENSMUST00000172276						0	7	8	45	2	8	0	0	0	0	0		
ENSMUST00000172278	ENSMUSG00000045613	6	36388084	36528414	1	20	21	35	62	26	17	0	0	0	0	0		Q9ERZ4
ENSMUST00000172279	ENSMUSG00000033857	11	118476829	118489209	1	1	0	0	53	0	1	0	0	0	0	0		Q8BX80
ENSMUST00000172280	ENSMUSG00000056617	9	46303361	46319986	-1	0	0	0	0	0	0	0	0	0	0	0	E9PVU2	
ENSMUST00000172281	ENSMUSG00000022561	15	76331231	76334907	1	8	0	0	0	6	0	125	544	57	40	155	E9PW03	
ENSMUST00000172282	ENSMUSG00000006498	10	79854427	79864771	1	0	0	0	50	6	0	559	638	455	31	274	Q922I7	
ENSMUST00000172284	ENSMUSG00000024037	17	31494323	31519974	-1	0	0	41	0	0	0	36	0	17	7	0	F6YNC4	
ENSMUST00000172287	ENSMUSG00000038305	1	57774162	57948394	1	4	5	8	9	6	3	0	0	0	0	0	E9Q1C3	
ENSMUST00000172288	ENSMUSG00000007379	3	103102604	103169769	1	7	9	0	2	14	0	0	0	13	6	7	E9Q4E4	
ENSMUST00000172289						9	8	14	62	14	13	0	0	0	0	0		
ENSMUST00000172297						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000172298	ENSMUSG00000004771	9	64715299	64737758	-1	1	1	7	28	1	1	156	227	46	30	40	Q0PD45	P62492
ENSMUST00000172299	ENSMUSG00000047496	1	105276914	105356710	-1	73	11	51	317	83	5	3	4	1	0	10		Q8BG47
ENSMUST00000172300						0	6	16	0	4	6	0	0	0	0	0		
ENSMUST00000172301	ENSMUSG00000023942	17	45585200	45599606	-1	0	0	0	0	0	0	0	0	0	0	0	E9PWD6	
ENSMUST00000172302	ENSMUSG00000024924	19	27216484	27254231	1	0	0	0	75	9	0	0	0	0	0	0	Q91YY0	
ENSMUST00000172303	ENSMUSG00000000631	11	77763246	77865980	1	14	0	29	0	9	0	328	772	336	0	186		Q9JMH9
ENSMUST00000172304						1	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000172305	ENSMUSG00000009073	11	4765845	4849536	-1	3	3	10	60	2	2	4	7	3	1	3	E9Q7I0	
ENSMUST00000172306	ENSMUSG00000053716	9	106368632	106375724	1	17	20	48	398	32	19	195	357	243	46	192		Q91Z46
ENSMUST00000172307	ENSMUSG00000078954	15	84720052	84772207	1	0	0	19	27	0	0	0	0	0	0	0		Q9CXP4
ENSMUST00000172308						5	0	0	4	0	0	0	0	1	0	0		
ENSMUST00000172314	ENSMUSG00000002996	12	31926254	31950535	-1	9	6	13	22	11	10	1861	7830	2895	3332	1702	E9Q1A8	
ENSMUST00000172320	ENSMUSG00000004994	8	84257795	84270380	-1	0	0	0	3	7	1	11	20	10	0	13	E9Q971	
ENSMUST00000172321	ENSMUSG00000053977	6	71373427	71379173	1	122	93	0	7	0	61	32	0	31	15	0	Q8CAX3	
ENSMUST00000172322	ENSMUSG00000094589	7	20911427	20912347	-1	0	0	0	0	0	0	0	0	0	0	0	L7N273	
ENSMUST00000172324						2	4	11	2	7	1	0	40	29	8	70		
ENSMUST00000172326	ENSMUSG00000056222	13	57421195	57908314	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BKQ3	
ENSMUST00000172330	ENSMUSG00000031284	X	143518591	143797796	1	0	0	0	0	0	0	0	0	0	0	0		Q61036
ENSMUST00000172331						0	2	0	3	0	0	0	0	0	0	0		
ENSMUST00000172332	ENSMUSG00000090946	12	32378704	32382943	1	10	10	17	328	22	17	352	1139	361	79	215	E9Q4T4	
ENSMUST00000172333	ENSMUSG00000028057	3	88716838	88731049	1	0	0	0	0	0	0	219	228	241	258	122	G3UWE0	
ENSMUST00000172334	ENSMUSG00000053559	15	100621342	100636865	-1	3	8	4	4	9	4	6	19	0	5	13		Q99KC7
ENSMUST00000172336						5	1	6	20	6	1	43	47	43	6	51		
ENSMUST00000172338	ENSMUSG00000091205	7	85615462	85624547	1	2	3	3	2	10	5	0	0	0	0	0	L7N2D8	
ENSMUST00000172341	ENSMUSG00000030970	7	132987563	133124354	-1	2	0	0	24	3	0	0	0	0	0	0	E9Q0T4	
ENSMUST00000172346						1	0	2	0	1	3	0	0	0	0	0		
ENSMUST00000172347						4	6	6	0	2	4	1	18	3	3	5		
ENSMUST00000172348	ENSMUSG00000025374	10	128401395	128411492	-1	0	0	0	0	0	0	0	0	6	0	0	E9PV68	
ENSMUST00000172350	ENSMUSG00000027703	3	30644507	30672431	1	0	2	0	84	5	0	0	0	0	0	0		A6H6A4
ENSMUST00000172352	ENSMUSG00000030699	7	126781483	126785560	1	0	7	3	4	0	3	29	70	40	0	39		P70327
ENSMUST00000172353	ENSMUSG00000001504	13	72628820	72634198	1	0	0	0	0	0	1	0	0	0	0	0	F6ZTI9	
ENSMUST00000172356	ENSMUSG00000032625	6	12311610	12749410	-1	41	32	85	60	38	23	1	11	5	0	6	E9PWD2	
ENSMUST00000172357						5	7	2	128	3	3	0	0	0	0	0		
ENSMUST00000172359	ENSMUSG00000091206	17	18085057	18136643	1	9	2	4	0	12	5	0	0	0	0	0	E9Q2U5	
ENSMUST00000172361	ENSMUSG00000000568	5	99955935	99978938	-1	9	8	17	22	21	9	7	27	22	6	39		Q60668
ENSMUST00000172362	ENSMUSG00000024908	19	3454933	3575749	-1	0	21	97	0	8	8	181	1077	568	133	355		Q922D4
ENSMUST00000172363						0	0	2	0	0	4	0	0	0	0	0		
ENSMUST00000172364						16	15	11	23	31	13	7	0	0	3	1		
ENSMUST00000172366						2	2	0	3	0	1	0	0	0	1	0		
ENSMUST00000172367	ENSMUSG00000104633	5	143928175	143937309	1	0	0	0	0	0	0	2	8	4	0	1	F6X8D5	
ENSMUST00000172370						24	17	7	10	23	10	10	10	18	1	21		
ENSMUST00000172371	ENSMUSG00000090673	19	41582370	41586536	1	47	27	110	38	41	26	39	47	122	10	103	F6RGI3	
ENSMUST00000172377						15	16	12	2	32	17	0	0	0	0	0		
ENSMUST00000172378	ENSMUSG00000040380	14	55878920	55884256	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JHG0
ENSMUST00000172380	ENSMUSG00000032503	9	112065091	112235938	-1	0	0	0	9	0	10	0	0	0	0	0		Q9DCB4
ENSMUST00000172382						1	1	1	0	5	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172386	ENSMUSG00000040046	7	46647130	46672537	-1	0	0	0	1	0	0	0	0	0	0	0	F7BYX2	
ENSMUST00000172387	ENSMUSG00000022370	15	55534094	55557748	-1	8	6	11	115	12	10	50	121	69	360	74		Q9D1P0
ENSMUST00000172388	ENSMUSG00000026358	1	144242296	144249242	-1	0	0	0	0	0	0	0	1	0	0	0	A0A0A0MQN0	
ENSMUST00000172391	ENSMUSG00000091620	6	123702821	123742291	1	7	14	15	4	13	4	0	0	0	0	0	E9PXI5	
ENSMUST00000172392						0	0	0	10	6	0	0	18	12	0	0		
ENSMUST00000172394						3	4	16	2	8	1	0	0	0	0	0		
ENSMUST00000172395						49	33	125	316	82	19	0	0	0	0	0		
ENSMUST00000172396	ENSMUSG00000005481	8	83715177	83726892	1	572	568	1189	475	770	370	75	466	142	18	470		Q8VDW0
ENSMUST00000172397						0	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000172398	ENSMUSG00000041708	15	83779467	83858494	1	1	0	4	0	0	0	0	0	0	0	0	E9Q2Q2	
ENSMUST00000172400						4	2	13	9	6	1	2	33	9	2	17		
ENSMUST00000172402						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172403	ENSMUSG00000042632	15	79286228	79328390	-1	0	0	0	0	0	0	0	0	0	2	4	Q3UN31	P97819
ENSMUST00000172405	ENSMUSG00000020530	11	84832361	84870817	-1	7	10	0	0	0	0	225	1624	0	0	0		Q5SV77
ENSMUST00000172407	ENSMUSG00000032301	9	54950790	54958030	1	0	0	3	1	1	0	13	12	30	138	20	E9PW69	
ENSMUST00000172409	ENSMUSG00000021262	12	108554720	108688513	1	5	4	28	5	8	7	117	184	73	30	148	E9PVP4	
ENSMUST00000172412	ENSMUSG00000091110	14	41278805	41288815	1	4	5	6	0	3	5	0	0	0	0	1	F7AEC7	
ENSMUST00000172416	ENSMUSG00000040865	1	62958418	63114667	-1	0	0	143	0	0	0	434	563	517	21	658	B1AT32	
ENSMUST00000172417	ENSMUSG00000058239	7	30945248	30956803	-1	0	0	2	0	2	0	0	0	0	0	0	E9PXC2	
ENSMUST00000172419	ENSMUSG00000021555	13	59585259	59634798	1	0	0	0	0	0	0	0	12	11	0	0	F7A8R0	
ENSMUST00000172422						0	1	1	6	0	1	172	126	139	27	111		
ENSMUST00000172429	ENSMUSG00000038500	17	35972541	35980236	-1	21	18	33	16	14	10	66	103	60	21	43	Q3V0R7	
ENSMUST00000172430						10	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000172431	ENSMUSG00000090363	14	7153511	7174533	-1	0	0	3	0	12	10	0	0	0	0	0	E9Q032	
ENSMUST00000172432						3	11	6	0	8	5	0	0	0	0	0		
ENSMUST00000172433	ENSMUSG00000091396	12	62687822	62688244	1	0	1	5	2	2	2	0	0	0	0	0	C0IQA4	
ENSMUST00000172434	ENSMUSG00000090523	18	32528322	32560034	-1	3	2	8	1	2	0	0	0	0	0	0	F7D1I5	
ENSMUST00000172435	ENSMUSG00000038552	5	31292242	31296080	-1	13	3	3	58	13	11	0	7	1	1	0	B9EI95	Q3TR08
ENSMUST00000172439						5	8	15	123	7	4	0	0	0	0	0		
ENSMUST00000172440						1	4	2	0	3	2	0	0	0	0	1		
ENSMUST00000172442						35	24	72	191	31	20	115	722	171	19	370		
ENSMUST00000172443	ENSMUSG00000038542	8	13077189	13105459	-1	0	0	0	0	0	0	13	3	0	0	3	E9Q1H5	
ENSMUST00000172444						2	4	0	0	2	0	20	0	0	60	37		
ENSMUST00000172445						4	0	0	0	4	0	4	0	0	0	0		
ENSMUST00000172447	ENSMUSG00000005125	15	66929321	66969640	-1	0	0	0	0	0	0	0	0	0	0	0	E9Q7G8	
ENSMUST00000172448	ENSMUSG00000062040	7	29893333	29906572	-1	0	0	0	0	0	1	0	7	11	0	6		P10077
ENSMUST00000172449						2	3	8	1	4	2	0	0	0	0	0		
ENSMUST00000172450	ENSMUSG00000003131	9	45965311	45984871	-1	33	18	60	66	40	12	440	1282	626	286	473		Q61206
ENSMUST00000172451	ENSMUSG00000005262	16	18811779	18835261	1	4	1	4	4	1	0	14	16	16	2	32	F6SYJ2	
ENSMUST00000172452	ENSMUSG00000020407	11	9118103	9136170	1	0	0	6	20	5	0	13	81	21	5	11	E9Q391	
ENSMUST00000172453						0	0	0	0	0	0	47	93	26	0	30		
ENSMUST00000172455						0	5	1	37	5	1	20	134	35	23	62		
ENSMUST00000172457	ENSMUSG00000008683	7	118104372	118116188	-1	61	75	116	70	88	34	11	28	4	5	16	Q5M9M4	P62245
ENSMUST00000172459	ENSMUSG00000023403	6	49395604	49469501	1	6	3	11	0	8	7	0	0	0	0	0	E9PWQ6	
ENSMUST00000172462						0	1	4	16	1	0	0	0	1	0	4		
ENSMUST00000172463	ENSMUSG00000054310	7	15388948	15556866	1	0	0	0	0	0	0	0	0	0	0	0	Q9D350	
ENSMUST00000172464	ENSMUSG00000047409	9	118926453	119043998	1	0	0	0	24	0	0	3	2	0	0	0	G3UXN0	
ENSMUST00000172465						0	1	1	9	2	1	0	0	0	0	0		
ENSMUST00000172466	ENSMUSG00000024109	17	90033631	91093071	-1	10	0	8	0	0	9	0	0	0	0	0	A0A0H2UH29	
ENSMUST00000172467	ENSMUSG00000002409	7	28179469	28187294	1	6	0	18	90	12	0	0	0	0	52	0		Q9Z188
ENSMUST00000172468						2	0	1	278	1	3	0	4	8	0	2		
ENSMUST00000172469	ENSMUSG00000039607	9	116572746	117629913	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYP9	
ENSMUST00000172470						3	4	4	32	5	0	0	1	0	0	0		
ENSMUST00000172471	ENSMUSG00000028382	4	59471868	59549364	-1	1	0	0	0	0	0	6	4	6	43	0	G3UXZ8	
ENSMUST00000172472	ENSMUSG00000029001	4	148152800	148160482	-1	0	0	0	3	0	0	0	0	0	0	0	G3UY69	
ENSMUST00000172474						0	0	0	0	0	0	4	3	0	2	3		
ENSMUST00000172475						0	0	1	0	0	0	8	1	0	5	2		
ENSMUST00000172476						26	33	10	17	59	0	1	3	2	1	5		
ENSMUST00000172478	ENSMUSG00000074369	7	15388721	15398545	1	2	0	1	0	2	0	0	0	0	0	0	E9PXV9	
ENSMUST00000172479	ENSMUSG00000025495	7	141122382	141157021	1	0	0	1	0	0	0	0	0	0	0	0	G3UXS3	
ENSMUST00000172481	ENSMUSG00000056900	3	32817546	32938071	1	0	0	0	0	0	3	0	0	0	0	0	G3UXT9	
ENSMUST00000172482	ENSMUSG00000033335	9	21424908	21507759	1	0	0	0	0	0	3	725	0	1100	0	164		P39054
ENSMUST00000172484						6	14	0	8	13	7	0	0	0	0	0		
ENSMUST00000172485	ENSMUSG00000090083	17	29614790	29641664	1	8	0	10	3	0	0	0	0	0	0	0	G3UZZ4	
ENSMUST00000172486	ENSMUSG00000015222	1	66175273	66442583	1	0	0	0	0	0	0	0	0	0	0	1	G3UYR3	
ENSMUST00000172487	ENSMUSG00000067786	2	157560078	157562522	1	0	1	1	60	0	0	0	0	0	0	0	G3UZA6	
ENSMUST00000172488	ENSMUSG00000022159	14	52261759	52279545	-1	0	0	0	0	0	0	0	0	0	2	4	G3UXQ7	
ENSMUST00000172489						0	0	6	2	0	0	26	0	42	4	70		
ENSMUST00000172490						1	0	0	21	0	0	0	0	0	0	0		
ENSMUST00000172491	ENSMUSG00000007035	17	35028605	35046745	-1	0	0	0	23	0	0	0	0	0	0	0	G3UWT5	
ENSMUST00000172492	ENSMUSG00000041961	11	5276324	5444847	-1	33	30	77	44	52	21	0	2	5	2	21		Q5SSZ7
ENSMUST00000172493	ENSMUSG00000031558	5	47983138	48307733	1	0	0	0	0	0	0	0	0	0	0	0	G3UZW0	
ENSMUST00000172494	ENSMUSG00000013766	17	35076902	35078804	1	1	0	0	0	0	0	0	0	0	0	0	G3UXD4	
ENSMUST00000172495	ENSMUSG00000030316	6	115004381	115037876	-1	0	0	0	0	0	0	1	0	4	12	0	G3UYJ1	
ENSMUST00000172496						0	0	0	0	0	0	6	0	0	0	20		
ENSMUST00000172497						4	2	16	12	8	1	1	11	1	0	6		
ENSMUST00000172498						1	2	0	0	3	1	1	0	0	4	4		
ENSMUST00000172499	ENSMUSG00000007030	17	35016579	35026741	1	26	32	53	109	37	27	0	0	0	1	0	B9EJA5	
ENSMUST00000172502						2	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000172503	ENSMUSG00000073411	17	35262730	35267499	1	0	0	7	0	0	0	242	529	186	45	191	G3UZP7	
ENSMUST00000172504						4	2	6	6	2	4	6	0	6	0	0		
ENSMUST00000172505	ENSMUSG00000022710	16	8689595	8792308	-1	0	0	0	0	0	0	0	0	15	0	0	G3UWR8	
ENSMUST00000172506						5	5	10	3	0	2	5	14	7	5	5		
ENSMUST00000172507						0	0	7	0	2	0	55	57	70	10	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172508	ENSMUSG00000032423	9	88447009	88482574	-1	0	0	0	34	0	0	0	0	10	3	0	G3XA76	
ENSMUST00000172509	ENSMUSG00000020661	12	3806007	3914443	1	0	0	0	0	0	0	3	0	0	0	4	G3UXY2	
ENSMUST00000172510	ENSMUSG00000030126	6	116018611	116193486	-1	2	10	20	2	5	0	140	2106	356	894	573	G3UXF1	
ENSMUST00000172511	ENSMUSG00000025316	8	121949750	122029258	1	2	4	3	8	0	0	0	0	0	0	8	G3UWN8	
ENSMUST00000172512						1	1	5	3	4	0	1	3	4	1	2		
ENSMUST00000172513						1	1	0	1	1	0	0	3	3	0	0		
ENSMUST00000172514						0	6	0	2	0	2	0	2	0	0	4		
ENSMUST00000172515	ENSMUSG00000000804	11	84984442	85140161	-1	0	0	0	0	0	0	3	9	35	0	17	G3UXQ4	
ENSMUST00000172516						0	0	1	1	1	0	0	0	15	0	10		
ENSMUST00000172517	ENSMUSG00000072672	14	26257962	26269436	1	0	0	1	0	2	1	0	0	0	0	0	G3UX37	
ENSMUST00000172518	ENSMUSG00000036315	17	36954356	36958559	-1	0	0	0	2	0	0	217	256	133	405	96		Q791N7
ENSMUST00000172519						0	4	1	0	2	1	0	0	0	0	0		
ENSMUST00000172520	ENSMUSG00000015120	17	25261916	25274622	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWJ1	
ENSMUST00000172521						0	0	0	0	0	0	0	0	4	4	13		
ENSMUST00000172523						24	44	62	209	47	16	1	6	5	0	4		
ENSMUST00000172524	ENSMUSG00000021952	14	57581002	57665430	-1	0	0	5	67	5	0	0	0	0	0	0	G3UX04	
ENSMUST00000172525	ENSMUSG00000033249	8	105269801	105275845	1	4	5	0	0	0	3	0	0	0	0	0	G3UYS8	
ENSMUST00000172527	ENSMUSG00000036036	17	37001163	37010635	1	0	0	0	2	0	0	0	0	0	0	0	G3UYK1	
ENSMUST00000172529	ENSMUSG00000015165	7	28808541	28822266	1	0	0	0	0	0	0	1504	1403	1257	221	999	G3UY38	
ENSMUST00000172530	ENSMUSG00000050994	10	10335703	10472326	-1	8	21	22	9	15	0	0	6	2	0	0		G3UZ78
ENSMUST00000172532	ENSMUSG00000042942	18	10325177	10562934	1	0	0	0	0	0	0	0	0	0	0	0	G3UYH8	
ENSMUST00000172533	ENSMUSG00000028479	4	44034075	44084177	-1	0	0	0	0	0	0	52	42	20	0	28	G3UYD5	
ENSMUST00000172534	ENSMUSG00000022905	16	35978750	36037131	1	3	3	4	2	0	0	29	0	0	0	13	G3UYD2	
ENSMUST00000172535						2	1	0	2	2	3	0	0	0	0	0		
ENSMUST00000172536	ENSMUSG00000007035	17	35028605	35046745	-1	0	0	0	0	8	0	0	10	0	0	47	G3UZB5	
ENSMUST00000172537	ENSMUSG00000027977	3	123526166	123690853	-1	2	0	0	0	5	0	0	0	0	0	0	E9PZJ4	
ENSMUST00000172538						3	0	2	37	3	2	55	171	48	27	77		
ENSMUST00000172539						13	24	50	56	10	8	0	4	1	3	3		
ENSMUST00000172540	ENSMUSG00000036036	17	37001163	37010635	1	0	0	0	2	0	0	0	0	0	0	0	G3UYC1	
ENSMUST00000172542	ENSMUSG00000031753	8	110846600	110882227	1	0	0	0	0	0	0	0	0	0	0	1	G3XA67	
ENSMUST00000172544						2	4	0	10	4	4	0	0	0	0	0		
ENSMUST00000172546						3	0	2	12	2	0	0	3	0	0	0		
ENSMUST00000172548	ENSMUSG00000046408	8	84001502	84004770	1	0	0	8	0	5	0	1	0	0	0	0	G3UZX3	
ENSMUST00000172549	ENSMUSG00000019432	17	35241746	35253707	1	6	0	0	0	0	0	17	41	18	0	103		Q9Z1N5
ENSMUST00000172550						0	0	0	0	5	1	0	4	1	0	2		
ENSMUST00000172551	ENSMUSG00000093871	7	22328794	22329717	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7G6	
ENSMUST00000172552	ENSMUSG00000020782	11	115824049	115855780	1	3	6	13	2	5	3	0	0	0	0	0	G3UXS2	
ENSMUST00000172553						0	2	4	3	3	0	0	0	0	1	4		
ENSMUST00000172554	ENSMUSG00000029736	6	43303674	43309554	-1	0	0	0	0	1	0	0	0	0	1	0	G3UWN1	
ENSMUST00000172555						17	19	26	26	21	14	0	2	1	0	0		
ENSMUST00000172556	ENSMUSG00000038056	5	25271798	25498783	-1	0	5	9	0	18	7	105	308	385	38	422	G3UY45	
ENSMUST00000172557	ENSMUSG00000022194	14	54892500	54898169	1	0	1	1	0	0	1	93	426	64	23	31	G3UWS5	
ENSMUST00000172558						8	0	3	2	5	0	3	21	7	0	25		
ENSMUST00000172559	ENSMUSG00000096719	7	47463806	47528862	-1	7	10	0	8	0	5	0	0	0	0	0	K4DID7	
ENSMUST00000172561						0	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000172563						3	3	8	0	0	0	0	0	0	0	0		
ENSMUST00000172564	ENSMUSG00000039607	9	116572746	117629913	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZJ9	
ENSMUST00000172565						4	0	8	8	6	7	0	0	0	0	0		
ENSMUST00000172566	ENSMUSG00000050751	8	124369049	124439658	-1	19	9	106	17	31	27	0	0	0	0	0	G3UX58	
ENSMUST00000172567	ENSMUSG00000025409	10	127281956	127289018	-1	1	0	0	16	0	0	0	0	0	3	0	G3UZJ8	
ENSMUST00000172568						0	0	0	0	2	0	0	18	0	0	0		
ENSMUST00000172569						1	0	8	2	0	3	10	14	22	3	39		
ENSMUST00000172570	ENSMUSG00000007029	17	35000987	35016322	1	2	1	16	1	3	3	0	0	0	0	0	G3UYW2	
ENSMUST00000172571	ENSMUSG00000024392	17	35135178	35147322	1	9	0	21	7	0	5	0	0	0	0	0	G3UYQ2	
ENSMUST00000172572	ENSMUSG00000092607	3	95129536	95134011	-1	1	4	3	0	5	2	128	284	95	349	80		
ENSMUST00000172573	ENSMUSG00000024446	17	36255645	36258069	-1	2	0	1	44	4	2	0	33	11	7	3	G3UWS0	
ENSMUST00000172574						4	31	221	6	0	0	1	2	5	0	11		
ENSMUST00000172576	ENSMUSG00000024448	17	36322858	36326155	-1	2	0	4	7	0	0	0	0	0	0	1	G3UWS8	
ENSMUST00000172577	ENSMUSG00000050373	2	164785823	164793816	1	0	0	0	0	0	0	26	25	4	0	0	G3UYL5	
ENSMUST00000172578	ENSMUSG00000092622	9	73101836	73104438	1	4	5	12	6	2	2	12	91	32	3	41	G3UXW5	
ENSMUST00000172579	ENSMUSG00000074832	13	66418114	66441118	-1	214	167	214	145	157	83	0	3	1	0	3	K7N769	
ENSMUST00000172580	ENSMUSG00000036036	17	37001163	37010635	1	0	0	0	0	0	0	0	0	0	0	0	G3UY05	
ENSMUST00000172581						4	1	3	42	4	0	0	0	0	0	0		
ENSMUST00000172582	ENSMUSG00000083947	17	37768607	37772789	1	3	5	0	0	10	3	0	0	0	0	0	Q7TRJ3	
ENSMUST00000172583						4	1	8	81	11	4	1	2	0	0	0		
ENSMUST00000172584						0	0	0	0	0	0	7	5	4	0	0		
ENSMUST00000172585	ENSMUSG00000029830	6	37983739	38046996	-1	0	1	0	0	3	0	0	0	0	0	0	G3UWK5	
ENSMUST00000172586						3	1	0	3	4	0	0	0	0	0	0		
ENSMUST00000172587	ENSMUSG00000015120	17	25261916	25274622	-1	0	0	4	25	0	0	0	0	0	1	0	Q8CFZ0	
ENSMUST00000172589						0	12	0	0	0	3	0	0	0	0	0		
ENSMUST00000172590	ENSMUSG00000028073	3	87747890	87824306	-1	0	0	0	0	0	0	0	0	0	2	0	G3UWZ1	
ENSMUST00000172592						3	3	4	1	5	3	0	0	4	0	0		
ENSMUST00000172593	ENSMUSG00000051860	3	30746293	30767174	1	7	0	4	0	10	2	0	0	0	0	0	G3UWL1	
ENSMUST00000172594	ENSMUSG00000019370	7	16915379	16924114	-1	1	2	0	0	8	5	136	316	67	114	122	G3UX57	
ENSMUST00000172595						0	0	1	32	2	0	0	0	0	0	5		
ENSMUST00000172596						0	0	0	0	0	0	3	0	0	0	5		
ENSMUST00000172597	ENSMUSG00000021519	13	66906968	66933088	-1	0	0	3	11	0	0	0	0	0	18	0	G3UWV0	
ENSMUST00000172598	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	3	0	24	49	35	9	33	G3UYK9	
ENSMUST00000172599						63	56	63	40	41	22	153	449	448	303	362		
ENSMUST00000172600						0	1	0	0	0	0	0	5	0	0	0		
ENSMUST00000172601	ENSMUSG00000030325	6	128778485	128789215	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYR0	
ENSMUST00000172602	ENSMUSG00000049811	11	23007531	23030788	1	7	4	0	41	3	7	0	0	0	0	5	B1AVK0	
ENSMUST00000172604						4	0	1	29	4	2	0	3	0	0	2		
ENSMUST00000172605	ENSMUSG00000003617	3	19957054	20009145	1	0	1	0	0	2	0	0	0	0	37	0	G3UZ53	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172606						4	1	4	4	6	0	1	2	3	1	0		
ENSMUST00000172607	ENSMUSG00000029767	6	29348069	29377110	1	4	2	1	0	0	0	17	10	12	0	27	G3UXA3	
ENSMUST00000172608						1	3	9	5	2	1	2	6	0	0	4		
ENSMUST00000172609						17	13	20	20	21	11	0	19	22	11	9		
ENSMUST00000172610						4	2	1	0	2	0	0	4	13	0	11		
ENSMUST00000172611	ENSMUSG00000020929	11	102838473	102880985	-1	0	0	0	0	1	1	0	5	0	2	0	G3UZ25	
ENSMUST00000172612	ENSMUSG00000040482	17	34837019	34839233	1	1	2	7	2	5	0	26	48	18	7	4	G3UWP7	
ENSMUST00000172613						2	3	14	2	4	2	372	252	611	10	277		
ENSMUST00000172614	ENSMUSG00000036990	8	79639618	79677724	1	30	20	73	20	17	10	5	4	23	4	37	G3UXQ0	
ENSMUST00000172615	ENSMUSG00000017428	11	80428615	80473248	1	0	0	6	0	0	3	0	0	0	0	0	G3UYL3	
ENSMUST00000172616	ENSMUSG00000028525	4	102087543	102607259	1	0	1	3	3	1	0	0	0	0	0	0	G3UZ46	
ENSMUST00000172618	ENSMUSG00000015120	17	25261916	25274622	-1	1	0	0	70	0	0	0	0	3	3	0		P63280
ENSMUST00000172619	ENSMUSG00000024308	17	33915899	33929288	1	1	0	0	24	2	0	3	0	5	0	5	G3UZZ2	
ENSMUST00000172620						21	14	50	46	49	27	0	4	4	0	10		
ENSMUST00000172621	ENSMUSG00000028073	3	87747890	87824306	-1	0	0	0	0	0	0	0	0	0	0	19		Q8VIK5
ENSMUST00000172622	ENSMUSG00000045751	4	24496451	24602950	1	0	0	0	0	0	0	0	0	0	0	0	G3UXE4	
ENSMUST00000172623						1	0	1	7	2	2	0	0	0	0	0		
ENSMUST00000172624						2	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000172625						1	7	11	2	5	3	0	0	0	0	0		
ENSMUST00000172626						19	9	39	61	18	11	0	0	1	0	17		
ENSMUST00000172627						0	0	0	31	0	2	0	0	0	0	0		
ENSMUST00000172628	ENSMUSG00000025316	8	121949750	122029258	1	0	0	0	0	3	0	0	0	0	0	0	G3UWM0	
ENSMUST00000172629						2	3	1	0	2	3	0	0	0	0	0		
ENSMUST00000172630	ENSMUSG00000030688	7	101317086	101346626	1	12	1	2	254	14	7	0	0	6	0	0	G3UYM0	
ENSMUST00000172631						6	17	56	24	18	0	0	11	0	0	19		
ENSMUST00000172632						0	6	5	3	4	1	0	0	0	0	0		
ENSMUST00000172633						44	28	67	61	54	29	107	528	119	454	177		
ENSMUST00000172634	ENSMUSG00000022159	14	52261759	52279545	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ24	
ENSMUST00000172635						3	0	6	2	7	7	4	25	15	0	16		
ENSMUST00000172636	ENSMUSG00000003662	2	127240938	127247816	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYS4	
ENSMUST00000172637						9	3	53	6	35	12	222	166	114	0	224		
ENSMUST00000172638	ENSMUSG00000029913	6	65778988	65937010	1	4	3	3	0	0	2	0	4	2	0	0	G3UWU3	
ENSMUST00000172639						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172640						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172641						77	132	131	111	85	32	5	11	5	6	11		
ENSMUST00000172642	ENSMUSG00000024436	17	35910379	35916389	-1	0	0	0	0	0	0	0	0	1	0	0	G3UYQ9	
ENSMUST00000172643						0	0	0	198	5	1	0	0	7	0	0		
ENSMUST00000172645	ENSMUSG00000028023	3	129199878	129219591	1	4	0	0	0	5	1	0	0	0	0	0	B1VD84	P97474
ENSMUST00000172646	ENSMUSG00000036972	9	91362413	91389348	1	0	0	14	0	0	0	0	0	0	0	0	G3UYE7	
ENSMUST00000172647						1	1	7	0	0	0	0	0	0	1	0		
ENSMUST00000172648						2	4	4	0	5	1	0	0	0	0	0		
ENSMUST00000172649	ENSMUSG00000042099	17	33810520	33822918	1	0	0	0	135	0	0	0	0	0	0	0	G3UXN4	
ENSMUST00000172650						0	1	11	9	4	0	0	0	0	1	0		
ENSMUST00000172651	ENSMUSG00000024406	17	35506018	35510772	1	0	0	0	0	0	0	0	0	0	0	0	E2JL30	
ENSMUST00000172652	ENSMUSG00000053046	7	141949751	142004247	1	5	3	15	17	0	6	0	0	0	0	0	G3UWV4	
ENSMUST00000172653						1	1	2	0	7	3	184	155	175	12	221		
ENSMUST00000172654	ENSMUSG00000019082	7	141429744	141437892	-1	0	0	0	0	0	0	2	0	0	0	0	V9GWS2	
ENSMUST00000172655						1	0	3	55	2	0	0	0	0	0	0		
ENSMUST00000172656						2	0	3	1	1	0	0	2	0	0	5		
ENSMUST00000172657						0	4	1	0	2	0	0	0	0	0	0		
ENSMUST00000172658						8158	7120	3086	118233	21237	2460	10	36	51	12	65		
ENSMUST00000172659						3	9	24	8	10	4	0	2	0	0	2		
ENSMUST00000172660						0	0	1	0	0	0	51	2	212	0	55		
ENSMUST00000172661	ENSMUSG00000038762	17	35956819	35969761	-1	2	4	7	49	4	1	0	1	8	2	6	G3UYI0	
ENSMUST00000172662	ENSMUSG00000030688	7	101317086	101346626	1	1	0	12	0	2	0	0	0	0	4	0	G3UYN6	
ENSMUST00000172663	ENSMUSG00000054128	17	36185572	36190287	-1	0	0	10	0	0	0	0	0	0	0	0	G3UZL7	
ENSMUST00000172665						2	0	0	16	0	0	0	8	12	0	0		
ENSMUST00000172666						7	3	3	5	9	2	3	14	5	2	2		
ENSMUST00000172667	ENSMUSG00000048502	14	25978577	25990088	1	11	0	0	0	0	5	0	0	0	0	0	Q3UY88	
ENSMUST00000172668	ENSMUSG00000031753	8	110846600	110882227	1	0	0	8	4	0	0	0	0	0	0	0	G3UYW8	
ENSMUST00000172669	ENSMUSG00000028073	3	87747890	87824306	-1	0	0	2	0	1	1	0	0	0	0	0	G3UZD5	
ENSMUST00000172670						15	3	18	38	19	8	0	6	2	1	3		
ENSMUST00000172672						13	11	139	14	10	4	0	0	3	1	0		
ENSMUST00000172674						1	0	0	0	0	0	0	0	10	0	4		
ENSMUST00000172675						1	2	5	0	3	2	0	0	0	0	0		
ENSMUST00000172676						36	42	31	25	34	33	0	2	5	0	3		
ENSMUST00000172677						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172678	ENSMUSG00000013766	17	35076902	35078804	1	0	0	0	1	0	0	0	0	0	0	0	Q9D7E5	
ENSMUST00000172679						4	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000172680	ENSMUSG00000042942	18	10325177	10562934	1	18	10	32	56	22	8	1	4	3	1	2	G3UZ23	
ENSMUST00000172681	ENSMUSG00000025316	8	121949750	122029258	1	0	0	0	0	0	0	0	0	3	0	4	G3UZ43	
ENSMUST00000172682	ENSMUSG00000031241	X	107667964	107688978	1	2	0	0	0	0	1	0	0	0	0	0	G3UXA1	
ENSMUST00000172683						5	5	13	4	3	3	0	0	2	0	0		
ENSMUST00000172685						4	0	5	5	8	11	11	3	0	0	18		
ENSMUST00000172686						0	5	0	0	5	1	0	0	0	0	0		
ENSMUST00000172687						6	3	1	6	0	1	1	3	2	1	8		
ENSMUST00000172688						35	22	18	59	28	18	0	0	0	0	0		
ENSMUST00000172689	ENSMUSG00000020661	12	3806007	3914443	1	17	29	274	54	17	10	28	27	48	0	47		O88508
ENSMUST00000172690	ENSMUSG00000004266	6	124720707	124738714	-1	0	0	0	0	0	0	2	1	1	1	2	G3UZU6	
ENSMUST00000172692						7	7	4	7	5	0	0	0	0	0	0		
ENSMUST00000172693	ENSMUSG00000024397	17	35170991	35176068	-1	1	2	0	0	0	0	0	98	17	604	9	Q4FJL9	O70200
ENSMUST00000172694	ENSMUSG00000027684	3	29951296	30548008	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ13	
ENSMUST00000172695	ENSMUSG00000022194	14	54892500	54898169	1	0	0	0	0	0	0	52	0	43	22	99	G3UX74	
ENSMUST00000172696	ENSMUSG00000037894	3	137864487	137866922	1	0	0	0	0	0	0	0	15	0	0	0	G3UX40	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172697	ENSMUSG00000027684	3	29951296	30548008	-1	13	6	11	30	0	5	0	0	0	0	0	G3UYK2	
ENSMUST00000172698						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000172699	ENSMUSG00000074480	3	88532395	88541396	1	54	47	253	506	77	28	2	11	8	7	33	G3UYU0	
ENSMUST00000172702	ENSMUSG00000032113	9	36708482	36727065	-1	32	0	47	122	29	9	0	6	0	6	13		O35280
ENSMUST00000172704	ENSMUSG00000078671	7	73426638	73541830	-1	4	2	1	2	2	0	2	0	3	0	0	G3UZG2	
ENSMUST00000172705	ENSMUSG00000002984	7	19701313	19715438	-1	2	1	9	5	2	0	0	2	0	0	0	G3UY77	
ENSMUST00000172706	ENSMUSG00000029381	5	92683435	92965318	1	5	0	5	2	0	6	0	0	0	0	0	G3UXH3	
ENSMUST00000172707						4	2	1	0	2	1	0	0	0	0	0		
ENSMUST00000172708						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172709						34	41	65	35	36	20	0	7	4	0	5		
ENSMUST00000172710	ENSMUSG00000029022	4	147860778	147868816	-1	0	0	12	0	0	0	0	0	0	0	0	C0KL25	A2A7Y5
ENSMUST00000172711	ENSMUSG00000073399	17	36881598	36890123	-1	11	0	9	6	0	7	0	0	0	0	0	B7ZWG4	
ENSMUST00000172712						6	5	0	1	2	0	0	0	0	0	0		
ENSMUST00000172713						2	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000172714	ENSMUSG00000020444	11	59183875	59192212	-1	0	1	0	1	1	0	0	0	0	0	0	G3UYV3	
ENSMUST00000172715	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYD0	
ENSMUST00000172716						1	1	0	2	4	0	0	0	1	0	0		
ENSMUST00000172717						11276	14489	34116	8586	9800	4476	74	284	163	22	139		
ENSMUST00000172718						4	0	19	2	1	0	0	2	0	0	0		
ENSMUST00000172719	ENSMUSG00000020661	12	3806007	3914443	1	0	0	0	0	0	0	0	0	0	0	0	G3UX07	
ENSMUST00000172722						0	1	0	0	0	0	0	0	0	1	1		
ENSMUST00000172723						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000172726						1	0	0	1	2	2	0	0	1	1	1		
ENSMUST00000172727	ENSMUSG00000021771	14	21831269	21845879	1	4	6	7	0	0	2	0	4	3	0	3	G3UX26	
ENSMUST00000172728						0	1	2	0	0	1	0	4	2	0	1		
ENSMUST00000172729						0	0	6	3	0	0	1	0	0	0	0		
ENSMUST00000172730						450	311	2938	646	285	133	62	343	86	25	118		
ENSMUST00000172731						2	1	3	3	1	2	0	2	0	0	0		
ENSMUST00000172732	ENSMUSG00000029191	5	65261850	65335670	-1	15	0	63	4	0	20	58	518	234	124	198	G3UZD0	
ENSMUST00000172733	ENSMUSG00000024083	17	64281005	64331916	-1	0	0	0	0	0	0	134	279	155	152	49		Q80U04
ENSMUST00000172734	ENSMUSG00000053644	18	56509687	56572951	-1	0	0	0	41	10	7	0	0	0	0	0	G3UYR8	
ENSMUST00000172735						2	3	7	0	8	0	0	0	0	1	3		
ENSMUST00000172736	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	0	0	0	0	0	0	0	0	G3UZS9	
ENSMUST00000172737	ENSMUSG00000037627	15	36009479	36140400	-1	0	0	0	0	0	0	0	0	0	0	0	G3UX14	
ENSMUST00000172738	ENSMUSG00000022216	14	55578123	55581529	1	0	0	0	0	0	0	228	545	310	320	205	G3UXY0	
ENSMUST00000172739						0	1	2	108	2	5	0	1	0	0	0		
ENSMUST00000172740						0	0	17	28	15	0	10	12	25	15	19		
ENSMUST00000172741						0	0	1	0	0	0	0	0	0	1	0		
ENSMUST00000172742	ENSMUSG00000032113	9	36708482	36727065	-1	2	0	0	26	1	0	0	2	0	0	3	G3UX84	
ENSMUST00000172743	ENSMUSG00000091045	7	12651706	12684991	-1	0	10	64	15	32	9	0	0	0	0	0	G3UWZ4	
ENSMUST00000172744						0	1	0	8	1	0	0	26	22	3	12		
ENSMUST00000172745						1	3	1	2	5	0	0	0	0	0	0		
ENSMUST00000172746						140	124	323	147	154	64	2	6	2	0	0		
ENSMUST00000172747	ENSMUSG00000028744	4	139294029	139310708	-1	0	0	0	0	0	0	54	0	0	0	14		Q8C4N4
ENSMUST00000172748	ENSMUSG00000022394	15	81663889	81688315	1	0	8	0	0	0	0	0	0	0	12	56	Q80XB1	
ENSMUST00000172749	ENSMUSG00000020661	12	3806007	3914443	1	0	0	0	0	0	0	0	0	0	0	0	G3UZN5	
ENSMUST00000172750	ENSMUSG00000035561	4	45799022	45804604	1	0	0	2	0	0	2	0	3	1	0	3	G3UYH1	
ENSMUST00000172752						4	5	3	1	10	6	0	0	0	0	0		
ENSMUST00000172753	ENSMUSG00000090877	17	34956436	34959238	-1	25	17	35	1515	57	19	23	84	55	11	102		P17879
ENSMUST00000172754	ENSMUSG00000027684	3	29951296	30548008	-1	15	8	14	13	17	4	0	0	0	0	0	G3UYN3	
ENSMUST00000172755						3	5	2	11	0	0	15	88	15	0	37		
ENSMUST00000172756	ENSMUSG00000015002	15	65787034	65873816	1	5	3	6	2	5	1	0	0	2	0	0	Q8BWC5	
ENSMUST00000172757						7	0	0	21	3	0	6	114	25	0	32		
ENSMUST00000172758	ENSMUSG00000041578	7	15865947	15879968	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZE2	
ENSMUST00000172759						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172761	ENSMUSG00000002409	7	28179469	28187294	1	0	11	16	0	4	12	170	64	165	0	102		Q9Z188
ENSMUST00000172762						3	7	3	10	5	7	2	33	6	13	19		
ENSMUST00000172763						0	0	0	0	0	0	292	1626	527	50	747		
ENSMUST00000172764	ENSMUSG00000041769	7	138846079	138883057	1	0	0	0	0	0	0	0	0	0	0	4	G3UXS9	
ENSMUST00000172765	ENSMUSG00000024387	17	35116196	35122053	-1	4	3	4	5	1	2	8	18	21	10	22	G3UZJ5	
ENSMUST00000172766						15	7	30	3	16	5	0	0	0	0	0		
ENSMUST00000172767	ENSMUSG00000079557	17	33685692	33718670	-1	6	7	9	12	26	2	1011	1281	602	534	448		Q99M02
ENSMUST00000172768	ENSMUSG00000028382	4	59471868	59549364	-1	2	2	0	29	8	0	0	0	0	0	0		Q8BHD7
ENSMUST00000172769						2	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000172770						3	3	16	10	16	6	0	0	5	0	4		
ENSMUST00000172771	ENSMUSG00000062563	12	24665838	24681813	-1	2	2	19	11	3	0	0	0	1	0	0	G3UZZ7	
ENSMUST00000172772	ENSMUSG00000009293	10	77622275	77645993	1	1	0	9	0	0	0	2	3	1	0	0	G3UZ92	
ENSMUST00000172773	ENSMUSG00000017428	11	80428615	80473248	1	0	0	0	0	0	0	0	0	0	0	0	G3UYI4	
ENSMUST00000172774	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	18	11	13	4	23	D6RDC0	
ENSMUST00000172775	ENSMUSG00000025469	7	140046157	140049089	-1	6	0	0	0	0	0	0	0	0	0	0	B2RPS3	P70354
ENSMUST00000172776						30	18	21	16	20	8	4	22	18	4	14		
ENSMUST00000172777						0	0	0	0	0	0	44	65	5	0	0		
ENSMUST00000172778						1	5	5	3	1	0	0	3	0	0	0		
ENSMUST00000172779	ENSMUSG00000047230	X	139800828	139811386	1	0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000172780						9	0	0	0	0	0	40	37	0	0	0		
ENSMUST00000172781	ENSMUSG00000038943	7	80294450	80316259	1	4	2	32	6	5	0	0	3	3	0	2	G3UXB1	
ENSMUST00000172782						11	6	24	252	28	19	90	186	121	14	224		
ENSMUST00000172783	ENSMUSG00000021281	12	111442469	111455018	1	0	0	0	0	0	1	398	12	495	0	289	G3UXC6	
ENSMUST00000172784	ENSMUSG00000070469	7	82335694	82614450	1	0	3	0	0	2	0	0	0	0	0	1	G3UYN1	
ENSMUST00000172785	ENSMUSG00000073411	17	35262730	35267499	1	12	18	45	308	23	14	23957	40277	17167	3294	18503	Q792Z7	P01899
ENSMUST00000172786						6	8	10	4	18	7	0	0	0	0	0		
ENSMUST00000172787	ENSMUSG00000025495	7	141122382	141157021	1	0	0	7	0	0	0	0	0	0	0	0	G3UWN0	
ENSMUST00000172788	ENSMUSG00000030549	7	79593363	79617657	-1	0	0	0	0	5	0	0	0	0	0	1	G3UYU7	
ENSMUST00000172789	ENSMUSG00000024462	17	37045966	37075067	1	5	9	9	78	9	6	16	28	11	0	19	Q3TWR2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172790						2	2	4	79	1	3	0	20	7	0	18		
ENSMUST00000172791	ENSMUSG00000026768	2	12106632	12301922	-1	0	0	0	10	4	0	0	0	1	0	0	G3UYN5	
ENSMUST00000172792	ENSMUSG00000024462	17	37045966	37075067	1	20	12	95	90	17	8	16	83	50	0	50		Q9WV18
ENSMUST00000172794	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	0	0	0	53	0	284	0	21	G3UYG6	
ENSMUST00000172795	ENSMUSG00000026456	1	134405559	134411740	1	3	0	0	0	0	3	15	29	51	3	60	G3UXV8	
ENSMUST00000172797						1	0	0	0	0	0	0	8	0	1	4		
ENSMUST00000172798						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000172799						143	141	382	72	119	38	17	74	41	22	44		
ENSMUST00000172800						4	2	8	5	0	2	153	117	157	408	72		
ENSMUST00000172802						2	3	2	9	2	1	0	0	0	0	0		
ENSMUST00000172803						0	3	0	4	7	3	3	25	10	11	0		
ENSMUST00000172804						0	0	0	2	2	1	0	16	10	4	4		
ENSMUST00000172805						2	1	7	27	8	4	10	13	13	3	17		
ENSMUST00000172806	ENSMUSG00000020140	10	115450311	115587780	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXX4	
ENSMUST00000172807						588	591	538	265	315	167	4	15	7	2	16		
ENSMUST00000172808	ENSMUSG00000002985	7	19696109	19699166	-1	0	0	0	0	2	0	40	0	0	0	0	G3UZM8	
ENSMUST00000172809	ENSMUSG00000025156	11	120784272	120789102	1	0	0	0	58	10	0	0	20	0	20	0	G3UXW9	
ENSMUST00000172810	ENSMUSG00000035469	14	59201209	59237265	1	1	0	4	0	4	0	0	0	0	3	0	G3UYZ5	
ENSMUST00000172811	ENSMUSG00000028399	4	75941238	78211961	-1	2	0	0	0	1	0	0	0	1	0	0	G3UYR6	
ENSMUST00000172813	ENSMUSG00000009293	10	77622275	77645993	1	0	0	0	21	2	0	18	14	0	0	0	G3UZX2	
ENSMUST00000172814	ENSMUSG00000092322	17	38416474	38420185	-1	1	1	0	2	0	0	0	0	0	0	0	G3UZD8	
ENSMUST00000172815	ENSMUSG00000092216	7	19852003	19858355	1	3	6	7	53	12	7	3	30	18	5	24	G3UYD9	
ENSMUST00000172816	ENSMUSG00000020661	12	3806007	3914443	1	0	2	5	7	3	1	0	0	1	0	0	G3UZU0	
ENSMUST00000172818	ENSMUSG00000024083	17	64281005	64331916	-1	0	22	22	37	0	12	84	222	276	267	280		Q80U04
ENSMUST00000172820	ENSMUSG00000001666	10	75771230	75773414	-1	6	0	5	7	4	2	0	8	0	0	0	G3UZN1	
ENSMUST00000172821	ENSMUSG00000006270	19	59166187	59170056	-1	3	5	9	102	5	5	0	0	0	0	0		Q2NKI2
ENSMUST00000172822						4	4	7	2	5	0	1	0	0	0	0		
ENSMUST00000172823	ENSMUSG00000036315	17	36954356	36958559	-1	1	0	0	0	0	0	6	0	0	0	0	G3UXD3	
ENSMUST00000172824						0	1	2	0	2	0	0	0	0	0	1		
ENSMUST00000172825						3	4	7	3	6	3	0	0	0	0	0		
ENSMUST00000172826	ENSMUSG00000051980	16	36493696	36562141	-1	21	0	38	21	21	0	0	0	0	0	0		Q9QY96
ENSMUST00000172827	ENSMUSG00000020173	11	12236608	12464960	-1	0	0	4	0	0	0	0	0	0	0	0	G3UWP1	
ENSMUST00000172828	ENSMUSG00000032423	9	88447009	88482574	-1	0	0	0	13	0	0	81	304	241	86	156	G3UXU5	
ENSMUST00000172829						1	1	2	0	0	0	0	3	1	1	3		
ENSMUST00000172830	ENSMUSG00000038518	13	44729474	44921643	1	1	4	7	79	1	1	0	0	3	0	3	G3UXE0	
ENSMUST00000172831	ENSMUSG00000037627	15	36009479	36140400	-1	15	24	0	35	28	8	0	0	0	0	0		G3UYX5
ENSMUST00000172832						26	19	27	302	41	15	59	224	113	6	119		
ENSMUST00000172833	ENSMUSG00000033335	9	21424908	21507759	1	1	0	0	0	2	1	0	15	13	0	15	G3UXX2	
ENSMUST00000172834	ENSMUSG00000062352	12	21240825	21286237	-1	0	0	5	11	3	3	157	620	234	782	152	Q3UGH2	
ENSMUST00000172835	ENSMUSG00000108585	7	18926080	18958618	1	0	0	0	0	0	0	1	0	0	0	0	G3UYX3	
ENSMUST00000172836	ENSMUSG00000028960	4	149328416	149426749	-1	16	9	0	2	0	0	6	0	235	0	96	G3UZD6	
ENSMUST00000172837	ENSMUSG00000020697	11	82781108	82804274	1	1	0	0	0	0	0	5	14	0	14	0	G3UYI8	
ENSMUST00000172841						3	4	9	6	6	1	4	41	20	2	23		
ENSMUST00000172843	ENSMUSG00000057443	17	38261067	38275711	1	0	0	0	0	0	0	0	0	0	0	0	Q7TRI7	
ENSMUST00000172844	ENSMUSG00000089682	14	54883377	54888234	1	0	0	0	0	0	0	0	0	0	0	0	G3XA70	
ENSMUST00000172845						0	3	4	2	0	0	0	0	0	0	0		
ENSMUST00000172846	ENSMUSG00000059714	17	35823230	35832791	1	7	5	4	26	5	9	43	92	86	6	28	G3UZZ5	
ENSMUST00000172847	ENSMUSG00000017428	11	80428615	80473248	1	0	0	0	0	0	0	0	0	2	41	0	G3UYL8	
ENSMUST00000172848						5	6	3	4	8	0	0	0	0	0	0		
ENSMUST00000172849						0	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000172850	ENSMUSG00000020940	11	103198944	103208558	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPM6	
ENSMUST00000172851						11	10	20	16	9	6	0	0	0	0	0		
ENSMUST00000172852	ENSMUSG00000046782	12	57564113	57737928	1	1	0	0	3	1	0	0	0	0	0	0	G3UWJ3	
ENSMUST00000172853						2	5	9	1	2	2	0	0	0	0	0		
ENSMUST00000172854	ENSMUSG00000043807	17	35113948	35115428	-1	4	11	19	21	10	0	0	41	12	3	14		Q8K1T4
ENSMUST00000172855	ENSMUSG00000024151	17	87672330	87723713	1	0	0	0	15	0	0	0	0	0	0	0	G3UXD8	
ENSMUST00000172856	ENSMUSG00000033545	8	111536097	111626030	1	7	0	0	371	10	8	87	148	97	7	118		Q91V17
ENSMUST00000172858						5	3	14	173	6	6	0	0	0	0	0		
ENSMUST00000172859						0	2	15	1	2	0	0	12	0	0	30		
ENSMUST00000172860	ENSMUSG00000003617	3	19957054	20009145	1	0	0	0	0	0	0	0	0	0	56	5	G3UWP5	
ENSMUST00000172861						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172862						5	0	0	1	4	0	0	0	0	0	0		
ENSMUST00000172863	ENSMUSG00000096513	7	21760531	21761475	-1	0	0	0	0	0	0	0	0	0	0	0	D3YTW8	
ENSMUST00000172864	ENSMUSG00000040606	4	142102390	142239401	-1	0	0	0	0	0	0	0	0	0	0	0	G3UY74	
ENSMUST00000172866	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	0	0	3	G3UYK4	
ENSMUST00000172868	ENSMUSG00000015120	17	25261916	25274622	-1	20	16	41	33	31	6	130	409	291	39	504	Q8CFZ0	
ENSMUST00000172869						2	2	5	147	24	5	3	13	3	7	4		
ENSMUST00000172870						1	2	0	24	0	0	0	0	0	0	0		
ENSMUST00000172871	ENSMUSG00000064120	17	49428362	49455435	1	0	0	1	0	0	0	0	0	0	0	0	G3UZD4	
ENSMUST00000172873						4	0	14	0	1	1	1	0	1	0	2		
ENSMUST00000172875	ENSMUSG00000035021	12	54892989	55014348	-1	0	0	1	0	0	0	0	0	0	0	4	G3UZ82	
ENSMUST00000172877						1	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000172878						5	1	7	7	7	0	11	49	9	0	42		
ENSMUST00000172879	ENSMUSG00000020661	12	3806007	3914443	1	33	18	74	24	42	15	0	1	0	0	2	G3UZY8	
ENSMUST00000172881	ENSMUSG00000054310	7	15388948	15556866	1	4	3	53	0	7	4	0	0	1	0	0	Q9D350	
ENSMUST00000172882						0	2	17	5	2	0	2	26	4	2	5		
ENSMUST00000172883	ENSMUSG00000030188	6	131284388	131293244	-1	0	0	0	0	0	0	3	2	1	4	0	G3UX51	
ENSMUST00000172884	ENSMUSG00000015165	7	28808541	28822266	1	0	0	0	0	2	0	0	0	3	0	0	G3UYY3	
ENSMUST00000172885						0	1	3	0	0	0	1	2	0	2	0		
ENSMUST00000172886	ENSMUSG00000015222	1	66175273	66442583	1	0	0	0	0	0	0	0	0	0	0	0	G3UWW1	
ENSMUST00000172887	ENSMUSG00000079298	6	128813706	128826331	-1	0	0	6	3	6	0	3	2	0	14	2	G3UZU5	
ENSMUST00000172888						6	0	6	65	4	3	2	14	7	3	7		
ENSMUST00000172889						1	1	23	4	3	4	0	4	0	0	5		
ENSMUST00000172890						0	0	0	0	0	0	11	0	1	6	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172892						1	1	0	2	2	3	2	7	3	2	8		
ENSMUST00000172893						104	129	413	116	120	49	0	9	6	2	4		
ENSMUST00000172894	ENSMUSG00000077450	17	33742484	33760530	-1	4	2	0	0	0	3	55	35	149	78	278	G3UZL4	
ENSMUST00000172895						0	0	0	0	2	0	23	7	13	4	26		
ENSMUST00000172897	ENSMUSG00000031753	8	110846600	110882227	1	0	0	0	0	0	0	6	0	0	0	0	G3UX78	
ENSMUST00000172898	ENSMUSG00000046367	1	134540941	134549682	-1	5	3	5	14	5	0	0	1	0	0	0		A6H684
ENSMUST00000172899						0	0	2	2	0	0	7	62	11	6	21		
ENSMUST00000172900	ENSMUSG00000038500	17	35972541	35980236	-1	0	0	0	4	0	0	1	0	0	0	0	E9Q601	
ENSMUST00000172901	ENSMUSG00000027347	2	117279993	117343001	-1	2	0	0	0	0	0	1	0	0	0	0	G3UWW4	
ENSMUST00000172902						10	4	3	5	4	1	0	0	0	0	0		
ENSMUST00000172903						0	5	6	2	2	0	0	0	0	0	0		
ENSMUST00000172904						0	0	30	8	0	9	91	214	14	33	70		
ENSMUST00000172906	ENSMUSG00000035569	8	122883337	122974793	-1	40	0	224	46	34	0	590	329	1822	51	1561	G3UY79	
ENSMUST00000172907	ENSMUSG00000040929	19	27761721	28011166	-1	0	0	0	4	0	0	0	7	0	0	12		P48381
ENSMUST00000172908	ENSMUSG00000042719	5	121397936	121444378	1	1	2	10	0	4	0	1	27	2	0	0	G3UZ51	
ENSMUST00000172909	ENSMUSG00000030126	6	116018611	116193486	-1	0	0	10	0	0	0	10	42	24	25	25	G3UZ99	
ENSMUST00000172911						8	6	9	14	13	4	0	3	7	2	0		
ENSMUST00000172912	ENSMUSG00000061232	17	33996017	34000333	-1	0	0	0	0	0	0	463	438	304	50	81	Q3TH01	
ENSMUST00000172913	ENSMUSG00000020661	12	3806007	3914443	1	0	0	0	0	0	2	0	0	0	0	0	G3UZH2	
ENSMUST00000172914						8	3	8	22	4	0	403	310	207	104	211		
ENSMUST00000172915						36	28	15	25	33	24	0	17	0	0	0		
ENSMUST00000172916						0	0	9	37	5	0	0	0	0	0	3		
ENSMUST00000172917	ENSMUSG00000063646	5	37028335	37148001	1	3	0	12	16	5	2	0	0	0	2	0	G3UY22	
ENSMUST00000172918						4	2	5	2	2	0	0	0	0	0	0		
ENSMUST00000172919	ENSMUSG00000020173	11	12236608	12464960	-1	7	0	9	2	0	0	0	0	0	1	0		Q5NBX1
ENSMUST00000172921	ENSMUSG00000013787	17	34898469	34914052	1	2	5	2	0	2	0	0	0	0	0	0	G3UYH7	
ENSMUST00000172922	ENSMUSG00000024299	17	33524204	33553782	1	0	0	2	0	0	0	29	0	0	4	0	G3UY03	
ENSMUST00000172923	ENSMUSG00000067438	5	35389108	35399730	1	0	0	0	16	0	0	0	0	0	0	0	A0A087WPM8	
ENSMUST00000172924						0	1	2	30	1	4	0	0	2	0	2		
ENSMUST00000172925						9	2	34	7	8	5	0	9	9	0	13		
ENSMUST00000172926	ENSMUSG00000003452	6	149408886	149563329	1	0	0	0	0	0	0	0	0	1	0	0	G3UY88	
ENSMUST00000172927	ENSMUSG00000043940	5	101832956	102069921	-1	0	0	0	0	7	0	0	0	0	0	10	G3UY81	
ENSMUST00000172928	ENSMUSG00000037025	2	148042877	148046969	-1	1	4	47	142	0	3	0	0	0	0	0	G3UYH0	
ENSMUST00000172929						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172930						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172931	ENSMUSG00000059791	17	35861318	35865402	1	0	0	9	0	0	3	0	0	0	2	0	G3UZN7	
ENSMUST00000172932						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000172933	ENSMUSG00000043312	17	38081970	38088693	-1	0	3	0	0	0	0	0	0	0	0	0	Q8VGC8	
ENSMUST00000172934	ENSMUSG00000079557	17	33685692	33718670	-1	0	0	0	12	0	0	0	0	0	0	0	G3UYC2	
ENSMUST00000172936	ENSMUSG00000042632	15	79286228	79328390	-1	3	4	6	3	3	1	0	0	0	0	0	G3UX73	
ENSMUST00000172937						11	7	13	9	19	4	0	0	0	0	0		
ENSMUST00000172938	ENSMUSG00000057836	X	73086293	73097095	-1	0	0	0	2	0	0	1	0	0	0	0	G3UZV3	
ENSMUST00000172939	ENSMUSG00000046782	12	57564113	57737928	1	25	13	10	9	12	11	0	0	0	0	0	G3UYY4	
ENSMUST00000172940						2	0	3	61	5	6	0	0	0	0	0		
ENSMUST00000172941						0	0	0	26	0	0	0	25	19	0	23		
ENSMUST00000172942	ENSMUSG00000068921	3	88920803	88951181	-1	0	0	0	0	1	1	0	0	0	6	8	G3UYM6	
ENSMUST00000172943						3	1	9	0	5	0	0	0	0	0	0		
ENSMUST00000172945						2	6	8	148	6	7	0	0	2	0	0		
ENSMUST00000172946						14	10	35	27	10	4	23	34	60	1	50		
ENSMUST00000172947	ENSMUSG00000030994	7	134265779	134385661	-1	0	0	15	0	0	12	0	0	0	0	0	G3UZF7	
ENSMUST00000172948						4	4	1	0	1	1	0	0	0	0	0		
ENSMUST00000172949						0	4	4	20	4	3	0	0	4	0	0		
ENSMUST00000172950						0	0	0	3	0	0	0	0	2	0	0		
ENSMUST00000172951	ENSMUSG00000056755	6	110645581	111567230	1	15	9	3	7	10	3	0	0	0	0	0		Q68ED2
ENSMUST00000172953						2	2	6	7	6	0	0	0	0	0	0		
ENSMUST00000172954						6	3	2	5	5	4	1	9	6	0	10		
ENSMUST00000172955						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172956	ENSMUSG00000020173	11	12236608	12464960	-1	7	0	0	0	0	0	0	0	0	0	2	G3UZ73	
ENSMUST00000172957						2	1	6	0	0	0	0	0	0	0	0		
ENSMUST00000172958	ENSMUSG00000092534	7	127001480	127016484	-1	0	0	0	0	0	0	216	42	23	2	8	F6V0H0	
ENSMUST00000172959	ENSMUSG00000013766	17	35076902	35078804	1	0	1	0	0	0	0	0	0	0	0	0	Q8K1T6	
ENSMUST00000172960						13	11	16	52	17	8	29	254	49	14	95		
ENSMUST00000172961						1	4	7	120	0	1	0	0	0	0	0		
ENSMUST00000172962						7	0	3	3	6	5	0	0	0	0	1		
ENSMUST00000172963						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172964	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	0	0	0	20	0	0	0	152	G3UWR2	
ENSMUST00000172965	ENSMUSG00000059319	7	86583903	86586206	1	0	0	9	0	0	0	0	0	0	0	0	Q7TS08	
ENSMUST00000172966	ENSMUSG00000040356	17	34839228	34850210	-1	3	0	0	0	0	0	0	3	0	0	0	G3UZ05	
ENSMUST00000172967	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	0	0	0	0	0	0	0	0	G3UXM5	
ENSMUST00000172968	ENSMUSG00000092243	17	36109719	36129425	-1	0	0	0	0	0	0	0	4	0	0	0	Q0WXH6	
ENSMUST00000172969						10	4	0	5	3	6	0	0	0	0	0		
ENSMUST00000172970						15	9	18	16	17	10	0	0	0	0	1		
ENSMUST00000172971	ENSMUSG00000025229	19	46135685	46148326	-1	3	0	0	4	0	1	0	0	0	0	0	G3UZN3	
ENSMUST00000172973	ENSMUSG00000034898	9	79815051	79977804	-1	5	2	12	1	7	4	0	0	0	0	2	G3UZB6	
ENSMUST00000172974	ENSMUSG00000029767	6	29348069	29377110	1	0	0	0	0	0	0	0	0	0	0	0	G3UWR0	
ENSMUST00000172975	ENSMUSG00000024955	19	6910977	6921813	-1	3	0	4	3	2	3	7	5	14	0	8	G3UY24	
ENSMUST00000172976						4	1	3	4	8	0	0	4	0	1	3		
ENSMUST00000172977	ENSMUSG00000038518	13	44729474	44921643	1	0	0	0	0	0	0	0	0	16	0	0	G3UYY7	
ENSMUST00000172978						1	1	4	5	3	6	0	0	0	0	0		
ENSMUST00000172979	ENSMUSG00000055413	17	35394126	35397800	1	7	4	7	0	12	5	149	219	106	26	204		
ENSMUST00000172980						2	0	13	70	2	3	0	0	0	0	0		
ENSMUST00000172981	ENSMUSG00000046768	12	75308322	75401456	1	0	0	0	1	0	0	0	0	0	0	2	G3UZM2	
ENSMUST00000172982						0	0	0	1	1	3	2	0	5	7	0		
ENSMUST00000172983	ENSMUSG00000002985	7	19696109	19699166	-1	1	0	9	39	0	2	12	59	25	0	50	G3UWN5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000172984						0	0	0	2	3	0	0	0	0	0	0		
ENSMUST00000172985						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000172987						26	25	41	22	23	15	0	4	6	0	10		
ENSMUST00000172988	ENSMUSG00000051504	7	55768178	55778925	1	0	0	0	0	3	0	1	0	0	0	0	G3UYB4	
ENSMUST00000172989	ENSMUSG00000095745	7	20333142	20334065	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7G6	
ENSMUST00000172990						0	5	11	36	7	2	0	0	0	0	0		
ENSMUST00000172991						17	11	3	12	14	3	0	1	2	1	2		
ENSMUST00000172992	ENSMUSG00000021057	12	76324891	76334153	1	9	1	2	62	4	0	0	0	0	0	0	H3BIV5	
ENSMUST00000172993	ENSMUSG00000024392	17	35135178	35147322	1	3	0	0	0	0	0	8	116	13	6	5	S4R224	
ENSMUST00000172994						15	18	56	215	30	16	5	46	4	0	22		
ENSMUST00000172996	ENSMUSG00000032187	9	21616169	21704230	1	5	0	5	35	13	6	77	48	221	0	100	G3UX35	
ENSMUST00000172997	ENSMUSG00000029546	5	139543494	139548179	1	0	12	0	230	12	6	0	0	0	0	0	G3UYF8	O08934
ENSMUST00000172998						24	10	42	293	15	14	0	0	1	0	0		
ENSMUST00000172999						2	3	6	1	4	4	0	0	4	0	5		
ENSMUST00000173001	ENSMUSG00000056755	6	110645581	111567230	1	0	0	0	0	0	2	0	0	0	0	0	G3UYV0	
ENSMUST00000173002	ENSMUSG00000046491	11	43474276	43491525	1	13	6	24	22	14	0	0	1	0	1	0	G3V001	
ENSMUST00000173003	ENSMUSG00000038518	13	44729474	44921643	1	1	0	0	0	0	0	0	0	13	0	0	G3UZ12	
ENSMUST00000173004	ENSMUSG00000007050	17	34981862	34985891	1	0	0	0	0	0	0	0	0	2	0	0	G3UZ96	
ENSMUST00000173005						2	2	9	6	0	0	15	0	7	1	4		
ENSMUST00000173006	ENSMUSG00000031442	8	12873806	13020905	1	0	0	0	0	1	0	0	0	15	0	30	G3UYM8	
ENSMUST00000173008						5	7	6	0	0	2	1	1	3	0	0		
ENSMUST00000173009	ENSMUSG00000020697	11	82781108	82804274	1	6	1	0	0	1	0	0	2	0	0	0	Q3TJN5	
ENSMUST00000173010	ENSMUSG00000027104	2	73816509	73892639	-1	0	0	0	0	0	0	0	183	200	106	149	G3UXC3	
ENSMUST00000173011	ENSMUSG00000032422	9	88376750	88438958	-1	0	2	4	0	0	6	0	0	0	0	0	G3UX13	
ENSMUST00000173012						61	46	137	44	93	50	0	0	4	0	0		
ENSMUST00000173013	ENSMUSG00000024299	17	33524204	33553782	1	17	0	16	0	20	0	73	0	112	0	94	G3UZ08	
ENSMUST00000173014	ENSMUSG00000075707	12	110279068	110281097	1	7	10	7	234	3	7	0	0	0	0	0		Q91ZI8
ENSMUST00000173015	ENSMUSG00000079557	17	33685692	33718670	-1	0	0	0	0	0	0	194	82	109	127	128	G3UXS1	
ENSMUST00000173016						0	0	0	0	0	0	1	30	0	0	9		
ENSMUST00000173017						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173018	ENSMUSG00000037627	15	36009479	36140400	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXI4	
ENSMUST00000173019	ENSMUSG00000067288	17	33819027	33824562	-1	7	0	2	5	2	0	3	0	4	4	20	Q059I1	P62858
ENSMUST00000173020						4	5	4	1	1	2	0	0	0	0	0		
ENSMUST00000173021	ENSMUSG00000068921	3	88920803	88951181	-1	0	0	0	0	0	0	0	0	0	4	5	G3UWJ4	
ENSMUST00000173022						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173023	ENSMUSG00000037860	1	173350879	173466040	1	0	0	0	3	0	0	23	93	65	57	48	G3UZ36	
ENSMUST00000173024						31	20	173	48	41	19	0	0	2	0	2		
ENSMUST00000173026						20	0	22	11	8	11	0	0	0	0	0		
ENSMUST00000173027						16	5	0	0	0	7	0	0	0	0	0		
ENSMUST00000173028	ENSMUSG00000002307	17	33909414	33915589	1	0	0	0	8	0	2	4	0	5	0	0	G3UWJ9	
ENSMUST00000173029						1	4	6	2	0	1	0	0	0	0	0		
ENSMUST00000173030	ENSMUSG00000024299	17	33524204	33553782	1	0	0	1	0	0	0	13	0	0	14	7	G3UZ08	
ENSMUST00000173031	ENSMUSG00000030126	6	116018611	116193486	-1	7	9	9	7	11	3	36	74	43	43	45	Q3TQU9	
ENSMUST00000173032	ENSMUSG00000024335	17	34112023	34122634	-1	0	0	0	0	0	0	0	0	0	0	9	G3UZR9	
ENSMUST00000173033	ENSMUSG00000064120	17	49428362	49455435	1	21	41	207	50	40	27	893	1429	901	48	671		Q5RKZ7
ENSMUST00000173034						0	3	0	1	0	2	0	131	0	14	0		
ENSMUST00000173035						0	2	2	3	1	0	0	3	0	1	0		
ENSMUST00000173036						6	4	0	7	2	3	0	0	0	0	0		
ENSMUST00000173037						11	13	6	5	0	0	5	64	0	0	6		
ENSMUST00000173038						11	6	6	2	11	5	0	0	0	0	0		
ENSMUST00000173039	ENSMUSG00000032422	9	88376750	88438958	-1	0	0	4	61	9	0	0	0	0	123	76	G3UXB6	
ENSMUST00000173040	ENSMUSG00000023852	17	15704967	17394898	1	2	0	0	2	0	0	0	26	40	0	33	G3UWS6	
ENSMUST00000173041	ENSMUSG00000067786	2	157560078	157562522	1	0	0	0	0	0	0	0	0	0	0	0	G3UYJ4	
ENSMUST00000173042	ENSMUSG00000043259	10	70440668	70558731	1	7	0	0	24	7	0	0	0	0	0	0	Q8BLV7	
ENSMUST00000173043	ENSMUSG00000092417	17	35121455	35124814	1	4	0	2	0	0	4	81	88	63	28	63	H3BL77	
ENSMUST00000173044						1	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000173045						9	11	25	15	14	6	0	0	0	0	0		
ENSMUST00000173046						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173047						10	4	20	33	12	5	1	0	0	0	0		
ENSMUST00000173048						2	3	4	2	1	1	1	0	0	0	1		
ENSMUST00000173050	ENSMUSG00000026077	1	39193731	39363236	1	2	0	0	29	1	1	0	0	0	0	0	G3UYV8	
ENSMUST00000173051						2	0	5	2	6	2	0	1	1	0	0		
ENSMUST00000173053	ENSMUSG00000074366	7	15750131	15759800	1	0	1	23	2	1	0	0	0	0	0	0	G3UZS7	
ENSMUST00000173054	ENSMUSG00000036972	9	91362413	91389348	1	0	0	0	0	0	0	0	0	0	0	0	G3UZ66	
ENSMUST00000173055	ENSMUSG00000092244	17	38554192	38560621	1	2	2	2	4	2	4	0	0	0	0	0	G3UXG0	
ENSMUST00000173057	ENSMUSG00000073418	17	34728380	34743882	-1	5	4	4	0	2	0	0	0	2	0	7	G3UZS2	
ENSMUST00000173058	ENSMUSG00000028033	1	21398403	21961942	-1	0	0	0	0	0	0	0	0	1	1	0	G3UYP4	
ENSMUST00000173059	ENSMUSG00000027684	3	29951296	30548008	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWJ0	
ENSMUST00000173060	ENSMUSG00000017428	11	80428615	80473248	1	1	0	0	0	0	0	6	11	11	0	0	G3UX15	
ENSMUST00000173061						2	0	0	1	1	3	0	4	2	0	7		
ENSMUST00000173062						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173063	ENSMUSG00000040482	17	34837019	34839233	1	0	0	0	0	0	0	21	75	21	0	0	G3UYP2	
ENSMUST00000173064						0	1	0	1	4	0	0	0	0	0	0		
ENSMUST00000173065	ENSMUSG00000024369	17	34850391	34856372	1	0	3	9	37	0	2	22	0	9	0	27	G3UY39	
ENSMUST00000173066						1	1	1	1	2	1	0	0	0	0	0		
ENSMUST00000173067	ENSMUSG00000021541	13	56773113	56895789	-1	0	0	1	0	5	2	0	0	0	0	0	G3UZF9	
ENSMUST00000173068	ENSMUSG00000040606	4	142102390	142239401	-1	0	0	2	0	0	0	0	0	0	0	0	G3UZH4	
ENSMUST00000173069	ENSMUSG00000037437	8	24836140	24948804	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXC2	
ENSMUST00000173071						0	8	7	8	0	4	0	0	13	1	14		
ENSMUST00000173072	ENSMUSG00000036492	17	36942918	36947986	1	2	2	4	15	2	2	0	0	3	0	0	G3UXJ0	
ENSMUST00000173073	ENSMUSG00000038056	5	25271798	25498783	-1	0	0	2	0	0	0	26	4	29	0	23	G3UZC8	
ENSMUST00000173074						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173075	ENSMUSG00000061232	17	33996017	34000333	-1	1	0	0	150	6	3	599	0	1164	0	718	G3UXW2	
ENSMUST00000173076						1	1	30	4	15	6	0	0	0	2	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173077						0	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000173078	ENSMUSG00000036990	8	79639618	79677724	1	0	0	50	79	0	0	93	0	126	52	259		B2RRE7
ENSMUST00000173079						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173080	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173081						9	5	23	3	3	0	0	1	0	1	0		
ENSMUST00000173082						10	10	14	8	6	6	0	0	0	0	3		
ENSMUST00000173083	ENSMUSG00000092443	14	54632329	54632781	1	0	0	0	4	0	0	0	3	2	0	0	G3UX18	
ENSMUST00000173084	ENSMUSG00000015120	17	25261916	25274622	-1	0	0	0	0	0	1	100	59	92	21	91		P63280
ENSMUST00000173085	ENSMUSG00000053110	9	7931999	8004596	-1	0	0	0	0	0	0	0	0	0	0	4	G3UYA6	
ENSMUST00000173086						0	0	0	0	0	0	62	79	33	247	44		
ENSMUST00000173087	ENSMUSG00000047146	10	62804570	62899118	-1	7	7	22	1	2	4	0	0	0	0	1	G3UXI7	
ENSMUST00000173088	ENSMUSG00000062181	8	105083753	105093929	1	0	0	4	1	0	1	0	0	0	1	0	G3UYS7	
ENSMUST00000173090						2	0	0	1	0	0	0	0	1	0	0		
ENSMUST00000173091	ENSMUSG00000024953	19	6906697	6910106	-1	2	3	0	18	0	0	8408	10822	5433	7821	2869	G3UZJ4	
ENSMUST00000173092						0	0	3	0	2	3	0	0	0	0	0		
ENSMUST00000173093	ENSMUSG00000049823	17	34879483	34896867	1	0	6	10	53	5	0	0	0	0	0	0	G3UY12	
ENSMUST00000173094	ENSMUSG00000068921	3	88920803	88951181	-1	0	0	0	0	0	0	0	193	2	15	0	G3UWZ6	
ENSMUST00000173095						3	2	7	9	6	1	0	1	0	0	0		
ENSMUST00000173096						12	12	17	94	17	8	0	0	0	0	1		
ENSMUST00000173097						2	2	2	5	4	1	0	0	3	0	7		
ENSMUST00000173098	ENSMUSG00000059070	7	45715457	45720835	1	3	0	0	0	0	0	75	35	97	271	132	G3UZJ6	
ENSMUST00000173099	ENSMUSG00000031442	8	12873806	13020905	1	9	16	25	38	21	14	0	0	0	0	0	G3UXP9	
ENSMUST00000173100						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000173101	ENSMUSG00000035523	7	23658316	23660663	1	7	4	4	0	0	1	0	0	0	0	0	Q9EPS4	
ENSMUST00000173102	ENSMUSG00000033249	8	105269801	105275845	1	10	0	21	0	0	3	0	0	0	0	0	G3UXZ1	
ENSMUST00000173103						4	5	3	1	6	2	0	0	0	0	14		
ENSMUST00000173104	ENSMUSG00000022479	15	97854425	97910630	-1	0	1	0	0	0	0	0	0	0	0	0	G3UZP9	
ENSMUST00000173105						2	2	4	4	0	0	0	0	0	0	5		
ENSMUST00000173106	ENSMUSG00000024397	17	35170991	35176068	-1	4	2	5	5	1	3	6	4	0	0	5	G3UYJ2	
ENSMUST00000173107	ENSMUSG00000031558	5	47983138	48307733	1	0	0	0	0	0	0	0	0	0	0	2	G3UXV6	Q9R1B9
ENSMUST00000173108	ENSMUSG00000030707	7	126699773	126707787	-1	0	0	0	3	2	8	6247	3107	2295	87	1332	G3UYK8	
ENSMUST00000173109	ENSMUSG00000042632	15	79286228	79328390	-1	3	4	3	2	8	10	0	0	0	0	2	G3UX52	
ENSMUST00000173110	ENSMUSG00000030126	6	116018611	116193486	-1	0	0	0	0	0	0	175	123	575	332	667	G3UXR4	
ENSMUST00000173111						0	0	2	5	8	3	0	7	4	0	12		
ENSMUST00000173112						4	0	7	3	3	0	0	0	0	0	0		
ENSMUST00000173113						0	0	4	0	2	2	3	2	0	0	0		
ENSMUST00000173114	ENSMUSG00000024387	17	35116196	35122053	-1	0	0	0	1	0	0	0	10	7	15	0		P67871
ENSMUST00000173115	ENSMUSG00000091705	17	35342242	35346762	1	9	2	0	4	6	0	2	7	4	2	1	G3UY91	
ENSMUST00000173116	ENSMUSG00000030707	7	126699773	126707787	-1	0	0	0	0	3	0	0	0	5	0	0	G3UX53	
ENSMUST00000173117						1	3	0	9	3	0	0	0	3	2	3		
ENSMUST00000173118	ENSMUSG00000092413	17	37609785	37627109	-1	3	10	6	0	3	0	0	0	0	0	0	B2RTB9	
ENSMUST00000173119	ENSMUSG00000028525	4	102087543	102607259	1	13	8	9	9	12	7	0	0	0	0	0	G3UWT3	
ENSMUST00000173120						3	0	22	14	8	2	0	0	0	0	0		
ENSMUST00000173121						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000173122						0	0	1	2	0	1	5	50	9	3	3		
ENSMUST00000173123						68	53	49	108	89	36	3	6	5	0	21		
ENSMUST00000173124						0	0	1	0	0	0	0	0	0	0	6		
ENSMUST00000173125						3	1	16	11	4	8	0	10	0	0	2		
ENSMUST00000173127						5	8	28	21	6	4	2	4	1	0	3		
ENSMUST00000173128	ENSMUSG00000092277	17	36121678	36129692	1	7	7	36	102	13	5	0	0	0	0	0	G3UZ45	
ENSMUST00000173129						3	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000173130						4	10	35	3	15	3	0	0	0	0	0		
ENSMUST00000173131	ENSMUSG00000092541	9	88407432	88456616	-1	0	0	0	0	0	0	0	0	0	2	0	G3UYK7	
ENSMUST00000173132	ENSMUSG00000041881	17	33824591	33838316	1	0	0	0	0	0	0	69	72	5	59	15	G3UXZ4	
ENSMUST00000173133	ENSMUSG00000054128	17	36185572	36190287	-1	0	0	0	0	0	6	0	2	0	0	3	Q05A75	
ENSMUST00000173134						2	2	3	41	0	3	2	3	14	10	8		
ENSMUST00000173135	ENSMUSG00000068921	3	88920803	88951181	-1	0	2	3	29	2	1	54	144	46	29	76		Q9ER88
ENSMUST00000173136	ENSMUSG00000022514	16	26581704	26730117	1	2	2	3	1	7	1	8	43	8	13	10	G3XA78	
ENSMUST00000173137						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000173138	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	0	0	3	0	0	0	0	5	0	G3UYB5	
ENSMUST00000173139	ENSMUSG00000019370	7	16915379	16924114	-1	0	1	1	0	4	1	0	0	0	0	0	G3UZ90	
ENSMUST00000173140	ENSMUSG00000030126	6	116018611	116193486	-1	2	1	5	0	3	3	57	0	21	0	0	G3UZD9	
ENSMUST00000173142	ENSMUSG00000007029	17	35000987	35016322	1	0	1	0	0	0	0	0	6	0	3	13	G3UZX1	
ENSMUST00000173143	ENSMUSG00000040147	X	16709282	16817366	-1	0	2	0	2	1	0	0	0	0	0	0	G3UZM5	
ENSMUST00000173144						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173145	ENSMUSG00000062563	12	24665838	24681813	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173146						6	3	11	6	3	0	4	20	9	0	7		
ENSMUST00000173147	ENSMUSG00000059714	17	35823230	35832791	1	0	0	0	0	0	0	311	54	230	9	133	G3UWW8	
ENSMUST00000173148	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	0	0	0	0	0	0	0	0	G3UZM3	
ENSMUST00000173150						3	0	4	1	2	0	0	2	1	0	2		
ENSMUST00000173151						137	107	569	163	186	89	2	2	5	5	4		
ENSMUST00000173152	ENSMUSG00000048000	1	87326998	87450796	1	0	1	0	2	0	1	0	0	0	0	0	G3UYH4	
ENSMUST00000173153						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173154						0	0	0	23	0	0	0	0	0	0	0		
ENSMUST00000173155	ENSMUSG00000048502	14	25978577	25990088	1	0	0	0	0	0	0	0	0	0	0	0	G3UZN2	
ENSMUST00000173156	ENSMUSG00000000804	11	84984442	85140161	-1	2	0	0	0	1	0	0	101	38	68	85	G3UX31	
ENSMUST00000173158	ENSMUSG00000021519	13	66906968	66933088	-1	0	0	0	0	0	0	0	43	0	12	0	G3UYC7	
ENSMUST00000173159						0	0	0	23	4	0	0	0	52	0	62		
ENSMUST00000173160						29	30	124	54	32	28	0	0	0	0	0		
ENSMUST00000173161						9	11	8	24	7	2	2	2	0	1	0		
ENSMUST00000173163	ENSMUSG00000042632	15	79286228	79328390	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UN31	P97819
ENSMUST00000173164						0	0	8	0	0	0	0	0	0	0	0		
ENSMUST00000173166	ENSMUSG00000037470	1	36140027	36244720	-1	0	0	0	0	0	0	7	0	0	0	9	G3UYG7	
ENSMUST00000173167	ENSMUSG00000073411	17	35262730	35267499	1	2	5	0	1	3	2	802	3278	741	81	995	G3UX20	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173168	ENSMUSG00000031976	8	124021508	124048505	1	49	34	158	143	51	41	0	22	48	20	61	G3UX45	
ENSMUST00000173169						1	2	6	2	0	4	5	6	2	0	0		
ENSMUST00000173170	ENSMUSG00000038943	7	80294450	80316259	1	0	0	0	0	0	0	0	9	0	0	0	G3UXT4	
ENSMUST00000173171	ENSMUSG00000041729	9	62419492	62537044	-1	0	1	0	1	2	0	0	0	0	0	0	G3V005	
ENSMUST00000173172						0	0	0	0	4	3	0	0	0	0	0		
ENSMUST00000173173	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	0	6	0	17	0	0	27	0	G3UYR9	
ENSMUST00000173174	ENSMUSG00000038056	5	25271798	25498783	-1	0	0	0	86	0	0	4	0	0	1	0	G3UWI5	
ENSMUST00000173175						0	0	0	0	0	0	18	47	20	105	11		
ENSMUST00000173176	ENSMUSG00000035021	12	54892989	55014348	-1	1	0	0	0	1	0	0	4	1	0	1	G3UYS9	
ENSMUST00000173177	ENSMUSG00000035021	12	54892989	55014348	-1	0	0	0	94	0	1	0	1	12	1	2	G3UXR5	
ENSMUST00000173179						1	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000173181						9	4	32	3	5	4	0	0	0	0	0		
ENSMUST00000173182						1	0	5	0	1	0	22	14	17	103	18		
ENSMUST00000173183						9	0	0	43	11	0	0	0	0	8	0		
ENSMUST00000173184	ENSMUSG00000028073	3	87747890	87824306	-1	0	0	0	0	0	1	3	0	0	0	0	G3UYI7	
ENSMUST00000173185	ENSMUSG00000092212	9	119220488	119231692	-1	15	8	35	10	11	6	16	62	20	3	31		
ENSMUST00000173186	ENSMUSG00000017428	11	80428615	80473248	1	0	0	0	0	0	0	0	0	0	0	0	G3UX67	
ENSMUST00000173187						0	0	0	0	3	1	4	0	3	0	8		
ENSMUST00000173189						1	2	2	1	5	0	3	74	17	6	38		
ENSMUST00000173190						5	2	10	4	6	1	6	20	9	0	7		
ENSMUST00000173191						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000173192						1	3	0	0	0	2	910	2119	1263	2951	690		
ENSMUST00000173193	ENSMUSG00000037709	6	58932090	59024549	-1	8	4	24	0	0	1	0	1	0	1	0	G3UYL7	
ENSMUST00000173194	ENSMUSG00000036591	2	20847919	20968881	-1	0	0	0	35	0	0	47	24	12	12	32	B7ZCJ0	
ENSMUST00000173195	ENSMUSG00000030994	7	134265779	134385661	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZQ0	
ENSMUST00000173196	ENSMUSG00000024319	17	33955812	33966984	1	0	0	0	0	0	2	353	362	433	36	345	G3UY33	
ENSMUST00000173197	ENSMUSG00000020661	12	3806007	3914443	1	5	9	10	6	5	6	0	2	0	0	0	G3UX63	
ENSMUST00000173198	ENSMUSG00000030188	6	131284388	131293244	-1	0	0	0	0	0	0	4	37	0	23	4	G3UZH0	
ENSMUST00000173199	ENSMUSG00000071454	12	3572381	3781796	1	0	0	1	2	3	1	0	11	8	0	0	G3UZ87	
ENSMUST00000173200						183	159	463	170	141	62	0	15	16	3	21		
ENSMUST00000173201						1	1	0	0	0	4	0	0	0	0	0		
ENSMUST00000173202						6	2	12	36	2	4	7	40	24	8	7		
ENSMUST00000173203						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000173204	ENSMUSG00000024335	17	34112023	34122634	-1	4	3	5	1	1	0	56	148	39	3	40	S4R1Z1	
ENSMUST00000173205	ENSMUSG00000029208	5	69556923	69575973	1	0	0	0	0	0	0	5	22	1	11	0	G3UWY0	
ENSMUST00000173206	ENSMUSG00000007379	3	103102604	103169769	1	0	0	7	79	14	10	4	7	0	2	0	G3UYA7	
ENSMUST00000173207	ENSMUSG00000092586	17	35065388	35070050	1	0	0	1	7	0	0	0	0	0	2	0	G3UYS0	
ENSMUST00000173209	ENSMUSG00000025473	7	139978932	139992562	-1	5	0	5	0	7	0	0	0	12	0	14	G3UXF8	
ENSMUST00000173210						3	6	2	7	1	2	0	0	0	0	0		
ENSMUST00000173211						2	0	3	24	0	1	0	33	4	15	9		
ENSMUST00000173213						0	0	0	61	5	0	3	5	4	0	12		
ENSMUST00000173214						14	3	21	14	15	5	0	0	0	0	0		
ENSMUST00000173215						1	0	0	0	0	0	0	0	0	25	0		
ENSMUST00000173216	ENSMUSG00000029767	6	29348069	29377110	1	1	0	5	39	2	0	0	0	0	21	0	G3V004	
ENSMUST00000173218						7	5	14	6	15	1	0	0	0	0	0		
ENSMUST00000173220						0	4	7	2	6	5	1	0	0	0	0		
ENSMUST00000173221						20	22	41	30	36	10	14	43	30	4	33		
ENSMUST00000173222						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000173223	ENSMUSG00000002409	7	28179469	28187294	1	4	0	4	0	10	0	0	0	0	0	0		Q9Z188
ENSMUST00000173225	ENSMUSG00000028073	3	87747890	87824306	-1	3	0	19	0	4	2	1	0	0	0	0	G3UYT5	
ENSMUST00000173226						7	5	9	4	4	5	0	0	0	0	0		
ENSMUST00000173227						1	1	0	38	2	0	0	0	0	0	0		
ENSMUST00000173228						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000173229						0	0	4	1	3	0	11	86	36	11	50		
ENSMUST00000173230						3	1	7	11	8	2	0	4	1	0	1		
ENSMUST00000173231	ENSMUSG00000015120	17	25261916	25274622	-1	0	5	19	27	5	2	4	8	7	0	9	G3UWL6	
ENSMUST00000173232	ENSMUSG00000067148	17	46243920	46248054	-1	0	0	0	0	0	0	3	10	10	11	0	G3UX92	
ENSMUST00000173234	ENSMUSG00000028479	4	44034075	44084177	-1	0	3	0	0	0	0	25	0	0	11	0	G3UX23	
ENSMUST00000173235	ENSMUSG00000048000	1	87326998	87450796	1	3	8	50	13	7	6	0	0	29	0	189	G3UZX7	
ENSMUST00000173236						5	11	9	4	8	6	24	121	73	19	79		
ENSMUST00000173237						5	2	5	3	5	2	0	0	0	0	0		
ENSMUST00000173238						4	4	5	18	10	3	7	39	7	6	15		
ENSMUST00000173239						0	0	0	0	0	0	33	32	0	4	10		
ENSMUST00000173240	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	0	0	0	0	G3UXK0	
ENSMUST00000173241	ENSMUSG00000024299	17	33524204	33553782	1	0	11	0	0	0	0	0	0	0	0	0	G3UZ08	
ENSMUST00000173242	ENSMUSG00000034254	17	34604262	34613449	1	1	0	0	0	0	0	0	0	0	0	0	G3UYV9	
ENSMUST00000173243	ENSMUSG00000059554	10	18213676	18234998	-1	0	0	4	2	0	0	0	0	0	0	0	G3UX80	
ENSMUST00000173244						5	1	2	0	3	0	0	0	0	0	0		
ENSMUST00000173245	ENSMUSG00000054310	7	15388948	15556866	1	0	3	0	4	1	1	0	0	0	0	0	G3UX03	
ENSMUST00000173246	ENSMUSG00000038518	13	44729474	44921643	1	19	6	35	21	11	4	309	887	469	79	340		Q62315
ENSMUST00000173247						5	0	10	6	11	1	28	28	28	0	27		
ENSMUST00000173248	ENSMUSG00000031543	8	22974844	23150497	1	0	0	0	0	0	0	0	0	0	0	0	B7ZW98	
ENSMUST00000173250						18	22	25	13	23	10	17	12	15	10	14		
ENSMUST00000173251						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000173252	ENSMUSG00000027347	2	117279993	117343001	-1	0	0	6	2	0	0	0	0	0	0	0	G3UZQ7	
ENSMUST00000173253						2	5	8	24	6	4	80	62	66	7	157		
ENSMUST00000173254	ENSMUSG00000025316	8	121949750	122029258	1	0	0	0	0	2	0	30	0	27	0	23		Q8VBU8
ENSMUST00000173255						7	10	12	6	12	4	0	0	0	0	0		
ENSMUST00000173256	ENSMUSG00000024406	17	35506018	35510772	1	0	0	0	0	0	0	0	0	0	0	0	E2JL30	
ENSMUST00000173258						1	2	23	13	2	4	69	144	61	7	101		
ENSMUST00000173259						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000173260						7	7	15	10	14	3	0	0	0	0	0		
ENSMUST00000173261						2	0	3	3	1	0	0	0	3	0	2		
ENSMUST00000173262						1	1	8	1	2	0	16	17	8	7	22		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173263	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	79	0	0	0	0	0	0	0	G3UY14	
ENSMUST00000173264	ENSMUSG00000053110	9	7931999	8004596	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYV4	
ENSMUST00000173265						19	16	15	16	10	2	0	0	0	0	0		
ENSMUST00000173266						1	0	0	0	2	0	9	2	10	0	5		
ENSMUST00000173267						23	14	29	23	29	5	15	17	37	2	50		
ENSMUST00000173268						0	1	4	0	7	6	44	367	288	125	257		
ENSMUST00000173269						22	8	44	45	22	16	212	1209	283	61	479		
ENSMUST00000173270	ENSMUSG00000030688	7	101317086	101346626	1	0	0	0	1	0	0	3	8	2	0	1	G3UY59	
ENSMUST00000173271						0	0	0	7	0	0	3	0	9	0	0		
ENSMUST00000173273						0	0	5	3	0	0	28	185	69	0	69		
ENSMUST00000173274	ENSMUSG00000028479	4	44034075	44084177	-1	0	0	0	1	0	0	0	0	0	0	0	G3UZ98	
ENSMUST00000173275						16	15	55	12	10	10	1	0	2	0	1		
ENSMUST00000173277						27	12	36	27	31	25	0	0	0	0	2		
ENSMUST00000173278						7	0	0	6	0	11	4	0	0	0	0		
ENSMUST00000173279						3	1	1	0	5	1	11	96	16	19	20		
ENSMUST00000173280	ENSMUSG00000056116	17	36037128	36042747	-1	0	0	0	0	0	0	231	345	192	150	176	G3UYB6	
ENSMUST00000173281						2	0	3	5	3	2	22	14	0	0	5		
ENSMUST00000173282						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000173283	ENSMUSG00000092335	7	42579783	42592547	-1	2	3	23	6	5	6	0	1	0	0	0	L7N2E7	
ENSMUST00000173284	ENSMUSG00000041354	17	33929543	33937687	1	0	0	0	0	0	2	213	643	159	13	166	G3UZ21	
ENSMUST00000173285						5	3	1	2	4	0	0	0	0	0	0		
ENSMUST00000173286	ENSMUSG00000036990	8	79639618	79677724	1	36	22	0	0	35	18	223	705	441	25	168		
ENSMUST00000173287	ENSMUSG00000070469	7	82335694	82614450	1	32	37	50	41	42	16	0	0	0	0	4	G3UXC7	
ENSMUST00000173289	ENSMUSG00000020782	11	115824049	115855780	1	2	0	3	2	6	0	0	0	0	0	0	G3UXR0	
ENSMUST00000173290						12	7	13	17	7	2	0	0	0	0	0		
ENSMUST00000173292	ENSMUSG00000036661	15	73512560	73572242	1	29	7	41	0	20	26	511	458	419	60	1067	G3UYA1	
ENSMUST00000173294						0	0	1	49	0	0	0	0	0	0	0		
ENSMUST00000173295						0	0	0	0	0	0	0	3	7	2	8		
ENSMUST00000173296						2	1	7	3	0	0	0	0	0	0	0		
ENSMUST00000173297	ENSMUSG00000055027	6	71213940	71322233	-1	17	10	22	8	9	4	0	0	0	0	0	G3UXZ0	
ENSMUST00000173298						54	28	45	26	52	41	0	0	2	0	5		
ENSMUST00000173299						9	8	18	8	14	9	145	399	349	10	572		
ENSMUST00000173300						3	2	1	4	0	2	1	0	0	0	2		
ENSMUST00000173302						7	7	10	6	14	4	0	9	0	2	4		
ENSMUST00000173303						0	1	3	0	2	1	0	0	0	0	0		
ENSMUST00000173305						4	2	18	3	7	0	6	12	6	1	24		
ENSMUST00000173306	ENSMUSG00000036139	15	102976439	102985099	1	0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000173307						0	0	126	0	0	5	1	8	8	0	6		
ENSMUST00000173308						0	0	0	10	2	0	16	56	30	2	16		
ENSMUST00000173309						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000173311	ENSMUSG00000023852	17	15704967	17394898	1	0	2	4	26	0	0	0	0	162	0	20	Q8C7Q2	
ENSMUST00000173312						0	5	2	11	4	1	0	0	0	0	0		
ENSMUST00000173313	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	0	0	0	0	0	0	0	0	G3UXY1	
ENSMUST00000173315	ENSMUSG00000004266	6	124720707	124738714	-1	0	0	0	0	0	0	0	700	0	26	0	G3UYY5	
ENSMUST00000173316						2	2	6	5	1	0	0	0	0	0	0		
ENSMUST00000173317						0	0	2	0	3	0	11	84	19	0	18		
ENSMUST00000173318						0	4	1	2	3	0	83	23	92	16	73		
ENSMUST00000173320	ENSMUSG00000045374	11	75440944	75454717	-1	46	0	24	314	82	24	316	291	607	0	921		Q5ND34
ENSMUST00000173321	ENSMUSG00000066463	9	78311972	78314797	-1	4	0	1	0	1	0	0	0	0	0	0	G3UY58	
ENSMUST00000173322	ENSMUSG00000092243	17	36109719	36129425	-1	0	0	0	0	0	0	0	0	0	0	0	Q0WXH6	
ENSMUST00000173323						4	0	0	0	0	3	2	0	0	4	2		
ENSMUST00000173324	ENSMUSG00000024397	17	35170991	35176068	-1	0	0	0	0	0	0	0	0	0	0	19	Q4FJL9	O70200
ENSMUST00000173325	ENSMUSG00000090165	1	88055388	88219004	1	2	0	0	4	0	2	0	0	0	0	0	G3UZC9	
ENSMUST00000173327						1	8	56	0	8	9	0	5	0	0	0		
ENSMUST00000173328	ENSMUSG00000034673	17	34591266	34597400	1	0	0	5	0	0	0	1255	1011	1032	121	596	Q3UR63	
ENSMUST00000173329	ENSMUSG00000079557	17	33685692	33718670	-1	18	16	15	24	19	13	14	37	30	3	27	G3UXU1	
ENSMUST00000173330						0	0	8	5	0	2	0	0	0	0	0		
ENSMUST00000173332	ENSMUSG00000030188	6	131284388	131293244	-1	2	0	5	0	2	1	0	0	4	0	0	G3UZH0	
ENSMUST00000173333						12	11	52	13	19	8	0	0	0	0	0		
ENSMUST00000173335						2	6	32	14	19	7	0	0	2	0	14		
ENSMUST00000173336						7	3	14	0	4	1	6	11	8	0	3		
ENSMUST00000173337						1	0	2	0	1	0	0	17	5	0	5		
ENSMUST00000173338						1	2	6	55	8	5	0	0	0	0	0		
ENSMUST00000173339						1	4	0	4	0	1	0	5	0	1	0		
ENSMUST00000173340						6	8	11	6	4	3	0	0	0	0	0		
ENSMUST00000173341	ENSMUSG00000060261	5	134237834	134314760	-1	8	0	0	0	0	0	27	94	93	0	121	Q3UHU8	
ENSMUST00000173342	ENSMUSG00000036972	9	91362413	91389348	1	0	1	3	12	2	0	0	0	0	0	0	G3UY76	
ENSMUST00000173344						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000173345	ENSMUSG00000057948	11	116062095	116077961	-1	16	11	0	27	23	27	0	45	77	0	75		
ENSMUST00000173346	ENSMUSG00000004231	19	44756045	44837871	1	17	7	37	95	29	10	0	0	0	0	1	G3UZ20	
ENSMUST00000173347	ENSMUSG00000020697	11	82781108	82804274	1	0	0	0	0	0	7	0	0	15	20	12	Q3UC82	
ENSMUST00000173348	ENSMUSG00000029112	5	33430734	33433976	-1	5	0	3	286	7	2	0	0	0	0	0	G3UXB3	
ENSMUST00000173349	ENSMUSG00000067148	17	46243920	46248054	-1	0	0	0	0	0	0	0	3	0	0	0	G3UXX5	
ENSMUST00000173350						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173351						3	2	5	8	3	0	13	27	11	0	20		
ENSMUST00000173352	ENSMUSG00000029001	4	148152800	148160482	-1	0	0	1	53	3	2	0	0	0	0	0	G3UZT3	
ENSMUST00000173353	ENSMUSG00000073402	17	36164443	36168537	-1	0	0	18	0	16	0	0	0	0	0	0	G3UXE9	
ENSMUST00000173354	ENSMUSG00000039656	17	34031812	34038393	1	0	0	3	0	0	3	233	36	162	0	147	Q8VCR0	
ENSMUST00000173355						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000173356						18	26	49	71	31	18	0	0	0	1	0		
ENSMUST00000173357	ENSMUSG00000024369	17	34850391	34856372	1	0	0	0	0	0	0	62	23	54	20	31	Q3UIA1	P19426
ENSMUST00000173358						5	2	2	3	6	4	0	0	0	0	0		
ENSMUST00000173359						7	2	0	2	0	3	11	4	10	0	13		
ENSMUST00000173360						0	4	8	4	4	3	0	0	0	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173361						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173362	ENSMUSG00000064120	17	49428362	49455435	1	0	3	0	2	8	0	401	10	516	0	239	G3UYX9	
ENSMUST00000173363	ENSMUSG00000024309	17	33938821	33940343	-1	3	2	2	6	3	6	0	15	0	4	0	G3UYF9	
ENSMUST00000173364						0	0	0	0	3	2	1	0	0	0	0		
ENSMUST00000173366						3	3	5	0	1	1	0	0	0	0	0		
ENSMUST00000173367	ENSMUSG00000038518	13	44729474	44921643	1	0	0	40	0	0	0	0	0	0	0	0	G3UZW3	
ENSMUST00000173368						1	4	7	0	0	1	0	0	0	0	0		
ENSMUST00000173369	ENSMUSG00000045409	17	36258873	36272247	-1	14	3	0	0	0	7	48	80	238	48	256	G3UWI0	
ENSMUST00000173370						5	10	9	1	6	1	0	2	2	3	0		
ENSMUST00000173372	ENSMUSG00000024300	17	33555719	33607764	1	0	0	0	0	0	0	117	54	127	57	340	G3V011	
ENSMUST00000173375						24	31	129	51	36	21	3	21	7	0	7		
ENSMUST00000173376	ENSMUSG00000028399	4	75941238	78211961	-1	0	0	0	0	0	0	0	0	0	0	0	B9EJA3	
ENSMUST00000173377						8	4	2	2	3	3	0	0	0	0	0		
ENSMUST00000173378	ENSMUSG00000067787	2	157556362	157571274	-1	4	0	0	3	16	0	0	0	0	0	0	G3UWQ6	
ENSMUST00000173379						0	0	0	0	0	3	45	25	43	0	14		
ENSMUST00000173380	ENSMUSG00000092417	17	35121455	35124814	1	5	1	6	8	7	2	19	23	9	2	19	G3UZZ1	
ENSMUST00000173381						0	4	0	1	0	0	162	515	187	53	171		
ENSMUST00000173382						2	0	1	5	2	2	0	0	0	0	0		
ENSMUST00000173383	ENSMUSG00000028479	4	44034075	44084177	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWV5	
ENSMUST00000173384						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173385						0	2	1	2	1	7	86	9	192	0	120		
ENSMUST00000173386	ENSMUSG00000079553	17	33875666	33890661	-1	0	0	0	0	0	0	0	0	8	0	0	G3UXN2	
ENSMUST00000173387	ENSMUSG00000066583	7	34021483	34022881	1	4	1	7	5	5	2	0	0	0	0	0	G3UXN8	
ENSMUST00000173388						0	0	0	0	0	0	6	27	13	13	0		
ENSMUST00000173389	ENSMUSG00000015468	17	34564268	34588503	1	36	0	36	150	0	11	0	0	0	0	0	G3UX69	
ENSMUST00000173391	ENSMUSG00000042104	14	118985039	119099430	-1	0	0	0	0	1	0	0	0	0	0	0	G3UXP5	
ENSMUST00000173392	ENSMUSG00000079557	17	33685692	33718670	-1	3	1	1	0	2	0	4	0	0	3	0	G3UYX1	
ENSMUST00000173393	ENSMUSG00000027510	2	173020498	173034734	1	6	0	6	59	16	5	7	21	7	0	0		Q62176
ENSMUST00000173394						2	2	0	8	5	1	0	0	0	0	0		
ENSMUST00000173395	ENSMUSG00000066772	7	15479825	15639902	-1	7	0	21	12	6	8	0	0	0	0	0	G3UXQ8	
ENSMUST00000173396	ENSMUSG00000025316	8	121949750	122029258	1	3	0	2	0	0	1	0	0	0	0	0	G3UYT4	
ENSMUST00000173397	ENSMUSG00000033335	9	21424908	21507759	1	0	2	0	37	0	1	979	1513	2059	129	1610	Q3TCR7	
ENSMUST00000173398						0	9	7	0	6	6	0	0	0	0	0		
ENSMUST00000173399						0	0	4	127	7	1	0	0	0	0	0		
ENSMUST00000173400	ENSMUSG00000019794	10	7726000	7763150	1	1	1	2	9	0	3	0	0	0	0	0	G3UX83	
ENSMUST00000173402						6	4	14	4	18	7	1	0	0	0	1		
ENSMUST00000173403						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000173404	ENSMUSG00000028033	1	21398403	21961942	-1	0	0	0	0	0	3	0	0	0	0	0	G3UYG5	
ENSMUST00000173405	ENSMUSG00000032423	9	88447009	88482574	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWM1	
ENSMUST00000173406						3	3	9	15	11	2	3	10	14	0	13		
ENSMUST00000173407	ENSMUSG00000021519	13	66906968	66933088	-1	1	1	5	3	1	0	3	5	0	0	5	G3UYC7	
ENSMUST00000173408	ENSMUSG00000003452	6	149408886	149563329	1	0	3	0	0	1	0	0	0	0	2	2	G3UXK5	
ENSMUST00000173409						5	1	12	1	5	1	4	0	1	15	0		
ENSMUST00000173410						7	4	61	6	11	3	0	0	1	0	1		
ENSMUST00000173411						26	18	58	238	51	22	2	0	1	0	0		
ENSMUST00000173412						5	6	24	10	17	6	0	0	0	0	0		
ENSMUST00000173414						1	1	1	4	1	1	0	2	0	0	1		
ENSMUST00000173415	ENSMUSG00000040356	17	34839228	34850210	-1	2	0	0	0	0	0	0	67	0	7	9	G3UYT1	
ENSMUST00000173416						1	1	3	2	2	0	0	0	0	0	0		
ENSMUST00000173417						3	1	11	11	2	1	0	2	2	0	4		
ENSMUST00000173418						2	5	9	157	13	4	4	1	0	3	2		
ENSMUST00000173419	ENSMUSG00000051890	12	69241176	69284632	1	5	4	0	0	5	1	0	2	4	0	0	G3UYQ6	
ENSMUST00000173420	ENSMUSG00000092517	7	101552453	101560865	-1	5	9	13	11	9	5	0	0	2	2	3		
ENSMUST00000173421						2	2	7	32	5	6	0	0	0	0	0		
ENSMUST00000173423						0	1	1	9	2	1	0	0	0	0	0		
ENSMUST00000173425						8	0	0	0	0	3	0	0	0	2	14		
ENSMUST00000173426						8	15	29	28	19	8	88	494	175	31	347		
ENSMUST00000173427						11	19	8	27	21	0	0	7	0	0	6		
ENSMUST00000173428						1	1	0	0	4	2	0	0	0	0	0		
ENSMUST00000173429	ENSMUSG00000039607	9	116572746	117629913	-1	0	0	0	0	0	0	0	0	0	0	0	G3UY10	
ENSMUST00000173430	ENSMUSG00000064120	17	49428362	49455435	1	0	0	0	0	0	0	8	9	0	7	0	G3UXN5	
ENSMUST00000173432	ENSMUSG00000000690	11	96292476	96301569	1	27	11	38	372	20	24	0	1	0	0	0		P09023
ENSMUST00000173433	ENSMUSG00000035021	12	54892989	55014348	-1	0	3	0	0	0	0	1194	3737	3836	519	2305	G3UWZ0	
ENSMUST00000173434						1	0	6	0	5	0	28	37	24	7	33		
ENSMUST00000173435						6	0	11	2	9	8	0	0	0	0	0		
ENSMUST00000173436						1	4	6	7	6	0	0	0	0	0	0		
ENSMUST00000173438						9	13	15	9	16	7	0	0	0	0	0		
ENSMUST00000173439						0	0	8	3	3	0	0	0	0	11	7		
ENSMUST00000173441	ENSMUSG00000024338	17	34197721	34201454	1	0	0	0	43	6	1	537	904	467	266	587	G3UZW8	
ENSMUST00000173442						180	147	190	200	182	86	6	10	18	0	27		
ENSMUST00000173443	ENSMUSG00000054310	7	15388948	15556866	1	0	0	0	0	0	0	0	0	0	0	0	Q9D350	
ENSMUST00000173444						3	0	3	1	1	0	0	0	0	0	0		
ENSMUST00000173445						1	2	2	5	2	1	8	29	0	0	6		
ENSMUST00000173446						13	16	40	24	11	6	0	0	0	0	0		
ENSMUST00000173447	ENSMUSG00000024176	17	25565892	25570686	-1	0	0	10	210	5	0	0	0	0	0	0	G3UWS3	
ENSMUST00000173448						0	1	0	0	0	0	0	10	18	0	12		
ENSMUST00000173449	ENSMUSG00000090083	17	29614790	29641664	1	5	3	6	4	10	8	0	0	0	0	0	G3UWU4	
ENSMUST00000173450						3	5	5	2	3	0	0	3	0	0	0		
ENSMUST00000173451						0	0	0	40	0	0	7	0	0	0	0		
ENSMUST00000173452						1	1	3	7	2	1	0	0	0	0	0		
ENSMUST00000173453						0	0	0	0	0	0	0	179	0	24	5		
ENSMUST00000173454	ENSMUSG00000079557	17	33685692	33718670	-1	0	0	0	0	0	0	3	0	14	41	31	G3UY44	
ENSMUST00000173455	ENSMUSG00000074366	7	15750131	15759800	1	11	10	7	6	8	7	0	0	0	0	0	G3UZE6	
ENSMUST00000173456	ENSMUSG00000021771	14	21831269	21845879	1	0	0	0	0	0	0	809	2361	972	961	399	G3UX26	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173457						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000173458						0	0	0	0	0	0	2	0	0	0	4		
ENSMUST00000173459	ENSMUSG00000070841	7	7670887	7689513	-1	17	17	31	38	8	11	0	0	0	0	0	E9PVI0	
ENSMUST00000173460						1	3	0	90	4	4	6	8	27	2	3		
ENSMUST00000173462	ENSMUSG00000092607	3	95129536	95134011	-1	0	0	1	0	0	0	36	183	57	156	65		Q8K136
ENSMUST00000173463						4	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000173464						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173465	ENSMUSG00000064068	3	89209081	89227088	-1	0	0	0	4	2	0	0	0	0	0	0	G3UXP6	
ENSMUST00000173466	ENSMUSG00000021541	13	56773113	56895789	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYZ6	
ENSMUST00000173467						2	1	6	3	0	0	0	0	0	0	0		
ENSMUST00000173468	ENSMUSG00000028073	3	87747890	87824306	-1	12	6	20	21	17	7	0	0	0	0	0	G3UY90	
ENSMUST00000173469						1	0	0	2	2	0	0	1	2	0	1		
ENSMUST00000173470						1	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000173471	ENSMUSG00000020185	10	110745439	110787384	1	0	4	14	15	3	0	9	0	4	0	15		Q6S7F2
ENSMUST00000173472	ENSMUSG00000049618	17	37336289	37339678	-1	0	6	0	0	0	0	0	0	0	0	0	Q920Y8	
ENSMUST00000173473						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173475	ENSMUSG00000064068	3	89209081	89227088	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYJ5	
ENSMUST00000173476						1	4	1	2	0	2	6	39	11	0	9		
ENSMUST00000173477	ENSMUSG00000064068	3	89209081	89227088	-1	0	0	0	0	0	0	32	27	21	25	0	G3XA66	
ENSMUST00000173478	ENSMUSG00000092586	17	35065388	35070050	1	61	42	499	99	45	30	0	2	2	0	5	Q545T2	Q9Z1Q4
ENSMUST00000173479						0	0	2	2	0	3	0	0	0	0	0		
ENSMUST00000173480						0	3	0	3	2	0	0	3	0	7	3		
ENSMUST00000173481						2	3	11	3	3	1	3	8	4	0	2		
ENSMUST00000173482	ENSMUSG00000006050	18	36666681	36679366	-1	0	0	0	0	0	0	361	1057	284	831	180	G3UZQ4	
ENSMUST00000173483	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	12	46	0	0	23	G3UZ85	
ENSMUST00000173484	ENSMUSG00000096304	7	22117322	22118245	-1	0	2	0	1	1	0	0	0	0	0	0	D3YZG3	
ENSMUST00000173485	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	1	4	0	14	0	2	9	0	G3UX27	
ENSMUST00000173486						4	0	4	39	7	2	122	144	61	222	34		
ENSMUST00000173487	ENSMUSG00000039431	8	40551095	40634797	-1	4	0	2	1	1	1	4	5	4	2	1	G3UYZ2	
ENSMUST00000173488						6	7	22	9	4	2	2	1	3	1	1		
ENSMUST00000173489	ENSMUSG00000092416	7	42473386	42505740	-1	0	4	0	8	1	7	0	0	4	0	0		
ENSMUST00000173490						3	0	0	3	9	0	8	20	15	4	1		
ENSMUST00000173491	ENSMUSG00000024392	17	35135178	35147322	1	0	2	3	97	0	0	108	0	88	0	65	G3UYZ0	
ENSMUST00000173492	ENSMUSG00000079553	17	33875666	33890661	-1	9	7	3	39	14	2	129	16	100	12	62		Q9QWT9
ENSMUST00000173493	ENSMUSG00000059714	17	35823230	35832791	1	0	1	0	21	4	3	66	6	17	0	0	G3UZZ5	
ENSMUST00000173494	ENSMUSG00000091415	10	41303980	41434534	1	45	61	131	47	50	20	4	6	2	2	2	G3UYQ4	
ENSMUST00000173495	ENSMUSG00000027684	3	29951296	30548008	-1	2	22	0	0	1	0	0	0	0	0	0	G3UZT5	
ENSMUST00000173496						4	3	18	83	4	1	0	0	0	0	0		
ENSMUST00000173497						27	25	49	23	42	17	14	59	78	13	49		
ENSMUST00000173498						0	0	0	1	0	0	0	0	0	1	5		
ENSMUST00000173500						1	0	1	1	3	1	0	0	0	0	0		
ENSMUST00000173501						0	0	0	2	0	1	0	3	0	0	5		
ENSMUST00000173502						7	4	12	21	9	3	66	244	102	3	204		
ENSMUST00000173503	ENSMUSG00000079025	15	63775968	63808759	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXG6	
ENSMUST00000173504	ENSMUSG00000060261	5	134237834	134314760	-1	2	0	0	0	4	1	0	0	0	0	0	G3UYD7	
ENSMUST00000173506	ENSMUSG00000033545	8	111536097	111626030	1	2	0	0	97	3	0	426	984	469	98	369		Q91V17
ENSMUST00000173507						0	0	1	0	0	0	0	0	2	0	2		
ENSMUST00000173508						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173509						5	6	7	7	5	4	1	2	2	1	7		
ENSMUST00000173510						5	5	24	92	15	20	137	339	138	80	219		
ENSMUST00000173511	ENSMUSG00000019794	10	7726000	7763150	1	0	0	0	3	0	0	0	6	2	3	0	G3UYX0	
ENSMUST00000173512	ENSMUSG00000092360	10	75771451	75780954	-1	0	0	0	0	0	0	0	0	0	1	0	G3UYJ7	
ENSMUST00000173513	ENSMUSG00000021541	13	56773113	56895789	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZW6	
ENSMUST00000173514	ENSMUSG00000026069	1	40429570	40465415	1	11	8	21	8	4	8	0	6	1	1	3	Q5D095	P14719
ENSMUST00000173515						1	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000173516	ENSMUSG00000022425	15	54838898	54920146	-1	0	0	19	0	0	0	0	0	0	39	11	G3UXY9	
ENSMUST00000173517	ENSMUSG00000091415	10	41303980	41434534	1	10	3	6	7	15	5	0	0	0	0	0	G3UZ50	
ENSMUST00000173518						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173520	ENSMUSG00000007039	17	35059035	35062095	1	0	0	0	15	7	1	0	6	0	0	0	G3UZR0	
ENSMUST00000173521						32	11	36	41	47	14	5	0	0	0	4		
ENSMUST00000173522	ENSMUSG00000034308	8	117661399	117673689	-1	9	8	19	23	34	30	38	64	51	16	30		Q9D665
ENSMUST00000173524						3	3	14	3	7	2	0	0	0	0	0		
ENSMUST00000173525						2	4	2	7	4	5	0	4	40	0	38		
ENSMUST00000173526						0	2	0	0	0	2	3	6	5	0	0		
ENSMUST00000173527						3	2	13	12	1	2	4	51	25	4	35		
ENSMUST00000173529	ENSMUSG00000035021	12	54892989	55014348	-1	5	0	0	0	4	1	0	0	0	0	0	G3UZD1	
ENSMUST00000173530	ENSMUSG00000024517	18	65872820	65886579	1	4	0	7	44	13	0	0	0	0	0	0	V9GX72	
ENSMUST00000173531						1	1	2	3	5	0	0	0	0	0	0		
ENSMUST00000173532	ENSMUSG00000029192	5	36490604	36593276	-1	0	0	0	0	0	0	0	2	9	0	16	G3UWY9	
ENSMUST00000173533	ENSMUSG00000040016	3	157566892	157645888	1	0	0	14	13	0	0	43	54	42	0	14	G3UYL9	
ENSMUST00000173534	ENSMUSG00000032113	9	36708482	36727065	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYB1	
ENSMUST00000173535	ENSMUSG00000024392	17	35135178	35147322	1	5	0	6	170	12	0	156	67	198	0	121	G3UXT8	
ENSMUST00000173536						2	3	9	2	5	2	0	0	0	0	0		
ENSMUST00000173537	ENSMUSG00000001665	10	75774115	75781414	-1	0	0	0	2	2	3	5	0	2	0	0	G3UX05	
ENSMUST00000173538						15	20	48	24	24	13	0	2	2	0	2		
ENSMUST00000173539	ENSMUSG00000040856	12	109452823	109463336	1	5	11	19	0	0	3	1	0	0	0	0	G3UWU8	
ENSMUST00000173540	ENSMUSG00000036398	17	36948356	36951741	-1	0	1	5	1	3	1	4	12	2	4	7	G3UZ30	
ENSMUST00000173541	ENSMUSG00000027347	2	117279993	117343001	-1	0	0	0	0	0	0	0	0	0	0	30	G3UYC3	
ENSMUST00000173542	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	0	0	0	0	G3UYD1	
ENSMUST00000173543						0	6	7	5	3	4	70	501	58	25	273		
ENSMUST00000173544						5	6	15	18	21	5	7	35	21	14	26		
ENSMUST00000173545						3	2	2	3	3	7	0	0	0	0	0		
ENSMUST00000173546						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000173547	ENSMUSG00000035469	14	59201209	59237265	1	0	0	0	17	0	0	0	0	0	0	1	G3UZ62	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173548	ENSMUSG00000030126	6	116018611	116193486	-1	0	0	0	0	2	2	0	0	189	10	70		
ENSMUST00000173550	ENSMUSG00000024392	17	35135178	35147322	1	0	0	0	0	0	6	880	1217	749	91	681	G3UZT6	
ENSMUST00000173551						0	2	28	0	0	7	0	0	0	0	0		
ENSMUST00000173552						5	9	4	6	3	2	0	0	0	0	1		
ENSMUST00000173554	ENSMUSG00000039656	17	34031812	34038393	1	1	0	13	54	0	3	0	3	3	0	5	G3UZ09	
ENSMUST00000173555	ENSMUSG00000022905	16	35978750	36037131	1	0	0	0	6	0	0	3	5	0	0	10	G3UWJ8	
ENSMUST00000173556						0	0	2	1	0	0	0	13	0	0	0		
ENSMUST00000173557						8	1	3	25	11	3	279	368	231	758	207		
ENSMUST00000173558						2	0	0	2	0	0	34	636	49	39	33		
ENSMUST00000173559	ENSMUSG00000037437	8	24836140	24948804	-1	0	0	0	2	0	0	0	0	0	0	1	G3UZF6	
ENSMUST00000173560						7	6	14	11	16	6	0	0	0	0	0		
ENSMUST00000173561						2	3	3	0	1	0	1	0	0	0	0		
ENSMUST00000173562						3	0	1	5	1	2	0	15	0	6	0		
ENSMUST00000173563						12	5	13	16	9	8	0	0	1	0	0		
ENSMUST00000173564						0	0	0	3	0	0	0	0	0	1	3		
ENSMUST00000173565	ENSMUSG00000017428	11	80428615	80473248	1	2	0	0	0	4	1	0	0	42	0	0	G3UZ33	
ENSMUST00000173566						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173567						2	5	10	13	9	7	0	5	3	2	1		
ENSMUST00000173568						7	5	10	4	6	6	0	0	0	1	2		
ENSMUST00000173569						2	0	3	147	7	0	0	0	0	0	0		
ENSMUST00000173570						1	0	1	125	2	3	0	0	0	0	0		
ENSMUST00000173571	ENSMUSG00000092456	7	24003091	24004247	1	3	5	3	4	0	0	0	0	0	0	0	Q3KNP5	
ENSMUST00000173572						0	0	12	1	7	4	0	0	0	0	0		
ENSMUST00000173573	ENSMUSG00000031543	8	22974844	23150497	1	0	0	45	0	0	0	0	0	0	0	0	G3UY11	
ENSMUST00000173574	ENSMUSG00000079637	X	37453680	37469861	1	9	10	5	12	4	7	0	0	0	0	0	G3UYU2	
ENSMUST00000173577						15	18	28	21	24	0	0	0	0	0	0		
ENSMUST00000173578						6	2	16	6	4	3	30	153	60	9	84		
ENSMUST00000173579						4	2	5	17	3	3	9	17	8	0	16		
ENSMUST00000173580	ENSMUSG00000048502	14	25978577	25990088	1	0	0	0	0	0	0	0	0	0	0	0	G3UX37	
ENSMUST00000173581	ENSMUSG00000021281	12	111442469	111455018	1	0	0	0	0	0	0	32	16	70	9	158	G3UXS6	
ENSMUST00000173582						0	2	5	3	3	3	0	1	0	0	5		
ENSMUST00000173583	ENSMUSG00000074832	13	66418114	66441118	-1	70	48	343	102	86	34	0	0	0	0	0	Q8C1L2	
ENSMUST00000173584	ENSMUSG00000007029	17	35000987	35016322	1	4	0	4	25	0	0	214	0	176	0	122	G3UY93	
ENSMUST00000173585	ENSMUSG00000038500	17	35972541	35980236	-1	3	0	2	1	0	0	0	4	3	0	0	Q3V0R7	
ENSMUST00000173586						0	3	11	12	13	0	0	0	0	0	0		
ENSMUST00000173587						0	4	0	8	0	3	0	0	0	0	0		
ENSMUST00000173588	ENSMUSG00000036036	17	37001163	37010635	1	2	3	0	1	2	0	0	0	0	0	0	H3BL53	
ENSMUST00000173589						0	0	0	0	0	0	0	41	0	0	0		
ENSMUST00000173590	ENSMUSG00000026028	1	58900449	58973430	-1	0	0	0	25	0	0	2	1	12	0	8	G3UZH5	
ENSMUST00000173591						0	1	3	3	2	0	0	0	0	0	0		
ENSMUST00000173592						0	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000173593	ENSMUSG00000064068	3	89209081	89227088	-1	0	0	0	0	0	0	20	0	0	0	12	G3UXX9	
ENSMUST00000173594						9	6	13	6	13	3	0	0	0	0	0		
ENSMUST00000173595	ENSMUSG00000067786	2	157560078	157562522	1	0	0	4	0	4	0	0	0	0	0	0	G3UWR7	
ENSMUST00000173596						0	0	1	0	0	0	0	8	0	4	4		
ENSMUST00000173598	ENSMUSG00000063765	15	81678296	81697287	-1	9	8	37	24	19	18	0	0	2	0	1	G3UXV0	
ENSMUST00000173599						2	2	0	0	2	0	0	3	0	10	0		
ENSMUST00000173600	ENSMUSG00000024399	17	35194439	35196320	1	0	2	0	21	0	0	810	2786	776	236	80	G3V002	
ENSMUST00000173601						2	0	12	19	1	1	4	0	0	0	0		
ENSMUST00000173602						12	0	28	0	8	5	7	122	20	5	52		
ENSMUST00000173604						4	2	4	1	1	6	0	0	0	0	0		
ENSMUST00000173607						1	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000173608						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173610	ENSMUSG00000063240	17	38145393	38149590	1	2	2	0	0	0	0	0	0	0	0	0	G3UXU0	
ENSMUST00000173611	ENSMUSG00000022479	15	97854425	97910630	-1	5	5	3	4	4	2	0	0	0	0	0	G3UWM9	
ENSMUST00000173612						39	38	457	112	57	36	0	0	1	0	0		
ENSMUST00000173613						2	3	5	13	4	2	0	2	0	0	4		
ENSMUST00000173614						5	5	1	4	4	1	4	42	5	1	26		
ENSMUST00000173615	ENSMUSG00000004591	3	142790902	142882004	-1	0	1	0	0	1	0	0	0	0	0	4	G3UWT9	
ENSMUST00000173616						0	1	0	6	4	0	0	9	0	0	3		
ENSMUST00000173617	ENSMUSG00000072675	14	26118349	26129763	1	3	0	0	0	0	0	0	0	0	0	0	G3UZN2	
ENSMUST00000173618	ENSMUSG00000021506	13	55825051	55836192	-1	4	0	2	91	0	5	0	0	0	0	0	G3UZS0	
ENSMUST00000173619						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000173620	ENSMUSG00000092210	10	115569986	115582448	1	4	6	15	4	6	7	0	0	0	1	0	G3UYI6	
ENSMUST00000173621	ENSMUSG00000015120	17	25261916	25274622	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYP0	
ENSMUST00000173623	ENSMUSG00000001815	2	74652991	74659557	-1	2	0	9	319	13	0	0	0	0	0	0		P49749
ENSMUST00000173625						1	0	3	63	9	0	734	840	393	153	701		
ENSMUST00000173626	ENSMUSG00000002307	17	33909414	33915589	1	0	0	3	108	5	1	0	0	3	0	0	G3UWI4	
ENSMUST00000173627	ENSMUSG00000025451	13	119428601	119458218	1	7	0	23	0	0	1	16	255	67	1	8	G3UYE5	
ENSMUST00000173628	ENSMUSG00000059714	17	35823230	35832791	1	2	2	8	0	11	0	574	1388	642	45	516	G3XA73	
ENSMUST00000173629	ENSMUSG00000054128	17	36185572	36190287	-1	5	5	0	4	2	2	0	0	0	0	0	G3UZR8	
ENSMUST00000173630	ENSMUSG00000006930	11	100347327	100356128	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYE4	
ENSMUST00000173631	ENSMUSG00000005354	15	77915047	77929006	-1	0	0	0	0	0	0	35	6	54	13	0	G3UZY2	
ENSMUST00000173632	ENSMUSG00000042632	15	79286228	79328390	-1	2	0	3	26	2	0	0	0	0	0	2	G3UY97	
ENSMUST00000173633	ENSMUSG00000024387	17	35116196	35122053	-1	2	0	0	0	3	0	6	6	3	3	6	G3UXU2	
ENSMUST00000173634	ENSMUSG00000020185	10	110745439	110787384	1	3	0	1	87	5	1	0	1	1	0	0	Q8BQ55	
ENSMUST00000173635	ENSMUSG00000024955	19	6910977	6921813	-1	3	6	2	5	0	2	82	9	15	0	3	G3UZQ2	
ENSMUST00000173636	ENSMUSG00000048000	1	87326998	87450796	1	2	0	0	3	4	0	0	7	0	0	0	G3UZW5	
ENSMUST00000173638						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000173639	ENSMUSG00000050747	17	36860691	36867210	-1	6	3	7	0	4	5	0	0	0	0	1	G3UXC8	
ENSMUST00000173640	ENSMUSG00000033249	8	105269801	105275845	1	0	0	0	0	0	0	0	0	0	0	2	G3UX32	
ENSMUST00000173641	ENSMUSG00000022905	16	35978750	36037131	1	1	0	0	0	0	0	6	21	9	19	0	G3UXF0	
ENSMUST00000173642	ENSMUSG00000024498	18	42511510	42575551	1	0	3	6	38	11	3	0	37	54	0	47		Q8CGF7
ENSMUST00000173643						0	0	0	0	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173644						3	0	0	30	5	3	15	63	32	8	17		
ENSMUST00000173645	ENSMUSG00000028023	3	129199878	129219591	1	4	5	2	45	5	6	0	0	1	0	0	G3UZ11	
ENSMUST00000173646						1	1	8	3	0	0	0	0	0	0	0		
ENSMUST00000173647	ENSMUSG00000004266	6	124720707	124738714	-1	0	0	0	2	0	0	3	0	7	0	4	G3UXM2	
ENSMUST00000173649						3	0	2	2	4	0	4	5	5	0	0		
ENSMUST00000173650	ENSMUSG00000051827	X	37244976	37249686	1	1	0	0	0	7	0	0	0	0	0	0	G3UYY0	
ENSMUST00000173651	ENSMUSG00000060261	5	134237834	134314760	-1	17	17	91	14	7	6	0	12	3	3	0	G3UY14	
ENSMUST00000173652						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000173653	ENSMUSG00000058831	6	29376671	29388468	-1	0	0	2	0	0	0	0	0	0	0	0	G3UX34	
ENSMUST00000173654						0	0	0	12	1	0	0	0	0	0	0		
ENSMUST00000173655	ENSMUSG00000018727	11	113698172	113710017	-1	0	0	0	2	2	0	0	0	0	0	0	G3UWW6	
ENSMUST00000173656	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	0	0	1	0	0	0	0	0	0	G3UXN3	
ENSMUST00000173657						4	0	5	6	3	1	0	0	0	0	0		
ENSMUST00000173658	ENSMUSG00000007564	17	20945311	20965916	1	0	0	0	0	0	0	0	0	0	0	0	G3UXQ1	
ENSMUST00000173659	ENSMUSG00000087166	4	98726734	98738480	1	19	11	17	129	17	7	1	0	0	1	0	G3UYN0	
ENSMUST00000173660	ENSMUSG00000051650	11	22834747	22860961	-1	0	0	7	0	1	0	44	126	232	37	146	G3UWI7	
ENSMUST00000173661						2	1	5	3	2	0	8	4	12	0	20		
ENSMUST00000173662	ENSMUSG00000028399	4	75941238	78211961	-1	0	0	1	0	0	0	0	0	0	0	0	G3UXU8	
ENSMUST00000173663	ENSMUSG00000048000	1	87326998	87450796	1	1	0	0	0	0	0	0	0	0	0	0	G3UWT6	
ENSMUST00000173664						26	13	34	25	28	15	0	0	0	0	0		
ENSMUST00000173665	ENSMUSG00000045409	17	36258873	36272247	-1	17	26	102	44	24	14	0	0	26	6	12	G3UX29	
ENSMUST00000173666						0	0	0	36	0	0	8	0	141	1478	112		
ENSMUST00000173668	ENSMUSG00000074311	7	22069057	22097907	1	2	0	0	3	3	3	0	0	0	0	0	Q4KL48	
ENSMUST00000173669						6	9	9	5	9	0	2	12	0	94	14		
ENSMUST00000173670						9	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173671						7	4	6	3	4	1	0	0	0	0	0		
ENSMUST00000173673						0	0	0	3	4	0	0	0	0	3	0		
ENSMUST00000173675						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173676						0	2	0	5	0	0	0	0	0	0	0		
ENSMUST00000173678						0	1	6	4	2	1	4	9	2	0	12		
ENSMUST00000173679	ENSMUSG00000020929	11	102838473	102880985	-1	4	0	0	2	18	0	0	0	0	0	59	G3UZ34	
ENSMUST00000173680	ENSMUSG00000092609	17	34969912	34972136	1	1	3	0	0	8	0	4	0	0	4	14	G3UXK4	
ENSMUST00000173681						0	2	23	7	9	2	0	0	2	2	10		
ENSMUST00000173682	ENSMUSG00000035969	4	43381979	43427088	1	26	0	0	0	0	0	0	0	5	0	0	G3UXJ5	
ENSMUST00000173684						4	1	2	4	3	0	27	26	34	6	56		
ENSMUST00000173685						0	1	0	0	1	0	0	32	12	5	2		
ENSMUST00000173686	ENSMUSG00000031558	5	47983138	48307733	1	0	0	5	1	2	2	0	0	1	0	1	G3UWQ3	
ENSMUST00000173687						0	7	0	14	0	0	0	0	0	0	0		
ENSMUST00000173688	ENSMUSG00000062352	12	21240825	21286237	-1	0	0	0	0	0	0	63	334	64	242	53	G3UX55	
ENSMUST00000173689	ENSMUSG00000037876	10	67096125	67256326	1	29	0	68	0	0	18	104	198	365	70	500		Q69ZK6
ENSMUST00000173690						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000173691	ENSMUSG00000020265	10	77606097	77641543	1	0	0	0	0	0	0	0	0	0	0	0	G3UZX6	
ENSMUST00000173692						2	0	2	1	7	1	1	6	1	2	1		
ENSMUST00000173694	ENSMUSG00000029767	6	29348069	29377110	1	0	0	0	0	0	0	0	0	0	0	0	G3UWV3	
ENSMUST00000173696	ENSMUSG00000022905	16	35978750	36037131	1	7	2	0	0	0	0	1	6	166	53	124	G3UZK5	
ENSMUST00000173697						3	0	1	2	0	1	0	0	0	0	0		
ENSMUST00000173698						0	0	0	1	6	1	0	0	0	0	0		
ENSMUST00000173699	ENSMUSG00000028382	4	59471868	59549364	-1	0	0	8	0	0	0	360	0	0	0	0	G3UZ01	
ENSMUST00000173700						48	28	86	160	55	32	0	1	0	1	1		
ENSMUST00000173701						2	4	0	0	1	1	4	11	0	16	8		
ENSMUST00000173702						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173704	ENSMUSG00000038518	13	44729474	44921643	1	0	0	0	36	9	0	48	5	310	0	227		Q62315
ENSMUST00000173705	ENSMUSG00000053046	7	141949751	142004247	1	0	2	3	3	0	0	0	0	0	0	0	G3UYP7	
ENSMUST00000173706						1	3	0	5	1	1	1	1	1	0	1		
ENSMUST00000173707	ENSMUSG00000064308	17	36977701	36981237	-1	0	0	0	6	7	0	0	0	0	0	0	G3UXK3	
ENSMUST00000173708						2	5	22	7	8	2	18	90	39	10	48		
ENSMUST00000173709						7	6	4	9	8	7	0	0	0	0	0		
ENSMUST00000173710						1	0	0	14	3	0	0	0	0	0	0		
ENSMUST00000173711						0	0	0	0	0	0	5	35	10	0	4		
ENSMUST00000173712						5	0	5	1	3	0	0	0	0	0	0		
ENSMUST00000173713	ENSMUSG00000015120	17	25261916	25274622	-1	0	0	0	0	0	2	145	247	136	113	120		P63280
ENSMUST00000173715						12	7	30	36	19	13	0	1	5	0	4		
ENSMUST00000173716						3	6	4	1	3	0	0	0	1	0	0		
ENSMUST00000173717						0	1	2	2	1	0	0	0	0	0	0		
ENSMUST00000173718						4	0	4	16	0	3	33	82	22	0	72		
ENSMUST00000173719						4	4	4	49	2	3	0	6	2	2	7		
ENSMUST00000173720	ENSMUSG00000027510	2	173020498	173034734	1	0	0	0	11	0	0	0	0	0	0	0	G3UXN1	
ENSMUST00000173721						1	1	0	48	0	2	0	2	0	2	0		
ENSMUST00000173722	ENSMUSG00000020697	11	82781108	82804274	1	0	0	13	0	0	0	161	515	320	0	202	Q80ZH7	
ENSMUST00000173723	ENSMUSG00000091638	7	20787285	20788208	1	0	0	0	0	0	0	0	0	0	0	0	G3UWI8	
ENSMUST00000173724	ENSMUSG00000038500	17	35972541	35980236	-1	2	0	0	72	2	0	0	0	0	0	0	G3UY06	
ENSMUST00000173725						0	0	2	108	0	2	0	0	0	0	0		
ENSMUST00000173726	ENSMUSG00000033545	8	111536097	111626030	1	0	0	0	0	5	1	54	78	104	3	122	G3UWY5	
ENSMUST00000173727	ENSMUSG00000020697	11	82781108	82804274	1	0	0	0	0	0	2	38	39	8	4	2	Q3UC82	
ENSMUST00000173728						0	2	3	0	2	0	0	23	20	9	0		
ENSMUST00000173729	ENSMUSG00000062352	12	21240825	21286237	-1	10	5	6	109	15	4	33	82	38	25	38		O35671
ENSMUST00000173730	ENSMUSG00000055027	6	71213940	71322233	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ94	
ENSMUST00000173731	ENSMUSG00000019432	17	35241746	35253707	1	6	12	55	79	23	0	41	73	37	0	29		Q9Z1N5
ENSMUST00000173732	ENSMUSG00000021959	14	57642077	57758388	-1	0	1	0	0	0	0	0	0	0	0	0	G3UXX1	
ENSMUST00000173733	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXF6	
ENSMUST00000173734	ENSMUSG00000092622	9	73101836	73104438	1	4	0	0	116	9	0	0	17	4	0	0		Q9CWU5
ENSMUST00000173735						0	2	0	2	1	2	0	1	0	0	0		
ENSMUST00000173736	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	0	14	0	0	G3UZJ3	
ENSMUST00000173737						0	0	0	5	0	0	0	14	0	0	26		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173739	ENSMUSG00000002985	7	19696109	19699166	-1	2	1	18	40	9	3	20	138	58	10	30	Q3TXU4	P08226
ENSMUST00000173740	ENSMUSG00000020140	10	115450311	115587780	-1	0	0	0	0	0	7	0	0	0	0	0	G3UXI8	
ENSMUST00000173741	ENSMUSG00000028403	4	82798738	82859958	-1	0	0	0	0	0	0	2	0	0	0	0	G3UXC1	
ENSMUST00000173742	ENSMUSG00000057836	X	73086293	73097095	-1	2	0	3	0	2	3	0	0	0	0	0	G3UZF3	
ENSMUST00000173744	ENSMUSG00000018395	11	53567379	53601967	1	0	0	0	0	0	0	0	0	0	0	0	Q3TET1	
ENSMUST00000173745	ENSMUSG00000000392	2	62500943	62574075	-1	2	0	0	0	0	0	0	0	0	0	0	G3UZ14	
ENSMUST00000173746						2	4	0	2	0	0	0	0	0	0	0		
ENSMUST00000173747						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173748	ENSMUSG00000053716	9	106368632	106375724	1	0	2	0	3	0	0	0	11	12	7	0	G3UX16	
ENSMUST00000173749						3	0	0	1	7	2	0	0	0	0	0		
ENSMUST00000173750						15	12	56	20	16	14	147	423	252	28	434		
ENSMUST00000173752						0	1	11	0	0	2	0	0	0	0	0		
ENSMUST00000173753						3	3	6	4	1	1	0	5	6	0	3		
ENSMUST00000173754	ENSMUSG00000030994	7	134265779	134385661	-1	10	9	19	7	6	4	0	1	0	0	0	G3UY66	
ENSMUST00000173755						4	1	15	6	0	0	0	57	9	0	0		
ENSMUST00000173756						8	5	9	0	6	4	0	0	0	0	0		
ENSMUST00000173757	ENSMUSG00000029192	5	36490604	36593276	-1	0	0	0	0	0	0	0	8	11	0	9	G3UZ97	
ENSMUST00000173758	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	4	0	7	0	0	G3UZQ3	
ENSMUST00000173759						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173760	ENSMUSG00000096458	12	102742230	102743661	-1	5	2	6	75	8	5	45	58	0	41	0		Q9ERH6
ENSMUST00000173761						5	0	25	1	9	0	0	1	0	0	0		
ENSMUST00000173762	ENSMUSG00000037876	10	67096125	67256326	1	4	2	12	2	3	4	25	535	86	202	165	G3UZX8	
ENSMUST00000173763	ENSMUSG00000037708	2	18694032	18750413	1	2	4	12	33	3	2	0	0	0	0	0	G3UWQ4	
ENSMUST00000173764	ENSMUSG00000041538	17	34238903	34245907	1	6	4	4	5	8	8	2	0	9	0	12	G3UY15	
ENSMUST00000173765						11	4	7	7	4	5	0	0	0	0	0		
ENSMUST00000173766						6	6	12	8	8	1	0	0	0	0	0		
ENSMUST00000173767						0	0	5	0	4	0	14	34	21	6	12		
ENSMUST00000173768	ENSMUSG00000040482	17	34837019	34839233	1	2	0	3	7	5	1	13	72	5	2	14	G3UYE6	
ENSMUST00000173769	ENSMUSG00000057191	9	21526176	21545333	1	0	0	2	0	0	0	1328	6105	1138	300	827	Z4YNA9	
ENSMUST00000173771						3	3	2	0	4	1	0	0	0	0	0		
ENSMUST00000173772	ENSMUSG00000034786	17	34589806	34591754	1	2	0	3	0	11	4	568	2474	665	154	502	G3UYL4	
ENSMUST00000173773	ENSMUSG00000021519	13	66906968	66933088	-1	0	0	0	0	0	0	0	0	0	3	0	G3UX91	
ENSMUST00000173774						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173775						4	2	7	8	2	3	0	4	7	0	5		
ENSMUST00000173776	ENSMUSG00000042345	17	31207873	31242202	1	0	0	0	3	2	1	0	0	0	2	2	G3UZM7	
ENSMUST00000173777						0	1	5	2	9	2	0	0	0	0	0		
ENSMUST00000173778	ENSMUSG00000015222	1	66175273	66442583	1	0	0	0	0	0	0	0	0	0	0	0	G3UZV6	
ENSMUST00000173779	ENSMUSG00000003617	3	19957054	20009145	1	0	2	4	2	1	0	0	0	3	0	1	G3UXD2	
ENSMUST00000173780	ENSMUSG00000041014	14	38368952	39473088	-1	0	0	0	94	0	0	0	0	0	0	0	G3V023	
ENSMUST00000173781	ENSMUSG00000033545	8	111536097	111626030	1	0	0	19	1	0	1	0	6	0	0	0	G3UYU9	
ENSMUST00000173782	ENSMUSG00000090794	7	5544197	5545129	-1	0	0	0	0	0	0	0	0	0	0	0	G3UY47	
ENSMUST00000173783	ENSMUSG00000030447	7	55841745	55932602	1	0	1	0	71	6	0	0	0	12	0	5	G3UZI5	
ENSMUST00000173784	ENSMUSG00000036591	2	20847919	20968881	-1	0	0	0	0	0	0	0	0	4	0	0	G3UX38	
ENSMUST00000173785	ENSMUSG00000078671	7	73426638	73541830	-1	0	0	0	2	3	0	0	3	11	0	0	G3UXJ4	
ENSMUST00000173786						0	1	0	3	2	0	100	100	46	347	49		
ENSMUST00000173787						11	5	2	5	8	7	0	0	0	0	0		
ENSMUST00000173788						320	263	491	429	417	145	79	303	77	40	548		
ENSMUST00000173789	ENSMUSG00000042099	17	33810520	33822918	1	0	3	0	0	0	0	0	13	0	17	1	Q6P8V1	
ENSMUST00000173790	ENSMUSG00000037894	3	137864487	137866922	1	1	0	15	9	11	1	0	73	273	1605	157	G3UWL7	
ENSMUST00000173791						0	0	3	0	7	0	0	0	0	0	0		
ENSMUST00000173792						3	4	21	9	9	5	1	0	0	0	1		
ENSMUST00000173793	ENSMUSG00000067786	2	157560078	157562522	1	0	0	0	0	0	0	1	2	3	1	6	G3UYJ4	
ENSMUST00000173794						1	1	2	2	2	3	0	3	3	2	3		
ENSMUST00000173795	ENSMUSG00000001029	11	106377656	106388075	-1	1	1	2	0	2	0	0	5	1	0	0	G3UWJ5	
ENSMUST00000173796						2	1	20	22	6	3	0	0	2	0	2		
ENSMUST00000173797	ENSMUSG00000017428	11	80428615	80473248	1	0	0	0	0	0	0	0	88	0	0	0	G3UXL5	
ENSMUST00000173798						18	16	12	17	9	10	0	0	0	0	0		
ENSMUST00000173800	ENSMUSG00000015222	1	66175273	66442583	1	0	0	19	0	0	0	0	0	0	0	0	G3UZJ2	
ENSMUST00000173801	ENSMUSG00000032423	9	88447009	88482574	-1	5	4	24	553	16	6	44	125	118	51	102		Q7TMK9
ENSMUST00000173802						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000173803	ENSMUSG00000092233	12	54986158	54986529	-1	1	2	2	12	1	0	1	3	5	1	3	G3UYB0	
ENSMUST00000173804	ENSMUSG00000072966	X	135839034	135844730	1	0	0	4	23	16	0	0	0	0	0	0		Q8BUY8
ENSMUST00000173805	ENSMUSG00000024406	17	35506018	35510772	1	0	2	5	1	0	1	0	0	0	0	0	E2JL30	
ENSMUST00000173806						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000173807						0	7	37	12	10	5	0	0	0	0	22		
ENSMUST00000173808	ENSMUSG00000074365	7	15882617	15904020	1	2	0	0	1	0	0	0	0	0	0	0	V9GWY4	
ENSMUST00000173809						2	0	0	0	0	1	677	685	455	0	472		
ENSMUST00000173810						0	1	0	22	1	0	0	4	0	0	2		
ENSMUST00000173812	ENSMUSG00000040856	12	109452823	109463336	1	0	0	0	0	0	0	1	0	0	0	0	G3UZ17	
ENSMUST00000173813						0	0	0	0	0	0	8	0	5	0	12		
ENSMUST00000173814	ENSMUSG00000036214	17	36958592	36965622	1	0	0	0	0	0	8	0	0	0	5	0		Q8R0E5
ENSMUST00000173815	ENSMUSG00000091528	7	43018798	43048106	1	8	3	0	8	7	2	0	0	0	0	0	G3UZC7	
ENSMUST00000173816	ENSMUSG00000092473	7	23952387	23953356	1	7	1	2	0	5	1	0	0	0	0	0	B9EK86	
ENSMUST00000173817	ENSMUSG00000021541	13	56773113	56895789	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWT1	
ENSMUST00000173818						2	3	1	4	8	1	3	14	10	1	47		
ENSMUST00000173819	ENSMUSG00000033545	8	111536097	111626030	1	0	0	0	0	0	0	0	8	0	0	0	G3UWN6	
ENSMUST00000173820						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000173821	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	0	0	15	G3V008	
ENSMUST00000173822						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000173823	ENSMUSG00000024462	17	37045966	37075067	1	0	0	19	0	0	0	28	145	11	7	108	G3UXR6	
ENSMUST00000173824	ENSMUSG00000038943	7	80294450	80316259	1	5	0	0	0	0	0	34	160	0	28	0	G3UY19	
ENSMUST00000173825						4	4	7	3	3	1	0	0	0	0	0		
ENSMUST00000173826	ENSMUSG00000045655	14	78081021	78089007	-1	0	0	6	3	6	3	0	0	0	0	0	G3UZG0	
ENSMUST00000173828	ENSMUSG00000070469	7	82335694	82614450	1	8	1	18	0	13	6	0	0	1	1	1	G3UWL5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173830	ENSMUSG00000004591	3	142790902	142882004	-1	0	2	0	0	0	0	24	88	88	4	67	G3UXH4	
ENSMUST00000173831	ENSMUSG00000096727	17	34181988	34187764	-1	0	0	2	1	0	0	33	29	19	13	16	G3UYK5	
ENSMUST00000173832						3	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000173833	ENSMUSG00000031552	8	24602246	24674755	-1	5	0	5	16	9	3	0	0	3	0	1	G3UWP9	
ENSMUST00000173834						0	0	1	1	1	1	0	0	0	0	0		
ENSMUST00000173835	ENSMUSG00000051504	7	55768178	55778925	1	0	0	0	0	0	0	3	0	0	0	0	B7ZMQ5	
ENSMUST00000173836	ENSMUSG00000063646	5	37028335	37148001	1	0	1	0	114	0	0	0	0	0	0	0	G3UXP1	
ENSMUST00000173837	ENSMUSG00000030188	6	131284388	131293244	-1	1	1	3	2	4	1	0	51	8	20	31	G3UZW7	
ENSMUST00000173838						5	7	30	10	19	5	0	0	0	0	0		
ENSMUST00000173839	ENSMUSG00000067786	2	157560078	157562522	1	3	0	0	0	11	0	0	0	0	1	0	G3UWR4	
ENSMUST00000173841	ENSMUSG00000057443	17	38261067	38275711	1	0	0	0	0	5	0	0	0	0	0	0	G3UXU4	
ENSMUST00000173842						11	6	3	4	2	3	0	0	0	0	0		
ENSMUST00000173843						2	6	4	4	2	1	0	0	0	0	0		
ENSMUST00000173844	ENSMUSG00000067288	17	33819027	33824562	-1	12	0	9	10	8	0	983	1448	954	5675	724	Q059I1	P62858
ENSMUST00000173846	ENSMUSG00000007036	17	35089263	35102987	1	15	0	0	19	20	9	54	232	63	97	138	G3UX11	
ENSMUST00000173848	ENSMUSG00000003617	3	19957054	20009145	1	2	0	0	0	1	0	0	0	0	3	0	G3UXG1	
ENSMUST00000173849	ENSMUSG00000068877	3	94693556	94704413	1	0	4	0	0	7	5	2	2	0	0	3	G3UYY2	
ENSMUST00000173850						8	3	5	14	9	2	1	3	4	0	2		
ENSMUST00000173851						6	3	48	15	9	1	0	0	0	0	0		
ENSMUST00000173852						2	2	5	0	5	0	0	0	0	0	0		
ENSMUST00000173853	ENSMUSG00000007739	11	22990519	23003780	1	1	3	0	141	12	0	0	0	0	91	11	G3UXG2	
ENSMUST00000173854	ENSMUSG00000001120	10	76761857	76961887	-1	0	0	0	0	0	0	1	0	0	0	0	G3UYM5	
ENSMUST00000173855	ENSMUSG00000015222	1	66175273	66442583	1	2	2	2	2	2	3	0	0	0	0	0	G3UZE9	
ENSMUST00000173857						2	0	8	271	8	0	2	2	2	0	0		
ENSMUST00000173858	ENSMUSG00000015002	15	65787034	65873816	1	0	2	2	0	0	2	0	8	143	0	114		Q8BG67
ENSMUST00000173859	ENSMUSG00000033249	8	105269801	105275845	1	0	5	0	5	0	3	0	0	0	0	0		Q9R0L1
ENSMUST00000173860	ENSMUSG00000077450	17	33742484	33760530	-1	20	0	62	94	42	17	1669	2096	1044	156	785	G3UZD3	
ENSMUST00000173861						3	2	8	3	3	2	0	0	0	0	0		
ENSMUST00000173862						3	4	0	1	2	2	0	0	0	0	0		
ENSMUST00000173863	ENSMUSG00000040929	19	27761721	28011166	-1	0	0	0	0	0	0	0	4	7	4	12	G3UWP0	
ENSMUST00000173864	ENSMUSG00000059070	7	45715457	45720835	1	0	0	0	0	0	0	5	0	0	0	0	G3UX28	
ENSMUST00000173865	ENSMUSG00000073888	4	41769467	41774247	-1	0	0	0	0	0	0	0	0	0	0	0	A2AMS8	
ENSMUST00000173867	ENSMUSG00000007739	11	22990519	23003780	1	0	4	5	46	14	12	137	969	263	355	127	Q564F4	P80315
ENSMUST00000173868						0	0	0	3	0	0	2	0	0	0	0		
ENSMUST00000173869	ENSMUSG00000002289	17	33773750	33781575	-1	13	2	20	48	5	8	7	14	6	14	15	G3UWT7	
ENSMUST00000173870	ENSMUSG00000020923	11	102304560	102319742	-1	6	1	8	116	9	1	0	16	39	0	19	A2AWT5	
ENSMUST00000173872	ENSMUSG00000038500	17	35972541	35980236	-1	0	0	0	6	0	4	3	2	1	0	3	G3UYB8	
ENSMUST00000173874	ENSMUSG00000040482	17	34837019	34839233	1	0	0	13	43	0	0	3	0	0	0	41	G3UZ39	
ENSMUST00000173875	ENSMUSG00000006050	18	36666681	36679366	-1	36	37	28	47	37	24	18	113	35	14	42		Q80VJ2
ENSMUST00000173876						2	2	2	2	0	0	0	0	0	0	0		
ENSMUST00000173877						637	561	1013	587	636	304	10	44	27	10	45		
ENSMUST00000173878	ENSMUSG00000027510	2	173020498	173034734	1	0	0	0	109	0	0	31	37	96	0	19	G3UWQ8	
ENSMUST00000173879	ENSMUSG00000067288	17	33819027	33824562	-1	2	0	9	2	2	0	0	8	2	8	8	G3UYV7	
ENSMUST00000173880						3	5	3	3	2	1	0	0	0	0	0		
ENSMUST00000173881	ENSMUSG00000026069	1	40429570	40465415	1	0	0	3	2	1	1	4	0	0	0	2	G3UYU3	
ENSMUST00000173884	ENSMUSG00000028382	4	59471868	59549364	-1	0	0	0	14	2	0	0	0	0	0	0	G3UY95	
ENSMUST00000173885						0	0	6	4	0	2	16	11	8	0	5		
ENSMUST00000173886	ENSMUSG00000096761	7	20544834	20545757	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7G9	
ENSMUST00000173887						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000173888	ENSMUSG00000060261	5	134237834	134314760	-1	6	7	0	18	4	0	0	0	41	0	0		Q9ESZ8
ENSMUST00000173890						1	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000173891	ENSMUSG00000021519	13	66906968	66933088	-1	0	2	3	1	3	4	0	4	0	1	0	G3UWK8	
ENSMUST00000173892						3	1	1	0	0	2	1	34	0	5	6		
ENSMUST00000173894						0	0	0	0	0	5	2	0	0	0	0		
ENSMUST00000173895	ENSMUSG00000042719	5	121397936	121444378	1	0	0	4	3	0	2	13	0	10	9	39	G3UZX9	
ENSMUST00000173896	ENSMUSG00000022160	14	52294668	52305128	-1	2	0	0	0	0	0	1	0	0	0	0	G3UYB5	
ENSMUST00000173898	ENSMUSG00000063765	15	81678296	81697287	-1	0	0	0	36	8	0	0	0	0	0	0	G3UY83	
ENSMUST00000173899	ENSMUSG00000027684	3	29951296	30548008	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWT0	
ENSMUST00000173901						0	3	1	1	1	2	0	0	0	0	0		
ENSMUST00000173902						1	0	2	1	5	2	0	0	0	0	0		
ENSMUST00000173903	ENSMUSG00000040312	17	35517100	35531015	1	32	15	39	33	29	14	0	0	0	0	0	G3UWS7	
ENSMUST00000173904						4	2	5	1	2	1	0	0	0	0	0		
ENSMUST00000173905	ENSMUSG00000047146	10	62804570	62899118	-1	0	0	0	0	0	0	0	0	1	0	0	G3UZN8	
ENSMUST00000173906	ENSMUSG00000038518	13	44729474	44921643	1	0	0	9	0	0	0	0	0	0	0	13	G3UZT8	
ENSMUST00000173907						0	1	6	6	2	0	61	73	17	0	69		
ENSMUST00000173908	ENSMUSG00000026456	1	134405559	134411740	1	0	0	0	0	0	0	17	8	21	12	10	G3UZG6	
ENSMUST00000173909						14	24	47	15	0	13	18	28	13	0	15		
ENSMUST00000173910	ENSMUSG00000021519	13	66906968	66933088	-1	0	0	0	0	0	0	0	7	0	0	1	G3UWX0	
ENSMUST00000173911						0	5	14	5	9	1	0	4	0	0	10		
ENSMUST00000173912	ENSMUSG00000066772	7	15479825	15639902	-1	10	7	13	11	8	8	0	0	0	0	0	Q3UT54	
ENSMUST00000173913	ENSMUSG00000004591	3	142790902	142882004	-1	0	0	0	3	8	3	0	144	210	62	144	G3UYE1	
ENSMUST00000173914						30	18	182	46	38	11	3	11	3	0	14		
ENSMUST00000173915	ENSMUSG00000024387	17	35116196	35122053	-1	0	2	3	21	1	4	0	3	2	0	0	G3UWU5	
ENSMUST00000173916	ENSMUSG00000036938	6	41311233	41316841	-1	13	3	94	34	11	8	2	0	0	0	1	G3UXD0	
ENSMUST00000173917	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	0	3	0	0	0	0	0	0	G3UWQ9	
ENSMUST00000173918						2	0	0	1	3	1	0	0	0	0	0		
ENSMUST00000173919						12	7	28	50	15	3	0	0	2	0	1		
ENSMUST00000173920	ENSMUSG00000026921	2	26580014	26593120	1	0	0	0	50	5	2	0	4	0	0	0	G3UZH9	
ENSMUST00000173921	ENSMUSG00000036036	17	37001163	37010635	1	0	0	0	5	0	0	0	0	0	0	0	G3UX77	
ENSMUST00000173922	ENSMUSG00000033545	8	111536097	111626030	1	0	0	3	0	0	0	153	152	91	26	51	G3UZ70	
ENSMUST00000173923	ENSMUSG00000049811	11	23007531	23030788	1	5	1	0	0	0	3	0	0	0	0	0	Q9CUP0	
ENSMUST00000173924	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	0	8	0	0	0	0	0	0	G3UYN4	
ENSMUST00000173925						3	3	14	0	3	1	0	0	0	0	0		
ENSMUST00000173926						0	4	1	1	11	0	0	0	0	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000173927	ENSMUSG00000029209	5	69573108	69592340	-1	0	0	0	0	0	0	0	24	0	38	14		Q9CRC9
ENSMUST00000173928						2	1	5	10	2	0	10	104	24	0	30		
ENSMUST00000173929	ENSMUSG00000026596	1	156558786	156649568	1	1	0	0	133	9	4	0	0	5	1	1	G3UWQ2	
ENSMUST00000173930	ENSMUSG00000024235	18	4331327	4353015	-1	0	0	0	8	0	0	32	318	92	0	15	G3UWY2	
ENSMUST00000173931	ENSMUSG00000024299	17	33524204	33553782	1	0	0	0	45	0	0	35	161	89	0	153	G3UZ08	
ENSMUST00000173932	ENSMUSG00000027971	3	125404076	125728899	1	0	0	0	0	0	0	0	0	0	0	0		Q9EQW8
ENSMUST00000173933	ENSMUSG00000036972	9	91362413	91389348	1	0	0	6	7	2	1	0	0	0	0	0	G3UYE7	
ENSMUST00000173934	ENSMUSG00000024406	17	35506018	35510772	1	7	12	21	7	11	7	0	0	0	0	0	E2JL30	
ENSMUST00000173935						5	5	8	4	10	3	7	24	19	1	18		
ENSMUST00000173936						0	0	0	0	0	2	2	0	0	0	5		
ENSMUST00000173937	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	0	0	0	0	0	D6RDC0	
ENSMUST00000173938	ENSMUSG00000017428	11	80428615	80473248	1	0	5	4	4	0	4	153	408	312	398	221	Q5BKQ9	Q8BG32
ENSMUST00000173939						0	2	0	2	2	1	4	7	13	0	22		
ENSMUST00000173940						0	0	2	2	0	0	0	0	0	0	0		
ENSMUST00000173941	ENSMUSG00000053046	7	141949751	142004247	1	2	0	4	6	11	2	0	0	0	0	0	G5E921	
ENSMUST00000173942	ENSMUSG00000037638	12	112678828	112682747	1	0	0	0	36	0	0	0	0	0	0	13	G3UY89	
ENSMUST00000173943						0	0	6	5	3	0	13	21	17	0	20		
ENSMUST00000173944						0	1	3	1	1	1	0	0	1	0	5		
ENSMUST00000173945						12	10	57	27	29	13	60	122	61	12	82		
ENSMUST00000173946						5	6	0	2	1	0	6	10	4	2	4		
ENSMUST00000173947						1	3	8	2	2	0	0	0	0	0	0		
ENSMUST00000173948	ENSMUSG00000020185	10	110745439	110787384	1	1	0	0	0	0	0	0	0	2	0	0	G3UYD4	
ENSMUST00000173949						9	8	28	0	0	12	2	0	0	0	6		
ENSMUST00000173950						19	19	151	34	34	15	0	5	0	0	5		
ENSMUST00000173951	ENSMUSG00000079608	18	70472454	70501066	1	0	1	0	1	2	3	0	0	0	0	0	G3UYT3	
ENSMUST00000173952	ENSMUSG00000024392	17	35135178	35147322	1	0	5	5	27	0	2	37	30	49	0	92	G3V013	
ENSMUST00000173953						2	1	1	6	1	1	0	0	0	0	0		
ENSMUST00000173954	ENSMUSG00000040123	14	56790585	56811716	-1	0	0	0	32	0	0	162	784	344	221	160		Q3U2E2
ENSMUST00000173955						7	3	16	27	10	11	7	43	0	14	39		
ENSMUST00000173956	ENSMUSG00000092579	7	5674627	5676383	1	0	0	0	0	2	3	0	0	0	0	0	Q8R2C0	
ENSMUST00000173957	ENSMUSG00000039431	8	40551095	40634797	-1	0	0	1	0	2	0	0	0	0	0	0	G3UYB7	
ENSMUST00000173958						0	5	0	0	0	2	0	0	0	0	4		
ENSMUST00000173960						0	0	0	16	11	7	0	0	0	0	0		
ENSMUST00000173961						3	0	6	5	3	0	0	1	3	0	3		
ENSMUST00000173962	ENSMUSG00000059554	10	18213676	18234998	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXW3	
ENSMUST00000173963	ENSMUSG00000032113	9	36708482	36727065	-1	0	0	0	0	0	0	0	13	5	27	9	G3UYC5	
ENSMUST00000173964	ENSMUSG00000021959	14	57642077	57758388	-1	0	0	0	49	0	2	0	0	1	1	26	G3UYM3	
ENSMUST00000173966						27	23	75	48	45	20	0	7	10	7	18		
ENSMUST00000173967	ENSMUSG00000024422	17	35879819	35892670	1	0	0	0	0	0	0	0	153	0	6	0	G3UXT5	
ENSMUST00000173968						3	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000173969	ENSMUSG00000091931	12	102753275	102757803	-1	22	37	89	49	35	20	67	243	103	60	74		P0C8B4
ENSMUST00000173970						3	4	7	2	4	0	2	0	0	0	0		
ENSMUST00000173971						2	1	3	1	4	0	0	0	0	0	0		
ENSMUST00000173972						21	9	45	20	4	22	11	46	12	2	20		
ENSMUST00000173973	ENSMUSG00000034254	17	34604262	34613449	1	1	0	0	96	0	0	14	12	15	0	20	G3UY51	
ENSMUST00000173974						74	60	295	97	57	24	1	5	0	0	3		
ENSMUST00000173975						26	13	40	720	22	25	67	381	146	24	351		
ENSMUST00000173976						0	4	0	1	2	0	3	0	6	0	0		
ENSMUST00000173977						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000173979	ENSMUSG00000027510	2	173020498	173034734	1	0	0	4	0	7	0	337	270	215	9	91	G3UXG4	
ENSMUST00000173981	ENSMUSG00000068877	3	94693556	94704413	1	0	0	3	0	5	0	4	5	4	0	3	G3UWK0	
ENSMUST00000173982	ENSMUSG00000079553	17	33875666	33890661	-1	1	1	7	0	3	0	0	10	0	0	0	G3UX22	
ENSMUST00000173983	ENSMUSG00000025977	1	55248658	55363469	-1	3	2	1	0	0	2	1	0	0	0	0	G3UYE8	
ENSMUST00000173984	ENSMUSG00000015461	17	34647146	34655074	1	17	0	0	61	17	0	13	11	160	0	155	G3UX19	
ENSMUST00000173985	ENSMUSG00000024517	18	65872820	65886579	1	10	5	11	13	9	0	0	0	0	0	0		Q8R1I2
ENSMUST00000173986						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000173987	ENSMUSG00000077450	17	33742484	33760530	-1	53	101	119	44	37	37	436	326	357	62	307	G3UY29	
ENSMUST00000173988						76	53	303	100	48	32	0	3	1	0	1		
ENSMUST00000173989						3	3	1	7	3	3	27	66	37	6	61		
ENSMUST00000173990	ENSMUSG00000021959	14	57642077	57758388	-1	13	7	32	61	15	7	11	14	8	4	45	G3UY78	
ENSMUST00000173991						2	1	0	4	1	1	0	0	0	0	0		
ENSMUST00000173992	ENSMUSG00000015452	17	34597862	34600936	1	2	0	4	0	2	0	9	21	11	0	0	C5H7W9	
ENSMUST00000173994						0	0	1	11	3	0	0	0	0	0	0		
ENSMUST00000173995	ENSMUSG00000040482	17	34837019	34839233	1	3	3	37	41	0	2	31	44	33	0	35	G3UZP8	
ENSMUST00000173996	ENSMUSG00000041353	X	150397773	150459154	-1	0	0	0	1	9	6	0	0	0	0	1	A2ANF5	
ENSMUST00000173997	ENSMUSG00000027510	2	173020498	173034734	1	0	3	0	0	0	0	120	0	0	0	19	G3UWX7	
ENSMUST00000173998	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	0	0	0	0	G3UXP7	
ENSMUST00000173999						13	16	21	28	16	8	5	373	8	106	58		
ENSMUST00000174000	ENSMUSG00000090523	18	32528322	32560034	-1	0	0	0	0	0	4	38	31	13	21	43	G3UXY6	
ENSMUST00000174001	ENSMUSG00000015120	17	25261916	25274622	-1	5	2	2	2	0	3	15	0	82	0	39		P63280
ENSMUST00000174003						1	2	5	2	5	3	0	0	0	0	5		
ENSMUST00000174004	ENSMUSG00000050088	17	14943184	14959570	1	0	0	1	0	0	0	200	108	179	237	139		Q9DAY5
ENSMUST00000174006	ENSMUSG00000028114	3	123368297	123386108	-1	2	0	0	0	0	1	4	28	2	0	0	G3UXL6	
ENSMUST00000174007	ENSMUSG00000019794	10	7726000	7763150	1	0	2	0	0	1	2	0	0	0	0	0	G3UWK1	
ENSMUST00000174008	ENSMUSG00000032187	9	21616169	21704230	1	0	0	0	0	0	0	600	768	1001	67	810		Q3TKT4
ENSMUST00000174009	ENSMUSG00000035469	14	59201209	59237265	1	0	0	0	63	0	0	0	0	0	0	0	G3UYZ5	
ENSMUST00000174010						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000174011						455	448	338	358	455	231	67	415	158	86	137		
ENSMUST00000174012						0	1	1	9	2	1	0	0	0	0	0		
ENSMUST00000174013						0	0	1	0	0	1	0	0	0	0	5		
ENSMUST00000174015	ENSMUSG00000053347	17	21962552	22071168	1	2	2	2	7	4	0	2	5	0	0	0	G3UXL1	
ENSMUST00000174016						0	0	0	32	0	0	0	0	0	0	0		
ENSMUST00000174017						2	1	4	1	0	2	0	3	7	0	2		
ENSMUST00000174018	ENSMUSG00000056755	6	110645581	111567230	1	11	11	7	8	12	0	0	0	0	0	0	G3UZU3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174019						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174020	ENSMUSG00000022159	14	52261759	52279545	-1	0	0	0	0	1	0	2	0	6	1	0	G3V022	
ENSMUST00000174021	ENSMUSG00000042632	15	79286228	79328390	-1	0	0	0	0	0	0	0	35	13	0	0		P97819
ENSMUST00000174022						4	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000174023	ENSMUSG00000028399	4	75941238	78211961	-1	0	0	0	0	0	0	0	0	0	0	0	G3UX60	
ENSMUST00000174024	ENSMUSG00000024387	17	35116196	35122053	-1	1	0	3	0	7	1	0	133	45	10	20	G3UZX4	
ENSMUST00000174026	ENSMUSG00000007035	17	35028605	35046745	-1	11	5	18	5	13	7	12	59	33	0	52	G3UZ06	
ENSMUST00000174027						4	0	14	0	0	0	0	0	0	0	0		
ENSMUST00000174028						3	3	1	0	3	2	0	0	0	0	1		
ENSMUST00000174029						0	0	7	0	0	1	0	14	0	0	0		
ENSMUST00000174030	ENSMUSG00000003662	2	127240938	127247816	-1	2	0	1	0	2	0	214	346	178	84	111	G3UYR5	
ENSMUST00000174031	ENSMUSG00000015120	17	25261916	25274622	-1	0	0	0	7	6	0	103	341	214	118	94		P63280
ENSMUST00000174033						7	2	8	9	3	1	2	33	18	0	19		
ENSMUST00000174034						0	0	13	0	3	0	4	10	6	4	14		
ENSMUST00000174035						0	0	2	6	3	1	19	2	16	0	0		
ENSMUST00000174036						4	0	0	11	5	3	0	0	0	0	0		
ENSMUST00000174037	ENSMUSG00000036185	17	35025959	35028016	-1	0	0	0	0	0	0	1	0	9	0	18	G3UXZ3	
ENSMUST00000174038	ENSMUSG00000041431	13	100778650	100786570	-1	0	0	0	0	0	0	60	132	103	193	63	G3UY65	
ENSMUST00000174040	ENSMUSG00000079557	17	33685692	33718670	-1	2	1	1	0	4	4	97	37	35	33	28	G3UZC4	
ENSMUST00000174041	ENSMUSG00000034254	17	34604262	34613449	1	3	3	6	62	4	6	3	2	0	0	0	G3UWV6	
ENSMUST00000174042	ENSMUSG00000020875	11	96271457	96276595	1	39	22	25	0	18	17	0	0	0	0	2	Q496Q8	
ENSMUST00000174043						4536	4829	7489	3635	4373	1998	97	406	215	42	162		
ENSMUST00000174044						7	3	13	10	5	4	4	10	2	1	10		
ENSMUST00000174045						13	6	18	63	12	1	4	6	0	2	4		
ENSMUST00000174046						9	8	7	7	4	4	0	0	0	0	0		
ENSMUST00000174047	ENSMUSG00000007739	11	22990519	23003780	1	0	0	2	0	0	0	0	0	0	0	0	G3UYW5	
ENSMUST00000174048	ENSMUSG00000024309	17	33938821	33940343	-1	0	0	0	0	0	0	56	169	34	64	40	Q792E4	Q03958
ENSMUST00000174049						43	36	107	615	69	33	2	12	4	0	2		
ENSMUST00000174050	ENSMUSG00000033335	9	21424908	21507759	1	6	0	0	0	0	0	720	0	273	0	0	G3UZZ3	
ENSMUST00000174051	ENSMUSG00000038943	7	80294450	80316259	1	10	9	4	0	9	0	0	0	0	23	0	G3UYX6	
ENSMUST00000174052						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000174053						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174054						23	5	15	29	17	10	21	71	23	3	29		
ENSMUST00000174055	ENSMUSG00000074289	7	23702342	23703313	1	3	2	2	0	0	1	0	0	0	0	0	E9Q8V7	
ENSMUST00000174056	ENSMUSG00000075046	10	58229979	58232675	-1	312	205	1494	520	495	240	0	0	0	0	0	G3UY18	
ENSMUST00000174058	ENSMUSG00000025495	7	141122382	141157021	1	0	0	0	26	0	0	0	0	0	0	0	G3UYQ3	
ENSMUST00000174059	ENSMUSG00000037437	8	24836140	24948804	-1	0	1	0	0	0	0	0	0	0	0	0	G3UZY0	
ENSMUST00000174060						0	0	7	0	0	3	0	8	11	0	0		
ENSMUST00000174061						0	0	0	26	10	6	0	0	0	0	3		
ENSMUST00000174062						15	16	29	120	22	7	0	5	4	0	0		
ENSMUST00000174063	ENSMUSG00000053835	17	36005695	36020560	-1	11	9	15	17	23	6	0	2	0	0	9	G3UWY8	
ENSMUST00000174064	ENSMUSG00000002985	7	19696109	19699166	-1	5	0	8	42	0	1	211	354	153	232	372	Q3TXU4	P08226
ENSMUST00000174065						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000174066	ENSMUSG00000092356	2	26586639	26635634	1	0	0	0	0	3	0	0	1	0	0	0	G3UXR8	
ENSMUST00000174068	ENSMUSG00000038518	13	44729474	44921643	1	1	0	2	18	0	0	0	0	7	0	0	G3UZQ8	
ENSMUST00000174069	ENSMUSG00000015452	17	34597862	34600936	1	0	0	0	0	0	0	0	38	12	7	11	C5H3H4	
ENSMUST00000174070	ENSMUSG00000050373	2	164785823	164793816	1	6	0	0	273	12	5	0	7	0	0	0	G3UWM2	
ENSMUST00000174071						1	6	6	2	4	0	0	2	0	0	0		
ENSMUST00000174072	ENSMUSG00000046157	12	78961795	79007627	-1	6	9	0	0	0	0	292	443	190	49	269		Q8BFQ2
ENSMUST00000174073	ENSMUSG00000028797	4	129600668	129624059	1	0	3	10	2	1	0	15	31	18	16	8	D6RDC0	
ENSMUST00000174075						4	2	0	5	2	2	0	1	0	0	1		
ENSMUST00000174076	ENSMUSG00000074369	7	15388721	15398545	1	0	0	8	3	2	0	0	0	0	0	0	E9PXV9	
ENSMUST00000174077	ENSMUSG00000068921	3	88920803	88951181	-1	1	0	1	0	0	0	5	2	0	0	30	G3UZC0	
ENSMUST00000174078	ENSMUSG00000041025	4	139530548	139620382	1	10	18	16	306	42	24	23	35	48	0	81		Q8R2V2
ENSMUST00000174080	ENSMUSG00000059714	17	35823230	35832791	1	0	0	0	0	0	4	183	0	140	25	31	G3UYU4	
ENSMUST00000174081						5	2	0	30	8	4	0	5	13	0	0		
ENSMUST00000174083	ENSMUSG00000030688	7	101317086	101346626	1	0	5	11	2	3	2	0	0	0	0	0	G3V020	
ENSMUST00000174084						11	7	51	136	12	6	0	20	2	6	11		
ENSMUST00000174086	ENSMUSG00000038518	13	44729474	44921643	1	0	1	0	0	1	1	0	0	0	0	0	G3UXT1	
ENSMUST00000174088	ENSMUSG00000092519	17	33432896	33434268	1	9	1	1	8	28	0	0	0	0	0	0		Q8CG27
ENSMUST00000174089						2	0	5	1	6	0	0	0	0	0	3		
ENSMUST00000174090	ENSMUSG00000041769	7	138846079	138883057	1	0	0	0	0	0	0	0	0	0	0	0	G3UZP6	
ENSMUST00000174091						0	2	1	1	0	1	0	0	0	1	0		
ENSMUST00000174092	ENSMUSG00000040482	17	34837019	34839233	1	0	0	0	0	0	0	0	0	0	0	0	G3UX82	
ENSMUST00000174093						2	2	10	0	2	0	0	0	0	6	14		
ENSMUST00000174094						0	1	5	70	4	1	304	263	276	0	138		
ENSMUST00000174095	ENSMUSG00000019082	7	141429744	141437892	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ58	
ENSMUST00000174096	ENSMUSG00000029767	6	29348069	29377110	1	0	0	0	0	0	0	11	0	78	82	49	G3UY49	
ENSMUST00000174097	ENSMUSG00000063646	5	37028335	37148001	1	0	0	0	0	0	0	1	0	0	0	0	G3UXP3	
ENSMUST00000174098						11	18	13	15	0	8	0	0	1	0	0		
ENSMUST00000174099						2	6	1	0	4	2	11	15	5	8	18		
ENSMUST00000174101	ENSMUSG00000054128	17	36185572	36190287	-1	0	0	0	0	0	2	0	1	0	0	1	S4R2A2	
ENSMUST00000174102	ENSMUSG00000020661	12	3806007	3914443	1	2	1	3	0	3	3	0	0	0	0	0	G3UZF8	
ENSMUST00000174103						1	0	0	0	0	1	0	21	0	1	0		
ENSMUST00000174104						0	0	20	0	11	0	5	0	25	0	0		
ENSMUST00000174105	ENSMUSG00000032113	9	36708482	36727065	-1	0	0	0	0	0	0	9	5	1	37	0	G3UZ93	
ENSMUST00000174106						10	8	8	3	5	5	0	0	0	0	0		
ENSMUST00000174107						11	4	70	10	4	2	0	0	0	0	0		
ENSMUST00000174108						7	0	126	0	11	0	0	0	0	2	0		
ENSMUST00000174109	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	12	0	4	0	G3UYN2	
ENSMUST00000174111	ENSMUSG00000038943	7	80294450	80316259	1	0	0	0	0	0	0	0	0	0	0	0	G3UYZ3	
ENSMUST00000174112						0	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000174113	ENSMUSG00000020265	10	77606097	77641543	1	0	0	0	1	4	2	0	0	3	30	0	G3UZ60	
ENSMUST00000174115						18	10	32	145	19	5	0	0	0	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174117	ENSMUSG00000036185	17	35025959	35028016	-1	0	2	3	0	3	1	4	45	3	0	4	G3UXZ3	
ENSMUST00000174118	ENSMUSG00000079608	18	70472454	70501066	1	0	2	1	7	0	0	0	0	0	0	0	Q9CPT8	P59096
ENSMUST00000174119						3	2	0	0	2	1	0	0	0	0	0		
ENSMUST00000174120	ENSMUSG00000026028	1	58900449	58973430	-1	6	0	0	0	8	0	165	3	1308	0	758	G3UYW9	
ENSMUST00000174121	ENSMUSG00000047146	10	62804570	62899118	-1	0	0	0	0	0	2	0	0	2	0	0	G3UZ35	
ENSMUST00000174122	ENSMUSG00000024228	17	58999618	59013372	-1	0	0	0	0	1	1	0	1	0	3	0		Q9DCN1
ENSMUST00000174123						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174124	ENSMUSG00000061607	17	35841515	35859670	1	0	2	5	4	1	0	7	0	3	0	7	G3UX64	
ENSMUST00000174125						1	1	1	5	1	0	0	2	2	0	6		
ENSMUST00000174126	ENSMUSG00000064068	3	89209081	89227088	-1	0	0	0	0	0	0	0	9	0	0	0	G3XA75	
ENSMUST00000174127						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000174128	ENSMUSG00000038762	17	35956819	35969761	-1	0	0	5	8	0	0	0	0	32	0	19	G3V012	
ENSMUST00000174129						2	2	1	1	1	4	0	0	0	0	0		
ENSMUST00000174130						0	1	2	2	3	0	2	2	3	0	13		
ENSMUST00000174132						5	1	7	3	6	3	0	5	10	0	5		
ENSMUST00000174133	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	0	0	2	2	2	0	0	0	G3UYJ6	
ENSMUST00000174134						3	1	2	0	0	0	21	58	6	0	8		
ENSMUST00000174135						8	0	7	24	9	6	0	4	0	0	0		
ENSMUST00000174137						64	42	133	102	86	26	12	26	31	6	45		
ENSMUST00000174138						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174139	ENSMUSG00000092292	17	37574454	37575448	-1	0	0	0	0	0	0	0	0	0	0	0	Q8VEU4	
ENSMUST00000174140	ENSMUSG00000030688	7	101317086	101346626	1	0	0	0	0	0	0	3	2	13	0	1	G3UZB9	
ENSMUST00000174142	ENSMUSG00000037470	1	36140027	36244720	-1	0	0	0	0	0	0	0	0	0	0	0	G3UY35	
ENSMUST00000174143	ENSMUSG00000079495	6	85808024	85820954	-1	94	77	158	86	122	45	1	0	0	0	4		Q9JIY8
ENSMUST00000174144	ENSMUSG00000002985	7	19696109	19699166	-1	0	0	2	10	3	5	21	236	49	0	42	G3UWN5	
ENSMUST00000174145						0	0	0	0	0	0	0	0	3	0	5		
ENSMUST00000174146	ENSMUSG00000002307	17	33909414	33915589	1	0	0	0	0	0	0	379	654	503	0	352	Q3UKR0	
ENSMUST00000174147	ENSMUSG00000074264	3	113555710	113606699	-1	0	0	0	0	0	0	0	2	0	3	0	G3UXY7	
ENSMUST00000174148						0	0	5	0	0	0	19	225	17	43	32		
ENSMUST00000174149	ENSMUSG00000024856	19	4097182	4099019	1	0	0	0	0	0	0	0	0	0	0	0	G3UX88	
ENSMUST00000174151	ENSMUSG00000066772	7	15479825	15639902	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXT3	
ENSMUST00000174152	ENSMUSG00000021952	14	57581002	57665430	-1	0	0	0	0	3	0	5	0	4	0	13	G3UX04	
ENSMUST00000174153						5	5	6	9	11	1	0	0	0	0	0		
ENSMUST00000174155	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	0	0	0	13	0	0	0	17		Q9ESZ8
ENSMUST00000174156						1	0	8	5	3	0	6	10	2	0	4		
ENSMUST00000174157	ENSMUSG00000059070	7	45715457	45720835	1	0	0	0	1	0	0	0	33	0	8	3	G3UYV6	
ENSMUST00000174158	ENSMUSG00000054054	7	86306185	86313509	-1	0	0	0	0	5	0	0	0	0	0	0	Q7TS01	
ENSMUST00000174159	ENSMUSG00000018752	11	69682577	69696098	-1	7	0	0	0	0	0	4	24	8	12	49	Q5F2A1	
ENSMUST00000174160	ENSMUSG00000039458	15	12205028	12272240	1	0	0	0	0	0	0	2	169	234	36	239	G3UZ04	
ENSMUST00000174161						67	35	168	444	68	46	65	775	143	23	344		
ENSMUST00000174162						3	1	93	13	5	1	0	0	0	0	0		
ENSMUST00000174163						4	4	2	0	7	1	3	10	4	4	1		
ENSMUST00000174164						16	11	28	33	18	6	230	630	323	37	547		
ENSMUST00000174165	ENSMUSG00000031753	8	110846600	110882227	1	0	0	0	22	2	0	5	0	5	4	14	G3UZ15	
ENSMUST00000174166	ENSMUSG00000021959	14	57642077	57758388	-1	1	1	2	1	3	0	0	0	0	0	0	G3UWQ0	
ENSMUST00000174169						3	5	3	1	2	0	0	1	0	0	0		
ENSMUST00000174170						0	0	7	48	5	5	0	5	5	4	7		
ENSMUST00000174171	ENSMUSG00000022514	16	26581704	26730117	1	1	0	3	0	1	0	114	0	757	375	706	G3UY13	
ENSMUST00000174172	ENSMUSG00000038943	7	80294450	80316259	1	0	0	0	0	0	0	52	0	60	0	86	G3UWQ7	
ENSMUST00000174174	ENSMUSG00000020534	11	60788104	60811718	-1	0	0	0	0	0	0	0	3	0	0	0	G3UZZ9	
ENSMUST00000174175						0	1	1	4	5	0	0	24	6	11	6		
ENSMUST00000174176	ENSMUSG00000024670	19	10789341	10830058	-1	3	2	0	7	6	2	0	0	0	2	1	G3UZU7	
ENSMUST00000174177	ENSMUSG00000092300	11	116216003	116220287	1	0	1	9	3	7	3	0	0	0	0	2		
ENSMUST00000174178						1	3	6	26	4	2	0	0	0	0	0		
ENSMUST00000174179	ENSMUSG00000079436	1	87386363	87394729	-1	0	0	2	0	0	0	0	0	0	0	3	G3UX25	
ENSMUST00000174180	ENSMUSG00000028399	4	75941238	78211961	-1	0	0	0	0	0	0	0	0	0	0	0	G3UY75	
ENSMUST00000174181						6	3	16	11	8	0	1	4	0	0	5		
ENSMUST00000174182						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174183	ENSMUSG00000028033	1	21398403	21961942	-1	8	0	19	0	0	0	1	0	0	0	0	G3UZ84	
ENSMUST00000174184						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174186	ENSMUSG00000028525	4	102087543	102607259	1	4	4	0	0	0	0	0	0	0	0	0	G3UZY9	
ENSMUST00000174187	ENSMUSG00000001665	10	75774115	75781414	-1	3	1	3	2	6	1	0	0	0	0	0	G3UX71	
ENSMUST00000174188	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	0	0	0	0	3	2	0	4	G3UZU4	
ENSMUST00000174189	ENSMUSG00000047146	10	62804570	62899118	-1	37	82	229	104	112	37	0	0	0	0	0	E9Q9Y4	
ENSMUST00000174190	ENSMUSG00000073414	17	35062693	35066184	-1	1	4	6	57	4	0	4	0	0	1	6	D7PDD4	
ENSMUST00000174191	ENSMUSG00000002985	7	19696109	19699166	-1	2	0	11	4	0	0	0	0	0	0	0	G3UWW2	
ENSMUST00000174192	ENSMUSG00000040263	8	121796313	121829569	-1	0	2	0	0	0	0	168	137	156	8	92	G3UZG5	
ENSMUST00000174193	ENSMUSG00000032517	9	120149742	120181484	1	21	9	11	17	21	9	0	0	0	0	0		Q9D2P8
ENSMUST00000174194	ENSMUSG00000029706	6	28442334	28449353	-1	0	0	0	0	0	1	0	0	0	0	0	G3UZE8	
ENSMUST00000174195	ENSMUSG00000050747	17	36860691	36867210	-1	1	2	0	23	8	4	0	1	1	0	0	G3UY57	
ENSMUST00000174196						0	0	0	26	0	3	36	64	55	11	81		
ENSMUST00000174197						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174199	ENSMUSG00000038943	7	80294450	80316259	1	1	13	8	13	6	6	22	0	81	41	37	G3XA79	
ENSMUST00000174200						3	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000174201						637	676	898	345	466	200	17	70	11	8	57		
ENSMUST00000174202	ENSMUSG00000022514	16	26581704	26730117	1	2	3	5	9	7	5	63	369	96	138	122	Q3UEL3	Q61730
ENSMUST00000174203	ENSMUSG00000092310	9	73102470	73117920	1	0	0	3	0	0	0	0	0	4	0	16	G3UZF1	
ENSMUST00000174204	ENSMUSG00000062818	6	90122643	90130990	1	0	0	0	14	0	0	0	0	0	0	0		
ENSMUST00000174205	ENSMUSG00000039431	8	40551095	40634797	-1	29	30	124	15	28	12	1	12	12	1	16	G3V027	
ENSMUST00000174206						3	6	13	0	6	7	0	34	3	0	3		
ENSMUST00000174208						8	3	18	5	3	7	0	0	0	0	0		
ENSMUST00000174209						71	151	47	37	95	59	1	4	9	10	4		
ENSMUST00000174210						5	12	16	6	8	7	0	0	17	0	59		
ENSMUST00000174211	ENSMUSG00000026921	2	26580014	26593120	1	0	0	0	0	0	0	11	0	0	0	4	Q3UTJ7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174212	ENSMUSG00000036972	9	91362413	91389348	1	0	0	4	4	2	0	0	0	0	0	0	G3UXS7	
ENSMUST00000174213	ENSMUSG00000021959	14	57642077	57758388	-1	15	5	35	101	21	7	18	0	260	0	121	G3UZ29	
ENSMUST00000174214	ENSMUSG00000020534	11	60788104	60811718	-1	3	0	0	0	0	0	0	3	6	3	0	G3UYY1	
ENSMUST00000174215						2	3	11	3	4	1	0	0	0	0	0		
ENSMUST00000174216	ENSMUSG00000015120	17	25261916	25274622	-1	2	3	9	9	3	0	39	274	82	9	129	G3UZL6	
ENSMUST00000174218						0	0	0	1	2	0	39	30	37	4	36		
ENSMUST00000174219	ENSMUSG00000028073	3	87747890	87824306	-1	2	0	2	2	0	0	0	0	0	0	0	G3UX62	
ENSMUST00000174220						4	4	0	145	0	0	5	1	9	0	15		
ENSMUST00000174221						4	1	0	1	3	0	0	0	0	0	0		
ENSMUST00000174222						2	4	4	0	1	0	0	0	0	0	0		
ENSMUST00000174223	ENSMUSG00000068877	3	94693556	94704413	1	0	0	0	0	0	0	0	0	0	0	0	G3UZT2	
ENSMUST00000174224	ENSMUSG00000037470	1	36140027	36244720	-1	0	2	0	0	2	0	0	0	7	0	0	G3UY73	
ENSMUST00000174225	ENSMUSG00000035021	12	54892989	55014348	-1	0	0	0	0	0	0	12	11	12	2	14	G3UWK3	
ENSMUST00000174226						0	13	36	25	18	21	187	603	91	0	217		
ENSMUST00000174227						2	2	0	6	1	0	2	12	11	0	17		
ENSMUST00000174228	ENSMUSG00000034254	17	34604262	34613449	1	0	0	0	0	6	0	0	0	85	0	39	G3UXY8	
ENSMUST00000174229	ENSMUSG00000022394	15	81663889	81688315	1	0	0	0	0	0	0	0	0	3	0	0	G3UY70	
ENSMUST00000174230	ENSMUSG00000021418	13	35893472	35906359	-1	0	0	0	0	0	0	0	0	0	38	0	G3UYU5	
ENSMUST00000174231	ENSMUSG00000021418	13	35893472	35906359	-1	0	0	0	0	0	0	0	0	0	6	0	G3UYT2	
ENSMUST00000174233						0	0	0	0	0	4	6	31	32	101	12		
ENSMUST00000174234	ENSMUSG00000000392	2	62500943	62574075	-1	0	0	0	0	0	0	0	0	0	0	0	G3UXR2	
ENSMUST00000174235						2	2	2	4	1	0	0	0	0	0	0		
ENSMUST00000174236	ENSMUSG00000038843	19	17326141	17356667	-1	0	0	0	6	0	0	231	1711	389	328	1208		Q09324
ENSMUST00000174237	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	0	0	0	0	0	0	0	0	G3UZN4	
ENSMUST00000174238						1	5	11	4	3	1	0	0	0	0	0		
ENSMUST00000174239						3	1	3	0	2	2	0	0	0	0	0		
ENSMUST00000174240						6	2	42	31	11	0	1	1	2	0	1		
ENSMUST00000174241						0	0	0	36	0	2	8	0	0	13	0		
ENSMUST00000174242	ENSMUSG00000014030	4	44524757	44710487	-1	5	4	2	3	9	0	0	0	0	0	0	G3UZ86	
ENSMUST00000174243						2	0	10	8	4	3	6	61	18	0	32		
ENSMUST00000174244						6	6	3	2	6	2	6	44	30	29	80		
ENSMUST00000174246						8	5	26	16	0	9	0	0	0	0	0		
ENSMUST00000174248						6	6	21	14	4	5	0	0	0	1	0		
ENSMUST00000174249	ENSMUSG00000045333	8	87661810	87959595	-1	0	2	5	2	1	0	0	0	0	0	0	G3UYI9	
ENSMUST00000174250						5	4	23	153	13	4	898	1947	683	154	834		
ENSMUST00000174251	ENSMUSG00000012520	5	67094399	67099301	-1	3	6	17	8	10	4	0	0	0	0	0	Q8C741	
ENSMUST00000174252	ENSMUSG00000069539	10	89638721	89686285	-1	19	19	47	200	30	14	156	343	137	31	68		Q8CFE4
ENSMUST00000174253						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174254						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000174255	ENSMUSG00000040263	8	121796313	121829569	-1	0	1	1	4	0	1	0	0	0	0	0	G3UZC6	
ENSMUST00000174256						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000174257	ENSMUSG00000039377	1	184727140	184732619	-1	0	0	9	0	5	0	48	272	0	7	0	G3V024	
ENSMUST00000174258						3	5	11	17	10	2	0	0	0	0	0		
ENSMUST00000174259	ENSMUSG00000022216	14	55578123	55581529	1	6	0	0	42	4	4	856	1726	575	958	643	Q5HZK3	P97371
ENSMUST00000174260	ENSMUSG00000007029	17	35000987	35016322	1	4	4	3	233	12	4	14	6	10	0	28	G3UZ22	
ENSMUST00000174261						2	0	2	1	1	0	0	1	0	0	0		
ENSMUST00000174262						0	4	3	0	4	2	0	0	0	0	0		
ENSMUST00000174263						1	4	3	0	1	0	0	5	2	2	3		
ENSMUST00000174264						9	4	28	15	10	10	0	2	13	3	15		
ENSMUST00000174265	ENSMUSG00000004266	6	124720707	124738714	-1	0	0	0	0	0	0	891	1793	931	234	564		P29351
ENSMUST00000174266	ENSMUSG00000037470	1	36140027	36244720	-1	0	0	0	0	0	0	675	1333	1626	105	1116	G3UZU8	
ENSMUST00000174267	ENSMUSG00000028073	3	87747890	87824306	-1	10	11	27	58	18	19	0	17	4	0	24	G3UXB8	
ENSMUST00000174268						1	3	6	1	4	1	17	9	28	1	26		
ENSMUST00000174269	ENSMUSG00000032423	9	88447009	88482574	-1	0	0	0	0	0	0	2	53	24	0	10	G3UZI2	
ENSMUST00000174270	ENSMUSG00000041375	7	16274042	16286795	-1	1	2	25	5	3	0	0	7	2	0	2	G3UXR7	
ENSMUST00000174271						1	0	5	0	1	2	0	0	0	0	0		
ENSMUST00000174272						1	3	6	1	9	0	0	0	0	0	0		
ENSMUST00000174273						41	28	241	85	45	19	14	24	12	1	24		
ENSMUST00000174274						0	0	0	0	0	0	5	0	0	0	0		
ENSMUST00000174275						1	4	7	76	1	0	8	21	18	0	10		
ENSMUST00000174276						0	8	0	3	11	0	0	0	0	1	0		
ENSMUST00000174278	ENSMUSG00000031562	8	48099092	48153233	1	4	11	81	0	0	3	4	6	3	0	5	G3X908	
ENSMUST00000174279						2	1	8	26	7	0	0	0	0	0	1		
ENSMUST00000174280						2	1	0	0	6	4	0	0	0	0	0		
ENSMUST00000174281	ENSMUSG00000024392	17	35135178	35147322	1	0	13	32	15	0	0	171	0	186	0	125	Q3TDL4	
ENSMUST00000174282	ENSMUSG00000032423	9	88447009	88482574	-1	0	0	0	0	0	0	72	148	65	89	72		
ENSMUST00000174284						10	3	2	28	5	3	0	0	0	1	0		
ENSMUST00000174286	ENSMUSG00000033735	6	85130176	85137766	-1	0	2	0	150	6	4	8	0	0	17	2	G3UXX3	
ENSMUST00000174288	ENSMUSG00000034850	2	127247908	127261107	1	0	0	3	0	0	0	29	0	1	0	58	G3UZT7	
ENSMUST00000174290	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	9	30	9	0	0	G3UXH9	
ENSMUST00000174291	ENSMUSG00000030688	7	101317086	101346626	1	0	0	0	0	2	0	19	6	0	7	10	G3UY87	
ENSMUST00000174292						2	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000174293						2	0	6	0	3	0	6	0	0	2	0		
ENSMUST00000174294	ENSMUSG00000032872	9	87022014	87077774	1	0	2	4	0	1	1	153	1028	89	18	1	G3UY26	
ENSMUST00000174295						34	29	22	15	32	14	4	12	3	0	8		
ENSMUST00000174296	ENSMUSG00000032238	9	68653786	69388246	1	6	0	5	1	0	0	0	0	0	0	0	G3UZ02	
ENSMUST00000174297						1	4	12	6	6	5	23	155	46	7	67		
ENSMUST00000174298	ENSMUSG00000021281	12	111442469	111455018	1	3	0	2	0	0	0	69	32	49	0	126	G3UWJ7	
ENSMUST00000174299	ENSMUSG00000039656	17	34031812	34038393	1	0	0	0	0	2	0	175	0	83	0	0	G3UXP8	
ENSMUST00000174300						164	169	876	278	165	74	4	36	22	5	25		
ENSMUST00000174301	ENSMUSG00000042506	11	61151785	61175055	-1	2	0	0	1	4	1	0	0	7	0	0	H3BLQ1	
ENSMUST00000174302	ENSMUSG00000020923	11	102304560	102319742	-1	0	81	160	172	0	42	11	6	0	0	0	A2AWT5	
ENSMUST00000174303						1	0	2	58	7	5	0	4	1	0	4		
ENSMUST00000174304						4	8	14	15	4	5	0	2	3	2	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174305	ENSMUSG00000074369	7	15388721	15398545	1	0	6	15	0	1	0	0	0	0	0	0	E9PXV9	
ENSMUST00000174306	ENSMUSG00000024387	17	35116196	35122053	-1	0	1	2	0	0	0	61	193	75	11	41	G3UZA4	
ENSMUST00000174307						2	0	6	0	4	0	0	0	0	0	0		
ENSMUST00000174308						4	1	6	2	0	0	0	164	3	6	0		
ENSMUST00000174309	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	0	0	0	0	0	0	0	0	G3UZ19	
ENSMUST00000174310	ENSMUSG00000056755	6	110645581	111567230	1	0	0	0	0	0	0	0	0	0	0	0	G3UY08	
ENSMUST00000174311						3	1	41	39	2	5	27	47	42	5	26		
ENSMUST00000174313	ENSMUSG00000031558	5	47983138	48307733	1	12	12	6	0	1	0	0	0	0	0	0	G3UY21	
ENSMUST00000174314						1	1	1	0	0	0	1	0	0	0	0		
ENSMUST00000174315						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174316						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000174317	ENSMUSG00000037876	10	67096125	67256326	1	0	5	14	6	4	6	25	2	127	0	76	G3UYW3	
ENSMUST00000174318	ENSMUSG00000041578	7	15865947	15879968	-1	172	168	128	123	228	83	6	21	15	2	18	A0A0A0MQN6	
ENSMUST00000174319	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	2	0	0	0	G3UY80	
ENSMUST00000174320	ENSMUSG00000096798	5	146167976	146170721	-1	7	3	13	7	5	6	0	0	0	0	0	L7N481	
ENSMUST00000174322						1	0	0	0	0	1	0	1	0	0	0		
ENSMUST00000174323	ENSMUSG00000028114	3	123368297	123386108	-1	1	0	2	0	6	0	2	5	0	0	0	G3UYS3	
ENSMUST00000174324						4	7	11	14	7	5	0	0	0	0	2		
ENSMUST00000174325						8	2	3	12	8	3	776	1376	497	10	545		
ENSMUST00000174326						0	0	0	1	0	0	3	0	0	3	6		
ENSMUST00000174327						2	4	2	2	4	2	0	4	0	0	0		
ENSMUST00000174328						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174329						8	3	3	5	3	3	0	0	0	0	0		
ENSMUST00000174330						3	2	6	0	2	2	5	12	1	1	5		
ENSMUST00000174331	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	0	0	0	0	0	0	0	0		Q9CS84
ENSMUST00000174333	ENSMUSG00000033545	8	111536097	111626030	1	0	3	0	1	2	0	16	42	14	0	13	E9PWL2	
ENSMUST00000174334	ENSMUSG00000048000	1	87326998	87450796	1	0	0	0	0	0	0	0	0	0	0	1	G3UXF2	
ENSMUST00000174335	ENSMUSG00000026069	1	40429570	40465415	1	0	1	0	0	0	0	2	2	15	0	3	Q5D095	P14719
ENSMUST00000174336						3	7	9	11	0	6	0	0	1	0	1		
ENSMUST00000174337	ENSMUSG00000024109	17	90033631	91093071	-1	0	13	0	122	18	0	0	0	0	0	0	G3UXK2	P0DI97
ENSMUST00000174339	ENSMUSG00000021519	13	66906968	66933088	-1	0	0	0	0	0	0	0	7	2	39	3	G3UYZ7	
ENSMUST00000174340						14	10	17	14	18	10	0	0	0	0	0		
ENSMUST00000174341						5	3	12	1	6	0	0	0	1	0	0		
ENSMUST00000174342						4	2	8	32	6	0	23	11	10	4	5		
ENSMUST00000174343	ENSMUSG00000028960	4	149328416	149426749	-1	0	0	0	0	0	5	282	0	250	0	153	G3UZM6	
ENSMUST00000174344						2	1	8	8	5	3	3	6	5	0	5		
ENSMUST00000174345						5	3	12	56	11	4	1	3	1	0	1		
ENSMUST00000174347	ENSMUSG00000024462	17	37045966	37075067	1	5	2	0	103	1	1	0	0	1	0	12	G3UZ52	
ENSMUST00000174348	ENSMUSG00000024299	17	33524204	33553782	1	3	4	5	6	6	0	7	60	34	0	44	G3UXX0	
ENSMUST00000174349	ENSMUSG00000024436	17	35910379	35916389	-1	7	1	0	0	2	0	0	0	0	0	0	G3UYX8	
ENSMUST00000174350						2	4	4	168	15	2	3	19	11	5	19		
ENSMUST00000174351	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	0	0	0	0	8	0	0	0	0	G5E922	
ENSMUST00000174352	ENSMUSG00000022217	14	55581516	55585302	-1	1	0	3	3	1	1	0	0	0	4	0	G3UWX6	
ENSMUST00000174353	ENSMUSG00000043969	19	59458372	59465357	1	0	0	0	7	0	6	0	0	0	0	0	A0A087WQN3	
ENSMUST00000174354	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	0	0	0	141	97	185	0	215		Q9ESZ8
ENSMUST00000174355	ENSMUSG00000002985	7	19696109	19699166	-1	0	1	0	2	0	0	1216	2836	979	4819	4309	Q3TXU4	P08226
ENSMUST00000174357						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000174358						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174359						0	0	0	0	2	0	0	2	0	0	0		
ENSMUST00000174360	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZP3	
ENSMUST00000174361	ENSMUSG00000032423	9	88447009	88482574	-1	0	0	0	0	0	0	0	37	90	19	0	G3V018	
ENSMUST00000174362	ENSMUSG00000061549	7	86403849	86413299	1	3	2	2	3	2	0	0	0	0	0	0	Q7TS04	
ENSMUST00000174363						18	0	42	30	11	0	106	267	96	22	233		
ENSMUST00000174364	ENSMUSG00000095837	7	20575321	20576241	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7H2	
ENSMUST00000174365						1	1	0	1	2	0	0	0	0	0	0		
ENSMUST00000174366	ENSMUSG00000024422	17	35879819	35892670	1	0	0	0	0	24	16	0	116	122	34	0	Q05BH3	
ENSMUST00000174367						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174368	ENSMUSG00000070847	7	7311723	7337531	-1	75	66	47	82	57	32	0	0	0	0	0	G3UYU1	
ENSMUST00000174369	ENSMUSG00000057103	6	85910154	85915687	-1	7	1	3	5	3	1	8	12	2	2	4	G3UWY7	
ENSMUST00000174370	ENSMUSG00000036962	1	119923341	119997234	-1	0	12	13	19	8	9	0	0	0	0	0		A9Q751
ENSMUST00000174372	ENSMUSG00000028645	4	119108711	119137983	1	0	0	14	2	0	7	236	52	21	9	211	G3V010	
ENSMUST00000174373	ENSMUSG00000025495	7	141122382	141157021	1	0	0	0	0	0	0	13	0	4	0	11	G3UXP2	
ENSMUST00000174375						0	2	6	0	2	0	0	0	3	0	8		
ENSMUST00000174376	ENSMUSG00000033545	8	111536097	111626030	1	2	0	0	0	0	0	9	0	0	0	7	G3UWW9	
ENSMUST00000174377						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174378						16	10	15	7	9	0	0	0	0	0	0		
ENSMUST00000174379	ENSMUSG00000031562	8	48099092	48153233	1	1	2	1	0	2	2	0	0	0	1	0	G3UYS1	
ENSMUST00000174381						17	7	43	47	29	26	0	0	2	0	4		
ENSMUST00000174382	ENSMUSG00000079491	17	36115876	36121465	-1	0	0	0	0	2	0	42	126	24	36	60		
ENSMUST00000174383						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174386						5	5	11	3	4	5	11	55	24	0	15		
ENSMUST00000174387	ENSMUSG00000032376	9	66514637	66593142	-1	0	0	0	45	0	0	273	956	451	0	226	G3UZF0	
ENSMUST00000174388	ENSMUSG00000096658	7	9014750	9030798	-1	38	29	21	4	22	13	0	0	0	0	0	L7N2E5	
ENSMUST00000174389						9	8	4	4	7	4	0	0	0	0	0		
ENSMUST00000174390	ENSMUSG00000061082	X	53069995	53240111	-1	3	0	6	1	0	4	0	0	0	0	0		Q9JI83
ENSMUST00000174391	ENSMUSG00000032423	9	88447009	88482574	-1	0	0	0	0	0	0	1	0	0	0	0	G3UZ48	
ENSMUST00000174392						4	0	10	1	1	1	3	5	2	3	0		
ENSMUST00000174393						3	4	3	1	3	0	0	0	0	0	0		
ENSMUST00000174394						0	5	10	40	6	3	1	0	0	0	2		
ENSMUST00000174395	ENSMUSG00000051860	3	30746293	30767174	1	28	26	86	20	29	17	0	1	1	0	0	G3UXH0	
ENSMUST00000174396						0	2	3	2	5	5	5	39	20	0	25		
ENSMUST00000174397	ENSMUSG00000026586	1	163245119	163313710	-1	72	43	75	657	121	65	2	3	0	2	0	G3UZ44	
ENSMUST00000174398	ENSMUSG00000031753	8	110846600	110882227	1	0	0	0	0	0	0	0	0	0	0	0	G3UWH9	
ENSMUST00000174399						0	0	0	0	0	0	27	54	15	0	55		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174400						5	3	8	39	9	0	1	10	3	0	8		
ENSMUST00000174401						0	1	0	0	1	0	0	0	1	0	1		
ENSMUST00000174402	ENSMUSG00000068921	3	88920803	88951181	-1	0	0	0	0	0	0	3	25	22	3	25	G3UWR5	
ENSMUST00000174403						38	23	53	375	42	16	38	68	28	7	32		
ENSMUST00000174404	ENSMUSG00000030325	6	128778485	128789215	-1	0	0	0	0	0	0	0	2	0	7	0	G3UZI0	
ENSMUST00000174405	ENSMUSG00000053046	7	141949751	142004247	1	0	0	0	4	8	0	0	0	0	0	0	G3UZ00	
ENSMUST00000174406	ENSMUSG00000027684	3	29951296	30548008	-1	7	3	14	0	1	2	0	0	0	0	0	G3UY46	
ENSMUST00000174407	ENSMUSG00000092416	7	42473386	42505740	-1	53	56	100	67	50	24	80	462	190	182	85	G3UY09	
ENSMUST00000174408	ENSMUSG00000037876	10	67096125	67256326	1	0	24	0	0	41	0	1260	2797	3172	617	1875	G3UZM1	
ENSMUST00000174409	ENSMUSG00000092518	7	4753226	4771302	-1	0	6	74	0	0	0	0	0	0	0	0	L7N480	
ENSMUST00000174410						2	1	4	1	1	1	10	49	7	2	33		
ENSMUST00000174411	ENSMUSG00000025880	18	75367529	75395935	1	1	4	5	1	12	3	5	0	29	0	24	G3UXH8	
ENSMUST00000174412						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000174413	ENSMUSG00000027684	3	29951296	30548008	-1	4	0	0	0	0	4	4	0	2	0	0	G3UYY9	
ENSMUST00000174414						0	2	0	2	0	0	0	7	4	1	10		
ENSMUST00000174415						132	174	12	63	93	20	1	14	2	0	8		
ENSMUST00000174416	ENSMUSG00000078886	2	175965331	175980303	1	0	0	0	0	0	0	1	0	2	7	0	G3UZB7	
ENSMUST00000174417	ENSMUSG00000055240	17	33360507	33394641	-1	0	3	2	2	2	3	1	0	2	5	0	G3UZE0	
ENSMUST00000174418	ENSMUSG00000039458	15	12205028	12272240	1	26	18	45	0	56	13	307	546	831	51	631	G3XA69	
ENSMUST00000174419	ENSMUSG00000022216	14	55578123	55581529	1	0	1	0	1	4	0	0	13	2	0	3	G3UXR1	
ENSMUST00000174420	ENSMUSG00000040929	19	27761721	28011166	-1	1	0	0	10	0	0	0	0	0	0	0	G3UZZ6	
ENSMUST00000174421	ENSMUSG00000031558	5	47983138	48307733	1	0	0	0	0	0	0	0	0	0	0	0	G3UYX7	
ENSMUST00000174422	ENSMUSG00000004591	3	142790902	142882004	-1	0	0	0	0	0	0	80	0	96	0	0	G3UZM9	
ENSMUST00000174423						8	11	6	8	7	0	0	0	0	0	0		
ENSMUST00000174424	ENSMUSG00000021952	14	57581002	57665430	-1	1	0	3	0	0	0	0	1	0	0	0	G3UXM9	
ENSMUST00000174426	ENSMUSG00000024309	17	33938821	33940343	-1	0	0	0	0	0	0	20	10	11	15	0	G3UYF9	
ENSMUST00000174427	ENSMUSG00000031621	8	74873173	74893506	1	4	6	18	9	0	3	0	0	0	0	0		A1A546
ENSMUST00000174428						17	13	25	48	17	9	0	0	0	0	0		
ENSMUST00000174429						25	19	116	51	15	7	1	3	2	0	4		
ENSMUST00000174430						2	2	5	2	4	4	0	0	0	0	0		
ENSMUST00000174431						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000174432	ENSMUSG00000040606	4	142102390	142239401	-1	3	0	0	0	4	0	0	0	0	0	0	G3UZT9	
ENSMUST00000174433	ENSMUSG00000096294	7	9546769	9572288	-1	29	24	137	21	37	9	0	0	0	0	0	K7N709	
ENSMUST00000174434						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000174435	ENSMUSG00000031543	8	22974844	23150497	1	0	1	0	4	0	0	0	0	0	0	1	G3UXF4	
ENSMUST00000174436						1	0	0	0	1	1	0	0	2	0	0		
ENSMUST00000174437						0	0	0	1	2	0	0	0	0	0	1		
ENSMUST00000174438						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174439	ENSMUSG00000041729	9	62419492	62537044	-1	24	35	27	31	27	22	1	8	3	0	3	G3UYG8	
ENSMUST00000174441						4	3	1	7	0	3	0	0	0	0	0		
ENSMUST00000174442						2	0	18	10	8	1	49	186	78	5	93		
ENSMUST00000174443	ENSMUSG00000066772	7	15479825	15639902	-1	9	1	60	29	2	20	0	0	0	0	0	Q3UT54	
ENSMUST00000174444						8	2	4	5	6	8	0	0	0	0	0		
ENSMUST00000174445	ENSMUSG00000025316	8	121949750	122029258	1	0	0	0	0	0	0	0	0	14	0	0	G3UZ43	
ENSMUST00000174447						3	1	4	0	2	0	19	30	16	3	19		
ENSMUST00000174448	ENSMUSG00000000392	2	62500943	62574075	-1	0	0	0	0	0	0	0	0	0	0	0		P97321
ENSMUST00000174449						5	0	0	4	2	0	0	10	3	0	6		
ENSMUST00000174450	ENSMUSG00000034308	8	117661399	117673689	-1	2	4	20	0	0	2	0	0	0	0	0	G3UXV3	
ENSMUST00000174451	ENSMUSG00000092297	7	22983714	22984673	-1	0	0	0	0	0	0	0	0	0	0	0	D3YTW8	
ENSMUST00000174454	ENSMUSG00000033545	8	111536097	111626030	1	2	1	0	13	4	1	9	18	0	0	5	G3UYU9	
ENSMUST00000174455	ENSMUSG00000079262	6	142085761	142208521	-1	16	10	18	17	5	9	0	0	1	0	1		
ENSMUST00000174456	ENSMUSG00000024462	17	37045966	37075067	1	0	0	0	73	0	0	0	1	0	0	0	Q3TWR2	
ENSMUST00000174457	ENSMUSG00000021541	13	56773113	56895789	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWI6	
ENSMUST00000174458	ENSMUSG00000036962	1	119923341	119997234	-1	0	0	0	7	0	0	0	0	0	0	0	G3V015	
ENSMUST00000174459	ENSMUSG00000090523	18	32528322	32560034	-1	14	3	28	100	26	0	0	79	20	0	0		Q78HU7
ENSMUST00000174460						2	1	1	1	4	1	0	0	0	0	0		
ENSMUST00000174461	ENSMUSG00000023852	17	15704967	17394898	1	0	0	3	2	9	6	25	206	148	2	103	G3V014	
ENSMUST00000174462	ENSMUSG00000060510	9	20495068	20521417	-1	28	30	120	74	34	27	82	219	125	101	90	E9Q2S7	
ENSMUST00000174463	ENSMUSG00000051390	17	33915904	33919324	1	0	0	2	0	1	0	3	2	0	0	6	G3UWM3	
ENSMUST00000174465						0	0	0	0	0	2	0	1	2	0	0		
ENSMUST00000174466						5	1	9	21	4	1	7	0	4	9	4		
ENSMUST00000174468	ENSMUSG00000005354	15	77915047	77929006	-1	0	0	0	0	0	0	0	0	0	0	0	G3UX46	
ENSMUST00000174469	ENSMUSG00000068302	6	85423886	85428877	1	1	0	11	20	3	1	0	0	0	0	0	G3UZB3	
ENSMUST00000174470						4	0	9	0	0	0	0	0	0	0	0		
ENSMUST00000174471						0	0	0	25	0	0	0	0	0	0	5		
ENSMUST00000174472						4	4	9	3	2	6	71	275	110	98	172		
ENSMUST00000174475						0	0	0	0	0	2	23	79	66	33	14		
ENSMUST00000174476						3	0	4	1	5	0	3	10	7	0	3		
ENSMUST00000174477	ENSMUSG00000015165	7	28808541	28822266	1	1	3	5	57	3	4	110	339	124	79	206	G5E924	
ENSMUST00000174478	ENSMUSG00000024392	17	35135178	35147322	1	2	3	7	49	4	4	2	12	2	0	10	S4R183	
ENSMUST00000174479	ENSMUSG00000071454	12	3572381	3781796	1	2088	2212	6412	2121	2695	1176	42	181	90	27	135	G3UXI3	
ENSMUST00000174480	ENSMUSG00000044067	12	31706867	31713947	-1	0	0	0	1	0	2	0	0	0	0	0	G3UZX5	
ENSMUST00000174481	ENSMUSG00000003644	4	133847290	133887797	-1	0	2	2	4	4	0	0	0	0	0	0	G3UZI3	
ENSMUST00000174482						5	0	4	1	6	0	4	9	4	3	13		
ENSMUST00000174483	ENSMUSG00000020661	12	3806007	3914443	1	0	0	0	0	0	0	0	47	5	5	11	G3UY43	
ENSMUST00000174484	ENSMUSG00000022216	14	55578123	55581529	1	4	1	7	13	4	1	0	18	0	0	0	G3UXZ5	
ENSMUST00000174485	ENSMUSG00000036990	8	79639618	79677724	1	0	0	22	0	5	1	7	0	42	8	46	G3UXM1	
ENSMUST00000174486						88	101	123	59	74	65	1	2	0	2	15		
ENSMUST00000174487						5	5	21	1	0	3	0	0	0	0	0		
ENSMUST00000174488						0	1	0	0	1	1	2	0	0	0	0		
ENSMUST00000174489						0	2	0	0	0	0	0	2	0	0	0		
ENSMUST00000174490	ENSMUSG00000004231	19	44756045	44837871	1	20	19	25	920	33	17	0	2	0	0	0		
ENSMUST00000174491	ENSMUSG00000068921	3	88920803	88951181	-1	0	1	1	2	1	2	4	1	9	0	13	G3UYP3	
ENSMUST00000174492	ENSMUSG00000069539	10	89638721	89686285	-1	1	2	0	0	0	1	2	10	0	0	0	Q80UY7	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174493	ENSMUSG00000007039	17	35059035	35062095	1	0	6	6	0	0	3	0	0	0	0	37	O08972	
ENSMUST00000174494	ENSMUSG00000072672	14	26257962	26269436	1	0	0	4	0	1	1	0	0	0	0	0	G3UZN2	
ENSMUST00000174495						0	1	17	4	6	4	0	0	0	0	0		
ENSMUST00000174496	ENSMUSG00000015452	17	34597862	34600936	1	0	0	3	0	3	0	0	70	0	13	0	C5H3H7	
ENSMUST00000174497	ENSMUSG00000022394	15	81663889	81688315	1	1	1	0	6	3	0	0	0	0	0	0	G3UX47	
ENSMUST00000174498						1	2	0	4	0	0	22	39	25	84	17		
ENSMUST00000174499	ENSMUSG00000053046	7	141949751	142004247	1	52	29	159	128	33	19	0	0	0	0	0		Q69Z98
ENSMUST00000174500	ENSMUSG00000022905	16	35978750	36037131	1	0	0	0	30	0	0	0	0	0	0	7	G3UXT6	
ENSMUST00000174501	ENSMUSG00000048000	1	87326998	87450796	1	8	4	0	8	0	1	0	0	0	0	0		Q6Y7W8
ENSMUST00000174503	ENSMUSG00000034850	2	127247908	127261107	1	0	0	0	147	6	1	1	0	0	0	7	G3UXI2	
ENSMUST00000174504	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	0	0	0	0	0	0	0	1	G3UYH5	
ENSMUST00000174505						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174507						15	7	32	35	32	6	16	9	27	0	29		
ENSMUST00000174508						12	8	8	8	5	0	8	40	11	4	15		
ENSMUST00000174509						5	4	3	4	3	0	0	0	0	0	0		
ENSMUST00000174510	ENSMUSG00000009293	10	77622275	77645993	1	15	11	56	29	23	11	1093	929	758	275	502	Q3U431	P60605
ENSMUST00000174512	ENSMUSG00000055240	17	33360507	33394641	-1	471	415	563	480	516	274	32	104	63	28	77	G3UXY5	
ENSMUST00000174513	ENSMUSG00000060261	5	134237834	134314760	-1	4	4	0	0	0	0	0	0	0	0	0		Q9ESZ8
ENSMUST00000174514	ENSMUSG00000024856	19	4097182	4099019	1	2	1	3	3	5	3	27	185	42	11	76	G3UYI1	
ENSMUST00000174515						11	12	12	8	0	3	0	0	1	0	0		
ENSMUST00000174516						6	3	19	13	7	7	0	0	0	0	0		
ENSMUST00000174518	ENSMUSG00000053644	18	56509687	56572951	-1	21	9	25	17	21	11	0	0	2	0	6		Q9DBF1
ENSMUST00000174519	ENSMUSG00000015461	17	34647146	34655074	1	0	0	0	0	0	2	0	0	0	0	0	G3UX56	
ENSMUST00000174520						1	1	8	1	5	0	0	0	0	0	0		
ENSMUST00000174521	ENSMUSG00000090509	17	35601549	35650571	1	30	12	70	978	75	28	0	0	0	0	0	G3UYT9	
ENSMUST00000174522	ENSMUSG00000028479	4	44034075	44084177	-1	1	0	0	0	0	0	0	9	26	2	0	G3UYR7	
ENSMUST00000174523						186	137	156	185	217	97	4	42	11	6	15		
ENSMUST00000174524	ENSMUSG00000036036	17	37001163	37010635	1	2	16	6	10	0	5	0	1	0	0	2		Q8C6P8
ENSMUST00000174525	ENSMUSG00000067235	17	35470089	35474563	1	0	0	0	0	0	0	0	88	0	3	0		P01898
ENSMUST00000174526						4	1	13	2	7	2	21	182	6	0	7		
ENSMUST00000174527						0	0	2	31	1	0	0	0	0	0	0		
ENSMUST00000174529	ENSMUSG00000005354	15	77915047	77929006	-1	6	1	6	6	0	1	2	0	1	0	3	G3UX99	
ENSMUST00000174531	ENSMUSG00000028399	4	75941238	78211961	-1	7	0	0	0	0	0	0	0	0	0	0	G3UYU6	
ENSMUST00000174532	ENSMUSG00000034673	17	34591266	34597400	1	1	4	3	7	8	1	5	28	15	12	18	G3UXL9	
ENSMUST00000174533	ENSMUSG00000025451	13	119428601	119458218	1	0	0	0	0	0	0	0	209	44	0	16	G3UZ67	
ENSMUST00000174534						20	20	0	0	9	10	0	0	0	0	0		
ENSMUST00000174535						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174536						9	7	20	12	8	0	27	55	22	26	31		
ENSMUST00000174537						0	0	0	13	0	0	0	0	0	0	0		
ENSMUST00000174538	ENSMUSG00000094284	7	20771185	20772078	1	0	0	0	0	0	0	0	0	0	0	0	G3UY48	
ENSMUST00000174539						1	2	5	38	2	0	0	0	0	0	0		
ENSMUST00000174540						1	2	0	0	1	0	0	5	0	0	0		
ENSMUST00000174541	ENSMUSG00000002307	17	33909414	33915589	1	0	0	0	0	0	0	0	0	1	1	0	G3UX50	
ENSMUST00000174542	ENSMUSG00000031255	X	133936385	133981812	-1	1	0	1	1	0	0	0	0	0	0	0	G3UYC6	
ENSMUST00000174543						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000174544	ENSMUSG00000079298	6	128813706	128826331	-1	2	0	0	0	0	0	0	1	0	0	0	G3UYB9	
ENSMUST00000174545	ENSMUSG00000021952	14	57581002	57665430	-1	12	17	25	14	13	6	37	62	61	9	58		
ENSMUST00000174546	ENSMUSG00000009293	10	77622275	77645993	1	0	0	0	0	0	0	24	0	11	2	4	G3UYT0	
ENSMUST00000174547	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	14	5	0	0	G3UY34	
ENSMUST00000174548	ENSMUSG00000015165	7	28808541	28822266	1	5	2	3	52	6	0	5	15	5	5	15		Q8R081
ENSMUST00000174551						6	7	27	19	9	1	14	179	39	15	49		
ENSMUST00000174552	ENSMUSG00000048264	13	9276528	9668928	1	25	20	26	79	32	5	16	30	31	12	49	B2RQ71	
ENSMUST00000174553						0	3	0	0	2	0	0	1	0	0	0		
ENSMUST00000174554						6	8	4	7	13	5	4	92	8	0	29		
ENSMUST00000174555						0	1	3	0	3	1	0	0	0	1	0		
ENSMUST00000174556	ENSMUSG00000007035	17	35028605	35046745	-1	21	19	22	30	21	13	14	165	53	22	62	G3UYF3	
ENSMUST00000174557						4	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000174558	ENSMUSG00000092225	7	42816829	42867234	-1	25	21	15	4	18	11	0	3	0	0	0	G3UY53	
ENSMUST00000174559	ENSMUSG00000041408	14	34673928	34747983	1	0	2	0	0	2	1	0	26	0	43	66	G3UXQ2	
ENSMUST00000174560	ENSMUSG00000024176	17	25565892	25570686	-1	0	1	0	0	0	0	0	0	0	0	0	G3UXL7	
ENSMUST00000174561	ENSMUSG00000037894	3	137864487	137866922	1	6	9	12	20	0	0	2692	3015	1177	1952	641	Q3UA95	
ENSMUST00000174563	ENSMUSG00000022216	14	55578123	55581529	1	0	0	0	0	0	0	205	746	214	279	226	G3UWN9	
ENSMUST00000174564	ENSMUSG00000072675	14	26118349	26129763	1	0	0	1	0	2	1	0	0	0	0	0	G3UX37	
ENSMUST00000174565						25	12	15	44	52	33	1	0	0	0	3		
ENSMUST00000174566						42	17	11	26	17	13	0	27	3	0	11		
ENSMUST00000174567	ENSMUSG00000020940	11	103198944	103208558	-1	1	5	2	3	5	0	0	0	0	0	0	G3UZ03	
ENSMUST00000174569	ENSMUSG00000040482	17	34837019	34839233	1	0	0	0	0	0	0	0	0	0	0	0	G3UWW3	
ENSMUST00000174570	ENSMUSG00000046408	8	84001502	84004770	1	3	6	0	31	0	2	0	5	0	0	4	G3UZG4	
ENSMUST00000174571	ENSMUSG00000068921	3	88920803	88951181	-1	0	0	0	0	0	0	45	130	64	59	40	G3UWM7	
ENSMUST00000174572						4	1	1	3	0	1	0	0	0	0	0		
ENSMUST00000174573						2	3	49	5	2	0	0	0	0	0	0		
ENSMUST00000174574						0	6	5	4	8	1	0	0	2	0	3		
ENSMUST00000174575						10	9	4	13	9	1	0	0	1	0	2		
ENSMUST00000174576	ENSMUSG00000096727	17	34181988	34187764	-1	2	2	4	39	7	2	1129	1588	722	1002	707		
ENSMUST00000174577	ENSMUSG00000053110	9	7931999	8004596	-1	0	0	0	0	0	0	0	0	0	0	0	G3UY62	
ENSMUST00000174578						2	1	6	0	2	1	10	11	0	0	12		
ENSMUST00000174579						0	0	9	0	0	0	21	99	6	0	40		
ENSMUST00000174580						14	0	11	0	15	50	0	0	0	0	0		
ENSMUST00000174581	ENSMUSG00000023084	3	87736923	87748625	-1	0	0	0	0	5	0	0	0	2	1	0	G3V007	
ENSMUST00000174582						2	2	0	1	0	1	0	0	0	0	0		
ENSMUST00000174583						11	10	17	10	22	4	14	26	3	5	7		
ENSMUST00000174584	ENSMUSG00000036591	2	20847919	20968881	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWM5	
ENSMUST00000174585						24	15	98	20	36	15	6	27	7	0	31		
ENSMUST00000174586	ENSMUSG00000028382	4	59471868	59549364	-1	15	8	51	14	17	0	3355	8925	3457	1318	1821	G3UXA6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174588						2	9	15	13	4	6	130	331	135	32	141		
ENSMUST00000174589						55	64	147	534	60	54	112	439	115	14	348		
ENSMUST00000174590						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174591						4	8	11	1	11	4	0	0	1	0	0		
ENSMUST00000174592	ENSMUSG00000059554	10	18213676	18234998	-1	5	2	0	0	0	1	13	0	10	98	8	G3UZ16	
ENSMUST00000174593						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000174594						4	0	12	2	9	14	0	0	0	0	0		
ENSMUST00000174595	ENSMUSG00000034254	17	34604262	34613449	1	6	0	23	0	0	0	790	553	545	24	227		
ENSMUST00000174596						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000174597						3	0	4	3	6	1	8	3	2	6	1		
ENSMUST00000174598	ENSMUSG00000043940	5	101832956	102069921	-1	44	28	35	0	0	25	42	0	1391	0	811	G3UYW1	
ENSMUST00000174599	ENSMUSG00000038943	7	80294450	80316259	1	2	0	0	1	1	4	3	0	2	1	0	G3UZL8	
ENSMUST00000174601						0	0	0	54	0	0	0	0	0	0	0		
ENSMUST00000174602	ENSMUSG00000000804	11	84984442	85140161	-1	1	0	0	3	0	0	5	27	35	0	30	G3UZF4	
ENSMUST00000174603	ENSMUSG00000007035	17	35028605	35046745	-1	7	0	5	0	0	0	0	0	28	5	0	G3UYF6	
ENSMUST00000174604	ENSMUSG00000053110	9	7931999	8004596	-1	1	0	0	2	4	4	1	0	0	0	10	G3UYW7	
ENSMUST00000174605						3	1	3	0	0	0	4	0	2	0	0		
ENSMUST00000174606						0	0	0	0	0	3	2	7	0	4	0		
ENSMUST00000174608	ENSMUSG00000042099	17	33810520	33822918	1	3	0	4	3	6	1	8	31	7	5	13	G3UZW1	
ENSMUST00000174609	ENSMUSG00000008668	17	33951999	33956001	-1	2	0	9	0	0	0	1400	1563	1009	4265	521	S4R1N6	
ENSMUST00000174610	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	16	8	29	8	17	G3UYJ0	
ENSMUST00000174611						7	4	7	16	17	11	0	0	0	0	0		
ENSMUST00000174612	ENSMUSG00000025495	7	141122382	141157021	1	1	1	9	0	7	0	0	0	0	0	0	G3UZC3	
ENSMUST00000174613						0	0	9	5	0	0	0	18	13	0	18		
ENSMUST00000174614	ENSMUSG00000015461	17	34647146	34655074	1	0	0	0	45	0	0	16	0	0	0	13	G3UXQ6	
ENSMUST00000174615						0	1	0	1	4	0	0	0	0	0	0		
ENSMUST00000174616	ENSMUSG00000018906	11	54100095	54131665	1	0	0	0	12	0	0	2	0	0	3	8	Q5SX74	Q60716
ENSMUST00000174617	ENSMUSG00000025215	19	45150680	45156943	1	4	2	10	15	5	2	0	0	0	0	0	G3UXB9	
ENSMUST00000174618						75	60	56	77	81	51	5	21	7	2	21		
ENSMUST00000174619						6	4	2	0	4	4	0	0	0	0	0		
ENSMUST00000174620						2	0	4	102	4	3	8	12	4	7	25		
ENSMUST00000174623	ENSMUSG00000028023	3	129199878	129219591	1	0	0	1	0	7	3	0	0	1	0	0	Q8BS64	
ENSMUST00000174624						0	0	0	0	0	0	1	0	1	0	0		
ENSMUST00000174625						16	23	19	54	28	16	36	65	40	5	32		
ENSMUST00000174626						3	2	1	3	2	0	0	0	0	0	0		
ENSMUST00000174628	ENSMUSG00000032058	9	50845301	50894229	1	0	0	25	122	0	0	0	0	39	0	0	G3UWS4	
ENSMUST00000174629	ENSMUSG00000063646	5	37028335	37148001	1	0	0	0	0	16	5	0	0	4	0	0	G3UYZ9	
ENSMUST00000174631						0	0	6	1	3	0	1	26	16	0	18		
ENSMUST00000174632	ENSMUSG00000030795	7	127967457	127985701	1	0	0	0	0	0	0	0	334	36	4	8	G3UXT7	
ENSMUST00000174633	ENSMUSG00000022479	15	97854425	97910630	-1	3	2	19	8	5	2	0	0	0	0	0	G3UXG5	
ENSMUST00000174634						1	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000174635	ENSMUSG00000006930	11	100347327	100356128	-1	0	1	0	0	0	0	0	0	0	0	0	G3UXU7	
ENSMUST00000174636						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000174637	ENSMUSG00000094748	7	22533964	22534887	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7G9	
ENSMUST00000174638						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000174639	ENSMUSG00000071454	12	3572381	3781796	1	2	2	4	2	0	0	0	0	0	0	0	G3UX96	
ENSMUST00000174640						0	0	0	0	0	0	16	27	3	8	41		
ENSMUST00000174641	ENSMUSG00000041444	9	32116136	32268446	1	87	68	299	157	107	47	0	6	0	1	3		Q811P8
ENSMUST00000174643	ENSMUSG00000094700	7	22789859	22790782	-1	0	0	0	0	0	0	0	0	0	0	0	G3UY92	
ENSMUST00000174644						0	1	0	0	1	0	0	7	1	0	3		
ENSMUST00000174645						0	0	0	0	1	0	0	8	0	3	5		
ENSMUST00000174646						0	0	6	0	0	0	0	39	16	6	23		
ENSMUST00000174647	ENSMUSG00000064120	17	49428362	49455435	1	0	0	0	0	2	0	112	13	51	0	87	G3UXJ3	
ENSMUST00000174648	ENSMUSG00000027971	3	125404076	125728899	1	5	0	2	5	2	2	0	0	0	0	0	G3UX70	
ENSMUST00000174649						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000174651	ENSMUSG00000041716	12	102741732	102758672	-1	3	9	13	192	19	12	98	240	79	17	56	F8WIA3	
ENSMUST00000174652						0	1	1	9	1	1	0	0	0	0	0		
ENSMUST00000174653	ENSMUSG00000063334	10	111972664	111988432	1	0	0	0	0	0	0	15	0	55	249	38	G3UZA0	
ENSMUST00000174655						15	5	30	10	15	6	0	0	0	0	0		
ENSMUST00000174656	ENSMUSG00000026921	2	26580014	26593120	1	0	0	6	0	0	0	0	0	0	1	0	G3UYR2	
ENSMUST00000174657						0	0	0	4	9	0	0	0	0	0	0		
ENSMUST00000174658	ENSMUSG00000031558	5	47983138	48307733	1	0	0	0	0	1	0	0	0	0	0	0	G3UZ61	
ENSMUST00000174659	ENSMUSG00000007739	11	22990519	23003780	1	0	0	0	0	0	0	0	0	0	0	0	G3UXF3	
ENSMUST00000174660						488	460	138	575	684	287	79	291	188	113	152		
ENSMUST00000174661	ENSMUSG00000028023	3	129199878	129219591	1	0	7	0	83	4	7	0	0	0	0	0		P97474
ENSMUST00000174662						2	4	5	1	3	2	12	48	7	7	27		
ENSMUST00000174663	ENSMUSG00000071454	12	3572381	3781796	1	0	0	0	0	0	0	0	0	0	0	0	G3UYM7	
ENSMUST00000174664	ENSMUSG00000092345	4	59003210	59041888	1	0	0	0	59	0	0	0	0	0	0	0	G3UZK1	
ENSMUST00000174665	ENSMUSG00000040263	8	121796313	121829569	-1	0	0	0	0	0	0	0	0	0	0	27	G3UZF2	
ENSMUST00000174666						2	0	3	11	4	0	0	175	14	6	59		
ENSMUST00000174667	ENSMUSG00000079608	18	70472454	70501066	1	1	0	0	0	0	0	0	0	0	0	0	G3UY60	
ENSMUST00000174668						1	2	2	37	3	0	4	16	20	7	22		
ENSMUST00000174669	ENSMUSG00000036492	17	36942918	36947986	1	0	1	2	0	4	5	0	0	0	0	1	G3UYJ8	
ENSMUST00000174670						8	0	12	5	22	11	0	0	0	5	6		
ENSMUST00000174671						11	10	29	2	15	7	89	488	82	86	84		
ENSMUST00000174672	ENSMUSG00000036036	17	37001163	37010635	1	5	2	8	3	11	0	0	0	0	0	0		Q8C6P8
ENSMUST00000174673						7	6	6	5	3	2	0	0	0	0	0		
ENSMUST00000174674	ENSMUSG00000068327	6	83068324	83070293	-1	0	7	3	269	3	0	0	0	0	0	0	G3UWU0	
ENSMUST00000174675	ENSMUSG00000081724	17	38054599	38059784	-1	4	5	5	0	5	0	0	0	0	0	0	Q7TRI9	
ENSMUST00000174676						1	1	5	2	1	0	0	4	0	0	10		
ENSMUST00000174677						1	1	5	1	1	3	0	0	0	0	0		
ENSMUST00000174678	ENSMUSG00000057443	17	38261067	38275711	1	1	0	2	1	0	0	0	0	0	0	0	G3UZE3	
ENSMUST00000174679	ENSMUSG00000031753	8	110846600	110882227	1	0	0	0	0	0	0	0	0	0	0	0	G3UWX2	
ENSMUST00000174680	ENSMUSG00000004591	3	142790902	142882004	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYD6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174681	ENSMUSG00000028736	4	139737062	139833528	-1	1	0	7	28	23	1	0	0	0	0	0	G3UX36	
ENSMUST00000174682						7	0	5	0	4	0	0	0	0	0	0		
ENSMUST00000174683						50	55	138	47	45	31	0	32	13	0	35		
ENSMUST00000174684	ENSMUSG00000040482	17	34837019	34839233	1	0	2	0	0	0	0	0	0	0	0	10	G3UZV8	
ENSMUST00000174685	ENSMUSG00000038375	2	155381059	155389850	1	0	0	0	58	2	0	7	3	6	2	4	G3UXZ2	
ENSMUST00000174686						1	1	8	3	6	1	0	0	0	0	0		
ENSMUST00000174687						5	5	28	1	9	5	0	0	0	0	0		
ENSMUST00000174688	ENSMUSG00000032423	9	88447009	88482574	-1	5	0	0	0	1	0	31	0	13	15	0	G3UXJ6	
ENSMUST00000174689						2	1	4	0	1	0	0	64	4	84	26		
ENSMUST00000174691	ENSMUSG00000025451	13	119428601	119458218	1	0	0	0	0	0	0	0	0	89	39	51	G3UZH8	
ENSMUST00000174692	ENSMUSG00000021281	12	111442469	111455018	1	0	0	0	0	0	0	597	0	445	0	167	G3UX17	
ENSMUST00000174693						0	0	0	0	0	0	0	22	165	0	0		
ENSMUST00000174694	ENSMUSG00000021959	14	57642077	57758388	-1	0	0	0	54	0	0	0	0	79	0	51	G3UXG3	
ENSMUST00000174695	ENSMUSG00000024300	17	33555719	33607764	1	1	0	7	2	0	1	0	0	32	0	10	G3UZR3	
ENSMUST00000174696	ENSMUSG00000070419	5	145345279	145390926	1	0	2	6	0	5	1	0	4	0	0	0	G3UX95	
ENSMUST00000174697	ENSMUSG00000046157	12	78961795	79007627	-1	30	24	82	132	28	8	0	0	0	0	0		Q8BFQ2
ENSMUST00000174698	ENSMUSG00000043940	5	101832956	102069921	-1	13	0	5	53	17	3	46	6	92	0	36		Q6VNB8
ENSMUST00000174699	ENSMUSG00000073409	17	35424850	35430055	1	390	319	252	580	513	276	189	556	209	129	556	P79568	
ENSMUST00000174700	ENSMUSG00000030994	7	134265779	134385661	-1	0	0	0	0	1	0	0	0	0	0	0	G3UZA2	
ENSMUST00000174701	ENSMUSG00000015134	7	66390892	66427517	-1	2	1	0	0	0	5	0	0	0	0	0	G3UWP3	
ENSMUST00000174702						3	2	0	0	1	2	1	1	2	0	2		
ENSMUST00000174703	ENSMUSG00000024151	17	87672330	87723713	1	0	0	0	0	0	0	2	1	0	0	6	G3UWZ8	
ENSMUST00000174704	ENSMUSG00000053644	18	56509687	56572951	-1	4	0	6	0	0	0	11	32	13	13	5	G3UY72	
ENSMUST00000174705						0	1	1	0	5	0	0	0	0	0	0		
ENSMUST00000174706						8	6	21	19	17	8	3	19	11	4	14		
ENSMUST00000174707						6	2	0	0	3	8	0	0	0	0	0		
ENSMUST00000174709						13	0	19	19	23	5	6	12	9	0	9		
ENSMUST00000174710	ENSMUSG00000002985	7	19696109	19699166	-1	0	2	0	0	3	2	6	32	0	9	9	G3UWW2	
ENSMUST00000174711	ENSMUSG00000036398	17	36948356	36951741	-1	0	1	2	0	0	0	243	297	128	627	82	A5A4Y9	
ENSMUST00000174713	ENSMUSG00000028073	3	87747890	87824306	-1	9	0	0	23	7	6	0	9	0	0	0	G3UYT5	
ENSMUST00000174715						0	2	2	7	0	0	0	3	0	0	4		
ENSMUST00000174716						34	33	109	48	38	13	2	5	10	0	6		
ENSMUST00000174717	ENSMUSG00000040263	8	121796313	121829569	-1	0	0	10	2	0	2	45	60	78	0	36	G3UZ63	
ENSMUST00000174718	ENSMUSG00000037820	2	158116402	158146436	-1	0	0	0	5	0	0	0	0	0	0	0	G3UXE8	
ENSMUST00000174719	ENSMUSG00000020534	11	60788104	60811718	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZ26	
ENSMUST00000174720	ENSMUSG00000053483	1	171281945	171287991	-1	0	0	6	0	1	0	23	5	0	0	8	G3UWN7	
ENSMUST00000174721	ENSMUSG00000046157	12	78961795	79007627	-1	2	0	0	0	5	0	0	0	0	0	0	G3UZR6	
ENSMUST00000174722						1	3	5	5	2	1	0	0	0	0	0		
ENSMUST00000174723	ENSMUSG00000031753	8	110846600	110882227	1	0	0	0	0	0	0	0	0	0	0	0	G3UWY4	
ENSMUST00000174724						6	5	6	17	9	3	0	0	0	0	12		
ENSMUST00000174726						1	0	1	0	1	1	0	6	0	0	0		
ENSMUST00000174727						5	3	15	3	5	1	0	0	0	0	0		
ENSMUST00000174729						6	0	1	4	0	0	0	0	0	4	0		
ENSMUST00000174730						38	28	140	47	60	23	0	2	1	1	0		
ENSMUST00000174731	ENSMUSG00000025041	19	46886831	47015153	-1	0	0	0	0	4	2	122	456	249	130	263	G3UZQ5	
ENSMUST00000174733	ENSMUSG00000020661	12	3806007	3914443	1	2	0	0	0	0	0	0	0	0	0	0	G3UZG8	
ENSMUST00000174734	ENSMUSG00000038056	5	25271798	25498783	-1	21	9	53	16	0	0	223	1004	354	89	360	G3UWZ3	
ENSMUST00000174735						22	0	10	8	17	4	0	0	0	0	0		
ENSMUST00000174736						3	0	0	0	0	0	7	0	0	115	6		
ENSMUST00000174737	ENSMUSG00000022905	16	35978750	36037131	1	0	0	4	0	0	1	0	0	0	0	0	G3UXW7	
ENSMUST00000174739						0	3	0	0	0	2	0	3	0	0	1		
ENSMUST00000174740						3	3	2	3	1	0	8	68	20	0	30		
ENSMUST00000174741						0	2	0	0	1	0	0	227	10	4	45		
ENSMUST00000174742	ENSMUSG00000092342	17	38639447	38645650	1	3	4	0	0	6	2	0	0	0	0	0	A8R0W3	
ENSMUST00000174743	ENSMUSG00000017428	11	80428615	80473248	1	0	0	0	0	0	0	8	0	19	113	78	G3UWV7	
ENSMUST00000174744						0	0	0	23	0	0	0	0	0	13	18		
ENSMUST00000174745						0	0	0	0	0	0	0	10	0	0	0		
ENSMUST00000174746						0	2	1	0	2	2	0	0	0	0	1		
ENSMUST00000174747	ENSMUSG00000036036	17	37001163	37010635	1	0	0	0	11	2	0	0	0	0	0	0	G3UWX4	
ENSMUST00000174748	ENSMUSG00000028382	4	59471868	59549364	-1	0	0	0	0	0	0	5	3	0	2	178	G3UXZ6	
ENSMUST00000174749						5	4	7	4	1	5	0	0	0	0	2		
ENSMUST00000174750						2	3	3	6	5	2	0	0	0	0	0		
ENSMUST00000174751	ENSMUSG00000036594	17	34282744	34287827	-1	7	3	11	0	2	0	39	63	6	430	220	G3UWR9	
ENSMUST00000174752						0	3	3	75	3	0	0	0	0	0	0		
ENSMUST00000174753	ENSMUSG00000025316	8	121949750	122029258	1	0	0	0	0	0	0	0	0	0	0	13	G3UYF0	
ENSMUST00000174754						0	0	0	1	0	0	0	0	0	0	1		
ENSMUST00000174755						0	0	0	4	0	0	0	0	91	0	0		
ENSMUST00000174757	ENSMUSG00000019432	17	35241746	35253707	1	0	0	0	0	0	0	11	20	32	3	42	G3UXI6	
ENSMUST00000174758						0	4	0	1	3	0	0	8	3	6	3		
ENSMUST00000174759	ENSMUSG00000028073	3	87747890	87824306	-1	0	0	0	0	0	0	0	0	0	0	11		Q8VIK5
ENSMUST00000174761						1	1	0	1	0	0	1	0	1	0	0		
ENSMUST00000174762						0	0	0	0	0	0	0	0	51	0	22		
ENSMUST00000174763						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000174764	ENSMUSG00000045333	8	87661810	87959595	-1	5	0	0	0	0	0	0	0	0	0	0	G3UZP1	
ENSMUST00000174765						0	1	0	2	4	0	30	19	13	22	0		
ENSMUST00000174766	ENSMUSG00000039089	10	26274468	26375185	-1	0	0	0	19	1	0	27	18	195	0	143		Q8BLB7
ENSMUST00000174767						3	0	0	1	2	1	0	0	0	0	0		
ENSMUST00000174769	ENSMUSG00000033735	6	85130176	85137766	-1	0	3	0	0	0	1	0	0	0	0	0	G3UZ79	
ENSMUST00000174770	ENSMUSG00000027347	2	117279993	117343001	-1	0	0	0	0	0	0	0	0	0	0	0	G3UYP5	
ENSMUST00000174772	ENSMUSG00000060261	5	134237834	134314760	-1	0	0	0	0	0	0	0	0	0	40	0		Q9ESZ8
ENSMUST00000174773						1	0	4	1	0	0	0	0	0	0	0		
ENSMUST00000174774	ENSMUSG00000020661	12	3806007	3914443	1	0	0	0	0	0	0	0	0	0	0	0	G3UZK0	
ENSMUST00000174775	ENSMUSG00000095984	7	22564423	22565343	-1	0	0	0	0	0	0	0	0	0	0	0	K9J7H2	
ENSMUST00000174776	ENSMUSG00000028073	3	87747890	87824306	-1	2	0	0	22	3	0	0	1	0	0	0	G3UXM4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174777						9	5	14	2	4	1	0	0	0	0	0		
ENSMUST00000174778						110	174	224	709	130	79	299	662	261	192	501		
ENSMUST00000174779	ENSMUSG00000024387	17	35116196	35122053	-1	0	1	0	0	0	0	0	201	0	67	0	G3UXG7	
ENSMUST00000174780	ENSMUSG00000037638	12	112678828	112682747	1	24	7	0	9	8	18	683	757	318	93	331	G3UYC4	
ENSMUST00000174781						7	4	6	153	2	2	0	0	0	0	4		
ENSMUST00000174782	ENSMUSG00000024406	17	35506018	35510772	1	5	3	5	2	8	0	0	0	0	0	0	G3UZG9	
ENSMUST00000174783						8	0	1	1	3	1	0	0	0	0	0		
ENSMUST00000174786	ENSMUSG00000038812	19	6909698	6911049	1	6	2	6	12	8	6	78	364	42	40	39	Q8VCR4	
ENSMUST00000174787	ENSMUSG00000004266	6	124720707	124738714	-1	0	0	0	1	1	0	0	3	0	0	1	G3UWU7	
ENSMUST00000174788						14	7	40	17	15	7	4	34	6	4	7		
ENSMUST00000174790						0	0	15	9	0	3	0	0	0	0	4		
ENSMUST00000174791						1	0	0	7	0	0	22	58	29	27	38		
ENSMUST00000174792	ENSMUSG00000029546	5	139543494	139548179	1	6	1	17	189	10	5	0	0	0	0	0	V9GXC0	
ENSMUST00000174793						1	3	1	4	0	0	0	13	2	0	0		
ENSMUST00000174794						0	0	1	1	0	0	2	0	1	1	4		
ENSMUST00000174795						2	1	0	79	7	3	1	0	2	0	2		
ENSMUST00000174796	ENSMUSG00000033739	17	34644764	34646324	1	1	1	2	3	0	1	1	3	2	3	2	G3UY63	
ENSMUST00000174797						3	0	3	2	0	0	5	19	8	0	0		
ENSMUST00000174798	ENSMUSG00000051611	17	37563228	37567094	-1	0	1	3	2	8	0	0	0	0	0	0	G3UXE1	
ENSMUST00000174799	ENSMUSG00000024856	19	4097182	4099019	1	0	1	0	0	3	3	1098	1224	459	247	568	G3UX88	
ENSMUST00000174800						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000174801						0	0	3	2	4	0	0	0	0	0	1		
ENSMUST00000174802						6	8	5	2	2	2	0	0	0	0	0		
ENSMUST00000174803						0	1	0	0	0	0	0	0	0	22	2		
ENSMUST00000174804						5	0	1	0	4	4	0	0	0	0	0		
ENSMUST00000174805	ENSMUSG00000024393	17	35149076	35164897	-1	26	31	133	30	28	37	1433	1704	994	91	1171	G3UX48	
ENSMUST00000174806	ENSMUSG00000032422	9	88376750	88438958	-1	12	0	0	0	0	0	52	43	0	25	23	G3UX33	
ENSMUST00000174807	ENSMUSG00000024436	17	35910379	35916389	-1	0	0	0	0	3	6	0	17	0	0	0	G3UX79	
ENSMUST00000174809						0	1	0	13	0	0	0	0	0	0	2		
ENSMUST00000174810						0	0	1	4	1	1	0	0	0	0	0		
ENSMUST00000174812						1	1	4	4	4	0	0	0	0	0	0		
ENSMUST00000174813						5	1	0	2	7	0	0	0	0	0	0		
ENSMUST00000174814						5	8	3	7	3	6	0	0	0	0	0		
ENSMUST00000174815	ENSMUSG00000071104	8	45934619	45944145	1	0	0	0	0	0	0	0	0	0	0	0	G3UZI6	
ENSMUST00000174816						66	55	67	60	59	35	0	4	3	0	3		
ENSMUST00000174817	ENSMUSG00000020661	12	3806007	3914443	1	0	0	116	42	2	14	51	11	82	2	193		O88508
ENSMUST00000174818	ENSMUSG00000031562	8	48099092	48153233	1	18	10	25	0	15	15	0	6	0	2	6	Q3UUA6	
ENSMUST00000174819	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	5	8	30	8	16	G3UXH7	
ENSMUST00000174822	ENSMUSG00000057948	11	116062095	116077961	-1	0	0	6	0	0	0	320	0	84	0	3		B2RUP2
ENSMUST00000174823						5	6	9	41	4	3	0	0	0	0	0		
ENSMUST00000174824						2	3	0	81	9	4	21	105	44	154	27		
ENSMUST00000174825						0	0	0	0	0	0	0	0	0	0	7		
ENSMUST00000174826						2	0	10	75	7	3	0	0	0	0	3		
ENSMUST00000174827						40	58	126	266	51	35	5	11	5	1	8		
ENSMUST00000174828	ENSMUSG00000033335	9	21424908	21507759	1	1	0	0	42	6	0	0	2	8	0	21	G3UY64	
ENSMUST00000174830	ENSMUSG00000035469	14	59201209	59237265	1	82	62	681	140	64	28	1	9	0	0	3	G3UWU1	
ENSMUST00000174831	ENSMUSG00000028399	4	75941238	78211961	-1	1	0	0	0	0	0	0	0	0	0	0	G3UWK6	
ENSMUST00000174832	ENSMUSG00000028399	4	75941238	78211961	-1	6	5	14	1	1	1	0	0	0	0	1	G3UX75	
ENSMUST00000174833						14	10	27	27	21	5	117	223	319	20	455		
ENSMUST00000174834						3	0	0	5	2	3	0	13	13	0	35		
ENSMUST00000174835						4	4	1	10	11	4	14	73	10	12	32		
ENSMUST00000174836	ENSMUSG00000038384	5	123142193	123168629	1	0	0	0	621	1	0	53	0	0	0	0		Q8CFT2
ENSMUST00000174837	ENSMUSG00000033249	8	105269801	105275845	1	5	0	9	0	10	0	1	1	0	0	0	G3UZF5	
ENSMUST00000174838						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000174839						0	0	67	0	15	0	159	1166	341	22	594		
ENSMUST00000174840	ENSMUSG00000039304	3	27317028	27342427	1	5	6	32	16	7	2	0	0	0	2	1	G3UY25	
ENSMUST00000174841						0	0	0	0	0	0	0	1	0	0	3		
ENSMUST00000174842	ENSMUSG00000066772	7	15479825	15639902	-1	0	0	0	0	0	0	0	0	0	0	0	G3UZJ7	
ENSMUST00000174843	ENSMUSG00000025880	18	75367529	75395935	1	0	0	0	142	0	0	0	0	0	0	0	G3UX42	
ENSMUST00000174846						0	0	0	12	0	0	19	29	0	0	0		
ENSMUST00000174847						2	3	8	7	0	3	3	5	0	2	12		
ENSMUST00000174848	ENSMUSG00000030316	6	115004381	115037876	-1	0	0	0	45	0	0	0	0	0	6	0	G3UWL8	
ENSMUST00000174849	ENSMUSG00000038500	17	35972541	35980236	-1	1	1	4	8	1	1	0	0	0	1	3	G3UZI1	
ENSMUST00000174850	ENSMUSG00000040929	19	27761721	28011166	-1	0	5	0	127	4	0	32	27	52	0	24		P48381
ENSMUST00000174852						39	70	109	40	57	28	10	8	11	5	15		
ENSMUST00000174853	ENSMUSG00000022160	14	52294668	52305128	-1	0	0	6	0	3	4	6	0	22	1	13	G3UXX7	
ENSMUST00000174854						12	14	38	245	32	6	49	161	80	9	232		
ENSMUST00000174855						2	2	5	57	2	0	0	3	2	0	5		
ENSMUST00000174856	ENSMUSG00000015002	15	65787034	65873816	1	0	0	0	0	0	0	0	0	5	0	0	G3UX01	
ENSMUST00000174857	ENSMUSG00000020185	10	110745439	110787384	1	266	235	530	342	362	190	12	31	23	7	23	Q8BQ55	
ENSMUST00000174858						0	0	1	2	0	0	0	1	0	0	0		
ENSMUST00000174859						3	3	3	0	0	5	0	16	2	2	9		
ENSMUST00000174860						3	2	11	56	5	4	0	8	2	0	0		
ENSMUST00000174862						1	5	2	4	1	0	0	0	0	0	0		
ENSMUST00000174863	ENSMUSG00000003662	2	127240938	127247816	-1	3	0	9	3	0	1	17	4	0	18	7	G3UYN9	
ENSMUST00000174865	ENSMUSG00000030325	6	128778485	128789215	-1	4	3	19	5	6	2	0	0	0	0	0	G3UYE9	
ENSMUST00000174866						3	3	0	1	3	0	1	0	0	0	0		
ENSMUST00000174867	ENSMUSG00000060261	5	134237834	134314760	-1	2	5	8	115	3	0	0	0	0	0	0	G3UWV2	
ENSMUST00000174868	ENSMUSG00000039607	9	116572746	117629913	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BWL5
ENSMUST00000174869						0	0	10	7	0	0	0	0	0	0	0		
ENSMUST00000174872						3	0	5	5	6	2	0	0	1	0	0		
ENSMUST00000174873	ENSMUSG00000059791	17	35861318	35865402	1	0	0	0	40	3	0	2	2	12	2	9	G3UWN3	
ENSMUST00000174874	ENSMUSG00000020173	11	12236608	12464960	-1	29	32	77	7	0	16	0	0	0	0	0	G3UWY3	
ENSMUST00000174875						1	2	7	2	1	2	0	5	0	3	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000174876	ENSMUSG00000092586	17	35065388	35070050	1	5	1	6	8	2	2	0	0	0	0	0	G3UXV4	
ENSMUST00000174877						7	2	6	9	10	4	0	0	0	0	0		
ENSMUST00000174878						5	2	5	6	2	5	24	141	36	4	61		
ENSMUST00000174879						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000174880						0	2	0	28	0	1	0	0	0	0	0		
ENSMUST00000174881	ENSMUSG00000037627	15	36009479	36140400	-1	5	0	16	0	0	3	0	0	0	0	0	G3UYR1	
ENSMUST00000174882	ENSMUSG00000015165	7	28808541	28822266	1	0	0	0	0	0	0	372	1456	331	51	195	G3UY56	
ENSMUST00000174885	ENSMUSG00000016933	2	160731300	160775760	1	1	0	0	87	1	0	0	0	0	0	0	G3V016	
ENSMUST00000174886						1	1	2	0	0	2	0	0	0	0	0		
ENSMUST00000174887						0	0	0	0	0	0	0	0	45	31	27		
ENSMUST00000174888						1	0	3	0	1	3	40	70	20	11	53		
ENSMUST00000174890	ENSMUSG00000025967	1	63176825	63180486	1	0	0	1	0	0	0	321	453	328	1256	241	G3UX43	
ENSMUST00000175634						3	2	3	9	4	1	0	1	0	0	2		
ENSMUST00000175635						3	5	2	0	1	0	0	0	0	0	0		
ENSMUST00000175636						25	15	36	486	26	15	1	6	3	1	5		
ENSMUST00000175637	ENSMUSG00000048996	13	21536974	21542775	-1	4	0	0	0	0	6	0	0	0	0	0	H3BKM1	
ENSMUST00000175640	ENSMUSG00000032058	9	50845301	50894229	1	3	0	0	0	0	1	0	0	0	7	0	H3BIV7	
ENSMUST00000175641						5	7	0	0	6	3	0	0	0	0	0		
ENSMUST00000175642						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175643	ENSMUSG00000058317	14	18573575	18894267	-1	0	0	0	0	0	1	0	0	2	0	0	H3BL69	
ENSMUST00000175644						3	1	3	0	1	0	0	6	0	0	4		
ENSMUST00000175645	ENSMUSG00000032058	9	50845301	50894229	1	0	0	0	0	0	0	0	0	1	0	0	H3BLQ0	
ENSMUST00000175646	ENSMUSG00000042410	2	75832177	75931350	1	3	0	1	22	7	2	126	130	544	35	229	H3BKN2	
ENSMUST00000175647	ENSMUSG00000064202	19	28893042	28967800	-1	0	3	0	4	6	15	0	0	0	0	0	H3BLJ4	
ENSMUST00000175648	ENSMUSG00000030788	7	110800432	110844457	-1	0	0	0	0	0	0	15	8	5	0	0	H3BJX9	
ENSMUST00000175649						2	1	1	3	1	4	0	0	0	0	0		
ENSMUST00000175650						10	5	31	20	14	6	0	0	0	11	0		
ENSMUST00000175651						0	0	0	0	3	4	0	66	0	0	0		
ENSMUST00000175652	ENSMUSG00000041359	12	105216750	105222793	-1	0	0	0	3	0	0	0	0	0	0	0	H3BJ18	
ENSMUST00000175654						39	53	0	116	57	20	0	0	0	0	0		
ENSMUST00000175655						0	3	0	0	3	0	0	1	0	1	2		
ENSMUST00000175656	ENSMUSG00000029413	5	92257659	92278170	-1	0	0	0	0	0	0	37	25	81	0	98	H3BL13	
ENSMUST00000175657						1	2	1	0	0	1	0	0	0	0	0		
ENSMUST00000175658	ENSMUSG00000019848	10	45178098	45318452	1	0	4	80	5	3	10	0	0	0	0	0	H3BKF9	
ENSMUST00000175659						65	65	265	96	62	24	16	29	19	2	43		
ENSMUST00000175660	ENSMUSG00000029088	5	48389502	49524907	-1	6	3	1	1	3	2	0	0	0	0	0	Q3UFC0	
ENSMUST00000175661	ENSMUSG00000020892	11	69125896	69149115	1	0	0	0	0	0	0	0	0	2	0	0	H3BJ21	
ENSMUST00000175662						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000175663	ENSMUSG00000001998	2	127008717	127067909	1	0	0	0	0	0	0	0	0	0	0	0	H3BL03	
ENSMUST00000175665	ENSMUSG00000022112	14	115092215	116525179	1	27	18	8	75	20	17	0	0	0	0	0	H3BLN8	
ENSMUST00000175666						0	0	0	1	0	1	13	28	11	20	22		
ENSMUST00000175667						1	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000175669	ENSMUSG00000026657	2	4017717	4614043	1	26	22	123	31	11	17	0	4	0	0	2	H3BK97	
ENSMUST00000175670	ENSMUSG00000030067	6	98925338	99522721	-1	4	4	38	17	2	7	1	1	2	0	2	H3BK38	
ENSMUST00000175672						2	0	7	1	4	1	0	0	0	0	0		
ENSMUST00000175673						5	2	0	9	0	0	3	3	2	0	8		
ENSMUST00000175676						53	43	299	70	44	44	5	7	5	4	6		
ENSMUST00000175677						0	3	12	73	4	4	0	0	0	1	1		
ENSMUST00000175678	ENSMUSG00000048280	13	67667437	67687071	-1	3	5	8	1	2	2	0	0	0	0	2	H3BJ65	
ENSMUST00000175679	ENSMUSG00000029036	4	155740641	155761093	-1	1	0	12	0	1	4	3	0	0	2	0	H3BK90	
ENSMUST00000175680	ENSMUSG00000049353	1	191977370	191988283	1	5	10	48	91	8	5	0	9	0	0	0	Q05D96	
ENSMUST00000175681	ENSMUSG00000092083	1	15287254	15723750	1	10	2	58	21	12	2	0	0	0	0	0		A6H8H5
ENSMUST00000175682						24	28	92	48	41	30	2	20	12	5	22		
ENSMUST00000175683	ENSMUSG00000093550	15	100364542	100383964	1	1	1	7	1	0	0	0	0	0	0	0	Q1XG80	Q76I25
ENSMUST00000175684						0	3	0	0	6	1	7	0	33	0	35		
ENSMUST00000175685						1	0	5	0	0	1	13	31	3	4	19		
ENSMUST00000175686	ENSMUSG00000002996	12	31926254	31950535	-1	2	1	0	5	1	0	18	19	12	5	10	H3BJQ4	
ENSMUST00000175687						1	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000175688						0	1	1	0	1	0	2	7	3	0	5		
ENSMUST00000175689	ENSMUSG00000006715	13	24751845	24761923	-1	3	4	5	1	6	1	0	43	32	73	0	H3BLK4	
ENSMUST00000175691						1	0	3	5	1	1	0	0	0	0	0		
ENSMUST00000175692	ENSMUSG00000031568	8	47533664	47552955	1	3	2	0	113	0	3	23	75	36	45	42	H3BJI4	
ENSMUST00000175693	ENSMUSG00000034460	12	73099609	73113456	-1	51	61	136	126	69	41	1	2	2	3	5	H3BL91	
ENSMUST00000175694						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000175695						16	6	11	15	32	4	0	1	0	0	0		
ENSMUST00000175697						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175698	ENSMUSG00000052752	17	24508562	24527938	-1	3	0	0	0	3	0	0	0	8	0	5	H3BKN1	
ENSMUST00000175700	ENSMUSG00000041134	16	85421533	85553397	-1	3	3	2	2	3	3	0	0	0	0	0	H3BKF0	
ENSMUST00000175701						2	3	7	3	6	6	0	0	0	0	0		
ENSMUST00000175702						2	2	4	4	7	1	0	2	0	2	6		
ENSMUST00000175703	ENSMUSG00000009734	13	18121101	18382041	-1	4	2	0	2	0	0	0	0	0	0	0	V9GXR5	
ENSMUST00000175704						0	1	5	5	3	0	0	9	0	2	0		
ENSMUST00000175705						4	1	0	0	2	2	22	45	20	0	0		
ENSMUST00000175706						5	2	0	1	1	0	0	0	0	2	0		
ENSMUST00000175707						0	3	0	0	1	3	0	0	0	0	0		
ENSMUST00000175708						0	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000175709						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000175710						2	0	1	17	5	0	0	0	3	0	1		
ENSMUST00000175711						0	0	9	1	1	0	0	0	0	0	0		
ENSMUST00000175712	ENSMUSG00000021996	14	74732297	74750765	1	0	0	0	0	0	0	82	257	165	971	134	H3BJC6	
ENSMUST00000175713						3	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000175714	ENSMUSG00000009585	15	79891659	79915906	1	0	0	0	0	0	0	68	244	184	36	77	H3BJL0	
ENSMUST00000175715						27	20	116	39	28	19	2	8	3	1	4		
ENSMUST00000175716	ENSMUSG00000093451	6	57955633	57956578	-1	2	3	1	2	5	2	0	0	0	0	0	Q8R2D6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000175718						0	0	4	0	0	0	7	0	0	0	0		
ENSMUST00000175719						0	0	0	2	3	0	0	6	3	0	4		
ENSMUST00000175720						10	3	2	2	4	3	0	0	1	0	0		
ENSMUST00000175722						2	1	0	0	2	0	0	53	5	0	6		
ENSMUST00000175724	ENSMUSG00000092049	3	64388621	64415296	-1	0	0	0	0	2	0	0	0	0	0	0	K7N784	
ENSMUST00000175725	ENSMUSG00000028710	4	115784812	115818828	1	0	2	2	0	0	0	0	0	0	0	6	H3BJP9	
ENSMUST00000175726	ENSMUSG00000046138	19	29714402	29805989	-1	17	25	10	0	7	5	76	112	166	14	95	H3BL88	
ENSMUST00000175727						1	0	5	40	10	3	299	1415	436	1373	214		
ENSMUST00000175728	ENSMUSG00000032059	9	50775019	50843542	1	5	4	10	6	11	2	4	12	0	6	3	H3BJK6	
ENSMUST00000175730						2	0	3	5	1	1	0	0	0	0	2		
ENSMUST00000175731	ENSMUSG00000070532	1	169928648	169934653	1	2	8	18	6	10	0	0	0	0	0	0	H3BLK0	
ENSMUST00000175732						0	0	0	0	0	0	6	5	0	0	0		
ENSMUST00000175733						5	2	19	3	5	1	0	0	0	0	0		
ENSMUST00000175734	ENSMUSG00000024347	18	35964830	36014715	1	45	0	0	0	37	8	0	0	0	0	15		Q6P1I6
ENSMUST00000175735						2	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000175736						5	2	1	3	0	1	0	0	0	0	0		
ENSMUST00000175737	ENSMUSG00000048277	11	117809668	117814283	1	6	3	0	0	2	0	32	0	9	0	0	H3BJ78	
ENSMUST00000175738						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175739						0	0	3	31	5	0	0	0	1	0	0		
ENSMUST00000175740						0	0	0	29	0	0	0	0	0	0	0		
ENSMUST00000175741	ENSMUSG00000018733	11	83294642	83302586	-1	0	0	0	0	0	0	0	165	0	0	40	Q5SWQ8	Q8VC48
ENSMUST00000175742						0	0	8	0	0	0	0	0	0	0	0		
ENSMUST00000175743	ENSMUSG00000036138	9	119339676	119350299	1	0	0	0	0	0	0	80	0	64	18	64	H3BKL5	
ENSMUST00000175744	ENSMUSG00000021972	14	64811600	64949871	-1	5	0	19	6	4	2	6	7	12	0	0	H3BK67	
ENSMUST00000175745	ENSMUSG00000028059	3	88607454	88648052	1	1	0	0	0	2	1	0	0	2	0	0	H3BJM4	
ENSMUST00000175747	ENSMUSG00000025224	19	46152509	46286510	1	3	0	8	1	0	3	0	8	0	0	0	H3BIX5	
ENSMUST00000175749						6	2	3	0	8	2	0	0	0	0	0		
ENSMUST00000175750	ENSMUSG00000025613	16	87483326	87495873	-1	0	0	0	0	0	3	0	111	0	0	0	H3BJB6	
ENSMUST00000175751	ENSMUSG00000038170	3	97689824	97888707	-1	12	9	8	15	18	7	28	0	33	0	67	H3BJ38	
ENSMUST00000175752	ENSMUSG00000009585	15	79891659	79915906	1	0	0	0	0	0	0	35	127	0	0	0	H3BKE5	
ENSMUST00000175754						2	1	7	6	5	1	0	0	0	0	2		
ENSMUST00000175755	ENSMUSG00000005980	16	4036942	4040024	1	0	0	0	0	0	0	0	0	0	0	0	H3BJN9	
ENSMUST00000175756	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	7	0	0	0	0	0	0	0	H3BKR9	
ENSMUST00000175757						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175758						0	0	1	0	0	0	38	704	217	117	151		
ENSMUST00000175759	ENSMUSG00000032595	9	107992497	107999684	1	0	0	0	0	0	0	0	0	0	0	0	H3BLD2	
ENSMUST00000175761						0	0	14	0	4	2	0	14	3	0	18		
ENSMUST00000175762	ENSMUSG00000022518	16	4835416	4867691	1	0	1	0	0	0	0	0	0	0	0	0	M0QWH1	
ENSMUST00000175763	ENSMUSG00000009563	2	32757234	32762244	1	0	0	0	0	0	0	0	137	0	0	0	H3BL93	
ENSMUST00000175764	ENSMUSG00000046138	19	29714402	29805989	-1	9	0	20	0	0	0	30	386	114	14	29	H3BJL2	
ENSMUST00000175765	ENSMUSG00000032041	9	35184551	35200291	-1	55	66	65	61	57	35	1225	3174	1782	249	1299	H3BKL1	
ENSMUST00000175766	ENSMUSG00000005220	5	72300025	72504473	-1	0	5	0	0	0	0	0	0	0	0	0	H3BLR7	
ENSMUST00000175767						0	0	10	6	5	3	0	6	1	19	9		
ENSMUST00000175768						0	0	22	16	2	4	0	0	1	0	0		
ENSMUST00000175769	ENSMUSG00000028249	4	6365650	6408423	1	0	0	0	89	4	0	218	509	1478	4590	1042	H3BLG5	
ENSMUST00000175770						5	2	10	13	8	1	9	44	24	20	4		
ENSMUST00000175771						7	8	15	4	6	2	0	0	0	0	0		
ENSMUST00000175772						4	5	3	0	0	0	0	0	0	0	0		
ENSMUST00000175773	ENSMUSG00000040037	3	156561794	157316445	1	2	2	1	22	1	2	0	0	0	0	0	H3BKU7	
ENSMUST00000175774	ENSMUSG00000008496	7	25087344	25159922	-1	0	3	102	0	0	2	70	261	112	36	140		Q00196
ENSMUST00000175776	ENSMUSG00000028552	4	109280268	109387817	1	3	0	0	0	0	0	107	241	766	508	310	H3BK65	
ENSMUST00000175777						2	0	1	0	4	0	0	7	3	0	4		
ENSMUST00000175778	ENSMUSG00000036529	15	89288236	89315311	-1	0	0	0	5	4	5	10	457	5	32	1	H3BKD9	
ENSMUST00000175779	ENSMUSG00000028059	3	88607454	88648052	1	0	2	2	1	0	3	93	0	42	0	0	H3BJ40	
ENSMUST00000175780						20	12	30	24	29	17	0	0	0	0	0		
ENSMUST00000175781	ENSMUSG00000008206	8	4493026	4531680	1	0	0	0	0	0	0	20	16	0	2	3		Q9D6J1
ENSMUST00000175783						36	26	99	0	24	16	34	52	115	23	160		
ENSMUST00000175784	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	8	1	2	0	0	0	0	0	H3BK68	
ENSMUST00000175785						1	1	0	0	0	0	1	0	0	0	0		
ENSMUST00000175786						0	0	2	0	1	0	0	0	0	0	2		
ENSMUST00000175788						2	3	0	0	1	1	0	0	0	0	0		
ENSMUST00000175789	ENSMUSG00000010601	15	77388221	77399110	-1	0	2	2	0	0	0	0	0	0	0	0	H3BKF5	
ENSMUST00000175790						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175791	ENSMUSG00000024921	19	26605115	26778321	1	0	0	0	0	0	0	2	96	31	5	67	H3BKJ3	
ENSMUST00000175792						1	0	0	0	0	0	3	1	4	4	5		
ENSMUST00000175793	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	0	0	8	64	231	254	48	0		Q9QWY8
ENSMUST00000175794						1	2	7	5	0	3	0	0	0	0	0		
ENSMUST00000175795	ENSMUSG00000031734	8	91798525	91801916	-1	12	0	16	289	13	15	0	0	0	4	28		P81067
ENSMUST00000175797						2	4	1	0	9	1	0	0	0	0	0		
ENSMUST00000175798						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175799	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	0	0	0	95	649	241	0	0	H3BKE6	
ENSMUST00000175800	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJ03	
ENSMUST00000175801						0	0	0	1	4	3	5	0	0	0	1		
ENSMUST00000175802	ENSMUSG00000032595	9	107992497	107999684	1	0	0	0	0	0	0	0	0	1	0	0	H3BJI8	
ENSMUST00000175803						2	1	0	0	0	0	0	0	0	0	2		
ENSMUST00000175804						5	5	6	6	9	0	2	0	0	0	3		
ENSMUST00000175805	ENSMUSG00000022361	15	58047003	58076541	-1	0	0	0	51	15	0	0	0	15	0	0		P70121
ENSMUST00000175806	ENSMUSG00000006705	17	31564749	31607684	1	8	2	14	14	10	0	19	9	33	2	18		O70477
ENSMUST00000175807	ENSMUSG00000029647	5	147430161	147548502	1	0	0	19	0	0	0	76	365	301	79	14	H3BLB9	
ENSMUST00000175808						0	0	0	17	0	0	0	0	0	0	0		
ENSMUST00000175809	ENSMUSG00000005982	16	3872375	3904780	1	0	0	0	0	0	0	0	0	0	0	0	H3BLJ2	
ENSMUST00000175810	ENSMUSG00000034795	14	77036772	77112257	1	0	0	0	0	0	0	0	3	0	4	0	H3BJX7	
ENSMUST00000175811						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175812						7	3	18	3	8	4	4	21	8	1	24		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000175813						0	6	8	5	0	0	0	0	0	0	2		
ENSMUST00000175815						0	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000175816	ENSMUSG00000032010	9	44067021	44095627	1	0	1	0	0	2	0	5	3	0	5	3	H3BLH3	
ENSMUST00000175817	ENSMUSG00000093376	6	57925842	57926838	-1	1	3	0	0	2	0	0	0	0	0	0	Q8R2D0	
ENSMUST00000175818						5	0	2	1	1	2	0	0	0	0	0		
ENSMUST00000175819	ENSMUSG00000017478	8	122376609	122417360	1	1	2	13	4	5	3	5	0	0	0	0	H3BJN4	
ENSMUST00000175820						29	23	66	40	52	24	5	36	19	0	64		
ENSMUST00000175821	ENSMUSG00000048280	13	67667437	67687071	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJN0	
ENSMUST00000175822						6	1	6	8	10	6	3	4	1	0	11		
ENSMUST00000175823						4	1	0	35	9	7	0	0	1	0	4		
ENSMUST00000175824						2	3	1	3	4	1	1	1	3	0	0		
ENSMUST00000175827						0	0	9	7	0	2	2	0	0	0	7		
ENSMUST00000175828						1	0	2	2	3	1	0	0	0	0	0		
ENSMUST00000175829						6	5	3	4	8	2	0	0	0	0	0		
ENSMUST00000175830	ENSMUSG00000050875	18	59062248	59076962	1	0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000175831						4	4	0	0	1	0	0	0	0	0	0		
ENSMUST00000175833						2	3	1	2	4	1	0	0	0	0	0		
ENSMUST00000175834						6	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000175835	ENSMUSG00000074634	13	119487941	119610458	1	17	9	0	97	18	0	0	9	16	4	11	H3BJ86	
ENSMUST00000175836	ENSMUSG00000022518	16	4835416	4867691	1	22	11	52	24	17	0	0	0	0	0	0	A0A075B687	
ENSMUST00000175837	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	27	188	149	38	95	H3BJ35	
ENSMUST00000175838						0	0	0	55	2	0	1	3	0	0	2		
ENSMUST00000175839						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175840						1005	766	2668	698	1386	363	14	54	27	1	35		
ENSMUST00000175842	ENSMUSG00000024921	19	26605115	26778321	1	1	2	0	3	4	1	0	0	0	0	0	H3BLI4	
ENSMUST00000175843	ENSMUSG00000033697	15	76723985	76818170	-1	1	0	1	98	6	4	0	0	0	0	0	H3BJU8	
ENSMUST00000175844	ENSMUSG00000012609	12	85824659	86061893	1	1	3	8	8	7	7	0	4	0	10	0	H3BJC7	
ENSMUST00000175847	ENSMUSG00000021546	13	58391142	58403343	-1	0	0	0	0	2	1	167	40	429	106	224	H3BJ43	
ENSMUST00000175848	ENSMUSG00000020684	11	83409137	83421039	1	0	0	0	96	4	7	0	0	0	0	0	H3BLI7	
ENSMUST00000175849						63	51	100	110	118	52	120	357	176	88	254		
ENSMUST00000175850						9	2	4	0	7	4	0	0	0	0	0		
ENSMUST00000175851						1	0	8	3	3	3	0	0	0	0	0		
ENSMUST00000175852	ENSMUSG00000019876	10	57631981	57741112	1	0	0	0	0	0	0	0	0	0	0	0	Q3TZU5	
ENSMUST00000175853	ENSMUSG00000095658	17	23061367	23077425	1	0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000175855	ENSMUSG00000038718	2	34171457	34373142	-1	0	0	0	0	0	0	4	0	10	0	8	H3BLL9	
ENSMUST00000175856	ENSMUSG00000044083	2	153780879	153844752	1	13	10	16	24	21	9	0	2	0	1	1	H3BJ05	
ENSMUST00000175857	ENSMUSG00000027699	3	27097222	27153878	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK10	
ENSMUST00000175858	ENSMUSG00000022421	15	79786352	79804766	-1	35	42	104	256	96	37	1	1	1	10	32	E9PZM8	
ENSMUST00000175859						6	3	6	7	5	1	0	7	2	0	10		
ENSMUST00000175860						0	0	0	0	0	0	13	86	56	28	15		
ENSMUST00000175862						7	11	5	3	6	6	0	0	0	0	0		
ENSMUST00000175863						0	1	0	2	2	1	0	2	2	0	1		
ENSMUST00000175864	ENSMUSG00000026858	2	30364233	30385521	1	0	0	0	0	1	0	2	0	0	0	0	H3BLJ3	
ENSMUST00000175865						0	1	0	3	0	2	2	2	0	0	0		
ENSMUST00000175866	ENSMUSG00000025255	3	5218526	5415857	1	41	21	220	68	51	26	0	0	0	0	0	H3BLK8	
ENSMUST00000175867	ENSMUSG00000020218	10	121033960	121100650	1	0	9	0	0	0	6	0	0	0	0	0	H3BKQ8	
ENSMUST00000175868						4	3	0	19	2	2	0	0	0	0	0		
ENSMUST00000175869						0	0	2	0	0	0	0	0	0	0	14		
ENSMUST00000175870						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175872	ENSMUSG00000010110	19	8741413	8756069	1	0	0	0	0	0	0	45	408	95	94	19	H3BKJ7	
ENSMUST00000175873						8	10	15	17	16	5	0	0	0	0	0		
ENSMUST00000175874	ENSMUSG00000032594	9	108002501	108048782	1	0	0	0	0	0	0	8	2	0	0	0	H3BLD6	
ENSMUST00000175875	ENSMUSG00000028890	4	124802104	124849800	1	12	7	12	53	13	1	0	3	0	0	8	A0A0G2JDC6	
ENSMUST00000175876	ENSMUSG00000023021	15	99734881	99772885	-1	4	5	7	55	10	0	29	55	25	7	39	H3BJ49	
ENSMUST00000175877	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	22	158	51	0	50	H3BKL6	
ENSMUST00000175878						3	1	7	7	6	5	3	2	2	0	8		
ENSMUST00000175879						6	6	2	8	8	2	0	0	0	0	0		
ENSMUST00000175880						2	2	4	0	2	2	0	0	3	0	7		
ENSMUST00000175881	ENSMUSG00000048756	10	42181841	42276755	-1	4	0	0	222	0	0	17	24	0	0	23		Q9WVH4
ENSMUST00000175882						6	7	8	3	11	5	0	0	0	0	0		
ENSMUST00000175883	ENSMUSG00000032547	9	102834917	102908305	1	0	5	2	13	0	0	9	13	19	1	30		Q01887
ENSMUST00000175884	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	2	3	0	0	0	1	0	0	H3BL74	
ENSMUST00000175885	ENSMUSG00000034906	2	127103809	127133954	-1	10	0	0	5	3	10	32	81	15	14	19	H3BL21	
ENSMUST00000175886	ENSMUSG00000030067	6	98925338	99522721	-1	3	5	5	1	1	0	0	0	8	2	19	H3BKT4	
ENSMUST00000175887	ENSMUSG00000021996	14	74732297	74750765	1	0	0	0	0	0	0	263	1892	446	1304	214	H3BK43	
ENSMUST00000175888	ENSMUSG00000055531	10	117344673	117380015	-1	0	0	1	0	0	1	0	0	0	0	0	H3BLM1	
ENSMUST00000175889	ENSMUSG00000032827	6	4902917	5165661	1	0	2	6	35	4	0	0	0	0	5	0	H3BL28	
ENSMUST00000175890						0	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000175892	ENSMUSG00000019893	10	52045721	52195244	-1	8	0	2	0	6	0	0	0	0	0	0	H3BK36	
ENSMUST00000175894	ENSMUSG00000022469	15	97744770	97767972	-1	0	0	0	0	0	0	1	0	0	0	15	H3BK02	
ENSMUST00000175896						8	7	15	11	9	2	0	0	0	0	0		
ENSMUST00000175897	ENSMUSG00000050875	18	59062248	59076962	1	0	0	0	0	0	0	0	0	0	0	0	H3BJK3	
ENSMUST00000175898	ENSMUSG00000038805	17	85613608	85629302	1	11	0	27	26	10	9	2	5	0	0	0		Q62233
ENSMUST00000175899						8	5	6	1	5	1	0	0	1	0	0		
ENSMUST00000175900	ENSMUSG00000031133	X	57231485	57338729	-1	0	2	0	0	0	0	10	18	39	11	45	H3BKQ0	
ENSMUST00000175901	ENSMUSG00000010110	19	8741413	8756069	1	0	0	0	0	0	0	37	13	23	7	22	H3BJE3	
ENSMUST00000175902						9	0	7	6	2	0	0	0	0	0	0		
ENSMUST00000175903	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	0	0	11	0	21	H3BJX8	
ENSMUST00000175904						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175905	ENSMUSG00000021972	14	64811600	64949871	-1	0	3	9	4	8	2	0	0	0	0	0	H3BL55	
ENSMUST00000175906	ENSMUSG00000064125	8	4209543	4217459	-1	4	4	35	72	7	3	0	0	0	0	0	H3BLA4	
ENSMUST00000175908						0	0	0	2	0	0	2	1	0	0	0		
ENSMUST00000175909	ENSMUSG00000034799	8	71624417	71671757	-1	4	0	0	0	0	0	0	0	0	0	0	H3BKU4	
ENSMUST00000175910						0	0	0	0	0	0	0	0	29	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000175911	ENSMUSG00000028059	3	88607454	88648052	1	2	2	3	0	5	4	46	12	44	0	72		Q60875
ENSMUST00000175912	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	0	0	32	30	0	H3BK48	
ENSMUST00000175914	ENSMUSG00000042106	9	107984223	107985879	-1	9	5	28	70	14	2	0	0	1	0	3	H3BJG7	
ENSMUST00000175915	ENSMUSG00000039375	8	54629055	54887184	-1	2	0	0	15	9	0	0	0	0	0	0	H3BLI8	
ENSMUST00000175916	ENSMUSG00000010175	1	190118035	190170714	-1	21	20	16	37	44	19	0	0	0	0	1		P48437
ENSMUST00000175918	ENSMUSG00000029705	5	136248135	136567490	-1	9	5	22	46	6	3	0	7	7	5	4	H3BL09	
ENSMUST00000175919	ENSMUSG00000010601	15	77388221	77399110	-1	12	0	15	0	13	1	0	0	0	3	0	B2RT54	
ENSMUST00000175920						1	1	2	1	1	0	2	0	0	0	2		
ENSMUST00000175922	ENSMUSG00000030982	7	118740226	118842966	1	0	2	6	0	3	0	6	22	7	6	17	H3BJE8	
ENSMUST00000175924	ENSMUSG00000055531	10	117344673	117380015	-1	0	0	0	0	1	0	0	0	0	0	0	H3BLM9	
ENSMUST00000175925	ENSMUSG00000024238	18	5591860	5775467	1	0	0	0	0	0	0	0	0	0	0	0	H3BJU2	
ENSMUST00000175926	ENSMUSG00000032058	9	50845301	50894229	1	7	0	4	5	2	4	16	8	36	0	0	H3BJ83	
ENSMUST00000175929	ENSMUSG00000093789	15	100353149	100383964	1	0	0	10	2	0	4	0	0	0	0	0	H3BJI7	
ENSMUST00000175930						0	0	3	0	4	0	0	46	0	0	5		
ENSMUST00000175931						0	1	11	7	5	0	0	0	0	0	0		
ENSMUST00000175932	ENSMUSG00000025007	19	40550257	40588463	-1	0	2	0	0	2	0	0	0	0	0	0	H3BKJ8	
ENSMUST00000175933						0	2	2	3	5	2	1	17	4	1	33		
ENSMUST00000175934	ENSMUSG00000024613	18	60813755	60848971	-1	9	18	1	0	17	17	88	86	219	31	105	H3BL37	
ENSMUST00000175935						2	4	1	0	6	0	85	254	141	28	209		
ENSMUST00000175936						4	0	0	0	3	0	10	5	12	6	43		
ENSMUST00000175937						0	0	0	47	2	0	0	0	0	0	0		
ENSMUST00000175938	ENSMUSG00000035934	9	36890982	37147322	-1	11	0	10	0	5	5	0	0	0	0	0	V9GWW7	
ENSMUST00000175939						0	0	0	0	1	0	24	20	12	0	22		
ENSMUST00000175940	ENSMUSG00000046691	8	106883863	106893601	-1	0	0	0	82	42	14	1459	651	582	202	762		P0CG15
ENSMUST00000175941	ENSMUSG00000043456	7	37472135	37773641	-1	13	18	94	0	10	20	0	0	0	0	0		Q8K083
ENSMUST00000175943						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175944	ENSMUSG00000026657	2	4017717	4614043	1	4	2	6	4	6	7	0	0	0	0	0	H3BL79	
ENSMUST00000175945	ENSMUSG00000032336	9	58582240	58657955	1	1	0	3	3	0	0	0	23	37	14	0	H3BKY2	
ENSMUST00000175946						0	0	0	4	2	0	2	0	0	0	0		
ENSMUST00000175947	ENSMUSG00000036834	3	63696234	63899472	-1	7	0	0	0	3	0	0	0	0	0	0	H3BKE1	
ENSMUST00000175948						0	0	0	0	1	0	0	0	0	0	9		
ENSMUST00000175949	ENSMUSG00000049281	9	40269216	40291618	1	0	5	0	0	0	0	0	0	0	0	0	H3BJ27	
ENSMUST00000175950	ENSMUSG00000032318	9	55538672	55546180	1	2	1	3	17	0	2	0	0	0	0	0	A0A087WNT5	
ENSMUST00000175952						1	0	0	0	2	0	0	138	4	35	8		
ENSMUST00000175953	ENSMUSG00000024921	19	26605115	26778321	1	0	0	3	6	0	0	0	0	0	0	0	H3BJM2	
ENSMUST00000175954						4	0	0	0	0	2	3	4	21	80	47		
ENSMUST00000175955	ENSMUSG00000093668	13	78024902	78026295	1	5	9	15	11	12	4	0	0	1	1	1		
ENSMUST00000175956						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175958	ENSMUSG00000021147	13	8802968	8871909	-1	0	1	5	0	2	0	0	0	0	0	0	H3BJZ0	
ENSMUST00000175959	ENSMUSG00000054611	19	4314419	4398285	-1	0	0	1	0	0	0	0	3	25	0	32	H3BL82	
ENSMUST00000175960						0	3	0	2	0	2	0	0	0	0	0		
ENSMUST00000175961						7	0	8	8	5	0	0	0	0	0	0		
ENSMUST00000175962	ENSMUSG00000032827	6	4902917	5165661	1	30	35	111	16	17	15	0	1	0	0	1	H3BKE7	
ENSMUST00000175963	ENSMUSG00000022377	15	64086857	64382919	-1	0	1	3	15	5	0	0	0	0	1	0	H3BJM7	
ENSMUST00000175964						15	28	136	56	26	13	6	22	9	0	38		
ENSMUST00000175965	ENSMUSG00000045991	18	64340364	64398488	1	50	54	353	210	53	25	1	2	0	0	0	H3BL85	
ENSMUST00000175966	ENSMUSG00000030340	6	125320659	125344943	1	0	0	8	30	2	0	48	0	16	4	96	H3BKW1	
ENSMUST00000175967	ENSMUSG00000025007	19	40550257	40588463	-1	1	0	0	1	0	0	0	0	0	0	0	H3BKK0	
ENSMUST00000175968	ENSMUSG00000093445	5	137629121	137641099	1	0	7	0	8	3	0	6	7	25	0	14	H3BIX9	
ENSMUST00000175969	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	0	0	0	0	0	0	0	H3BL54	
ENSMUST00000175970	ENSMUSG00000049957	11	120458115	120464358	1	0	0	0	0	0	0	0	0	0	0	0	H3BJB7	
ENSMUST00000175971						13	6	3	6	6	7	0	0	0	0	0		
ENSMUST00000175972	ENSMUSG00000010841	11	101984279	101992264	1	0	0	1	8	1	1	0	0	0	0	0		
ENSMUST00000175973	ENSMUSG00000032540	9	122351608	122381524	1	0	0	4	19	0	2	62	321	110	2	33	H3BLJ0	
ENSMUST00000175974	ENSMUSG00000057068	5	92555069	92591279	1	5	9	15	2	15	3	3	6	3	1	3	H3BK06	
ENSMUST00000175975	ENSMUSG00000029705	5	136248135	136567490	-1	5	0	3	5	8	0	113	0	97	0	0	H3BK24	
ENSMUST00000175977	ENSMUSG00000025613	16	87483326	87495873	-1	0	0	0	0	0	0	95	510	224	658	211	H3BL49	
ENSMUST00000175978						2	0	5	1	2	1	22	37	34	0	20		
ENSMUST00000175979						8	0	1	0	3	0	5	79	0	0	0		
ENSMUST00000175980						0	0	3	3	0	0	0	0	0	3	4		
ENSMUST00000175981	ENSMUSG00000030788	7	110800432	110844457	-1	36	31	50	15	43	23	25	176	134	68	101	H3BJU0	
ENSMUST00000175982	ENSMUSG00000029055	4	154983115	155056784	-1	0	7	5	0	0	0	0	2	0	0	0	H3BK11	
ENSMUST00000175983						4	0	0	4	3	1	0	0	0	0	0		
ENSMUST00000175984	ENSMUSG00000022010	14	76414961	76507765	1	0	0	0	0	0	0	0	0	1	0	0	H3BK98	
ENSMUST00000175985						10	2	12	15	13	2	0	0	0	0	0		
ENSMUST00000175986						26	30	51	31	42	14	11	47	32	3	76		
ENSMUST00000175987	ENSMUSG00000031910	8	106870242	106884566	1	0	7	21	16	18	9	1	0	0	0	0	H3BL01	
ENSMUST00000175988						5	3	0	3	6	2	0	0	0	0	0		
ENSMUST00000175990						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175991	ENSMUSG00000052997	7	34140688	34169599	-1	0	0	2	0	0	0	0	0	77	15	44	H3BLR3	
ENSMUST00000175992	ENSMUSG00000028776	4	130164454	130175122	-1	0	2	0	0	12	0	0	0	0	0	0	H3BJ97	
ENSMUST00000175993	ENSMUSG00000027610	2	155563181	155592810	-1	0	0	0	0	0	4	0	2	0	5	11	H3BKH4	
ENSMUST00000175995						0	0	0	4	0	0	1287	11446	1575	3171	1056		
ENSMUST00000175996	ENSMUSG00000045658	1	84036296	84364180	-1	6	3	5	6	5	3	0	0	0	0	2	H3BJG6	
ENSMUST00000175997						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000175998	ENSMUSG00000029705	5	136248135	136567490	-1	2	2	11	8	8	8	0	4	0	0	0	H3BLJ7	
ENSMUST00000175999	ENSMUSG00000034252	9	80066903	80144953	1	0	0	0	0	0	8	19	9	8	0	22	H3BKI2	
ENSMUST00000176000	ENSMUSG00000040302	5	3583978	3596585	-1	0	3	0	0	0	0	3	32	9	15	4	H3BLA0	
ENSMUST00000176001	ENSMUSG00000003949	11	90336536	90390895	-1	6	2	1	8	1	1	0	0	2	0	0	H3BKN8	
ENSMUST00000176003						1	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000176004						1	0	20	23	5	0	0	4	0	0	0		
ENSMUST00000176005						286	274	218	240	341	144	18	80	35	26	57		
ENSMUST00000176006						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000176007						0	0	0	3	1	0	21	15	2	0	12		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176008						37	22	42	28	39	19	0	6	3	1	1		
ENSMUST00000176009						0	0	0	0	0	1	21	59	29	3	27		
ENSMUST00000176010	ENSMUSG00000093674	10	128548114	128549305	-1	0	5	0	0	0	7	3698	4437	2144	14072	998		P62947
ENSMUST00000176011	ENSMUSG00000093445	5	137629121	137641099	1	4	0	4	105	8	4	10	14	15	0	7	H3BJU9	
ENSMUST00000176012	ENSMUSG00000032998	4	119537004	119629119	1	9	12	3	7	6	11	0	2	4	0	2	H3BKK7	
ENSMUST00000176013	ENSMUSG00000010110	19	8741413	8756069	1	0	0	0	0	0	0	10	118	16	50	23	H3BKP0	
ENSMUST00000176014	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	18	0	0	0	0	0	181	0	0	H3BJY2	
ENSMUST00000176015						0	8	3	55	5	7	0	0	1	0	0		
ENSMUST00000176017						3	2	0	1	1	1	0	0	0	0	0		
ENSMUST00000176018	ENSMUSG00000027035	2	68861441	69114282	1	0	0	0	0	0	0	28	4	72	5	54	H3BL08	
ENSMUST00000176019						3	0	0	1	0	0	0	5	0	0	0		
ENSMUST00000176021	ENSMUSG00000032041	9	35184551	35200291	-1	0	0	0	6	0	0	6	8	13	0	47	H3BLC8	
ENSMUST00000176022						0	1	0	0	0	0	3	24	0	0	0		
ENSMUST00000176023	ENSMUSG00000093379	6	58471898	58475343	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK49	
ENSMUST00000176024	ENSMUSG00000017631	11	76416734	76622314	-1	0	0	0	0	0	0	0	0	0	0	2	H3BL84	
ENSMUST00000176025						0	4	2	1	2	0	0	1	0	0	1		
ENSMUST00000176026						3	0	2	5	4	0	0	0	0	0	0		
ENSMUST00000176027	ENSMUSG00000069678	6	83077869	83080855	1	0	6	6	12	7	0	0	0	36	0	15	H3BL61	
ENSMUST00000176028						6	0	13	0	5	4	0	0	0	0	0		
ENSMUST00000176029	ENSMUSG00000022053	14	67233292	67430918	1	8	5	0	14	0	5	0	0	0	0	0		O08792
ENSMUST00000176030	ENSMUSG00000024921	19	26605115	26778321	1	9	8	71	0	0	0	449	684	989	51	700	H3BLH0	
ENSMUST00000176032						15	3	6	8	8	6	0	0	0	0	0		
ENSMUST00000176033						0	0	0	0	0	0	31	0	225	0	36		
ENSMUST00000176034	ENSMUSG00000043668	8	90247040	90348343	-1	0	3	0	15	0	0	0	0	0	0	0	H3BJC5	
ENSMUST00000176035	ENSMUSG00000050022	5	140724127	140761439	1	7	8	20	14	5	3	7	60	0	4	33	H3BKS3	
ENSMUST00000176036	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	0	10	0	0	0	0	0	0	0	H3BJJ5	
ENSMUST00000176037						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000176038	ENSMUSG00000004842	16	65520511	65535005	1	0	0	0	0	0	0	0	0	0	0	0	F8WGJ8	
ENSMUST00000176039						0	1	2	4	1	1	0	2	1	0	2		
ENSMUST00000176040	ENSMUSG00000036009	10	105763189	105841380	-1	1	0	0	4	0	0	0	2	2	0	0	H3BK52	
ENSMUST00000176041	ENSMUSG00000025613	16	87483326	87495873	-1	0	0	0	42	0	0	10	25	78	200	84	H3BKG2	
ENSMUST00000176042	ENSMUSG00000008206	8	4493026	4531680	1	0	0	0	1	0	0	0	0	0	0	0	H3BKZ9	
ENSMUST00000176043	ENSMUSG00000029036	4	155740641	155761093	-1	0	3	4	13	5	0	0	0	0	0	5	H3BKI6	
ENSMUST00000176044	ENSMUSG00000042258	13	116298281	116309689	-1	3	0	0	0	3	0	0	0	0	0	0		P61372
ENSMUST00000176046						0	4	11	21	6	3	10	50	0	4	0		
ENSMUST00000176047	ENSMUSG00000028710	4	115784812	115818828	1	0	0	0	4	17	0	9	12	22	0	0	H3BLL2	
ENSMUST00000176048						0	5	13	5	2	0	3	15	6	6	32		
ENSMUST00000176049						12	22	113	13	19	15	0	2	0	1	0		
ENSMUST00000176053						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176054	ENSMUSG00000055817	17	83706163	83821516	1	0	0	0	0	0	0	27	180	3	2	22	H3BIY7	
ENSMUST00000176055	ENSMUSG00000032058	9	50845301	50894229	1	0	0	3	0	1	0	0	1	3	0	3	H3BK50	
ENSMUST00000176056	ENSMUSG00000042410	2	75832177	75931350	1	0	4	1	0	1	0	1	7	0	0	1	H3BIY5	
ENSMUST00000176058						1	3	6	1	5	0	0	0	0	0	0		
ENSMUST00000176059	ENSMUSG00000093769	3	96246685	96248504	1	7	2	16	30	13	4	64	116	45	13	35	B9EI85	P84228
ENSMUST00000176060	ENSMUSG00000039031	10	26753421	26918648	1	5	1	0	1	0	0	22	16	39	111	47	H3BJL1	
ENSMUST00000176062						3	4	8	5	3	1	0	1	0	0	1		
ENSMUST00000176066	ENSMUSG00000017999	2	167015193	167034947	1	1	2	2	20	2	1	0	0	0	0	0	H3BLJ6	
ENSMUST00000176067	ENSMUSG00000038765	2	33560965	33640511	-1	3	0	8	181	2	0	0	0	0	0	0	H3BJD7	
ENSMUST00000176070						3	3	9	3	2	0	0	0	0	1	3		
ENSMUST00000176071						0	5	0	0	8	0	0	0	0	0	0		
ENSMUST00000176072	ENSMUSG00000011832	8	4166567	4211257	1	3	8	8	5	4	0	0	11	12	0	0	H3BJ67	
ENSMUST00000176073	ENSMUSG00000093785	6	57113396	57114367	1	3	0	2	0	4	2	0	0	0	0	0	W4VSP8	
ENSMUST00000176074	ENSMUSG00000010601	15	77388221	77399110	-1	2	6	0	22	0	0	0	0	0	0	0	B2RT54	
ENSMUST00000176075						3	3	1	4	0	0	8	78	6	4	12		
ENSMUST00000176076	ENSMUSG00000022362	15	58028243	58076425	-1	0	0	0	0	0	0	0	3	4	4	0	H3BKS2	
ENSMUST00000176077						5	2	15	2	1	1	0	0	0	0	0		
ENSMUST00000176078						4	2	1	41	3	7	0	0	2	1	1		
ENSMUST00000176079						0	1	0	0	0	1	0	0	5	0	6		
ENSMUST00000176080						8	5	14	32	16	11	1	3	1	0	5		
ENSMUST00000176081	ENSMUSG00000038805	17	85613608	85629302	1	44	36	61	801	87	44	0	10	0	0	4		Q62233
ENSMUST00000176082						4	0	10	15	4	2	0	1	4	0	2		
ENSMUST00000176084	ENSMUSG00000002996	12	31926254	31950535	-1	0	0	0	34	0	0	6	22	18	11	16	H3BKQ9	
ENSMUST00000176085	ENSMUSG00000093679	6	57431644	57432695	1	3	3	0	1	1	1	0	0	0	0	0	K7N778	
ENSMUST00000176086	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	281	133	79	41	159	H3BLM6	
ENSMUST00000176087						2	0	3	0	5	6	2	4	8	0	4		
ENSMUST00000176088						7	8	65	21	13	5	0	0	2	2	2		
ENSMUST00000176089	ENSMUSG00000069678	6	83077869	83080855	1	3	2	4	0	0	5	0	0	0	0	0	H3BK63	
ENSMUST00000176090	ENSMUSG00000046691	8	106883863	106893601	-1	0	0	4	0	0	0	52	0	0	0	11	H3BL81	
ENSMUST00000176091						3	1	14	55	6	1	0	0	0	2	0		
ENSMUST00000176092						0	3	3	1	2	0	0	2	3	0	13		
ENSMUST00000176093						109	86	351	146	83	67	40	144	79	9	124		
ENSMUST00000176094						14	6	13	3	17	8	0	0	0	0	0		
ENSMUST00000176096	ENSMUSG00000030142	6	123281789	123289870	-1	0	0	0	0	2	0	0	31	7	276	80	H3BL75	
ENSMUST00000176097						5	1	0	0	5	0	0	0	0	0	0		
ENSMUST00000176098	ENSMUSG00000021147	13	8802968	8871909	-1	0	0	0	0	0	0	0	0	16	3	0	H3BJR4	
ENSMUST00000176100	ENSMUSG00000069678	6	83077869	83080855	1	2	3	7	112	7	3	0	1	0	0	0	H3BLR0	
ENSMUST00000176101						4	5	2	5	3	2	0	0	0	0	0		
ENSMUST00000176102	ENSMUSG00000056459	12	76347782	76369602	-1	10	13	19	13	10	9	14	3	10	0	10	G3UW50	
ENSMUST00000176103	ENSMUSG00000002996	12	31926254	31950535	-1	0	2	0	0	0	0	37	43	51	23	66	H3BKS6	
ENSMUST00000176104	ENSMUSG00000044024	18	37955079	37959179	1	9	0	11	0	0	0	0	0	0	0	0		Q8BRJ3
ENSMUST00000176105						2	2	0	0	1	0	0	0	1	0	1		
ENSMUST00000176107	ENSMUSG00000090304	17	19362135	19394590	1	3	13	5	0	4	3	0	0	0	0	0	H3BK37	
ENSMUST00000176109	ENSMUSG00000044647	2	65845767	66031546	1	3	0	0	4	0	3	0	0	0	0	0		P59055
ENSMUST00000176110	ENSMUSG00000030340	6	125320659	125344943	1	21	3	19	0	10	0	172	579	134	21	103	H3BJC3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176111						0	0	5	2	0	0	0	7	1	0	3		
ENSMUST00000176112						9	3	19	14	2	3	0	0	0	0	1		
ENSMUST00000176113	ENSMUSG00000050966	4	134003330	134018841	-1	3	1	8	1	2	0	69	66	112	3	58	H3BK51	
ENSMUST00000176114	ENSMUSG00000043456	7	37472135	37773641	-1	7	0	1	80	12	0	0	0	0	0	0		Q8K083
ENSMUST00000176116	ENSMUSG00000040904	11	70235206	70239830	-1	2	0	4	76	2	0	126	182	80	10	44	H3BJV0	
ENSMUST00000176117	ENSMUSG00000027603	2	155490379	155518237	-1	0	2	16	6	0	2	0	0	0	0	1	H3BKA5	
ENSMUST00000176118	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK41	
ENSMUST00000176120	ENSMUSG00000049957	11	120458115	120464358	1	0	1	0	0	0	1	0	0	0	0	0	H3BLI5	
ENSMUST00000176121	ENSMUSG00000093632	6	66776144	66777179	-1	4	0	2	1	4	1	0	0	0	0	0	Q8R2E1	
ENSMUST00000176122						12	6	4	14	9	5	0	0	0	0	0		
ENSMUST00000176123						2	1	6	0	2	1	0	2	8	1	7		
ENSMUST00000176124	ENSMUSG00000073705	4	149127121	149137629	-1	2	1	3	32	4	0	8	5	6	0	0		
ENSMUST00000176125						3	1	1	0	1	0	6	26	5	0	10		
ENSMUST00000176126						0	0	0	0	0	0	0	0	0	5	0		
ENSMUST00000176127	ENSMUSG00000034799	8	71624417	71671757	-1	0	0	0	0	0	0	0	0	1	0	0	H3BKY4	
ENSMUST00000176128	ENSMUSG00000021972	14	64811600	64949871	-1	0	14	13	13	0	0	59	0	126	0	67	H3BKM3	
ENSMUST00000176129	ENSMUSG00000043456	7	37472135	37773641	-1	34	16	33	46	21	11	0	0	0	0	0	Q3TR09	
ENSMUST00000176130	ENSMUSG00000008206	8	4493026	4531680	1	0	0	2	0	2	0	3	0	0	1	0	H3BL50	
ENSMUST00000176131						2	5	3	3	0	0	0	0	0	0	0		
ENSMUST00000176133						7	5	5	3	11	5	0	0	0	0	0		
ENSMUST00000176135						0	0	0	0	0	1	4	0	0	5	0		
ENSMUST00000176136						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000176137						2	3	3	6	1	2	0	0	0	0	0		
ENSMUST00000176138						1	0	5	1	0	0	9	11	11	5	17		
ENSMUST00000176139						4	8	16	26	11	7	0	0	0	0	0		
ENSMUST00000176140	ENSMUSG00000009739	15	100575318	100599984	-1	0	0	0	0	0	0	10	5	3	0	0	A0A0A0MQN7	
ENSMUST00000176141	ENSMUSG00000035877	2	160748708	160872998	-1	0	0	0	0	0	0	1	0	0	0	0	H3BIX6	
ENSMUST00000176142						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176144	ENSMUSG00000031910	8	106870242	106884566	1	10	3	0	89	0	17	0	7	5	0	9		O08650
ENSMUST00000176145	ENSMUSG00000037845	9	50768236	50773348	1	0	0	0	0	0	0	0	0	0	2	0	H3BLI0	
ENSMUST00000176146	ENSMUSG00000022321	15	18818947	19014236	1	0	1	1	0	0	0	0	0	0	0	0	H3BKV8	
ENSMUST00000176147	ENSMUSG00000093379	6	58471898	58475343	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK49	
ENSMUST00000176148						0	5	10	0	0	0	0	4	0	0	1		
ENSMUST00000176149	ENSMUSG00000011832	8	4166567	4211257	1	0	0	0	0	0	0	0	0	0	0	12	H3BKQ3	
ENSMUST00000176150						0	0	0	31	0	6	0	0	0	0	0		
ENSMUST00000176151						0	1	0	52	5	2	0	0	0	0	0		
ENSMUST00000176153	ENSMUSG00000078934	9	35908423	35910796	1	0	0	0	0	0	0	0	0	0	0	0	D3YWX3	
ENSMUST00000176155	ENSMUSG00000031970	8	123504718	123515463	-1	8	5	15	61	16	0	0	2	7	0	11	H3BKU0	
ENSMUST00000176156	ENSMUSG00000049515	1	91322075	91348306	1	0	0	0	533	5	0	0	0	0	0	0	H3BLK9	
ENSMUST00000176158	ENSMUSG00000030879	7	105806658	105811099	-1	0	0	0	0	0	0	76	142	26	53	48	H3BJT9	
ENSMUST00000176159	ENSMUSG00000031979	8	124520767	124552008	1	0	0	0	29	0	0	0	0	0	0	0	H3BL04	
ENSMUST00000176160						0	0	7	4	1	0	0	0	0	0	0		
ENSMUST00000176161	ENSMUSG00000022053	14	67233292	67430918	1	15	17	51	16	18	11	0	0	0	0	1		O08792
ENSMUST00000176162						4	6	4	6	4	3	0	0	0	0	0		
ENSMUST00000176163						4	0	5	0	3	0	0	3	0	0	0		
ENSMUST00000176164						3	7	5	3	4	1	0	0	2	12	0		
ENSMUST00000176165						1	1	2	1	2	2	0	0	0	0	0		
ENSMUST00000176166						6	5	4	3	10	5	0	6	0	2	0		
ENSMUST00000176167						4	1	10	4	3	1	7	6	7	3	15		
ENSMUST00000176168	ENSMUSG00000056666	6	72598475	72608425	1	0	3	14	5	0	2	1	0	4	6	18	H3BKK1	
ENSMUST00000176169						0	2	0	76	0	0	0	0	0	0	0		
ENSMUST00000176170						7	3	7	2	7	0	5	6	5	0	10		
ENSMUST00000176171	ENSMUSG00000074634	13	119487941	119610458	1	0	0	0	0	0	0	0	0	0	1	0	H3BJ86	
ENSMUST00000176172	ENSMUSG00000029705	5	136248135	136567490	-1	1	5	38	0	0	0	0	28	175	5	192	H3BJQ9	
ENSMUST00000176173						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176175	ENSMUSG00000025255	3	5218526	5415857	1	2	2	1	3	1	0	0	0	0	0	0	V9GXP5	
ENSMUST00000176176	ENSMUSG00000050954	13	48487647	48513451	-1	6	3	7	7	8	0	0	30	0	0	0	G5E912	
ENSMUST00000176177	ENSMUSG00000093379	6	58471898	58475343	-1	0	0	0	0	2	1	0	0	0	0	0	L7N2F1	
ENSMUST00000176178	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	3	1	0	0	0	17	0	0	H3BJ15	
ENSMUST00000176179	ENSMUSG00000017631	11	76416734	76622314	-1	2	5	38	11	9	2	0	0	2	0	0	H3BKT3	
ENSMUST00000176180						133	152	684	242	150	87	1	3	0	0	0		
ENSMUST00000176181						7	5	58	10	9	2	1	0	2	0	3		
ENSMUST00000176182						0	0	0	0	0	0	10	167	42	0	37		
ENSMUST00000176183						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000176184						0	0	0	0	0	0	0	19	0	0	0		
ENSMUST00000176185	ENSMUSG00000049281	9	40269216	40291618	1	0	0	0	0	0	0	0	0	0	0	0	H3BJR6	
ENSMUST00000176186						6	6	29	101	11	0	0	0	2	0	7		
ENSMUST00000176187	ENSMUSG00000056459	12	76347782	76369602	-1	0	0	0	13	1	0	0	2	8	0	0	H3BKN3	
ENSMUST00000176188						2	1	1	1	0	1	5	14	3	0	3		
ENSMUST00000176189						0	0	3	0	0	0	0	0	1	0	2		
ENSMUST00000176190	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	0	17	0	1	0	9	0	0	0	H3BKB1	
ENSMUST00000176191	ENSMUSG00000029088	5	48389502	49524907	-1	40	33	17	37	21	11	0	7	5	3	20	Q3YAA7	Q6PHZ8
ENSMUST00000176192	ENSMUSG00000028710	4	115784812	115818828	1	0	0	4	0	0	0	10	53	7	7	0	H3BLD0	
ENSMUST00000176193	ENSMUSG00000030868	7	122133041	122149044	1	4	4	0	85	3	3	0	0	10	0	4	H3BJ75	
ENSMUST00000176194	ENSMUSG00000029055	4	154983115	155056784	-1	5	8	36	74	14	6	1	0	0	0	0	H3BIW6	
ENSMUST00000176195	ENSMUSG00000034674	10	82629828	82650799	1	0	0	0	0	3	0	0	0	0	0	6	H3BLR1	
ENSMUST00000176196						6	1	3	7	0	4	1	0	0	0	0		
ENSMUST00000176197						2	0	1	0	0	0	0	0	5	13	5		
ENSMUST00000176198	ENSMUSG00000032547	9	102834917	102908305	1	5	6	0	0	0	0	0	0	0	0	0	H3BKH8	
ENSMUST00000176199	ENSMUSG00000030513	7	65861734	66050386	1	0	2	0	10	3	0	0	0	0	0	0	H3BLN2	
ENSMUST00000176200	ENSMUSG00000063320	10	82619851	82623228	-1	3	12	42	124	19	14	0	0	0	0	0		Q8BTC1
ENSMUST00000176202						0	0	8	0	3	1	0	0	0	0	0		
ENSMUST00000176203	ENSMUSG00000090231	17	34856374	34862518	-1	0	12	23	0	18	5	0	0	0	0	0	B8JJM6	
ENSMUST00000176204	ENSMUSG00000092035	6	4747306	4760517	1	23	29	58	42	0	0	3	0	0	0	0		Q7TN75

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176205	ENSMUSG00000043456	7	37472135	37773641	-1	0	0	0	57	11	11	0	0	0	0	0		Q8K083
ENSMUST00000176207	ENSMUSG00000021546	13	58391142	58403343	-1	0	0	5	35	0	0	17	0	69	45	36		P61979
ENSMUST00000176209	ENSMUSG00000030513	7	65861734	66050386	1	0	14	10	0	0	23	0	0	1	0	0	H3BJL4	
ENSMUST00000176210	ENSMUSG00000030788	7	110800432	110844457	-1	0	0	0	0	0	0	2	0	0	0	0	H3BK28	
ENSMUST00000176211						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000176212						9	4	0	0	17	7	3	0	17	0	7		
ENSMUST00000176213						7	5	0	0	3	3	0	0	0	0	5		
ENSMUST00000176216	ENSMUSG00000029705	5	136248135	136567490	-1	0	0	0	0	0	0	216	540	123	63	0	H3BJN3	
ENSMUST00000176219	ENSMUSG00000033697	15	76723985	76818170	-1	6	0	0	11	0	3	2	3	0	0	7	H3BKC8	
ENSMUST00000176220	ENSMUSG00000026694	1	162532127	162548551	-1	0	0	0	0	0	3	0	0	4	0	0	H3BLQ8	
ENSMUST00000176221						0	4	1	13	2	0	0	0	0	0	3		
ENSMUST00000176222	ENSMUSG00000032089	9	45253837	45269149	-1	14	0	0	0	12	0	51	17	16	0	54	H3BKN6	
ENSMUST00000176223						0	1	0	0	0	0	0	0	0	2	0		
ENSMUST00000176224	ENSMUSG00000005982	16	3872375	3904780	1	0	2	4	1	0	0	4	2	7	0	9	H3BJW5	
ENSMUST00000176225						3908	4580	12908	2912	4878	2315	33	140	37	29	55		
ENSMUST00000176226						0	0	3	1	0	0	0	0	1	1	0		
ENSMUST00000176227	ENSMUSG00000064125	8	4209543	4217459	-1	0	0	1	59	0	2	0	0	0	0	0	H3BJX6	
ENSMUST00000176228	ENSMUSG00000019997	10	24595442	24598683	1	10	5	9	2	4	4	0	0	0	0	0	H3BJW0	
ENSMUST00000176229	ENSMUSG00000000247	2	38339281	38369733	1	0	0	3	18	5	1	0	0	0	0	0	H3BKI3	
ENSMUST00000176230						2	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000176231	ENSMUSG00000039166	10	25169090	25307870	-1	0	0	0	0	1	0	0	0	0	0	0	H3BKK9	
ENSMUST00000176232	ENSMUSG00000019737	7	30314807	30319046	1	1	0	1	0	0	0	0	0	0	2	0	H3BJV8	
ENSMUST00000176233	ENSMUSG00000093575	16	3884648	3919517	1	0	0	0	0	0	0	0	0	0	0	0	H3BLK7	
ENSMUST00000176234						0	1	0	3	2	1	0	0	0	0	0		
ENSMUST00000176236						2	1	0	2	1	3	0	0	0	0	0		
ENSMUST00000176237	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	3	0	12	0	46	H3BJD9	
ENSMUST00000176238	ENSMUSG00000037971	9	50762828	50775520	-1	0	0	0	0	0	0	5	0	9	60	14	H3BL73	
ENSMUST00000176239						4	3	0	0	0	3	0	0	0	0	0		
ENSMUST00000176240						10	2	6	9	0	1	0	0	0	0	0		
ENSMUST00000176241						0	0	0	0	0	1	3	28	5	4	7		
ENSMUST00000176242	ENSMUSG00000027699	3	27097222	27153878	-1	0	0	0	0	0	0	79	0	62	32	34		Q07139
ENSMUST00000176243	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	30	0	0	0	0	H3BLF9	
ENSMUST00000176244						4	0	3	5	3	0	0	0	0	0	0		
ENSMUST00000176245						0	1	0	91	2	0	0	0	0	0	0		
ENSMUST00000176246	ENSMUSG00000063232	12	103980243	103989957	-1	3	2	0	3	2	0	0	0	0	0	0	H3BJV3	
ENSMUST00000176247						2	3	5	12	1	2	0	0	3	0	0		
ENSMUST00000176248	ENSMUSG00000023021	15	99734881	99772885	-1	0	1	12	1	3	0	15	47	26	20	18	H3BJQ0	
ENSMUST00000176249	ENSMUSG00000070369	7	128154376	128223816	1	4	2	5	3	5	0	0	1	0	0	0	H3BKA0	
ENSMUST00000176250	ENSMUSG00000032336	9	58582240	58657955	1	8	3	11	5	11	5	16	30	23	12	34		P97300
ENSMUST00000176251	ENSMUSG00000028552	4	109280268	109387817	1	0	0	0	0	0	0	241	796	695	227	385	Q5JC28	
ENSMUST00000176252	ENSMUSG00000093696	6	57024106	57025324	-1	4	2	2	0	2	0	0	0	0	0	0	E9Q8T0	
ENSMUST00000176253						4	0	0	0	0	3	0	0	2	7	0		
ENSMUST00000176254	ENSMUSG00000026655	2	3613758	3782142	1	0	0	0	0	0	0	4	7	30	22	55	H3BLM7	
ENSMUST00000176255						2	0	0	3	3	1	0	0	0	0	0		
ENSMUST00000176256						0	0	0	0	0	0	11	56	0	2	0		
ENSMUST00000176257						0	2	0	0	5	3	27	138	37	28	0		
ENSMUST00000176258	ENSMUSG00000039166	10	25169090	25307870	-1	1	1	1	0	1	1	1	29	5	0	0	H3BJL8	
ENSMUST00000176259	ENSMUSG00000057156	14	54852736	54870961	-1	0	0	0	0	0	0	25	28	6	1	12	H3BL46	
ENSMUST00000176260						0	0	0	0	0	0	0	0	5	0	0		
ENSMUST00000176261	ENSMUSG00000003518	11	101971143	101987013	-1	0	0	0	15	1	1	0	0	7	0	4	H3BKL8	
ENSMUST00000176262	ENSMUSG00000045098	19	3767421	3818303	1	1	0	0	0	0	0	163	297	485	25	409		Q3U8K7
ENSMUST00000176263	ENSMUSG00000032827	6	4902917	5165661	1	10	2	3	0	7	0	0	0	0	0	0	H3BJD0	
ENSMUST00000176264						0	7	17	15	11	10	0	0	0	0	0		
ENSMUST00000176265	ENSMUSG00000029772	6	29768011	29912310	1	3	1	3	3	1	0	0	0	0	0	0	H3BLA5	
ENSMUST00000176266	ENSMUSG00000025154	19	41766588	41802084	-1	0	0	0	0	0	0	0	0	23	0	0	H3BJ36	
ENSMUST00000176267						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000176268	ENSMUSG00000040904	11	70235206	70239830	-1	0	5	0	0	0	2	0	0	0	0	0		Q8K3C0
ENSMUST00000176269						0	2	0	3	0	0	0	0	0	0	0		
ENSMUST00000176270						1	0	0	10	0	0	0	0	0	0	0		
ENSMUST00000176271	ENSMUSG00000009739	15	100575318	100599984	-1	23	16	88	89	35	17	48	24	58	13	56		Q07916
ENSMUST00000176272						3	0	2	0	0	0	0	0	23	7	57		
ENSMUST00000176273						3	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000176274	ENSMUSG00000053929	15	76643395	76660117	-1	12	3	20	37	18	7	437	392	308	95	241	H3BIV6	
ENSMUST00000176276	ENSMUSG00000070568	7	45277513	45288998	1	14	13	25	40	13	11	0	0	0	0	0	H3BL98	
ENSMUST00000176277						5	0	0	26	1	0	24	47	12	3	16		
ENSMUST00000176278	ENSMUSG00000056459	12	76347782	76369602	-1	0	0	0	21	0	0	0	61	8	31	0	G3UW50	
ENSMUST00000176279	ENSMUSG00000031979	8	124520767	124552008	1	0	0	0	0	0	0	3	0	0	0	0	H3BJK5	
ENSMUST00000176280						5	2	3	30	7	3	0	0	0	0	0		
ENSMUST00000176281						3	6	0	1	4	2	0	6	0	0	0		
ENSMUST00000176282	ENSMUSG00000061959	8	93201218	93229619	-1	0	11	0	14	0	0	0	0	0	0	0	H3BL34	
ENSMUST00000176284	ENSMUSG00000091662	7	10579756	10613576	-1	0	0	2	0	0	0	0	0	0	0	0	H3BJH9	
ENSMUST00000176285	ENSMUSG00000019984	10	24869986	24913681	1	6	0	4	0	8	1	93	196	157	58	126	H3BK33	
ENSMUST00000176286	ENSMUSG00000031970	8	123504718	123515463	-1	7	1	13	26	9	6	3	3	6	1	7	H3BIX2	
ENSMUST00000176287	ENSMUSG00000056487	15	100353200	100361840	1	5	0	12	4	0	2	0	0	0	0	0	Q76I24	
ENSMUST00000176288						5	2	12	6	3	1	4	0	2	0	7		
ENSMUST00000176289	ENSMUSG00000040434	2	92365046	92374869	-1	0	0	0	0	0	0	0	0	0	0	0		Q5XPT3
ENSMUST00000176292	ENSMUSG00000050966	4	134003330	134018841	-1	3	2	3	1	2	2	12	5	6	2	9	H3BL11	
ENSMUST00000176293						3	0	2	0	0	3	0	0	0	0	0		
ENSMUST00000176294	ENSMUSG00000020263	10	83600033	83648738	-1	0	0	0	33	0	0	0	0	0	0	0	H3BL43	
ENSMUST00000176295	ENSMUSG00000030868	7	122133041	122149044	1	6	3	0	6	10	6	0	39	2	2	3	H3BKU6	
ENSMUST00000176297						2	1	17	4	7	1	0	0	0	0	0		
ENSMUST00000176298						4	0	0	0	0	0	5	0	0	0	0		
ENSMUST00000176299	ENSMUSG00000032400	9	64137144	64173104	-1	0	0	0	0	0	0	12	0	2	0	4	H3BKZ0	
ENSMUST00000176300	ENSMUSG00000009739	15	100575318	100599984	-1	78	27	146	0	58	35	0	4	16	1	0	H3BKJ6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176301						1	0	2	1	2	1	0	0	3	0	0		
ENSMUST00000176302	ENSMUSG00000028101	3	96696384	96706070	1	0	1	0	51	4	0	0	2	6	0	4	H3BJ41	
ENSMUST00000176303						3	0	4	1	3	0	0	0	0	0	14		
ENSMUST00000176304	ENSMUSG00000019737	7	30314807	30319046	1	0	0	0	0	0	0	0	0	0	0	8	H3BL35	
ENSMUST00000176305	ENSMUSG00000021546	13	58391142	58403343	-1	2	0	8	8	0	5	416	1474	850	86	419	H3BK96	
ENSMUST00000176306	ENSMUSG00000032595	9	107992497	107999684	1	0	0	0	0	0	0	0	6	0	0	0	H3BK05	
ENSMUST00000176307	ENSMUSG00000028059	3	88607454	88648052	1	2	3	6	2	2	1	0	0	7	0	3	H3BJ48	
ENSMUST00000176308						0	0	0	7	0	0	897	1631	1197	273	799		
ENSMUST00000176310						5	5	10	6	5	4	0	0	0	1	1		
ENSMUST00000176311						4	0	2	5	1	0	0	0	1	0	1		
ENSMUST00000176312	ENSMUSG00000039826	2	29761224	29788502	-1	0	0	0	0	0	0	13	4	11	10	0	H3BLS1	
ENSMUST00000176313	ENSMUSG00000019984	10	24869986	24913681	1	1	0	0	11	1	2	0	0	0	0	0	H3BLE0	
ENSMUST00000176314	ENSMUSG00000010110	19	8741413	8756069	1	0	0	0	0	0	0	0	0	0	0	0	H3BKD6	
ENSMUST00000176315	ENSMUSG00000041530	4	126435012	126468583	-1	0	8	0	2	0	2	0	0	0	0	0	H3BJ70	
ENSMUST00000176316	ENSMUSG00000028059	3	88607454	88648052	1	0	1	0	0	0	1	0	0	0	0	0	H3BLJ1	
ENSMUST00000176317						1	1	8	2	3	1	0	0	0	0	0		
ENSMUST00000176318						1	0	5	2	1	0	0	7	0	0	3		
ENSMUST00000176320						0	5	0	4	0	1	0	0	0	0	0		
ENSMUST00000176321	ENSMUSG00000062082	16	44811733	44839150	1	9	6	24	0	7	4	0	125	43	15	95	H3BJX3	
ENSMUST00000176322	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	290	930	721	13	569	H3BJS0	
ENSMUST00000176324	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	1	0	0	0	0	13	H3BKC7	
ENSMUST00000176325	ENSMUSG00000009585	15	79891659	79915906	1	5	4	0	0	6	3	12	29	12	0	20	H3BJ44	
ENSMUST00000176326	ENSMUSG00000034674	10	82629828	82650799	1	0	0	0	0	0	0	0	0	0	0	0	H3BJJ4	
ENSMUST00000176327						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176328	ENSMUSG00000091572	3	64258961	64287495	-1	15	0	0	0	0	0	0	0	0	0	0	H3BJ88	
ENSMUST00000176329	ENSMUSG00000021147	13	8802968	8871909	-1	0	0	9	0	1	0	0	0	0	3	0	H3BJS1	
ENSMUST00000176330	ENSMUSG00000004842	16	65520511	65535005	1	46	21	142	1516	42	37	1	0	0	0	1		Q00286
ENSMUST00000176331						6	0	12	2	5	0	4	0	4	4	0		
ENSMUST00000176332	ENSMUSG00000090231	17	34856374	34862518	-1	0	1	0	0	0	0	0	20	0	35	20	H3BK95	
ENSMUST00000176333						3	2	1	15	4	2	0	3	2	4	0		
ENSMUST00000176334	ENSMUSG00000032595	9	107992497	107999684	1	0	0	2	0	0	0	0	0	0	0	0	H3BKF2	
ENSMUST00000176335	ENSMUSG00000037845	9	50768236	50773348	1	0	0	0	4	0	0	0	3	3	0	0		Q3UY23
ENSMUST00000176336	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	282	1539	586	55	101	H3BJ71	
ENSMUST00000176339	ENSMUSG00000040434	2	92365046	92374869	-1	0	2	1	13	3	4	0	2	0	0	2	H3BL20	
ENSMUST00000176340						0	1	0	6	7	0	11	18	0	8	6		
ENSMUST00000176341						3	4	4	0	1	3	0	0	0	0	0		
ENSMUST00000176342	ENSMUSG00000041420	7	16175090	16186504	1	0	3	5	22	0	2	0	0	0	2	0	H3BK94	
ENSMUST00000176343	ENSMUSG00000005803	2	122765237	122809569	1	1	0	2	0	0	0	0	1387	115	0	0	H3BLH2	
ENSMUST00000176345	ENSMUSG00000040732	16	95359169	95586593	-1	0	0	0	0	0	0	0	0	0	0	11	H3BKX4	
ENSMUST00000176346	ENSMUSG00000028487	4	84275095	84675275	-1	1	0	0	14	0	0	0	0	0	0	0	H3BJD5	
ENSMUST00000176347	ENSMUSG00000002233	3	104788375	104794459	1	3	3	0	0	3	0	49	0	27	14	29	H3BL56	
ENSMUST00000176348	ENSMUSG00000026798	2	29787493	29797935	1	0	0	0	9	0	0	36	0	0	14	0	D6RJJ8	
ENSMUST00000176349	ENSMUSG00000032058	9	50845301	50894229	1	2	0	0	3	0	2	0	0	0	0	0	H3BLE7	
ENSMUST00000176350	ENSMUSG00000032567	9	105395392	105412229	1	0	0	0	0	0	0	0	0	3	0	0	A0A087WNN6	
ENSMUST00000176351	ENSMUSG00000036138	9	119339676	119350299	1	0	0	0	70	0	0	0	0	0	0	0	H3BJC1	
ENSMUST00000176352						2	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000176353	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	374	407	318	82	175	Q8C2K8	
ENSMUST00000176354						0	0	0	1	1	0	18	232	92	167	35		
ENSMUST00000176355						2	0	0	46	2	2	0	0	0	0	0		
ENSMUST00000176356	ENSMUSG00000093456	9	107996349	108045270	1	0	0	0	0	0	0	0	0	0	0	0	H3BK64	
ENSMUST00000176357						0	0	0	0	0	0	7	0	34	4	12		
ENSMUST00000176358	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK40	
ENSMUST00000176359						0	0	0	0	0	0	328	1053	334	0	26		
ENSMUST00000176360	ENSMUSG00000034252	9	80066903	80144953	1	0	0	4	0	0	0	10	5	19	27	69	H3BJS8	
ENSMUST00000176361						3	1	3	6	5	2	5	9	8	0	17		
ENSMUST00000176362	ENSMUSG00000008489	4	91250763	91400785	-1	0	0	0	91	1	0	0	0	0	0	0	H3BJL9	
ENSMUST00000176363	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	0	0	0	0	0	4	0	0	32	H3BJY0	
ENSMUST00000176364	ENSMUSG00000056666	6	72598475	72608425	1	8	1	0	11	8	0	0	10	8	5	17	H3BJ51	
ENSMUST00000176365	ENSMUSG00000030340	6	125320659	125344943	1	0	0	0	0	0	0	0	0	0	0	0	H3BKP2	
ENSMUST00000176367						12	6	5	0	5	3	0	0	0	0	0		
ENSMUST00000176368						0	5	6	3	2	0	0	0	0	0	0		
ENSMUST00000176369	ENSMUSG00000078698	7	47588950	47601372	-1	8	11	11	13	8	5	0	0	0	1	0	H3BKL3	
ENSMUST00000176370	ENSMUSG00000028487	4	84275095	84675275	-1	2	0	0	1	1	0	0	0	0	0	0	H3BJE5	
ENSMUST00000176371	ENSMUSG00000030838	7	46195350	46238503	-1	4	5	21	4	12	5	0	0	0	0	0	H3BIZ2	
ENSMUST00000176372						0	0	1	1	1	2	6	8	1	4	2		
ENSMUST00000176373	ENSMUSG00000032595	9	107992497	107999684	1	0	0	7	0	2	1	0	2	0	0	1	H3BJ93	
ENSMUST00000176374	ENSMUSG00000018733	11	83294642	83302586	-1	2	4	17	31	8	2	0	4	2	5	2	H3BJF5	
ENSMUST00000176376	ENSMUSG00000093692	6	57232843	57234371	1	4	3	1	0	2	1	0	0	0	0	0	H3BJ46	
ENSMUST00000176378	ENSMUSG00000032400	9	64137144	64173104	-1	0	0	0	0	0	0	0	0	0	0	2	H3BIZ1	
ENSMUST00000176379	ENSMUSG00000031568	8	47533664	47552955	1	1	0	2	1	0	0	10	9	7	7	3	H3BJN8	
ENSMUST00000176381	ENSMUSG00000010110	19	8741413	8756069	1	14	8	25	17	4	4	20	64	14	7	51		Q8K1E0
ENSMUST00000176382						7	10	25	12	12	8	0	5	0	0	8		
ENSMUST00000176383	ENSMUSG00000025255	3	5218526	5415857	1	5	19	18	0	29	12	1	0	0	0	0	E9Q5A7	
ENSMUST00000176384	ENSMUSG00000022377	15	64086857	64382919	-1	0	3	0	0	3	0	0	0	0	0	105		Q9QWY8
ENSMUST00000176386						56	43	245	42	28	22	15	30	42	2	38		
ENSMUST00000176388						1	0	0	0	0	0	2	2	8	4	22		
ENSMUST00000176390	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	0	11	0	0	0	0	0	0	0	H3BK57	
ENSMUST00000176392						0	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000176394	ENSMUSG00000022518	16	4835416	4867691	1	108	95	198	128	209	128	2	9	10	52	11	H3BJT7	
ENSMUST00000176395	ENSMUSG00000093411	6	57360452	57361431	-1	3	3	1	3	2	1	0	0	0	0	0	Q8R2D8	
ENSMUST00000176397	ENSMUSG00000036138	9	119339676	119350299	1	0	0	0	0	0	0	0	0	0	7	0	H3BJZ9	
ENSMUST00000176398	ENSMUSG00000025916	1	9968624	10009136	-1	0	0	0	1	3	0	0	0	3	16	0	H3BK71	
ENSMUST00000176400						4	0	10	4	10	0	0	0	14	2	19		
ENSMUST00000176401						0	0	0	16	3	2	15	21	8	0	38		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176402						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176403	ENSMUSG00000049719	9	110844506	110856522	1	0	0	15	10	4	0	0	0	0	0	0		Q5M8S2
ENSMUST00000176404						0	0	0	0	0	1	0	115	14	11	41		
ENSMUST00000176407	ENSMUSG00000045098	19	3767421	3818303	1	0	0	0	0	0	0	0	0	0	0	0	H3BJ94	
ENSMUST00000176408	ENSMUSG00000008496	7	25087344	25159922	-1	3	6	11	17	6	4	0	0	0	0	6	H3BKB7	
ENSMUST00000176409						50	51	82	49	50	36	0	3	2	0	0		
ENSMUST00000176410						13	0	0	0	8	3	0	0	0	0	0		
ENSMUST00000176411	ENSMUSG00000029064	4	155491361	155559269	1	0	0	3	3	2	2	0	85	14	0	29	H3BLF7	
ENSMUST00000176412						4	7	18	9	12	2	0	0	0	0	0		
ENSMUST00000176413						2	2	6	6	5	0	0	0	0	0	0		
ENSMUST00000176414						2	1	0	2	2	1	0	0	0	0	0		
ENSMUST00000176415						0	3	0	0	0	0	0	4	2	6	3		
ENSMUST00000176416	ENSMUSG00000032010	9	44067021	44095627	1	0	2	0	159	4	5	22	37	88	3	30		O88623
ENSMUST00000176418	ENSMUSG00000028487	4	84275095	84675275	-1	20	19	3	10	15	5	1	10	8	0	8	H3BKX5	
ENSMUST00000176419	ENSMUSG00000014846	8	105467493	105471526	-1	0	0	7	4	2	1	144	35	9	36	52		Q9CRB6
ENSMUST00000176422						22	17	16	27	19	8	0	14	10	1	31		
ENSMUST00000176423	ENSMUSG00000029705	5	136248135	136567490	-1	0	0	0	0	0	0	56	22	67	0	51	H3BJL7	
ENSMUST00000176424						10	1	12	0	4	0	2	1	0	0	8		
ENSMUST00000176425	ENSMUSG00000001418	3	88325023	88331313	1	0	0	0	0	0	0	179	224	5	80	72	H3BKY1	
ENSMUST00000176426	ENSMUSG00000034799	8	71624417	71671757	-1	3	1	9	0	2	2	0	0	0	0	1	H3BJL3	
ENSMUST00000176427						4	0	0	2	2	1	0	0	3	0	3		
ENSMUST00000176429	ENSMUSG00000021147	13	8802968	8871909	-1	0	0	0	0	3	2	9	0	21	2	29	H3BJB3	
ENSMUST00000176430	ENSMUSG00000035152	11	83299024	83405035	1	18	9	22	24	9	2	16	19	22	0	24	H3BIY9	
ENSMUST00000176431						7	2	18	52	22	5	0	2	4	0	6		
ENSMUST00000176433	ENSMUSG00000011171	12	116077726	116146261	1	1	0	0	0	1	1	0	0	0	0	0	H3BJW2	
ENSMUST00000176434						4	0	5	4	2	0	3	2	7	0	23		
ENSMUST00000176435	ENSMUSG00000035394	18	74283090	74359986	1	0	0	0	0	0	0	0	2	0	0	0	H3BJA5	
ENSMUST00000176437	ENSMUSG00000046691	8	106883863	106893601	-1	0	0	0	0	2	0	5	3	7	0	6	H3BJ60	
ENSMUST00000176438	ENSMUSG00000026872	2	44983632	45117395	-1	1	0	129	48	25	14	35	28	0	0	0		Q9R0G7
ENSMUST00000176439						0	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000176440	ENSMUSG00000070385	3	103074014	103099720	1	2	0	1	4	4	0	0	0	0	0	0	H3BLC7	
ENSMUST00000176442	ENSMUSG00000030340	6	125320659	125344943	1	0	0	0	0	0	0	0	0	0	0	0	H3BKC4	
ENSMUST00000176443						6	7	0	0	0	12	0	0	0	0	0		
ENSMUST00000176444						0	3	0	34	5	3	0	0	0	0	0		
ENSMUST00000176445	ENSMUSG00000028124	3	122245557	122270732	1	0	0	0	1	0	0	7	31	12	0	5	H3BJA3	
ENSMUST00000176446	ENSMUSG00000041420	7	16175090	16186504	1	4	3	0	0	0	0	0	2	1	3	4	H3BJ55	
ENSMUST00000176448	ENSMUSG00000057068	5	92555069	92591279	1	1	0	2	0	0	0	0	0	0	0	0	H3BJN1	
ENSMUST00000176451						0	2	0	86	0	0	0	0	0	0	0		
ENSMUST00000176452						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000176453	ENSMUSG00000009995	X	74281912	74290151	1	0	0	0	0	0	0	0	11	0	5	20	H3BJJ8	
ENSMUST00000176454						2	0	2	3	2	1	0	0	0	0	0		
ENSMUST00000176456						65	61	79	90	70	40	11	37	31	7	42		
ENSMUST00000176457						0	0	0	0	0	0	91	0	0	0	0		
ENSMUST00000176458	ENSMUSG00000024213	17	27579382	27623465	-1	0	1	0	3	2	0	13	17	12	5	15	H3BJY4	
ENSMUST00000176459	ENSMUSG00000093456	9	107996349	108045270	1	0	0	0	0	0	0	0	2	0	3	9	H3BKU8	
ENSMUST00000176460	ENSMUSG00000012609	12	85824659	86061893	1	0	3	3	4	0	0	0	0	5	0	0	H3BK74	
ENSMUST00000176461						4	1	7	1	3	1	0	0	0	0	0		
ENSMUST00000176462						11	4	11	11	15	7	0	2	6	0	3		
ENSMUST00000176463	ENSMUSG00000027331	2	118814003	118853957	1	1	1	0	0	4	0	0	0	0	0	0	H3BKV9	
ENSMUST00000176464	ENSMUSG00000021000	12	59129720	59191583	1	110	104	149	108	94	50	12	29	23	12	32	H3BKH2	
ENSMUST00000176465						1	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000176466	ENSMUSG00000029647	5	147430161	147548502	1	0	0	0	0	0	0	18	38	73	0	45	H3BL68	
ENSMUST00000176467	ENSMUSG00000078606	7	105895139	105953967	-1	44	17	0	19	0	10	191	918	315	215	416		Q80SU7
ENSMUST00000176468						5	2	6	1	1	2	1	1	1	0	0		
ENSMUST00000176469						9	4	10	7	10	6	0	0	0	0	0		
ENSMUST00000176470						0	0	0	0	0	2	0	1	2	1	0		
ENSMUST00000176472	ENSMUSG00000024347	18	35964830	36014715	1	0	22	124	0	0	0	2	13	5	1	0	H3BK80	
ENSMUST00000176474						0	0	0	0	6	0	0	0	0	0	0		
ENSMUST00000176475	ENSMUSG00000024921	19	26605115	26778321	1	0	0	0	0	0	0	0	14	0	25	0	H3BK47	
ENSMUST00000176476						0	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000176477						0	1	41	4	0	0	29	0	51	0	20		
ENSMUST00000176478						16	4	32	19	19	4	6	84	15	0	109		
ENSMUST00000176479	ENSMUSG00000037816	13	50417864	50433780	1	0	5	0	0	0	0	0	15	0	0	5	H3BKU3	
ENSMUST00000176480	ENSMUSG00000055531	10	117344673	117380015	-1	1	0	0	0	3	0	1	96	36	17	17	H3BKW0	
ENSMUST00000176481	ENSMUSG00000090581	3	64537561	64565298	-1	13	0	0	11	2	0	0	0	0	0	0	H3BK29	
ENSMUST00000176482						4	3	3	2	8	1	0	0	0	0	0		
ENSMUST00000176483	ENSMUSG00000054611	19	4314419	4398285	-1	4	7	9	84	8	8	0	7	5	0	16	A0A087WQL9	
ENSMUST00000176484						0	1	0	1	1	0	3	15	6	14	4		
ENSMUST00000176485	ENSMUSG00000021595	13	69533746	69635780	1	8	0	2	0	3	0	29	0	35	39	23	H3BKN0	
ENSMUST00000176486	ENSMUSG00000029705	5	136248135	136567490	-1	0	0	0	1	0	7	0	0	0	0	0	H3BKF6	
ENSMUST00000176487						0	0	0	0	0	0	4	0	0	0	5		
ENSMUST00000176489	ENSMUSG00000021972	14	64811600	64949871	-1	2	0	1	0	0	0	0	0	0	0	0	H3BJ31	
ENSMUST00000176491	ENSMUSG00000037112	9	50892801	51009073	-1	0	0	0	0	0	0	0	69	88	0	158	H3BKG1	
ENSMUST00000176492						6	5	28	3	9	0	4	0	0	0	1		
ENSMUST00000176493						6	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000176494						0	0	5	0	1	0	0	0	0	0	0		
ENSMUST00000176495						22	21	48	35	25	10	0	10	8	1	14		
ENSMUST00000176496	ENSMUSG00000003680	19	8772522	8786417	-1	3	6	0	46	3	0	0	5	0	0	4	H3BJR2	
ENSMUST00000176497	ENSMUSG00000054611	19	4314419	4398285	-1	0	4	0	0	0	0	0	0	0	0	0	H3BKP6	
ENSMUST00000176498						0	0	14	0	0	0	141	231	93	58	73		
ENSMUST00000176499						11	0	14	0	6	2	0	0	0	2	14		
ENSMUST00000176500	ENSMUSG00000028059	3	88607454	88648052	1	8	19	24	13	13	17	0	0	2	19	32	H3BJ40	
ENSMUST00000176501						16	5	19	23	22	6	5	10	13	2	4		
ENSMUST00000176502	ENSMUSG00000019984	10	24869986	24913681	1	0	0	0	0	0	0	0	0	1	1	0	H3BJ42	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176503						1	1	14	13	0	3	0	4	0	0	0		
ENSMUST00000176504	ENSMUSG00000019737	7	30314807	30319046	1	0	0	0	0	0	0	0	0	0	0	0	H3BLM5	
ENSMUST00000176505						14	19	55	1	5	14	25	753	125	68	93		
ENSMUST00000176506	ENSMUSG00000041420	7	16175090	16186504	1	6	4	7	104	22	6	0	0	0	0	13		P97368
ENSMUST00000176508						4	0	16	7	2	3	1	6	3	0	11		
ENSMUST00000176509	ENSMUSG00000056459	12	76347782	76369602	-1	5	4	8	8	11	0	13	24	9	0	11	H3BLJ8	
ENSMUST00000176510	ENSMUSG00000035067	14	63606503	63820809	1	18	27	103	50	28	17	3	0	0	6	5	H3BJG3	
ENSMUST00000176511	ENSMUSG00000006720	13	21945094	21960779	1	5	4	0	19	0	0	0	0	0	0	0		Q7TSH9
ENSMUST00000176512	ENSMUSG00000045098	19	3767421	3818303	1	0	0	0	0	0	0	0	0	0	0	7	H3BJI9	
ENSMUST00000176513						6	1	0	0	5	1	0	0	5	0	4		
ENSMUST00000176514						2	5	6	8	0	2	2	8	3	2	2		
ENSMUST00000176515	ENSMUSG00000046691	8	106883863	106893601	-1	0	0	0	1	0	4	18	0	4	0	8	H3BL81	
ENSMUST00000176516						0	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000176517	ENSMUSG00000026858	2	30364233	30385521	1	0	1	7	0	0	3	0	0	0	0	0	H3BL42	
ENSMUST00000176518	ENSMUSG00000018733	11	83294642	83302586	-1	8	9	8	67	3	0	0	0	10	0	0	Q5SWQ8	Q8VC48
ENSMUST00000176519	ENSMUSG00000001418	3	88325023	88331313	1	0	0	0	0	0	0	0	0	0	0	46	H3BK59	
ENSMUST00000176520	ENSMUSG00000002996	12	31926254	31950535	-1	0	0	0	0	0	0	34	0	338	553	339	H3BJW8	
ENSMUST00000176522						2	1	0	0	0	0	0	0	6	0	0		
ENSMUST00000176523	ENSMUSG00000035152	11	83299024	83405035	1	0	0	0	0	0	0	0	0	0	0	0	H3BKM0	
ENSMUST00000176525						0	0	5	2	0	0	2	9	4	1	4		
ENSMUST00000176526						26	23	58	224	54	24	1	9	5	1	12		
ENSMUST00000176527	ENSMUSG00000034252	9	80066903	80144953	1	0	0	0	0	0	0	0	42	0	4	0	H3BLA9	
ENSMUST00000176528						2	1	2	0	0	1	0	8	6	0	15		
ENSMUST00000176529						73	40	79	93	80	53	0	0	3	0	4		
ENSMUST00000176530						0	0	0	0	0	0	0	12	15	4	0		
ENSMUST00000176531	ENSMUSG00000032041	9	35184551	35200291	-1	7	3	39	0	9	0	316	134	953	52	733	H3BKL1	
ENSMUST00000176532	ENSMUSG00000054611	19	4314419	4398285	-1	0	0	0	0	0	0	0	4	23	0	69	H3BKJ9	
ENSMUST00000176533	ENSMUSG00000079657	17	24527241	24534210	-1	4	0	0	2	0	0	0	0	0	0	0	H3BLG3	
ENSMUST00000176534	ENSMUSG00000043456	7	37472135	37773641	-1	0	3	0	0	0	2	0	0	0	0	0	H3BKM9	
ENSMUST00000176535	ENSMUSG00000027699	3	27097222	27153878	-1	0	0	0	0	0	0	0	0	0	0	0	H3BL29	
ENSMUST00000176536						1	3	6	4	12	0	0	0	1	0	0		
ENSMUST00000176538	ENSMUSG00000050860	11	95824499	95832140	1	0	0	0	88	0	1	5	78	149	46	52	H3BLB1	
ENSMUST00000176539	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	1	0	0	8	2	0	0	3	H3BL15	
ENSMUST00000176540	ENSMUSG00000052534	1	168119364	168432270	-1	45	41	394	115	57	24	913	3928	2264	278	1646		P41778
ENSMUST00000176541	ENSMUSG00000046519	3	95588934	95619247	1	0	0	0	0	0	0	0	0	25	0	0	H3BJN5	
ENSMUST00000176542						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176543	ENSMUSG00000037816	13	50417864	50433780	1	0	0	0	0	0	0	2	6	3	3	0	H3BJ96	
ENSMUST00000176546	ENSMUSG00000036138	9	119339676	119350299	1	0	0	0	0	0	0	109	0	0	0	4	H3BJG8	
ENSMUST00000176547	ENSMUSG00000049281	9	40269216	40291618	1	0	0	0	0	0	0	0	0	0	1	0	H3BKP5	
ENSMUST00000176548						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176550	ENSMUSG00000029556	5	114948980	114971094	-1	3	5	21	15	9	3	0	0	0	0	0	H3BL72	
ENSMUST00000176551	ENSMUSG00000092035	6	4747306	4760517	1	0	0	19	0	30	16	0	0	3	0	8	H3BJQ1	
ENSMUST00000176553	ENSMUSG00000029647	5	147430161	147548502	1	0	0	0	0	0	0	0	130	0	2	0	H3BJA8	
ENSMUST00000176554						2	4	7	5	13	1	0	0	0	2	3		
ENSMUST00000176555	ENSMUSG00000058317	14	18573575	18894267	-1	3	1	18	1	5	0	2	1	0	0	1	H3BJB5	
ENSMUST00000176557	ENSMUSG00000032336	9	58582240	58657955	1	0	5	11	0	1	0	530	702	0	0	0		P97300
ENSMUST00000176558	ENSMUSG00000021546	13	58391142	58403343	-1	5	6	1	1	3	7	17	57	23	5	33	Q8BT23	
ENSMUST00000176559	ENSMUSG00000045658	1	84036296	84364180	-1	37	20	45	26	41	18	0	0	10	0	46		Q3UBG2
ENSMUST00000176560						2	0	7	0	2	0	2	2	13	0	0		
ENSMUST00000176562						7	7	24	15	11	6	0	2	3	0	0		
ENSMUST00000176563						3	2	8	0	3	0	12	126	51	21	35		
ENSMUST00000176564						2	0	0	1	0	0	0	0	0	1	0		
ENSMUST00000176565	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	8	0	0	0	9	27	0	0	12	E2S038	
ENSMUST00000176566	ENSMUSG00000032594	9	108002501	108048782	1	0	0	0	0	0	0	19	0	7	0	1	H3BKD8	
ENSMUST00000176567						8	6	75	24	8	7	12	23	10	0	25		
ENSMUST00000176568						5	8	4	10	7	10	0	0	0	0	0		
ENSMUST00000176570	ENSMUSG00000010110	19	8741413	8756069	1	5	0	0	5	1	0	1	1	2	8	6	H3BJ89	
ENSMUST00000176571	ENSMUSG00000019737	7	30314807	30319046	1	0	1	0	0	0	0	0	0	0	0	0	H3BKW7	
ENSMUST00000176572	ENSMUSG00000094206	6	57978299	57979351	-1	3	1	0	2	3	1	0	0	0	0	0	H3BLP0	
ENSMUST00000176573						6	3	8	5	9	3	0	0	0	0	1		
ENSMUST00000176574	ENSMUSG00000025224	19	46152509	46286510	1	0	0	7	0	0	0	0	4	0	0	0	H3BLM8	
ENSMUST00000176575						0	0	0	26	3	0	0	0	12	0	15		
ENSMUST00000176576						0	4	10	5	9	4	6	8	7	0	19		
ENSMUST00000176577	ENSMUSG00000090173	11	62847069	62877465	1	0	0	0	0	0	4	0	0	5	0	0	H3BLP9	
ENSMUST00000176578						4	12	2	9	0	0	0	0	0	0	0		
ENSMUST00000176579	ENSMUSG00000041359	12	105216750	105222793	-1	2	1	0	0	3	3	0	0	0	0	0	H3BJP6	
ENSMUST00000176580	ENSMUSG00000006720	13	21945094	21960779	1	0	0	0	0	0	7	0	0	0	4	0	H3BKI5	
ENSMUST00000176581	ENSMUSG00000022010	14	76414961	76507765	1	0	0	6	0	0	0	1	0	1	0	0	H3BLH4	
ENSMUST00000176583						0	0	0	0	0	0	0	0	12	0	22		
ENSMUST00000176584	ENSMUSG00000024921	19	26605115	26778321	1	2	12	45	0	10	4	0	0	0	0	0	H3BKD2	
ENSMUST00000176585						4	0	0	4	13	0	41	51	31	14	50		
ENSMUST00000176586						0	2	0	1	1	0	1	0	0	0	1		
ENSMUST00000176587	ENSMUSG00000021147	13	8802968	8871909	-1	0	0	0	0	0	0	0	0	0	2	0	H3BK66	
ENSMUST00000176589						0	2	0	0	0	0	0	0	0	4	0		
ENSMUST00000176590						0	0	0	0	0	0	0	2	3	0	0		
ENSMUST00000176591	ENSMUSG00000025733	17	25838457	25844851	-1	0	0	0	0	0	0	11	0	0	0	0	H3BL14	
ENSMUST00000176592	ENSMUSG00000022603	15	74606029	74636353	-1	0	0	5	0	5	0	0	0	0	0	0	H3BLA6	
ENSMUST00000176593						2	4	12	0	1	2	0	0	0	0	0		
ENSMUST00000176594	ENSMUSG00000067010	5	108993412	109006471	-1	17	13	13	15	22	19	0	0	1	0	1	O35204	
ENSMUST00000176595	ENSMUSG00000091625	6	56701063	56704710	-1	0	0	0	7	0	0	0	0	5	19	0		
ENSMUST00000176596	ENSMUSG00000029647	5	147430161	147548502	1	0	0	0	0	0	0	357	631	301	0	428	H3BKQ1	
ENSMUST00000176597						5	0	8	41	2	3	0	0	1	0	2		
ENSMUST00000176600	ENSMUSG00000029647	5	147430161	147548502	1	13	17	18	3	17	7	173	507	332	32	254	H3BKF3	
ENSMUST00000176601	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	2	0	0	0	0	0	0	H3BKQ4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176602						2	0	0	0	9	0	0	17	0	1	0		
ENSMUST00000176604						0	0	3	29	2	0	36	6	12	0	10		
ENSMUST00000176605						1	0	2	2	0	1	0	0	0	0	0		
ENSMUST00000176606						68	74	173	309	98	47	31	18	22	0	26		
ENSMUST00000176607	ENSMUSG00000034252	9	80066903	80144953	1	0	0	0	0	2	0	8	0	17	0	22	H3BK32	
ENSMUST00000176608						197	115	738	759	231	114	4	1	2	0	3		
ENSMUST00000176609						0	0	3	1	0	0	11	12	9	0	31		
ENSMUST00000176610	ENSMUSG00000003680	19	8772522	8786417	-1	0	0	6	162	9	0	90	14	20	0	23	H3BK01	
ENSMUST00000176611	ENSMUSG00000032041	9	35184551	35200291	-1	1	1	8	2	0	0	0	12	25	0	57	H3BJH1	
ENSMUST00000176612	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	54	0	0	0	0	0	0	0	H3BLG6	
ENSMUST00000176613	ENSMUSG00000032594	9	108002501	108048782	1	0	0	0	0	0	0	0	4	0	0	3	H3BKZ2	
ENSMUST00000176614						2	1	3	14	5	2	0	0	0	0	0		
ENSMUST00000176616	ENSMUSG00000043668	8	90247040	90348343	-1	0	0	0	0	1	0	0	0	0	0	0	H3BL89	
ENSMUST00000176617	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	171	1188	44	204	456	H3BJS5	
ENSMUST00000176619						1	4	4	9	4	0	0	5	0	0	2		
ENSMUST00000176620						0	0	0	188	24	3	0	0	0	0	0		
ENSMUST00000176621	ENSMUSG00000057068	5	92555069	92591279	1	1	0	1	0	2	0	0	0	0	0	0	H3BKF1	
ENSMUST00000176622						13	8	10	20	9	9	0	0	1	0	1		
ENSMUST00000176623						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000176624	ENSMUSG00000003053	19	39269405	39330713	1	53	60	33	34	65	21	0	0	1	7	1	Q3UT49	
ENSMUST00000176625	ENSMUSG00000005982	16	3872375	3904780	1	0	0	3	30	0	0	15	23	42	0	16	H3BIY0	
ENSMUST00000176626						0	1	4	1	2	2	0	0	0	0	0		
ENSMUST00000176627	ENSMUSG00000023021	15	99734881	99772885	-1	0	2	3	25	3	1	3	0	0	0	3	H3BJH5	
ENSMUST00000176629	ENSMUSG00000017478	8	122376609	122417360	1	0	11	10	0	0	0	106	111	61	0	97	H3BIW0	
ENSMUST00000176630	ENSMUSG00000024613	18	60813755	60848971	-1	0	0	44	58	0	0	103	194	26	0	253		O08784
ENSMUST00000176632	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	0	0	0	0	H3BL33	
ENSMUST00000176633						2	1	5	3	0	0	5	41	21	0	34		
ENSMUST00000176634						0	0	11	0	0	0	0	0	0	0	1		
ENSMUST00000176636	ENSMUSG00000032015	9	43123939	43210369	-1	8	7	2	63	7	2	0	0	0	0	0	H3BJT4	
ENSMUST00000176637	ENSMUSG00000029064	4	155491361	155559269	1	0	19	40	0	26	10	1027	2992	780	150	343	Q3TQ70	P62874
ENSMUST00000176638	ENSMUSG00000025040	X	17556564	17572325	-1	0	0	0	0	3	0	12	27	73	267	60	H3BJZ1	
ENSMUST00000176639						35	34	94	155	53	28	46	266	122	5	310		
ENSMUST00000176640	ENSMUSG00000034252	9	80066903	80144953	1	1	2	0	215	0	1	3	10	38	1	23	H3BKR4	
ENSMUST00000176641	ENSMUSG00000067377	X	133891068	133898429	-1	0	0	2	0	0	2	0	0	0	1	0	H3BL26	
ENSMUST00000176642						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000176643	ENSMUSG00000002996	12	31926254	31950535	-1	0	0	0	0	0	0	0	128	31	17	6	H3BKV0	
ENSMUST00000176644						10	6	12	7	18	2	0	59	13	0	21		
ENSMUST00000176645	ENSMUSG00000011832	8	4166567	4211257	1	0	0	22	84	4	2	0	0	1	0	0	H3BLD3	
ENSMUST00000176646						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000176648	ENSMUSG00000034252	9	80066903	80144953	1	2	0	1	3	0	0	0	0	0	7	9	H3BK20	
ENSMUST00000176649						9	4	7	10	4	0	0	0	0	0	0		
ENSMUST00000176650						7	6	5	8	5	9	0	0	0	0	0		
ENSMUST00000176651	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	3	0	1	0	0	0	0	0	0	H3BLC2	
ENSMUST00000176652	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	72	18	11	0	18	F8WJF7	
ENSMUST00000176653	ENSMUSG00000054611	19	4314419	4398285	-1	2	0	5	12	7	0	0	2	14	2	40	H3BLD4	
ENSMUST00000176655	ENSMUSG00000030340	6	125320659	125344943	1	0	0	26	36	0	3	0	0	0	79	62	H3BLI2	
ENSMUST00000176656						0	0	0	0	0	0	9	27	12	7	18		
ENSMUST00000176657						17	12	39	19	21	10	2	1	3	1	4		
ENSMUST00000176658						12	5	2	4	4	3	0	0	0	0	0		
ENSMUST00000176659						2	1	3	1	3	2	0	0	0	0	0		
ENSMUST00000176661	ENSMUSG00000039990	7	133637543	133672971	1	0	0	1	0	1	0	4	102	10	9	3	H3BJF7	
ENSMUST00000176663	ENSMUSG00000037112	9	50892801	51009073	-1	0	0	1	0	0	0	136	91	192	0	127	H3BKG1	
ENSMUST00000176665						10	0	5	15	6	0	2	0	3	0	3		
ENSMUST00000176667	ENSMUSG00000093445	5	137629121	137641099	1	0	0	0	0	10	9	5123	5335	4001	590	3345	H3BLL3	
ENSMUST00000176668	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	222	179	315	0	42	H3BKZ1	
ENSMUST00000176669	ENSMUSG00000023927	17	51736187	51833290	-1	0	0	0	0	0	0	18	78	24	6	10		Q60611
ENSMUST00000176670	ENSMUSG00000055531	10	117344673	117380015	-1	0	0	0	0	0	0	152	450	338	45	176	H3BJW3	
ENSMUST00000176671	ENSMUSG00000032010	9	44067021	44095627	1	4	0	7	1	3	4	0	0	0	0	0	H3BLN9	
ENSMUST00000176672						12	8	60	14	11	5	0	2	0	0	0		
ENSMUST00000176673						12	8	59	15	26	19	45	384	79	11	283		
ENSMUST00000176674	ENSMUSG00000046519	3	95588934	95619247	1	2	0	0	0	6	3	9	0	100	134	45	H3BJ82	
ENSMUST00000176675	ENSMUSG00000020263	10	83600033	83648738	-1	1	1	1	0	1	0	2	42	13	22	35	H3BL67	
ENSMUST00000176677						0	0	0	0	1	0	0	0	3	4	2		
ENSMUST00000176678	ENSMUSG00000073434	17	25844771	25861501	-1	0	0	0	0	0	1	0	0	0	1	3	H3BKS4	
ENSMUST00000176680	ENSMUSG00000043456	7	37472135	37773641	-1	5	0	0	56	0	0	0	0	0	0	0	H3BK19	
ENSMUST00000176681	ENSMUSG00000029671	6	22288227	22298522	1	0	0	0	0	0	0	0	0	0	0	0	H3BL02	
ENSMUST00000176682						5	0	0	0	1	0	2	19	0	2	4		
ENSMUST00000176683	ENSMUSG00000093674	10	128548114	128549305	-1	17	3	41	54	24	1	3241	3980	1550	14335	1071		P62947
ENSMUST00000176684	ENSMUSG00000021604	13	73260479	73269608	1	14	11	0	200	18	15	0	0	0	0	0		Q9QY61
ENSMUST00000176685	ENSMUSG00000032041	9	35184551	35200291	-1	0	0	0	51	0	0	3	0	20	0	0	H3BKL1	
ENSMUST00000176686	ENSMUSG00000055531	10	117344673	117380015	-1	2	2	0	14	5	0	58	93	151	5	82	H3BJ30	
ENSMUST00000176687						3	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000176688						2	1	7	1	8	3	0	2	5	0	0		
ENSMUST00000176689						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000176690	ENSMUSG00000049577	8	122282141	122337251	1	2	1	21	2	3	0	12	0	7	0	1	H3BJR3	
ENSMUST00000176691	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	0	0	0	0	0	0	0		Q8BMQ3
ENSMUST00000176692						476	481	743	385	527	257	9	38	24	9	33		
ENSMUST00000176693						0	0	0	0	0	0	10	0	2	0	0		
ENSMUST00000176694						1	0	4	0	1	2	0	0	0	0	0		
ENSMUST00000176695	ENSMUSG00000012609	12	85824659	86061893	1	0	0	3	10	0	0	0	0	10	0	0	H3BLN3	
ENSMUST00000176696	ENSMUSG00000071192	17	25877630	25880305	-1	0	0	0	1	0	0	0	0	0	1	0	H3BJQ6	
ENSMUST00000176697						70	57	214	80	67	36	0	2	0	1	5		
ENSMUST00000176698	ENSMUSG00000024921	19	26605115	26778321	1	1	0	6	0	0	0	0	0	0	7	12	H3BKJ3	
ENSMUST00000176699	ENSMUSG00000017478	8	122376609	122417360	1	0	2	0	17	1	0	0	0	0	0	0	H3BKL4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176700						1	0	1	4	6	0	9	52	6	5	4		
ENSMUST00000176701	ENSMUSG00000006705	17	31564749	31607684	1	13	9	0	40	28	0	0	0	0	0	0		O70477
ENSMUST00000176702	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	1	0	0	0	0	0	0	H3BIY6	
ENSMUST00000176704						3	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000176705						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000176707	ENSMUSG00000091662	7	10579756	10613576	-1	2	1	0	0	2	0	0	0	0	0	0	H3BJH9	
ENSMUST00000176708	ENSMUSG00000026295	1	88406961	88426438	1	7	4	4	4	1	0	0	0	0	4	0	H3BLP2	
ENSMUST00000176709	ENSMUSG00000025733	17	25838457	25844851	-1	0	0	0	0	0	0	0	0	0	0	0	H3BKL2	
ENSMUST00000176710	ENSMUSG00000044067	12	31706867	31713947	-1	6	4	0	0	0	0	0	0	0	0	0		Q8BZL4
ENSMUST00000176711						1	1	1	0	4	1	0	0	0	0	0		
ENSMUST00000176712	ENSMUSG00000024459	17	36984061	36989537	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJA9	
ENSMUST00000176713						30	29	213	212	29	14	0	3	4	0	4		
ENSMUST00000176714						15	1	15	17	10	8	4	1	2	1	2		
ENSMUST00000176715	ENSMUSG00000021147	13	8802968	8871909	-1	0	0	0	0	0	0	0	0	18	0	18	H3BJH4	
ENSMUST00000176716						0	0	0	0	2	0	8	42	0	34	11		
ENSMUST00000176717						2	1	5	1	1	0	0	0	0	2	0		
ENSMUST00000176718	ENSMUSG00000067377	X	133891068	133898429	-1	0	0	3	0	0	0	0	0	0	1	0	H3BJJ0	
ENSMUST00000176719						3	2	3	0	0	0	0	0	2	0	0		
ENSMUST00000176720	ENSMUSG00000045658	1	84036296	84364180	-1	0	0	0	0	0	0	0	1	0	0	0	H3BJF2	
ENSMUST00000176722	ENSMUSG00000010841	11	101984279	101992264	1	0	0	3	4	1	0	0	0	0	0	0	H3BJ87	
ENSMUST00000176723						4	0	5	1	0	1	0	8	0	0	0		
ENSMUST00000176724						6	1	2	32	2	1	0	6	0	2	5		
ENSMUST00000176725						0	4	0	0	0	0	0	13	0	0	0		
ENSMUST00000176726	ENSMUSG00000021996	14	74732297	74750765	1	0	0	0	0	0	0	0	0	0	0	0	H3BL99	
ENSMUST00000176727	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	45	0	48	0	0	H3BL86	
ENSMUST00000176728	ENSMUSG00000021188	12	101834043	101913267	-1	0	0	0	0	0	0	0	0	8	0	0	H3BJH8	
ENSMUST00000176729	ENSMUSG00000032827	6	4902917	5165661	1	4	0	0	0	0	4	1	1	0	0	0	H3BJA6	
ENSMUST00000176730						1	1	3	0	2	0	0	0	0	0	0		
ENSMUST00000176731	ENSMUSG00000024921	19	26605115	26778321	1	0	0	1	0	0	0	63	792	75	60	96	H3BKN5	
ENSMUST00000176732	ENSMUSG00000026872	2	44983632	45117395	-1	2	0	2	0	2	1	0	0	0	0	23	H3BKH5	
ENSMUST00000176733						251	310	1522	289	216	127	19	81	13	56	33		
ENSMUST00000176734						8	13	21	11	17	4	0	0	1	0	2		
ENSMUST00000176735	ENSMUSG00000021175	12	117804289	117878706	1	0	0	0	0	0	3	0	0	9	3	8	H3BJV7	
ENSMUST00000176736	ENSMUSG00000033697	15	76723985	76818170	-1	0	1	2	0	0	0	0	0	0	0	0	H3BJW7	
ENSMUST00000176737						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176738						2	1	3	0	3	0	0	0	0	0	0		
ENSMUST00000176739						6	3	12	4	2	0	5	71	3	6	8		
ENSMUST00000176740	ENSMUSG00000026526	1	175600374	175625635	-1	0	0	0	0	0	0	0	93	2	37	14	H3BKG7	
ENSMUST00000176741						14	14	14	19	23	16	2	3	3	2	8		
ENSMUST00000176743						1	1	4	0	4	1	0	0	1	0	2		
ENSMUST00000176745	ENSMUSG00000029705	5	136248135	136567490	-1	0	0	0	0	0	0	581	1344	1288	56	797	H3BKT0	
ENSMUST00000176746	ENSMUSG00000030788	7	110800432	110844457	-1	0	0	0	15	0	0	17	5	8	8	0	H3BKH1	
ENSMUST00000176747						0	0	2	1	0	1	5	0	0	3	0		
ENSMUST00000176748						5	6	8	8	5	1	4	15	10	0	3		
ENSMUST00000176750	ENSMUSG00000025613	16	87483326	87495873	-1	0	0	0	68	1	2	0	0	0	0	0	H3BLL1	
ENSMUST00000176751	ENSMUSG00000093593	17	25834465	25841763	-1	2	8	17	3	9	0	0	54	0	0	30	H3BKJ1	
ENSMUST00000176752	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	0	0	0	0	0	H3BL86	
ENSMUST00000176753	ENSMUSG00000029647	5	147430161	147548502	1	0	0	0	0	0	0	16	0	190	0	127	H3BJH6	
ENSMUST00000176754						0	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000176755	ENSMUSG00000046519	3	95588934	95619247	1	0	0	0	0	0	2	4	152	11	37	0	H3BJ12	
ENSMUST00000176756	ENSMUSG00000018581	12	117877982	118199043	-1	25	0	17	0	0	6	0	0	0	0	0	H3BLD7	
ENSMUST00000176757						1	1	5	13	0	0	0	0	0	0	0		
ENSMUST00000176758						16	8	9	24	10	6	0	0	16	0	0		
ENSMUST00000176759	ENSMUSG00000038331	1	56793981	56978650	-1	0	0	0	23	2	1	0	0	0	0	0	H3BJX4	
ENSMUST00000176761						0	2	0	0	1	0	32	433	120	0	24		
ENSMUST00000176763						2	1	3	4	10	3	0	0	0	0	0		
ENSMUST00000176764	ENSMUSG00000011832	8	4166567	4211257	1	0	0	4	7	14	0	7	0	27	0	5	H3BJ57	
ENSMUST00000176765						0	1	0	10	0	0	2	0	0	0	0		
ENSMUST00000176766						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000176767	ENSMUSG00000022603	15	74606029	74636353	-1	0	1	2	6	0	1	0	0	0	0	0	H3BLE3	
ENSMUST00000176768	ENSMUSG00000093445	5	137629121	137641099	1	6	6	19	6	6	2	46	150	66	7	155	H3BK42	
ENSMUST00000176769	ENSMUSG00000024921	19	26605115	26778321	1	0	0	0	0	0	9	0	0	238	26	418	H3BJK2	
ENSMUST00000176770	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	1	0	0	0	104	399	419	44	35	H3BIX7	
ENSMUST00000176771	ENSMUSG00000052301	7	126847416	126852705	1	5	0	10	0	4	0	0	0	0	0	0	H3BJT3	
ENSMUST00000176772	ENSMUSG00000037816	13	50417864	50433780	1	0	0	0	0	0	0	0	9	0	0	0	H3BLQ7	
ENSMUST00000176773	ENSMUSG00000046138	19	29714402	29805989	-1	2	0	0	0	0	0	8	6	6	0	8	H3BJK8	
ENSMUST00000176774	ENSMUSG00000040434	2	92365046	92374869	-1	0	0	0	0	0	0	0	0	0	0	0	Q14AT0	
ENSMUST00000176775						1	0	0	4	4	1	0	0	0	0	0		
ENSMUST00000176777						0	0	0	13	0	1	2	1	1	0	0		
ENSMUST00000176778	ENSMUSG00000029705	5	136248135	136567490	-1	32	19	75	934	44	10	95	55	107	3	114	H3BLS0	
ENSMUST00000176780	ENSMUSG00000027699	3	27097222	27153878	-1	2	2	3	13	6	0	0	0	1	0	2	H3BIZ5	
ENSMUST00000176781	ENSMUSG00000062478	4	141814962	141846359	-1	0	0	0	0	0	0	0	0	0	0	0	H3BLM3	
ENSMUST00000176782	ENSMUSG00000049659	11	20685084	20741589	-1	2	1	0	0	0	0	34	255	118	46	50	H3BIZ9	
ENSMUST00000176784	ENSMUSG00000024459	17	36984061	36989537	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK58	
ENSMUST00000176785						3	3	3	2	4	0	0	0	0	0	0		
ENSMUST00000176787						1	1	8	2	2	1	13	6	20	0	40		
ENSMUST00000176788						1	1	0	11	1	4	1	0	1	0	2		
ENSMUST00000176789	ENSMUSG00000019737	7	30314807	30319046	1	0	0	2	0	2	3	0	0	0	0	0	H3BKP9	
ENSMUST00000176790	ENSMUSG00000052534	1	168119364	168432270	-1	0	0	0	0	0	0	137	42	306	48	322	Q71VB4	P41778
ENSMUST00000176791						47	45	236	74	46	27	5	12	12	1	23		
ENSMUST00000176792						20	9	0	0	7	10	0	0	0	0	0		
ENSMUST00000176793						141	122	202	107	182	87	36	55	50	10	66		
ENSMUST00000176794	ENSMUSG00000032400	9	64137144	64173104	-1	0	3	6	0	0	0	0	0	0	17	0	H3BJ52	
ENSMUST00000176795	ENSMUSG00000009734	13	18121101	18382041	-1	0	0	0	9	1	0	0	0	0	0	0	H3BIZ0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176796						37	30	77	37	43	23	128	210	122	29	178		
ENSMUST00000176797	ENSMUSG00000021546	13	58391142	58403343	-1	0	0	3	0	2	0	391	1028	808	365	696	H3BLP7	
ENSMUST00000176798	ENSMUSG00000032058	9	50845301	50894229	1	0	0	0	0	0	0	0	0	0	0	0	H3BKU1	
ENSMUST00000176799						2	4	0	3	0	0	38	161	31	61	21		
ENSMUST00000176800	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000176801						51	35	126	52	73	46	4	5	5	0	5		
ENSMUST00000176802	ENSMUSG00000094396	17	18049484	18074220	1	1	4	3	0	6	2	0	0	0	0	0	K7N789	
ENSMUST00000176803	ENSMUSG00000026657	2	4017717	4614043	1	0	0	0	0	0	0	0	0	0	0	0	H3BKK8	
ENSMUST00000176804	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	0	0	0	0	0	H3BKH9	
ENSMUST00000176805						2	7	0	6	5	0	9	86	2	0	14		
ENSMUST00000176806						0	1	1	1	0	0	9	7	11	0	11		
ENSMUST00000176808	ENSMUSG00000032089	9	45253837	45269149	-1	6	17	20	73	26	0	0	275	0	139	59	H3BKE8	
ENSMUST00000176809						2	2	2	0	0	3	0	0	0	0	0		
ENSMUST00000176810	ENSMUSG00000040434	2	92365046	92374869	-1	0	0	0	58	0	8	0	0	0	0	0	A2AHG6	
ENSMUST00000176812						1	2	16	0	10	6	0	0	0	0	0		
ENSMUST00000176813	ENSMUSG00000021147	13	8802968	8871909	-1	3	0	0	2	1	0	0	0	0	0	0	H3BJR7	
ENSMUST00000176814						3	2	7	2	2	2	0	0	0	0	0		
ENSMUST00000176815	ENSMUSG00000002732	2	76663044	76673116	-1	6	3	3	3	5	5	0	2	3	15	1	H3BJI5	
ENSMUST00000176816	ENSMUSG00000055817	17	83706163	83821516	1	0	0	0	0	3	0	0	41	0	4	10	H3BLE1	
ENSMUST00000176817						0	1	0	0	0	0	7	4	22	0	4		
ENSMUST00000176818	ENSMUSG00000003549	7	19344778	19356524	1	0	0	0	0	0	0	2	0	0	0	0	H3BLF5	
ENSMUST00000176819	ENSMUSG00000062082	16	44811733	44839150	1	0	0	0	3	0	0	37	0	0	60	15		Q6XJV4
ENSMUST00000176820						0	0	0	0	0	4	0	0	2	1	0		
ENSMUST00000176821						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000176822	ENSMUSG00000045658	1	84036296	84364180	-1	4	6	14	10	12	4	0	0	0	0	0	H3BKK5	
ENSMUST00000176823						3	3	10	2	8	2	0	0	0	0	0		
ENSMUST00000176824	ENSMUSG00000037112	9	50892801	51009073	-1	42	22	34	27	28	21	74	112	129	8	75	H3BJC9	
ENSMUST00000176825	ENSMUSG00000011832	8	4166567	4211257	1	0	0	0	0	0	0	82	127	39	9	82	H3BL92	
ENSMUST00000176826	ENSMUSG00000022146	15	6813577	6874969	-1	13	0	23	161	12	8	0	0	1	1	7		
ENSMUST00000176827						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176828	ENSMUSG00000026657	2	4017717	4614043	1	9	6	49	155	7	0	15	0	14	5	74	Q3TB04	
ENSMUST00000176829	ENSMUSG00000033713	12	99194980	99450111	-1	0	1	0	0	0	0	0	3	3	0	1	H3BKC0	
ENSMUST00000176830						3	2	12	1	4	0	0	0	2	0	1		
ENSMUST00000176831						19	23	96	51	27	12	330	2241	730	516	870		
ENSMUST00000176832	ENSMUSG00000021972	14	64811600	64949871	-1	0	0	0	0	0	0	0	0	0	0	9	H3BK13	
ENSMUST00000176834	ENSMUSG00000034120	11	116849901	116853094	-1	0	0	0	0	0	0	0	274	53	50	14	H3BJA4	
ENSMUST00000176836						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176837						0	19	32	0	0	0	0	0	0	1	4		
ENSMUST00000176838	ENSMUSG00000071893	6	56924015	56958100	1	0	7	13	7	9	7	0	0	0	1	0	Q8R2D3	
ENSMUST00000176839						0	0	10	2	1	2	0	0	0	0	0		
ENSMUST00000176840						7	3	5	4	3	0	0	0	0	0	0		
ENSMUST00000176842						0	0	0	0	0	0	0	7	6	0	12		
ENSMUST00000176843	ENSMUSG00000058317	14	18573575	18894267	-1	0	0	0	0	0	0	0	0	0	0	0	H3BL23	
ENSMUST00000176844						2	4	0	3	2	1	0	0	0	0	0		
ENSMUST00000176845						0	1	0	0	0	0	0	0	0	4	0		
ENSMUST00000176846						3	0	0	3	0	0	3	0	14	0	2		
ENSMUST00000176847						3	2	2	3	3	2	0	1	0	2	0		
ENSMUST00000176848						2	1	10	2	8	0	0	3	8	11	3		
ENSMUST00000176849	ENSMUSG00000021546	13	58391142	58403343	-1	0	0	0	0	0	0	253	439	621	63	307	H3BKD0	
ENSMUST00000176850	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJM1	
ENSMUST00000176851						6	4	16	10	3	2	2	0	0	0	2		
ENSMUST00000176853						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000176854	ENSMUSG00000032594	9	108002501	108048782	1	42	45	90	50	28	18	51	129	61	13	91	A0A0A6YVR5	
ENSMUST00000176855	ENSMUSG00000033697	15	76723985	76818170	-1	13	22	6	8	19	17	0	0	0	0	4	H3BJM3	
ENSMUST00000176856						0	0	1	2	2	0	22	27	59	2	43		
ENSMUST00000176857						1	0	0	2	2	4	3	5	0	2	7		
ENSMUST00000176858						0	0	7	0	1	0	15	442	182	56	715		
ENSMUST00000176859						0	1	1	0	2	1	0	0	0	0	0		
ENSMUST00000176860	ENSMUSG00000031845	8	117095854	117133720	1	4	4	0	0	0	2	0	0	0	0	0	E9Q321	
ENSMUST00000176861	ENSMUSG00000036834	3	63696234	63899472	-1	0	3	3	3	0	0	0	0	0	0	0	H3BKX1	
ENSMUST00000176862						1	0	4	1	2	1	0	0	0	0	0		
ENSMUST00000176863	ENSMUSG00000040407	5	3928054	4081310	1	0	1	12	3	2	0	0	19	5	3	0	H3BLL7	
ENSMUST00000176864	ENSMUSG00000026657	2	4017717	4614043	1	0	1	5	0	1	4	0	1	0	0	0	H3BJN6	
ENSMUST00000176866	ENSMUSG00000039375	8	54629055	54887184	-1	1	0	0	1	1	0	0	0	0	0	0	H3BJG5	
ENSMUST00000176867	ENSMUSG00000024913	19	3584828	3686564	-1	12	5	14	18	22	6	0	2	0	0	0	H3BL52	
ENSMUST00000176868	ENSMUSG00000009585	15	79891659	79915906	1	0	0	0	0	2	1	0	0	0	0	0	H3BL97	
ENSMUST00000176869						0	0	3	0	2	0	0	0	0	0	0		
ENSMUST00000176871	ENSMUSG00000093445	5	137629121	137641099	1	2	2	2	1	2	2	58	80	40	3	27	H3BL36	
ENSMUST00000176873	ENSMUSG00000024347	18	35964830	36014715	1	0	0	0	0	0	0	0	0	0	0	0		Q6P1I6
ENSMUST00000176874	ENSMUSG00000094291	6	58265078	58266162	1	3	6	1	0	3	0	0	0	0	0	0	Q8R2C9	
ENSMUST00000176875	ENSMUSG00000075046	10	58229979	58232675	-1	373	210	559	451	473	179	0	0	0	0	0		
ENSMUST00000176876	ENSMUSG00000024213	17	27579382	27623465	-1	0	0	1	10	0	0	0	0	0	2	8	H3BLR8	
ENSMUST00000176877						0	0	0	0	0	0	0	10	0	0	0		
ENSMUST00000176878	ENSMUSG00000072664	15	9273319	9315032	1	65	66	24	27	71	33	1	14	7	2	5	H3BLE9	
ENSMUST00000176879	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	0	0	0	0	0	H3BIX8	
ENSMUST00000176880	ENSMUSG00000064264	7	24507006	24515682	1	3	4	0	118	5	0	1	0	0	2	3	H3BL05	
ENSMUST00000176882						0	0	0	0	0	0	22	0	34	1	21		
ENSMUST00000176883						2	1	2	0	2	0	0	0	0	0	1		
ENSMUST00000176885						4	3	17	4	3	4	0	0	0	0	0		
ENSMUST00000176886	ENSMUSG00000022010	14	76414961	76507765	1	0	2	4	6	3	0	0	6	3	1	2	H3BK07	
ENSMUST00000176887	ENSMUSG00000030879	7	105806658	105811099	-1	0	0	0	53	0	0	18	59	50	38	25	H3BIZ3	
ENSMUST00000176888						4	0	0	1	7	0	25	335	9	0	0		
ENSMUST00000176889						0	0	0	0	0	0	11	0	6	0	0		
ENSMUST00000176890	ENSMUSG00000006715	13	24751845	24761923	-1	9	2	4	5	5	0	0	0	0	0	0	H3BJJ1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176891						3	2	1	1	4	1	0	0	0	0	0		
ENSMUST00000176892	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	184	796	694	17	146	H3BK44	
ENSMUST00000176893	ENSMUSG00000048482	2	109674700	109727007	1	0	2	0	1	2	0	0	1	0	2	12	Q541P3	P21237
ENSMUST00000176894						10	9	33	15	7	8	7	29	2	13	9		
ENSMUST00000176895						9	8	18	11	14	5	0	2	3	0	3		
ENSMUST00000176896	ENSMUSG00000032336	9	58582240	58657955	1	0	0	0	0	0	0	105	613	218	258	130	H3BIX4	
ENSMUST00000176897	ENSMUSG00000050966	4	134003330	134018841	-1	0	0	2	46	3	0	0	0	0	0	0	H3BLC6	
ENSMUST00000176898						0	6	0	7	3	0	0	0	0	0	0		
ENSMUST00000176899						0	6	2	3	4	3	0	0	0	0	0		
ENSMUST00000176900						0	1	3	0	0	3	16	69	32	0	53		
ENSMUST00000176901						2	2	1	0	2	0	0	0	0	0	0		
ENSMUST00000176902	ENSMUSG00000044024	18	37955079	37959179	1	0	0	0	0	0	0	0	2	0	0	0	H3BJY5	
ENSMUST00000176904	ENSMUSG00000009585	15	79891659	79915906	1	1	0	2	1	1	0	0	0	0	2	0	H3BKS1	
ENSMUST00000176905						4	2	2	5	7	4	0	0	0	0	0		
ENSMUST00000176906	ENSMUSG00000093674	10	128548114	128549305	-1	0	0	0	0	0	0	30	404	0	76	114	H3BK91	
ENSMUST00000176907						24	5	14	6	12	8	0	0	0	0	0		
ENSMUST00000176908						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000176909						0	1	1	0	4	0	0	0	0	2	0		
ENSMUST00000176910	ENSMUSG00000070733	5	73019987	73256619	-1	0	2	2	4	0	1	0	0	0	0	1	H3BLH9	
ENSMUST00000176911	ENSMUSG00000029556	5	114948980	114971094	-1	10	5	10	49	5	0	0	0	0	0	0	H3BKV2	
ENSMUST00000176912	ENSMUSG00000022112	14	115092215	116525179	1	3	7	5	4	11	3	0	0	0	0	0	H3BJQ8	
ENSMUST00000176913	ENSMUSG00000037816	13	50417864	50433780	1	0	0	5	15	6	0	3	0	0	3	0	H3BKU3	
ENSMUST00000176914						2	1	8	16	1	2	1	3	3	0	4		
ENSMUST00000176916	ENSMUSG00000032336	9	58582240	58657955	1	4	2	6	3	4	2	6	3	7	2	12		P97300
ENSMUST00000176918						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000176919						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000176920						0	2	2	2	2	1	0	0	0	0	0		
ENSMUST00000176922	ENSMUSG00000021147	13	8802968	8871909	-1	10	7	49	111	17	4	49	131	29	7	32	Q05BF4	
ENSMUST00000176923	ENSMUSG00000073434	17	25844771	25861501	-1	0	0	52	58	12	0	23	0	0	0	0		Q6ZPG2
ENSMUST00000176924	ENSMUSG00000036009	10	105763189	105841380	-1	0	0	0	0	4	0	0	0	0	0	0	H3BJ85	
ENSMUST00000176925						0	1	0	0	0	2	0	23	2	0	0		
ENSMUST00000176926	ENSMUSG00000045098	19	3767421	3818303	1	0	0	0	0	0	0	0	0	0	0	0	H3BLE5	
ENSMUST00000176927						4	3	10	12	4	0	0	0	0	0	0		
ENSMUST00000176928	ENSMUSG00000033713	12	99194980	99450111	-1	0	0	0	0	1	0	0	0	0	1	0	H3BLD8	
ENSMUST00000176931						2	0	20	8	8	0	0	0	0	0	0		
ENSMUST00000176932						18	0	18	37	27	14	0	4	0	0	0		
ENSMUST00000176933						5	7	5	0	2	3	0	0	0	0	0		
ENSMUST00000176935	ENSMUSG00000022362	15	58028243	58076425	-1	14	7	21	11	12	2	2	13	2	2	6	H3BIW7	
ENSMUST00000176936						0	0	5	3	3	0	10	3	0	0	0		
ENSMUST00000176937	ENSMUSG00000012609	12	85824659	86061893	1	5	2	0	0	0	0	1	0	4	0	7	H3BLC0	
ENSMUST00000176938	ENSMUSG00000032782	11	69299487	69323775	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK55	
ENSMUST00000176939	ENSMUSG00000025007	19	40550257	40588463	-1	11	12	16	0	0	4	83	142	59	12	116		Q9Z110
ENSMUST00000176940	ENSMUSG00000032567	9	105395392	105412229	1	0	0	0	0	0	0	1	0	2	0	0	H3BLN7	
ENSMUST00000176942						2	3	3	4	5	1	0	0	0	0	7		
ENSMUST00000176943						5	5	1	1	4	1	0	0	0	0	0		
ENSMUST00000176944	ENSMUSG00000035152	11	83299024	83405035	1	0	0	0	0	0	0	0	0	0	0	0	H3BJ06	
ENSMUST00000176945	ENSMUSG00000002588	6	5168090	5193946	-1	0	0	10	0	0	0	0	0	0	0	0	H3BLB8	
ENSMUST00000176946						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000176947	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	0	0	0	0	0	0	0	H3BKJ2	
ENSMUST00000176948						3	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000176949	ENSMUSG00000050954	13	48487647	48513451	-1	0	0	0	0	2	0	2	3	3	0	8	H3BL87	
ENSMUST00000176952						4	2	0	2	5	5	0	0	0	0	0		
ENSMUST00000176953						6	0	3	9	0	0	26	49	33	0	39		
ENSMUST00000176954	ENSMUSG00000093635	6	57137299	57138325	1	3	1	3	0	3	1	0	0	0	0	0	Q3SXA2	
ENSMUST00000176955	ENSMUSG00000025007	19	40550257	40588463	-1	1	0	2	0	0	0	0	0	0	0	0	H3BLE8	
ENSMUST00000176956						61	48	132	26	49	34	0	0	0	0	1		
ENSMUST00000176957	ENSMUSG00000021996	14	74732297	74750765	1	0	0	5	39	3	0	633	2152	650	1081	331	H3BKH6	
ENSMUST00000176959	ENSMUSG00000033713	12	99194980	99450111	-1	2	0	0	0	0	0	1	0	5	0	3	H3BLQ2	
ENSMUST00000176960						2	2	14	0	1	0	90	333	292	0	115		
ENSMUST00000176961	ENSMUSG00000073433	17	26196226	26207786	-1	19	14	17	4	26	7	0	0	0	0	2	Q3UNB6	Q62160
ENSMUST00000176962						0	0	0	7	0	0	0	0	0	0	0		
ENSMUST00000176963						0	3	3	7	2	3	8	0	0	0	0		
ENSMUST00000176964	ENSMUSG00000070568	7	45277513	45288998	1	0	0	10	0	0	0	0	0	0	0	0	H3BKC2	
ENSMUST00000176965						3	5	6	4	7	0	0	0	0	0	2		
ENSMUST00000176966						0	0	8	6	2	2	10	109	11	25	49		
ENSMUST00000176967	ENSMUSG00000056459	12	76347782	76369602	-1	0	0	0	9	0	0	0	0	0	0	0	H3BKL0	
ENSMUST00000176968	ENSMUSG00000010110	19	8741413	8756069	1	3	0	0	0	0	0	18	66	22	7	46	H3BKP3	
ENSMUST00000176969						2	5	0	0	2	0	0	0	0	6	7		
ENSMUST00000176970	ENSMUSG00000023021	15	99734881	99772885	-1	2	3	0	2	3	3	16	32	13	0	15	H3BLB3	
ENSMUST00000176971	ENSMUSG00000028487	4	84275095	84675275	-1	3	0	33	0	9	4	0	0	0	0	1	H3BL10	
ENSMUST00000176973	ENSMUSG00000042410	2	75832177	75931350	1	0	1	0	0	0	0	31	17	0	14	11	H3BJ14	
ENSMUST00000176974	ENSMUSG00000005220	5	72300025	72504473	-1	0	0	0	0	13	0	0	0	0	0	0	H3BLB2	
ENSMUST00000176975						0	0	4	75	0	0	0	0	0	0	0		
ENSMUST00000176976						0	0	1	3	7	1	0	0	0	0	3		
ENSMUST00000176978	ENSMUSG00000029088	5	48389502	49524907	-1	1	0	1	7	1	2	0	0	0	0	0	Q3YAA6	Q6PHZ8
ENSMUST00000176979						5	7	1	2	1	0	0	0	0	0	0		
ENSMUST00000176980						319	322	541	201	318	203	2	20	15	10	11		
ENSMUST00000176982	ENSMUSG00000022518	16	4835416	4867691	1	9	0	14	15	0	1	0	0	0	0	0	H3BJT7	
ENSMUST00000176983						2	3	18	5	5	0	3	6	1	0	9		
ENSMUST00000176984						9	2	17	13	4	2	0	0	0	0	2		
ENSMUST00000176985						15	0	46	10	5	9	0	0	0	0	0		
ENSMUST00000176986	ENSMUSG00000031133	X	57231485	57338729	-1	5	2	4	53	3	3	4	3	25	6	15	H3BJ53	
ENSMUST00000176988						8	4	10	37	5	5	3	38	43	0	44		
ENSMUST00000176989						1	2	2	1	3	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000176990						0	0	0	12	0	2	0	6	2	0	0		
ENSMUST00000176991						1	1	4	2	4	0	3	5	0	0	3		
ENSMUST00000176992	ENSMUSG00000025224	19	46152509	46286510	1	30	9	24	0	19	4	407	708	632	20	421	Q6A099	
ENSMUST00000176993						0	0	3	151	4	0	0	0	0	0	0		
ENSMUST00000176994	ENSMUSG00000078606	7	105895139	105953967	-1	2	0	10	5	3	3	9	3	73	60	118	H3BL64	
ENSMUST00000176996	ENSMUSG00000050954	13	48487647	48513451	-1	0	0	1	8	0	1	3	0	0	0	3	H3BKT6	
ENSMUST00000176997						5	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000176998	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK78	
ENSMUST00000176999						14	8	8	11	12	3	10	9	17	4	11		
ENSMUST00000177000						1	2	7	1	1	1	0	0	0	0	0		
ENSMUST00000177003	ENSMUSG00000043467	1	161002922	161034849	-1	0	0	0	4	0	0	0	0	5	0	0	H3BJ23	
ENSMUST00000177004	ENSMUSG00000060538	7	126886171	126922917	-1	0	0	0	0	0	0	0	6	0	0	0	H3BK56	
ENSMUST00000177005	ENSMUSG00000001418	3	88325023	88331313	1	48	75	76	73	91	37	283	282	154	48	141		Q9JHJ3
ENSMUST00000177006	ENSMUSG00000009585	15	79891659	79915906	1	0	0	0	0	3	0	43	5	36	18	0	H3BKS5	
ENSMUST00000177007						9	7	29	0	10	0	0	0	3	10	0		
ENSMUST00000177008						5	1	0	2	3	0	0	0	0	0	0		
ENSMUST00000177009						3	1	4	1	3	0	0	0	0	0	0		
ENSMUST00000177010	ENSMUSG00000008206	8	4493026	4531680	1	1	0	0	13	0	0	0	0	0	0	0	H3BLF1	
ENSMUST00000177011						28	24	44	16	34	12	9	14	10	2	13		
ENSMUST00000177013	ENSMUSG00000061689	2	156613705	156764363	1	0	2	0	0	0	0	0	11	0	0	0	H3BKJ0	
ENSMUST00000177014	ENSMUSG00000049659	11	20685084	20741589	-1	1	5	0	0	0	2	7	123	41	0	38	H3BKM5	
ENSMUST00000177016						26	33	33	35	50	32	0	2	1	0	2		
ENSMUST00000177017						5	1	5	2	13	1	1	4	0	0	2		
ENSMUST00000177018						2	1	0	14	1	0	6	7	0	0	0		
ENSMUST00000177019	ENSMUSG00000021546	13	58391142	58403343	-1	0	0	0	0	0	0	0	0	0	0	0	B2M1R6	
ENSMUST00000177020						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000177021						0	1	0	0	1	0	8	30	31	0	7		
ENSMUST00000177022						0	1	2	0	1	0	7	24	6	54	8		
ENSMUST00000177023	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	0	0	0	0	0	H3BJ59	
ENSMUST00000177024						35	13	66	39	32	18	28	124	62	0	107		
ENSMUST00000177025	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	0	3	0	0	0	H3BKC7	
ENSMUST00000177026	ENSMUSG00000033697	15	76723985	76818170	-1	40	43	44	34	37	34	5	19	13	1	26	H3BLS4	
ENSMUST00000177027						0	0	9	0	2	0	0	0	0	0	0		
ENSMUST00000177028						0	2	0	1	3	0	0	0	0	0	0		
ENSMUST00000177029	ENSMUSG00000035032	9	105162156	105395524	-1	0	1	0	0	1	0	0	0	0	0	0	H3BLL8	
ENSMUST00000177030						173	182	127	137	171	93	26	38	183	51	162		
ENSMUST00000177031						29	24	94	120	54	11	10	1	10	0	7		
ENSMUST00000177032						4	4	34	10	16	5	0	0	0	0	0		
ENSMUST00000177033						2	0	0	0	0	2	0	0	0	1	0		
ENSMUST00000177034	ENSMUSG00000052105	17	66336982	66449750	-1	13	5	36	0	29	6	0	0	0	5	23	H3BL83	
ENSMUST00000177035	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	0	0	0	217	0	437	0	525	H3BKD4	
ENSMUST00000177036	ENSMUSG00000066842	1	150562524	150993435	-1	0	0	1	0	0	0	0	0	0	1	0	H3BJH2	
ENSMUST00000177037	ENSMUSG00000026655	2	3613758	3782142	1	0	0	12	1	4	1	2	0	7	0	0	H3BKB6	
ENSMUST00000177038						6	0	6	5	0	3	6	32	3	0	6		
ENSMUST00000177039	ENSMUSG00000032596	9	107975505	107984060	1	0	0	4	8	3	2	39	311	126	48	149	H3BKY9	
ENSMUST00000177040	ENSMUSG00000028487	4	84275095	84675275	-1	3	0	25	3	0	0	0	0	1	0	0	H3BJR1	
ENSMUST00000177042	ENSMUSG00000022518	16	4835416	4867691	1	15	3	35	14	23	8	0	0	0	0	0	A0A075B686	
ENSMUST00000177044	ENSMUSG00000053411	15	79915807	79971119	-1	0	0	0	28	0	0	0	0	0	0	0	H3BK45	
ENSMUST00000177045	ENSMUSG00000032400	9	64137144	64173104	-1	3	1	6	2	3	0	2	0	10	0	0	H3BKB9	
ENSMUST00000177046	ENSMUSG00000024164	17	57203970	57228136	-1	0	0	2	0	0	0	0	1326	0	24	0	H3BKW9	
ENSMUST00000177047						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000177049	ENSMUSG00000017478	8	122376609	122417360	1	0	0	2	10	1	0	0	0	0	2	3	H3BJJ9	
ENSMUST00000177050	ENSMUSG00000041073	11	6597823	6606053	-1	3	0	0	0	2	1	5	0	0	0	2	H3BJG2	
ENSMUST00000177051						3	0	0	0	0	0	242	2013	336	94	307		
ENSMUST00000177052	ENSMUSG00000032041	9	35184551	35200291	-1	5	1	6	4	1	0	5	3	9	0	2	H3BKK6	
ENSMUST00000177053	ENSMUSG00000011832	8	4166567	4211257	1	0	2	18	33	0	0	7	20	13	3	5	H3BJX1	
ENSMUST00000177054	ENSMUSG00000032010	9	44067021	44095627	1	11	10	5	11	15	4	0	0	0	0	0		O88623
ENSMUST00000177055	ENSMUSG00000027699	3	27097222	27153878	-1	0	2	0	11	0	0	0	0	0	0	0	H3BIW1	
ENSMUST00000177056	ENSMUSG00000003680	19	8772522	8786417	-1	0	0	0	0	0	0	0	0	0	0	0		Q8R2K4
ENSMUST00000177057						2	1	1	2	2	4	0	0	0	0	0		
ENSMUST00000177058	ENSMUSG00000044024	18	37955079	37959179	1	0	0	0	0	0	0	2	0	0	0	0		Q8BRJ3
ENSMUST00000177060	ENSMUSG00000021546	13	58391142	58403343	-1	0	0	0	0	0	0	0	18	10	0	38	H3BKI8	
ENSMUST00000177061						2	0	3	1	1	0	0	0	0	0	0		
ENSMUST00000177062						0	0	3	2	2	0	0	6	4	0	3		
ENSMUST00000177064	ENSMUSG00000032336	9	58582240	58657955	1	0	0	0	0	0	0	29	127	64	182	0	H3BKA7	
ENSMUST00000177066						9	6	2	8	11	4	0	7	0	1	6		
ENSMUST00000177067						1	0	11	71	11	0	5	0	0	0	6		
ENSMUST00000177068	ENSMUSG00000046691	8	106883863	106893601	-1	0	0	0	0	0	0	426	623	787	52	442		P0CG15
ENSMUST00000177069	ENSMUSG00000055817	17	83706163	83821516	1	16	9	55	29	27	7	51	131	118	12	140	H3BJP3	
ENSMUST00000177070						0	0	2	4	1	0	0	0	0	0	0		
ENSMUST00000177071						2	0	3	0	0	0	0	82	7	20	18		
ENSMUST00000177072	ENSMUSG00000093764	6	66715902	66716930	-1	10	2	0	2	4	0	0	0	0	0	0	Q8R2E3	
ENSMUST00000177074	ENSMUSG00000032570	9	105403539	105527319	-1	0	0	0	0	0	0	328	686	714	73	258	H3BL44	
ENSMUST00000177077						7	9	8	2	3	0	0	1	0	0	1		
ENSMUST00000177078	ENSMUSG00000019737	7	30314807	30319046	1	0	0	0	0	0	0	0	0	1	0	0	H3BLS3	
ENSMUST00000177079						1	0	5	1	2	0	0	7	3	0	0		
ENSMUST00000177080						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177083	ENSMUSG00000022377	15	64086857	64382919	-1	0	11	0	0	0	0	608	1610	1118	70	891	E9QMJ1	
ENSMUST00000177084	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	6	0	2	3	0	H3BL70	
ENSMUST00000177085						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000177086	ENSMUSG00000049598	1	172555938	172563717	1	0	8	12	185	9	12	4	5	0	0	1		Q6P3A4
ENSMUST00000177087	ENSMUSG00000003053	19	39269405	39330713	1	3	2	4	7	11	7	0	0	0	0	0	H3BLM0	
ENSMUST00000177088						0	11	7	0	8	0	0	0	0	0	0		
ENSMUST00000177089	ENSMUSG00000028552	4	109280268	109387817	1	0	1	0	1	0	0	4	2	0	10	0	H3BJB8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177091						65	46	55	39	57	35	23	53	30	6	84		
ENSMUST00000177092	ENSMUSG00000017493	11	99041244	99054392	1	0	0	0	0	0	0	13	0	8	0	115	H3BJT2	
ENSMUST00000177093						0	1	4	7	0	2	0	0	0	0	0		
ENSMUST00000177094	ENSMUSG00000029064	4	155491361	155559269	1	3	2	2	6	2	1	741	246	1108	239	775	H3BKR2	
ENSMUST00000177095						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000177096						3	2	0	1	5	4	3	34	0	1	0		
ENSMUST00000177098	ENSMUSG00000009585	15	79891659	79915906	1	2	10	10	8	9	6	27	81	58	21	91	H3BJQ3	
ENSMUST00000177099						2	1	3	0	1	2	7	19	35	0	45		
ENSMUST00000177101	ENSMUSG00000035394	18	74283090	74359986	1	33	12	133	65	36	20	1	2	0	0	6	H3BJA5	
ENSMUST00000177102	ENSMUSG00000030523	7	64153835	64269775	1	14	11	36	16	6	0	0	0	0	0	0		Q2TV84
ENSMUST00000177103	ENSMUSG00000027331	2	118814003	118853957	1	0	0	0	0	0	0	26	0	4	71	0	H3BJ95	
ENSMUST00000177105						105	87	746	159	88	50	0	1	3	0	3		
ENSMUST00000177106						5	6	6	6	3	1	0	0	0	0	0		
ENSMUST00000177107	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000177108						2	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000177109	ENSMUSG00000008489	4	91250763	91400785	-1	0	0	7	0	0	0	0	0	0	0	0	H3BLG7	
ENSMUST00000177111	ENSMUSG00000070369	7	128154376	128223816	1	0	0	48	48	0	0	0	0	3	0	3	H3BKX8	
ENSMUST00000177112						0	0	0	0	0	0	8	3	5	8	0		
ENSMUST00000177113	ENSMUSG00000105827	3	96269752	96270132	1	2	0	5	3	6	2	14	12	12	14	19		Q64525
ENSMUST00000177114	ENSMUSG00000012609	12	85824659	86061893	1	0	0	0	0	0	0	0	0	0	0	0	H3BLN3	
ENSMUST00000177115						8	8	2	4	7	1	0	0	0	0	0		
ENSMUST00000177116	ENSMUSG00000024921	19	26605115	26778321	1	76	75	445	59	83	39	18	0	29	23	0	Q99KH6	
ENSMUST00000177117	ENSMUSG00000021546	13	58391142	58403343	-1	1	1	4	0	4	0	0	0	55	23	58	H3BJS9	
ENSMUST00000177118	ENSMUSG00000062327	17	8434423	8442496	1	0	3	2	1	0	0	0	1	0	0	0	H3BKU2	
ENSMUST00000177120						1	0	0	2	1	0	0	3	0	0	0		
ENSMUST00000177121						1	2	3	0	0	3	0	33	0	3	0		
ENSMUST00000177122						9	3	31	8	10	3	0	66	28	13	99		
ENSMUST00000177123						21	11	56	42	34	15	19	38	38	4	105		
ENSMUST00000177124	ENSMUSG00000039166	10	25169090	25307870	-1	0	0	0	0	0	0	0	0	4	0	3	H3BJV2	
ENSMUST00000177125	ENSMUSG00000026655	2	3613758	3782142	1	0	1	0	16	0	3	17	0	471	49	391	H3BLE6	
ENSMUST00000177126	ENSMUSG00000014846	8	105467493	105471526	-1	25	27	70	18	29	14	46	42	13	10	37		Q9CRB6
ENSMUST00000177129	ENSMUSG00000032041	9	35184551	35200291	-1	0	0	0	39	4	0	11	0	51	0	34	H3BKL1	
ENSMUST00000177131	ENSMUSG00000048277	11	117809668	117814283	1	0	0	0	6	0	0	0	0	0	0	0	H3BIZ8	
ENSMUST00000177133	ENSMUSG00000039826	2	29761224	29788502	-1	0	1	3	0	2	0	11	12	35	4	13	H3BLS1	
ENSMUST00000177134						16	11	85	63	31	29	0	0	0	0	0		
ENSMUST00000177135						6	4	4	6	5	1	1	1	1	0	1		
ENSMUST00000177137	ENSMUSG00000021996	14	74732297	74750765	1	0	0	0	0	0	0	0	0	0	0	0	H3BLJ9	
ENSMUST00000177138	ENSMUSG00000047284	11	69901072	69913820	1	0	0	0	28	6	0	0	0	104	8	47	H3BK72	
ENSMUST00000177139						0	0	0	0	0	0	0	0	0	3	0		
ENSMUST00000177140						0	0	0	0	0	1	0	0	0	0	2		
ENSMUST00000177142						0	0	0	4	1	0	2	0	7	26	0		
ENSMUST00000177143	ENSMUSG00000036834	3	63696234	63899472	-1	12	0	75	27	46	7	0	0	0	0	0	H3BKK4	
ENSMUST00000177144	ENSMUSG00000091625	6	56701063	56704710	-1	0	0	0	0	2	0	0	0	0	0	0	H3BKC5	
ENSMUST00000177145	ENSMUSG00000055531	10	117344673	117380015	-1	1	3	0	0	3	2	33	2	11	0	33		Q6NVF9
ENSMUST00000177147						4	2	0	2	5	0	0	0	0	0	0		
ENSMUST00000177148						16	16	16	36	33	11	34	60	102	5	201		
ENSMUST00000177149						0	0	4	4	2	3	0	0	0	0	0		
ENSMUST00000177151	ENSMUSG00000043897	3	64116432	64140543	-1	0	0	0	0	11	0	0	0	0	0	0	L7N2E9	
ENSMUST00000177152	ENSMUSG00000027165	2	101560781	101649532	-1	0	0	0	0	0	1	2	0	0	0	0	H3BKQ2	
ENSMUST00000177153	ENSMUSG00000032827	6	4902917	5165661	1	0	0	0	0	0	0	0	0	0	0	0	H3BKQ7	
ENSMUST00000177154	ENSMUSG00000052752	17	24508562	24527938	-1	0	2	4	0	2	0	0	0	20	0	0	H3BLQ3	
ENSMUST00000177155	ENSMUSG00000046138	19	29714402	29805989	-1	4	6	11	294	29	13	110	147	246	22	174	H3BKP8	
ENSMUST00000177156	ENSMUSG00000041420	7	16175090	16186504	1	4	0	2	0	5	3	0	6	0	0	0	Q148B2	
ENSMUST00000177157						7	8	6	10	10	5	0	0	0	0	0		
ENSMUST00000177158	ENSMUSG00000032594	9	108002501	108048782	1	0	0	0	0	1	0	221	27	126	0	114	H3BIW9	
ENSMUST00000177159	ENSMUSG00000002588	6	5168090	5193946	-1	0	0	4	1	0	0	0	0	0	0	0	H3BK03	
ENSMUST00000177160						11	3	10	44	15	6	9	5	15	0	25		
ENSMUST00000177162	ENSMUSG00000021000	12	59129720	59191583	1	0	0	0	0	0	0	0	0	0	19	0	H3BJI6	
ENSMUST00000177163	ENSMUSG00000093674	10	128548114	128549305	-1	9	24	0	0	9	5	494	359	365	1911	181		P62947
ENSMUST00000177164	ENSMUSG00000097437	7	43427622	43428873	1	6	4	5	28	0	7	0	0	0	0	0		H3BKT1
ENSMUST00000177165						2	0	2	161	9	3	0	3	9	1	3		
ENSMUST00000177167						2	2	16	6	4	0	0	0	0	1	0		
ENSMUST00000177168	ENSMUSG00000012609	12	85824659	86061893	1	0	0	0	0	20	2	0	30	0	4	0	H3BJ73	
ENSMUST00000177170						18	7	0	0	19	14	84	0	104	6	97		
ENSMUST00000177171						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177172	ENSMUSG00000024613	18	60813755	60848971	-1	0	0	0	3	0	17	28	0	45	0	0	H3BIX0	
ENSMUST00000177173	ENSMUSG00000032595	9	107992497	107999684	1	20	11	16	47	20	8	0	7	0	0	6	H3BJZ2	
ENSMUST00000177174						4	0	6	2	0	3	0	0	5	0	8		
ENSMUST00000177175						1	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000177176	ENSMUSG00000022362	15	58028243	58076425	-1	0	0	0	0	0	0	0	0	0	0	0	H3BKI4	
ENSMUST00000177177	ENSMUSG00000069678	6	83077869	83080855	1	5	0	0	0	0	0	34	129	0	49	14	H3BK85	
ENSMUST00000177178	ENSMUSG00000029915	6	40574894	40585821	-1	0	4	0	0	3	0	0	77	113	114	7		
ENSMUST00000177179						5	2	8	1	1	3	0	0	0	0	0		
ENSMUST00000177180	ENSMUSG00000022388	15	88890633	88954418	-1	0	3	5	62	5	12	0	0	0	0	0	H3BKG4	
ENSMUST00000177181	ENSMUSG00000021996	14	74732297	74750765	1	0	0	0	0	0	0	0	0	0	0	0	H3BJL6	
ENSMUST00000177182						6	2	16	2	5	1	0	0	0	0	0		
ENSMUST00000177183	ENSMUSG00000021188	12	101834043	101913267	-1	0	0	3	0	0	0	105	0	288	0	267	H3BJG4	
ENSMUST00000177184	ENSMUSG00000068999	3	64490821	64509735	-1	14	13	0	11	1	0	0	0	0	0	0	K7N788	
ENSMUST00000177186	ENSMUSG00000038291	8	46033261	46152159	-1	2	0	0	0	0	0	0	0	0	1	0	H3BJE1	
ENSMUST00000177187	ENSMUSG00000020263	10	83600033	83648738	-1	1	0	0	0	0	3	6	36	17	0	0	H3BJX0	
ENSMUST00000177188	ENSMUSG00000012609	12	85824659	86061893	1	0	1	0	1	0	0	3	0	1	0	3	H3BJC2	
ENSMUST00000177189						0	0	2	16	0	0	15	23	4	0	0		
ENSMUST00000177191						2	0	0	0	7	1	0	0	0	0	0		
ENSMUST00000177192	ENSMUSG00000028552	4	109280268	109387817	1	1	4	0	0	5	0	21	348	85	73	21	H3BLE4	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177193	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	0	0	0	0	14	H3BK82	
ENSMUST00000177194						4	0	3	103	3	2	1	0	0	0	1		
ENSMUST00000177195						2	0	6	3	3	0	1	3	3	0	7		
ENSMUST00000177196	ENSMUSG00000018001	5	143622447	143710250	1	1	0	4	39	1	1	0	0	0	0	0	A0A0G2JDC7	
ENSMUST00000177197	ENSMUSG00000032773	19	8663789	8683587	1	16	10	103	66	17	12	0	0	3	0	1	H3BKE3	
ENSMUST00000177198						0	0	6	0	0	0	0	0	0	0	0		
ENSMUST00000177199						0	0	0	6	1	0	0	0	0	0	0		
ENSMUST00000177200						1	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000177202	ENSMUSG00000009739	15	100575318	100599984	-1	0	3	0	838	36	0	11	17	0	0	14	H3BKJ6	
ENSMUST00000177203						1079	1063	4915	1283	1074	520	20	81	38	20	62		
ENSMUST00000177204						0	2	2	0	4	0	0	0	2	0	2		
ENSMUST00000177205	ENSMUSG00000064264	7	24507006	24515682	1	9	3	18	0	12	7	0	4	0	0	0	H3BLD9	
ENSMUST00000177206						3	4	4	8	5	3	0	0	0	0	0		
ENSMUST00000177207	ENSMUSG00000022010	14	76414961	76507765	1	0	0	12	26	0	0	0	32	0	0	0	H3BLI9	
ENSMUST00000177208	ENSMUSG00000030067	6	98925338	99522721	-1	0	1	0	0	1	0	0	0	0	0	3	H3BJZ5	
ENSMUST00000177210						0	10	2	0	7	3	0	0	0	0	0		
ENSMUST00000177211	ENSMUSG00000093550	15	100364542	100383964	1	0	2	3	0	4	0	0	0	0	0	0	Q1XG80	Q76I25
ENSMUST00000177212	ENSMUSG00000030838	7	46195350	46238503	-1	0	0	0	2	0	0	0	0	0	0	0	H3BLC4	
ENSMUST00000177213	ENSMUSG00000025040	X	17556564	17572325	-1	0	2	2	0	2	0	89	489	219	432	154	H3BJ77	
ENSMUST00000177214						0	0	0	0	12	0	0	0	0	0	0		
ENSMUST00000177215						0	0	19	0	1	1	0	5	3	0	5		
ENSMUST00000177216	ENSMUSG00000003680	19	8772522	8786417	-1	5	1	3	165	0	3	0	0	0	0	0	H3BK01	
ENSMUST00000177218	ENSMUSG00000035934	9	36890982	37147322	-1	3	20	51	0	26	5	0	0	17	11	0		Q8BG99
ENSMUST00000177219						5	2	5	0	0	1	0	0	0	0	0		
ENSMUST00000177221	ENSMUSG00000005983	16	3895179	3908689	-1	0	0	0	7	0	0	0	0	0	0	0	H3BJ08	
ENSMUST00000177222						0	0	0	0	0	0	0	35	0	0	3		
ENSMUST00000177223						11	7	48	23	6	5	0	0	0	0	0		
ENSMUST00000177224	ENSMUSG00000056458	12	110807798	110840939	-1	0	0	0	36	0	1	0	0	1	0	0	H3BLH6	
ENSMUST00000177225	ENSMUSG00000021000	12	59129720	59191583	1	2	2	18	33	1	1	0	0	0	0	9	H3BL19	
ENSMUST00000177226						0	1	0	13	0	2	0	0	0	0	0		
ENSMUST00000177227	ENSMUSG00000030067	6	98925338	99522721	-1	6	3	9	91	6	3	0	0	0	0	2	H3BK30	
ENSMUST00000177228	ENSMUSG00000064264	7	24507006	24515682	1	0	0	0	61	0	0	0	0	0	0	0	H3BLG0	
ENSMUST00000177229	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	1	91	0	336	0	57	H3BJ24	
ENSMUST00000177230	ENSMUSG00000030067	6	98925338	99522721	-1	6	4	3	3	3	6	0	13	13	0	18	H3BJR8	
ENSMUST00000177231						8	9	20	64	24	12	0	0	0	0	0		
ENSMUST00000177232	ENSMUSG00000019984	10	24869986	24913681	1	40	58	107	21	45	23	11	30	18	0	20	H3BJ66	
ENSMUST00000177233						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000177234	ENSMUSG00000007655	6	17306335	17341452	1	0	0	1	2	1	0	0	0	0	0	0	H3BLQ4	
ENSMUST00000177235						0	0	0	12	0	0	0	0	1	0	1		
ENSMUST00000177236	ENSMUSG00000030788	7	110800432	110844457	-1	15	9	38	17	9	4	371	1265	395	333	296		Q99MB7
ENSMUST00000177240	ENSMUSG00000031970	8	123504718	123515463	-1	3	0	0	0	6	3	2	0	0	0	0	H3BK17	
ENSMUST00000177241	ENSMUSG00000048277	11	117809668	117814283	1	0	0	0	3	0	0	0	3	0	0	0	H3BJY1	
ENSMUST00000177242						0	0	1	1	0	2	0	0	0	0	0		
ENSMUST00000177243						5	2	0	0	3	1	0	0	0	0	0		
ENSMUST00000177244	ENSMUSG00000091679	17	18581727	18598157	1	4	4	5	0	5	0	0	1	2	0	0	E9PZU5	
ENSMUST00000177245						1	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000177247						0	1	4	0	1	0	4	0	0	0	0		
ENSMUST00000177249	ENSMUSG00000029787	6	56714899	56761912	1	0	0	0	97	3	1	0	0	18	0	0		
ENSMUST00000177250	ENSMUSG00000070385	3	103074014	103099720	1	0	0	0	0	0	0	0	2	0	1	2	H3BIY4	
ENSMUST00000177252	ENSMUSG00000024921	19	26605115	26778321	1	0	0	5	0	0	1	0	44	0	0	0	H3BJI1	
ENSMUST00000177253	ENSMUSG00000006715	13	24751845	24761923	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJH3	
ENSMUST00000177254	ENSMUSG00000022388	15	88890633	88954418	-1	0	0	55	0	2	7	0	0	0	0	0	H3BJ58	
ENSMUST00000177255						2	3	3	11	13	1	1	2	0	0	1		
ENSMUST00000177256						1	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000177257	ENSMUSG00000019737	7	30314807	30319046	1	0	0	0	0	0	0	0	0	0	0	0	H3BKV7	
ENSMUST00000177258	ENSMUSG00000053178	5	4192367	4197651	1	3	3	1	0	3	2	7	68	23	23	16	A0A096P6K7	
ENSMUST00000177259	ENSMUSG00000058317	14	18573575	18894267	-1	0	0	0	0	0	0	0	0	0	0	0	H3BKX9	
ENSMUST00000177260						0	1	3	5	0	1	0	0	0	0	0		
ENSMUST00000177261						14	20	46	31	44	14	3	24	26	0	57		
ENSMUST00000177263						39	58	92	101	53	26	0	0	0	0	2		
ENSMUST00000177264						50	46	87	56	54	29	0	4	3	0	5		
ENSMUST00000177265						3	1	0	2	1	3	0	0	0	3	0		
ENSMUST00000177267	ENSMUSG00000093523	6	57322645	57323657	-1	2	4	4	0	3	0	0	0	0	0	0	K7N775	
ENSMUST00000177269	ENSMUSG00000033713	12	99194980	99450111	-1	3	2	0	0	1	1	0	2	0	0	0	H3BLJ5	
ENSMUST00000177271						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177272						7	7	46	5	5	6	0	0	0	0	1		
ENSMUST00000177273						7	0	27	6	7	8	0	0	0	0	0		
ENSMUST00000177274						4	2	5	2	2	5	1	0	0	0	1		
ENSMUST00000177275						0	0	0	0	0	0	0	30	0	8	2		
ENSMUST00000177276	ENSMUSG00000022361	15	58047003	58076541	-1	3	0	4	0	4	2	44	0	121	0	30	H3BK31	
ENSMUST00000177277	ENSMUSG00000028487	4	84275095	84675275	-1	0	0	0	0	0	0	0	0	0	0	0	H3BKY6	
ENSMUST00000177279	ENSMUSG00000026102	1	52785427	52817688	-1	0	0	4	0	0	0	131	229	204	69	144	H3BK26	
ENSMUST00000177280	ENSMUSG00000028710	4	115784812	115818828	1	0	0	0	224	5	0	0	0	3	8	7	H3BK16	
ENSMUST00000177281	ENSMUSG00000018001	5	143622447	143710250	1	0	1	2	0	1	0	0	0	0	0	0	H3BK81	
ENSMUST00000177282	ENSMUSG00000038331	1	56793981	56978650	-1	3	2	0	25	5	0	0	0	0	0	0	H3BKV4	
ENSMUST00000177283	ENSMUSG00000021996	14	74732297	74750765	1	0	2	0	0	5	3	456	1691	671	2493	401	H3BJP2	
ENSMUST00000177285						1	2	3	0	3	2	0	0	0	0	0		
ENSMUST00000177286						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177287						76	68	384	63	48	21	2	4	0	0	2		
ENSMUST00000177288	ENSMUSG00000010175	1	190118035	190170714	-1	14	6	28	114	11	4	0	0	0	0	0		P48437
ENSMUST00000177289	ENSMUSG00000042320	12	85086385	85106431	-1	25	13	56	41	31	10	9	24	21	3	23		Q8BII1
ENSMUST00000177290	ENSMUSG00000005220	5	72300025	72504473	-1	5	0	0	0	0	0	0	0	0	0	0	H3BKS9	
ENSMUST00000177291						0	3	0	4	3	0	0	0	0	0	0		
ENSMUST00000177292	ENSMUSG00000032336	9	58582240	58657955	1	1	2	7	8	4	1	6	9	9	3	9		P97300

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177293	ENSMUSG00000032570	9	105403539	105527319	-1	6	5	0	0	5	0	189	1881	910	183	645	H3BLI6	
ENSMUST00000177294	ENSMUSG00000024913	19	3584828	3686564	-1	0	0	0	0	0	0	8	22	0	3	0	H3BIY3	
ENSMUST00000177295						0	0	2	1	1	3	0	0	0	0	0		
ENSMUST00000177297	ENSMUSG00000029705	5	136248135	136567490	-1	0	0	0	0	0	0	10	0	125	0	1	H3BJ26	
ENSMUST00000177298						1	2	0	60	3	0	0	0	3	0	10		
ENSMUST00000177299						2	3	0	4	3	1	0	0	2	0	2		
ENSMUST00000177301						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177302	ENSMUSG00000026872	2	44983632	45117395	-1	10	0	0	44	16	5	91	80	503	223	458		Q9R0G7
ENSMUST00000177303	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	0	3	0	0	0	H3BJU7	
ENSMUST00000177304	ENSMUSG00000017311	11	102106676	102107832	-1	0	0	0	0	0	0	0	0	0	0	0	H3BK86	
ENSMUST00000177305						39	31	63	51	32	19	1	4	6	3	11		
ENSMUST00000177307	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	0	0	0	0	37	30	116	16	74	H3BLF2	
ENSMUST00000177308						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177309						11	13	24	18	22	15	0	2	1	0	4		
ENSMUST00000177310						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177311						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177312	ENSMUSG00000041650	14	122534324	122891100	1	0	0	0	0	0	1	1	0	0	6	0	H3BL62	
ENSMUST00000177313						0	2	7	5	6	1	0	0	0	0	0		
ENSMUST00000177315						0	0	0	78	0	0	0	2	0	0	3		
ENSMUST00000177318	ENSMUSG00000093379	6	58471898	58475343	-1	0	4	0	3	3	0	0	0	0	0	0	H3BKW5	
ENSMUST00000177320	ENSMUSG00000032059	9	50775019	50843542	1	1	0	7	0	3	0	0	0	3	0	1	H3BJ25	
ENSMUST00000177321						15	8	11	148	16	5	0	1	0	0	1		
ENSMUST00000177322	ENSMUSG00000010110	19	8741413	8756069	1	0	1	0	0	10	5	238	453	260	81	147	H3BL25	
ENSMUST00000177323	ENSMUSG00000005983	16	3895179	3908689	-1	0	0	0	0	0	0	27	33	18	12	1	H3BLF4	
ENSMUST00000177325	ENSMUSG00000019876	10	57631981	57741112	1	0	0	4	0	5	0	0	0	0	0	0	Q3TZU5	
ENSMUST00000177326	ENSMUSG00000021972	14	64811600	64949871	-1	0	2	0	0	0	0	3	2	0	0	5	H3BKF8	
ENSMUST00000177327						14	15	102	18	16	9	10	6	6	0	10		
ENSMUST00000177328						2	4	15	0	0	0	0	0	0	0	11		
ENSMUST00000177329	ENSMUSG00000030340	6	125320659	125344943	1	0	0	0	0	0	0	162	0	71	24	0	H3BJC3	
ENSMUST00000177330	ENSMUSG00000024913	19	3584828	3686564	-1	203	171	984	302	155	101	18	53	20	0	29	H3BJH0	
ENSMUST00000177333						2	1	7	4	1	0	0	0	0	0	0		
ENSMUST00000177334	ENSMUSG00000032570	9	105403539	105527319	-1	1	2	1	57	5	2	10	56	121	0	26	H3BJ99	
ENSMUST00000177335						15	6	17	2	17	18	16	80	0	9	7		
ENSMUST00000177336	ENSMUSG00000090173	11	62847069	62877465	1	0	0	0	23	0	0	0	9	0	5	0	H3BK87	
ENSMUST00000177337	ENSMUSG00000005980	16	4036942	4040024	1	0	0	0	0	0	0	0	0	0	0	0	H3BKL7	
ENSMUST00000177338	ENSMUSG00000032827	6	4902917	5165661	1	3	0	0	22	2	0	0	0	0	0	0	Q8BMP0	
ENSMUST00000177339	ENSMUSG00000021175	12	117804289	117878706	1	4	0	4	0	0	0	0	0	3	0	0	H3BJN2	
ENSMUST00000177340						2	5	58	20	8	7	0	2	0	0	2		
ENSMUST00000177341						2	0	7	2	0	0	0	0	0	0	1		
ENSMUST00000177342	ENSMUSG00000024109	17	90033631	91093071	-1	0	0	0	3	0	1	0	0	0	0	0	H3BK93	
ENSMUST00000177343	ENSMUSG00000024613	18	60813755	60848971	-1	2	0	0	2	2	0	0	0	0	0	0	H3BK88	
ENSMUST00000177346						282	238	1082	2381	456	254	7	15	13	1	25		
ENSMUST00000177347						0	3	5	0	1	1	0	5	4	0	5		
ENSMUST00000177350	ENSMUSG00000009585	15	79891659	79915906	1	0	0	2	0	0	1	0	0	3	0	5	H3BJD1	
ENSMUST00000177352	ENSMUSG00000022469	15	97744770	97767972	-1	34	30	154	57	26	5	0	9	6	0	0	H3BK39	
ENSMUST00000177353	ENSMUSG00000034674	10	82629828	82650799	1	0	0	0	0	0	0	0	2	0	0	0	H3BL22	
ENSMUST00000177354						5	0	15	10	9	2	12	113	49	0	87		
ENSMUST00000177355	ENSMUSG00000045098	19	3767421	3818303	1	0	0	0	10	0	0	0	0	0	0	6	H3BKZ5	
ENSMUST00000177356						4	0	2	1	0	0	0	0	0	0	4		
ENSMUST00000177357	ENSMUSG00000020160	11	18879817	19018985	-1	0	0	0	0	0	0	0	0	1	0	3	V9GXB5	
ENSMUST00000177358	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	0	1	0	H3BKX3	
ENSMUST00000177359	ENSMUSG00000053929	15	76643395	76660117	-1	0	0	22	22	8	4	0	42	18	5	9		Q9QXA1
ENSMUST00000177360	ENSMUSG00000024227	17	58878808	58991375	-1	0	2	1	1	3	4	0	0	0	1	0	H3BJY8	
ENSMUST00000177361	ENSMUSG00000074634	13	119487941	119610458	1	161	143	278	128	169	101	0	11	2	0	13	H3BIZ4	
ENSMUST00000177364						0	0	3	24	1	0	0	0	0	0	0		
ENSMUST00000177365						3	4	2	6	2	0	0	0	0	0	0		
ENSMUST00000177366	ENSMUSG00000025885	18	74440936	74771493	1	0	0	2	1	0	0	0	0	0	0	2	H3BLK6	
ENSMUST00000177367	ENSMUSG00000030142	6	123281789	123289870	-1	0	0	0	0	0	0	377	2990	1442	3089	1153	H3BJQ5	
ENSMUST00000177368	ENSMUSG00000079323	9	107983058	107995007	1	0	0	0	0	0	1	0	0	0	0	0	K7N787	
ENSMUST00000177369						4	6	0	0	2	0	0	0	0	0	0		
ENSMUST00000177370	ENSMUSG00000021000	12	59129720	59191583	1	1	1	3	0	0	0	4	65	0	0	0	H3BJY7	
ENSMUST00000177371	ENSMUSG00000022377	15	64086857	64382919	-1	33	7	83	31	7	7	385	1790	666	61	406	H3BL41	
ENSMUST00000177372	ENSMUSG00000001998	2	127008717	127067909	1	0	0	0	0	0	0	0	3	11	0	0	H3BKM4	
ENSMUST00000177373	ENSMUSG00000010110	19	8741413	8756069	1	0	0	0	0	0	0	55	109	36	0	0	H3BJ02	
ENSMUST00000177374	ENSMUSG00000022377	15	64086857	64382919	-1	0	0	0	0	11	0	0	0	0	0	0		Q9QWY8
ENSMUST00000177375	ENSMUSG00000093639	7	43427670	43435991	1	11	13	80	27	35	3	0	0	0	0	0		H3BKT1
ENSMUST00000177376	ENSMUSG00000025613	16	87483326	87495873	-1	0	0	2	0	0	0	226	1117	382	391	152	H3BKR8	
ENSMUST00000177377						3	1	0	1	3	0	0	11	0	6	22		
ENSMUST00000177378	ENSMUSG00000019893	10	52045721	52195244	-1	21	8	0	6	15	11	0	0	0	0	0	H3BJA2	
ENSMUST00000177379						13	8	15	23	26	9	0	0	0	0	0		
ENSMUST00000177380	ENSMUSG00000032336	9	58582240	58657955	1	0	0	0	8	0	1	0	0	38	254	45	A0A0A0MQN8	
ENSMUST00000177381	ENSMUSG00000041180	19	36554639	36621135	1	0	0	0	0	0	1	0	3	0	0	3	H3BJF4	
ENSMUST00000177382	ENSMUSG00000009563	2	32757234	32762244	1	0	0	0	44	0	0	0	0	0	0	0	H3BJF8	
ENSMUST00000177383	ENSMUSG00000070369	7	128154376	128223816	1	0	0	2	0	0	2	0	1	0	0	1	H3BJS4	
ENSMUST00000177384	ENSMUSG00000037845	9	50768236	50773348	1	1	1	1	0	0	0	5	3	0	8	0	H3BKY5	
ENSMUST00000177386						19	11	24	43	10	4	0	11	1	0	7		
ENSMUST00000177387						2	3	0	4	2	0	0	0	1	0	0		
ENSMUST00000177388						2	2	4	1	7	1	0	9	0	0	0		
ENSMUST00000177389	ENSMUSG00000046519	3	95588934	95619247	1	0	0	8	10	0	0	0	113	17	0	0	H3BKI7	
ENSMUST00000177390	ENSMUSG00000046519	3	95588934	95619247	1	0	0	0	0	0	0	229	483	270	628	212	H3BJ07	
ENSMUST00000177391	ENSMUSG00000041073	11	6597823	6606053	-1	0	0	7	5	2	0	0	0	0	0	1	H3BKC6	
ENSMUST00000177392	ENSMUSG00000032596	9	107975505	107984060	1	17	3	11	14	9	6	140	540	186	51	338	H3BJA7	
ENSMUST00000177393						5	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000177394	ENSMUSG00000028573	4	95557507	95926939	1	1	0	3	3	0	2	0	0	0	0	0	H3BJ80	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177395						0	0	0	0	0	0	0	2	0	0	1		
ENSMUST00000177396						0	0	0	0	0	0	0	0	8	0	0		
ENSMUST00000177397	ENSMUSG00000058258	13	8885501	8892451	1	0	0	0	0	0	0	0	0	15	4	0	H3BKD7	
ENSMUST00000177398						117	145	168	109	129	59	0	4	3	4	3		
ENSMUST00000177399	ENSMUSG00000046519	3	95588934	95619247	1	2	1	1	0	1	0	0	0	0	0	0	H3BJI3	
ENSMUST00000177400	ENSMUSG00000058258	13	8885501	8892451	1	0	0	0	0	0	0	0	0	0	0	5	H3BLF8	
ENSMUST00000177401	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	0	0	0	0	76	0	0	0	0	H3BKC9	
ENSMUST00000177402	ENSMUSG00000032567	9	105395392	105412229	1	0	0	0	0	0	0	0	16	3	0	0	H3BKA9	
ENSMUST00000177403	ENSMUSG00000072494	14	54872669	54877550	-1	0	0	0	186	8	0	0	0	0	0	0	H3BJB2	
ENSMUST00000177404	ENSMUSG00000021147	13	8802968	8871909	-1	1	0	7	18	0	0	2	3	4	6	0	H3BLH1	
ENSMUST00000177405	ENSMUSG00000052752	17	24508562	24527938	-1	7	3	0	2	4	0	9	0	0	0	0	H3BJU4	
ENSMUST00000177406						3	7	27	10	28	11	0	3	23	0	30		
ENSMUST00000177407						15	27	18	14	19	11	0	0	0	1	0		
ENSMUST00000177408	ENSMUSG00000073705	4	149127121	149137629	-1	0	0	0	0	0	0	12	3	10	23	5	H3BKU9	
ENSMUST00000177409						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000177410						4	0	2	2	0	0	0	31	10	12	0		
ENSMUST00000177411						3	3	0	10	1	1	0	0	0	0	0		
ENSMUST00000177412						49	55	175	93	42	23	0	3	0	0	3		
ENSMUST00000177413						4	10	6	3	8	1	0	0	0	0	0		
ENSMUST00000177415						3	3	0	2	0	0	0	0	0	2	4		
ENSMUST00000177416						3	2	4	2	2	0	0	0	0	0	0		
ENSMUST00000177417	ENSMUSG00000020160	11	18879817	19018985	-1	0	21	10	0	0	0	0	0	0	0	3	H3BLB6	
ENSMUST00000177418						0	0	0	0	0	0	0	2	33	0	29		
ENSMUST00000177419						2	2	0	5	1	0	0	0	0	0	0		
ENSMUST00000177420	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000177422						1	0	1	0	0	0	3	20	0	6	0		
ENSMUST00000177423	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	0	0	0	0	3	H3BKB8	
ENSMUST00000177424	ENSMUSG00000038331	1	56793981	56978650	-1	0	0	47	0	0	0	0	1	0	0	0	H3BKH3	
ENSMUST00000177425	ENSMUSG00000024164	17	57203970	57228136	-1	0	0	0	0	0	3	0	5	0	0	0	H3BL60	
ENSMUST00000177426						3	4	2	2	4	4	0	0	0	0	0		
ENSMUST00000177428	ENSMUSG00000034708	11	102430315	102437048	1	76	54	356	119	57	39	25	213	18	34	18	H3BJ90	
ENSMUST00000177429						0	0	0	0	0	0	0	512	0	2	0		
ENSMUST00000177431						2	5	5	3	4	0	2	2	3	0	3		
ENSMUST00000177432	ENSMUSG00000024347	18	35964830	36014715	1	0	0	18	3	0	0	0	0	0	0	0		Q6P1I6
ENSMUST00000177433						1	7	11	0	4	0	0	0	0	0	0		
ENSMUST00000177434						8	9	14	3	13	5	0	0	0	0	0		
ENSMUST00000177435	ENSMUSG00000093501	6	57899959	57901054	-1	4	2	1	3	0	2	0	0	0	0	0	Q8R2D1	
ENSMUST00000177437	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	7	8	0	0	203	237	308	62	290		
ENSMUST00000177438	ENSMUSG00000019876	10	57631981	57741112	1	0	0	0	2	1	0	0	0	0	0	0	H3BLG2	
ENSMUST00000177439						1	2	0	1	2	0	0	0	0	0	0		
ENSMUST00000177441						6	9	19	15	8	4	0	0	0	0	0		
ENSMUST00000177442	ENSMUSG00000015943	3	96196588	96219709	-1	2	0	0	100	11	7	8	16	22	54	9		Q9D8S9
ENSMUST00000177443						17	7	36	22	6	17	0	0	1	5	0		
ENSMUST00000177444	ENSMUSG00000035934	9	36890982	37147322	-1	0	0	0	0	5	0	0	0	0	0	0	H3BL39	
ENSMUST00000177445						0	0	0	4	3	1	7	0	15	81	33		
ENSMUST00000177446						2	4	3	0	3	0	0	0	0	0	0		
ENSMUST00000177447	ENSMUSG00000058258	13	8885501	8892451	1	0	0	0	0	2	0	0	0	0	0	0	H3BLP1	
ENSMUST00000177448						0	2	3	1	3	0	0	0	0	0	0		
ENSMUST00000177450	ENSMUSG00000040732	16	95359169	95586593	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJC4	
ENSMUST00000177451	ENSMUSG00000033713	12	99194980	99450111	-1	0	0	0	47	10	0	0	0	21	0	45		Q499D0
ENSMUST00000177452						5	3	18	3	6	2	0	0	0	0	0		
ENSMUST00000177454						3	7	12	6	2	1	0	1	3	0	0		
ENSMUST00000177455						3	0	9	5	2	2	0	0	0	0	0		
ENSMUST00000177456	ENSMUSG00000032827	6	4902917	5165661	1	0	0	0	0	0	0	0	0	0	0	4	H3BJD6	
ENSMUST00000177457	ENSMUSG00000026657	2	4017717	4614043	1	0	0	0	0	0	0	9	0	0	0	0	H3BIZ7	
ENSMUST00000177458	ENSMUSG00000045658	1	84036296	84364180	-1	74	82	1306	125	74	30	0	0	4	1	15	H3BJT8	
ENSMUST00000177460	ENSMUSG00000021000	12	59129720	59191583	1	2	0	0	39	2	4	0	0	0	0	0	H3BJ84	
ENSMUST00000177462	ENSMUSG00000030788	7	110800432	110844457	-1	0	0	0	0	0	0	21	61	52	43	51	H3BJB4	
ENSMUST00000177463	ENSMUSG00000036138	9	119339676	119350299	1	0	1	1	7	1	3	6	9	18	0	11	H3BKA1	
ENSMUST00000177464						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000177465	ENSMUSG00000029647	5	147430161	147548502	1	0	0	0	0	0	0	0	0	0	0	0	H3BJ17	
ENSMUST00000177466	ENSMUSG00000079165	5	137641334	137642902	1	0	0	4	19	1	0	17	37	9	0	42	H3BLC5	
ENSMUST00000177467	ENSMUSG00000039826	2	29761224	29788502	-1	0	0	0	0	0	0	41	0	0	0	0	H3BKT7	
ENSMUST00000177468						2	1	7	23	2	1	0	0	0	0	0		
ENSMUST00000177469						4	7	18	40	13	9	0	0	0	0	0		
ENSMUST00000177470						8	6	14	114	7	8	40	91	24	15	29		
ENSMUST00000177471	ENSMUSG00000022010	14	76414961	76507765	1	7	0	0	0	0	0	0	0	0	0	0	H3BJ00	
ENSMUST00000177472						105	72	302	1379	182	121	3	3	7	0	10		
ENSMUST00000177473	ENSMUSG00000019876	10	57631981	57741112	1	0	0	0	0	0	0	0	0	5	51	6	Q3TZU5	
ENSMUST00000177474						35	35	59	40	36	24	1	5	5	0	4		
ENSMUST00000177475						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177476	ENSMUSG00000047284	11	69901072	69913820	1	0	0	0	0	0	0	213	0	63	0	0	H3BJZ3	
ENSMUST00000177477	ENSMUSG00000093445	5	137629121	137641099	1	0	0	0	1	0	0	0	12	25	9	0	H3BLB4	
ENSMUST00000177478						1	3	1	5	2	0	1	0	0	0	0		
ENSMUST00000177479	ENSMUSG00000093626	15	75449457	75451406	1	7	3	5	8	8	3	0	0	0	0	0	H3BJG9	
ENSMUST00000177480	ENSMUSG00000021188	12	101834043	101913267	-1	0	0	0	0	0	0	0	0	0	4	0	H3BJU5	
ENSMUST00000177481						8	2	1	3	8	2	0	0	0	0	0		
ENSMUST00000177483	ENSMUSG00000009585	15	79891659	79915906	1	0	0	0	0	0	0	4	3	0	0	0	H3BJJ6	
ENSMUST00000177484	ENSMUSG00000024921	19	26605115	26778321	1	1	2	5	3	1	0	0	28	10	0	32	Q99KH6	
ENSMUST00000177485						1	0	1	3	0	0	0	19	0	0	0		
ENSMUST00000177486	ENSMUSG00000003549	7	19344778	19356524	1	0	0	0	0	0	0	7	6	2	8	0	H3BJX2	
ENSMUST00000177489						4	1	2	2	3	0	3	2	29	0	52		
ENSMUST00000177490						1	1	0	0	2	2	0	0	0	0	0		
ENSMUST00000177491	ENSMUSG00000064125	8	4209543	4217459	-1	0	0	0	0	0	0	0	0	0	0	0	H3BJU6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177493						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177494						7	12	15	0	10	4	205	437	47	0	265		
ENSMUST00000177495	ENSMUSG00000025154	19	41766588	41802084	-1	0	2	0	15	4	4	0	0	80	0	16		Q8BRH3
ENSMUST00000177496						0	0	0	0	0	0	11	2	0	0	4		
ENSMUST00000177497	ENSMUSG00000021546	13	58391142	58403343	-1	2	8	4	0	0	0	149	539	73	31	155	H3BLL4	
ENSMUST00000177498	ENSMUSG00000028059	3	88607454	88648052	1	0	0	0	0	0	0	0	0	35	0	0	H3BJ45	
ENSMUST00000177499						9	1	12	48	7	6	0	0	0	0	2		
ENSMUST00000177500	ENSMUSG00000035067	14	63606503	63820809	1	0	0	5	20	2	0	0	0	0	0	0	H3BL12	
ENSMUST00000177501	ENSMUSG00000025940	1	16665207	16678275	1	23	15	31	75	61	2	39	175	23	0	0		
ENSMUST00000177502	ENSMUSG00000052752	17	24508562	24527938	-1	0	0	3	2	4	0	0	3	8	0	16	H3BJF9	
ENSMUST00000177503						13	9	12	7	12	1	0	0	0	0	0		
ENSMUST00000177504	ENSMUSG00000022362	15	58028243	58076425	-1	0	0	0	41	2	2	0	0	3	0	0	H3BJT1	
ENSMUST00000177505						0	0	0	16	0	0	0	0	0	1	1		
ENSMUST00000177506						39	53	38	108	93	49	2	5	1	3	1		
ENSMUST00000177507	ENSMUSG00000030067	6	98925338	99522721	-1	0	0	1	1	0	0	0	0	0	0	0	H3BJ68	
ENSMUST00000177508	ENSMUSG00000032595	9	107992497	107999684	1	0	0	0	0	0	0	0	0	0	0	0	H3BKC1	
ENSMUST00000177509						10	4	4	0	2	0	0	0	0	0	0		
ENSMUST00000177510						3	3	7	0	6	1	0	0	0	0	0		
ENSMUST00000177511	ENSMUSG00000033510	7	63444751	63759028	1	2	0	0	63	0	0	0	0	0	0	0	H3BJ28	
ENSMUST00000177512	ENSMUSG00000025224	19	46152509	46286510	1	2	0	0	0	1	1	0	0	6	0	10	H3BLN1	
ENSMUST00000177513						5	3	0	0	5	0	54	125	15	133	16		
ENSMUST00000177514	ENSMUSG00000050063	7	43824499	43832030	1	0	2	0	1	0	0	0	0	0	0	0	H3BKZ6	
ENSMUST00000177515						6	3	67	6	5	5	0	0	0	0	0		
ENSMUST00000177516						2	1	4	6	0	0	0	0	0	0	0		
ENSMUST00000177517	ENSMUSG00000034799	8	71624417	71671757	-1	7	6	0	242	7	11	0	0	0	0	0	H3BJZ7	
ENSMUST00000177518	ENSMUSG00000024810	19	29925114	29960718	1	4	0	3	1	1	0	0	0	0	22	12	H3BLN5	
ENSMUST00000177519						0	4	0	0	2	0	8	33	10	66	1		
ENSMUST00000177520	ENSMUSG00000030788	7	110800432	110844457	-1	3	1	3	67	1	6	0	4	0	3	0	H3BJE9	
ENSMUST00000177521	ENSMUSG00000041359	12	105216750	105222793	-1	0	0	13	2	0	3	0	0	0	0	0	H3BJA0	
ENSMUST00000177522						380	329	910	272	532	237	32	118	59	6	84		
ENSMUST00000177523	ENSMUSG00000059934	6	132569809	132572941	1	0	0	31	23	0	0	0	0	0	0	0	D3Z1V5	
ENSMUST00000177525	ENSMUSG00000012609	12	85824659	86061893	1	3	4	14	7	0	1	9	7	12	2	7	H3BLA3	
ENSMUST00000177526						7	3	6	4	5	0	0	0	0	0	0		
ENSMUST00000177527	ENSMUSG00000021773	14	21845861	21848977	-1	2	0	0	49	0	0	68	60	44	18	18	H3BJ37	
ENSMUST00000177528						0	2	0	1	3	0	0	0	0	0	0		
ENSMUST00000177530	ENSMUSG00000050954	13	48487647	48513451	-1	13	16	16	28	8	12	51	66	105	12	100	E9Q3R6	
ENSMUST00000177531	ENSMUSG00000001909	8	84686307	84699808	1	0	0	0	0	0	0	3	0	0	0	0	H3BKV3	
ENSMUST00000177532						0	0	0	0	0	0	0	7	9	0	0		
ENSMUST00000177534	ENSMUSG00000033510	7	63444751	63759028	1	13	7	19	3	21	3	0	0	0	0	0	H3BKW8	
ENSMUST00000177536	ENSMUSG00000021188	12	101834043	101913267	-1	0	0	0	0	0	0	0	0	0	1	17	Q8BVJ9	
ENSMUST00000177537	ENSMUSG00000021147	13	8802968	8871909	-1	0	0	0	0	0	0	0	0	15	3	11	H3BKY3	
ENSMUST00000177538						0	0	0	0	0	1	4	0	9	8	3		
ENSMUST00000177540	ENSMUSG00000041420	7	16175090	16186504	1	0	0	0	0	0	0	0	0	0	2	1	H3BKH0	
ENSMUST00000177541						7	3	22	8	14	7	3	5	5	0	4		
ENSMUST00000177542	ENSMUSG00000048756	10	42181841	42276755	-1	3	3	7	30	0	3	0	0	0	0	0	H3BKE2	
ENSMUST00000177543	ENSMUSG00000049659	11	20685084	20741589	-1	0	0	6	0	0	0	187	0	738	78	424	H3BJH7	
ENSMUST00000177544						4	3	2	24	2	3	0	4	3	2	0		
ENSMUST00000177545	ENSMUSG00000029720	5	137629175	137642899	1	8	8	11	66	10	6	644	2895	950	104	1984		Q921G6
ENSMUST00000177546	ENSMUSG00000037971	9	50762828	50775520	-1	0	0	0	0	0	0	0	28	21	94	0	H3BJ69	
ENSMUST00000177549	ENSMUSG00000045404	12	99964499	100062682	1	23	0	0	0	0	0	0	0	0	0	31	Q3TYG8	Q8R1P5
ENSMUST00000177550						0	0	8	0	0	0	0	0	0	0	0		
ENSMUST00000177551	ENSMUSG00000049871	16	3945007	3976632	-1	46	56	46	11	82	30	2	5	7	0	51	J3QQ49	
ENSMUST00000177554	ENSMUSG00000094885	X	149074282	149138152	1	2	1	0	4	2	2	0	0	0	0	0	Q62012	
ENSMUST00000177556	ENSMUSG00000094370	14	5718336	5741577	-1	7	3	2	50	2	0	0	0	0	0	0	A6NAS7	
ENSMUST00000177559	ENSMUSG00000019178	5	135747220	135778385	-1	0	0	6	0	0	0	0	0	0	0	0	Q9DAR2	
ENSMUST00000177560	ENSMUSG00000095264	X	33399414	33400124	1	0	0	1	0	0	0	0	0	0	0	0	D3YU27	
ENSMUST00000177561	ENSMUSG00000094027	13	120214758	120215213	-1	0	5	0	0	0	0	0	0	0	9	0	Q3UPR8	
ENSMUST00000177562	ENSMUSG00000095092	GL456210.1	108390	110303	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177563	ENSMUSG00000095845	8	85067568	85067982	-1	0	1	5	2	2	1	0	2	1	0	1	B2RVA4	
ENSMUST00000177564	ENSMUSG00000096176	14	54122226	54122241	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177565	ENSMUSG00000096237	JH584294.1	138344	144557	-1	30	20	50	35	23	13	3	0	0	0	0		
ENSMUST00000177566	ENSMUSG00000094759	X	30820542	30843469	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000177567	ENSMUSG00000010064	9	107650634	107669530	-1	0	0	0	0	0	0	0	0	0	16	0		Q9DCP2
ENSMUST00000177568	ENSMUSG00000040899	17	8236043	8257127	1	0	0	0	8	0	0	0	9	0	0	0	Q542B6	O54689
ENSMUST00000177570	ENSMUSG00000042079	6	117900324	117925622	1	0	4	4	1	6	0	303	661	854	264	682	J3QM80	
ENSMUST00000177572						21	19	60	28	28	11	0	0	0	0	0		
ENSMUST00000177574	ENSMUSG00000093957	17	40632075	40637060	1	5	2	14	9	5	3	0	0	0	0	0	J3QN49	
ENSMUST00000177576	ENSMUSG00000068810	2	88540124	88540510	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177577	ENSMUSG00000035171	19	21581202	21652976	-1	6	3	0	3	7	0	0	0	1	1	0	J3QNC2	
ENSMUST00000177578	ENSMUSG00000096827	14	53166626	53167178	1	0	0	0	0	0	1	0	0	0	0	0	A0A075B6A1	
ENSMUST00000177579	ENSMUSG00000096885	Y	40775223	40775765	-1	1	0	67	0	0	2	0	0	0	0	0	J3QNW5	
ENSMUST00000177582	ENSMUSG00000094474	JH584299.1	173050	176134	1	0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000177584						3	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000177585	ENSMUSG00000079685	10	7444873	7473477	-1	19	16	32	15	19	7	88	216	210	110	78	Q8HWA3	
ENSMUST00000177586	ENSMUSG00000096361	17	47410363	47410740	1	0	0	0	60	0	1	0	0	0	0	0	J3QP80	
ENSMUST00000177587	ENSMUSG00000034271	12	85599105	85639878	1	0	0	0	8	0	0	3	0	3	0	0		P97875
ENSMUST00000177588	ENSMUSG00000056394	7	13277283	13311433	1	0	0	0	0	0	0	0	0	0	0	0	Q3U4X8	
ENSMUST00000177591	ENSMUSG00000096768	Y	90784738	90816464	1	0	0	0	16	0	0	0	0	0	0	9	J3QP13	
ENSMUST00000177592	ENSMUSG00000078515	4	141677549	141723419	-1	8	6	0	7	0	0	1234	0	1940	38	1073		Q9ER99
ENSMUST00000177594	ENSMUSG00000035151	8	83312632	83332486	-1	12	17	24	9	16	10	0	48	0	0	9		Q8BGF6
ENSMUST00000177595	ENSMUSG00000021065	12	77238104	77476338	1	0	0	0	0	0	0	0	27	49	0	0		Q9WTS2
ENSMUST00000177598						0	2	0	3	1	3	0	0	0	0	0		
ENSMUST00000177599						7	6	14	49	11	3	5	0	0	2	1		
ENSMUST00000177601	ENSMUSG00000095891	9	3025417	3033289	1	4595	4856	5199	4300	5356	4161	0	0	0	0	0	J3QNH6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177604	ENSMUSG00000036223	18	74195299	74207818	-1	21	13	0	0	0	16	0	0	0	20	0		
ENSMUST00000177605						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177606	ENSMUSG00000094885	X	149074282	149138152	1	2	1	0	4	2	2	0	0	0	0	0	Q62012	
ENSMUST00000177608	ENSMUSG00000016918	1	12692277	12861192	1	12	0	0	27	17	3	0	0	0	0	6		Q8K007
ENSMUST00000177612	ENSMUSG00000094346	Y	6237453	6237995	-1	54	54	1000	137	78	48	0	0	0	0	0	J3QMM6	
ENSMUST00000177615						1	1	0	0	4	2	0	0	0	0	0		
ENSMUST00000177616	ENSMUSG00000095346	5	67927261	67946421	-1	0	0	2	0	0	1	0	0	0	0	0	J3QJV5	
ENSMUST00000177622	ENSMUSG00000096908	14	53443249	53443839	1	0	2	8	0	3	3	0	5	0	8	1	Q5RII1	
ENSMUST00000177624						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177625	ENSMUSG00000008813	14	51918425	51920699	1	0	3	2	0	0	4	0	0	0	0	0		Q0P5Y3
ENSMUST00000177626						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177632	ENSMUSG00000094905	7	22658018	22658941	1	0	0	0	0	0	0	0	0	0	0	0	D3YTY1	
ENSMUST00000177633	ENSMUSG00000039671	2	165784152	165899016	-1	0	0	0	57	0	9	139	378	348	0	75	Q3U1M7	
ENSMUST00000177634	ENSMUSG00000063142	14	23289431	24004859	-1	0	7	0	0	8	0	0	0	0	0	0	J3QMT8	
ENSMUST00000177637	ENSMUSG00000052336	9	119901616	120068283	-1	0	0	0	0	0	0	6	0	15	0	13	Q543X3	Q9Z0D9
ENSMUST00000177638	ENSMUSG00000095061	7	63916857	63920539	1	6	3	54	13	2	2	5	2	11	12	16	J3QMS9	
ENSMUST00000177639	ENSMUSG00000094325	Y	17874741	17967603	1	0	0	13	0	0	0	0	0	0	0	0	Q3TTD8	
ENSMUST00000177642	ENSMUSG00000005506	2	90940382	91019497	1	0	0	0	0	0	0	0	0	0	0	0		P28659
ENSMUST00000177646	ENSMUSG00000096884	12	113460101	113460110	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177647	ENSMUSG00000028716	4	115088708	115093899	1	0	1	0	0	0	0	4	0	0	26	1		Q9CQH0
ENSMUST00000177648	ENSMUSG00000047109	16	93919031	94008837	-1	1	0	8	74	10	0	0	0	0	0	0	A2RSP0	Q9Z0S3
ENSMUST00000177649	ENSMUSG00000095213	4	144453009	144453317	-1	2	0	0	2	0	1	0	0	0	0	0	Q8C559	
ENSMUST00000177651	ENSMUSG00000063730	3	98709255	98724543	-1	0	0	0	0	0	0	0	0	0	0	0		P26149
ENSMUST00000177652						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177654	ENSMUSG00000039936	4	149649168	149702571	-1	0	0	0	0	0	0	3502	7529	3321	6	3236	Q3T9Y0	
ENSMUST00000177659	ENSMUSG00000095029	13	120026439	120027011	-1	2	0	12	7	3	1	0	9	0	0	6	Q3T9V6	
ENSMUST00000177660	ENSMUSG00000091022	14	4084120	4099306	1	0	0	2	0	0	0	0	0	0	0	0	J3QND1	
ENSMUST00000177662	ENSMUSG00000091882	14	6049469	6058267	-1	0	0	0	0	0	0	0	0	0	0	0	J3QMG0	
ENSMUST00000177663	ENSMUSG00000095785	Y	65205185	65207527	-1	0	0	0	0	0	0	0	0	0	0	0	Q810R8	
ENSMUST00000177664						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177665	ENSMUSG00000094030	16	82828382	82829881	1	3643	3726	27631	4929	2978	1477	21	75	38	0	41	J3QPK1	
ENSMUST00000177666	ENSMUSG00000094575	Y	37957811	37960145	1	0	0	0	6	0	4	0	0	0	0	0	Q810R8	
ENSMUST00000177667	ENSMUSG00000025226	19	46328184	46330446	1	3	5	8	268	0	0	0	32	0	14	0		Q91W61
ENSMUST00000177668	ENSMUSG00000095076	JH584298.1	179693	182203	1	0	0	0	3	0	5	0	0	0	0	0	L7N459	
ENSMUST00000177669						6	5	3	305	26	10	593	2775	794	227	1118		
ENSMUST00000177670	ENSMUSG00000094460	14	6210617	6219292	-1	0	0	0	2	1	0	0	0	0	0	0	J3QNJ1	
ENSMUST00000177671	ENSMUSG00000096768	Y	90784738	90816464	1	0	0	3	0	0	0	0	29	3	0	16	J3QJY2	
ENSMUST00000177675						1	0	24	0	0	0	0	0	0	0	1		
ENSMUST00000177676	ENSMUSG00000094404	Y	76378662	76379744	1	0	0	0	0	0	0	0	0	0	0	0	J3QPJ5	
ENSMUST00000177677	ENSMUSG00000095638	15	96766761	96767141	-1	7	3	8	36	8	0	0	0	0	0	0	J3QPX5	
ENSMUST00000177678	ENSMUSG00000096393	9	110914739	110916861	-1	5	1	7	9	7	3	0	0	0	2	0	J3QNP9	
ENSMUST00000177679	ENSMUSG00000052331	1	54645340	54926387	-1	1	1	0	1	8	3	0	0	10	0	53	J3QK37	
ENSMUST00000177680						11	7	0	14	12	3	0	0	0	0	0		
ENSMUST00000177684	ENSMUSG00000094584	19	10997025	11018031	-1	8	6	41	12	8	4	0	0	0	0	0	J3QN01	
ENSMUST00000177689	ENSMUSG00000035513	2	29194541	29253005	-1	0	0	0	0	0	0	7	26	13	0	76	J3QNA0	
ENSMUST00000177690						2	2	0	2	0	0	0	0	0	0	0		
ENSMUST00000177691						13	12	39	169	23	12	0	0	0	0	0		
ENSMUST00000177694	ENSMUSG00000020063	10	63319005	63381704	-1	0	0	0	0	0	0	0	9	26	19	30		Q923E4
ENSMUST00000177695	ENSMUSG00000094121	GL456350.1	394	1059	-1	0	0	0	0	0	0	0	0	0	0	0		P86793
ENSMUST00000177696	ENSMUSG00000071691	19	4625841	4698668	-1	18	8	10	199	21	11	1	0	0	0	0	J3QMY9	
ENSMUST00000177697	ENSMUSG00000094319	6	69631646	69632178	-1	1	1	0	2	1	0	0	3	0	0	1	J3QMZ0	
ENSMUST00000177698						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000177700	ENSMUSG00000094475	2	175643978	175653860	1	0	0	0	0	0	0	0	1	0	0	0	Q8BHI0	
ENSMUST00000177703	ENSMUSG00000094607	14	52929789	52930282	1	1	0	1	2	1	0	0	0	0	0	2	A0A075B6A4	
ENSMUST00000177704						14	10	40	9	12	9	0	11	7	0	5		
ENSMUST00000177705	ENSMUSG00000096541	14	53231433	53232102	1	0	0	0	0	0	0	1	0	0	1	1	A0A075B695	
ENSMUST00000177708						2	2	6	2	4	1	0	3	0	3	0		
ENSMUST00000177709						4	0	4	8	0	0	0	0	0	0	0		
ENSMUST00000177710	ENSMUSG00000031105	X	48623413	48662294	1	6	0	0	0	0	0	23	209	33	28	45		Q9Z2B2
ENSMUST00000177712	ENSMUSG00000095015	14	7185927	7194540	-1	0	0	0	0	0	0	0	0	0	0	0	J3QN10	
ENSMUST00000177713	ENSMUSG00000093895	Y	40290790	40316903	-1	0	0	0	0	0	0	0	0	0	0	0	J3QPW0	
ENSMUST00000177714	ENSMUSG00000074829	9	124291804	124312696	-1	25	32	91	26	21	17	26	75	21	13	20	J3QK55	
ENSMUST00000177715	ENSMUSG00000076617	12	113418558	113422730	-1	10	0	21	31	12	11	367	463	294	607	1622	A0A075B6A0	
ENSMUST00000177719	ENSMUSG00000096756	JH584297.1	108318	111392	-1	4	2	0	2	0	0	0	0	0	0	0		
ENSMUST00000177720						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000177721						8	6	11	9	10	0	0	1	0	0	1		
ENSMUST00000177722	ENSMUSG00000096385	9	3003346	3006948	1	104	114	35	34	120	85	0	0	0	0	0	J3QN50	
ENSMUST00000177727	ENSMUSG00000096846	5	11256033	11260494	1	0	0	0	0	0	0	0	0	0	0	0	J3QP00	
ENSMUST00000177731	ENSMUSG00000020817	11	70844778	70943105	1	0	0	2	25	2	3	0	28	26	0	0	J3QJV7	
ENSMUST00000177735	ENSMUSG00000095822	3	93936633	93943543	-1	5	6	11	6	8	2	0	0	0	0	0		P0DMR6
ENSMUST00000177736	ENSMUSG00000020782	11	115824049	115855780	1	0	13	76	15	24	0	22	24	40	0	0	J3QJU5	
ENSMUST00000177738	ENSMUSG00000031060	X	20617503	20650901	1	0	0	0	0	0	0	0	91	25	2	48		Q99KG3
ENSMUST00000177739						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177740	ENSMUSG00000094601	X	32650716	32651426	1	0	0	0	0	0	0	0	0	0	0	0	E9PWJ8	
ENSMUST00000177741	ENSMUSG00000096612	7	22582486	22583391	-1	0	0	0	0	0	0	0	0	0	0	0	J3KMT3	
ENSMUST00000177743	ENSMUSG00000042079	6	117900324	117925622	1	6	0	4	0	5	0	0	23	9	0	36	J3QMV8	
ENSMUST00000177744						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177747	ENSMUSG00000093847	12	88321047	88321481	-1	0	3	0	2	2	0	0	0	0	1	0	J3QNT6	
ENSMUST00000177748						0	0	2	0	0	2	0	8	1	0	19		
ENSMUST00000177750						11	7	0	14	12	3	0	0	0	0	0		
ENSMUST00000177752	ENSMUSG00000056629	19	6977741	6980461	-1	4	4	10	15	6	2	70	89	79	254	82	Q3TND1	P45878
ENSMUST00000177754	ENSMUSG00000004099	9	20907206	20959888	-1	6	4	19	2	27	5	292	240	172	0	216	J3QNW0	
ENSMUST00000177755	ENSMUSG00000031925	9	13619990	13709533	1	7	0	3	6	0	0	0	31	0	11	0	E9Q7L5	
ENSMUST00000177757	ENSMUSG00000056055	1	87803680	87845158	1	0	1	0	0	0	0	0	0	0	0	8	J3QNF6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177760						5	0	0	2	3	0	0	0	0	0	0		
ENSMUST00000177761	ENSMUSG00000045962	6	119923969	120038672	-1	0	20	48	14	33	36	0	0	1	21	0		P83741
ENSMUST00000177762						32	22	102	35	37	16	0	0	0	0	0		
ENSMUST00000177764	ENSMUSG00000095056	14	4397526	4406347	1	0	3	3	0	0	0	0	0	0	0	0	J3QPT1	
ENSMUST00000177765	ENSMUSG00000095634	Y	68537955	68540290	1	0	0	0	0	0	0	0	0	0	0	0	Q5FWD4	
ENSMUST00000177766	ENSMUSG00000095207	JH584293.1	203931	206144	-1	8	0	39	6	15	12	0	0	0	0	0		
ENSMUST00000177767						0	2	17	7	4	6	0	3710	0	846	0		
ENSMUST00000177768	ENSMUSG00000095595	12	55124528	55142078	1	28	32	72	29	33	23	101	381	129	51	117		Q8BR63
ENSMUST00000177770						2	0	5	12	1	2	0	0	0	0	0		
ENSMUST00000177771	ENSMUSG00000101163	4	88791550	88792098	1	0	0	0	0	0	0	0	0	0	0	0	Q8CD73	
ENSMUST00000177772	ENSMUSG00000039174	3	124556352	124581101	-1	0	0	0	0	1	0	0	0	0	0	0	J3QMZ7	
ENSMUST00000177774	ENSMUSG00000095543	7	22413583	22414506	1	0	0	0	0	0	0	0	0	0	0	0	Q9EPS5	
ENSMUST00000177775	ENSMUSG00000095153	Y	84097279	84123494	1	0	0	0	0	0	0	0	0	0	0	0	J3QJX2	
ENSMUST00000177776						0	0	0	0	0	0	9	0	11	0	5		
ENSMUST00000177778	ENSMUSG00000073197	12	18514738	18534191	1	0	0	0	90	17	12	0	0	0	0	0	J3QPX0	
ENSMUST00000177779	ENSMUSG00000004207	10	60277627	60302597	1	37	0	43	3	9	0	62	75	61	0	116	J3QPG5	
ENSMUST00000177780						27	0	14	0	27	14	5	14	0	7	21		
ENSMUST00000177783	ENSMUSG00000096776	GL456219.1	94186	95088	-1	1	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000177785	ENSMUSG00000096826	4	42655251	42656005	1	0	0	0	0	0	0	0	0	0	0	0		Q9Z1X0
ENSMUST00000177786	ENSMUSG00000096574	14	3332627	3354799	1	0	0	4	0	5	4	0	0	0	0	0	E9PVJ0	
ENSMUST00000177787	ENSMUSG00000094204	9	40670613	40671014	1	1	1	5	2	1	1	0	0	0	0	0	J3QPM7	
ENSMUST00000177789						79	48	57	624	145	73	2	1	1	0	4		
ENSMUST00000177792	ENSMUSG00000095022	10	104185533	104188000	1	0	0	0	0	0	0	0	0	0	0	0	J3QP73	
ENSMUST00000177793						0	7	13	6	9	2	0	0	0	0	0		
ENSMUST00000177795	ENSMUSG00000094262	6	69399810	69400344	-1	1	0	0	0	3	3	0	0	0	0	0	J3QNZ9	
ENSMUST00000177800	ENSMUSG00000029600	5	120594305	120612589	-1	0	0	11	0	15	0	0	42	7	0	0		Q9D1H0
ENSMUST00000177801	ENSMUSG00000021221	12	83213745	83487716	-1	0	7	3	2	5	0	0	1	0	0	0		P58269
ENSMUST00000177802						2	3	4	8	3	0	1	0	0	0	1		
ENSMUST00000177803						0	0	0	9	0	0	0	0	0	0	0		
ENSMUST00000177805						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000177806	ENSMUSG00000094271	4	88773834	88774801	1	5	0	0	68	13	10	0	0	0	0	0	Q8CD73	
ENSMUST00000177808	ENSMUSG00000037594	12	112808975	112816245	1	10	2	27	0	6	5	9	0	11	6	0		Q8BHN9
ENSMUST00000177811	ENSMUSG00000022995	1	181896384	182019990	-1	0	0	0	24	0	0	0	0	0	0	0	J3QNM3	
ENSMUST00000177813						0	0	0	0	10	0	0	0	0	0	0		
ENSMUST00000177814	ENSMUSG00000054423	14	12372563	12823079	-1	14	3	26	23	3	0	0	0	0	0	0	J3QJW3	
ENSMUST00000177815	ENSMUSG00000096386	7	20417942	20418865	1	0	0	0	0	0	0	0	0	0	0	0	Q9EPS5	
ENSMUST00000177817	ENSMUSG00000095280	14	19415857	19418930	-1	13139	14427	18661	10054	14055	10215	5	2	0	0	0	J3QP72	
ENSMUST00000177818	ENSMUSG00000094813	Y	10750004	10752450	-1	4	0	0	0	0	0	0	0	0	0	0	Q3TTD8	
ENSMUST00000177820	ENSMUSG00000096156	16	97490047	97491120	1	6	0	0	11	17	0	0	0	0	0	0	J3QNY1	
ENSMUST00000177822	ENSMUSG00000037544	14	47387779	47418407	-1	93	109	237	70	74	31	10	41	11	15	10	J3QPN1	
ENSMUST00000177824	ENSMUSG00000026601	1	156323509	156421159	-1	8	0	12	3	0	0	0	0	5	4	0	J3KMJ8	
ENSMUST00000177825	ENSMUSG00000017561	11	80046493	80080991	-1	0	0	2	0	0	0	0	0	121	61	168	J3QMV5	
ENSMUST00000177826	ENSMUSG00000096740	19	8883732	8892627	1	0	0	0	0	0	1	0	0	0	0	0	J3QPQ6	
ENSMUST00000177827	ENSMUSG00000090716	14	44402671	44410688	-1	0	1	0	0	1	0	0	0	0	0	0	J3QN98	
ENSMUST00000177828						0	0	0	0	3	0	2	0	0	0	0		
ENSMUST00000177834	ENSMUSG00000095135	Y	55731756	55757908	1	0	0	0	0	0	0	0	0	0	0	0	J3KMR5	
ENSMUST00000177837	ENSMUSG00000028218	4	12153409	12172015	-1	0	0	0	58	0	2	0	0	0	0	0	J3KMP6	
ENSMUST00000177839	ENSMUSG00000096568	12	113475400	113475416	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177840	ENSMUSG00000025510	7	141467362	141471479	1	0	0	0	0	0	0	252	267	134	242	172		O35566
ENSMUST00000177841	ENSMUSG00000045752	7	143069249	143071093	1	0	0	8	0	0	7	115	107	93	45	41		Q9JHE7
ENSMUST00000177842	ENSMUSG00000095263	Y	32588415	32620443	-1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000177843	ENSMUSG00000094172	JH584299.1	562161	564894	1	0	8	16	0	0	2	0	0	0	0	0		
ENSMUST00000177846	ENSMUSG00000096225	3	154306294	154330659	-1	9	5	0	8	12	6	0	0	0	0	0		O35652
ENSMUST00000177847	ENSMUSG00000095161	10	100351111	100351980	1	0	0	0	0	0	0	0	0	0	0	0	E9PZY4	
ENSMUST00000177848	ENSMUSG00000021635	13	100617165	100651059	-1	0	0	13	0	0	11	161	612	236	133	105	Q3UYY2	Q6NXW6
ENSMUST00000177850	ENSMUSG00000035242	10	80826656	80829290	1	0	0	0	0	0	0	54	86	33	46	38	J3QMV2	
ENSMUST00000177851	ENSMUSG00000036180	8	69907069	69996379	-1	0	0	0	52	0	0	11	7	500	0	514		Q8CHY6
ENSMUST00000177853	ENSMUSG00000096236	JH584297.1	31101	33667	1	3	5	0	12	3	0	0	0	0	0	0		
ENSMUST00000177856	ENSMUSG00000075704	16	18426384	18479073	1	5	3	12	5	4	2	9	13	0	0	0	J3QMQ8	
ENSMUST00000177857	ENSMUSG00000039601	17	43801851	44039516	1	1	0	0	0	0	1	0	0	0	2	3	Q543P2	Q9JHG2
ENSMUST00000177858						2	3	2	0	0	0	0	0	0	0	0		
ENSMUST00000177859						2	0	1	27	4	1	0	0	0	2	0		
ENSMUST00000177861	ENSMUSG00000024534	18	52767709	52915935	1	3	0	0	0	0	0	0	0	0	0	0	J3KMU0	
ENSMUST00000177870	ENSMUSG00000094790	8	89146747	89147247	-1	3	2	2	15	5	2	0	1	0	0	0	J3QPK6	
ENSMUST00000177874						5	1	4	2	6	1	0	0	1	0	0		
ENSMUST00000177875	ENSMUSG00000095891	9	3025417	3033289	1	1502	1581	2802	1968	2337	1375	0	0	0	0	1	J3QPP7	
ENSMUST00000177877	ENSMUSG00000091725	14	44285580	44291068	1	28	19	11	21	22	16	0	0	0	0	0	J3QMR5	
ENSMUST00000177878	ENSMUSG00000095602	Y	7405010	7405552	1	84	71	951	230	102	56	0	0	0	0	0	J3QNH3	
ENSMUST00000177879						4	1	4	2	3	1	0	0	0	0	0		
ENSMUST00000177880	ENSMUSG00000028629	4	120921196	120925017	-1	0	8	11	0	0	2	18	4	25	21	16		Q9CXP9
ENSMUST00000177881						5	4	13	4	13	3	2	0	0	0	0		
ENSMUST00000177882	ENSMUSG00000092322	17	38416474	38420185	-1	1	1	0	2	0	0	0	0	0	0	0	A8R0W9	
ENSMUST00000177883	ENSMUSG00000030638	7	82173840	82307419	1	0	0	0	0	0	0	0	0	0	0	0	J3QQ08	
ENSMUST00000177884	ENSMUSG00000095962	7	21994587	21995510	1	1	0	0	0	0	0	0	0	0	0	0	D3YTY1	
ENSMUST00000177891	ENSMUSG00000094719	5	67941669	67977070	1	126	97	303	188	155	76	0	2	0	0	8	J3QP01	
ENSMUST00000177892						8	9	22	9	5	11	0	0	0	0	0		
ENSMUST00000177893	ENSMUSG00000095366	Y	90754513	90754821	-1	0	0	0	0	0	0	0	0	0	2	0	Q3UE70	
ENSMUST00000177894						4	3	9	5	4	1	0	0	0	0	0		
ENSMUST00000177895	ENSMUSG00000030638	7	82173840	82307419	1	0	2	0	0	0	0	0	0	0	0	0	J3QQ08	
ENSMUST00000177904	ENSMUSG00000047996	X	78449613	78583896	-1	1	7	16	0	5	0	1	1	1	0	0	A2BFE8	
ENSMUST00000177905	ENSMUSG00000093828	JH584294.1	2012	3786	1	0	0	0	0	0	0	0	0	0	0	0		Q9Z1X0
ENSMUST00000177906						2	0	0	0	7	0	0	0	0	0	0		
ENSMUST00000177907	ENSMUSG00000021699	13	108449948	109953461	1	3	3	1	0	0	1	13	0	23	4	2	A2RSH1	Q01063
ENSMUST00000177908	ENSMUSG00000094282	5	120628335	120634235	-1	9	7	7	48	16	4	0	0	0	0	1	J3QPZ5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000177912	ENSMUSG00000095934	X	33657172	33658872	1	6	0	0	0	0	0	0	0	0	0	0	B8JKF6	
ENSMUST00000177913	ENSMUSG00000095533	14	3395093	3403525	1	0	0	0	0	0	0	0	0	0	0	0	Q497R9	
ENSMUST00000177915						5	10	22	9	10	7	0	0	0	0	0		
ENSMUST00000177916	ENSMUSG00000094870	13	119765187	119790805	-1	0	0	0	0	0	0	57	147	60	37	53		Q8K3J5
ENSMUST00000177917	ENSMUSG00000073255	X	30329772	30352645	1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000177918	ENSMUSG00000042079	6	117900324	117925622	1	0	0	0	0	0	0	3	0	0	0	3	J3QP45	
ENSMUST00000177919						3	0	0	0	0	0	0	0	0	0	15		
ENSMUST00000177921	ENSMUSG00000096808	GL456221.1	151235	152734	1	8669	9092	82957	13179	7013	3477	97	360	200	41	159		
ENSMUST00000177926	ENSMUSG00000099443	X	11321492	11321809	1	0	2	0	0	0	0	0	0	0	0	0	Q5M8Q2	
ENSMUST00000177927	ENSMUSG00000003154	6	122819914	122845366	1	26	8	145	0	0	26	416	769	440	34	347		Q9ES18
ENSMUST00000177929	ENSMUSG00000094841	7	83542800	83550258	-1	11	11	8	6	13	5	0	0	0	0	0	Q8C4H5	
ENSMUST00000177931	ENSMUSG00000074221	7	29983955	30028282	1	0	0	32	0	0	0	0	0	7	0	0	Q0VGV0	
ENSMUST00000177932	ENSMUSG00000067629	17	26941253	26972434	1	0	0	0	0	0	0	0	0	0	0	3	J3QQ18	
ENSMUST00000177934	ENSMUSG00000094186	10	82486535	82492618	-1	1	1	0	0	1	0	0	0	0	0	0	Q66VB7	
ENSMUST00000177936	ENSMUSG00000094208	7	21511780	21512703	1	1	0	0	0	0	0	0	0	0	0	0	D3YTY1	
ENSMUST00000177939	ENSMUSG00000024222	17	28399095	28517524	-1	6	12	28	3	0	0	0	21	29	0	0	Q4FJN2	Q64378
ENSMUST00000177942	ENSMUSG00000094252	X	124629893	124630390	1	0	0	0	0	2	2	0	0	0	0	0	B6ZB74	
ENSMUST00000177943	ENSMUSG00000026435	1	131962967	131982969	1	0	0	0	79	7	6	6	7	0	1	6		Q8K0H7
ENSMUST00000177945	ENSMUSG00000096744	10	100361338	100362247	1	0	0	0	0	0	0	0	0	0	0	0	E9PZY4	
ENSMUST00000177946	ENSMUSG00000029086	5	43993620	44102032	-1	0	4	2	2	12	0	48	291	116	129	54	Q8CDK8	
ENSMUST00000177947						11	7	0	14	12	3	0	0	0	0	0		
ENSMUST00000177948	ENSMUSG00000021388	13	49544443	49567557	1	8	6	0	7	4	0	0	0	0	0	0	A6H6K1	Q99MQ4
ENSMUST00000177949	ENSMUSG00000094174	12	114406474	114406961	-1	0	2	0	2	0	0	0	0	0	0	0	J3QNN6	
ENSMUST00000177950	ENSMUSG00000034928	13	54679399	54693907	-1	0	0	7	0	0	0	81	222	21	44	313		Q3UHJ8
ENSMUST00000177951	ENSMUSG00000057280	4	58285960	58374303	1	0	0	0	0	0	0	0	0	0	0	0	Q497X0	
ENSMUST00000177952	ENSMUSG00000051043	11	114851152	114872617	1	0	0	0	0	0	0	1	0	0	0	2	J3JS84	
ENSMUST00000177955	ENSMUSG00000031505	8	11497506	11514960	1	0	0	0	14	2	0	234	319	217	59	158	J3QMM7	
ENSMUST00000177957	ENSMUSG00000024073	17	74528295	74703356	1	0	0	4	0	11	0	8	0	7	0	1	J3QP64	
ENSMUST00000177958	ENSMUSG00000093805	1	93918311	93942650	1	0	0	0	0	0	0	0	0	0	0	0	J3QMJ1	
ENSMUST00000177959	ENSMUSG00000021221	12	83213745	83487716	-1	9	0	0	0	4	0	0	0	0	0	0		P58269
ENSMUST00000177962	ENSMUSG00000020650	12	31595354	31634658	-1	3	1	2	0	0	3	55	193	44	144	41	Q542A1	Q61334
ENSMUST00000177963	ENSMUSG00000051705	9	59734259	59750649	-1	0	0	0	0	0	0	0	0	0	12	0		Q9D2Z4
ENSMUST00000177964						2	1	8	4	0	0	0	0	0	0	0		
ENSMUST00000177965	ENSMUSG00000094057	12	113456720	113456736	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177966	ENSMUSG00000053702	2	17343909	17731464	-1	9	7	36	2	9	6	0	0	0	0	0	Q3TR73	
ENSMUST00000177967	ENSMUSG00000066839	9	22072246	22085438	-1	2	1	5	20	4	5	0	0	14	0	14	J3KMM6	
ENSMUST00000177969	ENSMUSG00000096201	9	3036877	3038316	1	542	445	587	495	589	361	0	0	0	0	0	J3QP74	
ENSMUST00000177970						9	0	0	7	7	0	0	0	0	0	0		
ENSMUST00000177972						9	11	7	9	6	2	0	0	0	0	0		
ENSMUST00000177973	ENSMUSG00000090539	14	4776337	4785002	1	0	0	0	0	0	0	0	0	0	0	0	J3QPD5	
ENSMUST00000177974	ENSMUSG00000029467	5	122453513	122502225	-1	16	8	5	33	9	11	30	251	82	15	71		O55143
ENSMUST00000177975						0	3	6	0	3	0	0	0	0	0	0		
ENSMUST00000177978	ENSMUSG00000094103	12	55199533	55214076	1	0	0	0	86	0	0	51	169	89	17	73		Q8BR63
ENSMUST00000177979	ENSMUSG00000096244	GL456219.1	149261	150163	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000177981	ENSMUSG00000094932	2	175741537	175751419	1	0	0	0	0	0	0	0	1	0	0	0	Q8BHI0	
ENSMUST00000177983	ENSMUSG00000054676	7	38183217	38197568	1	4	0	5	26	4	2	148	24	109	29	74	J3QPY0	
ENSMUST00000177984	ENSMUSG00000021198	12	102948859	103184065	1	4	3	0	1	0	0	0	0	0	0	0	J3QPJ0	
ENSMUST00000177985	ENSMUSG00000096405	14	36094917	36100114	1	2	5	5	5	10	5	0	0	0	0	0	Q8BVR5	
ENSMUST00000177986	ENSMUSG00000096003	14	5365794	5389049	-1	0	3	0	1	0	0	0	0	0	0	0	A6NAS7	
ENSMUST00000177990	ENSMUSG00000095754	X	31253894	31255381	1	6	7	14	10	5	2	0	0	0	0	0	J3QPU0	
ENSMUST00000177991	ENSMUSG00000096680	JH584296.1	130715	133448	-1	0	2	0	3	5	2	0	0	0	0	0		
ENSMUST00000177992	ENSMUSG00000037652	3	30899371	30969415	-1	0	0	0	0	0	0	18	8	3	0	45	D3YY34	
ENSMUST00000177994	ENSMUSG00000094577	X	154022780	154033827	-1	0	0	0	2	1	0	0	0	0	0	0	A2BED8	
ENSMUST00000177998	ENSMUSG00000090472	14	4555405	4562747	1	0	0	4	0	5	0	0	0	0	0	0	J3QNT1	
ENSMUST00000177999	ENSMUSG00000095224	11	64435156	64436653	-1	10	3	5	424	7	1	0	0	0	0	0	Q8C3A3	
ENSMUST00000178001	ENSMUSG00000021198	12	102948859	103184065	1	2	0	0	0	0	1	0	0	0	0	0	J3QP77	
ENSMUST00000178002	ENSMUSG00000079267	14	44330442	44338584	-1	0	0	0	0	0	0	0	0	0	0	0	J3QN40	
ENSMUST00000178003	ENSMUSG00000020744	11	115614178	115628295	-1	0	5	10	0	9	0	0	0	0	0	0		Q9DAM5
ENSMUST00000178004	ENSMUSG00000095965	X	125705444	125705941	1	0	0	0	0	2	2	0	0	0	0	0	B6ZB74	
ENSMUST00000178008	ENSMUSG00000102395	3	93281325	93282092	1	0	0	9	51	6	0	0	0	0	0	0	A0A0A6YXG4	
ENSMUST00000178011	ENSMUSG00000024534	18	52767709	52915935	1	5	0	5	82	0	15	0	0	0	0	0	E9Q4E2	
ENSMUST00000178012	ENSMUSG00000035171	19	21581202	21652976	-1	0	0	0	0	3	1	0	0	0	15	0	J3QNT0	
ENSMUST00000178014						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178015	ENSMUSG00000020594	12	8674134	8752581	1	9	0	0	0	0	0	1465	2984	268	224	707		Q80U58
ENSMUST00000178016	ENSMUSG00000096686	Y	6916300	6918282	-1	0	0	4	0	1	0	0	0	0	0	0	J3KML6	
ENSMUST00000178019						4	3	10	10	2	1	0	0	35	0	0		
ENSMUST00000178020						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178021	ENSMUSG00000065968	16	13981702	13986855	-1	55	39	294	74	48	33	0	12	2	0	9	Q9D3R8	
ENSMUST00000178024	ENSMUSG00000094127	1	85575676	85577295	1	1831	936	6478	7964	1600	998	0	0	0	0	0	J3QK25	
ENSMUST00000178025	ENSMUSG00000030655	7	118131308	118243637	-1	0	0	0	0	1	1	1	6	9	3	13	J3QMR1	
ENSMUST00000178026	ENSMUSG00000053219	10	22158569	22374139	1	1	6	0	0	0	0	0	0	0	0	0	D7F2B6	Q9CZQ6
ENSMUST00000178028						0	0	16	0	1	0	36	5	0	0	0		
ENSMUST00000178033	ENSMUSG00000098306	1	133309827	133329901	1	0	0	0	33	0	0	0	0	0	0	0	I0J0X7	Q6Y4S4
ENSMUST00000178034	ENSMUSG00000022218	14	55700009	55713492	-1	5	11	0	37	0	0	2256	3655	2246	199	1081		
ENSMUST00000178036	ENSMUSG00000026601	1	156323509	156421159	-1	3	11	0	21	15	6	0	7	0	0	7	J3QPL7	
ENSMUST00000178037	ENSMUSG00000096345	17	39536142	39540847	1	1	5	4	0	6	2	0	0	0	0	0	A8R0U9	
ENSMUST00000178039	ENSMUSG00000094168	17	39042634	39043341	-1	0	0	1	0	0	0	0	0	0	0	0	J3QMQ1	
ENSMUST00000178040						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178041	ENSMUSG00000025395	10	128015168	128030037	1	2	0	6	0	2	0	40	0	0	0	0	J3QN19	
ENSMUST00000178045	ENSMUSG00000096687	10	39890018	39899238	-1	34	25	65	5	28	15	18	36	17	0	25	J3QNS5	
ENSMUST00000178048	ENSMUSG00000050382	7	79698098	79715720	-1	0	19	17	0	0	0	1	1	1	0	3	J3QNW9	
ENSMUST00000178049						52	64	67	101	75	62	247	862	303	1054	281		
ENSMUST00000178050	ENSMUSG00000095759	Y	13223386	13223928	-1	0	0	22	0	0	0	0	0	0	0	0	A8HG57	
ENSMUST00000178051	ENSMUSG00000096316	9	99229376	99237239	-1	0	0	0	0	5	5	0	0	0	0	0	J3QPY3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000178052						4	1	28	3	9	4	17	41	16	0	0		
ENSMUST00000178056						24	19	34	20	32	22	0	0	2	1	11		
ENSMUST00000178057						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000178058	ENSMUSG00000096003	14	5365794	5389049	-1	1	0	0	0	0	0	0	0	0	0	0	J3QK73	
ENSMUST00000178060	ENSMUSG00000095195	14	3428103	3594220	1	8	0	5	4	0	0	0	0	0	0	0	J3QNM4	
ENSMUST00000178063	ENSMUSG00000094746	Y	79319565	79345707	1	0	0	0	0	0	0	0	0	0	0	0	J3QJX2	
ENSMUST00000178065	ENSMUSG00000094893	9	46998931	47003338	1	321	198	1916	417	397	169	4	13	15	4	23	J3QQ14	
ENSMUST00000178070	ENSMUSG00000094309	X	32560055	32562009	1	20	35	0	11	25	0	0	0	0	0	0	J3KMQ0	
ENSMUST00000178072	ENSMUSG00000017922	13	27196659	27203749	1	0	1	1	0	2	0	0	0	0	0	0	Z4YL38	
ENSMUST00000178075	ENSMUSG00000006676	9	108490602	108502337	1	0	0	0	0	0	2	1153	2004	1409	92	1399	J3KMM1	
ENSMUST00000178076	ENSMUSG00000021198	12	102948859	103184065	1	13	0	0	0	5	0	0	0	0	0	0	J3QNP0	
ENSMUST00000178077	ENSMUSG00000096385	9	3003346	3006948	1	744	922	1082	969	834	756	0	0	0	0	0	J3QNI2	
ENSMUST00000178078	ENSMUSG00000035642	7	97550331	97579497	-1	0	0	0	0	0	3	0	6	1	0	0	D3YZD8	
ENSMUST00000178079	ENSMUSG00000073702	1	39367842	39371911	1	0	0	0	6	10	0	25	363	0	136	37	Q5M9K9	P62900
ENSMUST00000178080	ENSMUSG00000096426	X	3193887	3195827	-1	0	4	15	4	0	0	0	0	0	0	0	J3QNQ5	
ENSMUST00000178081	ENSMUSG00000096873	JH584293.1	60162	60827	-1	0	0	0	0	0	0	0	0	0	0	0		P86793
ENSMUST00000178084						0	0	0	0	0	0	0	0	15	46	16		
ENSMUST00000178085	ENSMUSG00000045330	X	62283499	62292078	1	3	6	7	12	0	5	0	0	0	0	0	Q9D4D2	
ENSMUST00000178086						2	1	4	2	4	1	1	6	2	1	0		
ENSMUST00000178087	ENSMUSG00000035342	19	45015176	45027104	1	0	16	56	132	0	0	13	15	7	20	42		Q91YU6
ENSMUST00000178090						0	2	3	1	0	1	1	0	0	0	0		
ENSMUST00000178092	ENSMUSG00000021871	14	50944302	50965237	1	6	8	5	18	4	0	801	1364	694	1883	587	Q543K9	
ENSMUST00000178093	ENSMUSG00000075704	16	18426384	18479073	1	0	0	0	0	0	0	0	0	0	0	0	J3QMN4	
ENSMUST00000178095						0	2	1	0	4	0	0	0	2	0	0		
ENSMUST00000178096	ENSMUSG00000096192	13	13964487	13965860	-1	12	3	36	6	12	10	0	0	0	0	0	J3QMW8	
ENSMUST00000178097						3	6	11	14	7	2	0	1	1	0	0		
ENSMUST00000178098	ENSMUSG00000027708	3	35892105	35937445	-1	6	8	22	14	19	5	133	293	4	236	23	Q3UT23	
ENSMUST00000178100	ENSMUSG00000105080	14	53324632	53325208	1	24	23	64	22	24	11	2	21	14	8	12	A0A0B4J1N1	
ENSMUST00000178105	ENSMUSG00000020483	11	87979525	87987533	-1	4	14	11	0	0	0	149	219	60	26	70		Q9D0M5
ENSMUST00000178107						0	2	11	7	2	0	12	210	85	54	51		
ENSMUST00000178110	ENSMUSG00000004099	9	20907206	20959888	-1	49	30	54	389	37	23	0	0	0	0	8		P13864
ENSMUST00000178111						0	0	0	4	0	0	1	2	5	1	0		
ENSMUST00000178112						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178113	ENSMUSG00000032280	9	61372366	61418497	1	18	0	84	74	45	0	223	705	1530	38	1023	J3KMT7	
ENSMUST00000178114	ENSMUSG00000024781	19	34492318	34527474	-1	0	0	0	0	0	8	0	0	87	81	54		Q9Z0M5
ENSMUST00000178115	ENSMUSG00000094821	Y	62190866	62217137	1	0	0	0	0	0	0	0	0	0	0	0	J3QNI1	
ENSMUST00000178116	ENSMUSG00000026269	1	92910783	92924384	1	0	1	0	12	1	6	99	0	67	3	1	J3QJW7	
ENSMUST00000178117						3	3	3	70	5	0	16	36	17	9	14		
ENSMUST00000178118	ENSMUSG00000027209	2	125983483	126152004	-1	0	0	0	0	0	4	0	0	0	0	0		Q9D518
ENSMUST00000178120	ENSMUSG00000094475	2	175643978	175653860	1	0	0	0	0	0	0	0	0	0	0	0	A2ART4	
ENSMUST00000178121	ENSMUSG00000095850	X	125004163	125004660	1	0	0	0	0	2	2	0	0	0	0	0	B6ZB74	
ENSMUST00000178122						4	6	3	4	5	10	0	0	0	0	0		
ENSMUST00000178124	ENSMUSG00000096606	7	99624082	99627103	-1	20	12	28	416	33	22	1	3	0	1	7		Q8C013
ENSMUST00000178133	ENSMUSG00000094932	2	175741537	175751419	1	0	0	0	0	0	0	0	0	0	0	0	A2ART4	
ENSMUST00000178134	ENSMUSG00000058006	4	32657119	32775217	1	74	0	162	8	5	0	0	6	0	26	0	J3QMC5	
ENSMUST00000178135						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178136	ENSMUSG00000020865	11	94343295	94392997	-1	8	23	13	52	10	4	77	82	12	3	90	J3QML2	
ENSMUST00000178137	ENSMUSG00000091494	14	4838106	4846867	1	0	0	0	4	0	0	0	0	0	0	0	J3QQ25	
ENSMUST00000178140	ENSMUSG00000095440	15	101050194	101054399	-1	11	11	36	471	31	13	560	836	737	56	338	J3QK54	
ENSMUST00000178142	ENSMUSG00000095930	13	119710094	119755882	-1	23	24	41	87	30	19	7	23	20	9	18		Q8BHI9
ENSMUST00000178143	ENSMUSG00000094860	X	4952135	4954077	1	3	3	0	0	5	0	0	0	0	0	0	Q5FWA1	
ENSMUST00000178145	ENSMUSG00000094714	X	54622211	54639019	1	1	2	0	0	1	0	0	0	0	0	0	A6X8J1	
ENSMUST00000178147						1	25	15	19	40	0	0	0	0	0	0		
ENSMUST00000178148	ENSMUSG00000094620	X	123793665	123813765	1	0	1	0	2	0	0	0	0	0	0	0	J3QJW5	
ENSMUST00000178149	ENSMUSG00000095324	Y	8069168	8071507	-1	25	23	5	0	0	0	0	0	0	0	0	J3QM67	
ENSMUST00000178150						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178152	ENSMUSG00000095293	X	27924017	27946885	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000178155	ENSMUSG00000096215	16	5007288	5008309	1	0	0	0	0	4	0	0	0	0	0	0	J3QP37	
ENSMUST00000178156	ENSMUSG00000052331	1	54645340	54926387	-1	7	5	6	8	0	2	100	201	395	18	267	J3QNJ4	
ENSMUST00000178158	ENSMUSG00000094205	5	11770548	11775300	1	0	0	0	0	0	0	0	0	0	0	0	J3QMX3	
ENSMUST00000178159	ENSMUSG00000069476	11	74069955	74087292	1	0	0	11	0	0	0	0	0	0	0	0	J3QN14	
ENSMUST00000178160	ENSMUSG00000093916	X	108664004	108664891	-1	4	2	1	1	0	1	0	0	0	4	0	J3QQ19	
ENSMUST00000178161	ENSMUSG00000096144	14	57015134	57018982	1	45	40	50	48	52	30	2	6	2	1	1	J3QP07	
ENSMUST00000178162	ENSMUSG00000011427	7	29816072	29832042	1	0	0	0	0	0	7	0	83	0	38	0	Q80ZX2	
ENSMUST00000178163	ENSMUSG00000064179	7	4504570	4516382	-1	0	2	9	0	0	0	0	0	0	0	0	J3QPC8	
ENSMUST00000178164	ENSMUSG00000024260	18	31634371	31723061	1	30	1	2	0	1	0	119	105	111	0	96	J3QNK5	
ENSMUST00000178165	ENSMUSG00000041096	X	152336852	152342425	-1	0	0	0	0	0	0	12	0	5	0	0	J3QP69	
ENSMUST00000178167						9	4	27	4	4	4	0	0	0	0	0		
ENSMUST00000178168	ENSMUSG00000096596	4	42612195	42612860	1	0	0	0	0	0	0	0	0	0	0	0		P86792
ENSMUST00000178169	ENSMUSG00000095621	X	149447617	149487784	1	2	1	0	4	2	2	0	0	0	0	0	Q62012	
ENSMUST00000178170						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178171						6	3	20	4	10	9	29	91	46	212	39		
ENSMUST00000178172						2	0	0	0	1	0	0	0	0	3	0		
ENSMUST00000178173						2	1	0	0	7	2	0	0	0	0	0		
ENSMUST00000178174	ENSMUSG00000095139	4	22482780	22488366	-1	85	41	313	722	99	42	0	5	1	0	5		P31360
ENSMUST00000178178	ENSMUSG00000095384	14	43342383	43347811	-1	0	0	14	16	0	4	0	0	0	0	0	Q9DAR5	
ENSMUST00000178179	ENSMUSG00000094690	17	45732864	45733844	-1	6	0	7	36	4	4	0	0	0	0	0	Q9DAX4	
ENSMUST00000178180						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178181	ENSMUSG00000096122	Y	57531412	57533744	-1	6	0	9	5	21	3	0	0	0	0	0	Q5FWD5	
ENSMUST00000178182	ENSMUSG00000078875	2	177000956	177017787	1	0	0	0	0	0	0	0	0	0	0	0	J3KMS2	
ENSMUST00000178184	ENSMUSG00000092165	14	44556795	44562827	-1	1	0	0	0	0	2	0	0	0	0	0	J3QK24	
ENSMUST00000178185						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000178186						26	35	9	26	28	6	0	2	2	2	0		
ENSMUST00000178188	ENSMUSG00000023153	4	155469114	155470858	1	4	1	4	1	0	0	0	0	0	0	1	J3QNP8	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000178192	ENSMUSG00000093996	4	42318334	42323929	1	0	2	0	0	0	0	0	1	2	0	0		A2APU8
ENSMUST00000178195	ENSMUSG00000046634	11	8826708	8973266	-1	0	23	0	13	21	7	0	5	1	0	0	A0A0A0MQP1	
ENSMUST00000178196	ENSMUSG00000100448	X	9350627	9351136	1	0	0	0	3	0	1	1	0	0	0	2	J3QP08	
ENSMUST00000178198	ENSMUSG00000093993	Y	65377690	65403917	1	0	0	0	0	0	0	0	0	0	0	0	J3QNV4	
ENSMUST00000178199	ENSMUSG00000094874	GL456221.1	30394	32306	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178202	ENSMUSG00000001036	11	61517249	61579687	-1	20	21	0	0	14	0	0	0	0	0	0		Q8CHU3
ENSMUST00000178204	ENSMUSG00000026414	1	135836354	135852260	1	0	0	3	0	0	0	0	0	0	0	0	J3QQ13	
ENSMUST00000178205						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178207	ENSMUSG00000054676	7	38183217	38197568	1	0	0	0	0	12	0	0	0	0	0	0		
ENSMUST00000178209	ENSMUSG00000096283	7	22050599	22051504	-1	0	0	0	0	0	0	0	0	0	0	0	J3QK59	
ENSMUST00000178211	ENSMUSG00000079005	2	151098245	151103818	1	1	0	0	0	0	0	0	0	0	0	0	A2AQX6	
ENSMUST00000178213						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178215	ENSMUSG00000095619	7	22761697	22762590	1	0	0	0	0	0	0	0	0	0	0	0	E9Q069	
ENSMUST00000178218						463	487	317	511	305	129	9	40	38	9	50		
ENSMUST00000178219	ENSMUSG00000095558	X	34160003	34161499	-1	0	13	0	0	19	0	0	0	0	0	0	A2BFZ7	
ENSMUST00000178220	ENSMUSG00000095295	14	5501674	5522927	1	2	0	0	1	0	0	0	0	0	0	0	A6NAT8	
ENSMUST00000178221	ENSMUSG00000095388	3	98552542	98588807	-1	0	0	0	0	0	0	0	0	0	0	0		Q61767
ENSMUST00000178224	ENSMUSG00000094910	12	105453856	105493095	1	114	61	240	455	152	69	3	4	1	1	12	J3QPM6	
ENSMUST00000178226	ENSMUSG00000052331	1	54645340	54926387	-1	0	0	0	0	2	0	41	57	489	15	533	J3QK13	
ENSMUST00000178227						53	53	55	92	52	31	0	0	0	0	0		
ENSMUST00000178228	ENSMUSG00000045912	10	79606857	79614025	-1	116	45	432	121	119	44	0	2	1	0	1		Q5HZI2
ENSMUST00000178229	ENSMUSG00000094164	12	113611187	113611617	-1	7	8	13	2	4	2	0	2	3	1	12	A0A075B696	
ENSMUST00000178230	ENSMUSG00000096250	12	113461369	113461385	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178231	ENSMUSG00000035370	10	80602880	80615783	1	40	18	87	90	48	14	8	34	21	0	28		Q6PAT0
ENSMUST00000178232						0	2	8	0	0	1	0	0	0	0	0		
ENSMUST00000178234	ENSMUSG00000094294	Y	21164570	21166905	1	0	0	0	0	0	0	0	0	0	0	0	Q5FWB5	
ENSMUST00000178235	ENSMUSG00000006299	1	74279840	74284738	-1	4	0	9	0	5	1	478	444	226	54	167	J3QN89	
ENSMUST00000178236	ENSMUSG00000094995	9	35645117	35648202	-1	2	5	1	4	7	4	0	0	0	0	0		B3GLJ3
ENSMUST00000178238	ENSMUSG00000023153	4	155469114	155470858	1	0	0	0	0	7	0	0	0	0	0	0	B7ZN39	
ENSMUST00000178241	ENSMUSG00000048489	6	116650609	116652794	1	12	11	24	20	21	13	3	3	3	2	4		Q8K2F3
ENSMUST00000178243						0	0	13	4	11	0	0	0	0	0	0		
ENSMUST00000178244						41	35	156	68	31	25	10	10	12	5	12		
ENSMUST00000178245	ENSMUSG00000020817	11	70844778	70943105	1	0	1	0	0	0	1	14	0	0	6	74		O35551
ENSMUST00000178247						7	3	14	9	8	3	0	0	0	0	0		
ENSMUST00000178248						12	20	12	14	23	6	0	0	0	0	0		
ENSMUST00000178251	ENSMUSG00000096183	14	7255889	7264714	-1	2	0	0	0	1	0	0	0	0	0	0	J3QM54	
ENSMUST00000178252	ENSMUSG00000095495	14	52920443	52921112	1	0	0	0	0	0	0	1	0	0	1	1	A0A075B695	
ENSMUST00000178253	ENSMUSG00000040667	11	70943058	70969973	-1	5	3	14	35	9	7	6	6	6	0	7	J3QNZ2	
ENSMUST00000178254	ENSMUSG00000018293	11	70651850	70654644	-1	4	0	0	31	20	0	148	7682	54	99	282	J3QMC2	
ENSMUST00000178255						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178256	ENSMUSG00000096793	14	3810074	3966518	1	0	0	0	0	0	0	0	0	0	0	0	E9Q7N1	
ENSMUST00000178257	ENSMUSG00000030546	7	79720218	79732903	-1	0	0	0	92	0	14	0	0	0	0	1		Q8CGN5
ENSMUST00000178258	ENSMUSG00000094053	7	31703779	31705757	-1	0	0	0	0	0	1	0	0	0	0	0	D3YYY1	
ENSMUST00000178259						0	0	20	0	0	0	0	0	0	1	0		
ENSMUST00000178260						3	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000178261	ENSMUSG00000048031	3	87435773	87500678	1	0	0	0	0	0	0	0	0	0	0	0	J3QJU0	
ENSMUST00000178263						34	23	124	41	23	15	0	0	0	0	2		
ENSMUST00000178267	ENSMUSG00000041528	9	108051534	108083346	-1	0	0	0	0	0	0	0	3	0	24	68		Q5XPI3
ENSMUST00000178271	ENSMUSG00000094870	13	119765187	119790805	-1	7	4	9	9	14	2	107	677	295	233	211		Q8K3J5
ENSMUST00000178274	ENSMUSG00000095686	14	3998394	4007006	1	3	0	5	1	2	0	0	0	0	0	0	J3QPA5	
ENSMUST00000178276	ENSMUSG00000031565	8	25513654	25575714	1	0	0	0	8	0	0	0	0	0	0	0		P16092
ENSMUST00000178280						813	907	2729	580	1164	474	18	65	27	20	53		
ENSMUST00000178282	ENSMUSG00000095079	12	113254830	113260236	-1	0	3	5	0	10	0	43	29	20	122	1122	A0A075B6A3	
ENSMUST00000178284						3	2	56	0	4	0	0	0	0	0	0		
ENSMUST00000178288						4	3	0	0	7	4	0	0	0	0	0		
ENSMUST00000178289	ENSMUSG00000039182	13	14630245	14638202	1	0	3	0	0	8	0	0	78	20	3	15		Q91WD4
ENSMUST00000178291	ENSMUSG00000094741	GL456354.1	6366	8939	1	0	0	6	0	0	0	0	0	0	0	0		
ENSMUST00000178292						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178293	ENSMUSG00000046269	X	7371276	7375830	-1	17	17	74	23	19	13	2	4	2	0	6		Q8CEG8
ENSMUST00000178294						1	2	4	1	7	1	0	2	0	1	0		
ENSMUST00000178296	ENSMUSG00000096728	GL456354.1	158543	161339	1	0	4	4	0	0	4	0	0	0	0	0		
ENSMUST00000178301	ENSMUSG00000096803	12	88018337	88018771	-1	0	1	0	0	0	0	0	0	0	0	0	J3QPI8	
ENSMUST00000178303	ENSMUSG00000095194	9	39046614	39047549	-1	2	2	0	0	2	1	0	0	0	0	0	J3KMV2	
ENSMUST00000178304						0	1	1	4	3	2	0	0	0	0	0		
ENSMUST00000178308	ENSMUSG00000090643	14	5970744	5979137	-1	5	0	0	0	0	0	0	0	0	0	0	J3QK53	
ENSMUST00000178309	ENSMUSG00000095500	GL456221.1	32239	47294	1	0	0	0	1	0	0	0	0	0	0	1		
ENSMUST00000178310	ENSMUSG00000038274	19	6057888	6059524	1	15	0	25	0	0	0	696	1103	433	1735	355	Q642K5	
ENSMUST00000178312	ENSMUSG00000094472	16	15317458	15318957	1	12155	13090	150010	18356	10548	6138	44	99	63	7	88	J3KMP5	
ENSMUST00000178313						0	2	3	0	0	0	0	0	0	0	0		
ENSMUST00000178315						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178316	ENSMUSG00000090215	7	104300230	104336909	1	0	0	0	0	1	0	0	0	0	18	19	K7N6K2	
ENSMUST00000178317						11	3	20	11	6	6	0	0	0	0	0		
ENSMUST00000178318	ENSMUSG00000095763	JH584299.1	806210	809281	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178319	ENSMUSG00000094116	4	73622984	73627027	1	41	0	10	0	0	0	0	0	0	0	0	F2Z3W5	
ENSMUST00000178320	ENSMUSG00000004460	16	22857845	22879634	1	0	2	0	6	0	1	0	0	0	0	0		Q99KV1
ENSMUST00000178323						0	0	0	2	0	1	0	0	0	0	0		
ENSMUST00000178324	ENSMUSG00000031478	8	22128283	22166435	-1	9	0	12	0	13	3	8	17	12	8	9		Q9R0A5
ENSMUST00000178325	ENSMUSG00000094125	2	83955693	83958185	1	0	0	0	3	0	0	0	1	1	0	0	J3QNR0	
ENSMUST00000178327	ENSMUSG00000094855	JH584299.1	921942	924675	1	4	8	16	20	29	2	0	0	0	0	0		
ENSMUST00000178328	ENSMUSG00000019528	3	20122084	20155317	-1	9	0	34	0	0	0	3144	14085	4182	1661	1897		Q9R062
ENSMUST00000178330	ENSMUSG00000095074	5	94526287	94546423	1	4	2	0	0	0	0	0	0	0	0	0	J3QK78	
ENSMUST00000178332	ENSMUSG00000094354	Y	40380441	40381523	-1	76	43	65	152	59	32	0	0	0	0	0	J3QN86	
ENSMUST00000178335	ENSMUSG00000095505	JH584296.1	195181	197903	-1	4	4	19	11	0	0	0	0	0	0	0		
ENSMUST00000178336	ENSMUSG00000005763	1	165788681	165877277	1	0	0	0	0	0	0	0	0	0	0	0	J3QMU3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000178337	ENSMUSG00000096550	JH584299.1	477246	480331	1	0	0	0	0	0	0	0	0	0	0	0	Q3UL49	
ENSMUST00000178340	ENSMUSG00000032860	7	100996572	101011991	-1	0	13	11	80	16	1	290	141	255	4	217		
ENSMUST00000178341						0	29	0	0	32	0	0	0	0	0	0		
ENSMUST00000178342	ENSMUSG00000094802	X	154001590	154012640	-1	0	0	0	2	1	0	0	0	0	0	0	A2BED8	
ENSMUST00000178343	ENSMUSG00000095041	JH584304.1	52190	59690	-1	1213	925	2850	1603	1466	742	274	1659	352	63	724		
ENSMUST00000178344	ENSMUSG00000095115	7	118485114	118491975	-1	61	39	250	1083	71	35	591	1581	1212	111	814		Q3UV16
ENSMUST00000178345						23	15	79	31	21	11	0	0	0	0	0		
ENSMUST00000178347	ENSMUSG00000099518	4	88794487	88795035	1	0	1	0	0	0	0	0	0	0	0	0	B1AYI8	
ENSMUST00000178348	ENSMUSG00000096385	9	3003346	3006948	1	8222	9140	12011	8893	9246	6571	0	4	0	0	0	J3QK61	
ENSMUST00000178349	ENSMUSG00000095821	13	120317567	120318076	1	4	4	7	0	3	2	0	0	0	0	0	O70518	
ENSMUST00000178352						0	13	0	29	0	6	0	0	0	0	0		
ENSMUST00000178353	ENSMUSG00000096370	19	4742913	4811612	-1	6	9	38	52	9	3	4	12	8	1	3	J3QN51	
ENSMUST00000178355	ENSMUSG00000095789	5	129908540	129913789	1	25	21	38	81	35	18	1	6	5	1	6		Q497P3
ENSMUST00000178356						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000178359						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178361						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178363	ENSMUSG00000018566	11	69942539	69948188	-1	0	1	3	0	0	0	0	0	0	0	0	J3QMU2	
ENSMUST00000178364						8	2	19	2	13	4	9	9	13	2	33		
ENSMUST00000178365						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000178369						0	1	6	2	0	0	0	0	0	0	1		
ENSMUST00000178371						3	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000178372	ENSMUSG00000050064	3	98382461	98753812	1	14	30	43	389	54	0	2	0	0	0	4	G5E8C0	
ENSMUST00000178374	ENSMUSG00000096223	Y	9413518	9416148	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNZ6	
ENSMUST00000178376	ENSMUSG00000096869	14	7116798	7125412	-1	0	0	0	0	0	0	0	0	0	0	0	J3QN10	
ENSMUST00000178377						0	1	1	0	1	2	8	0	28	0	0		
ENSMUST00000178379						2	2	0	2	0	0	0	0	0	0	0		
ENSMUST00000178380						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178382						0	2	2	4	7	0	17	61	13	0	25		
ENSMUST00000178383	ENSMUSG00000023175	10	79704491	79711969	1	0	0	0	0	0	0	0	0	22	0	0	J3QP71	
ENSMUST00000178384	ENSMUSG00000096458	12	102742230	102743661	-1	0	0	0	12	0	0	3	99	73	0	74		Q9ERH6
ENSMUST00000178385	ENSMUSG00000030629	7	84615054	84679361	-1	0	2	3	8	0	5	836	2021	707	547	408		Q9DCH6
ENSMUST00000178386	ENSMUSG00000090764	14	4165030	4173503	1	0	0	3	0	0	2	0	0	0	0	0	J3QM98	
ENSMUST00000178389	ENSMUSG00000090827	14	4983935	4992409	1	0	0	4	0	5	0	0	0	0	0	0	J3QNT1	
ENSMUST00000178391	ENSMUSG00000096597	18	80089297	80089962	-1	1	2	4	12	9	2	0	0	0	0	0	J3QJU9	
ENSMUST00000178392	ENSMUSG00000096218	14	3884172	3921640	1	0	0	0	0	0	0	0	0	0	0	0	Q9D9B9	
ENSMUST00000178395	ENSMUSG00000101337	1	46425592	46807476	1	0	1	0	0	0	1	0	0	0	0	0	F6QYG9	
ENSMUST00000178396	ENSMUSG00000095324	Y	8069168	8071507	-1	0	0	0	0	0	0	0	0	0	0	0	J3QM67	
ENSMUST00000178399	ENSMUSG00000022221	14	55784996	55788857	-1	0	0	0	0	4	0	0	0	0	1	0	E9PZP3	
ENSMUST00000178400	ENSMUSG00000022701	16	43889800	43964314	1	0	0	0	0	0	4	0	8	28	18	14	J3QQ27	
ENSMUST00000178401	ENSMUSG00000095325	17	32879228	32886083	-1	64	63	93	49	92	27	7	55	11	16	30	J3QMA4	
ENSMUST00000178402	ENSMUSG00000075598	5	138053194	138066537	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSF2	
ENSMUST00000178403						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178404	ENSMUSG00000096370	19	4742913	4811612	-1	5	5	5	0	1	2	0	43	12	0	10	J3QQ01	
ENSMUST00000178408						58	48	475	142	54	31	0	2	0	0	7		
ENSMUST00000178410	ENSMUSG00000032503	9	112065091	112235938	-1	15	25	35	0	25	0	0	0	0	0	0		Q9DCB4
ENSMUST00000178412						0	0	3	2	3	0	0	0	0	0	0		
ENSMUST00000178414	ENSMUSG00000096629	14	5607620	5807982	-1	8	13	5	6	13	10	0	0	0	0	0	J3QQ59	
ENSMUST00000178416	ENSMUSG00000094147	X	125435542	125436039	1	0	0	0	0	2	2	0	0	0	0	0	B6ZB74	
ENSMUST00000178418	ENSMUSG00000090512	14	5821934	5830329	-1	0	4	0	0	13	0	0	0	0	0	0	J3QM74	
ENSMUST00000178421	ENSMUSG00000021417	13	34977748	35027094	-1	0	4	0	11	0	0	0	0	0	0	0		Q9WUR2
ENSMUST00000178422	ENSMUSG00000034974	10	81183007	81193197	1	0	0	0	2	0	0	392	415	272	32	184	Q05A21	O54784
ENSMUST00000178425	ENSMUSG00000095659	X	34237049	34238733	-1	1	5	6	6	5	0	0	0	0	0	0		
ENSMUST00000178426	ENSMUSG00000096478	14	52792316	52792777	1	1	1	1	0	2	0	4	0	2	0	0	A0A075B699	
ENSMUST00000178427						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000178428	ENSMUSG00000093883	Y	13465037	13465579	-1	1	0	84	2	3	4	0	0	0	0	0	J3QMH4	
ENSMUST00000178429	ENSMUSG00000094578	14	5484207	5492584	1	13	11	0	11	0	0	0	0	0	0	0	J3QJZ7	
ENSMUST00000178433						4	15	0	0	14	8	1	0	0	0	0		
ENSMUST00000178436						0	1	0	4	0	1	0	0	0	0	0		
ENSMUST00000178437						5	0	1	6	3	0	0	0	0	0	0		
ENSMUST00000178438	ENSMUSG00000095294	8	20615097	20639412	1	27	16	16	0	7	0	0	0	0	0	0	Q8C646	
ENSMUST00000178439						2	2	3	1	1	0	0	2	0	0	0		
ENSMUST00000178440	ENSMUSG00000041890	5	114727407	114775517	-1	0	0	0	0	0	0	0	0	0	0	0	J3QK07	
ENSMUST00000178443	ENSMUSG00000095199	2	176521056	176532479	1	0	0	1	0	1	1	0	0	5	2	0	A2ART2	
ENSMUST00000178444	ENSMUSG00000094352	X	31381959	31383918	-1	0	0	5	0	0	0	0	0	0	0	0	A2CG71	
ENSMUST00000178445	ENSMUSG00000031723	8	109565892	109574051	1	2	0	0	5	0	0	0	82	0	0	0		Q8BUH1
ENSMUST00000178446	ENSMUSG00000096178	Y	90401248	90433263	1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000178447	ENSMUSG00000094484	Y	7165068	7169293	-1	0	0	0	0	0	0	0	0	0	0	0	J3QK38	
ENSMUST00000178451	ENSMUSG00000095403	8	20550331	20581999	1	55	18	19	56	56	0	38	279	207	153	195	J3QPW4	
ENSMUST00000178455						0	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000178457	ENSMUSG00000095474	X	123581700	123602134	1	0	0	0	0	0	0	0	0	0	0	0	J3QNM1	
ENSMUST00000178458	ENSMUSG00000094328	3	94047981	94054885	-1	0	0	4	0	0	0	0	0	0	0	0		P0DMR6
ENSMUST00000178459	ENSMUSG00000094115	X	33234869	33235393	1	0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000178462	ENSMUSG00000020964	12	91806043	91849157	-1	16	19	0	5	22	0	0	785	0	0	0	J3QJX3	
ENSMUST00000178465	ENSMUSG00000095576	1	162916551	162937515	-1	4	10	0	0	0	0	0	0	0	0	0	J3QMN6	
ENSMUST00000178466	ENSMUSG00000095666	JH584296.1	41338	44417	-1	4	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000178467	ENSMUSG00000021198	12	102948859	103184065	1	2	1	1	0	0	0	0	0	0	0	0	J3QMH8	
ENSMUST00000178471	ENSMUSG00000094044	X	124500563	124501060	1	0	0	0	0	2	2	0	0	0	0	0	B6ZB74	
ENSMUST00000178472						66	66	127	81	84	47	0	0	0	0	3		
ENSMUST00000178473	ENSMUSG00000073684	4	155249802	155256687	1	0	2	0	0	0	0	157	268	97	34	111		Q3UN58
ENSMUST00000178474	ENSMUSG00000026341	1	125392905	125435727	-1	0	0	0	65	19	2	8374	23935	9198	2422	6667	Q3ULF7	Q99JY9
ENSMUST00000178477	ENSMUSG00000001496	12	56531958	56536908	-1	45	20	81	1887	69	26	2	1	0	1	1		P50220
ENSMUST00000178480	ENSMUSG00000100234	4	88788632	88789180	1	0	0	0	0	0	0	0	0	0	0	0	Q8CD73	
ENSMUST00000178483	ENSMUSG00000095592	12	113464524	113464552	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDD5	
ENSMUST00000178485	ENSMUSG00000039174	3	124556352	124581101	-1	2	2	0	0	0	0	0	1	0	0	0	J3QNW2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000178486	ENSMUSG00000048154	15	98831669	98871204	-1	7	120	452	21	0	0	374	1258	684	89	119		Q6PDK2
ENSMUST00000178487	ENSMUSG00000096045	5	25982030	25988650	-1	7	2	0	9	7	0	0	0	0	0	0	J3QK71	
ENSMUST00000178488						0	0	1	3	3	1	0	0	0	0	0		
ENSMUST00000178489	ENSMUSG00000095409	4	143511343	143517831	1	6	9	0	0	0	0	0	0	0	0	0	Q4FZF9	
ENSMUST00000178498	ENSMUSG00000095540	17	40598594	40602618	1	0	0	2	0	0	1	0	0	0	0	0	A8R0T8	
ENSMUST00000178500						15	7	8	4	2	1	0	0	0	0	0		
ENSMUST00000178504	ENSMUSG00000027546	2	168634438	168742409	-1	0	0	0	14	0	0	0	0	0	0	0		O70228
ENSMUST00000178505	ENSMUSG00000096902	Y	72220863	72247118	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNI1	
ENSMUST00000178508	ENSMUSG00000051054	13	59740842	59746752	-1	0	2	1	0	0	0	0	0	0	0	0	J3QNP7	
ENSMUST00000178509	ENSMUSG00000094437	9	44464243	44464602	1	0	4	10	0	0	0	133	588	316	954	203		Q9CQY2
ENSMUST00000178510	ENSMUSG00000096284	13	119893388	119894785	-1	15	7	10	7	9	4	0	1	0	0	1	O70619	
ENSMUST00000178514	ENSMUSG00000031486	8	27085583	27123436	1	0	0	7	333	66	0	9	0	0	4	2	J3QMG7	
ENSMUST00000178515	ENSMUSG00000019178	5	135747220	135778385	-1	0	0	10	23	23	0	3	8	8	0	8	Q9DAG7	
ENSMUST00000178519	ENSMUSG00000095462	Y	13348521	13349063	-1	0	0	22	0	0	0	0	0	0	0	0	A8HG57	
ENSMUST00000178522	ENSMUSG00000009035	15	79360684	79403303	-1	18	16	72	90	41	13	2787	1987	648	44	149		Q8BG09
ENSMUST00000178523	ENSMUSG00000035171	19	21581202	21652976	-1	0	3	2	8	0	2	0	2	0	0	0	J3QQ03	
ENSMUST00000178524	ENSMUSG00000094421	8	20828015	20835070	1	40	0	70	64	36	26	0	0	0	0	2	J3QN60	
ENSMUST00000178526	ENSMUSG00000030638	7	82173840	82307419	1	2	0	0	0	3	0	0	0	0	1	0	J3QK75	
ENSMUST00000178528	ENSMUSG00000095452	Y	40804914	40807356	1	0	0	0	0	0	0	0	0	0	0	0	J3QP49	
ENSMUST00000178531	ENSMUSG00000094511	Y	3326750	3345329	-1	0	0	0	0	0	0	0	0	0	0	0	J3QK27	
ENSMUST00000178532	ENSMUSG00000096697	17	39073691	39077037	-1	0	2	1	1	1	0	0	0	0	0	0	A8R0V5	
ENSMUST00000178533	ENSMUSG00000096337	2	83978933	83981425	1	7	7	16	6	9	4	0	0	0	0	0	A2AK42	
ENSMUST00000178534	ENSMUSG00000030850	7	130391526	130519961	-1	0	0	0	17	0	0	0	0	26	2	25	J3QNU1	
ENSMUST00000178537	ENSMUSG00000095668	6	41533201	41533212	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178539	ENSMUSG00000093812	9	102739648	102756685	1	11	6	16	10	10	4	0	0	0	0	0	Q3V3D0	
ENSMUST00000178542						1	1	1	1	3	3	0	0	0	0	0		
ENSMUST00000178543	ENSMUSG00000020366	11	49846751	49886421	1	0	0	15	26	0	5	0	0	0	0	0		Q9WTU6
ENSMUST00000178545	ENSMUSG00000095407	17	68837136	68843138	1	21	11	29	405	32	8	0	0	0	0	0	J3QK46	
ENSMUST00000178547						0	0	69	0	11	0	0	0	0	0	0		
ENSMUST00000178549	ENSMUSG00000095897	12	113466027	113466043	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178552	ENSMUSG00000096139	5	95731789	95736173	-1	17	4	4	20	17	4	0	0	0	0	0	Q6P8K3	
ENSMUST00000178553	ENSMUSG00000095108	X	123704324	123704791	-1	16	21	109	42	30	3	0	0	0	0	0	J3QNF7	
ENSMUST00000178555	ENSMUSG00000029673	5	131437333	132543344	-1	0	0	0	39	0	0	0	0	0	0	0	J3QNT9	
ENSMUST00000178556	ENSMUSG00000095979	Y	49571156	49597425	1	0	0	0	0	0	0	0	0	0	0	0	J3QNI1	
ENSMUST00000178557						3	10	51	8	11	2	800	1094	837	4155	592		
ENSMUST00000178558						0	0	0	0	2	0	19	22	11	5	0		
ENSMUST00000178559	ENSMUSG00000096120	Y	41406498	41407040	1	0	0	0	0	2	0	0	0	0	0	0	J3QMJ9	
ENSMUST00000178561	ENSMUSG00000035539	4	45890303	45950774	1	28	21	68	16	16	0	0	0	0	0	0	J3QNE4	
ENSMUST00000178562	ENSMUSG00000024340	17	34354822	34369493	1	0	11	29	28	0	6	6	0	5	6	0	J3QP12	
ENSMUST00000178563	ENSMUSG00000096687	10	39890018	39899238	-1	6	0	0	218	19	3	0	0	0	10	8	J3QPW5	
ENSMUST00000178564	ENSMUSG00000021431	13	38204939	38227663	1	2	0	4	45	2	2	7	83	18	91	32	J3QMA8	
ENSMUST00000178567	ENSMUSG00000000318	11	70156197	70170834	1	0	0	0	0	2	0	0	2	0	2	0	A2CF63	
ENSMUST00000178569	ENSMUSG00000095019	JH584303.1	81607	82689	1	44	37	47	133	57	25	0	0	0	0	0		
ENSMUST00000178571						2	2	5	2	1	1	0	0	0	1	0		
ENSMUST00000178572	ENSMUSG00000095266	17	24023859	24024182	1	3	0	1	2	3	1	0	0	0	0	0	J3QPL3	
ENSMUST00000178573	ENSMUSG00000022787	16	32247227	32257083	1	5	0	6	17	0	0	36	155	94	182	63		Q9DB94
ENSMUST00000178577	ENSMUSG00000090487	14	3030002	3038762	1	0	0	5	0	0	0	0	0	0	0	0	J3QPI7	
ENSMUST00000178578						5	3	4	0	0	1	0	0	0	0	0		
ENSMUST00000178581	ENSMUSG00000096380	10	77798387	77799133	-1	13	13	65	29	25	13	0	0	0	0	0	J3QMD1	
ENSMUST00000178585						0	5	3	0	2	3	0	0	0	0	0		
ENSMUST00000178589						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178590	ENSMUSG00000035818	19	56461637	56486729	1	8	6	12	10	10	6	8	0	34	6	5		Q8BW88
ENSMUST00000178591	ENSMUSG00000095363	7	22713611	22719710	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UTA8	
ENSMUST00000178594	ENSMUSG00000090707	14	5857918	5880382	-1	9	10	17	5	7	8	0	0	0	0	0	J3QN62	
ENSMUST00000178595	ENSMUSG00000094904	X	11308824	11309141	1	0	2	0	0	0	0	0	0	0	0	0	Q5M8Q2	
ENSMUST00000178597	ENSMUSG00000094845	11	69876684	69878018	-1	2	2	9	5	2	2	6	15	3	1	8		P0DJF3
ENSMUST00000178598						15	19	42	44	15	17	312	570	279	90	241		
ENSMUST00000178599	ENSMUSG00000093903	Y	13252442	13378804	1	0	0	0	0	0	0	0	0	0	0	0	J3QPX2	
ENSMUST00000178600						2	3	0	2	0	5	0	0	0	0	0		
ENSMUST00000178601	ENSMUSG00000074812	2	128591209	128598464	1	0	0	0	2	2	0	0	0	1	0	0	J3KMS1	
ENSMUST00000178602	ENSMUSG00000099420	4	88797397	88797945	1	0	0	0	0	0	0	0	0	0	0	0	Q8CD73	
ENSMUST00000178603	ENSMUSG00000095672	GL456211.1	160465	162404	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178604						10	4	14	24	13	3	0	0	0	0	0		
ENSMUST00000178605	ENSMUSG00000000420	18	24205344	24286818	1	16	17	0	0	0	13	372	1492	740	562	610		O08912
ENSMUST00000178611	ENSMUSG00000006057	11	96068852	96075670	-1	92	105	35	73	97	67	0	0	0	0	0		Q9CR84
ENSMUST00000178614	ENSMUSG00000096035	5	91987475	91995320	1	3	6	11	6	7	6	1	4	4	6	5	J3QNT8	
ENSMUST00000178615	ENSMUSG00000094936	19	4784293	4793901	-1	0	0	0	0	0	0	1	23	0	18	17	Q5CZX8	
ENSMUST00000178617						1	2	6	3	6	4	0	0	0	0	0		
ENSMUST00000178618	ENSMUSG00000095609	13	120034759	120035331	-1	2	3	0	7	3	1	45	146	54	51	49	Q3T9V6	
ENSMUST00000178621	ENSMUSG00000095716	X	3750934	3752885	-1	0	0	0	0	1	7	0	0	0	0	0	A2CG92	
ENSMUST00000178622	ENSMUSG00000020409	11	43433744	43447981	1	15	11	23	12	25	3	0	1000	0	0	0		Q8BHJ9
ENSMUST00000178623	ENSMUSG00000094706	14	7580617	7595592	-1	0	0	0	0	0	0	0	0	0	0	0	K7N692	
ENSMUST00000178627	ENSMUSG00000034343	1	91250304	91290337	1	3	1	0	0	0	0	176	582	170	243	123		Q9CY34
ENSMUST00000178630	ENSMUSG00000094219	19	47151609	47157764	-1	10	7	16	52	11	5	0	0	0	0	0	J3QMI4	
ENSMUST00000178631	ENSMUSG00000029155	5	73651379	73679512	1	6	7	0	0	0	0	0	0	0	0	0	J3QPR5	
ENSMUST00000178632	ENSMUSG00000046432	X	136270253	136271978	1	0	0	0	5	0	0	0	0	0	0	0		Q9WTZ9
ENSMUST00000178636	ENSMUSG00000037331	11	58009064	58062034	1	34	19	117	160	0	21	427	827	958	93	950		Q6ZQ58
ENSMUST00000178637						22	15	65	45	19	7	14	76	26	8	31		
ENSMUST00000178639	ENSMUSG00000094181	Y	44232123	44264444	-1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000178641	ENSMUSG00000096736	9	3034599	3035805	1	3081	3244	3528	2454	3500	2628	3	0	2	0	0	J3KMR8	
ENSMUST00000178644	ENSMUSG00000094439	4	139603186	139662691	1	20	9	33	7	4	4	3	0	0	0	0	J3QJZ1	
ENSMUST00000178645	ENSMUSG00000094514	GL456211.1	226405	229375	-1	2	3	0	0	1	1	0	3	0	0	0		
ENSMUST00000178646	ENSMUSG00000096742	5	94988626	95026536	1	0	11	6	0	8	7	0	0	0	0	0	Q8C6L9	
ENSMUST00000178647						3	3	2	2	2	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000178650	ENSMUSG00000095756	14	53007612	53008098	1	1	0	3	0	6	0	0	0	2	1	0	A0A075B6B0	
ENSMUST00000178654	ENSMUSG00000092244	17	38554192	38560621	1	0	0	0	0	0	0	0	0	0	0	0	A8R0W6	
ENSMUST00000178655	ENSMUSG00000096337	2	83978933	83981425	1	0	0	0	3	0	0	0	1	1	0	0	J3QNR0	
ENSMUST00000178657						11	5	36	7	10	12	2	28	8	19	21		
ENSMUST00000178658	ENSMUSG00000096330	13	98279887	98307154	1	0	2	0	0	4	0	0	0	0	0	0	J3QMM5	
ENSMUST00000178661						15	13	32	11	21	3	12	23	22	14	8		
ENSMUST00000178662						0	1	2	0	0	1	38	9	0	0	22		
ENSMUST00000178663						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178665	ENSMUSG00000017421	11	80383279	80405733	1	2	6	34	10	3	1	106	706	164	45	180		Q9JMD0
ENSMUST00000178666	ENSMUSG00000075028	2	92965151	93046167	-1	0	0	0	0	0	0	3	0	0	0	0		A2AGX3
ENSMUST00000178667						6	4	8	3	3	2	0	0	0	0	0		
ENSMUST00000178668	ENSMUSG00000037610	3	31902507	32200180	1	0	2	0	1	7	0	0	0	0	0	0		Q9CZM9
ENSMUST00000178669	ENSMUSG00000095860	Y	10553453	10553992	1	8	2	123	0	5	0	0	0	0	0	1	J3KMK6	
ENSMUST00000178670	ENSMUSG00000096039	14	3224440	3234351	1	0	0	0	0	0	0	0	0	0	0	0	Q8BGG1	
ENSMUST00000178672	ENSMUSG00000095887	X	28931821	28954702	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000178673	ENSMUSG00000095606	Y	52780040	52806254	1	0	0	0	0	0	0	0	0	0	0	0	J3QNV4	
ENSMUST00000178676						33	47	70	35	48	37	5146	21536	5697	2866	2273		
ENSMUST00000178678	ENSMUSG00000024534	18	52767709	52915935	1	0	0	0	0	0	0	0	0	0	0	0	G5E848	
ENSMUST00000178679	ENSMUSG00000094985	9	122747346	122802074	1	27	25	11	79	15	7	0	0	0	0	0		E5FYH1
ENSMUST00000178680						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178684	ENSMUSG00000020072	10	63024315	63077962	1	13	0	29	6	25	0	4	15	0	9	4		Q9DCG6
ENSMUST00000178685						22	21	75	24	25	23	10	43	12	3	8		
ENSMUST00000178686	ENSMUSG00000038612	3	95658788	95663176	1	0	0	0	44	1	0	0	0	408	91	0		P97287
ENSMUST00000178687	ENSMUSG00000094626	6	120488939	120493807	-1	34	21	94	585	47	21	5	8	2	0	5	B2RQD1	Q99MX7
ENSMUST00000178689	ENSMUSG00000094227	Y	13941738	13942280	1	0	1	0	2	1	0	0	0	0	0	0	J3QPV5	
ENSMUST00000178691	ENSMUSG00000015290	X	74365718	74373218	-1	1	0	3	45	0	2	108	69	54	43	28	Q3UK94	P21126
ENSMUST00000178693	ENSMUSG00000093806	X	170672644	170678054	1	0	0	0	106	8	4	0	1	0	0	2		
ENSMUST00000178694	ENSMUSG00000040632	14	55518978	55524981	-1	0	0	0	357	0	0	1	8	0	0	1	Q543Y0	P54846
ENSMUST00000178695	ENSMUSG00000103335	3	93284302	93285078	1	0	13	134	1396	54	0	0	0	0	0	0	A0A0A6YW46	
ENSMUST00000178696	ENSMUSG00000030170	6	119432531	119544347	-1	0	0	0	68	0	0	0	0	0	0	0		P22726
ENSMUST00000178697	ENSMUSG00000057963	12	102568582	102704930	-1	2	2	4	20	5	2	0	1	0	0	1	J3QPF8	
ENSMUST00000178698	ENSMUSG00000094802	X	154001590	154012640	-1	0	1	0	1	1	2	0	0	0	0	0	A2BED8	
ENSMUST00000178700	ENSMUSG00000040836	1	165295789	165326745	1	45	18	36	39	50	22	1	11	3	1	8		B2RPY5
ENSMUST00000178704	ENSMUSG00000020182	11	11814101	11898144	-1	0	0	0	0	0	4	0	0	0	0	0	Q5SUV8	O88533
ENSMUST00000178707						0	0	0	22	13	0	0	0	0	0	0		
ENSMUST00000178708						2	3	0	2	0	0	0	5	2	7	2		
ENSMUST00000178710	ENSMUSG00000064302	1	118389058	118612678	1	0	0	6	18	8	0	0	145	68	55	0	J3QP81	
ENSMUST00000178711	ENSMUSG00000091740	14	41747282	41750595	-1	0	0	0	0	0	5	0	0	0	0	0	J3QM56	
ENSMUST00000178715	ENSMUSG00000094886	13	49945096	49945335	-1	2	1	1	0	1	0	0	0	0	0	0	J3QMQ2	
ENSMUST00000178717						0	2	6	0	10	0	0	0	0	0	0		
ENSMUST00000178719						6	2	2	1	0	2	0	0	0	0	0		
ENSMUST00000178721	ENSMUSG00000031505	8	11497506	11514960	1	0	0	0	0	0	0	4	7	0	1	0	J3QN06	
ENSMUST00000178722	ENSMUSG00000096574	14	3332627	3354799	1	0	7	0	0	4	7	0	0	0	0	0	E9PZI7	
ENSMUST00000178723	ENSMUSG00000096646	JH584293.1	86316	87710	-1	0	0	28	19	0	8	0	0	0	0	0		
ENSMUST00000178724						312	293	515	479	484	229	5	12	7	9	18		
ENSMUST00000178725	ENSMUSG00000078773	4	11558922	11615805	1	0	3	0	0	1	3	0	0	0	0	3	J3QN23	
ENSMUST00000178727						0	0	0	10	0	0	20	0	17	8	6		
ENSMUST00000178728	ENSMUSG00000095195	14	3428103	3594220	1	0	27	0	0	4	0	0	0	0	0	0	E9PVJ0	
ENSMUST00000178730	ENSMUSG00000059456	14	66153257	66281052	-1	0	0	0	0	0	0	1345	2027	721	104	985	K7QD41	Q9QVP9
ENSMUST00000178732						4	4	20	7	9	4	0	0	0	0	0		
ENSMUST00000178733						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178735	ENSMUSG00000079342	19	33775521	33787462	-1	7	5	29	8	6	4	0	0	0	0	0	J3QME6	
ENSMUST00000178737						30	15	0	14	6	10	0	0	0	0	0		
ENSMUST00000178743						0	9	3	0	4	2	1	0	0	0	0		
ENSMUST00000178744	ENSMUSG00000079144	1	193168046	193177832	1	1	69	139	312	108	60	21	67	35	12	62		Q9DAE8
ENSMUST00000178745	ENSMUSG00000095546	X	27472031	27494882	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000178747	ENSMUSG00000093857	X	32047829	32049325	1	11	13	5	0	0	0	0	0	0	0	0	J3QN64	
ENSMUST00000178748	ENSMUSG00000094628	14	4726775	4747493	1	0	0	0	0	0	0	0	0	0	0	0	J3QPB3	
ENSMUST00000178750	ENSMUSG00000096083	11	62753100	62753498	1	1	3	0	1	3	0	0	0	0	0	0	J3QNV7	
ENSMUST00000178751	ENSMUSG00000095141	Y	60241202	60273250	1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000178752	ENSMUSG00000103777	3	93282826	93283581	1	33	23	184	2061	74	30	1	3	0	0	0	A0A0A6YVU7	
ENSMUST00000178756	ENSMUSG00000021221	12	83213745	83487716	-1	15	10	32	29	26	0	0	0	0	0	0		P58269
ENSMUST00000178757	ENSMUSG00000093805	1	93918311	93942650	1	22	18	51	20	20	22	6	14	10	3	5		Q6XQH0
ENSMUST00000178759	ENSMUSG00000091122	14	44583153	44588402	1	16	14	7	16	10	14	0	0	0	0	0	J3KMT2	
ENSMUST00000178760	ENSMUSG00000046572	5	38668484	38684826	-1	0	0	0	0	2	0	0	0	0	0	0	J3QNM2	
ENSMUST00000178761	ENSMUSG00000096666	Y	66739787	66742123	-1	0	0	0	0	0	0	0	0	0	0	0	Q5M8R5	
ENSMUST00000178764	ENSMUSG00000020827	11	70562881	70614483	1	0	0	0	0	0	0	7	0	0	0	4	J3QM71	
ENSMUST00000178765	ENSMUSG00000096271	GL456350.1	211325	212455	-1	0	8	0	0	15	5	0	0	0	0	0		P86792
ENSMUST00000178766						1	1	4	0	0	0	0	0	0	0	0		
ENSMUST00000178767	ENSMUSG00000096257	7	28756174	28758965	1	13	6	22	32	15	9	0	0	0	0	0	J3QPU5	
ENSMUST00000178768	ENSMUSG00000094023	14	52769753	52770392	1	0	0	2	5	6	2	0	1	0	6	2	Q5R1H9	
ENSMUST00000178772	ENSMUSG00000096140	17	43534174	43543639	-1	11	9	29	9	7	7	13	95	19	28	37	J3QNN4	
ENSMUST00000178773						2	2	0	0	0	0	0	0	10	0	4		
ENSMUST00000178774	ENSMUSG00000052146	17	27630422	27636629	-1	0	0	3	0	0	0	219	2684	1169	4467	959	Q5M9K7	P63325
ENSMUST00000178778						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000178779	ENSMUSG00000096036	Y	5942460	5945031	1	0	0	0	0	0	0	0	0	0	0	0	J3QMV3	
ENSMUST00000178781						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000178783						1	3	0	2	2	0	0	0	0	0	0		
ENSMUST00000178785	ENSMUSG00000095941	8	110109772	110111762	1	10	5	5	9	14	7	0	0	0	0	0	J3QNV0	
ENSMUST00000178787	ENSMUSG00000096734	9	124493731	124493793	-1	0	0	0	0	0	0	0	1	0	0	0	O88229	
ENSMUST00000178788	ENSMUSG00000094590	14	6638420	6684170	-1	0	0	0	0	0	0	0	0	0	0	0	J3QPM5	
ENSMUST00000178789	ENSMUSG00000095562	X	170009659	170019281	1	0	0	0	0	0	0	0	0	0	0	0	J3QM91	
ENSMUST00000178791						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000178794						3	3	2	1	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000178796	ENSMUSG00000019178	5	135747220	135778385	-1	0	0	0	5	0	0	3	6	4	28	7	J3QK74	
ENSMUST00000178797	ENSMUSG00000022885	16	23224740	23360350	1	0	11	31	0	13	0	97	105	3	45	120		Q64685
ENSMUST00000178798	ENSMUSG00000051497	11	110968033	111027968	1	0	19	0	62	23	0	0	0	0	0	0		Q9Z307
ENSMUST00000178799	ENSMUSG00000017412	2	52428320	52676831	-1	6	0	0	0	7	0	0	0	0	0	0	J3QK20	
ENSMUST00000178806	ENSMUSG00000096097	X	11305655	11305972	1	0	2	0	0	0	0	0	0	0	0	0	Q5M8Q2	
ENSMUST00000178807						4	2	2	1	5	1	0	0	0	0	0		
ENSMUST00000178808	ENSMUSG00000027890	3	108040408	108044894	-1	0	0	0	0	0	0	46	85	41	15	11	A2AE91	
ENSMUST00000178809						18	14	33	21	35	12	0	0	0	0	0		
ENSMUST00000178811						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178812	ENSMUSG00000006932	9	120929216	120960507	1	9	8	49	0	22	9	4562	11931	6312	1620	5513		Q02248
ENSMUST00000178814	ENSMUSG00000034912	12	66469568	67222549	-1	0	0	0	0	0	5	0	0	0	0	0		P60755
ENSMUST00000178815	ENSMUSG00000094957	12	113454942	113454951	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178816						1	0	0	0	0	0	438	429	399	24	342		
ENSMUST00000178817	ENSMUSG00000031505	8	11497506	11514960	1	25	12	47	15	26	3	4	15	8	0	14	J3QPU6	
ENSMUST00000178818						9	0	13	14	2	2	0	0	0	0	0		
ENSMUST00000178822	ENSMUSG00000018449	11	70970213	70977833	1	0	0	0	0	0	2	0	0	10	21	0	J3QN46	
ENSMUST00000178823	ENSMUSG00000094928	17	48036745	48038293	-1	9	6	31	5	10	1	0	0	0	0	0	J3QPW6	
ENSMUST00000178824	ENSMUSG00000094914	14	52892186	52892618	1	0	1	3	1	4	1	1	0	1	0	2	A0A075B6A9	
ENSMUST00000178826	ENSMUSG00000028124	3	122245557	122270732	1	0	0	0	8	0	0	732	1432	1078	143	427	Q4FJZ6	O09172
ENSMUST00000178827	ENSMUSG00000101500	X	33313379	33315286	1	0	0	0	11	0	0	0	0	0	0	0	A0A0A0MQP3	
ENSMUST00000178828	ENSMUSG00000095653	13	120173184	120173696	1	4	1	25	4	7	4	0	2	0	0	0	J3KMS6	
ENSMUST00000178829	ENSMUSG00000078862	2	177935993	177957297	-1	1	0	0	0	0	0	0	0	0	0	0	A2BFG5	
ENSMUST00000178830						4	3	10	10	2	1	0	0	35	0	0		
ENSMUST00000178832	ENSMUSG00000094487	3	54713176	54714353	-1	0	1	7	0	0	2	4	1	2	0	6	J3QPG7	
ENSMUST00000178833	ENSMUSG00000095872	X	147765991	147833456	1	0	0	3	0	0	0	0	0	0	0	0	A2ADW8	
ENSMUST00000178835						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178837	ENSMUSG00000095755	JH584293.1	83395	84475	-1	0	0	19	0	0	2	0	0	0	0	2		
ENSMUST00000178838	ENSMUSG00000073008	X	107255878	107296769	1	0	0	0	0	0	0	0	4	0	3	0		Q3U507
ENSMUST00000178839	ENSMUSG00000020923	11	102304560	102319742	-1	131	14	436	14	104	18	109	810	230	38	313	A2AWT6	
ENSMUST00000178840						4	3	3	8	0	11	9	125	20	37	13		
ENSMUST00000178843	ENSMUSG00000070683	4	136622621	136639110	1	14	17	23	205	36	16	0	0	0	0	0	S4R213	
ENSMUST00000178845						15	16	23	32	24	10	0	1	1	0	0		
ENSMUST00000178846						9	6	17	8	7	7	0	0	0	0	0		
ENSMUST00000178847						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178848						0	1	0	3	5	1	0	0	0	0	0		
ENSMUST00000178851	ENSMUSG00000030649	7	101881325	101901845	1	5	13	22	16	18	7	12	0	0	0	5		P60007
ENSMUST00000178852	ENSMUSG00000095717	12	88027004	88027438	1	2	0	0	2	5	0	0	0	0	0	0	J3QQ02	
ENSMUST00000178853						2	1	1	0	0	0	1	0	0	0	0		
ENSMUST00000178854	ENSMUSG00000026414	1	135836354	135852260	1	0	0	0	0	0	0	0	0	0	0	0		P50752
ENSMUST00000178855	ENSMUSG00000078974	11	16500530	16508484	-1	0	0	4	38	0	0	7	34	5	54	0	Q5SWJ8	P60060
ENSMUST00000178856						0	0	0	2	0	8	0	0	0	0	0		
ENSMUST00000178857						4	1	0	5	2	1	18	94	12	0	15		
ENSMUST00000178858	ENSMUSG00000079471	17	45600967	45602102	-1	5	2	5	25	13	5	0	0	2	0	0	Q2Q5T5	
ENSMUST00000178862	ENSMUSG00000094569	6	41542163	41542176	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178863	ENSMUSG00000094025	5	11127634	11132487	1	0	0	0	0	0	0	0	0	0	0	0	J3QNE1	
ENSMUST00000178864	ENSMUSG00000095675	4	42255767	42256432	1	0	0	0	0	0	0	0	0	0	0	0		P86793
ENSMUST00000178868						0	2	8	3	0	0	69	206	12	0	0		
ENSMUST00000178869						0	2	0	2	3	2	0	0	0	0	0		
ENSMUST00000178871	ENSMUSG00000095081	7	22691397	22692317	-1	0	0	0	1	0	0	0	0	0	0	0	E9PW18	
ENSMUST00000178872	ENSMUSG00000095648	2	176141591	176149825	-1	0	0	0	0	0	0	0	0	0	0	0	J3KMS2	
ENSMUST00000178875	ENSMUSG00000075410	11	116653534	116668389	1	0	0	0	12	0	5	0	0	0	0	0	J3QJU7	
ENSMUST00000178876	ENSMUSG00000054676	7	38183217	38197568	1	8	11	55	165	17	7	32	81	41	0	47		
ENSMUST00000178878	ENSMUSG00000093862	8	31737054	31739763	-1	13	4	9	8	5	1	0	1	0	0	0	J3QP10	
ENSMUST00000178879	ENSMUSG00000020639	12	4769295	4778266	1	0	2	0	0	0	0	0	0	0	0	1	Q6JEK6	Q9D6I3
ENSMUST00000178880	ENSMUSG00000095886	17	39953353	39955244	1	0	0	0	0	0	0	0	0	0	0	0	A8R0X1	
ENSMUST00000178882	ENSMUSG00000094293	4	42091207	42092287	1	0	0	19	0	0	2	0	0	0	0	2	E9Q1I1	
ENSMUST00000178883	ENSMUSG00000024534	18	52767709	52915935	1	0	0	0	0	0	0	0	0	0	0	0	J3QPG2	
ENSMUST00000178884	ENSMUSG00000027347	2	117279993	117343001	-1	0	6	38	0	0	0	48	127	48	20	175		Q9Z1S3
ENSMUST00000178887						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178888						2	6	11	3	0	1	4	13	5	4	11		
ENSMUST00000178889	ENSMUSG00000095650	Y	85528517	85530908	-1	0	0	0	0	0	0	0	0	0	0	0	Q62461	
ENSMUST00000178890						2	2	3	135	11	2	0	0	0	1	0		
ENSMUST00000178891	ENSMUSG00000094091	11	94284652	94285985	1	1	1	7	2	0	2	0	1	0	0	0	J3QP66	
ENSMUST00000178892	ENSMUSG00000025586	7	81347026	81455465	-1	0	0	0	12	0	4	0	0	0	0	0	Q059Z2	
ENSMUST00000178893	ENSMUSG00000017561	11	80046493	80080991	-1	0	4	0	18	0	0	35	381	203	0	90	J3QPM4	
ENSMUST00000178895	ENSMUSG00000095332	2	91945703	91947655	1	47	29	193	121	48	29	26	56	53	3	50	Q8K076	
ENSMUST00000178896	ENSMUSG00000090627	14	6528612	6537290	-1	5	2	1	0	0	0	0	0	0	0	0	J3QPD3	
ENSMUST00000178898	ENSMUSG00000096240	2	67413725	67433086	1	3	2	3	7	0	3	1	4	4	0	3	J3QMJ3	
ENSMUST00000178899						0	0	1	0	18	5	0	0	5	1	0		
ENSMUST00000178900	ENSMUSG00000096898	Y	77960873	77963204	-1	0	0	0	0	0	0	0	0	0	0	0	Q5FWD4	
ENSMUST00000178901	ENSMUSG00000074472	9	22188168	22202123	1	15	16	15	21	15	9	0	2	4	1	4	Q3UVL3	
ENSMUST00000178902						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178905						1	0	0	0	0	1	0	0	55	0	56		
ENSMUST00000178907	ENSMUSG00000095330	17	57741767	57742219	-1	2	4	2	5	5	4	0	0	0	0	0	J3QN05	
ENSMUST00000178908	ENSMUSG00000058835	2	22940073	23040241	-1	3	0	0	28	0	4	0	0	55	26	68	J3QNK8	
ENSMUST00000178909	ENSMUSG00000094268	12	113459864	113459892	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDD5	
ENSMUST00000178911						12	0	12	14	23	6	0	0	0	0	0		
ENSMUST00000178913	ENSMUSG00000095992	16	89010380	89010759	-1	1	1	4	3	1	0	0	0	0	0	0	J3QNX6	
ENSMUST00000178918	ENSMUSG00000090164	6	128849090	128891126	-1	0	0	2	1	0	0	1	0	0	3	1	J3QPI6	
ENSMUST00000178919	ENSMUSG00000095320	JH584294.1	121048	121713	-1	0	0	0	0	0	4	0	0	0	0	0		P84444
ENSMUST00000178921	ENSMUSG00000048583	7	142650766	142666816	-1	3	3	4	0	0	1	0	0	0	0	0	J3QJZ9	
ENSMUST00000178923	ENSMUSG00000094035	4	137572083	137574569	-1	3	2	29	24	12	5	0	0	0	0	0	Q3V0V0	
ENSMUST00000178925	ENSMUSG00000028282	4	32615451	32653265	1	0	19	35	0	0	5	160	510	347	242	220		Q9WUF3
ENSMUST00000178927	ENSMUSG00000096839	14	6613967	6622418	-1	0	2	0	0	0	0	0	0	0	0	0	J3QPJ1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000178929	ENSMUSG00000095104	17	39640957	39645666	1	1	0	2	3	1	0	0	0	0	0	0	A8R0U8	
ENSMUST00000178932						8	6	45	5	11	3	0	0	3	6	1		
ENSMUST00000178933						0	2	9	3	3	2	1	2	1	8	2		
ENSMUST00000178934	ENSMUSG00000094616	Y	70441882	70468158	1	0	0	0	0	0	0	0	0	0	0	0	J3QNI1	
ENSMUST00000178935						2	3	7	21	0	4	0	0	0	0	14		
ENSMUST00000178940	ENSMUSG00000095900	Y	13494026	13496466	1	0	0	0	0	0	0	0	0	0	0	0	J3QNP1	
ENSMUST00000178942	ENSMUSG00000096607	15	85492736	85503227	-1	31	15	48	370	28	14	2	10	5	2	3	J3QJX6	
ENSMUST00000178945	ENSMUSG00000000318	11	70156197	70170834	1	6	6	27	18	7	1	0	12	0	0	12	J3QPR7	
ENSMUST00000178946	ENSMUSG00000035165	7	100176670	100184869	1	7	1	5	7	5	2	0	0	0	3	0	Q545H9	Q9WTW2
ENSMUST00000178948	ENSMUSG00000094114	13	119606650	119610458	1	44	32	18	23	48	23	21	26	3	6	13	H3BJ86	
ENSMUST00000178949	ENSMUSG00000096355	12	115024026	115024459	-1	0	2	6	2	1	0	0	0	0	0	1	A0A075B693	
ENSMUST00000178950	ENSMUSG00000055746	X	155027201	155093666	-1	0	0	19	1	2	0	0	0	0	0	0	Q9R2A2	
ENSMUST00000178952	ENSMUSG00000094203	X	126017557	126018055	1	9	2	77	52	0	0	0	0	0	0	0	B6ZB74	
ENSMUST00000178953	ENSMUSG00000039174	3	124556352	124581101	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNU0	
ENSMUST00000178955	ENSMUSG00000078249	11	120762794	120764419	1	0	0	0	0	0	0	1	0	0	0	0	J3QK51	
ENSMUST00000178958	ENSMUSG00000095493	14	34051132	34102754	-1	6	8	13	5	10	2	0	0	0	0	0	J3QP60	
ENSMUST00000178959						13	4	12	7	18	7	0	0	0	0	0		
ENSMUST00000178960	ENSMUSG00000094336	2	83961503	83963995	1	7	7	16	6	9	4	0	0	0	0	0	A2AK42	
ENSMUST00000178961	ENSMUSG00000058295	6	132595913	132601236	1	5	7	18	640	11	2	0	0	0	0	0	F8VPU9	
ENSMUST00000178962	ENSMUSG00000096024	14	51586938	51592136	-1	228	189	907	410	222	132	0	0	1	0	1	M0QWQ9	
ENSMUST00000178966	ENSMUSG00000096457	X	28584992	28607842	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000178967	ENSMUSG00000091034	5	104070064	104077608	-1	4	0	0	2	1	0	0	0	0	0	0	B9UIU9	
ENSMUST00000178968						0	0	6	6	0	0	0	0	0	0	0		
ENSMUST00000178969	ENSMUSG00000024163	17	24892153	24936977	-1	0	0	0	24	32	0	0	50	0	0	43	J3QNR6	
ENSMUST00000178970	ENSMUSG00000096730	JH584292.1	3536	11935	1	7	0	0	3	2	0	0	0	0	0	0		
ENSMUST00000178971						3	5	2	4	4	2	5	7	0	0	0		
ENSMUST00000178973	ENSMUSG00000095930	13	119710094	119755882	-1	41	19	33	29	55	17	1	5	1	0	6	Q3UQ09	
ENSMUST00000178974	ENSMUSG00000073085	X	76393350	76397979	1	0	0	2	0	1	0	0	0	0	0	0	Q3V0X2	
ENSMUST00000178977	ENSMUSG00000031938	9	15283337	15306448	-1	7	0	0	13	7	6	77	276	86	137	64		Q91V76
ENSMUST00000178979	ENSMUSG00000095413	X	11311934	11312427	1	0	0	0	0	5	0	0	0	0	0	0	Q810S6	
ENSMUST00000178982	ENSMUSG00000036469	8	65617900	66471637	1	0	0	0	0	0	0	0	0	0	0	0		Q6NZQ8
ENSMUST00000178986	ENSMUSG00000093923	X	24753162	24775164	-1	0	0	0	0	0	0	0	0	0	0	0	Q497S0	
ENSMUST00000178987						38	30	36	151	40	25	19	105	26	25	37		
ENSMUST00000178988	ENSMUSG00000040883	9	21921010	21927535	-1	0	0	0	0	0	0	34	27	11	62	0		Q91XE8
ENSMUST00000178989	ENSMUSG00000094105	5	11681959	11686856	1	0	0	0	0	0	0	0	0	0	0	0	J3QP00	
ENSMUST00000178992	ENSMUSG00000094958	4	108719649	108781904	1	5	17	51	113	9	5	0	0	0	0	0	J3QMN2	
ENSMUST00000178993						0	0	0	31	0	0	0	441	393	644	156		
ENSMUST00000178995	ENSMUSG00000095403	8	20550331	20581999	1	109	158	564	65	85	94	543	1738	481	277	500	J3QMZ6	
ENSMUST00000178996						5	0	24	0	0	0	0	0	0	0	0		
ENSMUST00000178997	ENSMUSG00000027469	2	152847964	152895321	1	47	65	89	0	91	36	17	133	63	39	0		A2APB8
ENSMUST00000178998						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000178999	ENSMUSG00000058173	9	15505487	15545260	1	8	15	133	30	21	6	2	12	0	2	14		Q9JIS3
ENSMUST00000179000	ENSMUSG00000046811	11	70519196	70520736	1	1	2	0	86	10	0	0	0	0	0	0	Q8K1B3	
ENSMUST00000179001	ENSMUSG00000037902	2	129592835	129632228	1	22	0	0	0	10	14	1824	1704	3210	330	2693	Q6P6I8	
ENSMUST00000179002	ENSMUSG00000021198	12	102948859	103184065	1	0	16	0	2	9	0	0	0	0	0	0	E5CYJ9	
ENSMUST00000179004	ENSMUSG00000095655	X	11315158	11315475	1	0	2	0	0	0	0	0	0	0	0	0	Q5M8Q2	
ENSMUST00000179005	ENSMUSG00000074111	7	47234861	47252848	-1	0	6	23	0	0	0	0	0	0	0	0		
ENSMUST00000179008	ENSMUSG00000095247	JH584293.1	16864	21820	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179013	ENSMUSG00000095385	9	43259879	43280075	1	3	5	2	3	2	1	0	0	0	0	0	J3QPI1	
ENSMUST00000179014						234	354	133	106	268	65	4	0	0	6	12		
ENSMUST00000179020						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000179021	ENSMUSG00000094941	X	149272377	149305003	1	0	0	10	0	0	0	0	0	0	0	0	A2BI72	
ENSMUST00000179022	ENSMUSG00000062075	10	80901203	80918245	-1	0	0	0	90	13	0	157	96	104	22	96		P21619
ENSMUST00000179024						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179025						1	0	0	30	4	1	0	0	0	0	0		
ENSMUST00000179028	ENSMUSG00000094351	X	31573106	31574283	-1	4	6	6	16	6	5	0	0	0	0	0	J3QPV3	
ENSMUST00000179030	ENSMUSG00000052331	1	54645340	54926387	-1	0	0	0	23	0	4	943	1472	2082	141	1259		B2RXR6
ENSMUST00000179032	ENSMUSG00000096344	5	146481965	146484704	1	50	26	31	43	32	12	0	0	0	0	0	J3QNG1	
ENSMUST00000179036	ENSMUSG00000031085	7	143866871	143897506	1	1	8	23	5	0	8	0	0	0	0	0	J3QK70	
ENSMUST00000179038	ENSMUSG00000024534	18	52767709	52915935	1	1	0	8	57	6	2	0	0	0	0	0	A0A0G2JDC8	
ENSMUST00000179039						50	42	220	54	45	16	1	4	3	2	3		
ENSMUST00000179040						12	12	17	14	18	8	2	2	2	0	0		
ENSMUST00000179041	ENSMUSG00000072825	12	112722174	112746591	1	71	0	98	568	104	45	21	7	9	5	131		Q80U49
ENSMUST00000179042	ENSMUSG00000094811	14	6296365	6304843	-1	7	8	0	7	3	3	0	0	0	0	0	J3QPZ1	
ENSMUST00000179046						6	7	14	5	0	3	2	3	1	4	0		
ENSMUST00000179047	ENSMUSG00000030655	7	118131308	118243637	-1	0	0	0	84	0	0	2	0	4	0	14	J3QPA7	
ENSMUST00000179049	ENSMUSG00000039488	9	9660891	10904775	-1	0	0	18	0	0	0	0	0	0	0	0	E9PYK7	
ENSMUST00000179054	ENSMUSG00000097327	10	22113050	22149270	-1	0	0	154	1261	50	32	0	0	0	1	0	J3QML9	
ENSMUST00000179055	ENSMUSG00000060600	11	70657202	70662513	1	0	1	2	1	0	0	0	8	1	0	0	J3QPZ9	
ENSMUST00000179056	ENSMUSG00000095693	Y	5248359	5249441	-1	28	38	35	76	34	20	0	0	0	0	0	J3KMU2	
ENSMUST00000179059	ENSMUSG00000029086	5	43993620	44102032	-1	0	0	0	0	0	0	0	0	0	0	20	Q8R056	
ENSMUST00000179061	ENSMUSG00000095545	2	175692223	175703646	-1	0	0	1	0	1	1	0	0	5	2	0	A2ART2	
ENSMUST00000179062	ENSMUSG00000046873	X	157535371	157598715	-1	2	0	0	0	0	0	0	0	8	4	3		Q3TTC2
ENSMUST00000179064	ENSMUSG00000096879	3	93068823	93075505	1	0	0	0	0	0	0	0	0	0	0	0	Q3UT66	
ENSMUST00000179065	ENSMUSG00000032411	9	96196275	96323646	1	2	0	0	0	0	0	2	0	0	10	4	J3QK26	
ENSMUST00000179067						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000179069	ENSMUSG00000094361	X	32894625	32896121	1	4	0	0	0	5	0	0	0	0	0	0	J3QML3	
ENSMUST00000179070						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179071	ENSMUSG00000096323	13	120154627	120155136	1	2	2	3	0	3	0	0	0	0	0	0	O70517	
ENSMUST00000179072	ENSMUSG00000094682	7	23272801	23278900	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UTA8	
ENSMUST00000179073	ENSMUSG00000094647	Y	77692808	77719038	1	0	0	0	0	0	0	0	0	0	0	0	J3QNI1	
ENSMUST00000179074	ENSMUSG00000024069	17	74395608	74424229	1	0	0	0	0	0	0	0	0	0	0	15	J3QMX8	
ENSMUST00000179075	ENSMUSG00000095585	JH584293.1	41602	43114	-1	5	0	6	1	3	0	0	0	0	0	0		
ENSMUST00000179076	ENSMUSG00000094789	Y	31602724	31634756	-1	0	0	0	0	0	1	0	0	0	0	0	J3KMU1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000179077	ENSMUSG00000096768	Y	90784738	90816464	1	19	10	22	1534	36	18	3	61	24	15	59	J3QQ45	
ENSMUST00000179078	ENSMUSG00000043190	13	76001535	76018712	-1	9	6	4	47	7	1	23	86	52	61	26		Q8K2P6
ENSMUST00000179079	ENSMUSG00000095275	7	20668918	20669841	1	0	0	0	0	0	0	0	0	0	0	0	D3YTY1	
ENSMUST00000179086	ENSMUSG00000095637	X	31715660	31717156	-1	6	8	0	0	4	0	0	0	0	0	0	J3QMV9	
ENSMUST00000179088						4	4	3	5	0	1	1	0	1	0	0		
ENSMUST00000179089	ENSMUSG00000057715	1	11414105	11975901	1	0	0	3	1	0	3	0	0	0	0	0	B7ZN57	
ENSMUST00000179090						10	5	15	14	4	2	0	0	0	0	0		
ENSMUST00000179091	ENSMUSG00000096044	5	93481829	93540200	-1	0	0	0	0	5	0	0	0	0	0	0	J3QN52	
ENSMUST00000179094	ENSMUSG00000061306	11	120103960	120151346	-1	4	0	10	4	0	0	3178	2681	2567	312	1910	J3QNE8	
ENSMUST00000179095	ENSMUSG00000093848	Y	21241575	21243910	1	0	0	0	0	0	0	0	0	0	0	0	Q62460	
ENSMUST00000179096	ENSMUSG00000095240	X	39862919	39863604	-1	2	1	0	2	2	3	0	0	0	0	0	J3QPF7	
ENSMUST00000179097	ENSMUSG00000063142	14	23289431	24004859	-1	0	42	0	0	46	0	0	0	0	0	0	J3QN27	
ENSMUST00000179104	ENSMUSG00000031731	8	109778554	109864204	1	3	1	3	0	0	1	6	107	0	21	0	Q3TDN1	
ENSMUST00000179106	ENSMUSG00000043831	7	67222544	67228468	1	14	0	43	83	33	15	29	0	8	0	8		Q8CC84
ENSMUST00000179108	ENSMUSG00000035342	19	45015176	45027104	1	0	1	0	0	0	0	0	0	0	1	1		Q91YU6
ENSMUST00000179109	ENSMUSG00000093795	10	100306571	100307185	-1	1	0	2	1	1	0	0	0	0	0	0	J3QP31	
ENSMUST00000179114	ENSMUSG00000020817	11	70844778	70943105	1	1	5	4	58	11	6	20	37	19	2	8	Q3U983	
ENSMUST00000179115	ENSMUSG00000096730	JH584292.1	3536	11935	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179116	ENSMUSG00000093954	14	69363504	69503362	-1	10	7	6	22	10	5	0	0	0	0	1		Q920G8
ENSMUST00000179117	ENSMUSG00000067771	X	73117047	73129262	1	0	0	0	0	0	0	0	0	0	0	0	Q52KH6	
ENSMUST00000179118	ENSMUSG00000024963	19	6987911	6992503	-1	0	0	0	0	0	0	74	147	59	76	44		Q9D844
ENSMUST00000179119						0	0	4	1	5	0	0	0	0	0	0		
ENSMUST00000179120	ENSMUSG00000094112	15	40142188	40148689	1	3	3	2	3	3	0	0	0	0	0	0	J3QNB2	
ENSMUST00000179122						0	3	0	5	6	0	0	0	0	0	0		
ENSMUST00000179123						2	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000179124	ENSMUSG00000095787	GL456211.1	54469	54840	-1	15	17	56	9	12	5	2	16	6	10	3		
ENSMUST00000179125	ENSMUSG00000096533	Y	40651454	40651996	-1	0	0	22	0	0	0	0	0	0	0	0	A8HG57	
ENSMUST00000179126						5	4	4	2	3	1	0	0	0	0	0		
ENSMUST00000179127	ENSMUSG00000026269	1	92910783	92924384	1	0	0	0	25	0	0	611	861	443	86	276	J3QMP7	
ENSMUST00000179131	ENSMUSG00000095514	13	119836006	119846570	1	0	0	0	0	0	0	0	1	0	0	5	J3QMN9	
ENSMUST00000179133	ENSMUSG00000095470	12	19954505	19954840	1	0	1	1	137	3	1	0	0	0	0	0	J3KMP8	
ENSMUST00000179136	ENSMUSG00000095302	Y	67045743	67048072	-1	0	0	0	0	0	0	0	0	0	0	0	Q149W4	
ENSMUST00000179137	ENSMUSG00000094729	Y	53415953	53418291	-1	0	0	0	0	0	0	0	0	0	0	0	Q5FWB5	
ENSMUST00000179139	ENSMUSG00000096199	12	4234027	4240123	1	22	25	55	31	40	19	102	171	74	234	55		D3Z4S3
ENSMUST00000179140	ENSMUSG00000094337	GL456354.1	82993	86051	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179141	ENSMUSG00000093814	14	19401727	19402599	-1	4	5	10	6	3	3	0	0	0	0	0	J3QPW8	
ENSMUST00000179142	ENSMUSG00000038274	19	6057888	6059524	1	3	0	8	122	17	6	244	365	127	78	173	Q642K5	
ENSMUST00000179146	ENSMUSG00000095728	JH584298.1	168268	170838	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179149						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000179150						1	2	10	44	6	0	0	0	0	0	0		
ENSMUST00000179156						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000179158	ENSMUSG00000096582	4	88776922	88777470	1	0	0	0	0	0	0	0	0	0	0	0	Q8CD73	
ENSMUST00000179160	ENSMUSG00000095953	12	31184623	31185177	1	2	0	1	3	3	0	0	0	0	0	0	Q3UYS9	
ENSMUST00000179162	ENSMUSG00000037432	1	36372291	36422110	1	39	39	75	50	69	34	3	17	15	0	23		P0DM40
ENSMUST00000179163	ENSMUSG00000024142	17	24473550	24479078	-1	3	3	9	0	8	4	11	68	7	12	0		Q9DCJ1
ENSMUST00000179165	ENSMUSG00000022297	15	39006280	39038186	1	30	19	49	42	0	13	5	6	6	24	49	Q542J1	Q61089
ENSMUST00000179166	ENSMUSG00000096396	12	113469426	113469435	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179168						5	3	4	11	4	0	0	5	0	0	0		
ENSMUST00000179171	ENSMUSG00000064202	19	28893042	28967800	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0B4J1N4	
ENSMUST00000179172	ENSMUSG00000035242	10	80826656	80829290	1	0	0	0	12	0	0	0	83	503	152	559	J3QM96	
ENSMUST00000179174						1	1	3	1	4	1	0	0	0	0	0		
ENSMUST00000179175	ENSMUSG00000056300	4	146502027	146539395	1	11	12	0	16	6	2	0	0	1	1	0	A2A8V7	
ENSMUST00000179178						5	2	9	0	3	0	0	0	0	0	0		
ENSMUST00000179180	ENSMUSG00000032985	11	25602763	26210763	-1	3	0	0	1	0	1	0	0	0	0	0	J3QP50	
ENSMUST00000179181	ENSMUSG00000076757	13	19344558	19352756	1	1	3	0	0	2	1	0	0	1	0	1	A0A075B6C7	
ENSMUST00000179183						5	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179187	ENSMUSG00000093865	3	129787881	129804030	-1	0	3	19	0	7	1	0	0	0	0	0	J3QNQ8	
ENSMUST00000179189	ENSMUSG00000094936	19	4784293	4793901	-1	0	0	0	0	0	0	53	7	17	2	27	J3QPA9	
ENSMUST00000179191	ENSMUSG00000010721	5	29229802	29378390	-1	0	15	0	145	13	13	7	0	11	17	0	J3QM78	
ENSMUST00000179192	ENSMUSG00000094125	2	83955693	83958185	1	7	7	16	6	9	4	0	0	0	0	0	A2AK42	
ENSMUST00000179196	ENSMUSG00000034127	10	115817284	115849893	1	5	1	6	6	0	2	3	7	2	0	1		Q8R3G9
ENSMUST00000179197						10	8	26	74	10	3	0	0	0	0	0		
ENSMUST00000179199	ENSMUSG00000094021	14	7036535	7044970	-1	0	0	3	5	0	2	0	0	0	0	0	J3QPP2	
ENSMUST00000179200	ENSMUSG00000072601	14	43818765	43875517	-1	2	0	0	1	0	0	14	0	0	0	2	Q53ZF0	P97426
ENSMUST00000179201						4	2	0	3	9	2	6	6	7	0	0		
ENSMUST00000179202						0	2	1	1	3	1	0	0	0	0	0		
ENSMUST00000179203						85	35	42	0	68	0	0	0	0	0	0		
ENSMUST00000179205	ENSMUSG00000094504	5	138819370	138821619	1	4	0	22	224	12	6	93	216	133	85	60	J3QP53	
ENSMUST00000179206	ENSMUSG00000095163	7	22027977	22028897	-1	0	0	0	1	0	0	0	0	0	0	0	D3YTY2	
ENSMUST00000179207	ENSMUSG00000031486	8	27085583	27123436	1	1	2	0	0	13	2	0	0	0	0	0		
ENSMUST00000179209	ENSMUSG00000078552	4	129608331	129614257	-1	5	2	5	3	7	1	0	0	10	0	6	J3KML0	
ENSMUST00000179210	ENSMUSG00000057963	12	102568582	102704930	-1	0	0	0	0	0	1	5	4	5	0	6	J3QNS2	
ENSMUST00000179211	ENSMUSG00000095250	GL456211.1	30483	32396	-1	2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179212	ENSMUSG00000032417	9	86571991	86574899	1	0	0	0	0	0	0	12	21	0	2	0	Q14BN8	
ENSMUST00000179214	ENSMUSG00000095557	5	146556136	146558915	1	0	0	0	0	0	0	0	0	0	0	0	J3QMS8	
ENSMUST00000179215	ENSMUSG00000079265	14	44649204	44706456	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNS7	
ENSMUST00000179217	ENSMUSG00000095663	15	8518683	8519953	-1	3	3	6	5	3	5	0	0	0	0	0	J3QNJ2	
ENSMUST00000179218	ENSMUSG00000021192	12	102469134	102497902	1	0	0	0	53	0	0	33	191	205	53	229		Q9QYE6
ENSMUST00000179219	ENSMUSG00000095879	Y	18061270	18061812	-1	0	0	22	0	0	0	0	0	0	0	0	A8HG57	
ENSMUST00000179220	ENSMUSG00000095508	Y	12381981	12384008	1	0	4	0	0	0	0	0	0	0	0	0	J3QPZ4	
ENSMUST00000179224	ENSMUSG00000042079	6	117900324	117925622	1	0	0	0	7	0	0	29	0	72	0	14	J3QNH2	
ENSMUST00000179225						3	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000179226	ENSMUSG00000021669	13	96542618	96640167	1	2	0	3	30	12	0	120	0	1642	0	419		Q9EQG9
ENSMUST00000179227	ENSMUSG00000025515	7	141690340	141754693	1	2	0	0	0	0	0	0	0	0	0	0	Q9R1L0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000179228						0	2	0	2	5	5	13	11	7	5	0		
ENSMUST00000179230	ENSMUSG00000096449	13	85126999	85127514	-1	0	0	0	2	0	2	0	0	0	0	0	J3QPT4	
ENSMUST00000179231	ENSMUSG00000094258	14	4632352	4640802	1	0	0	4	0	5	0	0	0	0	0	0	J3QNT1	
ENSMUST00000179232						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179233	ENSMUSG00000008892	8	22577075	22593813	-1	1	1	1	7	0	0	0	0	0	0	0	J3QMG3	
ENSMUST00000179234	ENSMUSG00000059343	4	72850583	72852634	-1	8	3	25	15	12	4	1	0	1	0	0	Q9CPQ9	
ENSMUST00000179238	ENSMUSG00000004207	10	60277627	60302597	1	0	0	0	3	0	0	287	339	211	0	188	Q3UFE8	Q61207
ENSMUST00000179239						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000179240	ENSMUSG00000095623	JH584294.1	4164	9702	-1	0	0	0	0	0	0	0	0	0	0	0		P70225
ENSMUST00000179242						3	4	1	1	4	2	0	0	0	0	7		
ENSMUST00000179243	ENSMUSG00000039194	7	79374870	79387048	-1	0	0	0	0	26	7	0	0	0	0	1	Q544Y3	Q9Z275
ENSMUST00000179248	ENSMUSG00000094305	7	33364343	33366322	-1	4	0	17	8	4	0	0	0	0	0	0	J3QK77	
ENSMUST00000179250	ENSMUSG00000102829	3	93288095	93288859	1	29	7	13	1414	58	38	0	0	0	0	0	A0A0A6YWE2	
ENSMUST00000179251						45	53	14	67	79	31	0	0	0	0	0		
ENSMUST00000179253	ENSMUSG00000095456	JH584293.1	10948	16486	1	0	0	0	0	0	0	0	0	0	0	0		P70225
ENSMUST00000179256	ENSMUSG00000094081	Y	7632774	7638489	-1	0	0	0	0	0	0	0	0	0	0	0	J3QK38	
ENSMUST00000179258	ENSMUSG00000094144	10	104177024	104179491	1	0	0	0	0	0	0	0	0	0	0	0	J3QP73	
ENSMUST00000179262	ENSMUSG00000093876	12	113464761	113464770	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179263	ENSMUSG00000091931	12	102753275	102757803	-1	3	5	12	7	7	3	3	11	0	0	8	J3QK34	
ENSMUST00000179264	ENSMUSG00000095891	9	3025417	3033289	1	654	697	892	890	836	680	2	0	0	0	0	J3QPS1	
ENSMUST00000179265	ENSMUSG00000035247	12	51743722	51829536	-1	47	4	4	8	55	3	0	110	45	0	131		Q69ZR2
ENSMUST00000179266						3	0	0	6	6	0	0	2	0	1	0		
ENSMUST00000179267	ENSMUSG00000095711	14	53640701	53641225	1	0	0	3	5	0	2	0	0	0	3	0	A0A075B694	
ENSMUST00000179269	ENSMUSG00000096883	15	82206952	82212815	-1	3	4	6	429	16	10	1	2	1	0	4	J3QNX5	
ENSMUST00000179271	ENSMUSG00000009470	13	98839019	98926384	-1	0	2	1	19	2	0	0	0	0	0	0	J3QMX2	
ENSMUST00000179272	ENSMUSG00000095547	9	3017408	3021593	1	10994	12713	12563	9705	11653	8111	1	3	1	0	0	J3QM83	
ENSMUST00000179273	ENSMUSG00000079043	2	130613840	130630027	-1	9	0	0	0	0	1	2	0	18	18	5		
ENSMUST00000179276	ENSMUSG00000061288	5	117120129	117275219	1	1	0	0	0	0	0	499	856	1022	55	571		Q8BYC6
ENSMUST00000179279	ENSMUSG00000094311	10	38820541	38821779	-1	2	0	1	8	3	2	0	0	0	0	0	J3QPR6	
ENSMUST00000179281	ENSMUSG00000095247	JH584293.1	16864	21820	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z1X0
ENSMUST00000179282	ENSMUSG00000040328	11	48978889	49135387	1	0	2	0	0	2	0	0	0	0	0	0		Q8VGD6
ENSMUST00000179284	ENSMUSG00000095769	Y	13132950	13133492	-1	0	0	22	0	0	0	0	0	0	0	0	A8HG57	
ENSMUST00000179285	ENSMUSG00000096010	6	136801553	136804415	-1	790	683	1994	1186	704	360	34	82	43	19	122	B2RTM0	P62806
ENSMUST00000179290	ENSMUSG00000045268	4	119169513	119174195	-1	0	0	37	0	11	31	21	74	0	10	0	A2A7P4	
ENSMUST00000179291						36	47	145	206	32	25	3	16	6	0	11		
ENSMUST00000179292	ENSMUSG00000095450	GL456221.1	46295	46666	-1	15	17	56	9	12	5	2	16	6	10	3		
ENSMUST00000179295	ENSMUSG00000094374	12	82495419	82496537	-1	8	2	9	9	9	6	0	0	0	0	0	J3QNT2	
ENSMUST00000179296	ENSMUSG00000096685	14	6832231	6840311	-1	2	1	2	2	2	2	0	0	0	0	0	J3KMQ9	
ENSMUST00000179297	ENSMUSG00000024735	19	10895231	10909559	1	49	42	115	86	58	23	7	22	15	7	18		Q99KP6
ENSMUST00000179298	ENSMUSG00000018566	11	69942539	69948188	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNF4	
ENSMUST00000179300						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179301	ENSMUSG00000009470	13	98839019	98926384	-1	2	8	3	0	0	3	193	131	739	160	407	Q3TKD0	
ENSMUST00000179302	ENSMUSG00000095927	Y	18654482	18655024	1	0	1	0	2	1	0	0	0	0	0	0	J3QPV5	
ENSMUST00000179305	ENSMUSG00000025207	19	44989101	45003397	1	24	4	36	0	10	15	7	18	0	4	13		Q9WUH7
ENSMUST00000179306	ENSMUSG00000098530	12	102719975	102757765	-1	1	2	1	8	0	0	0	0	0	0	0	J3QMA2	
ENSMUST00000179308	ENSMUSG00000095105	13	12471209	12520450	-1	54	56	185	176	86	54	7	26	15	4	23	Q5D0F1	
ENSMUST00000179309	ENSMUSG00000096379	Y	38574609	38575691	-1	96	57	109	259	120	43	0	0	0	0	0	J3QM79	
ENSMUST00000179311	ENSMUSG00000096484	2	83973123	83975615	1	0	0	0	3	0	0	0	1	1	0	0	J3QNR0	
ENSMUST00000179312	ENSMUSG00000096904	14	6405827	6412482	-1	1	0	1	0	0	0	0	0	0	0	0	A6NAU3	
ENSMUST00000179313	ENSMUSG00000042761	9	87144306	87184045	1	37	0	37	119	19	0	0	0	0	0	0		D3Z1Q2
ENSMUST00000179314	ENSMUSG00000093931	3	113312455	113324052	-1	3	6	4	1	2	2	0	0	0	0	0		P00688
ENSMUST00000179317						2	0	4	1	2	4	1	2	2	0	2		
ENSMUST00000179318	ENSMUSG00000030638	7	82173840	82307419	1	4	11	3	3	4	5	0	0	0	0	0	J3QQ44	
ENSMUST00000179321	ENSMUSG00000037455	10	23796986	23827968	1	68	79	159	49	81	29	1	3	2	1	2		D3Z5L6
ENSMUST00000179322	ENSMUSG00000093938	11	79515056	79523762	-1	8	6	43	0	2	4	2892	14329	5293	6116	3163		Q8VD58
ENSMUST00000179323	ENSMUSG00000050188	4	126096623	126098584	1	0	0	0	0	0	0	75	316	33	50	25	Q3UPL7	Q8QZX5
ENSMUST00000179325	ENSMUSG00000094596	X	4289286	4291245	-1	0	0	5	0	0	0	0	0	0	0	0	A2CG71	
ENSMUST00000179326						10	12	11	16	8	3	0	1	0	0	0		
ENSMUST00000179327	ENSMUSG00000096901	14	3931756	3940185	1	0	1	0	0	0	0	0	0	0	0	0	J3QNT1	
ENSMUST00000179328						3	5	1	1	3	11	0	3	0	1	1		
ENSMUST00000179330	ENSMUSG00000094170	Y	47669242	47691098	-1	0	0	0	0	0	0	0	0	1	0	0	J3QPW0	
ENSMUST00000179331	ENSMUSG00000030655	7	118131308	118243637	-1	0	0	0	0	0	0	0	0	1370	0	1248	J3QQ22	
ENSMUST00000179332	ENSMUSG00000057181	11	80360492	80378034	-1	67	63	155	0	0	31	0	0	152	0	113	J3KMQ6	
ENSMUST00000179333						7	2	8	118	7	1	0	0	2	0	0		
ENSMUST00000179336						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000179337	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000179341	ENSMUSG00000035242	10	80826656	80829290	1	0	0	1	0	4	0	61	74	20	8	8	J3QME8	
ENSMUST00000179343	ENSMUSG00000094483	11	6467599	6475917	-1	26	27	35	220	30	17	1033	2521	1463	156	985		O35295
ENSMUST00000179344	ENSMUSG00000093908	12	19387809	19390286	1	264	193	628	1671	317	167	1	2	1	0	5	Q8BME7	
ENSMUST00000179346	ENSMUSG00000095993	19	61296902	61297069	-1	0	0	0	0	0	0	0	0	1	0	0	J3KMU4	
ENSMUST00000179347	ENSMUSG00000095026	8	70718543	70722635	1	5	4	16	9	10	5	0	0	0	0	1	J3QMQ6	
ENSMUST00000179348	ENSMUSG00000094885	X	149074282	149138152	1	2	1	0	4	2	2	0	0	0	0	0	Q62012	
ENSMUST00000179349	ENSMUSG00000095648	2	176141591	176149825	-1	0	0	0	0	0	0	0	0	0	0	0	A2BG90	
ENSMUST00000179350						2	0	0	23	0	0	0	1	0	0	1		
ENSMUST00000179351	ENSMUSG00000031486	8	27085583	27123436	1	9	0	4	74	0	2	0	0	0	0	0	J3QPS6	
ENSMUST00000179353	ENSMUSG00000026276	1	93478964	93510260	1	0	4	0	0	0	0	58	797	130	462	561		P42208
ENSMUST00000179355	ENSMUSG00000094939	Y	25308278	25309360	-1	46	42	9	58	57	37	0	0	0	0	0	J3QNB5	
ENSMUST00000179356						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000179360	ENSMUSG00000000948	7	59974149	60005064	-1	0	1	0	0	1	0	0	0	0	0	0		Q9WU12
ENSMUST00000179363	ENSMUSG00000096753	12	103310975	103317065	1	1	2	14	32	0	0	0	0	0	0	0	J3QNB7	
ENSMUST00000179364	ENSMUSG00000094500	8	33742112	33747770	-1	3	1	5	1	3	2	0	0	0	0	1	J3QNP2	
ENSMUST00000179365	ENSMUSG00000038301	6	51523901	51590679	1	5	5	12	1	10	8	428	1387	355	1045	247	Q4FJX6	Q9CWT3
ENSMUST00000179367	ENSMUSG00000093976	13	49899119	49904597	-1	24	10	52	33	21	13	0	0	0	0	0	J3QK40	
ENSMUST00000179368						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000179369	ENSMUSG00000094577	X	154022780	154033827	-1	0	1	0	1	1	2	0	0	0	0	0	A2BED8	
ENSMUST00000179372	ENSMUSG00000099545	4	88785709	88786257	1	3	0	3	5	1	0	0	0	0	0	0	A0A087WR18	
ENSMUST00000179375	ENSMUSG00000095296	5	11502685	11507417	1	0	0	0	0	0	0	0	0	0	0	0	J3QNA6	
ENSMUST00000179379	ENSMUSG00000021038	12	87238875	87266286	-1	0	10	29	20	30	4	0	503	0	0	0		Q8BGQ1
ENSMUST00000179382						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000179384	ENSMUSG00000094430	16	32804760	32810477	-1	5	3	5	8	7	0	1	1	0	1	0	J3QPC1	
ENSMUST00000179385						9	11	9	5	16	0	0	0	0	0	0		
ENSMUST00000179386	ENSMUSG00000091950	1	174151481	174152530	1	5	9	11	2	5	3	0	0	0	0	0		
ENSMUST00000179390	ENSMUSG00000093941	7	21545170	21546090	-1	0	0	0	1	0	0	0	0	0	0	0	D3YTY2	
ENSMUST00000179391	ENSMUSG00000078786	7	27195781	27210186	1	0	0	0	9	0	0	0	0	5	0	0	J3QPC3	
ENSMUST00000179392						1	0	0	4	3	1	0	0	0	0	0		
ENSMUST00000179393	ENSMUSG00000022307	15	41447482	41861048	1	12	7	36	0	13	12	13	13	26	0	13		Q4KMM3
ENSMUST00000179394	ENSMUSG00000060579	14	9550092	11162035	-1	0	3	0	0	0	0	0	0	1	0	0		O89106
ENSMUST00000179395	ENSMUSG00000032386	9	65828930	65908794	-1	128	114	270	81	107	56	61	362	167	46	108		Q9QXN3
ENSMUST00000179398						11	9	5	11	18	15	0	1	2	0	1		
ENSMUST00000179399	ENSMUSG00000094613	3	107230614	107234723	1	8	3	1	5	2	2	0	0	0	0	0	J3QQ32	
ENSMUST00000179402						11	7	0	14	12	3	0	0	0	0	0		
ENSMUST00000179404	ENSMUSG00000095852	Y	2830699	2873492	1	0	0	16	0	0	13	0	0	0	0	0	B2RWR6	
ENSMUST00000179408	ENSMUSG00000095365	Y	17400761	17402715	1	2	5	13	3	5	4	0	0	0	0	0	Q9D3U4	
ENSMUST00000179410	ENSMUSG00000095148	Y	6267098	6269548	1	0	0	0	0	0	0	0	0	0	0	0	J3QMQ9	
ENSMUST00000179411	ENSMUSG00000095797	14	5469438	5477830	-1	5	9	0	0	0	0	0	0	0	0	0	J3QNK3	
ENSMUST00000179412	ENSMUSG00000094840	5	137208813	137212389	-1	26	18	98	51	34	12	15	63	33	6	33	Q3U5A2	
ENSMUST00000179414						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000179416	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	0	0	0	0	0	0	0	0	Q8BHD2	
ENSMUST00000179417						5	2	1	7	2	2	0	0	0	0	4		
ENSMUST00000179418	ENSMUSG00000024309	17	33938821	33940343	-1	0	1	0	0	0	0	0	0	0	0	0	Q792E4	Q03958
ENSMUST00000179420						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000179422	ENSMUSG00000066839	9	22072246	22085438	-1	3	0	7	0	9	0	23	15	0	10	4		
ENSMUST00000179424						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179425	ENSMUSG00000096591	4	88779850	88780660	1	9	8	9	4	9	3	0	0	0	0	0	B1AYI3	
ENSMUST00000179426						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179429	ENSMUSG00000095143	3	98499071	98510514	-1	5	0	17	2	6	0	0	0	0	0	0		Q61767
ENSMUST00000179430	ENSMUSG00000095959	14	79863074	79868398	-1	27	56	24	27	26	9	0	1	1	0	0	Q3UNY9	
ENSMUST00000179433	ENSMUSG00000037263	19	3958645	3972103	1	8	23	2	24	17	21	8	0	0	2	4	J3QMK6	
ENSMUST00000179434	ENSMUSG00000024292	17	32905071	32917342	-1	9	14	8	26	5	0	13	7	10	5	10		Q9EP75
ENSMUST00000179435	ENSMUSG00000078877	2	176798612	176811223	1	0	1	0	0	0	0	0	4	2	10	1	J3KMS2	
ENSMUST00000179436	ENSMUSG00000095742	JH584295.1	66	1479	-1	0	0	0	22	0	0	29	380	219	289	149		
ENSMUST00000179437						0	3	1	0	3	1	0	0	0	0	0		
ENSMUST00000179441						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179443	ENSMUSG00000095276	7	45176349	45179597	-1	15	8	211	229	28	23	0	0	0	0	0		J3KML8
ENSMUST00000179445	ENSMUSG00000017781	11	75588097	75628804	1	0	10	59	33	3	10	1971	7729	2586	361	1594	J3QQ30	
ENSMUST00000179448	ENSMUSG00000094336	2	83961503	83963995	1	0	0	0	3	0	0	0	1	1	0	0	J3QNR0	
ENSMUST00000179450	ENSMUSG00000090097	2	88446019	88449121	-1	0	0	0	0	0	0	0	0	0	0	0	Q7TR17	
ENSMUST00000179455	ENSMUSG00000094237	13	119827961	119830216	-1	0	0	0	0	0	5	0	3	0	1	0	O70618	
ENSMUST00000179458	ENSMUSG00000036867	9	63953076	64022059	-1	0	0	0	33	1	0	0	0	0	0	0	J3QPR3	
ENSMUST00000179460						11	8	23	12	22	5	0	2	2	0	2		
ENSMUST00000179462						139	86	718	151	61	52	0	1	2	0	1		
ENSMUST00000179465						4	1	0	2	3	4	0	0	0	0	0		
ENSMUST00000179466	ENSMUSG00000096915	X	33955044	33956540	-1	10	0	0	0	0	19	0	0	0	0	0	J3QMW9	
ENSMUST00000179467	ENSMUSG00000044033	2	77009902	77170636	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNK9	
ENSMUST00000179468	ENSMUSG00000095799	12	88249666	88250100	-1	4	7	0	3	0	2	0	0	0	0	0	Q3UTA4	
ENSMUST00000179470	ENSMUSG00000094462	7	42578466	42578588	-1	1	0	0	0	0	0	0	0	0	0	0	J3QMU9	
ENSMUST00000179472	ENSMUSG00000064036	18	73859385	73881333	1	21	22	46	543	43	30	0	6	1	0	0	E9QNX2	
ENSMUST00000179473						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179474	ENSMUSG00000044465	7	105371211	105400054	-1	53	39	183	87	82	32	232	961	513	33	391	J3QP99	
ENSMUST00000179477	ENSMUSG00000102724	3	93286577	93287344	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXH0	
ENSMUST00000179478	ENSMUSG00000042079	6	117900324	117925622	1	6	6	3	53	0	8	155	560	708	118	269	J3QMT0	
ENSMUST00000179479						10	5	12	3	7	10	0	2	2	0	2		
ENSMUST00000179480	ENSMUSG00000096626	Y	58782567	58814597	-1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000179481	ENSMUSG00000095257	7	31375592	31376916	1	3	0	2	3	6	0	0	0	0	0	0	J3QJY4	
ENSMUST00000179482	ENSMUSG00000095829	5	11341516	11346286	1	0	0	0	0	0	0	0	0	0	0	0	J3QMX3	
ENSMUST00000179483	ENSMUSG00000096768	Y	90784738	90816464	1	8	0	26	82	17	2	10	19	12	5	15	J3QMM0	
ENSMUST00000179486	ENSMUSG00000095368	14	3634512	3642943	1	0	0	0	0	0	0	0	0	0	0	0	Q497R9	
ENSMUST00000179487						33	20	33	41	40	13	0	0	0	0	0		
ENSMUST00000179488	ENSMUSG00000096001	14	37102140	37114022	-1	2	7	23	3	0	6	0	0	0	0	1	A0A0B4J1N3	
ENSMUST00000179489	ENSMUSG00000038563	7	82648614	82777852	1	13	0	19	0	12	6	61	74	0	38	0		Q8C0D5
ENSMUST00000179490	ENSMUSG00000094648	4	88803254	88803802	1	0	0	0	0	0	0	0	0	0	0	0	B1AYI3	
ENSMUST00000179491	ENSMUSG00000095190	7	20724525	20730620	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UTA8	
ENSMUST00000179492						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000179493	ENSMUSG00000095976	7	21908665	21921291	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UT86	
ENSMUST00000179498						0	0	0	13	0	0	0	1	2	2	0		
ENSMUST00000179501	ENSMUSG00000031523	8	36567751	36953143	-1	0	0	2	1	0	1	0	0	0	0	0	J3QPV2	
ENSMUST00000179502	ENSMUSG00000096175	13	119912095	119929272	-1	0	0	0	0	0	0	0	0	0	0	0	J3QK00	
ENSMUST00000179503	ENSMUSG00000054676	7	38183217	38197568	1	0	6	0	1	0	0	141	13	172	0	201		
ENSMUST00000179504	ENSMUSG00000096729	2	83967313	83969805	1	0	0	0	0	0	0	0	0	0	0	0	J3QM48	
ENSMUST00000179505	ENSMUSG00000095041	JH584304.1	52190	59690	-1	100	86	45	21	119	68	292	948	338	57	733		
ENSMUST00000179506	ENSMUSG00000073208	5	15709501	15714271	-1	0	12	50	10	0	4	0	0	0	0	0	J3QMF9	
ENSMUST00000179508	ENSMUSG00000093918	Y	3294976	3306449	-1	0	0	0	0	0	0	0	0	0	0	0		O35698
ENSMUST00000179511	ENSMUSG00000095768	7	20702296	20703216	-1	0	6	0	1	0	0	0	0	0	0	0	D3YTY2	
ENSMUST00000179512	ENSMUSG00000095643	14	53032848	53033419	1	0	0	0	0	0	0	0	0	0	0	0	J3QMG8	
ENSMUST00000179513	ENSMUSG00000094228	10	100345990	100346859	1	0	0	0	0	0	0	0	0	0	0	0	E9PZY4	
ENSMUST00000179515						0	3	2	102	10	3	64	109	51	34	37		
ENSMUST00000179519						2	2	5	6	3	1	0	0	0	0	0		
ENSMUST00000179520	ENSMUSG00000094028	12	113430528	113430538	-1	0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000179521	ENSMUSG00000017781	11	75588097	75628804	1	17	14	34	0	23	13	0	0	0	0	0	J3QPW1	
ENSMUST00000179522	ENSMUSG00000094161	Y	17845724	17846266	-1	0	0	22	0	0	0	0	0	0	0	0	A8HG57	
ENSMUST00000179523	ENSMUSG00000094660	Y	84562572	84564907	-1	0	0	0	0	0	0	0	0	0	0	0	Q497R7	
ENSMUST00000179525	ENSMUSG00000054676	7	38183217	38197568	1	0	0	24	8	4	0	5613	10345	4356	1092	2823		
ENSMUST00000179526	ENSMUSG00000046593	4	40472180	40477168	1	2	5	6	50	5	0	3	6	2	1	1	B7ZN35	A7E1Z1
ENSMUST00000179528						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179531	ENSMUSG00000026269	1	92910783	92924384	1	20	12	34	38	28	25	50	108	60	3	73	J3QNU3	
ENSMUST00000179532	ENSMUSG00000094391	X	31117674	31119170	1	4	0	0	0	5	0	0	0	0	0	0	J3QML3	
ENSMUST00000179536						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179538	ENSMUSG00000094727	X	32973897	32975846	1	0	0	0	0	1	0	0	0	0	0	0		Q99N64
ENSMUST00000179539	ENSMUSG00000079710	17	14964189	15041537	-1	0	0	0	35	0	2	0	0	0	2	0		
ENSMUST00000179543	ENSMUSG00000095567	4	156236010	156247616	1	0	7	28	47	0	14	270	286	244	86	374	J3QK52	
ENSMUST00000179544	ENSMUSG00000094962	3	55461985	55472210	-1	0	0	0	0	0	0	0	0	0	0	0	J3QJU4	
ENSMUST00000179546	ENSMUSG00000009070	10	74957477	75032586	-1	0	0	0	0	0	0	0	0	0	0	0		Q9D3W1
ENSMUST00000179547	ENSMUSG00000094211	X	32941768	32942945	1	0	0	0	0	1	0	0	0	0	0	0	J3QMZ1	
ENSMUST00000179549	ENSMUSG00000095098	19	5456789	5457397	-1	1	2	4	318	8	6	9	43	28	35	19		Q6PDY0
ENSMUST00000179550	ENSMUSG00000094018	3	90590247	90591508	1	2	1	0	4	6	5	1	16	0	4	2	J3QMC7	
ENSMUST00000179551						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179552	ENSMUSG00000095824	2	83984743	83987235	1	0	0	0	3	0	0	0	1	1	0	0	J3QNR0	
ENSMUST00000179553	ENSMUSG00000035171	19	21581202	21652976	-1	2	4	0	0	0	0	23	39	47	160	45	J3QQ03	
ENSMUST00000179554	ENSMUSG00000095677	17	6648941	6655939	-1	0	0	5	208	0	0	1253	3268	999	4260	657		P51807
ENSMUST00000179555	ENSMUSG00000046572	5	38668484	38684826	-1	0	0	0	43	0	0	4	6	10	2	6	J3QPN0	
ENSMUST00000179556	ENSMUSG00000045252	7	25072567	25083492	1	16	25	46	34	0	23	362	488	379	0	252		Q8BY46
ENSMUST00000179558	ENSMUSG00000095242	Y	10322618	10324589	-1	0	1	2	1	0	0	0	0	0	0	0	J3QM72	
ENSMUST00000179560	ENSMUSG00000095444	12	113470694	113470710	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179562						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000179563	ENSMUSG00000041685	13	98723407	98815449	-1	0	0	0	25	0	0	4	0	106	0	6	J3QPQ1	
ENSMUST00000179564						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179565	ENSMUSG00000036292	16	43980350	44027945	-1	0	0	42	0	0	0	1	18	5	10	11		Q8CI52
ENSMUST00000179566						3	3	1	0	7	0	9	7	6	25	5		
ENSMUST00000179567						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000179568	ENSMUSG00000096770	3	113279843	113291449	-1	3	6	4	1	2	2	0	0	0	0	0		P00688
ENSMUST00000179569	ENSMUSG00000096255	17	6430112	6436293	1	0	3	0	74	8	2	1981	6845	1939	8940	1610		P51807
ENSMUST00000179570	ENSMUSG00000095353	Y	44980580	44981263	-1	0	0	4	0	0	0	0	0	0	0	0	J3QM57	
ENSMUST00000179572						54	59	34	23	52	25	2	8	2	0	3		
ENSMUST00000179573	ENSMUSG00000096094	1	75220095	75232102	-1	1	1	0	8	3	3	0	0	0	0	0	J3QMK5	
ENSMUST00000179574	ENSMUSG00000033491	9	86743649	86758443	1	0	0	0	0	0	0	0	41	0	0	0		Q8C0F9
ENSMUST00000179577						659	660	2357	1276	878	426	19	225	78	38	79		
ENSMUST00000179580	ENSMUSG00000096038	14	53337122	53337639	1	3	0	4	2	4	1	0	0	0	0	0	J3QMG8	
ENSMUST00000179583	ENSMUSG00000093915	14	53240745	53241244	1	1	0	1	2	1	0	0	0	0	0	2	A0A075B6A4	
ENSMUST00000179584	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	749	2324	1195	53	466	Q3U3S6	
ENSMUST00000179586						1	1	0	0	4	2	0	0	0	0	0		
ENSMUST00000179588						7	3	57	10	4	2	0	0	0	0	0		
ENSMUST00000179590	ENSMUSG00000094773	Y	9344836	9347184	-1	0	0	0	0	3	0	0	0	0	0	0	J3QN84	
ENSMUST00000179591						3	2	56	0	4	0	0	0	0	0	0		
ENSMUST00000179592	ENSMUSG00000031565	8	25513654	25575714	1	0	0	47	54	0	6	0	0	0	0	0	J3QN85	
ENSMUST00000179593						5	2	0	42	2	0	18	42	9	7	25		
ENSMUST00000179594	ENSMUSG00000095358	7	23217332	23218255	1	1	0	0	0	0	0	0	0	0	0	0	D3YTY1	
ENSMUST00000179595	ENSMUSG00000094679	Y	9199824	9202190	-1	0	0	0	0	0	0	0	0	0	0	0	J3QMK7	
ENSMUST00000179597						5	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000179598	ENSMUSG00000094410	1	133619940	133661318	-1	24	19	28	60	24	4	213	197	542	12	383	G0LE24	D2EAC2
ENSMUST00000179600	ENSMUSG00000058328	X	73107635	73292976	-1	0	4	0	1	0	0	0	0	0	0	0	A2BI45	
ENSMUST00000179601	ENSMUSG00000093922	17	87920977	87921393	1	2	1	9	5	5	1	0	0	0	0	0		
ENSMUST00000179602						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179605	ENSMUSG00000038895	9	22055460	22071345	-1	0	0	0	171	0	0	30	56	45	7	60		Q6YND2
ENSMUST00000179607	ENSMUSG00000095370	14	53318798	53319284	1	1	0	3	0	6	0	0	0	2	1	0	A0A075B6A6	
ENSMUST00000179611						0	2	7	8	9	3	2	4	0	0	2		
ENSMUST00000179612	ENSMUSG00000094867	Y	10616361	10616903	1	18	9	196	70	23	12	0	0	0	0	0	J3QP38	
ENSMUST00000179613	ENSMUSG00000089694	6	85706727	85713205	-1	0	0	0	0	0	0	0	0	0	0	0	E0CYR6	
ENSMUST00000179614	ENSMUSG00000075225	10	41538846	41709300	-1	15	9	14	16	7	2	0	0	0	0	0		Q0VG85
ENSMUST00000179618	ENSMUSG00000050468	2	127338639	127357651	1	0	0	0	0	0	7	0	0	0	0	0		Q6HA09
ENSMUST00000179619	ENSMUSG00000031785	8	94977109	95014208	1	13	14	26	42	21	0	0	27	47	0	20		Q8K209
ENSMUST00000179620	ENSMUSG00000035242	10	80826656	80829290	1	3	2	0	0	7	1	2446	2596	1182	218	680	J3QM60	
ENSMUST00000179623	ENSMUSG00000096850	Y	90838869	90839177	-1	0	0	0	0	0	0	0	0	0	2	0	Q3UE70	
ENSMUST00000179624	ENSMUSG00000023826	17	10840384	12063361	1	0	4	0	7	3	0	0	0	0	0	0	J3QMF8	
ENSMUST00000179625	ENSMUSG00000024534	18	52767709	52915935	1	0	5	23	0	0	0	0	0	0	0	1	J3QNK1	
ENSMUST00000179626	ENSMUSG00000095180	X	37804842	37808876	1	2	0	2	0	0	2	0	0	0	0	0	Q3UJH4	
ENSMUST00000179627	ENSMUSG00000094350	JH584294.1	137009	137560	1	8	7	6	5	4	2	0	0	0	0	0	Q8C8H0	
ENSMUST00000179629	ENSMUSG00000093927	Y	5043937	5046265	1	0	0	0	0	0	0	0	0	0	0	0	J3QN17	
ENSMUST00000179631						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179633						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179634						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179635						22	23	19	14	28	15	4	8	12	0	13		
ENSMUST00000179636	ENSMUSG00000019894	10	103367808	103419378	1	0	13	60	33	13	0	0	0	0	0	1		Q8BG16
ENSMUST00000179637						3	1	1	7	0	0	3	5	0	3	5		
ENSMUST00000179644	ENSMUSG00000095552	JH584293.1	140956	142665	1	0	0	4	0	0	2	0	0	0	0	0		
ENSMUST00000179647	ENSMUSG00000094447	15	34349176	34356421	-1	1	2	1	1	0	0	1	1	0	2	0	Q9CX21	
ENSMUST00000179648						127	128	86	135	134	85	1	9	6	5	5		
ENSMUST00000179649	ENSMUSG00000079389	14	4317283	4325721	1	0	0	8	5	8	5	0	0	0	0	0	J3QJX5	
ENSMUST00000179652						4	10	6	6	8	4	0	0	0	0	0		
ENSMUST00000179654	ENSMUSG00000094277	13	90583400	90583765	1	1	2	22	3	0	0	0	0	0	0	0	J3QMQ4	
ENSMUST00000179655						6	6	6	5	6	1	0	0	0	0	0		
ENSMUST00000179657	ENSMUSG00000096670	12	113716670	113717103	-1	9	13	11	13	8	3	1	0	1	0	8	A0A075B6A7	
ENSMUST00000179658	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	Z4YNB2	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000179659	ENSMUSG00000095912	14	5164535	5169233	1	2	0	0	1	0	0	0	0	0	0	0	A6NAT8	
ENSMUST00000179660						4	5	21	0	7	3	0	4	0	2	1		
ENSMUST00000179662						7	9	3	9	9	1	0	0	0	0	0		
ENSMUST00000179663	ENSMUSG00000093868	Y	24455057	24457399	1	0	0	0	0	0	0	0	0	0	0	0	Q62458	
ENSMUST00000179664						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179665	ENSMUSG00000095950	Y	10533609	10536042	-1	0	0	0	0	0	0	0	0	0	0	0	Q3TTD8	
ENSMUST00000179666						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179668						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179669	ENSMUSG00000020950	12	49382660	49386861	1	1	1	1	40	2	1	0	0	0	0	0	Q3V1Q8	Q60987
ENSMUST00000179671						7	5	3	4	9	3	9	30	0	15	2		
ENSMUST00000179672	ENSMUSG00000094782	Y	47450960	47482990	1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000179673						48	34	93	69	30	12	16	276	77	3	134		
ENSMUST00000179677	ENSMUSG00000094791	JH584299.1	314841	317584	1	2	2	4	2	0	1	0	0	0	0	0		
ENSMUST00000179679	ENSMUSG00000096732	5	11416418	11421235	1	0	0	0	0	0	0	0	0	0	0	0	J3QNG9	
ENSMUST00000179683						2	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000179684	ENSMUSG00000021203	12	103388682	103406350	1	1	3	0	5	0	5	0	0	0	0	0	D3Z0Y8	
ENSMUST00000179685	ENSMUSG00000096546	10	25527943	25536267	-1	7	1	1	10	7	5	0	0	0	2	0	J3QMJ4	
ENSMUST00000179687						0	0	0	69	3	1	0	2	3	0	3		
ENSMUST00000179688	ENSMUSG00000096467	7	33278370	33280338	-1	0	0	1	0	1	0	0	0	0	0	0	J3QM75	
ENSMUST00000179689	ENSMUSG00000024534	18	52767709	52915935	1	0	3	43	0	7	0	1	0	0	0	0	J3QP58	
ENSMUST00000179693	ENSMUSG00000070495	2	173093609	173119525	-1	15	37	104	18	5	8	0	16	3	2	5		A2APF3
ENSMUST00000179694	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179695	ENSMUSG00000095253	17	32815449	32830261	-1	144	140	604	146	108	63	12	63	35	15	44	J3QMI2	
ENSMUST00000179696						1	4	1	4	2	2	0	0	0	0	0		
ENSMUST00000179700	ENSMUSG00000094887	JH584299.1	587624	625594	1	18	0	0	0	1	0	0	0	0	0	0	Q5XK27	
ENSMUST00000179701	ENSMUSG00000096106	14	53001713	53002232	1	2	2	2	2	3	2	0	0	0	0	0	Q5R1F6	
ENSMUST00000179703						10	20	22	7	15	0	0	3	0	0	0		
ENSMUST00000179707	ENSMUSG00000096534	16	88962273	88962873	-1	2	0	5	2	4	0	0	0	0	0	0		Q8C1I6
ENSMUST00000179709	ENSMUSG00000020111	10	59702477	59864132	1	0	0	0	0	0	1	284	271	191	10	136		Q8VCX5
ENSMUST00000179715	ENSMUSG00000094915	GL456212.1	31967	34932	-1	3	0	2	6	1	0	0	0	0	2	5		
ENSMUST00000179716	ENSMUSG00000096645	X	31618216	31618920	-1	4	2	4	7	2	3	0	0	0	0	0	J3QNQ0	
ENSMUST00000179717	ENSMUSG00000038372	13	31819579	32338712	-1	0	0	0	56	0	1	0	0	0	0	0	J3QMC6	
ENSMUST00000179718						0	0	15	0	13	0	7	11	17	5	7		
ENSMUST00000179719						6	8	14	174	22	11	2	11	4	4	12		
ENSMUST00000179720						5	8	2	8	5	2	0	0	0	0	0		
ENSMUST00000179721	ENSMUSG00000031732	8	109868542	109944671	1	10	9	20	59	18	9	8	11	11	2	18	J3QM82	
ENSMUST00000179722						0	0	0	33	0	0	0	0	0	0	0		
ENSMUST00000179725	ENSMUSG00000095101	4	88799665	88801126	1	258	220	400	3499	438	178	0	3	1	0	0	B1AYI3	
ENSMUST00000179726	ENSMUSG00000096421	10	77726486	77726848	1	8	6	18	7	7	3	0	0	0	0	0	J3QK64	
ENSMUST00000179728	ENSMUSG00000094724	17	6978860	7011299	1	20	19	60	14	18	19	10	20	20	5	17	Q5FWA0	Q9CQ01
ENSMUST00000179729						2	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000179730						34	16	74	43	15	16	0	3	0	0	0		
ENSMUST00000179731						0	0	0	0	0	1	0	2	0	0	0		
ENSMUST00000179734	ENSMUSG00000095779	4	42466752	42589938	1	46	4	0	7	47	12	4	5	4	0	0	Q6PCY5	
ENSMUST00000179735	ENSMUSG00000095673	10	100366499	100367412	1	6	4	0	6	7	0	0	0	0	0	0	E9Q4V5	
ENSMUST00000179738						0	1	3	0	7	0	1	0	0	5	0		
ENSMUST00000179741	ENSMUSG00000094635	12	88284535	88286055	-1	35	23	59	39	60	30	0	0	0	0	0	J3QNS6	
ENSMUST00000179743	ENSMUSG00000096259	5	94218005	94222010	1	0	0	0	0	0	0	0	0	0	0	0	J3QPH3	
ENSMUST00000179744	ENSMUSG00000026601	1	156323509	156421159	-1	0	0	2	0	0	0	0	0	0	0	0	J3QMK9	
ENSMUST00000179745						16	4	22	25	0	8	0	0	0	0	0		
ENSMUST00000179747	ENSMUSG00000095360	14	6435796	6444611	-1	0	0	0	4	0	0	0	0	0	0	0	J3QQ25	
ENSMUST00000179748	ENSMUSG00000025817	2	5845019	5871895	1	0	0	0	0	0	0	35	83	32	170	47		Q9JKX6
ENSMUST00000179751	ENSMUSG00000095654	9	92192936	92209772	1	6	3	4	2	0	3	4	11	13	3	7	J3QM92	
ENSMUST00000179755	ENSMUSG00000018909	7	99535466	99606771	1	23	12	65	121	24	11	61	184	25	49	0	J3QNU6	
ENSMUST00000179756						0	0	7	0	0	0	5	2	2	2	8		
ENSMUST00000179757						5	1	3	3	5	0	0	1	0	1	0		
ENSMUST00000179758	ENSMUSG00000058022	13	41763148	41847684	-1	0	0	0	0	0	0	28	181	25	107	48		Q8C138
ENSMUST00000179759	ENSMUSG00000024049	17	71019521	71126856	1	1	0	0	0	0	0	2	10	5	0	3		Q62234
ENSMUST00000179760	ENSMUSG00000095562	X	170009659	170019281	1	7	2	4	1089	19	3	0	3	8	0	2	J3QM40	
ENSMUST00000179762	ENSMUSG00000079018	15	75044018	75048830	-1	4	0	8	11	13	3	941	2613	500	1251	516		P0CW02
ENSMUST00000179765	ENSMUSG00000018537	11	97688823	97700497	-1	0	15	42	97	7	0	0	0	0	0	0		P23798
ENSMUST00000179766	ENSMUSG00000041907	1	42952872	43035456	1	30	10	48	55	26	8	0	0	0	0	0	Q148B5	Q9EQQ4
ENSMUST00000179767	ENSMUSG00000094146	10	77715807	77716169	1	2	5	12	3	11	3	0	0	0	0	0	J3KMP7	
ENSMUST00000179768	ENSMUSG00000035171	19	21581202	21652976	-1	1	0	0	3	6	0	0	0	0	0	4	J3QNR9	
ENSMUST00000179769	ENSMUSG00000008373	7	3629985	3642486	1	9	7	43	0	22	9	0	0	0	0	0		Q8CCF0
ENSMUST00000179770	ENSMUSG00000020454	11	3202392	3244588	1	3	0	0	27	4	0	1	0	256	0	59		Q9EST3
ENSMUST00000179777	ENSMUSG00000094429	1	116802983	116823410	1	4	4	1	0	3	2	0	0	0	0	0	J3QNY8	
ENSMUST00000179780	ENSMUSG00000049580	7	98350668	98361328	-1	0	0	9	0	28	8	1	1	1	0	22	Q08EE6	Q8CBR6
ENSMUST00000179781	ENSMUSG00000023175	10	79704491	79711969	1	5	4	0	7	0	0	594	1781	539	587	563		P18572
ENSMUST00000179784	ENSMUSG00000078517	4	139352587	139378730	1	20	20	32	0	0	0	0	0	0	11	216		Q8C7X2
ENSMUST00000179787						42	23	101	56	32	28	1	5	7	1	5		
ENSMUST00000179788	ENSMUSG00000073077	X	79266559	79517285	-1	1	0	0	1	2	0	0	0	0	0	0	J3QP97	
ENSMUST00000179789	ENSMUSG00000096746	14	52744249	52744840	1	6	5	8	11	3	5	0	5	0	0	1	Q5R1I1	
ENSMUST00000179792						1	1	0	2	4	2	1	1	2	3	0		
ENSMUST00000179793	ENSMUSG00000095386	4	104857329	104859137	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDC9	
ENSMUST00000179796	ENSMUSG00000096407	12	114416596	114417053	-1	1	0	0	0	1	0	0	0	0	0	0	J3QK03	
ENSMUST00000179797	ENSMUSG00000096887	6	79817916	79818364	1	253	350	1037	620	614	564	1596	8458	2801	7711	1595	J3QJY3	
ENSMUST00000179799	ENSMUSG00000095522	3	59861051	59877313	1	2	0	2	1	2	0	0	0	0	0	0	J3QPI0	
ENSMUST00000179800						14	12	22	28	11	2	0	0	0	0	0		
ENSMUST00000179801	ENSMUSG00000102752	1	170298199	170306332	-1	24	17	35	37	26	13	414	625	533	12	282	J3QNH8	
ENSMUST00000179802	ENSMUSG00000096188	8	104348191	104395807	-1	47	31	132	152	58	32	33	40	31	13	73		Q8CJ61
ENSMUST00000179803	ENSMUSG00000095466	14	42763525	42768821	-1	19	12	0	5	13	2	0	0	0	0	0	J3QN18	
ENSMUST00000179804	ENSMUSG00000046798	5	5489537	5514958	-1	0	0	0	0	5	0	0	0	0	0	0		Q9ET43
ENSMUST00000179806						5	6	17	4	0	3	0	11	0	2	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000179811	ENSMUSG00000095578	Y	80133779	80159975	1	0	0	0	0	0	0	0	0	0	0	0	J3QNY0	
ENSMUST00000179814	ENSMUSG00000096872	19	9847562	9852808	1	3	6	9	2	3	2	0	0	0	0	0	J3KMP9	
ENSMUST00000179818	ENSMUSG00000032637	7	126491708	126503437	-1	2	0	0	24	4	0	16	23	16	2	10	J3QP59	
ENSMUST00000179820						105	78	682	102	84	51	9	84	32	9	59		
ENSMUST00000179821						5	0	0	0	0	0	0	3	0	9	2		
ENSMUST00000179824	ENSMUSG00000096230	5	93924777	93929052	-1	16	13	20	18	10	8	0	0	0	0	0	J3QMM8	
ENSMUST00000179826	ENSMUSG00000053963	1	180432387	180483504	-1	2	0	0	82	0	0	0	0	0	0	0	J3QP43	
ENSMUST00000179828	ENSMUSG00000047880	9	44511788	44556391	-1	25	23	66	13	27	0	0	13	0	13	66		Q04683
ENSMUST00000179829	ENSMUSG00000094556	Y	9781804	9784197	1	14	11	11	19	14	10	0	0	0	0	0	J3QPJ2	
ENSMUST00000179832	ENSMUSG00000045802	X	96306178	96456294	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BL67	
ENSMUST00000179836	ENSMUSG00000063142	14	23289431	24004859	-1	0	0	0	0	0	0	0	0	0	0	0	J3QP84	
ENSMUST00000179837	ENSMUSG00000026269	1	92910783	92924384	1	0	1	6	0	1	0	38	28	65	0	34	J3QNA8	
ENSMUST00000179839	ENSMUSG00000095891	9	3025417	3033289	1	728	610	584	596	745	609	1	0	0	0	0	J3QNK0	
ENSMUST00000179842	ENSMUSG00000035165	7	100176670	100184869	1	0	0	0	0	0	0	3	4	0	2	1	Q545H9	Q9WTW2
ENSMUST00000179847						19	32	38	35	43	20	4	5	10	3	17		
ENSMUST00000179848	ENSMUSG00000094024	17	39406359	39410992	1	0	6	13	4	3	4	0	0	0	0	0	A8R0V1	
ENSMUST00000179850						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179851						32	22	102	35	37	16	0	0	0	0	0		
ENSMUST00000179852	ENSMUSG00000021368	13	43151744	43171501	-1	0	0	17	65	21	0	12	27	5	12	11		Q9D0K0
ENSMUST00000179853						6	8	9	6	7	3	0	0	0	0	0		
ENSMUST00000179854						21	11	54	44	33	8	153	291	170	17	293		
ENSMUST00000179855	ENSMUSG00000017561	11	80046493	80080991	-1	0	0	0	0	0	0	0	48	39	10	19	J3QP70	
ENSMUST00000179856						3	2	56	0	4	0	0	0	0	0	0		
ENSMUST00000179857	ENSMUSG00000093904	8	126930664	126945921	-1	20	22	43	221	32	23	240	479	179	180	212	Q4KL41	Q9DCC8
ENSMUST00000179859	ENSMUSG00000095662	X	11318256	11318764	1	7	0	10	7	13	0	0	0	0	0	0	Q5M8Q2	
ENSMUST00000179860	ENSMUSG00000091698	14	43747866	43755948	1	1	0	0	0	0	0	0	0	0	0	0	J3QMB9	
ENSMUST00000179862	ENSMUSG00000094685	7	104949176	104950441	-1	4	6	10	6	7	3	76	487	111	54	67	Q542I7	O88653
ENSMUST00000179863	ENSMUSG00000026414	1	135836354	135852260	1	0	0	0	0	0	0	0	0	0	0	0	Q6P3Z7	
ENSMUST00000179865	ENSMUSG00000020368	11	50293961	50325673	-1	19	8	25	25	18	8	24	167	15	22	37	Q5SUC3	P35564
ENSMUST00000179868	ENSMUSG00000044033	2	77009902	77170636	-1	0	0	0	0	2	4	0	0	0	0	0	J3QN68	
ENSMUST00000179869	ENSMUSG00000093930	13	119690462	119708086	1	14	8	29	32	11	7	274	555	543	123	380		Q8JZK9
ENSMUST00000179871	ENSMUSG00000095247	JH584293.1	16864	21820	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z1X0
ENSMUST00000179873	ENSMUSG00000039958	6	149139849	149151171	1	0	0	0	0	0	0	0	0	0	0	0		Q80ZM3
ENSMUST00000179874	ENSMUSG00000094624	X	28270710	28293632	-1	0	0	0	0	1	0	0	0	0	0	0	Q62478	
ENSMUST00000179880	ENSMUSG00000094507	Y	74623896	74624978	1	44	37	47	133	57	25	0	0	0	0	0	J3KML9	
ENSMUST00000179881	ENSMUSG00000096385	9	3003346	3006948	1	12804	12879	13146	11213	13103	9412	3	1	1	4	0	J3QN11	
ENSMUST00000179882						6	1	7	11	5	0	0	0	3	2	1		
ENSMUST00000179883	ENSMUSG00000094552	12	113448214	113448229	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179884	ENSMUSG00000095011	Y	33511116	33543164	-1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000179886	ENSMUSG00000095567	4	156236010	156247616	1	24	0	0	6	24	0	23	74	0	0	0	Q8BHX6	
ENSMUST00000179890	ENSMUSG00000096100	GL456211.1	66955	67326	1	9	11	4	12	0	0	0	0	0	0	0		
ENSMUST00000179891	ENSMUSG00000021711	13	104142149	104178469	-1	0	0	0	0	0	0	44	126	107	257	53	J3QNW4	
ENSMUST00000179893	ENSMUSG00000030592	7	29003340	29125151	-1	46	93	275	526	161	36	20	36	32	13	17		E9PZQ0
ENSMUST00000179894						25	13	210	138	38	16	41	556	113	26	254		
ENSMUST00000179898	ENSMUSG00000092167	14	7083208	7100621	-1	2	0	4	0	0	0	0	0	0	0	0	K7N751	
ENSMUST00000179900	ENSMUSG00000096819	Y	17935713	17937330	-1	317	250	180	437	296	139	0	0	0	0	0	A8HG57	
ENSMUST00000179901	ENSMUSG00000096706	Y	5656986	5659574	1	0	0	0	0	0	0	0	0	0	0	0	J3QMZ8	
ENSMUST00000179905	ENSMUSG00000095071	13	120263114	120264517	1	8	8	9	16	11	8	0	0	0	0	0	O70616	
ENSMUST00000179907	ENSMUSG00000096528	18	3471630	3474315	1	575	484	707	874	763	428	59	138	93	30	237	Q3TL09	
ENSMUST00000179909	ENSMUSG00000096370	19	4742913	4811612	-1	2	0	5	11	15	4	61	133	75	11	35	B0LM42	
ENSMUST00000179915	ENSMUSG00000094945	X	37390848	37395621	1	0	6	0	0	0	0	0	0	0	28	2	Q9D3I8	
ENSMUST00000179916	ENSMUSG00000095034	X	123246440	123246907	-1	16	21	109	42	30	3	0	0	0	0	0	J3QNF7	
ENSMUST00000179917	ENSMUSG00000095870	3	92806291	92807891	-1	7	3	8	6	13	0	0	0	0	0	0	J3QP15	
ENSMUST00000179919	ENSMUSG00000096351	4	156246973	156255338	-1	25	9	89	48	28	16	21	23	52	2	43	J3QN61	
ENSMUST00000179922	ENSMUSG00000095867	Y	79148789	79151122	-1	0	0	0	0	0	0	0	0	0	0	0	Q62457	
ENSMUST00000179926	ENSMUSG00000078908	8	113635586	113645178	1	105	74	265	720	36	45	91	632	293	59	28		Q8BMQ8
ENSMUST00000179928	ENSMUSG00000023904	17	23673596	23675227	1	0	0	3	11	3	0	762	745	384	559	262	J3QPD4	
ENSMUST00000179929	ENSMUSG00000019888	10	101681487	102391469	1	5	0	0	12	0	8	0	0	0	0	0		Q9D306
ENSMUST00000179930						9	13	11	25	20	14	3	0	0	4	0		
ENSMUST00000179932						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179935	ENSMUSG00000094576	GL456350.1	23801	25222	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179936	ENSMUSG00000001036	11	61517249	61579687	-1	0	0	0	23	33	5	0	0	0	0	0	J3QNT7	
ENSMUST00000179937	ENSMUSG00000062210	18	49979427	50107173	1	12	11	21	26	10	15	33	189	44	45	29		Q921Z5
ENSMUST00000179938						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179939	ENSMUSG00000029467	5	122453513	122502225	-1	5	0	19	89	0	0	0	0	340	0	241	J3KMM5	O55143
ENSMUST00000179940						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179941	ENSMUSG00000049008	8	15041444	15046078	-1	0	0	40	0	19	7	0	0	0	0	0	Q8C5R5	
ENSMUST00000179943	ENSMUSG00000054520	5	34525838	34563641	1	0	0	19	0	3	12	0	74	0	0	27	Q5U3L0	
ENSMUST00000179944	ENSMUSG00000094443	8	63924694	63952170	-1	11	6	17	38	15	5	0	0	0	0	0	J3QMK1	
ENSMUST00000179946						1	1	7	1	6	0	0	0	0	0	0		
ENSMUST00000179947	ENSMUSG00000093945	14	41977873	41983325	-1	1	0	0	0	0	1	0	0	0	0	0	J3QN25	
ENSMUST00000179949	ENSMUSG00000093950	Y	62462504	62464845	-1	8	12	13	23	5	32	0	0	0	0	0	Q810R8	
ENSMUST00000179951	ENSMUSG00000057280	4	58285960	58374303	1	0	0	0	0	0	0	0	0	0	0	0	J3QPS3	
ENSMUST00000179953	ENSMUSG00000096508	X	135433835	135443830	1	17	0	19	0	0	0	0	0	0	0	0	Q1RLL5	
ENSMUST00000179954	ENSMUSG00000073702	1	39367842	39371911	1	2	4	4	114	4	0	4	20	3	34	7	Q5M9K9	P62900
ENSMUST00000179956	ENSMUSG00000050994	10	10335703	10472326	-1	8	0	12	0	9	0	3	0	1	0	15	J3QMP3	
ENSMUST00000179960	ENSMUSG00000025400	10	127724478	127731767	1	6	0	0	5	0	0	0	0	0	0	0		P55099
ENSMUST00000179968	ENSMUSG00000024457	17	36837134	36859398	1	0	0	0	0	0	0	0	0	0	0	0	J3QN94	
ENSMUST00000179970	ENSMUSG00000094399	Y	87116821	87142917	1	0	0	0	0	0	0	0	0	0	0	0	J3QJX2	
ENSMUST00000179971	ENSMUSG00000035191	7	5109787	5116911	-1	0	4	0	0	0	0	0	1	0	0	1		Q8VH31
ENSMUST00000179972	ENSMUSG00000095570	GL456354.1	146926	149659	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000179973	ENSMUSG00000094564	X	33985639	33986816	-1	17	22	7	10	21	14	0	0	0	0	0	J3QPN2	
ENSMUST00000179976	ENSMUSG00000102418	1	170277320	170286769	1	7	12	38	18	23	5	37	148	36	106	26	Q149T1	
ENSMUST00000179977	ENSMUSG00000095048	4	73668354	73672396	1	0	0	0	0	0	24	0	0	0	0	0	J3QM88	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000179981	ENSMUSG00000096107	13	3361029	3361533	1	10	6	19	181	21	2	23	31	41	4	30	J3QPN4	
ENSMUST00000179982	ENSMUSG00000095891	9	3025417	3033289	1	17876	17512	22899	16263	17037	11273	2	2	4	0	3	J3QMM9	
ENSMUST00000179984						26	13	25	0	29	14	0	0	0	0	0		
ENSMUST00000179985	ENSMUSG00000026601	1	156323509	156421159	-1	1	0	0	4	1	1	0	0	1	0	0	J3QMK9	
ENSMUST00000179986						6	0	5	1	2	0	0	0	0	0	0		
ENSMUST00000179987	ENSMUSG00000094925	14	41348609	41356839	1	0	0	0	0	0	0	0	0	0	0	0	J3QP19	
ENSMUST00000179989	ENSMUSG00000079442	2	32587095	32599698	1	0	2	24	0	0	10	145	15	94	0	24	Q8C3J2	
ENSMUST00000179990	ENSMUSG00000020022	10	94198955	94221443	1	0	0	0	17	0	0	60	100	73	546	64		
ENSMUST00000179991	ENSMUSG00000096194	X	32278394	32280342	1	0	0	0	0	18	0	0	0	0	0	0	J3QMS5	
ENSMUST00000179992	ENSMUSG00000054676	7	38183217	38197568	1	4	6	6	112	13	6	32	21	72	25	30		
ENSMUST00000179993	ENSMUSG00000026269	1	92910783	92924384	1	2	0	1	54	4	0	12	21	36	0	40	J3QQ46	
ENSMUST00000179994						1	1	3	1	7	2	0	0	0	0	0		
ENSMUST00000179996	ENSMUSG00000096433	17	22197265	22225614	-1	401	330	239	331	363	174	74	130	74	66	68	J3QM38	
ENSMUST00000179997	ENSMUSG00000096168	14	53312904	53313422	1	2	2	2	2	3	2	0	0	0	0	0	Q5R1F6	
ENSMUST00000179998	ENSMUSG00000025730	17	25882114	25919727	-1	0	0	12	0	0	0	121	2	0	0	0	Q0PD11	Q8VHQ4
ENSMUST00000179999						4	7	17	0	0	1	0	0	0	0	0		
ENSMUST00000180001	ENSMUSG00000095656	12	113450851	113450867	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180004	ENSMUSG00000094155	X	34450524	34452020	1	0	0	0	6	0	0	0	0	0	0	0	J3QQ50	
ENSMUST00000180006						2	3	9	4	0	0	0	0	0	0	0		
ENSMUST00000180008	ENSMUSG00000006456	19	4800569	4811634	-1	0	0	0	51	0	0	0	0	0	0	0	J3QPT3	
ENSMUST00000180009						6	1	19	7	7	4	0	0	0	0	0		
ENSMUST00000180011						8	14	59	13	13	0	0	0	0	7	1		
ENSMUST00000180013	ENSMUSG00000095565	12	113769850	113770302	-1	0	1	0	0	0	2	0	0	0	0	0	A0A075B697	
ENSMUST00000180014	ENSMUSG00000058186	4	145670685	145704441	1	1	3	8	12	0	6	0	0	0	0	0	A2A9J5	
ENSMUST00000180015	ENSMUSG00000011148	12	112620045	112641354	1	0	0	17	133	18	0	12	63	21	120	87	J3QN31	
ENSMUST00000180016	ENSMUSG00000046311	11	49203292	49218816	1	0	3	3	0	0	0	0	0	0	0	0		Q8C827
ENSMUST00000180020	ENSMUSG00000042079	6	117900324	117925622	1	0	0	0	26	0	14	0	42	0	0	0		Q9Z2X1
ENSMUST00000180021	ENSMUSG00000039217	9	50575273	50581837	1	2	1	0	0	2	0	5	258	9	24	8	Q2PMY2	P70380
ENSMUST00000180022						0	19	10	0	0	9	0	0	0	0	0		
ENSMUST00000180023	ENSMUSG00000051497	11	110968033	111027968	1	21	51	94	0	0	0	0	0	0	0	0		Q9Z307
ENSMUST00000180024	ENSMUSG00000096916	7	27984854	28014115	-1	0	0	3	0	0	3	7	8	6	2	1	J3QPC5	
ENSMUST00000180025	ENSMUSG00000072964	X	135885851	135891081	1	9	6	3	17	2	0	8	14	13	5	8		Q6PB60
ENSMUST00000180027						25	34	57	21	24	9	1	51	12	2	20		
ENSMUST00000180033	ENSMUSG00000039174	3	124556352	124581101	-1	0	2	0	0	0	0	0	0	0	0	0	J3QMC0	
ENSMUST00000180035						247	173	353	176	270	138	64	274	124	8	131		
ENSMUST00000180036	ENSMUSG00000035242	10	80826656	80829290	1	0	0	0	0	0	6	5574	6735	2950	741	1848		P54369
ENSMUST00000180037	ENSMUSG00000024073	17	74528295	74703356	1	17	0	42	85	31	13	0	59	31	0	53		O88738
ENSMUST00000180038	ENSMUSG00000094445	7	52011683	52015728	-1	2	0	5	0	2	3	0	0	0	0	0		J3QM76
ENSMUST00000180040	ENSMUSG00000094911	Y	24795161	24796243	-1	0	0	9	0	0	0	0	0	0	0	0	J3QNB5	
ENSMUST00000180041	ENSMUSG00000033705	2	120629126	120731895	1	0	0	17	16	119	57	192	48	132	0	0		Q80TF6
ENSMUST00000180043	ENSMUSG00000040482	17	34837019	34839233	1	0	0	0	0	10	0	44	0	0	11	0		
ENSMUST00000180044	ENSMUSG00000037624	1	189207930	189402273	-1	8	6	0	2	6	3	0	0	0	0	5		
ENSMUST00000180045	ENSMUSG00000056486	2	73610660	73775346	-1	0	0	0	0	0	0	0	0	0	0	0	A7VK14	Q91V57
ENSMUST00000180046	ENSMUSG00000056342	11	23306895	23490560	1	2	8	25	44	0	21	78	0	373	0	134		Q6ZQ93
ENSMUST00000180048						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180049						3	4	6	7	5	1	1	3	5	21	1		
ENSMUST00000180052	ENSMUSG00000087279	11	70615848	70616890	1	2	0	8	6	0	1	0	2	0	0	0	J3QK56	
ENSMUST00000180053	ENSMUSG00000096619	12	87919423	87919857	-1	0	2	3	1	1	0	0	0	0	0	0	J3QP87	
ENSMUST00000180056	ENSMUSG00000095267	Y	18089116	18091556	1	0	0	0	0	0	0	0	0	0	0	0	J3QPX2	
ENSMUST00000180058						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180059	ENSMUSG00000093954	14	69363504	69503362	-1	1	0	2	50	4	1	0	0	1	0	0	J3QPY4	
ENSMUST00000180062	ENSMUSG00000016918	1	12692277	12861192	1	5	13	13	0	0	0	0	0	0	1	6		Q8K007
ENSMUST00000180063	ENSMUSG00000045326	3	108853678	108890008	-1	28	18	48	32	0	19	0	3	1	0	1	J3QMB8	
ENSMUST00000180064						1	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000180066	ENSMUSG00000096330	13	98279887	98307154	1	3	0	0	0	0	0	0	0	0	0	0	J3QNN2	
ENSMUST00000180067						3	0	0	0	1	0	0	0	0	32	0		
ENSMUST00000180068	ENSMUSG00000048967	8	69887788	69902712	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A0MQP0	
ENSMUST00000180071						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000180072	ENSMUSG00000034566	11	115415689	115419962	-1	0	0	0	0	0	0	420	1065	433	1344	276		Q9DCX2
ENSMUST00000180075	ENSMUSG00000048400	8	95559133	95575455	-1	0	1	7	0	0	0	0	0	0	0	0		Q7M756
ENSMUST00000180076	ENSMUSG00000095954	5	94865436	94885388	1	0	0	1	0	0	0	0	0	0	0	0	D3YUJ6	
ENSMUST00000180077	ENSMUSG00000062691	17	78916500	78920306	1	3	0	0	0	0	0	18	62	4	103	15		Q8BTE5
ENSMUST00000180081	ENSMUSG00000096146	7	46098725	46099897	-1	12	8	24	35	19	5	0	0	0	0	0		Q61743
ENSMUST00000180084						12	0	1	87	0	28	0	0	0	0	0		
ENSMUST00000180086	ENSMUSG00000096210	15	79028212	79030498	1	14	5	125	348	38	13	231	354	155	277	621		P10922
ENSMUST00000180088	ENSMUSG00000034412	11	4186789	4215505	1	13	2	29	0	26	5	211	169	133	42	114		P58802
ENSMUST00000180089						34	29	66	617	40	22	7	17	10	0	0		
ENSMUST00000180092	ENSMUSG00000096700	4	73638121	73642161	1	10	0	23	34	19	0	0	0	0	0	0	J3QMS7	
ENSMUST00000180093	ENSMUSG00000029530	9	123678439	123783457	1	46	58	119	20	64	34	0	3	0	0	14		Q9WUT7
ENSMUST00000180095	ENSMUSG00000030120	6	124931386	124937238	1	0	7	20	82	12	12	1549	1771	976	229	753	Q3UNV7	Q99KX1
ENSMUST00000180097	ENSMUSG00000093813	14	53203122	53203554	1	0	1	3	1	4	1	1	0	1	0	2	A0A075B6A9	
ENSMUST00000180100	ENSMUSG00000096553	10	5069192	5071975	1	13	12	33	14	19	7	0	2	4	1	2	J3KMK7	
ENSMUST00000180101	ENSMUSG00000096094	1	75220095	75232102	-1	0	2	7	0	0	0	0	0	0	0	0	J3KMM7	
ENSMUST00000180103	ENSMUSG00000040899	17	8236043	8257127	1	0	0	0	0	0	0	0	0	0	0	0	Q542B6	O54689
ENSMUST00000180105	ENSMUSG00000094296	15	64817694	64937996	1	75	49	425	79	40	19	1	3	2	0	1	J3QNU5	
ENSMUST00000180106						3	6	13	5	7	0	0	0	0	0	0		
ENSMUST00000180109						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180110	ENSMUSG00000046876	13	45549758	45964991	-1	0	83	0	8	117	0	22	4	0	5	0	J3QPR1	
ENSMUST00000180112						0	15	35	14	13	10	0	0	0	0	0		
ENSMUST00000180119	ENSMUSG00000094728	GL456221.1	58743	59114	1	15	17	56	9	12	5	2	16	6	10	3		
ENSMUST00000180123						5	0	0	44	0	0	0	0	0	0	0		
ENSMUST00000180130	ENSMUSG00000095032	Y	10144735	10147183	-1	0	0	0	0	0	0	0	0	0	0	0	J3QQ23	
ENSMUST00000180131	ENSMUSG00000091594	7	42705469	42727017	-1	0	0	0	0	0	0	0	0	0	0	0	J3QMU6	
ENSMUST00000180132	ENSMUSG00000096529	12	20071882	20072217	1	1	0	0	79	1	0	0	0	0	0	0	J3KMV3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000180133	ENSMUSG00000096769	Y	51125220	51151484	1	0	0	2	0	0	0	0	0	0	0	0	J3QNE0	
ENSMUST00000180135						5	4	2	7	3	3	0	0	0	0	0		
ENSMUST00000180136	ENSMUSG00000090215	7	104300230	104336909	1	0	1	0	6	1	0	0	0	5	0	11	J3QNR8	
ENSMUST00000180138						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180139	ENSMUSG00000051054	13	59740842	59746752	-1	21	10	39	26	30	7	1	1	1	0	3	J3QMS2	
ENSMUST00000180140	ENSMUSG00000023904	17	23673596	23675227	1	10	7	0	0	0	5	126	502	3	116	48		Q9CYQ5
ENSMUST00000180142	ENSMUSG00000027048	2	69238282	69342616	-1	0	0	0	21	11	0	0	0	0	0	0	J3QNY6	
ENSMUST00000180143	ENSMUSG00000094825	14	5438065	5455467	-1	8	13	5	6	13	10	0	0	0	0	0	J3QQ59	
ENSMUST00000180149						3	1	3	3	7	1	2	9	5	0	8		
ENSMUST00000180150	ENSMUSG00000096468	X	54531208	54548016	1	1	2	0	0	1	0	0	0	0	0	0	A6X8J1	
ENSMUST00000180151	ENSMUSG00000096621	3	90775946	90777876	-1	2	0	1	6	2	2	0	0	0	0	0	J3QPE5	
ENSMUST00000180152	ENSMUSG00000061723	7	142498836	142516009	1	0	0	0	0	0	0	0	0	0	0	0	J3QP61	
ENSMUST00000180154	ENSMUSG00000032372	9	92275602	92297752	1	0	0	0	0	0	0	0	0	0	0	0		Q9DCW2
ENSMUST00000180157	ENSMUSG00000094913	10	77810967	77811845	-1	25	8	18	138	24	10	0	0	0	0	0	J3QK30	
ENSMUST00000180159	ENSMUSG00000045996	15	36174010	36177010	1	5	2	0	4	2	2	80	238	67	267	59	Q545V5	Q63871
ENSMUST00000180161	ENSMUSG00000095721	10	77787490	77788200	-1	29	9	45	105	0	4	0	0	0	0	0	J3QMW1	
ENSMUST00000180162	ENSMUSG00000039174	3	124556352	124581101	-1	0	0	0	0	0	0	0	0	0	0	0	J3QPK7	
ENSMUST00000180164	ENSMUSG00000054752	4	53631471	53707009	1	43	47	123	0	41	30	6	14	9	4	18	J3QM95	
ENSMUST00000180165	ENSMUSG00000050813	11	58489719	58492513	-1	14	9	10	10	19	10	0	0	0	0	0	Q5NC45	
ENSMUST00000180167						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180168	ENSMUSG00000094649	19	61174686	61176309	-1	432	508	217	521	440	194	20	121	65	12	35	J3QQ10	
ENSMUST00000180170	ENSMUSG00000095793	Y	35105684	35131833	-1	0	0	0	0	0	0	0	0	0	0	0	J3QJX2	
ENSMUST00000180173	ENSMUSG00000026601	1	156323509	156421159	-1	0	0	3	4	5	0	0	2	0	0	0	J3QNG8	
ENSMUST00000180176						21	22	118	87	20	14	0	3	2	0	1		
ENSMUST00000180177						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180178	ENSMUSG00000095503	5	94612069	94616342	-1	3	5	0	12	3	0	0	0	0	0	0	J3QPS7	
ENSMUST00000180179	ENSMUSG00000094052	Y	70271306	70273642	-1	0	0	0	0	0	0	0	0	0	0	0	J3QPK8	
ENSMUST00000180180	ENSMUSG00000066839	9	22072246	22085438	-1	1	5	0	13	0	6	23	28	25	1	0		
ENSMUST00000180181	ENSMUSG00000093844	12	87644246	87644467	-1	1	3	0	2	2	0	0	0	0	0	0	E9QJZ1	
ENSMUST00000180182	ENSMUSG00000054293	X	107148927	107173661	1	9	11	51	18	0	7	0	26	0	20	0	Q8BY68	
ENSMUST00000180183	ENSMUSG00000030638	7	82173840	82307419	1	0	0	0	0	0	0	0	0	0	0	0	J3QMW2	
ENSMUST00000180184	ENSMUSG00000079391	14	4182576	4204895	1	0	0	0	1	2	2	0	0	0	0	0	E9Q7N1	
ENSMUST00000180188	ENSMUSG00000096330	13	98279887	98307154	1	0	0	0	4	0	0	0	1	1	0	0	J3QN04	
ENSMUST00000180189						105	105	91	73	105	39	8	4	11	0	18		
ENSMUST00000180193	ENSMUSG00000074593	2	164715305	164718068	1	4	3	3	0	4	2	0	0	0	0	0	J3KMK8	
ENSMUST00000180194	ENSMUSG00000072955	X	136954988	136976869	-1	1	0	0	1	0	0	0	11	3	6	1	Q8C0W0	
ENSMUST00000180195	ENSMUSG00000074704	2	151645404	151668533	-1	0	0	0	0	0	0	0	0	0	0	0		A2AU37
ENSMUST00000180196	ENSMUSG00000053897	3	135825279	135888572	1	17	22	112	0	4	10	12	39	23	19	31		Q91W10
ENSMUST00000180197	ENSMUSG00000095229	X	31336454	31337950	1	0	0	12	15	0	0	0	0	0	0	0	J3QNK2	
ENSMUST00000180198	ENSMUSG00000094004	X	135373284	135383393	1	0	0	0	0	0	0	0	0	0	0	0	A2AWL1	
ENSMUST00000180200	ENSMUSG00000049871	16	3945007	3976632	-1	12	12	0	23	12	0	15	54	27	7	87		Q5DU56
ENSMUST00000180201	ENSMUSG00000094066	4	42522580	42528175	-1	0	2	0	0	0	0	0	1	2	0	0		A2APU8
ENSMUST00000180202	ENSMUSG00000096520	Y	3771673	3783267	1	0	0	0	6	0	0	0	0	0	0	0		Q60990
ENSMUST00000180204	ENSMUSG00000040118	5	15934691	16374511	1	4	0	3	0	0	0	0	0	0	0	0	Q14BH8	O08532
ENSMUST00000180207	ENSMUSG00000095887	X	28931821	28954702	-1	0	0	0	0	0	0	0	0	0	0	0	Q62478	
ENSMUST00000180208	ENSMUSG00000095475	JH584299.1	910289	913083	-1	0	0	0	0	0	8	0	0	0	0	0		
ENSMUST00000180210						1	6	1	0	0	0	0	3	0	1	0		
ENSMUST00000180214	ENSMUSG00000046572	5	38668484	38684826	-1	2	1	4	39	0	6	6	0	0	3	0	J3QNT5	
ENSMUST00000180215	ENSMUSG00000073491	1	173566284	173599274	-1	0	0	1	0	0	0	0	0	0	0	0	Q3UPZ5	
ENSMUST00000180217	ENSMUSG00000049657	4	44991242	45012412	-1	0	0	29	31	24	19	0	0	0	0	7		Q7TQG0
ENSMUST00000180219						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180221	ENSMUSG00000096322	9	43829963	43832516	1	3	0	4	13	2	2	0	0	0	0	0	J3QN29	
ENSMUST00000180222	ENSMUSG00000027583	2	181387762	181459426	-1	5	0	10	48	8	0	0	0	0	0	2		Q8BID6
ENSMUST00000180224						1	0	9	2	1	4	0	0	0	4	0		
ENSMUST00000180225						18	14	18	13	25	14	0	1	2	0	4		
ENSMUST00000180230	ENSMUSG00000004221	X	74393290	74453854	1	14	0	0	0	0	0	0	0	0	0	0	Q8VC91	
ENSMUST00000180231						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180232	ENSMUSG00000096066	5	95268493	95272768	-1	7	13	47	30	7	0	0	0	0	0	0	J3QNN3	
ENSMUST00000180233	ENSMUSG00000093803	9	124422622	124476861	-1	0	0	2	8	2	0	39	54	28	8	34	J3QPX4	
ENSMUST00000180234						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000180235						7	0	1	2	5	4	0	0	0	0	18		
ENSMUST00000180239	ENSMUSG00000094595	4	11579665	11587591	1	19	6	24	11	19	7	0	7	0	0	6		Q8BKE5
ENSMUST00000180242	ENSMUSG00000039781	11	120064430	120086827	-1	0	2	8	0	0	0	0	0	8	2	10	J3QMP9	
ENSMUST00000180243	ENSMUSG00000030638	7	82173840	82307419	1	6	2	3	52	3	1	0	0	0	0	0	J3QP51	
ENSMUST00000180245	ENSMUSG00000095625	17	39038285	39040117	1	0	0	1	2	0	0	0	0	0	0	0	A8R0V6	
ENSMUST00000180246	ENSMUSG00000074771	2	136501910	136562091	1	0	0	0	0	5	0	0	0	0	0	0		Q9D2J7
ENSMUST00000180248	ENSMUSG00000094936	19	4784293	4793901	-1	8	3	12	4	2	0	44	18	25	4	15	B7ZN14	Q8C7Q4
ENSMUST00000180249	ENSMUSG00000094570	Y	55213720	55239871	1	0	0	0	0	0	0	0	0	0	0	0	J3QJX2	
ENSMUST00000180250	ENSMUSG00000028886	4	132638987	132724765	1	3	19	0	0	28	0	0	0	0	0	0		P97480
ENSMUST00000180251	ENSMUSG00000095562	X	170009659	170019281	1	0	0	0	0	0	0	0	0	0	0	0	J3QQ04	
ENSMUST00000180252	ENSMUSG00000096847	17	45541940	45549677	-1	69	60	511	634	103	58	0	2	6	0	0		Q68FE7
ENSMUST00000180253						0	0	0	5	2	0	0	0	0	0	1		
ENSMUST00000180255						3	1	1	4	2	1	1	3	3	4	0		
ENSMUST00000180259	ENSMUSG00000024534	18	52767709	52915935	1	0	0	0	0	0	0	0	0	0	0	0	J3QPG2	
ENSMUST00000180260	ENSMUSG00000042208	11	23564961	23633639	-1	0	0	0	0	0	0	33	0	13	0	0		Q68FF0
ENSMUST00000180261						0	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000180262						0	0	0	0	1	0	1	1	0	0	0		
ENSMUST00000180266	ENSMUSG00000093818	12	113525313	113525329	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180268						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180269						3	3	0	0	4	2	24	39	23	6	33		
ENSMUST00000180270	ENSMUSG00000093803	9	124422622	124476861	-1	0	0	0	25	0	0	3	24	9	3	10	J3QNX1	
ENSMUST00000180277	ENSMUSG00000027281	2	136891218	137071950	1	0	0	4	0	0	0	2	0	23	0	3		Q9D7Y9
ENSMUST00000180278	ENSMUSG00000028550	4	99193934	99259787	1	0	0	0	0	0	0	39	272	69	28	11		Q811C2
ENSMUST00000180282	ENSMUSG00000096537	13	64481246	64497792	-1	2	5	3	5	2	7	0	0	0	0	0	J3QMB3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000180283	ENSMUSG00000012296	17	46257851	46283026	-1	13	4	17	98	24	15	75	62	38	9	70		Q9DCD5
ENSMUST00000180285	ENSMUSG00000096049	12	88011848	88012282	1	0	0	0	0	0	0	0	0	0	1	0	J3QMW5	
ENSMUST00000180286	ENSMUSG00000027341	2	132239492	132247807	-1	0	8	0	0	0	0	0	115	0	0	0		Q8CIB6
ENSMUST00000180288	ENSMUSG00000069303	13	21833743	21837530	1	0	0	0	2	2	3	25	313	25	27	87	Q8CBB6	
ENSMUST00000180289						2	0	5	12	1	2	0	0	0	0	0		
ENSMUST00000180290	ENSMUSG00000027088	2	69789623	69800005	1	44	70	216	58	75	31	33	78	49	7	53		Q9D9M5
ENSMUST00000180291	ENSMUSG00000094722	JH584298.1	90528	93623	1	0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000180293	ENSMUSG00000103750	3	93290366	93291133	1	58	25	139	2431	70	42	0	0	0	0	0	A0A0A6YX57	
ENSMUST00000180296						180	147	190	200	182	86	6	10	18	0	27		
ENSMUST00000180297	ENSMUSG00000095970	10	77689957	77690757	-1	21	12	56	139	42	15	0	0	0	0	0	J3QJV4	
ENSMUST00000180299						7	7	11	7	7	1	18	13	21	5	16		
ENSMUST00000180300	ENSMUSG00000028675	4	135870918	135873850	-1	0	0	0	0	1	0	8	5	44	210	44	J3QJZ8	
ENSMUST00000180303	ENSMUSG00000095523	JH584299.1	837364	840451	1	0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000180304	ENSMUSG00000035171	19	21581202	21652976	-1	3	2	0	1	2	3	0	0	0	0	2	J3KMS8	
ENSMUST00000180305	ENSMUSG00000062210	18	49979427	50107173	1	67	53	433	113	68	28	4	2	0	3	0	J3QNB8	
ENSMUST00000180306						13	12	37	121	23	12	43	60	73	5	60		
ENSMUST00000180308	ENSMUSG00000102439	3	93273523	93293686	1	3	4	29	71	7	0	0	0	0	0	0	A0A0A6YXI5	
ENSMUST00000180310	ENSMUSG00000095948	Y	3399188	3410167	-1	0	0	3	0	0	0	0	0	0	0	0		O35698
ENSMUST00000180318	ENSMUSG00000096820	Y	13161968	13164408	1	0	0	0	0	0	0	0	0	0	0	0	Q3TTD8	
ENSMUST00000180319						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000180321	ENSMUSG00000094935	12	93927004	93929102	-1	0	9	9	27	0	0	99	182	60	13	52	A6H624	Q9D0E3
ENSMUST00000180322	ENSMUSG00000051224	X	166499812	166518567	-1	0	0	0	0	0	0	0	3	3	0	8		Q3US16
ENSMUST00000180323						5	9	16	2	0	0	0	0	0	0	0		
ENSMUST00000180324	ENSMUSG00000094739	Y	78835721	78838056	-1	0	0	0	0	0	0	0	0	0	0	0	Q9D9T3	
ENSMUST00000180327						5	5	1	91	7	5	0	1	6	2	9		
ENSMUST00000180329	ENSMUSG00000096016	Y	68268651	68294898	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNI1	
ENSMUST00000180332	ENSMUSG00000096650	Y	35895328	35921526	-1	0	0	0	0	0	0	0	0	0	0	0	J3QJX2	
ENSMUST00000180335						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180336	ENSMUSG00000093910	5	143287755	143292356	-1	9	5	32	255	22	12	0	1	0	0	0	J3QPU9	
ENSMUST00000180339	ENSMUSG00000031938	9	15283337	15306448	-1	0	0	0	126	6	7	0	0	0	9	20		Q91V76
ENSMUST00000180341	ENSMUSG00000042079	6	117900324	117925622	1	0	0	5	0	17	12	1631	4738	2235	889	1103		Q9Z2X1
ENSMUST00000180344	ENSMUSG00000094759	X	30820542	30843469	-1	0	0	0	0	1	0	0	0	0	0	0	Q62478	
ENSMUST00000180347	ENSMUSG00000096484	2	83973123	83975615	1	7	7	16	6	9	4	0	0	0	0	0	A2AK42	
ENSMUST00000180350	ENSMUSG00000078441	10	80602882	80615783	1	4	0	9	0	7	0	14	0	15	0	0	Q3TGX0	Q9JKV5
ENSMUST00000180351	ENSMUSG00000024360	18	34902785	34932007	-1	0	0	0	14	0	0	0	0	0	0	0	J3QNS1	
ENSMUST00000180352	ENSMUSG00000094556	Y	9781804	9784197	1	0	0	0	0	0	0	0	0	0	0	0	J3QPJ2	
ENSMUST00000180353	ENSMUSG00000096014	8	12395295	12400126	1	33	26	132	429	39	16	0	2	1	0	0		P53783
ENSMUST00000180355						10	20	10	9	9	5	6	4	4	0	4		
ENSMUST00000180358	ENSMUSG00000000776	14	70438748	70443471	-1	0	9	12	142	14	11	8	27	0	13	0		Q91WD1
ENSMUST00000180359	ENSMUSG00000040997	14	54254188	54270637	1	17	7	11	0	8	0	8	19	42	0	24	Q8C0M2	
ENSMUST00000180360	ENSMUSG00000042302	11	22005828	22342292	-1	0	0	0	57	23	12	0	0	0	9	0		Q69ZW3
ENSMUST00000180362	ENSMUSG00000027523	2	174284320	174346744	1	2	0	0	277	0	6	0	0	0	0	0		Q9Z0F1
ENSMUST00000180365	ENSMUSG00000032182	9	21588709	21592831	-1	0	0	7	0	0	0	36	56	50	15	56		Q99LP8
ENSMUST00000180369	ENSMUSG00000023156	14	8080367	8091834	1	0	0	0	0	0	0	3	21	2	16	0	J3QMX0	
ENSMUST00000180372	ENSMUSG00000096268	Y	5725978	5728317	1	0	0	0	0	0	0	0	0	0	0	0	J3QME2	
ENSMUST00000180373	ENSMUSG00000094869	Y	29655497	29683370	-1	0	0	0	0	0	1	0	0	0	0	0	J3QP42	
ENSMUST00000180375	ENSMUSG00000036112	10	93858489	93897093	-1	1	0	0	0	5	0	0	0	44	195	31	M0QWM9	
ENSMUST00000180376	ENSMUSG00000037210	5	34369933	34486456	1	21	15	45	57	30	13	361	574	562	54	466	M0QWZ1	
ENSMUST00000180378						48	33	51	201	62	35	1	14	3	1	17		
ENSMUST00000180380	ENSMUSG00000094562	14	53757356	53757921	1	7	0	3	2	0	0	0	0	0	4	0	A0A075B6C2	
ENSMUST00000180384	ENSMUSG00000032021	9	40972753	41004628	-1	15	6	25	11	0	0	0	0	0	19	21	M0QWH9	
ENSMUST00000180388						4	2	6	2	5	1	3	0	1	1	0		
ENSMUST00000180392	ENSMUSG00000036112	10	93858489	93897093	-1	0	0	0	0	0	1	8	23	35	0	26	M0QW69	
ENSMUST00000180393	ENSMUSG00000097821	9	114515697	114516424	1	7	2	1	4	9	11	0	0	0	0	0	Q8C888	
ENSMUST00000180394						39	33	154	129	40	40	9	122	32	9	56		
ENSMUST00000180398						1	2	3	1	2	0	21	124	77	19	42		
ENSMUST00000180402						6	7	16	38	18	6	4	14	2	2	38		
ENSMUST00000180414						6	5	12	5	5	4	0	0	0	0	0		
ENSMUST00000180415						0	2	2	0	0	1	11	4	7	8	2		
ENSMUST00000180417	ENSMUSG00000031819	8	120653914	120668573	-1	0	1	1	143	7	1	7	33	20	5	29	M0QWC9	
ENSMUST00000180422						16	12	17	36	10	3	2624	3404	1955	2271	1196		
ENSMUST00000180430	ENSMUSG00000061578	5	117414000	117775003	1	135	121	447	170	166	69	2	12	5	2	8	M0QW59	
ENSMUST00000180433						4	1	2	74	8	2	0	0	0	0	0		
ENSMUST00000180435	ENSMUSG00000097485	CHR_MG153_PATCH	4097182	4099019	1	0	0	0	22	3	0	432	1073	711	261	891		Q9CPY4
ENSMUST00000180436	ENSMUSG00000097918	1	136050804	136051370	1	5	2	10	197	14	8	0	0	0	0	0	M0QWB7	
ENSMUST00000180438	ENSMUSG00000020216	10	80808496	80813498	-1	1	0	0	0	6	0	0	0	0	0	1	M0QW84	
ENSMUST00000180440						3	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000180446						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180448	ENSMUSG00000031822	8	120230536	120581390	1	4	2	11	12	2	5	0	0	0	0	1	M0QWG1	
ENSMUST00000180449						1	1	1	4	5	1	0	0	0	2	0		
ENSMUST00000180453						23	19	18	15	19	4	0	0	0	0	0		
ENSMUST00000180457						12	14	22	42	19	11	8	15	21	0	21		
ENSMUST00000180459	ENSMUSG00000030738	7	126546455	126566411	-1	1	1	3	201	5	2	1	0	9	1	1	M0QWV3	
ENSMUST00000180461						0	0	0	0	0	3	5	16	0	0	0		
ENSMUST00000180463	ENSMUSG00000049353	1	191977370	191988283	1	4	1	9	34	22	2	4	5	3	1	0		Q8BRE0
ENSMUST00000180464	ENSMUSG00000097185	10	112928501	112931155	1	3	3	0	70	6	0	1	0	0	0	1	Q3UPT2	
ENSMUST00000180473	ENSMUSG00000097704	10	52358767	52358853	1	0	0	0	0	0	0	0	0	1	0	0	M0QW83	
ENSMUST00000180475						7	4	23	6	14	3	0	0	0	0	0		
ENSMUST00000180476						4	3	5	2	8	4	0	0	3	0	3		
ENSMUST00000180480	ENSMUSG00000097830	CHR_MG153_PATCH	4035407	4037921	-1	7	1	13	13	4	1	156	224	76	71	157		P19157
ENSMUST00000180484						2	3	0	2	0	3	0	0	0	0	0		
ENSMUST00000180487	ENSMUSG00000097386	11	69120054	69122589	-1	15	15	100	162	26	17	0	2	0	0	1	Q3V3T2	
ENSMUST00000180498						3	1	4	2	4	3	0	0	0	0	0		
ENSMUST00000180499	ENSMUSG00000097611	CHR_MG4212_PATCH	15552440	15557206	-1	18	2	7	10	14	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000180500	ENSMUSG00000057132	14	52110704	52163546	1	0	0	0	0	0	0	0	0	0	1	3	M0QW58	
ENSMUST00000180502	ENSMUSG00000096916	7	27984854	28014115	-1	21	15	25	25	14	8	10	31	13	28	6	A0A087WSI7	
ENSMUST00000180504						2	2	7	2	3	2	0	0	0	0	0		
ENSMUST00000180507						44	39	121	64	47	24	1	2	2	5	7		
ENSMUST00000180510						1	2	2	3	2	0	2	1	0	0	3		
ENSMUST00000180513	ENSMUSG00000057132	14	52110704	52163546	1	1	0	0	0	0	0	0	0	0	0	0	M0QWT5	
ENSMUST00000180514						2	2	0	3	0	2	2	0	0	0	0		
ENSMUST00000180520						1	2	2	0	2	0	0	1	0	0	0		
ENSMUST00000180521	ENSMUSG00000097221	15	12321438	12321899	-1	0	0	0	116	0	2	0	30	62	71	36	Q3V2G9	
ENSMUST00000180522	ENSMUSG00000091831	17	71458327	71460395	-1	4	11	3	5	5	1	0	1	1	0	3	V9GWX6	
ENSMUST00000180526						4	5	0	0	5	10	0	0	0	0	0		
ENSMUST00000180531						167	134	209	162	188	127	57	204	76	44	70		
ENSMUST00000180532						0	0	0	0	1	0	1105	663	717	3539	552		
ENSMUST00000180536	ENSMUSG00000097333	13	67515781	67526177	-1	3	0	1	0	0	0	0	9	8	0	0	M0QWG2	
ENSMUST00000180539						6	8	14	10	4	3	15	61	22	4	26		
ENSMUST00000180540						6	4	4	8	6	1	0	0	0	0	0		
ENSMUST00000180541						32	21	34	351	41	22	0	2	0	0	1		
ENSMUST00000180542	ENSMUSG00000096968	1	170885065	170885881	1	9	11	12	216	13	9	1	1	0	0	0	Q9CY65	
ENSMUST00000180543	ENSMUSG00000078926	13	113035111	113091195	1	0	0	0	27	2	0	0	0	0	0	0	M0QW47	
ENSMUST00000180545						28	18	47	26	21	20	2	13	8	1	7		
ENSMUST00000180548						94	71	108	57	107	49	450	2412	690	122	1057		
ENSMUST00000180549	ENSMUSG00000094220	14	53428711	53430377	1	3	0	6	0	2	0	0	0	1	0	0	Q5R1E6	
ENSMUST00000180552	ENSMUSG00000097153	CHR_MG4136_PATCH	143437164	143450324	-1	5	0	0	0	4	2	0	0	0	0	0		
ENSMUST00000180554						36	23	60	28	35	18	11	48	45	9	34		
ENSMUST00000180559	ENSMUSG00000097025	2	70661248	70662108	-1	0	1	4	74	7	6	0	0	2	1	0	Q8BLW8	
ENSMUST00000180560						1	0	4	2	1	1	34	175	45	13	93		
ENSMUST00000180564						1	3	3	1	1	1	0	0	0	0	0		
ENSMUST00000180565						32	39	69	85	59	14	0	0	0	0	0		
ENSMUST00000180566	ENSMUSG00000022518	16	4835416	4867691	1	4	4	6	2	7	0	0	0	0	0	0	M0QWK8	
ENSMUST00000180568	ENSMUSG00000097550	10	104168515	104170983	1	0	0	0	1	0	0	0	0	0	0	0	M0QWR4	
ENSMUST00000180572	ENSMUSG00000041936	4	156165290	156197488	-1	26	23	37	118	36	0	189	107	219	10	540	M0QWP1	
ENSMUST00000180573						1	0	3	1	2	0	0	5	14	0	25		
ENSMUST00000180575	ENSMUSG00000096994	CHR_MG153_PATCH	4192157	4195418	1	4	4	14	29	9	8	6017	8330	4117	607	2669		P62137
ENSMUST00000180577						25	16	29	43	14	10	0	0	6	3	1		
ENSMUST00000180578	ENSMUSG00000097733	CHR_MG153_PATCH	4081578	4087340	1	5	4	14	3	6	3	0	0	0	0	0		
ENSMUST00000180580	ENSMUSG00000069206	13	67424549	67451624	-1	5	0	0	2	5	0	16	43	0	0	0	M0QWQ8	
ENSMUST00000180587	ENSMUSG00000018752	11	69682577	69696098	-1	0	11	10	143	10	6	20	55	8	18	45	Q8BXS2	
ENSMUST00000180588						34	23	22	21	43	20	0	0	0	0	0		
ENSMUST00000180600						0	2	2	0	3	1	8	198	23	7	23		
ENSMUST00000180605						0	3	0	2	0	0	0	0	13	0	0		
ENSMUST00000180607						0	1	4	1	1	2	6	11	2	0	12		
ENSMUST00000180611	ENSMUSG00000037416	18	49832670	49965473	1	21	0	9	77	23	6	167	243	348	51	206		Q6PNC0
ENSMUST00000180614	ENSMUSG00000097778	CHR_MG4136_PATCH	143412426	143421091	1	0	0	2	0	3	0	125	378	155	14	108		
ENSMUST00000180618						8	8	20	103	7	8	0	3	1	0	4		
ENSMUST00000180619	ENSMUSG00000097778	CHR_MG4136_PATCH	143412426	143421091	1	10	7	22	14	12	6	6	53	25	34	32		
ENSMUST00000180620	ENSMUSG00000097771	CHR_MG153_PATCH	4148618	4154034	1	0	0	0	4	0	0	28	0	17	3	2		
ENSMUST00000180621	ENSMUSG00000097508	CHR_MG153_PATCH	4231898	4233630	1	6	5	15	11	9	2	365	566	212	138	157	Q547B4	Q9CWP8
ENSMUST00000180626						7	10	12	6	11	3	0	0	6	0	8		
ENSMUST00000180627	ENSMUSG00000096949	5	111733924	111734574	1	0	1	1	4	1	0	0	0	0	0	0	M0QWX3	
ENSMUST00000180628	ENSMUSG00000097663	CHR_MG153_PATCH	4057477	4059446	-1	2	2	4	2	2	2	4	7	4	0	0		
ENSMUST00000180629						1	1	4	1	4	1	0	0	0	0	0		
ENSMUST00000180636	ENSMUSG00000022664	16	45139573	45158706	-1	0	6	0	0	0	0	94	23	244	226	138	M0QWG7	
ENSMUST00000180640						5	3	5	3	3	0	0	0	0	0	0		
ENSMUST00000180642	ENSMUSG00000097395	CHR_MG4212_PATCH	15605317	15610062	1	17	21	35	32	28	24	0	0	0	0	0		
ENSMUST00000180644						2	0	7	5	0	2	2	1	2	1	4		
ENSMUST00000180646	ENSMUSG00000057132	14	52110704	52163546	1	4	4	0	0	0	0	0	0	0	0	0	M0QWC0	
ENSMUST00000180647						24	18	26	21	21	14	9	1	3	10	6		
ENSMUST00000180648	ENSMUSG00000053219	10	22158569	22374139	1	6	10	29	1	14	8	0	0	0	0	4	M0QWQ3	
ENSMUST00000180649	ENSMUSG00000097643	15	95787856	95791642	-1	25	8	49	386	34	20	1	7	3	3	3	Q8CAU1	
ENSMUST00000180654						0	8	5	0	10	6	16	0	0	5	3		
ENSMUST00000180655						6	5	6	2	11	1	0	0	0	0	0		
ENSMUST00000180657	ENSMUSG00000033075	15	98038744	98093744	-1	0	2	0	149	17	6	64	79	133	34	112	M0QWX4	
ENSMUST00000180658						11	17	3	0	6	0	83	163	155	63	39		
ENSMUST00000180660	ENSMUSG00000097096	CHR_MG153_PATCH	4099998	4113965	1	0	0	0	50	0	1	948	589	789	73	381		O35954
ENSMUST00000180661						5	2	0	4	4	3	0	0	0	0	0		
ENSMUST00000180664	ENSMUSG00000091779	10	104142987	104153674	1	0	0	0	1	0	0	0	0	0	0	0	M0QWR4	
ENSMUST00000180665	ENSMUSG00000097436	CHR_MG4214_PATCH	37899547	37902220	-1	4	4	5	2	6	2	0	0	0	0	0		
ENSMUST00000180672						7	3	4	3	3	0	0	0	0	0	0		
ENSMUST00000180673						16	10	17	40	3	3	0	3	0	1	0		
ENSMUST00000180675						2	1	3	1	2	2	2	30	6	0	18		
ENSMUST00000180677	ENSMUSG00000043687	8	120608602	120647632	-1	4	0	8	5	5	7	0	0	0	0	0		Q8K1L6
ENSMUST00000180678	ENSMUSG00000024728	19	11139664	11165320	-1	0	0	0	0	0	0	0	0	0	0	0	Q6P8I0	
ENSMUST00000180683						2	3	8	9	5	2	0	0	0	0	0		
ENSMUST00000180687	ENSMUSG00000095426	14	52795165	52795633	1	1	0	0	0	0	0	0	0	2	0	0	A0A075B6B9	
ENSMUST00000180688	ENSMUSG00000036112	10	93858489	93897093	-1	0	0	0	78	1	0	52	112	116	363	161	M0QW48	
ENSMUST00000180692	ENSMUSG00000097427	10	104151497	104153965	1	0	0	0	1	0	0	0	0	0	0	0	M0QWR4	
ENSMUST00000180694	ENSMUSG00000097733	CHR_MG153_PATCH	4081578	4087340	1	0	0	2	1	0	3	0	1	0	0	0		
ENSMUST00000180697						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180702	ENSMUSG00000097153	CHR_MG4136_PATCH	143437164	143450324	-1	0	4	2	2	0	0	0	0	0	0	0		
ENSMUST00000180706	ENSMUSG00000096276	12	87954080	87960672	1	0	0	0	0	5	1	0	0	0	0	0	Q8C2W0	
ENSMUST00000180707	ENSMUSG00000096276	12	87954080	87960672	1	0	0	0	0	2	0	0	0	0	0	0	M0QWF7	
ENSMUST00000180710	ENSMUSG00000097132	CHR_MG153_PATCH	4154605	4156750	1	2	2	8	68	6	3	64	80	32	37	50	Q542J3	Q64697
ENSMUST00000180711	ENSMUSG00000094468	14	53454296	53454784	1	0	0	0	0	0	0	0	0	0	0	0	A0A075B6B4	
ENSMUST00000180714						10	6	4	4	9	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000180716	ENSMUSG00000033075	15	98038744	98093744	-1	3	2	0	36	2	0	26	17	59	0	26	M0QWV7	
ENSMUST00000180717	ENSMUSG00000095387	14	52753367	52753846	1	0	0	9	0	0	0	0	0	0	1	0	Q5R1I0	
ENSMUST00000180720						38	49	86	51	58	21	208	346	244	52	168		
ENSMUST00000180724						0	2	0	1	2	0	0	0	0	0	0		
ENSMUST00000180726						1256	1444	422	337	1320	599	85	207	90	36	147		
ENSMUST00000180736						2	3	2	1	3	1	0	0	0	0	0		
ENSMUST00000180739						3	0	4	102	6	1	0	0	0	0	3		
ENSMUST00000180744						2	1	5	7	0	2	0	0	0	1	1		
ENSMUST00000180745						3	2	5	1	4	1	0	0	0	0	0		
ENSMUST00000180746	ENSMUSG00000094328	3	94047981	94054885	-1	11	20	0	25	7	11	0	0	0	0	0		P0DMR6
ENSMUST00000180755						0	0	0	0	0	5	0	0	0	0	8		
ENSMUST00000180756						3	0	4	7	4	0	0	0	0	0	0		
ENSMUST00000180758	ENSMUSG00000097319	CHR_MG153_PATCH	4114446	4125858	-1	6	0	0	0	4	2	638	743	352	132	325		O08915
ENSMUST00000180760						0	0	0	0	0	0	20	26	9	7	9		
ENSMUST00000180762						0	5	2	2	5	5	10	35	13	0	6		
ENSMUST00000180765	ENSMUSG00000037349	19	6993018	6996117	-1	8	0	14	25	0	0	21	44	30	14	15		Q9DD16
ENSMUST00000180767						11	13	19	26	12	7	10	20	23	1	26		
ENSMUST00000180768	ENSMUSG00000078537	13	119949357	119950806	-1	18	9	21	7	15	17	0	1	0	0	0	Q3UT11	
ENSMUST00000180769						3	2	4	10	12	5	1	1	2	0	0		
ENSMUST00000180773	ENSMUSG00000097112	2	67432816	67433181	-1	3	4	19	3	7	2	0	0	0	0	1	M0QWT1	
ENSMUST00000180776						2	0	4	21	2	0	0	0	0	0	4		
ENSMUST00000180781						53	40	28	26	47	16	12	11	29	6	20		
ENSMUST00000180786						26	17	51	28	23	10	0	2	0	0	0		
ENSMUST00000180787						6	6	12	11	12	8	0	0	0	0	0		
ENSMUST00000180788	ENSMUSG00000095797	14	5469438	5477830	-1	14	0	0	0	0	0	0	0	0	0	0	M0QWX9	
ENSMUST00000180792	ENSMUSG00000071669	16	11322908	11755472	1	0	0	24	46	5	0	30	42	53	9	62		Q9D3S3
ENSMUST00000180794						3	3	9	6	4	0	2	5	14	0	19		
ENSMUST00000180795						5	5	3	9	4	2	8	29	22	2	16		
ENSMUST00000180803	ENSMUSG00000096276	12	87954080	87960672	1	3	4	4	5	0	0	0	0	0	0	0	M0QWH6	
ENSMUST00000180813						0	0	0	0	0	0	10	22	8	13	9		
ENSMUST00000180814						0	0	2	2	0	0	0	0	1	0	1		
ENSMUST00000180817	ENSMUSG00000097126	CHR_MG4214_PATCH	37875228	37879394	-1	20	17	46	361	20	13	0	11	0	0	1		
ENSMUST00000180826						8	4	7	9	7	2	0	0	0	0	0		
ENSMUST00000180827						1	0	0	5	1	0	0	0	0	0	1		
ENSMUST00000180829	ENSMUSG00000029769	6	29396309	29426994	1	0	11	0	0	0	4	0	0	0	0	0	E6Y2W7	
ENSMUST00000180840	ENSMUSG00000036112	10	93858489	93897093	-1	4	0	0	0	0	7	0	0	0	0	0	Q58E65	O08663
ENSMUST00000180843						211	135	1309	291	281	103	7	15	11	5	21		
ENSMUST00000180845	ENSMUSG00000060180	11	67321658	67371586	1	0	33	0	38	0	0	0	0	0	0	0	B1AR69	
ENSMUST00000180847	ENSMUSG00000097696	CHR_MG4212_PATCH	15647048	15651848	1	0	3	8	2	2	0	0	0	0	1	0		
ENSMUST00000180856						25	36	48	47	45	26	9	35	17	3	18		
ENSMUST00000180858	ENSMUSG00000097421	8	12554270	12573320	-1	2	4	1	5	1	0	0	0	0	0	0	Q8C3N8	
ENSMUST00000180859						1	3	10	2	4	2	0	0	0	0	0		
ENSMUST00000180867	ENSMUSG00000094825	14	5438065	5455467	-1	0	4	0	0	2	0	0	0	0	0	1	A6NAS6	
ENSMUST00000180872	ENSMUSG00000032021	9	40972753	41004628	-1	0	3	5	0	6	0	0	10	5	0	0		
ENSMUST00000180873						0	0	1	1	0	1	1	1	1	0	3		
ENSMUST00000180884	ENSMUSG00000078532	4	130531602	130574173	-1	5	5	7	0	6	1	0	2	0	0	3	M0QWW7	
ENSMUST00000180885						5	3	3	1	4	4	0	0	0	1	0		
ENSMUST00000180886	ENSMUSG00000057716	6	39873271	40255150	1	3	0	4	58	9	0	0	0	0	0	0	M0QWJ9	
ENSMUST00000180887	ENSMUSG00000034780	2	67565871	68122689	1	0	4	2	1	2	4	0	0	0	0	0	M0QWQ4	
ENSMUST00000180888						9	7	7	3	10	3	0	2	0	0	0		
ENSMUST00000180889	ENSMUSG00000094144	10	104177024	104179491	1	8	8	12	9	9	3	0	0	1	0	1	M0QWR4	
ENSMUST00000180890						3	7	5	5	9	1	1	0	0	0	2		
ENSMUST00000180891						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000180893	ENSMUSG00000097306	CHR_MG4214_PATCH	37804842	37808876	1	2	0	2	0	0	2	0	0	0	0	0		
ENSMUST00000180900						0	0	0	16	0	0	0	0	0	0	0		
ENSMUST00000180901						0	0	0	0	7	11	0	15	5	11	0		
ENSMUST00000180903	ENSMUSG00000097721	CHR_MG153_PATCH	4156712	4163353	-1	0	0	0	0	0	0	23	0	0	0	0		
ENSMUST00000180909						1	1	0	11	0	0	5	3	0	3	4		
ENSMUST00000180915						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180916	ENSMUSG00000097894	CHR_MG4151_PATCH	3422711	3434183	1	0	0	4	3	2	0	0	0	0	0	0		
ENSMUST00000180918	ENSMUSG00000097856	CHR_MG4136_PATCH	143527062	143573798	1	0	0	2	0	6	3	0	0	0	0	0		
ENSMUST00000180925	ENSMUSG00000097629	CHR_MG153_PATCH	4214237	4223489	1	2	0	0	18	0	0	3	14	5	5	29		Q9QZM3
ENSMUST00000180928	ENSMUSG00000097706	8	47713266	47715021	1	10	4	12	469	29	8	0	2	5	1	3	M0QWF9	
ENSMUST00000180929						3	1	3	2	2	0	0	0	0	0	1		
ENSMUST00000180934	ENSMUSG00000093887	14	3846245	3856085	1	0	0	0	25	0	0	0	0	0	0	0	M0QWI0	
ENSMUST00000180938	ENSMUSG00000076863	14	53875984	53876752	1	3	2	0	2	2	2	1	1	2	1	0	A0A075B6C4	
ENSMUST00000180939						5	2	10	9	4	2	0	0	1	0	1		
ENSMUST00000180940						0	5	16	0	0	3	0	0	0	14	0		
ENSMUST00000180947						6	6	2	3	4	2	0	0	0	1	1		
ENSMUST00000180949	ENSMUSG00000091694	15	77633951	77643286	-1	0	0	0	0	0	0	4	0	0	0	0	E9PUZ0	
ENSMUST00000180950						4	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000180952	ENSMUSG00000026017	1	60098247	60153953	1	0	0	0	0	0	0	0	0	9	0	0		Q8VHI4
ENSMUST00000180954						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000180956	ENSMUSG00000097485	CHR_MG153_PATCH	4097182	4099019	1	2	1	3	3	5	3	27	185	42	11	76		
ENSMUST00000180961	ENSMUSG00000097733	CHR_MG153_PATCH	4081578	4087340	1	2	0	5	6	2	0	0	0	0	0	0		
ENSMUST00000180966						3	3	0	2	0	0	0	0	0	0	0		
ENSMUST00000180971	ENSMUSG00000097100	12	112999964	113001926	1	10	8	15	203	21	3	2	5	4	0	3	M0QWX8	
ENSMUST00000180972	ENSMUSG00000096656	14	53616315	53616914	1	2	0	11	3	1	0	0	0	0	3	4	A0N8N6	
ENSMUST00000180973						7	7	9	6	12	4	5	6	3	6	0		
ENSMUST00000180976						53	53	55	92	52	31	0	0	0	0	0		
ENSMUST00000180978						7	3	14	7	8	2	0	0	0	0	0		
ENSMUST00000180979						6	3	28	82	10	5	40	104	52	5	55		
ENSMUST00000180990						4	0	7	12	12	0	0	0	0	0	0		
ENSMUST00000180994	ENSMUSG00000097696	CHR_MG4212_PATCH	15647048	15651848	1	5	5	3	11	7	3	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000180998	ENSMUSG00000097829	CHR_MG4151_PATCH	3289100	3298942	1	39	27	116	36	53	18	1140	801	1354	116	1213	Q0VE46	O35682
ENSMUST00000181001	ENSMUSG00000054310	7	15388948	15556866	1	0	0	0	0	0	0	0	0	0	0	0	Q9D350	
ENSMUST00000181004	ENSMUSG00000097192	CHR_MG4136_PATCH	143527071	143558234	1	0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000181006						4	2	3	1	3	5	0	0	0	0	0		
ENSMUST00000181009						6	11	21	16	10	7	0	4	2	0	4		
ENSMUST00000181010	ENSMUSG00000097808	CHR_MG153_PATCH	4040285	4042236	-1	4	4	3	2	5	1	2	0	0	0	1		P46425
ENSMUST00000181011						0	0	2	4	0	0	0	0	0	0	0		
ENSMUST00000181012	ENSMUSG00000096951	CHR_MG4136_PATCH	143267431	143299564	-1	1	2	9	0	1	1	0	0	0	3	0		
ENSMUST00000181017	ENSMUSG00000057132	14	52110704	52163546	1	0	0	0	0	0	0	0	0	0	0	1	M0QWM1	
ENSMUST00000181019	ENSMUSG00000097880	CHR_MG4136_PATCH	143394428	143400160	1	6	6	10	10	4	2	0	0	0	0	0		
ENSMUST00000181023	ENSMUSG00000037857	11	77686155	77741921	1	3	0	0	67	0	2	142	547	660	217	579		Q5F2E7
ENSMUST00000181024						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000181025	ENSMUSG00000097169	14	7791587	7792057	1	4	2	3	64	8	0	0	0	0	0	0	M0QWV4	
ENSMUST00000181026						1	2	8	3	4	0	6	17	4	4	14		
ENSMUST00000181027	ENSMUSG00000060180	11	67321658	67371586	1	5	0	4	4	2	4	0	0	0	0	0	M0QWL0	
ENSMUST00000181031						0	6	2	0	0	0	0	0	0	0	0		
ENSMUST00000181035						4	0	3	3	2	2	0	0	0	0	0		
ENSMUST00000181036	ENSMUSG00000090854	10	104194042	104196522	1	0	0	0	0	0	0	0	0	0	0	0	M0QWS9	
ENSMUST00000181037						8	5	14	18	12	6	2	21	9	4	6		
ENSMUST00000181038	ENSMUSG00000095854	14	52855614	52856166	1	0	3	0	1	0	0	1	3	1	5	2	A0A075B6B1	
ENSMUST00000181039	ENSMUSG00000020216	10	80808496	80813498	-1	0	3	14	0	0	0	0	0	0	0	0	M0QW57	
ENSMUST00000181040						8	3	8	22	4	0	403	310	207	104	211		
ENSMUST00000181042						56	56	223	91	69	40	9	17	3	6	10		
ENSMUST00000181051						9	10	14	6	40	0	2693	2286	1624	1902	1090		
ENSMUST00000181059	ENSMUSG00000097550	10	104168515	104170983	1	8	8	12	9	9	3	0	0	1	0	1	M0QWR4	
ENSMUST00000181061	ENSMUSG00000097319	CHR_MG153_PATCH	4114446	4125858	-1	0	0	0	0	0	0	69	21	56	13	20		
ENSMUST00000181062						47	20	146	118	61	25	37	107	24	9	173		
ENSMUST00000181063						2858	3173	3531	2002	3936	1877	41	168	63	35	142		
ENSMUST00000181069						0	1	0	0	0	0	21	88	19	0	38		
ENSMUST00000181071	ENSMUSG00000078994	13	67389309	67399767	-1	0	0	0	0	0	0	0	0	8	0	0	M0QWC3	
ENSMUST00000181074						0	5	8	1	2	5	0	0	0	0	1		
ENSMUST00000181079						2	0	0	4	5	2	0	0	0	0	0		
ENSMUST00000181080	ENSMUSG00000097687	CHR_MG153_PATCH	4135424	4139608	-1	8	9	14	10	8	10	0	3	2	0	2		Q8VHC5
ENSMUST00000181088	ENSMUSG00000095893	9	38046581	38048153	1	5	0	0	2	3	3	0	0	0	0	0	Q7TRE1	
ENSMUST00000181091	ENSMUSG00000036112	10	93858489	93897093	-1	0	0	0	0	0	0	0	283	2	373	0	Q3TMN1	
ENSMUST00000181104						0	5	4	0	5	0	2	3	0	0	0		
ENSMUST00000181108						0	0	0	0	0	0	0	66	113	102	67		
ENSMUST00000181110	ENSMUSG00000097129	10	62449489	62451322	1	5	2	12	86	10	3	1	1	0	0	0	Q8C9C9	
ENSMUST00000181111	ENSMUSG00000031819	8	120653914	120668573	-1	0	0	0	0	0	1	20	33	18	8	8	M0QWY0	
ENSMUST00000181115						5	5	1	6	2	0	0	0	0	1	0		
ENSMUST00000181117	ENSMUSG00000078926	13	113035111	113091195	1	0	0	0	0	0	0	0	1	0	0	0	M0QWN1	
ENSMUST00000181130						1	0	9	3	2	0	3	2	0	13	0		
ENSMUST00000181131	ENSMUSG00000097436	CHR_MG4214_PATCH	37899547	37902220	-1	1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000181136						1	0	1	0	1	0	0	1	0	2	0		
ENSMUST00000181143	ENSMUSG00000097871	4	154336127	154349918	1	4	3	20	6	7	2	0	0	0	0	0	Q3USW4	
ENSMUST00000181150						6	4	1	8	11	3	0	83	0	0	5		
ENSMUST00000181154	ENSMUSG00000091694	15	77633951	77643286	-1	6	0	15	3	4	0	1	0	0	0	0	M0QWF2	
ENSMUST00000181161						0	2	2	2	2	1	0	0	0	0	3		
ENSMUST00000181162						34	31	49	22	24	19	6	8	11	0	4		
ENSMUST00000181163	ENSMUSG00000093848	Y	21241575	21243910	1	0	11	10	0	0	0	0	0	0	0	0	Q62460	
ENSMUST00000181166	ENSMUSG00000097878	10	104160006	104162473	1	0	0	0	1	0	0	0	0	0	0	0	M0QWR4	
ENSMUST00000181168	ENSMUSG00000097411	13	118386630	118388124	1	34	40	91	155	37	23	5	4	1	0	3	Q8BQR5	
ENSMUST00000181171						4	6	0	1	3	2	0	0	0	0	1		
ENSMUST00000181172						1	5	8	0	10	0	97	330	127	59	81		
ENSMUST00000181173	ENSMUSG00000097148	14	11280735	11356726	-1	542	606	2437	755	598	265	16	44	35	15	22	S4R1W1	
ENSMUST00000181174	ENSMUSG00000097405	17	25951472	25963610	1	22	13	45	241	30	13	9	15	20	3	17	Q8C701	
ENSMUST00000181177	ENSMUSG00000022664	16	45139573	45158706	-1	0	0	0	0	0	0	202	704	617	745	447	M0QWE5	
ENSMUST00000181179	ENSMUSG00000097878	10	104160006	104162473	1	8	8	12	9	9	3	0	0	1	0	1	M0QWR4	
ENSMUST00000181181						38	23	188	48	68	38	33	104	69	53	10		
ENSMUST00000181182						2	2	3	4	4	4	0	0	0	1	0		
ENSMUST00000181188						2	0	1	0	1	2	0	0	0	0	0		
ENSMUST00000181201						11	6	3	8	3	1	0	0	0	0	0		
ENSMUST00000181205	ENSMUSG00000094294	Y	21164570	21166905	1	19	5	15	30	25	9	0	0	0	0	0	Q5FWB5	
ENSMUST00000181208						0	3	1	0	3	2	0	0	0	0	0		
ENSMUST00000181210	ENSMUSG00000096149	14	53491115	53491622	1	0	0	0	0	4	0	0	0	0	2	1	A0A075B6B5	
ENSMUST00000181217	ENSMUSG00000036112	10	93858489	93897093	-1	0	0	0	0	0	1	216	685	250	10	124	Q3UI33	
ENSMUST00000181219						1	0	9	5	2	2	31	153	40	10	54		
ENSMUST00000181221	ENSMUSG00000097449	CHR_MG4151_PATCH	3302048	3329611	1	0	1	1	1	0	0	14	3	9	0	17		
ENSMUST00000181223						117	83	442	168	167	80	45	150	76	26	66		
ENSMUST00000181228	ENSMUSG00000097708	CHR_MG153_PATCH	4184357	4191046	-1	10	8	26	21	14	4	1230	1812	937	524	1005		Q8C9V1
ENSMUST00000181233						12	14	0	2	14	9	0	0	0	6	0		
ENSMUST00000181236						0	0	6	19	3	0	0	0	19	20	57		
ENSMUST00000181239	ENSMUSG00000094144	10	104177024	104179491	1	0	0	0	1	0	0	0	0	0	0	0	M0QWR4	
ENSMUST00000181243	ENSMUSG00000097319	CHR_MG153_PATCH	4114446	4125858	-1	0	2	9	8	6	2	162	223	90	17	54		O08915
ENSMUST00000181244	ENSMUSG00000074785	10	94790866	94944578	-1	0	0	3	0	5	0	0	3	0	1	0	M0QWW0	
ENSMUST00000181245	ENSMUSG00000097721	CHR_MG153_PATCH	4156712	4163353	-1	3	0	4	4	0	0	69	45	13	0	38		Q9Z1M4
ENSMUST00000181246						35	30	230	57	34	12	2	5	4	0	4		
ENSMUST00000181249						4	5	9	4	4	4	0	0	0	0	1		
ENSMUST00000181256						4	7	0	4	4	0	0	0	0	0	0		
ENSMUST00000181261	ENSMUSG00000097328	11	69686250	69695849	-1	3	0	1	4	5	0	0	2	0	0	0	M9MMK6	
ENSMUST00000181263						3	2	8	12	5	3	0	0	1	0	0		
ENSMUST00000181276						10	11	25	3	5	6	8	25	9	4	8		
ENSMUST00000181283	ENSMUSG00000037926	11	77216287	77460220	1	0	0	0	0	0	0	601	3	2220	0	2478		
ENSMUST00000181284	ENSMUSG00000024728	19	11139664	11165320	-1	0	2	2	0	4	1	0	0	0	0	0	Q6P8I0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000181287	ENSMUSG00000097427	10	104151497	104153965	1	8	8	12	9	9	3	0	0	1	0	1	M0QWR4	
ENSMUST00000181294						8	7	50	0	16	5	0	2	1	0	0		
ENSMUST00000181297						2	1	12	5	3	0	0	0	0	0	0		
ENSMUST00000181298	ENSMUSG00000054252	5	33721674	33737068	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000181300	ENSMUSG00000096276	12	87954080	87960672	1	0	0	2	0	0	0	0	0	0	0	0	M0QWW9	
ENSMUST00000181313	ENSMUSG00000097581	12	87792580	87796877	1	10	4	3	8	17	6	0	0	0	0	0	M0QWL1	
ENSMUST00000181314	ENSMUSG00000097778	CHR_MG4136_PATCH	143412426	143421091	1	0	0	0	0	0	0	0	0	7	0	10		
ENSMUST00000181319	ENSMUSG00000090659	13	67779754	67792512	1	15	5	6	3	19	4	0	3	0	0	0	M0QWP5	
ENSMUST00000181320	ENSMUSG00000097297	CHR_MG4151_PATCH	3217458	3248370	-1	13	13	26	18	19	9	1024	4116	1946	480	2569		E9Q5R7
ENSMUST00000181321	ENSMUSG00000097854	10	79910856	79911140	1	0	0	1	0	1	0	111	83	0	5	23	M0QWA4	
ENSMUST00000181324	ENSMUSG00000097866	CHR_MG4151_PATCH	3108535	3111950	-1	8	13	33	14	28	9	0	0	0	0	0	D3Z081	
ENSMUST00000181326	ENSMUSG00000096276	12	87954080	87960672	1	17	13	8	17	14	3	0	0	0	0	0	M0QWA3	
ENSMUST00000181329	ENSMUSG00000097909	CHR_MG153_PATCH	4195197	4201602	-1	9	3	13	9	12	4	246	542	201	23	179		Q9Z0F6
ENSMUST00000181333	ENSMUSG00000097919	8	120608786	120668079	-1	0	0	0	20	0	0	0	0	0	0	0	M0QWE2	
ENSMUST00000181334	ENSMUSG00000031819	8	120653914	120668573	-1	0	0	0	4	0	0	1	0	7	0	2	M0QWI7	
ENSMUST00000181339	ENSMUSG00000030898	7	105425817	105470898	1	2	2	0	72	10	0	0	0	0	0	0	Q8BYG7	
ENSMUST00000181341	ENSMUSG00000097333	13	67515781	67526177	-1	0	0	0	1	0	0	0	0	13	58	14	M0QW75	
ENSMUST00000181346						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000181347	ENSMUSG00000096276	12	87954080	87960672	1	3	5	0	3	3	1	0	0	0	0	0	M0QWU7	
ENSMUST00000181349						160	211	247	31	101	49	3	10	8	2	20		
ENSMUST00000181350						4	7	5	3	5	3	0	0	0	0	0		
ENSMUST00000181351						2	2	0	2	2	2	1	3	0	1	8		
ENSMUST00000181352						0	0	0	0	0	0	2	20	3	4	0		
ENSMUST00000181353						11	0	0	9	6	3	1	1	0	0	0		
ENSMUST00000181354						12	7	33	4	6	4	3	9	5	2	14		
ENSMUST00000181357						6	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000181360	ENSMUSG00000095689	14	52844465	52845041	1	9	3	13	4	4	1	0	0	0	1	3	A0N8R0	
ENSMUST00000181363						10	5	28	4	9	6	0	0	0	1	0		
ENSMUST00000181366	ENSMUSG00000036027	9	51289686	51328917	-1	3	1	5	3	2	1	0	0	0	0	0	M0QWA8	
ENSMUST00000181369	ENSMUSG00000097602	2	154612937	154613437	-1	5	4	26	45	10	2	3	0	0	0	0	Q9CUJ8	
ENSMUST00000181372						4	1	6	4	1	4	5	64	5	5	32		
ENSMUST00000181375	ENSMUSG00000097394	CHR_MG153_PATCH	4125960	4132306	1	11	9	23	61	20	7	1351	1751	785	160	613		
ENSMUST00000181377						47	31	69	28	43	14	16	52	53	24	74		
ENSMUST00000181379	ENSMUSG00000037210	5	34369933	34486456	1	43	44	121	48	47	28	13	52	20	11	24	M0QWS6	
ENSMUST00000181386						0	0	9	0	0	0	8	63	18	3	0		
ENSMUST00000181391	ENSMUSG00000030446	13	67813740	67827002	1	0	4	10	1	5	3	0	23	5	0	0	Q7M6W8	
ENSMUST00000181394	ENSMUSG00000096276	12	87954080	87960672	1	0	0	0	2	0	0	0	0	0	0	0	M0QWT2	
ENSMUST00000181399	ENSMUSG00000096953	12	83950690	83951355	-1	0	0	0	91	0	0	0	0	0	0	0	M0QW80	
ENSMUST00000181401	ENSMUSG00000057132	14	52110704	52163546	1	0	0	0	0	0	0	0	0	0	0	0	E7CHD7	
ENSMUST00000181402						4	5	10	10	16	0	35	32	21	5	29		
ENSMUST00000181410	ENSMUSG00000096969	4	123917504	123918022	-1	0	1	0	65	2	0	0	0	0	0	0	Q9CUI2	
ENSMUST00000181413						2	2	1	2	0	0	5	4	8	2	2		
ENSMUST00000181415	ENSMUSG00000097721	CHR_MG153_PATCH	4156712	4163353	-1	0	1	0	0	0	0	12	114	77	9	1		
ENSMUST00000181419						2	4	1	2	3	2	0	0	0	0	0		
ENSMUST00000181421						6	6	0	0	8	3	0	0	0	0	0		
ENSMUST00000181423						5	5	0	0	2	0	0	0	0	2	0		
ENSMUST00000181429						19	22	14	54	13	8	0	2	4	2	5		
ENSMUST00000181431	ENSMUSG00000097270	CHR_MG4214_PATCH	37886889	37897682	-1	2	3	3	7	2	1	0	0	0	0	0		
ENSMUST00000181434						0	3	0	4	5	0	0	0	0	0	1		
ENSMUST00000181437						0	0	13	0	0	2	1	3	0	16	52		
ENSMUST00000181439						46	35	256	58	51	33	0	0	0	0	2		
ENSMUST00000181442						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000181445						9	3	12	6	8	2	1	0	0	2	5		
ENSMUST00000181451						9	8	7	6	7	6	0	0	0	0	1		
ENSMUST00000181455	ENSMUSG00000097449	CHR_MG4151_PATCH	3302048	3329611	1	34	24	162	106	45	18	40	146	79	8	145	Q3UN66	P63318
ENSMUST00000181459						2	0	1	1	1	0	0	0	0	0	0		
ENSMUST00000181461						5	3	9	1	7	1	0	2	2	2	1		
ENSMUST00000181464	ENSMUSG00000029769	6	29396309	29426994	1	0	0	0	0	13	0	0	0	0	0	0	E6Y2W6	
ENSMUST00000181467	ENSMUSG00000091694	15	77633951	77643286	-1	25	17	29	26	25	0	0	3	3	2	1	M0QWU4	
ENSMUST00000181468						1	0	13	1	2	0	0	98	10	13	28		
ENSMUST00000181470	ENSMUSG00000036112	10	93858489	93897093	-1	0	1	0	0	0	0	0	29	43	89	27	M0QWX0	
ENSMUST00000181477						0	0	5	94	0	0	2	4	1	0	1		
ENSMUST00000181483	ENSMUSG00000096600	14	52725299	52726919	1	0	0	0	2	0	0	1	0	0	0	0	A0A075B6B3	
ENSMUST00000181493						13	8	3	5	5	0	14	18	9	14	6		
ENSMUST00000181494	ENSMUSG00000097771	CHR_MG153_PATCH	4148618	4154034	1	6	2	9	11	10	5	4239	3699	2597	991	1669	A2RS22	Q9WUM3
ENSMUST00000181504	ENSMUSG00000042812	8	121084386	121088144	1	15	9	52	338	29	9	2	3	0	0	8		Q61080
ENSMUST00000181509	ENSMUSG00000071591	14	7374667	7412375	-1	0	17	9	7	6	0	0	0	0	0	0	Q9D9B9	
ENSMUST00000181512	ENSMUSG00000049353	1	191977370	191988283	1	0	5	8	21	0	1	74	133	67	5	38	Q05D96	
ENSMUST00000181513	ENSMUSG00000097046	CHR_MG4136_PATCH	143511343	143517831	1	6	9	0	0	0	0	0	0	0	0	0		
ENSMUST00000181518	ENSMUSG00000078747	4	41941572	41943124	1	0	0	0	0	0	0	0	0	0	0	0	A2APU9	
ENSMUST00000181521	ENSMUSG00000031812	8	121590361	121598760	1	0	0	0	34	0	0	0	342	78	211	159	M0QWT8	
ENSMUST00000181525						6	7	9	4	8	5	2	0	0	0	1		
ENSMUST00000181541	ENSMUSG00000094084	3	93669333	93676310	-1	11	11	0	4	0	0	0	0	0	0	0		P0DMR5
ENSMUST00000181542						1	1	2	3	1	2	0	0	1	0	0		
ENSMUST00000181544						2	2	3	0	2	0	17	24	6	2	0		
ENSMUST00000181545	ENSMUSG00000096923	11	6200029	6201643	1	7	4	18	41	11	4	0	0	1	1	2	Q8C4X0	
ENSMUST00000181548	ENSMUSG00000097905	CHR_MG153_PATCH	4139798	4145737	1	16	9	42	21	21	14	0	0	3	0	2		Q8BXS7
ENSMUST00000181549	ENSMUSG00000095650	Y	85528517	85530908	-1	33	36	46	35	44	23	0	0	0	0	0	Q62461	
ENSMUST00000181557						4	5	0	1	3	0	0	0	0	1	0		
ENSMUST00000181559	ENSMUSG00000097721	CHR_MG153_PATCH	4156712	4163353	-1	0	0	0	0	0	0	0	0	0	0	34		
ENSMUST00000181560						15	12	30	9	11	2	0	7	2	2	7		
ENSMUST00000181562	ENSMUSG00000095295	14	5501674	5522927	1	9	7	2	0	7	3	0	2	0	0	0	M0QW81	
ENSMUST00000181564	ENSMUSG00000097351	CHR_MG4136_PATCH	143349757	143371032	1	6	4	8	101	10	8	0	0	0	0	0		A2VDH3
ENSMUST00000181566	ENSMUSG00000097886	11	67774608	67789898	1	5	3	8	6	3	0	0	0	0	0	0	M0QWL6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000181567	ENSMUSG00000024728	19	11139664	11165320	-1	0	0	0	0	0	0	0	0	0	0	0	Q6P8I0	
ENSMUST00000181568	ENSMUSG00000078926	13	113035111	113091195	1	4	8	4	5	6	6	0	0	0	0	0	M0QWI6	
ENSMUST00000181571						5	6	0	0	3	4	0	0	0	0	0		
ENSMUST00000181573	ENSMUSG00000097333	13	67515781	67526177	-1	0	0	5	3	0	1	13	10	0	64	3	M0QWG2	
ENSMUST00000181579	ENSMUSG00000028797	4	129600668	129624059	1	0	0	0	0	0	0	0	0	0	0	3	M0QWT3	
ENSMUST00000181583						0	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000181584						0	0	1	0	0	1	53	26	30	163	34		
ENSMUST00000181585						4	1	5	5	2	3	0	1	0	1	0		
ENSMUST00000181586	ENSMUSG00000031818	8	120668222	120674207	1	0	0	0	0	0	0	45	14	41	12	0	A2RSV8	P19783
ENSMUST00000181589	ENSMUSG00000097733	CHR_MG153_PATCH	4081578	4087340	1	0	0	6	0	1	0	0	0	0	0	0		
ENSMUST00000181591						9	2	2	7	4	2	0	0	1	0	2		
ENSMUST00000181597						3	5	5	15	5	4	0	0	0	0	0		
ENSMUST00000181601	ENSMUSG00000097078	4	88721805	88722842	1	3	7	0	316	25	5	3	2	8	3	12	Q8CAC1	
ENSMUST00000181603	ENSMUSG00000094578	14	5484207	5492584	1	0	0	0	0	0	0	0	0	0	0	0	M0QWW3	
ENSMUST00000181606						0	0	7	16	18	11	54	125	185	43	40		
ENSMUST00000181607						3	3	5	4	3	0	0	0	0	0	0		
ENSMUST00000181608						1	0	0	2	1	0	200	322	61	41	68		
ENSMUST00000181609	ENSMUSG00000097084	8	121127940	121130644	1	30	22	65	236	47	18	0	0	3	0	1		Q64731
ENSMUST00000181613	ENSMUSG00000047117	13	96416134	96471198	-1	5	1	18	6	2	4	0	0	0	0	0	M0QWJ4	
ENSMUST00000181614						33	13	25	38	37	29	32	134	66	22	42		
ENSMUST00000181615	ENSMUSG00000090854	10	104194042	104196522	1	0	0	0	0	0	0	0	0	0	0	0	M0QWS9	
ENSMUST00000181616	ENSMUSG00000097490	CHR_MG4212_PATCH	15499687	15504507	-1	38	18	38	68	19	15	0	0	0	0	0		
ENSMUST00000181624	ENSMUSG00000097778	CHR_MG4136_PATCH	143412426	143421091	1	0	0	0	0	0	1	2	1	4	0	2		
ENSMUST00000181627	ENSMUSG00000057132	14	52110704	52163546	1	0	0	0	70	0	0	2	1	0	0	0	M0QWI1	
ENSMUST00000181628	ENSMUSG00000079263	6	141971845	142011414	-1	5	0	0	0	5	1	0	0	0	0	0	M0QWR8	
ENSMUST00000181634	ENSMUSG00000091779	10	104142987	104153674	1	8	8	12	9	9	3	0	0	1	0	1	M0QWR4	
ENSMUST00000181643						335	357	1174	424	302	145	19	38	5	22	15		
ENSMUST00000181645	ENSMUSG00000053219	10	22158569	22374139	1	12	6	13	153	25	2	0	10	8	0	0	D7F2B6	Q9CZQ6
ENSMUST00000181646						5	3	10	3	2	3	0	0	0	0	0		
ENSMUST00000181650						13	0	0	0	9	7	0	0	0	0	0		
ENSMUST00000181651						5	0	0	0	0	0	9	60	9	1	27		
ENSMUST00000181652	ENSMUSG00000069385	18	44156395	44159873	-1	0	0	0	0	0	0	0	0	0	0	0	M0QWD8	
ENSMUST00000181659	ENSMUSG00000097600	CHR_MG4214_PATCH	37832136	37841725	1	1	1	3	7	5	2	0	0	0	0	0		
ENSMUST00000181661						77	70	494	104	56	30	0	9	2	4	4		
ENSMUST00000181662						0	0	0	0	0	0	0	113	110	0	2		
ENSMUST00000181663	ENSMUSG00000052934	8	121549440	121578806	-1	8	3	10	20	9	6	21	26	21	2	18	M0QWM6	
ENSMUST00000181669	ENSMUSG00000107871	CHR_MG4151_PATCH	3154498	3169029	-1	43	28	64	279	52	53	1	5	3	2	5		
ENSMUST00000181673						12	9	9	16	5	2	0	3	0	0	1		
ENSMUST00000181677						18	20	17	27	23	16	52	92	86	24	67		
ENSMUST00000181678						3	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000181681						2	1	6	2	2	2	10	30	14	2	23		
ENSMUST00000181684	ENSMUSG00000097485	CHR_MG153_PATCH	4097182	4099019	1	0	1	0	0	3	3	1098	1224	459	247	568		
ENSMUST00000181686	ENSMUSG00000096998	CHR_MG4151_PATCH	3331471	3366737	1	4	4	11	36	10	7	0	0	0	0	0	B9EJ14	P62956
ENSMUST00000181691						6	4	4	5	3	1	0	0	0	0	0		
ENSMUST00000181698						37	28	134	48	55	22	5	3	7	1	1		
ENSMUST00000181703	ENSMUSG00000095022	10	104185533	104188000	1	8	8	12	9	9	3	0	0	1	0	1	M0QWR4	
ENSMUST00000181707	ENSMUSG00000095022	10	104185533	104188000	1	0	0	0	1	0	0	0	0	0	0	0	M0QWR4	
ENSMUST00000181709	ENSMUSG00000057132	14	52110704	52163546	1	0	0	0	0	0	0	0	0	0	0	0	M0QW56	
ENSMUST00000181711	ENSMUSG00000097187	2	84742169	84743655	-1	11	8	16	50	6	9	0	0	0	0	0	M0QWC7	
ENSMUST00000181715	ENSMUSG00000097096	CHR_MG153_PATCH	4099998	4113965	1	3	5	14	109	8	1	35	220	118	5	283		O35954
ENSMUST00000181716						14	7	20	2	8	4	0	0	0	0	0		
ENSMUST00000181721	ENSMUSG00000037991	16	10835059	10892966	1	7	8	5	7	7	3	0	0	1	0	4		Q3UPE3
ENSMUST00000181722						1	4	0	15	0	0	0	0	0	0	0		
ENSMUST00000181728	ENSMUSG00000094766	14	53461099	53461738	1	8	7	11	3	6	2	3	1	0	0	2	A0A075B6C1	
ENSMUST00000181733						0	0	0	0	0	0	2	17	10	6	10		
ENSMUST00000181734	ENSMUSG00000015189	6	4600839	4643355	1	0	0	0	0	0	4	20	0	0	0	7	M0QWG8	
ENSMUST00000181735						5	1	3	2	3	2	1	0	0	2	0		
ENSMUST00000181736	ENSMUSG00000057132	14	52110704	52163546	1	6	6	40	38	2	1	0	48	0	0	3	M0QWL3	
ENSMUST00000181740						0	0	1	5	0	0	0	0	0	0	0		
ENSMUST00000181741	ENSMUSG00000078926	13	113035111	113091195	1	2	0	0	0	0	0	0	0	0	0	0	M0QWC6	
ENSMUST00000181744						12	11	23	41	24	10	152	611	240	20	583		
ENSMUST00000181745	ENSMUSG00000096930	4	56740070	56741377	1	0	6	19	44	0	4	0	0	4	1	1	Q9CVR1	
ENSMUST00000181748	ENSMUSG00000095071	13	120263114	120264517	1	8	4	12	4	2	0	0	0	0	0	0	O70616	
ENSMUST00000181750	ENSMUSG00000022664	16	45139573	45158706	-1	0	0	0	0	0	0	0	0	0	3	0	M0QWP6	
ENSMUST00000181753						3	3	6	0	10	5	12	63	42	0	47		
ENSMUST00000181754	ENSMUSG00000096951	CHR_MG4136_PATCH	143267431	143299564	-1	4	2	3	13	3	1	1	4	0	8	10		Q62011
ENSMUST00000181761	ENSMUSG00000047117	13	96416134	96471198	-1	0	0	0	0	0	0	0	0	0	0	0	M0QWU9	
ENSMUST00000181763	ENSMUSG00000097856	CHR_MG4136_PATCH	143527062	143573798	1	4	5	0	6	0	0	0	0	0	0	0		
ENSMUST00000181767	ENSMUSG00000097333	13	67515781	67526177	-1	4	11	6	18	8	7	129	786	272	421	132	Q8K2A4	
ENSMUST00000181768	ENSMUSG00000094828	14	53665929	53666506	1	7	2	9	3	6	3	1	3	0	4	5	Q5R1C3	
ENSMUST00000181779	ENSMUSG00000096218	14	3884172	3921640	1	64	58	185	104	78	40	4	1	5	0	11	Q9D9B9	
ENSMUST00000181783						6	4	14	18	9	8	0	0	0	0	0		
ENSMUST00000181784	ENSMUSG00000097585	7	89980749	89981848	1	5	1	8	43	2	4	1	10	0	5	1	M0QW61	
ENSMUST00000181786	ENSMUSG00000094590	14	6638420	6684170	-1	55	21	104	73	49	21	0	4	0	2	0	J3QPM5	
ENSMUST00000181791	ENSMUSG00000079263	6	141971845	142011414	-1	0	0	0	0	0	0	0	0	0	0	0	L7N251	
ENSMUST00000181793	ENSMUSG00000076802	14	53132679	53133137	1	2	0	0	0	4	3	0	0	0	2	0	A0A075B6B2	
ENSMUST00000181795	ENSMUSG00000031818	8	120668222	120674207	1	0	0	0	0	0	0	100	623	239	12	168	M0QWX7	
ENSMUST00000181796	ENSMUSG00000097425	7	23984065	23985048	1	3	4	1	0	3	2	0	0	0	0	0	Q0P547	
ENSMUST00000181797						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000181798	ENSMUSG00000097096	CHR_MG153_PATCH	4099998	4113965	1	2	2	0	78	3	5	19	16	16	0	63		
ENSMUST00000181799						0	1	2	0	1	2	1	0	0	0	0		
ENSMUST00000181806	ENSMUSG00000097485	CHR_MG153_PATCH	4097182	4099019	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000181810	ENSMUSG00000097328	11	69686250	69695849	-1	4	3	24	21	7	2	59	48	14	18	55	Q5F2A0	O54907
ENSMUST00000181818						0	8	0	0	2	0	0	0	48	6	19		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000181822						0	2	0	0	4	6	0	0	0	0	0		
ENSMUST00000181823						57	74	129	102	93	38	5	10	3	0	8		
ENSMUST00000181826						11	14	59	217	26	12	56	194	123	19	202		
ENSMUST00000181828						13	11	34	79	17	10	0	2	1	0	2		
ENSMUST00000181835	ENSMUSG00000097407	10	93589413	93605245	1	8	10	9	168	14	7	0	0	1	0	0	Q9D475	
ENSMUST00000181836	ENSMUSG00000031819	8	120653914	120668573	-1	0	0	0	0	0	0	37	73	44	15	31	M0QWP2	
ENSMUST00000181843	ENSMUSG00000096276	12	87954080	87960672	1	3	1	18	0	8	5	0	0	0	0	0	M0QW82	
ENSMUST00000181844	ENSMUSG00000097721	CHR_MG153_PATCH	4156712	4163353	-1	0	0	0	11	0	0	24	51	7	3	42		
ENSMUST00000181847	ENSMUSG00000031818	8	120668222	120674207	1	1	2	0	3	2	2	12	18	12	0	12	M0QWX2	
ENSMUST00000181850	ENSMUSG00000097061	12	69197211	69199868	1	11	10	12	72	16	6	32	171	46	14	57	M0QWC1	
ENSMUST00000181853						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000181854						7	2	16	202	14	7	0	0	0	1	0		
ENSMUST00000181855						53	42	422	85	43	29	4	18	20	0	3		
ENSMUST00000181857						4	2	5	6	2	1	1	0	2	7	0		
ENSMUST00000181860	ENSMUSG00000027556	3	14766216	14808368	-1	0	0	0	0	0	0	0	0	0	8	0		P13634
ENSMUST00000181861						0	0	2	0	1	0	4	6	10	1	30		
ENSMUST00000181862						0	0	5	0	3	1	0	0	1	0	1		
ENSMUST00000181868	ENSMUSG00000071633	19	12599974	12628251	1	2	2	3	1	2	3	0	0	0	0	0	M0QWP3	
ENSMUST00000181869	ENSMUSG00000097064	CHR_MG153_PATCH	4164323	4175478	-1	12	8	31	96	22	8	120	454	184	26	465		
ENSMUST00000181878						2	4	2	2	2	1	0	0	0	0	0		
ENSMUST00000181879						2	3	12	7	9	3	6	3	29	1	29		
ENSMUST00000181880	ENSMUSG00000097853	14	5538496	5546373	1	6	2	7	13	3	6	0	0	0	0	0	M0QWL4	
ENSMUST00000181890						29	33	36	29	27	21	6	12	8	0	11		
ENSMUST00000181892	ENSMUSG00000095432	13	67538641	67553138	-1	9	8	16	15	6	5	94	368	156	201	81	Q7TPL6	
ENSMUST00000181894						0	13	26	0	11	0	3	27	0	7	7		
ENSMUST00000181896	ENSMUSG00000097298	9	75441122	75441652	-1	2	1	9	79	4	3	0	1	0	0	0	Q3UUU6	
ENSMUST00000181902						2	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000181904	ENSMUSG00000044365	3	134236484	134262161	1	13	15	27	39	7	8	1	0	0	0	0	M0QWU0	
ENSMUST00000181907						47	60	85	23	51	20	7	38	23	8	15		
ENSMUST00000181909						2	0	6	1	2	2	3	15	13	3	14		
ENSMUST00000181916	ENSMUSG00000097200	CHR_MG4214_PATCH	37827360	37830307	1	2	1	1	2	3	1	0	0	0	0	0		
ENSMUST00000181917	ENSMUSG00000097629	CHR_MG153_PATCH	4214237	4223489	1	0	3	8	4	0	4	0	0	0	0	0		
ENSMUST00000181922						3	2	0	13	4	1	0	0	0	0	0		
ENSMUST00000181923						11	6	19	13	15	6	2	2	3	1	1		
ENSMUST00000181924						4	3	2	3	4	1	1	2	1	0	0		
ENSMUST00000181935						0	0	0	0	0	4	1940	3685	1756	11516	1436		
ENSMUST00000181937						1	1	3	5	1	4	1	1	0	0	0		
ENSMUST00000181945	ENSMUSG00000020216	10	80808496	80813498	-1	6	0	0	17	17	3	0	0	0	0	0	M0QWR3	
ENSMUST00000181948	ENSMUSG00000031812	8	121590361	121598760	1	0	0	0	0	0	0	3177	5078	2000	8690	1584	M0QWC2	
ENSMUST00000181950	ENSMUSG00000031819	8	120653914	120668573	-1	0	0	0	0	0	0	32	84	17	17	7	M0QWS0	
ENSMUST00000181956	ENSMUSG00000097481	6	120294364	120295432	1	6	4	2	338	9	4	0	0	0	0	0	Q8C799	
ENSMUST00000181965						3	1	4	8	1	1	1	10	5	0	4		
ENSMUST00000181969	ENSMUSG00000053253	14	105258573	105309298	1	0	1	7	142	5	0	119	238	126	52	76	M0QWK1	
ENSMUST00000181970						0	0	4	7	10	5	0	0	0	0	0		
ENSMUST00000181971	ENSMUSG00000078671	7	73426638	73541830	-1	2	0	3	1	2	0	3	8	14	4	19	M0QWT0	
ENSMUST00000181974	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0		G5E8K5
ENSMUST00000181975	ENSMUSG00000030583	7	29320372	29518641	-1	0	2	0	2	0	0	10	4	20	0	6	S4R2C7	
ENSMUST00000181976	ENSMUSG00000035189	10	88948994	89344762	-1	5	0	0	1	0	0	0	0	0	0	0		Q8C5H1
ENSMUST00000181978						9	6	5	3	5	2	4	0	0	0	2		
ENSMUST00000181979						15	6	24	188	12	11	4	28	13	0	21		
ENSMUST00000181980	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	0	45	6	26	7	S4R254	
ENSMUST00000181981	ENSMUSG00000045659	7	116123485	116308376	-1	15	16	21	38	34	8	0	0	0	0	0		Q3UIL6
ENSMUST00000181982						9	3	8	10	6	2	0	0	0	0	0		
ENSMUST00000181983	ENSMUSG00000010608	12	83631236	83683123	1	127	133	64	41	71	19	56	225	488	134	449	S4R2B0	
ENSMUST00000181985	ENSMUSG00000024128	17	23941672	23945607	1	0	2	0	0	4	5	0	0	0	0	0	Q544L5	P15501
ENSMUST00000181986	ENSMUSG00000032582	9	107773559	107873237	-1	4	1	17	0	0	0	38	608	63	170	96	S4R1D1	
ENSMUST00000181987	ENSMUSG00000025656	X	95048935	95196856	-1	14	13	26	14	10	12	2	1	1	0	4		Q3UTH8
ENSMUST00000181989						0	0	0	0	0	0	0	0	0	0	7		
ENSMUST00000181990						7	4	5	8	8	2	0	0	0	0	0		
ENSMUST00000181991						0	0	0	0	0	0	0	0	38	38	53		
ENSMUST00000181992						1	2	2	1	3	2	1	1	0	0	0		
ENSMUST00000181993						9	14	9	55	18	6	8	5	8	0	15		
ENSMUST00000181994						0	1	0	26	1	2	0	0	0	0	0		
ENSMUST00000181995	ENSMUSG00000038510	10	40223246	40247036	-1	2	2	0	0	0	0	6	32	0	25	0	S4R1Y5	
ENSMUST00000181997						67	75	397	99	89	49	1	11	6	2	19		
ENSMUST00000181998	ENSMUSG00000045659	7	116123485	116308376	-1	19	20	4	22	0	6	0	2	0	0	6		Q3UIL6
ENSMUST00000181999						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000182000						1	0	8	3	3	3	1	1	1	0	0		
ENSMUST00000182001	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	0	0	0	0	0	0	0	0	0		Q3UTH8
ENSMUST00000182002	ENSMUSG00000035325	5	100361649	100416234	-1	0	0	5	0	0	0	3	16	1	4	7	S4R1Y8	
ENSMUST00000182003						4	0	3	1	3	2	0	0	0	0	0		
ENSMUST00000182004	ENSMUSG00000010608	12	83631236	83683123	1	0	0	0	0	0	0	0	10	0	0	0	S4R2B1	
ENSMUST00000182006	ENSMUSG00000102422	3	67892232	68626466	1	0	1	0	0	0	0	0	0	0	0	0		Q3TI53
ENSMUST00000182007						2	0	0	0	2	0	12	0	0	0	0		
ENSMUST00000182008	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	1	0	0	0	0		Q8C8R3
ENSMUST00000182009						0	0	0	2	0	0	16	0	52	0	131		
ENSMUST00000182011						22	5	35	81	21	9	51	10	106	0	77		
ENSMUST00000182013	ENSMUSG00000038094	16	29395853	29544864	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2B9	
ENSMUST00000182014	ENSMUSG00000056370	6	72304610	72314371	1	0	0	0	0	0	0	5	0	0	0	0	S4R239	
ENSMUST00000182015	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	0	13	122	329	73	S4R1G6	
ENSMUST00000182016						0	0	0	0	0	0	0	3	2	0	3		
ENSMUST00000182017						0	0	0	0	0	0	822	1810	425	1219	491		
ENSMUST00000182018	ENSMUSG00000026131	1	33908225	34308661	1	17	19	58	4	6	16	0	8	1	17	70	S4R1Y6	
ENSMUST00000182019						1	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182020						4	7	1	4	4	3	0	0	0	0	0		
ENSMUST00000182021						2	6	8	3	6	4	3	5	2	6	3		
ENSMUST00000182022	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	0	6	0	0	33	31	72	0	76	S4R1V5	
ENSMUST00000182023	ENSMUSG00000040528	11	106751226	106768794	1	7	4	15	8	7	0	98	409	155	214	93	A0A0B4J1N6	
ENSMUST00000182024	ENSMUSG00000025427	18	77456110	77565147	-1	2	0	79	2	2	0	0	0	0	0	0		
ENSMUST00000182025	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1B7	
ENSMUST00000182026	ENSMUSG00000032580	9	107740371	107770996	-1	1	3	4	5	5	6	18	73	10	44	26	S4R273	
ENSMUST00000182028						8	5	1	6	3	1	0	0	0	0	0		
ENSMUST00000182029	ENSMUSG00000069601	10	69533772	70027438	1	0	2	0	0	3	0	0	0	0	0	0		G5E8K5
ENSMUST00000182030						20	12	51	94	36	8	0	1	0	0	0		
ENSMUST00000182031						4	4	17	135	6	3	14	80	45	8	88		
ENSMUST00000182032						164	164	323	389	181	144	6	40	16	4	31		
ENSMUST00000182034	ENSMUSG00000030314	6	114643097	114860614	1	3	0	0	0	0	3	0	0	0	0	3	S4R1T0	
ENSMUST00000182035	ENSMUSG00000030314	6	114643097	114860614	1	0	0	0	0	0	0	0	5	0	0	0	S4R2P7	
ENSMUST00000182036	ENSMUSG00000010608	12	83631236	83683123	1	0	0	0	0	0	0	4	0	11	0	15	S4R2A4	
ENSMUST00000182037						52	33	53	53	54	32	0	1	0	0	1		
ENSMUST00000182038	ENSMUSG00000041225	18	6024427	6136098	-1	2	0	0	0	5	0	0	0	5	9	0	S4R1B0	
ENSMUST00000182039						24	14	4	20	22	3	0	0	0	0	0		
ENSMUST00000182040						51	48	119	160	55	26	232	498	188	29	124		
ENSMUST00000182041						2	4	38	134	11	4	0	0	0	0	0		
ENSMUST00000182042	ENSMUSG00000058690	14	36874936	36968777	-1	4	0	2	0	2	0	0	0	0	0	0	S4R211	
ENSMUST00000182044	ENSMUSG00000030666	7	114718643	114723365	1	2	4	1	6	4	0	0	0	0	0	0	S4R2C5	
ENSMUST00000182045	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0	S4R2K2	
ENSMUST00000182047	ENSMUSG00000029110	5	34336289	34355629	1	0	0	0	58	10	3	0	0	0	0	35		Q9QZS2
ENSMUST00000182048	ENSMUSG00000051811	7	4751792	4753094	-1	1	0	0	2	0	0	0	6	0	0	0	Q059Q8	Q80ZN9
ENSMUST00000182049						39	42	73	37	52	31	6	13	17	5	22		
ENSMUST00000182050						7	3	10	11	7	1	0	2	0	0	1		
ENSMUST00000182051						0	1	0	2	2	0	0	0	1	0	1		
ENSMUST00000182052	ENSMUSG00000057666	6	125161715	125166467	-1	0	0	0	0	0	0	17	36	9	6	0	S4R1W8	
ENSMUST00000182053	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	1	0	4	0	0	0	0	0	S4R2H3	
ENSMUST00000182055						2	5	6	5	0	4	2	8	3	1	4		
ENSMUST00000182056	ENSMUSG00000047507	17	25242659	25256364	-1	21	11	0	71	26	0	0	1	0	0	0	S4R1E7	
ENSMUST00000182057						6	3	7	16	6	1	0	1	0	0	0		
ENSMUST00000182058						19	10	18	16	24	9	0	11	12	6	5		
ENSMUST00000182059	ENSMUSG00000025077	19	56529167	56548222	-1	0	0	0	0	0	0	4	3	0	0	1	S4R1T3	
ENSMUST00000182060						2	4	4	2	2	4	62	301	84	191	95		
ENSMUST00000182061	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	12	15	0	0	23		Q3UPH7
ENSMUST00000182062	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	1	0	0	0	0	S4R1M4	
ENSMUST00000182063	ENSMUSG00000098164	17	22739944	22751509	1	3	6	4	6	6	1	0	0	0	0	0	S4R2D1	
ENSMUST00000182064	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	1	0	0	0	0	S4R2F3	
ENSMUST00000182065						54	34	125	55	53	21	16	68	32	9	47		
ENSMUST00000182066	ENSMUSG00000041225	18	6024427	6136098	-1	8	7	4	0	5	0	0	0	0	5	0	S4R248	
ENSMUST00000182067	ENSMUSG00000061099	7	30729775	30743681	-1	2	2	3	2	2	0	5	1	12	4	10	S4R2L8	
ENSMUST00000182068	ENSMUSG00000098112	15	100641077	100669553	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1Q1	
ENSMUST00000182069						2	3	9	7	7	2	0	0	0	0	0		
ENSMUST00000182070						0	0	0	0	1	0	16	12	15	7	21		
ENSMUST00000182071						1	8	4	8	11	0	0	1	1	0	0		
ENSMUST00000182072						4	0	7	2	9	1	0	0	0	0	1		
ENSMUST00000182073						6	7	30	6	7	8	9	27	14	3	26		
ENSMUST00000182076						2	2	0	0	2	0	13	52	42	9	50		
ENSMUST00000182078	ENSMUSG00000032826	3	126921612	127499350	-1	29	5	82	85	0	13	6	7	0	23	23	S4R2R5	
ENSMUST00000182079	ENSMUSG00000081607	X	141873409	141875235	-1	0	1	0	0	0	0	1	2	0	1	0	V9GXA7	
ENSMUST00000182080						0	0	0	3	1	1	0	7	4	4	0		
ENSMUST00000182081						1	0	1	1	8	0	0	0	0	0	0		
ENSMUST00000182082						9	3	4	2	7	5	0	0	0	0	0		
ENSMUST00000182083	ENSMUSG00000058589	10	89873509	90973300	1	0	2	0	3	0	0	0	0	0	0	0	S4R2B3	
ENSMUST00000182084						0	3	2	56	6	0	18	21	20	0	20		
ENSMUST00000182085	ENSMUSG00000026014	1	60482292	60567104	-1	0	1	0	0	0	0	0	0	1	0	6	S4R2K5	
ENSMUST00000182086						0	0	0	0	0	0	1	2	0	0	0		
ENSMUST00000182087	ENSMUSG00000030380	7	13042303	13054764	-1	0	0	0	458	0	0	20	29	26	7	8	S4R1C2	
ENSMUST00000182089	ENSMUSG00000098078	X	103422010	103481705	1	1	3	1	1	1	1	0	10	0	0	0	S4R1A3	
ENSMUST00000182090						7	3	3	5	2	4	0	0	1	1	0		
ENSMUST00000182092						1	1	14	7	4	0	0	10	9	0	0		
ENSMUST00000182093	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	4	0	2	2	6	S4R1J1	
ENSMUST00000182094						1	1	1	0	0	0	0	3	0	0	1		
ENSMUST00000182095	ENSMUSG00000066189	7	122670492	122769393	1	2	0	1	2	4	0	0	0	0	0	0	S4R2R7	
ENSMUST00000182096						4	3	5	12	5	2	0	0	0	0	0		
ENSMUST00000182097	ENSMUSG00000025027	19	52943417	53040214	-1	0	0	0	0	0	0	0	0	0	0	0	S4R228	
ENSMUST00000182098	ENSMUSG00000030314	6	114643097	114860614	1	1	1	0	5	5	0	0	0	0	0	0	S4R1K1	
ENSMUST00000182101						8	9	36	8	7	7	0	5	0	0	5		
ENSMUST00000182102	ENSMUSG00000067656	19	7864388	7966027	-1	5	3	0	0	4	1	0	0	0	0	0	Q76M71	
ENSMUST00000182104	ENSMUSG00000078958	13	90883433	90905355	-1	0	0	0	1	1	1	0	0	0	0	0	S4R1Q9	
ENSMUST00000182107						176	184	209	185	197	135	11	56	17	4	32		
ENSMUST00000182108						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000182110						3	6	4	5	2	1	0	0	0	0	0		
ENSMUST00000182111	ENSMUSG00000051811	7	4751792	4753094	-1	0	1	1	3	5	0	10	7	5	4	0	Q059Q8	Q80ZN9
ENSMUST00000182112						57	9	1	0	0	0	0	0	0	0	0		
ENSMUST00000182113	ENSMUSG00000058589	10	89873509	90973300	1	5	0	10	4	4	0	0	0	0	0	0	S4R2I2	
ENSMUST00000182114	ENSMUSG00000051285	1	7088920	7173628	1	0	0	0	15	0	0	1	0	0	0	0	S4R2K3	
ENSMUST00000182115						0	0	0	0	0	0	2122	3	1454	88	894		
ENSMUST00000182116	ENSMUSG00000020107	10	59987409	60003135	-1	0	0	0	0	0	0	0	0	10	0	10	S4R1V1	
ENSMUST00000182117	ENSMUSG00000041617	16	17646470	17650738	1	0	0	0	0	0	0	0	0	0	0	1	S4R2I4	
ENSMUST00000182118	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1Q5	
ENSMUST00000182122	ENSMUSG00000041258	18	82593593	82692883	-1	10	0	31	0	0	7	407	87	769	7	596	S4R299	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182123						8	9	33	9	11	6	0	192	35	62	244		
ENSMUST00000182126						0	7	9	2	6	8	0	3	0	0	3		
ENSMUST00000182128	ENSMUSG00000070796	7	18646736	18656725	-1	14	6	16	9	16	6	0	0	0	0	0	S4R1D2	
ENSMUST00000182129	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	42	1	0	25	0	23	9	17	S4R240	
ENSMUST00000182130						17	6	20	0	18	5	345	828	413	41	300		
ENSMUST00000182131						17	9	53	22	30	7	110	435	270	31	413		
ENSMUST00000182133	ENSMUSG00000024073	17	74528295	74703356	1	0	0	0	0	1	1	0	0	0	1	0		O88738
ENSMUST00000182134						5	4	10	30	0	2	0	0	0	0	0		
ENSMUST00000182135	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JFI4	
ENSMUST00000182136						63	77	207	110	84	37	9	17	14	0	20		
ENSMUST00000182137	ENSMUSG00000025656	X	95048935	95196856	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1J2	
ENSMUST00000182138						3	0	11	5	2	5	169	102	259	1	265		
ENSMUST00000182139	ENSMUSG00000098094	7	33054582	33056561	-1	0	1	1	3	2	2	0	0	0	0	0	S4R2G1	
ENSMUST00000182140	ENSMUSG00000042439	18	65580230	65689443	1	1	0	0	2	2	1	0	0	0	0	0	S4R2M5	
ENSMUST00000182142						65	43	258	74	55	12	0	1	0	0	2		
ENSMUST00000182143						0	1	3	0	3	0	0	0	0	0	0		
ENSMUST00000182144						1	1	1	105	6	4	0	1	4	0	2		
ENSMUST00000182146	ENSMUSG00000025427	18	77456110	77565147	-1	0	0	0	0	0	0	0	0	0	0	0	Q19SC8	
ENSMUST00000182147						0	4	2	0	3	3	0	0	45	0	43		
ENSMUST00000182148						66	93	106	71	83	44	4	1	4	0	7		
ENSMUST00000182149	ENSMUSG00000040225	1	162670725	162740556	-1	20	55	35	19	30	0	331	459	388	6	287	S4R294	
ENSMUST00000182150						8	1	10	9	9	3	0	2	0	0	0		
ENSMUST00000182151	ENSMUSG00000078350	4	154020470	154026230	-1	12	19	24	62	18	34	0	0	0	0	0		P0C8K7
ENSMUST00000182152	ENSMUSG00000020107	10	59987409	60003135	-1	0	4	5	14	1	0	20	16	3	3	0	S4R2B6	
ENSMUST00000182153	ENSMUSG00000025427	18	77456110	77565147	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1M1	
ENSMUST00000182154						4	2	2	25	3	0	0	0	0	0	1		
ENSMUST00000182155	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0		G5E8K5
ENSMUST00000182156						4	0	3	1	2	0	0	54	8	20	15		
ENSMUST00000182157						1	5	1	3	0	0	41	2	0	17	29		
ENSMUST00000182159						8	6	35	14	7	6	20	59	42	2	88		
ENSMUST00000182160						6	2	3	6	8	6	0	0	0	0	0		
ENSMUST00000182161	ENSMUSG00000098188	10	59221953	59226434	1	24	35	95	556	51	29	27	414	200	30	30		Q8C0J6
ENSMUST00000182162						2	6	2	5	3	4	0	0	0	0	0		
ENSMUST00000182163						0	0	8	26	0	1	1	0	0	0	0		
ENSMUST00000182164						25	32	25	3	22	8	6	0	1	7	17		
ENSMUST00000182165						5	0	2	0	4	0	12	4	0	0	0		
ENSMUST00000182166	ENSMUSG00000041482	18	63010213	63387183	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2R6	
ENSMUST00000182168	ENSMUSG00000038094	16	29395853	29544864	-1	0	0	1	0	0	0	0	6	0	1	0	S4R262	
ENSMUST00000182169	ENSMUSG00000030314	6	114643097	114860614	1	1	0	0	1	0	1	0	3	1	0	3	S4R1W9	
ENSMUST00000182170						3	5	19	8	6	5	4	1	1	2	1		
ENSMUST00000182171						10	4	4	1	13	5	0	0	0	0	0		
ENSMUST00000182172	ENSMUSG00000098176	15	75979872	75982455	-1	5	5	20	120	12	5	7	19	3	5	7	Q0P5Z5	
ENSMUST00000182173	ENSMUSG00000051811	7	4751792	4753094	-1	1	2	2	2	3	0	0	12	3	2	3	S4R1N0	
ENSMUST00000182175						5	1	5	2	5	4	0	0	0	0	0		
ENSMUST00000182176						3	3	10	6	4	1	0	0	0	0	0		
ENSMUST00000182177						11	3	40	42	9	15	0	0	0	1	0		
ENSMUST00000182178						0	0	0	6	1	1	0	0	0	0	0		
ENSMUST00000182179	ENSMUSG00000032525	9	121719169	121756843	1	0	1	0	5	0	0	1	0	11	0	16	Q3TQ51	
ENSMUST00000182180						3	3	0	1	0	0	0	0	0	0	0		
ENSMUST00000182181	ENSMUSG00000028004	3	82538383	82548084	-1	0	0	0	0	0	0	0	0	0	0	0	Q3SWR9	
ENSMUST00000182182						9	2	3	3	2	4	0	0	0	0	0		
ENSMUST00000182183	ENSMUSG00000020056	10	88201093	88246158	1	0	0	0	0	0	0	76	387	98	537	47	S4R287	
ENSMUST00000182184						2	0	3	0	0	0	5	1	3	4	0		
ENSMUST00000182187						5	2	2	3	4	5	0	0	0	0	0		
ENSMUST00000182188						91	141	169	79	128	31	8	4	8	4	7		
ENSMUST00000182189						9	15	0	0	9	9	1	1	0	0	3		
ENSMUST00000182190						7	1	2	3	6	1	0	0	0	0	2		
ENSMUST00000182191	ENSMUSG00000078350	4	154020470	154026230	-1	8	4	12	4	8	0	0	0	0	0	0	S4R2T3	
ENSMUST00000182192	ENSMUSG00000058589	10	89873509	90973300	1	0	0	1	2	1	1	0	0	0	0	0	S4R2M2	
ENSMUST00000182193	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	2	0	0	0	0	S4R2R3	
ENSMUST00000182194						29	24	45	33	36	19	2	2	1	1	2		
ENSMUST00000182196						2	3	7	0	4	2	0	0	0	0	0		
ENSMUST00000182198	ENSMUSG00000092572	1	107529003	107549271	1	0	1	0	0	0	0	31	81	19	64	42	G3UYR4	
ENSMUST00000182199	ENSMUSG00000040875	9	114978569	115232225	1	5	0	0	4	19	9	0	0	0	0	0	S4R1G3	
ENSMUST00000182200	ENSMUSG00000033760	19	4756543	4767065	1	0	0	0	0	0	0	0	0	0	0	0	S4R1A6	
ENSMUST00000182201						4	5	8	7	6	1	0	0	0	0	0		
ENSMUST00000182202	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0	S4R1W3	
ENSMUST00000182203	ENSMUSG00000027297	2	119751320	119760431	-1	0	0	0	42	2	2	2	0	1	1	0	Q0VGZ5	P08923
ENSMUST00000182205						110	105	2492	149	79	50	2	3	2	1	4		
ENSMUST00000182206						2	0	15	2	0	1	0	0	0	0	0		
ENSMUST00000182207	ENSMUSG00000069601	10	69533772	70027438	1	0	0	11	0	0	0	0	1	1	3	0	S4R278	
ENSMUST00000182208	ENSMUSG00000079055	12	81197915	81333180	-1	5	4	0	0	6	2	0	0	0	0	0	S4R2P9	
ENSMUST00000182209	ENSMUSG00000034165	17	47505051	47599691	1	0	0	1	50	0	0	9023	15438	8138	539	4411	Q3TSW4	P30282
ENSMUST00000182210						6	4	9	2	5	3	0	0	0	0	0		
ENSMUST00000182211						3	0	1	0	2	0	0	2	0	0	1		
ENSMUST00000182212						184	178	1483	309	235	109	3	9	8	2	10		
ENSMUST00000182213	ENSMUSG00000041225	18	6024427	6136098	-1	5	0	0	0	0	0	39	141	13	27	41	S4R221	
ENSMUST00000182214	ENSMUSG00000030433	7	4956134	4964390	-1	26	8	38	30	19	10	0	0	0	0	0		P0C5K1
ENSMUST00000182215						3	3	2	5	4	3	1	23	4	5	15		
ENSMUST00000182217	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	1	0	1	2	0	S4R2A6	
ENSMUST00000182218						6	3	10	1	6	3	0	0	1	0	0		
ENSMUST00000182220						5	3	7	4	9	4	0	0	1	0	1		
ENSMUST00000182221						1	7	51	5	2	2	3	0	0	3	5		
ENSMUST00000182222	ENSMUSG00000053395	7	3390683	3415648	1	4	2	2	68	11	5	0	0	0	0	0	F7CZ64	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182223						6	9	0	13	14	0	0	389	0	24	0		
ENSMUST00000182224						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182225	ENSMUSG00000032525	9	121719169	121756843	1	2	0	29	1	5	8	55	7	219	0	249	Q8CBP6	
ENSMUST00000182226	ENSMUSG00000037519	7	144476758	144553729	-1	0	0	19	3	0	11	118	83	159	18	211	B2RXQ2	
ENSMUST00000182227	ENSMUSG00000046056	7	30734739	30756134	1	0	0	2	0	0	0	0	0	0	0	0	S4R1Y7	
ENSMUST00000182228						10	1	4	14	6	0	0	0	0	0	0		
ENSMUST00000182229	ENSMUSG00000046056	7	30734739	30756134	1	0	3	0	2	1	1	0	0	0	13	2		
ENSMUST00000182230						3	0	6	5	6	2	0	2	1	5	0		
ENSMUST00000182233	ENSMUSG00000041482	18	63010213	63387183	-1	11	8	18	9	6	0	0	0	0	0	0	S4R1C9	
ENSMUST00000182234						12	4	6	14	4	5	0	1	0	1	1		
ENSMUST00000182235						4	6	2	5	6	3	0	0	0	0	0		
ENSMUST00000182236						0	1	0	23	6	1	2	0	0	0	2		
ENSMUST00000182237						7	2	14	5	10	7	1	2	0	3	0		
ENSMUST00000182239						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000182240						5	2	5	7	5	2	1	0	0	0	0		
ENSMUST00000182241	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	32	88	0	0	0	S4R1G6	
ENSMUST00000182242						58	79	440	72	62	31	7	8	15	0	16		
ENSMUST00000182243						10	5	4	4	10	4	24	13	20	11	3		
ENSMUST00000182246						2	0	6	5	3	0	57	157	67	18	35		
ENSMUST00000182247						3	5	4	14	8	3	2	5	0	0	0		
ENSMUST00000182248						3	2	6	44	6	3	1	4	0	2	1		
ENSMUST00000182249						3	1	5	1	3	3	0	0	0	0	0		
ENSMUST00000182251						8	19	35	14	14	6	0	6	12	0	0		
ENSMUST00000182252						2	4	0	4	4	0	0	0	0	0	0		
ENSMUST00000182253						5	9	4	6	9	5	0	0	0	0	0		
ENSMUST00000182254						0	3	0	9	0	0	0	0	0	0	0		
ENSMUST00000182255						8	2	4	10	10	2	188	411	156	60	214		
ENSMUST00000182256	ENSMUSG00000031586	8	33782643	33929863	-1	2	2	2	0	8	3	0	0	0	0	0	S4R1A1	
ENSMUST00000182257						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182260	ENSMUSG00000047417	10	80540922	80561560	-1	0	0	0	1	0	0	8	365	41	29	81	S4R246	
ENSMUST00000182262						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182263						0	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000182266						12	9	12	9	19	5	2	4	2	1	1		
ENSMUST00000182267	ENSMUSG00000024998	19	38481109	38785030	1	3	22	42	8	48	19	0	0	0	2	3	S4R1Q8	
ENSMUST00000182269	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	10	0	0	0	0	0	0	S4R187	
ENSMUST00000182270						8	1	0	9	7	3	0	0	0	0	0		
ENSMUST00000182271						2	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000182272						1	2	2	3	8	6	0	7	0	0	3		
ENSMUST00000182273						1	6	5	5	7	2	0	0	3	0	3		
ENSMUST00000182274						4	3	5	12	2	1	0	3	0	0	2		
ENSMUST00000182276	ENSMUSG00000025077	19	56529167	56548222	-1	2	0	2	7	0	0	16	130	45	33	54	S4R1N2	
ENSMUST00000182277	ENSMUSG00000057666	6	125161715	125166467	-1	4	3	11	136	4	0	6	4	11	5	5	S4R1N5	
ENSMUST00000182278	ENSMUSG00000024073	17	74528295	74703356	1	0	0	0	0	0	0	1	0	0	0	0	S4R1R8	
ENSMUST00000182279						7	3	5	8	4	4	1	3	1	0	1		
ENSMUST00000182280						6	6	5	7	3	6	0	0	0	0	0		
ENSMUST00000182281						28	21	138	71	55	26	274	683	290	40	275		
ENSMUST00000182282						3	1	6	2	2	2	0	0	0	0	0		
ENSMUST00000182283	ENSMUSG00000026395	1	138062861	138175708	-1	0	0	0	0	0	0	7660	24011	18728	18962	15427	S4R2V1	
ENSMUST00000182284	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	8	4	0	0	0	0	0	0		
ENSMUST00000182285						1	8	5	3	6	3	0	1	0	0	0		
ENSMUST00000182287						0	0	0	1	5	1	3	14	4	100	15		
ENSMUST00000182288						2	3	1	3	0	5	0	0	0	0	0		
ENSMUST00000182289	ENSMUSG00000051111	13	95954594	96132577	-1	0	0	7	0	0	0	0	0	0	0	0	A2RSH4	
ENSMUST00000182290						2	3	0	3	0	0	0	0	0	0	0		
ENSMUST00000182291	ENSMUSG00000042694	19	47501033	47537507	-1	0	0	3	32	0	0	2	0	0	3	0	S4R297	
ENSMUST00000182292	ENSMUSG00000059562	17	25162461	25171913	1	0	0	0	0	10	0	0	2	0	0	0	S4R1F0	
ENSMUST00000182293						9	12	17	70	29	9	0	0	5	0	2		
ENSMUST00000182294						15	5	51	22	10	1	0	0	0	0	0		
ENSMUST00000182295						7	6	7	6	12	5	0	0	1	0	0		
ENSMUST00000182297						0	2	2	15	4	1	1	0	2	1	2		
ENSMUST00000182298						0	0	2	0	4	0	0	0	0	1	0		
ENSMUST00000182299	ENSMUSG00000020056	10	88201093	88246158	1	2	0	0	0	2	1	0	0	0	8	0	S4R1K7	
ENSMUST00000182301						9	8	3	18	12	6	15	55	16	5	12		
ENSMUST00000182302						9	7	1	5	6	3	3	0	0	0	0		
ENSMUST00000182304	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	0	0	0	0	13	4	7	0	8	S4R1U7	
ENSMUST00000182305						8	3	33	8	9	5	3	2	0	3	6		
ENSMUST00000182306						0	1	0	0	2	0	2	0	0	2	0		
ENSMUST00000182307						9	8	6	7	7	3	0	0	0	0	0		
ENSMUST00000182308						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182309	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	72	800	543	1472	535	S4R2L4	
ENSMUST00000182310	ENSMUSG00000041444	9	32116136	32268446	1	0	0	0	0	0	0	1	0	1	0	3	S4R2G6	
ENSMUST00000182311	ENSMUSG00000032525	9	121719169	121756843	1	0	0	0	0	0	0	0	0	0	0	0	S4R2L3	
ENSMUST00000182312						2	2	0	3	1	5	0	0	0	0	0		
ENSMUST00000182313						2	0	5	2	7	4	0	0	0	0	1		
ENSMUST00000182314	ENSMUSG00000026131	1	33908225	34308661	1	57	32	0	0	27	26	0	0	0	0	5	A0A0A6YXR1	
ENSMUST00000182315						47	39	77	266	87	32	0	0	14	0	7		
ENSMUST00000182316						0	1	2	0	1	6	0	0	0	0	0		
ENSMUST00000182319	ENSMUSG00000042439	18	65580230	65689443	1	0	0	0	0	0	1	0	0	0	0	0	S4R1U0	
ENSMUST00000182320						7	4	4	5	3	2	0	0	0	0	0		
ENSMUST00000182321						3	1	0	3	2	1	3	3	0	3	2		
ENSMUST00000182322						1	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000182323	ENSMUSG00000024073	17	74528295	74703356	1	1	1	2	1	0	0	0	0	0	0	0	S4R2J7	
ENSMUST00000182324						0	0	0	0	0	0	0	10	0	4	3		
ENSMUST00000182326						4	2	4	5	1	4	0	2	1	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182327						2	5	6	4	10	5	0	0	0	0	0		
ENSMUST00000182328	ENSMUSG00000030591	7	29174188	29180701	-1	12	8	17	0	3	0	1476	3474	1321	1171	1004	Q9CPS5	
ENSMUST00000182329						10	2	3	8	1	5	0	1	0	1	0		
ENSMUST00000182331	ENSMUSG00000040225	1	162670725	162740556	-1	0	2	0	0	1	0	0	0	20	0	21	S4R298	
ENSMUST00000182332						1	0	2	0	0	0	3	55	11	14	18		
ENSMUST00000182334						0	2	0	18	4	0	0	0	0	0	0		
ENSMUST00000182335						17	7	12	22	15	6	0	0	0	0	1		
ENSMUST00000182336						9	5	6	15	6	2	0	1	4	4	2		
ENSMUST00000182337	ENSMUSG00000032525	9	121719169	121756843	1	0	2	0	9	0	0	0	0	0	0	0	S4R1C3	
ENSMUST00000182338	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	0	0	0	0	0	S4R237	
ENSMUST00000182339						0	0	0	0	0	0	6	0	7	0	0		
ENSMUST00000182340						0	1	6	3	5	2	0	0	0	0	0		
ENSMUST00000182341	ENSMUSG00000035189	10	88948994	89344762	-1	0	0	0	0	0	0	0	0	0	0	0		Q8C5H1
ENSMUST00000182343						2	3	0	2	0	0	0	0	0	0	0		
ENSMUST00000182344	ENSMUSG00000041617	16	17646470	17650738	1	1	0	0	0	3	0	0	0	1	0	0	S4R194	
ENSMUST00000182346						4	9	6	11	16	5	4	0	1	2	1		
ENSMUST00000182347	ENSMUSG00000010608	12	83631236	83683123	1	1	1	0	9	4	0	0	0	0	0	0	S4R1X5	
ENSMUST00000182348						2	2	3	7	1	2	0	0	0	0	0		
ENSMUST00000182350	ENSMUSG00000060509	9	123852315	123862029	-1	81	83	273	68	76	47	0	12	1	5	17	S4R1K3	
ENSMUST00000182351						136	92	1041	197	111	65	7	22	9	2	12		
ENSMUST00000182353						4	10	10	7	7	0	0	0	0	0	0		
ENSMUST00000182354						6	2	0	1	3	1	0	0	0	0	0		
ENSMUST00000182355						0	7	3	0	3	3	0	81	48	24	29		
ENSMUST00000182356	ENSMUSG00000058589	10	89873509	90973300	1	35	28	103	140	44	26	0	0	0	0	2		
ENSMUST00000182357						33	19	79	255	42	12	1	9	8	0	5		
ENSMUST00000182358						0	3	11	0	1	2	4	3	0	0	3		
ENSMUST00000182359						1	3	4	5	3	2	0	9	3	6	2		
ENSMUST00000182360						50	22	213	67	46	13	0	7	1	1	2		
ENSMUST00000182362						2	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000182363						6	12	14	17	19	6	0	0	0	0	0		
ENSMUST00000182364						0	0	0	32	0	0	0	0	0	0	0		
ENSMUST00000182365	ENSMUSG00000002342	8	70172356	70183681	1	0	0	0	0	0	0	0	0	0	0	6	S4R2H0	
ENSMUST00000182366	ENSMUSG00000079055	12	81197915	81333180	-1	6	2	2	1	1	2	0	0	0	0	0	S4R2V4	
ENSMUST00000182367						3	4	9	2	7	3	0	0	0	0	0		
ENSMUST00000182368	ENSMUSG00000041617	16	17646470	17650738	1	4	3	0	0	0	2	0	0	0	0	0	S4R1K8	
ENSMUST00000182369						7	4	12	3	5	1	2	2	2	1	0		
ENSMUST00000182371	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	0	0	0	0	392	3042	842	401	1179	S4R184	
ENSMUST00000182372						0	0	2	0	1	0	6	5	5	3	0		
ENSMUST00000182373						8	5	17	5	5	4	0	0	0	0	0		
ENSMUST00000182374						5	8	8	4	11	4	0	0	0	0	0		
ENSMUST00000182375						9	4	7	7	6	2	0	3	0	1	3		
ENSMUST00000182376						7	1	2	7	4	2	0	0	0	0	0		
ENSMUST00000182377						6	2	6	6	6	1	0	2	0	0	0		
ENSMUST00000182378						16	13	54	43	37	17	137	491	297	52	530		
ENSMUST00000182379						9	3	41	7	9	0	0	0	0	0	0		
ENSMUST00000182381						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000182382						5	5	7	60	6	5	0	0	0	0	0		
ENSMUST00000182383	ENSMUSG00000041225	18	6024427	6136098	-1	0	0	0	0	0	0	0	0	0	0	0	S4R203	
ENSMUST00000182384	ENSMUSG00000040875	9	114978569	115232225	1	12	0	24	1	5	9	1	0	0	0	0	S4R296	
ENSMUST00000182385						3	7	6	2	7	0	0	0	0	0	0		
ENSMUST00000182386	ENSMUSG00000034219	5	129683391	129708512	-1	26	7	15	8	11	8	0	0	1	0	0	S4R2P6	
ENSMUST00000182388						0	0	3	0	2	4	0	0	0	0	6		
ENSMUST00000182390						2	3	8	3	2	2	0	0	0	0	0		
ENSMUST00000182391						1	0	1	6	2	2	0	2	0	0	0		
ENSMUST00000182392						4	2	0	1	2	2	0	0	0	0	0		
ENSMUST00000182393	ENSMUSG00000040225	1	162670725	162740556	-1	0	17	13	0	2	0	221	515	295	18	292	S4R209	
ENSMUST00000182394						7	8	13	12	12	4	10	161	76	17	93		
ENSMUST00000182395						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182396	ENSMUSG00000034801	12	69583762	69681852	-1	0	0	0	0	0	0	98	684	531	15	427	S4R2C4	
ENSMUST00000182397						2	1	8	3	3	1	0	0	0	0	0		
ENSMUST00000182399						2	0	0	2	3	0	0	0	0	0	0		
ENSMUST00000182401						3	7	6	0	5	5	0	0	0	0	0		
ENSMUST00000182402						7	8	0	8	0	3	8	21	12	15	8		
ENSMUST00000182404	ENSMUSG00000002107	2	6539694	7509563	-1	1	0	0	2	0	0	9	0	0	0	0	S4R2S7	
ENSMUST00000182405	ENSMUSG00000021767	14	21481434	21672478	1	0	1	27	0	44	0	15	0	0	0	67		Q8BRB7
ENSMUST00000182407	ENSMUSG00000061601	5	14514918	14863459	1	31	31	559	149	59	5	0	0	0	0	0		Q9QYX7
ENSMUST00000182409						0	11	20	0	15	0	0	0	14	0	0		
ENSMUST00000182410						18	10	93	21	20	10	0	2	0	0	0		
ENSMUST00000182411	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	1	0	0	0	0	15	28	S4R1Z8	
ENSMUST00000182412	ENSMUSG00000004562	14	51984719	52006251	1	0	3	4	34	0	2	0	0	0	0	0	S4R1X0	
ENSMUST00000182413						0	1	6	0	12	0	0	0	0	0	2		
ENSMUST00000182415						11	0	3	3	3	0	15	122	40	135	17		
ENSMUST00000182416						3	2	0	1	3	0	0	0	0	0	0		
ENSMUST00000182417						3	0	2	5	4	1	0	0	0	0	0		
ENSMUST00000182418						4	2	7	8	3	1	0	0	0	0	0		
ENSMUST00000182419	ENSMUSG00000035189	10	88948994	89344762	-1	0	0	2	0	3	2	0	0	0	0	0	S4R1Z4	
ENSMUST00000182420						13	5	10	5	7	5	0	0	0	0	0		
ENSMUST00000182421	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2T4	
ENSMUST00000182422						0	0	0	0	2	0	4	23	18	0	10		
ENSMUST00000182425						7	3	3	3	3	1	0	0	0	0	0		
ENSMUST00000182426						66	42	197	141	84	40	3	5	5	0	1		
ENSMUST00000182427	ENSMUSG00000058589	10	89873509	90973300	1	2	1	0	3	0	0	0	0	0	0	0	S4R235	
ENSMUST00000182428	ENSMUSG00000030314	6	114643097	114860614	1	0	0	0	0	9	2	270	24	379	77	186	S4R2T5	
ENSMUST00000182430	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182431						1	0	0	0	0	0	5	24	0	1	5		
ENSMUST00000182432	ENSMUSG00000055044	19	40221173	40271842	-1	2	3	70	47	1	2	74	71	52	51	115	S4R1V0	
ENSMUST00000182433	ENSMUSG00000035325	5	100361649	100416234	-1	0	0	0	0	0	0	12	102	0	28	0	S4R1T5	
ENSMUST00000182434						3	3	10	2	3	0	0	0	0	0	0		
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ENSMUST00000182436						6	5	41	13	5	2	8	28	7	0	9		
ENSMUST00000182437	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	S4R2C1	
ENSMUST00000182438						1	4	2	2	7	1	0	0	0	0	0		
ENSMUST00000182439	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	G3X971	
ENSMUST00000182441						1618	1998	6837	1294	2019	928	7	58	25	4	50		
ENSMUST00000182442						15	19	34	18	18	5	0	1	0	0	0		
ENSMUST00000182443	ENSMUSG00000045659	7	116123485	116308376	-1	34	43	146	59	71	29	2	2	7	0	2		
ENSMUST00000182444						37	12	75	16	21	9	0	0	0	0	0		
ENSMUST00000182445						62	59	136	244	64	29	6	20	13	5	10		
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ENSMUST00000182448						2	5	1	0	1	1	0	0	0	0	1		
ENSMUST00000182449						4	5	7	4	9	2	2	4	2	3	3		
ENSMUST00000182450	ENSMUSG00000010608	12	83631236	83683123	1	4	0	0	0	0	0	60	1214	432	234	436	S4R1X9	
ENSMUST00000182451						1	4	0	4	4	4	2	0	1	0	2		
ENSMUST00000182452	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	0	0	0	1	0	S4R1U2	
ENSMUST00000182454						6	5	22	12	10	10	2	87	5	6	30		
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ENSMUST00000182456						4	5	2	3	1	1	17	11	20	25	14		
ENSMUST00000182457	ENSMUSG00000090658	13	65044613	65052760	-1	2	1	3	4	4	6	0	0	0	0	1		
ENSMUST00000182459						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000182461						4	0	0	8	3	1	2	27	11	0	18		
ENSMUST00000182462	ENSMUSG00000035189	10	88948994	89344762	-1	17	0	14	12	0	0	0	0	0	0	0	S4R1Z9	
ENSMUST00000182463						5	11	6	13	5	4	11	9	8	8	7		
ENSMUST00000182464						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000182465						3	3	5	4	5	2	0	0	0	0	0		
ENSMUST00000182466						6	6	3	3	3	4	0	1	0	0	0		
ENSMUST00000182467						9	9	16	6	11	6	6	11	6	1	0		
ENSMUST00000182468						5	2	3	3	4	0	0	0	0	0	0		
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ENSMUST00000182470						8	4	5	5	8	2	1	0	3	0	0		
ENSMUST00000182471						9	8	8	14	14	3	1	0	0	0	0		
ENSMUST00000182472						5	2	8	2	7	3	0	0	0	1	0		
ENSMUST00000182474						30	32	53	30	21	25	2	0	2	0	3		
ENSMUST00000182475						0	2	0	0	1	0	3	12	0	0	0		
ENSMUST00000182478	ENSMUSG00000042439	18	65580230	65689443	1	8	0	68	12	8	0	0	0	0	0	0		Q6NXK2
ENSMUST00000182479	ENSMUSG00000040528	11	106751226	106768794	1	0	0	0	0	0	0	0	0	0	222	57	S4R1V2	
ENSMUST00000182480						165	227	531	145	184	118	4	26	14	55	28		
ENSMUST00000182481	ENSMUSG00000024998	19	38481109	38785030	1	10	0	0	28	0	0	0	0	0	0	0		Q8K4S1
ENSMUST00000182482						4	0	3	2	7	4	0	2	0	1	0		
ENSMUST00000182483						4	12	49	14	25	5	0	0	0	0	0		
ENSMUST00000182484	ENSMUSG00000030583	7	29320372	29518641	-1	0	1	0	29	0	0	33	0	42	0	11	S4R2N4	
ENSMUST00000182485	ENSMUSG00000040327	17	46500572	46546388	-1	0	3	0	71	12	0	1	46	0	0	39	S4R1Y1	
ENSMUST00000182487	ENSMUSG00000045659	7	116123485	116308376	-1	0	0	0	8	0	0	3	0	2	0	0		Q3UIL6
ENSMUST00000182488						3	1	5	2	1	1	6	21	10	5	8		
ENSMUST00000182489	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	0	0	3	0	0	S4R265	
ENSMUST00000182490	ENSMUSG00000030380	7	13042303	13054764	-1	0	0	0	0	0	0	44	12	3	0	0	S4R1L6	
ENSMUST00000182491	ENSMUSG00000034009	3	79641611	79737880	-1	28	19	147	33	37	12	1	8	4	0	1	S4R2B5	
ENSMUST00000182492						4	6	4	7	4	2	0	0	0	0	0		
ENSMUST00000182493	ENSMUSG00000097894	CHR_MG4151_PATCH	3422711	3434183	1	8	4	13	8	2	4	0	0	0	0	0	Q14C42	Q8VHW3
ENSMUST00000182494						0	0	0	0	0	0	14	120	43	0	39		
ENSMUST00000182500	ENSMUSG00000025027	19	52943417	53040214	-1	669	470	2182	860	782	372	32	56	92	5	92	S4R167	
ENSMUST00000182501	ENSMUSG00000021917	14	30999826	31001672	-1	0	0	0	0	1	0	614	1538	556	2278	302		
ENSMUST00000182502	ENSMUSG00000081906	11	83645046	83645621	-1	1	3	0	0	2	1	0	2	1	1	1	S4R1R7	
ENSMUST00000182503	ENSMUSG00000032525	9	121719169	121756843	1	0	0	0	0	0	0	0	5	12	19	6	S4R220	
ENSMUST00000182504						0	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000182505						1	5	3	4	6	2	0	0	1	0	0		
ENSMUST00000182506	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	0	0	0	7	3	0	3	6	S4R1D9	
ENSMUST00000182507	ENSMUSG00000026131	1	33908225	34308661	1	3	0	3	25	5	0	0	0	0	0	0	S4R2C6	
ENSMUST00000182508						0	5	0	0	6	5	6	17	2	4	18		
ENSMUST00000182510	ENSMUSG00000030314	6	114643097	114860614	1	1	1	5	2	5	0	132	92	118	15	112	S4R1N8	
ENSMUST00000182511	ENSMUSG00000045659	7	116123485	116308376	-1	4	0	35	0	1	5	0	1	0	0	5		Q3UIL6
ENSMUST00000182512	ENSMUSG00000090121	12	70154142	70183887	1	0	0	0	0	0	0	0	0	0	0	0	S4R1Y3	
ENSMUST00000182513						17	0	72	44	0	0	0	0	0	3	0		
ENSMUST00000182514						5	5	9	9	10	3	1	0	2	0	0		
ENSMUST00000182515	ENSMUSG00000030380	7	13042303	13054764	-1	5	0	0	31	12	14	0	1	5	0	0	A1L358	
ENSMUST00000182518						25	19	35	28	19	21	3	4	4	2	8		
ENSMUST00000182519	ENSMUSG00000024128	17	23941672	23945607	1	1	0	0	0	0	0	0	0	0	0	0	S4R1R4	
ENSMUST00000182521						4	6	13	83	10	2	0	0	0	1	0		
ENSMUST00000182522						0	0	1	0	2	0	11	2	9	0	0		
ENSMUST00000182523						10	12	17	7	10	4	1	2	8	2	2		
ENSMUST00000182524						5	1	7	11	8	5	4	3	0	2	2		
ENSMUST00000182525						3	9	8	12	7	0	2	3	0	2	0		
ENSMUST00000182526						1	2	1	0	0	2	0	0	1	0	1		
ENSMUST00000182527						0	2	14	3	4	1	0	0	0	0	0		
ENSMUST00000182528						2	1	6	7	4	1	0	0	0	0	0		
ENSMUST00000182529						11	5	11	11	10	6	0	7	11	2	7		
ENSMUST00000182530						23	17	25	18	14	4	0	0	0	0	1		
ENSMUST00000182531						2	0	8	3	7	1	2	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182532	ENSMUSG00000027777	3	68064802	68626481	1	0	0	0	21	7	0	0	0	0	7	0		Q3TI53
ENSMUST00000182533	ENSMUSG00000071054	17	56584825	56606294	1	0	0	0	22	0	0	260	879	1145	66	623	S4R1M2	
ENSMUST00000182534						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182535						1	2	0	0	0	2	0	0	0	0	0		
ENSMUST00000182538	ENSMUSG00000066800	1	153749426	153764221	1	126	173	674	151	102	67	641	5149	1501	714	1197	Q3T9T6	
ENSMUST00000182539	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	0	3	0	561	188	357	85	204	S4R216	
ENSMUST00000182540						4	1	3	1	5	1	38	38	23	21	37		
ENSMUST00000182542						0	0	0	0	0	1	0	4	0	0	0		
ENSMUST00000182543						9	7	7	13	12	5	0	0	0	0	0		
ENSMUST00000182546	ENSMUSG00000098022	7	30054489	30072900	-1	0	0	0	0	0	1	0	8	0	0	0	S4R1G9	
ENSMUST00000182547	ENSMUSG00000032826	3	126921612	127499350	-1	6	0	5	5	0	0	0	0	0	0	0	S4R2D6	
ENSMUST00000182549						1	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000182550	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	1	0	0	0	0	0	S4R2H2	
ENSMUST00000182552						7	3	7	5	8	4	0	0	0	0	0		
ENSMUST00000182553						3	0	27	9	3	2	0	0	12	0	17		
ENSMUST00000182554	ENSMUSG00000025939	1	16540790	16619489	-1	5	2	5	5	3	0	1	17	9	5	0	S4R177	
ENSMUST00000182555						3	5	10	7	5	7	0	0	0	0	0		
ENSMUST00000182556	ENSMUSG00000029422	5	123728426	123749414	-1	4	1	2	0	0	0	0	0	0	10	0	S4R2G2	
ENSMUST00000182557	ENSMUSG00000069601	10	69533772	70027438	1	2	3	12	2	5	4	0	0	0	0	0	Q3UVY0	
ENSMUST00000182558						2	0	1	0	1	0	0	1	0	0	0		
ENSMUST00000182559	ENSMUSG00000041225	18	6024427	6136098	-1	0	10	10	78	9	0	0	44	49	36	11		Q8C0D4
ENSMUST00000182560						35	40	81	27	33	18	2	11	8	0	7		
ENSMUST00000182561						7	6	11	11	6	2	0	0	0	0	0		
ENSMUST00000182562	ENSMUSG00000025656	X	95048935	95196856	-1	2	2	0	0	0	0	0	0	0	0	0	S4R1A7	
ENSMUST00000182563	ENSMUSG00000066189	7	122670492	122769393	1	0	0	0	0	0	0	0	0	0	0	0	S4R247	
ENSMUST00000182564						76	92	66	150	88	91	1	7	2	3	6		
ENSMUST00000182565						7	3	4	8	14	8	6	4	1	3	0		
ENSMUST00000182566						2	2	1	7	0	1	4	4	2	5	5		
ENSMUST00000182569						0	1	5	3	6	6	0	10	9	3	18		
ENSMUST00000182571	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2Q9	
ENSMUST00000182572						21	21	46	17	19	10	1	2	1	0	0		
ENSMUST00000182573	ENSMUSG00000038094	16	29395853	29544864	-1	7	0	0	3	8	11	4	63	17	27	20	S4R2M1	
ENSMUST00000182574	ENSMUSG00000098112	15	100641077	100669553	-1	0	0	0	0	0	0	0	0	46	0	26	S4R171	
ENSMUST00000182575						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182576	ENSMUSG00000058690	14	36874936	36968777	-1	0	0	0	0	0	1	0	0	0	0	0	S4R1Q3	
ENSMUST00000182577	ENSMUSG00000046056	7	30734739	30756134	1	19	22	85	33	34	24	3	7	3	3	13	S4R1T6	
ENSMUST00000182579						3	1	5	0	1	1	0	0	0	0	0		
ENSMUST00000182581						10	6	8	8	11	9	20	28	6	25	9		
ENSMUST00000182582						11	12	29	72	12	4	2	0	2	0	5		
ENSMUST00000182583	ENSMUSG00000029110	5	34336289	34355629	1	0	0	0	52	0	0	0	6	12	30	3	S4R2C9	
ENSMUST00000182584	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	48	324	85	143	164	A0A0G2JDD3	
ENSMUST00000182585						3	5	7	3	3	4	0	0	0	0	0		
ENSMUST00000182588						0	20	0	0	13	0	2	0	0	0	0		
ENSMUST00000182589						29	18	23	14	27	12	0	0	0	0	0		
ENSMUST00000182591						0	0	0	0	0	1	0	0	0	65	0		
ENSMUST00000182593	ENSMUSG00000040225	1	162670725	162740556	-1	2	0	148	0	22	22	571	158	2036	47	1840	S4R2J9	
ENSMUST00000182594						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182595	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0	S4R1Q0	
ENSMUST00000182596						7	2	6	9	5	4	0	0	2	1	0		
ENSMUST00000182597	ENSMUSG00000024073	17	74528295	74703356	1	0	0	0	0	0	0	81	386	1721	0	650		O88738
ENSMUST00000182598	ENSMUSG00000035189	10	88948994	89344762	-1	1	0	6	0	4	0	0	0	0	0	0	S4R1D3	
ENSMUST00000182599						5	5	10	9	8	4	0	0	1	0	1		
ENSMUST00000182600	ENSMUSG00000058589	10	89873509	90973300	1	2	0	3	0	0	0	0	0	0	0	0	S4R2H8	
ENSMUST00000182602	ENSMUSG00000029551	5	139823592	139826885	-1	0	3	0	0	0	3	24	37	7	30	14		Q9CZH3
ENSMUST00000182603	ENSMUSG00000061544	17	21730795	21769342	1	0	0	128	0	38	14	4	26	4	0	15	E9PWT2	
ENSMUST00000182604						8	3	11	225	10	11	4	23	9	3	19		
ENSMUST00000182605						43	31	17	21	43	24	1	4	3	0	0		
ENSMUST00000182606						0	1	0	2	1	2	0	0	0	0	0		
ENSMUST00000182607						5	2	1	4	3	1	3	33	11	4	33		
ENSMUST00000182608						3	1	5	6	4	5	0	0	0	0	0		
ENSMUST00000182609						11	7	11	32	19	7	0	0	0	0	3		
ENSMUST00000182610	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1I1	
ENSMUST00000182611						3	2	0	0	1	0	9	8	10	0	0		
ENSMUST00000182612						0	17	0	7	0	0	0	0	30	0	0		
ENSMUST00000182613	ENSMUSG00000035189	10	88948994	89344762	-1	2	0	0	0	0	4	0	0	0	0	0	S4R1L3	
ENSMUST00000182614						0	0	0	15	0	0	0	0	0	3	0		
ENSMUST00000182615						1	4	0	6	4	1	0	0	2	0	0		
ENSMUST00000182616						7	5	8	4	8	5	0	0	0	0	0		
ENSMUST00000182617						0	2	0	49	0	0	0	0	0	0	1		
ENSMUST00000182618	ENSMUSG00000010608	12	83631236	83683123	1	0	0	0	0	0	0	3	0	15	0	5	S4R2J1	
ENSMUST00000182619	ENSMUSG00000020056	10	88201093	88246158	1	0	0	0	1	1	0	0	0	0	0	3	S4R1P7	
ENSMUST00000182621	ENSMUSG00000059562	17	25162461	25171913	1	0	0	0	0	0	0	0	0	0	0	0		Q6RUT8
ENSMUST00000182622						10	3	7	0	6	5	0	0	0	1	0		
ENSMUST00000182624	ENSMUSG00000035189	10	88948994	89344762	-1	3	0	2	1	0	3	0	0	0	0	0	S4R272	
ENSMUST00000182625	ENSMUSG00000051817	2	152393611	152398063	-1	25	20	39	433	37	22	10	13	7	1	10		Q04890
ENSMUST00000182626						0	0	0	2	0	0	0	0	0	4	0		
ENSMUST00000182627	ENSMUSG00000038094	16	29395853	29544864	-1	0	0	0	0	0	0	0	0	0	0	0	S4R234	
ENSMUST00000182628						1	2	2	4	4	2	0	0	0	0	0		
ENSMUST00000182629						59	70	83	71	64	44	6	75	14	29	28		
ENSMUST00000182630						0	3	0	0	0	0	14	2	9	4	6		
ENSMUST00000182631						4	0	1	1	2	1	0	0	0	0	0		
ENSMUST00000182632						0	0	0	10	0	0	0	0	0	0	0		
ENSMUST00000182633	ENSMUSG00000010608	12	83631236	83683123	1	0	0	0	0	0	0	0	0	0	0	0	S4R2F7	
ENSMUST00000182634	ENSMUSG00000061099	7	30729775	30743681	-1	11	0	6	37	2	0	5	14	0	0	2	S4R2G5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182635						0	3	10	1	2	1	0	0	1	0	0		
ENSMUST00000182636						23	20	117	63	27	13	0	4	0	0	5		
ENSMUST00000182637	ENSMUSG00000033882	3	82837228	82876483	-1	0	0	3	0	1	1	0	0	0	0	0	S4R2P5	
ENSMUST00000182638						10	2	6	2	7	0	8	2	8	7	3		
ENSMUST00000182640	ENSMUSG00000098094	7	33054582	33056561	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1X8	
ENSMUST00000182641						1	2	1	6	2	3	0	0	0	0	0		
ENSMUST00000182642	ENSMUSG00000025964	1	63445891	63596276	1	5	3	13	39	4	3	0	0	1	0	0	Q5SRA0	
ENSMUST00000182643						6	8	11	5	9	2	0	0	0	0	0		
ENSMUST00000182644						1	0	3	0	0	0	0	1	1	0	0		
ENSMUST00000182645						4	2	12	7	5	3	0	0	0	0	0		
ENSMUST00000182646						0	5	10	1	2	1	12	64	29	4	34		
ENSMUST00000182647						0	0	0	0	0	0	0	0	3	0	0		
ENSMUST00000182648						64	6	35	0	39	0	0	0	0	0	0		
ENSMUST00000182649	ENSMUSG00000004562	14	51984719	52006251	1	2	1	4	35	4	2	0	0	0	0	0	S4R2G8	
ENSMUST00000182651						5	4	8	5	6	3	0	0	0	0	0		
ENSMUST00000182652						5	2	4	2	4	0	0	0	0	0	0		
ENSMUST00000182654						1	1	0	0	2	1	0	2	0	0	0		
ENSMUST00000182655	ENSMUSG00000042439	18	65580230	65689443	1	2	1	3	0	0	0	0	0	0	0	0	S4R1F4	
ENSMUST00000182657	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	1	0	0	0	0	0	0	0	0	S4R2U1	
ENSMUST00000182658						4	4	15	6	10	4	0	3	4	0	3		
ENSMUST00000182659	ENSMUSG00000032580	9	107740371	107770996	-1	0	1	8	14	0	0	0	37	118	0	0		Q91YE7
ENSMUST00000182660	ENSMUSG00000040225	1	162670725	162740556	-1	29	0	18	48	15	0	0	230	0	0	0		Q3TLH4
ENSMUST00000182661						5	4	5	5	10	5	5	6	3	6	2		
ENSMUST00000182662						0	18	0	8	0	8	0	0	0	0	0		
ENSMUST00000182663						0	3	0	30	2	1	421	1029	895	290	757		
ENSMUST00000182664						3	4	3	1	4	1	2	4	2	0	2		
ENSMUST00000182665	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	2	0	0	0	0	0	0	A0A087WRU2	
ENSMUST00000182666	ENSMUSG00000028082	3	85971109	86130526	1	22	22	137	17	51	28	0	0	0	0	29		Q91X43
ENSMUST00000182667	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	0	0	0	0	0	S4R1Y4	
ENSMUST00000182668						22	19	67	35	43	21	0	6	3	1	0		
ENSMUST00000182669						0	1	0	0	0	0	0	2	1	0	0		
ENSMUST00000182670						0	0	0	0	6	0	21	17	14	16	19		
ENSMUST00000182671	ENSMUSG00000041617	16	17646470	17650738	1	0	0	0	0	0	0	0	0	0	0	0	S4R1C0	
ENSMUST00000182672						0	6	8	3	7	3	0	0	0	0	0		
ENSMUST00000182673	ENSMUSG00000098094	7	33054582	33056561	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2V3	
ENSMUST00000182674						1	1	2	1	1	1	0	0	0	0	0		
ENSMUST00000182675	ENSMUSG00000051285	1	7088920	7173628	1	0	2	0	0	0	0	4	11	59	3	47	S4R1A9	
ENSMUST00000182676						3	0	11	0	0	0	0	0	0	0	0		
ENSMUST00000182677	ENSMUSG00000078452	10	22360552	22374139	1	0	0	22	3	0	4	0	0	0	0	0		Q9JI58
ENSMUST00000182678						9	4	9	14	8	2	0	0	0	0	0		
ENSMUST00000182679						0	0	0	0	1	0	0	0	1	4	0		
ENSMUST00000182681						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000182682						8	8	15	7	19	9	19	39	19	0	41		
ENSMUST00000182683	ENSMUSG00000069601	10	69533772	70027438	1	2	0	0	3	0	2	0	0	0	0	0	S4R1U4	
ENSMUST00000182684	ENSMUSG00000042439	18	65580230	65689443	1	0	0	10	1	2	0	0	0	0	0	0	S4R2D8	
ENSMUST00000182685	ENSMUSG00000052920	19	30567551	31765033	-1	12	7	0	92	19	3	0	0	0	0	0	Q8BQ38	
ENSMUST00000182687						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182688						6	7	15	7	5	1	0	0	0	0	0		
ENSMUST00000182691						7	7	6	8	9	3	2	0	1	1	0		
ENSMUST00000182692	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	S4R2F5	
ENSMUST00000182693						1	1	15	1	0	2	0	0	0	0	0		
ENSMUST00000182694						6	6	9	9	13	7	0	0	0	0	0		
ENSMUST00000182695						5	2	2	9	5	5	0	0	0	0	0		
ENSMUST00000182696	ENSMUSG00000047507	17	25242659	25256364	-1	0	0	1	8	0	0	0	0	0	0	0	S4R212	
ENSMUST00000182697	ENSMUSG00000026131	1	33908225	34308661	1	0	19	286	76	11	16	0	0	0	0	0	A0A0A6YX28	
ENSMUST00000182698						0	5	9	6	0	3	0	0	0	0	0		
ENSMUST00000182700						4	7	18	2	5	3	1	3	2	0	1		
ENSMUST00000182702						1	0	0	11	0	0	2	0	14	0	7		
ENSMUST00000182703						2	1	3	4	3	2	0	0	0	0	0		
ENSMUST00000182704						33	0	245	100	67	74	0	0	0	0	0		
ENSMUST00000182705						3	7	5	3	15	4	2	3	4	0	0		
ENSMUST00000182706	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	0	0	0	0	0		Q9Z0H4
ENSMUST00000182707						7	3	1	10	5	4	0	0	0	0	0		
ENSMUST00000182708						55	47	304	348	76	39	0	11	5	1	11		
ENSMUST00000182709	ENSMUSG00000029110	5	34336289	34355629	1	0	0	0	6	0	0	351	613	568	362	276		Q9QZS2
ENSMUST00000182710						7	4	1	3	3	1	8	0	7	0	5		
ENSMUST00000182711	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	2	0	0	0	0	0	2	0	17	S4R2T7	
ENSMUST00000182712						0	1	2	0	0	0	0	0	1	0	0		
ENSMUST00000182713	ENSMUSG00000032525	9	121719169	121756843	1	0	0	0	0	0	0	1	0	0	0	0	S4R2C2	
ENSMUST00000182714						1	4	0	6	4	1	2	4	2	0	0		
ENSMUST00000182715	ENSMUSG00000002342	8	70172356	70183681	1	6	0	16	10	9	6	0	46	12	3	4	S4R1Z2	
ENSMUST00000182716						7	4	12	13	6	5	0	2	1	0	0		
ENSMUST00000182717						84	71	237	248	125	75	0	7	11	3	4		
ENSMUST00000182719	ENSMUSG00000027777	3	68064802	68626481	1	0	4	17	102	0	3	0	0	0	0	0		Q3TI53
ENSMUST00000182720						8	9	5	8	12	6	12	5	9	8	5		
ENSMUST00000182721	ENSMUSG00000046056	7	30734739	30756134	1	0	0	0	0	0	0	0	0	0	0	0	S4R2I1	
ENSMUST00000182722	ENSMUSG00000066800	1	153749426	153764221	1	0	0	0	0	0	0	380	1186	792	193	787	S4R1J5	
ENSMUST00000182723						2	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000182724						3	0	0	4	5	0	0	0	0	0	0		
ENSMUST00000182725						3	1	2	1	5	1	7	26	15	15	10		
ENSMUST00000182726						0	32	124	0	31	0	0	0	2	0	7		
ENSMUST00000182728						4	3	54	3	2	0	0	0	0	0	3		
ENSMUST00000182729	ENSMUSG00000020728	11	108425192	108860615	1	0	0	0	0	0	0	0	0	0	1	0	S4R1I4	
ENSMUST00000182730						7	4	6	8	5	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182731	ENSMUSG00000037519	7	144476758	144553729	-1	0	0	0	0	0	1	6	0	6	0	0	S4R1I7	
ENSMUST00000182732						16	29	9	21	24	8	4	5	8	0	13		
ENSMUST00000182734						2	2	2	0	0	2	0	0	0	0	0		
ENSMUST00000182735						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182736						0	0	6	0	5	0	0	2	0	4	9		
ENSMUST00000182738	ENSMUSG00000051811	7	4751792	4753094	-1	0	0	0	0	0	0	10	9	2	0	0	S4R2Q6	
ENSMUST00000182739	ENSMUSG00000031809	8	121530780	121544320	-1	5	3	14	0	0	0	0	0	0	0	0	S4R1L4	
ENSMUST00000182740						4	5	6	38	11	3	0	0	0	0	0		
ENSMUST00000182741	ENSMUSG00000022818	16	20308387	20323065	-1	5	4	8	8	16	7	3	0	2	9	12	S4R196	
ENSMUST00000182743						10	4	25	127	13	3	5	10	3	2	15		
ENSMUST00000182744						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182745						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182746	ENSMUSG00000058447	7	30056034	30090410	-1	0	0	0	0	0	0	7	15	0	11	8	S4R2A5	
ENSMUST00000182747						70	54	189	457	75	40	3	5	7	1	8		
ENSMUST00000182749						11	13	21	15	10	11	0	0	0	0	0		
ENSMUST00000182750	ENSMUSG00000070564	7	45684022	45694556	1	5	2	37	95	20	4	0	0	0	0	0	S4R1X6	
ENSMUST00000182751						4	10	27	0	3	0	158	191	373	82	340		
ENSMUST00000182752						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000182754						6	5	4	7	17	6	5	3	5	9	6		
ENSMUST00000182755	ENSMUSG00000026395	1	138062861	138175708	-1	0	6	42	16	0	14	1809	19989	964	1739	1538	S4R1M0	
ENSMUST00000182757						5	4	14	12	5	3	3	0	2	0	0		
ENSMUST00000182759						0	0	0	0	0	1	0	0	0	0	2		
ENSMUST00000182760	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	0	0	0	0	0	S4R189	
ENSMUST00000182762						0	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000182763	ENSMUSG00000032525	9	121719169	121756843	1	0	0	0	0	0	0	0	8	8	0	5	S4R1L7	
ENSMUST00000182764						6	6	0	2	5	5	0	0	0	0	3		
ENSMUST00000182765						19	16	102	34	22	14	2	1	0	1	0		
ENSMUST00000182766						4	4	1	1	1	2	0	0	0	0	0		
ENSMUST00000182767						3	2	9	61	7	5	1	1	0	8	2		
ENSMUST00000182769	ENSMUSG00000067882	17	23550965	23553566	-1	4	3	15	7	4	5	0	0	0	0	0		
ENSMUST00000182771	ENSMUSG00000030314	6	114643097	114860614	1	0	2	4	1	0	0	0	0	0	1	0	S4R1U3	
ENSMUST00000182772						4	3	2	0	3	0	2	4	7	0	4		
ENSMUST00000182773						6	6	7	6	4	4	1	2	0	0	1		
ENSMUST00000182774						12	9	26	74	21	12	0	0	0	0	0		
ENSMUST00000182775	ENSMUSG00000098112	15	100641077	100669553	-1	3	24	621	10	0	0	0	152	70	0	25	S4R2J8	
ENSMUST00000182776						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182777						3	0	0	5	0	2	0	0	0	0	1		
ENSMUST00000182779						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182780	ENSMUSG00000030583	7	29320372	29518641	-1	1	0	19	48	7	4	0	0	0	0	0	S4R1P8	
ENSMUST00000182781						3	3	0	5	1	0	0	0	0	0	0		
ENSMUST00000182782	ENSMUSG00000090121	12	70154142	70183887	1	1	8	0	0	9	1	5	19	23	2	20	S4R1Y3	
ENSMUST00000182783						8	2	3	3	5	1	0	0	0	0	0		
ENSMUST00000182784	ENSMUSG00000030162	6	129485244	129507165	-1	2	0	1	0	0	2	0	0	2	0	1	G4WK10	
ENSMUST00000182786	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0	S4R2N9	
ENSMUST00000182787						7	10	5	5	7	7	0	0	2	0	1		
ENSMUST00000182790	ENSMUSG00000035189	10	88948994	89344762	-1	0	16	0	7	15	0	0	0	0	0	0	S4R1L3	
ENSMUST00000182792						25	19	46	23	15	10	9	96	33	18	37		
ENSMUST00000182793	ENSMUSG00000030314	6	114643097	114860614	1	0	0	0	0	0	0	691	585	627	3	447		Q9D906
ENSMUST00000182794						1	1	4	1	0	0	1	0	1	2	1		
ENSMUST00000182795	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	S4R1X7	
ENSMUST00000182797	ENSMUSG00000058690	14	36874936	36968777	-1	0	4	0	2	3	3	0	0	0	0	0	S4R2U3	
ENSMUST00000182798						5	8	10	8	12	6	11	7	11	0	2		
ENSMUST00000182799						0	0	0	0	0	0	2	2	0	0	3		
ENSMUST00000182800	ENSMUSG00000071054	17	56584825	56606294	1	4	0	0	18	1	0	0	0	0	0	0	S4R2Q5	
ENSMUST00000182802	ENSMUSG00000041444	9	32116136	32268446	1	0	0	31	0	0	0	7	0	12	0	14		Q811P8
ENSMUST00000182803						3	6	1	5	4	6	0	0	0	0	0		
ENSMUST00000182804						14	13	18	9	17	7	0	3	2	1	3		
ENSMUST00000182805						2	0	4	0	2	1	0	0	0	0	0		
ENSMUST00000182806						0	4	0	6	0	1	0	0	0	0	0		
ENSMUST00000182807						4	5	6	6	4	2	0	0	0	0	0		
ENSMUST00000182808	ENSMUSG00000042694	19	47501033	47537507	-1	10	1	11	1	4	3	13	23	14	4	30	Q3UXU8	
ENSMUST00000182809						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000182810						0	1	1	2	1	5	0	0	0	0	0		
ENSMUST00000182812	ENSMUSG00000035325	5	100361649	100416234	-1	0	0	0	0	0	0	0	0	0	0	0	S4R256	
ENSMUST00000182813						0	3	3	3	6	4	40	72	10	22	53		
ENSMUST00000182814	ENSMUSG00000098112	15	100641077	100669553	-1	105	54	81	0	18	46	0	39	0	51	36	S4R1B8	
ENSMUST00000182815						4	2	4	1	4	2	0	0	0	0	0		
ENSMUST00000182816	ENSMUSG00000030666	7	114718643	114723365	1	7	3	5	10	4	4	0	0	0	0	0	S4R2N3	
ENSMUST00000182817	ENSMUSG00000024073	17	74528295	74703356	1	0	0	0	0	0	0	0	7	0	0	0	S4R1S3	
ENSMUST00000182818	ENSMUSG00000033882	3	82837228	82876483	-1	0	0	0	1	0	0	0	0	0	0	0	S4R1Y9	
ENSMUST00000182821						0	0	0	6	0	1	0	10	11	5	2		
ENSMUST00000182822						0	0	6	13	5	1	0	0	0	0	3		
ENSMUST00000182823						0	0	3	0	0	0	37	0	0	0	0		
ENSMUST00000182824						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000182825	ENSMUSG00000047507	17	25242659	25256364	-1	16	11	35	9	14	17	0	0	0	0	0	S4R1K2	
ENSMUST00000182827	ENSMUSG00000061544	17	21730795	21769342	1	192	178	364	151	178	39	4	15	6	3	11	S4R233	
ENSMUST00000182828	ENSMUSG00000004562	14	51984719	52006251	1	0	0	1	0	0	0	0	2	0	1	0	S4R1R5	
ENSMUST00000182829						377	321	1977	478	374	176	37	110	94	11	131		
ENSMUST00000182830						4	3	9	12	7	3	1	1	1	0	0		
ENSMUST00000182831	ENSMUSG00000028004	3	82538383	82548084	-1	11	3	12	2	1	6	0	0	0	0	0		P97295
ENSMUST00000182832						10	4	12	6	10	4	0	0	1	1	0		
ENSMUST00000182834	ENSMUSG00000045659	7	116123485	116308376	-1	0	0	0	51	19	0	0	0	0	0	0		Q3UIL6
ENSMUST00000182835						6	5	4	6	11	4	1	0	0	1	0		
ENSMUST00000182836						1	1	0	2	0	0	3	5	2	2	12		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182837						4	0	0	3	2	0	0	1	0	0	0		
ENSMUST00000182838						439	408	768	635	693	369	20	203	62	13	75		
ENSMUST00000182839	ENSMUSG00000098140	5	139807978	139826407	-1	0	0	0	0	0	0	0	0	0	0	0	S4R185	
ENSMUST00000182840						2	0	0	2	1	0	8	36	29	6	10		
ENSMUST00000182841						49	48	145	134	50	23	2	14	13	2	10		
ENSMUST00000182842						4	3	21	6	0	4	0	4	0	0	2		
ENSMUST00000182844						0	2	0	1	0	1	0	0	0	0	0		
ENSMUST00000182845	ENSMUSG00000024073	17	74528295	74703356	1	0	0	0	0	0	0	9	0	0	0	2	S4R2N7	
ENSMUST00000182846	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	0	0	0	0	3	0	3	0	S4R1R1	
ENSMUST00000182847						5	4	4	6	6	1	0	0	0	0	0		
ENSMUST00000182848	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	0	0	0	14	10	23	0	12	S4R2N5	
ENSMUST00000182849						32	27	146	41	27	16	0	3	0	0	2		
ENSMUST00000182850						4	6	15	2	1	0	0	0	0	0	0		
ENSMUST00000182851	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	150	66	112	0	101		Q9Z0H4
ENSMUST00000182852	ENSMUSG00000042439	18	65580230	65689443	1	3	0	13	0	0	0	0	0	0	0	28	S4R2I9	
ENSMUST00000182853	ENSMUSG00000004542	7	18789567	18798520	-1	0	0	0	6	0	0	0	1	0	0	0	S4R2F4	
ENSMUST00000182854						6	1	2	7	5	5	0	0	0	0	0		
ENSMUST00000182855	ENSMUSG00000021767	14	21481434	21672478	1	51	31	50	35	0	42	91	239	330	31	288		Q8BRB7
ENSMUST00000182856						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182857						5	0	5	6	6	3	1	0	0	0	0		
ENSMUST00000182858	ENSMUSG00000098132	7	112953962	112957457	1	16	6	39	229	29	11	0	0	0	0	0		Q8BL43
ENSMUST00000182859						0	0	0	40	0	0	1	0	0	0	0		
ENSMUST00000182860						2	0	0	1	1	4	0	148	0	7	0		
ENSMUST00000182861	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	0	659	24	173	0	A0A0G2JDD3	
ENSMUST00000182862						6	2	9	6	6	2	2	4	0	0	0		
ENSMUST00000182864						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000182866	ENSMUSG00000041258	18	82593593	82692883	-1	4	0	4	18	4	1	4	1	11	2	9	S4R1R9	
ENSMUST00000182867						3	3	5	4	4	2	0	0	0	0	0		
ENSMUST00000182868	ENSMUSG00000024128	17	23941672	23945607	1	2	7	11	0	6	3	0	0	0	0	0	S4R244	
ENSMUST00000182869	ENSMUSG00000090812	12	87199723	87213541	1	8	2	8	14	7	8	4	15	6	2	2		F6XZJ7
ENSMUST00000182871						2	4	5	2	3	1	0	0	0	0	0		
ENSMUST00000182873						1	3	15	0	1	2	58	274	60	164	54		
ENSMUST00000182874	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	17	0	0	0	0	0	0	0	S4R2N1	
ENSMUST00000182876						2	10	20	16	7	2	0	0	0	0	0		
ENSMUST00000182877						4	1	15	9	5	0	253	300	197	174	179		
ENSMUST00000182879	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	70	0	0	0	0		
ENSMUST00000182880						23	26	200	32	19	10	1	2	1	6	6		
ENSMUST00000182881						68	90	117	65	73	37	24	48	39	6	70		
ENSMUST00000182882						11	5	1	9	8	5	0	1	0	1	0		
ENSMUST00000182883						22	14	65	137	33	21	2	0	1	4	0		
ENSMUST00000182884	ENSMUSG00000069601	10	69533772	70027438	1	29	18	33	29	39	23	0	0	0	0	2		G5E8K5
ENSMUST00000182886	ENSMUSG00000035325	5	100361649	100416234	-1	0	0	8	0	0	0	74	0	140	0	91		Q3UPL0
ENSMUST00000182887						4	1	1	2	3	0	0	8	0	3	0		
ENSMUST00000182888						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182889						5	2	5	85	10	4	0	0	0	0	0		
ENSMUST00000182890						0	0	1	56	0	0	0	0	0	0	0		
ENSMUST00000182892						0	3	0	2	3	0	27	46	13	0	25		
ENSMUST00000182893						5	3	6	5	11	2	0	0	0	0	0		
ENSMUST00000182896	ENSMUSG00000040528	11	106751226	106768794	1	0	0	0	0	0	0	0	0	0	0	0	B7ZP19	
ENSMUST00000182897	ENSMUSG00000034413	17	26414829	26446349	1	0	0	0	124	0	0	0	0	0	0	0	S4R1Y0	
ENSMUST00000182898	ENSMUSG00000020107	10	59987409	60003135	-1	10	10	37	30	14	8	50	213	96	60	120		Q9CPV2
ENSMUST00000182899	ENSMUSG00000041347	12	105603085	105605428	1	8	0	0	6	14	0	0	0	0	5	0	Q0VBD7	Q61125
ENSMUST00000182901						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182902	ENSMUSG00000030314	6	114643097	114860614	1	0	0	0	0	0	0	257	153	194	0	132		Q9D906
ENSMUST00000182903						5	7	12	13	12	7	0	0	0	0	0		
ENSMUST00000182904						11	9	16	8	9	10	42	17	49	2	86		
ENSMUST00000182905	ENSMUSG00000004562	14	51984719	52006251	1	5	5	27	95	14	6	0	0	0	0	0	S4R2U9	
ENSMUST00000182906						9	4	7	5	16	9	8	4	1	3	4		
ENSMUST00000182907	ENSMUSG00000058589	10	89873509	90973300	1	0	0	24	0	0	8	0	0	0	0	0	S4R2E7	
ENSMUST00000182908	ENSMUSG00000040528	11	106751226	106768794	1	0	0	0	0	0	0	39	364	83	272	103		Q3TB92
ENSMUST00000182909	ENSMUSG00000004562	14	51984719	52006251	1	0	0	0	0	0	0	0	0	3	0	0		Q3UPH7
ENSMUST00000182910						14	14	17	11	29	11	0	0	0	0	0		
ENSMUST00000182911						26	23	46	91	36	12	8	9	5	1	6		
ENSMUST00000182912	ENSMUSG00000020107	10	59987409	60003135	-1	0	0	0	10	1	0	26	32	19	69	23	S4R1V1	
ENSMUST00000182913						3	0	7	4	0	0	6	30	17	3	14		
ENSMUST00000182914						2	0	0	0	0	0	0	0	7	25	22		
ENSMUST00000182915	ENSMUSG00000061601	5	14514918	14863459	1	35	29	7	0	13	21	0	4	1	0	6	S4R2E0	
ENSMUST00000182916						29	25	37	158	41	19	4	2	0	0	1		
ENSMUST00000182917						5	8	9	46	10	2	4	58	23	33	35		
ENSMUST00000182919	ENSMUSG00000098022	7	30054489	30072900	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2H1	
ENSMUST00000182920	ENSMUSG00000040875	9	114978569	115232225	1	3	0	7	1	3	0	0	0	0	0	0	S4R1L1	
ENSMUST00000182921	ENSMUSG00000041225	18	6024427	6136098	-1	0	0	2	0	0	0	0	0	0	0	0	S4R2V0	
ENSMUST00000182922						2	3	17	7	11	1	0	0	0	0	0		
ENSMUST00000182923						0	0	0	19	5	0	0	0	0	0	0		
ENSMUST00000182924	ENSMUSG00000033542	6	43265582	43289320	1	0	0	7	0	0	1	0	0	0	0	0	S4R1F1	
ENSMUST00000182925						20	16	22	21	40	24	12	12	0	4	9		
ENSMUST00000182926	ENSMUSG00000031586	8	33782643	33929863	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1T1	
ENSMUST00000182927	ENSMUSG00000090121	12	70154142	70183887	1	7	0	8	21	0	0	0	0	0	0	3	S4R2K4	
ENSMUST00000182928						7	8	7	6	5	1	0	1	0	0	0		
ENSMUST00000182929						7	6	4	5	7	2	0	1	0	0	0		
ENSMUST00000182930						2	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000182931						0	0	1	44	15	2	0	0	0	0	0		
ENSMUST00000182932						2	0	3	5	0	0	0	0	0	0	0		
ENSMUST00000182933						1	2	0	2	0	2	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000182934						8	3	11	1	2	2	0	3	3	0	3		
ENSMUST00000182935	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	4	0	0	0	0	0	0	0	S4R1L8	
ENSMUST00000182936	ENSMUSG00000058589	10	89873509	90973300	1	0	0	7	3	0	0	0	1	0	0	0	S4R1G5	
ENSMUST00000182938						6	4	4	6	9	2	0	0	0	0	0		
ENSMUST00000182939						2	2	7	6	1	0	0	0	0	0	0		
ENSMUST00000182940						3	3	7	1	5	2	2	1	5	0	6		
ENSMUST00000182941						5	4	10	7	9	4	1	3	0	0	0		
ENSMUST00000182942						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000182944	ENSMUSG00000024073	17	74528295	74703356	1	0	0	0	0	1	0	243	7	552	17	722	S4R2P8	
ENSMUST00000182945						0	4	4	4	5	2	0	0	1	0	0		
ENSMUST00000182946	ENSMUSG00000034206	16	37011786	37095417	1	0	0	0	0	0	0	0	0	0	0	0	Q8BGX6	
ENSMUST00000182947	ENSMUSG00000050901	9	15824528	15874556	-1	7	7	19	39	17	2	0	0	0	0	0	Q3SXF8	
ENSMUST00000182948						0	0	0	0	0	0	52	48	0	27	43		
ENSMUST00000182950						5	3	0	7	3	2	0	0	0	0	0		
ENSMUST00000182951	ENSMUSG00000071054	17	56584825	56606294	1	0	0	0	0	4	3	0	55	72	0	37	S4R1W0	
ENSMUST00000182954						8	5	8	5	15	6	5	8	3	4	4		
ENSMUST00000182955	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	95	440	39	152	0	S4R1M5	
ENSMUST00000182958	ENSMUSG00000037519	7	144476758	144553729	-1	0	0	12	0	14	0	95	168	108	25	105	S4R1D4	
ENSMUST00000182959	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	0	0	0	0	0	1	0	0	S4R1J9	
ENSMUST00000182960	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0	S4R1H2	
ENSMUST00000182961						66	46	245	160	67	40	0	13	4	2	6		
ENSMUST00000182962						6	10	11	7	9	1	1	6	2	5	1		
ENSMUST00000182963						2	6	2	2	0	1	0	0	0	0	0		
ENSMUST00000182964	ENSMUSG00000021767	14	21481434	21672478	1	0	0	8	0	0	0	50	11	120	0	0		Q8BRB7
ENSMUST00000182966	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	51	0	0	0	0	0	0	0	S4R2E3	
ENSMUST00000182967						5	5	4	3	6	1	0	0	0	0	0		
ENSMUST00000182968						17	20	128	15	16	16	32	48	29	26	66		
ENSMUST00000182969						0	0	0	30	3	1	0	0	0	0	0		
ENSMUST00000182970						16	18	15	40	25	11	18	35	52	14	34		
ENSMUST00000182972	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	1	0	0	0	S4R236	
ENSMUST00000182973	ENSMUSG00000042439	18	65580230	65689443	1	0	0	0	0	0	0	0	0	0	0	1	S4R1P1	
ENSMUST00000182974						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000182975	ENSMUSG00000097972	7	32827683	32829662	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2V3	
ENSMUST00000182976	ENSMUSG00000041617	16	17646470	17650738	1	0	0	0	0	0	0	0	0	0	0	0	S4R1R6	
ENSMUST00000182977						0	0	0	0	0	0	2	0	0	1	10		
ENSMUST00000182978						5	2	3	17	3	0	0	0	0	0	0		
ENSMUST00000182979	ENSMUSG00000042439	18	65580230	65689443	1	1	2	1	2	2	2	0	0	0	0	0	S4R1H5	
ENSMUST00000182980	ENSMUSG00000002342	8	70172356	70183681	1	1	3	0	0	0	0	118	165	102	41	117		Q8VCA6
ENSMUST00000182982						3	12	18	6	11	12	0	53	0	0	0		
ENSMUST00000182983	ENSMUSG00000003505	7	18345422	18355009	-1	3	2	0	6	4	5	0	0	0	0	0	S4R2S1	
ENSMUST00000182985						0	0	3	0	1	1	11	6	39	6	29		
ENSMUST00000182987	ENSMUSG00000031586	8	33782643	33929863	-1	0	0	0	0	0	0	0	0	0	0	0		Q9WVB0
ENSMUST00000182988	ENSMUSG00000035325	5	100361649	100416234	-1	9	6	15	3	0	1	24	51	95	10	67	S4R2A9	
ENSMUST00000182989						5	6	39	9	14	0	0	9	0	17	7		
ENSMUST00000182990						5	8	7	6	2	1	0	0	0	0	0		
ENSMUST00000182991						0	0	1	0	0	0	8	5	3	8	2		
ENSMUST00000182992	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	S4R2K9	
ENSMUST00000182993	ENSMUSG00000069601	10	69533772	70027438	1	0	0	3	0	2	0	0	0	0	0	0	W4VSQ0	
ENSMUST00000182994	ENSMUSG00000032826	3	126921612	127499350	-1	11	7	25	52	21	7	1	1	0	1	10		Q8C8R3
ENSMUST00000182995						6	3	7	12	7	2	10	18	11	6	6		
ENSMUST00000182996	ENSMUSG00000021767	14	21481434	21672478	1	18	0	0	0	0	5	0	0	0	0	0	S4R2Q8	
ENSMUST00000182997	ENSMUSG00000027777	3	68064802	68626481	1	4	1	0	0	6	4	0	0	0	0	0	S4R1J0	
ENSMUST00000182998						8	9	6	9	11	3	0	0	0	0	0		
ENSMUST00000182999	ENSMUSG00000024998	19	38481109	38785030	1	2	1	0	0	4	1	0	0	0	0	0	S4R168	
ENSMUST00000183000						4	6	4	5	8	0	1	0	0	1	0		
ENSMUST00000183001						1	0	0	5	0	0	0	0	0	0	1		
ENSMUST00000183002						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183003						6	1	6	5	5	0	1	1	0	0	0		
ENSMUST00000183004						2	4	0	8	5	2	0	0	2	0	0		
ENSMUST00000183005						7	4	12	4	8	1	0	0	0	0	1		
ENSMUST00000183006						9	9	12	8	20	7	0	0	0	1	0		
ENSMUST00000183007						1	1	14	2	3	0	0	3	0	0	0		
ENSMUST00000183008						17	24	0	21	47	5	2	19	14	16	28		
ENSMUST00000183010						0	0	0	0	0	0	0	3	2	0	2		
ENSMUST00000183011	ENSMUSG00000040225	1	162670725	162740556	-1	0	0	0	0	0	0	0	0	0	2	24	S4R2E2	
ENSMUST00000183012						2	1	6	2	5	3	0	0	0	0	0		
ENSMUST00000183013						10	6	8	211	16	5	0	0	0	0	0		
ENSMUST00000183014						0	2	0	2	2	0	40	92	42	76	72		
ENSMUST00000183015						2	0	9	0	2	0	0	0	0	0	0		
ENSMUST00000183016						0	0	0	2	0	0	3	9	6	0	0		
ENSMUST00000183017	ENSMUSG00000024128	17	23941672	23945607	1	0	0	0	0	0	0	0	0	0	0	0	S4R206	
ENSMUST00000183018	ENSMUSG00000056370	6	72304610	72314371	1	0	0	0	0	0	9	0	0	3	0	6	S4R2L6	
ENSMUST00000183020						6	5	6	5	8	4	2	2	0	0	0		
ENSMUST00000183022						1	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000183023	ENSMUSG00000069601	10	69533772	70027438	1	0	0	28	0	0	4	0	0	0	0	0	S4R208	
ENSMUST00000183024	ENSMUSG00000058589	10	89873509	90973300	1	1	0	0	52	7	0	0	0	0	0	0	S4R1K4	
ENSMUST00000183025						50	34	208	38	40	23	0	7	13	0	6		
ENSMUST00000183029						46	24	39	43	58	23	1	1	0	0	0		
ENSMUST00000183032	ENSMUSG00000032582	9	107773559	107873237	-1	0	0	0	0	0	0	199	1036	711	160	536	S4R1W5	
ENSMUST00000183033						5	3	5	13	6	3	0	0	0	0	0		
ENSMUST00000183034	ENSMUSG00000026131	1	33908225	34308661	1	63	114	0	12	53	29	0	0	0	0	62	S4R1P5	
ENSMUST00000183035	ENSMUSG00000032582	9	107773559	107873237	-1	2	0	0	9	0	0	1	0	8	2	4	S4R1I5	
ENSMUST00000183037	ENSMUSG00000075706	10	80047166	80056439	1	0	6	12	3	7	4	1772	2329	677	2663	627	S4R1E5	
ENSMUST00000183038	ENSMUSG00000058690	14	36874936	36968777	-1	0	2	2	3	0	0	0	26	69	12	38		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000183039						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183040						4	4	5	4	4	1	0	0	0	0	0		
ENSMUST00000183041						0	0	0	4	1	0	28	100	56	13	56		
ENSMUST00000183042						1	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000183044	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	0	0	0	1161	961	820	256	943	Q3TSW4	P30282
ENSMUST00000183046						4	2	1	1	3	5	1	5	4	0	10		
ENSMUST00000183047						0	0	0	0	0	0	0	0	0	5	0		
ENSMUST00000183048	ENSMUSG00000041258	18	82593593	82692883	-1	0	8	0	18	0	0	0	0	0	0	45	S4R1D8	
ENSMUST00000183049						7	4	9	5	9	2	5	3	3	1	1		
ENSMUST00000183050	ENSMUSG00000097972	7	32827683	32829662	-1	0	1	1	3	2	2	0	0	0	0	0	S4R2G1	
ENSMUST00000183051						0	0	0	5	1	0	0	0	0	0	0		
ENSMUST00000183052	ENSMUSG00000038510	10	40223246	40247036	-1	0	0	5	0	0	0	0	5	7	21	2	S4R2H5	
ENSMUST00000183053						7	2	9	7	15	4	1	2	2	6	2		
ENSMUST00000183055						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183057	ENSMUSG00000045659	7	116123485	116308376	-1	0	0	0	32	2	0	0	0	0	0	0	S4R243	
ENSMUST00000183058						6	3	3	8	5	2	0	0	0	0	0		
ENSMUST00000183059	ENSMUSG00000046101	1	9908638	9942085	1	1348	1265	4333	1075	1563	573	23	167	67	25	82	S4R1E1	
ENSMUST00000183060						1	2	11	1	3	0	0	0	0	0	0		
ENSMUST00000183061						31	19	89	41	59	24	14	58	69	13	138		
ENSMUST00000183062	ENSMUSG00000031586	8	33782643	33929863	-1	0	1	0	2	0	0	0	0	0	0	0	S4R2P3	
ENSMUST00000183063						5	1	7	1	0	2	3	9	0	1	4		
ENSMUST00000183064						1	5	6	5	4	2	2	0	0	2	2		
ENSMUST00000183065	ENSMUSG00000053747	9	99874106	99876170	-1	4	4	11	0	0	0	0	0	0	0	0	S4R1I8	
ENSMUST00000183067						7	7	14	6	13	4	0	2	0	0	2		
ENSMUST00000183069						7	6	6	14	16	8	0	0	0	0	0		
ENSMUST00000183070	ENSMUSG00000032525	9	121719169	121756843	1	5	5	14	24	11	4	18	22	43	1	55	Q3TQ51	
ENSMUST00000183071						0	0	0	0	1	0	2	2	9	0	3		
ENSMUST00000183072						4	3	4	3	5	0	0	0	0	0	0		
ENSMUST00000183073	ENSMUSG00000047417	10	80540922	80561560	-1	0	3	13	61	3	4	35	21	32	6	28	S4R1Q7	
ENSMUST00000183074	ENSMUSG00000069601	10	69533772	70027438	1	12	0	0	0	0	0	0	0	0	0	0	S4R2J6	
ENSMUST00000183075						0	3	0	0	3	0	0	0	0	0	0		
ENSMUST00000183076						4	5	3	6	6	1	1	0	0	1	0		
ENSMUST00000183077	ENSMUSG00000034413	17	26414829	26446349	1	1	0	3	247	2	0	0	0	0	0	1	S4R1D7	
ENSMUST00000183078						0	0	0	0	0	2	0	6	0	1	2		
ENSMUST00000183080						4	3	2	3	1	0	0	0	0	0	0		
ENSMUST00000183081						6	4	4	5	6	3	14	20	5	1	3		
ENSMUST00000183082	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	S4R162	
ENSMUST00000183085						0	5	0	8	1	0	0	0	0	0	0		
ENSMUST00000183086	ENSMUSG00000041347	12	105603085	105605428	1	2	0	9	6	4	0	0	1	0	3	0	S4R1G8	
ENSMUST00000183088	ENSMUSG00000031586	8	33782643	33929863	-1	4	0	2	1	4	3	0	0	0	1	0	S4R1Y2	
ENSMUST00000183090						7	0	5	0	13	0	5	2803	126	0	429		
ENSMUST00000183091	ENSMUSG00000002107	2	6539694	7509563	-1	1	0	0	0	0	0	6	0	123	36	126	S4R2U7	
ENSMUST00000183092						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183093						4	2	8	4	8	2	1	1	2	0	5		
ENSMUST00000183094						3	6	6	4	9	4	0	0	0	0	0		
ENSMUST00000183095	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	2	0	0	0	0	0	0	0	S4R241	
ENSMUST00000183096	ENSMUSG00000030583	7	29320372	29518641	-1	16	5	43	44	27	12	725	345	884	18	743	G3X9J0	
ENSMUST00000183097						8	9	19	11	8	2	0	0	0	0	1		
ENSMUST00000183098						26	22	56	30	28	10	14	12	40	3	76		
ENSMUST00000183100	ENSMUSG00000026131	1	33908225	34308661	1	0	0	0	0	0	0	0	0	0	0	0	S4R2A8	
ENSMUST00000183101						2	3	12	1	7	4	0	0	1	0	1		
ENSMUST00000183102						0	0	1	11	4	0	0	0	0	0	0		
ENSMUST00000183103						0	3	1	0	1	0	0	0	0	0	0		
ENSMUST00000183104	ENSMUSG00000040875	9	114978569	115232225	1	4	0	6	89	6	6	0	0	0	0	4	S4R1M9	S4R1M9
ENSMUST00000183105	ENSMUSG00000033075	15	98038744	98093744	-1	3	1	7	5	4	2	0	1	0	0	2	S4R1V9	
ENSMUST00000183106						137	116	276	986	161	88	9	24	19	0	20		
ENSMUST00000183107						0	4	14	0	0	0	0	5	0	3	4		
ENSMUST00000183108	ENSMUSG00000025027	19	52943417	53040214	-1	22	33	26	56	26	21	19	26	9	5	7	Q3UE92	
ENSMUST00000183109	ENSMUSG00000058589	10	89873509	90973300	1	12	9	18	7	12	3	0	0	0	0	0	S4R2J3	
ENSMUST00000183110	ENSMUSG00000098004	2	93956817	93996354	-1	0	0	1	2	0	0	0	0	0	0	0	S4R1M6	
ENSMUST00000183111	ENSMUSG00000040528	11	106751226	106768794	1	0	0	0	0	0	0	13	83	0	0	0		Q3TB92
ENSMUST00000183112	ENSMUSG00000034206	16	37011786	37095417	1	0	0	0	0	0	0	0	0	0	0	0	Q8BGX6	
ENSMUST00000183113						150	142	242	92	121	58	22	84	39	7	44		
ENSMUST00000183114	ENSMUSG00000038510	10	40223246	40247036	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2R2	
ENSMUST00000183115	ENSMUSG00000098022	7	30054489	30072900	-1	0	0	0	0	0	0	0	0	0	0	0	S4R2K1	
ENSMUST00000183118						14	24	33	25	25	5	0	3	5	2	5		
ENSMUST00000183119						1	1	3	0	0	0	0	0	0	0	0		
ENSMUST00000183120	ENSMUSG00000070564	7	45684022	45694556	1	0	0	0	0	7	0	0	0	0	0	0	S4R1A5	
ENSMUST00000183121	ENSMUSG00000041444	9	32116136	32268446	1	0	0	0	0	0	1	0	0	0	0	0	S4R2C0	
ENSMUST00000183122						0	1	5	8	6	2	0	0	0	0	0		
ENSMUST00000183125	ENSMUSG00000042063	12	116047724	116063360	1	19	12	37	10	24	4	28	97	41	41	46	Q1WWJ5	
ENSMUST00000183126	ENSMUSG00000098207	3	69222419	69223618	1	5	12	7	8	12	16	3	9	2	10	3	S4R1T9	
ENSMUST00000183127						3	2	0	3	10	2	2	3	6	0	6		
ENSMUST00000183128						0	0	0	0	0	0	2	0	3	1	2		
ENSMUST00000183129						17	20	25	11	11	7	0	0	0	0	0		
ENSMUST00000183130	ENSMUSG00000098176	15	75979872	75982455	-1	6	3	1	98	8	3	0	0	0	0	3	S4R181	
ENSMUST00000183131						29	23	121	35	17	16	2	4	1	0	0		
ENSMUST00000183132	ENSMUSG00000074151	8	94472763	94527272	1	0	0	2	8	0	0	0	0	0	0	12	S4R1C5	
ENSMUST00000183133						0	0	0	2	0	2	0	0	4	6	7		
ENSMUST00000183134						2	3	0	2	4	0	0	0	0	0	0		
ENSMUST00000183135						1	1	22	6	6	1	0	0	0	0	0		
ENSMUST00000183136	ENSMUSG00000058589	10	89873509	90973300	1	0	0	0	0	0	0	0	0	0	0	0	S4R2Q2	
ENSMUST00000183137						3	4	10	10	7	0	0	0	0	0	0		
ENSMUST00000183139						3	3	12	3	7	3	11	10	12	0	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000183140						6	1	5	1	3	0	0	0	0	0	0		
ENSMUST00000183141	ENSMUSG00000040875	9	114978569	115232225	1	5	1	3	1	4	0	0	0	0	0	0	S4R2S2	
ENSMUST00000183142						1	0	3	1	2	3	0	0	0	0	0		
ENSMUST00000183143	ENSMUSG00000025077	19	56529167	56548222	-1	32	28	67	57	36	22	25	17	22	0	17	S4R284	
ENSMUST00000183145						0	1	18	0	0	0	0	0	0	0	0		
ENSMUST00000183146	ENSMUSG00000098134	12	84417196	84418578	1	4	4	2	60	2	5	81	537	158	308	125	Q14B01	
ENSMUST00000183147	ENSMUSG00000029422	5	123728426	123749414	-1	0	0	0	0	0	0	0	0	61	256	105	S4R254	
ENSMUST00000183148	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	0	0	0	0	0	0	0	0	S4R2S8	
ENSMUST00000183150						8	3	2	5	5	5	0	0	0	0	0		
ENSMUST00000183151						6	1	3	4	3	1	0	0	0	0	0		
ENSMUST00000183152						28	23	56	32	32	12	10	28	8	6	17		
ENSMUST00000183153						23	22	114	24	16	14	1	8	2	1	9		
ENSMUST00000183154	ENSMUSG00000010608	12	83631236	83683123	1	0	0	0	37	0	0	5	6	30	5	26	S4R2J4	
ENSMUST00000183155	ENSMUSG00000024128	17	23941672	23945607	1	0	0	0	2	0	0	0	0	0	0	0	Q544L5	P15501
ENSMUST00000183156	ENSMUSG00000058589	10	89873509	90973300	1	0	0	2	28	0	0	0	0	0	0	0	S4R286	
ENSMUST00000183157						170	135	371	3555	203	71	7	17	6	3	8		
ENSMUST00000183158	ENSMUSG00000034165	17	47505051	47599691	1	8	1	2	31	4	0	14	9	12	0	9	S4R1C8	
ENSMUST00000183159						9	3	8	1	1	5	1	0	1	0	0		
ENSMUST00000183160	ENSMUSG00000047417	10	80540922	80561560	-1	3	0	7	4	3	2	10	21	9	2	7	S4R2E9	
ENSMUST00000183161						14	17	25	130	31	19	1	0	2	0	3		
ENSMUST00000183162	ENSMUSG00000078958	13	90883433	90905355	-1	0	0	0	0	4	0	0	0	0	0	0	S4R264	
ENSMUST00000183163						24	18	29	11	21	10	2	6	3	1	3		
ENSMUST00000183164						2	1	6	59	3	5	13	8	6	0	11		
ENSMUST00000183165	ENSMUSG00000030314	6	114643097	114860614	1	0	0	0	0	0	0	0	12	42	0	0	S4R2D5	
ENSMUST00000183167						42	34	615	166	54	18	2	3	1	3	4		
ENSMUST00000183169	ENSMUSG00000069601	10	69533772	70027438	1	0	8	0	0	4	0	0	0	0	0	0	S4R1S2	
ENSMUST00000183170	ENSMUSG00000030433	7	4956134	4964390	-1	0	0	2	0	0	1	0	0	0	0	0	S4R1E6	
ENSMUST00000183172						5	3	4	6	14	2	0	0	0	0	0		
ENSMUST00000183173						6	1	7	7	9	1	1	0	0	0	0		
ENSMUST00000183174						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000183175	ENSMUSG00000030659	7	116504369	116540584	1	0	0	0	3	0	2	5	5	5	15	10	Q3UKN6	
ENSMUST00000183176						104	75	216	1374	135	85	18	32	24	4	25		
ENSMUST00000183177	ENSMUSG00000034165	17	47505051	47599691	1	6	10	0	5	2	0	368	285	263	105	86	Q3TSW4	P30282
ENSMUST00000183178	ENSMUSG00000059562	17	25162461	25171913	1	18	21	40	16	13	9	0	0	1	0	0	S4R2I6	
ENSMUST00000183179						18	22	14	15	30	16	3	16	4	0	8		
ENSMUST00000183181						0	2	2	0	2	1	15	76	0	4	8		
ENSMUST00000183182	ENSMUSG00000050730	9	8994329	9239101	-1	2	1	2	27	2	4	0	0	0	0	0	Q9D333	
ENSMUST00000183183						3	4	12	17	4	3	1	1	0	0	5		
ENSMUST00000183184						8	10	55	36	7	8	2	3	3	0	13		
ENSMUST00000183185						5	0	3	5	7	0	0	0	0	0	0		
ENSMUST00000183187	ENSMUSG00000025519	8	66511756	66518335	1	20	13	13	13	20	10	0	0	0	0	0		
ENSMUST00000183188						1	0	4	1	5	0	0	0	0	0	0		
ENSMUST00000183189						95	97	218	95	66	45	0	8	4	2	8		
ENSMUST00000183190	ENSMUSG00000098022	7	30054489	30072900	-1	7	7	26	6	6	3	0	0	0	0	1		Q6P9Y7
ENSMUST00000183192	ENSMUSG00000061544	17	21730795	21769342	1	2	0	3	0	0	2	0	0	0	1	0	S4R1L0	
ENSMUST00000183193						1	5	1	4	2	4	54	253	86	4	176		
ENSMUST00000183195	ENSMUSG00000097982	7	32325286	32327245	-1	3	2	0	3	2	1	0	0	0	0	0	S4R2L0	
ENSMUST00000183196						7	3	6	4	2	2	0	5	0	8	3		
ENSMUST00000183197						0	2	0	6	2	0	0	0	0	0	0		
ENSMUST00000183198	ENSMUSG00000099269	13	3854143	3855016	1	10	11	29	10	8	2	0	0	0	0	0	A0A087WNL0	
ENSMUST00000183199						5	4	1	5	3	5	0	0	0	0	0		
ENSMUST00000183200	ENSMUSG00000078815	7	3424195	3435667	1	8	4	13	8	2	4	0	0	0	0	0	Q14C42	Q8VHW3
ENSMUST00000183201						0	8	18	11	16	0	0	0	0	0	0		
ENSMUST00000183202						57	43	60	31	62	28	3	3	1	6	9		
ENSMUST00000183204						1	0	3	6	4	7	0	217	79	55	47		
ENSMUST00000183205						4	3	11	19	3	3	0	0	0	0	0		
ENSMUST00000183206	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	1	0	0	44	31	29	3	6	S4R2Q7	
ENSMUST00000183207						0	1	0	0	2	0	1	1	0	0	0		
ENSMUST00000183208	ENSMUSG00000004562	14	51984719	52006251	1	2	5	9	0	14	0	0	0	0	7	0	S4R1S6	
ENSMUST00000183209	ENSMUSG00000002107	2	6539694	7509563	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1S7	
ENSMUST00000183210	ENSMUSG00000034165	17	47505051	47599691	1	0	1	0	16	0	0	1	0	0	0	2	S4R2I5	
ENSMUST00000183211	ENSMUSG00000098112	15	100641077	100669553	-1	0	0	0	203	89	0	2740	10488	5349	296	4639	S4R270	
ENSMUST00000183213						2	1	4	0	1	3	0	0	0	0	4		
ENSMUST00000183214	ENSMUSG00000002500	17	24727820	24736143	1	0	0	2	34	6	1	0	0	0	0	0	S4R242	
ENSMUST00000183216						0	0	0	0	1	0	0	8	3	0	0		
ENSMUST00000183217	ENSMUSG00000041482	18	63010213	63387183	-1	8	0	0	0	0	6	0	0	0	0	0	S4R2S0	
ENSMUST00000183219	ENSMUSG00000050100	7	131548773	131556589	1	14	9	91	14	20	0	0	0	0	0	0		P43687
ENSMUST00000183221						4	6	3	11	5	1	1	0	0	0	0		
ENSMUST00000183222						8	1	4	5	4	3	0	0	0	0	0		
ENSMUST00000183223	ENSMUSG00000040225	1	162670725	162740556	-1	12	5	0	14	9	14	38	963	52	55	0	S4R2L9	
ENSMUST00000183224	ENSMUSG00000024073	17	74528295	74703356	1	28	42	0	3	12	9	455	287	537	17	484	S4R1L5	
ENSMUST00000183227						0	2	0	1	0	1	0	0	0	1	0		
ENSMUST00000183228						29	37	51	133	47	40	2	48	9	4	9		
ENSMUST00000183229						0	1	0	0	0	0	1	3	3	4	6		
ENSMUST00000183230						5	7	4	6	4	2	0	0	0	0	0		
ENSMUST00000183232						3	0	4	15	2	2	0	0	0	0	0		
ENSMUST00000183233						0	0	0	0	0	0	123	0	103	0	41		
ENSMUST00000183234						16	14	21	13	21	11	0	0	0	0	0		
ENSMUST00000183236	ENSMUSG00000042439	18	65580230	65689443	1	0	0	0	0	1	0	0	0	0	0	0	S4R2T9	
ENSMUST00000183237						4	2	10	1	2	1	0	0	0	0	0		
ENSMUST00000183240	ENSMUSG00000069601	10	69533772	70027438	1	1	2	1	1	2	3	0	0	0	0	0	S4R229	
ENSMUST00000183241	ENSMUSG00000066800	1	153749426	153764221	1	0	0	0	0	0	0	230	827	751	280	685	S4R2R4	
ENSMUST00000183242						4	3	4	3	3	3	2	14	6	0	10		
ENSMUST00000183246						3	2	0	10	5	0	14	3	7	8	13		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000183247	ENSMUSG00000035325	5	100361649	100416234	-1	1	0	0	0	0	0	1	18	14	0	13	S4R192	
ENSMUST00000183248	ENSMUSG00000032580	9	107740371	107770996	-1	4	0	19	0	0	3	0	21	22	3	0	S4R1N4	
ENSMUST00000183249	ENSMUSG00000024073	17	74528295	74703356	1	4	2	6	0	4	0	82	593	157	106	170	S4R268	
ENSMUST00000183250						4	6	13	4	9	5	16	8	23	14	7		
ENSMUST00000183251						28	68	43	97	49	23	3	35	9	16	7		
ENSMUST00000183252	ENSMUSG00000024128	17	23941672	23945607	1	0	2	0	2	0	0	0	0	0	0	0	Q544L5	P15501
ENSMUST00000183253						44	24	40	25	38	25	39	54	19	37	96		
ENSMUST00000183254	ENSMUSG00000047535	7	103787313	103788275	-1	5	2	2	2	2	0	0	0	0	0	0	F8VPJ8	
ENSMUST00000183255	ENSMUSG00000033147	3	101855776	101924453	-1	2	8	9	14	11	2	17	80	73	3	57	S4R1S9	
ENSMUST00000183256	ENSMUSG00000034165	17	47505051	47599691	1	0	0	0	0	0	2	55	4	21	0	24	S4R275	
ENSMUST00000183257						5	8	8	10	7	1	0	0	0	1	0		
ENSMUST00000183258	ENSMUSG00000030162	6	129485244	129507165	-1	0	0	0	0	0	0	0	3	0	3	0	G4WK09	
ENSMUST00000183259						11	6	3	9	9	4	1	0	0	1	0		
ENSMUST00000183260						4	6	6	6	3	2	0	0	0	0	0		
ENSMUST00000183261	ENSMUSG00000069601	10	69533772	70027438	1	0	0	12	6	2	0	0	0	0	0	0	S4R165	
ENSMUST00000183262						0	0	0	0	0	0	0	0	30	0	0		
ENSMUST00000183265						54	58	87	46	41	25	24	52	35	4	28		
ENSMUST00000183267	ENSMUSG00000068923	3	88744700	88775164	-1	4	0	4	0	0	0	0	16	65	6	60	S4R1M8	
ENSMUST00000183268	ENSMUSG00000035189	10	88948994	89344762	-1	0	5	5	3	8	3	0	0	0	0	0	Q8CA69	
ENSMUST00000183269						29	18	75	14	21	16	1	14	22	2	29		
ENSMUST00000183270						4	3	7	6	7	4	2	3	1	1	0		
ENSMUST00000183271	ENSMUSG00000027901	3	106482405	106503030	1	10	3	16	2	7	8	370	1549	623	543	334	S4R219	
ENSMUST00000183272	ENSMUSG00000057666	6	125161715	125166467	-1	0	0	0	0	0	0	25	15	0	0	0	S4R257	
ENSMUST00000183273	ENSMUSG00000072720	5	112688876	112896362	-1	7	7	21	14	2	0	0	0	1	0	0	S4R2L2	
ENSMUST00000183274	ENSMUSG00000025027	19	52943417	53040214	-1	1	1	2	4	2	0	111	37	104	36	75	S4R1I3	
ENSMUST00000183275	ENSMUSG00000030583	7	29320372	29518641	-1	3	2	2	3	1	3	0	0	0	0	0	S4R1U8	
ENSMUST00000183277	ENSMUSG00000034801	12	69583762	69681852	-1	12	10	24	36	15	5	170	306	859	32	515		Q02384
ENSMUST00000183278	ENSMUSG00000056370	6	72304610	72314371	1	5	0	0	0	0	0	0	0	0	0	0	S4R239	
ENSMUST00000183279	ENSMUSG00000041617	16	17646470	17650738	1	2	5	0	0	0	4	0	0	0	0	0	S4R250	
ENSMUST00000183280	ENSMUSG00000031809	8	121530780	121544320	-1	0	0	0	0	0	0	0	0	0	0	0	S4R1A2	
ENSMUST00000183281	ENSMUSG00000045659	7	116123485	116308376	-1	0	0	0	0	0	0	0	0	0	0	0	S4R190	
ENSMUST00000183282						0	2	6	0	0	0	0	16	0	0	10		
ENSMUST00000183283						0	0	0	0	0	0	0	0	0	1	0		
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ENSMUST00000183285						8	20	66	10	17	3	0	0	0	0	0		
ENSMUST00000183286						0	0	0	48	0	0	0	0	0	0	1		
ENSMUST00000183287						7	4	6	8	14	4	0	8	4	1	15		
ENSMUST00000183288						6	5	5	13	6	2	0	0	1	0	0		
ENSMUST00000183291	ENSMUSG00000029605	5	120812635	120824163	1	124	224	506	0	281	0	105	508	120	89	233		
ENSMUST00000183292						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000183293						1	0	8	4	7	0	7	6	12	1	20		
ENSMUST00000183295						3	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000183296						3	7	3	2	5	5	0	0	0	0	0		
ENSMUST00000183298						5	1	4	3	6	2	0	0	0	0	0		
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ENSMUST00000183301	ENSMUSG00000026395	1	138062861	138175708	-1	0	0	0	2	11	0	410	827	1262	577	2014	S4R1S4	
ENSMUST00000183302	ENSMUSG00000026131	1	33908225	34308661	1	30	47	30	20	51	20	0	0	0	0	0		
ENSMUST00000183303						9	6	5	6	5	2	0	0	0	0	0		
ENSMUST00000183305						5	3	0	5	15	6	7	5	5	5	7		
ENSMUST00000183306						0	2	0	0	0	0	0	0	12	0	18		
ENSMUST00000183307						20	20	11	16	9	11	302	731	565	45	538		
ENSMUST00000183308						25	9	42	213	27	10	0	0	0	0	2		
ENSMUST00000183309	ENSMUSG00000038510	10	40223246	40247036	-1	0	6	0	30	4	2	15	84	8	54	16		Q9JJ80
ENSMUST00000183310	ENSMUSG00000073771	4	117119219	117125725	-1	3	1	0	3	2	0	16	15	21	4	9	S4R1I0	
ENSMUST00000183311						214	230	1026	184	322	128	25	160	65	22	103		
ENSMUST00000183312						3	5	5	23	8	4	0	0	0	0	0		
ENSMUST00000183313						365	305	1318	296	416	201	1	10	8	4	19		
ENSMUST00000183315						4	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000183316	ENSMUSG00000058690	14	36874936	36968777	-1	0	0	0	2	0	0	0	0	0	0	0	S4R170	
ENSMUST00000183318						0	0	0	0	0	0	0	8	0	9	4		
ENSMUST00000183319	ENSMUSG00000042439	18	65580230	65689443	1	1	0	5	0	5	1	0	0	0	0	0	S4R1F7	
ENSMUST00000183320						6	6	3	3	6	3	0	0	0	0	0		
ENSMUST00000183321						0	3	16	2	1	0	0	0	0	2	1		
ENSMUST00000183322						5	1	4	6	5	1	0	0	0	0	0		
ENSMUST00000183324	ENSMUSG00000041258	18	82593593	82692883	-1	0	0	6	5	0	0	111	259	166	25	104	S4R1Z3	
ENSMUST00000183325						6	4	3	4	3	4	0	0	0	0	0		
ENSMUST00000183326	ENSMUSG00000042439	18	65580230	65689443	1	0	0	0	0	0	0	0	0	0	0	0	S4R1B5	
ENSMUST00000183329						3	2	10	8	7	3	0	5	4	5	2		
ENSMUST00000183330	ENSMUSG00000030583	7	29320372	29518641	-1	4	0	10	30	4	10	22	43	28	11	9	S4R1S0	
ENSMUST00000183331						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183332						24	24	43	16	30	17	34	90	56	9	72		
ENSMUST00000183334	ENSMUSG00000051811	7	4751792	4753094	-1	1	0	0	3	0	0	0	0	4	0	12	S4R2M9	
ENSMUST00000183335	ENSMUSG00000030659	7	116504369	116540584	1	0	1	1	0	2	3	0	18	4	0	4	S4R2R9	
ENSMUST00000183336	ENSMUSG00000031586	8	33782643	33929863	-1	0	0	0	4	0	0	0	0	0	0	0	S4R280	
ENSMUST00000183337						45	33	146	109	63	23	4	5	1	2	4		
ENSMUST00000183338	ENSMUSG00000037174	3	51252720	51340663	-1	2	3	0	23	7	0	2	8	23	2	22	V9GXW8	
ENSMUST00000183345	ENSMUSG00000055963	4	12906838	12983553	1	0	8	3	12	7	3	0	1	0	0	1		B2B9E1
ENSMUST00000183347						0	1	5	0	0	0	0	65	6	3	2		
ENSMUST00000183349	ENSMUSG00000037514	2	131262495	131299188	1	3	3	11	3	7	2	10	59	14	8	47	V9GXL0	
ENSMUST00000183350						22	15	24	17	15	6	0	0	0	0	0		
ENSMUST00000183352	ENSMUSG00000098301	CHR_MG3829_PATCH	88047373	88053755	1	6	1	3	62	2	1	97	149	48	10	77		Q6PDM2
ENSMUST00000183353						3	4	2	0	8	3	4	0	1	0	11		
ENSMUST00000183354						25	15	22	12	16	5	0	2	0	0	2		
ENSMUST00000183355						11	5	14	3	12	5	20	48	9	2	21		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000183356						2	1	0	3	6	2	0	0	0	0	0		
ENSMUST00000183358	ENSMUSG00000042607	6	5383386	5433022	1	7	9	5	3	14	4	0	0	1	0	0	Q3V229	
ENSMUST00000183359	ENSMUSG00000026991	2	59160850	59355208	1	6	0	52	0	0	4	13	0	0	0	9	V9GXG7	
ENSMUST00000183360	ENSMUSG00000062762	9	36779159	36797361	-1	0	0	0	12	0	0	0	0	0	0	0	C3VDI2	
ENSMUST00000183363	ENSMUSG00000063320	10	82619851	82623228	-1	0	0	0	0	0	0	7	10	0	7	4		Q8BTC1
ENSMUST00000183367	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	12	0	19	19	20	6	0	0	0	0	0		
ENSMUST00000183368	ENSMUSG00000058897	3	130131501	130599877	1	8	10	19	13	4	4	0	0	0	0	0	V9GWX5	
ENSMUST00000183369						6	4	13	7	4	1	0	0	0	0	1		
ENSMUST00000183372	ENSMUSG00000037674	9	72532240	72622937	1	0	0	0	0	0	0	5	3	0	1	5	Q3TDE2	
ENSMUST00000183373	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	2	3	15	5	4	4	0	0	0	0	0		
ENSMUST00000183375	ENSMUSG00000032216	9	72662346	72749852	1	0	0	0	0	0	0	0	0	0	0	0	V9GWV8	
ENSMUST00000183377						37	34	164	199	33	7	3	23	9	2	11		
ENSMUST00000183378						41	43	84	30	64	38	2	3	2	0	2		
ENSMUST00000183380						14	10	39	18	21	2	0	3	0	8	0		
ENSMUST00000183381						0	0	3	0	0	0	0	1	0	0	0		
ENSMUST00000183383	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183386						0	0	6	6	0	0	33	103	134	52	73		
ENSMUST00000183388	ENSMUSG00000037514	2	131262495	131299188	1	0	0	0	0	0	0	22	51	36	7	4	V9GXK8	
ENSMUST00000183390	ENSMUSG00000098681	CHR_MG3829_PATCH	88294058	88295261	1	6	2	14	19	10	5	0	0	0	0	0		Q9D9C6
ENSMUST00000183393						0	0	0	9	0	0	4	0	0	0	1		
ENSMUST00000183397						6	0	5	6	3	0	0	0	2	0	5		
ENSMUST00000183399						7	6	19	6	14	9	0	6	2	1	5		
ENSMUST00000183400						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183401						5	0	7	47	0	0	4	0	0	0	0		
ENSMUST00000183402	ENSMUSG00000033253	4	118362743	118409273	-1	2	1	4	6	3	0	100	645	117	37	184	V9GXW1	
ENSMUST00000183403	ENSMUSG00000010505	2	181763332	181827797	1	0	0	0	0	0	0	0	0	0	0	0	V9GXW7	
ENSMUST00000183404	ENSMUSG00000032228	9	71842688	72111871	-1	39	32	189	32	45	28	14	25	26	10	25		Q61286
ENSMUST00000183407	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	0	0	0	0	F6ZGI7	
ENSMUST00000183409	ENSMUSG00000045868	7	106156556	106215326	-1	0	21	57	24	39	12	0	0	0	0	0	L7N451	
ENSMUST00000183410	ENSMUSG00000038535	9	72274860	72363777	1	0	0	7	0	0	0	0	0	0	0	0	V9GXP2	
ENSMUST00000183411						13	4	13	0	11	1	0	5	8	3	11		
ENSMUST00000183414						22	22	11	22	20	6	195	452	385	127	325		
ENSMUST00000183416	ENSMUSG00000063320	10	82619851	82623228	-1	0	10	18	169	11	8	0	0	2	0	1	V9GX89	
ENSMUST00000183421	ENSMUSG00000038679	15	50654752	50890463	-1	46	26	157	52	30	20	0	14	5	3	5	Q8BZ62	
ENSMUST00000183422						3	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000183424	ENSMUSG00000055942	7	14659496	14665996	1	2	1	14	0	2	1	0	0	0	0	0	V9GWX2	
ENSMUST00000183425	ENSMUSG00000007908	9	76014855	76136350	1	8	12	5	67	4	10	0	1	1	0	1	V9GXD2	
ENSMUST00000183428	ENSMUSG00000090626	9	72450394	72492212	-1	0	0	0	0	0	0	0	0	0	5	0	V9GXU5	
ENSMUST00000183430						3	1	5	0	0	1	0	7	5	0	0		
ENSMUST00000183431	ENSMUSG00000095304	14	25887932	25903100	-1	0	1	0	0	1	0	0	0	0	0	0	V9GXX6	
ENSMUST00000183432	ENSMUSG00000028521	4	103170649	103215164	-1	29	25	53	22	29	16	0	2	2	2	2	V9GX08	
ENSMUST00000183436						1	2	7	5	1	2	0	0	0	0	0		
ENSMUST00000183437	ENSMUSG00000032358	9	76490054	76567116	-1	0	0	0	37	5	9	0	0	0	0	0		Q0VBM2
ENSMUST00000183440						37	36	82	18	39	25	6	13	6	0	10		
ENSMUST00000183441						0	2	0	2	7	1	0	0	0	0	0		
ENSMUST00000183448	ENSMUSG00000042508	5	9118801	9161776	-1	10	0	0	0	0	0	0	0	48	10	77		Q8CE22
ENSMUST00000183451						1	4	2	0	2	2	2	0	0	7	0		
ENSMUST00000183452	ENSMUSG00000099083	15	102525946	102625464	-1	1	0	0	0	0	0	0	0	0	0	0	V9GXX5	
ENSMUST00000183453						2	2	2	2	1	0	0	0	0	0	0		
ENSMUST00000183456	ENSMUSG00000034940	11	83964428	84044578	1	0	2	1	0	7	0	208	193	532	18	290	V9GX40	
ENSMUST00000183459						5	13	76	12	20	6	2	0	0	0	0		
ENSMUST00000183461	ENSMUSG00000026933	2	25926838	25983282	-1	0	0	0	0	0	0	0	0	10	0	34		A2AHC3
ENSMUST00000183463	ENSMUSG00000037174	3	51252720	51340663	-1	0	0	18	1	0	0	119	728	202	101	133	Q80UM8	
ENSMUST00000183467	ENSMUSG00000032352	9	77430823	77544870	-1	6	0	12	0	6	0	0	20	0	0	0	V9GX13	
ENSMUST00000183468	ENSMUSG00000038535	9	72274860	72363777	1	6	13	7	44	13	5	0	17	6	1	2	Q8R2V6	
ENSMUST00000183469						2	5	0	3	4	4	0	0	0	0	0		
ENSMUST00000183471	ENSMUSG00000055675	8	15011025	15033333	1	46	63	135	118	85	24	46	45	40	4	177		Q8BNW9
ENSMUST00000183474						2	1	4	1	2	0	0	0	0	0	0		
ENSMUST00000183475	ENSMUSG00000021023	12	55299577	55382533	1	0	0	4	0	5	0	0	0	0	1	0	V9GXP4	
ENSMUST00000183477						0	0	0	0	0	0	0	0	0	0	0		
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ENSMUST00000183481						0	1	1	3	1	0	0	0	0	0	0		
ENSMUST00000183482	ENSMUSG00000049511	9	81628291	81633828	-1	171	95	491	385	139	61	8	57	12	4	11	Q0VES5	P28334
ENSMUST00000183484	ENSMUSG00000028044	3	89415472	89418383	-1	3	0	2	17	0	0	0	0	0	0	0	V9GWZ0	
ENSMUST00000183488	ENSMUSG00000096149	14	53491115	53491622	1	3	2	6	2	0	0	0	1	0	3	0	A0A075B6D4	
ENSMUST00000183489	ENSMUSG00000098306	1	133309827	133329901	1	0	0	0	6	13	5	0	0	0	1	0		Q9DCQ3
ENSMUST00000183492	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	56	1	0	0	0	0	0	5	V9GX18	
ENSMUST00000183493	ENSMUSG00000019590	11	105933702	105953336	-1	4	0	20	7	3	1	0	0	3	1	1	V9GXF4	
ENSMUST00000183496						16	9	23	21	12	10	1	1	3	1	5		
ENSMUST00000183499	ENSMUSG00000038671	2	181357690	181365404	-1	0	0	0	0	0	0	0	23	17	3	0	V9GX20	
ENSMUST00000183501	ENSMUSG00000090626	9	72450394	72492212	-1	0	0	0	0	0	0	1	3	0	0	0	V9GWX9	
ENSMUST00000183503						2	0	0	10	3	0	0	0	0	0	0		
ENSMUST00000183505						0	0	0	11	1	0	0	0	0	0	0		
ENSMUST00000183511						0	0	0	0	0	0	138	529	239	137	222		
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ENSMUST00000183516						4	7	5	2	2	0	23	133	34	28	52		
ENSMUST00000183518	ENSMUSG00000098950	2	156071845	156127092	-1	1	0	0	96	7	3	4	4	2	0	11	V9GX68	
ENSMUST00000183520	ENSMUSG00000015790	2	26913381	26916530	-1	0	0	0	0	2	0	85	191	65	30	43	V9GXE6	
ENSMUST00000183524						0	0	0	0	0	0	1	3	0	0	0		
ENSMUST00000183525	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	0	0	0	0	0	7	0	1	V9GXV6	
ENSMUST00000183527						9	2	12	7	11	4	0	0	0	0	0		
ENSMUST00000183528	ENSMUSG00000099164	CHR_MG3833_PATCH	18239784	18248732	-1	0	0	0	41	4	1	6	61	42	349	45		P34022
ENSMUST00000183531						19	26	59	52	25	17	0	0	0	1	0		
ENSMUST00000183532						0	0	2	0	0	1	0	42	6	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000183537						2	2	2	1	2	0	0	1	0	3	1		
ENSMUST00000183538	ENSMUSG00000026811	2	32599709	32620806	1	0	0	0	0	0	0	0	0	0	0	0		Q9JM95
ENSMUST00000183542	ENSMUSG00000026826	2	57106830	57124003	-1	2	0	0	115	0	0	0	9	0	0	0	Q9R1W4	
ENSMUST00000183543	ENSMUSG00000095601	X	37380028	37384493	1	0	0	0	0	0	0	0	0	0	0	0	V9GXK5	
ENSMUST00000183545						7	7	5	4	4	0	0	0	0	0	1		
ENSMUST00000183548						111	99	287	1095	96	78	5	9	0	0	14		
ENSMUST00000183549						4	3	3	4	3	0	0	0	0	0	0		
ENSMUST00000183550						6	15	8	15	14	8	0	0	0	0	0		
ENSMUST00000183551						1	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000183552	ENSMUSG00000027318	2	131050591	131063814	-1	0	0	0	0	0	0	0	0	0	0	0		Q923W9
ENSMUST00000183554						2	5	2	0	2	1	0	0	0	0	0		
ENSMUST00000183557						4	2	3	2	7	0	0	0	0	0	0		
ENSMUST00000183560	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0	V9GWS8	
ENSMUST00000183563						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183567						8	7	12	18	11	3	0	0	0	1	0		
ENSMUST00000183572						0	0	1	0	0	0	1	0	0	0	0		
ENSMUST00000183574	ENSMUSG00000090626	9	72450394	72492212	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZND9	
ENSMUST00000183575	ENSMUSG00000027333	2	131491496	131525922	1	1	0	0	0	0	1	1	26	15	0	62	V9GXD6	
ENSMUST00000183576						4	2	8	0	2	0	0	1	0	0	3		
ENSMUST00000183578						60	45	127	84	75	40	1	6	3	0	0		
ENSMUST00000183580						5	6	7	85	7	0	0	0	0	0	0		
ENSMUST00000183583	ENSMUSG00000035513	2	29194541	29253005	-1	0	6	9	239	17	4	163	634	287	20	299	V9GX85	
ENSMUST00000183586						0	0	0	0	0	0	10	33	7	9	10		
ENSMUST00000183587						1	0	0	1	0	0	7	9	26	0	33		
ENSMUST00000183589	ENSMUSG00000098930	CHR_MG3833_PATCH	18248679	18254772	1	1	2	2	4	2	4	2	30	5	0	0		Q8BNV1
ENSMUST00000183590	ENSMUSG00000098549	1	45889525	45890273	-1	0	0	0	0	0	0	0	0	0	0	1	V9GXF8	
ENSMUST00000183593	ENSMUSG00000098930	CHR_MG3833_PATCH	18248679	18254772	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183594	ENSMUSG00000032228	9	71842688	72111871	-1	0	1	0	27	0	0	0	0	0	0	0	V9GX29	
ENSMUST00000183595						5	4	8	0	4	5	0	0	0	0	0		
ENSMUST00000183601						47	51	68	66	51	19	0	7	7	2	12		
ENSMUST00000183604	ENSMUSG00000094220	14	53428711	53430377	1	0	1	0	3	1	2	0	1	0	4	0	A0A075B6D0	
ENSMUST00000183607						0	0	0	143	6	3	19	12	43	15	44		
ENSMUST00000183608						625	723	1287	105	333	94	0	4	0	3	15		
ENSMUST00000183610	ENSMUSG00000020717	11	106654217	106750628	-1	0	0	8	12	0	0	0	137	0	24	62		Q08481
ENSMUST00000183614	ENSMUSG00000032262	9	83778692	83806277	-1	3	1	3	97	7	2	0	0	0	0	0	V9GXI2	
ENSMUST00000183617						0	0	0	0	0	2	2	2	4	8	0		
ENSMUST00000183618	ENSMUSG00000098387	2	144368996	144373721	1	4	0	4	1	3	1	0	0	0	0	1		P0DJF2
ENSMUST00000183619						2	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000183623						50	59	47	60	77	29	0	1	1	1	2		
ENSMUST00000183625						3	3	0	3	1	1	0	0	0	1	2		
ENSMUST00000183626	ENSMUSG00000098892	CHR_MG3833_PATCH	18407771	18427737	-1	35	38	113	50	50	21	26	150	25	100	80		O88587
ENSMUST00000183629						0	0	17	6	5	8	0	0	0	0	0		
ENSMUST00000183630	ENSMUSG00000098377	CHR_MG3833_PATCH	18300825	18348103	-1	0	0	0	3	0	0	67	103	57	58	53		
ENSMUST00000183631						3	3	3	0	0	0	0	0	0	0	0		
ENSMUST00000183633						9	14	13	64	7	8	0	0	0	0	0		
ENSMUST00000183636						2	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000183637	ENSMUSG00000027849	3	103575231	103645569	1	2	2	5	39	2	3	0	0	0	0	0	V9GWX4	
ENSMUST00000183638	ENSMUSG00000033439	3	116581093	116614587	-1	0	0	0	0	0	0	8	40	10	29	18	V9GXM2	
ENSMUST00000183647	ENSMUSG00000032228	9	71842688	72111871	-1	1	0	0	0	1	0	0	0	0	0	0	V9GXG5	
ENSMUST00000183648						1	2	10	8	4	1	0	0	0	0	0		
ENSMUST00000183652	ENSMUSG00000095689	14	52844465	52845041	1	0	0	0	0	0	0	0	2	0	0	0	A0A075B605	
ENSMUST00000183654	ENSMUSG00000021023	12	55299577	55382533	1	2	7	0	0	2	0	0	0	0	0	0	V9GWT5	
ENSMUST00000183655	ENSMUSG00000079637	X	37453680	37469861	1	0	0	0	2	6	0	0	0	0	0	0	V9GX45	
ENSMUST00000183656						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183659	ENSMUSG00000052512	7	48908716	49610090	1	0	0	0	0	0	0	0	4	0	0	6	V9GXT3	
ENSMUST00000183662	ENSMUSG00000028226	4	17852893	18119145	1	57	66	128	90	83	35	0	9	2	0	5	V9GXD8	
ENSMUST00000183663	ENSMUSG00000021756	13	112464070	112510086	1	99	58	203	125	110	57	241	841	626	65	379		Q00560
ENSMUST00000183665						3	3	4	9	6	3	1	2	1	0	1		
ENSMUST00000183672						24	10	49	156	29	16	2	9	10	1	17		
ENSMUST00000183674						6	6	0	0	0	2	0	0	0	0	0		
ENSMUST00000183677						6	3	12	2	2	1	0	0	0	0	0		
ENSMUST00000183680						0	0	0	0	1	0	0	16	0	0	10		
ENSMUST00000183682	ENSMUSG00000029664	6	3962595	3988919	-1	2	1	0	0	0	2	0	0	0	1	0	V9GXA8	
ENSMUST00000183684	ENSMUSG00000034570	11	3494375	3504821	-1	7	14	52	16	25	10	5	12	6	0	11	V9GX61	
ENSMUST00000183686	ENSMUSG00000032355	9	77102081	77352969	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXW5	
ENSMUST00000183688	ENSMUSG00000098512	CHR_MG132_PATCH	124358303	124363500	-1	3	3	1	4	7	2	0	0	0	0	0		
ENSMUST00000183690	ENSMUSG00000026915	2	37483228	37703859	-1	34	19	115	61	34	14	0	8	35	0	0		Q91WM1
ENSMUST00000183691						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000183693	ENSMUSG00000027584	2	181715016	181720985	1	0	11	0	0	0	0	0	0	0	0	0		P35377
ENSMUST00000183694	ENSMUSG00000048004	12	119945957	120019211	1	2	1	0	9	4	0	0	0	0	0	0	V9GX04	
ENSMUST00000183695	ENSMUSG00000093954	14	69363504	69503362	-1	0	0	0	5	0	0	0	0	0	0	0		Q920G8
ENSMUST00000183696	ENSMUSG00000095510	X	37580992	37585496	1	0	0	0	0	0	0	0	0	0	0	0	V9GXR2	
ENSMUST00000183698	ENSMUSG00000021768	14	21733394	21751181	-1	0	0	0	3	0	0	0	0	0	0	0	V9GXA1	
ENSMUST00000183700						48	38	271	85	46	23	0	2	5	3	8		
ENSMUST00000183703	ENSMUSG00000030172	6	119570796	119848167	-1	39	0	0	38	21	0	0	0	246	2	99	F8VPM7	
ENSMUST00000183706						2	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000183712	ENSMUSG00000098633	R_MG4222_MG3908_PAT	55445355	55514554	1	10	10	38	15	16	8	0	0	0	0	0		Q76K27
ENSMUST00000183714	ENSMUSG00000034940	11	83964428	84044578	1	7	0	0	0	0	0	0	0	0	0	0	V9GXD9	
ENSMUST00000183715						15	9	16	9	18	7	3	6	0	0	2		
ENSMUST00000183716						1	3	0	2	1	0	0	0	0	0	0		
ENSMUST00000183722						0	2	5	1	4	4	0	0	0	0	0		
ENSMUST00000183723						1	0	3	5	0	0	0	0	0	0	0		
ENSMUST00000183725	ENSMUSG00000095304	14	25887932	25903100	-1	0	0	3	0	0	0	0	0	0	0	0	V9GXX6	
ENSMUST00000183727						22	36	25	33	38	22	2	25	6	0	10		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000183728	ENSMUSG00000098559	X	139713681	139714481	-1	2	2	2	1	2	0	0	1	0	3	1	V9GWY0	
ENSMUST00000183729						7	6	5	8	5	6	0	2	0	1	0		
ENSMUST00000183731	ENSMUSG00000037761	2	158624888	158639211	1	13	12	14	94	12	3	0	8	0	0	15	V9GXE4	
ENSMUST00000183733	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	0	0	96	7	154	30	133	V9GXM6	
ENSMUST00000183734	ENSMUSG00000032352	9	77430823	77544870	-1	9	6	3	7	12	2	0	0	3	0	0		Q80VQ1
ENSMUST00000183736						2	3	3	1	1	0	0	0	0	0	0		
ENSMUST00000183737	ENSMUSG00000071766	X	38104077	38110907	-1	6	0	0	6	0	0	0	0	0	0	0	V9GXS9	
ENSMUST00000183741						14	11	45	23	12	9	3	5	1	0	8		
ENSMUST00000183742	ENSMUSG00000098375	CHR_MG3829_PATCH	88204388	88211507	1	0	3	0	8	3	0	95	211	68	57	48		Q8VE22
ENSMUST00000183745						2	1	4	0	1	2	0	0	0	0	0		
ENSMUST00000183746	ENSMUSG00000079469	9	73007419	73040378	-1	41	46	79	78	53	25	72	403	174	158	327		Q9JJQ0
ENSMUST00000183748						12	2	10	117	18	0	0	0	0	0	1		
ENSMUST00000183755						8	3	5	405	22	5	0	3	3	1	0		
ENSMUST00000183756						0	0	0	0	0	0	45	49	4	0	0		
ENSMUST00000183757	ENSMUSG00000038679	15	50654752	50890463	-1	0	0	0	14	5	0	0	0	0	6	10	V9GX74	
ENSMUST00000183761						0	0	1	105	2	0	0	0	0	0	0		
ENSMUST00000183762						3	3	9	3	3	0	0	0	0	0	0		
ENSMUST00000183765	ENSMUSG00000099083	15	102525946	102625464	-1	1	0	5	0	0	0	0	2	4	0	0	V9GX99	
ENSMUST00000183767	ENSMUSG00000016087	9	32422204	32542861	-1	5	1	4	3	4	0	0	0	46	22	52	V9GX50	
ENSMUST00000183770						2	3	6	0	2	0	0	0	0	22	0		
ENSMUST00000183773	ENSMUSG00000028540	4	117888643	117892032	-1	0	0	0	0	0	0	43	49	22	9	33	V9GX25	
ENSMUST00000183775	ENSMUSG00000059173	2	79834453	80129458	-1	2	4	35	5	10	0	0	0	0	0	0	Q8BRR9	
ENSMUST00000183780						0	0	0	15	5	0	2	2	2	0	0		
ENSMUST00000183784						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000183785						0	0	9	0	4	0	0	5674	0	0	0		
ENSMUST00000183786						2	1	4	86	4	1	5	0	6	0	0		
ENSMUST00000183788	ENSMUSG00000055942	7	14659496	14665996	1	6	5	2	0	6	2	0	0	0	0	0	Q4KL20	
ENSMUST00000183790	ENSMUSG00000039523	4	153975194	154008732	1	8	0	0	0	0	4	8	9	32	7	14	V9GXW2	
ENSMUST00000183792						6	2	2	6	1	2	6	63	11	6	25		
ENSMUST00000183795						1	1	0	2	0	0	0	0	0	0	0		
ENSMUST00000183798						2	0	0	0	1	0	0	8	0	0	0		
ENSMUST00000183801	ENSMUSG00000038535	9	72274860	72363777	1	0	0	0	0	0	0	0	7	0	0	0	V9GXC9	
ENSMUST00000183807	ENSMUSG00000028803	4	135445420	135495038	-1	2	1	1	1	2	0	0	0	0	0	0	A2A987	
ENSMUST00000183809	ENSMUSG00000032221	9	72438011	72462025	1	0	0	7	3	5	1	0	0	0	0	1	V9GXE0	
ENSMUST00000183811	ENSMUSG00000072674	14	26167405	26182480	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXX6	
ENSMUST00000183813						2	1	6	1	0	0	0	0	0	0	0		
ENSMUST00000183816						0	1	0	0	4	0	0	0	0	0	0		
ENSMUST00000183817	ENSMUSG00000052040	7	63886351	63938915	-1	2	2	4	4	3	0	4	0	3	0	5	Q9DCC0	
ENSMUST00000183819	ENSMUSG00000026611	1	187044648	187215465	-1	4	3	8	6	3	5	0	0	0	1	1		Q9D552
ENSMUST00000183820	ENSMUSG00000095387	14	52753367	52753846	1	0	2	1	0	0	0	0	0	0	0	0	A0A075B6D2	
ENSMUST00000183821						0	0	0	3	0	4	0	0	1	1	1		
ENSMUST00000183822	ENSMUSG00000045691	14	55053884	55098986	1	2	9	8	4	6	3	0	0	0	0	0	A0A087WQW7	
ENSMUST00000183824						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000183827	ENSMUSG00000034673	17	34591266	34597400	1	0	0	0	0	0	0	45	0	88	0	175	V9GXB8	
ENSMUST00000183828						1	1	2	2	1	0	0	0	0	0	0		
ENSMUST00000183829	ENSMUSG00000021756	13	112464070	112510086	1	0	0	0	0	0	0	0	0	0	0	0	V9GX52	
ENSMUST00000183830	ENSMUSG00000039834	2	164891882	164911757	-1	0	15	3	283	3	24	0	0	0	73	0	Q6P5F4	
ENSMUST00000183831	ENSMUSG00000098456	11	33275758	33276737	-1	1	1	0	0	0	3	0	0	0	0	1	V9GXK0	
ENSMUST00000183833						0	2	0	21	0	0	0	0	0	0	0		
ENSMUST00000183835	ENSMUSG00000094828	14	53665929	53666506	1	0	0	0	0	0	0	0	0	0	0	0	A0A075B6D8	
ENSMUST00000183836	ENSMUSG00000038605	2	181595218	181599212	-1	0	6	0	0	0	7	153	292	112	10	0	V9GXE8	
ENSMUST00000183839						2	2	0	2	2	1	0	0	0	0	0		
ENSMUST00000183840	ENSMUSG00000093954	14	69363504	69503362	-1	4	5	4	60	10	1	0	0	1	0	3		Q920G8
ENSMUST00000183844						7	3	1	0	3	3	0	0	0	0	0		
ENSMUST00000183845	ENSMUSG00000038745	7	140920902	140929192	1	49	41	220	130	84	27	0	0	3	2	2		Q91WS2
ENSMUST00000183846	ENSMUSG00000050382	7	79698098	79715720	-1	28	0	0	261	28	0	0	0	0	0	0	J3QNW9	
ENSMUST00000183850	ENSMUSG00000054477	18	45268860	45686024	1	4	6	0	535	10	3	0	0	0	0	0		P58390
ENSMUST00000183855	ENSMUSG00000028524	4	102741297	102973628	1	2	1	4	2	2	0	1	0	0	0	0		Q8VD37
ENSMUST00000183856	ENSMUSG00000090626	9	72450394	72492212	-1	14	9	26	22	14	10	0	0	0	0	0	V9GXN9	
ENSMUST00000183862	ENSMUSG00000075139	2	88049678	88051112	-1	0	0	0	0	0	0	0	0	0	0	0	Q7TR28	
ENSMUST00000183868	ENSMUSG00000021756	13	112464070	112510086	1	2	1	5	1	2	2	0	0	0	0	0	V9GXJ5	
ENSMUST00000183869	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	138	35	156	4	231	A7UAK4	
ENSMUST00000183871	ENSMUSG00000041135	4	16122733	16163647	-1	8	13	5	0	0	0	0	0	0	0	0	V9GXY4	
ENSMUST00000183872						33	40	33	44	41	14	16	20	40	2	33		
ENSMUST00000183873	ENSMUSG00000032352	9	77430823	77544870	-1	8	0	0	14	6	0	0	30	26	0	0		Q80VQ1
ENSMUST00000183879						7	3	1	13	3	6	1	2	0	0	8		
ENSMUST00000183880	ENSMUSG00000030172	6	119570796	119848167	-1	2	0	0	0	0	0	0	0	0	0	0	V9GWT6	
ENSMUST00000183881	ENSMUSG00000027333	2	131491496	131525922	1	0	0	6	2	0	0	0	19	0	0	0	V9GXE5	
ENSMUST00000183882	ENSMUSG00000034248	14	69241848	69285112	-1	1	0	2	50	4	1	0	0	1	0	0	J3QPY4	
ENSMUST00000183883						4	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000183886	ENSMUSG00000021756	13	112464070	112510086	1	32	32	90	48	42	20	0	3	5	1	11	Q3TDT5	
ENSMUST00000183887	ENSMUSG00000020532	11	84129672	84401651	1	0	0	0	0	0	0	6	0	6	0	4	V9GXY1	
ENSMUST00000183888	ENSMUSG00000079629	X	37639115	37643470	-1	3	0	0	2	0	0	0	0	0	0	0	V9GXH1	
ENSMUST00000183889						2	4	6	113	13	0	3	23	5	3	4		
ENSMUST00000183893	ENSMUSG00000021768	14	21733394	21751181	-1	3	0	0	0	2	0	0	0	0	0	0	V9GXA3	
ENSMUST00000183895						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183897						6	11	20	72	11	0	0	0	0	0	0		
ENSMUST00000183898						0	1	0	0	0	0	0	11	0	0	0		
ENSMUST00000183899						0	0	3	1	2	1	0	0	0	0	0		
ENSMUST00000183901	ENSMUSG00000095601	X	37380028	37384493	1	0	0	0	0	0	0	0	0	0	0	0	V9GX94	
ENSMUST00000183902	ENSMUSG00000048911	2	131298064	131352892	-1	5	5	2	19	5	0	0	2	22	0	5	V9GXF9	
ENSMUST00000183904	ENSMUSG00000079469	9	73007419	73040378	-1	0	2	0	0	0	0	0	20	6	2	30	V9GWY8	
ENSMUST00000183906						25	25	26	31	32	17	2	11	7	7	3		
ENSMUST00000183907						12	9	80	9	20	4	40	39	107	7	75		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000183911	ENSMUSG00000030172	6	119570796	119848167	-1	0	0	0	6	0	0	0	0	0	0	6	V9GXF0	
ENSMUST00000183912						8	11	23	24	9	11	34	189	108	11	153		
ENSMUST00000183913	ENSMUSG00000045672	4	63214004	63334991	1	6	0	3	39	5	4	0	4	0	0	7	V9GXJ7	
ENSMUST00000183914	ENSMUSG00000045576	3	104864005	104930064	1	58	52	157	467	54	33	82	201	82	9	45	V9GXQ4	
ENSMUST00000183915						0	0	3	0	4	1	0	7	1	0	0		
ENSMUST00000183917	ENSMUSG00000093954	14	69363504	69503362	-1	0	0	0	9	0	0	0	0	0	0	0	V9GXC4	
ENSMUST00000183918	ENSMUSG00000032228	9	71842688	72111871	-1	9	7	19	19	10	12	0	0	0	0	0	V9GX46	
ENSMUST00000183924						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000183925	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	0	0	0	88	4	0	0	0	0	0	0		
ENSMUST00000183926						7	2	3	11	4	2	1	0	0	0	0		
ENSMUST00000183928						14	9	16	66	21	6	0	3	1	0	0		
ENSMUST00000183929	ENSMUSG00000025735	17	25834465	25837295	-1	6	0	13	3	5	0	9	0	9	2	0	V9GX92	
ENSMUST00000183931	ENSMUSG00000026611	1	187044648	187215465	-1	1	0	4	2	4	1	0	0	0	0	0	V9GXU8	
ENSMUST00000183934						7	8	10	10	11	2	0	2	1	0	0		
ENSMUST00000183935						0	0	0	0	0	1	2	1	0	1	5		
ENSMUST00000183936	ENSMUSG00000098814	6	68736297	68736780	-1	0	0	1	0	2	0	3	3	0	30	21	A0A075B6D5	
ENSMUST00000183937	ENSMUSG00000091831	17	71458327	71460395	-1	12	12	65	30	13	11	0	2	4	0	1	V9GXN5	
ENSMUST00000183939	ENSMUSG00000010097	19	8757073	8772475	1	1	2	0	0	0	0	14	0	65	1	107	V9GXW3	
ENSMUST00000183940	ENSMUSG00000011257	4	123262351	123298925	1	41	21	67	72	34	21	16	0	35	0	14	V9GXG3	
ENSMUST00000183942	ENSMUSG00000006398	4	118432901	118437352	-1	0	6	7	1	11	0	25	30	0	3	14	V9GXW0	
ENSMUST00000183943	ENSMUSG00000021768	14	21733394	21751181	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXH4	
ENSMUST00000183946	ENSMUSG00000044627	2	32278816	32288075	-1	0	0	0	0	0	1	374	594	335	984	146	E3WH32	Q8K3D3
ENSMUST00000183947	ENSMUSG00000027333	2	131491496	131525922	1	0	0	0	0	0	0	0	0	0	0	0		Q99K82
ENSMUST00000183948						2	1	1	3	5	2	0	3	1	0	1		
ENSMUST00000183951						1	4	0	2	2	1	0	0	0	0	0		
ENSMUST00000183952	ENSMUSG00000098923	1	119526160	119528983	1	7	7	10	90	10	5	202	596	238	30	167		Q8R3R5
ENSMUST00000183954	ENSMUSG00000076671	12	114357759	114358218	-1	0	0	0	0	0	1	0	0	0	0	1	A0A087WPN7	
ENSMUST00000183955	ENSMUSG00000032355	9	77102081	77352969	-1	5	6	20	0	10	7	0	0	0	0	0	V9GWW6	
ENSMUST00000183956						0	0	0	0	0	0	0	0	18	0	0		
ENSMUST00000183959	ENSMUSG00000098546	CHR_MG3829_PATCH	88068279	88084729	1	7	3	15	17	15	2	262	421	435	37	330		
ENSMUST00000183960						1	1	1	5	0	0	0	0	0	0	0		
ENSMUST00000183969	ENSMUSG00000098930	CHR_MG3833_PATCH	18248679	18254772	1	0	0	0	0	0	0	54	28	33	2	48		
ENSMUST00000183971	ENSMUSG00000051811	7	4751792	4753094	-1	0	0	0	0	0	0	0	0	5	4	0	V9GWZ7	
ENSMUST00000183972	ENSMUSG00000098950	2	156071845	156127092	-1	0	0	0	0	0	0	4	2	11	0	0	V9GX58	
ENSMUST00000183973	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	4	0	7	0	1	0	184	0	104	V9GXX1	
ENSMUST00000183974						66	107	204	85	66	46	0	4	2	0	0		
ENSMUST00000183976	ENSMUSG00000021867	14	26203369	26207041	-1	1	1	0	32	0	0	0	1	3	0	0	V9GX22	
ENSMUST00000183979	ENSMUSG00000007908	9	76014855	76136350	1	4	0	0	1	2	0	0	0	0	0	0	V9GWZ9	
ENSMUST00000183980						42	23	66	174	42	13	3	7	3	2	2		
ENSMUST00000183984	ENSMUSG00000002107	2	6539694	7509563	-1	3	0	0	17	1	0	0	0	99	0	252	V9GX43	
ENSMUST00000183985						2	1	2	0	2	0	5	23	0	3	5		
ENSMUST00000183988	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000183992	ENSMUSG00000032228	9	71842688	72111871	-1	2	1	0	88	8	0	0	0	0	0	0	V9GXC3	
ENSMUST00000183993						3	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000183995						2	2	3	9	2	0	0	0	0	0	0		
ENSMUST00000183996	ENSMUSG00000026611	1	187044648	187215465	-1	2	0	3	0	2	2	0	0	0	0	0	V9GXB4	
ENSMUST00000183997	ENSMUSG00000038679	15	50654752	50890463	-1	0	0	4	9	1	0	23	139	116	29	94	V9GXE9	
ENSMUST00000183999	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXI3	
ENSMUST00000184001						0	2	0	1	2	1	0	0	0	0	0		
ENSMUST00000184002						4	5	22	5	6	4	1	0	0	0	0		
ENSMUST00000184004						0	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000184006	ENSMUSG00000032355	9	77102081	77352969	-1	0	0	0	0	0	0	0	0	0	0	0	V9GX62	
ENSMUST00000184008						18	21	113	10	16	7	0	0	0	0	0		
ENSMUST00000184015	ENSMUSG00000037674	9	72532240	72622937	1	0	0	0	13	0	0	0	0	0	0	0	Q3TDE2	
ENSMUST00000184016	ENSMUSG00000095975	14	25938304	25956356	1	7	5	7	4	3	0	0	2	0	0	0	Q8BX39	
ENSMUST00000184019	ENSMUSG00000038535	9	72274860	72363777	1	0	0	0	0	0	0	0	0	0	0	0	V9GX57	
ENSMUST00000184020	ENSMUSG00000032216	9	72662346	72749852	1	0	0	0	0	0	0	15	49	0	0	0	V9GXS6	
ENSMUST00000184025						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184027						18	15	35	57	33	8	0	0	0	0	0		
ENSMUST00000184029	ENSMUSG00000032228	9	71842688	72111871	-1	2	3	17	1	0	0	0	0	0	0	0	V9GWS4	
ENSMUST00000184030						2	1	3	2	0	0	0	0	0	0	0		
ENSMUST00000184032						1	3	3	2	1	2	0	62	6	0	41		
ENSMUST00000184033						2	1	5	1	2	1	0	2	1	3	1		
ENSMUST00000184035	ENSMUSG00000079469	9	73007419	73040378	-1	0	0	6	0	0	0	96	0	194	0	250		Q9JJQ0
ENSMUST00000184036	ENSMUSG00000038535	9	72274860	72363777	1	0	0	0	32	0	0	18	9	28	0	20	V9GWW1	
ENSMUST00000184037						16	12	19	9	17	4	0	0	1	0	0		
ENSMUST00000184038						4	5	8	6	3	2	0	13	1	4	5		
ENSMUST00000184039						4	0	8	6	1	0	0	0	0	0	0		
ENSMUST00000184040						2	2	3	1	0	1	0	0	0	0	0		
ENSMUST00000184045						0	2	13	2	9	0	0	0	0	0	0		
ENSMUST00000184046	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	15	0	81	4	V9GX15	
ENSMUST00000184051						104	56	508	144	81	44	1	2	1	1	1		
ENSMUST00000184053	ENSMUSG00000038535	9	72274860	72363777	1	2	5	10	0	7	0	2	5	0	0	3	V9GWV5	
ENSMUST00000184058						6	3	2	1	3	1	0	0	0	0	0		
ENSMUST00000184061						1	0	15	4	0	1	0	0	0	0	0		
ENSMUST00000184063	ENSMUSG00000028804	4	127987857	128567656	1	89	68	135	172	133	70	0	2	1	0	2	V9GX34	
ENSMUST00000184066						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000184067	ENSMUSG00000045672	4	63214004	63334991	1	15	2	16	20	15	7	0	0	1	0	6	V9GXJ0	
ENSMUST00000184069	ENSMUSG00000048004	12	119945957	120019211	1	0	0	4	0	0	0	0	0	0	0	0	V9GX78	
ENSMUST00000184072	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXR6	
ENSMUST00000184076						7	7	13	9	7	8	9	60	11	4	25		
ENSMUST00000184077	ENSMUSG00000099083	15	102525946	102625464	-1	0	0	0	0	0	0	0	0	0	1	0	V9GXY2	
ENSMUST00000184082	ENSMUSG00000025241	9	123789510	123851899	-1	0	0	0	0	0	0	0	0	11	0	0		
ENSMUST00000184086	ENSMUSG00000019590	11	105933702	105953336	-1	0	2	47	0	0	0	0	0	0	0	0	V9GX11	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000184088	ENSMUSG00000079627	X	37668989	37673277	-1	0	4	2	0	3	0	0	0	0	0	0	V9GXS0	
ENSMUST00000184089						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000184093						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000184095	ENSMUSG00000042641	1	153779381	153844142	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXD4	
ENSMUST00000184099						4	0	0	2	3	1	0	0	0	0	0		
ENSMUST00000184101						8	4	3	0	4	4	0	0	0	0	0		
ENSMUST00000184102						15	15	98	25	27	12	0	2	2	1	0		
ENSMUST00000184103	ENSMUSG00000031789	8	95239045	95306585	-1	0	0	0	0	0	0	1	5	0	2	0	V9GXN8	
ENSMUST00000184105	ENSMUSG00000037514	2	131262495	131299188	1	0	0	0	10	0	0	54	63	103	30	48	V9GX56	
ENSMUST00000184106	ENSMUSG00000032355	9	77102081	77352969	-1	2	3	1	2	0	1	0	0	0	0	0	V9GWV7	
ENSMUST00000184107	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	0	0	6	0	8	0	8	V9GXP0	
ENSMUST00000184109	ENSMUSG00000052512	7	48908716	49610090	1	1	0	0	0	3	0	0	0	0	0	0	V9GWV3	
ENSMUST00000184110						56	40	347	86	45	22	0	4	2	0	0		
ENSMUST00000184112	ENSMUSG00000039853	4	46493781	46536141	-1	11	6	28	5	25	13	0	6	2	0	7		Q8BVW3
ENSMUST00000184113	ENSMUSG00000027699	3	27097222	27153878	-1	10	8	18	37	4	5	0	0	0	0	0	V9GXV8	
ENSMUST00000184117	ENSMUSG00000098810	CHR_MG132_PATCH	124291804	124312696	-1	25	32	91	26	21	17	26	75	21	13	20		
ENSMUST00000184118	ENSMUSG00000028863	4	125085134	125113238	1	0	0	0	0	0	0	0	17	0	13	7	V9GXH6	
ENSMUST00000184119						1	0	3	0	0	3	0	0	0	0	0		
ENSMUST00000184120	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	0	0	0	0	0	0	0	0	V9GWW5	
ENSMUST00000184121	ENSMUSG00000027327	2	131146324	131160081	-1	2	3	0	0	4	0	0	0	0	0	0	V9GXT6	
ENSMUST00000184123						144	114	182	207	194	110	12	80	43	15	40		
ENSMUST00000184124	ENSMUSG00000052512	7	48908716	49610090	1	58	42	229	151	58	60	1	1	2	1	1	V9GXT5	
ENSMUST00000184125	ENSMUSG00000090626	9	72450394	72492212	-1	0	0	0	0	0	0	0	0	0	4	0		Q9D845
ENSMUST00000184127	ENSMUSG00000027584	2	181715016	181720985	1	0	0	0	0	0	0	0	0	0	0	0		P35377
ENSMUST00000184129						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184130	ENSMUSG00000027669	3	32580332	32616585	-1	7	0	0	1	4	2	5	0	0	3	3	V9GWY1	
ENSMUST00000184131	ENSMUSG00000029036	4	155740641	155761093	-1	0	4	16	0	0	3	0	0	0	0	0	V9GWS6	
ENSMUST00000184132	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	5	11	19	0	0	3	1	0	0	0	0		
ENSMUST00000184135						7	2	7	4	4	1	0	0	0	0	1		
ENSMUST00000184137	ENSMUSG00000050382	7	79698098	79715720	-1	5	0	36	0	36	24	0	0	0	0	0	E9QMU1	
ENSMUST00000184138	ENSMUSG00000032355	9	77102081	77352969	-1	0	0	0	2	0	0	0	0	0	0	0	V9GXK2	
ENSMUST00000184139	ENSMUSG00000048186	2	4717831	4802142	1	0	0	6	2	0	7	0	0	0	0	0		Q8BSV3
ENSMUST00000184141						17	10	26	11	21	8	0	5	0	0	6		
ENSMUST00000184142	ENSMUSG00000072674	14	26167405	26182480	-1	4	0	9	105	10	5	0	0	0	0	0		Q8K262
ENSMUST00000184143	ENSMUSG00000051811	7	4751792	4753094	-1	0	0	0	0	0	0	0	11	0	9	0	V9GXN3	
ENSMUST00000184144						0	0	0	0	0	0	0	19	0	0	0		
ENSMUST00000184146	ENSMUSG00000032202	9	73044854	73097629	1	0	0	14	47	0	0	495	1186	840	160	679	Q544U7	Q9ERI2
ENSMUST00000184147						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000184149						11	11	17	6	5	8	32	132	100	69	117		
ENSMUST00000184151						4	5	2	3	5	5	0	5	2	2	0		
ENSMUST00000184152	ENSMUSG00000074643	2	156071842	156111965	-1	23	14	79	30	15	5	4	8	0	0	63	V9GX86	
ENSMUST00000184155						4	1	1	0	3	1	0	0	0	0	0		
ENSMUST00000184159	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	0	0	0	0	393	0	58	0		Q8CE22
ENSMUST00000184160						40	22	78	40	34	25	2	3	3	0	4		
ENSMUST00000184162						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000184164	ENSMUSG00000026870	2	34874396	34892132	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184165						25	25	26	31	32	17	2	11	7	7	3		
ENSMUST00000184169	ENSMUSG00000027010	2	71271063	71367749	-1	0	0	0	0	0	0	488	1221	736	173	454	V9GXX9	
ENSMUST00000184179	ENSMUSG00000028710	4	115784812	115818828	1	16	11	9	4	8	13	9	53	24	5	21	V9GX21	
ENSMUST00000184180						19	21	20	7	18	25	1	0	3	6	0		
ENSMUST00000184183	ENSMUSG00000099104	17	8565852	8566950	-1	1	0	0	0	0	0	0	3	3	1	0	V9GXQ2	
ENSMUST00000184186	ENSMUSG00000044345	19	42147400	42151703	1	18	24	49	21	29	19	50	195	73	3	68	V9GXP6	
ENSMUST00000184189	ENSMUSG00000098509	1	144516648	144567667	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXQ3	
ENSMUST00000184193						0	0	6	2	0	0	0	1	2	7	8		
ENSMUST00000184196						29	29	28	75	35	27	5	23	9	1	11		
ENSMUST00000184198						1	2	0	0	0	0	0	0	0	2	3		
ENSMUST00000184200						7	8	12	11	10	7	0	0	0	0	0		
ENSMUST00000184203	ENSMUSG00000032036	9	34485894	35036716	1	0	0	10	50	4	3	0	0	0	0	0	A0A087WNL2	
ENSMUST00000184205	ENSMUSG00000028863	4	125085134	125113238	1	2	1	3	0	2	0	50	85	30	17	72	V9GX42	
ENSMUST00000184206						1	3	4	1	4	0	0	0	0	0	0		
ENSMUST00000184208						0	0	4	4	5	0	0	0	0	0	0		
ENSMUST00000184209	ENSMUSG00000048004	12	119945957	120019211	1	0	0	11	18	0	0	0	0	0	0	0	V9GX84	
ENSMUST00000184210	ENSMUSG00000059626	X	37542019	37551082	1	0	0	0	0	0	0	0	0	0	0	0	V9GX94	
ENSMUST00000184214	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	0	7	0	0	F6ZGI7	
ENSMUST00000184216	ENSMUSG00000038535	9	72274860	72363777	1	2	3	0	0	0	2	0	26	1	38	11	V9GXF6	
ENSMUST00000184217						3	1	0	0	0	4	0	0	0	0	0		
ENSMUST00000184221	ENSMUSG00000017652	2	165055627	165072948	1	0	0	1	0	3	2	0	0	0	18	0		P27512
ENSMUST00000184222						0	0	0	0	0	0	70	252	192	262	60		
ENSMUST00000184223						5	1	1	0	0	0	2	10	8	0	5		
ENSMUST00000184231	ENSMUSG00000098571	CHR_MG3829_PATCH	88098058	88194140	1	0	0	0	0	0	0	16	36	0	0	0		Q8R3V6
ENSMUST00000184234						22	24	66	59	26	15	2	19	10	2	8		
ENSMUST00000184235	ENSMUSG00000062762	9	36779159	36797361	-1	1	1	0	8	4	3	3	0	18	0	0	V9GXU0	
ENSMUST00000184236						5	0	0	0	0	0	0	384	0	0	0		
ENSMUST00000184239						8	1	0	1	0	4	6	0	10	4	4		
ENSMUST00000184240	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184243						0	0	0	0	0	0	0	9	0	1	0		
ENSMUST00000184245	ENSMUSG00000015536	13	114818236	114832275	1	44	45	177	65	39	17	1	7	2	0	5	F6ZGI7	
ENSMUST00000184247						10	12	12	5	11	2	0	5	0	0	0		
ENSMUST00000184248						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184249						30	11	29	54	33	11	0	0	0	0	0		
ENSMUST00000184252	ENSMUSG00000099294	4	63662359	63663379	-1	0	3	0	0	1	1	0	1	0	0	0	V9GX06	
ENSMUST00000184253	ENSMUSG00000098633	R_MG4222_MG3908_PAT	55445355	55514554	1	4	3	3	5	4	1	0	0	0	0	0	B2RQY9	Q76K27
ENSMUST00000184254	ENSMUSG00000083780	4	105789869	105794711	1	0	0	0	0	0	0	0	0	0	1	0	V9GX31	
ENSMUST00000184255						5	5	12	1	5	1	2	3	2	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000184256	ENSMUSG00000096215	16	5007288	5008309	1	0	0	9	0	0	0	0	0	0	0	0	V9GX54	
ENSMUST00000184257						14	7	27	16	13	7	0	0	0	0	0		
ENSMUST00000184261	ENSMUSG00000033191	4	118471191	118490061	-1	12	7	20	48	11	6	0	0	0	0	3	Q6PAP2	
ENSMUST00000184263						0	0	1	3	3	0	0	0	0	0	0		
ENSMUST00000184265	ENSMUSG00000074643	2	156071842	156111965	-1	0	0	0	0	1	0	0	2	10	0	0	V9GWY2	
ENSMUST00000184266						10	12	15	21	13	4	2	0	2	2	0		
ENSMUST00000184269	ENSMUSG00000019590	11	105933702	105953336	-1	0	0	0	0	0	0	0	0	0	0	0	V9GWY3	
ENSMUST00000184270	ENSMUSG00000059626	X	37542019	37551082	1	0	0	0	0	0	0	0	0	0	0	0	V9GXK5	
ENSMUST00000184271	ENSMUSG00000099269	13	3854143	3855016	1	0	0	0	0	0	0	0	0	0	0	0	Q6W3E0	
ENSMUST00000184272	ENSMUSG00000094800	14	26027282	26042711	-1	0	0	0	0	0	0	0	0	0	3	4		
ENSMUST00000184274						0	0	1	0	4	0	0	0	0	0	0		
ENSMUST00000184276	ENSMUSG00000021756	13	112464070	112510086	1	0	0	0	2	0	0	0	0	32	0	0	V9GXA2	
ENSMUST00000184279						0	0	1	7	2	0	0	0	0	0	0		
ENSMUST00000184280	ENSMUSG00000030374	7	16815889	16840931	1	2	0	0	34	4	5	3	0	0	0	0	V9GXT1	
ENSMUST00000184282						17	17	97	33	26	9	2	8	4	3	4		
ENSMUST00000184287						5	7	5	5	3	2	0	1	1	0	0		
ENSMUST00000184292	ENSMUSG00000098724	CHR_MG4180_PATCH	109546348	109572236	1	8	3	10	18	9	0	2	5	0	2	2	Q8CCV7	
ENSMUST00000184294	ENSMUSG00000034032	2	119763304	119787537	-1	0	0	0	0	0	0	0	0	6	11	0	V9GWX3	
ENSMUST00000184296						2	1	4	1	3	1	0	0	0	0	0		
ENSMUST00000184297	ENSMUSG00000024095	17	80029487	80062334	-1	0	0	1	11	0	0	178	1178	423	48	286	V9GXB6	
ENSMUST00000184298	ENSMUSG00000099077	CHR_MG132_PATCH	124456062	124462462	-1	0	0	2	8	2	0	39	54	28	8	34		
ENSMUST00000184299	ENSMUSG00000009734	13	18121101	18382041	-1	5	0	1	0	0	3	0	0	0	0	0	Q8BY13	
ENSMUST00000184305	ENSMUSG00000099175	R_MG4222_MG3908_PAT	55592313	55624644	-1	4	0	2	2	1	2	0	0	0	0	0		
ENSMUST00000184306						8	11	0	4	8	7	0	0	0	0	0		
ENSMUST00000184310	ENSMUSG00000098810	CHR_MG132_PATCH	124291804	124312696	-1	0	0	0	0	0	0	0	7	0	3	0		
ENSMUST00000184311	ENSMUSG00000021756	13	112464070	112510086	1	0	0	0	0	0	0	0	0	0	0	0		Q00560
ENSMUST00000184312	ENSMUSG00000090626	9	72450394	72492212	-1	8	2	11	9	13	0	0	0	0	0	0	V9GWV2	
ENSMUST00000184314	ENSMUSG00000095463	14	69337174	69367270	1	53	40	339	73	54	26	2	12	5	0	3	Q80WR8	
ENSMUST00000184316	ENSMUSG00000032355	9	77102081	77352969	-1	0	0	0	0	0	0	0	0	0	0	0	V9GX17	
ENSMUST00000184320	ENSMUSG00000030172	6	119570796	119848167	-1	1	6	0	1	0	0	15	0	16	0	0	V9GXL1	
ENSMUST00000184322	ENSMUSG00000032355	9	77102081	77352969	-1	10	0	5	13	0	0	0	0	0	0	0	V9GXA0	
ENSMUST00000184324	ENSMUSG00000098377	CHR_MG3833_PATCH	18300825	18348103	-1	0	1	2	12	2	0	0	0	0	0	0		
ENSMUST00000184326	ENSMUSG00000035047	9	21273457	21287969	-1	6	6	25	31	10	0	0	48	123	105	33	V9GXJ9	
ENSMUST00000184328						0	2	0	3	2	2	11	19	10	4	13		
ENSMUST00000184330						42	21	172	47	33	15	0	1	0	0	2		
ENSMUST00000184332	ENSMUSG00000026991	2	59160850	59355208	1	0	0	0	0	0	0	0	0	4	0	0	V9GWY7	
ENSMUST00000184333	ENSMUSG00000032216	9	72662346	72749852	1	32	36	45	38	34	8	12	15	9	0	15	V9GXK3	
ENSMUST00000184335	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	0	6	0	0	F6ZGI7	
ENSMUST00000184336						6	5	8	0	3	0	0	1	0	0	0		
ENSMUST00000184339						2	2	2	41	2	6	2	2	2	4	2		
ENSMUST00000184342	ENSMUSG00000098633	R_MG4222_MG3908_PAT	55445355	55514554	1	4	4	5	88	3	2	0	0	0	0	0		
ENSMUST00000184348	ENSMUSG00000029074	4	156034840	156059414	-1	9	3	19	10	18	0	0	0	0	0	0	V9GXT8	
ENSMUST00000184350	ENSMUSG00000034247	11	103364275	103412687	-1	0	0	0	0	0	0	110	16	197	0	110	V9GWX7	
ENSMUST00000184356	ENSMUSG00000099216	7	14331436	14333557	-1	13	5	35	15	8	4	0	1	1	0	2	V9GWY9	
ENSMUST00000184363	ENSMUSG00000048154	15	98831669	98871204	-1	3	0	6	3	0	0	12	1	16	0	22	V9GX77	
ENSMUST00000184364	ENSMUSG00000032035	9	32636221	32757820	1	3	1	11	4	1	4	17	0	13	0	29	V9GXE2	
ENSMUST00000184366	ENSMUSG00000059852	18	80294546	80364254	-1	0	0	0	23	0	0	0	0	0	0	0	V9GX03	
ENSMUST00000184369						10	8	25	24	7	3	0	0	0	1	0		
ENSMUST00000184370	ENSMUSG00000042508	5	9118801	9161776	-1	0	4	3	2	0	2	12	25	2	3	0	V9GX14	
ENSMUST00000184371	ENSMUSG00000039943	2	135659011	136014593	1	0	0	0	0	0	0	1	6	17	0	0	V9GXQ9	
ENSMUST00000184372	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	7	0	0	0	0	0	0	0	V9GXK4	
ENSMUST00000184377						11	9	14	69	16	7	5	10	3	3	10		
ENSMUST00000184378	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	3	0	0	0	0	0	0	V9GXQ6	
ENSMUST00000184379						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184385						3	4	0	2	1	0	0	0	0	0	0		
ENSMUST00000184386						2	0	3	21	1	0	0	0	0	0	0		
ENSMUST00000184387						0	0	0	0	4	0	0	24	4	0	3		
ENSMUST00000184388						4	2	3	4	2	3	0	0	0	0	0		
ENSMUST00000184389	ENSMUSG00000079469	9	73007419	73040378	-1	0	0	0	0	0	0	0	0	0	0	0		Q9JJQ0
ENSMUST00000184390	ENSMUSG00000039536	2	166947549	166996299	-1	0	0	0	0	0	0	26	6	38	0	28	V9GX87	
ENSMUST00000184392	ENSMUSG00000041245	X	151198078	151320152	1	0	0	0	0	0	0	0	0	0	0	0		Q80XP9
ENSMUST00000184394	ENSMUSG00000027575	2	180967225	180982526	1	0	0	0	0	0	0	0	0	0	0	0	V9GWV1	
ENSMUST00000184395	ENSMUSG00000062762	9	36779159	36797361	-1	0	0	0	10	2	0	0	0	0	0	24	V9GXH2	
ENSMUST00000184399	ENSMUSG00000038535	9	72274860	72363777	1	0	0	8	0	0	0	5	5	9	0	6	V9GWZ2	
ENSMUST00000184401	ENSMUSG00000042508	5	9118801	9161776	-1	7	6	2	11	7	8	13	43	28	7	14		Q8CE22
ENSMUST00000184403						0	0	1	25	2	0	0	0	0	0	0		
ENSMUST00000184404	ENSMUSG00000074766	2	139678178	139758581	1	0	0	0	100	0	0	0	0	0	0	0	V9GXR4	
ENSMUST00000184409						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184410						5	0	3	1	2	0	11	185	39	58	72		
ENSMUST00000184411						0	0	0	0	0	0	1	0	2	0	0		
ENSMUST00000184413						1	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000184415	ENSMUSG00000032355	9	77102081	77352969	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXP3	
ENSMUST00000184416	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	1	0	0	0	0	0	0	V9GX66	
ENSMUST00000184422						6	2	12	0	4	8	0	0	0	0	3		
ENSMUST00000184423	ENSMUSG00000098639	CHR_MG4180_PATCH	109589702	109600838	-1	26	21	79	109	44	17	4	6	6	0	2	B4YB44	Q7M732
ENSMUST00000184424						125	184	421	2188	170	91	12	55	15	7	18		
ENSMUST00000184428	ENSMUSG00000030321	6	115810729	115838412	-1	0	0	0	0	0	0	1	3	0	1	0	V9GXH0	
ENSMUST00000184430	ENSMUSG00000098799	13	19342152	19342212	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JF87	
ENSMUST00000184431	ENSMUSG00000098847	9	35776524	35790101	-1	1	0	0	3	1	2	0	0	0	0	0	Q3UW50	
ENSMUST00000184432	ENSMUSG00000068173	X	38013173	38018815	-1	0	1	1	3	2	1	0	0	0	0	0	Q3V0S2	
ENSMUST00000184439	ENSMUSG00000096215	16	5007288	5008309	1	3	0	0	0	0	1	0	0	0	0	0	J3QP37	
ENSMUST00000184440						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184442	ENSMUSG00000042359	2	76406508	76600647	1	5	0	0	5	9	4	0	0	3	0	0	V9GXX3	
ENSMUST00000184443						2	3	3	3	3	1	0	1	5	0	7		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000184445	ENSMUSG00000021756	13	112464070	112510086	1	0	0	0	0	0	0	0	0	0	0	0	V9GXT4	
ENSMUST00000184446						1	1	3	5	6	1	0	0	0	0	0		
ENSMUST00000184448	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	0	0	16	0	0	5	6	Q3UXQ3	
ENSMUST00000184450	ENSMUSG00000032216	9	72662346	72749852	1	12	2	8	0	6	8	0	0	0	0	0	Q3V335	
ENSMUST00000184451	ENSMUSG00000095510	X	37580992	37585496	1	0	4	8	2	0	0	0	0	0	0	0	A2ANE1	
ENSMUST00000184452						3	2	8	3	5	3	0	0	0	0	0		
ENSMUST00000184454	ENSMUSG00000028894	4	124741850	124801511	1	22	0	20	136	18	0	63	108	65	0	137		Q8K337
ENSMUST00000184455	ENSMUSG00000040410	4	22357543	22434091	1	0	0	11	0	0	0	20	54	6	0	15	V9GWU9	
ENSMUST00000184457	ENSMUSG00000098377	CHR_MG3833_PATCH	18300825	18348103	-1	0	1	8	0	1	1	11	56	7	8	0		
ENSMUST00000184458	ENSMUSG00000038679	15	50654752	50890463	-1	0	0	0	0	0	0	44	5	15	0	0	V9GXA5	
ENSMUST00000184461						421	438	1147	490	416	171	15	7	5	0	15		
ENSMUST00000184462						222	124	1125	340	123	72	4	10	6	0	7		
ENSMUST00000184466						0	0	0	1	3	0	0	8	0	18	10		
ENSMUST00000184467						6	4	7	0	3	2	0	1	0	0	2		
ENSMUST00000184469	ENSMUSG00000027618	2	156123639	156144186	-1	0	0	0	4	0	0	0	0	0	0	0	V9GXS4	
ENSMUST00000184471						6	9	8	12	13	7	0	0	0	0	1		
ENSMUST00000184480	ENSMUSG00000033577	9	80165031	80311729	1	0	0	0	0	0	0	0	0	0	0	0	V9GX76	
ENSMUST00000184481						9	9	34	12	12	7	0	0	0	0	0		
ENSMUST00000184485	ENSMUSG00000099083	15	102525946	102625464	-1	0	0	0	0	0	0	0	0	0	0	50	Q3TZR9	
ENSMUST00000184486						5	5	6	2	6	0	0	0	0	1	0		
ENSMUST00000184487	ENSMUSG00000028064	3	88435959	88461182	-1	0	2	0	4	3	2	139	117	198	10	97	V9GXF5	
ENSMUST00000184496						0	0	0	0	0	0	0	0	7	10	0		
ENSMUST00000184497						49	22	52	22	59	15	838	2531	1617	116	1880		
ENSMUST00000184500						0	2	0	2	0	1	0	0	0	0	0		
ENSMUST00000184502	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	2	14	1	0	0	0	0	0	0	V9GXR0	
ENSMUST00000184503						0	15	5	7	4	4	0	0	0	0	2		
ENSMUST00000184506						22	24	66	59	26	15	2	19	10	2	8		
ENSMUST00000184507						8	3	16	1	6	6	0	0	0	0	0		
ENSMUST00000184509						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000184515	ENSMUSG00000027952	3	89454541	89469013	1	0	7	7	5	9	6	0	68	15	0	27		Q9D1G2
ENSMUST00000184517	ENSMUSG00000038535	9	72274860	72363777	1	2	3	20	2	0	5	2	0	0	2	0		Q68FE8
ENSMUST00000184518	ENSMUSG00000019082	7	141429744	141437892	-1	0	0	0	0	0	0	0	0	1	0	3	Q80X52	
ENSMUST00000184523	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	0	0	0	0	0	0	0	V9GWU2	
ENSMUST00000184525	ENSMUSG00000004842	16	65520511	65535005	1	0	1	0	0	0	1	0	0	0	0	0	F1T2M3	
ENSMUST00000184531						0	6	8	0	0	6	0	0	6	6	0		
ENSMUST00000184533						8	9	0	1	9	0	0	0	0	0	0		
ENSMUST00000184534						28	18	69	47	30	18	0	0	0	0	0		
ENSMUST00000184535	ENSMUSG00000027327	2	131146324	131160081	-1	0	0	23	18	8	5	22	124	16	0	15	Q6IR22	
ENSMUST00000184537	ENSMUSG00000028199	3	154596711	154623182	1	11	0	0	0	0	0	0	0	0	0	0	V9GXY8	
ENSMUST00000184538	ENSMUSG00000027406	2	130279309	130284547	-1	0	0	0	0	0	5	0	0	0	0	0	V9GXV0	
ENSMUST00000184539						2	2	0	0	0	0	91	0	143	0	186		
ENSMUST00000184540						26	17	31	29	16	3	250	787	693	200	495		
ENSMUST00000184543	ENSMUSG00000026611	1	187044648	187215465	-1	1	4	0	0	2	0	0	0	0	0	0	V9GX67	
ENSMUST00000184544						20	18	50	28	31	10	0	0	0	0	1		
ENSMUST00000184546	ENSMUSG00000095741	X	37571405	37576163	1	4	3	0	0	0	0	0	0	0	0	0	V9GXW4	
ENSMUST00000184548						66	86	84	69	89	44	6	42	18	2	23		
ENSMUST00000184550	ENSMUSG00000028163	3	135584655	135691547	-1	0	0	28	0	0	0	278	791	166	57	86	V9GX90	
ENSMUST00000184552	ENSMUSG00000019528	3	20122084	20155317	-1	0	0	0	0	0	0	7	124	14	30	0	V9GX26	
ENSMUST00000184557	ENSMUSG00000090626	9	72450394	72492212	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXL5	
ENSMUST00000184560	ENSMUSG00000038745	7	140920902	140929192	1	7	9	12	13	14	9	0	1	0	0	0	F8UKQ6	
ENSMUST00000184561						1	2	4	8	4	2	0	0	0	2	0		
ENSMUST00000184565	ENSMUSG00000095601	X	37380028	37384493	1	13	0	0	12	1	9	0	0	0	0	0	Q4TU90	
ENSMUST00000184566						1	5	0	0	2	2	0	0	0	0	0		
ENSMUST00000184571	ENSMUSG00000021768	14	21733394	21751181	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXV5	
ENSMUST00000184572	ENSMUSG00000020774	11	73304992	73329596	-1	4	4	10	4	6	3	0	0	0	0	0		Q8R3P0
ENSMUST00000184573						0	0	0	0	0	0	32	172	65	47	85		
ENSMUST00000184574	ENSMUSG00000059852	18	80294546	80364254	-1	1	0	0	57	1	0	0	0	0	0	0	V9GXB3	
ENSMUST00000184575						6	1	0	2	4	1	12	6	14	5	48		
ENSMUST00000184577	ENSMUSG00000094817	14	26082297	26235744	1	0	0	0	0	0	1	0	0	0	0	0	Q8BX39	
ENSMUST00000184578						12	13	84	89	15	5	54	82	49	5	78		
ENSMUST00000184581	ENSMUSG00000079293	6	129461591	129472779	-1	0	0	0	0	0	0	118	389	350	1065	271	V9GXI5	
ENSMUST00000184582	ENSMUSG00000040410	4	22357543	22434091	1	0	0	0	0	0	0	0	0	0	0	28	V9GXH8	
ENSMUST00000184588	ENSMUSG00000000827	2	181497142	181517966	1	1	0	0	33	0	0	99	180	109	330	90	V9GXN2	
ENSMUST00000184589						2	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000184590	ENSMUSG00000050315	3	123076519	123236149	-1	0	8	18	2	9	8	0	1	0	0	1	A0A0G2JDM5	
ENSMUST00000184591						1	0	2	21	8	0	0	0	0	0	0		
ENSMUST00000184598						0	3	7	58	4	5	0	1	0	0	3		
ENSMUST00000184600	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	5	3	12	5	4	2	9	13	0	0	0		
ENSMUST00000184601						2	3	18	4	2	0	0	0	0	0	0		
ENSMUST00000184602						90	81	105	97	140	55	4	18	15	0	13		
ENSMUST00000184603	ENSMUSG00000098306	1	133309827	133329901	1	0	0	0	0	0	0	0	0	0	0	0	A0A5C8	
ENSMUST00000184604	ENSMUSG00000032221	9	72438011	72462025	1	1	3	3	6	0	1	1	0	1	3	0	V9GXM7	
ENSMUST00000184609	ENSMUSG00000028597	4	108400390	108406961	-1	1	0	0	28	2	0	0	0	0	0	2	V9GXV4	
ENSMUST00000184611	ENSMUSG00000070313	9	36635754	36643376	-1	4	1	7	1	0	0	0	0	0	0	0	V9GXC5	
ENSMUST00000184613						0	0	0	18	0	0	0	0	19	0	10		
ENSMUST00000184615						1	0	0	0	0	0	6	6	0	1	0		
ENSMUST00000184616	ENSMUSG00000099083	15	102525946	102625464	-1	123	110	572	135	115	63	377	773	550	38	540	Q3TZR9	
ENSMUST00000184618						4	1	6	3	2	3	21	66	19	30	30		
ENSMUST00000184619						4	10	13	7	10	3	0	2	1	0	0		
ENSMUST00000184620	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	0	0	0	17	227	50	0	51	V9GWT2	
ENSMUST00000184621						1	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000184624						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184625						26	32	50	36	46	25	4	9	11	1	22		
ENSMUST00000184628						4	1	2	0	2	0	0	12	0	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000184631	ENSMUSG00000098377	CHR_MG3833_PATCH	18300825	18348103	-1	0	0	0	11	2	0	6	1	2	1	1		
ENSMUST00000184633						7	0	43	16	12	7	2	0	3	0	0		
ENSMUST00000184634						0	0	3	8	1	1	0	0	0	0	0		
ENSMUST00000184635	ENSMUSG00000024095	17	80029487	80062334	-1	2	2	0	0	0	0	73	39	0	43	0		Q921F4
ENSMUST00000184639						101	55	437	233	114	31	2	0	4	6	2		
ENSMUST00000184642						24	4	22	0	24	7	58	124	57	35	173		
ENSMUST00000184643	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	24	0	0		P25425
ENSMUST00000184644	ENSMUSG00000039795	3	10339953	10351317	-1	0	0	4	3	0	0	0	0	0	0	3	V9GXT9	
ENSMUST00000184646	ENSMUSG00000018698	11	84518284	84525535	-1	0	0	3	0	1	0	11	37	26	0	12	A0A087WNK8	
ENSMUST00000184647	ENSMUSG00000098470	6	124570294	124581171	1	10	9	57	21	16	14	0	8	0	10	10		Q8CFG9
ENSMUST00000184650	ENSMUSG00000094468	14	53454296	53454784	1	0	0	0	0	0	0	0	1	0	0	0	A0A075B6D6	
ENSMUST00000184651	ENSMUSG00000028041	3	89338542	89349996	-1	13	4	18	26	20	11	91	486	111	4	82		O88839
ENSMUST00000184652	ENSMUSG00000098773	14	69508632	69512549	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BI41	
ENSMUST00000184654	ENSMUSG00000098640	2	154769255	154770030	-1	0	3	0	0	0	0	0	0	0	0	2	V9GX35	
ENSMUST00000184657						6	3	0	0	2	3	0	0	0	0	3		
ENSMUST00000184659						4	5	7	15	0	4	8	46	15	6	27		
ENSMUST00000184663	ENSMUSG00000010097	19	8757073	8772475	1	0	0	0	0	0	0	0	0	0	3	0	V9GXC8	
ENSMUST00000184664	ENSMUSG00000033182	6	88545114	88637950	-1	9	7	18	10	7	3	0	0	0	0	0	V9GXB1	
ENSMUST00000184665						0	1	4	1	1	2	0	0	0	0	0		
ENSMUST00000184666	ENSMUSG00000062151	9	73479422	73968966	-1	32	28	69	36	36	32	0	0	1	0	0		Q8K0T7
ENSMUST00000184670						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000184672	ENSMUSG00000015536	13	114818236	114832275	1	0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000184675	ENSMUSG00000072674	14	26167405	26182480	-1	0	1	0	0	1	0	0	0	0	0	0	V9GXX6	
ENSMUST00000184677	ENSMUSG00000037174	3	51252720	51340663	-1	0	0	0	0	0	0	3	14	33	4	43	V9GXK9	
ENSMUST00000184679						0	3	2	1	5	3	0	0	0	0	0		
ENSMUST00000184683	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	0	0	0	0	0	0	1	0	0	0	0		
ENSMUST00000184684	ENSMUSG00000029074	4	156034840	156059414	-1	0	1	5	3	6	0	0	0	0	0	0	V9GXB7	
ENSMUST00000184686						12	16	38	28	14	12	0	0	0	0	0		
ENSMUST00000184687	ENSMUSG00000096138	14	53716716	53717291	1	0	0	0	1	0	0	0	0	0	0	0	A0A075B6D1	
ENSMUST00000184688	ENSMUSG00000079637	X	37453680	37469861	1	3	0	2	2	0	5	0	0	0	0	0	V9GXB9	
ENSMUST00000184693	ENSMUSG00000059383	9	76164102	76213657	-1	0	0	2	7	0	1	0	0	0	0	0		Q6SJE0
ENSMUST00000184694	ENSMUSG00000030374	7	16815889	16840931	1	0	0	0	0	0	0	3	9	9	0	11	V9GXE7	
ENSMUST00000184695						11	15	91	31	42	13	4	18	8	0	11		
ENSMUST00000184698						1	2	1	1	0	0	0	1	0	0	0		
ENSMUST00000184700						6	10	26	9	11	5	0	0	0	0	0		
ENSMUST00000184703	ENSMUSG00000021768	14	21733394	21751181	-1	0	0	0	0	0	0	0	0	0	0	0		Q9QYJ7
ENSMUST00000184704						2	2	6	35	4	2	0	5	4	3	6		
ENSMUST00000184705	ENSMUSG00000026991	2	59160850	59355208	1	1	0	0	0	0	0	0	0	0	0	0	V9GWY7	
ENSMUST00000184708	ENSMUSG00000030374	7	16815889	16840931	1	0	0	0	0	2	0	31	6	26	0	0	V9GXI9	
ENSMUST00000184716						4	0	11	2	3	1	0	0	0	0	0		
ENSMUST00000184717	ENSMUSG00000098615	CHR_MG3833_PATCH	18348182	18407957	1	2	0	4	11	0	1	0	0	0	0	0		P98203
ENSMUST00000184725						8	3	6	2	6	4	0	0	0	0	0		
ENSMUST00000184726						16	14	28	123	25	9	4	7	7	4	15		
ENSMUST00000184728	ENSMUSG00000044338	2	85136225	85139923	1	0	0	0	0	0	0	0	0	0	0	0	V9GXG8	
ENSMUST00000184730	ENSMUSG00000041245	X	151198078	151320152	1	2	0	0	0	0	1	0	0	0	0	0		Q80XP9
ENSMUST00000184731	ENSMUSG00000070810	7	14222403	14254870	-1	0	2	5	0	2	1	0	0	0	0	0	V9GWV0	
ENSMUST00000184732						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000184734						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184736	ENSMUSG00000098411	CHR_MG4180_PATCH	109452823	109463336	1	0	0	0	0	0	0	0	2	0	0	0		
ENSMUST00000184737						0	0	0	35	0	0	1	1	0	0	1		
ENSMUST00000184741						130	170	344	106	109	27	1	4	5	0	5		
ENSMUST00000184743						38	31	40	24	36	20	0	1	0	0	1		
ENSMUST00000184744	ENSMUSG00000098557	14	102976581	102982637	-1	28	18	22	596	52	45	3544	7430	3975	517	3761		
ENSMUST00000184746	ENSMUSG00000096788	X	37530452	37541813	1	0	0	0	0	0	3	0	0	0	0	0	V9GXL3	
ENSMUST00000184750						1	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000184751	ENSMUSG00000038685	2	181319739	181356616	1	0	0	0	0	0	0	0	0	0	0	0	V9GX41	
ENSMUST00000184752						0	0	0	0	0	0	0	16	3	54	8		
ENSMUST00000184753						27	14	51	98	22	18	0	1	3	0	0		
ENSMUST00000184756	ENSMUSG00000010097	19	8757073	8772475	1	0	2	0	0	1	0	0	0	0	0	0	V9GX96	
ENSMUST00000184757	ENSMUSG00000032360	9	76225880	76323856	-1	1	4	18	36	10	0	0	0	0	0	0		P58308
ENSMUST00000184766	ENSMUSG00000021023	12	55299577	55382533	1	0	0	0	0	0	0	4	22	5	0	3		Q8JZY4
ENSMUST00000184767						5	5	1	2	4	1	0	0	0	0	0		
ENSMUST00000184768						1	2	5	38	2	0	0	0	0	0	0		
ENSMUST00000184770						3	6	2	2	7	2	0	0	0	0	0		
ENSMUST00000184772	ENSMUSG00000052414	15	102523843	102625067	-1	0	0	0	0	0	0	5	0	0	0	0	Q3US59	
ENSMUST00000184775	ENSMUSG00000098835	R_MG4222_MG3908_PAT	55651997	55712600	-1	851	722	2029	902	1171	597	33	168	67	56	93		
ENSMUST00000184776						21	25	74	38	40	27	40	71	96	5	259		
ENSMUST00000184779						0	2	0	5	2	0	0	0	2	0	2		
ENSMUST00000184780						6	2	8	3	2	1	1	2	10	0	3		
ENSMUST00000184781	ENSMUSG00000015536	13	114818236	114832275	1	1	1	0	0	0	3	0	0	0	0	0	F6ZGI7	
ENSMUST00000184782						19	23	21	36	32	14	14	47	31	12	43		
ENSMUST00000184783	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	21	1	0	0	0	14	0	0		Q61286
ENSMUST00000184786	ENSMUSG00000038535	9	72274860	72363777	1	0	1	0	0	0	0	0	1	0	0	0	V9GX97	
ENSMUST00000184795	ENSMUSG00000027584	2	181715016	181720985	1	0	0	0	0	0	0	0	0	0	0	0	V9GX47	
ENSMUST00000184797						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184799	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	4	0	5	V9GXQ7	
ENSMUST00000184801						73	75	130	57	60	33	3	21	9	5	9		
ENSMUST00000184802	ENSMUSG00000028180	3	157534160	157548410	1	2	0	0	0	0	0	10	60	4	0	0	V9GX51	
ENSMUST00000184805						0	0	0	0	5	0	10	16	7	0	10		
ENSMUST00000184806						7	13	22	8	8	10	0	2	0	0	2		
ENSMUST00000184808						4	0	0	7	0	2	0	12	3	0	0		
ENSMUST00000184809						0	0	0	213	0	0	0	0	0	0	0		
ENSMUST00000184810						7	2	7	6	4	2	0	0	0	0	0		
ENSMUST00000184811						0	0	0	55	3	0	2	0	0	1	3		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000184813						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000184816	ENSMUSG00000093954	14	69363504	69503362	-1	17	8	23	0	12	7	0	0	0	0	0		Q920G8
ENSMUST00000184817						2	3	6	3	3	0	0	0	0	0	0		
ENSMUST00000184818						394	351	912	516	484	220	16	36	21	6	62		
ENSMUST00000184819	ENSMUSG00000097600	CHR_MG4214_PATCH	37832136	37841725	1	1	1	6	2	1	3	0	0	0	0	0		
ENSMUST00000184820	ENSMUSG00000048004	12	119945957	120019211	1	0	2	0	0	0	0	0	0	0	0	0	V9GX16	
ENSMUST00000184824	ENSMUSG00000071769	X	37657688	37668764	-1	0	0	1	0	2	0	0	0	0	0	0	V9GXU1	
ENSMUST00000184826	ENSMUSG00000010097	19	8757073	8772475	1	0	0	0	0	0	0	0	398	0	84	62	V9GXM5	
ENSMUST00000184828						4	5	0	5	6	4	1	0	0	0	0		
ENSMUST00000184830						5	5	3	2	4	3	0	0	0	1	0		
ENSMUST00000184831	ENSMUSG00000090626	9	72450394	72492212	-1	2	0	2	51	0	3	0	0	0	0	0	V9GX60	
ENSMUST00000184837						1	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000184838	ENSMUSG00000030172	6	119570796	119848167	-1	0	0	0	0	2	0	0	0	0	0	0		Q99MI1
ENSMUST00000184842						16	16	33	28	24	15	1378	6232	3653	2183	3670		
ENSMUST00000184843						21	8	20	8	22	2	0	0	0	6	16		
ENSMUST00000184845	ENSMUSG00000026790	2	29889221	29931746	1	0	0	0	0	0	3	0	0	0	0	0	V9GXZ0	
ENSMUST00000184846						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184848	ENSMUSG00000032355	9	77102081	77352969	-1	0	0	0	0	0	0	0	0	0	0	0		Q5FW52
ENSMUST00000184849	ENSMUSG00000000827	2	181497142	181517966	1	0	0	0	2	3	0	22	46	52	74	25	V9GWU5	
ENSMUST00000184850						11	5	16	5	7	5	7	18	6	0	13		
ENSMUST00000184851						199	191	437	333	207	130	13	48	21	8	27		
ENSMUST00000184852						9	1	2	5	3	5	0	0	0	0	0		
ENSMUST00000184858	ENSMUSG00000098678	15	75884137	75888770	-1	24	20	30	184	40	24	12	20	12	1	11	V9GX81	
ENSMUST00000184859						0	0	0	2	1	1	12	16	10	0	12		
ENSMUST00000184861						0	0	0	0	0	0	0	0	10	232	520		
ENSMUST00000184862	ENSMUSG00000039069	2	180070588	180085902	1	0	0	0	0	0	0	72	62	86	3	44	I6L986	
ENSMUST00000184863	ENSMUSG00000038055	16	10502531	10543054	-1	15	9	20	38	27	15	0	5	0	0	10		Q9WUQ7
ENSMUST00000184864	ENSMUSG00000030172	6	119570796	119848167	-1	0	0	0	0	0	0	1	0	109	0	5	V9GXP8	
ENSMUST00000184865	ENSMUSG00000025735	17	25834465	25837295	-1	1	0	2	31	6	2	0	2	0	1	2	V9GX09	
ENSMUST00000184866	ENSMUSG00000095180	X	37804842	37808876	1	0	1	0	2	0	0	0	0	0	6	0	V9GXJ4	
ENSMUST00000184867	ENSMUSG00000032228	9	71842688	72111871	-1	2	0	0	0	0	0	8	0	0	21	14	V9GXM8	
ENSMUST00000184874	ENSMUSG00000095711	14	53640701	53641225	1	0	0	0	0	3	0	0	0	0	0	0	A0A0B4J1N7	
ENSMUST00000184876	ENSMUSG00000028064	3	88435959	88461182	-1	0	0	0	0	0	0	86	74	107	3	63	V9GXH9	
ENSMUST00000184877	ENSMUSG00000001018	3	90488026	90491033	-1	0	0	0	0	0	0	104	130	32	86	26	V9GXT7	
ENSMUST00000184878	ENSMUSG00000033182	6	88545114	88637950	-1	0	4	11	1	9	3	0	0	0	0	0	V9GXV2	
ENSMUST00000184882	ENSMUSG00000027936	3	90254163	90264125	1	12	3	9	2	14	8	340	296	267	44	297	V9GXK6	
ENSMUST00000184883	ENSMUSG00000096600	14	52725299	52726919	1	0	0	0	0	0	0	0	0	0	0	0	A0A075B6D3	
ENSMUST00000184885	ENSMUSG00000038679	15	50654752	50890463	-1	0	0	0	0	0	0	0	0	88	0	63	Q80V18	
ENSMUST00000184887	ENSMUSG00000032035	9	32636221	32757820	1	0	0	0	0	0	0	0	0	0	0	0	V9GX28	
ENSMUST00000184888	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	0	0	0	0	0	0	34	0		Q8CE22
ENSMUST00000184889						10	12	23	5	13	9	24	67	35	9	59		
ENSMUST00000184890						5	2	3	0	5	0	0	0	0	0	0		
ENSMUST00000184891	ENSMUSG00000071767	X	37831686	37841275	1	1	1	6	2	1	3	0	0	0	0	0	V9GWS7	
ENSMUST00000184895	ENSMUSG00000098930	CHR_MG3833_PATCH	18248679	18254772	1	0	0	0	0	0	0	14	38	39	0	24		
ENSMUST00000184897	ENSMUSG00000032357	9	76951693	77045794	-1	7	0	3	0	8	0	0	0	0	0	0	V9GXH5	
ENSMUST00000184899	ENSMUSG00000098950	2	156071845	156127092	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXJ2	
ENSMUST00000184901						36	24	57	23	24	19	0	0	2	0	0		
ENSMUST00000184903						0	0	0	0	0	0	0	0	0	0	19		
ENSMUST00000184905	ENSMUSG00000094562	14	53757356	53757921	1	0	0	2	0	0	0	0	0	0	0	0	A0A075B6C9	
ENSMUST00000184906	ENSMUSG00000099083	15	102525946	102625464	-1	0	0	1	2	2	0	17	23	33	0	10	V9GXN6	
ENSMUST00000184908						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184913	ENSMUSG00000029036	4	155740641	155761093	-1	0	0	0	0	0	0	3	6	1	1	0	V9GWS5	
ENSMUST00000184914	ENSMUSG00000034248	14	69241848	69285112	-1	2	0	0	0	1	0	21	6	66	5	116		Q920G8
ENSMUST00000184915	ENSMUSG00000094800	14	26027282	26042711	-1	2	5	9	3	5	1	0	0	3	6	3		
ENSMUST00000184916						0	0	0	0	0	0	38	72	41	12	65		
ENSMUST00000184917	ENSMUSG00000068536	6	48974963	48978746	1	0	0	0	33	0	0	0	0	0	0	0	Q6IMK7	
ENSMUST00000184918						2	0	0	0	3	1	0	0	0	0	0		
ENSMUST00000184921	ENSMUSG00000027318	2	131050591	131063814	-1	0	0	0	0	0	0	0	0	0	0	2	V9GXX4	
ENSMUST00000184922						8	13	6	12	9	3	0	0	0	0	0		
ENSMUST00000184925						5	2	1	5	3	1	0	0	0	0	0		
ENSMUST00000184928						30	35	56	145	29	35	1	3	3	2	6		
ENSMUST00000184929	ENSMUSG00000099077	CHR_MG132_PATCH	124456062	124462462	-1	0	0	0	25	0	0	3	24	9	3	10		
ENSMUST00000184931	ENSMUSG00000027198	2	93661028	93822568	-1	10	11	17	18	16	1	0	0	0	0	0	V9GX32	
ENSMUST00000184932	ENSMUSG00000037514	2	131262495	131299188	1	7	5	31	17	5	7	137	558	199	94	327	V9GXP9	
ENSMUST00000184933						2	0	5	4	4	0	0	14	16	0	33		
ENSMUST00000184936						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184938						21	5	27	20	8	15	0	0	0	0	0		
ENSMUST00000184940	ENSMUSG00000099102	11	6835626	6837654	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXS8	
ENSMUST00000184941						0	2	0	0	4	1	8	49	28	20	21		
ENSMUST00000184944						97	72	354	491	110	65	4	9	6	0	5		
ENSMUST00000184945	ENSMUSG00000052512	7	48908716	49610090	1	48	20	272	0	67	17	88	111	86	9	94	V9GX91	
ENSMUST00000184947						6	5	6	11	10	4	7	8	28	4	39		
ENSMUST00000184949	ENSMUSG00000021756	13	112464070	112510086	1	0	0	1	0	2	0	0	0	0	0	0	V9GX00	
ENSMUST00000184951	ENSMUSG00000038126	5	124250959	124327972	-1	0	0	0	5	0	0	0	0	0	0	0	V9GX48	
ENSMUST00000184952						9	7	2	6	6	3	0	0	0	0	0		
ENSMUST00000184954	ENSMUSG00000062280	2	111408376	111409331	1	2	2	3	1	5	2	0	0	0	0	0		
ENSMUST00000184955						5	3	1	4	1	2	0	0	0	0	0		
ENSMUST00000184959						1	5	8	1	2	0	1	1	0	0	1		
ENSMUST00000184961						1	1	9	6	2	0	0	0	0	0	0		
ENSMUST00000184962						3	0	9	1	0	1	0	1	0	0	0		
ENSMUST00000184963	ENSMUSG00000033439	3	116581093	116614587	-1	0	0	0	0	0	0	7	35	17	7	4	V9GWW9	
ENSMUST00000184965						0	0	5	0	2	0	1697	10	2322	218	1392		
ENSMUST00000184968						44	19	249	83	57	42	2	9	7	0	16		
ENSMUST00000184969						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000184970	ENSMUSG00000010097	19	8757073	8772475	1	23	17	93	120	37	27	298	1668	705	178	1095	V9GXF3	
ENSMUST00000184972						0	2	3	5	3	3	0	2	0	0	10		
ENSMUST00000184973	ENSMUSG00000095463	14	69337174	69367270	1	5	3	10	11	7	3	36	80	44	18	55		Q9DBT4
ENSMUST00000184977						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000184978	ENSMUSG00000027966	3	114030540	114220718	1	2	5	9	5	4	1	0	1	0	0	0	V9GWX8	
ENSMUST00000184980	ENSMUSG00000021023	12	55299577	55382533	1	2	0	6	1	6	2	0	8	5	19	16	V9GXF2	
ENSMUST00000184985						1	1	1	11	0	0	0	0	0	0	0		
ENSMUST00000184986	ENSMUSG00000061762	6	7554879	7565834	1	0	0	0	0	0	0	0	0	0	0	0	B7ZMQ2	P41539
ENSMUST00000184988						30	16	57	132	26	16	47	32	18	6	46		
ENSMUST00000184996	ENSMUSG00000026754	2	39016155	39065541	-1	0	0	0	0	0	0	29	6	58	61	0		Q9CW79
ENSMUST00000185001	ENSMUSG00000028248	4	21847583	21876475	1	0	0	0	0	0	0	41	18	111	15	100	A2AJT3	
ENSMUST00000185005	ENSMUSG00000001018	3	90488026	90491033	-1	11	7	10	0	0	0	0	133	34	69	51	V9GXI0	
ENSMUST00000185006	ENSMUSG00000072676	14	25924000	25927672	-1	8	1	3	6	3	0	18	53	0	0	15		Q9DCV5
ENSMUST00000185008	ENSMUSG00000095510	X	37580992	37585496	1	4	0	0	0	0	0	0	0	0	0	0	V9GWT1	
ENSMUST00000185009						3	0	32	7	7	0	0	0	0	0	0		
ENSMUST00000185011	ENSMUSG00000030374	7	16815889	16840931	1	0	0	0	0	0	0	0	7	0	0	0	V9GXS1	
ENSMUST00000185012	ENSMUSG00000083780	4	105789869	105794711	1	0	0	0	0	0	0	0	0	0	1	0	V9GXC1	
ENSMUST00000185020	ENSMUSG00000038535	9	72274860	72363777	1	0	0	0	0	4	0	0	1	0	1	2	V9GWT3	
ENSMUST00000185024						3	0	2	1	3	0	1	4	2	0	1		
ENSMUST00000185025						23	21	57	64	45	20	0	0	0	0	0		
ENSMUST00000185027						3	7	12	9	9	1	19	56	49	2	76		
ENSMUST00000185028	ENSMUSG00000071772	X	37249919	37258983	1	0	0	0	0	0	0	0	0	0	0	0	V9GXK5	
ENSMUST00000185029	ENSMUSG00000040410	4	22357543	22434091	1	26	12	0	12	19	5	0	10	9	6	3	V9GWT8	
ENSMUST00000185030	ENSMUSG00000098892	CHR_MG3833_PATCH	18407771	18427737	-1	1	0	3	161	7	5	0	28	5	0	10		O88587
ENSMUST00000185034						11	4	11	2	3	3	6	0	6	3	13		
ENSMUST00000185036	ENSMUSG00000078570	4	124849080	124851196	-1	0	0	2	113	0	0	0	3	0	0	3	V9GXF1	
ENSMUST00000185039	ENSMUSG00000032355	9	77102081	77352969	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZMP8	
ENSMUST00000185040						0	0	0	0	0	0	0	0	0	2	0		
ENSMUST00000185042	ENSMUSG00000021768	14	21733394	21751181	-1	3	0	1	4	1	3	0	0	0	0	0	V9GXC2	
ENSMUST00000185049						2	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000185050	ENSMUSG00000071772	X	37249919	37258983	1	0	0	0	0	0	0	0	0	0	0	0	V9GX94	
ENSMUST00000185051	ENSMUSG00000047248	7	100372233	100470152	1	2	2	3	0	4	0	0	0	0	0	0	V9GXU2	
ENSMUST00000185052	ENSMUSG00000005583	13	83504034	83667080	1	2	3	45	0	13	8	10	3	30	2	45		Q8CFN5
ENSMUST00000185053						4	3	12	21	7	5	0	0	33	0	0		
ENSMUST00000185056						0	0	0	5	3	2	0	340	39	7	41		
ENSMUST00000185057						1	0	7	1	0	1	0	0	0	0	0		
ENSMUST00000185058	ENSMUSG00000099164	CHR_MG3833_PATCH	18239784	18248732	-1	1	3	4	3	0	0	44	138	35	27	60		
ENSMUST00000185066						16	9	43	19	18	5	1	1	3	0	3		
ENSMUST00000185068	ENSMUSG00000032343	9	80313330	80465481	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185070	ENSMUSG00000099083	15	102525946	102625464	-1	0	0	0	1	0	0	0	0	0	0	0	V9GXY2	
ENSMUST00000185072	ENSMUSG00000022066	14	69555424	69585520	1	5	3	10	11	7	3	36	80	44	18	55		Q9DBT4
ENSMUST00000185081	ENSMUSG00000099217	CHR_MG4212_PATCH	15605656	15662113	-1	114	103	32	111	131	76	0	0	0	0	0		
ENSMUST00000185083						3	0	4	1	2	1	0	0	0	0	0		
ENSMUST00000185084	ENSMUSG00000047248	7	100372233	100470152	1	3	0	0	0	1	0	3	7	0	2	5	V9GXB2	
ENSMUST00000185086						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000185087	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXI4	
ENSMUST00000185088						4	2	1	4	3	0	0	0	0	0	0		
ENSMUST00000185091	ENSMUSG00000051969	14	50357914	50363663	1	15	0	0	10	0	0	0	0	0	0	0	V9GWT0	
ENSMUST00000185097						0	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000185098	ENSMUSG00000033554	3	115887837	115934361	1	3	1	15	3	1	2	0	1	2	4	7	V9GXP1	
ENSMUST00000185100	ENSMUSG00000042508	5	9118801	9161776	-1	0	0	0	0	0	0	0	1	2	0	2	V9GX59	
ENSMUST00000185102	ENSMUSG00000029848	6	34920163	34939344	1	10	4	4	52	0	3	0	2	0	1	0	V9GXG4	
ENSMUST00000185104	ENSMUSG00000070498	5	125531774	125792583	1	8	4	1	20	4	4	0	0	0	0	0	V9GX71	
ENSMUST00000185106						4	0	2	0	6	0	0	0	0	0	0		
ENSMUST00000185113	ENSMUSG00000020220	4	144972622	145195005	-1	0	0	0	0	0	0	238	302	614	30	448	V9GX23	
ENSMUST00000185115	ENSMUSG00000027575	2	180967225	180982526	1	0	0	2	0	0	0	17	5	28	0	50	V9GXM1	
ENSMUST00000185117	ENSMUSG00000032228	9	71842688	72111871	-1	0	0	0	0	0	0	0	132	109	38	140		Q61286
ENSMUST00000185118	ENSMUSG00000038671	2	181357690	181365404	-1	0	0	0	0	0	0	0	18	83	10	0	Q80SX7	
ENSMUST00000185119	ENSMUSG00000027953	3	89268246	89270570	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXF7	
ENSMUST00000185121	ENSMUSG00000045691	14	55053884	55098986	1	13	10	21	23	25	12	0	0	0	0	0	A0A087WPV5	
ENSMUST00000185124						0	2	1	2	5	0	0	0	5	2	0		
ENSMUST00000185125	ENSMUSG00000079703	X	8684887	8690844	-1	0	0	0	0	2	0	0	0	0	0	0	B1AY40	
ENSMUST00000185127	ENSMUSG00000097306	CHR_MG4214_PATCH	37804842	37808876	1	0	1	0	2	0	0	0	0	0	6	0		
ENSMUST00000185128	ENSMUSG00000040412	3	108455694	108536536	-1	0	1	5	3	1	0	0	0	0	0	0	V9GWX1	
ENSMUST00000185130	ENSMUSG00000061762	6	7554879	7565834	1	3	1	3	6	1	3	0	0	0	0	0	V9GX83	
ENSMUST00000185131	ENSMUSG00000020160	11	18879817	19018985	-1	0	0	0	0	0	0	0	0	0	0	0		Q60954
ENSMUST00000185133						11	13	48	25	15	9	0	0	1	0	0		
ENSMUST00000185137	ENSMUSG00000028064	3	88435959	88461182	-1	3	4	11	16	6	4	55	129	74	4	128	V9GWW2	
ENSMUST00000185138	ENSMUSG00000071769	X	37657688	37668764	-1	3	0	0	0	0	0	0	0	0	0	0	V9GWW8	
ENSMUST00000185139	ENSMUSG00000030172	6	119570796	119848167	-1	0	0	0	0	0	0	0	0	0	0	36	V9GXH3	
ENSMUST00000185140						2	2	2	55	2	2	0	0	0	0	0		
ENSMUST00000185141						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000185143	ENSMUSG00000030172	6	119570796	119848167	-1	0	0	0	0	0	0	0	0	0	0	0	V9GX53	
ENSMUST00000185144	ENSMUSG00000032355	9	77102081	77352969	-1	8	0	3	0	15	0	0	0	0	0	0	V9GXX2	
ENSMUST00000185145	ENSMUSG00000056394	7	13277283	13311433	1	0	0	0	0	0	3	19	0	0	0	9	V9GWZ4	
ENSMUST00000185147	ENSMUSG00000096215	16	5007288	5008309	1	0	1	0	2	0	0	0	0	0	0	0	V9GXA9	
ENSMUST00000185148	ENSMUSG00000029066	4	155802878	155809975	1	1	0	3	0	0	0	0	125	18	10	0	V9GXI7	
ENSMUST00000185151	ENSMUSG00000090626	9	72450394	72492212	-1	0	0	0	19	0	0	0	0	0	2	0	V9GX10	
ENSMUST00000185153						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000185160	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	0	0	0	0	5	0	0	12	10	8	11		
ENSMUST00000185164	ENSMUSG00000042641	1	153779381	153844142	-1	11	6	24	12	0	0	0	0	0	0	0	V9GXV7	
ENSMUST00000185167	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0	V9GXY0	
ENSMUST00000185168	ENSMUSG00000063320	10	82619851	82623228	-1	9	11	0	10	0	0	0	5	1	0	3		Q8BTC1
ENSMUST00000185170	ENSMUSG00000098930	CHR_MG3833_PATCH	18248679	18254772	1	0	0	0	0	0	0	0	0	0	4	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000185174						1	2	10	8	4	1	0	0	0	0	0		
ENSMUST00000185175	ENSMUSG00000052040	7	63886351	63938915	-1	0	0	0	90	2	0	71	42	179	5	130	A0A087WQX4	
ENSMUST00000185176	ENSMUSG00000036306	8	69132669	69184225	-1	32	28	75	68	45	22	11	9	5	0	5		P60853
ENSMUST00000185177						3	2	0	0	0	0	0	0	0	1	0		
ENSMUST00000185178	ENSMUSG00000099115	13	96082054	96083231	1	7	9	44	4	12	6	0	0	0	0	0	V9GX38	
ENSMUST00000185183	ENSMUSG00000038679	15	50654752	50890463	-1	0	3	4	12	0	4	0	2	0	5	0	V9GX39	
ENSMUST00000185184	ENSMUSG00000099032	1	9960163	9967932	-1	11	12	19	161	21	9	11	48	15	0	6	V9GWT9	
ENSMUST00000185187	ENSMUSG00000061762	6	7554879	7565834	1	6	9	7	23	6	5	0	0	0	0	0	Q149W7	P41539
ENSMUST00000185188	ENSMUSG00000009621	2	27262104	27427033	-1	10	19	105	53	12	6	0	0	0	0	0	Q7TSI6	
ENSMUST00000185193						1	6	2	6	5	4	1	2	5	0	3		
ENSMUST00000185197						40	20	43	238	50	29	0	0	0	0	0		
ENSMUST00000185198	ENSMUSG00000026594	1	156804166	156939626	-1	2	2	1	2	1	1	0	0	0	0	2		Q9ERD6
ENSMUST00000185199						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185200	ENSMUSG00000079018	15	75044018	75048830	-1	1	0	0	7	3	0	10	56	21	22	11	A0A087WRG9	
ENSMUST00000185201						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000185202						1	2	0	3	2	2	0	0	0	0	0		
ENSMUST00000185205						0	2	0	0	0	0	0	5	0	0	0		
ENSMUST00000185208						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185209						0	1	0	0	0	0	0	0	0	1	0		
ENSMUST00000185210						3	3	5	1	2	1	0	0	0	1	1		
ENSMUST00000185212						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185214						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000185215						20	22	27	78	21	12	0	0	0	0	2		
ENSMUST00000185219	ENSMUSG00000052419	6	13867735	13871518	-1	9	4	2	2	7	0	2	14	2	7	2	F2Z3Y9	
ENSMUST00000185220	ENSMUSG00000100586	7	14560699	14562362	-1	5	3	2	0	0	0	0	0	0	0	0	A0A087WR36	
ENSMUST00000185223						4	6	5	3	3	3	0	0	0	0	0		
ENSMUST00000185224						0	0	4	0	1	0	2	1	0	3	0		
ENSMUST00000185225						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185228						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000185229						2	2	0	1	1	0	0	0	0	0	0		
ENSMUST00000185230						0	0	0	27	0	7	2	11	0	2	0		
ENSMUST00000185231	ENSMUSG00000037503	1	34813219	34843065	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNR1	
ENSMUST00000185232						0	0	0	0	1	0	6	0	0	0	0		
ENSMUST00000185233	ENSMUSG00000026409	1	130689182	130729253	-1	5	6	7	92	4	3	24	98	49	8	56	Q6GTL7	
ENSMUST00000185234	ENSMUSG00000050711	1	79434669	79440120	-1	0	0	19	0	0	0	0	0	0	1	0	Q4W8U9	
ENSMUST00000185235						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000185239	ENSMUSG00000047907	2	169633013	170071816	1	5	4	2	3	0	2	0	0	0	0	0	A0A087WS38	
ENSMUST00000185240	ENSMUSG00000100892	Y	38476061	38502238	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000185241						0	1	8	16	3	1	0	0	0	0	0		
ENSMUST00000185244						0	1	0	3	0	0	0	0	0	0	0		
ENSMUST00000185245	ENSMUSG00000102122	Y	50608251	50634461	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000185247						7	7	15	195	16	7	0	0	5	3	1		
ENSMUST00000185249						0	15	45	0	19	11	0	0	0	0	0		
ENSMUST00000185251	ENSMUSG00000026260	1	92439010	92473860	-1	0	0	0	0	0	0	0	0	2	0	0	A0A087WR38	
ENSMUST00000185253	ENSMUSG00000068349	15	74813452	74818815	-1	0	0	0	1	2	0	0	1	0	0	0	A0A087WQL5	
ENSMUST00000185254						7	8	11	7	6	2	0	3	0	0	0		
ENSMUST00000185256						9	7	19	8	12	7	0	0	0	0	0		
ENSMUST00000185257						0	0	0	0	0	0	2	4	5	20	15		
ENSMUST00000185258	ENSMUSG00000049252	2	40595246	42653624	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPQ4	
ENSMUST00000185259						0	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000185260	ENSMUSG00000070738	1	87853287	87945180	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ75	
ENSMUST00000185261						6	10	3	4	4	6	0	0	0	0	0		
ENSMUST00000185262						4	2	4	2	3	1	0	0	0	0	0		
ENSMUST00000185263	ENSMUSG00000025949	1	65186683	65278695	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS78	
ENSMUST00000185264						2	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000185265	ENSMUSG00000026021	1	59586558	59670834	-1	0	0	0	0	0	0	0	0	0	7	0	A0A087WRQ4	
ENSMUST00000185266						1	1	4	3	2	2	0	0	0	0	0		
ENSMUST00000185267						12	12	38	21	12	7	0	5	5	1	6		
ENSMUST00000185269	ENSMUSG00000026131	1	33908225	34308661	1	33	5	55	0	36	2	0	3	9	4	159	A0A087WSP0	
ENSMUST00000185273						38	36	106	48	60	23	2	12	9	1	12		
ENSMUST00000185275						8	5	21	16	11	7	3	10	6	4	27		
ENSMUST00000185276						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000185277						3	0	4	3	3	3	0	0	0	0	0		
ENSMUST00000185278						0	2	3	38	0	0	0	0	0	0	0		
ENSMUST00000185279						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000185280	ENSMUSG00000026341	1	125392905	125435727	-1	2	0	0	2	0	0	2	0	3	0	0	A0A087WQ83	
ENSMUST00000185282						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185284						6	2	6	6	6	3	0	0	0	0	0		
ENSMUST00000185285						4	3	3	1	1	1	0	0	0	0	0		
ENSMUST00000185291						8	6	33	9	7	5	0	0	1	1	1		
ENSMUST00000185296						24	0	24	0	32	8	0	0	0	0	0		
ENSMUST00000185297	ENSMUSG00000034973	9	86467154	86555923	1	1	1	0	0	0	0	3	24	0	0	0	A0A087WQM4	
ENSMUST00000185298						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000185299						0	2	6	9	4	1	2	2	0	5	4		
ENSMUST00000185301	ENSMUSG00000079036	12	87425840	87444017	-1	2	0	0	88	7	0	0	0	0	0	0	Q5XLJ1	
ENSMUST00000185305	ENSMUSG00000032555	9	103305215	103350428	1	0	0	0	0	0	0	0	3	0	9	0	A0A087WS20	
ENSMUST00000185306	ENSMUSG00000060036	15	80077794	80091868	-1	1	0	12	81	2	0	0	0	0	2	0	A0A087WQK0	
ENSMUST00000185307	ENSMUSG00000047728	15	75216376	75222661	1	3	2	10	2	2	0	0	1	0	3	2	A0A087WQT1	
ENSMUST00000185309						0	2	0	9	7	3	0	0	0	1	0		
ENSMUST00000185314						16	14	16	14	11	11	0	0	0	0	0		
ENSMUST00000185315	ENSMUSG00000066456	9	83109948	83146685	-1	9	8	6	57	15	6	0	3	0	8	7		Q9DCB1
ENSMUST00000185316						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185317						0	0	0	12	0	0	7	9	16	11	0		
ENSMUST00000185325						1	1	12	5	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000185326	ENSMUSG00000073962	7	102965102	102975160	1	2	3	3	2	4	2	0	0	0	0	0	A0A0G2JDQ4	
ENSMUST00000185327	ENSMUSG00000096769	Y	51125220	51151484	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPJ9	
ENSMUST00000185328						5	5	6	3	10	4	0	0	0	0	0		
ENSMUST00000185329						10	11	18	12	8	7	0	0	0	0	0		
ENSMUST00000185330						7	6	4	5	5	2	0	0	0	0	0		
ENSMUST00000185331	ENSMUSG00000055322	1	73910231	74124449	-1	0	0	0	0	0	0	0	0	0	0	24	A0A087WRU0	
ENSMUST00000185332						53	35	51	857	66	54	54	37	40	20	181		
ENSMUST00000185333	ENSMUSG00000038077	6	126708329	126740674	-1	10	0	33	270	0	4	0	0	0	0	0		Q61923
ENSMUST00000185334	ENSMUSG00000042210	9	106440051	106447678	-1	0	0	0	0	0	0	0	10	0	9	3	E9Q136	
ENSMUST00000185336	ENSMUSG00000041506	9	106475963	106485424	1	0	0	12	0	2	0	0	0	0	0	0	A0A087WS95	
ENSMUST00000185337						1	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000185338	ENSMUSG00000094746	Y	79319565	79345707	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000185340	ENSMUSG00000099740	Y	80926995	80953258	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP44	
ENSMUST00000185341						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000185342						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185343	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	4	0	10	19	0	0	A0A087WQG4	
ENSMUST00000185344						0	0	0	4	0	4	0	0	0	0	0		
ENSMUST00000185345	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	2	2	0	0	0	0	0	0	0	A0A087WRZ6	
ENSMUST00000185347	ENSMUSG00000042073	9	106447788	106452922	1	0	4	3	2	4	0	0	0	0	0	2	A0A087WQN8	
ENSMUST00000185348	ENSMUSG00000094081	Y	7632774	7638489	-1	0	0	0	0	0	0	0	0	0	0	0	J3QK38	
ENSMUST00000185349						3	2	0	2	2	0	0	2	3	0	3		
ENSMUST00000185352						42	59	116	64	39	32	1	40	6	35	20		
ENSMUST00000185353						13	8	34	23	13	14	0	0	7	0	0		
ENSMUST00000185354	ENSMUSG00000091402	12	111979111	111981317	-1	4	0	0	0	7	2	0	0	0	0	0	A0A087WSC5	
ENSMUST00000185355	ENSMUSG00000025223	19	46032593	46045214	-1	0	0	0	0	0	0	0	0	0	0	0		P70662
ENSMUST00000185356	ENSMUSG00000026479	1	153122756	153186447	-1	35	35	37	0	16	0	0	0	0	8	24	G5E874	
ENSMUST00000185357						15	0	0	5	22	0	0	0	0	0	0		
ENSMUST00000185358						5	6	12	4	3	0	0	0	0	0	0		
ENSMUST00000185359						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000185361	ENSMUSG00000052419	6	13867735	13871518	-1	0	0	0	7	0	1	176	614	153	521	74	F2Z3Y9	
ENSMUST00000185362	ENSMUSG00000018196	1	143716338	143749676	1	0	0	0	485	69	0	31	124	113	18	37	A2A5W4	Q923X4
ENSMUST00000185363						39	22	211	24	20	19	1	0	1	0	1		
ENSMUST00000185367						1006	810	8128	3379	1221	763	26	50	37	22	56		
ENSMUST00000185368						0	0	0	0	0	0	1	0	3	0	0		
ENSMUST00000185369						97	94	214	147	152	95	4	17	3	9	17		
ENSMUST00000185370	ENSMUSG00000029797	6	48448229	48501250	1	0	5	0	0	4	2	0	1	0	0	1	A0A087WNT4	
ENSMUST00000185371						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185372	ENSMUSG00000079018	15	75044018	75048830	-1	2	1	3	10	7	0	12	31	3	18	3	A0A087WPW7	
ENSMUST00000185373						14	9	39	12	11	6	0	0	0	0	0		
ENSMUST00000185374	ENSMUSG00000032418	9	86581371	86695953	-1	19	14	21	3	19	10	0	0	0	0	0	Q3TQP6	
ENSMUST00000185375						15	11	22	567	24	19	41	150	119	14	87		
ENSMUST00000185376						2	3	8	4	6	1	2	8	2	0	11		
ENSMUST00000185377						14	5	17	8	19	8	0	4	1	2	0		
ENSMUST00000185381	ENSMUSG00000100617	1	117965939	117986884	1	1	2	1	0	2	2	0	0	0	0	0	A0A087WS64	
ENSMUST00000185382						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000185383	ENSMUSG00000009545	7	143106362	143427042	1	7	0	5	0	3	2	0	0	0	0	0	A0A087WNY7	
ENSMUST00000185384	ENSMUSG00000078784	3	14606284	14611285	-1	1	0	2	4	0	0	42	126	19	144	15	G3UW58	
ENSMUST00000185386						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000185387						2	0	19	0	4	0	5	0	1	0	0		
ENSMUST00000185389						162	208	579	314	159	90	4	16	21	5	16		
ENSMUST00000185391						19	11	13	13	35	14	1	0	0	0	5		
ENSMUST00000185392						5	2	0	18	0	1	0	1	1	0	0		
ENSMUST00000185393	ENSMUSG00000079658	1	16641725	16657042	-1	0	3	0	0	0	0	71	513	112	213	52	A0A087WQE6	
ENSMUST00000185394	ENSMUSG00000019813	10	41718840	41809871	-1	7	2	17	0	5	2	0	0	0	0	0	A0A087WRG5	
ENSMUST00000185397						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185398	ENSMUSG00000054387	1	132959484	133030561	-1	0	0	0	0	0	0	0	0	9	0	11	A0A087WQ90	
ENSMUST00000185399	ENSMUSG00000066584	7	34011921	34013942	-1	0	0	5	0	1	0	0	0	0	0	0	A0A087WRN7	
ENSMUST00000185400						1	3	4	0	0	0	0	48	0	69	0		
ENSMUST00000185401						59	50	347	201	73	49	9	27	15	0	32		
ENSMUST00000185403	ENSMUSG00000026203	1	75236406	75245692	1	0	0	0	0	0	0	0	0	5	0	0	A0A087WPZ9	
ENSMUST00000185404						2	1	2	1	2	4	0	0	0	0	0		
ENSMUST00000185405	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP42	
ENSMUST00000185406	ENSMUSG00000025515	7	141690340	141754693	1	30	16	28	51	27	17	0	0	0	0	0	A0A087WSG8	
ENSMUST00000185407	ENSMUSG00000099900	7	33518481	33520458	-1	0	0	1	4	3	0	0	0	0	0	0	A0A087WQA9	
ENSMUST00000185408						14	14	24	2	2	3	48	2785	19	1150	267		
ENSMUST00000185411						125	116	291	145	183	71	12	20	11	1	12		
ENSMUST00000185412	ENSMUSG00000025968	1	63143596	63176833	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR47	
ENSMUST00000185413						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000185415						0	0	10	0	0	0	0	0	0	0	0		
ENSMUST00000185417						21	16	90	164	39	17	0	0	0	0	0		
ENSMUST00000185418						0	0	0	0	0	0	6	8	20	0	13		
ENSMUST00000185419	ENSMUSG00000026209	1	75307896	75317990	-1	15	10	10	13	17	14	25	61	37	7	48	Q8BPW9	
ENSMUST00000185421	ENSMUSG00000026271	1	92950865	92986391	1	1	0	1	1	1	2	0	2	1	0	0	A0A087WPK8	
ENSMUST00000185422						0	1	1	4	2	0	0	1	0	0	0		
ENSMUST00000185423	ENSMUSG00000078784	3	14606284	14611285	-1	0	0	0	0	0	0	0	11	0	0	0	A0A087WNL9	
ENSMUST00000185426						0	0	5	0	4	0	1	0	0	0	0		
ENSMUST00000185429						38	27	78	43	58	35	63	269	130	37	194		
ENSMUST00000185430						57	36	104	61	64	30	0	0	1	0	1		
ENSMUST00000185431						71	53	171	110	97	35	1	8	4	0	5		
ENSMUST00000185432	ENSMUSG00000079424	5	95305911	95343917	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSL7	
ENSMUST00000185433						22	35	121	14	49	18	1	3	7	1	10		
ENSMUST00000185434	ENSMUSG00000034157	12	86947043	86965362	1	1	10	17	0	0	0	0	0	32	5	0	A0A087WRF0	
ENSMUST00000185435						27	21	53	26	20	14	0	2	2	1	10		
ENSMUST00000185436	ENSMUSG00000079330	1	132191431	132259227	1	0	0	0	3	0	0	0	0	0	0	0	A0A087WR04	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000185437						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000185440						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185444						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185445	ENSMUSG00000026425	1	131285251	131527352	-1	0	0	3	0	1	1	6	0	2	1	3	A0A087WRV4	
ENSMUST00000185446						21	17	83	20	13	12	0	1	0	0	0		
ENSMUST00000185447						6	9	15	7	10	3	9	35	35	4	25		
ENSMUST00000185448	ENSMUSG00000026200	1	75198236	75210813	-1	0	0	0	7	0	0	0	0	6	0	0	A0A087WRY5	
ENSMUST00000185449						27	29	55	401	38	24	4	39	14	3	15		
ENSMUST00000185450	ENSMUSG00000029673	5	131437333	132543344	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSK2	
ENSMUST00000185452						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000185453	ENSMUSG00000025932	1	14168954	14310235	-1	1	0	0	0	0	0	1	0	0	0	0	A0A087WSJ4	
ENSMUST00000185454						7	6	5	10	12	2	0	1	1	0	0		
ENSMUST00000185457	ENSMUSG00000074217	8	84010222	84012171	-1	0	1	1	37	0	0	0	0	0	0	0	A0A087WQC3	
ENSMUST00000185459	ENSMUSG00000032359	9	90054152	90076089	1	0	0	0	0	2	0	104	619	114	241	82	A0A087WR20	
ENSMUST00000185462	ENSMUSG00000093865	3	129787881	129804030	-1	9	6	16	15	13	9	0	0	0	0	1	W8DXL4	
ENSMUST00000185466						2	0	1	4	1	0	87	123	86	114	100		
ENSMUST00000185467						3	1	2	0	4	0	0	0	0	0	0		
ENSMUST00000185468						0	0	2	4	0	0	0	0	0	0	0		
ENSMUST00000185469	ENSMUSG00000037503	1	34813219	34843065	-1	0	0	0	0	1	1	0	0	0	0	0	A0A087WSR1	
ENSMUST00000185470	ENSMUSG00000047606	9	89725239	89738475	-1	13	8	32	2	20	10	0	0	0	0	0	B2RPW9	Q8BLB8
ENSMUST00000185471						9	3	0	0	7	0	0	5	13	0	13		
ENSMUST00000185472	ENSMUSG00000032463	9	98986373	99002021	1	1	0	0	0	0	2	11	86	32	35	19	A0A087WRH2	
ENSMUST00000185473						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000185474						6	6	3	204	13	8	0	2	0	1	1		
ENSMUST00000185475	ENSMUSG00000100296	13	22591980	22592930	-1	2	1	0	0	1	0	0	0	0	0	0	Q8R276	
ENSMUST00000185476						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185477						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000185479	ENSMUSG00000053128	9	44066327	44113517	-1	5	2	3	77	2	1	0	0	0	0	0		Q8BUH7
ENSMUST00000185481	ENSMUSG00000045411	7	44246722	44252319	1	0	0	0	0	0	0	4	0	0	1	0	A0A087WPT9	
ENSMUST00000185482	ENSMUSG00000026280	1	93751500	93790610	1	0	0	0	0	0	0	347	245	169	60	99	A0A087WRT0	
ENSMUST00000185483	ENSMUSG00000043015	1	52630703	52651919	1	2	0	0	0	2	1	0	5	0	0	0		Q8CB65
ENSMUST00000185484						4	3	3	7	2	0	0	0	0	0	0		
ENSMUST00000185488	ENSMUSG00000071653	19	8888853	8890881	1	1	0	0	0	0	0	45	99	101	255	69	A0A087WQJ5	
ENSMUST00000185489						5	1	6	4	3	3	1	1	2	8	0		
ENSMUST00000185491						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185493	ENSMUSG00000018189	1	143777272	143807466	1	0	2	0	0	0	0	28	77	85	75	64	A0A087WP81	
ENSMUST00000185495						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185496						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185498	ENSMUSG00000026275	1	93342854	93373489	1	0	0	0	0	0	0	14	54	22	18	4	A0A087WRA7	
ENSMUST00000185502	ENSMUSG00000056222	13	57421195	57908314	-1	21	20	37	26	33	14	0	0	0	0	0	Q6DIC9	
ENSMUST00000185503	ENSMUSG00000032560	9	104151282	104262930	-1	6	2	0	0	0	0	0	0	0	0	0	A0A087WRC9	
ENSMUST00000185504						0	0	6	1	3	3	0	0	0	0	0		
ENSMUST00000185505						3	2	0	53	3	1	0	0	0	0	0		
ENSMUST00000185507	ENSMUSG00000023495	9	106453291	106464012	1	0	0	6	0	0	2	0	0	0	0	0	A0A087WRJ6	
ENSMUST00000185508						2	0	1	3	1	0	0	0	0	0	0		
ENSMUST00000185509						0	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000185510						3	8	5	4	7	2	1	0	3	1	1		
ENSMUST00000185511						0	0	6	2	2	1	0	0	0	0	0		
ENSMUST00000185513						3	5	2	2	2	0	0	0	0	0	0		
ENSMUST00000185514	ENSMUSG00000001248	7	31130127	31155896	-1	0	3	0	8	0	0	0	2	0	0	0	A0A087WP91	
ENSMUST00000185515	ENSMUSG00000032407	9	95456898	95511996	-1	1	0	0	0	0	0	0	0	0	0	0	A0A087WR93	
ENSMUST00000185517						0	6	5	0	7	4	0	0	0	0	0		
ENSMUST00000185518						7	1	7	15	6	3	0	1	3	0	1		
ENSMUST00000185519						0	2	1	0	1	0	0	10	2	0	4		
ENSMUST00000185520	ENSMUSG00000025986	1	46807544	46892852	-1	0	0	0	0	0	1	2	0	0	0	0	A0A087WRC8	
ENSMUST00000185521						0	1	10	0	0	0	11	14	13	2	7		
ENSMUST00000185522						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185523						13	6	7	22	1	3	6	18	15	0	13		
ENSMUST00000185524	ENSMUSG00000032468	9	99478372	99568899	-1	5	0	0	7	0	0	3	0	10	20	12		Q9DBR3
ENSMUST00000185525						10	8	11	84	9	5	0	0	0	0	5		
ENSMUST00000185526	ENSMUSG00000055827	15	63857724	63878558	-1	22	4	0	15	17	13	0	0	1	0	2		Q8CB12
ENSMUST00000185527	ENSMUSG00000042073	9	106447788	106452922	1	2	0	3	0	0	4	0	0	1	0	0	A0A087WPF8	
ENSMUST00000185528						19	23	20	345	49	38	4	5	9	2	9		
ENSMUST00000185529						1	4	3	1	1	1	0	0	0	0	0		
ENSMUST00000185530						2	0	1	2	6	0	0	0	1	0	2		
ENSMUST00000185531	ENSMUSG00000026305	1	90998737	91128944	1	2	0	13	6	2	0	0	0	0	0	0	A0A087WNU6	
ENSMUST00000185532						5	0	11	1	7	5	0	0	0	1	0		
ENSMUST00000185533	ENSMUSG00000032565	9	105128903	105131805	-1	137	146	1751	252	139	58	6	20	13	1	4	A0A087WSB5	
ENSMUST00000185534	ENSMUSG00000026107	1	51465862	51478425	-1	0	0	0	0	0	0	65	321	269	361	208		Q8BGW5
ENSMUST00000185539	ENSMUSG00000018189	1	143777272	143807466	1	0	1	0	0	0	0	22	162	3	2	7	A0A087WRL3	
ENSMUST00000185542						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185543						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185544						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185545						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185547						0	1	1	3	0	1	0	0	0	0	0		
ENSMUST00000185549						4	3	6	4	12	5	0	0	0	0	0		
ENSMUST00000185550	ENSMUSG00000093993	Y	65377690	65403917	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQC7	
ENSMUST00000185551						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185552						8	6	9	0	7	0	0	0	0	0	0		
ENSMUST00000185553	ENSMUSG00000101892	15	58022259	58034325	-1	2	0	0	99	0	1	0	0	0	2	0	A0A087WRX1	
ENSMUST00000185556						0	0	49	0	0	3	0	0	2	0	2		
ENSMUST00000185557						5	4	6	2	2	0	0	0	0	0	0		
ENSMUST00000185558	ENSMUSG00000078572	11	120098928	120100705	1	0	0	0	26	0	0	4	24	4	105	8	A0A087WQY7	
ENSMUST00000185559						0	0	2	170	0	0	0	0	0	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000185560	ENSMUSG00000026347	1	127486546	127679548	-1	79	65	172	381	120	63	0	2	0	0	8		Q8C996
ENSMUST00000185561						17	9	39	449	20	9	0	1	0	0	0		
ENSMUST00000185562						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000185563						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185565	ENSMUSG00000101933	Y	36709098	36735290	-1	0	0	0	1	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000185566	ENSMUSG00000032417	9	86571991	86574899	1	2	0	0	8	0	0	0	30	14	50	15	Q14BN8	
ENSMUST00000185567						3	3	4	2	2	0	0	0	4	0	6		
ENSMUST00000185569	ENSMUSG00000026223	1	85894281	85908675	1	0	0	0	0	0	0	199	216	109	98	191	A0A087WRM2	
ENSMUST00000185570						4	9	4	0	8	4	0	4	9	13	7		
ENSMUST00000185571						4	1	4	2	2	0	0	0	0	0	0		
ENSMUST00000185572						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185573						1	2	1	2	7	4	0	1	0	0	1		
ENSMUST00000185574						4	5	15	10	17	4	0	0	0	0	7		
ENSMUST00000185575	ENSMUSG00000099792	Y	78212993	78239189	1	0	0	2	0	0	0	0	0	0	0	0	A0A087WP44	
ENSMUST00000185576	ENSMUSG00000095242	Y	10322618	10324589	-1	3	0	0	3	0	0	0	0	0	0	0	J3QM72	
ENSMUST00000185578						153	186	446	199	228	100	7	28	12	3	17		
ENSMUST00000185579						2	4	1	70	6	0	3	18	7	15	3		
ENSMUST00000185580	ENSMUSG00000074139	9	92309377	92357876	1	0	0	2	0	0	0	0	0	0	0	0	A0A087WPD9	
ENSMUST00000185581	ENSMUSG00000057855	16	89084015	89084534	1	0	0	4	6	0	0	0	0	0	0	0	A0A087WQL6	
ENSMUST00000185582	ENSMUSG00000069601	10	69533772	70027438	1	0	0	0	2	0	0	0	0	0	0	0	A0A087WRP9	
ENSMUST00000185584						3	4	15	3	3	4	0	0	0	0	0		
ENSMUST00000185589						3	6	13	7	13	7	27	119	27	10	81		
ENSMUST00000185591						6	2	0	0	3	0	27	32	36	0	27		
ENSMUST00000185594	ENSMUSG00000025958	1	64532645	64604548	1	0	2	0	59	0	0	0	40	27	14	23	Q543W0	Q01147
ENSMUST00000185595	ENSMUSG00000041536	12	104112724	104121896	1	5	0	18	0	0	0	0	0	0	0	0	H7BWY0	
ENSMUST00000185596	ENSMUSG00000026425	1	131285251	131527352	-1	1	6	14	9	11	3	37	120	43	0	59	A0A087WSQ1	
ENSMUST00000185597						0	3	0	1	0	0	0	0	0	0	0		
ENSMUST00000185598						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185601	ENSMUSG00000026437	1	132112237	132139684	-1	0	0	0	0	0	0	5	3	1	0	0	A0A087WQ42	
ENSMUST00000185604						5	1	11	13	3	2	0	0	0	0	2		
ENSMUST00000185606	ENSMUSG00000036766	1	84369839	84696221	-1	0	1	3	0	0	0	0	0	0	0	0	A0A087WSC4	
ENSMUST00000185609						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000185610						22	22	26	176	26	7	4	10	12	0	17		
ENSMUST00000185612	ENSMUSG00000025481	7	140835018	140837971	1	2	2	0	1	0	0	0	0	0	15	0		Q9CRB3
ENSMUST00000185614						21	23	71	29	20	16	11	21	6	1	39		
ENSMUST00000185615						0	0	0	0	3	4	0	0	0	0	0		
ENSMUST00000185616						18	32	46	27	33	18	0	1	4	0	2		
ENSMUST00000185618	ENSMUSG00000039168	15	31224314	31274341	1	0	0	5	0	0	1	3	0	0	0	0	A0A087WRC6	
ENSMUST00000185619						6	6	13	46	8	5	0	1	1	0	2		
ENSMUST00000185621	ENSMUSG00000010453	1	36335730	36369181	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWN0	
ENSMUST00000185623						22	7	8	4	12	5	0	0	0	0	0		
ENSMUST00000185624						0	2	4	5	0	3	0	8	0	2	0		
ENSMUST00000185626						0	1	0	1	1	0	0	0	1	0	0		
ENSMUST00000185628						2	0	1	0	0	3	0	0	0	0	0		
ENSMUST00000185629						15	12	20	19	13	3	1	0	0	0	0		
ENSMUST00000185632						6	0	8	2	7	1	0	0	0	0	0		
ENSMUST00000185633	ENSMUSG00000032410	9	95954760	96057803	1	52	57	198	70	59	33	312	726	697	108	544	A0A087WQN7	
ENSMUST00000185634						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185636	ENSMUSG00000101286	Y	82225227	82251419	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000185639						1	3	0	1	2	0	0	0	0	0	0		
ENSMUST00000185640						0	3	0	0	2	0	0	0	0	0	0		
ENSMUST00000185641	ENSMUSG00000062683	15	102662864	102672352	-1	11	10	0	32	22	0	546	434	288	1096	244		P56383
ENSMUST00000185642						8	22	0	10	12	3	0	0	0	0	0		
ENSMUST00000185643						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185644	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	0	0	0	0	0	0	0	0	Q8BHD2	
ENSMUST00000185645						0	0	0	71	1	1	0	0	0	1	0		
ENSMUST00000185646						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185647						2	3	0	3	0	0	0	1	0	0	0		
ENSMUST00000185649						5	2	14	5	11	1	0	0	0	0	0		
ENSMUST00000185651	ENSMUSG00000076758	14	52427928	52428876	1	2	1	0	0	1	0	0	1	0	0	0	A0A087WRQ3	
ENSMUST00000185653						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000185654	ENSMUSG00000026203	1	75236406	75245692	1	0	0	0	34	0	0	0	2	0	0	6	A0A087WR37	
ENSMUST00000185655						0	0	0	0	7	0	0	0	0	0	0		
ENSMUST00000185656	ENSMUSG00000005267	11	62700356	62731905	-1	0	13	45	7	13	5	0	6	0	0	4		Q9EQB9
ENSMUST00000185657						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185658						2	4	3	1	2	0	0	0	0	0	0		
ENSMUST00000185659						3	2	12	6	4	7	0	0	0	0	0		
ENSMUST00000185660						6	6	2	2	4	5	0	0	0	0	0		
ENSMUST00000185661						10	7	12	17	14	5	18	19	27	6	24		
ENSMUST00000185664	ENSMUSG00000032261	9	83548327	83638801	1	2	3	4	9	3	0	0	0	0	0	3	A0A087WQX3	
ENSMUST00000185665	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNZ9	
ENSMUST00000185666	ENSMUSG00000026058	1	32172714	32658568	1	1	1	0	0	0	0	0	0	0	0	0	A0A087WR32	
ENSMUST00000185667	ENSMUSG00000100467	Y	30706533	30738561	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRT9	
ENSMUST00000185668						0	9	22	15	26	19	13	0	18	0	39		
ENSMUST00000185670						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185671						2	0	0	2	2	0	0	0	0	0	0		
ENSMUST00000185672						8	5	9	4	5	6	0	3	3	0	0		
ENSMUST00000185673	ENSMUSG00000041459	4	148612382	148627019	-1	2	2	1	11	1	0	0	2	7	5	14	A0A087WSE4	
ENSMUST00000185674	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPW1	
ENSMUST00000185675	ENSMUSG00000032252	9	62057248	62122655	-1	20	0	0	0	0	7	2	64	59	0	63		Q9EPS3
ENSMUST00000185676						1	3	0	0	2	0	560	3071	1384	4492	1451		
ENSMUST00000185677						2	13	7	7	4	5	0	0	0	0	0		
ENSMUST00000185682	ENSMUSG00000034730	15	74516195	74589465	1	0	0	0	0	0	0	0	0	0	0	0	E9Q4H5	
ENSMUST00000185684						0	1	5	0	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000185685						9	3	11	0	0	1	1	0	0	5	4		
ENSMUST00000185687	ENSMUSG00000026043	1	45311538	45349706	1	2	0	0	0	2	0	0	0	0	0	9	A0A087WPS3	
ENSMUST00000185688						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185690						0	1	4	1	0	0	0	0	0	0	0		
ENSMUST00000185691	ENSMUSG00000072754	5	110344730	110356094	1	0	5	0	0	0	0	0	0	0	0	0		Q3URS3
ENSMUST00000185692	ENSMUSG00000026319	1	105663861	105755191	1	0	4	6	0	5	5	47	441	0	32	0	A0A087WPW3	
ENSMUST00000185696						15	10	14	14	9	3	0	0	0	0	1		
ENSMUST00000185697						3	9	32	6	9	6	2	10	5	1	4		
ENSMUST00000185698	ENSMUSG00000006007	1	150319417	150333906	1	14	6	2	1	5	6	0	0	0	0	0	A0A087WRK4	
ENSMUST00000185699						6	10	8	2	7	4	0	0	0	0	0		
ENSMUST00000185700						6	7	41	18	6	10	0	29	5	0	26		
ENSMUST00000185701						0	0	1	0	0	1	0	0	0	0	4		
ENSMUST00000185702	ENSMUSG00000055322	1	73910231	74124449	-1	0	0	0	0	0	0	36	0	13	0	0	A0A087WQ94	
ENSMUST00000185703						2	7	11	4	4	5	0	0	0	0	0		
ENSMUST00000185704						3	0	4	3	4	2	0	0	0	0	0		
ENSMUST00000185705	ENSMUSG00000099861	Y	7994833	7997168	-1	0	4	0	0	0	0	0	0	0	0	0	A0A087WSM5	
ENSMUST00000185706						13	12	28	3	10	4	1	0	0	0	1		
ENSMUST00000185707	ENSMUSG00000074102	9	106880918	106887428	-1	2	0	26	0	0	0	86	2	57	6	43	A0A087WPD2	
ENSMUST00000185708						128	94	600	191	116	71	2	84	18	7	35		
ENSMUST00000185709						2254	2431	4756	2086	2495	1300	43	186	97	20	130		
ENSMUST00000185710						1	1	1	0	2	1	0	0	0	1	0		
ENSMUST00000185713	ENSMUSG00000095135	Y	55731756	55757908	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ24	
ENSMUST00000185714	ENSMUSG00000026358	1	144242296	144249242	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS51	
ENSMUST00000185715	ENSMUSG00000002102	2	91054009	91066369	1	0	0	0	0	0	0	91	223	151	346	123	A0A087WPH7	
ENSMUST00000185717						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000185718						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000185719						0	0	2	1	0	0	0	0	1	0	2		
ENSMUST00000185720						7	3	4	0	5	1	10	32	13	4	19		
ENSMUST00000185721	ENSMUSG00000032555	9	103305215	103350428	1	0	1	0	0	0	0	0	11	39	10	37	A0A087WS55	
ENSMUST00000185723						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185724	ENSMUSG00000030213	6	136506167	136610862	1	1	0	3	2	4	8	19	0	20	0	28	A0A087WR39	
ENSMUST00000185725						6	9	6	0	0	6	0	0	0	0	0		
ENSMUST00000185728						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185730						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185731	ENSMUSG00000044098	3	103914120	103966636	1	2	2	1	621	11	6	0	0	22	0	0	A0A0H2UH30	
ENSMUST00000185732	ENSMUSG00000025968	1	63143596	63176833	-1	0	1	0	3	4	0	2	3	0	9	0	A0A087WQR0	
ENSMUST00000185733	ENSMUSG00000006304	1	74236084	74268209	1	1	0	1	7	2	0	0	0	0	3	0	A0A087WRT2	
ENSMUST00000185734						561	638	964	549	529	258	12	26	25	3	14		
ENSMUST00000185735						2	6	0	2	10	4	0	0	0	1	0		
ENSMUST00000185736						37	37	49	371	60	25	1	15	7	0	17		
ENSMUST00000185739	ENSMUSG00000020659	12	31484829	31499616	-1	0	0	0	0	0	0	9	0	18	0	18	A0A087WSE1	
ENSMUST00000185742						16	15	19	219	31	14	2	1	0	5	3		
ENSMUST00000185743						2	5	11	2	9	4	0	2	6	0	0		
ENSMUST00000185744						5	2	33	4	5	2	0	0	1	2	0		
ENSMUST00000185745						2	0	0	82	4	4	0	0	0	0	0		
ENSMUST00000185748	ENSMUSG00000019429	7	30854330	30856178	-1	7	4	8	11	11	4	0	0	1	0	0	Q08AU6	Q3UFD7
ENSMUST00000185749						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185750						14	17	11	29	16	6	1	3	4	0	6		
ENSMUST00000185752	ENSMUSG00000003051	1	135253575	135258568	-1	0	0	0	0	0	6	0	9	0	1	2		Q3UPW2
ENSMUST00000185753						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185754						9	1	4	2	4	3	6	28	15	4	21		
ENSMUST00000185755	ENSMUSG00000101381	X	3955054	3957002	-1	0	0	10	0	0	0	0	0	0	0	0	A0A087WSN2	
ENSMUST00000185756						5	0	10	1	4	3	0	0	0	0	0		
ENSMUST00000185757						0	1	0	0	4	2	0	0	0	0	0		
ENSMUST00000185758	ENSMUSG00000094445	7	52011683	52015728	-1	0	2	0	0	0	0	0	0	0	0	0	A0A087WQJ9	
ENSMUST00000185759						28	36	115	64	45	13	0	5	3	1	3		
ENSMUST00000185760						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185762	ENSMUSG00000102018	15	76009888	76046111	1	0	0	2	5	2	2	0	0	0	0	0	A0A087WSC9	
ENSMUST00000185763	ENSMUSG00000026253	1	87204657	87212694	1	4	4	1	3	8	2	0	0	0	0	0	A0A087WP27	
ENSMUST00000185766						2	2	1	15	10	2	0	0	0	0	0		
ENSMUST00000185767	ENSMUSG00000052293	13	100651579	100656060	1	0	1	0	8	0	0	7	27	11	38	0	A0A087WR08	
ENSMUST00000185770						4	3	2	4	4	2	0	0	0	0	0		
ENSMUST00000185771	ENSMUSG00000079658	1	16641725	16657042	-1	0	0	0	0	0	0	0	0	0	7	5		P83940
ENSMUST00000185772	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	7	0	0	0	0	0	0	0	A0A087WNS6	
ENSMUST00000185773						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185775						10	9	41	108	9	10	0	0	0	0	4		
ENSMUST00000185776	ENSMUSG00000095153	Y	84097279	84123494	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR14	
ENSMUST00000185777						11	11	10	5	14	2	0	0	0	0	0		
ENSMUST00000185778						0	5	8	2	5	1	0	3	0	1	0		
ENSMUST00000185779	ENSMUSG00000023495	9	106453291	106464012	1	0	0	0	0	0	3	6	0	0	0	0	A0A087WRH3	
ENSMUST00000185780	ENSMUSG00000016918	1	12692277	12861192	1	0	4	0	0	0	3	0	0	0	0	0	A0A087WR86	
ENSMUST00000185781						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000185782						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185783	ENSMUSG00000034157	12	86947043	86965362	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRZ3	
ENSMUST00000185785	ENSMUSG00000026234	1	86344719	86359400	-1	5	0	9	191	6	1	4	3	0	13	9	A0A087WRM5	
ENSMUST00000185787						13	8	11	21	20	9	0	0	0	0	0		
ENSMUST00000185788	ENSMUSG00000026782	1	60409619	60481158	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNT3	
ENSMUST00000185790	ENSMUSG00000043015	1	52630703	52651919	1	0	0	0	0	0	2	0	13	48	1	96	A0A087WQU8	
ENSMUST00000185791						0	6	0	1	0	1	0	0	0	0	0		
ENSMUST00000185792						4	2	3	5	6	3	0	0	0	0	0		
ENSMUST00000185795	ENSMUSG00000041417	13	101680563	101768217	-1	1	1	1	37	2	0	3	2	4	0	8	P70305	
ENSMUST00000185796	ENSMUSG00000068130	2	150407141	150451486	-1	0	0	0	0	0	0	0	4	0	2	0	A0A087WQ98	
ENSMUST00000185797	ENSMUSG00000026209	1	75307896	75317990	-1	0	2	0	36	0	3	0	0	0	0	0	Q3TVK3	
ENSMUST00000185799	ENSMUSG00000056267	9	99243367	99300404	1	1	2	0	28	0	0	0	0	7	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000185800	ENSMUSG00000037608	10	20312469	20344613	1	9	5	6	0	0	3	291	1019	984	1597	735		Q8K019
ENSMUST00000185802						4	1	0	0	2	3	0	0	0	0	0		
ENSMUST00000185805						4	6	30	17	13	2	0	0	0	0	0		
ENSMUST00000185806						3	6	17	12	5	2	2	6	1	6	0		
ENSMUST00000185807	ENSMUSG00000026153	1	24011093	24100341	-1	0	0	0	0	0	0	0	1	0	1	0	A0A087WQ81	
ENSMUST00000185810						0	0	0	52	0	0	0	0	0	0	1		
ENSMUST00000185811						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185816						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185817						0	0	0	6	1	0	0	0	0	0	4		
ENSMUST00000185818						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185819						7	3	7	7	8	5	0	0	0	0	0		
ENSMUST00000185821						0	0	60	0	3	0	49	462	8	0	109		
ENSMUST00000185823	ENSMUSG00000025515	7	141690340	141754693	1	0	7	0	7	17	3	0	0	0	0	0	A0A087WS13	
ENSMUST00000185824	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	53	0	0	0	A0A087WQA5	
ENSMUST00000185825						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000185826						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185827						2	1	1	3	0	0	45	122	40	37	57		
ENSMUST00000185831						2	3	9	8	6	0	0	0	0	0	0		
ENSMUST00000185833						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185834	ENSMUSG00000094475	2	175643978	175653860	1	0	0	0	0	0	0	0	0	0	0	0	F7CEW8	
ENSMUST00000185836	ENSMUSG00000046367	1	134540941	134549682	-1	3	6	7	0	0	0	0	0	0	0	0	A0A087WPH6	
ENSMUST00000185837						303	324	598	1350	242	142	7	13	14	3	14		
ENSMUST00000185838						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185839						3	3	4	10	0	0	0	0	0	0	0		
ENSMUST00000185840						1	1	3	1	0	3	0	0	0	1	3		
ENSMUST00000185841	ENSMUSG00000094445	7	52011683	52015728	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSR9	
ENSMUST00000185845						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185846						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185847	ENSMUSG00000025968	1	63143596	63176833	-1	3	0	0	0	0	0	7	0	0	0	0	A0A087WSU3	
ENSMUST00000185849	ENSMUSG00000026204	1	75247027	75264502	-1	2	0	5	0	0	0	0	0	1	0	0	A0A087WQ67	
ENSMUST00000185850						0	0	3	0	3	2	0	0	0	0	0		
ENSMUST00000185851						165	187	370	101	144	39	9	25	22	1	20		
ENSMUST00000185852	ENSMUSG00000014850	13	92211872	92355003	-1	0	1	0	1	0	0	1	0	7	13	22	A0A087WQ16	
ENSMUST00000185853	ENSMUSG00000056211	1	128103301	128237736	1	1	0	1	0	0	1	9	4	17	0	23	A0A087WP65	
ENSMUST00000185854						5	3	1	101	4	0	0	0	0	0	0		
ENSMUST00000185855						10	7	28	18	8	6	0	0	0	0	1		
ENSMUST00000185856						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185858						1	2	3	0	2	3	0	0	0	0	0		
ENSMUST00000185859						2	1	2	4	0	0	0	0	0	0	0		
ENSMUST00000185860						4	3	1	3	2	2	0	0	0	0	0		
ENSMUST00000185861	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	0	0	0	0	0	0	0	0	Q99JA5	
ENSMUST00000185863	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	0	0	0	30	38	16	7	30	A0A087WQ65	
ENSMUST00000185864						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185865						0	5	4	0	0	0	0	0	0	0	0		
ENSMUST00000185866						9	1	27	3	4	1	0	0	0	0	0		
ENSMUST00000185867						3	3	4	11	8	5	2	20	7	26	13		
ENSMUST00000185868						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185869						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000185870						1	2	0	2	2	1	0	0	0	0	0		
ENSMUST00000185871	ENSMUSG00000026117	1	36761798	36782818	1	3	3	4	83	4	1	0	0	0	0	0	A0A087WQ05	
ENSMUST00000185872						3	2	7	0	1	0	0	0	0	0	0		
ENSMUST00000185873	ENSMUSG00000032252	9	62057248	62122655	-1	0	1	0	48	3	0	1	0	0	0	0	A0A087WRK5	
ENSMUST00000185874	ENSMUSG00000023495	9	106453291	106464012	1	4	2	14	19	13	3	0	0	0	0	4	A0A087WSI1	
ENSMUST00000185877						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185879	ENSMUSG00000041144	1	46066315	46373546	1	1	0	5	0	0	0	0	0	0	1	0	A0A087WPC9	
ENSMUST00000185882						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185883						3	2	3	0	3	3	0	0	0	0	0		
ENSMUST00000185884						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000185885						0	4	0	0	0	2	0	0	0	0	0		
ENSMUST00000185886						8	7	23	3	3	3	6	59	15	10	25		
ENSMUST00000185887						92	55	374	336	96	34	0	7	2	0	5		
ENSMUST00000185891						2	0	13	0	1	4	0	0	0	0	0		
ENSMUST00000185892						0	6	0	11	4	0	0	0	0	0	0		
ENSMUST00000185893	ENSMUSG00000008136	1	43123074	43196984	-1	4	4	8	2	8	3	1	0	0	0	0	Q543D7	O70433
ENSMUST00000185894	ENSMUSG00000066442	9	89210676	89377713	1	1	0	1	0	0	1	1	0	0	1	2	A0A087WPE2	
ENSMUST00000185895						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000185896	ENSMUSG00000004945	17	5410870	5440259	-1	0	1	13	0	0	0	5	0	0	7	4		Q8VCR3
ENSMUST00000185897	ENSMUSG00000026131	1	33908225	34308661	1	0	0	13	0	31	10	0	0	0	0	12	A0A087WPR7	
ENSMUST00000185899	ENSMUSG00000033272	18	36679215	36683861	1	1	2	3	0	2	2	6	0	15	0	4	A0A087WQH8	
ENSMUST00000185901						0	3	0	0	0	0	0	8	0	8	0		
ENSMUST00000185902						1	3	3	2	9	1	0	0	0	0	0		
ENSMUST00000185903	ENSMUSG00000042305	1	134346097	134361979	-1	0	3	3	6	4	2	0	3	8	0	10	A0A087WSE5	
ENSMUST00000185904	ENSMUSG00000028451	4	42969604	42983640	1	0	0	11	0	0	0	0	0	0	0	0	A0A087WR66	
ENSMUST00000185905						10	11	9	38	14	14	0	0	0	0	0		
ENSMUST00000185906						0	1	3	0	4	0	0	0	0	0	0		
ENSMUST00000185909	ENSMUSG00000026219	1	84721189	84840516	-1	3	0	2	19	0	0	71	59	257	7	255	A0A087WQ02	
ENSMUST00000185911						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185912	ENSMUSG00000010453	1	36335730	36369181	-1	28	18	105	0	46	23	0	866	29	34	20		A2RSY1
ENSMUST00000185913	ENSMUSG00000038379	9	83834689	83872389	1	0	0	0	0	0	0	0	0	0	3	0	Q3TPW2	
ENSMUST00000185914	ENSMUSG00000101436	7	21184317	21190423	-1	10	5	10	7	11	0	0	2	0	0	1	A0A087WRH8	
ENSMUST00000185915						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185917						1	1	4	2	1	1	0	0	0	0	0		
ENSMUST00000185918						11	10	46	18	18	5	1	0	1	0	1		
ENSMUST00000185919	ENSMUSG00000034973	9	86467154	86555923	1	16	12	13	0	14	8	34	35	49	0	0	A0A087WQ48	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000185920	ENSMUSG00000026094	1	53755506	53785224	-1	1	2	0	1	0	0	35	7	45	38	0	A0A087WPR0	
ENSMUST00000185921						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000185922						7	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185923						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185924	ENSMUSG00000100972	Y	48856497	48882617	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK3	
ENSMUST00000185925						2	4	4	1	5	0	0	2	1	3	0		
ENSMUST00000185926	ENSMUSG00000096036	Y	5942460	5945031	1	65	62	31	59	12	20	1	4	5	0	4	A0A087WNP8	
ENSMUST00000185927						8	2	7	4	8	4	2	2	0	1	2		
ENSMUST00000185928						0	3	4	0	3	1	0	0	0	1	1		
ENSMUST00000185929	ENSMUSG00000032737	7	101822632	101838076	-1	0	16	73	119	41	8	99	13	154	0	184	A0A087WPT7	
ENSMUST00000185930	ENSMUSG00000032712	6	149309414	149335663	1	0	0	0	1	0	3	0	6	8	0	10		
ENSMUST00000185932						0	0	35	0	12	8	0	0	0	0	0		
ENSMUST00000185933						6	4	3	1	2	1	0	0	0	0	0		
ENSMUST00000185934						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185936						120	113	532	203	110	65	5	14	23	3	21		
ENSMUST00000185937						2	0	7	2	14	2	1	0	0	0	1		
ENSMUST00000185940	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP48	
ENSMUST00000185942	ENSMUSG00000041670	1	22286251	22805724	-1	8	0	4	5	6	0	0	0	0	0	0	A0A087WSA4	
ENSMUST00000185944						20	19	65	34	33	17	6	20	11	1	15		
ENSMUST00000185945						0	1	0	0	3	1	7	97	56	75	76		
ENSMUST00000185947						55	42	169	70	42	29	0	11	2	2	1		
ENSMUST00000185948						3	8	0	32	7	0	0	0	0	8	0		
ENSMUST00000185949	ENSMUSG00000074829	9	124291804	124312696	-1	0	0	0	0	1	0	0	1	2	9	3	A0A087WQD2	
ENSMUST00000185950						2	1	13	14	3	1	0	28	2	0	2		
ENSMUST00000185951						4	4	0	1	0	0	3	1	1	0	0		
ENSMUST00000185952						2	2	6	11	4	1	1	3	1	1	0		
ENSMUST00000185953						8	7	12	10	16	10	0	0	0	0	0		
ENSMUST00000185954						4	1	0	1	2	3	0	1	0	0	9		
ENSMUST00000185956	ENSMUSG00000027523	2	174284320	174346744	1	1	1	0	0	4	3	0	0	0	0	0		Q6R0H7
ENSMUST00000185957						2	3	0	1	2	0	0	0	0	0	0		
ENSMUST00000185958						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185961						1	1	0	1	0	0	0	0	0	2	2		
ENSMUST00000185963						1	2	2	0	3	2	0	0	0	0	0		
ENSMUST00000185964	ENSMUSG00000026116	1	36792191	36943666	-1	1	1	5	1	1	2	0	0	0	0	0	A0A0A6YW65	
ENSMUST00000185965						7	3	38	6	8	3	0	0	0	0	1		
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ENSMUST00000185967	ENSMUSG00000055024	15	81585351	81652077	1	0	0	6	0	0	0	3	0	22	0	14	A0A087WPR8	
ENSMUST00000185968	ENSMUSG00000030228	6	139587221	139969284	1	0	0	5	0	0	0	0	0	0	0	0	A0A087WQW4	
ENSMUST00000185970						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185972						2	1	1	0	4	1	0	0	0	0	4		
ENSMUST00000185975						19	15	0	12	24	8	0	0	0	0	0		
ENSMUST00000185977						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185978						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000185981						0	3	11	0	1	0	0	0	0	0	0		
ENSMUST00000185983						2	8	5	3	5	6	0	0	0	0	0		
ENSMUST00000185984						6	7	40	2	3	4	0	0	0	0	0		
ENSMUST00000185985	ENSMUSG00000001248	7	31130127	31155896	-1	0	0	28	0	0	18	811	5565	1313	162	2021		
ENSMUST00000185986	ENSMUSG00000009210	11	106365472	106377558	1	0	0	0	6	0	0	0	0	0	0	0	A0A087WQW1	
ENSMUST00000185987						2	1	3	2	0	0	3	6	0	0	11		
ENSMUST00000185988						0	5	137	0	8	0	0	0	0	0	0		
ENSMUST00000185989	ENSMUSG00000101725	Y	70292585	70303287	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSA2	
ENSMUST00000185990	ENSMUSG00000026035	1	58430994	58445486	-1	0	0	0	0	0	0	17	24	12	48	17	A0A087WPZ6	
ENSMUST00000185993						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000185994						0	0	0	13	0	0	0	0	0	0	0		
ENSMUST00000185996						1	1	0	1	5	0	0	0	0	0	0		
ENSMUST00000185999						4	1	22	7	6	2	1	0	2	0	1		
ENSMUST00000186000						1	0	12	2	3	0	0	0	0	0	0		
ENSMUST00000186001						4	0	17	3	6	4	0	3	0	0	5		
ENSMUST00000186002	ENSMUSG00000026313	1	91928779	92180341	-1	2	1	5	2	0	3	2	0	9	0	2	A0A087WSF0	
ENSMUST00000186003	ENSMUSG00000026107	1	51465862	51478425	-1	14	19	0	0	27	9	133	235	143	98	102		Q8BGW5
ENSMUST00000186004	ENSMUSG00000101766	Y	64473266	64499452	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000186005						9	9	19	81	9	1	0	0	0	0	0		
ENSMUST00000186006						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186008						2	1	3	0	0	2	819	7081	859	171	239		
ENSMUST00000186009						18	13	11	6	19	6	6	11	4	5	3		
ENSMUST00000186012						31	20	186	20	23	24	0	1	0	0	0		
ENSMUST00000186014	ENSMUSG00000101026	15	74770908	74778859	-1	5	0	5	16	12	3	0	0	0	0	0	A0A087WQU7	
ENSMUST00000186017	ENSMUSG00000026393	1	138482875	138620141	-1	8	5	17	108	17	0	0	0	49	40	15		Q9ES74
ENSMUST00000186018						6	3	5	6	2	1	0	0	0	0	0		
ENSMUST00000186019						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000186021	ENSMUSG00000026043	1	45311538	45349706	1	2	1	0	0	0	0	0	0	0	7	27	A0A087WPJ5	
ENSMUST00000186022	ENSMUSG00000079557	17	33685692	33718670	-1	7	8	23	0	0	0	6	0	5	0	0	Q8CA25	
ENSMUST00000186023	ENSMUSG00000024681	19	11629496	11640851	-1	6	1	0	6	9	0	326	591	290	384	76	Q53ZU3	Q920C4
ENSMUST00000186024	ENSMUSG00000042686	1	16964560	17097889	-1	0	1	21	0	3	0	0	0	0	0	0	A0A087WRN3	
ENSMUST00000186026						0	3	0	0	7	2	0	0	0	0	0		
ENSMUST00000186028						0	0	0	69	0	0	0	0	0	0	5		
ENSMUST00000186029						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186031	ENSMUSG00000101638	7	32222840	32224156	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQJ0	
ENSMUST00000186032						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186033	ENSMUSG00000042590	13	106794439	106936958	-1	0	0	1	0	0	5	0	0	0	5	0		Q8K2V6
ENSMUST00000186035	ENSMUSG00000095267	Y	18089116	18091556	1	0	0	0	0	0	0	0	0	0	0	0	J3QPX2	
ENSMUST00000186037	ENSMUSG00000049339	1	75142778	75147913	1	10	15	16	2	25	12	2669	2482	1293	130	1084	A0A087WPR9	
ENSMUST00000186038	ENSMUSG00000026253	1	87204657	87212694	1	3	3	7	8	4	1	0	0	0	0	0	I0B502	
ENSMUST00000186039						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186040						9	12	12	1	9	5	0	0	0	0	0		
ENSMUST00000186041						3	7	4	8	4	6	3	2	2	3	4		
ENSMUST00000186043	ENSMUSG00000026159	1	82839483	82901182	1	0	0	0	32	0	2	4	0	0	0	10	A0A087WRL1	
ENSMUST00000186044						6	6	15	7	1	3	6	28	21	7	16		
ENSMUST00000186045	ENSMUSG00000039218	17	23790662	23824741	1	0	0	3	4	2	1	24	20	57	2	87	A0A087WPU0	
ENSMUST00000186046						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186047	ENSMUSG00000094511	Y	3326750	3345329	-1	0	0	0	0	2	0	0	0	0	0	0	J3QK27	
ENSMUST00000186049	ENSMUSG00000032468	9	99478372	99568899	-1	1	5	1	0	4	3	0	24	0	0	0		Q9DBR3
ENSMUST00000186050						2	6	13	7	10	7	0	7	5	5	2		
ENSMUST00000186051	ENSMUSG00000016918	1	12692277	12861192	1	5	7	16	14	15	7	0	0	0	0	0		
ENSMUST00000186052						0	0	3	0	0	0	0	0	0	2	1		
ENSMUST00000186053	ENSMUSG00000033029	15	79129349	79141253	-1	0	3	0	11	5	2	2	0	0	0	0	A0A087WQM6	
ENSMUST00000186056	ENSMUSG00000036098	19	10208272	10240748	-1	0	0	5	0	0	8	2	0	0	0	0		Q3UR85
ENSMUST00000186057	ENSMUSG00000026104	1	52119440	52161865	1	0	3	0	73	7	0	65	1124	21	40	0	A0A087WSP5	
ENSMUST00000186058						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186059	ENSMUSG00000051314	7	30818348	30823775	-1	1	2	0	0	0	0	3	19	5	6	15	A0A087WR60	
ENSMUST00000186061						24	18	15	243	43	14	0	3	0	0	4		
ENSMUST00000186062	ENSMUSG00000099611	13	22101727	22102665	-1	1	3	5	1	5	3	0	0	0	0	0	Q8K3N3	
ENSMUST00000186063						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186064						21	17	44	19	18	9	12	6	41	54	25		
ENSMUST00000186066						8	5	2	7	4	4	0	0	0	0	0		
ENSMUST00000186067						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186068	ENSMUSG00000026311	1	91540544	91559589	1	1	0	0	51	1	0	0	0	1	0	0	S4W2P0	
ENSMUST00000186069						3	5	82	2	2	3	0	5	0	0	1		
ENSMUST00000186070						0	0	0	65	2	1	0	0	0	0	0		
ENSMUST00000186071						148	142	65	126	152	50	0	0	0	0	0		
ENSMUST00000186072						4	0	0	0	3	1	0	0	0	0	0		
ENSMUST00000186075	ENSMUSG00000007805	1	91801461	91848028	1	13	5	29	149	21	6	0	0	0	0	0	A5D6P6	
ENSMUST00000186076						0	0	0	0	0	0	1	0	0	1	0		
ENSMUST00000186077						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186078						0	0	1	3	0	1	0	0	0	0	0		
ENSMUST00000186081	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	1	0	0	0	0	0	0	0	A0A087WQG6	
ENSMUST00000186082						3	0	3	0	6	0	0	0	0	0	0		
ENSMUST00000186086						10	9	123	15	15	7	0	0	0	0	0		
ENSMUST00000186087	ENSMUSG00000038608	1	80501073	80758527	-1	2	3	7	0	2	1	0	0	0	0	0	A0A087WQA1	
ENSMUST00000186089	ENSMUSG00000032253	9	82866159	82975516	-1	0	0	0	0	0	0	1	0	57	0	35	A0A087WP89	
ENSMUST00000186090						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186091						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186093						5	4	0	2	7	8	0	0	0	0	0		
ENSMUST00000186094						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186095						0	2	0	0	0	3	0	9	0	0	0		
ENSMUST00000186096	ENSMUSG00000073725	1	24678630	24766301	1	0	0	1	21	2	1	63	52	83	62	22	A0A087WS60	
ENSMUST00000186097	ENSMUSG00000026782	1	60409619	60481158	1	0	0	0	0	2	0	0	0	0	0	0	A0A087WNU9	
ENSMUST00000186099						3	2	10	0	5	7	1	1	1	0	1		
ENSMUST00000186100	ENSMUSG00000037608	10	20312469	20344613	1	0	0	3	8	13	2	25	117	264	179	239	A0A087WQA0	
ENSMUST00000186101						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186103						10	14	91	24	11	8	0	0	1	0	0		
ENSMUST00000186105						12	4	22	21	5	6	10	26	13	0	35		
ENSMUST00000186107	ENSMUSG00000026017	1	60098247	60153953	1	0	0	0	0	0	0	4	0	0	1	0	A8VI09	
ENSMUST00000186109	ENSMUSG00000039168	15	31224314	31274341	1	1	0	0	24	0	0	0	0	0	0	0	A0A087WSM4	
ENSMUST00000186110	ENSMUSG00000099840	Y	84746685	84772902	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000186111						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000186113	ENSMUSG00000022197	15	12359711	12739924	-1	2	0	3	0	2	1	0	0	0	0	0	A0A087WQ09	
ENSMUST00000186115						6	6	0	8	3	3	2	17	5	34	5		
ENSMUST00000186116	ENSMUSG00000030811	7	127744543	127769483	1	12	0	26	66	21	3	107	266	108	10	88	A0A087WQ84	
ENSMUST00000186120						5	4	13	11	7	5	0	0	1	0	1		
ENSMUST00000186121						0	1	2	0	1	0	0	0	0	0	0		
ENSMUST00000186122	ENSMUSG00000042268	1	131744022	131771504	1	0	0	0	2	0	0	0	0	0	0	0	A0A087WSS7	
ENSMUST00000186124						1	0	2	6	0	1	12	44	19	3	28		
ENSMUST00000186125	ENSMUSG00000068117	15	82069997	82126811	1	0	2	0	0	0	0	0	0	0	0	0	A0A087WQR2	
ENSMUST00000186126						3	2	9	105	6	3	0	0	0	0	2		
ENSMUST00000186127						3	3	7	6	6	2	0	0	0	0	0		
ENSMUST00000186128						3	8	5	4	5	5	0	0	3	0	1		
ENSMUST00000186129	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	65	70	14	0	1424	592	1556	0	6384	A0A087WSN6	
ENSMUST00000186131	ENSMUSG00000021917	14	30999826	31001672	-1	0	0	0	99	0	0	0	0	0	0	0		Q9D958
ENSMUST00000186136						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000186137						3	1	3	4	0	3	0	0	0	0	0		
ENSMUST00000186138						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000186139						59	64	201	72	58	26	2	11	9	1	10		
ENSMUST00000186140	ENSMUSG00000096520	Y	3771673	3783267	1	0	0	14	0	0	0	0	0	0	0	0		Q60990
ENSMUST00000186141						5	3	0	0	3	2	0	0	1	0	0		
ENSMUST00000186142						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000186144						2	0	14	3	1	4	0	0	0	0	0		
ENSMUST00000186145						5	3	1	8	0	0	0	0	0	0	0		
ENSMUST00000186148						1	0	5	2	0	1	0	16	0	1	7		
ENSMUST00000186149						4	3	10	7	2	2	0	0	0	0	0		
ENSMUST00000186150						2	2	1	3	4	0	0	0	0	0	0		
ENSMUST00000186152						0	0	0	0	0	0	10	0	5	11	2		
ENSMUST00000186154	ENSMUSG00000030577	7	30865402	30880342	-1	1	1	0	1	1	0	0	7	0	0	23	Q3UP36	
ENSMUST00000186155						2	1	0	4	3	0	0	0	0	0	0		
ENSMUST00000186156	ENSMUSG00000033722	1	155212471	155244444	-1	21	14	109	134	23	27	0	0	1	0	0	A0A087WP46	
ENSMUST00000186157						7	3	40	9	11	3	0	0	0	0	0		
ENSMUST00000186158						2	0	3	0	0	0	2	2	0	3	5		
ENSMUST00000186163						3	4	10	180	6	9	0	2	3	1	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186164	ENSMUSG00000034088	1	93405940	93478815	-1	0	0	0	0	8	0	302	665	506	1	230	A0A087WP83	
ENSMUST00000186165						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000186166	ENSMUSG00000071178	12	103728156	103830373	-1	0	0	9	0	0	0	0	0	0	0	0		P22599
ENSMUST00000186167						5	0	10	0	0	0	0	0	0	0	0		
ENSMUST00000186168						3	0	0	2	6	3	0	0	0	0	0		
ENSMUST00000186171						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186173	ENSMUSG00000026200	1	75198236	75210813	-1	2	0	0	0	0	0	3	0	0	6	15	A0A087WPH5	
ENSMUST00000186175						0	0	0	5	1	3	0	0	0	0	0		
ENSMUST00000186176						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000186177						0	0	1	3	0	1	0	0	0	0	0		
ENSMUST00000186178	ENSMUSG00000026204	1	75247027	75264502	-1	2	0	0	5	0	0	0	0	0	0	0	A0A087WPU7	
ENSMUST00000186179						3	1	1	0	3	4	0	0	0	0	0		
ENSMUST00000186181						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186182	ENSMUSG00000030591	7	29174188	29180701	-1	0	0	0	0	12	0	0	12	0	12	0		Q9CX56
ENSMUST00000186184						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186185						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000186186						1	2	0	6	2	3	0	4	0	0	0		
ENSMUST00000186187						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186188						0	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000186190	ENSMUSG00000073725	1	24678630	24766301	1	0	0	0	0	2	0	40	67	89	151	75	A0A087WPS2	
ENSMUST00000186191						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000186192						4	8	16	24	8	6	1	5	2	0	1		
ENSMUST00000186193						5	3	2	2	1	0	14	21	9	0	7		
ENSMUST00000186194	ENSMUSG00000100939	Y	7253787	7280017	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRP6	
ENSMUST00000186195	ENSMUSG00000056536	1	105518422	105663677	-1	25	32	32	29	29	12	1	8	3	1	0	A0A087WNT9	
ENSMUST00000186196						21	21	190	25	31	25	0	4	2	0	2		
ENSMUST00000186197	ENSMUSG00000094314	10	100335676	100336591	1	6	4	0	6	7	0	0	0	0	0	0	E9Q4V5	
ENSMUST00000186198						6	5	36	10	16	7	0	2	0	5	1		
ENSMUST00000186200						4	4	1	0	1	1	9	182	50	163	51		
ENSMUST00000186201						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186202	ENSMUSG00000061816	1	66924295	66945404	-1	2	2	2	0	6	2	0	0	0	0	0	A0A087WRZ7	
ENSMUST00000186203						0	1	5	2	10	5	1	0	0	0	0		
ENSMUST00000186204						2	1	0	11	2	0	0	0	0	0	0		
ENSMUST00000186205						0	0	0	44	0	0	0	0	0	0	0		
ENSMUST00000186207	ENSMUSG00000030811	7	127744543	127769483	1	10	17	43	0	13	15	113	0	28	5	65		Q6PB97
ENSMUST00000186208						1	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000186210						4	3	17	3	5	4	0	1	0	21	0		
ENSMUST00000186211	ENSMUSG00000036557	17	87389571	87427741	-1	2	2	0	0	0	1	0	0	1	0	1	A0A087WQI0	
ENSMUST00000186212	ENSMUSG00000095976	7	21908665	21921291	-1	97	102	67	82	108	40	0	13	11	2	4	Q3UT86	
ENSMUST00000186213	ENSMUSG00000026202	1	75214228	75219865	-1	19	11	58	16	30	13	88	290	137	23	110		P68368
ENSMUST00000186215	ENSMUSG00000095388	3	98552542	98588807	-1	0	0	29	8	9	0	0	0	0	0	1	Q3UIU9	Q61767
ENSMUST00000186217						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186218						1	2	2	0	3	2	0	0	0	0	0		
ENSMUST00000186219	ENSMUSG00000072774	5	104813169	104860070	-1	7	12	13	16	10	7	12	126	24	0	16	A0A087WRH0	
ENSMUST00000186220						29	24	20	21	28	16	1	3	0	3	3		
ENSMUST00000186221						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186222	ENSMUSG00000025950	1	65158616	65186500	-1	0	3	0	3	0	1	0	0	0	0	0	A0A087WRM4	
ENSMUST00000186224						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186225						76	59	80	1152	162	78	0	1	4	1	0		
ENSMUST00000186226						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186227	ENSMUSG00000026197	1	75168646	75171629	1	0	0	0	0	0	0	0	8	30	0	0	A0A087WPF5	
ENSMUST00000186228	ENSMUSG00000101031	19	11215010	11230540	-1	4	5	17	1	5	4	0	0	0	0	0	A0A087WSB9	
ENSMUST00000186229	ENSMUSG00000033061	1	75272199	75278415	-1	0	0	5	0	0	0	0	0	0	0	0	B9W0B0	
ENSMUST00000186231						0	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000186232						5	0	0	0	3	4	0	6	0	7	1		
ENSMUST00000186233						2	4	9	2	5	4	0	0	0	0	0		
ENSMUST00000186235	ENSMUSG00000032839	9	95705082	95750375	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSD0	
ENSMUST00000186239	ENSMUSG00000019813	10	41718840	41809871	-1	0	0	0	0	4	0	0	0	0	0	0	G5E828	
ENSMUST00000186242						10	14	28	16	25	7	7	28	14	3	5		
ENSMUST00000186243						0	0	0	17	0	1	0	0	1	0	0		
ENSMUST00000186244						3	4	0	52	3	3	0	1	2	0	3		
ENSMUST00000186245	ENSMUSG00000034867	7	35586244	35639226	1	12	3	13	11	19	11	10	18	26	8	27		
ENSMUST00000186246						38	53	163	55	64	36	24	120	28	10	27		
ENSMUST00000186247	ENSMUSG00000069601	10	69533772	70027438	1	40	36	178	64	84	27	0	0	0	0	1	A0A087WNU5	
ENSMUST00000186249						6	1	8	5	2	2	0	0	0	0	0		
ENSMUST00000186252						111	161	839	209	149	65	24	84	41	2	68		
ENSMUST00000186253						15	11	87	17	13	5	0	0	0	0	0		
ENSMUST00000186254						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186255	ENSMUSG00000026238	1	86526726	86530712	1	4	0	3	29	0	4	0	1570	1694	5490	1251	A0A087WP98	
ENSMUST00000186256						18	9	64	39	13	7	0	0	0	0	0		
ENSMUST00000186257						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186259	ENSMUSG00000039218	17	23790662	23824741	1	5	1	13	59	14	2	0	208	0	6	15	A0A087WR98	
ENSMUST00000186262						5	1	7	2	4	0	0	0	0	0	0		
ENSMUST00000186263	ENSMUSG00000024430	18	12741324	12755146	1	4	0	24	0	4	0	0	0	0	5	2		Q9D424
ENSMUST00000186264	ENSMUSG00000102030	1	118176542	118202307	1	5	6	5	5	7	8	0	0	0	1	0	A0A087WSP8	
ENSMUST00000186265	ENSMUSG00000029432	5	129725063	129758327	1	1	0	0	0	0	0	10	84	45	19	60	Q7TMG8	
ENSMUST00000186266	ENSMUSG00000043629	1	52922324	53020179	-1	0	0	0	0	0	0	0	0	0	1	0		Q9CPS8
ENSMUST00000186268						1	0	2	0	0	0	0	0	0	0	11		
ENSMUST00000186270						3	3	6	5	8	2	0	0	0	0	0		
ENSMUST00000186271	ENSMUSG00000056222	13	57421195	57908314	-1	8	0	0	17	1	3	0	0	0	0	0	Q8BKQ3	
ENSMUST00000186272						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186274						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186275						9	1	11	13	13	8	0	0	0	0	0		
ENSMUST00000186277						0	0	1	0	0	0	1	0	4	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186278						4	0	5	3	1	2	0	0	5	0	0		
ENSMUST00000186279						19	21	74	13	24	11	0	0	0	0	0		
ENSMUST00000186280						0	0	1	8	3	3	0	1	0	0	0		
ENSMUST00000186281						8	5	12	9	11	7	0	3	0	0	1		
ENSMUST00000186282	ENSMUSG00000033364	1	74435511	74544284	-1	1	2	0	6	1	1	1	0	0	0	0	A0A087WQE4	
ENSMUST00000186284	ENSMUSG00000009545	7	143106362	143427042	1	1	0	5	5	7	3	0	0	0	0	0	A0A087WQE3	
ENSMUST00000186286						6	5	12	0	5	1	0	0	0	0	0		
ENSMUST00000186287	ENSMUSG00000026277	1	93619751	93658659	-1	8	6	16	5	11	5	0	0	0	0	0	A0A087WQY6	
ENSMUST00000186288	ENSMUSG00000009545	7	143106362	143427042	1	0	0	2	1	0	0	0	0	0	0	0	A0A087WRU8	
ENSMUST00000186290						0	0	0	7	0	0	0	0	0	0	0		
ENSMUST00000186292	ENSMUSG00000037236	18	35562146	35593835	1	2	0	0	87	4	3	0	0	0	0	0	A0A087WNP3	
ENSMUST00000186294	ENSMUSG00000056763	1	10037987	10136768	1	0	0	5	2	15	5	0	18	112	8	148		B2RX88
ENSMUST00000186295						0	0	0	3	1	2	0	0	0	0	1		
ENSMUST00000186296	ENSMUSG00000022952	16	92601466	92826149	-1	2	0	0	0	0	0	2	4	4	4	8	A0A087WR05	
ENSMUST00000186298	ENSMUSG00000026271	1	92950865	92986391	1	0	0	0	0	0	0	226	274	200	85	402	Q3TBY9	Q9ES90
ENSMUST00000186299						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186301						3	2	3	0	2	3	0	0	0	0	0		
ENSMUST00000186302	ENSMUSG00000026159	1	82839483	82901182	1	0	6	0	0	0	0	537	1130	565	0	175		Q8K2K6
ENSMUST00000186303	ENSMUSG00000100235	13	67069399	67108604	-1	10	4	0	18	6	1	4	7	3	9	0	A0A087WQQ0	
ENSMUST00000186304						0	0	1	1	3	0	0	0	0	0	0		
ENSMUST00000186306						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186307						2	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000186308						0	0	0	0	0	1	0	6	0	0	0		
ENSMUST00000186309	ENSMUSG00000021219	12	82588292	83162056	1	1	2	6	2	2	0	0	0	0	0	0	A0A087WRN0	
ENSMUST00000186310						9	2	11	8	5	2	0	2	0	0	0		
ENSMUST00000186312						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186313						2	1	4	2	1	0	1	8	9	10	6		
ENSMUST00000186314	ENSMUSG00000036013	X	53273424	53331185	1	0	0	1	0	0	0	0	0	0	0	0	Q9D5J5	
ENSMUST00000186315						3	3	0	0	3	6	0	0	0	0	0		
ENSMUST00000186316						3	7	0	0	0	0	50	166	26	2	44		
ENSMUST00000186317						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000186319						0	4	128	36	28	1	0	0	0	0	0		
ENSMUST00000186320						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186322						14	9	20	8	9	10	5	36	25	0	7		
ENSMUST00000186323	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSJ9	
ENSMUST00000186324						2	0	3	4	2	1	0	0	0	0	0		
ENSMUST00000186329	ENSMUSG00000101294	X	33575398	33577314	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR44	
ENSMUST00000186330						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000186331	ENSMUSG00000026153	1	24011093	24100341	-1	0	3	0	3	0	0	0	2	2	0	5	A0A087WS93	
ENSMUST00000186333						0	0	0	0	0	0	0	0	2	0	2		
ENSMUST00000186335						1	1	5	0	0	1	10	0	0	0	5		
ENSMUST00000186336	ENSMUSG00000038750	9	78327589	78329620	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQL0	
ENSMUST00000186338						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186339	ENSMUSG00000051314	7	30818348	30823775	-1	0	0	0	0	0	0	24	15	5	0	5	A0A087WR67	
ENSMUST00000186341	ENSMUSG00000100265	1	117697131	117727441	1	7	4	4	1	0	0	0	0	0	0	0	A0A087WQW2	
ENSMUST00000186342	ENSMUSG00000070047	8	44935447	45052257	1	0	0	0	0	0	0	0	0	0	0	0	A7ISQ2	
ENSMUST00000186346						2	2	2	0	0	4	0	0	0	0	0		
ENSMUST00000186349	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	6	0	0	0	0	E9QKH0	
ENSMUST00000186350						3	0	0	3	7	3	6	63	7	0	28		
ENSMUST00000186351						12	6	15	10	5	5	0	0	0	0	1		
ENSMUST00000186352	ENSMUSG00000039257	7	40898328	40930594	1	2	0	2	12	5	0	0	0	0	0	0	A0A087WQL2	
ENSMUST00000186353						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186354						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000186356						6	1	15	4	2	5	0	0	0	0	0		
ENSMUST00000186358	ENSMUSG00000047407	17	70844205	70853546	-1	0	0	0	0	0	0	0	6	0	0	17	A0A087WNP4	
ENSMUST00000186359						4	2	1	1	8	3	0	2	0	2	1		
ENSMUST00000186360	ENSMUSG00000034730	15	74516195	74589465	1	0	0	0	218	0	0	0	14	0	0	12	A0A087WQV8	
ENSMUST00000186361	ENSMUSG00000042073	9	106447788	106452922	1	0	2	0	0	0	0	2	0	0	0	0	A0A087WSR2	
ENSMUST00000186362						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000186363	ENSMUSG00000067399	9	88839164	88848190	1	20	17	36	52	65	22	0	0	2	0	4	A0A087WPC1	
ENSMUST00000186364	ENSMUSG00000032369	9	92249750	92272278	1	3	6	5	25	6	0	2439	5573	3107	2316	1420		Q9JJ00
ENSMUST00000186365						13	0	1	0	7	0	0	11	0	0	0		
ENSMUST00000186366						3	3	5	0	1	3	0	0	0	5	0		
ENSMUST00000186367						15	8	5	12	10	8	0	0	0	0	0		
ENSMUST00000186368	ENSMUSG00000042751	1	152954993	153119261	1	40	37	138	53	47	24	0	1	1	0	0	A0A087WRE3	
ENSMUST00000186369	ENSMUSG00000048747	4	97568133	97778078	-1	1	1	0	0	0	0	0	0	0	0	0	A0A087WQA2	
ENSMUST00000186370	ENSMUSG00000096653	14	52863299	52863936	1	2	2	0	0	2	0	0	2	0	0	1	A0A075B608	
ENSMUST00000186373	ENSMUSG00000026251	1	87190607	87200070	1	52	0	280	31	49	21	0	0	0	0	0	A0A087WNX8	
ENSMUST00000186375	ENSMUSG00000005982	16	3872375	3904780	1	0	0	0	32	14	0	0	115	406	0	345		Q9DBU2
ENSMUST00000186376						8	9	14	11	5	1	1	0	7	2	0		
ENSMUST00000186380	ENSMUSG00000042699	1	153455758	153487660	-1	0	0	22	0	0	8	0	1081	111	61	58	A0A087WPL5	
ENSMUST00000186381						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000186382	ENSMUSG00000019865	10	14705591	14770850	1	12	10	3	3	0	3	0	0	0	0	0	A0A087WP36	
ENSMUST00000186383						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186384	ENSMUSG00000033633	8	111058920	111092426	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRN2	
ENSMUST00000186385						1	0	0	1	2	1	0	6	2	5	1		
ENSMUST00000186388						1	6	6	17	6	2	4	3	5	0	9		
ENSMUST00000186389	ENSMUSG00000026442	1	132564690	132741797	-1	2	0	0	2	3	0	0	0	0	0	0	A0A087WR56	
ENSMUST00000186392						0	0	3	0	0	3	0	0	0	11	0		
ENSMUST00000186393						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000186394	ENSMUSG00000074109	7	48478619	48499321	-1	2	3	4	3	0	0	0	0	0	0	0	Q3UG30	
ENSMUST00000186395	ENSMUSG00000038079	1	59100590	59120408	-1	0	0	0	25	3	0	0	5	1	7	0	A0A087WR42	
ENSMUST00000186396						1	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000186397						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186398						17	15	31	21	17	15	19	31	17	5	15		
ENSMUST00000186401						5	4	18	7	6	4	0	0	0	0	0		
ENSMUST00000186402	ENSMUSG00000040124	1	163384908	163403669	-1	7	0	0	0	5	0	0	13	9	21	0	A0A087WQS3	
ENSMUST00000186403						10	11	22	25	19	10	0	2	0	2	0		
ENSMUST00000186404						1925	1647	8756	2040	2117	1025	42	165	78	32	184		
ENSMUST00000186405	ENSMUSG00000016918	1	12692277	12861192	1	4	4	2	0	1	1	0	0	0	1	0	A0A087WS44	
ENSMUST00000186406	ENSMUSG00000023826	17	10840384	12063361	1	3	1	1	2	0	1	0	0	0	0	1	A0A087WQJ2	
ENSMUST00000186408	ENSMUSG00000072754	5	110344730	110356094	1	0	0	0	7	0	0	0	0	0	0	0	A0A087WQJ6	
ENSMUST00000186409						14	9	12	7	19	7	0	0	0	0	0		
ENSMUST00000186410	ENSMUSG00000032298	9	57142800	57148305	-1	3	1	8	3	0	4	8	7	3	0	18		Q8K4Q6
ENSMUST00000186412						3	0	1	1	1	1	0	0	0	0	0		
ENSMUST00000186413						1	1	1	0	1	0	0	3	3	9	3		
ENSMUST00000186414						11	6	13	9	9	5	0	0	0	0	6		
ENSMUST00000186415	ENSMUSG00000026484	1	151458004	151500955	-1	0	0	0	0	1	0	18	4	60	0	14	A0A087WRE9	
ENSMUST00000186416						4	1	2	3	1	1	0	0	0	0	0		
ENSMUST00000186417						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186418						76	63	375	69	87	34	19	80	39	6	53		
ENSMUST00000186419						4	1	3	2	0	1	0	0	0	0	0		
ENSMUST00000186420						2	1	0	4	1	0	3	27	5	0	4		
ENSMUST00000186421						3	1	1	0	2	2	0	0	0	0	0		
ENSMUST00000186422						8	12	19	140	9	4	0	0	2	0	2		
ENSMUST00000186423	ENSMUSG00000058470	19	11485938	11512577	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS47	
ENSMUST00000186425	ENSMUSG00000039168	15	31224314	31274341	1	0	0	16	0	2	0	0	4	16	5	29	A0A087WR57	
ENSMUST00000186427						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186429						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000186430						9	14	13	13	17	7	0	0	0	0	0		
ENSMUST00000186432	ENSMUSG00000026390	1	120474538	120505024	-1	1	0	0	0	0	1	0	0	0	0	0	A0A087WS94	
ENSMUST00000186433						5	0	15	1	5	1	14	48	10	4	18		
ENSMUST00000186434	ENSMUSG00000047361	1	59516264	59636417	1	5	6	10	3	11	1	0	0	0	0	0	A0A087WSM0	
ENSMUST00000186435						1	7	1	1	3	1	0	0	0	0	0		
ENSMUST00000186437	ENSMUSG00000020963	12	91400994	91540509	1	1	0	0	0	0	2	0	3	0	0	0	A0A087WP53	
ENSMUST00000186438	ENSMUSG00000054763	14	63046991	63058149	1	0	0	2	0	0	0	0	0	0	0	0	A0A087WR68	
ENSMUST00000186439						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000186440						4	4	1	11	8	3	0	1	1	0	0		
ENSMUST00000186441	ENSMUSG00000041763	1	43933647	44003000	1	3	1	1	0	0	1	9	0	29	0	0	A0A087WP19	
ENSMUST00000186442	ENSMUSG00000090272	1	173857220	173942491	-1	0	0	0	0	0	0	0	62	0	9	0	A0A087WRA4	
ENSMUST00000186443	ENSMUSG00000102045	Y	89052806	89079015	1	2	0	0	0	0	0	0	0	0	0	0	A0A087WS79	
ENSMUST00000186445	ENSMUSG00000035967	X	56454857	56507843	1	0	2	0	12	4	0	65	29	4	0	507		Q8BND4
ENSMUST00000186446						7	7	0	0	10	0	0	0	37	0	41		
ENSMUST00000186447						1	3	0	0	3	0	0	0	0	0	0		
ENSMUST00000186451	ENSMUSG00000037428	5	137026392	137033351	1	0	0	0	285	4	0	0	1	1	0	1	Q0VGU4	
ENSMUST00000186452	ENSMUSG00000041730	14	32599407	32649246	1	19	15	103	149	28	14	0	0	0	0	0		Q8BYH0
ENSMUST00000186455						6	12	24	4	7	3	1	0	0	0	0		
ENSMUST00000186456	ENSMUSG00000052303	7	47185707	47204920	-1	6	1	0	0	0	0	0	0	3	0	0	A0A087WQV0	
ENSMUST00000186458	ENSMUSG00000021219	12	82588292	83162056	1	56	44	127	605	81	36	0	3	0	0	0		Q9Z2H2
ENSMUST00000186459	ENSMUSG00000033029	15	79129349	79141253	-1	20	12	13	13	20	7	5	7	7	0	4	A0A087WPZ1	
ENSMUST00000186464						0	0	1	11	0	0	2	0	7	0	6		
ENSMUST00000186465	ENSMUSG00000026219	1	84721189	84840516	-1	0	18	59	0	20	21	338	1504	497	118	386		G5E870
ENSMUST00000186466	ENSMUSG00000021843	14	47648448	47736564	1	6	4	11	3	3	3	0	2	0	2	0	A0A087WR91	
ENSMUST00000186467	ENSMUSG00000025911	1	9547948	9580673	1	0	0	0	0	2	0	0	6	0	0	0	A0A087WS19	
ENSMUST00000186468						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186469	ENSMUSG00000029449	5	123103044	123132692	-1	21	15	37	0	26	18	11	20	21	0	25	Q4VA10	Q8BYP3
ENSMUST00000186470	ENSMUSG00000010453	1	36335730	36369181	-1	0	1	14	0	0	0	42	22	27	0	102		A2RSY1
ENSMUST00000186475	ENSMUSG00000099689	7	29908223	29916813	1	0	0	0	0	0	1	3	24	4	15	11	A0A087WRR7	
ENSMUST00000186476	ENSMUSG00000094410	1	133619940	133661318	-1	24	19	28	60	24	4	213	197	542	12	383	G0LE24	D2EAC2
ENSMUST00000186477	ENSMUSG00000079550	1	59120935	59163389	-1	0	0	7	0	0	0	0	0	0	0	0	A0A087WQU9	
ENSMUST00000186478						15	26	50	54	27	26	0	0	0	0	0		
ENSMUST00000186481						6	4	21	9	2	0	0	0	0	0	0		
ENSMUST00000186482						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186483						4	3	2	2	3	1	0	0	0	0	0		
ENSMUST00000186484						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186485	ENSMUSG00000056536	1	105518422	105663677	-1	0	0	0	0	0	0	231	324	347	179	168	G3X9F1	
ENSMUST00000186486	ENSMUSG00000026116	1	36792191	36943666	-1	2	1	4	0	0	0	0	0	0	0	0	A0A0A6YXP8	
ENSMUST00000186487						0	0	0	0	73	0	0	0	0	0	0		
ENSMUST00000186488	ENSMUSG00000009545	7	143106362	143427042	1	0	0	4	1	2	0	0	0	0	0	0	A0A087WRK7	
ENSMUST00000186489						5	1	10	13	8	5	12	40	4	0	10		
ENSMUST00000186490						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186491						2	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000186492						77	58	134	66	65	30	18	42	23	4	30		
ENSMUST00000186493	ENSMUSG00000099856	Y	87550966	87575691	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000186494						0	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000186495						5	7	10	0	5	3	0	0	1	1	0		
ENSMUST00000186496						1	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000186497						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186499	ENSMUSG00000034157	12	86947043	86965362	1	3	1	2	1	0	0	0	0	0	0	0	A0A087WNZ2	
ENSMUST00000186501						0	1	7	3	0	3	4	11	14	1	11		
ENSMUST00000186505						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186507						0	0	0	0	0	0	0	0	5	0	0		
ENSMUST00000186508						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186509	ENSMUSG00000062590	1	86154780	86278284	1	0	0	0	1	1	1	0	0	0	0	0	A0A087WNY0	
ENSMUST00000186511						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186512						0	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000186513						18	22	31	18	27	14	13	16	34	4	28		
ENSMUST00000186514						0	0	0	7	9	4	0	0	1	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186517						13	13	15	65	25	2	1	1	1	1	3		
ENSMUST00000186519						0	0	6	7	5	0	0	0	0	0	0		
ENSMUST00000186520						0	5	3	1	0	1	0	0	0	0	0		
ENSMUST00000186522						3	7	1	0	13	5	0	0	0	0	0		
ENSMUST00000186523						4	2	4	1	3	1	0	0	0	0	0		
ENSMUST00000186524						1	0	0	0	2	1	0	0	0	3	0		
ENSMUST00000186525	ENSMUSG00000068887	3	92788840	92790514	-1	2	0	0	5	2	1	0	0	0	0	0	D3YUU5	
ENSMUST00000186526	ENSMUSG00000075602	15	74994877	74998031	-1	0	0	6	2	11	0	0	16	0	11	0		P05533
ENSMUST00000186527	ENSMUSG00000062760	15	84379203	84447097	-1	1	0	1	3	1	0	0	0	0	0	0	A0A087WSA5	
ENSMUST00000186528	ENSMUSG00000025917	1	10024601	10038168	-1	0	0	0	0	0	0	45	199	149	507	83	A0A087WRH6	
ENSMUST00000186529	ENSMUSG00000100058	7	33171892	33173864	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPA9	
ENSMUST00000186530	ENSMUSG00000053024	1	132509427	132543256	-1	0	0	1	5	0	0	0	0	0	0	0	A0A087WPS6	
ENSMUST00000186534	ENSMUSG00000051314	7	30818348	30823775	-1	9	4	5	3	8	3	20	80	60	6	11	A0A087WQJ1	
ENSMUST00000186536						1	3	10	12	2	2	0	0	0	1	0		
ENSMUST00000186537						24	27	24	0	14	6	2	8	1	0	9		
ENSMUST00000186538	ENSMUSG00000033272	18	36679215	36683861	1	10	15	15	67	15	6	15	30	15	0	9		Q9D321
ENSMUST00000186539						0	2	8	0	5	3	0	0	0	0	0		
ENSMUST00000186541						0	0	5	10	0	1	0	0	0	0	0		
ENSMUST00000186542	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WST9	
ENSMUST00000186543	ENSMUSG00000026425	1	131285251	131527352	-1	4	3	93	0	0	0	144	50	274	0	175	A0A087WNM1	
ENSMUST00000186544						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186545	ENSMUSG00000096397	14	53806639	53807115	1	0	0	0	1	2	0	0	1	0	0	0	A0A087WQ87	
ENSMUST00000186546						6	3	5	3	1	4	0	0	0	0	0		
ENSMUST00000186547	ENSMUSG00000039168	15	31224314	31274341	1	0	0	0	51	4	1	0	0	0	0	0	A0A087WR57	
ENSMUST00000186548	ENSMUSG00000034832	6	83362373	83459084	-1	11	6	88	161	48	23	111	14	278	3	223	L0HN04	
ENSMUST00000186551						0	0	0	0	0	1	0	0	0	0	1		
ENSMUST00000186552						0	0	0	0	0	0	13	254	144	298	139		
ENSMUST00000186553						4	0	7	50	0	0	23	37	17	0	13		
ENSMUST00000186554						108	95	169	151	134	69	0	0	0	0	0		
ENSMUST00000186555						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186557	ENSMUSG00000041857	19	11667460	11691150	-1	0	0	0	0	0	0	1	0	0	0	0	A0A087WNQ0	
ENSMUST00000186558						76	27	17	87	143	20	0	0	0	0	0		
ENSMUST00000186559						0	0	0	0	0	0	1	67	5	20	0		
ENSMUST00000186561						5	1	10	6	7	6	6	4	0	0	2		
ENSMUST00000186565						0	0	0	87	0	0	6	9	0	9	0		
ENSMUST00000186566						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186568	ENSMUSG00000026480	1	152800194	152836991	1	31	31	61	18	44	36	4	36	4	4	12		O70145
ENSMUST00000186569						36	31	63	44	36	29	9	28	17	1	25		
ENSMUST00000186571						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186572	ENSMUSG00000006007	1	150319417	150333906	1	0	0	0	3	3	0	0	0	0	0	0	A0A087WS02	
ENSMUST00000186573	ENSMUSG00000076861	14	53831105	53831827	1	1	2	0	1	0	1	0	0	0	0	0	A0A087WRX6	
ENSMUST00000186574	ENSMUSG00000026104	1	52119440	52161865	1	7	0	22	28	0	6	472	884	738	172	1214	Q99K94	
ENSMUST00000186575						6	1	3	0	1	1	0	6	7	51	26		
ENSMUST00000186576						0	0	2	0	3	0	0	1	2	1	1		
ENSMUST00000186577	ENSMUSG00000030213	6	136506167	136610862	1	0	0	0	0	0	0	0	0	2	0	16	A0A087WQB3	
ENSMUST00000186578	ENSMUSG00000100045	Y	53843949	53870150	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000186579						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186583	ENSMUSG00000028053	3	88950622	89079375	1	51	40	70	65	52	0	93	127	40	31	233		Q99MY8
ENSMUST00000186585						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000186586						53	42	41	63	83	32	0	0	2	0	0		
ENSMUST00000186588						0	4	4	2	2	5	0	0	0	2	0		
ENSMUST00000186591	ENSMUSG00000032475	9	100492293	100546134	-1	2	1	4	0	0	5	42	345	191	130	82	A0A087WSB1	
ENSMUST00000186592	ENSMUSG00000074269	9	58652850	58743964	-1	0	1	0	0	0	0	5	0	2	0	0	A0A087WPF6	
ENSMUST00000186593						0	0	1	3	0	1	0	0	0	0	0		
ENSMUST00000186594						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186596						13	13	14	16	19	4	0	6	1	0	2		
ENSMUST00000186598	ENSMUSG00000029055	4	154983115	155056784	-1	4	0	0	97	0	0	0	2	0	0	0	A0A087WSR3	
ENSMUST00000186600						0	2	4	3	1	2	0	4	7	0	0		
ENSMUST00000186601						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000186602	ENSMUSG00000062563	12	24665838	24681813	-1	0	0	0	8	0	0	0	0	0	0	0		
ENSMUST00000186603						0	0	0	8	5	0	0	0	0	0	0		
ENSMUST00000186606	ENSMUSG00000045411	7	44246722	44252319	1	0	0	4	0	3	0	3	3	0	0	0	A0A087WSJ7	
ENSMUST00000186608						7	6	28	2	3	3	80	178	101	67	43		
ENSMUST00000186609	ENSMUSG00000032411	9	96196275	96323646	1	0	2	0	0	1	0	0	0	0	0	0	A0A087WPS0	
ENSMUST00000186613	ENSMUSG00000026193	1	71585520	71653200	-1	1	0	1	0	0	0	0	0	0	0	0	A0A087WQE0	
ENSMUST00000186614	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	0	0	0	0	0	6	0	0	A0A087WSU2	
ENSMUST00000186616						3	1	3	0	2	2	0	1	0	0	1		
ENSMUST00000186617	ENSMUSG00000054387	1	132959484	133030561	-1	55	40	108	75	58	34	3	20	9	0	9	A0A087WRX7	
ENSMUST00000186619	ENSMUSG00000071302	8	129216354	129234406	-1	65	54	170	66	67	25	29	111	43	71	36	A0A087WRJ1	
ENSMUST00000186620	ENSMUSG00000030790	7	110627661	110629820	1	0	0	0	83	0	0	0	0	0	0	0	A0A087WS43	
ENSMUST00000186621	ENSMUSG00000042751	1	152954993	153119261	1	0	0	0	13	0	0	0	0	1	0	0	A0A087WR71	
ENSMUST00000186622	ENSMUSG00000041460	6	119236526	119352407	1	0	0	15	0	0	6	0	0	0	0	0	A0A087WQH4	
ENSMUST00000186623						1	2	2	0	3	2	0	0	0	0	0		
ENSMUST00000186624						4	3	11	53	12	6	0	0	0	0	0		
ENSMUST00000186625						1	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000186626						0	2	0	0	3	3	0	0	0	0	0		
ENSMUST00000186627	ENSMUSG00000021843	14	47648448	47736564	1	5	0	0	0	0	0	37	108	19	0	17	A0A087WS29	
ENSMUST00000186628						0	0	8	4	0	2	1	4	0	0	0		
ENSMUST00000186633	ENSMUSG00000015882	5	45697181	45857615	-1	0	0	0	0	2	1	0	0	4	0	0	A0A087WST0	
ENSMUST00000186634	ENSMUSG00000001248	7	31130127	31155896	-1	7	0	0	0	0	0	287	248	156	0	210		Q8VEF1
ENSMUST00000186635						0	0	0	1	2	0	1	0	0	0	0		
ENSMUST00000186636	ENSMUSG00000101361	17	14000239	14001765	-1	4	0	0	13	7	1	0	0	0	0	0	A0A087WSA6	
ENSMUST00000186637						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000186638						0	0	0	4	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186639						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186640						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000186641	ENSMUSG00000034107	1	93373930	93404303	1	12	17	0	31	19	12	2	1	2	0	0		Q14AT5
ENSMUST00000186645						7	2	11	3	2	3	0	1	1	0	1		
ENSMUST00000186646						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186647						0	0	53	16	7	0	0	0	15	33	0		
ENSMUST00000186648	ENSMUSG00000026219	1	84721189	84840516	-1	0	2	0	0	7	0	1119	1537	2886	147	1478	A0A087WNZ7	
ENSMUST00000186649						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000186650						0	4	0	0	3	0	0	0	0	0	0		
ENSMUST00000186651	ENSMUSG00000025995	1	45795166	45823619	1	1	0	1	0	0	0	0	6	0	0	0	A0A087WQ22	
ENSMUST00000186652						2	4	9	3	2	4	0	0	0	0	1		
ENSMUST00000186653						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186655						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186657						0	0	0	0	0	0	0	0	4	0	0		
ENSMUST00000186658						59	53	157	67	86	26	1	3	2	0	1		
ENSMUST00000186659	ENSMUSG00000027263	2	121170654	121198770	1	1	0	2	0	0	0	26	14	0	9	0	Q8BYN2	
ENSMUST00000186660						2	2	9	11	8	3	0	0	0	0	0		
ENSMUST00000186661						26	14	75	34	21	17	1	13	3	1	7		
ENSMUST00000186664						47	53	50	48	101	44	0	0	0	0	0		
ENSMUST00000186667						5	4	3	0	3	0	5	0	0	0	0		
ENSMUST00000186668	ENSMUSG00000023577	9	106503225	106561631	-1	3	1	4	0	3	0	0	0	0	0	0	A0A087WQS8	
ENSMUST00000186669						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186670						6	15	15	13	14	2	9	8	5	2	12		
ENSMUST00000186672	ENSMUSG00000053877	7	127511983	127561219	1	0	0	0	13	2	0	0	0	0	0	0	A0A087WQY5	
ENSMUST00000186674						13	9	9	16	17	4	0	1	0	0	4		
ENSMUST00000186675						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000186676						25	27	24	28	21	5	0	0	0	0	0		
ENSMUST00000186678						1	2	6	12	0	2	0	0	0	0	0		
ENSMUST00000186680						1	0	3	4	3	2	0	0	0	0	0		
ENSMUST00000186682						3	3	0	2	3	3	0	0	0	0	0		
ENSMUST00000186684	ENSMUSG00000026107	1	51465862	51478425	-1	4	0	10	27	4	0	0	752	138	78	96		Q8BGW5
ENSMUST00000186685						0	0	0	9	0	0	0	0	0	0	0		
ENSMUST00000186687						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000186688						0	4	0	1	2	0	1	0	0	0	0		
ENSMUST00000186689						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186690						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186691						3	12	1	11	13	3	0	0	0	0	0		
ENSMUST00000186692						0	1	5	0	2	0	0	0	0	0	0		
ENSMUST00000186693	ENSMUSG00000035048	9	102626296	102634425	1	1	3	3	5	5	0	6	9	9	12	6		Q8R034
ENSMUST00000186694	ENSMUSG00000070939	1	43047200	43098637	-1	0	0	0	85	28	0	358	484	561	47	412		Q3UR70
ENSMUST00000186696	ENSMUSG00000056673	Y	897788	956786	1	0	0	0	0	0	0	0	0	0	0	0		Q62240
ENSMUST00000186698						0	0	0	28	1	0	0	0	0	0	0		
ENSMUST00000186699						30	42	14	0	55	24	0	0	0	0	0		
ENSMUST00000186700						15	13	10	9	11	12	0	10	0	0	4		
ENSMUST00000186701	ENSMUSG00000079658	1	16641725	16657042	-1	4	1	3	7	4	1	2	4	2	3	0	A0A087WPE4	
ENSMUST00000186702						0	0	1	25	2	1	0	0	0	1	1		
ENSMUST00000186704						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186705						3	1	3	0	0	2	0	0	0	0	0		
ENSMUST00000186706	ENSMUSG00000031927	9	14756587	14771030	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186710	ENSMUSG00000099356	2	89617267	89618190	-1	4	0	20	1	0	0	0	0	0	0	0	A0A087WQ53	
ENSMUST00000186711	ENSMUSG00000041459	4	148612382	148627019	-1	6	2	11	0	1	5	25	218	49	36	64	A0A087WQ63	
ENSMUST00000186715						0	2	3	0	7	1	5	7	13	11	16		
ENSMUST00000186718						1	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000186719	ENSMUSG00000036731	2	25238818	25242452	-1	0	4	2	10	4	4	0	0	0	0	0		Q9D1E4
ENSMUST00000186720						4	0	1	0	0	0	0	0	6	0	2		
ENSMUST00000186721						0	0	0	0	0	0	6	0	7	24	0		
ENSMUST00000186722	ENSMUSG00000096405	14	36094917	36100114	1	31	35	46	47	43	18	0	0	1	0	0	Q3V0P0	
ENSMUST00000186723	ENSMUSG00000001248	7	31130127	31155896	-1	1	3	15	9	3	3	103	142	134	13	123	A0A087WPB6	
ENSMUST00000186725						4	3	14	1	3	3	0	0	0	0	0		
ENSMUST00000186726	ENSMUSG00000056673	Y	897788	956786	1	671	578	1237	745	908	404	12	23	40	28	52	A0A087WR43	
ENSMUST00000186728						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000186729	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNY6	
ENSMUST00000186730	ENSMUSG00000026458	1	134296783	134332928	-1	0	0	0	0	0	6	9	8	0	0	13	A0A087WPJ3	
ENSMUST00000186731						8	8	28	12	19	12	11	11	22	1	31		
ENSMUST00000186733	ENSMUSG00000048874	1	30802339	30873921	-1	6	7	6	6	8	4	272	461	664	60	347	B2RQG2	
ENSMUST00000186734						19	19	47	32	19	16	1	0	5	1	5		
ENSMUST00000186735	ENSMUSG00000074305	9	56201126	56418067	-1	0	2	0	0	0	0	4	1	0	1	0	A0A087WQ82	
ENSMUST00000186736	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	0	110	0	2	0	0	0	0	5	A0A087WQW8	
ENSMUST00000186738						3	1	4	0	0	2	0	0	0	0	0		
ENSMUST00000186739	ENSMUSG00000101928	Y	8257907	8284105	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS97	
ENSMUST00000186740						4	6	33	10	11	2	0	55	5	0	35		
ENSMUST00000186741						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186742	ENSMUSG00000030213	6	136506167	136610862	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPT6	
ENSMUST00000186743						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000186744	ENSMUSG00000033124	1	75180860	75192196	-1	1	0	0	9	0	0	5	1	6	0	12	A0A087WRG3	
ENSMUST00000186745	ENSMUSG00000023150	1	151344477	151364422	1	5	10	25	0	5	0	81	347	224	171	414		Q920Q8
ENSMUST00000186750	ENSMUSG00000034432	1	90602981	90613341	1	0	0	0	0	0	0	35	31	11	31	16	A0A087WPM5	
ENSMUST00000186751						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000186752						7	4	0	0	0	2	0	0	0	0	0		
ENSMUST00000186754						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186755						16	8	15	71	19	8	12	51	37	9	50		
ENSMUST00000186757						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186758	ENSMUSG00000026202	1	75214228	75219865	-1	1	0	12	141	2	4	8	16	10	4	8	A0A087WRB4	
ENSMUST00000186759						4	1	0	0	3	0	0	3	10	0	6		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186761	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNW3	
ENSMUST00000186762	ENSMUSG00000026305	1	90998737	91128944	1	2	4	1	15	2	1	4	6	3	8	13	A0A087WPT0	
ENSMUST00000186763						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186764	ENSMUSG00000002881	1	52457294	52500679	-1	34	43	215	28	35	27	66	983	216	63	86	A0A087WSU4	
ENSMUST00000186766						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186767						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186770						0	0	0	2	2	2	0	0	0	0	0		
ENSMUST00000186774						1	2	1	0	2	0	0	0	0	0	0		
ENSMUST00000186776						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186777	ENSMUSG00000026409	1	130689182	130729253	-1	6	6	16	58	19	4	0	3	14	1	5	A0A087WRW5	
ENSMUST00000186778						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186779						61	56	275	79	56	22	0	6	3	0	8		
ENSMUST00000186780	ENSMUSG00000051185	1	95313623	95335284	1	20	12	9	15	16	2	8	19	16	4	26		Q9D3L0
ENSMUST00000186781						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186783	ENSMUSG00000073609	1	93824909	93852348	1	0	0	0	0	0	0	14	16	13	2	7	A0A087WPG6	
ENSMUST00000186784						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186787	ENSMUSG00000034088	1	93405940	93478815	-1	3	0	0	33	2	1	0	0	0	2	3	A0A087WPC5	
ENSMUST00000186788	ENSMUSG00000032560	9	104151282	104262930	-1	1	0	10	0	0	0	282	0	653	0	296	D4AFX7	
ENSMUST00000186789						130	70	126	947	203	125	3	7	4	3	6		
ENSMUST00000186790						3	2	1	10	8	8	0	0	0	0	1		
ENSMUST00000186792						3	0	3	3	0	0	0	0	0	0	0		
ENSMUST00000186794	ENSMUSG00000038079	1	59100590	59120408	-1	0	4	0	0	0	0	2	7	0	16	3		Q3V0J1
ENSMUST00000186796	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	16	0	0	9	525	109	208	70	A0A087WSP7	
ENSMUST00000186797						14	9	47	9	11	5	0	0	0	0	0		
ENSMUST00000186798	ENSMUSG00000009545	7	143106362	143427042	1	1	2	0	7	2	1	0	0	0	0	0	A0A087WPJ2	
ENSMUST00000186800						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000186802	ENSMUSG00000032258	9	83390293	83441127	-1	1	2	2	0	4	1	0	0	0	0	0	A0A087WNX0	
ENSMUST00000186803						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000186804	ENSMUSG00000025993	1	45908068	45926523	-1	0	0	0	0	0	0	0	0	0	0	0	C5H8V4	
ENSMUST00000186807	ENSMUSG00000026319	1	105663861	105755191	1	0	0	0	0	0	0	35	72	166	19	86	A0A087WRM8	
ENSMUST00000186808						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186809						4	3	17	6	4	0	0	0	0	0	0		
ENSMUST00000186810						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186811	ENSMUSG00000026280	1	93751500	93790610	1	0	1	0	6	0	3	56	80	45	22	11	A0A087WNR6	
ENSMUST00000186812						2	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000186813						4	1	2	2	8	0	0	0	0	0	0		
ENSMUST00000186814						4	5	3	6	7	4	0	0	0	1	0		
ENSMUST00000186815						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186816						1	1	4	1	0	0	0	0	0	0	0		
ENSMUST00000186820						3	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000186822						1	0	0	1	6	0	11	40	32	7	36		
ENSMUST00000186824						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186825	ENSMUSG00000056912	10	100590511	100618401	1	0	0	0	6	0	0	0	0	0	0	0	A0A087WQP6	
ENSMUST00000186826						113	114	349	125	117	63	13	75	38	31	40		
ENSMUST00000186828	ENSMUSG00000014602	1	93015464	93101951	-1	2	0	3	3	5	0	0	0	0	0	0	A0A087WNM0	
ENSMUST00000186831						0	1	8	1	3	1	0	0	0	0	0		
ENSMUST00000186832	ENSMUSG00000026166	1	83116766	83119167	1	0	0	0	1	1	0	0	0	0	0	0	Q642U4	O89093
ENSMUST00000186833						17	6	51	22	20	9	18	161	59	4	90		
ENSMUST00000186835						32	26	23	40	23	28	6	27	37	15	63		
ENSMUST00000186837						8	5	4	1	8	4	0	0	2	2	0		
ENSMUST00000186839						4	4	14	9	14	0	0	0	0	0	0		
ENSMUST00000186840						12	3	10	4	10	2	0	0	0	0	0		
ENSMUST00000186841						0	1	0	1	0	2	0	0	0	0	0		
ENSMUST00000186842						2	0	25	0	2	0	0	0	0	0	0		
ENSMUST00000186846						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186848	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSH2	
ENSMUST00000186851						2	2	1	0	7	2	0	2	0	0	0		
ENSMUST00000186852	ENSMUSG00000025986	1	46807544	46892852	-1	0	1	0	0	1	0	0	1	0	0	0	A0A087WQF7	
ENSMUST00000186853						78	80	377	225	84	52	4	18	3	7	3		
ENSMUST00000186854	ENSMUSG00000036098	19	10208272	10240748	-1	3	0	0	0	0	1	0	0	0	0	2	A0A087WRZ9	
ENSMUST00000186855						7	5	15	9	9	3	0	1	0	0	0		
ENSMUST00000186856						1	1	0	2	1	1	0	0	0	0	0		
ENSMUST00000186857	ENSMUSG00000026104	1	52119440	52161865	1	0	0	0	0	0	0	589	2307	1350	264	1230	Q8C3V4	
ENSMUST00000186859	ENSMUSG00000049755	11	58315114	58330339	-1	0	0	0	3	0	0	0	0	6	1	0	A0A087WQK7	
ENSMUST00000186860						0	0	0	5	3	0	0	0	0	0	0		
ENSMUST00000186861	ENSMUSG00000014602	1	93015464	93101951	-1	2	0	2	6	0	0	0	0	0	0	0	A0A087WSU7	
ENSMUST00000186862						1	2	2	0	3	2	0	0	0	0	0		
ENSMUST00000186863						1	2	0	36	0	0	0	0	0	0	0		
ENSMUST00000186864	ENSMUSG00000035504	10	80329953	80336441	1	0	7	25	43	0	0	0	2	6	4	1		Q9JM62
ENSMUST00000186865						8757	10281	4206	7177	7801	3490	693	4821	1396	1333	1375		
ENSMUST00000186867	ENSMUSG00000026409	1	130689182	130729253	-1	6	4	38	9	13	3	0	11	9	0	19	A0A087WRW5	
ENSMUST00000186868	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ58	
ENSMUST00000186869						1	2	3	0	1	3	0	0	0	0	0		
ENSMUST00000186870	ENSMUSG00000078784	3	14606284	14611285	-1	3	3	0	4	1	0	8	25	3	17	8	A0A087WNR7	
ENSMUST00000186874						8	12	44	125	41	14	0	0	0	0	0		
ENSMUST00000186877						0	2	2	0	1	0	0	0	0	0	0		
ENSMUST00000186878						2	0	2	1	4	0	1	0	0	0	0		
ENSMUST00000186879						29	18	60	52	19	10	2	18	4	5	10		
ENSMUST00000186881						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000186882	ENSMUSG00000034432	1	90602981	90613341	1	0	3	2	1	3	0	37	151	53	3	20		
ENSMUST00000186884						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186887						3	4	27	5	2	4	0	0	0	1	0		
ENSMUST00000186889	ENSMUSG00000051331	6	118587240	119196418	-1	82	89	430	149	127	73	0	0	2	0	1	Q0PCR6	
ENSMUST00000186890	ENSMUSG00000094616	Y	70441882	70468158	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQA3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000186891						19	35	35	34	34	12	0	0	0	1	0		
ENSMUST00000186894	ENSMUSG00000026219	1	84721189	84840516	-1	3	4	0	6	3	0	267	0	768	0	406	A0A0B4J1N9	
ENSMUST00000186896						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000186897						135	99	191	329	160	76	19	127	50	9	53		
ENSMUST00000186898						0	2	7	2	2	0	0	0	0	0	0		
ENSMUST00000186899						0	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000186900						5	0	0	0	0	0	0	0	0	0	5		
ENSMUST00000186903						9	8	12	0	6	0	77	132	63	7	99		
ENSMUST00000186904						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186905						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186906						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186907	ENSMUSG00000027523	2	174284320	174346744	1	1	1	0	0	4	3	0	0	0	0	0		Q6R0H6
ENSMUST00000186908						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186909						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186910	ENSMUSG00000095785	Y	65205185	65207527	-1	18	25	30	0	10	0	0	0	0	0	0	Q810R8	
ENSMUST00000186911	ENSMUSG00000096330	13	98279887	98307154	1	0	1	2	0	3	2	0	0	0	0	0	A0A087WPW4	
ENSMUST00000186913						0	0	1	34	1	0	14	22	9	64	12		
ENSMUST00000186914						2	7	19	2	15	11	212	918	451	60	988		
ENSMUST00000186915	ENSMUSG00000003721	1	121304353	121332589	-1	13	8	16	0	0	2	0	25	18	17	0	A0A087WQP7	
ENSMUST00000186917	ENSMUSG00000041757	1	133181321	133303435	1	0	0	0	0	0	0	13	0	4	0	5	E9PX43	
ENSMUST00000186919						1	0	4	2	4	1	0	0	0	0	0		
ENSMUST00000186920						2	0	1	4	0	0	0	0	0	0	0		
ENSMUST00000186922						109	100	337	128	123	52	5	21	11	2	15		
ENSMUST00000186924						2	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000186925	ENSMUSG00000032565	9	105128903	105131805	-1	0	0	0	60	0	0	0	0	0	0	0	A0A087WRE5	
ENSMUST00000186926						1	0	3	4	3	2	0	0	0	0	0		
ENSMUST00000186927						3	2	12	0	13	7	0	26	26	0	38		
ENSMUST00000186928	ENSMUSG00000095683	7	23131854	23144480	-1	97	102	67	82	108	40	0	13	11	2	4	Q3UT86	
ENSMUST00000186929						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186930	ENSMUSG00000026235	1	77367185	77515088	-1	0	0	0	2	2	0	0	0	0	0	0	A0A087WQW6	
ENSMUST00000186932						0	0	0	29	0	0	2	15	42	266	24		
ENSMUST00000186933						6	5	49	87	13	0	34	62	44	14	25		
ENSMUST00000186934						5	3	27	9	6	0	0	0	0	0	0		
ENSMUST00000186935						1	0	1	0	2	2	0	0	0	0	0		
ENSMUST00000186936						0	2	2	2	3	0	0	0	0	0	0		
ENSMUST00000186937	ENSMUSG00000054523	19	11273238	11283873	-1	3	0	11	5	0	6	0	0	0	0	0	Q2TVW9	
ENSMUST00000186938	ENSMUSG00000094821	Y	62190866	62217137	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQA3	
ENSMUST00000186939						0	0	2	0	0	1	0	0	0	0	0		
ENSMUST00000186940	ENSMUSG00000026193	1	71585520	71653200	-1	0	3	0	0	0	2	0	0	0	0	0	Q4KL80	
ENSMUST00000186941						125	79	463	164	120	65	0	0	0	0	0		
ENSMUST00000186942						45	21	264	60	39	25	0	0	0	0	0		
ENSMUST00000186943	ENSMUSG00000032571	9	105642978	105687657	1	0	2	0	1	1	0	0	0	18	0	2	A0A087WQR4	
ENSMUST00000186945	ENSMUSG00000072704	6	133104909	133110899	1	2	1	0	0	0	0	2	33	15	1	0	A0A087WNX5	
ENSMUST00000186946						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000186947	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	1	0	0	0	6	0	0	47	54	A0A087WR97	
ENSMUST00000186948	ENSMUSG00000079658	1	16641725	16657042	-1	0	0	0	11	6	0	50	156	80	67	12		P83940
ENSMUST00000186949	ENSMUSG00000051223	1	58392898	58407353	1	0	0	0	27	0	0	107	237	685	1513	411	A0A087WQS2	
ENSMUST00000186950						0	2	1	0	3	2	0	0	0	0	0		
ENSMUST00000186951						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186952	ENSMUSG00000062683	15	102662864	102672352	-1	0	3	10	129	6	5	0	0	0	0	0	A0A087WSE2	
ENSMUST00000186953						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186954	ENSMUSG00000053877	7	127511983	127561219	1	0	0	0	3137	1	0	151	189	350	28	2	A0A087WNX7	
ENSMUST00000186956	ENSMUSG00000099077	CHR_MG132_PATCH	124456062	124462462	-1	0	0	0	50	2	0	12	64	28	9	28		
ENSMUST00000186957						0	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000186960	ENSMUSG00000074269	9	58652850	58743964	-1	3	0	9	2	2	0	1	0	1	0	2	A0A087WP95	
ENSMUST00000186961	ENSMUSG00000039218	17	23790662	23824741	1	6	3	8	39	7	5	4	0	0	2	0	A0A087WRX8	
ENSMUST00000186963						3	2	15	2	0	0	0	0	0	0	0		
ENSMUST00000186964						0	0	4	14	3	0	27	216	0	19	32		
ENSMUST00000186965						0	0	19	2	2	0	0	0	0	0	0		
ENSMUST00000186966	ENSMUSG00000042699	1	153455758	153487660	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186969	ENSMUSG00000034359	4	112557194	112652248	1	8	11	11	14	15	14	0	0	0	1	0		A7XUX6
ENSMUST00000186970						6	2	2	3	2	2	0	0	0	0	0		
ENSMUST00000186971	ENSMUSG00000026202	1	75214228	75219865	-1	0	1	0	0	0	0	753	630	513	156	299	A0A087WQS4	
ENSMUST00000186972						0	0	4	72	0	0	0	0	0	0	0		
ENSMUST00000186975						16	25	90	28	15	12	5	15	10	1	15		
ENSMUST00000186976						209	174	151	166	197	91	18	98	37	21	63		
ENSMUST00000186978	ENSMUSG00000024680	19	11615523	11623719	-1	16	19	108	9	14	8	43	140	36	38	16	A0A0B4J1P0	
ENSMUST00000186980	ENSMUSG00000026220	1	84905898	84935134	-1	4	0	12	62	8	4	3	0	3	0	3	A0A087WQR7	
ENSMUST00000186983	ENSMUSG00000038866	1	105990406	106034074	1	6	0	74	0	7	3	51	5	36	3	62	A0A087WSQ9	
ENSMUST00000186984						27	29	37	7	28	15	0	3	0	0	1		
ENSMUST00000186985	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSU6	
ENSMUST00000186986	ENSMUSG00000026309	1	91373861	91398815	-1	0	0	0	0	0	0	0	18	0	3	0	A0A087WQ78	
ENSMUST00000186987						13	13	0	18	7	6	3	16	9	1	4		
ENSMUST00000186988						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000186989	ENSMUSG00000015501	10	13966075	14151374	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQF9	
ENSMUST00000186991						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186994						1	0	3	1	1	2	0	0	0	0	0		
ENSMUST00000186995						2	2	1	23	1	2	0	0	1	0	0		
ENSMUST00000186996	ENSMUSG00000095793	Y	35105684	35131833	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000186997						16	20	15	13	14	6	0	1	6	0	4		
ENSMUST00000186998						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000186999	ENSMUSG00000026153	1	24011093	24100341	-1	4	0	4	0	10	0	0	3	0	0	0	A0A087WQH5	
ENSMUST00000187000	ENSMUSG00000026209	1	75307896	75317990	-1	0	0	0	0	0	0	14	0	27	0	7	A0A087WSE6	
ENSMUST00000187001	ENSMUSG00000042210	9	106440051	106447678	-1	3	0	8	13	0	0	0	0	0	0	0	A0A087WQ50	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187003						32	21	48	51	38	12	2	0	1	0	2		
ENSMUST00000187005	ENSMUSG00000073643	1	79702262	79776143	-1	0	0	0	0	0	0	146	204	209	68	141	A0A087WPX9	
ENSMUST00000187006						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187007	ENSMUSG00000056091	6	72097592	72154571	1	0	0	0	27	0	0	0	0	0	8	8		
ENSMUST00000187009	ENSMUSG00000041417	13	101680563	101768217	-1	0	2	0	0	1	0	0	0	24	0	0	A0A087WQM2	
ENSMUST00000187010						7	5	10	25	5	5	0	0	1	0	0		
ENSMUST00000187012						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000187013						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187017	ENSMUSG00000029419	2	25575416	25581757	-1	0	5	10	21	2	0	0	0	0	0	1	A0A087WP25	
ENSMUST00000187020						2	0	5	5	2	2	2	0	0	0	1		
ENSMUST00000187021						4	1	5	0	1	0	2	0	4	0	2		
ENSMUST00000187022						3	2	0	2	3	1	0	0	0	0	0		
ENSMUST00000187023	ENSMUSG00000056211	1	128103301	128237736	1	0	2	0	0	0	0	0	0	0	0	0	A0A087WPF0	
ENSMUST00000187024						6	8	49	86	10	3	0	1	0	0	0		
ENSMUST00000187028	ENSMUSG00000099689	7	29908223	29916813	1	12	8	19	36	9	5	5	9	5	0	0	A0A087WSF1	
ENSMUST00000187031						0	0	0	0	0	0	53	60	164	22	90		
ENSMUST00000187032	ENSMUSG00000049643	7	27553233	27582099	1	2	0	21	0	5	2	0	12	0	0	0		
ENSMUST00000187033	ENSMUSG00000100338	Y	50097276	50122131	1	0	0	0	2	0	0	0	0	0	0	0	A0A0A6YW38	
ENSMUST00000187035						10	6	8	4	7	3	2	1	1	2	10		
ENSMUST00000187036						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000187037						2	3	15	6	7	8	8	29	4	15	0		
ENSMUST00000187038						6	2	6	200	9	4	0	2	2	1	4		
ENSMUST00000187039	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP48	
ENSMUST00000187040	ENSMUSG00000053877	7	127511983	127561219	1	23	0	94	278	144	44	150	574	610	65	495	A0A087WQ44	
ENSMUST00000187041						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187042	ENSMUSG00000026425	1	131285251	131527352	-1	0	2	0	0	0	3	10	4	6	0	30	A0A087WS73	
ENSMUST00000187046	ENSMUSG00000006299	1	74279840	74284738	-1	0	0	0	0	0	0	46	0	0	0	0	A0A087WNM5	
ENSMUST00000187048	ENSMUSG00000026484	1	151458004	151500955	-1	5	6	13	0	3	1	28	28	35	0	31		Q9CQJ4
ENSMUST00000187049	ENSMUSG00000026309	1	91373861	91398815	-1	10	11	26	10	22	7	13	78	27	9	21	A0A087WRS5	
ENSMUST00000187051	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPF4	
ENSMUST00000187053						3	0	1	0	1	3	0	0	1	0	2		
ENSMUST00000187056						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000187057	ENSMUSG00000037032	7	105558483	105581653	-1	2	3	0	5	2	3	4	0	0	3	0	A0A087WPS7	
ENSMUST00000187058	ENSMUSG00000026203	1	75236406	75245692	1	0	1	15	0	0	0	0	73	0	13	0		Q9QYI5
ENSMUST00000187059						0	1	1	0	1	0	0	1	1	2	0		
ENSMUST00000187060						5	14	18	67	9	5	0	3	0	0	1		
ENSMUST00000187062						14	17	14	30	23	7	0	5	1	0	1		
ENSMUST00000187063						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187064						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187065	ENSMUSG00000032555	9	103305215	103350428	1	0	0	0	5	0	3	0	0	3	0	2	A0A087WPG9	
ENSMUST00000187066						26	27	57	51	19	14	28	315	80	61	182		
ENSMUST00000187069						3	7	3	0	1	5	0	0	0	0	0		
ENSMUST00000187070						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187071						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187072						0	0	6	0	0	0	0	0	0	0	0		
ENSMUST00000187073						0	0	2	0	0	0	7	2	13	6	42		
ENSMUST00000187074						1	2	4	4	7	2	0	1	0	0	0		
ENSMUST00000187075	ENSMUSG00000026209	1	75307896	75317990	-1	0	0	2	10	4	3	0	3	10	0	3	A0A087WS31	
ENSMUST00000187077						33	37	150	43	46	21	1	6	3	0	7		
ENSMUST00000187078	ENSMUSG00000036557	17	87389571	87427741	-1	0	0	0	0	3	0	0	1	0	0	0	A0A087WRD7	
ENSMUST00000187081	ENSMUSG00000099898	7	33063449	33064765	1	1	0	0	0	0	0	0	0	0	0	0	A0A087WP50	
ENSMUST00000187082						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000187083	ENSMUSG00000015501	10	13966075	14151374	1	754	1162	398	374	704	342	0	28	70	10	135		Q3UHF7
ENSMUST00000187084						0	1	0	0	3	0	4	15	9	4	11		
ENSMUST00000187085						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187086						3	3	7	3	4	5	0	0	0	0	0		
ENSMUST00000187088						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000187089	ENSMUSG00000026409	1	130689182	130729253	-1	0	0	0	0	0	0	12	0	0	0	0	A0A087WRG0	
ENSMUST00000187092	ENSMUSG00000042046	1	132417555	132466958	1	0	0	0	1	0	0	0	3	8	0	4	A0A087WQX0	
ENSMUST00000187094						3	4	0	2	2	4	0	0	0	0	0		
ENSMUST00000187095						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187096	ENSMUSG00000033722	1	155212471	155244444	-1	0	0	4	3	5	0	0	0	0	0	0	A0A087WRH5	
ENSMUST00000187097						2	2	5	0	3	1	1	0	0	0	0		
ENSMUST00000187098						1	0	1	0	1	0	3	62	7	16	14		
ENSMUST00000187101						0	0	10	15	0	0	0	0	0	0	0		
ENSMUST00000187102						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187103						5	0	2	2	0	1	514	431	464	130	228		
ENSMUST00000187104						5	10	21	17	14	5	0	0	0	0	0		
ENSMUST00000187105						9	8	28	18	7	3	20	178	65	8	78		
ENSMUST00000187106	ENSMUSG00000042073	9	106447788	106452922	1	0	0	0	3	0	0	0	0	0	0	0	A0A087WP24	
ENSMUST00000187108						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187109						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000187111						3	7	4	8	4	6	3	2	2	3	4		
ENSMUST00000187113						8	7	38	17	27	7	65	280	118	17	204		
ENSMUST00000187115						0	2	2	3	1	0	0	15	4	3	2		
ENSMUST00000187116						1	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000187117						13	16	0	13	20	28	11787	62210	8879	8232	0		
ENSMUST00000187119	ENSMUSG00000056912	10	100590511	100618401	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSG1	
ENSMUST00000187120						2	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000187124						2	2	8	2	1	1	0	0	0	0	0		
ENSMUST00000187126	ENSMUSG00000093803	9	124422622	124476861	-1	0	1	3	13	0	0	20	40	13	6	16	A0A087WP99	
ENSMUST00000187128						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187132						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187134						1	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187135	ENSMUSG00000099894	Y	81458007	81484087	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSS0	
ENSMUST00000187136						7	6	18	3	13	8	1	1	1	1	3		
ENSMUST00000187137	ENSMUSG00000036634	7	30899176	30914873	-1	0	0	0	0	22	0	0	0	0	0	0		P20917
ENSMUST00000187138	ENSMUSG00000095854	14	52855614	52856166	1	0	0	0	0	0	1	0	0	0	0	0	A0A075B6A1	
ENSMUST00000187139						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000187140	ENSMUSG00000101578	13	22620097	22621035	-1	2	2	2	3	2	6	0	0	0	0	0	Q8R277	
ENSMUST00000187141						6	4	0	0	0	3	5	19	0	8	0		
ENSMUST00000187143	ENSMUSG00000019813	10	41718840	41809871	-1	8	4	7	0	3	1	4	0	2	12	7	B2RR53	
ENSMUST00000187144						0	0	9	0	0	0	0	0	0	0	0		
ENSMUST00000187145						24	8	23	321	36	6	0	0	0	0	0		
ENSMUST00000187146	ENSMUSG00000101915	Y	88053315	88079494	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQL3	
ENSMUST00000187148	ENSMUSG00000000103	Y	2106015	2170409	-1	0	1	0	0	0	0	0	0	0	0	0		P20662
ENSMUST00000187149						11	18	38	27	20	18	0	4	4	0	8		
ENSMUST00000187151						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000187153						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187155	ENSMUSG00000021209	12	103532283	103613831	1	3	0	6	0	0	0	1	0	0	0	0		Q8C0Y0
ENSMUST00000187156	ENSMUSG00000021901	14	31251450	31259944	1	0	0	0	0	0	0	3	20	11	0	9	A0A087WPT1	
ENSMUST00000187157	ENSMUSG00000038791	18	43764289	43767399	1	0	0	0	2	1	2	0	0	0	0	0	Q5D060	Q920H1
ENSMUST00000187159						2	2	1	36	4	2	0	0	0	0	0		
ENSMUST00000187160	ENSMUSG00000062683	15	102662864	102672352	-1	0	0	18	7	5	1	10	5	4	2	6	A0A087WQS5	
ENSMUST00000187161						0	1	0	0	0	0	1	1	0	0	1		
ENSMUST00000187163	ENSMUSG00000076864	14	53881612	53882217	1	3	0	1	0	0	0	0	0	0	0	0	A0A087WPH8	
ENSMUST00000187164						2	0	2	2	1	1	0	0	0	0	0		
ENSMUST00000187165	ENSMUSG00000099925	Y	83030947	83057301	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP44	
ENSMUST00000187166						20	10	18	11	17	8	0	4	7	0	0		
ENSMUST00000187167						0	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000187168	ENSMUSG00000022884	16	23107444	23114136	1	0	0	3	0	0	0	0	0	121	458	190	Q8BTU6	
ENSMUST00000187169						3	6	11	4	4	1	0	0	0	0	0		
ENSMUST00000187170	ENSMUSG00000070871	1	64690455	64725644	1	0	0	0	14	0	0	0	0	4	0	0	E9Q226	
ENSMUST00000187171	ENSMUSG00000075602	15	74994877	74998031	-1	2	0	0	0	0	0	0	0	2	0	0		P05533
ENSMUST00000187173						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187175						19	18	27	25	26	17	15	15	16	0	45		
ENSMUST00000187176						0	1	10	0	0	1	0	0	0	0	0		
ENSMUST00000187178						1	1	1	0	1	0	5	6	6	0	3		
ENSMUST00000187179						2	2	5	1	1	1	0	0	0	0	0		
ENSMUST00000187180						3	1	0	8	1	0	0	0	0	0	0		
ENSMUST00000187182	ENSMUSG00000032036	9	34485894	35036716	1	14	11	4	24	2	10	5	0	7	0	120		Q8BR86
ENSMUST00000187183	ENSMUSG00000095620	16	36221468	36257444	1	68	48	153	62	71	36	0	10	0	14	7	Q9D8D6	
ENSMUST00000187184	ENSMUSG00000025997	1	69531214	69687245	-1	0	4	3	11	8	0	0	0	0	0	0		P81183
ENSMUST00000187185	ENSMUSG00000061080	16	39984361	42181679	1	4	1	4	0	2	1	0	0	0	0	0	A0A087WP06	
ENSMUST00000187186						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187187						4	7	14	7	2	3	0	0	0	0	0		
ENSMUST00000187188						0	3	0	0	1	0	51	25	71	1	37		
ENSMUST00000187190	ENSMUSG00000030491	7	35469098	35537745	-1	8	0	16	9	4	4	0	0	0	0	0	A0A087WQS9	
ENSMUST00000187193	ENSMUSG00000066456	9	83109948	83146685	-1	0	0	0	0	0	0	0	2	0	0	0	A0A087WSB8	
ENSMUST00000187194	ENSMUSG00000026383	1	119545037	119649000	-1	5	2	4	90	9	4	0	0	0	0	0	A0A087WP93	
ENSMUST00000187195						53	41	104	732	63	32	2	12	3	0	7		
ENSMUST00000187196	ENSMUSG00000021148	13	8941575	8948231	-1	0	7	0	1	9	0	0	0	0	0	0		Q8BFZ6
ENSMUST00000187197						0	0	0	0	2	0	0	1	0	5	0		
ENSMUST00000187202						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000187207						1	1	1	1	1	1	0	0	0	0	0		
ENSMUST00000187208						6	5	3	0	0	0	0	0	0	0	0		
ENSMUST00000187210						0	0	4	3	2	0	0	0	0	0	0		
ENSMUST00000187211						55	46	135	298	46	24	5	13	7	1	17		
ENSMUST00000187212						2	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000187213	ENSMUSG00000009545	7	143106362	143427042	1	9	6	18	44	18	10	0	0	0	0	0	A0A087WPA8	
ENSMUST00000187214						1	0	3	0	0	1	0	0	0	0	2		
ENSMUST00000187216						3	3	6	3	2	2	0	0	0	0	0		
ENSMUST00000187217						0	0	19	24	0	0	0	0	0	0	0		
ENSMUST00000187219						0	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000187220	ENSMUSG00000071178	12	103728156	103830373	-1	1	3	1	5	1	3	0	0	0	0	0	A0A087WSE0	
ENSMUST00000187221						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187222						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000187223						20	14	15	11	14	4	0	0	0	0	0		
ENSMUST00000187226	ENSMUSG00000056763	1	10037987	10136768	1	0	0	0	1	0	0	2	49	0	17	5	A0A087WQ80	
ENSMUST00000187229						1	1	0	1	4	1	0	0	0	0	0		
ENSMUST00000187230						5	2	15	52	8	4	0	0	0	0	0		
ENSMUST00000187231	ENSMUSG00000026309	1	91373861	91398815	-1	0	1	5	2	2	5	8	21	17	8	31	A0A087WPY0	
ENSMUST00000187232						1	2	1	4	3	0	0	0	0	0	0		
ENSMUST00000187234						0	2	0	0	0	0	2	1	0	1	0		
ENSMUST00000187235						0	1	1	8	6	4	5	22	26	0	63		
ENSMUST00000187237	ENSMUSG00000072704	6	133104909	133110899	1	0	0	0	0	4	0	0	0	0	0	0	A0A087WPM1	
ENSMUST00000187238	ENSMUSG00000026167	1	74791516	74804179	1	0	0	0	0	2	0	0	0	0	1	0	A0A087WP71	
ENSMUST00000187239						15	14	15	11	12	1	0	0	0	0	0		
ENSMUST00000187240						0	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000187241	ENSMUSG00000066613	5	109996521	110010411	1	0	0	0	0	0	0	7	31	0	0	0	A0A087WR27	
ENSMUST00000187242	ENSMUSG00000022952	16	92601466	92826149	-1	1	1	7	3	4	0	0	0	0	0	0	A0A087WPL0	
ENSMUST00000187243						0	0	1	2	1	0	0	0	0	0	0		
ENSMUST00000187244						22	9	17	25	20	4	4	6	0	1	0		
ENSMUST00000187245	ENSMUSG00000095950	Y	10533609	10536042	-1	4	0	5	0	0	0	0	0	0	0	0	Q3TTD8	
ENSMUST00000187246						4	4	9	3	6	3	0	2	0	0	1		
ENSMUST00000187248						2	2	11	5	4	1	7	11	6	26	4		
ENSMUST00000187249						0	2	0	0	5	3	0	0	0	0	0		
ENSMUST00000187250						6	6	18	13	10	5	9	52	7	28	9		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187251						22	19	23	42	27	8	0	12	7	0	0		
ENSMUST00000187254						10	3	11	8	6	0	1	2	0	0	1		
ENSMUST00000187255						0	0	0	109	2	0	0	0	0	0	0		
ENSMUST00000187256						4	2	23	3	5	3	0	0	0	0	0		
ENSMUST00000187257	ENSMUSG00000099581	7	32100853	32102169	1	0	1	5	6	1	2	0	0	0	0	0	A0A087WPW0	
ENSMUST00000187261						0	7	0	0	15	0	0	0	0	0	0		
ENSMUST00000187262	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	17	35	0	0	A0A087WQI3	
ENSMUST00000187263						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187264						6	8	0	14	12	0	0	0	0	0	0		
ENSMUST00000187269						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000187271	ENSMUSG00000099550	Y	70004208	70014899	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR12	
ENSMUST00000187273	ENSMUSG00000026425	1	131285251	131527352	-1	2	1	0	0	0	0	0	0	0	0	0	A0A087WNR5	
ENSMUST00000187275						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187276						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187277	ENSMUSG00000093987	Y	3367147	3410167	-1	0	4	0	0	2	0	0	0	0	0	0		O35698
ENSMUST00000187278						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000187279						6	4	6	25	3	1	12	19	25	8	59		
ENSMUST00000187281	ENSMUSG00000055322	1	73910231	74124449	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP40	
ENSMUST00000187282	ENSMUSG00000044452	7	35772343	35803003	-1	0	1	0	14	2	3	0	3	8	0	6	A0A087WS86	
ENSMUST00000187284	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	0	0	0	8	5	8	0	0	Q99JA5	
ENSMUST00000187285	ENSMUSG00000041757	1	133181321	133303435	1	24	12	52	151	18	11	0	0	0	0	0	A0A087WRB7	
ENSMUST00000187287						24	19	249	220	25	9	1	6	2	0	4		
ENSMUST00000187291						7	3	5	3	8	3	0	0	0	0	0		
ENSMUST00000187293	ENSMUSG00000094570	Y	55213720	55239871	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000187294						34	56	74	28	30	18	0	0	0	0	0		
ENSMUST00000187296						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187297						6	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000187299	ENSMUSG00000041757	1	133181321	133303435	1	2	1	3	11	1	4	0	0	1	0	1	A0A087WPX6	
ENSMUST00000187301						6	0	23	0	4	1	0	0	0	0	1		
ENSMUST00000187302						6	7	21	7	9	5	0	0	0	0	0		
ENSMUST00000187303						0	0	3	1	1	2	1	9	3	9	5		
ENSMUST00000187304	ENSMUSG00000042888	14	101197690	101200330	-1	9	9	17	17	13	0	0	0	0	0	3		Q9D9B7
ENSMUST00000187305						5	1	3	0	3	0	0	0	0	0	0		
ENSMUST00000187306	ENSMUSG00000026309	1	91373861	91398815	-1	0	0	1	0	0	0	0	0	0	0	0	A0A087WPM3	
ENSMUST00000187307	ENSMUSG00000045690	12	75630596	75669537	-1	0	2	1	0	0	0	0	0	0	0	0		Q9D0R9
ENSMUST00000187308	ENSMUSG00000026313	1	91928779	92180341	-1	0	0	6	4	7	0	126	52	161	7	184	A0A087WQ92	
ENSMUST00000187309						0	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000187310						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187311						18	9	76	32	16	13	0	8	0	0	3		
ENSMUST00000187313	ENSMUSG00000005763	1	165788681	165877277	1	3	0	0	0	0	0	0	0	0	0	0		P29020
ENSMUST00000187316						2	0	0	0	1	2	0	8	1	2	5		
ENSMUST00000187317	ENSMUSG00000051331	6	118587240	119196418	-1	2	5	0	0	4	0	0	0	0	0	0	A0A087WRM3	
ENSMUST00000187319						0	3	0	19	6	2	0	0	2	4	4		
ENSMUST00000187321	ENSMUSG00000073609	1	93824909	93852348	1	1	0	5	4	3	1	0	0	3	0	3	A0A087WQG0	
ENSMUST00000187323						2	3	0	53	4	0	7	38	55	26	42		
ENSMUST00000187324						0	0	0	0	6	0	3	2	7	0	0		
ENSMUST00000187325						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187326						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187328						25	12	8	0	0	0	0	0	0	0	0		
ENSMUST00000187329						1	5	7	11	6	1	0	0	0	0	0		
ENSMUST00000187330						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187331						0	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000187333						3	0	0	9	8	0	0	0	0	0	0		
ENSMUST00000187334						0	0	4	0	0	3	0	0	0	0	0		
ENSMUST00000187336						1	1	0	2	4	0	4	38	8	12	16		
ENSMUST00000187338						0	0	0	18	1	0	4	0	0	1	1		
ENSMUST00000187339	ENSMUSG00000079330	1	132191431	132259227	1	0	0	3	0	1	0	0	0	0	0	0	A0A087WPB5	
ENSMUST00000187340						2	0	0	6	1	0	0	0	0	0	0		
ENSMUST00000187341						0	0	0	0	1	1	0	2	1	0	2		
ENSMUST00000187342	ENSMUSG00000026270	1	92934376	92947941	1	0	2	0	0	0	0	0	0	0	0	0	A0A087WSM6	
ENSMUST00000187346	ENSMUSG00000026235	1	77367185	77515088	-1	1	1	0	0	2	0	0	0	0	0	0	A0A087WRH4	
ENSMUST00000187347	ENSMUSG00000079018	15	75044018	75048830	-1	0	0	0	0	0	2	213	0	96	554	187		P0CW02
ENSMUST00000187348						2	4	7	7	3	0	7	10	9	2	5		
ENSMUST00000187353						142	120	244	154	151	85	17	50	30	22	27		
ENSMUST00000187354						4	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000187356						15	16	11	39	14	9	0	0	0	0	0		
ENSMUST00000187357	ENSMUSG00000008136	1	43123074	43196984	-1	6	0	0	0	2	0	1	0	0	0	5	A0A087WR06	
ENSMUST00000187358						16	19	3	13	13	4	1	9	7	3	3		
ENSMUST00000187359						37	23	40	29	40	14	4	17	12	2	20		
ENSMUST00000187360						2	1	1	4	6	0	0	0	0	0	0		
ENSMUST00000187362						46	58	68	660	97	44	6	36	8	23	26		
ENSMUST00000187363	ENSMUSG00000099909	2	89439333	89440277	-1	7	2	9	2	5	2	0	0	0	0	0	Q8VG73	
ENSMUST00000187364						140	153	470	60	146	61	0	6	5	0	12		
ENSMUST00000187365						0	2	0	4	5	1	0	0	0	0	0		
ENSMUST00000187367						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187369	ENSMUSG00000026153	1	24011093	24100341	-1	0	0	0	0	0	0	0	0	0	4	0	A0A087WRT5	
ENSMUST00000187371						5	3	9	1	4	3	0	1	1	0	0		
ENSMUST00000187373						2	1	0	11	2	0	0	0	0	0	0		
ENSMUST00000187375						2	0	0	1	4	2	7	32	20	0	26		
ENSMUST00000187376						16	8	3	11	9	13	0	0	0	0	0		
ENSMUST00000187377	ENSMUSG00000041730	14	32599407	32649246	1	0	0	0	76	8	0	0	0	0	0	0		Q8BYH0
ENSMUST00000187379						25	39	29	24	42	21	1	6	5	4	22		
ENSMUST00000187380						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187382	ENSMUSG00000037428	5	137026392	137033351	1	0	0	0	1	0	0	0	0	0	0	0	A0A087WQ93	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187386	ENSMUSG00000051331	6	118587240	119196418	-1	2	7	18	10	19	3	0	0	0	0	0	A0A087WQT9	
ENSMUST00000187388						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187389	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	0	0	0	12	16	7	0	9	Q5BL18	Q8K310
ENSMUST00000187390						0	2	2	0	0	1	0	1	2	0	0		
ENSMUST00000187391	ENSMUSG00000031452	8	13550733	13562461	-1	0	0	49	0	0	0	0	0	0	0	0	G3X906	
ENSMUST00000187392	ENSMUSG00000031585	8	33731833	33777173	1	0	0	0	53	5	0	0	0	5	2	2	A0A087WSS5	
ENSMUST00000187395						6	4	13	4	5	4	0	0	0	0	0		
ENSMUST00000187398						5	6	9	6	1	5	0	0	0	0	0		
ENSMUST00000187400	ENSMUSG00000026782	1	60409619	60481158	1	0	0	0	0	0	0	0	0	0	0	2	A0A087WP64	
ENSMUST00000187404						2	0	4	0	5	0	0	0	0	0	0		
ENSMUST00000187405						2	3	2	0	5	2	0	0	0	0	0		
ENSMUST00000187406	ENSMUSG00000025993	1	45908068	45926523	-1	0	0	0	0	0	3	0	0	0	0	7	C5H8V4	
ENSMUST00000187407	ENSMUSG00000026393	1	138482875	138620141	-1	32	24	29	10	29	7	319	914	497	94	244		Q9ES74
ENSMUST00000187410	ENSMUSG00000016524	1	130932656	130940115	-1	5	4	4	0	0	0	0	0	0	0	0	Q14BK1	Q8CJ70
ENSMUST00000187411	ENSMUSG00000051703	1	75479532	75485705	1	0	0	3	6	0	0	1	0	0	0	0	A0A087WRW1	
ENSMUST00000187413						0	1	0	0	0	3	0	0	0	0	0		
ENSMUST00000187414						0	0	0	0	0	0	0	8	0	0	0		
ENSMUST00000187416						47	83	83	39	43	33	0	0	0	0	0		
ENSMUST00000187417						2	0	6	8	0	1	13	140	35	22	30		
ENSMUST00000187418	ENSMUSG00000094052	Y	70271306	70273642	-1	12	4	5	31	11	9	0	0	0	0	0	J3QPK8	
ENSMUST00000187420	ENSMUSG00000025993	1	45908068	45926523	-1	0	0	0	0	0	0	0	0	100	72	280	C5H8V4	
ENSMUST00000187422						0	2	0	1	1	1	9	14	7	10	18		
ENSMUST00000187424	ENSMUSG00000014850	13	92211872	92355003	-1	0	1	0	0	0	1	0	0	0	0	0	A0A087WP45	
ENSMUST00000187425						2	3	0	1	2	0	0	0	0	0	0		
ENSMUST00000187427						9	11	42	1	8	5	6	44	29	25	7		
ENSMUST00000187428						0	0	9	0	0	0	0	0	0	0	0		
ENSMUST00000187429	ENSMUSG00000030213	6	136506167	136610862	1	0	1	1	0	16	11	292	0	782	7	418	A0A087WR75	
ENSMUST00000187430						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187431						175	276	9031	286	387	356	8	18	7	3	1		
ENSMUST00000187432	ENSMUSG00000047330	1	78816758	78820028	1	1	7	1	3	0	5	0	0	0	0	0	A0A087WQK6	
ENSMUST00000187433	ENSMUSG00000095578	Y	80133779	80159975	1	0	0	2	0	0	0	0	0	0	0	0	A0A087WP44	
ENSMUST00000187434	ENSMUSG00000094813	Y	10750004	10752450	-1	0	0	0	0	10	14	0	0	0	0	0	Q3TTD8	
ENSMUST00000187435	ENSMUSG00000066877	1	43444579	43570515	1	1	2	2	0	2	1	0	0	3	0	0	A0A087WQT7	
ENSMUST00000187436						3	2	4	1	1	1	0	0	4	1	0		
ENSMUST00000187437						4	3	0	3	2	2	1	2	0	0	0		
ENSMUST00000187438						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000187440						5	4	6	12	10	3	0	0	0	0	0		
ENSMUST00000187442						0	0	0	42	1	0	0	2	10	0	6		
ENSMUST00000187444						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187445	ENSMUSG00000026279	1	93701935	93754864	-1	0	2	6	1	1	0	2	2	0	0	4	A0A087WQL4	
ENSMUST00000187446						6	12	38	53	6	10	7	6	13	1	0		
ENSMUST00000187447						1	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000187448						2	0	11	5	4	3	0	0	0	0	0		
ENSMUST00000187449						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000187451						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187454						0	0	2	2	0	0	0	0	0	0	1		
ENSMUST00000187455	ENSMUSG00000100305	1	117830081	117854496	1	18	9	19	15	15	7	0	0	0	0	0	A0A087WR25	
ENSMUST00000187456						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187459						11	4	27	6	7	3	0	0	0	0	0		
ENSMUST00000187460	ENSMUSG00000026341	1	125392905	125435727	-1	0	0	0	0	1	0	0	0	510	0	0	A0A087WQ14	
ENSMUST00000187462						1	1	1	3	0	2	51	318	82	644	178		
ENSMUST00000187463						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187464						3	2	7	4	4	2	0	0	0	0	0		
ENSMUST00000187466						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187467	ENSMUSG00000099398	19	11301249	11314454	-1	27	17	555	63	29	11	0	0	0	0	1	A0A087WSD2	
ENSMUST00000187468						0	2	1	2	3	1	0	0	4	0	3		
ENSMUST00000187469						5	6	9	2	10	3	2	1	0	0	4		
ENSMUST00000187470						1	2	5	2	1	1	0	0	0	0	0		
ENSMUST00000187472						0	0	4	0	1	1	0	0	0	0	0		
ENSMUST00000187474	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	C7TQ59	
ENSMUST00000187475						7	5	33	181	20	10	5	11	3	1	10		
ENSMUST00000187477	ENSMUSG00000100485	Y	51852120	51878300	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000187478						2	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000187480						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000187481						9	21	14	14	15	10	0	0	0	0	0		
ENSMUST00000187482	ENSMUSG00000102053	Y	2785165	2796205	-1	0	0	0	7	0	0	0	0	0	0	0	A0A087WR82	
ENSMUST00000187485	ENSMUSG00000034730	15	74516195	74589465	1	43	35	121	41	62	23	50	44	61	8	60	A0A087WSA1	
ENSMUST00000187486	ENSMUSG00000026131	1	33908225	34308661	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRB8	
ENSMUST00000187487						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187490						57	36	90	29	49	19	1	1	5	2	2		
ENSMUST00000187491	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	0	0	0	0	6	9	32	6	A0A087WQ59	
ENSMUST00000187492						6	2	0	1	2	1	0	0	0	0	0		
ENSMUST00000187493	ENSMUSG00000074199	7	30787896	30791097	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRR2	
ENSMUST00000187494						1	5	3	3	9	7	0	1	1	1	0		
ENSMUST00000187499	ENSMUSG00000099077	CHR_MG132_PATCH	124456062	124462462	-1	1	0	0	49	0	1	3	13	6	2	8		
ENSMUST00000187500						3	2	5	14	0	2	549	534	446	220	848		
ENSMUST00000187501						1	4	1	0	0	1	0	0	0	0	0		
ENSMUST00000187504	ENSMUSG00000096740	19	8883732	8892627	1	37	20	90	48	33	21	52	98	47	27	36	A0A087WPA0	
ENSMUST00000187505	ENSMUSG00000026439	1	132477365	132505659	1	1	16	12	0	0	0	1	0	7	0	2	A0A087WST2	
ENSMUST00000187507	ENSMUSG00000026600	1	156424525	156474331	-1	0	0	0	40	0	2	0	0	217	0	97	A0A087WNN8	
ENSMUST00000187508						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000187509	ENSMUSG00000101874	11	49327413	49328348	1	8	4	3	3	7	2	0	1	0	0	0	Q8VFA4	
ENSMUST00000187510	ENSMUSG00000046159	13	9875486	10360844	-1	15	15	15	15	11	10	100	375	122	42	149	Q542R4	Q9ERZ3
ENSMUST00000187512	ENSMUSG00000046248	7	142201364	142203015	1	12	8	90	47	20	6	0	0	0	0	0	A0A087WSN0	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187513	ENSMUSG00000099703	18	35553404	35581609	1	0	0	2	9	0	0	3	0	1	1	0	A0A087WPQ5	
ENSMUST00000187516	ENSMUSG00000026177	1	74375195	74386062	1	2	3	0	0	8	2	45	39	30	0	90	A0A087WNR0	
ENSMUST00000187518						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187519	ENSMUSG00000042564	15	79609576	79658956	-1	0	0	0	0	0	0	0	0	18	0	0	Q9D3V8	
ENSMUST00000187520	ENSMUSG00000037681	9	99309963	99358557	-1	0	2	2	0	0	0	0	0	0	0	0	A0A087WRC5	
ENSMUST00000187521	ENSMUSG00000035941	9	85687360	85749334	-1	0	0	0	50	0	3	296	1056	700	173	638	A0A087WNN3	
ENSMUST00000187522						18	27	141	30	19	3	13	81	21	7	44		
ENSMUST00000187524	ENSMUSG00000045411	7	44246722	44252319	1	10	0	0	3	6	0	3	13	5	0	4	A0A087WQ29	
ENSMUST00000187525						4	3	4	0	0	0	0	1	0	0	0		
ENSMUST00000187527						0	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000187529						0	0	0	0	0	0	6	0	7	2	32		
ENSMUST00000187530	ENSMUSG00000096175	13	119912095	119929272	-1	50	48	28	28	44	31	0	0	0	0	0	J3QK00	
ENSMUST00000187531	ENSMUSG00000037572	14	47240944	47276857	-1	0	0	0	10	0	0	0	0	0	0	0		P59328
ENSMUST00000187532						0	4	4	4	5	3	0	13	6	3	5		
ENSMUST00000187533						2	3	11	3	4	5	0	1	0	0	0		
ENSMUST00000187535						1	0	0	16	1	1	0	0	0	0	0		
ENSMUST00000187537	ENSMUSG00000056536	1	105518422	105663677	-1	8	2	3	0	4	6	4	7	4	3	0	A0A087WQ32	
ENSMUST00000187538						0	2	2	1	0	1	3	6	1	0	7		
ENSMUST00000187539						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187540						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000187541	ENSMUSG00000004110	1	154390731	154884501	-1	93	22	121	68	67	32	7	67	13	0	27	A0A087WS83	
ENSMUST00000187543	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	0	0	0	0	3	0	0	0	A0A087WQP4	
ENSMUST00000187544	ENSMUSG00000029673	5	131437333	132543344	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPF7	
ENSMUST00000187545						24	22	9	19	20	4	0	0	0	0	0		
ENSMUST00000187546	ENSMUSG00000026592	1	157099139	157108680	-1	0	4	0	0	0	0	0	0	0	0	0	A0A087WNR4	
ENSMUST00000187547						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187548						181	182	233	184	194	90	8	15	21	2	9		
ENSMUST00000187549	ENSMUSG00000021103	12	73123717	73273988	1	18	16	46	18	16	14	4	7	0	4	7	A0A087WSG5	
ENSMUST00000187550	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	3	59	9	0	0	0	0	5	0	Q4V9V4	
ENSMUST00000187552						5	2	2	0	4	1	0	1	3	0	0		
ENSMUST00000187554						1	3	4	0	4	1	0	0	5	0	2		
ENSMUST00000187555						8	2	5	51	9	5	0	0	0	0	0		
ENSMUST00000187557	ENSMUSG00000056211	1	128103301	128237736	1	2	1	0	0	0	1	0	0	0	0	0	A0A087WRE1	
ENSMUST00000187559						2	5	41	19	0	7	0	0	0	0	0		
ENSMUST00000187562						1	1	0	3	2	1	5	81	54	10	8		
ENSMUST00000187563						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187565						5	5	40	0	8	2	0	0	0	0	1		
ENSMUST00000187566						2	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000187567						0	4	8	5	5	1	0	0	0	0	4		
ENSMUST00000187568						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187569						4	1	2	0	7	2	0	0	0	0	0		
ENSMUST00000187570	ENSMUSG00000100923	11	49317548	49318483	1	8	0	9	7	5	0	0	0	0	0	0		Q60883
ENSMUST00000187572						4	1	5	2	3	5	0	0	0	0	0		
ENSMUST00000187573						16	0	16	82	11	9	13	18	37	5	51		
ENSMUST00000187574						12	8	10	10	8	6	0	1	0	0	0		
ENSMUST00000187575						134	154	392	105	154	64	6	28	15	4	21		
ENSMUST00000187578						10	4	71	47	12	5	52	87	43	20	89		
ENSMUST00000187579						44	45	125	35	69	20	5	14	2	2	8		
ENSMUST00000187581						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187583						0	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000187584	ENSMUSG00000055322	1	73910231	74124449	-1	93	17	233	7	0	53	0	0	0	9	0	A0A087WQM0	
ENSMUST00000187585						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187586						18	19	111	40	23	16	449	905	1004	48	1150		
ENSMUST00000187588						10	6	0	4	6	2	0	17	0	0	0		
ENSMUST00000187590						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187591						4	5	1	1	1	3	0	0	0	0	0		
ENSMUST00000187593						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187596						4	5	11	6	1	0	1	0	0	3	3		
ENSMUST00000187599	ENSMUSG00000034730	15	74516195	74589465	1	0	0	0	6	0	0	0	0	1	0	0	A0A087WRZ4	
ENSMUST00000187600						0	0	0	0	0	2	0	0	5	0	0		
ENSMUST00000187601						5	1	2	3	7	2	10	24	29	0	35		
ENSMUST00000187602	ENSMUSG00000042215	1	33745484	33757795	-1	0	0	0	6	2	0	0	1	3	0	1	A0A087WNX9	
ENSMUST00000187603	ENSMUSG00000032666	1	151852403	152090125	-1	13	23	18	16	12	9	3	11	3	0	0	Q3TJL3	Q8K207
ENSMUST00000187605						70	45	178	79	50	43	6	7	9	3	17		
ENSMUST00000187606	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	0	0	0	0	7	0	0	0	Q99JA5	
ENSMUST00000187607						4	5	2	8	2	4	0	0	0	0	3		
ENSMUST00000187608						3	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000187609	ENSMUSG00000030717	7	126623249	126630861	-1	0	0	0	1	0	0	0	90	26	38	36		
ENSMUST00000187610						71	95	158	81	80	40	4	12	4	2	14		
ENSMUST00000187611						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187612						18	9	82	104	26	12	0	7	3	0	4		
ENSMUST00000187613						2	1	0	0	3	2	0	0	0	0	0		
ENSMUST00000187614						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187615	ENSMUSG00000015882	5	45697181	45857615	-1	0	0	0	0	0	0	0	0	15	0	5	A0A087WNR9	
ENSMUST00000187616	ENSMUSG00000074158	7	42609526	42642588	-1	0	0	1	0	0	0	0	0	2	0	0	A0A087WSF4	
ENSMUST00000187617						16	12	26	159	28	7	1	0	0	0	0		
ENSMUST00000187618	ENSMUSG00000030228	6	139587221	139969284	1	0	2	0	0	2	0	0	0	0	0	0	Q4FZD4	
ENSMUST00000187619	ENSMUSG00000026153	1	24011093	24100341	-1	0	3	1	0	4	0	0	0	0	0	0	A0A087WQ08	
ENSMUST00000187621						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187622						1	0	5	1	0	0	0	0	0	0	2		
ENSMUST00000187623						8	11	40	12	17	10	5	35	16	4	32		
ENSMUST00000187624						26	14	76	63	35	12	0	0	0	0	1		
ENSMUST00000187625	ENSMUSG00000032036	9	34485894	35036716	1	0	0	0	25	27	0	50	146	99	6	153	G5E8B6	
ENSMUST00000187627	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	0	0	0	0	168	65	102	11	780	A0A087WS99	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187628	ENSMUSG00000010453	1	36335730	36369181	-1	0	0	0	1	0	0	0	1	0	0	1	A0A087WQ64	
ENSMUST00000187631	ENSMUSG00000042429	1	134199223	134235431	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRW7	
ENSMUST00000187632						1	0	0	0	0	2	0	7	0	7	4		
ENSMUST00000187633						10	3	33	1	11	0	0	3	0	0	0		
ENSMUST00000187634						3	0	2	7	3	2	0	0	0	0	0		
ENSMUST00000187636						0	0	7	0	0	1	2	3	2	3	16		
ENSMUST00000187638	ENSMUSG00000070871	1	64690455	64725644	1	0	0	0	32	0	1	0	2	5	0	1	A0A087WPI4	
ENSMUST00000187639	ENSMUSG00000034730	15	74516195	74589465	1	7	2	11	148	0	0	4	0	0	0	8		
ENSMUST00000187640						9	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187641						478	414	1167	478	433	218	34	732	143	35	274		
ENSMUST00000187643	ENSMUSG00000068071	16	89140851	89141339	1	3	2	7	0	7	0	0	0	0	0	0	A0A087WPH4	
ENSMUST00000187646	ENSMUSG00000003346	10	80583654	80590341	-1	0	0	0	46	0	0	0	0	0	0	0	A0A087WR09	
ENSMUST00000187647	ENSMUSG00000023277	9	106203108	106215389	1	3	0	0	0	3	0	15	9	7	12	11	A0A087WRG4	
ENSMUST00000187648						0	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000187650	ENSMUSG00000026420	1	130882074	130887454	-1	0	4	0	9	9	1	0	0	0	0	0	A0A087WQD7	
ENSMUST00000187651	ENSMUSG00000025931	1	20890606	20939650	1	12	0	13	0	6	2	1	0	5	0	0		Q80ZE5
ENSMUST00000187652						5	7	15	9	4	2	2	7	2	4	4		
ENSMUST00000187653	ENSMUSG00000051590	1	127815253	127840321	-1	0	0	62	0	0	0	0	0	0	0	3	A0A087WS76	
ENSMUST00000187654						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187656	ENSMUSG00000094942	13	62368328	62383177	-1	10	10	15	4	7	6	15	31	7	15	8	A0A087WPN2	
ENSMUST00000187658						1	1	3	1	1	1	0	0	0	0	0		
ENSMUST00000187659	ENSMUSG00000086727	1	31135226	31222684	-1	0	0	0	0	0	0	0	0	0	0	0	B7ZWJ4	
ENSMUST00000187660						0	0	1	1	3	0	0	0	0	0	0		
ENSMUST00000187662						15	5	4	9	8	4	0	0	0	0	0		
ENSMUST00000187664						4	0	1	5	0	1	0	0	0	0	0		
ENSMUST00000187667	ENSMUSG00000038750	9	78327589	78329620	1	2	0	0	1	0	0	0	0	0	0	0	D3YX29	
ENSMUST00000187668						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187671						4	0	0	0	3	2	0	0	0	0	0		
ENSMUST00000187672						6	10	12	13	16	9	18	28	32	57	27		
ENSMUST00000187673						3	5	1	1	0	4	0	0	0	0	0		
ENSMUST00000187674						8	14	104	16	11	5	2	9	2	8	3		
ENSMUST00000187678	ENSMUSG00000026309	1	91373861	91398815	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQG1	
ENSMUST00000187679	ENSMUSG00000001248	7	31130127	31155896	-1	4	0	3	1	9	1	3	9	9	2	5	A0A087WRK8	
ENSMUST00000187680						2	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000187682						15	16	93	12	15	13	0	0	0	0	0		
ENSMUST00000187683	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	0	0	0	0	0	3	0	0	0	A0A087WNN4	
ENSMUST00000187684						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187688						144	122	82	68	99	62	0	0	0	1	0		
ENSMUST00000187689						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187690	ENSMUSG00000034595	17	35865593	35875596	1	0	29	24	115	0	0	468	494	833	0	397		Q8BQ30
ENSMUST00000187691	ENSMUSG00000055322	1	73910231	74124449	-1	0	4	3	12	0	4	29	0	26	0	34	Q9DBT6	
ENSMUST00000187694						24	20	32	55	13	14	0	5	1	0	1		
ENSMUST00000187695	ENSMUSG00000061080	16	39984361	42181679	1	0	8	16	2	3	1	0	0	0	0	1	A0A087WP80	
ENSMUST00000187698						16	11	20	25	11	9	0	0	0	0	1		
ENSMUST00000187699	ENSMUSG00000030168	6	119353150	119417704	-1	0	0	10	0	0	0	182	0	19	0	35	A0A087WPB1	
ENSMUST00000187701	ENSMUSG00000038065	6	54681624	54703851	1	0	0	0	58	0	0	0	0	0	2	0	A0A087WQV4	
ENSMUST00000187702						2	2	3	4	0	1	0	0	0	0	3		
ENSMUST00000187704						20	12	48	35	25	20	0	1	0	0	0		
ENSMUST00000187705						680	804	1148	883	697	263	19	138	54	44	81		
ENSMUST00000187707						17	22	28	22	19	12	0	1	0	1	3		
ENSMUST00000187709	ENSMUSG00000026782	1	60409619	60481158	1	0	0	0	0	0	0	0	0	0	0	5	A0A087WPP8	
ENSMUST00000187711	ENSMUSG00000032265	9	85320439	85327348	-1	29	0	23	168	33	0	0	32	120	0	192	A0A087WS27	
ENSMUST00000187712	ENSMUSG00000095011	Y	33511116	33543164	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000187713	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNW8	
ENSMUST00000187714						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187717	ENSMUSG00000038174	1	58522806	58586323	-1	0	0	4	0	2	2	0	0	0	5	9	A0A087WSI2	
ENSMUST00000187720						4	4	10	7	2	0	0	0	0	0	0		
ENSMUST00000187721	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	6	2	1	0	0	0	0	0	0	A0A087WQH0	
ENSMUST00000187722						2	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000187725	ENSMUSG00000026452	1	134646677	134762593	1	0	0	0	44	0	0	0	0	0	0	0	Q9JM87	
ENSMUST00000187729						22	0	0	0	28	0	0	0	0	0	0		
ENSMUST00000187732						0	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000187733	ENSMUSG00000026219	1	84721189	84840516	-1	3	1	7	0	0	0	4	865	183	23	0	A0A087WRK9	
ENSMUST00000187734						0	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000187737						6	2	11	4	2	5	0	0	0	0	0		
ENSMUST00000187738	ENSMUSG00000100704	5	87969517	88008277	1	0	1	0	2	0	0	0	0	0	0	0	A0A087WPU2	
ENSMUST00000187739						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187740						4	3	14	93	9	0	0	0	0	0	0		
ENSMUST00000187741						6	3	5	9	2	1	1	0	0	0	0		
ENSMUST00000187742	ENSMUSG00000095620	16	36221468	36257444	1	0	0	0	0	0	0	16	22	13	39	15	Q9D8D6	
ENSMUST00000187743						6	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000187744						2	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000187745	ENSMUSG00000048960	1	10993465	11303681	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRV5	
ENSMUST00000187747						92	139	110	85	75	30	4	21	8	0	16		
ENSMUST00000187748						1	2	7	6	3	2	1	0	0	0	0		
ENSMUST00000187749						3	0	21	2	3	0	0	0	0	0	0		
ENSMUST00000187750						9	0	0	0	19	0	0	0	0	0	0		
ENSMUST00000187751						3	3	9	21	6	5	0	0	0	0	0		
ENSMUST00000187752	ENSMUSG00000026153	1	24011093	24100341	-1	0	0	0	3	0	0	6	0	0	0	0	A0A087WP54	
ENSMUST00000187753	ENSMUSG00000048126	1	90765923	90843971	-1	0	0	0	9	4	0	0	0	0	0	0	A0A087WQN9	
ENSMUST00000187754	ENSMUSG00000025927	1	19208914	19238576	1	0	0	0	0	0	0	0	0	0	0	0	Q8CE69	
ENSMUST00000187755						0	3	5	8	3	4	0	0	0	0	0		
ENSMUST00000187756	ENSMUSG00000025968	1	63143596	63176833	-1	0	0	0	0	0	0	0	0	2	0	0	A0A087WQ77	
ENSMUST00000187758	ENSMUSG00000005501	1	87945119	88008551	-1	0	10	0	0	0	0	28	20	24	0	30		Q8BWR4

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187759						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187761						4	0	2	0	1	4	0	0	0	0	0		
ENSMUST00000187765						0	3	0	6	0	0	0	0	0	0	0		
ENSMUST00000187766						7	7	50	15	11	5	0	0	0	0	0		
ENSMUST00000187768	ENSMUSG00000100856	Y	63228427	63254644	1	0	0	0	0	0	0	0	0	0	0	0	Q810R0	
ENSMUST00000187770						12	19	100	41	15	11	0	1	0	0	5		
ENSMUST00000187771						0	0	6	0	4	9	525	2630	1589	4066	1285		
ENSMUST00000187772						0	0	0	35	0	0	0	0	0	0	0		
ENSMUST00000187774	ENSMUSG00000038608	1	80501073	80758527	-1	0	25	0	12	22	0	1	286	535	105	334	A0A087WQ86	
ENSMUST00000187776						1	4	15	7	6	5	22	83	57	2	39		
ENSMUST00000187778						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000187781						5	3	5	0	5	2	0	0	1	0	0		
ENSMUST00000187782						3	4	9	2	4	5	0	0	0	0	0		
ENSMUST00000187785	ENSMUSG00000033124	1	75180860	75192196	-1	0	0	0	0	0	0	0	4	0	0	11	A0A087WPL8	
ENSMUST00000187787						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000187788						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187789	ENSMUSG00000025515	7	141690340	141754693	1	2	1	4	3	6	1	0	1	0	0	0	A0A087WQU6	
ENSMUST00000187790	ENSMUSG00000025932	1	14168954	14310235	-1	0	0	0	2	0	0	0	0	0	0	0	A0A087WNY3	
ENSMUST00000187791						6	9	22	4	5	0	23	26	20	13	19		
ENSMUST00000187792	ENSMUSG00000052293	13	100651579	100656060	1	3	0	6	23	0	2	0	0	10	25	37	A0A087WQ57	
ENSMUST00000187793	ENSMUSG00000099703	18	35553404	35581609	1	0	0	0	0	0	0	0	0	0	52	20	A0A087WQ54	
ENSMUST00000187797						3	2	8	4	8	1	0	0	0	0	0		
ENSMUST00000187798						0	6	2	2	3	3	0	0	0	0	0		
ENSMUST00000187801						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187802						0	0	4	2	0	2	3	5	10	14	3		
ENSMUST00000187803						0	0	1	0	3	0	0	0	0	1	0		
ENSMUST00000187805						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187806						4	4	7	1	1	1	0	0	0	0	0		
ENSMUST00000187807	ENSMUSG00000034867	7	35586244	35639226	1	1	3	16	8	3	2	0	0	0	0	0	A0A087WS06	
ENSMUST00000187808						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000187809						8	1	5	0	1	4	0	3	0	2	0		
ENSMUST00000187810	ENSMUSG00000049866	1	88673125	88702221	-1	12	9	14	0	20	7	0	5	5	1	2		P61208
ENSMUST00000187811	ENSMUSG00000025958	1	64532645	64604548	1	4	4	9	137	15	0	0	18	30	26	86	A0A087WRI6	
ENSMUST00000187812						5	3	2	7	1	2	0	0	0	0	0		
ENSMUST00000187814	ENSMUSG00000034157	12	86947043	86965362	1	8	4	16	31	9	6	48	124	59	22	57		Q8R0W1
ENSMUST00000187816						6	5	18	4	1	1	0	0	0	0	0		
ENSMUST00000187818	ENSMUSG00000026219	1	84721189	84840516	-1	0	1	7	90	1	0	0	0	0	0	0	A0A087WS65	
ENSMUST00000187819						4	29	149	29	46	13	0	0	0	0	0		
ENSMUST00000187821						3	1	3	4	4	1	0	0	0	0	0		
ENSMUST00000187823	ENSMUSG00000022931	16	88820215	88829844	1	5	6	8	5	7	2	0	0	0	0	0		Q9QZU5
ENSMUST00000187824	ENSMUSG00000026280	1	93751500	93790610	1	0	0	0	0	0	0	73	43	38	10	11	A0A087WNY2	
ENSMUST00000187825						14	2	18	13	10	5	0	4	0	0	3		
ENSMUST00000187826						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187827						0	0	7	0	0	0	0	0	0	0	0		
ENSMUST00000187830						63	47	104	438	97	67	0	1	1	0	2		
ENSMUST00000187831						3	2	1	6	7	1	0	3	0	0	0		
ENSMUST00000187832	ENSMUSG00000060036	15	80077794	80091868	-1	0	0	0	0	0	0	3	8	0	10	4	A0A087WNS0	
ENSMUST00000187834						14	12	16	0	8	7	43	280	0	28	28		
ENSMUST00000187835						2	1	0	0	1	1	2	8	2	5	9		
ENSMUST00000187836	ENSMUSG00000026209	1	75307896	75317990	-1	9	1	10	25	2	7	80	54	46	27	38		Q9Z2W0
ENSMUST00000187837	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	0	0	0	4	53	10	49	17	A0A087WQ46	
ENSMUST00000187839	ENSMUSG00000021843	14	47648448	47736564	1	0	11	11	7	7	0	0	0	0	0	0	F8VQC7	
ENSMUST00000187842	ENSMUSG00000091987	Y	2900989	2912206	1	0	0	0	0	0	0	0	0	0	0	0	B2RWR6	
ENSMUST00000187843						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000187844						18	14	50	17	15	14	0	0	0	0	1		
ENSMUST00000187846	ENSMUSG00000095634	Y	68537955	68540290	1	11	0	0	0	0	0	0	0	0	0	0	Q5FWD4	
ENSMUST00000187849						4	6	4	6	7	1	0	0	0	0	0		
ENSMUST00000187850						5522	7212	9915	4399	5758	2825	40	296	148	40	139		
ENSMUST00000187852	ENSMUSG00000056222	13	57421195	57908314	-1	11	0	0	43	14	0	0	0	0	0	0	Q8BM07	
ENSMUST00000187856	ENSMUSG00000094729	Y	53415953	53418291	-1	19	5	15	30	25	9	0	0	0	0	0	Q5FWB5	
ENSMUST00000187857	ENSMUSG00000095148	Y	6267098	6269548	1	3	6	2	2	0	0	0	0	0	0	0	J3QMQ9	
ENSMUST00000187859						12	20	74	8	12	7	6	11	17	5	64		
ENSMUST00000187860						0	6	4	0	0	1	0	0	0	0	0		
ENSMUST00000187861	ENSMUSG00000026442	1	132564690	132741797	-1	4	7	28	0	3	0	0	1	0	0	0	A0A087WPX3	
ENSMUST00000187862						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187863						5	0	17	0	5	0	0	0	0	0	0		
ENSMUST00000187864						51	28	166	80	46	25	62	141	23	101	43		
ENSMUST00000187865						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187868						4	1	10	8	3	1	1	0	0	0	0		
ENSMUST00000187870						8	8	0	2	4	6	0	0	0	0	0		
ENSMUST00000187871						5	12	2	15	7	2	0	0	0	0	2		
ENSMUST00000187872						6	7	4	56	11	10	1	0	2	4	3		
ENSMUST00000187874	ENSMUSG00000014850	13	92211872	92355003	-1	1	0	0	0	0	0	0	0	0	0	0	A0A087WP43	
ENSMUST00000187877						1	4	3	5	3	0	0	0	0	0	0		
ENSMUST00000187881	ENSMUSG00000032712	6	149309414	149335663	1	0	0	2	0	0	0	0	0	0	0	0	A0A087WR65	
ENSMUST00000187883						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000187885						15	25	37	27	22	13	1	6	2	2	9		
ENSMUST00000187886						0	0	0	13	14	7	0	0	0	0	0		
ENSMUST00000187888						0	0	6	1	1	4	3	31	11	1	13		
ENSMUST00000187890						14	6	14	11	13	4	0	0	0	0	0		
ENSMUST00000187892	ENSMUSG00000086727	1	31135226	31222684	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNP0	
ENSMUST00000187893						1	2	0	3	1	0	0	0	0	0	0		
ENSMUST00000187895						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187896	ENSMUSG00000094651	1	93861306	93876494	1	4	1	8	13	2	6	0	0	0	0	0	A0A087WRM6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000187899	ENSMUSG00000026159	1	82839483	82901182	1	7	0	0	0	9	0	0	0	0	112	171	A0A087WNV1	
ENSMUST00000187900	ENSMUSG00000056211	1	128103301	128237736	1	0	4	15	3	13	8	5	0	0	0	0	Q80ZH9	
ENSMUST00000187901	ENSMUSG00000049339	1	75142778	75147913	1	2	0	18	17	3	1	5	9	1	0	6	A0A087WRH7	
ENSMUST00000187903						0	0	5	0	0	1	0	0	0	0	0		
ENSMUST00000187904	ENSMUSG00000101725	Y	70292585	70303287	-1	9	0	0	0	0	0	0	0	0	0	0	A0A087WSA2	
ENSMUST00000187905	ENSMUSG00000032454	9	98486115	98509781	1	1	0	0	0	2	0	0	0	0	15	3	Q059R7	Q08652
ENSMUST00000187909						10	24	17	20	21	14	0	5	6	0	5		
ENSMUST00000187910	ENSMUSG00000079658	1	16641725	16657042	-1	0	0	0	0	0	0	0	206	7	43	21	A0A087WNT1	
ENSMUST00000187912	ENSMUSG00000036452	18	38601534	39376284	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSU1	
ENSMUST00000187916	ENSMUSG00000016524	1	130932656	130940115	-1	1	2	0	3	2	0	0	1	0	0	0	A0A087WST1	
ENSMUST00000187917						0	0	0	1	4	0	0	3	2	0	10		
ENSMUST00000187919	ENSMUSG00000099077	CHR_MG132_PATCH	124456062	124462462	-1	0	1	3	13	0	0	20	40	13	6	16		
ENSMUST00000187922	ENSMUSG00000100231	Y	12273932	12306702	1	2	0	0	0	0	2	3	0	0	0	3	A0A087WNW4	
ENSMUST00000187925						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187928						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187931						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187935						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187936						2	0	1	2	3	0	0	1	0	2	2		
ENSMUST00000187937						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187938	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	0	2	0	22	10	238	14	0	237	Q3UHL6	
ENSMUST00000187939	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	1	0	0	1	0	4	0	0	0	A0A087WS74	
ENSMUST00000187940	ENSMUSG00000051331	6	118587240	119196418	-1	5	0	0	3	7	0	0	0	0	0	0	C7TQ57	
ENSMUST00000187943	ENSMUSG00000093868	Y	24455057	24457399	1	14	0	0	17	0	5	0	0	0	0	0	Q62458	
ENSMUST00000187944	ENSMUSG00000023277	9	106203108	106215389	1	3	3	10	24	12	4	0	3	3	0	12	A0A087WPT3	
ENSMUST00000187945	ENSMUSG00000025515	7	141690340	141754693	1	23	10	115	43	42	18	2	0	0	0	0	A0A087WSP1	
ENSMUST00000187949						36	24	55	18	38	12	4	1	3	0	3		
ENSMUST00000187951	ENSMUSG00000043019	1	151755371	151822051	1	7	6	0	0	3	0	0	3	167	6	102	B7ZNP0	
ENSMUST00000187952						3	0	2	3	4	0	42	2790	141	29	151		
ENSMUST00000187953	ENSMUSG00000030556	7	67513411	67645268	-1	12	2	9	0	11	5	0	0	0	0	0	A0A087WQI4	
ENSMUST00000187958						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187959						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000187960	ENSMUSG00000049643	7	27553233	27582099	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRI8	
ENSMUST00000187962						1	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000187963						21	22	23	30	28	10	9	11	31	6	3		
ENSMUST00000187965						0	1	1	1	0	0	0	0	0	0	0		
ENSMUST00000187968	ENSMUSG00000048874	1	30802339	30873921	-1	0	0	0	10	0	3	3	1	2	0	1	A0A087WNQ9	
ENSMUST00000187969						22	21	10	9	29	8	0	0	0	0	0		
ENSMUST00000187970						0	1	0	0	4	2	0	0	0	0	0		
ENSMUST00000187971						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000187972						0	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000187973						0	0	15	38	0	0	2993	6184	2754	14798	1939		
ENSMUST00000187974						0	0	0	0	0	13	0	0	0	0	0		
ENSMUST00000187975						6	2	5	3	4	0	1	0	1	0	0		
ENSMUST00000187976	ENSMUSG00000102018	15	76009888	76046111	1	2	0	5	71	10	6	0	0	0	0	0	A0A087WQQ1	
ENSMUST00000187977						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187978	ENSMUSG00000026017	1	60098247	60153953	1	41	29	92	32	28	15	11	64	15	16	25		Q8VHI4
ENSMUST00000187979						3	1	2	0	0	0	1	0	0	0	0		
ENSMUST00000187980						5	7	22	1	8	5	0	0	0	0	5		
ENSMUST00000187981						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187982						28	32	39	146	37	15	0	1	0	0	1		
ENSMUST00000187983	ENSMUSG00000042210	9	106440051	106447678	-1	2	0	0	0	0	0	0	0	0	0	0	A0A087WS50	
ENSMUST00000187984						5	0	13	0	1	1	0	0	0	0	0		
ENSMUST00000187985	ENSMUSG00000031506	1	135132700	135145317	1	4	1	0	2	0	0	34	5	82	0	40		Q8BUM3
ENSMUST00000187987						2	0	0	6	3	2	31	101	164	17	134		
ENSMUST00000187989	ENSMUSG00000030577	7	30865402	30880342	-1	2	0	0	1	0	0	0	0	0	0	24	A0A087WST4	
ENSMUST00000187990	ENSMUSG00000100224	2	89721165	89722109	-1	3	5	27	3	5	6	0	0	0	0	0	Q7TQZ2	
ENSMUST00000187991	ENSMUSG00000026484	1	151458004	151500955	-1	2	0	0	28	3	1	0	0	0	0	0	A0A087WQQ3	
ENSMUST00000187992						7	4	21	43	9	5	0	0	0	0	0		
ENSMUST00000187994	ENSMUSG00000075602	15	74994877	74998031	-1	3	0	5	8	4	10	0	0	0	0	6		P05533
ENSMUST00000187996						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000187997						76	75	78	69	84	32	1	2	6	1	5		
ENSMUST00000187998						4	2	2	30	4	2	0	1	0	0	0		
ENSMUST00000187999						5	3	12	1	3	3	0	0	0	0	0		
ENSMUST00000188000	ENSMUSG00000079355	9	104084157	104126933	-1	15	0	125	25	22	0	0	0	6	0	0		Q924I3
ENSMUST00000188001						5	2	11	2	4	9	0	0	0	0	0		
ENSMUST00000188002						11	4	16	109	16	3	0	10	2	10	11		
ENSMUST00000188004						8	8	31	9	8	1	0	0	0	0	0		
ENSMUST00000188005	ENSMUSG00000101315	1	83060930	83061921	1	34	11	96	913	46	13	0	2	1	1	3	A0A087WQP5	
ENSMUST00000188006						79	57	727	110	57	49	7	14	4	0	6		
ENSMUST00000188007						0	2	0	0	6	0	0	0	0	0	0		
ENSMUST00000188008	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	0	0	0	0	4	0	0	0	A0A087WSK4	
ENSMUST00000188009						4	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000188010						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188011	ENSMUSG00000096666	Y	66739787	66742123	-1	0	5	7	1	5	7	0	0	0	0	0	Q5M8R5	
ENSMUST00000188012						2	0	1	5	4	1	3	0	27	2	28		
ENSMUST00000188013						11	3	11	8	8	9	0	3	0	0	0		
ENSMUST00000188016						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000188017						9	7	23	119	21	7	0	0	0	0	1		
ENSMUST00000188018						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188019						2	0	0	0	0	0	2	7	3	7	7		
ENSMUST00000188020						2	0	1	0	3	0	0	0	0	0	0		
ENSMUST00000188021						4	3	5	1	5	0	0	0	0	0	0		
ENSMUST00000188022						0	3	1	1	5	1	0	0	0	0	0		
ENSMUST00000188023	ENSMUSG00000075189	2	86346724	86347764	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS05	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188025						10	2	12	0	14	0	3	106	6	17	18		
ENSMUST00000188027	ENSMUSG00000026600	1	156424525	156474331	-1	0	0	0	5	0	0	29	0	110	8	108	A0A087WSJ5	
ENSMUST00000188028	ENSMUSG00000026414	1	135836354	135852260	1	3	0	0	0	0	0	0	0	0	0	0	Q6P3Z7	
ENSMUST00000188030	ENSMUSG00000032261	9	83548327	83638801	1	33	17	123	21	27	22	0	1	5	2	1	A0A087WQU5	
ENSMUST00000188032						11	10	0	39	24	0	0	0	0	0	32		
ENSMUST00000188033						0	0	1	10	0	0	4	4	8	4	3		
ENSMUST00000188034	ENSMUSG00000036873	3	145938014	145944829	1	2	0	0	0	0	1	8	0	5	0	11	A0A087WQ79	
ENSMUST00000188035						3	0	8	1	4	0	0	0	0	0	0		
ENSMUST00000188036						1	2	4	0	1	0	0	0	0	0	0		
ENSMUST00000188037						31	41	167	39	49	23	21	82	29	10	51		
ENSMUST00000188039						3991	5089	7886	2683	4501	2005	53	352	135	83	181		
ENSMUST00000188041						0	1	4	5	8	0	0	0	0	0	0		
ENSMUST00000188042	ENSMUSG00000022587	15	74955051	74959905	1	2	3	11	8	6	0	23	71	37	4	66	Q99JA5	
ENSMUST00000188043						0	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000188044	ENSMUSG00000100725	1	178323074	178337728	-1	1	0	2	0	0	0	0	0	0	103	62	A0A087WPX7	
ENSMUST00000188045	ENSMUSG00000015242	4	52989272	53001162	1	0	0	9	0	0	0	0	0	0	0	0	G3X8S9	
ENSMUST00000188046	ENSMUSG00000034157	12	86947043	86965362	1	1	0	0	0	0	0	0	0	3	0	0	A0A087WPE5	
ENSMUST00000188047	ENSMUSG00000032068	9	50494525	50505482	1	6	0	0	1	7	0	0	0	1	0	0		Q8VEN2
ENSMUST00000188048	ENSMUSG00000068117	15	82069997	82126811	1	0	0	0	0	0	0	0	0	0	0	0		Q9D4I2
ENSMUST00000188049						0	0	1	0	2	2	0	6	4	0	1		
ENSMUST00000188050						11	4	12	31	24	9	0	0	0	0	0		
ENSMUST00000188051	ENSMUSG00000026107	1	51465862	51478425	-1	0	0	2	3	0	0	0	0	0	0	0		Q8BGW5
ENSMUST00000188052						5	4	7	6	13	3	0	0	0	0	0		
ENSMUST00000188053						2	2	31	3	3	3	13	40	20	2	36		
ENSMUST00000188054						56	45	546	181	75	53	0	0	0	0	0		
ENSMUST00000188057	ENSMUSG00000035934	9	36890982	37147322	-1	0	0	0	3	0	0	0	0	0	0	3	A0A087WRV9	
ENSMUST00000188059						4	4	13	5	4	3	0	0	0	0	0		
ENSMUST00000188060						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188062						1	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000188064						1	0	0	0	0	0	3	3	5	10	0		
ENSMUST00000188065	ENSMUSG00000053024	1	132509427	132543256	-1	0	0	10	0	0	0	0	0	0	0	0	A0A087WQQ9	
ENSMUST00000188066	ENSMUSG00000030228	6	139587221	139969284	1	4	0	0	3	0	0	0	0	0	0	0	A0A087WQB5	
ENSMUST00000188067						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188070						1	1	8	1	0	0	0	0	0	0	0		
ENSMUST00000188073	ENSMUSG00000006542	1	74738922	74749221	-1	17	12	44	161	30	16	0	3	0	0	3		Q8BGM7
ENSMUST00000188075						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000188077						33	10	9	25	44	10	0	0	0	0	0		
ENSMUST00000188078	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR02	
ENSMUST00000188080						6	3	13	2	7	3	0	0	0	0	0		
ENSMUST00000188081	ENSMUSG00000026311	1	91540544	91559589	1	4	1	12	17	4	9	0	2	2	0	0	A0A087WQE9	
ENSMUST00000188083						70	68	69	64	36	21	0	0	0	0	0		
ENSMUST00000188085	ENSMUSG00000100323	2	89666928	89667884	-1	8	2	7	9	4	1	0	0	0	0	0	Q7TQZ3	
ENSMUST00000188086						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000188088						20	26	41	16	15	7	2	0	4	0	3		
ENSMUST00000188090	ENSMUSG00000054387	1	132959484	133030561	-1	22	19	54	68	26	18	591	3449	1398	204	1412		O35618
ENSMUST00000188091	ENSMUSG00000095948	Y	3399188	3410167	-1	6	5	0	0	0	2	0	0	0	0	0		O35698
ENSMUST00000188092						5	2	0	0	3	2	2	2	7	2	58		
ENSMUST00000188094						27	38	143	92	55	28	2	2737	117	333	178		
ENSMUST00000188095	ENSMUSG00000070547	7	48444113	48456342	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR17	
ENSMUST00000188096	ENSMUSG00000094076	10	81812186	81826490	1	23	0	73	52	63	54	9	0	0	0	0	A0A087WNP5	
ENSMUST00000188097	ENSMUSG00000033021	1	75435930	75443179	1	0	4	0	6	0	0	17	10	0	3	0	A0A087WPV7	
ENSMUST00000188098						4	5	10	6	7	0	0	0	0	0	0		
ENSMUST00000188099						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000188100						11	6	23	9	27	6	1	1	0	0	5		
ENSMUST00000188101						459	442	964	1041	543	282	12	48	24	8	19		
ENSMUST00000188103						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188104						2	1	0	11	2	0	0	0	0	0	0		
ENSMUST00000188105						39	56	218	116	37	31	1	2	5	1	5		
ENSMUST00000188106	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS40	
ENSMUST00000188108	ENSMUSG00000055748	15	63891264	63912297	-1	0	0	0	0	9	0	0	0	0	0	0		Q3TR54
ENSMUST00000188109	ENSMUSG00000025950	1	65158616	65186500	-1	0	0	0	0	0	0	0	0	19	67	53	A0A087WRS9	
ENSMUST00000188110	ENSMUSG00000025997	1	69531214	69687245	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ74	
ENSMUST00000188111	ENSMUSG00000045411	7	44246722	44252319	1	0	0	0	0	29	7	0	0	25	0	0	Q3TE80	
ENSMUST00000188112						3	1	9	3	1	4	0	0	0	0	6		
ENSMUST00000188114	ENSMUSG00000095852	Y	2830699	2873492	1	0	0	0	0	3	0	0	0	0	0	0	B2RWR6	
ENSMUST00000188116	ENSMUSG00000032323	9	58006411	58027023	1	2	2	15	4	6	1	0	0	0	0	0	A0A087WRA8	
ENSMUST00000188117						2	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000188119						6	14	12	9	7	3	0	48	0	1	7		
ENSMUST00000188120						0	0	0	2	0	0	17	9	0	0	0		
ENSMUST00000188121						7	2	0	20	6	0	0	5	0	3	0		
ENSMUST00000188122						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188124	ENSMUSG00000053877	7	127511983	127561219	1	0	0	0	2	0	0	30	13	50	0	47	A0A087WS36	
ENSMUST00000188125						3	3	2	4	9	4	0	0	0	0	0		
ENSMUST00000188126						61	35	525	9	43	15	5	21	2	13	19		
ENSMUST00000188127						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000188131						0	1	2	0	0	0	0	0	0	0	0		
ENSMUST00000188132						3	1	2	2	5	0	0	0	0	0	0		
ENSMUST00000188133						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188134	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	0	0	0	0	Q8BLD4	
ENSMUST00000188136	ENSMUSG00000014602	1	93015464	93101951	-1	4	0	1	1	1	0	1	0	0	0	0	A0A087WRJ3	
ENSMUST00000188139						1	0	1	0	5	1	2	3	0	14	9		
ENSMUST00000188140						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188141						9	8	6	1	9	5	0	0	0	0	0		
ENSMUST00000188142	ENSMUSG00000074305	9	56201126	56418067	-1	42	21	66	29	50	24	108	217	202	52	436	A0A087WQ01	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188143						2	3	3	4	8	3	0	0	0	0	0		
ENSMUST00000188144						2	6	3	8	2	8	0	0	0	0	0		
ENSMUST00000188145	ENSMUSG00000043019	1	151755371	151822051	1	0	0	0	173	4	0	0	0	0	0	0	A0A087WR24	
ENSMUST00000188148	ENSMUSG00000026420	1	130882074	130887454	-1	2	0	8	1	0	0	0	0	0	0	0	A0A087WPT5	
ENSMUST00000188150						10	8	33	10	13	8	0	0	3	0	0		
ENSMUST00000188151	ENSMUSG00000028936	4	152325742	152334071	1	0	6	22	15	13	8	36	124	38	69	68	Q4VAG4	P67984
ENSMUST00000188154	ENSMUSG00000048960	1	10993465	11303681	1	90	58	133	99	112	50	1	7	5	1	5	A0A087WRD8	
ENSMUST00000188157	ENSMUSG00000030577	7	30865402	30880342	-1	0	0	0	0	0	0	3	0	2	0	0	A0A087WR31	
ENSMUST00000188161	ENSMUSG00000029419	2	25575416	25581757	-1	0	0	6	1156	18	3	0	0	0	0	1		A2AJA9
ENSMUST00000188164						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000188165	ENSMUSG00000034088	1	93405940	93478815	-1	0	0	0	14	0	0	0	3	0	0	0	A0A087WPH2	
ENSMUST00000188166						17	11	8	14	7	6	0	0	0	0	0		
ENSMUST00000188168						0	0	0	4	1	3	0	0	0	0	0		
ENSMUST00000188169	ENSMUSG00000079330	1	132191431	132259227	1	40	52	260	85	52	34	1	0	0	1	0	A0A087WR92	
ENSMUST00000188170						8	5	27	8	5	1	0	0	0	0	1		
ENSMUST00000188172						0	2	10	1	5	0	0	2	0	1	7		
ENSMUST00000188174						6	7	54	15	8	3	3	0	3	0	10		
ENSMUST00000188175						43	37	93	63	49	14	0	0	0	0	0		
ENSMUST00000188177	ENSMUSG00000026429	1	134962565	134974162	1	1	1	0	0	0	0	0	0	0	0	0	A0A087WPV1	
ENSMUST00000188178						1	1	0	2	2	2	0	0	0	0	0		
ENSMUST00000188179						1	0	4	13	0	0	3	11	6	3	3		
ENSMUST00000188180	ENSMUSG00000068600	15	74819071	74834871	1	0	1	0	3	0	0	0	0	0	0	0	A0A087WST8	
ENSMUST00000188181						5	6	14	10	8	0	0	0	0	0	0		
ENSMUST00000188182						0	0	0	2	0	3	12	0	6	0	5		
ENSMUST00000188184						1	2	0	0	1	0	0	0	0	0	0		
ENSMUST00000188187	ENSMUSG00000047897	9	87015537	87019917	1	8	2	3	125	6	0	0	0	0	0	0	A0A087WSI4	
ENSMUST00000188189	ENSMUSG00000048960	1	10993465	11303681	1	3	5	0	4	6	2	0	0	0	1	0	A0A087WRG8	
ENSMUST00000188190						7	9	57	21	14	2	0	0	0	0	0		
ENSMUST00000188191						10	7	7	9	8	2	0	0	0	0	0		
ENSMUST00000188192						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000188194	ENSMUSG00000022253	15	9071260	9110487	1	0	0	0	0	0	0	2	4	0	0	0	A0A087WQI8	
ENSMUST00000188195	ENSMUSG00000074217	8	84010222	84012171	-1	0	0	9	29	4	4	0	0	0	0	1	A0A087WR51	
ENSMUST00000188197	ENSMUSG00000042849	1	92511048	92518515	-1	0	3	0	12	5	7	0	0	0	0	0	A0A087WPA1	
ENSMUST00000188199						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188200						0	0	0	0	2	0	0	0	0	3	0		
ENSMUST00000188204	ENSMUSG00000026107	1	51465862	51478425	-1	0	0	0	0	0	1	74	440	52	117	60		Q8BGW5
ENSMUST00000188205						3	0	16	52	0	1	13	35	23	11	26		
ENSMUST00000188206	ENSMUSG00000026479	1	153122756	153186447	-1	6	3	27	6	5	1	0	0	0	0	0	Q9R086	
ENSMUST00000188208	ENSMUSG00000055322	1	73910231	74124449	-1	1	0	0	6	2	0	0	0	0	0	3	A0A087WRZ8	
ENSMUST00000188209						6	9	7	42	5	4	0	0	0	0	0		
ENSMUST00000188210	ENSMUSG00000063142	14	23289431	24004859	-1	0	0	0	84	0	0	0	0	0	0	0	A0A087WSJ2	
ENSMUST00000188211	ENSMUSG00000033499	13	9093881	9174451	1	6	0	9	14	11	7	256	224	980	42	589		Q6A0A2
ENSMUST00000188212	ENSMUSG00000025912	1	9667415	9700209	-1	0	0	1	1	2	0	0	1	0	0	0	A0A087WPK9	
ENSMUST00000188214	ENSMUSG00000022584	15	75108158	75111970	-1	0	0	0	0	0	0	204	462	170	422	120		P0CW03
ENSMUST00000188216						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000188219						9	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188220						0	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000188221						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188222	ENSMUSG00000101725	Y	70292585	70303287	-1	0	0	0	8	0	0	0	0	0	0	0	A0A087WSI5	
ENSMUST00000188223	ENSMUSG00000047428	17	46297421	46303271	1	3	0	14	63	5	0	0	0	0	0	0	A0A087WSS3	
ENSMUST00000188225						2	0	0	1	2	1	0	0	1	0	0		
ENSMUST00000188227						11	9	26	10	11	7	0	0	0	0	0		
ENSMUST00000188228						2	2	12	8	2	1	0	1	0	0	0		
ENSMUST00000188230						3	1	3	3	1	3	0	0	0	0	0		
ENSMUST00000188231						0	0	0	25	52	57	4041	13102	8098	45467	7381		
ENSMUST00000188235	ENSMUSG00000071613	14	3133997	3141609	1	0	0	0	0	0	0	0	0	0	0	0	L7N2B6	
ENSMUST00000188237						38	20	88	45	31	18	28	200	53	10	114		
ENSMUST00000188238						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188239						337	248	1618	448	197	108	2	31	0	2	7		
ENSMUST00000188240						7	1	20	5	3	0	0	0	0	0	0		
ENSMUST00000188241	ENSMUSG00000032261	9	83548327	83638801	1	6	23	15	6	10	0	0	0	0	0	0	A0A087WS96	
ENSMUST00000188244	ENSMUSG00000100667	Y	61102247	61134259	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000188246						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000188247	ENSMUSG00000026245	1	78417975	78488897	-1	0	0	0	0	0	0	2	0	0	0	0	A0A087WPV4	
ENSMUST00000188248						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188249						3	3	7	3	0	3	0	6	0	1	0		
ENSMUST00000188250						2	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000188251	ENSMUSG00000023341	16	97535308	97560900	1	2	0	1	1	1	0	0	30	0	0	24		
ENSMUST00000188252						0	0	0	0	0	0	0	0	0	51	129		
ENSMUST00000188253						0	1	3	0	3	0	0	0	0	0	0		
ENSMUST00000188254						4699	3793	1796	77850	6780	1100	18	96	61	9	117		
ENSMUST00000188257	ENSMUSG00000026058	1	32172714	32658568	1	157	125	729	155	168	83	1	13	7	8	5		Q9WU01
ENSMUST00000188259						4	0	10	34	5	2	0	0	0	0	0		
ENSMUST00000188261						1	3	5	2	5	2	0	0	0	0	0		
ENSMUST00000188263						1	0	0	2	1	0	0	2	0	0	0		
ENSMUST00000188264						0	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000188265						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188267	ENSMUSG00000054523	19	11273238	11283873	-1	0	1	0	0	0	0	0	0	0	0	0	A0A087WNU2	
ENSMUST00000188268						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188269	ENSMUSG00000100608	Y	89713424	89745532	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSS9	
ENSMUST00000188270						7	7	15	18	17	12	5	21	9	23	17		
ENSMUST00000188274	ENSMUSG00000066100	7	142296334	142297118	-1	28	19	82	36	28	8	0	0	0	0	0		Q64507
ENSMUST00000188275	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	123	3	8	0	16	0	0	7	A0A087WQZ1	
ENSMUST00000188280						1	0	0	1	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188281						10	4	9	4	10	4	0	0	0	0	0		
ENSMUST00000188282	ENSMUSG00000004945	17	5410870	5440259	-1	8	1	6	5	7	3	0	7	10	11	0		Q8VCR3
ENSMUST00000188283						1	2	3	1	1	0	0	0	0	0	0		
ENSMUST00000188284						5	4	27	5	3	1	0	0	0	0	0		
ENSMUST00000188285	ENSMUSG00000063142	14	23289431	24004859	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQN5	
ENSMUST00000188286						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188288						1	2	17	11	3	4	68	211	92	27	57		
ENSMUST00000188289						20	24	80	28	22	12	0	6	3	1	2		
ENSMUST00000188290	ENSMUSG00000026203	1	75236406	75245692	1	0	0	0	0	0	0	3	0	24	0	0		Q9QYI5
ENSMUST00000188291						18	21	5	18	7	5	0	0	0	0	0		
ENSMUST00000188293	ENSMUSG00000099729	7	32209173	32211145	-1	0	0	0	2	0	0	0	0	0	0	0	A0A087WR49	
ENSMUST00000188295						0	0	18	6	3	1	3	8	0	0	0		
ENSMUST00000188297						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188298	ENSMUSG00000025915	1	9798107	9900845	1	0	2	0	2	3	5	19	71	44	139	131	A0A087WPW2	
ENSMUST00000188299						1	3	0	0	2	1	249	428	38	542	44		
ENSMUST00000188301						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188302	ENSMUSG00000041763	1	43933647	44003000	1	0	0	0	0	0	0	67	0	91	0	0	Q05DJ9	
ENSMUST00000188303						15	15	70	66	32	14	4	7	2	1	8		
ENSMUST00000188304						2	0	18	6	6	7	0	0	0	0	0		
ENSMUST00000188306						6	4	0	2	5	4	0	6	0	0	3		
ENSMUST00000188307	ENSMUSG00000026442	1	132564690	132741797	-1	0	3	9	8	3	4	0	0	0	1	0	A0A087WNW2	
ENSMUST00000188310	ENSMUSG00000026246	1	87086694	87089928	-1	0	0	0	0	0	6	0	0	0	0	0		P24823
ENSMUST00000188313	ENSMUSG00000041763	1	43933647	44003000	1	4	0	5	0	13	0	73	910	217	109	150		Q64514
ENSMUST00000188314						0	0	11	0	0	0	0	0	0	0	0		
ENSMUST00000188316						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000188317	ENSMUSG00000100622	13	92305980	92307183	1	10	8	29	11	17	7	3	5	2	0	3	A0A087WR34	
ENSMUST00000188319						11	7	10	7	18	7	0	0	0	0	0		
ENSMUST00000188321						251	188	1697	404	181	106	9	12	16	1	15		
ENSMUST00000188325						8	13	13	13	18	6	0	0	0	0	0		
ENSMUST00000188326	ENSMUSG00000020659	12	31484829	31499616	-1	0	1	0	0	0	0	6	1	23	4	14	A0A087WPK1	
ENSMUST00000188327						13	4	11	12	17	3	0	0	0	0	0		
ENSMUST00000188330	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	1	0	0	14	A0A087WS04	
ENSMUST00000188332	ENSMUSG00000005501	1	87945119	88008551	-1	7	0	10	6	11	11	0	0	0	0	0	A0A087WRD2	
ENSMUST00000188333						7	7	20	3	18	8	27	38	41	12	60		
ENSMUST00000188334						2	1	2	3	2	1	0	0	0	0	0		
ENSMUST00000188335						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188336						5	2	4	5	7	0	0	0	0	0	0		
ENSMUST00000188338	ENSMUSG00000005493	3	153857149	153906138	-1	0	0	0	0	0	0	0	0	0	0	2	A0A087WQG8	
ENSMUST00000188339						18	18	95	23	14	7	0	0	0	0	0		
ENSMUST00000188340						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188341						9	1	10	10	6	2	0	0	0	0	0		
ENSMUST00000188343						32	39	54	53	43	22	2	8	4	1	14		
ENSMUST00000188344						7	2	7	6	4	1	0	2	2	0	0		
ENSMUST00000188345	ENSMUSG00000042699	1	153455758	153487660	-1	0	0	0	0	0	0	30	0	4	0	0	Q3UR42	
ENSMUST00000188346	ENSMUSG00000026203	1	75236406	75245692	1	0	0	0	0	0	0	55	5	0	0	39		Q9QYI5
ENSMUST00000188347	ENSMUSG00000033124	1	75180860	75192196	-1	0	0	9	30	0	0	1412	577	1197	95	612	Q3ZAQ4	
ENSMUST00000188348	ENSMUSG00000035934	9	36890982	37147322	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPZ3	
ENSMUST00000188350	ENSMUSG00000031927	9	14756587	14771030	-1	0	2	0	0	6	0	0	0	0	0	1	Q9DAE7	
ENSMUST00000188351						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188352						0	9	0	0	0	2	0	0	0	0	0		
ENSMUST00000188353						6	5	1	4	5	8	1	0	0	0	1		
ENSMUST00000188355	ENSMUSG00000101520	7	32334182	32335501	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP21	
ENSMUST00000188356	ENSMUSG00000090817	3	98445675	98457126	-1	0	3	0	4	0	0	0	0	0	0	0	A0A087WPY5	
ENSMUST00000188357						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000188358	ENSMUSG00000101667	Y	2932582	2939416	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPY7	
ENSMUST00000188359	ENSMUSG00000037236	18	35562146	35593835	1	2	0	0	34	3	0	0	4	7	28	5	A0A087WQD6	
ENSMUST00000188360						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188361						9	1	23	7	3	2	0	0	0	0	0		
ENSMUST00000188362						6	3	7	12	6	1	35	348	94	12	158		
ENSMUST00000188363						0	0	0	0	0	1	0	10	0	0	0		
ENSMUST00000188365						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000188366	ENSMUSG00000056091	6	72097592	72154571	1	0	3	0	0	10	0	80	136	91	21	68		
ENSMUST00000188367						3	3	0	7	0	1	1	1	2	0	5		
ENSMUST00000188368	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	3	0	0	0	0	0	0	0	0	A0A087WPI2	
ENSMUST00000188369						0	2	4	0	2	0	0	0	0	0	0		
ENSMUST00000188370	ENSMUSG00000025968	1	63143596	63176833	-1	0	0	0	0	0	0	0	2	3	0	3	A0A087WP77	
ENSMUST00000188371	ENSMUSG00000025925	1	15805646	15844052	1	46	64	248	137	59	29	25	77	29	5	28		P70371
ENSMUST00000188372						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188373						0	3	1	1	3	0	0	0	0	0	0		
ENSMUST00000188374	ENSMUSG00000056019	8	71882019	71895727	1	0	0	0	23	0	0	2	2	0	4	4	Q3THF1	
ENSMUST00000188375						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188376						17	8	11	180	15	8	1	2	3	0	6		
ENSMUST00000188377	ENSMUSG00000025935	1	13564698	13589910	-1	1	0	0	88	2	0	2	23	21	3	33	A0A087WR72	
ENSMUST00000188378						0	0	4	14	3	2	0	5	0	1	2		
ENSMUST00000188380						1	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000188381	ENSMUSG00000056211	1	128103301	128237736	1	0	0	0	6	0	0	2	0	0	0	0	Q3URW7	
ENSMUST00000188382	ENSMUSG00000045411	7	44246722	44252319	1	15	16	79	3	13	3	0	0	0	0	7	Q3TE80	
ENSMUST00000188383						0	0	0	5	10	0	0	0	0	0	0		
ENSMUST00000188384						80	57	194	292	99	46	0	0	0	0	0		
ENSMUST00000188385						2	0	8	1	0	0	0	0	0	0	0		
ENSMUST00000188386	ENSMUSG00000065987	8	3917655	3926844	-1	0	0	1	0	0	0	0	0	0	2	0		Q8CJ91
ENSMUST00000188387						3	0	6	3	5	2	0	0	0	0	0		
ENSMUST00000188388						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188389	ENSMUSG00000042046	1	132417555	132466958	1	0	5	2	81	3	8	22	0	55	0	74	A0A087WP69	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188390	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	0	0	0	6	19	4	51	14	A0A087WP00	
ENSMUST00000188391						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000188393						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000188394	ENSMUSG00000026278	1	93685660	93695764	1	2	3	7	81	6	2	0	0	0	0	0	A0A087WR00	
ENSMUST00000188395						13	11	12	4	16	6	0	1	0	2	1		
ENSMUST00000188396	ENSMUSG00000023495	9	106453291	106464012	1	1	0	0	64	8	0	3	5	1	0	10	A0A087WPG7	
ENSMUST00000188397						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188398	ENSMUSG00000035048	9	102626296	102634425	1	3	2	2	100	8	3	3	5	10	16	3		Q8R034
ENSMUST00000188399	ENSMUSG00000100016	2	89001348	89002286	-1	2	4	1	4	0	0	0	0	0	0	0	A0A087WSP6	
ENSMUST00000188400						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000188401						0	0	0	16	0	1	0	0	0	0	0		
ENSMUST00000188402	ENSMUSG00000026283	1	93803965	93822101	1	44	33	23	19	10	22	38	81	0	0	0	A0A087WRR4	
ENSMUST00000188403						1	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000188404	ENSMUSG00000056293	15	63824346	63845177	-1	18	5	0	4	4	0	0	0	0	0	0		Q2KHK6
ENSMUST00000188405						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000188406						42	51	196	29	52	21	6	14	1	3	3		
ENSMUST00000188407						8	5	3	1	6	2	0	0	0	0	0		
ENSMUST00000188408						11	9	5	9	9	7	0	0	0	0	0		
ENSMUST00000188409						2	5	10	2	8	2	0	0	0	0	0		
ENSMUST00000188410						3	0	0	1	5	0	0	4	1	0	6		
ENSMUST00000188413						3	1	1	1	2	0	0	2	0	2	1		
ENSMUST00000188414	ENSMUSG00000015112	6	6041218	6217173	-1	0	0	0	73	18	11	0	0	0	0	0		Q9QXX4
ENSMUST00000188415						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000188416						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000188419						0	0	0	2	0	0	1	0	2	0	0		
ENSMUST00000188422	ENSMUSG00000095172	Y	15882421	15884771	-1	0	2	0	2	5	0	0	0	0	0	0	J3KMI7	
ENSMUST00000188423						7	7	8	25	16	4	0	0	0	0	0		
ENSMUST00000188424						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188425						18	9	23	24	8	10	0	1	0	0	1		
ENSMUST00000188426						3	0	3	4	5	2	0	0	0	0	0		
ENSMUST00000188428						84	53	408	96	65	34	0	2	0	0	1		
ENSMUST00000188430						0	0	0	0	0	0	18	34	36	0	14		
ENSMUST00000188431						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188432						1	2	2	2	2	1	0	0	0	0	0		
ENSMUST00000188433						1	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000188436						27	25	94	133	39	28	1	0	2	0	5		
ENSMUST00000188437						2	1	5	1	5	2	0	0	0	0	5		
ENSMUST00000188439	ENSMUSG00000100626	X	11299257	11299757	1	17	0	13	0	2	0	0	0	0	0	0	Q5M8Q2	
ENSMUST00000188440	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	0	0	0	0	3	0	0	0	0	A0A087WRP1	
ENSMUST00000188441						1	5	1	1	1	2	0	0	1	0	0		
ENSMUST00000188442						7	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188444						5	2	1	2	5	2	77	186	71	5	89		
ENSMUST00000188445						8	8	6	11	10	4	0	0	0	15	30		
ENSMUST00000188446						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000188448						6	3	8	0	11	1	0	0	0	0	3		
ENSMUST00000188449	ENSMUSG00000056763	1	10037987	10136768	1	0	1	0	0	0	0	2	0	6	0	0	A0A087WRQ0	
ENSMUST00000188450						7	0	3	5	0	3	0	0	1	0	0		
ENSMUST00000188451						1	0	0	1	0	1	0	0	0	0	1		
ENSMUST00000188452						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188453	ENSMUSG00000021901	14	31251450	31259944	1	0	0	1	0	0	2	6	2	6	0	0	A0A087WPL4	
ENSMUST00000188454	ENSMUSG00000025938	1	12866549	12992650	-1	76	53	258	213	60	21	0	2	0	1	2	E9PVD9	
ENSMUST00000188455						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188458						0	0	31	11	16	0	0	0	0	0	0		
ENSMUST00000188459	ENSMUSG00000016528	1	131053700	131097826	-1	2	6	12	2	4	1	44	7	118	0	79	A0A087WSN7	
ENSMUST00000188460	ENSMUSG00000026201	1	75210838	75215606	1	0	0	0	0	0	0	50	0	8	0	2	A0A087WQ12	
ENSMUST00000188463						85	77	369	82	71	48	3	17	8	1	14		
ENSMUST00000188464	ENSMUSG00000057240	19	11169418	11196737	-1	7	2	1	0	8	2	0	0	0	0	0		Q5FWC3
ENSMUST00000188466	ENSMUSG00000033633	8	111058920	111092426	-1	6	0	0	0	0	1	0	0	0	0	0		Q7TSQ1
ENSMUST00000188467						2	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000188468	ENSMUSG00000040563	9	21937033	21948907	1	6	2	15	160	13	8	0	0	1	0	0	A0A087WQF0	
ENSMUST00000188469						9	9	5	6	11	9	0	0	1	0	0		
ENSMUST00000188470						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188472						1	4	13	7	1	3	0	0	0	1	0		
ENSMUST00000188475	ENSMUSG00000034353	1	91179822	91225196	1	0	1	0	5	1	2	0	0	1	0	4	A0A087WPC6	
ENSMUST00000188476						0	0	0	0	0	0	0	0	0	0	6		
ENSMUST00000188477						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188478						27	21	74	51	31	20	3	14	15	0	12		
ENSMUST00000188479						0	1	0	1	2	0	0	0	0	0	0		
ENSMUST00000188480						0	0	0	0	0	0	1	1	0	0	0		
ENSMUST00000188482	ENSMUSG00000022346	15	61985341	61990374	1	0	0	12	45	0	0	0	0	0	0	0	F8WID3	
ENSMUST00000188483						1	2	9	4	3	1	5	3	0	2	2		
ENSMUST00000188484	ENSMUSG00000069045	Y	1260771	1286629	-1	0	0	0	3	0	0	33	0	407	453	318	A0A087WQV7	
ENSMUST00000188486						103	96	230	111	103	58	14	60	19	1	68		
ENSMUST00000188487						1	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000188488	ENSMUSG00000041459	4	148612382	148627019	-1	5	0	3	0	3	0	0	10	0	2	0	A0A087WSC6	
ENSMUST00000188489	ENSMUSG00000017421	11	80383279	80405733	1	2	6	34	10	3	1	106	706	164	45	180		Q9JMD0
ENSMUST00000188491						4	2	6	3	5	2	1	0	0	0	0		
ENSMUST00000188492						25	14	46	22	32	5	0	0	0	0	0		
ENSMUST00000188493						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188494						0	9	0	9	0	7	0	0	5	0	0		
ENSMUST00000188495	ENSMUSG00000019982	10	21124936	21160905	-1	23	8	37	99	20	3	73	175	69	37	34	A0A087WPA7	
ENSMUST00000188496						11	10	0	20	12	0	0	0	0	0	0		
ENSMUST00000188497	ENSMUSG00000026341	1	125392905	125435727	-1	0	0	0	47	0	0	0	0	70	180	716	A0A087WRA1	
ENSMUST00000188500						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188501						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000188503						5	0	5	0	3	4	17	46	27	10	49		
ENSMUST00000188507	ENSMUSG00000043015	1	52630703	52651919	1	0	0	7	0	9	0	36	472	84	125	161	A0A087WQD9	
ENSMUST00000188509	ENSMUSG00000093803	9	124422622	124476861	-1	1	0	0	49	0	1	3	13	6	2	8	A0A087WQA6	
ENSMUST00000188511						3	1	3	0	2	0	0	0	0	0	8		
ENSMUST00000188512						0	0	0	0	1	0	78	208	108	97	89		
ENSMUST00000188513						21	9	0	3	13	7	0	0	0	0	0		
ENSMUST00000188514						2	3	3	1	5	3	0	0	0	0	0		
ENSMUST00000188515						3	2	0	0	1	2	0	0	0	0	0		
ENSMUST00000188516						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188517						5	4	0	0	5	0	0	0	0	0	0		
ENSMUST00000188518						12	2	24	5	7	3	0	0	0	0	0		
ENSMUST00000188520	ENSMUSG00000101904	1	130670209	130715799	-1	3	6	0	1	0	4	0	11	9	0	0	B2Z894	
ENSMUST00000188521						0	1	0	4	1	0	0	0	0	0	0		
ENSMUST00000188522	ENSMUSG00000051331	6	118587240	119196418	-1	9	2	2	71	14	8	0	0	0	0	0	A0A087WS67	
ENSMUST00000188523						0	2	19	0	1	3	0	0	0	0	0		
ENSMUST00000188524	ENSMUSG00000025967	1	63176825	63180486	1	4	0	0	12	5	3	519	2256	460	813	231	A0A087WS46	
ENSMUST00000188525						38	37	133	2519	19	39	0	7	2	0	0		
ENSMUST00000188528	ENSMUSG00000010453	1	36335730	36369181	-1	0	0	0	0	0	0	5	3	3	0	8	A0A087WPB8	
ENSMUST00000188531	ENSMUSG00000096914	8	57774052	58912640	-1	0	3	3	0	5	0	0	0	0	0	0	A0A087WP88	
ENSMUST00000188532	ENSMUSG00000073609	1	93824909	93852348	1	0	0	0	0	0	0	0	0	0	1	0	A0A087WPK4	
ENSMUST00000188533	ENSMUSG00000026238	1	86526726	86530712	1	0	0	5	0	6	0	0	1468	1113	3834	1037	A0A087WPN6	
ENSMUST00000188534						12	13	55	80	29	25	0	3	0	0	0		
ENSMUST00000188536						0	0	0	7	0	0	0	0	0	0	0		
ENSMUST00000188539	ENSMUSG00000032323	9	58006411	58027023	1	0	0	4	0	2	3	0	13	10	0	5	A0A087WRU6	
ENSMUST00000188543						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188545						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188546						0	0	0	1	2	0	12	262	9	88	7		
ENSMUST00000188548	ENSMUSG00000032258	9	83390293	83441127	-1	0	0	0	3	0	0	0	0	0	0	0	A0A087WQT5	
ENSMUST00000188549						17	8	13	5	13	3	0	0	0	0	1		
ENSMUST00000188550						4	2	0	5	1	1	0	0	0	0	0		
ENSMUST00000188552						0	23	0	0	0	3	0	0	0	0	0		
ENSMUST00000188553	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	6	9	72	0	A0A087WS23	
ENSMUST00000188554	ENSMUSG00000099550	Y	70004208	70014899	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNV3	
ENSMUST00000188555	ENSMUSG00000096316	9	99229376	99237239	-1	5	1	0	2	0	0	0	0	0	0	0	J3QPY3	
ENSMUST00000188557	ENSMUSG00000023259	9	108853283	108913049	1	0	0	0	0	0	0	24	33	0	0	0	A0A087WS07	
ENSMUST00000188558						5	0	7	0	6	0	0	0	0	2	0		
ENSMUST00000188559						55	45	483	95	70	40	0	0	0	0	0		
ENSMUST00000188561	ENSMUSG00000009210	11	106365472	106377558	1	0	0	0	6	0	0	0	0	0	0	0	A0A087WQH2	
ENSMUST00000188562	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	0	0	0	0	0	0	0	0	12	A0A087WPW6	
ENSMUST00000188563						6	2	2	4	8	1	0	0	0	0	0		
ENSMUST00000188567						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188569	ENSMUSG00000036634	7	30899176	30914873	-1	0	0	0	0	0	0	0	0	0	0	0	Q3ZB60	
ENSMUST00000188570						4	4	4	0	4	0	24	260	28	32	44		
ENSMUST00000188571						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188572						13	9	27	9	12	14	3	3	1	0	0		
ENSMUST00000188575	ENSMUSG00000026439	1	132477365	132505659	1	0	0	0	0	0	0	3	0	2	0	0	A0A087WQU2	
ENSMUST00000188576						2	2	14	14	0	1	0	10	3	0	2		
ENSMUST00000188578	ENSMUSG00000060962	7	30763756	30781063	1	5	1	0	0	0	2	0	0	0	1	0	A0A087WQH3	
ENSMUST00000188580	ENSMUSG00000030811	7	127744543	127769483	1	10	0	0	153	17	7	14	56	32	0	12		Q6PB97
ENSMUST00000188581	ENSMUSG00000026416	1	130906985	130911451	-1	2	0	0	0	0	0	0	0	0	0	0	Q2THG5	
ENSMUST00000188583						6	2	16	8	5	5	3	115	28	8	38		
ENSMUST00000188584						0	2	0	0	1	1	5	3	1	5	2		
ENSMUST00000188585	ENSMUSG00000096650	Y	35895328	35921526	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000188586						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000188587	ENSMUSG00000048126	1	90765923	90843971	-1	2	0	0	27	13	0	0	0	0	0	23	A0A087WS16	
ENSMUST00000188588						2	0	4	0	3	0	8	16	29	10	22		
ENSMUST00000188590						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188591						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188592						1	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000188593	ENSMUSG00000026202	1	75214228	75219865	-1	2	10	0	0	2	6	1654	2344	1245	572	786	A0A087WS35	
ENSMUST00000188594	ENSMUSG00000026782	1	60409619	60481158	1	0	0	0	30	0	0	0	0	0	0	0	A0A087WRS3	
ENSMUST00000188596						14	12	99	6	19	6	3	8	14	7	25		
ENSMUST00000188597						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188598						27	21	41	33	30	12	4	7	7	0	8		
ENSMUST00000188601						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000188604						0	0	0	1	0	0	1	2	0	0	0		
ENSMUST00000188606						7	4	8	113	13	6	0	0	0	0	0		
ENSMUST00000188607						4	7	2	3	7	1	0	0	0	0	0		
ENSMUST00000188609						0	0	0	0	0	4	0	0	0	0	0		
ENSMUST00000188612						1	1	5	0	5	4	0	0	2	0	5		
ENSMUST00000188614						1	0	0	40	1	3	0	0	0	0	0		
ENSMUST00000188615						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188617						0	0	4	134	3	2	0	0	0	0	0		
ENSMUST00000188618	ENSMUSG00000026782	1	60409619	60481158	1	16	13	29	0	9	4	0	10	0	0	0	Q6AXD2	
ENSMUST00000188619	ENSMUSG00000025917	1	10024601	10038168	-1	0	0	0	16	0	0	0	3	0	15	0	A0A087WQA8	
ENSMUST00000188621						9	15	36	79	10	6	0	2	0	1	1		
ENSMUST00000188622						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000188624						3	2	11	5	6	3	0	0	0	0	0		
ENSMUST00000188625						32	25	82	41	33	20	5	8	13	4	24		
ENSMUST00000188628						0	0	3	9	6	1	0	0	0	0	2		
ENSMUST00000188629						2	2	6	4	2	4	0	0	0	0	0		
ENSMUST00000188630	ENSMUSG00000051223	1	58392898	58407353	1	0	6	0	0	0	0	154	894	196	489	55	A0A087WS48	
ENSMUST00000188633	ENSMUSG00000058470	19	11485938	11512577	1	29	31	215	73	28	16	1	3	1	6	3	E9PZI3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188634						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188635						4	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000188636						7	3	10	3	8	5	0	0	0	0	0		
ENSMUST00000188637	ENSMUSG00000093927	Y	5043937	5046265	1	4	1	8	4	3	7	0	0	0	0	0	J3QN17	
ENSMUST00000188641	ENSMUSG00000079658	1	16641725	16657042	-1	6	3	1	8	3	2	53	369	46	230	72		P83940
ENSMUST00000188643						0	0	0	0	0	0	0	3	2	4	4		
ENSMUST00000188646						17	9	21	12	6	7	0	1	0	0	1		
ENSMUST00000188650	ENSMUSG00000023277	9	106203108	106215389	1	14	8	23	15	16	5	36	383	51	0	45		Q9Z0P5
ENSMUST00000188652	ENSMUSG00000026209	1	75307896	75317990	-1	0	0	0	17	0	0	0	0	0	0	0	A0A087WNX3	
ENSMUST00000188655						16	16	58	23	31	14	31	14	23	10	4		
ENSMUST00000188656	ENSMUSG00000026594	1	156804166	156939626	-1	9	10	13	5	8	0	0	0	0	0	7	A0A087WQU0	
ENSMUST00000188657						4	3	36	6	2	2	0	0	0	0	0		
ENSMUST00000188658	ENSMUSG00000032036	9	34485894	35036716	1	4	6	14	8	0	0	0	1	5	0	16		
ENSMUST00000188660						12	14	34	336	24	25	11	8	2	0	2		
ENSMUST00000188661						2	2	0	2	4	0	0	0	0	0	0		
ENSMUST00000188664	ENSMUSG00000032548	9	102988712	103096002	1	0	4	3	0	2	2	0	0	0	0	15		Q9EPT5
ENSMUST00000188665						1	2	12	2	6	3	0	7	0	3	5		
ENSMUST00000188666	ENSMUSG00000047180	1	36264597	36274679	-1	7	3	13	26	9	4	120	278	198	25	333	A0A087WP78	
ENSMUST00000188668						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000188669						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188670	ENSMUSG00000032475	9	100492293	100546134	-1	0	0	0	43	4	2	28	49	17	4	18	A0A087WQD1	
ENSMUST00000188671						1	0	0	1	1	0	1	0	0	2	1		
ENSMUST00000188672	ENSMUSG00000100902	Y	75715322	75741549	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000188674	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	0	0	0	2	3	151	1	155	72	A0A087WS56	
ENSMUST00000188675	ENSMUSG00000034973	9	86467154	86555923	1	0	0	0	0	0	0	10	0	54	5	26	A0A0B4J1N8	
ENSMUST00000188677	ENSMUSG00000026158	1	23366424	23397772	-1	0	0	0	0	0	5	257	811	397	0	80	A0A087WNQ8	
ENSMUST00000188679						90	78	513	168	76	43	2	14	12	0	25		
ENSMUST00000188680						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000188681	ENSMUSG00000026104	1	52119440	52161865	1	0	0	0	28	0	0	23	0	55	0	13	A0A087WSQ5	
ENSMUST00000188682						1	0	3	6	0	1	0	11	3	8	0		
ENSMUST00000188683						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188684						28	33	34	9	33	19	2	5	4	1	10		
ENSMUST00000188685	ENSMUSG00000056019	8	71882019	71895727	1	20	21	8	36	19	13	30	23	18	13	10	Q8VC29	
ENSMUST00000188686						0	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000188687						0	2	0	1	2	1	0	0	0	0	0		
ENSMUST00000188688						0	0	4	2	0	1	0	0	0	0	0		
ENSMUST00000188689						1	0	0	1	1	0	0	0	7	0	7		
ENSMUST00000188691	ENSMUSG00000056293	15	63824346	63845177	-1	1	10	21	10	20	0	0	0	0	0	0		Q2KHK6
ENSMUST00000188693						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000188695	ENSMUSG00000079445	1	86302832	86307305	1	0	4	0	0	5	4	0	0	0	1	5	A0A087WQY3	
ENSMUST00000188699	ENSMUSG00000026238	1	86526726	86530712	1	3	3	3	189	2	0	4	11	4	4	11	A0A087WQN2	
ENSMUST00000188700						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188702	ENSMUSG00000035085	11	83437677	83441233	1	0	0	0	107	7	0	75	87	86	38	28	A0A087WRJ9	
ENSMUST00000188705						10	9	7	11	12	1	0	2	1	0	2		
ENSMUST00000188706	ENSMUSG00000095867	Y	79148789	79151122	-1	9	0	0	0	0	5	0	0	0	0	0	Q62457	
ENSMUST00000188708						60	40	31	27	48	28	17	27	43	8	87		
ENSMUST00000188709						2	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000188710	ENSMUSG00000064302	1	118389058	118612678	1	358	259	2110	727	345	267	66	229	139	13	42	A0A087WRE8	
ENSMUST00000188712	ENSMUSG00000026153	1	24011093	24100341	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPF3	
ENSMUST00000188713						9	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188714						0	0	6	61	2	0	1	4	0	0	0		
ENSMUST00000188716						3	2	4	1	3	3	0	0	0	0	0		
ENSMUST00000188718						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188719						0	3	0	2	0	0	0	0	0	0	0		
ENSMUST00000188720						2	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000188723						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000188724						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188726	ENSMUSG00000037032	7	105558483	105581653	-1	2	0	7	0	6	2	1	4	0	0	0	A0A087WRY7	
ENSMUST00000188728	ENSMUSG00000070939	1	43047200	43098637	-1	0	0	0	16	0	1	17	0	7	0	0	A0A087WQF3	
ENSMUST00000188731	ENSMUSG00000049191	X	102066544	102071304	-1	3	0	13	52	10	5	0	18	14	2	23	Q8C065	Q5DTT4
ENSMUST00000188733						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000188734						0	0	0	4	0	2	0	0	0	0	0		
ENSMUST00000188735	ENSMUSG00000067028	1	99772765	100485942	1	7	5	0	5	10	0	0	0	0	0	0	A0A087WPQ7	
ENSMUST00000188736	ENSMUSG00000056912	10	100590511	100618401	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRQ1	
ENSMUST00000188738	ENSMUSG00000025915	1	9798107	9900845	1	0	0	3	0	0	0	8	104	237	107	79	A0A087WR70	
ENSMUST00000188739						2	3	2	1	1	2	0	0	0	0	0		
ENSMUST00000188740						4	4	11	87	14	2	0	1	0	0	0		
ENSMUST00000188741	ENSMUSG00000020870	11	94741782	94743033	1	0	0	0	64	0	0	0	0	0	0	0	A0A087WP01	
ENSMUST00000188744	ENSMUSG00000099541	Y	27495726	27521920	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR99	
ENSMUST00000188745	ENSMUSG00000067006	1	106861173	106883348	1	0	5	3	2	0	1	0	0	0	0	0	A0A087WQM9	
ENSMUST00000188746						0	22	30	10	20	13	7	276	130	23	126		
ENSMUST00000188748						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188749	ENSMUSG00000058884	2	85917927	85918865	1	4	1	0	0	5	1	0	0	0	0	0	A0A087WPP4	
ENSMUST00000188750	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPU8	
ENSMUST00000188751						1	0	3	4	3	2	0	0	0	0	0		
ENSMUST00000188752						11	15	18	16	27	6	0	0	0	0	1		
ENSMUST00000188754	ENSMUSG00000100240	Y	86061772	86087952	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPP3	
ENSMUST00000188755						2	2	10	1	4	0	0	0	1	0	0		
ENSMUST00000188756						44	30	61	257	32	34	0	13	1	6	2		
ENSMUST00000188757	ENSMUSG00000071302	8	129216354	129234406	-1	0	0	0	0	0	0	6	5	4	0	0	Q8BG62	
ENSMUST00000188759						3	4	1	10	2	4	0	0	0	0	0		
ENSMUST00000188760						18	12	14	19	20	10	0	0	0	0	0		
ENSMUST00000188761						2	3	10	2	1	0	0	0	0	0	0		
ENSMUST00000188762	ENSMUSG00000038252	6	125168007	125191701	-1	0	0	5	7	2	0	0	0	0	0	0	A0A087WRK6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188765						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188767	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	0	0	0	0	51	49	0	18	A0A087WSF8	
ENSMUST00000188768						1	5	4	0	1	0	4	65	0	0	0		
ENSMUST00000188770	ENSMUSG00000026425	1	131285251	131527352	-1	5	1	8	12	11	6	38	146	49	3	80	A0A087WS59	
ENSMUST00000188771	ENSMUSG00000097663	CHR_MG153_PATCH	4057477	4059446	-1	0	0	0	0	0	0	0	0	0	4	14		
ENSMUST00000188772	ENSMUSG00000047528	1	58646903	58695989	-1	3	7	6	0	5	0	0	0	0	1	0	A0A087WRU9	
ENSMUST00000188775	ENSMUSG00000101355	13	21717659	21718069	1	3	0	0	106	11	0	0	0	2	6	0		P68433
ENSMUST00000188779						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000188780	ENSMUSG00000048874	1	30802339	30873921	-1	0	0	0	29	0	1	5	0	35	3	12	A0A087WS81	
ENSMUST00000188782	ENSMUSG00000025915	1	9798107	9900845	1	0	2	3	0	0	0	0	42	0	0	0	A0A087WQS1	
ENSMUST00000188783						0	0	0	0	0	0	1	38	0	0	7		
ENSMUST00000188784	ENSMUSG00000032571	9	105642978	105687657	1	2	3	2	0	15	0	0	2	14	0	0		
ENSMUST00000188787						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188789	ENSMUSG00000048174	1	132506230	132508639	1	4	7	0	0	11	7	7	113	25	0	21		Q9D5K1
ENSMUST00000188794						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188795						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188796	ENSMUSG00000026253	1	87204657	87212694	1	0	0	0	0	0	0	0	0	0	0	0	H8YHW6	
ENSMUST00000188797	ENSMUSG00000026235	1	77367185	77515088	-1	0	0	0	0	0	0	0	0	0	0	0		Q03137
ENSMUST00000188799						4	3	10	4	9	0	3	0	0	0	0		
ENSMUST00000188801	ENSMUSG00000101303	1	117781133	117803359	1	6	3	2	3	2	4	0	0	0	0	0	A0A087WQI7	
ENSMUST00000188802						5	5	37	8	5	2	0	0	0	0	0		
ENSMUST00000188803						22	14	62	30	20	13	0	0	0	0	0		
ENSMUST00000188804	ENSMUSG00000090272	1	173857220	173942491	-1	4	2	0	6	6	10	26	0	12	97	41		D0QMC3
ENSMUST00000188805						149	161	653	152	124	63	5	10	5	0	4		
ENSMUST00000188806						4	4	0	7	7	2	0	0	0	0	0		
ENSMUST00000188807	ENSMUSG00000096878	5	15577333	15582078	1	15	12	18	14	12	4	0	1	0	0	1	A0A0G2JFD5	
ENSMUST00000188808						41	37	137	105	39	20	1	25	7	2	20		
ENSMUST00000188812						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188815	ENSMUSG00000024421	18	12333819	12583013	1	12	9	11	4	0	11	0	0	0	0	3		Q61789
ENSMUST00000188816						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000188818	ENSMUSG00000070732	1	91145089	91170795	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS12	
ENSMUST00000188822						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188823						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188825						1	3	2	0	2	0	0	0	0	0	0		
ENSMUST00000188827						2	8	6	7	0	2	2	2	8	5	23		
ENSMUST00000188828						7	3	15	32	14	4	0	0	0	0	0		
ENSMUST00000188829	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	0	0	0	1	0	0	0	0	A0A087WQV5	
ENSMUST00000188830						0	3	10	8	4	2	0	5	5	4	0		
ENSMUST00000188831						14	8	18	87	26	21	1	1	2	1	1		
ENSMUST00000188833						6	4	3	5	2	0	0	0	0	1	0		
ENSMUST00000188834						5	4	9	1	5	3	0	0	0	0	1		
ENSMUST00000188835						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000188837						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188838						15	8	30	14	16	4	0	0	4	0	4		
ENSMUST00000188839						5	3	3	18	4	3	0	0	0	0	0		
ENSMUST00000188840						18	19	73	20	21	5	4	14	6	1	10		
ENSMUST00000188842	ENSMUSG00000026452	1	134646677	134762593	1	36	31	154	51	29	27	0	4	0	0	3		
ENSMUST00000188843						58	48	98	74	59	31	8	66	50	6	91		
ENSMUST00000188844						12	8	30	34	21	4	0	1	3	0	0		
ENSMUST00000188845	ENSMUSG00000079018	15	75044018	75048830	-1	7	7	9	5	8	6	0	5	2	0	10	A0A087WNZ5	
ENSMUST00000188847						26	21	29	24	20	14	7	9	17	2	24		
ENSMUST00000188848	ENSMUSG00000032021	9	40972753	41004628	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPL6	
ENSMUST00000188850						36	19	34	18	27	16	2	5	6	1	2		
ENSMUST00000188851						3	5	13	15	4	7	35	79	89	10	112		
ENSMUST00000188853						1	1	2	6	0	1	0	0	0	0	0		
ENSMUST00000188855						0	3	0	1	0	0	5	0	4	0	6		
ENSMUST00000188857	ENSMUSG00000025932	1	14168954	14310235	-1	0	0	0	0	0	3	0	0	0	0	0	A0A087WQF4	
ENSMUST00000188858						3	4	5	4	5	3	0	0	0	0	1		
ENSMUST00000188859						0	0	0	0	0	0	28	48	8	9	58		
ENSMUST00000188860						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188861	ENSMUSG00000101918	2	89170275	89171210	-1	6	1	1	0	5	3	0	0	0	0	0	Q7TR01	
ENSMUST00000188862						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188863						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188864	ENSMUSG00000101158	Y	28245352	28271512	-1	0	0	0	1	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000188865	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPZ8	
ENSMUST00000188866	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	0	0	0	0	4	0	0	23	Q99JA5	
ENSMUST00000188867						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188868						8	7	25	6	4	2	12	28	199	33	116		
ENSMUST00000188869						4	2	0	5	1	1	0	0	0	0	0		
ENSMUST00000188871						0	0	0	0	0	0	5	8	0	0	0		
ENSMUST00000188873	ENSMUSG00000049339	1	75142778	75147913	1	0	0	0	1	0	0	145	636	104	36	85	A0A087WNV4	
ENSMUST00000188875						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000188876	ENSMUSG00000025950	1	65158616	65186500	-1	0	0	4	0	0	0	0	2	0	0	0	A0A087WPT4	
ENSMUST00000188877						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188878						0	0	0	0	6	0	0	0	0	0	0		
ENSMUST00000188879	ENSMUSG00000026311	1	91540544	91559589	1	0	0	0	0	0	0	2	0	0	0	0	G3X9J5	
ENSMUST00000188880						4	1	1	3	1	6	0	0	0	0	0		
ENSMUST00000188881	ENSMUSG00000094782	Y	47450960	47482990	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000188882						0	0	0	0	0	0	35	34	53	53	35		
ENSMUST00000188884						0	2	4	0	4	0	1	0	4	0	12		
ENSMUST00000188885	ENSMUSG00000032560	9	104151282	104262930	-1	0	0	3	0	0	0	0	34	10	16	10	A0A087WSI0	
ENSMUST00000188886						2	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000188887	ENSMUSG00000096268	Y	5725978	5728317	1	0	1	15	3	6	3	0	0	0	0	0	J3QME2	
ENSMUST00000188890						12	8	85	37	10	11	0	3	3	0	4		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000188892						5	2	0	21	3	2	0	7	21	0	9		
ENSMUST00000188894	ENSMUSG00000026193	1	71585520	71653200	-1	17	0	0	0	0	0	710	229	741	112	6491	A0A087WR50	
ENSMUST00000188895						0	2	2	0	4	5	0	0	1	0	0		
ENSMUST00000188896						36	35	50	31	53	22	7	7	10	1	9		
ENSMUST00000188897						2	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000188898	ENSMUSG00000051223	1	58392898	58407353	1	0	0	5	0	0	1	35	0	161	514	201	A0A087WPF9	
ENSMUST00000188899	ENSMUSG00000030858	7	131325944	131329516	-1	0	0	0	4	2	2	0	0	0	0	0		Q9DAL9
ENSMUST00000188900	ENSMUSG00000100963	2	130405239	130408256	1	6	0	0	0	0	0	0	0	0	0	0	A0A087WNV0	
ENSMUST00000188901						21	14	48	32	23	11	2	0	2	0	2		
ENSMUST00000188903						6	5	41	12	4	0	0	0	0	0	0		
ENSMUST00000188905						1	1	2	239	7	0	0	9	5	9	4		
ENSMUST00000188906	ENSMUSG00000034867	7	35586244	35639226	1	0	0	0	7	0	0	0	0	0	0	0	A0A087WPF2	
ENSMUST00000188907						1	0	2	19	2	0	0	0	0	0	2		
ENSMUST00000188908	ENSMUSG00000094773	Y	9344836	9347184	-1	5	0	7	0	0	2	0	0	0	0	0	J3QN84	
ENSMUST00000188910						90	89	242	82	105	45	2	0	8	1	5		
ENSMUST00000188912	ENSMUSG00000052534	1	168119364	168432270	-1	8	6	12	65	12	7	41	225	61	7	51	Q71VB4	P41778
ENSMUST00000188913						7	11	10	81	13	12	1	5	4	1	3		
ENSMUST00000188914	ENSMUSG00000095362	2	177831791	177840336	-1	0	3	0	3	0	2	0	0	0	0	5	A0A087WRL6	
ENSMUST00000188915						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188917	ENSMUSG00000094181	Y	44232123	44264444	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000188918	ENSMUSG00000070547	7	48444113	48456342	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR15	
ENSMUST00000188919						0	0	8	0	0	0	0	0	0	0	0		
ENSMUST00000188923						108	130	345	226	131	58	13	27	17	6	20		
ENSMUST00000188924						24	34	126	33	31	8	0	6	1	1	1		
ENSMUST00000188926						1	1	0	0	2	3	0	0	0	0	0		
ENSMUST00000188928	ENSMUSG00000102739	Y	17874741	17877179	1	0	0	0	0	16	0	0	0	0	0	0	Q3TTD8	
ENSMUST00000188930	ENSMUSG00000056912	10	100590511	100618401	1	2	4	0	1	3	0	0	0	0	0	0	A0A087WR40	
ENSMUST00000188931	ENSMUSG00000026203	1	75236406	75245692	1	26	9	52	66	25	19	83	144	100	18	100	Q3TB24	
ENSMUST00000188933	ENSMUSG00000032036	9	34485894	35036716	1	0	0	0	0	22	0	0	0	0	0	0	A0A087WNM9	
ENSMUST00000188934						1	1	10	4	3	5	0	0	0	0	0		
ENSMUST00000188937						2	0	3	0	2	1	9	24	14	0	36		
ENSMUST00000188939	ENSMUSG00000033499	13	9093881	9174451	1	0	0	0	2	0	6	0	0	0	0	0		Q6A0A2
ENSMUST00000188941						3	1	0	0	1	0	3	10	0	1	4		
ENSMUST00000188942						67	52	85	490	65	39	0	0	2	0	2		
ENSMUST00000188943	ENSMUSG00000053024	1	132509427	132543256	-1	1	3	4	0	3	4	0	0	0	0	0	A0A087WPI9	
ENSMUST00000188944						44	36	91	131	40	24	4	17	6	0	27		
ENSMUST00000188949						29	20	99	30	28	20	1	11	3	0	1		
ENSMUST00000188952	ENSMUSG00000026235	1	77367185	77515088	-1	0	37	174	52	34	14	0	5	1	1	7		Q03137
ENSMUST00000188953						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188954	ENSMUSG00000038866	1	105990406	106034074	1	0	0	0	0	0	0	10	7	25	0	0	A0A087WPY9	
ENSMUST00000188955						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188957	ENSMUSG00000010453	1	36335730	36369181	-1	0	0	0	10	1	0	0	0	0	0	0		
ENSMUST00000188958	ENSMUSG00000099531	Y	71469449	71495632	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000188959						3	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000188961	ENSMUSG00000010453	1	36335730	36369181	-1	0	0	0	3	0	0	25	0	37	5	0	A0A087WRK2	
ENSMUST00000188963						0	0	1	0	0	3	0	0	0	0	0		
ENSMUST00000188964	ENSMUSG00000060519	1	156653617	156674356	-1	2	0	4	0	0	0	26	4	32	10	41		Q9ER38
ENSMUST00000188965						23	29	91	142	26	14	1	1	2	0	0		
ENSMUST00000188967						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000188968						6	2	5	8	6	3	0	0	0	0	0		
ENSMUST00000188969						1	0	0	0	0	1	0	0	0	0	4		
ENSMUST00000188970	ENSMUSG00000029797	6	48448229	48501250	1	0	0	0	0	3	1	0	0	0	0	0	A0A087WRI0	
ENSMUST00000188971						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000188972	ENSMUSG00000026126	1	34459762	34475733	1	0	0	3	78	9	1	13	279	81	369	54	Q3V441	
ENSMUST00000188973						8	3	16	8	11	7	0	5	2	0	3		
ENSMUST00000188974						0	1	2	2	3	0	0	0	0	0	0		
ENSMUST00000188977						3	1	4	3	1	1	3	27	6	1	7		
ENSMUST00000188978						0	3	4	2	3	0	0	0	0	0	0		
ENSMUST00000188979						17	18	114	11	10	5	0	2	0	0	1		
ENSMUST00000188981						5	3	5	4	4	0	0	0	1	0	0		
ENSMUST00000188982						26	34	256	78	42	12	1	1	1	1	4		
ENSMUST00000188985						6	2	5	0	4	2	0	0	0	0	0		
ENSMUST00000188987						2	4	10	9	5	0	0	17	13	46	19		
ENSMUST00000188988	ENSMUSG00000034088	1	93405940	93478815	-1	0	5	0	0	1	0	0	0	3	0	3	A0A087WS92	
ENSMUST00000188989						9	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188991	ENSMUSG00000063142	14	23289431	24004859	-1	0	2	2	3	0	0	0	0	0	0	0	A0A087WRS4	
ENSMUST00000188992						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000188993						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000188994	ENSMUSG00000038872	8	108703100	108961630	1	30	13	138	128	11	13	3	5	4	0	2	A0A087WQ36	
ENSMUST00000188995	ENSMUSG00000101389	19	11375523	11392790	1	7	5	3	0	3	3	118	850	159	221	273	A0A087WRT7	
ENSMUST00000188996						9	7	33	13	0	4	1	0	0	0	0		
ENSMUST00000188997	ENSMUSG00000021709	13	103818787	103920514	-1	0	0	0	0	0	0	90	173	208	20	30	B2RUJ2	
ENSMUST00000188998	ENSMUSG00000032560	9	104151282	104262930	-1	0	2	0	0	0	0	0	0	0	13	23	A0A087WS25	
ENSMUST00000188999	ENSMUSG00000030209	6	135713233	136173511	-1	0	0	0	1	0	0	0	0	0	0	0	A0A087WR33	
ENSMUST00000189001						0	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000189003	ENSMUSG00000099530	Y	70271306	70303343	-1	13	22	21	3	45	6	0	0	0	0	0	A0A087WPG2	
ENSMUST00000189004						0	1	1	0	0	1	0	0	0	0	0		
ENSMUST00000189005						2	5	9	0	2	2	0	0	0	0	0		
ENSMUST00000189006	ENSMUSG00000101725	Y	70292585	70303287	-1	0	0	38	45	46	9	0	0	0	0	0	A0A087WRM1	
ENSMUST00000189007	ENSMUSG00000100645	Y	7722941	7749195	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRP6	
ENSMUST00000189008						7	2	4	159	16	4	8	9	6	2	5		
ENSMUST00000189009						15	3	15	16	15	10	0	0	0	0	0		
ENSMUST00000189010	ENSMUSG00000070939	1	43047200	43098637	-1	0	0	1	0	0	0	0	2	4	0	0	A0A087WR01	
ENSMUST00000189011	ENSMUSG00000026301	1	90042132	90153401	-1	1	1	3	0	0	1	0	1	0	0	0	A0A087WQW3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189012						0	3	2	1	1	1	0	0	0	0	0		
ENSMUST00000189013	ENSMUSG00000023791	16	32084418	32099738	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSN5	
ENSMUST00000189015						4	7	9	7	16	4	0	0	0	0	0		
ENSMUST00000189016						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000189017	ENSMUSG00000070047	8	44935447	45052257	1	13	14	92	7	5	13	3	1	0	5	21	A0A087WRT4	
ENSMUST00000189018						70	80	192	365	89	44	4	8	7	2	16		
ENSMUST00000189019						2	4	6	3	3	2	3	21	21	19	8		
ENSMUST00000189022	ENSMUSG00000041730	14	32599407	32649246	1	0	0	0	0	0	0	0	0	0	0	0		Q8BYH0
ENSMUST00000189023						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000189024						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189025	ENSMUSG00000034088	1	93405940	93478815	-1	0	1	1	7	1	3	4	3	20	2	9	A0A087WQY9	
ENSMUST00000189026						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000189027	ENSMUSG00000079502	2	28926949	29055066	-1	0	19	46	0	27	0	0	0	0	0	0	A0A087WQ85	
ENSMUST00000189029						17	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189030						1	5	4	3	4	0	0	0	0	0	0		
ENSMUST00000189031	ENSMUSG00000026333	1	97770172	97793709	1	0	0	0	0	0	0	2	0	0	1	1	A0A087WSG6	
ENSMUST00000189032	ENSMUSG00000054362	4	106590909	106617241	-1	0	0	0	7	8	0	0	0	0	0	0	A0A0F6T326	A2AVQ5
ENSMUST00000189034						32	28	18	23	13	6	0	0	0	0	0		
ENSMUST00000189037	ENSMUSG00000026387	1	120006894	120063536	1	7	3	16	12	12	0	0	0	0	0	0		Q5FWI2
ENSMUST00000189038						10	3	0	6	6	4	0	0	0	0	0		
ENSMUST00000189039	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	0	0	0	0	0	0	14	0	A0A087WNW7	
ENSMUST00000189041						0	1	0	0	1	0	13	0	0	0	0		
ENSMUST00000189042						10	7	19	15	14	7	6	31	16	4	19		
ENSMUST00000189043						15	12	51	16	7	5	7	185	27	0	29		
ENSMUST00000189044						17	14	19	24	27	6	2	4	4	0	3		
ENSMUST00000189047						9	7	4	2	8	3	0	0	0	0	0		
ENSMUST00000189048	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	36	27	0	14	0	Q8BLD4	
ENSMUST00000189049						1	6	20	4	9	4	1	0	0	0	1		
ENSMUST00000189050						0	0	0	5	2	0	2	2	6	0	3		
ENSMUST00000189051						0	0	1	0	0	0	0	34	22	5	22		
ENSMUST00000189055						15	6	152	36	13	8	0	0	0	0	0		
ENSMUST00000189057						4	1	8	7	1	4	0	0	0	0	0		
ENSMUST00000189059						20	15	93	28	21	22	0	1	0	0	3		
ENSMUST00000189061	ENSMUSG00000026358	1	144242296	144249242	-1	0	5	7	5	4	5	0	0	0	0	0		Q9JL25
ENSMUST00000189062						0	0	4	0	0	2	0	0	0	0	0		
ENSMUST00000189064						4	4	8	4	4	1	1	4	0	0	1		
ENSMUST00000189065						0	2	0	2	0	0	0	0	0	0	0		
ENSMUST00000189066	ENSMUSG00000042757	9	103482947	103761837	-1	7	0	45	118	12	10	0	1	0	1	3		Q8BHE4
ENSMUST00000189068	ENSMUSG00000075602	15	74994877	74998031	-1	2	5	0	0	0	0	0	0	2	15	16		P05533
ENSMUST00000189069	ENSMUSG00000056673	Y	897788	956786	1	0	1	1	3	0	1	0	0	0	0	0	Q8BQM3	
ENSMUST00000189070						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189072	ENSMUSG00000037032	7	105558483	105581653	-1	14	0	11	2	8	2	0	0	0	0	0	A0A087WR62	
ENSMUST00000189073	ENSMUSG00000079806	Y	6680421	6682872	-1	8	0	3	7	9	4	0	0	0	0	0	J3KMI9	
ENSMUST00000189075						7	4	14	7	6	3	4	18	8	5	36		
ENSMUST00000189076						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189078						4	3	4	0	8	3	0	0	1	0	0		
ENSMUST00000189079						2	0	3	0	0	1	0	0	0	0	0		
ENSMUST00000189081						0	0	0	2	0	2	0	0	0	0	0		
ENSMUST00000189082	ENSMUSG00000026782	1	60409619	60481158	1	0	0	0	10	0	0	0	0	0	0	0	A0A087WR90	
ENSMUST00000189083						4	2	4	3	0	5	3	21	5	1	8		
ENSMUST00000189084	ENSMUSG00000096016	Y	68268651	68294898	-1	0	0	0	0	0	0	0	0	0	0	0	J3QNI1	
ENSMUST00000189085						14	8	23	9	7	5	0	0	0	0	0		
ENSMUST00000189086						0	0	0	1	5	0	0	0	0	0	0		
ENSMUST00000189087						2	7	2	40	6	4	0	0	0	0	0		
ENSMUST00000189088						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000189089						6	4	14	4	7	5	3	22	9	2	7		
ENSMUST00000189091						0	0	2	16	0	0	1	0	0	0	0		
ENSMUST00000189092						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189094						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189095	ENSMUSG00000074419	7	3816781	3825687	-1	0	0	0	0	0	0	990	2571	1763	498	1334	A0A087WSB3	
ENSMUST00000189097						13	8	40	10	8	5	0	0	0	0	4		
ENSMUST00000189099	ENSMUSG00000023495	9	106453291	106464012	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ06	
ENSMUST00000189101	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQF8	
ENSMUST00000189102						8	5	6	1	1	2	0	0	0	0	0		
ENSMUST00000189103						3	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000189104						3	6	1	3	6	2	0	0	0	0	0		
ENSMUST00000189105						1	6	4	5	2	1	0	0	0	1	0		
ENSMUST00000189106	ENSMUSG00000032410	9	95954760	96057803	1	0	0	0	33	0	0	0	0	0	0	0	A0A087WQ18	
ENSMUST00000189107						1	1	4	0	0	2	7	19	7	0	6		
ENSMUST00000189108						1	1	11	22	4	0	0	0	0	0	0		
ENSMUST00000189109	ENSMUSG00000101155	Y	57187188	57213362	1	10	4	86	10	7	3	0	0	0	0	0	A0A087WSR0	
ENSMUST00000189110						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189112						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189113						1	3	7	2	4	2	0	0	0	0	0		
ENSMUST00000189114						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189115						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189118	ENSMUSG00000101232	7	32836554	32837870	1	1	0	0	0	0	0	0	0	0	0	0	A0A087WP50	
ENSMUST00000189119						4	3	3	5	5	0	0	0	0	0	0		
ENSMUST00000189120						3	2	2	3	3	1	0	0	0	0	0		
ENSMUST00000189121						12	20	12	3	13	0	1	19	4	2	5		
ENSMUST00000189122						13	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189124	ENSMUSG00000037263	19	3958645	3972103	1	41	0	125	24	27	14	0	32	8	0	7	A0A087WS45	
ENSMUST00000189126						17	17	49	30	34	15	0	3	2	4	4		
ENSMUST00000189127						0	0	0	0	4	1	0	0	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189128	ENSMUSG00000022594	15	74747852	74753046	-1	1	2	3	0	2	0	0	0	0	0	0	A0A087WNU3	
ENSMUST00000189131	ENSMUSG00000026202	1	75214228	75219865	-1	0	0	0	0	0	1	0	0	0	0	0	A0A087WSB0	
ENSMUST00000189133						37	36	192	54	41	24	2	18	7	0	8		
ENSMUST00000189134						4	0	3	47	5	1	0	0	0	0	0		
ENSMUST00000189135						0	0	0	0	0	0	655	378	564	92	341		
ENSMUST00000189136	ENSMUSG00000053877	7	127511983	127561219	1	2	3	1	4	6	3	0	0	3	0	9	A0A087WSL6	
ENSMUST00000189137	ENSMUSG00000032839	9	95705082	95750375	-1	34	27	46	25	28	11	0	10	3	0	18	B2RPS7	
ENSMUST00000189141						0	0	0	14	0	0	0	0	0	0	0		
ENSMUST00000189142						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189144						1	1	1	1	3	0	0	0	0	0	0		
ENSMUST00000189145						0	0	6	0	0	1	0	0	0	0	0		
ENSMUST00000189146						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000189151						4	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000189152						2	1	1	94	2	1	0	1	2	0	1		
ENSMUST00000189153						5	2	2	5	6	2	0	0	0	0	0		
ENSMUST00000189154	ENSMUSG00000073609	1	93824909	93852348	1	0	0	0	0	0	0	0	0	0	8	3	A0A087WR78	
ENSMUST00000189157						4	0	2	0	2	1	0	0	0	0	0		
ENSMUST00000189158	ENSMUSG00000037608	10	20312469	20344613	1	2	0	1	0	5	2	2	40	14	15	13	A0A087WRF8	
ENSMUST00000189159	ENSMUSG00000101892	15	58022259	58034325	-1	1	3	0	0	4	0	0	0	0	0	0	A0A087WSQ8	
ENSMUST00000189160						61	48	52	53	75	36	27	30	23	0	135		
ENSMUST00000189161						0	0	1	0	4	1	0	0	0	0	0		
ENSMUST00000189162						2	5	4	7	8	0	0	0	0	0	0		
ENSMUST00000189163	ENSMUSG00000099703	18	35553404	35581609	1	0	6	0	1	0	0	0	0	3	2	0	A0A087WPS1	
ENSMUST00000189165						1	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000189167	ENSMUSG00000026409	1	130689182	130729253	-1	0	0	0	0	2	0	0	0	11	0	0	B2Z894	
ENSMUST00000189168						8	9	11	162	17	3	0	0	0	1	0		
ENSMUST00000189173						3	2	2	4	13	6	89	81	132	23	56		
ENSMUST00000189174	ENSMUSG00000042849	1	92511048	92518515	-1	0	9	15	0	4	0	0	0	0	0	0	Q8VGU5	
ENSMUST00000189176						5	2	0	44	0	0	5	8	0	0	3		
ENSMUST00000189177						0	0	1	3	0	1	0	0	0	0	0		
ENSMUST00000189181	ENSMUSG00000031870	9	8899833	8968611	1	20	19	45	59	28	18	0	0	0	0	0	A6H6A5	
ENSMUST00000189182						0	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000189183						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000189184						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189185	ENSMUSG00000100967	15	84910438	84920038	-1	515	521	1007	432	654	295	27	74	58	40	48	A0A087WQ99	
ENSMUST00000189186	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	169	10	3	0	0	0	0	8	A0A087WNS9	
ENSMUST00000189188						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189189						37	31	45	38	26	29	0	4	2	0	7		
ENSMUST00000189190	ENSMUSG00000100249	X	3076875	3078817	1	0	4	0	3	8	7	0	0	0	0	0		
ENSMUST00000189192						0	2	5	2	0	1	10	41	29	6	43		
ENSMUST00000189193						2	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000189194						4	5	1	0	2	0	2	0	0	2	0		
ENSMUST00000189197						13	5	37	16	17	6	0	0	0	0	0		
ENSMUST00000189198						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000189199						2	2	4	1	1	3	0	0	0	0	0		
ENSMUST00000189200	ENSMUSG00000034730	15	74516195	74589465	1	0	0	0	0	2	0	2	4	5	0	5		
ENSMUST00000189201	ENSMUSG00000094484	Y	7165068	7169293	-1	6964	7780	8081	5586	7115	3370	381	1516	798	297	937	J3QK38	
ENSMUST00000189202						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189203						0	0	1	2	5	1	0	0	0	0	0		
ENSMUST00000189206						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189208						4	3	2	5	9	4	2	0	6	4	10		
ENSMUST00000189209						3	5	8	9	3	3	2	1	3	2	4		
ENSMUST00000189210						14	8	16	8	18	8	0	0	0	0	0		
ENSMUST00000189211						1	0	0	0	0	0	16	18	20	4	0		
ENSMUST00000189212						3	2	1	0	2	0	0	1	0	0	0		
ENSMUST00000189216						2	4	10	1	5	2	0	0	0	0	6		
ENSMUST00000189217						10	6	39	16	12	5	0	0	0	0	0		
ENSMUST00000189219						2	0	3	16	8	8	0	0	0	0	0		
ENSMUST00000189220	ENSMUSG00000026159	1	82839483	82901182	1	17	18	46	28	24	14	169	713	260	84	360		Q8K2K6
ENSMUST00000189222						68	55	186	84	62	43	6	16	6	8	12		
ENSMUST00000189223						5	3	6	3	5	2	0	0	0	0	0		
ENSMUST00000189225	ENSMUSG00000026295	1	88406961	88426438	1	0	0	1	0	0	2	0	0	0	0	0	A0A087WSF3	
ENSMUST00000189227						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000189228	ENSMUSG00000055322	1	73910231	74124449	-1	0	0	0	15	0	0	0	0	0	0	0	A0A087WPC7	
ENSMUST00000189229	ENSMUSG00000061080	16	39984361	42181679	1	0	1	2	10	8	3	0	0	0	0	0	A0A087WPK6	
ENSMUST00000189231						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189234						20	21	30	236	17	13	1	3	0	0	2		
ENSMUST00000189235						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000189238	ENSMUSG00000100708	Y	76761600	76787729	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK3	
ENSMUST00000189239						1	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000189241						24	26	54	37	16	8	2	14	4	6	19		
ENSMUST00000189242						4	0	10	5	1	3	0	0	0	0	11		
ENSMUST00000189243	ENSMUSG00000038750	9	78327589	78329620	1	0	0	0	0	0	3	0	0	0	0	0	A0A087WRQ7	
ENSMUST00000189244	ENSMUSG00000026104	1	52119440	52161865	1	31	23	94	0	26	13	0	77	0	3	0	Q8CFQ1	
ENSMUST00000189246	ENSMUSG00000034157	12	86947043	86965362	1	0	0	0	34	8	0	0	0	0	0	29	Z4YJJ0	
ENSMUST00000189248	ENSMUSG00000062760	15	84379203	84447097	-1	32	32	197	86	1	17	2	0	0	0	3	A0A087WSN1	
ENSMUST00000189249						72	87	61	77	102	44	2	7	5	0	4		
ENSMUST00000189252	ENSMUSG00000009418	1	135434580	135607295	-1	0	0	0	0	0	0	2	0	0	0	7	A0A087WSM9	
ENSMUST00000189253	ENSMUSG00000094679	Y	9199824	9202190	-1	6	0	10	6	0	11	0	0	0	0	0	J3QMK7	
ENSMUST00000189254						16	7	37	19	19	5	0	0	0	0	0		
ENSMUST00000189255						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189256						4	8	8	5	5	5	0	0	0	0	0		
ENSMUST00000189257	ENSMUSG00000033364	1	74435511	74544284	-1	0	6	7	6	0	0	0	0	43	0	20		
ENSMUST00000189258						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189259						84	72	415	87	60	33	5	16	13	1	17		
ENSMUST00000189260						9	3	20	4	8	3	0	0	1	1	0		
ENSMUST00000189262	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	13	0	436	0	245	A0A087WS18	
ENSMUST00000189263						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189264						1	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000189265	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	0	0	0	0	0	8	0	0	0	A0A087WQC5	
ENSMUST00000189268	ENSMUSG00000000384	11	6615598	6626067	-1	0	0	0	45	14	0	0	0	0	0	100		Q91YM4
ENSMUST00000189269						1	2	1	4	5	1	0	0	0	0	0		
ENSMUST00000189271						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189273						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189276						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189282	ENSMUSG00000026209	1	75307896	75317990	-1	0	0	0	37	0	0	7	4	0	0	1	A0A087WSU0	
ENSMUST00000189283						0	2	6	0	0	0	0	0	0	0	0		
ENSMUST00000189285						4	3	0	3	0	1	0	0	0	0	0		
ENSMUST00000189286						9	6	11	7	12	8	0	0	0	0	0		
ENSMUST00000189287						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189289						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000189290						56	36	93	66	63	36	7	10	14	1	51		
ENSMUST00000189292						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000189294	ENSMUSG00000035934	9	36890982	37147322	-1	0	2	4	6	5	2	0	0	0	0	0	A0A087WPD3	
ENSMUST00000189297						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189298						12	4	16	5	10	7	5	17	13	5	15		
ENSMUST00000189299						0	1	0	61	3	0	2	0	0	0	0		
ENSMUST00000189300	ENSMUSG00000019818	10	41519414	41531048	1	0	0	0	16	0	0	52	95	448	120	303	A0A087WP12	
ENSMUST00000189301	ENSMUSG00000041872	1	20777146	20790617	-1	59	98	138	55	63	15	1	0	0	0	3	A0A087WQB4	
ENSMUST00000189303						14	0	14	7	0	0	0	0	102	0	253		
ENSMUST00000189304	ENSMUSG00000101725	Y	70292585	70303287	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ00	
ENSMUST00000189305						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189307						0	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000189309						5	0	0	10	9	6	1	72	26	0	18		
ENSMUST00000189310						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189311						11	2	129	0	7	7	0	0	0	0	0		
ENSMUST00000189312						2	2	8	9	3	4	0	0	0	3	0		
ENSMUST00000189314	ENSMUSG00000048191	7	141633456	141655319	-1	11	5	32	15	11	13	1	1	0	0	0	Q0VAV1	
ENSMUST00000189315	ENSMUSG00000100535	Y	71692043	71718226	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000189316	ENSMUSG00000026594	1	156804166	156939626	-1	333	310	1807	444	427	208	12	107	33	12	92	Q8C134	
ENSMUST00000189317	ENSMUSG00000056211	1	128103301	128237736	1	0	0	0	0	0	0	0	0	2	0	0	A0A087WQF6	
ENSMUST00000189319						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189320						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189323						3	5	6	69	2	0	5	3	12	3	18		
ENSMUST00000189324	ENSMUSG00000022197	15	12359711	12739924	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS85	
ENSMUST00000189325						7	2	12	10	4	0	0	2	0	0	0		
ENSMUST00000189327	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	0	0	0	3	0	0	0	0	A0A087WNW0	
ENSMUST00000189328						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189329						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000189330						20	17	45	30	17	9	26	42	45	8	78		
ENSMUST00000189332						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189333	ENSMUSG00000095141	Y	60241202	60273250	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000189335						0	3	5	0	0	13	0	0	0	0	0		
ENSMUST00000189336	ENSMUSG00000026104	1	52119440	52161865	1	3	0	1	1	2	2	52	527	37	7	89	A0A087WRI1	
ENSMUST00000189337						7	4	7	3	4	1	0	0	0	0	0		
ENSMUST00000189338						5	4	0	0	3	4	3	1	7	0	0		
ENSMUST00000189339						1	3	3	0	7	2	0	0	0	0	0		
ENSMUST00000189341	ENSMUSG00000034292	1	91494647	91529307	1	8	7	23	34	20	6	0	0	0	5	9	A0A087WQD8	
ENSMUST00000189343						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000189345	ENSMUSG00000049339	1	75142778	75147913	1	0	0	0	0	0	0	0	2	1	0	0	A0A087WS58	
ENSMUST00000189346	ENSMUSG00000099782	Y	73669315	73695486	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000189347	ENSMUSG00000026104	1	52119440	52161865	1	0	0	0	0	0	0	0	375	441	12	245	Q99K94	
ENSMUST00000189349						2	2	1	0	0	0	0	35	21	4	14		
ENSMUST00000189351						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189352						3	0	0	1	2	0	0	0	0	0	1		
ENSMUST00000189353	ENSMUSG00000034730	15	74516195	74589465	1	0	0	0	1	0	3	0	0	0	0	0	A0A087WS42	
ENSMUST00000189354	ENSMUSG00000095979	Y	49571156	49597425	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQA3	
ENSMUST00000189355	ENSMUSG00000026414	1	135836354	135852260	1	0	0	0	0	0	0	0	0	0	0	0		P50752
ENSMUST00000189357						3	3	7	5	2	0	3	30	15	1	6		
ENSMUST00000189358	ENSMUSG00000061080	16	39984361	42181679	1	1	2	1	4	6	1	0	0	0	0	0	A0A087WNQ5	
ENSMUST00000189359	ENSMUSG00000041390	6	15720661	15802169	1	1	1	0	9	1	0	2	3	2	3	4		Q8BX65
ENSMUST00000189361	ENSMUSG00000026458	1	134296783	134332928	-1	0	0	0	0	49	26	0	3	11	0	14	A0A087WPM2	
ENSMUST00000189362						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189364						12	3	7	239	14	8	0	0	0	0	0		
ENSMUST00000189367						1	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000189368	ENSMUSG00000032826	3	126921612	127499350	-1	0	0	0	99	0	0	0	0	0	0	0	A0A087WRM9	
ENSMUST00000189369						0	0	3	2	1	0	0	0	0	0	0		
ENSMUST00000189370						11	1	13	172	8	5	0	0	0	0	8		
ENSMUST00000189371						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000189372						1	2	1	2	3	1	0	0	0	0	0		
ENSMUST00000189373	ENSMUSG00000056222	13	57421195	57908314	-1	0	5	3	0	0	8	0	0	0	0	0	A0A087WPP6	
ENSMUST00000189374						9	13	0	0	6	8	0	0	0	0	0		
ENSMUST00000189376						1	3	1	4	2	0	0	5	0	7	7		
ENSMUST00000189378	ENSMUSG00000037032	7	105558483	105581653	-1	7	6	0	97	24	0	0	0	0	0	17		
ENSMUST00000189380						3	1	1	0	0	5	2	10	4	3	4		
ENSMUST00000189382						5	2	2	5	4	4	3	0	0	0	0		
ENSMUST00000189383						3	2	10	5	1	5	0	1	1	0	1		
ENSMUST00000189384						8	15	14	12	14	3	0	3	7	0	9		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189385	ENSMUSG00000048960	1	10993465	11303681	1	5	0	4	5	0	0	0	0	0	0	0	A0A087WS21	
ENSMUST00000189388	ENSMUSG00000041763	1	43933647	44003000	1	0	5	0	0	0	6	35	0	197	0	5	A0A087WRC0	
ENSMUST00000189389	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPP1	
ENSMUST00000189390						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189391	ENSMUSG00000043289	9	81863670	82206007	1	0	0	0	0	1	0	0	0	0	0	0	A0A087WP18	
ENSMUST00000189392						6	11	19	12	20	6	0	0	0	0	0		
ENSMUST00000189393						9	3	2	4	3	2	0	3	1	0	0		
ENSMUST00000189395						3	3	2	1	1	0	2	13	8	7	6		
ENSMUST00000189396						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189398	ENSMUSG00000051590	1	127815253	127840321	-1	1	0	0	0	3	0	0	0	1	0	0	A0A087WR30	
ENSMUST00000189400	ENSMUSG00000025931	1	20890606	20939650	1	0	8	17	81	5	0	0	68	25	0	17		Q80ZE5
ENSMUST00000189402						0	1	0	0	5	0	0	0	0	0	2		
ENSMUST00000189403	ENSMUSG00000033159	1	75134554	75142711	-1	2	0	3	45	8	1	105	145	213	19	104	A0A087WSI6	
ENSMUST00000189406						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000189407	ENSMUSG00000023577	9	106503225	106561631	-1	1	4	0	0	0	1	0	0	0	0	0	A0A087WS34	
ENSMUST00000189409	ENSMUSG00000005501	1	87945119	88008551	-1	47	49	110	44	62	28	25	118	52	15	89	A0A087WQL1	
ENSMUST00000189411						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189412						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000189413	ENSMUSG00000041498	1	136466343	136531511	1	56	5	198	37	118	30	65	77	135	10	0		L0N7N1
ENSMUST00000189414						0	3	0	7	0	0	0	2	1	0	1		
ENSMUST00000189415						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189416						17	13	71	31	24	9	0	0	0	1	0		
ENSMUST00000189420						9	6	8	7	9	2	1	19	5	2	12		
ENSMUST00000189422	ENSMUSG00000096016	Y	68268651	68294898	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQA3	
ENSMUST00000189423						3	4	2	1	1	3	0	0	0	0	0		
ENSMUST00000189424						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000189425						1	1	1	5	4	1	0	0	1	0	0		
ENSMUST00000189426						19	14	69	280	33	21	0	1	14	0	4		
ENSMUST00000189427						6	3	6	19	7	1	0	1	0	0	0		
ENSMUST00000189430						1562	2046	2642	1012	1638	665	15	93	38	9	49		
ENSMUST00000189432	ENSMUSG00000000948	7	59974149	60005064	-1	0	0	0	2	3	1	1	0	0	0	1	A0A087WPV6	
ENSMUST00000189433						0	0	0	0	1	0	0	0	0	39	15		
ENSMUST00000189434						2	1	1	1	1	0	0	0	0	0	0		
ENSMUST00000189436						0	4	0	0	0	0	0	4	0	0	0		
ENSMUST00000189437						0	0	0	0	6	0	111	326	96	27	42		
ENSMUST00000189439						53	47	157	70	62	32	1	5	1	0	9		
ENSMUST00000189440						4	2	3	2	0	4	0	0	0	0	0		
ENSMUST00000189443	ENSMUSG00000026342	1	125560595	125595820	1	0	0	7	0	1	2	12	195	4	0	0	A0A087WS66	
ENSMUST00000189446	ENSMUSG00000032454	9	98486115	98509781	1	0	4	0	0	0	0	0	0	0	0	0	Q059R7	Q08652
ENSMUST00000189447						5	3	6	3	2	2	0	0	0	0	0		
ENSMUST00000189448	ENSMUSG00000070738	1	87853287	87945180	1	0	0	1	0	0	0	0	0	0	0	0	A0A087WP49	
ENSMUST00000189449						0	0	8	0	0	0	0	1	0	0	0		
ENSMUST00000189450	ENSMUSG00000100725	1	178323074	178337728	-1	0	0	0	0	4	0	58	286	85	17	77	A0A087WPF1	
ENSMUST00000189451	ENSMUSG00000100729	2	128458737	128460015	1	0	0	1	0	0	0	0	2	0	0	0	A0A087WRD5	
ENSMUST00000189452	ENSMUSG00000062101	17	55938381	55949500	-1	11	13	37	5	11	2	14	8	0	0	5	A0A087WPI5	
ENSMUST00000189453						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189454						7	5	35	7	13	0	0	0	0	0	0		
ENSMUST00000189455	ENSMUSG00000100726	Y	61646746	61672861	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK3	
ENSMUST00000189456	ENSMUSG00000047129	10	87058045	87230589	1	9	5	4	14	3	0	0	0	0	0	0	A0A087WR28	
ENSMUST00000189457	ENSMUSG00000101972	13	21782960	21783370	-1	7	3	6	174	0	2	0	0	0	10	1		P68433
ENSMUST00000189458						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189461						0	1	2	0	4	0	0	0	0	0	0		
ENSMUST00000189462						0	2	2	1	1	0	0	0	0	0	0		
ENSMUST00000189463	ENSMUSG00000094660	Y	84562572	84564907	-1	0	22	0	18	20	0	0	0	0	0	0	Q497R7	
ENSMUST00000189465						52	44	271	55	23	15	0	3	2	0	1		
ENSMUST00000189469						19	8	23	109	11	5	0	0	0	0	0		
ENSMUST00000189470	ENSMUSG00000026116	1	36792191	36943666	-1	1	2	0	1	0	0	2	6	2	1	7	A0A087WRG7	
ENSMUST00000189471						1	0	15	2	2	0	0	0	0	1	0		
ENSMUST00000189472	ENSMUSG00000026279	1	93701935	93754864	-1	0	2	4	3	5	2	39	19	31	7	20	A0A087WPE8	
ENSMUST00000189474						47	43	19	41	70	20	12	82	0	14	61		
ENSMUST00000189476						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189478						2	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000189479	ENSMUSG00000071398	12	17003319	17011727	-1	1	1	4	27	4	0	0	0	0	0	0	A0A087WQ37	
ENSMUST00000189482	ENSMUSG00000100512	7	30233439	30235725	-1	11	4	19	25	13	6	0	0	0	0	0		D3YYM0
ENSMUST00000189483						9	2	11	75	19	8	0	0	0	0	0		
ENSMUST00000189484						25	17	25	20	29	20	0	5	0	0	0		
ENSMUST00000189486	ENSMUSG00000038608	1	80501073	80758527	-1	3	9	4	4	12	0	18	137	26	23	60	A0A087WS26	
ENSMUST00000189487						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189488	ENSMUSG00000100181	10	41623182	41647149	-1	12	7	15	6	12	8	0	0	0	1	1	A0A087WRU3	
ENSMUST00000189490						4	29	149	29	46	13	0	0	0	0	0		
ENSMUST00000189491						1	0	0	1	0	1	0	0	0	0	0		
ENSMUST00000189492	ENSMUSG00000026621	1	184786767	184811313	-1	3	0	16	0	4	3	0	0	0	5	0	A0A087WPC2	
ENSMUST00000189494	ENSMUSG00000094932	2	175741537	175751419	1	0	0	0	0	0	0	0	0	0	0	0	F7CEW8	
ENSMUST00000189496	ENSMUSG00000026219	1	84721189	84840516	-1	2	3	11	11	2	3	0	0	0	0	0	A0A087WP92	
ENSMUST00000189498	ENSMUSG00000032527	9	100982032	101034898	-1	0	0	0	26	0	0	0	0	0	0	0	A0A087WQV1	
ENSMUST00000189501						6	5	22	16	11	18	2	0	0	0	0		
ENSMUST00000189503	ENSMUSG00000026260	1	92439010	92473860	-1	0	0	0	0	0	0	239	524	228	322	192	A0A087WRD4	
ENSMUST00000189504						0	1	0	0	0	1	3	40	6	0	7		
ENSMUST00000189505	ENSMUSG00000026305	1	90998737	91128944	1	0	0	0	54	3	0	0	0	0	0	0	A0A087WSF5	
ENSMUST00000189506						8	10	12	73	20	8	0	0	0	0	1		
ENSMUST00000189508						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189509						7	5	2	43	8	5	0	0	4	0	8		
ENSMUST00000189510						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189511	ENSMUSG00000101818	X	21743440	21745097	-1	3	1	1	0	0	1	0	0	0	0	0	A0A087WSG3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189512						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189513						0	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000189515						0	1	3	0	1	0	0	0	0	0	0		
ENSMUST00000189516						0	0	0	0	0	0	6	0	22	0	0		
ENSMUST00000189517						9	7	7	7	10	4	1	0	0	0	1		
ENSMUST00000189518	ENSMUSG00000100055	Y	26750605	26776799	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WR99	
ENSMUST00000189519						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189520	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQJ4	
ENSMUST00000189522						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000189524	ENSMUSG00000051998	1	133679091	133690108	-1	1	0	19	3	2	0	0	0	3	1	0	A0A087WQ47	
ENSMUST00000189526	ENSMUSG00000025932	1	14168954	14310235	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRG6	
ENSMUST00000189528	ENSMUSG00000053024	1	132509427	132543256	-1	33	38	114	56	36	14	0	0	2	0	0	A0A087WST5	
ENSMUST00000189529	ENSMUSG00000026245	1	78417975	78488897	-1	0	0	0	0	0	9	4	129	0	53	0	A0A087WQ15	
ENSMUST00000189531	ENSMUSG00000101819	X	11302432	11302926	1	0	0	0	2	0	2	0	0	0	0	0	A0A087WP11	
ENSMUST00000189533	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQD0	
ENSMUST00000189534	ENSMUSG00000026409	1	130689182	130729253	-1	0	0	0	0	0	1	3	0	9	10	3	B2Z893	
ENSMUST00000189535	ENSMUSG00000030213	6	136506167	136610862	1	0	0	5	0	0	0	0	0	0	0	0	A0A087WNQ2	
ENSMUST00000189537						11	8	13	6	12	2	0	0	0	1	0		
ENSMUST00000189539						1	1	5	1	1	1	0	0	0	0	0		
ENSMUST00000189540	ENSMUSG00000068117	15	82069997	82126811	1	23	0	29	8	27	26	0	0	0	0	0		Q9D4I2
ENSMUST00000189541	ENSMUSG00000016918	1	12692277	12861192	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDD4	
ENSMUST00000189542	ENSMUSG00000026107	1	51465862	51478425	-1	0	0	35	28	0	2	137	840	163	18	83		Q8BGW5
ENSMUST00000189543	ENSMUSG00000094399	Y	87116821	87142917	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000189544						7	0	5	81	9	2	2	2	0	0	1		
ENSMUST00000189545	ENSMUSG00000032356	9	89909908	90026977	1	137	84	316	1278	195	116	0	4	1	1	5	A0A087WS68	
ENSMUST00000189546						12	16	115	12	18	10	1	4	2	1	4		
ENSMUST00000189547	ENSMUSG00000026331	1	97059038	97128301	-1	1	0	0	0	0	0	0	0	0	0	0	Q9D4B7	
ENSMUST00000189548						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189549						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189550	ENSMUSG00000095508	Y	12381981	12384008	1	0	0	0	0	0	3	0	0	0	0	0	J3QPZ4	
ENSMUST00000189551	ENSMUSG00000026209	1	75307896	75317990	-1	2	0	0	1	0	2	0	0	0	0	0	A0A087WRC1	
ENSMUST00000189552						27	20	25	17	24	10	1	1	5	3	3		
ENSMUST00000189553	ENSMUSG00000040661	9	106688082	106789194	-1	0	0	0	0	1	0	0	0	0	0	0	A0A087WPJ6	
ENSMUST00000189556	ENSMUSG00000040710	1	95587682	95667571	-1	135	140	500	167	124	88	19	48	34	11	66	A0A087WRA0	
ENSMUST00000189557	ENSMUSG00000079162	9	89084624	89092835	-1	0	0	0	0	0	0	0	0	0	1	0	A0A087WNR2	
ENSMUST00000189559						11	7	0	4	8	4	0	0	0	0	0		
ENSMUST00000189561						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189562	ENSMUSG00000030811	7	127744543	127769483	1	0	0	1	43	0	2	0	0	0	0	0	A0A087WPZ0	
ENSMUST00000189563						13	9	34	11	7	9	244	1866	433	75	472		
ENSMUST00000189564						0	0	0	0	0	0	0	169	0	37	0		
ENSMUST00000189565						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189568						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189570	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	10	0	0	0	0	A0A087WQF1	
ENSMUST00000189571						0	0	0	0	0	0	0	0	2	0	6		
ENSMUST00000189572						0	2	3	0	2	0	0	41	0	23	33		
ENSMUST00000189575	ENSMUSG00000019899	10	26980036	27619758	-1	0	4	5	0	0	0	0	0	0	0	0	A0A087WRP2	
ENSMUST00000189577	ENSMUSG00000095263	Y	32588415	32620443	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000189580	ENSMUSG00000101725	Y	70292585	70303287	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ00	
ENSMUST00000189582						5	2	16	166	6	4	0	2	0	0	1		
ENSMUST00000189583						3	1	7	4	1	1	0	0	0	0	0		
ENSMUST00000189586						2	0	0	25	0	0	0	0	0	0	0		
ENSMUST00000189588	ENSMUSG00000042757	9	103482947	103761837	-1	9	0	52	86	9	0	0	0	0	0	0		Q8BHE4
ENSMUST00000189589						3	5	13	3	5	1	0	4	1	0	1		
ENSMUST00000189591						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000189592	ENSMUSG00000093918	Y	3294976	3306449	-1	24	0	8	36	2	0	0	0	0	0	0		O35698
ENSMUST00000189593	ENSMUSG00000038015	16	10791380	10796134	-1	15	12	18	2	15	5	0	0	0	0	1	Q545M0	P07978
ENSMUST00000189595						115	131	370	103	98	74	4	26	22	7	18		
ENSMUST00000189596						2	3	4	7	2	0	23	57	71	6	53		
ENSMUST00000189597						767	945	474	312	746	218	0	20	7	0	2		
ENSMUST00000189598	ENSMUSG00000041757	1	133181321	133303435	1	0	0	2	0	4	0	0	0	1	0	1	A0A087WP37	
ENSMUST00000189599						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189601						0	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000189602						16	13	18	23	22	9	2	0	1	0	1		
ENSMUST00000189603						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189605	ENSMUSG00000003346	10	80583654	80590341	-1	1	1	9	0	1	0	169	117	51	25	24	A0A087WST3	
ENSMUST00000189606	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	0	0	0	3	0	6	0	3	A0A087WSK4	
ENSMUST00000189610						5	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189612						5	1	22	1	3	1	0	2	3	0	2		
ENSMUST00000189613						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189614						11	6	12	5	8	6	0	0	0	0	0		
ENSMUST00000189615						92	77	156	111	104	45	19	115	89	0	81		
ENSMUST00000189616	ENSMUSG00000066415	9	101074101	101104800	1	7	5	0	211	4	9	72	140	598	39	340	A0A087WNL5	
ENSMUST00000189617	ENSMUSG00000026305	1	90998737	91128944	1	7	0	0	0	0	8	0	0	0	0	8	A0A087WPK3	
ENSMUST00000189618						8	11	37	346	30	14	0	1	0	0	0		
ENSMUST00000189620						344	289	952	352	446	199	17	65	29	11	50		
ENSMUST00000189621						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189622						10	9	15	6	18	8	0	0	1	0	0		
ENSMUST00000189624						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189626						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000189629	ENSMUSG00000107023	7	127519584	127567054	1	33	83	116	49	60	57	69	414	85	0	85	A0A087WP63	
ENSMUST00000189630	ENSMUSG00000095032	Y	10144735	10147183	-1	0	7	8	7	7	0	0	0	0	0	0	J3QQ23	
ENSMUST00000189631						5	3	4	44	4	4	0	0	0	0	0		
ENSMUST00000189633	ENSMUSG00000029280	5	88002549	88008534	1	3	0	0	0	0	0	0	0	0	0	0	A0A087WPN9	
ENSMUST00000189634	ENSMUSG00000046203	3	92373915	92375229	1	8	1	2	1	1	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189635						0	3	3	0	1	0	6	11	4	6	5		
ENSMUST00000189636	ENSMUSG00000076437	2	84669215	84670770	-1	0	0	0	0	0	0	0	0	0	86	1	A0A087WPM0	
ENSMUST00000189638						0	0	5	2	0	0	0	0	0	0	0		
ENSMUST00000189640						2	1	3	3	1	3	0	0	0	0	0		
ENSMUST00000189641	ENSMUSG00000024680	19	11615523	11623719	-1	2	0	7	3	3	0	10	0	2	2	0	A0A087WPM9	
ENSMUST00000189642						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189644	ENSMUSG00000021103	12	73123717	73273988	1	0	0	0	2	0	0	23	75	18	187	38	A0A087WSQ7	
ENSMUST00000189647						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189648	ENSMUSG00000026594	1	156804166	156939626	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQA4	
ENSMUST00000189649						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000189650	ENSMUSG00000049339	1	75142778	75147913	1	1	1	6	9	4	2	0	2	3	0	5	A0A087WNS5	
ENSMUST00000189651						19	20	23	27	32	11	8	7	11	2	10		
ENSMUST00000189652						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000189654	ENSMUSG00000022583	15	75268421	75272235	1	7	4	0	0	6	0	0	0	0	0	0		P35460
ENSMUST00000189655	ENSMUSG00000053286	1	151428542	151458161	1	0	0	0	0	12	5	155	923	160	88	219	A0A087WQ23	
ENSMUST00000189656						0	2	0	10	0	0	0	2	0	0	0		
ENSMUST00000189658	ENSMUSG00000098810	CHR_MG132_PATCH	124291804	124312696	-1	0	0	0	0	1	0	0	1	2	9	3		
ENSMUST00000189660						0	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000189661	ENSMUSG00000026600	1	156424525	156474331	-1	81	74	121	113	95	50	668	3721	1219	159	966		Q61263
ENSMUST00000189662						21	7	64	29	9	12	0	0	1	0	0		
ENSMUST00000189663	ENSMUSG00000026200	1	75198236	75210813	-1	0	0	0	0	0	0	0	79	0	2	0	A0A087WPD7	
ENSMUST00000189664	ENSMUSG00000025968	1	63143596	63176833	-1	5	8	15	9	5	1	6	9	30	14	40	A0A087WRY4	
ENSMUST00000189665	ENSMUSG00000033124	1	75180860	75192196	-1	7	2	13	29	4	11	752	1180	726	39	739	A0A087WQ26	
ENSMUST00000189666						3	0	3	0	6	0	1	1	1	0	0		
ENSMUST00000189667						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189668						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000189670	ENSMUSG00000026219	1	84721189	84840516	-1	0	0	0	12	0	0	281	2005	708	160	438	A0A087WRV6	
ENSMUST00000189671						0	3	0	1	0	0	0	0	0	0	0		
ENSMUST00000189672	ENSMUSG00000096856	10	81649059	81667361	1	23	40	0	25	0	0	9	86	41	41	22	A0A087WNP5	
ENSMUST00000189673	ENSMUSG00000074199	7	30787896	30791097	1	0	0	0	0	0	0	0	0	0	0	0	B7ZNU6	
ENSMUST00000189674						6	3	7	11	5	3	0	5	0	0	0		
ENSMUST00000189676						2	0	5	28	8	0	0	2	7	0	0		
ENSMUST00000189677						14	6	20	16	10	2	1	1	1	3	0		
ENSMUST00000189678						3	4	0	1	4	1	0	0	0	0	0		
ENSMUST00000189679	ENSMUSG00000022952	16	92601466	92826149	-1	8	9	8	18	8	8	7	40	23	15	12	A0A087WR69	
ENSMUST00000189681						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189684						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189685	ENSMUSG00000046441	8	110215665	110224486	1	4	5	9	88	5	2	0	0	0	0	0	A0A087WPV8	
ENSMUST00000189688	ENSMUSG00000003283	2	153108468	153151441	1	6	3	15	61	9	5	3497	6147	2935	722	2484		P08103
ENSMUST00000189690						14	7	12	0	23	10	0	0	0	0	0		
ENSMUST00000189691						4	5	9	6	6	3	5	15	5	0	11		
ENSMUST00000189692						0	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000189693						19	17	71	34	26	14	0	1	2	1	0		
ENSMUST00000189694	ENSMUSG00000035829	2	28446800	28455508	1	51	32	130	149	60	0	0	2	2	1	8		Q6A025
ENSMUST00000189695						3	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000189696						7	3	13	30	7	0	0	0	0	0	0		
ENSMUST00000189697	ENSMUSG00000026271	1	92950865	92986391	1	126	129	179	69	149	82	25	39	25	36	58	A0A087WPI1	
ENSMUST00000189698	ENSMUSG00000026201	1	75210838	75215606	1	3	0	15	16	9	0	105	11	67	9	32	A0A087WQT0	
ENSMUST00000189700						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189702	ENSMUSG00000033124	1	75180860	75192196	-1	2	0	2	44	0	0	41	29	22	0	61	Q3ZAQ4	
ENSMUST00000189704	ENSMUSG00000100937	19	5502767	5503787	-1	7	4	8	31	9	2	7	9	7	1	3	Q99PB1	
ENSMUST00000189705						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189706						2	0	1	1	3	1	0	0	3	0	5		
ENSMUST00000189707	ENSMUSG00000093803	9	124422622	124476861	-1	0	0	0	50	2	0	12	64	28	9	28	A0A087WS63	
ENSMUST00000189708						1	0	0	6	7	3	19	229	65	28	85		
ENSMUST00000189709						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189710	ENSMUSG00000030168	6	119353150	119417704	-1	2	4	1	2	1	0	0	0	0	0	0	A0A087WPS4	
ENSMUST00000189711	ENSMUSG00000079502	2	28926949	29055066	-1	22	0	0	16	0	7	19	31	17	0	15	A0A087WRI3	
ENSMUST00000189712						2	1	2	1	2	3	0	0	0	0	0		
ENSMUST00000189714						6	5	33	9	8	4	10	29	8	0	7		
ENSMUST00000189715						3	2	18	7	4	1	1	0	0	0	0		
ENSMUST00000189716						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189717						19	20	15	18	22	11	0	0	0	0	0		
ENSMUST00000189718	ENSMUSG00000030577	7	30865402	30880342	-1	39	35	251	33	27	16	0	22	27	0	14	Q3UP36	
ENSMUST00000189719						6	5	2	6	6	2	2	1	1	3	0		
ENSMUST00000189720						8	4	48	13	10	0	0	0	2	0	0		
ENSMUST00000189723						61	50	149	107	70	42	0	0	0	0	0		
ENSMUST00000189724	ENSMUSG00000099353	15	98398419	98416268	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQB2	
ENSMUST00000189725						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189726						9	0	5	0	2	0	5	2	15	0	23		
ENSMUST00000189727						81	55	476	136	70	21	0	0	0	0	2		
ENSMUST00000189728	ENSMUSG00000026279	1	93701935	93754864	-1	0	0	0	0	0	0	4	128	23	5	36		
ENSMUST00000189730						126	125	420	93	120	58	7	12	17	5	40		
ENSMUST00000189731						0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000189732	ENSMUSG00000026414	1	135836354	135852260	1	0	0	0	0	0	0	0	0	0	0	0		P50752
ENSMUST00000189733						1	2	2	11	2	3	0	0	0	0	0		
ENSMUST00000189734						5	1	19	15	3	1	2	0	0	0	4		
ENSMUST00000189735	ENSMUSG00000020633	12	28437795	28552303	-1	347	361	168	364	285	94	13	65	40	3	34		Q9D1B8
ENSMUST00000189736	ENSMUSG00000025777	1	17145362	17164271	1	0	0	0	0	1	0	0	0	0	0	0	A0A087WQZ4	
ENSMUST00000189737						0	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000189738	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	114	0	113	0	0	A0A087WRK0	
ENSMUST00000189739	ENSMUSG00000003680	19	8772522	8786417	-1	0	0	0	0	0	0	0	0	3	0	0	A0A087WQC4	
ENSMUST00000189740						8	7	26	9	4	0	0	0	0	0	0		
ENSMUST00000189741						3	5	3	69	5	1	0	1	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189742						59	57	51	70	59	22	0	0	0	0	0		
ENSMUST00000189743						9	4	24	13	11	12	0	0	0	0	2		
ENSMUST00000189745						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189746						3	5	4	0	11	6	0	0	0	0	0		
ENSMUST00000189747						1	3	4	1	4	2	0	0	0	0	0		
ENSMUST00000189749	ENSMUSG00000101337	1	46425592	46807476	1	41	32	43	36	52	16	0	0	0	0	0	A0A087WR13	
ENSMUST00000189750	ENSMUSG00000038791	18	43764289	43767399	1	0	0	0	0	0	0	0	0	0	0	0		Q920H1
ENSMUST00000189753	ENSMUSG00000005696	X	42502453	42529330	1	53	26	43	504	87	52	2	0	0	0	7	Q544F1	O88890
ENSMUST00000189755						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189756	ENSMUSG00000016526	1	131127455	131138340	-1	0	3	0	10	0	0	7	2	2	1	2	A0A087WQ56	
ENSMUST00000189758	ENSMUSG00000032567	9	105395392	105412229	1	1	0	0	0	0	0	0	0	0	0	0	H3BKA9	
ENSMUST00000189759	ENSMUSG00000091402	12	111979111	111981317	-1	3	7	0	6	2	0	0	0	0	0	0	B2RV38	
ENSMUST00000189760						2	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000189761	ENSMUSG00000033029	15	79129349	79141253	-1	0	2	3	5	0	0	0	0	0	0	0	A0A087WPE0	
ENSMUST00000189762						3	1	1	2	0	1	0	0	0	0	0		
ENSMUST00000189764						6	6	7	1	2	2	0	0	0	0	0		
ENSMUST00000189765	ENSMUSG00000101653	Y	48311855	48343871	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000189766						9	4	14	13	5	2	0	0	0	0	0		
ENSMUST00000189768						0	0	0	0	0	0	2	0	0	0	0		
ENSMUST00000189769	ENSMUSG00000026204	1	75247027	75264502	-1	0	0	0	14	0	0	0	0	0	0	0	A0A087WQF2	
ENSMUST00000189770	ENSMUSG00000019813	10	41718840	41809871	-1	2	0	0	7	0	0	0	14	0	19	0	B2RR53	
ENSMUST00000189771						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189772	ENSMUSG00000101645	2	84601439	84678041	-1	0	0	0	0	0	0	0	0	0	0	51		P30999
ENSMUST00000189774	ENSMUSG00000074928	16	88818667	88826145	-1	10	2	12	5	7	4	0	0	0	0	0		O08640
ENSMUST00000189775	ENSMUSG00000047129	10	87058045	87230589	1	3	4	12	1	4	7	0	0	0	0	0	Q9D9A9	
ENSMUST00000189776	ENSMUSG00000026018	1	59982490	60043184	-1	2	3	4	5	7	2	0	0	0	0	0	A0A087WSM1	
ENSMUST00000189777						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189779						10	16	87	25	19	11	0	0	2	2	4		
ENSMUST00000189782						2	3	19	6	5	0	0	0	0	0	0		
ENSMUST00000189783						0	1	0	0	1	0	1	1	1	0	2		
ENSMUST00000189785						2	0	3	2	2	2	0	0	0	0	0		
ENSMUST00000189786	ENSMUSG00000026439	1	132477365	132505659	1	7	2	11	6	1	2	0	3	0	0	0	A0A087WRV7	
ENSMUST00000189787						3	3	9	3	4	1	0	0	0	0	0		
ENSMUST00000189788	ENSMUSG00000101959	17	5417323	5418767	-1	7	9	14	17	10	5	0	1	2	0	1	Q8BVP2	
ENSMUST00000189789						0	3	3	2	2	1	0	0	1	1	0		
ENSMUST00000189790						8	8	12	1	10	6	0	4	1	0	3		
ENSMUST00000189791						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000189793	ENSMUSG00000026249	1	79794197	79861180	-1	1	3	3	0	2	0	5	12	0	4	0	A0A087WQ70	
ENSMUST00000189794						0	0	0	48	1	0	0	0	0	0	0		
ENSMUST00000189795						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000189797						0	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000189799	ENSMUSG00000033554	3	115887837	115934361	1	5	3	23	133	9	2	69	145	71	246	59		Q9CWQ0
ENSMUST00000189800						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189801						1	4	1	2	4	0	0	0	0	0	0		
ENSMUST00000189804						0	2	0	0	3	0	0	0	0	0	0		
ENSMUST00000189805	ENSMUSG00000026413	1	135871395	135919207	-1	0	0	0	56	0	0	0	0	0	0	0	A0A087WS37	
ENSMUST00000189806						3	0	2	1	4	5	1	2	0	0	0		
ENSMUST00000189807						1	2	4	1	3	2	0	0	0	0	0		
ENSMUST00000189808	ENSMUSG00000058216	19	4057477	4059446	-1	0	0	0	0	0	0	0	0	0	4	14	Q8VC73	
ENSMUST00000189809	ENSMUSG00000033159	1	75134554	75142711	-1	0	0	0	5	0	0	19	6	28	5	25	A0A087WQM7	
ENSMUST00000189810						3	1	0	2	3	0	0	0	0	0	0		
ENSMUST00000189811						8	3	13	2	14	6	0	0	0	0	0		
ENSMUST00000189812						6	12	11	11	13	9	0	2	3	0	5		
ENSMUST00000189813						0	0	3	4	3	0	0	50	4	0	0		
ENSMUST00000189816						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000189817	ENSMUSG00000034973	9	86467154	86555923	1	2	0	1	0	0	0	8	84	36	20	39	A0A087WP61	
ENSMUST00000189818						6	1	0	1	4	1	0	0	0	0	0		
ENSMUST00000189819						0	2	0	0	0	0	0	4	0	0	0		
ENSMUST00000189820	ENSMUSG00000033124	1	75180860	75192196	-1	37	26	106	54	52	20	200	743	175	0	307	A0A087WP33	
ENSMUST00000189821	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	0	0	0	0	750	584	309	4	3330	B7ZNJ1	
ENSMUST00000189822						0	5	5	0	0	3	0	0	0	0	0		
ENSMUST00000189824						8	5	17	12	4	5	0	0	1	0	8		
ENSMUST00000189826	ENSMUSG00000026414	1	135836354	135852260	1	2	2	7	5	4	0	0	0	0	0	0	A0A087WRX3	
ENSMUST00000189829						150	86	1216	236	76	51	1	4	2	3	9		
ENSMUST00000189830	ENSMUSG00000033276	1	74601445	74636894	1	4	1	3	3	0	1	0	0	4	0	1	A0A087WS61	
ENSMUST00000189832	ENSMUSG00000043289	9	81863670	82206007	1	3	2	4	0	2	1	0	0	0	0	0		Q8BRM6
ENSMUST00000189833						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189834						0	0	4	44	0	2	0	0	0	0	0		
ENSMUST00000189835						0	2	0	0	1	1	0	0	0	0	0		
ENSMUST00000189836	ENSMUSG00000030556	7	67513411	67645268	-1	0	0	0	5	1	0	5	9	0	1	7	A0A087WP31	
ENSMUST00000189837	ENSMUSG00000032712	6	149309414	149335663	1	15	24	61	0	5	12	1266	6419	2382	355	954	A0A087WP74	
ENSMUST00000189838						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189839						7	5	3	1	5	3	0	0	0	0	0		
ENSMUST00000189841	ENSMUSG00000026219	1	84721189	84840516	-1	1	0	0	0	0	0	2	0	78	0	79	A0A087WS33	
ENSMUST00000189844						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189846						0	0	4	5	0	2	13	7	11	5	8		
ENSMUST00000189847						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000189849	ENSMUSG00000062563	12	24665838	24681813	-1	9	0	16	0	9	8	0	0	0	0	0		
ENSMUST00000189850						2	4	7	6	7	2	0	0	0	0	0		
ENSMUST00000189851	ENSMUSG00000101750	11	49293323	49294258	1	8	3	6	5	10	5	0	0	0	1	0	Q8VFA6	
ENSMUST00000189852						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189854						7	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000189856						3	3	7	6	6	1	0	0	0	0	1		
ENSMUST00000189858						116	138	236	84	104	51	140	451	225	40	241		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189859	ENSMUSG00000015882	5	45697181	45857615	-1	0	0	0	0	0	0	0	0	0	1	0	A0A087WQ10	
ENSMUST00000189861						0	0	4	0	2	1	0	1	0	1	0		
ENSMUST00000189862						0	8	0	0	5	15	44	52	22	0	58		
ENSMUST00000189863						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189865	ENSMUSG00000021790	14	41072911	41092197	1	0	4	7	0	0	0	0	0	0	0	0		Q9D9T0
ENSMUST00000189866						8	9	40	12	14	5	0	0	0	0	0		
ENSMUST00000189870						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189871	ENSMUSG00000021209	12	103532283	103613831	1	0	0	2	4	8	5	0	0	0	0	0		Q8C0Y0
ENSMUST00000189872						2	0	12	0	2	2	4	19	10	4	25		
ENSMUST00000189873						17	9	84	18	24	8	0	0	0	0	0		
ENSMUST00000189874	ENSMUSG00000022579	15	75596628	75599481	1	12	7	13	9	11	8	0	0	0	0	0	A0A087WPI6	
ENSMUST00000189875	ENSMUSG00000032803	9	103353094	103365840	-1	0	0	0	0	0	0	7	5	4	3	1	A0A087WRM0	
ENSMUST00000189876						4	6	3	5	5	1	0	0	0	0	0		
ENSMUST00000189877	ENSMUSG00000030600	7	28451980	28468242	1	13	4	21	113	22	2	2	5	0	0	12		Q2WF71
ENSMUST00000189878	ENSMUSG00000026058	1	32172714	32658568	1	121	106	485	163	126	57	3	18	16	11	14	A0A087WSL3	
ENSMUST00000189881						0	0	3	147	0	0	276	0	398	0	327		
ENSMUST00000189882						2	0	3	0	4	0	0	1	0	2	0		
ENSMUST00000189884						13	10	31	18	14	0	0	0	0	0	0		
ENSMUST00000189885	ENSMUSG00000096753	12	103310975	103317065	1	4	7	1	107	8	3	0	0	0	0	0	A0A087WP32	
ENSMUST00000189886						1	2	2	0	5	4	0	0	0	0	0		
ENSMUST00000189888	ENSMUSG00000053211	Y	725128	797409	-1	3	0	0	0	0	0	0	0	0	0	0		P10925
ENSMUST00000189889						0	0	3	1	6	0	0	0	0	0	0		
ENSMUST00000189891						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189892						0	6	1	3	0	1	0	0	0	9	0		
ENSMUST00000189893						29	33	168	163	17	11	3	0	8	0	5		
ENSMUST00000189895						1	2	0	1	1	0	9	127	43	6	19		
ENSMUST00000189896	ENSMUSG00000032803	9	103353094	103365840	-1	1	0	5	202	0	0	0	0	3	0	10	A0A087WNP6	
ENSMUST00000189897	ENSMUSG00000036098	19	10208272	10240748	-1	10	0	3	74	13	9	3	0	0	0	9		Q3UR85
ENSMUST00000189900						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189902						2	0	3	4	0	0	0	0	0	0	0		
ENSMUST00000189906						1	2	0	3	0	1	0	0	0	0	0		
ENSMUST00000189907	ENSMUSG00000099353	15	98398419	98416268	1	0	0	0	3	0	0	0	0	0	0	0	A0A087WSJ6	
ENSMUST00000189908						1	1	0	0	2	0	0	0	0	0	0		
ENSMUST00000189909						0	0	0	0	0	0	19	36	15	102	9		
ENSMUST00000189910						4	6	10	45	12	6	0	0	0	0	0		
ENSMUST00000189911	ENSMUSG00000108265	11	58720069	58721094	-1	9	12	26	17	9	2	0	1	0	0	0	Q5NCD7	
ENSMUST00000189913						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189914						1	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000189915	ENSMUSG00000074829	9	124291804	124312696	-1	1	1	2	1	0	0	3	16	9	3	6	A0A087WRR3	
ENSMUST00000189916						0	0	3	1	0	0	0	0	0	0	0		
ENSMUST00000189917						11	0	0	9	0	0	0	0	0	0	0		
ENSMUST00000189918						0	0	0	8	2	1	0	0	0	0	0		
ENSMUST00000189919	ENSMUSG00000026020	1	59684971	59719044	1	3	1	3	1	0	0	0	0	0	0	0	A0A087WSU5	
ENSMUST00000189923						3	4	4	0	1	0	0	1	0	0	0		
ENSMUST00000189924	ENSMUSG00000101528	Y	74470531	74496958	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP44	
ENSMUST00000189925						1	1	0	0	0	0	0	11	8	11	17		
ENSMUST00000189926						1	1	2	6	5	1	0	0	1	0	0		
ENSMUST00000189927						0	2	3	3	1	0	0	0	0	0	0		
ENSMUST00000189930						37	38	54	47	40	28	0	0	0	0	2		
ENSMUST00000189931						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189932	ENSMUSG00000032712	6	149309414	149335663	1	0	0	0	0	0	0	0	9	348	0	51	B2KFD2	Q5DTW7
ENSMUST00000189933						14	12	42	15	11	7	0	0	0	0	2		
ENSMUST00000189934						60	30	32	448	94	48	0	3	2	0	0		
ENSMUST00000189935						16	7	65	13	10	3	5	1	5	3	9		
ENSMUST00000189936	ENSMUSG00000018189	1	143777272	143807466	1	0	0	4	10	1	2	42	503	150	62	39		Q9WUP7
ENSMUST00000189937						12	3	6	7	7	2	0	0	0	0	0		
ENSMUST00000189940						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189941						15	19	19	15	34	34	3125	21294	3721	11494	1421		
ENSMUST00000189944	ENSMUSG00000022579	15	75596628	75599481	1	1	1	0	0	3	0	0	0	0	2	0	A0A087WNV7	
ENSMUST00000189946	ENSMUSG00000026434	1	131910534	131936321	1	31	14	61	70	14	9	59	31	144	22	78	A0A087WRY3	
ENSMUST00000189949						10	26	14	11	16	11	0	0	0	0	0		
ENSMUST00000189950						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189951						8	7	10	0	7	7	7	40	30	2	62		
ENSMUST00000189952						0	7	17	11	16	7	0	0	0	0	3		
ENSMUST00000189954						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189955						3	14	1	2	10	2	0	1	2	1	0		
ENSMUST00000189956						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000189957						2	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000189958						6	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189959	ENSMUSG00000038252	6	125168007	125191701	-1	0	1	0	8	2	2	2	0	0	0	0	A0A087WNQ1	
ENSMUST00000189961	ENSMUSG00000027409	2	130405259	130406074	1	0	0	4	0	0	0	0	0	0	0	0	Q9DA59	
ENSMUST00000189962	ENSMUSG00000074199	7	30787896	30791097	1	0	2	4	2	0	0	0	0	0	0	0	A0A087WR64	
ENSMUST00000189964	ENSMUSG00000095852	Y	2830699	2873492	1	0	0	0	0	0	2	0	0	0	0	0	B2RWR6	
ENSMUST00000189965	ENSMUSG00000071302	8	129216354	129234406	-1	1	0	8	0	2	3	0	9	1	8	2	A0A087WQQ7	
ENSMUST00000189967						1	2	0	1	4	3	1	3	0	1	1		
ENSMUST00000189968						3	12	11	0	6	5	0	1	0	0	4		
ENSMUST00000189969	ENSMUSG00000078161	3	154663859	154767790	1	0	0	0	0	0	1	0	0	0	0	0	A0A087WS75	
ENSMUST00000189970						6	5	4	3	2	0	0	0	0	0	1		
ENSMUST00000189972	ENSMUSG00000006344	10	75589340	75617200	1	5	5	100	7	13	8	237	142	150	11	151	A0A087WNR3	
ENSMUST00000189973						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000189975						39	18	30	19	23	21	0	0	0	0	0		
ENSMUST00000189976						0	1	0	4	0	0	0	0	0	0	0		
ENSMUST00000189977						14	11	53	13	7	8	90	62	161	0	281		
ENSMUST00000189980	ENSMUSG00000026782	1	60409619	60481158	1	22	20	65	0	17	13	0	0	14	6	9	Q6AXH6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000189981						157	145	672	225	180	90	44	95	92	15	134		
ENSMUST00000189982						19	20	14	22	21	9	0	2	1	0	2		
ENSMUST00000189984						0	0	0	4	2	0	0	0	0	0	0		
ENSMUST00000189985	ENSMUSG00000032253	9	82866159	82975516	-1	0	0	0	2	3	0	0	1	3	0	2	A0A087WR26	
ENSMUST00000189986	ENSMUSG00000021843	14	47648448	47736564	1	8	0	0	0	0	0	0	0	0	0	0	A0A087WPY8	
ENSMUST00000189987	ENSMUSG00000038248	10	43002500	43174530	-1	0	0	0	123	4	0	0	0	0	0	0	A0A087WS24	
ENSMUST00000189988	ENSMUSG00000076437	2	84669215	84670770	-1	0	1	0	8	0	0	0	0	7	0	11	A0A087WNU1	
ENSMUST00000189990	ENSMUSG00000101716	11	22759738	22859545	-1	3	7	13	7	10	0	0	3	0	1	1	A0A087WR21	
ENSMUST00000189991	ENSMUSG00000006344	10	75589340	75617200	1	0	0	0	10	3	0	41	86	112	0	68	A0A087WSM3	
ENSMUST00000189992						2	1	10	3	3	6	2	2	2	0	2		
ENSMUST00000189993						0	10	0	0	8	0	0	0	0	0	0		
ENSMUST00000189994	ENSMUSG00000062760	15	84379203	84447097	-1	0	0	0	46	0	0	0	0	0	0	0	A0A087WRN8	
ENSMUST00000189997						1	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000189998	ENSMUSG00000090150	9	104063377	104127656	1	0	1	0	1	1	2	1	1	0	0	1	A0A087WSI8	
ENSMUST00000189999	ENSMUSG00000057329	1	106538178	106714274	-1	34	23	128	92	31	16	4	6	5	9	8	Q6NTH7	P10417
ENSMUST00000190001	ENSMUSG00000092073	5	94648382	94686353	1	0	0	8	0	16	0	0	0	0	0	0	E9PZS2	
ENSMUST00000190002						23	17	32	201	29	18	0	0	0	0	1		
ENSMUST00000190003						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190005						3	2	2	3	3	0	0	0	0	0	2		
ENSMUST00000190008	ENSMUSG00000006299	1	74279840	74284738	-1	0	2	2	24	5	1	3	14	0	0	6	A0A087WR11	
ENSMUST00000190009						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190010						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190012						0	1	2	1	1	2	0	0	0	0	0		
ENSMUST00000190013	ENSMUSG00000069053	Y	818649	844224	1	0	0	1	5	0	0	0	0	0	0	0		P31254
ENSMUST00000190014	ENSMUSG00000038079	1	59100590	59120408	-1	0	1	2	25	0	0	0	0	3	15	6	A0A087WQC2	
ENSMUST00000190015						31	11	35	26	28	21	0	0	0	0	0		
ENSMUST00000190016	ENSMUSG00000025997	1	69531214	69687245	-1	0	0	0	0	1	0	0	0	0	0	0	A0A087WQX2	
ENSMUST00000190018						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190019	ENSMUSG00000032407	9	95456898	95511996	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQT2	
ENSMUST00000190021						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190022	ENSMUSG00000019813	10	41718840	41809871	-1	0	0	0	0	0	0	0	11	0	0	0		
ENSMUST00000190024						0	1	2	1	0	1	0	0	0	0	0		
ENSMUST00000190025						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190026	ENSMUSG00000101243	Y	6583546	6615511	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP35	
ENSMUST00000190027						1	2	0	0	1	0	3	8	0	2	3		
ENSMUST00000190029	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	28	0	0	175	772	629	1146	347	Q5BL18	Q8K310
ENSMUST00000190030						2	5	19	4	0	5	0	0	0	0	0		
ENSMUST00000190032						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000190035						1	1	0	0	4	0	0	0	0	0	0		
ENSMUST00000190036	ENSMUSG00000015882	5	45697181	45857615	-1	0	0	0	0	0	0	0	0	7	0	0	A0A0H2UH31	
ENSMUST00000190037	ENSMUSG00000026342	1	125560595	125595820	1	4	0	6	47	3	5	2	3	19	18	16	A0A087WP59	
ENSMUST00000190038						3	0	0	1	3	0	0	0	0	0	0		
ENSMUST00000190039						0	0	12	0	1	0	0	0	8	11	3		
ENSMUST00000190041	ENSMUSG00000033499	13	9093881	9174451	1	0	2	9	40	2	2	4	2	2	2	1	A0A087WPU9	
ENSMUST00000190042						1	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000190044	ENSMUSG00000063142	14	23289431	24004859	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ41	
ENSMUST00000190045						0	3	0	3	0	0	0	0	0	0	3		
ENSMUST00000190046	ENSMUSG00000026159	1	82839483	82901182	1	0	0	9	5	2	0	2	64	421	56	223	A0A087WR52	
ENSMUST00000190047	ENSMUSG00000032531	9	102716672	102733418	1	3	0	0	0	0	0	0	0	0	0	0	A0A087WRL8	
ENSMUST00000190048	ENSMUSG00000026035	1	58430994	58445486	-1	0	0	0	0	0	0	0	0	0	4	0	A0A087WP41	
ENSMUST00000190049						0	5	0	0	0	1	0	0	0	0	0		
ENSMUST00000190050	ENSMUSG00000099908	16	18836584	18956247	1	4	3	0	0	2	1	0	0	10	0	49	A0A087WSL9	
ENSMUST00000190051						0	0	1	1	0	0	294	1945	233	469	200		
ENSMUST00000190052	ENSMUSG00000026159	1	82839483	82901182	1	4	3	0	0	0	0	74	11	16	0	16	A0A087WSR7	
ENSMUST00000190055						6	5	3	4	3	10	4	16	17	2	20		
ENSMUST00000190056	ENSMUSG00000056211	1	128103301	128237736	1	4	1	17	2	4	0	3	3	10	3	22	A0A087WQI5	
ENSMUST00000190057						0	1	1	21	2	0	0	4	9	0	4		
ENSMUST00000190058	ENSMUSG00000025949	1	65186683	65278695	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQI1	
ENSMUST00000190059						57	64	83	55	75	49	71	195	142	15	190		
ENSMUST00000190060						4	2	6	5	3	7	0	0	0	0	0		
ENSMUST00000190061	ENSMUSG00000070738	1	87853287	87945180	1	10	6	25	4	3	13	58	543	52	61	89	A0A087WP73	
ENSMUST00000190062						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190063						0	0	0	0	0	0	0	0	10	0	0		
ENSMUST00000190064						0	1	0	0	0	0	0	0	0	1	0		
ENSMUST00000190066	ENSMUSG00000078546	17	21879570	21909926	-1	4	6	3	1	6	5	0	5	0	10	3	E9Q6M3	
ENSMUST00000190067	ENSMUSG00000026219	1	84721189	84840516	-1	0	2	5	9	2	0	0	3	0	0	10	Q3TP48	
ENSMUST00000190068	ENSMUSG00000025507	7	141438113	141444025	-1	0	0	0	0	0	0	32	0	11	0	26	A0A087WPX5	
ENSMUST00000190070	ENSMUSG00000026484	1	151458004	151500955	-1	0	0	0	0	0	0	3	6	3	0	4	A0A087WP87	
ENSMUST00000190071	ENSMUSG00000090272	1	173857220	173942491	-1	0	0	5	0	0	0	1	0	0	44	30	A0A087WSH9	
ENSMUST00000190072						7	0	0	0	10	0	0	0	0	0	0		
ENSMUST00000190073						88	69	151	59	103	68	1	4	4	1	2		
ENSMUST00000190075						10	4	9	5	4	4	0	0	0	0	0		
ENSMUST00000190078	ENSMUSG00000056267	9	99243367	99300404	1	2	1	4	61	4	7	0	0	0	0	0	A0A087WSG9	
ENSMUST00000190079						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190081	ENSMUSG00000060568	1	167001417	167091302	1	0	0	0	54	2	0	0	0	0	0	0		Q8BQN5
ENSMUST00000190082						2	4	6	2	5	0	0	0	0	0	0		
ENSMUST00000190083						1	0	2	3	0	0	0	0	0	0	0		
ENSMUST00000190084						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000190086						1	3	3	0	0	0	0	0	0	0	0		
ENSMUST00000190087						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190089						0	1	6	1	1	0	0	0	0	0	0		
ENSMUST00000190090						0	4	2	0	0	0	0	0	0	0	0		
ENSMUST00000190091	ENSMUSG00000041476	X	157698910	157752591	1	2	0	0	0	0	0	0	0	0	0	0		Q9DC77
ENSMUST00000190092						0	0	0	0	1	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190093						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190094						1	2	6	3	2	0	0	0	0	0	0		
ENSMUST00000190095						13	9	8	9	11	2	2	23	10	4	5		
ENSMUST00000190096	ENSMUSG00000055013	1	89454806	89897617	1	1	6	28	19	0	0	345	333	428	9	367	A0A087WRF2	
ENSMUST00000190097						1	2	2	5	0	2	0	5	0	0	2		
ENSMUST00000190098						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190100	ENSMUSG00000100634	Y	5793395	5795728	1	0	2	0	6	3	3	0	0	0	0	0	A0A087WQ19	
ENSMUST00000190101						1	1	0	0	6	1	0	2	0	0	0		
ENSMUST00000190103	ENSMUSG00000026107	1	51465862	51478425	-1	0	0	0	0	0	0	11	739	175	0	0		Q8BGW5
ENSMUST00000190104	ENSMUSG00000032411	9	96196275	96323646	1	0	0	0	0	0	0	0	2	0	0	0	A0A087WRW3	
ENSMUST00000190106						112	88	30	129	134	88	0	0	0	0	0		
ENSMUST00000190107						4	4	17	13	7	0	0	0	0	0	0		
ENSMUST00000190108						11	16	32	61	15	11	3	12	8	2	14		
ENSMUST00000190110						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190111						3	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000190112						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000190114	ENSMUSG00000019865	10	14705591	14770850	1	0	1	3	0	0	0	0	0	0	0	0	A0A087WRS7	
ENSMUST00000190115						1	0	0	0	6	0	12	0	22	15	5		
ENSMUST00000190116	ENSMUSG00000026279	1	93701935	93754864	-1	82	60	148	97	74	40	2	27	18	4	26		Q6P3Z3
ENSMUST00000190119						9	6	12	6	12	5	0	0	0	0	0		
ENSMUST00000190121	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	0	0	0	225	0	10	243	43	A0A087WSP7	
ENSMUST00000190122	ENSMUSG00000026126	1	34459762	34475733	1	5	2	10	5	6	0	0	3	6	0	11	A0A087WPR5	
ENSMUST00000190125						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190127						16	30	185	73	18	5	2	3	0	0	4		
ENSMUST00000190128						8	3	8	2	13	5	8	12	10	3	19		
ENSMUST00000190130						12	0	24	60	16	5	0	0	7	0	6		
ENSMUST00000190131	ENSMUSG00000054115	15	9111985	9155425	-1	0	4	11	0	0	3	3	0	1	0	0	A0A087WQ11	
ENSMUST00000190134						19	20	15	18	22	11	0	0	0	0	0		
ENSMUST00000190135						5	13	19	8	7	9	0	3	2	2	5		
ENSMUST00000190136						5	2	7	2	3	1	5	5	5	0	7		
ENSMUST00000190137						0	3	7	0	0	0	0	0	0	0	0		
ENSMUST00000190139						35	28	216	106	31	13	4	34	38	2	12		
ENSMUST00000190141						2	0	0	1	1	0	0	3	0	0	1		
ENSMUST00000190142						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190143						5	0	4	3	6	4	0	0	0	0	0		
ENSMUST00000190145						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000190146						1	3	6	0	2	0	0	0	0	0	0		
ENSMUST00000190147						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190149	ENSMUSG00000026235	1	77367185	77515088	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQZ6	
ENSMUST00000190150						34	18	79	36	41	11	0	2	0	0	2		
ENSMUST00000190151	ENSMUSG00000021209	12	103532283	103613831	1	0	2	0	0	1	0	0	0	0	0	0	A0A087WPK7	
ENSMUST00000190152						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190153						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000190154	ENSMUSG00000066456	9	83109948	83146685	-1	0	0	1	0	0	0	0	6	1	18	0		Q9DCB1
ENSMUST00000190155	ENSMUSG00000025917	1	10024601	10038168	-1	0	0	4	0	2	0	82	418	96	337	48	A0A087WQ60	
ENSMUST00000190156	ENSMUSG00000037608	10	20312469	20344613	1	0	0	0	0	0	0	0	98	0	0	0		Q8K019
ENSMUST00000190157	ENSMUSG00000071302	8	129216354	129234406	-1	39	43	82	42	58	31	18	86	20	51	22	Q8BG62	
ENSMUST00000190158	ENSMUSG00000026782	1	60409619	60481158	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPE6	
ENSMUST00000190159						7	2	8	13	8	4	1	0	0	0	0		
ENSMUST00000190164						2	4	0	0	1	1	0	0	0	0	0		
ENSMUST00000190165	ENSMUSG00000052293	13	100651579	100656060	1	0	0	0	9	10	0	9	11	58	339	16	A0A087WNM2	
ENSMUST00000190166	ENSMUSG00000032263	9	83925145	84124240	1	0	0	0	0	0	0	4	24	1	0	2		Q6P3A8
ENSMUST00000190167	ENSMUSG00000042073	9	106447788	106452922	1	0	0	0	0	0	0	0	2	0	0	0	A0A087WRJ2	
ENSMUST00000190170						0	0	0	0	0	0	0	0	0	0	14		
ENSMUST00000190171						2	1	22	1	3	1	0	2	0	0	2		
ENSMUST00000190172						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190173	ENSMUSG00000101146	Y	75195856	75222058	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000190174						8	7	3	8	8	2	0	0	0	0	0		
ENSMUST00000190175						3	0	49	0	0	0	0	0	0	0	0		
ENSMUST00000190176						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000190177						5	12	3	3	5	2	0	0	0	1	0		
ENSMUST00000190178	ENSMUSG00000079583	X	60436052	60539249	-1	1	5	3	1	1	0	0	0	0	0	0	E9QAS1	
ENSMUST00000190182	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	20	4	88	1	A0A087WQQ5	
ENSMUST00000190185						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190186	ENSMUSG00000041757	1	133181321	133303435	1	0	0	0	0	0	0	0	17	8	0	8	A0A087WP13	
ENSMUST00000190187						0	1	0	0	1	2	0	0	0	0	0		
ENSMUST00000190188	ENSMUSG00000075602	15	74994877	74998031	-1	6	1	17	8	2	0	2	21	2	10	8	A0A087WNT7	
ENSMUST00000190190						1	1	0	1	0	0	0	0	2	0	0		
ENSMUST00000190191						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000190192						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190193	ENSMUSG00000091345	9	105856070	105960643	-1	34	37	65	45	41	16	0	0	0	4	7		A6H584
ENSMUST00000190195	ENSMUSG00000073725	1	24678630	24766301	1	0	1	1	1	1	0	49	377	90	26	21	A0A087WR85	
ENSMUST00000190196	ENSMUSG00000073600	18	35650351	35655238	-1	38	41	133	188	76	32	1	5	0	0	9	A0A087WR45	
ENSMUST00000190200						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000190202						960	935	1009	873	1024	624	10	114	28	23	51		
ENSMUST00000190205						7	2	9	153	14	2	0	0	0	0	0		
ENSMUST00000190207	ENSMUSG00000041763	1	43933647	44003000	1	0	5	0	0	0	5	7	0	0	0	0	A0A087WQR6	
ENSMUST00000190208						17	9	13	13	24	7	0	2	2	0	2		
ENSMUST00000190209						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190210						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190211						154	137	409	115	187	54	5	44	26	0	32		
ENSMUST00000190212	ENSMUSG00000034000	1	94020451	94028334	1	10	4	22	7	13	3	0	0	0	0	0	C5NTX9	Q8BZL1
ENSMUST00000190213	ENSMUSG00000026029	1	58795374	58847503	1	0	0	4	0	0	0	85	720	182	427	96	A0A087WQT6	
ENSMUST00000190215						0	2	6	4	5	0	0	1	4	0	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190216						5	3	5	2	3	0	0	1	0	0	0		
ENSMUST00000190217						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000190218	ENSMUSG00000073943	7	103682720	103683685	1	3	1	0	0	3	1	0	0	0	0	0	A0A087WQ52	
ENSMUST00000190219						1	1	1	0	0	3	0	0	0	0	0		
ENSMUST00000190220						4	3	31	2	4	3	0	0	0	0	0		
ENSMUST00000190222	ENSMUSG00000033633	8	111058920	111092426	-1	19	21	14	17	27	3	0	0	0	0	2	A0A087WP55	
ENSMUST00000190223						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190225						3	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000190226	ENSMUSG00000032803	9	103353094	103365840	-1	53	30	0	0	14	6	80	644	60	0	40	A0A087WS49	
ENSMUST00000190227						2	1	1	0	0	2	0	0	0	0	0		
ENSMUST00000190231	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRD9	
ENSMUST00000190232						4	2	6	2	3	1	2	0	4	4	4		
ENSMUST00000190233	ENSMUSG00000101113	15	77558239	77561892	-1	11	8	27	6	10	7	0	0	0	0	0	A0A087WNZ6	
ENSMUST00000190238						1	2	0	3	0	1	0	0	0	0	0		
ENSMUST00000190239						9	3	16	14	15	4	1	3	1	1	7		
ENSMUST00000190240	ENSMUSG00000049339	1	75142778	75147913	1	0	0	0	0	0	0	304	347	356	0	75		Q6NS82
ENSMUST00000190241						6	2	13	0	0	11	0	0	0	0	0		
ENSMUST00000190243						2	0	0	2	1	0	3	11	13	0	11		
ENSMUST00000190245	ENSMUSG00000032298	9	57142800	57148305	-1	37	35	87	50	40	19	29	89	25	6	52		Q8K4Q6
ENSMUST00000190246	ENSMUSG00000024731	19	10962293	10974670	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRZ0	
ENSMUST00000190247	ENSMUSG00000056553	12	116485720	117276849	1	0	0	27	0	17	0	0	0	0	0	0	Q3UU93	
ENSMUST00000190249						2	1	1	2	1	0	0	0	0	0	0		
ENSMUST00000190251						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190252	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	19	0	0	0	0	21	16	20	A0A087WQ25	
ENSMUST00000190255	ENSMUSG00000041390	6	15720661	15802169	1	3	2	1	28	4	0	9	18	6	11	21	A0A087WRH9	
ENSMUST00000190258						2	0	0	0	0	0	0	0	0	7	7		
ENSMUST00000190262	ENSMUSG00000022582	15	75155240	75159126	1	8	4	30	30	15	4	7298	23212	3115	8066	2260	A0A087WQF5	
ENSMUST00000190263						1	4	3	1	2	1	0	0	0	0	0		
ENSMUST00000190264	ENSMUSG00000096640	10	100381647	100382560	-1	6	4	0	6	7	0	0	0	0	0	0	E9Q4V5	
ENSMUST00000190265	ENSMUSG00000026020	1	59684971	59719044	1	0	0	0	0	0	0	1	14	7	0	0	A0A087WSL8	
ENSMUST00000190268	ENSMUSG00000009210	11	106365472	106377558	1	3	3	7	0	10	6	0	0	0	0	0	A0A087WPX8	
ENSMUST00000190270						6	2	0	5	12	0	0	0	0	0	0		
ENSMUST00000190271						0	0	0	0	0	11	0	0	0	0	0		
ENSMUST00000190273						1	0	1	3	3	1	0	0	0	0	0		
ENSMUST00000190274	ENSMUSG00000101725	Y	70292585	70303287	-1	0	0	0	0	0	1	0	0	0	0	0	A0A087WQ00	
ENSMUST00000190275						6	2	12	6	15	3	0	2	0	0	6		
ENSMUST00000190276	ENSMUSG00000030556	7	67513411	67645268	-1	0	0	0	0	0	0	5	20	0	14	0	A0A087WSB2	
ENSMUST00000190277						12	0	0	16	29	17	243	9699	7785	5189	3206		
ENSMUST00000190278	ENSMUSG00000106715	7	127561390	127566940	1	4	0	0	5	2	1	0	0	6	4	0		
ENSMUST00000190279	ENSMUSG00000035048	9	102626296	102634425	1	2	3	0	0	0	2	96	88	58	283	40		Q8R034
ENSMUST00000190282	ENSMUSG00000093993	Y	65377690	65403917	1	2	0	0	3	0	0	0	0	0	0	0	J3QNV4	
ENSMUST00000190283	ENSMUSG00000095948	Y	3399188	3410167	-1	0	0	0	25	3	0	0	0	0	0	0		O35698
ENSMUST00000190284						3	3	0	4	4	2	0	0	0	0	0		
ENSMUST00000190285	ENSMUSG00000051331	6	118587240	119196418	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSE7	
ENSMUST00000190286						2	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000190287	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS17	
ENSMUST00000190288						52	47	43	37	52	24	0	6	4	10	10		
ENSMUST00000190291						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000190292	ENSMUSG00000101155	Y	57187188	57213362	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000190293						0	1	0	0	0	0	0	0	0	1	5		
ENSMUST00000190295	ENSMUSG00000034832	6	83362373	83459084	-1	0	3	0	31	3	2	0	0	0	0	0	A0A087WP90	
ENSMUST00000190296						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190298	ENSMUSG00000009418	1	135434580	135607295	-1	15	6	18	49	18	3	16	18	17	0	114		Q8CH77
ENSMUST00000190300						0	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000190302						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190303						4	0	8	5	4	2	0	0	2	0	2		
ENSMUST00000190304						0	0	0	4	0	3	0	0	0	0	0		
ENSMUST00000190305						1	0	2	2	8	2	0	0	0	0	0		
ENSMUST00000190306						5	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000190307	ENSMUSG00000094445	7	52011683	52015728	-1	0	0	5	0	0	0	0	0	0	0	0	A0A087WSN4	
ENSMUST00000190309						12	4	18	11	4	2	0	0	0	0	0		
ENSMUST00000190310						0	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000190312						0	0	0	0	2	0	13	9	21	0	26		
ENSMUST00000190313	ENSMUSG00000048480	1	74191785	74194631	-1	4	4	9	10	10	3	67	157	68	18	94		Q810W6
ENSMUST00000190315	ENSMUSG00000096223	Y	9413518	9416148	-1	67	54	112	51	80	56	0	0	0	0	0	J3QNZ6	
ENSMUST00000190316						5	2	9	3	5	2	0	1	0	0	0		
ENSMUST00000190318						24	20	25	29	30	9	28	30	33	5	62		
ENSMUST00000190321	ENSMUSG00000034088	1	93405940	93478815	-1	0	1	0	13	0	0	0	0	0	0	8	A0A087WNQ4	
ENSMUST00000190322	ENSMUSG00000026435	1	131962967	131982969	1	6	2	11	0	5	4	3	0	2	0	0	A0A087WRT6	
ENSMUST00000190323	ENSMUSG00000026480	1	152800194	152836991	1	5	1	0	0	2	3	212	217	311	159	186	A0A087WPH0	
ENSMUST00000190324						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000190326						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190329	ENSMUSG00000091077	Y	9130999	9133924	-1	5	0	3	0	4	0	0	0	0	0	0	Q78EE2	
ENSMUST00000190330						16	23	34	28	18	5	0	0	0	1	1		
ENSMUST00000190331						2	3	0	0	2	0	0	0	0	0	0		
ENSMUST00000190333						78	51	173	47	51	18	0	0	0	0	0		
ENSMUST00000190334						2	0	2	2	1	1	0	0	0	0	0		
ENSMUST00000190336						3	0	1	2	8	4	3	19	13	12	9		
ENSMUST00000190337	ENSMUSG00000025932	1	14168954	14310235	-1	0	0	0	0	0	0	0	0	0	3	0		P97767
ENSMUST00000190338						0	0	0	0	0	0	9	7	0	3	36		
ENSMUST00000190339	ENSMUSG00000063142	14	23289431	24004859	-1	8	9	25	132	13	12	0	0	0	0	0	A0A087WSQ4	
ENSMUST00000190340	ENSMUSG00000034107	1	93373930	93404303	1	3	1	3	2	0	0	0	0	1	0	0	A0A087WPD8	
ENSMUST00000190341	ENSMUSG00000057367	9	7818227	7837064	-1	10	0	0	0	16	0	98	78	229	180	5		Q62210
ENSMUST00000190342						1	5	2	3	1	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190345	ENSMUSG00000062270	9	90091665	90114774	-1	0	0	0	39	0	0	2	4	5	5	3	A0A087WSL1	
ENSMUST00000190346						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190348	ENSMUSG00000025958	1	64532645	64604548	1	1	0	0	0	0	0	40	36	62	74	68	Q547S9	Q01147
ENSMUST00000190349	ENSMUSG00000094739	Y	78835721	78838056	-1	17	35	8	15	49	18	0	0	0	0	0	Q9D9T3	
ENSMUST00000190350						2	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000190351						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000190352						7	3	3	1	3	4	0	0	1	1	0		
ENSMUST00000190353						27	39	25	38	36	19	0	0	0	0	0		
ENSMUST00000190354						8	4	17	4	5	4	1	15	5	0	0		
ENSMUST00000190355						10	1	4	0	11	1	1	1	0	0	1		
ENSMUST00000190357						1	6	3	0	1	3	0	0	0	0	0		
ENSMUST00000190358	ENSMUSG00000032571	9	105642978	105687657	1	0	0	0	0	0	0	5	0	0	0	0	A0A087WP62	
ENSMUST00000190359						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190360						0	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000190361						1	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000190363	ENSMUSG00000040661	9	106688082	106789194	-1	1	2	6	2	0	1	0	3	1	0	0	A0A087WP96	
ENSMUST00000190365						9	0	22	18	14	11	0	0	2	0	3		
ENSMUST00000190366	ENSMUSG00000025779	1	16688051	16709611	1	0	0	0	0	0	0	0	28	0	7	0	A0A087WQZ9	
ENSMUST00000190368	ENSMUSG00000101540	13	6395716	6398258	1	67	48	360	94	50	40	15	65	41	2	36	A0A087WSK3	
ENSMUST00000190369	ENSMUSG00000037032	7	105558483	105581653	-1	2	0	3	2	0	0	0	0	0	0	0	A0A087WR62	
ENSMUST00000190370						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190371						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000190372						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190373						1	3	8	2	11	4	0	0	0	0	0		
ENSMUST00000190375						0	0	0	25	0	2	0	0	0	0	1		
ENSMUST00000190377						77	101	131	102	109	45	31	135	56	17	79		
ENSMUST00000190378	ENSMUSG00000049300	3	110246109	110250998	-1	17	0	23	0	0	13	11	33	10	4	0		Q6NZB1
ENSMUST00000190379						3	7	13	10	5	0	0	5	1	0	1		
ENSMUST00000190382						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190383						32	27	22	22	27	21	1	4	3	1	7		
ENSMUST00000190384						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000190385						4	6	1	6	3	3	0	0	0	0	0		
ENSMUST00000190386	ENSMUSG00000056912	10	100590511	100618401	1	0	0	2	0	0	5	0	0	0	0	0	A0A087WQ33	
ENSMUST00000190387	ENSMUSG00000040563	9	21937033	21948907	1	17	0	45	19	4	6	0	0	5	1	6		Q8VCY8
ENSMUST00000190388						79	65	353	104	63	26	0	1	2	0	2		
ENSMUST00000190389	ENSMUSG00000055322	1	73910231	74124449	-1	1	0	2	4	1	0	3	0	3	0	7	A0A087WR29	
ENSMUST00000190390	ENSMUSG00000053877	7	127511983	127561219	1	76	17	0	0	0	0	929	11	1148	0	1400	A0A087WNL7	
ENSMUST00000190391	ENSMUSG00000096706	Y	5656986	5659574	1	5	18	17	24	41	8	2	4	0	2	7	A0A087WNM4	
ENSMUST00000190393	ENSMUSG00000014850	13	92211872	92355003	-1	645	585	1492	946	646	318	24	100	84	10	111	A0A087WSS2	
ENSMUST00000190394						2	0	3	0	1	1	0	0	0	0	0		
ENSMUST00000190395						2	0	0	39	2	0	0	0	0	0	0		
ENSMUST00000190397						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190398						34	27	107	85	39	18	1	1	0	0	1		
ENSMUST00000190399						19	0	12	23	0	0	0	0	0	0	0		
ENSMUST00000190400	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	4	0	0	0	0	0	0	0	0	A0A087WSK0	
ENSMUST00000190401						19	24	51	22	30	22	2	6	4	1	8		
ENSMUST00000190402						1	0	13	2	0	0	0	0	0	0	0		
ENSMUST00000190403						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000190404	ENSMUSG00000026005	1	66700831	66719805	1	1	0	7	0	4	1	40	225	149	240	88	A0A087WQM3	
ENSMUST00000190405						0	0	0	0	1	0	0	0	0	0	1		
ENSMUST00000190406						5	8	35	9	12	6	0	0	0	0	0		
ENSMUST00000190407						1	2	1	1	3	2	0	0	0	0	0		
ENSMUST00000190410	ENSMUSG00000026432	1	131599239	131612000	1	4	0	2	0	2	0	0	0	0	0	0	A0A087WR95	
ENSMUST00000190413						2	1	0	11	2	0	0	0	0	0	0		
ENSMUST00000190414						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190416						15	18	128	58	51	24	0	0	0	0	0		
ENSMUST00000190418	ENSMUSG00000099550	Y	70004208	70014899	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNU4	
ENSMUST00000190419						4	0	2	1	1	2	0	0	0	0	0		
ENSMUST00000190420						2	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000190421						7	7	19	9	4	6	0	0	0	0	0		
ENSMUST00000190422	ENSMUSG00000101523	1	156524012	156526664	1	0	0	0	0	0	5	0	0	0	0	0		Q60737
ENSMUST00000190423						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190425						0	7	0	0	0	0	0	0	0	0	0		
ENSMUST00000190426	ENSMUSG00000096686	Y	6916300	6918282	-1	5	1	0	2	0	1	0	0	0	0	0	J3KML6	
ENSMUST00000190427	ENSMUSG00000070939	1	43047200	43098637	-1	0	0	0	50	1	0	0	0	0	0	0	A0A087WQX7	
ENSMUST00000190428	ENSMUSG00000023495	9	106453291	106464012	1	0	0	6	2	1	2	0	0	0	0	0	A0A087WP16	
ENSMUST00000190430	ENSMUSG00000023495	9	106453291	106464012	1	2	3	3	2	1	0	0	0	0	0	0	A0A087WR61	
ENSMUST00000190433	ENSMUSG00000022596	15	74724318	74728034	-1	17	15	76	30	33	16	0	0	0	0	0		Q9Z0K7
ENSMUST00000190436	ENSMUSG00000078932	15	91199494	91260894	1	5	0	8	53	10	0	2	0	0	1	0	A0A087WRU1	
ENSMUST00000190438						15	5	16	13	14	6	0	0	0	1	0		
ENSMUST00000190440						3	5	5	5	3	1	0	0	0	0	0		
ENSMUST00000190441	ENSMUSG00000026245	1	78417975	78488897	-1	1	0	0	11	2	1	0	0	2	3	0	A0A087WS80	
ENSMUST00000190442	ENSMUSG00000026116	1	36792191	36943666	-1	0	0	0	0	2	0	0	0	0	0	16	A0A087WQG5	
ENSMUST00000190444						3	1	1	0	2	0	0	0	0	0	0		
ENSMUST00000190445	ENSMUSG00000026203	1	75236406	75245692	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP03	
ENSMUST00000190446						5	4	31	11	3	6	2	0	0	0	0		
ENSMUST00000190447	ENSMUSG00000023341	16	97535308	97560900	1	16	9	17	15	21	11	0	0	0	0	0		
ENSMUST00000190448	ENSMUSG00000031155	X	7878262	7883432	1	20	11	32	34	20	16	128	271	107	12	136	A0A087WRF4	
ENSMUST00000190449	ENSMUSG00000005493	3	153857149	153906138	-1	3	5	0	1	3	4	0	0	0	0	0	A0A087WQN0	
ENSMUST00000190450						39	13	31	0	0	0	0	0	0	0	0		
ENSMUST00000190451	ENSMUSG00000026414	1	135836354	135852260	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQP1	
ENSMUST00000190452						1	0	0	0	1	0	0	0	0	3	0		
ENSMUST00000190453	ENSMUSG00000101471	Y	42550083	42582250	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNW5	
ENSMUST00000190454						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190455	ENSMUSG00000030577	7	30865402	30880342	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQV3	
ENSMUST00000190456	ENSMUSG00000054759	7	142174535	142176005	-1	23	11	70	65	13	11	0	0	0	0	0	A0A087WRV2	
ENSMUST00000190457	ENSMUSG00000074217	8	84010222	84012171	-1	4	4	7	247	10	2	0	0	0	0	0	A0A087WQ89	
ENSMUST00000190458	ENSMUSG00000099703	18	35553404	35581609	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPU5	
ENSMUST00000190459						2	3	19	2	3	0	15	36	19	0	29		
ENSMUST00000190460						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190462						5	10	41	21	16	4	0	2	0	0	0		
ENSMUST00000190464	ENSMUSG00000026219	1	84721189	84840516	-1	1	0	0	0	0	0	0	0	0	1	39	A0A087WSG4	
ENSMUST00000190465						2	3	0	0	3	1	0	0	0	0	0		
ENSMUST00000190467						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190468						34	20	163	66	47	13	1	0	1	1	1		
ENSMUST00000190469						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190470						17	9	45	65	28	23	0	2	0	0	0		
ENSMUST00000190471						6	9	26	156	16	7	0	0	0	0	0		
ENSMUST00000190472	ENSMUSG00000036873	3	145938014	145944829	1	0	0	0	0	0	0	42	174	29	12	0	A0A087WQ28	
ENSMUST00000190473						27	20	15	20	19	11	4	7	4	29	2		
ENSMUST00000190474						23	18	30	11	20	4	0	0	6	0	6		
ENSMUST00000190476	ENSMUSG00000026283	1	93803965	93822101	1	0	0	28	23	10	4	1	2	0	36	0		Q9D8Y8
ENSMUST00000190477						2	5	2	0	3	3	0	0	0	0	0		
ENSMUST00000190478						0	0	3	8	0	0	0	0	0	32	5		
ENSMUST00000190480						3	0	3	0	3	0	0	0	0	1	0		
ENSMUST00000190481						15	11	0	10	8	8	0	0	0	0	0		
ENSMUST00000190483						3	0	0	0	3	0	0	9	0	2	0		
ENSMUST00000190484	ENSMUSG00000026311	1	91540544	91559589	1	0	0	0	0	0	0	0	0	0	0	0	S4W6L8	
ENSMUST00000190489						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190490	ENSMUSG00000047361	1	59516264	59636417	1	5	2	5	3	8	1	0	2	0	0	0	A0A087WRV0	
ENSMUST00000190492	ENSMUSG00000032563	9	105053239	105079888	1	0	1	0	59	0	0	5	10	11	6	10	A0A087WQU4	
ENSMUST00000190494						19	9	42	26	24	8	0	3	0	0	0		
ENSMUST00000190495	ENSMUSG00000026355	1	128331590	128359664	-1	15	9	22	26	15	8	0	26	0	6	23	Q3ULG5	
ENSMUST00000190496	ENSMUSG00000034595	17	35865593	35875596	1	0	0	0	0	0	0	5788	7044	3019	801	2374	A0A087WRI9	
ENSMUST00000190497	ENSMUSG00000032839	9	95705082	95750375	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRB2	
ENSMUST00000190498						0	0	0	3	0	0	10	16	0	8	0		
ENSMUST00000190499						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000190500						0	2	2	0	6	0	0	0	0	0	0		
ENSMUST00000190501	ENSMUSG00000026319	1	105663861	105755191	1	4	0	0	0	0	0	0	0	69	0	6	A0A087WSS1	
ENSMUST00000190503	ENSMUSG00000034867	7	35586244	35639226	1	0	15	0	0	14	17	0	0	0	21	0		Q3UMR0
ENSMUST00000190506						0	0	0	0	0	7	0	0	0	0	0		
ENSMUST00000190507	ENSMUSG00000056220	1	149829618	149961290	-1	0	1	0	0	0	0	0	0	0	0	0	A0A087WPN8	
ENSMUST00000190509	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF9	
ENSMUST00000190510						4	2	6	7	2	0	0	0	0	0	0		
ENSMUST00000190511						0	0	27	0	0	0	45	117	0	66	24		
ENSMUST00000190512	ENSMUSG00000096284	13	119893388	119894785	-1	0	6	4	6	9	3	0	0	0	0	0	O70619	
ENSMUST00000190513						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190514	ENSMUSG00000032258	9	83390293	83441127	-1	1	2	2	4	3	3	0	0	0	0	0	A0A087WRS6	
ENSMUST00000190516	ENSMUSG00000094838	Y	11197024	11199374	-1	0	2	0	2	5	0	0	0	0	0	0	J3KMI7	
ENSMUST00000190518						0	6	0	7	0	0	0	0	0	0	0		
ENSMUST00000190519	ENSMUSG00000026309	1	91373861	91398815	-1	0	0	0	0	0	0	0	0	1	0	0	A0A087WQ55	
ENSMUST00000190520						0	0	3	1	6	0	0	0	0	0	0		
ENSMUST00000190522	ENSMUSG00000100855	10	41648876	41694487	-1	22	13	17	14	14	8	0	0	0	0	0	A0A087WS10	
ENSMUST00000190523						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190524	ENSMUSG00000034730	15	74516195	74589465	1	0	0	1	36	6	1	0	0	0	0	0	A0A087WQZ5	
ENSMUST00000190527						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000190529						0	0	0	0	3	3	0	0	0	0	0		
ENSMUST00000190530						0	0	0	0	0	0	68	194	16	172	42		
ENSMUST00000190531						1	3	0	0	4	1	10	17	6	3	17		
ENSMUST00000190532						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190533	ENSMUSG00000044367	11	70216789	70221064	-1	2	2	3	1	0	0	0	0	0	0	0	A0A087WPQ3	
ENSMUST00000190534						1	2	0	1	3	1	0	0	0	0	0		
ENSMUST00000190535	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	86	0	85	94	A0A087WPX0	
ENSMUST00000190536	ENSMUSG00000091402	12	111979111	111981317	-1	0	0	9	0	0	0	0	0	0	0	0	B2RV38	
ENSMUST00000190537						0	0	0	1	0	0	2	6	4	0	4		
ENSMUST00000190538						2	1	0	3	0	1	0	0	0	0	0		
ENSMUST00000190540						2	3	3	0	0	2	0	0	0	0	0		
ENSMUST00000190544	ENSMUSG00000042699	1	153455758	153487660	-1	4	7	8	1	3	2	8	25	26	11	50	A0A087WRT3	
ENSMUST00000190545						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190548						2	3	0	2	3	0	0	0	0	0	0		
ENSMUST00000190549	ENSMUSG00000032036	9	34485894	35036716	1	0	0	2	0	9	12	0	0	0	0	0	A0A087WPC0	
ENSMUST00000190551	ENSMUSG00000094647	Y	77692808	77719038	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSL2	
ENSMUST00000190552	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	312	0	0	0	A0A087WSH7	
ENSMUST00000190553						4	5	4	51	25	12	0	0	0	0	0		
ENSMUST00000190554	ENSMUSG00000095363	7	22713611	22719710	-1	0	0	0	0	6	1	0	0	0	0	0	Q3UTA8	
ENSMUST00000190555						4	3	4	3	5	2	0	0	0	0	0		
ENSMUST00000190556						16	5	59	40	18	5	0	0	0	0	0		
ENSMUST00000190557						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190558	ENSMUSG00000096178	Y	90401248	90433263	1	0	0	14	0	0	0	0	0	0	0	0	A0A087WP97	
ENSMUST00000190560						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190564	ENSMUSG00000020257	9	106170928	106191136	1	0	0	0	0	0	0	37	19	46	0	0	A0A087WQ38	
ENSMUST00000190565	ENSMUSG00000095302	Y	67045743	67048072	-1	16	17	16	24	0	0	0	0	0	0	0	Q149W4	
ENSMUST00000190566	ENSMUSG00000058883	13	67069398	67081545	-1	0	2	7	0	0	1	0	0	0	0	0	A0A087WPV0	
ENSMUST00000190568						6	1	14	6	6	4	80	1096	167	47	350		
ENSMUST00000190570						2	0	0	0	0	0	2	4	0	5	4		
ENSMUST00000190571	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ31	
ENSMUST00000190572	ENSMUSG00000101396	Y	10412737	10444691	1	0	0	0	1	0	0	0	0	0	0	0	A0A087WP28	
ENSMUST00000190573	ENSMUSG00000101399	Y	57705697	57731932	1	2	0	0	0	0	0	0	0	0	0	0	A0A087WPA5	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190574	ENSMUSG00000102049	1	133655879	133660885	-1	0	0	0	0	4	13	47	117	231	6	116	G0LE24	D2EAC2
ENSMUST00000190579						15	9	31	13	22	4	0	0	0	4	7		
ENSMUST00000190580						0	0	0	0	0	0	0	5	0	0	0		
ENSMUST00000190582	ENSMUSG00000079371	14	6105321	6125807	-1	0	1	0	0	0	0	0	0	0	0	0	Q5BKP9	
ENSMUST00000190583						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190584						4	8	19	19	8	2	0	0	0	0	0		
ENSMUST00000190585						0	1	0	9	0	0	0	0	0	0	1		
ENSMUST00000190586						0	2	9	0	8	4	0	0	0	0	0		
ENSMUST00000190587						6	4	9	14	4	4	0	0	0	0	0		
ENSMUST00000190588	ENSMUSG00000034157	12	86947043	86965362	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF0	
ENSMUST00000190589						2	0	3	1	5	2	0	0	0	0	0		
ENSMUST00000190591						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190592						0	0	0	12	0	0	0	0	0	0	1		
ENSMUST00000190593						0	0	0	1	6	0	0	0	0	0	0		
ENSMUST00000190594	ENSMUSG00000052293	13	100651579	100656060	1	0	6	0	0	0	0	2	12	2	7	8		Q8VI33
ENSMUST00000190595	ENSMUSG00000038608	1	80501073	80758527	-1	20	0	0	0	0	8	0	15	0	0	0		
ENSMUST00000190597						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000190599						2	1	10	39	9	4	0	0	0	0	0		
ENSMUST00000190600						1	0	2	7	3	3	0	0	0	0	0		
ENSMUST00000190601						71	44	76	21	18	49	0	0	0	0	0		
ENSMUST00000190603						6	3	9	1	13	0	0	0	0	1	0		
ENSMUST00000190604	ENSMUSG00000032839	9	95705082	95750375	-1	0	0	0	0	0	0	0	0	0	1	0	A0A087WP07	
ENSMUST00000190605						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190606						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000190607	ENSMUSG00000060519	1	156653617	156674356	-1	0	1	0	82	0	1	0	0	0	0	0	A0A087WQB9	
ENSMUST00000190609						1	0	3	2	3	5	0	0	0	0	0		
ENSMUST00000190610						9	2	14	49	8	5	2	1	2	1	0		
ENSMUST00000190613						22	16	32	88	64	22	0	0	0	0	0		
ENSMUST00000190617	ENSMUSG00000030577	7	30865402	30880342	-1	0	0	0	0	0	0	0	0	0	0	0	Q3UP36	
ENSMUST00000190618	ENSMUSG00000053333	1	86703808	87050095	1	14	9	12	11	19	15	0	0	0	3	0	A0A087WP08	
ENSMUST00000190620						19	18	47	278	30	16	14	37	21	3	18		
ENSMUST00000190621						0	8	0	0	6	2	0	0	0	0	0		
ENSMUST00000190623						2	0	7	4	1	1	0	0	0	0	0		
ENSMUST00000190624						83	87	86	82	115	61	1	5	15	2	9		
ENSMUST00000190625						2	0	0	0	1	1	0	0	7	0	5		
ENSMUST00000190626	ENSMUSG00000066392	12	88722876	90334935	1	5	16	61	17	0	0	0	0	2	0	0	A0A087WPQ9	
ENSMUST00000190630	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	9	0	0	0	0	A0A087WQX8	
ENSMUST00000190632						85	102	142	69	63	15	44	175	103	12	110		
ENSMUST00000190636						4	4	0	7	7	2	0	0	0	0	0		
ENSMUST00000190637	ENSMUSG00000032263	9	83925145	84124240	1	0	0	0	104	1	0	0	0	0	0	0		Q6P3A8
ENSMUST00000190638	ENSMUSG00000036634	7	30899176	30914873	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRD6	
ENSMUST00000190639	ENSMUSG00000031585	8	33731833	33777173	1	2	0	0	0	2	0	0	12	11	46	0	A0A087WSE8	
ENSMUST00000190641	ENSMUSG00000038065	6	54681624	54703851	1	36	28	69	114	45	25	25	45	38	12	52		Q8CGA4
ENSMUST00000190642						16	16	11	25	17	16	7	30	16	14	6		
ENSMUST00000190643						0	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000190644						0	2	2	5	4	4	0	0	0	0	2		
ENSMUST00000190646	ENSMUSG00000030577	7	30865402	30880342	-1	2	0	1	2	6	1	0	0	0	0	0	A0A087WR96	
ENSMUST00000190647	ENSMUSG00000040867	12	109032187	109068217	-1	25	8	24	31	33	13	0	0	0	0	3	F8WIG2	
ENSMUST00000190648	ENSMUSG00000026594	1	156804166	156939626	-1	0	5	13	14	11	8	0	4	0	0	5	A0A087WQ61	
ENSMUST00000190651	ENSMUSG00000090272	1	173857220	173942491	-1	0	0	0	0	0	0	10	4	0	4	9	A0A087WQG9	
ENSMUST00000190652						2	2	0	21	3	0	0	0	0	0	0		
ENSMUST00000190653	ENSMUSG00000037236	18	35562146	35593835	1	0	0	0	0	0	0	0	134	0	16	0	A0A087WSP7	
ENSMUST00000190654	ENSMUSG00000025911	1	9547948	9580673	1	11	8	4	6	6	5	0	3	5	0	1	A0A087WRE7	
ENSMUST00000190655						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190656	ENSMUSG00000049643	7	27553233	27582099	1	0	0	0	0	0	0	1	0	6	0	0	A0A087WSU8	
ENSMUST00000190658						2	1	0	0	0	0	0	0	0	1	2		
ENSMUST00000190659						3	10	6	3	6	1	0	0	0	0	0		
ENSMUST00000190661	ENSMUSG00000032566	9	105143342	105145092	-1	4	2	5	4	2	0	0	0	0	0	0	Q80ZT6	
ENSMUST00000190662						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190664	ENSMUSG00000021209	12	103532283	103613831	1	2	0	0	0	0	0	0	0	0	0	0	A0A087WQP9	
ENSMUST00000190665	ENSMUSG00000032410	9	95954760	96057803	1	0	1	0	0	0	1	3	11	0	0	0	A0A087WNV6	
ENSMUST00000190667						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000190669						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190670						2	1	0	3	4	3	0	0	0	0	0		
ENSMUST00000190671						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190672						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000190674						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190675	ENSMUSG00000031585	8	33731833	33777173	1	2	1	2	2	0	2	0	0	2	0	5	A0A087WQX6	
ENSMUST00000190676						53	55	54	75	61	47	0	0	0	0	0		
ENSMUST00000190677						2	3	3	0	2	0	0	2	0	0	4		
ENSMUST00000190678						8	3	11	4	5	7	0	0	0	0	2		
ENSMUST00000190679	ENSMUSG00000033159	1	75134554	75142711	-1	3	2	9	132	10	9	2482	5246	2083	320	1846		Q8K158
ENSMUST00000190680	ENSMUSG00000091402	12	111979111	111981317	-1	0	0	0	3	0	0	0	0	0	0	0	A0A087WRC7	
ENSMUST00000190682	ENSMUSG00000055827	15	63857724	63878558	-1	0	7	25	0	0	0	0	3	0	0	0		Q8CB12
ENSMUST00000190686	ENSMUSG00000039218	17	23790662	23824741	1	0	0	0	92	1	39	1403	1030	3769	43	5795		Q8BTI8
ENSMUST00000190687						33	21	44	13	32	10	1	16	4	0	14		
ENSMUST00000190689						33	35	88	36	35	17	1	9	12	0	5		
ENSMUST00000190691	ENSMUSG00000071398	12	17003319	17011727	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQY2	
ENSMUST00000190692						84	75	126	96	78	54	8	15	1	2	13		
ENSMUST00000190694						2	1	9	4	6	0	2	0	1	0	0		
ENSMUST00000190695	ENSMUSG00000026037	1	58462771	58505109	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPP9	
ENSMUST00000190696	ENSMUSG00000041459	4	148612382	148627019	-1	4	0	24	7	1	4	86	436	359	321	363	A0A087WP57	
ENSMUST00000190697						3	2	0	2	2	1	0	0	0	0	0		
ENSMUST00000190700						12	6	15	3	4	2	3	3	3	2	15		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190701						3	5	3	1	0	1	0	0	0	0	0		
ENSMUST00000190702						1	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000190703	ENSMUSG00000002831	17	56100591	56109803	-1	28	19	58	78	36	14	12	30	19	1	36		O88492
ENSMUST00000190706						7	14	14	8	11	9	0	0	0	0	0		
ENSMUST00000190708	ENSMUSG00000056912	10	100590511	100618401	1	0	4	0	0	2	0	0	0	0	0	0	A0A087WPJ1	
ENSMUST00000190709						0	0	0	34	0	0	0	0	0	0	0		
ENSMUST00000190710						4	3	3	1	5	0	0	0	0	0	0		
ENSMUST00000190711						146	121	143	126	154	87	3	8	9	0	12		
ENSMUST00000190712						100	92	143	44	76	27	8	65	26	5	46		
ENSMUST00000190713						3	2	0	2	1	0	0	0	0	0	0		
ENSMUST00000190715	ENSMUSG00000056267	9	99243367	99300404	1	7	7	23	2	9	5	0	0	0	0	0	A0A087WQX1	
ENSMUST00000190716						4	6	6	3	3	3	0	0	0	0	0		
ENSMUST00000190717	ENSMUSG00000026202	1	75214228	75219865	-1	0	0	6	5	0	0	25	40	35	9	63	A0A087WSL5	
ENSMUST00000190719	ENSMUSG00000025930	1	14753346	14755992	-1	0	4	0	0	2	0	0	0	0	0	0	A0A087WRR6	
ENSMUST00000190721						9	5	49	4	8	3	0	0	0	0	0		
ENSMUST00000190723	ENSMUSG00000014602	1	93015464	93101951	-1	35	16	25	678	74	13	0	0	0	0	0	A0A087WQE8	
ENSMUST00000190724	ENSMUSG00000026249	1	79794197	79861180	-1	3	6	2	0	0	2	3	0	1	0	0	A0A087WQM1	
ENSMUST00000190725						2	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000190726	ENSMUSG00000043629	1	52922324	53020179	-1	3	0	20	0	0	0	0	0	0	0	0		Q9CPS8
ENSMUST00000190727						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000190729	ENSMUSG00000078941	13	100650979	100666359	1	6	0	7	0	0	5	188	1007	243	34	128	A0A087WRI5	
ENSMUST00000190730	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	0	0	0	0	2	0	0	8	0	Q4V9V4	
ENSMUST00000190731	ENSMUSG00000030616	7	90348699	90410439	1	0	0	0	0	0	0	0	0	0	0	0		Q99N50
ENSMUST00000190733	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	0	0	132	0	0	A0A087WRU7	
ENSMUST00000190734	ENSMUSG00000100679	1	53297111	53318035	1	0	0	0	0	0	0	0	0	24	75	22	A0A087WSK7	
ENSMUST00000190735						54	39	105	77	60	24	2	19	4	2	8		
ENSMUST00000190736	ENSMUSG00000026353	1	128243964	128279378	1	0	0	0	2	1	0	58	116	90	0	0	A0A087WSK5	
ENSMUST00000190738						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190740						4	5	5	8	9	2	0	0	0	0	0		
ENSMUST00000190741	ENSMUSG00000031509	8	11654924	11701063	-1	0	1	0	1	3	1	0	0	0	0	0	A0A087WQK3	
ENSMUST00000190742						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190744						2	4	1	3	2	1	0	0	0	0	0		
ENSMUST00000190745						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190746						9	5	16	6	13	4	0	0	0	0	1		
ENSMUST00000190747	ENSMUSG00000026309	1	91373861	91398815	-1	0	0	0	0	0	0	0	13	8	0	0	A0A087WS54	
ENSMUST00000190748	ENSMUSG00000060715	1	53158577	53187636	-1	5	0	1	2	2	3	0	0	0	0	0	A0A087WPV9	
ENSMUST00000190749	ENSMUSG00000026596	1	156558786	156649568	1	0	1	1	0	1	0	2	0	0	0	7	A0A087WQB7	
ENSMUST00000190750						5	5	7	4	2	3	0	0	0	0	0		
ENSMUST00000190751	ENSMUSG00000019865	10	14705591	14770850	1	4	0	0	5	8	3	0	0	0	0	0	A0A087WQJ7	
ENSMUST00000190752						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190753	ENSMUSG00000030577	7	30865402	30880342	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ27	
ENSMUST00000190755						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190756						1	0	3	4	3	2	0	0	0	0	0		
ENSMUST00000190757	ENSMUSG00000099486	2	89248721	89249692	-1	5	1	1	4	4	1	0	0	0	0	0	Q8VGM9	
ENSMUST00000190758						1	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000190759						1	2	0	0	0	0	0	0	2	0	0		
ENSMUST00000190760						0	0	3	4	2	0	0	0	0	0	0		
ENSMUST00000190761	ENSMUSG00000014850	13	92211872	92355003	-1	2	0	0	0	0	0	0	7	0	0	0	A0A087WQZ2	
ENSMUST00000190762	ENSMUSG00000026594	1	156804166	156939626	-1	1	2	5	99	3	0	0	0	0	0	0	A0A087WPL3	
ENSMUST00000190763						2	5	2	0	0	0	0	0	0	0	0		
ENSMUST00000190764						8	1	4	8	4	2	0	0	0	0	0		
ENSMUST00000190766						1	1	1	2	1	3	0	0	0	0	0		
ENSMUST00000190767						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190768						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000190770						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190771	ENSMUSG00000025997	1	69531214	69687245	-1	0	3	0	4	7	0	0	0	0	0	5	A0A087WNY4	
ENSMUST00000190772						1	0	2	0	4	2	0	0	0	0	0		
ENSMUST00000190773						2	5	1	2	6	1	0	0	0	0	0		
ENSMUST00000190774						5	7	2	3	8	4	82	29	300	38	147		
ENSMUST00000190775						0	0	0	0	0	5	0	0	0	0	0		
ENSMUST00000190776						0	0	0	473	23	20	15	0	10	11	12		
ENSMUST00000190778	ENSMUSG00000033633	8	111058920	111092426	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPI3	
ENSMUST00000190779						13	7	11	0	0	0	0	0	0	0	0		
ENSMUST00000190780	ENSMUSG00000026193	1	71585520	71653200	-1	0	0	0	0	0	0	2333	1052	3124	0	11724	B9EHT6	
ENSMUST00000190781						0	0	7	1	6	0	2	24	0	0	10		
ENSMUST00000190782	ENSMUSG00000101157	Y	37233420	37259603	-1	0	0	0	1	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000190784	ENSMUSG00000032487	1	150100031	150108227	1	0	0	0	2	1	2	0	0	0	0	0	A0A087WPT2	
ENSMUST00000190785	ENSMUSG00000032712	6	149309414	149335663	1	0	0	0	0	0	0	8	0	0	0	0	A0A087WP47	
ENSMUST00000190786						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190787						1	0	0	7	1	0	0	0	0	0	0		
ENSMUST00000190788						14	22	31	19	19	16	16	96	21	0	83		
ENSMUST00000190790	ENSMUSG00000037529	1	34543968	34560943	-1	2	0	4	0	0	0	0	0	0	0	0	A0A087WS39	
ENSMUST00000190791						3	1	0	0	1	1	0	0	0	0	0		
ENSMUST00000190792						45	39	54	23	32	15	0	1	1	0	1		
ENSMUST00000190794						8	6	5	4	7	3	0	0	0	0	0		
ENSMUST00000190795	ENSMUSG00000009210	11	106365472	106377558	1	2	1	7	4	0	0	0	0	0	0	0		B1ARI9
ENSMUST00000190796						28	24	18	19	15	13	0	0	0	0	0		
ENSMUST00000190797						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190798	ENSMUSG00000042210	9	106440051	106447678	-1	3	0	0	0	0	0	0	0	0	0	5	A0A087WSL4	
ENSMUST00000190799						1	3	2	0	1	0	0	0	0	0	3		
ENSMUST00000190800						1	0	3	2	1	1	0	0	0	0	0		
ENSMUST00000190801	ENSMUSG00000042590	13	106794439	106936958	-1	6	3	3	0	8	0	3	57	7	130	36	A0A087WS00	
ENSMUST00000190802						2	2	7	0	3	0	0	0	0	0	0		
ENSMUST00000190803	ENSMUSG00000023262	9	106432981	106438319	-1	4	2	5	0	3	4	2	0	3	0	1	A0A087WPV3	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190805						1	3	5	7	6	0	0	0	1	0	1		
ENSMUST00000190806	ENSMUSG00000096626	Y	58782567	58814597	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRF5	
ENSMUST00000190807	ENSMUSG00000054387	1	132959484	133030561	-1	0	2	3	0	0	1	0	0	0	0	0	A0A087WQP2	
ENSMUST00000190809						0	3	1	6	1	0	0	0	0	0	0		
ENSMUST00000190810	ENSMUSG00000022587	15	74955051	74959905	1	4	0	0	0	0	0	0	0	7	0	9	A0A087WNT2	
ENSMUST00000190811	ENSMUSG00000056536	1	105518422	105663677	-1	0	0	0	0	0	0	10	4	93	0	64	A0A087WS03	
ENSMUST00000190812						70	68	69	64	36	21	0	0	0	0	0		
ENSMUST00000190813	ENSMUSG00000051747	2	76703980	76982547	-1	1	1	0	0	1	1	0	0	0	0	0	A0A087WRP0	
ENSMUST00000190814						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000190817						3	2	4	8	7	6	0	0	0	0	1		
ENSMUST00000190819						0	3	0	3	2	0	0	0	0	0	0		
ENSMUST00000190822	ENSMUSG00000032253	9	82866159	82975516	-1	0	0	0	0	0	0	6	4	0	0	0	A0A087WPP7	
ENSMUST00000190823						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000190824	ENSMUSG00000033147	3	101855776	101924453	-1	0	0	0	8	0	0	127	441	298	79	304	A0A087WNW1	
ENSMUST00000190825	ENSMUSG00000026439	1	132477365	132505659	1	10	0	0	31	17	4	119	15	11	0	17		
ENSMUST00000190826						959	983	3469	941	1172	531	19	83	46	9	95		
ENSMUST00000190827	ENSMUSG00000037428	5	137026392	137033351	1	10	9	24	119	20	16	0	0	0	0	0	Q0VGU4	
ENSMUST00000190829						0	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000190831	ENSMUSG00000043629	1	52922324	53020179	-1	0	5	0	1	5	3	0	0	0	0	0		Q9CPS8
ENSMUST00000190832						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000190833						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190834						12	3	31	6	11	9	1	0	3	1	3		
ENSMUST00000190835						7	6	4	3	0	3	0	1	0	0	0		
ENSMUST00000190836						8	5	2	7	4	4	0	0	0	0	0		
ENSMUST00000190837	ENSMUSG00000030616	7	90348699	90410439	1	0	0	28	0	0	0	0	6	0	0	0		Q99N50
ENSMUST00000190838						2	6	22	15	1	3	1	0	1	0	2		
ENSMUST00000190840	ENSMUSG00000031561	8	48227682	48844026	-1	42	38	61	136	61	26	0	0	0	0	0	G3X907	
ENSMUST00000190841						84	75	153	88	75	27	2	8	2	6	10		
ENSMUST00000190842						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000190843						10	4	11	0	0	3	0	0	0	0	0		
ENSMUST00000190844	ENSMUSG00000062497	1	92596495	92597492	1	8	7	20	10	12	8	0	0	0	0	0	Q8VFC4	
ENSMUST00000190846						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190847						1	0	1	0	0	0	0	4	2	0	0		
ENSMUST00000190848						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000190849						4	0	14	0	0	3	0	0	0	0	0		
ENSMUST00000190851						1	6	2	2	7	2	0	0	5	0	0		
ENSMUST00000190853						169	177	225	174	287	137	1	6	6	1	6		
ENSMUST00000190854						7	5	17	2	13	3	0	0	0	0	0		
ENSMUST00000190855	ENSMUSG00000025997	1	69531214	69687245	-1	7	0	0	0	0	4	0	0	4	0	1	A0A087WQ51	
ENSMUST00000190856						10	2	17	15	4	5	0	5	0	2	4		
ENSMUST00000190857						19	21	63	22	26	12	3	27	9	3	1		
ENSMUST00000190858						4	3	5	3	2	0	0	0	0	0	0		
ENSMUST00000190859						13	7	41	31	14	10	4	0	0	0	0		
ENSMUST00000190860						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190862	ENSMUSG00000017146	11	101488764	101551955	-1	0	1	1	3	2	0	0	0	0	0	0	A0A087WP26	
ENSMUST00000190869						3	2	2	2	1	1	0	0	0	0	0		
ENSMUST00000190870						200	184	1263	244	336	164	6	23	10	6	22		
ENSMUST00000190871						13	6	16	8	8	5	0	0	0	0	0		
ENSMUST00000190872	ENSMUSG00000023150	1	151344477	151364422	1	3	3	0	2	2	0	0	2	2	0	5	A0A087WQT3	
ENSMUST00000190873						1	1	8	3	1	2	0	0	0	0	0		
ENSMUST00000190874						0	4	0	0	0	0	9	54	84	40	94		
ENSMUST00000190875						1	0	0	1	0	2	0	0	0	0	0		
ENSMUST00000190876	ENSMUSG00000025958	1	64532645	64604548	1	0	0	0	0	2	0	21	40	66	34	31	Q61441	
ENSMUST00000190877						64682	91507	165745	73106	60958	31172	458	2340	1041	243	847		
ENSMUST00000190878						0	3	0	2	2	2	7	6	8	0	0		
ENSMUST00000190882	ENSMUSG00000025507	7	141438113	141444025	-1	0	0	12	0	0	0	0	0	0	4	3	A0A087WPI0	
ENSMUST00000190883						0	2	0	3	3	1	0	1	0	0	0		
ENSMUST00000190884						22	18	39	21	30	14	0	0	0	0	1		
ENSMUST00000190885						4	6	9	6	2	1	0	1	0	0	0		
ENSMUST00000190892						139	101	333	1442	219	121	4	5	2	1	6		
ENSMUST00000190893						116	77	116	91	116	54	4	13	6	4	17		
ENSMUST00000190894						14	20	36	11	6	8	0	0	3	0	3		
ENSMUST00000190900	ENSMUSG00000023262	9	106432981	106438319	-1	4	4	4	33	9	4	0	0	0	0	0	A0A087WRE0	
ENSMUST00000190902	ENSMUSG00000028451	4	42969604	42983640	1	2	9	3	0	0	1	0	0	0	0	0	A0A087WQV9	
ENSMUST00000190903						3	1	1	5	3	2	0	3	1	1	1		
ENSMUST00000190904						2	0	1	0	3	0	0	0	0	0	0		
ENSMUST00000190905						9	3	7	4	5	3	0	0	0	0	0		
ENSMUST00000190906						0	0	0	3	0	1	0	0	0	0	9		
ENSMUST00000190907	ENSMUSG00000048191	7	141633456	141655319	-1	242	168	1576	444	120	89	0	24	0	0	0	A0A087WR59	
ENSMUST00000190909	ENSMUSG00000095452	Y	40804914	40807356	1	0	0	7	0	0	0	0	0	0	0	0	J3QP49	
ENSMUST00000190913						4	1	0	2	1	0	0	0	0	0	0		
ENSMUST00000190915						0	0	2	22	2	1	3	10	39	22	24		
ENSMUST00000190916						3	0	0	0	0	3	0	0	0	0	0		
ENSMUST00000190920						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190921						15	12	27	15	20	8	6	7	6	1	15		
ENSMUST00000190922						14	15	76	39	15	9	4	0	0	0	0		
ENSMUST00000190923						0	0	0	1	1	1	0	0	0	0	0		
ENSMUST00000190924						3	2	8	3	0	2	0	4	2	6	13		
ENSMUST00000190926						2	8	31	5	4	1	0	14	4	12	26		
ENSMUST00000190928						1	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000190929	ENSMUSG00000022197	15	12359711	12739924	-1	0	2	0	0	3	0	0	0	0	0	0	A0A087WRL4	
ENSMUST00000190932						0	0	29	2	0	55	0	0	0	0	0		
ENSMUST00000190934						5	9	2	5	8	6	1	2	0	1	1		
ENSMUST00000190935						62	84	230	243	66	21	2	9	1	0	1		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000190936						8	9	27	0	7	0	1	0	2	4	2		
ENSMUST00000190937						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190939						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190940	ENSMUSG00000020888	11	70000595	70012301	1	12	5	22	28	22	16	9	45	29	6	25		Q60838
ENSMUST00000190942						2	0	3	0	1	0	0	0	0	0	0		
ENSMUST00000190943						2	2	2	0	0	0	0	0	0	5	4		
ENSMUST00000190944						1	0	5	0	0	0	10	0	0	2	5		
ENSMUST00000190945						17266	16263	28986	74074	17884	5432	72	261	201	54	323		
ENSMUST00000190946	ENSMUSG00000094789	Y	31602724	31634756	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRT9	
ENSMUST00000190948						4	0	2	2	0	0	0	6	5	0	2		
ENSMUST00000190950	ENSMUSG00000036634	7	30899176	30914873	-1	1	3	1	1	2	3	0	0	0	0	0	A0A087WPP5	
ENSMUST00000190952						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190954	ENSMUSG00000030600	7	28451980	28468242	1	0	1	7	0	0	0	2	0	0	0	0	A0A087WRA2	
ENSMUST00000190955						4	0	0	0	3	3	0	0	0	0	0		
ENSMUST00000190957	ENSMUSG00000034973	9	86467154	86555923	1	0	0	0	19	0	0	0	1	8	16	0	H7BWZ9	
ENSMUST00000190958						49	40	99	67	59	30	0	18	6	1	7		
ENSMUST00000190959	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	0	13	0	3	0	0	0	0	0	Q14AC9	Q9D9S1
ENSMUST00000190960						1	1	5	4	3	3	1	0	0	0	0		
ENSMUST00000190961						2	2	3	1	1	3	0	0	0	0	0		
ENSMUST00000190962	ENSMUSG00000030228	6	139587221	139969284	1	3	1	3	4	6	4	0	0	0	0	0	Q4FZD4	
ENSMUST00000190963	ENSMUSG00000072754	5	110344730	110356094	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQC1	
ENSMUST00000190964						8	4	8	4	5	2	0	0	0	0	0		
ENSMUST00000190965						15	8	11	10	14	5	0	0	0	0	0		
ENSMUST00000190968						34	48	0	91	81	37	0	0	0	0	0		
ENSMUST00000190969						3	0	19	8	5	0	0	0	0	0	0		
ENSMUST00000190972	ENSMUSG00000023262	9	106432981	106438319	-1	0	1	3	55	3	1	3	0	0	2	1	A0A087WPX1	
ENSMUST00000190973						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000190975	ENSMUSG00000023577	9	106503225	106561631	-1	5	2	0	0	0	0	0	0	0	0	0	A0A087WSD7	
ENSMUST00000190976						2	0	4	0	3	0	0	0	0	0	0		
ENSMUST00000190977						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190978						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190979						159	93	105	105	166	86	1	8	11	2	18		
ENSMUST00000190981						2	3	1	2	2	2	0	0	0	0	0		
ENSMUST00000190983	ENSMUSG00000038608	1	80501073	80758527	-1	9	0	24	0	0	0	89	33	0	10	54	A0A087WRP5	
ENSMUST00000190985	ENSMUSG00000063142	14	23289431	24004859	-1	0	1	0	1	2	0	0	0	0	0	0	A0A087WQE1	
ENSMUST00000190986						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000190987	ENSMUSG00000096898	Y	77960873	77963204	-1	0	0	0	0	0	0	0	0	0	0	0	Q5FWD4	
ENSMUST00000190988						2	4	2	1	4	3	0	0	0	0	0		
ENSMUST00000190990	ENSMUSG00000074199	7	30787896	30791097	1	0	0	0	0	0	0	0	0	0	0	0		Q3V2T4
ENSMUST00000190992						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000190993	ENSMUSG00000034120	11	116849901	116853094	-1	0	0	1	141	7	0	38	510	289	161	333		Q62093
ENSMUST00000190995	ENSMUSG00000101605	11	105994675	106005443	1	18	13	14	25	18	4	0	0	0	0	0	D0G895	
ENSMUST00000190996						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000190997	ENSMUSG00000026439	1	132477365	132505659	1	7	0	11	0	0	0	85	325	242	29	178		Q8BX09
ENSMUST00000190998	ENSMUSG00000047443	1	91366430	91374217	1	1	0	0	0	0	0	0	0	0	1	0	A0A087WR80	
ENSMUST00000190999	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	21	A0A087WP85	
ENSMUST00000191000						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000191001						0	0	0	8	0	0	0	0	0	0	0		
ENSMUST00000191002	ENSMUSG00000058132	7	12304802	12305719	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRV1	
ENSMUST00000191004	ENSMUSG00000026341	1	125392905	125435727	-1	0	0	0	39	0	0	6	18	79	20	48	A0A087WS98	
ENSMUST00000191005						11	7	4	5	10	4	0	0	0	0	0		
ENSMUST00000191006	ENSMUSG00000033029	15	79129349	79141253	-1	0	0	4	0	0	2	0	0	0	0	0	A0A087WSP2	
ENSMUST00000191009						0	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000191010	ENSMUSG00000073650	1	74362108	74369321	1	18	3	17	119	17	5	2	18	4	0	2		B9EKE5
ENSMUST00000191011	ENSMUSG00000037032	7	105558483	105581653	-1	9	17	7	28	5	0	0	0	0	0	0		
ENSMUST00000191012	ENSMUSG00000056763	1	10037987	10136768	1	0	0	0	0	0	1	0	0	0	0	0	A0A087WS14	
ENSMUST00000191013						8	3	6	5	10	6	0	0	0	0	0		
ENSMUST00000191014	ENSMUSG00000056267	9	99243367	99300404	1	2	0	0	4	3	0	0	3	2	1	4	A0A087WPS5	
ENSMUST00000191016						0	4	0	7	0	0	10	0	6	0	0		
ENSMUST00000191018	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP14	
ENSMUST00000191019						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191020						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191021						13	10	9	9	10	9	0	3	0	0	0		
ENSMUST00000191023						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191024						2	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000191025						4	7	8	4	5	3	0	0	1	0	0		
ENSMUST00000191026						13	6	2	203	14	6	0	0	0	0	0		
ENSMUST00000191028						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191030	ENSMUSG00000033633	8	111058920	111092426	-1	8	32	29	18	0	1	5	10	7	0	7		Q7TSQ1
ENSMUST00000191032	ENSMUSG00000034157	12	86947043	86965362	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ97	
ENSMUST00000191033	ENSMUSG00000056912	10	100590511	100618401	1	0	3	1	0	2	1	0	0	0	0	0	A0A087WPP2	
ENSMUST00000191035	ENSMUSG00000030556	7	67513411	67645268	-1	0	0	0	0	0	0	39	31	55	29	29	Q8C1S3	
ENSMUST00000191036						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191037	ENSMUSG00000099353	15	98398419	98416268	1	2	1	1	5	1	0	0	0	0	0	0	A0A087WSH0	
ENSMUST00000191039						4	3	0	4	2	1	0	0	0	1	0		
ENSMUST00000191040						20	8	28	20	25	8	2	5	0	21	0		
ENSMUST00000191041						2	6	1	2	2	2	0	0	0	0	0		
ENSMUST00000191043	ENSMUSG00000071302	8	129216354	129234406	-1	0	0	29	0	0	0	0	0	3	0	0	A0A087WNL1	
ENSMUST00000191044						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191046	ENSMUSG00000026383	1	119545037	119649000	-1	19	17	23	59	23	16	0	1	1	0	1		Q8BGS1
ENSMUST00000191047	ENSMUSG00000031927	9	14756587	14771030	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WS57	
ENSMUST00000191049						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191050						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000191051						1	4	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191053	ENSMUSG00000100828	2	89590169	89591113	-1	0	4	2	0	4	0	0	0	0	0	0	Q7TQZ6	
ENSMUST00000191055						25	22	80	36	43	16	0	1	0	0	1		
ENSMUST00000191056						2	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000191057						3	4	1	175	6	3	0	0	0	0	0		
ENSMUST00000191058						63	77	98	69	57	38	15	82	30	3	39		
ENSMUST00000191059						2	1	9	0	2	1	0	0	0	0	0		
ENSMUST00000191061						2	0	5	2	2	7	8	26	0	3	13		
ENSMUST00000191062						2	4	1	1	2	0	0	0	0	0	0		
ENSMUST00000191063						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000191064	ENSMUSG00000048874	1	30802339	30873921	-1	3	0	0	0	0	0	9	0	18	1	0	A0A087WRR9	
ENSMUST00000191065						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000191066						0	0	2	0	1	0	0	0	0	0	2		
ENSMUST00000191068						0	0	0	9	0	2	0	0	0	0	0		
ENSMUST00000191069						46	30	56	43	58	25	0	0	0	0	0		
ENSMUST00000191070	ENSMUSG00000043019	1	151755371	151822051	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQK5	
ENSMUST00000191073	ENSMUSG00000095190	7	20724525	20730620	-1	0	0	20	11	0	7	0	0	0	0	0	Q3UTA8	
ENSMUST00000191074						0	1	1	0	0	0	2	2	0	0	0		
ENSMUST00000191075						2	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000191076						0	0	35	2	9	0	8	18	25	0	18		
ENSMUST00000191078	ENSMUSG00000024430	18	12741324	12755146	1	0	0	0	0	0	0	0	0	0	0	0		Q9D424
ENSMUST00000191080						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000191081	ENSMUSG00000036634	7	30899176	30914873	-1	7	2	0	0	0	13	0	0	0	0	10	A0A087WPR1	
ENSMUST00000191082						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191083						2	4	7	4	18	1	0	1	5	1	2		
ENSMUST00000191086						2	8	5	8	7	2	0	0	0	0	0		
ENSMUST00000191088						0	1	0	18	2	0	0	0	0	0	0		
ENSMUST00000191089	ENSMUSG00000071652	19	8888926	8897890	1	0	0	0	0	0	0	32	0	22	7	1	A0A087WRC2	
ENSMUST00000191090						4	5	0	0	5	0	0	0	0	0	0		
ENSMUST00000191091						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191092						4	0	10	4	0	3	0	5	0	0	0		
ENSMUST00000191093						1	2	5	0	4	0	0	0	0	0	0		
ENSMUST00000191094						4	0	9	0	1	0	0	2	0	0	0		
ENSMUST00000191095						2	0	9	6	5	3	0	0	0	0	0		
ENSMUST00000191097						0	1	4	5	2	1	146	314	120	544	96		
ENSMUST00000191100						0	0	0	0	0	0	0	1	0	0	1		
ENSMUST00000191103						3	0	0	3	1	0	1	0	0	4	0		
ENSMUST00000191104	ENSMUSG00000055322	1	73910231	74124449	-1	0	0	0	136	99	0	363	708	563	35	867	A0A087WQS0	
ENSMUST00000191105						2	0	5	0	2	2	0	0	0	0	0		
ENSMUST00000191106						20	12	31	39	18	5	0	0	0	0	0		
ENSMUST00000191107	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	2	0	0	0	0	0	0	A0A087WPD1	
ENSMUST00000191108	ENSMUSG00000026201	1	75210838	75215606	1	0	7	0	0	0	0	399	887	359	83	304	Q05DP1	
ENSMUST00000191109						6	6	13	3	9	3	1	0	0	0	0		
ENSMUST00000191110						5	6	7	5	6	3	0	0	1	0	0		
ENSMUST00000191111						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191112	ENSMUSG00000100505	4	88760119	88761581	1	0	0	0	4	0	0	0	1	1	0	0	A0A087WPG5	
ENSMUST00000191116						20	8	0	90	22	13	1	0	0	3	0		
ENSMUST00000191117						11	10	25	36	11	4	2	3	0	0	2		
ENSMUST00000191118						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000191120						0	2	0	2	2	0	0	0	0	0	0		
ENSMUST00000191123	ENSMUSG00000100032	Y	68806596	68832728	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK3	
ENSMUST00000191124	ENSMUSG00000023826	17	10840384	12063361	1	2	2	19	0	12	0	0	0	0	0	0		Q9WVS6
ENSMUST00000191126	ENSMUSG00000049643	7	27553233	27582099	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPA4	
ENSMUST00000191127	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	0	0	0	348	326	192	29	347	A0A087WPY4	
ENSMUST00000191128						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000191130						0	2	2	0	4	2	0	0	0	0	0		
ENSMUST00000191133	ENSMUSG00000032411	9	96196275	96323646	1	4	1	1	1	1	1	0	0	0	2	0	A0A087WNL4	
ENSMUST00000191135						145	182	214	152	195	110	7	16	23	0	16		
ENSMUST00000191138	ENSMUSG00000015501	10	13966075	14151374	1	0	0	0	0	0	0	0	0	0	0	37		Q3UHF7
ENSMUST00000191142	ENSMUSG00000026020	1	59684971	59719044	1	171	132	377	191	172	96	14	82	18	27	47		Q6DFW4
ENSMUST00000191143						3	2	1	1	6	1	16	79	28	41	37		
ENSMUST00000191145	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	1	0	0	0	19	3	0	7	A0A087WRZ2	
ENSMUST00000191147						26	18	32	73	32	17	8	23	11	1	9		
ENSMUST00000191148						4	4	0	7	7	2	0	0	0	0	0		
ENSMUST00000191149						15	12	66	143	14	3	0	0	1	0	0		
ENSMUST00000191150						3	3	5	318	8	5	12	14	16	14	29		
ENSMUST00000191151	ENSMUSG00000099550	Y	70004208	70014899	-1	37	69	44	55	68	43	0	0	0	0	0	A0A087WP82	
ENSMUST00000191158						1	2	8	10	7	4	0	0	0	124	0		
ENSMUST00000191160						3	1	9	25	5	5	7	46	25	19	13		
ENSMUST00000191161						0	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000191162						2	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000191163						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000191164						10	7	2	6	6	1	0	0	0	0	0		
ENSMUST00000191167	ENSMUSG00000031927	9	14756587	14771030	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQX9	
ENSMUST00000191168						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191169	ENSMUSG00000094682	7	23272801	23278900	-1	25	21	2	8	10	3	0	3	0	2	4	Q3UTA8	
ENSMUST00000191171						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000191172						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000191174						13	8	9	2	10	5	0	0	0	0	0		
ENSMUST00000191176						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000191178	ENSMUSG00000022346	15	61985341	61990374	1	0	0	7	0	0	0	3	0	0	0	46	A0A087WSQ0	
ENSMUST00000191179						20	15	46	17	28	18	0	2	0	0	3		
ENSMUST00000191183						1	8	2	17	13	3	9	117	77	104	54		
ENSMUST00000191184						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191187						1	3	1	0	1	0	3	8	3	1	13		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191188						0	0	0	11	0	0	0	0	0	0	0		
ENSMUST00000191189	ENSMUSG00000062270	9	90091665	90114774	-1	0	0	0	19	0	0	28	127	1221	2608	786	A0A087WQB0	
ENSMUST00000191192	ENSMUSG00000030717	7	126623249	126630861	-1	0	0	0	0	0	0	69	361	112	175	26	A0A087WNT8	
ENSMUST00000191195						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000191196						6	5	3	60	2	4	0	0	0	0	0		
ENSMUST00000191197	ENSMUSG00000026100	1	53061640	53068079	1	0	0	0	2	5	0	0	0	0	0	0	A0A087WQL8	
ENSMUST00000191198	ENSMUSG00000017146	11	101488764	101551955	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPE1	
ENSMUST00000191199						2	2	0	2	1	0	7	2	0	0	0		
ENSMUST00000191200	ENSMUSG00000079550	1	59120935	59163389	-1	0	0	0	0	0	0	0	0	0	0	0		Q6P7F1
ENSMUST00000191201	ENSMUSG00000026029	1	58795374	58847503	1	0	0	0	24	2	0	22	165	106	174	138	A0A087WQT6	
ENSMUST00000191203	ENSMUSG00000096045	5	25982030	25988650	-1	0	47	26	0	26	0	0	0	0	0	0	A0A087WQP8	
ENSMUST00000191204	ENSMUSG00000055322	1	73910231	74124449	-1	0	0	7	0	0	0	2	0	0	0	0	A0A087WS32	
ENSMUST00000191205						6	2	46	9	7	2	2	8	6	0	2		
ENSMUST00000191206	ENSMUSG00000026037	1	58462771	58505109	-1	0	0	0	52	0	3	0	0	0	2	0	A0A087WSP9	
ENSMUST00000191208						2	3	0	2	0	2	0	0	0	0	0		
ENSMUST00000191210						0	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000191211						8	4	17	7	4	1	0	0	0	0	1		
ENSMUST00000191212	ENSMUSG00000054387	1	132959484	133030561	-1	0	0	0	0	0	0	11	16	58	0	20	A0A087WQ20	
ENSMUST00000191213	ENSMUSG00000032407	9	95456898	95511996	-1	0	4	0	0	5	0	63	431	307	381	203	A0A087WRG2	
ENSMUST00000191214						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191215						5	11	22	15	6	7	0	0	0	0	0		
ENSMUST00000191216	ENSMUSG00000079018	15	75044018	75048830	-1	0	0	0	0	0	0	0	9	13	95	53	A0A087WRP7	
ENSMUST00000191218	ENSMUSG00000096753	12	103310975	103317065	1	5	0	16	0	10	9	0	0	0	0	0	J3QNB7	
ENSMUST00000191219						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191220						0	0	0	6	6	0	0	0	0	0	0		
ENSMUST00000191224						0	1	0	1	3	1	0	0	0	0	0		
ENSMUST00000191225						3	2	2	0	3	0	0	0	0	0	2		
ENSMUST00000191226						0	2	0	1	0	2	0	0	0	1	0		
ENSMUST00000191227						2	4	7	7	8	3	0	0	0	1	0		
ENSMUST00000191228	ENSMUSG00000006007	1	150319417	150333906	1	1	3	3	0	0	3	0	0	0	0	0		Q9QW08
ENSMUST00000191229						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191230						1	0	2	8	2	0	7	36	16	0	21		
ENSMUST00000191231						13	12	84	12	13	5	0	0	0	0	0		
ENSMUST00000191232						102	69	272	184	92	54	1	11	11	2	13		
ENSMUST00000191233						2	5	5	10	7	2	0	0	0	0	0		
ENSMUST00000191234	ENSMUSG00000069670	10	31689310	32890462	-1	6	10	18	33	20	12	0	0	0	0	0		Q4PNJ2
ENSMUST00000191235						5	0	1	0	2	0	0	32	7	8	8		
ENSMUST00000191236						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000191237	ENSMUSG00000042305	1	134346097	134361979	-1	4	4	0	2	8	0	140	166	193	41	121	A0A087WPL2	
ENSMUST00000191238	ENSMUSG00000019865	10	14705591	14770850	1	2	0	3	0	0	0	0	0	0	0	0	A0A087WPA3	
ENSMUST00000191239						6	4	20	7	4	2	0	0	0	0	0		
ENSMUST00000191242						3	4	0	0	11	0	6	73	0	24	0		
ENSMUST00000191243						2	4	1	0	0	0	0	0	0	0	0		
ENSMUST00000191244						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191245						8	3	7	3	5	3	2	15	8	0	12		
ENSMUST00000191247						51	65	433	68	64	28	122	227	214	28	358		
ENSMUST00000191248						0	0	0	0	0	0	0	4	0	0	2		
ENSMUST00000191249						10	5	5	9	2	9	0	0	0	0	0		
ENSMUST00000191250						3	5	7	1	4	3	0	0	0	0	0		
ENSMUST00000191251	ENSMUSG00000026018	1	59982490	60043184	-1	5	5	12	0	0	3	2	6	6	1	10		Q3TY65
ENSMUST00000191252	ENSMUSG00000047528	1	58646903	58695989	-1	6	0	1	0	0	3	0	0	0	2	2	A0A087WRG1	
ENSMUST00000191254	ENSMUSG00000026209	1	75307896	75317990	-1	0	0	1	8	0	1	23	2	7	3	3	A0A087WSD3	
ENSMUST00000191255	ENSMUSG00000101401	7	33185568	33186868	1	0	0	3	3	0	0	0	0	0	0	0	A0A087WQJ0	
ENSMUST00000191256						0	0	0	0	0	0	0	0	0	11	0		
ENSMUST00000191257						3	2	0	1	2	1	0	0	0	0	0		
ENSMUST00000191258						3	7	10	11	5	2	7	42	6	4	14		
ENSMUST00000191260						0	1	4	2	4	2	0	5	0	0	8		
ENSMUST00000191262	ENSMUSG00000025997	1	69531214	69687245	-1	1	0	14	0	0	0	2	0	0	0	0	A0A087WNX1	
ENSMUST00000191264						12	1	28	12	13	7	0	0	0	0	5		
ENSMUST00000191265	ENSMUSG00000101415	1	117928015	117949988	1	8	2	0	4	2	2	0	0	0	0	0	A0A087WNP1	
ENSMUST00000191267						10	6	4	17	0	14	6	5	0	0	0		
ENSMUST00000191268	ENSMUSG00000032571	9	105642978	105687657	1	15	0	9	0	0	7	171	47	89	0	177		Q8VD65
ENSMUST00000191269						4	1	2	4	1	0	1	0	0	0	1		
ENSMUST00000191271	ENSMUSG00000096094	1	75220095	75232102	-1	4	3	9	5	4	2	0	0	0	0	0	A0A087WQ76	
ENSMUST00000191273	ENSMUSG00000028416	4	40936398	40948294	-1	0	0	0	113	0	0	0	0	0	0	0		Q60739
ENSMUST00000191274						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191275	ENSMUSG00000021709	13	103818787	103920514	-1	0	0	7	0	0	0	116	201	470	32	125	B2RUK2	Q80TH2
ENSMUST00000191276						4	14	10	5	5	9	0	0	0	0	0		
ENSMUST00000191279	ENSMUSG00000026420	1	130882074	130887454	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRY6	
ENSMUST00000191281	ENSMUSG00000098810	CHR_MG132_PATCH	124291804	124312696	-1	1	1	2	1	0	0	3	16	9	3	6		
ENSMUST00000191282						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191283						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000191284						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000191285						3	5	15	0	4	0	0	1	0	0	0		
ENSMUST00000191288						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191289						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191290	ENSMUSG00000033419	9	86765923	86880654	-1	0	0	0	4	0	2	0	0	0	0	0	A0A087WSI9	
ENSMUST00000191291						3	0	0	0	4	0	0	0	0	0	0		
ENSMUST00000191292	ENSMUSG00000044916	2	92382538	92385708	1	0	0	0	0	0	0	0	4	0	0	0	A0A087WR07	
ENSMUST00000191293						41	40	120	48	44	19	45	41	73	4	74		
ENSMUST00000191294						29	23	68	26	19	9	0	0	0	0	0		
ENSMUST00000191295						4	5	1	7	3	5	0	0	0	1	0		
ENSMUST00000191296						3	0	12	8	2	2	2	4	0	0	2		
ENSMUST00000191297						9	13	13	157	16	5	0	3	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191300						42	34	194	176	56	28	0	3	5	1	3		
ENSMUST00000191301	ENSMUSG00000026409	1	130689182	130729253	-1	0	0	0	1	0	0	0	0	0	0	58	B2Z891	
ENSMUST00000191303	ENSMUSG00000025982	1	54985169	55027481	-1	0	1	0	16	0	0	23	17	190	49	158	A0A087WNS2	
ENSMUST00000191304						0	0	0	0	0	6	12	37	19	6	15		
ENSMUST00000191305	ENSMUSG00000096902	Y	72220863	72247118	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQA3	
ENSMUST00000191306						5	4	6	21	7	2	0	0	0	0	0		
ENSMUST00000191307	ENSMUSG00000037503	1	34813219	34843065	-1	0	0	0	0	0	0	0	0	0	0	0	G3UWF0	
ENSMUST00000191308						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191310						2	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000191311	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRP8	
ENSMUST00000191312						3	0	10	1	3	0	3	2	1	2	3		
ENSMUST00000191316						8	6	16	17	8	5	0	0	0	0	0		
ENSMUST00000191317						6	0	15	4	3	0	0	9	1	6	0		
ENSMUST00000191319						6	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000191320	ENSMUSG00000057963	12	102568582	102704930	-1	2	3	1	0	3	1	0	0	0	0	0	A0A087WNL3	
ENSMUST00000191322						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191323						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191324						0	7	12	58	3	9	8	3	8	0	0		
ENSMUST00000191327						0	1	0	0	4	0	7	19	21	8	48		
ENSMUST00000191329	ENSMUSG00000048874	1	30802339	30873921	-1	18	8	92	24	19	13	73	881	379	197	406	A0A087WP76	
ENSMUST00000191331						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000191332						3	1	3	4	4	1	0	0	0	0	0		
ENSMUST00000191333	ENSMUSG00000051590	1	127815253	127840321	-1	0	2	0	0	0	1	0	0	0	0	0	A0A087WSG0	
ENSMUST00000191335	ENSMUSG00000056267	9	99243367	99300404	1	2	5	9	0	8	2	3	24	2	19	25		Q6IQY5
ENSMUST00000191336	ENSMUSG00000056912	10	100590511	100618401	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRP3	
ENSMUST00000191337						59	52	328	85	38	28	4	16	5	17	5		
ENSMUST00000191338						33	31	63	124	44	20	10	34	23	6	50		
ENSMUST00000191339						23	39	61	32	37	20	2	9	1	1	2		
ENSMUST00000191340						0	0	0	0	2	2	0	0	3	0	0		
ENSMUST00000191341						4	2	5	0	5	2	0	1	0	0	0		
ENSMUST00000191342						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191343	ENSMUSG00000024731	19	10962293	10974670	-1	3	0	0	0	3	0	0	0	0	0	0		Q99N03
ENSMUST00000191345						5	8	14	9	14	5	2	8	2	0	2		
ENSMUST00000191347	ENSMUSG00000026409	1	130689182	130729253	-1	0	0	0	0	0	0	0	0	0	0	6	A0A087WRM7	
ENSMUST00000191348						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191349						1	1	2	2	3	1	0	0	0	0	0		
ENSMUST00000191350	ENSMUSG00000031509	8	11654924	11701063	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP52	
ENSMUST00000191352	ENSMUSG00000021219	12	82588292	83162056	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPC4	
ENSMUST00000191353	ENSMUSG00000062270	9	90091665	90114774	-1	2	0	11	8	3	0	0	0	88	456	80	A0A087WQ34	
ENSMUST00000191355	ENSMUSG00000101155	Y	57187188	57213362	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WNQ6	
ENSMUST00000191358	ENSMUSG00000095520	Y	17093873	17095892	1	0	0	11	9	0	0	0	0	0	0	0	J3QPZ4	
ENSMUST00000191360						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191361						1	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000191365						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191366						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191367	ENSMUSG00000055322	1	73910231	74124449	-1	2	3	4	23	0	0	8	0	0	1	0	A0A087WSC8	
ENSMUST00000191368	ENSMUSG00000034343	1	91250304	91290337	1	1	6	0	0	0	10	154	619	220	214	79		Q9CY34
ENSMUST00000191370						1	0	0	10	1	0	0	1	2	0	0		
ENSMUST00000191371						34	52	182	47	69	21	2	11	5	4	10		
ENSMUST00000191373						1	5	3	18	2	0	0	0	0	0	2		
ENSMUST00000191376						0	0	4	2	0	0	0	0	0	0	0		
ENSMUST00000191377						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191378	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRP4	
ENSMUST00000191379						5	5	10	7	11	1	8	35	24	0	9		
ENSMUST00000191380						22	5	43	41	14	13	0	1	1	1	0		
ENSMUST00000191381						19	11	91	11	18	6	2	12	12	2	66		
ENSMUST00000191382						0	0	0	6	0	0	0	0	0	0	0		
ENSMUST00000191383						3	1	4	1	4	2	1	0	0	2	0		
ENSMUST00000191385	ENSMUSG00000039218	17	23790662	23824741	1	0	0	0	1	4	0	0	0	9	0	7	A0A087WPS9	
ENSMUST00000191386						0	1	0	2	2	2	0	2	0	7	0		
ENSMUST00000191387						47	52	123	69	63	32	11	53	19	13	41		
ENSMUST00000191388	ENSMUSG00000071632	16	18836578	18840160	1	92	63	96	238	113	47	0	61	7	3	2	A0A087WSJ3	
ENSMUST00000191390						6	12	54	12	15	8	0	0	0	0	0		
ENSMUST00000191392						0	0	0	0	3	0	0	0	0	0	0		
ENSMUST00000191395						7	5	4	4	1	6	83	142	92	36	60		
ENSMUST00000191397						4	0	2	0	2	0	0	0	0	0	0		
ENSMUST00000191399						2	3	5	11	1	0	0	0	0	0	0		
ENSMUST00000191401	ENSMUSG00000042564	15	79609576	79658956	-1	0	0	0	0	0	0	7	0	0	0	0	A0A087WRJ7	
ENSMUST00000191403						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000191404	ENSMUSG00000023259	9	108853283	108913049	1	4	4	18	3	2	1	8	24	7	5	9	A0A087WSC0	
ENSMUST00000191407	ENSMUSG00000101026	15	74770908	74778859	-1	11	9	54	9	13	8	0	0	0	0	0	A0A087WRX0	
ENSMUST00000191408						0	0	3	0	0	0	0	0	10	0	6		
ENSMUST00000191410						2	0	3	4	3	0	0	1	0	0	0		
ENSMUST00000191412						8	5	0	1	4	1	0	2	1	0	0		
ENSMUST00000191413						0	0	0	0	0	0	0	0	0	6	0		
ENSMUST00000191415						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000191416						1	3	2	7	5	3	0	0	0	0	0		
ENSMUST00000191417						30	27	81	23	43	19	3	10	2	1	3		
ENSMUST00000191418	ENSMUSG00000079330	1	132191431	132259227	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQH1	
ENSMUST00000191419						27	47	91	43	62	62	0	0	0	0	0		
ENSMUST00000191420						0	4	0	0	0	0	0	0	0	0	0		
ENSMUST00000191421						12	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191422						1	2	0	4	4	0	0	0	0	0	0		
ENSMUST00000191423						0	1	1	1	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191424						1	1	0	0	2	2	1	1	1	1	1		
ENSMUST00000191425	ENSMUSG00000026327	1	107361198	107380475	1	0	4	0	0	4	0	0	0	0	0	0	A0A087WST6	
ENSMUST00000191428	ENSMUSG00000070047	8	44935447	45052257	1	73	73	79	129	79	0	0	0	0	0	79	F2Z4A3	
ENSMUST00000191430						8	6	30	4	18	8	0	3	0	0	0		
ENSMUST00000191431	ENSMUSG00000003283	2	153108468	153151441	1	6	3	15	61	9	5	3497	6147	2935	722	2484	F6UND7	
ENSMUST00000191432						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191433						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191434	ENSMUSG00000023345	9	106281061	106350521	1	0	4	2	0	6	2	6	16	0	9	36		Q8JZX3
ENSMUST00000191435	ENSMUSG00000026104	1	52119440	52161865	1	0	8	0	0	12	0	0	0	0	0	0	Q99K94	
ENSMUST00000191436	ENSMUSG00000022587	15	74955051	74959905	1	0	0	0	0	0	0	2118	5440	1090	320	2108	Q99JA5	
ENSMUST00000191437						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000191438	ENSMUSG00000037608	10	20312469	20344613	1	8	6	8	1	4	0	5	315	38	325	19	A0A087WRN1	
ENSMUST00000191439						4	2	5	54	6	3	9	43	19	4	27		
ENSMUST00000191440	ENSMUSG00000003346	10	80583654	80590341	-1	0	0	0	15	0	0	15	20	10	0	0	A0A087WPG3	
ENSMUST00000191441	ENSMUSG00000043629	1	52922324	53020179	-1	3	0	0	1	0	5	0	0	0	0	0		Q9CPS8
ENSMUST00000191443	ENSMUSG00000093895	Y	40290790	40316903	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRL2	
ENSMUST00000191444						1	1	3	0	1	2	0	0	0	0	0		
ENSMUST00000191445	ENSMUSG00000064302	1	118389058	118612678	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQ95	
ENSMUST00000191446	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRS1	
ENSMUST00000191448						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191449	ENSMUSG00000038608	1	80501073	80758527	-1	0	0	0	0	0	2	0	0	8	2	0	Q8BLX9	
ENSMUST00000191450	ENSMUSG00000041459	4	148612382	148627019	-1	0	0	0	0	0	0	16	0	0	19	14	A0A087WRZ5	
ENSMUST00000191451	ENSMUSG00000022584	15	75108158	75111970	-1	0	0	0	0	0	3	314	149	175	615	219		P0CW03
ENSMUST00000191454						1	0	0	0	0	1	0	3	0	6	0		
ENSMUST00000191456						37	35	44	27	33	14	1	10	2	2	4		
ENSMUST00000191458						2	0	0	0	4	1	0	0	0	0	0		
ENSMUST00000191459	ENSMUSG00000025950	1	65158616	65186500	-1	0	0	1	0	4	0	0	0	0	0	0	A0A087WNN7	
ENSMUST00000191462	ENSMUSG00000072704	6	133104909	133110899	1	2	2	3	91	0	0	0	0	0	6	0	A0A087WNQ7	
ENSMUST00000191463	ENSMUSG00000034157	12	86947043	86965362	1	2	0	6	0	13	0	7	0	2	1	0		Q8R0W1
ENSMUST00000191464						12	8	45	12	9	6	0	0	0	0	0		
ENSMUST00000191465	ENSMUSG00000039313	9	89587216	89623125	-1	0	6	0	0	8	0	0	0	0	0	0	A0A087WS88	
ENSMUST00000191466						0	3	0	6	0	0	0	0	0	0	0		
ENSMUST00000191467						6	6	5	2	3	4	0	1	0	0	0		
ENSMUST00000191468						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191469	ENSMUSG00000033633	8	111058920	111092426	-1	26	0	23	26	47	25	0	0	0	0	0		Q7TSQ1
ENSMUST00000191470						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191471	ENSMUSG00000073725	1	24678630	24766301	1	0	0	0	26	0	0	380	751	448	398	229		Q8K0B2
ENSMUST00000191472						23	23	39	11	44	16	0	4	1	0	7		
ENSMUST00000191473	ENSMUSG00000031586	8	33782643	33929863	-1	0	0	0	0	5	0	0	0	16	10	42		Q9WVB0
ENSMUST00000191475						16	15	14	13	21	12	1	9	5	3	5		
ENSMUST00000191477						0	0	0	0	0	0	0	0	1	0	0		
ENSMUST00000191480						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191483						2	14	3	15	4	1	0	0	0	0	0		
ENSMUST00000191484	ENSMUSG00000038379	9	83834689	83872389	1	0	0	0	35	0	0	0	0	0	0	0	A0A087WPS8	
ENSMUST00000191485	ENSMUSG00000042626	3	89418443	89430027	1	0	25	0	17	8	0	173	320	377	19	363		P98083
ENSMUST00000191486						10	7	11	10	13	4	0	0	4	1	0		
ENSMUST00000191488						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191489						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191491						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191493						14	12	23	8	9	7	2	2	2	2	3		
ENSMUST00000191494						1	6	0	4	0	0	0	5	1	0	3		
ENSMUST00000191497	ENSMUSG00000046269	X	7371276	7375830	-1	17	17	74	23	19	13	2	4	2	0	6		Q8CEG8
ENSMUST00000191498	ENSMUSG00000019813	10	41718840	41809871	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WSK9	
ENSMUST00000191499						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000191500						0	1	0	0	0	0	0	13	3	1	4		
ENSMUST00000191501	ENSMUSG00000100241	14	32462438	32464850	-1	10	11	44	417	31	9	0	0	0	0	0	Q3TYJ1	
ENSMUST00000191502						1	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000191503						20	25	15	14	25	6	0	4	5	1	9		
ENSMUST00000191504						468	455	534	539	629	344	22	94	39	14	65		
ENSMUST00000191505						5	6	11	59	5	6	0	0	2	2	0		
ENSMUST00000191506	ENSMUSG00000028141	3	94432414	94443915	-1	10	10	12	7	15	7	0	0	0	0	0	A0A087WNM3	
ENSMUST00000191507						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000191509	ENSMUSG00000014850	13	92211872	92355003	-1	28	10	35	32	26	17	3	7	6	0	9	A0A087WSR8	
ENSMUST00000191510						10	14	14	9	11	4	14	51	25	7	41		
ENSMUST00000191511	ENSMUSG00000021843	14	47648448	47736564	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WPW5	
ENSMUST00000191512						142	231	283	143	191	86	3	127	17	58	54		
ENSMUST00000191513	ENSMUSG00000099353	15	98398419	98416268	1	2	2	3	0	2	0	0	0	0	0	0	A0A087WQB2	
ENSMUST00000191514						5	0	0	3	4	5	0	0	0	0	0		
ENSMUST00000191516	ENSMUSG00000013353	7	43492044	43505940	-1	7	3	10	5	4	2	2	2	3	0	14	A2RSL7	
ENSMUST00000191520						73	83	485	83	85	36	2	8	2	1	9		
ENSMUST00000191521						0	0	0	7	0	0	0	5	0	0	0		
ENSMUST00000191523	ENSMUSG00000074217	8	84010222	84012171	-1	0	0	0	0	0	0	0	1	0	0	0	A0A087WQV6	
ENSMUST00000191525						3	0	12	5	7	0	0	0	0	0	0		
ENSMUST00000191526						9	1	22	9	12	3	0	2	0	1	0		
ENSMUST00000191527						1	0	7	4	4	0	0	0	0	0	0		
ENSMUST00000191528						1	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000191529						485	407	1675	517	581	225	13	102	48	18	55		
ENSMUST00000191532						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191533	ENSMUSG00000034343	1	91250304	91290337	1	0	0	4	20	0	0	0	0	0	0	0	A0A087WQR9	
ENSMUST00000191534						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191535						0	0	0	1	0	0	0	3	0	22	0		
ENSMUST00000191536						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191537	ENSMUSG00000045411	7	44246722	44252319	1	1	0	0	0	0	0	0	0	10	0	7	A0A087WSJ7	
ENSMUST00000191538						4	0	0	2	3	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191540						4	4	11	4	4	0	0	0	0	0	1		
ENSMUST00000191541						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191543						0	4	6	4	5	0	0	0	0	0	0		
ENSMUST00000191544	ENSMUSG00000026341	1	125392905	125435727	-1	0	4	0	0	0	0	62	466	816	17	74	A0A087WP86	
ENSMUST00000191545						4	2	1	2	0	0	0	0	0	0	0		
ENSMUST00000191546	ENSMUSG00000036766	1	84369839	84696221	-1	1	0	0	3	5	1	0	0	0	0	0	A0A087WRJ8	
ENSMUST00000191548						14	0	0	0	1	0	0	1	0	0	0		
ENSMUST00000191549						3	4	3	4	5	3	0	0	0	0	0		
ENSMUST00000191550	ENSMUSG00000014850	13	92211872	92355003	-1	8	0	1	0	2	0	0	22	42	5	32	A0A087WRJ5	
ENSMUST00000191552						2	2	9	0	4	0	0	0	0	0	0		
ENSMUST00000191553	ENSMUSG00000095606	Y	52780040	52806254	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WQC7	
ENSMUST00000191554						0	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000191556	ENSMUSG00000040648	1	97706048	97770411	-1	0	1	0	0	2	0	1	0	0	0	0	A0A087WPZ7	
ENSMUST00000191557						2	0	3	4	0	1	0	0	0	0	0		
ENSMUST00000191558	ENSMUSG00000070047	8	44935447	45052257	1	0	0	0	0	1	0	0	0	1	0	0	A7ISQ1	
ENSMUST00000191559						0	0	0	3	0	0	0	0	0	0	0		
ENSMUST00000191560						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191562						1	3	2	2	2	4	0	0	0	0	0		
ENSMUST00000191565	ENSMUSG00000047528	1	58646903	58695989	-1	0	0	0	4	6	0	1	4	0	0	0	A0A087WNN1	
ENSMUST00000191566						13	23	8	13	21	4	0	0	0	0	0		
ENSMUST00000191567						1	2	0	0	1	2	0	0	0	0	0		
ENSMUST00000191568						26	36	30	23	37	26	15	32	32	7	47		
ENSMUST00000191569						7	6	5	2	8	3	0	0	0	0	0		
ENSMUST00000191571						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191572						23	24	47	28	22	10	1	15	9	1	9		
ENSMUST00000191574						5	11	22	14	13	4	0	0	0	0	0		
ENSMUST00000191575						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000191577	ENSMUSG00000042451	1	134193448	134201232	1	0	0	0	18	0	9	5	10	7	9	0		P70402
ENSMUST00000191578	ENSMUSG00000026341	1	125392905	125435727	-1	1	0	0	0	1	8	318	8344	5635	682	2114	A0A087WPR6	
ENSMUST00000191579						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191580	ENSMUSG00000053080	19	7417625	7425904	1	0	0	3	52	5	0	0	0	0	0	0	A0A087WQW5	
ENSMUST00000191582						128	94	600	191	116	71	2	84	18	7	35		
ENSMUST00000191583						0	0	4	2	2	0	0	0	0	0	0		
ENSMUST00000191584						5	2	9	0	3	0	0	0	0	0	2		
ENSMUST00000191587	ENSMUSG00000025515	7	141690340	141754693	1	7	3	2	4	1	3	0	0	0	0	1	A0A087WP72	
ENSMUST00000191589						0	2	11	4	5	4	2	15	2	0	4		
ENSMUST00000191590						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191591						1	0	0	0	1	2	0	0	0	0	0		
ENSMUST00000191592						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000191593						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191595						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000191596						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191597						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191598	ENSMUSG00000024038	17	31520115	31531326	1	5	0	6	11	7	3	17	138	40	17	28	A0A087WQ40	
ENSMUST00000191601	ENSMUSG00000037032	7	105558483	105581653	-1	0	0	23	0	0	0	0	0	6	5	0		
ENSMUST00000191602	ENSMUSG00000029419	2	25575416	25581757	-1	9	21	0	0	0	0	0	0	0	3	3		A2AJA9
ENSMUST00000191604	ENSMUSG00000026125	1	34498410	34503063	1	3	0	0	3	1	0	0	0	0	0	0	A0A087WR41	
ENSMUST00000191605	ENSMUSG00000026594	1	156804166	156939626	-1	0	0	0	0	0	0	0	0	0	0	0		Q9ERD6
ENSMUST00000191606						89	109	0	0	0	0	0	0	0	0	0		
ENSMUST00000191607						2	2	4	0	3	1	0	0	0	0	0		
ENSMUST00000191608						3	4	1	1	0	3	0	0	0	0	0		
ENSMUST00000191609						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191610	ENSMUSG00000061080	16	39984361	42181679	1	2	4	0	11	3	0	0	0	0	0	0	A0A087WQA7	
ENSMUST00000191611						2	1	0	4	0	0	0	0	2	0	0		
ENSMUST00000191613	ENSMUSG00000079144	1	193168046	193177832	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX20	
ENSMUST00000191615						10	8	10	87	19	2	54	632	206	27	376		
ENSMUST00000191617	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	2	0	0	0	1	0	0	0	0	0	0	Q9D8I4	
ENSMUST00000191618						0	2	1	1	4	1	0	0	0	0	0		
ENSMUST00000191621						6	0	8	4	5	0	0	0	0	0	0		
ENSMUST00000191622						1	4	3	9	0	4	2	2	0	0	3		
ENSMUST00000191626	ENSMUSG00000026510	1	182409172	182462432	1	0	0	0	0	2	1	0	0	5	2	10	A0A0A6YX89	
ENSMUST00000191627						1	2	0	26	4	0	0	0	0	0	0		
ENSMUST00000191629						1	2	2	39	5	1	0	0	0	0	0		
ENSMUST00000191631						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000191633	ENSMUSG00000027820	3	63241537	63386030	1	0	0	0	8	1	0	0	0	0	1	0	A0A0A6YWA6	
ENSMUST00000191638						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191639						2	2	8	0	1	1	0	0	2	0	0		
ENSMUST00000191640						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191642	ENSMUSG00000026121	1	36548639	36558349	-1	19	7	78	40	7	0	0	0	0	0	0		Q64151
ENSMUST00000191645						57	60	210	61	85	42	3	22	9	2	13		
ENSMUST00000191646	ENSMUSG00000076481	6	41281376	41281990	1	3	6	0	3	2	0	0	0	0	0	3	A0A0B4J1P1	
ENSMUST00000191647	ENSMUSG00000025902	1	4490931	4497354	-1	0	0	0	0	0	1	0	0	0	0	0	A0A0A6YXZ2	
ENSMUST00000191649						1	0	0	1	2	3	0	5	0	0	2		
ENSMUST00000191651	ENSMUSG00000026721	1	160219174	160793211	-1	1	1	0	0	2	1	3	8	1	0	4	A0A0A6YW18	
ENSMUST00000191653	ENSMUSG00000034755	X	120290259	120910619	1	1	1	12	0	0	0	0	0	0	0	0	Q2TJH7	
ENSMUST00000191657						3	0	2	2	6	1	0	231	10	20	6		
ENSMUST00000191659						1	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000191661						2	0	0	0	1	2	0	2	2	0	0		
ENSMUST00000191662						0	0	0	0	0	0	21	25	0	48	0		
ENSMUST00000191664						7	4	48	19	5	5	0	0	0	0	1		
ENSMUST00000191666	ENSMUSG00000059994	3	87376387	87402934	1	0	0	0	0	0	4	0	0	54	7	42	A0A0A6YXB2	
ENSMUST00000191667						0	0	0	19	0	4	0	0	0	0	0		
ENSMUST00000191668	ENSMUSG00000026773	2	11471433	11554077	-1	0	0	0	0	0	0	0	0	0	0	17	A7UAK5	
ENSMUST00000191670	ENSMUSG00000027531	3	10311956	10331439	-1	0	0	0	0	0	0	59	147	88	299	97	A0A0A6YW07	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191671	ENSMUSG00000026073	1	40074079	40125231	1	5	6	3	3	5	6	12	11	18	8	26	A0A0A6YX83	
ENSMUST00000191672						5	7	1	208	2	2	0	0	0	0	0		
ENSMUST00000191673						0	0	1	2	1	0	0	5	0	0	0		
ENSMUST00000191674						0	3	3	0	2	1	0	0	0	0	0		
ENSMUST00000191675	ENSMUSG00000102668	Y	20967477	20993657	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX04	
ENSMUST00000191677	ENSMUSG00000026121	1	36548639	36558349	-1	0	17	15	0	33	5	0	0	0	0	1		Q64151
ENSMUST00000191678	ENSMUSG00000027528	3	10193621	10197283	-1	0	0	0	4	0	0	0	0	0	0	0	A0A0A6YXI2	
ENSMUST00000191680	ENSMUSG00000039748	1	175880581	175913489	1	0	0	0	0	0	0	1	3	5	4	0	A0A0A6YWF4	
ENSMUST00000191681						5	5	6	69	1	0	0	0	0	0	0		
ENSMUST00000191683	ENSMUSG00000025909	1	8361475	9299878	-1	0	0	14	0	0	4	0	0	0	0	0	Q8C415	
ENSMUST00000191684						42	54	250	73	51	30	0	0	8	1	11		
ENSMUST00000191689	ENSMUSG00000026554	1	172148084	172197005	1	0	0	0	0	0	0	330	1321	438	95	458		Q8N7N5
ENSMUST00000191690						7	4	10	22	7	0	0	1	0	0	5		
ENSMUST00000191691						0	1	0	0	0	0	0	0	1	0	1		
ENSMUST00000191692						4	2	4	3	1	1	0	0	0	0	0		
ENSMUST00000191693	ENSMUSG00000094029	12	114196439	114196875	-1	0	0	4	1	0	0	0	0	0	0	0	A0A0A6YWL2	
ENSMUST00000191695						28	13	129	225	28	15	0	0	0	0	0		
ENSMUST00000191697						1	1	0	0	0	0	1	0	0	0	1		
ENSMUST00000191699						0	0	0	0	0	0	41	182	64	275	37		
ENSMUST00000191703						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191705						1	2	0	0	0	0	0	1	0	2	3		
ENSMUST00000191706						0	12	3	4	0	2	29	59	38	0	76		
ENSMUST00000191709	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000191711	ENSMUSG00000098301	CHR_MG3829_PATCH	88047373	88053755	1	0	1	0	0	0	0	19	79	128	11	63		
ENSMUST00000191713						50	46	131	99	65	31	3	25	6	0	18		
ENSMUST00000191715						2	2	2	0	2	6	0	4	0	0	3		
ENSMUST00000191719						7	6	6	185	13	6	1	2	0	1	0		
ENSMUST00000191721						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191722						0	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000191724						1	2	0	48	0	0	0	0	0	0	0		
ENSMUST00000191725						96	49	665	150	144	51	0	2	3	1	6		
ENSMUST00000191726						0	1	1	2	5	1	8	6	17	0	33		
ENSMUST00000191727						1	2	5	2	1	0	0	0	0	0	0		
ENSMUST00000191728						9	12	49	9	8	10	12	44	23	8	23		
ENSMUST00000191730						0	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000191731						0	1	13	0	2	0	0	0	0	0	0		
ENSMUST00000191732						2	0	1	5	0	0	0	0	0	0	0		
ENSMUST00000191733						1	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000191739						1	1	12	1	4	0	13	27	10	21	5		
ENSMUST00000191744						20	33	97	23	25	7	6	11	11	0	4		
ENSMUST00000191745	ENSMUSG00000026558	1	167222883	167285320	-1	1	1	9	3	3	0	0	0	0	0	0	A0A0A6YX11	
ENSMUST00000191746						5	3	2	2	1	1	0	1	0	1	0		
ENSMUST00000191747	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	4	0	389	45	12	7	99	Q3U570	
ENSMUST00000191752	ENSMUSG00000028078	3	86786151	86920852	-1	32	33	81	56	64	31	3	18	6	0	29		Q6PGN3
ENSMUST00000191754						2	1	0	0	3	0	0	12	0	0	2		
ENSMUST00000191755						0	1	0	0	0	0	2	9	2	0	7		
ENSMUST00000191757						27	29	139	31	43	17	0	3	0	0	1		
ENSMUST00000191758	ENSMUSG00000033767	3	83897655	84040175	-1	11	0	57	28	16	0	590	1034	968	40	514		Q3U3D7
ENSMUST00000191760						5	5	6	4	2	3	0	1	3	0	1		
ENSMUST00000191761	ENSMUSG00000026074	1	39900913	40026310	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVZ8	
ENSMUST00000191762						3	2	4	1	4	0	0	0	0	0	0		
ENSMUST00000191763						12	9	8	8	9	7	3	0	0	0	0		
ENSMUST00000191766						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191769						0	0	1	0	0	0	0	17	0	0	9		
ENSMUST00000191773						24	19	70	18	22	15	0	0	3	0	6		
ENSMUST00000191774	ENSMUSG00000047213	3	16183212	16217037	1	1	0	39	0	3	5	262	784	949	55	621		Q8BYK6
ENSMUST00000191775	ENSMUSG00000016481	1	195097382	195131586	-1	0	0	0	2	2	0	118	784	248	205	125	A0A0A6YVT1	
ENSMUST00000191776						1	0	0	6	4	1	0	0	0	0	0		
ENSMUST00000191777						22	18	43	35	35	17	2	0	5	0	3		
ENSMUST00000191781						0	0	3	2	0	2	0	0	0	0	0		
ENSMUST00000191782						0	0	0	21	0	0	0	0	0	0	0		
ENSMUST00000191783	ENSMUSG00000027667	3	32510259	32520833	1	0	0	0	8	0	0	34	62	31	32	18		Q99KZ6
ENSMUST00000191785						4	0	9	1	7	3	1	0	1	2	0		
ENSMUST00000191786						0	2	1	3	3	0	0	0	0	0	0		
ENSMUST00000191789						4	2	7	0	3	0	0	0	0	0	0		
ENSMUST00000191790						3	0	12	114	8	2	39	118	51	16	49		
ENSMUST00000191793						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191794	ENSMUSG00000037892	3	49743296	49757325	-1	24	16	0	31	36	15	0	0	0	0	1	A0A0A6YXH7	
ENSMUST00000191795						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191797						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000191799						33	29	53	176	46	25	6	35	20	3	35		
ENSMUST00000191801	ENSMUSG00000102888	12	114612243	114612675	-1	4	2	1	0	1	3	0	0	1	0	1	A0A0A6YWI9	
ENSMUST00000191802						4	6	0	0	4	1	2	11	9	4	30		
ENSMUST00000191803	ENSMUSG00000096499	12	114513330	114513807	-1	5	8	7	3	5	0	0	0	1	0	6	A0A0A6YWG2	
ENSMUST00000191804						10	6	46	0	9	0	23	166	0	0	93		
ENSMUST00000191805	ENSMUSG00000025762	3	40950354	41040234	1	0	3	10	0	0	0	0	127	0	0	0	Q8R3F0	
ENSMUST00000191808	ENSMUSG00000054003	12	111971559	112068854	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWV8	
ENSMUST00000191813						17	10	20	15	6	7	0	1	0	0	1		
ENSMUST00000191814						3	0	9	3	3	2	0	0	1	0	0		
ENSMUST00000191815						3	4	26	2	3	1	0	0	0	0	0		
ENSMUST00000191818	ENSMUSG00000026566	1	165592240	165634538	-1	0	0	0	0	1	0	0	0	4	0	0	A0A0A6YW22	
ENSMUST00000191820	ENSMUSG00000079164	1	182954788	182976044	1	27	25	14	22	28	12	0	0	0	0	0	Q05AH3	
ENSMUST00000191821						0	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000191823	ENSMUSG00000064302	1	118389058	118612678	1	0	0	1	0	0	0	0	0	0	0	0	A0A0A6YXZ1	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191826	ENSMUSG00000027536	3	10366907	10428856	1	27	24	17	21	40	16	2	0	0	0	0	A0A0A6YWM4	
ENSMUST00000191828						3	0	1	3	4	0	9	0	55	15	75		
ENSMUST00000191829	ENSMUSG00000102692	3	83127948	83357209	1	68	49	61	444	79	32	0	0	0	0	0	A0A0A6YW72	
ENSMUST00000191830						1	0	1	0	0	0	0	1	0	0	0		
ENSMUST00000191832						0	1	1	2	3	2	3	14	9	3	11		
ENSMUST00000191833						3	7	0	0	7	4	0	0	0	0	0		
ENSMUST00000191835	ENSMUSG00000063887	3	25426215	26332460	-1	0	0	0	1	0	0	0	0	0	0	0	E9QK34	
ENSMUST00000191836						4	1	40	6	4	3	0	0	0	0	0		
ENSMUST00000191837	ENSMUSG00000029108	5	57717967	58133230	1	17	14	14	75	20	16	0	0	0	1	2	A0A0A6YY83	
ENSMUST00000191838	ENSMUSG00000026792	2	32925216	32961614	-1	0	0	0	0	0	0	1	0	0	1	0	A0A0A6YWV2	
ENSMUST00000191841						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191842						0	0	1	0	0	0	3	2	0	4	24		
ENSMUST00000191844						3	14	3	3	3	7	0	0	3	0	0		
ENSMUST00000191845						6	4	1	13	8	8	0	0	0	0	0		
ENSMUST00000191847						134	90	653	320	126	63	0	5	3	0	7		
ENSMUST00000191848						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000191849	ENSMUSG00000067653	1	36530188	36547201	-1	6	10	3	17	15	0	13	16	13	0	0	Q8K1D0	
ENSMUST00000191851						84	26	55	1142	167	92	8	962	24	0	2		
ENSMUST00000191852						14	13	10	22	17	9	0	0	0	0	0		
ENSMUST00000191853						3	1	5	1	4	3	0	0	0	0	0		
ENSMUST00000191854	ENSMUSG00000052613	10	73099342	74649737	1	16	15	25	11	21	13	0	0	0	0	0		Q99PJ1
ENSMUST00000191855						0	0	2	1	0	0	4	6	0	9	0		
ENSMUST00000191859						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000191860						67	67	125	48	71	36	82	526	112	24	170		
ENSMUST00000191861	ENSMUSG00000094241	12	114772928	114773361	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY24	
ENSMUST00000191862	ENSMUSG00000094051	12	114879888	114880321	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXT2	
ENSMUST00000191864						2	2	6	2	0	1	0	0	0	0	0		
ENSMUST00000191865	ENSMUSG00000026074	1	39900913	40026310	1	5	5	0	0	1	0	0	0	0	4	0	A0A0A6YWJ2	
ENSMUST00000191868	ENSMUSG00000094652	12	114937113	114937544	-1	2	2	13	0	5	0	0	0	0	0	8	A0A0A6YY38	
ENSMUST00000191869	ENSMUSG00000037610	3	31902507	32200180	1	0	2	0	2	0	0	0	0	0	0	0	A0A0A6YXE4	
ENSMUST00000191870						28	25	220	32	23	25	1	0	1	0	0		
ENSMUST00000191871	ENSMUSG00000013593	1	171234853	171251388	-1	0	0	0	0	6	1	0	0	0	0	0	A0A0A6YXD3	
ENSMUST00000191872	ENSMUSG00000025762	3	40950354	41040234	1	14	7	22	38	19	7	0	53	8	22	8	Q3TQS1	
ENSMUST00000191874						3	2	9	1	2	1	0	0	0	0	0		
ENSMUST00000191876						0	0	3	1	0	1	2	5	1	5	0		
ENSMUST00000191878	ENSMUSG00000004880	1	181815335	181843046	-1	2	2	0	2	0	2	11	31	172	0	149	A0A0A6YXT6	
ENSMUST00000191881						0	0	0	0	0	0	1	18	4	12	10		
ENSMUST00000191882						6	11	4	9	13	0	2	25	14	0	3		
ENSMUST00000191883						0	0	26	13	2	1	0	0	0	0	0		
ENSMUST00000191886	ENSMUSG00000046259	3	92385685	92387324	1	0	0	9	0	0	0	0	0	0	0	0	A0A0A6YW71	
ENSMUST00000191889						3	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000191891	ENSMUSG00000026554	1	172148084	172197005	1	0	0	0	0	0	0	0	46	0	9	22	A0A0A6YWY2	
ENSMUST00000191896	ENSMUSG00000102976	1	133619862	133661380	-1	3	8	7	0	8	0	166	1361	0	148	3	Q3UL31	Q6NZF1
ENSMUST00000191897						0	0	13	0	2	2	54	320	56	6	84		
ENSMUST00000191899	ENSMUSG00000039952	9	108204634	108263958	-1	28	28	63	71	28	16	286	304	293	38	312	Q544G5	Q62165
ENSMUST00000191900	ENSMUSG00000026615	1	185363044	185428360	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWA4	
ENSMUST00000191903						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000191904						0	2	2	5	1	0	8	28	2	27	7		
ENSMUST00000191906	ENSMUSG00000032583	9	107888151	107903139	1	22	15	43	114	35	18	37	55	32	13	36		
ENSMUST00000191907						11	7	4	9	9	5	0	2	0	0	0		
ENSMUST00000191909	ENSMUSG00000026721	1	160219174	160793211	-1	0	0	0	0	0	0	7	7	16	5	14	A0A0A6YWT4	
ENSMUST00000191910						2	0	0	1	2	1	0	18	19	30	10		
ENSMUST00000191911						4	3	2	0	6	0	0	5	1	3	1		
ENSMUST00000191915						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191916	ENSMUSG00000040374	3	5560188	5576239	-1	0	1	3	0	0	0	0	373	0	0	0	Q91YZ5	
ENSMUST00000191918	ENSMUSG00000094174	12	114406474	114406961	-1	2	0	10	0	0	2	0	0	0	0	0	A0A0A6YX19	
ENSMUST00000191919						0	3	0	3	5	2	0	2	0	0	0		
ENSMUST00000191920						0	0	2	0	0	0	11	62	11	0	16		
ENSMUST00000191921						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191923						0	0	10	0	0	0	0	0	0	0	0		
ENSMUST00000191925	ENSMUSG00000026626	1	191351975	191403272	-1	0	0	0	1	1	1	33	169	29	0	63	A0A0A6YVV9	
ENSMUST00000191926						0	11	3	0	0	0	0	0	0	0	0		
ENSMUST00000191928						2	5	13	11	9	0	0	0	1	0	0		
ENSMUST00000191929						2	1	1	2	1	2	0	0	0	0	0		
ENSMUST00000191931						2	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000191932						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000191933						25	25	36	73	26	16	4	1	8	1	22		
ENSMUST00000191934						2	3	0	3	4	0	0	0	0	0	0		
ENSMUST00000191935						1	0	3	4	0	1	0	0	0	0	0		
ENSMUST00000191936	ENSMUSG00000026715	1	160978585	161005863	1	9	17	8	5	10	0	0	0	0	0	1	A0A0A6YXS8	
ENSMUST00000191939	ENSMUSG00000025902	1	4490931	4497354	-1	0	1	0	55	0	0	0	0	0	0	0	A0A0A6YXV3	
ENSMUST00000191940						1	2	0	3	0	0	0	0	0	0	0		
ENSMUST00000191941	ENSMUSG00000026721	1	160219174	160793211	-1	0	1	8	0	3	0	0	21	17	18	0	A0A0A6YX13	
ENSMUST00000191942						49	38	109	158	64	27	1	1	2	0	4		
ENSMUST00000191943						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000191946	ENSMUSG00000066595	1	191005847	191026158	-1	5	5	11	277	12	4	8	9	14	2	17	A0A0A6YWJ7	
ENSMUST00000191947	ENSMUSG00000026575	1	164304121	164437725	1	0	0	0	0	0	0	13	44	0	86	12	Q3UMG6	
ENSMUST00000191948						0	3	4	1	2	1	0	0	0	0	0		
ENSMUST00000191949						2	1	4	0	0	1	0	0	0	0	0		
ENSMUST00000191951						0	0	0	1	1	1	0	0	0	0	0		
ENSMUST00000191952	ENSMUSG00000025764	3	41555731	41616864	1	18	15	54	55	26	17	34	88	41	6	31		Q6ZPI0
ENSMUST00000191955	ENSMUSG00000102843	1	107535508	107547072	1	0	0	0	0	0	0	0	322	28	283	42	G3UYR4	
ENSMUST00000191956						3	0	1	1	4	0	0	0	0	0	0		
ENSMUST00000191957						3	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000191958						18	19	101	42	25	8	318	3768	379	617	360		
ENSMUST00000191959	ENSMUSG00000026727	2	13076821	13271415	-1	1	4	6	10	4	5	6	0	18	0	4	A0A0A6YWZ22	
ENSMUST00000191960	ENSMUSG00000103362	3	93651542	93652686	-1	10	5	0	3	4	5	0	0	0	0	0	A0A0A6YVW8	
ENSMUST00000191962						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000191964	ENSMUSG00000026074	1	39900913	40026310	1	0	0	5	0	2	1	0	0	0	0	21	A0A0A6YVR7	
ENSMUST00000191966						10	12	39	161	17	9	2	5	4	0	2		
ENSMUST00000191967						0	0	15	1	0	0	0	0	0	0	0		
ENSMUST00000191970	ENSMUSG00000025789	7	73939119	74013690	-1	3	0	0	58	0	1	0	0	0	0	0	A0A0A6YVX5	
ENSMUST00000191971						5	2	1	0	3	1	0	0	0	0	0		
ENSMUST00000191973	ENSMUSG00000048154	15	98831669	98871204	-1	0	4	0	5	3	0	65	248	116	12	160	A0A0A6YY77	
ENSMUST00000191975	ENSMUSG00000040297	1	161816114	161876682	-1	0	0	1	0	0	2	0	6	14	3	7	A0A0A6YWN8	
ENSMUST00000191976						12	8	16	10	13	3	0	0	0	0	0		
ENSMUST00000191977						9	11	8	21	7	3	2	6	4	0	3		
ENSMUST00000191980						0	1	2	0	2	1	2	1	0	1	1		
ENSMUST00000191981	ENSMUSG00000026114	1	37214434	37263384	1	1	0	8	0	3	0	0	0	0	0	0	A0A0A6YY14	
ENSMUST00000191983						8	10	13	264	13	10	0	0	1	0	2		
ENSMUST00000191984						22	8	37	18	18	3	0	0	0	0	1		
ENSMUST00000191985	ENSMUSG00000032590	9	108085413	108094606	-1	0	0	2	88	4	2	0	12	10	0	12	A0A0A6YXV0	
ENSMUST00000191989	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	3	0	0	0	2	0	0	0	0	0	10		
ENSMUST00000191990						0	0	1	0	0	1	0	0	0	0	0		
ENSMUST00000191995						4	0	2	6	0	0	0	0	0	0	0		
ENSMUST00000191997	ENSMUSG00000063856	9	108338903	108340343	1	0	0	0	53	16	0	1795	15868	8536	7585	4777	A0A0A6YY34	
ENSMUST00000191998						5	11	7	0	0	0	0	0	0	0	0		
ENSMUST00000191999						116	96	663	198	135	84	0	0	0	0	0		
ENSMUST00000192001	ENSMUSG00000041570	1	136268123	136346104	-1	21	4	9	0	0	0	60	85	95	0	44		Q8C1B1
ENSMUST00000192002	ENSMUSG00000027820	3	63241537	63386030	1	1	0	1	0	0	0	0	0	0	0	0	A0A0A6YWB9	
ENSMUST00000192007						0	0	0	3	3	0	1	0	6	0	7		
ENSMUST00000192009	ENSMUSG00000001415	3	88336260	88362338	1	1	0	0	0	0	0	0	0	0	0	10	A0A0A6YWQ7	
ENSMUST00000192011						9	5	37	14	9	2	0	0	0	0	0		
ENSMUST00000192014						69	74	158	224	78	35	6	9	3	0	13		
ENSMUST00000192015						8	10	24	7	11	4	0	0	1	0	0		
ENSMUST00000192019						0	1	0	1	0	0	0	0	0	6	8		
ENSMUST00000192020	ENSMUSG00000037318	1	193175453	193201703	-1	0	0	0	2	0	0	0	0	9	0	0	G3X949	
ENSMUST00000192021						17	7	22	380	22	8	0	0	0	0	0		
ENSMUST00000192024	ENSMUSG00000038179	1	171632403	171653035	-1	0	0	0	0	0	1	2	0	0	6	1	A0A0A6YW73	
ENSMUST00000192026						6	1	5	4	2	0	0	0	0	0	0		
ENSMUST00000192027	ENSMUSG00000103084	3	92737651	92739096	-1	3	4	18	14	5	0	0	0	0	0	0	A0A0A6YX29	
ENSMUST00000192028	ENSMUSG00000032599	9	108783796	108806337	1	0	0	2	0	0	0	1	6	0	0	0	Q6PAT6	
ENSMUST00000192029	ENSMUSG00000033793	1	5070018	5162529	1	0	0	0	0	0	0	0	3	0	0	0	A0A0A6YW86	
ENSMUST00000192031						10	11	28	5	10	1	56	114	94	3	170		
ENSMUST00000192032						1	4	0	14	8	3	1	1	2	0	1		
ENSMUST00000192034						1	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000192035						1	2	3	1	4	1	0	0	0	0	0		
ENSMUST00000192039						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192041	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	1	1	1	0	1	0	0	0	0	0	0		
ENSMUST00000192043						0	4	14	1	5	1	0	2	2	0	2		
ENSMUST00000192044	ENSMUSG00000040782	1	159232320	159347640	1	0	0	0	0	0	0	47	277	148	6	29	A0A0A6YWC5	
ENSMUST00000192045	ENSMUSG00000103034	3	5750806	5751295	1	6	9	13	15	10	6	1875	5518	2328	1599	2120	A0A0A6YW67	
ENSMUST00000192046						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000192047	ENSMUSG00000026581	1	164061982	164084181	1	24	26	40	69	28	20	3565	25474	7013	5394	5409	Q3TCF3	
ENSMUST00000192048	ENSMUSG00000029108	5	57717967	58133230	1	1	0	0	0	3	3	0	1	0	0	0	A0A0A6YWD5	
ENSMUST00000192049						99	120	89	688	115	73	10	22	14	4	15		
ENSMUST00000192054	ENSMUSG00000032577	9	107254927	107289877	-1	0	0	0	0	0	0	0	0	0	0	0		Q3UMW7
ENSMUST00000192055						2	2	4	2	10	3	1	11	4	0	14		
ENSMUST00000192057						18	25	52	78	34	16	42	91	87	6	89		
ENSMUST00000192058	ENSMUSG00000029999	6	86195223	86275719	1	0	0	0	15	0	0	0	0	0	0	0	A0A0A6YW49	
ENSMUST00000192061						3	2	2	0	0	1	0	0	0	0	0		
ENSMUST00000192065						5	0	10	2	3	3	0	0	12	0	10		
ENSMUST00000192067						1	4	16	60	6	5	0	0	0	0	1		
ENSMUST00000192068	ENSMUSG00000032601	9	108689314	108750436	1	0	0	0	0	0	0	0	0	2	0	0	A0A0A6YY28	
ENSMUST00000192069	ENSMUSG00000015829	1	159523769	159931729	1	264	183	1111	329	208	112	4	10	11	2	17		Q8BYI9
ENSMUST00000192071						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000192075						5	0	21	6	7	8	174	3003	282	77	448		
ENSMUST00000192076	ENSMUSG00000072258	1	183388981	183410198	1	8	5	6	8	9	0	7	33	16	14	6	A0A0A6YXZ8	
ENSMUST00000192077	ENSMUSG00000103254	12	114657353	114657786	-1	2	6	8	7	6	0	1	0	0	1	3	A0A0A6YXA5	
ENSMUST00000192080	ENSMUSG00000006675	9	108578862	108597667	-1	0	0	0	3	0	0	0	0	0	0	0	A0A0A6YXH5	
ENSMUST00000192084						0	10	0	0	5	0	0	0	0	0	0		
ENSMUST00000192086						0	0	29	10	5	0	2	0	3	0	0		
ENSMUST00000192089						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192090						9	10	12	1	4	5	6	16	17	3	10		
ENSMUST00000192091						53	38	260	55	51	28	5	15	14	0	20		
ENSMUST00000192093	ENSMUSG00000027674	3	32949408	33143247	-1	0	5	0	0	0	0	0	0	0	0	0	F8SLQ3	
ENSMUST00000192094						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000192095	ENSMUSG00000033767	3	83897655	84040175	-1	0	0	0	0	0	10	658	754	1085	64	939		Q3U3D7
ENSMUST00000192096						10	5	61	15	5	7	0	0	1	0	0		
ENSMUST00000192098						3	2	4	0	3	1	0	0	0	0	0		
ENSMUST00000192099	ENSMUSG00000003134	1	39371492	39478755	-1	0	1	6	0	0	0	48	321	25	25	22	A0A0A6YVT5	
ENSMUST00000192100						3	0	0	0	0	4	0	0	0	0	0		
ENSMUST00000192102						4	1	9	14	4	4	0	0	0	0	0		
ENSMUST00000192103	ENSMUSG00000102918	18	37806364	37841873	1	0	0	0	0	0	0	4	5	0	2	23	A0A0A6YWM6	
ENSMUST00000192106						7	7	38	15	16	9	1	3	1	1	4		
ENSMUST00000192107						0	3	0	3	1	0	0	5	2	0	5		
ENSMUST00000192108						0	1	5	3	1	0	0	0	0	0	0		
ENSMUST00000192115						2	0	1	4	3	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000192116						1	1	0	0	0	0	0	0	1	0	10		
ENSMUST00000192117						7	3	24	4	14	1	0	0	0	0	0		
ENSMUST00000192118	ENSMUSG00000029866	6	41686330	41704339	-1	0	0	2	0	0	0	0	0	0	0	0	A0A0A6YVT2	
ENSMUST00000192119						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192121						0	0	0	1	1	0	0	1	0	0	0		
ENSMUST00000192123	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	0	0	0	0	0	7	10	9	0	0		
ENSMUST00000192124						5	5	13	0	6	0	0	0	0	0	0		
ENSMUST00000192125	ENSMUSG00000054003	12	111971559	112068854	1	4	0	11	0	18	0	0	0	0	0	0	A0A0A6YY15	
ENSMUST00000192126						4	1	3	3	1	2	9	37	7	1	11		
ENSMUST00000192128	ENSMUSG00000037395	1	192098546	192138062	-1	0	6	0	0	0	0	11	9	17	0	14	A0A0A6YWP7	
ENSMUST00000192130	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	0	0	0	0	0	0	0	0	0	S4R184	
ENSMUST00000192135						3	6	6	6	1	1	0	0	0	0	0		
ENSMUST00000192138						5	7	3	8	11	8	1	0	0	0	0		
ENSMUST00000192142						7	9	5	8	2	4	1	5	0	1	1		
ENSMUST00000192144	ENSMUSG00000108680	CHR_MG184_PATCH	72347316	72353147	1	56	42	76	1596	81	41	545	1500	962	68	617		Q149G0
ENSMUST00000192145	ENSMUSG00000028080	3	86224680	86782692	1	30	16	15	7	20	19	0	0	0	0	0	A0A0A6YXX3	
ENSMUST00000192146	ENSMUSG00000091476	1	177983423	178172704	1	0	6	1	2	0	2	0	0	1	0	0	A0A0A6YXX9	
ENSMUST00000192148						0	1	6	3	0	0	0	0	0	0	0		
ENSMUST00000192150	ENSMUSG00000026708	1	161070713	161086724	1	0	0	0	0	2	0	46	100	45	79	1	M0QWX6	
ENSMUST00000192151	ENSMUSG00000057072	1	191036639	191042942	1	0	0	0	0	0	0	0	0	0	0	0		Q9CVW4
ENSMUST00000192152						5	3	12	1	0	1	0	0	0	0	0		
ENSMUST00000192155	ENSMUSG00000021466	13	63508328	63573598	-1	30	9	135	18	8	0	14	35	21	0	10	A0A0A6YWC4	
ENSMUST00000192157						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192158	ENSMUSG00000037395	1	192098546	192138062	-1	0	7	84	13	8	6	28	121	0	5	37	A0A0A6YX54	
ENSMUST00000192159						6	7	34	228	16	5	0	16	17	8	18		
ENSMUST00000192160						0	0	0	0	0	0	0	0	0	0	2		
ENSMUST00000192161	ENSMUSG00000098375	CHR_MG3829_PATCH	88204388	88211507	1	1	0	8	34	3	2	2	0	0	0	1		
ENSMUST00000192165						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192166						6	15	6	7	5	0	0	0	0	5	8		
ENSMUST00000192168	ENSMUSG00000103092	18	36960440	37187657	1	20	8	22	151	24	3	0	0	0	0	0	Q91Y15	
ENSMUST00000192171						0	0	0	39	0	0	0	0	0	0	0		
ENSMUST00000192172	ENSMUSG00000027739	3	51483920	51496232	1	0	0	0	69	2	0	0	0	0	4	19	A0A0A6YY00	
ENSMUST00000192174						0	0	2	33	0	0	18	141	78	3	67		
ENSMUST00000192175						95	103	220	150	100	65	4	13	11	0	12		
ENSMUST00000192177						4	4	5	3	19	3	0	3	3	2	0		
ENSMUST00000192179						11	8	9	89	10	3	1	1	2	0	3		
ENSMUST00000192180						16	15	10	11	18	9	4	10	0	1	6		
ENSMUST00000192181						0	8	16	0	0	7	0	0	0	0	0		
ENSMUST00000192183						8	1	8	21	2	1	0	0	0	0	0		
ENSMUST00000192185	ENSMUSG00000040848	1	165174337	165194438	-1	24	10	6	0	5	9	889	50	1377	17	822	A0A0A6YX21	
ENSMUST00000192187						3	0	2	3	5	3	0	0	0	0	0		
ENSMUST00000192188	ENSMUSG00000076613	12	113302965	113307933	-1	15	13	39	25	21	4	1	1	0	2	10	A0A0A6YVP0	
ENSMUST00000192189	ENSMUSG00000079144	1	193168046	193177832	1	0	0	0	1	0	0	0	0	0	0	0	A0A0A6YY07	
ENSMUST00000192191						3	2	2	0	2	1	0	0	0	0	0		
ENSMUST00000192193	ENSMUSG00000025766	3	41742611	41803320	1	10	3	2	0	7	6	7	0	0	0	0		Q8BGN2
ENSMUST00000192194						18	18	44	21	17	19	4	14	5	1	9		
ENSMUST00000192195	ENSMUSG00000038179	1	171632403	171653035	-1	21	20	35	27	27	15	5	46	13	8	55		
ENSMUST00000192196						0	0	0	0	0	0	0	1	0	0	0		
ENSMUST00000192197	ENSMUSG00000063273	3	51415148	51476507	1	0	0	1	0	1	0	6	0	14	0	0	A0A0A6YX86	
ENSMUST00000192198						57	58	49	55	75	33	4	8	8	2	17		
ENSMUST00000192199						112	111	1152	118	97	68	9	22	7	3	9		
ENSMUST00000192200						1	1	0	3	3	0	0	0	0	0	0		
ENSMUST00000192202	ENSMUSG00000040329	3	7569994	7613760	-1	0	0	0	0	0	3	0	0	0	0	0	Q3UT18	
ENSMUST00000192203	ENSMUSG00000026527	1	175059087	175492500	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVV6	
ENSMUST00000192204	ENSMUSG00000093903	Y	13252442	13378804	1	18	6	0	6	0	10	0	0	0	0	0	J3QPX2	
ENSMUST00000192205						11	9	13	10	9	5	0	2	0	0	1		
ENSMUST00000192208						2	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000192209	ENSMUSG00000039717	3	13946393	14182287	1	0	2	3	0	1	1	0	0	0	0	0	A0A0A6YXQ8	
ENSMUST00000192210						4	1	0	79	3	1	2	3	2	1	0		
ENSMUST00000192211	ENSMUSG00000010064	9	107650634	107669530	-1	0	0	0	5	0	0	0	0	0	0	0	A0A0A6YWI8	
ENSMUST00000192214						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000192215	ENSMUSG00000040782	1	159232320	159347640	1	0	0	0	0	0	0	116	215	160	10	54	A0A0A6YVV7	
ENSMUST00000192220						3	4	3	52	10	6	3	5	3	0	9		
ENSMUST00000192221	ENSMUSG00000055421	14	93013410	93890679	-1	11	0	12	21	0	7	0	0	0	0	0	A0A0A6YY37	
ENSMUST00000192222	ENSMUSG00000037395	1	192098546	192138062	-1	6	6	8	4	3	6	7	20	4	3	23	A0A0A6YVU5	
ENSMUST00000192223						8	4	17	6	13	6	0	0	0	0	1		
ENSMUST00000192225						5	0	5	1	2	1	0	0	0	0	1		
ENSMUST00000192226	ENSMUSG00000032599	9	108783796	108806337	1	1	0	3	0	0	0	0	0	0	0	0	A0A0A6YVS3	
ENSMUST00000192227	ENSMUSG00000026527	1	175059087	175492500	-1	6	0	0	0	0	5	0	0	0	0	0		O54829
ENSMUST00000192230						17	5	29	22	18	5	2	4	2	0	6		
ENSMUST00000192231						7	10	31	14	13	10	1	0	0	0	1		
ENSMUST00000192233	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	0	0	0	0	0	0	0	12	29	5		
ENSMUST00000192235	ENSMUSG00000023473	9	108826320	108852969	1	0	0	0	156	0	0	0	2	29	0	32	A0A0A6YW76	
ENSMUST00000192236						2	4	3	1	4	2	0	0	0	0	0		
ENSMUST00000192237	ENSMUSG00000058407	1	37985189	37997893	-1	0	0	0	0	0	0	37	39	110	466	91	A0A0A6YWP9	
ENSMUST00000192239						98	93	129	89	79	40	3	30	11	4	11		
ENSMUST00000192240						9	9	24	12	19	5	1	0	1	2	2		
ENSMUST00000192241	ENSMUSG00000026822	2	32384633	32388252	-1	3	5	13	4	20	3	44	59	63	48	27	A0A0A6YW77	
ENSMUST00000192242						11	7	22	8	7	1	1	2	0	0	3		
ENSMUST00000192243						0	2	10	1	5	0	0	0	0	0	0		
ENSMUST00000192245						16	16	121	17	25	11	0	8	1	0	7		
ENSMUST00000192247						5	9	37	11	4	2	1	2	1	0	0		
ENSMUST00000192248	ENSMUSG00000026683	1	169497934	169531464	-1	5	0	3	1	2	0	0	0	0	0	0	A0A0A6YW74	
ENSMUST00000192249	ENSMUSG00000098375	CHR_MG3829_PATCH	88204388	88211507	1	0	0	0	1	0	0	32	87	48	44	25		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000192250	ENSMUSG00000104213	12	113406604	113416324	-1	2	0	0	0	0	0	4	0	11	0	20	A0A0A6YXD7	
ENSMUST00000192252						11	11	20	215	21	13	0	1	1	1	4		
ENSMUST00000192255						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192260						0	0	0	7	0	1	2	0	0	0	0		
ENSMUST00000192262						0	1	0	82	0	1	0	0	0	0	0		
ENSMUST00000192264	ENSMUSG00000095210	12	113736111	113736630	-1	0	0	0	2	0	0	0	0	0	0	0	A0A0A6YVS4	
ENSMUST00000192268						0	0	1	20	1	3	0	0	0	0	0		
ENSMUST00000192269	ENSMUSG00000026558	1	167222883	167285320	-1	0	0	0	3	0	0	5	0	2	0	0	A0A0A6YXW7	
ENSMUST00000192270						5	3	5	2	4	3	0	0	0	0	0		
ENSMUST00000192271	ENSMUSG00000034837	9	107674474	107679712	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWJ0	
ENSMUST00000192273						0	2	9	4	3	0	0	0	0	0	0		
ENSMUST00000192274						4	0	0	0	13	9	0	0	0	0	0		
ENSMUST00000192278						4	4	10	9	6	2	0	3	0	0	3		
ENSMUST00000192280						6	5	6	3	11	1	0	0	0	0	0		
ENSMUST00000192281						376	294	1455	430	435	235	12	44	28	5	61		
ENSMUST00000192283						49	34	192	102	76	17	0	0	3	0	4		
ENSMUST00000192284						15	15	16	5	10	10	0	7	7	13	14		
ENSMUST00000192286						63	67	151	96	79	35	6	29	23	1	23		
ENSMUST00000192287	ENSMUSG00000029108	5	57717967	58133230	1	4	5	5	0	0	2	0	0	0	0	0	A0A0A6YY48	
ENSMUST00000192288	ENSMUSG00000062691	17	78916500	78920306	1	2	0	3	76	2	0	1	1	0	0	0	A0A0A6YXB8	
ENSMUST00000192289	ENSMUSG00000033910	3	82092427	82145789	-1	1	2	0	0	3	0	0	0	0	1	0	A0A0A6YWB4	
ENSMUST00000192290						0	0	0	0	0	1	0	0	0	2	0		
ENSMUST00000192293						0	2	0	0	0	0	7	0	0	0	5		
ENSMUST00000192294						5	7	4	3	2	4	0	0	0	0	0		
ENSMUST00000192295	ENSMUSG00000104252	18	36952648	37187661	1	0	0	0	0	0	0	0	0	0	0	0		O88689
ENSMUST00000192298	ENSMUSG00000096355	12	115024026	115024459	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW26	
ENSMUST00000192300						5	7	17	4	4	0	7	4	11	0	6		
ENSMUST00000192302						4	0	82	4	6	9	0	0	0	0	0		
ENSMUST00000192305	ENSMUSG00000025651	9	108936633	108949623	1	1	0	6	2	0	1	0	2	2	0	6	A0A0A6YVZ0	
ENSMUST00000192306						0	2	14	216	10	0	0	0	0	0	0		
ENSMUST00000192307	ENSMUSG00000032599	9	108783796	108806337	1	0	0	0	44	6	1	6	6	15	11	17	A0A0A6YXT7	
ENSMUST00000192311						2	2	0	1	3	1	0	4	12	2	18		
ENSMUST00000192312	ENSMUSG00000026674	1	169972307	170110762	-1	0	0	1	0	2	0	0	0	0	0	2	A0A0A6YXY2	
ENSMUST00000192313						0	1	0	0	0	0	0	1	0	1	0		
ENSMUST00000192314	ENSMUSG00000041570	1	136268123	136346104	-1	0	8	0	10	23	16	9	0	94	11	78	A0A0A6YY67	
ENSMUST00000192315						0	1	2	0	0	1	0	0	0	0	0		
ENSMUST00000192318						28	0	38	62	7	0	0	0	0	0	0		
ENSMUST00000192319						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192322	ENSMUSG00000026639	1	193207699	193343878	1	1	0	0	0	0	0	0	0	0	0	0	A0A0A6YVX1	
ENSMUST00000192323	ENSMUSG00000010064	9	107650634	107669530	-1	3	0	6	2	6	3	0	0	0	0	0	A0A0A6YX60	
ENSMUST00000192324						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000192327						7	1	1	4	5	0	0	0	0	0	0		
ENSMUST00000192328	ENSMUSG00000027630	3	22076652	22216594	1	20	18	29	36	27	10	274	100	820	40	406		Q8BHJ5
ENSMUST00000192329						3	1	3	2	7	3	4	2	3	0	2		
ENSMUST00000192331						0	0	0	181	4	3	0	4	2	0	2		
ENSMUST00000192332						4	4	2	30	2	5	0	0	0	0	0		
ENSMUST00000192333						6	6	5	10	9	4	0	0	0	1	1		
ENSMUST00000192334						6	0	0	0	2	1	43	97	100	10	131		
ENSMUST00000192341	ENSMUSG00000027956	3	79812564	79852773	-1	1	0	0	0	0	1	1	0	0	0	0	A0A0A6YY58	
ENSMUST00000192343	ENSMUSG00000026594	1	156804166	156939626	-1	0	0	0	0	3	3	0	0	0	0	8	A0A0A6YXI6	
ENSMUST00000192344	ENSMUSG00000032601	9	108689314	108750436	1	2	0	3	0	1	3	0	0	0	0	0	A0A0A6YWE5	
ENSMUST00000192345	ENSMUSG00000026062	1	40680574	40769273	1	9	9	2	12	11	5	0	0	1	0	0	Q3TM63	
ENSMUST00000192352						5	2	1	0	3	1	0	0	0	0	0		
ENSMUST00000192355	ENSMUSG00000026074	1	39900913	40026310	1	0	0	0	0	0	0	9	0	0	0	0	A0A0A6YXE5	
ENSMUST00000192357	ENSMUSG00000026398	1	136842571	136960448	-1	4	0	17	0	0	0	0	0	0	0	0	A0A0A6YY04	
ENSMUST00000192358	ENSMUSG00000051509	1	174424126	174431552	1	0	4	22	10	0	3	1	0	0	0	0	E9Q5P8	
ENSMUST00000192359						6	6	24	1	8	3	3	5	9	3	7		
ENSMUST00000192360						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192364						0	3	0	1	0	0	0	0	0	0	0		
ENSMUST00000192365						0	1	14	0	9	1	18	38	20	16	41		
ENSMUST00000192366	ENSMUSG00000076485	6	41534323	41534376	1	0	0	0	1	0	0	2	1	0	6	0	A0A0A6YXA0	
ENSMUST00000192368						2	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000192369	ENSMUSG00000026564	1	166098148	166127922	-1	0	19	0	11	50	0	0	0	0	0	0		Q148W8
ENSMUST00000192370						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192372	ENSMUSG00000078657	3	93144787	93149819	1	3	0	9	0	0	0	0	0	0	0	0	A0A0A6YXA1	
ENSMUST00000192374						2	3	1	2	4	3	0	0	0	0	0		
ENSMUST00000192376						3	4	2	0	2	1	0	0	0	0	0		
ENSMUST00000192377						6	2	16	16	3	3	5	23	4	0	28		
ENSMUST00000192378						1	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000192382	ENSMUSG00000095028	3	15495751	15575065	-1	0	4	0	0	0	0	8	8	0	8	0	A0A0A6YXN8	
ENSMUST00000192383	ENSMUSG00000028182	3	155093434	155194280	1	4	6	13	7	4	2	0	0	0	0	0		Q14DL3
ENSMUST00000192384	ENSMUSG00000044835	1	161142691	161170498	1	0	0	0	7	2	0	0	0	0	0	0	A0A0A6YVY8	
ENSMUST00000192387	ENSMUSG00000064302	1	118389058	118612678	1	0	1	3	2	1	0	0	0	0	0	0	A0A0A6YWK1	
ENSMUST00000192392						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192393						4	1	12	4	8	2	0	0	0	0	0		
ENSMUST00000192394						12	19	37	12	14	12	34	27	90	8	118		
ENSMUST00000192395						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192400						0	0	9	10	6	4	0	0	0	0	0		
ENSMUST00000192401						3	4	10	45	1	8	38	90	110	13	48		
ENSMUST00000192403	ENSMUSG00000007653	11	42419757	42629028	1	0	3	3	0	2	0	0	0	0	0	0		P63137
ENSMUST00000192405						0	0	0	0	0	1	0	0	5	0	8		
ENSMUST00000192409	ENSMUSG00000073591	18	37517871	37524479	1	448	502	856	390	508	247	11	55	19	23	33	Q91XZ8	
ENSMUST00000192410	ENSMUSG00000026471	1	155127277	155146814	-1	0	0	0	0	2	0	0	10	7	1	0	A0A0A6YWB2	
ENSMUST00000192411						21	14	14	13	21	10	1	10	2	3	8		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000192412						2	2	1	3	2	1	0	0	0	0	0		
ENSMUST00000192414						81	74	208	92	76	42	4	40	14	3	29		
ENSMUST00000192415						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192419	ENSMUSG00000063273	3	51415148	51476507	1	0	0	1	55	0	0	0	0	0	0	0	A0A0A6YXF4	
ENSMUST00000192420						81	63	124	63	66	29	8	13	19	4	26		
ENSMUST00000192422						45	56	52	41	72	31	3	35	9	6	17		
ENSMUST00000192424						0	3	3	4	2	1	0	0	0	0	0		
ENSMUST00000192425						27	13	7	162	34	14	0	0	0	0	0		
ENSMUST00000192426	ENSMUSG00000040612	1	166254139	166316823	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXF0	
ENSMUST00000192428						201	217	767	230	197	105	32	130	72	8	125		
ENSMUST00000192429	ENSMUSG00000037610	3	31902507	32200180	1	0	0	0	0	0	0	0	0	0	0	0		Q9CZM9
ENSMUST00000192430						2	1	0	2	3	3	0	0	0	0	0		
ENSMUST00000192433						6	10	11	155	11	5	4	4	3	0	4		
ENSMUST00000192434						2	0	3	0	3	2	0	0	0	0	0		
ENSMUST00000192435						6	3	29	0	10	0	0	0	0	0	0		
ENSMUST00000192436	ENSMUSG00000040843	1	165212286	165236996	-1	0	2	2	30	0	0	83	334	92	29	18	A0A0A6YWU8	
ENSMUST00000192438	ENSMUSG00000040774	3	106502260	106547802	-1	0	0	0	0	0	0	0	0	26	0	4	A0A0A6YXR0	
ENSMUST00000192439						2	1	3	3	4	3	0	0	0	0	0		
ENSMUST00000192442						0	1	4	35	3	1	31	119	68	375	42		
ENSMUST00000192445						3	0	9	2	7	7	4	5	0	1	2		
ENSMUST00000192447	ENSMUSG00000102206	18	37010712	37187657	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY44	
ENSMUST00000192449						4	1	0	3	4	0	0	0	0	0	0		
ENSMUST00000192450						2	1	4	3	3	3	0	0	0	0	0		
ENSMUST00000192451	ENSMUSG00000025764	3	41555731	41616864	1	0	0	0	0	0	0	0	0	3	0	0	A0A0A6YXU2	
ENSMUST00000192453						5	3	0	4	2	2	0	0	0	0	0		
ENSMUST00000192454						2	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000192455						0	4	2	1	2	4	0	0	0	0	3		
ENSMUST00000192456						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192457	ENSMUSG00000015829	1	159523769	159931729	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWD9	
ENSMUST00000192458						115	120	247	107	104	37	1	6	11	4	11		
ENSMUST00000192460	ENSMUSG00000026547	1	172500047	172507380	1	0	0	0	0	0	0	20	2	10	0	9	A0A0A6YXG6	
ENSMUST00000192461						2	1	0	1	1	0	0	4	4	0	3		
ENSMUST00000192462	ENSMUSG00000028199	3	154596711	154623182	1	4	10	19	82	15	6	14	39	21	20	15		P47199
ENSMUST00000192463	ENSMUSG00000033981	3	80681450	80802835	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW90	
ENSMUST00000192465	ENSMUSG00000103421	1	133309800	133323026	1	0	2	9	0	4	0	1	0	0	0	0	A0A0A6YXE9	
ENSMUST00000192466						2	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000192467						23	18	23	12	28	21	3	15	2	3	7		
ENSMUST00000192468	ENSMUSG00000027499	3	7366669	7445366	1	0	2	0	22	3	1	0	0	0	0	0	A0A0A6YXS7	
ENSMUST00000192470	ENSMUSG00000039449	2	4622058	4652113	-1	1	0	1	57	5	2	0	0	0	0	0	A0A0A6YW97	
ENSMUST00000192471						4	4	1	0	4	2	0	0	0	0	0		
ENSMUST00000192474						3	1	1	11	3	0	0	0	10	0	5		
ENSMUST00000192475						8	1	3	3	2	0	0	0	0	0	0		
ENSMUST00000192476						0	2	5	1	1	0	0	0	0	0	0		
ENSMUST00000192477	ENSMUSG00000048304	3	73047265	73057803	-1	31	17	109	49	20	26	0	0	0	0	0		Q810B9
ENSMUST00000192481						4	1	0	0	5	0	0	8	0	0	3		
ENSMUST00000192483						25	17	51	265	29	14	2	1	0	0	2		
ENSMUST00000192485						1	1	1	0	0	0	2	0	0	0	0		
ENSMUST00000192488	ENSMUSG00000103326	_MMCHR1_CHORI29_IDI	60935411	60942198	1	8	6	2	1	17	2	1	24	11	33	55		
ENSMUST00000192489						0	0	9	0	1	5	257	514	142	37	142		
ENSMUST00000192491	ENSMUSG00000037395	1	192098546	192138062	-1	6	0	8	4	3	0	0	0	0	2	0	A0A0A6YWY4	
ENSMUST00000192492						8	0	5	7	5	3	0	0	0	0	0		
ENSMUST00000192494						6	6	6	4	6	1	0	0	0	0	0		
ENSMUST00000192495	ENSMUSG00000041355	3	88575876	88588419	1	4	4	0	1	0	3	0	12	0	0	15	A0A0A6YXB7	
ENSMUST00000192497						0	4	1	0	1	0	0	0	0	0	0		
ENSMUST00000192499	ENSMUSG00000076668	12	114222788	114223328	-1	0	0	4	0	0	0	1	0	0	2	1	A0A0A6YXL5	
ENSMUST00000192503	ENSMUSG00000102312	18	36946105	37187657	1	20	19	31	157	18	7	0	0	0	0	0	Q91Y16	
ENSMUST00000192505						3	6	13	111	9	2	0	0	0	0	0		
ENSMUST00000192506						24	30	90	43	46	16	200	576	236	54	296		
ENSMUST00000192507	ENSMUSG00000023259	9	108853283	108913049	1	14	20	21	69	30	9	29	25	13	0	47	A0A087WS07	
ENSMUST00000192508						1	0	0	2	1	1	0	0	0	2	0		
ENSMUST00000192509	ENSMUSG00000026074	1	39900913	40026310	1	0	0	0	0	0	0	195	72	361	0	248	A0A0A6YWR8	
ENSMUST00000192510						10	3	9	8	5	5	0	0	0	0	0		
ENSMUST00000192511	ENSMUSG00000103472	18	37714764	37841873	1	4	8	5	11	4	0	0	0	0	2	4	Q6DD96	
ENSMUST00000192512	ENSMUSG00000104252	18	36952648	37187661	1	0	0	0	0	0	0	0	0	0	0	0		O88689
ENSMUST00000192518	ENSMUSG00000019039	9	108569886	108572774	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXN1	
ENSMUST00000192519						0	2	2	3	0	1	0	3	0	0	0		
ENSMUST00000192520						0	1	8	3	0	0	0	0	0	0	0		
ENSMUST00000192521	ENSMUSG00000103528	Y	22025164	22051353	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WP44	
ENSMUST00000192522						4	2	5	18	7	0	0	0	0	0	0		
ENSMUST00000192523						0	0	0	8	1	0	2	0	0	0	0		
ENSMUST00000192527	ENSMUSG00000053461	1	183418215	183436808	1	1	9	36	19	14	0	0	3	0	0	0		Q9D2G9
ENSMUST00000192529						1	1	6	3	2	1	0	0	0	0	0		
ENSMUST00000192530						7	0	11	35	3	7	8	0	7	0	0		
ENSMUST00000192531	ENSMUSG00000003134	1	39371492	39478755	-1	5	0	19	0	10	0	574	0	731	0	354	A0A0A6YXU3	
ENSMUST00000192532	ENSMUSG00000073406	17	36080115	36084223	-1	0	1	0	0	0	0	151	139	95	40	152		
ENSMUST00000192535	ENSMUSG00000103749	18	37731009	37841873	1	3	0	0	4	0	0	0	0	5	0	1	Q91XX5	
ENSMUST00000192538	ENSMUSG00000042165	3	92428032	92429423	-1	17	4	35	203	17	7	0	0	0	0	8	A0A0A6YVU8	
ENSMUST00000192539	ENSMUSG00000098571	CHR_MG3829_PATCH	88098058	88194140	1	6	2	33	167	11	5	0	0	11	6	30		
ENSMUST00000192544	ENSMUSG00000047539	1	182313102	182341629	-1	2	0	2	0	0	0	79	26	161	19	65	A0A0A6YX52	
ENSMUST00000192547						14	16	29	34	30	14	0	4	0	0	0		
ENSMUST00000192548						20	29	31	35	17	5	151	611	368	445	339		
ENSMUST00000192550						0	0	2	79	2	2	0	0	0	0	0		
ENSMUST00000192551						22	22	60	120	32	31	0	4	7	0	6		
ENSMUST00000192553						5	3	13	8	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000192554	ENSMUSG00000095204	12	115145487	115145919	-1	6	3	17	8	0	0	3	4	6	6	9	A0A0A6YXC3	
ENSMUST00000192555	ENSMUSG00000027777	3	68064802	68626481	1	5	0	4	281	1	0	0	0	0	0	4	A0A0A6YXQ5	
ENSMUST00000192557	ENSMUSG00000050505	14	88464743	88471396	-1	8	8	13	27	17	12	0	0	0	0	0		Q8BIZ0
ENSMUST00000192558						1	2	0	2	2	1	0	0	0	0	0		
ENSMUST00000192559	ENSMUSG00000023259	9	108853283	108913049	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWP3	
ENSMUST00000192561	ENSMUSG00000058729	1	180641150	180690694	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVZ7	
ENSMUST00000192564						0	0	0	0	0	0	0	1	1	1	3		
ENSMUST00000192565	ENSMUSG00000040848	1	165174337	165194438	-1	1	4	5	17	5	2	0	5	5	0	18	A0A0A6YY20	
ENSMUST00000192566						45	30	126	212	57	44	52	90	175	19	289		
ENSMUST00000192567						17	6	17	18	13	9	1	0	1	1	0		
ENSMUST00000192570	ENSMUSG00000040297	1	161816114	161876682	-1	0	0	0	0	0	0	2	22	15	0	1	A0A0A6YX94	
ENSMUST00000192573						3	8	6	2	3	4	0	10	2	0	5		
ENSMUST00000192575						0	0	0	0	0	0	0	6	5	0	2		
ENSMUST00000192577						8	11	10	9	7	3	0	0	0	0	0		
ENSMUST00000192578						6	10	22	19	17	9	4	0	8	0	15		
ENSMUST00000192584	ENSMUSG00000039542	9	49502136	49798925	-1	6	2	5	3	9	1	0	0	0	0	0	A0A0A6YWU2	
ENSMUST00000192585	ENSMUSG00000037375	1	192496711	192771223	-1	1	0	0	11	1	0	0	0	0	0	0	A0A0A6YWJ4	
ENSMUST00000192587						4	0	0	5	1	0	0	0	0	0	0		
ENSMUST00000192588						15	7	21	164	8	6	0	1	0	0	0		
ENSMUST00000192591	ENSMUSG00000104452	12	115294062	115294504	-1	10	7	25	7	17	14	0	0	0	1	6	A0A0A6YXQ0	
ENSMUST00000192594	ENSMUSG00000026082	1	38052786	38129801	-1	2	2	0	1	0	0	0	0	0	0	3	A0A0A6YW35	
ENSMUST00000192595	ENSMUSG00000033900	3	82358044	82395268	1	0	3	4	56	0	2	1	0	1	0	0		
ENSMUST00000192597						19	12	19	8	9	7	2	12	5	2	5		
ENSMUST00000192598						2	2	4	100	8	4	0	0	0	0	0		
ENSMUST00000192599						2	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192603	ENSMUSG00000103392	3	10321712	10335681	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWW8	
ENSMUST00000192604						8	0	9	6	4	1	0	0	0	0	3		
ENSMUST00000192606						0	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000192607	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	0	0	30	0	0	0	0		Q9JKP5
ENSMUST00000192608						7	5	9	4	11	4	0	4	8	0	0		
ENSMUST00000192609	ENSMUSG00000027562	3	14886273	14900770	1	3	0	5	63	0	0	0	4	0	0	0	A0A0A6YX78	
ENSMUST00000192610						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000192611						24	27	41	26	37	11	4	13	5	1	3		
ENSMUST00000192615	ENSMUSG00000032562	9	107614125	107635367	-1	2	0	0	3	0	0	2270	3835	1384	124	1109		P08752
ENSMUST00000192616						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192619						0	0	1	0	0	2	0	0	0	0	0		
ENSMUST00000192620						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192621						6	10	13	9	9	4	0	0	0	0	0		
ENSMUST00000192623						4	5	1	3	4	0	0	0	0	0	2		
ENSMUST00000192627						0	0	0	0	0	0	0	0	0	0	14		
ENSMUST00000192628	ENSMUSG00000026637	1	191997205	192092559	-1	0	0	0	0	0	0	7	53	10	2	27	A0A0A6YWK3	
ENSMUST00000192630	ENSMUSG00000103879	CHR_MG184_PATCH	72304610	72314372	1	8	9	37	22	19	0	0	7	0	0	0		P50405
ENSMUST00000192631	ENSMUSG00000104318	18	36973802	37187657	1	14	10	22	81	27	14	0	0	0	0	0	Q91Y13	
ENSMUST00000192633						2	1	2	0	2	0	0	0	0	0	0		
ENSMUST00000192637						8	4	2	7	20	9	1	0	0	1	1		
ENSMUST00000192638	ENSMUSG00000040612	1	166254139	166316823	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY76	
ENSMUST00000192639	ENSMUSG00000026701	1	161240112	161251219	-1	0	5	0	10	5	6	733	1240	470	102	274	A0A0A6YXQ7	
ENSMUST00000192641						3	7	20	14	4	4	0	4	0	1	0		
ENSMUST00000192643						3	0	0	1	1	0	0	2	6	0	0		
ENSMUST00000192645						49	65	124	41	57	18	5	11	5	4	12		
ENSMUST00000192649						5	5	4	0	4	4	0	0	0	0	0		
ENSMUST00000192650	ENSMUSG00000025902	1	4490931	4497354	-1	7	11	17	36	15	23	0	0	0	0	0	A0A0A6YXS3	
ENSMUST00000192651						1	2	7	0	0	2	11	51	18	0	29		
ENSMUST00000192653						0	4	10	6	4	3	2	3	2	1	4		
ENSMUST00000192657	ENSMUSG00000026620	1	184896789	184999570	-1	3	2	2	4	2	2	0	0	0	0	0	A0A0A6YY78	
ENSMUST00000192659						0	0	4	0	3	1	31	201	12	0	0		
ENSMUST00000192664	ENSMUSG00000057335	1	176733653	176814067	-1	0	0	3	2	5	7	4	19	10	6	5	A0A0A6YVZ3	
ENSMUST00000192665						3	3	25	7	4	6	0	0	0	0	0		
ENSMUST00000192666	ENSMUSG00000066595	1	191005847	191026158	-1	7	0	24	1	17	8	25	79	92	14	63	A0A0A6YXG8	
ENSMUST00000192667						4	0	2	4	5	1	0	0	0	0	0		
ENSMUST00000192670						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192671	ENSMUSG00000038599	1	182565007	182632352	1	0	0	2	15	11	0	0	1	0	0	0	A0A0A6YVU9	
ENSMUST00000192672						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192675						0	4	0	6	5	3	0	0	0	0	0		
ENSMUST00000192677	ENSMUSG00000034755	X	120290259	120910619	1	0	6	0	0	0	0	0	0	0	0	0	F6ZNL5	
ENSMUST00000192678	ENSMUSG00000032598	9	108808368	108818844	1	0	0	0	0	0	0	2	0	0	2	0	A0A0A6YX64	
ENSMUST00000192681						1	2	5	4	2	2	5	0	1	0	8		
ENSMUST00000192683	ENSMUSG00000104191	Y	14400710	14426798	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRL2	
ENSMUST00000192685						32	30	174	61	24	35	0	2	0	0	0		
ENSMUST00000192686						0	0	0	0	0	0	0	0	3	1	0		
ENSMUST00000192687						0	0	0	0	5	0	0	0	0	0	0		
ENSMUST00000192688	ENSMUSG00000041355	3	88575876	88588419	1	0	0	0	0	3	1	0	3	0	0	0	A0A0A6YWA8	
ENSMUST00000192690	ENSMUSG00000026470	1	155158715	155208256	1	6	1	7	4	3	1	0	2	0	0	0	A0A0A6YW23	
ENSMUST00000192695						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000192696						2	1	9	0	1	2	0	0	0	0	0		
ENSMUST00000192697						4	2	10	0	0	0	0	10	2	0	0		
ENSMUST00000192698	ENSMUSG00000033793	1	5070018	5162529	1	0	0	0	0	0	0	104	377	153	37	105	A0A0A6YX18	
ENSMUST00000192699	ENSMUSG00000063659	1	177442351	177450764	1	2	1	9	9	4	0	0	0	3	0	7		
ENSMUST00000192700	ENSMUSG00000095788	3	15371653	15426520	-1	0	0	0	0	2	0	620	5091	1236	4055	814	Q6F5F2	
ENSMUST00000192702	ENSMUSG00000026558	1	167222883	167285320	-1	0	2	8	0	0	0	0	0	9	18	0	A0A0A6YVQ3	
ENSMUST00000192704	ENSMUSG00000026554	1	172148084	172197005	1	2	0	0	31	2	0	126	153	225	100	283		Q8N7N5
ENSMUST00000192708						0	0	5	0	0	0	0	0	0	0	0		
ENSMUST00000192709						48	23	125	93	38	14	0	0	0	0	1		
ENSMUST00000192710						0	0	0	0	0	0	2	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000192712						3	0	18	1	0	2	1	0	0	0	2		
ENSMUST00000192714						0	0	0	0	0	0	0	0	15	1	0		
ENSMUST00000192715	ENSMUSG00000037730	3	30602065	30619873	1	11	7	35	76	21	13	0	22	10	9	14		Q99MD8
ENSMUST00000192716						0	5	4	0	7	1	0	0	0	0	0		
ENSMUST00000192718						7	6	11	2	2	5	0	0	0	0	0		
ENSMUST00000192719						0	3	1	0	4	0	0	0	0	0	5		
ENSMUST00000192723	ENSMUSG00000037624	1	189207930	189402273	-1	0	1	2	14	0	0	0	0	0	0	0		P97438
ENSMUST00000192724	ENSMUSG00000076710	12	115055223	115055656	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWX2	
ENSMUST00000192725	ENSMUSG00000058729	1	180641150	180690694	1	0	0	0	0	0	0	0	0	0	0	27	A0A0A6YWD3	
ENSMUST00000192726						4	1	0	2	1	3	5	68	5	6	7		
ENSMUST00000192727	ENSMUSG00000034684	9	107681500	107710475	-1	0	0	5	54	4	4	0	0	0	0	20		O88632
ENSMUST00000192729						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192730	ENSMUSG00000033701	1	155558120	155691330	1	0	0	0	0	0	0	6	9	1	1	3	A0A0A6YWZ1	
ENSMUST00000192731						0	0	0	0	0	2	0	1	0	0	0		
ENSMUST00000192732	ENSMUSG00000040612	1	166254139	166316823	1	0	0	0	39	0	0	0	0	0	0	0	A0A0A6YWD2	
ENSMUST00000192734						2	2	0	0	1	2	0	0	0	0	0		
ENSMUST00000192737						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192738						5	3	16	28	10	5	0	0	0	0	0		
ENSMUST00000192744						2	2	4	7	2	3	0	0	0	0	0		
ENSMUST00000192746	ENSMUSG00000076620	12	113429468	113429567	-1	0	0	0	0	0	0	2	4	1	4	35	A0A0A6YWJ8	
ENSMUST00000192747						0	0	1	2	2	0	0	0	0	0	0		
ENSMUST00000192749	ENSMUSG00000103468	Y	13252391	13254834	1	0	8	0	3	0	3	0	0	0	0	0	Q3TTD8	
ENSMUST00000192750						0	0	2	3	2	0	7	21	12	0	10		
ENSMUST00000192755						2	8	3	0	3	0	0	0	0	0	0		
ENSMUST00000192757	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	0	0	2	3	40	35	14	A0A0A6YXL7	
ENSMUST00000192758						17	10	33	33	27	7	83	242	157	0	123		
ENSMUST00000192761						6	1	5	5	5	5	0	0	0	0	0		
ENSMUST00000192762	ENSMUSG00000040782	1	159232320	159347640	1	0	0	2	6	0	0	99	670	345	6	99	A0A0A6YXK6	
ENSMUST00000192764						0	2	1	0	0	0	0	0	0	0	0		
ENSMUST00000192765						4	3	5	3	2	2	14	16	8	0	5		
ENSMUST00000192768						11	15	20	15	25	13	1	1	9	0	11		
ENSMUST00000192769						0	0	0	2	0	0	1	0	0	2	4		
ENSMUST00000192770						0	0	0	1	2	2	0	0	0	0	0		
ENSMUST00000192771						1	2	4	4	2	1	0	0	0	0	0		
ENSMUST00000192773	ENSMUSG00000028078	3	86786151	86920852	-1	16	13	66	13	26	18	3	3	9	0	12	A0A0A6YWI6	
ENSMUST00000192774						5	7	16	145	27	7	0	0	0	0	0		
ENSMUST00000192775						1	2	2	7	1	0	61	36	58	14	66		
ENSMUST00000192776						8	4	12	0	6	0	111	153	170	13	67		
ENSMUST00000192779						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000192783	ENSMUSG00000034684	9	107681500	107710475	-1	0	0	0	0	0	0	0	0	0	0	2	A0A0A6YWS0	
ENSMUST00000192784						0	3	10	6	7	3	0	0	0	0	0		
ENSMUST00000192787						5	1	1	4	3	0	0	0	0	1	1		
ENSMUST00000192788						5	0	5	2	0	0	6	0	30	0	28		
ENSMUST00000192789						23	38	511	51	18	18	4	3	2	3	2		
ENSMUST00000192792						4	5	1	1	1	5	0	0	0	0	0		
ENSMUST00000192793	ENSMUSG00000090919	3	46442197	46448219	-1	0	15	0	21	0	0	0	0	0	0	0	G5E8X2	
ENSMUST00000192795						0	3	0	0	0	1	0	0	0	0	0		
ENSMUST00000192796						1	4	13	4	4	0	0	0	0	1	0		
ENSMUST00000192799						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192801	ENSMUSG00000091537	9	109074568	109082587	-1	1	2	1	1	2	1	0	0	0	0	0	A0A0A6YXZ5	
ENSMUST00000192802						2	3	4	1	8	1	0	0	0	0	0		
ENSMUST00000192804						2	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000192807	ENSMUSG00000027763	3	60472830	60629750	1	6	0	1	0	0	0	230	0	132	108	34	Q3U581	
ENSMUST00000192809						2	3	22	3	6	0	0	2	0	4	0		
ENSMUST00000192810						2	1	2	1	0	0	0	0	0	0	1		
ENSMUST00000192811						3	2	17	442	9	3	20	9	23	3	14		
ENSMUST00000192812						3	0	7	2	3	2	0	69	18	19	17		
ENSMUST00000192815	ENSMUSG00000102412	._MMCHR1_CHORI29_IDI	60745208	60769374	1	0	2	11	8	3	6	0	0	3	0	0		
ENSMUST00000192817						3	2	1	3	4	0	0	0	0	0	0		
ENSMUST00000192818						3	2	0	7	2	0	0	0	0	0	0		
ENSMUST00000192819	ENSMUSG00000006673	9	108516806	108560163	1	0	0	0	0	0	0	3	1	18	0	12	A0A0A6YXK2	
ENSMUST00000192821	ENSMUSG00000026587	1	158362273	158691781	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVT7	
ENSMUST00000192823						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000192825						1	2	4	2	4	4	0	0	0	0	0		
ENSMUST00000192827						0	0	3	123	2	4	7	0	5	0	11		
ENSMUST00000192829	ENSMUSG00000046836	1	183276352	183297269	-1	8	6	19	6	11	4	2	9	2	2	7	A0A0A6YWK4	
ENSMUST00000192830						3	1	4	2	2	0	0	0	0	0	0		
ENSMUST00000192831						4	1	2	5	6	1	0	0	0	0	0		
ENSMUST00000192832						12	6	10	13	10	4	0	3	0	0	3		
ENSMUST00000192834						1	1	2	2	0	0	0	0	0	0	0		
ENSMUST00000192835						1	0	0	0	0	0	0	1	1	7	0		
ENSMUST00000192837	ENSMUSG00000032562	9	107614125	107635367	-1	0	0	1	11	0	0	0	5	3	0	8	A0A0A6YXC2	
ENSMUST00000192838						0	5	4	1	2	0	0	0	0	0	1		
ENSMUST00000192840						4	7	5	3	5	2	0	0	0	0	0		
ENSMUST00000192841						0	6	3	5	4	0	86	697	109	18	45		
ENSMUST00000192844						8	3	19	22	13	0	15	43	93	3	56		
ENSMUST00000192847	ENSMUSG00000033793	1	5070018	5162529	1	0	0	0	0	0	0	36	32	21	0	27	A0A0A6YWP6	
ENSMUST00000192848						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192849						4	1	2	4	8	0	0	0	0	0	0		
ENSMUST00000192850	ENSMUSG00000026708	1	161070713	161086724	1	0	0	0	0	0	0	0	0	0	0	35	Q05CX4	
ENSMUST00000192851	ENSMUSG00000063659	1	177442351	177450764	1	0	0	0	0	0	0	0	0	26	0	26	A0A0A6YY33	
ENSMUST00000192852	ENSMUSG00000025652	9	108914619	108915563	1	5	0	2	19	8	13	1	3	0	0	0		Q9DA04
ENSMUST00000192853						0	0	1	0	0	0	3	18	9	0	0		
ENSMUST00000192854						46	46	373	86	39	25	48	22	16	3	125		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000192855						7	4	12	1	9	3	0	0	0	0	0		
ENSMUST00000192856	ENSMUSG00000076490	6	41538218	41539881	1	0	0	0	0	3	3	31	120	6	92	39	A0A0A6YWV4	
ENSMUST00000192857						3	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000192859						2	2	5	6	4	1	3	7	11	6	6		
ENSMUST00000192866	ENSMUSG00000037395	1	192098546	192138062	-1	0	0	0	3	0	0	0	0	19	0	1	A0A0A6YXM5	
ENSMUST00000192867	ENSMUSG00000045876	18	37355121	37358604	1	0	0	0	0	3	0	0	0	0	0	0	A0A0A6YX31	
ENSMUST00000192869	ENSMUSG00000102671	CHR_MG184_PATCH	72368793	72380467	-1	0	15	22	15	0	7	209	284	125	137	110	Q791P0	Q9Z2P8
ENSMUST00000192870	ENSMUSG00000037957	12	110737944	110804238	1	0	0	0	0	0	0	6	0	5	8	13	A0A0A6YX87	
ENSMUST00000192872						5	0	14	3	3	4	0	0	0	0	0		
ENSMUST00000192874						100	84	143	262	142	80	72	166	195	17	311		
ENSMUST00000192875						35	34	52	154	76	28	0	1	0	0	0		
ENSMUST00000192876						6	8	0	0	2	0	0	6	0	0	1		
ENSMUST00000192877	ENSMUSG00000094134	12	113826646	113827129	-1	0	2	9	0	0	0	0	0	0	0	0	A0A0A6YWC7	
ENSMUST00000192878						0	0	0	2	0	0	0	0	0	0	0		
ENSMUST00000192880	ENSMUSG00000026365	1	140084708	140183764	-1	0	3	2	4	3	0	0	0	0	0	0	A0A0A6YVP8	
ENSMUST00000192882						9	4	29	148	26	15	2	1	0	0	1		
ENSMUST00000192883						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192884						4	4	22	7	4	3	6	28	14	2	29		
ENSMUST00000192886	ENSMUSG00000039461	9	108302958	108306160	-1	0	0	3	45	0	0	70	52	67	11	31	A0A0A6YXI4	
ENSMUST00000192887	ENSMUSG00000010047	9	107567945	107572779	1	0	0	0	0	2	0	1	0	0	0	0	A0A0A6YXZ3	
ENSMUST00000192888						2	2	1	3	0	2	0	0	0	0	1		
ENSMUST00000192890						41	26	44	34	22	19	6	12	3	0	6		
ENSMUST00000192892	ENSMUSG00000103919	Y	22835086	22861256	-1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRK1	
ENSMUST00000192893						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192899						10	6	15	112	25	6	4	37	8	1	8		
ENSMUST00000192901						0	0	0	7	5	1	0	0	0	0	1		
ENSMUST00000192903						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192905						0	0	1	1	2	0	3	35	10	16	2		
ENSMUST00000192906						2	4	2	2	0	0	0	0	0	0	0		
ENSMUST00000192907						1	2	3	5	8	0	0	0	0	0	0		
ENSMUST00000192909	ENSMUSG00000028066	3	88394143	88410331	-1	3	0	1	3	0	0	0	0	0	0	0	A0A0A6YVR2	
ENSMUST00000192911	ENSMUSG00000076646	12	113796138	113796567	-1	0	0	0	0	0	0	0	0	0	0	10	A0A0A6YWY9	
ENSMUST00000192912						0	1	0	0	1	0	0	0	0	0	0		
ENSMUST00000192913	ENSMUSG00000025902	1	4490931	4497354	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWS4	
ENSMUST00000192915						6	7	11	1	9	0	8	10	0	5	7		
ENSMUST00000192916						0	0	2	1	0	0	0	11	4	0	10		
ENSMUST00000192918						1	0	27	2	3	0	1	20	1	4	12		
ENSMUST00000192919	ENSMUSG00000026365	1	140084708	140183764	-1	0	0	0	0	0	0	0	0	0	17	0	A0A0A6YWP4	
ENSMUST00000192923						14	2	2	1	15	1	0	0	0	0	0		
ENSMUST00000192927	ENSMUSG00000057335	1	176733653	176814067	-1	7	0	15	0	0	1	0	165	0	11	24	A0A0A6YXK7	
ENSMUST00000192929	ENSMUSG00000026398	1	136842571	136960448	-1	0	5	0	5	9	2	1	0	1	0	0	Q1WLP7	
ENSMUST00000192931	ENSMUSG00000103037	18	37680233	37841870	1	0	10	0	0	5	0	0	0	0	0	2	Q91XX8	
ENSMUST00000192932	ENSMUSG00000006673	9	108516806	108560163	1	0	0	0	0	0	0	0	0	3	2	0	A0A0A6YVQ2	
ENSMUST00000192933						1	1	4	0	0	1	0	0	0	0	0		
ENSMUST00000192934						24	16	65	35	35	21	9	49	16	0	21		
ENSMUST00000192935						0	3	15	6	0	0	2	6	5	6	5		
ENSMUST00000192937	ENSMUSG00000103906	15	75909735	75914535	1	36	24	66	95	44	25	14	8	8	0	12		Q499M4
ENSMUST00000192938						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192939						0	0	0	0	0	0	0	0	6	0	0		
ENSMUST00000192944						5	0	0	3	8	0	0	0	0	0	0		
ENSMUST00000192945						3	2	5	3	2	1	0	0	0	0	0		
ENSMUST00000192946						0	1	7	2	1	1	0	0	0	0	0		
ENSMUST00000192948	ENSMUSG00000026080	1	38863867	38898161	-1	0	0	0	0	2	1	0	0	2	0	0	A0A0A6YWA7	
ENSMUST00000192949	ENSMUSG00000026773	2	11471433	11554077	-1	7	0	29	442	43	30	324	2350	695	37	273	A0A0A6YY64	
ENSMUST00000192950						1	0	4	45	4	6	0	0	0	0	0		
ENSMUST00000192951						4	4	26	5	6	2	2	4	0	0	2		
ENSMUST00000192954						1	0	0	36	0	0	0	0	0	3	0		
ENSMUST00000192955						4	2	3	5	0	1	0	0	0	0	0		
ENSMUST00000192956	ENSMUSG00000062729	1	171275990	171281186	-1	0	1	8	0	0	0	24	152	1	5	105	A0A0A6YX50	
ENSMUST00000192959						3	0	0	9	0	0	1	1	2	0	0		
ENSMUST00000192960	ENSMUSG00000058407	1	37985189	37997893	-1	0	0	0	0	0	0	35	194	60	229	13	A0A0A6YVV3	
ENSMUST00000192961	ENSMUSG00000057335	1	176733653	176814067	-1	6	2	2	75	7	6	0	5	7	0	0		Q6A065
ENSMUST00000192962	ENSMUSG00000008604	3	88553758	88569725	1	1	0	0	29	1	0	0	0	0	0	0	A0A0A6YXU5	
ENSMUST00000192964						2	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000192967	ENSMUSG00000022995	1	181896384	182019990	-1	0	1	0	25	2	2	7	1	4	0	4	A0A0A6YVZ6	
ENSMUST00000192969	ENSMUSG00000001143	1	36419871	36445271	-1	1	0	3	0	0	3	13	11	10	0	11	A0A0A6YX25	
ENSMUST00000192971	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	0	0	0	0	0	0	0	0	2	0	12		
ENSMUST00000192975						0	2	11	2	8	1	0	0	0	0	2		
ENSMUST00000192977						6	8	9	30	5	5	0	0	1	0	0		
ENSMUST00000192980	ENSMUSG00000103205	CHR_MG184_PATCH	72385222	72390702	-1	3	2	1	8	6	2	1445	2641	840	4383	550		
ENSMUST00000192985	ENSMUSG00000027667	3	32510259	32520833	1	0	0	0	0	0	0	0	1	0	1	0	A0A0A6YWH9	
ENSMUST00000192986						10	8	21	8	14	2	0	0	0	0	0		
ENSMUST00000192987						0	1	0	0	0	0	0	0	1	2	1		
ENSMUST00000192988	ENSMUSG00000053646	9	109095389	109119917	1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDM9	
ENSMUST00000192989						0	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000192990	ENSMUSG00000010064	9	107650634	107669530	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWF5	
ENSMUST00000192991	ENSMUSG00000057335	1	176733653	176814067	-1	0	0	0	0	0	0	0	62	0	0	0	A0A0A6YX99	
ENSMUST00000192992						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000192995	ENSMUSG00000032611	9	108392805	108410934	1	1	4	0	9	0	0	3	0	1	0	6	A0A0A6YWI5	
ENSMUST00000192998	ENSMUSG00000039254	2	32236590	32255005	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXZ7	
ENSMUST00000193000						0	1	8	27	3	1	0	0	0	0	0		
ENSMUST00000193002	ENSMUSG00000059146	7	78175959	78738012	-1	0	8	0	0	0	7	0	0	1	0	2	A0A0A6YWF9	
ENSMUST00000193003	ENSMUSG00000076499	6	41557691	41558452	-1	1	6	2	5	5	5	4	5	0	5	5	A0A0A6YW81	
ENSMUST00000193005						3	4	3	6	4	8	3	31	0	0	8		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193006						12	18	25	43	32	14	4	3	2	1	2		
ENSMUST00000193007						0	3	1	1	0	1	0	2	0	0	0		
ENSMUST00000193008						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000193010	ENSMUSG00000043542	3	7503483	7553836	1	0	3	2	0	0	2	0	3	0	14	5		Q8BJH1
ENSMUST00000193011						3	4	1	0	4	1	0	0	0	0	0		
ENSMUST00000193012	ENSMUSG00000103203	12	113469189	113469217	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0G2JDD5	
ENSMUST00000193013						4	4	0	1	2	0	0	1	0	0	0		
ENSMUST00000193016						8	6	0	3	0	0	0	0	0	0	0		
ENSMUST00000193017	ENSMUSG00000005339	1	173221284	173227214	-1	0	6	3	0	5	0	0	32	14	0	0	A0A0A6YXC5	
ENSMUST00000193018	ENSMUSG00000023087	3	51224447	51251644	1	0	87	0	268	396	151	227	1892	658	660	668	A0A0A6YY01	
ENSMUST00000193020	ENSMUSG00000026602	1	156310727	156328035	1	5	0	1	5	0	8	0	0	0	0	0	A0A0A6YVZ4	
ENSMUST00000193023	ENSMUSG00000026566	1	165592240	165634538	-1	0	1	0	99	0	0	0	0	0	0	0	A0A0A6YWA2	
ENSMUST00000193024						29	24	74	172	21	21	4	72	14	9	22		
ENSMUST00000193025						4	5	22	2	4	0	0	0	0	0	0		
ENSMUST00000193028	ENSMUSG00000004880	1	181815335	181843046	-1	0	1	6	0	0	0	9	14	19	3	4	A0A0A6YWS3	
ENSMUST00000193029						13	7	75	21	21	8	2	5	2	0	4		
ENSMUST00000193030	ENSMUSG00000004880	1	181815335	181843046	-1	0	0	3	12	1	0	34	29	164	13	74	A0A0A6YW01	
ENSMUST00000193031						4580	6958	16949	2086	5541	2555	17	223	60	99	75		
ENSMUST00000193033						3	2	11	2	2	0	0	1	0	1	0		
ENSMUST00000193038						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193039						0	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000193042	ENSMUSG00000026587	1	158362273	158691781	1	40	32	0	48	0	17	0	0	0	0	0		Q61137
ENSMUST00000193043						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000193044						0	2	12	153	12	6	0	3	7	1	11		
ENSMUST00000193045						57	55	256	168	57	30	2	8	6	0	4		
ENSMUST00000193046						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193047						2	1	0	1	2	1	1	0	0	0	0		
ENSMUST00000193048						1	3	0	1	1	0	4	58	5	1	5		
ENSMUST00000193050	ENSMUSG00000027669	3	32580332	32616585	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVN9	
ENSMUST00000193051						2	2	3	460	12	8	0	38	19	15	15		
ENSMUST00000193053	ENSMUSG00000037957	12	110737944	110804238	1	3	0	9	27	0	0	37	133	57	141	45	Q9D721	
ENSMUST00000193055	ENSMUSG00000032599	9	108783796	108806337	1	0	0	0	0	0	0	6	6	0	3	0	A0A0A6YWE4	
ENSMUST00000193056						0	0	1	3	0	1	8	19	4	3	7		
ENSMUST00000193058						0	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000193059	ENSMUSG00000026470	1	155158715	155208256	1	0	0	2	108	0	2	14	8	5	2	0	A0A0A6YXG0	
ENSMUST00000193060						0	0	0	1	0	0	0	0	0	0	2		
ENSMUST00000193061	ENSMUSG00000076489	6	41535642	41535687	1	0	0	0	0	0	0	0	0	1	1	0	A0A0A6YVP1	
ENSMUST00000193063						0	0	0	0	0	0	102	1	0	0	147		
ENSMUST00000193064	ENSMUSG00000076479	6	41227505	41227993	1	0	3	0	0	0	0	0	0	0	0	0	A0A0B4J1P5	
ENSMUST00000193068						2	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000193069	ENSMUSG00000041355	3	88575876	88588419	1	3	0	3	4	0	0	0	0	0	0	0	A0A0A6YW45	
ENSMUST00000193070						2	6	14	4	11	1	0	3	2	2	3		
ENSMUST00000193071						4	1	0	1	0	1	2	0	0	0	0		
ENSMUST00000193072						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193073						0	5	7	0	3	3	246	669	257	906	195		
ENSMUST00000193074	ENSMUSG00000022995	1	181896384	182019990	-1	0	0	0	0	0	0	0	0	8	4	35	A0A0A6YXC8	
ENSMUST00000193075	ENSMUSG00000025766	3	41742611	41803320	1	3	5	7	5	9	5	1	0	0	0	0	A0A0A6YWY5	
ENSMUST00000193077						1	0	2	0	4	2	0	0	0	0	0		
ENSMUST00000193078	ENSMUSG00000040181	1	162829561	162866610	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVP9	
ENSMUST00000193080						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193083	ENSMUSG00000067653	1	36530188	36547201	-1	12	0	0	0	0	0	0	53	15	2	52	A0A0A6YW48	
ENSMUST00000193085						1	2	0	7	4	3	0	0	0	0	0		
ENSMUST00000193088						0	0	1	1	2	0	2	1	1	0	0		
ENSMUST00000193089						3	3	0	0	2	0	0	0	0	0	0		
ENSMUST00000193091						0	0	2	3	3	3	0	0	0	0	14		
ENSMUST00000193093						53	66	157	232	57	52	5	10	15	1	9		
ENSMUST00000193094	ENSMUSG00000016481	1	195097382	195131586	-1	144	136	183	135	181	85	85	612	328	68	165	A0A0A6YY75	
ENSMUST00000193097						176	233	393	42	116	30	13	41	10	1	40		
ENSMUST00000193098						848	939	1659	632	987	535	14	46	34	11	64		
ENSMUST00000193101	ENSMUSG00000052428	1	167308378	167333978	1	0	0	0	0	0	0	0	92	0	0	1	A0A0A6YW31	
ENSMUST00000193104						5	3	0	7	5	8	0	0	0	0	0		
ENSMUST00000193105						23	37	208	53	41	23	147	623	266	54	184		
ENSMUST00000193108	ENSMUSG00000034684	9	107681500	107710475	-1	0	0	0	0	0	1	1	0	0	0	7	A0A0A6YX80	
ENSMUST00000193109						5	3	7	5	2	0	0	0	0	0	0		
ENSMUST00000193110						25	14	22	9	18	17	0	0	1	0	0		
ENSMUST00000193113						0	0	3	3	2	2	0	0	0	0	0		
ENSMUST00000193115						16	22	16	3	19	12	0	1	1	0	2		
ENSMUST00000193118						0	0	0	277	0	0	0	0	0	0	0		
ENSMUST00000193119	ENSMUSG00000027667	3	32510259	32520833	1	0	0	0	0	0	0	0	0	3	0	0	A0A0A6YY23	
ENSMUST00000193121						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000193123						30	11	65	24	12	8	0	0	0	0	1		
ENSMUST00000193128						3	1	1	5	2	1	7	17	9	7	21		
ENSMUST00000193130						0	0	0	0	0	0	0	0	10	4	0		
ENSMUST00000193132						94	60	515	116	38	22	1	2	0	1	2		
ENSMUST00000193133	ENSMUSG00000076653	12	113912025	113912483	-1	0	0	0	0	0	1	0	0	0	0	0	A0A0A6YX91	
ENSMUST00000193134						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193137	ENSMUSG00000051599	18	37294812	37297624	1	3	0	6	0	0	0	0	0	0	0	0	A0A0A6YW85	
ENSMUST00000193140	ENSMUSG00000010048	9	107587642	107593385	1	4	0	0	0	0	0	0	0	1	0	2	A0A0A6YW12	
ENSMUST00000193143	ENSMUSG00000026608	1	188971095	189007841	-1	29	15	17	0	17	20	0	0	17	17	36	A0A0A6YX67	
ENSMUST00000193144	ENSMUSG00000037395	1	192098546	192138062	-1	0	0	0	4	0	0	0	2	0	0	0	A0A0A6YXI3	
ENSMUST00000193145	ENSMUSG00000094505	12	115165777	115166220	-1	2	1	8	0	3	0	0	0	0	0	0	A0A0A6YXA3	
ENSMUST00000193146						8	2	9	5	7	0	0	0	0	0	2		
ENSMUST00000193149	ENSMUSG00000026567	1	165485183	165576774	1	0	0	2	0	0	1	3	0	0	0	0	A0A0A6YXI1	
ENSMUST00000193151						0	2	1	0	0	0	11	7	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193152						3	2	0	0	1	2	0	0	0	1	0		
ENSMUST00000193153						5	5	29	1	8	3	0	0	0	0	3		
ENSMUST00000193154						2	1	1	1	1	1	0	0	0	0	0		
ENSMUST00000193155						4	0	1	1	1	1	0	0	0	0	0		
ENSMUST00000193158						1	1	6	4	4	0	0	1	0	0	0		
ENSMUST00000193159						1	2	6	134	5	1	0	1	0	0	1		
ENSMUST00000193160						8	6	49	4	9	5	0	0	0	1	0		
ENSMUST00000193161						5	0	4	1	1	3	1	8	7	2	1		
ENSMUST00000193162						31	27	77	17	26	8	2	3	3	0	6		
ENSMUST00000193164						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000193165						0	5	0	0	0	0	0	0	0	0	0		
ENSMUST00000193167						3	2	3	2	2	2	0	0	0	0	0		
ENSMUST00000193168	ENSMUSG00000039221	3	28805436	28807424	1	0	0	0	0	0	0	13	124	15	35	12	A0A0A6YW21	
ENSMUST00000193170	ENSMUSG00000049305	9	108460527	108465938	1	0	19	80	34	22	12	383	210	90	0	139		Q8VEG0
ENSMUST00000193171	ENSMUSG00000038860	2	32986224	33131654	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXP5	
ENSMUST00000193172						0	3	4	28	1	1	0	0	0	0	0		
ENSMUST00000193174	ENSMUSG00000052613	10	73099342	74649737	1	0	2	0	0	0	0	0	0	0	0	0	A0A0A6YY17	
ENSMUST00000193175						1	3	3	4	3	3	9	21	15	3	20		
ENSMUST00000193179						0	0	3	29	2	0	0	0	0	0	0		
ENSMUST00000193180	ENSMUSG00000057969	9	107597674	107609229	-1	0	2	10	0	0	2	0	0	0	1	0	A0A0A6YWW1	
ENSMUST00000193182						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193183						0	0	0	2	2	2	8	0	37	0	15		
ENSMUST00000193185	ENSMUSG00000026721	1	160219174	160793211	-1	0	1	0	0	0	1	0	7	9	20	11	A0A0A6YY35	
ENSMUST00000193186						1	1	2	11	5	1	4	0	7	6	0		
ENSMUST00000193188						2	0	3	5	0	0	0	0	0	0	0		
ENSMUST00000193189						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193190	ENSMUSG00000064145	9	108602942	108649386	-1	3	0	6	2	17	0	117	121	327	21	187	A0A0A6YXB0	
ENSMUST00000193195						2	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000193196						0	0	0	7	3	6	0	0	0	0	0		
ENSMUST00000193197	ENSMUSG00000064145	9	108602942	108649386	-1	0	0	0	70	1	0	3	2	0	0	0	A0A0A6YXA7	
ENSMUST00000193200	ENSMUSG00000067629	17	26941253	26972434	1	11	7	11	29	16	4	0	6	0	0	0	A0A0A6YVS6	
ENSMUST00000193201	ENSMUSG00000027765	3	61002795	61008982	1	34	32	239	154	49	21	20	119	24	29	94	Q544J5	P49650
ENSMUST00000193203						0	2	4	1	0	0	0	0	0	0	0		
ENSMUST00000193204						14	14	61	29	14	12	1	25	1	0	1		
ENSMUST00000193205						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193206						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000193210	ENSMUSG00000061518	1	36691484	36693681	1	11	7	18	90	10	2	162	813	280	1154	172	Q9D881	
ENSMUST00000193212						2	2	4	0	1	1	0	0	0	0	0		
ENSMUST00000193213						2	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000193215						5	6	10	4	10	6	0	0	0	0	1		
ENSMUST00000193217						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193218						1	1	4	3	2	1	0	0	0	0	0		
ENSMUST00000193219						19	16	22	32	19	15	0	0	0	0	0		
ENSMUST00000193220						1	1	5	1	0	2	0	1	0	0	3		
ENSMUST00000193221						6	7	7	8	12	2	0	0	0	3	2		
ENSMUST00000193222						17	8	51	17	21	15	0	0	0	0	0		
ENSMUST00000193224						2	0	0	0	0	0	26	8	32	9	15		
ENSMUST00000193226						5	0	3	2	3	0	0	0	0	0	0		
ENSMUST00000193227						1	0	27	0	0	0	0	0	0	0	0		
ENSMUST00000193228	ENSMUSG00000025766	3	41742611	41803320	1	0	1	0	0	0	0	0	6	1	3	1	A0A0A6YXY8	
ENSMUST00000193229	ENSMUSG00000048031	3	87435773	87500678	1	9	10	23	12	10	6	0	0	0	0	0		Q68SN8
ENSMUST00000193230						0	1	11	3	1	2	0	0	0	0	0		
ENSMUST00000193231	ENSMUSG00000027671	3	32706298	32726973	1	0	0	1	1	0	0	0	42	0	0	0	A0A0A6YWR1	
ENSMUST00000193232						11	13	28	30	20	10	0	1	0	0	0		
ENSMUST00000193233						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000193234						1	2	7	0	3	2	0	0	0	0	0		
ENSMUST00000193235						0	0	0	0	0	2	472	822	260	874	226		
ENSMUST00000193237						8	10	23	13	14	8	0	4	1	5	5		
ENSMUST00000193238						0	1	2	12	2	1	0	3	0	2	3		
ENSMUST00000193242						2	0	6	10	9	2	20	56	18	77	19		
ENSMUST00000193243						2	3	6	0	4	0	0	0	0	0	0		
ENSMUST00000193247						1	0	0	0	2	1	0	1	1	1	0		
ENSMUST00000193248						7	10	3	12	5	2	0	0	0	0	0		
ENSMUST00000193251						7	8	41	11	10	5	0	0	0	0	0		
ENSMUST00000193252	ENSMUSG00000049100	3	45378398	45435623	1	11	6	39	187	11	6	0	0	0	0	0	Q6P0A6	
ENSMUST00000193254	ENSMUSG00000032590	9	108085413	108094606	-1	0	2	0	55	7	4	450	563	479	116	197		Q8R146
ENSMUST00000193255						1	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000193257						0	0	7	2	2	0	0	0	0	0	0		
ENSMUST00000193258	ENSMUSG00000006673	9	108516806	108560163	1	6	2	39	7	15	0	0	2	0	2	9	Q8BUN3	
ENSMUST00000193260						6	5	19	6	12	6	0	0	0	0	0		
ENSMUST00000193262						14	12	23	8	18	0	0	0	0	0	0		
ENSMUST00000193266	ENSMUSG00000063273	3	51415148	51476507	1	34	22	16	396	43	21	21	16	37	0	5	A0A0A6YW80	
ENSMUST00000193267						37	37	81	42	35	18	10	39	23	3	46		
ENSMUST00000193268						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193269	ENSMUSG00000049305	9	108460527	108465938	1	4	0	0	0	1	1	8	3	0	2	0	A0A0A6YXC9	
ENSMUST00000193270						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193271						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000193272						4	4	12	5	2	0	0	0	0	0	2		
ENSMUST00000193273						137	174	179	91	152	97	17	117	18	57	40		
ENSMUST00000193274						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193276						35	7	52	18	13	10	0	0	1	0	2		
ENSMUST00000193278						0	0	5	1	1	0	0	0	0	0	0		
ENSMUST00000193279	ENSMUSG00000037152	3	51404677	51408988	-1	0	0	0	0	0	0	62	91	48	188	28		Q9CQY9
ENSMUST00000193282						0	1	0	0	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193286	ENSMUSG00000032609	9	108447636	108461581	-1	0	0	0	2	0	0	0	0	0	0	0		Q9D2D9
ENSMUST00000193287	ENSMUSG00000027667	3	32510259	32520833	1	5	7	11	35	8	3	0	23	0	19	5		Q99KZ6
ENSMUST00000193288	ENSMUSG00000032612	9	108347853	108392545	1	0	0	2	0	0	0	16	582	35	0	82	A0A0A6YWM7	
ENSMUST00000193289	ENSMUSG00000027674	3	32949408	33143247	-1	0	0	0	0	0	0	0	0	0	0	0	F8SLQ1	
ENSMUST00000193290						1	2	1	4	3	2	0	2	0	0	2		
ENSMUST00000193291	ENSMUSG00000023259	9	108853283	108913049	1	0	0	9	85	3	0	24	33	47	12	19	A0A087WS07	
ENSMUST00000193292						0	0	4	14	1	1	2	4	5	1	4		
ENSMUST00000193297						0	8	36	1	5	3	0	0	0	0	0		
ENSMUST00000193299						6	8	46	10	9	5	0	0	1	0	0		
ENSMUST00000193301						1	0	5	40	7	5	2	1	2	0	0		
ENSMUST00000193303	ENSMUSG00000010044	9	107547298	107551319	1	0	0	6	7	0	3	0	0	0	0	0	A0A0A6YW68	
ENSMUST00000193305						0	1	10	0	4	1	0	0	0	0	0		
ENSMUST00000193306	ENSMUSG00000095900	Y	13494026	13496466	1	0	4	0	0	0	0	0	0	0	0	0	A0A0A6YXW2	
ENSMUST00000193307	ENSMUSG00000079144	1	193168046	193177832	1	4	1	3	8	3	2	0	0	0	0	1	A0A0A6YY45	
ENSMUST00000193308						0	0	1	0	0	1	0	3	2	0	2		
ENSMUST00000193311						7	8	12	4	4	8	1	0	2	0	2		
ENSMUST00000193313						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193316						4	0	1	4	1	1	0	0	0	0	0		
ENSMUST00000193319	ENSMUSG00000037624	1	189207930	189402273	-1	11	5	11	35	3	4	0	0	0	0	0		P97438
ENSMUST00000193320	ENSMUSG00000049528	1	174084331	174089980	1	5	0	0	5	5	0	0	0	0	0	0	Q7TRW1	
ENSMUST00000193321						26395	31679	81531	28299	25352	12221	305	1124	474	88	546		
ENSMUST00000193322						0	0	0	62	0	1	0	0	0	0	0		
ENSMUST00000193324						2	5	10	1	3	1	0	0	1	0	9		
ENSMUST00000193325	ENSMUSG00000015829	1	159523769	159931729	1	4	7	8	4	6	3	0	0	0	0	1	A0A0A6YWY3	
ENSMUST00000193326						3	0	0	0	4	2	2	0	13	0	0		
ENSMUST00000193327						1	1	1	2	1	1	0	0	0	0	0		
ENSMUST00000193328						2	0	2	4	5	2	0	0	0	0	0		
ENSMUST00000193329						1	5	12	3	4	1	0	0	0	0	0		
ENSMUST00000193330	ENSMUSG00000027499	3	7366669	7445366	1	1	3	3	0	1	3	0	0	0	0	1		P63248
ENSMUST00000193331						13	7	22	22	11	3	0	0	0	0	0		
ENSMUST00000193332						12	12	37	41	13	10	11	99	17	1	35		
ENSMUST00000193334	ENSMUSG00000104463	CHR_MG184_PATCH	72432798	72439557	-1	13	13	17	39	12	14	156	518	201	114	210	Q99J57	Q3THS6
ENSMUST00000193335						3	2	3	7	5	1	0	0	0	0	0		
ENSMUST00000193337	ENSMUSG00000074445	3	92285417	92291405	1	12	9	0	5	7	3	0	0	0	0	0		Q9CQK8
ENSMUST00000193338	ENSMUSG00000028066	3	88394143	88410331	-1	4	1	9	23	7	4	0	12	5	13	0		Q9CPV5
ENSMUST00000193339						1	1	1	3	5	1	0	0	0	0	0		
ENSMUST00000193340						2	1	2	0	2	1	0	0	0	0	0		
ENSMUST00000193341						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193342	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX44	
ENSMUST00000193343						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193346						1	3	2	2	6	1	0	0	0	0	0		
ENSMUST00000193348	ENSMUSG00000006673	9	108516806	108560163	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWT7	
ENSMUST00000193351						4	7	11	2	5	3	0	0	0	0	1		
ENSMUST00000193353						8	4	19	4	3	0	71	237	67	32	132		
ENSMUST00000193354						5	2	4	4	6	3	0	0	0	0	0		
ENSMUST00000193355						1047	1053	8379	1414	1064	495	44	48	36	6	51		
ENSMUST00000193356	ENSMUSG00000026616	1	195136811	195176716	-1	0	0	0	0	0	0	0	8	7	4	5	A0A0A6YWU7	
ENSMUST00000193359						0	2	5	0	9	0	47	252	45	72	0		
ENSMUST00000193360						3	6	6	7	7	8	0	0	0	0	0		
ENSMUST00000193361	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000193366						4	1	7	1	5	1	0	0	0	0	0		
ENSMUST00000193367	ENSMUSG00000026576	1	164437109	164458355	-1	5	6	3	3	9	3	1	0	5	3	14	A0A0A6YX05	
ENSMUST00000193368						3	2	5	7	1	0	0	0	0	0	0		
ENSMUST00000193370						0	2	4	0	1	3	0	0	0	0	5		
ENSMUST00000193371						3	1	0	2	1	3	0	0	0	0	0		
ENSMUST00000193372						155	183	439	161	144	76	62	189	105	30	139		
ENSMUST00000193373	ENSMUSG00000004105	2	33216069	33247717	1	0	0	0	6	0	0	0	0	0	0	0	A0A0A6YXQ1	
ENSMUST00000193374	ENSMUSG00000079283	1	138851983	138856852	-1	10	4	6	119	9	5	2	13	6	4	12	A0A0A6YWI4	
ENSMUST00000193375						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000193376	ENSMUSG00000051323	X	133582860	133688987	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193377						2	5	0	2	2	0	0	0	0	0	0		
ENSMUST00000193379						10	10	25	9	13	9	0	1	1	0	1		
ENSMUST00000193382	ENSMUSG00000026121	1	36548639	36558349	-1	0	0	14	68	0	0	0	0	0	0	2	A0A0A6YXK9	
ENSMUST00000193384	ENSMUSG00000048930	6	113366025	113377883	-1	0	0	0	16	0	0	2	2	0	2	0	A0A0A6YVW0	
ENSMUST00000193388	ENSMUSG00000070942	1	40324610	40367562	1	0	0	0	0	0	0	0	0	4	0	0	A0A0A6YWD7	
ENSMUST00000193389	ENSMUSG00000103707	18	36967631	37187657	1	26	18	15	37	0	0	0	0	0	0	0	B9EKB6	
ENSMUST00000193391	ENSMUSG00000026070	1	40465552	40500854	1	0	7	3	6	6	0	26	30	39	8	41	Q8C257	
ENSMUST00000193394	ENSMUSG00000032562	9	107614125	107635367	-1	0	0	4	5	4	5	67	0	85	0	245	A0A0A6YWA9	
ENSMUST00000193396						3	3	2	1	1	0	0	0	0	0	1		
ENSMUST00000193397	ENSMUSG00000087582	12	114455626	114456083	-1	0	0	2	0	3	1	0	0	0	0	2	A0A0A6YWU3	
ENSMUST00000193398	ENSMUSG00000028069	3	88043108	88055993	1	7	3	9	6	11	0	0	0	0	0	10		Q3TFK5
ENSMUST00000193399						2	1	8	2	3	2	0	0	0	0	0		
ENSMUST00000193400						2	0	1	0	4	0	0	0	2	0	1		
ENSMUST00000193404	ENSMUSG00000102222	18	37746993	37841873	1	23	7	87	24	34	7	2	8	4	0	9	Q91XY9	
ENSMUST00000193406						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193408	ENSMUSG00000103939	12	114253617	114254051	-1	1	0	3	2	1	1	0	0	0	1	3	A0A0A6YXF1	
ENSMUST00000193410	ENSMUSG00000027956	3	79812564	79852773	-1	0	2	6	2	0	0	0	0	0	0	0	A0A0A6YX47	
ENSMUST00000193411						0	0	0	0	0	0	28	0	57	9	24		
ENSMUST00000193412						22	16	24	15	22	6	3	18	16	2	9		
ENSMUST00000193414	ENSMUSG00000103567	18	37694380	37841873	1	14	8	33	58	25	14	0	4	0	0	0	Q91XY3	
ENSMUST00000193418	ENSMUSG00000010054	9	107563255	107566112	1	0	0	0	0	0	0	0	3	0	13	0	A0A0A6YWP5	
ENSMUST00000193421	ENSMUSG00000062867	9	108560286	108565584	1	0	0	0	0	3	0	6	0	0	0	0	A0A0A6YXS4	
ENSMUST00000193422						7	2	12	12	12	9	0	0	0	0	0		
ENSMUST00000193423						1	1	2	0	3	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193424						1	0	0	3	0	0	15	38	9	0	45		
ENSMUST00000193425						2	8	9	4	4	7	0	0	0	0	0		
ENSMUST00000193426	ENSMUSG00000019817	10	13060504	13131694	1	6	0	0	5	7	4	0	0	0	0	0	A0A0A6YWE3	
ENSMUST00000193427	ENSMUSG00000019039	9	108569886	108572774	1	2	0	4	0	2	1	25	1	29	6	0	A0A0A6YWX9	
ENSMUST00000193431						1	2	3	3	11	3	0	3	0	0	0		
ENSMUST00000193432	ENSMUSG00000027742	3	52981875	53017237	-1	5	3	0	2	4	1	13	35	85	32	50	Q8BRB0	
ENSMUST00000193433	ENSMUSG00000050144	3	88410498	88425139	-1	0	0	0	0	0	0	137	640	67	23	46		Q8BGF9
ENSMUST00000193435	ENSMUSG00000026080	1	38863867	38898161	-1	0	0	0	21	0	0	0	0	0	0	0	A0A0A6YWM2	
ENSMUST00000193436	ENSMUSG00000026616	1	195136811	195176716	-1	0	0	0	0	0	0	0	0	1	0	0	A0A0A6YXU7	
ENSMUST00000193437						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193439	ENSMUSG00000032558	9	104002544	104153483	1	6	0	0	0	2	0	0	0	0	0	0	A0A0A6YWG5	
ENSMUST00000193440	ENSMUSG00000063659	1	177442351	177450764	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW03	
ENSMUST00000193441	ENSMUSG00000026080	1	38863867	38898161	-1	48	31	117	63	66	27	0	5	0	0	5	A0A0A6YXK3	
ENSMUST00000193442						3	2	3	4	3	2	0	0	0	0	0		
ENSMUST00000193443						12	9	18	20	16	8	0	1	0	0	0		
ENSMUST00000193445						3	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193446	ENSMUSG00000052428	1	167308378	167333978	1	0	0	0	0	0	0	93	451	31	0	5	A0A0A6YVS2	
ENSMUST00000193449	ENSMUSG00000104250	CHR_MG184_PATCH	72318677	72345183	-1	3	7	11	53	10	4	195	555	283	109	170		Q3TIX9
ENSMUST00000193451						4	3	5	1	2	4	0	0	0	0	0		
ENSMUST00000193452						0	0	0	0	2	1	0	0	0	0	2		
ENSMUST00000193453						4	3	6	3	1	0	0	0	0	0	0		
ENSMUST00000193454						2	4	0	5	4	0	0	0	0	0	0		
ENSMUST00000193455	ENSMUSG00000036334	3	59316735	59344394	-1	7	0	0	0	0	0	0	0	0	0	0		Q3V1M1
ENSMUST00000193460	ENSMUSG00000016181	1	193091104	193130272	-1	0	3	0	0	0	1	6	11	6	1	3	A0A0A6YXM9	
ENSMUST00000193463						14	0	30	9	16	7	0	8	0	0	0		
ENSMUST00000193464						1	1	4	3	4	2	0	0	0	0	0		
ENSMUST00000193465	ENSMUSG00000030842	7	101905904	101926675	1	1	2	3	5	0	0	2	0	2	0	0	A0A0A6YX02	
ENSMUST00000193466						1	3	0	0	4	0	0	0	0	0	0		
ENSMUST00000193470						0	0	0	52	0	1	0	9	12	0	8		
ENSMUST00000193472	ENSMUSG00000026082	1	38052786	38129801	-1	4	0	0	0	3	0	0	3	0	0	0	A0A0A6YX77	
ENSMUST00000193474						0	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000193476	ENSMUSG00000103472	18	37714764	37841873	1	15	6	35	20	21	13	0	2	0	0	0	A0A0A6YXT1	
ENSMUST00000193477						105	109	588	206	116	65	1	15	9	3	15		
ENSMUST00000193478						1	2	0	2	2	1	0	0	0	0	0		
ENSMUST00000193480	ENSMUSG00000063659	1	177442351	177450764	1	0	0	0	0	0	0	61	274	83	29	75	A0A0A6YWR6	
ENSMUST00000193482						40	39	126	62	35	16	20	170	86	17	110		
ENSMUST00000193483						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193485						1	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000193486						0	1	7	14	2	1	0	0	0	0	0		
ENSMUST00000193487	ENSMUSG00000027528	3	10193621	10197283	-1	2	1	5	0	8	0	0	0	0	0	0	A0A0A6YXB9	
ENSMUST00000193489	ENSMUSG00000026078	1	38985608	38997238	1	0	1	0	77	4	1	0	0	0	0	0	A0A0A6YVT6	
ENSMUST00000193490	ENSMUSG00000007815	9	108306129	108337934	1	0	0	11	11	1	0	16	12	5	12	0	A0A0A6YWJ1	
ENSMUST00000193491	ENSMUSG00000098301	CHR_MG3829_PATCH	88047373	88053755	1	0	3	4	5	2	0	282	657	214	43	179		Q6PDM2
ENSMUST00000193493						0	3	1	2	0	0	0	9	0	0	0		
ENSMUST00000193495						2	9	21	14	11	5	0	0	0	0	0		
ENSMUST00000193502						47	13	73	156	38	17	11	9	10	2	12		
ENSMUST00000193503	ENSMUSG00000036899	6	41652173	41680769	-1	6	8	14	11	7	4	0	0	2	0	0	A0A0A6YW69	
ENSMUST00000193504	ENSMUSG00000102976	1	133619862	133661380	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX93	
ENSMUST00000193505						1	1	1	0	0	2	0	0	1	0	0		
ENSMUST00000193508						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000193509	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	3	6	21	0	4	534	613	428	299	320		Q9CY62
ENSMUST00000193510						1	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000193512						0	0	2	1	1	1	0	0	0	0	0		
ENSMUST00000193514						0	2	1	3	7	3	0	0	0	0	0		
ENSMUST00000193517	ENSMUSG00000027763	3	60472830	60629750	1	0	7	0	0	7	0	322	1676	262	372	103	A0A0A6YVV8	
ENSMUST00000193518	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	0	0	0	0	308	54	119	A0A0A6YXQ4	
ENSMUST00000193521	ENSMUSG00000102308	3	92532505	92534511	-1	2	6	6	12	3	1	0	0	0	0	0	A0A0A6YVW6	
ENSMUST00000193522	ENSMUSG00000057914	2	14603088	14987908	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWX5	
ENSMUST00000193525						3	3	3	4	4	2	0	0	0	0	0		
ENSMUST00000193526	ENSMUSG00000098375	CHR_MG3829_PATCH	88204388	88211507	1	0	0	0	0	0	0	17	31	27	31	16		
ENSMUST00000193529	ENSMUSG00000095822	3	93936633	93943543	-1	8	0	0	0	4	0	0	0	0	0	0		P0DMR6
ENSMUST00000193531						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000193533	ENSMUSG00000032936	9	107935674	107949691	1	0	0	0	21	4	1	0	0	0	0	0	A0A0A6YW08	
ENSMUST00000193535						2	3	10	140	6	2	0	2	3	0	1		
ENSMUST00000193538						0	0	0	2	0	0	131	436	67	15	198		
ENSMUST00000193539						6	7	18	12	10	4	12	18	5	3	7		
ENSMUST00000193543						10	7	11	0	9	6	0	0	0	0	0		
ENSMUST00000193547	ENSMUSG00000039542	9	49502136	49798925	-1	0	0	0	13	5	0	57	126	63	5	48	A0A0A6YY47	
ENSMUST00000193548						6	0	9	0	0	3	0	0	0	0	0		
ENSMUST00000193550						1	0	4	0	3	2	0	0	0	0	0		
ENSMUST00000193551						0	0	9	3	0	1	0	0	0	0	0		
ENSMUST00000193552	ENSMUSG00000064145	9	108602942	108649386	-1	2	1	0	4	0	0	33	20	15	4	31	A0A0A6YXR5	
ENSMUST00000193556						8	9	57	16	8	10	0	0	0	0	0		
ENSMUST00000193557						3	6	5	8	5	4	0	0	0	0	0		
ENSMUST00000193558	ENSMUSG00000006676	9	108490602	108502337	1	0	0	0	0	0	0	16	5	17	0	12	A0A0A6YXT9	
ENSMUST00000193559	ENSMUSG00000033900	3	82358044	82395268	1	0	0	11	8	0	0	0	0	0	0	0	A0A0A6YXJ3	
ENSMUST00000193560	ENSMUSG00000032599	9	108783796	108806337	1	0	0	9	10	15	5	226	462	296	100	242	A0A0A6YWM3	
ENSMUST00000193565	ENSMUSG00000103350	3	93692050	93693070	-1	11	8	10	9	11	10	0	0	0	0	0	A0A0A6YXL2	
ENSMUST00000193566						3	4	3	0	6	0	0	0	0	0	0		
ENSMUST00000193567						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193568						190	160	744	140	145	81	7	51	12	6	14		
ENSMUST00000193569	ENSMUSG00000037461	1	191575636	191623688	1	1	0	0	0	1	0	0	0	0	0	0	A0A0A6YWX4	
ENSMUST00000193571						3	1	6	0	4	0	11	12	0	4	12		
ENSMUST00000193575	ENSMUSG00000026568	1	165460637	165481214	1	0	0	0	0	2	0	0	0	0	0	0	A0A0A6YY89	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193578						1	2	2	2	1	0	0	0	0	0	0		
ENSMUST00000193579						5	1	14	18	7	5	0	0	0	0	0		
ENSMUST00000193583						4	3	2	3	4	1	0	0	0	0	0		
ENSMUST00000193586						3	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000193587						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193588						2	0	1	4	1	2	0	0	0	1	0		
ENSMUST00000193589	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193590						4	1	7	3	10	1	0	0	0	0	2		
ENSMUST00000193591						2	0	0	0	1	3	0	0	0	0	0		
ENSMUST00000193593	ENSMUSG00000102388	Y	69321132	69331861	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXW0	
ENSMUST00000193597	ENSMUSG00000028005	3	82032006	82074689	-1	0	10	0	0	0	1	3	5	0	0	0	Q80YP4	
ENSMUST00000193598						1	0	0	152	5	2	0	0	2	0	4		
ENSMUST00000193599	ENSMUSG00000026587	1	158362273	158691781	1	0	0	0	1	0	0	0	0	0	0	0	A0A0A6YWD1	
ENSMUST00000193600						0	1	1	54	4	1	0	0	0	0	0		
ENSMUST00000193603	ENSMUSG00000063887	3	25426215	26332460	-1	51	34	47	101	34	16	0	0	0	0	1		Q99K10
ENSMUST00000193606	ENSMUSG00000052726	1	140246158	140612067	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXD8	
ENSMUST00000193610						0	1	1	0	0	0	0	2	3	6	1		
ENSMUST00000193611						2	0	16	73	7	4	106	253	107	20	174		
ENSMUST00000193612						4	5	13	5	7	1	0	0	0	0	0		
ENSMUST00000193613						12	5	7	5	11	5	0	0	1	0	0		
ENSMUST00000193615	ENSMUSG00000027671	3	32706298	32726973	1	4	3	1	0	0	1	0	0	0	0	10	A0A0A6YW15	
ENSMUST00000193618						2	3	9	165	15	1	0	2	0	0	0		
ENSMUST00000193619						72	80	198	140	119	59	5	19	14	1	13		
ENSMUST00000193620	ENSMUSG00000037995	1	172481788	172498878	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXP1	
ENSMUST00000193621	ENSMUSG00000006675	9	108578862	108597667	-1	10	11	10	27	16	3	0	0	0	0	0	A0A0A6YX56	
ENSMUST00000193622						2	5	8	4	1	2	0	0	0	1	0		
ENSMUST00000193625	ENSMUSG00000042901	1	183296590	183325476	1	0	0	0	0	0	0	46	53	80	26	74		Q8C4Q6
ENSMUST00000193627						0	0	3	4	0	5	0	0	1	0	0		
ENSMUST00000193628						7	10	13	24	10	3	26	117	46	0	43		
ENSMUST00000193629						6	5	5	2	8	5	0	0	0	0	0		
ENSMUST00000193630						1	0	3	7	4	0	0	0	0	0	0		
ENSMUST00000193631						18	15	15	200	22	10	0	0	0	0	0		
ENSMUST00000193632	ENSMUSG00000028078	3	86786151	86920852	-1	0	0	0	0	2	0	0	0	2	0	0	A0A0A6YX71	
ENSMUST00000193633	ENSMUSG00000030491	7	35469098	35537745	-1	6	15	0	0	6	4	0	0	0	0	0	A0A0A6YX17	
ENSMUST00000193634						16	10	26	23	20	13	20	142	39	0	95		
ENSMUST00000193636	ENSMUSG00000026718	2	14074098	14149634	1	0	0	0	0	0	0	109	295	151	73	107	A0A0A6YVP6	
ENSMUST00000193638	ENSMUSG00000026554	1	172148084	172197005	1	1	1	0	19	5	2	59	129	133	13	161		Q8N7N5
ENSMUST00000193640						4	0	1	1	3	1	0	0	0	0	0		
ENSMUST00000193641						2	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000193642						0	0	0	193	0	0	0	0	1	0	0		
ENSMUST00000193643	ENSMUSG00000064145	9	108602942	108649386	-1	0	0	0	37	3	5	1	37	39	2	28	A0A0A6YW29	
ENSMUST00000193644						0	0	0	0	0	0	0	1	2	0	0		
ENSMUST00000193645						84	61	109	1002	129	67	1	31	9	12	20		
ENSMUST00000193646						9	6	27	9	20	14	22	120	54	0	25		
ENSMUST00000193647	ENSMUSG00000027763	3	60472830	60629750	1	2	0	2	0	3	0	0	0	144	92	137	A0A0A6YWG1	
ENSMUST00000193648	ENSMUSG00000000817	1	161780689	161788495	-1	1	0	0	0	0	0	0	0	0	1	0		P41047
ENSMUST00000193650	ENSMUSG00000026395	1	138062861	138175708	-1	2	1	1	2	0	1	0	0	0	0	0	A0A0A6YWF2	
ENSMUST00000193651						5	4	12	3	3	2	3	13	8	1	18		
ENSMUST00000193652	ENSMUSG00000094194	12	113838526	113839010	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0B4J1P4	
ENSMUST00000193654						3	2	0	1	0	0	0	0	0	0	0		
ENSMUST00000193658						1	4	4	9	5	7	0	0	2	0	0		
ENSMUST00000193659						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193660	ENSMUSG00000038576	1	182763860	182896591	1	2	3	2	28	4	0	0	0	0	0	0	A0A0A6YX15	
ENSMUST00000193661						10	13	15	27	11	6	0	1	3	0	1		
ENSMUST00000193662						5	2	15	2	8	4	0	0	0	0	0		
ENSMUST00000193664						18	42	64	32	26	8	5	15	14	1	11		
ENSMUST00000193665						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000193666						9	12	47	15	19	9	0	0	0	0	1		
ENSMUST00000193669	ENSMUSG00000060771	1	37754776	37866429	-1	0	0	0	0	0	0	0	0	5	3	7	Q3TR21	
ENSMUST00000193671						2	0	1	0	1	2	0	0	0	0	0		
ENSMUST00000193673	ENSMUSG00000026087	1	37890477	37898535	1	0	0	4	0	3	0	25	25	25	66	8		Q9D7N6
ENSMUST00000193675	ENSMUSG00000026728	2	13573927	13582826	1	8	0	0	0	0	0	12471	12173	14600	3458	11494	A0A0A6YWC8	
ENSMUST00000193676						2	1	4	0	2	0	0	0	0	0	0		
ENSMUST00000193677						0	2	1	1	1	0	0	0	0	0	0		
ENSMUST00000193678	ENSMUSG00000006676	9	108490602	108502337	1	0	0	0	0	0	0	8	1	1	26	0	A0A0A6YWX1	
ENSMUST00000193681	ENSMUSG00000027674	3	32949408	33143247	-1	0	0	0	0	0	0	0	0	0	0	0	F8SLQ1	
ENSMUST00000193682	ENSMUSG00000026074	1	39900913	40026310	1	0	0	0	0	0	0	896	1849	1862	60	1275	B2RUE8	
ENSMUST00000193683	ENSMUSG00000026575	1	164304121	164437725	1	0	0	0	0	0	0	9	87	32	73	13	Q3UMG6	
ENSMUST00000193686						0	0	5	1	1	1	0	0	0	0	1		
ENSMUST00000193687	ENSMUSG00000079164	1	182954788	182976044	1	0	0	8	19	0	0	11	0	37	0	41	A0A0A6YVY4	
ENSMUST00000193693	ENSMUSG00000102455	CHR_MG184_PATCH	72355446	72359761	1	0	0	9	11	4	0	0	11	8	0	6		Q91WN2
ENSMUST00000193694						0	2	0	0	1	0	8	8	24	0	5		
ENSMUST00000193695	ENSMUSG00000026791	2	32972990	32982083	-1	0	0	0	0	0	0	0	0	0	0	0	Q2TK27	
ENSMUST00000193696						14	6	28	10	13	6	1	6	5	2	3		
ENSMUST00000193697	ENSMUSG00000026082	1	38052786	38129801	-1	0	0	2	0	2	2	1	0	0	0	0	A0A0A6YWI0	
ENSMUST00000193699						3	2	2	1	5	0	0	0	0	0	0		
ENSMUST00000193700						3	0	21	3	6	0	155	352	132	0	66		
ENSMUST00000193701						1	1	1	16	3	0	0	1	0	0	0		
ENSMUST00000193702						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000193703	ENSMUSG00000022995	1	181896384	182019990	-1	344	230	1844	482	272	142	47	516	52	9	64		Q03173
ENSMUST00000193704						0	1	0	0	3	1	0	0	0	0	0		
ENSMUST00000193706						1	7	6	14	5	2	0	2	0	0	0		
ENSMUST00000193708						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193710						21	15	23	30	22	23	0	2	2	1	2		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193711						0	3	0	2	2	0	0	0	0	0	0		
ENSMUST00000193713	ENSMUSG00000026111	1	37430139	37439124	1	0	0	0	0	0	0	0	5	0	24	0	A0A0A6YWQ8	
ENSMUST00000193714	ENSMUSG00000040723	1	165646516	165709757	-1	0	0	0	37	0	0	5	56	93	6	72	A0A0A6YXA9	
ENSMUST00000193715						0	1	1	0	0	2	0	0	0	0	1		
ENSMUST00000193716						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193719						9	8	20	7	14	5	0	4	1	0	1		
ENSMUST00000193720	ENSMUSG00000102412	._MMCHR1_CHORI29_IDI	60745208	60769374	1	0	0	0	0	0	0	0	0	0	0	5		P31041
ENSMUST00000193721						3	7	20	5	6	6	0	0	0	0	0		
ENSMUST00000193722						3	6	0	5	5	2	8	0	0	0	0		
ENSMUST00000193726						0	2	0	3	3	0	41	12	54	0	32		
ENSMUST00000193727	ENSMUSG00000043263	1	173630917	173647928	1	0	2	2	0	5	0	6	249	23	101	61	A0A0A6YXV9	
ENSMUST00000193729						40	39	100	70	36	27	10	12	32	9	21		
ENSMUST00000193730						16	13	39	750	45	18	0	0	0	0	1		
ENSMUST00000193734	ENSMUSG00000027630	3	22076652	22216594	1	65	0	149	177	0	0	166	212	492	149	121		Q8BHJ5
ENSMUST00000193736						3	1	0	0	0	1	0	27	2	3	2		
ENSMUST00000193737						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193739	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0		Q99PJ1
ENSMUST00000193740						2	2	3	1	3	2	0	0	0	0	0		
ENSMUST00000193741						0	0	0	38	0	0	0	0	0	0	0		
ENSMUST00000193742						19	17	92	52	20	7	1	5	0	0	0		
ENSMUST00000193743						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000193747	ENSMUSG00000010047	9	107567945	107572779	1	0	0	0	10	0	1	0	0	0	0	0	Q8C309	
ENSMUST00000193749						2	5	2	6	4	5	0	0	0	0	0		
ENSMUST00000193752						1	0	1	3	8	4	0	0	0	0	0		
ENSMUST00000193754						0	0	4	0	0	1	27	59	45	2	61		
ENSMUST00000193755						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193757						4	3	7	4	2	2	0	0	0	0	0		
ENSMUST00000193758						165	164	772	712	218	118	3	14	3	3	19		
ENSMUST00000193763						2	4	8	8	2	0	0	0	0	0	0		
ENSMUST00000193765						1	1	3	8	3	1	1	2	0	1	2		
ENSMUST00000193766						15	18	22	2	15	5	0	0	0	0	0		
ENSMUST00000193767						25	25	197	48	18	11	21	172	17	29	27		
ENSMUST00000193768						1	4	2	4	0	0	0	0	0	0	0		
ENSMUST00000193769						0	1	4	1	0	0	2	3	0	0	0		
ENSMUST00000193771						0	0	0	0	6	0	3	1	0	0	0		
ENSMUST00000193772						3	2	2	0	5	0	0	0	0	0	1		
ENSMUST00000193773						2	0	6	4	4	0	0	0	0	1	0		
ENSMUST00000193774	ENSMUSG00000026113	1	37299865	37410736	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXS5	
ENSMUST00000193776						0	0	2	0	1	0	5	0	0	0	0		
ENSMUST00000193777	ENSMUSG00000103707	18	36967631	37187657	1	0	0	0	8	0	0	0	0	0	0	0	Q91Y14	
ENSMUST00000193779	ENSMUSG00000039286	3	27416162	27711307	-1	0	0	0	26	0	0	7	11	8	0	27	A0A0A6YX88	
ENSMUST00000193780						1	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000193784	ENSMUSG00000026698	1	161969186	161973435	1	13	12	14	72	11	4	5	42	10	2	5		Q9CXR4
ENSMUST00000193785						1	4	3	0	5	8	0	0	1	0	2		
ENSMUST00000193786						2	2	0	8	2	4	0	0	0	0	0		
ENSMUST00000193787						3	1	2	6	5	3	0	0	0	1	0		
ENSMUST00000193788						6	7	18	14	16	6	2	0	1	0	1		
ENSMUST00000193789	ENSMUSG00000027667	3	32510259	32520833	1	4	0	0	0	0	0	0	5	0	17	0	A0A0A6YXK4	
ENSMUST00000193791	ENSMUSG00000033488	1	157458577	157492638	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWV6	
ENSMUST00000193792	ENSMUSG00000025816	2	5870987	5895432	-1	0	0	0	0	0	0	0	17	13	8	13	Q9CYJ6	
ENSMUST00000193793	ENSMUSG00000026070	1	40465552	40500854	1	1	0	0	2	0	4	0	5	5	0	12	A0A0A6YWA3	
ENSMUST00000193795	ENSMUSG00000025762	3	40950354	41040234	1	4	2	0	3	3	0	0	0	6	0	5	A0A0A6YXJ7	
ENSMUST00000193797						3	3	1	5	5	0	0	0	0	0	0		
ENSMUST00000193798						27	23	225	25	20	18	2	2	3	0	1		
ENSMUST00000193800	ENSMUSG00000057914	2	14603088	14987908	1	0	0	13	0	0	0	0	0	0	0	0	C7IVS7	
ENSMUST00000193801	ENSMUSG00000026616	1	195136811	195176716	-1	0	4	0	0	0	1	1	2	0	1	0	Q32M14	
ENSMUST00000193803						0	0	4	1	0	0	0	2	1	0	2		
ENSMUST00000193804						6	3	20	7	4	2	5	24	5	3	14		
ENSMUST00000193805						1	4	6	0	6	3	0	0	0	0	0		
ENSMUST00000193806						0	0	4	0	2	0	0	0	0	0	0		
ENSMUST00000193808	ENSMUSG00000026575	1	164304121	164437725	1	4	3	9	1	3	1	0	0	4	6	5	Q3UMG6	
ENSMUST00000193810	ENSMUSG00000026721	1	160219174	160793211	-1	5	1	6	30	5	3	0	0	4	0	6	A0A0A6YWY0	
ENSMUST00000193818						2	0	2	7	1	0	13	18	17	4	18		
ENSMUST00000193821	ENSMUSG00000103019	CHR_MG184_PATCH	72414307	72430711	1	0	2	2	1	3	1	2	1	2	0	1		
ENSMUST00000193822	ENSMUSG00000039748	1	175880581	175913489	1	0	0	1	0	0	0	0	0	0	0	0	A0A0A6YWN5	
ENSMUST00000193823	ENSMUSG00000003134	1	39371492	39478755	-1	9	4	7	7	7	4	127	167	192	24	254	A0A0A6YWY1	
ENSMUST00000193824						6	5	19	7	7	6	0	0	0	0	0		
ENSMUST00000193825						0	1	6	25	2	0	0	1	1	0	0		
ENSMUST00000193826						5	0	5	0	0	1	0	0	0	0	0		
ENSMUST00000193827						8	6	10	1	4	4	0	0	0	0	0		
ENSMUST00000193828	ENSMUSG00000051375	18	38185914	38212053	-1	3	3	3	23	11	2	0	0	0	0	0	A0A0A6YY88	
ENSMUST00000193829	ENSMUSG00000016481	1	195097382	195131586	-1	0	0	0	0	1	0	7	12	19	7	0	A0A0A6YXH8	
ENSMUST00000193831						0	1	3	0	2	3	0	0	0	0	0		
ENSMUST00000193832	ENSMUSG00000058407	1	37985189	37997893	-1	35	38	57	33	48	26	11	61	23	20	29	A0A0A6YXY0	
ENSMUST00000193834						1	1	3	0	2	0	0	0	0	0	0		
ENSMUST00000193835						5	0	0	5	0	0	11	24	9	0	37		
ENSMUST00000193836	ENSMUSG00000017418	2	15049395	15082456	1	0	0	0	19	5	3	0	0	0	0	0	A0A0A6YWH0	
ENSMUST00000193838						16	14	76	17	11	4	0	7	4	1	1		
ENSMUST00000193839	ENSMUSG00000103442	18	36930184	37187661	1	18	10	35	143	15	4	0	0	0	0	0	Q641K6	
ENSMUST00000193843						18	4	10	6	15	6	0	0	0	0	0		
ENSMUST00000193844						2	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000193846						6	0	0	4	2	4	0	17	0	0	9		
ENSMUST00000193847						11	19	71	122	47	28	0	0	0	0	0		
ENSMUST00000193849						4	2	3	1	5	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193850						3	0	4	5	3	2	0	0	1	0	2		
ENSMUST00000193852						0	0	0	11	0	0	0	0	0	0	0		
ENSMUST00000193854						6	2	0	1	2	3	5	35	10	2	22		
ENSMUST00000193855	ENSMUSG00000096410	12	114708648	114709135	-1	9	4	8	0	2	0	0	0	0	11	10	A0A0A6YWX0	
ENSMUST00000193856	ENSMUSG00000102206	18	37010712	37187657	1	0	0	0	28	0	0	0	0	0	0	0	A0A0A6YX38	
ENSMUST00000193858	ENSMUSG00000039748	1	175880581	175913489	1	0	0	0	0	0	2	0	0	0	1	0	A0A0A6YWI7	
ENSMUST00000193860	ENSMUSG00000040612	1	166254139	166316823	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVY9	
ENSMUST00000193861						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193862						0	1	2	1	0	2	0	0	0	0	0		
ENSMUST00000193866						10	6	5	2	5	0	0	0	0	0	0		
ENSMUST00000193868						7	19	14	0	27	14	282	1292	247	760	110		
ENSMUST00000193869	ENSMUSG00000103332	18	37668953	37841870	1	18	13	20	31	14	10	0	0	0	0	0	Q91XY6	
ENSMUST00000193870	ENSMUSG00000098892	CHR_MG3833_PATCH	18407771	18427737	-1	0	0	0	0	0	0	0	0	2	0	0		
ENSMUST00000193872	ENSMUSG00000001420	3	88328655	88336148	-1	8	3	12	22	9	3	4	4	4	2	7	A0A0A6YX45	
ENSMUST00000193874	ENSMUSG00000023259	9	108853283	108913049	1	0	0	0	0	0	0	0	12	4	0	0	A0A0A6YWP3	
ENSMUST00000193876	ENSMUSG00000032562	9	107614125	107635367	-1	0	0	0	9	0	0	0	0	1	0	0	A0A0A6YXN0	
ENSMUST00000193878						0	0	0	0	0	0	9	16	0	0	0		
ENSMUST00000193879	ENSMUSG00000028011	3	81957090	81976202	-1	8	3	6	9	7	0	0	0	0	3	0	C5NSA7	
ENSMUST00000193880						4	6	6	1	1	1	0	1	0	0	0		
ENSMUST00000193882	ENSMUSG00000104043	3	84174104	84175132	1	3	8	5	3	5	2	0	0	0	1	0	A0A0A6YW33	
ENSMUST00000193883	ENSMUSG00000017418	2	15049395	15082456	1	0	0	0	0	0	0	0	15	12	6	2	A0A0A6YXH4	
ENSMUST00000193884						1	3	6	5	2	3	0	0	0	0	0		
ENSMUST00000193886						1	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000193888	ENSMUSG00000102367	1	133309827	133329722	1	3	0	0	0	0	0	0	0	0	0	0	I0J0X7	Q6Y4S4
ENSMUST00000193889						1	1	3	2	1	2	0	0	0	0	0		
ENSMUST00000193890	ENSMUSG00000102543	18	37819513	37841873	1	0	0	0	3	0	0	0	0	0	0	0	A0A0A6YXZ9	
ENSMUST00000193892	ENSMUSG00000058729	1	180641150	180690694	1	0	0	0	0	0	0	0	43	36	4	0	A0A0A6YWF7	
ENSMUST00000193893	ENSMUSG00000094694	12	114583569	114584002	-1	0	0	2	0	5	0	0	0	0	0	10	A0A0A6YW37	
ENSMUST00000193895	ENSMUSG00000032609	9	108447636	108461581	-1	0	0	0	9	0	0	0	2	0	0	0		Q9D2D9
ENSMUST00000193897						8	3	19	3	12	7	11	114	25	13	37		
ENSMUST00000193898	ENSMUSG00000091060	1	162647193	162658219	-1	0	0	0	0	0	0	0	0	2	0	0	A0A0A6YX39	
ENSMUST00000193899	ENSMUSG00000034755	X	120290259	120910619	1	0	0	4	0	0	0	0	0	0	0	0	A0A0A6YWK0	
ENSMUST00000193901	ENSMUSG00000055421	14	93013410	93890679	-1	12	15	0	0	9	0	0	0	0	0	0	A0A0A6YWY8	
ENSMUST00000193904						3	4	0	2	1	0	0	0	0	0	0		
ENSMUST00000193905						3	0	1	1	0	0	0	0	0	0	0		
ENSMUST00000193907	ENSMUSG00000062169	1	181144693	181168994	1	2	1	0	0	0	2	19	15	0	20	3	A0A0A6YW87	
ENSMUST00000193909						4	3	4	5	5	1	4	11	3	1	6		
ENSMUST00000193910	ENSMUSG00000026566	1	165592240	165634538	-1	1	1	2	1	0	4	0	0	0	0	1	A0A0A6YXL8	
ENSMUST00000193911						3	0	0	2	2	0	0	0	0	0	1		
ENSMUST00000193914						67	45	68	650	136	91	1	5	0	1	0		
ENSMUST00000193916						0	3	17	0	0	0	1735	3220	3649	109	2408		
ENSMUST00000193919						3	7	13	299	21	0	2	0	0	0	2		
ENSMUST00000193920						4	3	51	180	25	1	0	0	0	0	0		
ENSMUST00000193921						3	5	8	5	0	2	0	0	0	0	5		
ENSMUST00000193922						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000193923						33	26	60	96	31	20	23	142	62	7	76		
ENSMUST00000193924	ENSMUSG00000033910	3	82092427	82145789	-1	24	0	16	61	27	9	0	0	0	0	0		Q9ERL9
ENSMUST00000193925						5	1	7	61	3	3	34	80	66	16	97		
ENSMUST00000193931						7	5	7	177	4	8	0	0	0	0	3		
ENSMUST00000193932	ENSMUSG00000010064	9	107650634	107669530	-1	0	0	3	16	0	0	0	0	0	1	0		Q9DCP2
ENSMUST00000193933						2	0	0	1	1	0	5	10	4	0	9		
ENSMUST00000193934	ENSMUSG00000041355	3	88575876	88588419	1	0	0	3	0	0	0	11	0	0	0	0	A0A0A6YVZ1	
ENSMUST00000193935						0	0	0	0	2	1	0	0	0	0	0		
ENSMUST00000193936	ENSMUSG00000096407	12	114416596	114417053	-1	0	3	3	0	0	0	0	0	0	0	0	A0A0A6YWS9	
ENSMUST00000193937						5	12	3	2	9	2	0	1	0	0	2		
ENSMUST00000193938						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000193940						33	34	45	45	48	25	3	7	3	5	13		
ENSMUST00000193941	ENSMUSG00000102543	18	37819513	37841873	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVT4	
ENSMUST00000193942						2	1	3	0	1	3	0	0	0	0	0		
ENSMUST00000193943	ENSMUSG00000027765	3	61002795	61008982	1	12	15	5	327	28	15	166	576	332	63	206	Q544J5	P49650
ENSMUST00000193944	ENSMUSG00000027912	3	93017810	93019060	-1	2	0	2	3	0	0	0	0	0	0	0	A0A0A6YWC3	
ENSMUST00000193947	ENSMUSG00000040209	3	9427020	9610085	-1	12	11	47	3	15	9	5	6	3	1	3	A0A0A6YWL6	
ENSMUST00000193948	ENSMUSG00000026566	1	165592240	165634538	-1	0	0	0	0	1	1	0	0	0	0	0	A0A0A6YXX8	
ENSMUST00000193949						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193950	ENSMUSG00000095923	12	114896238	114896671	-1	5	0	0	0	0	0	0	0	0	0	0	A0A0A6YW32	
ENSMUST00000193952	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	4	1	3	2	6	1	0	0	0	0	0		
ENSMUST00000193953	ENSMUSG00000021466	13	63508328	63573598	-1	0	0	1	20	3	0	0	0	0	0	0	Q5R1U4	
ENSMUST00000193954						0	3	0	0	0	0	0	0	0	0	0		
ENSMUST00000193957						0	0	0	0	0	4	0	0	0	0	0		
ENSMUST00000193959	ENSMUSG00000042901	1	183296590	183325476	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXT3	
ENSMUST00000193961						63	58	58	47	60	29	0	5	0	2	5		
ENSMUST00000193963						2	1	9	0	2	1	0	0	0	2	0		
ENSMUST00000193967						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193970						0	0	0	0	0	0	9	43	16	3	1		
ENSMUST00000193971						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000193972						7	7	4	8	6	5	0	0	0	0	0		
ENSMUST00000193973	ENSMUSG00000058715	1	171229572	171234365	-1	6	0	0	8	0	0	48	459	133	109	179	A0A0A6YVS1	
ENSMUST00000193974						1	1	0	3	0	0	0	0	0	0	1		
ENSMUST00000193975						11	5	42	13	10	3	61	402	131	13	184		
ENSMUST00000193977	ENSMUSG00000037474	1	191537356	191575544	-1	40	33	76	52	44	23	0	2	2	1	1	A0A0A6YXS0	
ENSMUST00000193979	ENSMUSG00000026111	1	37430139	37439124	1	0	0	0	99	7	2	0	0	65	126	60	A0A0A6YX35	
ENSMUST00000193980						0	1	0	0	0	2	7	9	3	0	16		
ENSMUST00000193981						1	2	0	4	0	0	0	0	0	0	0		
ENSMUST00000193982	ENSMUSG00000003308	9	21229730	21239332	-1	0	0	0	67	0	0	32	0	0	0	32		Q9Z2X8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000193984	ENSMUSG00000103125	18	36975941	37833296	1	1	2	2	8	5	1	0	0	0	0	0	A0A0A6YY46	
ENSMUST00000193987	ENSMUSG00000063856	9	108338903	108340343	1	10	5	0	0	15	1	13238	7367	3553	3069	2088	A0A0A6YVV2	
ENSMUST00000193988						3	3	5	0	4	4	0	0	0	0	0		
ENSMUST00000193989	ENSMUSG00000104301	3	75274988	75482156	-1	9	11	4	11	12	3	0	0	0	0	0		
ENSMUST00000193991						27	25	90	39	36	14	4	31	13	4	7		
ENSMUST00000193997	ENSMUSG00000076478	6	41216073	41216526	1	0	0	0	0	0	0	0	2	0	0	0	A0A0A6YWQ1	
ENSMUST00000193998						4	3	5	17	1	3	0	0	0	0	0		
ENSMUST00000194003						2	0	0	28	2	1	0	2	0	0	4		
ENSMUST00000194006						0	0	0	0	0	0	0	0	0	0	14		
ENSMUST00000194007						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194010	ENSMUSG00000029004	5	23434441	23504235	1	1	0	0	0	0	0	18	23	27	0	68	A0A0A6YW47	
ENSMUST00000194011						0	0	4	11	0	0	1	0	0	0	3		
ENSMUST00000194012	ENSMUSG00000024440	18	38267092	38284402	-1	0	0	0	0	0	5	0	0	0	0	0	A0JNZ2	
ENSMUST00000194013						1	1	1	4	0	0	0	0	0	0	0		
ENSMUST00000194014						5	0	4	0	0	1	0	92	0	1	1		
ENSMUST00000194015						5	0	8	1	3	3	1	4	2	3	29		
ENSMUST00000194016	ENSMUSG00000027674	3	32949408	33143247	-1	12	5	23	23	20	21	0	0	0	0	0	F8SLQ1	
ENSMUST00000194020						2	0	3	1	3	1	0	0	0	0	0		
ENSMUST00000194022						0	4	2	1	5	0	0	0	0	0	0		
ENSMUST00000194023						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194025	ENSMUSG00000046337	1	36562692	36683183	-1	0	0	0	0	5	3	0	0	0	0	0	A0A0A6YWE8	
ENSMUST00000194026						3	2	6	47	6	0	0	0	0	0	1		
ENSMUST00000194027	ENSMUSG00000041842	3	84442198	84480429	-1	0	0	11	0	0	0	0	9	0	0	0	A0A0A6YXK5	
ENSMUST00000194028						3	4	4	8	3	2	0	0	0	0	0		
ENSMUST00000194029						1	4	28	3	7	4	9	93	16	4	23		
ENSMUST00000194033	ENSMUSG00000030768	1	183086266	183221522	-1	0	0	35	181	1	2	0	0	6	0	0	A0A0A6YWR7	
ENSMUST00000194034						0	2	2	2	0	0	4	2	3	0	2		
ENSMUST00000194035						4	2	10	5	1	1	2	3	2	0	2		
ENSMUST00000194036	ENSMUSG00000016494	1	194938819	194961279	1	0	0	1	0	0	1	0	0	0	0	0	A0A0A6YX84	
ENSMUST00000194037						3	4	2	1	11	2	4	0	2	5	4		
ENSMUST00000194038	ENSMUSG00000103800	18	36992371	37187657	1	19	18	48	31	32	5	0	0	0	0	0	Q91Y12	
ENSMUST00000194039	ENSMUSG00000034684	9	107681500	107710475	-1	7	1	0	138	9	0	0	0	0	0	12	A0A0A6YY06	
ENSMUST00000194041						3	3	7	0	5	4	0	0	0	0	0		
ENSMUST00000194042						0	0	0	216	7	0	0	0	0	0	1		
ENSMUST00000194044	ENSMUSG00000102367	1	133309827	133329722	1	0	0	0	0	0	0	0	0	0	0	0	I0J0X7	Q6Y4S4
ENSMUST00000194045	ENSMUSG00000032604	9	108507713	108515941	1	0	0	1	1	0	0	0	295	0	42	60	A0A0A6YY08	
ENSMUST00000194046	ENSMUSG00000037872	1	173331886	173333750	-1	1	0	0	6	3	4	0	0	0	0	1	A0A0A6YWZ3	
ENSMUST00000194047	ENSMUSG00000025651	9	108936633	108949623	1	0	0	0	0	5	5	44	200	75	0	32	A0A0A6YW82	
ENSMUST00000194048						1	2	0	6	2	1	0	0	0	0	0		
ENSMUST00000194049						0	3	5	0	0	4	18	0	68	0	0		
ENSMUST00000194050						10	13	35	154	10	12	0	0	0	0	0		
ENSMUST00000194051						180	143	407	227	194	100	90	250	275	369	215		
ENSMUST00000194054						45	60	106	155	70	44	3	7	6	0	6		
ENSMUST00000194056	ENSMUSG00000055421	14	93013410	93890679	-1	1	0	0	23	15	0	0	0	0	0	0	A0A0A6YWM0	
ENSMUST00000194057	ENSMUSG00000040629	1	166201201	166238747	-1	0	0	0	91	7	0	0	0	0	0	0	A0A0A6YWQ9	
ENSMUST00000194059	ENSMUSG00000102627	7	59995449	60005049	-1	0	0	0	0	0	1	0	0	0	0	0		Q9WU12
ENSMUST00000194061						12	0	23	6	23	10	0	0	3	4	4		
ENSMUST00000194062	ENSMUSG00000016481	1	195097382	195131586	-1	0	0	0	0	0	0	10	458	30	154	6	A0A0A6YXR6	
ENSMUST00000194063						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194064						4	5	2	1	1	1	0	0	0	0	2		
ENSMUST00000194065						36	47	117	57	55	36	2	42	21	2	33		
ENSMUST00000194066	ENSMUSG00000026791	2	32972990	32982083	-1	1	0	0	0	0	0	8	5	0	2	1	A0A0A6YXF7	
ENSMUST00000194069	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	0	3	63	20	40	0	22	A0A0A6YWB0	
ENSMUST00000194071	ENSMUSG00000094862	12	115242802	115243235	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXG2	
ENSMUST00000194073	ENSMUSG00000064145	9	108602942	108649386	-1	5	0	0	0	1	0	34	229	30	53	116	A0A0A6YW24	
ENSMUST00000194075	ENSMUSG00000014030	4	44524757	44710487	-1	0	0	0	0	0	1	1	0	0	0	0	A0A0A6YVX2	
ENSMUST00000194076						3	6	24	6	7	2	0	0	0	2	4		
ENSMUST00000194079	ENSMUSG00000023473	9	108826320	108852969	1	12	6	0	0	3	6	88	41	141	8	154	A0A0A6YX12	
ENSMUST00000194082						1	2	4	3	0	2	0	0	1	3	3		
ENSMUST00000194083						52	26	124	37	46	26	23	59	29	4	38		
ENSMUST00000194084						110	128	342	280	136	63	8	23	7	3	17		
ENSMUST00000194085	ENSMUSG00000028020	3	80843599	80913660	-1	7	7	2	0	8	1	0	0	0	0	0	A1KR23	
ENSMUST00000194086	ENSMUSG00000103371	Y	19113007	19139093	1	0	0	0	0	0	0	0	0	0	0	0	A0A087WRL2	
ENSMUST00000194087	ENSMUSG00000026523	1	175698593	175815734	1	7	7	0	0	1	0	0	0	0	0	0	A0A0A6YWX3	
ENSMUST00000194088						2641	2795	1503	1389	1620	566	29	170	138	22	183		
ENSMUST00000194089						0	1	2	1	2	0	0	7	20	2	0		
ENSMUST00000194091	ENSMUSG00000005705	8	105566698	105637393	-1	0	0	0	0	0	0	0	0	0	0	1	Q3UU47	P56473
ENSMUST00000194092						0	0	0	0	0	0	0	0	0	1	0		
ENSMUST00000194094						8	9	13	0	20	9	4	1	4	0	1		
ENSMUST00000194095						2	2	0	0	2	0	0	0	4	6	4		
ENSMUST00000194098						2	4	3	3	3	2	0	0	0	0	0		
ENSMUST00000194100						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194101						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194102	ENSMUSG00000048031	3	87435773	87500678	1	68	63	97	71	90	34	0	12	3	16	32		Q68SN8
ENSMUST00000194103						0	0	0	0	6	0	0	0	0	0	0		
ENSMUST00000194106						1	0	5	2	1	1	0	0	0	1	1		
ENSMUST00000194108						3	1	3	1	4	2	0	0	0	0	0		
ENSMUST00000194111	ENSMUSG00000016481	1	195097382	195131586	-1	3	5	9	46	5	14	217	354	175	162	209	A0A0A6YXN9	
ENSMUST00000194115						0	0	0	1	2	0	0	0	0	0	0		
ENSMUST00000194116						3	2	0	0	3	2	1	3	0	5	1		
ENSMUST00000194118						0	0	4	0	4	0	15	82	24	22	30		
ENSMUST00000194119						7	0	3	0	4	0	0	0	0	0	0		
ENSMUST00000194122						0	0	0	0	0	0	0	0	0	0	3		
ENSMUST00000194124						1	0	3	0	3	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000194125						3	2	3	0	0	0	0	0	0	0	0		
ENSMUST00000194126						8	15	31	17	13	10	6	36	25	5	28		
ENSMUST00000194127						0	7	0	103	3	5	0	0	0	0	3		
ENSMUST00000194128						12	10	6	11	9	7	3	10	5	2	4		
ENSMUST00000194129	ENSMUSG00000055421	14	93013410	93890679	-1	0	0	0	2	0	0	0	0	0	0	0	A0A0A6YVP5	
ENSMUST00000194132						0	7	14	7	0	4	0	2	0	2	0		
ENSMUST00000194134	ENSMUSG00000027820	3	63241537	63386030	1	181	217	226	297	213	133	1	11	6	1	2		Q61391
ENSMUST00000194139						5	1	8	2	9	0	0	176	19	28	15		
ENSMUST00000194142						3	2	1	2	1	2	0	0	0	0	0		
ENSMUST00000194144	ENSMUSG00000095788	3	15371653	15426520	-1	1	0	0	0	0	0	380	1997	723	2433	828	A0A0A6YWR3	
ENSMUST00000194147	ENSMUSG00000052911	9	108479736	108490530	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWI2	
ENSMUST00000194149						2	0	0	1	0	0	0	2	0	0	0		
ENSMUST00000194150	ENSMUSG00000027820	3	63241537	63386030	1	1	0	0	186	4	2	0	0	0	0	0		Q61391
ENSMUST00000194152						7	5	2	4	8	0	0	0	1	0	1		
ENSMUST00000194153						32	20	35	27	24	24	2	14	1	3	8		
ENSMUST00000194156	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194157						9	11	17	2	11	6	0	0	0	0	0		
ENSMUST00000194158						2	0	7	0	0	2	24	12	8	0	21		
ENSMUST00000194159	ENSMUSG00000094322	12	114299961	114300389	-1	3	3	4	2	4	0	0	0	0	0	14	A0A0A6YWH6	
ENSMUST00000194162	ENSMUSG00000104213	12	113406604	113416324	-1	25	12	52	20	22	11	99	103	140	208	298	A0A0A6YW14	
ENSMUST00000194163						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000194164						55	35	223	56	41	15	0	0	0	0	0		
ENSMUST00000194165						2	1	6	107	7	1	0	0	0	0	0		
ENSMUST00000194166						0	0	11	0	0	3	0	0	0	0	0		
ENSMUST00000194167						1	2	2	1	0	0	3	0	0	0	0		
ENSMUST00000194168						1	1	0	0	0	0	7	31	15	25	1		
ENSMUST00000194170						11	12	22	17	18	1	95	205	279	377	400		
ENSMUST00000194171	ENSMUSG00000006676	9	108490602	108502337	1	0	7	0	0	0	0	217	474	129	57	196	A0A0A6YWN9	
ENSMUST00000194172	ENSMUSG00000037624	1	189207930	189402273	-1	0	1	0	0	2	0	0	0	0	0	0	A0A0A6YXX0	
ENSMUST00000194173						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194175	ENSMUSG00000033860	3	83007724	83015049	1	0	0	0	0	0	0	0	0	0	0	0	Q3UER8	
ENSMUST00000194176						6	6	0	0	5	6	0	0	0	0	0		
ENSMUST00000194179						0	0	0	0	0	2	0	0	0	0	0		
ENSMUST00000194181	ENSMUSG00000025764	3	41555731	41616864	1	3	3	0	2	3	0	0	0	0	0	0	A0A0A6YWS2	
ENSMUST00000194182	ENSMUSG00000015314	1	171917515	171953170	1	0	3	3	6	2	0	0	0	0	0	1	A0A0A6YY21	
ENSMUST00000194183	ENSMUSG00000032558	9	104002544	104153483	1	0	1	1	0	0	0	0	0	0	0	1	A0A0A6YXM1	
ENSMUST00000194184	ENSMUSG00000040329	3	7569994	7613760	-1	5	3	1	20	0	2	0	2	0	1	0	Q3UT18	
ENSMUST00000194185						3	3	56	6	2	5	0	0	0	0	0		
ENSMUST00000194186	ENSMUSG00000033898	1	139804167	139858702	-1	2	3	12	6	1	1	0	0	0	1	0	Q61405	
ENSMUST00000194187						2	10	5	4	11	1	0	0	0	0	0		
ENSMUST00000194188						3	0	15	3	0	0	0	0	4	0	7		
ENSMUST00000194189						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194190	ENSMUSG00000103144	18	37661793	37841873	1	0	0	21	0	0	0	0	0	0	4	2	Q91XZ0	
ENSMUST00000194191						0	0	0	0	0	0	0	0	1	0	1		
ENSMUST00000194193	ENSMUSG00000004892	3	87987531	88000230	-1	0	2	2	36	0	0	0	0	0	0	0	A0A0A6YW95	
ENSMUST00000194195	ENSMUSG00000026114	1	37214434	37263384	1	0	0	0	0	0	0	0	0	0	0	0		Q9JJZ8
ENSMUST00000194196						153	210	379	153	178	91	4	11	3	1	5		
ENSMUST00000194197						0	0	0	0	0	0	0	0	0	0	1		
ENSMUST00000194199						10	11	13	148	11	7	0	0	0	0	0		
ENSMUST00000194201	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	3	0	0	0	0	0	0	A0A0A6YXE3	
ENSMUST00000194204	ENSMUSG00000038026	1	172320501	172329318	-1	3	3	20	8	5	9	0	2	2	0	0	Q544N3	P48543
ENSMUST00000194206	ENSMUSG00000032936	9	107935674	107949691	1	0	15	37	3	0	0	0	1	0	0	0	A0A0A6YW88	
ENSMUST00000194207	ENSMUSG00000103019	CHR_MG184_PATCH	72414307	72430711	1	17	18	42	42	21	11	16	35	19	3	27	B2RS80	Q9QYC7
ENSMUST00000194208						0	0	0	6	0	9	3	0	0	0	0		
ENSMUST00000194209						0	0	0	28	0	0	3	0	0	0	0		
ENSMUST00000194213	ENSMUSG00000047539	1	182313102	182341629	-1	1	0	0	16	0	2	20	30	52	0	14	A0A0A6YVQ6	
ENSMUST00000194214						1	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000194217	ENSMUSG00000026587	1	158362273	158691781	1	5	5	17	5	4	2	0	0	0	0	0	A0A0A6YWJ9	
ENSMUST00000194218						2	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000194219						5	3	7	1	1	3	0	0	0	0	0		
ENSMUST00000194220	ENSMUSG00000033488	1	157458577	157492638	1	57	56	120	55	86	60	7	15	10	7	10	A0A0A6YXW5	
ENSMUST00000194224	ENSMUSG00000032612	9	108347853	108392545	1	53	44	186	77	63	23	43	92	112	11	183	A0A0A6YVY7	
ENSMUST00000194225						5	0	2	4	7	3	9	0	0	0	11		
ENSMUST00000194226						10	5	6	311	22	12	0	3	7	1	7		
ENSMUST00000194228						2	2	1	1	0	0	0	0	0	0	0		
ENSMUST00000194229	ENSMUSG00000066671	1	174442159	174449602	1	0	7	3	8	3	0	0	0	0	0	0	E9Q050	
ENSMUST00000194230						3	0	4	0	0	0	0	0	0	0	0		
ENSMUST00000194231						3	1	0	2	3	0	0	0	0	0	0		
ENSMUST00000194232						4	13	5	8	9	11	0	0	1	1	1		
ENSMUST00000194233						1	1	1	4	0	1	1	0	0	0	0		
ENSMUST00000194234						1	1	0	1	0	1	0	0	0	0	0		
ENSMUST00000194235						0	16	0	144	28	0	0	0	0	0	0		
ENSMUST00000194236						96	105	86	132	140	86	4	25	9	2	18		
ENSMUST00000194237	ENSMUSG00000055067	1	178951960	179518041	-1	10	4	15	22	14	1	0	1	2	0	4	A0A0A6YWP2	
ENSMUST00000194240						35	29	83	64	49	20	0	3	0	1	1		
ENSMUST00000194242						0	1	4	6	7	2	1	0	0	0	0		
ENSMUST00000194244	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194248	ENSMUSG00000006395	4	118359990	118362744	1	2	0	0	0	0	0	19	56	13	19	0		
ENSMUST00000194250						4	1	0	0	0	0	0	0	2	0	0		
ENSMUST00000194251						2	4	7	0	5	9	0	0	0	0	0		
ENSMUST00000194252	ENSMUSG00000039542	9	49502136	49798925	-1	54	42	208	190	67	29	5	0	0	0	0	A0A0A6YY91	
ENSMUST00000194253						30	25	59	33	37	18	8	53	15	4	27		
ENSMUST00000194254						2	0	0	2	1	0	0	0	0	0	0		
ENSMUST00000194256						1	0	2	1	0	1	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000194257	ENSMUSG00000102364	12	115067560	115068002	-1	12	15	31	8	18	20	1	1	2	1	0	A0A0A6YY60	
ENSMUST00000194258	ENSMUSG00000028069	3	88043108	88055993	1	1	0	0	0	2	0	0	0	1	0	0	A0A0A6YWB3	
ENSMUST00000194259						3	6	11	3	7	1	0	0	0	0	0		
ENSMUST00000194260						0	0	0	0	0	1	0	18	0	6	8		
ENSMUST00000194263	ENSMUSG00000057335	1	176733653	176814067	-1	0	0	2	0	0	0	1	0	5	0	0	A0A0A6YWV9	
ENSMUST00000194265						1	0	2	0	1	0	0	0	0	0	0		
ENSMUST00000194269						0	0	0	0	0	0	0	2	2	0	2		
ENSMUST00000194271	ENSMUSG00000032586	9	107950136	107972270	1	0	0	0	0	0	0	0	0	5	0	5	A0A0A6YWT5	
ENSMUST00000194272						5	6	9	8	3	3	0	0	2	0	0		
ENSMUST00000194278	ENSMUSG00000037318	1	193175453	193201703	-1	0	8	7	0	0	3	11	137	0	0	39	A0A0A6YWR4	
ENSMUST00000194279	ENSMUSG00000040329	3	7569994	7613760	-1	24	22	28	29	34	15	0	0	0	0	0	Q544C8	P10168
ENSMUST00000194280						2	0	0	7	0	1	0	1	0	0	3		
ENSMUST00000194282						6	1	27	4	4	4	0	0	0	3	0		
ENSMUST00000194284						0	0	0	0	2	2	0	0	0	0	0		
ENSMUST00000194288	ENSMUSG00000026527	1	175059087	175492500	-1	0	0	0	0	0	0	0	0	0	0	0	Q45FE1	
ENSMUST00000194290						5	3	3	11	7	5	0	0	7	0	11		
ENSMUST00000194291						1	0	0	0	1	1	1	0	1	0	0		
ENSMUST00000194296	ENSMUSG00000070942	1	40324610	40367562	1	16	20	33	30	17	11	34	64	69	23	45	Q149G7	Q9ERS7
ENSMUST00000194297						0	0	0	0	8	0	0	0	0	0	0		
ENSMUST00000194298						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194299						5	4	3	6	9	4	0	0	0	0	0		
ENSMUST00000194300						0	1	0	0	3	0	0	0	0	0	0		
ENSMUST00000194301						14	9	14	14	13	14	3	8	6	0	4		
ENSMUST00000194302						8	6	17	10	3	5	4	6	7	5	26		
ENSMUST00000194303						2	5	4	28	3	8	0	8	0	2	12		
ENSMUST00000194304	ENSMUSG00000076614	12	113325240	113330523	-1	26	14	102	32	26	18	9	2	7	3	18	A0A0A6YWR2	
ENSMUST00000194305						11	4	18	6	5	7	0	0	0	0	0		
ENSMUST00000194306	ENSMUSG00000039748	1	175880581	175913489	1	1	0	4	3	3	0	1	0	0	0	0	A0A0A6YWZ8	
ENSMUST00000194307						0	0	0	0	1	0	0	0	0	0	1		
ENSMUST00000194309						3	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000194310						0	0	1	0	2	0	0	0	0	0	0		
ENSMUST00000194312	ENSMUSG00000051375	18	38185914	38212053	-1	1	1	4	0	0	2	0	0	1	0	0	A0A0A6YX79	
ENSMUST00000194313						57137	96148	33806	15967	28692	10541	108	797	383	220	491		
ENSMUST00000194315	ENSMUSG00000052613	10	73099342	74649737	1	0	3	0	0	4	0	0	0	0	0	0	A0A0A6YWL3	
ENSMUST00000194319	ENSMUSG00000063659	1	177442351	177450764	1	0	0	0	0	0	0	3	4	12	0	6	A0A0A6YX98	
ENSMUST00000194320						2	3	12	39	4	5	0	0	0	0	0		
ENSMUST00000194321						0	3	1	1	1	0	0	0	0	0	0		
ENSMUST00000194324	ENSMUSG00000027820	3	63241537	63386030	1	0	0	0	0	1	0	0	0	0	0	0	A0A0A6YY36	
ENSMUST00000194325						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000194326						2	2	1	1	2	1	0	0	0	0	0		
ENSMUST00000194327	ENSMUSG00000046836	1	183276352	183297269	-1	0	0	4	0	0	0	65	20	126	0	29	A0A0A6YVS9	
ENSMUST00000194329						7	6	22	12	11	10	0	0	0	0	0		
ENSMUST00000194333						0	4	0	0	0	3	0	0	0	0	0		
ENSMUST00000194335						0	2	1	0	1	0	0	0	2	0	1		
ENSMUST00000194338						0	3	23	10	4	3	0	0	0	0	0		
ENSMUST00000194344	ENSMUSG00000037190	9	107539007	107542193	-1	0	0	0	0	0	0	0	0	4	0	4	A0A0A6YWG0	
ENSMUST00000194345						0	0	2	0	0	1	0	0	0	1	0		
ENSMUST00000194346	ENSMUSG00000025766	3	41742611	41803320	1	0	0	0	0	0	0	0	0	1	4	1		Q8BGN2
ENSMUST00000194348						0	0	0	11	0	0	0	0	0	0	0		
ENSMUST00000194349						2	0	0	1	1	1	0	0	0	0	0		
ENSMUST00000194350	ENSMUSG00000076695	12	114682632	114683065	-1	0	0	3	6	0	0	0	0	0	2	9	A0A0A6YXN4	
ENSMUST00000194354						0	1	0	2	1	0	0	0	0	0	0		
ENSMUST00000194355						3	3	7	3	7	3	0	0	0	0	0		
ENSMUST00000194359						2	1	3	2	4	1	1	10	1	1	14		
ENSMUST00000194361	ENSMUSG00000026080	1	38863867	38898161	-1	0	0	0	16	0	0	0	0	0	0	0	A0A0A6YVW5	
ENSMUST00000194362						17	11	7	6	17	5	1	4	2	0	1		
ENSMUST00000194363						1	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000194365						0	0	3	2	2	0	0	6	1	0	6		
ENSMUST00000194366	ENSMUSG00000026565	1	165865154	166002678	-1	0	0	0	0	0	0	0	0	1	0	0	A0A0A6YWN1	
ENSMUST00000194367	ENSMUSG00000078780	3	15946870	16006437	-1	8	4	8	12	8	0	1049	8053	1142	3001	1134	Q1AN92	
ENSMUST00000194369	ENSMUSG00000026587	1	158362273	158691781	1	10	8	29	15	14	0	0	9	2	1	3	A0A0A6YXJ4	
ENSMUST00000194371	ENSMUSG00000057335	1	176733653	176814067	-1	0	0	0	0	0	0	0	0	14	2	2	A0A0A6YXT4	
ENSMUST00000194372						2	0	0	2	3	2	0	0	0	0	1		
ENSMUST00000194373						8	8	9	0	3	3	0	0	0	0	0		
ENSMUST00000194374						12	5	16	15	13	9	0	0	0	0	0		
ENSMUST00000194376	ENSMUSG00000028182	3	155093434	155194280	1	1	1	1	1	0	0	0	1	0	1	0		Q14DL3
ENSMUST00000194377						1	2	1	0	1	0	0	0	0	0	0		
ENSMUST00000194380						3	2	0	5	0	0	0	0	0	0	0		
ENSMUST00000194381	ENSMUSG00000070283	9	108565537	108567434	-1	0	0	0	0	0	0	45	29	17	70	20	A0A0A6YVW1	
ENSMUST00000194383						0	7	0	3	3	8	0	0	0	0	2		
ENSMUST00000194384						0	0	0	0	1	0	0	0	2	0	0		
ENSMUST00000194385	ENSMUSG00000006673	9	108516806	108560163	1	0	0	0	0	0	0	3	0	3	0	0	A0A0A6YXZ6	
ENSMUST00000194386	ENSMUSG00000026843	2	31572651	31617526	1	0	0	0	0	0	0	0	0	0	0	4	A0A0A6YY39	
ENSMUST00000194387						0	0	2	5	2	1	0	22	8	7	2		
ENSMUST00000194388						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194391	ENSMUSG00000104158	1	175920329	175922225	1	16	13	32	18	13	9	0	0	0	0	0		
ENSMUST00000194392	ENSMUSG00000036850	2	24974117	24975098	-1	9	7	13	71	12	5	0	0	2	3	0	A0A0A6YXF9	
ENSMUST00000194393						1	9	7	6	9	1	0	0	1	0	0		
ENSMUST00000194394						1	0	3	2	3	0	0	0	0	0	0		
ENSMUST00000194395						3	1	0	0	5	2	0	0	0	0	0		
ENSMUST00000194397						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194398						89	80	210	3443	160	110	2	11	11	1	6		
ENSMUST00000194399	ENSMUSG00000076467	6	41116007	41116468	1	4	0	2	0	6	0	0	18	0	30	13	A0A0B4J1P8	
ENSMUST00000194400	ENSMUSG00000032580	9	107740371	107770996	-1	0	0	4	0	0	0	11	27	2	2	8	A0A0A6YY86	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000194402	ENSMUSG00000037624	1	189207930	189402273	-1	0	0	0	0	3	0	0	0	0	0	0	A0A0A6YXK1	
ENSMUST00000194404	ENSMUSG00000102455	CHR_MG184_PATCH	72355446	72359761	1	4	4	4	14	6	5	4	5	0	2	4		
ENSMUST00000194405						17	14	29	33	28	13	0	0	0	0	0		
ENSMUST00000194407						218	195	664	247	313	150	8	7	11	1	10		
ENSMUST00000194408						15	9	40	18	9	0	0	26	0	4	12		
ENSMUST00000194410	ENSMUSG00000098546	CHR_MG3829_PATCH	88068279	88084729	1	4	1	4	0	0	6	0	277	4	3	7		
ENSMUST00000194411	ENSMUSG00000094325	Y	17874741	17967603	1	0	8	0	3	0	3	0	0	0	0	0	Q3TTD8	
ENSMUST00000194412	ENSMUSG00000016181	1	193091104	193130272	-1	4	0	0	2	0	0	0	0	0	0	2	A0A0A6YXR2	
ENSMUST00000194413						2	2	11	15	8	4	3	7	2	0	7		
ENSMUST00000194414						2	1	3	0	0	0	2	0	1	3	0		
ENSMUST00000194415	ENSMUSG00000004880	1	181815335	181843046	-1	2	0	0	0	3	4	0	0	370	110	282	A0A0A6YY12	
ENSMUST00000194418	ENSMUSG00000103677	18	37685210	37841873	1	7	14	44	20	8	6	0	0	0	0	5		Q91XY4
ENSMUST00000194419						1	3	11	1	6	0	0	0	0	0	2		
ENSMUST00000194421						2	2	7	9	1	1	0	2	0	0	1		
ENSMUST00000194423						4	4	10	2	4	2	0	0	0	0	0		
ENSMUST00000194424	ENSMUSG00000034684	9	107681500	107710475	-1	5	1	4	3	4	0	0	0	0	0	5	A0A0A6YXX2	
ENSMUST00000194427						2	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000194429						2	0	3	28	5	0	0	0	1	0	0		
ENSMUST00000194430						1	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000194432						46	28	66	58	40	25	82	139	36	6	96		
ENSMUST00000194433	ENSMUSG00000057969	9	107597674	107609229	-1	0	0	0	3	0	2	0	0	0	0	0	A0A0A6YW56	
ENSMUST00000194434	ENSMUSG00000026496	1	180568924	180601254	1	10	3	6	52	1	3	0	0	0	0	0	A0A0A6YX03	
ENSMUST00000194435						3	4	5	2	1	2	0	0	0	0	0		
ENSMUST00000194436	ENSMUSG00000032582	9	107773559	107873237	-1	2	0	0	1	0	2	0	3	0	0	0	A0A0A6YY54	
ENSMUST00000194437	ENSMUSG00000026566	1	165592240	165634538	-1	0	2	0	14	2	1	0	0	0	7	0	A0A0A6YXW1	
ENSMUST00000194438						1	0	2	6	2	0	0	1	0	0	4		
ENSMUST00000194440	ENSMUSG00000028068	3	88081971	88121048	1	21	16	63	15	38	9	0	41	0	9	0	Q3UQP1	
ENSMUST00000194441						4	10	21	11	7	3	3	0	0	18	1		
ENSMUST00000194443	ENSMUSG00000049133	3	93197278	93221391	1	1	0	0	0	0	0	0	0	0	0	0	A0A0A6YWQ2	
ENSMUST00000194445						1	3	5	1	3	2	0	0	0	0	0		
ENSMUST00000194446	ENSMUSG00000034751	13	102732486	103334497	-1	20	0	21	0	14	0	0	0	18	0	0	A0A0A6YXG1	
ENSMUST00000194447						35	27	87	296	40	9	0	0	0	0	0		
ENSMUST00000194448						0	0	4	0	0	2	1	0	0	16	0		
ENSMUST00000194449						0	3	4	3	2	0	0	0	0	0	0		
ENSMUST00000194450						0	0	0	1	1	0	0	0	0	0	0		
ENSMUST00000194452	ENSMUSG00000028078	3	86786151	86920852	-1	2	0	0	34	0	2	5	0	0	0	0	A0A0A6YX33	
ENSMUST00000194455	ENSMUSG00000026715	1	160978585	161005863	1	4	3	10	0	3	6	0	0	0	15	0	A0A0A6YX85	
ENSMUST00000194457						2	0	0	3	2	0	0	0	0	0	0		
ENSMUST00000194458						1312	1168	3029	921	1527	821	29	82	70	25	114		
ENSMUST00000194460						0	0	0	3	0	1	1	2	0	0	0		
ENSMUST00000194461	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	2	1	2	1	2	0	0	0	0	2	0		Q9CY62
ENSMUST00000194462	ENSMUSG00000027737	3	49892526	50443614	-1	3	4	23	1	4	2	0	0	5	4	0	A0A0B4J1P7	
ENSMUST00000194464						1	0	2	4	0	0	0	0	0	0	0		
ENSMUST00000194466						2	1	0	2	0	2	0	0	0	0	0		
ENSMUST00000194469	ENSMUSG00000025651	9	108936633	108949623	1	2	0	0	0	3	0	0	96	0	7	0	A0A0A6YWX6	
ENSMUST00000194471						9	5	15	2	10	4	0	0	0	0	0		
ENSMUST00000194473						3	3	0	0	1	0	1	0	0	0	0		
ENSMUST00000194475						1	0	6	1	0	2	1	1	0	0	0		
ENSMUST00000194476						0	0	0	0	0	0	19	84	29	5	15		
ENSMUST00000194477						1	2	5	3	1	0	0	0	0	0	0		
ENSMUST00000194478	ENSMUSG00000028559	4	109061145	109202272	-1	0	0	0	0	0	0	0	40	0	25	0	A0A0A6YXH3	
ENSMUST00000194480						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194489						0	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000194492	ENSMUSG00000103068	_MMCHR1_CHORI29_IDI	61011483	61032732	1	0	0	5	0	3	2	0	3	3	7	5	A2A6A7	
ENSMUST00000194493						14	8	52	455	23	14	1	17	2	1	4		
ENSMUST00000194494						4	2	1	3	2	0	0	0	0	0	0		
ENSMUST00000194496						0	0	0	5	0	0	0	0	0	0	1		
ENSMUST00000194499						8	3	5	10	5	4	0	10	9	2	19		
ENSMUST00000194501						9	16	27	55	23	8	0	0	0	0	0		
ENSMUST00000194504						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194505	ENSMUSG00000038034	1	172261641	172319841	1	2	1	0	0	5	4	14	67	5	0	0	A0A0A6YWK7	
ENSMUST00000194510						1	3	2	5	9	3	2	12	4	1	6		
ENSMUST00000194511						0	0	4	2	2	3	0	0	0	0	0		
ENSMUST00000194516						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194518						2	3	2	1	1	3	0	0	0	0	0		
ENSMUST00000194521	ENSMUSG00000095789	5	129908540	129913789	1	2	1	0	4	4	3	3	3	0	0	2		Q497P3
ENSMUST00000194522						1	1	4	3	3	1	2	4	9	0	3		
ENSMUST00000194523						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194527						7	3	13	6	8	2	0	1	0	0	2		
ENSMUST00000194528						8	8	5	8	12	8	0	0	0	0	0		
ENSMUST00000194531	ENSMUSG00000038179	1	171632403	171653035	-1	4	3	3	0	3	0	1	42	0	7	12		
ENSMUST00000194533						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194536						26	20	101	31	18	12	1	5	2	2	0		
ENSMUST00000194538						17	23	46	31	35	11	0	0	0	0	5		
ENSMUST00000194540						0	0	20	5	0	7	0	0	0	21	38		
ENSMUST00000194542	ENSMUSG00000003308	9	21229730	21239332	-1	5	2	11	248	31	9	295	646	354	96	288		Q9Z2X8
ENSMUST00000194543	ENSMUSG00000056050	1	183326725	183369553	-1	7	2	3	88	12	3	36	60	112	4	68		
ENSMUST00000194544	ENSMUSG00000102836	18	36969916	37833296	1	0	0	0	0	0	2	0	0	0	0	0	Q8K491	
ENSMUST00000194546	ENSMUSG00000036334	3	59316735	59344394	-1	0	16	101	45	7	37	0	0	0	0	0		Q3V1M1
ENSMUST00000194548						3	0	3	11	0	0	22	30	12	11	27		
ENSMUST00000194552	ENSMUSG00000026078	1	38985608	38997238	1	4	1	6	11	2	2	120	332	192	639	146	A0A0A6YXV1	
ENSMUST00000194554						81	60	461	119	47	50	1	11	1	0	4		
ENSMUST00000194555	ENSMUSG00000026527	1	175059087	175492500	-1	0	7	13	29	9	0	0	0	0	0	0	Q80XD3	
ENSMUST00000194557	ENSMUSG00000019230	1	138825186	138848577	-1	4	0	1	0	1	1	0	0	0	0	0	A0A0A6YY42	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000194558	ENSMUSG00000027782	3	69067149	69127113	-1	0	0	0	55	0	0	860	2497	1384	252	849	Q4FJX1	O35343
ENSMUST00000194559						22	24	127	99	37	19	0	0	0	0	0		
ENSMUST00000194561	ENSMUSG00000015314	1	171917515	171953170	1	0	0	0	0	0	0	0	8	3	30	21	C6ESQ1	
ENSMUST00000194562						4	3	2	0	1	1	0	0	0	0	0		
ENSMUST00000194563	ENSMUSG00000026116	1	36792191	36943666	-1	0	33	0	103	0	23	88	88	438	0	526		O70472
ENSMUST00000194565						16	13	29	16	8	11	5	11	4	4	8		
ENSMUST00000194566						4	2	20	1	1	5	0	1	0	0	0		
ENSMUST00000194568						7	9	8	6	4	2	0	2	0	14	3		
ENSMUST00000194574						0	1	0	0	0	2	0	0	0	0	0		
ENSMUST00000194575						85	47	95	1067	166	99	0	0	1	0	0		
ENSMUST00000194576						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194578						1	1	1	0	0	0	0	0	0	0	0		
ENSMUST00000194581	ENSMUSG00000096078	12	115446409	115446869	-1	0	0	0	13	1	0	0	0	0	0	4	A0A0A6YXZ4	
ENSMUST00000194582						0	0	1	4	0	0	0	0	0	0	0		
ENSMUST00000194585						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194587						28	36	147	134	47	18	1	2	4	1	5		
ENSMUST00000194589						0	5	0	0	2	0	23	58	0	2	0		
ENSMUST00000194591						6	8	39	12	10	2	0	0	0	0	0		
ENSMUST00000194592	ENSMUSG00000026715	1	160978585	161005863	1	8	4	18	0	9	10	0	0	0	0	0	A0A0A6YWH7	
ENSMUST00000194593						6	2	15	6	13	4	0	0	0	0	0		
ENSMUST00000194595	ENSMUSG00000096879	3	93068823	93075505	1	9	16	7	9	16	4	0	0	0	1	0	Q3UT66	
ENSMUST00000194596						1	2	13	12	7	0	0	0	0	0	0		
ENSMUST00000194597	ENSMUSG00000029866	6	41686330	41704339	-1	0	2	1	2	0	0	0	0	0	0	0	A0A0A6YXM8	
ENSMUST00000194598	ENSMUSG00000067629	17	26941253	26972434	1	7	13	70	66	36	10	9	17	11	1	18		F6SEU4
ENSMUST00000194603	ENSMUSG00000037892	3	49743296	49757325	-1	0	9	39	4	7	2	0	0	0	0	0	A0A0A6YXT8	
ENSMUST00000194604	ENSMUSG00000041355	3	88575876	88588419	1	2	1	0	0	1	0	0	11	7	16	0	A0A0A6YWL0	
ENSMUST00000194605						2	3	7	6	7	6	0	5	1	14	0		
ENSMUST00000194606	ENSMUSG00000057969	9	107597674	107609229	-1	1	0	0	7	0	0	0	0	0	0	0	A0A0A6YXC1	
ENSMUST00000194608	ENSMUSG00000026496	1	180568924	180601254	1	0	0	0	101	2	0	0	0	0	0	0	A0A0A6YY63	
ENSMUST00000194612	ENSMUSG00000026471	1	155127277	155146814	-1	3	5	2	4	8	0	0	27	10	34	8	A0A0A6YXY6	
ENSMUST00000194613						24	14	36	147	21	8	8	22	15	2	13		
ENSMUST00000194614						2	2	4	2	0	0	0	3	0	1	4		
ENSMUST00000194615						6	1	10	5	4	2	0	0	0	0	0		
ENSMUST00000194617						4	2	102	44	8	0	23	107	43	13	29		
ENSMUST00000194618						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194619						142	128	113	91	151	59	3	36	13	22	33		
ENSMUST00000194620						8	2	9	112	7	7	0	1	2	2	3		
ENSMUST00000194621						3	5	3	1	0	1	0	0	0	0	0		
ENSMUST00000194622						0	2	0	0	1	2	0	0	0	0	0		
ENSMUST00000194623						9	7	3	8	6	0	0	3	8	1	3		
ENSMUST00000194624						138	98	893	144	140	52	0	3	2	10	4		
ENSMUST00000194625	ENSMUSG00000103290	12	114764450	114764883	-1	0	0	0	0	1	0	0	0	0	1	3	A0A0A6YVW3	
ENSMUST00000194627						31	35	137	80	36	27	0	1	0	0	0		
ENSMUST00000194632	ENSMUSG00000033684	1	155776029	155812889	-1	0	0	0	0	0	0	9280	10036	6400	843	3615		Q8BND5
ENSMUST00000194633						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000194634						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194635						3	0	1	0	0	0	0	0	0	0	0		
ENSMUST00000194636	ENSMUSG00000039748	1	175880581	175913489	1	0	0	1	0	0	0	2	12	0	1	5	A0A0A6YVY2	
ENSMUST00000194638	ENSMUSG00000058729	1	180641150	180690694	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXQ9	
ENSMUST00000194639						9	12	33	28	31	9	4	5	2	1	12		
ENSMUST00000194641	ENSMUSG00000037174	3	51252720	51340663	-1	20	19	14	30	28	15	55	267	99	14	83		Q9JHC9
ENSMUST00000194649	ENSMUSG00000039221	3	28805436	28807424	1	0	0	0	0	2	0	234	422	151	515	98		Q9D7S7
ENSMUST00000194650						3	3	6	9	7	8	20	71	0	17	42		
ENSMUST00000194652						2	0	0	1	0	0	7	0	14	0	26		
ENSMUST00000194654	ENSMUSG00000005705	8	105566698	105637393	-1	0	4	0	3	0	0	0	0	0	0	0	A0A0A6YX09	
ENSMUST00000194655	ENSMUSG00000051678	18	37333921	37337674	1	0	0	5	3	0	0	0	0	0	0	0	A0A0A6YX01	
ENSMUST00000194656	ENSMUSG00000042197	1	33761545	33814595	-1	0	0	0	0	0	0	0	0	5	2	4	A0A0A6YX30	
ENSMUST00000194657	ENSMUSG00000026080	1	38863867	38898161	-1	8	9	12	17	16	7	1	0	0	0	0	A0A0A6YWB7	
ENSMUST00000194658						9	14	64	15	21	6	0	1	0	0	0		
ENSMUST00000194660						21	14	31	24	26	13	0	2	1	1	0		
ENSMUST00000194663	ENSMUSG00000021466	13	63508328	63573598	-1	0	0	37	182	30	23	0	0	0	6	0	A0A0A6YWZ4	
ENSMUST00000194666						8	5	4	78	7	1	43	45	25	75	15		
ENSMUST00000194668	ENSMUSG00000102976	1	133619862	133661380	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWW2	
ENSMUST00000194670						176	131	802	202	225	103	43	73	48	14	103		
ENSMUST00000194674						15	17	21	10	17	6	1	5	5	0	4		
ENSMUST00000194675						10	6	10	1	10	2	13	41	7	1	8		
ENSMUST00000194676	ENSMUSG00000033793	1	5070018	5162529	1	1	0	0	157	3	2	2	4	25	7	10	A0A0A6YVU0	
ENSMUST00000194677	ENSMUSG00000026639	1	193207699	193343878	1	25	11	13	25	7	0	14	55	24	9	33		Q61087
ENSMUST00000194681						32	14	28	40	40	23	0	0	4	0	0		
ENSMUST00000194682						0	1	2	0	0	0	0	8	0	0	14		
ENSMUST00000194684						0	1	0	0	0	0	0	0	0	0	1		
ENSMUST00000194685						10	4	12	1	7	4	2	1	0	1	1		
ENSMUST00000194687	ENSMUSG00000104267	Y	13042891	13045326	1	6	8	0	0	10	6	0	0	0	0	0	A0A0A6YXX7	
ENSMUST00000194688						1	2	0	0	0	0	0	0	0	0	0		
ENSMUST00000194689						0	0	3	1	1	2	1	0	0	0	0		
ENSMUST00000194690	ENSMUSG00000026674	1	169972307	170110762	-1	61	42	60	57	69	44	0	0	0	0	131		Q62371
ENSMUST00000194691						12	14	0	20	20	7	0	0	0	0	0		
ENSMUST00000194692						4	12	22	22	17	1	0	0	1	0	0		
ENSMUST00000194693						0	1	6	0	0	1	0	0	0	0	0		
ENSMUST00000194694						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000194695						2	3	1	3	4	0	0	1	11	0	6		
ENSMUST00000194696						0	1	1	0	0	2	0	0	0	0	0		
ENSMUST00000194698	ENSMUSG00000039952	9	108204634	108263958	-1	1	1	2	0	0	0	0	0	0	0	0	A0A0A6YXB6	
ENSMUST00000194700						0	0	0	0	0	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000194701	ENSMUSG00000007815	9	108306129	108337934	1	0	0	0	13	0	0	696	983	1283	838	991	A0A0A6YXF6	
ENSMUST00000194703						1	2	3	0	0	0	0	4	0	0	0		
ENSMUST00000194705						0	2	4	5	4	3	0	0	0	0	0		
ENSMUST00000194707	ENSMUSG00000049133	3	93197278	93221391	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVP3	
ENSMUST00000194713						135	125	349	119	132	58	3	20	17	2	26		
ENSMUST00000194717						1	2	0	10	0	0	0	0	0	0	0		
ENSMUST00000194721						4	3	2	0	6	1	0	0	0	0	0		
ENSMUST00000194725						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194727	ENSMUSG00000057335	1	176733653	176814067	-1	12	0	15	0	0	0	0	0	0	0	0		Q6A065
ENSMUST00000194729						25	30	213	76	47	35	0	4	2	1	2		
ENSMUST00000194730						7	5	9	238	9	3	0	0	0	0	0		
ENSMUST00000194731						0	0	0	0	2	1	0	0	0	1	0		
ENSMUST00000194732						23	22	12	15	22	10	44	167	80	22	79		
ENSMUST00000194733						3	3	1	9	6	6	0	3	0	0	0		
ENSMUST00000194734						3	3	3	1	21	0	0	0	0	0	0		
ENSMUST00000194735						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000194738	ENSMUSG00000095079	12	113254830	113260236	-1	19	9	13	23	21	7	0	5	0	5	16	A0A0A6YXW6	
ENSMUST00000194739						27	41	116	28	28	11	2	4	2	0	2		
ENSMUST00000194740	ENSMUSG00000039318	1	185204117	185286759	1	7	6	24	39	21	7	565	1087	1099	73	734	A0A0A6YWM5	
ENSMUST00000194741	ENSMUSG00000006673	9	108516806	108560163	1	0	0	0	0	1	0	0	3	0	0	0	A0A0A6YY13	
ENSMUST00000194743						19	21	33	63	18	9	35	33	25	0	33		
ENSMUST00000194745						3	3	9	5	3	0	0	1	0	0	1		
ENSMUST00000194746	ENSMUSG00000073702	1	39367842	39371911	1	12	10	10	8	3	8	629	586	692	5224	597	A0A0A6YX26	
ENSMUST00000194747						8	8	23	11	12	2	70	294	79	87	74		
ENSMUST00000194748						5	11	14	11	14	4	0	0	0	0	0		
ENSMUST00000194749						0	0	1	11	0	0	0	0	0	0	0		
ENSMUST00000194750	ENSMUSG00000037395	1	192098546	192138062	-1	0	2	0	0	4	1	2	0	8	0	1	A0A0A6YXP4	
ENSMUST00000194751	ENSMUSG00000103707	18	36967631	37187657	1	0	0	31	26	21	3	0	0	0	0	0	A0A0A6YY55	
ENSMUST00000194754						3	4	0	11	5	5	0	0	0	0	0		
ENSMUST00000194756						22	23	55	26	30	19	1	0	1	0	3		
ENSMUST00000194759	ENSMUSG00000028080	3	86224680	86782692	1	16	10	64	35	27	18	0	0	1	0	44	A0A0A6YXL6	
ENSMUST00000194764						5	1	3	0	6	0	0	0	0	0	0		
ENSMUST00000194766						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194768						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000194769						1	2	2	2	2	3	0	0	0	0	0		
ENSMUST00000194772						40	51	68	63	56	37	1	2	3	2	6		
ENSMUST00000194774	ENSMUSG00000032558	9	104002544	104153483	1	0	16	36	0	0	12	5	0	0	0	21	H9KV07	
ENSMUST00000194776						2	0	20	2	1	1	0	0	0	0	0		
ENSMUST00000194777						3	3	0	8	6	5	0	0	0	0	0		
ENSMUST00000194778	ENSMUSG00000013593	1	171234853	171251388	-1	6	3	6	0	0	0	28	0	17	0	0	A0A0A6YW30	
ENSMUST00000194779						322	306	218	213	363	130	23	309	78	59	81		
ENSMUST00000194781	ENSMUSG00000027671	3	32706298	32726973	1	0	2	0	0	0	0	0	0	0	0	0	A0A0A6YWG8	
ENSMUST00000194782	ENSMUSG00000032599	9	108783796	108806337	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWA1	
ENSMUST00000194783	ENSMUSG00000026523	1	175698593	175815734	1	0	2	0	0	4	2	0	0	0	0	0	A0A0A6YW40	
ENSMUST00000194785	ENSMUSG00000037461	1	191575636	191623688	1	0	4	0	0	0	0	68	132	50	14	90	A0A0A6YX34	
ENSMUST00000194786	ENSMUSG00000059994	3	87376387	87402934	1	9	2	22	8	19	0	0	24	13	49	22	A0A0A6YY56	
ENSMUST00000194787						1	0	1	0	3	1	0	3	1	0	0		
ENSMUST00000194788						9	7	22	19	13	8	0	0	0	0	0		
ENSMUST00000194789						2	2	0	0	0	1	0	0	0	0	0		
ENSMUST00000194791	ENSMUSG00000038179	1	171632403	171653035	-1	0	2	0	2	2	2	0	0	11	0	0	A0A0A6YWL9	
ENSMUST00000194794	ENSMUSG00000010047	9	107567945	107572779	1	2	2	0	14	2	2	0	0	2	0	0	A0A0A6YXJ6	
ENSMUST00000194796	ENSMUSG00000037610	3	31902507	32200180	1	2	2	2	0	0	0	0	0	0	0	0	B5BNW2	
ENSMUST00000194797	ENSMUSG00000004709	1	171559193	171609746	1	7	5	51	11	15	10	26	455	112	52	107	Q3TAZ6	
ENSMUST00000194798						5	0	3	2	0	0	40	374	165	56	122		
ENSMUST00000194800						3	0	5	4	2	0	0	0	0	0	0		
ENSMUST00000194801						2	3	8	0	8	0	143	1263	166	136	127		
ENSMUST00000194802						4	0	30	17	0	0	0	0	0	0	0		
ENSMUST00000194806						1	2	4	2	0	0	0	0	0	0	0		
ENSMUST00000194807	ENSMUSG00000056050	1	183326725	183369553	-1	0	0	0	0	0	0	13	33	23	0	30	A0A0A6YXE6	
ENSMUST00000194808	ENSMUSG00000041570	1	136268123	136346104	-1	12	4	20	1	6	9	30	184	47	21	43	A0A0A6YXV8	
ENSMUST00000194810	ENSMUSG00000026696	1	162570515	162599084	1	0	0	0	0	0	0	59	399	196	143	45	A0A0A6YY66	
ENSMUST00000194813						4	8	6	1	4	0	29	62	29	3	8		
ENSMUST00000194814						11	9	21	23	15	6	0	0	0	0	0		
ENSMUST00000194815	ENSMUSG00000026082	1	38052786	38129801	-1	0	0	1	0	1	1	0	0	4	0	0	A0A0A6YX32	
ENSMUST00000194816	ENSMUSG00000039748	1	175880581	175913489	1	2	1	3	1	4	0	0	0	0	0	0	A0A0A6YXQ6	
ENSMUST00000194819	ENSMUSG00000032598	9	108808368	108818844	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWU4	
ENSMUST00000194821						3	1	2	11	3	1	2	3	4	2	10		
ENSMUST00000194824						0	2	0	1	0	0	0	0	5	0	1		
ENSMUST00000194825						2	1	0	1	0	0	0	0	0	1	0		
ENSMUST00000194828						13	9	26	15	17	8	0	2	3	1	6		
ENSMUST00000194829						0	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000194831						37	50	108	50	39	17	1	9	1	0	2		
ENSMUST00000194832						13	11	19	17	16	9	1	11	6	0	2		
ENSMUST00000194833						1	0	0	61	0	0	0	1	0	0	3		
ENSMUST00000194834						3	4	28	81	11	6	1	0	0	0	0		
ENSMUST00000194836	ENSMUSG00000027820	3	63241537	63386030	1	0	1	0	67	0	0	0	0	0	0	0	A0A0A6YW93	
ENSMUST00000194839	ENSMUSG00000046337	1	36562692	36683183	-1	2	0	0	2	6	2	0	0	1	0	0	A0A0A6YWQ3	
ENSMUST00000194840						18	10	22	14	27	20	0	0	0	0	1		
ENSMUST00000194842						12	8	39	18	31	7	0	1	0	0	0		
ENSMUST00000194843						3	0	0	32	0	0	0	0	0	0	0		
ENSMUST00000194844	ENSMUSG00000039542	9	49502136	49798925	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWW5	
ENSMUST00000194846						0	4	10	6	5	5	0	0	0	0	0		
ENSMUST00000194847						3	3	0	0	1	0	0	0	0	16	0		
ENSMUST00000194848						1	0	2	4	2	1	0	8	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000194849						6	6	6	1	3	0	0	0	0	0	0		
ENSMUST00000194851	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	1	1	0	0	0	0	637	0	0	0		Q9CY62
ENSMUST00000194852						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194853	ENSMUSG00000067653	1	36530188	36547201	-1	0	1	0	9	0	4	3	0	0	1	0	B7ZNT7	
ENSMUST00000194855	ENSMUSG00000026708	1	161070713	161086724	1	0	0	0	0	0	0	0	0	33	6	3	Q05CX4	
ENSMUST00000194856						4	3	1	0	0	0	0	0	0	0	2		
ENSMUST00000194857	ENSMUSG00000026087	1	37890477	37898535	1	0	2	0	0	3	0	79	217	88	430	64	A0A0A6YXW4	
ENSMUST00000194860						3	5	12	310	8	6	0	0	0	0	1		
ENSMUST00000194861						2	5	3	32	3	3	0	3	0	1	1		
ENSMUST00000194863	ENSMUSG00000006676	9	108490602	108502337	1	4	0	0	0	0	2	25	17	10	0	20	A0A0A6YX42	
ENSMUST00000194865	ENSMUSG00000076709	12	114991108	114991580	-1	0	2	0	0	1	0	0	0	0	1	0	A0A0A6YY41	
ENSMUST00000194868						1	2	0	3	0	0	0	0	0	0	0		
ENSMUST00000194869	ENSMUSG00000026571	1	165328698	165460475	-1	1	0	0	0	7	2	0	0	20	11	8	A0A0A6YW54	
ENSMUST00000194870						16	13	42	27	25	16	0	0	0	0	0		
ENSMUST00000194872						2	2	9	12	8	3	0	0	0	0	0		
ENSMUST00000194873						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194875	ENSMUSG00000032599	9	108783796	108806337	1	0	0	5	0	0	0	0	5	0	0	0	A0A0A6YY18	
ENSMUST00000194876	ENSMUSG00000028199	3	154596711	154623182	1	0	0	0	0	0	0	0	0	4	0	0	A0A0A6YXR4	
ENSMUST00000194877	ENSMUSG00000037461	1	191575636	191623688	1	0	0	0	0	0	0	30	0	51	0	31	A0A0A6YWX4	
ENSMUST00000194885	ENSMUSG00000103124	3	10179852	10197262	-1	8	5	3	0	8	3	0	0	0	0	0	A0A0A6YW05	
ENSMUST00000194887						2	2	28	4	3	3	0	0	0	0	0		
ENSMUST00000194888	ENSMUSG00000103144	18	37661793	37841873	1	20	18	26	32	34	15	0	1	0	0	0	A0A0A6YW27	
ENSMUST00000194890						1	1	1	2	0	2	0	0	0	0	0		
ENSMUST00000194894	ENSMUSG00000079610	1	36539474	36547185	-1	0	0	0	26	2	0	12	8	8	3	0	A0A0A6YWV1	
ENSMUST00000194895						9	12	20	7	27	6	0	0	0	0	0		
ENSMUST00000194896						2	5	5	8	5	4	0	0	0	0	0		
ENSMUST00000194897						3	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000194898						2	1	0	1	1	1	0	0	0	0	0		
ENSMUST00000194900						2	1	0	0	0	1	0	2	0	0	1		
ENSMUST00000194901						0	2	0	1	0	1	0	0	0	0	0		
ENSMUST00000194902						0	0	0	0	0	0	1	1	0	0	2		
ENSMUST00000194903						5	2	3	2	1	1	0	0	0	0	0		
ENSMUST00000194904	ENSMUSG00000062867	9	108560286	108565584	1	0	0	1	0	8	0	0	110	22	34	41	A0A0A6YY72	
ENSMUST00000194905						2	2	3	1	3	0	0	0	0	0	0		
ENSMUST00000194906						0	0	0	0	0	2	7	0	0	0	0		
ENSMUST00000194908						0	0	0	4	0	0	0	0	0	0	0		
ENSMUST00000194912						2	0	0	0	1	1	0	0	0	0	0		
ENSMUST00000194913	ENSMUSG00000026073	1	40074079	40125231	1	1	3	0	1	4	1	235	457	309	380	378		
ENSMUST00000194914						39	33	69	41	55	33	32	57	195	3	344		
ENSMUST00000194915						2	4	8	1	15	4	0	0	37	0	95		
ENSMUST00000194917						3	0	0	2	0	0	36	253	14	7	0		
ENSMUST00000194918	ENSMUSG00000026645	2	3341982	3397210	-1	6	5	0	0	6	0	0	0	0	0	0		Q8R197
ENSMUST00000194921						7	5	0	3	2	0	0	0	2	0	0		
ENSMUST00000194922						4523	6941	5143	2897	3585	1542	26	249	99	41	157		
ENSMUST00000194924						1	3	7	12	5	2	0	0	0	0	0		
ENSMUST00000194928	ENSMUSG00000104063	18	37751600	37841873	1	22	8	46	140	16	11	24	34	30	0	19	Q91XX3	
ENSMUST00000194931						1	6	1	0	4	5	0	0	0	0	0		
ENSMUST00000194932						17	0	0	0	0	8	14	26	0	0	0		
ENSMUST00000194933	ENSMUSG00000025817	2	5845019	5871895	1	0	0	3	4	1	1	0	0	0	0	0	A0A0A6YVU1	
ENSMUST00000194936						0	1	3	2	1	1	0	0	0	0	0		
ENSMUST00000194939						8	4	7	2	9	5	36	311	14	57	33		
ENSMUST00000194940						2	2	0	1	2	0	0	47	0	0	14		
ENSMUST00000194941						2	0	2	1	2	0	0	0	0	0	0		
ENSMUST00000194942						2	0	2	31	3	0	0	0	0	0	0		
ENSMUST00000194947						0	2	6	4	4	0	0	0	0	0	0		
ENSMUST00000194948						0	3	19	2	6	2	4	9	82	18	77		
ENSMUST00000194951	ENSMUSG00000092572	1	107529003	107549271	1	0	0	2	0	2	0	60	230	109	336	117		
ENSMUST00000194953						11038	11416	16650	9475	10673	4942	2819	10388	3918	1007	5739		
ENSMUST00000194959	ENSMUSG00000032612	9	108347853	108392545	1	6	0	0	0	0	0	637	1549	684	118	576	A0A0A6YW28	
ENSMUST00000194960						1	1	1	0	3	0	0	0	0	0	0		
ENSMUST00000194961						1	2	4	3	9	1	0	2	2	0	2		
ENSMUST00000194964	ENSMUSG00000040612	1	166254139	166316823	1	0	0	0	87	0	0	0	0	0	0	0	A0A0A6YXV2	
ENSMUST00000194965	ENSMUSG00000074435	3	92583867	92588997	-1	12	0	21	16	7	0	0	0	0	0	0		P15265
ENSMUST00000194967	ENSMUSG00000037190	9	107539007	107542193	-1	3	0	17	0	0	0	0	13	6	0	0	A0A0A6YY22	
ENSMUST00000194968	ENSMUSG00000095761	12	114723772	114724205	-1	0	0	12	3	0	0	0	0	0	0	0	A0A0A6YX66	
ENSMUST00000194971						2	1	2	1	1	0	0	0	0	0	0		
ENSMUST00000194972						7	9	9	6	1	1	13	13	10	0	8		
ENSMUST00000194974						3	4	5	5	8	6	0	0	0	0	0		
ENSMUST00000194976	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	0	0	0	0	0	5	0	0	0	7		
ENSMUST00000194977						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194978						13	16	40	22	21	13	1	16	2	3	5		
ENSMUST00000194979	ENSMUSG00000037661	3	30855950	30897192	1	0	1	0	0	1	0	12	16	12	3	8		
ENSMUST00000194981	ENSMUSG00000038576	1	182763860	182896591	1	0	0	2	13	4	2	0	0	0	0	0	A0A0A6YWB1	
ENSMUST00000194982						3	2	0	0	4	0	0	0	0	0	0		
ENSMUST00000194983						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000194984						5	3	0	0	0	0	8	18	39	30	60		
ENSMUST00000194985						1	3	2	0	5	4	0	0	0	0	0		
ENSMUST00000194986						3	5	4	4	5	2	0	0	0	0	0		
ENSMUST00000194992	ENSMUSG00000025900	1	4290846	4409241	-1	4	10	0	5	6	1	1	0	0	0	2	A0A0A6YXU6	
ENSMUST00000194993						7	2	7	3	7	2	39	80	41	16	106		
ENSMUST00000195001	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	0	0	3	6	21	2	11	A0A0A6YX59	
ENSMUST00000195002	ENSMUSG00000063659	1	177442351	177450764	1	0	0	0	3	0	0	0	2	5	2	1	A0A0A6YXT0	
ENSMUST00000195006						0	0	0	65	0	0	0	0	3	2	5		
ENSMUST00000195008	ENSMUSG00000039286	3	27416162	27711307	-1	6	42	8	0	41	3	346	904	435	18	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000195009	ENSMUSG00000098301	CHR_MG3829_PATCH	88047373	88053755	1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195010						2	1	19	0	0	0	9	0	20	3	17		
ENSMUST00000195011						0	0	0	0	0	0	0	14	0	0	0		
ENSMUST00000195014	ENSMUSG00000041355	3	88575876	88588419	1	0	5	0	36	4	3	558	661	330	482	381		Q9CPW5
ENSMUST00000195015	ENSMUSG00000052428	1	167308378	167333978	1	5	0	2	129	9	5	134	231	236	488	156		Q921L3
ENSMUST00000195016						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195017						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195019	ENSMUSG00000102671	CHR_MG184_PATCH	72368793	72380467	-1	27	6	32	108	34	13	10	9	5	8	4	Q791P0	Q9Z2P8
ENSMUST00000195021						2	2	19	0	0	3	0	0	0	2	0		
ENSMUST00000195022						171	134	1337	200	200	92	4	0	2	2	8		
ENSMUST00000195023	ENSMUSG00000034684	9	107681500	107710475	-1	1	3	0	0	1	0	0	1	0	0	2	A0A0A6YW11	
ENSMUST00000195026						30	35	100	81	22	13	9	16	10	3	12		
ENSMUST00000195027						5	5	0	31	2	2	0	0	0	0	1		
ENSMUST00000195030	ENSMUSG00000025766	3	41742611	41803320	1	0	0	0	0	0	2	0	0	0	0	0	A0A0A6YY40	
ENSMUST00000195031						1	3	4	0	2	0	0	0	0	0	0		
ENSMUST00000195032	ENSMUSG00000058407	1	37985189	37997893	-1	0	4	0	0	0	5	22	139	47	179	24		Q9CQ79
ENSMUST00000195033						11	13	50	13	14	9	0	0	0	0	0		
ENSMUST00000195034						20	0	22	238	27	5	0	0	0	0	0		
ENSMUST00000195036						5	2	11	30	5	1	0	0	0	0	0		
ENSMUST00000195037	ENSMUSG00000102301	12	114462291	114462730	-1	5	5	2	7	2	1	0	0	0	0	1	A0A0A6YW58	
ENSMUST00000195038						17	17	62	36	19	5	0	0	0	0	0		
ENSMUST00000195041						3	4	21	4	5	0	0	0	0	0	1		
ENSMUST00000195042						4	1	3	3	4	0	55	291	43	29	84		
ENSMUST00000195043						67	55	175	136	91	46	2	10	11	0	14		
ENSMUST00000195044	ENSMUSG00000040782	1	159232320	159347640	1	0	0	0	0	0	2	98	494	137	10	38	A0A0A6YVP2	
ENSMUST00000195045						0	0	0	0	4	0	65	177	113	10	161		
ENSMUST00000195047						3	0	5	1	1	0	9	47	26	11	12		
ENSMUST00000195049						0	0	1	6	0	0	0	2	0	0	0		
ENSMUST00000195051						2	3	18	103	1	3	1	7	4	0	22		
ENSMUST00000195054	ENSMUSG00000046836	1	183276352	183297269	-1	0	0	0	0	0	0	0	0	0	0	12	A0A0A6YWP0	
ENSMUST00000195055						46	41	99	299	76	39	2	13	4	1	7		
ENSMUST00000195057	ENSMUSG00000057969	9	107597674	107609229	-1	1	0	0	0	0	0	0	0	0	0	0	A0A0G2JDD7	
ENSMUST00000195058	ENSMUSG00000052911	9	108479736	108490530	1	0	0	2	0	0	0	0	0	0	0	0	A0A0A6YWY6	
ENSMUST00000195059	ENSMUSG00000022995	1	181896384	182019990	-1	0	0	16	29	10	0	0	4	26	3	14	A0A0A6YW06	
ENSMUST00000195060						1	1	5	0	1	2	0	0	0	0	0		
ENSMUST00000195061	ENSMUSG00000047539	1	182313102	182341629	-1	0	0	5	0	2	0	0	0	0	0	47	A0A0A6YX00	
ENSMUST00000195062						7	0	0	34	6	2	1	0	0	1	6		
ENSMUST00000195067	ENSMUSG00000102976	1	133619862	133661380	-1	1	0	1	0	0	0	44	49	41	4	20	A0A0A6YX41	
ENSMUST00000195068						3	4	24	4	7	3	0	0	0	0	0		
ENSMUST00000195069						138	121	378	238	172	67	3	27	15	6	17		
ENSMUST00000195072						0	0	0	0	1	0	8	39	7	9	8		
ENSMUST00000195073						4	9	15	1	4	3	0	3	0	3	3		
ENSMUST00000195075						2	1	2	0	2	1	0	6	0	0	3		
ENSMUST00000195077	ENSMUSG00000027763	3	60472830	60629750	1	0	0	9	0	0	2	15	2	142	13	42	A0A0A6YXP3	
ENSMUST00000195078						6	6	1	6	5	3	0	0	0	0	0		
ENSMUST00000195080						1	1	0	0	0	0	0	0	0	0	11		
ENSMUST00000195081						3	0	18	2	1	1	0	0	0	0	0		
ENSMUST00000195084						2	0	0	0	1	0	61	505	229	58	84		
ENSMUST00000195085						1	1	4	4	7	1	0	0	0	0	0		
ENSMUST00000195086						2	0	0	5	0	0	0	0	0	0	0		
ENSMUST00000195087	ENSMUSG00000076477	6	41202550	41203044	1	0	0	1	0	0	2	0	0	0	0	0	A0A0A6YX06	
ENSMUST00000195088	ENSMUSG00000034755	X	120290259	120910619	1	9	0	0	0	3	0	0	0	0	0	0	A0JNT1	
ENSMUST00000195089						2	0	2	2	1	0	0	0	0	0	0		
ENSMUST00000195092						7	11	17	34	10	6	0	0	0	0	0		
ENSMUST00000195093	ENSMUSG00000102141	8	128745963	128798694	-1	1	4	0	0	2	1	0	0	0	0	0	A0A0A6YXJ1	
ENSMUST00000195094						125	106	885	173	125	68	2	1	6	1	14		
ENSMUST00000195095						10	2	8	5	15	3	0	0	0	0	0		
ENSMUST00000195096						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195099						6	7	3	2	7	4	0	0	0	0	0		
ENSMUST00000195100						3	1	6	2	2	4	0	0	0	0	0		
ENSMUST00000195101						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000195102						3	1	3	5	1	1	0	0	0	0	0		
ENSMUST00000195103	ENSMUSG00000028199	3	154596711	154623182	1	0	0	0	0	0	0	2	2	0	4	0	A0A0A6YVS7	
ENSMUST00000195104						188	211	297	216	255	100	0	23	4	2	2		
ENSMUST00000195106	ENSMUSG00000021466	13	63508328	63573598	-1	0	1	1	31	2	0	0	0	0	0	0	A0A0A6YVW7	
ENSMUST00000195107						4	1	0	0	2	1	0	0	0	0	0		
ENSMUST00000195112	ENSMUSG00000102748	18	37689828	37841873	1	0	0	0	0	0	0	0	0	0	0	2	Q91XX7	
ENSMUST00000195113						2	0	2	2	3	0	0	1	1	0	0		
ENSMUST00000195114						5	0	7	4	4	0	3	0	0	2	8		
ENSMUST00000195115						1	0	2	1	0	0	0	0	0	0	0		
ENSMUST00000195117	ENSMUSG00000026628	1	191170296	191218039	-1	11	4	15	7	9	3	73	39	0	34	0	Q4FJW1	Q60765
ENSMUST00000195120	ENSMUSG00000026616	1	195136811	195176716	-1	10	31	13	26	36	6	0	2	3	1	5	A0A0A6YWG3	
ENSMUST00000195123	ENSMUSG00000073702	1	39367842	39371911	1	0	0	0	0	0	0	596	1093	522	2812	285	A0A0A6YXL3	
ENSMUST00000195124	ENSMUSG00000076672	12	114288152	114288582	-1	2	4	2	2	0	0	2	0	0	0	26		P18531
ENSMUST00000195125						7	6	14	9	6	5	1	8	4	0	10		
ENSMUST00000195126						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195129						0	0	6	2	6	2	0	0	0	0	0		
ENSMUST00000195130						2	2	2	1	4	1	0	0	0	0	0		
ENSMUST00000195133						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195135						3	1	3	1	3	1	1	2	3	1	3		
ENSMUST00000195136	ENSMUSG00000048234	1	39551296	39577405	-1	4	2	4	0	3	0	116	1086	632	61	541	A0A0A6YWR9	
ENSMUST00000195140						0	2	1	3	3	0	0	0	0	0	0		
ENSMUST00000195142						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195144						7	3	10	5	2	1	0	1	0	1	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000195149						2	0	1	0	1	3	0	0	0	0	0		
ENSMUST00000195150	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	0	2	6	1	1	0	1	0	0	0	0		
ENSMUST00000195151	ENSMUSG00000061518	1	36691484	36693681	1	0	0	0	4	3	0	74	188	86	394	71	A0A0A6YVR0	
ENSMUST00000195155						5	0	0	3	0	0	5	8	4	0	0		
ENSMUST00000195156	ENSMUSG00000029108	5	57717967	58133230	1	7	0	0	0	0	0	0	0	0	0	0	A0A0A6YW34	
ENSMUST00000195157	ENSMUSG00000091685	3	79336661	79464129	1	2	0	5	1	4	2	0	0	0	0	0	A0A0A6YW13	
ENSMUST00000195158						1	0	2	0	3	0	0	0	0	0	0		
ENSMUST00000195159						9	3	18	8	13	1	1	0	0	1	0		
ENSMUST00000195160						7	5	23	6	11	2	2	0	1	0	0		
ENSMUST00000195161						1	0	1	1	0	0	0	10	1	0	2		
ENSMUST00000195162						3	1	3	6	4	5	0	0	0	0	0		
ENSMUST00000195163	ENSMUSG00000103677	18	37685210	37841873	1	0	2	3	1	4	1	0	0	0	0	0	A0A0A6YVU6	
ENSMUST00000195164	ENSMUSG00000042035	3	101377083	101463059	1	15	0	3	28	5	4	0	0	0	0	0	A0A0A6YX40	
ENSMUST00000195165						3	0	0	0	0	0	66	30	40	0	0		
ENSMUST00000195167						2	1	3	10	6	1	0	0	0	0	0		
ENSMUST00000195169	ENSMUSG00000098892	CHR_MG3833_PATCH	18407771	18427737	-1	0	0	0	1	1	0	41	64	32	34	85		O88587
ENSMUST00000195175						4	2	9	1	5	3	0	0	1	0	0		
ENSMUST00000195176						0	0	0	0	6	0	0	0	0	0	0		
ENSMUST00000195177	ENSMUSG00000041605	1	136213531	136234264	-1	1	1	8	2	5	1	0	0	0	0	1	A0A0A6YWD6	
ENSMUST00000195181						26	17	88	45	21	7	0	6	3	0	4		
ENSMUST00000195182						2	1	4	2	1	2	0	0	0	0	0		
ENSMUST00000195183	ENSMUSG00000027742	3	52981875	53017237	-1	0	3	0	74	3	1	0	0	0	0	0	A0A0A6YWW6	
ENSMUST00000195189						1	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000195190						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000195191	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	0	0	0	1	1	0	3	6	0	2		
ENSMUST00000195192	ENSMUSG00000076612	12	113285325	113288932	-1	8	1	10	3	6	2	2	3	0	20	42	A0A0A6YY53	
ENSMUST00000195194						2	2	5	0	8	2	0	0	0	0	1		
ENSMUST00000195195						10	5	55	13	8	0	0	0	1	8	0		
ENSMUST00000195196	ENSMUSG00000039748	1	175880581	175913489	1	0	0	0	14	0	0	0	0	0	0	0	A0A0A6YX74	
ENSMUST00000195199						5	2	6	0	6	1	0	0	0	0	1		
ENSMUST00000195200						4	5	7	4	1	7	1	0	0	0	0		
ENSMUST00000195201	ENSMUSG00000039239	1	186622792	186705989	-1	0	2	5	85	0	0	0	0	0	3	2	A0A0A6YXU9	
ENSMUST00000195203						26	13	26	7	24	12	6	12	5	0	6		
ENSMUST00000195206						0	1	0	0	0	0	4	19	3	14	1		
ENSMUST00000195207						1	4	2	7	4	3	0	3	3	0	7		
ENSMUST00000195209						1	0	0	0	1	0	9	85	26	10	37		
ENSMUST00000195212						5	3	20	5	7	3	1	1	1	0	1		
ENSMUST00000195217						3	6	7	3	2	2	0	0	0	0	0		
ENSMUST00000195218						0	0	3	1	1	1	0	0	0	0	0		
ENSMUST00000195219	ENSMUSG00000032936	9	107935674	107949691	1	2	1	42	7	4	1	0	0	0	0	0	A0A0A6YXI7	
ENSMUST00000195220	ENSMUSG00000026571	1	165328698	165460475	-1	0	0	0	0	0	0	13	26	17	2	33	A0A0A6YVW2	
ENSMUST00000195222						12	4	12	2	13	4	0	0	0	0	0		
ENSMUST00000195228						2	1	5	5	6	2	0	0	0	0	0		
ENSMUST00000195229	ENSMUSG00000024579	18	61696837	61707635	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY26	
ENSMUST00000195230						0	0	0	0	1	0	14	165	54	0	0		
ENSMUST00000195231						3	2	1	0	3	1	69	622	189	9	257		
ENSMUST00000195232						8	2	22	3	5	2	0	0	0	0	0		
ENSMUST00000195233	ENSMUSG00000056050	1	183326725	183369553	-1	0	0	3	0	0	0	34	202	95	4	41	A0A0A6YX61	
ENSMUST00000195234	ENSMUSG00000094237	13	119827961	119830216	-1	13	5	13	15	18	3	0	0	0	0	0	O70618	
ENSMUST00000195235	ENSMUSG00000037190	9	107539007	107542193	-1	0	2	2	14	0	0	31	60	21	18	23		Q9WUE3
ENSMUST00000195236						0	0	0	1	0	0	0	2	0	0	0		
ENSMUST00000195238						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195239	ENSMUSG00000023036	18	37815079	37841873	1	0	0	0	0	0	3	0	55	0	9	0	A0A0A6YVS5	
ENSMUST00000195242						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000195245						2	0	6	2	0	0	1	266	0	16	0		
ENSMUST00000195247	ENSMUSG00000058407	1	37985189	37997893	-1	4	0	6	45	4	0	64	479	24	153	15		Q9CQ79
ENSMUST00000195248	ENSMUSG00000040843	1	165212286	165236996	-1	1	0	2	14	3	1	0	5	5	8	11	A0A0A6YY87	
ENSMUST00000195249	ENSMUSG00000019039	9	108569886	108572774	1	5	4	0	0	0	0	4	7	17	0	11	A0A0A6YW92	
ENSMUST00000195254						1	4	0	1	2	2	0	0	0	0	0		
ENSMUST00000195255						4	3	12	7	0	0	9	18	26	3	37		
ENSMUST00000195256						1	2	3	3	3	0	0	0	0	0	1		
ENSMUST00000195257						0	0	7	0	0	0	0	0	0	0	0		
ENSMUST00000195258	ENSMUSG00000021466	13	63508328	63573598	-1	0	0	8	2	21	0	1	0	5	0	9	A0A0A6YVX7	
ENSMUST00000195259	ENSMUSG00000026074	1	39900913	40026310	1	0	0	0	0	0	0	0	0	0	0	0	B7ZNR9	
ENSMUST00000195260						4	3	6	12	9	5	6	7	6	0	3		
ENSMUST00000195261	ENSMUSG00000027833	3	66971727	66981771	-1	2	0	3	7	3	1	1	0	0	0	0	A0A0A6YWN6	
ENSMUST00000195262	ENSMUSG00000059146	7	78175959	78738012	-1	12	0	10	2	14	0	0	0	0	0	0	A0A0A6YWL7	
ENSMUST00000195263						0	0	0	0	0	0	2	1	0	0	0		
ENSMUST00000195264						9	3	19	10	9	3	6	9	11	1	9		
ENSMUST00000195265						1	2	0	0	2	0	0	0	0	0	0		
ENSMUST00000195267						9	13	28	0	13	0	2	4	3	1	0		
ENSMUST00000195268						2	0	0	4	3	0	3	5	0	0	6		
ENSMUST00000195269						3	3	1	0	1	1	0	0	0	0	0		
ENSMUST00000195270						2	0	11	0	0	0	0	7	2	0	7		
ENSMUST00000195271	ENSMUSG00000004031	1	158245269	158356326	-1	72	45	331	171	91	45	0	5	0	1	1	A0A0A6YWU9	
ENSMUST00000195272	ENSMUSG00000026114	1	37214434	37263384	1	1	3	1	0	5	0	0	0	0	0	0	A0A0A6YXW9	
ENSMUST00000195273						0	1	3	1	2	8	0	2	0	0	0		
ENSMUST00000195274	ENSMUSG00000041498	1	136466343	136531511	1	0	0	0	0	0	0	0	0	0	0	0	L0N759	
ENSMUST00000195275	ENSMUSG00000026468	1	155698031	155751684	-1	5	0	0	9	12	9	0	0	0	0	0	A0A0A6YWR5	
ENSMUST00000195278	ENSMUSG00000103523	3	92604718	92607492	-1	45	40	161	386	63	44	3	6	5	0	4	A0A0A6YVV1	
ENSMUST00000195283						10	7	18	56	15	7	4	5	1	0	7		
ENSMUST00000195285						0	0	2	1	2	0	0	0	0	0	2		
ENSMUST00000195286	ENSMUSG00000102367	1	133309827	133329722	1	0	0	4	8	3	0	0	0	0	0	0	I0J0X7	Q6Y4S4
ENSMUST00000195291	ENSMUSG00000016181	1	193091104	193130272	-1	0	0	0	0	0	37	0	62	30	9	0	A0A0A6YWS6	

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000195292						19	20	37	17	30	7	0	0	0	0	0		
ENSMUST00000195295						0	0	1	1	2	0	0	0	0	0	0		
ENSMUST00000195298						7	4	7	10	5	6	0	0	0	0	0		
ENSMUST00000195299	ENSMUSG00000004880	1	181815335	181843046	-1	0	0	0	5	0	0	0	0	0	0	0	A0A0A6YXW3	
ENSMUST00000195300						0	3	2	1	1	1	0	0	0	0	0		
ENSMUST00000195302	ENSMUSG00000026470	1	155158715	155208256	1	0	0	2	19	1	2	55	24	76	6	35		Q9JKK1
ENSMUST00000195305						19	10	24	31	20	9	34	274	114	37	187		
ENSMUST00000195307						12	6	23	26	16	4	0	0	0	0	0		
ENSMUST00000195311	ENSMUSG00000026587	1	158362273	158691781	1	0	0	0	41	3	0	0	0	0	0	0	A0A0A6YWE6	
ENSMUST00000195315						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195316						9	6	5	13	5	1	2	6	5	0	3		
ENSMUST00000195318						3	2	0	4	0	1	0	0	0	0	0		
ENSMUST00000195319						2	1	1	2	2	0	0	0	0	0	0		
ENSMUST00000195322						0	3	0	0	5	0	0	0	0	0	0		
ENSMUST00000195323	ENSMUSG00000032598	9	108808368	108818844	1	0	0	2	53	1	0	0	0	3	0	0	A0A0A6YWW3	
ENSMUST00000195324	ENSMUSG00000026527	1	175059087	175492500	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW36	
ENSMUST00000195325						4	3	2	1	7	3	0	0	0	2	3		
ENSMUST00000195329						1	2	1	1	1	1	0	0	0	0	0		
ENSMUST00000195330						6	4	1	6	6	1	0	0	0	0	0		
ENSMUST00000195333						2	3	2	0	3	0	0	0	0	0	0		
ENSMUST00000195334						0	1	0	0	0	0	0	25	8	0	0		
ENSMUST00000195336						2	3	4	2	2	2	0	0	0	0	0		
ENSMUST00000195337	ENSMUSG00000076688	12	114564578	114565012	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX72	
ENSMUST00000195339	ENSMUSG00000026121	1	36548639	36558349	-1	0	0	0	123	6	3	0	0	0	0	0	A0A0A6YX48	
ENSMUST00000195341						3	1	4	2	5	0	0	0	0	0	0		
ENSMUST00000195342	ENSMUSG00000026683	1	169497934	169531464	-1	0	0	0	0	0	0	0	0	0	0	2	A0A0A6YVY5	
ENSMUST00000195345	ENSMUSG00000026554	1	172148084	172197005	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX55	
ENSMUST00000195346						0	2	2	2	1	0	0	2	0	0	0		
ENSMUST00000195347						1	0	0	3	1	0	0	0	0	0	0		
ENSMUST00000195350						2	1	0	1	0	0	0	0	0	0	0		
ENSMUST00000195354	ENSMUSG00000016200	1	192891233	193035775	-1	39	31	26	21	31	16	0	2	0	0	0		Q7TN84
ENSMUST00000195355	ENSMUSG00000036422	14	79766775	79771312	-1	0	2	9	261	13	15	0	0	1	0	2		Q7TSK3
ENSMUST00000195356						2	1	2	3	5	0	0	0	2	0	2		
ENSMUST00000195358	ENSMUSG00000026581	1	164061982	164084181	1	0	0	0	0	0	0	257	1686	268	436	149	A0A0A6YW25	
ENSMUST00000195359	ENSMUSG00000095197	12	115335082	115335514	-1	0	0	6	2	5	0	0	0	0	4	0	A0A0A6YXE0	
ENSMUST00000195361						18	21	45	33	22	15	1	1	0	0	0		
ENSMUST00000195363	ENSMUSG00000103585	18	37720369	37841870	1	0	0	0	0	0	0	0	0	0	0	0	Q91XX6	
ENSMUST00000195364						0	0	0	4	4	0	0	0	0	0	0		
ENSMUST00000195367						6	7	15	17	6	3	0	0	0	0	0		
ENSMUST00000195370	ENSMUSG00000010057	9	107542226	107545706	1	0	0	0	0	0	0	0	3	0	0	0	A0A0A6YWX8	
ENSMUST00000195372	ENSMUSG00000030768	1	183086266	183221522	-1	0	0	49	87	56	9	0	0	0	0	0		Q3TDN0
ENSMUST00000195373	ENSMUSG00000026087	1	37890477	37898535	1	0	0	5	0	0	1	78	338	107	655	93		Q9D7N6
ENSMUST00000195376	ENSMUSG00000055421	14	93013410	93890679	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY09	
ENSMUST00000195381	ENSMUSG00000103033	12	113762249	113762708	-1	0	0	1	0	0	1	0	0	0	0	0	A0A0A6YWG4	
ENSMUST00000195383	ENSMUSG00000026082	1	38052786	38129801	-1	0	0	0	20	0	0	0	0	0	0	0	A0A0A6YWQ5	
ENSMUST00000195384						14	11	31	17	25	7	0	0	0	0	0		
ENSMUST00000195387						6	0	15	81	5	2	4	8	8	0	8		
ENSMUST00000195388	ENSMUSG00000063659	1	177442351	177450764	1	0	1	0	0	0	0	0	0	15	5	0	A0A0A6YWT8	
ENSMUST00000195390						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195391						1	1	2	1	2	1	0	0	0	0	0		
ENSMUST00000195392						6	1	7	2	4	0	0	0	0	0	0		
ENSMUST00000195394						27	26	43	19	33	12	95	423	246	33	292		
ENSMUST00000195395						1	0	0	1	0	0	0	0	0	0	0		
ENSMUST00000195396	ENSMUSG00000037730	3	30602065	30619873	1	0	1	0	0	0	0	3	81	8	21	20		Q99MD8
ENSMUST00000195398						13	9	6	6	10	9	0	1	0	0	0		
ENSMUST00000195399						2	1	1	1	1	1	0	0	0	0	0		
ENSMUST00000195402						4	2	8	35	3	7	0	0	0	0	1		
ENSMUST00000195403						27	31	168	21	24	23	0	6	3	0	3		
ENSMUST00000195405	ENSMUSG00000032601	9	108689314	108750436	1	2	0	4	205	2	0	0	0	8	0	15	A0A0A6YX73	
ENSMUST00000195406						2	2	6	2	4	1	0	3	0	3	0		
ENSMUST00000195408						0	1	0	0	0	0	13	16	7	47	27		
ENSMUST00000195410	ENSMUSG00000026566	1	165592240	165634538	-1	0	0	0	0	0	0	2	0	0	0	0	A0A0A6YX14	
ENSMUST00000195412						2	2	10	2	5	0	0	0	0	0	0		
ENSMUST00000195415						197	187	215	219	218	119	5	35	20	9	38		
ENSMUST00000195417	ENSMUSG00000095859	12	114945950	114946383	-1	0	0	0	3	1	0	0	0	0	0	5	A0A0A6YXN5	
ENSMUST00000195418						6	4	10	116	6	0	0	0	0	0	0		
ENSMUST00000195419						32	20	122	56	40	32	7	17	16	0	41		
ENSMUST00000195421						0	0	1	0	0	0	0	2	0	0	0		
ENSMUST00000195422						2	4	4	1	4	0	0	0	0	0	0		
ENSMUST00000195423						1	1	0	2	1	0	0	12	0	0	0		
ENSMUST00000195424	ENSMUSG00000102976	1	133619862	133661380	-1	0	0	0	6	0	0	0	0	0	0	0	A0A0A6YXN6	
ENSMUST00000195427						4	2	4	2	2	0	0	0	0	0	0		
ENSMUST00000195428	ENSMUSG00000026398	1	136842571	136960448	-1	0	0	0	42	0	0	0	0	0	0	0	A0A0A6YWQ4	
ENSMUST00000195429	ENSMUSG00000039952	9	108204634	108263958	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW41	
ENSMUST00000195430						102	105	125	75	90	35	0	2	4	1	8		
ENSMUST00000195432	ENSMUSG00000037174	3	51252720	51340663	-1	10	15	42	24	25	10	4	32	11	1	34	A0A0A6YY68	
ENSMUST00000195433	ENSMUSG00000057335	1	176733653	176814067	-1	0	34	4	10	27	5	41	48	416	44	268	A0A0A6YXR9	
ENSMUST00000195435	ENSMUSG00000032609	9	108447636	108461581	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWH8	
ENSMUST00000195436	ENSMUSG00000090919	3	46442197	46448219	-1	0	0	0	19	2	2	0	0	0	0	0	A0A0A6YWT2	
ENSMUST00000195438	ENSMUSG00000026715	1	160978585	161005863	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX49	
ENSMUST00000195440						5	0	1	2	3	1	0	0	0	0	0		
ENSMUST00000195442	ENSMUSG00000026721	1	160219174	160793211	-1	3	2	3	56	1	0	0	0	0	0	0		A6H6A9
ENSMUST00000195443	ENSMUSG00000026558	1	167222883	167285320	-1	0	0	4	0	0	0	17	24	53	40	18	A0A0A6YXG9	
ENSMUST00000195444						0	0	0	3	2	0	0	0	0	0	0		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000195447						14	10	16	16	11	11	0	0	0	0	0		
ENSMUST00000195449						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000195450	ENSMUSG00000050122	1	37026596	37187613	1	6	2	9	3	2	1	0	0	0	0	0	A0A0A6YXU0	
ENSMUST00000195456						7	1	2	12	5	1	2	6	2	0	7		
ENSMUST00000195459						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195461						242	197	516	157	348	144	6	13	11	2	18		
ENSMUST00000195464						11	9	15	10	11	5	0	0	0	0	0		
ENSMUST00000195465	ENSMUSG00000028068	3	88081971	88121048	1	29	20	48	27	39	25	0	5	5	3	11	A0A0A6YXJ2	
ENSMUST00000195467						0	1	1	0	4	1	0	0	0	0	0		
ENSMUST00000195468	ENSMUSG00000076633	12	113578504	113578990	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YVX8	
ENSMUST00000195469	ENSMUSG00000095416	12	114615850	114616318	-1	0	0	6	0	5	1	0	0	0	0	4	A0A0A6YXJ9	
ENSMUST00000195471	ENSMUSG00000033900	3	82358044	82395268	1	0	0	0	0	0	1	0	0	0	0	0	A0A0A6YVV4	
ENSMUST00000195472						9	3	4	4	10	0	0	0	0	1	4		
ENSMUST00000195474						13	26	41	17	27	6	5	6	2	0	4		
ENSMUST00000195477	ENSMUSG00000026527	1	175059087	175492500	-1	0	0	1	0	0	0	0	0	0	0	0	Q45FE2	
ENSMUST00000195481						0	0	6	15	2	1	0	0	0	1	0		
ENSMUST00000195483	ENSMUSG00000052911	9	108479736	108490530	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY71	
ENSMUST00000195484						5	2	9	3	1	4	0	0	0	0	0		
ENSMUST00000195485						4	2	5	12	1	0	0	0	0	0	0		
ENSMUST00000195488						7	8	18	15	7	5	0	1	0	0	0		
ENSMUST00000195492						7	5	4	6	6	0	0	0	0	0	0		
ENSMUST00000195498						9	9	13	4	10	2	1	6	3	0	8		
ENSMUST00000195502						2	2	4	1	1	0	0	6	0	0	0		
ENSMUST00000195504						0	10	0	0	0	0	0	0	0	0	0		
ENSMUST00000195505						2	2	4	8	2	6	0	0	1	0	0		
ENSMUST00000195511						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195513	ENSMUSG00000006673	9	108516806	108560163	1	0	0	0	0	0	0	0	4	20	0	5	A0A0A6YXK0	
ENSMUST00000195514	ENSMUSG00000032599	9	108783796	108806337	1	0	0	0	0	0	0	51	90	66	12	21	A0A0A6YX46	
ENSMUST00000195515	ENSMUSG00000078657	3	93144787	93149819	1	0	0	0	14	16	0	0	0	0	0	0	D3YUU6	
ENSMUST00000195516						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195517						1	0	1	0	1	0	0	8	3	3	2		
ENSMUST00000195519						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195520						2	0	2	0	1	1	0	0	0	0	0		
ENSMUST00000195521						4	3	2	2	0	0	0	0	0	0	0		
ENSMUST00000195523	ENSMUSG00000099282	CHR_MG3833_PATCH	18427269	18479958	1	2	1	0	1	2	1	4	5	0	1	1		
ENSMUST00000195524	ENSMUSG00000028080	3	86224680	86782692	1	11	11	9	0	11	6	5	59	0	12	2	Q8BSM6	
ENSMUST00000195525	ENSMUSG00000034349	3	69004738	69034623	1	0	0	0	0	2	2	0	0	0	0	14	A0A0A6YX07	
ENSMUST00000195526						5	3	7	3	9	14	0	0	2	5	0		
ENSMUST00000195530	ENSMUSG00000016200	1	192891233	193035775	-1	0	3	4	3	13	0	0	0	0	0	0	A0A0A6YWI3	
ENSMUST00000195531	ENSMUSG00000052613	10	73099342	74649737	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YXB5	
ENSMUST00000195533	ENSMUSG00000026395	1	138062861	138175708	-1	0	1	0	0	0	0	225	79	349	127	232	A0A0A6YXM4	
ENSMUST00000195534						0	1	4	5	5	0	5	9	3	0	7		
ENSMUST00000195537	ENSMUSG00000090919	3	46442197	46448219	-1	5	0	3	22	0	0	0	0	0	0	1	A0A0A6YX62	
ENSMUST00000195538						1	0	1	8	6	1	2	0	0	6	7		
ENSMUST00000195539						0	1	0	0	0	1	0	0	0	0	0		
ENSMUST00000195542						1	4	3	1	1	2	0	0	0	0	1		
ENSMUST00000195544						1	0	3	1	0	3	0	0	0	0	0		
ENSMUST00000195548						1	0	0	2	1	1	0	0	0	0	0		
ENSMUST00000195549	ENSMUSG00000063659	1	177442351	177450764	1	0	0	2	8	0	0	2	3	0	0	0	A0A0A6YXP2	
ENSMUST00000195554	ENSMUSG00000040782	1	159232320	159347640	1	0	0	0	0	0	0	0	6	6	0	0	A0A0A6YWI1	
ENSMUST00000195555	ENSMUSG00000025902	1	4490931	4497354	-1	4	2	0	17	2	0	0	0	0	0	0		Q61473
ENSMUST00000195557	ENSMUSG00000040612	1	166254139	166316823	1	0	0	0	0	5	2	0	0	1	0	0	A0A0A6YY19	
ENSMUST00000195558						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000195559						9	11	11	40	6	0	0	0	0	0	0		
ENSMUST00000195560	ENSMUSG00000026496	1	180568924	180601254	1	0	0	0	0	0	0	0	16	0	1	0	A0A0A6YVX0	
ENSMUST00000195561	ENSMUSG00000028078	3	86786151	86920852	-1	0	0	0	0	0	0	0	7	0	2	5		Q6PGN3
ENSMUST00000195563	ENSMUSG00000006673	9	108516806	108560163	1	5	0	14	86	8	1	0	0	11	0	4	A0A0A6YWV5	
ENSMUST00000195564						1	1	0	0	5	3	4	0	0	1	0		
ENSMUST00000195565						17	17	29	57	31	13	3	10	8	1	6		
ENSMUST00000195567	ENSMUSG00000003135	1	39534992	39546889	1	0	0	0	0	0	0	12	16	0	0	0	A0A0A6YW44	
ENSMUST00000195568						7	1	5	20	4	4	0	0	0	0	0		
ENSMUST00000195570						0	0	0	0	2	0	0	0	0	0	0		
ENSMUST00000195571	ENSMUSG00000026708	1	161070713	161086724	1	47	13	0	0	10	14	12	19	12	3	19	Q05CX4	
ENSMUST00000195574	ENSMUSG00000102388	Y	69321132	69331861	1	145	125	93	139	96	32	0	0	0	0	0	A0A087WNV3	
ENSMUST00000195575						2	10	28	3	11	8	1	0	1	1	2		
ENSMUST00000195576	ENSMUSG00000095576	1	162916551	162937515	-1	0	0	10	7	11	7	0	0	0	0	0		
ENSMUST00000195577						0	3	10	4	1	0	0	0	0	0	0		
ENSMUST00000195579						10	21	23	17	19	9	1	4	1	1	4		
ENSMUST00000195580						0	0	0	0	2	0	0	11	0	0	0		
ENSMUST00000195581						3	4	12	10	5	1	0	0	0	0	0		
ENSMUST00000195582						1	1	2	1	2	0	0	0	0	0	0		
ENSMUST00000195584	ENSMUSG00000026705	1	161088375	161131511	-1	0	2	6	3	0	0	0	33	0	1	0	Q8BL42	
ENSMUST00000195586						0	0	0	0	0	0	0	8	12	0	0		
ENSMUST00000195589	ENSMUSG00000079293	6	129461591	129472779	-1	12	7	34	25	7	8	1375	16720	2456	3670	2038		
ENSMUST00000195590	ENSMUSG00000104148	18	36939205	37187657	1	18	12	39	114	24	12	0	0	0	0	0	B9EJ92	
ENSMUST00000195591						1	0	2	4	4	2	0	0	0	0	0		
ENSMUST00000195592	ENSMUSG00000102720	CHR_MG184_PATCH	72359713	72366955	-1	0	0	0	4	1	2	3	2	3	0	10		
ENSMUST00000195594						1	4	26	2	4	3	6	4	9	4	15		
ENSMUST00000195595						4	4	2	1	6	0	0	0	0	0	0		
ENSMUST00000195596						0	0	1	2	2	0	0	0	0	0	0		
ENSMUST00000195597						1	2	1	1	0	1	0	0	0	1	0		
ENSMUST00000195598						16	11	60	15	17	2	0	5	0	0	3		
ENSMUST00000195604						0	3	1	1	1	0	0	0	0	0	0		
ENSMUST00000195605						0	0	0	0	0	0	541	94	664	0	132		

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000195607						3	1	2	0	3	0	0	0	0	0	0		
ENSMUST00000195608	ENSMUSG00000032612	9	108347853	108392545	1	0	2	0	0	1	0	0	0	5	21	1	A0A0A6YW63	
ENSMUST00000195612	ENSMUSG00000063659	1	177442351	177450764	1	0	0	10	0	8	0	124	263	106	35	147		Q9WUK6
ENSMUST00000195613						2	0	0	1	1	1	0	0	1	0	0		
ENSMUST00000195614						0	4	0	0	0	0	1	0	0	1	0		
ENSMUST00000195615	ENSMUSG00000039461	9	108302958	108306160	-1	1	0	0	25	2	0	16	0	11	3	6	A0A0A6YWL1	
ENSMUST00000195616						5	2	1	0	2	1	0	2	0	0	0		
ENSMUST00000195617	ENSMUSG00000032584	9	107906873	107920383	1	25	14	35	16	36	14	5	8	5	2	0	A0A0A6YXY9	
ENSMUST00000195619	ENSMUSG00000076670	12	114262652	114263087	-1	6	0	3	3	0	1	0	0	0	0	0	A0A0A6YWB6	
ENSMUST00000195620	ENSMUSG00000026121	1	36548639	36558349	-1	22	0	7	52	8	0	5	9	2	7	41		Q64151
ENSMUST00000195621	ENSMUSG00000028354	1	174501825	174822729	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YY57	
ENSMUST00000195622						53	42	234	71	35	20	5	21	12	1	7		
ENSMUST00000195623						0	5	1	35	0	1	0	1	4	0	0		
ENSMUST00000195624						19	11	36	77	21	13	0	0	0	0	0		
ENSMUST00000195626	ENSMUSG00000096820	Y	13161968	13164408	1	22	0	0	7	4	0	0	0	0	0	0	Q3TTD8	
ENSMUST00000195627						2	5	25	12	8	3	0	2	0	0	2		
ENSMUST00000195628						7	1	5	0	5	4	18	88	36	19	79		
ENSMUST00000195631						2	2	3	51	9	1	0	5	1	1	1		
ENSMUST00000195632						4	1	2	2	4	0	0	0	0	0	0		
ENSMUST00000195636	ENSMUSG00000026074	1	39900913	40026310	1	14	15	25	30	37	21	148	45	488	186	311	A0A0A6YWM8	
ENSMUST00000195638						1	1	0	0	0	1	0	0	0	1	7		
ENSMUST00000195640	ENSMUSG00000033900	3	82358044	82395268	1	0	0	0	53	27	0	0	4	0	1	1		Q3TRR0
ENSMUST00000195641	ENSMUSG00000076661	12	114068828	114069281	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW39	
ENSMUST00000195642						9	9	35	22	11	6	0	0	0	0	0		
ENSMUST00000195643						3	1	1	4	4	1	0	0	0	0	0		
ENSMUST00000195646						0	0	1	0	5	0	0	0	0	0	0		
ENSMUST00000195647						3	1	1	1	2	1	0	0	0	0	0		
ENSMUST00000195648						1	3	3	1	5	3	0	0	0	0	0		
ENSMUST00000195650	ENSMUSG00000037474	1	191537356	191575544	-1	1	2	224	0	66	1	0	0	0	0	0	A0A0A6YVQ5	
ENSMUST00000195651						5	4	1	2	3	0	0	0	0	0	0		
ENSMUST00000195654	ENSMUSG00000014226	1	160202367	160212875	-1	0	0	0	31	0	0	2	46	42	123	19	A0A0A6YY29	
ENSMUST00000195655						0	1	1	0	1	1	0	0	0	0	0		
ENSMUST00000195656	ENSMUSG00000015314	1	171917515	171953170	1	105	88	141	73	85	50	4	32	17	20	38	Q18PJ0	Q9ET39
ENSMUST00000195657	ENSMUSG00000050144	3	88410498	88425139	-1	0	0	0	0	0	0	158	177	231	0	39		Q8BGF9
ENSMUST00000195658	ENSMUSG00000026608	1	188971095	189007841	-1	2	0	0	0	0	0	1	0	0	0	0	A0A0A6YX69	
ENSMUST00000195659	ENSMUSG00000038034	1	172261641	172319841	1	0	0	0	0	0	0	0	0	0	2	0	A0A0A6YVX9	
ENSMUST00000195662	ENSMUSG00000057969	9	107597674	107609229	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWM9	
ENSMUST00000195663						2	6	14	10	3	2	0	4	0	1	0		
ENSMUST00000195664						1	0	0	7	0	0	0	0	11	0	9		
ENSMUST00000195667						0	0	1	2	0	0	0	0	0	0	0		
ENSMUST00000195668						0	0	0	0	1	0	0	0	0	0	0		
ENSMUST00000195669	ENSMUSG00000102976	1	133619862	133661380	-1	0	5	0	13	1	0	13	3	21	0	34	A0A0A6YXI9	
ENSMUST00000195671						3	2	5	3	4	1	0	0	0	0	0		
ENSMUST00000195678						0	0	2	0	0	0	0	0	0	0	0		
ENSMUST00000195681	ENSMUSG00000010047	9	107567945	107572779	1	13	15	23	8	29	9	0	5	0	0	0	A0A0A6YX37	
ENSMUST00000195682						2	0	10	4	4	0	0	0	0	0	0		
ENSMUST00000195684	ENSMUSG00000026070	1	40465552	40500854	1	0	0	0	0	0	0	0	0	0	0	0		Q61098
ENSMUST00000195686						5	2	1	90	3	5	8	22	28	0	68		
ENSMUST00000195688	ENSMUSG00000026668	2	4976122	4985748	1	0	0	0	0	0	2	0	0	1	1	0		Q14BU0
ENSMUST00000195689						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195690						1	4	2	6	6	2	0	0	0	0	0		
ENSMUST00000195691						3	2	2	2	6	1	0	1	0	0	2		
ENSMUST00000195693						0	0	0	0	0	2	4	6	8	0	6		
ENSMUST00000195695						1	0	2	3	6	0	0	0	0	0	0		
ENSMUST00000195701						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195702	ENSMUSG00000033488	1	157458577	157492638	1	1	0	0	0	0	0	1	0	0	0	0	A0A0A6YWZ0	
ENSMUST00000195703						0	0	0	0	0	0	7	0	7	3	0		
ENSMUST00000195705	ENSMUSG00000048234	1	39551296	39577405	-1	0	0	0	0	1	0	6	0	4	0	2	A0A0A6YVR6	
ENSMUST00000195706	ENSMUSG00000076666	12	114176438	114176867	-1	4	6	12	3	5	0	0	0	0	0	5	A0A0A6YVR1	
ENSMUST00000195707	ENSMUSG00000096498	12	113685482	113686045	-1	22	22	50	33	32	15	0	0	0	0	0	A0A0A6YY69	
ENSMUST00000195708	ENSMUSG00000062232	3	79062516	79286517	-1	25	10	19	151	0	0	412	418	942	61	546	A0A0A6YWG7	
ENSMUST00000195713	ENSMUSG00000026792	2	32925216	32961614	-1	0	0	3	0	2	0	0	2	6	0	0	A0A0A6YWS5	
ENSMUST00000195715						0	0	0	5	2	4	15	7	77	4	47		
ENSMUST00000195717	ENSMUSG00000057335	1	176733653	176814067	-1	0	0	0	40	0	0	266	434	468	90	388	H7BX26	
ENSMUST00000195721	ENSMUSG00000026817	2	32621758	32635058	1	0	0	0	2	0	0	0	0	1	0	0	A0A0A6YXW8	
ENSMUST00000195722						4	0	2	0	2	0	0	0	1	0	0		
ENSMUST00000195724	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	1	0	0	21	14	17	0	A0A0A6YXG7	
ENSMUST00000195725	ENSMUSG00000010048	9	107587642	107593385	1	0	9	3	63	3	1	8	0	4	5	3	A0A0A6YWV7	
ENSMUST00000195728						2	4	5	47	2	1	2	65	3	6	13		
ENSMUST00000195729						3	9	2	3	2	1	0	0	0	0	0		
ENSMUST00000195731						0	0	0	0	0	0	0	1	0	5	0		
ENSMUST00000195734						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195735	ENSMUSG00000096649	12	114829264	114829697	-1	0	0	0	0	3	0	0	0	0	0	0	A0A0A6YWK5	
ENSMUST00000195737						0	0	0	1	0	0	0	1	0	2	0		
ENSMUST00000195738	ENSMUSG00000025651	9	108936633	108949623	1	0	3	0	74	7	2	0	6	9	0	8	A0A0A6YWM1	
ENSMUST00000195739	ENSMUSG00000010064	9	107650634	107669530	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWC0	
ENSMUST00000195740						3128	2711	19927	9519	2726	1330	12	85	60	4	65		
ENSMUST00000195741						7	9	9	7	10	10	1	1	4	0	6		
ENSMUST00000195744						0	0	4	0	1	0	0	0	0	0	0		
ENSMUST00000195745						0	0	0	0	2	0	0	0	0	1	2		
ENSMUST00000195746	ENSMUSG00000010048	9	107587642	107593385	1	1	2	3	2	0	1	1	8	0	3	10	A0A0A6YY02	
ENSMUST00000195747						14	8	14	22	15	0	0	0	0	1	0		
ENSMUST00000195749	ENSMUSG00000026707	2	14995131	15055069	-1	10	15	12	0	2	10	0	0	35	21	0		Q7TS68
ENSMUST00000195751	ENSMUSG00000037730	3	30602065	30619873	1	0	0	0	0	0	0	16	171	56	80	0		Q99MD8

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Start_position	End_position	Strand	hpgl0681	hpgl0683	hpgl0526	hpgl0527	hpgl0682	hpgl0684	hpgl0685	hpgl0522	hpgl0687	hpgl0686	hpgl0688	Uniprot_Trembl	Uniprot_Swissprot
ENSMUST00000195752	ENSMUSG00000010047	9	107567945	107572779	1	4	3	14	111	12	7	0	0	0	0	0	Q3UZE4	O35632
ENSMUST00000195755						2	0	0	0	0	1	0	0	0	0	0		
ENSMUST00000195756	ENSMUSG00000021466	13	63508328	63573598	-1	1	0	7	11	3	0	0	0	0	0	0	Q5R1U4	
ENSMUST00000195757						3	1	1	1	1	1	0	0	0	0	0		
ENSMUST00000195758						5	1	11	3	9	4	3	8	9	0	13		
ENSMUST00000195760	ENSMUSG00000026715	1	160978585	161005863	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YX70	
ENSMUST00000195762						12	8	11	12	16	4	4	21	9	1	17		
ENSMUST00000195763						0	1	14	5	7	1	0	4	3	0	15		
ENSMUST00000195764	ENSMUSG00000103081	18	37761801	37841870	1	23	15	26	92	17	6	0	0	4	0	7		
ENSMUST00000195765						7	7	5	2	4	1	0	0	0	0	0		
ENSMUST00000195766	ENSMUSG00000095789	5	129908540	129913789	1	0	0	0	79	0	0	0	9	6	1	0		Q497P3
ENSMUST00000195768						14	8	9	25	8	6	0	0	0	0	0		
ENSMUST00000195770	ENSMUSG00000026073	1	40074079	40125231	1	12	7	0	0	2	1	0	3975	126	858	38	A0A0A6YX23	
ENSMUST00000195773						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195775						1	0	6	5	3	3	0	0	0	0	0		
ENSMUST00000195776						4	2	1	5	6	1	2	1	0	0	3		
ENSMUST00000195778	ENSMUSG00000095028	3	15495751	15575065	-1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YWF8	
ENSMUST00000195779	ENSMUSG00000026773	2	11471433	11554077	-1	13	23	9	0	10	4	31	1786	0	92	0	A0A0A6YW89	
ENSMUST00000195782						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195787						0	0	9	54	1	0	0	0	0	0	0		
ENSMUST00000195788						0	2	0	0	0	5	5	0	14	0	15		
ENSMUST00000195789						0	0	1	4	0	0	0	0	0	0	0		
ENSMUST00000195790						2	1	3	0	3	1	0	0	0	0	0		
ENSMUST00000195791						0	1	0	0	0	0	0	0	0	0	0		
ENSMUST00000195793	ENSMUSG00000033900	3	82358044	82395268	1	1	0	1	0	2	2	0	0	0	1	0	A0A0A6YVR4	
ENSMUST00000195794						0	0	3	0	0	0	0	0	0	0	0		
ENSMUST00000195797	ENSMUSG00000095514	13	119836006	119846570	1	10	10	14	11	12	9	0	2	0	3	2	Q3UPR8	
ENSMUST00000195798	ENSMUSG00000072258	1	183388981	183410198	1	30	29	110	32	30	12	6	45	11	12	23	A0A0A6YW00	
ENSMUST00000195800	ENSMUSG00000040782	1	159232320	159347640	1	0	0	0	59	0	0	0	28	72	6	21	A0A0A6YXD2	
ENSMUST00000195801						2	2	4	2	6	1	0	0	0	0	0		
ENSMUST00000195802	ENSMUSG00000098301	CHR_MG3829_PATCH	88047373	88053755	1	0	0	0	0	0	0	0	386	154	43	108		
ENSMUST00000195803						0	0	31	0	6	0	0	0	0	0	0		
ENSMUST00000195804						0	1	0	9	18	0	9	133	85	6	123		
ENSMUST00000195809						2	1	13	2	5	0	0	0	0	0	1		
ENSMUST00000195812						6	5	27	9	10	7	1	2	0	3	5		
ENSMUST00000195815	ENSMUSG00000026637	1	191997205	192092559	-1	0	0	0	0	0	0	0	11	0	0	3	A0A0A6YXC4	
ENSMUST00000195816						0	0	1	0	1	0	0	0	0	0	0		
ENSMUST00000195817	ENSMUSG00000027763	3	60472830	60629750	1	0	0	0	0	0	0	0	12	75	13	38	A0A0A6YWJ5	
ENSMUST00000195818						0	9	2	0	0	8	0	0	0	0	0		
ENSMUST00000195821						4	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195822	ENSMUSG00000027534	3	10417817	10440102	-1	1	0	3	25	2	0	0	17	1	7	9	Q8BLP0	
ENSMUST00000195823	ENSMUSG00000103793	18	37707039	37841873	1	8	9	20	32	22	8	0	2	0	0	9	Q91XY2	
ENSMUST00000195824	ENSMUSG00000026615	1	185363044	185428360	1	0	0	0	0	0	0	0	0	3	0	0	A0A0A6YWH3	
ENSMUST00000195825						2	0	0	6	1	0	0	0	0	0	0		
ENSMUST00000195826	ENSMUSG00000055421	14	93013410	93890679	-1	0	0	0	0	0	0	0	0	0	0	0	F8VPK8	
ENSMUST00000195827						0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195829						5	6	4	3	4	0	0	0	0	0	0		
ENSMUST00000195832						18	26	25	45	28	27	0	1	0	1	2		
ENSMUST00000195833	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195834						3	0	0	1	0	4	0	0	0	0	0		
ENSMUST00000195838	ENSMUSG00000073406	17	36080115	36084223	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195839						10	6	10	10	6	5	3	7	3	0	2		
ENSMUST00000195840						1	2	1	19	2	1	2	0	2	0	0		
ENSMUST00000195841	ENSMUSG00000057914	2	14603088	14987908	1	1	2	3	0	3	0	0	0	0	0	0	A0A0A6YY52	
ENSMUST00000195843	ENSMUSG00000010064	9	107650634	107669530	-1	8	0	0	0	0	0	0	0	0	0	0	A0A0A6YWH4	
ENSMUST00000195844						3	0	2	2	0	1	0	0	0	0	0		
ENSMUST00000195846	ENSMUSG00000025764	3	41555731	41616864	1	0	0	0	5	0	0	0	0	0	0	0	A0A0A6YWV0	
ENSMUST00000195847	ENSMUSG00000096879	3	93068823	93075505	1	4	0	0	6	0	4	0	0	0	0	0	A0A0A6YWS7	
ENSMUST00000195848	ENSMUSG00000016181	1	193091104	193130272	-1	0	0	0	0	0	1	2	0	0	1	0	A0A0A6YXE1	
ENSMUST00000195849						4	3	23	31	6	1	0	0	0	0	0		
ENSMUST00000195850						6	1	0	4	6	1	0	0	0	0	0		
ENSMUST00000195851						0	3	2	38	5	3	0	0	0	0	0		
ENSMUST00000195854						5	5	7	0	7	2	20	6	23	1	14		
ENSMUST00000195855	ENSMUSG00000040374	3	5560188	5576239	-1	0	0	0	0	0	0	87	162	106	262	96	Q91YZ5	
ENSMUST00000195856						3	2	6	6	5	0	0	0	0	0	0		
ENSMUST00000195857						0	1	8	4	2	3	4	4	11	0	8		
ENSMUST00000195858	ENSMUSG00000096420	12	113449588	113449599	-1	0	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195859						0	0	0	0	0	2	0	1	0	0	1		
ENSMUST00000195860	ENSMUSG00000026074	1	39900913	40026310	1	0	0	0	0	0	0	0	0	0	0	0	A0A0A6YW53	
ENSMUST00000195861						1	0	0	0	0	0	0	0	0	0	0		
ENSMUST00000195863	ENSMUSG00000026791	2	32972990	32982083	-1	1	0	0	0	0	0	6	0	0	0	0	A0A0A6YX81	
ENSMUST00000195866	ENSMUSG00000032582	9	107773559	107873237	-1	0	0	3	1	1	0	1	0	0	0	2	A0A0A6YWN4	
ENSMUST00000195867						4	4	3	1	7	2	0	0	0	0	0		
ENSMUST00000195869						24	21	41	10	33	14	0	0	0	0	0		
ENSMUST00000195870						19	12	29	9	17	15	15	17	63	0	38		
ENSMUST00000195872	ENSMUSG00000098375	CHR_MG3829_PATCH	88204388	88211507	1	5	0	4	0	0	3	25	41	9	21	15		
ENSMUST00000195875						1	1	1	2	3	2	0	0	0	0	0		
ENSMUST00000195876	ENSMUSG00000103205	CHR_MG184_PATCH	72385222	72390702	-1	10	18	75	17	21	12	96	331	115	39	142		
ENSMUST00000195878						17	11	29	24	15	9	0	0	0	0	0		
ENSMUST00000195882	ENSMUSG00000025766	3	41742611	41803320	1	0	1	0	0	0	0	0	0	0	0	0		Q8BGN2
ENSMUST00000195883	ENSMUSG00000032582	9	107773559	107873237	-1	0	0	0	0	0	0	0	0	0	4	0	A0A0A6YXE2	
ENSMUST00000195884	ENSMUSG00000096805	12	114093928	114094358	-1	0	4	6	0	1	0	0	0	0	0	13	A0A0B4J1P3	
ENSMUST00000195886	ENSMUSG00000037957	12	110737944	110804238	1	1	1	0	0	6	2	0	6	8	2	15	A0A0A6YXV5	

Differential Expression of mRNA transcript isoforms

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000000001	guanine nucleotide binding protein (G protein), alpha inhibiting 3 [Source:MGI Symbol;Acc:MGI:95773]		Q9DC51	-5.8	1.2E-06	-4.8	3.5E-05	0.9	1.5E-02	-0.1	8.8E-01
ENSMUST00000000010	homeobox B9 [Source:MGI Symbol;Acc:MGI:96190]		P20615	5.2	1.4E-02	7.5	1.9E-03	-0.6	7.4E-01	-3.0	2.2E-02
ENSMUST00000000028	cell division cycle 45 [Source:MGI Symbol;Acc:MGI:1338073]	Q3UI99	Q9Z1X9	-2.1	1.0E-01	-1.4	4.9E-01	1.4	2.5E-01	0.7	7.0E-01
ENSMUST00000000058	caveolin 2 [Source:MGI Symbol;Acc:MGI:107571]		Q9WVC3	-0.7	4.7E-01	-1.9	1.4E-01	-0.7	4.1E-01	0.5	6.9E-01
ENSMUST00000000080	Kruppel-like factor 6 [Source:MGI Symbol;Acc:MGI:1346318]	Q8BPQ2		-5.0	2.7E-04	-3.9	5.6E-03	0.7	2.2E-01	-0.3	7.9E-01
ENSMUST00000000087	sex comb on midleg homolog 1 [Source:MGI Symbol;Acc:MGI:1352762]		Q8K214	-2.7	3.3E-02	2.4	3.3E-01	7.1	2.8E-03	2.1	2.8E-01
ENSMUST00000000090	cytochrome c oxidase subunit Va [Source:MGI Symbol;Acc:MGI:88474]		P12787	-6.1	6.7E-07	-5.1	4.1E-05	1.3	2.0E-03	0.4	5.9E-01
ENSMUST00000000095	T-box 2 [Source:MGI Symbol;Acc:MGI:98494]		Q60707	6.3	6.0E-06	3.9	1.8E-04	-2.4	6.2E-03	0.0	9.7E-01
ENSMUST00000000096	T-box 4 [Source:MGI Symbol;Acc:MGI:102556]		P70325	7.1	6.2E-02	5.9	1.4E-01	-0.8	8.5E-01	0.4	8.5E-01
ENSMUST00000000109	contactin 1 [Source:MGI Symbol;Acc:MGI:105980]		P12960	6.3	1.6E-04	7.6	6.7E-05	-0.5	6.4E-01	-1.8	1.5E-02
ENSMUST00000000122	nerve growth factor receptor (TNFR superfamily, member 16) [Source:MGI Symbol;Acc:MGI:97323]	Q8CFT3		9.9	4.6E-06	6.2	1.1E-05	-4.0	2.9E-03	-0.3	4.7E-01
ENSMUST00000000127	wingless-type MMTV integration site family, member 3 [Source:MGI Symbol;Acc:MGI:98955]	A2A649	P17553	7.9	2.6E-05	7.5	7.5E-05	-0.6	6.2E-01	-0.2	7.2E-01
ENSMUST00000000128	wingless-type MMTV integration site family, member 9A [Source:MGI Symbol;Acc:MGI:2446084]	J3JS28		4.0	7.1E-02	5.3	1.3E-02	-2.1	3.2E-01	-3.4	2.8E-02
ENSMUST00000000129	fer (fms/fps related) protein kinase [Source:MGI Symbol;Acc:MGI:105917]		P70451	-2.9	1.9E-03	-4.3	3.3E-03	-0.4	4.7E-01	1.0	3.7E-01
ENSMUST00000000137	ARP2 actin-related protein 2 [Source:MGI Symbol;Acc:MGI:1913963]	Q5SW83	P61161	-6.9	1.5E-07	-6.2	3.1E-06	0.3	2.7E-01	-0.4	5.0E-01
ENSMUST00000000153	guanine nucleotide binding protein, alpha 12 [Source:MGI Symbol;Acc:MGI:95767]		P27600	-0.9	9.8E-02	-0.4	5.1E-01	0.0	9.9E-01	-0.5	4.3E-01
ENSMUST00000000161	integrin beta 2-like [Source:MGI Symbol;Acc:MGI:1277979]		Q3UV74	2.7	2.4E-01	-0.8	8.5E-01	0.8	7.9E-01	4.3	2.5E-01
ENSMUST00000000175	ccinate dehydrogenase complex, subunit D, integral membrane protein [Source:MGI Symbol;Acc:MGI:191417		Q9CXV1	-5.5	3.8E-06	-5.4	3.1E-05	-0.1	6.5E-01	-0.3	6.6E-01
ENSMUST00000000186	fibroblast growth factor 23 [Source:MGI Symbol;Acc:MGI:1891427]	Q3U1V5	Q9EPC2	8.6	2.5E-05	7.1	2.4E-04	-0.7	6.1E-01	0.8	2.2E-01
ENSMUST00000000187	fibroblast growth factor 6 [Source:MGI Symbol;Acc:MGI:95520]		P21658	7.1	4.1E-05	6.6	1.5E-04	-0.5	6.4E-01	0.0	9.7E-01
ENSMUST00000000188	cyclin D2 [Source:MGI Symbol;Acc:MGI:88314]	Q4FK45	P30280	1.3	4.2E-02	0.6	3.8E-01	-0.7	2.5E-01	0.0	9.9E-01
ENSMUST00000000193	chemokine (C-C motif) ligand 2 [Source:MGI Symbol;Acc:MGI:98259]	Q5SVU3	P10148	-1.0	3.4E-01	-3.2	3.7E-02	-1.4	1.2E-01	0.8	5.7E-01
ENSMUST00000000199	neuronal calcium sensor 1 [Source:MGI Symbol;Acc:MGI:109166]		Q8BNY6	5.6	2.0E-04	4.6	2.3E-03	-0.9	4.2E-01	0.2	8.1E-01
ENSMUST00000000201	sodium leak channel, non-selective [Source:MGI Symbol;Acc:MGI:2444306]	E9QLE4		7.9	3.1E-05	7.5	9.6E-05	-0.5	6.9E-01	-0.1	8.8E-01
ENSMUST00000000208	schlafen 4 [Source:MGI Symbol;Acc:MGI:1329010]	Q3UV66		-10.1	3.6E-04	-7.0	2.6E-03	0.0	9.9E-01	-3.1	1.7E-01
ENSMUST00000000219	tyrosine hydroxylase [Source:MGI Symbol;Acc:MGI:98735]		P24529	5.1	1.7E-02	6.4	6.8E-03	-0.7	7.3E-01	-1.9	1.3E-01
ENSMUST00000000221	sodium channel, nonvoltage-gated 1 gamma [Source:MGI Symbol;Acc:MGI:104695]		Q9WU39	7.6	4.1E-05	7.3	1.1E-04	-0.6	6.3E-01	-0.3	6.4E-01
ENSMUST00000000253	LIM homeobox protein 2 [Source:MGI Symbol;Acc:MGI:96785]	Q543C6	Q9Z0S2	6.3	6.1E-04	6.2	2.3E-02	-0.8	7.5E-01	-0.4	7.4E-01
ENSMUST00000000266	interferon activated gene 202B [Source:MGI Symbol;Acc:MGI:1347083]		Q9R002	-2.5	2.1E-02	6.9	5.6E-04	-0.6	7.0E-01	-1.2	1.4E-01
ENSMUST00000000260	guanosine monophosphate reductase [Source:MGI Symbol;Acc:MGI:1913605]		Q9DCZ1	1.5	7.2E-02	2.1	5.2E-02	0.5	5.4E-01	0.0	9.7E-01
ENSMUST00000000275	glycine receptor, alpha 3 subunit [Source:MGI Symbol;Acc:MGI:95749]	G5E811		4.7	1.8E-02	-2.4	4.4E-02	-1.2	9.9E-02	-1.3	2.6E-01
ENSMUST00000000284	tripartite motif-containing 25 [Source:MGI Symbol;Acc:MGI:102749]	Q5SU71		5.6	1.1E-03	5.9	8.7E-03	-0.4	8.5E-01	-1.6	1.6E-01
ENSMUST00000000291	max binding protein [Source:MGI Symbol;Acc:MGI:109150]		O08789	-1.6	1.7E-02	7.4	1.5E-03	1.6	3.4E-01	-0.2	7.9E-01
ENSMUST00000000287	serine carboxypeptidase 1 [Source:MGI Symbol;Acc:MGI:1921867]		Q920A5	-0.9	1.9E-01	-2.0	2.9E-02	-1.2	3.2E-02	-0.1	9.2E-01
ENSMUST00000000299	integrin beta 2 [Source:MGI Symbol;Acc:MGI:96611]	Q542I8		-7.3	7.0E-07	-0.5	5.1E-01	1.2	3.1E-02	0.2	8.1E-01
ENSMUST00000000305	tumor protein D52-like 1 [Source:MGI Symbol;Acc:MGI:1298386]		O54818	3.8	1.1E-02	-6.9	1.7E-05	0.9	2.2E-02	0.5	5.7E-01
ENSMUST00000000304	HD domain containing 2 [Source:MGI Symbol;Acc:MGI:1916942]		Q3SXD3	-1.3	4.8E-01	-6.2	5.9E-02	-3.2	4.5E-02	1.6	5.9E-01
ENSMUST00000000314	cadherin 4 [Source:MGI Symbol;Acc:MGI:99218]		P39038	10.0	2.4E-06	-0.2	8.1E-01	-4.9	2.0E-03	-0.8	3.9E-01
ENSMUST00000000312	cadherin 1 [Source:MGI Symbol;Acc:MGI:88354]			0.7	2.8E-01	1.2	1.8E-01	0.7	3.2E-01	0.2	8.2E-01
ENSMUST00000000326	B cell CLL/lymphoma 6, member B [Source:MGI Symbol;Acc:MGI:1278332]	Q5BKP3	O88282	7.7	2.8E-05	8.4	1.1E-05	-1.5	2.0E-01	0.1	8.3E-01
ENSMUST00000000317	creatine kinase, mitochondrial 1, ubiquitous [Source:MGI Symbol;Acc:MGI:99441]	Q545N7	P30275	3.5	6.2E-02	7.1	1.9E-03	-0.5	7.9E-01	-4.1	4.8E-03
ENSMUST00000000329	arachidonate 12-lipoxygenase [Source:MGI Symbol;Acc:MGI:87998]	A2CF85	P39655	4.3	3.1E-05	7.7	9.6E-05	0.0	9.8E-01	0.1	9.2E-01
ENSMUST00000000335	catechol-O-methyltransferase [Source:MGI Symbol;Acc:MGI:88470]		O88587	-4.0	8.8E-04	1.7	1.2E-02	-2.5	1.5E-03	0.1	7.9E-01
ENSMUST00000000342	chemokine (C-C motif) ligand 11 [Source:MGI Symbol;Acc:MGI:103576]		P48298	6.2	1.0E-04	-3.6	4.0E-03	-1.0	7.4E-02	-1.3	2.4E-01
ENSMUST00000000348	RNA 3'-terminal phosphate cyclase [Source:MGI Symbol;Acc:MGI:1913618]		Q9D7H3	-4.7	1.3E-03	4.9	6.5E-04	-1.3	2.4E-01	0.0	9.5E-01
ENSMUST00000000349	dihydrolipoamide branched chain transacylase E2 [Source:MGI Symbol;Acc:MGI:105386]		P53395	2.3	1.8E-03	-1.7	8.6E-02	0.1	9.1E-01	-2.9	2.7E-02
ENSMUST00000000356	DAZ associated protein 2 [Source:MGI Symbol;Acc:MGI:1344344]		Q9DCP9	-7.5	5.2E-08	1.0	1.1E-01	-1.3	3.0E-02	0.0	9.9E-01
ENSMUST00000000365	malignant T cell amplified sequence 1 [Source:MGI Symbol;Acc:MGI:1916245]		Q9DB27	-7.5	5.0E-06	-6.7	9.9E-07	0.3	1.8E-01	-0.5	4.5E-01
ENSMUST00000000369	rad and gem related GTP binding protein 1 [Source:MGI Symbol;Acc:MGI:1097696]		O35929	4.9	6.6E-04	-5.8	2.4E-04	0.8	5.2E-02	-0.9	3.9E-01
ENSMUST00000000384	trafficking protein particle complex 10 [Source:MGI Symbol;Acc:MGI:1336209]	F8VQF9		-2.2	7.3E-04	5.2	1.5E-03	-0.4	7.6E-01	-0.6	3.9E-01
ENSMUST00000000388	cerebral cavernous malformation 2 [Source:MGI Symbol;Acc:MGI:2384924]		Q8K2Y9	-6.3	1.4E-04	-1.1	8.1E-02	0.9	3.2E-02	-0.2	7.8E-01
ENSMUST00000000395	transmembrane protease, serine 2 [Source:MGI Symbol;Acc:MGI:1354381]		Q9JIQ8	7.9	3.1E-05	-3.4	4.5E-03	0.4	4.4E-01	-2.5	5.5E-02
ENSMUST00000000394	transforming growth factor beta regulated gene 4 [Source:MGI Symbol;Acc:MGI:1100868]		Q91YM4	-2.5	8.9E-02	-2.1	3.5E-01	1.7	2.0E-01	1.3	5.4E-01
ENSMUST00000000412	EGF-like-domain, multiple 6 [Source:MGI Symbol;Acc:MGI:1858599]		Q9JJZ5	8.7	2.8E-06	6.3	2.3E-04	-1.4	2.6E-01	0.1	8.4E-01
ENSMUST00000000421	testis-specific serine kinase 3 [Source:MGI Symbol;Acc:MGI:1929914]		Q9D2E1	4.0	1.0E-02	8.4	4.3E-05	0.8	5.0E-01	1.0	9.5E-02
ENSMUST00000000445	myogenic factor 5 [Source:MGI Symbol;Acc:MGI:97252]	A2RSK4	P24699	6.8	4.6E-05	3.7	3.5E-02	-0.6	6.9E-01	-0.3	7.7E-01
ENSMUST00000000430	acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI		O08912	4.2	5.6E-02	5.2	5.9E-02	0.7	7.5E-01	-0.3	8.8E-01
ENSMUST00000000451	v-raf-leukemia viral oncogene 1 [Source:MGI Symbol;Acc:MGI:97847]		Q99N57	-9.5	9.5E-06	7.1	6.2E-05	-0.6	6.0E-01	-0.9	1.4E-01
ENSMUST00000000449	makorin, ring finger protein, 2 [Source:MGI Symbol;Acc:MGI:1914277]		Q9ERV1	0.0	9.9E-01	0.3	6.8E-01	0.0	9.6E-01	-0.2	7.0E-01
ENSMUST00000000466	perilipin 2 [Source:MGI Symbol;Acc:MGI:87920]		P43883	-7.1	4.0E-07	-7.9	2.6E-04	0.8	6.4E-02	-0.8	6.2E-01
ENSMUST00000000500	platelet derived growth factor, B polypeptide [Source:MGI Symbol;Acc:MGI:97528]			5.1	2.1E-04	-7.6	2.3E-06	-0.1	7.0E-01	0.4	6.0E-01
ENSMUST00000000476	platelet derived growth factor receptor, alpha polypeptide [Source:MGI Symbol;Acc:MGI:97530]		P26618	3.7	6.9E-02	-0.1	9.3E-01	-5.6	7.1E-03	-1.8	2.6E-01
ENSMUST00000000505	minichromosome maintenance deficient 7 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1298398]	Q3U4T8	Q61881	-1.5	1.5E-02	3.9	2.0E-03	-1.9	5.7E-02	-0.7	3.5E-01
ENSMUST00000000514	serine (or cysteine) peptidase inhibitor, clade B, member 8 [Source:MGI Symbol;Acc:MGI:894657]		O08800	4.8	4.0E-04	-1.1	1.2E-01	0.3	4.8E-01	-0.1	9.1E-01
ENSMUST00000000543	P1 (general receptor for phosphoinositides 1)-associated scaffold protein [Source:MGI Symbol;Acc:MGI:18603		Q9JJA9	8.6	2.2E-05	1.7	9.5E-02	-2.1	3.9E-02	1.0	2.1E-01
ENSMUST00000000542	activin A receptor, type II-like 1 [Source:MGI Symbol;Acc:MGI:1338946]		Q61288	-3.6	8.7E-02	2.3	3.5E-01	2.5	2.4E-01	-3.5	1.3E-01
ENSMUST00000000544	activin A receptor, type 1B [Source:MGI Symbol;Acc:MGI:1338944]	Q3TZF1	Q61271	-2.7	1.3E-04	6.6	5.6E-04	-1.1	3.9E-01	0.8	2.7E-01
ENSMUST00000000572	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2 [Source:MGI Symbol;Acc:MGI:95614]	A0A0H2UKB5		7.2	8.5E-05	-1.2	5.3E-02	1.4	3.0E-03	-0.1	9.2E-01
ENSMUST00000000573	oviductal glycoprotein 1 [Source:MGI Symbol;Acc:MGI:106661]	Q54AJ4	Q62010	-4.3	5.1E-04	7.1	1.8E-04	-0.5	7.1E-01	-0.4	5.7E-01
ENSMUST00000000574	adenosine A3 receptor [Source:MGI Symbol;Acc:MGI:104847]	Q3U4C5		-2.2	5.4E-04	-4.6	1.7E-03	0.0	1.0E+00	0.3	8.2E-01
ENSMUST00000000579	SRY (sex determining region Y)-box 9 [Source:MGI Symbol;Acc:MGI:98371]		Q04887	9.6	3.1E-05	-1.7	1.0E-02	0.3	4.5E-01	-0.2	6.9E-01
ENSMUST00000000594	C1D nuclear receptor co-repressor [Source:MGI Symbol;Acc:MGI:1927354]		O35473	-4.3	1.5E-04	5.4	4.8E-04	-3.4	2.4E-02	0.7	2.7E-01
ENSMUST00000000590	radixin [Source:MGI Symbol;Acc:MGI:97887]		P26043	-0.7	7.3E-01	-3.2	2.5E-01	-2.2	1.9E-01	0.3	9.3E-01
ENSMUST00000000608	GM2 ganglioside activator protein [Source:MGI Symbol;Acc:MGI:95762]	Q5F1Z8	Q60648	-5.2	2.0E-06	-5.3	1.1E-03	-0.4	3.7E-01	0.5	6.6E-01
ENSMUST00000000631	glutamate receptor, metabotropic 6 [Source:MGI Symbol;Acc:MGI:1351343]		Q5NCH9	3.3	4.4E-03	-4.2	5.4E-05	0.4	2.4E-01	-0.6	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000000619	chloride channel, voltage-sensitive 4 [Source:MGI Symbol;Acc:MGI:104571]		Q61418	-1.0	1.3E-01	-0.9	2.8E-01	0.5	4.0E-01	0.4	6.0E-01
ENSMUST00000000641	ain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain [Source:MGI Symbol;Acc:MGI:		Q9Z123	2.6	5.5E-03	5.1	2.7E-03	1.1	3.6E-01	-0.7	3.4E-01
ENSMUST00000000642	hexokinase 2 [Source:MGI Symbol;Acc:MGI:1315197]		O08528	-1.4	1.5E-02	3.1	1.4E-02	1.1	2.3E-01	0.6	4.3E-01
ENSMUST00000000687	3-hydroxyanthranilate 3,4-dioxygenase [Source:MGI Symbol;Acc:MGI:1349444]		Q78JT3	-1.9	2.0E-02	-0.6	3.8E-01	0.8	9.5E-02	-0.1	9.1E-01
ENSMUST00000000696	CD52 antigen [Source:MGI Symbol;Acc:MGI:1346088]		Q64389	-9.8	2.3E-07	-0.8	4.0E-01	0.6	2.9E-01	-0.5	5.5E-01
ENSMUST00000000717	T cell leukemia/lymphoma 1B, 5 [Source:MGI Symbol;Acc:MGI:1351635]	Q3UT92	P56845	6.7	4.8E-05	-8.9	2.8E-06	-0.2	4.7E-01	-1.1	2.3E-01
ENSMUST00000000707	lysyl oxidase-like 3 [Source:MGI Symbol;Acc:MGI:1337004]		Q9Z175	3.9	8.0E-02	2.4	2.8E-01	-3.0	1.7E-01	-1.4	4.5E-01
ENSMUST00000000718	T cell leukemia/lymphoma 1B, 4 [Source:MGI Symbol;Acc:MGI:1351604]		P56844	6.7	1.8E-04	6.6	1.1E-04	-0.6	5.9E-01	-0.4	4.5E-01
ENSMUST00000000724	K(lysine) acetyltransferase 2B [Source:MGI Symbol;Acc:MGI:1343094]	B2RR30	Q9JHD1	-3.2	1.0E-03	6.4	4.5E-04	-0.6	6.3E-01	-0.4	6.1E-01
ENSMUST00000000727	RAB5B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105938]	B2RPS1	P61021	-5.0	2.1E-06	-1.5	7.8E-02	0.6	2.3E-01	-1.1	2.3E-01
ENSMUST00000000746	DNA (cytosine-5-)-methyltransferase 3-like [Source:MGI Symbol;Acc:MGI:1859287]	A3EWM2	Q9CWR8	6.0	2.6E-02	-3.4	2.1E-04	1.1	5.7E-03	-0.5	3.8E-01
ENSMUST00000000756	ribosomal protein L13 [Source:MGI Symbol;Acc:MGI:105922]		P47963	-5.3	5.4E-05	7.0	1.6E-02	-0.8	7.6E-01	-1.9	2.2E-01
ENSMUST00000000759	charged multivesicular body protein 1A [Source:MGI Symbol;Acc:MGI:1920159]		Q921W0	-4.0	3.0E-04	-5.6	1.3E-04	-0.8	8.2E-02	-0.4	6.5E-01
ENSMUST00000000767	replication protein A1 [Source:MGI Symbol;Acc:MGI:1915525]	Q5SWN2		-6.7	1.5E-05	-2.7	1.3E-02	0.9	8.9E-02	-0.3	7.1E-01
ENSMUST00000000769	serine (or cysteine) peptidase inhibitor, clade F, member 1 [Source:MGI Symbol;Acc:MGI:108080]		P97298	5.5	5.1E-04	-6.2	1.7E-04	-0.2	5.9E-01	-0.7	5.5E-01
ENSMUST00000000776	tubulin, gamma complex associated protein 3 [Source:MGI Symbol;Acc:MGI:2183752]		P58854	-4.8	2.0E-03	4.0	2.2E-03	-2.5	4.6E-02	-1.0	1.9E-01
ENSMUST00000000804	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Source:MGI Symbol;Acc:MGI:103064]	Q3TQX5	Q62167	-6.6	2.0E-07	-2.8	2.9E-02	-0.1	8.8E-01	-2.1	1.4E-01
ENSMUST00000000793	polymerase (RNA) III (DNA directed) polypeptide D [Source:MGI Symbol;Acc:MGI:1914315]		Q91WD1	1.6	4.2E-01	2.2	3.5E-01	-1.7	4.3E-01	-2.3	2.2E-01
ENSMUST00000000808	interleukin 12 receptor, beta 1 [Source:MGI Symbol;Acc:MGI:104579]		Q60837	3.0	5.5E-04	-6.0	2.4E-06	-0.2	3.6E-01	-0.8	1.8E-01
ENSMUST00000000809	solute carrier family 5 (sodium iodide symporter), member 5 [Source:MGI Symbol;Acc:MGI:2149330]	G3X8P5		8.3	1.6E-05	3.6	4.9E-04	0.3	5.8E-01	-0.3	5.8E-01
ENSMUST00000000821	ubiquitin specific peptidase 32 [Source:MGI Symbol;Acc:MGI:2144475]	F6XDW8		-5.8	3.7E-03	7.6	5.2E-05	-0.9	4.5E-01	-0.2	7.4E-01
ENSMUST00000000811	termediate/small conductance calcium-activated channel, subfamily N, member 3 [Source:MGI Symbol;Acc:M		P58391	0.5	3.8E-01	2.8	5.7E-03	2.2	6.6E-03	0.0	9.4E-01
ENSMUST00000000828	thioredoxin reductase 3 [Source:MGI Symbol;Acc:MGI:2386711]	G3X8P6		2.4	2.6E-03	-4.4	2.8E-02	-0.5	5.9E-01	-1.9	3.5E-01
ENSMUST00000000834	Fas ligand (TNF superfamily, member 6) [Source:MGI Symbol;Acc:MGI:99255]	Q544E9	P41047	2.4	9.6E-03	1.8	3.2E-02	-0.2	7.8E-01	0.4	4.6E-01
ENSMUST00000000844	tumor protein D52-like 2 [Source:MGI Symbol;Acc:MGI:1913564]	Q3TAI4		-6.0	6.4E-04	2.6	8.9E-03	-1.4	8.5E-02	-1.6	4.3E-02
ENSMUST00000000894	E2F transcription factor 1 [Source:MGI Symbol;Acc:MGI:101941]	Q9CYB4		7.8	9.1E-04	-4.1	3.4E-02	2.1	1.9E-02	0.1	9.4E-01
ENSMUST00000000881	B cell CLL/lymphoma 11A (zinc finger protein) [Source:MGI Symbol;Acc:MGI:106190]		Q9QYE3	0.1	9.5E-01	-0.3	8.0E-01	-0.3	7.3E-01	0.1	9.5E-01
ENSMUST00000000896	peroxisomal membrane protein 4 [Source:MGI Symbol;Acc:MGI:1891701]		Q9JJW0	1.2	2.1E-02	3.0	7.2E-02	-3.6	5.7E-02	1.2	2.9E-01
ENSMUST00000000901	discs, large homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1888986]	Q52KF7		7.2	2.8E-04	1.5	2.9E-02	1.0	6.3E-02	0.6	2.4E-01
ENSMUST00000000904	uanine nucleotide binding protein (G protein), beta polypeptide 1-like [Source:MGI Symbol;Acc:MGI:1338057	F8WH35		7.6	2.1E-04	4.6	1.1E-02	-0.5	7.5E-01	2.1	4.2E-02
ENSMUST00000000910	dopamine beta hydroxylase [Source:MGI Symbol;Acc:MGI:94864]		Q64237	8.7	1.1E-05	8.3	1.7E-04	-0.8	6.2E-01	-1.5	7.3E-02
ENSMUST00000000924	matrix metallopeptidase 11 [Source:MGI Symbol;Acc:MGI:97008]	Q3UQT3	Q02853	5.2	2.6E-02	8.4	2.9E-05	-0.7	5.8E-01	-0.4	4.7E-01
ENSMUST00000000939	huntingtin interacting protein 1 related [Source:MGI Symbol;Acc:MGI:1352504]		Q9JKY5	-2.2	3.6E-03	7.4	1.0E-02	0.3	9.1E-01	-1.9	1.7E-01
ENSMUST00000000925	d, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 [Source:MGI Symbol;Acc	Q6ZWP4	Q9Z0H3	-2.4	7.5E-02	0.6	7.1E-01	1.5	2.3E-01	-1.5	3.0E-01
ENSMUST00000000958	DNA topoisomerase 1, mitochondrial [Source:MGI Symbol;Acc:MGI:1920210]		Q8R4U6	3.4	3.2E-04	-1.1	1.6E-01	1.2	4.1E-02	0.0	9.6E-01
ENSMUST00000000940	NOL1/NOP2/Sun domain family, member 5 [Source:MGI Symbol;Acc:MGI:2140844]		Q8K4F6	1.0	3.4E-01	1.0	5.1E-01	1.1	3.7E-01	1.1	3.8E-01
ENSMUST00000000964	homeobox A1 [Source:MGI Symbol;Acc:MGI:96170]	B9EHK7		8.3	1.4E-05	2.7	2.5E-03	-1.3	5.8E-02	-0.7	2.5E-01
ENSMUST00000000984	e carrier family 7 (cationic amino acid transporter, y+ system), member 7 [Source:MGI Symbol;Acc:MGI:1337		Q9Z1K8	-2.4	1.3E-02	6.9	1.3E-04	-0.6	5.9E-01	0.8	1.8E-01
ENSMUST00000000985	oxidase assembly 1-like [Source:MGI Symbol;Acc:MGI:1916339]		Q8BGA9	-2.1	9.2E-04	-1.5	1.6E-01	0.7	2.7E-01	-0.2	8.5E-01
ENSMUST00000001008	chemokine (C-C motif) ligand 3 [Source:MGI Symbol;Acc:MGI:98260]	Q5QNW0	P10855	-3.0	5.7E-03	-1.5	2.8E-02	0.5	1.5E-01	-0.1	8.4E-01
ENSMUST00000001002	HEAT repeat containing 6 [Source:MGI Symbol;Acc:MGI:1919790]		Q6P1G0	-0.1	8.5E-01	0.5	6.0E-01	0.7	4.1E-01	0.0	9.7E-01
ENSMUST00000001009	WAP four-disulfide core domain 18 [Source:MGI Symbol;Acc:MGI:107506]		P62810	-5.3	1.4E-04	-1.9	7.1E-02	-0.8	2.5E-01	-1.8	9.7E-02
ENSMUST00000001036	tyrosine kinase 2 [Source:MGI Symbol;Acc:MGI:1929470]	E9QJS1		-1.7	9.6E-03	-2.6	5.5E-03	0.4	4.2E-01	-2.3	3.2E-02
ENSMUST00000001027	aldehyde oxidase 1 [Source:MGI Symbol;Acc:MGI:88035]	G3X8P9		1.2	1.7E-01	1.9	1.0E-01	0.4	6.5E-01	-0.3	7.4E-01
ENSMUST00000001040	intercellular adhesion molecule 4, Landsteiner-Wiener blood group [Source:MGI Symbol;Acc:MGI:1925619]	Q14AB0	Q9ERM2	5.6	5.4E-04	-0.3	6.3E-01	1.1	4.0E-02	-0.3	6.9E-01
ENSMUST00000001042	interleukin enhancer binding factor 2 [Source:MGI Symbol;Acc:MGI:1915031]		Q9CXY6	-1.9	2.5E-03	6.4	2.1E-03	1.0	5.1E-01	0.2	8.5E-01
ENSMUST00000001046	S100 calcium binding protein A4 [Source:MGI Symbol;Acc:MGI:1330282]	Q545V2	P07091	-7.8	1.9E-06	-2.5	1.8E-03	-0.4	3.2E-01	0.3	6.3E-01
ENSMUST00000001043	chromatin target of PRMT1 [Source:MGI Symbol;Acc:MGI:1913761]		Q9CY57	-6.7	3.9E-02	4.5	2.8E-01	9.3	1.2E-02	-1.9	6.0E-01
ENSMUST00000001047	S100 calcium binding protein A3 [Source:MGI Symbol;Acc:MGI:1338849]	Q496W1	P62818	1.8	2.3E-02	-9.9	1.8E-05	-2.0	4.4E-04	0.1	9.2E-01
ENSMUST00000001051	S100 calcium binding protein A6 (calcyclin) [Source:MGI Symbol;Acc:MGI:1339467]	Q54SI9	P14069	-9.5	7.1E-07	3.2	3.1E-03	0.7	3.5E-01	-0.7	2.9E-01
ENSMUST00000001079	Sec24 related gene family, member B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2139764]	Q80ZX0		-3.6	9.5E-03	-9.0	5.6E-06	0.0	9.8E-01	-0.5	5.8E-01
ENSMUST00000001055	intercellular adhesion molecule 2 [Source:MGI Symbol;Acc:MGI:96394]		P35330	-1.3	4.4E-02	-2.3	6.8E-03	-1.8	2.7E-03	-0.9	2.5E-01
ENSMUST00000001059	endoplasmic reticulum (ER) to nucleus signalling 1 [Source:MGI Symbol;Acc:MGI:1930134]		Q9EQY0	-1.3	3.7E-02	-0.2	7.6E-01	0.7	1.9E-01	-0.4	5.4E-01
ENSMUST00000001080	NEDD4 binding protein 3 [Source:MGI Symbol;Acc:MGI:2442218]		Q8C7U1	2.1	8.5E-03	-0.9	5.3E-01	1.3	1.8E-01	-1.5	3.1E-01
ENSMUST00000001081	required for meiotic nuclear division 5 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913339]		Q91YQ7	-2.7	7.1E-04	3.1	2.5E-03	0.3	6.7E-01	-0.7	2.6E-01
ENSMUST00000001092	zinc finger protein (C2H2 type) 276 [Source:MGI Symbol;Acc:MGI:1888495]		Q8CE64	-3.8	1.3E-02	-2.3	9.9E-03	0.7	1.2E-01	0.3	7.0E-01
ENSMUST00000001083				-2.4	3.6E-02	-3.1	1.7E-02	-1.8	2.7E-02	-1.2	3.3E-01
ENSMUST00000001109	major facilitator superfamily domain containing 10 [Source:MGI Symbol;Acc:MGI:1915544]		Q9D2V8	-5.6	1.1E-03	-0.4	7.6E-01	1.2	2.4E-01	-2.2	1.7E-01
ENSMUST00000001108	adducin 1 (alpha) [Source:MGI Symbol;Acc:MGI:87918]	F8WGR0		-1.9	6.5E-02	-4.3	3.3E-02	0.1	8.7E-01	2.5	1.6E-01
ENSMUST00000001115	G protein-coupled receptor kinase 6 [Source:MGI Symbol;Acc:MGI:1347078]		O70293	-6.4	1.8E-05	-4.2	3.1E-02	1.2	1.4E-01	-0.2	9.1E-01
ENSMUST00000001122	carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 [Source:MGI Symbol;Acc:MGI:127		Q9ES88	7.3	4.4E-05	-3.8	1.7E-03	1.3	1.6E-02	-1.3	2.1E-01
ENSMUST00000001116	leucine zipper protein 1 [Source:MGI Symbol;Acc:MGI:107629]		Q8R4U7	3.2	2.7E-01	-3.5	4.4E-01	-2.9	2.7E-01	3.8	3.9E-01
ENSMUST00000001126	solute carrier family 46, member 1 [Source:MGI Symbol;Acc:MGI:1098733]		Q6PEM8	5.6	9.1E-05	7.5	1.1E-04	0.0	9.8E-01	-0.2	7.7E-01
ENSMUST00000001125	potassium channel tetramerisation domain containing 10 [Source:MGI Symbol;Acc:MGI:2141207]	F8WGQ9		-3.1	4.0E-02	1.2	4.2E-01	1.9	1.2E-01	-2.4	1.3E-01
ENSMUST00000001127	polymerase (DNA-directed), delta interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915061]		Q91VA6	-2.2	6.0E-03	3.3	5.2E-03	-2.1	3.9E-02	0.3	7.1E-01
ENSMUST00000001130	SEBOX homeobox [Source:MGI Symbol;Acc:MGI:108012]		P70368	5.0	1.3E-02	-1.3	1.4E-01	0.6	2.6E-01	-0.3	6.7E-01
ENSMUST00000001147	collagen, type VI, alpha 1 [Source:MGI Symbol;Acc:MGI:88459]		Q04857	9.1	2.6E-06	6.4	4.9E-03	-0.7	7.3E-01	-2.1	8.2E-02
ENSMUST00000001155	v-raf murine sarcoma 3611 viral oncogene homolog [Source:MGI Symbol;Acc:MGI:88065]		P04627	-4.0	1.4E-04	-0.2	6.6E-01	-9.3	1.2E-06	-0.1	9.1E-01
ENSMUST00000001156	complement factor properdin [Source:MGI Symbol;Acc:MGI:97545]	A2AE15	P11680	-7.0	1.9E-07	-2.8	8.5E-03	1.2	3.5E-02	-0.1	9.4E-01
ENSMUST00000001171	lectin, mannose-binding 2-like [Source:MGI Symbol;Acc:MGI:2443010]	J3QNZ7		-7.6	1.9E-05	-6.4	2.3E-06	-0.2	5.1E-01	-0.7	2.7E-01
ENSMUST00000001181	collagen, type VI, alpha 2 [Source:MGI Symbol;Acc:MGI:88460]		Q02788	8.8	6.8E-06	-5.7	1.3E-03	-1.1	6.6E-02	0.0	9.8E-01
ENSMUST00000001166	cyclin M3 [Source:MGI Symbol;Acc:MGI:2151055]		Q32NY4	-0.3	7.6E-01	-1.9	2.2E-01	1.2	2.2E-01	2.8	7.2E-02
ENSMUST00000001184	MAX dimerization protein 1 [Source:MGI Symbol;Acc:MGI:96908]	Q8K1Z8		-6.3	1.1E-05	-1.1	4.2E-01	5.5	6.9E-05	-1.0	4.6E-01
ENSMUST00000001172	ankyrin repeat domain 23 [Source:MGI Symbol;Acc:MGI:1925571]	Q14A32	Q9D2X0	1.8	3.5E-01	3.4	1.7E-01	0.0	9.9E-01	-1.5	4.1E-01
ENSMUST00000001179	pericentrin (kendrin) [Source:MGI Symbol;Acc:MGI:102722]	F8VPV0		0.3	3.2E-01	1.0	4.5E-02	0.6	1.1E-01	-0.1	8.8E-01
ENSMUST00000001185	germ cell-less homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1345156]		Q920G9	-2.8	8.5E-04	1.1	7.4E-02	-8.0	8.8E-06	-0.4	4.9E-01
ENSMUST00000001186	small nuclear ribonucleoprotein 27 (U4/U6.U5) [Source:MGI Symbol;Acc:MGI:1913868]		Q8K194	-7.1	3.9E-05	-5.1	4.3E-04	1.2	2.5E-02	0.0	9.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000001187	annexin A4 [Source:MGI Symbol;Acc:MGI:88030]		P97429	-4.5	9.3E-04	-0.7	3.6E-01	1.0	6.1E-02	-1.2	1.2E-01
ENSMUST00000001226	SH3-domain binding protein 1 [Source:MGI Symbol;Acc:MGI:104603]	A2A5V4		-4.0	2.7E-04	-7.9	2.8E-04	-0.4	3.7E-01	0.4	8.0E-01
ENSMUST00000001240	1-acylglycerol-3-phosphate O-acyltransferase 3 [Source:MGI Symbol;Acc:MGI:1336186]		Q9D517	3.8	1.5E-03	-5.5	1.0E-03	-1.4	1.7E-02	-0.5	7.0E-01
ENSMUST00000001202	oculocerebrorenal syndrome of Lowe [Source:MGI Symbol;Acc:MGI:109589]		Q6NVF0	-1.9	1.2E-01	-3.2	5.7E-02	0.2	8.1E-01	1.5	3.3E-01
ENSMUST00000001204	calmodulin 1 [Source:MGI Symbol;Acc:MGI:88251]	Q3UKW2		2.5	3.0E-01	1.0	7.5E-01	-1.5	5.8E-01	-0.1	9.8E-01
ENSMUST00000001242	DNA segment, Chr 10, Johns Hopkins University 81 expressed [Source:MGI Symbol;Acc:MGI:1351861]		Q9D172	-2.8	1.0E-03	-2.3	2.1E-02	0.9	9.3E-02	-0.8	3.6E-01
ENSMUST00000001253	solute carrier family 26, member 4 [Source:MGI Symbol;Acc:MGI:1346029]		Q9R155	5.7	9.0E-05	1.6	1.1E-01	-2.3	2.0E-02	-0.1	9.3E-01
ENSMUST00000001256	ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B [Source:MGI Symbol;Acc:MGI:	Q3UTK5	O54951	2.9	8.6E-03	-1.7	4.4E-02	0.6	1.9E-01	-0.5	5.3E-01
ENSMUST00000001279	lipolysis stimulated lipoprotein receptor [Source:MGI Symbol;Acc:MGI:1927471]		Q99KG5	3.2	5.5E-03	6.6	1.4E-04	0.5	6.6E-01	-0.4	5.4E-01
ENSMUST00000001280	GRAM domain containing 1A [Source:MGI Symbol;Acc:MGI:105490]		Q8VEF1	-7.0	3.3E-04	-1.4	4.5E-01	1.4	2.8E-01	5.6	4.8E-03
ENSMUST00000001258	ubiquitin-like, containing PHD and RING finger domains, 1 [Source:MGI Symbol;Acc:MGI:1338889]		Q8VDF2	7.1	3.8E-02	2.8	4.3E-01	-3.6	3.2E-01	0.7	7.7E-01
ENSMUST00000001284	upstream transcription factor 1 [Source:MGI Symbol;Acc:MGI:99542]	F8WGH6		-5.2	1.1E-03	3.6	1.6E-02	0.0	9.7E-01	-0.3	6.9E-01
ENSMUST00000001304	creatine kinase, brain [Source:MGI Symbol;Acc:MGI:88407]		Q04447	2.8	8.4E-03	-4.1	7.4E-03	1.2	5.9E-02	-1.7	2.7E-01
ENSMUST00000001319	ephrin B2 [Source:MGI Symbol;Acc:MGI:105097]	Q4FJM3	P52800	5.3	3.0E-05	-3.6	3.5E-02	1.2	1.1E-01	-0.5	7.6E-01
ENSMUST00000001326	trans-acting transcription factor 1 [Source:MGI Symbol;Acc:MGI:98372]	G3X8Q0		-3.1	7.5E-05	0.1	8.9E-01	-2.3	1.4E-02	0.3	6.9E-01
ENSMUST00000001335	prefoldin 5 [Source:MGI Symbol;Acc:MGI:1928753]	H7BWX1		-8.5	2.1E-05	2.0	1.9E-02	-3.2	1.1E-03	0.1	8.8E-01
ENSMUST00000001339	ribosomal RNA processing 15 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914473]		Q9CYX7	-3.6	2.2E-03	-2.0	8.7E-03	1.1	1.4E-02	-0.1	9.0E-01
ENSMUST00000001327	integrin beta 7 [Source:MGI Symbol;Acc:MGI:96616]		P26011	-1.8	4.9E-02	-1.8	1.2E-01	0.0	9.4E-01	0.0	9.9E-01
ENSMUST00000001384	calponin 1 [Source:MGI Symbol;Acc:MGI:104979]	B2RSH3	Q08091	6.5	2.7E-05	-9.6	1.2E-04	-1.1	2.3E-02	-0.1	9.7E-01
ENSMUST00000001402	f-box protein 9 [Source:MGI Symbol;Acc:MGI:1918788]		Q8BK06	-5.6	3.2E-04	-3.1	1.3E-03	-2.3	1.1E-03	-2.8	9.8E-03
ENSMUST00000001347	Rho family GTPase 2 [Source:MGI Symbol;Acc:MGI:1338755]	A2A4Q3	Q9QYM5	1.6	3.7E-01	1.6	4.5E-01	-0.5	7.9E-01	-0.5	7.9E-01
ENSMUST00000001412	coiled-coil domain containing 132 [Source:MGI Symbol;Acc:MGI:1920538]		Q8CI71	-3.4	1.1E-02	6.5	1.5E-04	0.1	8.9E-01	0.2	7.8E-01
ENSMUST00000001419	zinc finger, matrin type 2 [Source:MGI Symbol;Acc:MGI:1913742]		Q9CPW7	-4.6	1.1E-04	-5.3	1.1E-02	1.3	6.8E-02	0.9	6.0E-01
ENSMUST00000001439	ubiquitin-conjugating enzyme E2C [Source:MGI Symbol;Acc:MGI:1915862]	A2A4Z1		6.8	2.1E-04	-4.1	9.7E-03	-1.7	3.0E-02	-1.0	5.0E-01
ENSMUST00000001415	steroid receptor RNA activator 1 [Source:MGI Symbol;Acc:MGI:1344414]	Q3UR23	Q8R1C9	-0.3	6.3E-01	-0.2	7.7E-01	0.2	7.5E-01	0.1	8.7E-01
ENSMUST00000001416	histidyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:108087]		Q61035	-1.2	5.9E-02	-1.9	3.4E-02	-0.4	4.3E-01	0.3	6.7E-01
ENSMUST00000001451	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans) [Source:MGI Symbol;Acc:MGI:2447364		Q6ZPY2	-2.3	2.3E-03	-4.7	4.6E-04	-0.6	1.7E-01	-0.5	5.8E-01
ENSMUST00000001452	chaperonin containing Tcp1, subunit 3 (gamma) [Source:MGI Symbol;Acc:MGI:104708]	Q3U4U6	P80318	-7.3	3.3E-06	6.9	5.0E-04	0.0	9.7E-01	-0.1	8.9E-01
ENSMUST00000001454	glycosylated lysosomal membrane protein [Source:MGI Symbol;Acc:MGI:1913318]	H9H9R4		-7.3	3.8E-05	-1.4	8.4E-02	0.7	1.5E-01	-0.3	6.8E-01
ENSMUST00000001455	myocyte enhancer factor 2D [Source:MGI Symbol;Acc:MGI:99533]	Q921S6		-2.3	7.9E-03	-8.0	1.5E-05	-1.2	3.0E-03	-0.5	6.4E-01
ENSMUST00000001460	staphylococcal nuclease and tudor domain containing 1 [Source:MGI Symbol;Acc:MGI:1929266]		Q78PY7	-3.5	4.4E-04	-5.4	1.9E-03	1.3	2.2E-02	-0.7	6.4E-01
ENSMUST00000001479	karyopherin (importin) beta 1 [Source:MGI Symbol;Acc:MGI:107532]		P70168	-2.7	8.1E-05	-0.9	3.1E-01	0.8	2.0E-01	-0.7	4.5E-01
ENSMUST00000001480	aminopeptidase puromycin sensitive [Source:MGI Symbol;Acc:MGI:1101358]		Q11011	-6.0	6.2E-05	-2.2	2.0E-02	0.5	3.4E-01	-0.8	3.6E-01
ENSMUST00000001484	T-box 21 [Source:MGI Symbol;Acc:MGI:1888984]	Q3U150	Q9JKD8	5.3	7.1E-05	-2.2	2.1E-03	0.4	2.0E-01	-0.1	8.3E-01
ENSMUST00000001485	mitochondrial ribosomal protein L10 [Source:MGI Symbol;Acc:MGI:1333801]		Q3TBW2	-2.8	4.1E-04	-3.6	8.6E-03	2.1	4.4E-03	-0.3	7.8E-01
ENSMUST00000001513	tubulin, beta 6 class V [Source:MGI Symbol;Acc:MGI:1915201]	Q3UMM1	Q922F4	-1.7	3.4E-02	5.5	5.2E-04	0.1	9.3E-01	-0.1	8.4E-01
ENSMUST00000001522	differentially expressed in FDCP 8 [Source:MGI Symbol;Acc:MGI:1346331]			4.9	6.9E-03	-1.5	4.5E-02	0.8	5.5E-02	-0.4	5.0E-01
ENSMUST00000001507	cytochrome P450, family 51 [Source:MGI Symbol;Acc:MGI:106040]		Q8K0C4	0.3	5.6E-01	0.7	2.4E-01	0.0	9.3E-01	-0.4	4.0E-01
ENSMUST00000001534	sclerostin [Source:MGI Symbol;Acc:MGI:1921749]	B2RQA5		7.4	7.6E-05	-2.7	1.2E-02	-1.0	8.3E-02	0.1	9.4E-01
ENSMUST00000001520	AFG3-like AAA ATPase 1 [Source:MGI Symbol;Acc:MGI:1928277]		Q920A7	-2.9	4.2E-02	-6.3	5.0E-02	0.9	3.6E-01	4.3	1.5E-01
ENSMUST00000001536	NK2 homeobox 1 [Source:MGI Symbol;Acc:MGI:108067]		P50220	8.3	8.9E-06	1.4	5.9E-01	0.4	8.0E-01	3.9	9.8E-02
ENSMUST00000001544	von Willebrand factor A domain containing 5A [Source:MGI Symbol;Acc:MGI:1915026]		Q99KC8	-3.8	4.1E-03	7.2	1.8E-04	-0.6	6.3E-01	-0.4	5.6E-01
ENSMUST00000001547	collagen, type I, alpha 1 [Source:MGI Symbol;Acc:MGI:88467]		P11087	7.4	8.7E-07	8.2	1.9E-05	-0.5	6.3E-01	-0.4	3.6E-01
ENSMUST00000001548	integrin alpha 3 [Source:MGI Symbol;Acc:MGI:96602]		Q62470	7.0	4.8E-03	-6.7	2.8E-03	-1.2	6.9E-02	1.7	3.5E-01
ENSMUST00000001562	tubby-like protein 3 [Source:MGI Symbol;Acc:MGI:1329045]		O88413	3.7	5.2E-04	2.8	7.1E-04	-4.7	3.9E-05	-0.1	8.9E-01
ENSMUST00000001566	tubulin, beta 5 class I [Source:MGI Symbol;Acc:MGI:107812]		P99024	-3.5	1.2E-04	-6.3	1.1E-02	-9.5	3.6E-04	3.7	8.8E-02
ENSMUST00000001559	integrin alpha FG-GAP repeat containing 2 [Source:MGI Symbol;Acc:MGI:1915450]		Q91WI7	-1.5	3.1E-01	-2.1	3.0E-01	0.2	8.6E-01	0.9	6.3E-01
ENSMUST00000001569	flotillin 1 [Source:MGI Symbol;Acc:MGI:1100500]	Q540I4	O08917	-8.4	1.0E-04	2.7	6.7E-03	-1.2	1.2E-01	-0.3	6.6E-01
ENSMUST00000001565	general transcription factor II H, polypeptide 4 [Source:MGI Symbol;Acc:MGI:1338799]	Q542U3	O70422	0.6	3.4E-01	1.1	1.8E-01	0.1	8.9E-01	-0.4	5.5E-01
ENSMUST00000001592	junction plakoglobin [Source:MGI Symbol;Acc:MGI:96650]		Q02257	-3.3	1.6E-02	-2.8	2.6E-03	0.3	3.9E-01	-0.3	6.3E-01
ENSMUST00000001595	FK506 binding protein 10 [Source:MGI Symbol;Acc:MGI:104769]		Q61576	6.5	2.0E-04	-6.4	4.7E-03	1.5	5.1E-02	-0.5	8.0E-01
ENSMUST00000001583	elongation factor RNA polymerase II 2 [Source:MGI Symbol;Acc:MGI:2183438]		Q3UKU1	-0.2	7.4E-01	-0.3	6.7E-01	0.2	7.0E-01	0.3	6.4E-01
ENSMUST00000001599	kelch-like 10 [Source:MGI Symbol;Acc:MGI:2181067]	B2RTD7	Q9D5V2	6.9	5.6E-05	-2.1	1.8E-01	2.0	5.5E-02	0.8	6.2E-01
ENSMUST00000001611	nucleolar protein with MIF4G domain 1 [Source:MGI Symbol;Acc:MGI:1861749]		Q3UFM5	1.6	1.8E-03	4.3	1.7E-03	-2.7	3.9E-02	-0.5	4.5E-01
ENSMUST00000001620	fragile X mental retardation gene 1, autosomal homolog [Source:MGI Symbol;Acc:MGI:104860]		Q61584	-2.0	3.2E-02	6.8	1.2E-04	-0.6	6.3E-01	-0.5	4.2E-01
ENSMUST00000001631	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 [Source:MGI Symbol;Acc:MGI:2388270]		Q8K2H4	-6.0	3.9E-04	1.7	4.7E-03	-0.2	6.1E-01	-0.2	5.4E-01
ENSMUST00000001619				1.8	4.2E-01	-1.8	6.1E-01	-0.6	7.6E-01	3.0	4.0E-01
ENSMUST00000001652	bradykinin receptor, beta 2 [Source:MGI Symbol;Acc:MGI:102845]		P32299	7.1	1.1E-04	-4.7	3.4E-03	-0.8	2.1E-01	1.9	1.5E-01
ENSMUST00000001667	casein kappa [Source:MGI Symbol;Acc:MGI:107461]		P06796	8.1	1.2E-03	-3.4	2.7E-02	1.1	1.3E-01	-1.5	3.2E-01
ENSMUST00000001675	serine/threonine kinase 38 like [Source:MGI Symbol;Acc:MGI:1922250]		Q7TSE6	1.5	3.4E-02	5.7	5.3E-04	-2.3	8.2E-02	-0.9	2.2E-01
ENSMUST00000001699	homeobox C10 [Source:MGI Symbol;Acc:MGI:96192]		P31257	8.3	1.2E-04	2.7	6.9E-02	-5.0	1.8E-02	0.5	6.6E-01
ENSMUST00000001672	interferon-related developmental regulator 1 [Source:MGI Symbol;Acc:MGI:1316717]		P19182	-0.3	7.1E-01	1.7	1.4E-01	1.8	5.5E-02	-0.2	8.3E-01
ENSMUST00000001700	homeobox C13 [Source:MGI Symbol;Acc:MGI:99560]		P50207	7.6	5.4E-05	2.3	1.2E-02	0.1	9.1E-01	-0.7	2.7E-01
ENSMUST00000001701	homeobox C11 [Source:MGI Symbol;Acc:MGI:96193]		P31313	6.6	6.0E-05	6.5	1.4E-03	-0.7	6.4E-01	1.1	2.0E-01
ENSMUST00000001703	homeobox C8 [Source:MGI Symbol;Acc:MGI:96198]		P09025	10.1	1.6E-05	7.0	1.8E-04	-0.6	6.2E-01	-0.1	9.0E-01
ENSMUST00000001706	homeobox C9 [Source:MGI Symbol;Acc:MGI:96199]		P09633	8.0	2.0E-05	6.8	8.9E-05	-0.5	6.2E-01	-0.7	2.1E-01
ENSMUST00000001709	homeobox C5 [Source:MGI Symbol;Acc:MGI:96196]		P32043	8.3	1.6E-05	7.1	2.2E-04	-2.1	1.6E-01	0.9	1.8E-01
ENSMUST00000001711	homeobox C6 [Source:MGI Symbol;Acc:MGI:96197]	B2RUB8	P10629	6.6	2.3E-04	8.4	1.1E-04	-0.4	7.8E-01	-0.8	1.9E-01
ENSMUST00000001715	glutathione S-transferase, theta 3 [Source:MGI Symbol;Acc:MGI:2143526]	Q99L20		3.1	1.2E-03	6.0	2.6E-04	-1.5	2.2E-01	0.8	1.8E-01
ENSMUST00000001716	D-dopachrome tautomerase [Source:MGI Symbol;Acc:MGI:1298381]	Q3UNI8	O35215	-3.7	2.1E-03	6.0	8.5E-04	-0.6	6.4E-01	0.0	9.6E-01
ENSMUST00000001712	calcineurin binding protein 1 [Source:MGI Symbol;Acc:MGI:1298375]	G3X8Q1		-0.4	3.6E-01	0.4	4.5E-01	0.7	1.1E-01	-0.1	8.2E-01
ENSMUST00000001720	tyrosine aminotransferase [Source:MGI Symbol;Acc:MGI:98487]		Q8QZR1	6.4	1.3E-04	3.6	1.0E-03	-0.2	7.8E-01	-0.7	2.6E-01
ENSMUST00000001722	MARVEL (membrane-associating) domain containing 3 [Source:MGI Symbol;Acc:MGI:1920858]	G3X8Q2		6.8	5.5E-05	-3.7	4.1E-03	-0.6	3.1E-01	-0.5	6.5E-01
ENSMUST00000001757	eukaryotic translation elongation factor 1 epsilon 1 [Source:MGI Symbol;Acc:MGI:1913393]		Q9D1M4	-2.5	1.8E-02	4.0	1.8E-03	-2.9	2.1E-02	-0.5	4.2E-01
ENSMUST00000001780	thymoma viral proto-oncogene 1 [Source:MGI Symbol;Acc:MGI:87986]		P31750	-6.2	5.7E-06	6.3	1.7E-04	-0.6	6.2E-01	-0.1	8.3E-01
ENSMUST00000001724	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 [Source:MGI Symbol;Acc:MGI:1914192]	B2RUM8	Q8K363	-1.1	9.1E-02	-2.1	1.3E-02	-1.3	1.4E-02	-0.3	6.7E-01
ENSMUST00000001790	claudin 15 [Source:MGI Symbol;Acc:MGI:1913103]		Q9Z0S5	-7.1	6.1E-05	-1.6	7.9E-02	-1.4	5.3E-02	-2.3	3.8E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000001801	, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3 [Source:MGI Symbol;Acc:MGI:135	Q9JHF5		-7.0	1.7E-04	-4.8	2.5E-04	1.0	2.1E-02	-0.4	6.3E-01
ENSMUST00000001806	Coenzyme A synthase [Source:MGI Symbol;Acc:MGI:1918993]		Q9DBL7	-3.7	2.7E-03	1.0	2.4E-01	2.4	2.7E-03	-5.6	4.4E-04
ENSMUST00000001792	interleukin 16 [Source:MGI Symbol;Acc:MGI:1270855]		O54824	1.4	1.0E-01	1.1	2.9E-01	-0.6	4.3E-01	-0.3	7.6E-01
ENSMUST00000001809	poly(A) binding protein, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:1349722]		P29341	-5.6	6.6E-06	-7.5	2.1E-03	0.6	3.1E-01	1.1	5.7E-01
ENSMUST00000001802	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB) [Source:MGI Symbol;Acc:MGI:1351641]	O88325		-0.9	2.1E-01	-0.3	7.0E-01	-0.3	5.7E-01	-0.9	2.8E-01
ENSMUST00000001812	smoothened, frizzled class receptor [Source:MGI Symbol;Acc:MGI:108075]	Q4VBD5	P56726	3.8	5.7E-04	-0.4	7.2E-01	1.1	1.4E-01	-2.3	5.6E-02
ENSMUST00000001818	Crn, crooked neck-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1914127]		P63154	-3.2	4.3E-04	-3.9	5.0E-04	1.3	6.3E-03	-0.5	5.3E-01
ENSMUST00000001825	ne and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 [Source:MGI Symbol;Acc:MGI:191		Q9D1P4	-2.9	1.3E-03	3.0	5.9E-03	-0.8	3.3E-01	0.0	9.4E-01
ENSMUST00000001834	RNA 2',3'-cyclic phosphate and 5'-OH ligase [Source:MGI Symbol;Acc:MGI:106379]		Q99LF4	-3.1	1.7E-04	-3.1	3.2E-03	-0.1	8.2E-01	-0.3	7.3E-01
ENSMUST00000001836	PWP1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914735]		Q99LL5	-3.2	1.3E-04	-2.8	5.8E-03	-0.1	8.7E-01	-0.1	8.6E-01
ENSMUST00000001845	calpain, small subunit 1 [Source:MGI Symbol;Acc:MGI:88266]			-3.4	1.3E-02	-3.7	2.9E-04	-0.5	2.0E-01	0.2	7.5E-01
ENSMUST00000001854	: carrier family 7 (cationic amino acid transporter, y+ system), member 10 [Source:MGI Symbol;Acc:MGI:185		P63115	5.8	2.1E-02	-2.2	5.3E-03	0.2	5.4E-01	-0.8	2.3E-01
ENSMUST00000001837	F-box protein 7 [Source:MGI Symbol;Acc:MGI:1917004]	F8WIP1		-1.2	5.7E-01	-3.0	2.2E-01	-1.8	2.5E-01	-0.1	9.8E-01
ENSMUST00000001867	even skipped homeotic gene 2 homolog [Source:MGI Symbol;Acc:MGI:95462]	G5E813		7.8	2.1E-05	-2.7	1.5E-01	1.4	1.6E-01	0.7	6.7E-01
ENSMUST00000001872	homeobox D13 [Source:MGI Symbol;Acc:MGI:96205]		P70217	7.1	4.8E-05	2.8	3.2E-01	-0.8	7.4E-01	2.1	3.2E-01
ENSMUST00000001878	homeobox D12 [Source:MGI Symbol;Acc:MGI:96204]		P23812	8.5	8.3E-06	7.3	6.6E-05	-0.6	6.3E-01	-0.1	8.4E-01
ENSMUST00000001884	ClpB caseinolytic peptidase B [Source:MGI Symbol;Acc:MGI:1100517]	Q3URM1	Q60649	5.8	3.7E-06	6.0	3.1E-04	-0.6	6.2E-01	0.5	4.1E-01
ENSMUST00000001900	zinc finger, DHHC domain containing 4 [Source:MGI Symbol;Acc:MGI:1920131]		Q9D6H5	-5.5	2.8E-04	7.5	4.6E-05	-0.6	6.0E-01	0.4	4.8E-01
ENSMUST00000001920	allograft inflammatory factor 1-like [Source:MGI Symbol;Acc:MGI:1919598]		Q9EQX4	6.4	8.7E-05	6.1	3.7E-05	0.4	5.7E-01	0.1	7.9E-01
ENSMUST00000001921	carboxypeptidase A3, mast cell [Source:MGI Symbol;Acc:MGI:88479]	Q542E3	P15089	-2.8	2.1E-04	-4.6	5.8E-03	1.2	4.8E-02	0.3	8.1E-01
ENSMUST00000001927	latent transforming growth factor beta binding protein 1 [Source:MGI Symbol;Acc:MGI:109151]		Q8CG19	9.4	1.2E-05	2.3	1.5E-02	-4.2	1.5E-03	-0.1	9.3E-01
ENSMUST00000001950	toll interacting protein [Source:MGI Symbol;Acc:MGI:1891808]		Q9QZ06	-3.2	2.3E-04	-2.4	5.1E-03	0.9	5.1E-02	0.5	4.7E-01
ENSMUST00000001965	otassium voltage-gated channel, subfamily H (eag-related), member 6 [Source:MGI Symbol;Acc:MGI:2684139	Q32ME0		8.2	2.1E-05	4.5	1.8E-03	-4.6	3.7E-03	0.3	6.2E-01
ENSMUST00000001984	carcinoembryonic antigen-related cell adhesion molecule 9 [Source:MGI Symbol;Acc:MGI:1347247]	Q78T27		6.5	9.2E-05	-2.1	1.7E-02	1.3	1.3E-02	0.2	7.4E-01
ENSMUST00000001963	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 [Source:MGI Symbol;Acc:MGI:87874]	Q3TU20	P09470	2.8	4.4E-02	3.5	6.3E-02	0.1	9.6E-01	-0.6	5.7E-01
ENSMUST00000001964	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 [Source:MGI Symbol;Acc:MGI:87874]		P09470	2.5	8.2E-02	5.4	1.1E-02	2.0	2.3E-01	-0.9	4.4E-01
ENSMUST00000001989	ubiquitin-like modifier activating enzyme 1 [Source:MGI Symbol;Acc:MGI:98890]	B9EHN0	Q02053	-6.1	4.9E-04	8.1	4.9E-05	-0.7	5.9E-01	-0.5	3.9E-01
ENSMUST00000001975	cleus accumbens associated 1, BEN and BTB (POZ) domain containing [Source:MGI Symbol;Acc:MGI:19140		Q7TSZ8	-1.2	9.2E-02	0.0	9.7E-01	0.9	1.4E-01	-0.2	8.0E-01
ENSMUST00000002008	V-set and immunoglobulin domain containing 2 [Source:MGI Symbol;Acc:MGI:1928009]		Q9Z109	6.8	1.1E-03	6.7	1.4E-04	-0.5	6.5E-01	-0.7	2.7E-01
ENSMUST00000002011	endothelial cell-specific adhesion molecule [Source:MGI Symbol;Acc:MGI:1916774]	Q3U102	Q925F2	4.7	6.6E-04	-3.0	3.2E-02	1.1	1.3E-01	-1.9	1.8E-01
ENSMUST00000001995				-1.7	3.2E-01	1.8	3.1E-01	0.2	8.9E-01	-3.4	7.5E-02
ENSMUST00000002007	sialic acid acetylesterase [Source:MGI Symbol;Acc:MGI:104803]		P70665	0.9	1.2E-01	0.3	5.7E-01	-1.0	5.9E-02	-0.5	4.3E-01
ENSMUST00000002025	transketolase-like 2 [Source:MGI Symbol;Acc:MGI:1921669]			5.5	1.6E-03	6.2	1.7E-03	-2.0	2.4E-01	-1.3	1.8E-01
ENSMUST00000002029	emerin [Source:MGI Symbol;Acc:MGI:108117]		O08579	-5.2	2.9E-04	2.0	6.4E-02	-2.5	2.2E-02	0.1	9.3E-01
ENSMUST00000002013	sperm autoantigenic protein 17 [Source:MGI Symbol;Acc:MGI:1333778]	Q545M2	Q62252	2.3	5.2E-02	0.6	5.8E-01	-1.5	1.7E-01	0.2	8.6E-01
ENSMUST00000002043	coiled-coil domain containing 47 [Source:MGI Symbol;Acc:MGI:1914413]	Q0VBU4	Q9D024	-1.6	4.1E-03	6.7	1.0E-03	0.0	9.9E-01	-1.2	1.7E-01
ENSMUST00000002044	mitogen-activated protein kinase kinase kinase 3 [Source:MGI Symbol;Acc:MGI:1346874]		Q61084	-5.3	6.9E-06	-3.8	9.2E-03	1.1	9.0E-02	-0.3	8.2E-01
ENSMUST00000002053	neuronal PAS domain protein 1 [Source:MGI Symbol;Acc:MGI:109205]	A2RSH6	P97459	4.7	2.1E-04	-1.4	2.5E-02	-0.2	5.0E-01	-0.5	4.0E-01
ENSMUST00000002064	biliverdin reductase A [Source:MGI Symbol;Acc:MGI:88170]		Q9CY64	-3.3	1.6E-04	-3.8	3.2E-04	0.7	5.3E-02	-0.7	3.1E-01
ENSMUST00000002048	nslational activator of mitochondrially encoded cytochrome c oxidase I [Source:MGI Symbol;Acc:MGI:191745		Q8K0Z7	-0.5	3.1E-01	-0.9	1.6E-01	0.1	8.3E-01	0.5	4.0E-01
ENSMUST00000002080	PDZ domain containing 4 [Source:MGI Symbol;Acc:MGI:2443483]		Q9QY39	4.4	2.1E-02	5.8	4.8E-04	1.4	2.1E-01	0.2	8.0E-01
ENSMUST00000002063	adaptor-related protein complex AP-4, epsilon 1 [Source:MGI Symbol;Acc:MGI:1336993]		Q80V94	1.3	6.6E-02	2.6	1.6E-02	1.1	1.6E-01	-0.2	8.1E-01
ENSMUST00000002084	ATP-binding cassette, sub-family D (ALD), member 1 [Source:MGI Symbol;Acc:MGI:1349215]		P48410	-4.8	4.0E-05	-4.8	5.9E-05	-1.8	8.0E-04	-0.4	5.9E-01
ENSMUST00000002073	latent transforming growth factor beta binding protein 2 [Source:MGI Symbol;Acc:MGI:99502]	E9QNQ3		7.4	4.3E-02	3.4	2.3E-01	-5.7	1.2E-01	-1.8	3.6E-01
ENSMUST00000002079	plexin B3 [Source:MGI Symbol;Acc:MGI:2154240]		Q9QY40	3.0	1.3E-01	6.6	7.2E-03	-0.4	8.6E-01	-3.9	1.3E-02
ENSMUST00000002087	pregnancy upregulated non-ubiquitously expressed CaM kinase [Source:MGI Symbol;Acc:MGI:1347357]	Q3TYC1	Q9QYK9	5.7	1.6E-02	3.4	1.2E-01	-1.4	4.8E-01	-0.4	8.0E-01
ENSMUST00000002090	signal sequence receptor, delta [Source:MGI Symbol;Acc:MGI:1099464]	Q3TVJ8	Q62186	-6.0	1.1E-03	-3.3	3.0E-03	1.2	1.5E-02	-0.3	7.3E-01
ENSMUST00000002091	B cell receptor associated protein 31 [Source:MGI Symbol;Acc:MGI:1350933]		Q61335	-5.1	9.9E-07	4.5	7.7E-02	-0.7	7.7E-01	0.6	7.2E-01
ENSMUST00000002099	intraflagellar transport 46 [Source:MGI Symbol;Acc:MGI:1923818]		Q9DB07	5.2	2.3E-04	-6.1	4.0E-03	-0.8	1.9E-01	-0.8	6.8E-01
ENSMUST00000002101	CD3 antigen, gamma polypeptide [Source:MGI Symbol;Acc:MGI:88333]	Q3U4Y3	P11942	-4.6	1.0E-03	-5.7	3.2E-06	-0.3	2.9E-01	0.3	6.4E-01
ENSMUST00000002095	lysine (K)-specific methyltransferase 2A [Source:MGI Symbol;Acc:MGI:96995]		P55200	0.4	6.8E-01	-2.6	1.8E-01	0.8	4.6E-01	3.8	4.9E-02
ENSMUST00000002112	trafficking protein particle complex 6A [Source:MGI Symbol;Acc:MGI:1914341]		Q78XR0	-6.6	2.4E-05	3.8	3.3E-03	-1.4	1.6E-01	0.0	9.5E-01
ENSMUST00000002100	transmembrane protein 25 [Source:MGI Symbol;Acc:MGI:1918937]		Q9DCF1	2.3	9.0E-02	5.8	1.4E-03	0.1	9.5E-01	-3.4	6.7E-03
ENSMUST00000002121	suppressor of Ty 6 [Source:MGI Symbol;Acc:MGI:107726]		Q62383	-1.9	4.0E-04	-3.6	1.8E-03	-1.6	1.0E-02	-2.7	3.0E-02
ENSMUST00000002127	unc-119 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1328357]	Q3V299	Q9Z2R6	-8.8	3.3E-05	-5.0	1.1E-03	0.9	5.5E-02	-0.7	5.5E-01
ENSMUST00000002128	RAB34, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:104606]	Q0PD20		5.1	2.9E-02	-1.2	2.1E-02	0.5	8.8E-02	-0.1	7.5E-01
ENSMUST00000002133	stromal cell derived factor 2 [Source:MGI Symbol;Acc:MGI:108019]			-4.7	4.2E-03	-9.6	3.7E-04	0.5	2.8E-01	1.3	4.8E-01
ENSMUST00000002145	heat shock transcription factor 2 binding protein [Source:MGI Symbol;Acc:MGI:1921627]	Q9D4G2		8.2	2.0E-05	-0.9	6.3E-01	-4.2	4.9E-02	1.7	3.2E-01
ENSMUST00000002152	BCL2 binding component 3 [Source:MGI Symbol;Acc:MGI:2181667]	B2RVL4	Q99ML1	-2.3	5.7E-03	-6.8	6.8E-03	-0.8	3.3E-01	1.3	5.1E-01
ENSMUST00000002180	spleen focus forming virus (SFFV) proviral integration oncogene [Source:MGI Symbol;Acc:MGI:98282]	Q3U5L4	P17433	-6.7	8.2E-06	7.9	3.4E-04	0.9	5.3E-01	1.2	1.3E-01
ENSMUST00000002259	calmegin [Source:MGI Symbol;Acc:MGI:107472]		P52194	7.6	1.5E-05	-0.6	4.8E-01	0.9	1.3E-01	-0.8	3.2E-01
ENSMUST00000002172	acid phosphatase 2, lysosomal [Source:MGI Symbol;Acc:MGI:87882]		P24638	-0.6	2.7E-01	0.2	7.4E-01	0.4	4.8E-01	-0.5	4.5E-01
ENSMUST00000002274	napsin A aspartic peptidase [Source:MGI Symbol;Acc:MGI:109365]	Q3U7H1	O09043	-4.2	3.9E-04	-4.7	4.7E-04	1.4	7.8E-03	-0.6	5.1E-01
ENSMUST00000002198	splicing factor 3a, subunit 1 [Source:MGI Symbol;Acc:MGI:1914715]		Q8K4Z5	-0.7	2.1E-01	-0.1	8.7E-01	0.9	8.2E-02	0.4	5.8E-01
ENSMUST00000002275	vaccinia related kinase 3 [Source:MGI Symbol;Acc:MGI:2182465]	Q3TAR6	Q8K3G5	-7.3	2.4E-05	6.9	7.1E-05	-0.5	6.1E-01	0.2	7.5E-01
ENSMUST00000002280	smg-9 homolog, nonsense mediated mRNA decay factor (C. elegans) [Source:MGI Symbol;Acc:MGI:1919247]		Q9DB90	-4.7	3.0E-04	-3.5	7.9E-03	1.0	9.3E-02	0.3	7.8E-01
ENSMUST00000002284	plasminogen activator, urokinase receptor [Source:MGI Symbol;Acc:MGI:97612]	Q545X5	P35456	-4.2	1.4E-04	-7.8	1.0E-03	1.2	3.1E-02	1.6	3.4E-01
ENSMUST00000002289	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) [Source:MGI Symbol;Acc:MGI:1355274]		Q9JKB1	-4.0	3.2E-04	-3.4	2.1E-02	1.3	5.4E-02	0.0	9.8E-01
ENSMUST00000002291	PAX interacting (with transcription-activation domain) protein 1 [Source:MGI Symbol;Acc:MGI:1890430]		Q6NZQ4	1.5	3.4E-03	-3.8	2.5E-03	0.7	1.4E-01	0.3	7.3E-01
ENSMUST00000002292	required for meiotic nuclear division 5 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915727]		Q80YQ8	-3.4	4.4E-04	-4.6	1.4E-03	-0.1	9.0E-01	0.5	6.2E-01
ENSMUST00000002303	ras homolog gene family, member C [Source:MGI Symbol;Acc:MGI:106028]		Q62159	-5.0	4.7E-04	1.5	1.3E-02	0.6	1.9E-01	0.5	2.9E-01
ENSMUST00000002305	lysine (K)-specific demethylase 7A [Source:MGI Symbol;Acc:MGI:2443388]		Q3UWM4	-4.0	6.1E-05	-2.7	8.5E-03	0.6	2.0E-01	-0.1	8.8E-01
ENSMUST00000002297	Moloney leukemia virus 10 [Source:MGI Symbol;Acc:MGI:97054]	D3YVL0		-4.3	4.7E-02	-3.5	3.5E-01	2.6	1.9E-01	1.9	6.0E-01
ENSMUST00000002298	protein phosphatase 1J [Source:MGI Symbol;Acc:MGI:1919137]		Q149T7	-0.4	4.0E-01	2.3	1.3E-02	2.7	1.9E-03	-0.1	8.4E-01
ENSMUST00000002310	proline rich 27 [Source:MGI Symbol;Acc:MGI:1921029]	E9Q591		6.5	6.3E-05	-6.2	4.5E-03	-0.3	5.6E-01	0.8	6.3E-01
ENSMUST00000002320	peroxisome proliferator activator receptor delta [Source:MGI Symbol;Acc:MGI:101884]	Q546I3	P35396	-3.2	5.1E-04	-3.6	1.6E-03	1.1	2.9E-02	0.6	4.5E-01
ENSMUST00000002327	differentially expressed in FDCP 6 [Source:MGI Symbol;Acc:MGI:1346328]			-3.9	2.8E-05	6.1	1.9E-04	-0.6	6.0E-01	-0.1	8.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000002318	zinc finger protein 523 [Source:MGI Symbol;Acc:MGI:2687278]		Q8BMU0	2.5	2.5E-01	4.8	5.0E-02	-0.5	8.4E-01	-2.8	1.2E-01
ENSMUST00000002336	zinc finger, imprinted 1 [Source:MGI Symbol;Acc:MGI:1341879]	Q8C393		7.9	8.0E-05	-2.1	3.1E-02	1.2	2.7E-02	0.1	9.4E-01
ENSMUST00000002350	nuclear prelamin A recognition factor-like [Source:MGI Symbol;Acc:MGI:1914813]		Q7TMW6	-3.8	2.0E-03	-2.2	4.8E-03	1.2	6.5E-03	-0.4	5.0E-01
ENSMUST00000002360	angiopoietin-like 4 [Source:MGI Symbol;Acc:MGI:1888999]		Q9Z1P8	5.2	2.1E-03	7.6	2.0E-04	-0.7	6.2E-01	-0.4	5.8E-01
ENSMUST00000002344	meteorin, glial cell differentiation regulator [Source:MGI Symbol;Acc:MGI:1917333]	A2RSN4	Q8C1Q4	-1.8	1.6E-01	-1.6	1.4E-01	-1.8	3.8E-02	-2.0	1.3E-01
ENSMUST00000002379	CD320 antigen [Source:MGI Symbol;Acc:MGI:1860083]		Q9Z1P5	7.4	2.5E-05	-5.2	1.1E-02	0.7	3.1E-01	2.1	2.2E-01
ENSMUST00000002391	transmembrane 9 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1921390]		Q9DBU0	-6.6	4.7E-04	4.6	2.9E-03	-1.8	2.0E-01	-1.2	1.6E-01
ENSMUST00000002395	REC8 meiotic recombination protein [Source:MGI Symbol;Acc:MGI:1929645]		Q8C5S7	6.7	9.4E-06	6.4	5.2E-05	-2.3	5.1E-02	-1.3	4.1E-02
ENSMUST00000002389	transglutaminase 1, K polypeptide [Source:MGI Symbol;Acc:MGI:98730]			1.0	6.1E-01	4.6	1.9E-01	5.0	1.2E-01	1.4	5.1E-01
ENSMUST00000002397	guanosine monophosphate reductase 2 [Source:MGI Symbol;Acc:MGI:1917903]		Q99L27	-3.0	2.6E-04	-2.6	4.0E-02	0.8	2.5E-01	-3.2	4.6E-02
ENSMUST00000002403	dehydrogenase/reductase (SDR family) member 1 [Source:MGI Symbol;Acc:MGI:1196314]		Q99L04	-6.7	1.4E-04	6.3	6.0E-05	-0.5	6.1E-01	0.0	9.6E-01
ENSMUST00000002412	neurocan [Source:MGI Symbol;Acc:MGI:104694]			8.8	2.9E-06	-3.2	7.7E-04	-0.3	4.0E-01	-0.1	8.6E-01
ENSMUST00000002398	adenylate cyclase 4 [Source:MGI Symbol;Acc:MGI:99674]		Q91WF3	4.4	1.2E-01	-0.5	9.0E-01	-2.2	4.5E-01	2.7	4.4E-01
ENSMUST00000002400	magnesium-dependent phosphatase 1 [Source:MGI Symbol;Acc:MGI:1915131]		Q9D967	-0.2	6.9E-01	0.1	9.3E-01	0.0	9.8E-01	-0.2	6.6E-01
ENSMUST00000002418	BLOC-1 related complex subunit 8 [Source:MGI Symbol;Acc:MGI:1919618]		Q9D6Y4	-2.3	5.2E-03	-5.0	4.3E-03	1.1	9.5E-02	-0.6	6.8E-01
ENSMUST00000002436	sorting nexin 9 [Source:MGI Symbol;Acc:MGI:1913866]	Q3U1P2	Q91VH2	-1.9	2.4E-03	6.8	2.2E-05	-1.7	9.1E-02	0.2	6.6E-01
ENSMUST00000002445	RAN binding protein 3 [Source:MGI Symbol;Acc:MGI:1919060]		Q9CT10	-2.1	3.6E-03	0.6	4.4E-01	1.5	3.4E-02	-1.4	8.3E-02
ENSMUST00000002452	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11 [Source:MGI Symbol;Acc:MGI:1917125]	G5E814		-2.6	6.6E-03	-1.3	5.2E-02	0.2	5.4E-01	-0.4	5.0E-01
ENSMUST00000002444	regulatory factor X, 2 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:106583]		P48379	4.5	1.1E-01	2.4	4.7E-01	-1.3	6.7E-01	0.8	7.5E-01
ENSMUST00000002456	5'-nucleotidase, cytosolic IB [Source:MGI Symbol;Acc:MGI:1918131]		Q91YE9	7.3	1.0E-02	-1.1	1.4E-01	0.6	1.9E-01	-0.4	5.8E-01
ENSMUST00000002457	bone morphogenetic protein 8b [Source:MGI Symbol;Acc:MGI:107335]		P55105	7.4	4.8E-05	-2.7	1.5E-02	-0.6	2.7E-01	-0.5	6.2E-01
ENSMUST00000002466	nuclear receptor subfamily 2, group F, member 6 [Source:MGI Symbol;Acc:MGI:1352453]		P43136	-3.4	1.1E-03	5.8	4.1E-02	-0.8	7.6E-01	0.7	6.4E-01
ENSMUST00000002469	occludin/ELL domain containing 1 [Source:MGI Symbol;Acc:MGI:1924340]	G5E815		-4.4	1.2E-03	6.8	1.8E-04	-0.9	4.9E-01	-0.2	6.9E-01
ENSMUST00000002473	BRISC and BRCA1 A complex member 1 [Source:MGI Symbol;Acc:MGI:1915501]		Q3UI43	-2.6	1.2E-03	-4.2	2.6E-03	0.1	8.3E-01	1.0	3.8E-01
ENSMUST00000002487	Braf transforming gene [Source:MGI Symbol;Acc:MGI:88190]		P28028	-3.1	1.0E-03	-5.6	6.1E-03	0.8	2.7E-01	2.0	2.3E-01
ENSMUST00000002502	helicase-like transcription factor [Source:MGI Symbol;Acc:MGI:1196437]		Q6PCN7	-6.3	1.6E-05	-1.7	4.2E-02	0.7	1.2E-01	-0.2	7.9E-01
ENSMUST00000002518	amino-terminal enhancer of split [Source:MGI Symbol;Acc:MGI:95806]	Q3TYD9	P63002	-5.7	6.0E-05	-2.0	4.1E-02	0.8	1.1E-01	-0.3	7.7E-01
ENSMUST00000002529	PRP6 pre-mRNA splicing factor 6 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1922946]		Q91YR7	-2.3	9.3E-03	-3.4	3.5E-03	0.0	9.4E-01	-1.2	2.6E-01
ENSMUST00000002532	regulator of G-protein signaling 19 [Source:MGI Symbol;Acc:MGI:1915153]	Q78NN4	Q9CX84	-8.8	1.3E-03	-5.7	2.1E-04	-0.1	8.0E-01	-0.7	5.0E-01
ENSMUST00000002533	regulator of G-protein signaling 20 [Source:MGI Symbol;Acc:MGI:1929866]		Q9QZB1	8.6	1.3E-06	-5.2	8.8E-04	1.0	6.0E-02	0.5	6.3E-01
ENSMUST00000002551	small nuclear ribonucleoprotein D1 [Source:MGI Symbol;Acc:MGI:98344]		P62315	-2.8	1.8E-04	-3.2	2.1E-02	0.5	3.9E-01	1.4	2.2E-01
ENSMUST00000002599	poly-U binding splicing factor 60 [Source:MGI Symbol;Acc:MGI:1915209]		Q3UEB3	-5.1	8.6E-04	-6.0	4.7E-02	2.7	3.0E-02	-0.1	9.7E-01
ENSMUST00000002603	scribbled homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2145950]		Q80U72	6.0	1.3E-02	11.1	6.3E-06	1.9	1.3E-01	-0.6	1.5E-01
ENSMUST00000002625	uridine-cytidine kinase 1 [Source:MGI Symbol;Acc:MGI:98904]	A2AN37		-1.5	3.1E-02	-4.4	4.5E-05	-1.0	1.3E-02	0.6	3.3E-01
ENSMUST00000002572	te carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2 [Source:MGI Symbol;Acc:MGI:18906			-0.2	8.1E-01	1.8	8.2E-02	1.9	2.3E-02	0.0	1.0E+00
ENSMUST00000002588	T cell lymphoma invasion and metastasis 1 [Source:MGI Symbol;Acc:MGI:103306]	G3UWG2		-1.7	6.2E-01	0.1	9.7E-01	0.3	9.3E-01	-1.6	6.6E-01
ENSMUST00000002640	scinderin [Source:MGI Symbol;Acc:MGI:1306794]		Q60604	3.0	2.5E-03	-2.2	8.2E-02	0.5	4.4E-01	-2.3	9.9E-02
ENSMUST00000002655	migration and invasion enhancer 1 [Source:MGI Symbol;Acc:MGI:1913678]		Q9CQ86	-5.0	2.1E-05	5.1	8.7E-02	1.5	5.4E-01	2.5	2.4E-01
ENSMUST00000002663	paraoxonase 1 [Source:MGI Symbol;Acc:MGI:103295]		P52430	4.5	1.9E-03	-0.3	7.4E-01	1.3	4.1E-02	0.0	9.5E-01
ENSMUST00000002678	transforming growth factor, beta 1 [Source:MGI Symbol;Acc:MGI:98725]	Q3UNK5	P04202	-4.0	4.5E-04	4.8	1.0E-03	1.6	1.1E-01	-0.2	8.0E-01
ENSMUST00000002683	coiled-coil domain containing 97 [Source:MGI Symbol;Acc:MGI:1196455]		Q9DBT3	-3.1	1.8E-03	-3.7	1.0E-03	0.8	8.7E-02	-0.5	5.3E-01
ENSMUST00000002708	sonic hedgehog [Source:MGI Symbol;Acc:MGI:98297]		Q62226	6.7	1.2E-04	4.0	2.2E-03	-2.1	8.2E-02	-1.5	6.4E-02
ENSMUST00000002677	AXL receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:1347244]		Q00993	3.0	8.2E-02	-1.2	4.0E-01	-5.3	2.4E-03	-1.1	4.7E-01
ENSMUST00000002710	programmed cell death 2-like [Source:MGI Symbol;Acc:MGI:1915329]		Q8C5N5	-2.3	8.8E-04	-2.8	1.4E-02	1.0	8.5E-02	-0.2	8.4E-01
ENSMUST00000002733	general transcription factor IIF, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1923848]		Q3THK3	-3.3	6.6E-05	-1.8	7.1E-02	1.1	6.3E-02	-0.1	9.0E-01
ENSMUST00000002699	A kinase (PRKA) anchor protein 8 [Source:MGI Symbol;Acc:MGI:1928488]	Q059U9	Q9DBR0	-1.3	8.6E-02	-1.2	2.1E-01	-0.1	8.8E-01	-0.2	8.1E-01
ENSMUST00000002756	mediator complex subunit 6 [Source:MGI Symbol;Acc:MGI:1917042]			-7.1	1.3E-04	5.5	8.2E-04	-1.1	3.8E-01	0.2	8.0E-01
ENSMUST00000002757	cytochrome c oxidase assembly protein 16 [Source:MGI Symbol;Acc:MGI:1913522]		Q9CR63	6.7	1.5E-04	-2.4	3.1E-03	-0.1	7.8E-01	0.0	9.5E-01
ENSMUST00000002765	protein kinase D1 [Source:MGI Symbol;Acc:MGI:99879]		Q62101	6.3	3.5E-04	-3.7	1.6E-04	-0.9	2.1E-02	-0.5	4.6E-01
ENSMUST00000002735	caseinolytic mitochondrial matrix peptidase proteolytic subunit [Source:MGI Symbol;Acc:MGI:1858213]		O88696	-0.7	3.4E-01	-0.4	6.7E-01	-0.4	5.6E-01	-0.7	4.2E-01
ENSMUST00000002737	alkB, alkylation repair homolog 7 (E. coli) [Source:MGI Symbol;Acc:MGI:1913650]		Q9D6Z0	-1.5	1.0E-01	0.6	5.5E-01	0.3	6.8E-01	-1.8	8.1E-02
ENSMUST00000002790	chromosome segregation 1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1339951]		Q9ERK4	-3.4	3.3E-02	-3.5	3.5E-02	2.6	4.1E-03	-1.0	5.2E-01
ENSMUST00000002808	in kinase, interferon inducible double stranded RNA dependent activator [Source:MGI Symbol;Acc:MGI:1344		Q9WTX2	-4.2	1.6E-05	5.4	2.2E-03	-0.8	5.5E-01	0.6	4.7E-01
ENSMUST00000002818	YKT6 homolog (S. Cerevisiae) [Source:MGI Symbol;Acc:MGI:1927550]		Q9CQW1	-3.4	8.3E-05	6.7	4.5E-04	-0.4	7.4E-01	-0.8	2.8E-01
ENSMUST00000002825	bromodomain adjacent to zinc finger domain, 1B [Source:MGI Symbol;Acc:MGI:1353499]		Q9Z277	-2.5	2.8E-04	-3.8	2.7E-02	-1.3	1.4E-01	-0.9	6.0E-01
ENSMUST00000002837	transmembrane emp24 protein transport domain containing 5 [Source:MGI Symbol;Acc:MGI:1921586]	A2RS96	Q9CXE7	-5.6	2.7E-04	-3.4	4.0E-04	0.1	8.8E-01	-0.8	2.4E-01
ENSMUST00000002840	peroxisomal biogenesis factor 6 [Source:MGI Symbol;Acc:MGI:2385054]		Q99LC9	-7.1	5.7E-04	-3.0	2.4E-03	1.1	1.8E-02	0.6	4.0E-01
ENSMUST00000002844	mitochondrial ribosomal protein L2 [Source:MGI Symbol;Acc:MGI:1351622]		Q9D773	-5.1	5.9E-05	-1.6	1.7E-02	0.6	9.4E-02	-0.3	6.0E-01
ENSMUST00000002845	male enhanced antigen 1 [Source:MGI Symbol;Acc:MGI:96957]		Q64327	-3.9	1.4E-04	-6.3	1.9E-03	0.3	6.1E-01	1.0	5.2E-01
ENSMUST00000002839	protein phosphatase 2, regulatory subunit B', delta [Source:MGI Symbol;Acc:MGI:2388481]	Q91V89		-0.7	2.5E-01	-0.3	7.1E-01	0.8	1.8E-01	0.4	6.3E-01
ENSMUST00000002848	glutamate receptor, ionotropic, NMDA2D (epsilon 4) [Source:MGI Symbol;Acc:MGI:95823]		Q03391	5.7	3.1E-05	-5.1	1.8E-02	1.4	6.6E-02	-0.6	7.7E-01
ENSMUST00000002850	ATP-binding cassette, sub-family C (CFTR/MRP), member 6 [Source:MGI Symbol;Acc:MGI:1351634]		Q9R1S7	8.3	2.1E-05	-5.3	3.3E-04	-0.3	4.6E-01	-0.1	9.4E-01
ENSMUST00000002855	L (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 [Source:MGI Symbol;Acc:MGI:1915		Q99JH8	-6.8	3.4E-05	-3.8	7.4E-04	-0.4	3.6E-01	-0.4	6.3E-01
ENSMUST00000002846	glycine N-methyltransferase [Source:MGI Symbol;Acc:MGI:1202304]		Q9QXF8	0.2	7.3E-01	0.9	2.2E-01	-0.6	3.0E-01	-1.3	6.3E-02
ENSMUST00000002883	secreted frizzled-related protein 4 [Source:MGI Symbol;Acc:MGI:892010]		Q9Z1N6	7.9	9.2E-05	4.6	3.0E-04	-1.2	1.6E-01	-0.1	8.7E-01
ENSMUST00000002885	ependymin related protein 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:2145369]		Q99M71	4.0	2.8E-04	7.2	4.6E-05	-1.9	1.3E-01	-0.8	1.5E-01
ENSMUST00000002889	flightless I homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1342286]		Q9JJ28	-4.8	2.0E-05	-4.1	7.9E-04	0.9	6.3E-02	-1.8	1.1E-01
ENSMUST00000002874				-1.0	3.5E-01	-1.4	3.6E-01	0.2	8.8E-01	0.5	7.3E-01
ENSMUST00000002880	BTB (POZ) domain containing 6 [Source:MGI Symbol;Acc:MGI:3026623]	G5E817		2.8	1.3E-01	5.2	1.2E-02	-0.6	7.4E-01	-3.0	4.6E-02
ENSMUST00000002881	nudix (nucleoside diphosphate linked moiety X)-type motif 14 [Source:MGI Symbol;Acc:MGI:1913424]		Q9D142	-0.8	2.0E-01	0.3	7.4E-01	0.1	8.3E-01	-1.0	2.1E-01
ENSMUST00000002908	perilipin 4 [Source:MGI Symbol;Acc:MGI:1929709]		O88492	3.7	2.5E-03	5.8	1.6E-03	-0.7	6.4E-01	1.4	8.2E-02
ENSMUST00000002911	hepatoma-derived growth factor, related protein 2 [Source:MGI Symbol;Acc:MGI:1194492]		Q3UMU9	-1.8	8.2E-03	3.7	8.7E-04	-0.7	3.2E-01	-0.4	5.1E-01
ENSMUST00000002923	ADP-ribosylarginine hydrolase [Source:MGI Symbol;Acc:MGI:1098234]	Q3U5N4	P54923	-4.4	4.3E-04	-3.1	2.1E-03	1.0	2.3E-02	-0.7	3.6E-01
ENSMUST00000002891	topoisomerase (DNA) III alpha [Source:MGI Symbol;Acc:MGI:1197527]	Q5NCT2	O70157	-1.7	2.6E-01	0.9	6.1E-01	0.5	7.2E-01	-2.1	2.3E-01
ENSMUST00000002902	queuine tRNA-ribosyltransferase 1 [Source:MGI Symbol;Acc:MGI:1931441]		Q9JMA2	1.0	1.8E-01	0.1	8.9E-01	-1.1	1.1E-01	-0.2	7.8E-01
ENSMUST00000002925	translocase of inner mitochondrial membrane domain containing 1 [Source:MGI Symbol;Acc:MGI:1922139]		Q8BUY5	2.2	3.3E-03	4.6	1.8E-03	0.1	9.3E-01	-0.8	3.1E-01
ENSMUST00000002926	phospholipase A1 member A [Source:MGI Symbol;Acc:MGI:1934677]		Q8VI78	6.0	2.6E-04	-0.7	3.4E-01	0.7	1.3E-01	-0.4	5.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000002914	chromatin assembly factor 1, subunit A (p150) [Source:MGI Symbol;Acc:MGI:1351331]		Q9QWF0	0.5	4.1E-01	1.6	9.0E-02	0.8	2.5E-01	-0.3	7.2E-01
ENSMUST00000002964	adhesion G protein-coupled receptor E5 [Source:MGI Symbol;Acc:MGI:1347095]	A0A0D9SEG8		-9.0	1.7E-04	-3.2	1.5E-02	1.5	2.4E-02	0.4	7.3E-01
ENSMUST00000002976	interleukin 17 receptor A [Source:MGI Symbol;Acc:MGI:107399]		Q60943	-2.8	1.4E-03	2.3	1.3E-02	0.6	3.5E-01	0.5	3.9E-01
ENSMUST00000002979	laminin B1 [Source:MGI Symbol;Acc:MGI:96743]	E9QN70		6.6	1.6E-03	0.1	8.7E-01	-6.1	1.3E-04	-0.2	7.2E-01
ENSMUST00000003017	thromboxane A synthase 1, platelet [Source:MGI Symbol;Acc:MGI:98497]		P36423	-5.2	3.8E-04	-6.0	1.2E-03	0.9	1.3E-01	-2.0	2.5E-01
ENSMUST00000003029	translocase of inner mitochondrial membrane 44 [Source:MGI Symbol;Acc:MGI:1343262]		O35857	-4.9	6.5E-04	-2.8	1.0E-02	1.0	9.7E-02	0.9	2.8E-01
ENSMUST00000003038	adaptor-related protein complex 2, alpha 2 subunit [Source:MGI Symbol;Acc:MGI:101920]		P17427	-3.2	1.4E-05	-1.3	2.1E-01	-7.8	2.7E-04	0.2	8.7E-01
ENSMUST00000002989	arrestin domain containing 2 [Source:MGI Symbol;Acc:MGI:1918057]		Q9D668	-1.1	5.4E-02	-0.9	2.3E-01	0.5	2.8E-01	0.2	7.3E-01
ENSMUST00000003044	polynucleotide kinase 3'- phosphatase [Source:MGI Symbol;Acc:MGI:1891698]	G5E8N7		-5.8	1.2E-03	-5.4	4.9E-04	-2.0	1.7E-03	-1.8	1.6E-01
ENSMUST00000003049	mediator complex subunit 25 [Source:MGI Symbol;Acc:MGI:1922863]		Q8VCB2	-1.6	1.9E-02	-6.5	1.8E-03	-0.7	2.2E-01	0.9	5.9E-01
ENSMUST00000003035	dispatched homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1916147]		Q3TDN0	-2.7	1.6E-01	-1.4	6.6E-01	2.0	3.3E-01	0.7	8.1E-01
ENSMUST00000003061	basal cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1929940]		Q9R069	7.2	3.2E-05	-2.0	2.7E-03	1.2	2.4E-03	0.0	9.3E-01
ENSMUST00000003071	apolipoprotein C-IV [Source:MGI Symbol;Acc:MGI:87878]		Q61268	4.1	1.7E-02	-5.3	1.4E-02	1.8	5.8E-02	1.3	4.9E-01
ENSMUST00000003074	apolipoprotein C-II [Source:MGI Symbol;Acc:MGI:88054]	Q3UJG0	Q05020	-7.0	3.4E-05	-0.8	3.1E-01	0.8	1.2E-01	0.0	9.9E-01
ENSMUST00000003079	protein kinase, cAMP dependent regulatory, type II beta [Source:MGI Symbol;Acc:MGI:97760]		P31324	-6.3	5.7E-04	1.6	4.2E-02	-5.5	1.9E-04	0.2	7.9E-01
ENSMUST00000003100	cytochrome P450, family 2, subfamily f, polypeptide 2 [Source:MGI Symbol;Acc:MGI:88608]		P33267	6.9	2.8E-04	0.5	6.8E-01	-4.3	1.2E-02	-0.6	5.3E-01
ENSMUST00000003115	cyclin-dependent kinase inhibitor 1B [Source:MGI Symbol;Acc:MGI:104565]		P46414	-6.2	1.8E-05	-6.7	3.6E-04	-0.4	3.3E-01	-0.8	5.6E-01
ENSMUST00000003117	adaptor-related protein complex AP-1, mu subunit 1 [Source:MGI Symbol;Acc:MGI:102776]	Q3UG16	P35585	-4.9	9.5E-05	-3.3	1.7E-02	1.0	1.2E-01	-1.9	2.0E-01
ENSMUST00000003121	RAB8A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:96960]	Q0PD50	P55258	-2.7	3.0E-05	5.4	1.3E-03	-1.9	1.8E-01	-0.4	6.1E-01
ENSMUST00000003123	family with sequence similarity 32, member A [Source:MGI Symbol;Acc:MGI:1915172]		Q9CR80	-6.0	1.1E-06	-6.2	1.0E-04	0.1	7.5E-01	0.1	9.3E-01
ENSMUST00000003135	E74-like factor 3 [Source:MGI Symbol;Acc:MGI:1101781]		Q3UPW2	7.3	3.5E-03	-3.4	4.9E-03	1.1	3.8E-02	-0.3	7.3E-01
ENSMUST00000003152	serine/threonine kinase 11 [Source:MGI Symbol;Acc:MGI:1341870]		Q9WTK7	-6.2	2.3E-04	-2.3	5.8E-04	0.4	2.2E-01	0.0	9.4E-01
ENSMUST00000003154	ephrin A2 [Source:MGI Symbol;Acc:MGI:102707]		P52801	7.2	7.0E-05	-6.6	5.3E-06	-0.6	6.3E-02	0.1	9.1E-01
ENSMUST00000003156	ITP synthase, H+ transporting, mitochondrial F1 complex, delta subunit [Source:MGI Symbol;Acc:MGI:191329		Q4FK74	-5.2	5.3E-04	5.3	3.0E-02	-0.5	8.2E-01	1.4	2.7E-01
ENSMUST00000003183	protein phosphatase 5, catalytic subunit [Source:MGI Symbol;Acc:MGI:102666]		Q9D3D9	-3.9	3.3E-03	-5.4	3.8E-03	1.9	7.6E-03	1.0	5.2E-01
ENSMUST00000003203	cyclin-dependent kinase 12 [Source:MGI Symbol;Acc:MGI:1098802]		Q60676	5.5	5.0E-03	4.7	6.2E-04	-2.5	4.3E-02	-0.1	9.3E-01
ENSMUST00000003268	SH3-domain GRB2-like 1 [Source:MGI Symbol;Acc:MGI:700010]	Q3TRJ7	Q14AX6	-3.4	4.7E-04	-3.6	1.1E-02	1.1	9.8E-02	-0.4	7.5E-01
ENSMUST00000003274	Epstein-Barr virus induced gene 3 [Source:MGI Symbol;Acc:MGI:1354171]	Q3U1K3	Q62419	-4.3	2.8E-04	-0.6	5.1E-01	0.8	2.8E-01	-2.5	4.7E-02
ENSMUST00000003191	protein kinase D3 [Source:MGI Symbol;Acc:MGI:1922542]		O35228	-2.1	1.2E-01	-2.8	9.2E-02	0.2	8.0E-01	1.0	5.4E-01
ENSMUST00000003310	RAN binding protein 2 [Source:MGI Symbol;Acc:MGI:894323]		Q8K1Y2	-3.4	8.4E-05	0.7	7.6E-01	-1.4	4.3E-01	3.4	1.0E-01
ENSMUST00000003207	lipase, hormone sensitive [Source:MGI Symbol;Acc:MGI:96790]		Q9ERU9	-0.4	6.2E-01	0.7	5.0E-01	1.2	1.4E-01	0.1	8.8E-01
ENSMUST00000003219	CCR4-NOT transcription complex, subunit 11 [Source:MGI Symbol;Acc:MGI:106580]		P54310	-0.4	6.2E-01	0.7	5.0E-01	1.2	1.4E-01	0.1	8.8E-01
ENSMUST00000003238	forkhead box J2 [Source:MGI Symbol;Acc:MGI:1926805]		Q9CWN7	-2.8	7.1E-02	-2.5	1.7E-01	0.5	6.7E-01	0.2	9.1E-01
ENSMUST00000003312	ectodysplasin-A receptor [Source:MGI Symbol;Acc:MGI:1343498]		Q9ES18	1.3	5.3E-02	1.3	1.3E-01	0.5	4.0E-01	0.5	4.9E-01
ENSMUST00000003313	G protein-coupled receptor kinase 5 [Source:MGI Symbol;Acc:MGI:109161]	Q3TST4	Q9R187	7.7	2.4E-05	-10.0	2.4E-06	0.4	1.2E-01	-0.8	4.7E-01
ENSMUST00000003319	ATP-binding cassette, sub-family F (GCN20), member 3 [Source:MGI Symbol;Acc:MGI:1351656]		Q8VEB1	-1.6	4.9E-03	-1.8	3.9E-02	0.9	7.0E-02	-0.6	4.4E-01
ENSMUST00000003284	interferon regulatory factor 3 [Source:MGI Symbol;Acc:MGI:1859179]	Q3U9K6	Q8K268	-2.3	1.8E-03	-2.9	1.6E-02	1.5	1.8E-02	0.1	9.5E-01
ENSMUST00000003290	BCL2-like 12 (proline rich) [Source:MGI Symbol;Acc:MGI:1922986]	Q9D3J3	P70671	1.5	1.5E-01	-0.3	8.1E-01	-0.4	6.6E-01	1.4	2.4E-01
ENSMUST00000003320	eukaryotic translation initiation factor 2B, subunit 5 epsilon [Source:MGI Symbol;Acc:MGI:2446176]			-0.4	7.2E-01	-1.2	5.1E-01	1.4	2.7E-01	2.1	2.2E-01
ENSMUST00000003345	amphiphysin [Source:MGI Symbol;Acc:MGI:103574]		Q8CHW4	-1.3	1.3E-02	-3.1	1.1E-03	0.2	5.3E-01	0.0	9.5E-01
ENSMUST00000003360	carbonic anhydrase 11 [Source:MGI Symbol;Acc:MGI:1336193]	Q541E9	Q7TQF7	7.4	1.5E-05	8.0	3.5E-05	-0.5	6.6E-01	-0.8	1.4E-01
ENSMUST00000003318	dishevelled 3, dsh homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108100]		O70354	5.3	6.2E-04	-1.2	5.3E-02	0.6	1.3E-01	0.2	6.6E-01
ENSMUST00000003369	pleiomorphic adenoma gene 1 [Source:MGI Symbol;Acc:MGI:1891916]		Q61062	1.0	2.1E-01	2.9	3.0E-02	2.2	4.9E-02	0.3	7.2E-01
ENSMUST00000003370	hemopoietic cell kinase [Source:MGI Symbol;Acc:MGI:96052]	F6UND7	Q9QYE0	3.6	2.5E-04	-2.2	1.0E-02	0.0	9.1E-01	-0.1	9.3E-01
ENSMUST00000003386	mitochondrial ribosomal protein L4 [Source:MGI Symbol;Acc:MGI:2137210]		Q9DCU6	-2.7	7.4E-04	7.5	4.5E-05	0.1	9.6E-01	-0.1	8.6E-01
ENSMUST00000003351	glutamate receptor, ionotropic, NMDA2C (epsilon 3) [Source:MGI Symbol;Acc:MGI:95822]	A2A6S2	Q01098	3.0	4.2E-02	6.7	4.5E-04	-0.5	6.9E-01	-4.2	1.8E-03
ENSMUST00000003395	phosphodiesterase 4A, cAMP specific [Source:MGI Symbol;Acc:MGI:99558]		O89084	8.1	1.1E-05	5.7	7.2E-04	-0.8	4.9E-01	-1.2	9.7E-02
ENSMUST00000003413	cytochrome P450, family 4, subfamily f, polypeptide 39 [Source:MGI Symbol;Acc:MGI:2445210]	Q8BGU0		6.6	1.6E-04	3.9	2.7E-04	-0.5	4.1E-01	-0.9	1.3E-01
ENSMUST00000003416	cytochrome P450, family 4, subfamily f, polypeptide 16 [Source:MGI Symbol;Acc:MGI:1917351]	Q99N17		-4.3	5.2E-03	-4.6	2.0E-04	1.4	3.8E-03	-0.4	6.3E-01
ENSMUST00000003433	MAP kinase-interacting serine/threonine kinase 2 [Source:MGI Symbol;Acc:MGI:894279]			-4.6	1.3E-04	-0.7	2.9E-01	1.0	3.4E-02	-0.9	1.7E-01
ENSMUST00000003436	abhydrolase domain containing 17A [Source:MGI Symbol;Acc:MGI:106388]		Q99JW1	-4.1	5.9E-04	4.3	8.3E-04	-3.1	1.2E-02	0.7	2.5E-01
ENSMUST00000003397	adaptor protein complex AP-1, mu 2 subunit [Source:MGI Symbol;Acc:MGI:1336974]			1.1	4.7E-02	1.5	4.7E-02	0.5	3.4E-01	0.2	7.7E-01
ENSMUST00000003404	golgi apparatus protein 1 [Source:MGI Symbol;Acc:MGI:104967]	F8WHM5		0.9	6.6E-01	4.7	9.6E-02	1.8	4.0E-01	-2.0	4.1E-01
ENSMUST00000003438	MOB kinase activator 3A [Source:MGI Symbol;Acc:MGI:3050117]		Q8BSU7	-5.6	9.1E-06	7.0	2.8E-04	-0.1	9.4E-01	-0.5	4.7E-01
ENSMUST00000003442	calcium channel, voltage-dependent, beta 3 subunit [Source:MGI Symbol;Acc:MGI:103307]		P54285	4.6	3.0E-02	-2.5	1.5E-01	1.4	1.5E-01	-0.4	8.1E-01
ENSMUST00000003444	coiled-coil domain containing 65 [Source:MGI Symbol;Acc:MGI:2146001]		Q8VHI7	6.8	2.0E-04	-3.4	4.6E-03	1.1	4.8E-02	-0.1	9.3E-01
ENSMUST00000003450	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 [Source:MGI Symbol;Acc:MGI:1921601]	D3Z0M9		-2.1	4.9E-04	-1.8	8.7E-02	1.1	8.5E-02	-1.2	2.7E-01
ENSMUST00000003451	Rho family GTPase 1 [Source:MGI Symbol;Acc:MGI:2444878]		Q8BLR7	-3.4	5.2E-05	-4.5	3.8E-04	1.0	2.4E-02	-0.1	9.0E-01
ENSMUST00000003459	myosin IG [Source:MGI Symbol;Acc:MGI:1927091]		Q5SUA5	-6.4	1.4E-04	5.3	2.0E-02	-0.7	7.4E-01	-1.3	3.5E-01
ENSMUST00000003461	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) [Source:MGI Symbol;Acc:MGI:1098267]		Q60597	-5.5	2.1E-03	4.8	2.6E-03	-1.4	3.0E-01	0.6	4.1E-01
ENSMUST00000003445	FK506 binding protein 11 [Source:MGI Symbol;Acc:MGI:1913370]		Q9D1M7	0.8	1.8E-01	-0.4	5.1E-01	-1.5	1.6E-02	-0.3	6.0E-01
ENSMUST00000003468	glutamate receptor, ionotropic, kainate 5 (gamma 2) [Source:MGI Symbol;Acc:MGI:95818]		Q61626	2.6	2.1E-03	-1.5	1.8E-02	0.6	1.1E-01	-0.1	8.6E-01
ENSMUST00000003501	VAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C) [Source:MGI Symbol;Acc:MGI:109		Q60900	8.7	3.5E-06	-2.1	6.0E-03	1.0	1.7E-02	-0.2	7.5E-01
ENSMUST00000003509	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6 [Source:MGI Symbol;Acc:MGI:2386797]	Q148N5	Q8K4T1	4.3	1.6E-04	-7.9	5.7E-03	1.3	6.7E-02	2.7	2.4E-01
ENSMUST00000003512	Fc receptor, IgG, alpha chain transporter [Source:MGI Symbol;Acc:MGI:103017]		Q61559	-1.9	2.3E-02	-4.6	2.3E-02	0.9	2.6E-01	0.0	9.8E-01
ENSMUST00000003513	nitric oxide synthase interacting protein [Source:MGI Symbol;Acc:MGI:1913644]		Q9D6T0	2.5	7.1E-03	2.9	3.7E-03	0.2	7.3E-01	-0.1	8.3E-01
ENSMUST00000003469	CD79A antigen (immunoglobulin-associated alpha) [Source:MGI Symbol;Acc:MGI:101774]		P11911	0.2	8.0E-01	-0.9	2.5E-01	-1.6	1.3E-02	-0.5	4.9E-01
ENSMUST00000003493	protein kinase C substrate 80K-H [Source:MGI Symbol;Acc:MGI:107877]	Q3U518	O08795	-2.1	2.6E-01	-2.1	4.3E-01	1.7	3.5E-01	1.7	5.0E-01
ENSMUST00000003521	ribosomal protein S11 [Source:MGI Symbol;Acc:MGI:1351329]	Q3UC02	P62281	-5.9	3.5E-07	7.8	1.1E-05	-1.1	2.8E-01	-0.2	6.5E-01
ENSMUST00000003527	suppressor of Ty 5 [Source:MGI Symbol;Acc:MGI:1202400]		O55201	-2.8	1.2E-04	3.5	1.3E-03	-0.9	2.5E-01	-0.1	8.4E-01
ENSMUST00000003529	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923988]		Q8K2T8	-4.1	7.4E-05	-3.3	3.0E-03	-2.4	8.3E-04	-1.1	2.5E-01
ENSMUST00000003550	nicastrin [Source:MGI Symbol;Acc:MGI:1891700]		P57716	-10.1	2.7E-05	3.1	6.6E-03	-0.1	8.7E-01	-0.7	3.4E-01
ENSMUST00000003554	calsequestrin 1 [Source:MGI Symbol;Acc:MGI:1309468]		O09165	6.1	1.7E-04	-6.2	2.5E-06	-0.5	8.9E-02	-0.2	7.8E-01
ENSMUST00000003561	phytanoyl-CoA hydroxylase interacting protein [Source:MGI Symbol;Acc:MGI:1860417]	B9EIC7	Q8K0S0	7.4	3.6E-05	-1.9	8.1E-03	0.7	6.6E-02	-0.3	6.3E-01
ENSMUST00000003568	corticotropin releasing hormone receptor 2 [Source:MGI Symbol;Acc:MGI:894312]	Q3UQP0		7.7	1.1E-04	-2.7	5.5E-03	0.8	8.2E-02	-0.6	4.7E-01
ENSMUST00000003536	mediator complex subunit 29 [Source:MGI Symbol;Acc:MGI:1914474]		Q9DB91	-0.5	4.1E-01	-0.3	6.5E-01	-0.4	4.1E-01	-0.6	4.0E-01
ENSMUST00000003569	indolethylamine N-methyltransferase [Source:MGI Symbol;Acc:MGI:102963]		P40936	5.3	9.6E-04	-8.0	8.5E-04	1.3	2.2E-02	-0.7	7.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000003572	glycyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:2449057]		Q9CZD3	-3.9	1.6E-05	6.9	1.3E-04	-0.5	6.5E-01	-1.3	6.0E-02
ENSMUST00000003574	cytochrome P450, family 4, subfamily f, polypeptide 18 [Source:MGI Symbol;Acc:MGI:1919304]		Q99N16	-6.6	2.2E-07	6.5	1.3E-04	-1.4	2.3E-01	-0.6	3.4E-01
ENSMUST00000003575	tropomyosin 4 [Source:MGI Symbol;Acc:MGI:2449202]		Q6IRU2	-5.7	2.4E-05	7.3	3.3E-04	-0.7	6.4E-01	-0.3	7.2E-01
ENSMUST00000003599	protocadherin gamma subfamily B, 6 [Source:MGI Symbol;Acc:MGI:1935197]	Q91XX4		2.9	1.4E-03	3.1	1.2E-02	-2.4	6.3E-02	-0.2	7.8E-01
ENSMUST00000003612	ual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) [Source:MGI Symbol;Acc:MGI:191959		Q9D7X3	-6.4	3.1E-05	-3.1	6.0E-04	0.8	3.8E-02	-0.1	8.5E-01
ENSMUST00000003620	proline dehydrogenase [Source:MGI Symbol;Acc:MGI:97770]		Q9WU79	5.4	9.2E-03	-7.3	1.1E-06	-0.1	8.2E-01	0.6	3.6E-01
ENSMUST00000003622	te carrier family 25 (mitochondrial carrier, citrate transporter), member 1 [Source:MGI Symbol;Acc:MGI:1345		Q8JZU2	-2.7	3.4E-03	-5.5	2.6E-04	0.1	8.1E-01	-0.1	9.0E-01
ENSMUST00000003635	immediate early response 3 [Source:MGI Symbol;Acc:MGI:104814]	Q91VZ5		-4.3	5.4E-05	2.9	4.1E-03	0.7	3.0E-01	0.7	2.9E-01
ENSMUST00000003642	kinesin light chain 4 [Source:MGI Symbol;Acc:MGI:1922014]		Q9DBS5	-2.3	3.0E-03	-6.4	2.4E-04	0.4	3.0E-01	0.5	7.1E-01
ENSMUST00000003643	creatine kinase, muscle [Source:MGI Symbol;Acc:MGI:88413]	A2RTA0	P07310	5.8	2.4E-03	7.6	1.4E-02	2.3	3.6E-01	0.1	9.4E-01
ENSMUST00000003621	DiGeorge syndrome critical region gene 14 [Source:MGI Symbol;Acc:MGI:107854]	Q3UFM6		-0.8	1.2E-01	0.4	5.0E-01	1.0	5.4E-02	-0.3	6.6E-01
ENSMUST00000003659	cartilage oligomeric matrix protein [Source:MGI Symbol;Acc:MGI:88469]		Q9R0G6	6.0	8.0E-05	-0.8	3.5E-01	1.0	1.0E-01	-0.9	3.4E-01
ENSMUST00000003677	ring finger protein 215 [Source:MGI Symbol;Acc:MGI:1918923]		Q5SPX3	-2.5	3.1E-02	-3.1	2.4E-03	0.9	4.9E-02	-0.3	6.8E-01
ENSMUST00000003640	FBJ osteosarcoma oncogene B [Source:MGI Symbol;Acc:MGI:95575]	A2RSD4	P13346	-0.4	8.5E-01	2.5	4.4E-01	2.7	3.3E-01	-0.2	9.4E-01
ENSMUST00000003681	SEC14-like lipid binding 2 [Source:MGI Symbol;Acc:MGI:1915065]		Q99J08	6.2	4.5E-04	-0.9	2.5E-01	0.9	7.7E-02	-0.5	5.1E-01
ENSMUST00000003687	transforming growth factor, beta 3 [Source:MGI Symbol;Acc:MGI:98727]	Q91YU7		7.3	8.0E-06	4.1	1.6E-02	-1.9	2.1E-01	-0.2	8.3E-01
ENSMUST00000003645	repair cross-complementing rodent repair deficiency, complementation group 1 [Source:MGI Symbol;Acc:MG		P07903	1.8	3.7E-02	0.7	3.9E-01	-1.2	1.3E-01	-0.1	8.7E-01
ENSMUST00000003655	arsenic (+3 oxidation state) methyltransferase [Source:MGI Symbol;Acc:MGI:1929882]		Q91WU5	-1.0	6.1E-02	-1.1	8.2E-02	-0.4	3.8E-01	-0.2	7.0E-01
ENSMUST00000003705	apoptosis, caspase activation inhibitor [Source:MGI Symbol;Acc:MGI:1921518]		Q9D9K3	3.5	4.1E-04	5.7	2.1E-04	-0.5	6.1E-01	-0.3	6.9E-01
ENSMUST00000003669	homer homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1347359]		Q99JP6	-3.0	1.4E-01	-2.8	3.8E-01	0.8	6.7E-01	0.6	8.3E-01
ENSMUST00000003710	AP2 associated kinase 1 [Source:MGI Symbol;Acc:MGI:1098687]		Q3UHJ0	7.3	1.0E-04	-0.3	7.9E-01	0.7	4.3E-01	-1.5	2.4E-01
ENSMUST00000003717	ATP-binding cassette, sub-family B (MDR/TAP), member 4 [Source:MGI Symbol;Acc:MGI:97569]		P21440	6.0	7.7E-05	3.6	3.5E-03	-3.6	1.1E-02	-0.9	2.4E-01
ENSMUST00000003720	carnitine O-octanoyltransferase [Source:MGI Symbol;Acc:MGI:1921364]		Q9DC50	-5.0	3.4E-05	3.5	4.3E-04	-4.1	5.5E-04	-0.3	4.9E-01
ENSMUST00000003754	calbindin 2 [Source:MGI Symbol;Acc:MGI:101914]		Q08331	6.9	5.6E-05	3.0	2.5E-03	-0.6	4.0E-01	-0.2	7.9E-01
ENSMUST00000003759	cytosolic iron-sulfur protein assembly 1 [Source:MGI Symbol;Acc:MGI:1346998]		Q99KN2	-2.1	1.7E-02	4.3	6.1E-03	-1.7	2.2E-01	1.4	1.2E-01
ENSMUST00000003714	ceruloplasmin [Source:MGI Symbol;Acc:MGI:88476]	G3X8Q5		-0.7	5.7E-01	-2.9	2.3E-02	-4.1	4.8E-04	-1.8	1.7E-01
ENSMUST00000003762	hyaluronan synthase1 [Source:MGI Symbol;Acc:MGI:106590]		Q61647	5.6	9.5E-05	4.1	4.3E-04	-2.7	1.1E-02	-0.8	1.9E-01
ENSMUST00000003808	growth differentiation factor 15 [Source:MGI Symbol;Acc:MGI:1346047]		Q9Z0J7	5.2	3.0E-03	-4.5	3.4E-04	-0.3	4.6E-01	-0.8	3.7E-01
ENSMUST00000003726	bromodomain containing 4 [Source:MGI Symbol;Acc:MGI:1888520]	Q3UH70		-3.2	4.7E-02	2.4	9.9E-02	1.3	2.9E-01	-4.4	1.2E-02
ENSMUST00000003741	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:104558]		P18653	1.0	6.7E-01	1.3	6.7E-01	0.5	8.4E-01	0.2	9.5E-01
ENSMUST00000003818	insulin induced gene 2 [Source:MGI Symbol;Acc:MGI:1920249]		Q91WG1	-2.1	1.0E-02	6.6	1.5E-04	-0.6	6.2E-01	-0.2	6.8E-01
ENSMUST00000003826	5-hydroxytryptamine (serotonin) receptor 3A [Source:MGI Symbol;Acc:MGI:96282]	E9QLC0		7.8	1.8E-05	-0.3	7.9E-01	1.4	6.4E-02	-0.4	6.2E-01
ENSMUST00000003857	Sh3kbp1 binding protein 1 [Source:MGI Symbol;Acc:MGI:2385803]		Q6P7W2	-6.6	8.9E-04	2.8	1.1E-02	-2.5	1.7E-02	0.3	6.7E-01
ENSMUST00000003860	aarF domain containing kinase 4 [Source:MGI Symbol;Acc:MGI:1924139]	E9QLB8		-4.4	1.3E-03	2.6	1.4E-01	-2.1	2.1E-01	0.6	5.9E-01
ENSMUST00000003870	MAX interactor 1, dimerization protein [Source:MGI Symbol;Acc:MGI:97245]	Q3U3X2		-5.4	3.7E-05	-1.2	1.5E-01	0.2	6.4E-01	-0.6	4.4E-01
ENSMUST00000003876	bromodomain containing 8 [Source:MGI Symbol;Acc:MGI:1925906]		Q8R3B7	4.3	2.7E-02	7.5	5.0E-05	-0.6	6.0E-01	-0.3	5.6E-01
ENSMUST00000003828	karyopherin (importin) alpha 6 [Source:MGI Symbol;Acc:MGI:1100836]	Q4FJZ2		-0.2	9.5E-01	0.6	8.8E-01	0.0	9.9E-01	-0.8	8.2E-01
ENSMUST00000003843	mannosidase 1, alpha [Source:MGI Symbol;Acc:MGI:104677]	Q544T7	P45700	-1.6	4.0E-02	-2.1	3.1E-02	-0.4	4.2E-01	0.1	8.8E-01
ENSMUST00000003850	inositol 1,4,5-trisphosphate 3-kinase C [Source:MGI Symbol;Acc:MGI:2442554]		Q7TS72	1.0	1.6E-01	1.8	6.2E-02	0.7	3.2E-01	-0.1	8.9E-01
ENSMUST00000003906	phenylalanyl-tRNA synthetase, alpha subunit [Source:MGI Symbol;Acc:MGI:1913840]		Q8C0C7	-5.3	3.0E-04	-7.8	8.3E-03	1.1	1.3E-01	2.4	3.5E-01
ENSMUST00000003911	RAD23a homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:105126]	Q8CAP3		-4.1	3.1E-02	-0.9	3.9E-01	0.8	2.3E-01	-2.6	4.9E-02
ENSMUST00000003912	calreticulin [Source:MGI Symbol;Acc:MGI:88252]	B2MWM9	P14211	-6.2	1.1E-05	-2.1	1.8E-02	1.1	3.5E-02	-2.3	2.3E-02
ENSMUST00000003946	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914869]	Q148S3	Q8BW10	-4.6	1.9E-04	1.9	2.1E-01	-5.6	5.8E-03	-3.2	3.7E-02
ENSMUST00000003947	NAD(P)H dehydrogenase, quinone 1 [Source:MGI Symbol;Acc:MGI:103187]	Q542Y0	Q64669	-2.4	2.0E-03	-5.4	1.8E-03	0.4	4.7E-01	0.4	7.5E-01
ENSMUST00000003907	glutaryl-Coenzyme A dehydrogenase [Source:MGI Symbol;Acc:MGI:104541]	A0A0A0MQ68		3.3	1.3E-01	2.7	3.7E-01	0.4	8.7E-01	1.0	6.1E-01
ENSMUST00000003908	microtubule associated serine/threonine kinase 2 [Source:MGI Symbol;Acc:MGI:894676]	B1AST8		1.1	5.2E-01	2.7	1.5E-01	-0.5	7.6E-01	-2.0	2.3E-01
ENSMUST00000003910	deoxyribonuclease II alpha [Source:MGI Symbol;Acc:MGI:1329019]	Q3UM14	P56542	-0.5	2.5E-01	-0.6	2.9E-01	-0.3	4.5E-01	-0.2	6.8E-01
ENSMUST00000003964	glycogen synthase 1, muscle [Source:MGI Symbol;Acc:MGI:101805]		Q9Z1E4	-3.2	9.2E-04	-2.0	4.1E-01	1.8	2.5E-01	-0.2	9.2E-01
ENSMUST00000004036	ephrin B3 [Source:MGI Symbol;Acc:MGI:109196]	Q543Q7	O35393	5.2	3.3E-04	-6.8	7.3E-05	0.2	6.6E-01	0.8	4.5E-01
ENSMUST00000004051	hepatic leukemia factor [Source:MGI Symbol;Acc:MGI:96108]		Q8BW74	2.6	6.0E-03	-4.8	6.6E-04	-1.0	4.5E-02	-0.8	4.7E-01
ENSMUST00000004054	karyopherin (importin) alpha 1 [Source:MGI Symbol;Acc:MGI:103560]		Q60960	-5.0	8.4E-05	-1.5	4.5E-02	-0.2	6.6E-01	-1.1	1.5E-01
ENSMUST00000003961	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3 [Source:MGI Symbol;Ac	B8QI35	P60469	2.9	3.0E-01	3.2	2.5E-01	-0.5	8.6E-01	-0.8	7.1E-01
ENSMUST00000004055	DAZ interacting protein 1 [Source:MGI Symbol;Acc:MGI:1914311]		Q8BMD2	5.1	5.8E-04	-0.7	4.3E-01	1.8	8.6E-03	-0.7	3.9E-01
ENSMUST00000003981	interleukin 7 receptor [Source:MGI Symbol;Acc:MGI:96562]		P16872	0.4	3.4E-01	-0.6	2.4E-01	-1.2	6.1E-03	-0.3	5.5E-01
ENSMUST00000004057	family with sequence similarity 162, member A [Source:MGI Symbol;Acc:MGI:1917436]		Q9D6U8	-4.9	9.4E-06	5.3	2.4E-03	0.1	9.4E-01	0.0	9.6E-01
ENSMUST00000004050	monocyte to macrophage differentiation-associated [Source:MGI Symbol;Acc:MGI:1914718]		Q9CQY7	-2.0	4.2E-02	-2.5	6.1E-02	-0.4	5.6E-01	0.1	9.5E-01
ENSMUST00000004072	ribosomal protein L8 [Source:MGI Symbol;Acc:MGI:1350927]		P62918	-5.5	8.7E-06	3.0	8.9E-03	0.7	3.7E-01	0.3	6.7E-01
ENSMUST00000004076	glutamate receptor, metabotropic 3 [Source:MGI Symbol;Acc:MGI:1351340]		Q9QYS2	6.8	3.8E-05	-1.8	5.0E-02	0.8	1.4E-01	-2.4	2.5E-02
ENSMUST00000004094	single-stranded DNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1914220]	Q540I3	Q9CYZ8	3.9	4.6E-04	1.0	3.3E-01	-3.6	4.8E-03	0.5	5.4E-01
ENSMUST00000004136	glutathione S-transferase, mu 3 [Source:MGI Symbol;Acc:MGI:106026]		P19639	7.0	8.4E-05	-5.4	3.2E-05	-1.1	1.1E-02	-0.6	3.9E-01
ENSMUST00000004137	glutathione S-transferase, mu 7 [Source:MGI Symbol;Acc:MGI:1915562]		Q80W21	4.3	1.7E-03	-4.8	1.3E-04	0.4	3.2E-01	-0.3	7.3E-01
ENSMUST00000004140	glutathione S-transferase, mu 1 [Source:MGI Symbol;Acc:MGI:95860]		P10649	-2.8	3.9E-03	7.2	1.0E-04	0.4	7.0E-01	0.0	9.8E-01
ENSMUST00000004143	signal transducer and activator of transcription 5B [Source:MGI Symbol;Acc:MGI:103035]		P42232	-6.7	6.1E-04	4.1	1.3E-03	-0.2	8.0E-01	-0.3	6.2E-01
ENSMUST00000004097	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	E9QKE9		-0.5	3.6E-01	-0.4	6.2E-01	0.8	1.3E-01	0.7	3.1E-01
ENSMUST00000004120	Fanconi anemia, complementation group L [Source:MGI Symbol;Acc:MGI:1914280]		Q9CR14	1.2	8.0E-02	1.2	1.0E-01	-0.8	2.2E-01	-0.8	2.0E-01
ENSMUST00000004134	glutathione S-transferase, mu 5 [Source:MGI Symbol;Acc:MGI:1309466]		P48774	0.1	9.5E-01	-0.8	4.4E-01	-2.3	3.3E-02	-1.4	2.0E-01
ENSMUST00000004145	signal transducer and activator of transcription 5A [Source:MGI Symbol;Acc:MGI:103036]	Q9JIA0	P42230	7.5	3.1E-04	6.8	2.1E-04	-0.5	6.8E-01	-0.3	6.5E-01
ENSMUST00000004156	mitogen-activated protein kinase kinase kinase 11 [Source:MGI Symbol;Acc:MGI:1346880]		Q80XI6	-3.5	7.2E-04	5.8	1.2E-03	1.2	3.5E-01	-0.3	6.7E-01
ENSMUST00000004172	heme oxygenase 2 [Source:MGI Symbol;Acc:MGI:109373]	Q544R7	O70252	-6.8	2.8E-05	-0.8	3.6E-01	0.7	2.4E-01	-1.2	1.9E-01
ENSMUST00000004200	CWC15 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913320]		Q9JHS9	-5.5	7.8E-07	-6.3	5.5E-03	0.7	3.1E-01	0.2	9.0E-01
ENSMUST00000004201	collagen, type V, alpha 3 [Source:MGI Symbol;Acc:MGI:1858212]	Q9JLI2		5.9	6.7E-06	2.1	1.5E-01	-4.3	1.5E-02	1.0	3.1E-01
ENSMUST00000004202	DNA methyltransferase (cytosine-5) 1 [Source:MGI Symbol;Acc:MGI:94912]		P13864	-1.8	1.9E-03	-2.0	3.5E-02	1.1	5.3E-02	-0.3	7.4E-01
ENSMUST00000004206	eukaryotic translation initiation factor 3, subunit G [Source:MGI Symbol;Acc:MGI:1858258]	Q544H0	Q9Z1D1	-2.2	8.0E-03	-5.5	1.6E-04	-0.5	2.5E-01	-1.8	1.2E-01
ENSMUST00000004173	cell death inducing Trp53 target 1 [Source:MGI Symbol;Acc:MGI:1913876]		Q9DB75	1.3	1.6E-01	1.2	2.9E-01	0.2	8.7E-01	0.3	7.7E-01
ENSMUST00000004208	angiopoietin-like 2 [Source:MGI Symbol;Acc:MGI:1347002]		Q9R045	3.9	7.1E-05	-6.4	2.1E-06	-0.5	8.1E-02	0.3	5.7E-01
ENSMUST00000004222	histone cell cycle regulation defective homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:99430]		Q61666	-1.7	8.9E-03	3.6	3.2E-04	-2.7	2.3E-03	-0.4	4.1E-01
ENSMUST00000004294	kinesin family member C2 [Source:MGI Symbol;Acc:MGI:109187]	G3X8Q6		3.1	6.0E-03	-1.3	4.6E-02	1.0	1.9E-02	0.5	3.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000004203	peter pan homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2178445]		Q91YU8	-1.6	1.9E-01	-0.7	5.9E-01	0.4	6.4E-01	-0.4	7.6E-01
ENSMUST00000004326	plexin A3 [Source:MGI Symbol;Acc:MGI:107683]		P70208	6.8	1.3E-04	-2.6	1.4E-02	0.1	7.7E-01	0.5	5.5E-01
ENSMUST00000004327	glucose-6-phosphate dehydrogenase X-linked [Source:MGI Symbol;Acc:MGI:105979]	Q790Y8	Q00612	-8.5	2.9E-08	0.3	5.7E-01	-3.9	3.1E-05	-0.4	4.9E-01
ENSMUST00000004214	calcium channel, voltage-dependent, R type, alpha 1E subunit [Source:MGI Symbol;Acc:MGI:106217]	E9QK20		1.9	3.7E-01	1.3	5.7E-01	-2.6	2.2E-01	-1.9	3.6E-01
ENSMUST00000004343	tryptophanyl tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1917810]		Q9CYK1	4.4	7.2E-05	-0.3	6.9E-01	1.1	3.8E-02	-0.3	6.1E-01
ENSMUST00000004281	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 [Source:MGI Symbol;Acc:MGI:1330301]		Q5U4C9	0.3	4.8E-01	0.1	8.2E-01	0.2	6.4E-01	0.4	4.9E-01
ENSMUST00000004375	prohibitin 2 [Source:MGI Symbol;Acc:MGI:102520]	Q3V235	O35129	-7.4	3.2E-05	3.3	1.2E-02	0.0	9.8E-01	-0.1	8.6E-01
ENSMUST00000004316	prosaposin [Source:MGI Symbol;Acc:MGI:97783]	K3W4L3		-1.9	5.9E-01	0.3	9.4E-01	-1.3	6.4E-01	-3.5	3.4E-01
ENSMUST00000004377	protein tyrosine phosphatase, non-receptor type 6 [Source:MGI Symbol;Acc:MGI:96055]	Q3UCJ0	P29351	-3.7	2.2E-03	4.0	3.2E-03	-2.9	2.5E-02	0.0	9.5E-01
ENSMUST00000004378	enolase 2, gamma neuronal [Source:MGI Symbol;Acc:MGI:95394]	Q545V3	P17183	5.9	9.6E-03	-7.4	8.2E-07	0.9	5.2E-03	-0.2	7.2E-01
ENSMUST00000004330	inhibitor of kappaB kinase gamma [Source:MGI Symbol;Acc:MGI:1338074]	Q7TSS3		-0.8	7.4E-01	-1.9	6.0E-01	0.3	9.1E-01	1.4	6.7E-01
ENSMUST00000004379	EMG1 nucleolar protein homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1315195]	Q542P8	O35130	-6.8	1.4E-04	3.1	2.2E-03	-1.1	1.6E-01	0.3	6.1E-01
ENSMUST00000004381	lysophosphatidylcholine acyltransferase 3 [Source:MGI Symbol;Acc:MGI:1315211]		Q91V01	-5.8	9.5E-06	-6.3	3.7E-04	0.7	1.2E-01	-0.4	7.7E-01
ENSMUST00000004389	gene rich cluster, C10 gene [Source:MGI Symbol;Acc:MGI:1315201]		O35127	-3.8	1.2E-04	-1.3	2.0E-01	0.8	2.1E-01	-1.5	1.7E-01
ENSMUST00000004392	interferon regulatory factor 5 [Source:MGI Symbol;Acc:MGI:1350924]	Q3U169	P56477	-7.1	9.3E-04	3.3	1.2E-01	-2.4	2.6E-01	0.2	9.0E-01
ENSMUST00000004396	ATPase, H+ transporting, lysosomal V1 subunit F [Source:MGI Symbol;Acc:MGI:1913394]		Q9D1K2	-7.0	1.1E-06	-7.3	1.4E-04	-1.0	5.1E-02	-0.5	7.0E-01
ENSMUST00000004470	UTP20, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1917933	E9QK83		2.4	1.7E-03	-6.6	7.1E-04	1.5	5.6E-03	2.3	1.1E-01
ENSMUST00000004473	Spi-C transcription factor (Spi-1/PU.1 related) [Source:MGI Symbol;Acc:MGI:1341168]		Q6P3D7	6.5	1.4E-06	-3.0	1.8E-03	-0.7	1.1E-01	-1.5	6.4E-02
ENSMUST00000004480	somatostatin [Source:MGI Symbol;Acc:MGI:98326]	Q545V6	P60041	6.2	2.2E-03	-6.7	1.7E-03	0.5	4.8E-01	0.0	1.0E+00
ENSMUST00000004505	NPC1-like 1 [Source:MGI Symbol;Acc:MGI:2685089]	Z4YJC9		8.5	1.3E-05	-6.2	1.3E-05	-0.5	1.4E-01	-1.3	1.1E-01
ENSMUST00000004428	chloride channel, voltage-sensitive 5 [Source:MGI Symbol;Acc:MGI:99486]		Q9WVD4	-1.3	5.1E-02	0.0	9.5E-01	0.8	1.5E-01	-0.6	4.6E-01
ENSMUST00000004508	transmembrane emp24 protein transport domain containing 4 [Source:MGI Symbol;Acc:MGI:1915070]		Q8R1V4	-3.1	1.7E-04	1.6	3.4E-02	-1.0	1.1E-01	-0.2	7.5E-01
ENSMUST00000004554	ribosomal protein S5 [Source:MGI Symbol;Acc:MGI:1097682]	Q91V55		-9.1	1.8E-04	6.3	4.0E-06	-0.6	3.4E-01	-0.4	3.1E-01
ENSMUST00000004560	BH3 interacting domain death agonist [Source:MGI Symbol;Acc:MGI:108093]		P70444	-6.7	6.1E-05	4.8	1.7E-02	-0.6	7.5E-01	0.8	4.7E-01
ENSMUST00000004494	transcriptional regulator, SIN3B (yeast) [Source:MGI Symbol;Acc:MGI:107158]		Q62141	-0.4	5.2E-01	0.6	4.5E-01	0.9	1.6E-01	-0.1	8.8E-01
ENSMUST00000004497	like-glycosyltransferase [Source:MGI Symbol;Acc:MGI:1342270]	Q059X9	Q9Z1M7	0.9	6.2E-01	1.0	6.9E-01	0.8	6.9E-01	0.7	7.3E-01
ENSMUST00000004565	v-ral simian leukemia viral oncogene homolog B (ras related) [Source:MGI Symbol;Acc:MGI:1927244]		Q9JIW9	-5.1	5.1E-06	7.9	3.3E-05	-1.1	3.4E-01	-0.5	3.0E-01
ENSMUST00000004507	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 [Source:MGI Symbol;Acc:MGI:1277172]	Q5SVX3	Q9D0R4	-0.6	2.6E-01	-0.6	4.2E-01	0.0	9.6E-01	-0.1	9.0E-01
ENSMUST00000004574	DnaJ (Hsp40) homolog, subfamily B, member 11 [Source:MGI Symbol;Acc:MGI:1915088]		Q99KV1	-5.6	3.0E-05	-2.7	2.4E-03	0.7	8.8E-02	0.3	6.7E-01
ENSMUST00000004587	C-type lectin domain family 11, member a [Source:MGI Symbol;Acc:MGI:1298219]		O88200	4.1	3.3E-04	-10.6	1.1E-03	-1.0	1.7E-01	0.5	8.5E-01
ENSMUST00000004614	zinc finger protein 110 [Source:MGI Symbol;Acc:MGI:1890378]			-2.5	4.2E-03	-4.5	2.5E-03	0.3	5.4E-01	-1.9	1.5E-01
ENSMUST00000004622	growth factor receptor bound protein 2-associated protein 2 [Source:MGI Symbol;Acc:MGI:1333854]	Q3ZB57		-2.3	6.4E-04	-3.9	2.4E-04	0.9	2.5E-02	-0.3	6.9E-01
ENSMUST00000004646	coronin, actin binding protein 1C [Source:MGI Symbol;Acc:MGI:1345964]	Q499X7	Q9WUM4	-6.1	1.6E-03	-7.1	6.9E-04	0.7	1.6E-01	2.2	1.5E-01
ENSMUST00000004576	TBCC domain containing 1 [Source:MGI Symbol;Acc:MGI:1917823]		Q640P7	-0.3	5.5E-01	-0.8	2.1E-01	0.0	9.5E-01	0.5	4.1E-01
ENSMUST00000004655	pregnancy specific glycoprotein 17 [Source:MGI Symbol;Acc:MGI:1347250]	Q62056		6.6	4.8E-05	4.5	3.4E-04	-0.1	8.8E-01	-0.6	3.8E-01
ENSMUST00000004657	pregnancy specific glycoprotein 19 [Source:MGI Symbol;Acc:MGI:1347252]	Q4KL31		8.3	6.0E-05	-2.5	1.5E-02	-0.3	5.0E-01	-0.4	6.8E-01
ENSMUST00000004683	mucolipin 1 [Source:MGI Symbol;Acc:MGI:1890498]		Q99J21	-5.1	4.7E-04	-1.6	2.0E-02	0.5	2.0E-01	-0.2	7.3E-01
ENSMUST00000004634	te carrier family 1 (glutamate/neutral amino acid transporter), member 4 [Source:MGI Symbol;Acc:MGI:2135	Q5SSP3		3.8	1.7E-01	1.2	6.3E-01	-3.1	2.4E-01	-0.6	8.0E-01
ENSMUST00000004684	rho/rac guanine nucleotide exchange factor (GEF) 18 [Source:MGI Symbol;Acc:MGI:2142567]		Q6P9R4	-8.2	6.5E-05	-3.8	4.8E-02	0.7	3.8E-01	-1.6	4.0E-01
ENSMUST00000004686	peroxisomal biogenesis factor 11 gamma [Source:MGI Symbol;Acc:MGI:1920905]		Q6P6M5	1.6	1.1E-02	4.3	1.6E-04	-3.3	3.9E-03	-1.0	9.7E-02
ENSMUST00000004715	motile sperm domain containing 2 [Source:MGI Symbol;Acc:MGI:1924013]	B1AU74		-5.2	5.8E-04	6.7	3.6E-04	-1.5	2.9E-01	0.1	9.3E-01
ENSMUST00000004673	N-myc downstream regulated gene 2 [Source:MGI Symbol;Acc:MGI:1352498]		Q9QYG0	5.7	5.3E-02	3.5	3.7E-01	1.2	7.2E-01	3.3	2.9E-01
ENSMUST00000004681	patatin-like phospholipase domain containing 6 [Source:MGI Symbol;Acc:MGI:1354723]		Q3TRM4	-0.5	7.6E-01	-1.6	4.0E-01	-0.2	8.8E-01	0.9	6.1E-01
ENSMUST00000004728	CD33 antigen [Source:MGI Symbol;Acc:MGI:99440]		Q63994	-7.3	5.3E-04	-2.9	2.5E-02	0.9	1.3E-01	-1.3	3.1E-01
ENSMUST00000004729	electron transferring flavoprotein, beta polypeptide [Source:MGI Symbol;Acc:MGI:106098]		Q9DCW4	-4.0	2.8E-05	-7.0	2.3E-03	1.1	5.8E-02	-0.1	9.7E-01
ENSMUST00000004745	syntaxin binding protein 2 [Source:MGI Symbol;Acc:MGI:107370]	F8WGM5		-11.2	5.7E-06	2.2	7.2E-03	0.2	7.6E-01	-0.4	4.3E-01
ENSMUST00000004770	tyrosinase [Source:MGI Symbol;Acc:MGI:98880]	Q91XK0	P11344	4.6	7.5E-04	-5.1	1.8E-03	-0.3	5.6E-01	-0.4	7.6E-01
ENSMUST00000004774	aquaporin 1 [Source:MGI Symbol;Acc:MGI:103201]		Q02013	3.2	1.0E-02	-5.5	5.2E-03	0.0	9.6E-01	-1.8	3.1E-01
ENSMUST00000004780	AT rich interactive domain 3B (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1930768]		Q9Z1N7	-4.8	9.5E-03	-4.0	1.4E-04	0.0	9.7E-01	0.1	9.1E-01
ENSMUST00000004784	calponin 2 [Source:MGI Symbol;Acc:MGI:105093]	Q543F3	Q08093	-5.9	7.7E-06	-9.6	1.3E-04	0.9	4.8E-02	-0.7	6.9E-01
ENSMUST00000004756	WW domain-containing oxidoreductase [Source:MGI Symbol;Acc:MGI:1931237]		Q91WL8	-0.5	4.5E-01	-0.6	4.7E-01	0.1	8.6E-01	0.2	7.7E-01
ENSMUST00000004786	polymerase (RNA) II (DNA directed) polypeptide E [Source:MGI Symbol;Acc:MGI:1913670]	Q3V214	Q80UW8	-6.3	7.6E-04	6.0	1.1E-03	0.3	7.8E-01	-1.0	1.8E-01
ENSMUST00000004829	CD244 natural killer cell receptor 2B4 [Source:MGI Symbol;Acc:MGI:109294]		Q07763	-3.8	8.7E-03	1.6	1.5E-01	-2.1	5.3E-02	-0.5	5.7E-01
ENSMUST00000004868	mitochondrial fission process 1 [Source:MGI Symbol;Acc:MGI:1916686]		Q9CRB8	2.9	4.1E-03	-6.0	4.6E-02	0.8	4.0E-01	2.0	4.7E-01
ENSMUST00000004892	RAB11A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1858202]	F8WGS1		-5.7	3.0E-03	-4.4	3.9E-04	1.1	1.6E-02	-0.4	6.6E-01
ENSMUST00000004910	eukaryotic translation initiation factor 2B, subunit 2 beta [Source:MGI Symbol;Acc:MGI:2145118]		Q99LD9	-4.5	1.0E-04	-6.7	5.7E-04	-0.6	3.3E-01	-0.1	9.4E-01
ENSMUST00000004827	lymphocyte antigen 9 [Source:MGI Symbol;Acc:MGI:96885]	E9PX73		-4.3	5.6E-02	-6.1	3.5E-02	-2.3	6.0E-02	-0.4	8.7E-01
ENSMUST00000004913	placental growth factor [Source:MGI Symbol;Acc:MGI:105095]	Q544A5	P49764	5.6	3.0E-04	-6.9	3.4E-03	-0.4	6.1E-01	2.7	1.6E-01
ENSMUST00000004850	adhesion G protein-coupled receptor E1 [Source:MGI Symbol;Acc:MGI:106912]	Q3U9R0	Q61549	-3.3	5.7E-02	-4.9	3.4E-02	-1.6	1.5E-01	0.1	9.8E-01
ENSMUST00000004920	unc-51 like kinase 2 [Source:MGI Symbol;Acc:MGI:1352758]		Q9QY01	-2.6	8.9E-04	5.1	4.8E-04	1.0	3.0E-01	-1.2	1.2E-01
ENSMUST00000004949	TNF receptor-associated factor 6 [Source:MGI Symbol;Acc:MGI:108072]		P70196	-1.0	3.0E-02	-7.6	3.1E-03	-1.5	4.0E-02	0.4	8.6E-01
ENSMUST00000004964	POU domain, class 1, transcription factor 1 [Source:MGI Symbol;Acc:MGI:97588]	F8WGJ8		5.3	2.3E-04	-1.9	4.5E-02	1.3	2.6E-02	-1.3	1.7E-01
ENSMUST00000004965	charged multivesicular body protein 2B [Source:MGI Symbol;Acc:MGI:1916192]		Q8BJF9	-4.2	2.4E-05	5.5	7.3E-04	-0.6	6.1E-01	-0.5	4.6E-01
ENSMUST00000004968	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 [Source:MGI Symbol;Acc:MGI:1347008]		Q9R0E1	-3.9	5.6E-04	-1.0	1.8E-01	1.6	7.9E-03	0.0	9.5E-01
ENSMUST00000004936	chemokine (C-C motif) ligand 24 [Source:MGI Symbol;Acc:MGI:1928953]	Q3U0A4	Q9JKC0	-0.5	4.0E-01	-4.5	1.4E-04	-3.8	1.4E-05	0.2	8.1E-01
ENSMUST00000004986	mitogen-activated protein kinase 13 [Source:MGI Symbol;Acc:MGI:1346864]	Q3UIB2	Q9Z1B7	-6.6	2.5E-05	-0.1	7.8E-01	0.7	6.5E-02	-0.1	8.3E-01
ENSMUST00000004959	GRB2-related adaptor protein [Source:MGI Symbol;Acc:MGI:1918770]		Q9CX99	0.7	2.1E-01	1.6	3.3E-02	-0.1	8.5E-01	-1.0	1.2E-01
ENSMUST00000004990	mitogen-activated protein kinase 14 [Source:MGI Symbol;Acc:MGI:1346865]	Q5U421	P47811	-5.0	5.9E-05	4.9	1.7E-03	0.2	8.9E-01	0.6	4.1E-01
ENSMUST00000004994	paired box 3 [Source:MGI Symbol;Acc:MGI:97487]	Q8BRF1		6.0	1.3E-03	-3.1	1.3E-03	1.1	1.4E-02	0.1	9.2E-01
ENSMUST00000005003	lamin B receptor [Source:MGI Symbol;Acc:MGI:2138281]		Q3U9G9	-7.3	1.6E-06	-2.8	1.5E-02	0.8	1.4E-01	-0.4	7.2E-01
ENSMUST00000004985	bromodomain and PHD finger containing, 3 [Source:MGI Symbol;Acc:MGI:2146836]	B2KF05		-1.3	3.6E-02	0.0	9.6E-01	0.7	1.8E-01	-0.7	3.4E-01
ENSMUST00000005015	papillary renal cell carcinoma (translocation-associated) [Source:MGI Symbol;Acc:MGI:2137738]	Q9EQC8		-1.9	7.6E-03	-6.1	1.0E-03	1.6	9.0E-03	1.1	4.3E-01
ENSMUST00000004987	serine/arginine-rich protein specific kinase 1 [Source:MGI Symbol;Acc:MGI:106908]	F8WGJ7		-3.4	3.9E-02	-3.8	5.8E-02	-0.9	3.1E-01	-0.5	8.0E-01
ENSMUST00000005017	hepatoma-derived growth factor [Source:MGI Symbol;Acc:MGI:1194494]		P51859	-3.4	2.9E-04	-7.3	5.3E-04	0.2	6.3E-01	2.5	1.1E-01
ENSMUST00000005019	cellular retinoic acid binding protein II [Source:MGI Symbol;Acc:MGI:88491]		P22935	5.6	1.1E-03	6.2	3.7E-04	-1.7	2.1E-01	-2.0	3.5E-02
ENSMUST00000005041	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 [Source:MGI Symbol;Acc:MGI:98886]		P26369	-2.6	9.1E-04	-7.7	2.7E-05	0.7	5.4E-02	1.1	3.0E-01
ENSMUST00000005053	transmembrane protein 242 [Source:MGI Symbol;Acc:MGI:1917794]		Q8VCR3	-3.1	4.6E-04	-0.9	2.2E-01	1.2	2.9E-02	0.3	6.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000005057	thimet oligopeptidase 1 [Source:MGI Symbol;Acc:MGI:1354165]			1.9	1.6E-02	-2.5	9.2E-03	0.6	1.9E-01	-0.4	6.3E-01
ENSMUST00000005064	protein inhibitor of activated STAT 4 [Source:MGI Symbol;Acc:MGI:2136940]	Q3ULQ6	Q9JM05	-3.7	1.2E-03	1.9	6.9E-02	-4.0	6.5E-03	-0.3	7.2E-01
ENSMUST00000005066	mitogen-activated protein kinase kinase 1 [Source:MGI Symbol;Acc:MGI:1346866]	Q3TMJ8	P31938	-5.2	4.2E-06	-1.4	6.9E-02	0.9	5.5E-02	-0.2	7.5E-01
ENSMUST00000005051	lactate dehydrogenase A [Source:MGI Symbol;Acc:MGI:96759]	G5E8N5		1.8	5.9E-02	3.2	3.5E-02	1.4	2.6E-01	0.0	9.9E-01
ENSMUST00000005067	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha [Source:MGI Symbol;Acc:MGI:1098703		Q8BJU0	-3.4	4.4E-04	-2.1	1.3E-02	-0.5	2.8E-01	-1.5	6.5E-02
ENSMUST00000005069	nicotinamide riboside kinase 2 [Source:MGI Symbol;Acc:MGI:1916814]		Q9D7C9	6.6	3.7E-05	1.5	7.1E-02	-0.9	2.0E-01	-0.4	5.2E-01
ENSMUST00000005073	zona pellucida glycoprotein 3 [Source:MGI Symbol;Acc:MGI:99215]		P10761	6.6	9.5E-05	-1.8	7.4E-02	0.8	2.0E-01	-1.1	2.7E-01
ENSMUST00000005077	heat shock protein 1 [Source:MGI Symbol;Acc:MGI:96240]	Q545F4	P14602	4.7	5.3E-03	-3.8	2.3E-04	1.0	1.5E-02	-0.4	5.5E-01
ENSMUST00000005103	nuclear factor, erythroid derived 2, like 3 [Source:MGI Symbol;Acc:MGI:1339958]	Q3UZC1	Q9WTM4	3.1	5.8E-03	-2.1	2.5E-02	1.0	4.5E-02	-0.2	8.4E-01
ENSMUST00000005114	FXYD domain-containing ion transport regulator 4 [Source:MGI Symbol;Acc:MGI:1889005]		Q9D2W0	3.6	1.1E-03	5.6	5.4E-04	-0.8	4.4E-01	0.2	7.8E-01
ENSMUST00000005120	coiled-coil domain containing 130 [Source:MGI Symbol;Acc:MGI:1914986]		Q9D516	-5.7	8.4E-05	6.3	2.6E-04	-0.5	6.6E-01	-0.2	7.5E-01
ENSMUST00000005164	protein kinase, cAMP dependent, catalytic, beta [Source:MGI Symbol;Acc:MGI:97594]		P68181	-3.0	8.4E-03	0.8	4.2E-01	-5.3	1.9E-03	-1.3	1.6E-01
ENSMUST00000005175	chromodomain helicase DNA binding protein 5 [Source:MGI Symbol;Acc:MGI:3036258]		A2A8L1	8.3	3.7E-03	3.1	1.2E-02	-0.2	8.6E-01	-0.2	8.0E-01
ENSMUST00000005108	lysine (K)-specific demethylase 5A [Source:MGI Symbol;Acc:MGI:2136980]	E9Q8F1	Q3UXZ9	3.7	3.2E-01	5.6	1.6E-01	-0.5	9.0E-01	-2.4	3.3E-01
ENSMUST00000005185	cystatin B [Source:MGI Symbol;Acc:MGI:109514]		Q62426	-7.3	2.2E-05	3.4	2.7E-03	-1.3	1.3E-01	-1.2	1.2E-01
ENSMUST00000005233	eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427]	A2AUM0		-3.3	2.9E-03	-2.9	6.5E-03	0.1	7.9E-01	-2.7	2.4E-02
ENSMUST00000005234	WD repeat domain 1 [Source:MGI Symbol;Acc:MGI:1337100]	Q3TJY2	O88342	-6.1	4.0E-07	-2.6	3.5E-02	-0.7	2.8E-01	-1.2	3.1E-01
ENSMUST00000005173	N-sulfoglucosamine sulfohydrolase (sulfamidase) [Source:MGI Symbol;Acc:MGI:1350341]	Q9EQ08		-3.6	9.3E-02	0.5	8.4E-01	1.8	3.5E-01	-2.3	3.4E-01
ENSMUST00000005255	WNT1 inducible signaling pathway protein 1 [Source:MGI Symbol;Acc:MGI:1197008]	Q3UFJ5	O54775	5.1	6.5E-05	6.0	3.4E-02	-0.3	9.1E-01	2.0	1.8E-01
ENSMUST00000005256	N-myc downstream regulated gene 1 [Source:MGI Symbol;Acc:MGI:1341799]	Q545R3	Q62433	-2.9	2.1E-03	-6.0	2.3E-04	-0.6	2.2E-01	-1.9	1.2E-01
ENSMUST00000005188	SH2B adaptor protein 2 [Source:MGI Symbol;Acc:MGI:1345171]		Q9JID9	1.4	7.4E-02	2.3	4.1E-02	0.8	3.4E-01	0.0	9.8E-01
ENSMUST00000005218	CD44 antigen [Source:MGI Symbol;Acc:MGI:88338]	A2APM2		-2.7	7.2E-02	-6.0	6.3E-02	-0.2	8.6E-01	3.1	3.0E-01
ENSMUST00000005292	peroxiredoxin 2 [Source:MGI Symbol;Acc:MGI:109486]		Q61171	-5.4	1.5E-03	-3.3	1.1E-02	0.4	4.6E-01	0.5	6.7E-01
ENSMUST00000005334	sex hormone binding globulin [Source:MGI Symbol;Acc:MGI:98295]		P97497	6.8	4.9E-04	-5.0	1.8E-05	0.9	9.8E-03	-0.2	7.1E-01
ENSMUST00000005336	SUMO/sentrin specific peptidase 3 [Source:MGI Symbol;Acc:MGI:2158736]		Q9EP97	-5.0	2.0E-03	4.2	3.9E-04	-1.2	1.2E-01	-0.4	5.0E-01
ENSMUST00000005352	corin [Source:MGI Symbol;Acc:MGI:1349451]		Q9Z319	7.5	8.9E-05	-1.8	6.7E-02	0.9	1.2E-01	-0.2	8.5E-01
ENSMUST00000005279	Kruppel-like factor 5 [Source:MGI Symbol;Acc:MGI:1338056]		Q9Z0Z7	-0.7	2.2E-01	-0.3	6.8E-01	1.1	4.8E-02	0.8	2.9E-01
ENSMUST00000005365	C25, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:19136		Q3UA16	-2.9	1.0E-02	-6.6	2.4E-03	-1.3	4.9E-02	-0.1	9.4E-01
ENSMUST00000005371	transformation related protein 53 [Source:MGI Symbol;Acc:MGI:98834]		P02340	-3.5	1.2E-02	4.8	8.5E-03	-0.6	6.9E-01	1.3	1.8E-01
ENSMUST00000005394	ubiquitin fusion degradation 1 like [Source:MGI Symbol;Acc:MGI:109353]		P70362	-1.9	6.6E-03	-2.1	1.6E-01	1.1	1.9E-01	-1.8	2.3E-01
ENSMUST00000005399	zinc finger protein 287 [Source:MGI Symbol;Acc:MGI:2176561]	Q5SVS9		6.3	1.8E-04	7.6	1.5E-04	-0.6	6.3E-01	-0.7	3.1E-01
ENSMUST00000005364	glucose-6-phosphatase, catalytic, 2 [Source:MGI Symbol;Acc:MGI:1277193]		Q9Z186	3.5	1.4E-01	6.1	2.8E-02	-0.3	9.2E-01	-2.9	8.1E-02
ENSMUST00000005406	amyloid beta (A4) precursor protein [Source:MGI Symbol;Acc:MGI:88059]	Q6GR78	P12023	-5.7	6.2E-07	-1.4	1.5E-01	0.1	9.2E-01	-1.4	1.8E-01
ENSMUST00000005413	zinc finger protein 112 [Source:MGI Symbol;Acc:MGI:1929115]		Q0VAW7	7.0	4.8E-05	-0.6	6.3E-01	1.4	1.7E-01	-1.4	3.0E-01
ENSMUST00000005431	leucine zipper-EF-hand containing transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1932557]		Q9Z2I0	-1.0	2.6E-02	-1.1	1.1E-01	0.2	6.4E-01	-0.5	4.5E-01
ENSMUST00000005452	fibroblast growth factor receptor 4 [Source:MGI Symbol;Acc:MGI:95525]			7.3	1.2E-05	4.8	3.4E-03	-0.6	6.4E-01	0.9	2.7E-01
ENSMUST00000005477	cytochrome P450, family 2, subfamily b, polypeptide 10 [Source:MGI Symbol;Acc:MGI:88598]	G3X8Q9		4.2	1.6E-02	-5.0	1.8E-05	0.7	3.4E-02	-0.1	9.3E-01
ENSMUST00000005487	thioredoxin 2 [Source:MGI Symbol;Acc:MGI:1929468]		P97493	-6.9	3.7E-04	5.2	9.7E-04	-1.2	2.8E-01	0.5	4.5E-01
ENSMUST00000005488	caspase 14 [Source:MGI Symbol;Acc:MGI:1335092]	Q542Q1	O89094	7.2	3.1E-05	-0.3	6.3E-01	0.8	5.9E-02	0.0	9.7E-01
ENSMUST00000005490	carrier family 1 (high affinity aspartate/glutamate transporter), member 6 [Source:MGI Symbol;Acc:MGI:109	B2RQX4	O35544	7.4	3.5E-05	7.9	2.2E-05	0.1	9.3E-01	-0.5	3.0E-01
ENSMUST00000005493	lute carrier family 1 (glial high affinity glutamate transporter), member 3 [Source:MGI Symbol;Acc:MGI:9991	Q543U3	P56564	6.5	1.4E-04	4.4	4.9E-03	-2.5	1.0E-01	-2.8	2.1E-02
ENSMUST00000005504	F-box protein 11 [Source:MGI Symbol;Acc:MGI:2147134]		Q7TPD1	-5.1	5.7E-03	-4.2	6.4E-03	0.6	2.8E-01	-2.1	1.9E-01
ENSMUST00000005507	MLX interacting protein-like [Source:MGI Symbol;Acc:MGI:1927999]		Q99MZ3	4.7	1.0E-04	6.5	1.4E-04	-0.6	6.0E-01	0.2	7.6E-01
ENSMUST00000005532	nidogen 1 [Source:MGI Symbol;Acc:MGI:97342]		P10493	6.9	7.5E-07	6.7	1.6E-04	-0.5	6.5E-01	0.2	7.4E-01
ENSMUST00000005548	heme oxygenase 1 [Source:MGI Symbol;Acc:MGI:96163]	Q3U5U6	P14901	-5.7	6.8E-06	6.8	1.9E-04	-0.5	6.6E-01	-0.9	1.9E-01
ENSMUST00000005503	mutS homolog 6 (E. coli) [Source:MGI Symbol;Acc:MGI:1343961]		P54276	0.4	4.4E-01	0.2	7.2E-01	0.1	8.4E-01	0.2	6.8E-01
ENSMUST00000005606	protein kinase, cAMP dependent, catalytic, alpha [Source:MGI Symbol;Acc:MGI:97592]		P05132	-2.4	4.8E-03	-2.0	1.5E-01	0.1	9.0E-01	-3.0	9.2E-02
ENSMUST00000005607	anti-silencing function 1B histone chaperone [Source:MGI Symbol;Acc:MGI:1914179]		Q9DAP7	-2.7	9.1E-03	1.4	6.8E-02	-4.2	1.5E-04	-0.8	1.9E-01
ENSMUST00000005611	myosin, light chain 10, regulatory [Source:MGI Symbol;Acc:MGI:1891705]	E9QNY3		5.3	5.9E-04	3.4	2.6E-04	-3.0	5.8E-04	0.5	2.9E-01
ENSMUST00000005616	protein kinase N1 [Source:MGI Symbol;Acc:MGI:108022]		P70268	-7.6	8.5E-05	-4.8	1.2E-04	0.3	4.1E-01	-0.6	4.9E-01
ENSMUST00000005578	capicua homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1918972]	E9QP01		3.0	8.8E-02	4.8	1.6E-02	-0.5	7.6E-01	-2.3	9.8E-02
ENSMUST00000005583	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3 [Source:MGI Symbol;Acc:MGI:108414]	Q3TJC2	Q61205	-0.9	3.5E-01	-0.9	4.1E-01	-1.2	1.7E-01	-1.3	2.5E-01
ENSMUST00000005600	regulatory factor X, 1 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:105982]		P48377	-1.1	8.5E-02	-0.1	9.3E-01	0.7	2.0E-01	-0.3	6.5E-01
ENSMUST00000005601	interleukin 27 receptor, alpha [Source:MGI Symbol;Acc:MGI:1355318]		O70394	1.2	9.3E-02	1.0	2.1E-01	-0.8	2.5E-01	-0.6	4.3E-01
ENSMUST00000005620	DnaJ (Hsp40) homolog, subfamily B, member 1 [Source:MGI Symbol;Acc:MGI:1931874]	Q3TU79	Q9QYJ3	-1.6	2.9E-02	-1.9	6.8E-02	1.2	4.8E-02	0.7	4.6E-01
ENSMUST00000005630	mutS homolog 4 (E. coli) [Source:MGI Symbol;Acc:MGI:1860077]	A6H6D5	Q99MT2	5.0	6.3E-03	-0.9	4.1E-01	1.0	1.5E-01	-0.8	4.8E-01
ENSMUST00000005647	NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Source:MGI Symbol;Acc:MGI:1915599]		Q9DCT2	-4.1	3.6E-03	6.3	3.4E-04	-0.5	6.8E-01	-1.5	4.8E-02
ENSMUST00000005651	P450 (cytochrome) oxidoreductase [Source:MGI Symbol;Acc:MGI:97744]		P37040	-9.5	1.7E-04	-5.8	3.2E-03	1.3	3.5E-02	-0.5	7.5E-01
ENSMUST00000005669	cytochrome P450, family 2, subfamily b, polypeptide 13 [Source:MGI Symbol;Acc:MGI:88599]	A6H6J2		4.8	2.7E-04	-1.4	1.3E-01	0.5	3.2E-01	0.3	6.8E-01
ENSMUST00000005671	insulin-like growth factor I receptor [Source:MGI Symbol;Acc:MGI:96433]	E9QNX9		-2.3	4.4E-04	5.4	5.8E-03	-0.6	7.1E-01	-1.0	3.0E-01
ENSMUST00000005678	Fc receptor, IgE, low affinity II, alpha polypeptide [Source:MGI Symbol;Acc:MGI:95497]		P20693	4.6	1.3E-05	-4.1	9.7E-03	-0.4	4.9E-01	-0.5	7.4E-01
ENSMUST00000005685	cytochrome P450, family 2, subfamily a, polypeptide 5 [Source:MGI Symbol;Acc:MGI:88597]	Q91X75		5.0	5.2E-04	-8.8	1.1E-03	1.0	1.4E-01	0.4	8.6E-01
ENSMUST00000005705	tripartite motif-containing 28 [Source:MGI Symbol;Acc:MGI:109274]	Q5EBP9	Q62318	-5.5	6.6E-04	4.6	4.8E-04	-0.8	3.8E-01	-0.6	3.5E-01
ENSMUST00000005711	charged multivesicular body protein 2A [Source:MGI Symbol;Acc:MGI:1916203]		Q9DB34	-6.4	6.4E-07	-1.5	2.6E-02	0.8	5.5E-02	-0.1	8.8E-01
ENSMUST00000005714	ubiquitin-conjugating enzyme E2M [Source:MGI Symbol;Acc:MGI:108278]		P61082	-3.1	6.3E-03	3.4	2.8E-04	-1.4	3.4E-02	-0.2	7.2E-01
ENSMUST00000005749	9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1093		Q62018	-1.2	1.1E-02	4.6	5.0E-04	-2.1	5.8E-02	-1.7	2.1E-02
ENSMUST00000005692	ATPase, H+/K+ exchanging, gastric, alpha polypeptide [Source:MGI Symbol;Acc:MGI:88113]	E9QNX7		5.8	5.2E-02	5.6	7.9E-02	-0.8	8.1E-01	-0.6	7.6E-01
ENSMUST00000005751	MRV integration site 1 [Source:MGI Symbol;Acc:MGI:1338023]		Q9WUX5	9.4	2.0E-05	-2.7	4.4E-02	0.7	2.9E-01	-2.0	1.6E-01
ENSMUST00000005768	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha [Source:MGI Symbol;Acc:MGI:107929]	F8WI18		-6.4	5.9E-04	-6.6	3.2E-06	-0.7	2.5E-02	-0.5	4.7E-01
ENSMUST00000005791	calcium binding protein 5 [Source:MGI Symbol;Acc:MGI:1352746]	Q543X4	Q9JLK3	6.8	1.5E-04	-1.9	3.8E-02	-0.8	1.8E-01	-2.0	6.2E-02
ENSMUST00000005719	adenylate cyclase 9 [Source:MGI Symbol;Acc:MGI:108450]		P51830	1.4	5.4E-01	1.6	5.4E-01	0.7	7.5E-01	0.5	8.4E-01
ENSMUST00000005722	myocyte enhancer factor 2C [Source:MGI Symbol;Acc:MGI:99458]	A0A0H2UKB6		5.1	6.3E-02	1.4	4.6E-01	-5.1	5.3E-02	-1.4	4.1E-01
ENSMUST00000005798	sorting nexin 6 [Source:MGI Symbol;Acc:MGI:1919433]		Q6P8X1	-6.0	4.6E-06	-0.4	3.6E-01	0.5	1.3E-01	-0.2	6.2E-01
ENSMUST00000005810	drofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase [Source:MGI Symbol;A		P18155	-1.9	4.8E-03	5.2	1.0E-03	-4.4	6.8E-03	-0.2	7.6E-01
ENSMUST00000005817	ranslocase of outer mitochondrial membrane 40 homolog-like (yeast) [Source:MGI Symbol;Acc:MGI:3589112		Q9CZR3	5.4	1.9E-03	-4.8	3.5E-02	2.0	2.4E-02	0.4	8.5E-01
ENSMUST00000005826	citrate synthase [Source:MGI Symbol;Acc:MGI:88529]		Q9CZU6	-4.8	1.1E-05	8.2	1.2E-04	0.2	9.1E-01	-1.3	7.1E-02
ENSMUST00000005829	adenosine monophosphate deaminase 3 [Source:MGI Symbol;Acc:MGI:1096344]		O08739	-5.8	2.2E-03	-7.0	5.0E-05	-0.2	5.2E-01	0.7	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000005830	breast carcinoma amplified sequence 2 [Source:MGI Symbol;Acc:MGI:1915433]		Q9D287	-3.4	1.0E-02	-0.3	6.8E-01	1.0	5.3E-02	-0.6	3.5E-01
ENSMUST00000005815	kit oncogene [Source:MGI Symbol;Acc:MGI:96677]		P05532	-3.0	6.4E-02	-1.4	5.6E-01	2.7	1.5E-01	1.1	5.9E-01
ENSMUST00000005841	CCCTC-binding factor [Source:MGI Symbol;Acc:MGI:109447]		Q61164	-4.1	1.9E-04	2.9	2.4E-02	-2.6	6.0E-02	-0.1	9.1E-01
ENSMUST00000005825	PAN2 polyA specific ribonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1918984]		Q8BGF7	-1.2	1.1E-01	-0.2	8.2E-01	0.6	3.0E-01	-0.3	7.1E-01
ENSMUST00000005862	transcription factor AP4 [Source:MGI Symbol;Acc:MGI:103239]	Q9JIZ5		3.1	3.7E-03	-3.3	8.9E-04	0.9	2.7E-02	-0.6	3.8E-01
ENSMUST00000005889	vav 1 oncogene [Source:MGI Symbol;Acc:MGI:98923]	Q3U9E2	P27870	-5.9	1.7E-04	-2.8	1.5E-01	2.5	3.0E-02	-0.5	7.7E-01
ENSMUST00000005891	kallikrein related-peptidase 9 [Source:MGI Symbol;Acc:MGI:1921082]	Q32M27		7.8	1.5E-05	-1.9	6.6E-02	-1.2	8.1E-02	-2.7	4.2E-02
ENSMUST00000005923	proteasome (prosome, macropain) subunit, beta type 4 [Source:MGI Symbol;Acc:MGI:1098257]		P99026	-5.0	7.3E-06	-2.5	1.7E-02	1.1	4.4E-02	-0.6	5.4E-01
ENSMUST00000005933	kallikrein 1-related peptidase b16 [Source:MGI Symbol;Acc:MGI:891982]		P04071	7.1	5.8E-05	3.4	9.9E-03	0.9	3.7E-01	0.5	5.1E-01
ENSMUST00000005952	solute carrier family 30 (zinc transporter), member 4 [Source:MGI Symbol;Acc:MGI:1345282]		O35149	2.9	3.0E-04	-3.0	1.9E-02	1.1	8.9E-02	-1.8	1.5E-01
ENSMUST00000005953	sulfide quinone reductase-like (yeast) [Source:MGI Symbol;Acc:MGI:1929899]		Q9R112	-9.0	3.4E-05	5.9	1.2E-04	-1.9	9.0E-02	0.0	9.6E-01
ENSMUST00000005907	CD247 antigen [Source:MGI Symbol;Acc:MGI:88334]		P24161	0.3	6.2E-01	-0.5	5.1E-01	-0.8	1.4E-01	0.0	9.6E-01
ENSMUST00000005954	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin [Source:MGI Symbol;Acc:MGI:1927580]		Q9R0C0	-2.2	7.0E-03	-5.6	4.0E-05	-0.2	5.7E-01	0.3	6.7E-01
ENSMUST00000005964	alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI Symbol;Acc:MGI:87929]	Q6P5I3	P28474	-3.6	6.2E-05	6.5	2.1E-04	-0.6	6.1E-01	-0.1	9.1E-01
ENSMUST00000005975	G protein-coupled receptor 108 [Source:MGI Symbol;Acc:MGI:1925558]		Q91WD0	-3.0	2.4E-04	3.4	4.6E-04	0.0	9.8E-01	-0.4	3.6E-01
ENSMUST00000005976	tumor necrosis factor (ligand) superfamily, member 14 [Source:MGI Symbol;Acc:MGI:1355317]		Q9QYH9	-4.8	1.5E-05	-7.7	2.4E-04	0.1	7.7E-01	-1.2	4.5E-01
ENSMUST00000006005	parathyroid hormone 1 receptor [Source:MGI Symbol;Acc:MGI:97801]		P41593	5.8	2.1E-02	-0.5	5.5E-01	0.7	2.0E-01	-1.0	2.1E-01
ENSMUST00000006027	receptor accessory protein 5 [Source:MGI Symbol;Acc:MGI:1270152]	G3X8R0		-4.6	7.0E-06	-3.5	3.0E-04	-0.7	5.6E-02	-0.8	2.4E-01
ENSMUST00000006035	ERGIC and golgi 3 [Source:MGI Symbol;Acc:MGI:1913616]		Q9CQE7	-7.5	2.0E-04	-1.9	1.6E-02	0.8	7.0E-02	-0.4	5.9E-01
ENSMUST00000006046	thyrotropin releasing hormone [Source:MGI Symbol;Acc:MGI:98823]		Q62361	6.7	5.4E-05	-4.5	2.4E-04	0.4	3.3E-01	0.1	9.3E-01
ENSMUST00000006053	sphingomyelin phosphodiesterase 4 [Source:MGI Symbol;Acc:MGI:1924876]		Q6ZPR5	4.9	3.4E-02	2.4	3.9E-01	-0.8	7.5E-01	2.6	2.3E-01
ENSMUST00000006094	cytochrome P450, family 2, subfamily d, polypeptide 26 [Source:MGI Symbol;Acc:MGI:1923529]			4.7	4.0E-04	-3.9	1.5E-04	0.4	2.4E-01	-0.3	6.9E-01
ENSMUST00000006101	integrin alpha E, epithelial-associated [Source:MGI Symbol;Acc:MGI:1298377]		Q60677	3.1	1.6E-03	-4.7	2.6E-03	0.6	2.6E-01	-2.2	1.6E-01
ENSMUST00000006037	nuclear receptor coactivator 2 [Source:MGI Symbol;Acc:MGI:1276533]		Q61026	-0.1	8.8E-01	1.2	2.7E-01	1.0	2.1E-01	-0.3	7.6E-01
ENSMUST00000006103	cystinosis, nephropathic [Source:MGI Symbol;Acc:MGI:1932872]	Q542U5	P57757	-9.2	2.4E-05	6.2	1.2E-04	-1.3	2.4E-01	-0.8	1.8E-01
ENSMUST00000006104	purinergic receptor P2X, ligand-gated ion channel, 5 [Source:MGI Symbol;Acc:MGI:2137026]	Q3UYI1		8.2	2.0E-05	3.6	9.8E-02	-3.4	1.3E-01	-2.1	2.0E-01
ENSMUST00000006061	peroxisomal biogenesis factor 1 [Source:MGI Symbol;Acc:MGI:1918632]		Q5BL07	3.0	2.3E-01	4.4	9.7E-02	-3.1	2.5E-01	-4.5	3.5E-02
ENSMUST00000006071	orthodenticle homolog 1 [Source:MGI Symbol;Acc:MGI:97450]	Q5SS54	P80205	3.7	1.6E-01	4.1	7.5E-02	-2.2	3.8E-01	-2.5	1.6E-01
ENSMUST00000006112	Eph receptor B3 [Source:MGI Symbol;Acc:MGI:104770]		P54754	7.2	7.5E-05	5.0	3.7E-04	-1.0	2.8E-01	-1.3	6.5E-02
ENSMUST00000006123	tuftelin 1 [Source:MGI Symbol;Acc:MGI:109572]	Q3V1F5	O08970	2.3	3.9E-03	1.3	1.5E-01	-1.3	9.0E-02	0.5	4.9E-01
ENSMUST00000006137	TNF receptor-associated protein 1 [Source:MGI Symbol;Acc:MGI:1915265]		Q9CQN1	-1.4	3.5E-02	-7.4	6.8E-04	0.8	9.4E-02	-0.9	5.9E-01
ENSMUST00000006138	N(alpha)-acetyltransferase 60, NatF catalytic subunit [Source:MGI Symbol;Acc:MGI:1922013]		Q9DBU2	-5.9	5.6E-05	5.7	1.2E-04	-2.5	4.0E-02	0.0	9.6E-01
ENSMUST00000006105	sedoheptulokinase [Source:MGI Symbol;Acc:MGI:1921887]		Q9D5J6	-1.9	1.3E-01	0.0	9.9E-01	0.6	5.8E-01	-1.3	3.4E-01
ENSMUST00000006178	kaptin [Source:MGI Symbol;Acc:MGI:1890380]	G3X8R1		-2.6	7.8E-03	7.0	1.8E-04	-0.5	6.9E-01	-0.3	6.5E-01
ENSMUST00000006181	N-ethylmaleimide sensitive fusion protein attachment protein alpha [Source:MGI Symbol;Acc:MGI:104563]		Q9DB05	-3.9	1.0E-04	1.5	6.2E-02	-0.9	1.7E-01	-0.1	8.9E-01
ENSMUST00000006128	reticulocalbin 1 [Source:MGI Symbol;Acc:MGI:104559]		Q05186	0.9	2.5E-01	0.1	9.3E-01	-1.3	8.0E-02	-0.5	5.3E-01
ENSMUST00000006209	steroid receptor RNA activator 1 [Source:MGI Symbol;Acc:MGI:1344414]	G3X8R2		-5.8	7.0E-05	-1.2	1.3E-01	-0.3	4.9E-01	-0.6	4.5E-01
ENSMUST00000006217	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1343161]		Q9CZ28	-7.2	1.5E-05	-7.8	1.1E-03	0.8	1.1E-01	2.7	1.3E-01
ENSMUST00000006235	cathepsin B [Source:MGI Symbol;Acc:MGI:88561]		P10605	-6.2	5.3E-07	-0.7	5.1E-01	1.3	8.2E-02	-0.6	5.3E-01
ENSMUST00000006254	tubulin folding cofactor B [Source:MGI Symbol;Acc:MGI:1913661]		Q9D1E6	-2.9	1.1E-03	-2.8	4.1E-03	0.8	6.7E-02	-0.2	7.8E-01
ENSMUST00000006205	ankyrin repeat and KH domain containing 1 [Source:MGI Symbol;Acc:MGI:1921733]	E9Q1M6		2.8	9.7E-02	4.9	9.0E-03	-0.6	7.2E-01	-2.8	4.2E-02
ENSMUST00000006286	inositol polyphosphate 5-phosphatase K [Source:MGI Symbol;Acc:MGI:1194899]	Q5ND43	Q8C5L6	-7.9	1.2E-04	-7.0	1.4E-04	-1.3	1.0E-02	-0.1	9.6E-01
ENSMUST00000006293	v-crk sarcoma virus CT10 oncogene homolog (avian)-like [Source:MGI Symbol;Acc:MGI:104686]	A2RS58	P47941	-1.7	2.3E-03	-5.5	2.3E-04	0.6	1.2E-01	-1.1	3.3E-01
ENSMUST00000006221	vacuolar protein sorting 54 (yeast) [Source:MGI Symbol;Acc:MGI:2178798]		Q5SPW0	-3.7	9.5E-02	-2.6	4.2E-01	1.8	3.7E-01	0.8	8.0E-01
ENSMUST00000006301	leucine-rich repeats and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:1918985]		Q8BUI3	-5.6	3.7E-04	-5.7	6.0E-06	0.0	9.9E-01	-0.5	4.3E-01
ENSMUST00000006311	TEA domain family member 4 [Source:MGI Symbol;Acc:MGI:106907]			3.2	1.6E-03	-2.0	3.2E-02	0.6	2.2E-01	-0.4	6.6E-01
ENSMUST00000006341	protease, serine 16 (thymus) [Source:MGI Symbol;Acc:MGI:1859181]	Q5SZ30	Q9QXE5	-2.9	1.2E-04	-6.4	6.3E-04	0.3	5.6E-01	-1.1	4.6E-01
ENSMUST00000006353	CDK5 regulatory subunit associated protein 1-like 1 [Source:MGI Symbol;Acc:MGI:1921765]		Q91WE6	2.6	6.0E-03	-0.9	1.2E-01	1.0	2.3E-02	0.1	7.9E-01
ENSMUST00000006367	HtrA serine peptidase 1 [Source:MGI Symbol;Acc:MGI:1929076]		Q9R118	3.3	3.2E-02	-4.5	1.2E-02	0.8	2.2E-01	-0.3	8.4E-01
ENSMUST00000006377	zinc finger and BTB domain containing 17 [Source:MGI Symbol;Acc:MGI:107410]		Q60821	-6.0	1.2E-03	4.2	1.4E-03	1.0	2.3E-01	0.1	9.1E-01
ENSMUST00000006380	family with sequence similarity 131, member C [Source:MGI Symbol;Acc:MGI:2685539]	A2ADB2		6.5	7.3E-05	-0.1	8.0E-01	2.0	6.8E-04	-0.7	2.1E-01
ENSMUST00000006392	serine (or cysteine) peptidase inhibitor, clade B, member 9b [Source:MGI Symbol;Acc:MGI:894668]	Q9DAV6		2.9	4.3E-03	1.2	2.1E-01	-0.8	2.8E-01	0.6	4.8E-01
ENSMUST00000006397	erythropoietin receptor [Source:MGI Symbol;Acc:MGI:95408]	Q3UTV9	P14753	6.3	1.2E-04	0.3	7.1E-01	-7.0	9.8E-05	-4.0	2.4E-03
ENSMUST00000006431	ATPase, H+ transporting, lysosomal V1 subunit B1 [Source:MGI Symbol;Acc:MGI:103285]	Q91YH6		7.1	5.6E-05	-2.6	6.8E-02	1.3	8.4E-02	-2.1	2.0E-01
ENSMUST00000006378	chloride channel, voltage-sensitive Kb [Source:MGI Symbol;Acc:MGI:1930643]		Q9WUB6	3.7	1.2E-01	1.6	6.3E-01	0.3	9.1E-01	2.5	3.4E-01
ENSMUST00000006435	ATPase, H+ transporting, lysosomal V1 subunit B2 [Source:MGI Symbol;Acc:MGI:109618]		P62814	-6.7	1.7E-05	6.1	2.2E-04	-0.5	6.3E-01	-0.1	8.4E-01
ENSMUST00000006391	serine (or cysteine) peptidase inhibitor, clade B, member 9 [Source:MGI Symbol;Acc:MGI:106603]	O08797		2.4	5.6E-02	-1.9	1.7E-01	-2.7	2.4E-02	1.6	2.2E-01
ENSMUST00000006444	telomerase associated protein 1 [Source:MGI Symbol;Acc:MGI:109573]		P97499	0.9	2.6E-02	1.2	1.6E-01	-2.1	1.8E-02	-0.4	5.6E-01
ENSMUST00000006451	tetratricopeptide repeat domain 5 [Source:MGI Symbol;Acc:MGI:2683584]		Q99LG4	-2.3	7.9E-04	6.1	2.9E-04	-0.9	4.5E-01	-0.7	3.0E-01
ENSMUST00000006403	coiled-coil domain containing 159 [Source:MGI Symbol;Acc:MGI:1914369]		Q8C963	1.8	3.6E-01	2.3	3.1E-01	-0.9	6.5E-01	-1.4	4.8E-01
ENSMUST00000006415				-0.2	8.0E-01	-1.1	4.3E-01	0.3	7.2E-01	1.2	3.6E-01
ENSMUST00000006462	angio-associated migratory protein [Source:MGI Symbol;Acc:MGI:107809]	Q3TJ22		-7.4	2.0E-04	6.8	1.6E-04	-0.6	6.2E-01	-0.2	6.8E-01
ENSMUST00000006467	actin related protein 2/3 complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1923959]		Q9CVB6	-11.0	7.4E-05	-5.7	4.3E-04	1.2	2.5E-02	0.2	8.4E-01
ENSMUST00000006476	uroplakin 1A [Source:MGI Symbol;Acc:MGI:98911]	A2RSB9	Q9D132	4.7	2.9E-04	0.8	9.0E-02	-0.4	2.3E-01	-0.3	4.4E-01
ENSMUST00000006478	transmembrane protein 147 [Source:MGI Symbol;Acc:MGI:1915011]	B2RVQ1	Q9CQG6	-3.3	7.8E-04	-1.3	3.8E-02	0.0	9.7E-01	-1.0	1.2E-01
ENSMUST00000006496	ribosomal protein S9 [Source:MGI Symbol;Acc:MGI:1924096]		Q6ZWN5	-8.1	8.7E-06	-5.2	2.2E-03	0.7	2.2E-01	-1.6	3.1E-01
ENSMUST00000006523	cysteine-rich protein 1 (intestinal) [Source:MGI Symbol;Acc:MGI:88501]		P63254	-6.4	1.5E-03	-7.2	2.2E-04	0.0	9.5E-01	-3.8	5.3E-02
ENSMUST00000006470	lysine (K)-specific methyltransferase 2B [Source:MGI Symbol;Acc:MGI:109565]	F8WJ40		-1.9	6.8E-02	0.4	7.4E-01	1.2	1.6E-01	-1.0	3.6E-01
ENSMUST00000006544	ycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase) [Source:MGI Symbol;Acc:MGI:134938		O88986	2.2	2.2E-02	5.7	6.3E-04	0.3	8.0E-01	-0.7	3.3E-01
ENSMUST00000006556	myeloproliferative leukemia virus oncogene [Source:MGI Symbol;Acc:MGI:97076]	A2A9D4		5.8	2.5E-02	-2.0	2.9E-02	0.2	7.4E-01	-1.1	1.9E-01
ENSMUST00000006559	trophoblast glycoprotein [Source:MGI Symbol;Acc:MGI:1341264]		Q9Z0L0	7.6	4.6E-03	-6.1	1.3E-04	0.3	5.4E-01	-1.8	1.3E-01
ENSMUST00000006508	gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:95706]	Q4FK56	Q60928	-1.4	3.8E-01	0.9	6.9E-01	1.9	3.2E-01	-0.4	8.3E-01
ENSMUST00000006578	poliovirus receptor-related 4 [Source:MGI Symbol;Acc:MGI:1918990]		Q8R007	8.7	1.7E-02	-7.3	1.4E-03	-2.4	9.9E-03	-1.5	4.1E-01
ENSMUST00000006525	-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human) [Source:MGI Symbol;Acc:MGI:1338		O54972	1.8	3.8E-01	0.5	8.5E-01	-0.3	9.0E-01	0.9	6.6E-01
ENSMUST00000006579	prefoldin 2 [Source:MGI Symbol;Acc:MGI:1276111]	F8WJ30		-4.8	2.0E-04	-0.2	7.8E-01	-3.3	1.1E-03	-0.9	2.7E-01
ENSMUST00000006587	transmembrane protein 189 [Source:MGI Symbol;Acc:MGI:2142624]		Q99LQ7	-3.7	6.8E-04	4.3	8.9E-02	-2.1	4.0E-01	-0.6	7.4E-01
ENSMUST00000006557	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 [Source:MGI Symbol;Acc:MGI:185	Q548M4	Q9JLJ5	-0.9	3.5E-01	1.0	4.7E-01	1.9	8.6E-02	0.0	9.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000006614	Eph receptor A2 [Source:MGI Symbol;Acc:MGI:95278]		Q03145	7.1	1.1E-04	5.6	3.3E-02	-0.6	8.0E-01	1.3	3.3E-01
ENSMUST00000006565	cell division cycle 20 [Source:MGI Symbol;Acc:MGI:1859866]		Q9JJ66	-1.3	1.3E-01	0.2	8.2E-01	0.7	3.3E-01	-0.8	4.0E-01
ENSMUST00000006618	Rho guanine nucleotide exchange factor (GEF) 19 [Source:MGI Symbol;Acc:MGI:1925912]		Q8BWA8	8.1	3.2E-05	2.4	4.6E-01	-3.2	3.5E-01	3.1	1.8E-01
ENSMUST00000006625	RNA binding motif protein 14 [Source:MGI Symbol;Acc:MGI:1929092]		Q8C2Q3	-2.2	1.9E-02	-5.4	4.7E-04	-1.1	3.1E-02	-0.4	6.9E-01
ENSMUST00000006626	actinin alpha 3 [Source:MGI Symbol;Acc:MGI:99678]		O88990	7.7	2.7E-05	-2.2	4.6E-02	1.3	3.3E-02	-0.1	8.9E-01
ENSMUST00000006611	spermidine synthase [Source:MGI Symbol;Acc:MGI:102690]	Q543H0	Q64674	1.5	4.8E-02	0.9	3.0E-01	-0.8	2.6E-01	-0.1	8.8E-01
ENSMUST00000006638	solute carrier family 34 (sodium phosphate), member 3 [Source:MGI Symbol;Acc:MGI:2159410]		Q80SU6	6.7	6.8E-04	1.2	2.2E-01	-5.5	5.7E-04	0.3	6.8E-01
ENSMUST00000006669	pyruvate dehydrogenase kinase, isoenzyme 1 [Source:MGI Symbol;Acc:MGI:1926119]		Q8BFP9	1.7	1.5E-02	5.7	1.7E-04	-2.3	6.4E-02	0.0	9.4E-01
ENSMUST00000006679	proteinase 3 [Source:MGI Symbol;Acc:MGI:893580]			-5.1	4.2E-04	-2.6	5.7E-02	1.0	1.4E-01	1.5	2.3E-01
ENSMUST00000006692	mevalonate (diphospho) decarboxylase [Source:MGI Symbol;Acc:MGI:2179327]	Q3UYC1	Q99JF5	-2.9	1.3E-03	6.9	7.7E-05	-1.4	2.5E-01	-0.6	2.6E-01
ENSMUST00000006629	spectrin beta, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98388]		Q62261	1.9	1.2E-01	-2.5	1.8E-02	-6.5	3.8E-05	-2.1	5.8E-02
ENSMUST00000006632	zinc finger, DHHC domain containing 24 [Source:MGI Symbol;Acc:MGI:1917855]		Q6IR37	-1.0	4.5E-01	1.2	5.5E-01	2.0	2.1E-01	-0.1	9.3E-01
ENSMUST00000006697	inter-alpha trypsin inhibitor, heavy chain 3 [Source:MGI Symbol;Acc:MGI:96620]		Q61704	5.1	2.2E-03	5.7	3.3E-03	-0.6	7.1E-01	0.4	6.4E-01
ENSMUST00000006646	MDA receptor synaptonuclear signaling and neuronal migration factor [Source:MGI Symbol;Acc:MGI:186175		Q99NF2	2.1	4.3E-01	-1.2	7.1E-01	-3.8	1.5E-01	-0.5	8.7E-01
ENSMUST00000006701	transmembrane protein 110 [Source:MGI Symbol;Acc:MGI:1921500]		Q3UF25	-1.8	2.7E-02	2.2	1.5E-02	0.6	3.5E-01	0.0	9.4E-01
ENSMUST00000006716	wingless-type MMTV integration site family, member 6 [Source:MGI Symbol;Acc:MGI:98960]		P22727	6.6	1.7E-04	-3.1	2.8E-02	1.8	1.8E-02	-0.2	9.0E-01
ENSMUST00000006687	orosomucoid 3 [Source:MGI Symbol;Acc:MGI:97445]	J3JRU4		2.0	3.8E-02	0.0	9.7E-01	-1.4	1.1E-01	0.6	5.2E-01
ENSMUST00000006718	wingless-type MMTV integration site family, member 10A [Source:MGI Symbol;Acc:MGI:108071]		P70701	8.1	1.7E-05	-1.2	1.2E-01	0.5	2.7E-01	-1.1	1.7E-01
ENSMUST00000006742	ATPase, Cu++ transporting, beta polypeptide [Source:MGI Symbol;Acc:MGI:103297]		Q64446	8.2	4.7E-05	1.7	1.4E-01	-4.8	3.2E-03	-1.4	1.4E-01
ENSMUST00000006749	solute carrier family 4 (anion exchanger), member 1 [Source:MGI Symbol;Acc:MGI:109393]	Q53ZN9	P04919	4.0	1.1E-02	-0.5	5.6E-01	0.8	2.1E-01	-0.5	5.9E-01
ENSMUST00000006703	inter alpha-trypsin inhibitor, heavy chain 4 [Source:MGI Symbol;Acc:MGI:109536]		A6X935	3.3	7.0E-02	2.2	2.6E-01	-0.3	8.7E-01	0.8	5.7E-01
ENSMUST00000006704	inter-alpha trypsin inhibitor, heavy chain 1 [Source:MGI Symbol;Acc:MGI:96618]	F8WJ05		2.4	4.2E-02	4.4	6.4E-03	0.4	7.1E-01	-1.6	1.3E-01
ENSMUST00000006761	runt-related transcription factor 1; translocated to, 1 (cyclin D-related) [Source:MGI Symbol;Acc:MGI:104793]	Q3UQX8		5.7	2.4E-02	5.3	8.2E-04	-1.5	2.2E-01	-0.1	8.4E-01
ENSMUST00000006762	snail family zinc finger 3 [Source:MGI Symbol;Acc:MGI:1353563]		Q9QY31	6.3	8.3E-05	4.2	1.8E-04	-4.4	1.2E-03	-0.5	4.0E-01
ENSMUST00000006764	adenine phosphoribosyl transferase [Source:MGI Symbol;Acc:MGI:88061]		P08030	-4.5	6.0E-05	8.7	1.2E-04	0.0	9.8E-01	-0.5	4.1E-01
ENSMUST00000006774	general transcription factor II H, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1277216]	G3X8R4		-4.9	1.8E-05	1.9	1.6E-01	-2.7	5.0E-02	-0.6	5.6E-01
ENSMUST00000006760	chromatin licensing and DNA replication factor 1 [Source:MGI Symbol;Acc:MGI:1914427]		Q8R4E9	-0.9	1.6E-01	0.3	7.5E-01	1.0	1.1E-01	-0.2	8.3E-01
ENSMUST00000006786	solute carrier family 17 (sodium phosphate), member 2 [Source:MGI Symbol;Acc:MGI:2443098]		Q5SZA1	8.0	1.4E-05	5.5	2.0E-02	-1.8	4.3E-01	-1.7	2.5E-01
ENSMUST00000006818	transcription factor 23 [Source:MGI Symbol;Acc:MGI:1934960]		Q9JLR5	7.0	3.4E-06	5.6	5.8E-04	-0.5	6.8E-01	0.2	7.2E-01
ENSMUST00000006825	nephrosis 1, nephrin [Source:MGI Symbol;Acc:MGI:1859637]		Q9QZS7	9.7	1.5E-06	-3.8	9.3E-04	0.4	3.3E-01	-0.3	7.6E-01
ENSMUST00000006828	amyloid beta (A4) precursor-like protein 1 [Source:MGI Symbol;Acc:MGI:88046]			2.8	3.1E-03	-4.1	2.8E-04	-0.3	3.8E-01	-1.1	1.7E-01
ENSMUST00000006838	glutaminyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1915851]	Q8BML9		-3.8	5.0E-03	7.8	3.3E-05	-0.6	6.0E-01	-0.4	4.2E-01
ENSMUST00000006853	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum) [Source:MGI Symbol;Acc:MGI:1921693]	Q2M2M8	Q8BG58	4.4	1.8E-03	5.4	5.4E-05	-1.4	8.9E-02	0.2	6.6E-01
ENSMUST00000006893	RIKEN cDNA D130043K22 gene [Source:MGI Symbol;Acc:MGI:3036268]		Q5SZV5	7.7	2.3E-02	8.5	3.7E-06	-1.3	2.1E-01	-0.1	8.6E-01
ENSMUST00000006898	geminin [Source:MGI Symbol;Acc:MGI:1927344]	Q3V295	O88513	3.4	2.8E-02	3.0	6.2E-03	0.3	7.2E-01	0.0	9.7E-01
ENSMUST00000006900	acyl-CoA thioesterase 13 [Source:MGI Symbol;Acc:MGI:1914084]	Q4VA32	Q9CQR4	-5.0	4.3E-04	-3.5	2.5E-02	0.3	6.9E-01	0.0	9.9E-01
ENSMUST00000006851	glutamine-rich 1 [Source:MGI Symbol;Acc:MGI:1916482]	G3X8R5		-2.3	1.4E-01	-2.5	3.9E-01	2.2	2.4E-01	2.4	3.6E-01
ENSMUST00000006911	cyclin-dependent kinase 4 [Source:MGI Symbol;Acc:MGI:88357]	Q545C3	P30285	-5.3	8.8E-05	3.7	1.7E-02	-0.1	9.3E-01	0.6	5.2E-01
ENSMUST00000006854	ubiquitin specific peptidase 19 [Source:MGI Symbol;Acc:MGI:1918722]		Q3UJD6	-1.9	1.5E-01	-0.5	7.5E-01	1.0	3.0E-01	-0.4	8.0E-01
ENSMUST00000006856	polymerase (DNA directed), alpha 1 [Source:MGI Symbol;Acc:MGI:99660]		P33609	-1.7	6.3E-02	-1.3	2.0E-01	-0.7	3.0E-01	-1.1	2.5E-01
ENSMUST00000006912	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha [Source:MGI Symbol;Acc:MGI:1298206]	Q544E3	O70172	-4.2	3.5E-05	9.3	1.1E-02	-1.0	7.7E-01	-2.7	1.3E-01
ENSMUST00000006914	beta-1,4-N-acetyl-galactosaminyl transferase 1 [Source:MGI Symbol;Acc:MGI:1342057]	Q3UN35	Q09200	-4.0	4.2E-04	5.5	2.2E-03	-0.5	7.1E-01	-2.6	2.0E-02
ENSMUST00000006949	tryptophan hydroxylase 2 [Source:MGI Symbol;Acc:MGI:2651811]		Q8CGV2	3.3	1.6E-03	-4.8	1.7E-03	-0.9	1.1E-01	-1.1	3.8E-01
ENSMUST00000006952	serum amyloid A 4 [Source:MGI Symbol;Acc:MGI:98224]		P31532	7.6	3.1E-04	-5.5	4.4E-04	0.0	9.2E-01	0.3	8.0E-01
ENSMUST00000006956	serum amyloid A 3 [Source:MGI Symbol;Acc:MGI:98223]		P04918	-10.1	1.2E-04	-2.9	1.7E-03	0.7	7.1E-02	-0.6	4.3E-01
ENSMUST00000006963	keratin 28 [Source:MGI Symbol;Acc:MGI:1918093]		A6BLY7	7.0	1.0E-04	-2.9	1.1E-02	1.1	6.4E-02	0.0	9.9E-01
ENSMUST00000006915	methyltransferase like 1 [Source:MGI Symbol;Acc:MGI:1339986]		Q9Z120	1.1	2.8E-01	0.9	4.5E-01	-0.5	6.1E-01	-0.3	7.7E-01
ENSMUST00000006948				-1.1	2.1E-01	-0.8	4.3E-01	0.8	3.0E-01	0.6	5.6E-01
ENSMUST00000006969	keratin 23 [Source:MGI Symbol;Acc:MGI:2148866]	Q544I8	Q99PS0	6.2	1.6E-04	4.2	1.5E-03	0.6	4.9E-01	-0.3	6.9E-01
ENSMUST00000006973	K(lysine) acetyltransferase 2A [Source:MGI Symbol;Acc:MGI:1343101]	Q6P3Z8		-3.6	4.4E-03	6.3	2.6E-03	-0.3	8.4E-01	0.9	3.2E-01
ENSMUST00000006976	tetratricopeptide repeat domain 25 [Source:MGI Symbol;Acc:MGI:1921657]	B8A5X0		5.5	5.1E-04	-8.3	9.2E-04	0.1	9.0E-01	-1.7	4.1E-01
ENSMUST00000006991	hyperpolarization-activated, cyclic nucleotide-gated K+ 1 [Source:MGI Symbol;Acc:MGI:1096392]		O88704	8.1	4.3E-05	6.6	3.3E-04	-0.6	6.5E-01	-0.1	8.8E-01
ENSMUST00000007007	Wilms tumour 1-associating protein [Source:MGI Symbol;Acc:MGI:1926395]	E0CYH0		-3.5	1.8E-03	5.9	4.2E-04	-0.7	5.3E-01	-0.4	5.2E-01
ENSMUST00000007012	superoxide dismutase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:98352]	Q4FJX9	P09671	-1.2	5.1E-03	0.7	3.7E-01	0.2	8.0E-01	-4.2	2.2E-03
ENSMUST00000007042	IK cytokine [Source:MGI Symbol;Acc:MGI:1345142]		Q9Z1M8	-5.1	1.6E-05	7.1	2.7E-04	0.4	7.5E-01	-1.2	1.1E-01
ENSMUST00000007046	transmembrane and coiled-coil domains 6 [Source:MGI Symbol;Acc:MGI:1919233]		Q8BQX5	-2.0	1.2E-02	7.8	1.8E-04	0.0	9.8E-01	0.3	6.9E-01
ENSMUST00000007005	acetyl-Coenzyme A acetyltransferase 2 [Source:MGI Symbol;Acc:MGI:87871]		Q8CAY6	-1.3	1.0E-01	0.6	5.4E-01	0.7	3.3E-01	-1.1	2.0E-01
ENSMUST00000007130	catenin (cadherin associated protein), beta 1 [Source:MGI Symbol;Acc:MGI:88276]		Q02248	-6.6	6.1E-04	-6.0	1.5E-03	-0.2	7.3E-01	2.4	1.1E-01
ENSMUST00000007139	eukaryotic translation initiation factor 1B [Source:MGI Symbol;Acc:MGI:1916219]		Q9CXU9	-4.6	3.0E-05	-1.3	1.3E-02	0.1	7.5E-01	0.2	6.1E-01
ENSMUST00000007156	kallikrein 1-related peptidase b11 [Source:MGI Symbol;Acc:MGI:892023]		P15946	6.1	4.5E-04	-5.3	5.7E-05	-1.0	1.5E-02	-0.8	3.0E-01
ENSMUST00000007161	kallikrein related-peptidase 4 (prostase, enamel matrix, prostate) [Source:MGI Symbol;Acc:MGI:1861379]	Q9Z0M1		7.7	2.0E-04	-1.1	2.2E-01	0.6	2.6E-01	-0.3	7.1E-01
ENSMUST00000007212	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 [Source:MGI Symbol;Acc:MGI:1096584]	Q3TKV1	Q8VDM4	-5.3	7.5E-05	-6.5	4.1E-03	0.5	4.3E-01	0.3	8.6E-01
ENSMUST00000007131	ATP citrate lyase [Source:MGI Symbol;Acc:MGI:103251]		Q91V92	2.6	2.9E-01	0.8	7.7E-01	-1.4	5.4E-01	0.4	8.8E-01
ENSMUST00000007216	adaptor-related protein complex 2, mu 1 subunit [Source:MGI Symbol;Acc:MGI:1298405]	Q5FWI9	P84091	1.3	3.0E-03	-3.1	2.4E-03	0.9	5.7E-02	-0.7	4.0E-01
ENSMUST00000007236	synaptogyrin 3 [Source:MGI Symbol;Acc:MGI:1341881]		Q8R191	6.7	1.5E-04	6.7	4.4E-04	-0.6	6.4E-01	-1.2	1.3E-01
ENSMUST00000007245	von Willebrand factor A domain containing 7 [Source:MGI Symbol;Acc:MGI:1306798]	B2RQ76	Q9JHA8	4.6	9.6E-04	4.7	1.5E-03	-3.1	3.6E-02	-0.2	8.2E-01
ENSMUST00000007248	heat shock protein 1-like [Source:MGI Symbol;Acc:MGI:96231]	A1L347	P16627	4.7	4.0E-03	-3.8	2.9E-03	0.6	2.2E-01	-1.0	3.4E-01
ENSMUST00000007250	mutS homolog 5 (E. coli) [Source:MGI Symbol;Acc:MGI:1329021]			-4.9	1.3E-02	2.0	7.8E-04	0.3	4.2E-01	-0.4	2.1E-01
ENSMUST00000007251	abhydrolase domain containing 16A [Source:MGI Symbol;Acc:MGI:99476]		Q9Z1Q2	-3.8	1.3E-02	6.8	3.7E-04	-0.1	9.2E-01	-0.2	7.6E-01
ENSMUST00000007253	neuraminidase 1 [Source:MGI Symbol;Acc:MGI:97305]	Q3UL64	O35657	-6.4	8.2E-05	4.8	5.3E-03	0.1	9.7E-01	-0.1	8.6E-01
ENSMUST00000007255	dimethylarginine dimethylaminohydrolase 2 [Source:MGI Symbol;Acc:MGI:1859016]		Q99LD8	-3.0	1.5E-02	4.9	1.1E-02	-0.5	7.4E-01	-0.7	5.1E-01
ENSMUST00000007257	chloride intracellular channel 1 [Source:MGI Symbol;Acc:MGI:2148924]	Q542F1	Q9Z1Q5	-7.8	7.4E-07	-4.1	6.2E-02	1.1	3.3E-01	0.4	8.6E-01
ENSMUST00000007272	keratin 14 [Source:MGI Symbol;Acc:MGI:96688]		Q61781	8.5	6.3E-05	-6.0	5.3E-02	1.3	2.0E-01	3.5	2.3E-01
ENSMUST00000007275	keratin 13 [Source:MGI Symbol;Acc:MGI:101925]		P08730	7.2	5.8E-04	-3.4	4.6E-03	1.0	7.4E-02	-2.0	9.7E-02
ENSMUST00000007280	keratin 16 [Source:MGI Symbol;Acc:MGI:96690]	Q3SYP5	Q9Z2K1	9.6	1.3E-05	0.3	7.7E-01	0.6	4.4E-01	-2.7	3.0E-02
ENSMUST00000007296	polymerase (DNA directed), epsilon [Source:MGI Symbol;Acc:MGI:1196391]		Q9WVF7	2.6	4.7E-03	-7.4	7.6E-06	0.1	7.3E-01	-0.2	7.7E-01
ENSMUST00000007301	myosin, heavy polypeptide 3, skeletal muscle, embryonic [Source:MGI Symbol;Acc:MGI:1339709]		P13541	6.0	2.3E-03	3.9	1.8E-03	-4.3	5.2E-03	0.2	7.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000007317	keratin 19 [Source:MGI Symbol;Acc:MGI:96693]	B1AQ78	P19001	6.7	3.8E-05	3.8	1.5E-02	-3.2	5.3E-02	0.1	8.7E-01
ENSMUST00000007318	keratin 31 [Source:MGI Symbol;Acc:MGI:1309993]		Q61765	5.3	1.7E-03	7.4	8.9E-05	-1.8	1.7E-01	0.3	5.7E-01
ENSMUST00000007340	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Source:MGI Symbol;Acc:MGI:1926943]		Q9Z1W8	7.2	1.1E-04	3.5	4.0E-03	0.4	6.2E-01	-0.5	5.0E-01
ENSMUST00000007482	mitochondrial ribosomal protein L49 [Source:MGI Symbol;Acc:MGI:108180]		Q9CQ40	-1.8	3.8E-03	3.9	3.7E-02	-0.1	9.7E-01	2.1	9.7E-02
ENSMUST00000007559	GATA zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1914460]		Q920S3	-4.5	3.8E-05	1.6	3.0E-02	-5.7	8.7E-05	-0.6	2.9E-01
ENSMUST00000007584	protocadherin alpha subfamily C, 1 [Source:MGI Symbol;Acc:MGI:1891442]	Q91Y10		7.9	4.8E-05	6.3	9.6E-04	-0.4	7.8E-01	-1.4	8.8E-02
ENSMUST00000007602	mannose-6-phosphate receptor, cation dependent [Source:MGI Symbol;Acc:MGI:96904]	Q3UKQ5	P24668	-6.5	3.5E-04	7.4	1.8E-04	-0.5	7.3E-01	-0.6	3.6E-01
ENSMUST00000007444	STE20-related kinase adaptor alpha [Source:MGI Symbol;Acc:MGI:1919399]		Q3UUJ4	-3.6	3.8E-02	-1.8	3.6E-01	0.9	4.6E-01	-0.8	6.8E-01
ENSMUST00000007708	protein phosphatase 2, regulatory subunit A, alpha [Source:MGI Symbol;Acc:MGI:1926334]		Q76MZ3	-4.8	5.3E-05	-1.5	3.0E-02	0.1	7.8E-01	-0.2	7.9E-01
ENSMUST00000007733	Terf1 (TRF1)-interacting nuclear factor 2 [Source:MGI Symbol;Acc:MGI:107246]	Q8K1K3		-2.3	9.6E-04	-2.6	5.9E-03	0.9	4.8E-02	-1.0	2.1E-01
ENSMUST00000007738	hyaluronan and proteoglycan link protein 4 [Source:MGI Symbol;Acc:MGI:2679531]		Q80WM4	7.2	3.7E-05	7.4	1.5E-04	-0.5	6.8E-01	-0.1	9.1E-01
ENSMUST00000007754	GTP binding protein 3 [Source:MGI Symbol;Acc:MGI:1917609]	B2RRS4	Q923K4	1.8	8.9E-03	-8.5	3.7E-03	0.3	6.8E-01	2.3	3.3E-01
ENSMUST00000007757	transforming growth factor, beta receptor I [Source:MGI Symbol;Acc:MGI:98728]	Q4FJL1	Q64729	-3.1	3.6E-04	-3.0	4.5E-03	1.1	2.7E-02	-0.6	4.6E-01
ENSMUST00000007797	gamma-aminobutyric acid (GABA) A receptor, subunit beta 2 [Source:MGI Symbol;Acc:MGI:95620]		P63137	7.3	2.3E-05	-1.8	1.6E-02	0.4	2.4E-01	-0.1	9.1E-01
ENSMUST00000007799	caveolin 1, caveolae protein [Source:MGI Symbol;Acc:MGI:102709]		P49817	4.7	3.4E-03	6.5	1.8E-04	-1.1	3.4E-01	-0.4	4.5E-01
ENSMUST00000007747	dihydrouridine synthase 3-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2147092]			-0.8	1.9E-01	-0.4	6.7E-01	0.7	2.3E-01	0.2	8.0E-01
ENSMUST00000007803	BCL2-like 1 [Source:MGI Symbol;Acc:MGI:88139]	Q5HZH3	Q64373	-6.7	6.6E-04	3.4	1.2E-03	1.8	1.5E-02	0.2	6.9E-01
ENSMUST00000007814	KH-type splicing regulatory protein [Source:MGI Symbol;Acc:MGI:1336214]		Q3U0V1	-1.5	5.2E-03	-2.1	1.9E-02	0.9	5.4E-02	-0.1	8.4E-01
ENSMUST00000007865	coiled-coil domain containing 124 [Source:MGI Symbol;Acc:MGI:1916403]		Q9D8X2	-4.0	1.5E-04	6.8	8.9E-05	-0.6	6.1E-01	0.0	9.8E-01
ENSMUST00000007921	RIKEN cDNA 0610009B22 gene [Source:MGI Symbol;Acc:MGI:1913300]	Q8R3W2		-4.0	9.2E-05	-4.5	1.0E-02	-6.4	2.7E-04	2.8	6.9E-02
ENSMUST00000007959	ras homolog gene family, member A [Source:MGI Symbol;Acc:MGI:1096342]	Q4VAE6	Q9QUI0	-6.5	2.8E-07	-2.0	9.0E-02	0.6	3.6E-01	-4.1	1.8E-02
ENSMUST00000007961	zinc finger, MIZ-type containing 1 [Source:MGI Symbol;Acc:MGI:3040693]		Q6P1E1	3.9	1.1E-03	-0.8	1.5E-01	0.9	4.0E-02	0.2	6.8E-01
ENSMUST00000007980	heterogeneous nuclear ribonucleoprotein A0 [Source:MGI Symbol;Acc:MGI:1924384]		Q9CX86	-4.2	9.7E-06	-3.5	1.8E-03	0.4	3.4E-01	-0.1	9.3E-01
ENSMUST00000007884	zinc finger protein 54 [Source:MGI Symbol;Acc:MGI:99201]	E9PW05		-0.1	9.2E-01	1.0	6.2E-01	0.5	7.5E-01	-0.6	7.2E-01
ENSMUST00000007981	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2 [Source:MGI Symbol;Acc:MGI:1929596]		Q8R182	-4.4	5.5E-03	-3.4	9.7E-04	-0.5	2.7E-01	-1.0	1.8E-01
ENSMUST00000007993	RNA binding motif protein 28 [Source:MGI Symbol;Acc:MGI:2655711]		Q8CGC6	3.0	2.3E-04	-5.3	1.1E-05	0.7	2.2E-02	-0.4	4.8E-01
ENSMUST00000008021	titin-cap [Source:MGI Symbol;Acc:MGI:1330233]	Q545G3	O70548	4.7	2.6E-04	4.5	4.1E-03	1.3	2.3E-01	0.7	4.1E-01
ENSMUST00000007977	aldehyde dehydrogenase 16 family, member A1 [Source:MGI Symbol;Acc:MGI:1916998]			-2.4	1.1E-01	0.5	7.6E-01	1.4	2.4E-01	-1.5	3.8E-01
ENSMUST00000008032	cytokine receptor-like factor 1 [Source:MGI Symbol;Acc:MGI:1340030]		Q9JM58	5.8	1.6E-03	-2.8	7.3E-04	0.8	3.4E-02	-0.6	3.6E-01
ENSMUST00000008036	ribosomal protein, large, P1 [Source:MGI Symbol;Acc:MGI:1927099]	Q58E35	P47955	-7.0	2.5E-05	-5.6	1.9E-02	0.8	2.9E-01	2.1	3.3E-01
ENSMUST00000008088	tetratricopeptide repeat domain 9B [Source:MGI Symbol;Acc:MGI:1920282]		Q9D6E4	6.0	4.6E-04	3.7	2.1E-04	0.3	6.1E-01	-0.5	3.3E-01
ENSMUST00000008004	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 [Source:MGI Symbol;Acc:MGI:2136689]		Q4FZF3	-2.9	4.1E-02	-1.8	2.5E-01	-0.1	9.5E-01	-1.1	4.8E-01
ENSMUST00000008016	inhibitor of DNA binding 3 [Source:MGI Symbol;Acc:MGI:96398]	Q545W1	P41133	1.2	1.4E-01	1.4	1.6E-01	0.0	1.0E+00	-0.2	8.4E-01
ENSMUST00000008090	paired-like homeobox 2a [Source:MGI Symbol;Acc:MGI:106633]		Q62066	6.9	2.6E-04	5.4	9.5E-04	0.4	6.8E-01	-0.3	6.8E-01
ENSMUST00000008024	AT rich interactive domain 1A (SWI-like) [Source:MGI Symbol;Acc:MGI:1935147]		A2BH40	1.8	3.0E-01	1.8	4.2E-01	0.2	9.0E-01	0.2	9.3E-01
ENSMUST00000008179	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish)) [Source:MGI Symbol;Acc:MGI:1915291	Q4FK31	Q9CQ20	-5.1	8.9E-04	5.9	2.4E-03	-0.6	7.2E-01	-0.7	4.1E-01
ENSMUST00000008273	prokineticin 2 [Source:MGI Symbol;Acc:MGI:1354178]	G3X8R6		-5.8	7.4E-03	-7.0	1.5E-04	-0.4	4.1E-01	-0.3	7.8E-01
ENSMUST00000008297	calsyntenin 3 [Source:MGI Symbol;Acc:MGI:2178323]		Q99JH7	6.8	1.0E-04	5.4	1.0E-03	-1.4	2.8E-01	-0.9	2.4E-01
ENSMUST00000008350	ceramide synthase 4 [Source:MGI Symbol;Acc:MGI:1914510]		Q9D6J1	7.5	7.6E-06	6.8	4.7E-04	-0.6	6.6E-01	-0.6	4.3E-01
ENSMUST00000008094	abhydrolase domain containing 8 [Source:MGI Symbol;Acc:MGI:1918946]		Q8R0P8	0.8	2.7E-01	1.1	2.1E-01	0.1	8.4E-01	-0.2	7.8E-01
ENSMUST00000008131	intraflagellar transport 22 [Source:MGI Symbol;Acc:MGI:1914536]	A0A0H2UKB7		-0.6	2.5E-01	-1.1	9.8E-02	-0.7	1.6E-01	-0.2	7.5E-01
ENSMUST00000008462	RELT tumor necrosis factor receptor [Source:MGI Symbol;Acc:MGI:2443373]		Q8BX43	-4.9	4.4E-04	-2.9	4.9E-02	1.1	1.5E-01	-1.2	4.1E-01
ENSMUST00000008477	U2 small nuclear ribonucleoprotein B [Source:MGI Symbol;Acc:MGI:104805]		Q9CQI7	-5.5	4.8E-04	-3.1	9.4E-02	1.9	1.1E-01	-0.8	7.0E-01
ENSMUST00000008280	four and a half LIM domains 2 [Source:MGI Symbol;Acc:MGI:1338762]	Q543D7	O70433	2.0	1.2E-01	-1.2	2.5E-01	-4.4	2.3E-03	-1.1	2.9E-01
ENSMUST00000008517	PRP31 pre-mRNA processing factor 31 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916238]		Q8CCF0	-4.5	1.6E-04	-2.5	1.2E-01	0.6	4.4E-01	-2.0	2.6E-01
ENSMUST00000008528	SERTA domain containing 1 [Source:MGI Symbol;Acc:MGI:1913438]		Q9JL10	-3.9	4.2E-05	7.5	2.7E-04	0.5	6.9E-01	-0.2	8.0E-01
ENSMUST00000008537	calcium regulated heat stable protein 1 [Source:MGI Symbol;Acc:MGI:1196368]	Q5M9P7	Q9CR86	-5.3	1.4E-05	6.9	3.0E-05	-0.8	4.1E-01	-0.1	7.7E-01
ENSMUST00000008445	phosphorylated adaptor for RNA export [Source:MGI Symbol;Acc:MGI:1891839]		Q9JJT9	-1.0	1.3E-01	-2.8	5.9E-03	-1.4	2.2E-02	0.4	6.4E-01
ENSMUST00000008573	HERPUD family member 2 [Source:MGI Symbol;Acc:MGI:1915393]		Q9JJC9	-3.6	4.2E-05	-2.7	2.7E-02	0.9	1.4E-01	-1.2	3.0E-01
ENSMUST00000008579	retinol dehydrogenase 13 (all-trans and 9-cis) [Source:MGI Symbol;Acc:MGI:1918732]		Q8CEE7	3.3	4.5E-05	-3.5	3.6E-03	-0.8	1.8E-01	-2.7	3.9E-02
ENSMUST00000008582	a disintegrin and metallopeptidase domain 21 [Source:MGI Symbol;Acc:MGI:1861229]		Q9JI76	4.3	5.8E-04	-4.4	1.2E-03	0.3	4.5E-01	0.2	8.6E-01
ENSMUST00000008605	fucosyltransferase 1 [Source:MGI Symbol;Acc:MGI:109375]	P97327		9.0	8.2E-06	-2.5	4.1E-03	0.9	4.0E-02	-0.6	3.6E-01
ENSMUST00000008626	ring finger protein 151 [Source:MGI Symbol;Acc:MGI:1914754]		Q9CQ29	5.4	1.0E-03	-3.9	9.3E-04	1.2	1.5E-02	-0.2	8.1E-01
ENSMUST00000008542	ELK3, member of ETS oncogene family [Source:MGI Symbol;Acc:MGI:101762]		P41971	-1.4	6.4E-02	-0.7	4.5E-01	0.3	6.2E-01	-0.5	5.9E-01
ENSMUST00000008684	microsomal glutathione S-transferase 1 [Source:MGI Symbol;Acc:MGI:1913850]	Q53ZD4	Q91VS7	-4.4	1.8E-04	-2.9	1.2E-03	1.0	1.9E-02	0.3	6.9E-01
ENSMUST00000008734	5-hydroxytryptamine (serotonin) receptor 3B [Source:MGI Symbol;Acc:MGI:1861899]		Q9JHJ5	7.3	2.9E-05	2.7	6.3E-04	-0.6	2.1E-01	0.0	9.5E-01
ENSMUST00000008745	RAB25, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1858203]	Q0PD30	Q9WTL2	4.2	6.5E-03	5.6	2.0E-04	0.2	8.4E-01	-1.1	9.9E-02
ENSMUST00000008594	nuclear transport factor 2 [Source:MGI Symbol;Acc:MGI:1915301]		P61971	0.3	6.8E-01	1.5	1.3E-01	-0.1	9.0E-01	-1.3	1.4E-01
ENSMUST00000008748	ubiquilin 4 [Source:MGI Symbol;Acc:MGI:2150152]		Q99NB8	-1.8	1.1E-02	8.8	2.2E-05	-0.5	6.8E-01	-0.2	6.3E-01
ENSMUST00000008801	cytochrome P450, family 4, subfamily f, polypeptide 15 [Source:MGI Symbol;Acc:MGI:2146921]	Q8VCA4		3.6	1.6E-02	5.3	2.6E-03	-0.9	5.2E-01	-0.8	3.5E-01
ENSMUST00000008878	G protein-coupled receptor, family C, group 5, member B [Source:MGI Symbol;Acc:MGI:1927596]		Q923Z0	7.7	1.6E-05	-4.9	3.8E-04	-1.2	2.8E-02	-0.7	4.8E-01
ENSMUST00000008733	DnaJ (Hsp40) homolog, subfamily B, member 6 [Source:MGI Symbol;Acc:MGI:1344381]		O54946	-0.9	1.3E-01	-0.6	4.0E-01	0.4	3.9E-01	0.2	8.1E-01
ENSMUST00000008893	coronin, actin binding protein 1B [Source:MGI Symbol;Acc:MGI:1345963]	A2RS22	Q9WUM3	-6.9	1.5E-05	6.6	8.7E-05	-1.2	2.7E-01	-0.5	3.8E-01
ENSMUST00000008907	mannosidase, alpha, class 1A, member 2 [Source:MGI Symbol;Acc:MGI:104676]		P39098	-2.2	1.6E-03	4.5	2.0E-02	0.6	6.9E-01	0.3	7.9E-01
ENSMUST00000008966	acylphosphatase 1, erythrocyte (common) type [Source:MGI Symbol;Acc:MGI:1913454]		P56376	-4.5	5.2E-04	0.1	9.2E-01	0.7	1.5E-01	-1.1	1.3E-01
ENSMUST00000008987	claudin 13 [Source:MGI Symbol;Acc:MGI:1913102]	Q547B2	Q9Z0S4	6.5	3.6E-03	7.1	2.2E-04	-0.6	6.3E-01	-4.2	9.8E-04
ENSMUST00000008812	ribosomal protein S18 [Source:MGI Symbol;Acc:MGI:98146]	Q561N5	P62270	-3.4	1.1E-01	-6.6	2.3E-02	-3.3	1.2E-02	-0.1	9.6E-01
ENSMUST00000008826	ribosomal protein L10 [Source:MGI Symbol;Acc:MGI:105943]		Q6ZWV3	-2.8	5.5E-02	-1.9	1.5E-01	-0.9	3.0E-01	-1.8	2.4E-01
ENSMUST00000008847				-0.7	4.4E-01	-0.4	7.7E-01	0.5	6.0E-01	0.1	9.1E-01
ENSMUST00000008991	spectrin beta, non-erythrocytic 2 [Source:MGI Symbol;Acc:MGI:1313261]	Q68FG2		7.2	9.0E-07	1.5	5.4E-02	-6.1	7.2E-05	0.1	8.6E-01
ENSMUST00000009003	v-ral simian leukemia viral oncogene homolog A (ras related) [Source:MGI Symbol;Acc:MGI:1927243]		P63321	-4.2	8.7E-05	-5.1	6.5E-04	0.8	1.1E-01	-1.0	3.6E-01
ENSMUST00000009018	C-type lectin domain family 3, member a [Source:MGI Symbol;Acc:MGI:2685642]	B2RVD1	Q9EPW4	6.5	5.4E-04	-0.9	1.9E-01	0.9	5.6E-02	-0.5	4.7E-01
ENSMUST00000009036	voltage-dependent anion channel 3 [Source:MGI Symbol;Acc:MGI:106922]	Q3TX38	Q60931	-5.0	4.1E-06	-5.6	6.6E-04	-1.2	2.4E-02	-0.1	9.2E-01
ENSMUST00000009058	ATP-binding cassette, sub-family B (MDR/TAP), member 1B [Source:MGI Symbol;Acc:MGI:97568]	B2RUR3	P06795	2.4	5.2E-03	5.9	1.1E-02	-0.3	9.0E-01	0.3	7.8E-01
ENSMUST00000009120	GA repeat binding protein, alpha [Source:MGI Symbol;Acc:MGI:95610]		Q00422	-2.5	9.0E-04	6.4	5.5E-06	-1.0	1.5E-01	-0.3	5.2E-01
ENSMUST00000008995	histone deacetylase 4 [Source:MGI Symbol;Acc:MGI:3036234]		Q6NZM9	0.6	7.9E-01	3.2	2.3E-01	1.2	5.8E-01	-1.4	5.6E-01
ENSMUST00000008999	histone deacetylase 5 [Source:MGI Symbol;Acc:MGI:1333784]	B7ZDF5		-0.8	3.3E-01	0.4	7.5E-01	1.5	1.5E-01	0.3	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000009138	serine/threonine kinase 38 [Source:MGI Symbol;Acc:MGI:2442572]		Q91VJ4	-6.7	1.0E-04	-3.5	1.4E-03	0.3	4.6E-01	-0.4	6.6E-01
ENSMUST00000009143	bone morphogenetic protein 7 [Source:MGI Symbol;Acc:MGI:103302]		P23359	8.9	2.0E-05	5.4	3.1E-03	-0.7	6.5E-01	0.4	6.3E-01
ENSMUST00000009157	dynein light chain LC8-type 1 [Source:MGI Symbol;Acc:MGI:1861457]		P63168	3.6	2.2E-05	-6.7	2.8E-05	-0.1	7.8E-01	1.6	9.3E-02
ENSMUST00000009039	ribosomal protein L30 [Source:MGI Symbol;Acc:MGI:98037]	Q58DZ3	P62889	-1.9	4.2E-02	-1.8	1.2E-01	0.2	7.3E-01	0.1	8.9E-01
ENSMUST00000009174	phosducin-like [Source:MGI Symbol;Acc:MGI:1914716]		Q9DBX2	-5.6	8.0E-05	0.5	4.8E-01	-2.4	2.9E-03	-0.5	4.3E-01
ENSMUST00000009102	vacuolar protein sorting 72 (yeast) [Source:MGI Symbol;Acc:MGI:1202305]		Q62481	-0.6	3.3E-01	-0.2	8.0E-01	0.7	2.1E-01	0.3	6.6E-01
ENSMUST00000009219	calcium binding protein 7 [Source:MGI Symbol;Acc:MGI:2183437]	Q5NCJ7	Q91ZM8	7.3	3.8E-05	-2.4	6.4E-03	0.4	3.0E-01	0.3	6.7E-01
ENSMUST00000009220	zinc finger, matrin type 5 [Source:MGI Symbol;Acc:MGI:1914428]		Q9CQR5	-4.9	1.3E-03	-6.6	1.7E-03	1.1	9.0E-02	1.0	5.4E-01
ENSMUST00000009234	adaptor protein complex AP-1, beta 1 subunit [Source:MGI Symbol;Acc:MGI:1096368]		O35643	-3.7	9.3E-03	5.6	8.4E-04	-2.5	7.0E-02	0.9	2.4E-01
ENSMUST00000009236	Der1-like domain family, member 3 [Source:MGI Symbol;Acc:MGI:1917627]	Q14C34	Q9D8K3	5.9	3.6E-05	3.2	3.3E-04	0.1	7.8E-01	0.5	2.1E-01
ENSMUST00000009256	BCL2-like 13 (apoptosis facilitator) [Source:MGI Symbol;Acc:MGI:2136959]		P59017	-1.0	1.4E-02	-4.1	1.1E-03	-0.2	7.5E-01	-1.6	1.4E-01
ENSMUST00000009214	radial spoke head homolog 14 (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1918486]		Q9D3W1	3.2	7.6E-02	6.1	4.2E-03	-0.5	7.9E-01	-3.4	1.4E-02
ENSMUST00000009259	spermatogenesis and centriole associated 1 like [Source:MGI Symbol;Acc:MGI:1923823]		Q9D9W0	6.7	8.0E-05	7.0	1.7E-04	-0.5	6.8E-01	-0.1	8.6E-01
ENSMUST00000009321	DiGeorge syndrome critical region gene 8 [Source:MGI Symbol;Acc:MGI:2151114]		Q9EQM6	-4.0	1.5E-03	-5.8	5.7E-03	-0.4	5.4E-01	0.5	7.6E-01
ENSMUST00000009344	exportin 6 [Source:MGI Symbol;Acc:MGI:2429950]		Q924Z6	-9.6	1.9E-04	-1.5	2.9E-01	0.7	4.4E-01	-1.6	2.8E-01
ENSMUST00000009354	proline rich 29 [Source:MGI Symbol;Acc:MGI:1922823]		B1ARI9	5.5	7.6E-04	4.1	1.5E-03	-1.5	1.1E-01	0.3	6.2E-01
ENSMUST00000009358	transmembrane protein 8C [Source:MGI Symbol;Acc:MGI:1913389]		Q9D1N4	5.5	1.9E-02	-0.2	7.0E-01	0.9	1.7E-02	0.1	9.0E-01
ENSMUST00000009396	tetraspanin 32 [Source:MGI Symbol;Acc:MGI:1350360]		Q9JHH2	-3.4	4.6E-03	7.3	7.1E-05	-0.6	6.0E-01	-1.3	5.7E-02
ENSMUST00000009435	pituitary tumor-transforming 1 interacting protein [Source:MGI Symbol;Acc:MGI:2652132]		Q8R143	-5.1	7.9E-06	-3.4	1.4E-02	0.0	9.3E-01	-0.7	5.9E-01
ENSMUST00000009340	myeloid cell nuclear differentiation antigen [Source:MGI Symbol;Acc:MGI:3041120]		Q08619	-0.5	5.1E-01	-3.2	4.1E-03	-3.2	7.9E-04	-0.5	5.6E-01
ENSMUST00000009522	olute carrier family 16 (monocarboxylic acid transporters), member 12 [Source:MGI Symbol;Acc:MGI:214771(		Q8BGC3	3.5	1.5E-04	-7.0	7.5E-03	1.9	2.1E-02	-0.8	7.4E-01
ENSMUST00000009538	synapsin II [Source:MGI Symbol;Acc:MGI:103020]		Q64332	7.3	2.6E-05	6.0	7.3E-04	-0.5	6.9E-01	-1.1	1.6E-01
ENSMUST00000009356	serine (or cysteine) peptidase inhibitor, clade B, member 2 [Source:MGI Symbol;Acc:MGI:97609]	Q542A3	P12388	2.0	2.4E-01	-3.8	9.2E-02	-5.4	3.5E-03	0.4	8.5E-01
ENSMUST00000009617	potassium voltage gated channel, Shaw-related subfamily, member 4 [Source:MGI Symbol;Acc:MGI:96670]		Q8R1C0	8.8	2.1E-05	7.3	6.4E-03	-0.6	7.9E-01	-2.4	7.1E-02
ENSMUST00000009667	Usher syndrome 1C [Source:MGI Symbol;Acc:MGI:1919338]	E9QMN1		7.4	2.4E-02	-1.5	2.4E-01	1.4	9.4E-02	-0.5	6.9E-01
ENSMUST00000009411	Zinc finger protein 212 [Source:MGI Symbol;Acc:MGI:2682609]	G3X8R7		-0.9	9.2E-02	-0.3	6.4E-01	0.8	1.0E-01	0.2	7.5E-01
ENSMUST00000009679	RNA (guanine-7-) methyltransferase [Source:MGI Symbol;Acc:MGI:1915147]		Q9D0L8	-4.0	4.6E-03	-4.2	2.1E-04	0.6	8.4E-02	-0.2	7.6E-01
ENSMUST00000009689	potassium voltage-gated channel, subfamily Q, member 1 [Source:MGI Symbol;Acc:MGI:108083]		P97414	8.8	1.4E-05	2.4	5.1E-03	-0.3	6.6E-01	0.8	1.7E-01
ENSMUST00000009530	tissue inhibitor of metalloproteinase 1 [Source:MGI Symbol;Acc:MGI:98752]		P12032	1.8	1.6E-01	-5.9	3.1E-03	-6.6	7.3E-05	1.1	4.8E-01
ENSMUST00000009693	signal recognition particle 14 [Source:MGI Symbol;Acc:MGI:107169]		P16254	-7.8	2.2E-05	6.5	8.9E-05	-1.3	2.4E-01	-0.5	3.4E-01
ENSMUST00000009550	ELK1, member of ETS oncogene family [Source:MGI Symbol;Acc:MGI:101833]		P41969	-0.8	2.1E-01	0.1	9.0E-01	1.0	1.2E-01	0.1	9.1E-01
ENSMUST00000009699	cyclin-dependent kinase 9 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1328368]		Q99J95	-8.6	9.8E-05	8.0	8.8E-05	-0.7	6.1E-01	0.2	7.9E-01
ENSMUST00000009705	endoglin [Source:MGI Symbol;Acc:MGI:95392]		Q63961	5.4	1.0E-02	5.9	8.4E-02	-0.9	7.9E-01	0.6	7.5E-01
ENSMUST00000009707	torsin family 2, member A [Source:MGI Symbol;Acc:MGI:1353596]		Q8R1J9	-8.2	2.9E-05	-0.4	6.6E-01	0.1	8.9E-01	-3.5	1.3E-02
ENSMUST00000009727	synaptogyrin 1 [Source:MGI Symbol;Acc:MGI:1328323]		O55100	5.6	9.6E-05	7.1	5.7E-05	-1.9	1.3E-01	-0.3	6.5E-01
ENSMUST00000009732	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 [Source:MGI Symbo		Q9QZ39	9.7	1.0E-05	-6.2	3.9E-05	-0.6	1.2E-01	-2.2	6.8E-02
ENSMUST00000009695	RIKEN cDNA 6330409D20 gene [Source:MGI Symbol;Acc:MGI:1917980]	A2AK85		0.1	8.5E-01	1.5	9.0E-02	0.8	2.2E-01	-0.5	4.5E-01
ENSMUST00000009774	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform [Source:MGI Symbol;Acc:MGI:1321161]		P62715	-5.6	7.4E-06	-6.5	3.4E-03	1.5	2.4E-02	-0.6	7.5E-01
ENSMUST00000009777	G0/G1 switch gene 2 [Source:MGI Symbol;Acc:MGI:1316737]	Q545U0	Q61585	-4.5	4.6E-04	7.4	8.3E-03	0.8	7.4E-01	-1.2	3.6E-01
ENSMUST00000009790	phospholipase A2, group XIIB [Source:MGI Symbol;Acc:MGI:1917086]	Q8VC81		6.5	6.9E-05	-6.9	6.3E-04	0.7	1.5E-01	-0.6	6.9E-01
ENSMUST00000009713	MKL/myocardin-like 2 [Source:MGI Symbol;Acc:MGI:3050795]	G3X8R8		-0.4	8.1E-01	2.9	2.6E-01	3.9	6.3E-02	0.6	7.8E-01
ENSMUST00000009798	oncoprotein induced transcript 3 [Source:MGI Symbol;Acc:MGI:1201782]		Q8R4V5	5.5	1.1E-05	7.8	1.0E-04	1.4	2.5E-01	-0.8	2.6E-01
ENSMUST00000009831	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	F8WJA1		-11.2	2.6E-06	7.4	6.0E-05	-2.1	1.1E-01	0.2	7.7E-01
ENSMUST00000009772	testis expressed gene 15 [Source:MGI Symbol;Acc:MGI:1934816]	F8VPN2		0.7	3.3E-01	1.1	2.7E-01	1.0	2.1E-01	0.6	4.6E-01
ENSMUST00000009875	potassium voltage-gated channel, Shal-related family, member 1 [Source:MGI Symbol;Acc:MGI:96671]	A2AEX0	Q03719	2.4	3.0E-02	-4.3	3.3E-04	0.9	3.0E-02	-0.3	7.3E-01
ENSMUST00000009877	transcription factor CP2 [Source:MGI Symbol;Acc:MGI:98509]		Q9ERA0	1.6	1.5E-02	-4.8	1.4E-03	-0.4	4.7E-01	-0.1	9.4E-01
ENSMUST00000009789	proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide [Source:MGI Symbol;Acc:		Q60715	-0.2	6.2E-01	-0.1	8.8E-01	0.2	6.9E-01	0.0	9.5E-01
ENSMUST00000009972	intestinal cell kinase [Source:MGI Symbol;Acc:MGI:1934157]	Q9D7Q7		7.4	1.9E-03	6.2	1.9E-04	-0.6	6.2E-01	-0.2	7.0E-01
ENSMUST00000010007	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) [Source:MGI Symbol;Acc:MGI:1914930]		Q9CQA3	-7.0	4.2E-06	7.1	2.6E-05	1.4	1.3E-01	-0.2	7.0E-01
ENSMUST00000010044	wingless-type MMTV integration site family, member 3A [Source:MGI Symbol;Acc:MGI:98956]		P27467	8.2	1.3E-05	-11.3	2.0E-05	-0.8	4.2E-02	-0.7	6.4E-01
ENSMUST00000010049	3-ketodihydrosphingosine reductase [Source:MGI Symbol;Acc:MGI:1918000]	Q8CII3	Q6GV12	1.8	4.9E-03	2.3	1.0E-01	0.4	7.3E-01	0.5	6.7E-01
ENSMUST00000010189	transmembrane protein 115 [Source:MGI Symbol;Acc:MGI:1930765]	Q543Y8	Q9WUH1	-1.8	1.3E-02	2.3	1.2E-02	0.6	3.0E-01	0.0	9.6E-01
ENSMUST00000009885	upstream binding protein 1 [Source:MGI Symbol;Acc:MGI:104889]		Q811S7	-3.5	8.8E-02	-0.7	7.5E-01	1.2	4.3E-01	-1.6	5.0E-01
ENSMUST00000010191	hyaluronoglucosaminidase 2 [Source:MGI Symbol;Acc:MGI:1196334]	Q3UZE4	O35632	-3.4	1.3E-02	5.9	1.3E-02	-0.3	8.8E-01	1.2	3.2E-01
ENSMUST00000010195	hyaluronoglucosaminidase 1 [Source:MGI Symbol;Acc:MGI:96298]		Q91ZJ9	6.9	6.2E-05	-6.7	4.1E-05	-0.3	3.9E-01	-0.6	5.4E-01
ENSMUST00000010038	synaptosomal-associated protein, 47 [Source:MGI Symbol;Acc:MGI:1915076]		Q8R570	-0.9	1.1E-01	-0.4	5.3E-01	-0.4	3.7E-01	-0.9	1.7E-01
ENSMUST00000010198	tumor suppressor candidate 2 [Source:MGI Symbol;Acc:MGI:1931086]	Q542N4	Q9WVF8	-2.9	6.2E-04	7.9	3.5E-05	-0.6	6.0E-01	-0.3	6.3E-01
ENSMUST00000010201	nitrogen permease regulator-like 2 [Source:MGI Symbol;Acc:MGI:1914482]		Q9WUE4	-5.9	2.6E-04	1.5	3.8E-02	0.0	9.6E-01	0.3	6.3E-01
ENSMUST00000010205	guanine nucleotide binding protein, alpha transducing 1 [Source:MGI Symbol;Acc:MGI:95778]		P20612	6.7	5.1E-05	-0.9	2.6E-01	0.9	8.0E-02	0.1	9.2E-01
ENSMUST00000010208	solute carrier family 38, member 3 [Source:MGI Symbol;Acc:MGI:1923507]		Q9DCP2	5.6	2.3E-02	-3.5	3.3E-02	-0.8	3.2E-01	-0.7	6.4E-01
ENSMUST00000010192	interferon-related developmental regulator 2 [Source:MGI Symbol;Acc:MGI:1316708]	Q9D8U0		-0.8	5.6E-01	0.3	8.3E-01	-0.7	5.0E-01	-1.8	2.3E-01
ENSMUST00000010211	Ras association (RalGDS/AF-6) domain family member 1 [Source:MGI Symbol;Acc:MGI:1928386]		Q99MK9	-4.8	2.7E-05	7.0	1.0E-04	-0.5	6.4E-01	-0.7	2.7E-01
ENSMUST00000010241	nuclear RNA export factor 1 [Source:MGI Symbol;Acc:MGI:1858330]		Q99JX7	-7.3	7.4E-05	-1.2	1.2E-01	1.2	2.8E-02	-0.6	4.3E-01
ENSMUST00000010248	nuclear RNA export factor 1 [Source:MGI Symbol;Acc:MGI:1858330]		Q9CQE2	-2.5	2.0E-02	-4.2	4.6E-03	0.2	7.1E-01	-1.5	2.7E-01
ENSMUST00000010249	ke RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor [Source:MGI Symbol;Acc:MGI:2		Q9CY24	-5.8	6.7E-06	8.0	2.1E-05	-0.6	5.7E-01	-1.9	6.2E-03
ENSMUST00000010250	solute carrier family 22 (organic anion transporter), member 6 [Source:MGI Symbol;Acc:MGI:892001]		Q8VC69	8.2	1.5E-05	5.7	2.7E-02	-0.8	7.5E-01	-0.9	5.4E-01
ENSMUST00000010251	solute carrier family 22 (organic anion transporter), member 8 [Source:MGI Symbol;Acc:MGI:1336187]		O88909	9.4	1.7E-02	-5.3	3.0E-04	0.0	9.8E-01	0.4	6.5E-01
ENSMUST00000010224				3.9	5.3E-02	4.6	4.5E-02	-0.5	8.3E-01	-1.1	4.1E-01
ENSMUST00000010239	rrier family 3 (activators of dibasic and neutral amino acid transport), member 2 [Source:MGI Symbol;Acc:MC		P10852	-1.3	4.0E-02	-0.5	4.9E-01	0.9	1.0E-01	0.1	8.4E-01
ENSMUST00000010267	solute carrier family 47, member 1 [Source:MGI Symbol;Acc:MGI:1914723]		Q8K0H1	5.7	8.1E-04	-7.3	1.1E-03	0.4	3.7E-01	0.5	7.8E-01
ENSMUST00000010278	WD repeat domain 77 [Source:MGI Symbol;Acc:MGI:1917715]		Q99J09	-8.4	6.4E-04	0.0	9.9E-01	1.8	6.8E-02	-0.6	5.7E-01
ENSMUST00000010286	tumor necrosis factor receptor superfamily, member 13b [Source:MGI Symbol;Acc:MGI:1889411]	A5D8Y6	Q9ET35	-4.7	5.1E-06	-4.9	1.6E-04	0.3	3.7E-01	-0.6	4.9E-01
ENSMUST00000010298	spire homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2446256]		Q8K1S6	6.4	1.8E-04	8.5	2.1E-05	-0.6	5.9E-01	-0.9	9.5E-02
ENSMUST00000010319	prospero homeobox 1 [Source:MGI Symbol;Acc:MGI:97772]		P48437	6.3	2.5E-02	9.5	2.0E-02	-1.0	8.0E-01	-1.1	5.2E-01
ENSMUST00000010254	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]	I1E4X1		-3.5	2.7E-01	-3.1	4.3E-01	0.1	9.8E-01	-0.3	9.4E-01
ENSMUST00000010421	RIKEN cDNA 2610507B11 gene [Source:MGI Symbol;Acc:MGI:1919753]		Q5SYL3	-2.6	6.1E-05	5.9	8.1E-04	-1.2	3.9E-01	-1.4	9.0E-02
ENSMUST00000010502	interferon-induced protein 35 [Source:MGI Symbol;Acc:MGI:1917360]		Q9D8C4	-6.8	2.4E-04	-5.5	3.4E-02	2.4	1.7E-02	-0.5	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000010506	RAD52 motif 1 [Source:MGI Symbol;Acc:MGI:1913849]		Q9CQK3	-4.3	2.8E-03	-2.7	1.6E-03	1.5	1.2E-03	-0.5	4.4E-01
ENSMUST00000010520	neural precursor cell expressed, developmentally down-regulated gene 8 [Source:MGI Symbol;Acc:MGI:97301	Q3UI46	P29595	-6.9	1.1E-04	3.9	3.7E-03	-2.7	3.0E-02	-0.2	7.6E-01
ENSMUST00000010536	golgi SNAP receptor complex member 1 [Source:MGI Symbol;Acc:MGI:1858260]		O88630	-2.2	2.6E-04	4.4	1.5E-01	-0.7	8.0E-01	1.2	5.3E-01
ENSMUST00000010348	ferredoxin 1-like [Source:MGI Symbol;Acc:MGI:1915415]		Q9CPW2	-0.2	7.3E-01	0.2	7.5E-01	-0.5	3.8E-01	-0.9	1.8E-01
ENSMUST00000010550	mitochondrial ribosomal protein L52 [Source:MGI Symbol;Acc:MGI:1916086]		Q9D0Y8	-5.0	3.2E-04	-2.4	7.3E-04	0.1	7.8E-01	-0.1	8.5E-01
ENSMUST00000010434	expressed sequence AI597479 [Source:MGI Symbol;Acc:MGI:2138299]		Q922M7	-0.6	2.1E-01	-0.1	8.6E-01	0.3	5.4E-01	-0.3	6.7E-01
ENSMUST00000010451	transmembrane protein 86A [Source:MGI Symbol;Acc:MGI:1915143]		Q9D8N3	-1.7	3.6E-02	-0.3	7.3E-01	1.4	5.2E-02	0.0	9.7E-01
ENSMUST00000010597	KAT8 regulatory NSL complex subunit 3 [Source:MGI Symbol;Acc:MGI:1918055]		A2RSY1	-5.2	3.7E-03	-3.9	4.5E-03	0.0	9.6E-01	-2.9	5.9E-02
ENSMUST00000010673	predicted gene 266 [Source:MGI Symbol;Acc:MGI:2685112]	A6H634		3.2	2.1E-03	-4.7	8.8E-03	-0.2	7.1E-01	0.2	9.0E-01
ENSMUST00000010804	phospholipase C, delta 1 [Source:MGI Symbol;Acc:MGI:97614]		Q8R3B1	5.5	1.0E-03	-6.8	7.7E-04	-0.5	4.3E-01	-0.6	7.1E-01
ENSMUST00000010899	cysteinyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1351477]		Q9ER72	2.8	2.2E-02	-1.3	1.8E-02	0.2	5.0E-01	-0.7	1.6E-01
ENSMUST00000010904	pleckstrin homology-like domain, family A, member 2 [Source:MGI Symbol;Acc:MGI:1202307]		O08969	5.5	2.0E-04	-5.1	9.0E-04	-0.7	1.9E-01	-0.6	5.8E-01
ENSMUST00000010941	wingless-type MMTV integration site family, member 2 [Source:MGI Symbol;Acc:MGI:98954]		P21552	6.2	7.2E-03	-6.0	9.0E-03	0.1	8.7E-01	0.9	6.7E-01
ENSMUST00000010974	L (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 [Source:MGI Symbol;Acc:MGI:2145		Q8R1L4	4.7	3.7E-03	5.2	8.9E-04	1.4	2.1E-01	-0.6	3.2E-01
ENSMUST00000010795	acetyl-Coenzyme A acyltransferase 1B [Source:MGI Symbol;Acc:MGI:3605455]	Q3UKM0	Q8VCH0	-0.9	2.9E-01	0.7	5.5E-01	1.5	9.5E-02	0.0	9.7E-01
ENSMUST00000011055	APAF1 interacting protein [Source:MGI Symbol;Acc:MGI:1926788]		Q9WVQ5	-5.5	1.4E-04	5.4	6.3E-03	-0.5	7.3E-01	-0.3	7.3E-01
ENSMUST00000010807	fatty acid desaturase 1 [Source:MGI Symbol;Acc:MGI:1923517]		Q920L1	0.7	1.4E-01	0.7	2.3E-01	0.0	9.8E-01	0.0	9.7E-01
ENSMUST00000011058	pyruvate dehydrogenase complex, component X [Source:MGI Symbol;Acc:MGI:1351627]		Q8BKZ9	-2.3	3.2E-03	2.7	1.1E-01	1.1	4.3E-01	1.2	2.8E-01
ENSMUST00000011152	mucolipin 2 [Source:MGI Symbol;Acc:MGI:1915529]		Q8K595	5.8	2.4E-03	4.1	9.5E-04	-2.1	5.7E-02	-0.7	2.3E-01
ENSMUST00000011178	solute carrier family 5 (sodium/glucose cotransporter), member 1 [Source:MGI Symbol;Acc:MGI:107678]	Q9QXI6		7.0	3.5E-05	6.9	6.5E-03	-0.7	7.4E-01	-1.4	2.5E-01
ENSMUST00000011262	pannexin 3 [Source:MGI Symbol;Acc:MGI:1918881]	Q6IMP0	Q8CEG0	6.2	2.8E-04	1.7	1.3E-01	-4.1	6.2E-03	-1.1	2.5E-01
ENSMUST00000011285	fibroblast growth factor 11 [Source:MGI Symbol;Acc:MGI:109167]	Q6NXW2		4.8	3.3E-03	-3.0	4.1E-03	-0.1	8.3E-01	-2.6	2.5E-02
ENSMUST00000011302	g, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae) [Source:MGI Symbol;Acc:M	G3X8S2		-1.7	2.1E-02	-1.6	4.8E-02	0.2	7.1E-01	-0.5	4.8E-01
ENSMUST00000011315	vasoactive intestinal peptide receptor 2 [Source:MGI Symbol;Acc:MGI:107166]	Q546Q8	P41588	6.7	1.2E-04	0.0	9.8E-01	-5.2	3.4E-03	0.6	6.0E-01
ENSMUST00000011391	protease, serine 45 [Source:MGI Symbol;Acc:MGI:3605764]		Q8K4I7	6.3	2.1E-02	7.4	1.2E-04	0.5	7.0E-01	0.0	9.8E-01
ENSMUST00000011400	a disintegrin and metallopeptidase domain 19 (meltrin beta) [Source:MGI Symbol;Acc:MGI:105377]	Q3UHT3	O35674	-2.9	1.1E-03	6.4	4.3E-04	-0.5	7.1E-01	-0.6	3.7E-01
ENSMUST00000011407	exocyst complex component 3-like 2 [Source:MGI Symbol;Acc:MGI:1921713]	E9Q180		5.0	1.8E-02	6.5	1.8E-03	-0.2	8.7E-01	-1.9	5.7E-02
ENSMUST00000011450	SURP and G patch domain containing 1 [Source:MGI Symbol;Acc:MGI:1917866]		Q8CH02	-2.3	1.3E-03	-0.8	3.5E-01	0.5	3.3E-01	-0.4	6.0E-01
ENSMUST00000011492	acyl-Coenzyme A dehydrogenase family, member 9 [Source:MGI Symbol;Acc:MGI:1914272]		Q8JZN5	5.6	1.2E-07	8.4	7.9E-04	2.1	2.2E-01	0.4	6.4E-01
ENSMUST00000011493	doublesex and mab-3 related transcription factor like family C2 [Source:MGI Symbol;Acc:MGI:1918491]		Q8CGW9	7.3	9.4E-05	2.9	3.4E-01	-0.9	7.5E-01	2.5	3.0E-01
ENSMUST00000011398	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913878]		Q9CY52	0.4	4.2E-01	-0.4	5.2E-01	-1.3	1.9E-02	-0.5	4.4E-01
ENSMUST00000011526	dihydrodiol dehydrogenase (dimeric) [Source:MGI Symbol;Acc:MGI:1919005]		Q9DBB8	5.1	1.1E-05	-2.4	1.4E-02	0.7	1.8E-01	0.2	7.6E-01
ENSMUST00000011607	carboxypeptidase B1 (tissue) [Source:MGI Symbol;Acc:MGI:1923953]	B2RS76		9.6	4.0E-05	5.3	3.0E-02	0.5	8.3E-01	0.2	9.0E-01
ENSMUST00000011623	DENN/MADD domain containing 1C [Source:MGI Symbol;Acc:MGI:1918035]		Q8CFK6	-3.4	3.5E-03	-1.2	8.6E-02	0.7	1.1E-01	-0.4	5.6E-01
ENSMUST00000011733	fibronectin type 3 and SPRY domain-containing protein [Source:MGI Symbol;Acc:MGI:1934858]		Q7TPM6	7.5	1.0E-04	5.7	3.5E-07	-0.3	4.6E-01	-0.4	2.1E-01
ENSMUST00000011877	spectrin beta, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98388]		Q62261	-8.6	4.9E-05	6.7	3.2E-04	-0.7	6.2E-01	-0.1	9.0E-01
ENSMUST00000011896	phosphoglycerate mutase 1 [Source:MGI Symbol;Acc:MGI:97552]	Q3U7Z6	Q9DBJ1	-5.0	1.7E-05	4.5	1.4E-04	0.1	9.4E-01	0.6	2.2E-01
ENSMUST00000011934	titin [Source:MGI Symbol;Acc:MGI:98864]		A2ASS6	9.4	1.0E-03	8.6	2.1E-04	-0.3	8.3E-01	0.6	3.8E-01
ENSMUST00000012028	glycolipid transfer protein [Source:MGI Symbol;Acc:MGI:1929253]		Q9JL62	-4.6	1.1E-04	-2.6	4.7E-02	0.7	3.1E-01	-0.1	9.1E-01
ENSMUST00000012152	DiGeorge syndrome critical region gene 2 [Source:MGI Symbol;Acc:MGI:892866]	Q6P5A9		-5.4	3.6E-03	7.4	2.2E-04	-0.7	6.3E-01	-0.5	4.5E-01
ENSMUST00000012161	scavenger receptor class F, member 2 [Source:MGI Symbol;Acc:MGI:1858430]	Q58A84	P59222	7.7	1.4E-05	-4.8	7.4E-04	0.2	6.6E-01	-3.6	2.3E-02
ENSMUST00000011895	spectrin beta, non-erythrocytic 4 [Source:MGI Symbol;Acc:MGI:1890574]	E9PX29		5.1	6.9E-02	6.7	4.5E-02	-0.1	9.8E-01	-1.7	3.3E-01
ENSMUST00000012186	RIKEN cDNA 4930579F01 gene [Source:MGI Symbol;Acc:MGI:1914991]	E9Q3L6		8.0	3.7E-04	-3.1	2.7E-03	1.7	2.7E-03	-0.2	8.2E-01
ENSMUST00000012259	mediator complex subunit 15 [Source:MGI Symbol;Acc:MGI:2137379]	G3X8S4		-5.3	2.5E-03	3.1	2.2E-01	-2.0	4.0E-01	4.4	3.0E-02
ENSMUST00000011981	small nuclear RNA activating complex, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1914861]		Q91XA5	-0.8	1.8E-01	0.8	3.1E-01	1.3	4.7E-02	-0.3	6.3E-01
ENSMUST00000012279	goosecoid homebox 2 [Source:MGI Symbol;Acc:MGI:892006]	A2RTU1		6.3	1.5E-04	-1.8	5.1E-02	1.6	8.8E-03	-1.2	1.9E-01
ENSMUST00000012104	cyclin T1 [Source:MGI Symbol;Acc:MGI:1328363]		Q9QWV9	0.6	7.7E-01	0.5	8.1E-01	-2.9	1.1E-01	-2.8	2.1E-01
ENSMUST00000012281	bone morphogenetic protein 5 [Source:MGI Symbol;Acc:MGI:88181]		P49003	7.9	8.7E-05	-3.9	8.2E-02	1.9	1.0E-01	0.4	8.4E-01
ENSMUST00000012314	zinc finger protein 729a [Source:MGI Symbol;Acc:MGI:3036250]	Q4QQP3		-2.2	1.5E-03	2.4	3.4E-03	-5.4	1.7E-04	-0.1	8.4E-01
ENSMUST00000012348	glutathione S-transferase, mu 2 [Source:MGI Symbol;Acc:MGI:95861]		P15626	6.2	3.5E-04	6.7	2.3E-03	-0.8	6.5E-01	0.5	5.7E-01
ENSMUST00000012355	testis expressed gene 22 [Source:MGI Symbol;Acc:MGI:1922921]		Q9D9U4	7.1	5.6E-05	-0.8	5.2E-01	0.5	5.7E-01	-4.0	2.1E-02
ENSMUST00000012262	dehydrodolichyl diphosphate synthase [Source:MGI Symbol;Acc:MGI:1914672]		Q99KU1	-3.8	4.1E-01	-3.1	6.0E-01	-0.3	9.3E-01	-0.9	8.8E-01
ENSMUST00000012426	wingless-type MMTV integration site family, member 8A [Source:MGI Symbol;Acc:MGI:107924]		Q64527	7.2	4.9E-05	6.3	2.8E-04	-0.5	6.7E-01	-0.5	4.0E-01
ENSMUST00000012566	transmembrane protein 167 [Source:MGI Symbol;Acc:MGI:1913324]		Q9CR64	-4.4	9.9E-06	6.7	2.6E-03	-0.5	7.5E-01	0.8	3.8E-01
ENSMUST00000012627	replication protein A3 [Source:MGI Symbol;Acc:MGI:1915490]		Q9CQ71	-5.4	1.8E-04	-1.4	5.0E-02	0.7	9.6E-02	-0.1	9.0E-01
ENSMUST00000012664	paired-like homeobox 2b [Source:MGI Symbol;Acc:MGI:1100882]		O35690	6.7	8.2E-05	-0.2	8.3E-01	-6.9	9.9E-05	-0.5	5.2E-01
ENSMUST00000012679	transportin 3 [Source:MGI Symbol;Acc:MGI:1196412]		Q6P2B1	-3.8	7.6E-03	6.6	1.8E-04	-0.6	6.0E-01	-0.2	7.9E-01
ENSMUST00000012798	sialic acid binding Ig-like lectin F [Source:MGI Symbol;Acc:MGI:2681107]		Q920G3	-6.7	4.3E-03	7.1	1.0E-04	-0.6	6.2E-01	-0.5	4.1E-01
ENSMUST00000012440	tight junction associated protein 1 [Source:MGI Symbol;Acc:MGI:1921344]		Q9DCD5	1.4	1.6E-01	0.1	9.5E-01	0.3	7.9E-01	1.6	2.1E-01
ENSMUST00000012540	Nanog homeobox [Source:MGI Symbol;Acc:MGI:1919200]	A2RS90	Q80Z64	4.7	9.8E-02	6.6	4.2E-02	-0.2	9.4E-01	-2.2	2.1E-01
ENSMUST00000012847	CD209a antigen [Source:MGI Symbol;Acc:MGI:2157942]		Q91ZX1	3.7	8.2E-03	-4.4	7.2E-04	0.9	4.0E-02	0.9	3.4E-01
ENSMUST00000012580	Hermansky-Pudlak syndrome 3 homolog (human) [Source:MGI Symbol;Acc:MGI:2153839]		Q91VB4	3.0	1.3E-01	1.5	4.2E-01	-2.2	2.4E-01	-0.6	7.0E-01
ENSMUST00000012587	kinesin family member 11 [Source:MGI Symbol;Acc:MGI:1098231]		Q6P9P6	-0.5	2.9E-01	0.1	9.3E-01	0.8	8.5E-02	0.3	6.6E-01
ENSMUST00000012612	zinc finger, MIZ-type containing 2 [Source:MGI Symbol;Acc:MGI:106374]		Q8CIE2	-0.5	8.2E-01	-1.0	7.5E-01	-1.0	6.3E-01	-0.5	8.5E-01
ENSMUST00000012873	zinc finger protein 729b [Source:MGI Symbol;Acc:MGI:2145180]	Q80VN4		-4.0	5.6E-04	-4.0	2.5E-03	0.1	8.3E-01	-1.3	2.8E-01
ENSMUST00000013130	striatin, calmodulin binding protein 3 [Source:MGI Symbol;Acc:MGI:2151064]		Q9ERG2	-3.1	2.5E-02	7.3	8.0E-05	-0.5	6.9E-01	-1.1	9.7E-02
ENSMUST00000013220	angiomotin-like 1 [Source:MGI Symbol;Acc:MGI:1922973]		Q9D4H4	7.8	2.8E-05	-3.2	4.6E-02	0.1	9.1E-01	-0.5	7.2E-01
ENSMUST00000013235	transmembrane protein 190 [Source:MGI Symbol;Acc:MGI:1925302]		Q9D2E9	6.1	3.4E-04	-2.5	1.5E-01	1.1	2.6E-01	-3.1	1.5E-01
ENSMUST00000013294	glucose-fructose oxidoreductase domain containing 2 [Source:MGI Symbol;Acc:MGI:1917825]		Q9CYH5	4.5	6.2E-06	0.1	9.6E-01	-3.4	1.0E-02	0.3	7.7E-01
ENSMUST00000012849	resistin [Source:MGI Symbol;Acc:MGI:1888506]	Q5BMX4	Q99P87	0.9	4.4E-02	0.6	2.6E-01	-0.8	7.6E-02	-0.4	4.0E-01
ENSMUST00000013302	RIKEN cDNA 4933405L10 gene [Source:MGI Symbol;Acc:MGI:1918296]		Q9D4A5	6.2	1.2E-04	-1.8	8.4E-02	0.6	2.8E-01	-1.6	1.3E-01
ENSMUST00000013304	ATPase, H+ transporting, lysosomal V0 subunit D1 [Source:MGI Symbol;Acc:MGI:1201778]		P51863	-6.4	1.3E-05	-5.2	4.0E-02	0.0	9.6E-01	2.0	3.7E-01
ENSMUST00000013338	ariadne homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1344361]	Q3TK92	Q9Z1K6	-7.8	3.6E-04	3.9	1.3E-03	-4.5	1.3E-03	-0.5	4.3E-01
ENSMUST00000013455	alcohol dehydrogenase 6A (class V) [Source:MGI Symbol;Acc:MGI:1916367]	E9Q4Y1		7.5	3.0E-04	6.0	6.7E-04	-0.6	6.5E-01	-0.5	4.8E-01
ENSMUST00000013262	zinc finger with KRAB and SCAN domains 17 [Source:MGI Symbol;Acc:MGI:2679270]		Q5SXI5	0.2	8.8E-01	-2.5	2.1E-01	-0.4	7.6E-01	2.3	2.4E-01
ENSMUST00000013497	RIKEN cDNA 4931406B18 gene [Source:MGI Symbol;Acc:MGI:1921304]	A2RSL7		5.7	2.8E-05	4.6	3.7E-05	0.3	5.5E-01	0.2	5.8E-01
ENSMUST00000013299	enkurin domain containing 1 [Source:MGI Symbol;Acc:MGI:2142593]		Q7TSV9	0.7	2.3E-01	1.6	6.0E-02	1.1	9.4E-02	0.2	7.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000013559	insulin-like growth factor 2 mRNA binding protein 1 [Source:MGI Symbol;Acc:MGI:1890357]		O88477	9.1	1.6E-05	6.8	1.1E-04	-0.6	6.3E-01	-1.2	7.0E-02
ENSMUST00000013633	fibroblast growth factor receptor-like 1 [Source:MGI Symbol;Acc:MGI:2150920]		Q91V87	8.3	5.1E-06	-4.0	1.3E-03	1.3	1.2E-02	-1.0	2.9E-01
ENSMUST00000013667	breast carcinoma amplified sequence 1 [Source:MGI Symbol;Acc:MGI:1924210]		Q80YN3	6.5	2.4E-02	-7.0	6.2E-03	0.7	2.8E-01	-0.1	9.6E-01
ENSMUST00000013693	COMM domain containing 8 [Source:MGI Symbol;Acc:MGI:1343485]	Q4QQP1	Q9CZG3	-1.8	1.1E-03	5.9	1.9E-03	-1.4	3.6E-01	0.1	8.9E-01
ENSMUST00000013737	NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Source:MGI Symbol;Acc:MGI:2385112]		Q91WD5	-8.6	1.1E-04	4.7	2.3E-04	-0.8	3.5E-01	0.2	7.4E-01
ENSMUST00000013759	formin binding protein 4 [Source:MGI Symbol;Acc:MGI:1860513]			-2.7	1.1E-02	7.4	6.7E-05	-2.0	1.4E-01	-0.3	6.3E-01
ENSMUST00000013615	serine/arginine repetitive matrix 3 [Source:MGI Symbol;Acc:MGI:1920309]	H7BWX3		2.9	1.5E-01	2.1	2.9E-01	-0.5	7.9E-01	0.3	8.5E-01
ENSMUST00000013766	all-trans retinoic acid induced differentiation factor [Source:MGI Symbol;Acc:MGI:1918918]	A8C1S6	Q6PGD0	-6.3	1.4E-04	4.0	8.6E-05	-5.1	1.8E-04	-0.7	1.2E-01
ENSMUST00000013771	tripartite motif-containing 54 [Source:MGI Symbol;Acc:MGI:1889623]		Q9ERP3	6.1	2.4E-02	4.9	1.1E-01	-0.9	7.5E-01	0.7	7.4E-01
ENSMUST00000013807	phosphatase and tensin homolog [Source:MGI Symbol;Acc:MGI:109583]		O08586	-4.3	1.0E-04	-1.9	4.1E-03	-0.1	6.9E-01	0.0	9.8E-01
ENSMUST00000013842	phosphoprotein enriched in astrocytes 15A [Source:MGI Symbol;Acc:MGI:104799]		Q62048	-3.0	7.6E-03	-4.6	2.2E-03	0.5	3.6E-01	-3.5	4.0E-02
ENSMUST00000013755	sorting nexin 31 [Source:MGI Symbol;Acc:MGI:1913946]		Q6P8Y7	4.0	1.0E-01	5.7	4.6E-02	-0.3	9.3E-01	-1.9	2.2E-01
ENSMUST00000013845	translocase of inner mitochondrial membrane 23 [Source:MGI Symbol;Acc:MGI:1858317]	Q9CXU4		-5.8	4.3E-04	-1.6	1.4E-01	0.3	6.9E-01	-0.8	4.7E-01
ENSMUST00000013851	tumor necrosis factor, alpha-induced protein 8-like 2 [Source:MGI Symbol;Acc:MGI:1917019]		Q9D8Y7	-5.7	1.9E-05	-6.2	4.7E-04	-0.6	2.4E-01	-0.7	6.3E-01
ENSMUST00000013882	cereblon [Source:MGI Symbol;Acc:MGI:1913277]		Q8C7D2	-3.7	1.9E-03	7.4	1.4E-02	-0.6	8.2E-01	-1.9	2.0E-01
ENSMUST00000013773	oyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase [Source:MGI Symbol;Acc:MGI:19		B2RQC6	1.2	6.9E-02	1.6	6.7E-02	-0.1	9.0E-01	-0.4	5.3E-01
ENSMUST00000013910	lymphocyte antigen 6 complex, locus G6E [Source:MGI Symbol;Acc:MGI:1917524]	Q9D7E5		6.7	2.0E-03	-2.8	1.0E-02	1.7	6.7E-03	0.2	7.9E-01
ENSMUST00000013931	euchromatic histone lysine N-methyltransferase 2 [Source:MGI Symbol;Acc:MGI:2148922]		Q9Z148	-4.4	2.2E-02	-1.4	1.8E-01	-0.4	4.9E-01	-2.1	7.9E-02
ENSMUST00000013949	baculoviral IAP repeat-containing 3 [Source:MGI Symbol;Acc:MGI:1197007]	A2CGA5		-7.6	9.5E-06	-7.9	1.1E-03	-0.7	1.9E-01	1.3	4.6E-01
ENSMUST00000013966	elongation factor 1 homolog (ELF1, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913376]	Q545S6	P60003	-4.8	8.6E-04	-5.5	1.9E-04	0.2	6.7E-01	0.0	9.9E-01
ENSMUST00000013970	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma [Source:MGI Symbol;Acc:MGI:2152214]		Q91XU3	-2.6	4.0E-04	-5.6	3.3E-03	-1.0	1.2E-01	1.0	5.0E-01
ENSMUST00000013886	protein phosphatase 1, regulatory (inhibitor) subunit 12C [Source:MGI Symbol;Acc:MGI:1924258]		Q3UMT1	-4.8	1.6E-01	-4.0	3.6E-01	0.3	8.7E-01	-0.5	9.1E-01
ENSMUST00000013995	ATP-binding cassette, sub-family A (ABC1), member 4 [Source:MGI Symbol;Acc:MGI:109424]		O35600	6.6	1.3E-04	6.5	3.9E-03	-0.8	6.9E-01	-0.6	5.6E-01
ENSMUST00000014058	kallikrein related-peptidase 10 [Source:MGI Symbol;Acc:MGI:1916790]	Q99M20		7.2	5.5E-05	-0.1	9.3E-01	0.6	6.5E-01	-3.7	6.2E-02
ENSMUST00000014063	kallikrein related-peptidase 12 [Source:MGI Symbol;Acc:MGI:1916761]	B2RVZ0		6.1	1.0E-03	-7.4	1.2E-04	-0.1	7.3E-01	-0.4	7.4E-01
ENSMUST00000014065	CAP-GLY domain containing linker protein 3 [Source:MGI Symbol;Acc:MGI:1923936]		B9EHT4	8.6	8.2E-05	-4.5	5.6E-03	0.1	9.4E-01	-0.2	8.7E-01
ENSMUST00000014118	mast cell expressed membrane protein 1 [Source:MGI Symbol;Acc:MGI:1916439]		Q9D8U6	-8.2	3.5E-07	-1.6	2.8E-02	0.9	3.6E-02	0.0	9.5E-01
ENSMUST00000014218	ring finger protein 168 [Source:MGI Symbol;Acc:MGI:1917488]		Q80XJ2	1.5	1.2E-02	6.1	1.8E-04	-1.5	2.0E-01	-1.0	1.3E-01
ENSMUST00000014022	ring finger protein 170 [Source:MGI Symbol;Acc:MGI:1924983]		Q8CBG9	-1.3	6.4E-02	-0.7	4.0E-01	0.1	8.3E-01	-0.5	5.3E-01
ENSMUST00000014220	Tctex1 domain containing 2 [Source:MGI Symbol;Acc:MGI:1913311]		Q9CQ66	-5.8	9.0E-05	6.4	2.7E-04	-0.6	6.5E-01	0.3	6.6E-01
ENSMUST00000014221	calcineurin-like EF hand protein 1 [Source:MGI Symbol;Acc:MGI:1927185]		P61022	-5.7	5.0E-06	5.9	2.2E-03	-0.7	6.7E-01	-0.5	5.9E-01
ENSMUST00000014290	beta (A4) precursor protein-binding, family B, member 1 interacting protein [Source:MGI Symbol;Acc:MGI:1	B1AYC9	Q8R5A3	-6.0	1.1E-04	5.7	1.2E-03	-2.0	1.7E-01	0.9	2.8E-01
ENSMUST00000014072	THAP domain containing 8 [Source:MGI Symbol;Acc:MGI:1922879]	E9Q695		2.5	1.2E-01	5.3	3.3E-03	-1.1	4.6E-01	-3.9	5.9E-03
ENSMUST00000014321	trans-golgi network vesicle protein 23B [Source:MGI Symbol;Acc:MGI:1914760]		Q9D8T4	-2.4	4.8E-03	-7.7	3.8E-06	-0.2	6.0E-01	-0.6	4.6E-01
ENSMUST00000014339	DnaJ (Hsp40) homolog, subfamily C, member 7 [Source:MGI Symbol;Acc:MGI:1928373]		Q9QYI3	-4.5	3.8E-05	2.1	5.7E-03	0.3	5.7E-01	-0.4	4.5E-01
ENSMUST00000014370	calcyclin binding protein [Source:MGI Symbol;Acc:MGI:1270839]		Q9CXW3	-4.2	1.4E-04	-5.5	4.1E-04	-0.6	2.1E-01	-0.9	4.1E-01
ENSMUST00000014389	phosphatidylinositol glycan anchor biosynthesis, class L [Source:MGI Symbol;Acc:MGI:2681271]		Q5SX19	2.3	1.1E-03	-5.3	1.7E-04	1.4	3.6E-03	1.0	2.8E-01
ENSMUST00000014263	UDP glucuronosyltransferase 1 family, polypeptide A6A [Source:MGI Symbol;Acc:MGI:2137698]		Q64435	2.8	2.6E-01	-1.3	5.7E-01	-4.9	5.1E-02	-0.8	7.2E-01
ENSMUST00000014438	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 [Source:MGI Symbol;Acc:MGI:1343103]		Q9CQ75	-5.5	6.0E-05	-6.0	3.0E-03	1.7	1.6E-02	1.7	2.9E-01
ENSMUST00000014457	cytochrome c oxidase subunit VIc [Source:MGI Symbol;Acc:MGI:104614]		Q9CPQ1	-7.2	1.2E-04	-4.3	2.7E-03	-0.4	5.0E-01	1.5	1.8E-01
ENSMUST00000014499	anaphase promoting complex subunit 1 [Source:MGI Symbol;Acc:MGI:103097]		P53995	-1.6	3.3E-03	-3.8	4.0E-04	-0.6	1.5E-01	-1.3	1.2E-01
ENSMUST00000014505	c-mer proto-oncogene tyrosine kinase [Source:MGI Symbol;Acc:MGI:96965]		Q60805	4.2	8.8E-05	-3.1	3.6E-03	-0.4	3.4E-01	-1.6	8.2E-02
ENSMUST00000014546	tumor susceptibility gene 101 [Source:MGI Symbol;Acc:MGI:106581]	Q3UCW0	Q61187	-4.2	8.7E-06	2.2	5.7E-03	0.0	1.0E+00	0.1	8.8E-01
ENSMUST00000014421	ankyrin repeat domain 17 [Source:MGI Symbol;Acc:MGI:1932101]		Q99NH0	0.8	3.9E-01	2.9	4.7E-02	1.2	2.9E-01	-0.8	4.0E-01
ENSMUST00000014578	plasminogen [Source:MGI Symbol;Acc:MGI:97620]		P20918	5.9	1.4E-03	-6.5	1.7E-04	-0.9	7.0E-02	0.1	9.4E-01
ENSMUST00000014445	presequence translocase-asssociated motor 16 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913699		Q9CQV1	-1.7	1.4E-01	-4.7	3.5E-02	-1.0	3.0E-01	1.9	3.2E-01
ENSMUST00000014447	GLIS family zinc finger 2 [Source:MGI Symbol;Acc:MGI:1932535]		Q8VDL9	4.6	5.5E-02	3.3	9.6E-02	-4.4	7.0E-02	-3.1	5.6E-02
ENSMUST00000014597	B lymphoid kinase [Source:MGI Symbol;Acc:MGI:88169]		P16277	3.6	5.1E-04	-6.6	5.4E-04	-0.7	2.7E-01	-1.2	4.1E-01
ENSMUST00000014473	bicaudal C homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1933388]	G3X8S6		5.9	4.2E-02	5.6	7.4E-02	-0.7	8.2E-01	-0.4	8.4E-01
ENSMUST00000014614	ring finger protein 166 [Source:MGI Symbol;Acc:MGI:1915968]	A2RS02	Q3U9F6	-5.3	7.6E-05	-0.7	2.3E-01	0.8	3.8E-02	-0.1	8.9E-01
ENSMUST00000014640	ankyrin repeat domain 28 [Source:MGI Symbol;Acc:MGI:2145661]		Q505D1	-2.3	9.2E-04	2.1	1.2E-02	-2.1	7.5E-03	0.0	9.8E-01
ENSMUST00000014545	lactate dehydrogenase C [Source:MGI Symbol;Acc:MGI:96764]	Q548Z6	P00342	0.7	3.7E-01	1.8	7.0E-02	1.1	1.7E-01	0.0	1.0E+00
ENSMUST00000014673	transmembrane BAX inhibitor motif containing 7 [Source:MGI Symbol;Acc:MGI:1922305]	Q9D592		6.4	3.1E-04	-4.1	8.6E-05	0.3	3.0E-01	0.2	7.5E-01
ENSMUST00000014562	Hermansky-Pudlak syndrome 5 homolog (human) [Source:MGI Symbol;Acc:MGI:2180307]		P59438	1.2	3.4E-01	-1.8	4.1E-01	0.2	8.7E-01	3.2	1.1E-01
ENSMUST00000014684	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1 [Source:MGI Symbol;Acc:MGI:98884]	Q14C24	Q9D883	-5.5	3.0E-04	2.7	3.7E-02	-4.5	8.2E-03	-1.3	1.6E-01
ENSMUST00000014686	C-type lectin domain family 4, member f [Source:MGI Symbol;Acc:MGI:1859834]			6.5	1.4E-04	1.4	1.1E-01	-2.0	1.7E-02	0.3	7.1E-01
ENSMUST00000014687	killer cell lectin-like receptor, subfamily A, member 17 [Source:MGI Symbol;Acc:MGI:2180674]	Q9JMA4		-9.6	8.0E-06	-3.0	1.1E-02	1.3	3.2E-02	-1.0	3.3E-01
ENSMUST00000014691	WD repeat and FYVE domain containing 2 [Source:MGI Symbol;Acc:MGI:2442811]		Q8BUB4	-1.6	1.4E-02	-1.8	1.8E-02	0.5	2.1E-01	0.0	9.9E-01
ENSMUST00000014642	ankyrin repeat domain 52 [Source:MGI Symbol;Acc:MGI:2444029]		Q8BTI7	-0.5	3.8E-01	0.5	5.1E-01	1.1	6.8E-02	0.1	8.6E-01
ENSMUST00000014694	rabenosyn, RAB effector [Source:MGI Symbol;Acc:MGI:1925537]		Q80Y56	-1.2	1.6E-02	7.3	2.7E-04	-0.5	7.4E-01	-1.4	5.4E-02
ENSMUST00000014698	deoxyguanosine kinase [Source:MGI Symbol;Acc:MGI:1351602]		Q9QX60	-4.8	5.8E-04	-3.5	7.7E-03	-0.7	2.3E-01	-2.6	4.7E-02
ENSMUST00000014743	colony stimulating factor 1 (macrophage) [Source:MGI Symbol;Acc:MGI:1339753]		P07141	-3.8	7.7E-04	4.4	8.5E-04	-2.2	6.3E-02	-0.1	8.7E-01
ENSMUST00000014747	aristaless-like homeobox 3 [Source:MGI Symbol;Acc:MGI:1277097]	Q3UQX2	O70137	6.8	1.1E-04	-9.2	7.7E-05	-0.7	1.2E-01	-1.1	4.8E-01
ENSMUST00000014750	carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11 [Source:MGI Symbol;Acc:MGI:191	Q5SX53	Q9CR62	-6.9	3.4E-05	-0.3	6.6E-01	0.5	2.9E-01	-0.8	2.1E-01
ENSMUST00000014830	carcinoembryonic antigen-related cell adhesion molecule 16 [Source:MGI Symbol;Acc:MGI:2685615]		E9QA28	2.2	6.9E-03	-0.3	5.8E-01	1.2	1.3E-02	0.3	5.9E-01
ENSMUST00000014848	homeobox A2 [Source:MGI Symbol;Acc:MGI:96174]		P31245	7.1	5.8E-05	-5.3	2.2E-03	-0.3	5.9E-01	0.2	8.7E-01
ENSMUST00000014891	ankyrin repeat domain 53 [Source:MGI Symbol;Acc:MGI:1922555]		Q3V0J4	5.3	1.6E-04	-1.7	8.2E-02	1.4	2.9E-02	-0.6	5.1E-01
ENSMUST00000014892	testis expressed gene 261 [Source:MGI Symbol;Acc:MGI:1096575]		Q62302	-3.2	7.3E-04	6.9	1.9E-04	-0.5	7.2E-01	-0.5	4.1E-01
ENSMUST00000014913	proteasome (prosome, macropain) subunit, beta type 1 [Source:MGI Symbol;Acc:MGI:104884]	Q6RI64	O09061	-6.1	1.8E-06	-5.6	8.7E-04	1.0	7.0E-02	-0.3	8.2E-01
ENSMUST00000014777	copine VIII [Source:MGI Symbol;Acc:MGI:1914121]	Q9DB19		0.4	8.1E-01	0.1	9.7E-01	-1.0	4.8E-01	-0.7	6.8E-01
ENSMUST00000014812	checkpoint with forkhead and ring finger domains [Source:MGI Symbol;Acc:MGI:2444898]		Q810L3	-3.4	5.5E-02	0.3	8.6E-01	2.1	1.8E-01	-1.7	3.8E-01
ENSMUST00000014917	delta-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:104659]		Q61483	9.0	5.1E-06	1.9	4.8E-02	0.5	4.8E-01	0.8	2.6E-01
ENSMUST00000014920	nucleolar protein 3 (apoptosis repressor with CARD domain) [Source:MGI Symbol;Acc:MGI:1925938]	Q53YU5	Q9D1X0	6.8	2.4E-06	4.1	5.5E-04	-3.5	5.5E-03	-0.5	4.1E-01
ENSMUST00000014957	stanniocalcin 1 [Source:MGI Symbol;Acc:MGI:1091131]	Q3UYZ1	O55183	8.4	5.1E-06	5.4	9.1E-04	-0.2	8.8E-01	-0.2	7.3E-01
ENSMUST00000014981	RIKEN cDNA 4931428F04 gene [Source:MGI Symbol;Acc:MGI:1921606]		Q810A5	4.5	2.5E-05	-2.1	2.5E-02	0.7	1.6E-01	-0.4	6.6E-01
ENSMUST00000014911	TATA box binding protein [Source:MGI Symbol;Acc:MGI:101838]	Q6RI65	P29037	-3.0	2.6E-01	-3.5	2.5E-01	-1.6	3.5E-01	-1.2	7.3E-01
ENSMUST00000014990	tubulin polymerization-promoting protein family member 3 [Source:MGI Symbol;Acc:MGI:1915221]		Q9CRB6	-2.5	3.1E-02	-6.5	7.3E-06	-0.6	6.9E-02	-0.2	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000014996	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 13 [Source:MGI Symbol;Acc:M	A2ALB3		6.7	1.6E-04	4.3	5.1E-04	-3.3	6.7E-03	1.3	3.6E-02
ENSMUST00000015000	transmembrane protein 208 [Source:MGI Symbol;Acc:MGI:1913570]		Q9CR96	-6.5	6.2E-04	6.3	1.0E-05	-0.2	8.3E-01	0.3	5.3E-01
ENSMUST00000014922	formin homology 2 domain containing 1 [Source:MGI Symbol;Acc:MGI:2679008]		Q6P9Q4	0.4	5.8E-01	-2.3	1.4E-01	1.1	2.3E-01	3.8	1.8E-02
ENSMUST00000015003	E2F transcription factor 4 [Source:MGI Symbol;Acc:MGI:103012]		Q8R0K9	-2.5	1.6E-03	6.7	4.7E-05	-1.2	2.6E-01	0.6	2.7E-01
ENSMUST00000015011	surfeit gene 4 [Source:MGI Symbol;Acc:MGI:98445]	Q545Q2	Q64310	-5.1	2.1E-05	6.0	6.6E-06	0.6	3.9E-01	-1.0	4.3E-02
ENSMUST00000015049	DnaJ (Hsp40) homolog, subfamily B, member 9 [Source:MGI Symbol;Acc:MGI:1351618]		Q9QYI6	-4.3	4.2E-04	-2.2	9.6E-02	-0.7	3.6E-01	-1.0	4.3E-01
ENSMUST00000015100	protein phosphatase 1, catalytic subunit, beta isoform [Source:MGI Symbol;Acc:MGI:104871]		P62141	-2.4	1.9E-02	5.6	1.7E-04	-2.1	7.6E-02	-1.1	1.1E-01
ENSMUST00000015107	tousled-like kinase 2 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1346023]		O55047	-5.2	3.2E-03	-5.5	1.6E-03	-0.3	6.1E-01	-1.2	4.3E-01
ENSMUST00000015138	elastin [Source:MGI Symbol;Acc:MGI:95317]		P54320	9.5	2.1E-05	-1.8	3.9E-02	0.9	6.2E-02	0.2	7.7E-01
ENSMUST00000015146	EFR3 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923990]		Q8BG67	-2.6	4.0E-04	-3.7	1.3E-03	1.3	9.1E-03	-0.1	9.0E-01
ENSMUST00000015157	trafficking protein particle complex 2-like [Source:MGI Symbol;Acc:MGI:1916295]		Q9JME7	-4.5	2.2E-05	-2.2	5.2E-02	1.4	4.5E-02	-0.7	5.1E-01
ENSMUST00000015160	acyl-CoA synthetase family member 3 [Source:MGI Symbol;Acc:MGI:2182591]		Q3URE1	2.7	1.3E-03	-0.9	4.1E-01	1.1	1.7E-01	-0.4	7.0E-01
ENSMUST00000015171	galactosamine (N-acetyl)-6-sulfate sulfatase [Source:MGI Symbol;Acc:MGI:1355303]		Q571E4	-3.0	1.5E-03	-5.9	5.5E-03	-1.4	5.1E-02	-0.7	6.9E-01
ENSMUST00000015137	LIM-domain containing, protein kinase [Source:MGI Symbol;Acc:MGI:104572]		P53668	-1.0	4.7E-01	-0.5	8.4E-01	1.8	2.7E-01	1.3	5.4E-01
ENSMUST00000015236	endothelial differentiation-related factor 1 [Source:MGI Symbol;Acc:MGI:1891227]		Q9JMG1	-7.9	2.7E-05	4.8	2.8E-04	-4.5	3.3E-03	0.1	8.8E-01
ENSMUST00000015267	protease, serine 28 [Source:MGI Symbol;Acc:MGI:2149951]			5.4	1.3E-03	-1.5	2.8E-02	0.4	3.1E-01	-0.7	2.4E-01
ENSMUST00000015271	unkempt-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1921404]		Q5FWH2	-3.5	2.8E-02	-5.2	7.5E-05	-0.2	6.3E-01	0.5	5.5E-01
ENSMUST00000015277	leucine-rich repeat kinase 1 [Source:MGI Symbol;Acc:MGI:2142227]		Q3UHC2	1.4	1.1E-02	3.0	1.8E-03	-0.1	8.4E-01	-0.5	3.7E-01
ENSMUST00000015278	aldehyde dehydrogenase family 1, subfamily A3 [Source:MGI Symbol;Acc:MGI:1861722]	Q3UIA4	Q9JHW9	7.2	5.1E-05	-1.8	7.3E-02	1.4	2.7E-02	0.2	8.5E-01
ENSMUST00000015197	GATA binding protein 2 [Source:MGI Symbol;Acc:MGI:95662]	Q3U320	O09100	0.9	6.1E-01	1.3	5.9E-01	-0.2	9.3E-01	-0.5	7.9E-01
ENSMUST00000015333	CAS1 domain containing 1 [Source:MGI Symbol;Acc:MGI:2384865]		Q7TN73	-3.0	2.0E-04	-8.4	1.5E-04	0.0	9.5E-01	0.6	7.0E-01
ENSMUST00000015239	F-box and WD-40 domain protein 5 [Source:MGI Symbol;Acc:MGI:1354731]		Q9QXW2	-0.7	2.5E-01	0.2	8.1E-01	0.9	1.6E-01	-0.1	9.4E-01
ENSMUST00000015256	r family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13 [Source:MGI Symbol;Acc:MC		Q9QXX4	0.2	8.0E-01	-3.1	4.4E-02	0.3	7.0E-01	3.5	2.2E-02
ENSMUST00000015346	Cnksr family member 3 [Source:MGI Symbol;Acc:MGI:2674130]		Q8BMA3	3.7	8.1E-04	5.6	3.0E-03	0.0	9.9E-01	-0.3	7.6E-01
ENSMUST00000015358	myotubularin related protein 1 [Source:MGI Symbol;Acc:MGI:1858271]		Q9Z2C4	-5.2	1.2E-03	-3.2	2.0E-01	1.4	2.7E-01	1.1	6.5E-01
ENSMUST00000015391	nipsnap homolog 3B (C. elegans) [Source:MGI Symbol;Acc:MGI:1913786]		Q9CQE1	-6.6	1.4E-04	1.9	8.8E-03	0.0	9.5E-01	-0.5	3.0E-01
ENSMUST00000015433	L antigen family, member 3 [Source:MGI Symbol;Acc:MGI:1913442]		Q9CR70	-5.7	6.7E-05	5.2	2.2E-04	-2.5	3.5E-02	-0.5	3.7E-01
ENSMUST00000015435	guanosine diphosphate (GDP) dissociation inhibitor 1 [Source:MGI Symbol;Acc:MGI:99846]		P50396	-4.2	2.6E-02	-2.8	2.0E-03	0.8	5.0E-02	0.6	3.7E-01
ENSMUST00000015449	SAM and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1917347]	F8VQK5		7.2	5.6E-07	4.3	3.1E-03	0.8	4.7E-01	0.2	7.5E-01
ENSMUST00000015456	growth arrest and DNA-damage-inducible 45 beta [Source:MGI Symbol;Acc:MGI:107776]		P22339	-3.9	9.8E-05	-4.5	1.5E-02	0.1	8.7E-01	-0.6	7.1E-01
ENSMUST00000015361	high mobility group box 3 [Source:MGI Symbol;Acc:MGI:1098219]	Q544R9	O54879	6.2	6.4E-02	7.3	5.6E-02	-0.8	8.3E-01	-1.9	3.9E-01
ENSMUST00000015460	signaling lymphocytic activation molecule family member 1 [Source:MGI Symbol;Acc:MGI:1351314]	Q544K1	Q9QUM4	2.3	1.8E-02	-7.6	4.7E-04	0.0	9.4E-01	1.0	5.1E-01
ENSMUST00000015467	solute carrier family 39 (zinc transporter), member 1 [Source:MGI Symbol;Acc:MGI:1353474]		Q9QZ03	-2.1	2.9E-03	-6.1	2.4E-04	-1.0	2.8E-02	-0.6	6.0E-01
ENSMUST00000015434	ubiquitin-like 4A [Source:MGI Symbol;Acc:MGI:95049]	F8WHM4		-2.2	1.5E-01	-4.0	4.6E-02	-2.0	5.6E-02	-0.3	8.7E-01
ENSMUST00000015484	cytochrome b-245, beta polypeptide [Source:MGI Symbol;Acc:MGI:88574]	Q3U6G0	Q61093	-6.1	9.2E-06	-5.8	3.6E-02	1.0	4.0E-01	2.5	3.2E-01
ENSMUST00000015486	Kell blood group precursor (McLeod phenotype) homolog [Source:MGI Symbol;Acc:MGI:103569]	Q059K7	Q9QXY7	2.1	9.1E-03	2.7	5.6E-04	-4.3	4.2E-05	0.2	6.8E-01
ENSMUST00000015498	procollagen C-endopeptidase enhancer 2 [Source:MGI Symbol;Acc:MGI:1923727]		Q8R4W6	7.6	2.2E-05	-3.4	1.8E-03	0.8	9.2E-02	0.2	8.2E-01
ENSMUST00000015501	caseinolytic mitochondrial matrix peptidase chaperone subunit [Source:MGI Symbol;Acc:MGI:1346017]		Q9JHS4	-5.9	4.1E-04	-1.3	1.5E-01	-3.2	1.6E-03	0.4	6.0E-01
ENSMUST00000015540	CD83 antigen [Source:MGI Symbol;Acc:MGI:1328316]		O88324	2.7	6.4E-03	-1.0	1.4E-01	0.8	8.6E-02	-0.2	7.7E-01
ENSMUST00000015481	endonuclease G [Source:MGI Symbol;Acc:MGI:1261433]	Q3UN47	O08600	1.6	7.6E-02	1.4	1.5E-01	-0.6	4.5E-01	-0.5	5.4E-01
ENSMUST00000015576	mast cell protease 2 [Source:MGI Symbol;Acc:MGI:96938]	Q541U2	P15119	6.3	2.0E-04	-5.5	2.8E-04	1.1	2.8E-02	0.5	6.3E-01
ENSMUST00000015578	granzyme G [Source:MGI Symbol;Acc:MGI:109253]	Q4KL28	P13366	6.0	4.3E-04	2.7	1.4E-02	1.0	1.9E-01	0.4	5.4E-01
ENSMUST00000015583	cathepsin G [Source:MGI Symbol;Acc:MGI:88563]	Q059V7	P28293	-4.5	8.9E-04	2.4	5.3E-03	-5.3	2.7E-04	-0.1	8.6E-01
ENSMUST00000015585	granzyme C [Source:MGI Symbol;Acc:MGI:109256]	Q0VB76	P08882	5.2	5.3E-04	-5.6	7.3E-04	0.1	7.8E-01	-0.2	8.9E-01
ENSMUST00000015509	Moloney leukemia virus 10-like 1 [Source:MGI Symbol;Acc:MGI:1891384]	G3X8T0		3.1	1.8E-01	7.3	8.8E-03	-0.5	8.5E-01	-4.7	1.0E-02
ENSMUST00000015511	plexin D1 [Source:MGI Symbol;Acc:MGI:2154244]		Q3UH93	1.5	3.5E-02	2.5	1.6E-02	0.8	2.6E-01	-0.1	8.9E-01
ENSMUST00000015594	mast cell protease 8 [Source:MGI Symbol;Acc:MGI:1261780]	Q3UWB6	P43430	-5.0	1.9E-04	-0.5	5.6E-01	-2.7	3.5E-03	0.4	5.7E-01
ENSMUST00000015605	activating transcription factor 6 beta [Source:MGI Symbol;Acc:MGI:105121]	A0A0A0MQ69		-5.2	2.3E-03	5.7	7.9E-04	-0.5	6.8E-01	0.1	8.6E-01
ENSMUST00000015612	notch 4 [Source:MGI Symbol;Acc:MGI:107471]	A2CG28		3.2	1.1E-03	1.5	1.1E-01	-3.9	4.5E-03	0.5	5.1E-01
ENSMUST00000015581	granzyme B [Source:MGI Symbol;Acc:MGI:109267]	Q3TZH4	P04187	0.7	2.4E-01	0.0	9.9E-01	-1.9	5.0E-03	-1.2	8.5E-02
ENSMUST00000015620	proline-rich transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1932118]	A2CG20	O35449	6.8	1.4E-04	-4.2	5.3E-03	-0.1	9.2E-01	-0.3	7.8E-01
ENSMUST00000015622	ring finger protein 5 [Source:MGI Symbol;Acc:MGI:1860076]		O35445	-4.8	3.8E-04	2.0	3.7E-02	-3.1	9.6E-03	0.1	9.2E-01
ENSMUST00000015628	family with sequence similarity 163, member A [Source:MGI Symbol;Acc:MGI:3618859]	A9ZNB6	Q8CAA5	8.5	2.8E-05	-4.8	4.0E-03	0.4	4.1E-01	0.2	9.0E-01
ENSMUST00000015596	advanced glycosylation end product-specific receptor [Source:MGI Symbol;Acc:MGI:893592]	O35444		-3.2	1.0E-01	-2.2	3.8E-01	0.3	8.3E-01	-0.7	7.8E-01
ENSMUST00000015667	cathepsin S [Source:MGI Symbol;Acc:MGI:107341]	F6WR04		-4.3	8.1E-05	-2.3	1.5E-01	1.5	1.1E-01	-1.4	4.1E-01
ENSMUST00000015680	molybdenum cofactor synthesis 2 [Source:MGI Symbol;Acc:MGI:1336894]			-6.1	4.1E-04	4.7	2.2E-04	0.4	5.7E-01	-1.1	9.3E-02
ENSMUST00000015712	lipoprotein lipase [Source:MGI Symbol;Acc:MGI:96820]		P11152	4.1	6.5E-05	5.4	1.0E-03	-1.7	2.0E-01	-0.2	7.6E-01
ENSMUST00000015719	ATPase, H+ transporting, lysosomal V0 subunit E [Source:MGI Symbol;Acc:MGI:1328318]		Q9CQD8	-9.0	1.6E-04	-3.7	7.1E-03	0.5	3.8E-01	-0.6	6.1E-01
ENSMUST00000015723	NK2 homeobox 5 [Source:MGI Symbol;Acc:MGI:97350]	Q3UQU2	P42582	7.1	4.0E-04	7.3	1.2E-04	-1.0	4.6E-01	0.3	6.5E-01
ENSMUST00000015645	human immunodeficiency virus type I enhancer binding protein 2 [Source:MGI Symbol;Acc:MGI:1338076]		Q3UHF7	1.1	7.5E-02	1.5	6.1E-02	-0.2	7.6E-01	-0.5	4.4E-01
ENSMUST00000015664	cathepsin K [Source:MGI Symbol;Acc:MGI:107823]	Q545T0	P55097	1.1	2.5E-01	-0.1	9.1E-01	-1.8	5.4E-02	-0.6	5.5E-01
ENSMUST00000015749	serum response factor [Source:MGI Symbol;Acc:MGI:106658]		Q9JM73	-2.2	7.8E-03	-5.4	3.5E-05	-2.1	5.7E-04	-1.0	2.3E-01
ENSMUST00000015771	GATA binding protein 5 [Source:MGI Symbol;Acc:MGI:109497]		P97489	7.5	5.4E-06	-5.5	3.2E-03	-0.5	4.3E-01	-1.0	5.2E-01
ENSMUST00000015791	laminin, alpha 5 [Source:MGI Symbol;Acc:MGI:105382]		Q61001	4.5	3.2E-05	4.2	1.7E-04	-0.3	6.4E-01	-0.3	4.9E-01
ENSMUST00000015796	six transmembrane epithelial antigen of the prostate 1 [Source:MGI Symbol;Acc:MGI:1917608]		Q9CWR7	4.6	1.1E-03	-7.8	4.5E-04	0.1	9.0E-01	-1.2	5.2E-01
ENSMUST00000015816	mitochondrial ribosomal protein L32 [Source:MGI Symbol;Acc:MGI:2137226]		Q9DCI9	-4.8	3.5E-05	7.0	7.4E-04	-0.7	6.7E-01	-0.6	4.9E-01
ENSMUST00000015725	BCL2/adenovirus E1B interacting protein 1 [Source:MGI Symbol;Acc:MGI:109328]		Q6QD59	-1.1	4.4E-01	-1.4	5.1E-01	0.4	7.5E-01	0.7	7.0E-01
ENSMUST00000015829	acyl-Coenzyme A dehydrogenase, short/branched chain [Source:MGI Symbol;Acc:MGI:1914135]		Q9DBL1	-5.3	2.1E-04	-1.1	2.1E-01	1.1	8.0E-02	0.0	9.7E-01
ENSMUST00000015855	prune homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1925152]		Q8BIW1	-2.1	3.5E-03	5.2	8.2E-05	-2.0	3.9E-02	0.3	6.0E-01
ENSMUST00000015858	ceramide synthase 2 [Source:MGI Symbol;Acc:MGI:1924143]		Q924Z4	-6.7	4.2E-06	2.2	6.5E-03	-2.6	1.7E-03	-0.3	6.0E-01
ENSMUST00000015877	capping protein (actin filament) muscle Z-line, alpha 2 [Source:MGI Symbol;Acc:MGI:106222]	Q5DQJ3	P47754	-7.8	2.9E-06	-1.3	1.1E-01	-6.4	6.9E-05	-0.5	4.6E-01
ENSMUST00000015812	PDZ domain containing 11 [Source:MGI Symbol;Acc:MGI:1919871]		Q9CZG9	-1.7	1.4E-01	-2.8	6.2E-02	-1.3	1.7E-01	-0.2	8.6E-01
ENSMUST00000015893	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Source:MGI Symbol;Acc:MGI:1913721]		P97822	-3.3	1.4E-02	-3.7	5.5E-04	-0.6	1.8E-01	-1.6	6.0E-02
ENSMUST00000015894	anterior pharynx defective 1a homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2385110]	Q6GTF1	Q8BVF7	-4.6	1.8E-04	-5.3	1.3E-03	-0.2	7.0E-01	-0.3	8.2E-01
ENSMUST00000015841	SET domain, bifurcated 1 [Source:MGI Symbol;Acc:MGI:1934229]	D3YYC3		-1.5	5.9E-01	3.1	3.4E-01	1.0	7.3E-01	-3.6	2.0E-01
ENSMUST00000015846	annexin A9 [Source:MGI Symbol;Acc:MGI:1923711]		Q9JHQ0	-1.9	1.5E-01	-0.8	5.9E-01	0.3	7.2E-01	-0.8	6.1E-01
ENSMUST00000015901	peptidylprolyl isomerase (cyclophilin)-like 4 [Source:MGI Symbol;Acc:MGI:1914668]		Q9CXG3	-3.3	5.0E-04	-0.8	2.5E-01	1.1	3.5E-02	-0.1	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000015903	cornichon homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1277202]		O35372	-3.6	7.9E-03	-5.2	1.8E-04	1.2	1.3E-02	-0.3	7.6E-01
ENSMUST00000015941	betaine-homocysteine methyltransferase 2 [Source:MGI Symbol;Acc:MGI:1891379]		Q91WS4	4.5	2.0E-05	-6.9	6.2E-05	0.5	2.5E-01	-0.4	6.7E-01
ENSMUST00000015889	pleckstrin homology domain containing, family O member 1 [Source:MGI Symbol;Acc:MGI:1914470]		Q9JIY0	-1.7	1.9E-01	0.5	7.0E-01	0.1	9.2E-01	-2.1	1.4E-01
ENSMUST00000015891	vacuolar protein sorting 45 (yeast) [Source:MGI Symbol;Acc:MGI:891965]		P97390	-0.2	7.5E-01	0.1	9.3E-01	-0.2	7.0E-01	-0.4	5.1E-01
ENSMUST00000015892	PRP3 pre-mRNA processing factor 3 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1918017]		Q922U1	1.7	5.8E-02	-0.4	6.8E-01	-1.6	6.0E-02	0.5	5.6E-01
ENSMUST00000015987	retinoid X receptor gamma [Source:MGI Symbol;Acc:MGI:98216]		P28705	6.8	5.5E-05	-5.2	3.1E-03	-2.7	2.4E-03	-0.8	6.0E-01
ENSMUST00000015994	ADAMTS-like 4 [Source:MGI Symbol;Acc:MGI:2389008]		Q80T21	-4.2	8.4E-03	-2.5	2.2E-02	1.3	2.5E-02	-0.8	4.2E-01
ENSMUST00000015998	CD5 antigen-like [Source:MGI Symbol;Acc:MGI:1334419]		Q9QWK4	6.1	2.4E-04	-3.2	2.7E-03	-0.2	6.4E-01	-0.2	7.7E-01
ENSMUST00000016023	family with sequence similarity 184, member B [Source:MGI Symbol;Acc:MGI:2442958]		Q0KK56	6.3	6.5E-06	-1.7	2.3E-01	0.5	5.8E-01	-1.5	2.8E-01
ENSMUST00000015934	surfeit gene 1 [Source:MGI Symbol;Acc:MGI:98443]		P09925	-0.2	7.9E-01	-1.6	1.9E-01	-0.4	6.2E-01	1.0	3.7E-01
ENSMUST00000016033	leukotriene A4 hydrolase [Source:MGI Symbol;Acc:MGI:96836]		P24527	-6.0	1.0E-05	5.0	3.5E-05	0.2	7.6E-01	-0.3	4.8E-01
ENSMUST00000016034	amidohydrolase domain containing 1 [Source:MGI Symbol;Acc:MGI:1919011]		Q9DBA8	4.1	6.5E-04	-4.8	4.2E-03	0.1	8.0E-01	-0.1	9.7E-01
ENSMUST00000015950	quinoid dihydropteridine reductase [Source:MGI Symbol;Acc:MGI:97836]		Q8BVI4	-1.0	3.9E-01	-0.2	8.7E-01	0.1	9.3E-01	-0.7	6.1E-01
ENSMUST00000015981	sequestosome 1 [Source:MGI Symbol;Acc:MGI:107931]		Q64337	-2.6	5.3E-02	-2.1	2.1E-01	0.2	8.1E-01	-0.3	8.7E-01
ENSMUST00000016072	ribosome binding protein 1 [Source:MGI Symbol;Acc:MGI:1932395]	A2AVJ7		-3.0	3.8E-04	6.3	6.2E-05	-1.7	1.2E-01	-1.2	5.7E-02
ENSMUST00000016081	H2A histone family, member Y [Source:MGI Symbol;Acc:MGI:1349392]		Q9QZQ8	-9.5	6.0E-07	-5.5	5.3E-02	1.2	2.2E-01	2.5	3.4E-01
ENSMUST00000016086	GTF2I repeat domain containing 2 [Source:MGI Symbol;Acc:MGI:2149780]		Q99NI3	-2.0	6.2E-03	-3.2	8.9E-04	-10.2	1.9E-06	-0.9	2.4E-01
ENSMUST00000016088	GATS protein-like 2 [Source:MGI Symbol;Acc:MGI:1933384]		Q8CAB8	3.6	9.4E-05	7.0	5.5E-05	0.9	3.4E-01	0.2	6.4E-01
ENSMUST00000016026	ligand dependent nuclear receptor corepressor-like [Source:MGI Symbol;Acc:MGI:2651932]		Q3U285	-1.1	6.7E-01	-2.6	4.1E-01	-2.0	2.9E-01	-0.5	8.9E-01
ENSMUST00000016031	histidine ammonia lyase [Source:MGI Symbol;Acc:MGI:96010]	F8WH73		-1.9	7.9E-02	-5.0	1.5E-02	-1.5	7.0E-02	1.6	3.6E-01
ENSMUST00000016094	neutrophil cytosolic factor 1 [Source:MGI Symbol;Acc:MGI:97283]	F8WH69		-7.8	3.9E-03	-4.1	8.9E-04	1.4	8.1E-03	-0.5	5.7E-01
ENSMUST00000016105	adenylosuccinate synthetase, non muscle [Source:MGI Symbol;Acc:MGI:87948]	B9EIE9	P46664	-6.6	1.7E-05	4.3	1.3E-03	-0.1	8.9E-01	-0.4	5.6E-01
ENSMUST00000016115	ARP8 actin-related protein 8 [Source:MGI Symbol;Acc:MGI:1860775]		Q8R2S9	-1.3	1.2E-02	-2.0	1.1E-02	0.0	9.1E-01	-0.9	2.0E-01
ENSMUST00000016138	farnesyltransferase, CAAX box, alpha [Source:MGI Symbol;Acc:MGI:104683]	Q541Z2	Q61239	-4.2	7.7E-05	-8.0	8.8E-06	1.1	2.7E-03	-0.4	6.8E-01
ENSMUST00000016143	WAS protein family, member 3 [Source:MGI Symbol;Acc:MGI:2658986]		Q8VHI6	8.1	1.4E-05	-0.6	4.2E-01	1.0	6.8E-02	-0.4	5.9E-01
ENSMUST00000016087	bolA-like 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1916418]		Q9D8S9	-1.7	3.7E-01	-1.9	3.0E-01	-1.6	2.3E-01	-1.4	4.8E-01
ENSMUST00000016144	phosphatidic acid phosphatase type 2A [Source:MGI Symbol;Acc:MGI:108412]		Q61469	4.3	3.5E-03	2.8	2.5E-03	-0.3	5.9E-01	0.5	3.6E-01
ENSMUST00000016168	lipopolysaccharide binding protein [Source:MGI Symbol;Acc:MGI:1098776]		Q61805	-3.4	1.5E-04	-5.8	5.1E-02	1.1	2.9E-01	-0.9	7.7E-01
ENSMUST00000016172	n, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) [Source:MGI Symbol;Acc:MGI:11		O35161	5.7	1.4E-05	-4.1	1.0E-03	0.7	1.6E-01	-1.8	9.0E-02
ENSMUST00000016231	Friend leukemia integration 1 [Source:MGI Symbol;Acc:MGI:95554]	Q544B3	P26323	-1.9	1.3E-03	-1.2	6.1E-02	0.1	7.1E-01	0.0	9.5E-01
ENSMUST00000016124	leucine rich repeat containing 27 [Source:MGI Symbol;Acc:MGI:1923862]		Q80YS5	-0.1	8.6E-01	-2.1	4.7E-02	-0.5	3.6E-01	1.4	1.4E-01
ENSMUST00000016125	serine/threonine kinase 32C [Source:MGI Symbol;Acc:MGI:2385336]		Q8QZV4	3.8	8.6E-02	5.9	1.9E-02	-0.5	8.4E-01	-2.6	9.0E-02
ENSMUST00000016279	NEDD4 binding protein 2-like 1 [Source:MGI Symbol;Acc:MGI:2140872]		Q3V2Q8	-4.3	1.0E-04	-3.0	3.1E-03	0.5	2.7E-01	-0.8	3.4E-01
ENSMUST00000016309	transmembrane BAX inhibitor motif containing 1 [Source:MGI Symbol;Acc:MGI:1916910]	Q3U717		-3.2	1.8E-02	8.0	3.2E-05	-0.5	6.5E-01	-0.4	4.2E-01
ENSMUST00000016315	laminin, beta 3 [Source:MGI Symbol;Acc:MGI:99915]		Q61087	8.3	1.1E-05	1.4	1.7E-01	-3.6	8.1E-03	-0.6	4.5E-01
ENSMUST00000016323	calcium/calmodulin-dependent protein kinase I gamma [Source:MGI Symbol;Acc:MGI:2388073]		Q91VB2	7.3	2.4E-05	-1.8	2.4E-02	1.1	1.9E-02	-0.5	5.0E-01
ENSMUST00000016338	hydroxysteroid 11-beta dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:103562]	Q4JHD9	P50172	-3.6	8.1E-04	5.9	6.0E-05	-0.1	8.8E-01	-0.3	5.8E-01
ENSMUST00000016396	P synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit [Source:MGI Symbol;Acc:MGI:18556	Q545F5	P56382	-9.1	3.4E-05	-1.3	2.6E-02	0.3	3.8E-01	-0.3	5.9E-01
ENSMUST00000016397	negative elongation factor complex member C/D, Th1l [Source:MGI Symbol;Acc:MGI:1926424]	Q3TW27		4.6	1.5E-02	-3.1	4.3E-03	0.9	6.7E-02	-0.3	7.2E-01
ENSMUST00000016399	tubulin, beta 1 class VI [Source:MGI Symbol;Acc:MGI:107814]		A2AQ07	1.9	2.3E-02	-4.0	1.5E-02	-0.4	5.9E-01	0.4	7.9E-01
ENSMUST00000016400	cathepsin Z [Source:MGI Symbol;Acc:MGI:1891190]	Q545I6	Q9WUU7	-5.2	2.4E-05	1.9	1.4E-01	-1.5	1.9E-01	4.9	6.9E-04
ENSMUST00000016401	slowmo homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913640]		Q9CYY7	-3.3	6.5E-04	7.3	4.8E-05	-0.6	6.1E-01	-0.6	3.2E-01
ENSMUST00000016406	SERTA domain containing 4 [Source:MGI Symbol;Acc:MGI:2443496]		A7DTG3	8.2	8.2E-06	-2.3	1.8E-02	-0.4	4.4E-01	-1.7	8.3E-02
ENSMUST00000016383	LON peptidase N-terminal domain and ring finger 3 [Source:MGI Symbol;Acc:MGI:1921615]		Q9D4H7	-0.7	4.6E-01	-0.1	9.3E-01	1.6	1.6E-01	1.0	4.8E-01
ENSMUST00000016427	histocompatibility 2, M region locus 2 [Source:MGI Symbol;Acc:MGI:95914]	Q6W9J6		5.1	2.4E-03	-8.7	9.1E-05	-0.2	5.8E-01	-0.7	6.7E-01
ENSMUST00000016452	ubiquitin-conjugating enzyme E2A [Source:MGI Symbol;Acc:MGI:102959]	Q3UCS1	Q9Z255	-6.0	1.8E-05	1.5	3.0E-01	-5.0	1.0E-02	-1.8	1.3E-01
ENSMUST00000016463	er family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 [Source:MGI Symbol;Acc:MG	Q545A2	P51881	-7.7	2.6E-07	0.1	9.0E-01	-2.1	8.7E-03	-0.3	6.3E-01
ENSMUST00000016498	kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites [Source:MGI Symbol;Acc:M(	Q0VBH4		6.8	5.9E-05	-3.9	5.0E-04	0.2	6.5E-01	-1.1	1.8E-01
ENSMUST00000016511	PTK6 protein tyrosine kinase 6 [Source:MGI Symbol;Acc:MGI:99683]	Q05AA8	Q64434	6.0	9.5E-06	-4.5	3.9E-04	-0.8	7.5E-02	0.4	6.2E-01
ENSMUST00000016569	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2140945]		Q4VA53	-5.5	4.2E-04	5.7	1.8E-04	-1.5	1.6E-01	1.0	1.1E-01
ENSMUST00000016571	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 [Source:MGI Symbol;Acc:MGI:1929511]	Q545K0	O35683	-3.0	1.4E-04	4.6	5.5E-03	-0.5	7.0E-01	0.0	9.9E-01
ENSMUST00000016638	CD34 antigen [Source:MGI Symbol;Acc:MGI:88329]	Q543B6	Q64314	-3.4	6.6E-03	-3.6	9.6E-04	1.1	2.1E-02	-1.3	1.6E-01
ENSMUST00000016640	CD274 antigen [Source:MGI Symbol;Acc:MGI:1926446]	Q3U472	Q9EP73	2.7	6.3E-03	-6.5	5.6E-06	-0.3	2.8E-01	-1.5	6.1E-02
ENSMUST00000016488	l differentiation and proliferation factor homolog (zebrafish)RIKEN cDNA 2700038C09 gene [Source:MGI Sy		Q9CR37	0.1	9.3E-01	1.3	3.2E-01	0.0	9.8E-01	-1.2	3.1E-01
ENSMUST00000016654	mitochondrial translational initiation factor 3 [Source:MGI Symbol;Acc:MGI:1923616]	A4QMQ0	Q9CZD5	-3.4	6.8E-03	5.3	1.5E-04	-1.9	7.7E-02	-0.4	4.7E-01
ENSMUST00000016672	MAP kinase-activated protein kinase 2 [Source:MGI Symbol;Acc:MGI:109298]	Q3U2P8	P49138	-5.0	5.0E-05	6.0	5.6E-05	0.3	7.1E-01	0.3	6.1E-01
ENSMUST00000016553	NFKB activating protein [Source:MGI Symbol;Acc:MGI:1914300]		Q9D0F4	1.3	1.0E-01	1.0	3.5E-01	0.8	3.3E-01	1.1	2.5E-01
ENSMUST00000016673	interleukin 10 [Source:MGI Symbol;Acc:MGI:96537]		P18893	4.7	3.1E-04	-6.1	1.2E-03	-0.6	2.2E-01	0.0	9.8E-01
ENSMUST00000016678	lysosomal-associated membrane protein 2 [Source:MGI Symbol;Acc:MGI:96748]		P17047	-9.3	1.0E-05	-3.8	1.8E-04	-0.9	2.3E-02	-0.1	8.8E-01
ENSMUST00000016631	PTPRF interacting protein, binding protein 1 (liprin beta 1) [Source:MGI Symbol;Acc:MGI:1914783]		Q8C8U0	-0.5	8.6E-01	-1.3	5.3E-01	-3.9	4.8E-02	-3.1	2.4E-01
ENSMUST00000016680	cullin 4A [Source:MGI Symbol;Acc:MGI:1914487]		Q3TCH7	-6.6	1.3E-04	-0.7	5.0E-01	0.8	2.8E-01	-2.0	9.8E-02
ENSMUST00000016639	plasminogen receptor, C-terminal lysine transmembrane protein [Source:MGI Symbol;Acc:MGI:1915009]		Q9D3P8	-0.4	8.7E-01	-1.4	7.3E-01	-0.4	8.7E-01	0.5	8.9E-01
ENSMUST00000016681	cullin 4B [Source:MGI Symbol;Acc:MGI:1919834]	E9PXY1		-4.5	3.0E-02	0.9	3.3E-01	-1.3	1.3E-01	0.5	5.3E-01
ENSMUST00000016703	H3 histone, family 3B [Source:MGI Symbol;Acc:MGI:1101768]		P84244	-8.3	1.1E-04	-3.3	3.2E-02	-0.5	5.2E-01	-0.6	6.7E-01
ENSMUST00000016664	ligand of numb-protein X 2 [Source:MGI Symbol;Acc:MGI:2155959]		Q91XL2	1.0	3.9E-02	1.1	7.3E-02	0.3	5.1E-01	0.2	7.3E-01
ENSMUST00000016670	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 [Source:MGI Symbol;Acc:MGI:1330300]		Q922Y0	1.0	1.2E-01	1.8	5.2E-02	0.4	5.1E-01	-0.3	6.7E-01
ENSMUST00000016768	PHD finger protein 21B [Source:MGI Symbol;Acc:MGI:2443812]	F8WGM2		4.8	3.1E-02	-4.2	1.6E-03	1.3	1.8E-02	0.5	6.1E-01
ENSMUST00000016771	myosin, heavy polypeptide 9, non-muscle [Source:MGI Symbol;Acc:MGI:107717]		Q8VDD5	-5.9	1.2E-07	4.3	6.4E-04	-1.3	1.6E-01	-0.9	1.9E-01
ENSMUST00000016902	BCL2-interacting killer [Source:MGI Symbol;Acc:MGI:1206591]		O70337	4.2	4.7E-04	-10.7	1.2E-04	-0.5	1.9E-01	0.8	6.4E-01
ENSMUST00000016907	signal peptide, CUB domain, EGF-like 1 [Source:MGI Symbol;Acc:MGI:1890616]		Q6NZL8	6.5	2.1E-03	-5.6	6.7E-04	1.0	8.0E-02	0.0	9.9E-01
ENSMUST00000016977	mitochondrial ribosomal protein S18C [Source:MGI Symbol;Acc:MGI:1915985]		Q8R2L5	-7.6	2.3E-05	-3.6	2.8E-01	1.9	3.1E-01	0.9	7.6E-01
ENSMUST00000016696	FAD-dependent oxidoreductase domain containing 2 [Source:MGI Symbol;Acc:MGI:106315]		Q3USW5	-0.2	8.8E-01	7.6	2.5E-03	5.1	1.6E-02	-2.7	2.6E-02
ENSMUST00000017065	serine/arginine-rich splicing factor 6 [Source:MGI Symbol;Acc:MGI:1915246]	A0A0A6YXX6		-6.8	3.0E-04	7.4	1.7E-04	0.1	9.6E-01	-0.5	4.9E-01
ENSMUST00000017086	transmembrane serine protease 6 [Source:MGI Symbol;Acc:MGI:1919003]		Q9DBI0	7.7	3.3E-04	-8.4	3.9E-03	0.7	2.9E-01	0.8	7.1E-01
ENSMUST00000017090	potassium channel tetramerisation domain containing 5 [Source:MGI Symbol;Acc:MGI:1916509]			-1.8	8.0E-03	4.0	1.3E-01	-1.5	5.4E-01	-0.6	7.1E-01
ENSMUST00000017126	POM121 membrane glycoprotein-like 2 (rat) [Source:MGI Symbol;Acc:MGI:2684870]		Q5SW25	6.6	2.0E-05	-4.1	1.2E-05	1.3	7.4E-04	-0.5	3.0E-01
ENSMUST00000016781	intraflagellar transport 27 [Source:MGI Symbol;Acc:MGI:1914292]		Q9D0P8	-0.7	2.8E-01	-0.1	9.5E-01	0.9	1.7E-01	0.2	7.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000016897	tubulin tyrosine ligase-like 1 [Source:MGI Symbol;Acc:MGI:2443047]		Q91V51	1.0	4.1E-02	1.3	5.1E-02	0.6	2.6E-01	0.2	6.5E-01
ENSMUST00000016901	tubulin tyrosine ligase-like family, member 12 [Source:MGI Symbol;Acc:MGI:3039573]		Q3UDE2	0.5	5.1E-01	1.2	1.9E-01	0.0	9.7E-01	-0.8	3.5E-01
ENSMUST00000017147	seminal vesicle secretory protein 3A [Source:MGI Symbol;Acc:MGI:1927635]	F2Z472		7.7	5.8E-04	3.6	2.1E-03	-1.0	2.6E-01	-0.4	5.9E-01
ENSMUST00000017151	mbination signal binding protein for immunoglobulin kappa J region-like [Source:MGI Symbol;Acc:MGI:1196	Q3V2I2	O08674	7.6	5.4E-05	5.1	1.5E-02	-0.6	7.4E-01	0.8	4.7E-01
ENSMUST00000017153	syndecan 4 [Source:MGI Symbol;Acc:MGI:1349164]	Q3U5S6	O35988	3.6	1.9E-03	-5.2	1.7E-04	0.5	2.9E-01	-2.0	9.4E-02
ENSMUST00000017255	keratin 24 [Source:MGI Symbol;Acc:MGI:1922956]		A1L317	7.8	8.0E-05	-7.0	3.1E-03	0.5	4.2E-01	0.7	7.2E-01
ENSMUST00000017270	keratin 42 [Source:MGI Symbol;Acc:MGI:1915489]		Q6IFX2	6.7	2.2E-03	3.9	5.3E-02	-2.8	1.5E-01	-1.5	2.3E-01
ENSMUST00000017276	cytohesin 1 [Source:MGI Symbol;Acc:MGI:1334257]	Q8K3E8	Q9QX11	-5.4	1.8E-02	4.9	3.1E-03	-3.3	4.8E-02	-0.5	5.5E-01
ENSMUST00000017290	breast cancer 1, early onset [Source:MGI Symbol;Acc:MGI:104537]		P48754	1.7	2.5E-03	-0.8	2.5E-01	0.6	1.8E-01	-0.4	6.0E-01
ENSMUST00000017316	amine oxidase, copper containing 3 [Source:MGI Symbol;Acc:MGI:1306797]	A2A4I8		7.2	1.3E-04	7.6	1.0E-04	1.5	1.8E-01	0.5	4.3E-01
ENSMUST00000017332	cytochrome C oxidase assembly factor 3 [Source:MGI Symbol;Acc:MGI:1098757]		Q9D2R6	-4.6	3.6E-05	4.9	1.8E-02	-0.7	6.8E-01	2.0	9.6E-02
ENSMUST00000017348	gasdermin A [Source:MGI Symbol;Acc:MGI:1889509]		Q9EST1	5.5	1.1E-05	7.1	1.8E-04	-0.6	6.1E-01	-0.1	9.0E-01
ENSMUST00000017354	mediator complex subunit 24 [Source:MGI Symbol;Acc:MGI:1344385]		Q99K74	-6.3	3.6E-04	-0.9	2.6E-01	-4.6	1.3E-04	-0.2	8.4E-01
ENSMUST00000017355	gasdermin A2 [Source:MGI Symbol;Acc:MGI:1921490]		Q32M21	4.6	8.9E-03	7.1	3.3E-04	-0.7	6.3E-01	0.1	9.3E-01
ENSMUST00000017365	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 [Source:MGI Symbol;Acc:MGI:98858]		P14685	-5.6	1.8E-04	5.1	1.8E-02	-0.7	7.0E-01	0.9	4.6E-01
ENSMUST00000017384	cancer susceptibility candidate 3 [Source:MGI Symbol;Acc:MGI:2179723]		Q8K3W3	-4.4	2.9E-03	-0.6	7.1E-01	0.9	4.3E-01	-3.8	9.4E-02
ENSMUST00000017288	Rho family GTPase 3 [Source:MGI Symbol;Acc:MGI:1921444]		P61588	-1.3	1.3E-01	-1.3	1.9E-01	-0.6	3.7E-01	-0.6	5.1E-01
ENSMUST00000017408	exosome component 10 [Source:MGI Symbol;Acc:MGI:1355322]		P56960	-6.6	1.1E-05	1.4	2.8E-02	-0.3	5.2E-01	0.1	8.6E-01
ENSMUST00000017430	glyoxalase domain containing 4 [Source:MGI Symbol;Acc:MGI:1914451]		Q9CPV4	-5.1	1.4E-05	7.1	4.0E-04	0.0	9.8E-01	0.1	8.4E-01
ENSMUST00000017435	TAO kinase 1 [Source:MGI Symbol;Acc:MGI:1914490]	B2RX66	Q5F2E8	-3.4	1.5E-02	-2.5	6.9E-03	0.7	1.0E-01	-1.3	1.1E-01
ENSMUST00000017443	deoxynucleotidyltransferase, terminal, interacting protein 1 [Source:MGI Symbol;Acc:MGI:1923483]	Q3THA4	Q99LB0	-3.8	9.4E-05	4.5	9.7E-05	-1.1	1.3E-01	-0.1	8.3E-01
ENSMUST00000017453	CD300 antigen like family member G [Source:MGI Symbol;Acc:MGI:1289168]		Q1ERP8	3.3	9.6E-05	-5.3	7.4E-03	0.8	1.8E-01	-0.2	9.3E-01
ENSMUST00000017458	embrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2) [Source:MGI Symbol;Acc:MGI:185825		Q9WV34	7.9	2.0E-05	3.9	5.0E-02	-0.4	8.3E-01	0.4	7.6E-01
ENSMUST00000017534	aldolase C, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:101863]		P05063	2.8	1.1E-03	-3.7	3.5E-03	0.9	9.5E-02	-1.0	3.6E-01
ENSMUST00000017544	SH3 and cysteine rich domain 2 [Source:MGI Symbol;Acc:MGI:2144518]		Q8R1B0	5.2	7.8E-04	-3.8	2.6E-02	1.0	2.0E-01	0.4	8.1E-01
ENSMUST00000017548	ribosomal protein L19 [Source:MGI Symbol;Acc:MGI:98020]	Q5I0T8	P84099	-7.8	3.5E-04	-6.5	1.1E-04	0.3	4.0E-01	0.2	8.7E-01
ENSMUST00000017552	calcium channel, voltage-dependent, beta 1 subunit [Source:MGI Symbol;Acc:MGI:102522]	A2A543		5.2	5.3E-04	-7.2	1.0E-04	-0.8	4.9E-02	1.3	2.7E-01
ENSMUST00000017561	plexin domain containing 1 [Source:MGI Symbol;Acc:MGI:1919574]		Q91ZV7	3.1	4.0E-03	-4.6	1.7E-02	0.6	4.5E-01	1.8	2.8E-01
ENSMUST00000017562	ADP-ribosylation factor-like 5B [Source:MGI Symbol;Acc:MGI:1923119]	Q8BLF9		8.4	3.1E-05	-2.3	1.0E-02	0.9	5.7E-02	-0.6	3.9E-01
ENSMUST00000017567	zinc finger protein 207 [Source:MGI Symbol;Acc:MGI:1340045]		Q9JMD0	-6.1	2.9E-06	3.4	3.5E-04	0.1	9.0E-01	0.0	9.9E-01
ENSMUST00000017572	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 [Source:MGI Symbol;Acc:MGI:1916327]	Q5BKQ9	Q8BG32	-2.8	1.3E-03	7.6	6.0E-05	-0.5	6.9E-01	-0.1	7.9E-01
ENSMUST00000017488	vitronectin [Source:MGI Symbol;Acc:MGI:98940]		P29788	3.6	9.5E-02	1.5	4.1E-01	-4.5	4.7E-02	-2.4	1.3E-01
ENSMUST00000017530	TNF receptor associated factor 4 [Source:MGI Symbol;Acc:MGI:1202880]		Q61382	-3.1	9.1E-02	-1.9	2.5E-01	-0.5	6.6E-01	-1.6	4.0E-01
ENSMUST00000017576	RNA binding protein, fox-1 homolog (C. elegans) 3 [Source:MGI Symbol;Acc:MGI:106368]		Q8BIF2	8.2	2.6E-04	3.0	2.8E-03	0.6	3.5E-01	0.4	5.7E-01
ENSMUST00000017597	pipecolic acid oxidase [Source:MGI Symbol;Acc:MGI:1197006]	Q3UEJ8	Q9D826	6.5	4.3E-04	3.8	1.3E-02	-1.0	4.3E-01	0.4	6.5E-01
ENSMUST00000017604	cytochrome b-245, alpha polypeptide [Source:MGI Symbol;Acc:MGI:1316658]	B3VQI8	Q61462	-7.0	1.1E-05	-6.9	1.2E-03	-1.1	1.3E-01	-2.0	2.7E-01
ENSMUST00000017610	tissue inhibitor of metalloproteinase 2 [Source:MGI Symbol;Acc:MGI:98753]	Q6PI17		-3.8	2.4E-05	7.4	1.1E-03	2.2	1.7E-01	-0.1	9.4E-01
ENSMUST00000017620	calcium activated nucleotidase 1 [Source:MGI Symbol;Acc:MGI:1923275]		Q8VCF1	-1.6	1.6E-02	3.6	4.0E-03	-0.1	8.7E-01	-0.6	4.1E-01
ENSMUST00000017622	zinc finger CCCH-type containing 18 [Source:MGI Symbol;Acc:MGI:1923264]	G3X8T2		-5.1	2.0E-04	8.3	7.8E-05	-0.7	6.2E-01	-0.5	4.4E-01
ENSMUST00000017629	topoisomerase (DNA) II beta [Source:MGI Symbol;Acc:MGI:98791]		Q64511	-3.8	6.1E-05	-4.9	4.2E-05	0.0	9.6E-01	-1.2	1.3E-01
ENSMUST00000017637	insulin-like growth factor binding protein 4 [Source:MGI Symbol;Acc:MGI:96439]		P47879	2.6	8.5E-04	-1.3	1.4E-01	1.2	3.6E-02	-0.3	6.8E-01
ENSMUST00000017692	suppressor of zeste 12 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1261758]		Q80U70	-6.7	1.1E-02	8.0	5.3E-04	-0.8	6.5E-01	-0.6	4.6E-01
ENSMUST00000017590	C1q and tumor necrosis factor related protein 1 [Source:MGI Symbol;Acc:MGI:1919254]		Q9QXP7	4.9	8.0E-02	5.8	4.6E-02	-0.8	7.7E-01	-1.8	3.3E-01
ENSMUST00000017694	ATPase family, AAA domain containing 5 [Source:MGI Symbol;Acc:MGI:2442925]		Q4QY64	4.9	7.1E-03	4.5	3.1E-03	-2.4	9.1E-02	-0.3	6.9E-01
ENSMUST00000017732	keratin 27 [Source:MGI Symbol;Acc:MGI:1339999]		Q9Z320	7.1	8.6E-05	-5.9	3.1E-04	1.3	1.6E-02	0.2	8.7E-01
ENSMUST00000017741	keratin 12 [Source:MGI Symbol;Acc:MGI:96687]	Z4YJD9		8.0	1.2E-04	-3.0	7.7E-04	0.6	7.2E-02	-0.1	8.4E-01
ENSMUST00000017743	keratin 20 [Source:MGI Symbol;Acc:MGI:1914059]		Q9D312	6.8	7.6E-05	0.2	8.1E-01	1.3	2.7E-02	-0.5	5.0E-01
ENSMUST00000017751	tensin 4 [Source:MGI Symbol;Acc:MGI:2144377]		Q8BZ33	6.4	3.4E-05	-4.0	6.2E-03	1.6	1.2E-02	0.4	7.2E-01
ENSMUST00000017799	CD40 antigen [Source:MGI Symbol;Acc:MGI:88336]		P27512	4.6	1.3E-05	-3.3	1.0E-03	0.6	1.0E-01	0.1	8.4E-01
ENSMUST00000017808	solute carrier family 35, member C2 [Source:MGI Symbol;Acc:MGI:2385166]	Q5GMH2	Q8VCX2	-7.5	7.6E-04	0.0	1.0E+00	-2.2	2.0E-03	0.4	4.2E-01
ENSMUST00000017821	WD repeat and SOCS box-containing 1 [Source:MGI Symbol;Acc:MGI:1926139]	Q3TFQ2	O54927	-5.1	3.5E-04	-0.6	7.7E-01	2.2	2.0E-01	-3.9	1.2E-01
ENSMUST00000017831	ras homolog gene family, member T1 [Source:MGI Symbol;Acc:MGI:1926078]		Q8BG51	-5.7	9.4E-04	4.5	4.0E-02	-0.2	9.0E-01	0.2	8.7E-01
ENSMUST00000017836	rhomboid, veinlet-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2179276]		P58873	8.6	1.4E-05	6.6	2.9E-04	-0.5	6.7E-01	0.0	9.6E-01
ENSMUST00000017851	serine incorporator 3 [Source:MGI Symbol;Acc:MGI:1349457]		Q9QZI9	-7.6	6.3E-08	7.4	4.2E-04	-0.7	6.4E-01	0.0	9.5E-01
ENSMUST00000017859	phosphatidylglycerophosphate synthase 1 [Source:MGI Symbol;Acc:MGI:1921701]	F8WI04		-9.0	1.1E-04	7.1	1.2E-04	-0.1	9.2E-01	-0.5	4.6E-01
ENSMUST00000017867	WAP four-disulfide core domain 2 [Source:MGI Symbol;Acc:MGI:1914951]	Q4FZJ6	Q9DAU7	4.6	5.6E-03	1.8	3.3E-02	-4.2	6.0E-04	0.5	4.5E-01
ENSMUST00000017759	tumor necrosis factor, alpha-induced protein 1 (endothelial) [Source:MGI Symbol;Acc:MGI:104961]		O70479	-1.1	1.6E-01	-0.1	8.8E-01	0.4	5.4E-01	-0.6	5.5E-01
ENSMUST00000017783	RAB11 family interacting protein 4 (class II) [Source:MGI Symbol;Acc:MGI:2442920]		Q8BQP8	-1.0	6.3E-02	-0.3	5.9E-01	0.6	2.0E-01	-0.1	9.2E-01
ENSMUST00000017881	matrix metallopeptidase 9 [Source:MGI Symbol;Acc:MGI:97011]		P41245	-7.8	2.4E-06	4.1	9.6E-05	-0.6	3.3E-01	-0.1	8.2E-01
ENSMUST00000017891	GH3 domain containing [Source:MGI Symbol;Acc:MGI:1931556]		Q99J23	1.1	1.3E-02	-5.4	2.0E-02	1.2	1.3E-01	-0.9	6.9E-01
ENSMUST00000017911	spermatogenesis associated 25 [Source:MGI Symbol;Acc:MGI:1922892]		Q9DA57	7.5	8.3E-05	-5.0	3.4E-03	1.2	7.0E-02	1.1	4.0E-01
ENSMUST00000017920	v-crk sarcoma virus CT10 oncogene homolog (avian) [Source:MGI Symbol;Acc:MGI:88508]	Q5ND51	Q64010	-8.0	3.1E-04	-4.3	1.7E-02	0.6	4.0E-01	-0.8	6.4E-01
ENSMUST00000017946	family with sequence similarity 134, member C [Source:MGI Symbol;Acc:MGI:1915248]		Q9CQV4	-6.0	5.4E-04	6.3	3.3E-04	-1.3	2.7E-01	0.9	1.9E-01
ENSMUST00000017839	ring finger protein 135 [Source:MGI Symbol;Acc:MGI:1919206]	B2RRA5	Q9CWS1	-0.6	2.6E-01	0.6	3.1E-01	0.5	3.1E-01	-0.8	2.2E-01
ENSMUST00000017841	adenosine deaminase [Source:MGI Symbol;Acc:MGI:87916]	Q4FK28	P03958	-0.3	6.8E-01	-0.6	4.3E-01	-0.8	1.9E-01	-0.4	6.0E-01
ENSMUST00000017961	junctophilin 2 [Source:MGI Symbol;Acc:MGI:1891496]		Q9ET78	6.7	2.9E-02	-6.7	1.0E-06	0.2	3.2E-01	-0.7	2.7E-01
ENSMUST00000017974	DEXH (Asp-Glu-X-His) box polypeptide 58 [Source:MGI Symbol;Acc:MGI:1931560]		Q99J87	-2.4	4.5E-03	-6.9	1.5E-03	1.0	1.0E-01	-1.2	5.2E-01
ENSMUST00000017975	RAB5A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105926]		Q9CQD1	-4.1	4.9E-05	-3.8	4.2E-03	-8.4	4.7E-05	0.0	9.9E-01
ENSMUST00000017878	dysbindin (dystrobrevin binding protein 1) domain containing 2 [Source:MGI Symbol;Acc:MGI:106562]	Q330P7	Q9CRD4	2.6	1.3E-01	3.7	1.1E-01	0.5	8.2E-01	-0.7	6.6E-01
ENSMUST00000017981	NFKB inhibitor interacting Ras-like protein 2 [Source:MGI Symbol;Acc:MGI:1919216]		Q9CR56	-3.7	8.7E-04	-5.6	1.2E-04	1.6	4.0E-03	-0.7	4.8E-01
ENSMUST00000018002	intraflagellar transport 52 [Source:MGI Symbol;Acc:MGI:2387217]		Q62559	-3.3	1.6E-03	1.7	4.7E-03	0.6	1.4E-01	-0.1	9.0E-01
ENSMUST00000017900	solute carrier family 12, member 7 [Source:MGI Symbol;Acc:MGI:1342283]	B9EIV8	Q9WVL3	0.5	2.7E-01	1.0	1.4E-01	0.5	3.3E-01	0.0	9.7E-01
ENSMUST00000017904	cathepsin A [Source:MGI Symbol;Acc:MGI:97748]	G3X8T3		2.6	2.6E-01	5.6	2.7E-02	-0.6	8.0E-01	-3.6	5.8E-02
ENSMUST00000017908	zinc finger SWIM-type containing 1 [Source:MGI Symbol;Acc:MGI:1919221]		Q9CWV7	0.8	1.9E-01	1.4	1.3E-01	0.9	1.8E-01	0.4	6.0E-01
ENSMUST00000018005	myeloblastosis oncogene-like 2 [Source:MGI Symbol;Acc:MGI:101785]		P48972	1.7	2.5E-02	5.8	4.9E-04	-1.9	1.5E-01	-0.1	8.4E-01
ENSMUST00000018012	serum/glucocorticoid regulated kinase 2 [Source:MGI Symbol;Acc:MGI:1351318]		Q9QZS5	5.7	5.6E-04	-7.0	8.1E-04	0.6	2.9E-01	-0.4	8.1E-01
ENSMUST00000018087	ganglioside-induced differentiation-associated protein 1-like 1 [Source:MGI Symbol;Acc:MGI:2385163]	Q3USC7		6.7	2.5E-02	-5.3	1.3E-03	-1.3	5.5E-02	-2.4	1.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000017945	MAX-like protein X [Source:MGI Symbol;Acc:MGI:108398]	A2BFB0		-4.9	4.0E-02	-3.5	2.9E-01	1.1	5.3E-01	-0.2	9.5E-01
ENSMUST00000018113	prostaglandin I2 (prostacyclin) synthase [Source:MGI Symbol;Acc:MGI:1097156]		O35074	7.8	2.0E-05	-7.4	1.0E-02	1.0	2.0E-01	2.4	3.2E-01
ENSMUST00000018156	RAS-related C3 botulinum substrate 3 [Source:MGI Symbol;Acc:MGI:2180784]	Q14A12	P60764	5.2	3.5E-02	8.3	2.6E-02	0.0	9.9E-01	-1.6	3.5E-01
ENSMUST00000018246	histone cluster 1, H2bc [Source:MGI Symbol;Acc:MGI:1915274]		Q6ZWY9	-6.7	9.3E-05	-1.3	1.3E-01	0.6	2.7E-01	-0.5	5.7E-01
ENSMUST00000018287	naf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian) [Source:MGI Symbol;Acc:MGI:9995	Q3UP84	Q61827	-5.7	7.6E-04	-3.5	8.6E-04	0.8	5.6E-02	0.3	7.4E-01
ENSMUST00000018304	mediator complex subunit 1 [Source:MGI Symbol;Acc:MGI:1100846]		Q925J9	5.7	1.3E-03	-2.7	2.4E-02	1.3	3.7E-02	0.4	7.1E-01
ENSMUST00000018311	START domain containing 3 [Source:MGI Symbol;Acc:MGI:1929618]	Q544C3	Q61542	-3.4	1.7E-04	-3.4	7.2E-03	0.5	3.3E-01	0.6	5.7E-01
ENSMUST00000018315	vacuole membrane protein 1 [Source:MGI Symbol;Acc:MGI:1923159]		Q99KU0	-3.7	4.9E-04	3.2	4.8E-03	1.1	1.7E-01	-0.4	5.6E-01
ENSMUST00000018333	ubiquitin carboxyl-terminal esterase L5 [Source:MGI Symbol;Acc:MGI:1914848]		Q9WUP7	-5.8	3.7E-05	5.3	5.8E-04	-2.1	9.9E-02	-1.7	3.4E-02
ENSMUST00000018353	serine/threonine kinase 4 [Source:MGI Symbol;Acc:MGI:1929004]		Q9JI11	-6.7	1.3E-04	5.6	7.5E-02	-0.9	7.8E-01	0.2	8.9E-01
ENSMUST00000018094	hepatic nuclear factor 4, alpha [Source:MGI Symbol;Acc:MGI:109128]		P49698	0.0	9.9E-01	5.6	8.9E-03	1.5	3.6E-01	-4.0	1.5E-02
ENSMUST00000018361	peripheral myelin protein 22 [Source:MGI Symbol;Acc:MGI:97631]	Q5SXS3		5.1	2.3E-03	0.3	6.1E-01	-7.3	2.1E-05	0.2	7.6E-01
ENSMUST00000018143	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 [Source:MGI Symbol;Acc:MGI:2385884]		Q921N6	-1.0	8.3E-02	-1.0	1.8E-01	0.1	8.5E-01	0.0	9.6E-01
ENSMUST00000018382	growth differentiation factor 9 [Source:MGI Symbol;Acc:MGI:95692]	Q3UWR9	Q07105	4.8	6.7E-04	0.8	7.1E-01	-2.8	2.1E-01	1.7	3.5E-01
ENSMUST00000018184	ribosomal RNA processing 7 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1922028]		Q9D1C9	-1.3	5.1E-02	0.4	5.8E-01	0.8	1.4E-01	-0.9	2.4E-01
ENSMUST00000018186	cytochrome b5 reductase 3 [Source:MGI Symbol;Acc:MGI:94893]		Q9DCN2	0.5	2.9E-01	0.2	7.8E-01	-0.1	7.6E-01	0.2	7.2E-01
ENSMUST00000018212	integrator complex subunit 2 [Source:MGI Symbol;Acc:MGI:1917672]		Q80UK8	0.3	6.0E-01	0.4	5.9E-01	0.5	3.5E-01	0.4	5.0E-01
ENSMUST00000018399	keratin 33A [Source:MGI Symbol;Acc:MGI:1919138]		Q8K0Y2	7.0	7.3E-05	-5.2	6.0E-04	0.1	8.2E-01	-1.4	2.6E-01
ENSMUST00000018274	casein kinase 1, delta [Source:MGI Symbol;Acc:MGI:1355272]		Q9DC28	-2.8	5.0E-02	-0.3	7.9E-01	0.4	7.1E-01	-2.1	1.6E-01
ENSMUST00000018407	T-box 5 [Source:MGI Symbol;Acc:MGI:102541]	Q5CZX7	P70326	8.2	9.2E-07	-3.2	4.2E-02	1.0	1.8E-01	-1.4	3.4E-01
ENSMUST00000018295	protein interacting with C kinase 1 [Source:MGI Symbol;Acc:MGI:894645]	E9PUZ5		-2.3	3.7E-02	-3.5	2.2E-02	-0.6	3.5E-01	0.6	6.6E-01
ENSMUST00000018430	proteasome (prosome, macropain) subunit, beta type 6 [Source:MGI Symbol;Acc:MGI:104880]		Q60692	-7.9	1.4E-05	5.0	3.0E-03	-1.4	3.3E-01	-0.7	4.4E-01
ENSMUST00000018437	profilin 1 [Source:MGI Symbol;Acc:MGI:97549]	Q5SX50	P62962	-8.7	1.9E-05	-2.6	6.5E-03	1.0	3.1E-02	0.2	7.8E-01
ENSMUST00000018313	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase [Source:MGI Symbol;Acc:MGI:1095404]	Q3UPI0	O09008	0.4	5.6E-01	1.0	2.9E-01	0.3	7.1E-01	-0.3	7.0E-01
ENSMUST00000018449	pre-mRNA processing factor 8 [Source:MGI Symbol;Acc:MGI:2179381]		Q99PV0	-4.9	5.3E-03	-4.6	1.2E-03	0.0	9.5E-01	1.0	3.6E-01
ENSMUST00000018470	ionooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Source:MGI Symbol;Acc:M(	A2A5N2	Q9CQV8	-4.9	5.4E-06	-3.8	3.2E-03	1.1	3.8E-02	-0.8	4.3E-01
ENSMUST00000018337	cell division cycle 73, Paf1/RNA polymerase II complex component [Source:MGI Symbol;Acc:MGI:2384876]		Q8JZM7	0.3	5.3E-01	0.2	7.2E-01	0.6	2.0E-01	0.7	2.7E-01
ENSMUST00000018476	serine/threonine kinase 3 [Source:MGI Symbol;Acc:MGI:1928487]		Q9JI10	-1.6	1.7E-02	2.4	3.2E-02	-2.2	4.1E-02	-0.4	6.4E-01
ENSMUST00000018478	kinase suppressor of ras 1 [Source:MGI Symbol;Acc:MGI:105051]		Q61097	-2.5	7.1E-04	-5.1	2.6E-03	0.3	6.6E-01	-1.3	3.5E-01
ENSMUST00000018485	interleukin 12 receptor, beta 2 [Source:MGI Symbol;Acc:MGI:1270861]		P97378	5.5	4.4E-04	-4.2	1.6E-03	-8.8	2.4E-05	0.6	5.7E-01
ENSMUST00000018516	centrosomal protein 95 [Source:MGI Symbol;Acc:MGI:2443502]		Q8BVV7	-6.2	5.8E-04	4.8	9.8E-04	-0.7	5.1E-01	-0.7	3.6E-01
ENSMUST00000018521	vascular endothelial zinc finger 1 [Source:MGI Symbol;Acc:MGI:1313291]	Q5SXC4		-2.6	1.1E-03	6.5	2.4E-04	-0.6	6.3E-01	-0.1	8.7E-01
ENSMUST00000018547	gametogenetin binding protein 2 [Source:MGI Symbol;Acc:MGI:2387356]		Q5SV77	-4.6	2.1E-02	8.3	4.3E-06	-0.4	6.5E-01	-0.5	2.1E-01
ENSMUST00000018429	phospholipase D2 [Source:MGI Symbol;Acc:MGI:892877]	Q5SXG5	P97813	0.5	8.2E-01	1.1	6.3E-01	-1.6	4.5E-01	-2.2	3.3E-01
ENSMUST00000018556	KAT8 regulatory NSL complex subunit 1 [Source:MGI Symbol;Acc:MGI:1923969]		Q80TG1	-4.1	4.3E-04	-8.3	1.1E-04	-0.4	3.4E-01	0.0	9.9E-01
ENSMUST00000018431	sperm associated antigen 7 [Source:MGI Symbol;Acc:MGI:107380]		Q7TNE3	-0.7	2.6E-01	-1.5	8.7E-02	-0.4	5.0E-01	0.5	5.5E-01
ENSMUST00000018571	yippee-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925114]	Q0VA86	Q65Z95	2.2	6.2E-03	-10.3	1.7E-04	1.3	3.2E-02	2.9	1.2E-01
ENSMUST00000018572	A kinase (PRKA) anchor protein 1 [Source:MGI Symbol;Acc:MGI:104729]		O08715	4.5	6.8E-03	1.9	1.7E-01	1.5	2.2E-01	-5.4	3.4E-03
ENSMUST00000018466	translocase of outer mitochondrial membrane 34 [Source:MGI Symbol;Acc:MGI:1914395]		Q9CYG7	-2.8	8.3E-02	-0.6	6.7E-01	-0.7	5.5E-01	-2.8	1.1E-01
ENSMUST00000018586	Der1-like domain family, member 2 [Source:MGI Symbol;Acc:MGI:2151483]	J3QMF4		-3.0	4.9E-03	-4.6	1.4E-04	1.2	6.5E-03	0.9	2.6E-01
ENSMUST00000018593	RPA interacting protein [Source:MGI Symbol;Acc:MGI:1916973]		Q9CWY9	-4.8	1.2E-03	-5.2	1.4E-03	-0.5	3.3E-01	3.1	2.0E-02
ENSMUST00000018610	nitric oxide synthase 2, inducible [Source:MGI Symbol;Acc:MGI:97361]		P29477	-4.3	5.0E-05	-1.1	1.2E-01	1.2	2.0E-02	-0.3	6.8E-01
ENSMUST00000018625	amyloid beta precursor protein (cytoplasmic tail) binding protein 2 [Source:MGI Symbol;Acc:MGI:1914134]		Q9DAX9	-2.3	1.7E-04	3.0	2.0E-02	-1.6	1.7E-01	0.9	3.0E-01
ENSMUST00000018491	zinc finger with KRAB and SCAN domains 6 [Source:MGI Symbol;Acc:MGI:1289293]		Q810A1	-0.8	7.7E-01	2.3	4.9E-01	0.4	8.8E-01	-2.7	3.3E-01
ENSMUST00000018506	karyopherin (importin) alpha 2 [Source:MGI Symbol;Acc:MGI:103561]	Q52L97	P52293	-0.8	5.4E-01	-4.3	4.7E-02	-2.1	6.7E-02	1.5	4.6E-01
ENSMUST00000018630	wingless-type MMTV integration site family, member 9B [Source:MGI Symbol;Acc:MGI:1197020]	Q2TBA6	O35468	8.5	1.3E-05	-3.0	2.4E-02	0.2	7.3E-01	-3.0	5.7E-02
ENSMUST00000018632	myosin, heavy polypeptide 4, skeletal muscle [Source:MGI Symbol;Acc:MGI:1339713]		Q5SX39	7.9	6.4E-05	-1.6	4.7E-02	0.8	1.0E-01	-0.2	8.1E-01
ENSMUST00000018641	myosin, heavy polypeptide 2, skeletal muscle, adult [Source:MGI Symbol;Acc:MGI:1339710]	G3UW82		8.7	1.2E-05	-2.0	4.4E-01	2.3	1.6E-01	-0.2	9.4E-01
ENSMUST00000018549	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2443470]		Q99J25	0.6	2.4E-01	1.4	4.1E-02	0.7	2.1E-01	-0.2	7.1E-01
ENSMUST00000018681	polycomb group ring finger 2 [Source:MGI Symbol;Acc:MGI:99161]		P23798	5.3	6.5E-03	0.4	7.8E-01	4.7	7.2E-04	0.2	8.3E-01
ENSMUST00000018568	developmentally regulated GTP binding protein 2 [Source:MGI Symbol;Acc:MGI:1342307]		Q9QXB9	-0.8	1.1E-01	-0.4	4.7E-01	-0.1	8.9E-01	-0.4	4.5E-01
ENSMUST00000018569	DEAH (Asp-Glu-Ala-His) box polypeptide 40 [Source:MGI Symbol;Acc:MGI:1914737]		Q6PE54	-1.0	9.8E-02	-0.4	6.0E-01	0.9	9.6E-02	0.3	6.1E-01
ENSMUST00000018685	CWC25 spliceosome-associated protein homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914730]		Q9DBF7	-1.2	2.9E-02	1.6	6.0E-02	-0.4	5.0E-01	0.1	8.6E-01
ENSMUST00000018711	gamma-aminobutyric acid receptor associated protein [Source:MGI Symbol;Acc:MGI:1861742]		Q9DCD6	-7.0	1.7E-07	2.1	9.6E-02	-4.8	3.9E-03	-2.3	4.1E-02
ENSMUST00000018577	nucleolar protein 11 [Source:MGI Symbol;Acc:MGI:1916229]		Q8BJW5	-0.8	7.8E-01	-4.3	2.4E-01	-2.8	1.7E-01	0.7	8.5E-01
ENSMUST00000018713	claudin 7 [Source:MGI Symbol;Acc:MGI:1859285]		Q9Z261	5.6	3.0E-04	-3.9	1.4E-02	0.0	9.5E-01	0.9	4.9E-01
ENSMUST00000018716	PHD finger protein 23 [Source:MGI Symbol;Acc:MGI:1925496]		Q8BSN5	-5.2	2.7E-03	-3.3	1.4E-02	0.0	9.6E-01	-1.5	2.4E-01
ENSMUST00000018719	dynein, axonemal, heavy chain 17 [Source:MGI Symbol;Acc:MGI:1917176]	A2A519		6.5	1.1E-04	-1.9	2.3E-02	1.6	4.2E-03	-0.8	3.2E-01
ENSMUST00000018614	assium voltage-gated channel, shaker-related subfamily, beta member 3 [Source:MGI Symbol;Acc:MGI:13362	Q8VD73		3.8	3.6E-02	6.6	6.8E-03	0.5	8.0E-01	-2.3	6.1E-02
ENSMUST00000018737	secreted acidic cysteine rich glycoprotein [Source:MGI Symbol;Acc:MGI:98373]	Q5NCU5	P07214	7.0	5.9E-05	-1.0	5.7E-02	0.7	4.0E-02	-0.6	2.0E-01
ENSMUST00000018765	matrix metallopeptidase 8 [Source:MGI Symbol;Acc:MGI:1202395]		O70138	-9.9	5.8E-08	8.8	2.0E-05	-0.6	6.3E-01	-0.8	1.3E-01
ENSMUST00000018792	dual specificity phosphatase 14 [Source:MGI Symbol;Acc:MGI:1927168]	Q542U4	Q9JLY7	7.5	6.8E-05	8.7	5.8E-05	-0.6	6.9E-01	-1.3	5.9E-02
ENSMUST00000018637	myosin, heavy polypeptide 1, skeletal muscle, adult [Source:MGI Symbol;Acc:MGI:1339711]		Q5SX40	2.6	2.0E-01	6.1	6.9E-03	-0.5	8.1E-01	-4.0	1.6E-02
ENSMUST00000018795	transcriptional adaptor 2A [Source:MGI Symbol;Acc:MGI:2144471]		Q8CHV6	1.7	1.1E-02	8.7	2.5E-05	-0.7	6.0E-01	-0.6	2.4E-01
ENSMUST00000018644	adenosine A2b receptor [Source:MGI Symbol;Acc:MGI:99403]		Q60614	-0.5	3.1E-01	0.4	5.4E-01	0.5	3.2E-01	-0.4	4.8E-01
ENSMUST00000018645	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	Q5RIM6		-1.4	6.5E-01	-5.0	2.1E-01	-3.0	1.6E-01	0.6	8.8E-01
ENSMUST00000018651	transient receptor potential cation channel, subfamily V, member 2 [Source:MGI Symbol;Acc:MGI:1341836]		Q9WTR1	-0.9	8.7E-02	-0.4	5.0E-01	0.9	7.1E-02	0.5	4.6E-01
ENSMUST00000018803	pyridoxine 5'-phosphate oxidase [Source:MGI Symbol;Acc:MGI:2144151]		Q91XF0	-4.9	2.2E-03	4.5	1.1E-02	-2.7	1.3E-01	-1.9	8.5E-02
ENSMUST00000018805	component of oligomeric golgi complex 1 [Source:MGI Symbol;Acc:MGI:1333873]		Q9Z160	-1.8	6.0E-03	-1.2	1.1E-01	0.8	8.5E-02	0.8	2.5E-01
ENSMUST00000018691	phosphatidylinositol-5-phosphate 4-kinase, type II, beta [Source:MGI Symbol;Acc:MGI:1934234]	Q3UJ95	Q80XI4	-0.7	1.1E-01	0.0	9.5E-01	0.9	5.0E-02	0.2	7.1E-01
ENSMUST00000018700	discs, large homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1277959]		Q62108	-3.0	6.7E-02	-2.5	2.1E-01	-0.1	9.4E-01	-0.6	7.5E-01
ENSMUST00000018810	chromobox 1 [Source:MGI Symbol;Acc:MGI:105369]	Q7TPM0		4.1	3.6E-04	-7.4	1.1E-06	0.1	5.8E-01	0.5	4.3E-01
ENSMUST00000018821	solute carrier family 25, member 39 [Source:MGI Symbol;Acc:MGI:1196386]	Q14BQ5	Q9D8K8	-7.3	1.8E-03	5.6	5.8E-04	-0.6	6.4E-01	-0.6	4.0E-01
ENSMUST00000018841	apoptosis antagonizing transcription factor [Source:MGI Symbol;Acc:MGI:1929608]		Q9JKX4	-4.9	1.5E-03	-3.0	4.3E-02	0.9	2.3E-01	-1.3	4.3E-01
ENSMUST00000018718	acyl-Coenzyme A dehydrogenase, very long chain [Source:MGI Symbol;Acc:MGI:895149]	B1AR28		-0.9	7.4E-01	-1.2	6.3E-01	-2.6	2.5E-01	-2.3	3.9E-01
ENSMUST00000018851	dynein cytoplasmic 1 heavy chain 1 [Source:MGI Symbol;Acc:MGI:103147]		Q9JHU4	-1.5	2.2E-03	5.9	7.4E-04	-1.2	3.5E-01	-0.5	4.7E-01
ENSMUST00000018727	GTPase activating protein (SH3 domain) binding protein 1 [Source:MGI Symbol;Acc:MGI:1351465]		P97855	-0.2	5.7E-01	-0.5	3.8E-01	-0.1	8.6E-01	0.2	7.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000018875	adaptor-related protein complex 2, beta 1 subunit [Source:MGI Symbol;Acc:MGI:1919020]	Q5SWR1	Q9DBG3	-3.7	1.5E-05	0.5	4.5E-01	-7.4	2.1E-05	-0.9	1.6E-01
ENSMUST00000018743	mitochondrial elongation factor 2 [Source:MGI Symbol;Acc:MGI:2144199]		Q5NCS9	-0.6	3.8E-01	0.7	4.7E-01	1.5	4.8E-02	0.2	7.7E-01
ENSMUST00000018744	serine hydroxymethyltransferase 1 (soluble) [Source:MGI Symbol;Acc:MGI:98299]		P50431	0.5	4.0E-01	1.1	1.5E-01	0.4	5.5E-01	-0.3	6.6E-01
ENSMUST00000018755	PDZ and LIM domain 4 [Source:MGI Symbol;Acc:MGI:1353470]		P70271	0.9	4.0E-01	1.6	1.9E-01	-1.3	2.1E-01	-2.0	8.7E-02
ENSMUST00000018877	peroxisomal biogenesis factor 12 [Source:MGI Symbol;Acc:MGI:2144177]	Q5SWQ8	Q8VC48	5.1	2.6E-02	-8.7	5.9E-07	0.0	9.3E-01	-1.2	1.2E-01
ENSMUST00000018880	nuclear distribution gene E-like homolog 1 (A. nidulans) [Source:MGI Symbol;Acc:MGI:1932915]		Q9ERR1	-5.6	3.4E-06	5.8	7.6E-04	-0.6	6.2E-01	1.0	1.8E-01
ENSMUST00000018884	solute carrier family 25, member 35 [Source:MGI Symbol;Acc:MGI:1919248]	A0A0A0MQ70		5.0	1.2E-03	0.8	2.5E-01	-0.8	1.9E-01	0.2	7.2E-01
ENSMUST00000018798	IKAROS family zinc finger 1 [Source:MGI Symbol;Acc:MGI:1342540]	Q5SWU0		1.1	6.4E-01	-1.1	7.3E-01	-0.6	7.6E-01	1.5	6.1E-01
ENSMUST00000018887	myosin, heavy polypeptide 10, non-muscle [Source:MGI Symbol;Acc:MGI:1930780]	Q5SV64		4.7	3.5E-02	-2.7	4.9E-02	0.8	2.7E-01	-1.4	3.4E-01
ENSMUST00000018896	tumor necrosis factor (ligand) superfamily, member 13 [Source:MGI Symbol;Acc:MGI:1916833]	Q5F2A4		-4.8	2.0E-03	-0.8	2.5E-01	0.7	1.5E-01	-0.3	6.1E-01
ENSMUST00000018905	mannose-P-dolichol utilization defect 1 [Source:MGI Symbol;Acc:MGI:1346040]	Q8R0J2		-4.6	3.4E-04	3.8	4.6E-03	-0.1	9.1E-01	0.2	7.6E-01
ENSMUST00000018909	fragile X mental retardation, autosomal homolog 2 [Source:MGI Symbol;Acc:MGI:1346074]	Q6P5B5		-3.5	1.2E-04	-5.4	1.2E-02	1.0	2.2E-01	-0.8	6.9E-01
ENSMUST00000018914	nthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9) [Source:MGI Symbol;Acc:MGI:24	Q14BC2	P56384	-6.6	1.6E-05	-1.8	9.7E-02	0.4	5.5E-01	-2.7	5.1E-02
ENSMUST00000018842	LIM homeobox protein 1 [Source:MGI Symbol;Acc:MGI:99783]	Q569N5	P63006	0.7	4.1E-01	2.1	1.0E-01	1.7	9.8E-02	0.3	7.3E-01
ENSMUST00000018918	CD68 antigen [Source:MGI Symbol;Acc:MGI:88342]		P31996	-6.8	3.1E-04	-0.6	1.9E-01	0.7	6.1E-02	-0.2	6.6E-01
ENSMUST00000018966	secreted frizzled-related sequence protein 5 [Source:MGI Symbol;Acc:MGI:1860298]			3.9	1.4E-04	-2.4	1.9E-03	1.0	9.8E-03	-0.3	5.9E-01
ENSMUST00000018988	fibronectin type III domain containing 8 [Source:MGI Symbol;Acc:MGI:1926169]	B2RQ03	Q9D2H8	7.8	4.6E-05	5.0	7.0E-02	0.1	9.7E-01	0.2	9.1E-01
ENSMUST00000018990	pantothenate kinase 3 [Source:MGI Symbol;Acc:MGI:2387464]	Q5SXA7	Q8R2W9	-1.5	3.1E-03	-4.3	1.4E-04	0.6	8.1E-02	-0.7	3.4E-01
ENSMUST00000018992	arginyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1914297]		Q9D0I9	-5.0	4.1E-05	5.0	2.2E-03	-1.1	3.6E-01	-1.1	2.2E-01
ENSMUST00000018993	WW, C2 and coiled-coil domain containing 1 [Source:MGI Symbol;Acc:MGI:2388637]		Q5SXA9	8.7	1.1E-05	0.3	8.6E-01	-3.8	6.0E-02	0.5	7.5E-01
ENSMUST00000019012	patatin-like phospholipase domain containing 5 [Source:MGI Symbol;Acc:MGI:1923022]		Q32LZ8	7.6	5.7E-05	-4.8	6.3E-03	-1.0	1.4E-01	-1.0	5.3E-01
ENSMUST00000019026	mitochondrial ribosomal protein L45 [Source:MGI Symbol;Acc:MGI:1914286]		Q9D0Q7	-1.1	8.9E-03	-2.8	2.3E-02	1.2	6.8E-02	-0.6	5.9E-01
ENSMUST00000019038	septin 9 [Source:MGI Symbol;Acc:MGI:1858222]		Q80UG5	7.1	1.4E-04	-3.0	1.7E-03	0.6	1.3E-01	0.2	7.8E-01
ENSMUST00000019051	arachidonate lipoxygenase, epidermal [Source:MGI Symbol;Acc:MGI:1274790]	Q5F2E4	P55249	5.4	2.9E-04	-7.5	2.0E-04	0.5	2.1E-01	1.4	3.0E-01
ENSMUST00000019063	transmembrane 4 superfamily member 5 [Source:MGI Symbol;Acc:MGI:1922854]	Q91XF2		4.8	2.5E-03	-4.4	6.5E-03	0.4	5.6E-01	-2.1	1.8E-01
ENSMUST00000018965	arginine vasopressin-induced 1 [Source:MGI Symbol;Acc:MGI:1916784]		Q9D7H4	0.9	3.4E-01	-0.3	7.4E-01	-1.7	5.5E-02	-0.5	5.6E-01
ENSMUST00000019064	chemokine (C-X-C motif) ligand 16 [Source:MGI Symbol;Acc:MGI:1932682]		Q8BSU2	2.9	2.6E-03	4.7	9.3E-05	0.2	7.3E-01	-0.6	3.0E-01
ENSMUST00000018985	RAD51 homolog D [Source:MGI Symbol;Acc:MGI:1261809]	Q3UGT8	O55230	-2.0	1.5E-01	-3.5	1.0E-01	0.8	5.1E-01	2.3	2.6E-01
ENSMUST00000019067	mediator complex subunit 11 [Source:MGI Symbol;Acc:MGI:1913422]		Q9D8C6	-5.7	4.4E-04	7.8	1.1E-04	-0.2	8.6E-01	-0.2	7.3E-01
ENSMUST00000019068	arachidonate 15-lipoxygenase [Source:MGI Symbol;Acc:MGI:87997]	A2CF88	P39654	1.4	2.3E-02	-1.0	6.6E-02	0.4	2.3E-01	-0.1	8.3E-01
ENSMUST00000019069	HEAT repeat containing 9 [Source:MGI Symbol;Acc:MGI:3650286]		Q5QNV8	5.9	1.3E-04	-4.1	5.2E-04	-0.8	6.9E-02	-1.7	7.1E-02
ENSMUST00000019071	chemokine (C-C motif) ligand 6 [Source:MGI Symbol;Acc:MGI:98263]		P27784	-7.4	8.8E-07	6.0	5.8E-05	-3.0	1.7E-02	-0.2	6.3E-01
ENSMUST00000019006	otopetrin 3 [Source:MGI Symbol;Acc:MGI:1916852]	F8VQ32		7.1	4.3E-02	5.0	1.7E-01	-0.9	8.0E-01	1.2	6.0E-01
ENSMUST00000019074	chemokine (C-C motif) ligand 4 [Source:MGI Symbol;Acc:MGI:98261]	Q5QNV9	P14097	-3.1	2.1E-03	7.2	1.8E-04	-0.7	6.1E-01	-0.2	7.7E-01
ENSMUST00000019076	mitogen-activated protein kinase kinase 3 [Source:MGI Symbol;Acc:MGI:1346868]	Q5SWN9	O09110	-9.4	7.6E-05	-0.6	1.7E-01	0.3	4.1E-01	-0.2	6.0E-01
ENSMUST00000019109	monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide [Source:MGI Symbol;Acc:M(		P68510	-5.4	5.2E-06	0.1	8.4E-01	-7.1	9.4E-05	-0.1	9.3E-01
ENSMUST00000019043	interferon regulatory factor 1 [Source:MGI Symbol;Acc:MGI:96590]	Q5SX13	P15314	-2.3	1.6E-01	-1.3	4.5E-01	-1.0	4.1E-01	-2.0	2.8E-01
ENSMUST00000019044	solute carrier family 22 (organic cation transporter), member 5 [Source:MGI Symbol;Acc:MGI:1329012]	Q5SX17	Q9Z0E8	0.3	6.1E-01	0.4	6.2E-01	0.2	7.3E-01	0.1	8.6E-01
ENSMUST00000019117	homeobox B1 [Source:MGI Symbol;Acc:MGI:96182]		P17919	9.3	8.3E-05	4.9	8.4E-04	-1.2	2.7E-01	-0.6	4.1E-01
ENSMUST00000019118	squamous cell carcinoma antigen recognized by T cells 3 [Source:MGI Symbol;Acc:MGI:1858230]		Q9JLI8	-1.3	1.9E-02	6.0	1.1E-03	-0.4	7.7E-01	-1.6	6.3E-02
ENSMUST00000019133	calcium/calmodulin-dependent protein kinase II, beta [Source:MGI Symbol;Acc:MGI:88257]	Q5SVJ0		6.2	1.6E-04	1.5	8.4E-02	-1.9	2.4E-02	-0.4	5.1E-01
ENSMUST00000019065	proline, glutamic acid and leucine rich protein 1 [Source:MGI Symbol;Acc:MGI:1922523]		Q9DBD5	0.1	8.5E-01	1.3	8.4E-02	0.5	3.4E-01	-0.7	2.9E-01
ENSMUST00000019135	olgi associated, gamma adaptin ear containing, ARF binding protein 3 [Source:MGI Symbol;Acc:MGI:238415(		Q8BMI3	-7.1	1.5E-04	-4.5	5.6E-03	-0.3	7.1E-01	-1.4	3.2E-01
ENSMUST00000019169	unconventional SNARE in the ER 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914273]		Q9CQ56	-8.8	8.4E-05	-2.4	1.9E-03	-4.3	3.5E-06	-0.5	4.2E-01
ENSMUST00000019183	DALR anticodon binding domain containing 3 [Source:MGI Symbol;Acc:MGI:1915039]		Q6PJN8	-5.4	1.3E-03	5.1	7.6E-04	-0.6	6.0E-01	0.2	8.1E-01
ENSMUST00000019192	crystallin, alpha A [Source:MGI Symbol;Acc:MGI:88515]	Q546L9	P24622	7.5	4.6E-05	-8.2	1.7E-06	-1.9	1.8E-04	-1.1	1.9E-01
ENSMUST00000019198	fission 1 (mitochondrial outer membrane) homolog (yeast) [Source:MGI Symbol;Acc:MGI:1913687]		Q9CQ92	-7.0	1.3E-05	-3.7	4.0E-03	-0.4	4.6E-01	0.2	8.6E-01
ENSMUST00000019075	N-acetyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:1344388]		Q9DBW3	-0.7	1.9E-01	0.4	6.1E-01	1.2	3.6E-02	0.1	8.3E-01
ENSMUST00000019199	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 [Source:MGI Symbol;Acc:MGI:99907]		Q9R0E2	-4.9	8.8E-04	-3.5	7.3E-03	1.5	2.1E-02	-4.4	1.4E-02
ENSMUST00000019224	major facilitator superfamily domain containing 3 [Source:MGI Symbol;Acc:MGI:1916822]			2.4	7.3E-03	-4.8	1.4E-04	1.1	1.1E-02	0.4	5.7E-01
ENSMUST00000019226	olute carrier family 25 (mitochondrial carrier, glutamate), member 22 [Source:MGI Symbol;Acc:MGI:1915517		Q9D6M3	6.4	2.1E-02	8.9	6.5E-04	0.7	6.9E-01	1.2	2.1E-01
ENSMUST00000019229	mediator complex subunit 8 [Source:MGI Symbol;Acc:MGI:1915269]		Q9D7W5	-8.7	8.4E-07	-0.3	5.6E-01	0.9	6.2E-02	-0.1	9.0E-01
ENSMUST00000019130	schlafen 3 [Source:MGI Symbol;Acc:MGI:1329005]	Q9Z0I5		0.5	4.2E-01	0.2	7.6E-01	-0.9	1.2E-01	-0.6	3.5E-01
ENSMUST00000019231	ATPase, H+ transporting, lysosomal accessory protein 1 [Source:MGI Symbol;Acc:MGI:109629]	Q3TWN7	Q9R1Q9	-9.4	2.9E-05	6.4	2.4E-04	-0.6	6.3E-01	-0.8	2.4E-01
ENSMUST00000019232	deoxyribonuclease 1-like 1 [Source:MGI Symbol;Acc:MGI:109628]		Q9D7J6	-5.0	4.6E-04	-5.4	4.9E-03	1.1	7.6E-02	-0.6	7.2E-01
ENSMUST00000019143	solute carrier family 35, member B4 [Source:MGI Symbol;Acc:MGI:1931249]		Q8CIA5	0.1	8.0E-01	1.8	3.8E-02	1.0	1.2E-01	-0.7	3.4E-01
ENSMUST00000019248	CD22 antigen [Source:MGI Symbol;Acc:MGI:88322]	Q3UP36		5.5	1.9E-06	-8.8	3.5E-04	-1.0	5.1E-02	-1.0	5.7E-01
ENSMUST00000019266	chemokine (C-C motif) ligand 9 [Source:MGI Symbol;Acc:MGI:104533]	Q3U9T8	P51670	-2.4	2.8E-04	-2.2	9.3E-02	1.1	1.5E-01	-2.2	1.5E-01
ENSMUST00000019268	secernin 1 [Source:MGI Symbol;Acc:MGI:1917188]		Q9CZC8	7.6	1.1E-04	5.5	1.5E-04	-3.0	1.8E-02	-1.0	1.2E-01
ENSMUST00000019276	cDNA sequence BC005537 [Source:MGI Symbol;Acc:MGI:2441726]	Q3TVJ4	Q99LU8	-4.4	3.5E-04	-8.5	2.4E-04	-0.1	7.3E-01	1.3	3.7E-01
ENSMUST00000019287	histidyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:1918041]	G5E823		-4.9	4.4E-03	-2.4	6.6E-02	0.8	2.4E-01	-1.6	2.3E-01
ENSMUST00000019220	striatin, calmodulin binding protein 4 [Source:MGI Symbol;Acc:MGI:2142346]		P58404	-1.9	4.3E-01	-2.7	3.0E-01	-1.2	5.0E-01	-0.4	8.8E-01
ENSMUST00000019290	calcium channel, voltage-dependent, gamma subunit 2 [Source:MGI Symbol;Acc:MGI:1316660]	Q3ZB20	O88602	8.9	2.6E-05	2.2	3.0E-02	-0.3	7.2E-01	0.0	9.6E-01
ENSMUST00000019291	pregnancy-specific glycoprotein 28 [Source:MGI Symbol;Acc:MGI:1891360]	Q4KL66		8.9	9.2E-05	5.4	6.8E-02	-0.8	7.6E-01	0.2	9.0E-01
ENSMUST00000019302	transmembrane protein 160 [Source:MGI Symbol;Acc:MGI:1916344]		Q9D938	-3.4	8.9E-04	-7.5	2.1E-05	0.4	1.9E-01	-0.8	4.2E-01
ENSMUST00000019317	RAB5C, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105306]	Q8C266		-4.5	9.5E-03	-9.7	1.6E-03	1.2	6.3E-02	1.5	5.1E-01
ENSMUST00000019323	malate dehydrogenase 2, NAD (mitochondrial) [Source:MGI Symbol;Acc:MGI:97050]		P08249	-7.8	5.4E-05	-4.5	3.8E-03	-0.1	8.8E-01	-0.6	6.3E-01
ENSMUST00000019333	ring finger protein 145 [Source:MGI Symbol;Acc:MGI:1921565]		Q5SWK7	-4.6	2.0E-05	5.1	7.1E-06	-1.2	5.0E-02	-0.8	5.4E-02
ENSMUST00000019354	ATPase, H+ transporting, lysosomal V1 subunit E1 [Source:MGI Symbol;Acc:MGI:894326]		P50518	-6.2	5.5E-07	-3.7	5.8E-05	-1.7	4.9E-04	-0.4	4.6E-01
ENSMUST00000019362	dishevelled 2, dsh homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:106613]		Q60838	-4.5	1.3E-02	4.8	6.1E-04	-3.1	2.5E-02	-0.3	6.3E-01
ENSMUST00000019374	LIM homeobox protein 9 [Source:MGI Symbol;Acc:MGI:1316721]		Q9WUH2	7.1	6.9E-05	-3.3	1.4E-02	1.5	2.9E-02	0.3	7.7E-01
ENSMUST00000019281	BCL2-like 11 (apoptosis facilitator) [Source:MGI Symbol;Acc:MGI:1197519]	Q3U7X3	O54918	4.0	4.5E-02	5.9	1.9E-02	0.8	6.7E-01	-1.1	5.0E-01
ENSMUST00000019283	myo-inositol 1-phosphate synthase A1 [Source:MGI Symbol;Acc:MGI:1919030]		Q9JHU9	-0.7	2.3E-01	-1.3	1.1E-01	0.0	9.8E-01	0.6	4.5E-01
ENSMUST00000019379	ribosomal protein S6 kinase-like 1 [Source:MGI Symbol;Acc:MGI:2443413]		Q8R2S1	5.2	5.8E-05	-3.1	5.4E-02	0.5	5.3E-01	-1.3	4.3E-01
ENSMUST00000019382	trans-2,3-enoyl-CoA reductase [Source:MGI Symbol;Acc:MGI:1915408]		Q9CY27	-5.2	4.5E-03	9.0	2.0E-04	0.8	6.1E-01	0.6	3.5E-01
ENSMUST00000019422	dipeptidase 1 (renal) [Source:MGI Symbol;Acc:MGI:94917]		P31428	6.8	1.8E-04	7.4	8.4E-04	-0.7	6.7E-01	0.9	3.2E-01
ENSMUST00000019426	desmoglein 4 [Source:MGI Symbol;Acc:MGI:2661061]		Q7TMD7	7.9	1.3E-05	-3.4	4.3E-03	-0.1	9.2E-01	-0.1	9.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000019439	transmembrane protein 129 [Source:MGI Symbol;Acc:MGI:1915616]		Q8K304	-5.1	4.2E-03	-4.1	4.5E-02	0.2	8.1E-01	-0.2	9.4E-01
ENSMUST00000019443	ring finger protein 31 [Source:MGI Symbol;Acc:MGI:1934704]		Q924T7	-7.0	6.6E-05	-5.9	5.6E-04	0.4	4.0E-01	-1.6	2.6E-01
ENSMUST00000019445	hydroxysteroid (17-beta) dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:105077]	Q790P4	P51656	3.1	3.8E-03	-3.3	1.1E-03	0.8	5.3E-02	-0.5	4.9E-01
ENSMUST00000019464	NADPH oxidase organizer 1 [Source:MGI Symbol;Acc:MGI:1919143]		Q8VCM2	1.8	3.3E-02	-5.9	5.0E-06	-0.3	2.9E-01	-0.6	3.8E-01
ENSMUST00000019469	glucose-6-phosphatase, catalytic [Source:MGI Symbol;Acc:MGI:95607]		P35576	7.1	3.4E-05	-1.0	5.4E-01	1.5	1.8E-01	-2.0	2.9E-01
ENSMUST00000019470	oteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki) [Source:MGI Symbol;Acc:MGI:10963(	Q4FK54	P61290	-3.4	1.1E-04	7.6	7.7E-05	-0.5	7.0E-01	-0.9	1.3E-01
ENSMUST00000019378	mutL homolog 3 (E coli) [Source:MGI Symbol;Acc:MGI:1353455]	Q68FG1		2.9	3.0E-01	-1.0	7.7E-01	-1.5	5.8E-01	2.3	4.4E-01
ENSMUST00000019482	zinc finger protein 687 [Source:MGI Symbol;Acc:MGI:1925516]		Q9D2D7	-4.3	2.2E-03	6.4	1.5E-04	0.9	3.5E-01	-0.2	6.8E-01
ENSMUST00000019506	DNA segment, Chr 8, ERATO Doi 738, expressed [Source:MGI Symbol;Acc:MGI:1289231]		Q8R1F0	-4.9	9.8E-06	-1.6	2.9E-01	0.8	3.9E-01	-2.9	1.1E-01
ENSMUST00000019386	receptor-interacting serine-threonine kinase 4 [Source:MGI Symbol;Acc:MGI:1919638]		Q9ERK0	3.4	9.5E-02	3.2	6.5E-02	-2.5	1.7E-01	-2.3	1.3E-01
ENSMUST00000019405	microtubule-associated protein 1S [Source:MGI Symbol;Acc:MGI:2443304]		Q8C052	0.4	3.7E-01	0.9	1.7E-01	0.7	1.9E-01	0.2	7.4E-01
ENSMUST00000019514	calmodulin 3 [Source:MGI Symbol;Acc:MGI:103249]		P62204	-5.5	5.1E-05	5.6	9.7E-04	-1.3	3.1E-01	-0.1	8.8E-01
ENSMUST00000019516	nuclear receptor binding protein 2 [Source:MGI Symbol;Acc:MGI:2385017]			5.1	1.8E-04	7.4	4.9E-05	-0.6	6.0E-01	-0.1	9.1E-01
ENSMUST00000019517	(constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	Q3UQL2	O88543	-7.3	1.2E-04	-0.7	6.6E-01	2.2	7.9E-02	-2.2	1.8E-01
ENSMUST00000019441	NOP9 nucleolar protein [Source:MGI Symbol;Acc:MGI:1915092]		Q8BMC4	-0.9	1.1E-01	0.0	9.5E-01	1.0	7.0E-02	0.1	8.6E-01
ENSMUST00000019576	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 [Source:MGI Symbol;Acc:MGI:1915528]		Q8VDW0	-5.4	6.3E-03	-6.8	6.3E-04	0.7	1.6E-01	0.5	7.3E-01
ENSMUST00000019605	phospholipid scramblase 3 [Source:MGI Symbol;Acc:MGI:1917560]	Q5F283	Q9JIZ9	-3.6	2.4E-03	3.9	7.4E-03	0.6	5.5E-01	-0.1	8.8E-01
ENSMUST00000019614	XPA binding protein 2 [Source:MGI Symbol;Acc:MGI:1914689]		Q9DCD2	-8.0	6.1E-05	2.8	8.6E-03	0.7	3.9E-01	-0.4	6.2E-01
ENSMUST00000019615	cell division cycle 37 [Source:MGI Symbol;Acc:MGI:109531]		Q61081	-3.2	3.8E-05	6.2	1.1E-04	-1.3	2.4E-01	-0.5	4.0E-01
ENSMUST00000019616	intercellular adhesion molecule 5, telencephalin [Source:MGI Symbol;Acc:MGI:109430]		Q60625	7.4	1.1E-05	-1.8	2.0E-02	1.1	1.8E-02	-0.5	4.7E-01
ENSMUST00000019625	myosin, heavy polypeptide 8, skeletal muscle, perinatal [Source:MGI Symbol;Acc:MGI:1339712]		P13542	8.0	6.7E-05	-5.9	8.2E-03	0.8	2.7E-01	2.3	2.2E-01
ENSMUST00000019631	thyroid hormone receptor interactor 10 [Source:MGI Symbol;Acc:MGI:2146901]		Q8CJ53	1.8	5.4E-03	-5.2	3.1E-05	-0.9	2.1E-02	-0.5	4.6E-01
ENSMUST00000019633	CD70 antigen [Source:MGI Symbol;Acc:MGI:1195273]	Q05A52	O55237	6.7	6.5E-05	-5.5	4.4E-04	0.5	2.7E-01	0.4	6.8E-01
ENSMUST00000019638	(constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	Q3UIT2	O88545	-2.1	1.4E-02	4.2	1.4E-03	-1.2	1.9E-01	-0.3	6.6E-01
ENSMUST00000019649	ubiquitin B [Source:MGI Symbol;Acc:MGI:98888]	Q78XY9	P0CG49	-8.2	6.6E-08	-7.0	5.2E-04	-0.1	7.7E-01	-0.4	7.8E-01
ENSMUST00000019572	zinc finger protein 874b [Source:MGI Symbol;Acc:MGI:3040702]	Q7M6X2		0.0	9.4E-01	0.2	7.1E-01	0.2	6.4E-01	0.0	9.7E-01
ENSMUST00000019662	adaptor-related protein complex AP-4, mu 1 [Source:MGI Symbol;Acc:MGI:1337063]		Q9JKC7	-3.8	6.4E-03	-3.2	8.2E-02	1.1	2.4E-01	-1.1	5.7E-01
ENSMUST00000019577	GIPC PDZ domain containing family, member 1 [Source:MGI Symbol;Acc:MGI:1926252]		Q9Z0G0	-1.2	5.0E-02	0.5	5.2E-01	1.3	2.8E-02	-0.4	6.0E-01
ENSMUST00000019677	MAP kinase-interacting serine/threonine kinase 1 [Source:MGI Symbol;Acc:MGI:894316]	A2A8W8		-8.4	3.3E-05	-1.1	3.0E-01	1.6	5.2E-02	-0.9	4.1E-01
ENSMUST00000019608	prostaglandin E receptor 1 (subtype EP1) [Source:MGI Symbol;Acc:MGI:97793]	B2RS62	P35375	-0.2	8.7E-01	-0.1	9.6E-01	0.1	9.1E-01	0.0	9.9E-01
ENSMUST00000019611	Rho guanine nucleotide exchange factor (GEF) 25 [Source:MGI Symbol;Acc:MGI:1277173]	G5E825		3.5	2.1E-01	3.4	2.6E-01	-0.4	8.9E-01	-0.3	8.9E-01
ENSMUST00000019679	armadillo repeat containing 6 [Source:MGI Symbol;Acc:MGI:1924063]		Q8BNU0	-5.0	7.6E-04	-7.2	1.1E-03	0.9	7.3E-02	0.1	9.5E-01
ENSMUST00000019683	reticulocalbin 3, EF-hand calcium binding domain [Source:MGI Symbol;Acc:MGI:1277122]		Q8BH97	7.8	1.4E-02	-3.2	4.0E-04	0.3	3.4E-01	0.3	6.3E-01
ENSMUST00000019701	dual specificity phosphatase 9 [Source:MGI Symbol;Acc:MGI:2387107]	Q7TNL7		5.9	1.3E-05	8.0	2.2E-05	0.1	9.3E-01	-0.5	3.1E-01
ENSMUST00000019708	AT rich interactive domain 3A (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1328360]		Q62431	-6.5	3.6E-04	8.2	1.1E-04	-0.7	6.1E-01	-0.9	2.1E-01
ENSMUST00000019721	pyruvate dehydrogenase kinase, isoenzyme 4 [Source:MGI Symbol;Acc:MGI:1351481]	Q544J2	O70571	5.7	1.6E-05	1.5	3.9E-02	-0.3	5.1E-01	0.0	9.7E-01
ENSMUST00000019722	UBX domain protein 6 [Source:MGI Symbol;Acc:MGI:1913780]		Q99PL6	-3.9	3.7E-04	5.5	3.1E-04	-1.5	2.0E-01	-0.3	6.4E-01
ENSMUST00000019726	perilipin 3 [Source:MGI Symbol;Acc:MGI:1914155]		Q9DBG5	-2.5	2.0E-04	1.1	1.9E-01	1.4	4.9E-02	-1.7	4.5E-02
ENSMUST00000019734	cytochrome b-561 [Source:MGI Symbol;Acc:MGI:103253]		Q60720	5.0	1.3E-04	-7.6	9.3E-07	0.1	8.3E-01	-0.5	4.3E-01
ENSMUST00000019660	zinc finger with KRAB and SCAN domains 1 [Source:MGI Symbol;Acc:MGI:1921820]		Q8BGS3	-1.3	2.8E-01	0.6	6.7E-01	0.0	9.9E-01	-1.9	1.7E-01
ENSMUST00000019749	homeobox D8 [Source:MGI Symbol;Acc:MGI:96209]		P23463	7.3	2.3E-03	-3.3	3.8E-02	-0.1	9.0E-01	-0.6	6.9E-01
ENSMUST00000019803	coiled-coil domain containing 12 [Source:MGI Symbol;Acc:MGI:1919904]		Q8R344	-5.3	1.5E-05	-3.8	3.3E-03	1.0	6.1E-02	-3.6	1.7E-02
ENSMUST00000019808	perilipin 5 [Source:MGI Symbol;Acc:MGI:1914218]		Q8BVZ1	-4.9	3.5E-03	-0.5	5.9E-01	0.9	1.6E-01	-3.7	7.6E-03
ENSMUST00000019833	RIKEN cDNA 1110001J03 gene [Source:MGI Symbol;Acc:MGI:1913367]		Q9CR13	-3.5	1.4E-02	4.0	1.3E-01	-4.5	1.2E-01	-0.7	7.2E-01
ENSMUST00000019684	tte carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2 [Source:MGI Symbol;Acc:MGI:18906			-0.2	8.4E-01	-0.7	6.1E-01	0.1	9.2E-01	0.6	6.4E-01
ENSMUST00000019697	HAUS augmin-like complex, subunit 5 [Source:MGI Symbol;Acc:MGI:1919159]		Q9D786	-0.6	3.1E-01	1.0	2.2E-01	1.1	9.3E-02	-0.5	4.6E-01
ENSMUST00000019854	mitochondrial ribosomal protein L24 [Source:MGI Symbol;Acc:MGI:1914957]		Q9CQ06	-6.2	5.1E-05	2.4	9.5E-03	-2.6	4.7E-03	0.9	1.4E-01
ENSMUST00000019861	zinc finger protein 451 [Source:MGI Symbol;Acc:MGI:2137896]		Q8C0P7	-4.4	3.9E-03	-5.5	8.3E-03	1.0	1.8E-01	0.0	1.0E+00
ENSMUST00000019896	iodotyrosine deiodinase [Source:MGI Symbol;Acc:MGI:1917587]		Q9DCX8	6.5	7.3E-04	5.1	8.4E-05	-0.4	5.7E-01	0.1	8.1E-01
ENSMUST00000019908	mitochondrial translational release factor 1-like [Source:MGI Symbol;Acc:MGI:1918830]		Q8BJU9	1.7	2.0E-02	-2.6	1.4E-02	0.8	1.5E-01	-0.5	6.1E-01
ENSMUST00000019723	myeloid derived growth factor [Source:MGI Symbol;Acc:MGI:2156020]		Q9CPT4	0.7	1.6E-01	-0.2	7.6E-01	-0.6	2.2E-01	0.3	5.7E-01
ENSMUST00000019911	histone deacetylase 2 [Source:MGI Symbol;Acc:MGI:1097691]			-4.4	7.6E-04	-1.1	8.4E-02	1.7	1.4E-03	0.3	6.5E-01
ENSMUST00000019917	RWD domain containing 1 [Source:MGI Symbol;Acc:MGI:1913771]		Q9CQK7	-5.6	1.4E-04	2.7	1.0E-02	-2.7	7.5E-03	-0.4	6.1E-01
ENSMUST00000019920	clavesin 2 [Source:MGI Symbol;Acc:MGI:2443223]		Q8BG92	5.4	1.3E-03	5.4	2.0E-02	-0.8	7.2E-01	1.1	3.7E-01
ENSMUST00000019924	hairy/enhancer-of-split related with YRPW motif 2 [Source:MGI Symbol;Acc:MGI:1341884]	Q0VGJ1	Q9QUS4	7.3	4.2E-05	-4.6	2.2E-04	0.2	6.4E-01	-0.5	5.3E-01
ENSMUST00000019929	katanin p60 (ATPase-containing) subunit A1 [Source:MGI Symbol;Acc:MGI:1344353]	E9QKG2		-4.8	3.0E-05	-0.2	8.5E-01	1.7	5.9E-02	-3.0	5.5E-02
ENSMUST00000019932	RIKEN cDNA 1700021F05 gene [Source:MGI Symbol;Acc:MGI:1915101]		Q9CQF4	-5.2	6.3E-05	-3.6	1.3E-02	-0.8	2.8E-01	-0.7	6.0E-01
ENSMUST00000019938	nuclear receptor subfamily 2, group E, member 1 [Source:MGI Symbol;Acc:MGI:1100526]	Q78ZM1	Q64104	7.7	8.3E-06	-5.8	5.6E-04	0.1	9.0E-01	-0.3	7.8E-01
ENSMUST00000019859	GLE1 RNA export mediator (yeast) [Source:MGI Symbol;Acc:MGI:1921662]		Q8R322	-0.2	6.3E-01	0.5	4.2E-01	0.8	8.7E-02	0.1	8.6E-01
ENSMUST00000019939	sorting nexin 3 [Source:MGI Symbol;Acc:MGI:1860188]	Q78ZM0		-6.1	2.1E-05	-2.9	5.4E-02	-0.1	9.1E-01	-1.6	3.0E-01
ENSMUST00000019878	leukocyte receptor cluster (LRC) member 1 [Source:MGI Symbol;Acc:MGI:1917007]		Q9DB98	-0.2	7.8E-01	0.3	6.3E-01	0.3	6.0E-01	-0.2	7.3E-01
ENSMUST00000019882	polymerase (RNA) II (DNA directed) polypeptide I [Source:MGI Symbol;Acc:MGI:1917170]		P60898	0.4	8.7E-01	-2.8	3.3E-01	-3.2	1.1E-01	0.0	9.9E-01
ENSMUST00000019944	adenosine deaminase, tRNA-specific 2 [Source:MGI Symbol;Acc:MGI:1914007]		Q6P6J0	1.3	3.2E-02	6.3	1.5E-03	-0.7	6.4E-01	-0.5	5.2E-01
ENSMUST00000019907	F-box protein 5 [Source:MGI Symbol;Acc:MGI:1914391]		Q7TSG3	-0.8	1.2E-01	0.3	6.4E-01	0.6	2.1E-01	-0.5	4.1E-01
ENSMUST00000019945	peroxisomal biogenesis factor 3 [Source:MGI Symbol;Acc:MGI:1929646]	Q3UIG2	Q9QXY9	-4.8	2.3E-04	1.4	7.5E-02	-0.3	6.1E-01	-0.1	9.1E-01
ENSMUST00000019950	LTV1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2447810]		Q6NSQ7	-2.3	1.2E-03	-3.7	5.3E-03	-0.2	6.7E-01	-0.9	4.1E-01
ENSMUST00000019913	fyn-related kinase [Source:MGI Symbol;Acc:MGI:103265]		Q922K9	5.9	5.9E-02	3.7	2.6E-01	-2.1	5.2E-01	0.1	9.8E-01
ENSMUST00000019962	CD164 antigen [Source:MGI Symbol;Acc:MGI:1859568]		Q9R0L9	-5.6	4.0E-06	-4.5	6.8E-04	-0.4	3.5E-01	-1.6	1.6E-01
ENSMUST00000019965	sphingomyelin phosphodiesterase 2, neutral [Source:MGI Symbol;Acc:MGI:1278330]		O70572	-6.5	6.0E-05	6.1	1.1E-03	-0.4	7.6E-01	-1.1	1.8E-01
ENSMUST00000019967	tubule associated monooxygenase, calponin and LIM domain containing 1 [Source:MGI Symbol;Acc:MGI:238		Q8VDP3	-5.4	4.1E-04	7.1	9.8E-05	-0.6	6.1E-01	-0.4	5.1E-01
ENSMUST00000019927	tRNA methyltransferase 11 [Source:MGI Symbol;Acc:MGI:1920931]	E9QKG3		-0.6	3.5E-01	-0.2	7.3E-01	-0.5	3.5E-01	-0.9	2.1E-01
ENSMUST00000019974	RAB32, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1915094]	Q0PD23	Q9CZE3	-5.8	2.4E-05	-3.9	6.8E-04	0.4	3.6E-01	-0.5	5.6E-01
ENSMUST00000019931	low density lipoprotein receptor-related protein 11 [Source:MGI Symbol;Acc:MGI:2442989]		Q8CB67	1.5	3.1E-01	6.6	3.8E-03	1.5	3.9E-01	-3.6	9.3E-03
ENSMUST00000019975	WAS protein family, member 1 [Source:MGI Symbol;Acc:MGI:1890563]		Q8R5H6	6.5	1.3E-04	-6.1	1.4E-04	-0.9	4.0E-02	0.0	9.9E-01
ENSMUST00000019937	SEC63-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2155302]		Q8VHE0	-0.1	8.7E-01	-0.3	6.9E-01	0.5	3.1E-01	0.7	2.9E-01
ENSMUST00000019977	D-aspartate oxidase [Source:MGI Symbol;Acc:MGI:1925528]		Q922Z0	7.1	1.5E-04	7.0	2.9E-05	-0.8	4.0E-01	-0.2	6.6E-01
ENSMUST00000019982	general transcription factor IIIC, polypeptide 6, alpha [Source:MGI Symbol;Acc:MGI:1914621]		Q9D8P7	-2.4	1.9E-03	-5.6	7.0E-04	0.7	1.1E-01	0.3	8.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000019987	TRAF3 interacting protein 2 [Source:MGI Symbol;Acc:MGI:2143599]	Q8N7N6		3.8	1.8E-04	0.3	6.4E-01	-0.8	1.5E-01	0.2	6.9E-01
ENSMUST00000019992	laminin, alpha 4 [Source:MGI Symbol;Acc:MGI:109321]		P97927	7.5	6.5E-05	-1.0	1.8E-01	0.3	4.8E-01	-3.5	2.8E-03
ENSMUST00000019994	popeye domain containing 3 [Source:MGI Symbol;Acc:MGI:1930153]		Q9ES81	5.7	9.5E-03	-2.9	9.0E-04	-0.8	4.9E-02	-0.2	7.9E-01
ENSMUST00000019998	PERP, TP53 apoptosis effector [Source:MGI Symbol;Acc:MGI:1929938]		Q9JK95	4.6	1.6E-03	-4.7	1.2E-04	1.0	1.7E-02	0.1	9.2E-01
ENSMUST00000019999	ARFGEF family member 3 [Source:MGI Symbol;Acc:MGI:106387]		Q3UGY8	7.6	4.8E-07	-5.3	1.5E-03	0.6	2.2E-01	-0.7	6.2E-01
ENSMUST00000020000	heme binding protein 2 [Source:MGI Symbol;Acc:MGI:1860084]		Q9WU63	4.2	5.7E-04	-5.0	3.6E-03	0.7	2.7E-01	0.3	8.3E-01
ENSMUST00000020002	ABRA C-terminal like [Source:MGI Symbol;Acc:MGI:1920362]	E9QMV2		-5.4	1.1E-06	-4.2	1.3E-03	1.2	2.0E-02	-0.4	6.9E-01
ENSMUST00000020004	anti-silencing function 1A histone chaperone [Source:MGI Symbol;Acc:MGI:1913653]		Q9CQE6	-2.5	1.5E-03	4.4	8.2E-04	-2.8	2.0E-02	-0.7	2.9E-01
ENSMUST00000020016	gap junction protein, epsilon 1 [Source:MGI Symbol;Acc:MGI:1923993]		Q9CX92	5.6	5.2E-05	7.8	5.0E-04	1.1	4.9E-01	0.4	5.8E-01
ENSMUST00000019978	solute carrier family 22 (organic cation transporter), member 16 [Source:MGI Symbol;Acc:MGI:1918090]		Q497L8	3.5	1.2E-01	6.2	2.1E-02	-0.3	9.1E-01	-2.9	5.8E-02
ENSMUST00000020018	Vps20-associated 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913451]	F8WJC2		-3.9	4.7E-05	-3.6	4.0E-04	-1.3	8.9E-03	0.0	9.6E-01
ENSMUST00000019986	-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:13		Q61493	3.7	1.8E-01	5.1	1.1E-01	-0.4	8.9E-01	-1.8	3.7E-01
ENSMUST00000020022	sphingomyelin phosphodiesterase, acid-like 3A [Source:MGI Symbol;Acc:MGI:1931437]		P70158	-8.9	3.7E-07	2.7	4.3E-03	-0.8	2.2E-01	0.3	6.5E-01
ENSMUST00000019991	epsilon-tubulin 1 [Source:MGI Symbol;Acc:MGI:1919174]		Q9D6T1	1.1	4.0E-02	1.4	5.6E-02	0.5	3.2E-01	0.3	6.0E-01
ENSMUST00000020023	receptor accessory protein 3 [Source:MGI Symbol;Acc:MGI:88930]		Q99KK1	-1.7	1.4E-04	4.2	6.1E-04	-4.1	3.5E-03	-0.8	2.6E-01
ENSMUST00000020027	serine incorporator 1 [Source:MGI Symbol;Acc:MGI:1926228]	A9CLV6	Q9QZI8	-6.2	1.1E-06	6.2	9.9E-03	-0.7	7.5E-01	-1.1	3.4E-01
ENSMUST00000019997	tumor necrosis factor, alpha-induced protein 3 [Source:MGI Symbol;Acc:MGI:1196377]		Q60769	1.8	3.9E-01	2.5	3.5E-01	-0.2	9.4E-01	-0.9	7.0E-01
ENSMUST00000020039	MGAT4 family, member C [Source:MGI Symbol;Acc:MGI:1914819]		Q9D306	6.2	3.6E-03	4.6	5.8E-03	0.2	8.9E-01	0.1	8.8E-01
ENSMUST00000020049	coiled-coil domain containing 59 [Source:MGI Symbol;Acc:MGI:1289302]		Q8R2N0	-5.4	6.1E-04	7.7	4.2E-06	0.2	7.9E-01	0.0	9.0E-01
ENSMUST00000020062	G protein-coupled receptor, family C, group 6, member A [Source:MGI Symbol;Acc:MGI:2429498]		Q8K4Z6	6.7	4.9E-05	1.8	4.6E-02	-2.7	6.6E-03	-0.3	6.5E-01
ENSMUST00000020071	single-minded homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:98306]		Q61045	10.1	3.0E-05	-4.4	2.1E-05	-0.2	4.2E-01	-1.1	7.8E-02
ENSMUST00000020078	LIM and senescent cell antigen-like domains 1 [Source:MGI Symbol;Acc:MGI:1195263]			-5.6	7.6E-07	-1.6	4.6E-02	0.2	6.3E-01	-0.7	3.4E-01
ENSMUST00000020008	golgi associated PDZ and coiled-coil motif containing [Source:MGI Symbol;Acc:MGI:2149946]		Q8BH60	-1.1	6.5E-02	-0.1	9.2E-01	1.2	4.1E-02	0.2	8.1E-01
ENSMUST00000020012	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 [Source:MGI Symbol;Acc:MGI:1923813]		Q9CZN8	-0.9	1.1E-01	-0.5	4.6E-01	0.0	1.0E+00	-0.4	4.8E-01
ENSMUST00000020081	ZW10 interactor [Source:MGI Symbol;Acc:MGI:1289227]		Q9CQU5	-2.8	4.2E-04	4.8	4.4E-04	-0.8	3.4E-01	0.0	9.9E-01
ENSMUST00000020017	absent in melanoma 1 [Source:MGI Symbol;Acc:MGI:109544]	E9PVP1		0.4	3.9E-01	0.5	4.3E-01	-0.1	8.5E-01	-0.1	8.0E-01
ENSMUST00000020085	ubiquitin-conjugating enzyme E2D 1 [Source:MGI Symbol;Acc:MGI:2384911]	Q3UFQ4	P61080	-6.4	1.8E-04	-6.7	1.7E-04	0.0	9.9E-01	2.8	2.8E-02
ENSMUST00000020099	cyclin-dependent kinase 1 [Source:MGI Symbol;Acc:MGI:88351]		P11440	3.1	2.6E-02	-6.9	1.4E-05	0.4	2.4E-01	-1.6	8.6E-02
ENSMUST00000020101	Rho-related BTB domain containing 1 [Source:MGI Symbol;Acc:MGI:1916538]		Q9DAK3	6.8	1.3E-05	-0.7	4.0E-02	0.4	1.1E-01	-0.5	1.1E-01
ENSMUST00000020024	fatty acid binding protein 7, brain [Source:MGI Symbol;Acc:MGI:101916]		P51880	-0.1	8.9E-01	-3.0	1.3E-02	-4.7	3.7E-04	-1.9	1.1E-01
ENSMUST00000020102	ier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8 [Source:MGI Symbol;Acc:MG		Q8BFU8	5.9	3.0E-05	-6.4	7.5E-06	-0.5	1.1E-01	-0.3	6.4E-01
ENSMUST00000020107	ATPase, Ca++ transporting, plasma membrane 1 [Source:MGI Symbol;Acc:MGI:104653]		G5E829	-2.5	7.4E-05	2.0	3.0E-01	-1.4	4.4E-01	2.7	7.3E-02
ENSMUST00000020045	Ros1 proto-oncogene [Source:MGI Symbol;Acc:MGI:97999]		Q78DX7	5.9	5.4E-02	3.5	2.8E-01	-0.6	8.7E-01	1.9	3.7E-01
ENSMUST00000020109	ARP6 actin-related protein 6 [Source:MGI Symbol;Acc:MGI:1914269]			-3.7	5.5E-04	-3.7	4.5E-03	0.0	9.6E-01	-1.7	1.9E-01
ENSMUST00000020112	UHRF1 (ICBP90) binding protein 1-like [Source:MGI Symbol;Acc:MGI:2442888]		A2RSJ4	-3.1	2.4E-05	6.6	1.1E-04	-0.6	6.1E-01	-0.5	4.4E-01
ENSMUST00000020113	POC1 centriolar protein homolog B (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1918511]		Q8BHD1	-3.4	7.9E-03	8.2	3.3E-04	-0.8	6.2E-01	1.1	1.5E-01
ENSMUST00000020123	thymopoietin [Source:MGI Symbol;Acc:MGI:106920]		Q61033	-3.6	4.4E-04	-5.0	1.4E-05	0.4	1.7E-01	-0.2	7.7E-01
ENSMUST00000020145	serum/glucocorticoid regulated kinase 1 [Source:MGI Symbol;Acc:MGI:1340062]		Q9WVC6	-10.9	1.7E-06	-3.1	1.3E-03	-0.3	4.1E-01	0.0	9.5E-01
ENSMUST00000020149	IKBKB interacting protein [Source:MGI Symbol;Acc:MGI:1914704]	E9QMH7		3.3	2.0E-04	-3.2	2.4E-02	1.7	1.9E-02	-1.5	2.7E-01
ENSMUST00000020153	Hbs1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1891704]		Q69ZS7	-2.1	5.2E-03	3.0	4.5E-02	-1.3	3.1E-01	-1.1	3.2E-01
ENSMUST00000020157	apoptotic peptidase activating factor 1 [Source:MGI Symbol;Acc:MGI:1306796]		O88879	-4.0	2.9E-03	6.4	1.4E-04	-0.2	8.5E-01	0.3	6.5E-01
ENSMUST00000020158	myeloblastosis oncogene [Source:MGI Symbol;Acc:MGI:97249]		P06876	-4.6	2.6E-04	5.8	1.4E-04	0.5	5.8E-01	0.7	2.4E-01
ENSMUST00000020106	AT rich interactive domain 5B (MRF1-like) [Source:MGI Symbol;Acc:MGI:2175912]		Q8BM75	0.5	2.3E-01	0.5	4.5E-01	0.7	1.3E-01	0.8	1.8E-01
ENSMUST00000020159	mediator complex subunit 23 [Source:MGI Symbol;Acc:MGI:1917458]	F8WJB0		-4.2	7.9E-04	-2.6	4.0E-04	0.0	9.7E-01	0.1	8.0E-01
ENSMUST00000020165	phosphodiesterase 7B [Source:MGI Symbol;Acc:MGI:1352752]		Q9QXQ1	-2.4	6.1E-03	-2.1	2.6E-02	0.1	8.8E-01	-1.5	9.7E-02
ENSMUST00000020169	ectonucleotide pyrophosphatase/phosphodiesterase 3 [Source:MGI Symbol;Acc:MGI:2143702]		Q6DYE8	5.9	1.5E-03	-1.9	3.8E-03	1.1	3.9E-03	0.0	9.4E-01
ENSMUST00000020171	connective tissue growth factor [Source:MGI Symbol;Acc:MGI:95537]		P29268	5.4	1.4E-03	-1.8	3.4E-01	3.1	2.5E-02	1.5	4.0E-01
ENSMUST00000020118	dual specificity phosphatase 6 [Source:MGI Symbol;Acc:MGI:1914853]		Q9DBB1	-0.8	3.0E-01	-0.8	3.5E-01	-0.4	4.6E-01	-0.4	6.5E-01
ENSMUST00000020173	microtubule-associated protein 7 [Source:MGI Symbol;Acc:MGI:1328328]	E9QMU3		7.1	4.1E-05	-1.9	4.5E-02	1.3	2.7E-02	-0.4	6.5E-01
ENSMUST00000020174	syntaxin 7 [Source:MGI Symbol;Acc:MGI:1858210]	Q8BH40		-5.3	1.5E-06	-9.1	6.1E-05	1.0	1.4E-02	-0.7	6.3E-01
ENSMUST00000020182	peroxisomal biogenesis factor 7 [Source:MGI Symbol;Acc:MGI:1321392]		P97865	-3.7	3.1E-03	2.2	5.6E-03	-0.8	1.7E-01	0.2	6.8E-01
ENSMUST00000020150	IKBKB interacting protein [Source:MGI Symbol;Acc:MGI:1914704]		Q9DBZ1	-0.6	2.3E-01	-1.9	1.4E-02	-0.8	9.0E-02	0.4	4.9E-01
ENSMUST00000020185	interleukin 20 receptor, alpha [Source:MGI Symbol;Acc:MGI:3605069]		Q6PHB0	7.3	6.6E-05	-1.2	1.4E-01	0.4	3.8E-01	-0.5	4.7E-01
ENSMUST00000020188	interferon gamma receptor 1 [Source:MGI Symbol;Acc:MGI:107655]		P15261	-7.9	7.0E-08	-0.8	4.5E-01	0.4	5.6E-01	-2.7	4.3E-02
ENSMUST00000020190	vanin 3 [Source:MGI Symbol;Acc:MGI:1347055]		Q9QZ25	2.0	2.7E-02	-1.4	2.1E-01	2.5	1.7E-03	-0.7	5.2E-01
ENSMUST00000020203	small nuclear ribonucleoprotein polypeptide F [Source:MGI Symbol;Acc:MGI:1917128]	Q497K3	P62307	-4.2	2.5E-04	2.4	1.0E-01	6.0	2.4E-04	-0.6	5.9E-01
ENSMUST00000020161	arginase, liver [Source:MGI Symbol;Acc:MGI:88070]		Q61176	1.2	3.9E-01	-7.5	2.2E-04	-10.1	7.1E-06	-1.5	3.1E-01
ENSMUST00000020163	ieural precursor cell expressed, developmentally down-regulated gene 1 [Source:MGI Symbol;Acc:MGI:97293		P33215	-0.1	8.1E-01	-0.5	4.5E-01	-0.9	1.1E-01	-0.5	4.9E-01
ENSMUST00000020204	netrin 4 [Source:MGI Symbol;Acc:MGI:1888978]		Q9JI33	5.4	3.5E-05	-2.9	1.1E-02	0.4	4.8E-01	0.9	3.5E-01
ENSMUST00000020208	FYVE, RhoGEF and PH domain containing 6 [Source:MGI Symbol;Acc:MGI:1261419]		Q69ZL1	1.2	3.4E-02	5.1	1.5E-03	-2.2	1.3E-01	-1.4	1.3E-01
ENSMUST00000020209	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 [Source:MGI Symbol;Acc:MGI:1913664]		Q7TMF3	2.5	1.1E-02	3.5	6.3E-03	-2.9	3.3E-02	-1.0	2.5E-01
ENSMUST00000020212	centrosomal protein 83 [Source:MGI Symbol;Acc:MGI:1924298]		Q9D5R3	-3.7	4.7E-04	7.1	5.3E-05	-0.5	6.2E-01	-0.6	3.4E-01
ENSMUST00000020215	suppressor of cytokine signaling 2 [Source:MGI Symbol;Acc:MGI:1201787]	Q548Q7	O35717	5.5	2.1E-02	-4.7	2.1E-05	0.1	7.9E-01	-0.5	3.9E-01
ENSMUST00000020217	nudix (nucleoside diphosphate linked moiety X)-type motif 4 [Source:MGI Symbol;Acc:MGI:1918457]	Q4FJR0	Q8R2U6	-6.0	1.2E-05	-2.9	4.0E-02	0.6	3.8E-01	-0.2	8.8E-01
ENSMUST00000020220	NUAK family, SNF1-like kinase, 1 [Source:MGI Symbol;Acc:MGI:1925226]		Q641K5	5.9	5.4E-06	6.3	3.7E-04	-0.6	6.3E-01	0.4	5.6E-01
ENSMUST00000020223	t-complex 11 (mouse) like 2 [Source:MGI Symbol;Acc:MGI:2444679]		Q8K1H7	-6.6	9.8E-07	-6.5	2.5E-06	0.9	4.3E-03	-0.5	4.7E-01
ENSMUST00000020227	cryptochrome 1 (photolyase-like) [Source:MGI Symbol;Acc:MGI:1270841]		P97784	-3.2	5.8E-05	3.0	8.4E-03	0.1	9.5E-01	-0.9	2.4E-01
ENSMUST00000020197	eyes absent 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109339]		P97480	5.6	6.5E-02	6.2	5.7E-02	-0.7	8.3E-01	-1.2	5.0E-01
ENSMUST00000020231	BTB (POZ) domain containing 11 [Source:MGI Symbol;Acc:MGI:1921257]	H7BWX5		5.8	8.7E-04	-6.1	2.7E-04	-1.1	2.3E-02	0.9	4.4E-01
ENSMUST00000020234	tissue inhibitor of metalloproteinase 3 [Source:MGI Symbol;Acc:MGI:98754]	Q54AE5	P39876	8.0	1.4E-06	7.3	1.9E-05	1.1	2.5E-01	-0.8	1.4E-01
ENSMUST00000020238	heat shock protein 90, beta (Grp94), member 1 [Source:MGI Symbol;Acc:MGI:98817]	Q3UAD6	P08113	-6.1	7.3E-06	2.3	1.0E-02	1.1	7.8E-02	0.1	8.4E-01
ENSMUST00000020241	phenylalanine hydroxylase [Source:MGI Symbol;Acc:MGI:97473]		P16331	6.1	2.6E-04	2.2	4.1E-02	-0.5	5.2E-01	-0.2	7.9E-01
ENSMUST00000020243	achaete-scute complex homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:96919]		Q02067	7.8	5.0E-05	-3.3	3.5E-03	0.0	9.7E-01	-0.4	7.0E-01
ENSMUST00000020248	coiled-coil domain containing 53 [Source:MGI Symbol;Acc:MGI:1914532]		Q9CR27	-5.1	3.2E-03	5.7	4.0E-02	0.7	7.8E-01	0.5	7.6E-01
ENSMUST00000020249	DNA-damage regulated autophagy modulator 1 [Source:MGI Symbol;Acc:MGI:1918962]		Q9DC58	-6.5	6.3E-04	-4.8	4.3E-04	1.0	4.0E-02	-0.3	7.8E-01
ENSMUST00000020255	solute carrier family 5 (iodide transporter), member 8 [Source:MGI Symbol;Acc:MGI:2384916]		Q8BYF6	7.7	4.1E-05	5.6	1.9E-05	-0.4	5.6E-01	-0.1	8.0E-01
ENSMUST00000020257	sirtuin 1 [Source:MGI Symbol;Acc:MGI:2135607]	Q53Z05	Q923E4	-3.4	6.5E-03	-4.6	6.6E-05	1.1	4.7E-03	-0.8	2.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000020258	hect domain and RLD 4 [Source:MGI Symbol;Acc:MGI:1914595]		Q6PAV2	-5.0	5.2E-05	6.9	1.3E-04	-0.6	6.0E-01	-1.2	9.1E-02
ENSMUST00000020262	phenazine biosynthesis-like protein domain containing 2 [Source:MGI Symbol;Acc:MGI:1914557]		Q9CXN7	6.4	2.0E-04	-2.2	3.1E-03	1.0	1.4E-02	0.1	9.2E-01
ENSMUST00000020266	phenazine biosynthesis-like protein domain containing 2 [Source:MGI Symbol;Acc:MGI:1914557]	K3W4L7		7.7	8.6E-05	7.5	2.0E-03	1.6	3.8E-01	-0.2	8.1E-01
ENSMUST00000020268	cell division cycle and apoptosis regulator 1 [Source:MGI Symbol;Acc:MGI:1914750]		Q8CH18	-4.4	1.6E-04	3.7	9.0E-05	-4.9	7.0E-05	-0.6	1.5E-01
ENSMUST00000020270	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50 [Source:MGI Symbol;Acc:MGI:2182303]		Q99MJ9	-4.7	3.7E-05	-8.3	1.5E-05	-1.0	1.9E-02	1.2	2.5E-01
ENSMUST00000020271	serglycin [Source:MGI Symbol;Acc:MGI:97756]		P13609	-11.0	1.6E-03	5.6	5.6E-04	-1.4	2.7E-01	-0.9	1.9E-01
ENSMUST00000020277	hexokinase domain containing 1 [Source:MGI Symbol;Acc:MGI:2384910]		Q91W97	7.9	2.5E-05	7.2	2.4E-04	-0.2	8.7E-01	0.4	5.6E-01
ENSMUST00000020278	tachykinin receptor 2 [Source:MGI Symbol;Acc:MGI:98477]	Q3KP20	P30549	8.0	2.5E-05	-4.7	8.5E-03	-0.8	2.6E-01	-1.2	4.6E-01
ENSMUST00000020283	H2A histone family, member Y2 [Source:MGI Symbol;Acc:MGI:3037658]		Q8CCK0	3.0	8.3E-04	-4.2	1.5E-02	0.7	3.4E-01	-1.6	3.3E-01
ENSMUST00000020251	ı-acetylglucosamine-1-phosphate transferase, alpha and beta subunits [Source:MGI Symbol;Acc:MGI:3643902		Q69ZN6	-3.0	3.8E-02	-2.6	1.7E-01	1.2	2.7E-01	0.9	6.2E-01
ENSMUST00000020285	SAR1 gene homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:98230]	Q99JZ4		-4.1	2.5E-05	6.7	2.5E-04	-0.5	6.7E-01	0.5	4.4E-01
ENSMUST00000020287	neuropeptide FF receptor 1 [Source:MGI Symbol;Acc:MGI:2685082]	E9Q468		7.5	9.9E-04	-1.3	3.3E-01	1.5	6.8E-02	-0.6	6.6E-01
ENSMUST00000020288	eukaryotic translation initiation factor 4E binding protein 2 [Source:MGI Symbol;Acc:MGI:109198]	Q3UFP6	P70445	-4.5	1.4E-04	-4.6	6.4E-04	0.4	3.6E-01	0.0	1.0E+00
ENSMUST00000020289	phosphatase domain containing, paladin 1 [Source:MGI Symbol;Acc:MGI:1351623]			5.0	2.0E-04	5.7	5.5E-04	-1.2	3.2E-01	-0.5	4.8E-01
ENSMUST00000020298	nolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1 [Source:MGI Symb		P61458	4.2	6.3E-04	6.9	2.4E-04	-1.0	4.5E-01	-0.2	7.2E-01
ENSMUST00000020301	RIKEN cDNA 4632428N05 gene [Source:MGI Symbol;Acc:MGI:1921298]		Q9D659	-6.7	1.0E-05	-4.1	1.1E-03	-0.2	6.4E-01	-0.5	6.0E-01
ENSMUST00000020307	anaphase promoting complex subunit 16 [Source:MGI Symbol;Acc:MGI:1289325]	S4R2B6		-6.1	1.7E-04	-4.3	3.1E-04	-0.4	3.4E-01	-0.7	3.7E-01
ENSMUST00000020312	mitochondrial calcium uniporter [Source:MGI Symbol;Acc:MGI:3026965]		Q3UMR5	-2.9	6.5E-04	-10.9	7.8E-03	-0.6	5.1E-01	-0.6	8.7E-01
ENSMUST00000020273	suppressor of var1, 3-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2441711]		Q80YD1	-2.7	1.6E-01	-2.5	1.6E-01	-0.2	8.7E-01	-0.3	8.6E-01
ENSMUST00000020315	cullin associated and neddylation disassociated 1 [Source:MGI Symbol;Acc:MGI:1261820]		Q6ZQ38	-1.5	9.2E-03	7.9	5.3E-05	-0.5	6.5E-01	-0.5	3.5E-01
ENSMUST00000020316	TANK-binding kinase 1 [Source:MGI Symbol;Acc:MGI:1929658]	A1L361	Q9WUN2	-4.1	6.2E-04	6.4	2.3E-04	-1.0	4.3E-01	0.6	3.3E-01
ENSMUST00000020317	partner of NOB1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913499]		Q9CPS7	-2.8	4.9E-03	3.9	5.4E-04	0.8	2.4E-01	0.0	9.6E-01
ENSMUST00000020284	trypsin domain containing 1 [Source:MGI Symbol;Acc:MGI:1919017]		Q9DBA6	-0.1	9.3E-01	1.0	2.5E-01	0.9	1.9E-01	-0.2	8.3E-01
ENSMUST00000020321	pleckstrin [Source:MGI Symbol;Acc:MGI:1860485]	Q8CAG6		-10.4	3.8E-04	-4.4	1.5E-04	0.1	7.0E-01	0.3	6.4E-01
ENSMUST00000020286	pyrophosphatase (inorganic) 1 [Source:MGI Symbol;Acc:MGI:97831]	Q4FK49	Q9D819	-1.8	5.0E-02	-3.0	2.1E-02	-1.2	1.1E-01	0.0	9.8E-01
ENSMUST00000020323	arginine vasopressin receptor 1A [Source:MGI Symbol;Acc:MGI:1859216]	Q3U1H9	Q62463	8.1	8.1E-05	6.2	5.1E-03	-0.7	7.0E-01	0.5	6.0E-01
ENSMUST00000020329	epidermal growth factor receptor [Source:MGI Symbol;Acc:MGI:95294]		Q01279	7.1	4.4E-07	-2.8	1.1E-02	1.1	3.9E-02	-0.6	5.3E-01
ENSMUST00000020334	ubiquitin specific peptidase 15 [Source:MGI Symbol;Acc:MGI:101857]		Q8R5H1	-4.5	5.6E-05	4.3	1.0E-03	-0.9	3.1E-01	-0.3	6.7E-01
ENSMUST00000020339	TBC1 domain family, member 15 [Source:MGI Symbol;Acc:MGI:1913937]		Q9CXF4	-6.7	2.7E-07	3.8	1.4E-03	-1.0	2.7E-01	-0.6	3.5E-01
ENSMUST00000020341	RIKEN cDNA 2310011J03 gene [Source:MGI Symbol;Acc:MGI:1913624]		Q9D7E4	-3.4	9.4E-04	-5.6	3.1E-04	1.2	1.8E-02	0.2	8.8E-01
ENSMUST00000020343	RAB21, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:894308]	Q0PD35	P35282	-5.3	1.7E-05	-5.4	4.1E-03	0.7	2.0E-01	0.0	1.0E+00
ENSMUST00000020308	DNA-damage-inducible transcript 4 [Source:MGI Symbol;Acc:MGI:1921997]	B7ZNP9	Q9D3F7	-0.7	2.3E-01	-0.9	1.9E-01	-0.5	2.5E-01	-0.3	6.5E-01
ENSMUST00000020309	DnaJ (Hsp40) homolog, subfamily B, member 12 [Source:MGI Symbol;Acc:MGI:1931881]		Q9QYI4	-2.3	1.8E-01	-2.6	3.5E-01	1.6	3.4E-01	2.0	4.5E-01
ENSMUST00000020311	mitochondrial calcium uptake 1 [Source:MGI Symbol;Acc:MGI:2384909]		Q8VCX5	0.5	8.3E-01	-3.9	1.1E-01	-5.7	8.7E-03	-1.3	6.1E-01
ENSMUST00000020350	leucine rich repeat containing G protein coupled receptor 5 [Source:MGI Symbol;Acc:MGI:1341817]		Q9Z1P4	6.1	1.0E-04	-1.2	1.3E-01	1.3	1.6E-02	-0.4	6.2E-01
ENSMUST00000020358	RAB1A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:97842]	Q5SW88		-8.8	6.2E-03	-0.3	5.8E-01	0.8	6.1E-02	-0.3	5.7E-01
ENSMUST00000020361	NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Source:MGI Symbol;Acc:MGI:1922656]		Q9DC70	-7.2	3.9E-05	-3.0	1.2E-02	0.1	8.1E-01	-1.0	3.5E-01
ENSMUST00000020362	m large conductance calcium-activated channel, subfamily M, beta member 1 [Source:MGI Symbol;Acc:MGI:1	Q5SQK1		9.3	7.9E-07	-3.4	4.6E-03	-1.4	2.5E-02	-0.9	3.8E-01
ENSMUST00000020366	gamma-aminobutyric acid (GABA) A receptor, pi [Source:MGI Symbol;Acc:MGI:2387597]		Q8QZW7	6.9	5.1E-05	1.4	6.7E-01	10.6	1.2E-03	-1.1	6.8E-01
ENSMUST00000020322	SLIT-ROBO Rho GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2152936]		Q91Z69	0.4	8.7E-01	-0.3	9.4E-01	2.2	3.9E-01	2.8	4.0E-01
ENSMUST00000020372	ubiquinol-cytochrome c reductase, complex III subunit XI [Source:MGI Symbol;Acc:MGI:1913844]		Q9CPX8	-5.8	8.1E-04	7.5	2.6E-04	-0.7	6.3E-01	-0.1	8.8E-01
ENSMUST00000020378	bestrophin 3 [Source:MGI Symbol;Acc:MGI:3580298]		Q6H1V1	8.3	1.7E-05	5.4	4.2E-06	-2.5	2.2E-03	-0.8	3.9E-02
ENSMUST00000020382	YEATS domain containing 4 [Source:MGI Symbol;Acc:MGI:1927224]		Q9CR11	-3.8	1.3E-04	-4.5	3.5E-04	-0.4	3.7E-01	-0.5	6.0E-01
ENSMUST00000020383	ATPase, class I, type 8B, member 3 [Source:MGI Symbol;Acc:MGI:1914581]		Q6UQ17	9.2	5.2E-06	-6.2	2.8E-06	-0.4	1.4E-01	-0.9	1.9E-01
ENSMUST00000020397	small nuclear ribonucleoprotein D3 [Source:MGI Symbol;Acc:MGI:1914582]		P62320	-2.9	1.5E-04	-2.6	1.9E-02	1.0	7.4E-02	0.2	8.0E-01
ENSMUST00000020399	carboxypeptidase M [Source:MGI Symbol;Acc:MGI:1917824]		Q80V42	5.7	5.0E-04	-3.6	1.7E-03	1.3	1.4E-02	-0.5	5.5E-01
ENSMUST00000020346	THAP domain containing, apoptosis associated protein 2 [Source:MGI Symbol;Acc:MGI:1914066]		Q9D305	0.9	1.5E-01	2.0	1.7E-02	0.6	3.5E-01	-0.6	3.2E-01
ENSMUST00000020349	adenomatosis polyposis coli 2 [Source:MGI Symbol;Acc:MGI:1346052]	G5E832		3.6	9.4E-02	8.5	1.3E-02	1.9	5.1E-01	-3.0	6.2E-02
ENSMUST00000020400	leucine rich repeat transmembrane neuronal 1 [Source:MGI Symbol;Acc:MGI:2389173]		Q8K377	6.8	4.3E-05	4.6	1.3E-03	-0.7	4.7E-01	0.8	3.0E-01
ENSMUST00000020403	cysteine and glycine-rich protein 2 [Source:MGI Symbol;Acc:MGI:1202907]		P97314	-1.7	1.4E-02	-8.7	2.7E-02	-0.1	9.3E-01	-0.2	9.5E-01
ENSMUST00000020408	transformed mouse 3T3 cell double minute 2 [Source:MGI Symbol;Acc:MGI:96952]		P23804	-7.4	4.1E-04	-5.8	1.1E-03	0.7	1.3E-01	-0.7	6.2E-01
ENSMUST00000020420	adaptor-related protein complex 3, delta 1 subunit [Source:MGI Symbol;Acc:MGI:107734]		O54774	-3.0	3.9E-04	8.1	2.1E-05	-0.8	4.5E-01	0.4	3.7E-01
ENSMUST00000020365	melanoma associated antigen (mutated) 1 [Source:MGI Symbol;Acc:MGI:1915364]		Q6DID5	-3.7	5.8E-02	-2.9	9.9E-02	0.2	8.8E-01	-0.6	7.5E-01
ENSMUST00000020437	transformed mouse 3T3 cell double minute 1 [Source:MGI Symbol;Acc:MGI:96951]		Q9D067	-3.6	1.6E-02	7.3	6.8E-05	-0.5	6.5E-01	-0.9	1.5E-01
ENSMUST00000020439	Wnt inhibitory factor 1 [Source:MGI Symbol;Acc:MGI:1344332]	Q3TYU1	Q9WUA1	7.1	2.1E-02	-8.0	3.9E-03	-0.8	2.1E-01	1.3	5.3E-01
ENSMUST00000020375	RAB3A interacting protein [Source:MGI Symbol;Acc:MGI:105933]		Q68EF0	0.5	2.9E-01	1.1	1.1E-01	0.4	4.1E-01	-0.2	7.9E-01
ENSMUST00000020377	transcription factor 3 [Source:MGI Symbol;Acc:MGI:98510]			-3.6	5.8E-02	-3.3	1.7E-01	0.3	8.0E-01	0.0	1.0E+00
ENSMUST00000020440	translocase of inner mitochondrial membrane 13 [Source:MGI Symbol;Acc:MGI:1353432]		P62075	-2.3	5.2E-03	7.2	1.1E-04	-0.6	6.2E-01	0.5	3.9E-01
ENSMUST00000020379	transcription factor 3 [Source:MGI Symbol;Acc:MGI:98510]			-1.3	2.3E-01	-4.1	3.0E-02	-0.6	4.3E-01	2.1	2.2E-01
ENSMUST00000020381	fibroblast growth factor receptor substrate 2 [Source:MGI Symbol;Acc:MGI:1100860]		Q8C180	-0.7	1.3E-01	0.1	9.1E-01	0.7	8.3E-02	0.0	9.9E-01
ENSMUST00000020444	LLP homolog, long-term synaptic facilitation (Aplysia) [Source:MGI Symbol;Acc:MGI:1913475]		Q9D945	-1.4	2.7E-02	-3.3	2.0E-03	0.8	1.0E-01	0.3	7.5E-01
ENSMUST00000020446	transmembrane BAX inhibitor motif containing 4 [Source:MGI Symbol;Acc:MGI:1915462]		Q9DA39	-8.3	8.3E-06	8.6	1.9E-05	-0.6	5.9E-01	0.0	9.6E-01
ENSMUST00000020448	interleukin-1 receptor-associated kinase 3 [Source:MGI Symbol;Acc:MGI:1921164]	Q0VB14	Q8K4B2	-3.8	1.5E-02	-3.0	4.4E-04	-0.8	2.9E-02	-0.7	2.6E-01
ENSMUST00000020450	solute carrier family 5, member 4a [Source:MGI Symbol;Acc:MGI:1927848]	G5E836		6.9	1.1E-04	5.3	1.1E-03	-1.2	3.3E-01	-0.7	3.6E-01
ENSMUST00000020457	fizzy/cell division cycle 20 related 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1926790]	F8WJ80		-5.7	2.0E-03	7.5	1.0E-04	0.5	7.0E-01	-0.2	7.1E-01
ENSMUST00000020478	host cell factor C2 [Source:MGI Symbol;Acc:MGI:1915183]	G5E837		3.2	4.5E-03	-2.3	7.6E-03	-1.0	4.6E-02	-0.4	5.4E-01
ENSMUST00000020484	thioredoxin reductase 1 [Source:MGI Symbol;Acc:MGI:1354175]		Q9JMH6	-2.5	7.9E-04	-7.7	2.1E-03	-0.4	5.2E-01	-0.1	9.6E-01
ENSMUST00000020413	zona pellucida binding protein [Source:MGI Symbol;Acc:MGI:1855701]	Q5NC84		2.5	4.2E-02	4.0	1.4E-02	0.3	8.4E-01	-1.2	2.3E-01
ENSMUST00000020490	WD repeat domain containing 82 [Source:MGI Symbol;Acc:MGI:1924555]	B2RXQ8	Q8BFQ4	-3.4	7.0E-05	-1.7	2.9E-02	0.8	9.2E-02	-0.5	4.7E-01
ENSMUST00000020493	protein O-fucosyltransferase 2 [Source:MGI Symbol;Acc:MGI:1916863]	B2RV73	Q8VHI3	-1.9	4.7E-03	-5.1	3.5E-02	0.2	8.1E-01	1.7	4.3E-01
ENSMUST00000020497	aldehyde dehydrogenase 1 family, member L2 [Source:MGI Symbol;Acc:MGI:2444680]		Q8K009	7.6	3.9E-05	6.0	6.2E-02	-0.9	7.8E-01	0.3	8.8E-01
ENSMUST00000020500	otein, phosphotyrosine interaction, PH domain and leucine zipper containing 2 [Source:MGI Symbol;Acc:MGI	Q3TVI6	Q8K3G9	-4.0	4.9E-03	-1.4	8.8E-02	0.3	5.8E-01	-0.6	4.4E-01
ENSMUST00000020441	vacuolar protein sorting 13 D (yeast) [Source:MGI Symbol;Acc:MGI:2448530]	B1ART1		-1.7	4.6E-01	0.4	9.0E-01	1.3	5.6E-01	-0.8	7.6E-01
ENSMUST00000020504	histidine triad nucleotide binding protein 1 [Source:MGI Symbol;Acc:MGI:1321133]		P70349	-7.1	2.3E-04	-3.2	1.8E-03	-1.3	1.2E-02	0.5	5.0E-01
ENSMUST00000020507	fibroblast growth factor 18 [Source:MGI Symbol;Acc:MGI:1277980]		O89101	6.9	1.2E-02	-5.1	1.9E-04	0.7	6.9E-02	-2.4	4.6E-02
ENSMUST00000020513	poly(A) polymerase gamma [Source:MGI Symbol;Acc:MGI:2442119]		Q6PCL9	-3.0	5.2E-05	-1.0	4.0E-01	0.4	6.1E-01	-2.3	1.3E-01
ENSMUST00000020449	helicase (DNA) B [Source:MGI Symbol;Acc:MGI:2152895]		Q6NVF4	-0.8	1.1E-01	-0.7	2.9E-01	0.2	5.7E-01	0.1	8.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000020522	phosphofructokinase, liver, B-type [Source:MGI Symbol;Acc:MGI:97547]		P12382	-2.1	3.8E-03	6.4	3.8E-04	-0.6	6.3E-01	0.0	9.7E-01
ENSMUST00000020452	protein arginine N-methyltransferase 2 [Source:MGI Symbol;Acc:MGI:1316652]	Q3UKX1		-1.9	2.5E-01	-2.0	1.7E-01	-2.1	7.0E-02	-2.0	2.5E-01
ENSMUST00000020454	high mobility group 20B [Source:MGI Symbol;Acc:MGI:1341190]	Q3U1L0	Q9Z104	0.9	7.4E-01	-0.9	7.9E-01	-1.4	5.4E-01	0.4	9.1E-01
ENSMUST00000020528	N-methylpurine-DNA glycosylase [Source:MGI Symbol;Acc:MGI:97073]		Q04841	-4.5	8.9E-04	-5.1	1.8E-02	1.1	1.4E-01	0.5	8.1E-01
ENSMUST00000020461	nuclear factor I/C [Source:MGI Symbol;Acc:MGI:109591]		P70255	4.2	4.2E-02	1.5	5.9E-01	1.0	6.0E-01	3.7	1.7E-01
ENSMUST00000020463	nicalin homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1926081]		Q8VCM8	-0.5	6.6E-01	0.6	6.1E-01	0.1	9.3E-01	-1.0	4.1E-01
ENSMUST00000020531	hemoglobin X, alpha-like embryonic chain in Hba complex [Source:MGI Symbol;Acc:MGI:96019]	Q78PA4	P06467	5.8	2.3E-03	2.5	5.7E-02	0.7	4.9E-01	1.4	1.7E-01
ENSMUST00000020535	hemoglobin, theta 1A [Source:MGI Symbol;Acc:MGI:2685722]	Q8BYM1		5.3	9.3E-03	-1.7	4.0E-02	1.1	3.0E-02	0.2	7.9E-01
ENSMUST00000020488	DNA segment, Chr 10, Wayne State University 102, expressed [Source:MGI Symbol;Acc:MGI:106381]		Q9CX66	-0.2	7.3E-01	0.6	3.3E-01	0.5	2.8E-01	-0.2	6.4E-01
ENSMUST00000020537	neuron specific gene family member 2 [Source:MGI Symbol;Acc:MGI:1202070]	Q5SS02	P47759	2.7	2.7E-03	-2.6	2.6E-03	0.6	9.4E-02	-0.1	8.4E-01
ENSMUST00000020538	exportin 1, CRM1 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2144013]		Q6P5F9	-5.2	6.4E-04	-1.2	1.1E-01	0.6	2.1E-01	-0.2	7.8E-01
ENSMUST00000020546	stanniocalcin 2 [Source:MGI Symbol;Acc:MGI:1316731]	Q5SS12	O88452	5.9	6.2E-05	6.3	2.7E-04	-1.1	3.5E-01	0.2	7.7E-01
ENSMUST00000020547	vomeronasal 2, receptor 81 [Source:MGI Symbol;Acc:MGI:2684056]	Q80Z09		6.0	2.5E-04	-1.9	1.2E-01	0.5	4.8E-01	-1.6	2.3E-01
ENSMUST00000020501	small ubiquitin-like modifier 3 [Source:MGI Symbol;Acc:MGI:1336201]		Q9Z172	1.6	1.4E-01	0.3	8.2E-01	-0.1	9.2E-01	1.2	3.2E-01
ENSMUST00000020551	ankyrin repeat and SOCS box-containing 3 [Source:MGI Symbol;Acc:MGI:1929749]		Q9WV72	-3.4	4.0E-03	-7.6	7.3E-05	-1.4	1.6E-02	-0.9	5.1E-01
ENSMUST00000020552	tubulin polyglutamylase complex subunit 1 [Source:MGI Symbol;Acc:MGI:106618]	B2RRP1	Q99MS8	-3.6	6.2E-05	6.6	2.0E-02	-0.9	7.4E-01	-0.6	6.5E-01
ENSMUST00000020554	mucosal vascular addressin cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:103579]	G5E838		7.4	2.6E-04	-2.3	1.2E-03	-0.2	4.6E-01	-0.9	1.1E-01
ENSMUST00000020562	chaperonin containing Tcp1, subunit 4 (delta) [Source:MGI Symbol;Acc:MGI:104689]	G5E839		-7.9	8.6E-05	-1.4	8.1E-02	0.6	1.8E-01	-0.1	8.8E-01
ENSMUST00000020523	peroxisomal biogenesis factor 13 [Source:MGI Symbol;Acc:MGI:1919379]		Q9D0K1	0.6	3.0E-01	0.7	2.9E-01	0.2	7.4E-01	0.0	9.9E-01
ENSMUST00000020566	testicular haploid expressed gene [Source:MGI Symbol;Acc:MGI:1338756]		Q9JMB1	7.7	4.3E-05	-1.7	9.5E-02	0.1	8.0E-01	-2.7	3.6E-02
ENSMUST00000020529	AHA1, activator of heat shock protein ATPase 2 [Source:MGI Symbol;Acc:MGI:1916133]		Q8N9S3	-5.0	1.4E-01	-5.8	1.7E-01	-1.3	4.6E-01	-0.5	9.1E-01
ENSMUST00000020573	protease, serine 57 [Source:MGI Symbol;Acc:MGI:1920356]		Q14B24	-5.0	6.7E-03	5.8	4.0E-03	-0.6	7.0E-01	-0.6	5.1E-01
ENSMUST00000020576	cyclin G1 [Source:MGI Symbol;Acc:MGI:102890]	Q5NC86	P51945	-4.3	1.5E-05	2.5	8.1E-02	-3.2	6.8E-02	-0.4	7.3E-01
ENSMUST00000020577	fibroblast growth factor 22 [Source:MGI Symbol;Acc:MGI:1914362]		Q9ESS2	6.4	2.3E-04	2.6	6.1E-03	-0.9	1.9E-01	-0.8	2.0E-01
ENSMUST00000020578	NudC domain containing 2 [Source:MGI Symbol;Acc:MGI:1277103]		Q9CQ48	-3.3	9.8E-03	-6.3	3.5E-03	0.0	9.6E-01	1.1	5.1E-01
ENSMUST00000020543	cytoplasmic polyadenylation element binding protein 4 [Source:MGI Symbol;Acc:MGI:1914829]		Q7TN98	0.4	6.5E-01	0.0	9.7E-01	0.5	5.5E-01	0.8	4.3E-01
ENSMUST00000020579	hyaluronan mediated motility receptor (RHAMM) [Source:MGI Symbol;Acc:MGI:104667]		Q00547	3.4	2.3E-05	6.6	9.4E-04	2.1	1.3E-01	1.4	7.7E-02
ENSMUST00000020581	hyperpolarization-activated, cyclic nucleotide-gated K+ 2 [Source:MGI Symbol;Acc:MGI:1298210]		O88703	6.2	1.4E-02	5.7	6.7E-04	-0.5	7.0E-01	-0.1	8.3E-01
ENSMUST00000020550	cell division cycle 34 [Source:MGI Symbol;Acc:MGI:102657]		Q8CFI2	-2.1	3.1E-01	-2.7	2.6E-01	-0.9	5.5E-01	-0.3	9.1E-01
ENSMUST00000020608	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform [Source:MGI Symbol;Acc:MGI:1321159]		P63330	-2.3	9.2E-04	-3.4	7.0E-02	1.7	6.2E-02	1.7	3.2E-01
ENSMUST00000020617	FMS-like tyrosine kinase 4 [Source:MGI Symbol;Acc:MGI:95561]	Q5SU94	P35917	8.8	7.5E-06	-2.4	3.5E-03	0.3	3.9E-01	-1.0	1.6E-01
ENSMUST00000020624	CCR4-NOT transcription complex, subunit 6 [Source:MGI Symbol;Acc:MGI:2144529]		Q8K3P5	-4.5	2.5E-03	6.9	7.4E-04	-0.7	6.4E-01	-0.2	7.7E-01
ENSMUST00000020629	glutamine fructose-6-phosphate transaminase 2 [Source:MGI Symbol;Acc:MGI:1338883]		Q9Z2Z9	6.9	2.0E-04	-8.0	9.1E-04	-0.2	7.3E-01	-0.1	9.5E-01
ENSMUST00000020630	heat shock protein 4 [Source:MGI Symbol;Acc:MGI:1342292]	Q3U2G2		-3.6	2.1E-04	6.8	1.3E-04	-1.5	2.3E-01	-0.6	3.7E-01
ENSMUST00000020568	WD repeat containing planar cell polarity effector [Source:MGI Symbol;Acc:MGI:2144467]	B1ATJ7	Q8C456	2.9	3.5E-02	0.6	6.4E-01	-2.9	3.0E-02	-0.6	5.9E-01
ENSMUST00000020634	mitogen-activated protein kinase 9 [Source:MGI Symbol;Acc:MGI:1346862]	Q5NCK8	Q9WTU6	-5.3	3.0E-03	-3.1	5.7E-02	1.2	2.0E-01	-0.7	6.6E-01
ENSMUST00000020637	calnexin [Source:MGI Symbol;Acc:MGI:88261]	Q5SUC3	P35564	-5.8	6.5E-05	-4.0	1.4E-04	-0.1	8.3E-01	-0.3	6.1E-01
ENSMUST00000020640	uanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Source:MGI Symbol;Acc:MGI:10184		P68040	-8.2	1.8E-04	5.6	1.3E-03	-0.2	8.9E-01	0.6	4.0E-01
ENSMUST00000020643	RUN and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:2429762]		Q8BIJ7	-2.9	8.4E-04	-1.2	2.5E-01	0.4	5.8E-01	-1.7	1.5E-01
ENSMUST00000020647	RIKEN cDNA 3010026O09 gene [Source:MGI Symbol;Acc:MGI:1915317]		Q9D1F5	2.0	2.6E-02	3.4	5.7E-05	-0.5	2.4E-01	-0.5	1.6E-01
ENSMUST00000020580	polymerase (RNA) mitochondrial (DNA directed) [Source:MGI Symbol;Acc:MGI:1915843]	Q3U3J3	Q8BKF1	-0.1	9.6E-01	3.6	3.0E-01	3.5	1.7E-01	-0.2	9.4E-01
ENSMUST00000020650	interleukin 13 [Source:MGI Symbol;Acc:MGI:96541]		P20109	4.9	1.8E-04	5.0	4.1E-02	-1.0	6.6E-01	0.1	9.1E-01
ENSMUST00000020586	solute carrier family 22 (organic cation transporter), member 4 [Source:MGI Symbol;Acc:MGI:1353479]		Q9Z306	0.8	2.7E-01	1.2	2.0E-01	0.6	4.0E-01	0.2	8.0E-01
ENSMUST00000020653	SAR1 gene homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913647]	Q0VGU0	Q9CQC9	-4.4	2.1E-05	-1.7	2.8E-02	1.1	3.3E-02	0.4	5.3E-01
ENSMUST00000020657	ubiquitin-conjugating enzyme E2B [Source:MGI Symbol;Acc:MGI:102944]	A2RSE4	P63147	-6.6	1.8E-06	6.3	1.2E-05	-3.0	1.2E-02	-0.5	3.2E-01
ENSMUST00000020662	kringle containing transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1933988]		Q99N43	-1.5	2.2E-02	-1.0	4.8E-01	3.7	4.7E-03	0.2	8.8E-01
ENSMUST00000020665	mediator complex subunit 7 [Source:MGI Symbol;Acc:MGI:1913463]		Q9CZB6	-7.1	7.9E-04	3.5	4.2E-03	-4.1	5.8E-03	-0.6	4.4E-01
ENSMUST00000020679	NIPA-like domain containing 4 [Source:MGI Symbol;Acc:MGI:2444671]		Q8BZF2	6.6	1.3E-05	-3.2	2.5E-03	0.2	6.6E-01	-0.3	7.1E-01
ENSMUST00000020681	SLU7 splicing factor homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2385598]		Q8BHJ9	-8.3	2.9E-05	-3.7	1.3E-02	-0.4	5.5E-01	-2.0	2.1E-01
ENSMUST00000020685	pituitary tumor-transforming gene 1 [Source:MGI Symbol;Acc:MGI:1353578]		Q9CQJ7	-5.0	2.3E-03	-8.1	5.3E-04	-0.2	7.1E-01	2.0	2.1E-01
ENSMUST00000020692	B cell translocation gene 2, anti-proliferative [Source:MGI Symbol;Acc:MGI:108384]	Q3TF68	Q04211	-5.2	2.5E-04	-8.2	1.1E-03	-0.4	5.2E-01	-0.4	8.2E-01
ENSMUST00000020695	tensin 3 [Source:MGI Symbol;Acc:MGI:2443012]		Q5SSZ5	1.9	3.5E-03	-1.0	1.7E-01	0.6	1.9E-01	-1.3	1.0E-01
ENSMUST00000020699	GATS protein-like 3 [Source:MGI Symbol;Acc:MGI:1919212]		Q9CWQ8	2.2	2.5E-02	0.8	3.7E-01	-1.7	4.3E-02	-0.5	5.3E-01
ENSMUST00000020649	RAD50 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:109292]	Q5SV02		-0.3	5.8E-01	0.2	7.4E-01	0.2	6.1E-01	-0.3	6.8E-01
ENSMUST00000020702	insulin-like growth factor binding protein 3 [Source:MGI Symbol;Acc:MGI:96438]		P47878	5.9	2.0E-03	4.9	5.7E-04	-0.5	6.2E-01	-0.5	4.6E-01
ENSMUST00000020704	insulin-like growth factor binding protein 1 [Source:MGI Symbol;Acc:MGI:96436]		P47876	6.7	1.8E-04	-3.9	2.4E-04	-0.5	1.5E-01	-1.1	1.5E-01
ENSMUST00000020655	jade family PHD finger 2 [Source:MGI Symbol;Acc:MGI:1924151]		Q6ZQF7	-0.9	7.4E-01	-2.0	5.7E-01	-0.5	8.2E-01	0.6	8.6E-01
ENSMUST00000020705	pescadillo homolog 1, containing BRCT domain (zebrafish) [Source:MGI Symbol;Acc:MGI:1890613]		Q9EQ61	-3.9	5.6E-03	-5.6	4.3E-05	0.5	1.8E-01	-0.6	4.8E-01
ENSMUST00000020706	adenylate cyclase 1 [Source:MGI Symbol;Acc:MGI:99677]		O88444	8.9	3.1E-06	-0.2	7.4E-01	0.9	1.1E-01	-0.4	5.2E-01
ENSMUST00000020664	IL2 inducible T cell kinase [Source:MGI Symbol;Acc:MGI:96621]	Q5STT8		-2.2	9.0E-02	-2.3	2.9E-01	1.9	1.4E-01	2.0	3.3E-01
ENSMUST00000020707	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1 [Source:MGI Symbol;Acc:MGI:95613]	Q544F7	P62812	6.7	8.5E-05	-4.7	1.4E-02	0.9	2.2E-01	-1.5	4.2E-01
ENSMUST00000020668	hepatitis A virus cellular receptor 2 [Source:MGI Symbol;Acc:MGI:2159682]		Q8VIM0	-2.1	4.4E-01	0.5	8.5E-01	0.0	9.9E-01	-2.6	3.1E-01
ENSMUST00000020673	voltage-dependent anion channel 1 [Source:MGI Symbol;Acc:MGI:106919]		Q60932	-2.0	5.2E-01	-3.0	4.6E-01	-1.3	5.6E-01	-0.3	9.4E-01
ENSMUST00000020677	uridine phosphorylase 1 [Source:MGI Symbol;Acc:MGI:1097668]	Q5SUC8	P52624	0.4	6.4E-01	2.1	1.1E-01	0.6	5.8E-01	-1.1	2.6E-01
ENSMUST00000020710	transcobalamin 2 [Source:MGI Symbol;Acc:MGI:98534]		O88968	-9.3	1.6E-03	7.0	2.0E-05	-0.2	8.0E-01	-0.6	2.4E-01
ENSMUST00000020712	RIKEN cDNA 4921536K21 gene [Source:MGI Symbol;Acc:MGI:1914680]		Q9CR34	5.7	1.7E-05	-9.3	1.2E-04	-1.1	1.7E-02	-0.2	9.1E-01
ENSMUST00000020683	Hus1 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1277962]		Q8BQY8	-2.7	4.6E-02	-3.8	8.2E-02	0.3	7.3E-01	1.4	4.8E-01
ENSMUST00000020717	ADP-ribosylation factor 5 [Source:MGI Symbol;Acc:MGI:99434]		P84084	-4.9	4.4E-04	-4.7	1.2E-02	-0.4	5.7E-01	-0.7	6.8E-01
ENSMUST00000020687	pituitary tumor-transforming gene 1 [Source:MGI Symbol;Acc:MGI:1353578]		Q9CQJ7	-3.2	2.0E-01	-3.3	3.5E-01	-0.1	9.7E-01	0.1	9.8E-01
ENSMUST00000020718	smoothelin [Source:MGI Symbol;Acc:MGI:1354727]	D3YVS1		8.1	5.2E-05	-4.0	6.3E-03	0.9	1.4E-01	-0.3	8.0E-01
ENSMUST00000020719	RIKEN cDNA 2310033P09 gene [Source:MGI Symbol;Acc:MGI:1915112]		Q99LX5	-1.7	2.1E-02	1.6	2.9E-02	-0.3	5.7E-01	0.0	9.6E-01
ENSMUST00000020732	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF [Source:MGI Symbol;Acc:MGI:2681862]	Z4YJE4		9.7	3.5E-06	2.7	2.3E-02	-0.1	8.9E-01	-0.6	4.8E-01
ENSMUST00000020734	eukaryotic translation initiation factor 4E nuclear import factor 1 [Source:MGI Symbol;Acc:MGI:1921453]		Q9EST3	-7.2	2.4E-04	2.3	5.9E-02	-3.8	1.9E-02	-0.2	8.5E-01
ENSMUST00000020741	developmentally regulated GTP binding protein 1 [Source:MGI Symbol;Acc:MGI:1343297]	Q5NBZ3	P32233	-6.1	1.2E-04	5.9	7.5E-04	-0.6	6.2E-01	0.1	8.8E-01
ENSMUST00000020754	cilia and flagella associated protein 36 [Source:MGI Symbol;Acc:MGI:1913994]		Q8C6E0	-4.1	3.4E-03	-2.4	7.7E-02	-0.5	5.2E-01	-2.0	1.6E-01
ENSMUST00000020755	SMEK homolog 2, suppressor of mek1 (Dictyostelium) [Source:MGI Symbol;Acc:MGI:2144474]		Q922R5	-5.2	3.0E-05	9.1	9.7E-06	0.1	9.5E-01	-0.1	8.2E-01
ENSMUST00000020756	polyribonucleotide nucleotidyltransferase 1 [Source:MGI Symbol;Acc:MGI:1918951]		Q8K1R3	-5.0	1.2E-03	5.7	5.1E-04	-0.5	6.5E-01	0.5	4.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000020768	phosphoglycerate mutase 2 [Source:MGI Symbol;Acc:MGI:1933118]	Q5NCI4	O70250	-2.4	3.9E-03	-7.8	1.8E-02	0.7	4.0E-01	-0.8	8.0E-01
ENSMUST00000020776	coiled-coil domain containing 117 [Source:MGI Symbol;Acc:MGI:2144383]		Q6PB51	-2.5	5.9E-04	5.1	3.1E-04	0.2	8.4E-01	0.8	1.9E-01
ENSMUST00000020779	myeloperoxidase [Source:MGI Symbol;Acc:MGI:97137]		P11247	-3.5	1.9E-03	-4.3	6.3E-03	1.2	7.0E-02	0.7	6.0E-01
ENSMUST00000020794	spindle and kinetochore associated complex subunit 2 [Source:MGI Symbol;Acc:MGI:1913390]		Q9CR46	2.8	1.4E-04	5.9	3.7E-04	-2.5	6.5E-02	-0.3	6.2E-01
ENSMUST00000020801	smg-8 homolog, nonsense mediated mRNA decay factor (C. elegans) [Source:MGI Symbol;Acc:MGI:1921383]		Q8VE18	-1.3	1.7E-02	0.4	5.9E-01	1.0	1.1E-01	-1.1	1.6E-01
ENSMUST00000020721	smoothelin [Source:MGI Symbol;Acc:MGI:1354727]		Q921U8	1.6	4.5E-01	0.9	8.0E-01	0.6	8.1E-01	1.3	6.6E-01
ENSMUST00000020804	glycerophosphodiester phosphodiesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:1913819]		Q9CRY7	4.0	2.0E-03	10.5	3.9E-06	-0.5	6.7E-01	-1.3	1.1E-02
ENSMUST00000020820	mitochondrial ribosomal protein L22 [Source:MGI Symbol;Acc:MGI:1333794]		Q8BU88	-3.8	1.1E-03	-2.7	1.4E-02	0.2	7.2E-01	-4.3	8.7E-03
ENSMUST00000020822	CCR4-NOT transcription complex, subunit 8 [Source:MGI Symbol;Acc:MGI:1916375]		Q9D8X5	-7.6	4.5E-05	-5.4	2.4E-03	0.2	7.2E-01	-0.5	7.4E-01
ENSMUST00000020749	mitochondrial translational initiation factor 2 [Source:MGI Symbol;Acc:MGI:1924034]		Q91YJ5	2.6	4.8E-02	-1.3	4.6E-01	-0.9	4.5E-01	3.0	7.8E-02
ENSMUST00000020826	SAP30-like [Source:MGI Symbol;Acc:MGI:1354709]		Q5SQF8	-4.7	3.0E-05	-3.9	7.9E-03	-1.2	1.1E-01	-1.4	2.8E-01
ENSMUST00000020827	ring finger protein, transmembrane 1 [Source:MGI Symbol;Acc:MGI:1924142]		Q9DCN7	-2.0	7.8E-03	-4.3	6.2E-04	0.5	2.8E-01	-0.5	6.1E-01
ENSMUST00000020831	family with sequence similarity 114, member A2 [Source:MGI Symbol;Acc:MGI:1917629]		Q8VE88	-2.8	5.1E-04	-4.0	1.6E-02	0.2	7.7E-01	-0.8	5.7E-01
ENSMUST00000020759	ermal growth factor-containing fibulin-like extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:1339		Q8BPB5	3.8	7.9E-02	5.4	3.3E-02	-0.3	9.0E-01	-1.9	1.8E-01
ENSMUST00000020767	polymerase (DNA directed), mu [Source:MGI Symbol;Acc:MGI:1860191]		Q9JIW4	1.7	1.4E-01	-0.5	7.4E-01	-0.4	7.4E-01	1.9	2.1E-01
ENSMUST00000020835	protein phosphatase 1D magnesium-dependent, delta isoform [Source:MGI Symbol;Acc:MGI:1858214]		Q9QZ67	-2.5	7.1E-04	-0.5	5.1E-01	0.9	1.3E-01	-1.0	2.3E-01
ENSMUST00000020769	drebrin-like [Source:MGI Symbol;Acc:MGI:700006]		Q62418	-2.5	6.2E-02	-2.1	2.0E-01	0.1	8.9E-01	-0.2	8.8E-01
ENSMUST00000020837	myosin XIX [Source:MGI Symbol;Acc:MGI:1913446]		Q5SV80	7.0	2.7E-04	-7.0	1.7E-04	-0.2	6.7E-01	-0.3	8.2E-01
ENSMUST00000020775	dynein light chain LC8-type 2 [Source:MGI Symbol;Acc:MGI:1915347]		Q9D0M5	-1.9	4.4E-01	-3.7	2.3E-01	-1.4	4.1E-01	0.4	8.9E-01
ENSMUST00000020843	acetyl-Coenzyme A carboxylase alpha [Source:MGI Symbol;Acc:MGI:108451]		Q5SWU9	-5.8	6.3E-05	-1.0	1.1E-01	0.9	3.3E-02	-0.5	4.1E-01
ENSMUST00000020846	sterol regulatory element binding transcription factor 1 [Source:MGI Symbol;Acc:MGI:107606]		Q9WTN3	-4.1	1.0E-02	0.2	8.7E-01	1.5	5.5E-02	-2.2	4.8E-02
ENSMUST00000020849	target of myb1-like 1 (chicken) [Source:MGI Symbol;Acc:MGI:1919193]		Q923U0	2.5	2.5E-02	2.5	1.0E-03	-0.4	3.9E-01	-0.1	8.6E-01
ENSMUST00000020851	cytochrome c oxidase assembly protein 11 [Source:MGI Symbol;Acc:MGI:1917052]		Q6P8I6	-2.2	3.3E-02	-0.4	4.9E-01	1.0	3.4E-02	0.1	8.3E-01
ENSMUST00000020856	basic leucine zipper and W2 domains 2 [Source:MGI Symbol;Acc:MGI:1914162]		Q91VK1	-2.2	2.4E-03	1.7	7.9E-02	-2.8	1.3E-02	-0.4	5.9E-01
ENSMUST00000020864	phosphatidylcholine transfer protein [Source:MGI Symbol;Acc:MGI:107375]	Q5SV41		1.7	5.6E-03	-3.7	2.0E-03	-1.0	7.7E-02	-1.1	2.7E-01
ENSMUST00000020877	twist basic helix-loop-helix transcription factor 1 neighbor [Source:MGI Symbol;Acc:MGI:106292]	B2RT77	Q78WZ7	-3.5	2.4E-04	-4.5	1.2E-03	0.5	2.9E-01	-2.6	5.3E-02
ENSMUST00000020885	synaptophysin-like protein [Source:MGI Symbol;Acc:MGI:108081]	Q3TVX7	O09117	-8.1	1.5E-05	-5.8	9.7E-03	0.0	1.0E+00	1.4	4.5E-01
ENSMUST00000020886	nicotinamide phosphoribosyltransferase [Source:MGI Symbol;Acc:MGI:1929865]		Q99KQ4	-4.2	1.2E-04	-3.2	1.2E-03	0.1	7.7E-01	-1.4	9.3E-02
ENSMUST00000020896	tetraspanin 13 [Source:MGI Symbol;Acc:MGI:1913359]		Q9D8C2	-5.0	6.4E-05	-0.9	2.5E-01	0.8	1.6E-01	-0.4	6.4E-01
ENSMUST00000020830	microfibrillar-associated protein 3 [Source:MGI Symbol;Acc:MGI:1924068]			0.2	7.9E-01	3.7	1.4E-02	1.6	1.8E-01	-1.9	6.4E-02
ENSMUST00000020899	matrilin 3 [Source:MGI Symbol;Acc:MGI:1328350]		O35701	5.6	2.0E-04	-2.3	6.8E-03	0.1	8.9E-01	-0.5	5.1E-01
ENSMUST00000020904	Rho-associated coiled-coil containing protein kinase 2 [Source:MGI Symbol;Acc:MGI:107926]	F8VPK5		-2.1	5.1E-03	-1.5	4.5E-02	0.9	5.4E-02	-0.2	7.5E-01
ENSMUST00000020909	lysosomal-associated protein transmembrane 4A [Source:MGI Symbol;Acc:MGI:108017]	E9QLR3		-6.1	1.0E-06	5.2	1.9E-03	-1.8	1.8E-01	0.0	9.8E-01
ENSMUST00000020911	syndecan 1 [Source:MGI Symbol;Acc:MGI:1349162]	Q3V1F2	P18828	4.4	1.0E-02	-5.5	8.5E-04	0.1	8.0E-01	-0.2	8.5E-01
ENSMUST00000020922	tribbles homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2145021]		Q8K4K3	1.3	3.4E-02	-1.7	2.5E-01	0.6	4.8E-01	-1.8	2.9E-01
ENSMUST00000020926	family with sequence similarity 84, member A [Source:MGI Symbol;Acc:MGI:2145011]			8.4	3.2E-05	3.3	3.7E-02	1.2	3.6E-01	0.4	6.5E-01
ENSMUST00000020929	archaelysin family metallopeptidase 2 [Source:MGI Symbol;Acc:MGI:104837]	B1AT60		-5.3	1.0E-03	-0.6	5.1E-01	0.4	5.2E-01	-1.1	2.8E-01
ENSMUST00000020930	guanine nucleotide binding protein, alpha 13 [Source:MGI Symbol;Acc:MGI:95768]		P27601	-1.3	3.4E-02	-2.6	1.8E-03	-1.4	4.1E-03	-0.9	1.6E-01
ENSMUST00000020938	family with sequence similarity 20, member A [Source:MGI Symbol;Acc:MGI:2388266]		Q8CID3	5.5	9.0E-03	2.3	5.9E-03	0.6	2.4E-01	0.1	9.0E-01
ENSMUST00000020939	neuronal cell adhesion molecule [Source:MGI Symbol;Acc:MGI:104750]		Q810U4	8.7	1.6E-02	-2.1	1.7E-02	0.7	1.2E-01	-0.7	4.1E-01
ENSMUST00000020947	retinol dehydrogenase 14 (all-trans and 9-cis) [Source:MGI Symbol;Acc:MGI:1920402]		Q9ERI6	-2.2	2.2E-03	-6.7	2.3E-04	1.0	2.6E-02	-0.4	7.6E-01
ENSMUST00000020948	ATP-binding cassette, sub-family A (ABC1), member 8b [Source:MGI Symbol;Acc:MGI:1351668]	A2AM56	Q8K440	5.5	4.2E-06	-5.5	1.8E-04	-0.4	3.6E-01	0.9	3.6E-01
ENSMUST00000020949	mitogen-activated protein kinase kinase 6 [Source:MGI Symbol;Acc:MGI:1346870]	Q543Z5	P70236	-3.0	3.0E-03	-4.2	1.2E-03	0.3	4.8E-01	-0.5	5.9E-01
ENSMUST00000020957	acireductone dioxygenase 1 [Source:MGI Symbol;Acc:MGI:2144929]		Q99JT9	3.8	7.4E-05	6.0	6.5E-04	0.1	9.1E-01	-0.3	6.4E-01
ENSMUST00000020958	kelch-like 29 [Source:MGI Symbol;Acc:MGI:2683857]		Q80T74	9.0	3.6E-06	-1.7	4.9E-02	0.4	4.3E-01	0.0	9.9E-01
ENSMUST00000020908	E2F transcription factor 6 [Source:MGI Symbol;Acc:MGI:1354159]		O54917	1.3	6.2E-02	0.7	3.7E-01	0.2	8.1E-01	0.7	3.5E-01
ENSMUST00000020959	ribonuclease H1 [Source:MGI Symbol;Acc:MGI:1335073]	E9QLN8		-1.8	2.7E-03	-4.7	4.0E-05	0.6	4.9E-02	-0.8	2.7E-01
ENSMUST00000020964	FK506 binding protein 1b [Source:MGI Symbol;Acc:MGI:1336205]	A9E3L2	Q9Z212	-1.6	7.5E-03	-1.5	2.8E-01	-4.7	4.3E-03	1.3	3.4E-01
ENSMUST00000020915	pumilio RNA-binding family member 2 [Source:MGI Symbol;Acc:MGI:1931751]	Q3TQ29		-1.0	4.2E-01	-0.7	6.9E-01	-0.1	9.6E-01	-0.4	8.1E-01
ENSMUST00000020920	regulator of G-protein signaling 9 [Source:MGI Symbol;Acc:MGI:1338824]		O54828	4.0	6.9E-02	2.6	2.3E-01	-0.5	8.0E-01	0.8	5.9E-01
ENSMUST00000020965	allantoicase [Source:MGI Symbol;Acc:MGI:2136971]		Q9JHX6	6.2	2.0E-02	0.9	1.8E-01	-1.0	9.5E-02	-0.5	4.0E-01
ENSMUST00000020967	profilin family, member 4 [Source:MGI Symbol;Acc:MGI:1920121]	Q6JEK6	Q9D6I3	6.0	9.7E-04	7.1	1.1E-04	-1.4	2.7E-01	-0.2	7.9E-01
ENSMUST00000020927	HCLS1 binding protein 3 [Source:MGI Symbol;Acc:MGI:1913224]		Q3TC93	-1.2	7.4E-02	0.5	5.5E-01	1.4	3.2E-02	-0.2	7.5E-01
ENSMUST00000020971	ring finger protein 144A [Source:MGI Symbol;Acc:MGI:1344401]		Q925F3	-4.6	1.6E-02	-3.7	3.5E-02	1.4	8.0E-02	-0.2	8.9E-01
ENSMUST00000020974	inhibitor of DNA binding 2 [Source:MGI Symbol;Acc:MGI:96397]	Q545T4	P41136	-6.8	6.9E-06	-1.1	1.7E-01	0.9	1.0E-01	0.7	3.7E-01
ENSMUST00000020931	structural maintenance of chromosomes 6 [Source:MGI Symbol;Acc:MGI:1914491]		Q924W5	-0.8	1.0E-01	-1.5	5.3E-02	0.2	6.4E-01	0.8	2.1E-01
ENSMUST00000020980	ribonucleotide reductase M2 [Source:MGI Symbol;Acc:MGI:98181]		P11157	-2.0	3.1E-03	-3.8	1.0E-01	-6.1	3.2E-03	3.2	1.5E-01
ENSMUST00000020981	centromere protein O [Source:MGI Symbol;Acc:MGI:1923800]	B8JK52		-6.3	9.1E-06	2.9	4.9E-01	-1.0	7.9E-01	4.9	1.4E-01
ENSMUST00000020982	Kruppel-like factor 11 [Source:MGI Symbol;Acc:MGI:2653368]		Q8K1S5	2.0	2.6E-02	-1.1	1.1E-01	-0.2	6.6E-01	-1.3	5.6E-02
ENSMUST00000020986	DnaJ (Hsp40) homolog, subfamily C, member 27 [Source:MGI Symbol;Acc:MGI:2443036]		Q8CFP6	3.8	6.7E-05	5.7	7.2E-06	-0.4	4.9E-01	-0.6	1.3E-01
ENSMUST00000020990	pro-opiomelanocortin-alpha [Source:MGI Symbol;Acc:MGI:97742]		P01193	5.6	5.8E-04	1.2	8.9E-02	0.0	9.5E-01	-4.2	3.6E-04
ENSMUST00000020954	trafficking protein particle complex 12 [Source:MGI Symbol;Acc:MGI:2445089]		Q8K2L8	-1.2	2.7E-01	0.5	7.1E-01	0.0	9.7E-01	-1.7	2.0E-01
ENSMUST00000020991	DNA methyltransferase 3A [Source:MGI Symbol;Acc:MGI:1261827]		O88508	6.1	1.0E-02	4.6	9.0E-05	0.3	6.6E-01	-0.6	2.4E-01
ENSMUST00000020997	Sh3 domain YSC-like 1 [Source:MGI Symbol;Acc:MGI:1346118]		O08641	-2.3	2.7E-02	7.9	1.1E-05	-0.9	4.1E-01	0.2	6.7E-01
ENSMUST00000020999	kinesin family member 3C [Source:MGI Symbol;Acc:MGI:107979]		O35066	3.3	2.6E-04	-1.6	1.7E-02	-0.4	2.5E-01	-0.7	2.3E-01
ENSMUST00000020962	UBX domain protein 2A [Source:MGI Symbol;Acc:MGI:2442310]		Q99KJ0	0.9	1.9E-01	0.8	4.2E-01	0.5	5.2E-01	0.6	4.7E-01
ENSMUST00000021001	RAB10, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105066]	Q4FJL0	P61027	-4.1	1.1E-05	-0.4	4.8E-01	0.9	6.3E-02	-0.2	6.7E-01
ENSMUST00000021005	thyroid peroxidase [Source:MGI Symbol;Acc:MGI:98813]		P35419	7.7	3.1E-05	5.5	5.3E-02	-0.8	7.7E-01	-0.1	9.6E-01
ENSMUST00000021009	myelin transcription factor 1-like [Source:MGI Symbol;Acc:MGI:1100511]	E9QLD2		6.9	1.2E-04	5.5	3.7E-03	0.0	9.8E-01	0.4	6.2E-01
ENSMUST00000020969	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:99830]		Q3U5Q7	-0.1	9.0E-01	0.6	5.2E-01	0.4	6.0E-01	-0.3	7.1E-01
ENSMUST00000020970	radical S-adenosyl methionine domain containing 2 [Source:MGI Symbol;Acc:MGI:1929628]		Q8CBB9	1.3	2.1E-01	-1.0	4.0E-01	-1.5	1.2E-01	0.8	4.9E-01
ENSMUST00000021018	5 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:191	Q8BQ46		-2.6	2.9E-03	-4.7	3.9E-02	0.4	6.8E-01	0.5	8.1E-01
ENSMUST00000021039	ligase III, DNA, ATP-dependent [Source:MGI Symbol;Acc:MGI:109152]	K4DI59		5.3	2.4E-02	-6.5	6.1E-05	-0.2	5.6E-01	-0.6	5.6E-01
ENSMUST00000020977	dihydrouridine synthase 4-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919166]			0.7	2.6E-01	0.5	5.3E-01	-0.2	7.7E-01	0.1	9.2E-01
ENSMUST00000021044	RIKEN cDNA 5530401A14 gene [Source:MGI Symbol;Acc:MGI:1918638]	Q9D3H9		5.1	1.4E-02	0.1	9.0E-01	1.5	7.6E-03	-0.6	3.6E-01
ENSMUST00000021045	acid-sensing (proton-gated) ion channel 2 [Source:MGI Symbol;Acc:MGI:1100867]	B2RRQ1	Q925H0	8.4	6.2E-05	-5.3	2.7E-04	0.6	1.2E-01	-0.4	6.6E-01
ENSMUST00000021046	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 [Source:MGI Symbol;Acc:MGI:1919297]		Q810A7	-2.6	9.4E-04	1.2	2.7E-01	0.5	5.5E-01	1.3	1.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000021048	FtsJ homolog 3 (E. coli) [Source:MGI Symbol;Acc:MGI:1860295]		Q9DBE9	-1.8	1.2E-02	4.1	9.9E-05	-0.3	5.8E-01	-0.6	2.0E-01
ENSMUST00000021049	protease (prosome, macropain) 26S subunit, ATPase 5 [Source:MGI Symbol;Acc:MGI:105047]		P62196	-7.2	3.9E-04	6.3	1.4E-03	0.3	8.5E-01	-0.4	5.8E-01
ENSMUST00000021050	ArfGAP with dual PH domains 2 [Source:MGI Symbol;Acc:MGI:2663075]	Q5SSK2	Q8R2V5	3.0	7.3E-04	3.8	5.7E-02	-2.8	1.8E-01	-0.5	7.0E-01
ENSMUST00000021052	d, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 [Source:MGI Symbol;Acc		Q99JR8	-5.7	8.4E-04	-2.5	6.5E-02	0.7	3.5E-01	0.9	4.9E-01
ENSMUST00000021056	sodium channel, voltage-gated, type IV, alpha [Source:MGI Symbol;Acc:MGI:98250]	G3X8T7		6.0	1.1E-05	3.3	1.2E-03	-0.2	8.1E-01	-0.2	7.7E-01
ENSMUST00000021062	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Source:MGI Symbol;Acc:MGI:105037]	Q8BTS0		-7.9	1.8E-04	-3.1	4.7E-04	0.8	3.0E-02	-0.2	7.6E-01
ENSMUST00000021004	syntrophin, gamma 2 [Source:MGI Symbol;Acc:MGI:1919541]		Q925E0	4.4	1.4E-01	2.9	3.8E-01	-0.2	9.5E-01	1.2	5.6E-01
ENSMUST00000021063	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 [Source:MGI Symbol;Acc:MGI:1914247]		Q9D8W5	-2.5	6.5E-04	7.0	1.4E-04	-0.6	6.1E-01	0.1	8.2E-01
ENSMUST00000021065	calcium channel, voltage-dependent, gamma subunit 1 [Source:MGI Symbol;Acc:MGI:1206582]	Q4KL26	O70578	7.1	4.4E-05	6.8	1.6E-04	-1.4	2.6E-01	-1.3	5.5E-02
ENSMUST00000021016	HNF1 homeobox B [Source:MGI Symbol;Acc:MGI:98505]		P27889	3.2	2.4E-01	3.4	2.4E-01	-0.4	9.0E-01	-0.6	7.7E-01
ENSMUST00000021066	calcium channel, voltage-dependent, gamma subunit 4 [Source:MGI Symbol;Acc:MGI:1859167]	A2AAU2	Q9JJV4	7.5	2.4E-05	-2.0	4.0E-02	0.5	3.5E-01	-0.2	8.6E-01
ENSMUST00000021020	matrix metallopeptidase 28 (epilysin) [Source:MGI Symbol;Acc:MGI:2153062]	Q8CGV5		2.5	5.3E-02	6.2	2.9E-04	-0.5	6.6E-01	-4.2	7.1E-04
ENSMUST00000021028	integrin beta 3 [Source:MGI Symbol;Acc:MGI:96612]		O54890	0.6	2.9E-01	0.9	1.8E-01	0.0	9.5E-01	-0.3	5.9E-01
ENSMUST00000021033	RAD51 homolog D [Source:MGI Symbol;Acc:MGI:1261809]	Q9EP85		-1.7	2.5E-01	6.6	8.2E-03	4.8	2.6E-02	-3.5	3.1E-02
ENSMUST00000021036	ring finger and FYVE like domain containing protein [Source:MGI Symbol;Acc:MGI:1914588]	Q148A8	Q6ZQM0	0.8	5.5E-01	-1.4	4.5E-01	-1.6	2.0E-01	0.5	7.5E-01
ENSMUST00000021071	G protein-coupled receptor, family C, group 5, member C [Source:MGI Symbol;Acc:MGI:1917605]	J3JS84		3.9	2.1E-02	5.4	6.8E-02	0.3	9.1E-01	0.2	8.9E-01
ENSMUST00000021040	chaperonin containing Tcp1, subunit 6b (zeta) [Source:MGI Symbol;Acc:MGI:1329013]	Q497N0	Q61390	1.5	3.8E-01	-1.7	5.0E-01	-1.5	3.5E-01	1.7	4.9E-01
ENSMUST00000021076	RAB37, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1929945]	Q544E8		-2.6	5.6E-04	4.8	3.3E-02	-0.5	8.1E-01	-0.2	8.8E-01
ENSMUST00000021077	ute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1 [Source:MGI Symbol;Acc:MGI:13494	Q3TG37	P70441	-5.2	5.9E-05	7.7	2.4E-04	-0.6	6.6E-01	0.1	8.3E-01
ENSMUST00000021082	5',3'-nucleotidase, cytosolic [Source:MGI Symbol;Acc:MGI:1354954]		Q9JM14	-4.4	1.6E-03	-1.6	3.0E-02	0.4	3.7E-01	-0.5	4.3E-01
ENSMUST00000021083	hematological and neurological expressed sequence 1 [Source:MGI Symbol;Acc:MGI:1096361]		P97825	-3.4	4.6E-04	-2.9	2.4E-03	-1.4	8.8E-03	-0.3	7.3E-01
ENSMUST00000021087	MIF4G domain containing [Source:MGI Symbol;Acc:MGI:1916924]		Q3UBZ5	-5.2	9.3E-04	-6.1	1.8E-03	-0.3	6.9E-01	-1.3	4.3E-01
ENSMUST00000021090	growth factor receptor bound protein 2 [Source:MGI Symbol;Acc:MGI:95805]	Q3U5I5	Q60631	-9.6	2.6E-06	1.7	2.6E-02	-1.8	1.2E-02	-0.5	3.8E-01
ENSMUST00000021091	platelet-activating factor acetylhydrolase, isoform 1b, subunit 1 [Source:MGI Symbol;Acc:MGI:109520]	Q5SW18	P63005	-8.8	4.4E-06	-5.3	7.5E-03	1.0	2.0E-01	0.5	7.5E-01
ENSMUST00000021097	RecQ protein-like 5 [Source:MGI Symbol;Acc:MGI:2156841]		Q8VID5	-5.5	2.9E-03	5.5	3.7E-05	-0.9	2.5E-01	-0.5	3.6E-01
ENSMUST00000021130	TEN1 telomerase capping complex subunit [Source:MGI Symbol;Acc:MGI:1916785]		Q9D7K2	-5.8	1.9E-04	-6.2	4.0E-03	1.0	1.8E-01	-0.7	7.0E-01
ENSMUST00000021133	signal recognition particle 68 [Source:MGI Symbol;Acc:MGI:1917447]		Q8BMA6	-4.9	2.2E-04	-3.1	7.0E-04	-0.3	3.6E-01	0.3	6.5E-01
ENSMUST00000021135	RIKEN cDNA 1200014J11 gene [Source:MGI Symbol;Acc:MGI:1914124]		Q8BZR9	-2.2	2.4E-03	6.4	1.9E-04	-0.6	6.0E-01	0.1	8.6E-01
ENSMUST00000021142	ATPase, Ca++ transporting, ubiquitous [Source:MGI Symbol;Acc:MGI:1194503]		Q64518	-8.3	9.9E-04	8.0	2.9E-04	0.9	5.1E-01	0.5	4.6E-01
ENSMUST00000021148	ubiquitin-conjugating enzyme E2G 1 [Source:MGI Symbol;Acc:MGI:1914378]	Q5F239	P62254	-2.6	1.5E-02	6.3	2.2E-03	-0.5	7.7E-01	-2.9	1.4E-02
ENSMUST00000021157	mediator complex subunit 31 [Source:MGI Symbol;Acc:MGI:1914529]		Q9CXU1	-3.2	2.5E-03	-1.7	1.7E-02	0.1	7.2E-01	-0.8	2.5E-01
ENSMUST00000021158	thioredoxin domain containing 17 [Source:MGI Symbol;Acc:MGI:1289248]		Q9CQM5	-4.8	3.8E-06	-4.3	1.2E-03	0.9	6.6E-02	0.1	9.4E-01
ENSMUST00000021078	ferredoxin reductase [Source:MGI Symbol;Acc:MGI:104724]		Q61578	-1.8	1.2E-01	-1.4	3.6E-01	0.5	6.0E-01	0.1	9.5E-01
ENSMUST00000021079				3.4	7.3E-02	4.8	2.4E-02	-0.5	7.8E-01	-1.9	1.8E-01
ENSMUST00000021161	ute carrier family 13 (sodium-dependent citrate transporter), member 5 [Source:MGI Symbol;Acc:MGI:30371		Q67BT3	7.3	4.4E-05	-5.0	8.6E-03	-0.4	5.8E-01	0.2	8.9E-01
ENSMUST00000021166	cytoglobin [Source:MGI Symbol;Acc:MGI:2149481]	Q546K1	Q9CX80	8.4	1.5E-05	-2.8	6.6E-03	0.4	4.1E-01	-0.2	8.4E-01
ENSMUST00000021085	nucleoporin 85 [Source:MGI Symbol;Acc:MGI:3046173]		Q8R480	-1.8	8.6E-02	0.0	9.8E-01	0.0	9.9E-01	-1.8	1.2E-01
ENSMUST00000021168	WSC domain containing 1 [Source:MGI Symbol;Acc:MGI:2448493]		Q80XH4	8.6	7.6E-05	-6.5	7.1E-03	0.9	2.0E-01	2.1	3.0E-01
ENSMUST00000021089	arrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 [Source:MGI Symbol;Acc:MGI:1		Q9DAM5	-1.9	1.0E-01	-0.3	8.4E-01	0.7	4.6E-01	-0.9	5.0E-01
ENSMUST00000021170	matrix-remodelling associated 7 [Source:MGI Symbol;Acc:MGI:1914872]		Q9CZH7	4.3	6.8E-04	-8.6	6.2E-05	1.2	6.1E-03	0.2	8.9E-01
ENSMUST00000021179	vitelline membrane outer layer 1 homolog (chicken) [Source:MGI Symbol;Acc:MGI:2685587]		Q5SXG7	6.5	7.1E-04	-8.8	8.2E-05	0.8	3.7E-02	0.9	5.4E-01
ENSMUST00000021197	bleomycin hydrolase [Source:MGI Symbol;Acc:MGI:1345186]		Q8R016	-1.9	2.4E-03	-4.0	1.9E-02	1.0	2.1E-01	-0.6	7.3E-01
ENSMUST00000021201	carboxypeptidase D [Source:MGI Symbol;Acc:MGI:107265]		O89001	-5.8	9.6E-07	-7.1	2.3E-03	-1.5	3.2E-02	0.1	9.7E-01
ENSMUST00000021114	galactokinase 1 [Source:MGI Symbol;Acc:MGI:95730]		Q9R0N0	0.7	3.8E-01	-0.4	6.6E-01	-1.4	5.8E-02	-0.3	6.9E-01
ENSMUST00000021116	unkempt homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2442456]		Q8BL48	-1.6	5.8E-01	2.4	4.4E-01	0.5	8.5E-01	-3.5	2.4E-01
ENSMUST00000021120	tripartite motif-containing 47 [Source:MGI Symbol;Acc:MGI:1917374]		Q8C0E3	4.5	4.1E-02	2.8	1.0E-01	-4.3	4.2E-02	-2.7	8.0E-02
ENSMUST00000021204	nucleoredoxin [Source:MGI Symbol;Acc:MGI:109331]		P97346	-3.0	6.7E-04	-5.0	2.3E-03	0.2	6.7E-01	-0.6	6.8E-01
ENSMUST00000021207	family with sequence similarity 101, member B [Source:MGI Symbol;Acc:MGI:1923816]		Q5SVD0	-3.3	3.9E-04	-2.6	6.7E-03	0.2	6.2E-01	-2.1	5.1E-02
ENSMUST00000021134	tRNA splicing endonuclease 54 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923515]		Q8C2A2	-3.4	3.6E-02	-2.6	8.9E-02	0.4	6.6E-01	-0.4	8.0E-01
ENSMUST00000021208	rabphilin 3A-like (without C2 domains) [Source:MGI Symbol;Acc:MGI:1923492]		Q768S4	5.6	4.2E-04	-2.3	1.0E-02	0.3	4.3E-01	0.4	5.5E-01
ENSMUST00000021141	purinergic receptor P2X, ligand-gated ion channel, 1 [Source:MGI Symbol;Acc:MGI:1098235]		P51576	-1.1	7.1E-02	-0.2	7.9E-01	0.5	2.9E-01	-0.4	5.9E-01
ENSMUST00000021209	double C2, beta [Source:MGI Symbol;Acc:MGI:1100497]		P70169	8.6	2.0E-05	-4.1	1.9E-02	0.7	3.2E-01	-3.5	1.0E-01
ENSMUST00000021217	NME/NM23 nucleoside diphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:97356]	Q5NC82	Q01768	-2.7	5.3E-03	-4.3	5.2E-02	2.0	3.9E-02	3.7	7.4E-02
ENSMUST00000021154	spinster homolog 3 [Source:MGI Symbol;Acc:MGI:1924827]		Q9D232	-0.7	8.0E-01	-0.1	9.8E-01	-2.2	2.9E-01	-2.8	3.2E-01
ENSMUST00000021220	NME/NM23 nucleoside diphosphate kinase 1 [Source:MGI Symbol;Acc:MGI:97355]	Q5NC80		-2.5	3.4E-02	-3.9	3.0E-03	-0.7	2.1E-01	0.1	9.5E-01
ENSMUST00000021239	leucine rich repeat containing 59 [Source:MGI Symbol;Acc:MGI:2138133]		Q922Q8	-3.0	8.3E-05	-4.9	2.1E-05	-0.4	1.4E-01	-0.4	5.7E-01
ENSMUST00000021240	cell division cycle 34 homolog, pseudogene (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1858429]			6.8	1.5E-03	6.7	1.0E-04	-1.3	2.7E-01	-0.7	2.3E-01
ENSMUST00000021164	family with sequence similarity 64, member A [Source:MGI Symbol;Acc:MGI:1924434]		Q8BFY7	0.4	5.7E-01	0.9	3.7E-01	0.3	7.0E-01	-0.2	8.4E-01
ENSMUST00000021241	distal-less homeobox 4 [Source:MGI Symbol;Acc:MGI:94904]		P70436	8.0	2.7E-05	5.7	7.2E-05	-2.8	2.1E-02	-0.2	7.2E-01
ENSMUST00000021242	tachykinin 4 [Source:MGI Symbol;Acc:MGI:1931130]		Q99N14	6.3	6.3E-05	7.7	3.5E-04	-0.8	6.2E-01	0.2	8.0E-01
ENSMUST00000021259	guanylate cyclase 2e [Source:MGI Symbol;Acc:MGI:105123]		P52785	8.4	4.6E-05	3.8	5.8E-03	0.2	8.0E-01	0.7	3.6E-01
ENSMUST00000021173	major facilitator superfamily domain containing 11 [Source:MGI Symbol;Acc:MGI:1917150]		Q8BJ51	0.2	7.2E-01	0.2	7.3E-01	-0.6	1.6E-01	-0.6	2.4E-01
ENSMUST00000021177	SEC14-like lipid binding 1 [Source:MGI Symbol;Acc:MGI:1921386]	A2A9B9		-3.3	1.7E-01	-3.2	3.0E-01	-0.1	9.3E-01	-0.2	9.4E-01
ENSMUST00000021262	arachidonate 8-lipoxygenase [Source:MGI Symbol;Acc:MGI:1098228]		O35936	4.9	7.4E-05	6.2	1.7E-03	-0.7	6.5E-01	-0.4	6.5E-01
ENSMUST00000021183	Era (G-protein)-like 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1889295]		Q9CZU4	0.1	9.3E-01	2.8	2.0E-01	1.3	4.5E-01	-1.4	4.6E-01
ENSMUST00000021187	dehydrogenase/reductase (SDR family) member 13 [Source:MGI Symbol;Acc:MGI:1917701]		Q5SS80	-0.4	7.2E-01	0.4	8.1E-01	1.3	2.6E-01	0.6	6.6E-01
ENSMUST00000021195	olute carrier family 6 (neurotransmitter transporter, serotonin), member 4 [Source:MGI Symbol;Acc:MGI:9628		Q60857	1.3	4.5E-01	-1.3	5.5E-01	-1.6	3.3E-01	1.0	6.3E-01
ENSMUST00000021271	period circadian clock 1 [Source:MGI Symbol;Acc:MGI:1098283]		O35973	-6.5	1.8E-02	-1.8	1.3E-02	0.3	4.2E-01	0.2	7.2E-01
ENSMUST00000021273	vesicle-associated membrane protein 2 [Source:MGI Symbol;Acc:MGI:1313277]	Q8CHR4	P63044	-2.8	2.1E-02	-4.5	4.7E-05	1.2	3.3E-03	0.0	9.7E-01
ENSMUST00000021203	translocase of inner mitochondrial membrane 22 [Source:MGI Symbol;Acc:MGI:1929742]		Q9CQ85	0.1	8.7E-01	1.2	1.0E-01	0.3	5.1E-01	-0.7	2.4E-01
ENSMUST00000021286	syntaxin 8 [Source:MGI Symbol;Acc:MGI:1890156]	Q9D0J1		3.0	4.1E-04	-1.2	1.4E-01	1.2	2.2E-02	-0.6	4.6E-01
ENSMUST00000021287	cilia and flagella associated protein 52 [Source:MGI Symbol;Acc:MGI:1919110]	Q147Z1	Q5F201	6.1	3.5E-04	-2.7	9.1E-03	1.1	5.0E-02	0.5	5.7E-01
ENSMUST00000021289	glucagon-like peptide 2 receptor [Source:MGI Symbol;Acc:MGI:2136733]	Q8BM22		6.7	5.8E-05	5.7	1.6E-03	-0.3	8.1E-01	-0.4	6.5E-01
ENSMUST00000021297	LSM12 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919592]		Q9D0R8	-7.3	1.2E-05	8.0	7.1E-05	-0.6	6.2E-01	0.0	9.6E-01
ENSMUST00000021302	HIG1 domain family, member 1B [Source:MGI Symbol;Acc:MGI:1922939]		Q99JY6	5.1	9.5E-04	-3.1	5.2E-03	-1.3	3.0E-02	-0.9	3.3E-01
ENSMUST00000021307	coiled-coil domain containing 103 [Source:MGI Symbol;Acc:MGI:1920543]		Q9D9P2	5.1	4.4E-04	-4.5	1.6E-02	-1.6	5.4E-02	0.4	7.8E-01
ENSMUST00000021227	ankyrin repeat domain 40 [Source:MGI Symbol;Acc:MGI:1918702]		Q5SUE8	-0.2	7.9E-01	2.6	2.5E-02	1.7	7.3E-02	-1.1	1.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000021231	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 [Source:MGI Symbol;Acc:MGI:1923658]			4.7	6.6E-02	2.8	1.7E-01	-4.0	8.4E-02	-2.1	2.5E-01
ENSMUST00000021311	kinesin family member 18B [Source:MGI Symbol;Acc:MGI:2446979]		Q6PFD6	1.5	2.2E-02	-2.3	2.7E-03	0.4	2.1E-01	-0.3	6.0E-01
ENSMUST00000021314	N-myristoyltransferase 1 [Source:MGI Symbol;Acc:MGI:102579]	Q3UJC3	O70310	-3.5	5.5E-05	6.2	4.1E-03	-0.7	6.9E-01	-0.2	8.7E-01
ENSMUST00000021323	RIKEN cDNA 1700023F06 gene [Source:MGI Symbol;Acc:MGI:1916691]	A2AB62		6.1	9.9E-03	6.5	1.1E-04	-1.9	1.2E-01	-0.4	5.4E-01
ENSMUST00000021328	lysozyme-like 6 [Source:MGI Symbol;Acc:MGI:1916694]	A0A077S2U3	Q9DA11	6.1	1.7E-04	4.5	6.6E-04	-1.5	1.5E-01	0.4	5.5E-01
ENSMUST00000021243	solute carrier family 35, member B1 [Source:MGI Symbol;Acc:MGI:1343133]		P97858	-2.8	5.0E-02	-2.9	6.5E-02	-1.0	2.5E-01	-0.9	5.8E-01
ENSMUST00000021246	sorting nexin 11 [Source:MGI Symbol;Acc:MGI:1921729]		Q91WL6	-1.8	5.4E-02	-0.6	6.1E-01	0.9	2.5E-01	-0.4	7.4E-01
ENSMUST00000021249	secernin 2 [Source:MGI Symbol;Acc:MGI:1343092]		Q8VCA8	0.1	9.3E-01	1.9	3.1E-01	0.0	9.8E-01	-1.7	2.9E-01
ENSMUST00000021251	leucine rich repeat containing 46 [Source:MGI Symbol;Acc:MGI:1916547]		Q9DAP0	0.6	2.8E-01	1.8	2.5E-02	0.2	7.7E-01	-1.0	1.2E-01
ENSMUST00000021329	golgi SNAP receptor complex member 2 [Source:MGI Symbol;Acc:MGI:1927204]		O35166	-3.6	1.3E-05	7.9	2.3E-04	-0.7	6.2E-01	-0.2	7.5E-01
ENSMUST00000021331	kelch-like 28 [Source:MGI Symbol;Acc:MGI:1913939]		Q9CR40	-1.5	7.3E-03	5.5	2.0E-04	0.6	5.0E-01	0.0	9.7E-01
ENSMUST00000021268	arachidonate lipoxygenase 3 [Source:MGI Symbol;Acc:MGI:1345140]		Q9WV07	0.9	1.3E-01	3.2	2.0E-03	1.5	4.0E-02	-0.8	2.2E-01
ENSMUST00000021332	FK506 binding protein 3 [Source:MGI Symbol;Acc:MGI:1353460]	Q3UBU9	Q62446	-3.2	7.2E-04	-4.8	8.8E-02	1.2	4.5E-01	-0.4	8.8E-01
ENSMUST00000021335	Sec1 family domain containing 1 [Source:MGI Symbol;Acc:MGI:1924233]		Q8BRF7	-4.4	1.4E-03	-2.2	1.3E-01	0.7	3.8E-01	0.2	9.1E-01
ENSMUST00000021277	aurora kinase B [Source:MGI Symbol;Acc:MGI:107168]		O70126	-2.4	5.5E-02	-3.4	1.3E-01	1.1	2.9E-01	2.1	3.3E-01
ENSMUST00000021282	hosphoribosylformylglycinamidine synthase (FGAR amidotransferase) [Source:MGI Symbol;Acc:MGI:268486		Q5SUR0	0.6	6.7E-01	2.3	2.0E-01	0.9	5.1E-01	-0.8	5.9E-01
ENSMUST00000021283	phosphoinositide-3-kinase, regulatory subunit 5, p101 [Source:MGI Symbol;Acc:MGI:2443588]	A1A4T4	Q5SW28	-0.3	6.7E-01	-0.8	4.2E-01	0.7	2.8E-01	1.2	1.8E-01
ENSMUST00000021284	netrin 1 [Source:MGI Symbol;Acc:MGI:105088]		O09118	2.2	2.8E-01	-1.2	3.9E-01	-6.3	2.6E-03	-2.9	1.0E-01
ENSMUST00000021285	syntaxin 8 [Source:MGI Symbol;Acc:MGI:1890156]		O88983	0.1	8.0E-01	-0.3	5.6E-01	-1.1	1.9E-02	-0.7	1.9E-01
ENSMUST00000021338	adaptor-related protein complex AP-4, sigma 1 [Source:MGI Symbol;Acc:MGI:1337065]		Q9WVL1	-2.3	1.6E-03	2.7	2.2E-03	-0.3	5.7E-01	-0.1	8.9E-01
ENSMUST00000021339	D-tyrosyl-tRNA deacylase 2 [Source:MGI Symbol;Acc:MGI:1923485]		Q8BHA3	2.2	7.4E-03	5.6	1.1E-03	-0.5	6.9E-01	0.0	9.5E-01
ENSMUST00000021343	thyroid stimulating hormone receptor [Source:MGI Symbol;Acc:MGI:98849]	Q78U67		4.8	2.0E-02	6.5	7.4E-05	-1.5	1.8E-01	-1.4	3.7E-02
ENSMUST00000021296	transmembrane protein 101 [Source:MGI Symbol;Acc:MGI:1923797]		Q91VP7	-1.0	1.2E-01	0.4	6.0E-01	1.3	4.9E-02	-0.1	8.7E-01
ENSMUST00000021346	thyroid stimulating hormone receptor [Source:MGI Symbol;Acc:MGI:98849]		P47750	2.1	4.9E-03	-6.4	1.2E-04	0.6	1.2E-01	-0.3	8.0E-01
ENSMUST00000021347	sel-1 suppressor of lin-12-like (C. elegans) [Source:MGI Symbol;Acc:MGI:1329016]		Q9Z2G6	-7.8	1.0E-04	6.3	4.1E-04	-0.6	6.3E-01	-1.8	2.8E-02
ENSMUST00000021306	elongation factor Tu GTP binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1336880]	A2AH85		-1.8	4.8E-01	-2.0	5.6E-01	-0.2	9.4E-01	0.1	9.8E-01
ENSMUST00000021356	dynein, axonemal assembly factor 2 [Source:MGI Symbol;Acc:MGI:1923566]		Q8BPI1	1.9	4.8E-03	5.4	1.3E-03	1.0	4.3E-01	0.6	3.8E-01
ENSMUST00000021362	kelch domain containing 2 [Source:MGI Symbol;Acc:MGI:1916804]		Q4G5Y1	-4.2	2.6E-04	2.6	7.4E-03	1.1	9.3E-02	0.0	9.5E-01
ENSMUST00000021313	dephospho-CoA kinase domain containing [Source:MGI Symbol;Acc:MGI:1915337]		Q8BHC4	-1.8	1.2E-01	-1.4	3.6E-01	0.3	7.2E-01	0.0	9.8E-01
ENSMUST00000021368	nuclear export mediator factor [Source:MGI Symbol;Acc:MGI:1918305]		Q8CCP0	-3.5	2.7E-03	-2.5	1.7E-03	0.1	8.0E-01	-0.9	1.7E-01
ENSMUST00000021370	L-2-hydroxyglutarate dehydrogenase [Source:MGI Symbol;Acc:MGI:2384968]		Q91YP0	4.8	5.0E-05	-1.6	2.1E-01	0.9	2.6E-01	-0.3	8.3E-01
ENSMUST00000021375	SEC23 homolog A, COPII coat complex component [Source:MGI Symbol;Acc:MGI:1349635]		Q01405	-2.2	1.7E-03	7.0	7.1E-03	-0.8	7.2E-01	-1.8	1.7E-01
ENSMUST00000021324	mitogen-activated protein kinase kinase kinase 14 [Source:MGI Symbol;Acc:MGI:1858204]	Q544K4	Q9WUL6	-1.5	6.4E-02	-0.3	7.6E-01	0.9	1.8E-01	-0.3	7.4E-01
ENSMUST00000021377	cyclin-dependent kinase-like 1 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1918341]	Q14BG3	Q8CEQ0	5.8	4.9E-04	5.2	9.4E-04	-0.6	5.9E-01	0.3	6.2E-01
ENSMUST00000021380	trafficking protein particle complex 6B [Source:MGI Symbol;Acc:MGI:1925482]		Q9D289	-4.3	8.1E-06	-2.5	8.4E-04	0.7	3.4E-02	-0.4	4.9E-01
ENSMUST00000021381	pinin [Source:MGI Symbol;Acc:MGI:1100514]	Q3TUQ5		-3.9	4.1E-04	-1.7	1.3E-02	-0.2	6.1E-01	0.0	9.4E-01
ENSMUST00000021390	galactosylceramidase [Source:MGI Symbol;Acc:MGI:95636]		P54818	-2.9	3.7E-04	-4.0	6.8E-04	-1.2	2.5E-02	-0.4	6.1E-01
ENSMUST00000021405	polymerase (RNA) II (DNA directed) polypeptide H [Source:MGI Symbol;Acc:MGI:2384309]		Q923G2	-3.4	3.2E-05	-4.7	3.8E-03	-0.7	2.8E-01	-0.5	7.3E-01
ENSMUST00000021407	signal recognition particle 54A [Source:MGI Symbol;Acc:MGI:1346087]		P14576	-6.9	1.1E-04	-1.7	1.9E-02	-0.2	5.8E-01	-0.8	2.3E-01
ENSMUST00000021410	protein phosphatase 2, regulatory subunit B", gamma [Source:MGI Symbol;Acc:MGI:1930009]		Q9JK24	-3.9	2.9E-04	2.7	5.2E-03	0.0	9.4E-01	-0.5	4.2E-01
ENSMUST00000021412	proteasome (prosome, macropain) subunit, alpha type 6 [Source:MGI Symbol;Acc:MGI:1347006]		Q9QUM9	-9.2	2.7E-06	2.5	2.8E-01	-0.2	9.2E-01	2.1	2.5E-01
ENSMUST00000021345	general transcription factor II A, 1 [Source:MGI Symbol;Acc:MGI:1933277]		Q99PM3	-0.7	1.4E-01	-0.7	2.5E-01	0.2	5.6E-01	0.3	6.6E-01
ENSMUST00000021413	ır factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha [Source:MGI Symbol;Acc:MGI:10		Q9Z1E3	-4.9	5.0E-06	5.0	8.5E-05	2.4	5.4E-03	-0.6	3.0E-01
ENSMUST00000021416	MAP3K12 binding inhibitory protein 1 [Source:MGI Symbol;Acc:MGI:1918320]		Q99LQ1	-2.7	6.7E-03	-3.9	6.6E-03	1.6	1.5E-02	-2.4	1.2E-01
ENSMUST00000021423	NADP+ dependent oxidoreductase domain containing 1 [Source:MGI Symbol;Acc:MGI:1918525]		Q9D3S5	-3.7	5.0E-04	1.4	7.6E-02	0.1	8.6E-01	0.7	2.6E-01
ENSMUST00000021359	polymerase (DNA directed), epsilon 2 (p59 subunit) [Source:MGI Symbol;Acc:MGI:1197514]		O54956	-0.3	6.7E-01	-1.1	2.2E-01	-1.0	1.5E-01	-0.2	8.0E-01
ENSMUST00000021424	serine palmitoyltransferase, long chain base subunit 2 [Source:MGI Symbol;Acc:MGI:108074]	Q542D6	P97363	-3.4	3.2E-04	-3.2	6.3E-03	0.9	1.1E-01	-0.1	8.8E-01
ENSMUST00000021425	AHA1, activator of heat shock protein ATPase 1 [Source:MGI Symbol;Acc:MGI:2387603]		Q8BK64	-5.1	5.1E-06	-3.9	4.8E-03	-0.9	1.3E-01	-0.5	6.8E-01
ENSMUST00000021428	SNW domain containing 1 [Source:MGI Symbol;Acc:MGI:1913604]	A0A0B4J1E2		-4.5	4.6E-05	3.2	2.5E-03	-0.9	2.2E-01	0.7	2.3E-01
ENSMUST00000021438	neuro-oncological ventral antigen 1 [Source:MGI Symbol;Acc:MGI:104297]		Q9JKN6	8.3	2.1E-05	-2.4	4.4E-03	-0.2	5.3E-01	-0.1	9.1E-01
ENSMUST00000021443	genase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase [Source		Q922D8	1.4	1.7E-02	5.6	1.3E-03	-0.4	7.9E-01	-0.2	8.2E-01
ENSMUST00000021379	gem (nuclear organelle) associated protein 2 [Source:MGI Symbol;Acc:MGI:1913853]		Q9CQQ4	-1.2	3.6E-01	-0.4	8.1E-01	-0.4	7.0E-01	-1.3	4.1E-01
ENSMUST00000021447	protein phosphatase 2, regulatory subunit B', epsilon [Source:MGI Symbol;Acc:MGI:1349473]		Q61151	-1.6	3.9E-03	-3.6	2.6E-04	0.8	4.0E-02	0.1	9.3E-01
ENSMUST00000021450	sphingosine-1-phosphate phosphatase 1 [Source:MGI Symbol;Acc:MGI:2135760]	Q3UDY2	Q9JI99	-3.1	3.4E-05	-3.3	3.4E-03	-0.7	1.7E-01	-1.3	1.8E-01
ENSMUST00000021384	melanoma inhibitory activity 2 [Source:MGI Symbol;Acc:MGI:2159614]		Q91ZV0	1.3	1.3E-01	1.6	1.1E-01	-0.5	5.4E-01	-0.8	3.5E-01
ENSMUST00000021453	testis expressed gene 21 [Source:MGI Symbol;Acc:MGI:1931131]	Q9R0U9		7.1	3.3E-05	-1.8	2.3E-02	0.9	5.4E-02	-0.2	7.7E-01
ENSMUST00000021458	spectrin beta, erythrocytic [Source:MGI Symbol;Acc:MGI:98387]	Q3UGX2		3.7	3.5E-05	-2.7	7.4E-04	0.2	5.3E-01	-0.5	3.9E-01
ENSMUST00000021459	RAB15, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1916865]	Q3TYH2		5.2	3.4E-05	-5.9	1.9E-03	0.2	6.9E-01	-0.9	5.6E-01
ENSMUST00000021466	atlastin GTPase 1 [Source:MGI Symbol;Acc:MGI:1921241]		Q8BH66	3.8	2.3E-04	-4.0	1.3E-03	0.2	7.2E-01	0.2	8.0E-01
ENSMUST00000021467	salvador homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1927144]		Q8VEB2	-4.0	2.8E-04	-9.7	2.4E-05	-0.1	6.8E-01	0.4	7.9E-01
ENSMUST00000021471	thioredoxin-related transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1919986]		Q8VBT0	-3.2	8.4E-04	-4.8	5.8E-05	0.3	4.0E-01	0.1	8.6E-01
ENSMUST00000021479	ARP10 actin-related protein 10 [Source:MGI Symbol;Acc:MGI:1891654]		Q9QZB7	-3.1	1.0E-05	-3.3	7.5E-03	-0.7	2.5E-01	0.0	9.7E-01
ENSMUST00000021420	neuroglobin [Source:MGI Symbol;Acc:MGI:2151886]	Q5ZPR7	Q9ER97	3.9	6.9E-02	2.6	2.7E-01	-0.5	8.2E-01	0.8	6.7E-01
ENSMUST00000021494	coiled-coil domain containing 175 [Source:MGI Symbol;Acc:MGI:1921186]		E9PVB3	5.9	1.1E-03	-2.3	2.3E-02	0.7	2.2E-01	-0.7	4.2E-01
ENSMUST00000021495	serine (or cysteine) peptidase inhibitor, clade A, member 5 [Source:MGI Symbol;Acc:MGI:107817]		P70458	5.6	8.0E-05	-2.5	1.0E-02	0.7	1.4E-01	-0.2	7.8E-01
ENSMUST00000021506	serine (or cysteine) peptidase inhibitor, clade A, member 3N [Source:MGI Symbol;Acc:MGI:105045]	G3X8T9		5.8	5.5E-05	-3.9	2.6E-04	0.9	1.8E-02	-0.3	6.8E-01
ENSMUST00000021426	B interacting protein, apical-basolateral polarity regulator, spe-39 homolog [Source:MGI Symbol;Acc:MGI:21		Q8BGQ1	-0.9	7.4E-01	-1.0	8.0E-01	0.1	9.7E-01	0.2	9.5E-01
ENSMUST00000021512	dehydrogenase/reductase (SDR family) member 7 [Source:MGI Symbol;Acc:MGI:1913625]		Q9CXR1	-7.2	4.2E-07	-5.4	8.6E-05	-0.9	4.5E-02	0.1	9.2E-01
ENSMUST00000021514	protein phosphatase 1A, magnesium dependent, alpha isoform [Source:MGI Symbol;Acc:MGI:99878]		P49443	-4.6	7.7E-06	6.6	2.7E-04	-0.6	6.1E-01	1.1	1.1E-01
ENSMUST00000021519	sine oculis-related homeobox 6 [Source:MGI Symbol;Acc:MGI:1341840]	B2RSE8	Q9QZ28	7.9	2.5E-05	0.5	4.3E-01	-0.9	8.2E-02	0.0	9.5E-01
ENSMUST00000021522	glutaredoxin 5 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1920296]		Q80Y14	-1.7	2.0E-02	-0.5	3.5E-01	1.2	1.0E-02	0.1	8.1E-01
ENSMUST00000021523	menage a trois 1 [Source:MGI Symbol;Acc:MGI:106207]		P51949	3.1	3.5E-02	-2.5	8.7E-04	0.5	1.3E-01	-0.1	7.8E-01
ENSMUST00000021527	protein kinase C, eta [Source:MGI Symbol;Acc:MGI:97600]		P23298	-2.7	6.9E-03	7.6	3.6E-05	-0.6	6.1E-01	-1.1	6.8E-02
ENSMUST00000021530	hypoxia inducible factor 1, alpha subunit [Source:MGI Symbol;Acc:MGI:106918]		Q61221	-8.7	1.1E-05	4.1	6.8E-05	0.3	5.8E-01	-0.1	7.8E-01
ENSMUST00000021532	small nuclear RNA activating complex, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1922877]		Q8K0S9	-1.5	2.0E-02	6.5	9.0E-05	1.1	2.7E-01	-0.2	7.2E-01
ENSMUST00000021535	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:109301]		Q61183	-5.0	1.1E-03	4.1	3.5E-04	0.0	9.4E-01	-0.4	5.3E-01
ENSMUST00000021536	ATPase, H+ transporting, lysosomal V1 subunit D [Source:MGI Symbol;Acc:MGI:1921084]	Q3U861	P57746	-5.7	3.6E-06	-2.9	1.0E-02	1.0	7.5E-02	-0.1	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000021468	ninein [Source:MGI Symbol;Acc:MGI:105108]		Q61043	-3.8	7.7E-02	-1.0	6.9E-01	2.5	1.9E-01	-0.3	9.1E-01
ENSMUST00000021544	pleckstrin 2 [Source:MGI Symbol;Acc:MGI:1351466]		Q9WV52	5.4	1.0E-04	-4.4	8.0E-04	-0.2	5.9E-01	0.9	3.3E-01
ENSMUST00000021548	retinol dehydrogenase 12 [Source:MGI Symbol;Acc:MGI:1925224]		Q8BYK4	-10.9	2.4E-06	-3.0	1.2E-04	0.0	9.7E-01	-0.1	8.2E-01
ENSMUST00000021550	arginase type II [Source:MGI Symbol;Acc:MGI:1330806]		O08691	-7.9	2.4E-07	4.9	5.9E-03	-0.4	7.7E-01	0.5	5.2E-01
ENSMUST00000021552	zinc finger protein 36, C3H type-like 1 [Source:MGI Symbol;Acc:MGI:107946]	Q543H2	P23950	-6.7	4.3E-04	5.7	1.2E-04	-0.5	5.6E-01	-0.7	2.4E-01
ENSMUST00000021554	actinin, alpha 1 [Source:MGI Symbol;Acc:MGI:2137706]		Q7TPR4	-5.9	1.7E-05	0.2	7.7E-01	-6.0	2.3E-05	-0.4	4.9E-01
ENSMUST00000021558	:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 16 [Source:MGI Symbol;Acc:MGI		Q9JJ61	8.3	6.2E-06	-5.9	9.9E-06	0.4	1.4E-01	-0.8	2.7E-01
ENSMUST00000021559	enhancer of rudimentary homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108089]	Q4FZH7	P84089	-2.5	2.9E-04	-3.4	4.0E-04	0.6	1.1E-01	-0.7	2.9E-01
ENSMUST00000021572	WD repeat domain 37 [Source:MGI Symbol;Acc:MGI:1920393]		Q8CBE3	-4.3	2.6E-03	5.8	3.6E-04	-1.6	2.1E-01	0.6	3.6E-01
ENSMUST00000021595	protease (prosome, macropain) 26S subunit, ATPase 1 [Source:MGI Symbol;Acc:MGI:106054]	Q542I9	P62192	-4.4	2.7E-05	-1.6	9.1E-02	0.7	2.1E-01	0.6	5.0E-01
ENSMUST00000021596	nrde-2 necessary for RNA interference, domain containing [Source:MGI Symbol;Acc:MGI:2670969]		Q80XC6	-1.2	1.9E-02	1.9	2.0E-01	-1.5	2.6E-01	-0.3	8.2E-01
ENSMUST00000021603	fibulin 5 [Source:MGI Symbol;Acc:MGI:1346091]		Q9WVH9	7.3	2.6E-05	-1.7	1.1E-01	0.5	4.4E-01	-0.5	6.2E-01
ENSMUST00000021605	thyroid hormone receptor interactor 11 [Source:MGI Symbol;Acc:MGI:1924393]	E9Q512		-1.5	2.8E-02	-8.1	1.7E-04	0.4	3.1E-01	-0.2	8.7E-01
ENSMUST00000021606	ataxin 3 [Source:MGI Symbol;Acc:MGI:1099442]	Q546X9	Q9CVD2	-2.4	1.2E-03	-1.8	2.1E-02	-0.6	1.8E-01	-0.3	6.6E-01
ENSMUST00000021607	legumain [Source:MGI Symbol;Acc:MGI:1330838]	A2RTI3	O89017	-4.4	1.3E-02	1.5	4.0E-01	6.5	8.4E-04	-0.1	9.6E-01
ENSMUST00000021609	golgi autoantigen, golgin subfamily a, 5 [Source:MGI Symbol;Acc:MGI:1351475]		Q9QYE6	-3.5	6.2E-04	-5.4	3.2E-05	-0.4	2.5E-01	-0.7	3.3E-01
ENSMUST00000021539	vaccinia related kinase 1 [Source:MGI Symbol;Acc:MGI:1261847]		Q80X41	-2.6	1.3E-01	-2.4	1.4E-01	-1.6	1.3E-01	-1.8	3.1E-01
ENSMUST00000021610	chromogranin A [Source:MGI Symbol;Acc:MGI:88394]		P26339	8.4	6.8E-04	3.9	4.4E-04	-2.2	2.2E-02	-0.7	2.1E-01
ENSMUST00000021547	zinc finger, FYVE domain containing 26 [Source:MGI Symbol;Acc:MGI:1924767]		Q5DU37	-0.9	1.1E-01	0.6	4.1E-01	1.1	6.0E-02	-0.4	5.2E-01
ENSMUST00000021614	phosphofructokinase, platelet [Source:MGI Symbol;Acc:MGI:1891833]	Q8C605		-7.7	3.0E-05	-10.2	3.2E-05	0.1	7.9E-01	-0.6	6.7E-01
ENSMUST00000021617	ankyrin repeat and SOCS box-containing 2 [Source:MGI Symbol;Acc:MGI:1929743]		Q8K0L0	5.7	2.0E-03	-7.0	3.7E-06	-0.1	6.6E-01	-1.0	1.9E-01
ENSMUST00000021631	protein phosphatase 4, regulatory subunit 4 [Source:MGI Symbol;Acc:MGI:1921771]		Q8C0Y0	6.8	7.1E-05	-3.5	5.2E-02	2.3	1.7E-02	-0.9	5.9E-01
ENSMUST00000021639	tubulin, alpha-like 3 [Source:MGI Symbol;Acc:MGI:3588215]		Q3UX10	6.6	1.8E-04	-4.1	1.4E-03	1.6	4.4E-03	-0.2	8.7E-01
ENSMUST00000021641	teashirt zinc finger family member 3 [Source:MGI Symbol;Acc:MGI:2442819]			7.2	1.0E-05	7.0	1.9E-05	-1.9	8.5E-02	-0.5	2.7E-01
ENSMUST00000021645	DDB1 and CUL4 associated factor 4 [Source:MGI Symbol;Acc:MGI:1921078]	Q99LF7		3.3	2.0E-04	-2.4	1.3E-03	-0.8	2.8E-02	-1.0	9.8E-02
ENSMUST00000021564	SPARC related modular calcium binding 1 [Source:MGI Symbol;Acc:MGI:1929878]	E9QKW2		4.0	1.5E-01	1.9	5.9E-01	-0.2	9.6E-01	2.0	4.5E-01
ENSMUST00000021567	pecanex homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1891924]		Q9QYC1	0.0	9.8E-01	0.9	1.5E-01	0.8	9.2E-02	-0.1	8.7E-01
ENSMUST00000021649	acyl-CoA thioesterase 2 [Source:MGI Symbol;Acc:MGI:2159605]		Q9QYR9	4.7	1.5E-03	-3.3	3.5E-02	0.7	3.3E-01	-0.3	8.6E-01
ENSMUST00000021574	GTP binding protein 4 [Source:MGI Symbol;Acc:MGI:1916487]		Q99ME9	-0.8	2.3E-01	-1.9	2.7E-02	-1.4	1.8E-02	-0.2	7.7E-01
ENSMUST00000021592	cell division cycle associated 7 like [Source:MGI Symbol;Acc:MGI:2384982]		Q922M5	0.3	5.0E-01	0.0	9.8E-01	-0.3	5.2E-01	0.0	9.3E-01
ENSMUST00000021652	acyl-CoA thioesterase 4 [Source:MGI Symbol;Acc:MGI:2159621]	Q14DI6	Q8BWN8	6.1	2.7E-04	-5.7	2.8E-05	-0.9	2.7E-02	0.5	5.5E-01
ENSMUST00000021653	acyl-CoA thioesterase 3 [Source:MGI Symbol;Acc:MGI:2159619]	Q53YL1	Q9QYR7	7.1	6.6E-05	-0.5	3.3E-01	0.4	3.3E-01	-0.3	5.9E-01
ENSMUST00000021665	visual system homeobox 2 [Source:MGI Symbol;Acc:MGI:88401]	Q80WF9	Q61412	8.2	1.4E-02	6.1	1.5E-04	-0.9	4.2E-01	0.4	4.9E-01
ENSMUST00000021666	ATP-binding cassette, sub-family D (ALD), member 4 [Source:MGI Symbol;Acc:MGI:1349217]		O89016	2.3	1.4E-03	-0.5	4.9E-01	0.5	3.1E-01	-0.4	5.4E-01
ENSMUST00000021667	iron-sulfur cluster assembly 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1921566]		Q9DCB8	-3.5	1.1E-04	-2.1	1.3E-02	0.3	4.1E-01	0.0	9.6E-01
ENSMUST00000021668	Niemann-Pick type C2 [Source:MGI Symbol;Acc:MGI:1915213]		Q9Z0J0	-4.8	4.8E-06	-5.6	5.4E-03	-2.7	6.4E-03	-1.5	4.2E-01
ENSMUST00000021669	F1 small subunit (SSU) processome component homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:19209		Q9CTH6	-5.4	4.4E-04	-3.3	2.8E-03	0.3	5.8E-01	0.0	9.5E-01
ENSMUST00000021670	YLP motif containing 1 [Source:MGI Symbol;Acc:MGI:1926195]	D3YWX2		6.2	3.2E-03	8.2	1.3E-03	-0.8	6.9E-01	-0.7	4.9E-01
ENSMUST00000021611	pitrilysin metallepetidase 1 [Source:MGI Symbol;Acc:MGI:1916867]		Q8K411	0.7	1.6E-01	-0.1	8.1E-01	-1.3	1.2E-02	-0.4	4.1E-01
ENSMUST00000021676	RIKEN cDNA 0610007P14 gene [Source:MGI Symbol;Acc:MGI:1915571]		Q9ERY9	-3.4	1.6E-04	-6.0	4.3E-04	0.4	3.7E-01	-1.3	3.2E-01
ENSMUST00000021681	vasohibin 1 [Source:MGI Symbol;Acc:MGI:2442543]		Q8C1W1	6.5	5.7E-05	7.2	1.6E-03	0.1	9.7E-01	-1.4	1.6E-01
ENSMUST00000021682	angel homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1915987]		Q8VCU0	4.0	2.5E-04	4.8	3.0E-04	-2.8	1.9E-02	-0.9	1.7E-01
ENSMUST00000021634	aldo-keto reductase family 1, member C13 [Source:MGI Symbol;Acc:MGI:1351662]		Q8VC28	-0.6	4.9E-01	-2.1	3.9E-02	-2.4	8.4E-03	-0.8	3.7E-01
ENSMUST00000021684	cytochrome P450, family 46, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1341877]	Q3US73	Q9WVK8	7.8	5.7E-05	6.1	1.0E-03	-0.2	8.6E-01	0.3	7.5E-01
ENSMUST00000021685	hedgehog interacting protein-like 1 [Source:MGI Symbol;Acc:MGI:1919265]		Q14DK5	6.9	9.5E-05	6.4	2.1E-04	-0.5	6.3E-01	0.3	5.8E-01
ENSMUST00000021691	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase [Source:MGI Symbol;Acc:MGI:1917309]		Q8R2F2	5.8	8.8E-04	1.6	2.7E-02	-1.5	2.3E-02	0.2	6.8E-01
ENSMUST00000021646	papilin, proteoglycan-like sulfated glycoprotein [Source:MGI Symbol;Acc:MGI:2386139]		Q9EPX2	4.0	7.7E-02	6.2	9.4E-03	-2.5	2.7E-01	-4.7	5.7E-03
ENSMUST00000021647	numb gene homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:107423]		Q9QZS3	1.5	5.3E-01	1.5	5.7E-01	-0.4	8.4E-01	-0.5	8.5E-01
ENSMUST00000021692	YY1 transcription factor [Source:MGI Symbol;Acc:MGI:99150]		Q00899	-4.0	1.1E-04	4.0	1.7E-02	0.4	7.3E-01	1.1	2.7E-01
ENSMUST00000021693	er family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29 [Source:MGI Symbol;Acc:MG		Q8BL03	2.4	5.7E-03	5.1	1.7E-03	-0.9	5.0E-01	0.2	8.2E-01
ENSMUST00000021698	heat shock protein 90, alpha (cytosolic), class A member 1 [Source:MGI Symbol;Acc:MGI:96250]	Q80Y52	P07901	-7.2	3.0E-05	7.3	1.0E-04	-0.5	6.6E-01	-0.7	2.8E-01
ENSMUST00000021662	ectonucleoside triphosphate diphosphohydrolase 5 [Source:MGI Symbol;Acc:MGI:1321385]		Q9WUZ9	-3.0	1.8E-01	7.5	1.7E-02	4.5	8.9E-02	-6.0	1.4E-02
ENSMUST00000021707	amnionless [Source:MGI Symbol;Acc:MGI:1934943]		Q99JB7	4.7	2.2E-03	9.1	1.1E-02	-0.9	7.9E-01	-1.7	2.6E-01
ENSMUST00000021719	RIKEN cDNA 2010107E04 gene [Source:MGI Symbol;Acc:MGI:1917507]		P56379	-7.3	8.3E-06	2.4	4.8E-03	0.3	5.8E-01	0.1	7.9E-01
ENSMUST00000021726	adenylosuccinate synthetase like 1 [Source:MGI Symbol;Acc:MGI:87947]	Q3UBP0	P28650	-6.9	1.4E-03	-2.9	1.5E-03	-0.2	6.2E-01	-0.8	2.6E-01
ENSMUST00000021728	SIVA1, apoptosis-inducing factor [Source:MGI Symbol;Acc:MGI:1353606]		O54926	-4.8	2.6E-04	-4.6	4.3E-05	-0.1	7.3E-01	-0.3	6.2E-01
ENSMUST00000021734	guanine nucleotide binding protein (G protein), gamma 4 [Source:MGI Symbol;Acc:MGI:102703]		P50153	4.5	6.1E-05	-4.2	4.8E-03	-0.9	1.9E-01	-2.1	1.2E-01
ENSMUST00000021738	G protein-coupled receptor 137B [Source:MGI Symbol;Acc:MGI:1891463]			-2.3	1.3E-03	7.1	6.7E-03	1.3	5.2E-01	0.3	8.0E-01
ENSMUST00000021674	FBJ osteosarcoma oncogene [Source:MGI Symbol;Acc:MGI:95574]		P01101	-4.9	7.8E-02	-4.2	2.5E-01	0.8	6.5E-01	0.0	1.0E+00
ENSMUST00000021750	ryanodine receptor 2, cardiac [Source:MGI Symbol;Acc:MGI:99685]		E9Q401	8.7	8.0E-06	-2.8	1.1E-03	-0.7	8.0E-02	-1.3	6.6E-02
ENSMUST00000021770	secretagogin, EF-hand calcium binding protein [Source:MGI Symbol;Acc:MGI:2384873]		Q91WD9	6.5	2.2E-04	6.9	2.6E-04	0.0	9.8E-01	-0.4	5.7E-01
ENSMUST00000021773	glycosylphosphatidylinositol specific phospholipase D1 [Source:MGI Symbol;Acc:MGI:106604]	Q8VCU2		-1.4	8.2E-03	4.4	4.7E-04	0.4	6.2E-01	-0.1	8.9E-01
ENSMUST00000021784	interferon regulatory factor 4 [Source:MGI Symbol;Acc:MGI:1096873]	Q5SUZ4	Q64287	2.0	1.3E-02	5.2	5.3E-04	-2.2	7.9E-02	0.3	6.2E-01
ENSMUST00000021785	exocyst complex component 2 [Source:MGI Symbol;Acc:MGI:1913732]		Q9D4H1	-4.5	5.5E-03	6.8	2.0E-04	-0.9	4.7E-01	-0.8	2.5E-01
ENSMUST00000021787	transcription factor AP-2, alpha [Source:MGI Symbol;Acc:MGI:104671]	Q8BPN4		8.4	3.3E-03	6.1	1.1E-03	-0.5	7.5E-01	-0.7	3.4E-01
ENSMUST00000021790	transmembrane protein 14C [Source:MGI Symbol;Acc:MGI:1913404]		Q9CQN6	-5.5	3.7E-05	-2.8	6.2E-03	1.4	1.1E-02	0.2	8.0E-01
ENSMUST00000021791	glial cells missing homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1861438]			9.3	5.3E-06	3.1	4.9E-03	0.8	3.2E-01	0.1	9.2E-01
ENSMUST00000021794	eural precursor cell expressed, developmentally down-regulated gene 9 [Source:MGI Symbol;Acc:MGI:97302		O35177	-3.9	7.0E-06	-9.4	3.2E-04	-0.8	9.0E-02	1.4	4.2E-01
ENSMUST00000021796	endothelin 1 [Source:MGI Symbol;Acc:MGI:95283]	Q544E0	P22387	7.0	5.1E-05	4.8	1.5E-04	-0.2	7.3E-01	-0.1	8.9E-01
ENSMUST00000021706	TNF receptor-associated factor 3 [Source:MGI Symbol;Acc:MGI:108041]		Q60803	-3.3	1.3E-01	-3.7	3.8E-01	2.1	3.4E-01	2.5	5.3E-01
ENSMUST00000021800	mitochondrial calcium uniporter regulator 1 [Source:MGI Symbol;Acc:MGI:1923387]		Q9CXD6	-1.9	2.5E-03	4.4	1.4E-02	-0.2	9.1E-01	0.1	9.1E-01
ENSMUST00000021714	zinc finger, FYVE domain containing 21 [Source:MGI Symbol;Acc:MGI:1915770]		Q8VCM3	0.5	3.5E-01	0.4	5.5E-01	-0.3	4.9E-01	-0.2	7.1E-01
ENSMUST00000021715	-ray repair complementing defective repair in Chinese hamster cells 3 [Source:MGI Symbol;Acc:MGI:192158		Q9CXE6	2.4	7.6E-02	-0.4	8.2E-01	-0.6	6.5E-01	2.2	1.5E-01
ENSMUST00000021802	CAP, adenylate cyclase-associated protein, 2 (yeast) [Source:MGI Symbol;Acc:MGI:1914502]		Q9CYT6	7.4	2.0E-04	-6.2	3.7E-05	-0.5	2.1E-01	-1.6	1.3E-01
ENSMUST00000021803	nucleoporin 153 [Source:MGI Symbol;Acc:MGI:2385621]	E9Q3G8		-3.6	1.3E-05	-5.1	2.0E-02	1.0	3.0E-01	-0.8	7.1E-01
ENSMUST00000021807	DEK oncogene (DNA binding) [Source:MGI Symbol;Acc:MGI:1926209]		Q7TNV0	-6.6	2.8E-04	-3.2	5.2E-03	0.1	8.1E-01	-1.5	1.5E-01
ENSMUST00000021729	G protein-coupled receptor 132 [Source:MGI Symbol;Acc:MGI:1890220]		Q9Z282	-0.1	9.5E-01	-0.2	8.4E-01	0.1	9.1E-01	0.3	8.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000021813	BarH-like homeobox 1 [Source:MGI Symbol;Acc:MGI:103124]		Q9ER42	6.3	3.0E-04	4.7	1.4E-04	0.1	8.7E-01	-0.2	7.7E-01
ENSMUST00000021828	nucleoredoxin-like 2 [Source:MGI Symbol;Acc:MGI:1922374]		Q9D531	6.2	8.8E-04	-1.8	2.2E-02	0.3	4.6E-01	-0.2	7.1E-01
ENSMUST00000021844	receptor (TNFRSF)-interacting serine-threonine kinase 1 [Source:MGI Symbol;Acc:MGI:108212]		Q60855	-8.3	1.2E-05	7.7	5.3E-05	-0.9	4.7E-01	0.1	8.7E-01
ENSMUST00000021757	acyloxyacyl hydrolase [Source:MGI Symbol;Acc:MGI:1350928]		O35298	1.0	1.5E-01	1.2	1.6E-01	0.3	6.4E-01	0.0	9.7E-01
ENSMUST00000021761	tripartite motif-containing 27 [Source:MGI Symbol;Acc:MGI:97904]		Q62158	0.9	9.9E-02	1.6	3.7E-02	1.2	4.8E-02	0.5	4.3E-01
ENSMUST00000021769	solute carrier family 17 (sodium phosphate), member 4 [Source:MGI Symbol;Acc:MGI:2442850]	A0A044PY53		3.6	8.8E-02	2.0	4.2E-01	-0.5	8.3E-01	1.1	5.7E-01
ENSMUST00000021847	PX domain containing 1 [Source:MGI Symbol;Acc:MGI:1914145]		Q8JZU6	7.2	8.8E-03	5.6	1.1E-03	-0.5	7.0E-01	0.3	6.2E-01
ENSMUST00000021772	MRS2 magnesium homeostasis factor homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2685748]		Q5NCE8	-0.8	8.7E-02	-1.4	3.5E-02	0.1	7.9E-01	0.7	2.4E-01
ENSMUST00000021851	family with sequence similarity 217, member A [Source:MGI Symbol;Acc:MGI:1919114]	F8WGE0		7.9	2.9E-05	-0.9	1.2E-01	0.6	1.0E-01	0.2	7.0E-01
ENSMUST00000021853	enoyl-Coenzyme A delta isomerase 3 [Source:MGI Symbol;Acc:MGI:1916373]	Q78JN3		6.0	2.3E-03	1.3	1.1E-01	-0.9	2.0E-01	-0.2	7.7E-01
ENSMUST00000021854	enoyl-Coenzyme A delta isomerase 2 [Source:MGI Symbol;Acc:MGI:1346064]		Q9WUR2	-3.3	3.7E-03	-2.3	1.6E-01	0.5	5.5E-01	-1.7	3.0E-01
ENSMUST00000021860	lymphocyte antigen 86 [Source:MGI Symbol;Acc:MGI:1321404]		O88188	-2.9	2.7E-03	4.2	1.3E-01	-1.2	6.4E-01	3.0	1.0E-01
ENSMUST00000021866	RIO kinase 1 (yeast) [Source:MGI Symbol;Acc:MGI:1918590]		Q922Q2	-2.2	1.9E-03	-4.6	6.6E-04	0.6	1.8E-01	-0.2	8.0E-01
ENSMUST00000021880	cytotoxic T lymphocyte-associated protein 2 alpha [Source:MGI Symbol;Acc:MGI:88554]		P12399	3.3	7.7E-04	7.0	5.0E-05	-1.9	1.1E-01	0.5	3.8E-01
ENSMUST00000021793	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 [Source:MGI Symbol;Acc:MGI:185	Q543J1	Q9JLJ4	4.2	1.0E-01	-0.1	9.8E-01	-1.7	5.0E-01	2.6	3.8E-01
ENSMUST00000021891	cathepsin 8 [Source:MGI Symbol;Acc:MGI:1860275]	Q9JI81		9.6	4.4E-05	-3.5	1.2E-04	0.1	6.1E-01	-0.3	6.1E-01
ENSMUST00000021898	src homology 2 domain-containing transforming protein C3 [Source:MGI Symbol;Acc:MGI:106179]		Q61120	6.7	2.6E-04	7.7	7.4E-05	0.0	9.8E-01	-0.7	2.8E-01
ENSMUST00000021900	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D [Source:MGI		O09126	-5.9	4.0E-03	-1.3	6.7E-02	0.8	5.4E-02	0.2	7.2E-01
ENSMUST00000021903	growth arrest and DNA-damage-inducible 45 gamma [Source:MGI Symbol;Acc:MGI:1346325]	Q9R0S0		-4.1	1.7E-04	6.7	7.1E-04	-0.6	6.6E-01	0.0	9.7E-01
ENSMUST00000021907	fructose bisphosphatase 2 [Source:MGI Symbol;Acc:MGI:95491]	Q3TKP4	P70695	5.5	1.2E-03	-2.3	8.8E-04	0.4	1.7E-01	-0.8	1.3E-01
ENSMUST00000021911	RIKEN cDNA 2010111I01 gene [Source:MGI Symbol;Acc:MGI:1919311]	F8WGB2		-1.7	7.2E-03	-6.4	3.7E-03	0.7	2.5E-01	0.5	7.6E-01
ENSMUST00000021913	AU RNA binding protein/enoyl-coenzyme A hydratase [Source:MGI Symbol;Acc:MGI:1338011]			-7.9	1.6E-05	6.7	3.2E-04	-0.6	6.5E-01	-1.1	1.4E-01
ENSMUST00000021816	sushi domain containing 3 [Source:MGI Symbol;Acc:MGI:1913579]		Q9D176	1.2	6.1E-01	2.0	4.8E-01	0.3	9.1E-01	-0.5	8.5E-01
ENSMUST00000021817	inositol 1,3,4,5,6-pentakisphosphate 2-kinase [Source:MGI Symbol;Acc:MGI:1922928]		Q6P1C1	0.1	9.1E-01	0.6	3.1E-01	0.5	2.8E-01	-0.1	8.9E-01
ENSMUST00000021818	centromere protein P [Source:MGI Symbol;Acc:MGI:1913586]	B2RVI6	Q9CZ92	-0.5	5.4E-01	-0.4	6.6E-01	-0.7	3.8E-01	-0.7	4.0E-01
ENSMUST00000021824	nucleolar protein 8 [Source:MGI Symbol;Acc:MGI:1918180]	E9QKD1		-0.2	7.4E-01	-0.5	4.0E-01	-1.0	5.6E-02	-0.6	3.2E-01
ENSMUST00000021920	serine palmitoyltransferase, long chain base subunit 1 [Source:MGI Symbol;Acc:MGI:1099431]		O35704	-2.6	1.1E-04	5.9	1.6E-03	-0.9	5.3E-01	-0.6	4.7E-01
ENSMUST00000021832	Werner helicase interacting protein 1 [Source:MGI Symbol;Acc:MGI:1926153]		Q91XU0	-0.6	2.5E-01	-0.2	7.7E-01	0.5	2.8E-01	0.1	8.7E-01
ENSMUST00000021837	serine (or cysteine) peptidase inhibitor, clade B, member 9c [Source:MGI Symbol;Acc:MGI:894669]	I7HJI5		3.5	1.5E-01	5.1	5.6E-02	-0.3	9.0E-01	-2.0	2.1E-01
ENSMUST00000021843	NAD(P)H dehydrogenase, quinone 2 [Source:MGI Symbol;Acc:MGI:104513]		Q9JI75	-0.3	9.1E-01	0.7	8.7E-01	1.4	6.7E-01	0.4	9.0E-01
ENSMUST00000021922	msh homeobox 2 [Source:MGI Symbol;Acc:MGI:97169]	Q3UZH5	Q03358	8.3	1.2E-06	-6.2	1.5E-04	0.4	3.1E-01	-1.6	2.0E-01
ENSMUST00000021929	hyaluronic acid binding protein 4 [Source:MGI Symbol;Acc:MGI:1891713]	E9QKB2		1.7	2.4E-02	1.9	4.4E-01	-3.1	2.4E-01	2.3	1.9E-01
ENSMUST00000021932	dopamine receptor D1 [Source:MGI Symbol;Acc:MGI:99578]		Q61616	8.2	1.9E-05	6.6	1.3E-04	-1.5	2.3E-01	-0.2	7.6E-01
ENSMUST00000021933	cathepsin L [Source:MGI Symbol;Acc:MGI:88564]	Q543M3	P06797	-5.6	1.2E-05	3.6	5.7E-02	-0.5	7.9E-01	1.9	1.2E-01
ENSMUST00000021938	AhpC/TSA antioxidant enzyme domain containing 1 [Source:MGI Symbol;Acc:MGI:1913379]		Q9D1A0	-4.9	1.9E-05	-6.0	5.1E-03	-0.6	3.5E-01	2.0	2.3E-01
ENSMUST00000021857	phenylalanine-tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1917205]		Q99M01	-0.5	5.2E-01	-0.2	8.4E-01	-0.1	8.3E-01	-0.4	6.3E-01
ENSMUST00000021940	lectin, mannose-binding 2 [Source:MGI Symbol;Acc:MGI:1914140]		Q9DBH5	-4.0	4.9E-05	-4.2	7.7E-04	-2.1	1.8E-03	-0.8	3.7E-01
ENSMUST00000021864	signal sequence receptor, alpha [Source:MGI Symbol;Acc:MGI:105082]		Q9CY50	-1.0	3.7E-02	-0.6	2.5E-01	0.6	1.5E-01	0.3	6.1E-01
ENSMUST00000021941	Max dimerization protein 3 [Source:MGI Symbol;Acc:MGI:104987]		Q80US8	-3.1	2.7E-02	-2.2	6.8E-03	-0.2	5.9E-01	-0.2	7.5E-01
ENSMUST00000021870	solute carrier family 35, member B3 [Source:MGI Symbol;Acc:MGI:1913978]	F8WGD7		3.2	1.8E-01	4.3	1.9E-01	1.6	5.7E-01	0.5	8.3E-01
ENSMUST00000021942	PRELI domain containing 1 [Source:MGI Symbol;Acc:MGI:1913744]		Q8R107	-6.2	4.3E-06	0.5	4.8E-01	-2.9	1.6E-03	0.0	9.4E-01
ENSMUST00000021884	cytotoxic T lymphocyte-associated protein 2 beta [Source:MGI Symbol;Acc:MGI:88555]		P12400	-2.5	4.1E-02	-6.1	2.0E-03	-3.2	9.9E-04	0.4	8.1E-01
ENSMUST00000021948	coagulation factor XII (Hageman factor) [Source:MGI Symbol;Acc:MGI:1891012]		Q80YC5	2.2	1.7E-02	7.2	4.8E-04	-1.4	3.7E-01	1.0	1.8E-01
ENSMUST00000021956	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 [Source:MGI Symbol;Acc:MGI:1920185]		Q91VN6	-4.1	5.9E-05	7.6	1.8E-04	-0.5	7.0E-01	-1.4	5.9E-02
ENSMUST00000021957	family with sequence similarity 193, member B [Source:MGI Symbol;Acc:MGI:2385851]		Q3U2K0	-2.2	3.0E-02	-5.1	4.8E-02	1.4	1.7E-01	0.6	7.9E-01
ENSMUST00000021958	olamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2 [Source:MGI Symbol		Q9CZL5	-5.2	2.4E-04	-2.9	8.8E-03	1.5	1.4E-02	0.3	7.3E-01
ENSMUST00000021959	thioredoxin domain containing 15 [Source:MGI Symbol;Acc:MGI:1916922]		Q6P6J9	-3.2	1.4E-04	5.0	2.7E-03	-1.2	3.7E-01	-0.7	3.6E-01
ENSMUST00000021961	cation channel, sperm associated 3 [Source:MGI Symbol;Acc:MGI:1924106]	E0Z0E0	Q80W99	7.0	2.9E-03	-1.9	1.1E-02	-0.4	3.0E-01	-0.2	7.4E-01
ENSMUST00000021963	calcium modulating ligand [Source:MGI Symbol;Acc:MGI:104728]		P49070	-4.0	1.3E-03	-6.1	6.1E-04	0.9	6.5E-02	-0.9	5.2E-01
ENSMUST00000021918	receptor tyrosine kinase-like orphan receptor 2 [Source:MGI Symbol;Acc:MGI:1347521]		Q9Z138	2.8	5.3E-02	4.5	7.2E-03	-0.6	6.7E-01	-2.2	5.8E-02
ENSMUST00000021968	paired-like homeodomain transcription factor 1 [Source:MGI Symbol;Acc:MGI:107374]	Q3UQH0	P70314	7.7	4.8E-05	-1.5	1.2E-02	0.5	1.3E-01	-0.6	2.5E-01
ENSMUST00000021921	patched homolog 1 [Source:MGI Symbol;Acc:MGI:105373]		Q61115	6.9	5.6E-02	3.5	2.3E-01	-5.0	1.7E-01	-1.6	4.3E-01
ENSMUST00000021970	chemokine (C-X-C motif) ligand 14 [Source:MGI Symbol;Acc:MGI:1888514]		Q9WUQ5	5.2	6.9E-05	7.6	6.8E-06	-0.8	3.7E-01	-0.1	8.3E-01
ENSMUST00000021971	solute carrier family 25, member 48 [Source:MGI Symbol;Acc:MGI:2145373]		Q8BW66	7.8	1.3E-05	1.6	6.7E-02	-0.3	6.7E-01	-0.2	7.7E-01
ENSMUST00000021930	sideroflexin 1 [Source:MGI Symbol;Acc:MGI:2137677]		Q99JR1	-0.2	6.8E-01	0.4	5.4E-01	-0.1	8.0E-01	-0.8	2.5E-01
ENSMUST00000021990	phosphatidylserine synthase 1 [Source:MGI Symbol;Acc:MGI:1276575]		Q99LH2	-2.7	1.6E-04	7.1	7.7E-05	-1.5	2.3E-01	-0.3	5.4E-01
ENSMUST00000021991	mitochondrial transcription termination factor 3 [Source:MGI Symbol;Acc:MGI:1913660]		Q8R3J4	-5.2	4.0E-04	-7.6	6.3E-06	-2.6	4.5E-05	-0.6	4.8E-01
ENSMUST00000021937	zinc finger protein 346 [Source:MGI Symbol;Acc:MGI:1349417]		Q9R0B7	0.2	7.6E-01	0.9	2.5E-01	0.7	2.2E-01	0.0	9.8E-01
ENSMUST00000021993	ubiquinol-cytochrome c reductase binding protein [Source:MGI Symbol;Acc:MGI:1914780]	Q9CQB4		-6.0	8.3E-06	-3.8	5.0E-04	0.0	9.9E-01	-1.1	1.6E-01
ENSMUST00000021939	cyclin-dependent kinase 20 [Source:MGI Symbol;Acc:MGI:2145349]		Q9JHU3	-0.5	3.6E-01	1.1	1.8E-01	1.0	9.5E-02	-0.6	4.1E-01
ENSMUST00000022007	RIKEN cDNA 1700001L19 gene [Source:MGI Symbol;Acc:MGI:1916565]		Q9DAR0	5.9	1.8E-03	-3.1	1.6E-03	0.8	6.0E-02	0.0	9.8E-01
ENSMUST00000022009	centrin 3 [Source:MGI Symbol;Acc:MGI:1097706]	Q545L8	O35648	-5.5	3.0E-05	0.9	5.4E-01	1.9	9.8E-02	-2.1	1.5E-01
ENSMUST00000022013	adenylate cyclase 2 [Source:MGI Symbol;Acc:MGI:99676]	Q3V1Q3		6.8	2.8E-04	-4.8	1.1E-04	0.7	8.1E-02	-0.7	3.9E-01
ENSMUST00000022028	RIKEN cDNA 1700067P10 gene [Source:MGI Symbol;Acc:MGI:1915474]	G3X8U2		6.3	3.2E-04	3.2	7.7E-03	0.8	3.5E-01	-0.2	7.7E-01
ENSMUST00000021950	drebrin 1 [Source:MGI Symbol;Acc:MGI:1931838]		Q9QXS6	2.5	1.8E-01	5.2	1.3E-02	-0.6	7.5E-01	-3.3	3.3E-02
ENSMUST00000022032	RIKEN cDNA 2210016F16 gene [Source:MGI Symbol;Acc:MGI:1917403]	G3X8U3		1.8	9.3E-04	-3.5	9.8E-04	0.5	1.9E-01	-0.1	9.4E-01
ENSMUST00000022036	te carrier family 28 (sodium-coupled nucleoside transporter), member 3 [Source:MGI Symbol;Acc:MGI:21373		Q9ERH8	3.8	5.5E-05	-1.6	1.8E-01	0.4	5.7E-01	-0.2	8.7E-01
ENSMUST00000022038	N(alpha)-acetyltransferase 35, NatC auxiliary subunit [Source:MGI Symbol;Acc:MGI:1925939]		Q6PHQ8	-5.5	6.3E-05	-4.1	3.6E-03	0.0	9.5E-01	-1.0	4.0E-01
ENSMUST00000022039	golgi membrane protein 1 [Source:MGI Symbol;Acc:MGI:1917329]		Q91XA2	-2.7	2.1E-02	-3.1	1.1E-03	0.4	3.4E-01	0.3	6.8E-01
ENSMUST00000022040	ATP/GTP binding protein 1 [Source:MGI Symbol;Acc:MGI:2159437]		Q641K1	-7.6	4.5E-05	3.2	1.2E-01	-1.5	4.6E-01	2.3	1.0E-01
ENSMUST00000022048	solute carrier family 6 (neurotransmitter transporter), member 19 [Source:MGI Symbol;Acc:MGI:1921588]	Q3KN89	Q9D687	6.0	9.8E-04	-1.7	4.8E-02	-0.3	5.8E-01	-2.6	2.3E-02
ENSMUST00000022051	naked cuticle 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1919543]		Q8VE28	8.7	1.3E-05	4.1	4.3E-04	-4.2	2.5E-03	-0.6	3.5E-01
ENSMUST00000022057	tubulin polymerization promoting protein [Source:MGI Symbol;Acc:MGI:1920198]	Q3URG1	Q7TQD2	2.7	1.6E-03	0.7	2.3E-01	-4.9	6.1E-05	-0.5	4.2E-01
ENSMUST00000022059	aryl-hydrocarbon receptor repressor [Source:MGI Symbol;Acc:MGI:1333776]			4.9	1.3E-03	5.2	5.8E-05	-3.2	5.8E-03	-0.6	2.4E-01
ENSMUST00000022060	programmed cell death 6 [Source:MGI Symbol;Acc:MGI:109283]		P12815	-5.4	4.6E-06	-1.6	1.5E-02	0.8	3.9E-02	-0.4	5.2E-01
ENSMUST00000022062	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) [Source:MGI Symbol;Acc:MGI:1914195]		Q8K2B3	-4.6	1.2E-04	-4.0	8.1E-03	0.2	6.6E-01	-0.9	4.8E-01
ENSMUST00000022063	coiled-coil domain containing 127 [Source:MGI Symbol;Acc:MGI:1914683]		Q3TC33	1.5	5.7E-03	-6.2	2.9E-04	0.1	8.8E-01	0.3	8.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000022064	leucine rich repeat containing 14B [Source:MGI Symbol;Acc:MGI:2145269]		Q3UJB3	7.3	1.2E-03	6.1	2.3E-03	-0.5	7.4E-01	-0.8	3.9E-01
ENSMUST00000022075	proprotein convertase subtilisin/kexin type 1 [Source:MGI Symbol;Acc:MGI:97511]	Q32MU0	P63239	6.6	1.4E-04	-6.3	2.3E-04	-0.5	2.3E-01	0.3	7.7E-01
ENSMUST00000022078	Rho-related BTB domain containing 3 [Source:MGI Symbol;Acc:MGI:1920546]		Q9CTN4	4.7	3.7E-04	5.7	7.5E-04	-1.7	2.3E-01	-0.6	4.4E-01
ENSMUST00000022023	transient receptor potential cation channel, subfamily C, member 7 [Source:MGI Symbol;Acc:MGI:1349470]	Q0VFY2	Q9WVC5	5.0	6.2E-02	2.3	5.1E-01	-0.3	9.0E-01	2.4	3.8E-01
ENSMUST00000022082	glutaredoxin [Source:MGI Symbol;Acc:MGI:2135625]	Q3U6L3	Q9QUH0	-8.3	4.4E-08	5.3	1.8E-03	-0.6	6.8E-01	0.4	5.6E-01
ENSMUST00000022087	NOL1/NOP2/Sun domain family member 2 [Source:MGI Symbol;Acc:MGI:107252]		Q1HFZ0	6.6	1.0E-04	2.9	2.7E-04	0.8	7.5E-02	-0.2	6.1E-01
ENSMUST00000022089	mediator complex subunit 10 [Source:MGI Symbol;Acc:MGI:106331]		Q9CXU0	-3.7	4.6E-05	4.8	8.1E-05	1.1	1.1E-01	0.1	7.8E-01
ENSMUST00000022095	Iroquois related homeobox 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1355275]		Q9QY61	7.1	1.1E-02	-4.1	1.4E-03	0.3	5.8E-01	-1.1	2.7E-01
ENSMUST00000022097	NADH dehydrogenase (ubiquinone) Fe-S protein 6 [Source:MGI Symbol;Acc:MGI:107932]		P52503	-5.6	2.7E-04	-3.6	2.9E-02	0.5	4.9E-01	1.4	3.3E-01
ENSMUST00000022098	mitochondrial ribosomal protein L36 [Source:MGI Symbol;Acc:MGI:2137228]		Q99N90	-3.4	6.5E-05	-5.6	2.1E-03	1.1	4.2E-02	-0.8	5.7E-01
ENSMUST00000022100	lute carrier family 6 (neurotransmitter transporter, dopamine), member 3 [Source:MGI Symbol;Acc:MGI:9486		Q61327	8.1	1.0E-05	6.3	1.3E-03	-0.5	7.6E-01	-0.7	3.8E-01
ENSMUST00000022102	CLPTM1-like [Source:MGI Symbol;Acc:MGI:2442892]		Q8BXA5	-4.1	1.1E-04	8.1	4.8E-05	-0.6	6.2E-01	0.0	9.5E-01
ENSMUST00000022053	thyroid hormone receptor interactor 13 [Source:MGI Symbol;Acc:MGI:1916966]		Q3UA06	0.6	2.6E-01	1.9	1.5E-02	0.6	2.6E-01	-0.7	2.3E-01
ENSMUST00000022104	telomerase reverse transcriptase [Source:MGI Symbol;Acc:MGI:1202709]		O70372	6.6	9.5E-06	1.9	2.6E-02	-0.7	2.7E-01	0.0	9.9E-01
ENSMUST00000022108	hyaluronan and proteoglycan link protein 1 [Source:MGI Symbol;Acc:MGI:1337006]		Q9QUP5	9.9	5.4E-05	4.8	2.3E-03	-0.5	6.5E-01	-0.4	6.4E-01
ENSMUST00000022115	-ray repair complementing defective repair in Chinese hamster cells 4 [Source:MGI Symbol;Acc:MGI:133379			-6.1	2.2E-04	-5.5	2.5E-05	-0.4	1.8E-01	-0.3	6.4E-01
ENSMUST00000022119	autophagy related 10 [Source:MGI Symbol;Acc:MGI:1914045]			1.5	3.0E-02	-5.7	4.7E-04	0.3	5.0E-01	1.4	2.2E-01
ENSMUST00000022120	acyl-CoA thioesterase 12 [Source:MGI Symbol;Acc:MGI:1921406]	A2RSC2	Q9DBK0	6.3	1.8E-04	1.6	1.1E-02	-0.1	8.0E-01	-0.2	6.1E-01
ENSMUST00000022121	zinc finger, CCHC domain containing 9 [Source:MGI Symbol;Acc:MGI:1916335]		Q8R1J3	-5.6	2.2E-03	5.1	1.8E-02	-0.7	7.2E-01	1.5	2.0E-01
ENSMUST00000022122	creatine kinase, mitochondrial 2 [Source:MGI Symbol;Acc:MGI:1923972]		Q6P8J7	7.0	7.8E-04	6.6	2.9E-04	-0.5	7.1E-01	-0.4	5.2E-01
ENSMUST00000022135	adenylate kinase 6 [Source:MGI Symbol;Acc:MGI:5510732]		Q8VCP8	-2.9	2.1E-03	2.5	2.6E-02	-1.6	9.2E-02	0.5	5.0E-01
ENSMUST00000022137	MARVEL (membrane-associating) domain containing 2 [Source:MGI Symbol;Acc:MGI:2446166]	A1BQX3	Q3UZP0	6.4	8.9E-04	-8.4	3.8E-07	-0.4	1.0E-01	-0.3	6.1E-01
ENSMUST00000022140	occludin [Source:MGI Symbol;Acc:MGI:106183]	B2RS24	Q61146	5.8	1.6E-02	5.5	1.8E-03	-0.9	4.9E-01	0.2	8.3E-01
ENSMUST00000022142	NLR family, apoptosis inhibitory protein 1 [Source:MGI Symbol;Acc:MGI:1298223]		Q9QWK5	4.6	2.6E-05	-3.6	3.3E-04	-0.2	5.2E-01	-0.4	5.4E-01
ENSMUST00000022147	survival motor neuron 1 [Source:MGI Symbol;Acc:MGI:109257]	Q549F9	P97801	-6.3	8.7E-05	2.6	4.0E-01	-0.9	7.5E-01	3.6	1.4E-01
ENSMUST00000022148	methylcrotonoyl-Coenzyme A carboxylase 2 (beta) [Source:MGI Symbol;Acc:MGI:1925288]	B2RUK5	Q3ULD5	3.0	7.6E-04	-6.5	1.2E-03	-0.6	2.7E-01	0.3	8.3E-01
ENSMUST00000022153	pentatricopeptide repeat domain 2 [Source:MGI Symbol;Acc:MGI:1916177]		Q8R3K3	-1.8	2.6E-03	-3.6	2.9E-04	0.3	4.6E-01	0.4	5.0E-01
ENSMUST00000022099	lysophosphatidylcholine acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2384812]		Q3TFD2	-2.6	7.7E-02	-1.3	4.9E-01	1.5	2.3E-01	0.2	9.1E-01
ENSMUST00000022164	ankyrin repeat, family A (RFXANK-like), 2 [Source:MGI Symbol;Acc:MGI:1915808]		Q99PE2	-6.0	3.3E-05	7.7	3.1E-05	-0.4	6.9E-01	0.0	9.6E-01
ENSMUST00000022169	hexosaminidase B [Source:MGI Symbol;Acc:MGI:96074]	Q3TXR9	P20060	-5.3	2.9E-06	-2.7	6.7E-03	1.2	2.3E-02	-0.2	8.4E-01
ENSMUST00000022172	polymerase (DNA directed), kappa [Source:MGI Symbol;Acc:MGI:1349767]		Q9QUG2	-1.7	6.5E-03	5.9	1.2E-04	-0.8	4.0E-01	-0.1	8.6E-01
ENSMUST00000022176	3-hydroxy-3-methylglutaryl-Coenzyme A reductase [Source:MGI Symbol;Acc:MGI:96159]		Q01237	-4.2	2.1E-03	8.4	3.7E-04	-0.9	6.2E-01	0.6	4.4E-01
ENSMUST00000022185	coagulation factor II (thrombin) receptor-like 1 [Source:MGI Symbol;Acc:MGI:101910]	Q3TU81	P55086	5.4	2.4E-04	-5.5	1.7E-03	-0.4	4.9E-01	-1.0	4.9E-01
ENSMUST00000022189	angiogenic factor with G patch and FHA domains 1 [Source:MGI Symbol;Acc:MGI:1913799]		Q7TN31	-4.7	5.1E-05	0.5	4.9E-01	-0.2	7.4E-01	0.8	2.8E-01
ENSMUST00000022195	orthopedia homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:99835]		O09113	9.9	3.6E-05	6.7	2.2E-04	-0.4	7.2E-01	-0.8	2.3E-01
ENSMUST00000022196	adaptor-related protein complex 3, beta 1 subunit [Source:MGI Symbol;Acc:MGI:1333879]		Q9Z1T1	-3.7	6.7E-06	-5.4	1.8E-03	-0.3	6.9E-01	-0.4	7.8E-01
ENSMUST00000022197	secretory carrier membrane protein 1 [Source:MGI Symbol;Acc:MGI:1349480]	Q3TD71	Q8K021	-2.8	2.3E-04	6.0	3.5E-03	-0.7	6.7E-01	0.3	7.7E-01
ENSMUST00000022124	CD180 antigen [Source:MGI Symbol;Acc:MGI:1194924]		Q62192	-0.6	2.6E-01	-0.9	2.2E-01	-0.2	6.1E-01	0.0	1.0E+00
ENSMUST00000022204	kinesin family member 2A [Source:MGI Symbol;Acc:MGI:108390]		P28740	-3.6	7.0E-04	-3.9	2.7E-03	-0.8	1.5E-01	0.2	8.7E-01
ENSMUST00000022136	RAD17 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1333807]	Q3UYY2	Q6NXW6	-0.1	9.7E-01	-1.8	4.4E-01	-2.0	2.5E-01	-0.3	8.9E-01
ENSMUST00000022207	ELOVL family member 7, elongation of long chain fatty acids (yeast) [Source:MGI Symbol;Acc:MGI:1921809		Q9D2Y9	5.8	2.2E-05	5.3	3.3E-03	-2.1	1.8E-01	-1.0	2.9E-01
ENSMUST00000022212	polo-like kinase 2 [Source:MGI Symbol;Acc:MGI:1099790]	Q548A9	P53351	-1.7	3.4E-02	6.7	1.2E-02	-0.6	7.9E-01	-1.5	2.5E-01
ENSMUST00000022213	thrombospondin 4 [Source:MGI Symbol;Acc:MGI:1101779]	B2RTL6	Q9Z1T2	5.8	2.1E-04	2.4	2.7E-03	-2.4	2.7E-03	-0.2	6.9E-01
ENSMUST00000022217	zinc finger, FYVE domain containing 16 [Source:MGI Symbol;Acc:MGI:2145181]		Q80U44	-1.7	1.7E-02	-4.6	2.4E-03	1.2	3.6E-02	-0.5	7.1E-01
ENSMUST00000022220	mutS homolog 3 (E. coli) [Source:MGI Symbol;Acc:MGI:109519]	E9QPY6		-3.4	1.6E-02	2.4	9.1E-03	-0.3	6.2E-01	0.3	6.1E-01
ENSMUST00000022222	Erbb2 interacting protein [Source:MGI Symbol;Acc:MGI:1890169]		Q80TH2	-3.3	1.8E-02	-0.9	1.1E-01	0.0	9.1E-01	-0.9	1.1E-01
ENSMUST00000022163	basic transcription factor 3 [Source:MGI Symbol;Acc:MGI:1202875]		Q64152	-0.1	9.5E-01	-0.2	8.8E-01	-1.2	2.8E-01	-1.1	4.1E-01
ENSMUST00000022225	tripartite motif-containing 23 [Source:MGI Symbol;Acc:MGI:1933161]		Q8BGX0	-4.9	4.0E-04	-4.5	1.4E-03	0.7	1.4E-01	-0.8	4.4E-01
ENSMUST00000022226	peptidylprolyl isomerase domain and WD repeat containing 1 [Source:MGI Symbol;Acc:MGI:2443069]		Q8CEC6	-2.6	3.8E-03	-4.3	9.1E-05	0.6	7.3E-02	-0.4	5.3E-01
ENSMUST00000022170	G elongation factor, mitochondrial 2 [Source:MGI Symbol;Acc:MGI:2444783]		Q8R2Q4	1.9	5.1E-01	-1.4	6.9E-01	-3.8	1.8E-01	-0.5	8.8E-01
ENSMUST00000022228	CWC27 spliceosome-associated protein homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914535]		Q3TKY6	-2.4	8.4E-03	-1.2	8.3E-02	0.4	3.7E-01	-0.1	8.6E-01
ENSMUST00000022230	plicing regulatory glutamine/lysine-rich protein 1interacting protein 1 [Source:MGI Symbol;Acc:MGI:1914538		Q4V9W2	-2.8	3.2E-02	-2.5	6.4E-02	0.4	5.5E-01	-1.3	3.3E-01
ENSMUST00000022182	coagulation factor II (thrombin) receptor-like 2 [Source:MGI Symbol;Acc:MGI:1298208]		O08675	-0.3	4.9E-01	1.3	5.4E-02	0.9	6.8E-02	-0.7	2.3E-01
ENSMUST00000022232	RIKEN cDNA 4933425L06 gene [Source:MGI Symbol;Acc:MGI:1914013]	Q9D3Z8		6.3	1.1E-04	3.4	8.7E-03	-1.2	2.4E-01	0.8	3.4E-01
ENSMUST00000022235	5-hydroxytryptamine (serotonin) receptor 1A [Source:MGI Symbol;Acc:MGI:96273]		Q64264	8.2	1.3E-05	-2.5	8.1E-03	0.5	2.4E-01	-1.6	7.1E-02
ENSMUST00000022239	poly (ADP-ribose) polymerase family, member 8 [Source:MGI Symbol;Acc:MGI:1098713]	F8WIK2		-2.7	3.7E-03	8.4	1.7E-04	-0.4	8.2E-01	1.2	1.2E-01
ENSMUST00000022242	embigin [Source:MGI Symbol;Acc:MGI:95321]		P21995	-8.3	3.7E-06	-2.6	4.9E-04	0.8	1.5E-02	-0.3	5.8E-01
ENSMUST00000022245	mitochondrial ribosomal protein S30 [Source:MGI Symbol;Acc:MGI:1926237]		Q9D0G0	-3.2	1.2E-03	-2.7	2.9E-03	0.9	4.5E-02	0.8	2.7E-01
ENSMUST00000022203	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913504]		Q9D0D4	0.8	3.0E-01	-0.3	7.1E-01	-1.6	2.9E-02	-0.6	4.3E-01
ENSMUST00000022246	fibroblast growth factor 10 [Source:MGI Symbol;Acc:MGI:1099809]		O35565	7.3	8.9E-05	-1.7	8.3E-02	1.0	8.1E-02	-0.9	3.3E-01
ENSMUST00000022256	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 [Source:MGI Symbol;Acc:MGI:1913663]		Q99JI4	-6.6	8.4E-05	3.8	8.9E-04	-1.3	1.3E-01	0.7	2.1E-01
ENSMUST00000022262	Fez family zinc finger 2 [Source:MGI Symbol;Acc:MGI:1859823]		Q9ESP5	7.5	9.3E-05	-1.4	1.1E-01	-0.2	7.6E-01	-0.4	6.4E-01
ENSMUST00000022264	protein tyrosine phosphatase, receptor type, G [Source:MGI Symbol;Acc:MGI:97814]	F8VQD7		7.6	2.3E-05	8.2	5.1E-04	2.1	1.9E-01	-0.3	6.8E-01
ENSMUST00000022268	pyruvate dehydrogenase (lipoamide) beta [Source:MGI Symbol;Acc:MGI:1915513]		Q9D051	-3.4	1.8E-03	-0.5	5.1E-01	0.5	3.5E-01	-0.8	3.2E-01
ENSMUST00000022218	dihydrofolate reductase [Source:MGI Symbol;Acc:MGI:94890]	Q544T5	P00375	1.1	7.1E-02	0.8	3.0E-01	-0.3	5.5E-01	0.1	9.3E-01
ENSMUST00000022269	oncoprotein induced transcript 1 [Source:MGI Symbol;Acc:MGI:1201784]		P97805	9.4	6.3E-05	2.0	3.8E-01	6.1	4.4E-03	0.8	6.7E-01
ENSMUST00000022271	acyl-Coenzyme A oxidase 2, branched chain [Source:MGI Symbol;Acc:MGI:1934852]		Q9QXD1	-4.0	4.0E-03	-3.7	4.6E-02	-0.3	7.5E-01	0.1	9.4E-01
ENSMUST00000022272	potassium channel tetramerisation domain containing 6 [Source:MGI Symbol;Acc:MGI:1918643]	A2RS47	Q8BNL5	-3.8	1.0E-02	-5.3	2.7E-03	0.2	7.1E-01	0.7	6.4E-01
ENSMUST00000022281	superkiller viralicidic activity 2-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919448]		Q9CZU3	-3.2	9.2E-04	-3.1	5.2E-03	-0.3	5.3E-01	0.2	8.6E-01
ENSMUST00000022282	glutathione peroxidase 8 (putative) [Source:MGI Symbol;Acc:MGI:1916840]		Q9D7B7	2.6	1.5E-02	-2.8	7.4E-03	-1.2	5.6E-02	-0.7	4.4E-01
ENSMUST00000022286	NADH dehydrogenase (ubiquinone) Fe-S protein 4 [Source:MGI Symbol;Acc:MGI:1343135]	E9QPX3		-4.2	8.8E-05	-1.4	2.9E-01	-0.7	4.6E-01	-2.0	1.6E-01
ENSMUST00000022292	sterile alpha motif domain containing 8 [Source:MGI Symbol;Acc:MGI:1914880]	Q14AQ4	Q9DA37	-3.1	1.0E-02	6.3	1.9E-04	-0.5	6.3E-01	-0.6	3.4E-01
ENSMUST00000022293	voltage-dependent anion channel 2 [Source:MGI Symbol;Acc:MGI:106915]		Q60930	-7.4	3.7E-06	7.9	3.5E-05	-0.6	6.1E-01	-0.3	6.0E-01
ENSMUST00000022296	ubiquitin-conjugating enzyme E2E 1 [Source:MGI Symbol;Acc:MGI:107411]	Q541Z5	P52482	-3.2	5.6E-04	-2.0	3.7E-02	0.1	8.6E-01	-0.6	5.3E-01
ENSMUST00000022303	thyroid hormone receptor beta [Source:MGI Symbol;Acc:MGI:98743]		P37242	6.6	1.1E-04	-8.7	2.7E-05	0.2	5.5E-01	0.7	5.6E-01
ENSMUST00000022304	thyroid hormone receptor beta [Source:MGI Symbol;Acc:MGI:98743]		P37242	7.3	2.9E-03	-1.4	1.4E-01	1.1	9.1E-02	-0.7	4.5E-01
ENSMUST00000022310	N-glycanase 1 [Source:MGI Symbol;Acc:MGI:1913276]		Q9JI78	-5.3	1.0E-05	7.7	5.9E-04	0.5	7.3E-01	0.1	8.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000022311	3-oxoacyl-ACP synthase, mitochondrial [Source:MGI Symbol;Acc:MGI:1918397]		Q9D404	3.8	3.6E-04	-7.0	7.6E-04	-0.5	3.3E-01	-0.2	9.1E-01
ENSMUST00000022257	ataxin 7 [Source:MGI Symbol;Acc:MGI:2179277]		Q8R4I1	0.5	4.1E-01	0.5	5.7E-01	0.4	5.3E-01	0.4	5.7E-01
ENSMUST00000022322	glutamate dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:95753]		P26443	-4.8	1.5E-05	7.1	2.4E-04	-0.6	6.4E-01	-0.3	6.7E-01
ENSMUST00000022330	LIM domain binding 3 [Source:MGI Symbol;Acc:MGI:1344412]		Q9JKS4	7.5	6.6E-05	7.3	6.7E-05	-0.6	6.3E-01	-0.2	6.9E-01
ENSMUST00000022331	opsin 4 (melanopsin) [Source:MGI Symbol;Acc:MGI:1353425]		Q9QXZ9	7.6	1.3E-04	-4.5	2.3E-03	-0.1	8.5E-01	1.1	3.5E-01
ENSMUST00000022337	cadherin-related family member 1 [Source:MGI Symbol;Acc:MGI:2157782]		Q8VHP6	8.5	8.9E-06	7.5	7.8E-04	-0.8	6.3E-01	1.2	1.7E-01
ENSMUST00000022340	nidogen 2 [Source:MGI Symbol;Acc:MGI:1298229]		O88322	4.9	1.4E-05	-2.3	1.6E-01	1.7	5.6E-02	0.0	9.9E-01
ENSMUST00000022341	RIKEN cDNA 2700060E02 gene [Source:MGI Symbol;Acc:MGI:1915295]	Q4VA29	Q9CQE8	-4.9	7.5E-06	-0.5	7.1E-01	1.3	2.0E-01	-2.0	1.6E-01
ENSMUST00000022345	DnaJ (Hsp40) homolog, subfamily C, member 9 [Source:MGI Symbol;Acc:MGI:1915326]		Q91WN1	-2.4	1.6E-03	-3.3	2.7E-03	-0.5	2.5E-01	-0.4	6.5E-01
ENSMUST00000022353	MSS51 mitochondrial translational activator [Source:MGI Symbol;Acc:MGI:1922093]		Q9D5Z5	2.2	2.0E-02	-2.6	6.0E-03	-6.2	2.3E-05	-1.0	2.2E-01
ENSMUST00000022355	protein phosphatase 3, catalytic subunit, beta isoform [Source:MGI Symbol;Acc:MGI:107163]	G3X8U7		-2.9	5.8E-03	-4.0	4.7E-04	-0.7	9.1E-02	-0.9	2.7E-01
ENSMUST00000022287	follistatin [Source:MGI Symbol;Acc:MGI:95586]			0.6	2.9E-01	2.1	1.2E-02	1.2	6.6E-02	-0.4	5.1E-01
ENSMUST00000022358	zinc finger SWIM-type containing 8 [Source:MGI Symbol;Acc:MGI:1919156]		Q3UHH1	-1.5	1.6E-02	0.3	7.4E-01	0.4	5.7E-01	-3.0	1.4E-02
ENSMUST00000022369	vinculin [Source:MGI Symbol;Acc:MGI:98927]		Q64727	-3.5	3.2E-05	-4.8	5.9E-05	0.2	5.9E-01	-2.5	1.5E-02
ENSMUST00000022294	NFKB inhibitor interacting Ras-like protein 1 [Source:MGI Symbol;Acc:MGI:1916971]	F8WIJ8		-2.0	1.8E-01	-2.2	2.3E-01	-0.3	7.8E-01	-0.1	9.4E-01
ENSMUST00000022295				-2.6	7.9E-02	-1.4	3.4E-01	0.5	6.1E-01	-0.6	7.0E-01
ENSMUST00000022371	adaptor-related protein complex 3, mu 1 subunit [Source:MGI Symbol;Acc:MGI:1929212]	H7BWY2		-4.3	7.0E-04	-3.2	1.9E-03	-0.6	1.9E-01	-0.5	5.2E-01
ENSMUST00000022378	ERO1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1354385]	Q4FK57	Q8R180	-3.4	1.7E-04	6.0	2.8E-04	-1.1	3.3E-01	-0.5	4.3E-01
ENSMUST00000022380	proteasome (prosome, macropain) 26S subunit, ATPase, 6 [Source:MGI Symbol;Acc:MGI:1914339]	Q14AQ1	P62334	-6.5	5.9E-05	5.3	2.7E-02	-0.5	8.1E-01	1.4	2.6E-01
ENSMUST00000022416	annexin A11 [Source:MGI Symbol;Acc:MGI:108481]		P97384	-9.0	2.1E-05	-4.6	1.7E-04	0.1	7.9E-01	-0.6	4.6E-01
ENSMUST00000022419	peptidylprolyl isomerase F (cyclophilin F) [Source:MGI Symbol;Acc:MGI:2145814]		Q99KR7	-4.4	4.4E-04	5.0	4.0E-04	1.1	2.3E-01	-0.2	7.9E-01
ENSMUST00000022315	DPY30 domain containing 1 [Source:MGI Symbol;Acc:MGI:1916746]		Q9D9T0	2.8	9.6E-02	6.4	2.3E-03	-0.5	7.6E-01	-4.1	4.8E-03
ENSMUST00000022317	family with sequence similarity 213, member A [Source:MGI Symbol;Acc:MGI:1917814]		Q9CYH2	1.9	2.7E-01	-1.2	5.0E-01	-2.3	1.6E-01	0.8	6.2E-01
ENSMUST00000022428	ribonuclease, RNase A family 4 [Source:MGI Symbol;Acc:MGI:1926217]	Q8C7E4		-5.9	1.1E-03	-3.7	6.4E-04	0.9	3.5E-02	-0.2	7.7E-01
ENSMUST00000022327	LIM domain binding 3 [Source:MGI Symbol;Acc:MGI:1344412]		Q9JKS4	3.9	7.8E-02	1.8	4.8E-01	-0.5	8.3E-01	1.6	4.4E-01
ENSMUST00000022429	ADP-ribosylation factor 4 [Source:MGI Symbol;Acc:MGI:99433]	Q14BR4	P61750	-5.1	1.9E-04	7.3	1.5E-04	-0.7	6.1E-01	-0.5	4.7E-01
ENSMUST00000022433	dynein, axonemal, heavy chain 12 [Source:MGI Symbol;Acc:MGI:107720]	E9QPU2		6.3	1.8E-04	6.6	7.0E-04	-0.7	6.3E-01	0.3	6.7E-01
ENSMUST00000022446	ELL associated factor 1 [Source:MGI Symbol;Acc:MGI:1921677]		Q9D4C5	-1.7	3.8E-03	7.6	4.4E-05	-0.6	6.0E-01	0.2	6.6E-01
ENSMUST00000022450	family with sequence similarity 208, member A [Source:MGI Symbol;Acc:MGI:1921694]		Q69ZR9	1.0	2.3E-02	3.3	3.0E-04	-2.1	6.4E-03	-0.5	2.8E-01
ENSMUST00000022451	calpain 7 [Source:MGI Symbol;Acc:MGI:1338030]		Q9R1S8	-4.8	2.4E-04	-4.3	1.1E-04	-0.2	5.6E-01	-0.9	2.2E-01
ENSMUST00000022343	nudix (nucleoside diphosphate linked moiety X)-type motif 13 [Source:MGI Symbol;Acc:MGI:1914975]		Q8JZU0	-0.4	5.0E-01	0.9	2.4E-01	0.6	2.9E-01	-0.7	3.2E-01
ENSMUST00000022344	ecdysoneless homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1917851]		Q9CS74	0.1	7.5E-01	0.3	6.3E-01	0.1	8.7E-01	-0.1	8.9E-01
ENSMUST00000022458	Brca1 associated protein 1 [Source:MGI Symbol;Acc:MGI:1206586]		Q99PU7	-4.8	7.2E-04	-1.6	4.7E-02	0.6	1.6E-01	-0.2	7.7E-01
ENSMUST00000022349	cilia and flagella associated protein 70 [Source:MGI Symbol;Acc:MGI:1923920]	E9Q7X8		3.6	1.4E-01	4.9	7.3E-02	-0.4	8.8E-01	-1.7	3.0E-01
ENSMUST00000022460	:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15 [Source:MGI Symbol;Acc:MGI		Q9D2N8	9.4	5.1E-06	1.4	1.7E-01	0.3	7.3E-01	1.1	2.2E-01
ENSMUST00000022462	oxidoreductase NAD-binding domain containing 1 [Source:MGI Symbol;Acc:MGI:1916953]		Q8VE38	-4.6	3.6E-03	0.0	1.0E+00	0.3	6.0E-01	-2.6	2.2E-02
ENSMUST00000022356	ubiquitin specific peptidase 54 [Source:MGI Symbol;Acc:MGI:1926037]		Q8BL06	0.5	6.4E-01	-2.6	2.7E-01	0.8	4.8E-01	3.9	9.1E-02
ENSMUST00000022470	poly (ADP-ribose) glycohydrolase [Source:MGI Symbol;Acc:MGI:1347094]	G3X8U8		-4.2	2.4E-03	-0.5	4.7E-01	0.8	1.3E-01	-0.3	6.6E-01
ENSMUST00000022368	plasminogen activator, urokinase [Source:MGI Symbol;Acc:MGI:97611]	Q0VBA8	P06869	-0.2	5.2E-01	0.7	1.7E-01	0.5	1.9E-01	-0.4	3.4E-01
ENSMUST00000022480	oxoglutarate dehydrogenase-like [Source:MGI Symbol;Acc:MGI:3616088]	E9Q7L0		7.7	6.5E-06	-2.0	6.4E-03	1.2	4.9E-03	-0.2	7.1E-01
ENSMUST00000022496	karyopherin (importin) alpha 3 [Source:MGI Symbol;Acc:MGI:1100863]	Q543M7	O35344	-1.8	6.3E-03	-4.1	1.9E-03	-1.2	4.9E-02	-1.4	2.1E-01
ENSMUST00000022497	SPRY domain containing 7 [Source:MGI Symbol;Acc:MGI:1913924]		Q3TFQ1	3.0	2.3E-03	-1.9	2.5E-02	1.3	1.4E-02	-0.2	7.7E-01
ENSMUST00000022499	ribonuclease H2, subunit B [Source:MGI Symbol;Acc:MGI:1914403]		Q80ZV0	-2.4	8.3E-04	-6.2	3.5E-04	-0.3	5.7E-01	-0.6	6.4E-01
ENSMUST00000022386	sterile alpha motif domain containing 4 [Source:MGI Symbol;Acc:MGI:1921730]		Q8CBY1	4.6	7.5E-02	4.8	9.7E-02	-0.4	9.0E-01	-0.6	7.2E-01
ENSMUST00000022501	guanylate cyclase 1, soluble, beta 2 [Source:MGI Symbol;Acc:MGI:2660873]	Q8BXH3		7.4	1.3E-03	-6.1	1.4E-03	1.7	1.2E-02	-1.2	4.2E-01
ENSMUST00000022504	mitogen-activated protein kinase 8 [Source:MGI Symbol;Acc:MGI:1346861]	G3X8U9		-5.1	2.1E-04	-4.5	2.2E-03	0.3	5.3E-01	0.4	7.2E-01
ENSMUST00000022424	ribonuclease, RNase A family, 10 (non-active) [Source:MGI Symbol;Acc:MGI:1922269]	E9QPU5		4.3	1.7E-01	3.3	3.5E-01	-0.2	9.6E-01	0.9	6.9E-01
ENSMUST00000022507	paraspeckle protein 1 [Source:MGI Symbol;Acc:MGI:1913895]		Q8R326	-2.2	5.4E-03	-6.2	5.8E-03	-0.7	3.3E-01	-0.4	8.3E-01
ENSMUST00000022511	zinc finger, MYM-type 2 [Source:MGI Symbol;Acc:MGI:1923257]		Q9CU65	-3.5	7.9E-05	-1.3	1.2E-01	1.3	2.5E-02	-2.5	2.2E-02
ENSMUST00000022518	N-6 adenine-specific DNA methyltransferase 2 (putative) [Source:MGI Symbol;Acc:MGI:1915293]	A0A0D2X7Z2		-2.9	8.0E-04	5.0	5.4E-04	-2.1	8.6E-02	-0.8	2.5E-01
ENSMUST00000022519	annexin A8 [Source:MGI Symbol;Acc:MGI:1201374]		O35640	5.3	1.3E-03	-0.9	1.7E-01	1.1	1.9E-02	0.3	6.3E-01
ENSMUST00000022522	L-threonine dehydrogenase [Source:MGI Symbol;Acc:MGI:1926231]		Q8K3F7	7.4	3.3E-05	1.2	3.6E-02	0.8	7.5E-02	0.5	2.4E-01
ENSMUST00000022529	transketolase [Source:MGI Symbol;Acc:MGI:105992]		P40142	-7.4	1.1E-06	-6.1	2.3E-03	0.9	1.2E-01	2.2	1.7E-01
ENSMUST00000022531	large tumor suppressor 2 [Source:MGI Symbol;Acc:MGI:1354386]		Q7TSJ6	-2.9	8.2E-04	-4.4	1.7E-02	1.3	7.5E-02	0.9	5.7E-01
ENSMUST00000022459	PHD finger protein 7 [Source:MGI Symbol;Acc:MGI:1919088]	A2RTI5	Q9DAG9	-0.8	1.6E-01	-0.7	3.2E-01	0.7	1.6E-01	0.6	3.4E-01
ENSMUST00000022532	RIKEN cDNA 4930578I06 gene [Source:MGI Symbol;Acc:MGI:1915000]		Q80ZQ3	7.1	1.0E-04	6.0	1.4E-05	-3.8	3.5E-03	-0.4	4.4E-01
ENSMUST00000022536	spindle and kinetochore associated complex subunit 3 [Source:MGI Symbol;Acc:MGI:3041235]		Q8C263	2.1	1.1E-03	-1.7	1.3E-01	-0.3	6.8E-01	-3.2	3.6E-02
ENSMUST00000022469	nischarin [Source:MGI Symbol;Acc:MGI:1928323]		Q80TM9	1.6	2.9E-01	-3.1	8.8E-02	-4.7	4.6E-03	0.1	9.7E-01
ENSMUST00000022538	mitochondrial ribosomal protein L53 [Source:MGI Symbol;Acc:MGI:1915090]		Q9CQF8	-1.1	2.8E-02	-1.3	4.0E-01	2.5	2.0E-02	-0.4	7.6E-01
ENSMUST00000022474	polybromo 1 [Source:MGI Symbol;Acc:MGI:1923998]	E9Q7L2		2.1	3.6E-01	4.6	2.3E-01	4.1	1.5E-01	1.6	6.0E-01
ENSMUST00000022476	glycosyltransferase 8 domain containing 1 [Source:MGI Symbol;Acc:MGI:1923735]		Q6NSU3	2.8	1.9E-01	-1.0	7.7E-01	-0.7	7.8E-01	3.1	3.1E-01
ENSMUST00000022543	mitochondrial calcium uptake 2 [Source:MGI Symbol;Acc:MGI:1915764]		Q8CD10	-4.0	2.2E-04	6.7	2.4E-05	-1.4	1.6E-01	-0.4	4.1E-01
ENSMUST00000022545	fibroblast growth factor 9 [Source:MGI Symbol;Acc:MGI:104723]		P54130	6.3	1.7E-04	3.0	2.4E-02	-2.4	9.0E-02	0.8	3.9E-01
ENSMUST00000022494	emopamil binding protein-like [Source:MGI Symbol;Acc:MGI:1915427]		Q9D0P0	1.1	4.1E-02	1.6	2.0E-02	0.4	4.1E-01	-0.1	7.7E-01
ENSMUST00000022553	calcium binding protein 39-like [Source:MGI Symbol;Acc:MGI:1914081]		Q9DB16	-2.4	5.6E-04	-1.9	1.8E-02	-0.2	6.6E-01	-0.1	8.3E-01
ENSMUST00000022563	myotubularin related protein 6 [Source:MGI Symbol;Acc:MGI:2145637]		Q8VE11	-4.7	7.2E-06	3.8	1.2E-03	0.1	9.4E-01	-0.8	2.5E-01
ENSMUST00000022567	calcium channel, voltage-dependent, alpha2/delta subunit 3 [Source:MGI Symbol;Acc:MGI:1338890]		Q9Z1L5	7.7	1.6E-05	-1.3	5.9E-02	0.0	9.1E-01	-1.2	6.9E-02
ENSMUST00000022574	leucine rich repeat containing 63 [Source:MGI Symbol;Acc:MGI:1918109]	G3X8V0		3.4	6.7E-04	5.3	1.7E-02	-0.6	7.7E-01	1.6	1.7E-01
ENSMUST00000022576	carboxypeptidase B2 (plasma) [Source:MGI Symbol;Acc:MGI:1891837]		Q9JHH6	5.4	6.2E-04	-4.5	2.1E-03	-0.3	5.8E-01	-0.9	4.6E-01
ENSMUST00000022577	zinc finger CCCH type containing 13 [Source:MGI Symbol;Acc:MGI:1914552]	E9Q784	E9Q784	-1.2	1.9E-02	-3.1	7.6E-03	-0.1	8.0E-01	0.7	4.4E-01
ENSMUST00000022580	solute carrier family 25, member 30 [Source:MGI Symbol;Acc:MGI:1914804]		Q9CR58	-2.8	3.5E-04	-2.8	1.8E-03	0.3	3.7E-01	-0.3	6.6E-01
ENSMUST00000022517	crystallin, lambda 1 [Source:MGI Symbol;Acc:MGI:1915881]	A7VMV2	Q99KP3	0.1	9.1E-01	-2.1	2.3E-02	-1.4	2.4E-02	0.8	3.4E-01
ENSMUST00000022586	nuclear fragile X mental retardation protein interacting protein 1 [Source:MGI Symbol;Acc:MGI:1351474]		Q9QXX8	2.6	1.4E-03	-3.5	9.0E-04	-1.0	4.0E-02	-0.4	5.7E-01
ENSMUST00000022587	TSC22 domain family, member 1 [Source:MGI Symbol;Acc:MGI:109127]	Q3UXU0	P62500	-2.5	2.7E-03	0.2	8.1E-01	-6.0	3.1E-04	-1.0	2.4E-01
ENSMUST00000022521	protein kinase C, delta [Source:MGI Symbol;Acc:MGI:97598]		P28867	-4.8	6.7E-02	-3.4	4.0E-01	2.5	2.7E-01	1.1	7.6E-01
ENSMUST00000022589	ecto-NOX disulfide-thiol exchanger 1 [Source:MGI Symbol;Acc:MGI:2444896]		Q8BHR2	7.7	4.3E-05	7.3	6.7E-05	-0.6	6.0E-01	-0.6	3.4E-01
ENSMUST00000022528	PIN2/TERF1 interacting, telomerase inhibitor 1 [Source:MGI Symbol;Acc:MGI:1919650]		Q9CZX5	0.8	2.8E-01	-2.0	2.7E-02	-2.0	7.2E-03	0.7	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000022590	DnaJ (Hsp40) homolog, subfamily C, member 15 [Source:MGI Symbol;Acc:MGI:1913398]		Q78YY6	-2.4	5.6E-03	-5.9	6.1E-05	1.4	3.1E-03	-0.1	9.0E-01
ENSMUST00000022592	tumor necrosis factor (ligand) superfamily, member 11 [Source:MGI Symbol;Acc:MGI:1100089]		O35235	3.3	1.9E-02	-1.5	7.4E-02	1.0	5.3E-02	-0.4	5.9E-01
ENSMUST00000022593	A kinase (PRKA) anchor protein 11 [Source:MGI Symbol;Acc:MGI:2684060]	E9Q774		5.1	3.5E-03	6.2	5.1E-04	-0.7	6.1E-01	0.2	7.2E-01
ENSMUST00000022535	DCP1 decapping enzyme homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923151]		Q91YD3	-0.5	2.9E-01	0.5	3.6E-01	0.8	7.8E-02	-0.2	7.2E-01
ENSMUST00000022599	diaphanous homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1927222]	F8WIG5		3.3	2.2E-04	2.8	8.7E-04	0.4	4.1E-01	-0.3	5.6E-01
ENSMUST00000022603	leukocyte cell derived chemotaxin 1 [Source:MGI Symbol;Acc:MGI:1341171]		Q9Z1F6	5.6	1.9E-02	-0.4	4.8E-01	0.5	2.2E-01	-0.2	6.5E-01
ENSMUST00000022610	scavenger receptor class A, member 5 (putative) [Source:MGI Symbol;Acc:MGI:1918395]		Q8K299	7.5	1.7E-05	-3.3	3.7E-03	0.4	3.4E-01	-0.2	7.8E-01
ENSMUST00000022544	homeobox containing 1 [Source:MGI Symbol;Acc:MGI:2445066]		Q8BJA3	-0.8	1.7E-01	-0.4	6.0E-01	0.5	3.2E-01	0.1	8.9E-01
ENSMUST00000022618	a disintegrin and metallopeptidase domain 2 [Source:MGI Symbol;Acc:MGI:1340894]		Q60718	6.8	6.5E-05	5.9	4.7E-04	-0.6	6.2E-01	-0.2	7.3E-01
ENSMUST00000022550	exostoses (multiple)-like 3 [Source:MGI Symbol;Acc:MGI:1860765]	Q6P1H4		0.4	3.8E-01	1.0	8.8E-02	0.5	2.5E-01	-0.1	7.6E-01
ENSMUST00000022620	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal) [Source:MGI Symbol;Acc:MGI:87886]		Q91X60	4.1	1.5E-04	-1.6	1.6E-02	0.0	9.9E-01	-0.8	2.1E-01
ENSMUST00000022555	cytidine and dCMP deaminase domain containing 1 [Source:MGI Symbol;Acc:MGI:1919141]		Q8BMD5	-0.7	7.7E-01	-0.2	9.4E-01	0.7	7.6E-01	0.3	9.2E-01
ENSMUST00000022561	APC membrane recruitment 2 [Source:MGI Symbol;Acc:MGI:1919375]			0.3	5.3E-01	1.0	1.5E-01	0.5	2.9E-01	-0.1	8.3E-01
ENSMUST00000022629	dihydropyrimidinase-like 2 [Source:MGI Symbol;Acc:MGI:1349763]		O08553	4.1	1.4E-03	-4.2	1.2E-04	0.4	2.5E-01	-0.1	8.7E-01
ENSMUST00000022566	spermatogenesis associated 13 [Source:MGI Symbol;Acc:MGI:104838]	E9Q3I3		-0.3	8.5E-01	2.7	2.0E-01	0.7	6.9E-01	-2.3	1.9E-01
ENSMUST00000022634	BCL2/adenovirus E1B interacting protein 3-like [Source:MGI Symbol;Acc:MGI:1332659]		Q9Z2F7	-6.3	1.0E-06	7.5	4.0E-05	-0.6	6.0E-01	-0.4	4.7E-01
ENSMUST00000022573	esterase D/formylglutathione hydrolase [Source:MGI Symbol;Acc:MGI:95421]		Q9R0P3	-0.4	4.3E-01	-0.1	8.1E-01	-0.1	7.8E-01	-0.4	5.0E-01
ENSMUST00000022638	neurofilament, medium polypeptide [Source:MGI Symbol;Acc:MGI:97314]			8.1	9.0E-05	2.6	6.6E-03	-0.7	3.3E-01	0.1	9.3E-01
ENSMUST00000022639	neurofilament, light polypeptide [Source:MGI Symbol;Acc:MGI:97313]		P08551	6.1	5.4E-04	2.4	3.3E-02	-3.1	1.8E-02	-0.2	8.0E-01
ENSMUST00000022640	a disintegrin and metallopeptidase domain 7 [Source:MGI Symbol;Acc:MGI:107247]		O35227	6.2	1.9E-04	-0.7	1.9E-01	0.3	4.5E-01	-0.1	7.7E-01
ENSMUST00000022641	ADAM-like, decysin 1 [Source:MGI Symbol;Acc:MGI:1917650]	Q3U0T4	Q9R0X2	3.7	2.9E-03	-1.6	2.1E-02	0.2	6.7E-01	-1.0	1.5E-01
ENSMUST00000022585	GPALPP motifs containing 1 [Source:MGI Symbol;Acc:MGI:1914717]		Q69ZC8	0.0	9.0E-01	-0.1	9.1E-01	-0.1	7.6E-01	0.0	9.9E-01
ENSMUST00000022646	NK-3 transcription factor, locus 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:97352]	Q3UVH8	P97436	8.2	1.5E-05	2.6	5.6E-03	-0.1	8.8E-01	0.0	1.0E+00
ENSMUST00000022660	lysyl oxidase-like 2 [Source:MGI Symbol;Acc:MGI:2137913]		P58022	4.2	3.0E-05	-4.9	1.1E-04	-2.7	1.5E-04	-0.3	7.2E-01
ENSMUST00000022663	tumor necrosis factor receptor superfamily, member 10b [Source:MGI Symbol;Acc:MGI:1341090]		Q9QZM4	4.9	2.3E-06	6.5	1.5E-04	-1.5	2.3E-01	-0.3	6.4E-01
ENSMUST00000022665	Rho-related BTB domain containing 2 [Source:MGI Symbol;Acc:MGI:2180557]		Q91V93	-2.0	7.4E-03	-4.0	3.4E-03	-1.0	9.0E-02	0.7	5.1E-01
ENSMUST00000022591	epithelial stromal interaction 1 (breast) [Source:MGI Symbol;Acc:MGI:1915168]			-1.0	3.0E-01	-3.3	1.7E-02	-1.7	5.2E-02	0.6	6.1E-01
ENSMUST00000022666	kelch-like 1 [Source:MGI Symbol;Acc:MGI:2136335]		Q9JI74	6.1	5.9E-05	4.0	6.9E-03	-1.4	2.6E-01	-2.1	4.2E-02
ENSMUST00000022678	phosphatidylethanolamine binding protein 4 [Source:MGI Symbol;Acc:MGI:1920773]	G3X8V3		5.9	3.8E-04	-0.9	4.7E-01	-6.1	8.8E-04	0.0	9.9E-01
ENSMUST00000022595	regulator of cell cycle [Source:MGI Symbol;Acc:MGI:1913464]		Q9DBX1	-0.4	5.1E-01	-0.6	4.3E-01	-0.7	2.1E-01	-0.5	4.6E-01
ENSMUST00000022597	N(alpha)-acetyltransferase 16, NatA auxiliary subunit [Source:MGI Symbol;Acc:MGI:1914147]		Q9DBB4	0.1	9.4E-01	0.2	8.8E-01	0.5	6.3E-01	0.4	7.8E-01
ENSMUST00000022680	bridging integrator 3 [Source:MGI Symbol;Acc:MGI:1929883]		Q9JI08	-6.5	6.0E-08	3.2	9.8E-04	0.0	9.7E-01	0.1	9.0E-01
ENSMUST00000022600	mitochondrial translational release factor 1 [Source:MGI Symbol;Acc:MGI:2384815]		Q8K126	-0.1	8.9E-01	-0.3	6.5E-01	-1.2	8.5E-02	-0.9	2.2E-01
ENSMUST00000022601	WW domain binding protein 4 [Source:MGI Symbol;Acc:MGI:109568]		Q61048	-1.0	1.5E-01	-1.5	1.1E-01	0.0	9.6E-01	0.6	5.1E-01
ENSMUST00000022681	PDZ and LIM domain 2 [Source:MGI Symbol;Acc:MGI:2384850]		Q8R1G6	-4.5	5.5E-03	5.4	3.5E-02	-0.6	8.0E-01	-0.4	7.8E-01
ENSMUST00000022609	elongator acetyltransferase complex subunit 3 [Source:MGI Symbol;Acc:MGI:1921445]		Q9CZX0	-0.2	6.9E-01	0.0	9.4E-01	-0.2	6.8E-01	-0.3	5.8E-01
ENSMUST00000022682	sorbin and SH3 domain containing 3 [Source:MGI Symbol;Acc:MGI:700013]		Q9R1Z8	4.1	2.6E-05	1.2	5.9E-02	-7.0	1.8E-05	-0.6	2.3E-01
ENSMUST00000022612	PDZ binding kinase [Source:MGI Symbol;Acc:MGI:1289156]		Q9JJ78	-0.7	2.0E-01	-0.1	8.6E-01	0.3	4.5E-01	-0.2	7.4E-01
ENSMUST00000022613	establishment of cohesion 1 homolog 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919238]		Q8CIB9	-0.7	3.9E-01	0.6	5.8E-01	0.6	4.9E-01	-0.7	4.5E-01
ENSMUST00000022614	coiled-coil domain containing 25 [Source:MGI Symbol;Acc:MGI:1914429]	A0PK78	Q78PG9	1.5	7.3E-02	0.3	7.6E-01	-0.4	6.0E-01	0.8	3.7E-01
ENSMUST00000022616	clusterin [Source:MGI Symbol;Acc:MGI:88423]	Q549A5	Q06890	0.7	2.2E-01	-2.0	1.3E-02	-2.6	4.2E-04	0.2	8.0E-01
ENSMUST00000022690	family with sequence similarity 160, member B2 [Source:MGI Symbol;Acc:MGI:3036290]		Q80YR2	2.4	1.8E-03	6.3	2.3E-04	-0.5	6.5E-01	0.0	9.9E-01
ENSMUST00000022692	surfactant associated protein C [Source:MGI Symbol;Acc:MGI:109517]	Q6P8P8		6.4	1.8E-04	5.1	7.9E-05	0.4	6.2E-01	-0.7	2.1E-01
ENSMUST00000022622	PTK2 protein tyrosine kinase 2 beta [Source:MGI Symbol;Acc:MGI:104908]	K7QD41	Q9QVP9	1.1	6.3E-01	8.1	6.7E-03	0.7	7.6E-01	-6.3	6.5E-03
ENSMUST00000022623	tripartite motif-containing 35 [Source:MGI Symbol;Acc:MGI:1914104]			0.0	9.5E-01	-0.3	6.9E-01	0.3	4.9E-01	0.6	3.4E-01
ENSMUST00000022693	bone morphogenetic protein 1 [Source:MGI Symbol;Acc:MGI:88176]		P98063	6.2	4.9E-06	2.6	4.2E-02	-0.7	4.8E-01	0.8	3.7E-01
ENSMUST00000022694	dematin actin binding protein [Source:MGI Symbol;Acc:MGI:99670]		Q9WV69	7.6	9.3E-04	-4.4	5.6E-05	0.3	3.5E-01	-1.6	3.8E-02
ENSMUST00000022695	dematin actin binding protein [Source:MGI Symbol;Acc:MGI:99670]		Q9WV69	5.7	1.5E-02	7.8	2.2E-04	-0.7	6.3E-01	-0.4	5.6E-01
ENSMUST00000022696	exportin 7 [Source:MGI Symbol;Acc:MGI:1929705]		Q9EPK7	2.2	5.9E-04	6.1	9.1E-04	-0.4	7.5E-01	-0.5	5.0E-01
ENSMUST00000022697	fibroblast growth factor 17 [Source:MGI Symbol;Acc:MGI:1202401]	Q0VF19	P63075	6.2	8.7E-05	5.9	5.2E-04	-0.5	7.0E-01	-0.2	8.1E-01
ENSMUST00000022698	docking protein 2 [Source:MGI Symbol;Acc:MGI:1332623]	Q3TX09	O70469	-4.2	9.5E-04	2.1	5.5E-02	-2.1	4.5E-02	-0.5	5.7E-01
ENSMUST00000022699	glial cell line derived neurotrophic factor family receptor alpha 2 [Source:MGI Symbol;Acc:MGI:1195462]		O08842	8.2	3.6E-06	7.7	5.1E-05	-0.5	6.5E-01	0.0	9.8E-01
ENSMUST00000022650	progesterone immunomodulatory binding factor 1 [Source:MGI Symbol;Acc:MGI:1261910]	E9Q6K3		-1.3	7.5E-02	-1.4	1.0E-01	-0.4	4.7E-01	-0.2	7.5E-01
ENSMUST00000022656	bora, aurora kinase A activator [Source:MGI Symbol;Acc:MGI:1924994]		Q8BS90	0.9	1.4E-01	1.3	8.7E-02	0.3	5.7E-01	-0.1	8.5E-01
ENSMUST00000022701	retinoblastoma 1 [Source:MGI Symbol;Acc:MGI:97874]		P13405	-3.7	4.1E-04	3.2	5.2E-04	-0.9	1.4E-01	0.1	8.1E-01
ENSMUST00000022704	integral membrane protein 2B [Source:MGI Symbol;Acc:MGI:1309517]		O89051	-7.8	1.5E-07	5.9	3.5E-06	0.7	2.2E-01	-0.3	4.0E-01
ENSMUST00000022705	mediator complex subunit 4 [Source:MGI Symbol;Acc:MGI:1914631]		Q9CQA5	-3.1	1.7E-04	-0.2	8.1E-01	1.4	2.9E-02	-0.5	5.3E-01
ENSMUST00000022706	succinate-Coenzyme A ligase, ADP-forming, beta subunit [Source:MGI Symbol;Acc:MGI:1306775]		Q9Z2I9	-7.2	3.9E-04	6.5	1.6E-04	0.5	6.6E-01	0.1	9.1E-01
ENSMUST00000022708	tripartite motif-containing 52 [Source:MGI Symbol;Acc:MGI:3045276]	Q8CDV4		7.9	2.1E-05	6.3	6.3E-04	0.0	9.8E-01	-0.4	6.0E-01
ENSMUST00000022716	ring finger protein 219 [Source:MGI Symbol;Acc:MGI:1919736]	G3X8V5		3.8	8.9E-04	-6.0	7.5E-07	-0.2	4.5E-01	-0.6	2.4E-01
ENSMUST00000022721	ceroid-lipofuscinosis, neuronal 5 [Source:MGI Symbol;Acc:MGI:2442253]	B2RUP8	Q3UMW8	-4.9	8.9E-05	-3.8	1.1E-01	2.1	5.7E-02	1.4	5.3E-01
ENSMUST00000022722	immunoresponsive gene 1 [Source:MGI Symbol;Acc:MGI:103206]			-3.3	4.7E-03	2.0	4.3E-03	-2.7	5.5E-04	-0.5	2.9E-01
ENSMUST00000022725	dopachrome tautomerase [Source:MGI Symbol;Acc:MGI:102563]		P29812	7.5	1.8E-05	2.1	1.7E-02	0.7	2.8E-01	1.0	1.3E-01
ENSMUST00000022727	TDP-glucose 4,6-dehydratase [Source:MGI Symbol;Acc:MGI:1923605]		Q8VDR7	-2.2	1.3E-03	6.9	2.4E-04	-0.2	8.7E-01	-0.6	3.6E-01
ENSMUST00000022728	G protein-coupled receptor 180 [Source:MGI Symbol;Acc:MGI:1930949]		Q8BPS4	7.3	2.2E-04	1.5	2.7E-02	-5.1	1.8E-05	-0.3	5.3E-01
ENSMUST00000022734	DnaJ (Hsp40) homolog, subfamily C, member 3 [Source:MGI Symbol;Acc:MGI:107373]	Q3UFV9	Q91YW3	-3.3	6.1E-05	4.8	2.7E-02	-0.4	8.2E-01	2.4	5.8E-02
ENSMUST00000022744	glial cell line derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:107430]		P48540	7.6	6.6E-05	5.8	1.3E-02	-1.8	4.0E-01	-1.9	1.6E-01
ENSMUST00000022746	oncostatin M receptor [Source:MGI Symbol;Acc:MGI:1330819]	G3X8V6		6.2	1.5E-03	3.2	3.2E-04	1.0	6.1E-02	0.0	9.9E-01
ENSMUST00000022767	methyltransferase like 3 [Source:MGI Symbol;Acc:MGI:1927165]			-3.2	2.7E-03	7.1	1.6E-04	0.5	6.8E-01	-0.3	5.8E-01
ENSMUST00000022781	defender against cell death 1 [Source:MGI Symbol;Acc:MGI:101912]		P61804	-4.6	1.1E-03	-2.5	4.3E-02	1.1	8.9E-02	-0.6	6.2E-01
ENSMUST00000022782	low-density lipoprotein receptor-related protein 10 [Source:MGI Symbol;Acc:MGI:1929480]		Q7TQH7	-4.6	6.9E-05	7.2	4.8E-05	-0.6	5.5E-01	0.4	4.0E-01
ENSMUST00000022787	e carrier family 7 (cationic amino acid transporter, y+ system), member 8 [Source:MGI Symbol;Acc:MGI:1355		Q9QXW9	2.9	1.4E-03	-1.9	5.2E-02	1.1	6.7E-02	-0.8	4.0E-01
ENSMUST00000022791	F-box protein 4 [Source:MGI Symbol;Acc:MGI:2146220]		Q8CHQ0	-3.1	6.2E-04	-6.8	3.4E-06	0.7	2.4E-02	-0.2	7.6E-01
ENSMUST00000022803	proteasome (prosome, macropain) subunit, beta type 5 [Source:MGI Symbol;Acc:MGI:1194513]		O55234	-4.3	2.0E-04	-4.2	1.1E-04	-0.7	5.5E-02	0.4	5.6E-01
ENSMUST00000022813	embryonal Fyn-associated substrate [Source:MGI Symbol;Acc:MGI:105311]		Q64355	8.9	4.1E-06	-5.7	6.9E-04	-0.7	2.1E-01	-2.2	1.6E-01
ENSMUST00000022815	neuroguidin, EIF4E binding protein [Source:MGI Symbol;Acc:MGI:1916216]		Q9DB96	-4.3	1.5E-05	6.7	1.5E-04	-0.6	6.2E-01	0.6	3.0E-01
ENSMUST00000022709	sprouty homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1345138]	B2RS85	Q9QXV8	-0.5	4.5E-01	-0.3	7.4E-01	0.4	5.6E-01	0.2	8.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000022715	RNA binding motif protein 26 [Source:MGI Symbol;Acc:MGI:1921463]		Q6NZN0	2.1	2.4E-01	-1.4	6.4E-01	-0.5	8.2E-01	3.1	2.5E-01
ENSMUST00000022816	SUB1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:104811]		P11031	-2.1	1.3E-02	2.2	4.3E-02	-0.7	4.1E-01	0.9	2.6E-01
ENSMUST00000022718	endothelin receptor type B [Source:MGI Symbol;Acc:MGI:102720]		P48302	-0.7	6.0E-01	-1.7	2.5E-01	-2.6	3.4E-02	-1.7	2.9E-01
ENSMUST00000022720	F-box and leucine-rich repeat protein 3 [Source:MGI Symbol;Acc:MGI:1354702]	Q5PRF6	Q8C4V4	1.1	4.8E-02	1.1	1.1E-01	0.6	2.6E-01	0.5	3.9E-01
ENSMUST00000022819	junctophilin 4 [Source:MGI Symbol;Acc:MGI:2443113]		Q80WT0	7.3	4.0E-05	-3.7	3.0E-03	1.1	3.6E-02	0.0	9.9E-01
ENSMUST00000022826	fat storage-inducing transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1915930]		Q91V79	6.2	1.6E-04	-3.1	2.3E-02	-0.1	8.9E-01	-0.3	8.0E-01
ENSMUST00000022830	receptor-interacting serine-threonine kinase 3 [Source:MGI Symbol;Acc:MGI:2154952]		Q9QZL0	-6.8	8.1E-06	6.8	7.7E-05	-0.6	6.0E-01	0.1	9.0E-01
ENSMUST00000022831	KH and NYN domain containing [Source:MGI Symbol;Acc:MGI:2451333]		Q80U38	-2.4	4.7E-03	-2.2	5.2E-03	-0.4	2.8E-01	-0.4	5.1E-01
ENSMUST00000022842	chaperonin containing Tcp1, subunit 5 (epsilon) [Source:MGI Symbol;Acc:MGI:107185]		P80316	-6.3	1.2E-05	4.3	1.3E-02	-0.9	5.1E-01	2.1	6.0E-02
ENSMUST00000022857	tetratricopeptide repeat domain 23-like [Source:MGI Symbol;Acc:MGI:1923027]		A6H6E9	6.8	5.2E-05	-4.1	9.9E-05	-0.7	5.1E-02	0.1	8.4E-01
ENSMUST00000022861	UDP glycosyltransferases 3 family, polypeptide A1 [Source:MGI Symbol;Acc:MGI:2146055]		Q3UP75	6.9	7.3E-05	7.6	1.3E-04	-0.4	7.5E-01	-0.4	5.1E-01
ENSMUST00000022865	metadherin [Source:MGI Symbol;Acc:MGI:1914404]		Q80WJ7	-5.0	1.0E-03	-1.4	2.1E-01	-6.5	6.9E-04	1.1	2.9E-01
ENSMUST00000022751	tetratricopeptide repeat domain 33 [Source:MGI Symbol;Acc:MGI:1914765]		Q9D6K7	0.2	9.0E-01	-1.8	2.8E-01	-2.6	7.8E-02	-0.6	7.2E-01
ENSMUST00000022765	RAB2B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1923588]	Q0PD64	P59279	-2.4	2.1E-01	4.2	1.0E-01	3.4	1.3E-01	-3.2	1.1E-01
ENSMUST00000022766	TOX high mobility group box family member 4 [Source:MGI Symbol;Acc:MGI:1915389]		Q8BU11	-0.6	1.7E-01	-0.2	7.6E-01	1.0	4.6E-02	0.5	3.7E-01
ENSMUST00000022871	syndecan 2 [Source:MGI Symbol;Acc:MGI:1349165]		P43407	4.9	5.5E-05	-5.2	6.3E-03	0.0	9.8E-01	2.0	2.1E-01
ENSMUST00000022881	family with sequence similarity 134, member B [Source:MGI Symbol;Acc:MGI:1913520]		Q8VE91	-5.2	2.5E-05	-5.8	3.1E-03	-0.9	1.7E-01	0.2	8.7E-01
ENSMUST00000022882	myosin X [Source:MGI Symbol;Acc:MGI:107716]	E9Q5G1		5.2	5.3E-03	-3.5	3.1E-03	1.2	2.7E-02	0.1	9.5E-01
ENSMUST00000022784	HAUS augmin-like complex, subunit 4 [Source:MGI Symbol;Acc:MGI:1261794]		Q8BFT2	-1.3	6.7E-02	-0.6	5.0E-01	0.5	3.7E-01	-0.2	7.7E-01
ENSMUST00000022786	RIKEN cDNA 4931414P19 gene [Source:MGI Symbol;Acc:MGI:1921609]		Q8K2W9	1.4	1.1E-01	2.7	2.9E-02	1.2	1.9E-01	-0.1	9.5E-01
ENSMUST00000022890	ring finger protein 19A [Source:MGI Symbol;Acc:MGI:1353623]		P50636	-2.3	4.4E-04	1.7	5.9E-02	-0.9	1.7E-01	0.3	6.4E-01
ENSMUST00000022894	nonooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Source:MGI Symbol;Acc:M		P63101	-6.9	3.7E-06	-2.0	3.6E-02	1.4	2.3E-02	0.3	7.0E-01
ENSMUST00000022794	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]	B8JJ92		-5.1	3.8E-02	-3.6	2.8E-01	1.1	5.2E-01	-0.3	9.2E-01
ENSMUST00000022895	grainyhead-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2182543]		Q8K5C0	6.5	1.4E-02	-4.5	8.1E-04	0.0	1.0E+00	0.2	8.5E-01
ENSMUST00000022806	BCL2-like 2 [Source:MGI Symbol;Acc:MGI:108052]		P70345	-1.7	1.5E-01	-3.2	1.1E-01	0.6	5.5E-01	2.1	2.7E-01
ENSMUST00000022808	poly(A) binding protein, nuclear 1 [Source:MGI Symbol;Acc:MGI:1859158]		Q8CCS6	-4.3	2.3E-01	-5.2	2.5E-01	-1.2	5.6E-01	-0.3	9.5E-01
ENSMUST00000022904	ATPase, H+ transporting, lysosomal V1 subunit C1 [Source:MGI Symbol;Acc:MGI:1913585]		Q9Z1G3	-4.3	2.6E-05	6.6	1.5E-05	-2.5	2.6E-02	-0.2	7.0E-01
ENSMUST00000022906	frizzled homolog 6 (Drosophila) [Source:MGI Symbol;Acc:MGI:108474]	Q542J1	Q61089	5.1	7.6E-05	-4.5	4.8E-05	-1.0	9.5E-03	-0.9	2.0E-01
ENSMUST00000022908	solute carrier family 25, member 32 [Source:MGI Symbol;Acc:MGI:1917156]		Q8BMG8	-1.8	3.5E-03	-2.3	2.1E-02	-0.5	3.7E-01	-0.3	7.5E-01
ENSMUST00000022909	DDB1 and CUL4 associated factor 13 [Source:MGI Symbol;Acc:MGI:2684929]		Q6PAC3	-3.4	1.7E-04	7.6	5.4E-05	-0.6	6.2E-01	-0.9	1.4E-01
ENSMUST00000022821	dehydrogenase/reductase (SDR family) member 4 [Source:MGI Symbol;Acc:MGI:90169]		Q99LB2	-1.0	8.0E-02	-0.4	5.9E-01	-0.1	9.0E-01	-0.7	2.7E-01
ENSMUST00000022913	dentrocyte expressed seven transmembrane protein [Source:MGI Symbol;Acc:MGI:1923016]		Q7TNJ0	6.9	1.4E-04	5.7	4.0E-04	-1.3	2.6E-01	-0.9	1.9E-01
ENSMUST00000022828	ER membrane protein complex subunit 9 [Source:MGI Symbol;Acc:MGI:1934682]	Q793L1	Q9DB76	1.4	7.8E-02	-0.9	3.7E-01	-0.6	4.2E-01	1.7	8.8E-02
ENSMUST00000022915	dihydropyrimidinase [Source:MGI Symbol;Acc:MGI:1928679]		Q9EQF5	6.2	2.6E-04	-5.9	2.1E-04	0.7	7.4E-02	-0.2	8.5E-01
ENSMUST00000022918	oxidation resistance 1 [Source:MGI Symbol;Acc:MGI:2179326]		Q4KMM3	-4.1	9.9E-03	-1.2	1.8E-01	1.1	6.6E-02	0.0	9.5E-01
ENSMUST00000022834	chymase 1, mast cell [Source:MGI Symbol;Acc:MGI:96941]	A4QPC5		2.8	4.9E-02	1.0	4.4E-01	-2.2	8.7E-02	-0.5	6.9E-01
ENSMUST00000022921	angiopoietin 1 [Source:MGI Symbol;Acc:MGI:108448]		O08538	2.9	8.6E-04	-6.7	5.1E-05	-1.1	2.4E-02	-0.8	4.4E-01
ENSMUST00000022849	threonyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:106314]		Q9D0R2	-0.9	6.7E-02	-2.3	3.3E-03	-1.2	8.9E-03	0.2	7.3E-01
ENSMUST00000022925	eukaryotic translation initiation factor 3, subunit H [Source:MGI Symbol;Acc:MGI:1915385]	Q5M9L0	Q91WK2	-4.4	5.3E-07	6.2	4.7E-03	-0.7	7.1E-01	-0.9	3.7E-01
ENSMUST00000022853	C1q and tumor necrosis factor related protein 3 [Source:MGI Symbol;Acc:MGI:1932136]	Q4ZJN6	Q9ES30	4.1	6.8E-02	5.2	3.5E-02	-1.4	5.7E-01	-2.4	1.0E-01
ENSMUST00000022855	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915082]		Q9DCA5	-0.1	8.7E-01	-1.0	1.1E-01	-1.3	1.3E-02	-0.3	5.5E-01
ENSMUST00000022927	RAD21 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:108016]		Q61550	-4.9	5.3E-07	6.5	1.4E-04	-0.6	5.9E-01	-0.3	5.9E-01
ENSMUST00000022952	odd-skipped related 2 [Source:MGI Symbol;Acc:MGI:1930813]		Q91ZD1	8.1	1.2E-05	6.6	2.2E-04	-0.5	6.9E-01	-0.1	8.3E-01
ENSMUST00000022953	family with sequence similarity 135, member B [Source:MGI Symbol;Acc:MGI:1917613]		Q9DAI6	7.2	4.9E-05	-4.3	2.0E-02	1.2	1.2E-01	0.4	7.8E-01
ENSMUST00000022867	lysosomal-associated protein transmembrane 4B [Source:MGI Symbol;Acc:MGI:1890494]	B2CZK6	Q91XQ6	-0.3	6.0E-01	-0.1	9.2E-01	0.4	4.0E-01	0.2	7.4E-01
ENSMUST00000022954	CH domain containing, RNA binding, signal transduction associated 3 [Source:MGI Symbol;Acc:MGI:1313312		Q9R226	4.1	1.6E-04	-1.0	1.3E-01	-5.7	6.5E-06	0.1	8.7E-01
ENSMUST00000022875	progressive ankylosis [Source:MGI Symbol;Acc:MGI:3045421]	Q3UG85	Q9JHZ2	0.5	3.2E-01	-0.5	3.5E-01	-1.7	1.9E-03	-0.7	1.9E-01
ENSMUST00000022960	eukaryotic translation initiation factor 3, subunit E [Source:MGI Symbol;Acc:MGI:99257]	Q3UIG0	P60229	-5.0	3.5E-05	-3.8	1.5E-03	1.3	1.3E-02	-0.2	8.6E-01
ENSMUST00000022962	ER membrane protein complex subunit 2 [Source:MGI Symbol;Acc:MGI:1913986]	Q6A0D1	Q9CRD2	-6.0	2.5E-05	2.5	1.5E-01	-2.4	1.4E-01	0.4	7.8E-01
ENSMUST00000022964	estrogen receptor-binding fragment-associated gene 9 [Source:MGI Symbol;Acc:MGI:1859920]		Q9D0V7	-2.3	2.8E-03	-2.1	5.8E-03	0.5	1.9E-01	0.2	7.1E-01
ENSMUST00000022967	potassium channel, subfamily V, member 1 [Source:MGI Symbol;Acc:MGI:1914748]		Q8BZN2	7.4	5.0E-05	-5.8	1.4E-04	1.4	5.4E-03	0.2	8.0E-01
ENSMUST00000022976	RIKEN cDNA E430025E21 gene [Source:MGI Symbol;Acc:MGI:2146110]		Q8C2E7	-2.0	8.3E-04	1.4	6.2E-01	-1.9	4.4E-01	3.2	1.7E-01
ENSMUST00000022901	ribonucleotide reductase M2 B (TP53 inducible) [Source:MGI Symbol;Acc:MGI:2155865]		Q6PEE3	-0.9	4.4E-02	-1.0	6.7E-02	-0.2	6.5E-01	0.0	9.7E-01
ENSMUST00000022977	squalene epoxidase [Source:MGI Symbol;Acc:MGI:109296]	Q3TQK8	P52019	-5.9	2.4E-05	-4.4	1.8E-04	0.4	2.9E-01	0.4	5.6E-01
ENSMUST00000022980	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 [Source:MGI Symbol;Acc:MGI:1913468]		Q9CQJ8	-5.8	1.2E-06	3.0	2.5E-03	-2.9	3.3E-03	-0.8	2.1E-01
ENSMUST00000022985	kelch-like 38 [Source:MGI Symbol;Acc:MGI:3045310]		Q8BSF5	7.1	5.6E-05	-0.7	2.1E-01	0.2	6.7E-01	-0.9	1.4E-01
ENSMUST00000022986	F-box protein 32 [Source:MGI Symbol;Acc:MGI:1914981]		Q9CPU7	3.6	4.0E-05	-6.4	9.5E-05	-0.8	4.8E-02	2.1	5.4E-02
ENSMUST00000022993	Der1-like domain family, member 1 [Source:MGI Symbol;Acc:MGI:1915069]		Q99J56	-3.7	1.3E-05	4.8	2.3E-03	-1.5	2.6E-01	0.6	4.2E-01
ENSMUST00000022998	Mdm2, transformed 3T3 cell double minute p53 binding protein [Source:MGI Symbol;Acc:MGI:2146005]		Q8BJS8	-3.2	1.9E-02	6.7	2.9E-04	-0.5	6.9E-01	-1.0	1.8E-01
ENSMUST00000022916	low density lipoprotein-related protein 12 [Source:MGI Symbol;Acc:MGI:2443132]		Q8BUJ9	-1.0	3.6E-01	-2.0	1.8E-01	0.3	7.2E-01	1.3	3.7E-01
ENSMUST00000023006	leucine rich repeat containing 6 (testis) [Source:MGI Symbol;Acc:MGI:1859553]		O88978	5.9	3.1E-04	3.8	9.0E-02	6.2	5.4E-03	-1.7	2.8E-01
ENSMUST00000023007	adenylate cyclase 8 [Source:MGI Symbol;Acc:MGI:1341110]		P97490	8.1	2.2E-05	1.4	5.2E-02	-1.8	1.2E-02	-0.3	5.7E-01
ENSMUST00000023015	wingless-type MMTV integration site family, member 7B [Source:MGI Symbol;Acc:MGI:98962]		P28047	4.3	9.3E-03	-4.1	9.4E-06	0.3	2.2E-01	0.0	9.8E-01
ENSMUST00000023036	ring-box 1 [Source:MGI Symbol;Acc:MGI:1891829]		P62878	-2.6	6.6E-05	-4.1	1.2E-05	0.4	1.2E-01	-0.4	4.6E-01
ENSMUST00000022945	Shc SH2-domain binding protein 1 [Source:MGI Symbol;Acc:MGI:1338802]		Q9Z179	-1.3	7.3E-02	-1.0	2.6E-01	0.0	9.9E-01	-0.4	6.4E-01
ENSMUST00000022947	matrilin 2 [Source:MGI Symbol;Acc:MGI:109613]		O08746	3.9	1.1E-01	0.7	7.7E-01	-2.8	2.3E-01	0.5	8.1E-01
ENSMUST00000023039	suppression of tumorigenicity 13 [Source:MGI Symbol;Acc:MGI:1917606]	F8WJK8		-6.0	1.8E-04	4.1	2.2E-04	-4.2	1.2E-03	-0.2	7.0E-01
ENSMUST00000023040	r family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17 [Source:MGI Symbol;Acc:MC		O70579	-3.2	2.3E-04	7.8	5.3E-05	-0.5	6.8E-01	-1.0	8.9E-02
ENSMUST00000023043	adenylosuccinate lyase [Source:MGI Symbol;Acc:MGI:103202]		P54822	6.1	2.0E-04	2.4	7.7E-03	-1.6	3.7E-02	0.1	8.1E-01
ENSMUST00000023044	family with sequence similarity 83, member F [Source:MGI Symbol;Acc:MGI:2146227]			4.9	3.4E-04	-4.2	4.1E-04	-0.6	1.8E-01	-1.4	1.3E-01
ENSMUST00000023048	mitochondrial elongation factor 1 [Source:MGI Symbol;Acc:MGI:2146020]	B2RPW2	Q8BGV8	-1.4	2.6E-02	-5.7	2.5E-04	-0.2	7.2E-01	-0.5	6.4E-01
ENSMUST00000023053	collagen, type XIV, alpha 1 [Source:MGI Symbol;Acc:MGI:1341272]		Q80X19	8.3	4.9E-04	-2.5	6.4E-03	-0.4	4.2E-01	-0.2	8.3E-01
ENSMUST00000023056	DEP domain containing MTOR-interacting protein [Source:MGI Symbol;Acc:MGI:2146322]	B2ZRS7	Q570Y9	9.5	5.6E-04	6.2	3.6E-04	-0.6	6.4E-01	0.6	3.5E-01
ENSMUST00000022971	myelocytomatosis oncogene [Source:MGI Symbol;Acc:MGI:97250]	F8WID3		-1.0	4.4E-01	2.1	1.8E-01	0.8	5.1E-01	-2.2	1.1E-01
ENSMUST00000023061	Josephin domain containing 1 [Source:MGI Symbol;Acc:MGI:1921408]		Q9DBJ6	-3.8	4.0E-05	-1.7	1.5E-02	0.7	7.0E-02	0.3	5.6E-01
ENSMUST00000023062	translocase of outer mitochondrial membrane 22 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2450248]		Q9CPQ3	-6.5	2.3E-05	-5.1	4.2E-04	0.2	6.6E-01	-0.6	5.4E-01
ENSMUST00000023064	chibby homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1920989]		Q9D1C2	-2.6	2.9E-03	-6.7	3.4E-06	-0.5	8.1E-02	0.4	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000023067	RIB43A domain with coiled-coils 2 [Source:MGI Symbol;Acc:MGI:1914997]	G3X8W0		6.8	3.4E-05	7.0	1.2E-04	-0.6	6.4E-01	-0.4	4.7E-01
ENSMUST00000023068	structural maintenance of chromosomes 1B [Source:MGI Symbol;Acc:MGI:2154049]	A1L2Z0	Q920F6	5.2	2.1E-04	3.4	2.5E-04	-0.2	7.2E-01	0.0	9.9E-01
ENSMUST00000022992	TBC1 domain family, member 31 [Source:MGI Symbol;Acc:MGI:2684931]		Q6NXY1	-1.4	6.0E-02	-2.4	3.6E-02	-0.5	3.9E-01	0.4	6.5E-01
ENSMUST00000023069	family with sequence similarity 118, member A [Source:MGI Symbol;Acc:MGI:1920475]		Q91YN1	-1.5	6.1E-03	-3.0	4.5E-04	0.7	4.5E-02	0.0	9.8E-01
ENSMUST00000023070	uroplakin 3A [Source:MGI Symbol;Acc:MGI:98914]		Q9JKX8	6.3	3.3E-04	-3.0	2.0E-02	-1.7	3.7E-02	-1.8	1.9E-01
ENSMUST00000023071	orting and assembly machinery component 50 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191590		Q8BGH2	-2.8	4.0E-04	5.5	3.9E-04	-1.5	2.0E-01	-1.1	1.2E-01
ENSMUST00000023072	parvin, beta [Source:MGI Symbol;Acc:MGI:2153063]	Q3UGT9	Q9ES46	1.9	7.0E-03	8.3	3.7E-05	-0.5	7.0E-01	-0.6	2.7E-01
ENSMUST00000023008	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]	E9QN63		2.7	1.2E-01	5.0	9.8E-03	-0.6	7.3E-01	-2.9	3.9E-02
ENSMUST00000023074	parvin, gamma [Source:MGI Symbol;Acc:MGI:2158329]		Q9ERD8	-6.8	8.9E-04	-4.5	8.1E-03	-6.9	1.7E-04	1.9	1.9E-01
ENSMUST00000023024	thyrotroph embryonic factor [Source:MGI Symbol;Acc:MGI:98663]		Q9JLC6	-1.0	4.2E-01	-0.3	8.7E-01	1.3	4.0E-01	0.6	7.3E-01
ENSMUST00000023029	l(3)mbt-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443584]		P59178	-0.2	8.9E-01	-1.6	5.7E-01	2.2	2.2E-01	3.6	1.7E-01
ENSMUST00000023083	cytochrome P450, family 2, subfamily d, polypeptide 22 [Source:MGI Symbol;Acc:MGI:1929474]	Q9JKY7		2.4	2.1E-03	-2.5	5.5E-04	-0.3	3.3E-01	-0.5	3.3E-01
ENSMUST00000023085	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) [Source:MGI Symbol;Acc:MGI:1914380]		Q9CQZ5	-5.9	1.9E-05	-5.1	9.5E-04	-0.9	7.0E-02	-1.9	1.6E-01
ENSMUST00000023086	single-pass membrane protein with aspartate rich tail 1 [Source:MGI Symbol;Acc:MGI:1916279]		Q9DB10	-6.3	6.9E-05	-4.3	1.5E-04	-0.7	7.3E-02	0.4	5.9E-01
ENSMUST00000023087	twinfilin, actin-binding protein, homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1100520]		Q91YR1	-3.4	1.7E-04	5.0	1.4E-03	-0.7	5.2E-01	0.4	6.6E-01
ENSMUST00000023088	N-acetyl galactosaminidase, alpha [Source:MGI Symbol;Acc:MGI:1261422]		Q9QWR8	-3.4	2.7E-04	5.7	5.4E-04	0.6	5.7E-01	-0.2	7.8E-01
ENSMUST00000023089	WBP2 N-terminal like [Source:MGI Symbol;Acc:MGI:1921966]		Q9D529	5.4	9.2E-04	0.5	4.5E-01	1.4	2.1E-02	-0.6	4.2E-01
ENSMUST00000023050	TGF-beta activated kinase 1/MAP3K7 binding protein 1 [Source:MGI Symbol;Acc:MGI:1913763]		Q8CF89	-0.9	1.6E-01	0.7	3.8E-01	1.0	9.4E-02	-0.6	4.6E-01
ENSMUST00000023095	septin 3 [Source:MGI Symbol;Acc:MGI:1345148]		Q9Z1S5	6.4	1.1E-05	2.2	1.5E-01	-4.5	1.8E-02	1.6	1.9E-01
ENSMUST00000023055	dynein, axonemal, light chain 4 [Source:MGI Symbol;Acc:MGI:1859217]		Q9DCM4	-1.1	1.7E-01	0.3	7.7E-01	1.2	1.3E-01	-0.2	8.1E-01
ENSMUST00000023099	solute carrier family 38, member 2 [Source:MGI Symbol;Acc:MGI:1915010]		Q8CFE6	-4.2	1.5E-05	4.7	4.1E-02	-1.3	5.4E-01	3.4	2.9E-02
ENSMUST00000023100	sterol regulatory element binding factor 2 [Source:MGI Symbol;Acc:MGI:107585]		Q3U1N2	-2.3	8.4E-04	-2.6	3.6E-03	1.6	2.3E-03	0.4	5.9E-01
ENSMUST00000023101	solute carrier family 38, member 4 [Source:MGI Symbol;Acc:MGI:1916604]		Q8R1S9	6.0	2.0E-04	-4.8	7.1E-04	0.3	5.3E-01	-1.5	1.8E-01
ENSMUST00000023113	polymerase (RNA) III (DNA directed) polypeptide H [Source:MGI Symbol;Acc:MGI:1926179]		Q9D2C6	2.3	2.7E-03	-2.1	2.9E-02	0.1	7.8E-01	-0.4	6.2E-01
ENSMUST00000023116	aconitase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:87880]		Q99KI0	-3.2	1.7E-05	5.4	1.1E-04	-2.1	5.1E-02	-0.7	2.2E-01
ENSMUST00000023117	PHD finger protein 5A [Source:MGI Symbol;Acc:MGI:2156864]		P83870	-3.0	1.8E-04	5.2	4.0E-04	-0.6	5.4E-01	-0.6	3.2E-01
ENSMUST00000023119	vitamin D receptor [Source:MGI Symbol;Acc:MGI:103076]		P48281	3.5	1.7E-04	-0.7	2.3E-01	0.5	1.7E-01	-0.3	5.8E-01
ENSMUST00000023128	integrin alpha 5 (fibronectin receptor alpha) [Source:MGI Symbol;Acc:MGI:96604]		P11688	-2.4	3.0E-03	6.2	6.6E-04	-0.7	6.2E-01	-0.6	4.3E-01
ENSMUST00000023132	phosphodiesterase 1B, Ca2+-calmodulin dependent [Source:MGI Symbol;Acc:MGI:97523]		Q01065	-3.0	1.7E-02	-2.0	1.1E-02	0.4	3.5E-01	-0.5	4.6E-01
ENSMUST00000023133	protein phosphatase 1, regulatory (inhibitor) subunit 1A [Source:MGI Symbol;Acc:MGI:1889595]		Q9ERT9	3.5	1.1E-02	1.2	8.6E-02	-1.5	2.3E-02	-0.7	2.4E-01
ENSMUST00000023140	tumor necrosis factor receptor superfamily, member 17 [Source:MGI Symbol;Acc:MGI:1343050]		O88472	6.0	7.2E-04	-7.0	8.0E-03	1.3	1.4E-01	1.6	4.9E-01
ENSMUST00000023075	C1q and tumor necrosis factor related protein 6 [Source:MGI Symbol;Acc:MGI:1919959]		Q6IR41	1.2	4.2E-01	0.1	9.4E-01	-1.2	4.3E-01	-0.1	9.7E-01
ENSMUST00000023076	Nfat activating molecule with ITAM motif 1 [Source:MGI Symbol;Acc:MGI:1921289]		Q8R4V1	0.7	7.9E-01	2.6	3.9E-01	1.4	5.9E-01	-0.5	8.5E-01
ENSMUST00000023143	LPS-induced TN factor [Source:MGI Symbol;Acc:MGI:1929512]		Q9JLJ0	-6.7	2.1E-05	3.3	1.1E-03	0.3	5.9E-01	-0.5	3.5E-01
ENSMUST00000023146	nucleotide binding protein 1 [Source:MGI Symbol;Acc:MGI:1347073]		Q9R060	-3.6	1.2E-02	-6.8	6.0E-05	-0.9	4.8E-02	0.0	9.9E-01
ENSMUST00000023147	class II transactivator [Source:MGI Symbol;Acc:MGI:108445]	Q3U5G4	P79621	5.0	7.0E-05	-5.2	1.6E-03	0.8	1.2E-01	-0.3	8.3E-01
ENSMUST00000023150	RIKEN cDNA 1810013L24 gene [Source:MGI Symbol;Acc:MGI:1916303]		Q14AM7	-3.3	2.0E-03	-3.6	7.2E-04	0.3	4.9E-01	0.5	5.1E-01
ENSMUST00000023151	B cell leukemia/lymphoma 6 [Source:MGI Symbol;Acc:MGI:107187]	Q544F9	P41183	-4.3	2.1E-04	-1.9	2.5E-02	0.8	7.7E-02	-0.7	3.9E-01
ENSMUST00000023156	interleukin 1 receptor accessory protein [Source:MGI Symbol;Acc:MGI:104975]		Q61730	-5.3	7.0E-07	6.4	6.8E-04	-0.1	9.6E-01	-1.1	1.8E-01
ENSMUST00000023157	ankyrin repeat and sterile alpha motif domain containing 3 [Source:MGI Symbol;Acc:MGI:1919865]		Q9CZK6	-2.0	4.3E-03	3.6	1.2E-03	-2.6	7.4E-03	0.2	7.1E-01
ENSMUST00000023161	sarcalumenin [Source:MGI Symbol;Acc:MGI:2146620]		Q7TQ48	8.6	4.8E-06	-3.0	1.1E-03	1.0	1.4E-02	-0.2	8.0E-01
ENSMUST00000023171	hairy and enhancer of split 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:104853]	Q3UZZ2	P35428	3.1	6.5E-03	-1.4	5.3E-02	1.2	1.3E-02	0.3	6.6E-01
ENSMUST00000023176	zinc finger protein 263 [Source:MGI Symbol;Acc:MGI:1921370]	Q8CF60		-2.9	1.0E-02	4.2	1.4E-03	-2.7	2.7E-02	-0.9	2.0E-01
ENSMUST00000023104	RNA polymerase II associated protein 3 [Source:MGI Symbol;Acc:MGI:1277218]		Q9D706	1.1	1.1E-01	1.4	1.0E-01	-0.6	4.0E-01	-0.8	2.8E-01
ENSMUST00000023112	phosphomannomutase 1 [Source:MGI Symbol;Acc:MGI:1353418]	Q545Q8	O35621	-1.9	3.2E-01	-0.9	6.0E-01	-1.4	3.0E-01	-2.4	2.6E-01
ENSMUST00000023180	Mediterranean fever [Source:MGI Symbol;Acc:MGI:1859396]		Q9JJ26	-6.1	4.7E-03	3.1	1.5E-03	0.3	6.7E-01	-0.5	3.5E-01
ENSMUST00000023189	glyoxylate reductase 1 homolog (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1921272]		Q922P9	-3.6	2.1E-02	-2.6	5.9E-04	0.4	2.0E-01	-0.3	5.6E-01
ENSMUST00000023191	rogdi homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913299]		Q3TDK6	-4.6	1.7E-04	-1.7	1.7E-02	0.3	4.2E-01	-1.0	1.3E-01
ENSMUST00000023203	glutamic pyruvic transaminase, soluble [Source:MGI Symbol;Acc:MGI:95802]	Q566C3	Q8QZR5	1.4	2.0E-02	2.3	7.1E-03	-1.0	1.2E-01	0.3	6.4E-01
ENSMUST00000023123	collagen, type II, alpha 1 [Source:MGI Symbol;Acc:MGI:88452]		P28481	2.7	4.7E-02	7.5	1.0E-04	-0.5	6.8E-01	-5.3	1.8E-04
ENSMUST00000023210	cytochrome c-1 [Source:MGI Symbol;Acc:MGI:1913695]		Q9D0M3	-3.5	4.7E-04	-1.1	1.7E-01	1.0	5.7E-02	-0.2	7.6E-01
ENSMUST00000023211	SHANK-associated RH domain interacting protein [Source:MGI Symbol;Acc:MGI:1913331]		Q91WA6	-7.2	2.6E-04	-2.6	7.3E-02	-0.1	9.1E-01	-0.4	7.4E-01
ENSMUST00000023212	MAF1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916127]		Q9D0U6	-9.5	1.4E-04	3.9	2.7E-02	0.1	9.7E-01	-0.4	7.1E-01
ENSMUST00000023138	shisa family member 9 [Source:MGI Symbol;Acc:MGI:1919805]	E9QN38		3.9	8.3E-02	6.2	2.1E-02	-0.3	9.0E-01	-2.6	8.6E-02
ENSMUST00000023213	HGH1 homolog [Source:MGI Symbol;Acc:MGI:1930628]		Q8C3I8	1.8	1.1E-02	4.2	5.3E-03	-1.9	1.8E-01	-0.1	8.8E-01
ENSMUST00000023214	diacylglycerol O-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:1333825]	Q54AA6	Q9Z2A7	-5.7	7.8E-04	-5.2	1.1E-03	1.6	9.0E-03	0.1	9.0E-01
ENSMUST00000023219	F-box and leucine-rich repeat protein 6 [Source:MGI Symbol;Acc:MGI:1354705]		Q9QXW0	-2.7	1.8E-03	-2.9	1.1E-01	0.4	6.9E-01	-0.3	8.7E-01
ENSMUST00000023221	GPI anchor attachment protein 1 [Source:MGI Symbol;Acc:MGI:1202392]		Q9WTK3	-3.4	1.0E-02	3.8	1.7E-03	-0.9	3.1E-01	0.3	5.9E-01
ENSMUST00000023225	ceptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding) [Source:MGI Symbol;Acc:M		Q9ESF4	-8.3	1.2E-05	-2.9	2.5E-02	1.1	9.5E-02	0.7	5.4E-01
ENSMUST00000023231	tissue specific transplantation antigen P35B [Source:MGI Symbol;Acc:MGI:98857]	Q5HZI6	P23591	-3.4	4.5E-04	-3.7	4.6E-03	1.0	6.5E-02	0.4	7.0E-01
ENSMUST00000023154	claudin 1 [Source:MGI Symbol;Acc:MGI:1276109]	Q4FJV3	O88551	0.8	1.6E-01	1.5	5.1E-02	0.1	7.9E-01	-0.5	3.8E-01
ENSMUST00000023235	ic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Source:MGI Symbol;Acc:MGI:1	E9QN08		-6.0	1.3E-04	-4.8	8.7E-06	-0.3	1.7E-01	-0.9	1.2E-01
ENSMUST00000023238	gasdermin D [Source:MGI Symbol;Acc:MGI:1916396]		Q9D8T2	-5.0	1.3E-05	-1.1	1.3E-01	0.6	1.9E-01	-0.3	6.9E-01
ENSMUST00000023159	mahogunin, ring finger 1 [Source:MGI Symbol;Acc:MGI:2447670]		Q9D074	-3.0	4.9E-02	1.3	4.5E-01	2.2	1.3E-01	-2.0	2.0E-01
ENSMUST00000023246	lymphocyte antigen 6 complex, locus G [Source:MGI Symbol;Acc:MGI:109440]		P35461	-9.3	1.1E-05	8.6	1.0E-05	-0.6	6.0E-01	-0.5	2.4E-01
ENSMUST00000023165	CREB binding protein [Source:MGI Symbol;Acc:MGI:1098280]	F8VPR5		-0.1	7.1E-01	0.2	7.8E-01	0.8	7.1E-02	0.5	3.3E-01
ENSMUST00000023259	Ly6/neurotoxin 1 [Source:MGI Symbol;Acc:MGI:1345180]		Q9WVC2	6.0	4.6E-05	2.0	5.6E-02	-2.2	3.4E-02	-1.1	1.8E-01
ENSMUST00000023265	prostate stem cell antigen [Source:MGI Symbol;Acc:MGI:1919623]	Q9D7U0		5.7	3.1E-03	-3.2	3.1E-02	0.4	5.9E-01	0.7	5.8E-01
ENSMUST00000023179	zinc finger protein 7 [Source:MGI Symbol;Acc:MGI:99208]	Q3TFZ4		0.9	6.6E-02	1.1	8.8E-02	0.0	9.2E-01	-0.1	8.2E-01
ENSMUST00000023268	activity regulated cytoskeletal-associated protein [Source:MGI Symbol;Acc:MGI:88067]		Q9WV31	8.5	4.7E-04	-7.6	2.2E-02	0.1	9.5E-01	1.6	6.0E-01
ENSMUST00000023269	ribosomal protein L24 [Source:MGI Symbol;Acc:MGI:1915443]		Q8BP67	-6.1	1.2E-05	-2.3	1.6E-01	-0.3	7.2E-01	-1.6	3.3E-01
ENSMUST00000023270	centrosomal protein 97 [Source:MGI Symbol;Acc:MGI:1921451]		Q9CZ62	4.5	2.6E-05	-2.6	1.8E-02	1.3	3.0E-02	-0.7	4.7E-01
ENSMUST00000023271	maestro heat-like repeat family member 4 [Source:MGI Symbol;Acc:MGI:1916689]	G3X8W1		7.6	1.7E-05	1.5	3.9E-02	0.3	5.7E-01	0.1	7.9E-01
ENSMUST00000023206	epair cross-complementing rodent repair deficiency, complementation group 4 [Source:MGI Symbol;Acc:MGI:		Q9QZD4	-1.3	5.9E-02	-1.2	1.9E-01	0.6	3.1E-01	0.5	5.6E-01
ENSMUST00000023285	thymidine phosphorylase [Source:MGI Symbol;Acc:MGI:1920212]		Q99N42	5.7	4.6E-05	-2.3	2.2E-02	1.0	6.9E-02	-0.3	7.2E-01
ENSMUST00000023289	choline kinase beta [Source:MGI Symbol;Acc:MGI:1328313]	Q54AG5	O55229	-5.6	3.2E-04	-4.6	4.8E-03	1.0	1.3E-01	-1.6	3.0E-01
ENSMUST00000023291	mitogen-activated protein kinase 8 interacting protein 2 [Source:MGI Symbol;Acc:MGI:1926555]	Q548W8	Q9ERE9	9.6	1.6E-05	-4.9	3.6E-03	1.1	8.9E-02	-3.5	6.5E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000023295	acrosin preppeptide [Source:MGI Symbol;Acc:MGI:87884]		P23578	7.2	5.6E-05	2.2	1.4E-02	0.1	8.6E-01	-0.2	7.2E-01
ENSMUST00000023330	microrchidia 1 [Source:MGI Symbol;Acc:MGI:1316740]		Q9WVL5	5.9	6.9E-04	-3.8	1.5E-02	1.1	1.2E-01	-0.8	5.8E-01
ENSMUST00000023217	block of proliferation 1 [Source:MGI Symbol;Acc:MGI:1334460]		P97452	0.0	9.2E-01	0.1	8.9E-01	0.0	9.2E-01	-0.1	8.8E-01
ENSMUST00000023335	poliovirus receptor-related 3 [Source:MGI Symbol;Acc:MGI:1930171]		Q9JLB9	9.5	4.2E-06	-0.8	2.9E-01	0.9	9.1E-02	-1.0	2.3E-01
ENSMUST00000023220	solute carrier protein 52, member 2 [Source:MGI Symbol;Acc:MGI:1289288]		Q9D8F3	0.2	7.1E-01	1.2	1.7E-01	0.8	2.1E-01	-0.1	8.6E-01
ENSMUST00000023339	germinal center associated, signaling and motility [Source:MGI Symbol;Acc:MGI:102969]		Q6RFH4	8.0	9.9E-06	-0.8	5.6E-01	1.3	1.7E-01	-1.4	3.1E-01
ENSMUST00000023222	5-oxoprolinase (ATP-hydrolysing) [Source:MGI Symbol;Acc:MGI:1922725]		Q8K010	-1.1	4.8E-01	-2.4	3.4E-01	0.6	6.4E-01	2.0	4.4E-01
ENSMUST00000023343	autophagy related 3 [Source:MGI Symbol;Acc:MGI:1915091]		Q9CPX6	-7.9	3.3E-06	-6.9	3.3E-04	1.2	4.3E-02	-0.2	8.8E-01
ENSMUST00000023226	plectin [Source:MGI Symbol;Acc:MGI:1277961]		Q9QXS1	-0.7	5.0E-01	-0.1	9.6E-01	0.9	3.7E-01	0.2	8.6E-01
ENSMUST00000023344	solute carrier family 35, member A5 [Source:MGI Symbol;Acc:MGI:1921352]		Q921R7	-6.1	6.6E-06	-2.9	5.0E-03	0.1	7.9E-01	-0.4	6.2E-01
ENSMUST00000023352	protein kinase, DNA activated, catalytic polypeptide [Source:MGI Symbol;Acc:MGI:104779]		P97313	1.4	2.1E-02	-5.6	1.0E-03	-0.4	4.3E-01	-0.7	5.9E-01
ENSMUST00000023237	nicotinate phosphoribosyltransferase [Source:MGI Symbol;Acc:MGI:2442664]		Q8CC86	-1.7	4.3E-02	-0.1	9.5E-01	1.9	2.3E-02	0.3	7.6E-01
ENSMUST00000023353	minichromosome maintenance deficient 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:103199]	Q542F4	P49717	-2.0	1.6E-03	-4.0	3.3E-04	0.4	2.7E-01	-0.6	4.7E-01
ENSMUST00000023356	snail family zinc finger 2 [Source:MGI Symbol;Acc:MGI:1096393]	Q3UZ96	P97469	8.1	2.1E-05	-9.0	4.8E-05	-0.3	3.9E-01	-0.6	6.8E-01
ENSMUST00000023250	lymphocyte antigen 6 complex, locus I [Source:MGI Symbol;Acc:MGI:1888480]		Q9WU67	0.5	4.5E-01	1.5	8.6E-02	0.2	7.5E-01	-0.8	2.9E-01
ENSMUST00000023357	Fgfr1op N-terminal like [Source:MGI Symbol;Acc:MGI:1913336]		Q9CZS3	-7.1	8.1E-05	4.8	2.2E-04	-1.7	6.9E-02	-0.5	3.7E-01
ENSMUST00000023361	pyridoxal-dependent decarboxylase domain containing 1 [Source:MGI Symbol;Acc:MGI:1920909]			1.6	1.4E-02	6.2	2.4E-03	-1.5	3.9E-01	-2.0	4.8E-02
ENSMUST00000023362	N-terminal Asn amidase [Source:MGI Symbol;Acc:MGI:108471]		Q64311	-5.5	2.2E-03	3.1	1.3E-01	-1.5	4.3E-01	3.9	1.6E-02
ENSMUST00000023364	phospholipase A2, group X [Source:MGI Symbol;Acc:MGI:1347522]		Q9QXX3	6.5	3.7E-04	-6.8	3.1E-05	-1.2	1.1E-02	-0.4	6.3E-01
ENSMUST00000023365	bifunctional apoptosis regulator [Source:MGI Symbol;Acc:MGI:1914368]			-1.9	3.0E-02	3.8	3.9E-04	-0.3	6.7E-01	0.4	4.3E-01
ENSMUST00000023370	ll adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein [Source:MGI Symbol;Acc:M			8.1	1.6E-04	8.0	2.2E-05	-0.5	6.2E-01	-0.9	8.8E-02
ENSMUST00000023276	trafficking protein particle complex 9 [Source:MGI Symbol;Acc:MGI:1923760]		Q3U0M1	-2.3	7.1E-02	-2.4	1.7E-01	1.1	2.6E-01	1.3	4.5E-01
ENSMUST00000023283	lipase maturation factor 2 [Source:MGI Symbol;Acc:MGI:2146015]		Q8C3X8	-0.4	4.6E-01	0.5	5.3E-01	1.0	1.0E-01	0.1	9.2E-01
ENSMUST00000023390	dopamine receptor D3 [Source:MGI Symbol;Acc:MGI:94925]	Q0VEC4	P30728	6.8	6.9E-05	4.2	3.8E-04	-1.6	7.1E-02	-0.2	7.7E-01
ENSMUST00000023396	phosphomannomutase 2 [Source:MGI Symbol;Acc:MGI:1859214]	Q545N8	Q9Z2M7	-2.4	2.9E-04	-4.8	5.5E-03	0.8	1.7E-01	0.1	9.7E-01
ENSMUST00000023400	transmembrane protein 114 [Source:MGI Symbol;Acc:MGI:1921970]		Q9D563	8.1	1.9E-05	8.5	5.2E-05	-0.9	5.0E-01	0.2	7.4E-01
ENSMUST00000023407	myc induced nuclear antigen [Source:MGI Symbol;Acc:MGI:1914264]		Q8CD15	-4.4	2.2E-04	-1.3	1.7E-01	1.0	9.5E-02	-0.1	8.8E-01
ENSMUST00000023426	claudin domain containing 1 [Source:MGI Symbol;Acc:MGI:2447860]		Q9CQX5	-5.7	3.2E-04	7.2	1.1E-04	-0.6	6.1E-01	-0.6	3.6E-01
ENSMUST00000023312	activated leukocyte cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1313266]	Q54AJ5	Q61490	-0.5	4.8E-01	-0.3	7.2E-01	0.1	9.2E-01	-0.1	8.8E-01
ENSMUST00000023329	resistin like alpha [Source:MGI Symbol;Acc:MGI:1888504]	G3X8W2		-1.5	2.3E-01	-3.7	1.8E-02	-3.2	6.0E-03	-1.0	4.7E-01
ENSMUST00000023431	TBC1 domain family, member 23 [Source:MGI Symbol;Acc:MGI:1914831]		Q8K0F1	-5.2	6.8E-06	6.2	5.4E-04	-1.1	4.2E-01	-1.4	8.4E-02
ENSMUST00000023434	transmembrane protein 30C [Source:MGI Symbol;Acc:MGI:1918277]		Q9D4D7	6.0	7.5E-03	7.9	4.8E-05	-1.0	3.8E-01	0.6	2.7E-01
ENSMUST00000023336	CD96 antigen [Source:MGI Symbol;Acc:MGI:1934368]		Q3U0X8	1.5	7.9E-02	0.3	7.1E-01	-1.7	3.7E-02	-0.5	5.2E-01
ENSMUST00000023437	adhesion G protein-coupled receptor G7 [Source:MGI Symbol;Acc:MGI:2441732]		Q8BM96	4.0	2.9E-04	4.6	6.3E-05	-4.0	1.3E-03	-0.6	2.5E-01
ENSMUST00000023341	CD200 antigen [Source:MGI Symbol;Acc:MGI:1196990]	E9QMY1		4.0	6.3E-02	5.8	3.1E-02	0.4	8.6E-01	-1.5	3.4E-01
ENSMUST00000023441	purinergic receptor P2X, ligand-gated ion channel, 6 [Source:MGI Symbol;Acc:MGI:1337113]	G3X8W3		6.7	3.7E-04	-9.8	5.3E-05	0.1	8.6E-01	1.9	1.8E-01
ENSMUST00000023442	leucine rich repeat containing 74B [Source:MGI Symbol;Acc:MGI:1921935]		Q14BP6	8.1	8.5E-05	-4.8	2.2E-04	0.9	3.6E-02	-0.4	6.7E-01
ENSMUST00000023351	mitotic spindle organizing protein 2 [Source:MGI Symbol;Acc:MGI:1922845]		Q9CQ25	-0.9	2.5E-01	-0.9	3.7E-01	0.1	8.7E-01	0.1	9.1E-01
ENSMUST00000023444	leucine-zipper-like transcriptional regulator, 1 [Source:MGI Symbol;Acc:MGI:1914113]		Q9CQ33	-7.0	5.4E-04	1.5	3.4E-02	-0.3	5.2E-01	-0.5	4.0E-01
ENSMUST00000023448	apoptosis-inducing factor, mitochondrion-associated 3 [Source:MGI Symbol;Acc:MGI:1919418]		Q3TY86	5.4	1.3E-02	-1.3	4.5E-02	0.6	1.3E-01	-0.1	9.3E-01
ENSMUST00000023449	synaptosomal-associated protein 29 [Source:MGI Symbol;Acc:MGI:1914724]		Q9ERB0	-5.1	1.3E-05	6.9	8.2E-04	-0.2	9.1E-01	1.0	1.7E-01
ENSMUST00000023450	serine (or cysteine) peptidase inhibitor, clade D, member 1 [Source:MGI Symbol;Acc:MGI:96051]		P49182	5.1	1.7E-02	-7.2	1.5E-03	0.3	5.5E-01	0.5	7.8E-01
ENSMUST00000023359	nuclear distribution gene E homolog 1 (A nidulans) [Source:MGI Symbol;Acc:MGI:1914453]		Q9CZA6	-1.1	6.9E-01	1.8	5.5E-01	0.4	8.7E-01	-2.5	3.6E-01
ENSMUST00000023360	Mpv17 transgene, kidney disease mutant-like [Source:MGI Symbol;Acc:MGI:2135951]		Q99MS3	4.0	7.2E-02	5.5	3.3E-02	-0.1	9.8E-01	-1.6	3.3E-01
ENSMUST00000023452	coiled-coil domain containing 116 [Source:MGI Symbol;Acc:MGI:1924122]		Q80X53	4.9	1.2E-04	1.2	9.1E-02	-0.7	2.1E-01	-0.3	6.4E-01
ENSMUST00000023455	peptidylprolyl isomerase (cyclophilin)-like 2 [Source:MGI Symbol;Acc:MGI:2447857]		Q9D787	-5.2	1.7E-05	-6.7	3.5E-03	-1.0	1.4E-01	0.3	8.9E-01
ENSMUST00000023363	RRN3 RNA polymerase I transcription factor homolog (yeast) [Source:MGI Symbol;Acc:MGI:1925255]		B2RS91	0.0	9.3E-01	0.6	4.1E-01	0.7	2.1E-01	0.1	8.4E-01
ENSMUST00000023460	nuclear cap binding protein subunit 2 [Source:MGI Symbol;Acc:MGI:1915342]		Q9CQ49	-2.4	8.6E-03	4.6	8.2E-03	-0.6	6.7E-01	1.4	1.6E-01
ENSMUST00000023462	mitogen-activated protein kinase 1 [Source:MGI Symbol;Acc:MGI:1346858]		P63085	-6.6	9.9E-05	-2.8	2.8E-02	0.4	5.6E-01	1.3	2.6E-01
ENSMUST00000023464	97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 [Source:MGI Symbol;Acc:MGI:	Q544J8	Q9R0R1	8.0	2.6E-05	5.7	1.9E-04	-3.6	1.9E-02	-1.2	1.2E-01
ENSMUST00000023387	queuine tRNA-ribosyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:1922194]	Z4YJE9		1.3	4.2E-01	2.0	2.8E-01	-0.8	6.2E-01	-1.5	3.6E-01
ENSMUST00000023467	p21 protein (Cdc42/Rac)-activated kinase 2 [Source:MGI Symbol;Acc:MGI:1339984]		Q8CIN4	-5.2	1.3E-05	7.3	9.1E-05	-0.1	9.1E-01	-0.6	3.0E-01
ENSMUST00000023391	mitochondrial ribosomal protein L40 [Source:MGI Symbol;Acc:MGI:1332635]	Q3UKS6	Q9Z2Q5	0.2	7.2E-01	-1.2	5.0E-02	-0.9	3.3E-02	0.5	4.1E-01
ENSMUST00000023478	immunoglobulin superfamily, member 11 [Source:MGI Symbol;Acc:MGI:2388477]		P0C673	7.7	4.8E-04	-1.8	7.9E-03	0.3	4.2E-01	-0.4	4.8E-01
ENSMUST00000023487	Rho GTPase activating protein 31 [Source:MGI Symbol;Acc:MGI:1333857]	B2RSI0	A6X8Z5	3.5	3.7E-05	6.9	1.4E-04	-0.6	6.4E-01	0.7	2.7E-01
ENSMUST00000023489	forty-two-three domain containing 1 [Source:MGI Symbol;Acc:MGI:1917955]		Q91Z49	-5.8	6.3E-05	-4.7	9.0E-04	-0.1	8.9E-01	0.2	8.4E-01
ENSMUST00000023491	ucine-rich repeats and calponin homology (CH) domain containing 3 [Source:MGI Symbol;Acc:MGI:1917394		Q8BVU0	-2.4	1.2E-03	-3.5	1.5E-02	1.1	1.0E-01	-1.2	3.9E-01
ENSMUST00000023494	popeye domain containing 2 [Source:MGI Symbol;Acc:MGI:1930150]	Q6P3F7		8.0	2.2E-04	-5.0	5.5E-05	-0.2	6.3E-01	-0.4	6.2E-01
ENSMUST00000023432	nitrilase family, member 2 [Source:MGI Symbol;Acc:MGI:1261838]		Q9JHW2	-1.2	6.8E-02	-1.6	4.5E-02	-0.6	2.1E-01	-0.2	7.4E-01
ENSMUST00000023497	leishmanolysin-like (metallopeptidase M8 family) [Source:MGI Symbol;Acc:MGI:2444736]		Q8BMN4	5.3	6.5E-06	6.6	2.3E-02	0.8	7.5E-01	0.2	8.8E-01
ENSMUST00000023501	MYCBP-associated, testis expressed 1 [Source:MGI Symbol;Acc:MGI:2443598]		Q8BRC6	6.8	8.8E-05	7.0	1.1E-04	1.9	9.0E-02	-1.1	9.8E-02
ENSMUST00000023502	sorting nexin 4 [Source:MGI Symbol;Acc:MGI:1916400]		Q91YJ2	-4.3	1.5E-05	6.7	7.5E-04	-0.5	7.5E-01	-0.4	5.6E-01
ENSMUST00000023504	nuclear receptor subfamily 1, group I, member 2 [Source:MGI Symbol;Acc:MGI:1337040]	Q0P525	O54915	7.0	4.0E-05	7.3	4.0E-04	-0.3	8.6E-01	0.5	4.8E-01
ENSMUST00000023509	kelch-like 24 [Source:MGI Symbol;Acc:MGI:1923035]		Q8BRG6	-3.4	3.1E-06	-2.6	4.8E-02	1.0	1.6E-01	-3.5	4.3E-02
ENSMUST00000023514	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4 [Source:MGI Symbol;Acc:MGI:1915444]		Q9CQC7	-1.9	3.3E-02	6.2	1.2E-02	-0.1	9.6E-01	-1.0	4.2E-01
ENSMUST00000023524	RAB, member RAS oncogene family-like 3 [Source:MGI Symbol;Acc:MGI:1914907]		Q9D4V7	-5.6	2.4E-04	-3.7	6.2E-04	0.8	6.0E-02	-0.6	4.4E-01
ENSMUST00000023525	general transcription factor II E, polypeptide 1 (alpha subunit) [Source:MGI Symbol;Acc:MGI:1921447]		Q9D0D5	-1.2	1.9E-02	2.4	3.0E-01	-0.7	7.2E-01	2.0	2.7E-01
ENSMUST00000023531	hematopoietic cell specific Lyn substrate 1 [Source:MGI Symbol;Acc:MGI:104568]		P49710	-6.9	1.4E-05	6.4	2.8E-04	1.4	2.1E-01	-0.1	8.9E-01
ENSMUST00000023453	stromal cell-derived factor 2-like 1 [Source:MGI Symbol;Acc:MGI:2149842]		Q9ESP1	-0.8	2.0E-01	0.1	9.1E-01	0.1	8.8E-01	-0.8	2.7E-01
ENSMUST00000023454	discs, large homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:107231]	H7BWY4		-1.6	5.6E-01	-3.4	3.3E-01	-2.2	2.7E-01	-0.3	9.3E-01
ENSMUST00000023532	coiled-coil domain containing 14 [Source:MGI Symbol;Acc:MGI:2443448]		Q8K2J4	2.2	4.6E-03	-5.4	4.3E-04	0.5	2.6E-01	0.6	5.5E-01
ENSMUST00000023457	SUMO/sentrin specific peptidase 5 [Source:MGI Symbol;Acc:MGI:2443596]		Q6NXL6	0.2	6.8E-01	1.3	5.7E-02	0.2	6.2E-01	-0.8	1.5E-01
ENSMUST00000023538	myosin, light polypeptide kinase [Source:MGI Symbol;Acc:MGI:894806]	B1B1A8		5.1	2.9E-06	-2.4	2.4E-02	-0.1	8.6E-01	-0.1	9.3E-01
ENSMUST00000023550	protein disulfide isomerase associated 5 [Source:MGI Symbol;Acc:MGI:1919849]		Q921X9	2.5	1.1E-03	-4.2	1.4E-03	0.9	7.2E-02	-1.4	2.3E-01
ENSMUST00000023554	disrupted in renal carcinoma 2 (human) [Source:MGI Symbol;Acc:MGI:2387188]		Q8BFQ6	1.4	2.3E-02	8.3	6.0E-05	-0.1	9.4E-01	-0.4	5.2E-01
ENSMUST00000023465	topoisomerase (DNA) III beta [Source:MGI Symbol;Acc:MGI:1333803]	Q3UJF5	Q9Z321	-3.1	4.9E-02	-2.6	1.7E-01	0.1	9.5E-01	-0.5	8.0E-01
ENSMUST00000023559	oyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase [Source:MGI Symbol;Acc:MGI:12779(		Q9DBM2	4.4	1.6E-04	-3.8	9.5E-04	1.3	8.4E-03	-0.1	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000023561	SUMO/sentrin specific peptidase 2 [Source:MGI Symbol;Acc:MGI:1923076]		Q91ZX6	-3.0	3.4E-03	2.2	4.5E-02	-0.7	4.0E-01	0.5	5.4E-01
ENSMUST00000023474	WD repeat domain 53 [Source:MGI Symbol;Acc:MGI:1916230]		Q9DB94	-0.2	6.8E-01	0.7	3.4E-01	0.4	4.7E-01	-0.6	4.3E-01
ENSMUST00000023477	dynamin 1-like [Source:MGI Symbol;Acc:MGI:1921256]		Q8K1M6	0.0	9.9E-01	-2.2	1.3E-01	-0.3	7.2E-01	1.9	1.7E-01
ENSMUST00000023562	transmembrane protein 41a [Source:MGI Symbol;Acc:MGI:1913914]		Q9D8U2	2.1	8.1E-03	6.9	1.8E-03	-0.6	7.3E-01	0.2	8.1E-01
ENSMUST00000023486	transferrin receptor [Source:MGI Symbol;Acc:MGI:98822]	Q542D9	Q62351	-1.4	5.2E-02	-3.0	4.4E-03	-0.7	1.5E-01	0.9	2.8E-01
ENSMUST00000023564	transformer 2 beta homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:106016]	F8WJG3		-3.5	2.1E-03	2.4	2.5E-03	-0.6	2.6E-01	0.5	2.5E-01
ENSMUST00000023572	coxsackie virus and adenovirus receptor [Source:MGI Symbol;Acc:MGI:1201679]		P97792	2.0	1.9E-02	-2.5	4.8E-03	0.0	9.1E-01	-3.2	5.7E-03
ENSMUST00000023580	ubiquitin specific peptidase 25 [Source:MGI Symbol;Acc:MGI:1353655]		P57080	-4.7	7.9E-05	-1.6	4.7E-02	0.9	5.5E-02	0.1	9.2E-01
ENSMUST00000023583	alpha-2-HS-glycoprotein [Source:MGI Symbol;Acc:MGI:107189]	Q3UEK9	P29699	5.0	4.4E-03	6.1	9.7E-04	-2.8	8.6E-02	-0.9	2.6E-01
ENSMUST00000023590	histidine-rich glycoprotein [Source:MGI Symbol;Acc:MGI:2146636]			5.8	6.1E-04	5.2	2.1E-05	-0.1	8.2E-01	0.0	9.8E-01
ENSMUST00000023593	adiponectin, C1Q and collagen domain containing [Source:MGI Symbol;Acc:MGI:106675]		Q60994	5.1	1.3E-03	6.0	4.0E-04	-0.5	6.6E-01	0.2	7.2E-01
ENSMUST00000023598	replication factor C (activator 1) 4 [Source:MGI Symbol;Acc:MGI:2146571]		Q99J62	-4.7	1.1E-04	-4.9	5.0E-05	-0.4	2.8E-01	0.3	7.2E-01
ENSMUST00000023600	roundabout homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1274781]	G5E843		9.0	1.4E-05	6.5	8.3E-05	-1.3	2.4E-01	-0.8	1.5E-01
ENSMUST00000023507	glycogen synthase kinase 3 beta [Source:MGI Symbol;Acc:MGI:1861437]	Q5KU03	Q9WV60	0.2	6.4E-01	0.4	4.7E-01	0.8	7.4E-02	0.6	2.4E-01
ENSMUST00000023608	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F [Source:MGI Symbol;Acc:MGI:107777]		P97450	-8.0	2.4E-05	-3.1	5.2E-05	0.4	1.3E-01	0.2	7.0E-01
ENSMUST00000023510	uridine monophosphate synthetase [Source:MGI Symbol;Acc:MGI:1298388]	Q544K9	P13439	-0.4	6.1E-01	-2.3	8.4E-02	-0.1	9.2E-01	1.8	1.5E-01
ENSMUST00000023610	ı-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1 [Source:MGI Symbol;Acc:M		P97857	6.7	5.1E-05	-2.4	3.0E-02	-1.0	1.3E-01	-0.6	5.5E-01
ENSMUST00000023520	mucin 13, epithelial transmembrane [Source:MGI Symbol;Acc:MGI:103190]	Q3V1S6	P19467	2.3	2.8E-01	3.5	1.3E-01	0.3	9.0E-01	-0.9	6.1E-01
ENSMUST00000023611	l metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) [Source:MGI Symbo		Q9R001	2.9	2.4E-03	-3.7	1.3E-02	1.0	1.2E-01	-0.9	5.0E-01
ENSMUST00000023612	E26 avian leukemia oncogene 2, 3' domain [Source:MGI Symbol;Acc:MGI:95456]	Q3UP99	P15037	-3.3	2.2E-03	-0.9	1.2E-01	0.0	9.1E-01	-0.3	5.6E-01
ENSMUST00000023615	Down syndrome critical region gene 3 [Source:MGI Symbol;Acc:MGI:1206040]		O35075	-4.1	3.8E-06	-4.7	8.3E-04	1.2	2.1E-02	-0.9	3.9E-01
ENSMUST00000023616	solute carrier family 15 (H+/peptide transporter), member 2 [Source:MGI Symbol;Acc:MGI:1890457]	E9QMN8		4.9	1.4E-02	1.5	4.9E-02	-0.7	2.4E-01	-0.1	8.7E-01
ENSMUST00000023619	stefin A2 [Source:MGI Symbol;Acc:MGI:106197]		P35174	-9.8	6.5E-06	3.8	3.8E-05	-1.7	7.3E-03	-0.4	2.4E-01
ENSMUST00000023622	poly (ADP-ribose) polymerase family, member 9 [Source:MGI Symbol;Acc:MGI:1933117]	H7BWY5		-9.3	5.6E-05	1.5	4.2E-02	-0.8	1.7E-01	0.2	6.4E-01
ENSMUST00000023630	proteasome (prosome, macropain) assembly chaperone 1 [Source:MGI Symbol;Acc:MGI:1860263]		Q9JK23	-3.5	1.6E-02	2.1	9.9E-03	0.4	4.6E-01	-0.3	5.6E-01
ENSMUST00000023555	Hspb associated protein 1 [Source:MGI Symbol;Acc:MGI:1913917]		Q8BK58	0.1	7.5E-01	0.8	2.0E-01	0.2	5.8E-01	-0.4	4.7E-01
ENSMUST00000023660	ripply3 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2181192]		Q924S9	7.0	3.4E-05	3.2	3.1E-03	-1.2	1.4E-01	0.0	9.4E-01
ENSMUST00000023670	chloride intracellular channel 6 [Source:MGI Symbol;Acc:MGI:2146607]		Q8BHB9	8.8	1.0E-05	-2.4	4.7E-02	0.9	1.6E-01	0.3	8.1E-01
ENSMUST00000023672	regulator of calcineurin 1 [Source:MGI Symbol;Acc:MGI:1890564]	Q542V6	Q9JHG6	-2.5	2.9E-02	1.3	1.0E-01	-0.8	2.6E-01	0.1	9.3E-01
ENSMUST00000023677	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit [Source:MGI Symbol;Acc:MGI:106341]		Q9DB20	-6.7	9.6E-05	-3.8	6.0E-03	0.2	7.8E-01	0.5	6.7E-01
ENSMUST00000023570	B cell translocation gene 3 [Source:MGI Symbol;Acc:MGI:109532]	Q52L83	P50615	1.8	4.5E-01	2.2	5.1E-01	0.6	8.1E-01	0.2	9.3E-01
ENSMUST00000023682	downstream neighbor of SON [Source:MGI Symbol;Acc:MGI:1890621]		Q9QXP4	-6.4	7.7E-04	1.2	1.3E-01	-1.7	3.4E-02	-0.9	2.4E-01
ENSMUST00000023578	diacylglycerol kinase, gamma [Source:MGI Symbol;Acc:MGI:105060]	Q8C413		2.3	1.9E-01	1.1	6.2E-01	-0.9	6.5E-01	0.3	8.9E-01
ENSMUST00000023686	transmembrane protein 50B [Source:MGI Symbol;Acc:MGI:1925225]		Q9D1X9	-6.0	1.5E-06	-3.2	4.3E-03	0.6	2.1E-01	-0.9	3.2E-01
ENSMUST00000023687	interferon gamma receptor 2 [Source:MGI Symbol;Acc:MGI:107654]	Q63953		-6.3	6.2E-04	0.7	5.4E-01	-5.5	2.6E-03	-1.2	2.6E-01
ENSMUST00000023689	interferon (alpha and beta) receptor 1 [Source:MGI Symbol;Acc:MGI:107658]		P33896	-3.7	7.3E-04	3.0	1.8E-02	-3.0	3.1E-02	-0.2	8.0E-01
ENSMUST00000023691	interleukin 10 receptor, beta [Source:MGI Symbol;Acc:MGI:109380]	Q8VHM7		-10.3	1.1E-06	6.6	3.9E-04	-0.4	7.5E-01	-2.0	1.9E-02
ENSMUST00000023693	interferon (alpha and beta) receptor 2 [Source:MGI Symbol;Acc:MGI:1098243]		O35664	-4.3	6.5E-04	-3.3	2.9E-03	0.2	6.9E-01	-1.1	2.4E-01
ENSMUST00000023694	RIKEN cDNA 1110004E09 gene [Source:MGI Symbol;Acc:MGI:1915251]		Q8BL95	-3.0	9.0E-03	8.3	3.4E-05	-1.0	4.5E-01	-0.2	6.3E-01
ENSMUST00000023601	beta galactoside alpha 2,6 sialyltransferase 1 [Source:MGI Symbol;Acc:MGI:108470]		Q64685	1.7	1.6E-01	3.3	4.4E-02	0.1	9.3E-01	-1.4	2.1E-01
ENSMUST00000023698	PAX3 and PAX7 binding protein 1 [Source:MGI Symbol;Acc:MGI:1914617]	F6YY19		-7.3	5.6E-04	-9.2	8.3E-05	-0.9	3.6E-02	0.2	8.8E-01
ENSMUST00000023707	superoxide dismutase 1, soluble [Source:MGI Symbol;Acc:MGI:98351]		P08228	-6.0	5.3E-05	2.8	6.9E-03	-3.7	2.8E-03	0.1	8.4E-01
ENSMUST00000023709	keratin 5 [Source:MGI Symbol;Acc:MGI:96702]	Q32P04	Q922U2	9.2	1.6E-04	3.2	6.9E-03	0.6	4.4E-01	0.4	5.7E-01
ENSMUST00000023710	keratin 71 [Source:MGI Symbol;Acc:MGI:1861586]		Q9R0H5	7.7	1.6E-05	-2.3	3.5E-02	0.5	4.0E-01	-0.5	6.4E-01
ENSMUST00000023614	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a [Source:MGI Symbol;Acc:MGI:1330299]	A9C475	Q61214	2.8	2.6E-01	0.1	9.5E-01	-3.6	1.1E-01	-0.9	6.8E-01
ENSMUST00000023712	keratin 2 [Source:MGI Symbol;Acc:MGI:96699]		Q3TTY5	8.7	3.3E-05	-4.0	3.8E-05	0.1	6.3E-01	0.0	9.7E-01
ENSMUST00000023713	keratin 82 [Source:MGI Symbol;Acc:MGI:2149248]		Q99M74	8.1	3.2E-05	5.6	1.0E-02	-0.8	6.7E-01	-1.4	2.2E-01
ENSMUST00000023617	immunoglobulin-like domain containing receptor 1 [Source:MGI Symbol;Acc:MGI:2146574]		Q8CBR1	2.8	9.7E-02	4.9	9.0E-03	-0.6	7.2E-01	-2.8	4.2E-02
ENSMUST00000023714	RIKEN cDNA 4732456N10 gene [Source:MGI Symbol;Acc:MGI:3045312]	E9Q1Z0		8.4	1.8E-05	-10.3	4.0E-05	-0.5	3.0E-01	-0.1	9.4E-01
ENSMUST00000023718	RIKEN cDNA 5430421N21 gene [Source:MGI Symbol;Acc:MGI:3690448]	E9Q1Y9		4.0	1.0E-02	-8.8	5.0E-04	-0.5	3.3E-01	-1.0	5.9E-01
ENSMUST00000023629	protein S (alpha) [Source:MGI Symbol;Acc:MGI:1095733]	Q3TR66	Q08761	-1.0	8.7E-02	-2.4	5.9E-03	-0.5	3.0E-01	1.0	1.6E-01
ENSMUST00000023720	keratin 84 [Source:MGI Symbol;Acc:MGI:96700]		Q99M73	9.1	7.8E-05	-4.5	7.2E-03	-0.6	4.1E-01	0.4	7.7E-01
ENSMUST00000023631	bromodomain and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:1890651]		Q921C3	-1.9	1.8E-01	-3.0	8.6E-02	0.1	9.4E-01	1.2	4.8E-01
ENSMUST00000023722	zinc finger protein 641 [Source:MGI Symbol;Acc:MGI:2442788]		Q8BZ34	7.2	3.8E-03	6.3	4.6E-04	-1.0	4.2E-01	-0.2	7.2E-01
ENSMUST00000023666	chromatin assembly factor 1, subunit B (p60) [Source:MGI Symbol;Acc:MGI:1314881]		Q9D0N7	3.9	1.3E-01	-0.2	9.2E-01	-5.4	2.9E-02	-1.3	5.7E-01
ENSMUST00000023728	RIKEN cDNA 4930415O20 gene [Source:MGI Symbol;Acc:MGI:1921113]	Q8CDT5		4.1	1.2E-03	7.9	5.1E-05	-0.6	6.0E-01	0.3	5.8E-01
ENSMUST00000023732	wingless-type MMTV integration site family, member 10B [Source:MGI Symbol;Acc:MGI:108061]		P48614	6.1	7.8E-04	-2.4	1.3E-01	1.4	1.2E-01	1.3	3.8E-01
ENSMUST00000023673	runt related transcription factor 1 [Source:MGI Symbol;Acc:MGI:99852]	Q3UM65		-1.1	3.7E-02	0.8	2.3E-01	1.2	2.7E-02	-0.7	2.2E-01
ENSMUST00000023734	wingless-type MMTV integration site family, member 1 [Source:MGI Symbol;Acc:MGI:98953]	Q3UR96	P04426	8.3	3.5E-05	-6.6	2.4E-04	-0.9	9.5E-02	-0.9	4.6E-01
ENSMUST00000023736	limb region 1 like [Source:MGI Symbol;Acc:MGI:1289247]		Q9D1E5	-5.9	4.4E-04	-1.1	5.7E-01	4.5	3.9E-03	-0.8	6.4E-01
ENSMUST00000023684	phosphoribosylglycinamide formyltransferase [Source:MGI Symbol;Acc:MGI:95654]		Q64737	-1.5	2.7E-01	0.4	7.8E-01	-0.7	4.9E-01	-2.6	9.1E-02
ENSMUST00000023737	desert hedgehog [Source:MGI Symbol;Acc:MGI:94891]	Q544P6	Q61488	8.5	9.0E-06	-5.2	3.5E-05	0.9	1.5E-02	0.1	8.8E-01
ENSMUST00000023747	NCK-associated protein 5-like [Source:MGI Symbol;Acc:MGI:3609653]		Q6GQX2	4.9	3.0E-04	-7.9	4.5E-03	1.2	1.4E-01	2.8	2.2E-01
ENSMUST00000023749	transmembrane BAX inhibitor motif containing 6 [Source:MGI Symbol;Acc:MGI:99682]		Q9D2C7	-7.2	1.5E-05	-1.7	8.1E-02	0.8	1.5E-01	-1.2	2.0E-01
ENSMUST00000023750	Fas apoptotic inhibitory molecule 2 [Source:MGI Symbol;Acc:MGI:1919643]		Q8K097	7.5	6.0E-06	-8.1	3.2E-05	0.6	1.1E-01	-1.7	1.8E-01
ENSMUST00000023752	aquaporin 2 [Source:MGI Symbol;Acc:MGI:1096865]	Q3UQD4	P56402	8.1	1.5E-05	-5.7	3.5E-03	2.2	7.6E-03	3.5	3.6E-02
ENSMUST00000023754	aquaporin 6 [Source:MGI Symbol;Acc:MGI:1341204]		Q8C4A0	7.6	1.6E-05	-3.9	9.8E-03	-0.9	1.5E-01	0.0	9.8E-01
ENSMUST00000023756	Rac GTPase-activating protein 1 [Source:MGI Symbol;Acc:MGI:1349423]		Q9WVM1	-6.0	4.2E-03	-5.2	1.7E-02	1.2	1.2E-01	-0.9	6.6E-01
ENSMUST00000023758	acid-sensing (proton-gated) ion channel 1 [Source:MGI Symbol;Acc:MGI:1194915]		Q6NXK8	2.4	1.3E-03	-5.1	7.0E-04	0.0	9.4E-01	-1.0	3.9E-01
ENSMUST00000023760	glycerol-3-phosphate dehydrogenase 1 (soluble) [Source:MGI Symbol;Acc:MGI:95679]		P13707	5.5	3.2E-04	7.7	1.1E-03	-0.8	6.5E-01	0.7	4.5E-01
ENSMUST00000023761	cytochrome c oxidase assembly protein 14 [Source:MGI Symbol;Acc:MGI:1913629]		Q8BH51	-5.0	2.3E-05	8.1	2.2E-05	-0.6	6.1E-01	-0.9	9.2E-02
ENSMUST00000023762	ceramide synthase 5 [Source:MGI Symbol;Acc:MGI:1919199]		Q9D6K9	-8.0	3.8E-06	8.1	1.0E-04	-0.7	6.3E-01	-0.1	8.1E-01
ENSMUST00000023769	activating transcription factor 1 [Source:MGI Symbol;Acc:MGI:1298366]		P81269	-3.1	4.2E-03	7.7	8.7E-05	-0.6	6.2E-01	-0.3	6.5E-01
ENSMUST00000023774	arrier family 11 (proton-coupled divalent metal ion transporters), member 2 [Source:MGI Symbol;Acc:MGI:13		P49282	4.5	1.6E-04	8.0	5.3E-05	-0.7	6.0E-01	-0.3	6.2E-01
ENSMUST00000023775	chymotrypsin-like elastase family, member 1 [Source:MGI Symbol;Acc:MGI:95314]		Q91X79	-1.8	2.7E-02	5.2	1.6E-02	0.7	6.8E-01	-0.5	6.4E-01
ENSMUST00000023776	solute carrier family 4 (anion exchanger), member 8 [Source:MGI Symbol;Acc:MGI:1928745]		Q8JZR6	6.4	4.2E-06	8.6	2.3E-04	-0.8	6.3E-01	-0.3	6.8E-01
ENSMUST00000023781	RIKEN cDNA 1700011A15 gene [Source:MGI Symbol;Acc:MGI:1913572]	Q9CPR6		6.1	1.8E-04	5.3	3.1E-02	-0.5	8.1E-01	1.3	3.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000023727	KAT8 regulatory NSL complex subunit 2 [Source:MGI Symbol;Acc:MGI:1916862]	F8WJE3		-1.0	1.0E-01	-0.1	8.4E-01	0.3	5.6E-01	-0.6	4.0E-01
ENSMUST00000023786	keratin 6B [Source:MGI Symbol;Acc:MGI:1333768]	Q3UV11		7.9	4.7E-05	5.9	3.0E-04	0.1	9.0E-01	-1.6	2.4E-02
ENSMUST00000023788	keratin 6A [Source:MGI Symbol;Acc:MGI:1100845]		P50446	7.8	6.7E-05	4.1	2.8E-03	-2.8	4.4E-02	-0.8	3.3E-01
ENSMUST00000023790	keratin 1 [Source:MGI Symbol;Acc:MGI:96698]		P04104	8.7	6.6E-06	7.2	2.0E-04	-0.6	6.3E-01	0.4	4.9E-01
ENSMUST00000023797	keratin 4 [Source:MGI Symbol;Acc:MGI:96701]		P07744	7.8	2.8E-05	-5.2	3.9E-03	0.8	2.1E-01	0.1	9.7E-01
ENSMUST00000023799	keratin 79 [Source:MGI Symbol;Acc:MGI:2385030]		Q8VED5	8.1	2.1E-05	5.9	1.0E-04	-2.4	3.9E-02	0.1	8.5E-01
ENSMUST00000023741	lysine (K)-specific methyltransferase 2D [Source:MGI Symbol;Acc:MGI:2682319]	A0A0A0MQ73		-1.0	4.9E-01	1.6	3.1E-01	0.7	5.7E-01	-1.8	2.2E-01
ENSMUST00000023803	keratin 18 [Source:MGI Symbol;Acc:MGI:96692]		P05784	3.9	9.2E-05	5.3	1.0E-03	0.5	6.3E-01	0.1	8.5E-01
ENSMUST00000023807	insulin-like growth factor binding protein 6 [Source:MGI Symbol;Acc:MGI:96441]		P47880	-5.7	6.6E-06	-5.3	6.4E-04	1.3	2.2E-02	-0.6	5.8E-01
ENSMUST00000023809	anti-Mullerian hormone type 2 receptor [Source:MGI Symbol;Acc:MGI:105062]		Q8K592	3.4	2.5E-04	6.3	2.2E-05	-1.7	8.1E-02	-0.5	3.2E-01
ENSMUST00000023810	proline rich 13 [Source:MGI Symbol;Acc:MGI:1913401]		Q9CQJ5	-7.7	5.2E-04	6.8	6.4E-05	-1.4	2.1E-01	-0.1	8.1E-01
ENSMUST00000023812	mitogen-activated protein kinase kinase kinase 12 [Source:MGI Symbol;Acc:MGI:1346881]		Q60700	4.3	3.3E-02	7.7	3.1E-05	-0.6	6.0E-01	-0.6	2.5E-01
ENSMUST00000023813	TAR (HIV) RNA binding protein 2 [Source:MGI Symbol;Acc:MGI:103027]		P97473	-5.4	1.3E-03	-4.1	1.9E-02	1.0	2.5E-01	-0.9	6.4E-01
ENSMUST00000023818	calcium binding and coiled coil domain 1 [Source:MGI Symbol;Acc:MGI:1914738]		Q8CGU1	-4.1	1.1E-04	3.8	3.2E-04	0.9	1.5E-01	-0.5	3.3E-01
ENSMUST00000023759	d, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1 [Source:MGI Symbol;Acc		Q61466	-0.7	1.6E-01	1.1	9.9E-02	0.9	8.0E-02	-0.9	1.3E-01
ENSMUST00000023826	synuclein, gamma [Source:MGI Symbol;Acc:MGI:1298397]	Q5GQ64	Q9Z0F7	5.2	2.8E-03	4.5	1.4E-03	-1.6	1.3E-01	-0.6	4.4E-01
ENSMUST00000023828	rotatin [Source:MGI Symbol;Acc:MGI:2179288]		Q8R4Y8	1.9	1.2E-02	-4.6	3.2E-04	0.1	7.8E-01	-0.3	7.6E-01
ENSMUST00000023829	cyclin-dependent kinase inhibitor 1A (P21) [Source:MGI Symbol;Acc:MGI:104556]	Q564P6	P39689	-1.8	3.1E-02	-4.4	6.0E-05	0.3	2.9E-01	-3.2	4.3E-03
ENSMUST00000023835	solute carrier family 10, member 2 [Source:MGI Symbol;Acc:MGI:1201406]	Q0VBB8	P70172	3.8	3.7E-03	-2.5	5.3E-02	1.0	1.3E-01	0.4	7.3E-01
ENSMUST00000023840	chemokine (C-X-C motif) ligand 13 [Source:MGI Symbol;Acc:MGI:1888499]	Q3U1E8	O55038	5.2	2.4E-04	3.1	6.1E-03	-0.6	4.9E-01	0.8	2.6E-01
ENSMUST00000023845	histocompatibility 2, M region locus 10.2 [Source:MGI Symbol;Acc:MGI:1276525]	Q85ZW9		6.8	5.3E-05	-1.0	2.4E-01	-0.4	4.7E-01	-1.2	1.7E-01
ENSMUST00000023846	leucine rich repeat containing 71 [Source:MGI Symbol;Acc:MGI:1921735]		Q9D3W5	3.8	4.7E-03	6.5	2.1E-05	0.1	9.0E-01	0.0	9.1E-01
ENSMUST00000023779	nuclear receptor subfamily 4, group A, member 1 [Source:MGI Symbol;Acc:MGI:1352454]	Q545Q1	P12813	-0.1	9.3E-01	0.0	9.8E-01	-0.5	5.9E-01	-0.6	6.0E-01
ENSMUST00000023856	methionine sulfoxide reductase B2 [Source:MGI Symbol;Acc:MGI:1923717]		Q78J03	-3.2	4.9E-03	5.4	1.1E-03	-0.5	6.8E-01	0.2	8.1E-01
ENSMUST00000023867	replication factor C (activator 1) 2 [Source:MGI Symbol;Acc:MGI:1341868]	Q4KL82	Q9WUK4	-4.3	2.2E-05	7.2	1.3E-04	-1.4	2.7E-01	-0.7	2.5E-01
ENSMUST00000023882	symplekin [Source:MGI Symbol;Acc:MGI:1915438]	F8WJD4		-4.5	3.1E-03	7.5	1.8E-04	-0.7	6.2E-01	-0.4	6.0E-01
ENSMUST00000023884	predicted gene 853 [Source:MGI Symbol;Acc:MGI:2685699]	Q3UNZ2		7.7	3.4E-05	7.0	4.3E-05	-1.4	2.0E-01	0.3	6.0E-01
ENSMUST00000023886	sulfotransferase family, cytosolic, 1C, member 2 [Source:MGI Symbol;Acc:MGI:1916333]		Q9D939	6.4	6.4E-05	7.3	9.6E-05	-0.6	6.3E-01	0.0	9.5E-01
ENSMUST00000023897	granzyme A [Source:MGI Symbol;Acc:MGI:109266]	Q3U0N0	P11032	-4.2	1.0E-02	7.4	9.5E-05	-0.6	6.0E-01	0.1	8.4E-01
ENSMUST00000023911	l-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase [Source:MGI Symbol;Acc:MGI:1351598		Q8BJ48	-3.2	1.2E-02	-2.2	2.1E-03	-6.2	7.3E-07	-0.1	8.9E-01
ENSMUST00000023805	cysteine sulfinic acid decarboxylase [Source:MGI Symbol;Acc:MGI:2180098]		Q9DBE0	0.1	9.4E-01	0.0	1.0E+00	-0.1	9.3E-01	0.0	9.9E-01
ENSMUST00000023806	sterol O-acyltransferase 2 [Source:MGI Symbol;Acc:MGI:1332226]		O88908	-1.0	1.5E-01	-0.7	4.4E-01	0.1	9.1E-01	-0.3	7.1E-01
ENSMUST00000023913	tryptophan rich basic protein [Source:MGI Symbol;Acc:MGI:2136882]		Q8K0D7	1.9	1.8E-02	-5.5	5.7E-05	0.1	7.7E-01	-0.1	8.9E-01
ENSMUST00000023918	influenza virus NS1A binding protein [Source:MGI Symbol;Acc:MGI:2152389]		Q920Q8	-6.4	6.1E-05	3.6	5.4E-04	-0.2	6.9E-01	-0.4	4.9E-01
ENSMUST00000023952	keratin 8 [Source:MGI Symbol;Acc:MGI:96705]		P11679	8.0	1.8E-05	-3.2	6.6E-02	1.5	1.0E-01	-3.1	1.2E-01
ENSMUST00000023958	prolyl 3-hydroxylase 3 [Source:MGI Symbol;Acc:MGI:1315208]		Q8CG70	4.8	3.0E-03	4.8	3.8E-02	-0.3	8.9E-01	-0.8	5.5E-01
ENSMUST00000023959	glutamate receptor, metabotropic 2 [Source:MGI Symbol;Acc:MGI:1351339]		Q14BI2	8.4	1.9E-05	-2.0	2.7E-01	3.4	4.5E-03	0.1	9.6E-01
ENSMUST00000023965	complement factor H-related 1 [Source:MGI Symbol;Acc:MGI:2138169]	Q61406		3.1	4.6E-03	-2.3	1.5E-02	0.9	6.3E-02	-0.8	3.2E-01
ENSMUST00000023978	lipocalin 9 [Source:MGI Symbol;Acc:MGI:1924954]		Q9D267	7.2	1.3E-04	-1.3	1.7E-01	-6.7	3.0E-04	-0.3	7.7E-01
ENSMUST00000023987	erythrocyte membrane protein band 4.2 [Source:MGI Symbol;Acc:MGI:95402]	Q3UV95		6.0	5.4E-04	2.3	1.2E-02	0.0	1.0E+00	-0.4	4.8E-01
ENSMUST00000023994	serine (or cysteine) peptidase inhibitor, clade G, member 1 [Source:MGI Symbol;Acc:MGI:894696]		P97290	5.7	5.1E-04	-2.1	4.9E-02	0.1	8.7E-01	0.4	6.5E-01
ENSMUST00000023830	uclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:119636		Q99LJ8	0.7	3.2E-01	-0.4	6.8E-01	0.4	5.8E-01	1.4	1.3E-01
ENSMUST00000024011	potassium channel, subfamily K, member 5 [Source:MGI Symbol;Acc:MGI:1336175]	Q9JK62		5.2	8.8E-06	4.4	7.1E-03	1.4	2.4E-01	0.8	3.8E-01
ENSMUST00000023836	motile sperm domain containing 1 [Source:MGI Symbol;Acc:MGI:1917630]		Q8VEL0	2.1	2.2E-01	-1.2	4.6E-01	-3.5	2.7E-02	-0.3	8.4E-01
ENSMUST00000024042	cysteine-rich with EGF-like domains 2 [Source:MGI Symbol;Acc:MGI:1923987]		Q9CYA0	-2.0	2.5E-03	-2.8	1.9E-03	-7.5	6.7E-06	0.4	5.4E-01
ENSMUST00000024044	CD4 antigen [Source:MGI Symbol;Acc:MGI:88335]	Q3TSV7	P06332	2.6	7.9E-03	6.3	1.1E-04	-0.9	4.2E-01	-0.4	5.4E-01
ENSMUST00000024047	twinfilin, actin-binding protein, homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1346078]		Q9Z0P5	-9.8	3.0E-05	4.5	7.6E-03	1.2	3.7E-01	0.4	6.3E-01
ENSMUST00000023851	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 [Source:MGI Symbol;Acc:MGI:1915452]		Q9CPP6	0.5	6.5E-01	-1.7	2.2E-01	-2.0	8.0E-02	0.2	8.7E-01
ENSMUST00000024078	membrane-associated ring finger (C3HC4) 5 [Source:MGI Symbol;Acc:MGI:1915207]	A2RTC8	Q3KNM2	-3.2	1.0E-03	-4.6	5.5E-03	0.8	2.7E-01	2.2	1.2E-01
ENSMUST00000024099	acetylcholinesterase [Source:MGI Symbol;Acc:MGI:87876]	Q543Z1	P21836	5.5	2.9E-02	-3.5	5.8E-04	0.5	1.6E-01	-0.3	6.5E-01
ENSMUST00000023869	density-regulated protein [Source:MGI Symbol;Acc:MGI:1915434]		Q9CQJ6	-0.2	7.7E-01	-0.2	7.0E-01	-0.8	1.3E-01	-0.7	2.8E-01
ENSMUST00000023873	protein arginine N-methyltransferase 5 [Source:MGI Symbol;Acc:MGI:1351645]			0.1	8.7E-01	0.2	7.3E-01	-0.3	5.1E-01	-0.5	4.7E-01
ENSMUST00000024104	glial cells missing homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:108045]	Q3UQD1	P70348	6.5	3.5E-05	-3.3	6.4E-02	1.4	1.1E-01	0.3	8.5E-01
ENSMUST00000024107	WAP four-disulfide core domain 1 [Source:MGI Symbol;Acc:MGI:1915116]	Q3UQ76	Q9ESH5	6.1	1.7E-04	7.3	1.1E-04	-0.6	6.0E-01	-0.2	7.0E-01
ENSMUST00000024118	C-type lectin domain family 4, member n [Source:MGI Symbol;Acc:MGI:1861231]	Q3V2N1	Q9JKF4	-6.4	1.3E-04	6.9	6.9E-05	-0.6	6.0E-01	-1.1	8.6E-02
ENSMUST00000024121	RIKEN cDNA 4921501E09 gene [Source:MGI Symbol;Acc:MGI:1921292]			6.1	1.6E-04	-3.4	4.3E-02	-0.5	6.2E-01	-1.3	4.3E-01
ENSMUST00000024155	potassium channel, subfamily K, member 16 [Source:MGI Symbol;Acc:MGI:1921821]	G5E845		6.6	1.0E-04	-0.9	5.1E-01	1.2	1.8E-01	-1.1	3.9E-01
ENSMUST00000024159	distal-less homeobox 2 [Source:MGI Symbol;Acc:MGI:94902]	Q52KJ2	P40764	7.8	6.2E-05	2.6	1.3E-02	0.5	5.2E-01	-0.2	7.5E-01
ENSMUST00000024200	chymotrypsin-like elastase family, member 3A [Source:MGI Symbol;Acc:MGI:3651647]	A2A9U8		6.9	3.3E-04	-3.2	1.8E-03	-0.1	8.7E-01	-3.3	9.1E-03
ENSMUST00000023924	ribonuclease P 14 subunit [Source:MGI Symbol;Acc:MGI:1914303]		Q9CQH8	-0.1	8.2E-01	-0.6	3.8E-01	-0.8	1.3E-01	-0.3	6.2E-01
ENSMUST00000023934	hemoglobin, beta adult s chain [Source:MGI Symbol;Acc:MGI:5474852]	A8DUK4		-2.6	3.7E-02	-4.1	4.4E-03	-4.1	8.2E-04	-2.7	4.5E-02
ENSMUST00000024206	guanine nucleotide binding protein (G protein), beta 3 [Source:MGI Symbol;Acc:MGI:95785]	Q54AE3	Q61011	5.6	3.1E-04	-2.0	2.8E-03	-10.5	1.1E-06	-0.4	4.0E-01
ENSMUST00000024470	2-oxoglutarate and iron-dependent oxygenase domain containing 2 [Source:MGI Symbol;Acc:MGI:1913877]		Q9CQ04	-4.7	6.3E-03	2.7	6.0E-02	-2.2	1.1E-01	-0.1	9.2E-01
ENSMUST00000024486	mitochondrial ribosomal protein S23 [Source:MGI Symbol;Acc:MGI:1928138]		Q8VE22	-5.0	4.3E-04	8.0	5.7E-05	-0.6	6.4E-01	-0.2	7.6E-01
ENSMUST00000024543	hairy and enhancer of split 7 (Drosophila) [Source:MGI Symbol;Acc:MGI:2135679]		Q8BKT2	9.7	8.5E-07	2.2	4.2E-02	-0.3	7.6E-01	0.6	4.8E-01
ENSMUST00000024572	radial spoke 3B homolog (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:3630308]		Q9DA80	-3.4	7.4E-03	6.0	9.6E-04	-0.7	6.1E-01	0.6	4.3E-01
ENSMUST00000024594	ol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) [Source:MGI Symbol;Acc:M		Q8K4X7	2.6	4.4E-03	5.8	1.8E-03	0.1	9.7E-01	0.2	7.8E-01
ENSMUST00000024595	solute carrier family 22 (organic cation transporter), member 3 [Source:MGI Symbol;Acc:MGI:1333817]	Q547K2	Q9WTW5	2.5	4.3E-03	-0.3	6.6E-01	-7.5	3.8E-05	-1.5	5.9E-02
ENSMUST00000024596	solute carrier family 22 (organic cation transporter), member 1 [Source:MGI Symbol;Acc:MGI:108111]		O08966	6.5	1.6E-03	3.3	4.4E-04	-2.0	8.2E-03	0.0	9.3E-01
ENSMUST00000024031	aminoacylase 1 [Source:MGI Symbol;Acc:MGI:87913]			-1.1	5.8E-01	-3.9	1.6E-01	-2.3	1.3E-01	0.5	8.7E-01
ENSMUST00000024627	chromodomain helicase DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:88393]		P40201	-3.1	1.7E-04	-2.3	4.7E-03	0.0	9.2E-01	0.4	5.6E-01
ENSMUST00000024636	Fgfr1 oncogene partner [Source:MGI Symbol;Acc:MGI:1922546]		Q66JX5	-5.8	9.9E-05	1.2	2.3E-01	-0.9	2.6E-01	0.4	6.4E-01
ENSMUST00000024657	PHD finger protein 10 [Source:MGI Symbol;Acc:MGI:1919307]	K4DI61		-7.6	7.0E-06	-9.6	3.1E-04	0.8	1.1E-01	0.6	7.7E-01
ENSMUST00000024056	ubiquitin-conjugating enzyme E2J 2 [Source:MGI Symbol;Acc:MGI:2153608]	B1ASK8		0.8	6.1E-01	0.6	7.7E-01	0.0	1.0E+00	0.2	8.9E-01
ENSMUST00000024660	SPARC related modular calcium binding 2 [Source:MGI Symbol;Acc:MGI:1929881]		Q8CD91	7.3	1.3E-04	-3.4	5.5E-03	0.7	1.8E-01	1.0	3.1E-01
ENSMUST00000024696	matrix metallopeptidase 25 [Source:MGI Symbol;Acc:MGI:2443938]		Q3U435	-3.8	1.9E-04	5.4	4.1E-02	-0.7	7.6E-01	-0.6	6.8E-01
ENSMUST00000024697	host cell factor C1 regulator 1 (XPO1-dependent) [Source:MGI Symbol;Acc:MGI:2663619]		Q9CYQ5	-3.3	1.1E-02	5.5	2.2E-04	-0.8	4.4E-01	0.2	7.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000024699	claudin 6 [Source:MGI Symbol;Acc:MGI:1859284]	Q0GH64	Q9Z262	7.4	8.3E-05	5.9	4.2E-04	-0.8	5.1E-01	-0.6	4.1E-01
ENSMUST00000024702	progestin and adipoQ receptor family member IV [Source:MGI Symbol;Acc:MGI:1923748]		Q9JJE4	3.8	3.3E-04	-6.9	3.8E-04	-1.4	1.2E-02	-0.9	5.4E-01
ENSMUST00000024119	thyroid hormone receptor interactor 6 [Source:MGI Symbol;Acc:MGI:1343458]	B2RS30	Q9Z1Y4	-0.4	6.3E-01	-0.1	9.5E-01	-0.1	9.0E-01	-0.5	6.7E-01
ENSMUST00000024705	solute carrier family 25, member 27 [Source:MGI Symbol;Acc:MGI:1921261]	Q9D6D0		3.5	4.6E-03	6.5	3.1E-04	0.1	9.1E-01	-0.3	6.8E-01
ENSMUST00000024123	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3 [Source:MGI Symbol;Acc:MGI:2183446]	F8VQE9		-1.2	8.3E-02	-0.5	5.8E-01	0.9	1.5E-01	0.1	8.6E-01
ENSMUST00000024706	holipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) [Source:MGI Symbol;Acc:MGI:135		Q60963	-8.1	6.5E-06	6.5	2.2E-04	-0.6	6.1E-01	-0.5	4.7E-01
ENSMUST00000024707	meprin 1 alpha [Source:MGI Symbol;Acc:MGI:96963]			5.1	1.5E-02	7.1	2.3E-04	-0.6	6.4E-01	0.1	9.0E-01
ENSMUST00000024708	tumor necrosis factor receptor superfamily, member 21 [Source:MGI Symbol;Acc:MGI:2151075]		Q9EPU5	-1.8	8.0E-03	6.9	5.8E-04	-0.7	6.3E-01	-0.7	3.5E-01
ENSMUST00000024709	CD2-associated protein [Source:MGI Symbol;Acc:MGI:1330281]		Q9JLQ0	1.3	2.0E-02	6.1	3.5E-04	-0.5	6.9E-01	-0.9	1.9E-01
ENSMUST00000024238	n, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) [Source:MGI Symbol;Acc:MGI:18		Q91ZI0	-0.8	8.6E-02	0.3	5.5E-01	1.0	4.9E-02	-0.2	6.8E-01
ENSMUST00000024270	cell division cycle associated 3 [Source:MGI Symbol;Acc:MGI:1315198]		Q99M54	-1.2	1.2E-01	-1.5	1.2E-01	-0.5	4.6E-01	-0.2	8.5E-01
ENSMUST00000024338	family with sequence similarity 132, member A [Source:MGI Symbol;Acc:MGI:1914639]		Q8R2Z0	0.7	2.1E-01	0.9	2.0E-01	0.1	8.1E-01	-0.1	9.1E-01
ENSMUST00000024711	adhesion G protein-coupled receptor F4 [Source:MGI Symbol;Acc:MGI:1925499]	A0A0D9SEG9		6.7	2.2E-02	-5.5	3.0E-02	0.4	6.1E-01	1.2	6.0E-01
ENSMUST00000024721	Rhesus blood group-associated A glycoprotein [Source:MGI Symbol;Acc:MGI:1202713]		Q9QUT0	4.5	5.3E-05	-3.1	1.6E-02	0.7	2.3E-01	-1.2	3.3E-01
ENSMUST00000024725	EF hand domain family, member B [Source:MGI Symbol;Acc:MGI:3045296]		Q8CDU5	6.5	1.3E-04	9.4	1.2E-05	0.0	9.7E-01	0.3	4.9E-01
ENSMUST00000024731	spermatogenesis associated, serine-rich 1 [Source:MGI Symbol;Acc:MGI:1918270]		A2RRY8	6.1	4.6E-04	-3.4	4.0E-02	0.3	6.8E-01	0.3	8.2E-01
ENSMUST00000024575	ribosomal protein S6 kinase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1342290]		Q9WUT3	-1.1	7.4E-02	0.8	2.6E-01	1.4	2.4E-02	-0.5	4.8E-01
ENSMUST00000024733	alanyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:2681839]		Q14CH7	3.2	1.4E-03	1.7	8.7E-02	-0.1	9.2E-01	0.8	3.0E-01
ENSMUST00000024734	mitochondrial ribosomal protein L14 [Source:MGI Symbol;Acc:MGI:1333864]		Q9D1I6	-7.8	8.1E-05	4.3	7.5E-04	1.4	9.8E-02	-0.4	5.7E-01
ENSMUST00000024739	heat shock protein 90 alpha (cytosolic), class B member 1 [Source:MGI Symbol;Acc:MGI:96247]	Q71LX8	P11499	-4.7	6.8E-05	5.0	2.8E-03	-2.2	1.6E-01	-0.7	4.9E-01
ENSMUST00000024599	insulin-like growth factor 2 receptor [Source:MGI Symbol;Acc:MGI:96435]		Q07113	-0.4	2.9E-01	0.6	2.0E-01	0.8	4.2E-02	-0.2	6.3E-01
ENSMUST00000024620	chromodomain helicase DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:88393]		Q9CQS5	-0.6	3.5E-01	-0.3	6.4E-01	-1.0	8.5E-02	-1.2	9.5E-02
ENSMUST00000024748	GTP binding protein 2 [Source:MGI Symbol;Acc:MGI:1860138]		Q3UJK4	-5.8	1.3E-03	-2.8	2.8E-03	0.6	1.4E-01	0.3	6.7E-01
ENSMUST00000024755	chloride intracellular channel 5 [Source:MGI Symbol;Acc:MGI:1917912]		Q8BXK9	7.2	1.2E-05	-5.3	9.2E-04	-0.4	4.3E-01	-0.8	5.0E-01
ENSMUST00000024762	radial spoke head 9 homolog (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1922814]		Q9D9V4	3.0	4.3E-03	-3.7	3.3E-04	0.7	6.8E-02	-3.2	5.9E-03
ENSMUST00000024763	mitochondrial ribosomal protein S18A [Source:MGI Symbol;Acc:MGI:1915815]	Q5U5I3		-3.8	1.7E-03	5.3	1.1E-03	-1.9	1.6E-01	0.1	9.2E-01
ENSMUST00000024766	ribosomal RNA processing 36 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2385053]			-1.6	9.0E-03	-2.0	3.5E-02	1.7	6.8E-03	-0.1	9.2E-01
ENSMUST00000024773	peripherin 2 [Source:MGI Symbol;Acc:MGI:102791]	Q3UWK3	P15499	6.1	2.8E-04	-2.4	1.5E-01	1.3	1.6E-01	0.4	7.9E-01
ENSMUST00000024698	tumor necrosis factor receptor superfamily, member 12a [Source:MGI Symbol;Acc:MGI:1351484]		Q9CR75	0.0	9.7E-01	-3.0	5.8E-03	-1.2	3.6E-02	1.8	5.2E-02
ENSMUST00000024774	guanylate cyclase activator 1B [Source:MGI Symbol;Acc:MGI:1194489]		Q8VBV8	6.9	4.5E-05	6.6	3.8E-04	-0.6	6.2E-01	0.2	8.0E-01
ENSMUST00000024701	protein kinase, membrane associated tyrosine/threonine 1 [Source:MGI Symbol;Acc:MGI:2137630]		Q9ESG9	1.4	4.1E-02	3.4	1.6E-03	1.3	7.0E-02	-0.7	3.0E-01
ENSMUST00000024778	mediator complex subunit 20 [Source:MGI Symbol;Acc:MGI:1929648]		Q9R0X0	-4.4	3.0E-03	3.5	1.3E-03	-0.7	3.5E-01	-0.3	5.9E-01
ENSMUST00000024779	ubiquitin specific peptidase 49 [Source:MGI Symbol;Acc:MGI:2685391]		Q6P9L4	2.5	2.0E-03	3.5	1.4E-02	0.2	8.8E-01	0.2	8.5E-01
ENSMUST00000024782	progastricsin (pepsinogen C) [Source:MGI Symbol;Acc:MGI:98909]		Q9D7R7	6.4	8.3E-04	-7.0	8.7E-05	-0.2	7.2E-01	-1.3	2.6E-01
ENSMUST00000024791	triggering receptor expressed on myeloid cells 2 [Source:MGI Symbol;Acc:MGI:1913150]		Q99NH8	-4.1	3.3E-03	6.9	3.4E-03	-0.7	7.2E-01	-2.5	5.0E-02
ENSMUST00000024792	triggering receptor expressed on myeloid cells-like 1 [Source:MGI Symbol;Acc:MGI:1918576]		Q8K558	2.2	1.1E-02	-0.5	5.3E-01	1.4	1.9E-02	0.0	9.7E-01
ENSMUST00000024797	molybdenum cofactor synthesis 1 [Source:MGI Symbol;Acc:MGI:1928904]		Q5RKZ7	-8.2	9.7E-06	-0.1	8.4E-01	-1.1	4.3E-02	0.4	4.8E-01
ENSMUST00000024805	copine V [Source:MGI Symbol;Acc:MGI:2385908]		Q8JZW4	9.4	3.3E-05	7.9	1.4E-02	-0.9	7.6E-01	-2.1	2.1E-01
ENSMUST00000024717	TBC1 domain family, member 5 [Source:MGI Symbol;Acc:MGI:1919488]		Q80XQ2	-0.3	3.9E-01	0.2	6.8E-01	0.4	2.4E-01	-0.1	8.3E-01
ENSMUST00000024810	FYVE, RhoGEF and PH domain containing 2 [Source:MGI Symbol;Acc:MGI:1347084]		Q8BY35	-4.3	9.1E-03	5.6	7.7E-05	0.7	3.9E-01	-0.4	4.3E-01
ENSMUST00000024811	proviral integration site 1 [Source:MGI Symbol;Acc:MGI:97584]	Q8CFN8		-4.7	5.7E-05	6.2	2.4E-04	-1.3	2.8E-01	-0.9	1.6E-01
ENSMUST00000024727	cell division cycle 5-like (S. pombe) [Source:MGI Symbol;Acc:MGI:1918952]	Q3UCF2	Q6A068	-0.9	4.3E-02	-1.4	1.8E-02	-0.4	2.6E-01	0.1	8.2E-01
ENSMUST00000024816	cap methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1921407]		Q9DBC3	-2.9	3.8E-04	5.9	1.1E-03	-0.5	7.3E-01	-0.2	7.4E-01
ENSMUST00000024817	ring finger protein 8 [Source:MGI Symbol;Acc:MGI:1929069]		Q8VC56	-3.9	2.6E-03	4.5	8.6E-04	0.8	3.5E-01	-0.5	4.7E-01
ENSMUST00000024823	glyoxalase 1 [Source:MGI Symbol;Acc:MGI:95742]	A5GZX3	Q9CPU0	-2.0	1.9E-02	-5.8	1.4E-03	0.4	4.2E-01	-1.6	3.1E-01
ENSMUST00000024736	shugoshin-like 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:1919665]		Q9CXH7	-0.2	7.5E-01	-0.8	3.1E-01	-0.2	7.1E-01	0.4	5.9E-01
ENSMUST00000024829	ATP-binding cassette, sub-family G (WHITE), member 1 [Source:MGI Symbol;Acc:MGI:107704]	Q0VDW9	Q64343	-2.7	2.2E-03	-3.8	1.4E-03	0.4	3.5E-01	-0.5	5.9E-01
ENSMUST00000024742	factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon [Source:MGI Symbol;Acc:MGI:11		O54910	-0.7	3.6E-01	0.0	9.8E-01	0.9	2.6E-01	0.2	8.5E-01
ENSMUST00000024747	vascular endothelial growth factor A [Source:MGI Symbol;Acc:MGI:103178]		Q00731	4.0	4.3E-02	5.0	4.4E-02	0.6	7.6E-01	-0.3	8.3E-01
ENSMUST00000024831	trefoil factor 1 [Source:MGI Symbol;Acc:MGI:88135]	Q149Y8	Q08423	4.6	1.1E-02	-7.0	1.5E-02	1.1	1.6E-01	2.3	3.5E-01
ENSMUST00000024749	polymerase (DNA directed), eta (RAD 30 related) [Source:MGI Symbol;Acc:MGI:1891457]		Q9JJN0	-0.3	4.5E-01	0.6	3.3E-01	0.8	9.0E-02	-0.1	8.3E-01
ENSMUST00000024833	transmembrane protease, serine 3 [Source:MGI Symbol;Acc:MGI:2155445]		Q8K1T0	4.7	5.5E-05	7.7	1.0E-04	0.9	4.6E-01	0.4	5.1E-01
ENSMUST00000024756	ectonucleotide pyrophosphatase/phosphodiesterase 5 [Source:MGI Symbol;Acc:MGI:1933830]		Q9EQG7	0.2	8.1E-01	2.8	8.4E-02	2.4	9.4E-02	-0.2	8.5E-01
ENSMUST00000024757	ectonucleotide pyrophosphatase/phosphodiesterase 4 [Source:MGI Symbol;Acc:MGI:2682634]		Q8BTJ4	-0.2	8.8E-01	8.2	8.2E-03	5.3	4.7E-02	-3.1	4.5E-02
ENSMUST00000024761	F-box and leucine-rich repeat protein 17 [Source:MGI Symbol;Acc:MGI:1354704]		Q9QZN1	-1.7	1.1E-01	0.0	9.7E-01	0.6	5.3E-01	-1.2	3.2E-01
ENSMUST00000024840	Rho GTPase activating protein 28 [Source:MGI Symbol;Acc:MGI:2147003]		Q8BN58	5.6	3.3E-05	2.1	4.9E-02	-0.7	3.9E-01	0.2	8.0E-01
ENSMUST00000024846	myosin, light chain 12A, regulatory, non-sarcomeric [Source:MGI Symbol;Acc:MGI:1914518]	Q6ZWQ9		-9.8	1.4E-04	-2.3	6.0E-02	0.8	2.5E-01	-0.7	5.5E-01
ENSMUST00000024849	elastin microfibril interfacer 2 [Source:MGI Symbol;Acc:MGI:2389136]	Q3U1J9	Q8K482	-6.1	4.4E-07	-0.7	2.7E-01	0.3	5.3E-01	-0.7	2.9E-01
ENSMUST00000024854	CAP-GLY domain containing linker protein family, member 4 [Source:MGI Symbol;Acc:MGI:1919100]		Q8CI96	6.8	1.6E-05	8.4	9.9E-05	0.5	7.4E-01	-1.8	2.1E-02
ENSMUST00000024858	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 [Source:MGI Symbol;Acc:MGI	Q08EC9		10.0	1.5E-05	7.1	6.7E-05	-0.6	6.1E-01	-0.8	1.9E-01
ENSMUST00000024860	EH-domain containing 3 [Source:MGI Symbol;Acc:MGI:1928900]		Q9QXY6	4.8	3.4E-05	-3.6	5.1E-02	0.8	3.3E-01	0.0	9.9E-01
ENSMUST00000024866	xanthine dehydrogenase [Source:MGI Symbol;Acc:MGI:98973]		Q00519	-5.3	1.5E-05	3.3	2.0E-03	0.4	5.2E-01	-0.3	5.9E-01
ENSMUST00000024869	spastin [Source:MGI Symbol;Acc:MGI:1858896]		Q9QYY8	-2.4	3.1E-03	5.9	2.4E-03	-0.7	6.7E-01	-0.2	8.6E-01
ENSMUST00000024783	bystin-like [Source:MGI Symbol;Acc:MGI:1858419]		O54825	0.8	1.8E-01	1.3	1.0E-01	0.9	1.5E-01	0.3	6.3E-01
ENSMUST00000024786	transcription factor EB [Source:MGI Symbol;Acc:MGI:103270]	Q3UKG7		1.9	5.9E-01	6.2	2.6E-01	2.7	6.0E-01	-1.6	6.1E-01
ENSMUST00000024870	solute carrier family 30 (zinc transporter), member 6 [Source:MGI Symbol;Acc:MGI:2386741]		Q8BJM5	-1.9	3.7E-03	-6.1	3.4E-03	-1.3	5.3E-02	0.7	6.8E-01
ENSMUST00000024873	Yip1 domain family, member 4 [Source:MGI Symbol;Acc:MGI:1915114]		Q8C407	-4.1	8.9E-05	1.0	2.4E-01	-1.2	1.1E-01	0.0	9.6E-01
ENSMUST00000024880	vitrin [Source:MGI Symbol;Acc:MGI:1921449]		Q8VHI5	10.6	2.7E-05	-6.8	2.5E-04	0.6	1.3E-01	-0.8	5.7E-01
ENSMUST00000024882	tetratricopeptide repeat domain 27 [Source:MGI Symbol;Acc:MGI:1921446]		Q8CD92	1.6	3.1E-02	5.7	4.9E-02	-0.9	7.5E-01	-0.3	8.6E-01
ENSMUST00000024802	peptidylprolyl isomerase (cyclophilin)-like 1 [Source:MGI Symbol;Acc:MGI:1916066]	B9EJX8	Q9D0W5	-0.9	1.5E-01	-1.0	1.9E-01	-0.3	5.8E-01	-0.2	8.0E-01
ENSMUST00000024884	eukaryotic translation initiation factor 2-alpha kinase 2 [Source:MGI Symbol;Acc:MGI:1353449]		Q03963	5.0	6.5E-06	6.8	2.3E-04	-2.8	6.8E-02	-0.2	7.2E-01
ENSMUST00000024885	CCAAT/enhancer binding protein zeta [Source:MGI Symbol;Acc:MGI:109386]			-2.4	3.7E-03	-3.9	4.8E-02	0.0	9.6E-01	-0.4	8.2E-01
ENSMUST00000024887	UDH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 7 [Source:MGI Symbol;Acc:MGI:19209		Q9CWG8	1.2	2.9E-02	-3.8	1.7E-03	1.0	5.4E-02	0.1	9.4E-01
ENSMUST00000024888	praja 2, RING-H2 motif containing [Source:MGI Symbol;Acc:MGI:2159342]		Q80U04	-4.8	2.2E-03	-1.3	6.7E-02	0.8	6.9E-02	-0.9	2.1E-01
ENSMUST00000024889	praja 2, RING-H2 motif containing [Source:MGI Symbol;Acc:MGI:2159342]		Q80U04	3.9	2.2E-02	-1.3	2.3E-01	0.7	3.6E-01	-2.0	1.1E-01
ENSMUST00000024894	cytochrome P450, family 1, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88590]		Q64429	8.6	1.4E-05	-3.0	7.4E-03	-1.0	8.4E-02	0.0	9.7E-01
ENSMUST00000024897	vesicle-associated membrane protein, associated protein A [Source:MGI Symbol;Acc:MGI:1353561]		Q9WV55	-6.7	7.6E-05	-1.3	1.3E-01	0.8	1.4E-01	-0.6	4.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000024905	ralA binding protein 1 [Source:MGI Symbol;Acc:MGI:108466]		Q62172	-8.7	1.0E-06	5.4	7.9E-03	-0.4	8.4E-01	-1.1	2.5E-01
ENSMUST00000024832	radial spoke head 1 homolog (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1194909]	Q3YEA4	Q8VIG3	-0.7	2.4E-01	-0.5	4.8E-01	0.0	9.3E-01	-0.2	7.4E-01
ENSMUST00000024909	NADH dehydrogenase (ubiquinone) flavoprotein 2 [Source:MGI Symbol;Acc:MGI:1920150]		Q9D6J6	-8.4	6.7E-07	7.1	4.9E-05	2.2	4.0E-02	-0.2	6.8E-01
ENSMUST00000024839	salt inducible kinase 1 [Source:MGI Symbol;Acc:MGI:104754]		Q60670	-0.9	2.3E-01	-1.2	2.3E-01	0.3	6.1E-01	0.6	4.8E-01
ENSMUST00000024914	thymocyte selection associated family member 3 [Source:MGI Symbol;Acc:MGI:1921806]		Q9CU24	6.5	7.3E-05	3.3	2.3E-03	-2.2	1.9E-02	0.1	8.1E-01
ENSMUST00000024916	luteinizing hormone/choriogonadotropin receptor [Source:MGI Symbol;Acc:MGI:96783]		P30730	6.8	2.9E-04	-7.2	3.3E-03	1.5	3.7E-02	-1.1	6.1E-01
ENSMUST00000024928	protease, serine 21 [Source:MGI Symbol;Acc:MGI:1916698]	Q54AE4	Q9JHJ7	6.1	3.1E-04	-5.5	8.4E-06	0.6	5.7E-02	-0.1	9.3E-01
ENSMUST00000024851	NDC80 homolog, kinetochore complex component (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914302]		Q9D0F1	-0.8	2.9E-01	-1.0	2.7E-01	-0.6	3.3E-01	-0.4	6.5E-01
ENSMUST00000024931	TBC1 domain family, member 24 [Source:MGI Symbol;Acc:MGI:2443456]	Q52KG2	Q9R1A3	8.0	1.5E-05	3.3	9.7E-04	-3.4	1.9E-03	0.1	8.9E-01
ENSMUST00000024857	limb-bud and heart [Source:MGI Symbol;Acc:MGI:1925139]		Q9CX60	-0.7	2.9E-01	-0.3	7.3E-01	0.5	3.9E-01	0.1	8.9E-01
ENSMUST00000024932	ATPase, H+ transporting, lysosomal V0 subunit C [Source:MGI Symbol;Acc:MGI:88116]	A3KML5	P63082	-6.3	2.7E-05	8.1	3.7E-05	-1.8	2.0E-01	0.0	9.4E-01
ENSMUST00000024936	protease, serine 30 [Source:MGI Symbol;Acc:MGI:1353645]		Q9QYZ9	6.4	1.1E-06	3.6	7.9E-04	-0.7	3.3E-01	0.5	4.1E-01
ENSMUST00000024939	spermine binding protein-like [Source:MGI Symbol;Acc:MGI:3694550]	Q3TUY3		6.6	1.0E-04	-3.9	6.4E-04	0.9	6.0E-02	-0.5	5.8E-01
ENSMUST00000024944	solute carrier family 3, member 1 [Source:MGI Symbol;Acc:MGI:1195264]		Q91WV7	3.5	4.7E-03	-1.4	9.6E-02	0.8	1.1E-01	-0.2	8.1E-01
ENSMUST00000024954	endothelial PAS domain protein 1 [Source:MGI Symbol;Acc:MGI:109169]		P97481	5.7	3.4E-05	-1.1	8.8E-02	0.2	6.1E-01	-0.6	3.8E-01
ENSMUST00000024956	ras homolog gene family, member Q [Source:MGI Symbol;Acc:MGI:1931553]		Q8R527	-1.8	5.2E-03	-3.5	3.1E-03	1.5	1.2E-02	0.8	3.6E-01
ENSMUST00000024958	CASK interacting protein 1 [Source:MGI Symbol;Acc:MGI:2442952]		Q6P9K8	6.5	1.2E-04	9.6	3.1E-04	0.5	7.6E-01	1.4	9.6E-02
ENSMUST00000024881	striatin, calmodulin binding protein [Source:MGI Symbol;Acc:MGI:1333757]	F8WH41		1.5	4.8E-01	1.5	5.1E-01	-1.0	6.0E-01	-1.0	6.4E-01
ENSMUST00000024959	cysteine-rich PDZ-binding protein [Source:MGI Symbol;Acc:MGI:1929655]		O70333	-5.5	9.7E-07	0.1	8.3E-01	-1.9	1.0E-02	-0.4	5.6E-01
ENSMUST00000024963	multiple coagulation factor deficiency 2 [Source:MGI Symbol;Acc:MGI:2183439]	D0EW11	Q8K5B2	-6.0	1.1E-03	4.3	5.0E-05	-0.7	2.1E-01	0.0	9.3E-01
ENSMUST00000024970	general transcription factor IIA, 1-like [Source:MGI Symbol;Acc:MGI:1919078]		Q8R4I4	6.3	8.8E-05	-2.6	7.8E-03	-0.7	1.4E-01	-0.5	5.3E-01
ENSMUST00000024978	NME/NM23 nucleoside diphosphate kinase 3 [Source:MGI Symbol;Acc:MGI:1930182]		Q9WV85	-4.6	2.4E-04	1.0	1.2E-01	-0.2	7.1E-01	0.0	9.5E-01
ENSMUST00000024984	transmembrane protein 204 [Source:MGI Symbol;Acc:MGI:3039635]		Q7TQI0	3.2	1.5E-02	-5.9	1.2E-02	-0.3	7.3E-01	0.8	6.8E-01
ENSMUST00000024988	complement component 3 [Source:MGI Symbol;Acc:MGI:88227]		P01027	-5.1	1.1E-06	3.5	1.5E-02	-4.7	6.8E-03	-4.3	2.9E-03
ENSMUST00000024993	protease, serine 29 [Source:MGI Symbol;Acc:MGI:2149952]	E9QLD5		7.0	5.2E-05	3.1	2.1E-03	-5.1	5.7E-04	0.4	4.7E-01
ENSMUST00000025000	beta galactoside alpha 2,6 sialyltransferase 2 [Source:MGI Symbol;Acc:MGI:2445190]		Q76K27	7.5	4.8E-05	-5.0	3.1E-03	1.1	7.6E-02	-0.6	6.7E-01
ENSMUST00000025002	tektin 4 [Source:MGI Symbol;Acc:MGI:1919090]			7.6	2.9E-05	-8.3	1.4E-05	1.0	5.4E-03	0.6	5.7E-01
ENSMUST00000024906	twisted gastrulation homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2137520]		Q9EP52	0.1	9.1E-01	-0.8	2.0E-01	-0.8	8.5E-02	0.1	8.8E-01
ENSMUST00000025003	SRY (sex determining region Y)-box 8 [Source:MGI Symbol;Acc:MGI:98370]	Q543C3	Q04886	8.0	3.1E-05	-7.1	1.1E-05	0.2	4.8E-01	-1.1	2.4E-01
ENSMUST00000025010	transmembrane protein 8 (five membrane-spanning domains) [Source:MGI Symbol;Acc:MGI:1926283]		Q9ESN3	-2.0	7.0E-03	6.5	1.4E-04	-0.6	6.0E-01	-0.6	3.4E-01
ENSMUST00000025014	mitochondrial ribosomal protein L28 [Source:MGI Symbol;Acc:MGI:1915861]		Q9D1B9	-2.9	3.1E-03	6.8	5.3E-04	-0.4	7.8E-01	-0.4	5.4E-01
ENSMUST00000025023	Luc7 homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:1914228]			-3.5	6.7E-03	6.8	2.5E-04	-0.5	6.8E-01	-1.2	9.2E-02
ENSMUST00000024930	RIKEN cDNA 1600002H07 gene [Source:MGI Symbol;Acc:MGI:1919266]		Q6GQV0	1.3	1.4E-01	4.3	2.7E-03	1.9	8.1E-02	-1.2	1.4E-01
ENSMUST00000025025	dual specificity phosphatase 1 [Source:MGI Symbol;Acc:MGI:105120]	Q3U8K3	P28563	-8.4	7.5E-04	8.0	3.6E-05	-0.5	6.6E-01	-0.5	3.3E-01
ENSMUST00000025027	cutA divalent cation tolerance homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1914925]		Q9CQ89	-5.7	9.3E-05	-5.6	5.0E-04	0.9	7.1E-02	0.2	8.8E-01
ENSMUST00000025034	BCL2-antagonist/killer 1 [Source:MGI Symbol;Acc:MGI:1097161]	Q91WX5		-6.7	7.9E-05	6.1	3.6E-06	-0.7	2.8E-01	-0.4	2.9E-01
ENSMUST00000025045	ubiquinol-cytochrome c reductase complex assembly factor 2 [Source:MGI Symbol;Acc:MGI:1914517]		Q9CQY6	-4.8	4.7E-03	6.2	3.1E-04	-0.6	6.2E-01	-0.1	8.2E-01
ENSMUST00000025046	inositol hexaphosphate kinase 3 [Source:MGI Symbol;Acc:MGI:3045325]		Q8BWD2	4.6	5.7E-04	3.0	1.8E-02	-0.4	6.7E-01	0.0	1.0E+00
ENSMUST00000024946	enoyl-Coenzyme A delta isomerase 1 [Source:MGI Symbol;Acc:MGI:94871]		P42125	0.9	1.7E-01	-0.1	8.8E-01	-0.2	8.0E-01	0.9	2.6E-01
ENSMUST00000025048	RIKEN cDNA 1700061G19 gene [Source:MGI Symbol;Acc:MGI:1925875]	Q08EE8		2.0	2.4E-02	4.6	6.1E-04	-0.2	8.0E-01	0.8	1.8E-01
ENSMUST00000025050	nudix (nucleotide diphosphate linked moiety X)-type motif 3 [Source:MGI Symbol;Acc:MGI:1928484]		Q9JI46	-3.3	8.6E-05	-0.8	2.5E-01	0.6	1.7E-01	-0.4	4.8E-01
ENSMUST00000024957	phosphatidylinositol glycan anchor biosynthesis, class F [Source:MGI Symbol;Acc:MGI:99462]		O09101	-1.6	5.2E-02	-2.1	9.8E-02	0.3	6.7E-01	0.8	4.8E-01
ENSMUST00000025052	ribosomal protein S10 [Source:MGI Symbol;Acc:MGI:1914347]	Q3UW83		-9.6	2.2E-05	5.8	8.8E-04	-0.2	8.5E-01	0.5	5.2E-01
ENSMUST00000025054	SAM pointed domain containing ets transcription factor [Source:MGI Symbol;Acc:MGI:1353422]		Q9WTP3	6.5	2.4E-02	-5.1	1.1E-05	0.2	5.0E-01	-0.2	7.4E-01
ENSMUST00000025057	1 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:191		Q99JX1	-3.9	1.2E-03	-5.4	1.8E-02	0.9	2.9E-01	0.3	8.8E-01
ENSMUST00000024967	mutS homolog 2 (E. coli) [Source:MGI Symbol;Acc:MGI:101816]	Q3TZI5	P43247	0.7	2.7E-01	0.7	3.7E-01	0.0	9.5E-01	0.0	9.9E-01
ENSMUST00000025064	PDZ and pleckstrin homology domains 1 [Source:MGI Symbol;Acc:MGI:1916489]	Q8BGR1		7.7	6.6E-05	5.8	3.1E-04	-0.5	6.5E-01	0.0	9.8E-01
ENSMUST00000024974	hydroxyacyl glutathione hydrolase [Source:MGI Symbol;Acc:MGI:95745]			-2.2	2.1E-01	-2.3	3.4E-01	-0.4	7.8E-01	-0.3	9.1E-01
ENSMUST00000024976	splA/ryanodine receptor domain and SOCS box containing 3 [Source:MGI Symbol;Acc:MGI:1891471]		Q571F5	0.0	9.9E-01	-0.3	7.8E-01	0.7	4.3E-01	1.0	3.5E-01
ENSMUST00000025065	nudix (nucleoside diphosphate linked moiety X)-type motif 12 [Source:MGI Symbol;Acc:MGI:1915243]		Q9DCN1	8.4	2.6E-07	-4.1	5.3E-03	0.3	5.4E-01	-0.2	8.5E-01
ENSMUST00000024981	hematological and neurological expressed 1-like [Source:MGI Symbol;Acc:MGI:1196260]	Q3TM10	Q6PGH2	0.9	4.8E-02	0.7	2.3E-01	0.2	6.1E-01	0.4	3.9E-01
ENSMUST00000024983	intraflagellar transport 140 [Source:MGI Symbol;Acc:MGI:2146906]	E9PY46		0.3	6.5E-01	1.1	2.2E-01	1.0	1.3E-01	0.2	7.8E-01
ENSMUST00000025075	BMP and activin membrane-bound inhibitor [Source:MGI Symbol;Acc:MGI:1915260]		Q9D0L6	2.5	1.8E-02	4.8	7.7E-03	0.5	7.3E-01	-1.1	2.6E-01
ENSMUST00000025077	mitochondrial poly(A) polymerase [Source:MGI Symbol;Acc:MGI:1914690]		Q9D0D3	-2.3	1.3E-03	-3.5	1.4E-04	1.4	1.1E-03	-0.2	7.3E-01
ENSMUST00000025078	mitogen-activated protein kinase kinase kinase 8 [Source:MGI Symbol;Acc:MGI:1346878]	Q3UEB8	Q07174	-4.5	2.4E-04	6.9	1.1E-04	-0.6	5.9E-01	-0.5	4.1E-01
ENSMUST00000025081	zinc finger E-box binding homeobox 1 [Source:MGI Symbol;Acc:MGI:1344313]		Q64318	-2.3	8.0E-04	7.0	1.6E-04	-0.6	6.0E-01	-0.2	7.7E-01
ENSMUST00000025083	kinesin family member 5B [Source:MGI Symbol;Acc:MGI:1098268]		Q61768	-1.1	4.1E-03	7.6	5.6E-05	-0.6	6.1E-01	-0.6	3.0E-01
ENSMUST00000025092	transmembrane protein 178 [Source:MGI Symbol;Acc:MGI:1915277]		Q9CZ16	4.7	3.0E-04	7.1	8.4E-05	-1.5	2.4E-01	-0.5	3.7E-01
ENSMUST00000025004	adhesion G protein-coupled receptor E4 [Source:MGI Symbol;Acc:MGI:1196464]		Q91ZE5	0.7	3.9E-01	-0.7	4.1E-01	-2.2	8.2E-03	-0.9	3.1E-01
ENSMUST00000025007	NME/NM23 nucleoside diphosphate kinase 4 [Source:MGI Symbol;Acc:MGI:1931148]		Q9WV84	1.0	2.8E-01	-0.4	7.0E-01	-1.3	1.5E-01	0.1	9.4E-01
ENSMUST00000025093	THUMP domain containing 2 [Source:MGI Symbol;Acc:MGI:1919417]		Q9CZB3	1.9	2.5E-02	-0.9	2.3E-01	0.3	5.4E-01	-0.8	2.6E-01
ENSMUST00000025095	cytochrome c oxidase subunit VIIa polypeptide 2-like [Source:MGI Symbol;Acc:MGI:106015]	Q3UDK5	Q61387	-7.8	4.5E-05	-1.1	2.5E-01	0.5	4.0E-01	-1.4	1.7E-01
ENSMUST00000025101	dynein cytoplasmic 2 light intermediate chain 1 [Source:MGI Symbol;Acc:MGI:1913996]		Q8K0T2	-3.5	2.0E-04	-1.5	1.6E-01	-0.4	5.4E-01	-2.5	5.3E-02
ENSMUST00000025106	polymerase (RNA) II (DNA directed) polypeptide D [Source:MGI Symbol;Acc:MGI:1916491]		Q9D7M8	-4.2	1.2E-04	-6.8	8.0E-03	0.5	5.4E-01	-1.1	6.4E-01
ENSMUST00000025110	synaptotagmin IV [Source:MGI Symbol;Acc:MGI:101759]		P40749	7.1	5.5E-05	-2.7	6.9E-03	0.4	3.6E-01	-2.5	2.6E-02
ENSMUST00000025117	CUGBP, Elav-like family member 4 [Source:MGI Symbol;Acc:MGI:1932407]		Q7TSY6	6.0	4.1E-03	-6.9	3.0E-03	1.2	5.2E-02	1.4	4.4E-01
ENSMUST00000025036	lysine (K)-specific demethylase 4B [Source:MGI Symbol;Acc:MGI:2442355]		Q91VY5	-0.2	7.8E-01	0.6	5.0E-01	0.9	1.7E-01	0.2	8.4E-01
ENSMUST00000025120	elongator acetyltransferase complex subunit 2 [Source:MGI Symbol;Acc:MGI:1889642]		Q91WG4	-1.7	2.4E-03	1.1	1.8E-01	-2.0	2.6E-02	0.4	6.1E-01
ENSMUST00000025127	microtubule-associated protein, RP/EB family, member 2 [Source:MGI Symbol;Acc:MGI:106271]		Q8R001	-3.8	3.5E-03	-6.6	2.1E-03	-1.5	4.5E-02	0.3	8.8E-01
ENSMUST00000025137	THO complex 1 [Source:MGI Symbol;Acc:MGI:1919668]		Q8R3N6	-1.5	1.7E-02	4.8	3.2E-03	-0.2	8.6E-01	-0.4	5.9E-01
ENSMUST00000025142	establishment of cohesion 1 homolog 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925055]		Q69Z69	-3.3	1.2E-04	2.2	3.0E-02	-0.4	5.8E-01	-0.6	4.1E-01
ENSMUST00000025160	coiled coil domain containing 178 [Source:MGI Symbol;Acc:MGI:1918200]		Q8CDV0	5.6	1.6E-03	-1.9	1.5E-02	1.4	4.1E-03	0.0	9.7E-01
ENSMUST00000025161	TAP binding protein [Source:MGI Symbol;Acc:MGI:1201689]	Q3TCU5		-3.9	7.2E-05	-4.6	1.7E-02	3.9	6.7E-04	-1.0	5.5E-01
ENSMUST00000025053	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1 [Source:MGI Symbol;Acc:I	Q9ERL0		0.4	5.2E-01	1.3	1.0E-01	0.8	2.0E-01	-0.2	8.0E-01
ENSMUST00000025163	prefoldin subunit 6 [Source:MGI Symbol;Acc:MGI:95908]	Q792E4	Q03958	-3.3	1.5E-02	5.7	6.2E-02	-0.8	7.8E-01	0.0	1.0E+00
ENSMUST00000025166	cadherin 2 [Source:MGI Symbol;Acc:MGI:88355]		P15116	9.0	2.0E-05	-5.3	7.3E-03	0.0	9.5E-01	1.4	3.7E-01
ENSMUST00000025058	ankyrin repeat and SAM domain containing 1 [Source:MGI Symbol;Acc:MGI:2446180]	Q3UHP6		3.4	2.3E-01	9.0	8.1E-03	-0.5	8.8E-01	-6.1	4.2E-03

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000025060	armadillo repeat containing 12 [Source:MGI Symbol;Acc:MGI:1914895]		Q80X86	1.1	1.0E-01	1.4	8.6E-02	-0.2	7.8E-01	-0.5	4.8E-01
ENSMUST00000025177	trafficking protein particle complex 8 [Source:MGI Symbol;Acc:MGI:2443008]	E9PWG2		-3.9	3.6E-04	7.3	2.1E-04	-0.7	6.1E-01	-0.2	7.4E-01
ENSMUST00000025181	histocompatibility 2, K1, K region [Source:MGI Symbol;Acc:MGI:95904]	Q7JJ15	P01901	-10.1	1.9E-04	8.4	2.4E-06	-0.1	8.9E-01	-0.1	7.7E-01
ENSMUST00000025073	cullin 2 [Source:MGI Symbol;Acc:MGI:1918995]		Q9D4H8	2.7	2.6E-01	1.4	6.0E-01	-2.2	3.6E-01	-0.8	7.3E-01
ENSMUST00000025186	solute carrier family 39 (zinc transporter), member 7 [Source:MGI Symbol;Acc:MGI:95909]	A0A068BIT0	Q31125	-7.9	4.3E-05	2.4	5.9E-02	0.1	9.2E-01	0.2	7.8E-01
ENSMUST00000025193	bromodomain containing 2 [Source:MGI Symbol;Acc:MGI:99495]	B2RS09	Q7JJ13	-7.7	8.9E-05	-2.3	5.4E-03	0.1	8.5E-01	0.1	9.2E-01
ENSMUST00000025196	e (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7) [Source:MGI Symbol;Acc:MGI		P28063	-3.3	2.9E-04	-3.0	6.7E-03	0.0	1.0E+00	-1.5	1.4E-01
ENSMUST00000025198	butyrophilin-like 2 [Source:MGI Symbol;Acc:MGI:1859549]		O70355	3.3	1.4E-02	-1.7	1.6E-02	0.5	2.2E-01	-0.1	8.9E-01
ENSMUST00000025202	potassium voltage gated channel, Shaw-related subfamily, member 1 [Source:MGI Symbol;Acc:MGI:96667]	Q3UHB6	P15388	9.6	6.2E-07	-0.9	4.6E-02	0.3	2.9E-01	0.0	9.2E-01
ENSMUST00000025089	mitogen-activated protein kinase kinase kinase kinase 3 [Source:MGI Symbol;Acc:MGI:2154405]		Q99JP0	0.1	7.6E-01	0.4	4.7E-01	0.3	5.4E-01	0.0	9.7E-01
ENSMUST00000025204	prefoldin 1 [Source:MGI Symbol;Acc:MGI:1914449]	Q9CQF7		-4.2	4.8E-05	5.7	3.6E-04	0.2	8.1E-01	-0.8	2.5E-01
ENSMUST00000025208	DnaJ (Hsp40) homolog, subfamily C, member 18 [Source:MGI Symbol;Acc:MGI:1923844]		Q9CZJ9	2.6	1.8E-03	0.1	9.2E-01	-1.2	1.3E-01	0.7	3.7E-01
ENSMUST00000025211	marginal zone B and B1 cell-specific protein 1 [Source:MGI Symbol;Acc:MGI:1917066]		Q9D8I1	2.3	2.3E-02	-6.8	6.4E-04	-0.1	9.2E-01	-1.1	4.7E-01
ENSMUST00000025212	solute carrier family 23 (nucleobase transporters), member 1 [Source:MGI Symbol;Acc:MGI:1341903]		Q9Z2J0	6.0	2.9E-04	-3.1	1.8E-03	-0.2	6.1E-01	-0.6	4.2E-01
ENSMUST00000025217	heat shock protein 9 [Source:MGI Symbol;Acc:MGI:96245]		P38647	-3.0	4.7E-04	-3.9	7.2E-04	-0.6	2.0E-01	-1.0	2.6E-01
ENSMUST00000025109	Sin3A associated protein [Source:MGI Symbol;Acc:MGI:1919782]			-2.5	7.1E-02	-1.5	3.5E-01	0.5	6.3E-01	-0.6	7.1E-01
ENSMUST00000025218	eukaryotic translation termination factor 1 [Source:MGI Symbol;Acc:MGI:2385071]		Q8BWY3	-4.4	5.2E-06	5.5	6.7E-04	-0.6	6.0E-01	1.0	1.4E-01
ENSMUST00000025223	cytochrome P450, family 21, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88591]			7.8	1.4E-05	1.1	5.6E-01	-2.3	1.9E-01	2.6	1.2E-01
ENSMUST00000025224	glial cell line derived neurotrophic factor family receptor alpha 3 [Source:MGI Symbol;Acc:MGI:1201403]		O35118	7.2	3.1E-05	-2.0	3.9E-03	-0.6	8.0E-02	-0.3	5.2E-01
ENSMUST00000025230	complement component 2 (within H-2S) [Source:MGI Symbol;Acc:MGI:88226]		P21180	7.9	2.0E-05	-2.5	4.0E-02	0.2	7.2E-01	-1.1	3.7E-01
ENSMUST00000025234	erythrocyte membrane protein band 4.1 like 4a [Source:MGI Symbol;Acc:MGI:103007]		P52963	7.4	1.7E-05	-1.3	6.6E-02	-0.7	1.0E-01	-1.0	1.4E-01
ENSMUST00000025239	bridging integrator 1 [Source:MGI Symbol;Acc:MGI:108092]		O08539	5.3	4.7E-04	-3.2	6.1E-04	-0.2	6.1E-01	-0.2	7.1E-01
ENSMUST00000025241	repair cross-complementing rodent repair deficiency, complementation group 3 [Source:MGI Symbol;Acc:MG		P49135	-2.6	8.0E-04	5.6	2.8E-03	-0.4	8.0E-01	-0.4	6.5E-01
ENSMUST00000025243	IWS1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1920723]		Q8C1D8	1.5	6.7E-03	-3.2	2.2E-03	0.8	8.8E-02	0.0	9.9E-01
ENSMUST00000025246	casein kinase 2, beta polypeptide [Source:MGI Symbol;Acc:MGI:88548]		P67871	-6.5	4.1E-05	-4.5	3.0E-02	-0.6	4.5E-01	0.5	7.7E-01
ENSMUST00000025249	apolipoprotein M [Source:MGI Symbol;Acc:MGI:1930124]		Q9Z1R3	2.7	1.2E-02	7.6	2.1E-04	-0.3	8.5E-01	1.2	9.3E-02
ENSMUST00000025170	WD repeat domain 46 [Source:MGI Symbol;Acc:MGI:1931871]		Q9Z0H1	-0.4	5.0E-01	0.0	9.8E-01	0.6	3.0E-01	0.2	8.1E-01
ENSMUST00000025250	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]		Q9Z1R2	-8.0	1.7E-03	-2.4	2.4E-02	1.0	6.1E-02	-0.5	6.1E-01
ENSMUST00000025178	vacuolar protein sorting 52 (yeast) [Source:MGI Symbol;Acc:MGI:1330304]		Q8C754	-1.5	7.8E-02	-1.2	2.9E-01	1.2	1.3E-01	0.9	4.3E-01
ENSMUST00000025253	proline-rich coiled-coil 2A [Source:MGI Symbol;Acc:MGI:1915467]		Q7TSC1	-5.1	1.5E-03	-10.0	2.0E-03	0.1	9.3E-01	-0.1	9.6E-01
ENSMUST00000025183	ring finger protein 1 [Source:MGI Symbol;Acc:MGI:1101770]		O35730	-2.0	7.3E-02	-1.2	3.7E-01	0.6	5.0E-01	-0.2	8.8E-01
ENSMUST00000025254	LIM and senescent cell antigen like domains 2 [Source:MGI Symbol;Acc:MGI:2385067]		Q91XD2	7.0	7.8E-05	-5.9	1.9E-03	1.3	2.2E-02	-0.7	6.7E-01
ENSMUST00000025262	lymphotoxin B [Source:MGI Symbol;Acc:MGI:104796]		P41155	-5.7	1.7E-04	-6.0	3.3E-03	0.9	1.3E-01	-0.8	6.2E-01
ENSMUST00000025263	tumor necrosis factor [Source:MGI Symbol;Acc:MGI:104798]	Q3U593	P06804	-2.4	4.8E-03	-2.7	3.9E-03	-0.1	8.7E-01	-0.7	3.4E-01
ENSMUST00000025197	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) [Source:MGI Symbol;Acc:MGI:98484]	Q792S7	P36371	-0.4	4.6E-01	1.0	2.0E-01	1.0	9.5E-02	-0.4	5.5E-01
ENSMUST00000025266	lymphotoxin A [Source:MGI Symbol;Acc:MGI:104797]	Q542S2	P09225	3.1	8.8E-03	2.8	4.6E-02	-1.2	3.2E-01	-0.7	5.3E-01
ENSMUST00000025270	RIO kinase 3 [Source:MGI Symbol;Acc:MGI:1914128]		Q9DBU3	-2.1	1.3E-03	8.6	8.8E-06	-0.6	5.3E-01	0.4	4.0E-01
ENSMUST00000025271	POU domain, class 5, transcription factor 1 [Source:MGI Symbol;Acc:MGI:101893]		P20263	7.3	3.2E-05	-4.3	1.7E-04	-0.8	5.6E-02	-0.7	3.4E-01
ENSMUST00000025273	psoriasis susceptibility 1 candidate 2 (human) [Source:MGI Symbol;Acc:MGI:1930025]	Q3UUY0		6.4	2.3E-04	1.9	2.6E-02	-0.5	4.3E-01	0.2	7.5E-01
ENSMUST00000025209	spermatogenesis associated 24 [Source:MGI Symbol;Acc:MGI:1918492]		Q6P926	0.3	7.8E-01	0.7	5.7E-01	-1.3	2.5E-01	-1.6	1.7E-01
ENSMUST00000025276	RIKEN cDNA 3110002H16 gene [Source:MGI Symbol;Acc:MGI:1916528]	Q3U4H5	Q8VC42	-8.3	1.8E-06	-0.1	8.9E-01	-3.4	1.7E-03	-0.9	3.0E-01
ENSMUST00000025288	zinc finger protein 521 [Source:MGI Symbol;Acc:MGI:95459]		Q6KAS7	6.0	5.3E-06	4.1	7.8E-03	-0.8	5.1E-01	1.1	2.3E-01
ENSMUST00000025215	endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1932040]		Q9EPK6	1.1	6.3E-02	0.9	1.9E-01	-0.7	1.8E-01	-0.5	4.2E-01
ENSMUST00000025292	DEAH (Asp-Glu-Ala-His) box polypeptide 16 [Source:MGI Symbol;Acc:MGI:1916442]	G3X8X0		-2.0	1.6E-02	-2.9	1.8E-03	-0.7	8.8E-02	-0.8	2.7E-01
ENSMUST00000025293	Nedd4 family interacting protein 1 [Source:MGI Symbol;Acc:MGI:1929601]		Q8R0W6	-7.1	3.8E-05	-3.6	1.2E-04	0.2	5.9E-01	-0.7	2.6E-01
ENSMUST00000025295	sprouty homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1345144]		Q9WTP2	8.6	2.9E-05	7.9	2.7E-05	-0.6	6.0E-01	-0.6	2.3E-01
ENSMUST00000025305	mitochondrial ribosomal protein S18B [Source:MGI Symbol;Acc:MGI:1914223]		Q99N84	-3.5	4.5E-03	7.4	5.0E-05	-0.6	6.2E-01	-0.7	2.2E-01
ENSMUST00000025228	CDC23 cell division cycle 23 [Source:MGI Symbol;Acc:MGI:1098815]	G3X8W7		-2.0	3.7E-02	-0.9	3.7E-01	-0.1	8.9E-01	-1.2	2.3E-01
ENSMUST00000025229	complement factor B [Source:MGI Symbol;Acc:MGI:105975]	B8JJM5		4.2	3.5E-02	0.0	9.8E-01	-4.4	2.8E-02	-0.2	8.5E-01
ENSMUST00000025311	protocadherin 12 [Source:MGI Symbol;Acc:MGI:1855700]		O55134	6.0	2.6E-02	5.0	4.2E-04	-3.3	1.1E-02	-0.4	4.6E-01
ENSMUST00000025312	histocompatibility 2, T region locus 3 [Source:MGI Symbol;Acc:MGI:95959]	F6TIX5		7.8	3.3E-04	2.8	1.1E-03	-5.4	1.4E-04	-0.8	1.1E-01
ENSMUST00000025236	StAR-related lipid transfer (START) domain containing 4 [Source:MGI Symbol;Acc:MGI:2156764]	Q80SX0		-0.6	3.0E-01	-0.7	4.1E-01	0.5	3.1E-01	0.6	4.4E-01
ENSMUST00000025237	thymic stromal lymphopoietin [Source:MGI Symbol;Acc:MGI:1855696]		Q9JIE6	0.9	2.3E-01	-0.1	8.9E-01	-2.5	4.2E-03	-1.5	5.8E-02
ENSMUST00000025322	histocompatibility 2, M region locus 10.1 [Source:MGI Symbol;Acc:MGI:1276522]	O19443		5.9	1.4E-04	2.8	8.0E-03	-3.0	1.2E-02	-0.6	4.2E-01
ENSMUST00000025329	tripartite motif-containing 15 [Source:MGI Symbol;Acc:MGI:1916347]	Q8R096		6.8	1.4E-02	-2.5	6.5E-03	0.4	3.4E-01	0.3	7.1E-01
ENSMUST00000025337	diaphanous homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1194490]	E9PV41		-8.4	3.3E-04	1.1	8.2E-02	0.2	6.8E-01	0.6	2.4E-01
ENSMUST00000025338	gamma-aminobutyric acid (GABA) B receptor, 1 [Source:MGI Symbol;Acc:MGI:1860139]		Q9WV18	6.1	3.7E-03	-5.1	8.7E-04	0.7	1.5E-01	-0.6	5.9E-01
ENSMUST00000025356	mal, T cell differentiation protein 2 [Source:MGI Symbol;Acc:MGI:2146021]	Q2KHK7	Q8BI08	7.6	2.8E-04	2.8	1.7E-02	-0.9	3.5E-01	-1.0	2.4E-01
ENSMUST00000025357	adaptor-related protein complex 3, sigma 1 subunit [Source:MGI Symbol;Acc:MGI:1337062]	Q3U8S0	Q9DCR2	-5.4	1.8E-05	-3.1	5.5E-02	1.1	2.2E-01	-3.9	7.8E-02
ENSMUST00000025358	laeverin [Source:MGI Symbol;Acc:MGI:1921824]	E9QJR0		5.6	2.6E-05	-2.2	1.2E-01	1.4	1.0E-01	-1.5	3.0E-01
ENSMUST00000025363	heparin-binding EGF-like growth factor [Source:MGI Symbol;Acc:MGI:96070]	Q5FW64	Q06186	5.3	6.3E-05	6.7	1.9E-04	-0.8	5.1E-01	-0.5	4.0E-01
ENSMUST00000025364	Yip1 domain family, member 5 [Source:MGI Symbol;Acc:MGI:1914430]		Q9EQQ2	-3.1	1.0E-04	-5.7	3.7E-03	1.3	5.2E-02	1.3	4.1E-01
ENSMUST00000025374	POU domain, class 4, transcription factor 3 [Source:MGI Symbol;Acc:MGI:102523]		Q63955	8.3	3.7E-05	-0.3	7.1E-01	1.8	1.4E-02	-0.3	7.1E-01
ENSMUST00000025264	WD repeat domain 33 [Source:MGI Symbol;Acc:MGI:1921570]		Q8K4P0	-0.9	6.7E-02	-0.5	4.0E-01	0.5	1.9E-01	0.2	7.7E-01
ENSMUST00000025385	hydroxysteroid (17-beta) dehydrogenase 4 [Source:MGI Symbol;Acc:MGI:105089]		P51660	-2.9	1.1E-04	2.6	3.1E-02	-1.1	2.8E-01	-0.6	4.8E-01
ENSMUST00000025388	ferritin mitochondrial [Source:MGI Symbol;Acc:MGI:1914884]		Q9D5H4	5.9	3.6E-04	-2.2	5.9E-03	0.5	2.3E-01	0.6	3.1E-01
ENSMUST00000025393	SMAD family member 4 [Source:MGI Symbol;Acc:MGI:894293]		P97471	-5.6	2.7E-04	6.5	1.6E-04	-0.6	6.0E-01	0.2	7.0E-01
ENSMUST00000025394	SEC11 homolog C, signal peptidase complex subunit [Source:MGI Symbol;Acc:MGI:1913536]		Q9D8V7	-7.9	1.0E-04	5.3	9.8E-04	-1.5	2.5E-01	-0.4	5.7E-01
ENSMUST00000025396	retina and anterior neural fold homeobox [Source:MGI Symbol;Acc:MGI:109632]		O35602	6.7	4.8E-05	-7.3	3.5E-05	0.2	5.3E-01	-0.8	4.5E-01
ENSMUST00000025278	mitochondrial ribosomal protein L27 [Source:MGI Symbol;Acc:MGI:2137224]		Q99N92	0.3	4.4E-01	-0.2	5.1E-01	-1.3	2.2E-03	-0.8	5.8E-02
ENSMUST00000025279	Niemann-Pick type C1 [Source:MGI Symbol;Acc:MGI:1097712]		O35604	-0.7	5.7E-02	0.2	7.2E-01	1.2	7.0E-03	0.3	5.2E-01
ENSMUST00000025399	phorbol-12-myristate-13-acetate-induced protein 1 [Source:MGI Symbol;Acc:MGI:1930146]		Q9JM54	-1.4	2.5E-02	5.7	1.4E-05	-0.7	3.4E-01	-0.4	4.0E-01
ENSMUST00000025290	impact, RWD domain protein [Source:MGI Symbol;Acc:MGI:1098233]		O55091	-1.6	3.8E-02	-1.8	5.5E-02	-0.9	1.1E-01	-0.8	3.6E-01
ENSMUST00000025403	inositol (myo)-1(or 4)-monophosphatase 2 [Source:MGI Symbol;Acc:MGI:2149728]	Q3U3B7	Q91UZ5	-2.0	3.5E-03	-6.0	5.9E-03	1.1	8.3E-02	5.2	1.2E-02
ENSMUST00000025404	death-inducing DNA fragmentation factor, alpha subunit-like effector A [Source:MGI Symbol;Acc:MGI:1270		O70302	6.5	1.7E-04	-5.1	2.4E-03	1.6	1.5E-02	-0.4	7.7E-01
ENSMUST00000025294	tetratricopeptide repeat domain 39C [Source:MGI Symbol;Acc:MGI:1919997]	G3X8X1		0.0	9.9E-01	0.5	7.7E-01	-1.3	3.8E-01	-1.8	3.5E-01
ENSMUST00000025409	lysyl oxidase [Source:MGI Symbol;Acc:MGI:96817]	Q3TXH3	P28301	6.0	5.3E-03	5.2	2.0E-04	-3.2	1.6E-02	0.2	7.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000025411	slowmo homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2442865]		Q8VE85	8.0	2.9E-05	-4.9	7.1E-03	-0.9	1.7E-01	0.5	7.3E-01
ENSMUST00000025419	peptidylprolyl isomerase C [Source:MGI Symbol;Acc:MGI:97751]	Q3UC73	P30412	2.2	1.6E-02	7.7	1.1E-02	-0.6	8.2E-01	-2.3	1.2E-01
ENSMUST00000025420	protein tyrosine phosphatase, non-receptor type 2 [Source:MGI Symbol;Acc:MGI:97806]		Q06180	-8.0	4.4E-05	5.0	1.2E-02	-0.6	7.0E-01	2.1	5.7E-02
ENSMUST00000025314	RIKEN cDNA 0610009O20 gene [Source:MGI Symbol;Acc:MGI:1914089]		Q9DCV6	-0.7	2.0E-01	0.1	9.2E-01	0.6	2.0E-01	-0.1	8.7E-01
ENSMUST00000025319	ribonuclease P 21 subunit [Source:MGI Symbol;Acc:MGI:1914926]		Q8R040	-3.1	4.1E-02	-5.2	3.1E-02	-1.1	2.7E-01	1.0	6.3E-01
ENSMUST00000025421	SEH1-like (S. cerevisiae [Source:MGI Symbol;Acc:MGI:1919374]		Q8R2U0	-2.1	1.8E-03	6.3	1.6E-04	-0.5	6.4E-01	-0.9	1.4E-01
ENSMUST00000025427	RNA (guanine-7-) methyltransferase [Source:MGI Symbol;Acc:MGI:1915147]		Q9D0L8	-6.0	3.1E-04	2.8	3.8E-01	-0.9	7.5E-01	3.1	2.0E-01
ENSMUST00000025430	SET binding protein 1 [Source:MGI Symbol;Acc:MGI:1933199]	F2Z3U2	Q9Z180	6.1	6.1E-05	-7.6	3.4E-03	0.4	4.5E-01	-0.3	8.9E-01
ENSMUST00000025434	solute carrier family 14 (urea transporter), member 2 [Source:MGI Symbol;Acc:MGI:1351653]	G5E849		8.5	4.4E-05	4.7	3.2E-02	-2.1	3.0E-01	-0.7	5.7E-01
ENSMUST00000025350	DCP2 decapping enzyme homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1917890]		Q9CYC6	0.7	6.0E-02	1.4	6.8E-03	0.6	1.1E-01	-0.2	6.3E-01
ENSMUST00000025354	protein geranylgeranyltransferase type I, beta subunit [Source:MGI Symbol;Acc:MGI:1917514]		Q8BUY9	0.1	7.8E-01	-0.2	7.8E-01	-0.1	8.0E-01	0.2	7.3E-01
ENSMUST00000025439	malic enzyme 2, NAD(+)-dependent, mitochondrial [Source:MGI Symbol;Acc:MGI:2147351]		Q99KE1	-5.1	1.0E-06	5.4	4.6E-03	-0.7	6.4E-01	1.4	1.3E-01
ENSMUST00000025444	CXXC finger 1 (PHD domain) [Source:MGI Symbol;Acc:MGI:1921572]	Q541B1	Q9CWW7	-1.9	4.1E-03	-4.3	6.1E-04	1.2	1.8E-02	0.0	9.6E-01
ENSMUST00000025453	SMAD family member 2 [Source:MGI Symbol;Acc:MGI:108051]		Q62432	-6.6	9.5E-04	6.2	1.2E-04	0.4	6.6E-01	-0.2	7.5E-01
ENSMUST00000025462	ribosome binding factor A [Source:MGI Symbol;Acc:MGI:1915981]	Q3UKZ0	Q6P3B9	-3.5	1.3E-04	1.7	6.3E-02	-3.0	3.4E-03	0.7	3.2E-01
ENSMUST00000025468	phosphodiesterase 6A, cGMP-specific, rod, alpha [Source:MGI Symbol;Acc:MGI:97524]	Q8K0A8		7.9	1.3E-05	-2.3	3.0E-03	0.3	3.5E-01	-0.5	4.5E-01
ENSMUST00000025472	prenylcysteine oxidase 1 like [Source:MGI Symbol;Acc:MGI:3606062]		Q8C7K6	3.7	5.9E-03	6.4	5.1E-04	-0.6	6.3E-01	1.2	9.5E-02
ENSMUST00000025375	transcription elongation regulator 1 (CA150) [Source:MGI Symbol;Acc:MGI:1926421]	Q3TH57	Q8CGF7	-0.7	2.3E-01	-0.9	2.2E-01	0.2	6.3E-01	0.5	5.0E-01
ENSMUST00000025474	N-ethylmaleimide sensitive fusion protein attachment protein gamma [Source:MGI Symbol;Acc:MGI:104561]		Q9CWZ7	-3.6	1.3E-04	-2.2	3.4E-03	0.5	1.3E-01	-0.2	7.9E-01
ENSMUST00000025476	thioredoxin-like 1 [Source:MGI Symbol;Acc:MGI:1860078]		Q8CDN6	-4.2	1.4E-05	6.2	4.1E-04	-0.6	6.3E-01	-1.0	1.6E-01
ENSMUST00000025477	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 [Source:MGI Symbol;Acc:MGI:106019]		Q64689	9.9	4.9E-06	-5.9	4.2E-03	1.4	5.3E-02	1.8	2.8E-01
ENSMUST00000025482	ATPase, class I, type 8B, member 1 [Source:MGI Symbol;Acc:MGI:1859665]		Q148W0	7.1	7.3E-06	-7.6	1.1E-04	-0.8	1.0E-01	-1.1	4.7E-01
ENSMUST00000025483	asparaginyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1917473]		Q8BP47	-4.7	7.4E-06	6.5	2.1E-04	0.1	9.6E-01	0.3	6.4E-01
ENSMUST00000025484	ferrochelatase [Source:MGI Symbol;Acc:MGI:95513]	Q544X6		-1.6	3.4E-03	-0.3	6.5E-01	0.7	1.6E-01	-0.4	5.4E-01
ENSMUST00000025402	guanine nucleotide binding protein, alpha stimulating, olfactory type [Source:MGI Symbol;Acc:MGI:95774]	Q66L47		2.9	4.9E-02	6.7	3.8E-04	-0.5	6.9E-01	-4.3	1.1E-03
ENSMUST00000025486	lamin B1 [Source:MGI Symbol;Acc:MGI:96795]		P14733	-6.0	8.8E-08	-0.5	4.8E-01	1.5	9.6E-03	0.0	9.8E-01
ENSMUST00000025497	fibrillin 2 [Source:MGI Symbol;Acc:MGI:95490]		Q61555	9.7	2.9E-06	5.7	6.3E-04	-1.0	4.4E-01	-0.1	8.4E-01
ENSMUST00000025406	serum response factor binding protein 1 [Source:MGI Symbol;Acc:MGI:1914472]		Q9CZ91	0.8	2.6E-01	-0.1	9.5E-01	-1.4	5.3E-02	-0.5	5.2E-01
ENSMUST00000025408	AFG3-like AAA ATPase 2 [Source:MGI Symbol;Acc:MGI:1916847]		Q8JZQ2	-0.9	5.6E-02	-1.1	6.4E-02	-0.4	2.2E-01	-0.3	6.3E-01
ENSMUST00000025500	solute carrier family 27 (fatty acid transporter), member 6 [Source:MGI Symbol;Acc:MGI:3036230]	E9Q9W4		6.4	2.6E-04	3.8	1.5E-02	-3.7	4.7E-02	-1.5	1.8E-01
ENSMUST00000025503	isochorismatase domain containing 1 [Source:MGI Symbol;Acc:MGI:1913557]		Q91V64	1.8	2.4E-02	7.9	1.1E-04	0.0	9.9E-01	0.2	7.9E-01
ENSMUST00000025418	proteasome (prosome, macropain) assembly chaperone 2 [Source:MGI Symbol;Acc:MGI:1922901]		Q9EST4	-0.9	1.2E-01	-1.5	4.6E-02	-0.9	6.8E-02	-0.4	5.4E-01
ENSMUST00000025505	dynactin 4 [Source:MGI Symbol;Acc:MGI:1914915]	Q3TQY2	Q8CBY8	-4.0	1.1E-05	1.7	7.5E-02	-0.6	4.6E-01	-0.1	9.0E-01
ENSMUST00000025506	RNA binding motif protein 22 [Source:MGI Symbol;Acc:MGI:1914060]		Q8BHS3	-4.3	1.5E-04	-7.1	5.9E-04	-0.1	8.6E-01	-1.0	5.4E-01
ENSMUST00000025511	ribosomal protein S14 [Source:MGI Symbol;Acc:MGI:98107]		P62264	-8.7	7.0E-05	-1.7	2.1E-02	0.0	9.2E-01	-0.4	5.1E-01
ENSMUST00000025425	centrosomal protein 192 [Source:MGI Symbol;Acc:MGI:1918049]	E9Q4Y4		0.1	7.8E-01	0.8	1.6E-01	0.3	5.0E-01	-0.4	4.2E-01
ENSMUST00000025515	thioredoxin-related transmembrane protein 3 [Source:MGI Symbol;Acc:MGI:2442418]		Q8BXZ1	-4.9	1.3E-06	-5.5	1.1E-03	-1.2	4.1E-02	-1.7	2.4E-01
ENSMUST00000025520	ute carrier family 6 (neurotransmitter transporter, L-proline), member 7 [Source:MGI Symbol;Acc:MGI:21473		Q6PGE7	8.3	2.0E-05	6.1	5.9E-04	-0.7	5.3E-01	-0.7	3.1E-01
ENSMUST00000025521	caudal type homeobox 1 [Source:MGI Symbol;Acc:MGI:88360]		P18111	7.3	3.5E-05	8.1	1.4E-04	-0.3	8.6E-01	0.1	8.9E-01
ENSMUST00000025522	platelet derived growth factor receptor, beta polypeptide [Source:MGI Symbol;Acc:MGI:97531]	E9QPE2		3.0	4.1E-03	-4.8	1.6E-05	0.5	6.3E-02	0.2	7.2E-01
ENSMUST00000025523	colony stimulating factor 1 receptor [Source:MGI Symbol;Acc:MGI:1339758]	Q0P635	P09581	-6.4	4.1E-04	-0.8	2.1E-01	0.7	1.1E-01	-0.3	5.9E-01
ENSMUST00000025546	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:MGI Symbol;Acc:MGI:1913304]		Q9D1A2	-3.3	3.7E-05	-5.6	1.8E-02	1.1	1.8E-01	0.0	9.9E-01
ENSMUST00000025547	tranlocase of inner mitochondrial membrane 21 [Source:MGI Symbol;Acc:MGI:1920595]	Q3THX0	Q8CCM6	-1.8	2.2E-02	-3.0	2.4E-03	0.7	9.0E-02	0.1	8.4E-01
ENSMUST00000025463	predicted gene 16286 [Source:MGI Symbol;Acc:MGI:3833940]	Q9CQX6		0.7	8.4E-01	7.3	1.5E-01	6.1	1.4E-01	-0.5	9.0E-01
ENSMUST00000025549	cytochrome b5 type A (microsomal) [Source:MGI Symbol;Acc:MGI:1926952]	G5E850		-6.0	1.1E-04	6.8	4.0E-05	-1.4	2.0E-01	-0.3	5.2E-01
ENSMUST00000025561	annexin A1 [Source:MGI Symbol;Acc:MGI:96819]	Q4FJV4	P10107	-10.1	8.2E-07	3.6	2.3E-02	0.5	6.4E-01	0.7	5.3E-01
ENSMUST00000025563	ferritin heavy polypeptide 1 [Source:MGI Symbol;Acc:MGI:95588]		P09528	-7.3	9.5E-07	-2.8	2.7E-03	0.3	4.5E-01	-0.5	5.4E-01
ENSMUST00000025567	fatty acid desaturase 2 [Source:MGI Symbol;Acc:MGI:1930079]		Q9Z0R9	2.8	1.3E-03	-3.9	2.0E-04	0.5	1.6E-01	0.2	7.6E-01
ENSMUST00000025568	transmembrane protein 138 [Source:MGI Symbol;Acc:MGI:1920232]		Q9D6G5	-1.7	3.1E-03	9.0	2.2E-05	-0.7	6.0E-01	0.3	6.0E-01
ENSMUST00000025569	transmembrane protein 216 [Source:MGI Symbol;Acc:MGI:1920020]		Q9CQC4	-5.9	4.8E-05	7.8	4.3E-05	1.1	3.1E-01	0.4	4.5E-01
ENSMUST00000025570	succinate dehydrogenase complex assembly factor 2 [Source:MGI Symbol;Acc:MGI:1913322]		Q8C6I2	-3.8	3.1E-05	-4.6	6.8E-05	0.1	7.8E-01	0.0	9.8E-01
ENSMUST00000025580	membrane-spanning 4-domains, subfamily A, member 6B [Source:MGI Symbol;Acc:MGI:1917024]		Q99N09	-8.5	1.1E-04	-0.7	1.6E-01	-0.2	5.6E-01	-1.0	5.1E-02
ENSMUST00000025581	membrane-spanning 4-domains, subfamily A, member 4D [Source:MGI Symbol;Acc:MGI:1913857]		Q99N05	5.8	3.3E-03	-6.1	4.4E-07	-0.5	3.9E-02	-0.3	4.8E-01
ENSMUST00000025488	RIKEN cDNA C330018D20 gene [Source:MGI Symbol;Acc:MGI:1924672]		Q9CWB7	-1.6	4.6E-02	-0.1	8.8E-01	0.3	6.5E-01	-1.2	1.7E-01
ENSMUST00000025490	proline-rich coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1916106]		Q3UPH1	0.3	4.4E-01	1.3	4.8E-02	1.0	5.6E-02	0.0	1.0E+00
ENSMUST00000025582	membrane-spanning 4-domains, subfamily A, member 6D [Source:MGI Symbol;Acc:MGI:1916024]	Q2TVW7		-5.9	1.3E-05	8.1	1.3E-05	-1.4	2.1E-01	0.2	6.4E-01
ENSMUST00000025585	gastric intrinsic factor [Source:MGI Symbol;Acc:MGI:1202394]		P52787	6.1	5.1E-04	6.0	4.4E-04	-1.3	3.2E-01	-1.0	1.9E-01
ENSMUST00000025590	oxysterol binding protein [Source:MGI Symbol;Acc:MGI:97447]		Q3B7Z2	-2.5	3.2E-03	1.9	4.4E-02	-0.4	5.8E-01	-0.5	5.0E-01
ENSMUST00000025595	family with sequence similarity 111, member A [Source:MGI Symbol;Acc:MGI:1915508]		Q9D2L9	-8.8	2.9E-04	-3.1	3.8E-04	0.3	3.2E-01	-0.7	2.8E-01
ENSMUST00000025601	leupaxin [Source:MGI Symbol;Acc:MGI:2147677]		Q99N69	-2.4	8.5E-04	-3.0	8.3E-03	1.2	3.7E-02	-0.1	9.0E-01
ENSMUST00000025602	guanine nucleotide binding protein, alpha 14 [Source:MGI Symbol;Acc:MGI:95769]		P30677	6.4	6.0E-05	-8.3	3.8E-04	-0.7	2.1E-01	-1.2	4.7E-01
ENSMUST00000025618	proprotein convertase subtilisin/kexin type 5 [Source:MGI Symbol;Acc:MGI:97515]		Q04592	8.2	1.4E-05	-4.5	2.2E-05	0.4	1.5E-01	0.0	9.4E-01
ENSMUST00000025631	osteoclast stimulating factor 1 [Source:MGI Symbol;Acc:MGI:700012]		Q62422	-1.6	6.3E-04	8.1	4.7E-05	-0.6	6.0E-01	-0.4	4.4E-01
ENSMUST00000025636	membrane-spanning 4-domains, subfamily A, member 8A [Source:MGI Symbol;Acc:MGI:1927657]		Q99N10	-4.0	3.3E-05	6.0	3.1E-04	-0.5	6.4E-01	0.8	2.1E-01
ENSMUST00000025641	zona pellucida glycoprotein 1 [Source:MGI Symbol;Acc:MGI:103073]	Q059L1	Q62005	7.1	1.3E-04	4.5	7.1E-04	-0.1	9.0E-01	-1.6	3.7E-02
ENSMUST00000025642	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:106247]		Q99KP6	-6.6	5.4E-05	-4.5	6.7E-03	0.1	8.5E-01	-1.7	2.7E-01
ENSMUST00000025541	guanine nucleotide binding protein, alpha q polypeptide [Source:MGI Symbol;Acc:MGI:95776]	Q3UHH5	P21279	-0.5	3.0E-01	0.4	5.7E-01	0.8	1.3E-01	-0.1	8.4E-01
ENSMUST00000025542	phosphoserine aminotransferase 1 [Source:MGI Symbol;Acc:MGI:2183441]	Q543K5	Q99K85	0.0	9.6E-01	-1.2	1.3E-01	-0.1	8.3E-01	1.1	1.4E-01
ENSMUST00000025645	transmembrane protein 132A [Source:MGI Symbol;Acc:MGI:2147810]		Q922P8	3.2	1.6E-02	-7.2	6.7E-05	0.5	1.5E-01	4.4	1.9E-03
ENSMUST00000025646	solute carrier family 15, member 3 [Source:MGI Symbol;Acc:MGI:1929691]		Q8BPX9	-6.7	3.3E-06	-1.5	6.8E-02	-0.8	1.7E-01	-1.0	2.2E-01
ENSMUST00000025647	pepsinogen 5, group I [Source:MGI Symbol;Acc:MGI:1915935]	Q9D106		7.3	9.5E-05	-7.6	5.3E-04	-1.2	3.7E-02	0.4	7.7E-01
ENSMUST00000025649	damage specific DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:1202384]		Q3U1J4	-3.0	4.2E-05	-9.8	5.4E-06	-0.3	5.3E-01	-0.6	5.8E-01
ENSMUST00000025562	inner centromere protein [Source:MGI Symbol;Acc:MGI:1313288]		Q9WU62	-0.7	1.3E-01	-0.3	6.0E-01	0.7	9.3E-02	0.3	5.6E-01
ENSMUST00000025651	flap structure specific endonuclease 1 [Source:MGI Symbol;Acc:MGI:102779]	Q91Z50		2.4	2.0E-02	-5.8	2.4E-05	0.7	6.1E-02	-0.7	3.4E-01
ENSMUST00000025656	aldehyde dehydrogenase family 1, subfamily A7 [Source:MGI Symbol;Acc:MGI:1347050]	B2RTL5	O35945	6.0	3.6E-04	2.4	9.5E-03	-0.2	7.4E-01	0.2	7.1E-01
ENSMUST00000025659	zinc finger, AN1-type domain 5 [Source:MGI Symbol;Acc:MGI:1278334]		O88878	-5.6	4.4E-05	-0.4	4.9E-01	0.4	3.1E-01	-1.0	8.9E-02
ENSMUST00000025663	transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1890373]		Q5FWI3	-7.6	4.9E-06	-0.2	7.5E-01	1.5	1.1E-02	-4.2	8.8E-04

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000025667	reticulon 3 [Source:MGI Symbol;Acc:MGI:1339970]		Q9ES97	-8.9	7.4E-06	-3.2	3.7E-04	-0.3	4.1E-01	-0.8	2.1E-01
ENSMUST00000025571	CD5 antigen [Source:MGI Symbol;Acc:MGI:88340]	Q3UP78	P13379	1.4	1.1E-01	1.9	6.3E-02	-0.8	3.3E-01	-1.3	1.3E-01
ENSMUST00000025572				1.6	8.9E-02	1.6	1.0E-01	-1.4	1.2E-01	-1.4	1.2E-01
ENSMUST00000025668	atlastin GTPase 3 [Source:MGI Symbol;Acc:MGI:1924270]		Q91YH5	-1.3	8.2E-03	-6.1	1.4E-03	-0.3	5.6E-01	-2.7	1.3E-01
ENSMUST00000025679	OTU domain, ubiquitin aldehyde binding 1 [Source:MGI Symbol;Acc:MGI:2147616]		Q7TQI3	-3.6	1.3E-04	5.4	8.2E-03	-0.6	7.3E-01	-0.2	8.2E-01
ENSMUST00000025681	CDC42 binding protein kinase gamma (DMPK-like) [Source:MGI Symbol;Acc:MGI:2652845]		Q80UW5	1.3	1.6E-02	-6.4	3.3E-05	-1.3	8.2E-03	-0.8	3.9E-01
ENSMUST00000025684	EH-domain containing 1 [Source:MGI Symbol;Acc:MGI:1341878]	Q80ZZ0	Q9WVK4	-5.2	1.2E-04	6.2	7.8E-04	-0.4	7.5E-01	-0.6	4.2E-01
ENSMUST00000025686	ankyrin repeat domain 22 [Source:MGI Symbol;Acc:MGI:1277101]		Q9D3J5	-7.3	4.7E-06	-1.1	2.1E-01	1.2	4.9E-02	-0.2	7.8E-01
ENSMUST00000025691	Fas (TNF receptor superfamily member 6) [Source:MGI Symbol;Acc:MGI:95484]		P25446	-5.0	3.3E-05	-9.3	4.0E-03	0.0	9.5E-01	0.5	8.5E-01
ENSMUST00000025696	adenylate kinase 3 [Source:MGI Symbol;Acc:MGI:1860835]		Q9WTP7	-1.6	6.5E-03	-3.5	2.3E-04	-1.5	2.4E-03	-0.4	5.0E-01
ENSMUST00000025702	sorting nexin 15 [Source:MGI Symbol;Acc:MGI:1916274]		Q91WE1	-1.6	2.3E-02	6.7	4.4E-04	0.7	5.8E-01	0.4	5.8E-01
ENSMUST00000025617	riboflavin kinase [Source:MGI Symbol;Acc:MGI:1914688]		Q8CFV9	-0.2	7.6E-01	-0.3	8.0E-01	0.6	4.1E-01	0.6	5.1E-01
ENSMUST00000025704	cell division cycle associated 5 [Source:MGI Symbol;Acc:MGI:1915099]		Q9CPY3	2.4	2.5E-02	7.7	3.5E-05	-1.1	3.5E-01	-0.6	2.6E-01
ENSMUST00000025705	Janus kinase 2 [Source:MGI Symbol;Acc:MGI:96629]	G5E852		-7.3	3.6E-04	-1.0	2.7E-02	0.4	1.9E-01	-0.2	5.5E-01
ENSMUST00000025706	tumor necrosis factor receptor superfamily, member 25 [Source:MGI Symbol;Acc:MGI:1934667]	B1AWN9		6.4	1.1E-04	-5.8	6.0E-06	-2.9	1.3E-05	-1.0	1.4E-01
ENSMUST00000025639	coiled-coil domain containing 86 [Source:MGI Symbol;Acc:MGI:1277220]		Q9JJ89	-1.8	1.4E-01	-2.3	1.6E-01	-0.3	7.6E-01	0.3	8.6E-01
ENSMUST00000025707	zinc finger like protein 1 [Source:MGI Symbol;Acc:MGI:1891017]		Q9DB43	-3.7	4.2E-03	7.8	1.1E-04	-0.7	6.1E-01	-1.3	7.2E-02
ENSMUST00000025711	vacuolar protein sorting 51 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915755]		Q3UVL4	-7.3	9.4E-05	-6.9	2.9E-04	0.0	9.3E-01	0.3	8.0E-01
ENSMUST00000025718	ankyrin repeat domain 1 (cardiac muscle) [Source:MGI Symbol;Acc:MGI:1097717]		Q9CR42	5.9	1.3E-04	-0.7	3.8E-01	-5.5	2.1E-04	-1.5	1.2E-01
ENSMUST00000025719	melan-A [Source:MGI Symbol;Acc:MGI:108454]	Q2TA50		5.5	7.1E-03	-6.7	4.2E-05	0.4	2.7E-01	0.4	6.7E-01
ENSMUST00000025723	synovial apoptosis inhibitor 1, synoviolin [Source:MGI Symbol;Acc:MGI:1921376]	E9QQ99		-6.8	6.5E-04	7.1	2.2E-04	-0.6	6.4E-01	-0.5	5.0E-01
ENSMUST00000025727	tumor protein D52-like 3 [Source:MGI Symbol;Acc:MGI:1913995]	Q9CQ14		6.8	6.0E-05	-2.2	2.3E-03	0.7	5.7E-02	-0.2	7.1E-01
ENSMUST00000025728	FERM domain containing 8 [Source:MGI Symbol;Acc:MGI:1914707]		Q3UFK8	-3.1	4.3E-04	2.8	1.9E-01	5.2	7.4E-03	4.8	1.1E-02
ENSMUST00000025729	ankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 [Source:MGI Symbol;Acc:MGI:1921743		Q3UES3	-4.0	2.6E-05	5.1	1.3E-03	-1.1	3.8E-01	-0.2	7.9E-01
ENSMUST00000025732	solute carrier family 25, member 45 [Source:MGI Symbol;Acc:MGI:2147731]		Q8CFJ7	-4.5	4.2E-04	-4.2	4.4E-03	2.1	2.8E-03	0.7	5.3E-01
ENSMUST00000025739	ubiquitin-like, containing PHD and RING finger domains 2 [Source:MGI Symbol;Acc:MGI:1923718]		Q7TMI3	-4.3	1.1E-03	-1.1	5.2E-02	1.3	4.1E-03	-5.2	1.0E-04
ENSMUST00000025740	RAD9 homolog A [Source:MGI Symbol;Acc:MGI:1328356]		Q9Z0F6	-2.8	7.4E-03	-8.2	2.3E-04	1.0	3.4E-02	0.3	8.6E-01
ENSMUST00000025745	mitochondrial ribosomal protein L21 [Source:MGI Symbol;Acc:MGI:2660674]		Q9D1N9	4.8	2.2E-03	-1.5	2.0E-02	0.2	4.8E-01	0.5	4.0E-01
ENSMUST00000025675	pha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1918		Q8VE10	-0.5	2.8E-01	0.3	6.3E-01	0.6	1.4E-01	-0.1	8.1E-01
ENSMUST00000025746	D4, zinc and double PHD fingers family 2 [Source:MGI Symbol;Acc:MGI:109529]	F8WIP7		-4.1	2.6E-02	-2.5	7.8E-03	0.9	5.7E-02	-0.3	6.8E-01
ENSMUST00000025755	doublesex and mab-3 related transcription factor 1 [Source:MGI Symbol;Acc:MGI:1354733]		Q9QZ59	6.8	1.3E-02	2.4	3.9E-03	0.8	1.3E-01	-0.2	7.2E-01
ENSMUST00000025760	choline kinase alpha [Source:MGI Symbol;Acc:MGI:107760]		O54804	-5.3	3.1E-04	-3.7	5.7E-03	1.3	3.5E-02	-0.2	8.9E-01
ENSMUST00000025685	lipase, family member M [Source:MGI Symbol;Acc:MGI:1926003]		Q8K2A6	0.9	1.7E-01	3.6	1.1E-03	1.3	7.5E-02	-1.4	5.7E-02
ENSMUST00000025761	calcium binding protein 4 [Source:MGI Symbol;Acc:MGI:1920910]		Q8VHC5	5.1	3.8E-04	-7.2	1.5E-04	0.1	8.1E-01	-0.1	9.5E-01
ENSMUST00000025762	barrier to autointegration factor 1 [Source:MGI Symbol;Acc:MGI:1346330]		O54962	-5.7	3.7E-04	-6.0	7.8E-05	-0.6	1.7E-01	0.4	6.8E-01
ENSMUST00000025695	protein phosphatase 2, regulatory subunit B', beta [Source:MGI Symbol;Acc:MGI:2388480]	Q6PD28		-0.8	1.7E-01	0.5	5.3E-01	1.0	8.2E-02	-0.3	7.2E-01
ENSMUST00000025764	cystatin E/M [Source:MGI Symbol;Acc:MGI:1920970]	Q9D1B1		9.8	7.9E-05	-1.1	1.0E-01	0.3	4.4E-01	-0.3	6.4E-01
ENSMUST00000025767	aryl-hydrocarbon receptor-interacting protein [Source:MGI Symbol;Acc:MGI:109622]		O08915	-7.0	3.7E-04	0.1	8.6E-01	1.1	7.7E-02	-0.6	4.0E-01
ENSMUST00000025773	polymerase (DNA-directed), delta 4 [Source:MGI Symbol;Acc:MGI:1916995]	Q547B4	Q9CWP8	-3.4	3.2E-04	0.0	9.7E-01	-0.3	7.3E-01	2.1	9.1E-02
ENSMUST00000025774	splicing factor 3b, subunit 2 [Source:MGI Symbol;Acc:MGI:2441856]	Q3UJB0		-5.3	2.6E-06	3.5	1.1E-01	8.2	7.4E-04	-2.6	1.3E-01
ENSMUST00000025778	glycine decarboxylase [Source:MGI Symbol;Acc:MGI:1341155]		Q91W43	8.1	1.0E-05	7.0	1.0E-04	-0.5	6.5E-01	-1.1	9.5E-02
ENSMUST00000025779	CDK2-associated protein 2 [Source:MGI Symbol;Acc:MGI:1098779]		Q9CPY4	-7.6	2.5E-06	-4.8	1.2E-02	0.4	5.5E-01	1.5	3.8E-01
ENSMUST00000025786	phosphofurin acidic cluster sorting protein 1 [Source:MGI Symbol;Acc:MGI:1277113]		Q8K212	-3.6	2.1E-04	-5.5	3.6E-03	1.2	4.4E-02	-0.6	7.0E-01
ENSMUST00000025714	ribonuclease P/MRP 30 subunit [Source:MGI Symbol;Acc:MGI:1859683]		O88796	-1.1	1.1E-01	-2.5	9.7E-03	-1.3	3.0E-02	0.0	9.6E-01
ENSMUST00000025791	adrenergic receptor kinase, beta 1 [Source:MGI Symbol;Acc:MGI:87940]	Q7TS64		-9.4	2.6E-04	0.7	3.0E-01	-6.2	5.0E-05	-1.0	1.1E-01
ENSMUST00000025797	mannose-binding lectin (protein C) 2 [Source:MGI Symbol;Acc:MGI:96924]	Q3UEK1	P41317	4.9	3.7E-03	4.6	2.5E-02	-1.5	4.3E-01	-0.5	6.2E-01
ENSMUST00000025800	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta [Source:MGI Symbol;Acc:MGI:107930]		P70181	-4.8	1.7E-03	-5.6	8.8E-03	0.4	5.0E-01	-0.7	7.1E-01
ENSMUST00000025724	interleukin 33 [Source:MGI Symbol;Acc:MGI:1924375]		Q8BVZ5	3.2	6.7E-02	-1.2	2.6E-01	-6.7	7.1E-04	-2.3	6.4E-02
ENSMUST00000025802	nudix (nucleoside diphosphate linked moiety X)-type motif 8 [Source:MGI Symbol;Acc:MGI:1913637]		Q9CR24	-4.6	7.8E-03	6.7	1.4E-04	-0.5	6.5E-01	-0.4	5.3E-01
ENSMUST00000025803	dickkopf homolog 1 (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1329040]		O54908	7.5	9.0E-06	-1.4	7.1E-02	1.3	2.1E-02	-0.4	5.8E-01
ENSMUST00000025804	RAB1B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1923558]	Q0PD66	Q9D1G1	-5.6	1.0E-04	-3.6	6.0E-04	0.9	2.5E-02	0.5	5.0E-01
ENSMUST00000025811	Yip1 interacting factor homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915340]		Q91XB7	-1.8	1.1E-02	-5.8	3.6E-03	0.7	2.0E-01	2.0	2.1E-01
ENSMUST00000025815	COBW domain containing 1 [Source:MGI Symbol;Acc:MGI:2385089]		Q8VEH6	-2.0	1.5E-02	-4.2	1.7E-02	0.7	2.8E-01	0.6	6.8E-01
ENSMUST00000025818	Ras and Rab interactor 1 [Source:MGI Symbol;Acc:MGI:2385695]		Q921Q7	4.4	2.1E-05	-0.9	4.1E-01	1.2	1.0E-01	-0.6	5.5E-01
ENSMUST00000025743	mitochondrial ribosomal protein L21 [Source:MGI Symbol;Acc:MGI:2660674]		Q9D1N9	-1.5	4.7E-02	-4.6	2.1E-03	-0.9	1.2E-01	2.2	6.6E-02
ENSMUST00000025826	solute carrier family 29 (nucleoside transporters), member 2 [Source:MGI Symbol;Acc:MGI:1345278]		Q61672	4.9	1.0E-04	3.7	2.4E-02	-0.5	7.1E-01	0.6	5.2E-01
ENSMUST00000025830	amyloid beta (A4) precursor protein binding, family A, member 1 [Source:MGI Symbol;Acc:MGI:1860297]		B2RUJ5	3.3	3.0E-04	-3.0	1.5E-01	0.7	5.3E-01	-0.4	8.4E-01
ENSMUST00000025749	ribosomal protein S6 kinase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1927343]		Q9Z1M4	-0.8	6.0E-01	-2.0	4.7E-01	0.5	7.5E-01	1.7	4.7E-01
ENSMUST00000025751	immunoglobulin mu binding protein 2 [Source:MGI Symbol;Acc:MGI:99954]	A0A0B4J1E3		0.0	9.8E-01	2.1	1.9E-01	-0.2	8.7E-01	-2.4	1.2E-01
ENSMUST00000025752	polymerase (DNA directed), alpha 2 [Source:MGI Symbol;Acc:MGI:99690]		P33611	-0.7	1.0E-01	-0.3	5.5E-01	0.3	3.9E-01	-0.1	8.6E-01
ENSMUST00000025831	dedicator of cytokinesis 8 [Source:MGI Symbol;Acc:MGI:1921396]		Q8C147	-3.3	4.6E-05	6.3	2.7E-02	-0.8	7.6E-01	-0.3	8.3E-01
ENSMUST00000025759	eukaryotic translation initiation factor 1A domain containing [Source:MGI Symbol;Acc:MGI:1917110]		Q3THJ3	0.6	3.3E-01	-0.1	9.0E-01	0.5	4.3E-01	1.3	1.6E-01
ENSMUST00000025833	3'-phosphoadenosine 5'-phosphosulfate synthase 2 [Source:MGI Symbol;Acc:MGI:1330223]		O88428	4.3	6.0E-04	-3.3	2.3E-02	1.3	5.8E-02	-0.8	5.7E-01
ENSMUST00000025834	pellino 3 [Source:MGI Symbol;Acc:MGI:1924963]			3.9	9.7E-03	5.4	9.2E-04	-0.1	9.0E-01	-0.5	5.2E-01
ENSMUST00000025835	carnitine palmitoyltransferase 1a, liver [Source:MGI Symbol;Acc:MGI:1098296]	Q7TQD5	P97742	-3.5	5.9E-04	-2.5	1.3E-02	0.0	9.7E-01	-3.2	1.9E-02
ENSMUST00000025841	MUS81 endonuclease homolog (yeast) [Source:MGI Symbol;Acc:MGI:1918961]	F8WIN9		-5.3	5.8E-05	5.7	4.4E-04	-3.5	3.5E-02	0.5	4.7E-01
ENSMUST00000025842	galanin [Source:MGI Symbol;Acc:MGI:95637]	Q3V002	P47212	4.5	9.1E-04	-3.6	1.1E-02	0.8	2.5E-01	-2.7	8.8E-02
ENSMUST00000025847	fibroblast growth factor (acidic) intracellular binding protein [Source:MGI Symbol;Acc:MGI:1926233]	Q8K2D8		-3.8	7.9E-05	-2.7	6.0E-03	0.7	1.2E-01	0.0	9.5E-01
ENSMUST00000025850	fos-like antigen 1 [Source:MGI Symbol;Acc:MGI:107179]	Q3UMK5	P48755	4.2	9.3E-04	-3.7	1.7E-04	0.9	1.8E-02	-0.7	3.0E-01
ENSMUST00000025851	dipeptidylpeptidase 3 [Source:MGI Symbol;Acc:MGI:1922471]		Q99KK7	-3.0	1.3E-03	4.8	8.0E-05	-3.2	5.7E-03	0.2	7.6E-01
ENSMUST00000025853	Dr1 associated protein 1 (negative cofactor 2 alpha) [Source:MGI Symbol;Acc:MGI:1913806]	Q4FJW2	Q9D6N5	-5.8	1.1E-04	-6.1	2.1E-05	-0.1	6.3E-01	-1.6	9.9E-02
ENSMUST00000025856	low density lipoprotein receptor-related protein 5 [Source:MGI Symbol;Acc:MGI:1278315]		Q91VN0	-4.2	6.1E-03	-2.9	6.7E-03	1.3	1.8E-02	0.6	4.8E-01
ENSMUST00000025864	ribonuclease H2, subunit C [Source:MGI Symbol;Acc:MGI:1915459]		Q9CQ18	-5.8	9.2E-05	-5.4	4.8E-03	1.5	4.7E-02	-2.4	2.2E-01
ENSMUST00000025867	v-rel reticuloendotheliosis viral oncogene homolog A (avian) [Source:MGI Symbol;Acc:MGI:103290]	Q548Y4	Q04207	-4.2	9.3E-05	3.9	8.4E-03	-2.0	1.6E-01	-1.0	2.8E-01
ENSMUST00000025798	kinesin light chain 2 [Source:MGI Symbol;Acc:MGI:107953]	D3YXZ3		2.6	2.4E-01	0.5	8.6E-01	-0.9	6.7E-01	1.1	6.6E-01
ENSMUST00000025875	nily 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 [Source:MGI Symbol;A		P51906	5.4	1.6E-04	-6.6	1.8E-02	0.6	4.2E-01	2.4	3.1E-01
ENSMUST00000025885	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human) [Source:MGI Symbol;Acc:MGI:1913482]	Q545N1	P56873	-3.7	4.1E-03	-4.2	2.1E-02	0.3	6.9E-01	-0.1	9.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000025890	SCY1-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1931787]		Q9EQC5	-2.4	1.5E-03	7.3	1.5E-04	0.2	8.4E-01	0.5	4.1E-01
ENSMUST00000025891	calpain 1 [Source:MGI Symbol;Acc:MGI:88263]	Q3TI07	O35350	-5.3	4.7E-05	-3.8	3.9E-03	0.9	1.0E-01	-0.9	4.2E-01
ENSMUST00000025893	ADP-ribosylation factor-like 2 [Source:MGI Symbol;Acc:MGI:1928393]		Q9D0J4	-3.2	2.4E-02	-0.8	2.6E-01	0.3	5.2E-01	-0.7	3.6E-01
ENSMUST00000025897	mitogen-activated protein kinase kinase kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346883]		Q61161	-8.4	2.0E-03	-1.0	2.4E-01	-0.2	7.5E-01	-1.2	1.5E-01
ENSMUST00000025903	ribosomal protein S6 kinase, polypeptide 4 [Source:MGI Symbol;Acc:MGI:1930076]		Q9Z2B9	-2.2	7.8E-03	3.9	8.7E-05	-1.1	7.9E-02	-0.7	1.5E-01
ENSMUST00000025823	RCE1 homolog, prenyl protein peptidase (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1336895]		P57791	-1.4	5.7E-02	-0.6	4.7E-01	0.9	1.5E-01	0.1	8.6E-01
ENSMUST00000025904	peroxiredoxin 5 [Source:MGI Symbol;Acc:MGI:1859821]		P99029	-9.1	3.1E-04	3.4	2.6E-03	-1.2	1.5E-01	0.3	6.9E-01
ENSMUST00000025827	multiple inositol polyphosphate histidine phosphatase 1 [Source:MGI Symbol;Acc:MGI:1336159]		Q9Z2L6	-0.2	5.3E-01	-0.1	9.1E-01	0.2	5.1E-01	0.0	9.2E-01
ENSMUST00000025906	estrogen related receptor, alpha [Source:MGI Symbol;Acc:MGI:1346831]		O08580	-4.7	6.6E-05	3.3	1.3E-03	0.0	9.7E-01	0.0	9.9E-01
ENSMUST00000025908	potassium channel, subfamily K, member 4 [Source:MGI Symbol;Acc:MGI:1298234]	Q0VD85	O88454	7.3	3.5E-05	-2.1	5.5E-03	1.1	1.0E-02	0.0	9.5E-01
ENSMUST00000025910	BCL2-associated agonist of cell death [Source:MGI Symbol;Acc:MGI:1096330]		Q61337	-1.9	7.3E-03	4.8	2.5E-03	1.3	2.4E-01	0.8	3.1E-01
ENSMUST00000025912	phospholipase C, beta 3 [Source:MGI Symbol;Acc:MGI:104778]		P51432	-1.4	1.5E-02	6.4	1.0E-03	0.1	9.6E-01	-2.4	2.0E-02
ENSMUST00000025918	stress-induced phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:109130]		Q60864	-2.7	5.3E-04	-2.3	2.5E-02	0.9	1.1E-01	-0.4	6.9E-01
ENSMUST00000025836	mitochondrial ribosomal protein L11 [Source:MGI Symbol;Acc:MGI:2137215]		Q9CQF0	0.9	8.4E-02	-0.3	5.4E-01	-1.2	1.9E-02	0.0	9.5E-01
ENSMUST00000025840	metallothionein-like 5, testis-specific (tesmin) [Source:MGI Symbol;Acc:MGI:1340029]		Q9WTJ6	0.5	6.6E-01	0.7	6.5E-01	1.3	2.9E-01	1.0	4.9E-01
ENSMUST00000025921	MAP/microtubule affinity regulating kinase 2 [Source:MGI Symbol;Acc:MGI:99638]	Q3T9A3		-2.8	4.6E-03	-3.8	2.7E-03	0.8	9.6E-02	-0.7	5.3E-01
ENSMUST00000025925	phospholipase A2, group XVI [Source:MGI Symbol;Acc:MGI:2179715]		Q8R3U1	3.6	6.8E-03	4.2	3.8E-03	-0.7	5.3E-01	-0.4	5.8E-01
ENSMUST00000025844	cathepsin W [Source:MGI Symbol;Acc:MGI:1338045]	Q8C2M0	P56203	0.7	2.2E-01	0.3	6.8E-01	-0.5	4.0E-01	0.0	9.9E-01
ENSMUST00000025846	protein phosphatase 6, regulatory subunit 3 [Source:MGI Symbol;Acc:MGI:1921807]		Q922D4	-2.2	1.9E-01	0.2	9.1E-01	0.5	7.7E-01	-2.0	3.0E-01
ENSMUST00000025930	structural maintenance of chromosomes 3 [Source:MGI Symbol;Acc:MGI:1339795]	Q1HL32	Q9CW03	-2.8	6.6E-04	-3.1	1.6E-03	0.2	5.2E-01	-0.5	5.1E-01
ENSMUST00000025931	programmed cell death 4 [Source:MGI Symbol;Acc:MGI:107490]		Q61823	-7.8	4.5E-04	1.3	1.5E-01	-3.6	1.7E-03	-0.7	3.5E-01
ENSMUST00000025932	soc-2 (suppressor of clear) homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1927197]		O88520	-7.8	8.4E-04	-0.9	2.5E-01	1.2	3.9E-02	-0.9	3.0E-01
ENSMUST00000025940	C1q and tumor necrosis factor related protein 9 [Source:MGI Symbol;Acc:MGI:3045252]		Q4ZJN1	2.8	4.7E-03	-5.8	1.1E-03	0.7	1.3E-01	0.7	6.1E-01
ENSMUST00000025944	hematopoietically expressed homeobox [Source:MGI Symbol;Acc:MGI:96086]		P43120	-2.8	4.0E-03	-4.7	1.2E-02	-1.1	1.3E-01	-0.5	7.5E-01
ENSMUST00000025861	OVO homolog-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1330290]		Q9WTJ2	1.0	5.8E-02	1.2	6.1E-02	0.0	1.0E+00	-0.2	6.8E-01
ENSMUST00000025862	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	F2Z4A9		4.2	1.1E-01	0.6	8.1E-01	-3.8	1.2E-01	-0.2	9.3E-01
ENSMUST00000025946	cytochrome P450, family 26, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1096359]			4.4	8.7E-04	-4.5	6.3E-04	-0.1	7.7E-01	-1.5	1.8E-01
ENSMUST00000025951	retinol binding protein 4, plasma [Source:MGI Symbol;Acc:MGI:97879]	H7BWY6		6.6	1.8E-04	-2.5	8.2E-03	1.0	3.5E-02	-0.7	4.2E-01
ENSMUST00000025955	eukaryotic translation initiation factor 3, subunit A [Source:MGI Symbol;Acc:MGI:95301]		P23116	-3.9	2.5E-05	6.9	1.0E-04	0.5	6.5E-01	-1.0	1.1E-01
ENSMUST00000025957	family with sequence similarity 45, member A [Source:MGI Symbol;Acc:MGI:1915144]		Q9D8N2	-7.5	6.8E-06	-3.5	1.6E-02	-0.6	3.4E-01	-0.8	5.6E-01
ENSMUST00000025961	peroxiredoxin 3 [Source:MGI Symbol;Acc:MGI:88034]		P20108	-4.4	8.6E-06	-1.4	7.6E-02	0.8	7.7E-02	-0.2	7.4E-01
ENSMUST00000025963	nucleolar complex associated 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1932610]		Q8VI84	4.1	5.2E-05	-3.7	3.1E-03	1.4	1.4E-02	-0.2	8.8E-01
ENSMUST00000025986	tolloid-like 2 [Source:MGI Symbol;Acc:MGI:1346044]		Q9WVM6	8.6	8.5E-05	-1.2	3.0E-01	0.2	7.9E-01	-1.7	2.1E-01
ENSMUST00000025989	transmembrane 9 superfamily member 3 [Source:MGI Symbol;Acc:MGI:1914262]		Q9ET30	-4.6	3.1E-05	-6.7	3.0E-02	1.4	1.3E-01	-0.2	9.4E-01
ENSMUST00000025992	potassium channel tetramerisation domain containing 1 [Source:MGI Symbol;Acc:MGI:1918269]		Q5M956	5.1	6.4E-03	-1.3	1.7E-01	1.2	5.3E-02	0.3	7.4E-01
ENSMUST00000025993	slit homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1315203]		Q80TR4	7.2	1.2E-02	-5.8	1.5E-03	0.4	4.7E-01	-2.8	1.5E-01
ENSMUST00000025997	survival motor neuron domain containing 1 [Source:MGI Symbol;Acc:MGI:1923729]		Q8BGT7	-4.6	5.7E-05	-2.5	1.4E-02	1.2	2.9E-02	-1.0	2.6E-01
ENSMUST00000025998	MAX interactor 1, dimerization protein [Source:MGI Symbol;Acc:MGI:97245]	Q3USD3	P50540	-7.5	5.6E-05	7.2	1.1E-04	-0.1	9.0E-01	0.0	9.7E-01
ENSMUST00000025909	G protein-coupled receptor 137 [Source:MGI Symbol;Acc:MGI:2147529]		Q80ZU9	-1.9	1.3E-01	1.1	4.2E-01	0.2	8.7E-01	-2.8	5.8E-02
ENSMUST00000025999	adducin 3 (gamma) [Source:MGI Symbol;Acc:MGI:1351615]		Q9QYB5	-9.7	6.6E-06	-0.6	3.7E-01	0.5	3.0E-01	-0.7	2.9E-01
ENSMUST00000026008	tripartite motif-containing 8 [Source:MGI Symbol;Acc:MGI:1933302]		Q99PJ2	-2.3	8.2E-04	-0.3	6.2E-01	1.1	3.4E-02	0.0	9.9E-01
ENSMUST00000025914	vascular endothelial growth factor B [Source:MGI Symbol;Acc:MGI:106199]		P49766	0.7	5.1E-01	0.9	4.8E-01	-0.8	4.6E-01	-0.9	4.0E-01
ENSMUST00000025915	DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:MGI Symbol;Acc:MGI:1927346]	Q6GTN1		-1.0	1.9E-01	0.0	9.6E-01	-0.1	8.9E-01	-1.2	2.1E-01
ENSMUST00000026009	ADP-ribosylation factor-like 3 [Source:MGI Symbol;Acc:MGI:1929699]	Q543P7	Q9WUL7	-3.2	1.1E-04	-2.4	4.7E-03	-0.2	5.5E-01	-0.6	3.9E-01
ENSMUST00000026011	sideroflexin 2 [Source:MGI Symbol;Acc:MGI:2137678]	Q3UC14	Q925N2	3.0	1.2E-03	-0.5	6.3E-01	1.6	3.2E-02	-0.7	4.5E-01
ENSMUST00000025924	expressed sequence AI846148 [Source:MGI Symbol;Acc:MGI:2147611]		Q05AH6	0.3	6.2E-01	1.5	8.2E-02	0.6	3.5E-01	-0.6	3.9E-01
ENSMUST00000026012	cytochrome P450, family 17, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88586]	Q53YJ1	P27786	6.7	8.3E-05	1.2	2.6E-01	-2.9	1.8E-02	-0.4	6.4E-01
ENSMUST00000026013	monoamine oxidase A [Source:MGI Symbol;Acc:MGI:96915]		Q64133	6.6	2.9E-07	-2.4	6.1E-03	0.0	9.9E-01	-0.3	6.5E-01
ENSMUST00000026016	FUN14 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919268]		Q9DB70	-6.7	1.5E-04	-3.0	3.6E-02	1.0	1.7E-01	-3.9	4.0E-02
ENSMUST00000026021	macrophage scavenger receptor 1 [Source:MGI Symbol;Acc:MGI:98257]		P30204	-3.7	5.1E-03	-5.6	2.4E-03	-0.8	2.2E-01	-3.0	1.3E-01
ENSMUST00000026027	5 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:2442	F8VPY2		-1.9	6.8E-03	2.9	7.7E-03	-0.3	7.4E-01	-0.4	5.4E-01
ENSMUST00000026036	nuclear receptor subfamily 0, group B, member 1 [Source:MGI Symbol;Acc:MGI:1352460]	Q53ZY9	Q61066	6.6	1.5E-04	-0.8	3.8E-01	0.8	2.0E-01	-1.2	2.1E-01
ENSMUST00000026039	glycerol kinase [Source:MGI Symbol;Acc:MGI:106594]		Q64516	-6.0	8.0E-04	3.1	7.8E-03	-1.5	1.2E-01	-0.2	7.8E-01
ENSMUST00000026043	STE20-like kinase [Source:MGI Symbol;Acc:MGI:103241]	A2RRK3	O54988	-3.8	8.5E-05	6.8	2.5E-04	-0.6	6.5E-01	-0.8	2.5E-01
ENSMUST00000026045	collagen, type XVII, alpha 1 [Source:MGI Symbol;Acc:MGI:88450]		Q07563	8.1	3.3E-02	-3.7	2.5E-04	-0.1	7.8E-01	-0.3	6.0E-01
ENSMUST00000026050	glutathione S-transferase omega 1 [Source:MGI Symbol;Acc:MGI:1342273]		O09131	-3.0	1.9E-04	-5.1	7.4E-04	1.3	1.4E-02	-1.2	3.1E-01
ENSMUST00000026062	caspase 7 [Source:MGI Symbol;Acc:MGI:109383]	Q4FJQ4	P97864	-3.0	7.6E-05	-4.9	3.1E-05	-0.5	1.1E-01	-0.1	9.2E-01
ENSMUST00000026068	von Willebrand factor A domain containing 2 [Source:MGI Symbol;Acc:MGI:2684334]		Q70UZ7	9.4	5.1E-06	3.1	7.8E-04	-1.1	8.3E-02	-0.1	8.6E-01
ENSMUST00000025965	helicase, lymphoid specific [Source:MGI Symbol;Acc:MGI:106209]		Q60848	1.2	3.9E-02	2.2	6.0E-03	0.5	3.4E-01	-0.5	3.2E-01
ENSMUST00000025979	aldehyde dehydrogenase 18 family, member A1 [Source:MGI Symbol;Acc:MGI:1888908]		Q9Z110	2.5	1.6E-01	3.8	3.7E-02	-1.5	3.7E-01	-2.8	7.8E-02
ENSMUST00000025981	tectonic family member 3 [Source:MGI Symbol;Acc:MGI:1914840]		Q8R2Q6	0.0	9.5E-01	1.3	2.4E-01	0.2	8.3E-01	-1.0	2.9E-01
ENSMUST00000025983	cyclin J [Source:MGI Symbol;Acc:MGI:2443297]		Q3TZI6	-2.9	5.5E-02	-2.8	1.6E-01	0.7	5.2E-01	0.6	7.6E-01
ENSMUST00000026072	TruB pseudouridine (psi) synthase homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1919383]		Q8C0D0	5.2	9.5E-04	7.0	8.2E-04	-0.6	7.1E-01	1.0	2.1E-01
ENSMUST00000026073	TruB pseudouridine (psi) synthase homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1919383]		Q8C0D0	5.1	1.8E-05	-3.4	1.9E-03	1.2	1.7E-02	-0.1	8.9E-01
ENSMUST00000026076	glial cell line derived neurotrophic factor family receptor alpha 1 [Source:MGI Symbol;Acc:MGI:1100842]		P97785	7.7	2.2E-03	5.4	1.5E-02	-0.7	6.9E-01	-1.0	4.0E-01
ENSMUST00000026078	cDNA sequence BC051665 [Source:MGI Symbol;Acc:MGI:2682300]	E9Q623		5.8	5.2E-04	7.6	1.3E-02	-0.8	7.7E-01	-1.2	4.2E-01
ENSMUST00000026081	pancreatic lipase-related protein 2 [Source:MGI Symbol;Acc:MGI:1336202]	Q4VBW7		6.3	9.4E-05	-3.0	6.0E-03	1.3	2.3E-02	-0.4	6.8E-01
ENSMUST00000026093	BTB (POZ) domain containing 1 [Source:MGI Symbol;Acc:MGI:1933765]		P58544	-4.1	7.1E-05	-6.1	3.8E-04	0.3	4.5E-01	-1.1	4.1E-01
ENSMUST00000026094	hepatoma-derived growth factor, related protein 3 [Source:MGI Symbol;Acc:MGI:1352760]		Q9JMG7	5.9	1.7E-05	-8.2	1.6E-04	0.6	1.4E-01	-0.8	5.8E-01
ENSMUST00000026096	basonuclin 1 [Source:MGI Symbol;Acc:MGI:1097164]	F8VPY0		8.6	6.4E-06	-1.2	7.5E-02	1.0	2.6E-02	-0.2	7.8E-01
ENSMUST00000026120	basic helix-loop-helix family, member e22 [Source:MGI Symbol;Acc:MGI:1930001]			6.3	1.0E-04	-3.3	3.6E-04	-0.5	1.4E-01	-0.4	4.9E-01
ENSMUST00000026121	protein phosphatase 1, regulatory subunit 27 [Source:MGI Symbol;Acc:MGI:1915951]		Q9D119	5.6	2.4E-04	3.4	4.1E-03	0.7	3.7E-01	0.3	6.0E-01
ENSMUST00000026122	prolyl 4-hydroxylase, beta polypeptide [Source:MGI Symbol;Acc:MGI:97464]		P09103	-4.5	1.1E-05	7.2	1.4E-04	-0.1	9.3E-01	-0.5	4.1E-01
ENSMUST00000026128	anaphase promoting complex subunit 11 [Source:MGI Symbol;Acc:MGI:1913406]		Q9CPX9	2.4	1.6E-03	5.8	8.1E-07	-1.2	4.3E-02	-0.4	1.8E-01
ENSMUST00000026129	phosphate cytidylyltransferase 2, ethanolamine [Source:MGI Symbol;Acc:MGI:1915921]	Q3USD5	Q922E4	-2.2	6.1E-03	-5.9	8.8E-04	0.5	3.5E-01	-0.3	8.2E-01
ENSMUST00000026133	pyrroline-5-carboxylate reductase 1 [Source:MGI Symbol;Acc:MGI:2384795]	Q3UTR5	Q922W5	5.8	2.4E-05	-7.6	6.5E-04	-3.6	3.2E-04	0.4	8.1E-01
ENSMUST00000026134	myeloid-associated differentiation marker-like 2 [Source:MGI Symbol;Acc:MGI:1915765]		Q08AU7	4.8	6.7E-04	-0.5	4.5E-01	1.2	4.3E-02	-0.2	7.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000026032	polycomb group ring finger 6 [Source:MGI Symbol;Acc:MGI:1918291]		Q99NA9	0.8	3.1E-01	1.0	3.0E-01	0.6	4.7E-01	0.3	6.9E-01
ENSMUST00000026139	leucine rich repeat containing 45 [Source:MGI Symbol;Acc:MGI:2387183]		Q8CIM1	-4.3	2.2E-02	6.6	2.6E-04	-0.5	6.6E-01	-0.6	3.7E-01
ENSMUST00000026142	melanoma antigen, family D, 1 [Source:MGI Symbol;Acc:MGI:1930187]		Q9QYH6	-3.9	5.3E-03	-6.9	1.0E-03	-0.6	3.6E-01	0.3	8.4E-01
ENSMUST00000026144	dicarbonyl L-xylulose reductase [Source:MGI Symbol;Acc:MGI:1915130]		Q91X52	-2.7	7.3E-03	-3.1	1.8E-03	0.3	4.0E-01	-0.4	6.4E-01
ENSMUST00000026150	Rho GTPase activating protein 19 [Source:MGI Symbol;Acc:MGI:1918335]		Q8BRH3	-4.7	1.3E-02	6.4	1.0E-01	-0.9	8.2E-01	0.9	6.9E-01
ENSMUST00000026154	zinc finger, DHHC domain containing 16 [Source:MGI Symbol;Acc:MGI:1921418]		Q9ESG8	-2.2	9.0E-04	4.4	1.1E-02	-1.4	3.5E-01	-0.8	3.9E-01
ENSMUST00000026156	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase [Source:MGI Symbol;Acc:MGI:894275]		O09009	-3.9	1.1E-02	-2.8	1.3E-03	-0.3	4.1E-01	-0.5	4.5E-01
ENSMUST00000026162	secreted and transmembrane 1A [Source:MGI Symbol;Acc:MGI:2384805]	A2ABP9		7.7	4.6E-05	-1.9	8.1E-03	0.9	1.8E-02	-0.2	6.9E-01
ENSMUST00000026170	ubiquitin domain containing 1 [Source:MGI Symbol;Acc:MGI:2385092]		Q91WB7	-3.8	3.5E-04	8.0	1.3E-05	-1.9	1.1E-01	-0.5	2.6E-01
ENSMUST00000026172	ankyrin repeat domain 2 (stretch responsive muscle) [Source:MGI Symbol;Acc:MGI:1861447]		Q9WV06	4.8	1.9E-03	3.9	9.9E-03	-1.6	2.0E-01	-0.2	8.5E-01
ENSMUST00000026173	WD repeat domain 45B [Source:MGI Symbol;Acc:MGI:1914090]		Q9CR39	-4.3	7.2E-06	5.6	2.2E-05	-0.2	7.8E-01	-0.7	1.6E-01
ENSMUST00000026175	fructosamine 3 kinase [Source:MGI Symbol;Acc:MGI:1926834]		Q9ER35	6.5	1.1E-04	5.5	2.4E-02	-0.6	7.8E-01	1.6	2.2E-01
ENSMUST00000026188	R3H domain and coiled-coil containing 1 like [Source:MGI Symbol;Acc:MGI:1196316]		Q8BJM3	-3.4	7.4E-04	6.3	5.6E-04	-0.5	6.8E-01	-1.0	1.8E-01
ENSMUST00000026190	lysyl oxidase-like 4 [Source:MGI Symbol;Acc:MGI:1914823]		Q924C6	6.3	2.5E-05	6.5	1.4E-04	-0.6	6.2E-01	-0.8	2.2E-01
ENSMUST00000026084	solute carrier family 18 (vesicular monoamine), member 2 [Source:MGI Symbol;Acc:MGI:106677]		Q8BRU6	1.1	1.3E-01	2.7	1.7E-02	1.6	5.5E-02	0.1	9.4E-01
ENSMUST00000026196	glutamic-oxaloacetic transaminase 1, soluble [Source:MGI Symbol;Acc:MGI:95791]		P05201	-3.1	2.6E-04	-4.3	5.5E-04	0.7	1.1E-01	0.8	3.4E-01
ENSMUST00000026199	cutC copper transporter homolog (E.coli) [Source:MGI Symbol;Acc:MGI:1913638]	F8WHX2		-3.6	1.8E-02	5.0	4.3E-04	-0.2	8.1E-01	0.7	2.4E-01
ENSMUST00000026208	ATP-binding cassette, sub-family C (CFTR/MRP), member 2 [Source:MGI Symbol;Acc:MGI:1352447]		Q8VI47	6.7	1.8E-05	4.1	1.4E-04	-4.7	4.7E-04	-0.3	5.3E-01
ENSMUST00000026210	carboxypeptidase N, polypeptide 1 [Source:MGI Symbol;Acc:MGI:2135874]		Q9JJN5	5.6	2.6E-04	6.7	2.1E-04	0.1	9.1E-01	-0.3	6.4E-01
ENSMUST00000026211	cytochrome P450, family 2, subfamily c, polypeptide 44 [Source:MGI Symbol;Acc:MGI:1888897]	E9Q5K4		6.5	1.8E-04	5.1	5.7E-04	-1.5	2.0E-01	-1.0	1.4E-01
ENSMUST00000026217	conserved helix-loop-helix ubiquitous kinase [Source:MGI Symbol;Acc:MGI:99484]	E9QNL4		-6.8	2.4E-05	-4.3	1.3E-04	0.4	2.5E-01	0.2	7.6E-01
ENSMUST00000026125	Aly/REF export factor [Source:MGI Symbol;Acc:MGI:1341044]		O08583	0.6	2.8E-01	0.9	2.1E-01	0.0	9.8E-01	-0.3	6.3E-01
ENSMUST00000026126	integrator complex subunit 4 [Source:MGI Symbol;Acc:MGI:1917164]		Q8CIM8	-0.8	1.1E-01	-1.1	9.6E-02	-0.4	3.5E-01	-0.1	8.8E-01
ENSMUST00000026220	stearoyl-coenzyme A desaturase 3 [Source:MGI Symbol;Acc:MGI:1353437]		Q99PL7	7.4	1.3E-05	2.8	3.0E-03	0.3	6.5E-01	-0.1	8.6E-01
ENSMUST00000026221	stearoyl-Coenzyme A desaturase 2 [Source:MGI Symbol;Acc:MGI:98240]		P13011	-1.7	1.1E-03	-0.9	2.6E-01	0.9	1.1E-01	-0.4	6.3E-01
ENSMUST00000026222	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 [Source:MGI Symbol;Acc:MGI:1914514]		Q9D6J5	-7.0	5.2E-05	7.2	4.1E-05	1.2	2.4E-01	-0.2	7.4E-01
ENSMUST00000026227	progressive external ophthalmoplegia 1 (human) [Source:MGI Symbol;Acc:MGI:2137410]		Q8CIW5	1.6	1.1E-02	5.7	2.5E-03	0.7	5.9E-01	-0.2	8.5E-01
ENSMUST00000026135	alveolar soft part sarcoma chromosome region, candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1916188]		Q8VBT9	-3.7	5.7E-02	0.8	7.5E-01	3.7	5.1E-02	-0.7	7.4E-01
ENSMUST00000026236	T cell leukemia, homeobox 1 [Source:MGI Symbol;Acc:MGI:98769]	Q9QX99		6.9	1.5E-04	-3.6	4.2E-02	0.2	8.5E-01	-0.5	8.0E-01
ENSMUST00000026239	polymerase (DNA directed), lambda [Source:MGI Symbol;Acc:MGI:1889000]		Q9QXE2	-1.5	3.3E-02	-2.2	3.8E-02	-1.4	3.5E-02	-3.2	2.2E-02
ENSMUST00000026240	fibroblast growth factor 8 [Source:MGI Symbol;Acc:MGI:99604]	Q80ZL6		6.0	2.5E-02	-4.0	3.0E-03	-1.0	9.4E-02	0.3	7.5E-01
ENSMUST00000026148	carbonyl reductase 2 [Source:MGI Symbol;Acc:MGI:107200]	Q542P5	P08074	1.1	4.3E-01	-5.1	1.1E-03	-8.0	2.1E-05	-1.8	1.9E-01
ENSMUST00000026241	fibroblast growth factor 8 [Source:MGI Symbol;Acc:MGI:99604]		P37237	6.9	1.0E-02	-6.1	7.8E-02	1.3	2.5E-01	2.6	4.2E-01
ENSMUST00000026243	meningioma expressed antigen 5 (hyaluronidase) [Source:MGI Symbol;Acc:MGI:1932139]		Q9EQQ9	-4.1	1.4E-04	-1.1	8.1E-02	0.9	2.7E-02	-0.1	8.7E-01
ENSMUST00000026252	LIM domain binding 1 [Source:MGI Symbol;Acc:MGI:894762]		P70662	-5.8	7.7E-04	-2.0	2.1E-01	1.4	1.5E-01	-0.6	7.2E-01
ENSMUST00000026159	CD7 antigen [Source:MGI Symbol;Acc:MGI:88344]	Q3U4A8	P50283	-0.4	6.5E-01	0.1	9.6E-01	-0.5	5.8E-01	-0.9	3.6E-01
ENSMUST00000026254	golgi-specific brefeldin A-resistance factor 1 [Source:MGI Symbol;Acc:MGI:1861607]	Q6DFZ1		-5.8	2.0E-04	7.0	2.0E-04	-0.6	6.1E-01	0.1	9.3E-01
ENSMUST00000026168	MMS19 (MET18 S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919449]		Q9D071	-0.3	9.1E-01	3.6	4.4E-01	3.8	2.6E-01	-0.1	9.8E-01
ENSMUST00000026169	2-oxoglutarate and iron-dependent oxygenase domain containing 3 [Source:MGI Symbol;Acc:MGI:1913429]		Q9D136	0.7	3.2E-01	0.7	4.2E-01	0.0	9.8E-01	0.0	9.7E-01
ENSMUST00000026256	F-box and leucine-rich repeat protein 15 [Source:MGI Symbol;Acc:MGI:1915681]		Q91W61	-4.0	5.5E-04	-2.6	1.5E-02	1.1	5.0E-02	-0.2	8.6E-01
ENSMUST00000026259	paired-like homeodomain transcription factor 3 [Source:MGI Symbol;Acc:MGI:1100498]		O35160	6.9	7.0E-05	5.8	1.0E-03	-0.4	7.8E-01	-1.4	1.0E-01
ENSMUST00000026262	hexosaminidase A [Source:MGI Symbol;Acc:MGI:96073]		P29416	-5.1	1.1E-04	-3.7	1.3E-04	0.2	4.5E-01	-0.4	5.0E-01
ENSMUST00000026266	ADP-dependent glucokinase [Source:MGI Symbol;Acc:MGI:1919391]			-7.3	1.9E-05	6.8	3.0E-04	0.2	8.8E-01	-0.1	8.4E-01
ENSMUST00000026267	poly (ADP-ribose) polymerase family, member 6 [Source:MGI Symbol;Acc:MGI:1914537]	G5E856		-2.8	1.3E-02	-2.6	1.0E-02	0.0	9.9E-01	-0.7	4.0E-01
ENSMUST00000026270	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1933169]		Q9EP69	-4.2	2.8E-05	2.1	2.3E-02	-4.0	6.5E-04	0.2	7.6E-01
ENSMUST00000026194	Hermansky-Pudlak syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:2177763]			-5.0	1.0E-01	-3.7	3.0E-01	0.2	9.1E-01	-1.1	7.7E-01
ENSMUST00000026289	hydroxysteroid (17-beta) dehydrogenase 10 [Source:MGI Symbol;Acc:MGI:1333871]	Q99N15		-6.7	8.5E-05	-2.3	7.7E-03	0.6	1.3E-01	-0.2	8.2E-01
ENSMUST00000026292	HECT, UBA and WWE domain containing 1 [Source:MGI Symbol;Acc:MGI:1926884]	A2AFQ0		-5.0	1.7E-02	-2.9	5.0E-02	0.7	4.1E-01	0.0	9.8E-01
ENSMUST00000026296	FYVE, RhoGEF and PH domain containing 1 [Source:MGI Symbol;Acc:MGI:104566]		P52734	5.8	8.4E-03	6.1	4.3E-05	-0.9	3.1E-01	-0.3	5.3E-01
ENSMUST00000026209	dynamin binding protein [Source:MGI Symbol;Acc:MGI:1917352]			0.0	9.8E-01	1.1	7.0E-02	0.9	5.2E-02	-0.2	7.0E-01
ENSMUST00000026297	guanine nucleotide binding protein-like 3 (nucleolar)-like [Source:MGI Symbol;Acc:MGI:2448557]		Q6PGG6	7.5	4.6E-06	5.6	5.4E-04	-0.9	4.5E-01	-0.8	2.4E-01
ENSMUST00000026315	deoxyribonuclease 1-like 3 [Source:MGI Symbol;Acc:MGI:1314633]		O55070	6.9	2.5E-06	6.3	3.8E-04	-0.9	4.8E-01	-0.7	3.2E-01
ENSMUST00000026318	spermidine/spermine N1-acetyl transferase 1 [Source:MGI Symbol;Acc:MGI:98233]		P48026	-8.0	1.0E-06	-5.1	1.6E-03	1.9	2.4E-03	0.1	9.3E-01
ENSMUST00000026218	CWF19-like 1, cell cycle control (S. pombe) [Source:MGI Symbol;Acc:MGI:1919752]		Q8CI33	-0.1	8.9E-01	1.2	7.7E-02	0.5	3.3E-01	-0.8	1.9E-01
ENSMUST00000026324	acyl-CoA thioesterase 9 [Source:MGI Symbol;Acc:MGI:1928939]		Q9R0X4	-7.0	6.5E-05	5.9	1.6E-04	-0.8	4.5E-01	0.8	2.0E-01
ENSMUST00000026328	peroxiredoxin 4 [Source:MGI Symbol;Acc:MGI:1859815]		O08807	-6.2	1.5E-05	-0.6	2.7E-01	1.1	5.2E-03	0.0	9.6E-01
ENSMUST00000026354	BTG3 associated nuclear protein [Source:MGI Symbol;Acc:MGI:1889023]		Q8VBU8	-4.2	1.7E-03	-7.7	5.0E-04	0.4	3.9E-01	1.0	5.3E-01
ENSMUST00000026357	junctophilin 3 [Source:MGI Symbol;Acc:MGI:1891497]		Q9ET77	-1.5	1.5E-02	1.7	3.4E-02	0.7	2.5E-01	0.5	3.5E-01
ENSMUST00000026360	integrin beta 8 [Source:MGI Symbol;Acc:MGI:1338035]	Q0VBD0		7.7	4.6E-05	6.6	3.9E-04	-0.6	6.7E-01	-0.2	7.4E-01
ENSMUST00000026377	peptidyl arginine deiminase, type III [Source:MGI Symbol;Acc:MGI:1338891]		Q9Z184	-2.5	3.3E-02	-0.4	6.7E-01	1.0	1.0E-01	-0.2	8.0E-01
ENSMUST00000026378	peptidyl arginine deiminase, type I [Source:MGI Symbol;Acc:MGI:1338893]	Q544I4	Q9Z185	7.1	7.9E-05	6.6	2.1E-02	-0.8	7.7E-01	-1.4	3.6E-01
ENSMUST00000026381	peptidyl arginine deiminase, type IV [Source:MGI Symbol;Acc:MGI:1338898]		Q9Z183	-5.8	6.5E-05	4.7	9.0E-02	-0.8	7.5E-01	1.4	4.2E-01
ENSMUST00000026387	Shwachman-Bodian-Diamond syndrome homolog (human) [Source:MGI Symbol;Acc:MGI:1913961]		P70122	-4.2	2.8E-05	-3.0	4.0E-03	0.7	1.2E-01	-0.3	7.3E-01
ENSMUST00000026398	methyltransferase like 7B [Source:MGI Symbol;Acc:MGI:1918914]		Q9DD20	6.4	9.5E-05	-5.7	1.0E-02	0.8	2.5E-01	0.7	7.1E-01
ENSMUST00000026405	biogenesis of lysosomal organelles complex-1, subunit 1 [Source:MGI Symbol;Acc:MGI:1195276]		O55102	-8.0	4.2E-05	-5.2	3.4E-03	1.2	4.8E-02	0.5	7.3E-01
ENSMUST00000026407	CD63 antigen [Source:MGI Symbol;Acc:MGI:99529]	Q549D0	P41731	-5.8	7.7E-04	0.8	2.1E-01	0.7	1.9E-01	-4.2	5.3E-04
ENSMUST00000026408	growth differentiation factor 11 [Source:MGI Symbol;Acc:MGI:1338027]		Q9Z1W4	5.9	1.3E-05	7.1	1.1E-04	-0.5	6.6E-01	-0.7	2.5E-01
ENSMUST00000026409	ORM1-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914094]		Q9CQZ0	-2.9	3.2E-04	-3.2	8.4E-03	1.4	2.4E-02	-0.6	5.7E-01
ENSMUST00000026264	ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:13	H7BWY7		1.4	6.2E-01	-3.6	3.3E-01	-3.6	1.3E-01	1.4	7.1E-01
ENSMUST00000026265	Bardet-Biedl syndrome 4 (human) [Source:MGI Symbol;Acc:MGI:2143311]	A6H669	Q8C1Z7	-0.5	4.5E-01	-0.7	3.7E-01	-0.7	2.3E-01	-0.5	5.4E-01
ENSMUST00000026410	DnaJ (Hsp40) homolog, subfamily C, member 14 [Source:MGI Symbol;Acc:MGI:1921580]		Q921R4	-3.7	2.2E-05	-5.1	1.2E-03	1.7	7.9E-03	-0.5	6.9E-01
ENSMUST00000026411	matrix metallopeptidase 19 [Source:MGI Symbol;Acc:MGI:1927899]	Q2KHP2	Q9JHI0	-3.3	8.5E-04	-0.8	4.2E-01	0.5	4.4E-01	-1.5	1.9E-01
ENSMUST00000026269	LIM domains containing 1 [Source:MGI Symbol;Acc:MGI:1352502]		Q9QXD8	-0.8	7.4E-02	0.1	8.5E-01	0.5	1.9E-01	-0.4	4.4E-01
ENSMUST00000026414	diacylglycerol kinase, alpha [Source:MGI Symbol;Acc:MGI:102952]		O88673	-3.2	1.2E-04	-3.4	5.6E-04	0.0	9.1E-01	-0.8	2.9E-01
ENSMUST00000026284	zinc finger homeodomain 4 [Source:MGI Symbol;Acc:MGI:2137668]	E9Q5A7		3.4	8.6E-02	1.8	4.5E-01	-0.4	8.4E-01	1.2	5.3E-01
ENSMUST00000026415	cyclin-dependent kinase 2 [Source:MGI Symbol;Acc:MGI:104772]	Q3U6X7	P97377	-2.2	1.5E-03	-3.8	1.6E-03	-0.4	4.2E-01	-3.3	1.3E-02
ENSMUST00000026416	cyclin-dependent kinase 2 [Source:MGI Symbol;Acc:MGI:104772]	Q3UGB9	P97377	-7.9	1.0E-04	-4.1	1.9E-01	1.1	4.4E-01	0.3	9.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000026420	ribosomal protein S26 [Source:MGI Symbol;Acc:MGI:1351628]	Q497N1	P62855	-7.6	2.1E-04	5.6	1.5E-02	-0.7	7.5E-01	-0.5	6.8E-01
ENSMUST00000026425	proliferation-associated 2G4 [Source:MGI Symbol;Acc:MGI:894684]	Q3TGU7	P50580	-2.5	2.7E-04	8.6	2.1E-05	1.2	3.0E-01	0.1	8.4E-01
ENSMUST00000026313	abhydrolase domain containing 6 [Source:MGI Symbol;Acc:MGI:1913332]		Q8R2Y0	4.5	6.1E-02	4.1	6.9E-02	-2.3	3.1E-01	-1.9	2.3E-01
ENSMUST00000026427	extended synaptotagmin-like protein 1 [Source:MGI Symbol;Acc:MGI:1344426]		Q3U7R1	-3.7	2.0E-04	5.5	2.9E-05	-1.3	9.4E-02	0.1	9.1E-01
ENSMUST00000026433	d, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 [Source:MGI Symbol;Acc		Q6PDG5	-5.6	5.0E-03	-7.7	2.9E-05	1.0	1.7E-02	0.7	4.8E-01
ENSMUST00000026322	polymerase (RNA) III (DNA directed) polypeptide A [Source:MGI Symbol;Acc:MGI:2681836]	B2RXC6		0.5	2.5E-01	0.8	1.3E-01	0.2	5.5E-01	-0.1	7.7E-01
ENSMUST00000026434	charged multivesicular body protein 6 [Source:MGI Symbol;Acc:MGI:3583942]	B1AZ39	P0C0A3	-2.7	2.5E-03	-5.6	6.0E-04	-0.1	8.8E-01	-1.5	2.7E-01
ENSMUST00000026439	nucleic acid binding protein 2 [Source:MGI Symbol;Acc:MGI:1917167]		Q8R2Y9	-3.6	6.7E-03	-5.2	1.4E-05	-2.2	1.0E-04	-3.2	2.9E-03
ENSMUST00000026445	homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus) [Source:MGI Symbol;Acc:MGI:24		Q32M02	4.4	1.3E-03	-4.4	5.3E-03	-0.7	2.1E-01	-0.6	6.7E-01
ENSMUST00000026446	canopy 2 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1928477]		Q9QXT0	-2.1	1.6E-03	-0.9	2.1E-01	0.6	1.7E-01	0.0	9.4E-01
ENSMUST00000026448	Fanconi anemia core complex associated protein 100 [Source:MGI Symbol;Acc:MGI:1919135]		A2ACJ2	-4.4	1.6E-02	5.0	2.7E-04	-3.4	1.1E-02	-0.7	2.4E-01
ENSMUST00000026367	trans-acting transcription factor 4 [Source:MGI Symbol;Acc:MGI:107595]	K4DI62		-0.8	1.3E-01	-0.9	1.7E-01	-0.3	5.3E-01	-0.1	8.2E-01
ENSMUST00000026449	interleukin 23, alpha subunit p19 [Source:MGI Symbol;Acc:MGI:1932410]		Q9EQ14	5.4	5.2E-04	-1.3	3.0E-01	0.3	7.5E-01	-1.0	4.4E-01
ENSMUST00000026455	major intrinsic protein of lens fiber [Source:MGI Symbol;Acc:MGI:96990]		P51180	7.7	3.9E-05	2.7	1.3E-02	-4.5	1.9E-03	-0.1	9.2E-01
ENSMUST00000026459	\TP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Source:MGI Symbol;Acc:MGI:107801		P56480	-8.1	1.3E-05	-3.8	4.9E-03	1.5	1.7E-02	-0.5	6.6E-01
ENSMUST00000026462	hydroxysteroid (17-beta) dehydrogenase 6 [Source:MGI Symbol;Acc:MGI:1351670]		Q9R092	5.9	2.3E-04	-4.1	1.4E-04	-0.8	4.2E-02	-0.9	2.2E-01
ENSMUST00000026466	tachykinin 2 [Source:MGI Symbol;Acc:MGI:98476]		P55099	4.3	8.4E-03	4.5	7.9E-04	-2.0	7.3E-02	-0.1	8.4E-01
ENSMUST00000026472	inhibin beta-C [Source:MGI Symbol;Acc:MGI:105932]		P55104	7.2	3.7E-05	-7.5	2.1E-04	-0.9	7.1E-02	-1.4	3.4E-01
ENSMUST00000026406	retinol dehydrogenase 5 [Source:MGI Symbol;Acc:MGI:1201412]		O55240	-0.5	6.8E-01	0.9	5.2E-01	-0.3	7.7E-01	-1.7	2.0E-01
ENSMUST00000026474	GLI-Kruppel family member GLI1 [Source:MGI Symbol;Acc:MGI:95727]		P47806	3.8	3.1E-04	-5.8	3.7E-03	0.1	9.0E-01	0.1	9.3E-01
ENSMUST00000026475	DNA-damage inducible transcript 3 [Source:MGI Symbol;Acc:MGI:109247]		P35639	-4.5	2.5E-03	4.9	2.1E-04	-1.2	1.4E-01	-0.2	7.1E-01
ENSMUST00000026476	methyl-CpG binding domain protein 6 [Source:MGI Symbol;Acc:MGI:106378]	E9Q572		-2.8	1.4E-02	-3.5	2.8E-04	-0.9	3.1E-02	-0.3	7.0E-01
ENSMUST00000026479	dynactin 2 [Source:MGI Symbol;Acc:MGI:107733]	Q3TPZ5	Q99KJ8	-5.0	2.4E-06	-3.2	5.1E-04	0.5	1.2E-01	0.1	8.9E-01
ENSMUST00000026487	immediate early response 3 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1913441]		Q9CR20	-4.6	3.7E-06	-2.0	5.5E-02	1.5	2.0E-02	0.2	8.2E-01
ENSMUST00000026494	ring finger protein 165 [Source:MGI Symbol;Acc:MGI:2444521]		E9QAU8	8.2	1.5E-06	-3.0	8.8E-04	0.0	9.3E-01	-0.2	7.6E-01
ENSMUST00000026495	TP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1 [Source:MGI Symbol;Acc:MGI:8811		Q03265	-6.3	8.0E-07	-0.2	7.4E-01	2.0	1.9E-03	0.0	9.7E-01
ENSMUST00000026504	XRCC6 binding protein 1 [Source:MGI Symbol;Acc:MGI:1916984]		Q9CWQ3	4.6	1.8E-02	-3.9	7.1E-03	1.1	8.1E-02	-3.0	5.9E-02
ENSMUST00000026506	chloride channel, nucleotide-sensitive, 1A [Source:MGI Symbol;Acc:MGI:109638]	Q923F1		-3.0	2.2E-04	-7.3	9.2E-04	-1.5	4.7E-02	-1.7	3.2E-01
ENSMUST00000026507	ubiquitin specific peptidase 33 [Source:MGI Symbol;Acc:MGI:2159711]	A0A0H2UKB8		-3.7	7.5E-03	-2.5	1.3E-03	-0.4	2.3E-01	-0.4	4.5E-01
ENSMUST00000026519	RIKEN cDNA 4833420G17 gene [Source:MGI Symbol;Acc:MGI:1914642]		Q3UJC8	-3.8	4.5E-03	-2.2	2.0E-02	1.4	1.4E-02	-0.1	8.6E-01
ENSMUST00000026428	myosin, light polypeptide 6B [Source:MGI Symbol;Acc:MGI:1917789]		Q8CI43	0.9	1.5E-01	1.8	2.5E-02	0.7	2.4E-01	-0.3	6.4E-01
ENSMUST00000026538	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Source:MGI Symbol;Acc:MGI:2136460]		Q8BH95	-5.5	3.0E-04	-2.2	4.4E-01	3.6	3.7E-02	0.2	9.4E-01
ENSMUST00000026541	calcyon neuron-specific vesicular protein [Source:MGI Symbol;Acc:MGI:1915816]		Q9DCA7	7.8	4.7E-05	-1.9	5.0E-02	0.8	1.5E-01	0.0	9.8E-01
ENSMUST00000026436	brain-specific angiogenesis inhibitor 1-associated protein 2 [Source:MGI Symbol;Acc:MGI:2137336]		Q8BKX1	1.7	4.4E-01	-0.3	8.9E-01	-2.5	2.2E-01	-0.4	8.6E-01
ENSMUST00000026546	a disintegrin and metallopeptidase domain 8 [Source:MGI Symbol;Acc:MGI:107825]	Q3U7G2		-11.3	3.2E-05	-1.9	1.4E-01	0.9	2.6E-01	-0.9	4.9E-01
ENSMUST00000026548	adhesion G protein-coupled receptor A1 [Source:MGI Symbol;Acc:MGI:1277167]		Q8C4G9	8.0	4.1E-05	4.9	2.3E-03	0.1	9.2E-01	-0.3	7.0E-01
ENSMUST00000026551	dihydropyrimidinase-like 4 [Source:MGI Symbol;Acc:MGI:1349764]	Q3TMU8		5.9	3.1E-04	-2.4	2.6E-03	-0.5	1.6E-01	-0.3	6.8E-01
ENSMUST00000026552	cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88607]		Q05421	4.4	2.9E-04	-3.5	5.5E-02	1.2	2.5E-01	0.3	8.8E-01
ENSMUST00000026553	synaptonemal complex central element protein 1 [Source:MGI Symbol;Acc:MGI:1921325]		Q9D495	4.7	5.5E-04	2.0	2.6E-02	-4.9	7.7E-04	-1.5	5.1E-02
ENSMUST00000026557	blocked early in transport 1 homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:1913128]		O35153	-3.8	1.2E-04	7.7	6.9E-05	-0.6	6.1E-01	-0.7	2.6E-01
ENSMUST00000026558	resistance to inhibitors of cholinesterase 8 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2141866]		Q3TIR3	-4.8	5.7E-05	-7.3	2.5E-04	0.8	1.3E-01	-0.1	9.6E-01
ENSMUST00000026461	DNA primase, p49 subunit [Source:MGI Symbol;Acc:MGI:97757]	Q5FW94	P20664	-3.4	1.8E-01	-5.3	9.5E-02	-2.5	1.2E-01	-0.6	8.6E-01
ENSMUST00000026560	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 [Source:MGI Symbol;Acc:MGI:1345192]	B2RT97	Q9WVJ2	-4.8	3.3E-05	3.4	4.9E-03	-2.0	8.8E-02	0.5	4.7E-01
ENSMUST00000026564	interferon induced transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1915963]		Q9D103	-7.6	2.1E-05	6.5	1.0E-03	-0.6	6.9E-01	-2.8	1.1E-02
ENSMUST00000026469	Ngfi-A binding protein 2 [Source:MGI Symbol;Acc:MGI:107563]		Q61127	4.1	6.9E-02	3.3	2.5E-01	-0.6	8.2E-01	0.2	9.0E-01
ENSMUST00000026470	serine hydroxymethyltransferase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1277989]	Q9CZN7		-0.4	5.7E-01	0.0	9.9E-01	0.2	7.6E-01	-0.2	8.1E-01
ENSMUST00000026565	interferon induced transmembrane protein 3 [Source:MGI Symbol;Acc:MGI:1913391]		Q9CQW9	-7.6	1.6E-06	5.9	2.3E-04	-1.3	2.6E-01	0.0	9.9E-01
ENSMUST00000026569	dopamine receptor D4 [Source:MGI Symbol;Acc:MGI:94926]		P51436	7.4	2.6E-04	4.0	6.2E-04	-0.1	8.5E-01	-0.3	6.0E-01
ENSMUST00000026571	interferon regulatory factor 7 [Source:MGI Symbol;Acc:MGI:1859212]	Q542T3	P70434	-5.3	7.8E-04	-5.4	4.9E-03	-0.8	2.6E-01	0.1	9.4E-01
ENSMUST00000026572	Harvey rat sarcoma virus oncogene [Source:MGI Symbol;Acc:MGI:96224]		Q61411	5.5	1.4E-04	-0.9	4.5E-01	1.1	1.7E-01	-0.7	5.3E-01
ENSMUST00000026576	transaldolase 1 [Source:MGI Symbol;Acc:MGI:1274789]		Q93092	-8.6	1.2E-07	-4.1	8.4E-05	0.8	1.5E-02	-0.1	9.2E-01
ENSMUST00000026480	tetratricopeptide repeat domain 4 [Source:MGI Symbol;Acc:MGI:1919604]		Q8R3H9	-2.5	3.9E-02	-1.8	1.9E-01	-0.1	8.6E-01	-0.9	5.1E-01
ENSMUST00000026577	EPS8-like 2 [Source:MGI Symbol;Acc:MGI:2138828]		Q99K30	5.5	1.8E-03	-4.2	8.1E-05	0.5	1.6E-01	0.1	8.6E-01
ENSMUST00000026578	transmembrane protein 80 [Source:MGI Symbol;Acc:MGI:1918698]		Q9D3H0	-3.8	1.6E-02	9.3	1.2E-05	1.2	2.9E-01	0.0	9.6E-01
ENSMUST00000026583	patatin-like phospholipase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914103]	H3BIT5		-10.3	1.2E-04	-5.3	2.2E-05	0.7	4.4E-02	-0.4	6.0E-01
ENSMUST00000026500	advillin [Source:MGI Symbol;Acc:MGI:1333798]		O88398	2.5	7.6E-02	2.9	1.1E-01	-0.2	9.1E-01	-0.6	6.1E-01
ENSMUST00000026586	chitinase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915288]			6.0	1.2E-02	5.6	1.8E-02	0.3	8.6E-01	-0.6	6.2E-01
ENSMUST00000026595	transmembrane protein 192 [Source:MGI Symbol;Acc:MGI:1920317]		Q9CXT7	-3.5	6.4E-05	-2.1	8.2E-03	0.2	6.7E-01	-0.8	2.4E-01
ENSMUST00000026599	apolipoprotein O-like [Source:MGI Symbol;Acc:MGI:1915367]		Q78IK4	-2.7	2.2E-03	-3.7	5.6E-02	0.8	3.2E-01	0.8	6.5E-01
ENSMUST00000026601	spermidine/spermine N1-acetyl transferase-like 1 [Source:MGI Symbol;Acc:MGI:1921059]		Q9D5N8	8.6	9.8E-04	-2.7	6.2E-02	0.5	5.0E-01	-0.6	6.5E-01
ENSMUST00000026520	polyadenylate binding protein-interacting protein 1 [Source:MGI Symbol;Acc:MGI:2384993]		Q8VE62	-1.8	1.6E-01	0.2	8.6E-01	0.9	4.6E-01	-1.2	3.9E-01
ENSMUST00000026537	polyamine oxidase (exo-N4-amino) [Source:MGI Symbol;Acc:MGI:1916983]		Q8C0L6	-0.1	9.2E-01	-0.1	9.5E-01	-0.6	3.8E-01	-0.6	5.0E-01
ENSMUST00000026607	choroideremia (RAB escort protein 1) [Source:MGI Symbol;Acc:MGI:892979]	A2AD03		-6.6	1.1E-04	-4.8	1.2E-03	-0.4	4.0E-01	-1.2	3.5E-01
ENSMUST00000026539	fucose mutarotase [Source:MGI Symbol;Acc:MGI:1916314]		Q8R2K1	-2.0	8.0E-02	-3.8	4.2E-02	-0.4	6.4E-01	1.4	3.9E-01
ENSMUST00000026608	calcitonin gene-related peptide-receptor component protein [Source:MGI Symbol;Acc:MGI:1100818]		O35427	-3.7	1.0E-04	6.9	2.3E-04	-0.6	6.2E-01	0.2	7.0E-01
ENSMUST00000026613	glucuronidase, beta [Source:MGI Symbol;Acc:MGI:95872]		P12265	-4.1	3.2E-05	-9.5	7.0E-04	1.0	6.5E-02	-0.8	7.2E-01
ENSMUST00000026547	tubulin, gamma complex associated protein 2 [Source:MGI Symbol;Acc:MGI:1921487]		Q921G8	-0.6	1.5E-01	-0.3	5.4E-01	0.2	5.8E-01	-0.1	8.3E-01
ENSMUST00000026617	phosphorylase kinase gamma 1 [Source:MGI Symbol;Acc:MGI:97579]		P07934	8.1	2.7E-05	8.1	3.3E-04	0.1	9.5E-01	0.1	9.3E-01
ENSMUST00000026550	inositol polyphosphate-5-phosphatase A [Source:MGI Symbol;Acc:MGI:2686961]	E9QAS7		-4.2	5.1E-02	-2.4	3.5E-01	0.8	6.0E-01	-1.0	7.0E-01
ENSMUST00000026624	transmembrane 9 superfamily member 2 [Source:MGI Symbol;Acc:MGI:1915309]	Q542E4	P58021	-6.0	6.2E-05	7.0	1.5E-04	-0.5	6.6E-01	-1.7	2.6E-02
ENSMUST00000026625	citrate lyase beta like [Source:MGI Symbol;Acc:MGI:1916884]		Q8R4N0	2.8	8.7E-03	2.3	8.9E-03	-2.9	4.0E-03	-0.9	1.7E-01
ENSMUST00000026631	fibroblast growth factor 14 [Source:MGI Symbol;Acc:MGI:109189]			6.8	1.3E-04	4.0	2.5E-03	-0.8	4.3E-01	0.0	9.5E-01
ENSMUST00000026635	, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived) [Source:MGI Symbol;Acc:MGI:24		F8VPU2	2.1	1.7E-03	-3.6	9.1E-04	0.1	8.5E-01	-0.1	8.6E-01
ENSMUST00000026649	synaptogyrin 2 [Source:MGI Symbol;Acc:MGI:1328324]		O55101	-7.6	9.1E-05	-4.4	1.4E-03	0.7	1.5E-01	0.2	8.1E-01
ENSMUST00000026559	sirtuin 3 [Source:MGI Symbol;Acc:MGI:1927665]	Q4FJK3	Q8R104	-3.2	9.0E-02	0.6	7.6E-01	1.3	4.1E-01	-2.4	2.2E-01
ENSMUST00000026658	trinucleotide repeat containing 6C [Source:MGI Symbol;Acc:MGI:2443265]	B1ATC3		-4.5	3.0E-03	-4.0	6.3E-04	0.5	2.7E-01	-0.2	7.7E-01
ENSMUST00000026562	interferon induced transmembrane protein 5 [Source:MGI Symbol;Acc:MGI:1934923]		O88728	0.3	6.1E-01	0.0	9.4E-01	-0.6	3.0E-01	-0.2	7.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000026659	transmembrane channel-like gene family 6 [Source:MGI Symbol;Acc:MGI:1098686]	B1ATB3		-8.5	8.2E-05	-8.5	7.9E-05	-0.5	2.9E-01	0.4	7.8E-01
ENSMUST00000026662	chromobox 2 [Source:MGI Symbol;Acc:MGI:88289]		P30658	5.0	1.6E-03	-7.9	1.3E-05	-0.1	7.2E-01	0.2	8.3E-01
ENSMUST00000026568	phosphatidylserine synthase 2 [Source:MGI Symbol;Acc:MGI:1351664]		Q9Z1X2	1.1	4.6E-02	2.1	1.0E-02	0.8	1.5E-01	-0.2	7.6E-01
ENSMUST00000026667	eukaryotic translation initiation factor 4A3 [Source:MGI Symbol;Acc:MGI:1923731]		Q91VC3	-5.5	8.4E-05	6.4	1.2E-03	-0.7	6.6E-01	0.4	6.6E-01
ENSMUST00000026670	neuronal pentraxin 1 [Source:MGI Symbol;Acc:MGI:107811]	A2ACL9	Q62443	10.1	3.1E-06	-2.0	4.6E-02	-0.3	6.2E-01	-3.6	1.3E-02
ENSMUST00000026672	phosphodiesterase 8A [Source:MGI Symbol;Acc:MGI:1277116]		O88502	-3.0	2.0E-04	5.0	9.4E-04	-0.7	5.1E-01	-0.2	7.9E-01
ENSMUST00000026573	lamin tail domain containing 2 [Source:MGI Symbol;Acc:MGI:1919250]		Q0VET5	1.2	4.3E-01	3.9	3.9E-02	0.2	9.2E-01	-2.5	9.6E-02
ENSMUST00000026698	podocalyxin-like [Source:MGI Symbol;Acc:MGI:1351317]	Q791G4	Q9R0M4	8.3	7.9E-07	-7.2	2.6E-06	0.4	1.5E-01	-1.1	1.8E-01
ENSMUST00000026699	muskelin 1, intracellular mediator containing kelch motifs [Source:MGI Symbol;Acc:MGI:1351638]		O89050	2.0	2.9E-03	3.0	2.1E-02	-3.0	3.6E-02	-0.5	5.8E-01
ENSMUST00000026700	Map3k7 C-terminal like [Source:MGI Symbol;Acc:MGI:2446584]	Q544C0	P58500	2.9	1.6E-02	0.6	7.1E-01	2.3	8.6E-02	-2.1	2.0E-01
ENSMUST00000026703	BTB and CNC homology 1 [Source:MGI Symbol;Acc:MGI:894680]	Q3URL4	P97302	-4.9	2.1E-06	-8.6	2.4E-03	1.0	1.1E-01	-0.7	7.6E-01
ENSMUST00000026585	tetraspanin 4 [Source:MGI Symbol;Acc:MGI:1928097]	Q4FJW7	Q9DCK3	1.8	2.7E-01	0.4	7.1E-01	-4.8	3.1E-03	-3.4	2.4E-02
ENSMUST00000026704	chaperonin containing Tcp1, subunit 8 (theta) [Source:MGI Symbol;Acc:MGI:107183]	Q3UL22	P42932	-3.2	3.5E-03	-0.1	9.7E-01	-2.8	1.9E-01	3.2	1.3E-01
ENSMUST00000026723	hypoxanthine guanine phosphoribosyl transferase [Source:MGI Symbol;Acc:MGI:96217]		P00493	-5.9	8.5E-06	-2.4	4.8E-03	1.3	9.1E-03	0.2	8.2E-01
ENSMUST00000026737	shisa family member 5 [Source:MGI Symbol;Acc:MGI:1915044]		Q9D7I0	-6.2	1.1E-03	-1.9	3.3E-02	-0.3	5.8E-01	-1.1	1.9E-01
ENSMUST00000026743	ubiquinol-cytochrome c reductase core protein 1 [Source:MGI Symbol;Acc:MGI:107876]		Q9CZ13	-6.8	1.5E-04	6.6	8.6E-03	-0.9	7.0E-01	1.1	3.4E-01
ENSMUST00000026750	connector enhancer of kinase suppressor of Ras 2 [Source:MGI Symbol;Acc:MGI:2661175]		Q80YA9	8.0	1.3E-04	-6.5	1.9E-03	0.4	4.6E-01	0.3	8.5E-01
ENSMUST00000026795	arachidonate 5-lipoxygenase [Source:MGI Symbol;Acc:MGI:87999]		P48999	-7.0	8.4E-07	-4.3	1.6E-04	-0.8	6.0E-02	-0.1	8.6E-01
ENSMUST00000026818	SEC11 homolog A, signal peptidase complex subunit [Source:MGI Symbol;Acc:MGI:1929464]		Q9R0P6	-6.5	1.0E-04	-2.9	2.1E-03	0.7	6.8E-02	-0.6	4.4E-01
ENSMUST00000026823	phosphatidylinositol glycan anchor biosynthesis, class Q [Source:MGI Symbol;Acc:MGI:1333114]	Q3TF56	Q9QYT7	-5.8	5.1E-04	6.7	1.1E-04	-1.9	1.2E-01	-0.5	4.1E-01
ENSMUST00000026827	RIKEN cDNA 0610011F06 gene [Source:MGI Symbol;Acc:MGI:1915597]		Q9DCS2	-4.5	1.3E-02	-3.6	6.8E-03	1.8	9.2E-03	-0.6	6.0E-01
ENSMUST00000026828	family with sequence similarity 195, member A [Source:MGI Symbol;Acc:MGI:1915491]		Q9CQB2	2.5	5.1E-03	1.0	2.7E-01	-2.0	3.5E-02	-0.2	7.8E-01
ENSMUST00000026832	jumonji domain containing 8 [Source:MGI Symbol;Acc:MGI:1919356]			-5.2	2.4E-03	5.8	7.9E-04	-0.5	6.7E-01	0.5	4.7E-01
ENSMUST00000026839	phosphoribosyl pyrophosphate synthetase 2 [Source:MGI Symbol;Acc:MGI:97776]		Q9CS42	1.9	1.5E-02	2.3	4.6E-03	0.1	8.7E-01	-0.1	8.3E-01
ENSMUST00000026841	enase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit [Sour		Q99JY0	-7.7	2.5E-06	-7.9	1.2E-03	0.8	1.1E-01	1.2	5.3E-01
ENSMUST00000026846	thymidylate synthase [Source:MGI Symbol;Acc:MGI:98878]	Q544L2	P07607	6.3	7.3E-06	-2.9	8.2E-02	1.0	2.3E-01	-0.5	7.5E-01
ENSMUST00000026854	ATP/GTP binding protein-like 1 [Source:MGI Symbol;Acc:MGI:3646469]		Q09M05	9.5	3.4E-04	-7.2	1.9E-03	1.1	6.0E-02	-0.2	9.1E-01
ENSMUST00000026661	thymidine kinase 1 [Source:MGI Symbol;Acc:MGI:98763]		P04184	-1.2	1.5E-01	-1.5	1.3E-01	-0.5	4.0E-01	-0.2	8.4E-01
ENSMUST00000026862	La ribonucleoprotein domain family, member 1B [Source:MGI Symbol;Acc:MGI:1914604]	Q497V3		9.3	1.8E-05	5.2	8.8E-03	0.2	9.0E-01	0.0	9.7E-01
ENSMUST00000026663	chromobox 8 [Source:MGI Symbol;Acc:MGI:1353589]		Q9QXV1	-0.8	1.0E-01	0.7	3.1E-01	1.2	2.9E-02	-0.3	5.7E-01
ENSMUST00000026665	chromobox 4 [Source:MGI Symbol;Acc:MGI:1195985]		O55187	-0.7	2.7E-01	-0.4	6.1E-01	0.9	1.5E-01	0.6	4.4E-01
ENSMUST00000026666	glucosidase, alpha, acid [Source:MGI Symbol;Acc:MGI:95609]		P70699	-3.2	7.9E-02	-3.8	1.0E-01	0.0	9.9E-01	0.6	8.0E-01
ENSMUST00000026865	jade family PHD finger 1 [Source:MGI Symbol;Acc:MGI:1925835]		Q6ZPI0	-2.2	2.6E-03	-3.1	7.0E-03	0.5	2.8E-01	-1.9	8.5E-02
ENSMUST00000026886	inter-alpha (globulin) inhibitor H5 [Source:MGI Symbol;Acc:MGI:1925751]		Q8BJD1	4.2	1.5E-05	5.3	3.4E-05	-4.6	1.1E-03	0.2	6.3E-01
ENSMUST00000026671	regulatory associated protein of MTOR, complex 1 [Source:MGI Symbol;Acc:MGI:1921620]	A2ACM0		-3.5	5.1E-02	-4.0	8.6E-02	0.3	7.7E-01	0.8	7.4E-01
ENSMUST00000026887	ynthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 [Source:MGI Symbol;Acc:MGI:12(	A2AKU9		-5.3	6.3E-05	-1.5	5.2E-02	1.6	2.9E-03	0.1	9.2E-01
ENSMUST00000026888	3 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:2388	A2ASY1	Q5HZG4	-3.8	5.4E-03	5.2	4.2E-05	-2.6	6.5E-03	0.5	2.5E-01
ENSMUST00000026889	RIKEN cDNA 4930412O13 gene [Source:MGI Symbol;Acc:MGI:1921185]	Q9D5M9		7.5	5.5E-05	2.0	1.3E-02	0.1	8.8E-01	0.1	8.6E-01
ENSMUST00000026891	exosome component 7 [Source:MGI Symbol;Acc:MGI:1913696]		Q9D0M0	-3.6	1.1E-04	3.6	2.5E-02	0.2	9.0E-01	-0.5	5.7E-01
ENSMUST00000026892	zinc finger, DHHC domain containing 3 [Source:MGI Symbol;Acc:MGI:1926134]	D6RHA3		-9.1	1.5E-05	-3.5	1.6E-04	0.8	1.5E-02	-0.5	3.6E-01
ENSMUST00000026893	transglutaminase 4 (prostate) [Source:MGI Symbol;Acc:MGI:3027002]			3.1	3.3E-03	-5.0	3.7E-03	-0.6	3.4E-01	1.3	3.5E-01
ENSMUST00000026710	ubiquitin specific peptidase 16 [Source:MGI Symbol;Acc:MGI:1921362]		Q99LG0	-1.8	8.4E-02	0.5	7.1E-01	1.6	1.4E-01	-0.7	5.3E-01
ENSMUST00000026896	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2 [Source:MGI Symbol;Acc:MGI:106020]		O35696	8.7	7.4E-06	-6.4	6.6E-05	0.0	9.6E-01	0.5	6.2E-01
ENSMUST00000026735	coiled-coil domain containing 51 [Source:MGI Symbol;Acc:MGI:1913908]		Q3URS9	0.1	8.4E-01	0.4	5.7E-01	0.0	9.5E-01	-0.4	6.2E-01
ENSMUST00000026900	HGF-regulated tyrosine kinase substrate [Source:MGI Symbol;Acc:MGI:104681]	Q3UMA3		-3.7	1.4E-02	-5.2	1.1E-02	0.6	3.8E-01	-0.3	8.7E-01
ENSMUST00000026740	collagen, type VII, alpha 1 [Source:MGI Symbol;Acc:MGI:88462]		Q63870	3.1	1.8E-01	-2.9	4.7E-01	-1.5	4.9E-01	4.5	2.5E-01
ENSMUST00000026902	Ras association (RalGDS/AF-6) domain family member 3 [Source:MGI Symbol;Acc:MGI:2179722]		Q99P51	-5.1	2.3E-05	-7.5	4.6E-03	1.2	7.4E-02	1.9	3.8E-01
ENSMUST00000026907	cytochrome P450, family 4, subfamily v, polypeptide 3 [Source:MGI Symbol;Acc:MGI:2142763]	H9H9R5		5.5	8.4E-03	7.3	7.6E-04	0.0	9.9E-01	0.7	3.5E-01
ENSMUST00000026911	chemokine (C-C motif) receptor 1 [Source:MGI Symbol;Acc:MGI:104618]		P51675	-8.1	4.6E-06	-5.2	6.0E-05	1.5	1.3E-03	-0.2	7.5E-01
ENSMUST00000026816	WD repeat domain 73 [Source:MGI Symbol;Acc:MGI:1919218]		Q9CWR1	-2.5	2.0E-01	-2.0	4.2E-01	0.2	8.8E-01	-0.3	9.2E-01
ENSMUST00000026817	neuromedin B [Source:MGI Symbol;Acc:MGI:1915289]		Q9CR53	-0.8	4.6E-01	-2.1	2.3E-01	-0.3	7.6E-01	1.0	5.4E-01
ENSMUST00000026917	neuropilin 1 [Source:MGI Symbol;Acc:MGI:106206]		P97333	2.0	2.1E-03	-4.9	1.0E-03	-0.8	1.2E-01	-2.4	8.0E-02
ENSMUST00000026820	te carrier family 28 (sodium-coupled nucleoside transporter), member 1 [Source:MGI Symbol;Acc:MGI:36050	E9PXX9		1.9	3.4E-01	7.5	5.4E-03	0.6	7.8E-01	-4.9	6.1E-03
ENSMUST00000026922	homer homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1347354]		Q9QWW1	4.8	3.3E-02	-0.1	8.7E-01	1.1	8.0E-02	-4.5	3.5E-03
ENSMUST00000026826	Rab40C, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2183454]	Q0PD11	Q8VHQ4	-4.3	1.5E-01	2.3	6.0E-01	5.8	1.0E-01	-0.8	8.2E-01
ENSMUST00000026927	nudix (nucleoside diphosphate linked moiety X)-type motif 5 [Source:MGI Symbol;Acc:MGI:1858232]		Q9JKX6	2.2	5.3E-03	-2.2	3.0E-01	1.6	2.3E-01	-0.8	7.2E-01
ENSMUST00000026937	IscU iron-sulfur cluster scaffold homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1913633]		Q9D7P6	-6.3	2.0E-04	3.0	2.8E-03	-0.6	4.2E-01	-1.1	9.8E-02
ENSMUST00000026831	rhomboid, veinlet-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2384891]	Q3USF1	Q8VC82	0.4	8.4E-01	2.3	2.3E-01	-0.8	6.5E-01	-2.7	1.5E-01
ENSMUST00000026957	preferentially expressed antigen in melanoma like 7 [Source:MGI Symbol;Acc:MGI:2156391]	Q810Y8		5.8	6.8E-04	-3.4	6.2E-02	1.0	2.1E-01	-0.8	6.7E-01
ENSMUST00000026833	WD repeat domain 24 [Source:MGI Symbol;Acc:MGI:2446285]		Q8CFJ9	-1.6	1.3E-01	-2.1	1.6E-01	0.6	4.6E-01	1.2	4.1E-01
ENSMUST00000026972	family with sequence similarity 20, member C [Source:MGI Symbol;Acc:MGI:2136853]		Q5MJS3	-4.9	1.5E-05	1.3	1.6E-01	-0.3	6.4E-01	0.4	6.3E-01
ENSMUST00000026975	dynein, axonemal, assembly factor 5 [Source:MGI Symbol;Acc:MGI:3616079]		B9EJR8	1.5	1.2E-02	-7.5	3.0E-05	0.0	9.7E-01	-0.2	8.8E-01
ENSMUST00000026976	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914854]		Q9D1H7	-2.1	9.6E-03	-6.4	2.5E-03	0.3	6.6E-01	-1.1	5.5E-01
ENSMUST00000026845	interleukin 6 [Source:MGI Symbol;Acc:MGI:96559]	A2RTD1	P08505	1.1	1.6E-01	-0.4	5.9E-01	-2.7	3.5E-03	-1.2	1.6E-01
ENSMUST00000026985	complexin 2 [Source:MGI Symbol;Acc:MGI:104726]		P84086	8.5	7.2E-06	5.4	5.6E-05	-0.7	3.3E-01	0.2	7.6E-01
ENSMUST00000026986	HIG1 domain family, member 2A [Source:MGI Symbol;Acc:MGI:1914294]		Q9CQJ1	-5.7	2.8E-05	7.4	2.4E-03	-1.7	4.1E-01	0.5	6.0E-01
ENSMUST00000026858	polo-like kinase 4 [Source:MGI Symbol;Acc:MGI:101783]		Q64702	-3.0	6.2E-02	-1.3	5.4E-01	2.1	1.3E-01	0.4	8.4E-01
ENSMUST00000026859	major facilitator superfamily domain containing 8 [Source:MGI Symbol;Acc:MGI:1919425]		Q8BH31	-0.5	5.6E-01	1.2	2.6E-01	1.3	1.4E-01	-0.4	6.9E-01
ENSMUST00000026987	NOP16 nucleolar protein [Source:MGI Symbol;Acc:MGI:107862]		Q9CPT5	1.3	2.8E-02	7.1	5.9E-05	-3.1	3.3E-02	-0.8	1.3E-01
ENSMUST00000026989	RIKEN cDNA 4833439L19 gene [Source:MGI Symbol;Acc:MGI:1921162]		Q9DBN4	-5.9	1.1E-03	-5.2	1.8E-03	0.8	8.8E-02	3.8	9.5E-03
ENSMUST00000026881	lymphocyte antigen 96 [Source:MGI Symbol;Acc:MGI:1341909]	Q14AM4	Q9JHF9	-0.3	6.4E-01	0.8	4.5E-01	1.7	5.1E-02	0.6	5.3E-01
ENSMUST00000026991	Fas associated factor family member 2 [Source:MGI Symbol;Acc:MGI:1923827]		Q3TDN2	-5.8	1.1E-04	4.4	7.6E-05	0.5	3.6E-01	0.3	4.6E-01
ENSMUST00000026994	unc-5 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:894682]		Q8K1S4	5.8	3.1E-02	-6.3	1.5E-04	-1.3	2.0E-02	-0.3	7.9E-01
ENSMUST00000026997	ubiquitin interaction motif containing 1 [Source:MGI Symbol;Acc:MGI:103185]			-6.1	6.1E-04	-0.2	8.6E-01	0.8	2.6E-01	-2.8	3.2E-02
ENSMUST00000027012	caspase 4, apoptosis-related cysteine peptidase [Source:MGI Symbol;Acc:MGI:107700]		P70343	-10.5	1.1E-04	5.9	2.8E-04	-1.9	1.3E-01	-0.3	6.2E-01
ENSMUST00000027015	caspase 1 [Source:MGI Symbol;Acc:MGI:96544]		P29452	-6.0	4.1E-04	-2.3	5.4E-03	-0.2	6.9E-01	-1.4	5.8E-02
ENSMUST00000027020	glutamate receptor, ionotropic, AMPA4 (alpha 4) [Source:MGI Symbol;Acc:MGI:95811]	G5E863		6.7	2.0E-02	-7.6	6.0E-04	1.5	7.1E-03	0.0	9.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000027027	CWF19-like 2, cell cycle control (S. pombe) [Source:MGI Symbol;Acc:MGI:1918023]		Q8BG79	-3.3	6.3E-04	4.7	2.6E-03	2.0	7.8E-02	0.5	5.3E-01
ENSMUST00000027032	retinitis pigmentosa 1 (human) [Source:MGI Symbol;Acc:MGI:1341105]		P56716	7.0	4.6E-05	8.4	2.1E-05	-0.6	5.9E-01	-0.3	5.6E-01
ENSMUST00000026897	solute carrier organic anion transporter family, member 3a1 [Source:MGI Symbol;Acc:MGI:1351867]		Q8R3L5	-0.2	8.0E-01	0.2	8.3E-01	0.4	6.3E-01	-0.1	9.6E-01
ENSMUST00000026899	rrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10 [Source:MGI Symbol;Acc:MGI:1		Q9QZD8	0.2	7.9E-01	-0.1	9.5E-01	-0.1	9.2E-01	0.2	8.4E-01
ENSMUST00000027036	lysophospholipase 1 [Source:MGI Symbol;Acc:MGI:1344588]		P97823	-2.3	3.4E-03	-5.9	5.7E-02	1.4	1.7E-01	3.7	2.1E-01
ENSMUST00000026901				-3.2	1.2E-01	-1.6	5.9E-01	1.6	4.7E-01	0.0	9.9E-01
ENSMUST00000027050	(constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13		O35864	-6.2	2.0E-04	-4.0	1.1E-03	1.1	2.8E-02	-0.1	8.9E-01
ENSMUST00000027056	osphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2 [Source:MGI Symbol;Acc:MGI:19233		Q3LAC4	4.7	2.1E-03	2.5	1.2E-01	-2.6	1.3E-01	0.4	7.1E-01
ENSMUST00000027057	telomeric repeat binding factor 1 [Source:MGI Symbol;Acc:MGI:109634]	Q3V252		-6.3	1.2E-04	-7.5	3.8E-05	-0.4	2.9E-01	-1.0	3.5E-01
ENSMUST00000027059	transcription factor AP-2 beta [Source:MGI Symbol;Acc:MGI:104672]		Q61313	8.7	1.9E-05	0.7	2.4E-01	-1.3	1.8E-02	0.0	9.5E-01
ENSMUST00000027062	musculin [Source:MGI Symbol;Acc:MGI:1333884]		O88940	6.7	5.2E-03	1.4	6.8E-01	0.3	9.0E-01	3.8	1.6E-01
ENSMUST00000027064	transmembrane protein 14A [Source:MGI Symbol;Acc:MGI:1922962]	D3YV08		5.4	6.8E-03	2.4	1.1E-02	0.1	8.7E-01	-0.1	8.7E-01
ENSMUST00000027065	transmembrane protein 14A [Source:MGI Symbol;Acc:MGI:1922962]		P56983	3.6	2.8E-02	-7.5	1.9E-03	0.2	7.9E-01	1.3	4.7E-01
ENSMUST00000027066	eyes absent 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109344]		P97767	6.3	8.1E-03	6.3	7.1E-04	-0.4	7.6E-01	-0.9	2.3E-01
ENSMUST00000027068	translocating chain-associating membrane protein 1 [Source:MGI Symbol;Acc:MGI:1919515]	Q4FK14	Q91V04	-4.3	1.0E-04	-2.8	2.3E-03	1.5	3.4E-03	-0.6	4.0E-01
ENSMUST00000026973	protein kinase, cAMP dependent regulatory, type I beta [Source:MGI Symbol;Acc:MGI:97759]		P12849	3.6	8.9E-02	2.0	4.3E-01	-0.5	8.3E-01	1.2	5.5E-01
ENSMUST00000027071	lactamase, beta 2 [Source:MGI Symbol;Acc:MGI:2442551]		Q99KR3	4.4	1.8E-04	2.1	1.2E-02	0.8	1.7E-01	0.2	7.2E-01
ENSMUST00000027083	parathyroid hormone 2 receptor [Source:MGI Symbol;Acc:MGI:2180917]		Q91V95	7.3	8.2E-05	-1.0	2.7E-01	1.3	4.6E-02	0.2	8.4E-01
ENSMUST00000026978	X-linked inhibitor of apoptosis [Source:MGI Symbol;Acc:MGI:107572]		Q60989	-1.2	4.7E-01	0.5	8.3E-01	1.6	3.8E-01	-0.1	9.7E-01
ENSMUST00000027089	crystallin, gamma C [Source:MGI Symbol;Acc:MGI:88523]	A3RLD4	Q61597	5.7	6.0E-03	5.8	1.4E-04	-2.5	3.0E-02	0.2	6.8E-01
ENSMUST00000027102	RIKEN cDNA 4933402D24 gene [Source:MGI Symbol;Acc:MGI:1921676]	Q9D4D3		7.0	1.8E-04	-4.7	4.8E-04	0.0	1.0E+00	-0.9	3.4E-01
ENSMUST00000027103	FAST kinase domains 2 [Source:MGI Symbol;Acc:MGI:1922869]		Q922E6	2.2	1.4E-02	1.9	1.5E-02	0.0	9.4E-01	-0.5	3.5E-01
ENSMUST00000026988	ADP-ribosylation factor-like 10 [Source:MGI Symbol;Acc:MGI:1930788]		Q9QXJ4	0.2	8.1E-01	1.3	1.8E-01	-0.2	8.4E-01	-1.2	1.8E-01
ENSMUST00000027111	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Source:MGI Symbol;Acc:MGI:2443241]		Q91VD9	-5.9	5.3E-05	-5.3	2.1E-03	0.6	3.3E-01	0.1	9.7E-01
ENSMUST00000026990	THO complex 3 [Source:MGI Symbol;Acc:MGI:1920916]		Q8VE80	-0.7	9.2E-02	-0.2	6.9E-01	0.4	2.5E-01	-0.1	8.4E-01
ENSMUST00000027112	neuropilin 2 [Source:MGI Symbol;Acc:MGI:1100492]		O35375	5.7	3.0E-02	-5.9	5.6E-04	-0.5	3.0E-01	-0.4	7.7E-01
ENSMUST00000026993	tetraspanin 17 [Source:MGI Symbol;Acc:MGI:1921507]	Q3TAQ3		-1.3	9.2E-02	0.9	3.3E-01	0.8	2.7E-01	-1.5	1.1E-01
ENSMUST00000027121	raftlin family member 2 [Source:MGI Symbol;Acc:MGI:1921263]		Q8CHX7	2.6	5.0E-03	5.7	4.5E-02	-0.7	7.9E-01	-0.6	7.3E-01
ENSMUST00000027123	heat shock protein 1 (chaperonin) [Source:MGI Symbol;Acc:MGI:96242]		P63038	-3.0	3.7E-04	-4.7	4.4E-03	-0.6	3.0E-01	-2.0	2.0E-01
ENSMUST00000026999	SMAD family member 7 [Source:MGI Symbol;Acc:MGI:1100518]	B2RPW6	O35253	-0.4	6.5E-01	-0.2	8.9E-01	0.8	3.0E-01	0.6	5.6E-01
ENSMUST00000027127	splicing factor 3b, subunit 1 [Source:MGI Symbol;Acc:MGI:1932339]	G5E866		-6.7	3.6E-05	-9.0	2.2E-03	0.6	3.4E-01	-0.9	7.2E-01
ENSMUST00000027137	solute carrier family 40 (iron-regulated transporter), member 1 [Source:MGI Symbol;Acc:MGI:1315204]		Q9JHI9	-7.6	1.1E-05	-5.0	4.5E-03	0.0	9.6E-01	-1.0	4.9E-01
ENSMUST00000027144	carbamoyl-phosphate synthetase 1 [Source:MGI Symbol;Acc:MGI:891996]		Q8C196	6.4	1.5E-04	6.5	3.5E-02	-0.8	7.8E-01	-0.6	7.2E-01
ENSMUST00000027146	IKAROS family zinc finger 2 [Source:MGI Symbol;Acc:MGI:1342541]		P81183	3.2	2.3E-03	-3.2	2.8E-03	-0.7	1.6E-01	-0.8	3.6E-01
ENSMUST00000027153	acyl-Coenzyme A dehydrogenase, long-chain [Source:MGI Symbol;Acc:MGI:87866]			-6.2	2.1E-06	7.2	6.9E-05	-0.5	6.4E-01	-0.8	2.0E-01
ENSMUST00000027157	ribulose-5-phosphate-3-epimerase [Source:MGI Symbol;Acc:MGI:1913896]		Q8VEE0	-6.4	2.0E-04	-2.5	1.3E-02	0.2	6.0E-01	0.4	6.3E-01
ENSMUST00000027040	RB1-inducible coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1341850]		Q9ESK9	-1.4	1.6E-01	-0.8	4.5E-01	-0.8	3.2E-01	-1.4	2.0E-01
ENSMUST00000027165	CD28 antigen [Source:MGI Symbol;Acc:MGI:88327]		P31041	2.6	1.8E-02	-7.0	5.6E-04	-0.9	7.8E-02	-0.1	9.7E-01
ENSMUST00000027053	retinol dehydrogenase 10 (all-trans) [Source:MGI Symbol;Acc:MGI:1924238]		Q8VCH7	-1.0	1.1E-01	-0.6	4.0E-01	0.7	2.0E-01	0.3	6.7E-01
ENSMUST00000027173	WD repeat domain 12 [Source:MGI Symbol;Acc:MGI:1927241]	Q4V9X1	Q9JJA4	4.4	5.9E-05	3.8	8.2E-03	-1.5	2.1E-01	-1.1	2.3E-01
ENSMUST00000027174	NOP58 ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1933184]	A0A0A0MQ76		-4.7	6.7E-04	7.8	2.6E-03	3.2	1.0E-01	0.1	8.8E-01
ENSMUST00000027186	trafficking protein, kinesin binding 2 [Source:MGI Symbol;Acc:MGI:1918077]	Q6P9N8		-4.4	1.6E-06	-5.4	1.7E-03	0.0	9.8E-01	-0.9	5.1E-01
ENSMUST00000027189	caspase 8 [Source:MGI Symbol;Acc:MGI:1261423]	Q3U607	O89110	1.8	1.2E-02	8.1	3.2E-04	0.3	8.1E-01	0.9	2.0E-01
ENSMUST00000027193	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 [Source:MGI Symbol;Acc:MGI:1913745]		Q9CQZ6	-4.5	7.0E-05	3.9	9.7E-02	-0.7	7.6E-01	2.1	1.6E-01
ENSMUST00000027217	RIKEN cDNA 1500015O10 gene [Source:MGI Symbol;Acc:MGI:1926146]		Q99LS0	5.1	1.2E-03	3.3	6.4E-02	-1.7	3.4E-01	0.4	7.2E-01
ENSMUST00000027231	solute carrier family 9 (sodium/hydrogen exchanger), member 2 [Source:MGI Symbol;Acc:MGI:105075]	Q3ZAS0		7.3	1.9E-05	3.9	2.1E-02	-1.3	3.9E-01	-1.6	1.8E-01
ENSMUST00000027232	protein tyrosine phosphatase 4a1 [Source:MGI Symbol;Acc:MGI:1277096]	B9EKL6	Q63739	-4.4	3.2E-05	5.4	1.5E-02	-2.6	2.3E-01	-1.7	1.9E-01
ENSMUST00000027233	solute carrier family 9 (sodium/hydrogen exchanger), member 4 [Source:MGI Symbol;Acc:MGI:105074]		Q8BUE1	6.3	1.0E-04	-2.8	6.8E-03	1.1	3.6E-02	-0.4	6.2E-01
ENSMUST00000027237	interleukin 18 receptor accessory protein [Source:MGI Symbol;Acc:MGI:1338888]	Q0VBK3	Q9Z2B1	-6.4	8.7E-06	3.5	1.9E-03	-0.8	3.1E-01	0.1	8.2E-01
ENSMUST00000027241	interleukin 1 receptor, type I [Source:MGI Symbol;Acc:MGI:96545]	Q32MH0	P13504	5.9	3.8E-04	6.4	4.6E-04	-0.6	6.4E-01	0.4	5.7E-01
ENSMUST00000027243	interleukin 1 receptor, type II [Source:MGI Symbol;Acc:MGI:96546]	Q4FK69	P27931	-10.7	5.9E-05	5.9	6.8E-03	-0.7	7.1E-01	-1.0	3.8E-01
ENSMUST00000027257	MIT, microtubule interacting and transport, domain containing 1 [Source:MGI Symbol;Acc:MGI:1916278]		Q8VDV8	-4.2	1.6E-03	6.6	4.9E-04	-0.6	6.5E-01	-0.3	7.2E-01
ENSMUST00000027263	serine/threonine kinase 17b (apoptosis-inducing) [Source:MGI Symbol;Acc:MGI:2138162]		Q8BG48	-8.1	5.0E-06	3.8	1.9E-03	0.4	6.6E-01	-1.3	7.5E-02
ENSMUST00000027264	asparagine synthetase domain containing 1 [Source:MGI Symbol;Acc:MGI:1917646]		Q8BFS9	-7.1	7.1E-06	-7.0	6.6E-04	0.3	4.6E-01	1.5	3.1E-01
ENSMUST00000027265	O-sialoglycoprotein endopeptidase-like 1 [Source:MGI Symbol;Acc:MGI:1919335]		Q6PEB4	-4.0	2.9E-03	2.0	4.5E-01	-2.3	3.6E-01	1.4	5.2E-01
ENSMUST00000027114	RIKEN cDNA 9430016H08 gene [Source:MGI Symbol;Acc:MGI:1915365]		Q8BHE8	-1.1	6.0E-02	0.8	2.4E-01	0.8	1.3E-01	-1.1	1.0E-01
ENSMUST00000027266	ORM1-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2181669]		Q921I0	-3.9	3.7E-05	3.2	2.9E-03	-0.3	6.9E-01	-0.9	1.8E-01
ENSMUST00000027122	MOB family member 4, phocein [Source:MGI Symbol;Acc:MGI:104899]	G8JL35		-2.9	2.3E-01	-3.5	2.2E-01	-1.5	3.3E-01	-0.9	7.7E-01
ENSMUST00000027271	inositol polyphosphate-1-phosphatase [Source:MGI Symbol;Acc:MGI:104848]		P49442	1.7	7.7E-03	-3.0	1.5E-03	-0.5	1.6E-01	-0.5	4.5E-01
ENSMUST00000027125	coenzyme Q10 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915126]			-2.0	6.3E-02	-2.1	1.4E-01	0.2	8.3E-01	0.3	7.9E-01
ENSMUST00000027279	nucleic acid binding protein 1 [Source:MGI Symbol;Acc:MGI:1923258]		Q8BGW5	-5.2	2.2E-02	-5.4	6.7E-04	0.4	4.6E-01	-1.0	4.2E-01
ENSMUST00000027131	solute carrier family 39 (zinc transporter), member 10 [Source:MGI Symbol;Acc:MGI:1914515]		Q6P5F6	-0.2	7.3E-01	-0.5	4.0E-01	-1.0	3.7E-02	-0.7	2.5E-01
ENSMUST00000027285	unc-50 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1914637]		Q9CQ61	-5.9	1.8E-05	-6.5	2.7E-04	1.1	3.6E-02	0.0	9.9E-01
ENSMUST00000027139	WD repeat domain 75 [Source:MGI Symbol;Acc:MGI:1920924]	Q3U821		0.6	4.8E-01	-3.4	1.6E-02	-2.3	7.8E-03	1.7	1.7E-01
ENSMUST00000027286	cytochrome C oxidase assembly factor 5 [Source:MGI Symbol;Acc:MGI:1923428]		Q99M07	-2.1	8.2E-04	3.8	3.1E-03	-3.4	1.1E-02	-0.7	2.7E-01
ENSMUST00000027287	inositol polyphosphate-4-phosphatase, type I [Source:MGI Symbol;Acc:MGI:1931123]	F6V2U0		-2.1	6.6E-03	3.2	1.0E-02	0.4	6.2E-01	0.5	5.5E-01
ENSMUST00000027288	cyclic nucleotide gated channel alpha 3 [Source:MGI Symbol;Acc:MGI:1341818]		Q9JJZ8	7.5	9.3E-06	-4.4	1.9E-04	1.4	2.7E-03	-0.4	6.5E-01
ENSMUST00000027289	von Willebrand factor A domain containing 3B [Source:MGI Symbol;Acc:MGI:1918103]	J9JI28		7.3	4.5E-05	-5.7	2.6E-03	0.3	6.5E-01	-0.4	8.0E-01
ENSMUST00000027290	transmembrane protein 131 [Source:MGI Symbol;Acc:MGI:1927110]		O70472	-5.3	1.1E-02	1.7	1.5E-01	-1.0	3.0E-01	-0.1	9.3E-01
ENSMUST00000027172	islet cell autoantigen 1-like [Source:MGI Symbol;Acc:MGI:1917625]		Q3TY65	2.5	1.0E-01	4.7	7.5E-03	-0.6	7.0E-01	-2.7	3.1E-02
ENSMUST00000027297	leckstrin homology domain containing, family B (evectins) member 2 [Source:MGI Symbol;Acc:MGI:2385825		Q9QZC7	-3.0	7.4E-04	3.8	7.1E-04	-0.2	7.6E-01	0.4	5.1E-01
ENSMUST00000027298	cripto, FRL-1, cryptic family 1 [Source:MGI Symbol;Acc:MGI:109448]		P97766	6.4	1.9E-04	-6.4	3.3E-04	-2.6	5.6E-04	-0.9	4.7E-01
ENSMUST00000027178	amyotrophic lateral sclerosis 2 (juvenile) [Source:MGI Symbol;Acc:MGI:1921268]		Q920R0	-1.2	1.2E-01	0.2	7.8E-01	0.1	8.6E-01	-1.3	1.5E-01
ENSMUST00000027185	STE20-related kinase adaptor beta [Source:MGI Symbol;Acc:MGI:2144047]		Q8K4T3	0.1	8.2E-01	3.7	3.5E-03	3.2	3.7E-03	-0.4	5.8E-01
ENSMUST00000027299	protease, serine 39 [Source:MGI Symbol;Acc:MGI:1270856]		O70169	7.1	5.4E-05	-3.0	2.8E-04	1.4	7.7E-04	-0.1	9.0E-01
ENSMUST00000027302	protein tyrosine phosphatase, non-receptor type 18 [Source:MGI Symbol;Acc:MGI:108410]		Q61152	-4.3	2.6E-03	0.5	4.0E-01	-1.7	1.0E-02	-0.4	4.8E-01
ENSMUST00000027322	rhomboid domain containing 1 [Source:MGI Symbol;Acc:MGI:1924117]		Q8BHC7	-1.9	1.9E-03	-3.7	8.5E-04	-1.0	4.1E-02	-1.7	5.9E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000027198	origin recognition complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1328306]	Q543F8	Q60862	0.2	7.7E-01	-0.5	6.1E-01	0.1	8.6E-01	0.8	3.7E-01
ENSMUST00000027202	shugoshin-like 2a (S. pombe) [Source:MGI Symbol;Acc:MGI:1098767]		Q7TSY8	0.7	3.2E-01	0.2	8.0E-01	0.1	8.9E-01	0.6	4.9E-01
ENSMUST00000027214	repair cross-complementing rodent repair deficiency, complementation group 5 [Source:MGI Symbol;Acc:MGI	E9QM61		-3.2	6.3E-02	-2.4	1.9E-01	-0.4	7.2E-01	-1.2	5.3E-01
ENSMUST00000027337	family with sequence similarity 135, member A [Source:MGI Symbol;Acc:MGI:1915437]		Q6NS59	7.6	7.6E-05	3.1	1.1E-02	-2.2	7.2E-02	-0.2	7.6E-01
ENSMUST00000027338	succinate dehydrogenase complex assembly factor 4 [Source:MGI Symbol;Acc:MGI:1915252]		Q8BTE0	-2.3	7.5E-03	7.9	5.8E-05	0.5	6.9E-01	-0.2	7.4E-01
ENSMUST00000027339	small ArfGAP 1 [Source:MGI Symbol;Acc:MGI:2138261]		Q91VZ6	-5.6	1.4E-03	-2.9	2.3E-03	0.7	8.9E-02	-0.7	3.5E-01
ENSMUST00000027343	opioid growth factor receptor-like 1 [Source:MGI Symbol;Acc:MGI:1917405]		Q8VE52	-4.9	3.6E-06	4.3	7.7E-04	-2.2	4.6E-02	-0.2	8.0E-01
ENSMUST00000027357	ring finger protein 25 [Source:MGI Symbol;Acc:MGI:1890215]		Q9QZR0	-4.9	4.5E-03	-5.9	9.1E-05	-0.2	6.5E-01	-0.7	4.7E-01
ENSMUST00000027366	villin 1 [Source:MGI Symbol;Acc:MGI:98930]		Q62468	5.9	7.3E-05	3.7	5.9E-03	-3.1	1.8E-02	-1.0	2.6E-01
ENSMUST00000027367	oxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1 [Source:MGI Symbol;Acc:MGI	Q5I0X8	P58466	-6.7	6.8E-04	-9.3	1.1E-04	-1.2	5.0E-02	-2.6	1.8E-01
ENSMUST00000027247	phosducin-like 3 [Source:MGI Symbol;Acc:MGI:1916083]		Q8BVF2	-0.5	4.3E-01	-1.1	1.5E-01	-1.0	6.5E-02	-0.4	6.0E-01
ENSMUST00000027251	REV1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1929074]		Q920Q2	-1.1	9.1E-02	-2.7	2.0E-02	-0.1	9.2E-01	1.5	1.4E-01
ENSMUST00000027252	eukaryotic translation initiation factor 5B [Source:MGI Symbol;Acc:MGI:2441772]		Q05D44	-0.8	2.8E-01	-1.5	1.5E-01	-0.7	2.7E-01	-0.1	9.3E-01
ENSMUST00000027256	mitochondrial ribosomal protein L30 [Source:MGI Symbol;Acc:MGI:1333820]		Q9D7N6	-1.3	1.2E-01	-4.5	6.7E-03	-1.5	4.4E-02	1.8	1.9E-01
ENSMUST00000027368	arrier family 11 (proton-coupled divalent metal ion transporters), member 1 [Source:MGI Symbol;Acc:MGI:13		P41251	-5.6	8.0E-04	-6.2	2.7E-03	-0.9	1.4E-01	1.1	5.1E-01
ENSMUST00000027372	chemokine (C-X-C motif) receptor 2 [Source:MGI Symbol;Acc:MGI:105303]		P35343	-7.8	8.1E-04	-8.1	3.1E-05	-0.6	1.8E-01	-0.6	6.0E-01
ENSMUST00000027377	insulin-like growth factor binding protein 5 [Source:MGI Symbol;Acc:MGI:96440]	Q3UQV0	Q07079	9.7	1.3E-06	-6.6	7.8E-05	0.4	3.1E-01	0.0	9.6E-01
ENSMUST00000027380	transmembrane protein 169 [Source:MGI Symbol;Acc:MGI:2442781]		Q8BG50	5.3	4.0E-04	-3.8	2.5E-02	0.6	4.1E-01	0.4	8.0E-01
ENSMUST00000027393	BRCA1 associated RING domain 1 [Source:MGI Symbol;Acc:MGI:1328361]		O70445	3.4	3.8E-04	-2.6	2.7E-03	0.5	1.8E-01	-0.9	2.2E-01
ENSMUST00000027394	zinc finger, AN1 type domain 2B [Source:MGI Symbol;Acc:MGI:1916068]		Q91X58	-5.4	4.0E-04	2.3	9.9E-03	1.2	7.6E-02	0.6	3.3E-01
ENSMUST00000027277	signal transducer and activator of transcription 4 [Source:MGI Symbol;Acc:MGI:103062]	Q3V157		2.8	7.6E-02	-0.1	9.2E-01	-2.6	7.8E-02	0.4	8.0E-01
ENSMUST00000027404	protein tyrosine phosphatase, receptor type, N [Source:MGI Symbol;Acc:MGI:102765]	A6MDD2		6.4	2.1E-05	-3.7	9.4E-02	0.1	9.1E-01	-1.3	5.8E-01
ENSMUST00000027405	solute carrier family 23 (nucleobase transporters), member 3 [Source:MGI Symbol;Acc:MGI:104516]			2.6	1.1E-02	-5.5	2.7E-04	0.3	4.6E-01	-0.2	8.5E-01
ENSMUST00000027409	desmin [Source:MGI Symbol;Acc:MGI:94885]	Q3V1K9	P31001	8.7	5.2E-06	-1.9	1.1E-02	0.6	1.1E-01	0.4	5.1E-01
ENSMUST00000027422	olute carrier family 16 (monocarboxylic acid transporters), member 14 [Source:MGI Symbol;Acc:MGI:191903		Q8K1C7	2.9	3.9E-04	-0.9	3.0E-01	1.3	4.3E-02	0.0	1.0E+00
ENSMUST00000027425	integral membrane protein 2C [Source:MGI Symbol;Acc:MGI:1927594]		Q91VK4	-3.1	2.8E-03	7.2	3.2E-05	-0.4	6.8E-01	-0.1	8.8E-01
ENSMUST00000027431	5-hydroxytryptamine (serotonin) receptor 2B [Source:MGI Symbol;Acc:MGI:109323]		Q02152	6.0	1.6E-03	7.1	1.2E-04	-0.6	6.0E-01	-0.4	5.4E-01
ENSMUST00000027432	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 [Source:MGI Symbol;Acc:MGI:1917497]		Q3TXS7	-3.6	3.2E-03	-4.0	7.5E-02	1.2	2.8E-01	0.0	1.0E+00
ENSMUST00000027291	zeta-chain (TCR) associated protein kinase [Source:MGI Symbol;Acc:MGI:99613]		P43404	2.1	5.2E-02	2.2	8.0E-02	0.1	9.1E-01	0.0	9.7E-01
ENSMUST00000027434	armadillo repeat containing 9 [Source:MGI Symbol;Acc:MGI:1926045]		Q9D2I5	6.7	2.3E-04	-2.1	2.8E-02	1.1	4.3E-02	0.2	8.2E-01
ENSMUST00000027440	neuromedin U receptor 1 [Source:MGI Symbol;Acc:MGI:1341898]	G5E871		6.2	4.7E-04	6.4	3.5E-04	-0.6	6.2E-01	-0.6	3.6E-01
ENSMUST00000027444	phosphodiesterase 6D, cGMP-specific, rod, delta [Source:MGI Symbol;Acc:MGI:1270843]	Q3TDQ8	O55057	-3.9	2.0E-04	7.0	1.3E-04	-0.6	6.1E-01	-0.4	5.0E-01
ENSMUST00000027446	constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13		Q8BV13	-5.7	5.0E-05	-3.1	3.3E-02	-0.4	6.1E-01	-1.6	2.7E-01
ENSMUST00000027303	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast) [Source:MGI Symbol;Acc:MGI:106572]		Q8VHZ7	-0.3	5.4E-01	0.0	9.6E-01	0.0	9.6E-01	-0.3	6.8E-01
ENSMUST00000027312	DNA primase, p58 subunit [Source:MGI Symbol;Acc:MGI:97758]		P33610	-1.3	1.1E-01	-2.9	1.9E-02	-0.5	4.2E-01	1.1	3.0E-01
ENSMUST00000027315	zinc finger protein 142 [Source:MGI Symbol;Acc:MGI:1924514]	G5E869		1.2	1.2E-01	1.6	1.1E-01	0.3	6.5E-01	-0.1	8.7E-01
ENSMUST00000027449	natriuretic peptide type C [Source:MGI Symbol;Acc:MGI:97369]	Q544K5	Q61839	6.5	7.3E-05	-5.7	3.2E-04	0.5	1.7E-01	4.3	1.8E-03
ENSMUST00000027451	Eph receptor A4 [Source:MGI Symbol;Acc:MGI:98277]		Q03137	7.3	7.2E-04	5.0	1.1E-03	-3.6	1.4E-02	-1.0	1.8E-01
ENSMUST00000027455	alkaline phosphatase, placental-like 2 [Source:MGI Symbol;Acc:MGI:108009]		P24823	7.7	1.4E-03	-2.4	1.1E-02	-1.2	5.7E-02	-1.0	2.2E-01
ENSMUST00000027470	cholinergic receptor, nicotinic, gamma polypeptide [Source:MGI Symbol;Acc:MGI:87895]	F8VQK4		7.3	5.5E-05	-1.9	1.6E-01	1.8	4.8E-02	-2.0	2.0E-01
ENSMUST00000027475	GRB10 interacting GYF protein 2 [Source:MGI Symbol;Acc:MGI:2138584]		Q6Y7W8	-6.7	9.8E-05	-4.4	7.3E-05	0.5	1.2E-01	0.0	9.6E-01
ENSMUST00000027356	cytochrome P450, family 27, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88594]		Q9DBG1	1.2	2.9E-01	0.7	5.7E-01	-1.1	3.0E-01	-0.6	5.9E-01
ENSMUST00000027487	arginyl aminopeptidase (aminopeptidase B)-like 1 [Source:MGI Symbol;Acc:MGI:1914170]	G5E872		-6.3	8.7E-04	-6.3	2.3E-02	0.4	6.0E-01	1.8	4.7E-01
ENSMUST00000027358	BCS1-like (yeast) [Source:MGI Symbol;Acc:MGI:1914071]		Q9CZP5	0.6	5.0E-01	3.0	3.5E-02	1.5	1.9E-01	-0.9	3.2E-01
ENSMUST00000027491	alanine-glyoxylate aminotransferase [Source:MGI Symbol;Acc:MGI:1329033]		O35423	7.0	1.3E-04	8.0	1.7E-04	1.6	2.2E-01	-0.4	5.0E-01
ENSMUST00000027492	mitochondrial transcription termination factor 4 [Source:MGI Symbol;Acc:MGI:1918355]		Q8BVN4	-3.7	1.7E-03	-3.9	1.9E-02	1.1	1.7E-01	-1.7	3.1E-01
ENSMUST00000027493	PAS domain containing serine/threonine kinase [Source:MGI Symbol;Acc:MGI:2155936]		Q8CEE6	3.7	8.2E-05	-5.4	5.9E-03	0.8	2.9E-01	0.6	7.3E-01
ENSMUST00000027370	paroxysmal nonkinesiogenic dyskinesia [Source:MGI Symbol;Acc:MGI:1930773]		Q69ZP3	2.9	2.7E-01	-0.6	8.6E-01	-3.1	2.7E-01	0.4	8.9E-01
ENSMUST00000027494	protein phosphatase 1, regulatory (inhibitor) subunit 7 [Source:MGI Symbol;Acc:MGI:1913635]		Q3UM45	2.2	5.5E-05	-5.0	2.8E-02	1.7	5.1E-02	-1.2	6.0E-01
ENSMUST00000027373	protein phosphatase 1F (PP2C domain containing) [Source:MGI Symbol;Acc:MGI:1918464]		Q8CGA0	0.9	9.3E-02	1.1	1.2E-01	0.4	4.0E-01	0.2	7.0E-01
ENSMUST00000027498	serine/threonine kinase 25 (yeast) [Source:MGI Symbol;Acc:MGI:1891699]		Q9Z2W1	2.9	5.6E-03	3.4	1.8E-04	-6.4	3.0E-05	-0.1	8.0E-01
ENSMUST00000027379	(-ray repair complementing defective repair in Chinese hamster cells 5 [Source:MGI Symbol;Acc:MGI:104517		P27641	0.3	5.3E-01	-0.6	3.0E-01	-1.5	8.7E-03	-0.5	3.7E-01
ENSMUST00000027502	autophagy related 4B, cysteine peptidase [Source:MGI Symbol;Acc:MGI:1913865]			-1.9	4.7E-03	6.9	3.3E-04	0.8	5.3E-01	-0.8	2.6E-01
ENSMUST00000027384	midazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Source:MGI Symbol;Acc:MGI:		Q9CWJ9	0.8	2.4E-01	-0.2	7.9E-01	-0.5	4.2E-01	0.5	5.3E-01
ENSMUST00000027503	deoxythymidylate kinase [Source:MGI Symbol;Acc:MGI:108396]		P97930	-3.3	1.1E-03	5.3	3.9E-04	1.8	7.2E-02	-0.1	8.5E-01
ENSMUST00000027505	inhibitor of growth family, member 5 [Source:MGI Symbol;Acc:MGI:1922816]		Q9D8Y8	-4.7	1.0E-02	-3.2	3.2E-02	1.5	4.3E-02	-0.7	6.0E-01
ENSMUST00000027396	ATP-binding cassette, sub-family B (MDR/TAP), member 6 [Source:MGI Symbol;Acc:MGI:1921354]		Q9DC29	0.2	8.5E-01	-0.8	5.1E-01	0.9	3.1E-01	2.0	1.1E-01
ENSMUST00000027507	programmed cell death 1 [Source:MGI Symbol;Acc:MGI:104879]	Q544F3	Q02242	6.1	3.2E-04	5.2	6.5E-05	-2.1	2.6E-02	-0.9	9.6E-02
ENSMUST00000027512	autophagy related 16-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924290]		Q8C0J2	-4.5	2.2E-03	3.0	1.3E-02	0.3	7.6E-01	-0.1	9.1E-01
ENSMUST00000027517	diacylglycerol kinase, delta [Source:MGI Symbol;Acc:MGI:2138334]	E9PUQ8		-2.6	1.8E-03	5.9	3.0E-05	-2.8	1.4E-02	-0.1	8.4E-01
ENSMUST00000027414	serine/threonine kinase 11 interacting protein [Source:MGI Symbol;Acc:MGI:1918978]		Q3TAA7	0.2	8.1E-01	1.0	3.2E-01	-0.5	5.1E-01	-1.3	1.7E-01
ENSMUST00000027421	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]		G5E870	-2.3	1.4E-01	1.7	5.5E-01	5.2	3.3E-02	1.2	5.8E-01
ENSMUST00000027521	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:2653690]		Q8BXK8	3.1	1.3E-04	3.1	1.2E-03	0.4	4.4E-01	0.2	6.7E-01
ENSMUST00000027528	melanophilin [Source:MGI Symbol;Acc:MGI:2176380]			7.5	6.8E-06	-2.4	2.8E-02	0.2	7.2E-01	-0.5	6.1E-01
ENSMUST00000027529	RAB17, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:104640]	Q0PD39	P35292	6.2	1.4E-02	4.9	1.3E-02	-0.2	9.2E-01	0.9	3.6E-01
ENSMUST00000027533	kelch-like 30 [Source:MGI Symbol;Acc:MGI:1918038]		Q8C3F7	6.1	1.9E-05	-4.4	6.3E-03	0.0	9.4E-01	0.7	5.9E-01
ENSMUST00000027534	integrin-linked kinase-associated serine/threonine phosphatase 2C [Source:MGI Symbol;Acc:MGI:1914694]		Q8R0F6	-6.1	7.2E-05	6.6	4.1E-04	-0.6	6.2E-01	-0.6	4.0E-01
ENSMUST00000027438	nucleolin [Source:MGI Symbol;Acc:MGI:97286]		P09405	0.5	2.4E-01	0.7	1.7E-01	-0.2	6.2E-01	-0.4	3.7E-01
ENSMUST00000027538	ankyrin repeat and SOCS box-containing 1 [Source:MGI Symbol;Acc:MGI:1929735]	A0A0A0MQ78		1.6	3.1E-03	5.0	3.6E-03	-1.0	5.0E-01	0.2	8.0E-01
ENSMUST00000027554	ceroid-lipofuscinosis, neuronal 8 [Source:MGI Symbol;Acc:MGI:1349447]	Q542J5	Q9QUK3	2.7	5.2E-05	-2.4	1.1E-02	1.1	3.7E-02	-0.4	6.5E-01
ENSMUST00000027559	mor necrosis factor receptor superfamily, member 11a, NFKB activator [Source:MGI Symbol;Acc:MGI:131489		O35305	6.1	1.1E-05	-2.6	2.8E-02	2.3	1.6E-03	-0.7	5.0E-01
ENSMUST00000027560	5 hydroxytryptamine (serotonin) receptor 4 [Source:MGI Symbol;Acc:MGI:109246]		P97288	7.9	1.7E-05	5.7	3.5E-04	-0.6	6.2E-01	0.2	7.3E-01
ENSMUST00000027564	rine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 13 [Source:MGI Symbol;Acc:MGI:304225		Q8CDC0	8.7	2.5E-05	5.4	8.5E-03	-0.6	7.3E-01	1.3	1.9E-01
ENSMUST00000027565	serine (or cysteine) peptidase inhibitor, clade B, member 3C [Source:MGI Symbol;Acc:MGI:1277952]	A2RSF9		5.8	6.3E-04	5.4	1.9E-02	-0.6	7.8E-01	1.7	1.6E-01
ENSMUST00000027464	mitochondrial ribosomal protein L44 [Source:MGI Symbol;Acc:MGI:1916413]		Q9CY73	-1.2	4.9E-02	0.2	7.9E-01	1.0	7.1E-02	-0.4	5.6E-01
ENSMUST00000027467	serine (or cysteine) peptidase inhibitor, clade E, member 2 [Source:MGI Symbol;Acc:MGI:101780]	Q543R5	Q07235	-0.4	5.3E-01	-1.5	8.5E-02	-1.7	1.8E-02	-0.6	4.5E-01
ENSMUST00000027569	solute carrier organic anion transporter family, member 6c1 [Source:MGI Symbol;Acc:MGI:1921691]	Q8C0X7		4.7	1.2E-04	7.1	1.6E-04	-0.2	8.7E-01	0.0	9.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000027472	EF hand domain containing 1 [Source:MGI Symbol;Acc:MGI:1921607]		Q9D4J1	4.0	8.3E-02	6.5	2.4E-02	0.1	9.7E-01	-2.4	1.2E-01
ENSMUST00000027580	solute carrier family 35, member F5 [Source:MGI Symbol;Acc:MGI:1921400]		Q8R314	-3.5	2.7E-04	-3.8	3.3E-03	0.5	2.8E-01	-2.4	7.4E-02
ENSMUST00000027477	neuronal guanine nucleotide exchange factor [Source:MGI Symbol;Acc:MGI:1858414]		Q8CHT1	0.1	9.0E-01	2.3	5.0E-02	-0.3	7.3E-01	-2.5	3.6E-02
ENSMUST00000027478	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Source:MGI Symbol;Acc:MGI:1914523]		Q99LC3	-0.8	2.7E-01	-0.1	9.3E-01	0.7	3.3E-01	-0.1	9.5E-01
ENSMUST00000027581	G protein-coupled receptor 39 [Source:MGI Symbol;Acc:MGI:1918361]	A0A0B4J1E4		7.2	7.9E-05	-5.0	1.8E-02	1.4	6.1E-02	0.1	9.5E-01
ENSMUST00000027488	calpain 10 [Source:MGI Symbol;Acc:MGI:1344392]		Q9ESK3	-0.8	2.2E-01	1.4	1.0E-01	1.0	1.3E-01	-1.2	1.2E-01
ENSMUST00000027489	G protein-coupled receptor 35 [Source:MGI Symbol;Acc:MGI:1929509]	A0A0A0MQ77		-1.2	3.8E-01	-2.1	3.0E-01	0.7	5.4E-01	1.6	3.9E-01
ENSMUST00000027592	UBX domain protein 4 [Source:MGI Symbol;Acc:MGI:1915062]			-1.8	1.1E-02	6.5	4.3E-04	-0.6	6.5E-01	-0.1	9.1E-01
ENSMUST00000027601	omosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1	Q542I2	P97311	-5.2	1.4E-04	-3.6	1.2E-02	-0.2	7.7E-01	-0.3	7.8E-01
ENSMUST00000027602	aspartyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:2442544]		Q922B2	-5.3	2.6E-05	4.3	1.9E-04	0.8	2.2E-01	0.3	6.2E-01
ENSMUST00000027603	regulator of G-protein signaling 18 [Source:MGI Symbol;Acc:MGI:1927498]	Q544K2	Q99PG4	-7.0	3.0E-05	2.0	3.9E-04	-0.2	4.5E-01	0.0	9.1E-01
ENSMUST00000027495	septin 2 [Source:MGI Symbol;Acc:MGI:97298]		P42208	-0.3	7.7E-01	-1.5	2.7E-01	-0.5	5.9E-01	0.8	5.6E-01
ENSMUST00000027606	regulator of G-protein signaling 2 [Source:MGI Symbol;Acc:MGI:1098271]	A0A087WPY2		-8.5	2.2E-05	2.3	4.0E-02	-0.7	4.2E-01	0.0	9.7E-01
ENSMUST00000027499	BCL2-related ovarian killer [Source:MGI Symbol;Acc:MGI:1858494]	Q3TH93	O35425	4.3	4.1E-02	-0.2	8.8E-01	-5.4	1.1E-02	-0.8	5.7E-01
ENSMUST00000027626	nucleolar protein interacting with the FHA domain of MKI67 [Source:MGI Symbol;Acc:MGI:1915199]		Q91VE6	-1.7	8.3E-03	-0.9	1.8E-01	0.8	9.9E-02	-0.2	8.0E-01
ENSMUST00000027629	transcription factor CP2-like 1 [Source:MGI Symbol;Acc:MGI:2444691]		Q3UNW5	7.9	8.6E-06	-2.9	5.9E-03	-0.7	2.2E-01	-1.1	2.4E-01
ENSMUST00000027634	diazepam binding inhibitor [Source:MGI Symbol;Acc:MGI:94865]	Q548W7	P31786	-7.6	2.8E-04	-3.4	9.1E-02	0.8	4.0E-01	-0.5	8.1E-01
ENSMUST00000027639	macrophage receptor with collagenous structure [Source:MGI Symbol;Acc:MGI:1309998]	A2RT24	Q60754	7.4	4.9E-05	1.9	9.5E-02	-4.4	2.5E-03	-0.2	8.5E-01
ENSMUST00000027642	NIMA (never in mitosis gene a)-related expressed kinase 7 [Source:MGI Symbol;Acc:MGI:1890645]	Q3TN15		-3.8	2.9E-02	-5.4	3.5E-03	-0.4	4.8E-01	0.6	7.1E-01
ENSMUST00000027649	nuclear receptor subfamily 5, group A, member 2 [Source:MGI Symbol;Acc:MGI:1346834]		P45448	7.5	3.8E-05	-0.9	2.2E-01	0.9	9.5E-02	-0.8	3.2E-01
ENSMUST00000027650	CD55 molecule, decay accelerating factor for complement [Source:MGI Symbol;Acc:MGI:104850]		Q61475	-1.4	2.6E-02	3.7	3.1E-04	0.6	3.3E-01	0.0	9.7E-01
ENSMUST00000027667	plakophilin 1 [Source:MGI Symbol;Acc:MGI:1328359]		P97350	8.9	1.9E-05	8.1	1.8E-05	0.3	7.4E-01	-0.2	6.7E-01
ENSMUST00000027670	Fc receptor, IgA, IgM, high affinity [Source:MGI Symbol;Acc:MGI:1927803]		Q2TB54	6.0	2.9E-02	7.3	9.0E-03	-0.8	7.6E-01	-1.9	1.7E-01
ENSMUST00000027532	selenocysteine lyase [Source:MGI Symbol;Acc:MGI:1355310]			0.0	9.4E-01	0.0	9.9E-01	0.2	8.0E-01	0.2	7.9E-01
ENSMUST00000027673	interleukin 20 [Source:MGI Symbol;Acc:MGI:1890473]	Q2NKI0	Q9JKV9	7.0	3.5E-03	7.2	5.0E-05	0.4	7.0E-01	-0.7	1.8E-01
ENSMUST00000027675	polymeric immunoglobulin receptor [Source:MGI Symbol;Acc:MGI:103080]		O70570	7.4	3.1E-05	-6.1	9.0E-04	0.5	2.9E-01	0.6	6.8E-01
ENSMUST00000027677	cysteine and glycine-rich protein 1 [Source:MGI Symbol;Acc:MGI:88549]	Q4FJX4	P97315	-3.9	2.4E-03	1.7	8.7E-03	0.4	4.0E-01	0.2	6.5E-01
ENSMUST00000027682	G protein-coupled receptor 37-like 1 [Source:MGI Symbol;Acc:MGI:1928503]		Q99JG2	8.5	2.7E-05	2.5	4.2E-04	-0.2	6.1E-01	0.0	9.7E-01
ENSMUST00000027684	ADP-ribosylation factor-like 8A [Source:MGI Symbol;Acc:MGI:1915974]		Q8VEH3	-5.0	7.5E-05	5.1	2.0E-04	-0.1	8.6E-01	0.9	1.3E-01
ENSMUST00000027690	arginine vasopressin receptor 1B [Source:MGI Symbol;Acc:MGI:1347010]		Q9WU02	7.0	2.0E-05	6.5	9.3E-05	-1.5	2.0E-01	-0.1	8.4E-01
ENSMUST00000027693	RAB29, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2385107]	E9QLQ7		-6.0	2.8E-04	6.5	3.3E-04	-1.5	2.6E-01	0.8	2.5E-01
ENSMUST00000027695	solute carrier family 45, member 3 [Source:MGI Symbol;Acc:MGI:1922082]		Q8K0H7	7.8	8.2E-05	6.3	6.5E-04	-0.5	7.1E-01	-1.0	1.9E-01
ENSMUST00000027697	cyclin-dependent kinase 18 [Source:MGI Symbol;Acc:MGI:97518]	Q0VDL6	Q04899	4.1	9.9E-05	6.5	6.3E-05	1.5	1.3E-01	-0.4	5.0E-01
ENSMUST00000027579	ARP3 actin-related protein 3 [Source:MGI Symbol;Acc:MGI:1921367]	Q3ULF7	Q99JY9	-3.8	1.1E-01	1.7	7.1E-01	6.7	5.9E-02	1.2	7.4E-01
ENSMUST00000027700	retinoblastoma binding protein 5 [Source:MGI Symbol;Acc:MGI:1918367]		Q8BX09	-4.4	2.9E-03	-2.6	7.3E-03	0.6	1.6E-01	-0.2	7.7E-01
ENSMUST00000027706	leucine rich repeat protein 2, neuronal [Source:MGI Symbol;Acc:MGI:106037]	Q6PHP6		8.0	9.5E-06	2.5	8.6E-03	-5.3	5.8E-04	-0.6	3.7E-01
ENSMUST00000027587	cyclin T2 [Source:MGI Symbol;Acc:MGI:1920199]	Q7TQK0		-4.2	5.8E-02	0.7	7.1E-01	1.1	4.8E-01	-3.8	8.0E-02
ENSMUST00000027719	RIKEN cDNA 2010107G23 gene [Source:MGI Symbol;Acc:MGI:1917144]	F8WHN9		8.2	6.1E-05	-1.7	4.2E-02	0.2	6.7E-01	0.1	8.5E-01
ENSMUST00000027725	kelch-like 12 [Source:MGI Symbol;Acc:MGI:2385619]		Q8BZM0	-3.6	3.7E-03	-4.3	1.5E-03	0.2	6.2E-01	-0.7	5.4E-01
ENSMUST00000027727	adiponectin receptor 1 [Source:MGI Symbol;Acc:MGI:1919924]	Q53YY4	Q91VH1	-5.6	1.2E-04	-3.4	9.0E-04	-0.4	4.0E-01	-2.3	1.5E-02
ENSMUST00000027730	myogenin [Source:MGI Symbol;Acc:MGI:97276]		P12979	7.5	7.0E-05	-4.3	1.4E-03	0.5	3.0E-01	-2.1	7.4E-02
ENSMUST00000027736	zinc finger CCCH type containing 11A [Source:MGI Symbol;Acc:MGI:1917829]	Q3UL31	Q6NZF1	-4.4	1.4E-03	-9.7	1.5E-04	-0.5	2.0E-01	0.7	6.7E-01
ENSMUST00000027623	translin [Source:MGI Symbol;Acc:MGI:109263]	Q545E6	Q62348	0.9	8.9E-02	1.3	7.1E-02	0.0	9.6E-01	-0.3	5.4E-01
ENSMUST00000027740	LIM homeobox protein 4 [Source:MGI Symbol;Acc:MGI:101776]		P53776	9.9	4.1E-05	-2.3	5.3E-03	-1.0	3.8E-02	-0.4	5.2E-01
ENSMUST00000027741	xenotropic and polytropic retrovirus receptor 1 [Source:MGI Symbol;Acc:MGI:97932]		Q9Z0U0	-2.3	5.5E-03	7.3	1.3E-04	-0.7	5.5E-01	-0.1	8.4E-01
ENSMUST00000027743	syntaxin 6 [Source:MGI Symbol;Acc:MGI:1926235]		Q9JKK1	-1.9	1.0E-02	-9.1	2.3E-03	-0.7	2.6E-01	0.7	7.5E-01
ENSMUST00000027748	regulator of G-protein signaling 16 [Source:MGI Symbol;Acc:MGI:108407]	Q542U0	P97428	5.5	1.7E-04	1.2	1.1E-01	-6.0	1.6E-04	0.1	8.3E-01
ENSMUST00000027752	laminin, gamma 1 [Source:MGI Symbol;Acc:MGI:99914]	F8VQJ3		1.3	9.7E-03	-3.2	1.2E-01	0.6	6.0E-01	-0.1	9.8E-01
ENSMUST00000027754	neutrophil cytosolic factor 2 [Source:MGI Symbol;Acc:MGI:97284]		O70145	-12.8	8.1E-08	7.2	1.1E-04	-0.6	6.1E-01	-0.3	6.0E-01
ENSMUST00000027760	ral guanine nucleotide dissociation stimulator,-like 1 [Source:MGI Symbol;Acc:MGI:107484]		Q60695	5.5	3.0E-04	-1.8	4.1E-02	0.7	1.9E-01	1.0	2.0E-01
ENSMUST00000027655	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59 [Source:MGI Symbol;Acc:MGI:1915247]		Q9DBN9	-0.3	5.8E-01	-1.6	3.2E-02	-0.7	1.4E-01	0.6	3.5E-01
ENSMUST00000027764	RIKEN cDNA A530064D06 gene [Source:MGI Symbol;Acc:MGI:2443476]	Q8C239		-4.2	8.7E-03	8.6	4.9E-05	-0.6	6.3E-01	-0.3	5.6E-01
ENSMUST00000027768	AT hook containing transcription factor 1 [Source:MGI Symbol;Acc:MGI:1915033]		Q8CJF7	-3.1	2.1E-04	6.0	2.9E-02	-1.4	5.9E-01	-1.5	3.4E-01
ENSMUST00000027671	troponin T2, cardiac [Source:MGI Symbol;Acc:MGI:104597]		P50752	3.1	7.7E-02	5.5	4.9E-03	-1.4	4.0E-01	-3.9	6.5E-03
ENSMUST00000027778	Mix1 homeobox-like 1 (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1351322]		Q9WUI0	8.1	2.3E-05	5.5	2.2E-02	-0.8	7.2E-01	0.7	5.6E-01
ENSMUST00000027780	acyl-Coenzyme A binding domain containing 3 [Source:MGI Symbol;Acc:MGI:2181074]			-3.4	7.7E-04	6.0	2.5E-04	-1.3	2.7E-01	0.1	8.3E-01
ENSMUST00000027781	COX20 Cox2 chaperone [Source:MGI Symbol;Acc:MGI:1913609]		Q9D7J4	-4.6	3.0E-04	-1.0	3.1E-01	0.3	5.9E-01	-2.6	3.8E-02
ENSMUST00000027783	desumoylating isopeptidase 2 [Source:MGI Symbol;Acc:MGI:1926075]		Q9D291	2.7	9.1E-04	8.3	6.7E-05	-0.7	6.0E-01	-0.5	4.5E-01
ENSMUST00000027785	serologically defined colon cancer antigen 8 [Source:MGI Symbol;Acc:MGI:1924066]		Q80UF4	-6.6	3.0E-04	-4.2	1.3E-03	0.9	8.3E-02	0.1	9.6E-01
ENSMUST00000027687	ubiquitin-conjugating enzyme E2T (putative) [Source:MGI Symbol;Acc:MGI:1914446]		Q9CQ37	-1.6	1.8E-01	0.2	8.9E-01	-0.2	8.5E-01	-1.9	1.3E-01
ENSMUST00000027792	signal recognition particle 9 [Source:MGI Symbol;Acc:MGI:1350930]	Q5EAT0	P49962	-5.0	1.2E-04	8.5	2.4E-05	0.8	5.1E-01	-0.7	1.6E-01
ENSMUST00000027795	cornichon homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1920228]		Q6ZWS4	10.0	2.0E-05	-3.5	4.1E-03	0.0	9.6E-01	-2.5	5.3E-02
ENSMUST00000027797	nuclear VCP-like [Source:MGI Symbol;Acc:MGI:1914709]		Q9DBY8	3.8	1.4E-06	7.3	2.9E-04	-0.6	6.7E-01	-0.1	8.9E-01
ENSMUST00000027800	transmembrane protein 63a [Source:MGI Symbol;Acc:MGI:2384789]		Q91YT8	-1.5	1.1E-02	5.0	1.0E-04	0.8	2.5E-01	-0.1	8.1E-01
ENSMUST00000027802	pyrroline-5-carboxylate reductase family, member 2 [Source:MGI Symbol;Acc:MGI:1277956]	Q3TMZ1	Q922Q4	-4.8	2.2E-03	-4.8	1.6E-02	0.3	6.3E-01	0.7	6.8E-01
ENSMUST00000027809	opsin 3 [Source:MGI Symbol;Acc:MGI:1338022]		Q9WUK7	2.4	1.4E-02	7.1	4.0E-05	-1.0	3.3E-01	-0.1	8.8E-01
ENSMUST00000027810	fumarate hydratase 1 [Source:MGI Symbol;Acc:MGI:95530]		P97807	2.3	6.9E-03	6.9	2.4E-04	-1.4	2.9E-01	-0.1	8.7E-01
ENSMUST00000027817	spectrin alpha, erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98385]		P08032	6.4	2.6E-04	-4.2	6.3E-03	-1.1	7.5E-02	-0.6	6.6E-01
ENSMUST00000027726	cytochrome b5 reductase 1 [Source:MGI Symbol;Acc:MGI:1919267]		Q9DB73	-2.4	8.0E-02	-4.2	8.2E-02	2.0	1.1E-01	3.9	9.3E-02
ENSMUST00000027826	dual specificity phosphatase 23 [Source:MGI Symbol;Acc:MGI:1915690]		Q6NT99	3.5	9.5E-04	-3.6	8.0E-03	1.3	5.0E-02	-0.7	5.2E-01
ENSMUST00000027830	SLAM family member 9 [Source:MGI Symbol;Acc:MGI:1923692]			1.6	3.2E-02	7.2	1.9E-04	-0.7	6.1E-01	-0.3	6.1E-01
ENSMUST00000027833	coatomer protein complex subunit alpha [Source:MGI Symbol;Acc:MGI:1334462]	F8WHL2		-9.2	2.6E-05	-3.1	2.2E-02	-0.3	6.0E-01	-1.6	2.2E-01
ENSMUST00000027738	torsin A interacting protein 1 [Source:MGI Symbol;Acc:MGI:3582693]		Q921T2	0.5	7.8E-01	-4.2	4.3E-02	-4.9	7.5E-03	-0.2	9.0E-01
ENSMUST00000027837	vang-like 2 (van gogh, Drosophila) [Source:MGI Symbol;Acc:MGI:2135272]		Q91ZD4	6.2	4.8E-04	9.3	1.9E-04	-0.2	9.2E-01	0.4	5.1E-01
ENSMUST00000027843	flavin containing monooxygenase 9 [Source:MGI Symbol;Acc:MGI:3606068]	Q8C116		5.4	2.4E-02	-1.4	1.4E-01	1.1	6.4E-02	0.2	8.1E-01
ENSMUST00000027846	transcriptional adaptor 1 [Source:MGI Symbol;Acc:MGI:1196415]		Q99LM9	-5.3	2.7E-04	-1.4	1.2E-01	1.0	7.9E-02	0.5	5.5E-01
ENSMUST00000027852	adenylate cyclase 10 [Source:MGI Symbol;Acc:MGI:2660854]		Q8C0T9	3.9	2.3E-02	4.3	4.0E-04	-2.2	3.2E-02	-1.0	1.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000027853	mitochondrial pyruvate carrier 2 [Source:MGI Symbol;Acc:MGI:1917706]		Q9D023	-6.0	1.6E-04	0.8	1.2E-01	-1.2	8.2E-03	-0.7	1.2E-01
ENSMUST00000027753	laminin, gamma 2 [Source:MGI Symbol;Acc:MGI:99913]	G5E874		3.3	4.3E-02	7.4	3.5E-04	-0.5	7.3E-01	-4.6	1.0E-03
ENSMUST00000027856	DDB1 and CUL4 associated factor 6 [Source:MGI Symbol;Acc:MGI:1921356]		Q9DC22	-2.2	1.2E-03	-10.5	3.8E-07	0.3	2.5E-01	-2.0	6.4E-02
ENSMUST00000027859	T-box 19 [Source:MGI Symbol;Acc:MGI:1891158]		Q99ME7	7.8	1.5E-05	1.8	9.4E-02	-3.1	9.4E-03	0.6	4.5E-01
ENSMUST00000027861	dermatopontin [Source:MGI Symbol;Acc:MGI:1928392]		Q9QZZ6	6.2	8.6E-05	-1.1	4.1E-01	0.2	8.0E-01	-2.8	9.1E-02
ENSMUST00000027766	aarF domain containing kinase 3 [Source:MGI Symbol;Acc:MGI:1914676]		Q60936	-2.5	5.0E-01	2.4	5.5E-01	1.5	6.4E-01	-3.4	3.9E-01
ENSMUST00000027871	selectin, lymphocyte [Source:MGI Symbol;Acc:MGI:98279]	Q3UV83	P18337	-13.0	7.3E-07	-1.9	1.7E-02	0.8	6.0E-02	-0.4	5.8E-01
ENSMUST00000027769	transcription factor B2, mitochondrial [Source:MGI Symbol;Acc:MGI:107937]	B2RSE6	Q3TL26	0.0	9.5E-01	1.6	1.6E-02	0.0	9.9E-01	-1.6	1.3E-02
ENSMUST00000027775	EF-hand calcium binding domain 2 [Source:MGI Symbol;Acc:MGI:1915476]		Q9CQ46	0.3	6.2E-01	0.3	6.6E-01	-0.6	2.1E-01	-0.7	3.0E-01
ENSMUST00000027777	poly (ADP-ribose) polymerase family, member 1 [Source:MGI Symbol;Acc:MGI:1340806]	Q921K2		0.0	9.7E-01	-0.1	8.7E-01	-0.3	5.9E-01	-0.2	8.0E-01
ENSMUST00000027874	selectin, endothelial cell [Source:MGI Symbol;Acc:MGI:98278]	Q3U5F6		2.3	2.8E-03	7.1	1.2E-04	-0.6	6.3E-01	0.4	5.2E-01
ENSMUST00000027876	SCY1-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1921385]		Q9DBQ7	-3.8	3.6E-03	-3.1	7.0E-03	0.8	1.5E-01	0.5	6.0E-01
ENSMUST00000027878	paired related homeobox 1 [Source:MGI Symbol;Acc:MGI:97712]		P63013	9.8	1.9E-06	-4.1	2.9E-03	0.3	5.9E-01	-0.3	8.2E-01
ENSMUST00000027885	angiopoietin-like 1 [Source:MGI Symbol;Acc:MGI:1919963]		Q640P2	8.7	7.7E-06	3.2	1.5E-03	0.6	3.8E-01	0.0	9.4E-01
ENSMUST00000027896	nephrosis 2, podocin [Source:MGI Symbol;Acc:MGI:2157018]	C0LL94	Q91X05	5.3	1.6E-03	-4.2	6.4E-03	0.3	5.8E-01	-2.1	1.7E-01
ENSMUST00000027906	estrogen-related receptor gamma [Source:MGI Symbol;Acc:MGI:1347056]		P62509	7.3	4.7E-05	-4.2	1.3E-03	0.0	9.5E-01	-0.9	3.7E-01
ENSMUST00000027916	bisphosphate 3'-nucleotidase 1 [Source:MGI Symbol;Acc:MGI:1338800]		Q9Z0S1	5.1	4.2E-05	8.6	7.2E-05	-0.8	5.7E-01	0.6	3.5E-01
ENSMUST00000027929	MAP/microtubule affinity regulating kinase 1 [Source:MGI Symbol;Acc:MGI:2664902]		Q8VHJ5	7.5	2.7E-05	4.0	3.9E-06	-0.1	8.4E-01	-0.2	4.2E-01
ENSMUST00000027931	NIMA (never in mitosis gene a)-related expressed kinase 2 [Source:MGI Symbol;Acc:MGI:109359]		O35942	2.0	1.3E-03	-1.2	1.2E-01	1.0	4.6E-02	0.6	3.8E-01
ENSMUST00000027933	denticleless homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1924093]		Q3TLR7	3.8	1.2E-02	-3.4	2.4E-02	0.6	3.9E-01	-0.8	5.9E-01
ENSMUST00000027940	transmembrane protein 206 [Source:MGI Symbol;Acc:MGI:1914200]		Q9D771	2.8	4.5E-04	2.7	1.3E-02	-0.6	5.0E-01	-0.9	2.5E-01
ENSMUST00000027952	plexin A2 [Source:MGI Symbol;Acc:MGI:107684]		P70207	9.1	3.3E-06	1.0	2.1E-01	-1.5	4.3E-02	-0.2	8.0E-01
ENSMUST00000027956	suppressor of variegation 3-9 homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1890396]			3.6	7.9E-04	2.8	2.0E-02	-3.9	6.4E-03	-0.3	6.8E-01
ENSMUST00000027961	heat shock protein 14 [Source:MGI Symbol;Acc:MGI:1354164]		Q99M31	-6.7	3.0E-05	2.9	8.3E-03	-0.2	8.4E-01	0.5	5.2E-01
ENSMUST00000027965	family with sequence similarity 107, member B [Source:MGI Symbol;Acc:MGI:1913790]		Q3TGF2	-5.8	3.3E-05	-1.5	3.3E-02	-4.6	2.0E-05	-1.5	4.1E-02
ENSMUST00000027974	activating transcription factor 6 [Source:MGI Symbol;Acc:MGI:1926157]		F6VAN0	-1.8	2.9E-03	-4.4	1.6E-03	0.9	9.8E-02	-4.0	1.3E-02
ENSMUST00000027975	phytanoyl-CoA hydroxylase [Source:MGI Symbol;Acc:MGI:891978]	Q3TPC7	O35386	-6.0	1.6E-05	5.4	2.7E-03	-0.2	9.0E-01	0.6	5.2E-01
ENSMUST00000027986	optineurin [Source:MGI Symbol;Acc:MGI:1918898]		Q8K3K8	-5.0	1.4E-03	5.1	4.5E-02	-0.4	8.6E-01	-0.2	9.1E-01
ENSMUST00000027988	coiled-coil domain containing 3 [Source:MGI Symbol;Acc:MGI:1921436]		Q9D6Y1	8.4	3.4E-05	-3.4	1.1E-02	0.6	3.5E-01	-1.4	2.5E-01
ENSMUST00000027989	hydroxysteroid (17-beta) dehydrogenase 7 [Source:MGI Symbol;Acc:MGI:1330808]		O88736	1.2	1.6E-02	4.9	6.2E-03	-1.6	3.1E-01	-2.6	2.7E-02
ENSMUST00000027997	regulator of G-protein signaling 5 [Source:MGI Symbol;Acc:MGI:1098434]		O08850	7.1	3.1E-05	-7.1	6.0E-04	-0.1	7.6E-01	0.9	5.5E-01
ENSMUST00000028000	UF2, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191422		Q99P69	-6.1	1.1E-04	-1.1	1.2E-01	0.8	5.7E-02	-0.3	5.9E-01
ENSMUST00000028003	LIM homeobox transcription factor 1 alpha [Source:MGI Symbol;Acc:MGI:1888519]	Q543W2	Q9JKU8	7.1	2.2E-04	7.8	3.0E-05	-0.6	6.1E-01	-0.6	2.5E-01
ENSMUST00000028017	methyltransferase like 13 [Source:MGI Symbol;Acc:MGI:1918699]		Q91YR5	2.3	6.6E-03	5.3	1.5E-04	-2.1	5.4E-02	-1.2	6.0E-02
ENSMUST00000027863	ATPase, Na+/K+ transporting, beta 1 polypeptide [Source:MGI Symbol;Acc:MGI:88108]	Q545P0	P14094	0.6	3.8E-01	0.6	5.3E-01	-0.1	9.2E-01	0.0	9.9E-01
ENSMUST00000027866	basic leucine zipper nuclear factor 1 [Source:MGI Symbol;Acc:MGI:1201607]		Q8R2X8	1.0	1.6E-01	1.5	9.2E-02	0.3	6.7E-01	-0.2	7.6E-01
ENSMUST00000027867	coiled-coil domain containing 181 [Source:MGI Symbol;Acc:MGI:1922145]		Q80ZU5	-0.7	2.1E-01	-1.4	7.7E-02	-0.7	1.8E-01	-0.1	9.3E-01
ENSMUST00000028020	myocilin [Source:MGI Symbol;Acc:MGI:1202864]	Q05AC1	O70624	5.8	9.7E-04	-11.6	1.5E-05	0.4	2.4E-01	-1.0	5.1E-01
ENSMUST00000028021	phosphatidylinositol glycan anchor biosynthesis, class C [Source:MGI Symbol;Acc:MGI:1914542]		Q9CXR4	-6.6	2.8E-04	1.5	3.5E-02	-1.5	2.5E-02	-0.7	2.5E-01
ENSMUST00000028024	tumor necrosis factor (ligand) superfamily, member 4 [Source:MGI Symbol;Acc:MGI:104511]	B6DXE3	P43488	6.6	2.2E-04	-4.5	2.2E-02	1.6	5.2E-02	2.3	1.9E-01
ENSMUST00000027877	kinesin-associated protein 3 [Source:MGI Symbol;Acc:MGI:107566]		P70188	0.8	4.2E-01	-0.1	9.3E-01	0.2	8.5E-01	1.1	3.5E-01
ENSMUST00000028035	centromere protein L [Source:MGI Symbol;Acc:MGI:1917704]		Q3U3S3	8.5	2.9E-03	6.8	7.0E-06	-3.4	5.5E-03	-0.4	3.6E-01
ENSMUST00000028045	mannose receptor, C type 1 [Source:MGI Symbol;Acc:MGI:97142]	Q2HZ94	Q61830	1.8	2.5E-02	6.4	6.0E-05	-2.3	5.2E-02	-0.1	9.1E-01
ENSMUST00000027888	bl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene) [Source:MGI Symbol;Acc:MGI:878	F8VQH0		2.0	1.4E-01	1.3	4.7E-01	0.1	9.4E-01	0.8	5.9E-01
ENSMUST00000028049	RAB GTPase activating protein 1-like [Source:MGI Symbol;Acc:MGI:1352507]		A6H6A9	-2.8	4.3E-03	6.0	1.8E-03	0.7	6.1E-01	-0.8	3.2E-01
ENSMUST00000028059	Ras suppressor protein 1 [Source:MGI Symbol;Acc:MGI:103040]	Q9D031		-7.6	2.3E-07	6.3	1.9E-03	0.7	6.6E-01	-0.4	6.6E-01
ENSMUST00000027897	SET and MYND domain containing 2 [Source:MGI Symbol;Acc:MGI:1915889]		Q8R5A0	-2.2	4.3E-02	-1.5	7.4E-02	-2.4	3.6E-03	-3.1	1.1E-02
ENSMUST00000028062	vimentin [Source:MGI Symbol;Acc:MGI:98932]	Q5FWJ3	P20152	-6.4	1.2E-05	6.8	1.6E-04	-0.6	5.9E-01	-0.2	7.8E-01
ENSMUST00000028080	nebulette [Source:MGI Symbol;Acc:MGI:1921353]		Q9DC07	6.8	3.6E-04	4.5	5.9E-04	0.3	7.1E-01	0.9	1.5E-01
ENSMUST00000027921	isoleucine-tRNA synthetase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1919586]		Q8BIJ6	-2.1	4.3E-02	-4.5	8.5E-03	0.1	8.8E-01	2.5	9.6E-02
ENSMUST00000028081	plexin domain containing 2 [Source:MGI Symbol;Acc:MGI:1914698]		Q9DC11	4.8	1.5E-04	7.0	6.2E-05	-1.3	2.7E-01	-0.7	1.9E-01
ENSMUST00000028083	proteasome (prosome, macropain) subunit, beta type 7 [Source:MGI Symbol;Acc:MGI:107637]		P70195	-6.6	7.5E-07	0.9	1.3E-01	-0.5	2.5E-01	0.6	2.6E-01
ENSMUST00000028084	nuclear receptor subfamily 5, group A, member 1 [Source:MGI Symbol;Acc:MGI:1346833]		P33242	6.3	3.2E-04	-0.4	8.1E-01	0.1	9.3E-01	4.3	2.3E-02
ENSMUST00000028087	protein phosphatase 6, catalytic subunit [Source:MGI Symbol;Acc:MGI:1915107]		Q9CQR6	-4.6	1.6E-05	2.3	3.7E-03	-0.7	2.2E-01	-0.2	6.8E-01
ENSMUST00000027941	activating transcription factor 3 [Source:MGI Symbol;Acc:MGI:109384]	Q4FJW1	Q60765	-1.7	2.1E-01	0.2	9.0E-01	1.1	4.8E-01	-0.9	5.8E-01
ENSMUST00000027945	TatD DNase domain containing 3 [Source:MGI Symbol;Acc:MGI:1916222]	D3YXH9		-2.4	1.9E-01	-1.8	2.7E-01	-1.9	1.3E-01	-2.5	1.9E-01
ENSMUST00000027947	angel homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1196310]		Q8K1C0	-1.4	3.7E-01	2.4	3.6E-01	3.1	1.9E-01	-0.8	6.7E-01
ENSMUST00000028098	origin recognition complex, subunit 4 [Source:MGI Symbol;Acc:MGI:1347043]		O88708	-2.3	7.0E-03	8.4	1.0E-05	-0.9	4.1E-01	-0.3	5.1E-01
ENSMUST00000028100	enhancer of polycomb homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1278322]		Q8C9X6	-5.1	9.0E-03	3.0	6.1E-03	-0.5	5.4E-01	0.1	8.7E-01
ENSMUST00000028102	kinesin family member 5C [Source:MGI Symbol;Acc:MGI:1098269]		P28738	6.1	1.6E-05	-4.6	2.1E-04	0.0	9.8E-01	-2.1	5.8E-02
ENSMUST00000028105	family with sequence similarity 188, member A [Source:MGI Symbol;Acc:MGI:1914210]		Q9CV28	-7.2	3.3E-05	-5.2	7.3E-04	1.2	2.8E-02	0.6	5.8E-01
ENSMUST00000027966	Fc receptor, IgG, low affinity IIb [Source:MGI Symbol;Acc:MGI:95499]	A0A0B4J1E6		0.7	2.3E-01	0.6	3.9E-01	-0.2	6.7E-01	-0.1	8.7E-01
ENSMUST00000027973	selenophosphate synthetase 1 [Source:MGI Symbol;Acc:MGI:1923580]		Q8BH69	0.9	1.3E-01	0.1	8.9E-01	-0.8	1.4E-01	0.0	9.9E-01
ENSMUST00000028106	integrin alpha 8 [Source:MGI Symbol;Acc:MGI:109442]		A2ARA8	7.1	1.3E-04	-0.8	1.7E-01	0.3	3.7E-01	-0.7	2.4E-01
ENSMUST00000028110	speckle-type POZ protein-like [Source:MGI Symbol;Acc:MGI:1924107]	A0A0A6YWE7		-3.3	5.5E-03	-4.9	4.2E-04	0.5	2.8E-01	-0.7	4.9E-01
ENSMUST00000027979	U2AF homology motif (UHM) kinase 1 [Source:MGI Symbol;Acc:MGI:1341908]		P97343	0.5	8.5E-01	1.4	6.8E-01	2.2	3.5E-01	1.2	7.1E-01
ENSMUST00000027980	minichromosome maintenance deficient 10 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1917274]		Q0VBD2	-0.9	3.2E-01	-1.8	1.4E-01	-0.9	2.2E-01	-0.1	9.5E-01
ENSMUST00000028111	interleukin 2 receptor, alpha chain [Source:MGI Symbol;Acc:MGI:96549]	Q544I2	P01590	5.7	2.6E-05	-4.7	1.5E-02	0.9	2.0E-01	0.7	7.0E-01
ENSMUST00000028113	RIKEN cDNA 4931423N10 gene [Source:MGI Symbol;Acc:MGI:1918231]	Q9D4J9		5.4	2.3E-04	7.8	2.3E-04	0.0	9.9E-01	0.6	4.0E-01
ENSMUST00000028117	YME1-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1351651]		O88967	-4.9	5.2E-05	1.6	1.5E-02	0.7	1.5E-01	0.2	7.1E-01
ENSMUST00000027991	regulator of G-protein signaling 4 [Source:MGI Symbol;Acc:MGI:108409]	Q5D078		3.9	9.3E-02	5.7	3.7E-02	-0.2	9.3E-01	-2.0	1.8E-01
ENSMUST00000028119	microtubule associated serine/threonine kinase-like [Source:MGI Symbol;Acc:MGI:1914371]		Q8C0P0	2.5	5.2E-04	6.2	1.9E-04	-0.7	5.0E-01	0.2	6.8E-01
ENSMUST00000028123	glutamic acid decarboxylase 2 [Source:MGI Symbol;Acc:MGI:95634]	Q548L4	P48320	7.4	2.4E-06	-5.3	1.5E-03	0.0	9.6E-01	-0.8	5.4E-01
ENSMUST00000028129	solute carrier family 2, (facilitated glucose transporter), member 8 [Source:MGI Symbol;Acc:MGI:1860103]		Q9JIF3	-2.8	1.6E-02	8.9	6.7E-05	-0.4	7.5E-01	-2.2	6.7E-03
ENSMUST00000028004	aldehyde dehydrogenase 9, subfamily A1 [Source:MGI Symbol;Acc:MGI:1861622]	Q3U367		-0.5	4.7E-01	0.2	8.0E-01	0.7	2.9E-01	0.0	9.9E-01
ENSMUST00000028005	microsomal glutathione S-transferase 3 [Source:MGI Symbol;Acc:MGI:1913697]		Q9CPU4	-1.4	6.1E-02	-1.3	1.3E-01	-1.3	4.1E-02	-1.5	8.7E-02
ENSMUST00000028016	proline-rich coiled-coil 2C [Source:MGI Symbol;Acc:MGI:1913754]	A0A0A0MQ79		0.4	8.5E-01	0.4	9.0E-01	0.8	7.2E-01	0.8	8.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000028137	coenzyme Q4 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1098826]	B9EID1	Q8BGB8	-6.4	2.2E-05	3.4	1.7E-03	0.1	8.4E-01	-1.0	1.2E-01
ENSMUST00000028139	mediator complex subunit 27 [Source:MGI Symbol;Acc:MGI:1916225]		Q9DB40	-5.0	4.1E-04	5.1	5.8E-03	-1.3	3.8E-01	-0.6	5.1E-01
ENSMUST00000028151	dolichol-phosphate (beta-D) mannosyltransferase 2 [Source:MGI Symbol;Acc:MGI:1330238]	Q545R7	Q9Z324	-7.2	2.7E-05	-2.6	2.7E-02	1.2	6.2E-02	-2.8	5.5E-02
ENSMUST00000028161	carboxyl ester lipase [Source:MGI Symbol;Acc:MGI:88374]	Q3V2H7	Q64285	7.4	5.0E-05	2.8	1.3E-02	-3.1	1.7E-02	0.7	3.8E-01
ENSMUST00000028162	prostaglandin E synthase 2 [Source:MGI Symbol;Acc:MGI:1917592]		Q8BWM0	2.1	1.5E-03	7.7	8.3E-03	-0.7	7.9E-01	0.0	9.9E-01
ENSMUST00000028167	glycerol phosphate dehydrogenase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:99778]		Q64521	-4.6	1.9E-02	-4.1	3.0E-04	-5.9	3.3E-06	0.1	9.4E-01
ENSMUST00000028175	cytohesin 1 interacting protein [Source:MGI Symbol;Acc:MGI:2183535]		Q91VY6	-4.4	1.4E-06	-1.6	8.4E-02	0.0	1.0E+00	-1.2	2.1E-01
ENSMUST00000028050	ignal transducing adaptor molecule (SH3 domain and ITAM motif) 1 [Source:MGI Symbol;Acc:MGI:1329014	Q3UGN9		1.2	2.0E-01	4.3	1.1E-02	2.2	9.5E-02	-0.8	3.9E-01
ENSMUST00000028052	RAB GTPase activating protein 1-like [Source:MGI Symbol;Acc:MGI:1352507]		A6H6A9	-0.4	4.7E-01	-1.4	7.1E-02	-0.5	2.9E-01	0.5	5.0E-01
ENSMUST00000028178	activin A receptor, type IC [Source:MGI Symbol;Acc:MGI:2661081]		Q8K348	6.3	7.6E-05	-2.5	4.6E-02	-0.4	6.2E-01	-1.2	3.2E-01
ENSMUST00000028179	ficolin B [Source:MGI Symbol;Acc:MGI:1341158]		O70497	-4.5	1.3E-03	-8.7	7.5E-06	-0.4	1.3E-01	0.6	5.5E-01
ENSMUST00000028187	laminin gamma 3 [Source:MGI Symbol;Acc:MGI:1344394]		Q9R0B6	9.2	1.1E-05	-4.4	9.7E-04	1.6	5.9E-03	-0.4	6.5E-01
ENSMUST00000028076	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 [Source:MGI Symbol;Acc:		O54826	-1.0	3.9E-01	-4.6	1.1E-01	1.0	3.9E-01	4.6	9.1E-02
ENSMUST00000028188	fibrinogen C domain containing 1 [Source:MGI Symbol;Acc:MGI:2138953]		A2AV25	9.3	2.7E-06	5.4	1.9E-03	-1.1	4.1E-01	0.2	7.7E-01
ENSMUST00000028190	c-abl oncogene 1, non-receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:87859]		P00520	2.9	2.1E-04	2.2	2.1E-02	-2.7	6.7E-03	-0.1	9.1E-01
ENSMUST00000028199	torsin family 1, member B [Source:MGI Symbol;Acc:MGI:1353605]		Q9ER41	-5.5	9.0E-04	-5.3	1.3E-05	-0.9	1.6E-02	-2.1	1.1E-02
ENSMUST00000028200	torsin family 1, member A (torsin A) [Source:MGI Symbol;Acc:MGI:1353568]	Q3TV62	Q9ER39	-7.8	2.3E-05	7.4	3.0E-04	0.1	9.2E-01	-0.9	2.0E-01
ENSMUST00000028205	cDNA sequence BC005624 [Source:MGI Symbol;Acc:MGI:2385132]		Q3TQI7	-1.6	3.2E-03	-4.1	2.4E-04	0.4	3.1E-01	-0.1	8.4E-01
ENSMUST00000028207	carnitine acetyltransferase [Source:MGI Symbol;Acc:MGI:109501]		P47934	-4.2	1.8E-02	-1.9	5.1E-02	0.4	4.7E-01	0.0	1.0E+00
ENSMUST00000028214	SH3-domain GRB2-like endophilin B2 [Source:MGI Symbol;Acc:MGI:2385131]		Q8R3V5	-6.3	4.9E-04	-3.7	5.4E-02	0.3	7.1E-01	-1.1	5.8E-01
ENSMUST00000028222	heat shock protein 5 [Source:MGI Symbol;Acc:MGI:95835]		P20029	3.1	1.1E-03	5.4	7.9E-05	-0.4	6.4E-01	0.2	6.7E-01
ENSMUST00000028103	LY6/PLAUR domain containing 6B [Source:MGI Symbol;Acc:MGI:1919147]		Q9D7F2	0.8	3.0E-01	1.6	1.0E-01	0.5	4.7E-01	-0.3	7.0E-01
ENSMUST00000028223	kynureninase (L-kynurenine hydrolase) [Source:MGI Symbol;Acc:MGI:1918039]	A2ARD6		2.6	7.4E-04	-1.1	3.2E-01	3.6	6.0E-04	-2.5	4.9E-02
ENSMUST00000028225	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 [Source:MGI Symbol;Acc:MGI:1914248]		Q8BJY1	-6.0	1.3E-04	6.3	3.5E-04	-1.4	2.8E-01	-0.6	3.9E-01
ENSMUST00000028229	zinc finger E-box binding homeobox 2 [Source:MGI Symbol;Acc:MGI:1344407]			-6.9	4.8E-04	-3.5	1.5E-02	-0.2	6.9E-01	0.0	9.7E-01
ENSMUST00000028234	TNF receptor-associated factor 1 [Source:MGI Symbol;Acc:MGI:101836]		P39428	-3.1	4.6E-03	5.5	6.0E-05	-1.1	2.0E-01	-0.8	1.3E-01
ENSMUST00000028237	centriolin [Source:MGI Symbol;Acc:MGI:1889576]		A2AL36	-4.9	8.1E-03	3.9	4.0E-04	-3.1	6.4E-03	-1.6	2.8E-02
ENSMUST00000028114	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:MGI Symbol;Acc:MGI:2181202]	Q7TS91		3.9	2.4E-01	1.3	7.5E-01	-1.5	6.7E-01	1.0	7.5E-01
ENSMUST00000028238	RAB14, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1915615]	Q50HX4	Q91V41	-6.3	6.1E-05	-4.5	4.5E-04	0.0	9.1E-01	-0.3	7.5E-01
ENSMUST00000028118	protein kinase C, theta [Source:MGI Symbol;Acc:MGI:97601]	A6H667	Q02111	1.7	6.1E-02	1.5	1.2E-01	-0.7	3.6E-01	-0.6	4.8E-01
ENSMUST00000028239	gelsolin [Source:MGI Symbol;Acc:MGI:95851]		P13020	-6.1	1.1E-05	1.5	1.5E-02	-1.3	2.1E-02	-0.3	4.9E-01
ENSMUST00000028121	acyl-Coenzyme A binding domain containing 5 [Source:MGI Symbol;Acc:MGI:1921409]		Q5XG73	2.7	4.1E-01	-1.5	6.6E-01	-3.4	2.4E-01	0.8	8.2E-01
ENSMUST00000028241	stomatin [Source:MGI Symbol;Acc:MGI:95403]		P54116	-5.1	1.4E-06	6.9	6.1E-05	0.2	8.5E-01	0.6	2.1E-01
ENSMUST00000028125	zinc finger and BTB domain containing 43 [Source:MGI Symbol;Acc:MGI:1919084]		Q9DAI4	-1.6	4.1E-01	4.3	6.8E-02	3.1	9.6E-02	-2.8	2.0E-01
ENSMUST00000028251	RNA binding motif protein 18 [Source:MGI Symbol;Acc:MGI:1915139]		Q9CR83	-4.1	3.0E-05	-2.1	1.2E-01	0.2	8.1E-01	-0.6	6.5E-01
ENSMUST00000028132	leucine rich repeat and sterile alpha motif containing 1 [Source:MGI Symbol;Acc:MGI:2684789]		Q80ZI6	3.8	9.2E-02	2.4	3.4E-01	-1.1	6.3E-01	0.4	8.5E-01
ENSMUST00000028135	family with sequence similarity 129, member B [Source:MGI Symbol;Acc:MGI:2442910]		Q8R1F1	-1.1	4.2E-02	-0.7	2.9E-01	0.7	1.5E-01	0.3	6.8E-01
ENSMUST00000028252	growth factor receptor bound protein 14 [Source:MGI Symbol;Acc:MGI:1355324]	A2ASX2	Q9JLM9	4.4	3.5E-03	-3.5	6.8E-03	2.1	2.0E-03	-0.8	4.8E-01
ENSMUST00000028256	MORN repeat containing 5 [Source:MGI Symbol;Acc:MGI:1922745]		Q9DAI9	5.7	2.7E-04	-4.3	6.2E-03	0.7	2.1E-01	0.0	9.9E-01
ENSMUST00000028148	folylpolyglutamyl synthetase [Source:MGI Symbol;Acc:MGI:95576]		P48760	-1.8	3.4E-01	0.0	9.8E-01	0.0	9.9E-01	-1.7	3.9E-01
ENSMUST00000028257	grancalcin [Source:MGI Symbol;Acc:MGI:1918521]		Q8VC88	-2.4	6.9E-04	-6.6	4.2E-04	0.6	1.9E-01	0.0	9.7E-01
ENSMUST00000028155	tuberous sclerosis 1 [Source:MGI Symbol;Acc:MGI:1929183]		Q9EP53	-1.5	6.7E-01	-0.7	9.0E-01	1.0	7.8E-01	0.2	9.7E-01
ENSMUST00000028156	growth factor independent 1B [Source:MGI Symbol;Acc:MGI:1276578]		O70237	-0.8	5.1E-01	-2.5	2.3E-01	0.1	9.1E-01	1.8	3.4E-01
ENSMUST00000028157	general transcription factor IIIC, polypeptide 5 [Source:MGI Symbol;Acc:MGI:1917489]	Q3UI98	Q8R2T8	-1.1	3.5E-01	-3.8	1.3E-01	0.4	7.1E-01	3.1	1.9E-01
ENSMUST00000028160	e carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 [Source:MGI Symbol;Acc:MGI:1915		A2ASZ8	-1.6	5.8E-01	4.7	2.7E-01	4.3	2.7E-01	-2.0	4.9E-01
ENSMUST00000028278	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 [Source:MGI Symbol;Acc:MGI:1913284]		O35593	-4.1	1.3E-04	7.4	1.0E-04	-0.6	6.5E-01	-0.5	3.9E-01
ENSMUST00000028279	spermatid perinuclear RNA binding protein [Source:MGI Symbol;Acc:MGI:104626]		Q91WM1	5.6	5.6E-06	3.3	5.6E-04	1.2	5.1E-02	0.0	9.5E-01
ENSMUST00000028286	rol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) [Source:MGI Symbol;Acc:MC	Q059U0	Q8K3K7	-7.7	3.0E-05	-3.8	8.3E-02	0.9	4.3E-01	0.0	9.9E-01
ENSMUST00000028170	ral guanine nucleotide dissociation stimulator [Source:MGI Symbol;Acc:MGI:107485]		Q03385	-1.0	5.3E-01	-0.3	8.7E-01	-0.8	5.2E-01	-1.6	3.7E-01
ENSMUST00000028288	notch 1 [Source:MGI Symbol;Acc:MGI:97363]		Q01705	-2.5	1.8E-03	-4.3	9.6E-06	-0.3	2.3E-01	-0.5	3.7E-01
ENSMUST00000028177	olfactomedin 1 [Source:MGI Symbol;Acc:MGI:1860437]	Q8R357		0.7	8.1E-01	0.7	7.7E-01	-3.6	1.4E-01	-3.6	2.3E-01
ENSMUST00000028293	serologically defined colon cancer antigen 3 [Source:MGI Symbol;Acc:MGI:1915362]		A2AIW0	-6.2	1.5E-04	6.4	1.8E-04	-0.6	6.0E-01	-0.6	3.1E-01
ENSMUST00000028294	caspase recruitment domain family, member 9 [Source:MGI Symbol;Acc:MGI:2685628]		A2AIV8	-7.1	3.6E-04	-4.0	2.2E-02	1.3	8.6E-02	0.8	6.1E-01
ENSMUST00000028299	RIKEN cDNA 1700019N19 gene [Source:MGI Symbol;Acc:MGI:1914757]			5.8	2.3E-04	5.7	8.8E-05	-3.9	5.3E-03	-0.4	4.4E-01
ENSMUST00000028300	cleus accumbens associated 2, BEN and BTB (POZ) domain containing [Source:MGI Symbol;Acc:MGI:19152		Q9DCM7	3.7	5.4E-03	8.0	7.3E-06	-1.3	2.2E-01	0.0	9.7E-01
ENSMUST00000028304	lipocalin 3 [Source:MGI Symbol;Acc:MGI:102669]	Q14AJ3		6.4	2.5E-04	1.2	5.4E-02	-1.7	5.5E-03	0.1	9.1E-01
ENSMUST00000028307	ficolin A [Source:MGI Symbol;Acc:MGI:1340905]	Q4FJM1	O70165	4.3	9.0E-05	-3.3	1.1E-02	-0.2	7.7E-01	-2.4	9.7E-02
ENSMUST00000028309	coiled-coil domain containing 183 [Source:MGI Symbol;Acc:MGI:1924308]		A2AJB1	5.9	9.6E-03	-6.5	1.4E-04	0.1	7.9E-01	-1.2	3.4E-01
ENSMUST00000028320	nebulin [Source:MGI Symbol;Acc:MGI:97292]	A2AQB2		7.5	6.2E-04	-2.4	2.1E-03	-0.3	4.0E-01	0.4	4.4E-01
ENSMUST00000028328	ectonucleoside triphosphate diphosphohydrolase 2 [Source:MGI Symbol;Acc:MGI:1096863]	Q921R1	O55026	5.6	1.8E-02	-2.9	1.5E-01	1.0	3.5E-01	-0.3	9.0E-01
ENSMUST00000028209	dolichyl pyrophosphate phosphatase 1 [Source:MGI Symbol;Acc:MGI:1914093]		Q9JMF7	-1.9	1.4E-01	2.6	1.2E-01	2.4	1.0E-01	-2.2	1.2E-01
ENSMUST00000028329	suppressor APC domain containing 2 [Source:MGI Symbol;Acc:MGI:1919330]		Q9D818	3.2	1.7E-03	-2.1	2.4E-01	3.4	6.9E-03	-0.8	6.1E-01
ENSMUST00000028332	dipeptidylpeptidase 7 [Source:MGI Symbol;Acc:MGI:1933213]		Q9ET22	-2.9	9.1E-03	2.3	1.3E-02	-0.7	2.9E-01	0.0	9.6E-01
ENSMUST00000028336	ADP-ribosylation factor-like 6 interacting protein 6 [Source:MGI Symbol;Acc:MGI:1929507]		Q8BH07	-2.3	2.4E-02	3.1	6.2E-04	-0.1	8.5E-01	-0.6	2.1E-01
ENSMUST00000028224	GTPase activating protein and VPS9 domains 1 [Source:MGI Symbol;Acc:MGI:1913941]		Q6PAR5	-0.5	8.4E-01	1.3	7.0E-01	1.6	4.8E-01	-0.2	9.4E-01
ENSMUST00000028337	leucine rich repeat containing 26 [Source:MGI Symbol;Acc:MGI:2385129]		Q91W20	7.6	2.5E-05	-6.4	5.7E-04	-0.2	6.0E-01	0.2	9.1E-01
ENSMUST00000028340	transmembrane protein 210 [Source:MGI Symbol;Acc:MGI:1925467]		Q9D2F0	7.6	3.4E-04	-4.8	1.9E-02	1.6	4.5E-02	-0.4	8.2E-01
ENSMUST00000028232	PHD finger protein 19 [Source:MGI Symbol;Acc:MGI:1921266]		Q9CXG9	-0.9	4.7E-01	-3.0	2.3E-01	1.0	4.2E-01	3.1	2.0E-01
ENSMUST00000028233	hemolytic complement [Source:MGI Symbol;Acc:MGI:96031]		P06684	-0.1	7.9E-01	0.6	3.9E-01	0.6	2.6E-01	-0.2	8.2E-01
ENSMUST00000028341	anaphase promoting complex subunit 2 [Source:MGI Symbol;Acc:MGI:2139135]		Q8BZQ7	-3.5	3.6E-04	-2.8	2.2E-02	-0.4	5.3E-01	-0.6	5.9E-01
ENSMUST00000028342	Sjogren's syndrome nuclear autoantigen 1 [Source:MGI Symbol;Acc:MGI:1915725]		Q9JJ94	-8.2	6.2E-05	3.7	3.0E-01	9.9	8.8E-03	1.3	5.4E-01
ENSMUST00000028346	family with sequence similarity 166, member A [Source:MGI Symbol;Acc:MGI:3605773]		Q9D4K5	5.6	2.7E-03	-3.7	5.7E-03	1.3	3.5E-02	-1.3	2.7E-01
ENSMUST00000028347	RNA binding motif, single stranded interacting protein 1 [Source:MGI Symbol;Acc:MGI:1861774]		Q91W59	-5.1	8.7E-05	-4.8	3.9E-04	1.1	2.1E-02	-0.2	8.5E-01
ENSMUST00000028349	arrestin domain containing 1 [Source:MGI Symbol;Acc:MGI:2446136]		Q99KN1	-7.8	5.4E-04	-3.4	2.6E-04	1.6	5.4E-04	-0.1	8.4E-01
ENSMUST00000028250	mitochondrial ribosome recycling factor [Source:MGI Symbol;Acc:MGI:1915121]		Q9D6S7	0.4	3.8E-01	0.8	1.2E-01	-0.8	7.6E-02	-1.2	3.0E-02
ENSMUST00000028350	zinc finger, MYND domain containing 19 [Source:MGI Symbol;Acc:MGI:1914437]		Q9CQG3	2.5	6.9E-03	-4.5	1.5E-04	0.1	7.5E-01	0.5	4.6E-01
ENSMUST00000028355	paired box 8 [Source:MGI Symbol;Acc:MGI:97492]		Q00288	3.0	1.8E-02	5.8	1.6E-03	0.0	9.9E-01	-1.4	1.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000028360	interleukin 1 family, member 5 (delta) [Source:MGI Symbol;Acc:MGI:1859325]		Q9QYY1	6.6	3.0E-04	4.9	6.4E-04	-1.6	1.7E-01	-0.7	2.7E-01
ENSMUST00000028362	lymphocyte antigen 75 [Source:MGI Symbol;Acc:MGI:106662]		Q60767	-2.7	3.5E-02	-2.1	1.0E-02	0.8	6.4E-02	0.6	4.0E-01
ENSMUST00000028259	interferon induced with helicase C domain 1 [Source:MGI Symbol;Acc:MGI:1918836]	D2CGM4	Q8R5F7	-0.6	5.2E-01	1.0	4.1E-01	0.3	7.3E-01	-1.3	2.5E-01
ENSMUST00000028382	nucleoporin 35 [Source:MGI Symbol;Acc:MGI:1916732]		Q8R4R6	-5.0	9.5E-05	-4.0	8.2E-04	0.1	7.9E-01	0.0	1.0E+00
ENSMUST00000028384	dual specificity phosphatase 19 [Source:MGI Symbol;Acc:MGI:1915332]	Q99N12		3.8	6.4E-03	5.5	3.8E-05	0.3	6.5E-01	0.4	3.9E-01
ENSMUST00000028280	collagen, type V, alpha 1 [Source:MGI Symbol;Acc:MGI:88457]	B1AWB9	O88207	-0.2	6.1E-01	2.0	1.8E-03	2.3	2.0E-04	0.1	8.6E-01
ENSMUST00000028282	bromodomain containing 3 [Source:MGI Symbol;Acc:MGI:1914632]	Q3TUI3	Q8K2F0	2.1	3.7E-01	6.5	2.8E-02	1.8	4.7E-01	-2.6	2.2E-01
ENSMUST00000028386	NCK-associated protein 1 [Source:MGI Symbol;Acc:MGI:1355333]		P28660	3.1	7.3E-03	-6.0	3.0E-04	0.3	4.7E-01	-1.4	2.8E-01
ENSMUST00000028389	frizzled-related protein [Source:MGI Symbol;Acc:MGI:892032]		P97401	7.5	1.2E-04	-1.2	1.3E-01	1.1	4.4E-02	-0.2	8.2E-01
ENSMUST00000028291				4.6	4.9E-02	4.9	1.0E-01	0.0	9.9E-01	-0.3	8.7E-01
ENSMUST00000028392	DnaJ (Hsp40) homolog, subfamily C, member 10 [Source:MGI Symbol;Acc:MGI:1914111]		Q9DC23	-5.3	1.9E-05	2.1	2.6E-01	8.2	1.6E-04	-0.1	9.7E-01
ENSMUST00000028398	ubiquitin-conjugating enzyme E2E 3 [Source:MGI Symbol;Acc:MGI:107412]		P52483	-2.0	2.9E-02	-5.5	4.0E-03	0.5	4.2E-01	-1.1	5.1E-01
ENSMUST00000028295	DNL-type zinc finger [Source:MGI Symbol;Acc:MGI:106559]		Q9D113	-1.5	2.4E-01	-1.3	4.5E-01	0.5	6.4E-01	0.4	8.2E-01
ENSMUST00000028403	cytochrome b reductase 1 [Source:MGI Symbol;Acc:MGI:2654575]		Q925G2	6.9	1.3E-05	6.7	1.6E-04	-0.5	6.6E-01	-1.4	4.8E-02
ENSMUST00000028408	histone aminotransferase 1 [Source:MGI Symbol;Acc:MGI:96013]		Q8BY71	-4.6	2.0E-03	2.7	5.3E-02	-0.8	4.9E-01	0.2	8.4E-01
ENSMUST00000028410	xin actin-binding repeat containing 2 [Source:MGI Symbol;Acc:MGI:2685198]		Q4U4S6	8.8	4.5E-06	6.0	7.6E-04	-0.6	6.4E-01	-0.1	8.5E-01
ENSMUST00000028426	ceramide synthase 6 [Source:MGI Symbol;Acc:MGI:2442564]		Q8C172	-2.8	1.8E-03	-4.4	1.5E-05	-9.4	4.6E-08	-0.7	2.4E-01
ENSMUST00000028465	purinergic receptor P2X, ligand-gated ion channel, 3 [Source:MGI Symbol;Acc:MGI:1097160]		Q3UR32	6.4	1.5E-02	6.3	1.0E-02	-0.8	7.3E-01	-1.2	3.3E-01
ENSMUST00000028311	TNF receptor-associated factor 2 [Source:MGI Symbol;Acc:MGI:101835]	Q3U8L1	P39429	-1.5	5.5E-02	-1.5	1.2E-01	0.2	7.5E-01	0.2	7.9E-01
ENSMUST00000028314	N-myc (and STAT) interactor [Source:MGI Symbol;Acc:MGI:1928368]	Q3UJ82	O35309	-2.2	2.6E-01	-4.0	1.0E-01	-2.3	8.9E-02	-0.5	8.5E-01
ENSMUST00000028466	proteoglycan 3 [Source:MGI Symbol;Acc:MGI:1858200]		Q9JL95	3.9	3.0E-02	3.8	1.2E-02	-3.8	2.6E-02	-0.1	9.3E-01
ENSMUST00000028471	smoothelin-like 1 [Source:MGI Symbol;Acc:MGI:1915928]		Q99LM3	7.5	6.2E-05	6.5	1.1E-02	-0.7	7.4E-01	-1.6	2.5E-01
ENSMUST00000028475	CLP1, cleavage and polyadenylation factor I subunit [Source:MGI Symbol;Acc:MGI:2138968]		Q99LI9	-4.6	7.7E-04	3.8	1.7E-03	0.2	8.3E-01	-0.4	6.0E-01
ENSMUST00000028494	phosphatase, orphan 2 [Source:MGI Symbol;Acc:MGI:1920623]		Q9D9M5	-7.4	2.5E-05	-4.6	9.8E-03	-0.6	3.4E-01	1.1	4.6E-01
ENSMUST00000028509	golgi reassembly stacking protein 2 [Source:MGI Symbol;Acc:MGI:2135962]		Q99JX3	-7.2	6.6E-05	-2.0	1.1E-01	0.9	2.4E-01	0.6	6.1E-01
ENSMUST00000028515	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) [Source:MGI Symbol;Acc:MGI:87885]	Q05A24	P04756	7.3	8.8E-06	6.3	2.1E-04	-0.6	6.1E-01	0.7	2.4E-01
ENSMUST00000028525	Rap guanine nucleotide exchange factor (GEF) 4 [Source:MGI Symbol;Acc:MGI:1917723]	A2ASW8		6.9	1.8E-04	6.3	2.2E-03	-0.7	6.7E-01	0.6	5.0E-01
ENSMUST00000028533	follicle stimulating hormone beta [Source:MGI Symbol;Acc:MGI:95582]	A0A0F7RQR1	Q60687	5.7	3.7E-04	-2.2	2.4E-02	1.1	3.7E-02	-0.2	8.3E-01
ENSMUST00000028536	ADP-ribosylation factor-like 14 effector protein [Source:MGI Symbol;Acc:MGI:1926020]		Q8BIX3	-1.9	5.3E-03	-7.6	6.4E-04	-0.1	8.4E-01	-0.7	6.8E-01
ENSMUST00000028549	solute carrier family 12, member 6 [Source:MGI Symbol;Acc:MGI:2135960]		Q924N4	-9.7	7.0E-06	5.7	1.9E-02	1.2	5.5E-01	1.1	3.8E-01
ENSMUST00000028551	ER membrane protein complex subunit 4 [Source:MGI Symbol;Acc:MGI:1915282]		Q9CZX9	-3.4	6.4E-04	-4.2	1.6E-03	0.9	9.8E-02	0.0	9.8E-01
ENSMUST00000028552	katanin p80 subunit B like 1 [Source:MGI Symbol;Acc:MGI:1919675]		Q9CWJ3	-1.5	2.8E-02	-6.1	1.8E-03	1.2	9.4E-02	-0.5	7.6E-01
ENSMUST00000028553	NOP10 ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1913431]		Q9CQS2	-2.2	5.0E-03	3.5	3.8E-03	0.4	6.4E-01	-0.5	4.5E-01
ENSMUST00000028351	diphthamine biosynthesis 7 [Source:MGI Symbol;Acc:MGI:1914478]		Q9CYU6	0.6	7.8E-01	-0.7	8.0E-01	-1.5	4.7E-01	-0.2	9.3E-01
ENSMUST00000028554	lysophosphatidylcholine acyltransferase 4 [Source:MGI Symbol;Acc:MGI:2138993]		Q6NVG1	-2.9	1.3E-03	2.5	1.1E-01	0.7	5.6E-01	1.3	2.8E-01
ENSMUST00000028356	CD302 antigen [Source:MGI Symbol;Acc:MGI:1913455]		Q9DCG2	-1.6	5.0E-01	-3.3	1.4E-01	-3.1	5.8E-02	-1.3	6.0E-01
ENSMUST00000028583	lin-7 homolog C (C. elegans) [Source:MGI Symbol;Acc:MGI:1330839]		O88952	-4.0	7.0E-06	6.8	4.7E-04	-0.5	7.2E-01	-0.7	3.7E-01
ENSMUST00000028592	eukaryotic translation initiation factor 3, subunit M [Source:MGI Symbol;Acc:MGI:1351744]		Q99JX4	-4.7	3.2E-04	-3.2	1.3E-01	1.2	2.0E-01	1.7	4.0E-01
ENSMUST00000028368	WD repeat, SAM and U-box domain containing 1 [Source:MGI Symbol;Acc:MGI:1919387]		Q9D0I6	0.5	3.8E-01	1.0	2.0E-01	0.3	6.5E-01	-0.2	7.4E-01
ENSMUST00000028369	death associated protein-like 1 [Source:MGI Symbol;Acc:MGI:1923997]		Q9D757	-0.8	5.0E-01	-1.4	2.6E-01	-2.2	4.9E-02	-1.6	2.2E-01
ENSMUST00000028378	acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 [Source:MGI Symbol;Acc:MGI		P70419	-1.4	1.0E-01	-0.1	8.9E-01	1.0	2.2E-01	-0.3	7.6E-01
ENSMUST00000028593	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane) [Source:MGI Symbol;Acc:MGI:2442211]	Q4KL73	Q8BGN6	7.7	1.2E-04	-3.8	8.0E-04	-0.7	8.9E-02	-1.9	6.4E-02
ENSMUST00000028599	cleavage stimulation factor, 3' pre-RNA, subunit 3 [Source:MGI Symbol;Acc:MGI:1351825]		Q99LI7	-3.5	6.1E-04	1.0	3.5E-01	-2.2	6.0E-02	0.6	5.2E-01
ENSMUST00000028600	homeodomain interacting protein kinase 3 [Source:MGI Symbol;Acc:MGI:1314882]		Q9ERH7	-2.8	9.2E-04	-2.5	5.5E-02	-3.2	4.3E-03	2.5	5.0E-02
ENSMUST00000028608	N-acetyltransferase 10 [Source:MGI Symbol;Acc:MGI:2138939]		Q8K224	-4.4	6.8E-03	6.9	4.1E-04	-0.5	7.2E-01	0.1	8.9E-01
ENSMUST00000028609	E74-like factor 5 [Source:MGI Symbol;Acc:MGI:1335079]	Q3V1F7	Q8VDK3	7.2	1.9E-04	-4.9	1.7E-04	-0.3	4.5E-01	-0.7	4.3E-01
ENSMUST00000028612	peptidase domain containing associated with muscle regeneration 1 [Source:MGI Symbol;Acc:MGI:2445082]		Q8BU25	6.9	7.3E-05	-0.9	4.3E-01	1.4	1.0E-01	0.2	8.3E-01
ENSMUST00000028617	apoptosis inhibitor 5 [Source:MGI Symbol;Acc:MGI:1888993]		O35841	-5.2	9.3E-06	7.5	9.1E-05	0.2	8.7E-01	-0.4	5.0E-01
ENSMUST00000028619	hydroxysteroid (17-beta) dehydrogenase 12 [Source:MGI Symbol;Acc:MGI:1926967]	Q0VGQ1	O70503	-5.4	5.1E-04	2.6	7.8E-03	-1.4	6.7E-02	-0.5	4.3E-01
ENSMUST00000028623	exostoses (multiple) 2 [Source:MGI Symbol;Acc:MGI:108050]		P70428	-2.2	5.7E-03	-5.8	1.4E-02	-0.1	9.3E-01	1.2	5.5E-01
ENSMUST00000028624	glycine amidinotransferase (L-arginine:glycine amidinotransferase) [Source:MGI Symbol;Acc:MGI:1914342]		Q9D964	-4.0	7.7E-06	8.3	1.7E-05	-0.6	5.9E-01	0.0	9.7E-01
ENSMUST00000028635	(constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13		P61202	-4.6	1.2E-04	-2.6	1.9E-02	0.9	1.2E-01	0.7	4.7E-01
ENSMUST00000028644	CD82 antigen [Source:MGI Symbol;Acc:MGI:104651]	Q3UII2	P40237	-5.8	5.1E-05	6.4	2.2E-02	-0.8	7.5E-01	-0.8	5.8E-01
ENSMUST00000028648	synaptotagmin XIII [Source:MGI Symbol;Acc:MGI:1933945]		Q9EQT6	8.6	5.3E-06	4.4	5.5E-02	-0.2	9.1E-01	-0.7	6.3E-01
ENSMUST00000028467	proteoglycan 2, bone marrow [Source:MGI Symbol;Acc:MGI:103294]	Q545D8	Q61878	0.8	5.8E-01	0.3	8.6E-01	-0.7	6.1E-01	-0.2	9.0E-01
ENSMUST00000028470	translocase of inner mitochondrial membrane 10 [Source:MGI Symbol;Acc:MGI:1353429]		P62073	-0.8	4.6E-01	-1.0	3.7E-01	-1.3	1.9E-01	-1.0	3.9E-01
ENSMUST00000028650	peroxisomal biogenesis factor 16 [Source:MGI Symbol;Acc:MGI:1338829]		Q91XC9	-2.2	2.3E-02	7.2	1.6E-04	-0.6	6.1E-01	-0.4	5.4E-01
ENSMUST00000028652	ute carrier family 28 (sodium-coupled nucleoside transporter), member 2 [Source:MGI Symbol;Acc:MGI:19131		O88627	-2.9	4.1E-04	-5.8	4.8E-03	0.1	8.3E-01	1.3	4.2E-01
ENSMUST00000028656	dual oxidase maturation factor 2 [Source:MGI Symbol;Acc:MGI:1914061]		Q9D311	7.2	9.0E-04	-6.2	5.6E-04	0.3	4.5E-01	-0.9	5.0E-01
ENSMUST00000028499	integrin alpha V [Source:MGI Symbol;Acc:MGI:96608]		P43406	-1.5	2.4E-01	1.8	2.2E-01	1.2	3.1E-01	-2.1	1.4E-01
ENSMUST00000028661	RIKEN cDNA 4933406J08 gene [Source:MGI Symbol;Acc:MGI:1921651]		Q9D494	6.3	3.0E-04	-4.7	2.2E-03	0.9	8.9E-02	-1.6	2.4E-01
ENSMUST00000028511	metaxin 2 [Source:MGI Symbol;Acc:MGI:1859652]		O88441	1.0	5.1E-02	1.0	7.1E-02	-0.5	2.4E-01	-0.6	2.4E-01
ENSMUST00000028663	cAMP responsive element binding protein 3-like 1 [Source:MGI Symbol;Acc:MGI:1347062]			4.7	5.5E-04	7.5	5.9E-05	0.5	6.4E-01	0.3	5.5E-01
ENSMUST00000028517	Obg-like ATPase 1 [Source:MGI Symbol;Acc:MGI:1914309]		Q9CZ30	-1.0	1.4E-01	-1.1	1.7E-01	-0.3	6.4E-01	-0.1	8.5E-01
ENSMUST00000028522	integrin alpha 6 [Source:MGI Symbol;Acc:MGI:96605]	Q8CC06	Q61739	-1.6	5.3E-01	-2.3	3.0E-01	-3.7	4.3E-02	-3.0	2.7E-01
ENSMUST00000028665	protein associated with topoisomerase II homolog 2 (yeast) [Source:MGI Symbol;Acc:MGI:1914828]		A2ARM1	7.3	2.6E-05	7.1	2.5E-04	-0.5	6.9E-01	-0.7	3.5E-01
ENSMUST00000028527	kinesin family member 18A [Source:MGI Symbol;Acc:MGI:2446977]		Q91WD7	0.2	7.9E-01	-0.1	9.6E-01	0.2	8.2E-01	0.5	6.5E-01
ENSMUST00000028679	elongation factor RNA polymerase II-like 3 [Source:MGI Symbol;Acc:MGI:2673679]		Q80VR2	6.8	3.1E-05	6.3	3.6E-04	-0.5	7.1E-01	-1.0	1.6E-01
ENSMUST00000028683	protein disulfide isomerase associated 3 [Source:MGI Symbol;Acc:MGI:95834]		P27773	-5.0	1.6E-04	-1.0	1.4E-01	-0.2	7.1E-01	-1.1	1.2E-01
ENSMUST00000028689	low density lipoprotein receptor-related protein 4 [Source:MGI Symbol;Acc:MGI:2442252]		Q8VI56	4.5	1.0E-05	-7.8	2.5E-04	1.2	1.7E-02	-0.7	6.2E-01
ENSMUST00000028691	ADP-ribosylation factor GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:1924288]		Q99K28	-4.0	2.6E-03	-2.7	6.0E-03	-0.3	5.6E-01	-1.0	2.2E-01
ENSMUST00000028721	transglutaminase 5 [Source:MGI Symbol;Acc:MGI:1921426]		Q9D7I9	7.8	3.3E-05	-1.2	1.4E-01	0.2	6.9E-01	-0.1	9.0E-01
ENSMUST00000028727	synaptosomal-associated protein 25 [Source:MGI Symbol;Acc:MGI:98331]		P60879	6.1	2.5E-02	-3.4	1.4E-03	-1.1	3.4E-02	0.1	9.0E-01
ENSMUST00000028728	ubiquitin protein ligase E3 component n-recognin 1 [Source:MGI Symbol;Acc:MGI:1277977]		O70481	-3.0	1.3E-03	-1.5	8.9E-02	1.3	2.6E-02	0.0	9.6E-01
ENSMUST00000028580	coiled-coil domain containing 34 [Source:MGI Symbol;Acc:MGI:1915451]		Q3UI66	-2.9	4.6E-02	-1.2	3.4E-01	-0.3	7.4E-01	-1.9	2.0E-01
ENSMUST00000028735	jagged 1 [Source:MGI Symbol;Acc:MGI:1095416]	Q3UVN4	Q9QXX0	2.2	7.3E-03	-4.2	3.1E-05	-0.4	1.3E-01	-0.2	6.6E-01
ENSMUST00000028584	COMM domain containing 9 [Source:MGI Symbol;Acc:MGI:1923751]		Q8K2Q0	-1.3	4.2E-02	-0.1	9.1E-01	0.2	7.4E-01	-1.1	1.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000028740	tau tubulin kinase 2 [Source:MGI Symbol;Acc:MGI:2155779]	A2AW15		2.7	1.2E-02	-7.9	4.3E-04	-1.0	8.9E-02	2.3	1.4E-01
ENSMUST00000028741	HAUS augmin-like complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1913546]	H7BWZ0		-4.0	5.5E-03	5.5	4.7E-03	-1.2	4.3E-01	1.1	2.7E-01
ENSMUST00000028595	DEP domain containing 7 [Source:MGI Symbol;Acc:MGI:2139258]		Q91WS7	-0.6	5.0E-01	-0.6	5.5E-01	-1.1	2.3E-01	-1.1	2.9E-01
ENSMUST00000028597	t-complex 11 like 1 [Source:MGI Symbol;Acc:MGI:2444263]		Q8BTG3	4.7	6.3E-02	5.4	8.5E-02	0.1	9.6E-01	-0.5	7.8E-01
ENSMUST00000028752	vacuolar protein sorting 39 (yeast) [Source:MGI Symbol;Acc:MGI:2443189]	Q5KU38	Q8R5L3	-5.7	2.4E-02	-1.4	1.3E-01	0.7	2.0E-01	-1.4	1.2E-01
ENSMUST00000028758	inositol 1,4,5-trisphosphate 3-kinase A [Source:MGI Symbol;Acc:MGI:1333822]		Q8R071	6.5	3.1E-05	-1.6	6.0E-02	1.2	2.9E-02	-0.1	9.2E-01
ENSMUST00000028603	F-box protein 3 [Source:MGI Symbol;Acc:MGI:1929084]		Q9DC63	-1.9	1.7E-01	-2.7	1.3E-01	-0.2	8.3E-01	0.6	7.3E-01
ENSMUST00000028607	cell cycle associated protein 1 [Source:MGI Symbol;Acc:MGI:1858234]		Q60865	0.3	7.0E-01	1.9	6.3E-02	1.2	1.3E-01	-0.4	5.9E-01
ENSMUST00000028759	leukocyte tyrosine kinase [Source:MGI Symbol;Acc:MGI:96840]		P08923	7.3	3.3E-03	-1.6	2.2E-01	-0.2	8.3E-01	-3.0	6.4E-02
ENSMUST00000028764	oxytocin [Source:MGI Symbol;Acc:MGI:97453]	Q545V4	P35454	5.2	7.9E-05	3.9	2.5E-02	-0.7	6.2E-01	2.6	3.3E-02
ENSMUST00000028610	catalase [Source:MGI Symbol;Acc:MGI:88271]		P24270	-1.1	9.2E-02	-0.8	3.3E-01	0.6	2.8E-01	0.3	6.9E-01
ENSMUST00000028769	protein tyrosine phosphatase, receptor type, A [Source:MGI Symbol;Acc:MGI:97808]	Q91V35		-6.8	1.5E-04	6.4	2.5E-04	-0.5	6.6E-01	0.0	9.8E-01
ENSMUST00000028771	nucleolar and spindle associated protein 1 [Source:MGI Symbol;Acc:MGI:2675669]		Q9ERH4	2.3	3.1E-03	-4.2	3.1E-04	0.6	1.4E-01	-0.5	5.4E-01
ENSMUST00000028781	attractin [Source:MGI Symbol;Acc:MGI:1341628]		Q9WU60	-2.7	6.9E-05	-6.1	4.4E-04	-0.9	8.2E-02	-0.2	8.5E-01
ENSMUST00000028783	serine protease inhibitor, Kunitz type 1 [Source:MGI Symbol;Acc:MGI:1338033]		Q9R097	-3.9	1.1E-02	-2.2	1.7E-02	-0.4	3.7E-01	-0.5	5.7E-01
ENSMUST00000028794	sialic acid binding Ig-like lectin 1, sialoadhesin [Source:MGI Symbol;Acc:MGI:99668]	G3X8X6		6.3	1.4E-05	-3.0	2.7E-04	-0.3	3.7E-01	-1.3	4.0E-02
ENSMUST00000028633	fibrillin 1 [Source:MGI Symbol;Acc:MGI:95489]	A2AQ53		1.3	9.4E-02	2.5	3.0E-02	1.5	7.8E-02	0.3	7.3E-01
ENSMUST00000028796	RNA pseudouridylate synthase domain containing 2 [Source:MGI Symbol;Acc:MGI:1918066]		Q149F1	5.2	1.5E-05	-2.7	8.8E-03	0.0	9.3E-01	-1.8	6.5E-02
ENSMUST00000028640	diphthamine biosynthesis 6 [Source:MGI Symbol;Acc:MGI:1913882]		Q9CQ28	3.9	3.8E-02	0.6	7.5E-01	-1.8	3.0E-01	1.4	4.0E-01
ENSMUST00000028801	sperm flagellar 1 [Source:MGI Symbol;Acc:MGI:3513546]		Q99JL1	4.7	5.8E-03	-6.9	9.8E-04	0.9	8.2E-02	2.0	1.9E-01
ENSMUST00000028802	cancer susceptibility candidate 5 [Source:MGI Symbol;Acc:MGI:1923714]	A3KGI3		1.4	4.1E-03	0.8	1.5E-01	-7.7	8.0E-06	0.1	8.3E-01
ENSMUST00000028803	kinetochore-localized astrin/SPAG5 binding [Source:MGI Symbol;Acc:MGI:1289298]	A3KGG6		-4.3	2.3E-03	-1.1	3.3E-01	1.0	1.9E-01	-0.2	8.6E-01
ENSMUST00000028804	cell division cycle 25B [Source:MGI Symbol;Acc:MGI:99701]	Q3U535	P30306	-4.8	3.8E-03	-1.4	5.0E-02	0.2	6.0E-01	-1.3	7.1E-02
ENSMUST00000028807	isovaleryl coenzyme A dehydrogenase [Source:MGI Symbol;Acc:MGI:1929242]		Q9JHI5	-2.8	2.2E-03	6.0	4.8E-03	-0.7	6.9E-01	0.5	6.0E-01
ENSMUST00000028814	Ras association (RalGDS/AF-6) domain family member 2 [Source:MGI Symbol;Acc:MGI:2442060]		Q8BMS9	2.2	5.1E-03	6.3	5.8E-04	-0.6	6.4E-01	-0.6	4.3E-01
ENSMUST00000028816	transmembrane protein 230 [Source:MGI Symbol;Acc:MGI:1917862]		Q8CIB6	-6.2	2.8E-03	5.4	2.2E-03	1.0	4.0E-01	0.4	6.5E-01
ENSMUST00000028817	proliferating cell nuclear antigen [Source:MGI Symbol;Acc:MGI:97503]	Q542J9	P17918	-4.7	2.1E-05	6.9	5.2E-05	-0.9	4.0E-01	-0.5	3.9E-01
ENSMUST00000028667	diacylglycerol kinase zeta [Source:MGI Symbol;Acc:MGI:1278339]		Q80UP3	-3.0	8.4E-02	-3.2	1.8E-01	0.1	9.4E-01	0.3	9.0E-01
ENSMUST00000028668	eukaryotic translation initiation factor 3, subunit J1 [Source:MGI Symbol;Acc:MGI:1925905]		Q3UGC7	0.9	2.3E-01	0.8	4.0E-01	-0.4	5.4E-01	-0.3	7.3E-01
ENSMUST00000028672	midkine [Source:MGI Symbol;Acc:MGI:96949]		P12025	3.0	4.1E-02	2.0	1.9E-01	-1.0	4.6E-01	0.0	9.9E-01
ENSMUST00000028821	fibrous sheath-interacting protein 1 [Source:MGI Symbol;Acc:MGI:1918563]		Q9D3V5	6.5	1.2E-04	5.2	8.3E-04	-1.5	2.0E-01	0.2	7.4E-01
ENSMUST00000028822	lycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:10489	B0R058		-3.9	1.6E-04	-4.6	1.9E-03	0.6	2.2E-01	0.2	8.4E-01
ENSMUST00000028825	family with sequence similarity 98, member B [Source:MGI Symbol;Acc:MGI:1915465]		Q80VD1	-3.7	7.7E-05	5.5	1.0E-05	0.6	3.0E-01	-0.4	3.1E-01
ENSMUST00000028826	chromogranin B [Source:MGI Symbol;Acc:MGI:88395]	Q3TY66	P16014	8.2	1.4E-04	-5.9	1.3E-02	0.8	2.3E-01	2.7	1.9E-01
ENSMUST00000028696	damage specific DNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1355314]		Q99J79	2.5	2.8E-01	-0.5	8.2E-01	-3.5	1.1E-01	-0.5	8.3E-01
ENSMUST00000028702	adenosine deaminase-like [Source:MGI Symbol;Acc:MGI:1923144]		Q80SY6	-1.7	4.4E-01	-3.0	2.5E-01	-2.1	1.7E-01	-0.8	7.8E-01
ENSMUST00000028704	hydroxyacid oxidase 1, liver [Source:MGI Symbol;Acc:MGI:96011]	Q3UEE8	Q9WU19	2.8	3.5E-02	2.3	1.2E-01	-0.4	7.7E-01	0.1	9.0E-01
ENSMUST00000028835	cardiolipin synthase 1 [Source:MGI Symbol;Acc:MGI:1913836]		Q80ZM8	-5.2	7.8E-05	7.7	6.8E-05	-0.6	6.0E-01	-0.6	3.2E-01
ENSMUST00000028836	bone morphogenetic protein 2 [Source:MGI Symbol;Acc:MGI:88177]		P21274	6.6	2.8E-05	5.4	6.0E-02	-0.7	8.0E-01	0.1	9.7E-01
ENSMUST00000028838	histidine decarboxylase [Source:MGI Symbol;Acc:MGI:96062]		P23738	-7.6	1.1E-05	-1.2	1.5E-01	1.1	5.2E-02	-0.6	4.4E-01
ENSMUST00000028730	McKusick-Kaufman syndrome [Source:MGI Symbol;Acc:MGI:1891836]		Q9JI70	-1.7	2.2E-01	-0.4	7.8E-01	-0.1	9.1E-01	-1.4	3.2E-01
ENSMUST00000028841	ubiquitin specific peptidase 8 [Source:MGI Symbol;Acc:MGI:1934029]		Q80U87	-3.4	4.8E-05	2.5	1.5E-02	0.3	6.3E-01	0.0	9.7E-01
ENSMUST00000028844	signal peptide peptidase like 2A [Source:MGI Symbol;Acc:MGI:1913802]		Q9JJF9	-2.2	5.0E-04	3.6	8.2E-02	4.9	1.2E-02	4.0	1.0E-02
ENSMUST00000028852	mitochondrial ribosomal protein S5 [Source:MGI Symbol;Acc:MGI:1924971]		Q99N87	4.2	4.7E-05	-2.8	7.6E-02	0.6	4.2E-01	-0.6	7.1E-01
ENSMUST00000028743	synaptosomal-associated protein 23 [Source:MGI Symbol;Acc:MGI:109356]	A2AKH4	O09044	-4.8	4.7E-02	-0.5	8.2E-01	1.1	4.7E-01	-3.2	1.9E-01
ENSMUST00000028854	myelin and lymphocyte protein, T cell differentiation protein [Source:MGI Symbol;Acc:MGI:892970]		O09198	7.8	1.1E-05	-3.8	1.2E-01	0.3	8.2E-01	-1.7	5.2E-01
ENSMUST00000028755	EH-domain containing 4 [Source:MGI Symbol;Acc:MGI:1919619]	Q3TM70	Q9EQP2	-0.6	3.1E-01	-0.8	3.4E-01	-0.2	7.3E-01	0.0	9.5E-01
ENSMUST00000028855	prominin 2 [Source:MGI Symbol;Acc:MGI:2138997]		Q3UUY6	9.0	1.9E-04	5.1	2.8E-04	-1.1	2.6E-01	0.3	6.0E-01
ENSMUST00000028856	mal, T cell differentiation protein-like [Source:MGI Symbol;Acc:MGI:2385152]		Q91X49	7.0	4.2E-05	5.7	2.1E-02	-0.7	7.5E-01	0.9	4.7E-01
ENSMUST00000028761	U box domain containing 5 [Source:MGI Symbol;Acc:MGI:2154658]	Q543N0	Q925F4	1.1	6.2E-02	2.1	1.0E-02	0.5	3.9E-01	-0.6	3.4E-01
ENSMUST00000028857	nephronophthisis 1 (juvenile) homolog (human) [Source:MGI Symbol;Acc:MGI:1858233]	A2APS1		3.1	1.3E-03	6.9	2.1E-04	1.6	1.7E-01	-0.1	8.7E-01
ENSMUST00000028767	1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:13094		A2AQ19	-1.3	4.0E-02	-0.8	2.9E-01	0.3	4.7E-01	-0.2	8.2E-01
ENSMUST00000028858	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1100510]	A2APR8		-1.5	1.9E-02	-3.1	3.3E-03	0.0	9.9E-01	-3.7	9.8E-03
ENSMUST00000028859	acyl-Coenzyme A oxidase-like [Source:MGI Symbol;Acc:MGI:1921371]		Q9DBS4	7.2	4.8E-05	1.2	1.0E-01	-1.4	3.8E-02	-0.2	7.4E-01
ENSMUST00000028780	ChaC, cation transport regulator 1 [Source:MGI Symbol;Acc:MGI:1916315]		Q8R3J5	1.1	1.2E-01	2.0	3.7E-02	1.1	1.4E-01	0.1	8.9E-01
ENSMUST00000028864	fibulin 7 [Source:MGI Symbol;Acc:MGI:1917620]		Q501P1	4.7	1.6E-02	-1.4	1.5E-02	0.9	2.0E-02	-0.4	4.1E-01
ENSMUST00000028874	polymerase (RNA) I polypeptide B [Source:MGI Symbol;Acc:MGI:108014]	A2AP84		7.6	5.2E-05	-1.6	3.2E-01	1.5	1.3E-01	-0.8	6.1E-01
ENSMUST00000028880	solute carrier family 20, member 1 [Source:MGI Symbol;Acc:MGI:108392]		Q61609	-3.5	4.4E-04	0.4	5.2E-01	-5.3	3.2E-05	0.5	4.3E-01
ENSMUST00000028795	RAD51 homolog [Source:MGI Symbol;Acc:MGI:97890]		Q08297	-1.3	3.1E-01	3.8	9.0E-03	1.0	4.1E-01	-4.1	4.5E-03
ENSMUST00000028881	interleukin 1 beta [Source:MGI Symbol;Acc:MGI:96543]		P10749	-8.7	2.9E-04	5.2	1.1E-04	0.3	6.8E-01	0.4	4.6E-01
ENSMUST00000028799	cancer susceptibility candidate 5 [Source:MGI Symbol;Acc:MGI:1923714]		Q66JQ7	3.9	3.5E-02	5.3	1.7E-02	1.1	5.4E-01	-0.3	8.2E-01
ENSMUST00000028883	prodynorphin [Source:MGI Symbol;Acc:MGI:97535]	O35852		6.8	1.6E-04	6.3	1.4E-03	-0.6	6.9E-01	-2.1	3.7E-02
ENSMUST00000028892	isocitrate dehydrogenase 3 (NAD+) beta [Source:MGI Symbol;Acc:MGI:2158650]	Q91VA7		-3.1	1.7E-04	2.2	2.9E-03	1.0	4.0E-02	0.3	5.1E-01
ENSMUST00000028897	carboxypeptidase X 1 (M14 family) [Source:MGI Symbol;Acc:MGI:1934569]		Q9Z100	6.8	4.0E-05	-4.1	6.8E-03	-0.9	1.9E-01	-1.1	4.2E-01
ENSMUST00000028900	vacuolar protein sorting 16 (yeast) [Source:MGI Symbol;Acc:MGI:2136772]	G3X8X7		-2.4	1.2E-03	-2.1	1.4E-01	1.5	8.9E-02	-1.2	4.4E-01
ENSMUST00000028806	spermine oxidase [Source:MGI Symbol;Acc:MGI:2445356]	Q3UPW5	Q99K82	-2.3	3.7E-01	-0.9	7.0E-01	-0.6	7.4E-01	-2.0	4.5E-01
ENSMUST00000028905	proprotein convertase subtilisin/kexin type 2 [Source:MGI Symbol;Acc:MGI:97512]	Q547J8	P21661	9.0	7.9E-05	-1.1	2.2E-01	1.2	4.9E-02	-0.5	5.6E-01
ENSMUST00000028907	beaded filament structural protein 1, in lens-CP94 [Source:MGI Symbol;Acc:MGI:101770]		A2AMT1	7.3	2.4E-03	3.0	5.6E-03	0.9	2.5E-01	0.1	8.3E-01
ENSMUST00000028815	solute carrier family 23 (nucleobase transporters), member 2 [Source:MGI Symbol;Acc:MGI:1859682]		Q9EPR4	0.5	2.9E-01	0.5	4.6E-01	0.3	5.0E-01	0.4	5.6E-01
ENSMUST00000028909	sorting nexin 5 [Source:MGI Symbol;Acc:MGI:1916428]		Q9D8U8	-4.7	4.0E-04	-1.7	2.5E-01	1.2	2.0E-01	-3.4	7.8E-02
ENSMUST00000028910	mitochondrial genome maintainance exonuclease 1 [Source:MGI Symbol;Acc:MGI:1921778]		Q9CXC3	5.6	2.3E-04	-5.3	6.0E-05	-0.4	2.4E-01	0.1	8.7E-01
ENSMUST00000028916	SEC23 homolog B, COPII coat complex component [Source:MGI Symbol;Acc:MGI:1350925]		Q9D662	-7.0	8.9E-05	6.1	3.4E-04	-0.6	6.2E-01	-0.2	7.0E-01
ENSMUST00000028921	5'-3' exoribonuclease 2 [Source:MGI Symbol;Acc:MGI:894687]		Q9DBR1	-4.4	1.1E-05	-3.1	2.6E-03	-0.2	5.8E-01	-1.0	2.3E-01
ENSMUST00000028926	N-ethylmaleimide sensitive fusion protein attachment protein beta [Source:MGI Symbol;Acc:MGI:104562]		P28663	6.4	3.4E-02	-2.7	2.7E-03	0.3	4.1E-01	-0.7	3.2E-01
ENSMUST00000028928	GDNF-inducible zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1921783]		Q4VBD9	-2.0	3.5E-03	7.2	5.1E-04	-1.5	3.5E-01	-0.5	5.3E-01
ENSMUST00000028829	sprouty protein with EVH-1 domain 1, related sequence [Source:MGI Symbol;Acc:MGI:2150016]		Q924S8	1.3	4.4E-02	0.4	6.1E-01	-0.8	1.5E-01	0.1	8.8E-01
ENSMUST00000028938	cystatin C [Source:MGI Symbol;Acc:MGI:102519]		P21460	-8.1	8.0E-07	-2.5	1.5E-02	1.3	2.5E-02	-1.4	1.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000028944	acyl-CoA synthetase short-chain family member 1 [Source:MGI Symbol;Acc:MGI:1915988]	Q569W4	Q99NB1	4.4	1.1E-04	3.0	1.4E-03	-4.0	8.6E-04	-0.4	4.6E-01
ENSMUST00000028949	NSFL1 (p97) cofactor (p47) [Source:MGI Symbol;Acc:MGI:3042273]		Q9CZ44	-7.4	3.9E-06	-6.2	2.4E-04	0.6	1.9E-01	-0.9	4.6E-01
ENSMUST00000028950	syndecan binding protein (syntenin) 2 [Source:MGI Symbol;Acc:MGI:2385156]	Q3UN51	Q99JZ0	3.1	8.8E-04	-3.0	8.0E-04	0.4	2.7E-01	0.0	9.8E-01
ENSMUST00000028843	transient receptor potential cation channel, subfamily M, member 7 [Source:MGI Symbol;Acc:MGI:1929996]	A2AI57		-6.2	4.0E-02	-2.5	4.4E-01	2.2	3.4E-01	-1.6	6.3E-01
ENSMUST00000028951	syntaphilin [Source:MGI Symbol;Acc:MGI:2139270]		Q80U23	8.0	1.8E-02	-2.0	4.8E-03	0.0	9.3E-01	-0.2	7.0E-01
ENSMUST00000028846	dual specificity phosphatase 2 [Source:MGI Symbol;Acc:MGI:101911]		Q05922	1.5	1.1E-01	0.1	8.9E-01	-0.8	3.2E-01	0.5	6.0E-01
ENSMUST00000028848	fumarylacetoacetate hydrolase domain containing 2A [Source:MGI Symbol;Acc:MGI:1915376]			-2.9	4.3E-02	0.5	7.7E-01	1.4	2.7E-01	-2.0	1.9E-01
ENSMUST00000028850	Kv channel interacting protein 3, calsenilin [Source:MGI Symbol;Acc:MGI:1929258]	A2AHT3		6.7	4.8E-02	-0.2	9.6E-01	-2.2	4.7E-01	4.6	1.9E-01
ENSMUST00000028955	angiopoietin 4 [Source:MGI Symbol;Acc:MGI:1336887]	Q3V0P7	Q9WVH6	6.9	4.2E-05	3.0	1.5E-03	-0.8	2.1E-01	0.4	4.2E-01
ENSMUST00000028963	TBC1 domain family, member 20 [Source:MGI Symbol;Acc:MGI:1914481]	Q0P648	Q9D9I4	-7.4	1.7E-04	6.6	5.1E-05	-1.5	1.7E-01	-0.2	6.6E-01
ENSMUST00000028966	defensin beta 22 [Source:MGI Symbol;Acc:MGI:3045368]	Q8BVC1		6.2	4.5E-04	8.5	5.3E-04	-0.8	6.7E-01	-0.2	7.6E-01
ENSMUST00000028970	myosin, light polypeptide kinase 2, skeletal muscle [Source:MGI Symbol;Acc:MGI:2139434]		Q8VCR8	8.9	9.8E-05	6.8	1.1E-04	-0.5	6.4E-01	-0.3	6.1E-01
ENSMUST00000028972	p53 and DNA damage regulated 1 [Source:MGI Symbol;Acc:MGI:1915809]	Q3UKN2	P59048	-3.8	6.6E-03	1.8	3.2E-02	-2.1	1.1E-02	-0.7	2.6E-01
ENSMUST00000028977	kinesin family member 3B [Source:MGI Symbol;Acc:MGI:107688]	Q3UHC4	Q61771	-3.5	1.0E-04	-0.6	3.7E-01	0.3	5.2E-01	-0.6	3.8E-01
ENSMUST00000028981	microtubule-associated protein, RP/EB family, member 1 [Source:MGI Symbol;Acc:MGI:891995]	Q3U4H0	Q61166	-2.6	1.1E-04	6.5	2.3E-04	-0.2	8.8E-01	0.5	4.5E-01
ENSMUST00000028982	Sad1 and UNC84 domain containing 5 [Source:MGI Symbol;Acc:MGI:1923657]			6.2	1.3E-04	5.8	2.1E-02	0.4	8.3E-01	-0.6	6.5E-01
ENSMUST00000028866	zinc finger CCCH type containing 8 [Source:MGI Symbol;Acc:MGI:1930128]		Q9JI48	0.7	2.9E-01	0.7	3.8E-01	-1.0	1.4E-01	-0.9	1.9E-01
ENSMUST00000028983	BPI fold containing family B, member 2 [Source:MGI Symbol;Acc:MGI:1913807]	Q14AV3	Q8C1E1	7.3	1.5E-04	4.2	2.4E-03	-3.1	2.2E-02	0.2	7.2E-01
ENSMUST00000028990	CDK5 regulatory subunit associated protein 1 [Source:MGI Symbol;Acc:MGI:1914221]		Q8BTW8	-4.5	3.2E-03	-1.9	2.6E-02	-0.3	4.8E-01	-1.9	3.7E-02
ENSMUST00000028991	syntrophin, acidic 1 [Source:MGI Symbol;Acc:MGI:101772]		Q61234	5.9	2.9E-02	-8.7	1.1E-03	-1.5	6.2E-02	-1.5	4.8E-01
ENSMUST00000028999	protein kinase inhibitor, alpha [Source:MGI Symbol;Acc:MGI:104747]		P63248	5.4	4.3E-04	6.2	3.9E-04	-1.5	2.6E-01	-0.9	2.2E-01
ENSMUST00000028888	transglutaminase 6 [Source:MGI Symbol;Acc:MGI:3044321]	Q8BM11		6.3	7.4E-02	6.2	9.1E-02	-0.9	8.0E-01	-0.8	7.1E-01
ENSMUST00000028890	NOP56 ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1914384]	A2APD7		-0.4	8.6E-01	-4.2	2.5E-01	-2.3	2.5E-01	1.6	6.6E-01
ENSMUST00000029002	stathmin-like 2 [Source:MGI Symbol;Acc:MGI:98241]	Q545S4	P55821	5.6	5.0E-04	-3.5	4.6E-04	-0.1	7.0E-01	0.3	7.1E-01
ENSMUST00000029005	replication termination factor 2 domain containing 1 [Source:MGI Symbol;Acc:MGI:1913654]		Q99K95	-7.4	6.0E-05	6.7	1.2E-04	-0.5	6.3E-01	-0.4	4.8E-01
ENSMUST00000029013	RAE1 RNA export 1 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1913929]		Q8C570	-3.0	3.5E-04	-2.0	1.5E-02	0.7	1.1E-01	0.4	6.1E-01
ENSMUST00000029014	RNA binding motif protein 38 [Source:MGI Symbol;Acc:MGI:1889294]		Q62176	-9.0	1.4E-05	8.2	3.1E-04	-0.7	6.8E-01	0.1	9.2E-01
ENSMUST00000029018	Z-DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:1927449]	A2APF7		-5.2	1.9E-03	5.3	2.3E-02	-0.6	7.8E-01	1.4	2.6E-01
ENSMUST00000029024	RAB22A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105072]	Q0PD34	P35285	-6.7	4.3E-03	-7.0	5.9E-04	-0.3	5.8E-01	2.0	1.7E-01
ENSMUST00000029025	zinc finger, DBF-type containing 2 [Source:MGI Symbol;Acc:MGI:1921134]		Q5SS00	8.1	9.6E-03	4.6	1.9E-03	-0.8	4.3E-01	0.2	8.4E-01
ENSMUST00000028911	cysteine and glycine-rich protein 2 binding protein [Source:MGI Symbol;Acc:MGI:1917264]		Q8C1D0	-0.4	4.2E-01	0.4	4.9E-01	0.4	3.4E-01	-0.4	5.1E-01
ENSMUST00000028914	polymerase (RNA) III (DNA directed) polypeptide F [Source:MGI Symbol;Acc:MGI:1924086]		Q921X6	1.0	5.8E-02	0.6	3.7E-01	0.2	6.4E-01	0.7	2.8E-01
ENSMUST00000028915	retinoblastoma binding protein 9 [Source:MGI Symbol;Acc:MGI:1347074]	A2AN96	O88851	0.2	8.1E-01	-0.8	3.1E-01	-1.5	3.5E-02	-0.6	4.7E-01
ENSMUST00000029030	endothelin 3 [Source:MGI Symbol;Acc:MGI:95285]	A2APU5	P48299	6.4	4.4E-04	-4.2	2.0E-03	0.7	1.7E-01	-2.2	1.1E-01
ENSMUST00000028917	D-tyrosyl-tRNA deacylase 1 [Source:MGI Symbol;Acc:MGI:1913294]		Q9DD18	-1.9	8.6E-02	-3.0	3.0E-02	-1.2	1.5E-01	-0.1	9.2E-01
ENSMUST00000029043	fatty acid binding protein 12 [Source:MGI Symbol;Acc:MGI:1922747]		Q9DAK4	8.3	2.5E-05	-4.0	1.4E-04	0.3	3.4E-01	-0.1	9.0E-01
ENSMUST00000029046	fatty acid binding protein 5, epidermal [Source:MGI Symbol;Acc:MGI:101790]	Q497I3	Q05816	-4.8	9.5E-06	2.0	5.7E-01	-0.5	8.7E-01	3.9	1.8E-01
ENSMUST00000029049	charged multivesicular body protein 4C [Source:MGI Symbol;Acc:MGI:1913621]		Q9D7F7	6.2	1.8E-06	-1.1	1.3E-01	0.5	2.2E-01	-0.4	5.4E-01
ENSMUST00000029053	protein tyrosine phosphatase, non-receptor type 1 [Source:MGI Symbol;Acc:MGI:97805]	Q3TZW9	P35821	-7.5	9.2E-04	-8.4	4.7E-06	-0.6	1.0E-01	-0.2	8.2E-01
ENSMUST00000029061	sal-like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2139360]		Q8BX22	9.3	3.5E-05	3.3	3.1E-03	-0.7	3.7E-01	0.4	4.8E-01
ENSMUST00000028948	GINS complex subunit 1 (Psf1 homolog) [Source:MGI Symbol;Acc:MGI:1916520]		Q9CZ15	-0.7	2.5E-01	-2.1	3.5E-02	-0.6	2.8E-01	0.8	3.6E-01
ENSMUST00000029071	carbonic anhydrase 13 [Source:MGI Symbol;Acc:MGI:1931322]		Q9D6N1	1.6	2.7E-02	-6.8	4.9E-05	-0.2	5.5E-01	-0.8	4.6E-01
ENSMUST00000029075	docking protein 5 [Source:MGI Symbol;Acc:MGI:1924079]		Q91ZM9	8.0	9.4E-06	1.4	8.0E-02	-2.0	1.2E-02	-0.2	7.7E-01
ENSMUST00000029076	carbonic anhydrase 3 [Source:MGI Symbol;Acc:MGI:88270]		P16015	7.4	1.5E-04	6.0	7.8E-02	-0.8	8.1E-01	1.2	5.1E-01
ENSMUST00000029078	carbonic anhydrase 2 [Source:MGI Symbol;Acc:MGI:88269]		P00920	2.2	3.4E-02	7.5	6.7E-05	0.1	9.0E-01	-0.4	5.1E-01
ENSMUST00000029082	proteasome (prosome, macropain) subunit, alpha type 7 [Source:MGI Symbol;Acc:MGI:1347070]	Q542H2	Q9Z2U0	-9.4	5.9E-06	-7.2	6.5E-03	1.0	1.4E-01	0.8	6.9E-01
ENSMUST00000028964	RanBP-type and C3HC4-type zinc finger containing 1 [Source:MGI Symbol;Acc:MGI:1344372]		Q9WUB0	-0.6	5.4E-01	2.1	2.7E-01	3.9	3.0E-02	1.2	3.7E-01
ENSMUST00000029084	neurotensin receptor 1 [Source:MGI Symbol;Acc:MGI:97386]	A2ACT4	O88319	7.9	3.5E-05	5.8	1.3E-03	-0.6	6.4E-01	-0.2	7.6E-01
ENSMUST00000029085	MRG/MORF4L binding protein [Source:MGI Symbol;Acc:MGI:1920497]		Q9DAT2	-5.2	1.3E-04	8.7	3.2E-04	0.0	9.8E-01	0.2	7.6E-01
ENSMUST00000029087	opioid growth factor receptor [Source:MGI Symbol;Acc:MGI:1919325]		Q99PG2	-3.0	1.1E-03	-3.8	5.2E-02	0.1	8.9E-01	0.1	9.7E-01
ENSMUST00000029090	GID complex subunit 8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923675]		Q9D7M1	-6.3	1.8E-05	-2.7	3.2E-03	0.6	1.6E-01	-0.3	7.0E-01
ENSMUST00000029092	ADP-ribosylation factor GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2183559]		Q9EPJ9	-2.2	2.2E-02	-2.6	6.9E-04	-0.2	5.4E-01	-0.2	6.7E-01
ENSMUST00000029106	zinc finger and BTB domain containing 46 [Source:MGI Symbol;Acc:MGI:1919397]		Q8BID6	6.8	4.8E-05	6.5	1.7E-04	-0.5	6.4E-01	-0.9	1.9E-01
ENSMUST00000029116	:in-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 [Source:MGI Symbol;Acc:MGI:1923		Q8BHD8	-5.1	5.1E-04	6.8	5.1E-04	-0.6	6.5E-01	-0.1	9.0E-01
ENSMUST00000029126	itchy, E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1202301]		Q8C863	-6.8	7.8E-05	-2.6	5.4E-02	0.2	8.1E-01	-1.8	2.0E-01
ENSMUST00000029128	microtubule-associated protein 1 light chain 3 alpha [Source:MGI Symbol;Acc:MGI:1915661]		Q91VR7	-2.7	9.9E-03	7.2	1.5E-02	-0.8	7.7E-01	-2.2	1.7E-01
ENSMUST00000028995	family with sequence similarity 210, member B [Source:MGI Symbol;Acc:MGI:1914267]		Q9D8B6	-0.1	8.3E-01	1.0	1.2E-01	0.9	8.9E-02	-0.2	6.6E-01
ENSMUST00000029129	mitochondrial fission regulator 1 [Source:MGI Symbol;Acc:MGI:1914722]	F8WI92		-6.8	1.5E-05	4.5	1.0E-03	-1.5	1.9E-01	-0.6	3.5E-01
ENSMUST00000029131	gamma-glutamyltransferase 7 [Source:MGI Symbol;Acc:MGI:1913385]		Q99JP7	7.1	6.1E-05	3.5	6.2E-03	-2.9	2.9E-02	-0.7	3.3E-01
ENSMUST00000029135	acyl-CoA synthetase short-chain family member 2 [Source:MGI Symbol;Acc:MGI:1890410]		Q9QXG4	-3.8	7.3E-05	-4.9	2.6E-03	0.6	2.9E-01	-1.8	1.9E-01
ENSMUST00000029007	family with sequence similarity 209 [Source:MGI Symbol;Acc:MGI:1923676]	A2APA5		1.2	2.3E-01	2.1	7.9E-02	0.0	9.7E-01	-0.9	3.4E-01
ENSMUST00000029139	tripartite motif-containing 55 [Source:MGI Symbol;Acc:MGI:3036269]	G3X8Y1		7.0	4.9E-05	-2.3	9.2E-03	1.0	4.7E-02	0.2	7.4E-01
ENSMUST00000029142	eukaryotic translation initiation factor 6 [Source:MGI Symbol;Acc:MGI:1196288]	Q545K4	O55135	-4.7	9.3E-04	-6.8	7.0E-04	1.6	6.0E-03	-0.6	6.7E-01
ENSMUST00000029017	phosphoenolpyruvate carboxykinase 1, cytosolic [Source:MGI Symbol;Acc:MGI:97501]		Q9Z2V4	6.5	8.8E-02	2.0	5.7E-01	-2.5	4.9E-01	2.0	4.7E-01
ENSMUST00000029143	family with sequence similarity 83, member C [Source:MGI Symbol;Acc:MGI:1918655]	A2ARK0		9.1	4.0E-06	-3.3	1.2E-02	-0.9	1.8E-01	-2.8	6.2E-02
ENSMUST00000029147	nitrogen fixation gene 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1316706]		Q9Z1J3	-2.7	4.0E-04	-3.3	9.1E-02	0.8	4.5E-01	-2.6	2.3E-01
ENSMUST00000029158	AAR2 splicing factor homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915545]		Q9D2V5	1.7	2.1E-02	4.3	9.9E-02	-2.2	4.4E-01	1.6	3.2E-01
ENSMUST00000029165	RIKEN cDNA 1110008F13 gene [Source:MGI Symbol;Acc:MGI:1914638]		Q9CQT9	-10.1	3.0E-06	6.3	8.8E-04	-0.4	7.6E-01	-0.4	6.1E-01
ENSMUST00000029170	retinoblastoma-like 1 (p107) [Source:MGI Symbol;Acc:MGI:103300]		Q64701	-1.5	8.9E-03	7.4	1.3E-04	-0.7	6.0E-01	0.2	6.9E-01
ENSMUST00000029178	catenin, beta like 1 [Source:MGI Symbol;Acc:MGI:1913892]		Q9CWL8	-2.4	9.1E-04	-5.6	9.9E-05	-0.2	5.2E-01	0.6	4.9E-01
ENSMUST00000029188	WNT1 inducible signaling pathway protein 2 [Source:MGI Symbol;Acc:MGI:1328326]	A2AHD1		6.4	7.8E-04	6.0	7.1E-06	0.0	9.8E-01	0.2	5.7E-01
ENSMUST00000029196	solute carrier family 2 (facilitated glucose transporter), member 10 [Source:MGI Symbol;Acc:MGI:2156687]	A2A4V1	Q8VHD6	6.8	2.7E-05	-7.6	6.2E-03	1.0	2.7E-01	1.0	6.7E-01
ENSMUST00000029199	zinc finger matrin type 3 [Source:MGI Symbol;Acc:MGI:1195270]	B9EI21		6.0	1.3E-02	8.1	2.0E-04	-0.7	6.3E-01	0.4	5.3E-01
ENSMUST00000029201	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide [Source:MGI Symbol;Acc:MGI:1206581]		P42337	3.1	7.6E-05	-0.2	7.4E-01	-2.7	9.6E-04	-0.9	1.6E-01
ENSMUST00000029203	zinc finger protein 639 [Source:MGI Symbol;Acc:MGI:1915028]		Q99KZ6	-5.1	2.5E-03	8.0	3.2E-05	-0.5	6.8E-01	-0.4	4.4E-01
ENSMUST00000029208	carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 [Source:MGI Symbol;Acc:MGI:214	Q3UUJ6	Q91Y63	5.9	2.2E-03	5.2	1.3E-03	-2.2	1.1E-01	-0.1	8.9E-01
ENSMUST00000029213	osteoclast stimulatory transmembrane protein [Source:MGI Symbol;Acc:MGI:1921864]		Q9D611	5.9	1.7E-06	0.1	9.5E-01	-2.6	1.2E-02	-0.4	6.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000029214	actin-like 6A [Source:MGI Symbol;Acc:MGI:1861453]	Q505L1	Q9Z2N8	-4.9	1.7E-03	-9.9	4.0E-05	-0.5	1.9E-01	0.1	9.5E-01
ENSMUST00000029222	coiled-coil domain containing 39 [Source:MGI Symbol;Acc:MGI:1289263]		Q9D5Y1	3.0	1.1E-02	7.7	8.0E-05	-0.4	7.2E-01	-0.3	5.7E-01
ENSMUST00000029252	leucine rich repeat containing 34 [Source:MGI Symbol;Acc:MGI:1919077]	Q14B04	Q9DAM1	3.9	1.6E-03	-4.2	2.5E-03	0.1	7.5E-01	-0.8	4.6E-01
ENSMUST00000029256	SEC62 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916526]		Q8BU14	-4.8	2.5E-05	-2.1	2.3E-02	0.7	1.5E-01	-0.1	8.7E-01
ENSMUST00000029257	ATPase, class VI, type 11B [Source:MGI Symbol;Acc:MGI:1923545]	Q6DFW5		-5.8	1.2E-05	-7.2	2.9E-04	0.1	8.0E-01	1.0	4.3E-01
ENSMUST00000029266	annexin A5 [Source:MGI Symbol;Acc:MGI:106008]		P48036	-4.3	2.0E-06	-4.3	8.4E-03	0.4	5.1E-01	2.5	8.3E-02
ENSMUST00000029268	RIKEN cDNA 1810062G17 gene [Source:MGI Symbol;Acc:MGI:1919532]	G3X8Y2		5.1	1.6E-04	4.6	6.6E-04	-2.4	3.8E-02	-0.1	8.2E-01
ENSMUST00000029269	exosome component 9 [Source:MGI Symbol;Acc:MGI:1355319]		Q9JHI7	-6.3	6.1E-05	-3.4	1.5E-02	0.6	3.3E-01	-1.0	4.4E-01
ENSMUST00000029120	hnRNP-associated with lethal yellow [Source:MGI Symbol;Acc:MGI:97850]		Q64012	0.7	8.0E-01	3.7	3.1E-01	1.2	7.2E-01	-1.8	5.4E-01
ENSMUST00000029270	cyclin A2 [Source:MGI Symbol;Acc:MGI:108069]		P51943	-3.1	3.6E-03	7.4	5.9E-04	-0.7	6.6E-01	-0.9	3.0E-01
ENSMUST00000029125	armadillo repeat containing 1 [Source:MGI Symbol;Acc:MGI:1921502]		Q9D7A8	-0.9	9.4E-02	-0.8	2.6E-01	0.3	5.2E-01	0.2	8.2E-01
ENSMUST00000029271	transient receptor potential cation channel, subfamily C, member 3 [Source:MGI Symbol;Acc:MGI:109526]	B1ATV3		7.0	1.1E-04	-7.9	6.8E-04	0.7	2.5E-01	1.8	2.7E-01
ENSMUST00000029273	interleukin 21 [Source:MGI Symbol;Acc:MGI:1890474]	Q5SUE2	Q9ES17	7.0	3.6E-05	-0.6	5.6E-01	1.3	1.0E-01	-0.7	4.7E-01
ENSMUST00000029297	carrier family 7 (cationic amino acid transporter, y+ system), member 11 [Source:MGI Symbol;Acc:MGI:134	Q542C8	Q9WTR6	3.1	4.0E-03	0.0	9.8E-01	4.4	1.2E-04	-2.4	3.8E-02
ENSMUST00000029303	N(alpha)-acetyltransferase 15, NatA auxiliary subunit [Source:MGI Symbol;Acc:MGI:1922088]	G3X8Y3		-4.2	7.4E-03	6.8	1.0E-04	-1.3	2.6E-01	-1.1	8.4E-02
ENSMUST00000029307	stomatin (Epb7.2)-like 3 [Source:MGI Symbol;Acc:MGI:2388072]	B2RS16	Q6PE84	9.3	1.7E-05	-1.4	6.2E-02	1.2	1.4E-02	-1.2	1.2E-01
ENSMUST00000029311	transient receptor potential cation channel, subfamily C, member 4 [Source:MGI Symbol;Acc:MGI:109525]	Q0VB97	Q9QUQ5	6.6	9.9E-05	6.8	1.3E-04	-0.6	6.1E-01	-0.3	5.9E-01
ENSMUST00000029140	protein C receptor, endothelial [Source:MGI Symbol;Acc:MGI:104596]		Q64695	-0.6	6.8E-01	0.5	7.3E-01	-0.7	5.8E-01	-1.7	2.4E-01
ENSMUST00000029141	matrix metallopeptidase 24 [Source:MGI Symbol;Acc:MGI:1341867]		Q9R0S2	0.4	4.5E-01	1.9	2.4E-02	0.8	2.0E-01	-0.7	2.7E-01
ENSMUST00000029315	suppressor of Ty 20 [Source:MGI Symbol;Acc:MGI:1929651]	Z4YJG1		-3.6	4.3E-04	-2.2	7.4E-02	0.9	1.9E-01	-1.5	2.3E-01
ENSMUST00000029316	exosome component 8 [Source:MGI Symbol;Acc:MGI:1916889]	Q546F8	Q9D753	-4.7	4.3E-04	8.4	4.1E-05	-0.5	7.0E-01	0.3	6.4E-01
ENSMUST00000029326	succinate receptor 1 [Source:MGI Symbol;Acc:MGI:1934135]		Q99MT6	4.9	4.5E-03	-2.4	3.6E-03	0.3	4.0E-01	0.0	9.5E-01
ENSMUST00000029149	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	Q3U313	Q8VH51	-2.9	4.3E-01	-7.1	1.8E-01	-4.2	8.4E-02	0.0	1.0E+00
ENSMUST00000029336	DEAH (Asp-Glu-Ala-His) box polypeptide 36 [Source:MGI Symbol;Acc:MGI:1919412]		Q8VHK9	-2.4	8.6E-04	2.4	1.7E-02	1.1	1.5E-01	0.3	6.5E-01
ENSMUST00000029164	Src-like-adaptor 2 [Source:MGI Symbol;Acc:MGI:1925049]		Q8R4L0	-0.2	9.2E-01	0.2	9.2E-01	-2.1	2.2E-01	-2.5	2.4E-01
ENSMUST00000029344	major facilitator superfamily domain containing 1 [Source:MGI Symbol;Acc:MGI:1914118]		Q9DC37	-3.6	7.5E-05	-8.9	2.2E-05	1.0	1.7E-02	-0.2	8.5E-01
ENSMUST00000029347	intraflagellar transport 80 [Source:MGI Symbol;Acc:MGI:1915509]		Q8K057	-4.8	1.5E-02	-0.7	2.9E-01	1.2	1.9E-02	0.4	5.4E-01
ENSMUST00000029355	protein phosphatase 1 (formerly 2C)-like [Source:MGI Symbol;Acc:MGI:2139740]		Q8BHN0	3.0	2.7E-04	-1.3	5.6E-02	0.3	3.6E-01	-0.7	2.6E-01
ENSMUST00000029179	TELO2 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1922675]		Q91V83	-2.2	8.0E-02	0.0	1.0E+00	-0.2	8.0E-01	-2.4	8.6E-02
ENSMUST00000029180	regulation of nuclear pre-mRNA domain containing 1B [Source:MGI Symbol;Acc:MGI:1917720]		Q9CSU0	-3.7	4.3E-02	-2.4	2.3E-01	0.9	4.6E-01	-0.4	8.5E-01
ENSMUST00000029183	family with sequence similarity 83, member D [Source:MGI Symbol;Acc:MGI:1919128]		Q9D7I8	1.0	4.2E-01	3.5	2.7E-02	0.8	5.1E-01	-1.7	1.5E-01
ENSMUST00000029186	DEAH (Asp-Glu-Ala-His) box polypeptide 35 [Source:MGI Symbol;Acc:MGI:1918965]	Q8K1G9		4.4	9.6E-02	7.3	2.9E-02	2.2	4.6E-01	-0.8	6.9E-01
ENSMUST00000029358	NMD3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2140103]		Q99L48	2.5	4.7E-03	1.1	2.8E-01	-5.1	2.4E-03	0.2	8.5E-01
ENSMUST00000029194	SKI-like [Source:MGI Symbol;Acc:MGI:106203]		Q60665	1.1	6.7E-01	4.7	2.2E-01	3.0	4.0E-01	-0.6	8.0E-01
ENSMUST00000029367	butyrylcholinesterase [Source:MGI Symbol;Acc:MGI:894278]		Q03311	6.0	8.2E-04	6.9	3.3E-04	0.5	6.7E-01	0.4	5.2E-01
ENSMUST00000029368	cyclin A1 [Source:MGI Symbol;Acc:MGI:108042]		Q61456	6.4	1.1E-04	5.1	7.9E-02	-0.5	8.5E-01	0.4	8.0E-01
ENSMUST00000029369	spermatogenesis and oogenesis specific basic helix-loop-helix 2 [Source:MGI Symbol;Acc:MGI:1921684]		Q9D489	6.9	7.7E-05	3.0	5.3E-04	-0.1	9.0E-01	0.0	9.1E-01
ENSMUST00000029371	SMAD family member 9 [Source:MGI Symbol;Acc:MGI:1859993]	Q3UVC6	Q9JIW5	8.5	2.0E-05	-5.2	1.1E-02	-0.3	6.5E-01	-0.2	9.3E-01
ENSMUST00000029374	neurobeachin [Source:MGI Symbol;Acc:MGI:1347075]		Q9EPN1	9.2	4.2E-06	4.9	2.3E-02	-1.2	5.0E-01	-0.2	8.6E-01
ENSMUST00000029377	transmembrane 4 superfamily member 4 [Source:MGI Symbol;Acc:MGI:2385173]	Q3TMT3		5.5	1.1E-03	6.0	5.5E-06	-0.1	8.2E-01	-0.3	4.3E-01
ENSMUST00000029380	WW domain containing transcription regulator 1 [Source:MGI Symbol;Acc:MGI:1917649]		Q9EPK5	2.6	1.1E-02	-6.0	1.6E-03	-0.9	1.3E-01	0.2	8.8E-01
ENSMUST00000029382	peptidylprolyl isomerase D (cyclophilin D) [Source:MGI Symbol;Acc:MGI:1914988]		Q9CR16	-3.4	2.9E-03	4.8	2.4E-03	0.5	6.7E-01	-1.3	1.4E-01
ENSMUST00000029385	stress-associated endoplasmic reticulum protein 1 [Source:MGI Symbol;Acc:MGI:92638]		Q9Z1W5	-6.3	8.7E-06	4.4	7.7E-04	-0.5	6.1E-01	-1.0	1.6E-01
ENSMUST00000029386	electron transferring flavoprotein, dehydrogenase [Source:MGI Symbol;Acc:MGI:106100]		Q921G7	-6.7	3.0E-04	-4.9	8.1E-05	-0.8	4.3E-02	-0.6	4.2E-01
ENSMUST00000029387	eukaryotic translation initiation factor 2A [Source:MGI Symbol;Acc:MGI:1098684]		Q8BJW6	-3.8	2.0E-02	-4.4	6.1E-04	1.3	8.4E-03	-0.1	9.5E-01
ENSMUST00000029259	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Source:MGI Symbol;Acc:MGI:1919289]		Q99MR8	0.5	3.5E-01	-0.3	6.0E-01	-0.8	1.2E-01	0.0	9.5E-01
ENSMUST00000029388	RIKEN cDNA 4930579G24 gene [Source:MGI Symbol;Acc:MGI:1923189]		Q3UUX7	2.6	4.7E-04	-4.5	9.1E-06	-0.3	2.0E-01	-0.1	9.2E-01
ENSMUST00000029402	solute carrier family 33 (acetyl-CoA transporter), member 1 [Source:MGI Symbol;Acc:MGI:1332247]		Q99J27	-2.9	9.7E-03	3.2	1.6E-03	-2.0	2.9E-02	-0.1	8.2E-01
ENSMUST00000029404	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 [Source:MGI Symbol;Ac	B8QI34		7.0	9.3E-05	-6.4	2.9E-04	-1.1	3.5E-02	-1.0	4.4E-01
ENSMUST00000029414	signal sequence receptor, gamma [Source:MGI Symbol;Acc:MGI:1914687]	Q4FK79	Q9DCF9	-5.0	8.4E-07	-1.8	1.5E-01	1.3	8.7E-02	-0.1	9.5E-01
ENSMUST00000029419	ventricular zone expressed PH domain-containing 1 [Source:MGI Symbol;Acc:MGI:1920039]		A1A535	6.7	5.2E-06	6.8	2.6E-04	-0.5	6.8E-01	-0.3	6.4E-01
ENSMUST00000029421	pentraxin related gene [Source:MGI Symbol;Acc:MGI:104641]		P48759	7.1	7.1E-05	6.5	1.3E-04	-0.6	6.0E-01	0.0	9.5E-01
ENSMUST00000029277	spermatogenesis associated 5 [Source:MGI Symbol;Acc:MGI:1927170]	A0A0A0MQ80		-2.9	1.2E-01	-4.0	8.1E-02	-1.9	1.1E-01	-0.9	7.0E-01
ENSMUST00000029422	short stature homeobox 2 [Source:MGI Symbol;Acc:MGI:1201673]		P70390	5.2	4.5E-03	2.2	6.9E-02	-0.3	7.4E-01	0.6	4.7E-01
ENSMUST00000029423	serine (or cysteine) peptidase inhibitor, clade I, member 1 [Source:MGI Symbol;Acc:MGI:1194506]		O35684	4.5	1.2E-05	-4.7	3.2E-02	0.1	9.1E-01	0.6	7.8E-01
ENSMUST00000029424	programmed cell death 10 [Source:MGI Symbol;Acc:MGI:1928396]	F8WI55		-9.1	9.5E-06	7.3	2.6E-04	-0.8	5.5E-01	1.3	9.8E-02
ENSMUST00000029429	wingless-type MMTV integration site family, member 2B [Source:MGI Symbol;Acc:MGI:1261834]		O70283	4.9	1.7E-05	5.6	4.4E-04	-1.3	2.8E-01	-0.3	6.5E-01
ENSMUST00000029433	protein tyrosine phosphatase, non-receptor type 22 (lymphoid) [Source:MGI Symbol;Acc:MGI:107170]		P29352	-3.4	3.2E-04	-2.2	1.8E-02	0.0	9.3E-01	-1.4	1.2E-01
ENSMUST00000029435	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2156057]		Q8C7W7	-5.5	1.0E-02	-6.1	4.0E-04	-1.1	3.9E-02	0.4	7.7E-01
ENSMUST00000029440	olfactomedin-like 3 [Source:MGI Symbol;Acc:MGI:1914877]			6.2	3.5E-02	5.5	4.7E-03	-0.1	9.7E-01	-0.7	4.5E-01
ENSMUST00000029331	purinergic receptor P2Y, G-protein coupled 1 [Source:MGI Symbol;Acc:MGI:105049]	Q544J5	P49650	-2.1	1.1E-01	-1.3	4.4E-01	2.0	9.2E-02	1.3	4.3E-01
ENSMUST00000029441	synaptotagmin X [Source:MGI Symbol;Acc:MGI:1859546]	Q059J3	Q9R0N4	7.5	5.2E-05	-1.2	7.3E-02	0.8	6.6E-02	-0.4	5.7E-01
ENSMUST00000029444	tripartite motif-containing 33 [Source:MGI Symbol;Acc:MGI:2137357]	E9QP19		-6.6	2.9E-03	-3.1	1.3E-03	0.6	1.2E-01	0.1	8.5E-01
ENSMUST00000029445	neuroblastoma ras oncogene [Source:MGI Symbol;Acc:MGI:97376]	Q9D091		-1.7	5.8E-03	-4.7	4.1E-02	-0.8	4.1E-01	-0.9	7.0E-01
ENSMUST00000029353	karyopherin (importin) alpha 4 [Source:MGI Symbol;Acc:MGI:1100848]	A0A0B4J1E7		0.3	7.0E-01	0.6	6.1E-01	0.5	5.7E-01	0.2	8.3E-01
ENSMUST00000029446	cold shock domain containing E1, RNA binding [Source:MGI Symbol;Acc:MGI:92356]	Q3U1S6	Q91W50	-4.4	2.5E-05	2.6	1.9E-03	-0.5	3.4E-01	-0.2	6.7E-01
ENSMUST00000029448	synaptonemal complex protein 1 [Source:MGI Symbol;Acc:MGI:105931]		Q62209	3.2	1.4E-03	1.4	9.0E-02	-1.0	1.9E-01	0.1	8.9E-01
ENSMUST00000029454	calsequestrin 2 [Source:MGI Symbol;Acc:MGI:1309469]		O09161	7.0	1.1E-03	6.2	1.3E-03	-0.5	7.6E-01	-0.6	4.6E-01
ENSMUST00000029456	CD2 antigen [Source:MGI Symbol;Acc:MGI:88320]	Q549Q4	P08920	-2.1	1.8E-02	5.6	5.5E-04	-0.5	6.4E-01	0.3	6.6E-01
ENSMUST00000029459	ganglioside-induced differentiation-associated-protein 2 [Source:MGI Symbol;Acc:MGI:1338001]		Q9DBL2	-4.2	8.9E-06	6.4	2.6E-04	-0.5	7.0E-01	0.0	9.9E-01
ENSMUST00000029462	T-box 15 [Source:MGI Symbol;Acc:MGI:1277234]		O70306	8.8	1.0E-05	8.2	7.9E-05	-0.7	5.8E-01	-0.4	4.3E-01
ENSMUST00000029463	roxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 6 [Source:MGI Symbol;Acc:MGI:1095		O35469	6.5	6.3E-05	4.9	4.1E-05	-4.3	1.0E-03	-0.1	8.5E-01
ENSMUST00000029376	transmembrane 4 superfamily member 1 [Source:MGI Symbol;Acc:MGI:104678]		Q64302	2.4	4.9E-02	-3.2	7.3E-03	-6.4	5.5E-05	-0.8	4.0E-01
ENSMUST00000029469	regenerating islet-derived family, member 4 [Source:MGI Symbol;Acc:MGI:1914959]		Q9D8G5	6.0	4.3E-04	3.2	1.4E-02	-2.5	6.5E-02	-0.2	7.9E-01
ENSMUST00000029477	e carrier family 25 (mitochondrial carrier, phosphate carrier), member 24 [Source:MGI Symbol;Acc:MGI:1917		Q8BMD8	-4.0	1.5E-05	-1.3	2.5E-01	-1.8	4.0E-02	2.0	7.0E-02
ENSMUST00000029480	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B [Source:MGI Symbol;Acc:MGI:1914171]		Q80SY5	-4.5	5.2E-03	-3.3	8.6E-03	-0.5	4.0E-01	-0.6	5.8E-01
ENSMUST00000029489	glutathione S-transferase, mu 4 [Source:MGI Symbol;Acc:MGI:95862]	Q8R5I6		3.0	3.1E-03	-5.8	1.6E-04	1.3	9.8E-03	0.8	4.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000029490	S-adenosylhomocysteine hydrolase-like 1 [Source:MGI Symbol;Acc:MGI:2385184]		Q80SW1	-2.8	1.6E-04	-6.5	2.3E-03	0.0	9.8E-01	-0.2	9.2E-01
ENSMUST00000029504	chymosin [Source:MGI Symbol;Acc:MGI:2684977]	B7ZWD6		6.1	2.6E-04	-5.8	8.6E-03	-1.6	7.7E-02	0.5	7.9E-01
ENSMUST00000029507	DNA-damage regulated autophagy modulator 2 [Source:MGI Symbol;Acc:MGI:1914421]	Q9D835		-4.9	3.3E-03	3.1	1.1E-03	0.6	3.0E-01	0.2	7.6E-01
ENSMUST00000029508	DENN/MADD domain containing 2D [Source:MGI Symbol;Acc:MGI:2181193]		Q91VV4	-3.4	1.3E-03	-3.7	5.8E-02	1.4	1.2E-01	2.1	2.3E-01
ENSMUST00000029515	S100 calcium binding protein A11 [Source:MGI Symbol;Acc:MGI:1338798]		P50543	-9.7	2.0E-08	6.8	2.2E-04	-0.5	6.8E-01	-0.4	5.9E-01
ENSMUST00000029405	guanine monophosphate synthetase [Source:MGI Symbol;Acc:MGI:2448526]	B2RRH9	Q3THK7	-1.0	4.4E-02	-0.8	1.6E-01	-0.1	8.1E-01	-0.3	6.0E-01
ENSMUST00000029516	trichohyalin-like 1 [Source:MGI Symbol;Acc:MGI:1918575]		Q9D3P1	8.8	3.8E-05	-4.5	1.6E-05	0.3	1.8E-01	-0.2	6.7E-01
ENSMUST00000029520	late cornified envelope 1M [Source:MGI Symbol;Acc:MGI:1913453]	Q9CR91		6.2	1.9E-04	8.0	6.5E-06	0.8	3.8E-01	-0.5	2.4E-01
ENSMUST00000029524	late cornified envelope 1D [Source:MGI Symbol;Acc:MGI:1916861]	Q9D731		5.8	4.1E-03	5.6	4.5E-04	-1.5	2.2E-01	-0.1	9.3E-01
ENSMUST00000029535	late cornified envelope-like proline-rich 1 [Source:MGI Symbol;Acc:MGI:1916582]		Q9DAE3	7.0	5.5E-05	4.7	9.9E-03	-1.4	3.9E-01	-0.9	3.5E-01
ENSMUST00000029540	natriuretic peptide receptor 1 [Source:MGI Symbol;Acc:MGI:97371]	Q2TAY4	P18293	7.8	5.8E-05	3.8	4.6E-05	-1.5	1.9E-02	-0.8	4.6E-02
ENSMUST00000029545	CREB regulated transcription coactivator 2 [Source:MGI Symbol;Acc:MGI:1921593]		Q3U182	-3.8	5.1E-03	-8.0	1.6E-04	0.1	7.7E-01	-0.9	5.2E-01
ENSMUST00000029546	jumping translocation breakpoint [Source:MGI Symbol;Acc:MGI:1346082]	Q542D4	O88824	-6.4	1.8E-04	4.3	1.3E-04	-0.8	2.0E-01	-0.3	5.8E-01
ENSMUST00000029548	nucleoporin 210-like [Source:MGI Symbol;Acc:MGI:1924845]		Q9D2F7	3.4	1.4E-03	-3.2	1.3E-03	-0.1	7.5E-01	-0.3	7.0E-01
ENSMUST00000029549	tropomyosin 3, gamma [Source:MGI Symbol;Acc:MGI:1890149]	Q58E70	P21107	-3.7	3.2E-04	-3.8	9.2E-02	1.5	2.3E-01	-0.2	9.2E-01
ENSMUST00000029438	homeodomain interacting protein kinase 1 [Source:MGI Symbol;Acc:MGI:1314873]		O88904	1.3	7.2E-01	5.3	2.1E-01	0.9	8.1E-01	-3.1	3.9E-01
ENSMUST00000029553	ubiquitin-associated protein 2-like [Source:MGI Symbol;Acc:MGI:1921633]		Q80X50	-2.6	2.0E-03	6.2	4.6E-02	-0.9	7.8E-01	-0.8	6.3E-01
ENSMUST00000029559	interleukin 6 receptor, alpha [Source:MGI Symbol;Acc:MGI:105304]		P22272	-3.1	3.9E-05	6.8	2.0E-04	-0.6	6.1E-01	0.0	9.6E-01
ENSMUST00000029562	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal) [Source:MGI Symbol;Acc:MGI:87891]		Q9ERK7	4.5	1.2E-05	-3.9	1.2E-01	2.0	1.2E-01	-0.7	7.7E-01
ENSMUST00000029565	solute carrier family 50 (sugar transporter), member 1 [Source:MGI Symbol;Acc:MGI:107417]		Q9CXK4	-3.6	8.3E-03	-1.5	4.9E-02	0.8	9.8E-02	0.6	3.9E-01
ENSMUST00000029570	hippocampus abundant gene transcript 1 [Source:MGI Symbol;Acc:MGI:1201609]		P70187	-5.5	1.2E-06	-3.6	4.5E-04	0.1	8.4E-01	-0.7	3.2E-01
ENSMUST00000029447	suppressor of IKBKE 1 [Source:MGI Symbol;Acc:MGI:1913891]		Q9CPR7	-0.1	9.1E-01	-0.1	8.7E-01	0.6	3.4E-01	0.7	4.2E-01
ENSMUST00000029573	leucine rich repeat containing 39 [Source:MGI Symbol;Acc:MGI:1924557]	Q0VDT4	Q8BGI7	1.9	3.4E-02	2.2	3.1E-02	-0.3	7.4E-01	0.8	2.9E-01
ENSMUST00000029451	tetraspanin 2 [Source:MGI Symbol;Acc:MGI:1917997]		Q922J6	-1.0	2.3E-01	-0.5	6.5E-01	0.4	6.1E-01	-0.2	8.6E-01
ENSMUST00000029574	vascular cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:98926]	Q3UPN1		4.7	1.7E-04	4.0	4.3E-02	-0.6	7.6E-01	2.4	6.1E-02
ENSMUST00000029587	neurogenin 2 [Source:MGI Symbol;Acc:MGI:109619]	Q6GTH9		7.4	3.4E-05	-4.7	1.8E-03	-1.9	5.7E-03	0.7	5.4E-01
ENSMUST00000029598	RIKEN cDNA 1700006A11 gene [Source:MGI Symbol;Acc:MGI:1919074]	B9EHI3		5.3	9.1E-04	-3.7	1.5E-04	0.4	2.0E-01	-0.1	8.4E-01
ENSMUST00000029603	protease, serine 12 neurotrypsin (motopsin) [Source:MGI Symbol;Acc:MGI:1100881]		O08762	6.7	3.0E-05	6.0	5.8E-04	-1.7	1.9E-01	1.1	1.3E-01
ENSMUST00000029623	toll-like receptor 2 [Source:MGI Symbol;Acc:MGI:1346060]	G3X8Y8		-4.8	1.2E-05	5.8	3.9E-04	-0.5	6.7E-01	0.1	8.3E-01
ENSMUST00000029624	coiled-coil domain containing 109B [Source:MGI Symbol;Acc:MGI:1914065]		Q810S1	-3.0	5.4E-03	5.5	1.0E-03	-1.5	2.6E-01	-1.0	2.0E-01
ENSMUST00000029476	SEC22 homolog B, vesicle trafficking protein [Source:MGI Symbol;Acc:MGI:1338759]		O08547	-0.8	2.0E-01	1.1	2.1E-01	1.5	3.6E-02	-0.4	5.9E-01
ENSMUST00000029625	secreted frizzled-related protein 2 [Source:MGI Symbol;Acc:MGI:108078]	Q3UI35	P97299	6.9	7.2E-05	-2.7	1.9E-03	1.1	7.5E-03	-0.2	7.4E-01
ENSMUST00000029626	caspase 6 [Source:MGI Symbol;Acc:MGI:1312921]	Q3TPJ9	O08738	-6.2	2.4E-05	-7.6	2.2E-02	0.2	8.0E-01	3.2	2.7E-01
ENSMUST00000029482	G-protein signalling modulator 2 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:1923373]	Q3UPG3	Q8VDU0	-0.4	4.1E-01	-0.7	2.1E-01	0.3	4.5E-01	0.7	2.3E-01
ENSMUST00000029483	chloride channel CLIC-like 1 [Source:MGI Symbol;Acc:MGI:2385186]		Q99LI2	3.6	5.7E-02	2.6	3.2E-01	0.2	9.1E-01	1.3	5.0E-01
ENSMUST00000029486				4.8	1.0E-01	5.4	6.9E-02	-2.0	5.2E-01	-2.6	1.6E-01
ENSMUST00000029632	ıin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase) [Source:MGI Symbol;Acc:MGI:1891	B2RUR5	Q9JI60	7.1	3.6E-05	1.9	6.4E-02	-0.7	3.9E-01	0.4	5.7E-01
ENSMUST00000029644	pyrophosphatase (inorganic) 2 [Source:MGI Symbol;Acc:MGI:1922026]		Q91VM9	-5.8	3.2E-05	-2.3	3.6E-03	0.8	4.7E-02	0.3	6.4E-01
ENSMUST00000029499	solute carrier family 6 (neurotransmitter transporter), member 17 [Source:MGI Symbol;Acc:MGI:2442535]			6.7	7.0E-02	1.1	8.4E-01	-0.6	8.8E-01	5.0	3.0E-01
ENSMUST00000029650	integrator complex subunit 12 [Source:MGI Symbol;Acc:MGI:1919043]		Q9D168	-5.0	5.2E-05	5.1	4.9E-04	-2.1	8.8E-02	-1.1	1.1E-01
ENSMUST00000029651	glutathione S-transferase, C-terminal domain containing [Source:MGI Symbol;Acc:MGI:1914803]		Q5RL51	-3.5	6.3E-03	-4.2	2.2E-02	-0.1	8.4E-01	-0.8	6.5E-01
ENSMUST00000029653	epidermal growth factor [Source:MGI Symbol;Acc:MGI:95290]		P01132	6.7	1.4E-04	-2.4	3.5E-02	0.8	1.8E-01	-0.2	8.2E-01
ENSMUST00000029662	alpha-kinase 1 [Source:MGI Symbol;Acc:MGI:1918731]	E9QNX4		-6.5	1.1E-04	-9.2	2.2E-07	-0.1	6.2E-01	-0.6	3.7E-01
ENSMUST00000029663	ıinoacyl tRNA synthetase complex-interacting multifunctional protein 1 [Source:MGI Symbol;Acc:MGI:10277	Q3UZG4		-3.9	2.1E-04	7.5	2.9E-04	-0.8	6.0E-01	0.6	4.1E-01
ENSMUST00000029665	dickkopf homolog 2 (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1890663]		Q9QYZ8	6.1	1.1E-04	6.0	4.7E-04	-0.5	6.7E-01	-0.3	6.7E-01
ENSMUST00000029667	potassium voltage-gated channel, subfamily Q, member 5 [Source:MGI Symbol;Acc:MGI:1924937]		Q9JK45	6.2	3.2E-03	4.3	3.3E-02	-0.7	7.0E-01	0.9	4.5E-01
ENSMUST00000029670	prostaglandin F receptor [Source:MGI Symbol;Acc:MGI:97796]	Q60I90	P43117	7.4	4.4E-05	5.9	3.4E-04	-0.6	6.0E-01	0.4	5.1E-01
ENSMUST00000029671	interferon-induced protein 44 [Source:MGI Symbol;Acc:MGI:2443016]		Q8BV66	5.2	2.9E-03	3.5	1.4E-03	-4.5	2.2E-03	-0.2	7.0E-01
ENSMUST00000029542	integrator complex subunit 3 [Source:MGI Symbol;Acc:MGI:2140050]		Q7TPD0	-3.1	7.4E-02	-2.2	3.4E-01	1.6	2.5E-01	0.7	7.6E-01
ENSMUST00000029673	ephrin A3 [Source:MGI Symbol;Acc:MGI:106644]		O08545	7.2	3.5E-05	-2.8	5.5E-02	1.2	1.2E-01	0.1	9.2E-01
ENSMUST00000029674	ephrin A4 [Source:MGI Symbol;Acc:MGI:106643]	Q3UQB5	O08542	4.7	1.1E-03	-5.0	1.4E-03	0.1	8.0E-01	-1.3	3.4E-01
ENSMUST00000029676	a disintegrin and metallopeptidase domain 15 (metargidin) [Source:MGI Symbol;Acc:MGI:1333882]		O88839	-9.0	7.2E-05	5.8	5.8E-04	1.5	1.9E-01	-0.8	2.1E-01
ENSMUST00000029677	zinc finger and BTB domain containing 7B [Source:MGI Symbol;Acc:MGI:102755]	Q5BJ24	Q64321	-8.2	7.8E-05	-6.6	2.1E-03	1.6	1.2E-02	4.5	1.7E-02
ENSMUST00000029551	RIKEN cDNA 4933434E20 gene [Source:MGI Symbol;Acc:MGI:1914027]			1.0	2.5E-01	1.3	2.2E-01	0.2	8.2E-01	-0.2	8.6E-01
ENSMUST00000029679	CDC28 protein kinase 1b [Source:MGI Symbol;Acc:MGI:1889208]		P61025	-1.9	1.2E-02	-1.7	6.0E-02	0.5	3.7E-01	-0.5	5.7E-01
ENSMUST00000029684	secretory carrier membrane protein 3 [Source:MGI Symbol;Acc:MGI:1346346]		O35609	-6.1	8.9E-03	-2.5	1.6E-03	1.1	6.2E-03	0.6	3.2E-01
ENSMUST00000029686	hyperpolarization-activated, cyclic nucleotide-gated K+ 3 [Source:MGI Symbol;Acc:MGI:1298211]	B2RRB5	O88705	7.7	2.3E-05	5.1	2.6E-05	0.7	2.6E-01	0.1	8.5E-01
ENSMUST00000029563	adenosine deaminase, RNA-specific [Source:MGI Symbol;Acc:MGI:1889575]		Q99MU3	-0.5	8.7E-01	0.4	9.4E-01	1.7	5.7E-01	0.8	8.5E-01
ENSMUST00000029564	phosphomevalonate kinase [Source:MGI Symbol;Acc:MGI:1915853]		Q9D1G2	-1.6	7.9E-02	-3.2	3.4E-02	0.3	6.1E-01	1.9	1.6E-01
ENSMUST00000029692	Ras-like without CAAX 1 [Source:MGI Symbol;Acc:MGI:108053]		P70426	-7.3	2.3E-04	-3.0	2.2E-02	-0.3	6.4E-01	-0.9	4.9E-01
ENSMUST00000029567	family with sequence similarity 198, member B [Source:MGI Symbol;Acc:MGI:1915909]		Q3UPI1	4.3	8.1E-02	-0.1	9.8E-01	-1.5	5.4E-01	2.9	2.4E-01
ENSMUST00000029569	er family 35 (UDP-N-acetylglucosamine (UDP-GleNAc) transporter), member 3 [Source:MGI Symbol;Acc:MG		Q8R1T4	-0.6	1.3E-01	-0.3	5.6E-01	0.6	1.2E-01	0.3	5.6E-01
ENSMUST00000029694	rho/rac guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:103264]		Q60875	-5.3	3.4E-04	-5.0	1.6E-05	0.3	3.0E-01	-0.2	7.8E-01
ENSMUST00000029571	spindle assembly 6 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1920026]			0.7	1.1E-01	0.7	2.1E-01	0.4	3.3E-01	0.4	4.6E-01
ENSMUST00000029696	RIKEN cDNA 2810403A07 gene [Source:MGI Symbol;Acc:MGI:1921450]		Q3TCX3	-3.5	3.1E-04	4.0	1.4E-03	0.6	4.9E-01	-1.5	6.2E-02
ENSMUST00000029698	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2 [Source:MGI Symbol;Acc:MGI:1932697]		Q9JHS3	-7.8	8.2E-05	-0.7	2.3E-01	-6.2	9.1E-06	-0.8	2.2E-01
ENSMUST00000029700	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI		Q62178	-6.6	8.5E-05	7.1	9.0E-05	-0.6	6.2E-01	-0.3	6.4E-01
ENSMUST00000029588	La ribonucleoprotein domain family, member 7 [Source:MGI Symbol;Acc:MGI:107634]		Q05CL8	-1.4	4.1E-02	-1.9	2.1E-02	-1.1	3.6E-02	-0.5	4.7E-01
ENSMUST00000029708	apolipoprotein A-I binding protein [Source:MGI Symbol;Acc:MGI:2180167]		Q8K4Z3	-2.3	2.2E-03	6.4	4.6E-04	-0.4	7.4E-01	-1.5	5.2E-02
ENSMUST00000029709	SH2 domain containing 2A [Source:MGI Symbol;Acc:MGI:1351596]	Q5D0E4	Q9QXK9	3.9	1.5E-03	6.6	1.2E-04	0.1	9.2E-01	0.2	7.7E-01
ENSMUST00000029610	hydroxyacyl-Coenzyme A dehydrogenase [Source:MGI Symbol;Acc:MGI:96009]		Q61425	-1.2	8.1E-02	-1.2	1.3E-01	-0.3	4.9E-01	-0.3	7.1E-01
ENSMUST00000029611	lymphoid enhancer binding factor 1 [Source:MGI Symbol;Acc:MGI:96770]	Q3TYB0	P27782	0.7	7.8E-01	3.4	1.9E-01	-0.4	8.4E-01	-3.1	2.3E-01
ENSMUST00000029711	insulin receptor-related receptor [Source:MGI Symbol;Acc:MGI:1346037]		Q9WTL4	8.8	8.1E-06	-3.4	7.3E-04	0.9	2.9E-02	-0.5	4.7E-01
ENSMUST00000029712	neurotrophic tyrosine kinase, receptor, type 1 [Source:MGI Symbol;Acc:MGI:97383]		Q3UFB7	7.9	3.7E-05	-3.3	1.5E-02	-0.5	4.5E-01	-0.1	9.0E-01
ENSMUST00000029717	CD1d1 antigen [Source:MGI Symbol;Acc:MGI:107674]			-3.4	3.3E-02	2.2	1.7E-02	-4.4	1.2E-03	0.3	6.2E-01
ENSMUST00000029719	doublecortin-like kinase 2 [Source:MGI Symbol;Acc:MGI:1918012]		Q6PGN3	2.9	2.7E-02	-5.5	3.8E-04	0.5	3.1E-01	-0.3	8.0E-01
ENSMUST00000029628	pleiotropic regulator 1, PRL1 homolog (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1858197]	F8WI31		-5.0	5.5E-02	-5.3	8.6E-02	-1.4	3.0E-01	-1.1	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000029629	phospholipase A2, group XIIA [Source:MGI Symbol;Acc:MGI:1913600]		Q9EPR2	0.5	4.5E-01	-1.4	1.7E-01	-1.0	1.8E-01	1.0	3.0E-01
ENSMUST00000029630	fibrinogen alpha chain [Source:MGI Symbol;Acc:MGI:1316726]		E9PV24	4.3	3.8E-02	-0.6	7.0E-01	-5.2	1.7E-02	-0.2	8.9E-01
ENSMUST00000029722	ribosomal protein S3A1 [Source:MGI Symbol;Acc:MGI:1202063]	Q564F3	P97351	-7.2	4.3E-06	5.7	1.7E-04	-1.5	1.8E-01	0.0	9.6E-01
ENSMUST00000029635	guanylate cyclase 1, soluble, beta 3 [Source:MGI Symbol;Acc:MGI:1860604]		O54865	4.5	5.8E-02	0.2	9.3E-01	-4.6	4.4E-02	-0.3	8.7E-01
ENSMUST00000029643	GAR1 ribonucleoprotein homolog (yeast) [Source:MGI Symbol;Acc:MGI:1930948]		Q9CY66	0.7	4.6E-01	-0.7	6.7E-01	0.9	4.0E-01	2.3	1.2E-01
ENSMUST00000029729	flavin containing monooxygenase 5 [Source:MGI Symbol;Acc:MGI:1310004]		P97872	-3.5	4.1E-04	-5.1	5.8E-04	0.4	3.8E-01	-0.3	7.6E-01
ENSMUST00000029649	cathepsin O [Source:MGI Symbol;Acc:MGI:2139628]		Q8BM88	-1.0	1.2E-01	-1.5	9.2E-02	0.1	8.6E-01	0.6	4.9E-01
ENSMUST00000029738	G protein-coupled receptor 89 [Source:MGI Symbol;Acc:MGI:1914799]		Q8BS95	3.1	2.0E-02	-5.3	2.4E-04	-0.2	6.7E-01	0.2	8.7E-01
ENSMUST00000029740	ring finger protein 115 [Source:MGI Symbol;Acc:MGI:1915095]		Q9D0C1	-5.8	7.0E-07	-0.7	5.9E-01	1.5	6.8E-02	-1.4	3.0E-01
ENSMUST00000029652	platelet-derived growth factor, C polypeptide [Source:MGI Symbol;Acc:MGI:1859631]		Q8CI19	4.1	4.1E-02	6.3	8.4E-03	-0.4	8.5E-01	-2.7	4.2E-02
ENSMUST00000029741	polymerase (RNA) III (DNA directed) polypeptide C [Source:MGI Symbol;Acc:MGI:1921664]	B2RX77	Q9D483	-7.5	6.5E-06	5.4	2.8E-04	-1.8	1.3E-01	-0.5	5.0E-01
ENSMUST00000029742	nudix (nucleoside diphosphate linked moiety X)-type motif 17 [Source:MGI Symbol;Acc:MGI:1925623]		Q9CWD3	5.2	2.6E-02	-5.6	1.9E-03	0.3	5.4E-01	-0.6	6.6E-01
ENSMUST00000029752	threonyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:1919057]		Q3UQ84	-5.8	1.3E-04	-4.5	3.0E-04	-1.2	2.2E-02	-0.6	5.1E-01
ENSMUST00000029753	extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:103060]	F8WI14		-5.4	2.2E-03	6.8	1.7E-02	1.2	6.0E-01	-0.4	7.8E-01
ENSMUST00000029766	breast cancer anti-estrogen resistance 3 [Source:MGI Symbol;Acc:MGI:1352501]		Q9QZK2	3.4	4.0E-04	6.7	1.1E-03	1.0	5.0E-01	0.4	5.9E-01
ENSMUST00000029666	3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Source:MGI Symbol;Acc:MGI:1330587]	Q3U647	Q60967	-0.6	1.9E-01	-0.3	5.5E-01	0.1	8.2E-01	-0.2	7.4E-01
ENSMUST00000029769	glutamate-cysteine ligase, modifier subunit [Source:MGI Symbol;Acc:MGI:104995]	Q4FJZ6	O09172	-3.3	1.1E-04	4.4	4.2E-02	-0.6	7.6E-01	1.2	3.5E-01
ENSMUST00000029773	calponin 3, acidic [Source:MGI Symbol;Acc:MGI:1919244]		Q9DAW9	3.4	2.5E-04	7.5	6.9E-05	-0.5	7.0E-01	-0.6	2.7E-01
ENSMUST00000029777	transmembrane protein 56 [Source:MGI Symbol;Acc:MGI:1923195]		Q8CGF5	6.6	2.6E-04	1.2	3.5E-01	-3.4	2.2E-02	0.5	6.4E-01
ENSMUST00000029780	polypyrimidine tract binding protein 2 [Source:MGI Symbol;Acc:MGI:1860489]		Q91Z31	-2.3	1.7E-03	6.6	1.3E-04	-0.5	6.6E-01	0.1	8.9E-01
ENSMUST00000029783	sorting nexin family member 27 [Source:MGI Symbol;Acc:MGI:1923992]		Q3UHD6	-3.3	7.3E-04	4.0	2.8E-03	-1.7	1.2E-01	-0.9	2.7E-01
ENSMUST00000029784	CUGBP, Elav-like family member 3 [Source:MGI Symbol;Acc:MGI:1926034]		Q8CIN6	6.8	2.5E-05	-7.9	1.3E-03	1.3	3.2E-02	0.2	9.2E-01
ENSMUST00000029786	mitochondrial ribosomal protein L9 [Source:MGI Symbol;Acc:MGI:2137211]	Q14B21	Q99N94	-1.2	1.3E-02	-5.0	9.3E-04	0.5	3.1E-01	-2.6	8.1E-02
ENSMUST00000029794	thioesterase superfamily member 5 [Source:MGI Symbol;Acc:MGI:1913448]		Q9CQJ0	7.1	5.4E-05	-2.5	7.3E-03	-1.4	1.2E-02	-0.9	2.8E-01
ENSMUST00000029682	thrombospondin 3 [Source:MGI Symbol;Acc:MGI:98739]		Q05895	-3.4	4.8E-02	-2.4	2.4E-01	0.5	6.0E-01	-0.4	8.4E-01
ENSMUST00000029795	RAR-related orphan receptor gamma [Source:MGI Symbol;Acc:MGI:104856]			7.0	1.5E-05	-4.6	1.1E-01	1.8	2.3E-01	0.4	8.9E-01
ENSMUST00000029796	RAP1, GTP-GDP dissociation stimulator 1 [Source:MGI Symbol;Acc:MGI:2385189]	E9Q6Q4		-6.1	7.2E-03	6.6	1.5E-04	-1.0	4.0E-01	0.1	8.7E-01
ENSMUST00000029803	eukaryotic translation initiation factor 4E [Source:MGI Symbol;Acc:MGI:95305]	Q3TK95	P63073	-2.6	2.3E-04	-5.2	1.5E-03	0.1	8.0E-01	-2.0	2.0E-01
ENSMUST00000029804	methionyl aminopeptidase 1 [Source:MGI Symbol;Acc:MGI:1922874]	Q4VAA9	Q8BP48	-2.2	2.7E-04	-1.9	7.9E-02	0.9	1.5E-01	-2.4	4.9E-02
ENSMUST00000029805	microsomal triglyceride transfer protein [Source:MGI Symbol;Acc:MGI:106926]		O08601	5.3	1.2E-02	-2.8	6.1E-03	0.5	2.8E-01	-0.2	7.7E-01
ENSMUST00000029806	dual adaptor for phosphotyrosine and 3-phosphoinositides 1 [Source:MGI Symbol;Acc:MGI:1347063]	Q3UK44	Q9QXT1	-3.8	2.0E-02	-5.8	1.7E-04	-0.9	7.1E-02	-2.9	4.4E-02
ENSMUST00000029699	lamin A [Source:MGI Symbol;Acc:MGI:96794]		P48678	-1.6	1.3E-01	-0.7	4.9E-01	-1.7	4.9E-02	-2.6	4.2E-02
ENSMUST00000029812	uclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 [Source:MGI Symbol;Acc:MGI:9731		P25799	-4.9	3.2E-03	-6.3	1.4E-03	0.8	1.8E-01	0.5	7.5E-01
ENSMUST00000029707	G patch domain containing 4 [Source:MGI Symbol;Acc:MGI:1913864]		Q3TFK5	-2.1	1.9E-01	-3.4	6.3E-02	-2.4	6.2E-02	-1.1	5.4E-01
ENSMUST00000029814	mannosidase, beta A, lysosomal [Source:MGI Symbol;Acc:MGI:88175]			-2.6	2.5E-03	-1.9	2.0E-02	0.5	3.0E-01	0.1	8.7E-01
ENSMUST00000029815	CDGSH iron sulfur domain 2 [Source:MGI Symbol;Acc:MGI:1914256]		Q9CQB5	-1.6	1.2E-02	2.7	4.8E-02	0.0	9.7E-01	1.2	2.2E-01
ENSMUST00000029822	tachykinin receptor 3 [Source:MGI Symbol;Acc:MGI:892968]		P47937	7.8	1.4E-05	8.5	2.2E-05	-0.6	5.9E-01	-0.3	5.0E-01
ENSMUST00000029836	deoxyribonuclease II beta [Source:MGI Symbol;Acc:MGI:1913283]		Q9QY48	3.9	1.2E-04	7.3	1.4E-04	-0.6	6.4E-01	0.0	9.9E-01
ENSMUST00000029837	urate oxidase [Source:MGI Symbol;Acc:MGI:98907]	Q543J0	P25688	5.1	1.6E-03	-1.1	4.4E-01	0.1	9.4E-01	-2.3	1.7E-01
ENSMUST00000029838	ribosome production factor 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1917535]		Q7TND5	-3.7	1.8E-04	5.2	1.0E-03	-0.6	6.4E-01	-2.8	8.3E-03
ENSMUST00000029842	B cell leukemia/lymphoma 10 [Source:MGI Symbol;Acc:MGI:1337994]	B7ZWE5	Q9Z0H7	-5.9	1.9E-06	-7.7	1.5E-05	-1.1	1.0E-02	-0.6	5.1E-01
ENSMUST00000029845	dimethylarginine dimethylaminohydrolase 1 [Source:MGI Symbol;Acc:MGI:1916469]		Q9CWS0	7.6	8.7E-05	-1.9	3.8E-02	1.5	1.1E-02	-0.1	9.5E-01
ENSMUST00000029730	chromodomain helicase DNA binding protein 1-like [Source:MGI Symbol;Acc:MGI:1915308]		Q9CXF7	0.0	9.9E-01	1.1	1.1E-01	0.8	1.2E-01	-0.3	6.2E-01
ENSMUST00000029846	cysteine rich protein 61 [Source:MGI Symbol;Acc:MGI:88613]	Q3TX21	P18406	6.8	1.3E-04	1.7	1.5E-01	-2.1	7.1E-02	-0.7	4.6E-01
ENSMUST00000029848	collagen, type XXIV, alpha 1 [Source:MGI Symbol;Acc:MGI:1918605]		Q30D77	7.6	2.6E-05	-5.3	1.2E-05	0.4	1.4E-01	-0.1	8.5E-01
ENSMUST00000029865	transformation related protein 53 inducible nuclear protein 1 [Source:MGI Symbol;Acc:MGI:1926609]	Q3UQK9	Q9QXE4	-8.0	2.9E-04	-2.5	2.4E-03	0.7	5.8E-02	-4.3	6.8E-04
ENSMUST00000029875	transmembrane protein 55A [Source:MGI Symbol;Acc:MGI:1919769]		Q9CZX7	-2.3	9.5E-04	4.7	5.0E-02	-2.3	3.2E-01	-1.8	2.3E-01
ENSMUST00000029744	integrin, alpha 10 [Source:MGI Symbol;Acc:MGI:2153482]	E9Q6R1		4.2	1.0E-01	5.3	5.7E-02	-1.3	6.4E-01	-2.4	1.4E-01
ENSMUST00000029748	Fc receptor, IgG, high affinity I [Source:MGI Symbol;Acc:MGI:95498]		P26151	-0.9	7.9E-02	-2.4	1.6E-03	-2.3	1.6E-04	-0.8	2.0E-01
ENSMUST00000029877	2,4-dienoyl CoA reductase 1, mitochondrial [Source:MGI Symbol;Acc:MGI:1914710]	Q4FJK0	Q9CQ62	1.8	7.2E-03	-5.1	1.7E-03	0.1	8.9E-01	-0.6	6.2E-01
ENSMUST00000029885	copine III [Source:MGI Symbol;Acc:MGI:1917818]		Q8BT60	-2.0	2.3E-04	-6.8	1.2E-02	0.2	7.7E-01	1.6	4.9E-01
ENSMUST00000029759	methyltransferase like 14 [Source:MGI Symbol;Acc:MGI:2442926]		Q3UIK4	-1.4	3.6E-02	-0.6	3.9E-01	0.1	8.8E-01	-0.7	3.4E-01
ENSMUST00000029888	regulator of microtubule dynamics 1 [Source:MGI Symbol;Acc:MGI:1913552]		Q9DCV4	-4.3	3.6E-04	2.4	8.1E-03	-0.8	2.2E-01	0.1	8.8E-01
ENSMUST00000029891	transmembrane protein 68 [Source:MGI Symbol;Acc:MGI:1919348]		Q9D850	-1.7	2.2E-02	-1.6	3.7E-02	1.7	1.8E-03	0.1	9.2E-01
ENSMUST00000029770	ATP-binding cassette, sub-family D (ALD), member 3 [Source:MGI Symbol;Acc:MGI:1349216]		P55096	-0.6	3.1E-01	-1.0	2.2E-01	0.0	9.4E-01	0.3	6.6E-01
ENSMUST00000029771	coagulation factor III [Source:MGI Symbol;Acc:MGI:88381]			1.3	2.2E-01	2.4	6.4E-02	-0.1	9.0E-01	-1.2	2.3E-01
ENSMUST00000029772	regulatory factor X, 5 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:1858421]		Q9JL61	4.1	1.2E-01	4.1	1.3E-01	-3.2	2.4E-01	-3.3	1.1E-01
ENSMUST00000029900	ATPase, H+ transporting, lysosomal V0 subunit D2 [Source:MGI Symbol;Acc:MGI:1924415]		Q80SY3	7.1	4.7E-04	-0.9	1.0E-01	-4.9	6.7E-06	-0.5	3.5E-01
ENSMUST00000029905	cytochrome P450, family 7, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:106091]		Q64505	6.0	5.0E-05	5.6	1.4E-03	-0.5	7.1E-01	0.5	5.2E-01
ENSMUST00000029907	UBX domain protein 2B [Source:MGI Symbol;Acc:MGI:1915303]		Q0KL01	2.9	1.5E-03	-2.6	3.4E-03	0.0	9.8E-01	0.3	6.5E-01
ENSMUST00000029910	neutral sphingomyelinase (N-SMase) activation associated factor [Source:MGI Symbol;Acc:MGI:1341864]		O35242	-5.5	1.8E-04	-1.7	6.6E-02	1.1	4.9E-02	-0.4	6.1E-01
ENSMUST00000029911	PNN interacting serine/arginine-rich [Source:MGI Symbol;Acc:MGI:1913875]	A2AJT5		-2.8	1.8E-03	5.9	3.0E-04	-0.7	5.2E-01	0.2	7.6E-01
ENSMUST00000029912	syndecan binding protein [Source:MGI Symbol;Acc:MGI:1337026]		O08992	-5.4	1.2E-06	-0.9	1.1E-01	0.2	5.2E-01	-0.1	8.2E-01
ENSMUST00000029919	chloride channel accessory 1 [Source:MGI Symbol;Acc:MGI:1346342]		Q9D7Z6	6.9	4.3E-05	7.0	1.2E-04	-0.5	6.4E-01	-0.5	4.6E-01
ENSMUST00000029929	chloride channel accessory 3A2 [Source:MGI Symbol;Acc:MGI:1931471]	Q9EQR4		5.9	3.9E-05	3.5	6.0E-04	-3.4	2.3E-03	0.1	8.4E-01
ENSMUST00000029932	chloride channel accessory 3A1 [Source:MGI Symbol;Acc:MGI:1316732]	Q91Z28		6.8	7.1E-05	-3.2	3.3E-01	3.7	6.2E-02	0.8	7.8E-01
ENSMUST00000029800	tetraspanin 5 [Source:MGI Symbol;Acc:MGI:1928096]		P62080	-4.5	1.6E-01	-0.2	9.7E-01	4.1	2.2E-01	-0.2	9.5E-01
ENSMUST00000029936	guanylate binding protein 2b [Source:MGI Symbol;Acc:MGI:95666]	A4UUI2		-4.0	2.2E-03	-3.2	2.6E-04	-1.0	7.8E-03	-0.5	4.2E-01
ENSMUST00000029938	general transcription factor IIB [Source:MGI Symbol;Acc:MGI:2385191]	Q3ULN2	P62915	-6.1	7.7E-06	-2.5	8.1E-04	0.1	7.0E-01	0.4	4.3E-01
ENSMUST00000029941	PDZ and LIM domain 5 [Source:MGI Symbol;Acc:MGI:1927489]		Q8CI51	-2.7	1.0E-03	2.9	1.7E-01	-2.4	2.4E-01	0.0	9.8E-01
ENSMUST00000029942	RNA guanylyltransferase and 5'-phosphatase [Source:MGI Symbol;Acc:MGI:1329041]	Q9DCC1		-5.1	3.7E-04	-1.7	2.3E-01	-0.2	8.7E-01	-2.2	1.9E-01
ENSMUST00000029810	solute carrier family 39 (metal ion transporter), member 8 [Source:MGI Symbol;Acc:MGI:1914797]		Q91W10	3.6	5.0E-02	4.8	1.9E-02	-0.5	7.6E-01	-1.7	1.8E-01
ENSMUST00000029944	ubiquitin-conjugating enzyme E2J 1 [Source:MGI Symbol;Acc:MGI:1926245]	B1AWT7		-3.8	2.4E-03	-4.3	5.4E-02	0.9	2.7E-01	0.4	8.4E-01
ENSMUST00000029946	Ras-related GTP binding D [Source:MGI Symbol;Acc:MGI:1098604]	B1AWT3		8.9	1.3E-04	-1.7	5.7E-02	0.3	5.5E-01	-0.6	4.4E-01
ENSMUST00000029947	gamma-aminobutyric acid (GABA) C receptor, subunit rho 1 [Source:MGI Symbol;Acc:MGI:95625]		P56475	7.1	4.9E-05	-1.2	1.2E-01	0.7	1.3E-01	0.3	6.3E-01
ENSMUST00000029948	bone morphogenetic protein receptor, type 1B [Source:MGI Symbol;Acc:MGI:107191]	B2RRZ4	P36898	6.3	2.8E-04	6.8	8.5E-05	-0.5	6.3E-01	0.4	4.3E-01
ENSMUST00000029964	Eph receptor A7 [Source:MGI Symbol;Acc:MGI:95276]		Q61772	9.2	1.7E-02	4.4	1.9E-04	-0.3	6.6E-01	-0.7	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000029968	arginyl-tRNA synthetase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1923596]		Q3U186	-5.4	5.4E-03	0.2	7.9E-01	-5.2	1.0E-03	-0.3	6.8E-01
ENSMUST00000029971	RIKEN cDNA 1700003M02 gene [Source:MGI Symbol;Acc:MGI:1916579]		Q6PE87	6.7	1.9E-04	-3.1	2.3E-03	-0.3	4.7E-01	-0.9	2.4E-01
ENSMUST00000029972	small integral membrane protein 8 [Source:MGI Symbol;Acc:MGI:1913541]		Q9CQQ0	-5.3	3.9E-04	-4.5	7.9E-05	0.7	5.2E-02	-0.6	3.9E-01
ENSMUST00000029987	aldolase B, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:87995]	Q3UER1	Q91Y97	5.1	7.1E-03	6.3	4.8E-04	-1.5	2.9E-01	-0.1	9.2E-01
ENSMUST00000029989	ring finger protein 20 [Source:MGI Symbol;Acc:MGI:1925927]		Q5DTM8	-7.7	2.1E-04	0.5	5.5E-01	-5.9	2.3E-04	0.4	5.3E-01
ENSMUST00000029991	n phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II) [Source:MGI Symbol;Acc:MGI:1(	Q497S1	Q63811	7.2	3.3E-05	6.6	1.0E-04	-1.3	2.5E-01	-0.4	5.3E-01
ENSMUST00000029995	topoisomerase I binding, arginine/serine-rich like [Source:MGI Symbol;Acc:MGI:1915524]	Q9D2F8		5.4	2.2E-02	-5.8	2.6E-03	-0.1	8.4E-01	-2.4	1.9E-01
ENSMUST00000029866	cyclin E2 [Source:MGI Symbol;Acc:MGI:1329034]	A2API1		2.6	2.0E-01	-0.6	8.0E-01	-2.3	2.4E-01	0.9	6.9E-01
ENSMUST00000029868	GTP binding protein (gene overexpressed in skeletal muscle) [Source:MGI Symbol;Acc:MGI:99844]	Q3TH76	P55041	1.1	5.1E-01	1.2	4.8E-01	-2.2	1.5E-01	-2.3	1.8E-01
ENSMUST00000030010	ATP-binding cassette, sub-family A (ABC1), member 1 [Source:MGI Symbol;Acc:MGI:99607]		P41233	-1.5	2.0E-03	-1.6	1.9E-02	0.3	4.6E-01	-0.3	5.7E-01
ENSMUST00000030013	xeroderma pigmentosum, complementation group A [Source:MGI Symbol;Acc:MGI:99135]		Q64267	-6.1	2.8E-04	-0.1	8.2E-01	-1.4	1.8E-02	0.5	3.8E-01
ENSMUST00000029879	nibrin [Source:MGI Symbol;Acc:MGI:1351625]		Q9R207	-1.1	7.6E-02	-1.0	1.7E-01	-0.5	2.9E-01	-0.7	3.4E-01
ENSMUST00000030014	nuclear cap binding protein subunit 1 [Source:MGI Symbol;Acc:MGI:1891840]		Q3UYV9	-4.7	2.6E-06	-1.3	1.6E-02	0.9	1.5E-02	0.1	7.4E-01
ENSMUST00000030018	N-acetylneuraminic acid synthase (sialic acid synthase) [Source:MGI Symbol;Acc:MGI:2149820]	Q99J77		-3.4	6.2E-04	-1.1	2.3E-01	1.4	4.3E-02	-1.9	6.4E-02
ENSMUST00000030025	nuclear receptor subfamily 4, group A, member 3 [Source:MGI Symbol;Acc:MGI:1352457]		Q9QZB6	7.9	5.4E-04	-1.7	5.1E-02	-0.5	3.3E-01	-0.6	4.4E-01
ENSMUST00000030028	endoplasmic reticulum protein 44 [Source:MGI Symbol;Acc:MGI:1923549]		Q9D1Q6	-4.0	1.7E-05	5.1	3.7E-03	-2.2	1.6E-01	-0.3	7.7E-01
ENSMUST00000030029	inversin [Source:MGI Symbol;Acc:MGI:1335082]	A2AM57		2.1	2.2E-03	7.5	9.6E-05	1.1	3.3E-01	-0.3	5.6E-01
ENSMUST00000030030	testis expressed gene 10 [Source:MGI Symbol;Acc:MGI:1344413]		Q3URQ0	-4.6	1.6E-03	2.2	2.5E-02	-0.1	8.7E-01	0.6	3.7E-01
ENSMUST00000029909	coenzyme Q3 homolog, methyltransferase (yeast) [Source:MGI Symbol;Acc:MGI:101813]		Q8BMS4	1.1	2.1E-01	0.7	4.7E-01	-0.6	4.7E-01	-0.2	8.2E-01
ENSMUST00000030033	muscle-related coiled-coil protein [Source:MGI Symbol;Acc:MGI:1915266]		A2AMM0	6.4	9.4E-05	-5.7	7.2E-04	-0.9	6.1E-02	-0.8	5.5E-01
ENSMUST00000030036	bone morphogenic protein/retinoic acid inducible neural specific 1 [Source:MGI Symbol;Acc:MGI:1928478]		Q920P3	8.6	2.8E-05	-2.6	6.1E-03	-1.1	3.7E-02	-1.3	1.4E-01
ENSMUST00000030039	formin 2 [Source:MGI Symbol;Acc:MGI:1859252]		Q9JL04	8.8	7.4E-06	-6.5	2.3E-06	-0.7	2.1E-02	0.4	5.4E-01
ENSMUST00000029915	thiosulfate sulfurtransferase (rhodanese)-like domain containing 3 [Source:MGI Symbol;Acc:MGI:1924282]		Q9D0B5	1.1	4.8E-02	0.6	3.7E-01	-0.5	3.6E-01	0.1	8.8E-01
ENSMUST00000030041	alpha 1 microglobulin/bikunin [Source:MGI Symbol;Acc:MGI:88002]		Q07456	-3.1	8.5E-04	7.1	6.6E-05	-0.5	6.4E-01	-0.7	2.1E-01
ENSMUST00000029923	chloride channel accessory 4A [Source:MGI Symbol;Acc:MGI:2139744]	G3X8Z1		3.7	9.0E-02	6.0	2.0E-02	-0.3	9.1E-01	-2.6	7.4E-02
ENSMUST00000029925	DH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4 [Source:MGI Symbol;Acc:MGI:19157		Q9D1H6	3.5	5.4E-02	1.1	5.1E-01	-1.9	2.4E-01	0.4	7.6E-01
ENSMUST00000030044	orosomucoid 1 [Source:MGI Symbol;Acc:MGI:97443]		Q60590	-4.8	3.4E-04	6.3	4.8E-05	-0.5	6.2E-01	-0.9	1.2E-01
ENSMUST00000030051	thioredoxin 1 [Source:MGI Symbol;Acc:MGI:98874]		P10639	-7.6	2.7E-08	7.5	5.7E-05	-0.6	5.9E-01	-1.4	4.7E-02
ENSMUST00000030069	prostaglandin reductase 1 [Source:MGI Symbol;Acc:MGI:1914353]		Q91YR9	-2.2	7.6E-04	-4.7	3.2E-03	-1.3	5.4E-02	-0.6	6.4E-01
ENSMUST00000030074	UDP-glucose ceramide glucosyltransferase [Source:MGI Symbol;Acc:MGI:1332243]		O88693	-3.3	1.2E-03	-5.1	1.2E-04	-0.8	5.9E-02	-1.8	6.0E-02
ENSMUST00000030078	hydroxysteroid dehydrogenase like 2 [Source:MGI Symbol;Acc:MGI:1919729]		Q2TPA8	-3.9	3.2E-03	-2.1	2.4E-02	0.8	8.7E-02	0.2	7.7E-01
ENSMUST00000030080	sorting nexin family member 30 [Source:MGI Symbol;Acc:MGI:2443882]		Q8CE50	3.0	2.9E-04	-2.9	9.3E-03	0.2	7.6E-01	-2.0	9.5E-02
ENSMUST00000030081	solute carrier family 46, member 2 [Source:MGI Symbol;Acc:MGI:1353616]		Q8CA03	8.5	2.5E-05	-3.1	1.3E-02	-0.4	4.8E-01	-1.1	3.2E-01
ENSMUST00000030102	lysine (K)-specific demethylase 4C [Source:MGI Symbol;Acc:MGI:1924054]		Q8VCD7	-3.3	3.2E-03	8.3	4.4E-04	-0.8	6.5E-01	-0.1	8.9E-01
ENSMUST00000030103	transmembrane protein 261 [Source:MGI Symbol;Acc:MGI:1914178]		Q9CQ00	-3.4	1.2E-04	7.5	6.6E-05	-0.5	6.7E-01	-0.9	1.6E-01
ENSMUST00000030110	zinc finger, DHHC domain containing 21 [Source:MGI Symbol;Acc:MGI:1915518]		Q9D270	1.8	6.2E-03	6.7	3.6E-04	-0.4	7.4E-01	-0.8	2.5E-01
ENSMUST00000029950	caspase 8 associated protein 2 [Source:MGI Symbol;Acc:MGI:1349399]		Q9WUF3	-1.0	6.6E-01	1.1	6.9E-01	0.1	9.8E-01	-2.1	4.0E-01
ENSMUST00000030117	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1915546]		Q3UKJ7	-4.8	9.7E-05	9.2	2.2E-02	-1.0	8.0E-01	-1.0	5.9E-01
ENSMUST00000030118	DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:MGI Symbol;Acc:MGI:1270129]	Q5NTY0	P63037	-6.5	1.3E-04	-5.3	3.6E-03	-1.0	1.9E-01	-1.1	5.1E-01
ENSMUST00000029970	solute carrier family 35 (CMP-sialic acid transporter), member 1 [Source:MGI Symbol;Acc:MGI:1345622]		Q61420	1.0	1.6E-01	0.7	3.8E-01	-0.5	4.6E-01	-0.2	8.2E-01
ENSMUST00000030119	aprataxin [Source:MGI Symbol;Acc:MGI:1913658]		Q7TQC5	5.2	9.0E-03	7.5	1.6E-04	-0.6	6.4E-01	-1.4	7.0E-02
ENSMUST00000030121	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 [Source:MGI Symbol;Acc:MGI:95705]	Q3U478	P15535	-4.0	9.3E-05	-4.9	2.5E-03	0.0	9.5E-01	-0.4	7.5E-01
ENSMUST00000030124	T cell acute lymphocytic leukemia 2 [Source:MGI Symbol;Acc:MGI:99540]	Q2TB09	Q62282	4.1	5.2E-04	1.0	4.7E-01	-3.6	3.8E-02	0.4	7.3E-01
ENSMUST00000030125	BCL2-associated athanogene 1 [Source:MGI Symbol;Acc:MGI:108047]	F6TCF9		-4.3	6.2E-04	-7.7	4.2E-03	0.4	4.9E-01	0.4	8.4E-01
ENSMUST00000030128	charged multivesicular body protein 5 [Source:MGI Symbol;Acc:MGI:1924209]		Q9D7S9	-6.1	4.5E-07	6.8	1.0E-04	-0.6	6.0E-01	-0.2	7.4E-01
ENSMUST00000030134	RAD23b homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:105128]		P54728	-2.7	5.3E-04	6.0	2.0E-02	-0.6	8.1E-01	-1.2	3.8E-01
ENSMUST00000030003	exosome component 3 [Source:MGI Symbol;Acc:MGI:1913612]		Q7TQK4	-2.2	6.1E-02	-3.3	5.6E-02	0.3	7.6E-01	1.4	3.6E-01
ENSMUST00000030136	aquaporin 7 [Source:MGI Symbol;Acc:MGI:1314647]	Q5DX24	O54794	8.2	3.2E-05	-0.2	7.4E-01	1.1	9.1E-03	-0.3	4.8E-01
ENSMUST00000030138	nucleolar protein family 6 (RNA-associated) [Source:MGI Symbol;Acc:MGI:2140151]		Q8R5K4	1.2	3.4E-02	-6.9	1.3E-03	-0.1	8.1E-01	0.7	6.8E-01
ENSMUST00000030142	erythrocyte membrane protein band 4.1 like 4b [Source:MGI Symbol;Acc:MGI:1859149]		Q9JMC8	2.8	2.8E-02	-3.0	2.3E-04	0.4	1.9E-01	-1.3	3.3E-02
ENSMUST00000030143	ubiquitin-associated protein 2 [Source:MGI Symbol;Acc:MGI:1916176]		Q91VX2	-4.8	1.9E-02	-1.9	2.6E-02	-0.5	2.6E-01	-2.0	3.3E-02
ENSMUST00000030021	coronin, actin binding protein 2A [Source:MGI Symbol;Acc:MGI:1345966]	B1AVH4	Q8C0P5	-2.5	2.0E-01	0.0	9.9E-01	4.3	1.2E-01	1.8	4.5E-01
ENSMUST00000030145	DDB1 and CUL4 associated factor 12 [Source:MGI Symbol;Acc:MGI:1916220]		Q8BGZ3	-2.7	8.1E-04	5.0	6.3E-03	-3.4	7.2E-02	-0.5	5.6E-01
ENSMUST00000030158	dynactin 3 [Source:MGI Symbol;Acc:MGI:1859251]		Q9Z0Y1	-5.3	4.5E-04	-2.5	1.9E-03	0.9	2.3E-02	-0.5	4.0E-01
ENSMUST00000030163	RIKEN cDNA 1700022I11 gene [Source:MGI Symbol;Acc:MGI:1914567]		Q3V0E1	7.8	3.8E-05	2.8	1.7E-03	0.5	3.7E-01	-0.2	6.3E-01
ENSMUST00000030164	valosin containing protein [Source:MGI Symbol;Acc:MGI:99919]		Q01853	-4.9	8.9E-06	-5.7	7.2E-03	0.2	8.1E-01	1.3	4.6E-01
ENSMUST00000030169	stomatin (Epb7.2)-like 2 [Source:MGI Symbol;Acc:MGI:1913842]		Q99JB2	2.5	3.4E-02	6.8	1.1E-04	-0.6	6.1E-01	-1.0	1.1E-01
ENSMUST00000030170	unc-13 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:3051532]		Q4KUS2	5.4	9.0E-05	7.7	1.3E-04	-0.7	6.2E-01	0.2	7.2E-01
ENSMUST00000030183	carbonic anhydrase 9 [Source:MGI Symbol;Acc:MGI:2447188]	Q3UUZ9	Q8VHB5	5.9	2.5E-03	8.2	2.7E-05	-0.5	6.4E-01	0.0	9.3E-01
ENSMUST00000030187	talin 1 [Source:MGI Symbol;Acc:MGI:1099832]		P26039	-5.5	3.9E-06	-3.0	4.5E-03	0.0	9.3E-01	-0.1	8.9E-01
ENSMUST00000030042	kinesin family member 12 [Source:MGI Symbol;Acc:MGI:1098232]		Q9D2Z8	2.6	7.6E-02	5.2	2.7E-03	-0.5	7.1E-01	-3.1	1.2E-02
ENSMUST00000030189	glucosidase beta 2 [Source:MGI Symbol;Acc:MGI:2654325]		Q69ZF3	-6.7	1.9E-04	-5.1	2.2E-03	0.1	8.7E-01	0.4	7.3E-01
ENSMUST00000030047	tumor necrosis factor (ligand) superfamily, member 8 [Source:MGI Symbol;Acc:MGI:88328]	Q544U1	P32972	0.1	8.4E-01	0.4	5.0E-01	-0.9	1.2E-01	-1.2	8.3E-02
ENSMUST00000030191	natriuretic peptide receptor 2 [Source:MGI Symbol;Acc:MGI:97372]		Q6VVW5	6.4	2.5E-02	-7.6	2.8E-07	-0.1	7.5E-01	-0.1	8.4E-01
ENSMUST00000030192	histidine triad nucleotide binding protein 2 [Source:MGI Symbol;Acc:MGI:1916167]	Q5M9J2	Q9D0S9	-4.2	1.4E-03	-1.8	8.1E-03	-0.4	2.9E-01	-0.8	1.9E-01
ENSMUST00000030198	reversion-inducing-cysteine-rich protein with kazal motifs [Source:MGI Symbol;Acc:MGI:1855698]		Q9Z0J1	-4.2	2.8E-02	-2.2	4.4E-02	1.0	9.7E-02	-0.2	8.4E-01
ENSMUST00000030076	polypyrimidine tract binding protein 3 [Source:MGI Symbol;Acc:MGI:1923334]		Q8BHD7	2.2	5.8E-01	-2.1	6.1E-01	-4.4	2.4E-01	-0.1	9.8E-01
ENSMUST00000030201	ucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase [Source:MGI Symbol;Acc:MGI:135495	Q3UW64		3.1	6.9E-04	-4.0	1.1E-02	-0.6	3.6E-01	-0.5	7.0E-01
ENSMUST00000030202	GLI pathogenesis-related 2 [Source:MGI Symbol;Acc:MGI:1917770]		Q9CYL5	-6.0	2.9E-05	2.5	3.5E-03	-0.5	3.5E-01	0.0	9.2E-01
ENSMUST00000030206	small nuclear RNA activating complex, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1916338]		Q9D2C9	-3.5	9.7E-03	8.2	6.7E-05	-0.7	6.0E-01	-0.4	5.4E-01
ENSMUST00000030090	aminolevulinate, delta-, dehydratase [Source:MGI Symbol;Acc:MGI:96853]		P10518	-1.1	3.8E-01	0.4	7.5E-01	-0.2	8.5E-01	-1.8	2.2E-01
ENSMUST00000030091	polymerase (DNA directed), epsilon 3 (p17 subunit) [Source:MGI Symbol;Acc:MGI:1933378]			-3.6	6.5E-02	-3.0	1.5E-01	-0.6	6.6E-01	-1.1	6.0E-01
ENSMUST00000030095	transducin-like enhancer of split 1, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104636]	Q5SQA3		-0.1	9.7E-01	0.2	9.4E-01	-0.9	5.9E-01	-1.2	6.5E-01
ENSMUST00000030207	PC4 and SFRS1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2142116]		Q99JF8	-4.6	3.0E-05	-4.0	7.9E-03	0.1	8.7E-01	0.8	5.4E-01
ENSMUST00000030212	SH3-domain GRB2-like 2 [Source:MGI Symbol;Acc:MGI:700009]		Q62420	4.3	3.3E-03	-2.3	4.6E-03	0.0	9.9E-01	-1.1	1.0E-01
ENSMUST00000030216	stablizer of axonemal microtubules 1 [Source:MGI Symbol;Acc:MGI:1923061]	B1AXP3		7.0	9.5E-04	1.6	3.3E-02	-0.2	6.6E-01	0.0	9.6E-01
ENSMUST00000030243	protein kinase, AMP-activated, alpha 2 catalytic subunit [Source:MGI Symbol;Acc:MGI:1336173]		Q8BRK8	7.5	1.8E-05	-5.7	1.9E-04	-0.3	5.0E-01	0.6	5.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000030247	mesoderm induction early response 1 homolog (Xenopus laevis [Source:MGI Symbol;Acc:MGI:1918398]		Q5UAK0	-8.2	9.7E-04	-4.8	6.2E-04	-0.5	3.3E-01	-2.2	8.2E-02
ENSMUST00000030254	leptin receptor overlapping transcript [Source:MGI Symbol;Acc:MGI:2687005]		O89013	-8.6	2.2E-05	6.0	9.0E-03	0.8	6.9E-01	-0.1	9.3E-01
ENSMUST00000030257	cache domain containing 1 [Source:MGI Symbol;Acc:MGI:2444177]		Q6PDJ1	9.9	1.8E-06	-2.0	2.3E-02	1.4	7.7E-03	-0.6	4.7E-01
ENSMUST00000030263	ST3 beta-galactoside alpha-2,3-sialyltransferase 3 [Source:MGI Symbol;Acc:MGI:1316659]		P97325	3.5	1.3E-03	5.3	2.5E-04	0.7	4.7E-01	-0.5	4.2E-01
ENSMUST00000030265	DPH2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914978]		Q9CR25	7.5	4.7E-05	-5.7	4.0E-03	0.8	1.9E-01	2.2	1.8E-01
ENSMUST00000030127	transmembrane protein 38B [Source:MGI Symbol;Acc:MGI:1098718]		Q9DAV9	1.3	4.5E-01	0.7	7.6E-01	0.9	6.2E-01	1.4	4.7E-01
ENSMUST00000030279	autophagy related 4C, cysteine peptidase [Source:MGI Symbol;Acc:MGI:2651854]		Q811C2	5.1	8.0E-05	-5.9	3.1E-06	-0.5	6.9E-02	-0.6	3.0E-01
ENSMUST00000030133	nuclear transcription factor, X-box binding 1 [Source:MGI Symbol;Acc:MGI:1921414]		B1AY10	1.4	7.7E-02	2.1	5.0E-02	1.0	2.2E-01	0.3	7.4E-01
ENSMUST00000030286	dedicator of cytokinesis 7 [Source:MGI Symbol;Acc:MGI:1914549]	A2A9M5		5.2	1.2E-02	-1.6	3.8E-02	1.0	3.4E-02	-0.1	8.9E-01
ENSMUST00000030289	ubiquitin specific peptidase 1 [Source:MGI Symbol;Acc:MGI:2385198]		Q8BJQ2	-3.7	1.4E-02	8.7	3.6E-05	-0.6	6.2E-01	-1.2	5.6E-02
ENSMUST00000030296	thioredoxin domain containing 12 (endoplasmic reticulum) [Source:MGI Symbol;Acc:MGI:1913323]		Q9CQU0	-5.3	2.9E-05	1.7	2.9E-02	0.0	9.7E-01	-0.4	5.0E-01
ENSMUST00000030140	kappa light polypeptide enhancer in B cells, kinase complex-associated protein [Source:MGI Symbol;Acc:MG		Q7TT37	0.6	1.2E-01	0.1	7.9E-01	-0.3	3.9E-01	0.2	6.8E-01
ENSMUST00000030299	cytochrome P450, family 2, subfamily j, polypeptide 5 [Source:MGI Symbol;Acc:MGI:1270149]	Q3TNC5	O54749	8.1	1.1E-04	5.7	2.5E-03	1.0	4.5E-01	-1.9	6.4E-02
ENSMUST00000030303	cytochrome P450, family 2, subfamily j, polypeptide 6 [Source:MGI Symbol;Acc:MGI:1270148]		O54750	6.5	5.9E-05	-1.5	3.8E-01	0.4	7.0E-01	-2.8	1.8E-01
ENSMUST00000030305	cytochrome P450, family 2, subfamily j, polypeptide 13 [Source:MGI Symbol;Acc:MGI:2385197]	Q3UNV4		6.5	8.6E-07	-2.1	2.0E-02	1.0	4.5E-02	0.4	5.7E-01
ENSMUST00000030154	nudix (nucleoside diphosphate linked moiety X)-type motif 2 [Source:MGI Symbol;Acc:MGI:1913651]		P56380	-1.5	1.2E-01	-2.2	7.2E-02	-1.0	2.2E-01	-0.4	7.4E-01
ENSMUST00000030306	hook homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925213]		Q8BIL5	-5.5	9.2E-05	-2.8	3.8E-02	0.9	1.8E-01	-1.6	2.3E-01
ENSMUST00000030313	caspase activity and apoptosis inhibitor 1 [Source:MGI Symbol;Acc:MGI:1915020]		Q8VDY9	-4.3	1.5E-03	6.7	2.9E-04	-0.7	5.8E-01	0.3	6.2E-01
ENSMUST00000030320	coiled-coil and C2 domain containing 1B [Source:MGI Symbol;Acc:MGI:2443076]		Q8BRN9	-5.7	2.7E-04	-3.7	3.5E-04	0.6	1.0E-01	-0.6	3.7E-01
ENSMUST00000030165	Fanconi anemia, complementation group G [Source:MGI Symbol;Acc:MGI:1926471]		Q9EQR6	-1.8	1.9E-01	0.9	6.2E-01	2.5	9.4E-02	-0.2	8.9E-01
ENSMUST00000030326	PRAME family member 12 [Source:MGI Symbol;Acc:MGI:1924882]	Q9D2F1		6.9	6.0E-05	4.0	2.0E-02	1.2	3.9E-01	-0.3	7.4E-01
ENSMUST00000030328	RIKEN cDNA 9430007A20 gene [Source:MGI Symbol;Acc:MGI:2685880]		Q8BM81	6.8	7.3E-04	5.2	3.4E-04	-0.3	7.8E-01	0.0	9.8E-01
ENSMUST00000030179	CD72 antigen [Source:MGI Symbol;Acc:MGI:88345]	Q3UZ35		1.2	3.9E-01	-3.9	2.1E-02	-4.9	9.1E-04	0.2	9.2E-01
ENSMUST00000030180	suppression inducing transmembrane adaptor 1 [Source:MGI Symbol;Acc:MGI:1889342]		Q8C503	3.5	5.5E-02	0.8	6.8E-01	-2.1	2.2E-01	0.6	7.0E-01
ENSMUST00000030181	coiled-coil domain containing 107 [Source:MGI Symbol;Acc:MGI:1913423]		Q9DCC3	-0.8	5.1E-01	-1.1	4.2E-01	-0.9	3.7E-01	-0.6	6.7E-01
ENSMUST00000030332	glutathione peroxidase 7 [Source:MGI Symbol;Acc:MGI:1914555]	Q3TNK3	Q99LJ6	4.8	1.7E-04	-2.0	3.6E-01	-3.6	3.4E-02	4.4	4.8E-02
ENSMUST00000030184	tropomyosin 2, beta [Source:MGI Symbol;Acc:MGI:98810]	A2AIM4		6.5	4.2E-02	5.7	9.7E-02	-0.7	8.3E-01	0.1	9.6E-01
ENSMUST00000030336	tumor necrosis factor receptor superfamily, member 1b [Source:MGI Symbol;Acc:MGI:1314883]	Q545P4	P25119	-3.2	1.3E-03	-3.8	3.1E-04	1.3	7.5E-03	-0.5	5.0E-01
ENSMUST00000030339	tumor necrosis factor receptor superfamily, member 8 [Source:MGI Symbol;Acc:MGI:99908]	A1L3C9	Q60846	2.3	3.0E-02	-1.3	1.3E-01	1.4	2.8E-02	-4.0	7.1E-03
ENSMUST00000030340	sterol carrier protein 2, liver [Source:MGI Symbol;Acc:MGI:98254]		P32020	-7.7	5.5E-06	6.9	2.6E-02	-0.6	8.4E-01	-1.1	4.8E-01
ENSMUST00000030345	carnitine palmitoyltransferase 2 [Source:MGI Symbol;Acc:MGI:109176]		P52825	-3.3	3.1E-04	-4.8	3.7E-03	-0.4	4.7E-01	0.1	9.3E-01
ENSMUST00000030348	mago homolog, exon junction complex core component [Source:MGI Symbol;Acc:MGI:1330312]		P61327	-4.5	2.7E-06	-3.4	1.1E-01	0.6	5.7E-01	-0.1	9.6E-01
ENSMUST00000030360	leucine rich repeat containing 42 [Source:MGI Symbol;Acc:MGI:1925059]		Q8R2U7	-1.6	2.5E-02	3.6	1.2E-03	0.4	6.2E-01	-0.1	8.0E-01
ENSMUST00000030365	mitochondrial ribosomal protein L37 [Source:MGI Symbol;Acc:MGI:1926268]		Q921S7	-3.4	1.7E-02	-5.1	3.3E-04	0.3	4.3E-01	-0.5	6.2E-01
ENSMUST00000030367	single-stranded DNA binding protein 3 [Source:MGI Symbol;Acc:MGI:1919725]		Q9D032	-2.0	6.4E-03	-1.0	4.3E-01	1.2	1.5E-01	-1.3	3.5E-01
ENSMUST00000030372	collagen, type IX, alpha 2 [Source:MGI Symbol;Acc:MGI:88466]	I7HJR1		6.5	1.5E-05	-3.0	2.6E-03	0.6	1.6E-01	-1.0	2.1E-01
ENSMUST00000030376	potassium voltage-gated channel, subfamily Q, member 4 [Source:MGI Symbol;Acc:MGI:1926803]		Q9JK97	9.2	4.1E-06	5.5	5.7E-03	0.8	6.1E-01	-0.5	6.1E-01
ENSMUST00000030384	endothelin 2 [Source:MGI Symbol;Acc:MGI:95284]		P22389	7.3	4.6E-05	3.4	8.3E-02	-0.7	7.0E-01	3.0	3.8E-02
ENSMUST00000030221	3-hydroxyacyl-CoA dehydratase 4 [Source:MGI Symbol;Acc:MGI:1914025]		A2AKM2	-0.8	8.6E-01	-1.9	7.2E-01	-1.6	6.5E-01	-0.5	9.3E-01
ENSMUST00000030391	transcription factor AP-2, gamma [Source:MGI Symbol;Acc:MGI:106032]	A0A023UF19	Q61312	3.4	2.8E-02	8.0	3.7E-05	0.1	9.3E-01	-0.4	4.7E-01
ENSMUST00000030394	RIKEN cDNA 4930538K18 gene [Source:MGI Symbol;Acc:MGI:1922430]	Q9D4Y8		7.0	6.0E-05	4.0	1.1E-01	8.1	2.2E-03	-4.1	6.2E-02
ENSMUST00000030251	phosphodiesterase 4B, cAMP specific [Source:MGI Symbol;Acc:MGI:99557]	Q3TTI9		0.5	7.8E-01	-3.6	1.8E-01	-3.7	2.6E-02	0.4	8.8E-01
ENSMUST00000030395	coiled-coil domain containing 23 [Source:MGI Symbol;Acc:MGI:1916466]		Q99LQ4	-6.3	5.1E-05	-6.4	1.3E-04	0.2	5.7E-01	-2.0	1.5E-01
ENSMUST00000030396	erythroblast membrane-associated protein [Source:MGI Symbol;Acc:MGI:1349816]	E9QKE5		9.1	1.2E-06	7.5	1.3E-05	-1.9	8.8E-02	0.4	3.6E-01
ENSMUST00000030398	solute carrier family 2 (facilitated glucose transporter), member 1 [Source:MGI Symbol;Acc:MGI:95755]		P17809	-5.2	1.9E-05	3.7	8.0E-03	0.7	4.8E-01	0.6	4.2E-01
ENSMUST00000030399	Ras-related GTP binding C [Source:MGI Symbol;Acc:MGI:1858751]		Q99K70	-7.6	8.9E-05	4.6	1.2E-03	-3.6	1.1E-02	-0.7	3.1E-01
ENSMUST00000030274	BEN domain containing 5 [Source:MGI Symbol;Acc:MGI:1914871]		Q8C6D4	2.4	9.8E-02	3.0	5.6E-02	-0.8	5.9E-01	-1.4	2.4E-01
ENSMUST00000030400	c-myc binding protein [Source:MGI Symbol;Acc:MGI:1891750]		Q9EQS3	-2.2	1.4E-02	3.9	3.8E-03	-0.7	5.0E-01	0.6	4.0E-01
ENSMUST00000030281	epidermal growth factor receptor pathway substrate 15 [Source:MGI Symbol;Acc:MGI:104583]			-5.1	1.7E-01	-5.9	1.9E-01	-1.9	3.3E-01	-1.1	8.3E-01
ENSMUST00000030284	ring finger protein 11 [Source:MGI Symbol;Acc:MGI:1352759]		Q9QYK7	0.2	7.3E-01	0.0	9.8E-01	0.6	4.0E-01	0.8	3.8E-01
ENSMUST00000030285	calreticulin 4 [Source:MGI Symbol;Acc:MGI:2140435]	Q3TQS0		3.3	9.4E-02	4.7	3.3E-02	-0.5	8.0E-01	-1.9	2.0E-01
ENSMUST00000030401	NADH dehydrogenase (ubiquinone) Fe-S protein 5 [Source:MGI Symbol;Acc:MGI:1890889]		Q99LY9	-7.9	3.0E-05	2.2	1.9E-01	-5.4	1.1E-02	-2.4	9.3E-02
ENSMUST00000030404	peptidylprolyl isomerase E (cyclophilin E) [Source:MGI Symbol;Acc:MGI:1917118]		Q9QZH3	-1.9	1.0E-02	-1.0	3.7E-01	-0.4	5.9E-01	-3.1	4.6E-02
ENSMUST00000030412	palmitoyl-protein thioesterase 1 [Source:MGI Symbol;Acc:MGI:1298204]	Q3U6J9	O88531	-10.8	4.4E-06	-5.8	1.2E-04	-0.2	6.7E-01	0.3	7.3E-01
ENSMUST00000030417	cell division cycle 42 [Source:MGI Symbol;Acc:MGI:106211]		P60766	-2.6	2.9E-02	4.6	3.5E-03	-2.5	8.7E-02	1.0	2.1E-01
ENSMUST00000030420	Eph receptor A8 [Source:MGI Symbol;Acc:MGI:109378]		O09127	9.3	9.3E-06	2.4	3.8E-03	-5.2	2.1E-04	-1.2	5.2E-02
ENSMUST00000030427	transcription elongation factor B (SIII), polypeptide 3 [Source:MGI Symbol;Acc:MGI:1351315]		Q8CB77	-3.7	1.9E-05	6.8	1.5E-06	-0.3	6.6E-01	-0.5	1.3E-01
ENSMUST00000030432	3-hydroxy-3-methylglutaryl-Coenzyme A lyase [Source:MGI Symbol;Acc:MGI:96158]		P38060	-7.6	6.5E-05	-0.3	6.8E-01	2.0	4.1E-03	-3.3	4.8E-03
ENSMUST00000030311	intraflagellar transport 74 [Source:MGI Symbol;Acc:MGI:1914944]		Q8BKE9	-1.9	4.7E-02	-3.1	3.0E-02	0.0	9.6E-01	1.2	3.3E-01
ENSMUST00000030434	fucosidase, alpha-L- 1, tissue [Source:MGI Symbol;Acc:MGI:95593]		Q99LJ1	-2.1	1.2E-04	-2.4	6.8E-02	0.7	2.8E-01	-1.2	3.4E-01
ENSMUST00000030315	pumilio RNA-binding family member 1 [Source:MGI Symbol;Acc:MGI:1931749]		Q80U78	-4.5	4.7E-02	-2.7	3.5E-01	1.7	3.9E-01	-0.2	9.5E-01
ENSMUST00000030316	lysosomal-associated protein transmembrane 5 [Source:MGI Symbol;Acc:MGI:108046]	F8WH95		1.7	5.4E-01	0.7	8.7E-01	2.2	4.5E-01	3.2	4.7E-01
ENSMUST00000030436	proline-rich nuclear receptor coactivator 2 [Source:MGI Symbol;Acc:MGI:106512]		Q9CR73	-6.2	3.1E-06	-1.3	1.7E-01	1.1	8.0E-02	-3.3	1.3E-02
ENSMUST00000030439	ring finger protein 220 [Source:MGI Symbol;Acc:MGI:1913993]		Q6PDX6	4.1	1.4E-03	6.7	1.6E-04	-0.6	6.3E-01	-0.3	6.3E-01
ENSMUST00000030443	patched homolog 2 [Source:MGI Symbol;Acc:MGI:1095405]		O35595	8.2	1.3E-02	7.1	9.4E-04	-0.7	6.6E-01	-1.0	2.5E-01
ENSMUST00000030451	target of EGR1, member 1 (nuclear) [Source:MGI Symbol;Acc:MGI:1915526]		Q9D2E2	-1.4	1.5E-02	2.8	3.4E-03	-2.9	4.9E-03	-0.8	1.7E-01
ENSMUST00000030453	methylmalonic aciduria cblC type, with homocystinuria [Source:MGI Symbol;Acc:MGI:1914346]		Q9CZD0	4.2	1.4E-05	-3.1	1.1E-02	0.8	1.6E-01	0.8	4.4E-01
ENSMUST00000030455	aldo-keto reductase family 1, member A1 (aldehyde reductase) [Source:MGI Symbol;Acc:MGI:1929955]	Q540D7	Q9JII6	-7.4	2.2E-06	5.4	2.0E-03	2.1	1.0E-01	-1.0	2.8E-01
ENSMUST00000030456	nuclear autoantigenic sperm protein (histone-binding) [Source:MGI Symbol;Acc:MGI:1355328]	B1AU75		2.3	3.6E-03	-6.3	8.3E-05	0.0	9.6E-01	-1.4	1.8E-01
ENSMUST00000030457	nuclear autoantigenic sperm protein (histone-binding) [Source:MGI Symbol;Acc:MGI:1355328]	B1AU76		-3.8	1.6E-03	-1.2	1.2E-01	1.2	2.0E-02	-0.9	2.7E-01
ENSMUST00000030460	GC-rich promoter binding protein 1-like 1 [Source:MGI Symbol;Acc:MGI:1924360]		Q6NZP2	-4.1	2.9E-04	-4.8	1.1E-02	-1.1	1.5E-01	0.8	6.1E-01
ENSMUST00000030464	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55) [Source:MGI Symbol;Acc:MGI:109277]	Q3UXE9	Q64143	5.1	4.6E-04	-4.4	1.7E-05	-0.3	3.0E-01	-0.4	4.9E-01
ENSMUST00000030356	density lipoprotein receptor-related protein 8, apolipoprotein e receptor [Source:MGI Symbol;Acc:MGI:13400	B1AXJ4		0.2	9.1E-01	2.9	6.5E-02	0.5	6.7E-01	-2.2	1.3E-01
ENSMUST00000030357	NDC1 transmembrane nucleoporin [Source:MGI Symbol;Acc:MGI:1920037]	J3QMD9		-2.3	1.2E-01	-1.0	4.8E-01	1.3	2.5E-01	0.0	9.9E-01
ENSMUST00000030465	tetraspanin 1 [Source:MGI Symbol;Acc:MGI:1914055]		Q99J59	6.9	4.7E-05	-0.6	4.2E-01	0.5	4.0E-01	-0.5	5.1E-01
ENSMUST00000030361	transmembrane protein 59 [Source:MGI Symbol;Acc:MGI:1929278]		Q9QY73	-1.7	4.7E-01	-3.8	1.2E-01	-3.7	5.0E-02	-1.6	5.3E-01
ENSMUST00000030469	leucine rich adaptor protein 1 [Source:MGI Symbol;Acc:MGI:1915325]	A2A8F6	Q9D6I9	5.5	9.6E-06	-0.4	7.3E-01	0.1	9.4E-01	-2.9	4.4E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000030471	leucine rich repeat containing 41 [Source:MGI Symbol;Acc:MGI:2441984]		Q8K1C9	-2.0	7.5E-03	-0.7	3.6E-01	1.1	4.2E-02	-0.1	8.4E-01
ENSMUST00000030474	NOL1/NOP2/Sun domain family, member 4 [Source:MGI Symbol;Acc:MGI:1919431]	A0A0A0MQ81		5.6	1.9E-02	8.2	8.2E-05	1.8	1.5E-01	0.1	8.9E-01
ENSMUST00000030375	exonuclease 5 [Source:MGI Symbol;Acc:MGI:1920422]		Q9CXP9	0.6	8.4E-01	1.9	5.2E-01	-0.8	7.6E-01	-2.1	4.3E-01
ENSMUST00000030475	NOL1/NOP2/Sun domain family, member 4 [Source:MGI Symbol;Acc:MGI:1919431]		Q9CZ57	-4.9	1.3E-04	8.0	1.4E-05	-1.5	1.9E-01	-0.3	5.4E-01
ENSMUST00000030381	cytidine 5'-triphosphate synthase [Source:MGI Symbol;Acc:MGI:1858304]		P70698	1.0	7.0E-02	1.3	4.2E-02	-0.6	1.9E-01	-1.0	9.0E-02
ENSMUST00000030477	MOB kinase activator 3C [Source:MGI Symbol;Acc:MGI:2140623]	B1ASD4	Q8BJG4	1.9	2.7E-02	6.5	2.3E-04	-0.6	6.1E-01	0.2	6.9E-01
ENSMUST00000030385	phosphopantothenoylcysteine synthetase [Source:MGI Symbol;Acc:MGI:1915237]		Q8VDG5	-1.6	2.1E-01	0.9	4.1E-01	-0.3	7.9E-01	-2.8	4.3E-02
ENSMUST00000030480	cytochrome P450, family 4, subfamily a, polypeptide 31 [Source:MGI Symbol;Acc:MGI:3028580]	Q91WU1		7.5	2.3E-04	5.4	2.4E-03	-0.5	7.1E-01	-2.6	2.4E-02
ENSMUST00000030393	prolyl 3-hydroxylase 1 [Source:MGI Symbol;Acc:MGI:1888921]	A6PW84		4.1	8.4E-02	4.2	1.3E-01	-0.7	7.7E-01	-0.8	6.3E-01
ENSMUST00000030486	cytochrome P450, family 4, subfamily a, polypeptide 31 [Source:MGI Symbol;Acc:MGI:3028580]	F8WGU9		7.9	9.7E-04	6.9	1.3E-04	-0.6	6.1E-01	-0.5	4.1E-01
ENSMUST00000030487	cytochrome P450, family 4, subfamily a, polypeptide 14 [Source:MGI Symbol;Acc:MGI:1096550]		O35728	7.8	2.4E-05	-7.0	2.0E-04	-0.4	3.6E-01	0.3	8.2E-01
ENSMUST00000030491	cytidine monophosphate (UMP-CMP) kinase 1 [Source:MGI Symbol;Acc:MGI:1913838]			-3.4	1.2E-05	7.2	1.1E-05	-1.7	7.6E-02	0.3	5.8E-01
ENSMUST00000030508	paired box 7 [Source:MGI Symbol;Acc:MGI:97491]		P47239	8.7	1.1E-05	-3.8	9.2E-04	1.0	2.6E-02	-0.3	7.0E-01
ENSMUST00000030510	taste receptor, type 1, member 2 [Source:MGI Symbol;Acc:MGI:1933546]		Q925I4	6.8	7.8E-04	-5.0	5.1E-03	1.5	2.7E-02	-1.1	4.7E-01
ENSMUST00000030513	mRNA turnover 4, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1917152]	A2AMV1		-6.5	3.0E-02	-2.4	5.9E-02	0.5	4.6E-01	0.7	5.5E-01
ENSMUST00000030518	capping protein (actin filament) muscle Z-line, beta [Source:MGI Symbol;Acc:MGI:104652]		P47757	-4.7	1.5E-03	-5.7	8.1E-05	-0.7	1.1E-01	-2.8	3.1E-02
ENSMUST00000030526	phospholipase A2, group IIF [Source:MGI Symbol;Acc:MGI:1349661]		Q9QZT4	7.9	4.1E-05	-1.4	7.2E-02	-0.7	1.4E-01	-1.2	1.1E-01
ENSMUST00000030407	c myelocytomatosis viral oncogene homolog, lung carcinoma derived (avian) [Source:MGI Symbol;Acc:MGI:9	Q3UIE0	P10166	2.9	1.6E-01	6.6	2.8E-02	1.6	5.4E-01	-2.1	1.9E-01
ENSMUST00000030408	major facilitator superfamily domain containing 2A [Source:MGI Symbol;Acc:MGI:1923824]		Q9DA75	0.6	5.0E-01	0.9	5.0E-01	1.5	1.6E-01	1.2	3.1E-01
ENSMUST00000030528	phospholipase A2, group IID [Source:MGI Symbol;Acc:MGI:1341796]	Q3TYT9	Q9WVF6	9.4	1.1E-05	-5.3	9.6E-05	1.0	2.7E-02	-4.5	3.8E-03
ENSMUST00000030533	von Willebrand factor A domain containing 5B1 [Source:MGI Symbol;Acc:MGI:1922968]	B1AZ81	A9Z1V5	9.2	2.8E-06	-1.1	3.7E-01	0.6	5.1E-01	-0.8	5.0E-01
ENSMUST00000030535	cytidine deaminase [Source:MGI Symbol;Acc:MGI:1919519]		P56389	4.6	1.2E-03	8.9	2.5E-05	-0.7	6.0E-01	-0.3	5.7E-01
ENSMUST00000030536	PTEN induced putative kinase 1 [Source:MGI Symbol;Acc:MGI:1916193]		Q99MQ3	-6.8	7.1E-05	-3.8	1.7E-04	0.2	5.2E-01	0.3	6.2E-01
ENSMUST00000030538	dolichyl-di-phosphooligosaccharide-protein glycotransferase [Source:MGI Symbol;Acc:MGI:1194508]		O54734	-1.9	6.4E-03	-7.5	5.0E-04	1.0	9.4E-02	0.9	5.7E-01
ENSMUST00000030541	heterochromatin protein 1, binding protein 3 [Source:MGI Symbol;Acc:MGI:109369]		Q3TEA8	-9.2	1.6E-05	-1.1	2.2E-02	0.5	8.6E-02	-0.5	2.0E-01
ENSMUST00000030547	perlecan (heparan sulfate proteoglycan 2) [Source:MGI Symbol;Acc:MGI:96257]	B1B0C7		10.1	1.5E-05	-6.4	2.0E-05	0.1	7.3E-01	0.4	6.5E-01
ENSMUST00000030551	alkaline phosphatase, liver/bone/kidney [Source:MGI Symbol;Acc:MGI:87983]		P09242	6.8	2.3E-05	2.8	2.9E-02	0.3	7.9E-01	1.5	1.2E-01
ENSMUST00000030556	protein tyrosine phosphatase, non-receptor type 12 [Source:MGI Symbol;Acc:MGI:104673]		P35831	-5.0	2.4E-04	2.7	4.7E-01	-0.9	7.8E-01	4.6	1.2E-01
ENSMUST00000030446	uroporphyrinogen decarboxylase [Source:MGI Symbol;Acc:MGI:98916]		P70697	-0.8	1.7E-01	-0.9	2.2E-01	0.0	9.5E-01	0.2	8.2E-01
ENSMUST00000030563	penta-EF hand domain containing 1 [Source:MGI Symbol;Acc:MGI:1915148]		Q8BFY6	-7.7	3.6E-04	-2.0	7.6E-03	-0.3	4.8E-01	0.4	5.6E-01
ENSMUST00000030578	protein tyrosine phosphatase 4a2 [Source:MGI Symbol;Acc:MGI:1277117]		O70274	-6.8	3.6E-05	3.1	4.7E-04	-0.8	1.7E-01	0.4	4.1E-01
ENSMUST00000030454	peroxiredoxin 1 [Source:MGI Symbol;Acc:MGI:99523]	B1AXW6		-4.3	4.3E-02	-2.4	3.8E-01	1.4	3.8E-01	-0.4	8.7E-01
ENSMUST00000030583	adenylate kinase 2 [Source:MGI Symbol;Acc:MGI:87978]		Q9WTP6	-3.9	1.7E-03	-7.4	5.9E-05	0.3	4.4E-01	0.3	7.7E-01
ENSMUST00000030585	alpha 1,3-galactosyltransferase 2 (isoglobotriaosylceramide synthase) [Source:MGI Symbol;Acc:MGI:2685279		Q3V1N9	8.1	6.4E-05	1.0	1.5E-01	-1.7	1.4E-02	-0.4	4.9E-01
ENSMUST00000030586	coiled coil domain containing 28B [Source:MGI Symbol;Acc:MGI:1913514]		Q8CEG5	-6.4	6.9E-04	-2.3	4.2E-02	-0.4	4.8E-01	-2.0	8.7E-02
ENSMUST00000030606	regulator of calcineurin 3 [Source:MGI Symbol;Acc:MGI:1858220]		Q9JKK0	2.8	1.2E-03	-2.5	1.4E-02	0.5	2.8E-01	-1.0	2.7E-01
ENSMUST00000030610	zinc finger and BTB domain containing 8a [Source:MGI Symbol;Acc:MGI:1920930]		Q9CWH1	5.5	2.3E-05	4.4	2.6E-03	-0.8	4.3E-01	-0.1	9.2E-01
ENSMUST00000030614	cDNA sequence CK137956 [Source:MGI Symbol;Acc:MGI:3616080]	B1AYM9		8.6	2.9E-05	6.8	9.6E-05	-0.6	6.2E-01	-0.5	4.0E-01
ENSMUST00000030622	SYF2 homolog, RNA splicing factor (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915842]		Q9D198	-6.9	5.5E-07	5.9	3.5E-05	0.7	3.4E-01	0.4	4.4E-01
ENSMUST00000030623	actor proline/glutamine rich (polypyrimidine tract binding protein associated) [Source:MGI Symbol;Acc:MGI:		Q8VIJ6	-5.0	5.4E-06	-1.6	7.9E-02	0.7	1.9E-01	0.2	8.0E-01
ENSMUST00000030626	transmembrane protein 50A [Source:MGI Symbol;Acc:MGI:1919067]	Q52KP1	Q9CXL1	-4.1	2.3E-06	1.5	5.1E-01	-2.0	3.6E-01	2.0	2.7E-01
ENSMUST00000030627	Rh blood group, D antigen [Source:MGI Symbol;Acc:MGI:1202882]			3.7	1.5E-04	-1.1	1.1E-01	0.3	4.6E-01	-3.5	1.9E-03
ENSMUST00000030628	transmembrane protein 57 [Source:MGI Symbol;Acc:MGI:1913396]		Q7TQE6	-2.2	4.3E-03	1.8	9.7E-02	0.7	3.9E-01	0.8	3.4E-01
ENSMUST00000030636	stathmin 1 [Source:MGI Symbol;Acc:MGI:96739]	Q545B6	P54227	-2.7	1.6E-03	6.0	4.1E-03	-0.5	7.8E-01	1.0	3.0E-01
ENSMUST00000030642	proteasome (prosome, macropain) subunit, beta type 2 [Source:MGI Symbol;Acc:MGI:1347045]		Q9R1P3	-6.1	1.5E-04	8.0	1.7E-03	-0.5	8.1E-01	-0.6	5.2E-01
ENSMUST00000030643	exostoses (multiple)-like 1 [Source:MGI Symbol;Acc:MGI:1888742]		Q9JKV7	8.7	5.3E-06	6.6	1.8E-04	-0.6	5.9E-01	0.5	3.7E-01
ENSMUST00000030489	T cell acute lymphocytic leukemia 1 [Source:MGI Symbol;Acc:MGI:98480]	Q3TZH7	P22091	0.9	2.4E-01	1.9	5.1E-02	0.2	7.7E-01	-0.8	3.0E-01
ENSMUST00000030490	Scl/Tal1 interrupting locus [Source:MGI Symbol;Acc:MGI:107477]	A2AD39		-1.8	1.8E-01	-2.1	3.2E-01	1.3	2.7E-01	1.6	4.4E-01
ENSMUST00000030651	SH3 domain binding glutamic acid-rich protein-like 3 [Source:MGI Symbol;Acc:MGI:1920973]		Q91VW3	-8.8	2.5E-05	-2.8	3.9E-04	0.4	1.5E-01	-0.2	6.4E-01
ENSMUST00000030501	EBNA1 binding protein 2 [Source:MGI Symbol;Acc:MGI:1916322]		Q9D903	1.3	4.2E-02	0.6	4.0E-01	-0.6	2.7E-01	0.1	8.8E-01
ENSMUST00000030658	tektin 2 [Source:MGI Symbol;Acc:MGI:1346335]		Q922G7	6.7	6.0E-05	8.6	2.5E-05	-0.5	6.6E-01	-0.4	4.5E-01
ENSMUST00000030660	trafficking protein particle complex 3 [Source:MGI Symbol;Acc:MGI:1351486]	Q3U9K9	O55013	-4.7	2.1E-05	4.5	1.8E-02	-0.6	7.1E-01	1.6	1.4E-01
ENSMUST00000030661	GPN-loop GTPase 2 [Source:MGI Symbol;Acc:MGI:2140368]		Q8VEJ1	-1.9	8.8E-03	2.0	6.0E-01	7.2	2.1E-02	-1.3	7.0E-01
ENSMUST00000030665	nuclear distribution gene C homolog (Aspergillus) [Source:MGI Symbol;Acc:MGI:106014]		O35685	-3.5	8.6E-05	-5.1	4.7E-03	0.1	9.0E-01	0.5	7.5E-01
ENSMUST00000030673	colony stimulating factor 3 receptor (granulocyte) [Source:MGI Symbol;Acc:MGI:1339755]		P40223	-5.9	1.6E-05	7.6	1.1E-04	-0.6	6.2E-01	-0.4	5.4E-01
ENSMUST00000030674	synaptotagmin-like 1 [Source:MGI Symbol;Acc:MGI:1933365]	A2AE94		-4.0	5.0E-03	8.7	4.7E-05	-0.4	7.9E-01	0.4	5.2E-01
ENSMUST00000030675	mitochondrial ribosomal protein S15 [Source:MGI Symbol;Acc:MGI:1913657]		Q9DC71	-3.8	1.3E-03	9.7	1.0E-05	0.4	7.1E-01	-0.1	8.1E-01
ENSMUST00000030676	glutamate receptor, ionotropic, kainate 3 [Source:MGI Symbol;Acc:MGI:95816]		B1AS29	8.5	7.1E-06	3.3	4.4E-03	-2.4	3.7E-02	-1.1	1.3E-01
ENSMUST00000030677	mitogen-activated protein kinase kinase kinase 6 [Source:MGI Symbol;Acc:MGI:1855691]	A0A0A0MQ82		3.6	5.2E-04	-3.4	8.2E-03	0.7	2.2E-01	-2.7	4.3E-02
ENSMUST00000030683	hepatocyte growth factor [Source:MGI Symbol;Acc:MGI:96079]		Q08048	-2.0	6.4E-03	-1.6	4.9E-02	0.3	5.3E-01	0.0	1.0E+00
ENSMUST00000030684	guanine nucleotide binding protein-like 2 (nucleolar) [Source:MGI Symbol;Acc:MGI:2385207]		Q99LH1	-2.2	6.6E-03	-7.7	3.9E-04	0.7	1.3E-01	-0.8	6.2E-01
ENSMUST00000030687	R-spondin 1 [Source:MGI Symbol;Acc:MGI:2183426]	B1ASC1		7.3	2.8E-04	2.8	8.1E-03	-7.3	1.6E-04	0.0	1.0E+00
ENSMUST00000030690	cell division cycle associated 8 [Source:MGI Symbol;Acc:MGI:1196274]		Q8BHX3	6.2	4.4E-03	4.4	1.4E-04	-3.2	3.7E-03	-0.8	1.4E-01
ENSMUST00000030693	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog [Source:MGI Symbol;Acc:MGI:95527]		P14234	-6.9	2.8E-05	-5.2	1.2E-03	0.1	7.8E-01	0.3	8.1E-01
ENSMUST00000030560	tubulointerstitial nephritis antigen-like 1 [Source:MGI Symbol;Acc:MGI:2137617]		Q99JR5	2.5	5.6E-02	2.9	4.9E-02	-0.4	7.6E-01	-0.8	5.0E-01
ENSMUST00000030696	family with sequence similarity 76, member A [Source:MGI Symbol;Acc:MGI:2385211]		Q922G2	-2.2	3.4E-03	-6.6	7.8E-03	0.8	3.1E-01	-0.3	9.0E-01
ENSMUST00000030568	ain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C [Source:MGI Symbol;Acc:M		Q62181	4.5	7.3E-02	0.2	9.1E-01	-5.0	4.2E-02	-0.7	6.7E-01
ENSMUST00000030571	adhesion G protein-coupled receptor B2 [Source:MGI Symbol;Acc:MGI:2451244]	H7BWZ2		2.7	2.4E-01	5.6	2.5E-02	-0.6	7.9E-01	-3.5	6.1E-02
ENSMUST00000030577	transmembrane protein 54 [Source:MGI Symbol;Acc:MGI:1913510]	A2A7R2		4.2	5.6E-02	6.8	8.0E-03	-0.2	9.4E-01	-2.8	6.6E-02
ENSMUST00000030698	syntaxin 12 [Source:MGI Symbol;Acc:MGI:1931027]		Q9ER00	-3.5	4.0E-05	-6.9	3.0E-04	0.3	4.8E-01	0.3	8.2E-01
ENSMUST00000030702	protein phosphatase 1, regulatory (inhibitor) subunit 8 [Source:MGI Symbol;Acc:MGI:2140494]		Q8R3G1	-2.9	1.8E-03	-4.2	2.9E-03	-0.2	6.6E-01	0.1	9.3E-01
ENSMUST00000030584	ring finger protein 19B [Source:MGI Symbol;Acc:MGI:1922484]		A2A7Q9	2.0	3.3E-01	5.7	2.6E-02	1.4	5.2E-01	-2.3	2.1E-01
ENSMUST00000030709	sphingomyelin phosphodiesterase, acid-like 3B [Source:MGI Symbol;Acc:MGI:1916022]	Q3TLX9	P58242	2.1	1.6E-02	5.4	2.0E-03	-2.6	8.6E-02	0.1	8.8E-01
ENSMUST00000030714	ain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A [Source:MGI Symbol;Acc:M		O08665	5.8	1.7E-04	-4.9	5.9E-03	-0.3	6.8E-01	-1.7	3.0E-01
ENSMUST00000030588	polyhomeotic-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1860454]		Q9QWH1	3.8	1.1E-01	1.9	5.0E-01	-0.5	8.6E-01	1.4	5.4E-01
ENSMUST00000030723	metal response element binding transcription factor 1 [Source:MGI Symbol;Acc:MGI:101786]		Q07243	-5.6	9.6E-03	3.0	5.0E-03	0.7	3.2E-01	0.4	4.8E-01
ENSMUST00000030724	sestrin 2 [Source:MGI Symbol;Acc:MGI:2651874]		P58043	-3.0	1.9E-03	4.6	2.2E-04	-0.6	4.2E-01	0.2	6.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000030730	tRNA selenocysteine 1 associated protein 1 [Source:MGI Symbol;Acc:MGI:1919037]		Q80VC6	-4.9	2.9E-04	8.1	1.3E-04	-1.0	4.9E-01	-0.5	4.2E-01
ENSMUST00000030734	splicing factor 3a, subunit 3 [Source:MGI Symbol;Acc:MGI:1922312]	Q58E59	Q9D554	-3.2	6.4E-05	-6.9	3.7E-06	-0.6	5.2E-02	-0.6	4.0E-01
ENSMUST00000030739	erythrocyte membrane protein band 4.1 [Source:MGI Symbol;Acc:MGI:95401]		P48193	2.9	2.4E-02	-3.6	3.9E-04	0.9	2.5E-02	-0.6	4.0E-01
ENSMUST00000030747	caspase 9 [Source:MGI Symbol;Acc:MGI:1277950]		Q8C3Q9	-2.1	9.7E-03	-3.6	5.0E-05	0.4	1.7E-01	-0.1	8.7E-01
ENSMUST00000030757	F-box protein 42 [Source:MGI Symbol;Acc:MGI:1924992]		Q6PDJ6	-1.3	2.9E-02	3.5	6.7E-04	-0.4	5.0E-01	-0.2	7.1E-01
ENSMUST00000030760	NECAP endocytosis associated 2 [Source:MGI Symbol;Acc:MGI:1913397]		Q9D1J1	-5.1	5.0E-03	-5.2	2.2E-03	0.3	5.7E-01	3.2	2.3E-02
ENSMUST00000030765	peptidyl arginine deiminase, type II [Source:MGI Symbol;Acc:MGI:1338892]		Q08642	3.9	2.3E-04	-1.4	1.1E-01	1.6	1.1E-02	0.4	6.6E-01
ENSMUST00000030637	neurochondrin [Source:MGI Symbol;Acc:MGI:1347351]		Q9Z0E0	0.1	9.1E-01	0.6	4.5E-01	0.6	3.0E-01	0.1	9.1E-01
ENSMUST00000030769	proteasome (prosome, macropain) 26S subunit, ATPase 2 [Source:MGI Symbol;Acc:MGI:109555]	Q8BVQ9		-4.0	3.7E-05	-7.3	1.1E-03	-0.7	2.5E-01	0.4	7.8E-01
ENSMUST00000030771	DnaJ (Hsp40) homolog, subfamily C, member 2 [Source:MGI Symbol;Acc:MGI:99470]		P54103	-3.9	1.5E-02	7.7	1.9E-05	-1.1	3.1E-01	0.0	9.3E-01
ENSMUST00000030644	zinc finger protein 593 [Source:MGI Symbol;Acc:MGI:1915290]		Q9DB42	-0.6	6.3E-01	-3.6	1.4E-01	-0.4	7.5E-01	2.6	2.5E-01
ENSMUST00000030645	connector enhancer of kinase suppressor of Ras 1 [Source:MGI Symbol;Acc:MGI:2670958]	A2A9K7		3.8	8.6E-02	7.2	7.0E-03	-0.5	8.4E-01	-3.8	1.7E-02
ENSMUST00000030773	-ray repair complementing defective repair in Chinese hamster cells 2 [Source:MGI Symbol;Acc:MGI:192734		Q9CX47	4.0	3.7E-04	-7.1	4.8E-04	0.5	4.0E-01	-1.3	3.9E-01
ENSMUST00000030775	chromodomain helicase DNA binding protein 5 [Source:MGI Symbol;Acc:MGI:3036258]	E9PYL1		6.9	6.8E-04	2.7	5.6E-02	-0.6	5.7E-01	3.4	5.1E-03
ENSMUST00000030782	hairy and enhancer of split 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1098624]		O54792	6.9	2.7E-05	-3.8	4.4E-04	0.2	6.1E-01	-0.7	3.9E-01
ENSMUST00000030787	Ras homolog enriched in brain [Source:MGI Symbol;Acc:MGI:97912]	Q540E6	Q921J2	-3.5	1.0E-04	-0.8	2.5E-01	0.0	9.5E-01	-1.0	1.7E-01
ENSMUST00000030662	G patch domain containing 3 [Source:MGI Symbol;Acc:MGI:2442492]		Q8BIY1	-0.8	2.4E-01	0.8	3.8E-01	1.6	4.4E-02	-0.1	9.2E-01
ENSMUST00000030795	ATP-binding cassette, sub-family F (GCN20), member 2 [Source:MGI Symbol;Acc:MGI:1351657]		Q99LE6	-2.1	4.4E-04	-2.3	3.9E-03	-0.1	7.6E-01	-1.3	7.6E-02
ENSMUST00000030669	solute carrier family 9 (sodium/hydrogen exchanger), member 1 [Source:MGI Symbol;Acc:MGI:102462]	Q3UDC9	Q61165	-1.3	3.6E-02	0.2	7.4E-01	1.2	3.7E-02	-0.3	6.5E-01
ENSMUST00000030797	vesicle-associated membrane protein 3 [Source:MGI Symbol;Acc:MGI:1321389]		P63024	-3.0	1.7E-04	-5.3	2.9E-04	0.9	8.6E-02	0.3	7.1E-01
ENSMUST00000030799	transmembrane and ubiquitin-like domain containing 1 [Source:MGI Symbol;Acc:MGI:1923764]		Q9JMG3	-3.4	9.7E-03	-1.7	2.3E-01	1.1	2.0E-01	-1.1	4.3E-01
ENSMUST00000030800	Fas-activated serine/threonine kinase [Source:MGI Symbol;Acc:MGI:1913837]	Q8C725		-3.9	2.9E-02	-3.0	1.6E-02	0.0	9.3E-01	-0.7	4.9E-01
ENSMUST00000030805	Parkinson disease (autosomal recessive, early onset) 7 [Source:MGI Symbol;Acc:MGI:2135637]		Q99LX0	-6.8	1.5E-04	9.0	6.3E-05	1.0	4.4E-01	0.4	4.3E-01
ENSMUST00000030811	ERBB receptor feedback inhibitor 1 [Source:MGI Symbol;Acc:MGI:1921405]	Q3TK48	Q99JZ7	-4.6	7.6E-04	3.9	8.0E-04	0.0	9.9E-01	-0.4	5.6E-01
ENSMUST00000030814	cyclin-dependent kinase 5 [Source:MGI Symbol;Acc:MGI:101765]	Q543F6	P49615	-2.7	2.4E-03	-1.6	3.5E-02	-0.6	1.6E-01	-1.0	1.9E-01
ENSMUST00000030815	cortistatin [Source:MGI Symbol;Acc:MGI:109538]		P56469	5.4	4.1E-04	-3.7	1.5E-03	-1.0	4.6E-02	0.4	6.4E-01
ENSMUST00000030816	DNA fragmentation factor, alpha subunit [Source:MGI Symbol;Acc:MGI:1196227]		O54786	-1.3	1.8E-02	5.9	8.7E-03	-0.2	9.0E-01	1.1	2.8E-01
ENSMUST00000030826	solute carrier family 2 (facilitated glucose transporter), member 5 [Source:MGI Symbol;Acc:MGI:1928369]		Q9WV38	8.3	2.5E-05	3.4	7.9E-02	-2.5	2.1E-01	0.4	7.5E-01
ENSMUST00000030839	catenin beta interacting protein 1 [Source:MGI Symbol;Acc:MGI:1915756]		Q9JJN6	-3.2	6.2E-05	-5.4	9.3E-04	1.1	5.3E-02	-0.3	7.8E-01
ENSMUST00000030840	angiopoietin-like 7 [Source:MGI Symbol;Acc:MGI:3605801]		Q8R1Q3	4.3	4.7E-04	-2.3	1.9E-02	0.7	1.7E-01	0.7	3.8E-01
ENSMUST00000030849	family with sequence similarity 126, member A [Source:MGI Symbol;Acc:MGI:2149839]			-1.7	3.8E-03	-3.6	1.8E-04	-0.2	6.1E-01	0.0	9.6E-01
ENSMUST00000030851	translocase of outer mitochondrial membrane 7 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1913419]		Q9D173	-5.6	1.5E-06	-1.2	1.7E-01	0.3	5.0E-01	-1.4	1.2E-01
ENSMUST00000030858	F-box protein 6 [Source:MGI Symbol;Acc:MGI:1354743]		Q9QZN4	-4.0	3.3E-03	1.3	1.2E-01	-1.5	5.4E-02	-0.7	3.4E-01
ENSMUST00000030860	MAD2 mitotic arrest deficient-like 2 [Source:MGI Symbol;Acc:MGI:1919140]		Q9D752	2.7	1.1E-02	5.0	4.6E-04	-1.4	1.9E-01	-0.6	3.7E-01
ENSMUST00000030862	dorsal inhibitory axon guidance protein [Source:MGI Symbol;Acc:MGI:1917683]		Q6PAL1	5.7	5.5E-05	-3.4	7.6E-02	0.9	3.8E-01	-1.3	5.3E-01
ENSMUST00000030865	angiotensin II, type I receptor-associated protein [Source:MGI Symbol;Acc:MGI:1339977]		Q9WVK0	-1.8	7.9E-04	-1.4	1.3E-01	1.3	3.7E-02	-0.2	8.0E-01
ENSMUST00000030726	regulator of chromosome condensation 1 [Source:MGI Symbol;Acc:MGI:1913989]	Q6PFB2		0.4	8.5E-01	0.8	6.0E-01	-4.3	1.5E-02	-4.7	2.6E-02
ENSMUST00000030868	in, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D [Source:MGI Symbol;Acc:MC		Q8BH34	6.6	6.6E-05	-4.7	1.8E-03	-0.6	2.5E-01	-0.8	4.8E-01
ENSMUST00000030731	2 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:191		Q8VE65	0.9	2.0E-01	0.4	6.4E-01	0.3	6.7E-01	0.8	3.5E-01
ENSMUST00000030733	glucocorticoid modulatory element binding protein 1 [Source:MGI Symbol;Acc:MGI:2135604]		Q9JL60	-2.1	5.9E-02	-1.0	4.9E-01	1.4	1.8E-01	0.3	8.3E-01
ENSMUST00000030872	origin recognition complex, subunit 5 [Source:MGI Symbol;Acc:MGI:1347044]		Q9WUV0	-4.1	1.1E-02	-3.8	1.0E-04	-0.9	1.5E-02	-0.4	5.3E-01
ENSMUST00000030738	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) [Source:MGI Symbol;Acc:MGI:1914455]		Q9CZJ1	-0.9	1.2E-01	-2.1	1.3E-02	-0.9	7.6E-02	0.4	5.9E-01
ENSMUST00000030882	peptidase (mitochondrial processing) beta [Source:MGI Symbol;Acc:MGI:1920328]		Q9CXT8	-6.8	1.1E-04	0.2	9.1E-01	-0.7	5.5E-01	2.1	1.3E-01
ENSMUST00000030895	WD repeat containing, antisense to Trp73 [Source:MGI Symbol;Acc:MGI:1891749]		Q9JM98	-4.6	1.0E-02	3.3	1.7E-02	0.6	5.8E-01	-0.3	6.7E-01
ENSMUST00000030896	transformation related protein 63 regulated like [Source:MGI Symbol;Acc:MGI:1915058]		Q9DBS2	-6.6	2.6E-06	-1.0	3.1E-01	1.6	2.0E-02	0.5	5.8E-01
ENSMUST00000030751	trin homology domain containing, family M (with RUN domain) member 2 [Source:MGI Symbol;Acc:MGI:19	A2ADE0		-0.3	9.0E-01	2.7	5.9E-01	4.6	2.4E-01	1.6	6.7E-01
ENSMUST00000030897	multiple EGF-like-domains 6 [Source:MGI Symbol;Acc:MGI:1919351]	A0A0A0MQ83		9.4	4.9E-06	-0.2	7.3E-01	1.1	3.9E-02	0.1	9.0E-01
ENSMUST00000030901	cleavage and polyadenylation specific factor 3-like [Source:MGI Symbol;Acc:MGI:1919207]		Q9CWS4	-6.2	4.2E-05	-6.3	1.4E-02	1.1	2.4E-01	2.3	3.1E-01
ENSMUST00000030763	cyclin-dependent kinase 14 [Source:MGI Symbol;Acc:MGI:894318]		O35495	-1.6	1.9E-01	-1.2	4.4E-01	0.4	7.0E-01	0.1	9.5E-01
ENSMUST00000030905	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916241]		Q9CY97	-7.4	9.8E-06	3.7	1.0E-03	-0.7	3.9E-01	-0.4	4.6E-01
ENSMUST00000030768	tassium voltage-gated channel, shaker-related subfamily, beta member 2 [Source:MGI Symbol;Acc:MGI:10923	Q3UPV6		-4.8	3.6E-02	-1.6	6.4E-01	3.3	1.3E-01	0.0	1.0E+00
ENSMUST00000030914	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915080]		Q9CQU3	-9.0	7.8E-07	-4.8	8.3E-05	-0.6	8.4E-02	0.1	9.0E-01
ENSMUST00000030922	protein kinase C, zeta [Source:MGI Symbol;Acc:MGI:97602]		Q02956	4.0	9.8E-04	-5.1	8.4E-03	-0.8	3.0E-01	0.4	8.3E-01
ENSMUST00000030935	family with sequence similarity 213, member B [Source:MGI Symbol;Acc:MGI:1913719]		Q9DB60	1.6	1.7E-02	4.5	5.2E-04	0.1	8.9E-01	-0.3	5.8E-01
ENSMUST00000030937	matrix metallopeptidase 23 [Source:MGI Symbol;Acc:MGI:1347361]		O88676	6.3	7.7E-04	1.8	3.5E-01	-0.3	8.4E-01	4.8	8.0E-03
ENSMUST00000030779	acyl-CoA thioesterase 7 [Source:MGI Symbol;Acc:MGI:1917275]		Q91V12	2.2	4.1E-01	-1.3	6.8E-01	-4.0	1.3E-01	-0.5	8.7E-01
ENSMUST00000030939	NAD kinase [Source:MGI Symbol;Acc:MGI:2183149]		P58058	-8.6	1.8E-04	7.2	6.6E-05	0.1	9.4E-01	-0.2	7.3E-01
ENSMUST00000030784	protein kinase, AMP-activated, gamma 2 non-catalytic subunit [Source:MGI Symbol;Acc:MGI:1336153]		Q91WG5	0.1	8.3E-01	0.0	9.8E-01	0.0	9.9E-01	0.1	8.7E-01
ENSMUST00000030940	guanine nucleotide binding protein (G protein), beta 1 [Source:MGI Symbol;Acc:MGI:95781]	Q3TQ70	P62874	-7.2	3.3E-02	-3.1	1.0E-03	-0.1	7.3E-01	-0.5	4.4E-01
ENSMUST00000030942	mitochondrial ribosomal protein L20 [Source:MGI Symbol;Acc:MGI:2137221]		Q9CQL4	-6.8	2.8E-03	-1.5	9.9E-03	0.0	9.0E-01	-0.6	2.3E-01
ENSMUST00000030948	dishevelled, dsh homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:94941]		P51141	-6.3	1.1E-03	-2.7	3.4E-03	0.6	1.2E-01	0.3	6.6E-01
ENSMUST00000030949	taste receptor, type 1, member 3 [Source:MGI Symbol;Acc:MGI:1933547]		Q925D8	4.6	9.9E-05	-2.1	1.6E-01	1.2	1.8E-01	-0.2	9.2E-01
ENSMUST00000030971	adhesion G protein-coupled receptor A3 [Source:MGI Symbol;Acc:MGI:1917943]		Q7TT36	4.1	5.5E-04	-3.3	9.2E-02	1.4	1.8E-01	0.9	6.6E-01
ENSMUST00000030985	hepatocyte growth factor activator [Source:MGI Symbol;Acc:MGI:1859281]	Q545J3	Q9R098	6.1	4.1E-04	-6.4	4.8E-04	-0.6	2.3E-01	-1.0	4.8E-01
ENSMUST00000030806	kinesin family member 1B [Source:MGI Symbol;Acc:MGI:108426]	A2AH75		0.1	8.2E-01	0.8	2.6E-01	0.8	1.4E-01	0.1	8.8E-01
ENSMUST00000030986	low density lipoprotein receptor-related protein associated protein 1 [Source:MGI Symbol;Acc:MGI:96829]	Q52KI7	P55302	-2.2	3.8E-04	-2.5	1.3E-02	0.0	9.5E-01	-2.1	7.4E-02
ENSMUST00000030813	apoptosis-inducing, TAF9-like domain 1 [Source:MGI Symbol;Acc:MGI:1917178]		Q9D084	1.3	7.9E-02	0.9	2.6E-01	-0.8	2.0E-01	-0.5	5.0E-01
ENSMUST00000030992	ring finger protein 4 [Source:MGI Symbol;Acc:MGI:1201691]		Q9QZS2	-7.0	1.3E-03	-2.3	2.3E-02	0.6	2.6E-01	0.2	8.4E-01
ENSMUST00000030993	negative elongation factor complex member A, Whsc2 [Source:MGI Symbol;Acc:MGI:1346098]		Q8BG30	-1.8	4.9E-03	5.1	1.4E-03	-1.0	4.2E-01	-0.7	3.7E-01
ENSMUST00000031002	mannosidase 2, alpha B2 [Source:MGI Symbol;Acc:MGI:1195262]		O54782	-2.5	1.3E-03	-0.1	8.7E-01	1.0	3.9E-02	-0.2	7.1E-01
ENSMUST00000031003	protein phosphatase 2, regulatory subunit B, gamma [Source:MGI Symbol;Acc:MGI:2442660]		Q8BG02	9.4	3.3E-05	8.0	6.5E-05	-0.6	6.1E-01	-0.4	5.2E-01
ENSMUST00000030830	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) [Source:MGI Symbol;Acc:MGI:2140356]	A2A7A7		-3.1	9.1E-02	-1.3	4.1E-01	-0.6	5.6E-01	-2.4	2.3E-01
ENSMUST00000030834	nitric oxide synthase 3, endothelial cell [Source:MGI Symbol;Acc:MGI:97362]		P70313	3.2	1.5E-01	3.5	2.3E-01	-0.2	9.4E-01	-0.4	8.4E-01
ENSMUST00000031004	collapsin response mediator protein 1 [Source:MGI Symbol;Acc:MGI:107793]		P97427	5.7	3.3E-05	-1.4	3.4E-02	1.3	4.6E-03	-0.5	3.7E-01
ENSMUST00000031005	Ellis van Creveld gene syndrome [Source:MGI Symbol;Acc:MGI:1890596]		P57680	7.6	4.2E-04	3.3	3.3E-03	-1.8	5.3E-02	-0.8	2.2E-01
ENSMUST00000030841	kelch-like 7 [Source:MGI Symbol;Acc:MGI:1196453]		Q8BUL5	-1.2	5.8E-02	-5.1	1.1E-03	-0.5	2.6E-01	3.4	1.1E-02
ENSMUST00000030842	leucine zipper and CTNNBIP1 domain containing [Source:MGI Symbol;Acc:MGI:1916401]		Q8K3C3	-0.9	4.8E-02	-0.6	2.8E-01	0.1	8.3E-01	-0.3	5.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000031008	syntaxin 18 [Source:MGI Symbol;Acc:MGI:1918366]		Q8VDS8	-5.3	1.0E-04	-0.6	2.7E-01	0.9	3.9E-02	-0.1	8.1E-01
ENSMUST00000031009	neuron specific gene family member 1 [Source:MGI Symbol;Acc:MGI:109149]		Q62092	8.8	7.1E-05	-6.5	4.1E-06	-0.6	6.4E-02	0.3	7.0E-01
ENSMUST00000030852	RAD50 interactor 1 [Source:MGI Symbol;Acc:MGI:1916233]		Q8BZ36	-0.2	9.2E-01	-0.3	9.1E-01	0.3	8.9E-01	0.4	8.6E-01
ENSMUST00000031011	RAB28, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1917285]	Q3TWY9	Q99KL7	-4.5	4.7E-06	-2.8	5.9E-02	0.9	2.5E-01	-0.3	8.4E-01
ENSMUST00000031017	fos-like antigen 2 [Source:MGI Symbol;Acc:MGI:102858]		P47930	-4.1	2.1E-04	2.8	5.5E-02	1.2	3.3E-01	1.1	2.3E-01
ENSMUST00000031018	ribokinase [Source:MGI Symbol;Acc:MGI:1918586]		Q8R1Q9	-2.8	6.5E-04	3.5	3.1E-03	-1.4	1.4E-01	0.8	2.4E-01
ENSMUST00000031020	RIKEN cDNA 4930548H24 gene [Source:MGI Symbol;Acc:MGI:1914906]	Q9D496		7.2	1.7E-04	-0.9	1.1E-01	1.2	7.2E-03	0.2	7.1E-01
ENSMUST00000031024	mitochondrial ribosomal protein L33 [Source:MGI Symbol;Acc:MGI:2137225]		Q9CQP0	-9.6	2.3E-06	4.1	2.7E-04	-3.3	4.8E-03	-0.9	1.6E-01
ENSMUST00000031029	sorting nexin 17 [Source:MGI Symbol;Acc:MGI:2387801]		Q8BVL3	-7.9	2.4E-04	-2.5	9.4E-02	-0.4	6.3E-01	-2.1	2.1E-01
ENSMUST00000030878	solute carrier family 26, member 5 [Source:MGI Symbol;Acc:MGI:1933154]		Q99NH7	2.6	1.0E-01	5.4	3.1E-03	-0.5	7.4E-01	-3.4	1.0E-02
ENSMUST00000031032	:in phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform [Source:MGI Symbol;Acc:MGI:106		Q61074	-3.8	1.4E-04	-6.6	2.3E-04	-0.2	6.5E-01	-0.4	7.5E-01
ENSMUST00000030884	mitofusin 2 [Source:MGI Symbol;Acc:MGI:2442230]		Q80U63	5.3	7.3E-02	6.6	8.7E-02	1.8	6.0E-01	0.5	8.1E-01
ENSMUST00000030886	migration and invasion inhibitory protein [Source:MGI Symbol;Acc:MGI:106506]	C0KL25	A2A7Y5	-1.9	1.6E-01	-2.4	3.0E-01	1.4	2.2E-01	2.0	3.7E-01
ENSMUST00000030893	DNA fragmentation factor, beta subunit [Source:MGI Symbol;Acc:MGI:1196287]		O54788	-0.9	7.3E-02	-0.4	4.8E-01	0.9	4.2E-02	0.5	3.8E-01
ENSMUST00000030894	leucine rich repeat containing 47 [Source:MGI Symbol;Acc:MGI:1920196]	B1AX98	Q505F5	-1.0	1.1E-01	-0.8	3.7E-01	1.0	1.1E-01	0.7	3.8E-01
ENSMUST00000031034	nuclear receptor binding protein 1 [Source:MGI Symbol;Acc:MGI:2183436]		Q99J45	-8.6	6.0E-06	-3.6	5.4E-02	1.3	1.9E-01	0.2	8.9E-01
ENSMUST00000031038	OCIA domain containing 1 [Source:MGI Symbol;Acc:MGI:1915345]		Q9CRD0	-7.7	1.9E-05	-4.8	1.5E-04	0.9	3.3E-02	-0.9	2.8E-01
ENSMUST00000031040	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2444131]		Q91YL7	7.3	1.1E-04	6.7	4.1E-05	-2.8	2.5E-02	-0.2	6.8E-01
ENSMUST00000031051	cell growth regulator with EF hand domain 1 [Source:MGI Symbol;Acc:MGI:1915817]	E9QPK1		4.2	8.4E-04	-1.3	8.3E-02	1.0	4.0E-02	-3.9	1.8E-03
ENSMUST00000030903	ATPase family, AAA domain containing 3A [Source:MGI Symbol;Acc:MGI:1919214]		Q925I1	1.3	9.7E-02	1.0	2.7E-01	-0.8	2.6E-01	-0.5	5.3E-01
ENSMUST00000031055	elastin microfibril interfacer 1 [Source:MGI Symbol;Acc:MGI:1926189]		Q99K41	-2.1	9.5E-03	-8.3	9.1E-05	-0.5	2.4E-01	0.4	7.5E-01
ENSMUST00000031061	DEAH (Asp-Glu-Ala-His) box polypeptide 15 [Source:MGI Symbol;Acc:MGI:1099786]	Q3UKJ6	O35286	-3.9	6.4E-05	-7.8	2.5E-05	1.0	7.0E-03	-0.2	8.7E-01
ENSMUST00000030917	ski sarcoma viral oncogene homolog (avian) [Source:MGI Symbol;Acc:MGI:98310]	B1AUF1		-3.0	7.3E-02	-4.0	1.6E-01	1.3	4.0E-01	2.3	3.9E-01
ENSMUST00000031077	zinc finger, CCHC domain containing 4 [Source:MGI Symbol;Acc:MGI:1926046]		Q8BKW4	4.9	5.5E-06	0.6	6.5E-01	-0.7	4.6E-01	2.7	2.9E-02
ENSMUST00000030925	gamma-aminobutyric acid (GABA) A receptor, subunit delta [Source:MGI Symbol;Acc:MGI:95622]	Q14AH9	P22933	4.6	4.6E-02	3.0	1.9E-01	-0.6	7.9E-01	1.0	5.5E-01
ENSMUST00000030931	pantothenate kinase 4 [Source:MGI Symbol;Acc:MGI:2387466]		Q80YV4	-1.9	1.3E-01	-4.0	8.8E-02	0.7	4.6E-01	2.9	2.0E-01
ENSMUST00000031080	family with sequence similarity 114, member A1 [Source:MGI Symbol;Acc:MGI:1915553]		Q9D281	-2.1	3.1E-03	-1.2	5.0E-02	-3.7	3.6E-05	-0.9	1.5E-01
ENSMUST00000031081	phosphatidylinositol 4-kinase type 2 beta [Source:MGI Symbol;Acc:MGI:1914323]		Q8CBQ5	-2.2	4.0E-03	4.2	1.0E-02	-2.4	1.2E-01	-0.3	7.5E-01
ENSMUST00000031090	sel-1 suppressor of lin-12-like 3 (C. elegans) [Source:MGI Symbol;Acc:MGI:1916941]		Q80TS8	8.4	7.1E-06	-9.0	1.1E-03	0.6	3.9E-01	1.0	6.3E-01
ENSMUST00000031091	DNA segment, Chr 5, ERATO Doi 579, expressed [Source:MGI Symbol;Acc:MGI:1261849]	E9QPJ5		-4.7	3.7E-03	2.0	6.9E-01	9.0	2.6E-02	-0.3	9.5E-01
ENSMUST00000031093	cholecystokinin A receptor [Source:MGI Symbol;Acc:MGI:99478]		O08786	11.1	7.5E-06	-4.9	4.1E-03	-1.1	1.5E-01	-2.9	1.4E-01
ENSMUST00000030944	cyclin L2 [Source:MGI Symbol;Acc:MGI:1927119]		Q9JJA7	-2.5	3.6E-02	-2.0	1.6E-01	0.3	7.0E-01	-0.2	8.8E-01
ENSMUST00000030947	matrix-remodelling associated 8 [Source:MGI Symbol;Acc:MGI:1922011]		Q9DBV4	3.7	3.7E-02	-1.4	4.2E-01	-3.2	5.8E-02	1.9	2.4E-01
ENSMUST00000031096	klotho beta [Source:MGI Symbol;Acc:MGI:1932466]		Q99N32	4.4	3.1E-04	-4.8	2.0E-02	0.6	3.9E-01	-0.9	6.4E-01
ENSMUST00000031099	GrpE-like 1, mitochondrial [Source:MGI Symbol;Acc:MGI:1334417]		Q99LP6	-3.4	1.1E-04	4.3	9.1E-04	0.4	5.9E-01	0.8	2.3E-01
ENSMUST00000030950	ceramide-1-phosphate transfer protein [Source:MGI Symbol;Acc:MGI:1933107]		Q8BS40	0.6	7.3E-01	2.3	4.1E-01	1.3	5.8E-01	-0.3	8.6E-01
ENSMUST00000031103	UDP-glucose dehydrogenase [Source:MGI Symbol;Acc:MGI:1306785]	Q3TS38	O70475	-7.6	1.4E-06	6.3	6.2E-04	-0.7	6.1E-01	-0.2	8.0E-01
ENSMUST00000030952	tumor necrosis factor receptor superfamily, member 4 [Source:MGI Symbol;Acc:MGI:104512]	B1ASL3		1.8	3.2E-01	0.9	6.0E-01	-2.4	1.7E-01	-1.4	3.8E-01
ENSMUST00000030964	CD38 antigen [Source:MGI Symbol;Acc:MGI:107474]	Q4FJL8	P56528	-0.3	4.2E-01	-0.1	7.8E-01	-0.3	4.4E-01	-0.5	3.4E-01
ENSMUST00000030968	PARK2 co-regulated-like [Source:MGI Symbol;Acc:MGI:1914018]		Q9D3X5	-1.2	3.6E-02	-0.6	3.4E-01	-0.1	8.4E-01	-0.7	2.4E-01
ENSMUST00000031104	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1918771]	E9QPI5		-2.6	7.6E-04	1.9	4.7E-02	-2.2	2.0E-02	0.0	9.9E-01
ENSMUST00000030980	tRNA methyltransferase 44 [Source:MGI Symbol;Acc:MGI:1926140]		Q9D2Q2	0.4	3.8E-01	1.5	4.6E-02	1.0	6.7E-02	0.0	9.6E-01
ENSMUST00000030984	regulator of G-protein signaling 12 [Source:MGI Symbol;Acc:MGI:1918979]		Q8CGE9	1.1	5.1E-01	-1.1	7.2E-01	0.1	9.7E-01	2.3	3.8E-01
ENSMUST00000031106	ras homolog gene family, member H [Source:MGI Symbol;Acc:MGI:1921984]	Q504M6	Q9D3G9	1.3	1.4E-02	7.2	4.0E-04	0.0	9.9E-01	-1.1	1.5E-01
ENSMUST00000031117	glucosamine-6-phosphate deaminase 2 [Source:MGI Symbol;Acc:MGI:1915230]		Q9CRC9	-3.7	2.0E-03	-2.0	2.5E-03	-0.3	2.8E-01	-0.5	3.4E-01
ENSMUST00000031121	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 4 [Source:MGI Symbol;Acc:MGI:95616]	Q543Z0	Q9D6F4	7.7	3.1E-05	-6.2	1.7E-02	0.7	3.4E-01	-0.1	9.6E-01
ENSMUST00000031122	gamma-aminobutyric acid (GABA) A receptor, subunit beta 1 [Source:MGI Symbol;Acc:MGI:95619]	Q53WT3	P50571	6.7	1.8E-05	-0.7	2.5E-01	0.7	9.8E-02	-0.3	6.0E-01
ENSMUST00000031124	predicted gene 5868 [Source:MGI Symbol;Acc:MGI:3645333]	Q8BJG1		7.6	1.6E-04	-1.4	7.4E-02	0.7	1.2E-01	-0.4	5.8E-01
ENSMUST00000031127	ute carrier family 10 (sodium/bile acid cotransporter family), member 4 [Source:MGI Symbol;Acc:MGI:36064	A2RTJ6	Q3UEZ8	9.1	8.0E-06	8.5	1.5E-04	-0.8	6.1E-01	0.2	7.8E-01
ENSMUST00000031143	steroid 5 alpha-reductase 3 [Source:MGI Symbol;Acc:MGI:1930252]		Q9WUP4	-6.7	3.9E-05	5.1	6.4E-04	-0.2	8.3E-01	0.4	5.4E-01
ENSMUST00000031144	transmembrane protein 165 [Source:MGI Symbol;Acc:MGI:894407]		P52875	-5.6	1.5E-05	2.0	1.3E-01	-4.5	9.6E-03	1.2	2.5E-01
ENSMUST00000031146	neuromedin U [Source:MGI Symbol;Acc:MGI:1860476]	Q059S5	Q9QXK8	6.5	1.9E-04	-4.8	6.0E-04	-0.1	7.4E-01	-0.6	5.5E-01
ENSMUST00000031161	theg spermatid protein like [Source:MGI Symbol;Acc:MGI:1919118]		Q9DA15	6.3	1.5E-04	6.2	8.5E-04	-2.0	2.0E-01	0.6	4.7E-01
ENSMUST00000031167	polymerase (RNA) II (DNA directed) polypeptide B [Source:MGI Symbol;Acc:MGI:2388280]		Q8CFI7	-4.5	5.3E-05	-3.8	1.1E-04	0.7	3.3E-02	0.0	9.5E-01
ENSMUST00000031171	signal transducing adaptor family member 1 [Source:MGI Symbol;Acc:MGI:1926193]	A0A0H2UKC0		-6.5	5.0E-05	-3.0	7.4E-03	1.0	8.3E-02	-0.2	8.2E-01
ENSMUST00000031181	UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI Symbol;Acc:MGI:2140962]	Q8K154		7.0	7.6E-05	-2.6	3.3E-03	-0.6	1.7E-01	-0.8	2.3E-01
ENSMUST00000031183	UDP glucuronosyltransferase 2 family, polypeptide B1 [Source:MGI Symbol;Acc:MGI:1919023]	Q8R084		6.2	1.6E-04	6.0	5.7E-04	-2.0	1.5E-01	-0.7	3.1E-01
ENSMUST00000031186	UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI Symbol;Acc:MGI:3576100]	Q8BJL9		5.9	4.3E-04	-8.4	6.9E-06	-0.3	3.7E-01	-1.5	2.0E-01
ENSMUST00000031190	down-regulator of transcription 1 [Source:MGI Symbol;Acc:MGI:1100515]		Q91WV0	-2.8	2.1E-04	-6.0	7.3E-03	1.2	8.7E-02	-0.7	7.3E-01
ENSMUST00000031198	family with sequence similarity 69, member A [Source:MGI Symbol;Acc:MGI:1914516]		Q9D6I7	-4.2	1.4E-03	-2.4	9.5E-03	0.9	6.3E-02	-0.5	5.1E-01
ENSMUST00000031205	growth factor independent 1 [Source:MGI Symbol;Acc:MGI:103170]			3.8	2.0E-02	-6.9	6.4E-05	0.6	1.0E-01	-1.0	3.9E-01
ENSMUST00000031037	solute carrier family 30 (zinc transporter), member 3 [Source:MGI Symbol;Acc:MGI:1345280]	Q3TMQ7	P97441	2.8	4.5E-02	6.8	2.3E-04	-0.5	6.8E-01	-4.5	5.8E-04
ENSMUST00000031215	bromodomain, testis-specific [Source:MGI Symbol;Acc:MGI:1891374]		Q91Y44	6.8	3.8E-05	-5.8	2.0E-04	0.2	6.4E-01	-1.7	1.7E-01
ENSMUST00000031222	enamelin [Source:MGI Symbol;Acc:MGI:1333772]	Q548P8	O55196	9.5	4.5E-05	6.7	3.5E-04	-0.7	6.2E-01	-0.1	8.7E-01
ENSMUST00000031224	transforming growth factor, beta receptor III [Source:MGI Symbol;Acc:MGI:104637]			3.7	2.8E-04	3.8	1.2E-02	0.9	4.6E-01	1.3	1.6E-01
ENSMUST00000031053	ketohexokinase [Source:MGI Symbol;Acc:MGI:1096353]	E9Q1Q9		-1.0	2.3E-01	0.4	7.1E-01	0.6	4.3E-01	-0.8	4.2E-01
ENSMUST00000031226	ameloblastin [Source:MGI Symbol;Acc:MGI:104655]		O55189	6.8	7.7E-04	-0.9	3.1E-01	1.0	9.9E-02	-0.3	7.5E-01
ENSMUST00000031229	RUN and FYVE domain containing 3 [Source:MGI Symbol;Acc:MGI:106484]		Q9D394	3.7	9.6E-04	-3.5	8.7E-04	0.5	1.8E-01	0.2	8.2E-01
ENSMUST00000031069	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase [Source:MGI Symbol;Acc:MGI:1098791]		Q6P6M7	7.1	6.6E-02	-0.5	8.8E-01	-5.4	1.6E-01	2.2	3.9E-01
ENSMUST00000031072	anaphase promoting complex subunit 4 [Source:MGI Symbol;Acc:MGI:1098673]	Q3TM92	Q91W96	1.0	3.5E-01	1.0	4.1E-01	-0.8	4.3E-01	-0.8	4.8E-01
ENSMUST00000031073	centromere protein A [Source:MGI Symbol;Acc:MGI:88375]	D6RJ71		-5.0	3.7E-02	-1.3	6.5E-01	2.1	2.7E-01	-1.6	5.5E-01
ENSMUST00000031239	ATP-binding cassette, sub-family G (WHITE), member 3 [Source:MGI Symbol;Acc:MGI:1351624]		Q99P81	3.6	5.3E-03	4.6	2.5E-05	-0.4	4.4E-01	-0.2	7.0E-01
ENSMUST00000031243	secreted phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:98389]	Q547B5	P10923	-4.7	5.3E-03	-3.5	8.8E-04	-0.7	1.2E-01	0.8	3.2E-01
ENSMUST00000031246	integrin binding sialoprotein [Source:MGI Symbol;Acc:MGI:96389]		Q61711	6.3	3.8E-04	-1.6	4.5E-02	-0.9	8.4E-02	-1.6	5.2E-02
ENSMUST00000031249	SPARC-like 1 [Source:MGI Symbol;Acc:MGI:108110]		P70663	7.2	2.9E-04	2.8	1.3E-01	-4.9	2.5E-02	-1.2	3.8E-01
ENSMUST00000031250	nudix (nucleoside diphosphate linked moiety X)-type motif 9 [Source:MGI Symbol;Acc:MGI:1921417]		Q8BVU5	-2.7	9.0E-04	5.2	3.9E-05	-3.5	3.3E-03	-0.4	4.6E-01
ENSMUST00000031251	hydroxysteroid (17-beta) dehydrogenase 11 [Source:MGI Symbol;Acc:MGI:2149821]		Q9EQ06	-7.3	1.4E-07	-5.1	2.5E-02	-0.1	8.9E-01	0.3	8.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000031263	ute carrier family 10 (sodium/bile acid cotransporter family), member 6 [Source:MGI Symbol;Acc:MGI:192306		Q9CXB2	6.9	6.0E-05	-3.5	4.3E-02	0.0	9.7E-01	-1.9	2.9E-01
ENSMUST00000031264	placenta-specific 8 [Source:MGI Symbol;Acc:MGI:2445289]		Q9JI48	-10.3	4.2E-07	7.7	9.8E-05	-2.1	1.5E-01	1.3	5.4E-02
ENSMUST00000031094	TBC1 domain family, member 14 [Source:MGI Symbol;Acc:MGI:1098708]	E9Q8K4		-4.0	6.1E-02	-1.6	5.8E-01	3.0	7.3E-02	0.6	8.4E-01
ENSMUST00000031273	CDP-diacylglycerol synthase 1 [Source:MGI Symbol;Acc:MGI:1921846]		P98191	3.4	3.8E-03	3.2	3.8E-03	-1.5	8.3E-02	-0.4	5.8E-01
ENSMUST00000031097	transcriptional adaptor 2B [Source:MGI Symbol;Acc:MGI:3035274]	D3Z4Z0		-0.6	2.3E-01	0.8	2.1E-01	1.2	2.8E-02	-0.2	7.1E-01
ENSMUST00000031276	RasGEF domain family, member 1B [Source:MGI Symbol;Acc:MGI:2443755]		Q8JZL7	4.1	1.2E-03	-3.1	6.4E-04	-0.6	8.4E-02	-0.9	2.0E-01
ENSMUST00000031101	lipoic acid synthetase [Source:MGI Symbol;Acc:MGI:1934604]			0.1	8.4E-01	1.7	7.1E-02	1.3	9.1E-02	-0.3	6.6E-01
ENSMUST00000031278	bone morphogenetic protein 3 [Source:MGI Symbol;Acc:MGI:88179]	Q149J9	Q8BHE5	6.4	1.4E-05	-5.6	7.2E-06	0.1	6.6E-01	-1.9	3.2E-02
ENSMUST00000031280	fibroblast growth factor 5 [Source:MGI Symbol;Acc:MGI:95519]		P15656	11.2	8.8E-05	-1.9	1.9E-02	0.5	2.6E-01	-0.2	7.5E-01
ENSMUST00000031281	anthrax toxin receptor 2 [Source:MGI Symbol;Acc:MGI:1919164]	Q3TCL6	Q6DFX2	-3.1	9.6E-05	-6.6	1.4E-04	-0.7	1.1E-01	-0.7	5.8E-01
ENSMUST00000031286	crystallin, beta B1 [Source:MGI Symbol;Acc:MGI:104992]		Q9WVJ5	5.2	1.8E-02	0.8	1.6E-01	-0.7	1.1E-01	-0.2	6.8E-01
ENSMUST00000031287	protein-tyrosine sulfotransferase 2 [Source:MGI Symbol;Acc:MGI:1309516]	Q3TQN1		-7.5	1.3E-04	-3.9	2.3E-02	0.9	2.3E-01	1.0	4.8E-01
ENSMUST00000031288	tuftelin interacting protein 11 [Source:MGI Symbol;Acc:MGI:1930075]	Q3TTV6	Q9ERA6	-2.2	3.9E-03	5.8	2.4E-04	-2.0	1.0E-01	-0.1	9.0E-01
ENSMUST00000031291	aspartate beta-hydroxylase domain containing 2 [Source:MGI Symbol;Acc:MGI:1920148]		Q80VP9	8.4	9.1E-05	5.6	8.8E-05	-1.1	2.2E-01	-0.1	8.7E-01
ENSMUST00000031309	WD repeat and SOCS box-containing 2 [Source:MGI Symbol;Acc:MGI:2144041]		O54929	-2.6	2.9E-03	6.1	8.6E-04	-1.5	3.1E-01	0.0	9.8E-01
ENSMUST00000031311	deoxycytidine kinase [Source:MGI Symbol;Acc:MGI:102726]	Q545E8	P43346	-4.6	4.4E-05	8.2	3.8E-05	-0.6	6.2E-01	0.3	5.3E-01
ENSMUST00000031314	albumin [Source:MGI Symbol;Acc:MGI:87991]	Q546G4	P07724	4.5	1.2E-02	-4.9	2.4E-03	2.3	1.3E-03	0.5	6.8E-01
ENSMUST00000031317	Ras association (RalGDS/AF-6) domain family member 6 [Source:MGI Symbol;Acc:MGI:1920496]	G3X8Z9		3.6	2.4E-03	-6.2	6.4E-04	1.3	1.6E-02	1.9	1.5E-01
ENSMUST00000031318	chemokine (C-X-C motif) ligand 5 [Source:MGI Symbol;Acc:MGI:1096868]		P50228	5.8	2.0E-04	5.8	7.5E-04	-0.6	6.3E-01	0.1	9.1E-01
ENSMUST00000031158				-2.0	8.2E-02	-3.7	2.5E-02	-1.6	6.0E-02	0.1	9.7E-01
ENSMUST00000031160	izole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase [Source:MGI S		Q9DCL9	2.1	1.8E-01	-0.5	7.5E-01	-3.2	3.4E-02	-0.6	6.7E-01
ENSMUST00000031322	chemokine (C-X-C motif) ligand 15 [Source:MGI Symbol;Acc:MGI:1339941]		Q9WVL7	8.2	4.1E-07	7.5	6.3E-05	-0.5	6.5E-01	-1.8	1.5E-02
ENSMUST00000031324	epiregulin [Source:MGI Symbol;Acc:MGI:107508]		Q61521	6.4	2.6E-04	-4.2	4.3E-04	-0.3	4.4E-01	-0.6	4.6E-01
ENSMUST00000031170	centromere protein C1 [Source:MGI Symbol;Acc:MGI:99700]		P49452	-1.0	5.6E-02	-0.7	2.6E-01	0.0	9.6E-01	-0.4	5.5E-01
ENSMUST00000031325	amphiregulin [Source:MGI Symbol;Acc:MGI:88068]	Q4FJT2	P31955	4.4	2.1E-03	-5.4	1.1E-03	0.1	7.5E-01	-0.9	4.7E-01
ENSMUST00000031175	transmembrane protease, serine 11d [Source:MGI Symbol;Acc:MGI:2385221]		Q8VHK8	3.1	2.5E-01	4.7	1.1E-01	-0.4	9.0E-01	-2.1	2.9E-01
ENSMUST00000031326	chemokine (C-X-C motif) ligand 3 [Source:MGI Symbol;Acc:MGI:3037818]		Q6W5C0	5.4	1.5E-04	6.5	2.6E-04	-0.6	6.4E-01	-0.1	9.0E-01
ENSMUST00000031327	chemokine (C-X-C motif) ligand 1 [Source:MGI Symbol;Acc:MGI:108068]	A2RTH0	P12850	3.7	3.1E-03	5.9	4.0E-04	-0.5	6.5E-01	-0.3	6.9E-01
ENSMUST00000031341	CDK2 (cyclin-dependent kinase 2)-associated protein 1 [Source:MGI Symbol;Acc:MGI:1202069]		O35207	-5.1	1.3E-03	5.9	8.2E-04	-0.5	7.0E-01	-0.4	5.4E-01
ENSMUST00000031189	phosphatidylinositol glycan anchor biosynthesis, class G [Source:MGI Symbol;Acc:MGI:3576484]	D3Z4I0		2.6	2.8E-01	6.4	7.2E-02	2.4	4.3E-01	-1.4	5.4E-01
ENSMUST00000031344	M-phase phosphoprotein 9 [Source:MGI Symbol;Acc:MGI:2443138]	E9QPF8		2.4	3.3E-03	-1.5	2.6E-02	0.8	4.1E-02	-0.5	4.3E-01
ENSMUST00000031345	ring finger and CHY zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1915348]		Q9CR50	-5.8	3.2E-05	-3.8	1.9E-02	0.3	6.8E-01	-0.1	9.2E-01
ENSMUST00000031347	Rab interacting lysosomal protein-like 2 [Source:MGI Symbol;Acc:MGI:1933112]		Q99LE1	-3.0	6.9E-04	6.5	1.7E-02	3.0	1.8E-01	0.4	7.7E-01
ENSMUST00000031351	ADP-ribosylation factor-like 6 interacting protein 4 [Source:MGI Symbol;Acc:MGI:1929500]		Q9JM93	-3.6	2.5E-03	5.1	1.6E-04	-1.6	1.1E-01	0.0	9.6E-01
ENSMUST00000031221	cell division cycle 7 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1309511]		Q9Z0H0	-1.2	5.3E-01	-2.6	1.6E-01	-2.1	1.4E-01	-0.8	7.0E-01
ENSMUST00000031354	ATP-binding cassette, sub-family B (MDR/TAP), member 9 [Source:MGI Symbol;Acc:MGI:1861729]		Q9JJ59	1.8	1.9E-02	8.4	2.4E-04	-0.8	6.2E-01	0.3	6.6E-01
ENSMUST00000031355	USO1 vesicle docking factor [Source:MGI Symbol;Acc:MGI:1929095]		Q9Z1Z0	-3.3	1.2E-04	1.4	6.1E-02	-2.3	5.4E-03	0.0	9.8E-01
ENSMUST00000031356	cDNA sequence U90926 [Source:MGI Symbol;Acc:MGI:1930915]	O08546		6.0	4.8E-04	6.4	1.9E-03	-0.8	6.5E-01	-0.4	6.6E-01
ENSMUST00000031227	zinc finger protein 326 [Source:MGI Symbol;Acc:MGI:1927246]			-1.4	1.6E-01	-0.8	3.3E-01	-1.8	2.9E-02	-2.3	3.1E-02
ENSMUST00000031359	protein phosphatase, EF hand calcium-binding domain 2 [Source:MGI Symbol;Acc:MGI:1342304]		O35385	3.7	5.4E-03	3.4	8.4E-03	0.5	5.7E-01	0.8	3.3E-01
ENSMUST00000031235	guanylate-binding protein 8 [Source:MGI Symbol;Acc:MGI:1923324]	Q2V6D6		1.8	1.2E-01	0.2	8.5E-01	-2.1	6.4E-02	-0.5	6.3E-01
ENSMUST00000031238	guanylate-binding protein 9 [Source:MGI Symbol;Acc:MGI:3605620]	Q8BTS3		0.2	8.4E-01	-0.1	9.7E-01	-0.7	4.7E-01	-0.5	7.1E-01
ENSMUST00000031366	kinetochore associated 1 [Source:MGI Symbol;Acc:MGI:2673709]		Q8C3Y4	1.2	1.2E-02	1.8	1.1E-01	-2.7	1.9E-02	-0.9	3.4E-01
ENSMUST00000031376	zinc finger, CCHC domain containing 8 [Source:MGI Symbol;Acc:MGI:1917900]		Q9CYA6	-1.9	1.7E-02	-9.0	1.5E-04	-5.1	2.6E-05	-0.8	6.2E-01
ENSMUST00000031377	scavenger receptor class B, member 2 [Source:MGI Symbol;Acc:MGI:1196458]		O35114	-4.8	3.1E-05	2.7	1.7E-02	-3.7	8.9E-03	-0.1	8.7E-01
ENSMUST00000031382	CAP-GLY domain containing linker protein 1 [Source:MGI Symbol;Acc:MGI:1928401]	F8WIA1		-7.6	3.3E-05	4.6	3.5E-03	-2.6	8.8E-02	0.1	9.3E-01
ENSMUST00000031383	RAN, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1333112]		P62827	-3.1	5.6E-04	-2.4	6.8E-03	-0.6	1.9E-01	-1.0	2.0E-01
ENSMUST00000031388	vacuolar protein sorting 33A (yeast) [Source:MGI Symbol;Acc:MGI:1924823]		Q9D2N9	-2.5	9.4E-05	-7.5	1.0E-06	0.1	7.7E-01	0.2	7.0E-01
ENSMUST00000031254	kelch-like 8 [Source:MGI Symbol;Acc:MGI:2179430]		P59280	4.2	3.5E-02	3.0	2.3E-01	-0.8	7.3E-01	0.5	7.8E-01
ENSMUST00000031255	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:MGI Symbol;Acc:MGI:3603816]		Q8C0N2	-3.6	6.5E-02	-2.9	4.3E-01	3.2	1.5E-01	2.5	4.5E-01
ENSMUST00000031256	AF4/FMR2 family, member 1 [Source:MGI Symbol;Acc:MGI:1100819]	E9Q921		0.1	9.5E-01	-4.6	1.8E-01	0.8	6.1E-01	5.5	9.0E-02
ENSMUST00000031262	coenzyme Q2 homolog, prenyltransferase (yeast) [Source:MGI Symbol;Acc:MGI:1919133]		Q66JT7	-1.3	6.2E-02	-0.3	6.7E-01	0.4	4.1E-01	-0.5	5.1E-01
ENSMUST00000031390	matrix metallopeptidase 17 [Source:MGI Symbol;Acc:MGI:1346076]		Q9R0S3	7.0	4.3E-05	4.8	2.7E-04	-2.4	3.4E-02	-0.4	5.1E-01
ENSMUST00000031391	B cell CLL/lymphoma 7A [Source:MGI Symbol;Acc:MGI:1924295]		Q9CXE2	3.2	3.8E-03	-11.9	1.8E-05	-0.4	2.6E-01	1.2	4.0E-01
ENSMUST00000031268	enolase-phosphatase 1 [Source:MGI Symbol;Acc:MGI:1915120]		Q8BGB7	3.0	2.3E-01	2.9	2.8E-01	-1.1	6.6E-01	-1.0	6.3E-01
ENSMUST00000031399	phosphoserine phosphatase [Source:MGI Symbol;Acc:MGI:97788]		Q99LS3	-4.2	6.8E-04	3.8	6.8E-03	0.0	1.0E+00	-0.3	7.0E-01
ENSMUST00000031401	ras homolog gene family, member f [Source:MGI Symbol;Acc:MGI:1345629]	Q4VA10	Q8BYP3	-4.1	3.2E-04	3.4	1.2E-02	0.2	8.1E-01	1.0	2.4E-01
ENSMUST00000031411	aldehyde dehydrogenase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:99600]	Q544B1	P47738	-5.0	1.7E-05	5.9	1.5E-04	-0.6	5.3E-01	-0.1	8.7E-01
ENSMUST00000031412	acyl-Coenzyme A dehydrogenase family, member 10 [Source:MGI Symbol;Acc:MGI:1919235]		Q8K370	8.6	1.3E-05	9.9	4.6E-04	-0.4	8.3E-01	0.8	3.3E-01
ENSMUST00000031414	BRCA1 associated protein [Source:MGI Symbol;Acc:MGI:1919649]		Q99MP8	-7.3	7.4E-05	-3.1	1.0E-03	0.7	8.1E-02	0.7	2.7E-01
ENSMUST00000031420	GPN-loop GTPase 3 [Source:MGI Symbol;Acc:MGI:1289326]		Q9D3W4	-4.8	1.6E-03	6.1	1.3E-02	-0.5	8.0E-01	-1.5	2.4E-01
ENSMUST00000031421	actin related protein 2/3 complex, subunit 3 [Source:MGI Symbol;Acc:MGI:1928375]	H7BWZ3		-5.8	4.2E-07	-5.9	2.2E-03	0.6	2.7E-01	-0.9	5.6E-01
ENSMUST00000031422	anaphase promoting complex subunit 7 [Source:MGI Symbol;Acc:MGI:1929711]		Q9WVM3	-7.3	1.9E-05	-0.7	3.7E-01	1.1	5.4E-02	-0.5	4.9E-01
ENSMUST00000031423	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Source:MGI Symbol;Acc:MGI:88110]		O55143	-2.8	2.5E-03	7.5	4.2E-04	-0.7	6.3E-01	0.2	7.8E-01
ENSMUST00000031429	purinergic receptor P2X, ligand-gated ion channel 4 [Source:MGI Symbol;Acc:MGI:1338859]	Q9Z257		3.2	2.0E-03	5.5	1.1E-03	-1.3	3.2E-01	-0.7	3.6E-01
ENSMUST00000031434	ring finger protein 34 [Source:MGI Symbol;Acc:MGI:2153340]		Q99KR6	-4.8	2.5E-06	-1.1	1.9E-01	1.0	8.9E-02	-0.5	5.5E-01
ENSMUST00000031435	lysine (K)-specific demethylase 2B [Source:MGI Symbol;Acc:MGI:1354737]		Q6P1G2	-3.2	2.3E-02	-2.9	3.5E-03	1.0	4.0E-02	-0.8	3.4E-01
ENSMUST00000031445	acetoacetyl-CoA synthetase [Source:MGI Symbol;Acc:MGI:1926144]		Q9D2R0	-3.3	2.4E-04	-2.4	7.1E-02	-7.5	3.5E-04	-0.6	6.4E-01
ENSMUST00000031446	transmembrane protein 132B [Source:MGI Symbol;Acc:MGI:3609245]	F7BAB2		4.9	4.9E-05	1.6	5.8E-02	-3.1	4.0E-03	-1.1	1.5E-01
ENSMUST00000031447	annexin A3 [Source:MGI Symbol;Acc:MGI:1201378]		O35639	-6.9	4.6E-07	1.1	1.4E-01	-5.3	2.8E-04	-0.6	3.7E-01
ENSMUST00000031319	pro-platelet basic protein [Source:MGI Symbol;Acc:MGI:1888712]	Q9EQI5		-0.9	1.6E-01	-2.7	2.9E-03	-2.8	2.8E-04	-1.0	1.6E-01
ENSMUST00000031320	platelet factor 4 [Source:MGI Symbol;Acc:MGI:1888711]	Q3TVN6	Q9Z126	-1.9	1.2E-01	-5.3	2.3E-03	-4.3	3.9E-04	-0.9	5.0E-01
ENSMUST00000031472	peroxisomal membrane protein 2 [Source:MGI Symbol;Acc:MGI:107487]	Q5D073		3.6	1.6E-02	6.9	3.7E-06	-1.2	1.1E-01	0.1	8.2E-01
ENSMUST00000031474	ankyrin repeat and LEM domain containing 2 [Source:MGI Symbol;Acc:MGI:1261856]		Q6P1H6	-2.0	1.1E-02	5.2	7.2E-04	-1.5	2.1E-01	-0.3	7.1E-01
ENSMUST00000031477	golgi autoantigen, golgin subfamily a, 3 [Source:MGI Symbol;Acc:MGI:96958]	E9QP99		-7.0	9.9E-06	0.7	4.1E-01	-4.3	1.7E-03	-0.6	4.1E-01
ENSMUST00000031478	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 [Source:MGI Symbol;Acc:MGI:1916913]		Q6P9R1	2.3	4.8E-04	2.3	1.4E-02	-3.0	5.7E-03	0.1	8.4E-01
ENSMUST00000031486	protein kinase, AMP-activated, beta 1 non-catalytic subunit [Source:MGI Symbol;Acc:MGI:1336167]	Q542K0	Q9R078	-6.9	1.4E-06	-0.4	6.3E-01	-4.8	3.9E-04	-0.7	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000031331	cyclin G2 [Source:MGI Symbol;Acc:MGI:1095734]	Q5HZK4	O08918	-3.3	3.5E-02	-5.2	4.7E-02	-0.6	5.7E-01	1.3	5.7E-01
ENSMUST00000031333	general transcription factor IIH, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1277143]	Q3UZB8	Q8VD76	-0.2	8.0E-01	3.0	1.5E-02	2.6	1.1E-02	-0.6	4.9E-01
ENSMUST00000031334	eukaryotic translation initiation factor 2B, subunit 1 (alpha) [Source:MGI Symbol;Acc:MGI:2384802]	Q3UZR8	Q99LC8	-0.9	7.4E-02	-1.1	8.4E-02	-0.7	9.7E-02	-0.6	3.4E-01
ENSMUST00000031490	unc-51 like kinase 1 [Source:MGI Symbol;Acc:MGI:1270126]			-3.3	3.8E-04	-2.0	1.7E-01	1.2	1.6E-01	-1.9	2.0E-01
ENSMUST00000031492	RAB35, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1924657]	Q3U0T9	Q6PHN9	-4.6	9.0E-05	2.0	3.0E-02	-0.4	5.2E-01	0.0	9.5E-01
ENSMUST00000031501	RIKEN cDNA 1700123K08 gene [Source:MGI Symbol;Acc:MGI:1923908]	Q9D991		6.4	2.6E-04	-4.9	5.0E-04	0.4	3.5E-01	-0.5	6.0E-01
ENSMUST00000031508	TP53 regulated inhibitor of apoptosis 1 [Source:MGI Symbol;Acc:MGI:1916326]		Q9D8Z2	-3.4	1.1E-04	-1.8	3.8E-02	0.9	6.2E-02	-0.3	7.1E-01
ENSMUST00000031349	small nuclear ribonucleoprotein 35 (U11/U12) [Source:MGI Symbol;Acc:MGI:1923417]		Q9D384	-0.7	3.3E-01	0.4	5.9E-01	-0.4	5.4E-01	-1.5	7.7E-02
ENSMUST00000031513	serine/arginine-rich splicing factor 9 [Source:MGI Symbol;Acc:MGI:104896]		Q9D0B0	-3.8	1.1E-04	-3.7	1.3E-02	0.2	7.0E-01	0.3	7.8E-01
ENSMUST00000031519	calcium binding protein 1 [Source:MGI Symbol;Acc:MGI:1352750]		Q9JLK7	8.0	2.1E-05	3.2	6.4E-03	1.7	4.7E-02	0.3	6.5E-01
ENSMUST00000031521	cytochrome P450, family 2, subfamily w, polypeptide 1 [Source:MGI Symbol;Acc:MGI:3616076]		E9Q816	7.0	1.6E-04	-2.7	2.2E-03	0.5	2.1E-01	-0.1	9.1E-01
ENSMUST00000031524	acyl-Coenzyme A dehydrogenase, short chain [Source:MGI Symbol;Acc:MGI:87868]		Q07417	-6.0	7.3E-04	5.6	1.2E-03	-0.6	6.6E-01	-0.3	6.9E-01
ENSMUST00000031530	signal peptide peptidase 3 [Source:MGI Symbol;Acc:MGI:1891433]		Q9CUS9	-3.8	2.8E-04	4.0	1.0E-02	0.0	1.0E+00	-0.3	7.6E-01
ENSMUST00000031364	SDA1 domain containing 1 [Source:MGI Symbol;Acc:MGI:2140779]			0.0	9.3E-01	-0.5	3.3E-01	-0.5	1.9E-01	0.0	9.8E-01
ENSMUST00000031531	proteasome (prosome, macropain) assembly chaperone 3 [Source:MGI Symbol;Acc:MGI:1913756]		Q9CZH3	-3.5	9.5E-03	2.3	1.9E-03	0.8	8.2E-02	-0.2	5.8E-01
ENSMUST00000031367	solute carrier family 15, member 4 [Source:MGI Symbol;Acc:MGI:2140796]		Q91W98	-3.0	6.5E-02	-2.2	2.9E-01	0.9	4.5E-01	0.1	9.7E-01
ENSMUST00000031533	transcription factor EC [Source:MGI Symbol;Acc:MGI:1333760]		Q9WTW4	-3.1	6.0E-04	-1.2	1.9E-01	0.6	2.6E-01	-0.1	9.3E-01
ENSMUST00000031535	HNF1 homeobox A [Source:MGI Symbol;Acc:MGI:98504]		P22361	6.1	1.9E-02	-4.3	4.8E-04	0.6	1.3E-01	0.2	8.5E-01
ENSMUST00000031378	syntaxin 2 [Source:MGI Symbol;Acc:MGI:108059]	Q80W45		-3.0	6.2E-02	-2.0	3.2E-01	0.8	5.1E-01	-0.2	9.2E-01
ENSMUST00000031540	2'-5' oligoadenylate synthetase-like 1 [Source:MGI Symbol;Acc:MGI:2180849]		Q8VI94	-3.2	1.3E-02	-5.9	1.4E-03	1.1	4.6E-02	-0.6	6.8E-01
ENSMUST00000031547	RIKEN cDNA 4930519G04 gene [Source:MGI Symbol;Acc:MGI:1914843]	Q9CPT7		2.2	2.2E-02	-3.3	2.7E-03	0.0	9.6E-01	0.2	7.8E-01
ENSMUST00000031385	diablo homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913843]	D3Z3K5		-0.2	8.1E-01	0.8	5.2E-01	1.0	3.5E-01	-0.1	9.5E-01
ENSMUST00000031549	predicted gene 4951 [Source:MGI Symbol;Acc:MGI:3644953]	Q3UED7		5.0	1.3E-04	-1.9	4.1E-03	0.7	3.7E-02	0.1	8.7E-01
ENSMUST00000031554	transmembrane protein 168 [Source:MGI Symbol;Acc:MGI:1921794]		Q91VX9	-3.3	9.3E-04	6.6	2.3E-04	-0.7	5.4E-01	-0.3	6.7E-01
ENSMUST00000031555	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase [Source:MGI Symbol;Acc:MGI:1095413]	B2RRW2	O09010	-4.4	1.9E-04	1.1	3.2E-01	-0.4	6.8E-01	1.7	9.2E-02
ENSMUST00000031556	transmembrane protein 106B [Source:MGI Symbol;Acc:MGI:1919150]		Q80X71	-3.3	1.1E-04	-3.6	2.3E-03	-0.6	2.3E-01	-1.3	2.1E-01
ENSMUST00000031560	ethylmalonic aciduria (cobalamin deficiency) type B homolog (human) [Source:MGI Symbol;Acc:MGI:192494		Q9D273	4.0	8.5E-05	-3.5	8.2E-03	1.0	8.0E-02	0.3	7.5E-01
ENSMUST00000031565	cin homolog 1, actin bundling protein (Strongylocentrotus purpuratus) [Source:MGI Symbol;Acc:MGI:135274		Q61553	7.3	2.6E-05	-4.5	5.1E-04	-0.7	1.4E-01	0.3	7.4E-01
ENSMUST00000031410	MAP kinase-activated protein kinase 5 [Source:MGI Symbol;Acc:MGI:1333110]		O54992	-3.4	4.9E-02	-4.3	5.2E-02	-0.4	6.6E-01	0.4	8.5E-01
ENSMUST00000031574	speedy/RINGO cell cycle regulator family, member E4B [Source:MGI Symbol;Acc:MGI:3612701]	Q8CDE8		6.1	2.5E-03	-3.0	3.4E-03	1.7	2.4E-03	-0.3	7.3E-01
ENSMUST00000031590	RNA binding motif protein 19 [Source:MGI Symbol;Acc:MGI:1921361]		Q8R3C6	2.2	2.1E-03	5.2	4.5E-04	-3.5	1.1E-02	0.0	9.7E-01
ENSMUST00000031591	LIM homeobox protein 5 [Source:MGI Symbol;Acc:MGI:107792]	Q543P4	P61375	9.8	2.8E-06	-5.9	2.5E-03	1.4	2.3E-02	0.0	9.9E-01
ENSMUST00000031419	family with sequence similarity 216, member A [Source:MGI Symbol;Acc:MGI:1916198]		Q9DB54	-0.7	1.5E-01	-1.1	8.2E-02	-0.6	1.6E-01	-0.3	6.5E-01
ENSMUST00000031594	serine dehydratase-like [Source:MGI Symbol;Acc:MGI:2182607]		Q8R238	6.9	4.9E-04	-2.8	4.3E-02	0.5	4.9E-01	-1.5	2.7E-01
ENSMUST00000031598	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54 [Source:MGI Symbol;Acc:MGI:1919240]		Q8K4L0	-1.6	2.1E-02	-4.5	9.5E-06	-0.1	8.2E-01	-1.3	3.6E-02
ENSMUST00000031607	deltex 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1352744]		Q61010	3.6	1.5E-03	-5.9	5.5E-04	0.7	1.2E-01	-0.7	5.9E-01
ENSMUST00000031617	ribosomal protein L6 [Source:MGI Symbol;Acc:MGI:108057]	Q3UCH0	P47911	-6.3	2.2E-05	-2.1	3.3E-02	0.0	9.9E-01	-0.7	4.3E-01
ENSMUST00000031426	intraflagellar transport 81 [Source:MGI Symbol;Acc:MGI:1098597]		O35594	-0.5	7.3E-01	-1.2	3.7E-01	-2.6	3.5E-02	-1.8	2.3E-01
ENSMUST00000031621	CCZ1 vacuolar protein trafficking and biogenesis associated [Source:MGI Symbol;Acc:MGI:2141070]		Q8C1Y8	-4.8	7.1E-06	3.6	2.8E-03	0.0	9.9E-01	-0.4	5.4E-01
ENSMUST00000031624	RIKEN cDNA 1700018F24 gene [Source:MGI Symbol;Acc:MGI:1916646]	B2RW27		5.8	1.1E-03	-4.1	3.7E-05	-0.1	6.9E-01	-0.8	2.1E-01
ENSMUST00000031625	actin related protein 2/3 complex, subunit 1A [Source:MGI Symbol;Acc:MGI:1928896]		Q9R0Q6	-7.8	8.3E-06	0.0	9.7E-01	1.4	2.2E-01	-1.9	2.1E-01
ENSMUST00000031627	PDGFA associated protein 1 [Source:MGI Symbol;Acc:MGI:2448536]	B2RTB0	Q3UHX2	-1.9	1.2E-03	-1.7	3.3E-02	1.1	2.6E-02	-0.5	4.8E-01
ENSMUST00000031628	pentatricopeptide repeat domain 1 [Source:MGI Symbol;Acc:MGI:1919049]		Q8C2E4	-1.6	1.2E-02	5.8	6.5E-05	0.9	2.6E-01	0.0	9.6E-01
ENSMUST00000031632	zinc finger with KRAB and SCAN domains 14 [Source:MGI Symbol;Acc:MGI:1914485]		Q9Z1D9	-1.9	3.0E-03	-6.6	4.4E-06	-0.2	5.8E-01	-0.4	5.4E-01
ENSMUST00000031455	major facilitator superfamily domain containing 7A [Source:MGI Symbol;Acc:MGI:2442629]		Q8CE47	0.0	9.3E-01	0.1	8.3E-01	0.4	4.0E-01	0.2	7.3E-01
ENSMUST00000031456	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide [Source:MGI Symbol;Acc:MGI:97525]		P23440	4.9	6.0E-02	5.5	5.6E-02	-0.2	9.4E-01	-0.8	6.4E-01
ENSMUST00000031637	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Source:MGI Symbol;Acc:MGI:107686]		Q62425	-5.8	4.6E-05	2.7	6.2E-02	-1.1	3.9E-01	-0.3	7.8E-01
ENSMUST00000031640	cyclin-dependent kinase 8 [Source:MGI Symbol;Acc:MGI:1196224]		Q8R3L8	-4.3	9.0E-03	-1.3	1.5E-01	0.6	2.7E-01	-0.1	8.9E-01
ENSMUST00000031646	RAS-like, family 11, member A [Source:MGI Symbol;Acc:MGI:1916145]		Q6IMB1	5.0	2.2E-04	-2.3	3.3E-03	0.0	9.5E-01	-4.7	3.1E-04
ENSMUST00000031650	caudal type homeobox 2 [Source:MGI Symbol;Acc:MGI:88361]	Q543L9	P43241	7.8	7.0E-05	2.3	2.3E-03	-0.2	6.9E-01	-0.1	7.6E-01
ENSMUST00000031483	pseudouridine synthase 1 [Source:MGI Symbol;Acc:MGI:1929237]		Q9WU56	0.0	9.9E-01	2.3	3.3E-01	-0.5	8.1E-01	-2.9	1.9E-01
ENSMUST00000031653	FMS-like tyrosine kinase 1 [Source:MGI Symbol;Acc:MGI:95558]			5.6	1.3E-05	-4.3	2.2E-04	1.3	4.2E-03	-1.3	1.1E-01
ENSMUST00000031654	proteasome maturation protein [Source:MGI Symbol;Acc:MGI:1913787]		Q9CQT5	-5.5	6.7E-06	7.3	7.4E-04	-0.8	6.3E-01	0.9	2.8E-01
ENSMUST00000031655	solute carrier family 46, member 3 [Source:MGI Symbol;Acc:MGI:1918956]		Q9DC26	5.3	7.7E-03	-2.0	2.8E-02	1.1	4.3E-02	-0.2	7.6E-01
ENSMUST00000031663	complement component 8, beta polypeptide [Source:MGI Symbol;Acc:MGI:88236]		Q8BH35	6.1	1.3E-03	-2.9	8.4E-03	1.2	2.3E-02	-0.5	5.8E-01
ENSMUST00000031667	testis expressed 26 [Source:MGI Symbol;Acc:MGI:1923110]			6.7	8.9E-05	5.8	8.8E-04	-0.5	6.7E-01	0.0	9.9E-01
ENSMUST00000031668	collagen, type I, alpha 2 [Source:MGI Symbol;Acc:MGI:88468]	Q3TX57	Q01149	8.4	6.0E-06	-3.3	6.6E-04	-0.4	3.1E-01	-0.6	4.2E-01
ENSMUST00000031673	ucleotide binding protein (G protein), gamma transducing activity polypeptide 1 [Source:MGI Symbol;Acc:MG		Q61012	5.4	2.3E-05	-3.0	4.1E-03	0.9	6.7E-02	0.1	9.3E-01
ENSMUST00000031674	tissue factor pathway inhibitor 2 [Source:MGI Symbol;Acc:MGI:108543]	Q3V1S9	O35536	5.8	3.9E-04	5.8	2.2E-04	-1.6	1.7E-01	0.5	3.7E-01
ENSMUST00000031680	inhibitor of growth family, member 3 [Source:MGI Symbol;Acc:MGI:1919027]		Q8VEK6	-2.6	2.6E-02	6.3	7.7E-04	-0.2	8.9E-01	0.5	4.9E-01
ENSMUST00000031691	hyaluronoglucosaminidase 4 [Source:MGI Symbol;Acc:MGI:1924292]	L0MX76	Q05A56	5.5	7.4E-04	8.7	1.7E-03	1.1	5.6E-01	1.5	1.2E-01
ENSMUST00000031692	B cell CLL/lymphoma 7B [Source:MGI Symbol;Acc:MGI:1332238]		Q921K9	-6.4	1.4E-04	-4.9	1.3E-02	1.4	6.4E-02	0.3	8.8E-01
ENSMUST00000031694	leiomodin 2 (cardiac) [Source:MGI Symbol;Acc:MGI:2135672]		Q3UHZ5	6.0	7.6E-04	-3.5	3.4E-03	1.1	4.2E-02	0.8	4.1E-01
ENSMUST00000031695	Wiskott-Aldrich syndrome-like (human) [Source:MGI Symbol;Acc:MGI:1920428]	Q3TXX8	Q91YD9	-1.9	1.4E-02	-2.7	8.7E-02	0.6	4.9E-01	-0.2	8.8E-01
ENSMUST00000031697	cullin 1 [Source:MGI Symbol;Acc:MGI:1349658]		Q9WTX6	-6.4	4.6E-05	-3.1	1.9E-03	-1.4	1.1E-02	-1.4	8.2E-02
ENSMUST00000031534	MAD1 mitotic arrest deficient 1-like 1 [Source:MGI Symbol;Acc:MGI:1341857]		Q9WTX8	-1.8	1.9E-01	-1.8	3.1E-01	0.5	6.3E-01	0.6	7.4E-01
ENSMUST00000031707	aminoadipate-semialdehyde synthase [Source:MGI Symbol;Acc:MGI:1353573]	Q3UEQ9	Q99K67	6.8	4.0E-05	7.1	1.2E-02	-1.4	5.9E-01	-2.4	9.6E-02
ENSMUST00000031536	FtsJ homolog 2 (E. coli) [Source:MGI Symbol;Acc:MGI:1915267]		Q9CPY0	-0.6	3.5E-01	1.3	9.1E-02	0.5	4.3E-01	-1.4	5.2E-02
ENSMUST00000031538	RIKEN cDNA 2210016L21 gene [Source:MGI Symbol;Acc:MGI:1919607]			-0.5	3.1E-01	0.3	7.0E-01	0.4	3.7E-01	-0.4	5.7E-01
ENSMUST00000031539	sorting nexin 8 [Source:MGI Symbol;Acc:MGI:2443816]		Q8CFD4	0.8	1.9E-01	0.7	3.3E-01	-0.2	7.8E-01	-0.1	8.8E-01
ENSMUST00000031709	Fez family zinc finger 1 [Source:MGI Symbol;Acc:MGI:1920441]		Q0VDQ9	7.9	1.9E-05	-3.8	3.2E-02	1.0	2.6E-01	1.6	3.1E-01
ENSMUST00000031542	2'-5' oligoadenylate synthetase-like 2 [Source:MGI Symbol;Acc:MGI:1344390]		Q9Z2F2	-0.3	8.4E-01	-3.9	1.2E-01	-1.6	2.9E-01	2.0	4.0E-01
ENSMUST00000031719	omolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus) [Source:MGI Symbol;Acc:MGI:1		Q9QXW4	5.7	3.9E-04	1.4	1.4E-01	-1.3	1.3E-01	-0.5	4.9E-01
ENSMUST00000031725	actin-like 6B [Source:MGI Symbol;Acc:MGI:1933548]	F8WI57		7.1	2.3E-03	2.2	1.6E-02	-3.2	2.9E-03	-0.4	5.3E-01
ENSMUST00000031726	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	Q3U9V4	P62880	-4.7	1.6E-03	-5.0	1.6E-03	0.4	3.8E-01	2.2	8.1E-02
ENSMUST00000031727	GRB10 interacting GYF protein 1 [Source:MGI Symbol;Acc:MGI:1888677]		Q99MR1	-1.7	2.3E-02	-3.5	3.6E-03	0.8	1.3E-01	-0.1	9.0E-01
ENSMUST00000031728	processing of precursor 7, ribonuclease P family, (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1921347]		Q9DCH2	-4.5	4.7E-03	-2.3	5.0E-03	0.3	3.5E-01	-0.7	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000031729	transferrin receptor 2 [Source:MGI Symbol;Acc:MGI:1354956]		Q9JKX3	3.2	2.7E-03	3.8	7.2E-04	0.3	6.4E-01	0.5	3.5E-01
ENSMUST00000031562	zinc finger protein 513 [Source:MGI Symbol;Acc:MGI:2141255]		Q6PD29	-1.4	3.9E-02	-0.3	7.6E-01	1.4	3.3E-02	0.2	7.5E-01
ENSMUST00000031736	ArfGAP with FG repeats 2 [Source:MGI Symbol;Acc:MGI:2443267]		Q80WC7	-4.4	7.4E-03	0.5	4.0E-01	-7.1	1.7E-05	-0.3	5.7E-01
ENSMUST00000031739	protein phosphatase 1, regulatory subunit 35 [Source:MGI Symbol;Acc:MGI:1922853]		Q9D8C8	-3.8	1.7E-03	3.3	8.6E-02	-0.5	7.8E-01	2.3	7.3E-02
ENSMUST00000031583	acetyl-Coenzyme A carboxylase beta [Source:MGI Symbol;Acc:MGI:2140940]		E9Q4Z2	3.1	2.1E-01	-1.0	7.9E-01	-1.8	4.4E-01	2.3	5.2E-01
ENSMUST00000031587	uracil DNA glycosylase [Source:MGI Symbol;Acc:MGI:109352]		P97931	5.0	8.0E-02	4.2	1.4E-01	-2.5	4.0E-01	-1.7	3.4E-01
ENSMUST00000031588	ubiquitin specific peptidase 30 [Source:MGI Symbol;Acc:MGI:2140991]		Q3UN04	0.3	6.4E-01	1.7	4.6E-02	1.1	8.7E-02	-0.3	6.0E-01
ENSMUST00000031740	methylphosphate capping enzyme [Source:MGI Symbol;Acc:MGI:106477]		Q8K3A9	-2.8	1.4E-03	2.0	1.0E-02	-0.6	2.7E-01	-0.4	4.7E-01
ENSMUST00000031749	NOBOX oogenesis homeobox [Source:MGI Symbol;Acc:MGI:108011]		Q8VIH1	6.5	1.2E-04	7.8	1.1E-05	-2.2	6.1E-02	-0.2	7.0E-01
ENSMUST00000031750	Rho guanine nucleotide exchange factor (GEF) 5 [Source:MGI Symbol;Acc:MGI:1858952]	E9Q7D5		7.1	3.9E-06	4.1	1.6E-02	-2.2	1.7E-01	0.7	4.4E-01
ENSMUST00000031597	phospholipase B domain containing 2 [Source:MGI Symbol;Acc:MGI:1919022]		Q3TCN2	-0.8	1.5E-01	-0.3	6.3E-01	0.4	4.6E-01	-0.1	8.3E-01
ENSMUST00000031766	asparagine synthetase [Source:MGI Symbol;Acc:MGI:1350929]		Q61024	-5.5	2.3E-06	-0.5	5.2E-01	0.9	1.0E-01	-0.2	7.7E-01
ENSMUST00000031599	RBPJ interacting and tubulin associated 1 [Source:MGI Symbol;Acc:MGI:1922021]		Q9D1H0	3.4	1.4E-01	-1.2	6.7E-01	-2.1	3.3E-01	2.4	3.4E-01
ENSMUST00000031779	calumenin [Source:MGI Symbol;Acc:MGI:1097158]	Q3TUF3	O35887	-4.5	2.1E-03	2.6	1.1E-02	-1.5	8.1E-02	-0.6	4.4E-01
ENSMUST00000031613	inoacyl tRNA synthetase complex-interacting multifunctional protein 2 [Source:MGI Symbol;Acc:MGI:23852		Q8R010	-1.8	7.0E-02	-0.3	8.0E-01	-0.2	7.8E-01	-1.8	1.0E-01
ENSMUST00000031787	even skipped homeotic gene 1 homolog [Source:MGI Symbol;Acc:MGI:95461]		P23683	7.6	7.7E-05	-7.4	5.5E-05	-1.2	1.7E-02	-0.2	8.9E-01
ENSMUST00000031788	3-hydroxyisobutyrate dehydrogenase [Source:MGI Symbol;Acc:MGI:1889802]		Q99L13	-3.5	8.8E-05	-3.0	9.0E-04	0.7	6.7E-02	-1.1	1.3E-01
ENSMUST00000031793	5'-nucleotidase, cytosolic III [Source:MGI Symbol;Acc:MGI:1927186]		Q9D020	-5.6	2.2E-04	5.7	2.0E-03	-0.5	7.5E-01	-0.4	6.2E-01
ENSMUST00000031795	FK506 binding protein 9 [Source:MGI Symbol;Acc:MGI:1350921]		Q9Z247	3.2	6.2E-04	-7.2	2.0E-04	0.9	4.0E-02	0.3	8.2E-01
ENSMUST00000031805	AVL9 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1926187]		Q80U56	-2.6	7.8E-04	-0.9	9.0E-02	0.4	2.8E-01	-0.6	2.4E-01
ENSMUST00000031806	carboxypeptidase A1, pancreatic [Source:MGI Symbol;Acc:MGI:88478]		Q7TPZ8	7.3	8.1E-05	-0.2	7.8E-01	0.8	1.0E-01	-0.7	3.2E-01
ENSMUST00000031815	KRAB-A domain containing 1 [Source:MGI Symbol;Acc:MGI:1925077]		Q6NXZ1	2.9	6.5E-03	-1.1	9.2E-02	0.4	3.4E-01	-0.4	5.0E-01
ENSMUST00000031823	hect domain and RLD 3 [Source:MGI Symbol;Acc:MGI:1921248]	G5E876		4.2	8.4E-03	-4.7	7.1E-04	-0.7	1.6E-01	-1.8	1.0E-01
ENSMUST00000031835	amine oxidase, copper-containing 1 [Source:MGI Symbol;Acc:MGI:1923757]	E9PYN9		5.0	1.9E-02	-0.5	8.1E-01	3.6	2.2E-02	-0.2	9.3E-01
ENSMUST00000031837	RIKEN cDNA 1600015I10 gene [Source:MGI Symbol;Acc:MGI:1917011]	E9Q745		8.4	2.7E-05	5.4	2.4E-04	-0.6	5.3E-01	-1.0	1.0E-01
ENSMUST00000031838	insulin-like growth factor 2 mRNA binding protein 3 [Source:MGI Symbol;Acc:MGI:1890359]		Q9CPN8	6.1	9.4E-05	7.0	2.7E-04	-0.7	6.3E-01	0.1	9.0E-01
ENSMUST00000031651	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919837]		Q640Q5	-1.8	1.2E-01	0.4	7.7E-01	0.9	3.9E-01	-1.3	3.1E-01
ENSMUST00000031840	glycoprotein (transmembrane) nmb [Source:MGI Symbol;Acc:MGI:1934765]		Q99P91	3.6	1.0E-04	4.6	1.0E-04	-1.4	7.5E-02	-0.4	4.8E-01
ENSMUST00000031841	transformer 2 alpha homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1933972]	E9QP00		-5.3	9.4E-05	-6.3	1.7E-05	-0.7	7.6E-02	0.1	8.8E-01
ENSMUST00000031850	zinc finger CCCH type, antiviral 1 [Source:MGI Symbol;Acc:MGI:1926031]		Q3UPF5	-5.1	1.4E-03	6.0	1.7E-02	0.6	7.5E-01	-0.1	9.6E-01
ENSMUST00000031851	transmembrane protein 213 [Source:MGI Symbol;Acc:MGI:1924772]			6.8	2.2E-03	6.1	2.3E-03	-0.7	6.5E-01	-0.7	4.3E-01
ENSMUST00000031852	RIKEN cDNA 4921507P07 gene [Source:MGI Symbol;Acc:MGI:1918071]		Q9D5Y0	1.6	1.9E-02	5.4	5.5E-04	-1.5	2.1E-01	-0.1	8.4E-01
ENSMUST00000031866	myotrophin [Source:MGI Symbol;Acc:MGI:99445]		P62774	-4.0	2.1E-04	-0.1	9.1E-01	-8.6	2.8E-06	-0.1	8.0E-01
ENSMUST00000031670	guanine nucleotide binding protein (G protein), gamma 11 [Source:MGI Symbol;Acc:MGI:1913316]		P61953	-1.5	4.3E-02	-3.0	1.8E-03	-2.8	2.5E-04	-1.2	1.4E-01
ENSMUST00000031868	solute carrier family 13 (sodium/sulfate symporters), member 4 [Source:MGI Symbol;Acc:MGI:2442367]	Q8BZ82		8.0	3.8E-05	5.0	3.7E-04	0.2	7.9E-01	0.6	3.2E-01
ENSMUST00000031876	stimulated by retinoic acid gene 8 [Source:MGI Symbol;Acc:MGI:107917]		P70278	6.5	5.0E-03	6.1	5.4E-04	-0.1	9.4E-01	-0.5	5.0E-01
ENSMUST00000031879	TRPM8 channel-associated factor 2 [Source:MGI Symbol;Acc:MGI:2385258]		Q921K8	7.2	2.7E-05	3.7	2.7E-02	4.1	8.7E-03	-2.2	6.6E-02
ENSMUST00000031894	chloride channel, voltage-sensitive 1 [Source:MGI Symbol;Acc:MGI:88417]		Q64347	7.3	4.4E-03	6.4	4.4E-04	-0.5	7.2E-01	-1.4	6.8E-02
ENSMUST00000031895	caspase 2 [Source:MGI Symbol;Acc:MGI:97295]		P29594	-2.8	7.2E-04	-5.4	2.9E-03	1.3	3.4E-02	0.3	8.4E-01
ENSMUST00000031899	Kell blood group [Source:MGI Symbol;Acc:MGI:1346053]		Q9EQF2	6.5	3.5E-04	6.0	1.5E-03	-0.2	9.1E-01	-0.2	8.3E-01
ENSMUST00000031902	transient receptor potential cation channel, subfamily V, member 6 [Source:MGI Symbol;Acc:MGI:1927259]			9.0	4.7E-06	-0.1	8.8E-01	0.8	1.9E-01	-1.0	2.0E-01
ENSMUST00000031910	protease, serine 1 (trypsin 1) [Source:MGI Symbol;Acc:MGI:98839]	Q9Z1R9		5.9	8.2E-03	-4.3	8.6E-04	0.2	6.4E-01	-1.9	9.5E-02
ENSMUST00000031914	coiled-coil domain containing 184 [Source:MGI Symbol;Acc:MGI:2146066]		Q8BMK5	8.3	1.6E-04	4.7	2.1E-04	-2.4	2.6E-02	-0.3	5.5E-01
ENSMUST00000031931	RIKEN cDNA 2210010C04 gene [Source:MGI Symbol;Acc:MGI:1914623]	Q9CPN9		7.0	3.2E-05	7.4	5.9E-05	-0.6	6.1E-01	-0.1	8.3E-01
ENSMUST00000031718	paired box 4 [Source:MGI Symbol;Acc:MGI:97488]	A2RRY5	P32115	4.0	9.4E-02	2.3	4.1E-01	-0.3	9.2E-01	1.4	4.9E-01
ENSMUST00000031937	monooxygenase, DBH-like 2 [Source:MGI Symbol;Acc:MGI:2388042]		Q7TT41	6.5	6.1E-05	5.7	1.4E-03	0.4	7.5E-01	0.5	5.3E-01
ENSMUST00000031977	acylglycerol kinase [Source:MGI Symbol;Acc:MGI:1917173]		Q9ESW4	2.2	1.2E-03	5.3	1.9E-02	-0.6	7.8E-01	1.2	3.1E-01
ENSMUST00000031978	mitochondrial ribosomal protein S33 [Source:MGI Symbol;Acc:MGI:1338046]	Q58DZ5	Q9D2R8	-3.2	1.2E-03	-3.7	2.6E-02	0.2	7.4E-01	-0.8	6.1E-01
ENSMUST00000031982	hematopoietic prostaglandin D synthase [Source:MGI Symbol;Acc:MGI:1859384]		Q9JHF7	5.1	4.0E-05	-0.5	5.1E-01	0.8	1.6E-01	-0.3	6.9E-01
ENSMUST00000031985	makorin, ring finger protein, 1 [Source:MGI Symbol;Acc:MGI:1859353]	Q8C5V4		-7.2	6.8E-05	-3.2	5.4E-02	0.8	2.7E-01	-0.4	7.9E-01
ENSMUST00000032065	prenylcysteine oxidase 1 [Source:MGI Symbol;Acc:MGI:1914131]		Q9CQF9	-1.9	1.2E-03	4.3	1.2E-03	0.4	6.7E-01	-0.7	3.1E-01
ENSMUST00000031731	procollagen C-endopeptidase enhancer protein [Source:MGI Symbol;Acc:MGI:105099]	Q3UIP2	Q61398	1.4	3.1E-01	-1.3	2.9E-01	-4.3	2.1E-03	-1.7	2.1E-01
ENSMUST00000031732	F-box protein 24 [Source:MGI Symbol;Acc:MGI:1918426]		Q9D417	1.2	4.7E-01	3.0	1.8E-01	0.5	7.8E-01	-1.3	3.9E-01
ENSMUST00000031734	eucine-rich repeats and calponin homology (CH) domain containing 4 [Source:MGI Symbol;Acc:MGI:1917193		Q921G6	4.7	4.2E-02	4.4	7.9E-02	-1.6	4.9E-01	-1.3	4.0E-01
ENSMUST00000032066	transforming growth factor alpha [Source:MGI Symbol;Acc:MGI:98724]	Q545E4	P48030	8.6	3.2E-06	0.4	8.3E-01	3.6	2.3E-02	-1.2	4.7E-01
ENSMUST00000032069	adducin 2 (beta) [Source:MGI Symbol;Acc:MGI:87919]		Q9QYB8	8.2	1.3E-05	-1.4	1.5E-01	0.6	3.4E-01	-1.7	1.2E-01
ENSMUST00000032071	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) [Source:MGI Symbol;Acc:MGI:1919352]		Q6NXK5	-3.7	3.0E-05	-1.7	5.4E-02	1.0	5.9E-02	-0.1	9.0E-01
ENSMUST00000031741	cytochrome P450, family 3, subfamily a, polypeptide 13 [Source:MGI Symbol;Acc:MGI:88610]	Q3UW87	Q64464	0.8	2.3E-01	1.8	4.6E-02	0.3	6.8E-01	-0.7	3.1E-01
ENSMUST00000032073	N-acetyltransferase 8 (GCN5-related, putative) [Source:MGI Symbol;Acc:MGI:1915646]		Q9JIY7	5.8	1.9E-04	6.6	2.0E-04	-0.6	6.1E-01	-0.7	3.0E-01
ENSMUST00000032078	chaperonin containing Tcp1, subunit 7 (eta) [Source:MGI Symbol;Acc:MGI:107184]	Q3TIJ7	P80313	-3.7	8.2E-06	3.7	6.0E-04	-3.1	2.1E-03	0.4	4.7E-01
ENSMUST00000032080	protease-associated domain containing 1 [Source:MGI Symbol;Acc:MGI:1920577]		Q9D9N8	-5.9	6.2E-05	-4.0	1.8E-04	1.0	1.3E-02	-0.5	4.8E-01
ENSMUST00000031773	paraoxonase 3 [Source:MGI Symbol;Acc:MGI:106686]		Q62087	-2.3	5.7E-02	-3.2	2.0E-02	-2.4	1.3E-02	-1.5	2.7E-01
ENSMUST00000032088	zinc finger protein 638 [Source:MGI Symbol;Acc:MGI:1203484]	E9QML5		-4.2	2.3E-04	-3.8	1.4E-02	-0.8	2.4E-01	-1.6	2.8E-01
ENSMUST00000032093	prickle homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925144]	A7YQ68		6.3	1.9E-02	7.5	1.5E-04	-0.6	6.4E-01	-0.5	4.3E-01
ENSMUST00000032094	F-box and leucine-rich repeat protein 14 [Source:MGI Symbol;Acc:MGI:2141676]		Q8BID8	-3.2	2.1E-04	-2.0	1.3E-02	1.0	3.2E-02	-0.5	4.4E-01
ENSMUST00000032105	leucine-rich repeats and immunoglobulin-like domains 1 [Source:MGI Symbol;Acc:MGI:107935]		P70193	5.6	2.7E-04	-6.3	6.2E-04	-0.8	9.5E-02	-0.1	9.5E-01
ENSMUST00000032106	RIKEN cDNA 1700003E16 gene [Source:MGI Symbol;Acc:MGI:1919087]		Q9DAQ4	4.7	1.7E-04	1.0	1.7E-01	-2.1	6.0E-03	0.1	8.7E-01
ENSMUST00000032109	INO80 complex subunit B [Source:MGI Symbol;Acc:MGI:1917270]			-3.1	2.8E-02	-1.6	4.5E-02	0.9	5.6E-02	-0.1	8.6E-01
ENSMUST00000032111	WW domain binding protein 1 [Source:MGI Symbol;Acc:MGI:104710]		P97764	-7.1	3.0E-05	6.8	2.6E-04	-0.7	6.1E-01	-0.2	7.9E-01
ENSMUST00000031810	centrosomal protein 41 [Source:MGI Symbol;Acc:MGI:1891414]		Q99NF3	2.3	1.1E-01	3.1	1.4E-01	1.2	4.7E-01	0.4	7.5E-01
ENSMUST00000032114	mannosyl-oligosaccharide glucosidase [Source:MGI Symbol;Acc:MGI:1929872]		Q80UM7	-1.4	1.4E-02	2.4	2.5E-02	-1.1	2.3E-01	-0.6	4.4E-01
ENSMUST00000031817	hect domain and RLD 6 [Source:MGI Symbol;Acc:MGI:1914388]		F2Z461	-0.7	3.2E-01	-0.7	3.8E-01	-0.5	4.2E-01	-0.4	6.3E-01
ENSMUST00000031822	ATP-binding cassette, sub-family G (WHITE), member 2 [Source:MGI Symbol;Acc:MGI:1347061]			0.3	8.8E-01	0.1	9.5E-01	-1.7	3.2E-01	-1.5	4.3E-01
ENSMUST00000032122	tachykinin receptor 1 [Source:MGI Symbol;Acc:MGI:98475]		P30548	8.2	1.8E-06	6.0	2.9E-03	0.7	6.4E-01	-1.1	2.6E-01
ENSMUST00000032124	mitochondrial ribosomal protein L19 [Source:MGI Symbol;Acc:MGI:1926274]		Q9D338	1.7	7.2E-04	7.1	3.5E-03	-0.7	7.3E-01	-2.8	3.6E-02
ENSMUST00000032125	bone morphogenetic protein 10 [Source:MGI Symbol;Acc:MGI:1338820]		Q9R229	6.3	1.2E-04	7.5	1.4E-04	-0.7	6.1E-01	0.3	6.8E-01
ENSMUST00000032127	gastrokine 3 [Source:MGI Symbol;Acc:MGI:1916138]		Q9D0T7	6.8	1.1E-04	4.8	2.0E-03	-1.2	3.2E-01	0.2	8.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000032129	gastrokine 1 [Source:MGI Symbol;Acc:MGI:1913533]	Q53YU8		5.9	2.9E-04	-3.4	8.0E-04	0.0	9.5E-01	-1.7	6.5E-02
ENSMUST00000032132	EF hand and coiled-coil domain containing 1 [Source:MGI Symbol;Acc:MGI:3611451]	A0A0A0MQ84		7.6	1.9E-05	4.7	7.3E-05	0.9	1.7E-01	-0.2	6.5E-01
ENSMUST00000032138	cellular nucleic acid binding protein [Source:MGI Symbol;Acc:MGI:88431]	Q5QJQ9	P53996	-2.3	3.0E-02	-5.3	7.8E-04	0.2	7.0E-01	0.2	8.5E-01
ENSMUST00000031843	neuropeptide Y [Source:MGI Symbol;Acc:MGI:97374]		P57774	-0.5	5.8E-01	-1.6	1.3E-01	-2.7	7.3E-03	-1.7	1.2E-01
ENSMUST00000031845	deafness, autosomal dominant 5 (human) [Source:MGI Symbol;Acc:MGI:1889850]		Q9Z2D3	3.0	4.8E-02	4.0	7.6E-02	2.2	2.6E-01	1.2	3.9E-01
ENSMUST00000032141	5-hydroxymethylcytosine (hmC) binding, ES cell specific [Source:MGI Symbol;Acc:MGI:1914053]		Q8R1M0	-5.7	5.1E-04	-2.2	7.4E-02	0.5	4.9E-01	-2.4	9.5E-02
ENSMUST00000032143	ribophorin I [Source:MGI Symbol;Acc:MGI:98084]		Q91YQ5	-2.9	9.4E-05	7.1	2.8E-03	-0.7	7.0E-01	-1.1	3.2E-01
ENSMUST00000032146	FERM domain containing 4B [Source:MGI Symbol;Acc:MGI:2141794]		Q920B0	4.9	1.3E-02	0.8	2.3E-01	-0.7	2.6E-01	0.1	8.6E-01
ENSMUST00000031862	chromobox 3 [Source:MGI Symbol;Acc:MGI:108515]	Q9DCC5		-1.9	5.1E-02	-6.3	2.0E-03	-1.2	8.1E-02	3.2	5.7E-02
ENSMUST00000032151	eukaryotic translation initiation factor 4E member 3 [Source:MGI Symbol;Acc:MGI:1914142]		Q9DBB5	-2.7	4.7E-03	-2.8	8.3E-03	1.1	4.4E-02	0.0	9.8E-01
ENSMUST00000032152	prokineticin 2 [Source:MGI Symbol;Acc:MGI:1354178]	Q14AB2	Q9QXU7	-7.6	2.2E-04	8.2	6.2E-05	-0.6	6.3E-01	-0.8	1.9E-01
ENSMUST00000032157	glucoside xylosyltransferase 2 [Source:MGI Symbol;Acc:MGI:2682940]		Q810K9	5.0	2.4E-03	5.6	1.9E-02	-0.7	7.4E-01	0.3	8.2E-01
ENSMUST00000032159	contactin 3 [Source:MGI Symbol;Acc:MGI:99534]		Q07409	8.8	6.7E-05	5.4	9.4E-05	-2.1	4.6E-02	-0.4	4.9E-01
ENSMUST00000032168	Sec61 alpha 1 subunit (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1858417]		P61620	-4.3	1.2E-05	4.5	4.2E-02	-2.2	3.2E-01	0.5	6.9E-01
ENSMUST00000032169	ankyrin repeat and BTB (POZ) domain containing 1 [Source:MGI Symbol;Acc:MGI:1933148]			-5.6	8.1E-05	-1.9	3.0E-02	1.3	1.9E-02	0.4	6.4E-01
ENSMUST00000031897	glutathione S-transferase kappa 1 [Source:MGI Symbol;Acc:MGI:1923513]		Q9DCM2	0.0	9.9E-01	-1.1	2.5E-01	-0.9	2.3E-01	0.2	8.1E-01
ENSMUST00000032172	coiled-coil-helix-coiled-coil-helix domain containing 6 [Source:MGI Symbol;Acc:MGI:1913348]		Q91VN4	2.3	1.2E-02	7.3	5.9E-04	0.2	9.1E-01	-0.7	4.0E-01
ENSMUST00000032180	wingless-type MMTV integration site family, member 7A [Source:MGI Symbol;Acc:MGI:98961]		P24383	8.6	3.1E-05	6.3	5.7E-05	-2.5	3.4E-02	0.2	7.0E-01
ENSMUST00000032182	xeroderma pigmentosum, complementation group C [Source:MGI Symbol;Acc:MGI:103557]		P51612	-4.6	5.6E-05	6.6	7.2E-03	-0.8	7.2E-01	-1.4	2.4E-01
ENSMUST00000032183	transmembrane protein 43 [Source:MGI Symbol;Acc:MGI:1921372]		Q9DBS1	-4.2	6.4E-05	6.6	1.2E-03	-1.5	3.6E-01	0.1	8.5E-01
ENSMUST00000032185	olute carrier family 6 (neurotransmitter transporter, taurine), member 6 [Source:MGI Symbol;Acc:MGI:98488	Q3UPI8	O35316	-2.4	1.9E-03	7.7	4.4E-05	-0.5	6.9E-01	-1.2	4.8E-02
ENSMUST00000032192	inositol 1,4,5-trisphosphate receptor 1 [Source:MGI Symbol;Acc:MGI:96623]		P11881	1.6	6.5E-03	7.1	5.6E-05	-0.6	6.1E-01	-1.2	6.1E-02
ENSMUST00000032194	basic helix-loop-helix family, member e40 [Source:MGI Symbol;Acc:MGI:1097714]	Q542A5	O35185	-2.5	3.8E-03	-4.4	2.6E-03	-0.1	8.5E-01	-2.5	6.0E-02
ENSMUST00000031976	PR domain containing 5 [Source:MGI Symbol;Acc:MGI:1918029]		Q9CXE0	3.6	8.4E-02	4.6	4.5E-02	-0.5	8.1E-01	-1.5	3.1E-01
ENSMUST00000032196	ADP-ribosylation factor-like 8B [Source:MGI Symbol;Acc:MGI:1914416]		Q9CQW2	-4.6	1.1E-04	1.8	1.1E-02	-0.5	3.2E-01	-0.1	8.3E-01
ENSMUST00000032200	e carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 [Source:MGI Symbol;Acc:MGI:9	Q8VCS9		5.9	1.1E-04	-3.5	2.7E-03	-0.7	1.7E-01	-0.4	6.2E-01
ENSMUST00000032201	ret proto-oncogene [Source:MGI Symbol;Acc:MGI:97902]		P35546	5.5	1.0E-02	2.1	1.5E-02	-2.6	4.8E-03	0.4	4.9E-01
ENSMUST00000031984	rix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 [Source:MGI Sy		Q04692	-0.1	8.0E-01	0.1	8.7E-01	0.4	3.1E-01	0.2	6.9E-01
ENSMUST00000032203	alpha-2-macroglobulin [Source:MGI Symbol;Acc:MGI:2449119]		Q6GQT1	7.0	1.3E-04	-3.1	6.1E-03	0.7	1.7E-01	-3.4	1.5E-02
ENSMUST00000031986	RAB19, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:103292]		P35294	0.4	4.0E-01	-0.2	7.6E-01	-1.2	3.2E-02	-0.5	3.7E-01
ENSMUST00000032057	glutamine fructose-6-phosphate transaminase 1 [Source:MGI Symbol;Acc:MGI:95698]		P47856	0.1	9.8E-01	-0.6	7.6E-01	-3.1	6.6E-02	-2.4	3.1E-01
ENSMUST00000032211	growth differentiation factor 3 [Source:MGI Symbol;Acc:MGI:95686]		Q07104	7.3	1.4E-05	-1.3	3.5E-02	0.6	1.1E-01	0.0	9.9E-01
ENSMUST00000032214	myeloid leukemia factor 2 [Source:MGI Symbol;Acc:MGI:1353554]	Q3UNV7	Q99KX1	-3.8	3.0E-02	5.0	7.1E-05	-3.9	1.5E-03	-0.3	5.4E-01
ENSMUST00000032216	parathymosin [Source:MGI Symbol;Acc:MGI:1916452]		Q9D0J8	-4.5	6.1E-04	7.9	2.1E-05	-0.9	4.4E-01	-0.5	3.5E-01
ENSMUST00000032217	lymphocyte-activation gene 3 [Source:MGI Symbol;Acc:MGI:106588]		Q61790	5.5	7.7E-05	-3.4	3.4E-04	0.0	9.2E-01	-0.3	6.6E-01
ENSMUST00000032220	constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13		Q9CZ04	-4.0	3.5E-03	6.8	1.7E-04	0.0	9.8E-01	-0.9	1.8E-01
ENSMUST00000032222	transmembrane and coiled coil domains 1 [Source:MGI Symbol;Acc:MGI:2442368]	F8WJ98		-7.4	6.1E-05	-3.4	1.3E-04	0.4	2.2E-01	0.0	9.7E-01
ENSMUST00000032228	murinoglobulin 1 [Source:MGI Symbol;Acc:MGI:99837]		P28665	5.1	1.1E-02	-4.5	2.6E-03	1.2	2.7E-02	-0.1	9.2E-01
ENSMUST00000032234	CD163 antigen [Source:MGI Symbol;Acc:MGI:2135946]		Q2VLH6	5.6	1.1E-02	-3.5	3.4E-03	0.3	4.6E-01	-0.4	7.0E-01
ENSMUST00000032237	BMS1 homolog, ribosome assembly protein (yeast) [Source:MGI Symbol;Acc:MGI:2446132]	Q6PGF5		-1.4	1.7E-02	6.2	3.0E-02	-0.8	7.8E-01	-0.7	6.5E-01
ENSMUST00000032238	vomeronasal 2, receptor 26 [Source:MGI Symbol;Acc:MGI:2678394]		Q6TAC4	5.9	1.6E-03	-2.3	8.5E-03	1.1	2.0E-02	0.2	7.6E-01
ENSMUST00000032239	C-type lectin domain family 4, member e [Source:MGI Symbol;Acc:MGI:1861232]	Q4FK29	Q9R0Q8	-8.4	3.4E-05	7.6	2.8E-04	1.6	2.6E-01	-0.4	5.1E-01
ENSMUST00000032240	C-type lectin domain family 4, member d [Source:MGI Symbol;Acc:MGI:1298389]	Q4KL29	Q9Z2H6	-8.2	3.5E-07	4.7	9.1E-04	0.2	8.0E-01	0.3	6.6E-01
ENSMUST00000032107	kelch repeat and BTB (POZ) domain containing 8 [Source:MGI Symbol;Acc:MGI:2661430]		Q3UQV5	0.8	6.8E-01	2.4	3.1E-01	0.0	1.0E+00	-1.7	3.6E-01
ENSMUST00000032248	C-type lectin domain family 4, member a2 [Source:MGI Symbol;Acc:MGI:1349412]	Q923C7		-8.7	1.3E-05	-4.1	7.0E-02	0.6	4.8E-01	1.6	4.4E-01
ENSMUST00000032258	C-type lectin domain family 2, member e [Source:MGI Symbol;Acc:MGI:3028921]	H7BWZ4		7.7	1.2E-04	-5.4	1.1E-03	0.9	7.0E-02	-0.7	5.7E-01
ENSMUST00000032260	C-type lectin domain family 2, member d [Source:MGI Symbol;Acc:MGI:2135589]	F5BFH0	Q91V08	-7.4	5.0E-05	-1.2	8.4E-02	0.5	2.1E-01	0.3	6.2E-01
ENSMUST00000032263	transmembrane protein 52B [Source:MGI Symbol;Acc:MGI:2442838]		Q0VBF2	6.9	1.4E-05	8.9	1.3E-05	0.7	5.2E-01	-0.1	8.8E-01
ENSMUST00000032264	amma-aminobutyric acid (GABA) A receptor-associated protein-like 1 [Source:MGI Symbol;Acc:MGI:191498		Q8R3R8	-1.6	8.1E-03	1.9	2.3E-03	0.3	3.6E-01	0.2	5.4E-01
ENSMUST00000032272	adiponectin receptor 2 [Source:MGI Symbol;Acc:MGI:93830]	Q53YY3	Q8BQS5	-5.1	5.1E-06	6.8	1.4E-04	-0.5	6.7E-01	-1.0	1.4E-01
ENSMUST00000032326	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 [Source:MGI Symbol;Acc:MGI:1915005]	Q4VBG1	Q9CWX9	-8.2	2.0E-06	5.9	5.6E-04	-0.6	6.4E-01	0.3	6.4E-01
ENSMUST00000032330	epithelial membrane protein 1 [Source:MGI Symbol;Acc:MGI:107941]	Q4FK43	P47801	-7.2	6.9E-06	6.1	4.2E-04	-0.6	6.5E-01	-0.7	2.7E-01
ENSMUST00000032130	aprataxin and PNKP like factor [Source:MGI Symbol;Acc:MGI:1919353]		Q9D842	4.2	6.7E-02	0.6	8.1E-01	-1.1	6.3E-01	2.5	2.7E-01
ENSMUST00000032331	glutamate receptor, ionotropic, NMDA2A (epsilon 1) [Source:MGI Symbol;Acc:MGI:95820]		P35436	7.6	2.3E-02	7.1	1.1E-04	0.0	9.7E-01	0.5	4.1E-01
ENSMUST00000032133	glycoprotein 9 (platelet) [Source:MGI Symbol;Acc:MGI:1860137]		O88186	0.1	9.4E-01	-2.5	2.7E-02	-2.6	5.6E-03	0.0	9.8E-01
ENSMUST00000032134	RAB43, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1917084]	Q91Z34		2.5	6.2E-02	3.6	4.6E-02	1.1	4.6E-01	-0.1	9.6E-01
ENSMUST00000032335	activating transcription factor 7 interacting protein [Source:MGI Symbol;Acc:MGI:1858965]		Q7TT18	-1.8	6.4E-03	-3.2	1.1E-02	-1.5	4.4E-02	-0.6	5.8E-01
ENSMUST00000032336	phospholipase B domain containing 1 [Source:MGI Symbol;Acc:MGI:1914107]			-6.6	2.1E-05	-4.3	4.6E-03	0.9	1.4E-01	-0.4	7.6E-01
ENSMUST00000032338	guanylate cyclase 2c [Source:MGI Symbol;Acc:MGI:106903]		Q3UWA6	9.3	3.7E-05	-2.9	6.2E-04	0.1	7.4E-01	0.1	8.0E-01
ENSMUST00000032341	ADP-ribosyltransferase 4 [Source:MGI Symbol;Acc:MGI:1202710]		Q9CRA0	4.0	5.6E-04	4.0	4.6E-02	-1.9	3.1E-01	-1.0	4.2E-01
ENSMUST00000032342	matrix Gla protein [Source:MGI Symbol;Acc:MGI:96976]		P19788	2.9	1.6E-02	-0.6	4.9E-01	1.4	3.9E-02	-0.6	5.0E-01
ENSMUST00000032344	Rho, GDP dissociation inhibitor (GDI) beta [Source:MGI Symbol;Acc:MGI:101940]		Q61599	-7.5	1.2E-05	-4.6	2.0E-02	2.2	1.0E-02	-0.8	6.7E-01
ENSMUST00000032371	glycogen synthase 2 [Source:MGI Symbol;Acc:MGI:2385254]		Q8VCB3	7.0	3.9E-05	4.9	5.0E-03	-0.8	5.8E-01	-0.7	4.1E-01
ENSMUST00000032376	LIM and cysteine-rich domains 1 [Source:MGI Symbol;Acc:MGI:1353635]	Q3TVW6	Q8VEE1	7.1	4.3E-05	8.4	8.0E-04	0.3	8.4E-01	0.8	3.7E-01
ENSMUST00000032165	RuvB-like protein 1 [Source:MGI Symbol;Acc:MGI:1928760]	Q3U1C2	P60122	-0.7	1.1E-01	-0.6	2.6E-01	-0.5	1.6E-01	-0.7	2.1E-01
ENSMUST00000032383	sarcospan [Source:MGI Symbol;Acc:MGI:1353511]	Q3TRE0		7.3	2.1E-03	-3.6	3.8E-04	0.7	4.4E-02	0.0	9.8E-01
ENSMUST00000032386	basic helix-loop-helix family, member e41 [Source:MGI Symbol;Acc:MGI:1930704]	Q6L8F5	Q99PV5	6.4	3.7E-06	-3.9	3.2E-03	1.2	4.7E-02	-0.5	6.4E-01
ENSMUST00000032396	lymphoid-restricted membrane protein [Source:MGI Symbol;Acc:MGI:108424]	G5E880		-6.7	5.0E-05	6.5	4.9E-04	3.7	1.0E-02	-0.5	4.6E-01
ENSMUST00000032174	Kruppel-like factor 15 [Source:MGI Symbol;Acc:MGI:1929988]		Q9EPW2	4.4	1.0E-01	2.4	3.6E-01	-1.4	6.2E-01	0.6	7.5E-01
ENSMUST00000032177	solute carrier family 41, member 3 [Source:MGI Symbol;Acc:MGI:1918949]		Q921R8	2.8	3.9E-02	-0.1	9.7E-01	-0.3	8.3E-01	2.6	1.0E-01
ENSMUST00000032179	nucleoporin 210 [Source:MGI Symbol;Acc:MGI:1859555]		Q9QY81	-0.3	8.8E-01	2.3	3.7E-01	1.4	5.4E-01	-1.2	5.3E-01
ENSMUST00000032398	THUMP domain containing 3 [Source:MGI Symbol;Acc:MGI:1277973]		P97770	-5.3	1.2E-04	7.5	1.7E-04	-0.7	6.1E-01	0.3	6.0E-01
ENSMUST00000032399	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog [Source:MGI Symbol;Acc:MGI:96680]	Q5J7N1	P32883	-2.7	1.8E-03	-4.3	6.2E-04	0.2	5.9E-01	-0.1	9.2E-01
ENSMUST00000032402	branched chain aminotransferase 1, cytosolic [Source:MGI Symbol;Acc:MGI:104861]	Q8CBC8		7.4	1.3E-05	-3.2	2.8E-03	1.0	3.6E-02	0.1	9.4E-01
ENSMUST00000032406	8-oxoguanine DNA-glycosylase 1 [Source:MGI Symbol;Acc:MGI:1097693]	Q3UIL3	O08760	-4.4	3.3E-04	-2.0	2.6E-02	1.0	6.6E-02	0.6	4.2E-01
ENSMUST00000032191	sulfatase modifying factor 1 [Source:MGI Symbol;Acc:MGI:1889844]		Q8R0F3	-0.9	7.3E-02	0.1	7.9E-01	0.5	2.2E-01	-0.5	3.5E-01
ENSMUST00000032409	calcium/calmodulin-dependent protein kinase I [Source:MGI Symbol;Acc:MGI:1098535]	Q3UY68	Q91YS8	-5.7	9.5E-05	1.9	9.6E-03	-0.2	6.5E-01	-0.5	3.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000032413	ethanolamine kinase 1 [Source:MGI Symbol;Acc:MGI:1922570]		Q9D4V0	-2.1	4.0E-03	-1.9	5.8E-02	0.9	1.2E-01	0.3	7.6E-01
ENSMUST00000032419	cytidine monophospho-N-acetylneuraminic acid synthetase [Source:MGI Symbol;Acc:MGI:1337124]			-6.4	9.5E-06	-2.7	1.3E-02	1.6	1.1E-02	-0.3	7.5E-01
ENSMUST00000032198	ubiquitin specific peptidase 18 [Source:MGI Symbol;Acc:MGI:1344364]		Q9WTV6	0.2	8.2E-01	0.0	9.9E-01	-1.0	3.2E-01	-0.7	5.3E-01
ENSMUST00000032421	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1 [Source:MGI Symbol;Acc:MGI:106011]		Q64687	4.7	7.1E-05	7.4	1.3E-04	0.7	5.6E-01	-0.8	2.1E-01
ENSMUST00000032425	ER membrane protein complex subunit 3 [Source:MGI Symbol;Acc:MGI:1913337]		Q99KI3	-2.8	3.6E-05	7.1	2.0E-03	-0.7	7.0E-01	-2.3	7.3E-02
ENSMUST00000032427	asunder, spermatogenesis regulator [Source:MGI Symbol;Acc:MGI:1918427]		Q8QZV7	-2.8	3.9E-03	7.2	2.2E-04	-0.5	7.2E-01	-0.6	3.4E-01
ENSMUST00000032206	olute carrier family 16 (monocarboxylic acid transporters), member 6 [Source:MGI Symbol;Acc:MGI:2144585	H9KUY0		-1.7	1.7E-01	-1.5	4.2E-01	0.7	5.9E-01	0.4	8.0E-01
ENSMUST00000032429	mediator complex subunit 21 [Source:MGI Symbol;Acc:MGI:1347064]		Q9CQ39	-7.4	2.8E-06	6.0	1.7E-04	-0.8	4.4E-01	0.5	4.1E-01
ENSMUST00000032440	SEC13 homolog, nuclear pore and COPII coat complex component [Source:MGI Symbol;Acc:MGI:99832]		Q9D1M0	-4.3	9.5E-05	-1.8	4.7E-01	2.1	2.0E-01	0.1	9.6E-01
ENSMUST00000032443	fatty acyl CoA reductase 2 [Source:MGI Symbol;Acc:MGI:2687035]		Q7TNT2	3.8	1.1E-04	-3.4	1.2E-02	0.8	2.2E-01	-0.3	8.0E-01
ENSMUST00000032446	ERGIC and golgi 2 [Source:MGI Symbol;Acc:MGI:1914706]	F8WJ78		-7.2	6.5E-05	5.9	2.2E-04	0.8	4.1E-01	0.4	5.0E-01
ENSMUST00000032451	olute carrier family 6 (neurotransmitter transporter, GABA), member 11 [Source:MGI Symbol;Acc:MGI:9563(		P31650	8.2	1.4E-05	-2.4	8.5E-02	0.6	4.2E-01	-1.0	4.6E-01
ENSMUST00000032454	olute carrier family 6 (neurotransmitter transporter, GABA), member 1 [Source:MGI Symbol;Acc:MGI:95627		P31648	8.7	6.0E-06	-6.4	1.4E-03	0.0	9.4E-01	-1.0	5.3E-01
ENSMUST00000032457	autophagy related 7 [Source:MGI Symbol;Acc:MGI:1921494]		Q9D906	-5.6	2.9E-03	1.8	2.3E-01	-4.6	1.9E-02	-1.3	2.8E-01
ENSMUST00000032233	tubulin, alpha 8 [Source:MGI Symbol;Acc:MGI:1858225]		Q9JJZ2	1.5	3.5E-02	2.6	8.2E-03	0.7	2.8E-01	-0.4	5.4E-01
ENSMUST00000032462	tissue inhibitor of metalloproteinase 4 [Source:MGI Symbol;Acc:MGI:109125]	Q3USH7	Q9JHB3	6.8	1.0E-04	-4.1	5.9E-02	-6.4	3.1E-03	3.3	1.1E-01
ENSMUST00000032471	rhodopsin [Source:MGI Symbol;Acc:MGI:97914]		P15409	7.2	1.2E-05	-0.2	7.8E-01	0.4	3.6E-01	-0.8	1.8E-01
ENSMUST00000032472	killer cell lectin-like receptor subfamily B member 1B [Source:MGI Symbol;Acc:MGI:107539]		Q99JB4	5.9	8.3E-04	1.1	3.4E-01	-3.8	1.5E-02	1.0	3.3E-01
ENSMUST00000032473	interferon inducible GTPase 1 [Source:MGI Symbol;Acc:MGI:1926259]	J7NNX8	Q9QZ85	6.8	2.5E-02	-7.9	1.1E-03	0.4	4.9E-01	-0.1	9.4E-01
ENSMUST00000032476	solute carrier family 2 (facilitated glucose transporter), member 3 [Source:MGI Symbol;Acc:MGI:95757]	Q3TPL8	P32037	-9.5	6.0E-06	-8.2	2.5E-06	-0.5	1.1E-01	-0.5	5.4E-01
ENSMUST00000032480	inhibitor of growth family, member 4 [Source:MGI Symbol;Acc:MGI:107307]		Q8C0D7	-9.3	2.2E-04	-7.3	2.9E-04	0.3	4.4E-01	-1.1	4.7E-01
ENSMUST00000032257	killer cell lectin-like receptor subfamily B member 1F [Source:MGI Symbol;Acc:MGI:2442965]	I3QI43	Q8VD98	0.2	8.0E-01	0.6	5.0E-01	0.4	5.8E-01	0.0	9.8E-01
ENSMUST00000032485	mitochondrial ribosomal protein L51 [Source:MGI Symbol;Acc:MGI:1913743]		Q9CPY1	2.9	7.6E-05	8.0	1.8E-04	-0.8	5.9E-01	-1.1	1.0E-01
ENSMUST00000032259	CD69 antigen [Source:MGI Symbol;Acc:MGI:88343]	Q3U6A8	P37217	-0.9	2.6E-01	-0.9	3.0E-01	-1.4	4.3E-02	-1.4	1.3E-01
ENSMUST00000032486	CD27 antigen [Source:MGI Symbol;Acc:MGI:88326]	Q3U4X0	P41272	3.5	3.5E-03	-4.0	6.1E-03	1.5	2.9E-02	-1.9	1.6E-01
ENSMUST00000032261	C-type lectin domain family 12, member B [Source:MGI Symbol;Acc:MGI:1918433]			-1.5	2.9E-01	0.6	6.7E-01	-0.5	6.9E-01	-2.6	9.1E-02
ENSMUST00000032262	C-type lectin domain family 1, member b [Source:MGI Symbol;Acc:MGI:1913287]		Q9JL99	-1.9	1.1E-01	-3.9	1.3E-02	-2.4	1.9E-02	-0.4	7.6E-01
ENSMUST00000032489	lymphotoxin B receptor [Source:MGI Symbol;Acc:MGI:104875]	B2RRV3	P50284	-4.6	1.3E-04	5.6	2.8E-04	-0.6	5.3E-01	0.7	2.9E-01
ENSMUST00000032491	tumor necrosis factor receptor superfamily, member 1a [Source:MGI Symbol;Acc:MGI:1314884]	Q3U479	P25118	-6.2	1.5E-05	-1.0	1.4E-01	0.6	1.9E-01	-0.1	9.1E-01
ENSMUST00000032265	oxidized low density lipoprotein (lectin-like) receptor 1 [Source:MGI Symbol;Acc:MGI:1261434]		Q9EQ09	1.3	7.1E-02	0.7	4.3E-01	0.1	9.1E-01	0.7	4.1E-01
ENSMUST00000032269	RAD52 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:101949]	G5E879		-1.8	4.1E-01	-0.9	6.3E-01	-2.3	1.4E-01	-3.2	1.6E-01
ENSMUST00000032492	CD9 antigen [Source:MGI Symbol;Acc:MGI:88348]		P40240	-7.0	6.1E-07	-3.4	4.8E-04	0.8	2.9E-02	-0.9	1.9E-01
ENSMUST00000032279	ELKS/RAB6-interacting/CAST family member 1 [Source:MGI Symbol;Acc:MGI:2151013]	F8VPM7		-2.1	2.0E-01	0.8	6.3E-01	0.5	7.3E-01	-2.5	1.8E-01
ENSMUST00000032283	coiled-coil domain containing 77 [Source:MGI Symbol;Acc:MGI:1914450]		Q9CZH8	-2.4	1.3E-01	-2.7	2.1E-01	0.8	5.6E-01	1.0	6.0E-01
ENSMUST00000032306	killer cell lectin-like receptor, subfamily A, member 2 [Source:MGI Symbol;Acc:MGI:101906]	Q9D3R1		0.0	1.0E+00	-0.9	3.9E-01	0.0	9.6E-01	0.9	3.5E-01
ENSMUST00000032309	Y box protein 3 [Source:MGI Symbol;Acc:MGI:2137670]		Q9JKB3	0.0	1.0E+00	1.5	2.7E-01	-0.3	8.1E-01	-1.8	1.7E-01
ENSMUST00000032322	low density lipoprotein receptor-related protein 6 [Source:MGI Symbol;Acc:MGI:1298218]			0.9	4.2E-02	1.0	8.4E-02	0.2	6.7E-01	0.1	8.5E-01
ENSMUST00000032497	DNA segment, Chr 6, Wayne State University 163, expressed [Source:MGI Symbol;Acc:MGI:107893]		Q91YN0	-2.4	1.5E-03	-7.0	4.6E-05	0.4	2.3E-01	-0.8	4.7E-01
ENSMUST00000032500	protein arginine N-methyltransferase 8 [Source:MGI Symbol;Acc:MGI:3043083]		Q6PAK3	10.0	4.9E-05	-8.6	1.2E-05	-2.1	9.5E-05	-0.7	5.0E-01
ENSMUST00000032501	tetraspanin 11 [Source:MGI Symbol;Acc:MGI:1915748]		Q9D1D1	8.5	2.7E-05	8.4	1.9E-02	-1.0	7.6E-01	-1.8	3.2E-01
ENSMUST00000032508	FK506 binding protein 4 [Source:MGI Symbol;Acc:MGI:95543]		P30416	-6.9	1.1E-04	-1.3	1.1E-01	1.2	2.9E-02	0.7	3.6E-01
ENSMUST00000032512	killer cell lectin-like receptor subfamily B member 1A [Source:MGI Symbol;Acc:MGI:107540]	G5E882		5.9	3.3E-04	-5.7	3.7E-04	0.9	8.2E-02	0.0	9.9E-01
ENSMUST00000032518	C-type lectin domain family 2, member h [Source:MGI Symbol;Acc:MGI:2136934]		Q8C1T8	6.2	1.6E-04	8.0	2.5E-04	-0.8	6.1E-01	0.5	4.6E-01
ENSMUST00000032551	zinc finger protein interacting with K protein 1 [Source:MGI Symbol;Acc:MGI:108070]		Q80YP6	3.7	4.0E-04	3.6	2.4E-03	-0.6	4.8E-01	-0.2	8.1E-01
ENSMUST00000032557	MAP/microtubule affinity regulating kinase 2 [Source:MGI Symbol;Acc:MGI:99638]			-5.4	8.9E-05	-4.3	7.8E-05	-9.6	1.5E-06	-2.4	9.3E-03
ENSMUST00000032559	reticulon 2 (Z-band associated protein) [Source:MGI Symbol;Acc:MGI:107612]	Q6IM75	O70622	5.5	1.3E-04	-8.7	6.1E-05	-0.5	2.7E-01	0.7	5.8E-01
ENSMUST00000032347	RAS-like, estrogen-regulated, growth-inhibitor [Source:MGI Symbol;Acc:MGI:2665139]		Q8R367	4.2	1.1E-01	1.2	7.0E-01	-1.3	6.5E-01	1.7	5.0E-01
ENSMUST00000032359	AE binding protein 2 [Source:MGI Symbol;Acc:MGI:1338038]		Q9Z248	-0.2	8.1E-01	1.0	3.0E-01	0.7	3.4E-01	-0.5	5.8E-01
ENSMUST00000032370	RecQ protein-like [Source:MGI Symbol;Acc:MGI:103021]	Q3UUK0	Q9Z129	-2.4	6.5E-02	-4.4	3.8E-02	-1.3	1.4E-01	0.6	7.6E-01
ENSMUST00000032560	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative) [Source:MGI Symbol;Acc:MGI:2142330]		Q8BGL1	5.8	6.2E-05	7.0	1.2E-04	0.0	9.9E-01	0.0	9.5E-01
ENSMUST00000032372	golgi transport 1 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914214]		Q9CR60	-0.2	7.0E-01	-0.1	8.6E-01	0.2	7.1E-01	0.1	8.9E-01
ENSMUST00000032373	lactate dehydrogenase B [Source:MGI Symbol;Acc:MGI:96763]		P16125	-1.1	3.8E-02	-1.5	2.9E-02	-0.5	2.6E-01	-0.1	8.2E-01
ENSMUST00000032374	potassium inwardly-rectifying channel, subfamily J, member 8 [Source:MGI Symbol;Acc:MGI:1100508]			1.0	2.5E-01	2.2	7.7E-02	1.0	2.9E-01	-0.1	8.9E-01
ENSMUST00000032561	vasodilator-stimulated phosphoprotein [Source:MGI Symbol;Acc:MGI:109268]		P70460	-7.3	1.7E-05	4.6	5.7E-04	-2.1	6.3E-02	0.3	6.3E-01
ENSMUST00000032568	dystrophia myotonica-protein kinase [Source:MGI Symbol;Acc:MGI:94906]		P54265	4.9	3.1E-02	5.2	1.0E-02	-3.8	7.1E-02	-1.7	1.4E-01
ENSMUST00000032571	neuro-oncological ventral antigen 2 [Source:MGI Symbol;Acc:MGI:104296]	D3YVV7		7.9	6.6E-06	4.2	1.9E-04	-1.5	5.2E-02	0.7	1.8E-01
ENSMUST00000032573	peptidoglycan recognition protein 1 [Source:MGI Symbol;Acc:MGI:1345092]	Q4FK86	O88593	-9.0	1.0E-06	4.8	2.1E-03	-2.0	1.4E-01	0.2	7.8E-01
ENSMUST00000032585	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913411		Q9CR08	-3.6	1.1E-04	-5.9	6.8E-04	-0.1	8.6E-01	-0.9	4.7E-01
ENSMUST00000032590	RIKEN cDNA A430033K04 gene [Source:MGI Symbol;Acc:MGI:3583896]	Q3V2D1		5.9	4.8E-04	-4.7	7.6E-04	-0.1	7.8E-01	-0.8	4.8E-01
ENSMUST00000032591	zinc finger protein 12 [Source:MGI Symbol;Acc:MGI:99157]		Q7TSI0	4.6	6.8E-05	-1.9	3.8E-02	0.5	2.7E-01	-0.3	7.5E-01
ENSMUST00000032597	ribosomal protein L28 [Source:MGI Symbol;Acc:MGI:101839]	Q5M9J8	P41105	-6.3	3.1E-05	8.1	4.0E-05	0.8	5.1E-01	0.1	8.5E-01
ENSMUST00000032622	zinc finger protein 773 [Source:MGI Symbol;Acc:MGI:1923623]		Q9CZ29	7.4	4.1E-04	0.1	8.5E-01	0.4	4.6E-01	-4.2	6.5E-04
ENSMUST00000032635	on imprinted in Prader-Willi/Angelman syndrome 2 homolog (human) [Source:MGI Symbol;Acc:MGI:191391		Q9JJC8	-6.4	1.4E-04	-6.1	7.3E-04	0.4	3.4E-01	0.8	5.5E-01
ENSMUST00000032410	transcriptional adaptor 3 [Source:MGI Symbol;Acc:MGI:1915724]		Q8R0L9	0.7	2.8E-01	1.9	5.9E-02	1.5	4.9E-02	0.3	6.5E-01
ENSMUST00000032648	RIKEN cDNA 4933421I07 gene [Source:MGI Symbol;Acc:MGI:1918412]	Q9D420		6.6	4.2E-05	-1.2	1.2E-01	1.0	5.6E-02	0.2	8.1E-01
ENSMUST00000032414	tubulin tyrosine ligase-like family, member 3 [Source:MGI Symbol;Acc:MGI:2141418]		A4Q9E5	1.2	5.3E-01	2.9	1.1E-01	-1.8	3.2E-01	-3.4	6.0E-02
ENSMUST00000032416	cell death-inducing DFFA-like effector c [Source:MGI Symbol;Acc:MGI:95585]		P56198	3.6	1.0E-01	7.2	5.9E-03	-0.4	8.5E-01	-4.1	1.2E-02
ENSMUST00000032663	carcinoembryonic antigen-related cell adhesion molecule 18 [Source:MGI Symbol;Acc:MGI:1919681]		Q9D871	3.3	4.0E-03	-4.2	1.1E-03	1.4	9.8E-03	-0.8	4.2E-01
ENSMUST00000032667	sialic acid binding Ig-like lectin E [Source:MGI Symbol;Acc:MGI:1932475]		Q91Y57	-5.2	4.7E-05	3.9	1.1E-03	0.1	8.8E-01	0.9	1.7E-01
ENSMUST00000032422	cysteine-rich with EGF-like domains 1 [Source:MGI Symbol;Acc:MGI:2152539]	A8C1T7	Q91XD7	0.3	6.7E-01	1.4	1.7E-01	0.3	7.2E-01	-0.8	3.8E-01
ENSMUST00000032696	zinc finger protein 93 [Source:MGI Symbol;Acc:MGI:107611]		Q61116	5.6	8.6E-04	-3.5	9.2E-05	0.1	7.3E-01	0.8	1.6E-01
ENSMUST00000032705	rhophilin, Rho GTPase binding protein 2 [Source:MGI Symbol;Acc:MGI:1289234]		Q8BWR8	6.5	4.1E-05	-3.2	9.0E-03	0.2	7.8E-01	0.5	5.9E-01
ENSMUST00000032710	ier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 [Source:MGI Symbol;Acc:MG			7.7	2.4E-05	-5.8	1.2E-04	0.7	5.6E-02	-0.9	3.8E-01
ENSMUST00000032717	developing brain homeobox 1 [Source:MGI Symbol;Acc:MGI:94867]		P52950	7.8	2.3E-05	-4.6	3.3E-04	-0.2	5.7E-01	0.0	9.6E-01
ENSMUST00000032441	coiled-coil domain containing 91 [Source:MGI Symbol;Acc:MGI:1914265]		Q9D8L5	-0.4	5.9E-01	-0.3	7.2E-01	-0.6	3.0E-01	-0.7	3.8E-01
ENSMUST00000032719	neuron navigator 3 [Source:MGI Symbol;Acc:MGI:2183703]	E9QMF5		10.5	1.4E-06	3.6	7.0E-04	0.4	5.5E-01	0.5	3.4E-01
ENSMUST00000032726	TM2 domain containing 3 [Source:MGI Symbol;Acc:MGI:1915884]		Q8BJ83	-4.5	3.1E-03	-7.3	3.5E-04	-0.9	6.2E-02	-0.9	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000032729	tight junction protein 1 [Source:MGI Symbol;Acc:MGI:98759]	B9EHJ3		6.5	9.7E-03	7.7	4.6E-05	-0.6	6.1E-01	-0.1	8.4E-01
ENSMUST00000032732	amyloid beta (A4) precursor protein-binding, family A, member 2 [Source:MGI Symbol;Acc:MGI:1261791]		P98084	7.7	3.4E-05	8.5	1.5E-05	-0.6	5.9E-01	-0.4	4.1E-01
ENSMUST00000032735	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) [Source:MGI Symbol;Acc:MGI:1915223]		Q810V0	-3.8	5.3E-04	-2.3	1.3E-01	1.0	2.6E-01	-2.3	1.9E-01
ENSMUST00000032459	vestigial like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2652840]		Q80V24	-1.5	6.2E-02	-0.4	6.7E-01	1.1	1.3E-01	0.0	9.6E-01
ENSMUST00000032461	chondrial translocator assembly and maintenance protein, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:M	G5E881		-1.0	2.4E-01	-3.4	3.9E-02	-0.2	8.1E-01	2.2	1.3E-01
ENSMUST00000032736	myotubularin related protein 10 [Source:MGI Symbol;Acc:MGI:2142292]		Q7TPM9	-1.8	2.6E-03	6.0	4.7E-04	-0.6	6.4E-01	0.2	7.2E-01
ENSMUST00000032469	methyl-CpG binding domain protein 4 [Source:MGI Symbol;Acc:MGI:1333850]			0.5	4.6E-01	1.2	1.8E-01	0.5	4.4E-01	-0.2	7.9E-01
ENSMUST00000032738	cholinergic receptor, nicotinic, alpha polypeptide 7 [Source:MGI Symbol;Acc:MGI:99779]	Q53YJ9	P49582	7.2	4.2E-05	8.1	1.7E-05	0.1	9.4E-01	-0.7	1.4E-01
ENSMUST00000032748	unc-45 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:2142246]		Q99KD5	-7.5	1.8E-04	3.0	1.1E-02	-3.5	1.4E-02	-0.6	4.9E-01
ENSMUST00000032754	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B [Source:MGI		Q62179	1.3	2.3E-02	3.6	1.8E-01	-3.5	2.3E-01	-0.4	8.4E-01
ENSMUST00000032760	mesoderm posterior 1 [Source:MGI Symbol;Acc:MGI:107785]		P97309	6.5	1.2E-04	-7.2	1.6E-04	1.1	3.4E-02	-1.1	3.9E-01
ENSMUST00000032477	NECAP endocytosis associated 1 [Source:MGI Symbol;Acc:MGI:1914852]	Q0VB06	Q9CR95	-1.5	4.4E-02	-0.5	5.8E-01	0.7	2.4E-01	-0.3	7.0E-01
ENSMUST00000032761	peroxisomal biogenesis factor 11 alpha [Source:MGI Symbol;Acc:MGI:1338788]		Q9Z211	2.0	1.3E-02	-7.2	5.6E-03	1.1	1.3E-01	-1.0	6.5E-01
ENSMUST00000032762	perilipin 1 [Source:MGI Symbol;Acc:MGI:1890505]		Q8CGN5	7.8	4.9E-03	2.8	4.2E-04	-0.1	8.7E-01	0.0	9.1E-01
ENSMUST00000032766	Rhesus blood group-associated C glycoprotein [Source:MGI Symbol;Acc:MGI:1888517]		Q9QXP0	4.2	1.3E-04	3.1	2.5E-02	0.0	9.6E-01	0.4	7.0E-01
ENSMUST00000032487	vesicle-associated membrane protein 1 [Source:MGI Symbol;Acc:MGI:1313276]		Q62442	1.0	5.2E-01	1.9	4.1E-01	1.6	4.3E-01	0.6	7.0E-01
ENSMUST00000032768	nuclear receptor subfamily 2, group F, member 2 [Source:MGI Symbol;Acc:MGI:1352452]	Q3UST6	P43135	9.0	9.6E-06	-3.4	4.6E-03	1.2	3.3E-02	-0.1	9.6E-01
ENSMUST00000032770	pyroglutamyl-peptidase I-like [Source:MGI Symbol;Acc:MGI:1925694]	E9QM76		4.7	1.1E-04	-4.6	7.2E-04	1.2	1.9E-02	-0.4	6.9E-01
ENSMUST00000032779	cathepsin C [Source:MGI Symbol;Acc:MGI:109553]	Q3UBY5	P97821	-6.4	5.6E-06	-7.2	4.6E-06	-0.3	2.6E-01	-0.1	8.5E-01
ENSMUST00000032800	TYRO protein tyrosine kinase binding protein [Source:MGI Symbol;Acc:MGI:1277211]	Q3U419	O54885	-7.9	6.9E-07	-2.7	3.2E-03	-0.6	1.4E-01	-0.4	6.0E-01
ENSMUST00000032808	RIKEN cDNA 2200002D01 gene [Source:MGI Symbol;Acc:MGI:1919525]	Q9D809		7.1	3.9E-04	8.2	4.6E-04	-0.8	6.3E-01	1.0	2.0E-01
ENSMUST00000032811	RAS guanyl releasing protein 4 [Source:MGI Symbol;Acc:MGI:2386851]		Q8BTM9	-6.9	5.0E-05	4.3	3.1E-04	-4.7	1.6E-03	-0.6	3.0E-01
ENSMUST00000032818	F-box protein 17 [Source:MGI Symbol;Acc:MGI:1354707]	Q3V064	Q9QZM8	7.2	2.6E-03	-6.3	1.3E-03	0.0	9.5E-01	-0.7	6.5E-01
ENSMUST00000032823	p21 protein (Cdc42/Rac)-activated kinase 4 [Source:MGI Symbol;Acc:MGI:1917834]		Q8BTW9	4.8	1.2E-03	2.1	2.7E-02	-4.0	3.1E-03	-0.2	7.3E-01
ENSMUST00000032824	proteasome (prosome, macropain) 26S subunit, ATPase, 4 [Source:MGI Symbol;Acc:MGI:1346093]		P54775	-6.3	9.0E-06	5.2	5.7E-04	-1.2	2.9E-01	-0.2	8.0E-01
ENSMUST00000032539	solute carrier family 27 (fatty acid transporter), member 5 [Source:MGI Symbol;Acc:MGI:1347100]		Q4LDG0	4.6	4.8E-02	2.7	1.4E-01	-3.0	1.6E-01	-1.2	4.3E-01
ENSMUST00000032827	hyaluronan and proteoglycan link protein 3 [Source:MGI Symbol;Acc:MGI:1914916]		Q80WM5	7.5	1.1E-04	3.8	9.1E-04	-0.3	7.1E-01	-0.4	5.7E-01
ENSMUST00000032835	aggrecan [Source:MGI Symbol;Acc:MGI:99602]		Q61282	9.9	8.0E-06	-3.4	7.5E-03	1.3	2.8E-02	-0.7	5.1E-01
ENSMUST00000032841	mitochondrial ribosomal protein L46 [Source:MGI Symbol;Acc:MGI:1914558]		Q9EQI8	-1.8	8.2E-03	6.3	2.8E-04	0.2	8.7E-01	-0.6	3.9E-01
ENSMUST00000032843	transmembrane protein 126B [Source:MGI Symbol;Acc:MGI:1915722]		Q9D1R1	-2.5	1.0E-02	6.1	2.1E-04	0.0	9.9E-01	-0.3	6.0E-01
ENSMUST00000032844	transmembrane protein 126A [Source:MGI Symbol;Acc:MGI:1913521]		Q9D8Y1	-4.1	7.2E-04	-5.4	7.5E-04	1.7	7.5E-03	-0.2	8.6E-01
ENSMUST00000032566	glutaminyl-peptide cyclotransferase-like [Source:MGI Symbol;Acc:MGI:1914619]		Q8BH73	-0.6	2.9E-01	0.3	6.8E-01	0.7	2.3E-01	-0.2	7.3E-01
ENSMUST00000032856	malic enzyme 3, NADP(+)-dependent, mitochondrial [Source:MGI Symbol;Acc:MGI:1916679]		Q8BMF3	5.6	5.8E-04	5.3	2.7E-02	-0.7	7.4E-01	-1.1	4.3E-01
ENSMUST00000032570	dystrophia myotonica-containing WD repeat motif [Source:MGI Symbol;Acc:MGI:94907]		Q08274	2.7	1.0E-01	4.9	9.1E-03	-0.6	7.2E-01	-2.8	4.1E-02
ENSMUST00000032865	fumarylacetoacetate hydrolase [Source:MGI Symbol;Acc:MGI:95482]		P35505	-4.5	1.3E-05	8.4	3.4E-05	0.5	6.9E-01	0.0	1.0E+00
ENSMUST00000032877	DNA damage-induced apoptosis suppressor [Source:MGI Symbol;Acc:MGI:1921291]	E9QLR9		1.5	3.2E-02	-7.5	2.5E-05	0.9	3.2E-02	-0.5	5.9E-01
ENSMUST00000032888	ADP-ribosylation factor-like 6 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1858943]	Q80ZW9	Q9JKW0	-5.7	1.1E-06	-3.1	1.1E-03	-0.7	8.4E-02	-1.3	9.6E-02
ENSMUST00000032891	tG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans) [Source:MGI Symbol;Acc:MGI:19197		Q8BKX6	-2.1	3.5E-03	5.5	3.3E-03	0.2	9.0E-01	0.6	5.4E-01
ENSMUST00000032895	nucleobindin 2 [Source:MGI Symbol;Acc:MGI:1858179]		P81117	-4.2	7.9E-05	2.1	2.0E-02	-1.4	6.5E-02	1.0	1.2E-01
ENSMUST00000032898	importin 5 [Source:MGI Symbol;Acc:MGI:1917822]		Q8BKC5	-1.3	8.9E-03	-9.2	3.4E-04	-0.7	1.6E-01	2.3	2.0E-01
ENSMUST00000032899	RIKEN cDNA 1110004F10 gene [Source:MGI Symbol;Acc:MGI:1929274]		Q9R0P4	-3.3	2.4E-03	4.8	8.2E-03	-2.3	1.6E-01	0.3	7.6E-01
ENSMUST00000032627	tubulin, gamma complex associated protein 5 [Source:MGI Symbol;Acc:MGI:2178836]		Q8BKN5	-1.3	4.5E-02	-1.5	5.0E-02	-0.7	1.3E-01	-0.5	4.8E-01
ENSMUST00000032629	cytoplasmic FMR1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1338801]		Q7TMB8	-2.9	1.5E-01	-2.5	3.0E-01	1.4	3.3E-01	1.0	6.9E-01
ENSMUST00000032909	phosphodiesterase 3B, cGMP-inhibited [Source:MGI Symbol;Acc:MGI:1333863]	E9QLQ3		2.9	4.9E-04	-5.7	1.5E-03	-0.1	7.7E-01	-0.8	5.8E-01
ENSMUST00000032912	quinolinate phosphoribosyltransferase [Source:MGI Symbol;Acc:MGI:1914625]		Q91X91	5.2	9.7E-06	6.2	2.3E-04	0.0	9.7E-01	0.5	3.8E-01
ENSMUST00000032916	YC-associated zinc finger protein (purine-binding transcription factor) [Source:MGI Symbol;Acc:MGI:133882	F8VPK3		-3.7	3.1E-04	3.3	2.4E-02	0.7	4.9E-01	0.8	3.8E-01
ENSMUST00000032920	cylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) [Source:MGI Symbol;Acc:MGI:		Q8VDP6	-4.4	1.5E-04	-3.9	2.3E-03	1.1	4.5E-02	-0.2	8.0E-01
ENSMUST00000032673	zinc finger protein 94 [Source:MGI Symbol;Acc:MGI:107610]	Q61117		2.0	1.9E-01	6.0	8.3E-03	1.2	4.8E-01	-2.7	6.1E-02
ENSMUST00000032926	transmembrane protein 219 [Source:MGI Symbol;Acc:MGI:1915992]		Q9D123	-6.9	1.3E-04	5.1	1.4E-03	-1.6	2.0E-01	-1.1	1.9E-01
ENSMUST00000032704	Fanconi anemia core complex associated protein 24 [Source:MGI Symbol;Acc:MGI:2142208]		Q8BHL6	-0.6	3.1E-01	1.6	3.9E-02	0.6	2.9E-01	-1.6	2.9E-02
ENSMUST00000032931	FCH and double SH3 domains 2 [Source:MGI Symbol;Acc:MGI:2448475]		Q3USJ8	6.3	2.0E-02	4.8	6.1E-04	-1.7	1.0E-01	0.0	9.6E-01
ENSMUST00000032934	aldolase A, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:87994]	Q5FWB7	P05064	-8.5	5.3E-06	6.6	1.1E-04	-1.5	2.1E-01	-0.4	5.2E-01
ENSMUST00000032715	protein arginine N-methyltransferase 3 [Source:MGI Symbol;Acc:MGI:1919224]		Q922H1	-1.3	6.7E-02	-1.4	8.4E-02	-0.7	2.0E-01	-0.6	4.5E-01
ENSMUST00000032936	protein phosphatase 4, catalytic subunit [Source:MGI Symbol;Acc:MGI:1891763]	Q3UNF2	P97470	-5.1	3.5E-05	7.4	6.3E-05	-0.6	6.2E-01	-0.2	7.0E-01
ENSMUST00000032944	glycerophosphodiester phosphodiesterase domain containing 3 [Source:MGI Symbol;Acc:MGI:1915866]		Q99LY2	-2.0	3.5E-03	6.9	2.7E-05	-3.4	8.2E-03	0.2	7.3E-01
ENSMUST00000032946	RAB6A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:894313]	Q0PD54	P35279	-7.9	4.6E-04	-3.9	1.5E-02	-0.6	3.9E-01	-1.1	4.6E-01
ENSMUST00000032728	threonyl-tRNA synthetase-like 2 [Source:MGI Symbol;Acc:MGI:2444486]		Q8BLY2	1.4	1.3E-01	1.9	8.4E-02	-0.4	6.1E-01	-0.9	2.9E-01
ENSMUST00000032949	coronin, actin binding protein 1A [Source:MGI Symbol;Acc:MGI:1345961]	Q3U1N0	O89053	-9.7	6.6E-06	5.2	3.7E-02	-3.1	1.9E-01	-1.8	2.5E-01
ENSMUST00000032955	kallikrein related-peptidase 7 (chymotryptic, stratum corneum) [Source:MGI Symbol;Acc:MGI:1346336]	A0A0B6VPC4	Q91VE3	7.5	2.1E-05	7.9	4.9E-05	-0.6	6.1E-01	-0.8	1.6E-01
ENSMUST00000032956	coiled-coil domain containing 101 [Source:MGI Symbol;Acc:MGI:1922815]		Q9DA08	-2.4	2.4E-02	-4.1	1.5E-03	-0.5	3.1E-01	-0.2	8.7E-01
ENSMUST00000032958	uncoupling protein 3 (mitochondrial, proton carrier) [Source:MGI Symbol;Acc:MGI:1099787]	B2RTM2	P56501	5.4	1.0E-03	-0.8	1.6E-01	0.0	9.3E-01	-1.0	1.0E-01
ENSMUST00000032961	nuclear protein transcription regulator 1 [Source:MGI Symbol;Acc:MGI:1891834]		Q9WTK0	-3.6	8.8E-04	7.1	9.2E-05	-0.5	6.4E-01	-0.4	4.8E-01
ENSMUST00000032747	HD domain containing 3 [Source:MGI Symbol;Acc:MGI:1915945]		Q9D114	-1.2	9.2E-02	-2.2	2.3E-02	-0.9	1.3E-01	0.0	9.9E-01
ENSMUST00000032963	protein phosphatase methylesterase 1 [Source:MGI Symbol;Acc:MGI:1919840]		Q8BVQ5	-1.9	4.0E-03	-6.2	4.5E-03	1.0	1.1E-01	-0.3	8.6E-01
ENSMUST00000032749	vacuolar protein sorting 33B (yeast) [Source:MGI Symbol;Acc:MGI:2446237]		P59016	-0.6	6.9E-01	-4.0	2.5E-01	0.5	7.4E-01	3.9	2.4E-01
ENSMUST00000032967	lipoyl(octanoyl) transferase 2 (putative) [Source:MGI Symbol;Acc:MGI:1914414]		Q9D009	2.7	8.6E-03	1.7	2.7E-02	0.7	2.2E-01	0.2	6.6E-01
ENSMUST00000032969	polymerase (DNA-directed), delta 3, accessory subunit [Source:MGI Symbol;Acc:MGI:1915217]	Q8BH76		-2.1	3.6E-03	6.6	2.2E-04	-0.5	7.0E-01	-0.6	3.7E-01
ENSMUST00000032974	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 [Source:MGI Symbol;Acc:MGI:105058]		Q8R429	4.0	4.4E-04	2.1	1.6E-02	-0.9	2.2E-01	-1.0	1.5E-01
ENSMUST00000032977	chordin-like 2 [Source:MGI Symbol;Acc:MGI:1916371]	A0A0B4J1E8		6.6	2.1E-02	5.8	3.4E-02	-0.7	7.9E-01	1.3	3.7E-01
ENSMUST00000032978	SH2B adaptor protein 1 [Source:MGI Symbol;Acc:MGI:1201407]		Q91ZM2	-1.5	3.5E-02	5.8	2.1E-04	1.6	1.1E-01	0.0	9.7E-01
ENSMUST00000032981	predicted pseudogene 9755 [Source:MGI Symbol;Acc:MGI:3642279]	D3YVN7		5.0	8.2E-03	8.2	1.7E-05	-1.4	2.4E-01	-0.6	2.5E-01
ENSMUST00000032985	solute carrier organic anion transporter family, member 2b1 [Source:MGI Symbol;Acc:MGI:1351872]		Q8BXB6	6.3	9.3E-05	4.0	1.2E-03	-0.4	6.3E-01	0.3	6.4E-01
ENSMUST00000032776	myocyte enhancer factor 2A [Source:MGI Symbol;Acc:MGI:99532]		Q60929	-2.6	8.2E-02	-0.4	8.1E-01	0.9	3.8E-01	-1.3	4.8E-01
ENSMUST00000032988	protease, serine 8 (prostasin) [Source:MGI Symbol;Acc:MGI:1923810]	Q99L44		5.4	2.7E-04	-6.6	5.2E-05	0.1	7.9E-01	0.3	7.4E-01
ENSMUST00000032796	zinc finger protein 790 [Source:MGI Symbol;Acc:MGI:1923431]	Q80ZX2		-0.4	6.8E-01	-2.2	1.0E-01	-0.1	9.1E-01	1.8	1.7E-01
ENSMUST00000032992	eukaryotic translation initiation factor 3, subunit C [Source:MGI Symbol;Acc:MGI:1926966]		Q8R1B4	-4.4	3.4E-06	-8.8	5.7E-06	-0.5	1.9E-01	0.5	6.2E-01
ENSMUST00000032802	zinc finger protein 84 [Source:MGI Symbol;Acc:MGI:107780]	Q9D654		-0.8	1.1E-01	-1.1	9.9E-02	-0.4	3.1E-01	-0.1	8.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000032803	zinc finger protein 30 [Source:MGI Symbol;Acc:MGI:99178]	Q78FW7		1.6	3.0E-01	0.2	9.4E-01	1.5	4.4E-01	2.9	2.2E-01
ENSMUST00000032998	ribosomal protein S3 [Source:MGI Symbol;Acc:MGI:1350917]	Q5YLW3	P62908	-5.7	3.5E-05	1.4	1.7E-01	-5.0	3.0E-03	0.6	4.6E-01
ENSMUST00000032809	Yip1 interacting factor homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924504]		Q9CX30	0.8	7.2E-01	1.4	6.4E-01	0.8	7.1E-01	0.2	9.6E-01
ENSMUST00000033000	interleukin 21 receptor [Source:MGI Symbol;Acc:MGI:1890475]	Q3TAI3	Q9JHX3	4.8	3.1E-05	-8.3	6.2E-04	1.0	9.0E-02	2.5	1.6E-01
ENSMUST00000032813	ryanodine receptor 1, skeletal muscle [Source:MGI Symbol;Acc:MGI:99659]	K3W4M2		-0.1	9.4E-01	0.0	9.9E-01	0.3	8.5E-01	0.2	9.4E-01
ENSMUST00000032815	ar factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta [Source:MGI Symbol;Acc:MGI:10		Q60778	0.2	7.6E-01	1.2	1.2E-01	0.4	4.6E-01	-0.6	3.6E-01
ENSMUST00000033001	diacylglycerol O-acyltransferase 2 [Source:MGI Symbol;Acc:MGI:1915050]		Q9DCV3	-5.1	5.9E-05	1.5	3.6E-01	-4.0	4.4E-02	1.7	2.4E-01
ENSMUST00000032820	zinc finger and SCAN domain containing 26 [Source:MGI Symbol;Acc:MGI:3531417]	F8WJ31		0.2	7.2E-01	1.4	1.2E-01	0.5	4.3E-01	-0.7	4.1E-01
ENSMUST00000033004	interleukin 4 receptor, alpha [Source:MGI Symbol;Acc:MGI:105367]	Q3U905	P16382	-5.7	6.6E-06	4.9	4.5E-03	0.7	5.9E-01	0.5	5.8E-01
ENSMUST00000033006	non-SMC element 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914961]			-5.2	1.6E-04	-7.6	1.8E-04	0.2	5.8E-01	1.4	2.7E-01
ENSMUST00000032825	milk fat globule-EGF factor 8 protein [Source:MGI Symbol;Acc:MGI:102768]		P21956	-0.5	7.3E-01	-0.9	5.2E-01	-2.0	8.9E-02	-1.6	3.0E-01
ENSMUST00000033008	proteasome (prosome, macropain) subunit, alpha type 1 [Source:MGI Symbol;Acc:MGI:1347005]	Q3TS44	Q9R1P4	-7.6	7.2E-07	6.6	3.6E-04	-1.0	4.8E-01	-0.1	9.1E-01
ENSMUST00000033010	lysine (K)-specific demethylase 8 [Source:MGI Symbol;Acc:MGI:1924285]		Q9CXT6	1.4	1.8E-02	9.4	2.6E-05	-0.7	5.9E-01	-0.2	7.5E-01
ENSMUST00000032839	de-etiolated homolog 1 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1923625]		Q9D0A0	-0.9	2.2E-01	-0.3	7.6E-01	0.7	2.9E-01	0.1	9.3E-01
ENSMUST00000033012	coatomer protein complex, subunit beta 1 [Source:MGI Symbol;Acc:MGI:1917599]		Q9JIF7	-5.2	9.8E-06	-3.3	1.2E-03	-0.7	1.4E-01	0.8	2.8E-01
ENSMUST00000032842	coiled-coil domain containing 90B [Source:MGI Symbol;Acc:MGI:1913615]		Q8C3X2	-2.5	5.2E-02	-3.0	3.9E-02	-1.3	1.1E-01	-0.8	6.0E-01
ENSMUST00000033018	fatty acyl CoA reductase 1 [Source:MGI Symbol;Acc:MGI:1914670]		Q922J9	-7.7	9.7E-05	-2.9	2.1E-02	-0.2	7.0E-01	0.2	8.6E-01
ENSMUST00000033020	alkaline ceramidase 3 [Source:MGI Symbol;Acc:MGI:1913440]		Q9D099	-3.5	3.2E-02	-4.2	4.9E-03	0.7	2.3E-01	0.8	5.1E-01
ENSMUST00000033023	aquaporin 8 [Source:MGI Symbol;Acc:MGI:1195271]		P56404	7.0	4.3E-04	6.4	1.4E-03	-0.4	8.0E-01	-1.2	1.5E-01
ENSMUST00000033025	leucine carboxyl methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1353593]	A2RTH5		-1.6	1.1E-02	-1.7	2.5E-02	1.8	1.1E-03	-1.1	1.4E-01
ENSMUST00000033030	parvin, alpha [Source:MGI Symbol;Acc:MGI:1931144]		Q9EPC1	8.0	1.1E-05	2.9	2.6E-03	1.1	9.5E-02	-0.3	5.7E-01
ENSMUST00000032882	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 [Source:MGI Symbol;Acc:MGI:1344370]		Q9CQ54	-1.9	9.3E-02	-1.8	1.7E-01	-1.0	2.4E-01	-1.1	3.8E-01
ENSMUST00000033033	MICAL C-terminal like [Source:MGI Symbol;Acc:MGI:1918127]		Q9D5U9	8.1	2.5E-05	-3.9	6.6E-03	-0.8	1.7E-01	-0.8	5.3E-01
ENSMUST00000032887	demethyl-Q 7 [Source:MGI Symbol;Acc:MGI:107207]		P97478	-1.4	8.1E-02	-2.5	3.2E-02	-1.0	1.3E-01	0.1	9.3E-01
ENSMUST00000033036	dickkopf homolog 3 (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1354952]		Q9QUN9	9.1	1.3E-05	-5.5	1.5E-05	0.4	1.5E-01	0.2	7.8E-01
ENSMUST00000033040	p21 protein (Cdc42/Rac)-activated kinase 1 [Source:MGI Symbol;Acc:MGI:1339975]	G5E884		-3.1	6.5E-03	-0.6	3.8E-01	0.9	7.2E-02	-0.6	4.0E-01
ENSMUST00000032892	xylosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2451073]	F8VPK6		-0.4	4.5E-01	0.4	6.0E-01	0.8	1.2E-01	0.1	9.2E-01
ENSMUST00000033050	lymphatic vessel endothelial hyaluronan receptor 1 [Source:MGI Symbol;Acc:MGI:2136348]		Q8BHC0	3.5	1.7E-04	-5.0	1.2E-04	-0.9	5.1E-02	-0.1	9.2E-01
ENSMUST00000033054	adrenomedullin [Source:MGI Symbol;Acc:MGI:108058]		P97297	7.1	1.3E-04	-1.7	8.3E-03	-0.5	1.4E-01	-0.1	8.5E-01
ENSMUST00000033056	PYD and CARD domain containing [Source:MGI Symbol;Acc:MGI:1931465]	Q54AA2	Q9EPB4	-3.7	1.8E-03	-4.4	2.9E-03	-0.2	7.5E-01	1.0	3.9E-01
ENSMUST00000033057	dickkopf-like 1 [Source:MGI Symbol;Acc:MGI:1354963]		Q9QZL9	2.8	3.3E-03	1.4	6.5E-02	-0.7	2.1E-01	0.7	2.2E-01
ENSMUST00000032910	myosin light chain, phosphorylatable, fast skeletal muscle [Source:MGI Symbol;Acc:MGI:97273]	Q545G1	P97457	0.5	5.1E-01	0.8	3.0E-01	-1.1	1.2E-01	-1.4	6.3E-02
ENSMUST00000033063	CD37 antigen [Source:MGI Symbol;Acc:MGI:88330]	Q3U429		-4.9	1.3E-04	4.3	1.3E-04	-0.4	5.4E-01	0.4	3.5E-01
ENSMUST00000032915	kinesin family member 22 [Source:MGI Symbol;Acc:MGI:109233]		Q3V300	-0.8	1.2E-01	-0.4	5.2E-01	0.5	2.4E-01	0.1	8.1E-01
ENSMUST00000033070	K(lysine) acetyltransferase 8 [Source:MGI Symbol;Acc:MGI:1915023]		Q9D1P2	-1.9	4.6E-03	-2.9	7.5E-03	1.0	5.4E-02	0.2	8.5E-01
ENSMUST00000033075	syntaxin 4A (placental) [Source:MGI Symbol;Acc:MGI:893577]		P70452	-3.7	3.5E-05	-0.7	3.9E-01	1.0	6.7E-02	-0.1	9.3E-01
ENSMUST00000033086	phosphorylase kinase, gamma 2 (testis) [Source:MGI Symbol;Acc:MGI:1916211]		Q9DB30	-7.5	1.7E-05	-3.4	4.0E-03	0.8	9.7E-02	-0.2	8.3E-01
ENSMUST00000032924	potassium channel tetramerisation domain containing 13 [Source:MGI Symbol;Acc:MGI:1923739]		Q8BGV7	-1.2	1.0E-01	-0.8	3.9E-01	0.9	1.8E-01	0.5	5.8E-01
ENSMUST00000033087	RuvB-like protein 2 [Source:MGI Symbol;Acc:MGI:1342299]	Q3TXT7	Q9WTM5	1.9	3.4E-02	-6.5	1.2E-03	-0.2	6.6E-01	-0.7	6.8E-01
ENSMUST00000033088	ring finger protein 40 [Source:MGI Symbol;Acc:MGI:2142048]		Q3U319	-2.9	4.0E-04	7.3	1.5E-02	-0.8	7.6E-01	-1.8	2.3E-01
ENSMUST00000033093	BCL2-associated X protein [Source:MGI Symbol;Acc:MGI:99702]	Q544Z6	Q07813	-4.4	1.9E-04	-6.9	1.7E-04	1.2	1.8E-02	-0.4	7.4E-01
ENSMUST00000033095	proline rich 14 [Source:MGI Symbol;Acc:MGI:2384565]		Q7TPN9	-2.9	4.3E-04	-3.8	1.4E-03	1.0	3.3E-02	-0.3	7.4E-01
ENSMUST00000033096	nucleobindin 1 [Source:MGI Symbol;Acc:MGI:97388]		Q02819	-3.4	5.0E-04	-2.0	9.3E-03	-0.6	1.4E-01	-0.6	3.3E-01
ENSMUST00000033099	fibroblast growth factor 21 [Source:MGI Symbol;Acc:MGI:1861377]		Q9JJN1	6.7	8.9E-05	-3.7	2.1E-02	1.3	9.4E-02	-2.9	1.2E-01
ENSMUST00000033123	ATP-binding cassette, sub-family C (CFTR/MRP), member 8 [Source:MGI Symbol;Acc:MGI:1352629]	B2RUS7		5.7	1.5E-05	-8.0	1.3E-04	1.0	5.4E-02	-0.7	6.4E-01
ENSMUST00000033131	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 [Source:MGI Symbol;Acc:MGI:1913758]		Q9CQ22	-4.9	5.3E-05	7.4	4.7E-05	-0.5	6.2E-01	-0.5	4.1E-01
ENSMUST00000033133	regulator of G-protein signalling 10 [Source:MGI Symbol;Acc:MGI:1915115]	Q32MD7	Q9CQE5	-5.1	7.2E-05	-1.3	2.3E-01	-0.1	8.6E-01	-1.2	2.7E-01
ENSMUST00000033135	Tia1 cytotoxic granule-associated RNA binding protein-like 1 [Source:MGI Symbol;Acc:MGI:107913]	Q921W2		-7.0	1.1E-03	5.2	3.1E-03	-1.2	3.8E-01	-1.1	2.3E-01
ENSMUST00000033136	BCL2-associated athanogene 3 [Source:MGI Symbol;Acc:MGI:1352493]		Q9JLV1	1.6	2.2E-02	-5.4	1.7E-03	-0.7	2.1E-01	1.2	3.5E-01
ENSMUST00000033149	carboxypeptidase X 2 (M14 family) [Source:MGI Symbol;Acc:MGI:1926006]			8.1	1.8E-05	-1.4	5.0E-02	0.4	3.5E-01	-0.1	9.1E-01
ENSMUST00000033152	calcineurin-like EF hand protein 2 [Source:MGI Symbol;Acc:MGI:1917511]		Q9D869	5.9	2.5E-03	3.6	8.9E-03	1.7	1.2E-01	0.8	3.4E-01
ENSMUST00000032968	CD19 antigen [Source:MGI Symbol;Acc:MGI:88319]		P25918	1.7	3.7E-02	0.1	8.9E-01	-1.6	3.5E-02	0.0	9.7E-01
ENSMUST00000033153	endoplasmic reticulum (ER) to nucleus signalling 2 [Source:MGI Symbol;Acc:MGI:1349436]		Q9Z2E3	8.4	2.3E-05	-1.9	2.6E-02	0.5	2.8E-01	0.2	7.5E-01
ENSMUST00000033156	dynactin 5 [Source:MGI Symbol;Acc:MGI:1891689]		Q9QZB9	-7.2	8.0E-05	3.8	1.6E-03	-0.5	5.6E-01	-0.2	7.6E-01
ENSMUST00000033157	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 [Source:MGI Symbol;Acc:MGI:1917566]	Q569N0	Q9CR21	3.0	5.2E-04	5.6	6.2E-02	-0.9	7.6E-01	0.1	9.6E-01
ENSMUST00000033160	olgi associated, gamma adaptin ear containing, ARF binding protein 2 [Source:MGI Symbol;Acc:MGI:192135		Q6P5E6	5.9	2.0E-06	-0.4	6.5E-01	1.0	1.0E-01	-0.1	8.7E-01
ENSMUST00000033161	sodium channel, nonvoltage-gated 1 beta [Source:MGI Symbol;Acc:MGI:104696]	A2RS45	Q9WU38	8.0	2.8E-05	7.4	3.1E-03	0.9	6.5E-01	-1.5	1.9E-01
ENSMUST00000033163	methyltransferase like 9 [Source:MGI Symbol;Acc:MGI:1914862]		Q9EPL4	-6.7	1.7E-06	6.7	1.0E-04	-0.5	6.5E-01	-1.0	1.2E-01
ENSMUST00000033166	RIKEN cDNA 4933427G17 gene [Source:MGI Symbol;Acc:MGI:1921716]	Q9D3Y2		3.6	1.6E-03	5.0	5.4E-04	-1.1	2.8E-01	-0.7	3.2E-01
ENSMUST00000033173	polymerase (RNA) III (DNA directed) polypeptide E [Source:MGI Symbol;Acc:MGI:1349452]		Q9CZT4	-4.3	4.1E-03	-4.2	3.7E-05	-0.1	8.1E-01	-0.3	6.5E-01
ENSMUST00000032994	spinster homolog 1 [Source:MGI Symbol;Acc:MGI:1920908]		Q8R0G7	-1.8	3.8E-01	-1.4	6.3E-01	0.4	8.4E-01	0.0	9.9E-01
ENSMUST00000032997	linker for activation of T cells [Source:MGI Symbol;Acc:MGI:1342293]	Q546H1	O54957	0.1	9.2E-01	-0.4	6.4E-01	-0.4	4.7E-01	0.0	9.7E-01
ENSMUST00000033176	ubiquinol cytochrome c reductase core protein 2 [Source:MGI Symbol;Acc:MGI:1914253]		Q9DB77	-7.1	2.0E-05	-6.8	1.2E-04	-0.8	1.0E-01	0.4	7.3E-01
ENSMUST00000033182	integrin linked kinase [Source:MGI Symbol;Acc:MGI:1195267]		O55222	-9.4	1.4E-05	2.7	2.8E-03	-1.8	2.1E-02	0.3	5.2E-01
ENSMUST00000033184	tripeptidyl peptidase I [Source:MGI Symbol;Acc:MGI:1336194]		O89023	-3.4	2.4E-04	-3.7	3.6E-03	1.4	1.3E-02	0.0	1.0E+00
ENSMUST00000033187	cyclic nucleotide gated channel alpha 4 [Source:MGI Symbol;Acc:MGI:2664099]		Q3UW12	1.5	2.1E-02	-4.5	2.9E-04	1.2	1.5E-02	0.0	9.7E-01
ENSMUST00000033189	cholecystokinin B receptor [Source:MGI Symbol;Acc:MGI:99479]	Q3ZB46	P56481	8.1	3.3E-05	-4.8	1.2E-03	-0.1	8.9E-01	-0.4	7.0E-01
ENSMUST00000033198	crystallin, mu [Source:MGI Symbol;Acc:MGI:102675]	Q3UPX0	O54983	6.8	1.1E-04	-7.4	6.8E-06	-0.5	9.9E-02	-0.7	4.2E-01
ENSMUST00000033009	rferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) [Source:MGI Symbol;.		Q9CUX1	0.1	7.5E-01	0.4	5.0E-01	-0.1	7.8E-01	-0.4	5.1E-01
ENSMUST00000033201	ankyrin repeat and sterile alpha motif domain containing 4B [Source:MGI Symbol;Acc:MGI:1919324]		Q8K3X6	6.2	1.5E-04	3.0	1.3E-03	0.9	1.5E-01	-0.7	2.0E-01
ENSMUST00000033207	zona pellucida glycoprotein 2 [Source:MGI Symbol;Acc:MGI:99214]		P20239	6.6	5.2E-05	-5.6	5.2E-05	0.2	4.9E-01	0.6	4.8E-01
ENSMUST00000033015	interleukin 4 induced 1 [Source:MGI Symbol;Acc:MGI:109552]			2.1	2.8E-01	2.6	2.3E-01	-0.9	6.4E-01	-1.4	4.6E-01
ENSMUST00000033230	threonine aldolase 1 [Source:MGI Symbol;Acc:MGI:1919026]	Q6XPS7		-3.1	1.2E-02	-6.8	2.2E-04	0.2	6.4E-01	-0.6	6.6E-01
ENSMUST00000033255	glycoprotein 2 (zymogen granule membrane) [Source:MGI Symbol;Acc:MGI:1914383]			6.6	6.4E-05	-4.5	4.7E-02	0.7	5.1E-01	1.7	4.1E-01
ENSMUST00000033257	methyltransferase like 10 [Source:MGI Symbol;Acc:MGI:1919346]		Q9D853	-3.5	1.1E-03	3.4	5.7E-02	-0.6	7.0E-01	3.0	2.1E-02
ENSMUST00000033263	uromodulin [Source:MGI Symbol;Acc:MGI:102674]		Q91X17	8.2	3.7E-05	-0.8	2.1E-01	0.2	5.7E-01	-0.5	4.2E-01
ENSMUST00000033265	zinc finger, RAN-binding domain containing 1 [Source:MGI Symbol;Acc:MGI:106441]		Q7M760	-4.9	3.0E-03	1.1	8.7E-02	-7.0	2.0E-05	-0.1	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000033267	protein disulfide isomerase-like, testis expressed [Source:MGI Symbol;Acc:MGI:1919080]		Q9DAN1	7.0	3.3E-05	7.3	1.2E-04	-0.7	5.9E-01	0.1	8.5E-01
ENSMUST00000033035	solute carrier family 5 (sodium/glucose cotransporter), member 11 [Source:MGI Symbol;Acc:MGI:1919316]		Q8K0E3	4.4	8.6E-02	5.7	5.1E-02	-0.2	9.3E-01	-1.6	3.2E-01
ENSMUST00000033269	C-terminal binding protein 2 [Source:MGI Symbol;Acc:MGI:1201686]	Q3UGL5	P56546	-5.6	4.3E-05	5.8	1.2E-04	-3.2	1.7E-02	0.0	9.7E-01
ENSMUST00000033276	uroporphyrinogen III synthase [Source:MGI Symbol;Acc:MGI:98917]	Q3UG55	P51163	3.3	2.2E-02	-4.9	5.0E-03	0.5	4.3E-01	2.4	1.1E-01
ENSMUST00000033044	cDNA sequence BC017158 [Source:MGI Symbol;Acc:MGI:2384572]			-1.5	3.1E-01	2.9	1.3E-01	1.2	4.6E-01	-3.2	5.0E-02
ENSMUST00000033280	RIKEN cDNA 9030624J02 gene [Source:MGI Symbol;Acc:MGI:1918767]		Q8BWQ6	3.7	2.4E-04	-1.3	3.1E-02	-5.0	3.4E-06	-0.3	6.1E-01
ENSMUST00000033051	integrin, alpha D [Source:MGI Symbol;Acc:MGI:3578624]	E9PXZ7		3.9	1.4E-01	6.2	3.8E-02	-0.2	9.4E-01	-2.6	1.4E-01
ENSMUST00000033053	integrin alpha X [Source:MGI Symbol;Acc:MGI:96609]		Q9QXH4	0.1	9.3E-01	0.0	9.7E-01	-0.4	6.0E-01	-0.4	7.2E-01
ENSMUST00000033282	BRCA2 and CDKN1A interacting protein [Source:MGI Symbol;Acc:MGI:1913415]		Q9CWI3	-4.7	6.6E-04	5.3	6.1E-04	-2.2	7.5E-02	-0.4	6.3E-01
ENSMUST00000033283	ribonucleotide reductase M1 [Source:MGI Symbol;Acc:MGI:98180]		P07742	-1.9	2.7E-03	-4.9	1.8E-03	-0.9	1.2E-01	0.3	8.1E-01
ENSMUST00000033289	stromal interaction molecule 1 [Source:MGI Symbol;Acc:MGI:107476]		P70302	-3.1	4.3E-04	4.6	5.6E-04	1.4	9.8E-02	-0.4	5.6E-01
ENSMUST00000033058	SET binding factor 2 [Source:MGI Symbol;Acc:MGI:1921831]	E9PXF8		2.5	2.7E-01	3.1	1.9E-01	-0.5	8.4E-01	-1.0	5.7E-01
ENSMUST00000033300	ADP-ribosyltransferase 1 [Source:MGI Symbol;Acc:MGI:107511]	Q545U9	Q60935	7.1	1.5E-04	-2.7	1.2E-02	0.9	1.1E-01	-1.3	1.8E-01
ENSMUST00000033310	antigen identified by monoclonal antibody Ki 67 [Source:MGI Symbol;Acc:MGI:106035]	E9PVX6		-1.7	1.7E-02	-1.7	2.6E-02	-0.2	6.9E-01	-0.4	5.5E-01
ENSMUST00000033074	vitamin K epoxide reductase complex, subunit 1 [Source:MGI Symbol;Acc:MGI:106442]		Q9CRC0	-0.2	8.0E-01	-1.5	2.5E-01	-0.8	3.6E-01	0.4	7.1E-01
ENSMUST00000033313	ATPase, H+ transporting, lysosomal accessory protein 2 [Source:MGI Symbol;Acc:MGI:1917745]	Q1XID4	Q9CYN9	-5.5	1.8E-06	-3.4	6.5E-04	0.6	1.2E-01	0.3	6.9E-01
ENSMUST00000033081	F-box and leucine-rich repeat protein 19 [Source:MGI Symbol;Acc:MGI:3039600]		Q6PB97	-0.1	9.8E-01	2.8	2.6E-01	0.3	8.9E-01	-2.6	2.6E-01
ENSMUST00000033321	alcium/calmodulin-dependent serine protein kinase (MAGUK family) [Source:MGI Symbol;Acc:MGI:130948		O70589	-7.7	8.4E-06	-7.2	1.6E-04	-0.3	5.0E-01	-0.6	6.3E-01
ENSMUST00000033325	SWA-70 protein [Source:MGI Symbol;Acc:MGI:1298390]		Q6A028	-3.0	9.8E-04	3.3	1.1E-02	0.4	6.8E-01	-1.0	1.9E-01
ENSMUST00000033333	TMEM9 domain family, member B [Source:MGI Symbol;Acc:MGI:1915254]		Q9JJR8	-6.7	6.1E-05	-1.8	2.4E-02	0.9	5.3E-02	-0.2	7.6E-01
ENSMUST00000033341	tubby candidate gene [Source:MGI Symbol;Acc:MGI:2651573]	Q4VA41	P50586	8.1	2.9E-06	-3.5	3.5E-03	0.0	9.7E-01	-0.9	3.4E-01
ENSMUST00000033342	eukaryotic translation initiation factor 3, subunit F [Source:MGI Symbol;Acc:MGI:1913335]		Q9DCH4	-5.1	4.1E-05	-2.0	1.5E-02	0.6	1.6E-01	-0.3	6.7E-01
ENSMUST00000033372	retinitis pigmentosa 2 homolog (human) [Source:MGI Symbol;Acc:MGI:1277953]		Q9EPK2	-3.8	1.4E-04	-2.2	2.4E-02	0.9	8.1E-02	-0.3	7.2E-01
ENSMUST00000033098	branched chain aminotransferase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1276534]	Q3ULU3	O35855	-2.3	1.4E-01	1.6	4.7E-01	2.8	1.1E-01	-1.1	5.5E-01
ENSMUST00000033378	early B cell factor 3 [Source:MGI Symbol;Acc:MGI:894289]		O08791	10.5	2.2E-02	6.0	3.5E-04	-0.6	6.1E-01	0.1	9.3E-01
ENSMUST00000033121	nodal modulator 1 [Source:MGI Symbol;Acc:MGI:2385850]		Q6GQT9	0.2	6.3E-01	0.5	4.1E-01	0.4	3.8E-01	0.1	8.6E-01
ENSMUST00000033380	cyclin-dependent kinase 16 [Source:MGI Symbol;Acc:MGI:97516]	Q543G3	Q04735	-5.8	1.8E-03	6.8	5.5E-05	0.9	3.7E-01	-0.3	6.1E-01
ENSMUST00000033127	secretion regulating guanine nucleotide exchange factor [Source:MGI Symbol;Acc:MGI:1351630]		Q80YD6	-0.6	4.1E-01	0.0	9.9E-01	0.4	6.0E-01	-0.2	7.9E-01
ENSMUST00000033388	oral cancer overexpressed 1 [Source:MGI Symbol;Acc:MGI:1919534]	Q3TF33		-2.3	2.2E-03	-3.7	2.0E-03	0.9	5.8E-02	-0.3	7.5E-01
ENSMUST00000033389	fibroblast growth factor 15 [Source:MGI Symbol;Acc:MGI:1096383]	Q790L8	O35622	6.4	7.3E-05	-4.6	1.2E-04	-1.1	2.0E-02	-1.5	1.1E-01
ENSMUST00000033394	Fas (TNFRSF6)-associated via death domain [Source:MGI Symbol;Acc:MGI:109324]		Q61160	3.2	2.4E-04	-4.3	5.1E-02	1.8	5.6E-02	-0.9	6.9E-01
ENSMUST00000033407	cortactin [Source:MGI Symbol;Acc:MGI:99695]	Q921L6		-3.0	5.2E-03	1.2	1.4E-01	-0.3	6.1E-01	0.1	8.5E-01
ENSMUST00000033139	arginyltransferase 1 [Source:MGI Symbol;Acc:MGI:1333870]		Q9Z2A5	-1.9	1.5E-01	1.7	2.6E-01	1.6	2.1E-01	-2.1	1.6E-01
ENSMUST00000033141	transforming, acidic coiled-coil containing protein 2 [Source:MGI Symbol;Acc:MGI:1928899]	E9QL08		4.5	6.1E-02	6.5	2.2E-02	-0.3	9.1E-01	-2.3	1.2E-01
ENSMUST00000033142	protein tyrosine phosphatase, non-receptor type 5 [Source:MGI Symbol;Acc:MGI:97807]		P54830	4.3	7.2E-02	2.7	2.9E-01	-0.4	8.7E-01	1.2	4.8E-01
ENSMUST00000033418	interleukin 13 receptor, alpha 1 [Source:MGI Symbol;Acc:MGI:105052]		O09030	-7.4	4.9E-06	7.4	8.3E-05	-0.6	6.2E-01	0.2	7.6E-01
ENSMUST00000033419	dedicator of cytokinesis 11 [Source:MGI Symbol;Acc:MGI:1923224]		A2AF47	-4.0	1.1E-03	2.0	9.5E-02	-4.1	1.4E-02	-0.2	8.0E-01
ENSMUST00000033427	SAM and SH3 domain containing 3 [Source:MGI Symbol;Acc:MGI:1921381]		Q8K352	-6.1	1.9E-05	7.6	1.1E-04	-0.7	6.0E-01	0.1	8.2E-01
ENSMUST00000033154	polo-like kinase 1 [Source:MGI Symbol;Acc:MGI:97621]	Q3TPZ2	Q07832	0.6	2.9E-01	1.7	5.6E-02	1.6	2.6E-02	0.5	4.9E-01
ENSMUST00000033429	E74-like factor 4 (ets domain transcription factor) [Source:MGI Symbol;Acc:MGI:1928377]		Q9Z2U4	-4.2	1.7E-03	-4.2	2.1E-03	0.2	7.4E-01	-2.9	4.2E-02
ENSMUST00000033430	RAB33A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:109493]	Q3SXA7	P97950	5.3	5.6E-04	2.6	6.3E-03	0.3	6.3E-01	0.7	2.3E-01
ENSMUST00000033158	ubiquitin family domain containing 1 [Source:MGI Symbol;Acc:MGI:107301]		Q78JW9	1.0	9.0E-02	1.3	9.0E-02	0.6	2.8E-01	0.3	6.7E-01
ENSMUST00000033444	serine/threonine kinase 26 [Source:MGI Symbol;Acc:MGI:1917665]	A2AD85	Q99JT2	-3.9	1.5E-03	4.4	3.5E-05	-1.3	4.8E-02	0.2	6.7E-01
ENSMUST00000033450	glypican 4 [Source:MGI Symbol;Acc:MGI:104902]		P51655	4.3	2.9E-04	8.1	7.8E-05	0.0	9.8E-01	-0.1	8.4E-01
ENSMUST00000033464	bombesin-like receptor 3 [Source:MGI Symbol;Acc:MGI:1100501]		O54798	5.6	1.8E-04	-6.7	2.0E-05	0.5	1.3E-01	0.6	5.1E-01
ENSMUST00000033468	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Source:MGI Symbol;Acc:MGI:1920591]	F6WMJ3		-9.0	1.1E-05	6.2	6.3E-04	1.7	1.6E-01	-0.8	2.5E-01
ENSMUST00000033169	cerebellar degeneration-related 2 [Source:MGI Symbol;Acc:MGI:1100885]		P97817	-2.9	6.0E-02	2.3	2.0E-01	2.4	1.2E-01	-2.7	8.4E-02
ENSMUST00000033171	ADP-ribosylation factor interacting protein 2 [Source:MGI Symbol;Acc:MGI:1924182]	H7BWZ6		-3.7	5.4E-02	-2.1	2.6E-01	0.0	9.8E-01	-1.7	4.1E-01
ENSMUST00000033473	fibroblast growth factor 13 [Source:MGI Symbol;Acc:MGI:109178]		P70377	5.8	1.1E-02	-1.6	1.3E-01	-0.6	3.7E-01	-3.3	2.5E-02
ENSMUST00000033477	coagulation factor IX [Source:MGI Symbol;Acc:MGI:88384]		P16294	5.0	8.5E-04	-6.4	8.3E-05	-0.7	1.3E-01	-1.3	2.4E-01
ENSMUST00000033178	PDZ domain containing 9 [Source:MGI Symbol;Acc:MGI:1915233]	B9EJT5	Q9D9M4	3.4	1.3E-01	2.8	2.6E-01	-0.5	8.5E-01	0.2	9.1E-01
ENSMUST00000033179	ribosomal RNA processing 8, methyltransferase, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914251]		Q9DB85	-2.1	7.8E-02	-0.3	8.5E-01	0.8	4.5E-01	-1.1	4.1E-01
ENSMUST00000033480	ATPase, class VI, type 11C [Source:MGI Symbol;Acc:MGI:1859661]	E9QKK8		-4.4	5.0E-03	-7.9	3.6E-04	0.9	5.0E-02	-0.6	7.1E-01
ENSMUST00000033483	coiled-coil domain containing 22 [Source:MGI Symbol;Acc:MGI:1859608]		Q9JIG7	-3.2	3.5E-04	-2.5	7.5E-03	0.4	3.3E-01	-0.5	5.3E-01
ENSMUST00000033185	hemopexin [Source:MGI Symbol;Acc:MGI:105112]		Q91X72	1.4	1.0E-01	-0.9	2.6E-01	-2.9	2.2E-03	-0.6	4.3E-01
ENSMUST00000033486	proteolipid protein 2 [Source:MGI Symbol;Acc:MGI:1298382]	Q0VEW4	Q9R1Q7	-10.0	3.3E-05	2.0	1.3E-02	-0.1	8.6E-01	-0.6	3.1E-01
ENSMUST00000033490	coiled-coil domain containing 120 [Source:MGI Symbol;Acc:MGI:1859619]	A2AEV7		7.0	5.8E-05	7.4	1.4E-04	-0.6	6.1E-01	0.1	8.4E-01
ENSMUST00000033494	OTU domain containing 5 [Source:MGI Symbol;Acc:MGI:1859615]		Q3U2S4	-3.8	4.2E-03	3.2	4.2E-03	-3.3	9.5E-03	0.4	5.9E-01
ENSMUST00000033497	polyglutamine binding protein 1 [Source:MGI Symbol;Acc:MGI:1859638]	A2AER7	Q91VJ5	-7.0	6.5E-06	6.7	1.7E-04	-0.5	6.7E-01	-1.0	1.5E-01
ENSMUST00000033498	translocase of inner mitochondrial membrane 17b [Source:MGI Symbol;Acc:MGI:1343176]	Q545H3	Q9Z0V7	3.1	1.1E-04	5.8	2.6E-04	-0.5	6.3E-01	0.3	6.3E-01
ENSMUST00000033210	transmembrane protein 159 [Source:MGI Symbol;Acc:MGI:1925752]		Q922Z1	0.0	9.8E-01	-0.1	9.2E-01	0.5	5.8E-01	0.6	6.0E-01
ENSMUST00000033211	tripartite motif-containing 30D [Source:MGI Symbol;Acc:MGI:3035181]	E9PWL0		-1.0	2.0E-01	-1.6	8.9E-02	-1.0	1.2E-01	-0.4	6.3E-01
ENSMUST00000033218	RIKEN cDNA 2610020H08 gene [Source:MGI Symbol;Acc:MGI:1919402]	Q7TSF9		3.4	6.2E-02	6.1	2.4E-02	1.3	5.6E-01	-1.4	3.4E-01
ENSMUST00000033505	Wiskott-Aldrich syndrome homolog (human) [Source:MGI Symbol;Acc:MGI:105059]	Q53WY0	P70315	-3.4	3.4E-04	-0.1	9.0E-01	0.4	5.7E-01	-2.5	3.8E-02
ENSMUST00000033236	THUMP domain containing 1 [Source:MGI Symbol;Acc:MGI:2444479]		Q99J36	-0.1	8.5E-01	-1.3	1.6E-01	-0.7	2.4E-01	0.5	6.0E-01
ENSMUST00000033241	hospholysine phosphohistidine inorganic pyrophosphate phosphatase [Source:MGI Symbol;Acc:MGI:1923679		Q9D7I5	1.9	4.8E-02	0.6	5.9E-01	0.0	9.9E-01	1.3	1.9E-01
ENSMUST00000033509	phenylalkylamine Ca2+ antagonist (emopamil) binding protein [Source:MGI Symbol;Acc:MGI:107822]		P70245	-3.6	1.3E-04	7.0	7.9E-05	-0.5	6.4E-01	-0.9	1.4E-01
ENSMUST00000033513	FtsJ homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1859648]	Q8CBC7		5.4	8.1E-05	-2.0	3.7E-02	0.5	3.7E-01	-0.9	3.1E-01
ENSMUST00000033519	dynein light chain Tctex-type 3 [Source:MGI Symbol;Acc:MGI:1914367]	Q542J7	P56387	-3.7	2.0E-04	7.6	1.4E-04	-0.6	6.3E-01	-0.1	9.2E-01
ENSMUST00000033264	tripartite motif-containing 21 [Source:MGI Symbol;Acc:MGI:106657]	Q3U7K7		-3.6	3.7E-02	-3.6	7.0E-02	-0.6	5.5E-01	-0.6	7.6E-01
ENSMUST00000033532	AF4/FMR2 family, member 2 [Source:MGI Symbol;Acc:MGI:1202294]		O55112	3.5	3.7E-04	-4.9	1.4E-02	-0.6	4.2E-01	-0.6	7.3E-01
ENSMUST00000033540	von Hippel-Lindau binding protein 1 [Source:MGI Symbol;Acc:MGI:1333804]		P61759	-6.9	1.4E-05	7.3	5.0E-05	-0.5	6.2E-01	-0.8	1.7E-01
ENSMUST00000033541	FUN14 domain containing 2 [Source:MGI Symbol;Acc:MGI:1914641]		Q9D6K8	-1.3	1.7E-02	-4.0	2.5E-03	1.0	4.4E-02	-0.6	5.9E-01
ENSMUST00000033545	RAB39B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1915040]	Q0PD14	Q8BHC1	5.0	5.8E-04	1.2	2.9E-01	-2.9	3.2E-02	-0.8	3.8E-01
ENSMUST00000033277	lysine rich nucleolar protein 1 [Source:MGI Symbol;Acc:MGI:1913606]	E9QKQ3		3.3	1.2E-01	-0.9	6.4E-01	-4.2	3.6E-02	0.0	1.0E+00
ENSMUST00000033556	G protein-coupled receptor 15-like [Source:MGI Symbol;Acc:MGI:2676330]	Q80T54		5.7	1.2E-03	2.5	4.9E-03	-1.4	5.4E-02	-0.3	6.2E-01
ENSMUST00000033560	oligophrenin 1 [Source:MGI Symbol;Acc:MGI:2151070]		Q99J31	5.7	3.3E-04	-7.1	9.6E-04	-1.2	3.5E-02	1.1	4.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000033570	immunoglobulin (CD79A) binding protein 1 [Source:MGI Symbol;Acc:MGI:1346500]		Q61249	-5.3	2.2E-05	-2.5	3.5E-03	-0.3	3.5E-01	0.2	7.5E-01
ENSMUST00000033575	melanoma antigen, family E, 2 [Source:MGI Symbol;Acc:MGI:2148316]	Q52KG3		8.9	9.1E-05	-1.5	6.2E-02	1.4	1.3E-02	-0.2	8.2E-01
ENSMUST00000033290	DEAH (Asp-Glu-Ala-His) box polypeptide 32 [Source:MGI Symbol;Acc:MGI:2141813]		Q8BZS9	-0.4	7.3E-01	5.2	3.9E-03	1.9	1.8E-01	-3.8	5.9E-03
ENSMUST00000033577	polysaccharide biosynthesis domain containing 1 [Source:MGI Symbol;Acc:MGI:1914933]		Q9D0B6	-2.2	8.4E-03	7.0	2.7E-04	-0.5	6.8E-01	-0.5	4.4E-01
ENSMUST00000033578	melanoma antigen, family E, 1 [Source:MGI Symbol;Acc:MGI:2148149]		Q6PCZ4	2.9	4.2E-03	-1.4	9.5E-02	0.6	2.8E-01	0.3	6.8E-01
ENSMUST00000033581	fibroblast growth factor 16 [Source:MGI Symbol;Acc:MGI:1931627]		Q9ESL8	5.9	1.9E-04	-5.7	1.9E-05	0.7	4.2E-02	1.0	1.9E-01
ENSMUST00000033582	cytochrome c oxidase subunit VIIb [Source:MGI Symbol;Acc:MGI:1913392]	Q5FW98	P56393	-6.8	4.6E-05	-6.9	1.2E-04	-0.1	8.6E-01	-0.8	5.1E-01
ENSMUST00000033585	phosphoglycerate kinase 2 [Source:MGI Symbol;Acc:MGI:97563]		P09041	6.0	9.2E-04	-1.5	8.1E-02	1.0	7.6E-02	-0.5	4.9E-01
ENSMUST00000033326	WEE 1 homolog 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:103075]		P47810	1.0	8.2E-02	1.5	4.6E-02	0.4	4.4E-01	-0.1	9.3E-01
ENSMUST00000033331	nuclear receptor interacting protein 3 [Source:MGI Symbol;Acc:MGI:1925843]		Q9JJR9	3.5	1.5E-01	1.8	5.2E-01	0.5	8.5E-01	2.1	3.4E-01
ENSMUST00000033597	high-mobility group nucleosome binding domain 5 [Source:MGI Symbol;Acc:MGI:1355295]		Q9JL35	-3.5	4.3E-04	-5.7	2.0E-03	0.6	2.7E-01	-0.4	7.6E-01
ENSMUST00000033335	A kinase (PRKA) interacting protein 1 [Source:MGI Symbol;Acc:MGI:3041226]		Q9JJR5	-1.3	2.4E-01	0.5	6.3E-01	-0.2	8.5E-01	-2.0	9.5E-02
ENSMUST00000033598	SH3-binding domain glutamic acid-rich protein like [Source:MGI Symbol;Acc:MGI:1930849]		Q9JJU8	-4.2	8.3E-05	6.2	2.7E-05	-1.7	7.0E-02	0.2	6.5E-01
ENSMUST00000033606	sushi-repeat-containing protein, X-linked 2 [Source:MGI Symbol;Acc:MGI:1916042]		Q8R054	4.9	8.1E-03	-3.5	2.8E-03	1.2	2.5E-02	-0.5	5.9E-01
ENSMUST00000033609	cleavage stimulation factor, 3' pre-RNA subunit 2 [Source:MGI Symbol;Acc:MGI:1343054]		Q8BIQ5	-6.0	3.6E-04	-6.9	5.6E-04	0.5	2.4E-01	3.5	2.3E-02
ENSMUST00000033611	Kell blood group complex subunit-related, X-linked [Source:MGI Symbol;Acc:MGI:3584011]		Q5GH68	8.8	1.4E-05	6.6	1.2E-01	-1.8	6.8E-01	2.1	4.1E-01
ENSMUST00000033617	Bruton agammaglobulinemia tyrosine kinase [Source:MGI Symbol;Acc:MGI:88216]		P35991	-6.2	4.3E-05	-5.5	1.3E-02	1.0	2.7E-01	0.7	7.1E-01
ENSMUST00000033383	ubiquitin specific peptidase 11 [Source:MGI Symbol;Acc:MGI:2384312]		Q99K46	0.4	3.9E-01	1.5	4.6E-02	0.7	1.7E-01	-0.3	6.1E-01
ENSMUST00000033386	MAS-related GPR, member F [Source:MGI Symbol;Acc:MGI:2384823]		Q8VCJ6	4.6	5.5E-02	2.2	3.1E-01	-3.6	1.4E-01	-1.2	4.7E-01
ENSMUST00000033621	galactosidase, alpha [Source:MGI Symbol;Acc:MGI:1347344]	Q8BGZ6		-1.2	3.4E-02	-1.3	8.6E-02	0.6	1.9E-01	-0.4	6.0E-01
ENSMUST00000033642	doublecortin [Source:MGI Symbol;Acc:MGI:1277171]		O88809	8.3	4.5E-06	6.5	2.3E-04	0.1	9.1E-01	0.1	9.2E-01
ENSMUST00000033393	anoctamin 1, calcium activated chloride channel [Source:MGI Symbol;Acc:MGI:2142149]		Q8BHY3	2.7	1.2E-01	5.1	1.0E-02	-0.6	7.3E-01	-3.0	3.9E-02
ENSMUST00000033643	glycosyltransferase 28 domain containing 2 [Source:MGI Symbol;Acc:MGI:2443773]	Q8BML3		5.5	2.3E-04	3.2	1.6E-03	0.5	4.4E-01	0.5	3.7E-01
ENSMUST00000033650	retinoschisis (X-linked, juvenile) 1 (human) [Source:MGI Symbol;Acc:MGI:1336189]		Q9Z1L4	8.4	3.5E-05	-0.2	7.1E-01	-2.3	1.4E-03	-5.1	1.8E-04
ENSMUST00000033415	NAD synthetase 1 [Source:MGI Symbol;Acc:MGI:1926164]		Q711T7	-2.0	2.6E-01	0.5	8.0E-01	0.6	7.2E-01	-1.9	3.4E-01
ENSMUST00000033662	pyruvate dehydrogenase E1 alpha 1 [Source:MGI Symbol;Acc:MGI:97532]	Q3UFJ3	P35486	-5.7	1.3E-06	-6.9	7.3E-05	0.6	1.7E-01	0.0	9.6E-01
ENSMUST00000033664	interleukin 2 receptor, gamma chain [Source:MGI Symbol;Acc:MGI:96551]	Q3UPA9	P34902	-4.7	6.9E-04	-2.1	6.0E-02	0.8	2.1E-01	-1.1	3.2E-01
ENSMUST00000033671	ribosomal protein S6 kinase polypeptide 3 [Source:MGI Symbol;Acc:MGI:104557]		P18654	-4.4	3.8E-05	-3.9	1.8E-03	1.3	1.6E-02	-1.0	3.4E-01
ENSMUST00000033673	non-POU-domain-containing, octamer binding protein [Source:MGI Symbol;Acc:MGI:1855692]	Q4FK11	Q99K48	-4.6	3.7E-06	-5.4	8.7E-03	1.4	6.3E-02	2.6	1.4E-01
ENSMUST00000033683	ribosomal protein S4, X-linked [Source:MGI Symbol;Acc:MGI:98158]	Q545X8	P62702	-7.1	8.0E-07	3.1	3.9E-03	-3.1	1.1E-02	-0.9	2.1E-01
ENSMUST00000033433	RNA binding motif protein, X-linked 2 [Source:MGI Symbol;Acc:MGI:1919414]		Q8R0F5	-1.1	5.6E-02	-1.9	1.3E-02	-1.2	2.6E-02	-0.4	5.2E-01
ENSMUST00000033442	immunoglobulin superfamily, member 1 [Source:MGI Symbol;Acc:MGI:2147913]		Q7TQA1	3.0	5.1E-02	5.9	1.6E-03	-0.5	7.4E-01	-3.4	6.6E-03
ENSMUST00000033689	caudal type homeobox 4 [Source:MGI Symbol;Acc:MGI:88362]	Q78Z64	Q07424	4.5	8.8E-04	-4.6	2.6E-03	-0.7	2.2E-01	0.0	9.8E-01
ENSMUST00000033695	ATP-binding cassette, sub-family B (MDR/TAP), member 7 [Source:MGI Symbol;Acc:MGI:109533]		Q61102	-2.0	4.8E-03	1.3	1.5E-01	-2.4	1.1E-02	0.7	3.5E-01
ENSMUST00000033463	solute carrier family 9 (sodium/hydrogen exchanger), member 9 [Source:MGI Symbol;Acc:MGI:2679732]		Q8BZ00	0.4	5.4E-01	0.2	8.3E-01	-0.3	5.8E-01	-0.1	8.9E-01
ENSMUST00000033700	X-linked myotubular myopathy gene 1 [Source:MGI Symbol;Acc:MGI:1099452]		Q9Z2C5	-6.5	1.1E-04	6.4	1.1E-04	-0.6	5.9E-01	-1.5	3.2E-02
ENSMUST00000033713	centrin 2 [Source:MGI Symbol;Acc:MGI:1347085]	Z4YJH1		-5.9	2.2E-03	-7.1	1.6E-04	0.5	2.6E-01	-1.5	3.0E-01
ENSMUST00000033715	NAD(P) dependent steroid dehydrogenase-like [Source:MGI Symbol;Acc:MGI:1099438]	Q3US15	Q9R1J0	-3.7	1.2E-03	7.4	4.7E-03	-0.2	9.2E-01	-1.8	1.4E-01
ENSMUST00000033717	holocytochrome c synthetase [Source:MGI Symbol;Acc:MGI:106911]		P53702	-5.3	1.9E-03	5.8	8.1E-04	0.0	9.8E-01	-0.8	3.1E-01
ENSMUST00000033721	Rho GTPase activating protein 6 [Source:MGI Symbol;Acc:MGI:1196332]		O54834	7.2	3.4E-05	-3.8	2.4E-02	1.3	1.1E-01	0.7	6.4E-01
ENSMUST00000033723	synapse associated protein 1 [Source:MGI Symbol;Acc:MGI:1914293]		Q9D5V6	-4.3	2.2E-05	-2.4	8.4E-03	0.6	1.7E-01	-0.1	8.8E-01
ENSMUST00000033485	prickle homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1859635]		Q80VL3	-1.0	7.0E-01	-2.5	4.4E-01	-1.6	4.7E-01	-0.1	9.8E-01
ENSMUST00000033725	male-specific lethal 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1341851]		Q9WVG9	-3.3	1.6E-02	-5.4	2.3E-03	1.5	2.8E-02	-3.2	7.0E-02
ENSMUST00000033489	PRA1 domain family 2 [Source:MGI Symbol;Acc:MGI:1859607]		Q9JIG8	0.3	6.4E-01	-0.3	6.4E-01	-0.1	8.0E-01	0.5	5.0E-01
ENSMUST00000033727	cytidine 5'-triphosphate synthase 2 [Source:MGI Symbol;Acc:MGI:1933185]		P70303	-3.7	1.1E-03	4.7	5.8E-04	-2.1	7.0E-02	0.2	8.1E-01
ENSMUST00000033730	gastrin releasing peptide receptor [Source:MGI Symbol;Acc:MGI:95836]	Q53WV4	P21729	10.1	4.0E-05	-1.1	3.9E-01	1.4	1.1E-01	-1.3	3.2E-01
ENSMUST00000033731	zinc finger protein 275 [Source:MGI Symbol;Acc:MGI:1350985]	G3X904		-4.3	1.9E-02	-6.6	8.2E-05	0.0	9.2E-01	-0.5	6.6E-01
ENSMUST00000033734	adaptor-related protein complex 1, sigma 2 subunit [Source:MGI Symbol;Acc:MGI:1889383]	Q3TIV9		-7.9	1.1E-04	3.2	5.9E-04	0.5	3.3E-01	0.5	3.3E-01
ENSMUST00000033502	GATA binding protein 1 [Source:MGI Symbol;Acc:MGI:95661]		P17679	1.2	1.8E-01	2.1	5.1E-02	-0.1	9.0E-01	-1.1	2.2E-01
ENSMUST00000033739	carbonic anhydrase 5b, mitochondrial [Source:MGI Symbol;Acc:MGI:1926249]		Q9QZA0	3.6	1.4E-05	-2.2	2.0E-02	1.3	1.8E-02	0.2	7.7E-01
ENSMUST00000033506	WD repeat domain 13 [Source:MGI Symbol;Acc:MGI:1914661]	Q32P16	Q91V09	-5.0	1.1E-01	0.1	9.9E-01	2.9	2.8E-01	-2.1	5.2E-01
ENSMUST00000033740	zinc finger protein 92 [Source:MGI Symbol;Acc:MGI:108094]		Q62396	8.0	4.8E-06	-3.8	4.5E-04	-0.1	7.1E-01	0.1	9.3E-01
ENSMUST00000033741	biglycan [Source:MGI Symbol;Acc:MGI:88158]	Q3TNY9	P28653	8.9	3.3E-05	4.5	9.3E-04	-0.2	8.3E-01	0.7	3.3E-01
ENSMUST00000033752	lute carrier family 6 (neurotransmitter transporter, creatine), member 8 [Source:MGI Symbol;Acc:MGI:214783		Q8VBW1	6.9	4.6E-03	-3.4	1.7E-03	0.2	7.2E-01	-0.1	8.6E-01
ENSMUST00000033754	phosphatidylinositol glycan anchor biosynthesis, class A [Source:MGI Symbol;Acc:MGI:99461]	A2AIH5	Q64323	-6.1	3.9E-05	3.5	3.0E-03	1.0	2.1E-01	1.1	1.1E-01
ENSMUST00000033539	coagulation factor VIII [Source:MGI Symbol;Acc:MGI:88383]		Q06194	4.5	8.9E-02	6.5	3.6E-02	-0.2	9.4E-01	-2.2	1.8E-01
ENSMUST00000033763	N(alpha)-acetyltransferase 10, NatA catalytic subunit [Source:MGI Symbol;Acc:MGI:1915255]	Q540H0	Q9QY36	4.2	2.5E-02	-5.7	4.4E-04	0.4	3.8E-01	-0.9	4.6E-01
ENSMUST00000033770	methyl CpG binding protein 2 [Source:MGI Symbol;Acc:MGI:99918]		Q9Z2D6	-2.4	1.1E-02	-0.6	2.9E-01	-0.5	2.3E-01	-1.2	4.9E-02
ENSMUST00000033775	membrane protein, palmitoylated [Source:MGI Symbol;Acc:MGI:105941]	Q542P4	P70290	-7.1	1.4E-05	3.4	6.5E-03	-1.7	1.3E-01	0.0	9.7E-01
ENSMUST00000033547	plastin 3 (T-isoform) [Source:MGI Symbol;Acc:MGI:104807]		Q99K51	2.4	2.1E-01	-0.6	7.2E-01	-3.4	7.2E-02	-0.4	8.3E-01
ENSMUST00000033800	proteolipid protein (myelin) 1 [Source:MGI Symbol;Acc:MGI:97623]	Q3UYM8	P60202	8.3	7.3E-06	6.3	1.2E-03	-0.5	7.6E-01	-1.0	2.3E-01
ENSMUST00000033804	zinc finger, CCHC domain containing 18 [Source:MGI Symbol;Acc:MGI:1914245]		Q8VD24	7.6	3.3E-05	5.2	1.3E-03	-1.6	2.1E-01	-1.0	1.9E-01
ENSMUST00000033805	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 [Source:MGI Symbol;Acc:MGI:1858898]		Q9Z2X2	-8.0	1.1E-05	-5.6	7.0E-05	-1.1	2.2E-02	-0.8	3.6E-01
ENSMUST00000033809	phosphoribosyl pyrophosphate synthetase 1 [Source:MGI Symbol;Acc:MGI:97775]		Q9D7G0	-4.0	1.6E-05	6.5	1.2E-03	-1.2	4.3E-01	1.2	1.8E-01
ENSMUST00000033810	RNA binding motif protein 41 [Source:MGI Symbol;Acc:MGI:2444923]		Q8JZV4	5.8	8.4E-03	-3.0	3.9E-03	-1.0	7.9E-02	-0.2	8.0E-01
ENSMUST00000033818	ATPase, class VI, type 11A [Source:MGI Symbol;Acc:MGI:1354735]	E9Q3G7		-9.3	5.3E-05	3.3	6.0E-03	0.8	3.5E-01	0.3	6.6E-01
ENSMUST00000033821	coagulation factor X [Source:MGI Symbol;Acc:MGI:103107]	Q3U3V1		-7.8	1.4E-04	5.4	6.0E-04	-0.6	6.3E-01	-0.1	8.3E-01
ENSMUST00000033822	protein Z, vitamin K-dependent plasma glycoprotein [Source:MGI Symbol;Acc:MGI:1860488]		Q9CQW3	1.6	2.2E-02	-6.4	9.9E-05	-1.2	2.4E-02	-1.6	1.8E-01
ENSMUST00000033583	magnesium transporter 1 [Source:MGI Symbol;Acc:MGI:1914325]	A2ADH1		0.9	1.2E-01	1.1	9.0E-02	-0.4	4.0E-01	-0.7	2.4E-01
ENSMUST00000033824	lysosomal-associated membrane protein 1 [Source:MGI Symbol;Acc:MGI:96745]	Q3TA96	P11438	-5.9	1.2E-06	5.8	1.9E-03	-0.4	7.8E-01	-0.3	7.3E-01
ENSMUST00000033591	integral membrane protein 2A [Source:MGI Symbol;Acc:MGI:107706]		Q61500	-0.8	4.0E-01	-0.8	4.3E-01	-1.4	1.2E-01	-1.4	1.8E-01
ENSMUST00000033825	ADP-ribosylhydrolase like 1 [Source:MGI Symbol;Acc:MGI:2442168]		Q8BGK2	6.9	7.1E-05	-3.7	1.1E-03	-0.8	1.2E-01	-0.6	4.7E-01
ENSMUST00000033826	ATPase, H+/K+ exchanging, beta polypeptide [Source:MGI Symbol;Acc:MGI:88114]	Q0VBB6	P50992	7.5	9.7E-04	-5.4	9.9E-05	-0.8	7.2E-02	0.4	6.3E-01
ENSMUST00000033827	G protein-coupled receptor kinase 1 [Source:MGI Symbol;Acc:MGI:1345146]	G3X905		8.9	1.0E-06	6.2	3.4E-03	-0.6	7.3E-01	-1.9	8.4E-02
ENSMUST00000033608	synaptotagmin-like 4 [Source:MGI Symbol;Acc:MGI:1351606]	Q549X6	Q9R0Q1	3.5	8.3E-02	2.6	2.0E-01	-1.9	3.1E-01	-1.1	5.2E-01
ENSMUST00000033828	growth arrest specific 6 [Source:MGI Symbol;Acc:MGI:95660]		Q61592	6.5	7.0E-06	-3.8	2.2E-02	1.3	6.3E-02	-0.8	5.8E-01
ENSMUST00000033839	coordinator of PRMT5, differentiation stimulator [Source:MGI Symbol;Acc:MGI:1913673]		Q9CQ13	2.5	5.1E-03	6.2	4.6E-04	-0.5	6.6E-01	2.1	1.3E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000033842	myomesin 2 [Source:MGI Symbol;Acc:MGI:1328358]	Q14BI5		8.2	9.2E-06	-8.8	8.8E-04	0.1	7.6E-01	2.8	1.5E-01
ENSMUST00000033846	angiopoietin 2 [Source:MGI Symbol;Acc:MGI:1202890]	B9EHQ4	O35608	5.8	1.1E-04	-1.0	1.5E-01	-0.1	7.6E-01	-0.4	5.3E-01
ENSMUST00000033634	acyl-CoA synthetase long-chain family member 4 [Source:MGI Symbol;Acc:MGI:1354713]		Q9QUJ7	0.6	7.8E-01	1.7	3.5E-01	-2.3	1.9E-01	-3.4	1.3E-01
ENSMUST00000033847	l-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) [Source:MGI Symbol;Acc:M	F8WGD9		-6.1	1.6E-05	7.5	9.2E-06	-1.2	2.3E-01	-0.4	4.0E-01
ENSMUST00000033866	vacuolar protein sorting 36 (yeast) [Source:MGI Symbol;Acc:MGI:1917410]	Q3TSR1	Q91XD6	-1.6	1.8E-02	4.6	8.4E-04	-1.3	2.2E-01	-0.3	6.5E-01
ENSMUST00000033871	carrier family 25 (mitochondrial carrier ornithine transporter), member 15 [Source:MGI Symbol;Acc:MGI:134	Q543E2	Q9WVD5	2.2	1.8E-03	7.9	2.2E-04	-0.1	9.2E-01	0.4	5.6E-01
ENSMUST00000033652	phosphorylase kinase alpha 2 [Source:MGI Symbol;Acc:MGI:97577]		Q8BWJ3	-2.5	7.5E-02	-1.4	4.5E-01	0.9	4.5E-01	-0.3	8.8E-01
ENSMUST00000033873	ER lipid raft associated 2 [Source:MGI Symbol;Acc:MGI:2387215]		Q8BFZ9	-1.4	1.3E-02	-4.6	3.9E-05	0.1	7.7E-01	-1.1	1.2E-01
ENSMUST00000033875	proline synthetase co-transcribed [Source:MGI Symbol;Acc:MGI:1891207]	Q544R1	Q9Z2Y8	-2.4	3.7E-03	-2.7	2.0E-02	-0.1	8.5E-01	-2.0	9.6E-02
ENSMUST00000033665	mitogen-activated protein kinase kinase kinase 15 [Source:MGI Symbol;Acc:MGI:2448588]		A2AQW0	-2.2	4.1E-02	-2.9	4.8E-02	0.2	8.1E-01	0.9	5.0E-01
ENSMUST00000033876	adhesion G protein-coupled receptor A2 [Source:MGI Symbol;Acc:MGI:1925810]		Q91ZV8	7.6	3.9E-03	-3.4	1.4E-03	0.9	3.9E-02	-0.1	9.0E-01
ENSMUST00000033880	eukaryotic translation initiation factor 4E binding protein 1 [Source:MGI Symbol;Acc:MGI:103267]		Q60876	-6.3	4.6E-06	-4.5	2.3E-05	-0.5	1.0E-01	-0.5	3.8E-01
ENSMUST00000033882	cholinergic receptor, nicotinic, alpha polypeptide 6 [Source:MGI Symbol;Acc:MGI:106213]		Q9R0W9	7.4	7.8E-05	-7.0	3.9E-06	-0.9	1.6E-02	-1.0	1.9E-01
ENSMUST00000033888	CD209e antigen [Source:MGI Symbol;Acc:MGI:2157948]	Q3KNN8	Q91ZW7	6.0	1.3E-03	2.6	9.2E-03	-2.6	1.8E-02	-0.7	3.5E-01
ENSMUST00000033898	collagen, type IV, alpha 1 [Source:MGI Symbol;Acc:MGI:88454]		P02463	6.1	1.4E-05	-0.7	2.9E-01	0.2	6.2E-01	-1.1	1.3E-01
ENSMUST00000033699	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]		Q8BTM8	-1.9	6.5E-01	0.9	8.9E-01	3.6	3.4E-01	0.8	9.0E-01
ENSMUST00000033899	collagen, type IV, alpha 2 [Source:MGI Symbol;Acc:MGI:88455]	B2RQQ8	P08122	3.5	4.9E-05	-6.3	7.2E-04	-0.7	1.6E-01	-0.9	5.2E-01
ENSMUST00000033900	RAB20, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:102789]	Q3TPA7	P35295	-3.2	5.4E-04	-4.6	2.5E-02	0.2	8.3E-01	-1.2	5.5E-01
ENSMUST00000033906	RIKEN cDNA 1700016D06 gene [Source:MGI Symbol;Acc:MGI:1923663]	Q9DAA5		5.3	7.8E-05	-1.8	8.7E-02	0.1	8.9E-01	-1.8	9.2E-02
ENSMUST00000033908	Rho guanine nucleotide exchange factor (GEF7) [Source:MGI Symbol;Acc:MGI:1860493]			4.8	5.4E-05	-3.9	5.1E-02	1.4	9.6E-02	0.0	9.8E-01
ENSMUST00000033720	retinoblastoma binding protein 7 [Source:MGI Symbol;Acc:MGI:1194910]		Q60973	-2.2	3.6E-01	-3.1	3.0E-01	-0.9	5.9E-01	0.0	1.0E+00
ENSMUST00000033909	testis expressed 29 [Source:MGI Symbol;Acc:MGI:1922778]		Q9DA77	5.1	1.2E-03	6.9	9.2E-05	-0.6	6.1E-01	-0.3	6.5E-01
ENSMUST00000033910	leptin receptor overlapping transcript-like 1 [Source:MGI Symbol;Acc:MGI:1915442]		Q9CQ74	-3.5	2.8E-05	-3.7	3.3E-04	0.3	4.5E-01	-0.4	5.9E-01
ENSMUST00000033919	vascular endothelial growth factor C [Source:MGI Symbol;Acc:MGI:109124]		P97953	5.6	7.5E-04	0.6	6.6E-01	2.0	8.8E-02	-2.0	1.7E-01
ENSMUST00000033927	exoribonuclease 1 [Source:MGI Symbol;Acc:MGI:1914526]			-1.6	3.1E-03	-3.2	1.0E-02	-0.1	7.8E-01	-0.7	5.1E-01
ENSMUST00000033930	dual specificity phosphatase 4 [Source:MGI Symbol;Acc:MGI:2442191]		Q8BFV3	6.4	4.3E-06	8.3	3.3E-04	-0.3	8.6E-01	1.6	8.0E-02
ENSMUST00000033933	store-operated calcium entry-associated regulatory factor [Source:MGI Symbol;Acc:MGI:1915137]			-4.1	2.3E-05	-2.4	3.7E-01	2.1	1.8E-01	0.2	9.4E-01
ENSMUST00000033935	small integral membrane protein 19 [Source:MGI Symbol;Acc:MGI:2142501]		Q80ZU4	-4.8	2.3E-04	-6.1	4.4E-03	1.7	1.7E-02	-0.1	9.6E-01
ENSMUST00000033737	HAUS augmin-like complex, subunit 7 [Source:MGI Symbol;Acc:MGI:1920988]		Q8BKT8	0.1	8.2E-01	-0.1	9.1E-01	-1.4	2.7E-02	-1.1	1.1E-01
ENSMUST00000033936	dickkopf homolog 4 (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:2385299]		Q8VEJ3	6.8	5.8E-05	2.8	2.9E-04	-0.6	2.3E-01	0.3	4.9E-01
ENSMUST00000033938	polymerase (DNA directed), beta [Source:MGI Symbol;Acc:MGI:97740]		Q8K409	-3.9	2.1E-04	6.8	6.2E-05	0.1	9.3E-01	1.3	3.7E-02
ENSMUST00000033939	inhibitor of kappaB kinase beta [Source:MGI Symbol;Acc:MGI:1338071]	Q5D0E0		-8.7	6.4E-06	3.9	1.8E-03	-4.4	3.9E-03	0.7	3.2E-01
ENSMUST00000033941	plasminogen activator, tissue [Source:MGI Symbol;Acc:MGI:97610]		P11214	5.9	3.0E-05	5.5	1.1E-02	-3.0	1.6E-01	-1.5	2.4E-01
ENSMUST00000033950	GINS complex subunit 4 (Sld5 homolog) [Source:MGI Symbol;Acc:MGI:1923847]		Q99LZ3	-3.2	1.2E-04	-5.4	7.0E-04	0.7	1.2E-01	0.0	9.8E-01
ENSMUST00000033761	host cell factor C1 [Source:MGI Symbol;Acc:MGI:105942]		Q61191	-3.0	1.6E-01	-2.0	5.1E-01	1.9	3.6E-01	0.9	7.3E-01
ENSMUST00000033952	secreted frizzled-related protein 1 [Source:MGI Symbol;Acc:MGI:892014]		Q8C4U3	9.4	1.1E-05	-0.2	8.8E-01	-4.3	1.9E-02	0.1	9.3E-01
ENSMUST00000033769	interleukin-1 receptor-associated kinase 1 [Source:MGI Symbol;Acc:MGI:107420]	B1AUW6		1.4	2.4E-01	2.0	2.2E-01	0.8	5.2E-01	0.2	8.5E-01
ENSMUST00000033961	TM2 domain containing 2 [Source:MGI Symbol;Acc:MGI:1916992]		Q8R0I4	-5.8	2.2E-06	-5.1	5.7E-03	-0.4	5.4E-01	2.3	1.3E-01
ENSMUST00000033975	DDHD domain containing 2 [Source:MGI Symbol;Acc:MGI:1919358]		Q80Y98	1.6	1.4E-02	-6.1	4.7E-04	0.9	7.9E-02	0.0	9.9E-01
ENSMUST00000033776	dyskeratosis congenita 1, dyskerin [Source:MGI Symbol;Acc:MGI:1861727]		Q9ESX5	1.2	5.3E-02	0.8	2.7E-01	-0.6	3.1E-01	-0.1	8.5E-01
ENSMUST00000033979	steroidogenic acute regulatory protein [Source:MGI Symbol;Acc:MGI:102760]		P51557	2.6	6.8E-04	6.4	2.3E-04	-1.2	3.0E-01	0.7	2.5E-01
ENSMUST00000033983	MAK16 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915170]		Q8BGS0	-2.6	6.3E-03	6.1	1.7E-04	-2.0	1.0E-01	-0.4	4.9E-01
ENSMUST00000033992	glutathione reductase [Source:MGI Symbol;Acc:MGI:95804]		P47791	-5.8	2.5E-06	-7.9	8.0E-05	-0.4	2.8E-01	-0.5	7.0E-01
ENSMUST00000033999	FSHD region gene 1 [Source:MGI Symbol;Acc:MGI:893597]	Q78P92	P97376	-3.7	1.8E-04	-3.8	1.5E-04	0.0	9.8E-01	-0.1	8.6E-01
ENSMUST00000034000	N-acylsphingosine amidohydrolase 1 [Source:MGI Symbol;Acc:MGI:1277124]	Q78P93	Q9WV54	-6.3	1.4E-04	1.6	4.2E-01	-1.8	3.7E-01	2.4	1.2E-01
ENSMUST00000034003	fibrinogen-like protein 1 [Source:MGI Symbol;Acc:MGI:102795]			-3.2	2.4E-03	-5.5	8.2E-04	0.7	1.4E-01	-3.1	6.5E-02
ENSMUST00000033820	coagulation factor VII [Source:MGI Symbol;Acc:MGI:109325]	Q542C2	P70375	1.3	5.0E-02	0.3	5.9E-01	-1.8	6.9E-03	-0.8	1.9E-01
ENSMUST00000034014	fibroblast growth factor 20 [Source:MGI Symbol;Acc:MGI:1891346]		Q9ESL9	5.8	2.8E-04	-7.4	1.4E-03	0.2	6.3E-01	-0.1	9.3E-01
ENSMUST00000034015	methylsterol monoxygenase 1 [Source:MGI Symbol;Acc:MGI:1913484]		Q9CRA4	-7.5	4.1E-06	2.5	6.5E-03	0.0	1.0E+00	-0.9	1.7E-01
ENSMUST00000034017	kelch-like 2, Mayven [Source:MGI Symbol;Acc:MGI:1924363]		Q8JZP3	-4.8	1.9E-06	-5.3	2.5E-05	0.5	8.9E-02	0.0	9.9E-01
ENSMUST00000034021	cetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7 [Source:MGI Symbol;Acc:MGI:		Q80VA0	-5.0	2.8E-03	7.0	1.2E-04	-0.6	6.2E-01	-0.7	2.9E-01
ENSMUST00000034022	sin3 associated polypeptide [Source:MGI Symbol;Acc:MGI:1929129]		O88574	-5.4	8.1E-06	6.0	6.5E-03	-0.8	6.9E-01	0.7	4.7E-01
ENSMUST00000034023	scrapie responsive gene 1 [Source:MGI Symbol;Acc:MGI:1328308]	Q543T5	O88745	-4.9	6.7E-06	8.7	5.3E-06	0.0	9.8E-01	0.2	7.0E-01
ENSMUST00000034029	endothelin receptor type A [Source:MGI Symbol;Acc:MGI:105923]		Q61614	2.0	1.9E-02	0.7	2.1E-01	-5.8	1.0E-05	0.0	9.9E-01
ENSMUST00000034034	intestine specific homeobox [Source:MGI Symbol;Acc:MGI:1918847]	B1Q2M1	A1A546	6.2	2.9E-04	1.6	6.2E-02	-0.3	6.3E-01	0.5	4.9E-01
ENSMUST00000034041	interferon regulatory factor 2 [Source:MGI Symbol;Acc:MGI:96591]	Q3U2Z2	P23906	-5.0	1.2E-04	7.9	2.7E-05	-0.6	6.0E-01	-0.3	6.1E-01
ENSMUST00000034046	acyl-CoA synthetase long-chain family member 1 [Source:MGI Symbol;Acc:MGI:102797]		P41216	-8.6	7.8E-05	2.0	4.1E-02	-3.0	8.6E-03	0.8	2.8E-01
ENSMUST00000034049	er family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4 [Source:MGI Symbol;Acc:MG		P48962	-2.1	3.9E-03	-5.9	1.7E-04	0.1	8.2E-01	-0.1	8.9E-01
ENSMUST00000033865	NIMA (never in mitosis gene a)-related expressed kinase 3 [Source:MGI Symbol;Acc:MGI:1344371]	F8WGD4		3.3	8.9E-02	1.8	4.2E-01	-0.4	8.3E-01	1.0	5.8E-01
ENSMUST00000034051	UFM1-specific peptidase 2 [Source:MGI Symbol;Acc:MGI:1913679]		Q99K23	-7.2	1.5E-04	-2.2	2.0E-02	-0.3	5.2E-01	0.2	7.5E-01
ENSMUST00000034053	PDZ and LIM domain 3 [Source:MGI Symbol;Acc:MGI:1859274]		O70209	6.9	1.2E-04	2.3	5.6E-03	0.0	9.5E-01	-0.1	8.4E-01
ENSMUST00000034056	toll-like receptor 3 [Source:MGI Symbol;Acc:MGI:2156367]		Q99MB1	6.4	2.4E-02	-0.5	3.8E-01	0.7	1.1E-01	-0.1	8.0E-01
ENSMUST00000034057	palladin, cytoskeletal associated protein [Source:MGI Symbol;Acc:MGI:1919583]		Q9ET54	8.1	5.9E-05	-0.3	6.5E-01	0.5	2.8E-01	-1.5	6.1E-02
ENSMUST00000034058	carbonyl reductase 4 [Source:MGI Symbol;Acc:MGI:2384567]		Q91VT4	-2.2	1.7E-02	2.3	3.9E-01	-1.7	5.2E-01	3.6	6.2E-02
ENSMUST00000033877	', subunit of RNA polymerase III transcription initiation factor, BRF1-like [Source:MGI Symbol;Acc:MGI:191			-0.2	8.1E-01	1.5	8.2E-02	1.0	1.5E-01	-0.7	3.2E-01
ENSMUST00000033878	RAB11 family interacting protein 1 (class I) [Source:MGI Symbol;Acc:MGI:1923017]		Q9D620	-2.1	9.3E-02	-3.4	8.0E-02	0.5	6.0E-01	1.8	3.1E-01
ENSMUST00000034060	SH3 domain containing ring finger 1 [Source:MGI Symbol;Acc:MGI:1913066]	E9QQ33		4.1	8.9E-05	-5.4	7.0E-05	0.2	5.7E-01	-0.7	4.0E-01
ENSMUST00000034064	coagulation factor XI [Source:MGI Symbol;Acc:MGI:99481]		Q91Y47	5.9	1.9E-04	6.5	4.4E-04	-0.6	6.4E-01	0.4	5.9E-01
ENSMUST00000034074	NEDD4 binding protein 1 [Source:MGI Symbol;Acc:MGI:2136825]		Q6A037	-1.7	6.8E-03	2.1	6.5E-02	-3.6	1.8E-02	0.3	7.1E-01
ENSMUST00000033892	tumor necrosis factor (ligand) superfamily, member 13b [Source:MGI Symbol;Acc:MGI:1344376]	Q3KP92	Q9WU72	0.2	7.2E-01	0.3	5.8E-01	-0.6	1.8E-01	-0.8	2.0E-01
ENSMUST00000034076	cerebellin 1 precursor protein [Source:MGI Symbol;Acc:MGI:88281]	Q7TNF5	Q9R171	5.7	1.4E-03	1.6	3.4E-02	-4.4	1.2E-04	0.1	8.9E-01
ENSMUST00000034085	bromodomain containing 7 [Source:MGI Symbol;Acc:MGI:1349766]		O88665	-2.6	3.3E-04	1.2	5.3E-02	-1.9	2.9E-03	0.4	3.9E-01
ENSMUST00000034086	naked cuticle 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2135954]		Q99MH6	8.6	1.5E-05	-2.9	5.3E-03	0.4	3.9E-01	0.0	9.9E-01
ENSMUST00000033901	carbohydrate kinase domain containing [Source:MGI Symbol;Acc:MGI:1913353]	K3W4M4		-3.1	1.7E-01	2.5	2.8E-01	2.4	2.4E-01	-3.1	1.6E-01
ENSMUST00000033905	ankyrin repeat domain 10 [Source:MGI Symbol;Acc:MGI:1921840]		Q99LW0	0.0	9.9E-01	-0.9	2.4E-01	-0.2	7.3E-01	0.7	3.3E-01
ENSMUST00000034087	sorting nexin 20 [Source:MGI Symbol;Acc:MGI:1918857]			-5.4	2.3E-06	5.5	1.6E-04	-0.3	7.2E-01	-0.5	3.9E-01
ENSMUST00000034090	sal-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1889585]	Q6P5E3		7.9	3.5E-05	6.0	1.2E-04	0.8	3.7E-01	-0.4	5.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000034091	retinoblastoma-like 2 [Source:MGI Symbol;Acc:MGI:105085]		Q64700	-3.5	1.0E-04	6.3	5.4E-04	-0.4	7.5E-01	-1.6	4.4E-02
ENSMUST00000034093	eukaryotic translation initiation factor 2 alpha kinase 3 [Source:MGI Symbol;Acc:MGI:1341830]	E9QQ30		-4.0	5.7E-05	-2.5	1.7E-03	0.7	4.0E-02	-0.3	6.2E-01
ENSMUST00000034097	glutamatic-oxaloacetic transaminase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:95792]		P05202	-3.9	3.7E-05	3.4	1.5E-02	-2.2	1.1E-01	0.0	9.9E-01
ENSMUST00000033920	aspartylglucosaminidase [Source:MGI Symbol;Acc:MGI:104873]	A2RSS6	Q64191	-0.1	8.2E-01	-0.7	3.6E-01	-0.7	2.3E-01	-0.1	8.4E-01
ENSMUST00000033923	deleted in liver cancer 1 [Source:MGI Symbol;Acc:MGI:1354949]	E9QKB1		5.9	7.0E-02	5.6	4.8E-02	-3.9	2.4E-01	-3.6	4.7E-02
ENSMUST00000034109	RIKEN cDNA 1700011L22 gene [Source:MGI Symbol;Acc:MGI:1914937]		Q9DAF8	6.3	3.9E-04	-1.2	5.6E-02	0.7	7.0E-02	0.2	6.4E-01
ENSMUST00000033929	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase [Source:MGI Symbol;Acc:MGI:1341087]		Q6PFX9	-1.0	3.5E-02	-0.1	8.7E-01	0.6	1.4E-01	-0.3	5.3E-01
ENSMUST00000034115	POU domain, class 4, transcription factor 2 [Source:MGI Symbol;Acc:MGI:102524]		Q63934	8.9	2.6E-05	4.7	2.8E-04	-1.2	1.5E-01	0.5	3.3E-01
ENSMUST00000034121	mannosidase 2, alpha B1 [Source:MGI Symbol;Acc:MGI:107286]		O09159	-5.3	2.2E-05	-3.4	5.2E-04	0.4	2.8E-01	-0.4	5.8E-01
ENSMUST00000033934	mitochondrial ribosomal protein S31 [Source:MGI Symbol;Acc:MGI:1913153]		Q61733	-0.5	4.4E-01	-1.9	2.9E-02	-1.1	5.5E-02	0.3	7.0E-01
ENSMUST00000034131	vacuolar protein sorting 35 [Source:MGI Symbol;Acc:MGI:1890467]	Q3TRJ1	Q9EQH3	-6.0	4.0E-06	-2.2	3.6E-02	1.3	4.2E-02	-1.3	2.3E-01
ENSMUST00000034132	origin recognition complex, subunit 6 [Source:MGI Symbol;Acc:MGI:1929285]	Q66JV6		-2.1	3.5E-03	7.0	5.7E-05	-0.9	4.1E-01	-1.1	9.4E-02
ENSMUST00000034133	myosin light chain kinase 3 [Source:MGI Symbol;Acc:MGI:2443063]		Q3UIZ8	6.3	8.6E-05	-3.2	2.3E-03	-0.7	1.3E-01	-1.4	1.1E-01
ENSMUST00000034136	glutamic pyruvate transaminase (alanine aminotransferase) 2 [Source:MGI Symbol;Acc:MGI:1915391]		Q8BGT5	3.7	6.3E-04	-7.1	2.1E-04	0.9	3.7E-02	-0.7	5.9E-01
ENSMUST00000034138	DnaJ (Hsp40) homolog, subfamily A, member 2 [Source:MGI Symbol;Acc:MGI:1931882]		Q9QYJ0	-4.2	4.0E-05	2.7	4.5E-03	-3.6	1.0E-03	-0.4	5.2E-01
ENSMUST00000034140	integrin alpha FG-GAP repeat containing 1 [Source:MGI Symbol;Acc:MGI:106419]		Q99KW9	-4.7	8.1E-06	-3.6	3.2E-04	-0.3	3.6E-01	0.0	1.0E+00
ENSMUST00000034141	lon peptidase 2, peroxisomal [Source:MGI Symbol;Acc:MGI:1914137]		Q9DBN5	-9.0	2.9E-05	3.2	1.4E-03	-6.0	2.8E-04	0.2	7.7E-01
ENSMUST00000033958	a disintegrin and metallopeptidase domain 3 (cyritestin) [Source:MGI Symbol;Acc:MGI:102518]	F8VQ03		-1.0	4.5E-01	-0.4	8.0E-01	-1.1	3.6E-01	-1.7	2.6E-01
ENSMUST00000034146	uncoupling protein 1 (mitochondrial, proton carrier) [Source:MGI Symbol;Acc:MGI:98894]		P12242	6.7	6.9E-05	-4.1	1.3E-04	0.7	4.9E-02	-1.0	1.8E-01
ENSMUST00000033973	RWD domain containing 4A [Source:MGI Symbol;Acc:MGI:2681000]		Q9CPR1	-0.6	3.8E-01	1.7	6.4E-02	0.5	4.4E-01	-1.8	3.6E-02
ENSMUST00000034147	zinc finger protein 330 [Source:MGI Symbol;Acc:MGI:1353574]		Q922H9	-3.7	1.3E-04	1.7	3.5E-02	0.1	8.2E-01	0.0	9.7E-01
ENSMUST00000034159	thioredoxin-like 4B [Source:MGI Symbol;Acc:MGI:2443724]		Q8BUH1	-2.9	1.0E-03	2.5	3.4E-03	0.1	8.8E-01	0.2	6.9E-01
ENSMUST00000034162	polyamine modulated factor 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1930136]	B2RR67	Q9WVQ0	8.4	1.8E-05	-3.9	2.2E-03	-1.1	7.1E-02	0.2	8.0E-01
ENSMUST00000033990	Werner syndrome homolog (human) [Source:MGI Symbol;Acc:MGI:109635]		O09053	1.2	5.0E-01	1.1	6.9E-01	1.4	5.2E-01	1.5	5.1E-01
ENSMUST00000033991	Werner syndrome homolog (human) [Source:MGI Symbol;Acc:MGI:109635]		O09053	-3.8	2.1E-01	0.7	8.4E-01	2.4	3.8E-01	-2.1	5.0E-01
ENSMUST00000034163	zinc finger protein 821 [Source:MGI Symbol;Acc:MGI:1923121]		Q6PD05	-2.5	1.5E-03	-4.5	1.2E-04	1.0	1.4E-02	-0.3	6.6E-01
ENSMUST00000033995	RNA binding protein gene with multiple splicing [Source:MGI Symbol;Acc:MGI:1334446]		Q9WVB0	1.3	5.4E-01	-0.7	7.9E-01	-1.5	4.5E-01	0.4	8.6E-01
ENSMUST00000034164	increased sodium tolerance 1 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1919205]		Q9CX00	-4.9	7.4E-06	-3.8	7.5E-04	-0.4	3.2E-01	-0.3	6.9E-01
ENSMUST00000034171	adaptor protein complex AP-1, gamma 1 subunit [Source:MGI Symbol;Acc:MGI:101919]		P22892	-7.6	6.2E-06	-5.0	1.5E-03	-1.1	7.5E-02	-2.4	8.1E-02
ENSMUST00000034172	carboxylesterase 1D [Source:MGI Symbol;Acc:MGI:2148202]		Q8VCT4	6.2	1.8E-04	-2.6	2.3E-02	-0.2	8.0E-01	-0.7	4.6E-01
ENSMUST00000034012	CCR4-NOT transcription complex, subunit 7 [Source:MGI Symbol;Acc:MGI:1298230]	Q543X5	Q60809	-5.5	1.9E-01	-5.7	2.7E-01	-1.0	6.5E-01	-0.8	8.9E-01
ENSMUST00000034173	carboxylesterase 1E [Source:MGI Symbol;Acc:MGI:95432]	Q3UN14	Q64176	6.3	3.2E-02	5.8	5.0E-04	-0.6	6.3E-01	-0.6	3.5E-01
ENSMUST00000034175	PH domain and leucine rich repeat protein phosphatase 2 [Source:MGI Symbol;Acc:MGI:2444928]		Q8BXA7	2.9	7.9E-04	-7.5	4.0E-05	-0.1	7.5E-01	-0.1	9.3E-01
ENSMUST00000034184	Iroquois related homeobox 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:1859086]		Q9JKQ4	6.4	3.5E-04	-3.8	9.5E-05	0.8	1.6E-02	-0.3	6.4E-01
ENSMUST00000034185	Iroquois related homeobox 6 (Drosophila) [Source:MGI Symbol;Acc:MGI:1927642]	Q8BFT1		7.7	6.1E-04	-3.1	4.9E-02	0.4	5.9E-01	-1.5	3.5E-01
ENSMUST00000034187	matrix metallopeptidase 2 [Source:MGI Symbol;Acc:MGI:97009]	Q3UG07	P33434	2.9	3.4E-04	-3.7	5.0E-04	0.4	2.7E-01	-1.2	1.3E-01
ENSMUST00000034189	carboxylesterase 1C [Source:MGI Symbol;Acc:MGI:95420]		P23953	4.9	1.9E-03	-4.8	6.8E-05	-0.5	1.8E-01	-0.6	4.2E-01
ENSMUST00000034026	hydroxyprostaglandin dehydrogenase 15 (NAD) [Source:MGI Symbol;Acc:MGI:108085]		Q8VCC1	0.9	2.8E-01	0.1	9.2E-01	-1.6	5.6E-02	-0.8	3.4E-01
ENSMUST00000034198	guanine nucleotide binding protein, alpha O [Source:MGI Symbol;Acc:MGI:95775]	Q543S2	P18872	3.3	3.4E-02	1.1	2.2E-01	-0.5	4.9E-01	0.4	6.3E-01
ENSMUST00000034030	transmembrane protein 184C [Source:MGI Symbol;Acc:MGI:2384562]		Q3TPR7	-1.5	3.8E-02	-0.8	3.3E-01	0.3	6.3E-01	-0.5	5.7E-01
ENSMUST00000034031	nuclear receptor subfamily 3, group C, member 2 [Source:MGI Symbol;Acc:MGI:99459]	E9Q8M8		5.1	6.5E-02	3.1	2.7E-01	-1.5	6.0E-01	0.5	8.0E-01
ENSMUST00000034203	component of oligomeric golgi complex 4 [Source:MGI Symbol;Acc:MGI:2142808]		Q8R1U1	-3.9	4.9E-05	6.1	5.7E-04	-0.5	7.2E-01	-0.4	5.5E-01
ENSMUST00000034204	nudix (nucleoside diphosphate linked moiety X)-type motif 21 [Source:MGI Symbol;Acc:MGI:1915469]		Q9CQF3	-1.2	1.3E-02	-3.3	7.1E-03	1.1	4.6E-02	-0.5	6.2E-01
ENSMUST00000034045	centromere protein U [Source:MGI Symbol;Acc:MGI:1919126]		Q8C4M7	-2.7	6.2E-02	-3.6	5.3E-02	-1.1	2.3E-01	-0.3	8.8E-01
ENSMUST00000034214	metallothionein 2 [Source:MGI Symbol;Acc:MGI:97172]		P02798	5.2	2.4E-03	-2.5	2.3E-02	1.8	9.3E-03	-4.4	9.6E-03
ENSMUST00000034048	cilia and flagella associated protein 97 [Source:MGI Symbol;Acc:MGI:1914006]		Q6ZPR1	-1.3	4.2E-01	-4.0	6.4E-02	-1.0	4.1E-01	1.8	3.9E-01
ENSMUST00000034218	solute carrier family 12, member 3 [Source:MGI Symbol;Acc:MGI:108114]	Q543E4	P59158	6.3	9.4E-05	-3.1	1.2E-03	-0.9	5.0E-02	0.1	8.3E-01
ENSMUST00000034219	synaptonemal complex central element protein 1 like [Source:MGI Symbol;Acc:MGI:1922247]		Q5D525	4.6	1.2E-03	-6.6	2.1E-04	-0.8	1.3E-01	-1.4	3.2E-01
ENSMUST00000034226	family with sequence similarity 192, member A [Source:MGI Symbol;Acc:MGI:1919637]		Q91WE2	-3.4	8.4E-05	5.1	1.4E-03	-1.4	2.8E-01	0.5	5.0E-01
ENSMUST00000034227	plasma membrane proteolipid [Source:MGI Symbol;Acc:MGI:1915051]		Q9DCU2	5.3	3.2E-05	1.4	4.9E-01	-4.9	5.8E-02	0.2	9.3E-01
ENSMUST00000034228	ADP-ribosylation factor-like 2 binding protein [Source:MGI Symbol;Acc:MGI:1349429]		Q9D385	-4.6	6.5E-04	7.3	3.0E-04	-0.7	6.2E-01	0.2	8.2E-01
ENSMUST00000034230	chemokine (C-X3-C motif) ligand 1 [Source:MGI Symbol;Acc:MGI:1097153]		O35188	8.8	1.6E-05	-5.0	6.8E-03	-0.8	2.4E-01	2.0	1.8E-01
ENSMUST00000034231	chemokine (C-C motif) ligand 22 [Source:MGI Symbol;Acc:MGI:1306779]	Q546S6	O88430	7.3	9.7E-06	4.5	1.2E-04	-0.2	7.7E-01	-0.6	2.7E-01
ENSMUST00000034232	chemokine (C-C motif) ligand 17 [Source:MGI Symbol;Acc:MGI:1329039]	F6R5P4		4.5	1.0E-03	4.6	7.9E-04	-1.7	1.3E-01	-0.5	4.7E-01
ENSMUST00000034065	NIMA (never in mitosis gene a)-related expressed kinase 1 [Source:MGI Symbol;Acc:MGI:97303]		P51954	-0.3	5.8E-01	0.9	2.0E-01	-0.2	7.5E-01	-1.5	5.0E-02
ENSMUST00000034233	cytokine induced apoptosis inhibitor 1 [Source:MGI Symbol;Acc:MGI:1922083]	F8WIK0		-4.6	5.1E-03	-1.5	5.4E-02	0.9	7.6E-02	0.7	3.3E-01
ENSMUST00000034234	coenzyme Q9 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1915164]		Q8K1Z0	-3.6	2.7E-04	6.2	1.5E-03	-0.4	7.9E-01	-0.9	2.6E-01
ENSMUST00000034079	HEAT repeat containing 3 [Source:MGI Symbol;Acc:MGI:2444491]		Q8BQM4	1.1	5.5E-02	1.0	1.0E-01	-1.0	5.3E-02	-0.9	1.1E-01
ENSMUST00000034243	matrix metallopeptidase 15 [Source:MGI Symbol;Acc:MGI:109320]		O54732	6.8	3.1E-06	-2.3	4.6E-03	0.3	3.7E-01	0.0	9.7E-01
ENSMUST00000034245	U6 snRNA biogenesis 1 [Source:MGI Symbol;Acc:MGI:2142454]			-4.6	4.8E-05	7.9	6.0E-05	-0.6	6.4E-01	0.1	8.6E-01
ENSMUST00000034249	cilia and flagella associated protein 20 [Source:MGI Symbol;Acc:MGI:107428]		Q8BTU1	-1.6	1.2E-02	-4.6	4.4E-05	0.4	1.6E-01	-0.4	5.3E-01
ENSMUST00000034260	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3 [Source:MGI Symbol;Acc:MGI:2152535]		Q5JCS9	3.3	1.4E-03	6.8	1.1E-04	-1.1	3.5E-01	-0.1	9.1E-01
ENSMUST00000034264	6-phosphogluconolactonase [Source:MGI Symbol;Acc:MGI:1913421]		Q9CQ60	-6.8	8.1E-05	-2.6	5.1E-03	0.8	5.4E-02	-0.1	8.6E-01
ENSMUST00000034267	solute carrier family 27 (fatty acid transporter), member 1 [Source:MGI Symbol;Acc:MGI:1347098]	Q544D7	Q60714	4.4	9.4E-05	-2.2	6.8E-03	0.5	2.1E-01	-1.3	8.4E-02
ENSMUST00000034094	GINS complex subunit 3 (Psf3 homolog) [Source:MGI Symbol;Acc:MGI:1926083]		Q9CY94	0.5	3.0E-01	1.5	2.0E-02	0.2	7.0E-01	-0.9	1.1E-01
ENSMUST00000034096	SET domain containing 6 [Source:MGI Symbol;Acc:MGI:1913333]		Q9CWY3	2.0	7.6E-02	3.5	3.8E-02	1.2	3.6E-01	-0.3	8.0E-01
ENSMUST00000034270	microtubule-associated protein 1 light chain 3 beta [Source:MGI Symbol;Acc:MGI:1914693]		Q9CQV6	-6.5	1.4E-06	-2.6	3.3E-03	1.2	9.9E-03	-0.1	8.4E-01
ENSMUST00000034272	multivesicular body subunit 12A [Source:MGI Symbol;Acc:MGI:1920961]		Q78HU3	-3.5	5.6E-04	5.0	1.9E-03	-2.0	1.5E-01	-0.6	4.3E-01
ENSMUST00000034111	ute carrier family 10 (sodium/bile acid cotransporter family), member 7 [Source:MGI Symbol;Acc:MGI:19240		Q5PT53	-0.9	7.0E-02	-0.1	8.4E-01	0.1	7.2E-01	-0.6	2.5E-01
ENSMUST00000034276	cytochrome c oxidase subunit IV isoform 1 [Source:MGI Symbol;Acc:MGI:88473]	A2RSV8	P19783	-9.4	1.5E-04	7.7	1.7E-04	-0.6	6.5E-01	0.6	3.7E-01
ENSMUST00000034277	ER membrane protein complex subunit 8 [Source:MGI Symbol;Acc:MGI:1343095]	Q3TPU5	O70378	3.7	1.1E-03	-4.6	6.1E-04	1.0	4.5E-02	0.3	7.5E-01
ENSMUST00000034280	zinc finger, DHHC domain containing 7 [Source:MGI Symbol;Acc:MGI:2142662]		Q91WU6	-2.5	3.6E-03	-5.4	5.5E-05	0.2	6.6E-01	-0.4	5.8E-01
ENSMUST00000034285	coactosin-like 1 (Dictyostelium) [Source:MGI Symbol;Acc:MGI:1919292]	Q544F6	Q9CQI6	-9.0	9.5E-05	-5.7	3.0E-04	-0.9	3.9E-02	2.7	2.1E-02
ENSMUST00000034296	osphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta) [Source:MGI Symbol;Acc:MGI:10987		O08908	-1.9	2.9E-02	7.8	2.8E-05	-0.5	6.3E-01	-2.0	4.5E-03
ENSMUST00000034299	interferon gamma inducible protein 30 [Source:MGI Symbol;Acc:MGI:2137648]		Q9ESY9	-5.8	1.6E-05	2.5	1.3E-02	-1.2	1.4E-01	0.0	9.7E-01
ENSMUST00000034300	heat shock factor binding protein 1 [Source:MGI Symbol;Acc:MGI:1915446]		Q9CQZ1	-5.4	1.1E-06	-3.4	8.0E-04	0.3	3.8E-01	-0.4	6.1E-01
ENSMUST00000034307	phosphodiesterase 4C, cAMP specific [Source:MGI Symbol;Acc:MGI:99556]		Q3UEI1	3.5	1.1E-03	-3.6	3.1E-04	0.4	2.0E-01	-0.7	3.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000034308	beta-carotene oxygenase 1 [Source:MGI Symbol;Acc:MGI:1926923]	Q05AC0	Q9JJS6	7.0	8.7E-05	-7.2	1.5E-04	0.9	6.8E-02	-1.0	5.1E-01
ENSMUST00000034145	TBC1 domain family, member 9 [Source:MGI Symbol;Acc:MGI:1918560]		Q3UYK3	2.9	1.7E-01	5.6	5.3E-02	0.8	7.5E-01	-1.9	2.9E-01
ENSMUST00000034311	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1354692]	Q9CY46		-3.3	6.6E-04	4.4	4.1E-04	-2.7	2.1E-02	-0.3	6.1E-01
ENSMUST00000034313	nucleoside-triphosphatase, cancer-related [Source:MGI Symbol;Acc:MGI:1913816]		Q9CQA9	-3.9	8.2E-05	-3.6	6.6E-04	-0.5	1.8E-01	-0.6	3.9E-01
ENSMUST00000034148	interleukin 15 [Source:MGI Symbol;Acc:MGI:103014]	Q3U1Z6	P48346	-1.0	2.2E-01	-1.1	2.5E-01	-0.8	2.2E-01	-0.7	4.9E-01
ENSMUST00000034150	growth factor receptor bound protein 2-associated protein 1 [Source:MGI Symbol;Acc:MGI:108088]	Q505A4	Q9QYY0	-0.7	1.0E-01	0.9	1.1E-01	1.2	1.2E-02	-0.4	4.1E-01
ENSMUST00000034316	cDNA sequence BC021891 [Source:MGI Symbol;Acc:MGI:2385307]		Q8VDG6	8.1	1.2E-05	-1.8	4.2E-02	0.5	2.7E-01	-0.6	4.7E-01
ENSMUST00000034326	ATPase type 13A1 [Source:MGI Symbol;Acc:MGI:2180801]		Q9EPE9	-1.3	2.5E-02	8.2	4.1E-05	-0.6	6.0E-01	-0.5	4.0E-01
ENSMUST00000034339	cadherin 5 [Source:MGI Symbol;Acc:MGI:105057]		P55284	6.2	2.5E-05	-1.2	1.0E-01	0.7	1.4E-01	-0.5	4.6E-01
ENSMUST00000034342	chemokine-like factor [Source:MGI Symbol;Acc:MGI:1922708]		Q9DAS1	-5.5	5.7E-06	-4.0	2.0E-04	0.5	1.4E-01	-0.4	5.8E-01
ENSMUST00000034343	CKLF-like MARVEL transmembrane domain containing 3 [Source:MGI Symbol;Acc:MGI:2447162]		Q99LJ5	-2.1	5.1E-03	-5.6	3.0E-04	0.8	4.0E-02	-1.1	3.3E-01
ENSMUST00000034346	carboxylesterase 2A [Source:MGI Symbol;Acc:MGI:2142491]		Q8QZR3	6.8	4.5E-05	5.3	6.1E-04	-1.3	2.7E-01	-0.5	4.6E-01
ENSMUST00000034349	NEDD8 activating enzyme E1 subunit 1 [Source:MGI Symbol;Acc:MGI:2384561]	Q3UK27	Q8VBW6	-7.6	3.0E-04	6.7	3.0E-02	-1.6	5.9E-01	-2.0	2.4E-01
ENSMUST00000034351	Ras-related associated with diabetes [Source:MGI Symbol;Acc:MGI:1930943]	Q6PGA2		3.1	3.3E-04	3.6	6.2E-04	-0.3	6.9E-01	-0.9	1.4E-01
ENSMUST00000034355	carboxylesterase 2E [Source:MGI Symbol;Acc:MGI:2443170]		Q8BK48	6.2	3.5E-03	6.1	7.6E-04	-0.9	5.3E-01	-0.5	4.6E-01
ENSMUST00000034359	TNFRSF1A-associated via death domain [Source:MGI Symbol;Acc:MGI:109200]	B2RRZ7	Q3U0V2	-3.1	8.4E-04	6.8	2.4E-03	-0.7	6.9E-01	0.2	8.4E-01
ENSMUST00000034361	RIKEN cDNA D230025D16 gene [Source:MGI Symbol;Acc:MGI:2443049]		Q922R1	-7.7	7.5E-06	1.8	1.6E-02	-1.0	9.6E-02	0.2	7.2E-01
ENSMUST00000034363	hydroxysteroid 11-beta dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:104720]		P51661	6.6	2.9E-05	2.4	4.0E-02	-3.4	1.8E-02	-0.9	2.9E-01
ENSMUST00000034190	Vac14 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2157980]		Q80WQ2	-0.8	1.2E-01	0.0	9.4E-01	0.8	7.0E-02	0.0	9.4E-01
ENSMUST00000034197	ST3 beta-galactoside alpha-2,3-sialyltransferase 2 [Source:MGI Symbol;Acc:MGI:99427]		Q11204	0.0	9.5E-01	1.0	1.7E-01	1.1	5.2E-02	0.1	8.7E-01
ENSMUST00000034365	translin-associated factor X (Tsnax) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1919486]		Q99P25	6.6	1.6E-04	4.9	4.8E-03	-1.6	2.7E-01	-3.2	1.5E-02
ENSMUST00000034368	chymotrypsin-like [Source:MGI Symbol;Acc:MGI:88558]	Q9ER05		4.4	7.5E-04	-4.1	1.9E-04	-0.1	7.4E-01	0.1	9.1E-01
ENSMUST00000034369	proteasome (prosome, macropain) subunit, beta type 10 [Source:MGI Symbol;Acc:MGI:1096380]		O35955	-2.4	1.3E-03	-0.6	2.3E-01	0.3	4.2E-01	-0.3	5.6E-01
ENSMUST00000034205	centromere protein N [Source:MGI Symbol;Acc:MGI:1919405]		Q9CZW2	0.4	5.6E-01	-0.2	8.1E-01	-0.8	1.9E-01	-0.3	7.1E-01
ENSMUST00000034206	Bardet-Biedl syndrome 2 (human) [Source:MGI Symbol;Acc:MGI:2135267]		Q9CWF6	0.4	5.1E-01	0.3	7.1E-01	0.2	7.6E-01	0.3	7.0E-01
ENSMUST00000034373	dipeptidase 2 [Source:MGI Symbol;Acc:MGI:2442042]		Q8C255	-6.4	1.0E-03	-3.4	5.1E-03	-9.0	2.0E-05	-0.5	6.3E-01
ENSMUST00000034215	metallothionein 1 [Source:MGI Symbol;Acc:MGI:97171]		P02802	-3.3	5.4E-02	-5.0	2.7E-02	-1.6	1.4E-01	0.1	9.5E-01
ENSMUST00000034377	phospholipase A2, group XV [Source:MGI Symbol;Acc:MGI:2178076]		Q8VEB4	-3.1	6.6E-04	6.5	2.8E-04	-0.3	7.6E-01	-0.5	4.7E-01
ENSMUST00000034378	e carrier family 7 (cationic amino acid transporter, y+ system), member 6 [Source:MGI Symbol;Acc:MGI:2142		Q8BGK6	1.6	3.3E-02	6.5	6.2E-04	1.2	3.8E-01	-0.7	3.4E-01
ENSMUST00000034220	inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 [Source:MGI Symbol;Acc:I	Q8C4N0		-0.3	9.0E-01	-3.4	2.6E-01	-2.4	2.7E-01	0.7	8.1E-01
ENSMUST00000034382	zinc finger protein 90 [Source:MGI Symbol;Acc:MGI:104786]		Q61967	3.1	1.1E-03	-3.2	1.1E-03	0.7	7.0E-02	0.5	4.6E-01
ENSMUST00000034385	hyaluronan synthase 3 [Source:MGI Symbol;Acc:MGI:109599]		O08650	6.5	1.4E-05	4.6	2.9E-04	-1.0	2.3E-01	-0.2	6.6E-01
ENSMUST00000034388	vacuolar protein sorting 4a (yeast) [Source:MGI Symbol;Acc:MGI:1890520]		Q8VEJ9	-3.5	8.1E-05	-1.3	2.2E-01	1.2	9.3E-02	-2.1	7.6E-02
ENSMUST00000034391	component of oligomeric golgi complex 8 [Source:MGI Symbol;Acc:MGI:2142885]		Q9JJA2	-7.9	6.6E-05	4.8	4.0E-04	-4.0	4.7E-03	0.0	1.0E+00
ENSMUST00000034396	myotubularin related protein 2 [Source:MGI Symbol;Acc:MGI:1924366]		Q9Z2D1	4.6	7.4E-04	4.3	1.4E-04	-3.2	3.0E-03	-0.2	6.5E-01
ENSMUST00000034400	cytochrome b5 type B [Source:MGI Symbol;Acc:MGI:1913677]		Q9CQX2	-1.3	5.4E-03	0.1	9.1E-01	-2.9	1.2E-02	1.5	1.6E-01
ENSMUST00000034405	meiotic recombination 11 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1100512]	Q3URU4	Q61216	-3.6	1.2E-03	-3.0	4.1E-02	0.2	8.1E-01	-1.4	3.7E-01
ENSMUST00000034406	ankyrin repeat domain 49 [Source:MGI Symbol;Acc:MGI:1930842]		Q8VE42	-2.2	4.3E-03	-1.7	4.8E-02	0.8	1.0E-01	-1.0	2.2E-01
ENSMUST00000034239	katanin p80 (WD40-containing) subunit B 1 [Source:MGI Symbol;Acc:MGI:1921437]		Q8BG40	-0.8	2.3E-01	1.1	2.4E-01	1.3	7.8E-02	-0.6	4.5E-01
ENSMUST00000034240	kinesin family member C3 [Source:MGI Symbol;Acc:MGI:109202]		O35231	-2.1	4.5E-02	-0.1	9.5E-01	0.5	5.4E-01	-1.6	1.7E-01
ENSMUST00000034408	G protein-coupled receptor 83 [Source:MGI Symbol;Acc:MGI:95712]	Q542Q9	P30731	4.4	2.9E-02	6.4	3.0E-05	-0.5	5.3E-01	-0.1	8.4E-01
ENSMUST00000034244	transmembrane protein 38A [Source:MGI Symbol;Acc:MGI:1921416]		Q3TMP8	-0.1	8.6E-01	0.4	5.4E-01	0.9	1.3E-01	0.3	6.3E-01
ENSMUST00000034411	mediator complex subunit 17 [Source:MGI Symbol;Acc:MGI:2182585]		Q8VCD5	-1.9	7.8E-04	-2.7	6.1E-03	0.9	7.0E-02	-1.0	2.4E-01
ENSMUST00000034413	V-set and transmembrane domain containing 5 [Source:MGI Symbol;Acc:MGI:1916387]		Q9D806	7.3	1.0E-04	-2.3	9.4E-03	0.0	9.2E-01	0.7	3.4E-01
ENSMUST00000034414	RIKEN cDNA 4931406C07 gene [Source:MGI Symbol;Acc:MGI:1918234]		Q91V76	7.3	7.4E-05	2.7	7.2E-03	-0.8	2.9E-01	-0.2	7.1E-01
ENSMUST00000034261	insulin-like 3 [Source:MGI Symbol;Acc:MGI:108427]	Q5RL10		-0.4	8.4E-01	0.8	7.4E-01	-0.1	9.4E-01	-1.3	5.2E-01
ENSMUST00000034415	\TA box binding protein (Tbp)-associated factor, RNA polymerase I, D [Source:MGI Symbol;Acc:MGI:19225(		Q9D4V4	-3.6	1.6E-02	-6.1	2.2E-04	0.6	2.3E-01	-0.2	8.7E-01
ENSMUST00000034265	RIKEN cDNA 1700018B08 gene [Source:MGI Symbol;Acc:MGI:1923655]	Q9DA83		2.5	6.4E-02	5.8	6.8E-04	-0.5	6.8E-01	-3.8	2.0E-03
ENSMUST00000034426	lysyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1934754]	Q3TIV6	Q99MN1	-4.6	3.7E-03	3.4	1.9E-03	-0.5	4.8E-01	0.4	4.8E-01
ENSMUST00000034427	adenosine deaminase, tRNA-specific 1 [Source:MGI Symbol;Acc:MGI:1353631]		Q9JHI2	5.7	1.3E-04	-5.8	2.7E-05	0.7	4.0E-02	0.0	9.5E-01
ENSMUST00000034428	amma-aminobutyric acid (GABA) A receptor-associated protein-like 2 [Source:MGI Symbol;Acc:MGI:189060		P60521	-3.9	3.5E-06	-2.2	2.4E-02	0.5	3.2E-01	-0.8	3.6E-01
ENSMUST00000034429	transmembrane protein 231 [Source:MGI Symbol;Acc:MGI:2685024]		Q3U284	5.7	2.2E-05	-7.8	6.9E-04	1.1	6.6E-02	-0.5	8.1E-01
ENSMUST00000034430	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5 [Source:MGI Symbol;Acc:MGI:1931825]		Q9QUP4	7.2	4.8E-05	3.0	1.1E-02	-0.6	4.8E-01	0.1	9.1E-01
ENSMUST00000034278	GINS complex subunit 2 (Psf2 homolog) [Source:MGI Symbol;Acc:MGI:1921019]		Q9D600	-1.0	4.2E-01	-0.9	5.4E-01	-0.8	4.5E-01	-0.9	5.2E-01
ENSMUST00000034279	genetic suppressor element 1 [Source:MGI Symbol;Acc:MGI:1098275]		Q3U3C9	0.6	4.8E-01	1.5	3.1E-01	1.5	2.3E-01	0.6	5.6E-01
ENSMUST00000034431	transmembrane protein 170 [Source:MGI Symbol;Acc:MGI:106426]		Q9D342	2.1	2.0E-02	-1.4	1.4E-01	1.2	4.5E-02	0.1	8.9E-01
ENSMUST00000034281	RIKEN cDNA 6430548M08 gene [Source:MGI Symbol;Acc:MGI:2443793]		Q8R0A7	-4.2	1.7E-01	1.7	7.7E-01	7.0	1.1E-01	1.0	8.2E-01
ENSMUST00000034282	cysteine-rich secretory protein LCCL domain containing 2 [Source:MGI Symbol;Acc:MGI:1926142]		Q8BZQ2	-2.9	1.8E-01	0.9	6.9E-01	1.0	5.3E-01	-2.8	2.6E-01
ENSMUST00000034432	craniofacial development protein 1 [Source:MGI Symbol;Acc:MGI:1344403]		O88271	-3.6	1.8E-04	-6.4	3.5E-03	1.5	5.1E-02	-1.1	5.5E-01
ENSMUST00000034287	kelch-like 36 [Source:MGI Symbol;Acc:MGI:2385305]		Q8R124	-0.7	3.0E-01	0.5	6.2E-01	1.4	6.7E-02	0.2	8.1E-01
ENSMUST00000034435	chymotrypsinogen B1 [Source:MGI Symbol;Acc:MGI:88559]		Q9CR35	6.4	1.3E-04	-1.0	3.2E-01	1.0	1.4E-01	0.1	9.4E-01
ENSMUST00000034437	WD repeat domain 59 [Source:MGI Symbol;Acc:MGI:2442115]	D3Z1F9		4.7	6.5E-04	-5.8	8.3E-05	-0.8	8.3E-02	-0.7	4.4E-01
ENSMUST00000034441	alanyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:2384560]		Q8BGQ7	-2.6	9.8E-04	-4.5	1.6E-05	-0.6	4.9E-02	-1.5	3.0E-02
ENSMUST00000034303	M phase phosphoprotein 6 [Source:MGI Symbol;Acc:MGI:1915783]		Q9D1Q1	-1.3	4.6E-02	-1.9	2.0E-02	-1.1	4.0E-02	-0.5	4.5E-01
ENSMUST00000034304	hydroxysteroid (17-beta) dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:1096386]		P51658	-0.3	6.3E-01	-0.3	7.3E-01	0.0	9.7E-01	-0.1	9.5E-01
ENSMUST00000034443	cadherin 15 [Source:MGI Symbol;Acc:MGI:106672]		P33146	8.1	1.5E-05	6.6	1.3E-04	2.1	6.4E-02	-1.0	1.2E-01
ENSMUST00000034448	galactosidase, beta 1 like 3 [Source:MGI Symbol;Acc:MGI:1918143]	F8WIH9		6.8	1.2E-04	7.9	1.3E-04	0.4	7.7E-01	-0.5	3.9E-01
ENSMUST00000034453	actin, alpha 1, skeletal muscle [Source:MGI Symbol;Acc:MGI:87902]		P68134	4.6	1.4E-04	-2.4	1.9E-02	0.7	2.0E-01	-0.2	8.0E-01
ENSMUST00000034458	acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI		Q6PB93	-5.1	1.2E-04	-3.3	3.9E-03	1.2	1.8E-02	0.7	4.6E-01
ENSMUST00000034460	component of oligomeric golgi complex 2 [Source:MGI Symbol;Acc:MGI:1923582]		Q921L5	-2.8	3.4E-04	7.4	3.4E-05	-1.3	2.4E-01	-0.6	2.2E-01
ENSMUST00000034325	lysophosphatidic acid receptor 2 [Source:MGI Symbol;Acc:MGI:1858422]	Q6P290		-1.6	3.4E-01	3.1	6.7E-02	-0.2	8.6E-01	-4.9	9.9E-03
ENSMUST00000034463	ARV1 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916115]	Q0VBH5	Q9D0U9	1.7	1.2E-02	-0.3	6.4E-01	0.7	1.4E-01	-0.3	6.0E-01
ENSMUST00000034328	integrator complex subunit 10 [Source:MGI Symbol;Acc:MGI:1918135]		Q8K2A7	1.7	2.4E-01	0.2	9.3E-01	2.2	2.0E-01	3.7	7.0E-02
ENSMUST00000034466	glyceronephosphate O-acyltransferase [Source:MGI Symbol;Acc:MGI:1343460]	Q545P6	P98192	-2.1	7.4E-04	4.5	3.6E-04	-1.9	4.4E-02	-0.2	6.9E-01
ENSMUST00000034469	egl-9 family hypoxia-inducible factor 1 [Source:MGI Symbol;Acc:MGI:1932286]		Q91YE3	-1.8	1.8E-03	-4.6	3.4E-04	0.6	1.2E-01	-0.2	7.9E-01
ENSMUST00000034470	vacuolar protein sorting 26 homolog B (yeast) [Source:MGI Symbol;Acc:MGI:1917656]		Q8C0E2	-2.7	3.2E-04	-1.7	4.8E-02	0.4	4.0E-01	-0.1	9.4E-01
ENSMUST00000034478	suppression of tumorigenicity 14 (colon carcinoma) [Source:MGI Symbol;Acc:MGI:1338881]	Q543E3	P56677	3.8	3.4E-04	2.3	9.0E-02	-0.5	6.2E-01	4.0	1.9E-03

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000034483	RIKEN cDNA 1700128F08 gene [Source:MGI Symbol;Acc:MGI:1923919]	Q9D970		10.9	1.8E-05	-3.9	5.4E-02	2.7	1.7E-02	-1.0	5.8E-01
ENSMUST00000034487	matrix metallopeptidase 20 (enamelysin) [Source:MGI Symbol;Acc:MGI:1353466]		P57748	7.0	5.0E-05	1.9	1.2E-02	-1.1	8.8E-02	0.1	8.1E-01
ENSMUST00000034497	matrix metallopeptidase 3 [Source:MGI Symbol;Acc:MGI:97010]	Q922W6		5.6	2.6E-04	5.1	1.7E-02	-0.6	7.6E-01	0.5	6.8E-01
ENSMUST00000034499	∛1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924		Q9CXV9	-5.0	2.6E-06	-1.5	8.8E-02	1.3	2.5E-02	-0.3	7.1E-01
ENSMUST00000034507	sestrin 3 [Source:MGI Symbol;Acc:MGI:1922997]	A2RSF4	Q9CYP7	1.7	5.5E-03	-4.6	2.4E-04	1.0	1.9E-02	-2.2	4.8E-02
ENSMUST00000034510	poliovirus receptor-related 1 [Source:MGI Symbol;Acc:MGI:1926483]		Q9JKF6	3.7	5.9E-04	5.4	1.9E-04	-1.4	1.6E-01	-0.1	7.9E-01
ENSMUST00000034511	tripartite motif-containing 29 [Source:MGI Symbol;Acc:MGI:1919419]		Q8R2Q0	7.4	6.1E-05	7.7	1.2E-04	-0.1	9.6E-01	-1.1	1.1E-01
ENSMUST00000034512	OAF homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:94852]		Q8QZR4	3.3	1.7E-03	3.8	4.3E-03	-1.2	2.5E-01	-0.5	4.9E-01
ENSMUST00000034513	POU domain, class 2, transcription factor 3 [Source:MGI Symbol;Acc:MGI:102565]	Q3U5D1		6.4	6.6E-04	-3.0	1.6E-03	-0.7	9.7E-02	-0.1	8.7E-01
ENSMUST00000034370	solute carrier family 12, member 4 [Source:MGI Symbol;Acc:MGI:1309465]	F8WIJ0		-1.7	5.6E-01	3.5	3.6E-01	3.8	2.7E-01	-1.3	6.5E-01
ENSMUST00000034371	dipeptidase 3 [Source:MGI Symbol;Acc:MGI:1919104]		Q9DA79	-0.3	7.0E-01	0.6	4.9E-01	0.8	2.4E-01	0.0	9.6E-01
ENSMUST00000034521	RIKEN cDNA 4931429I11 gene [Source:MGI Symbol;Acc:MGI:1918239]	E9Q793		5.8	1.8E-04	-8.0	4.6E-03	-0.1	8.7E-01	1.5	5.3E-01
ENSMUST00000034375	dihydrouridine synthase 2 [Source:MGI Symbol;Acc:MGI:1913619]	Q14A90	Q9D7B1	-1.1	6.5E-02	-3.6	9.4E-03	0.6	2.6E-01	3.0	1.7E-02
ENSMUST00000034524	REX2, RNA exonuclease 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1888981]		Q9D8S4	-2.7	3.7E-04	-1.7	7.5E-02	1.6	8.9E-03	0.2	7.9E-01
ENSMUST00000034527	neurexophilin and PC-esterase domain family, member 2 [Source:MGI Symbol;Acc:MGI:1925502]			5.7	7.1E-04	1.5	1.1E-01	-0.1	8.8E-01	0.1	9.4E-01
ENSMUST00000034529	cullin 5 [Source:MGI Symbol;Acc:MGI:1922967]	G3X914		-3.7	1.4E-03	1.2	1.0E-01	-2.0	1.3E-02	-0.1	8.8E-01
ENSMUST00000034533	potassium inwardly-rectifying channel, subfamily J, member 5 [Source:MGI Symbol;Acc:MGI:104755]		P48545	7.4	1.3E-05	5.7	2.9E-04	-0.7	4.9E-01	0.0	9.4E-01
ENSMUST00000034534	E26 avian leukemia oncogene 1, 5' domain [Source:MGI Symbol;Acc:MGI:95455]	Q540Q5	P27577	-2.1	1.0E-02	-2.7	2.4E-03	0.5	1.5E-01	-0.3	7.0E-01
ENSMUST00000034537	ST3 beta-galactoside alpha-2,3-sialyltransferase 4 [Source:MGI Symbol;Acc:MGI:1316743]		Q91Y74	-5.2	1.4E-05	-5.6	3.6E-03	1.6	1.6E-02	-0.7	6.6E-01
ENSMUST00000034392	nuclear import 7 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913414]		Q9CXK8	-1.3	5.1E-02	-1.8	4.7E-02	-0.4	4.6E-01	0.1	8.8E-01
ENSMUST00000034539	decapping enzyme, scavenger [Source:MGI Symbol;Acc:MGI:1916555]		Q9DAR7	-3.7	2.0E-05	4.1	3.1E-03	-0.4	7.0E-01	0.1	9.0E-01
ENSMUST00000034398	centrosomal protein 57 [Source:MGI Symbol;Acc:MGI:1915551]		Q8CEE0	2.5	1.2E-01	-2.7	1.6E-01	-4.4	1.1E-02	0.9	6.1E-01
ENSMUST00000034541	signal recognition particle receptor ('docking protein') [Source:MGI Symbol;Acc:MGI:1914648]		Q9DBG7	-3.3	3.4E-04	-0.5	2.7E-01	0.3	3.6E-01	-0.5	2.7E-01
ENSMUST00000034543	RNA pseudouridylate synthase domain containing 4 [Source:MGI Symbol;Acc:MGI:1919239]		Q9CWX4	-1.5	1.8E-02	-4.4	2.5E-03	-0.5	3.5E-01	0.3	8.1E-01
ENSMUST00000034554	POU domain, class 2, associating factor 1 [Source:MGI Symbol;Acc:MGI:105086]	Q542H4	Q64693	1.6	1.3E-02	-1.8	3.1E-02	-0.3	4.9E-01	-0.8	2.8E-01
ENSMUST00000034562	crystallin, alpha B [Source:MGI Symbol;Acc:MGI:88516]	Q52L78	P23927	2.8	2.6E-03	7.8	3.4E-03	1.0	6.3E-01	-2.5	1.1E-01
ENSMUST00000034409	IZUMO1 receptor, JUNO [Source:MGI Symbol;Acc:MGI:1929185]		Q9EQF4	0.4	7.3E-01	2.7	4.4E-02	-0.2	8.4E-01	-2.5	3.9E-02
ENSMUST00000034564	RIKEN cDNA 2310030G06 gene [Source:MGI Symbol;Acc:MGI:1914202]		Q9D8L0	5.2	1.3E-03	-1.0	6.3E-02	0.6	1.1E-01	-0.3	4.9E-01
ENSMUST00000034567	ɔamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Source:MGI Symbol;Acc:MG		Q8BMF4	-1.2	3.3E-02	7.7	1.7E-04	-0.2	8.9E-01	-0.5	4.3E-01
ENSMUST00000034570	6-pyruvoyl-tetrahydropterin synthase [Source:MGI Symbol;Acc:MGI:1338783]		Q9R1Z7	-4.5	2.9E-04	5.8	7.3E-04	-0.7	6.0E-01	0.8	2.3E-01
ENSMUST00000034583	ZPR1 zinc finger [Source:MGI Symbol;Acc:MGI:1330262]	F8WIG4		-5.0	8.4E-05	-3.6	2.9E-02	-1.0	2.5E-01	-1.0	5.4E-01
ENSMUST00000034585	apolipoprotein A-IV [Source:MGI Symbol;Acc:MGI:88051]		P06728	8.0	3.1E-04	-4.2	1.9E-02	-0.7	3.8E-01	-1.0	5.2E-01
ENSMUST00000034588	apolipoprotein A-I [Source:MGI Symbol;Acc:MGI:88049]		Q00623	5.1	9.7E-03	3.8	4.9E-03	-0.8	4.5E-01	1.1	1.7E-01
ENSMUST00000034591	beta-site APP cleaving enzyme 1 [Source:MGI Symbol;Acc:MGI:1346542]		P56818	2.5	2.1E-04	-3.8	4.1E-05	0.1	6.3E-01	0.0	9.5E-01
ENSMUST00000034592	Down syndrome cell adhesion molecule like 1 [Source:MGI Symbol;Acc:MGI:2150309]	E9QPR7		9.7	5.5E-06	4.2	4.8E-04	-1.3	1.2E-01	0.2	7.0E-01
ENSMUST00000034594	interleukin 10 receptor, alpha [Source:MGI Symbol;Acc:MGI:96538]	Q3UDL4	Q61727	-5.4	1.2E-02	6.8	2.0E-04	-0.2	8.9E-01	0.3	6.8E-01
ENSMUST00000034597	transmembrane protease, serine 13 [Source:MGI Symbol;Acc:MGI:2682935]	E9QPR6		7.8	7.2E-05	2.4	5.9E-02	1.4	1.4E-01	1.2	2.3E-01
ENSMUST00000034600	myelin protein zero-like 2 [Source:MGI Symbol;Acc:MGI:1289160]	Q91WI4		6.2	3.6E-04	-4.4	1.7E-04	-1.5	4.6E-03	-0.6	4.0E-01
ENSMUST00000034607	archain 1 [Source:MGI Symbol;Acc:MGI:2387591]		Q5XJY5	-2.6	3.7E-04	7.0	1.3E-04	-0.5	6.5E-01	-1.1	1.0E-01
ENSMUST00000034612	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 [Source:MGI Symbol;Acc:MGI:1353582]		Q9QY15	3.5	8.0E-04	5.1	6.6E-03	1.5	3.0E-01	1.1	2.1E-01
ENSMUST00000034615	pseudouridine synthase 3 [Source:MGI Symbol;Acc:MGI:1914299]		Q9JI38	-4.4	2.6E-03	-1.5	3.9E-02	0.6	1.8E-01	-0.5	4.8E-01
ENSMUST00000034621	NLR family member X1 [Source:MGI Symbol;Acc:MGI:2429611]		Q3TL44	-2.4	8.0E-03	7.3	5.8E-05	-0.9	4.3E-01	-0.1	8.4E-01
ENSMUST00000034623	trafficking protein particle complex 4 [Source:MGI Symbol;Acc:MGI:1926211]	Q544R8	Q9ES56	-5.0	2.2E-06	6.6	3.0E-04	-0.5	6.8E-01	-0.3	6.5E-01
ENSMUST00000034452	centriole, cilia and spindle associated protein [Source:MGI Symbol;Acc:MGI:1920670]		Q8QZT2	-0.9	3.5E-01	0.0	9.7E-01	0.7	4.2E-01	-0.2	8.6E-01
ENSMUST00000034630	fasciculation and elongation protein zeta 1 (zygin I) [Source:MGI Symbol;Acc:MGI:2670976]		Q8K0X8	3.9	2.8E-02	6.4	2.2E-04	1.3	2.0E-01	-0.5	4.5E-01
ENSMUST00000034457	URB2 ribosome biogenesis 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2681124]	E9Q7L1		-2.1	1.6E-01	0.8	7.1E-01	1.5	3.7E-01	-1.4	4.1E-01
ENSMUST00000034644	vacuolar protein sorting 11 (yeast) [Source:MGI Symbol;Acc:MGI:1918982]		Q91W86	-2.2	1.6E-04	-4.3	2.5E-03	1.0	6.5E-02	0.2	8.7E-01
ENSMUST00000034648	ATP-binding cassette, sub-family G (WHITE), member 4 [Source:MGI Symbol;Acc:MGI:1890594]	Q91WA9		5.7	8.5E-03	-1.3	6.7E-02	0.8	7.4E-02	-0.8	2.2E-01
ENSMUST00000034650	melanoma cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1933966]		Q8R2Y2	-5.6	9.1E-04	0.6	3.7E-01	-0.8	1.6E-01	0.3	5.8E-01
ENSMUST00000034464	RIKEN cDNA 2310022B05 gene [Source:MGI Symbol;Acc:MGI:1916801]		Q8C3W1	-1.0	1.3E-01	0.4	5.9E-01	1.0	1.2E-01	-0.5	5.4E-01
ENSMUST00000034465	RIKEN cDNA 2810004N23 gene [Source:MGI Symbol;Acc:MGI:1913773]		Q8CIL4	-0.2	7.2E-01	-0.5	3.3E-01	0.0	9.2E-01	0.4	4.1E-01
ENSMUST00000034692	olfactomedin 2 [Source:MGI Symbol;Acc:MGI:3045350]		Q8BM13	7.4	7.0E-05	-1.0	1.1E-01	0.9	2.6E-02	-0.3	6.4E-01
ENSMUST00000034467	SprT-like N-terminal domain [Source:MGI Symbol;Acc:MGI:2685351]		G3X912	-0.9	7.4E-02	-0.4	4.9E-01	0.8	1.0E-01	0.3	6.6E-01
ENSMUST00000034697	solute carrier family 44, member 2 [Source:MGI Symbol;Acc:MGI:1915932]		Q8BY89	-4.9	6.7E-05	-1.0	8.8E-02	0.8	4.7E-02	0.0	9.7E-01
ENSMUST00000034699	secretogranin III [Source:MGI Symbol;Acc:MGI:103032]		P47867	7.2	4.9E-05	-1.5	4.1E-02	1.4	7.8E-03	0.2	8.1E-01
ENSMUST00000034472	junction adhesion molecule 3 [Source:MGI Symbol;Acc:MGI:1933825]		Q9D8B7	0.0	9.5E-01	1.5	8.1E-02	0.7	2.7E-01	-0.8	2.5E-01
ENSMUST00000034707	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 [Source:MGI Symbol;Ac		Q3TKT4	8.7	2.7E-04	3.6	1.0E-03	-0.7	3.4E-01	-0.5	4.5E-01
ENSMUST00000034709	Bcl2-like 10 [Source:MGI Symbol;Acc:MGI:1330841]		Q9Z0F3	4.3	9.9E-04	9.4	1.1E-04	-0.8	6.1E-01	0.7	3.4E-01
ENSMUST00000034713	low density lipoprotein receptor [Source:MGI Symbol;Acc:MGI:96765]		P35951	-1.1	2.9E-02	6.9	1.1E-04	-0.5	6.5E-01	-0.5	4.5E-01
ENSMUST00000034717	KN motif and ankyrin repeat domains 2 [Source:MGI Symbol;Acc:MGI:2384568]		Q8BX02	6.8	7.6E-06	-3.4	4.4E-04	-9.3	2.6E-06	-0.3	6.9E-01
ENSMUST00000034720	polymerase (RNA) II (DNA directed) polypeptide M [Source:MGI Symbol;Acc:MGI:107282]		Q6P6I6	-5.6	2.0E-04	-2.9	9.7E-04	1.3	3.1E-03	-0.8	1.9E-01
ENSMUST00000034722	RAB27A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1861441]	Q544U7	Q9ERI2	-3.7	1.7E-04	0.9	1.5E-01	-0.7	1.8E-01	0.1	8.2E-01
ENSMUST00000034508	ubiquitin specific peptidase 2 [Source:MGI Symbol;Acc:MGI:1858178]		O88623	-1.4	1.4E-01	-0.1	9.6E-01	1.4	1.2E-01	0.1	9.5E-01
ENSMUST00000034723	aldehyde dehydrogenase family 1, subfamily A2 [Source:MGI Symbol;Acc:MGI:107928]		Q62148	6.6	2.3E-04	3.6	2.5E-03	-0.1	8.7E-01	-0.1	9.4E-01
ENSMUST00000034728	dedicator of cytokinesis 6 [Source:MGI Symbol;Acc:MGI:1914789]	E9QPN7		5.1	7.4E-06	6.3	1.6E-04	-1.4	2.4E-01	-0.3	6.7E-01
ENSMUST00000034731	lipase, hepatic [Source:MGI Symbol;Acc:MGI:96216]		P27656	2.9	2.3E-03	0.2	7.5E-01	-2.7	3.3E-03	0.3	6.9E-01
ENSMUST00000034734	dyslexia susceptibility 1 candidate 1 homolog (human) [Source:MGI Symbol;Acc:MGI:1914935]		Q8R368	6.2	5.8E-04	7.2	4.9E-04	-0.7	6.6E-01	-1.5	8.3E-02
ENSMUST00000034738	ribosomal L24 domain containing 1 [Source:MGI Symbol;Acc:MGI:2681840]	Q5EBK7	Q99L28	-3.2	2.6E-04	1.8	7.2E-02	-3.3	6.3E-03	0.7	4.0E-01
ENSMUST00000034522	CXADR-like membrane protein [Source:MGI Symbol;Acc:MGI:1918816]		Q8R373	0.6	4.9E-01	1.5	1.9E-01	0.4	6.4E-01	-0.5	6.3E-01
ENSMUST00000034740	neural precursor cell expressed, developmentally down-regulated 4 [Source:MGI Symbol;Acc:MGI:97297]	B2RSC8	P46935	-1.5	1.2E-02	-2.3	3.3E-03	-0.4	3.1E-01	-0.8	2.3E-01
ENSMUST00000034742	cyclin B2 [Source:MGI Symbol;Acc:MGI:88311]		P30276	-2.2	5.2E-04	4.5	3.1E-03	-2.6	5.9E-02	-1.4	1.0E-01
ENSMUST00000034745	myosin IE [Source:MGI Symbol;Acc:MGI:106621]		E9Q634	2.1	5.3E-04	-1.7	8.0E-02	0.7	2.3E-01	-1.3	2.0E-01
ENSMUST00000034746	meiosis-specific nuclear structural protein 1 [Source:MGI Symbol;Acc:MGI:107933]		Q61884	1.6	2.1E-02	8.8	1.1E-04	1.7	2.3E-01	0.3	6.0E-01
ENSMUST00000034749	family with sequence similarity 81, member A [Source:MGI Symbol;Acc:MGI:1924136]		Q3UXZ6	7.6	4.2E-05	-1.5	9.9E-02	0.3	5.7E-01	-0.3	7.5E-01
ENSMUST00000034751	glucosaminyl (N-acetyl) transferase 3, mucin type [Source:MGI Symbol;Acc:MGI:1919327]		Q5JCT0	8.2	8.3E-06	-4.9	2.4E-04	0.7	7.6E-02	0.5	5.9E-01
ENSMUST00000034754	BCL2/adenovirus E1B interacting protein 2 [Source:MGI Symbol;Acc:MGI:109327]		O54940	-6.4	1.3E-04	-2.5	7.7E-04	-0.8	2.6E-02	-2.0	5.5E-03
ENSMUST00000034756	annexin A2 [Source:MGI Symbol;Acc:MGI:88246]	Q542G9	P07356	-11.6	1.4E-06	-2.3	1.2E-02	0.6	1.6E-01	-0.4	5.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000034763	retinitis pigmentosa 9 (human) [Source:MGI Symbol;Acc:MGI:2157166]	Q3TH81	P97762	-3.7	3.4E-04	-1.4	5.7E-02	-0.2	6.2E-01	-0.3	6.2E-01
ENSMUST00000034547	acetyl-Coenzyme A acetyltransferase 1 [Source:MGI Symbol;Acc:MGI:87870]		Q8QZT1	-1.1	4.1E-02	-2.2	4.1E-03	-1.5	2.7E-03	-0.4	4.7E-01
ENSMUST00000034766	RAR-related orphan receptor alpha [Source:MGI Symbol;Acc:MGI:104661]		P51448	4.9	3.4E-05	0.8	2.4E-01	-1.2	4.5E-02	-0.3	5.8E-01
ENSMUST00000034560	protein phosphatase 2, regulatory subunit A, beta [Source:MGI Symbol;Acc:MGI:1920949]	Q3TTF6		-0.7	5.4E-01	-1.4	3.7E-01	-0.6	5.4E-01	0.0	9.8E-01
ENSMUST00000034561	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase) [Source:MGI Symbol;Acc:MGI:1924753]		Q8VDI9	-0.9	4.5E-01	-2.9	1.7E-01	-0.2	8.3E-01	1.7	3.7E-01
ENSMUST00000034774	integrin alpha 11 [Source:MGI Symbol;Acc:MGI:2442114]	A0A0B4J1F0		8.7	7.7E-06	0.7	3.4E-01	-2.0	1.5E-02	0.1	9.1E-01
ENSMUST00000034787	pleckstrin homology domain interacting protein [Source:MGI Symbol;Acc:MGI:1932404]	F8VQ93		-4.5	5.2E-06	2.0	4.3E-02	-4.2	3.7E-03	-1.0	2.0E-01
ENSMUST00000034791	Leber congenital amaurosis 5 (human) [Source:MGI Symbol;Acc:MGI:1923032]	G5E886		4.6	9.6E-04	-0.1	8.7E-01	0.9	7.3E-02	-0.2	7.1E-01
ENSMUST00000034792	ankyrin repeat and kinase domain containing 1 [Source:MGI Symbol;Acc:MGI:3045301]		Q8BZ25	7.8	1.9E-05	-3.8	3.2E-03	0.0	9.2E-01	-0.7	4.9E-01
ENSMUST00000034796	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 [Source:MGI Symbol;Acc:MGI:193		Q9EQC4	4.0	1.4E-03	-5.5	3.1E-04	-0.6	1.5E-01	-0.1	9.3E-01
ENSMUST00000034584	apolipoprotein A-V [Source:MGI Symbol;Acc:MGI:1913363]		Q8C7G5	3.4	2.3E-01	1.2	6.2E-01	-3.7	1.8E-01	-1.5	4.9E-01
ENSMUST00000034801	branched chain ketoacid dehydrogenase E1, beta polypeptide [Source:MGI Symbol;Acc:MGI:88137]		Q6P3A8	2.6	3.4E-02	5.9	1.3E-03	-2.7	1.1E-01	-0.6	4.7E-01
ENSMUST00000034802	family with sequence similarity 46, member A [Source:MGI Symbol;Acc:MGI:2670964]	D3Z5S8		-3.7	1.8E-02	-0.5	7.1E-01	-6.3	2.8E-03	-0.6	6.2E-01
ENSMUST00000034590	transgelin [Source:MGI Symbol;Acc:MGI:106012]		P37804	-0.2	7.6E-01	0.5	4.9E-01	0.4	5.0E-01	-0.3	6.5E-01
ENSMUST00000034803	zw10 kinetochore protein [Source:MGI Symbol;Acc:MGI:1349478]		O54692	-1.2	2.2E-02	1.9	6.2E-03	-0.1	8.7E-01	0.5	2.9E-01
ENSMUST00000034811	cytochrome P450, family 19, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88587]	Q3ZAT3	P28649	8.8	3.0E-05	9.3	1.6E-05	-0.7	6.0E-01	-0.3	5.8E-01
ENSMUST00000034815	kinesin family member 23 [Source:MGI Symbol;Acc:MGI:1919069]		E9Q5G3	-3.4	9.5E-05	-3.2	1.0E-01	0.4	7.1E-01	-1.8	4.1E-01
ENSMUST00000034817	progestin and adipoQ receptor family member V [Source:MGI Symbol;Acc:MGI:1921340]		Q9DCU0	8.1	3.4E-04	8.6	4.0E-04	1.2	4.6E-01	0.4	5.7E-01
ENSMUST00000034599	transmembrane protease, serine 4 [Source:MGI Symbol;Acc:MGI:2384877]		Q8VCA5	3.7	1.3E-01	6.9	1.9E-02	-0.3	9.2E-01	-3.4	4.3E-02
ENSMUST00000034822	acyl-CoA synthetase bubblegum family member 1 [Source:MGI Symbol;Acc:MGI:2385656]		Q99PU5	3.7	3.5E-04	5.4	4.4E-03	-1.0	4.8E-01	-0.2	8.2E-01
ENSMUST00000034602	CD3 antigen, delta polypeptide [Source:MGI Symbol;Acc:MGI:88331]	Q3U4T1	P04235	-0.3	4.9E-01	-1.1	1.1E-01	-0.7	1.4E-01	0.0	9.7E-01
ENSMUST00000034827	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916119]		Q921Y2	-4.1	8.6E-04	-1.6	2.2E-02	0.5	1.7E-01	-0.4	4.5E-01
ENSMUST00000034611	pleckstrin homology-like domain, family B, member 1 [Source:MGI Symbol;Acc:MGI:2143230]		Q6PDH0	4.9	8.8E-02	7.3	2.9E-02	-0.2	9.5E-01	-2.6	1.2E-01
ENSMUST00000034830	cellular retinoic acid binding protein I [Source:MGI Symbol;Acc:MGI:88490]		P62965	7.3	4.6E-05	3.2	2.5E-03	-0.6	4.3E-01	-0.3	6.4E-01
ENSMUST00000034832	protein tyrosine phosphatase, non-receptor type 9 [Source:MGI Symbol;Acc:MGI:1928376]	Q2M4G8	O35239	-1.6	6.8E-03	-4.5	1.1E-02	-0.3	6.3E-01	-0.3	8.6E-01
ENSMUST00000034618	PDZ domain containing 3 [Source:MGI Symbol;Acc:MGI:2429554]			0.0	9.9E-01	1.0	4.1E-01	0.2	8.5E-01	-0.8	4.6E-01
ENSMUST00000034834	pyruvate kinase, muscle [Source:MGI Symbol;Acc:MGI:97591]		P52480	-7.2	7.6E-07	-1.2	2.7E-01	1.6	3.3E-02	0.3	7.5E-01
ENSMUST00000034836	mannosidase, alpha, class 2C, member 1 [Source:MGI Symbol;Acc:MGI:1920994]	F8WIE1		-4.8	1.5E-02	-4.6	2.9E-05	0.2	6.0E-01	-0.3	6.0E-01
ENSMUST00000034625	checkpoint kinase 1 [Source:MGI Symbol;Acc:MGI:1202065]		O35280	5.2	1.0E-01	3.1	2.7E-01	-2.6	4.0E-01	-0.5	8.1E-01
ENSMUST00000034629	histone H4 transcription factor [Source:MGI Symbol;Acc:MGI:2429620]		Q8K1K9	-0.5	3.7E-01	-0.5	5.3E-01	0.7	1.8E-01	0.7	3.1E-01
ENSMUST00000034843	iron responsive element binding protein 2 [Source:MGI Symbol;Acc:MGI:1928268]		Q811J3	-3.5	2.8E-05	4.9	9.9E-03	-0.6	7.1E-01	-1.6	1.8E-01
ENSMUST00000034632	transmembrane protein 218 [Source:MGI Symbol;Acc:MGI:1913529]		Q9CQ44	0.3	5.1E-01	0.1	8.7E-01	-0.6	2.6E-01	-0.3	5.8E-01
ENSMUST00000034848	proteasome (prosome, macropain) subunit, alpha type 4 [Source:MGI Symbol;Acc:MGI:1347060]		Q9R1P0	-7.0	6.3E-05	-1.6	7.6E-03	0.5	8.2E-02	-0.1	8.4E-01
ENSMUST00000034851	cholinergic receptor, nicotinic, alpha polypeptide 3 [Source:MGI Symbol;Acc:MGI:87887]	Q0VBK4		7.3	4.5E-05	6.6	5.8E-03	-0.7	7.4E-01	-1.6	1.7E-01
ENSMUST00000034854	cholinergic receptor, nicotinic, beta polypeptide 4 [Source:MGI Symbol;Acc:MGI:87892]	Q3USV2	Q8R493	7.9	3.0E-06	-5.4	1.8E-02	1.6	5.3E-02	1.4	5.0E-01
ENSMUST00000034654	membrane-type frizzled-related protein [Source:MGI Symbol;Acc:MGI:2385957]		Q8K480	1.2	4.7E-01	5.5	1.4E-02	1.1	5.3E-01	-3.2	4.6E-02
ENSMUST00000034689	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 [Source:MGI Symbol;Acc:MGI:1346036]		Q9QUR7	-0.8	1.3E-01	-0.8	2.1E-01	0.1	8.9E-01	0.1	8.5E-01
ENSMUST00000034859	F-box protein 22 [Source:MGI Symbol;Acc:MGI:1926014]		Q78JE5	-3.6	8.8E-03	6.3	2.6E-04	-1.5	2.4E-01	-0.4	5.0E-01
ENSMUST00000034860	cytochrome P450, family 1, subfamily a, polypeptide 2 [Source:MGI Symbol;Acc:MGI:88589]	B6VGH4	P00186	6.8	8.1E-05	-3.2	5.3E-03	1.3	2.2E-02	-0.4	6.6E-01
ENSMUST00000034698	transmembrane emp24 domain containing 1 [Source:MGI Symbol;Acc:MGI:106201]	B2RRM5	Q3V009	-0.2	7.1E-01	-0.7	3.5E-01	-0.7	2.3E-01	-0.2	8.2E-01
ENSMUST00000034863	c-src tyrosine kinase [Source:MGI Symbol;Acc:MGI:88537]		P41241	-4.8	6.6E-05	6.8	1.5E-04	-0.6	6.2E-01	-0.2	7.8E-01
ENSMUST00000034700	Yip1 domain family, member 2 [Source:MGI Symbol;Acc:MGI:1922016]		Q99LP8	2.4	4.3E-02	3.5	6.7E-02	2.7	9.3E-02	1.7	1.9E-01
ENSMUST00000034865	cytochrome P450, family 1, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88588]	Q05A20	P00184	6.4	1.9E-04	4.4	9.7E-03	-3.9	3.7E-02	0.4	6.6E-01
ENSMUST00000034866	electron transferring flavoprotein, alpha polypeptide [Source:MGI Symbol;Acc:MGI:106092]		Q99LC5	-3.9	5.4E-04	4.5	7.1E-04	-0.9	3.6E-01	-1.0	1.5E-01
ENSMUST00000034868	CDC-like kinase 1 [Source:MGI Symbol;Acc:MGI:107403]		P22518	-8.9	9.1E-05	-0.5	4.2E-01	1.0	3.4E-02	0.4	5.2E-01
ENSMUST00000034878	transmembrane protein 30A [Source:MGI Symbol;Acc:MGI:106402]		Q8VEK0	-9.6	1.5E-05	3.7	7.2E-04	-2.5	1.0E-02	0.6	3.0E-01
ENSMUST00000034879	high mobility group 20A [Source:MGI Symbol;Acc:MGI:1914117]		Q9DC33	-1.7	5.1E-03	-2.7	1.3E-02	1.0	7.9E-02	-1.9	1.1E-01
ENSMUST00000034880	stimulated by retinoic acid gene 6 [Source:MGI Symbol;Acc:MGI:107742]			7.6	2.3E-05	-2.3	1.3E-02	1.1	4.1E-02	-0.2	7.6E-01
ENSMUST00000034881	cytochrome c oxidase subunit VIIa 2 [Source:MGI Symbol;Acc:MGI:1316715]		P48771	-6.2	6.4E-05	2.2	2.5E-02	-4.9	1.4E-03	-0.5	5.2E-01
ENSMUST00000034889	hyperpolarization-activated, cyclic nucleotide-gated K+ 4 [Source:MGI Symbol;Acc:MGI:1298209]	B2RY58		7.4	8.9E-06	4.7	3.0E-05	-0.7	2.9E-01	-0.3	4.9E-01
ENSMUST00000034898	Mab-21 domain containing 1 [Source:MGI Symbol;Acc:MGI:2442261]	D3Z5R0		6.0	4.3E-03	2.2	2.0E-02	-1.2	1.1E-01	-0.5	4.6E-01
ENSMUST00000034900	oocyte expressed protein [Source:MGI Symbol;Acc:MGI:1915218]		Q9CWE6	5.9	9.7E-06	4.3	2.2E-02	0.3	8.5E-01	2.3	6.1E-02
ENSMUST00000034737	KH domain containing 3, subcortical maternal complex member [Source:MGI Symbol;Acc:MGI:1914241]		Q9CWU5	-0.6	4.9E-01	1.6	2.0E-01	1.0	3.0E-01	-1.2	2.6E-01
ENSMUST00000034904	ELOVL family member 5, elongation of long chain fatty acids (yeast) [Source:MGI Symbol;Acc:MGI:1916051		Q8BHI7	-3.6	1.7E-05	-3.0	2.7E-03	0.7	9.7E-02	0.5	5.4E-01
ENSMUST00000034739	ring finger 111 [Source:MGI Symbol;Acc:MGI:1934919]		Q99ML9	-2.0	4.3E-02	-0.9	4.9E-01	1.7	5.2E-02	0.6	6.5E-01
ENSMUST00000034912	RAS protein-specific guanine nucleotide-releasing factor 1 [Source:MGI Symbol;Acc:MGI:99694]	B2RS27	P27671	8.3	1.1E-05	-1.2	8.2E-02	0.2	6.4E-01	-0.1	8.6E-01
ENSMUST00000034913	family with sequence similarity 195, member B [Source:MGI Symbol;Acc:MGI:2384752]		Q3UGS4	-6.3	1.0E-03	-2.0	5.2E-03	0.4	2.9E-01	0.2	7.7E-01
ENSMUST00000034915	cathepsin H [Source:MGI Symbol;Acc:MGI:107285]		P49935	-2.3	2.2E-03	1.6	1.2E-02	-0.2	6.0E-01	0.3	5.7E-01
ENSMUST00000034927	zinc finger protein of the cerebellum 1 [Source:MGI Symbol;Acc:MGI:106683]		P46684	5.4	5.3E-05	1.6	2.9E-02	-0.7	2.3E-01	-0.8	2.0E-01
ENSMUST00000034929	lactamase, beta [Source:MGI Symbol;Acc:MGI:1933395]	B2RWI2	Q9EP89	-2.4	1.4E-03	8.1	8.2E-05	-0.4	7.3E-01	-0.9	1.2E-01
ENSMUST00000034934	anterior pharynx defective 1b homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:3522097]		Q8C7N7	-2.7	7.6E-04	7.4	2.0E-05	-0.9	3.8E-01	-0.1	8.2E-01
ENSMUST00000034941	phospholipid scramblase 4 [Source:MGI Symbol;Acc:MGI:2143267]		P58196	4.4	3.7E-03	-4.1	1.5E-03	0.2	7.3E-01	-2.1	9.4E-02
ENSMUST00000034945	family with sequence similarity 96, member A [Source:MGI Symbol;Acc:MGI:1915500]		Q9DCL2	-4.4	7.8E-06	-9.0	8.9E-06	-0.3	5.0E-01	-2.8	3.8E-02
ENSMUST00000034761	interactor of little elongation complex ELL subunit 2 [Source:MGI Symbol;Acc:MGI:2135947]		Q3UZ18	-2.4	3.8E-02	0.3	7.6E-01	-0.4	6.0E-01	-3.1	1.6E-02
ENSMUST00000034946	sorting nexin 1 [Source:MGI Symbol;Acc:MGI:1928395]	Q6NZD2		-6.4	3.6E-07	-2.9	7.1E-03	0.8	1.2E-01	0.0	9.9E-01
ENSMUST00000034947	peptidylprolyl isomerase B [Source:MGI Symbol;Acc:MGI:97750]	Q9DCY1	P24369	-6.5	5.5E-06	4.3	2.7E-04	-0.5	4.6E-01	0.1	8.7E-01
ENSMUST00000034949	casein kinase 1, gamma 1 [Source:MGI Symbol;Acc:MGI:2660884]		Q8BTH8	-2.5	2.6E-03	7.4	2.0E-05	-1.4	2.1E-01	-0.1	8.0E-01
ENSMUST00000034775	feminization 1 homolog b (C. elegans) [Source:MGI Symbol;Acc:MGI:1335087]		Q9Z2G0	-0.1	7.7E-01	0.3	4.9E-01	0.6	8.9E-02	0.2	6.5E-01
ENSMUST00000034776	ceroid-lipofuscinosis, neuronal 6 [Source:MGI Symbol;Acc:MGI:2159324]	Q3U466		0.1	8.8E-01	0.3	7.1E-01	0.6	3.8E-01	0.3	6.9E-01
ENSMUST00000034777	calmodulin-like 4 [Source:MGI Symbol;Acc:MGI:1922850]		Q91WQ9	3.2	7.4E-02	-1.6	1.4E-01	-7.4	4.2E-04	-2.6	4.7E-02
ENSMUST00000034785	glucuronyl C5-epimerase [Source:MGI Symbol;Acc:MGI:2136405]		Q9EPS3	-1.6	2.9E-01	-0.2	9.3E-01	1.4	3.6E-01	0.0	9.8E-01
ENSMUST00000034955	spastic paraplegia 21 homolog (human) [Source:MGI Symbol;Acc:MGI:106403]	A2RT57	Q9CQC8	-4.8	1.0E-05	-3.5	1.8E-04	0.3	2.8E-01	-0.6	3.0E-01
ENSMUST00000034960	dipeptidylpeptidase 8 [Source:MGI Symbol;Acc:MGI:1921638]		Q80YA7	-3.9	2.6E-05	3.3	8.5E-03	-1.8	9.4E-02	-0.5	5.2E-01
ENSMUST00000034961	immunoglobulin superfamily, DCC subclass, member 3 [Source:MGI Symbol;Acc:MGI:1202390]		Q8BQC3	8.5	1.2E-05	7.7	4.7E-05	-0.6	6.1E-01	-0.4	4.7E-01
ENSMUST00000034964	timeless interacting protein [Source:MGI Symbol;Acc:MGI:1921571]		Q91WA1	-3.1	1.1E-03	6.9	5.9E-04	1.7	2.1E-01	-1.2	1.3E-01
ENSMUST00000034965	small nuclear RNA activating complex, polypeptide 5 [Source:MGI Symbol;Acc:MGI:1914282]	E9QPK5		-4.8	1.7E-05	2.5	4.3E-02	-2.6	3.3E-02	-2.4	3.3E-02
ENSMUST00000034966	ribosomal protein L4 [Source:MGI Symbol;Acc:MGI:1915141]	Q564E8	Q9D8E6	-6.2	4.4E-07	-2.2	1.9E-01	0.7	4.9E-01	-0.8	6.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000034969	lactase-like [Source:MGI Symbol;Acc:MGI:2183549]		Q8K1F9	5.3	3.2E-02	-0.4	4.3E-01	0.6	1.3E-01	-0.1	8.3E-01
ENSMUST00000034982	transcription factor Dp 2 [Source:MGI Symbol;Acc:MGI:107167]	Q8BHD2		3.4	9.2E-05	9.5	6.2E-04	1.6	3.9E-01	1.0	2.2E-01
ENSMUST00000034983	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:MGI Symbol;Acc:MGI:107788]	Q544Q7	P97370	-5.0	8.3E-06	-2.7	1.6E-03	-0.3	4.4E-01	-1.0	1.5E-01
ENSMUST00000034984	RAS p21 protein activator 2 [Source:MGI Symbol;Acc:MGI:2149960]		P58069	-1.6	2.2E-02	5.3	4.0E-03	-2.8	1.1E-01	0.0	9.7E-01
ENSMUST00000034820	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	F8WIE2		-6.0	1.1E-01	-2.9	5.3E-01	1.9	4.5E-01	-1.2	8.0E-01
ENSMUST00000034987	dopey family member 1 [Source:MGI Symbol;Acc:MGI:1289294]	H7BWZ9		-6.4	7.6E-05	3.4	1.3E-03	-1.0	1.7E-01	-0.6	3.1E-01
ENSMUST00000034991	T-box18 [Source:MGI Symbol;Acc:MGI:1923615]	G3X919		7.4	5.1E-06	-4.3	3.2E-03	0.0	9.6E-01	0.2	8.5E-01
ENSMUST00000035007	CKLF-like MARVEL transmembrane domain containing 6 [Source:MGI Symbol;Acc:MGI:2447165]		Q9CZ69	-4.4	9.1E-05	6.8	1.6E-04	-0.6	6.2E-01	0.0	9.4E-01
ENSMUST00000035009	CKLF-like MARVEL transmembrane domain containing 7 [Source:MGI Symbol;Acc:MGI:2447166]		Q9ESD6	-4.7	3.8E-05	-0.7	2.5E-01	0.7	1.2E-01	-0.3	6.5E-01
ENSMUST00000035010	subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:19			-3.9	2.9E-05	-5.5	2.4E-05	1.0	1.7E-02	-0.7	3.7E-01
ENSMUST00000035014	transforming growth factor, beta receptor II [Source:MGI Symbol;Acc:MGI:98729]		Q62312	-2.5	9.3E-04	-3.9	8.7E-02	0.2	8.7E-01	-0.7	7.7E-01
ENSMUST00000035024	solute carrier family 25, member 36 [Source:MGI Symbol;Acc:MGI:1924909]	Q8BZJ4		-3.2	2.0E-02	-2.6	1.8E-03	1.2	5.3E-03	0.3	6.6E-01
ENSMUST00000034846	RIKEN cDNA 1700017B05 gene [Source:MGI Symbol;Acc:MGI:1921461]		Q3TEI4	-1.3	4.5E-02	0.0	9.6E-01	1.2	4.8E-02	-0.1	9.1E-01
ENSMUST00000035026	tripartite motif-containing 42 [Source:MGI Symbol;Acc:MGI:1926161]		Q9D2H5	7.4	2.1E-05	-5.6	6.6E-04	-0.8	1.5E-01	-2.2	1.1E-01
ENSMUST00000035033	coatomer protein complex, subunit beta 2 (beta prime) [Source:MGI Symbol;Acc:MGI:1354962]		O55029	-5.3	3.9E-06	6.9	1.5E-04	-0.5	7.0E-01	0.0	9.8E-01
ENSMUST00000035034	mitochondrial ribosomal protein S22 [Source:MGI Symbol;Acc:MGI:1928137]		Q9CXW2	-3.5	3.6E-03	5.7	7.7E-05	-1.9	4.8E-02	0.4	5.1E-01
ENSMUST00000034856	mannose phosphate isomerase [Source:MGI Symbol;Acc:MGI:97075]	Q3V100	Q924M7	0.0	9.3E-01	-0.9	2.2E-01	0.0	9.7E-01	0.8	2.3E-01
ENSMUST00000035038	Fas apoptotic inhibitory molecule [Source:MGI Symbol;Acc:MGI:1344387]		Q9WUD8	-3.0	3.7E-03	0.6	5.4E-01	0.1	8.9E-01	-4.1	6.0E-03
ENSMUST00000035045	muscle and microspikes RAS [Source:MGI Symbol;Acc:MGI:1100856]	Q3TPX5	O08989	6.7	8.6E-06	6.3	1.7E-04	-1.3	2.7E-01	-0.8	1.9E-01
ENSMUST00000035048	claudin 18 [Source:MGI Symbol;Acc:MGI:1929209]		P56857	7.2	3.6E-05	-3.2	3.5E-03	1.2	2.8E-02	-0.5	6.0E-01
ENSMUST00000035055	microtubule-associated protein 4 [Source:MGI Symbol;Acc:MGI:97178]	A0A0B4J1F2	P27546	-8.4	2.1E-04	5.9	6.0E-04	-1.1	3.7E-01	-0.6	4.0E-01
ENSMUST00000035058	chondroitin sulfate proteoglycan 5 [Source:MGI Symbol;Acc:MGI:1352747]		Q71M36	8.2	2.2E-05	-3.9	6.6E-03	0.4	5.1E-01	0.3	8.0E-01
ENSMUST00000035061	neutrophilic granule protein [Source:MGI Symbol;Acc:MGI:105983]		O08692	-10.1	2.6E-08	-8.1	9.8E-04	-0.2	7.1E-01	-1.0	6.1E-01
ENSMUST00000034874	cytochrome P450, family 11, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88582]		Q9QZ82	-0.9	3.2E-01	1.3	2.5E-01	1.2	1.8E-01	-1.0	3.3E-01
ENSMUST00000034876	tetraspanin 3 [Source:MGI Symbol;Acc:MGI:1928098]	Q545L1	Q9QY33	0.1	8.6E-01	-0.7	3.0E-01	-1.1	3.9E-02	-0.3	6.0E-01
ENSMUST00000035065	prostaglandin-endoperoxide synthase 2 [Source:MGI Symbol;Acc:MGI:97798]		Q05769	3.8	3.3E-02	-7.4	6.4E-04	1.3	1.7E-02	-0.9	6.0E-01
ENSMUST00000035075	teratocarcinoma-derived growth factor 1 [Source:MGI Symbol;Acc:MGI:98658]	Q7TQ06		2.0	9.6E-03	-0.8	1.8E-01	0.3	4.5E-01	-0.6	3.4E-01
ENSMUST00000035076	leucine rich repeat containing 2 [Source:MGI Symbol;Acc:MGI:1921499]			3.3	8.2E-04	7.1	8.3E-05	-0.6	5.9E-01	-0.1	8.8E-01
ENSMUST00000035077	lactotransferrin [Source:MGI Symbol;Acc:MGI:96837]		P08071	-8.9	1.1E-06	-6.1	3.9E-04	-0.5	3.6E-01	-0.6	6.1E-01
ENSMUST00000034883	stomatin-like 1 [Source:MGI Symbol;Acc:MGI:1916356]	A0A0B4J1F1		1.1	9.1E-02	1.5	6.0E-02	-0.1	9.3E-01	-0.5	4.5E-01
ENSMUST00000035078	leucine rich repeat (in FLII) interacting protein 2 [Source:MGI Symbol;Acc:MGI:1918518]	E9QN52		-4.9	1.5E-03	8.0	1.9E-05	0.1	9.0E-01	-0.4	3.8E-01
ENSMUST00000034896	mitochondrial translation optimization 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915541]	G5E889		-1.1	1.2E-01	0.3	7.1E-01	0.6	3.2E-01	-0.8	3.1E-01
ENSMUST00000035079	mutL homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:101938]		Q9JK91	-3.7	6.0E-03	3.6	4.4E-02	-3.0	1.1E-01	-0.6	6.1E-01
ENSMUST00000035086	programmed cell death 6 interacting protein [Source:MGI Symbol;Acc:MGI:1333753]		Q9WU78	-2.8	2.4E-03	5.5	4.3E-05	-0.9	2.5E-01	-0.4	3.8E-01
ENSMUST00000035092	myeloid differentiation primary response gene 88 [Source:MGI Symbol;Acc:MGI:108005]	Q3U7M4	P22366	-7.5	5.9E-06	-2.3	2.0E-03	0.8	2.8E-02	-0.5	3.4E-01
ENSMUST00000034905	glutamate-cysteine ligase, catalytic subunit [Source:MGI Symbol;Acc:MGI:104990]	Q3TEF1	P97494	-0.1	8.6E-01	0.0	9.7E-01	0.1	8.2E-01	0.0	1.0E+00
ENSMUST00000034911	tubulointerstitial nephritis antigen [Source:MGI Symbol;Acc:MGI:1349477]	Q9WUR0		3.2	2.1E-01	3.1	2.5E-01	-0.4	8.9E-01	-0.3	8.6E-01
ENSMUST00000035094	endo/exonuclease (5'-3'), endonuclease G-like [Source:MGI Symbol;Acc:MGI:2143333]		Q8C163	5.3	2.2E-05	7.7	4.2E-05	-0.6	6.1E-01	0.0	9.3E-01
ENSMUST00000035099	golgi reassembly stacking protein 1 [Source:MGI Symbol;Acc:MGI:1921748]	Q3TCN5	Q91X51	2.1	3.5E-03	-5.3	1.1E-02	1.1	1.7E-01	0.1	9.4E-01
ENSMUST00000035100	tetratricopeptide repeat domain 21A [Source:MGI Symbol;Acc:MGI:1921302]		Q8C0S4	3.9	7.8E-04	-2.3	5.4E-03	-0.7	9.8E-02	-0.6	3.6E-01
ENSMUST00000034920	mitogen-activated protein kinase kinase 5 [Source:MGI Symbol;Acc:MGI:1346345]		Q9WVS7	-1.0	4.0E-02	0.2	7.0E-01	0.6	1.7E-01	-0.7	2.2E-01
ENSMUST00000035101	cysteine-serine-rich nuclear protein 1 [Source:MGI Symbol;Acc:MGI:2387989]		P59054	-2.5	1.1E-02	7.2	3.0E-05	1.1	2.4E-01	-0.6	2.3E-01
ENSMUST00000035105	ribosomal protein SA [Source:MGI Symbol;Acc:MGI:105381]		P14206	-6.1	1.4E-05	-1.9	2.0E-02	0.5	2.8E-01	-0.1	9.2E-01
ENSMUST00000034932	phospholipid scramblase 2 [Source:MGI Symbol;Acc:MGI:1270860]		Q9DCW2	-0.8	2.7E-01	-1.2	1.6E-01	-0.9	1.6E-01	-0.5	5.4E-01
ENSMUST00000035106	solute carrier family 25, member 38 [Source:MGI Symbol;Acc:MGI:2384782]		Q91XD8	-5.3	3.1E-05	-0.8	2.3E-01	1.3	1.6E-02	-0.6	3.9E-01
ENSMUST00000034940				1.0	6.3E-01	-3.0	2.4E-01	-3.7	6.5E-02	0.3	9.1E-01
ENSMUST00000035110	hedgehog acyltransferase-like [Source:MGI Symbol;Acc:MGI:1922020]		Q9D1G3	7.5	6.3E-05	1.1	2.9E-01	-2.6	4.5E-02	0.7	4.3E-01
ENSMUST00000034944	death-associated protein kinase 2 [Source:MGI Symbol;Acc:MGI:1341297]		Q8VDF3	0.2	7.8E-01	0.7	3.1E-01	-0.1	8.0E-01	-0.7	2.8E-01
ENSMUST00000035112	natural killer tumor recognition sequence [Source:MGI Symbol;Acc:MGI:97346]		P30415	-2.0	1.2E-02	-3.5	2.3E-04	0.2	5.5E-01	-0.7	2.5E-01
ENSMUST00000035113	differentially expressed in B16F10 1 [Source:MGI Symbol;Acc:MGI:1349474]		Q9D174	-6.0	2.2E-05	-5.8	6.4E-06	0.4	1.4E-01	-0.2	7.6E-01
ENSMUST00000035115	vasoactive intestinal peptide receptor 1 [Source:MGI Symbol;Acc:MGI:109272]		P97751	4.0	4.4E-04	-6.0	5.0E-05	-0.6	1.2E-01	-1.1	2.4E-01
ENSMUST00000035128	abhydrolase domain containing 5 [Source:MGI Symbol;Acc:MGI:1914719]	H3BKV1		-6.7	3.6E-05	-1.1	1.8E-01	1.1	5.4E-02	-0.3	7.4E-01
ENSMUST00000035129	Eph receptor B1 [Source:MGI Symbol;Acc:MGI:1096337]		Q8CBF3	7.3	5.3E-03	-3.7	3.8E-04	0.7	6.7E-02	-0.4	5.7E-01
ENSMUST00000035142	receptor-like tyrosine kinase [Source:MGI Symbol;Acc:MGI:101766]	H9H9R6		3.8	1.1E-02	-3.9	2.7E-04	0.8	4.2E-02	0.8	2.8E-01
ENSMUST00000035148	solute carrier organic anion transporter family, member 2a1 [Source:MGI Symbol;Acc:MGI:1346021]	Q3TED0	Q9EPT5	7.9	1.6E-06	7.5	3.6E-05	-1.5	2.1E-01	-0.5	4.1E-01
ENSMUST00000035155	RAB6B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:107283]	Q0PD53	P61294	8.2	2.2E-05	-3.9	2.1E-03	-0.7	1.8E-01	0.1	9.3E-01
ENSMUST00000035158	transferrin [Source:MGI Symbol;Acc:MGI:98821]		Q921I1	-7.0	2.4E-07	-4.9	7.9E-05	-0.5	1.6E-01	-0.5	5.4E-01
ENSMUST00000035164	topoisomerase (DNA) II binding protein 1 [Source:MGI Symbol;Acc:MGI:1920018]		Q6ZQF0	-2.0	2.6E-03	-6.4	2.9E-06	-0.6	5.3E-02	-0.5	4.7E-01
ENSMUST00000035166	ubiquitin-like modifier activating enzyme 5 [Source:MGI Symbol;Acc:MGI:1913913]		Q8VE47	-1.8	2.4E-02	5.3	4.3E-02	-0.8	7.5E-01	-0.8	6.1E-01
ENSMUST00000034973	SMAD family member 3 [Source:MGI Symbol;Acc:MGI:1201674]		Q8BUN5	-0.6	2.7E-01	-0.1	9.1E-01	0.4	4.1E-01	-0.1	8.5E-01
ENSMUST00000034980	ataxia telangiectasia and Rad3 related [Source:MGI Symbol;Acc:MGI:108028]	E9QPK4		-1.2	1.3E-01	0.0	9.7E-01	0.0	9.8E-01	-1.1	2.0E-01
ENSMUST00000034981	5'-3' exoribonuclease 1 [Source:MGI Symbol;Acc:MGI:891964]	F8VQ87		0.1	9.5E-01	0.6	8.0E-01	0.6	7.1E-01	0.1	9.6E-01
ENSMUST00000035167	nephronophthisis 3 (adolescent) [Source:MGI Symbol;Acc:MGI:1921275]		Q7TNH6	4.7	2.9E-02	3.6	2.4E-04	-0.1	8.7E-01	-0.3	4.6E-01
ENSMUST00000035170	DnaJ (Hsp40) homolog, subfamily C, member 13 [Source:MGI Symbol;Acc:MGI:2676368]	G3X922		-3.0	2.6E-03	-4.8	1.3E-04	1.1	1.2E-02	0.9	2.8E-01
ENSMUST00000035177	mitochondrial ribosomal protein L3 [Source:MGI Symbol;Acc:MGI:2137204]		Q99N95	3.6	3.2E-04	-0.5	5.1E-01	0.7	1.9E-01	-0.4	5.9E-01
ENSMUST00000035194	mitogen-activated protein kinase-activated protein kinase 3 [Source:MGI Symbol;Acc:MGI:2143163]		Q3UMW7	-5.4	6.6E-05	-5.2	1.8E-03	0.6	1.9E-01	-0.6	6.6E-01
ENSMUST00000034988	RWD domain containing 2A [Source:MGI Symbol;Acc:MGI:1916769]	Q14BN8		1.7	4.8E-02	2.8	2.0E-02	1.3	1.7E-01	0.2	7.9E-01
ENSMUST00000035196	HemK methyltransferase family member 1 [Source:MGI Symbol;Acc:MGI:1916786]		Q921L7	2.3	2.1E-02	6.3	5.8E-05	-0.6	5.0E-01	0.4	4.3E-01
ENSMUST00000034992	5' nucleotidase, ecto [Source:MGI Symbol;Acc:MGI:99782]	Q0VEE0	Q61503	-1.1	5.2E-02	-1.7	2.1E-02	-0.4	3.3E-01	0.2	7.4E-01
ENSMUST00000035199	RNA binding motif protein 5 [Source:MGI Symbol;Acc:MGI:1933204]		Q91YE7	-6.1	3.0E-03	-3.9	2.4E-03	1.3	2.7E-02	0.8	4.3E-01
ENSMUST00000035201	RNA binding motif protein 6 [Source:MGI Symbol;Acc:MGI:1338037]	Q3ULB0		-3.9	1.2E-02	-4.1	7.5E-04	1.1	2.2E-02	0.5	5.6E-01
ENSMUST00000035202	MON1 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1920075]			-5.1	1.2E-03	-2.8	1.4E-03	0.8	4.4E-02	-0.4	5.7E-01
ENSMUST00000035203	macrophage stimulating 1 receptor (c-met-related tyrosine kinase) [Source:MGI Symbol;Acc:MGI:99614]		Q62190	7.4	8.1E-05	-1.5	5.3E-02	1.0	4.4E-02	-0.1	9.3E-01
ENSMUST00000035020	comesodermin homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1201683]		O54839	0.5	7.9E-01	2.7	1.8E-01	-0.1	9.6E-01	-2.3	1.8E-01
ENSMUST00000035208	bassoon [Source:MGI Symbol;Acc:MGI:1277955]		O88737	9.3	2.3E-06	-4.5	7.0E-02	1.2	2.1E-01	2.5	2.7E-01
ENSMUST00000035211	macrophage stimulating 1 (hepatocyte growth factor-like) [Source:MGI Symbol;Acc:MGI:96080]		P26928	6.6	6.7E-03	7.5	4.0E-05	-0.6	6.1E-01	-0.6	2.9E-01
ENSMUST00000035214	inositol hexaphosphate kinase 1 [Source:MGI Symbol;Acc:MGI:1351633]		Q6PD10	-4.1	3.5E-04	-5.3	2.5E-05	-0.3	4.2E-01	-0.2	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000035222	rier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20 [Source:MGI Symbol;Acc:MGI:		Q9Z2Z6	-4.4	2.8E-04	-2.3	1.5E-02	-1.1	7.2E-02	-2.3	4.2E-02
ENSMUST00000035037	phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Source:MGI Symbol;Acc:MGI:1922019]		Q8BTI9	-1.1	1.5E-01	0.6	5.5E-01	1.4	8.3E-02	-0.3	7.1E-01
ENSMUST00000035227	nicolin 1 [Source:MGI Symbol;Acc:MGI:1913507]		Q9CQM0	1.9	6.4E-03	-3.9	3.2E-03	-0.5	3.6E-01	0.4	7.4E-01
ENSMUST00000035043	armadillo repeat containing 8 [Source:MGI Symbol;Acc:MGI:1921375]	G3X920		-0.1	9.0E-01	-0.7	3.2E-01	0.1	7.5E-01	0.8	2.4E-01
ENSMUST00000035230	aminomethyltransferase [Source:MGI Symbol;Acc:MGI:3646700]	A2RSW6	Q8CFA2	3.7	6.1E-04	4.8	1.8E-04	-2.1	2.7E-02	-0.1	8.3E-01
ENSMUST00000035237	ubiquitin specific peptidase 4 (proto-oncogene) [Source:MGI Symbol;Acc:MGI:98905]		P35123	-8.1	5.9E-05	7.0	8.4E-05	-0.6	6.2E-01	-0.4	4.7E-01
ENSMUST00000035053	NME/NM23 nucleoside diphosphate kinase 6 [Source:MGI Symbol;Acc:MGI:1861676]		O88425	-0.4	6.3E-01	-0.6	5.2E-01	-1.0	1.9E-01	-0.7	4.4E-01
ENSMUST00000035240	armadillo repeat containing 7 [Source:MGI Symbol;Acc:MGI:2679719]		Q3UJZ3	-3.8	2.0E-04	-3.6	1.4E-02	1.3	6.3E-02	-3.6	4.7E-02
ENSMUST00000035242	RAB24, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105065]	Q0PD31	P35290	-5.8	1.2E-04	8.1	4.4E-05	-0.6	6.3E-01	-0.5	3.5E-01
ENSMUST00000035243	spermatid associated [Source:MGI Symbol;Acc:MGI:1915176]		Q32MG2	5.6	2.5E-02	-8.3	4.3E-07	1.0	1.0E-02	-0.8	2.3E-01
ENSMUST00000035250	olfactory receptor 720 [Source:MGI Symbol;Acc:MGI:3030554]	Q8VF37		6.6	1.5E-04	0.1	9.3E-01	-4.1	1.4E-02	-0.5	7.4E-01
ENSMUST00000035069	neurotrophin receptor associated death domain [Source:MGI Symbol;Acc:MGI:1914419]		Q8CJ26	-0.5	6.2E-01	0.4	7.6E-01	0.3	7.5E-01	-0.6	6.2E-01
ENSMUST00000035258	membrane-spanning 4-domains, subfamily A, member 4B [Source:MGI Symbol;Acc:MGI:1913083]	Q9ES61		-6.2	1.0E-04	1.8	4.0E-02	-0.5	4.7E-01	-0.2	7.6E-01
ENSMUST00000035266	interferon gamma induced GTPase [Source:MGI Symbol;Acc:MGI:107729]	Q9DCE9		-2.5	3.9E-03	2.9	7.4E-03	-0.1	9.4E-01	0.4	5.6E-01
ENSMUST00000035269	muscle glycogen phosphorylase [Source:MGI Symbol;Acc:MGI:97830]		Q9WUB3	5.3	8.1E-03	-6.6	5.2E-05	1.8	2.1E-03	-0.5	6.2E-01
ENSMUST00000035275	tumor necrosis factor receptor superfamily, member 25 [Source:MGI Symbol;Acc:MGI:1934667]	Q8VD70		3.7	3.1E-02	-0.9	5.8E-01	3.3	9.0E-03	-0.7	6.6E-01
ENSMUST00000035276	dCTP pyrophosphatase 1 [Source:MGI Symbol;Acc:MGI:1913672]		Q9QY93	-2.8	1.4E-03	-3.7	7.1E-03	-1.0	1.5E-01	-0.9	4.8E-01
ENSMUST00000035083	src homology three (SH3) and cysteine rich domain [Source:MGI Symbol;Acc:MGI:1201400]	Q3UPL9	P97306	6.0	4.9E-02	5.6	8.7E-02	-0.7	8.4E-01	-0.3	8.9E-01
ENSMUST00000035279	Hermansky-Pudlak syndrome 4 homolog (human) [Source:MGI Symbol;Acc:MGI:2177742]	Q541V2	Q99KG7	-2.9	2.2E-02	-0.4	6.5E-01	1.4	3.1E-02	-1.0	2.4E-01
ENSMUST00000035090	F-box and leucine-rich repeat protein 2 [Source:MGI Symbol;Acc:MGI:1919429]	Q4VA21	Q8BH16	0.6	3.8E-01	1.2	1.4E-01	-0.2	7.2E-01	-0.9	2.3E-01
ENSMUST00000035288	stabilin 2 [Source:MGI Symbol;Acc:MGI:2178743]	E5RKF9	Q8R4U0	8.3	1.4E-05	-5.8	2.3E-04	1.2	1.9E-02	-0.5	6.1E-01
ENSMUST00000035295	degenerative spermatocyte homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1097711]		O09005	-6.9	4.7E-07	4.7	9.5E-05	-1.4	6.0E-02	-0.8	1.3E-01
ENSMUST00000035301	ATPase, H+ transporting, lysosomal V1 subunit G1 [Source:MGI Symbol;Acc:MGI:1913540]	Q5HZY7	Q9CR51	-6.4	2.0E-06	2.8	2.6E-03	0.4	5.0E-01	-0.3	5.8E-01
ENSMUST00000035323	Spi-B transcription factor (Spi-1/PU.1 related) [Source:MGI Symbol;Acc:MGI:892986]		O35906	4.8	9.9E-05	5.3	1.0E-03	1.3	2.3E-01	-0.1	8.7E-01
ENSMUST00000035325	quiescin Q6 sulfhydryl oxidase 1 [Source:MGI Symbol;Acc:MGI:1330818]		Q8BND5	-6.9	8.2E-04	-2.3	7.4E-02	0.8	2.6E-01	0.5	6.4E-01
ENSMUST00000035336	interleukin 17 receptor D [Source:MGI Symbol;Acc:MGI:2159727]		Q8JZL1	6.7	1.9E-05	-6.4	8.8E-05	-0.4	4.0E-01	-0.1	9.5E-01
ENSMUST00000035342	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 20 [Source:MGI Symbol;Acc:M		P59511	8.4	2.1E-05	-2.5	1.3E-02	1.1	3.9E-02	-1.7	7.2E-02
ENSMUST00000035351	synaptotagmin XV [Source:MGI Symbol;Acc:MGI:2442166]		Q8C6N3	8.6	1.2E-06	6.8	2.7E-04	-0.6	6.5E-01	0.1	8.3E-01
ENSMUST00000035371	synaptic vesicle glycoprotein 2 a [Source:MGI Symbol;Acc:MGI:1927139]		Q9JIS5	7.3	1.3E-04	-1.5	9.3E-02	0.1	8.3E-01	-0.4	6.5E-01
ENSMUST00000035372	achaete-scute complex homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928820]		Q9JIR7	3.5	2.0E-03	-4.5	1.1E-04	0.0	9.7E-01	-1.4	1.2E-01
ENSMUST00000035390	alpha-2-glycoprotein 1, zinc [Source:MGI Symbol;Acc:MGI:103163]		Q64726	5.4	2.7E-03	3.4	4.1E-03	-0.4	6.6E-01	0.3	7.2E-01
ENSMUST00000035116	propionyl Coenzyme A carboxylase, beta polypeptide [Source:MGI Symbol;Acc:MGI:1914154]		Q99MN9	-0.1	9.1E-01	-0.3	8.3E-01	0.8	3.7E-01	1.0	4.0E-01
ENSMUST00000035121	angiomotin-like 2 [Source:MGI Symbol;Acc:MGI:1929286]		Q8K371	-5.2	8.0E-02	-3.1	4.3E-01	1.4	4.9E-01	-0.7	8.7E-01
ENSMUST00000035399	PDZ domain containing RING finger 4 [Source:MGI Symbol;Acc:MGI:3056996]	E9Q5P6		7.3	2.6E-04	-6.9	6.9E-04	0.7	1.2E-01	0.9	5.5E-01
ENSMUST00000035419	perforin 1 (pore forming protein) [Source:MGI Symbol;Acc:MGI:97551]	A2RSY7	P10820	2.6	1.0E-02	5.6	3.2E-02	-0.6	8.1E-01	1.1	4.1E-01
ENSMUST00000035430	aspartyl-tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:2442510]		Q8BIP0	2.6	1.1E-03	1.3	3.1E-01	-3.6	1.0E-02	-1.1	3.5E-01
ENSMUST00000035458	arginyltransferase 1 [Source:MGI Symbol;Acc:MGI:1333870]	Q80YP1	Q9Z2A5	-5.8	3.1E-03	2.0	4.6E-03	-5.7	1.7E-05	0.1	7.7E-01
ENSMUST00000035154	RIKEN cDNA 1110059G10 gene [Source:MGI Symbol;Acc:MGI:1913452]		Q8K039	-0.2	7.2E-01	-1.1	1.3E-01	-1.1	5.1E-02	-0.2	7.8E-01
ENSMUST00000035462	dermatan sulfate epimerase-like [Source:MGI Symbol;Acc:MGI:2442948]		Q0VBN2	1.9	1.7E-02	6.6	1.1E-04	-1.6	2.0E-01	0.1	8.7E-01
ENSMUST00000035157	signal recognition particle receptor, B subunit [Source:MGI Symbol;Acc:MGI:102964]		P47758	-0.7	3.7E-01	0.8	4.0E-01	0.4	5.5E-01	-1.1	2.4E-01
ENSMUST00000035471	laminin, alpha 1 [Source:MGI Symbol;Acc:MGI:99892]	F8VQ40		9.4	3.8E-06	-6.4	4.2E-06	0.3	2.3E-01	-0.3	6.6E-01
ENSMUST00000035481	coiled-coil-helix-coiled-coil-helix domain containing 5 [Source:MGI Symbol;Acc:MGI:1913420]	Q52KC5	Q9CQP3	-3.4	1.2E-02	-1.0	1.5E-01	0.5	2.1E-01	-0.5	4.1E-01
ENSMUST00000035488	cytochrome P450, family 2, subfamily c, polypeptide 38 [Source:MGI Symbol;Acc:MGI:1306819]		P56655	5.0	2.2E-03	-0.8	3.1E-01	0.2	6.9E-01	-0.7	3.9E-01
ENSMUST00000035493	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]		Q9Z2X1	-9.0	9.9E-05	4.1	1.5E-01	1.0	7.0E-01	1.6	3.6E-01
ENSMUST00000035497	organic solute carrier partner 1 [Source:MGI Symbol;Acc:MGI:1916308]	A2A8Y5	Q8BHW2	4.5	4.1E-05	-1.6	1.1E-01	0.6	2.8E-01	-0.8	3.9E-01
ENSMUST00000035501	lipoxygenase homology domains 1 [Source:MGI Symbol;Acc:MGI:1914609]	E9PVB2		7.1	1.2E-03	4.0	4.8E-04	-0.2	7.2E-01	-0.6	3.4E-01
ENSMUST00000035179	nudix (nucleoside diphosphate linked moiety X)-type motif 16 [Source:MGI Symbol;Acc:MGI:1922936]		Q6P3D0	-1.6	4.0E-02	-0.5	6.0E-01	0.8	1.9E-01	-0.3	7.3E-01
ENSMUST00000035515	ATP-binding cassette, sub-family B (MDR/TAP), member 5 [Source:MGI Symbol;Acc:MGI:1924956]		B5X0E4	6.0	1.3E-03	-4.1	3.0E-03	1.6	1.4E-02	0.3	8.0E-01
ENSMUST00000035519	OTU domain containing 7B [Source:MGI Symbol;Acc:MGI:2654703]		B2RUR8	-2.8	2.8E-02	4.7	7.2E-03	2.5	7.1E-02	0.1	9.2E-01
ENSMUST00000035521	radial spoke head 6 homolog A (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1927643]	B2RQM5	Q8CDR2	5.4	7.5E-03	-3.7	1.2E-01	1.7	1.5E-01	-0.6	7.8E-01
ENSMUST00000035532	osphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) [Source:MGI Symbol;Acc:MGI:9758	Q80UI5		5.6	8.7E-04	-0.9	4.7E-01	0.5	5.6E-01	-2.5	1.1E-01
ENSMUST00000035538	WNK lysine deficient protein kinase 2 [Source:MGI Symbol;Acc:MGI:1922857]	E0CZE3		6.1	1.8E-04	-5.7	7.2E-03	1.1	1.1E-01	1.7	3.5E-01
ENSMUST00000035548	alpha-kinase 2 [Source:MGI Symbol;Acc:MGI:2449492]		Q91ZB0	9.4	5.7E-05	2.6	8.7E-02	-2.0	1.5E-01	2.7	2.0E-02
ENSMUST00000035560	acyl-Coenzyme A binding domain containing 6 [Source:MGI Symbol;Acc:MGI:1919732]	Q14BV7	Q9D061	7.7	1.4E-04	7.2	4.1E-05	-1.7	1.2E-01	0.5	4.0E-01
ENSMUST00000035565	polycystic kidney disease 1 homolog [Source:MGI Symbol;Acc:MGI:97603]		O08852	1.9	6.9E-03	5.6	3.2E-02	0.0	1.0E+00	1.0	4.4E-01
ENSMUST00000035579	F-box protein 21 [Source:MGI Symbol;Acc:MGI:1924223]		Q8VDH1	3.4	4.2E-05	-3.4	7.8E-03	0.9	1.1E-01	0.2	8.5E-01
ENSMUST00000035216	ubiquitin-like modifier activating enzyme 7 [Source:MGI Symbol;Acc:MGI:1349462]	Q9DBK7		-1.6	6.0E-01	-0.4	9.2E-01	1.0	6.8E-01	-0.2	9.6E-01
ENSMUST00000035218	NCK interacting protein with SH3 domain [Source:MGI Symbol;Acc:MGI:1931834]		Q9ESJ4	-0.2	6.7E-01	1.1	1.2E-01	0.6	2.4E-01	-0.7	2.6E-01
ENSMUST00000035220	protein kinase, cAMP dependent regulatory, type II alpha [Source:MGI Symbol;Acc:MGI:108025]	Q8K1M3		0.4	3.0E-01	1.0	6.8E-02	0.0	9.6E-01	-0.6	2.2E-01
ENSMUST00000035606	activating signal cointegrator 1 complex subunit 3 [Source:MGI Symbol;Acc:MGI:1925237]		E9PZJ8	-1.8	1.0E-02	-3.9	3.0E-03	0.8	1.3E-01	0.4	7.0E-01
ENSMUST00000035608	oligodendrocyte transcription factor 2 [Source:MGI Symbol;Acc:MGI:1355331]	Q542S0	Q9EQW6	7.6	6.6E-05	2.3	6.6E-03	-0.1	8.2E-01	-0.5	3.7E-01
ENSMUST00000035612	cell cycle activator and apoptosis regulator 2 [Source:MGI Symbol;Acc:MGI:2444228]		Q8VDP4	-1.2	3.0E-02	3.7	2.9E-03	0.3	6.8E-01	0.4	5.7E-01
ENSMUST00000035622	WD repeat domain 93 [Source:MGI Symbol;Acc:MGI:3646885]		Q402B2	7.8	1.2E-05	-5.9	6.4E-04	0.7	1.4E-01	-1.5	3.0E-01
ENSMUST00000035625	cytochrome P450, family 7, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:104978]		Q60991	3.9	4.0E-03	-2.2	2.3E-02	1.3	1.7E-02	-0.3	7.2E-01
ENSMUST00000035635	BMP2 inducible kinase [Source:MGI Symbol;Acc:MGI:2155456]		Q91Z96	-1.4	2.0E-02	-4.1	4.9E-03	1.1	6.7E-02	-0.5	6.9E-01
ENSMUST00000035648	autophagy related 12 [Source:MGI Symbol;Acc:MGI:1914776]		Q9CQY1	-3.2	1.2E-04	5.0	5.8E-02	-0.8	7.5E-01	-0.2	9.2E-01
ENSMUST00000035657	tumor suppressing subtransferable candidate 1 [Source:MGI Symbol;Acc:MGI:1289332]		Q8K0G5	-1.9	5.9E-03	5.8	7.4E-04	-0.6	6.3E-01	0.3	6.9E-01
ENSMUST00000035661	chondroitin sulfate proteoglycan 4 [Source:MGI Symbol;Acc:MGI:2153093]		Q8VHY0	10.6	1.3E-06	-5.9	5.2E-04	-1.0	4.1E-02	-1.3	3.1E-01
ENSMUST00000035264	p21 protein (Cdc42/Rac)-activated kinase 7 [Source:MGI Symbol;Acc:MGI:1920334]		Q8C015	5.7	3.8E-02	6.6	3.1E-02	-0.6	8.4E-01	-1.4	3.7E-01
ENSMUST00000035667	tripartite motif-containing 62 [Source:MGI Symbol;Acc:MGI:1914775]		Q80V85	2.8	2.2E-04	-2.1	2.4E-02	-0.5	3.0E-01	-1.0	2.6E-01
ENSMUST00000035672	periplakin [Source:MGI Symbol;Acc:MGI:1194898]	G5E898		7.1	1.3E-06	4.5	5.5E-02	-1.4	4.8E-01	-0.6	6.4E-01
ENSMUST00000035673	von Hippel-Lindau tumor suppressor [Source:MGI Symbol;Acc:MGI:103223]	Q3TTE7	P40338	-3.2	8.6E-05	2.1	2.7E-01	-0.7	6.8E-01	0.9	5.8E-01
ENSMUST00000035682	yippee-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913303]	Q65Z96	Q9ESC7	3.5	3.8E-03	-2.6	6.6E-03	-0.5	2.8E-01	-0.7	3.8E-01
ENSMUST00000035689	RIKEN cDNA 4932438H23 gene [Source:MGI Symbol;Acc:MGI:1921637]		Q9D4G1	5.4	6.7E-04	-3.7	7.5E-02	0.9	3.1E-01	1.8	3.6E-01
ENSMUST00000035695	retinol binding protein 3, interstitial [Source:MGI Symbol;Acc:MGI:97878]			8.9	9.3E-06	8.6	2.0E-05	-0.5	6.7E-01	-0.8	1.1E-01
ENSMUST00000035701	follicle stimulating hormone receptor [Source:MGI Symbol;Acc:MGI:95583]	B2RQM3	P35378	6.4	2.0E-04	-5.0	3.4E-05	1.0	7.3E-03	-0.9	2.1E-01
ENSMUST00000035715	protease, serine 42 [Source:MGI Symbol;Acc:MGI:2665280]		Q8VIF2	9.2	5.1E-05	-6.2	1.5E-05	-0.3	3.4E-01	-0.5	4.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000035716	RAS, guanyl releasing protein 2 [Source:MGI Symbol;Acc:MGI:1333849]		Q9QUG9	-7.4	8.2E-05	-3.1	7.5E-02	-1.0	2.2E-01	6.8	1.1E-03
ENSMUST00000035721	PRP18 pre-mRNA processing factor 18 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914479]		Q8BM39	-3.3	4.6E-04	-4.8	2.7E-02	1.2	1.6E-01	-0.8	6.8E-01
ENSMUST00000035724	AT-hook transcription factor [Source:MGI Symbol;Acc:MGI:2140340]		Q80VW7	-3.2	4.7E-04	5.9	1.1E-04	-0.7	4.4E-01	0.1	9.2E-01
ENSMUST00000035340	ubiquitin specific peptidase 54 [Source:MGI Symbol;Acc:MGI:1926037]		Q8BL06	1.4	7.4E-02	2.8	7.5E-03	-0.3	6.3E-01	-1.7	3.7E-02
ENSMUST00000035725	BRICK1, SCAR/WAVE actin-nucleating complex subunit [Source:MGI Symbol;Acc:MGI:1915406]		Q91VR8	-5.9	5.3E-07	8.4	4.3E-05	-0.7	6.0E-01	-0.7	2.6E-01
ENSMUST00000035346	nucleolar protein 4-like [Source:MGI Symbol;Acc:MGI:1918765]	Q3UH85		2.6	8.4E-02	5.4	1.6E-03	-0.9	5.2E-01	-3.7	5.9E-03
ENSMUST00000035350	aftiphilin [Source:MGI Symbol;Acc:MGI:1923012]		Q80WT5	-4.8	2.5E-01	-4.4	2.7E-01	-2.1	3.5E-01	-2.5	6.1E-01
ENSMUST00000035732	tektin 3 [Source:MGI Symbol;Acc:MGI:1918312]	Q5SXS5	Q6X6Z7	7.4	4.3E-05	7.9	1.1E-05	-0.3	7.5E-01	0.4	4.3E-01
ENSMUST00000035735	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2 [Source:MGI Symbol;Acc:MGI:3039567]		Q4FZG9	7.2	5.6E-05	5.2	1.6E-03	-1.9	1.5E-01	0.1	9.1E-01
ENSMUST00000035771	CD2 antigen (cytoplasmic tail) binding protein 2 [Source:MGI Symbol;Acc:MGI:1917483]		Q9CWK3	-2.3	2.8E-02	5.1	1.1E-03	0.7	4.8E-01	-0.9	2.4E-01
ENSMUST00000035773	son of sevenless homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:98355]	A0A0A0MQ87		-8.6	5.6E-06	1.3	3.0E-01	-4.1	1.5E-02	0.0	9.9E-01
ENSMUST00000035776	deoxynucleotidyltransferase, terminal, interacting protein 2 [Source:MGI Symbol;Acc:MGI:1923173]		Q8R2M2	-5.1	1.2E-04	6.7	9.2E-04	-0.7	6.5E-01	-0.1	9.5E-01
ENSMUST00000035779	acyl-CoA synthetase long-chain family member 3 [Source:MGI Symbol;Acc:MGI:1921455]		Q9CZW4	4.5	9.1E-04	2.7	1.5E-02	-0.8	3.5E-01	-0.9	2.4E-01
ENSMUST00000035426	RIKEN cDNA 3110001I22 gene [Source:MGI Symbol;Acc:MGI:1913848]	Q9CZ70		-1.5	4.1E-02	-0.2	7.8E-01	0.4	5.2E-01	-0.9	2.5E-01
ENSMUST00000035427	small nuclear RNA activating complex, polypeptide 4 [Source:MGI Symbol;Acc:MGI:2443935]		Q8BP86	6.0	4.9E-02	0.3	9.1E-01	-5.3	5.7E-02	0.4	8.7E-01
ENSMUST00000035780	OMA1 homolog, zinc metallopeptidase (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914263]		Q9D8H7	-2.4	1.4E-03	2.6	5.4E-03	0.3	6.3E-01	0.3	6.6E-01
ENSMUST00000035785	signal sequence receptor, beta [Source:MGI Symbol;Acc:MGI:1913506]		Q9CPW5	5.4	5.2E-03	-6.0	3.5E-02	0.4	6.3E-01	0.6	8.2E-01
ENSMUST00000035797	RAB26, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2443284]	Q148R0	Q504M8	6.2	7.0E-03	3.1	3.1E-03	0.2	8.3E-01	-1.0	1.4E-01
ENSMUST00000035799	fibrinogen-like protein 2 [Source:MGI Symbol;Acc:MGI:103266]	Q544K3	P12804	-6.0	1.4E-07	9.3	8.8E-06	-0.6	6.1E-01	-0.5	2.9E-01
ENSMUST00000035800	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 1 [Source:MGI Symbol;Acc:MGI:102469	Q9DBQ6		-3.0	8.1E-04	-1.6	2.1E-01	-0.2	7.9E-01	-2.0	1.5E-01
ENSMUST00000035484	carnitine deficiency-associated gene expressed in ventricle 3 [Source:MGI Symbol;Acc:MGI:2448759]		Q4VAA2	-2.3	3.9E-01	0.6	6.9E-01	-2.4	1.6E-01	-5.3	4.6E-02
ENSMUST00000035812	tubulin tyrosine ligase [Source:MGI Symbol;Acc:MGI:1916987]		P38585	2.8	4.1E-04	5.5	1.3E-03	-1.1	4.2E-01	-1.6	6.3E-02
ENSMUST00000035813	protein phosphatase 1, regulatory (inhibitor) subunit 9A [Source:MGI Symbol;Acc:MGI:2442401]	Q7TN74		3.1	8.3E-03	-8.9	3.2E-03	0.6	3.5E-01	0.5	8.3E-01
ENSMUST00000035495	Fanconi anemia, complementation group A [Source:MGI Symbol;Acc:MGI:1341823]		Q9JL70	0.9	2.3E-01	3.0	1.3E-02	1.9	4.5E-02	-0.2	7.7E-01
ENSMUST00000035824	protein tyrosine phosphatase domain containing 1 [Source:MGI Symbol;Acc:MGI:2145430]		Q6NZK8	4.4	2.4E-04	5.0	1.1E-04	0.3	6.7E-01	-0.2	7.1E-01
ENSMUST00000035840	zinc finger, DHHC domain containing 5 [Source:MGI Symbol;Acc:MGI:1923573]		Q8VDZ4	-2.5	2.7E-04	5.2	1.5E-02	-0.7	7.2E-01	1.3	2.6E-01
ENSMUST00000035842	Ras association (RalGDS/AF-6) domain family member 4 [Source:MGI Symbol;Acc:MGI:2386853]		Q8CB96	-2.9	8.0E-06	6.6	1.3E-03	-0.4	7.8E-01	-1.0	2.6E-01
ENSMUST00000035852	zinc finger, CW type with PWWP domain 1 [Source:MGI Symbol;Acc:MGI:2685899]		Q6IR42	3.0	7.1E-03	-4.7	1.8E-02	0.5	5.4E-01	2.4	1.9E-01
ENSMUST00000035854	CMT1A duplicated region transcript 4 [Source:MGI Symbol;Acc:MGI:1913588]		Q9DA64	7.0	5.8E-04	6.9	1.8E-03	-1.4	4.4E-01	-2.9	1.5E-02
ENSMUST00000035861	peroxisomal biogenesis factor 5 [Source:MGI Symbol;Acc:MGI:1098808]		O09012	-5.3	7.0E-04	0.4	6.2E-01	-5.5	6.3E-04	-0.4	6.3E-01
ENSMUST00000035870	Fancd2 opposite strand [Source:MGI Symbol;Acc:MGI:1918229]			6.8	3.2E-03	6.8	1.4E-04	-0.5	6.8E-01	-1.2	7.6E-02
ENSMUST00000035539	dynein, axonemal, heavy chain 2 [Source:MGI Symbol;Acc:MGI:107731]		P0C6F1	-0.5	8.2E-01	3.1	1.7E-01	0.3	8.6E-01	-3.3	1.4E-01
ENSMUST00000035540	PHD finger protein 2 [Source:MGI Symbol;Acc:MGI:1338034]		Q9WTU0	-0.8	9.9E-02	0.1	8.6E-01	1.0	3.4E-02	0.1	7.9E-01
ENSMUST00000035871	transmembrane protein 127 [Source:MGI Symbol;Acc:MGI:1916720]		Q8BGP5	-3.9	4.3E-05	9.0	1.6E-04	-0.8	6.2E-01	-0.4	5.8E-01
ENSMUST00000035889	myosin VI [Source:MGI Symbol;Acc:MGI:104785]	E9Q3L1		4.2	7.9E-03	6.8	5.3E-04	-1.1	4.3E-01	-0.2	7.4E-01
ENSMUST00000035890	carrier family 7, (cationic amino acid transporter, y+ system) member 13 [Source:MGI Symbol;Acc:MGI:192		Q91WN3	8.9	1.0E-05	2.5	8.5E-03	0.5	4.8E-01	-0.1	8.4E-01
ENSMUST00000035908	early growth response 3 [Source:MGI Symbol;Acc:MGI:1306780]		P43300	6.1	1.1E-04	2.9	4.1E-04	-0.6	2.2E-01	-0.2	7.0E-01
ENSMUST00000035597	signal peptide peptidase like 2B [Source:MGI Symbol;Acc:MGI:1920468]		Q3TD49	-1.3	5.0E-02	-0.6	4.3E-01	0.8	1.2E-01	0.2	8.1E-01
ENSMUST00000035604	gem (nuclear organelle) associated protein 5 [Source:MGI Symbol;Acc:MGI:2449311]		Q8BX17	0.2	7.5E-01	-0.8	4.4E-01	0.1	8.7E-01	1.2	2.5E-01
ENSMUST00000035914	cDNA sequence BC034090 [Source:MGI Symbol;Acc:MGI:2672904]	F6T2X5		6.2	1.6E-03	-1.4	8.5E-02	0.1	8.3E-01	-0.3	6.3E-01
ENSMUST00000035918	cytochrome P450, family 3, subfamily a, polypeptide 11 [Source:MGI Symbol;Acc:MGI:88609]	Q3UEN8	Q64459	5.9	3.9E-04	7.1	2.0E-04	-0.6	6.6E-01	-0.1	8.8E-01
ENSMUST00000035925	solute carrier family 7, member 6 opposite strand [Source:MGI Symbol;Acc:MGI:1916951]		Q7TPE5	-2.5	7.0E-03	-0.4	5.2E-01	0.9	7.2E-02	0.1	9.1E-01
ENSMUST00000035930	zinc finger protein 800 [Source:MGI Symbol;Acc:MGI:1889334]	B7ZMR9	Q0VEE6	4.9	3.0E-03	7.2	5.3E-05	-0.6	6.1E-01	0.1	8.8E-01
ENSMUST00000035934	exocyst complex component 3 [Source:MGI Symbol;Acc:MGI:2443972]	Q8K0E2	Q6KAR6	-2.6	2.7E-04	3.1	1.2E-02	-1.7	1.2E-01	-0.9	2.8E-01
ENSMUST00000035935	coiled-coil domain containing 40 [Source:MGI Symbol;Acc:MGI:2443893]		Q8BI79	7.9	5.0E-05	-0.9	2.1E-01	0.6	2.3E-01	0.0	9.6E-01
ENSMUST00000035960	4HAUS augmin-like complex, subunit 8 [Source:MGI Symbol;Acc:MGI:1923728]		Q99L00	-2.0	2.8E-02	-3.2	1.0E-03	0.3	4.2E-01	0.3	7.0E-01
ENSMUST00000035651	leucine rich repeat containing 17 [Source:MGI Symbol;Acc:MGI:1921761]		Q9CXD9	0.5	4.8E-01	2.0	2.9E-02	0.1	8.5E-01	-1.4	7.7E-02
ENSMUST00000035977	TOPBP1-interacting checkpoint and replication regulator [Source:MGI Symbol;Acc:MGI:1924261]		Q8BQ33	4.2	2.1E-05	-1.2	8.7E-02	-0.1	8.8E-01	-0.8	2.9E-01
ENSMUST00000035983	ribosomal protein L21 [Source:MGI Symbol;Acc:MGI:1278340]	Q9CQM8		3.1	3.0E-03	9.3	4.1E-06	-1.5	2.0E-01	-0.1	7.3E-01
ENSMUST00000035987	mitogen-activated protein kinase kinase kinase 9 [Source:MGI Symbol;Acc:MGI:2449952]		Q3U1V8	-2.7	2.3E-04	3.8	8.7E-05	0.2	6.3E-01	-0.8	1.1E-01
ENSMUST00000035988	thioredoxin domain containing 5 [Source:MGI Symbol;Acc:MGI:2145316]	Q3TEE8	Q91W90	-6.5	2.4E-04	2.6	1.2E-03	-4.5	4.8E-05	-0.1	8.7E-01
ENSMUST00000036004	heterogeneous nuclear ribonucleoprotein A1 [Source:MGI Symbol;Acc:MGI:104820]	Q5EBP8		1.5	3.1E-02	-2.0	8.1E-03	1.1	1.4E-02	-0.1	8.2E-01
ENSMUST00000036016	anti-Mullerian hormone [Source:MGI Symbol;Acc:MGI:88006]	Q5EC55		3.2	1.4E-03	5.8	1.3E-03	1.7	1.9E-01	-0.6	4.4E-01
ENSMUST00000036018	forkhead box A3 [Source:MGI Symbol;Acc:MGI:1347477]		P35584	8.5	9.6E-05	3.7	6.2E-03	-2.0	1.1E-01	-0.3	7.0E-01
ENSMUST00000036019	Fraser syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:2385368]		Q80T14	9.8	1.4E-06	8.8	2.0E-05	-0.6	6.0E-01	-0.6	2.8E-01
ENSMUST00000035700	CaM kinase-like vesicle-associated [Source:MGI Symbol;Acc:MGI:2384296]		Q3UHL1	2.6	5.3E-02	7.3	1.2E-04	-0.5	6.8E-01	-5.2	1.9E-04
ENSMUST00000036031	gamma-secretase activating protein [Source:MGI Symbol;Acc:MGI:2442259]		Q3TCV3	-3.0	1.2E-03	6.8	2.5E-04	-0.4	7.3E-01	-0.8	2.4E-01
ENSMUST00000036033	DIP2 disco-interacting protein 2 homolog A (Drosophila) [Source:MGI Symbol;Acc:MGI:2385920]	F8WI56		-4.6	1.7E-02	7.3	5.7E-04	-1.0	5.3E-01	1.0	2.2E-01
ENSMUST00000036049	hydroxysteroid dehydrogenase like 1 [Source:MGI Symbol;Acc:MGI:1919802]		Q8BTX9	-2.3	2.6E-03	-6.7	9.3E-04	0.1	8.6E-01	-0.6	7.1E-01
ENSMUST00000036060	ISL1 transcription factor, LIM/homeodomain [Source:MGI Symbol;Acc:MGI:101791]	A2RSV5	P61372	5.8	2.8E-03	-2.9	7.0E-03	0.4	3.4E-01	0.0	9.9E-01
ENSMUST00000036069	MAM domain containing 2 [Source:MGI Symbol;Acc:MGI:1918988]			5.3	1.2E-04	-2.6	1.1E-02	1.0	5.9E-02	0.4	6.0E-01
ENSMUST00000036070	family with sequence similarity 107, member A [Source:MGI Symbol;Acc:MGI:3041256]	Q78TU8		8.3	2.8E-04	-5.4	9.5E-06	0.5	9.0E-02	-0.1	9.2E-01
ENSMUST00000036072	RIKEN cDNA 5031414D18 gene [Source:MGI Symbol;Acc:MGI:2685590]	F8WGX2		-2.8	1.7E-04	6.8	1.7E-04	-0.6	6.4E-01	0.1	9.2E-01
ENSMUST00000036074	Gem-interacting protein [Source:MGI Symbol;Acc:MGI:1926066]		Q6PGG2	-3.9	2.6E-04	5.9	2.7E-04	-1.4	2.3E-01	-0.2	8.0E-01
ENSMUST00000035742	tumor necrosis factor receptor superfamily, member 23 [Source:MGI Symbol;Acc:MGI:1930269]	F8WH78		-1.3	7.4E-02	-0.1	9.3E-01	0.8	1.8E-01	-0.4	6.2E-01
ENSMUST00000035766	WD repeat domain 44 [Source:MGI Symbol;Acc:MGI:1919654]		Q6NVE8	-0.2	8.4E-01	-0.1	9.7E-01	2.0	5.3E-02	1.9	1.3E-01
ENSMUST00000036085	F-box and WD-40 domain protein 10 [Source:MGI Symbol;Acc:MGI:3052463]		Q5SUS0	7.5	8.1E-04	-2.9	5.7E-02	0.0	9.8E-01	0.6	6.6E-01
ENSMUST00000036089	tripartite motif-containing 69 [Source:MGI Symbol;Acc:MGI:1918178]		Q80X56	3.3	1.1E-03	-4.2	5.8E-03	3.7	3.9E-05	-0.7	5.8E-01
ENSMUST00000035775	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913344]		Q9CQQ8	-1.4	4.4E-01	-2.2	1.0E-01	-4.5	4.4E-03	-3.6	4.7E-02
ENSMUST00000036092	otassium voltage-gated channel, subfamily H (eag-related), member 2 [Source:MGI Symbol;Acc:MGI:1341722	Q53Z09		8.5	1.0E-04	-4.9	6.7E-04	-0.6	2.6E-01	-0.7	5.0E-01
ENSMUST00000035777	MON1 homolog b (yeast) [Source:MGI Symbol;Acc:MGI:1923231]		Q8BMQ8	-2.5	7.7E-02	0.5	7.4E-01	1.1	3.2E-01	-1.9	2.2E-01
ENSMUST00000036109	family with sequence similarity 101, member A [Source:MGI Symbol;Acc:MGI:1920371]		Q7TS73	7.1	1.0E-04	5.7	1.0E-03	1.2	3.4E-01	0.0	9.6E-01
ENSMUST00000036111	mitochondrial ribosomal protein S35 [Source:MGI Symbol;Acc:MGI:2385255]			-5.4	1.1E-04	-3.4	1.1E-03	0.1	8.3E-01	1.1	1.6E-01
ENSMUST00000036113	TBC1 domain family, member 16 [Source:MGI Symbol;Acc:MGI:2652878]	A2ABG4		3.9	1.4E-04	6.1	4.4E-03	-0.6	7.2E-01	-1.3	2.2E-01
ENSMUST00000036116	tetratricopeptide repeat domain 9 [Source:MGI Symbol;Acc:MGI:1916730]		Q3V038	6.6	1.9E-05	5.7	1.7E-02	-0.7	7.3E-01	-0.3	8.1E-01
ENSMUST00000036125	eukaryotic translation initiation factor 4H [Source:MGI Symbol;Acc:MGI:1341822]	Q3TG58	Q9WUK2	-4.6	6.4E-06	-5.7	1.0E-06	-0.4	8.2E-02	-0.7	1.9E-01
ENSMUST00000036126	poly (ADP-ribose) polymerase family, member 2 [Source:MGI Symbol;Acc:MGI:1341112]		O88554	-1.7	2.9E-02	-2.1	2.8E-02	1.0	6.3E-02	0.1	9.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000035804	cysteine dioxygenase 1, cytosolic [Source:MGI Symbol;Acc:MGI:105925]		P60334	0.4	5.9E-01	0.3	7.3E-01	-0.5	3.9E-01	-0.4	5.5E-01
ENSMUST00000036127	heat shock transcription factor 4 [Source:MGI Symbol;Acc:MGI:1347058]	B2RQY2	Q9R0L1	4.9	3.2E-02	2.3	5.4E-03	-0.3	5.7E-01	0.2	7.2E-01
ENSMUST00000036136	collectin sub-family member 11 [Source:MGI Symbol;Acc:MGI:1918943]			3.8	1.6E-03	4.6	6.8E-03	0.7	5.8E-01	-0.8	3.5E-01
ENSMUST00000035822	calcium homeostasis modulator 2 [Source:MGI Symbol;Acc:MGI:1919941]		Q8VEC4	-2.7	4.1E-02	-1.0	5.0E-01	0.8	4.0E-01	-0.8	5.7E-01
ENSMUST00000036153	(constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:19		Q8VBV7	-2.8	2.0E-04	2.8	6.4E-03	-1.9	3.3E-02	-0.4	5.5E-01
ENSMUST00000035836	inositol polyphosphate phosphatase-like 1 [Source:MGI Symbol;Acc:MGI:1333787]		Q6P549	1.9	5.0E-01	1.8	6.2E-01	-0.9	7.8E-01	-0.8	7.8E-01
ENSMUST00000036155	X-ray radiation resistance associated 1 [Source:MGI Symbol;Acc:MGI:2181647]		Q3U3V8	5.5	3.8E-05	-1.3	4.5E-02	1.0	1.8E-02	-0.2	6.8E-01
ENSMUST00000036158	solute carrier family 35, member A4 [Source:MGI Symbol;Acc:MGI:1915093]		Q9D321	-4.8	8.1E-03	-1.9	7.8E-04	0.5	6.6E-02	-0.5	2.2E-01
ENSMUST00000035844	Josephin domain containing 2 [Source:MGI Symbol;Acc:MGI:1913374]		Q9CR30	-0.1	9.1E-01	1.7	2.9E-01	1.4	3.2E-01	-0.5	6.9E-01
ENSMUST00000035850	nuclear protein in the AT region [Source:MGI Symbol;Acc:MGI:107605]		Q8BMA5	0.3	5.6E-01	0.0	9.5E-01	-0.1	7.9E-01	0.2	7.3E-01
ENSMUST00000036172	sphingosine-1-phosphate phosphotase 2 [Source:MGI Symbol;Acc:MGI:3589109]		Q810K3	7.4	2.0E-06	0.9	4.2E-01	-0.8	3.5E-01	1.3	1.7E-01
ENSMUST00000036174	GRAM domain containing 1C [Source:MGI Symbol;Acc:MGI:2443024]		Q8CI52	7.1	5.6E-04	6.5	1.7E-03	-0.7	6.8E-01	-0.1	8.6E-01
ENSMUST00000036177	engrailed 2 [Source:MGI Symbol;Acc:MGI:95390]	Q3TZM2	P09066	7.5	2.2E-04	-2.2	1.7E-01	2.9	9.1E-03	-0.1	9.4E-01
ENSMUST00000036181	carbonic anhydrase 14 [Source:MGI Symbol;Acc:MGI:1344341]		Q9WVT6	4.3	2.7E-03	5.3	2.1E-02	-0.7	7.4E-01	0.9	4.7E-01
ENSMUST00000036188	zinc finger CCCH type containing 12A [Source:MGI Symbol;Acc:MGI:2385891]		Q5D1E7	-1.9	1.1E-02	-3.1	1.9E-03	1.1	1.7E-02	0.3	6.7E-01
ENSMUST00000036208	solute carrier family 9 (sodium/hydrogen exchanger), member 3 [Source:MGI Symbol;Acc:MGI:105064]		G3X939	8.3	5.3E-05	-0.6	6.7E-01	-4.4	4.8E-03	0.3	7.8E-01
ENSMUST00000036210	protein O-glucosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2444232]		Q8BYB9	-3.0	1.1E-02	8.0	4.8E-05	-0.5	6.6E-01	0.3	5.7E-01
ENSMUST00000035899	biogenesis of lysosomal organelles complex-1, subunit 5, muted [Source:MGI Symbol;Acc:MGI:2178598]		Q8R015	-0.9	9.3E-02	-0.2	7.3E-01	0.0	9.1E-01	-0.7	2.2E-01
ENSMUST00000036211	G-protein coupled receptor 12 [Source:MGI Symbol;Acc:MGI:101909]		P35412	6.6	1.2E-04	4.7	2.0E-03	-1.6	1.9E-01	-0.1	8.4E-01
ENSMUST00000035911	RING CCCH (C3H) domains 1 [Source:MGI Symbol;Acc:MGI:2685397]	H7BX02		-1.4	5.7E-02	-2.0	6.7E-02	0.1	8.0E-01	0.7	4.6E-01
ENSMUST00000036215	forkhead box J1 [Source:MGI Symbol;Acc:MGI:1347474]		Q61660	7.5	2.1E-05	5.4	6.0E-03	-0.5	7.7E-01	0.3	7.6E-01
ENSMUST00000036225	embrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) [Source:MGI Symbol;Acc:MGI:192734	Q3UN60	Q9JLB0	-4.4	8.6E-04	2.9	9.1E-03	-3.0	1.9E-02	0.1	9.2E-01
ENSMUST00000036226	fem-1 homolog c (C.elegans) [Source:MGI Symbol;Acc:MGI:2444737]	B2RRW5	Q8CEF1	-3.2	2.0E-03	-2.1	4.4E-02	0.4	4.4E-01	0.1	9.2E-01
ENSMUST00000036227	5-hydroxytryptamine (serotonin) receptor 5A [Source:MGI Symbol;Acc:MGI:96283]		P30966	8.8	9.0E-06	2.9	1.0E-01	-0.9	5.5E-01	1.0	3.6E-01
ENSMUST00000036229	xy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 [Source:MGI Symbol;Acc:MC		Q7TSG2	-1.6	4.6E-03	-2.3	3.4E-03	0.2	6.3E-01	-0.1	8.8E-01
ENSMUST00000036248	prostate transmembrane protein, androgen induced 1 [Source:MGI Symbol;Acc:MGI:1929600]	A2APF4		5.3	1.0E-04	7.1	2.3E-04	-0.6	6.7E-01	0.2	7.4E-01
ENSMUST00000035938	chemokine (C-C motif) ligand 5 [Source:MGI Symbol;Acc:MGI:98262]	Q5XZF2	P30882	-1.8	3.7E-02	-2.5	1.6E-02	-1.2	5.0E-02	-0.5	5.4E-01
ENSMUST00000036267	carbohydrate sulfotransferase 2 [Source:MGI Symbol;Acc:MGI:1891160]		Q80WV3	8.8	4.2E-06	6.0	1.1E-03	-0.6	6.7E-01	0.7	3.2E-01
ENSMUST00000035952	nerve growth factor [Source:MGI Symbol;Acc:MGI:97321]		P01139	4.0	6.4E-02	4.9	3.5E-02	-1.4	5.5E-01	-2.3	1.0E-01
ENSMUST00000036274	signal peptidase complex subunit 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913874]		Q9CYN2	-3.7	6.0E-06	-0.8	4.0E-01	0.9	2.3E-01	-0.3	7.5E-01
ENSMUST00000036288	R3H domain containing 1 [Source:MGI Symbol;Acc:MGI:2448514]	E9Q9Q2		-5.7	3.3E-04	4.7	8.2E-05	1.1	1.0E-01	0.6	2.3E-01
ENSMUST00000035982	WW domain containing E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1861728]		Q8BZZ3	-1.2	3.2E-01	-1.1	4.1E-01	-0.1	9.3E-01	-0.1	9.3E-01
ENSMUST00000036300	collagen, type XXVII, alpha 1 [Source:MGI Symbol;Acc:MGI:2672118]		Q5QNQ9	4.1	3.8E-03	2.0	4.5E-02	-1.2	1.6E-01	-0.1	9.1E-01
ENSMUST00000036321	zinc finger, DHHC domain containing 23 [Source:MGI Symbol;Acc:MGI:2685625]	B7ZNY8		5.1	4.7E-03	-1.2	6.7E-02	1.5	4.2E-03	0.0	9.4E-01
ENSMUST00000036328	zinc finger homeobox 2 [Source:MGI Symbol;Acc:MGI:2686934]	Q2MHN3		5.2	8.6E-06	-5.3	7.2E-04	-0.7	1.6E-01	-1.8	1.9E-01
ENSMUST00000035991	basic, immunoglobulin-like variable motif containing [Source:MGI Symbol;Acc:MGI:2179809]		Q8CBX9	-2.4	8.9E-02	1.5	4.5E-01	3.2	6.6E-02	-0.7	6.7E-01
ENSMUST00000036003	kelch-like 42 [Source:MGI Symbol;Acc:MGI:2444786]	B2KFS7	Q8BFQ9	0.9	5.1E-02	1.3	3.7E-02	0.8	7.0E-02	0.4	3.9E-01
ENSMUST00000036329	WD repeat domain 26 [Source:MGI Symbol;Acc:MGI:1923825]	F8WH48		-7.1	2.6E-04	-0.3	6.5E-01	-2.0	5.3E-03	-0.1	8.2E-01
ENSMUST00000036331	neuraminidase 3 [Source:MGI Symbol;Acc:MGI:1355305]	Q543I9	Q9JMH7	5.6	2.0E-06	4.0	1.1E-03	0.4	6.2E-01	-0.4	5.3E-01
ENSMUST00000036340	Fanconi anemia, complementation group D2 [Source:MGI Symbol;Acc:MGI:2448480]	B2RSU4	Q80V62	1.7	5.3E-03	7.5	4.2E-04	-0.7	6.5E-01	0.2	7.7E-01
ENSMUST00000036350	cerebral dopamine neurotrophic factor [Source:MGI Symbol;Acc:MGI:3606576]		Q8CC36	5.9	6.9E-05	7.0	8.6E-06	-3.0	1.1E-02	-0.2	6.3E-01
ENSMUST00000036025	coiled-coil domain containing 93 [Source:MGI Symbol;Acc:MGI:1918079]		Q7TQK5	0.0	9.4E-01	0.8	3.2E-01	0.5	4.0E-01	-0.2	7.4E-01
ENSMUST00000036362	linker for activation of T cells family, member 2 [Source:MGI Symbol;Acc:MGI:1926479]		Q9JHL0	-7.0	6.9E-05	-2.8	8.3E-03	0.3	6.0E-01	0.1	9.4E-01
ENSMUST00000036370	T cell activation Rho GTPase activating protein [Source:MGI Symbol;Acc:MGI:3615484]		B2RWW0	-1.6	4.8E-03	-2.8	1.6E-01	0.7	5.5E-01	-1.0	6.1E-01
ENSMUST00000036041	adaptor protein complex AP-1, gamma 2 subunit [Source:MGI Symbol;Acc:MGI:1328307]		O88512	0.4	8.6E-01	3.8	1.1E-01	0.5	8.0E-01	-2.9	1.8E-01
ENSMUST00000036044	zinc finger, C3H1-type containing [Source:MGI Symbol;Acc:MGI:2446143]	B2RT41		-1.2	7.7E-02	-0.5	5.7E-01	0.8	1.6E-01	0.1	9.1E-01
ENSMUST00000036372	chondroitin sulfate synthase 1 [Source:MGI Symbol;Acc:MGI:2681120]		Q6ZQ11	-4.3	4.6E-05	-1.3	1.2E-01	1.3	2.5E-02	0.3	7.3E-01
ENSMUST00000036376	transmembrane and ubiquitin-like domain containing 2 [Source:MGI Symbol;Acc:MGI:1919303]		Q3V209	-8.6	2.6E-04	5.4	7.9E-03	-0.5	7.8E-01	0.0	9.9E-01
ENSMUST00000036380	ATPase, H+ transporting, lysosomal V0 subunit B [Source:MGI Symbol;Acc:MGI:1890510]	Q3U889	Q91V37	-9.9	3.0E-05	4.7	1.4E-03	-0.7	4.7E-01	-0.2	7.6E-01
ENSMUST00000036381	charged multivesicular body protein 7 [Source:MGI Symbol;Acc:MGI:1913922]		Q8R1T1	-2.3	1.6E-03	6.7	6.0E-03	-0.2	9.1E-01	1.4	2.3E-01
ENSMUST00000036382	glycerate kinase [Source:MGI Symbol;Acc:MGI:2444085]			9.9	1.0E-05	-1.5	2.7E-02	0.9	2.3E-02	-0.4	5.5E-01
ENSMUST00000036383	dynein, axonemal, light intermediate polypeptide 1 [Source:MGI Symbol;Acc:MGI:1922813]	Q0IIN3	Q8BVN8	5.6	1.1E-04	-3.1	8.2E-03	1.1	5.5E-02	0.3	7.9E-01
ENSMUST00000036387	S100 protein, beta polypeptide, neural [Source:MGI Symbol;Acc:MGI:98217]	Q3UY00	P50114	7.0	1.2E-04	8.0	8.3E-04	-0.8	6.7E-01	-1.3	1.8E-01
ENSMUST00000036088	ucleotide binding protein (G protein), gamma transducing activity polypeptide 2 [Source:MGI Symbol;Acc:MG	A2A614	Q61017	0.9	2.9E-01	0.3	7.4E-01	-0.6	4.2E-01	-0.1	9.5E-01
ENSMUST00000036407	family with sequence similarity 160, member B1 [Source:MGI Symbol;Acc:MGI:2147545]		Q8CDM8	-2.7	9.4E-05	4.0	7.2E-04	-0.6	4.6E-01	-1.2	9.5E-02
ENSMUST00000036424	arachidonate 12-lipoxygenase, 12R type [Source:MGI Symbol;Acc:MGI:1274782]	Q2KHL0	O70582	7.3	3.2E-05	5.8	5.3E-04	-2.5	9.5E-02	0.2	8.0E-01
ENSMUST00000036426	protease, serine 35 [Source:MGI Symbol;Acc:MGI:2444800]		Q8C0F9	9.5	9.8E-06	6.2	5.1E-04	-0.6	6.3E-01	0.3	6.5E-01
ENSMUST00000036439	cadherin 6 [Source:MGI Symbol;Acc:MGI:107435]		P97326	7.3	2.2E-05	-5.9	1.9E-03	0.8	1.4E-01	1.3	3.8E-01
ENSMUST00000036456	centrosomal protein 72 [Source:MGI Symbol;Acc:MGI:1921720]		Q9D3R3	1.8	6.5E-03	3.6	7.9E-04	-0.6	3.6E-01	-0.3	5.6E-01
ENSMUST00000036467	ankyrin repeat and SOCS box-containing 16 [Source:MGI Symbol;Acc:MGI:2654437]		Q8VHS5	6.3	3.6E-05	3.3	8.8E-04	-3.6	1.3E-03	-0.3	6.2E-01
ENSMUST00000036470	coiled-coil domain containing 32 [Source:MGI Symbol;Acc:MGI:2685477]	Q3UHY7		-1.7	3.9E-03	-3.4	3.9E-04	1.0	1.3E-02	-0.2	7.0E-01
ENSMUST00000036473	protein-O-mannosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2138994]		Q8R2R1	-4.3	2.0E-02	-2.3	1.9E-02	-0.2	7.4E-01	0.5	5.7E-01
ENSMUST00000036489	round spermatid basic protein 1-like [Source:MGI Symbol;Acc:MGI:3036237]	D3Z0K6		-2.6	1.4E-04	5.4	2.7E-02	-0.7	7.4E-01	-1.2	4.2E-01
ENSMUST00000036493	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:MGI Symbol;Acc:MGI:88105]		Q8VDN2	-4.7	2.0E-06	6.2	6.4E-04	0.9	4.7E-01	-1.5	6.0E-02
ENSMUST00000036503	zinc finger, AN1-type domain 4 [Source:MGI Symbol;Acc:MGI:1914742]	D3Z5M1		-7.8	4.6E-04	-2.6	1.9E-03	0.4	2.5E-01	0.2	7.6E-01
ENSMUST00000036509	ubiquitin associated domain containing 1 [Source:MGI Symbol;Acc:MGI:1920995]		Q8VDI7	-1.6	1.6E-02	4.2	5.0E-04	-1.5	7.1E-02	-0.3	6.6E-01
ENSMUST00000036156	importin 13 [Source:MGI Symbol;Acc:MGI:2385205]		Q8K0C1	-0.8	1.4E-01	-0.2	7.8E-01	0.9	9.9E-02	0.3	7.1E-01
ENSMUST00000036540	family with sequence similarity 117, member B [Source:MGI Symbol;Acc:MGI:1920000]		Q3U3E2	-2.6	3.5E-04	-2.9	1.1E-01	1.1	2.9E-01	-0.8	6.8E-01
ENSMUST00000036161	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide [Source:MGI Symbol;Acc:MGI:2448506]	E9Q3L2		-2.1	1.1E-01	-3.3	6.8E-02	0.5	5.9E-01	1.7	3.1E-01
ENSMUST00000036541	ADP-ribosylation factor-like 5A [Source:MGI Symbol;Acc:MGI:1922673]	Q498A0	Q80ZU0	-2.6	8.1E-04	5.6	1.2E-05	-2.2	1.3E-02	-0.3	4.7E-01
ENSMUST00000036554	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 [Source:MGI Symbol;Acc:MGI:2443111]	E9Q236		-4.2	3.0E-02	6.6	1.5E-03	-0.7	6.6E-01	-0.2	8.0E-01
ENSMUST00000036176	Rho GTPase activating protein 39 [Source:MGI Symbol;Acc:MGI:107858]	G3X932		-0.9	5.7E-01	0.2	9.4E-01	0.6	6.6E-01	-0.4	8.4E-01
ENSMUST00000036555	myosin VC [Source:MGI Symbol;Acc:MGI:2442485]	E9Q1F5		7.2	9.4E-07	7.3	4.5E-04	-0.6	6.7E-01	-0.5	5.5E-01
ENSMUST00000036561	WD repeat domain 48 [Source:MGI Symbol;Acc:MGI:1914811]		Q8BH57	-3.8	8.0E-05	4.8	3.8E-03	-0.3	8.0E-01	-0.8	3.0E-01
ENSMUST00000036187	quiescin Q6 sulfhydryl oxidase 2 [Source:MGI Symbol;Acc:MGI:2387194]		Q3TMX7	0.3	7.4E-01	1.9	5.3E-02	0.3	7.2E-01	-1.4	1.1E-01
ENSMUST00000036570	otein, phosphotyrosine interaction, PH domain and leucine zipper containing 1 [Source:MGI Symbol;Acc:MGI		Q8K3H0	-1.6	2.9E-03	-0.3	7.2E-01	0.9	1.2E-01	-0.8	3.2E-01
ENSMUST00000036195	ly 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 [Source:MGI Symbol;A	A2AKQ0		0.7	5.1E-01	1.1	4.2E-01	0.2	8.1E-01	-0.1	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000036206	coiled-coil domain containing 92 [Source:MGI Symbol;Acc:MGI:106485]		Q8VDN4	0.5	7.2E-01	1.7	3.0E-01	0.6	6.5E-01	-0.7	6.3E-01
ENSMUST00000036576	coiled-coil domain containing 138 [Source:MGI Symbol;Acc:MGI:1923388]		Q0VF22	3.8	1.1E-03	8.2	1.7E-04	-0.1	9.6E-01	0.0	9.6E-01
ENSMUST00000036584	pantothenate kinase 1 [Source:MGI Symbol;Acc:MGI:1922985]		Q8K4K6	4.9	5.0E-03	-1.2	3.1E-01	0.1	9.2E-01	-1.8	1.5E-01
ENSMUST00000036592	RIKEN cDNA 1700034J05 gene [Source:MGI Symbol;Acc:MGI:1920594]		Q80W69	8.3	7.3E-06	7.1	1.2E-04	-0.5	7.0E-01	-1.0	1.4E-01
ENSMUST00000036618	stabilin 1 [Source:MGI Symbol;Acc:MGI:2178742]	G3X973		1.7	3.8E-03	7.4	9.8E-05	0.1	9.4E-01	0.1	8.2E-01
ENSMUST00000036221	F-box and leucine-rich repeat protein 8 [Source:MGI Symbol;Acc:MGI:1354697]	Q3TD55	Q8CIG9	-1.3	8.1E-02	0.2	8.1E-01	1.2	9.7E-02	-0.4	6.7E-01
ENSMUST00000036643	leucine rich repeat containing 52 [Source:MGI Symbol;Acc:MGI:1924118]		Q5M8M9	6.4	2.1E-04	-1.9	1.1E-01	1.0	1.1E-01	-1.5	2.2E-01
ENSMUST00000036653	5-hydroxytryptamine (serotonin) receptor 2A [Source:MGI Symbol;Acc:MGI:109521]	Q543D4	P35363	3.4	1.3E-02	-1.9	7.0E-02	1.0	9.5E-02	-0.2	8.4E-01
ENSMUST00000036665	component of oligomeric golgi complex 6 [Source:MGI Symbol;Acc:MGI:1914792]			-6.2	3.3E-05	7.9	4.6E-05	-0.6	6.1E-01	0.3	5.9E-01
ENSMUST00000036680	THAP domain containing, apoptosis associated protein 3 [Source:MGI Symbol;Acc:MGI:1917126]	Q52KE1	Q8BJ25	-2.7	8.5E-03	-0.6	2.7E-01	0.8	5.2E-02	-0.2	7.7E-01
ENSMUST00000036247	leucine rich repeat containing 24 [Source:MGI Symbol;Acc:MGI:3605040]		Q8VE95	-0.3	5.6E-01	0.9	2.4E-01	1.4	2.6E-02	0.2	7.3E-01
ENSMUST00000036682	PX domain containing serine/threonine kinase [Source:MGI Symbol;Acc:MGI:1289230]		Q8BX57	-5.5	3.8E-04	2.5	1.9E-02	-2.4	1.8E-02	0.4	5.8E-01
ENSMUST00000036252	lamin A [Source:MGI Symbol;Acc:MGI:96794]		P48678	1.9	4.4E-01	-0.3	9.1E-01	-3.2	1.7E-01	-1.0	6.7E-01
ENSMUST00000036253				-0.8	3.9E-01	0.6	5.9E-01	0.9	3.3E-01	-0.5	6.4E-01
ENSMUST00000036691	proline-rich coiled-coil 2B [Source:MGI Symbol;Acc:MGI:1923304]		Q7TPM1	-4.1	1.2E-02	5.7	1.8E-04	-2.0	6.5E-02	1.1	9.7E-02
ENSMUST00000036273	ır factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta [Source:MGI Symbol;Acc:MGI:193		Q9EST8	5.2	7.0E-02	5.9	5.3E-02	-0.9	7.7E-01	-1.5	4.2E-01
ENSMUST00000036700	adrenergic receptor, alpha 2a [Source:MGI Symbol;Acc:MGI:87934]	Q3URE6		3.3	3.5E-04	-3.4	6.3E-05	-0.1	7.5E-01	-0.3	5.5E-01
ENSMUST00000036715	predicted gene 3402 [Source:MGI Symbol;Acc:MGI:3781580]	K7N5P2		6.5	1.1E-02	-4.8	8.5E-03	0.9	1.6E-01	-0.1	9.7E-01
ENSMUST00000036299	calmodulin binding transcription activator 2 [Source:MGI Symbol;Acc:MGI:2135957]		Q80Y50	2.2	4.5E-01	-1.7	6.2E-01	-4.4	1.2E-01	-0.5	8.9E-01
ENSMUST00000036719	osphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1 [Source:MGI Symbol;Acc:MGI:30406		Q69ZK0	-4.9	1.1E-04	2.7	4.6E-02	-0.9	4.1E-01	0.5	6.2E-01
ENSMUST00000036315	glutamate receptor, ionotropic, AMPA1 (alpha 1) [Source:MGI Symbol;Acc:MGI:95808]		P23818	6.2	6.5E-02	4.0	2.6E-01	-0.6	8.6E-01	1.6	4.6E-01
ENSMUST00000036720	FK506 binding protein-like [Source:MGI Symbol;Acc:MGI:1932127]		O35450	-2.5	7.6E-04	6.0	2.3E-03	-1.0	5.0E-01	-1.9	9.8E-02
ENSMUST00000036732	cDNA sequence, BC016579 [Source:MGI Symbol;Acc:MGI:2384848]	E9QP50		5.2	2.3E-04	5.1	3.5E-05	0.0	9.4E-01	0.1	9.0E-01
ENSMUST00000036737	collectin sub-family member 10 [Source:MGI Symbol;Acc:MGI:3606482]		Q8CF98	7.2	4.1E-05	-5.4	8.5E-03	1.4	3.2E-02	-0.3	8.7E-01
ENSMUST00000036742	meteorin, glial cell differentiation regulator-like [Source:MGI Symbol;Acc:MGI:2384806]		Q8VE43	-3.4	3.7E-04	5.0	1.6E-05	-0.3	5.8E-01	0.3	4.7E-01
ENSMUST00000036333	protein kinase, X-linked [Source:MGI Symbol;Acc:MGI:1309999]		Q922R0	-0.4	4.6E-01	0.2	7.7E-01	1.2	6.2E-02	0.5	4.6E-01
ENSMUST00000036744	RNA binding motif protein 4B [Source:MGI Symbol;Acc:MGI:1913954]		Q8VE92	-4.0	1.5E-03	2.2	7.1E-03	0.7	1.9E-01	0.2	6.5E-01
ENSMUST00000036748	solute carrier family 38, member 8 [Source:MGI Symbol;Acc:MGI:2685433]		Q5HZH7	8.9	5.9E-05	4.8	5.9E-04	-1.0	3.2E-01	0.2	8.0E-01
ENSMUST00000036354	praja ring finger 1, E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1101765]	Q05CG5	O55176	-0.4	5.8E-01	-0.3	7.4E-01	-0.8	2.1E-01	-0.9	2.7E-01
ENSMUST00000036355	pleckstrin homology-like domain, family B, member 2 [Source:MGI Symbol;Acc:MGI:2444981]		Q8K1N2	5.3	3.8E-02	6.5	3.5E-02	0.1	9.6E-01	-1.1	4.7E-01
ENSMUST00000036360	cDNA sequence BC028528 [Source:MGI Symbol;Acc:MGI:2385885]		Q8R2K8	-2.3	9.1E-02	-5.9	3.8E-02	-0.8	4.3E-01	2.8	2.7E-01
ENSMUST00000036759	family with sequence similarity 21 [Source:MGI Symbol;Acc:MGI:106463]		Q6PGL7	-4.7	3.2E-05	-6.8	1.3E-03	0.5	3.6E-01	0.3	8.6E-01
ENSMUST00000036796	follistatin-like 4 [Source:MGI Symbol;Acc:MGI:2443199]		Q5STE3	9.1	1.2E-05	-1.0	8.2E-02	0.2	5.0E-01	-0.3	5.9E-01
ENSMUST00000036805	pleckstrin homology domain containing, family J member 1 [Source:MGI Symbol;Acc:MGI:1925920]		Q9D240	-4.8	2.3E-05	-3.8	8.5E-04	0.4	2.6E-01	0.0	9.5E-01
ENSMUST00000036374	prohibitin [Source:MGI Symbol;Acc:MGI:97572]	Q5SQG5		-2.6	6.9E-02	-2.8	7.8E-02	-1.2	2.0E-01	-1.0	5.1E-01
ENSMUST00000036819	RIKEN cDNA 9130409I23 gene [Source:MGI Symbol;Acc:MGI:3588271]	Q3TS87		6.7	8.7E-05	-6.3	8.5E-03	1.5	4.5E-02	-0.8	7.2E-01
ENSMUST00000036825	synuclein, beta [Source:MGI Symbol;Acc:MGI:1889011]		Q91ZZ3	6.3	8.2E-04	-6.2	2.9E-04	1.1	4.2E-02	-2.6	9.9E-02
ENSMUST00000036852	RecQ protein-like 4 [Source:MGI Symbol;Acc:MGI:1931028]			4.8	3.2E-05	-0.7	3.2E-01	1.3	1.6E-02	-0.4	5.9E-01
ENSMUST00000036854	EF hand domain containing 2 [Source:MGI Symbol;Acc:MGI:106504]	Q8C845		-6.0	1.5E-06	9.1	4.2E-05	-0.8	5.8E-01	0.0	9.4E-01
ENSMUST00000036862	component of oligomeric golgi complex 5 [Source:MGI Symbol;Acc:MGI:2145130]		Q8C0L8	-1.6	1.8E-02	5.7	1.6E-04	-0.7	4.5E-01	-0.8	1.8E-01
ENSMUST00000036872	WD repeat domain, phosphoinositide interacting 2 [Source:MGI Symbol;Acc:MGI:1923831]		Q80W47	-2.2	3.5E-03	6.1	6.1E-04	-0.7	6.1E-01	0.2	7.2E-01
ENSMUST00000036877	DENN/MADD domain containing 2A [Source:MGI Symbol;Acc:MGI:2444961]		Q8C4S8	1.4	1.4E-02	-1.3	2.4E-02	0.8	3.0E-02	-0.6	2.8E-01
ENSMUST00000036423	leucine rich repeat containing 14 [Source:MGI Symbol;Acc:MGI:2445060]		Q8VC16	-2.2	4.7E-01	-2.0	6.2E-01	0.6	8.0E-01	0.4	9.2E-01
ENSMUST00000036904	ring finger protein 139 [Source:MGI Symbol;Acc:MGI:1923091]			-3.6	8.1E-05	8.4	3.3E-05	0.0	9.8E-01	-1.0	8.9E-02
ENSMUST00000036932	doublecortin domain containing 2a [Source:MGI Symbol;Acc:MGI:2652818]		Q5DU00	6.5	1.5E-04	8.2	7.0E-05	-1.5	2.6E-01	-0.2	7.7E-01
ENSMUST00000036437	mitochondrial ribosomal protein L1 [Source:MGI Symbol;Acc:MGI:2137202]		Q99N96	-3.0	6.5E-02	1.6	3.8E-01	1.8	2.2E-01	-2.8	1.2E-01
ENSMUST00000036934	nebulin [Source:MGI Symbol;Acc:MGI:97292]	E9Q1W3		11.3	1.0E-03	7.3	4.2E-05	-0.6	6.1E-01	-0.6	3.0E-01
ENSMUST00000036450	spastic paraplegia 11 [Source:MGI Symbol;Acc:MGI:2444989]		Q3UHA3	-0.9	6.5E-02	-0.3	6.3E-01	0.5	2.1E-01	-0.1	8.7E-01
ENSMUST00000036453	mitogen-activated protein kinase kinase kinase 10 [Source:MGI Symbol;Acc:MGI:1346879]		Q66L42	3.5	9.1E-02	3.6	1.8E-01	0.5	8.2E-01	0.5	7.9E-01
ENSMUST00000036938	r carrier family 7 (cationic amino acid transporter, y+ system), member 15 [Source:MGI Symbol;Acc:MGI:304		Q8BZV2	8.0	4.4E-05	2.7	2.0E-03	0.1	7.9E-01	-0.7	1.7E-01
ENSMUST00000036951	phosphatidylethanolamine binding protein 1 [Source:MGI Symbol;Acc:MGI:1344408]	Q5EBQ2	P70296	-1.5	2.1E-02	6.3	9.4E-05	-0.7	5.1E-01	-0.7	2.7E-01
ENSMUST00000036952	RIKEN cDNA 9530068E07 gene [Source:MGI Symbol;Acc:MGI:2654705]	Q3U339	Q8K201	-6.9	4.8E-05	-1.0	8.9E-02	0.2	5.8E-01	-0.5	4.1E-01
ENSMUST00000036954	gastrulation brain homeobox 2 [Source:MGI Symbol;Acc:MGI:95668]		P48031	5.0	1.9E-03	-1.4	4.9E-01	1.5	2.9E-01	-1.5	4.5E-01
ENSMUST00000036476	kazrin, periplakin interacting protein [Source:MGI Symbol;Acc:MGI:1918779]		Q69ZS8	2.7	6.9E-02	4.5	7.2E-03	-0.6	6.9E-01	-2.4	4.4E-02
ENSMUST00000036991	heat shock protein 8 [Source:MGI Symbol;Acc:MGI:2135756]		Q9JK92	7.2	4.4E-05	-2.5	9.7E-04	0.3	3.7E-01	0.2	6.7E-01
ENSMUST00000036996	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 [Source:MGI Symbol;Acc:MGI:1914166]		Q9CR61	-7.6	2.1E-04	-4.0	5.6E-05	0.6	6.4E-02	-0.1	8.0E-01
ENSMUST00000036497	protein kinase, cAMP dependent regulatory, type II beta [Source:MGI Symbol;Acc:MGI:97760]		P31324	2.8	2.1E-01	-2.4	1.0E-01	-7.3	1.6E-03	-2.1	2.2E-01
ENSMUST00000036999	CAP-GLY domain containing linker protein 2 [Source:MGI Symbol;Acc:MGI:1313136]		Q9Z0H8	1.4	2.9E-02	-7.7	2.8E-04	-1.0	9.6E-02	-1.1	5.2E-01
ENSMUST00000037007	envoplakin [Source:MGI Symbol;Acc:MGI:107507]		Q9D952	6.7	1.2E-05	-5.3	1.3E-03	-0.1	7.9E-01	3.6	1.1E-02
ENSMUST00000037011	tripartite motif-containing 36 [Source:MGI Symbol;Acc:MGI:106264]		Q80WG7	8.0	2.0E-06	-1.8	2.2E-02	1.3	7.7E-03	0.5	4.9E-01
ENSMUST00000037012	potassium voltage-gated channel, shaker-related subfamily, member 4 [Source:MGI Symbol;Acc:MGI:96661]		Q61423	9.3	9.6E-06	-1.7	3.9E-02	0.9	5.3E-02	0.0	9.9E-01
ENSMUST00000037023	ribosomal protein S29 [Source:MGI Symbol;Acc:MGI:107681]		P62274	-7.0	5.0E-05	2.2	2.4E-01	1.6	3.2E-01	-4.9	1.8E-02
ENSMUST00000037029	RIKEN cDNA 9430020K01 gene [Source:MGI Symbol;Acc:MGI:2685174]	B7ZN02	Q5DTX6	7.2	4.8E-06	4.9	1.5E-05	-2.7	2.2E-03	-0.4	3.6E-01
ENSMUST00000036557	WD repeat domain 78 [Source:MGI Symbol;Acc:MGI:2385328]		E9PYY5	1.8	2.6E-01	4.5	1.0E-02	-1.0	5.0E-01	-3.7	1.5E-02
ENSMUST00000037035	receptor (TNFRSF)-interacting serine-threonine kinase 2 [Source:MGI Symbol;Acc:MGI:1891456]	Q547H1	P58801	-3.5	3.0E-03	-3.4	6.6E-04	-0.4	3.0E-01	-0.8	2.8E-01
ENSMUST00000036564	interleukin 22 receptor, alpha 2 [Source:MGI Symbol;Acc:MGI:2665114]		Q80XF5	0.0	9.8E-01	0.4	7.6E-01	-1.1	3.4E-01	-1.4	2.5E-01
ENSMUST00000037048	monocyte to macrophage differentiation-associated 2 [Source:MGI Symbol;Acc:MGI:1922354]	Q3V1Z9	Q8R189	9.3	3.8E-06	-1.1	4.7E-02	-0.1	8.2E-01	-0.6	2.6E-01
ENSMUST00000036572	transmembrane protein 51 [Source:MGI Symbol;Acc:MGI:2384874]		Q99LG1	0.2	8.2E-01	-0.2	8.3E-01	-0.5	5.4E-01	0.0	9.7E-01
ENSMUST00000037055	ATPase type 13A2 [Source:MGI Symbol;Acc:MGI:1922022]		Q9CTG6	-10.1	3.8E-05	2.8	2.0E-02	-0.1	9.4E-01	0.9	2.7E-01
ENSMUST00000036578	bromo adjacent homology domain containing 1 [Source:MGI Symbol;Acc:MGI:2139371]	Z4YJL0		-0.3	5.5E-01	0.6	3.8E-01	1.1	5.8E-02	0.1	8.2E-01
ENSMUST00000036579	vacuolar protein sorting 13 D (yeast) [Source:MGI Symbol;Acc:MGI:2448530]	B1ART2		-1.3	5.8E-01	-2.3	4.7E-01	0.1	9.8E-01	1.1	7.3E-01
ENSMUST00000037056	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 [Source:MGI Symbol;Acc:MGI:1927558	F8WHP8		-4.8	2.5E-03	4.0	2.2E-02	-1.9	2.1E-01	-0.9	4.2E-01
ENSMUST00000037064	solute carrier family 25, member 37 [Source:MGI Symbol;Acc:MGI:1914962]		Q920G8	-5.3	6.6E-03	6.5	4.7E-05	-2.0	7.5E-02	-0.2	7.2E-01
ENSMUST00000036606	START domain containing 8 [Source:MGI Symbol;Acc:MGI:2448556]		Q8K031	-1.0	7.0E-02	0.2	8.1E-01	0.8	1.0E-01	-0.3	6.0E-01
ENSMUST00000036615	3-hydroxyacyl-CoA dehydratase 3 [Source:MGI Symbol;Acc:MGI:1889341]		Q8K2C9	0.5	3.9E-01	0.1	9.2E-01	-0.4	5.0E-01	0.1	9.3E-01
ENSMUST00000037071	olfactory receptor 796 [Source:MGI Symbol;Acc:MGI:3030630]	Q8VGJ1		6.6	2.7E-04	0.5	3.2E-01	-1.3	1.1E-02	-0.2	7.2E-01
ENSMUST00000036619	expressed sequence AW554918 [Source:MGI Symbol;Acc:MGI:2147376]	E9QPX6		1.0	4.2E-01	4.0	1.9E-03	-3.1	1.7E-02	-6.1	1.2E-04

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000037096	cyclic nucleotide binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1918123]		Q9D5U8	-5.5	2.0E-03	6.6	3.3E-04	-0.6	6.5E-01	-0.7	3.0E-01
ENSMUST00000036646	CCR4-NOT transcription complex, subunit 6-like [Source:MGI Symbol;Acc:MGI:2443154]	F8WJG1		0.0	9.9E-01	2.3	4.9E-01	2.1	3.7E-01	-0.2	9.4E-01
ENSMUST00000036647	cy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2 [Source:MGI Symbol;Acc:M		Q8BG15	3.2	1.1E-01	1.1	5.8E-01	-2.1	2.5E-01	0.0	9.9E-01
ENSMUST00000037097	formin homology 2 domain containing 3 [Source:MGI Symbol;Acc:MGI:1925847]		Q76LL6	8.6	9.6E-06	1.9	1.5E-01	-1.2	2.9E-01	0.2	8.7E-01
ENSMUST00000037115	mediator complex subunit 30 [Source:MGI Symbol;Acc:MGI:1917040]		Q9CQI9	-4.9	1.4E-04	-4.4	9.1E-04	0.6	1.5E-01	-1.3	2.5E-01
ENSMUST00000037119	distal-less homeobox 1 [Source:MGI Symbol;Acc:MGI:94901]		Q64317	6.6	1.1E-03	-1.3	2.3E-01	0.4	5.4E-01	-1.0	3.3E-01
ENSMUST00000037134	homeodomain interacting protein kinase 4 [Source:MGI Symbol;Acc:MGI:2685008]		Q3V016	7.5	3.2E-05	-3.3	2.1E-02	0.7	2.7E-01	-1.5	2.5E-01
ENSMUST00000037141	SET domain containing (lysine methyltransferase) 7 [Source:MGI Symbol;Acc:MGI:1920501]		Q8VHL1	-2.3	6.8E-04	-0.8	5.9E-01	0.9	3.6E-01	-2.4	1.6E-01
ENSMUST00000037145	cadherin-related family member 2 [Source:MGI Symbol;Acc:MGI:2687323]	E9Q7P9		8.6	8.9E-06	3.5	7.9E-04	0.5	4.0E-01	0.3	5.5E-01
ENSMUST00000037165	lymphoblastomic leukemia 1 [Source:MGI Symbol;Acc:MGI:96891]		P27792	-2.1	1.2E-02	-7.0	9.6E-04	1.0	4.9E-02	-0.6	7.1E-01
ENSMUST00000037190	RIKEN cDNA 2700029M09 gene [Source:MGI Symbol;Acc:MGI:1919862]		Q8CFE2	-6.6	6.7E-05	3.9	1.4E-01	-0.8	7.3E-01	1.7	3.6E-01
ENSMUST00000037198	oxidative stress induced growth inhibitor family member 2 [Source:MGI Symbol;Acc:MGI:2384798]	Q3TEE9		-3.5	2.3E-03	-3.1	7.6E-03	1.2	3.5E-02	-0.6	5.7E-01
ENSMUST00000037205	methylmalonyl CoA epimerase [Source:MGI Symbol;Acc:MGI:1920974]		Q9D1I5	-3.6	1.5E-04	-2.1	8.7E-03	0.2	5.3E-01	-0.2	7.7E-01
ENSMUST00000037206	ATP/GTP binding protein-like 2 [Source:MGI Symbol;Acc:MGI:2443254]		Q8CDK2	6.5	8.3E-04	6.0	6.7E-04	0.9	4.6E-01	0.0	9.7E-01
ENSMUST00000036734	owth arrest and DNA-damage-inducible, gamma interacting protein 1 [Source:MGI Symbol;Acc:MGI:191494		Q9CR59	0.4	4.3E-01	0.8	2.5E-01	0.7	2.0E-01	0.3	6.5E-01
ENSMUST00000037218	RAS-like, family 10, member A [Source:MGI Symbol;Acc:MGI:1922918]		Q8K5A4	7.2	2.1E-04	6.5	1.1E-04	-1.3	2.5E-01	-0.6	2.9E-01
ENSMUST00000037220	RIKEN cDNA 1700028J19 gene [Source:MGI Symbol;Acc:MGI:1917254]	Q9D9U7		2.6	8.0E-03	-4.3	1.6E-03	0.3	5.0E-01	1.2	2.4E-01
ENSMUST00000037232	ras responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:2443664]		Q3UH06	-4.1	2.7E-02	-3.3	1.5E-02	-0.1	9.2E-01	-0.7	5.7E-01
ENSMUST00000037235	X Kell blood group precursor related family member 7 homolog [Source:MGI Symbol;Acc:MGI:3526711]		Q5GH64	7.5	2.9E-05	8.4	2.7E-04	-0.1	9.3E-01	0.4	5.9E-01
ENSMUST00000037240	solute carrier family 30 (zinc transporter), member 8 [Source:MGI Symbol;Acc:MGI:2442682]		Q8BGG0	8.1	1.1E-05	-3.7	7.2E-04	0.4	3.5E-01	-0.6	4.4E-01
ENSMUST00000036765	eukaryotic translation initiation factor 4E binding protein 3 [Source:MGI Symbol;Acc:MGI:1270847]		Q80VV3	0.5	7.3E-01	-0.4	8.0E-01	-2.3	1.1E-01	-1.4	3.7E-01
ENSMUST00000037261	prostaglandin D2 receptor 2 [Source:MGI Symbol;Acc:MGI:1330275]		Q9Z2J6	8.0	9.7E-06	8.2	5.7E-05	-0.7	6.1E-01	0.3	6.3E-01
ENSMUST00000037268	coiled-coil domain containing 182 [Source:MGI Symbol;Acc:MGI:1921547]		Q9D9C6	6.2	3.6E-04	-3.9	7.6E-04	0.8	7.8E-02	-0.1	8.9E-01
ENSMUST00000036807	THAP domain containing, apoptosis associated protein 1 [Source:MGI Symbol;Acc:MGI:1921004]		Q8CHW1	-0.2	8.5E-01	-1.2	3.2E-01	0.2	7.8E-01	1.3	2.7E-01
ENSMUST00000037270	DNA segment, Chr 15, ERATO Doi 621, expressed [Source:MGI Symbol;Acc:MGI:1277178]	B6YY24	Q3UVG3	-1.5	3.3E-03	6.5	2.0E-04	-0.6	6.3E-01	-0.4	5.3E-01
ENSMUST00000037275	coiled-coil domain containing 15 [Source:MGI Symbol;Acc:MGI:2444488]		Q8C9M2	4.2	1.1E-04	5.9	2.2E-03	-0.6	7.2E-01	-0.2	8.4E-01
ENSMUST00000037286	complement component 1, q subcomponent-like 2 [Source:MGI Symbol;Acc:MGI:3032521]		Q8CFR0	7.6	3.4E-05	4.9	1.0E-04	0.1	9.2E-01	0.0	9.7E-01
ENSMUST00000037294	transcription factor AP-2, delta [Source:MGI Symbol;Acc:MGI:2153466]		Q91ZK0	7.0	5.2E-05	-4.8	7.3E-05	1.1	6.8E-03	-0.1	9.0E-01
ENSMUST00000037299	YTH domain family 1 [Source:MGI Symbol;Acc:MGI:1917431]		P59326	-4.0	2.6E-04	-2.2	1.2E-02	-0.5	2.4E-01	0.1	9.2E-01
ENSMUST00000036865	Fanconi anemia, complementation group I [Source:MGI Symbol;Acc:MGI:2384790]		Q8K368	-3.7	3.7E-02	2.3	1.7E-01	2.4	9.8E-02	-3.6	4.7E-02
ENSMUST00000037302	TBC1D12: TBC1 domain family, member 12 [Source:MGI Symbol;Acc:MGI:2384803]	E9QQ68		3.7	2.8E-04	-1.1	1.6E-01	0.8	1.1E-01	-0.3	6.8E-01
ENSMUST00000037315	abhydrolase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914344]		Q9QXM0	-2.5	7.7E-05	2.8	1.0E-03	0.6	2.5E-01	-0.8	1.2E-01
ENSMUST00000036880	cyclin-dependent kinase 10 [Source:MGI Symbol;Acc:MGI:2448549]		Q3UMM4	0.5	5.2E-01	0.8	4.3E-01	0.7	3.5E-01	0.4	6.7E-01
ENSMUST00000036884	Kruppel-like factor 9 [Source:MGI Symbol;Acc:MGI:1333856]	Q8CEC4		0.1	8.1E-01	0.6	3.9E-01	0.6	2.5E-01	0.1	8.4E-01
ENSMUST00000037324	S-phase kinase-associated protein 1A [Source:MGI Symbol;Acc:MGI:103575]	Q5SUR3	Q9WTX5	-7.8	6.9E-05	-2.3	7.2E-03	1.1	2.1E-02	-0.2	7.3E-01
ENSMUST00000036917	heart and neural crest derivatives expressed transcript 1 [Source:MGI Symbol;Acc:MGI:103577]	Q5SQG1	Q64279	3.4	1.3E-01	5.0	4.4E-02	-0.5	8.3E-01	-2.2	1.9E-01
ENSMUST00000036928	epoxide hydrolase 1, microsomal [Source:MGI Symbol;Acc:MGI:95405]		Q9D379	2.2	3.0E-01	0.3	9.1E-01	-0.5	8.1E-01	1.3	6.4E-01
ENSMUST00000037330	inhibin alpha [Source:MGI Symbol;Acc:MGI:96569]		Q04997	7.4	3.6E-05	6.7	2.2E-04	-0.5	7.0E-01	-0.7	2.7E-01
ENSMUST00000037333	cyclin D3 [Source:MGI Symbol;Acc:MGI:88315]	Q3TSW4	P30282	-7.8	1.7E-03	2.3	3.8E-01	-5.6	7.4E-02	3.3	7.5E-02
ENSMUST00000036937	tRNA methyltranferase 12 [Source:MGI Symbol;Acc:MGI:1915510]		Q8BG71	-0.7	1.6E-01	0.3	6.5E-01	0.6	2.3E-01	-0.5	4.7E-01
ENSMUST00000037337	TBC1 domain family, member 19 [Source:MGI Symbol;Acc:MGI:1914499]	Q8VDV7		2.0	1.2E-02	7.7	1.3E-04	-0.7	6.1E-01	-0.3	6.4E-01
ENSMUST00000037349	apoptosis-inducing factor, mitochondrion-associated 1 [Source:MGI Symbol;Acc:MGI:1349419]		Q9Z0X1	-3.6	2.1E-03	-2.1	1.6E-02	-0.5	2.7E-01	0.1	8.9E-01
ENSMUST00000037353	ectodysplasin A2 receptor [Source:MGI Symbol;Acc:MGI:2442860]	Q3KP88	Q8BX35	5.6	6.8E-04	-3.3	1.2E-02	1.7	1.4E-02	-1.9	1.3E-01
ENSMUST00000037356	PRAME family member 8 [Source:MGI Symbol;Acc:MGI:2140473]	Q8CE24		-5.4	1.3E-03	3.6	5.7E-03	-2.7	4.5E-02	-1.3	1.3E-01
ENSMUST00000036972	RIKEN cDNA 3632451O06 gene [Source:MGI Symbol;Acc:MGI:1914669]		Q8BT18	6.2	5.1E-02	5.8	8.7E-02	-0.7	8.3E-01	-0.4	8.4E-01
ENSMUST00000037359	kelch-like 35 [Source:MGI Symbol;Acc:MGI:1919434]		Q9CZ49	5.1	1.7E-02	-2.0	2.2E-01	1.7	9.9E-02	-1.4	4.0E-01
ENSMUST00000036977	mitochondrial GTPase 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2685015]		Q8R2R6	-2.6	4.9E-02	-1.5	2.0E-01	-0.9	2.7E-01	-2.0	1.4E-01
ENSMUST00000036987	non-SMC condensin II complex, subunit H2 [Source:MGI Symbol;Acc:MGI:1289164]	E9PY48		-3.0	6.4E-02	1.6	2.3E-01	-0.2	8.4E-01	-4.9	8.3E-03
ENSMUST00000037360	ras homolog gene family, member V [Source:MGI Symbol;Acc:MGI:2444227]		Q8VDU1	-3.0	1.5E-03	-0.5	4.7E-01	-7.4	2.0E-05	0.2	6.8E-01
ENSMUST00000036992	LIM domain only 1 [Source:MGI Symbol;Acc:MGI:102812]	Q3UZX1	Q924W9	-1.3	6.6E-02	0.6	5.2E-01	1.6	2.5E-02	-0.2	7.8E-01
ENSMUST00000037361	left right determination factor 1 [Source:MGI Symbol;Acc:MGI:107405]		Q64280	2.8	3.6E-03	-6.2	5.4E-04	-0.2	7.0E-01	-1.6	2.9E-01
ENSMUST00000037370	sortilin-related VPS10 domain containing receptor 2 [Source:MGI Symbol;Acc:MGI:1932289]		Q9EPR5	9.5	1.2E-05	1.6	6.0E-02	0.3	6.4E-01	0.1	8.1E-01
ENSMUST00000037001	LETM1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1915864]		Q924L1	-0.1	8.0E-01	0.8	2.0E-01	1.0	5.5E-02	0.0	9.5E-01
ENSMUST00000037372	NLR family, pyrin domain containing 4F [Source:MGI Symbol;Acc:MGI:2145528]	L7N1W9		7.0	2.0E-04	6.0	7.6E-05	-0.9	3.4E-01	-0.2	7.2E-01
ENSMUST00000037375	EPS8-like 3 [Source:MGI Symbol;Acc:MGI:2139743]		Q91WL0	6.8	1.5E-04	5.8	1.1E-04	-0.7	4.1E-01	1.4	2.3E-02
ENSMUST00000037378	RIKEN cDNA 1700020L24 gene [Source:MGI Symbol;Acc:MGI:1913580]		Q8C1R3	-4.1	3.2E-03	6.8	9.4E-05	-1.9	1.3E-01	0.5	3.5E-01
ENSMUST00000037014	cDNA sequence BC022687 [Source:MGI Symbol;Acc:MGI:2443738]		Q8BHN9	0.4	4.8E-01	1.5	9.8E-02	1.3	7.8E-02	0.2	7.3E-01
ENSMUST00000037380	ase, aminophospholipid transporter (APLT), class I, type 8A, member 1 [Source:MGI Symbol;Acc:MGI:1330		P70704	-4.1	3.6E-04	-7.9	1.4E-04	-1.1	4.8E-02	-0.2	8.8E-01
ENSMUST00000037025	lysine (K)-specific demethylase 1B [Source:MGI Symbol;Acc:MGI:2145261]		Q8C1G3	0.9	1.1E-01	0.5	4.7E-01	-0.4	4.7E-01	0.1	9.3E-01
ENSMUST00000037383	lipid droplet associated hydrolase [Source:MGI Symbol;Acc:MGI:1916082]	A0A0F6AIX5		-4.3	2.7E-03	4.6	2.0E-04	-2.6	8.8E-03	0.0	9.3E-01
ENSMUST00000037397	centrosomal protein 126 [Source:MGI Symbol;Acc:MGI:2680221]		Q0VBV7	5.8	7.4E-05	-1.0	2.1E-01	0.0	9.6E-01	-2.5	2.7E-02
ENSMUST00000037044	CT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:24461		Q3U0D9	-1.4	6.3E-02	-1.7	1.2E-01	0.6	3.5E-01	0.8	3.9E-01
ENSMUST00000037399	biliverdin reductase B (flavin reductase (NADPH)) [Source:MGI Symbol;Acc:MGI:2385271]	Q3U6G1	Q923D2	-4.9	1.4E-03	9.4	6.7E-06	-0.6	6.3E-01	-0.7	1.1E-01
ENSMUST00000037049	leucine zipper, putative tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2684762]		P60853	2.2	3.2E-01	4.0	1.1E-01	-0.8	7.4E-01	-2.5	1.8E-01
ENSMUST00000037401	PHD finger protein 20 [Source:MGI Symbol;Acc:MGI:2444148]		Q8BLG0	-2.8	3.0E-02	-7.7	1.6E-03	1.8	7.0E-03	-0.6	7.4E-01
ENSMUST00000037408	S phase cyclin A-associated protein in the ER [Source:MGI Symbol;Acc:MGI:1925976]	F8VQ70		-2.3	3.0E-03	-4.0	1.8E-02	-0.7	4.1E-01	-1.5	3.2E-01
ENSMUST00000037409	tripartite motif-containing 45 [Source:MGI Symbol;Acc:MGI:1918187]		Q6PFY8	6.7	9.2E-03	-2.1	2.2E-01	1.4	1.8E-01	-1.7	3.6E-01
ENSMUST00000037418	transmembrane emp24 domain containing 8 [Source:MGI Symbol;Acc:MGI:1923480]		Q3UHI4	-2.3	1.7E-03	5.7	1.2E-03	-0.6	6.8E-01	0.3	7.1E-01
ENSMUST00000037072	ankyrin repeat and KH domain containing 1 [Source:MGI Symbol;Acc:MGI:1921733]	F7DE17		-1.3	6.2E-01	-0.3	9.3E-01	-0.1	9.5E-01	-1.2	6.6E-01
ENSMUST00000037422	ring finger protein 44 [Source:MGI Symbol;Acc:MGI:2145310]		Q3UHJ8	-7.7	1.0E-03	-5.4	2.3E-03	-0.1	8.6E-01	-0.3	8.5E-01
ENSMUST00000037423	ovo-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1338039]		Q8CIV7	5.7	1.2E-02	4.3	1.3E-04	-4.5	9.3E-04	-0.3	5.8E-01
ENSMUST00000037099	chloride intracellular channel 4 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1352754]	Q543N5	Q9QYB1	0.2	7.2E-01	0.1	8.6E-01	-0.5	3.3E-01	-0.4	5.1E-01
ENSMUST00000037434	calcium channel, voltage-dependent, alpha 2/delta subunit 4 [Source:MGI Symbol;Acc:MGI:2442632]	F8VPL1		5.6	7.5E-05	-6.3	5.4E-04	0.0	9.4E-01	1.4	2.9E-01
ENSMUST00000037117	general transcription factor IIIC, polypeptide 4 [Source:MGI Symbol;Acc:MGI:2138937]		Q8BMQ2	-0.2	6.6E-01	0.8	1.6E-01	0.7	1.0E-01	-0.3	5.9E-01
ENSMUST00000037448	zinc finger protein 109 [Source:MGI Symbol;Acc:MGI:1929099]	Q9R166		5.6	1.0E-05	7.3	9.3E-04	-0.7	6.9E-01	-1.3	1.4E-01
ENSMUST00000037127	exoribonuclease 3 [Source:MGI Symbol;Acc:MGI:2153887]		Q8C460	-1.9	1.1E-01	-0.4	7.5E-01	0.7	3.8E-01	-0.7	5.7E-01
ENSMUST00000037453	protease, serine 34 [Source:MGI Symbol;Acc:MGI:2681414]	Q80UR4		-2.9	6.3E-03	6.9	1.8E-04	-0.4	7.7E-01	0.2	7.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000037472	leukocyte receptor cluster (LRC) member 8 [Source:MGI Symbol;Acc:MGI:2142195]		Q8CBY3	-9.1	1.3E-03	-0.8	1.7E-01	1.0	2.7E-02	-0.5	3.6E-01
ENSMUST00000037473	adaptor-related protein complex 5, mu 1 subunit [Source:MGI Symbol;Acc:MGI:1921635]			-2.3	2.1E-03	8.7	2.0E-05	-0.2	8.8E-01	-0.3	6.1E-01
ENSMUST00000037478	solute carrier family 18 (vesicular monoamine), member 1 [Source:MGI Symbol;Acc:MGI:106684]	Q32XG7	Q8R090	5.7	8.4E-04	-1.9	8.3E-02	1.4	4.0E-02	1.2	2.4E-01
ENSMUST00000037181	MAM domain containing glycosylphosphatidylinositol anchor 2 [Source:MGI Symbol;Acc:MGI:2444706]	B2RQF5		4.3	8.1E-02	4.6	9.6E-02	-0.3	9.3E-01	-0.6	7.2E-01
ENSMUST00000037182	hook homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443554]		Q8BUK6	-0.3	3.8E-01	-0.9	1.1E-01	0.5	1.8E-01	1.0	5.3E-02
ENSMUST00000037481	C-type lectin domain family 1, member a [Source:MGI Symbol;Acc:MGI:2444151]		Q8BWY2	2.2	2.0E-02	-5.2	1.8E-03	0.5	3.3E-01	-0.9	5.1E-01
ENSMUST00000037488	dedicator of cytokinesis 4 [Source:MGI Symbol;Acc:MGI:1918006]		P59764	2.2	1.3E-03	-3.1	2.0E-02	0.6	3.4E-01	0.1	9.0E-01
ENSMUST00000037489	ol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) [Source:MGI Symbol;Acc:M			-5.5	2.4E-04	-5.0	5.5E-04	-0.3	5.2E-01	1.0	2.9E-01
ENSMUST00000037491	coagulation factor XIII, A1 subunit [Source:MGI Symbol;Acc:MGI:1921395]		Q8BH61	-6.9	4.2E-04	4.9	8.8E-03	-0.6	7.0E-01	0.9	3.4E-01
ENSMUST00000037499	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913791]		Q9CQU8	-3.5	2.1E-04	4.6	3.3E-03	-3.2	3.8E-02	-0.6	4.0E-01
ENSMUST00000037502	family with sequence similarity 117, member A [Source:MGI Symbol;Acc:MGI:2144564]		Q7TNF9	-2.3	2.2E-03	3.9	2.0E-03	0.8	3.6E-01	-0.5	4.8E-01
ENSMUST00000037504	von Willebrand factor A domain containing 9 [Source:MGI Symbol;Acc:MGI:1917132]		Q8R3P6	5.6	2.4E-03	-3.0	1.4E-01	-0.1	9.4E-01	-1.2	5.7E-01
ENSMUST00000037522	RAN binding protein 17 [Source:MGI Symbol;Acc:MGI:1929706]	Q5SSA5		7.0	4.8E-06	7.6	4.5E-05	-0.6	6.3E-01	-0.7	2.2E-01
ENSMUST00000037528	glycerophosphodiester phosphodiesterase domain containing 5 [Source:MGI Symbol;Acc:MGI:2686926]		Q640M6	4.4	4.6E-05	8.7	2.1E-04	1.4	3.4E-01	0.8	2.3E-01
ENSMUST00000037246	copper chaperone for superoxide dismutase [Source:MGI Symbol;Acc:MGI:1333783]	Q543K2	Q9WU84	-1.3	5.1E-02	-0.9	2.7E-01	0.3	5.5E-01	-0.1	8.6E-01
ENSMUST00000037248	HIRA interacting protein 3 [Source:MGI Symbol;Acc:MGI:2142364]		Q8BLH7	0.1	8.8E-01	0.1	9.4E-01	-0.3	5.5E-01	-0.3	6.8E-01
ENSMUST00000037260	zinc finger protein 623 [Source:MGI Symbol;Acc:MGI:1926084]	Q9CY99		0.9	1.4E-01	0.4	5.8E-01	-0.4	4.7E-01	0.1	8.5E-01
ENSMUST00000037534	ring finger protein 167 [Source:MGI Symbol;Acc:MGI:1917760]		Q91XF4	-8.4	6.7E-05	6.3	7.3E-05	-1.5	1.8E-01	0.2	6.6E-01
ENSMUST00000037540	purinergic receptor P2Y, G-protein coupled 2 [Source:MGI Symbol;Acc:MGI:105107]			-2.2	3.8E-03	6.3	6.0E-04	-0.6	6.3E-01	-0.7	3.3E-01
ENSMUST00000037547	dispatched homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2388733]		Q8CIP5	8.8	2.9E-06	-2.1	3.7E-03	-0.2	4.9E-01	0.3	5.3E-01
ENSMUST00000037548	ring finger protein 146 [Source:MGI Symbol;Acc:MGI:1915281]		Q9CZW6	-5.4	1.4E-02	4.5	3.6E-04	0.2	7.9E-01	0.0	9.3E-01
ENSMUST00000037280	vacuolar protein sorting 18 (yeast) [Source:MGI Symbol;Acc:MGI:2443626]		Q8R307	-2.7	6.2E-02	-1.7	3.6E-01	1.0	3.9E-01	0.0	9.8E-01
ENSMUST00000037551	protein phosphatase 1, regulatory (inhibitor) subunit 16A [Source:MGI Symbol;Acc:MGI:1920312]		Q923M0	-5.5	3.2E-03	8.8	8.6E-04	0.2	9.2E-01	0.8	3.2E-01
ENSMUST00000037285	G protein-coupled receptor kinase-interactor 1 [Source:MGI Symbol;Acc:MGI:1927140]		Q68FF6	-2.3	3.2E-01	1.7	6.1E-01	4.1	1.4E-01	0.1	9.7E-01
ENSMUST00000037553	galanin-like peptide [Source:MGI Symbol;Acc:MGI:2663979]		Q810H5	7.2	6.4E-05	7.4	7.2E-05	-0.6	6.3E-01	-0.4	4.5E-01
ENSMUST00000037287	cyclin-dependent kinase inhibitor 1C (P57) [Source:MGI Symbol;Acc:MGI:104564]	Q791X1	P49919	0.1	9.7E-01	4.1	3.3E-02	0.7	6.6E-01	-3.4	4.1E-02
ENSMUST00000037290	methionine-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1345633]		Q68FL6	-1.6	6.4E-02	-0.3	7.9E-01	1.4	7.9E-02	0.1	9.4E-01
ENSMUST00000037557	MON2 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914324]		Q80TL7	-2.8	7.0E-03	6.3	2.1E-04	-0.6	6.1E-01	0.1	8.8E-01
ENSMUST00000037575	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	E9Q9Y2		-5.6	2.2E-04	-1.8	5.7E-02	1.3	2.4E-02	-0.8	3.6E-01
ENSMUST00000037585	DENN/MADD domain containing 6A [Source:MGI Symbol;Acc:MGI:2442980]		Q8BH65	2.0	1.6E-03	2.3	1.2E-02	-0.7	2.9E-01	0.7	2.9E-01
ENSMUST00000037603	solute carrier family 26 (sulfate transporter), member 2 [Source:MGI Symbol;Acc:MGI:892977]	F8WI08		6.7	1.8E-03	-1.9	3.8E-03	0.8	2.6E-02	0.1	7.6E-01
ENSMUST00000037607	mitogen-activated protein kinase kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346877]	Q923A8		-5.1	2.4E-03	-7.7	1.4E-03	0.5	3.6E-01	0.4	8.4E-01
ENSMUST00000037609	heparan-alpha-glucosaminide N-acetyltransferase [Source:MGI Symbol;Acc:MGI:1196297]		Q3UDW8	-4.1	1.6E-04	6.9	1.2E-04	-0.6	6.2E-01	0.0	9.7E-01
ENSMUST00000037615	aldhehyde dehydrogenase family 5, subfamily A1 [Source:MGI Symbol;Acc:MGI:2441982]	B2RS41	Q8BWF0	5.0	3.5E-05	-7.3	3.4E-02	1.2	2.1E-01	0.7	8.3E-01
ENSMUST00000037623	neuritin 1 [Source:MGI Symbol;Acc:MGI:1915654]		Q8CFV4	4.4	5.2E-04	0.2	7.9E-01	-1.4	4.9E-02	0.4	5.3E-01
ENSMUST00000037341	NHS-like 1 [Source:MGI Symbol;Acc:MGI:106390]		Q8CAF4	5.0	1.5E-01	5.1	1.9E-01	-0.3	9.4E-01	-0.3	8.8E-01
ENSMUST00000037633	zinc finger CCCH type containing 7 A [Source:MGI Symbol;Acc:MGI:2445044]	E9PWW6		-3.8	2.0E-04	-6.4	4.1E-03	-0.2	7.0E-01	2.7	1.4E-01
ENSMUST00000037636	internexin neuronal intermediate filament protein, alpha [Source:MGI Symbol;Acc:MGI:96568]		P46660	8.3	4.8E-05	5.0	1.8E-03	-1.3	3.2E-01	-0.7	3.8E-01
ENSMUST00000037646	PR domain containing 4 [Source:MGI Symbol;Acc:MGI:1920093]		Q80V63	-1.4	1.3E-02	-2.4	9.7E-02	1.3	9.9E-02	-1.6	3.0E-01
ENSMUST00000037666	malignant fibrous histiocytoma amplified sequence 1 [Source:MGI Symbol;Acc:MGI:1098644]		Q3V1N1	3.6	6.9E-05	4.6	2.3E-02	-2.3	2.6E-01	-1.8	1.5E-01
ENSMUST00000037682	neuromedin U receptor 2 [Source:MGI Symbol;Acc:MGI:2441765]		Q8BZ39	7.2	3.5E-05	-1.3	1.4E-01	1.4	2.1E-02	-0.2	8.4E-01
ENSMUST00000037685	mucin-like 2 [Source:MGI Symbol;Acc:MGI:98392]	Q9DA65		6.1	5.4E-04	3.0	5.5E-03	0.0	9.5E-01	-0.2	7.7E-01
ENSMUST00000037696	seminal vesicle secretory protein 1 [Source:MGI Symbol;Acc:MGI:2682321]	Q6WIZ7		7.6	2.9E-05	4.1	4.8E-04	-5.2	8.5E-04	0.1	8.4E-01
ENSMUST00000037708	acid-sensing (proton-gated) ion channel family member 4 [Source:MGI Symbol;Acc:MGI:2652846]		Q7TNS7	4.9	1.5E-02	5.2	9.9E-04	-2.0	1.3E-01	-0.2	7.8E-01
ENSMUST00000037374	growth factor receptor bound protein 2-associated protein 3 [Source:MGI Symbol;Acc:MGI:2387324]		Q8BSM5	-1.4	1.4E-01	-0.1	8.9E-01	0.5	5.2E-01	-0.7	4.8E-01
ENSMUST00000037728	NLR family, pyrin domain containing 4C [Source:MGI Symbol;Acc:MGI:1890518]		Q3TKR3	7.2	3.5E-05	7.0	8.0E-04	0.6	6.9E-01	0.4	6.1E-01
ENSMUST00000037376	N-acetylglucosamine kinase [Source:MGI Symbol;Acc:MGI:1860418]	Q3U2G9	Q9QZ08	-1.9	5.5E-02	-0.8	4.6E-01	0.2	8.2E-01	-0.9	3.8E-01
ENSMUST00000037739	guanine nucleotide binding protein-like 3 (nucleolar) [Source:MGI Symbol;Acc:MGI:1353651]		Q8CI11	-2.5	7.1E-04	-4.5	2.5E-02	1.4	1.1E-01	1.8	3.2E-01
ENSMUST00000037746	T cell leukemia, homeobox 3 [Source:MGI Symbol;Acc:MGI:1351209]		O55144	6.2	1.0E-03	-2.2	3.6E-02	1.0	7.2E-02	-0.9	3.3E-01
ENSMUST00000037748	heterogeneous nuclear ribonucleoprotein U [Source:MGI Symbol;Acc:MGI:1858195]		Q8VEK3	-4.3	2.6E-04	-6.5	1.9E-02	0.8	3.0E-01	3.0	2.2E-01
ENSMUST00000037762	hypoxia inducible factor 3, alpha subunit [Source:MGI Symbol;Acc:MGI:1859778]		Q0VBL6	8.0	2.8E-04	4.0	5.9E-04	-1.7	6.9E-02	0.0	9.5E-01
ENSMUST00000037764	death inducer-obliterator 1 [Source:MGI Symbol;Acc:MGI:1344352]			6.6	1.5E-03	-4.0	5.0E-03	-0.5	4.2E-01	-1.4	2.9E-01
ENSMUST00000037776	serine/arginine-rich splicing factor 3 [Source:MGI Symbol;Acc:MGI:98285]	Q3U781	P84104	-8.3	2.1E-06	-6.2	2.8E-02	0.0	9.8E-01	3.4	1.9E-01
ENSMUST00000037783	coiled-coil domain containing 174 [Source:MGI Symbol;Acc:MGI:2444652]			-5.2	2.4E-03	-1.2	1.1E-01	0.2	6.8E-01	-1.0	2.1E-01
ENSMUST00000037785	neural cell adhesion molecule 2 [Source:MGI Symbol;Acc:MGI:97282]		O35136	7.1	1.1E-04	4.4	1.2E-01	0.6	8.2E-01	2.9	8.7E-02
ENSMUST00000037788	protein-O-mannosyltransferase 2 [Source:MGI Symbol;Acc:MGI:2444430]		Q8BGQ4	1.9	1.5E-03	-1.2	1.3E-01	1.3	1.7E-02	0.2	7.9E-01
ENSMUST00000037796	GDP-mannose pyrophosphorylase A [Source:MGI Symbol;Acc:MGI:1916330]		Q922H4	-5.2	5.5E-04	-5.0	1.7E-02	1.3	1.3E-01	-1.4	5.1E-01
ENSMUST00000037798	ute carrier family 24 (sodium/potassium/calcium exchanger), member 1 [Source:MGI Symbol;Acc:MGI:23848	Q91WD8		5.9	1.7E-04	6.3	1.6E-02	-0.1	9.6E-01	-0.6	6.2E-01
ENSMUST00000037807	ventral anterior homeobox 2 [Source:MGI Symbol;Acc:MGI:1346018]	Q14B19	Q9WTP9	8.2	4.8E-05	6.0	3.9E-04	-0.3	8.1E-01	-0.7	3.1E-01
ENSMUST00000037811	apolipoprotein B [Source:MGI Symbol;Acc:MGI:88052]		E9Q414	8.6	7.1E-05	5.8	8.2E-05	0.1	9.0E-01	-0.1	8.4E-01
ENSMUST00000037814	CKLF-like MARVEL transmembrane domain containing 5 [Source:MGI Symbol;Acc:MGI:2447164]		Q9D6G9	6.4	2.3E-04	0.0	1.0E+00	2.5	1.0E-02	-0.5	6.8E-01
ENSMUST00000037820	haloacid dehalogenase-like hydrolase domain containing 3 [Source:MGI Symbol;Acc:MGI:1919998]		Q9CYW4	4.5	2.1E-04	-7.8	1.4E-02	0.4	6.2E-01	-0.9	7.6E-01
ENSMUST00000037824	forkhead box H1 [Source:MGI Symbol;Acc:MGI:1347465]	Q0VEP8	O88621	7.9	3.4E-04	-2.3	7.3E-03	0.2	6.6E-01	0.3	7.2E-01
ENSMUST00000037827	solute carrier family 45, member 1 [Source:MGI Symbol;Acc:MGI:2653235]		Q8BIV7	4.5	1.2E-04	7.1	2.2E-03	1.4	4.0E-01	-0.1	9.3E-01
ENSMUST00000037480	WAS/WASL interacting protein family, member 2 [Source:MGI Symbol;Acc:MGI:1924462]		Q6PEV3	0.6	1.5E-01	1.3	4.2E-02	1.1	3.3E-02	0.4	3.8E-01
ENSMUST00000037828	low density lipoprotein receptor adaptor protein 1 [Source:MGI Symbol;Acc:MGI:2140175]		Q8C142	-1.9	1.5E-02	2.1	4.1E-02	-0.8	3.1E-01	-0.7	3.4E-01
ENSMUST00000037484	SUMO/sentrin specific peptidase 6 [Source:MGI Symbol;Acc:MGI:1922075]		Q6P7W0	0.7	5.4E-01	-1.8	3.3E-01	0.1	9.6E-01	2.5	1.6E-01
ENSMUST00000037839	zinc finger, AN1-type domain 1 [Source:MGI Symbol;Acc:MGI:1913611]		Q8BFR6	-5.1	9.6E-05	2.5	3.4E-03	0.4	4.9E-01	0.1	8.8E-01
ENSMUST00000037843	UBA-like domain containing 1 [Source:MGI Symbol;Acc:MGI:1916255]		Q6P3B2	-3.4	7.6E-04	-6.3	3.5E-03	0.6	2.9E-01	1.4	4.2E-01
ENSMUST00000037850	sorting nexin 2 [Source:MGI Symbol;Acc:MGI:1915054]		Q9CWK8	-6.0	4.3E-06	-7.4	1.8E-03	-0.7	3.1E-01	-0.3	8.8E-01
ENSMUST00000037853	KDEL (Lys-Asp-Glu-Leu) containing 2 [Source:MGI Symbol;Acc:MGI:1923765]	G5E897		5.8	9.6E-06	-1.6	4.0E-02	0.7	1.5E-01	-1.1	1.4E-01
ENSMUST00000037863	interleukin 25 [Source:MGI Symbol;Acc:MGI:2155888]	Q8VHH8		7.5	8.8E-05	-1.4	7.4E-02	0.8	8.5E-02	-0.1	9.2E-01
ENSMUST00000037865	ATPase, H+ transporting, lysosomal V0 subunit A2 [Source:MGI Symbol;Acc:MGI:104855]		P15920	-1.5	1.1E-02	2.7	8.7E-02	-2.9	5.7E-02	0.0	9.8E-01
ENSMUST00000037520	apolipoprotein B [Source:MGI Symbol;Acc:MGI:88052]		E9Q1Y3	3.4	2.7E-01	5.1	1.3E-01	-0.3	9.2E-01	-2.0	3.3E-01
ENSMUST00000037877	transcription factor-like 5 (basic helix-loop-helix) [Source:MGI Symbol;Acc:MGI:2672878]	Q32NY8		4.9	1.7E-03	6.7	5.3E-05	-0.5	6.2E-01	-0.2	7.1E-01
ENSMUST00000037526	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 [Source:MGI Symbol;Acc:MGI:1914110]		Q0VGY8	2.1	3.2E-01	7.3	2.2E-02	2.3	4.0E-01	-2.8	1.1E-01
ENSMUST00000037879	headcase homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2685715]	Q3V1N5		-3.5	1.9E-05	4.4	1.4E-04	-0.2	7.4E-01	-0.2	7.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000037882	CD207 antigen [Source:MGI Symbol;Acc:MGI:2180021]		Q8VBX4	5.0	3.8E-04	-8.3	3.7E-03	1.1	8.0E-02	1.0	6.5E-01
ENSMUST00000037901	transient receptor potential cation channel, subfamily M, member 3 [Source:MGI Symbol;Acc:MGI:2443101]	B2RUS0		6.3	3.3E-04	-1.4	8.9E-02	0.7	1.8E-01	-0.2	8.0E-01
ENSMUST00000037906	transmembrane protein 177 [Source:MGI Symbol;Acc:MGI:1913593]		Q8BPE4	3.1	7.2E-04	8.1	1.5E-05	-0.8	4.7E-01	-0.1	9.1E-01
ENSMUST00000037907	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 [Source:MGI Symbol;Acc:MGI:2442858]		Q6Q899	-7.6	1.3E-04	-1.3	4.4E-01	1.0	3.7E-01	-3.1	1.4E-01
ENSMUST00000037912	slingshot homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2679255]		Q5SW75	-3.7	1.0E-04	-1.8	2.0E-01	1.7	6.5E-02	-2.0	2.4E-01
ENSMUST00000037552	leptin receptor [Source:MGI Symbol;Acc:MGI:104993]		P48356	2.0	3.4E-01	4.6	1.2E-01	1.6	5.6E-01	-1.1	5.5E-01
ENSMUST00000037913	RMI2, RecQ mediated genome instability 2, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2685383]		Q3UPE3	6.3	5.1E-07	6.6	2.4E-04	-0.7	5.9E-01	0.0	9.5E-01
ENSMUST00000037915	male-specific lethal 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1921276]		Q6PDM1	-3.1	8.0E-03	-5.5	2.5E-03	0.6	3.8E-01	3.3	3.6E-02
ENSMUST00000037923	RNA binding motif protein 24 [Source:MGI Symbol;Acc:MGI:3610364]		D3Z4I3	6.3	1.8E-04	-0.4	7.5E-01	4.7	2.8E-04	-0.5	7.1E-01
ENSMUST00000037930	male-specific lethal 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1921276]		Q6PDM1	-4.1	5.3E-05	1.9	1.0E-02	0.0	9.3E-01	0.2	6.8E-01
ENSMUST00000037593	ankyrin repeat domain 13b [Source:MGI Symbol;Acc:MGI:2144501]		Q5F259	2.7	2.0E-01	5.1	1.2E-01	2.8	3.5E-01	0.4	8.3E-01
ENSMUST00000037596	BCL6 co-repressor-like 1 [Source:MGI Symbol;Acc:MGI:2443910]		A2AQH4	-1.6	2.1E-01	1.7	2.9E-01	1.8	1.6E-01	-1.5	3.1E-01
ENSMUST00000037942	tubulin tyrosine ligase-like family, member 7 [Source:MGI Symbol;Acc:MGI:1918142]	A0A0G2LB90		8.7	7.7E-04	4.3	5.5E-02	-1.6	4.1E-01	0.8	5.4E-01
ENSMUST00000037947	myeloid cell leukemia sequence 1 [Source:MGI Symbol;Acc:MGI:101769]		P97287	-7.7	5.7E-06	-6.1	4.1E-03	0.0	9.6E-01	1.0	5.7E-01
ENSMUST00000037958	Rho GTPase activating protein 29 [Source:MGI Symbol;Acc:MGI:2443818]		Q8CGF1	4.6	8.1E-05	-4.7	7.7E-04	0.5	2.3E-01	1.1	2.9E-01
ENSMUST00000037960	zinc finger, DHHC domain containing 9 [Source:MGI Symbol;Acc:MGI:2444393]		P59268	-1.6	1.6E-02	4.9	1.1E-04	-0.2	8.3E-01	0.0	9.7E-01
ENSMUST00000037618	ecombination signal binding protein for immunoglobulin kappa J region [Source:MGI Symbol;Acc:MGI:96522		P31266	0.8	4.7E-01	-0.6	7.3E-01	0.2	9.0E-01	1.6	2.9E-01
ENSMUST00000037620	motile sperm domain containing 3 [Source:MGI Symbol;Acc:MGI:1916179]	Q05DT5	Q8BGG6	-0.6	3.1E-01	2.4	1.0E-02	1.5	3.2E-02	-1.5	4.5E-02
ENSMUST00000037964	taxilin beta [Source:MGI Symbol;Acc:MGI:2671945]		Q8VBT1	6.2	2.3E-04	3.6	2.0E-03	-1.5	1.2E-01	-0.7	2.7E-01
ENSMUST00000037967	olute carrier family 10 (sodium/bile acid cotransporter family), member 3 [Source:MGI Symbol;Acc:MGI:9504		P21129	-3.7	2.7E-03	-4.3	4.8E-04	-0.2	6.1E-01	0.3	7.3E-01
ENSMUST00000037974	protein tyrosine phosphatase, receptor type, M [Source:MGI Symbol;Acc:MGI:102694]		P28828	6.5	3.0E-05	7.8	1.8E-04	-0.3	8.5E-01	0.2	7.8E-01
ENSMUST00000037977	cell cycle progression 1 [Source:MGI Symbol;Acc:MGI:1196419]		Q640L3	-4.2	6.0E-03	7.0	3.2E-04	-0.5	7.1E-01	-1.4	6.7E-02
ENSMUST00000037644	Casitas B-lineage lymphoma [Source:MGI Symbol;Acc:MGI:88279]		P22682	-0.6	1.9E-01	0.1	8.2E-01	1.3	1.5E-02	0.6	3.2E-01
ENSMUST00000037983	endosulfine alpha [Source:MGI Symbol;Acc:MGI:1891189]		P60840	-5.1	8.0E-05	-0.9	1.7E-01	0.8	7.3E-02	0.3	6.3E-01
ENSMUST00000037649	RAB3 GTPase activating protein subunit 1 [Source:MGI Symbol;Acc:MGI:2445001]		Q80UJ7	-1.0	5.4E-02	-0.6	3.9E-01	0.8	9.0E-02	0.3	5.8E-01
ENSMUST00000037991	tubule associated monooxygenase, calponin and LIM domain containing 2 [Source:MGI Symbol;Acc:MGI:244		Q8BML1	5.2	8.9E-04	2.6	2.6E-03	-0.6	2.7E-01	0.4	4.5E-01
ENSMUST00000037678	triokinase, FMN cyclase [Source:MGI Symbol;Acc:MGI:2385084]		Q8VC30	0.0	9.9E-01	1.1	1.2E-01	1.1	4.7E-02	0.0	9.9E-01
ENSMUST00000037994	schlafen 1 [Source:MGI Symbol;Acc:MGI:1313259]	Q9Z0I7		-7.4	3.0E-07	7.2	7.1E-05	-0.5	6.3E-01	-0.5	3.7E-01
ENSMUST00000038004	keratin 25 [Source:MGI Symbol;Acc:MGI:1918060]		Q8VCW2	7.5	4.0E-05	6.4	6.8E-04	-0.7	6.3E-01	-1.0	2.1E-01
ENSMUST00000038006	amino carboxymuconate semialdehyde decarboxylase [Source:MGI Symbol;Acc:MGI:2386323]		Q8R519	3.8	6.4E-03	7.5	6.2E-05	-0.6	6.1E-01	-0.5	3.6E-01
ENSMUST00000037698	family with sequence similarity 149, member B [Source:MGI Symbol;Acc:MGI:2145567]		Q6NSV7	0.5	4.2E-01	-1.1	2.0E-01	0.1	8.2E-01	1.8	4.4E-02
ENSMUST00000038027	glucose phosphate isomerase 1 [Source:MGI Symbol;Acc:MGI:95797]		P06745	-7.2	1.2E-06	6.9	3.2E-03	-0.6	7.5E-01	-2.6	3.1E-02
ENSMUST00000037709	transmembrane 7 superfamily member 3 [Source:MGI Symbol;Acc:MGI:1914873]			-0.5	3.8E-01	0.2	8.1E-01	0.6	2.7E-01	-0.1	9.2E-01
ENSMUST00000038038	schlafen 2 [Source:MGI Symbol;Acc:MGI:1313258]	Q9Z0I6		-7.2	2.4E-07	7.0	9.5E-05	-0.5	6.4E-01	-0.3	6.2E-01
ENSMUST00000038069	carcinoembryonic antigen-related cell adhesion molecule 10 [Source:MGI Symbol;Acc:MGI:1347248]			-8.3	2.9E-07	-3.0	6.4E-04	-1.4	4.7E-03	-0.9	1.8E-01
ENSMUST00000038080	fer (fms/fps related) protein kinase [Source:MGI Symbol;Acc:MGI:105917]		P70451	4.4	7.2E-03	6.2	1.9E-03	-0.6	7.0E-01	-0.6	5.1E-01
ENSMUST00000038091	SDE2 telomere maintenance homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:2384788]		Q8K1J5	-1.8	6.4E-03	-2.7	1.6E-02	1.0	7.7E-02	-0.7	5.0E-01
ENSMUST00000038096	fructosamine 3 kinase related protein [Source:MGI Symbol;Acc:MGI:2679256]		Q8K274	4.6	1.1E-05	7.4	8.6E-04	-0.7	6.6E-01	-0.1	8.6E-01
ENSMUST00000037763	YTH domain containing 2 [Source:MGI Symbol;Acc:MGI:2448561]		B2RR83	0.6	2.6E-01	1.4	6.5E-02	0.3	5.9E-01	-0.5	4.4E-01
ENSMUST00000038107	00-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 [Source:MGI Symbol;Acc:MGI:1		O35740	-3.6	4.4E-04	5.0	1.3E-02	-1.1	5.0E-01	0.5	6.7E-01
ENSMUST00000038108	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 [Source:MGI Symbol;Acc:MGI:1913627]		Q9CQY9	4.5	5.1E-05	-9.0	1.1E-05	-0.6	5.4E-02	0.1	9.4E-01
ENSMUST00000038116	ankyrin repeat domain 12 [Source:MGI Symbol;Acc:MGI:1914357]	G5E893		-2.0	1.2E-03	-5.6	8.3E-03	-0.6	4.1E-01	-0.1	9.4E-01
ENSMUST00000038118	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]		Q80XR2	-6.6	2.8E-03	5.6	3.7E-03	-0.5	7.4E-01	1.0	2.5E-01
ENSMUST00000038128	transmembrane protein 109 [Source:MGI Symbol;Acc:MGI:1915789]		Q3UBX0	-1.9	2.1E-02	2.5	1.5E-03	0.5	2.8E-01	-0.1	8.7E-01
ENSMUST00000038131	replication factor C (activator 1) 3 [Source:MGI Symbol;Acc:MGI:1916513]	Q3TKD1	Q8R323	-3.7	4.2E-03	-2.5	3.8E-02	0.3	6.1E-01	-2.4	8.0E-02
ENSMUST00000038142	interferon-stimulated protein [Source:MGI Symbol;Acc:MGI:1928895]	Q4FK39	Q9JL16	-2.5	2.7E-02	4.7	1.7E-03	-0.8	4.8E-01	0.4	5.8E-01
ENSMUST00000038144	endothelial cell-specific molecule 1 [Source:MGI Symbol;Acc:MGI:1918940]	B9EJX9	Q9QYY7	5.1	1.5E-04	6.5	7.4E-04	-0.4	7.8E-01	1.2	1.4E-01
ENSMUST00000038145	C-type lectin domain family 16, member A [Source:MGI Symbol;Acc:MGI:1921624]		Q80U30	3.1	1.7E-03	6.8	3.1E-04	-2.0	1.9E-01	-0.2	7.6E-01
ENSMUST00000037813	guanine nucleotide binding protein, alpha z subunit [Source:MGI Symbol;Acc:MGI:95780]	Q542R8	O70443	6.7	6.1E-02	5.2	1.7E-01	-0.5	8.9E-01	1.0	6.7E-01
ENSMUST00000038149	pre B cell leukemia homeobox 2 [Source:MGI Symbol;Acc:MGI:1341793]	Q4FJL3	O35984	-4.0	1.5E-04	6.3	4.6E-04	-0.7	6.1E-01	-0.6	4.2E-01
ENSMUST00000038161	agmatine ureohydrolase (agmatinase) [Source:MGI Symbol;Acc:MGI:1923236]		A2AS89	7.4	7.9E-05	4.1	7.8E-04	-0.9	2.9E-01	-0.5	4.1E-01
ENSMUST00000038163	PNMA-like 1 [Source:MGI Symbol;Acc:MGI:1918941]		Q80VM8	7.9	4.0E-05	6.4	2.7E-03	-0.7	6.7E-01	0.8	3.6E-01
ENSMUST00000038169	macrophage migration inhibitory factor [Source:MGI Symbol;Acc:MGI:96982]	Q545F0	P34884	-3.0	2.4E-03	5.0	6.2E-04	0.8	4.1E-01	0.2	7.2E-01
ENSMUST00000038174	glutamic-oxaloacetic transaminase 1-like 1 [Source:MGI Symbol;Acc:MGI:1923865]		Q7TSV6	5.5	8.4E-04	-0.9	3.3E-01	1.3	4.6E-02	0.3	7.5E-01
ENSMUST00000037836	FGFR1 oncogene partner 2 [Source:MGI Symbol;Acc:MGI:1914779]	F8WGG1		-4.3	7.3E-02	3.1	3.7E-01	6.8	2.9E-02	-0.6	8.3E-01
ENSMUST00000038176	te immunoglobulin-like receptor, subfamily A (with TM domain), member 6 [Source:MGI Symbol;Acc:MGI:1	A0A0B4J1F3		-9.1	5.0E-05	-3.7	3.5E-03	0.4	3.9E-01	-1.0	3.5E-01
ENSMUST00000038185	exonuclease 3'-5' domain containing 2 [Source:MGI Symbol;Acc:MGI:1922485]	F8WID1		2.9	1.6E-03	-2.3	2.6E-02	0.8	1.4E-01	-0.3	7.1E-01
ENSMUST00000038191	adenosine A1 receptor [Source:MGI Symbol;Acc:MGI:99401]		Q60612	11.1	9.3E-05	-5.7	3.2E-05	-0.8	3.8E-02	-1.1	2.0E-01
ENSMUST00000038196	Meckel syndrome, type 1 [Source:MGI Symbol;Acc:MGI:3584243]	Q284W0	Q5SW45	2.6	1.9E-03	4.2	2.1E-04	-1.3	8.5E-02	0.3	5.1E-01
ENSMUST00000037854	diaphanous homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1858500]	Q6W4W7		-0.1	9.7E-01	2.1	5.0E-01	2.0	3.4E-01	-0.2	9.4E-01
ENSMUST00000038207	DnaJ (Hsp40) homolog, subfamily C, member 6 [Source:MGI Symbol;Acc:MGI:1919935]		Q80TZ3	7.7	5.8E-03	7.5	1.6E-04	-0.7	6.3E-01	-0.7	3.2E-01
ENSMUST00000038210	Sec24 related gene family, member A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924621]	A2AA71		-3.5	9.0E-03	-0.4	5.6E-01	0.9	5.8E-02	-0.3	6.8E-01
ENSMUST00000037875	ribosome binding protein 1 [Source:MGI Symbol;Acc:MGI:1932395]		Q99PL5	1.1	4.5E-01	2.0	2.5E-01	0.4	7.9E-01	-0.6	7.0E-01
ENSMUST00000038211	schlafen 9 [Source:MGI Symbol;Acc:MGI:2445121]	B1ARD6		6.4	6.6E-06	5.5	2.2E-03	0.1	9.5E-01	-0.5	5.4E-01
ENSMUST00000038213	syntaxin binding protein 5 (tomosyn) [Source:MGI Symbol;Acc:MGI:1926058]		Q8K400	-1.6	5.6E-03	-3.2	4.4E-04	0.7	3.6E-02	0.4	5.5E-01
ENSMUST00000038217	deltex 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2135752]		Q80V91	-5.6	1.6E-03	4.2	1.5E-03	-0.9	3.7E-01	-0.1	8.9E-01
ENSMUST00000038227	atypical chemokine receptor 1 (Duffy blood group) [Source:MGI Symbol;Acc:MGI:1097689]			5.8	4.9E-03	5.9	9.2E-04	-0.6	6.3E-01	-0.2	7.4E-01
ENSMUST00000037903	plakophilin 4 [Source:MGI Symbol;Acc:MGI:109281]	A2AS45		1.9	3.5E-01	1.5	3.3E-01	-4.1	3.4E-02	-3.7	4.0E-02
ENSMUST00000038228	thioredoxin-related transmembrane protein 4 [Source:MGI Symbol;Acc:MGI:106558]	Q0P5W2	Q8C0L0	-3.2	7.2E-05	2.7	4.1E-03	-0.9	1.9E-01	-0.4	4.4E-01
ENSMUST00000038229	nei like 2 (E. coli) [Source:MGI Symbol;Acc:MGI:2686058]		Q6R2P8	6.1	7.1E-04	-6.8	1.7E-03	0.1	8.9E-01	-0.8	6.6E-01
ENSMUST00000038237	THO complex 5 [Source:MGI Symbol;Acc:MGI:1351333]			-6.6	1.0E-05	-3.0	2.9E-03	1.0	5.0E-02	0.3	7.1E-01
ENSMUST00000038244	G-protein signalling modulator 3 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:2146785]	Q0VGT5	Q3U1Z5	-5.6	8.6E-05	6.2	2.5E-06	0.1	9.2E-01	0.2	6.0E-01
ENSMUST00000038252	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1349461]		O54905	6.2	5.6E-05	-2.5	7.6E-02	1.0	2.2E-01	0.3	8.1E-01
ENSMUST00000037918	transmembrane protein 33 [Source:MGI Symbol;Acc:MGI:1915128]		Q9CR67	-1.0	1.1E-01	-0.2	7.6E-01	0.8	1.4E-01	0.1	9.2E-01
ENSMUST00000038257	glutathione S-transferase, theta 2 [Source:MGI Symbol;Acc:MGI:106188]		Q61133	2.1	1.3E-02	6.4	3.1E-04	-0.5	7.1E-01	-0.5	4.0E-01
ENSMUST00000038280	fermitin family homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443583]		P59113	9.2	3.2E-06	-5.3	1.1E-03	1.0	4.1E-02	2.1	8.2E-02
ENSMUST00000037941	CD81 antigen [Source:MGI Symbol;Acc:MGI:1096398]		P35762	-2.2	6.8E-02	-2.4	8.6E-02	-1.0	2.1E-01	-0.8	5.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000038281	dexamethasone-induced transcript [Source:MGI Symbol;Acc:MGI:1926236]		Q9WUQ7	-3.0	1.1E-02	4.0	5.0E-02	-3.0	1.6E-01	1.8	1.6E-01
ENSMUST00000038287	dual specificity phosphatase 5 [Source:MGI Symbol;Acc:MGI:2685183]	Q1HL35		-2.7	1.7E-02	-6.3	1.6E-04	1.1	3.9E-02	-0.3	7.8E-01
ENSMUST00000038295	pleckstrin homology domain containing, family A member 6 [Source:MGI Symbol;Acc:MGI:2388662]		Q7TQG1	6.6	1.3E-04	2.1	1.7E-02	-2.1	1.3E-02	0.3	6.0E-01
ENSMUST00000038332	cytosolic thiouridylase subunit 1 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:2385277]		Q99J10	2.2	8.8E-03	-6.8	1.2E-03	0.6	2.2E-01	5.7	3.1E-03
ENSMUST00000038336	polycystic kidney and hepatic disease 1-like 1 [Source:MGI Symbol;Acc:MGI:2183153]	F8WH29		7.0	1.9E-04	6.8	5.1E-04	0.7	6.2E-01	0.0	9.6E-01
ENSMUST00000038341	udding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1333885		Q9Z1S0	-1.2	2.3E-02	-5.5	3.7E-03	-0.3	6.0E-01	1.6	3.2E-01
ENSMUST00000037968	UV radiation resistance associated gene [Source:MGI Symbol;Acc:MGI:1925860]		Q8K245	-0.4	6.0E-01	0.2	8.8E-01	0.6	3.9E-01	0.1	9.1E-01
ENSMUST00000038343	beta-1,4-N-acetyl-galactosaminyl transferase 2 [Source:MGI Symbol;Acc:MGI:1342058]	A2A615	Q09199	5.9	3.0E-04	5.7	1.7E-04	-1.2	2.3E-01	-0.4	5.4E-01
ENSMUST00000038356	ubiquitin-conjugating enzyme E2Q (putative) 1 [Source:MGI Symbol;Acc:MGI:1917343]		Q7TSS2	-4.6	9.2E-05	-4.1	1.8E-02	-0.3	6.8E-01	-0.3	8.3E-01
ENSMUST00000038361	mannoside acetylglucosaminyltransferase 5 [Source:MGI Symbol;Acc:MGI:894701]	Q059T5	Q8R4G6	1.0	2.0E-02	-5.9	5.4E-04	0.7	1.8E-01	1.4	2.5E-01
ENSMUST00000038364	follistatin-like 5 [Source:MGI Symbol;Acc:MGI:2442179]		Q8BFR2	6.9	5.0E-05	6.6	3.1E-04	-0.5	7.2E-01	-1.9	2.1E-02
ENSMUST00000037992	slingshot homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2683546]		Q8K330	-3.9	3.8E-02	-4.6	8.1E-02	1.2	3.4E-01	1.9	4.5E-01
ENSMUST00000038368	inhibitor of DNA binding 1 [Source:MGI Symbol;Acc:MGI:96396]	Q6GTZ3	P20067	-8.1	2.3E-06	-7.8	3.2E-06	-0.1	6.0E-01	0.2	8.1E-01
ENSMUST00000037998	translocating chain-associating membrane protein 2 [Source:MGI Symbol;Acc:MGI:1924817]		Q924Z5	0.0	9.5E-01	1.1	1.4E-01	1.0	1.1E-01	-0.2	7.5E-01
ENSMUST00000038377	B cell translocation gene 1, anti-proliferative [Source:MGI Symbol;Acc:MGI:88215]	Q3UEG0	P62325	-6.3	1.1E-04	7.2	1.0E-04	-0.6	6.4E-01	-0.3	5.6E-01
ENSMUST00000038379	cleavage and polyadenylation specific factor 7 [Source:MGI Symbol;Acc:MGI:1917826]		Q8BTV2	-3.1	1.6E-03	4.2	5.4E-03	-1.3	2.7E-01	-1.6	1.2E-01
ENSMUST00000038014	DnaJ (Hsp40) homolog, subfamily C, member 16 [Source:MGI Symbol;Acc:MGI:2442146]		Q80TN4	0.7	9.5E-02	1.9	7.0E-03	1.0	3.9E-02	-0.1	8.0E-01
ENSMUST00000038382	junctophilin 1 [Source:MGI Symbol;Acc:MGI:1891495]		Q9ET80	7.1	1.3E-05	-5.1	6.6E-05	1.3	5.2E-03	-0.8	3.4E-01
ENSMUST00000038384	YTH domain containing 1 [Source:MGI Symbol;Acc:MGI:2443713]		E9Q5K9	-7.3	2.8E-03	-6.8	2.1E-06	-0.5	1.1E-01	-1.0	1.6E-01
ENSMUST00000038039	tyrosyl-DNA phosphodiesterase 2 [Source:MGI Symbol;Acc:MGI:1860486]		Q9JJX7	-1.3	1.2E-01	0.6	6.0E-01	2.2	3.1E-02	0.2	8.1E-01
ENSMUST00000038053	LIM domain containing preferred translocation partner in lipoma [Source:MGI Symbol;Acc:MGI:2441849]		Q8BFW7	-1.3	4.1E-01	-2.5	3.0E-01	0.8	5.4E-01	2.0	3.9E-01
ENSMUST00000038388	RIKEN cDNA A230046K03 gene [Source:MGI Symbol;Acc:MGI:2441787]		Q3UMB9	-2.9	1.4E-04	-6.2	8.8E-06	0.3	4.0E-01	-1.9	3.1E-02
ENSMUST00000038073	cation channel, sperm associated 2 [Source:MGI Symbol;Acc:MGI:2387404]	A0A0A0MQ85		2.8	4.4E-02	3.4	6.3E-02	0.6	6.8E-01	0.0	9.8E-01
ENSMUST00000038075	gamma-glutamylamine cyclotransferase [Source:MGI Symbol;Acc:MGI:2385008]		Q923B0	1.2	7.5E-02	0.3	6.3E-01	-2.3	4.0E-03	-1.3	5.7E-02
ENSMUST00000038389	stereocilin [Source:MGI Symbol;Acc:MGI:2153816]		Q8VIM6	8.4	9.2E-06	5.6	1.0E-02	0.7	6.8E-01	-0.6	6.3E-01
ENSMUST00000038398	poly (ADP-ribose) polymerase family, member 12 [Source:MGI Symbol;Acc:MGI:2143990]		Q8BZ20	-2.1	1.5E-02	3.3	5.7E-02	-3.8	6.0E-02	-0.4	7.1E-01
ENSMUST00000038406	aldo-keto reductase family 1, member B8 [Source:MGI Symbol;Acc:MGI:107673]		P45377	4.2	1.3E-03	-0.6	4.0E-01	1.0	5.2E-02	-0.2	7.1E-01
ENSMUST00000038407	La ribonucleoprotein domain family, member 6 [Source:MGI Symbol;Acc:MGI:1914807]		Q8BN59	7.8	4.3E-05	3.9	1.4E-04	-0.4	5.1E-01	0.3	4.4E-01
ENSMUST00000038099	suppressor of cytokine signaling 1 [Source:MGI Symbol;Acc:MGI:1354910]		O35716	-0.3	6.5E-01	-0.1	9.1E-01	-0.3	6.8E-01	-0.4	5.3E-01
ENSMUST00000038101	histamine receptor H2 [Source:MGI Symbol;Acc:MGI:108482]		P97292	-1.1	7.4E-02	-0.4	5.9E-01	0.8	1.2E-01	0.2	8.3E-01
ENSMUST00000038104	e prime 1, subunit of RNA polymerase III transcription initiation factor IIIB [Source:MGI Symbol;Acc:MGI:1		Q571C7	-0.8	4.1E-01	1.7	2.7E-01	2.1	1.2E-01	-0.4	7.0E-01
ENSMUST00000038409	podocalyxin-like 2 [Source:MGI Symbol;Acc:MGI:2442488]	G3X9D3		5.9	1.1E-02	-2.3	2.1E-02	1.1	4.8E-02	-0.2	7.9E-01
ENSMUST00000038421	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914457]	Q544C9	Q8VC85	-2.9	1.4E-04	4.6	2.0E-04	0.4	5.8E-01	0.2	6.4E-01
ENSMUST00000038423	receptor transporter protein 4 [Source:MGI Symbol;Acc:MGI:1915025]		Q9ER80	-4.0	6.9E-03	-2.0	8.5E-03	0.4	3.1E-01	0.4	5.5E-01
ENSMUST00000038424	thioredoxin domain containing 11 [Source:MGI Symbol;Acc:MGI:1923620]		Q8K2W3	-1.8	8.7E-03	-3.0	1.1E-01	1.6	1.1E-01	-2.0	3.4E-01
ENSMUST00000038431	pyruvate dehydrogenase kinase, isoenzyme 2 [Source:MGI Symbol;Acc:MGI:1343087]		Q9JK42	1.7	1.4E-02	-1.0	2.5E-01	0.3	5.7E-01	-0.6	5.3E-01
ENSMUST00000038434	ribonuclease P/MRP 25 subunit-like [Source:MGI Symbol;Acc:MGI:1917211]		Q99JH1	-2.4	3.9E-03	-3.0	1.0E-02	-1.0	9.7E-02	-1.7	1.5E-01
ENSMUST00000038141	schlafen 8 [Source:MGI Symbol;Acc:MGI:2672859]	B1ARD8		-1.2	1.5E-01	-1.7	1.0E-01	-1.0	1.4E-01	-0.5	6.4E-01
ENSMUST00000038439	DnaJ (Hsp40) homolog, subfamily C, member 17 [Source:MGI Symbol;Acc:MGI:1916658]		Q91WT4	-4.6	1.4E-03	-4.4	5.6E-03	-1.1	1.2E-01	0.8	5.5E-01
ENSMUST00000038445	myosin binding protein H [Source:MGI Symbol;Acc:MGI:1858196]		P70402	5.1	1.4E-02	6.3	3.0E-04	1.1	3.0E-01	-0.1	9.2E-01
ENSMUST00000038446	myosin, light chain 12B, regulatory [Source:MGI Symbol;Acc:MGI:107494]		Q3THE2	-7.2	6.0E-07	2.9	6.8E-03	-0.1	8.4E-01	0.1	8.4E-01
ENSMUST00000038447	EF-hand domain (C-terminal) containing 1 [Source:MGI Symbol;Acc:MGI:1919127]	B2CKC6		3.4	1.5E-03	-3.0	5.0E-03	1.0	4.6E-02	0.0	9.9E-01
ENSMUST00000038154	mitochondria localized glutamic acid rich protein [Source:MGI Symbol;Acc:MGI:1914999]		Q8VI64	3.4	1.8E-01	1.6	4.7E-01	-1.9	4.4E-01	-0.1	9.6E-01
ENSMUST00000038448	transmembrane protease, serine 11B [Source:MGI Symbol;Acc:MGI:2442893]		Q14C59	6.1	1.6E-06	5.0	1.3E-03	-1.5	2.3E-01	0.9	2.0E-01
ENSMUST00000038463	ribonucleoprotein, PTB-binding 2 [Source:MGI Symbol;Acc:MGI:2443623]		Q7TPD6	3.9	1.3E-03	7.0	2.2E-04	-0.7	6.1E-01	0.3	6.8E-01
ENSMUST00000038166	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 [Source:MGI Symbol;Acc:MGI:2147067]		Q6P5D3	-4.5	1.0E-01	-3.1	3.6E-01	1.3	4.8E-01	-0.1	9.8E-01
ENSMUST00000038472	highly divergent homeobox [Source:MGI Symbol;Acc:MGI:2685226]		Q14B70	6.3	2.6E-03	-3.7	2.9E-03	-0.6	2.6E-01	0.2	8.7E-01
ENSMUST00000038172	myotubularin related protein 12 [Source:MGI Symbol;Acc:MGI:2443034]		Q80TA6	-3.9	1.7E-01	1.4	7.4E-01	5.3	1.1E-01	0.0	9.9E-01
ENSMUST00000038474	exosome component 2 [Source:MGI Symbol;Acc:MGI:2385133]	Q3TKQ3	Q8VBV3	1.7	4.5E-03	6.7	5.6E-04	0.1	9.4E-01	-1.1	1.7E-01
ENSMUST00000038482	lipocalin 8 [Source:MGI Symbol;Acc:MGI:2135945]		Q924P3	6.0	2.5E-04	-7.9	1.4E-04	-0.1	8.9E-01	-1.2	4.4E-01
ENSMUST00000038488	SID1 transmembrane family, member 2 [Source:MGI Symbol;Acc:MGI:2446134]	Q3U1L8	Q8CIF6	-7.7	2.1E-05	2.3	3.7E-02	0.8	3.1E-01	1.4	8.0E-02
ENSMUST00000038188	LIM and calponin homology domains 1 [Source:MGI Symbol;Acc:MGI:1924819]		Q3UH68	4.1	9.4E-02	6.6	2.3E-02	-0.2	9.3E-01	-2.7	8.7E-02
ENSMUST00000038489	pygopus 1 [Source:MGI Symbol;Acc:MGI:1919385]	Q1JPR5	Q9D0P5	8.7	6.2E-06	8.8	5.6E-04	-1.4	5.0E-01	1.0	2.3E-01
ENSMUST00000038193	WD repeat domain 59 [Source:MGI Symbol;Acc:MGI:2442115]		Q8C0M0	-0.2	9.2E-01	2.1	2.5E-01	0.4	8.0E-01	-1.9	2.8E-01
ENSMUST00000038194	ATPase family, AAA domain containing 2 [Source:MGI Symbol;Acc:MGI:1917722]	G3X963		-0.3	4.1E-01	-0.5	3.1E-01	0.0	9.6E-01	0.2	6.9E-01
ENSMUST00000038495	C-reactive protein, pentraxin-related [Source:MGI Symbol;Acc:MGI:88512]		P14847	7.9	7.3E-05	2.9	3.4E-03	0.1	8.3E-01	-0.2	7.9E-01
ENSMUST00000038507	lymphocyte antigen 6 complex, locus G6F [Source:MGI Symbol;Acc:MGI:3616082]	B2RXM6		6.7	6.6E-05	5.4	2.8E-02	-3.1	2.1E-01	-0.9	5.4E-01
ENSMUST00000038514	nucleoporin 54 [Source:MGI Symbol;Acc:MGI:1920460]		Q8BTS4	-2.3	1.5E-03	-0.3	7.6E-01	1.0	2.0E-01	-2.1	1.2E-01
ENSMUST00000038521	tRNA splicing endonuclease 34 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913328]	H7BX14		-3.8	3.8E-03	5.7	6.5E-05	0.1	9.1E-01	0.7	1.9E-01
ENSMUST00000038212	granzyme K [Source:MGI Symbol;Acc:MGI:1298232]		O35205	0.3	8.3E-01	2.7	2.1E-02	-1.7	1.1E-01	-4.1	4.3E-03
ENSMUST00000038522	sarcolemma associated protein [Source:MGI Symbol;Acc:MGI:1933549]		Q3URD3	-5.4	5.2E-03	-0.7	3.1E-01	1.2	1.4E-02	0.3	6.6E-01
ENSMUST00000038529	RBBP8 N-terminal like [Source:MGI Symbol;Acc:MGI:3606212]	A2ABX0		8.3	8.4E-05	-4.2	2.9E-02	0.7	3.8E-01	-0.8	6.7E-01
ENSMUST00000038532	melanocortin 3 receptor [Source:MGI Symbol;Acc:MGI:96929]	Q544G7	P33033	8.1	1.2E-05	2.8	9.6E-02	-2.1	2.3E-01	0.9	4.4E-01
ENSMUST00000038537	WT1-interacting protein [Source:MGI Symbol;Acc:MGI:2141920]		Q7TQJ8	5.5	1.3E-04	-2.0	8.3E-03	1.0	1.8E-02	-0.2	7.3E-01
ENSMUST00000038539	RIKEN cDNA 1700123O20 gene [Source:MGI Symbol;Acc:MGI:1920893]		Q9JJ93	-3.5	6.1E-05	6.0	1.0E-03	-1.4	3.2E-01	-1.3	1.3E-01
ENSMUST00000038234	intraflagellar transport 122 [Source:MGI Symbol;Acc:MGI:1932386]		Q6NWV3	1.6	4.2E-01	3.8	1.7E-01	1.8	4.7E-01	-0.4	8.4E-01
ENSMUST00000038551	protein phosphatase 1, regulatory subunit 21 [Source:MGI Symbol;Acc:MGI:1921075]		Q3TDD9	-2.8	2.1E-04	-2.7	1.1E-03	-0.3	4.3E-01	-4.2	4.8E-04
ENSMUST00000038552	coronin 7 [Source:MGI Symbol;Acc:MGI:1926135]		Q9D2V7	-3.0	2.2E-04	-3.9	4.8E-03	1.2	3.9E-02	-0.6	6.1E-01
ENSMUST00000038562	splA/ryanodine receptor domain and SOCS box containing 1 [Source:MGI Symbol;Acc:MGI:1921896]		Q9D5L7	1.4	2.7E-02	4.6	7.7E-04	-1.2	2.1E-01	0.3	6.2E-01
ENSMUST00000038563	golgi integral membrane protein 4 [Source:MGI Symbol;Acc:MGI:1920374]		Q8BXA1	2.4	5.4E-04	1.5	8.6E-02	-0.8	2.5E-01	-0.2	7.2E-01
ENSMUST00000038259	solute carrier organic anion transporter family, member 4a1 [Source:MGI Symbol;Acc:MGI:1351866]		Q8K078	0.8	7.2E-01	5.6	4.7E-02	1.6	5.2E-01	-3.3	1.2E-01
ENSMUST00000038275	myosin regulatory light chain interacting protein [Source:MGI Symbol;Acc:MGI:2388271]		Q8BM54	-0.9	5.3E-02	0.1	8.3E-01	0.4	3.5E-01	-0.7	1.9E-01
ENSMUST00000038569	sprouty homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1345139]	Q53ZU1	Q9QXV9	5.2	1.7E-02	7.0	9.2E-06	-2.5	2.5E-02	-0.3	5.0E-01
ENSMUST00000038584	tousled-like kinase 1 [Source:MGI Symbol;Acc:MGI:2441683]		Q8C0V0	-7.7	3.5E-05	-0.6	5.0E-01	0.8	2.5E-01	-1.5	1.6E-01
ENSMUST00000038598	isopentenyl-diphosphate delta isomerase 2 [Source:MGI Symbol;Acc:MGI:2444315]		Q8BFZ6	7.5	2.8E-05	-0.9	4.4E-01	1.3	1.2E-01	-0.4	7.3E-01
ENSMUST00000038608	membrane bound O-acyltransferase domain containing 7 [Source:MGI Symbol;Acc:MGI:1924832]		Q8CHK3	-4.1	1.1E-03	7.7	7.3E-05	-0.6	6.5E-01	-1.6	2.5E-02
ENSMUST00000038614	yippee-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913340]		P61237	-8.4	9.5E-06	5.2	1.1E-02	-0.6	7.3E-01	0.9	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000038618	latent transforming growth factor beta binding protein 4 [Source:MGI Symbol;Acc:MGI:1321395]		Q8K4G1	8.7	7.9E-04	2.5	1.8E-02	1.0	1.9E-01	0.6	3.9E-01
ENSMUST00000038626	MPV17 mitochondrial membrane protein-like 2 [Source:MGI Symbol;Acc:MGI:2681846]		Q8VIK2	-2.3	3.9E-03	4.0	1.5E-03	-3.8	7.9E-03	-0.9	2.5E-01
ENSMUST00000038627	zinc finger protein 91 [Source:MGI Symbol;Acc:MGI:104854]		Q62511	-3.3	2.2E-04	0.2	6.8E-01	0.7	8.0E-02	-0.7	2.4E-01
ENSMUST00000038648	NIMA (never in mitosis gene a)-related expressed kinase 11 [Source:MGI Symbol;Acc:MGI:2442276]		Q8C0Q4	6.8	6.0E-04	6.6	5.2E-04	0.2	8.6E-01	-0.5	5.2E-01
ENSMUST00000038658	MOB kinase activator 1A [Source:MGI Symbol;Acc:MGI:2442631]		Q921Y0	-5.4	2.6E-03	-3.1	5.1E-03	0.9	7.2E-02	-0.6	4.9E-01
ENSMUST00000038359	RIKEN cDNA 2210018M11 gene [Source:MGI Symbol;Acc:MGI:1924203]		Q8BMB0	-0.8	9.8E-02	-1.2	6.4E-02	-0.4	2.9E-01	0.0	9.7E-01
ENSMUST00000038661	solute carrier family 25, member 34 [Source:MGI Symbol;Acc:MGI:2686215]		A2ADF7	6.8	1.6E-05	1.9	2.9E-03	0.9	3.4E-02	0.0	9.3E-01
ENSMUST00000038671	KRI1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2384899]	F6WIU1		-9.0	3.7E-05	7.0	9.0E-05	-0.5	6.4E-01	-0.6	3.2E-01
ENSMUST00000038673	anaphase promoting complex subunit 13 [Source:MGI Symbol;Acc:MGI:1916260]		Q8R034	-5.3	7.5E-04	4.2	5.4E-03	-1.9	1.3E-01	-0.6	4.8E-01
ENSMUST00000038676	carboxypeptidase Z [Source:MGI Symbol;Acc:MGI:88487]		Q8R4V4	7.6	1.9E-05	-7.5	3.1E-05	-0.1	7.3E-01	-0.8	4.9E-01
ENSMUST00000038369	CLOCK interacting protein, circadian [Source:MGI Symbol;Acc:MGI:1919185]	Z4YJJ0		-0.6	2.8E-01	0.0	9.5E-01	0.3	4.9E-01	-0.3	6.5E-01
ENSMUST00000038374	propionyl-Coenzyme A carboxylase, alpha polypeptide [Source:MGI Symbol;Acc:MGI:97499]	Q3UGC8	Q91ZA3	-1.3	1.1E-01	-2.0	7.5E-02	-0.5	4.1E-01	0.1	8.8E-01
ENSMUST00000038677	ribosomal RNA processing 12 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2147437]	Q3UJA1	Q6P5B0	2.6	6.2E-04	-4.6	3.8E-03	1.1	9.4E-02	-0.5	6.8E-01
ENSMUST00000038693	claudin 22 [Source:MGI Symbol;Acc:MGI:1922927]		Q9D7U6	7.1	1.5E-04	-1.7	7.0E-02	0.7	1.9E-01	-0.6	5.0E-01
ENSMUST00000038695	potassium voltage-gated channel, shaker-related subfamily, member 2 [Source:MGI Symbol;Acc:MGI:96659]		P63141	7.4	2.7E-05	6.9	2.3E-04	0.4	7.0E-01	0.7	2.9E-01
ENSMUST00000038383	aldo-keto reductase family 1, member B10 (aldose reductase) [Source:MGI Symbol;Acc:MGI:1915111]	G5E895		-0.8	7.3E-01	-0.4	8.2E-01	-2.7	1.3E-01	-3.1	1.8E-01
ENSMUST00000038696	protein phosphatase 1, regulatory subunit 9B [Source:MGI Symbol;Acc:MGI:2387581]		Q6R891	-3.4	1.3E-04	-2.3	4.2E-01	4.6	1.9E-02	-0.4	8.8E-01
ENSMUST00000038705	UFM1 specific ligase 1 [Source:MGI Symbol;Acc:MGI:1914740]		Q8CCJ3	-6.1	1.5E-04	-2.6	1.4E-03	-0.1	7.6E-01	-0.4	5.5E-01
ENSMUST00000038709	cDNA sequence BC017643 [Source:MGI Symbol;Acc:MGI:2384959]		Q3TYS2	-8.3	1.0E-04	8.4	1.9E-05	-0.6	5.9E-01	-0.6	2.4E-01
ENSMUST00000038710	desmocollin 1 [Source:MGI Symbol;Acc:MGI:109173]	Q32ME9		6.3	2.4E-04	-1.0	2.7E-01	0.5	3.7E-01	-0.5	5.7E-01
ENSMUST00000038404	cyclin O [Source:MGI Symbol;Acc:MGI:2145534]	B2RWG0	P0C242	-1.2	1.2E-01	-0.5	5.9E-01	0.5	4.5E-01	-0.2	7.9E-01
ENSMUST00000038720	coiled-coil domain containing 114 [Source:MGI Symbol;Acc:MGI:2446120]		Q3UX62	2.4	2.4E-03	-0.5	4.6E-01	-6.1	4.5E-05	-1.4	6.2E-02
ENSMUST00000038730	receptor transporter protein 1 [Source:MGI Symbol;Acc:MGI:2685450]	B2RSL5	Q8C8C1	7.3	2.4E-05	7.6	9.9E-05	-0.6	6.2E-01	-0.4	4.9E-01
ENSMUST00000038738	CDKN2A interacting protein [Source:MGI Symbol;Acc:MGI:1918175]		Q8BI72	-2.5	7.8E-04	7.1	6.3E-03	-0.8	7.1E-01	-2.0	1.2E-01
ENSMUST00000038411	adenosine deaminase, tRNA-specific 3 [Source:MGI Symbol;Acc:MGI:1924344]		Q6PAT0	0.5	7.5E-01	-1.1	5.3E-01	-0.8	5.5E-01	0.8	6.6E-01
ENSMUST00000038739	ring finger and WD repeat domain 3 [Source:MGI Symbol;Acc:MGI:2384584]		Q8CIK8	-2.0	1.6E-03	-2.8	8.5E-04	-0.1	7.7E-01	-0.2	7.3E-01
ENSMUST00000038422	interferon regulatory factor 2 binding protein-like [Source:MGI Symbol;Acc:MGI:2442463]		Q8K3X4	-0.8	7.5E-02	0.2	7.1E-01	0.9	2.7E-02	0.0	1.0E+00
ENSMUST00000038749	peptidyl arginine deiminase, type VI [Source:MGI Symbol;Acc:MGI:2655198]		Q8K3V4	6.3	3.8E-04	-3.6	2.3E-02	-1.1	1.6E-01	-1.6	3.1E-01
ENSMUST00000038753	SH3 and PX domains 2B [Source:MGI Symbol;Acc:MGI:2442062]		A2AAY5	2.9	1.8E-04	-0.5	4.8E-01	0.9	1.0E-01	-0.4	5.3E-01
ENSMUST00000038757	cold shock domain containing C2, RNA binding [Source:MGI Symbol;Acc:MGI:2146027]		Q91YQ3	9.8	1.0E-05	2.8	3.7E-03	0.7	3.0E-01	-0.4	4.8E-01
ENSMUST00000038760	ladinin [Source:MGI Symbol;Acc:MGI:109343]		P57016	8.3	1.7E-05	-1.7	5.4E-02	0.0	9.6E-01	-0.7	3.9E-01
ENSMUST00000038765	inhibin beta-B [Source:MGI Symbol;Acc:MGI:96571]		Q04999	8.0	1.1E-05	-3.1	8.2E-03	-0.6	2.8E-01	-2.1	8.8E-02
ENSMUST00000038770	vasorin [Source:MGI Symbol;Acc:MGI:2177651]		Q9CZT5	2.8	2.0E-03	3.0	2.0E-01	-1.0	6.3E-01	1.1	5.0E-01
ENSMUST00000038772	transmembrane protein 5 [Source:MGI Symbol;Acc:MGI:2384919]	Q5XK09		-5.3	7.1E-05	-7.2	6.4E-06	0.1	6.4E-01	0.1	8.7E-01
ENSMUST00000038775	necdin [Source:MGI Symbol;Acc:MGI:97290]		P25233	5.6	5.9E-05	4.0	2.1E-03	0.6	4.7E-01	0.0	9.8E-01
ENSMUST00000038791	glycerophosphodiester phosphodiesterase 1 [Source:MGI Symbol;Acc:MGI:1891827]		Q9JL56	-1.4	1.9E-02	6.6	3.5E-06	0.3	6.6E-01	-0.2	6.2E-01
ENSMUST00000038794	dipeptidylpeptidase 9 [Source:MGI Symbol;Acc:MGI:2443967]		Q8BVG4	-1.3	2.0E-02	4.3	2.1E-04	0.0	9.7E-01	-0.1	8.3E-01
ENSMUST00000038824	cytochrome P450, family 24, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88593]	Q3TWW0	Q64441	7.8	1.5E-05	4.8	1.3E-03	0.3	7.5E-01	-0.6	4.5E-01
ENSMUST00000038829	Fc fragment of IgM receptor [Source:MGI Symbol;Acc:MGI:1916419]	A0A0G2LB91		2.6	4.5E-03	4.6	2.0E-02	-0.9	6.1E-01	0.8	4.5E-01
ENSMUST00000038830	RIKEN cDNA 1110059E24 gene [Source:MGI Symbol;Acc:MGI:1913456]		Q9CQ90	-4.7	7.4E-04	1.1	6.8E-02	-0.5	3.2E-01	0.1	8.5E-01
ENSMUST00000038475	fatty acid 2-hydroxylase [Source:MGI Symbol;Acc:MGI:2443327]		Q5MPP0	2.7	4.2E-02	6.3	2.6E-04	-0.5	6.6E-01	-4.2	7.2E-04
ENSMUST00000038841	clavesin 1 [Source:MGI Symbol;Acc:MGI:1921688]		Q9D4C9	6.8	3.5E-02	6.1	4.4E-04	-0.6	6.4E-01	-0.6	3.7E-01
ENSMUST00000038845	CD53 antigen [Source:MGI Symbol;Acc:MGI:88341]	Q3U0W1	Q61451	-8.8	5.3E-08	-1.5	3.5E-02	1.0	3.7E-02	-5.2	4.7E-04
ENSMUST00000038856	thyrotropin releasing hormone receptor [Source:MGI Symbol;Acc:MGI:98824]	Q32MS1	P21761	7.1	2.6E-04	7.1	2.2E-05	-1.6	1.5E-01	0.0	1.0E+00
ENSMUST00000038859	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]	Q8CI98		-8.4	1.4E-04	5.7	1.4E-04	-2.7	4.1E-02	-0.6	3.7E-01
ENSMUST00000038498	BCL2-associated athanogene 4 [Source:MGI Symbol;Acc:MGI:1914634]	A6H6S8	Q8CI61	-1.1	9.2E-02	0.6	4.8E-01	1.0	1.2E-01	-0.7	3.5E-01
ENSMUST00000038867	optic atrophy 1 [Source:MGI Symbol;Acc:MGI:1921393]	H7BX01		-5.7	1.3E-04	7.2	7.1E-05	-0.6	6.0E-01	-1.1	8.6E-02
ENSMUST00000038868	spermatogenesis associated 6 [Source:MGI Symbol;Acc:MGI:1915196]		Q3U6K5	-5.9	3.5E-03	-2.4	5.1E-03	0.0	9.0E-01	0.0	9.9E-01
ENSMUST00000038876	epithelial membrane protein 3 [Source:MGI Symbol;Acc:MGI:1098729]		O35912	-5.4	3.8E-05	-0.7	6.3E-01	2.5	2.2E-02	-0.6	6.5E-01
ENSMUST00000038886	colony stimulating factor 3 (granulocyte) [Source:MGI Symbol;Acc:MGI:1339751]	Q0VB73	P09920	6.5	1.1E-04	-1.5	4.4E-01	2.5	5.7E-02	-1.5	4.5E-01
ENSMUST00000038523	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:2682307]		Q80XE1	-0.5	7.6E-01	1.9	3.7E-01	2.1	2.4E-01	-0.3	8.5E-01
ENSMUST00000038890	DENN/MADD domain containing 4A [Source:MGI Symbol;Acc:MGI:2142979]	E9Q8V6		-4.6	4.6E-07	6.7	6.2E-04	-1.5	3.2E-01	0.1	8.6E-01
ENSMUST00000038896	lecithin cholesterol acyltransferase [Source:MGI Symbol;Acc:MGI:96755]		P16301	7.0	1.6E-04	7.3	2.9E-05	-1.5	1.9E-01	-0.8	1.6E-01
ENSMUST00000038907	WEE1 homolog 2 (S. pombe) [Source:MGI Symbol;Acc:MGI:3027899]		Q66JT0	3.0	4.6E-03	3.3	1.4E-03	-2.7	9.2E-03	-0.6	3.6E-01
ENSMUST00000038913	CCR4-NOT transcription complex, subunit 3 [Source:MGI Symbol;Acc:MGI:2385261]		Q8K0V4	-7.3	1.6E-03	-3.6	2.6E-04	-0.3	4.2E-01	-0.2	7.5E-01
ENSMUST00000038920	G protein-coupled receptor 63 [Source:MGI Symbol;Acc:MGI:2135884]		Q9EQQ3	5.0	3.9E-04	-2.4	3.6E-03	0.5	1.7E-01	0.1	8.9E-01
ENSMUST00000038928	histone H1-like protein in spermatids 1 [Source:MGI Symbol;Acc:MGI:2136691]	Q5SWB1	Q9QYL0	7.2	1.5E-04	-1.9	2.4E-02	1.4	7.9E-03	0.2	7.7E-01
ENSMUST00000038558	Kruppel-like factor 16 [Source:MGI Symbol;Acc:MGI:2153049]	B2RPU7	P58334	-0.1	9.4E-01	0.2	8.8E-01	0.9	2.6E-01	0.7	4.9E-01
ENSMUST00000038942	pre B cell leukemia transcription factor interacting protein 1 [Source:MGI Symbol;Acc:MGI:2441670]		Q3TVI8	-4.3	2.5E-05	2.0	1.3E-02	-0.3	5.8E-01	-0.9	1.5E-01
ENSMUST00000038945	pleckstrin homology-like domain, family A, member 3 [Source:MGI Symbol;Acc:MGI:1351485]		Q9WV95	4.6	1.1E-03	3.3	2.6E-04	0.2	7.0E-01	-0.7	1.4E-01
ENSMUST00000038949	adrenergic receptor, beta 1 [Source:MGI Symbol;Acc:MGI:87937]		P34971	6.1	3.2E-04	2.4	3.2E-01	-0.7	7.3E-01	2.1	2.6E-01
ENSMUST00000038570	hosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans) [Source:MGI Symbol;Acc:	Q5SVF7	O55125	0.2	7.3E-01	0.2	8.1E-01	-1.0	9.3E-02	-1.0	1.5E-01
ENSMUST00000038572	heterogeneous nuclear ribonucleoprotein L [Source:MGI Symbol;Acc:MGI:104816]		Q8R081	-6.2	4.6E-02	-3.4	3.8E-01	2.0	2.7E-01	-0.9	8.3E-01
ENSMUST00000038574	DEAH (Asp-Glu-Ala-His) box polypeptide 29 [Source:MGI Symbol;Acc:MGI:2145374]		Q6PGC1	-0.4	3.7E-01	0.8	1.5E-01	0.8	7.4E-02	-0.4	4.3E-01
ENSMUST00000038580	histocompatibility 2, M region locus 3 [Source:MGI Symbol;Acc:MGI:95915]	Q31093		0.2	7.2E-01	-0.8	2.7E-01	-1.1	4.1E-02	-0.2	8.1E-01
ENSMUST00000038956	leucine rich repeat containing 18 [Source:MGI Symbol;Acc:MGI:1914830]		Q9CQ07	6.2	4.7E-04	-4.1	1.7E-03	1.0	4.4E-02	-2.6	5.3E-02
ENSMUST00000038959	pleckstrin and Sec7 domain containing 3 [Source:MGI Symbol;Acc:MGI:1918215]	F6Z9E6		6.6	2.7E-04	6.7	1.4E-04	-0.8	5.0E-01	0.0	9.5E-01
ENSMUST00000038600	mitochondrial ribosomal protein S2 [Source:MGI Symbol;Acc:MGI:2153089]		Q924T2	0.4	8.6E-01	3.8	1.3E-01	0.3	9.1E-01	-3.2	1.5E-01
ENSMUST00000038973	N-acetylglucosamine-1-phosphotransferase, gamma subunit [Source:MGI Symbol;Acc:MGI:2147006]			-3.7	7.8E-04	-3.8	1.5E-02	1.0	1.3E-01	0.8	5.7E-01
ENSMUST00000039008	RIKEN cDNA E330009J07 gene [Source:MGI Symbol;Acc:MGI:2444256]		Q3UHG7	6.0	5.2E-05	-5.2	3.8E-04	1.0	2.8E-02	-2.2	8.7E-02
ENSMUST00000039011	ubiquitin carboxyl-terminal esterase L4 [Source:MGI Symbol;Acc:MGI:1890440]	B2RTM4	P58321	4.7	4.1E-04	4.5	3.1E-02	-2.8	1.8E-01	1.5	2.3E-01
ENSMUST00000039013	ATP-binding cassette, sub-family A (ABC1), member 3 [Source:MGI Symbol;Acc:MGI:1351617]		Q8R420	-5.6	1.9E-02	-0.6	4.0E-01	0.8	1.7E-01	-0.9	2.5E-01
ENSMUST00000039026	apelin [Source:MGI Symbol;Acc:MGI:1353624]	Q544B5	Q9R0R4	2.8	1.6E-03	-2.5	5.4E-03	0.3	4.0E-01	-0.5	5.3E-01
ENSMUST00000038628	mannosidase, alpha, class 1C, member 1 [Source:MGI Symbol;Acc:MGI:2446214]	Q6NXK9		0.7	3.7E-01	2.1	5.0E-02	1.4	8.8E-02	0.0	9.8E-01
ENSMUST00000039044	urotensin 2 receptor [Source:MGI Symbol;Acc:MGI:2183450]	Q05AD1	Q8VIH9	7.9	1.1E-04	6.2	1.4E-03	-1.4	3.6E-01	-0.9	3.0E-01
ENSMUST00000039049	synaptogyrin 4 [Source:MGI Symbol;Acc:MGI:1928903]			5.5	2.3E-02	-2.2	1.6E-01	1.5	1.0E-01	-1.7	3.3E-01
ENSMUST00000039059	proprotein convertase subtilisin/kexin type 7 [Source:MGI Symbol;Acc:MGI:107421]		Q61139	-2.1	4.9E-04	7.0	6.4E-05	0.2	8.2E-01	0.1	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000039061	trafficking protein particle complex 11 [Source:MGI Symbol;Acc:MGI:2444585]		B2RXC1	-6.6	4.5E-04	-7.1	3.3E-04	0.3	5.0E-01	-1.7	2.9E-01
ENSMUST00000039064	family with sequence similarity 124, member A [Source:MGI Symbol;Acc:MGI:3645930]	D3Z5V4		7.1	6.2E-06	-6.4	1.8E-03	-1.0	9.9E-02	0.1	9.7E-01
ENSMUST00000039074	SH3/ankyrin domain gene 3 [Source:MGI Symbol;Acc:MGI:1930016]		Q4ACU6	8.7	3.2E-05	5.9	4.5E-05	-2.5	2.7E-02	-0.8	1.4E-01
ENSMUST00000039088	testis expressed gene 19.1 [Source:MGI Symbol;Acc:MGI:1920929]		Q99MV2	8.5	1.8E-04	2.6	3.9E-03	0.1	8.4E-01	0.2	7.5E-01
ENSMUST00000038684	four and a half LIM domains 3 [Source:MGI Symbol;Acc:MGI:1341092]		Q9R059	-0.7	2.5E-01	0.7	4.2E-01	1.5	2.7E-02	0.2	8.0E-01
ENSMUST00000038690	expressed sequence AW209491 [Source:MGI Symbol;Acc:MGI:2145422]		Q91WD4	2.8	2.0E-01	-3.4	2.0E-01	-3.6	7.3E-02	2.5	3.2E-01
ENSMUST00000039090	ATPase type 13A4 [Source:MGI Symbol;Acc:MGI:1924456]			5.8	9.8E-03	7.1	3.0E-04	-0.7	6.3E-01	-0.6	4.2E-01
ENSMUST00000039118	zinc finger protein of the cerebellum 5 [Source:MGI Symbol;Acc:MGI:1929518]			8.3	5.0E-06	6.7	1.5E-04	-0.3	8.0E-01	0.5	4.8E-01
ENSMUST00000039121	family with sequence similarity 170, member A [Source:MGI Symbol;Acc:MGI:2684939]		Q66LM6	6.6	9.2E-04	-2.9	1.6E-03	0.6	1.4E-01	0.1	9.4E-01
ENSMUST00000038699	adaptor-related protein complex 5, zeta 1 subunit [Source:MGI Symbol;Acc:MGI:1924908]		Q3U829	-0.5	3.5E-01	0.5	4.9E-01	1.1	7.9E-02	0.0	9.9E-01
ENSMUST00000038701	zinc finger protein 324 [Source:MGI Symbol;Acc:MGI:2444641]	Q78F42		1.3	4.6E-01	-1.2	6.3E-01	0.5	7.9E-01	3.0	2.2E-01
ENSMUST00000039132	zinc finger protein 472 [Source:MGI Symbol;Acc:MGI:2385049]	B0V2W5		-2.5	3.7E-03	-6.5	5.8E-04	-0.8	1.0E-01	-0.4	7.6E-01
ENSMUST00000039135	dedicator of cytokinesis 5 [Source:MGI Symbol;Acc:MGI:2652871]		B2RY04	-2.2	1.5E-03	-8.2	2.0E-04	0.0	9.8E-01	-0.1	9.3E-01
ENSMUST00000039144	calsyntenin 1 [Source:MGI Symbol;Acc:MGI:1929895]		Q9EPL2	5.1	1.7E-02	6.7	4.6E-04	0.1	9.1E-01	-0.3	7.0E-01
ENSMUST00000038719	NudC domain containing 1 [Source:MGI Symbol;Acc:MGI:1914679]		Q6PIP5	0.2	6.9E-01	-0.7	2.5E-01	-1.6	5.3E-03	-0.7	2.2E-01
ENSMUST00000039146	testis expressed gene 19.2 [Source:MGI Symbol;Acc:MGI:1918206]	B2RUP5	Q9D5S1	8.5	4.1E-05	2.6	4.4E-03	-0.2	7.9E-01	-0.4	5.2E-01
ENSMUST00000039152	DEAH (Asp-Glu-Ala-His) box polypeptide 8 [Source:MGI Symbol;Acc:MGI:1306823]		A2A4P0	-2.0	1.0E-03	7.4	4.2E-05	-0.6	6.2E-01	-0.7	2.4E-01
ENSMUST00000039153	choline/ethanolaminephosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2139793]		Q8BGS7	-4.5	1.9E-03	-1.3	6.8E-02	0.5	1.9E-01	-0.7	2.9E-01
ENSMUST00000039160	G protein-coupled receptor 176 [Source:MGI Symbol;Acc:MGI:2685858]		Q80WT4	7.5	9.4E-06	-1.0	1.3E-01	0.8	7.2E-02	-0.3	6.1E-01
ENSMUST00000039161	thymocyte nuclear protein 1 [Source:MGI Symbol;Acc:MGI:1925112]		Q91YJ3	-3.1	1.2E-02	7.2	6.6E-04	0.5	7.6E-01	-0.4	6.0E-01
ENSMUST00000039164	lysophosphatidic acid receptor 3 [Source:MGI Symbol;Acc:MGI:1929469]	Q544B4	Q9EQ31	8.1	6.4E-06	1.7	1.5E-02	-1.2	3.9E-02	0.1	8.9E-01
ENSMUST00000039174	PR domain containing 1, with ZNF domain [Source:MGI Symbol;Acc:MGI:99655]		Q60636	4.6	1.4E-02	8.2	9.5E-05	-0.7	6.0E-01	0.9	1.7E-01
ENSMUST00000039177	dihydropyrimidine dehydrogenase [Source:MGI Symbol;Acc:MGI:2139667]		Q8CHR6	6.3	1.8E-04	6.7	1.0E-04	-1.5	2.2E-01	0.1	8.7E-01
ENSMUST00000039178	tenascin N [Source:MGI Symbol;Acc:MGI:2665790]		Q80Z71	7.4	5.0E-05	5.1	6.4E-05	-3.1	8.1E-03	-0.1	8.3E-01
ENSMUST00000039197	solute carrier family 44, member 3 [Source:MGI Symbol;Acc:MGI:2384860]		Q921V7	7.5	2.3E-05	2.0	2.8E-02	-0.8	2.6E-01	0.0	9.8E-01
ENSMUST00000039205	galactose mutarotase [Source:MGI Symbol;Acc:MGI:2442420]		Q8K157	-2.2	2.4E-03	-5.5	3.6E-04	-0.6	1.6E-01	-0.4	7.1E-01
ENSMUST00000039213	inhibitor of Bruton agammaglobulinemia tyrosine kinase [Source:MGI Symbol;Acc:MGI:1918677]		Q6ZPR6	-4.6	1.7E-03	4.1	3.1E-04	-1.8	4.8E-02	-0.3	5.3E-01
ENSMUST00000039229	CUB domain containing protein 1 [Source:MGI Symbol;Acc:MGI:2442010]		Q5U462	6.5	2.2E-06	-1.6	3.8E-02	0.2	7.1E-01	0.3	6.6E-01
ENSMUST00000039267	chromodomain helicase DNA binding protein 7 [Source:MGI Symbol;Acc:MGI:2444748]		A2AJK6	8.4	9.6E-03	-0.1	9.3E-01	1.2	2.0E-02	0.0	9.8E-01
ENSMUST00000038811	GTPase, IMAP family member 3 [Source:MGI Symbol;Acc:MGI:1932723]		Q99MI6	-1.5	7.3E-02	-2.4	2.5E-02	-1.4	3.8E-02	-0.5	6.0E-01
ENSMUST00000039286	autophagy related 5 [Source:MGI Symbol;Acc:MGI:1277186]		Q99J83	-4.4	4.4E-05	7.8	2.7E-05	-0.6	6.2E-01	-0.6	2.5E-01
ENSMUST00000039303	neuropeptide Y receptor Y1 [Source:MGI Symbol;Acc:MGI:104963]	Q3V1K5	Q04573	8.2	8.0E-06	1.1	2.3E-01	-0.6	4.0E-01	0.9	2.6E-01
ENSMUST00000039305	solute carrier family 36 (proton/amino acid symporter), member 2 [Source:MGI Symbol;Acc:MGI:1891430]		Q8BHK3	5.6	2.8E-04	-2.0	8.2E-02	0.6	4.0E-01	-2.1	9.6E-02
ENSMUST00000039309	secreted and transmembrane 1B [Source:MGI Symbol;Acc:MGI:1929083]	Q9D966		6.6	6.0E-05	5.9	7.7E-02	-0.8	8.1E-01	0.1	9.4E-01
ENSMUST00000038842	protein phosphatase 1, regulatory subunit 32 [Source:MGI Symbol;Acc:MGI:1915002]			2.1	4.0E-02	1.8	1.0E-01	-0.7	4.6E-01	-0.4	6.4E-01
ENSMUST00000039317	transmembrane channel-like gene family 3 [Source:MGI Symbol;Acc:MGI:2669033]	F8VQI4		3.6	7.3E-04	-7.9	8.2E-07	0.0	9.7E-01	-0.9	2.2E-01
ENSMUST00000039323	expressed sequence AA986860 [Source:MGI Symbol;Acc:MGI:2138143]		Q8BI29	3.2	1.9E-03	7.6	4.2E-04	0.0	1.0E+00	-0.5	5.2E-01
ENSMUST00000039327	diacylglycerol lipase, alpha [Source:MGI Symbol;Acc:MGI:2677061]		Q6WQJ1	8.8	6.7E-03	-3.4	1.4E-02	0.5	4.6E-01	-4.5	1.4E-02
ENSMUST00000038863	leucyl-tRNA synthetase, mitochondrial [Source:MGI Symbol;Acc:MGI:2142973]		Q8VDC0	1.2	1.2E-01	1.9	4.5E-02	0.2	7.9E-01	-0.5	5.1E-01
ENSMUST00000039331	immunoglobulin superfamily, member 21 [Source:MGI Symbol;Acc:MGI:2681842]		Q7TNR6	7.4	3.5E-05	-4.2	4.7E-03	0.7	2.1E-01	-0.9	5.0E-01
ENSMUST00000039349	WD repeat domain 60 [Source:MGI Symbol;Acc:MGI:2445085]		Q8C761	3.8	9.9E-05	-5.9	1.5E-02	-0.2	7.8E-01	-0.2	9.3E-01
ENSMUST00000038874	suppressor of cancer cell invasion [Source:MGI Symbol;Acc:MGI:2443716]		Q8C8N2	-0.1	8.1E-01	0.2	8.3E-01	-0.2	7.5E-01	-0.4	5.1E-01
ENSMUST00000039366	otassium voltage-gated channel, subfamily H (eag-related), member 8 [Source:MGI Symbol;Acc:MGI:244516(	F6TUN6		7.6	1.4E-05	-6.0	1.4E-04	-0.1	7.3E-01	0.5	6.2E-01
ENSMUST00000039373	ubiquitin-like modifier activating enzyme 6 [Source:MGI Symbol;Acc:MGI:1913894]		Q8C7R4	-3.6	1.2E-02	1.2	1.3E-01	-5.5	2.7E-04	-0.2	7.7E-01
ENSMUST00000038889	tubulin tyrosine ligase-like family, member 3 [Source:MGI Symbol;Acc:MGI:2141418]	H7BX03		0.8	3.2E-01	3.0	1.4E-02	0.1	9.1E-01	-2.0	3.1E-02
ENSMUST00000039374	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B [Source:MGI Symbol;Acc:MGI:2442593]		Q8BND4	-8.6	4.4E-05	-4.3	7.3E-06	0.2	3.2E-01	-0.1	7.6E-01
ENSMUST00000038893	regulator of chromosome condensation 2 [Source:MGI Symbol;Acc:MGI:1919784]		Q8BK67	-2.7	6.5E-02	-1.2	4.6E-01	0.6	5.7E-01	-0.9	5.8E-01
ENSMUST00000039380	gap junction protein, beta 6 [Source:MGI Symbol;Acc:MGI:107588]	Q3URC5	P70689	6.8	2.1E-04	3.9	1.4E-03	-3.5	1.1E-02	-0.3	6.4E-01
ENSMUST00000038900	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2140945]	F8WHU5		-0.2	8.8E-01	3.0	1.3E-01	1.9	2.4E-01	-1.3	3.6E-01
ENSMUST00000039388	ADP-ribosylation factor-like 4D [Source:MGI Symbol;Acc:MGI:1933155]		Q99PE9	3.0	2.9E-03	4.6	2.6E-03	1.0	3.4E-01	-0.6	4.7E-01
ENSMUST00000039390	kyphoscoliosis peptidase [Source:MGI Symbol;Acc:MGI:96709]	F8VQF8		8.0	5.4E-06	-5.2	6.3E-02	2.0	6.6E-02	-0.1	9.7E-01
ENSMUST00000039412	microcephaly, primary autosomal recessive 1 [Source:MGI Symbol;Acc:MGI:2443308]		Q7TT79	4.7	5.9E-05	5.8	8.0E-04	0.5	6.5E-01	-0.3	7.3E-01
ENSMUST00000038926	bromodomain adjacent to zinc finger domain 1A [Source:MGI Symbol;Acc:MGI:1309478]		O88379	0.8	3.0E-01	1.7	1.1E-01	0.3	6.9E-01	-0.6	5.2E-01
ENSMUST00000039413	phosphodiesterase 4A, cAMP specific [Source:MGI Symbol;Acc:MGI:99558]	B2RTL2	O89084	2.4	5.4E-03	6.4	6.8E-04	-0.7	6.2E-01	0.1	8.7E-01
ENSMUST00000039431	neurotrophic tyrosine kinase, receptor, type 3 [Source:MGI Symbol;Acc:MGI:97385]		Q6VNS1	6.3	8.4E-03	-2.9	2.1E-03	1.1	1.7E-02	-0.2	7.4E-01
ENSMUST00000039442	asparagine-linked glycosylation 14 [Source:MGI Symbol;Acc:MGI:1914039]		Q9D081	-1.8	2.1E-02	2.7	1.5E-02	-2.3	3.8E-02	-0.4	5.8E-01
ENSMUST00000039443	coiled-coil domain containing 50 [Source:MGI Symbol;Acc:MGI:1914751]		Q810U5	6.1	2.7E-04	5.3	2.3E-03	-0.8	5.7E-01	0.0	9.7E-01
ENSMUST00000039447	fibronectin type III domain containing 3C1 [Source:MGI Symbol;Acc:MGI:2685630]		Q6DFV6	5.5	5.4E-04	4.2	6.7E-03	-1.5	2.9E-01	0.5	4.8E-01
ENSMUST00000039449	listerin E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1926163]		Q6A009	-1.6	1.8E-03	6.6	3.8E-04	-1.2	3.8E-01	-1.2	1.1E-01
ENSMUST00000039450	mucolipin 3 [Source:MGI Symbol;Acc:MGI:1890500]	Q3KP78	Q8R4F0	4.1	9.7E-04	-2.7	1.5E-02	0.2	6.7E-01	-0.7	4.7E-01
ENSMUST00000038980	transformation/transcription domain-associated protein [Source:MGI Symbol;Acc:MGI:2153272]	E9PZA7		-2.9	1.6E-01	-2.6	4.4E-01	0.6	7.0E-01	0.3	9.2E-01
ENSMUST00000039007	transformation related protein 53 regulating kinase A [Source:MGI Symbol;Acc:MGI:1918294]	Q5U452		1.5	4.2E-02	2.4	2.2E-02	0.7	3.7E-01	-0.2	8.3E-01
ENSMUST00000039476	Rho guanine nucleotide exchange factor (GEF) 11 [Source:MGI Symbol;Acc:MGI:2441869]	Q68FM7		-5.1	1.5E-03	4.6	2.5E-03	0.1	9.2E-01	1.4	8.6E-02
ENSMUST00000039480	zinc finger SWIM-type containing 4 [Source:MGI Symbol;Acc:MGI:2443726]		Q8C7B8	-2.0	8.8E-03	4.5	1.2E-03	-0.5	6.4E-01	-0.2	7.3E-01
ENSMUST00000039490	tumor necrosis factor (ligand) superfamily, member 9 [Source:MGI Symbol;Acc:MGI:1101058]	Q3U1Z9	P41274	4.6	2.5E-04	-5.2	7.5E-02	0.2	8.5E-01	-0.2	9.3E-01
ENSMUST00000039016	leucine zipper, putative tumor suppressor 2 [Source:MGI Symbol;Acc:MGI:2385095]		Q91YU6	4.2	6.2E-02	7.4	5.6E-03	-0.5	8.3E-01	-3.7	1.7E-02
ENSMUST00000039492	kininogen 1 [Source:MGI Symbol;Acc:MGI:1097705]		O08677	3.9	1.6E-02	2.5	6.8E-03	-0.3	6.8E-01	0.0	9.6E-01
ENSMUST00000039043	CD6 antigen [Source:MGI Symbol;Acc:MGI:103566]		Q61003	3.4	1.3E-01	0.9	7.5E-01	-1.3	5.8E-01	1.1	6.3E-01
ENSMUST00000039500	transmembrane channel-like gene family 1 [Source:MGI Symbol;Acc:MGI:2151016]		Q8R4P5	7.3	1.8E-05	7.7	2.4E-04	-0.7	6.3E-01	-0.5	4.9E-01
ENSMUST00000039048	RIKEN cDNA 1810055G02 gene [Source:MGI Symbol;Acc:MGI:1919306]		Q9D8N1	1.0	2.9E-01	1.2	3.8E-01	1.0	3.5E-01	0.8	5.0E-01
ENSMUST00000039507	osteoclast associated receptor [Source:MGI Symbol;Acc:MGI:2179720]		Q8VBT3	5.9	3.3E-02	6.4	1.4E-02	-0.8	7.4E-01	-1.7	2.2E-01
ENSMUST00000039516	egl-9 family hypoxia-inducible factor 3 [Source:MGI Symbol;Acc:MGI:1932288]			-3.7	3.2E-05	-1.8	9.2E-03	0.6	7.3E-02	0.3	6.1E-01
ENSMUST00000039517	synapse defective 1, Rho GTPase, homolog 2 (C. elegans) [Source:MGI Symbol;Acc:MGI:3036264]	E9PUP1		7.8	7.2E-05	-6.6	8.3E-03	0.5	4.7E-01	0.5	8.2E-01
ENSMUST00000039522	apolipoprotein B receptor [Source:MGI Symbol;Acc:MGI:2176230]		Q8VBT6	-5.4	8.0E-06	7.8	5.2E-05	0.9	4.1E-01	0.2	6.3E-01
ENSMUST00000039071	calcium channel, voltage-dependent, gamma subunit 5 [Source:MGI Symbol;Acc:MGI:2157946]	Q544Q4	Q8VHW4	3.3	2.7E-01	3.6	2.6E-01	-0.3	9.1E-01	-0.7	7.5E-01
ENSMUST00000039535	WD repeat domain 38 [Source:MGI Symbol;Acc:MGI:1923896]		Q9D994	4.5	8.1E-03	8.5	6.7E-05	-0.7	6.4E-01	-0.5	4.0E-01
ENSMUST00000039541	tubulin, gamma complex associated protein 4 [Source:MGI Symbol;Acc:MGI:1196293]	Q543T6	Q9D4F8	-6.1	3.1E-03	5.7	2.0E-03	-2.1	1.9E-01	0.7	4.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000039545	Kruppel-like factor 8 [Source:MGI Symbol;Acc:MGI:2442430]		Q8BLM0	1.8	2.2E-02	4.9	3.5E-02	-0.4	8.4E-01	0.5	7.2E-01
ENSMUST00000039101	RWD domain containing 2B [Source:MGI Symbol;Acc:MGI:1858215]		Q99M03	-0.4	5.0E-01	0.6	4.2E-01	0.4	5.4E-01	-0.7	3.5E-01
ENSMUST00000039110	src homology 2 domain-containing transforming protein C1 [Source:MGI Symbol;Acc:MGI:98296]		P98083	-1.6	3.3E-01	-1.7	4.6E-01	0.7	6.2E-01	0.7	7.4E-01
ENSMUST00000039554	tRNA methyltransferase 6 [Source:MGI Symbol;Acc:MGI:1914176]		Q8CE96	-5.9	8.1E-04	6.6	3.8E-05	-1.1	2.8E-01	0.6	2.3E-01
ENSMUST00000039557	Rho GTPase activating protein 18 [Source:MGI Symbol;Acc:MGI:1921160]		Q8K0Q5	-4.0	7.1E-03	6.1	2.6E-03	-0.7	6.5E-01	-0.2	7.9E-01
ENSMUST00000039127	ubinuclein 2 [Source:MGI Symbol;Acc:MGI:2444236]		Q80WC1	1.9	3.1E-01	0.9	7.0E-01	-1.4	4.4E-01	-0.3	8.7E-01
ENSMUST00000039559	thrombospondin 1 [Source:MGI Symbol;Acc:MGI:98737]	Q80YQ1		3.4	1.2E-03	-0.2	7.7E-01	0.5	4.1E-01	-1.8	4.1E-02
ENSMUST00000039577	zinc finger protein 51 [Source:MGI Symbol;Acc:MGI:99198]	Q3U4L8		-2.2	6.6E-03	-0.8	2.1E-01	1.2	1.7E-02	-0.1	8.8E-01
ENSMUST00000039581	transmembrane protein 106A [Source:MGI Symbol;Acc:MGI:1922056]		Q8VC04	-4.4	1.2E-02	7.1	3.2E-03	-0.7	7.3E-01	-2.8	3.7E-02
ENSMUST00000039601	small nuclear ribonucleoprotein 25 (U11/U12) [Source:MGI Symbol;Acc:MGI:1925622]		Q8VIK1	-5.0	9.9E-04	8.0	1.2E-04	-0.7	6.3E-01	-0.2	7.5E-01
ENSMUST00000039605	family with sequence similarity 50, member B [Source:MGI Symbol;Acc:MGI:1351640]		Q9WTJ8	7.3	6.0E-05	-1.2	5.4E-02	0.8	5.0E-02	0.0	9.8E-01
ENSMUST00000039608	dymeclin [Source:MGI Symbol;Acc:MGI:1918480]		Q8CHY3	-3.1	3.8E-04	-1.7	1.8E-01	1.5	8.0E-02	-1.3	3.4E-01
ENSMUST00000039156	phosphohistidine phosphatase 1 [Source:MGI Symbol;Acc:MGI:1922704]		Q9DAK9	0.3	7.3E-01	-3.7	1.6E-02	-1.4	7.3E-02	2.6	6.3E-02
ENSMUST00000039610	xylulokinase homolog (H. influenzae) [Source:MGI Symbol;Acc:MGI:2142985]		Q3TNA1	5.0	4.6E-05	7.0	4.0E-05	-0.6	5.7E-01	-0.1	8.1E-01
ENSMUST00000039620	carbonyl reductase 3 [Source:MGI Symbol;Acc:MGI:1309992]		Q8K354	-4.1	1.8E-05	-3.2	1.3E-02	-1.7	3.9E-02	-1.6	1.9E-01
ENSMUST00000039627	benzodiazepine receptor associated protein 1 [Source:MGI Symbol;Acc:MGI:2450877]		Q7TNF8	5.1	4.7E-05	9.4	9.0E-06	0.4	6.9E-01	-0.9	7.0E-02
ENSMUST00000039165	golgi autoantigen, golgin subfamily a, 1 [Source:MGI Symbol;Acc:MGI:1924149]		Q9CW79	-1.9	2.0E-01	-0.2	9.0E-01	-0.8	4.9E-01	-2.5	1.3E-01
ENSMUST00000039171	chemokine (C-C motif) receptor 3 [Source:MGI Symbol;Acc:MGI:104616]		P51678	-0.3	7.4E-01	-1.1	3.2E-01	-0.6	4.3E-01	0.1	8.9E-01
ENSMUST00000039630	receptor tyrosine kinase-like orphan receptor 1 [Source:MGI Symbol;Acc:MGI:1347520]		Q9Z139	8.6	4.1E-06	2.8	1.2E-01	-2.2	2.0E-01	-0.4	7.8E-01
ENSMUST00000039631	actin, alpha 2, smooth muscle, aorta [Source:MGI Symbol;Acc:MGI:87909]		P62737	-1.9	1.3E-02	3.4	5.7E-03	-2.6	3.6E-02	0.3	6.5E-01
ENSMUST00000039652	insulin I [Source:MGI Symbol;Acc:MGI:96572]	Q545I7	P01325	6.1	1.8E-04	8.2	4.1E-05	-0.7	5.9E-01	-1.5	3.1E-02
ENSMUST00000039191	RIKEN cDNA 1810011H11 gene [Source:MGI Symbol;Acc:MGI:1916319]	E9PVZ2		-0.4	4.8E-01	-0.7	3.1E-01	-0.6	2.2E-01	-0.3	6.4E-01
ENSMUST00000039662	talin 2 [Source:MGI Symbol;Acc:MGI:1917799]	E9PUM4		3.9	3.0E-02	5.2	7.7E-05	-2.8	1.3E-02	-0.5	3.3E-01
ENSMUST00000039665	trophinin associated protein [Source:MGI Symbol;Acc:MGI:1925983]		B7ZNG4	2.0	9.8E-03	-1.6	3.3E-02	0.1	8.6E-01	-0.5	4.7E-01
ENSMUST00000039212	solute carrier family 4, sodium bicarbonate cotransporter, member 5 [Source:MGI Symbol;Acc:MGI:2443220]	D3YVG0		3.4	2.6E-01	5.3	1.2E-01	-0.4	9.0E-01	-2.3	2.9E-01
ENSMUST00000039672	major facilitator superfamily domain containing 9 [Source:MGI Symbol;Acc:MGI:2443548]		Q8C0T7	-3.6	2.4E-02	-2.0	1.9E-01	2.8	1.0E-02	0.2	9.0E-01
ENSMUST00000039694	STARD3 N-terminal like [Source:MGI Symbol;Acc:MGI:1923455]		Q9DCI3	-3.3	8.1E-05	3.7	2.9E-04	-2.6	2.8E-03	0.3	5.1E-01
ENSMUST00000039247	desmocollin 2 [Source:MGI Symbol;Acc:MGI:103221]	Q544V1	P55292	3.8	7.2E-02	6.1	1.1E-02	-0.5	8.2E-01	-2.9	5.1E-02
ENSMUST00000039259	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2 [Source:MGI Symbol;Acc:MGI:3580016]		Q3UHD9	-0.6	3.0E-01	0.5	5.1E-01	1.1	6.8E-02	0.0	9.7E-01
ENSMUST00000039695	Fras1 related extracellular matrix protein 3 [Source:MGI Symbol;Acc:MGI:2685641]	F8WHZ0		8.8	5.3E-06	6.1	8.3E-02	-0.5	8.6E-01	1.7	4.7E-01
ENSMUST00000039271	RIKEN cDNA 2610008E11 gene [Source:MGI Symbol;Acc:MGI:1919378]	G3X964		0.3	6.4E-01	0.8	2.2E-01	-0.1	8.0E-01	-0.7	2.7E-01
ENSMUST00000039280	SR-related CTD-associated factor 4 [Source:MGI Symbol;Acc:MGI:2146350]	Q6PFF0		0.6	1.2E-01	0.6	2.9E-01	0.8	7.0E-02	0.8	1.1E-01
ENSMUST00000039725	exonuclease 1 [Source:MGI Symbol;Acc:MGI:1349427]		Q9QZ11	5.7	3.7E-06	-4.6	1.9E-04	-0.4	3.2E-01	-0.2	7.9E-01
ENSMUST00000039726	RIKEN cDNA 3110052M02 gene [Source:MGI Symbol;Acc:MGI:1920479]	E9PUT0		-2.4	1.5E-02	6.2	1.1E-04	-1.5	1.7E-01	0.6	3.5E-01
ENSMUST00000039733	oxysterol binding protein-like 11 [Source:MGI Symbol;Acc:MGI:2146553]	G5E8A0		-2.7	9.3E-05	5.4	3.0E-04	-1.6	1.4E-01	-1.4	4.6E-02
ENSMUST00000039734	unkempt-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1921404]		Q5FWH2	-4.7	1.7E-04	7.0	1.2E-04	0.0	9.9E-01	-0.4	5.6E-01
ENSMUST00000039742	hydroxylysine kinase 1 [Source:MGI Symbol;Acc:MGI:2443139]		Q5U5V2	6.2	5.2E-06	3.7	1.8E-03	-0.1	8.9E-01	-0.2	7.5E-01
ENSMUST00000039318	CDC14 cell division cycle 14B [Source:MGI Symbol;Acc:MGI:2441808]		Q6PFY9	1.5	5.7E-01	4.1	1.3E-01	-1.3	6.1E-01	-3.9	9.7E-02
ENSMUST00000039750	leucine-rich repeat LGI family, member 2 [Source:MGI Symbol;Acc:MGI:2180196]		Q8K4Z0	6.7	1.6E-04	3.3	6.2E-03	0.3	6.8E-01	0.3	7.3E-01
ENSMUST00000039752	olute carrier family 16 (monocarboxylic acid transporters), member 8 [Source:MGI Symbol;Acc:MGI:1929519	Q5UB50	O35308	7.5	2.6E-04	6.7	1.3E-02	-5.1	8.7E-02	-3.0	6.0E-02
ENSMUST00000039758	cytochrome c oxidase subunit VIIIa [Source:MGI Symbol;Acc:MGI:105959]		Q64445	-5.8	7.0E-07	7.3	7.7E-05	-0.6	6.1E-01	-0.4	4.7E-01
ENSMUST00000039333	pyruvate dehydrogenase phosphatase regulatory subunit [Source:MGI Symbol;Acc:MGI:2442188]		Q7TSQ8	-0.9	4.9E-02	0.1	8.3E-01	1.1	2.3E-02	0.0	9.8E-01
ENSMUST00000039769	syntrophin, basic 1 [Source:MGI Symbol;Acc:MGI:101781]		Q99L88	4.5	1.9E-04	1.2	8.2E-02	-2.2	3.0E-03	0.4	4.9E-01
ENSMUST00000039775	leucine-rich repeat LGI family, member 4 [Source:MGI Symbol;Acc:MGI:2180197]		Q8K1S1	6.0	2.0E-04	7.5	3.4E-05	-0.5	6.1E-01	-0.4	4.4E-01
ENSMUST00000039784	acetyl-Coenzyme A acyltransferase 1A [Source:MGI Symbol;Acc:MGI:2148491]		Q921H8	-5.9	1.8E-04	-4.2	1.1E-02	-0.3	6.4E-01	0.3	8.4E-01
ENSMUST00000039788	CD276 antigen [Source:MGI Symbol;Acc:MGI:2183926]	A6MDC5	Q8VE98	2.9	5.4E-03	-6.1	2.8E-03	1.8	7.1E-03	-0.8	6.4E-01
ENSMUST00000039798	Bardet-Biedl syndrome 9 (human) [Source:MGI Symbol;Acc:MGI:2442833]		Q811G0	5.2	4.9E-03	6.1	8.0E-04	-0.7	6.2E-01	0.0	9.6E-01
ENSMUST00000039803	ubiquitin associated domain containing 2 [Source:MGI Symbol;Acc:MGI:1916139]		Q8R1K1	-3.0	9.3E-04	3.0	7.1E-03	-0.4	6.6E-01	-0.3	6.6E-01
ENSMUST00000039818	aldehyde dehydrogenase 4 family, member A1 [Source:MGI Symbol;Acc:MGI:2443883]		Q8CHT0	-3.2	3.4E-03	8.9	1.3E-05	0.5	6.7E-01	-0.4	3.8E-01
ENSMUST00000039861	CD33 antigen [Source:MGI Symbol;Acc:MGI:99440]		Q63994	-5.9	1.7E-06	3.9	1.2E-03	0.3	7.4E-01	1.0	1.2E-01
ENSMUST00000039894	tubulin-specific chaperone E [Source:MGI Symbol;Acc:MGI:1917680]		Q8CIV8	-5.6	2.0E-02	2.0	3.3E-02	-0.3	6.6E-01	0.1	9.1E-01
ENSMUST00000039419	immunoglobulin superfamily, member 10 [Source:MGI Symbol;Acc:MGI:1923481]		Q3V1M1	3.6	6.2E-02	3.6	1.7E-01	0.9	7.0E-01	0.9	5.9E-01
ENSMUST00000039900	prolyl-tRNA synthetase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915189]		Q9D820	-2.3	1.3E-03	5.6	2.2E-02	-0.8	7.4E-01	-0.1	9.3E-01
ENSMUST00000039925	ureidopropionase, beta [Source:MGI Symbol;Acc:MGI:2143535]	Q3UEK4	Q8VC97	6.4	7.6E-07	-2.0	2.7E-02	-1.0	1.0E-01	-0.8	3.3E-01
ENSMUST00000039926	dual specificity phosphatase 8 [Source:MGI Symbol;Acc:MGI:106626]		O09112	7.5	7.0E-05	3.4	3.8E-03	-3.0	1.6E-02	-0.3	6.7E-01
ENSMUST00000039928	in homology domain containing, family H (with MyTH4 domain) member 1 [Source:MGI Symbol;Acc:MGI:2		Q80TI1	9.5	1.4E-06	5.2	6.4E-04	-1.6	1.8E-01	-1.3	7.8E-02
ENSMUST00000039949	essential meiotic endonuclease 1 homolog 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:3576783]		Q8BJW7	2.3	4.4E-03	-1.5	1.5E-02	0.5	1.3E-01	0.4	4.0E-01
ENSMUST00000039956	solute carrier family 41, member 2 [Source:MGI Symbol;Acc:MGI:2442940]	B2RQZ3	Q8BYR8	6.4	3.2E-04	4.4	1.6E-03	-0.3	7.2E-01	-0.7	3.9E-01
ENSMUST00000039961	RIKEN cDNA 6820408C15 gene [Source:MGI Symbol;Acc:MGI:3045333]	Q8BJX2		5.8	2.2E-02	0.0	9.8E-01	0.5	4.5E-01	-4.6	4.5E-03
ENSMUST00000039987	thymocyte selection-associated high mobility group box [Source:MGI Symbol;Acc:MGI:2181659]		Q66JW3	4.8	4.1E-04	-1.3	1.4E-01	0.9	1.2E-01	0.2	8.5E-01
ENSMUST00000039484	zinc finger CCCH type containing 12D [Source:MGI Symbol;Acc:MGI:3045313]	E9QNR7		-0.7	1.5E-01	0.3	6.4E-01	1.4	1.7E-02	0.4	5.4E-01
ENSMUST00000039487	general transcription factor IIH, polypeptide 5 [Source:MGI Symbol;Acc:MGI:107227]		Q8K2X8	-0.9	1.2E-01	-2.0	1.3E-02	-0.8	7.9E-02	0.3	6.4E-01
ENSMUST00000039990	prolyl 3-hydroxylase 2 [Source:MGI Symbol;Acc:MGI:2146663]		Q8CG71	8.6	2.9E-04	3.6	3.5E-03	-0.9	3.0E-01	0.0	9.7E-01
ENSMUST00000039991	solute carrier family 12 (potassium/chloride transporters), member 9 [Source:MGI Symbol;Acc:MGI:1933532]		Q99MR3	-2.4	5.9E-03	-0.3	8.2E-01	-5.1	4.1E-03	-0.9	4.0E-01
ENSMUST00000040001	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 [Source:MGI Symbol;Acc:MGI:	G3X942		7.1	7.0E-05	5.5	9.0E-05	-2.1	4.8E-02	-0.3	5.2E-01
ENSMUST00000039506	immunoglobulin superfamily, member 8 [Source:MGI Symbol;Acc:MGI:2154090]			-4.1	3.2E-01	-5.5	2.9E-01	-1.1	6.4E-01	0.2	9.7E-01
ENSMUST00000040005	alkB, alkylation repair homolog 3 (E. coli) [Source:MGI Symbol;Acc:MGI:1916363]		Q8K1E6	-5.7	4.3E-05	4.2	1.6E-01	-0.8	7.8E-01	0.9	6.5E-01
ENSMUST00000040008	ubiquitin-conjugating enzyme E2R 2 [Source:MGI Symbol;Acc:MGI:1914865]		Q6ZWZ2	-3.3	6.5E-04	-2.9	1.0E-03	0.8	4.4E-02	-0.1	9.3E-01
ENSMUST00000040017	missing oocyte, meiosis regulator, homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2182066]		Q8VE19	-1.7	2.4E-02	5.6	2.6E-04	-2.8	4.2E-02	-0.5	4.5E-01
ENSMUST00000040019	SRY (sex determining region Y)-box 10 [Source:MGI Symbol;Acc:MGI:98358]		Q04888	7.9	1.6E-05	-3.6	4.4E-04	0.7	9.1E-02	-1.1	1.4E-01
ENSMUST00000040025	talin 2 [Source:MGI Symbol;Acc:MGI:1917799]	E9PUM4		5.5	1.9E-06	4.3	9.7E-03	-1.4	3.0E-01	-1.3	2.4E-01
ENSMUST00000039540	membrane-associated ring finger (C3HC4) 1 [Source:MGI Symbol;Acc:MGI:1920175]		Q6NZQ8	-0.5	7.1E-01	-4.4	5.5E-02	-1.1	3.4E-01	2.7	2.1E-01
ENSMUST00000040056	PTPRF interacting protein, binding protein 2 (liprin beta 2) [Source:MGI Symbol;Acc:MGI:894649]	G3X957		2.9	8.4E-03	-1.3	3.5E-01	1.5	1.3E-01	-3.3	7.5E-02
ENSMUST00000040059	hyaluronoglucosaminidase 3 [Source:MGI Symbol;Acc:MGI:1330288]		Q8VEI3	7.0	1.5E-06	3.3	3.5E-03	1.0	2.3E-01	-0.6	4.0E-01
ENSMUST00000039551	polymerase (RNA) III (DNA directed) polypeptide K [Source:MGI Symbol;Acc:MGI:1914255]		Q9CQZ7	0.3	3.5E-01	0.1	7.9E-01	-0.8	3.9E-02	-0.5	1.9E-01
ENSMUST00000040065	toll-like receptor 13 [Source:MGI Symbol;Acc:MGI:3045213]		Q6R5N8	-6.7	1.5E-06	-4.4	6.6E-03	-0.3	6.8E-01	-1.8	2.5E-01
ENSMUST00000040069	collectin sub-family member 12 [Source:MGI Symbol;Acc:MGI:2152907]		Q8K4Q8	2.8	1.0E-03	-5.0	1.1E-02	-1.3	1.3E-01	-0.3	8.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000040077	polymerase (RNA) II (DNA directed) polypeptide F [Source:MGI Symbol;Acc:MGI:1349393]		P61219	-2.9	1.3E-03	-1.9	3.3E-02	-5.1	2.6E-05	0.1	8.6E-01
ENSMUST00000039562	tripartite motif-containing 13 [Source:MGI Symbol;Acc:MGI:1913847]		Q9CYB0	-1.5	5.0E-01	-0.8	6.5E-01	-2.1	2.0E-01	-2.8	2.2E-01
ENSMUST00000039564	lipid phosphate phosphatase-related protein type 5 [Source:MGI Symbol;Acc:MGI:1923019]		Q8BJ52	5.2	3.6E-02	5.0	6.2E-02	-0.7	8.0E-01	-0.5	7.7E-01
ENSMUST00000039568	protocadherin 8 [Source:MGI Symbol;Acc:MGI:1306800]		Q7TSK3	3.7	7.2E-02	1.5	5.4E-01	-0.5	8.3E-01	1.8	3.7E-01
ENSMUST00000039571	RIKEN cDNA 2410004B18 gene [Source:MGI Symbol;Acc:MGI:1913671]		Q9CWU4	-1.0	4.0E-01	-4.1	2.8E-02	-1.6	1.1E-01	1.4	3.9E-01
ENSMUST00000040090	nucleotide binding protein-like [Source:MGI Symbol;Acc:MGI:1924076]		Q9CWD8	-1.9	1.5E-02	-1.1	2.0E-01	0.5	3.3E-01	-0.6	4.3E-01
ENSMUST00000040097	palmdelphin [Source:MGI Symbol;Acc:MGI:2148896]			3.9	3.2E-03	-4.9	6.3E-02	0.4	6.5E-01	0.9	7.1E-01
ENSMUST00000040104	heart and neural crest derivatives expressed transcript 2 [Source:MGI Symbol;Acc:MGI:103580]		Q61039	7.3	4.1E-05	-5.5	3.0E-03	-0.5	3.7E-01	0.0	9.8E-01
ENSMUST00000040106	family with sequence similarity 151, member B [Source:MGI Symbol;Acc:MGI:1921192]	D3YUE4		-1.5	2.3E-02	7.4	9.5E-05	-0.6	6.5E-01	-0.7	2.8E-01
ENSMUST00000040110	carbohydrate sulfotransferase 11 [Source:MGI Symbol;Acc:MGI:1927166]	B9EHC3	Q9JME2	-2.6	1.3E-03	-1.3	1.1E-01	1.4	9.8E-03	-0.5	5.4E-01
ENSMUST00000040112	iron/zinc purple acid phospatase-like [Source:MGI Symbol;Acc:MGI:2142121]	B2RRA7		7.6	2.1E-05	5.1	1.6E-04	-0.2	8.3E-01	-0.3	6.0E-01
ENSMUST00000040128	ATPase, class I, type 8B, member 4 [Source:MGI Symbol;Acc:MGI:1859664]	A2ANX3		-2.2	1.5E-02	-3.4	3.5E-04	0.6	1.1E-01	0.0	9.4E-01
ENSMUST00000040134	Norrie disease (pseudoglioma) (human) [Source:MGI Symbol;Acc:MGI:102570]		P48744	9.6	2.1E-06	5.6	3.4E-04	0.7	4.7E-01	0.2	6.7E-01
ENSMUST00000040147	BEN domain containing 3 [Source:MGI Symbol;Acc:MGI:2677212]		Q6PAL0	4.9	2.8E-05	5.7	1.8E-05	-2.8	9.6E-03	0.0	9.4E-01
ENSMUST00000040149	ATPase, class I, type 8B, member 4 [Source:MGI Symbol;Acc:MGI:1859664]	A2ANX3		-4.3	3.4E-02	-0.9	2.9E-01	0.4	4.2E-01	-0.6	4.3E-01
ENSMUST00000040153	RAR-related orphan receptor beta [Source:MGI Symbol;Acc:MGI:1343464]		Q8R1B8	6.4	8.0E-05	6.3	2.7E-04	-0.5	6.6E-01	-0.7	2.9E-01
ENSMUST00000039659	carbonyl reductase 1 [Source:MGI Symbol;Acc:MGI:88284]	B2RXY7	P48758	1.0	1.3E-01	0.3	7.1E-01	-1.0	1.1E-01	-0.3	7.1E-01
ENSMUST00000040154	cytochrome c oxidase subunit VIa polypeptide 1 [Source:MGI Symbol;Acc:MGI:103099]	Q9DCW5		-5.6	9.4E-06	2.6	2.3E-01	-0.6	7.4E-01	0.6	6.7E-01
ENSMUST00000040159	ynthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 [Source:MGI Symbol;Acc:MGI:21		Q9JJ06	-4.0	2.3E-05	2.5	9.9E-03	0.2	8.0E-01	-0.3	6.1E-01
ENSMUST00000039666	pleckstrin homology domain containing, family S member 1 [Source:MGI Symbol;Acc:MGI:2443041]		Q8BW88	1.3	3.5E-01	2.5	1.5E-01	0.3	8.5E-01	-0.8	5.4E-01
ENSMUST00000040161	G protein-coupled receptor 33 [Source:MGI Symbol;Acc:MGI:1277106]	D8VER2	O88416	6.5	3.8E-04	-2.2	2.1E-01	0.7	4.5E-01	-0.6	7.4E-01
ENSMUST00000039674	Pbx/knotted 1 homeobox 2 [Source:MGI Symbol;Acc:MGI:2445415]		Q8BG99	-3.7	8.8E-02	1.0	6.5E-01	2.1	2.5E-01	-2.5	2.4E-01
ENSMUST00000039680	poly (ADP-ribose) polymerase family, member 11 [Source:MGI Symbol;Acc:MGI:2141505]		Q8CFF0	-2.4	3.8E-02	-4.1	2.7E-02	-0.4	5.6E-01	1.2	4.6E-01
ENSMUST00000040162	growth differentiation factor 5 [Source:MGI Symbol;Acc:MGI:95688]		P43027	7.5	4.2E-05	-3.1	6.2E-04	0.2	5.6E-01	0.0	9.4E-01
ENSMUST00000040166	sushi domain containing 1 [Source:MGI Symbol;Acc:MGI:3651543]	E9Q3H4		-3.3	3.0E-02	8.9	1.3E-05	-0.1	9.0E-01	-0.2	6.1E-01
ENSMUST00000039720	Ras-related GTP binding B [Source:MGI Symbol;Acc:MGI:3038613]		Q6NTA4	1.5	4.0E-01	3.5	4.5E-02	-0.5	7.6E-01	-2.5	9.6E-02
ENSMUST00000039721	solute carrier family 17 (sodium phosphate), member 3 [Source:MGI Symbol;Acc:MGI:2389216]	G5E894		4.7	1.3E-01	4.8	1.7E-01	-0.3	9.4E-01	-0.3	8.7E-01
ENSMUST00000040167	methionine adenosyltransferase II, beta [Source:MGI Symbol;Acc:MGI:1913667]		Q99LB6	-7.6	4.6E-04	6.5	1.2E-05	0.8	2.8E-01	0.0	9.3E-01
ENSMUST00000040177	Znrd1 antisense [Source:MGI Symbol;Acc:MGI:1923666]			3.6	3.3E-02	-0.2	8.8E-01	1.4	9.5E-02	-0.8	4.2E-01
ENSMUST00000039729	LYR motif containing 5 [Source:MGI Symbol;Acc:MGI:1914886]		Q91V16	1.1	5.7E-01	-0.4	8.6E-01	-1.6	3.9E-01	-0.1	9.6E-01
ENSMUST00000040184	transient receptor potential cation channel, subfamily C, member 5 [Source:MGI Symbol;Acc:MGI:109524]	Q2KHN9	Q9QX29	8.0	6.4E-05	-2.6	7.7E-04	0.3	3.5E-01	0.2	7.2E-01
ENSMUST00000040202	ataxin 2-like [Source:MGI Symbol;Acc:MGI:2446242]		Q7TQH0	-4.8	1.5E-03	-4.3	2.4E-03	0.5	3.3E-01	0.0	1.0E+00
ENSMUST00000040210	transient receptor potential cation channel, subfamily M, member 8 [Source:MGI Symbol;Acc:MGI:2181435]		Q8R4D5	7.7	3.2E-05	5.4	7.1E-05	-1.0	2.1E-01	-0.1	7.8E-01
ENSMUST00000040217	TBC1 domain family, member 21 [Source:MGI Symbol;Acc:MGI:1921536]	Q9D9D3		6.5	1.3E-04	5.4	6.4E-04	-1.8	1.5E-01	-0.6	4.1E-01
ENSMUST00000040218	F-box protein 8 [Source:MGI Symbol;Acc:MGI:1354696]		Q9QZN3	-3.6	3.3E-03	7.5	8.0E-04	0.2	8.9E-01	0.2	7.8E-01
ENSMUST00000040219	l(3)mbt-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2143628]		Q8BLB7	-6.0	1.8E-02	-4.5	2.3E-05	0.3	3.3E-01	-1.0	1.1E-01
ENSMUST00000039763	glycoprotein integral membrane 1 [Source:MGI Symbol;Acc:MGI:2384905]		Q91WR6	-4.0	6.8E-02	-4.1	1.6E-01	0.0	9.8E-01	0.1	9.6E-01
ENSMUST00000040222	ciliary rootlet coiled-coil, rootletin [Source:MGI Symbol;Acc:MGI:3529431]		Q8CJ40	5.4	1.8E-02	3.3	4.7E-03	-0.6	4.7E-01	0.6	4.1E-01
ENSMUST00000040227	claudin domain containing 2 [Source:MGI Symbol;Acc:MGI:1921526]	A1A539	Q9D9H2	3.9	8.9E-03	8.4	4.0E-04	1.9	2.2E-01	-0.4	5.4E-01
ENSMUST00000039782	chromodomain helicase DNA binding protein 6 [Source:MGI Symbol;Acc:MGI:1918639]		A3KFM7	0.8	8.0E-02	1.1	8.4E-02	0.0	9.3E-01	-0.3	6.1E-01
ENSMUST00000040234	tRNA splicing endonuclease 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2141599]		Q6P7W5	3.3	3.3E-02	-3.8	1.3E-02	1.4	4.0E-02	-0.6	6.5E-01
ENSMUST00000040241	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b [Source:MGI Symbol;Acc:MGI:2148251]	Q8R3C7		1.9	4.7E-03	2.3	2.6E-02	-0.9	2.5E-01	-0.4	5.8E-01
ENSMUST00000039796	guanylyl cyclase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916028]		Q8BZI6	-1.2	3.0E-01	-0.2	8.6E-01	-0.2	8.3E-01	-1.1	3.9E-01
ENSMUST00000040248	scaffolding protein involved in DNA repair [Source:MGI Symbol;Acc:MGI:1924834]		Q8BGX7	-3.3	1.8E-04	4.3	4.4E-02	-0.2	9.3E-01	0.8	5.8E-01
ENSMUST00000040254	enhancer of mRNA decapping 4 [Source:MGI Symbol;Acc:MGI:2446249]	G5E896		-1.4	2.4E-02	-2.2	2.4E-02	1.0	6.9E-02	0.1	8.9E-01
ENSMUST00000039810	exportin, tRNA (nuclear export receptor for tRNAs) [Source:MGI Symbol;Acc:MGI:1920442]		Q9CRT8	0.6	2.3E-01	1.5	4.9E-02	0.4	4.7E-01	-0.5	4.4E-01
ENSMUST00000039812	zinc finger, MYM-type 5 [Source:MGI Symbol;Acc:MGI:3041170]		Q3U2E2	1.6	6.7E-01	0.8	8.5E-01	-1.4	7.1E-01	-0.5	8.9E-01
ENSMUST00000040260	ferric-chelate reductase 1 [Source:MGI Symbol;Acc:MGI:108076]	A0A0G2JFP4		-1.2	2.7E-02	-1.0	3.6E-01	1.1	1.4E-01	-1.2	2.8E-01
ENSMUST00000039827	AF4/FMR2 family, member 3 [Source:MGI Symbol;Acc:MGI:106927]	F8WJA7		5.5	3.8E-02	0.0	1.0E+00	-1.1	6.9E-01	4.4	1.6E-01
ENSMUST00000039840	ectonucleotide pyrophosphatase/phosphodiesterase 6 [Source:MGI Symbol;Acc:MGI:2445171]		Q8BGN3	5.1	4.3E-02	6.2	4.3E-02	0.2	9.5E-01	-0.9	5.9E-01
ENSMUST00000039855	golgi autoantigen, golgin subfamily b, macrogolgin 1 [Source:MGI Symbol;Acc:MGI:1099447]	E9PVZ8		-2.6	6.1E-02	-0.7	5.6E-01	-0.4	6.4E-01	-2.3	1.2E-01
ENSMUST00000040270	ARP1 actin-related protein 1A, centractin alpha [Source:MGI Symbol;Acc:MGI:1858964]		P61164	-4.2	9.6E-06	-5.2	3.4E-05	0.2	4.4E-01	-0.5	4.6E-01
ENSMUST00000039867	zinc finger and BTB domain containing 41 homolog [Source:MGI Symbol;Acc:MGI:2444487]		Q811F1	-0.4	2.7E-01	-0.4	3.9E-01	0.0	9.7E-01	0.0	9.7E-01
ENSMUST00000039881	elongation factor Tu GTP binding domain containing 1 [Source:MGI Symbol;Acc:MGI:2141969]		Q8C0D5	1.7	3.9E-01	-0.9	6.7E-01	-2.2	2.2E-01	0.4	8.5E-01
ENSMUST00000039882	ectonucleotide pyrophosphatase/phosphodiesterase 1 [Source:MGI Symbol;Acc:MGI:97370]	E9QQ26		1.2	4.0E-01	-0.8	5.4E-01	-3.4	1.8E-02	-1.4	2.9E-01
ENSMUST00000039892	TBC1 domain family, member 25 [Source:MGI Symbol;Acc:MGI:2444862]		A1A5B6	2.4	2.0E-01	6.2	3.9E-02	2.1	4.3E-01	-1.6	2.9E-01
ENSMUST00000040275	sine oculis-binding protein homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1924427]		Q0P5V2	9.7	1.5E-05	-4.5	5.9E-02	-0.4	7.3E-01	-1.5	5.5E-01
ENSMUST00000040280	e carrier family 25 (mitochondrial carrier; phosphate carrier), member 23 [Source:MGI Symbol;Acc:MGI:1914		Q6GQS1	3.3	1.1E-03	-2.0	1.2E-02	-0.1	7.4E-01	-0.5	4.6E-01
ENSMUST00000039913	Trp53 induced glycolysis repulatory phosphatase [Source:MGI Symbol;Acc:MGI:2442752]	B2RWB7	Q8BZA9	0.8	9.5E-02	1.4	4.0E-02	0.4	4.5E-01	-0.2	6.9E-01
ENSMUST00000039922	suppressor of fused homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1345643]		Q9Z0P7	0.3	5.9E-01	0.9	2.1E-01	0.7	2.0E-01	0.1	9.0E-01
ENSMUST00000040284	cDNA sequence BC031181 [Source:MGI Symbol;Acc:MGI:3039614]		Q91WE4	-5.3	4.3E-06	5.9	3.5E-06	-0.7	2.5E-01	-0.1	7.2E-01
ENSMUST00000040298	cellular repressor of E1A-stimulated genes 1 [Source:MGI Symbol;Acc:MGI:1344382]	K4DI63		-7.0	1.5E-04	5.5	7.6E-04	-1.5	2.1E-01	0.4	5.6E-01
ENSMUST00000040307	membrane-associated ring finger (C3HC4) 9 [Source:MGI Symbol;Acc:MGI:2446144]		Q3TZ87	3.8	2.2E-03	8.3	3.0E-06	-1.6	1.1E-01	-0.5	2.5E-01
ENSMUST00000039939				-2.7	4.2E-02	-0.8	6.0E-01	0.7	4.5E-01	-1.2	4.2E-01
ENSMUST00000040311	thrombospondin, type I, domain containing 7B [Source:MGI Symbol;Acc:MGI:2443925]	Q8BHP3		6.5	6.8E-05	1.6	4.0E-02	-0.9	1.9E-01	-0.2	7.2E-01
ENSMUST00000040314	RNA binding motif protein 17 [Source:MGI Symbol;Acc:MGI:1924188]		Q8JZX4	-4.1	3.9E-05	3.3	1.8E-02	-2.3	8.6E-02	0.8	3.7E-01
ENSMUST00000040321	tRNA methyltransferase 10A [Source:MGI Symbol;Acc:MGI:1920421]			2.8	2.0E-03	5.6	3.4E-02	-1.5	5.5E-01	-1.3	3.6E-01
ENSMUST00000040324	protein phosphatase 1, regulatory subunit 26 [Source:MGI Symbol;Acc:MGI:2685193]		Q6A025	7.9	3.4E-05	3.4	9.8E-03	-1.0	3.2E-01	0.3	6.9E-01
ENSMUST00000040325	mediator complex subunit 12-like [Source:MGI Symbol;Acc:MGI:2139916]		Q8BQM9	-7.8	4.9E-06	5.9	2.0E-03	-1.9	2.6E-01	0.8	3.6E-01
ENSMUST00000040340	FCH domain only 2 [Source:MGI Symbol;Acc:MGI:3505790]		Q3UQN2	-5.3	5.8E-07	-1.7	8.5E-02	0.9	1.2E-01	0.3	7.6E-01
ENSMUST00000040344	glucosamine (N-acetyl)-6-sulfatase [Source:MGI Symbol;Acc:MGI:1922862]		Q8BFR4	-3.6	2.8E-05	6.6	2.4E-04	-0.5	6.7E-01	0.0	9.9E-01
ENSMUST00000040357	RCSD domain containing 1 [Source:MGI Symbol;Acc:MGI:2676394]		Q3UZA1	-9.8	1.4E-05	-5.4	3.3E-04	-0.5	2.0E-01	-0.8	4.6E-01
ENSMUST00000040359	arylsulfatase i [Source:MGI Symbol;Acc:MGI:2670959]		Q32KI9	7.4	2.6E-05	-1.9	4.0E-02	1.0	7.0E-02	-0.4	6.2E-01
ENSMUST00000040010	RNA binding motif protein 3 [Source:MGI Symbol;Acc:MGI:1099460]	Q8BG13		0.1	9.3E-01	3.6	4.7E-02	1.3	3.7E-01	-2.2	9.5E-02
ENSMUST00000040361	ATPase, H+ transporting, lysosomal V0 subunit E2 [Source:MGI Symbol;Acc:MGI:1923502]		Q91XE7	2.7	6.5E-03	-0.3	6.7E-01	1.0	1.1E-01	-0.4	6.5E-01
ENSMUST00000040372	transmembrane protein 258 [Source:MGI Symbol;Acc:MGI:1916288]	Q60FD1	P61166	-7.6	4.2E-05	8.5	2.8E-05	0.0	9.8E-01	-0.6	2.6E-01
ENSMUST00000040021	protein tyrosine phosphatase, non-receptor type 23 [Source:MGI Symbol;Acc:MGI:2144837]		Q6PB44	0.0	9.8E-01	0.9	3.2E-01	0.8	2.5E-01	-0.1	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000040023	intermediate filament family orphan 2 [Source:MGI Symbol;Acc:MGI:2140675]	B1AZL1		3.6	1.0E-01	1.3	6.6E-01	0.7	7.5E-01	3.0	2.4E-01
ENSMUST00000040374	RIKEN cDNA A930018P22 gene [Source:MGI Symbol;Acc:MGI:1915493]		Q9D1Z2	5.6	5.1E-04	5.2	8.0E-06	-0.5	3.9E-01	-0.2	6.7E-01
ENSMUST00000040043	large tumor suppressor [Source:MGI Symbol;Acc:MGI:1333883]		Q8BYR2	0.2	9.3E-01	1.8	5.5E-01	0.9	6.5E-01	-0.7	8.1E-01
ENSMUST00000040381	nuclear receptor coactivator 5 [Source:MGI Symbol;Acc:MGI:2385165]		Q91W39	-3.5	1.6E-02	2.4	3.2E-02	-1.1	2.4E-01	-0.6	4.8E-01
ENSMUST00000040402	protein phosphatase 1, regulatory (inhibitor) subunit 11 [Source:MGI Symbol;Acc:MGI:1923747]	A5A4Y9		-3.5	3.1E-04	6.1	2.4E-05	-0.3	6.9E-01	0.6	2.1E-01
ENSMUST00000040404	lymphocyte antigen 6 complex, locus D [Source:MGI Symbol;Acc:MGI:96881]		P35459	5.0	2.7E-03	-7.0	1.4E-05	-0.1	7.8E-01	0.2	8.1E-01
ENSMUST00000040411	RAB42, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2441753]	Q0PD08		6.6	7.4E-05	2.1	9.9E-03	-1.0	1.3E-01	-0.3	6.1E-01
ENSMUST00000040416	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a [Source:MGI Symbol;Acc:MGI:99526]		Q61655	-2.6	2.1E-03	-3.1	2.8E-03	-0.9	6.0E-02	-0.8	3.6E-01
ENSMUST00000040089	ring finger protein 43 [Source:MGI Symbol;Acc:MGI:2442609]	A3KMI3	Q5NCP0	3.9	1.1E-01	0.8	7.3E-01	-1.1	6.5E-01	2.0	3.6E-01
ENSMUST00000040418	chondroadherin [Source:MGI Symbol;Acc:MGI:1096866]	Q3TYW1	O55226	7.5	4.3E-05	-0.8	3.8E-01	1.2	6.4E-02	0.1	9.3E-01
ENSMUST00000040428	ribonuclease, RNase K [Source:MGI Symbol;Acc:MGI:106369]		Q8K3C0	-5.7	5.5E-04	2.1	8.0E-02	-1.5	1.6E-01	0.3	7.5E-01
ENSMUST00000040434	tubulin-specific chaperone C [Source:MGI Symbol;Acc:MGI:1919976]			-1.9	8.9E-03	5.6	3.2E-04	-1.4	2.1E-01	0.2	7.2E-01
ENSMUST00000040105	perm antigen with calponin homology and coiled-coil domains 1-like [Source:MGI Symbol;Acc:MGI:1921642			0.3	5.4E-01	1.2	4.3E-02	0.3	4.6E-01	-0.7	1.9E-01
ENSMUST00000040440	calmodulin 2 [Source:MGI Symbol;Acc:MGI:103250]		P62204	-8.0	1.2E-05	-0.8	2.5E-01	-0.8	1.2E-01	-1.5	4.3E-02
ENSMUST00000040442	aldehyde oxidase 4 [Source:MGI Symbol;Acc:MGI:1919122]		Q3TYQ9	7.4	5.1E-05	-1.5	6.6E-02	1.1	3.6E-02	0.0	9.6E-01
ENSMUST00000040111	tetratricopeptide repeat domain 28 [Source:MGI Symbol;Acc:MGI:2140873]	A0A0A0MQN9		2.8	4.4E-02	7.5	1.0E-04	-0.5	6.8E-01	-5.2	1.9E-04
ENSMUST00000040445	THAP domain containing 11 [Source:MGI Symbol;Acc:MGI:1930964]		Q9JJD0	-3.4	2.6E-04	7.0	8.4E-05	-0.5	6.5E-01	0.1	8.8E-01
ENSMUST00000040117	SECIS binding protein 2 [Source:MGI Symbol;Acc:MGI:1922670]	Q3U1C4		-0.8	2.4E-01	-1.1	2.3E-01	0.4	5.1E-01	0.7	4.2E-01
ENSMUST00000040448	myotubularin related protein 3 [Source:MGI Symbol;Acc:MGI:1921552]	B1ATD5		-5.3	2.0E-03	-2.3	5.7E-02	0.7	2.9E-01	0.8	4.5E-01
ENSMUST00000040131	E74-like factor 1 [Source:MGI Symbol;Acc:MGI:107180]	Q3V1H4	Q60775	-0.8	4.6E-01	0.8	5.4E-01	-0.3	7.4E-01	-2.0	1.4E-01
ENSMUST00000040454	Bardet-Biedl syndrome 10 (human) [Source:MGI Symbol;Acc:MGI:1919019]		Q9DBI2	2.3	4.4E-03	7.4	1.0E-05	-2.2	5.0E-02	0.0	9.2E-01
ENSMUST00000040135	nucleoporin 43 [Source:MGI Symbol;Acc:MGI:1917162]		P59235	-1.3	9.3E-02	-3.2	3.8E-03	-1.9	9.5E-03	0.1	9.4E-01
ENSMUST00000040455	hypoxia-inducible factor 1, alpha subunit inhibitor [Source:MGI Symbol;Acc:MGI:2442345]		Q8BLR9	-1.9	3.2E-03	4.7	8.2E-05	-0.5	4.3E-01	-0.4	4.4E-01
ENSMUST00000040148	Bardet-Biedl syndrome 7 (human) [Source:MGI Symbol;Acc:MGI:1918742]		Q8K2G4	2.8	2.1E-01	1.4	6.4E-01	-1.0	6.9E-01	0.4	8.5E-01
ENSMUST00000040461	major facilitator superfamily domain containing 7C [Source:MGI Symbol;Acc:MGI:2384974]			8.5	6.9E-06	-3.8	9.5E-02	-0.4	7.1E-01	-0.8	7.4E-01
ENSMUST00000040465	chloride channel accessory 2 [Source:MGI Symbol;Acc:MGI:2139758]		Q8BG22	6.7	6.1E-05	7.3	2.7E-04	0.3	8.0E-01	-0.6	4.1E-01
ENSMUST00000040467	predicted gene 8909 [Source:MGI Symbol;Acc:MGI:3704134]	A7VMS6		6.5	3.9E-03	-8.4	2.1E-04	0.7	8.6E-02	3.5	3.2E-02
ENSMUST00000040468	primase and polymerase (DNA-directed) [Source:MGI Symbol;Acc:MGI:3603756]		Q6P1E7	-3.5	1.4E-03	-2.7	2.5E-03	1.2	1.1E-02	-0.1	8.5E-01
ENSMUST00000040489	transient receptor potential cation channel, subfamily M, member 6 [Source:MGI Symbol;Acc:MGI:2675603]		Q8CIR4	4.4	1.6E-04	4.3	5.2E-03	-2.0	1.6E-01	0.2	7.9E-01
ENSMUST00000040496	bone morphogenetic protein 8a [Source:MGI Symbol;Acc:MGI:104515]	Q80VZ0	P34821	5.4	1.0E-05	7.2	1.1E-04	-0.6	6.3E-01	-0.3	5.9E-01
ENSMUST00000040498	ring finger protein 39 [Source:MGI Symbol;Acc:MGI:2156378]	A2RT81		6.1	2.6E-04	-0.7	6.9E-01	1.4	2.1E-01	-1.3	4.6E-01
ENSMUST00000040500	diacylglycerol kinase, beta [Source:MGI Symbol;Acc:MGI:2442474]		Q6NS52	6.9	1.2E-04	-4.6	7.7E-03	0.8	2.2E-01	-2.2	2.2E-01
ENSMUST00000040506	family with sequence similarity 13, member B [Source:MGI Symbol;Acc:MGI:2447834]		Q8K2H3	-3.8	2.1E-04	-0.6	7.4E-01	-2.5	1.0E-01	1.7	3.0E-01
ENSMUST00000040179	tubulin tyrosine ligase-like family, member 5 [Source:MGI Symbol;Acc:MGI:2443657]		Q8CHB8	-1.1	3.7E-01	2.7	5.8E-02	0.6	5.8E-01	-3.1	2.4E-02
ENSMUST00000040182	coiled coil domain containing 88A [Source:MGI Symbol;Acc:MGI:1925177]		Q5SNZ0	0.2	6.8E-01	0.1	9.0E-01	-0.5	2.8E-01	-0.3	5.2E-01
ENSMUST00000040518	eukaryotic translation initiation factor 3, subunit L [Source:MGI Symbol;Acc:MGI:2386251]		Q8QZY1	-4.1	2.6E-05	8.0	1.3E-04	-0.6	6.5E-01	-0.6	3.9E-01
ENSMUST00000040188	spindle and kinetochore associated complex subunit 1 [Source:MGI Symbol;Acc:MGI:1913718]			-0.9	5.4E-01	1.0	5.7E-01	1.3	3.5E-01	-0.6	7.1E-01
ENSMUST00000040523	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2 [Source:MGI Symbol;Acc:M		Q8C9W3	4.7	1.3E-05	-2.2	1.0E-01	0.6	3.8E-01	-2.0	1.6E-01
ENSMUST00000040531	p21 protein (Cdc42/Rac)-activated kinase 4 [Source:MGI Symbol;Acc:MGI:1917834]	G5E8A7		-1.8	1.1E-02	8.0	4.8E-05	-0.6	6.5E-01	-0.9	1.5E-01
ENSMUST00000040213	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2141161]		Q8BJM7	-0.3	6.1E-01	0.2	8.0E-01	0.1	8.4E-01	-0.3	6.0E-01
ENSMUST00000040532	small integral membrane protein 14 [Source:MGI Symbol;Acc:MGI:1915802]	F8WHW8		-7.3	1.6E-05	6.6	2.2E-04	-0.5	6.6E-01	-0.7	3.1E-01
ENSMUST00000040536	basic leucine zipper transcription factor, ATF-like [Source:MGI Symbol;Acc:MGI:1859147]		O35284	-4.5	6.0E-05	-1.2	2.6E-01	-0.1	8.6E-01	-2.6	3.7E-02
ENSMUST00000040555	ring finger protein 10 [Source:MGI Symbol;Acc:MGI:1859162]	H7BX06		-7.0	1.1E-03	0.8	7.5E-01	3.7	1.1E-01	-3.1	2.2E-01
ENSMUST00000040561	RUN domain containing 1 [Source:MGI Symbol;Acc:MGI:2144506]		Q0VDN7	-1.3	1.3E-02	4.7	3.5E-02	-2.0	3.8E-01	-1.3	3.2E-01
ENSMUST00000040576	prostate androgen-regulated mucin-like protein 1 [Source:MGI Symbol;Acc:MGI:2443349]		Q923D3	9.1	5.6E-06	5.9	3.2E-03	1.1	4.7E-01	-0.9	3.0E-01
ENSMUST00000040580	synapse defective 1, Rho GTPase, homolog 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1918959]	G3X960		8.6	6.4E-05	2.9	6.0E-02	-2.0	1.5E-01	-1.6	1.9E-01
ENSMUST00000040594	ER membrane associated RNA degradation [Source:MGI Symbol;Acc:MGI:1917317]	Q3TVE4		2.7	2.9E-02	1.9	2.3E-02	0.2	6.9E-01	0.3	6.4E-01
ENSMUST00000040603	amylo-1,6-glucosidase, 4-alpha-glucanotransferase [Source:MGI Symbol;Acc:MGI:1924809]	F8VPN4		2.6	3.9E-04	-2.9	1.8E-03	-0.1	8.5E-01	-0.5	5.2E-01
ENSMUST00000040250	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) [Source:MGI Symbol;Acc:MGI:2138151]		Q91WN4	-0.3	8.4E-01	-3.0	1.7E-01	-1.8	1.4E-01	0.9	6.6E-01
ENSMUST00000040607	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914928]		P62311	-4.1	1.1E-04	-1.0	2.1E-01	0.5	2.6E-01	0.1	9.1E-01
ENSMUST00000040616	potassium channel tetramerisation domain containing 7 [Source:MGI Symbol;Acc:MGI:2442265]		Q8BJK1	1.1	2.8E-02	-0.1	8.8E-01	0.8	7.6E-02	-0.3	6.3E-01
ENSMUST00000040261	MACRO domain containing 1 [Source:MGI Symbol;Acc:MGI:2147583]		Q922B1	1.3	6.4E-02	2.8	4.5E-03	0.4	5.5E-01	-1.1	1.1E-01
ENSMUST00000040622	purinergic receptor P2Y, G-protein coupled 13 [Source:MGI Symbol;Acc:MGI:1921441]		Q9D8I2	-5.8	2.1E-05	-3.0	6.6E-04	0.7	4.0E-02	-0.5	4.6E-01
ENSMUST00000040271	centrosomal protein 85 [Source:MGI Symbol;Acc:MGI:1917262]		Q8BMK0	3.5	1.8E-01	3.7	1.5E-01	-4.0	1.5E-01	-4.2	5.1E-02
ENSMUST00000040636	secretory blood group 1 [Source:MGI Symbol;Acc:MGI:1928893]	Q8CDC9		8.7	6.7E-06	8.0	6.5E-05	-1.0	4.4E-01	0.7	2.7E-01
ENSMUST00000040647	fibroblast growth factor 1 [Source:MGI Symbol;Acc:MGI:95515]	Q6ZWS1	P61148	6.4	2.2E-04	3.2	5.4E-03	0.3	7.5E-01	0.3	6.7E-01
ENSMUST00000040655	histocompatibility 2, class II antigen A, alpha [Source:MGI Symbol;Acc:MGI:95895]		P14434	-6.2	1.7E-03	-5.0	3.7E-05	-0.3	3.3E-01	-0.6	3.9E-01
ENSMUST00000040667	zinc finger protein 300 [Source:MGI Symbol;Acc:MGI:3045326]	A2AE21		8.5	7.9E-08	-5.0	4.8E-03	0.7	2.1E-01	-1.4	3.9E-01
ENSMUST00000040668	oxysterol binding protein-like 2 [Source:MGI Symbol;Acc:MGI:2442832]		Q8BX94	-5.8	1.1E-06	3.8	5.5E-03	0.1	9.4E-01	0.0	9.5E-01
ENSMUST00000040676	ankyrin repeat domain 54 [Source:MGI Symbol;Acc:MGI:2444209]	A7YB12	Q91WK7	-3.0	1.0E-02	5.7	3.3E-04	-0.5	6.4E-01	0.3	6.7E-01
ENSMUST00000040312	tribbles homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1345675]		Q8K4K2	0.5	4.1E-01	3.1	2.0E-03	1.1	1.1E-01	-1.5	2.8E-02
ENSMUST00000040313	BCDIN3 domain containing [Source:MGI Symbol;Acc:MGI:1922534]		Q91YP1	-0.5	4.0E-01	0.5	4.8E-01	1.1	6.5E-02	0.1	8.3E-01
ENSMUST00000040677	endonuclease/exonuclease/phosphatase family domain containing 1 [Source:MGI Symbol;Acc:MGI:1914734]		Q3TGW2	-2.0	9.0E-04	-2.2	7.4E-03	0.6	1.6E-01	-1.4	7.3E-02
ENSMUST00000040320	bule associated monooxygenase, calponin and LIM domain containing -like 1 [Source:MGI Symbol;Acc:MGI:		Q8BGT6	-0.1	8.2E-01	0.3	6.8E-01	0.5	2.4E-01	0.2	7.4E-01
ENSMUST00000040687	Tax1 (human T cell leukemia virus type I) binding protein 3 [Source:MGI Symbol;Acc:MGI:1923531]		Q9DBG9	-3.3	2.0E-03	-1.7	1.7E-01	-0.2	7.8E-01	4.3	2.7E-03
ENSMUST00000040689	autophagy related 9A [Source:MGI Symbol;Acc:MGI:2138446]	Q3ZAQ4		-8.6	1.0E-05	6.4	8.9E-05	-1.9	1.1E-01	-0.5	4.3E-01
ENSMUST00000040695	somatomedin B and thrombospondin, type 1 domain containing [Source:MGI Symbol;Acc:MGI:2684952]		Q3UPR9	4.3	1.1E-04	-7.1	8.5E-05	0.8	3.4E-02	0.2	8.7E-01
ENSMUST00000040330	centrosomal protein 44 [Source:MGI Symbol;Acc:MGI:3525111]		Q5HZK1	-3.4	7.5E-02	-4.3	8.0E-02	-0.8	4.8E-01	0.1	9.7E-01
ENSMUST00000040336	solute carrier family 22, member 23 [Source:MGI Symbol;Acc:MGI:1920352]		Q3UHH2	3.5	8.3E-02	1.4	3.0E-01	-4.5	2.1E-02	-2.4	9.2E-02
ENSMUST00000040700	dedicator of cytokinesis 9 [Source:MGI Symbol;Acc:MGI:106321]	F8VPN7		-1.5	5.5E-03	-4.4	1.5E-05	0.1	6.4E-01	-0.8	1.6E-01
ENSMUST00000040703	myosin XVB [Source:MGI Symbol;Acc:MGI:2685534]	F6V1P1		5.8	1.9E-02	-2.0	4.3E-03	0.7	7.0E-02	-0.9	1.2E-01
ENSMUST00000040715	musculoskeletal, embryonic nuclear protein 1 [Source:MGI Symbol;Acc:MGI:1913425]		Q99JI1	-4.2	4.1E-04	-9.5	3.1E-04	1.0	5.9E-02	0.7	6.8E-01
ENSMUST00000040718	osteopetrosis associated transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:2655574]		Q8BGT0	-4.3	1.6E-05	6.8	1.5E-04	-0.7	5.4E-01	-0.1	8.7E-01
ENSMUST00000040729	chloride channel, voltage-sensitive 7 [Source:MGI Symbol;Acc:MGI:1347048]	Q6RUT9	O70496	-6.1	1.3E-03	2.3	3.2E-02	0.0	9.8E-01	0.3	6.6E-01
ENSMUST00000040368	regulator of microtubule dynamics 2 [Source:MGI Symbol;Acc:MGI:2147043]		Q8BSE0	1.3	6.5E-02	2.2	1.4E-02	0.2	8.2E-01	-0.8	2.3E-01
ENSMUST00000040735	amidohydrolase domain containing 2 [Source:MGI Symbol;Acc:MGI:2443978]		Q8JZV7	-3.7	2.1E-03	-8.0	1.8E-04	-1.2	2.0E-02	-0.8	5.8E-01
ENSMUST00000040750	leukemia inhibitory factor [Source:MGI Symbol;Acc:MGI:96787]	F8WH42		5.0	1.6E-03	5.9	7.0E-04	-0.5	7.1E-01	-0.8	2.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000040380	phosphatidylinositol transfer protein, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:1919045]	A0A0A0MQ88		-2.5	1.3E-01	1.1	5.7E-01	2.3	1.7E-01	-1.4	4.4E-01
ENSMUST00000040751	potassium voltage-gated channel, shaker-related, subfamily, member 6 [Source:MGI Symbol;Acc:MGI:96663]		Q61923	7.3	3.9E-04	-4.1	9.2E-02	1.8	9.6E-02	2.3	3.1E-01
ENSMUST00000040383	coiled-coil and C2 domain containing 1A [Source:MGI Symbol;Acc:MGI:2384831]		Q8K1A6	-2.7	5.1E-02	-1.0	5.5E-01	1.1	3.2E-01	-0.7	6.5E-01
ENSMUST00000040766	transmembrane emp24-like trafficking protein 10 (yeast) [Source:MGI Symbol;Acc:MGI:1915831]		Q9D1D4	-4.4	5.7E-06	-2.8	4.4E-03	-0.1	8.5E-01	-0.7	3.6E-01
ENSMUST00000040772	fermitin family homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2147790]	Q3TEE6	Q8K1B8	-5.3	1.0E-05	1.5	1.6E-01	-4.5	4.3E-03	-0.9	3.1E-01
ENSMUST00000040783	ubiquitin specific peptidase 40 [Source:MGI Symbol;Acc:MGI:2443184]		Q8BWR4	-4.4	1.4E-02	6.2	2.2E-04	-0.6	6.1E-01	-0.2	7.8E-01
ENSMUST00000040787	ankyrin repeat domain 13c [Source:MGI Symbol;Acc:MGI:2139746]		Q3UX43	-3.1	1.1E-03	-0.9	2.2E-01	0.7	1.6E-01	-0.9	2.4E-01
ENSMUST00000040789	glutaminyl-peptide cyclotransferase (glutaminyl cyclase) [Source:MGI Symbol;Acc:MGI:1917786]			4.0	2.3E-04	6.2	1.5E-04	-2.1	9.0E-02	-0.8	2.2E-01
ENSMUST00000040421	coenzyme Q5 homolog, methyltransferase (yeast) [Source:MGI Symbol;Acc:MGI:1098643]		Q9CXI0	-0.1	9.3E-01	-0.6	4.4E-01	-0.2	7.6E-01	0.4	6.1E-01
ENSMUST00000040423	CD59a antigen [Source:MGI Symbol;Acc:MGI:109177]	A2BI31	O55186	4.2	5.5E-02	2.8	1.5E-01	-3.2	1.2E-01	-1.8	2.7E-01
ENSMUST00000040791	NIPA-like domain containing 2 [Source:MGI Symbol;Acc:MGI:1924488]			6.9	1.6E-04	-4.6	1.1E-02	1.2	1.1E-01	0.1	9.7E-01
ENSMUST00000040429	ubiquitin specific petidase 45 [Source:MGI Symbol;Acc:MGI:101850]		Q8K387	-3.2	2.9E-01	-3.4	3.3E-01	-1.3	4.6E-01	-1.1	7.7E-01
ENSMUST00000040430	vesicle amine transport protein 1 homolog (T californica) [Source:MGI Symbol;Acc:MGI:1349450]	Q499X4	Q62465	-1.4	9.4E-02	-1.7	9.0E-02	-0.7	2.4E-01	-0.4	6.7E-01
ENSMUST00000040802	zinc finger protein 957 [Source:MGI Symbol;Acc:MGI:2145729]	Q3UT76		6.5	1.4E-04	-1.2	1.4E-01	0.7	1.7E-01	-0.1	9.5E-01
ENSMUST00000040821	hairy/enhancer-of-split related with YRPW motif-like [Source:MGI Symbol;Acc:MGI:1860511]		Q9DBX7	6.5	5.9E-06	-8.6	3.3E-04	0.1	7.8E-01	0.8	6.2E-01
ENSMUST00000040824	dolichyl-phosphate mannosyltransferase polypeptide 3 [Source:MGI Symbol;Acc:MGI:1915813]		Q9D1Q4	-5.6	9.8E-04	6.6	1.5E-04	-1.3	2.9E-01	-0.5	4.2E-01
ENSMUST00000040826	succinate dehydrogenase complex assembly factor 3 [Source:MGI Symbol;Acc:MGI:1913288]	Q0VF92	Q8BQU3	3.8	2.0E-03	-2.9	4.2E-03	0.9	4.7E-02	0.5	5.7E-01
ENSMUST00000040833	ER degradation enhancer, mannosidase alpha-like 2 [Source:MGI Symbol;Acc:MGI:1915540]	Q8BJT9		-4.7	6.4E-05	-6.9	2.7E-02	0.9	2.6E-01	2.5	3.6E-01
ENSMUST00000040844	ankyrin repeat domain 27 (VPS9 domain) [Source:MGI Symbol;Acc:MGI:2444103]		Q3UMR0	-2.4	2.4E-02	2.9	2.9E-03	0.0	9.4E-01	-0.6	3.0E-01
ENSMUST00000040853	oxidative-stress responsive 1 [Source:MGI Symbol;Acc:MGI:1917378]		Q6P9R2	-3.2	2.7E-04	-0.5	4.5E-01	1.3	1.3E-02	-0.1	9.0E-01
ENSMUST00000040865	transmembrane protein 98 [Source:MGI Symbol;Acc:MGI:1923457]		Q91X86	4.0	1.2E-03	7.1	3.1E-05	-1.4	1.9E-01	-0.1	8.8E-01
ENSMUST00000040873	serrate RNA effector molecule homolog (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1933527]		Q99MR6	-2.0	9.7E-03	5.8	2.3E-04	-1.3	2.6E-01	-0.4	5.3E-01
ENSMUST00000040876	adenylate kinase 7 [Source:MGI Symbol;Acc:MGI:1926051]	F8WIC0		4.4	1.5E-03	3.3	1.2E-01	-0.4	8.4E-01	2.7	5.6E-02
ENSMUST00000040880	MAP6 domain containing 1 [Source:MGI Symbol;Acc:MGI:3607784]		Q14BB9	4.4	1.3E-04	-2.1	5.3E-02	0.6	2.9E-01	-0.8	4.4E-01
ENSMUST00000040474	TBC1 domain family, member 24 [Source:MGI Symbol;Acc:MGI:2443456]		Q3UUG6	1.8	4.7E-01	4.3	3.1E-01	4.1	2.0E-01	1.6	6.4E-01
ENSMUST00000040481	solute carrier family 38, member 7 [Source:MGI Symbol;Acc:MGI:2679005]		Q8BWH0	-1.2	5.5E-02	0.0	9.7E-01	0.9	9.3E-02	-0.3	7.2E-01
ENSMUST00000040484	glycine cleavage system protein H (aminomethyl carrier) [Source:MGI Symbol;Acc:MGI:1915383]		Q91WK5	0.6	2.9E-01	0.9	1.4E-01	-0.6	1.9E-01	-1.0	9.3E-02
ENSMUST00000040881	clusterin associated protein 1 [Source:MGI Symbol;Acc:MGI:1924029]		Q8R3P7	-2.4	1.1E-03	6.8	7.4E-04	-0.7	6.5E-01	0.3	6.9E-01
ENSMUST00000040487	radical S-adenosyl methionine domain containing 1 [Source:MGI Symbol;Acc:MGI:3039628]		Q5SUV1	4.2	8.3E-02	7.1	1.7E-02	-0.1	9.6E-01	-3.0	1.1E-01
ENSMUST00000040907	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal [Source:MGI Symbol;Acc:MGI:1347059]	Q3UVJ7	Q9WV68	5.2	8.3E-06	2.9	3.6E-03	-1.9	3.0E-02	-0.3	5.8E-01
ENSMUST00000040914	histone cluster 1, H1c [Source:MGI Symbol;Acc:MGI:1931526]	Q5SZA3	P15864	-4.3	4.8E-04	6.3	4.1E-05	0.8	3.3E-01	-0.1	8.8E-01
ENSMUST00000040915	peptidyl-prolyl isomerase G (cyclophilin G) [Source:MGI Symbol;Acc:MGI:2445173]		A2AR02	-3.1	3.3E-02	6.8	2.2E-04	-0.5	7.0E-01	-1.2	8.4E-02
ENSMUST00000040917	ribosomal protein S27-like [Source:MGI Symbol;Acc:MGI:1915191]		Q6ZWY3	-6.8	8.3E-05	6.6	3.2E-04	-0.5	6.7E-01	-0.2	7.2E-01
ENSMUST00000040924	synovial sarcoma translocation, Chromosome 18 [Source:MGI Symbol;Acc:MGI:107708]		Q62280	-4.5	1.3E-02	-2.5	1.1E-02	0.8	9.3E-02	-0.4	5.9E-01
ENSMUST00000040514	insulin receptor substrate 2 [Source:MGI Symbol;Acc:MGI:109334]		P81122	0.2	6.6E-01	0.5	3.5E-01	0.6	1.9E-01	0.2	6.6E-01
ENSMUST00000040941	endogenous retroviral sequence 3 [Source:MGI Symbol;Acc:MGI:1919245]	Q9DAX3		7.2	5.0E-05	-5.0	4.5E-05	-0.8	3.5E-02	0.1	8.7E-01
ENSMUST00000040519	apoptogenic, mitochondrial 1 [Source:MGI Symbol;Acc:MGI:1915270]		Q9CQW7	-0.2	7.6E-01	0.4	5.2E-01	-0.4	4.4E-01	-0.9	1.4E-01
ENSMUST00000040944	cytochrome P450, family 2, subfamily g, polypeptide 1 [Source:MGI Symbol;Acc:MGI:109612]	Q9WV19		6.8	4.3E-05	5.0	3.2E-05	-0.1	8.6E-01	-0.4	3.9E-01
ENSMUST00000040960	solute carrier family 6 (neurotransmitter transporter), member 20A [Source:MGI Symbol;Acc:MGI:2143217]		Q8VDB9	7.7	2.7E-05	-0.4	5.5E-01	0.9	9.4E-02	-0.5	5.2E-01
ENSMUST00000040967	vacuolar protein sorting 37B (yeast) [Source:MGI Symbol;Acc:MGI:1916724]		Q8R0J7	-2.7	2.0E-03	-7.1	1.3E-04	-0.5	2.2E-01	-0.7	5.8E-01
ENSMUST00000040971	calpain 5 [Source:MGI Symbol;Acc:MGI:1100859]	Q3TPL4	O08688	4.3	8.6E-05	-4.4	3.3E-04	-0.4	3.0E-01	-0.5	5.4E-01
ENSMUST00000040548	myelin-associated glycoprotein [Source:MGI Symbol;Acc:MGI:96912]		P20917	-0.9	4.4E-01	-2.6	2.7E-01	1.0	4.1E-01	2.7	2.3E-01
ENSMUST00000040986	RIKEN cDNA 1700021K19 gene [Source:MGI Symbol;Acc:MGI:1915160]		Q80U62	-4.4	3.0E-02	-6.9	1.5E-03	0.8	2.5E-01	0.6	7.4E-01
ENSMUST00000040987	aldo-keto reductase family 1, member D1 [Source:MGI Symbol;Acc:MGI:2384785]		Q8VCX1	4.3	2.3E-04	0.0	9.7E-01	0.7	9.3E-02	-0.6	2.6E-01
ENSMUST00000040572	zinc finger CCCH type containing 10 [Source:MGI Symbol;Acc:MGI:2143670]		Q8R205	-0.9	1.3E-01	0.1	8.6E-01	0.9	9.4E-02	-0.1	9.3E-01
ENSMUST00000040990	von Willebrand factor A domain containing 8 [Source:MGI Symbol;Acc:MGI:1919008]		Q8CC88	1.2	1.4E-02	8.2	2.3E-05	-0.4	7.2E-01	0.5	3.7E-01
ENSMUST00000040992	NIMA (never in mitosis gene a)-related expressed kinase 9 [Source:MGI Symbol;Acc:MGI:2387995]		Q8K1R7	-3.1	1.6E-04	4.2	2.4E-03	-4.0	9.4E-03	0.5	5.4E-01
ENSMUST00000040583	HEAT repeat containing 5A [Source:MGI Symbol;Acc:MGI:2444133]		Q5PRF0	0.0	9.8E-01	0.0	9.4E-01	0.6	9.6E-02	0.5	2.1E-01
ENSMUST00000041005	FXYD domain-containing ion transport regulator 2 [Source:MGI Symbol;Acc:MGI:1195260]	Q6ITT1	Q04646	7.5	2.0E-05	2.8	7.6E-02	-0.3	8.0E-01	-0.4	6.8E-01
ENSMUST00000040599	neuron navigator 1 [Source:MGI Symbol;Acc:MGI:2183683]		Q8CH77	3.3	8.8E-02	1.8	3.7E-01	-1.4	4.1E-01	0.0	9.9E-01
ENSMUST00000041007	gap junction protein, delta 4 [Source:MGI Symbol;Acc:MGI:2444990]		Q8BSD4	7.6	2.2E-05	3.1	5.2E-04	0.2	7.7E-01	-0.3	4.7E-01
ENSMUST00000041010	coiled-coil domain containing 9 [Source:MGI Symbol;Acc:MGI:1921443]	G3X927		-2.6	4.3E-03	-5.0	2.0E-04	-0.6	1.6E-01	0.2	8.0E-01
ENSMUST00000041012	pre T cell antigen receptor alpha [Source:MGI Symbol;Acc:MGI:104857]			4.8	1.8E-04	2.3	4.6E-03	1.4	1.7E-02	0.2	6.4E-01
ENSMUST00000041029	SMAD family member 6 [Source:MGI Symbol;Acc:MGI:1336883]		O35182	4.3	2.3E-04	-4.9	2.4E-04	-0.4	3.7E-01	-1.3	1.9E-01
ENSMUST00000040624	GLTSCR1-like [Source:MGI Symbol;Acc:MGI:2673855]	B2RX81	Q8CHH5	-0.7	1.1E-01	0.5	3.5E-01	0.9	3.4E-02	-0.2	6.2E-01
ENSMUST00000040628	zinc finger protein 182 [Source:MGI Symbol;Acc:MGI:2442220]	A2AE18		-2.1	7.1E-02	-3.0	8.6E-02	-0.1	8.8E-01	0.8	6.1E-01
ENSMUST00000041045	H2A histone family, member Z [Source:MGI Symbol;Acc:MGI:1888388]		P0C0S6	-6.2	1.8E-02	6.6	4.5E-05	-2.2	5.7E-02	-0.1	8.9E-01
ENSMUST00000041047	leucyl/cystinyl aminopeptidase [Source:MGI Symbol;Acc:MGI:2387123]		Q8C129	-3.5	7.0E-06	3.1	5.1E-03	-3.4	8.8E-03	-0.1	8.8E-01
ENSMUST00000041048	ORAI calcium release-activated calcium modulator 2 [Source:MGI Symbol;Acc:MGI:2443195]	Q14BR6	Q8BH10	-2.8	2.6E-04	5.2	3.6E-03	-0.6	6.8E-01	0.4	6.1E-01
ENSMUST00000041053	oenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Source:MGI Symbol;Acc:MGI:1		Q8BWT1	-3.5	2.0E-05	-5.7	4.8E-04	-3.0	5.2E-04	-3.5	4.2E-02
ENSMUST00000040656	hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen) [Source:MGI Symbol;Acc:MGI:1		Q8R164	-0.4	5.6E-01	-1.2	1.9E-01	0.1	9.3E-01	0.9	3.1E-01
ENSMUST00000041055	autophagy related 2B [Source:MGI Symbol;Acc:MGI:1923809]		Q80XK6	1.4	6.2E-03	8.1	2.7E-07	-0.5	4.1E-01	-0.1	6.9E-01
ENSMUST00000041059	receptor potential cation channel, subfamily C, member 4 associated protein [Source:MGI Symbol;Acc:MGI:1	Q3TDP6	Q9JLV2	-7.2	4.8E-05	-4.7	4.1E-05	0.8	1.7E-02	-0.4	6.0E-01
ENSMUST00000041065	myosin ID [Source:MGI Symbol;Acc:MGI:107728]		Q5SYD0	-1.6	1.5E-02	-4.0	5.4E-02	1.2	1.7E-01	2.2	2.5E-01
ENSMUST00000041080	frizzled homolog 8 (Drosophila) [Source:MGI Symbol;Acc:MGI:108460]		Q61091	6.3	3.4E-05	-0.9	1.3E-01	0.8	3.7E-02	-0.4	5.1E-01
ENSMUST00000041093	cAMP responsive element binding protein 3-like 2 [Source:MGI Symbol;Acc:MGI:2442695]		Q8BH52	2.8	1.3E-04	-4.7	4.4E-03	0.7	2.7E-01	2.1	1.2E-01
ENSMUST00000041095	amine oxidase, copper containing 2 (retina-specific) [Source:MGI Symbol;Acc:MGI:2668431]		Q812C9	1.7	1.4E-02	-6.1	8.4E-04	1.8	2.0E-03	-0.7	6.2E-01
ENSMUST00000041096	proprotein convertase subtilisin/kexin type 1 inhibitor [Source:MGI Symbol;Acc:MGI:1353431]		Q9QXV0	5.7	1.1E-03	5.5	2.7E-04	1.1	2.2E-01	0.0	9.9E-01
ENSMUST00000041099	neurogenic differentiation 1 [Source:MGI Symbol;Acc:MGI:1339708]		Q60867	7.1	1.7E-04	-0.5	4.4E-01	0.8	6.7E-02	-0.3	5.5E-01
ENSMUST00000041100	alkB, alkylation repair homolog 4 (E. coli) [Source:MGI Symbol;Acc:MGI:1919291]		Q9D8F1	-5.5	1.3E-03	5.9	1.8E-02	-1.3	5.7E-01	-1.5	2.9E-01
ENSMUST00000040706	consortin, connexin sorting protein [Source:MGI Symbol;Acc:MGI:2445141]		Q8CBC4	-0.9	9.2E-02	-0.2	7.3E-01	0.6	2.2E-01	-0.1	8.5E-01
ENSMUST00000041110	tetratricopeptide repeat domain 7 [Source:MGI Symbol;Acc:MGI:1920999]		Q8BGB2	-9.9	2.8E-04	-2.7	1.8E-02	0.7	2.3E-01	-0.9	3.9E-01
ENSMUST00000040717	kinesin family member 15 [Source:MGI Symbol;Acc:MGI:1098258]		Q6P9L6	0.5	2.9E-01	0.6	4.0E-01	0.6	2.0E-01	0.6	3.5E-01
ENSMUST00000041111	split hand/foot malformation (ectrodactyly) type 1 [Source:MGI Symbol;Acc:MGI:109238]	Q3TV35	P60897	-8.7	3.1E-06	-4.5	9.9E-05	0.5	1.8E-01	0.6	3.8E-01
ENSMUST00000040721	protein-tyrosine sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1298231]	Q4FK50	O70281	2.3	1.6E-01	3.8	2.0E-02	-2.3	1.4E-01	-3.8	1.3E-02
ENSMUST00000041115	glutamate rich 6 [Source:MGI Symbol;Acc:MGI:3588212]		D3Z6S9	7.0	5.0E-05	-2.9	5.1E-02	0.9	2.2E-01	-2.3	1.8E-01
ENSMUST00000041124	zinc finger protein 704 [Source:MGI Symbol;Acc:MGI:2180715]		Q9ERQ3	5.0	4.4E-06	-3.7	2.0E-02	1.2	8.4E-02	1.2	3.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000041126	synovial sarcoma translocation gene on chromosome 18-like 1 [Source:MGI Symbol;Acc:MGI:2444061]		Q8BW22	2.7	2.0E-03	0.2	9.2E-01	-1.1	4.2E-01	3.7	3.2E-02
ENSMUST00000041133	family with sequence similarity 110, member C [Source:MGI Symbol;Acc:MGI:1918813]		Q8VE94	1.4	1.5E-02	8.6	2.2E-04	-0.1	9.3E-01	-1.4	8.7E-02
ENSMUST00000041138	elaC homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1890495]		Q8VEB6	-3.2	2.3E-03	-3.4	2.5E-04	0.9	1.7E-02	0.0	9.6E-01
ENSMUST00000041139	RAB8B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2442982]	Q0PD49	P61028	-3.5	9.0E-05	-3.6	8.2E-04	1.2	9.6E-03	-0.5	5.4E-01
ENSMUST00000040776	centromere protein T [Source:MGI Symbol;Acc:MGI:2443939]		Q3TJM4	-0.9	2.0E-01	0.5	5.7E-01	1.0	1.6E-01	-0.5	6.0E-01
ENSMUST00000041142	mucin 1, transmembrane [Source:MGI Symbol;Acc:MGI:97231]			1.9	2.2E-02	-3.4	4.2E-02	0.5	5.8E-01	-0.5	7.5E-01
ENSMUST00000041160	guanine nucleotide binding protein (G protein), gamma 10 [Source:MGI Symbol;Acc:MGI:1336169]		Q9CXP8	-8.1	5.1E-06	-2.5	2.0E-02	1.0	7.9E-02	0.4	6.3E-01
ENSMUST00000041163	wingless-type MMTV integration site family, member 8B [Source:MGI Symbol;Acc:MGI:109485]	Q8BQD1		7.9	3.0E-05	3.4	1.2E-03	-0.9	2.3E-01	-0.3	5.9E-01
ENSMUST00000040790	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:106299]		Q6P1D7	0.7	7.1E-01	2.1	4.0E-01	0.5	8.0E-01	-0.9	7.0E-01
ENSMUST00000041164	nucleolar protein 12 [Source:MGI Symbol;Acc:MGI:2146285]	F8WGP0		-6.0	1.5E-04	7.1	2.5E-04	-0.4	7.5E-01	-0.6	3.7E-01
ENSMUST00000041168	adhesion G protein-coupled receptor G6 [Source:MGI Symbol;Acc:MGI:1916151]		Q6F3F9	5.3	3.4E-06	7.0	1.6E-04	-0.5	7.1E-01	-0.9	1.7E-01
ENSMUST00000041180	trace amine-associated receptor 9 [Source:MGI Symbol;Acc:MGI:3527454]		Q5QD04	6.7	6.4E-05	8.2	2.5E-05	1.4	1.8E-01	-0.2	6.1E-01
ENSMUST00000041183	mesenchyme homeobox 2 [Source:MGI Symbol;Acc:MGI:103219]		P32443	7.6	3.2E-04	-5.9	4.2E-03	-0.3	5.7E-01	-0.1	9.5E-01
ENSMUST00000041190	microspherule protein 1 [Source:MGI Symbol;Acc:MGI:1858420]		Q99L90	-4.1	4.6E-03	2.6	2.4E-02	-1.6	1.1E-01	-0.3	6.9E-01
ENSMUST00000040828	histocompatibility 2, class II antigen A, beta 1 [Source:MGI Symbol;Acc:MGI:103070]	Q3TD53	P14483	-2.3	5.3E-02	-3.6	1.7E-02	-2.0	2.3E-02	-0.7	6.2E-01
ENSMUST00000041197	abhydrolase domain containing 4 [Source:MGI Symbol;Acc:MGI:1915938]	Q3U7M5		-3.6	2.8E-03	-3.6	2.8E-03	1.3	1.5E-02	0.2	8.1E-01
ENSMUST00000040835	coiled-coil-helix-coiled-coil-helix domain containing 4 [Source:MGI Symbol;Acc:MGI:1919420]		Q8VEA4	-0.1	8.1E-01	-1.1	1.0E-01	-0.8	1.0E-01	0.2	7.3E-01
ENSMUST00000041208	achalasia, adrenocortical insufficiency, alacrimia [Source:MGI Symbol;Acc:MGI:2443767]		P58742	-1.9	1.8E-02	-2.7	6.4E-02	0.9	2.4E-01	1.2	3.6E-01
ENSMUST00000041213	cyclin Pas1/PHO80 domain containing 1 [Source:MGI Symbol;Acc:MGI:1916421]		Q8K158	-8.7	5.7E-05	-2.4	7.7E-03	0.5	2.3E-01	-0.4	6.3E-01
ENSMUST00000040860	proteasome (prosome, macropain) subunit, alpha type, 8 [Source:MGI Symbol;Acc:MGI:1920927]		Q9CWH6	2.1	5.7E-02	3.4	1.4E-02	-0.5	6.3E-01	-1.8	5.5E-02
ENSMUST00000041229	bradykinin receptor, beta 1 [Source:MGI Symbol;Acc:MGI:88144]	Q0VBD7	Q61125	6.4	6.8E-04	2.9	1.3E-02	-1.4	1.4E-01	-0.3	7.4E-01
ENSMUST00000041231	proteasome (prosome, macropain) activator subunit 4 [Source:MGI Symbol;Acc:MGI:2143994]		Q5SSW2	-3.3	4.8E-04	-1.1	1.9E-01	0.6	2.9E-01	-0.4	6.5E-01
ENSMUST00000041240	shisa family member 4 [Source:MGI Symbol;Acc:MGI:1924802]		Q8CA71	5.6	3.6E-03	4.5	1.5E-03	-0.7	5.2E-01	-0.8	3.0E-01
ENSMUST00000041262	churchill domain containing 1 [Source:MGI Symbol;Acc:MGI:1923684]		Q6DG52	-1.7	2.7E-02	3.5	1.5E-03	-0.8	3.0E-01	0.1	9.1E-01
ENSMUST00000041265	ladybird homeobox homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1342288]		Q9WUN8	5.8	1.3E-04	-2.0	1.2E-02	0.0	9.9E-01	-0.4	5.2E-01
ENSMUST00000040888	keratinocyte associated protein 2 [Source:MGI Symbol;Acc:MGI:1913309]		Q5RL79	0.6	7.6E-01	-1.7	5.2E-01	-0.6	7.5E-01	1.7	5.0E-01
ENSMUST00000041266	fibronectin type III domain containing 4 [Source:MGI Symbol;Acc:MGI:1917195]	B9EI95	Q3TR08	5.6	1.6E-02	4.5	7.8E-05	-0.6	4.0E-01	0.2	7.2E-01
ENSMUST00000040912	anillin, actin binding protein [Source:MGI Symbol;Acc:MGI:1920174]		Q8K298	0.0	9.6E-01	-1.4	6.2E-02	-1.3	2.2E-02	0.2	7.5E-01
ENSMUST00000041272	trin homology domain containing, family M (with RUN domain) member 1 [Source:MGI Symbol;Acc:MGI:24		Q7TSI1	-1.6	9.5E-03	-3.1	1.6E-02	1.2	5.7E-02	0.0	1.0E+00
ENSMUST00000041301	phenylethanolamine-N-methyltransferase [Source:MGI Symbol;Acc:MGI:97724]	Q0VB50	P40935	7.3	6.5E-04	-2.5	1.0E-01	-1.2	2.0E-01	-1.8	2.5E-01
ENSMUST00000041314	polyadenylate-binding protein-interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915119]		Q9D6V8	-10.1	2.3E-06	-8.5	2.3E-04	-0.9	6.0E-02	0.8	6.3E-01
ENSMUST00000041318	N-myc downstream regulated gene 4 [Source:MGI Symbol;Acc:MGI:2384590]		Q8BTG7	2.8	3.2E-02	-4.3	6.1E-02	0.2	8.1E-01	0.1	9.7E-01
ENSMUST00000041331	stearoyl-Coenzyme A desaturase 1 [Source:MGI Symbol;Acc:MGI:98239]	Q547C4	P13516	2.6	6.4E-04	8.0	2.2E-04	0.9	5.0E-01	0.2	7.7E-01
ENSMUST00000041357	leucine-rich alpha-2-glycoprotein 1 [Source:MGI Symbol;Acc:MGI:1924155]	Q91XL1		-8.1	1.2E-06	6.3	1.6E-04	-0.5	6.3E-01	0.0	1.0E+00
ENSMUST00000041362	mitochondrial antiviral signaling protein [Source:MGI Symbol;Acc:MGI:2444773]		Q8VCF0	-4.7	3.3E-02	6.5	1.2E-04	-1.5	2.1E-01	-0.3	6.5E-01
ENSMUST00000040962	nudix (nucleoside diphosphate linked moiety X)-type motif 19 [Source:MGI Symbol;Acc:MGI:94203]		P11930	0.8	3.0E-01	0.3	7.4E-01	-0.8	2.4E-01	-0.3	6.9E-01
ENSMUST00000041366	polymerase (RNA) II (DNA directed) polypeptide J [Source:MGI Symbol;Acc:MGI:109582]	Q6PI63		-6.6	4.9E-04	-1.5	7.8E-02	0.8	1.3E-01	-0.4	6.6E-01
ENSMUST00000041370	taxilin gamma [Source:MGI Symbol;Acc:MGI:3590652]		Q8BHN1	-5.5	4.2E-03	2.9	1.4E-03	-2.1	9.0E-03	-0.7	1.9E-01
ENSMUST00000040972	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast) [Source:MGI Symbol;Acc:MGI:2145443]		Q8C7V3	0.7	1.5E-01	0.4	5.6E-01	-0.1	8.3E-01	0.3	6.6E-01
ENSMUST00000041377	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog [Source:MGI Symbol;Acc:MGI:96892]	Q3TCS3	P25911	-7.5	3.0E-04	-5.0	1.2E-03	-0.2	6.3E-01	-0.1	9.2E-01
ENSMUST00000041385	Rho GTPase activating protein 27 [Source:MGI Symbol;Acc:MGI:1916903]		A2AB59	-4.8	2.0E-03	0.6	7.0E-01	1.3	2.9E-01	-3.7	7.5E-02
ENSMUST00000041388	serine (or cysteine) peptidase inhibitor, clade E, member 1 [Source:MGI Symbol;Acc:MGI:97608]	G5E899		8.9	6.2E-05	4.4	7.5E-04	-0.1	9.5E-01	-0.2	8.1E-01
ENSMUST00000041398	histocompatibility 2, M region locus 10.6 [Source:MGI Symbol;Acc:MGI:2687364]	Q85ZW5		6.7	6.0E-04	1.3	2.0E-02	-0.4	3.6E-01	-0.5	2.7E-01
ENSMUST00000041403	beclin 1, autophagy related [Source:MGI Symbol;Acc:MGI:1891828]	E9QAM0		-9.8	1.5E-05	-2.1	1.0E-02	1.0	2.8E-02	0.0	9.9E-01
ENSMUST00000040999	aldehyde oxidase 3 [Source:MGI Symbol;Acc:MGI:1918974]		G3X982	2.0	7.7E-02	4.4	1.1E-02	1.7	1.8E-01	-0.7	5.4E-01
ENSMUST00000041407	sclerostin domain containing 1 [Source:MGI Symbol;Acc:MGI:1913292]		Q9CQN4	7.4	7.0E-05	5.3	2.1E-04	-2.2	4.9E-02	-0.1	9.2E-01
ENSMUST00000041415	otassium voltage-gated channel, subfamily H (eag-related), member 3 [Source:MGI Symbol;Acc:MGI:1341723	B2RU85		7.4	3.0E-05	8.6	2.5E-05	0.1	9.4E-01	-0.9	9.0E-02
ENSMUST00000041008	farnesyltransferase, CAAX box, beta [Source:MGI Symbol;Acc:MGI:1861305]		Q8K2I1	-0.6	4.6E-01	0.5	6.1E-01	-0.1	9.3E-01	-1.2	2.2E-01
ENSMUST00000041418	stromal antigen 1 [Source:MGI Symbol;Acc:MGI:1098658]	F8WHU7		-7.2	7.1E-06	-1.2	2.1E-01	1.4	5.2E-02	0.0	9.9E-01
ENSMUST00000041422	spermatogenesis associated 18 [Source:MGI Symbol;Acc:MGI:1920722]	E9QAP8		5.8	2.0E-02	6.5	2.5E-04	1.4	2.0E-01	-0.3	6.8E-01
ENSMUST00000041023	importin 9 [Source:MGI Symbol;Acc:MGI:1918944]	E9QKZ2		-1.0	1.3E-01	-0.1	9.0E-01	0.4	5.2E-01	-0.6	4.8E-01
ENSMUST00000041024	lactation elevated 1 [Source:MGI Symbol;Acc:MGI:2148801]		Q3V384	-1.0	3.1E-01	1.5	1.3E-01	-0.1	8.8E-01	-2.6	2.1E-02
ENSMUST00000041425	neuronal growth regulator 1 [Source:MGI Symbol;Acc:MGI:2444846]	A0A4W9		5.3	9.2E-04	5.6	1.8E-04	0.7	4.3E-01	-0.6	3.5E-01
ENSMUST00000041438	sestrin 1 [Source:MGI Symbol;Acc:MGI:2155278]		P58006	-4.6	7.0E-03	-2.5	2.2E-01	0.9	4.3E-01	-2.8	2.7E-01
ENSMUST00000041447	transient receptor potential cation channel, subfamily A, member 1 [Source:MGI Symbol;Acc:MGI:3522699]		Q8BLA8	5.2	2.2E-04	-3.5	1.0E-04	0.7	1.8E-02	0.7	2.3E-01
ENSMUST00000041463	PARK2 co-regulated [Source:MGI Symbol;Acc:MGI:1916560]	Q0VB91	Q9DAK2	5.6	4.0E-04	-2.0	1.1E-02	0.8	5.1E-02	0.1	9.2E-01
ENSMUST00000041466	zinc finger, BED type containing 5 [Source:MGI Symbol;Acc:MGI:1919220]	B2RPU8		4.5	9.9E-03	-3.7	1.0E-04	0.0	8.8E-01	0.2	6.9E-01
ENSMUST00000041477	immunoglobulin superfamily containing leucine-rich repeat [Source:MGI Symbol;Acc:MGI:1349645]		Q6GU68	7.0	2.9E-04	1.7	1.2E-02	0.6	2.0E-01	0.3	4.9E-01
ENSMUST00000041524	tRNA methyltransferase 13 [Source:MGI Symbol;Acc:MGI:1925219]		Q8BYH3	3.8	8.0E-03	-4.6	2.6E-03	0.9	1.3E-01	-1.8	1.8E-01
ENSMUST00000041531	histocompatibility 2, M region locus 10.5 [Source:MGI Symbol;Acc:MGI:1276526]	Q85ZW7		7.0	3.8E-05	0.5	4.7E-01	1.5	1.5E-02	-0.6	3.9E-01
ENSMUST00000041544	fibulin 2 [Source:MGI Symbol;Acc:MGI:95488]		P37889	8.7	1.5E-03	6.0	2.5E-04	-0.3	7.7E-01	0.1	9.0E-01
ENSMUST00000041550	macrophage galactose N-acetyl-galactosamine specific lectin 2 [Source:MGI Symbol;Acc:MGI:2385729]	Q8JZN1		3.8	1.3E-02	3.0	7.0E-04	0.4	4.6E-01	0.2	6.1E-01
ENSMUST00000041551	alpha- and gamma-adaptin binding protein [Source:MGI Symbol;Acc:MGI:1914189]		Q8R2R3	-3.4	2.4E-05	2.0	2.2E-02	0.1	9.3E-01	-0.3	6.7E-01
ENSMUST00000041555	multivesicular body subunit 12B [Source:MGI Symbol;Acc:MGI:1919793]		Q6KAU4	-1.4	1.0E-02	6.0	1.4E-03	-0.6	6.7E-01	-0.9	2.9E-01
ENSMUST00000041569	coiled-coil domain containing 113 [Source:MGI Symbol;Acc:MGI:3606076]		Q8C5T8	5.9	1.6E-04	6.9	3.8E-04	-0.6	6.8E-01	-0.3	6.3E-01
ENSMUST00000041587	olgi associated, gamma adaptin ear containing, ARF binding protein 1 [Source:MGI Symbol;Acc:MGI:214620		Q8R0H9	-3.7	8.2E-04	-3.5	4.1E-02	1.1	1.3E-01	-0.8	6.2E-01
ENSMUST00000041588	BRCA1-associated ATM activator 1 [Source:MGI Symbol;Acc:MGI:1891679]		Q8C3R1	-6.1	1.4E-03	-9.1	3.7E-03	1.5	4.3E-02	0.6	8.2E-01
ENSMUST00000041589	transducer of ErbB-2.1 [Source:MGI Symbol;Acc:MGI:1349721]		Q61471	-3.5	1.1E-04	-8.1	2.7E-05	-0.8	8.2E-02	-1.4	2.3E-01
ENSMUST00000041606	N-terminal EF-hand calcium binding protein 1 [Source:MGI Symbol;Acc:MGI:1916602]		Q8BG18	6.3	5.0E-04	7.2	7.9E-05	-0.5	6.8E-01	-0.7	2.7E-01
ENSMUST00000041122	coiled-coil-helix-coiled-coil-helix domain containing 7 [Source:MGI Symbol;Acc:MGI:1913683]		Q8K2Q5	-2.7	8.3E-02	-1.1	5.8E-01	1.3	3.5E-01	-0.2	9.0E-01
ENSMUST00000041123	mucin 20 [Source:MGI Symbol;Acc:MGI:2385039]		Q8BUE7	1.6	1.8E-01	1.5	3.7E-01	1.7	1.9E-01	1.8	2.2E-01
ENSMUST00000041614	tetratricopeptide repeat domain 13 [Source:MGI Symbol;Acc:MGI:2384573]	Q3UMK4		-5.5	2.3E-02	4.6	2.9E-05	-0.2	7.2E-01	0.2	6.1E-01
ENSMUST00000041616	pyridoxal (pyridoxine, vitamin B6) kinase [Source:MGI Symbol;Acc:MGI:1351869]		Q8K183	2.3	1.1E-03	2.8	1.1E-02	0.8	3.2E-01	0.7	3.1E-01
ENSMUST00000041627	sidekick homolog 2 (chicken) [Source:MGI Symbol;Acc:MGI:2443847]		Q6V4S5	8.4	1.5E-06	2.2	7.0E-03	1.1	6.7E-02	0.2	6.4E-01
ENSMUST00000041633	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) [Source:MGI Symbol;Acc:MGI:98483]	Q3TBA3		-8.2	6.1E-04	-1.8	8.8E-02	0.7	2.2E-01	-0.7	4.9E-01
ENSMUST00000041643	PDX1 C-terminal inhibiting factor 1 [Source:MGI Symbol;Acc:MGI:2443858]	Q542C3	P59114	-2.6	1.7E-03	-3.1	1.3E-03	0.6	1.3E-01	0.3	6.5E-01
ENSMUST00000041646	dopamine receptor D5 [Source:MGI Symbol;Acc:MGI:94927]	B2RQS5	Q8BLD9	8.2	3.1E-05	2.6	2.4E-02	0.8	3.2E-01	0.2	8.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000041159				1.0	6.1E-01	-2.1	2.7E-01	-4.3	1.6E-02	-1.2	5.5E-01
ENSMUST00000041649	protease, serine 22 [Source:MGI Symbol;Acc:MGI:1918085]	Q7TML0		4.3	1.6E-03	-8.6	3.4E-05	-0.5	1.8E-01	0.0	9.9E-01
ENSMUST00000041674	butyrophilin, subfamily 1, member A1 [Source:MGI Symbol;Acc:MGI:103118]	Q3UQC0	Q62556	10.6	1.3E-05	6.8	1.3E-04	-1.0	4.2E-01	0.1	8.8E-01
ENSMUST00000041676	histamine receptor H4 [Source:MGI Symbol;Acc:MGI:2429635]		Q91ZY2	5.0	5.1E-04	-6.2	6.1E-04	-1.0	5.6E-02	-0.8	5.7E-01
ENSMUST00000041683	ubiquitin specific peptidase 22 [Source:MGI Symbol;Acc:MGI:2144157]		Q5DU02	-3.7	8.7E-05	1.5	1.4E-02	-3.5	8.5E-05	0.3	5.1E-01
ENSMUST00000041175	prostaglandin E receptor 3 (subtype EP3) [Source:MGI Symbol;Acc:MGI:97795]	Q6PDF2		0.0	9.8E-01	2.5	1.2E-01	0.5	7.0E-01	-2.1	1.3E-01
ENSMUST00000041684	CASK-interacting protein 2 [Source:MGI Symbol;Acc:MGI:2157062]		Q8VHK1	2.5	2.9E-03	6.1	2.3E-04	-0.6	5.9E-01	0.0	9.4E-01
ENSMUST00000041685	neurogenic differentiation 2 [Source:MGI Symbol;Acc:MGI:107755]	Q3TYB2	Q62414	9.8	1.7E-05	6.0	3.9E-03	0.0	9.8E-01	1.6	9.8E-02
ENSMUST00000041686	nudix (nucleoside diphosphate linked moiety X)-type motif 22 [Source:MGI Symbol;Acc:MGI:1915573]		Q9DD16	-4.7	1.0E-03	-1.4	2.8E-01	0.7	4.1E-01	-2.1	1.5E-01
ENSMUST00000041705	spermatogenesis associated 20 [Source:MGI Symbol;Acc:MGI:2183449]		Q80YT5	7.0	2.2E-03	-2.2	7.2E-02	0.6	3.6E-01	-0.8	4.8E-01
ENSMUST00000041723	zinc finger, DHHC domain containing 17 [Source:MGI Symbol;Acc:MGI:2445110]		Q80TN5	-1.5	1.4E-02	-0.2	8.1E-01	0.6	2.9E-01	-1.1	1.8E-01
ENSMUST00000041726	ankyrin repeat and SOCS box-containing 6 [Source:MGI Symbol;Acc:MGI:1919573]		Q91ZU1	5.1	2.8E-05	-5.6	1.7E-03	1.5	1.9E-02	-1.6	3.1E-01
ENSMUST00000041730	LIM homeobox transcription factor 1 beta [Source:MGI Symbol;Acc:MGI:1100513]			9.1	1.5E-05	5.6	2.2E-04	0.2	8.5E-01	-1.1	1.1E-01
ENSMUST00000041732	kin of IRRE like (Drosophila) [Source:MGI Symbol;Acc:MGI:1891396]		Q80W68	6.0	1.9E-04	4.6	4.0E-03	-2.7	7.5E-02	-0.9	2.8E-01
ENSMUST00000041733	2 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:2443	B9EJX5		-1.0	2.8E-02	-2.3	2.0E-02	1.2	3.4E-02	0.2	8.6E-01
ENSMUST00000041736	histone deacetylase 11 [Source:MGI Symbol;Acc:MGI:2385252]	Q543U1	Q91WA3	5.0	9.4E-05	5.2	3.5E-03	-2.6	1.1E-01	-2.3	3.1E-02
ENSMUST00000041252	acyl-Coenzyme A dehydrogenase family, member 12 [Source:MGI Symbol;Acc:MGI:2443320]	D3Z7X0		-0.2	7.8E-01	0.9	3.6E-01	0.8	3.1E-01	-0.3	7.1E-01
ENSMUST00000041761	protease, serine 23 [Source:MGI Symbol;Acc:MGI:1923703]		Q9D6X6	6.7	2.7E-04	-4.0	3.4E-03	-0.3	5.8E-01	2.0	7.4E-02
ENSMUST00000041767	TBC1 domain family, member 2B [Source:MGI Symbol;Acc:MGI:1914266]		Q3U0J8	-3.3	5.4E-05	6.4	3.3E-04	0.7	5.3E-01	0.2	7.9E-01
ENSMUST00000041776	regulator of G-protein signaling 8 [Source:MGI Symbol;Acc:MGI:108408]		Q8BXT1	9.5	1.7E-05	1.6	4.0E-01	-3.1	1.4E-01	0.9	5.5E-01
ENSMUST00000041778	zinc finger protein 174 [Source:MGI Symbol;Acc:MGI:2686600]	B9EJW5		4.1	3.3E-05	-0.2	8.1E-01	1.3	2.0E-02	-0.2	7.8E-01
ENSMUST00000041282	tripartite motif-containing 37 [Source:MGI Symbol;Acc:MGI:2153072]		Q6PCX9	0.7	1.1E-01	1.0	8.4E-02	-0.2	7.0E-01	-0.4	3.9E-01
ENSMUST00000041297	zinc finger, BED type containing 4 [Source:MGI Symbol;Acc:MGI:2682302]		Q80WQ9	-0.6	2.6E-01	1.1	1.5E-01	1.1	5.5E-02	-0.5	4.0E-01
ENSMUST00000041779	C-type lectin domain family 4, member a2 [Source:MGI Symbol;Acc:MGI:1349412]		Q9QZ15	-3.1	5.8E-04	6.0	4.2E-03	-0.7	6.9E-01	0.7	4.8E-01
ENSMUST00000041782	activator of basal transcription 1 [Source:MGI Symbol;Acc:MGI:1353636]		Q9QYL7	-1.3	2.4E-02	-7.5	2.0E-05	0.1	7.0E-01	-2.4	6.0E-02
ENSMUST00000041317	mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1 [Source:MGI Symbol;A		Q9JHT5	-0.4	4.4E-01	0.8	2.0E-01	1.3	1.7E-02	0.1	8.2E-01
ENSMUST00000041804	lemur tyrosine kinase 2 [Source:MGI Symbol;Acc:MGI:3036247]		Q3TYD6	-1.3	5.8E-03	6.3	2.4E-04	-0.5	6.5E-01	-4.0	8.2E-04
ENSMUST00000041806	presenilin 1 [Source:MGI Symbol;Acc:MGI:1202717]	Q3UYK2	P49769	-4.5	9.4E-04	0.7	2.1E-01	-2.3	9.4E-04	-0.4	4.1E-01
ENSMUST00000041353	solute carrier family 35, member B2 [Source:MGI Symbol;Acc:MGI:1921086]	Q3TJQ2	Q91ZN5	-1.7	5.2E-02	-1.0	3.0E-01	0.5	4.0E-01	-0.1	9.0E-01
ENSMUST00000041826	ring finger protein 13 [Source:MGI Symbol;Acc:MGI:1346341]		O54965	-5.7	8.6E-06	-6.2	3.9E-05	1.4	3.2E-03	-0.5	5.8E-01
ENSMUST00000041361	zinc finger protein 335 [Source:MGI Symbol;Acc:MGI:2682313]		A2A5K6	-3.1	1.8E-01	-2.2	4.7E-01	1.1	6.3E-01	0.2	9.5E-01
ENSMUST00000041827	solute carrier family 22 (organic anion transporter), member 20 [Source:MGI Symbol;Acc:MGI:2685809]		Q80UJ1	-2.1	6.3E-03	-1.8	2.8E-01	0.3	7.8E-01	-2.5	2.4E-01
ENSMUST00000041364	NOP14 nucleolar protein [Source:MGI Symbol;Acc:MGI:1922666]		Q8R3N1	0.2	6.4E-01	-0.6	3.8E-01	-1.0	5.8E-02	-0.2	8.0E-01
ENSMUST00000041845	NLR family, pyrin domain containing 9C [Source:MGI Symbol;Acc:MGI:3028627]		Q66X01	6.2	2.7E-04	-5.9	1.1E-03	-0.5	3.2E-01	-1.3	4.2E-01
ENSMUST00000041367	DDB1 and CUL4 associated factor 15 [Source:MGI Symbol;Acc:MGI:2684420]		Q6PFH3	-1.6	3.9E-02	-1.0	2.9E-01	0.6	3.3E-01	-0.1	9.5E-01
ENSMUST00000041369	suppressor of cytokine signaling 5 [Source:MGI Symbol;Acc:MGI:2385459]		O54928	0.2	6.7E-01	1.3	3.1E-02	0.8	8.2E-02	-0.4	4.3E-01
ENSMUST00000041852	pyridine nucleotide-disulphide oxidoreductase domain 1 [Source:MGI Symbol;Acc:MGI:2676395]		Q3TMV7	-3.5	7.7E-03	-5.2	1.7E-02	-0.7	3.8E-01	-0.9	6.6E-01
ENSMUST00000041374	mannosidase, endo-alpha [Source:MGI Symbol;Acc:MGI:2444484]		Q6NXH2	0.2	5.1E-01	0.8	1.1E-01	0.1	6.8E-01	-0.4	3.3E-01
ENSMUST00000041375	salt inducible kinase 2 [Source:MGI Symbol;Acc:MGI:2445031]	F8VPT7		2.8	2.9E-01	0.1	9.7E-01	-1.9	4.5E-01	0.8	7.6E-01
ENSMUST00000041859	GDP-mannose 4, 6-dehydratase [Source:MGI Symbol;Acc:MGI:1891112]		Q8K0C9	-1.6	1.5E-02	-8.4	2.2E-03	1.2	1.2E-01	2.1	3.3E-01
ENSMUST00000041382	fucokinase [Source:MGI Symbol;Acc:MGI:1916071]	Q7TMC8		0.5	3.2E-01	1.6	3.4E-02	0.8	1.4E-01	-0.3	6.4E-01
ENSMUST00000041860	glycerophosphodiester phosphodiesterase domain containing 4 [Source:MGI Symbol;Acc:MGI:3606573]		Q3TT99	8.0	1.1E-05	-2.5	1.1E-01	1.3	1.3E-01	-1.0	5.0E-01
ENSMUST00000041866	bromodomain and WD repeat domain containing 3 [Source:MGI Symbol;Acc:MGI:3029414]	G3UZT0		-4.0	1.9E-02	4.4	6.4E-03	-3.9	2.0E-02	0.5	5.6E-01
ENSMUST00000041391	pleckstrin and Sec7 domain containing [Source:MGI Symbol;Acc:MGI:1920978]		Q5DTT2	-0.4	7.9E-01	0.2	9.4E-01	0.9	5.8E-01	0.3	8.8E-01
ENSMUST00000041871	T-box 10 [Source:MGI Symbol;Acc:MGI:1261436]		Q810F8	7.6	3.7E-05	6.2	1.8E-03	-0.7	6.7E-01	-0.2	8.6E-01
ENSMUST00000041400	RAN binding protein 10 [Source:MGI Symbol;Acc:MGI:1921584]			-0.9	4.6E-02	-0.1	7.9E-01	0.7	8.0E-02	-0.1	9.1E-01
ENSMUST00000041401	hect domain and RLD 3 [Source:MGI Symbol;Acc:MGI:1921248]	A6H6S0		-0.2	6.3E-01	0.4	5.5E-01	0.5	3.1E-01	-0.1	8.2E-01
ENSMUST00000041890	transmembrane 6 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1933209]		P58749	-6.7	3.5E-05	-8.2	3.7E-04	0.7	1.3E-01	-0.9	5.9E-01
ENSMUST00000041901	calcium and integrin binding family member 2 [Source:MGI Symbol;Acc:MGI:1929293]	Q544Z8	Q9Z309	-3.2	1.0E-04	6.8	2.5E-04	-0.6	6.1E-01	0.0	9.5E-01
ENSMUST00000041413	RIKEN cDNA E330034G19 gene [Source:MGI Symbol;Acc:MGI:2145557]	Q3UWX6		2.1	8.4E-02	6.7	1.1E-04	-0.5	6.4E-01	-5.2	1.4E-04
ENSMUST00000041905	nucleoporin like 1 [Source:MGI Symbol;Acc:MGI:1919094]		Q8R332	-2.1	1.1E-03	6.5	5.8E-05	-1.1	3.1E-01	-0.2	6.9E-01
ENSMUST00000041954	COMM domain containing 2 [Source:MGI Symbol;Acc:MGI:1098806]	G3X955		-7.4	1.1E-05	-4.6	1.2E-03	1.8	2.0E-03	-0.9	4.3E-01
ENSMUST00000041956	sperm associated antigen 9 [Source:MGI Symbol;Acc:MGI:1918084]		Q58A65	-7.5	4.5E-06	2.3	4.0E-01	-0.8	7.6E-01	2.7	2.1E-01
ENSMUST00000041965	CDC42 binding protein kinase beta [Source:MGI Symbol;Acc:MGI:2136459]		Q7TT50	1.7	4.3E-03	6.2	6.2E-04	-0.4	7.4E-01	-1.3	9.4E-02
ENSMUST00000041968	transmembrane protein 135 [Source:MGI Symbol;Acc:MGI:1920009]		Q9CYV5	-2.1	1.4E-02	-6.0	2.2E-03	-1.3	9.3E-02	0.1	9.4E-01
ENSMUST00000041982	histocompatibility 2, class II, locus Mb2 [Source:MGI Symbol;Acc:MGI:95923]	Q31099		4.2	7.0E-05	6.6	1.9E-04	0.5	6.3E-01	-0.8	2.1E-01
ENSMUST00000041459	cytochrome b-561 domain containing 2 [Source:MGI Symbol;Acc:MGI:1929280]		Q9WUE3	1.7	7.3E-02	3.5	8.1E-03	0.9	3.3E-01	-0.8	3.3E-01
ENSMUST00000041460	nuclear receptor interacting protein 3 [Source:MGI Symbol;Acc:MGI:1925843]	Q6GQT2		5.9	4.6E-02	6.0	5.7E-02	-0.8	8.0E-01	-0.8	6.6E-01
ENSMUST00000042009	discs, large homolog 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:1918478]	F6YZU5		7.3	6.3E-05	3.8	1.7E-03	-2.7	2.4E-02	-0.9	2.0E-01
ENSMUST00000042012	splicing factor 3b, subunit 3 [Source:MGI Symbol;Acc:MGI:1289341]	B2RSV4	Q921M3	-1.9	2.3E-03	4.2	3.4E-02	-0.2	8.9E-01	0.2	8.8E-01
ENSMUST00000041475	myoferlin [Source:MGI Symbol;Acc:MGI:1919192]		Q69ZN7	-1.1	9.1E-02	-1.3	6.7E-02	-1.3	1.6E-02	-1.0	1.7E-01
ENSMUST00000042021	testis-specific protein, Y-encoded-like 5 [Source:MGI Symbol;Acc:MGI:2442458]		Q69ZB3	7.6	1.6E-05	7.1	5.3E-04	-0.4	7.8E-01	-0.5	5.0E-01
ENSMUST00000041500	sulfiredoxin 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:104971]	A2AQU8		-0.8	8.8E-02	0.1	8.9E-01	0.3	4.0E-01	-0.5	3.1E-01
ENSMUST00000042025	anthrax toxin receptor 1 [Source:MGI Symbol;Acc:MGI:1916788]		Q9CZ52	8.1	4.8E-06	2.2	9.5E-02	-1.8	1.5E-01	-0.2	8.3E-01
ENSMUST00000042042	solute carrier family 51, alpha subunit [Source:MGI Symbol;Acc:MGI:2146634]		Q8R000	7.0	1.3E-04	6.9	8.8E-05	-0.6	6.1E-01	-0.4	4.7E-01
ENSMUST00000041543	VGF nerve growth factor inducible [Source:MGI Symbol;Acc:MGI:1343180]	Q0VGU4		2.9	7.0E-02	4.8	8.5E-03	-0.6	7.0E-01	-2.5	5.5E-02
ENSMUST00000042046	scavenger receptor class A, member 3 [Source:MGI Symbol;Acc:MGI:2444418]		Q8C850	8.4	1.9E-05	5.7	2.7E-02	-0.8	7.5E-01	2.1	1.2E-01
ENSMUST00000042052	HECT domain containing 1 [Source:MGI Symbol;Acc:MGI:2384768]	F8WIE5		-5.6	5.8E-03	4.2	8.4E-02	3.4	1.2E-01	3.0	4.3E-02
ENSMUST00000042054	forkhead box F2 [Source:MGI Symbol;Acc:MGI:1347479]		O54743	6.4	8.3E-05	-2.5	1.1E-03	0.5	1.2E-01	-0.4	4.9E-01
ENSMUST00000042055	protein phosphatase 2A activator, regulatory subunit B [Source:MGI Symbol;Acc:MGI:1346006]	Q543N6	P58389	-7.6	2.2E-03	-0.2	7.0E-01	1.3	1.0E-02	0.1	8.2E-01
ENSMUST00000041558	E1A binding protein p400 [Source:MGI Symbol;Acc:MGI:1276124]		Q8CHI8	-1.7	6.4E-02	-0.7	5.4E-01	1.1	1.3E-01	0.1	9.3E-01
ENSMUST00000041565	intraflagellar transport 172 [Source:MGI Symbol;Acc:MGI:2682064]		Q6VH22	0.3	4.2E-01	0.7	1.9E-01	-0.5	1.8E-01	-0.8	9.4E-02
ENSMUST00000042057	midnolin [Source:MGI Symbol;Acc:MGI:1890222]		Q3TPJ7	-6.9	5.6E-04	6.1	2.3E-04	-0.5	6.4E-01	-0.7	2.4E-01
ENSMUST00000041577	B cell scaffold protein with ankyrin repeats 1 [Source:MGI Symbol;Acc:MGI:2442120]		Q80VH0	1.0	1.2E-01	-1.3	7.3E-02	-2.3	9.9E-04	-0.1	9.2E-01
ENSMUST00000042065	mitogen-activated protein kinase kinase kinase 13 [Source:MGI Symbol;Acc:MGI:2444243]		Q1HKZ5	9.2	2.7E-06	-2.6	2.4E-02	1.1	6.9E-02	0.0	1.0E+00
ENSMUST00000042070	zinc finger, DHHC domain containing 15 [Source:MGI Symbol;Acc:MGI:1915336]		Q8BGJ0	3.3	2.5E-03	-3.6	9.5E-02	2.6	3.4E-02	0.1	9.6E-01
ENSMUST00000042078	aristaless-like homeobox 4 [Source:MGI Symbol;Acc:MGI:108359]		O35137	8.7	4.7E-06	-2.5	5.3E-03	0.8	5.6E-02	-0.2	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000041591	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Source:MGI Symbol;Acc:MGI:1321390]		Q9R1E6	3.2	9.3E-02	-4.1	4.4E-02	-6.5	1.9E-03	0.8	6.5E-01
ENSMUST00000042096	ER membrane protein complex subunit 1 [Source:MGI Symbol;Acc:MGI:2443696]		Q8C7X2	-1.6	1.5E-02	7.1	3.7E-04	-0.5	7.2E-01	-1.3	9.9E-02
ENSMUST00000041611	growth arrest specific 7 [Source:MGI Symbol;Acc:MGI:1202388]	B1ATI9		1.0	6.7E-01	2.2	5.6E-01	2.5	3.4E-01	1.3	7.0E-01
ENSMUST00000042103	myosin XVI [Source:MGI Symbol;Acc:MGI:2685951]	F8WGF8		9.1	2.6E-05	-2.8	3.4E-01	1.8	3.0E-01	-0.9	7.7E-01
ENSMUST00000042105	protein phosphatase 1, regulatory (inhibitor) subunit 15A [Source:MGI Symbol;Acc:MGI:1927072]	B2RRL7	P17564	-3.8	2.8E-02	2.4	4.2E-03	0.1	9.2E-01	0.0	9.8E-01
ENSMUST00000041618	A RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:215	E9QAP7		-0.3	7.9E-01	0.4	7.5E-01	1.2	2.5E-01	0.5	7.1E-01
ENSMUST00000041621	lipoyltransferase 1 [Source:MGI Symbol;Acc:MGI:3645211]		Q8VCM4	1.3	1.1E-01	0.7	4.2E-01	-0.7	3.4E-01	-0.1	8.6E-01
ENSMUST00000041623	ectodermal-neural cortex 1 [Source:MGI Symbol;Acc:MGI:109610]		O35709	1.2	9.6E-02	1.6	8.8E-02	0.4	6.0E-01	-0.1	9.4E-01
ENSMUST00000042118	forkhead box Q1 [Source:MGI Symbol;Acc:MGI:1298228]		O70220	6.6	6.3E-04	8.1	3.1E-05	-0.2	8.3E-01	0.1	7.6E-01
ENSMUST00000042122	single-stranded DNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1914220]		Q9CYZ8	-4.4	7.7E-04	-5.8	1.4E-02	1.0	1.9E-01	-1.5	5.1E-01
ENSMUST00000041638	general transcription factor IIIC, polypeptide 3 [Source:MGI Symbol;Acc:MGI:2138383]	Q3TMP1		1.2	4.2E-02	0.4	5.6E-01	-0.5	3.6E-01	0.3	5.8E-01
ENSMUST00000041639	spectrin repeat containing, nuclear envelope 1 [Source:MGI Symbol;Acc:MGI:1927152]		Q6ZWR6	-0.6	2.4E-01	-0.5	4.6E-01	0.1	7.6E-01	0.0	9.7E-01
ENSMUST00000041640	ankyrin repeat and MYND domain containing 2 [Source:MGI Symbol;Acc:MGI:2144755]		Q3TPE9	0.1	8.9E-01	0.0	9.5E-01	-1.3	1.4E-02	-1.2	5.2E-02
ENSMUST00000041641	calpain 15 [Source:MGI Symbol;Acc:MGI:1355075]		Q9JLG8	0.9	1.3E-01	1.7	3.7E-02	0.9	1.4E-01	0.0	9.5E-01
ENSMUST00000042125	tubulin tyrosine ligase-like family, member 4 [Source:MGI Symbol;Acc:MGI:1914784]		Q80UG8	5.0	3.5E-05	-1.3	1.2E-01	1.0	6.2E-02	-0.3	7.3E-01
ENSMUST00000042141	DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Source:MGI Symbol;Acc:MGI:108177]	E9QNN1		-5.2	2.4E-03	7.3	1.4E-04	-0.7	6.1E-01	0.2	7.5E-01
ENSMUST00000042146	syntaxin 18 [Source:MGI Symbol;Acc:MGI:1918366]		Q8VDS8	-6.1	1.4E-04	4.5	5.4E-03	0.6	6.2E-01	0.5	6.0E-01
ENSMUST00000041654	fucosyltransferase 7 [Source:MGI Symbol;Acc:MGI:107692]	Q3SWS0	Q11131	2.0	2.2E-01	2.0	3.2E-01	-0.1	9.5E-01	0.0	9.8E-01
ENSMUST00000041656	tubulin, gamma complex associated protein 6 [Source:MGI Symbol;Acc:MGI:2146071]	E9Q6P4		2.9	2.3E-01	5.5	1.4E-01	3.2	3.0E-01	0.6	8.2E-01
ENSMUST00000042148	mitochondrial ribosomal protein S28 [Source:MGI Symbol;Acc:MGI:1913480]		Q9CY16	-1.7	9.4E-03	8.5	5.4E-05	-1.8	2.3E-01	0.3	6.3E-01
ENSMUST00000042158	extended synaptotagmin-like protein 3 [Source:MGI Symbol;Acc:MGI:1098699]		Q5DTI8	6.3	2.1E-04	3.8	6.3E-03	-1.5	1.8E-01	-0.2	7.9E-01
ENSMUST00000042166	family with sequence similarity 103, member A1 [Source:MGI Symbol;Acc:MGI:1914398]		Q9CQY2	-4.3	2.2E-05	-2.1	1.4E-02	1.3	9.8E-03	-0.3	6.7E-01
ENSMUST00000042190	tectorin alpha [Source:MGI Symbol;Acc:MGI:109575]		O08523	8.5	5.1E-03	3.2	3.6E-03	0.9	2.2E-01	0.2	7.5E-01
ENSMUST00000042191	mitochondrial ribosomal protein S17 [Source:MGI Symbol;Acc:MGI:1913508]		Q9CQE3	-6.6	2.7E-05	7.7	1.4E-04	-0.7	5.9E-01	1.4	5.3E-02
ENSMUST00000042194	transient receptor potential cation channel, subfamily M, member 4 [Source:MGI Symbol;Acc:MGI:1915917]		Q7TN37	-1.1	2.4E-02	-1.5	1.4E-01	1.0	1.5E-01	-2.2	8.1E-02
ENSMUST00000042196	von Willebrand factor A domain containing 1 [Source:MGI Symbol;Acc:MGI:2179729]		Q8R2Z5	8.0	1.1E-05	3.9	7.4E-02	-0.6	7.7E-01	2.6	6.4E-02
ENSMUST00000042217	R-spondin 4 [Source:MGI Symbol;Acc:MGI:1924467]	Q0P5Y9	Q8BJ73	7.4	2.6E-05	-1.2	8.6E-02	-0.1	8.5E-01	-0.4	5.3E-01
ENSMUST00000041725	mannoside acetylglucosaminyltransferase 4, isoenzyme B [Source:MGI Symbol;Acc:MGI:2143974]		Q812F8	-0.7	2.9E-01	0.1	9.1E-01	-0.2	6.5E-01	-1.0	1.8E-01
ENSMUST00000042227	DNA segment, Chr 11, Wayne State University 47, expressed [Source:MGI Symbol;Acc:MGI:106356]		Q6PIX9	-4.6	4.0E-04	5.4	2.5E-04	0.6	4.5E-01	0.4	4.8E-01
ENSMUST00000042235	eukaryotic translation elongation factor 1 alpha 1 [Source:MGI Symbol;Acc:MGI:1096881]	Q58E64	P10126	-6.4	7.3E-09	8.7	4.4E-05	-0.7	6.0E-01	-0.2	6.6E-01
ENSMUST00000042246	SHC (Src homology 2 domain containing) family, member 4 [Source:MGI Symbol;Acc:MGI:2655364]		Q6S5L9	8.7	1.1E-04	6.4	2.1E-04	-0.6	6.3E-01	-1.0	1.4E-01
ENSMUST00000042251	required for meiotic nuclear division 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913334]		Q8CI78	1.8	1.4E-02	-0.6	2.5E-01	0.5	2.0E-01	0.1	8.5E-01
ENSMUST00000042261	solute carrier family 2 (facilitated glucose transporter), member 12 [Source:MGI Symbol;Acc:MGI:3052471]	B2RRB2	Q8BFW9	6.8	1.2E-04	5.9	1.9E-04	0.6	5.3E-01	-0.3	5.9E-01
ENSMUST00000041759	HMG box domain containing 4 [Source:MGI Symbol;Acc:MGI:1918073]	Q80Y32		4.9	4.2E-02	-1.4	6.1E-01	-3.5	1.4E-01	2.8	2.6E-01
ENSMUST00000042275	inositol polyphosphate-5-phosphatase D [Source:MGI Symbol;Acc:MGI:107357]		Q9ES52	-7.8	2.2E-03	3.1	8.1E-03	-4.1	5.1E-03	-0.5	5.0E-01
ENSMUST00000042281	dehydrogenase/reductase (SDR family) member 7B [Source:MGI Symbol;Acc:MGI:2384931]	I7DM66	Q99J47	-4.5	1.1E-03	-2.3	3.2E-03	0.8	3.7E-02	-0.1	8.6E-01
ENSMUST00000041769	dynein, cytoplasmic 1 light intermediate chain 2 [Source:MGI Symbol;Acc:MGI:107738]		Q6PDL0	-1.2	4.2E-02	-1.0	1.7E-01	0.3	4.8E-01	0.1	8.8E-01
ENSMUST00000042286	formin-like 1 [Source:MGI Symbol;Acc:MGI:1888994]		Q9JL26	-9.9	4.6E-05	8.9	5.9E-05	-0.7	6.1E-01	-0.1	8.9E-01
ENSMUST00000042288	ankyrin repeat and SOCS box-containing 13 [Source:MGI Symbol;Acc:MGI:2145525]		Q8VBX0	4.9	8.6E-05	4.1	1.5E-04	0.0	9.6E-01	0.0	9.2E-01
ENSMUST00000042290	inter-alpha trypsin inhibitor, heavy chain 2 [Source:MGI Symbol;Acc:MGI:96619]	G3X977		6.7	1.2E-04	0.0	9.5E-01	1.6	9.0E-03	-1.5	4.9E-02
ENSMUST00000042299	otassium voltage-gated channel, subfamily H (eag-related), member 5 [Source:MGI Symbol;Acc:MGI:358450		Q920E3	6.3	5.8E-05	-1.2	7.9E-02	0.0	9.2E-01	0.0	9.4E-01
ENSMUST00000041783	IQ motif containing E [Source:MGI Symbol;Acc:MGI:1921489]		Q6PCQ0	0.5	4.4E-01	2.3	1.3E-02	0.7	2.8E-01	-1.1	1.1E-01
ENSMUST00000042312	TRAF type zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1923551]		Q3UDK1	-6.5	3.3E-04	-0.2	6.9E-01	1.4	3.2E-03	0.3	5.2E-01
ENSMUST00000042318	fibronectin type III and SPRY domain containing 2 [Source:MGI Symbol;Acc:MGI:2444310]			7.9	1.3E-05	-1.7	1.3E-01	1.0	1.5E-01	-1.8	1.3E-01
ENSMUST00000042334	ribosomal protein L10A [Source:MGI Symbol;Acc:MGI:1343877]	Q5XJF6		-5.5	2.7E-03	-6.2	3.5E-05	-0.2	6.6E-01	0.4	6.5E-01
ENSMUST00000042344	RIKEN cDNA 4930556J24 gene [Source:MGI Symbol;Acc:MGI:1922592]	Q9D4U7		5.4	4.6E-04	-1.7	4.3E-02	-0.3	5.2E-01	-0.7	3.6E-01
ENSMUST00000041830	N-terminal Xaa-Pro-Lys N-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1913867]		Q8R2U4	1.2	9.6E-02	2.1	2.8E-02	0.6	3.9E-01	-0.3	6.8E-01
ENSMUST00000042345	catenin (cadherin associated protein), alpha 1 [Source:MGI Symbol;Acc:MGI:88274]	Q545R0	P26231	-3.1	5.8E-05	7.1	2.3E-04	-0.1	9.6E-01	-1.0	1.8E-01
ENSMUST00000042352	zinc finger, matrin type 4 [Source:MGI Symbol;Acc:MGI:2443497]		Q8BZ94	6.7	9.9E-05	-2.7	5.1E-02	-0.6	4.1E-01	-1.5	2.5E-01
ENSMUST00000042365	cyclin-dependent kinase 13 [Source:MGI Symbol;Acc:MGI:1916812]		Q69ZA1	-1.9	5.0E-03	-1.4	7.0E-02	0.7	1.9E-01	0.5	5.0E-01
ENSMUST00000042373	Shc SH2-domain binding protein 1-like [Source:MGI Symbol;Acc:MGI:1919086]		Q3TTP0	3.4	7.3E-03	7.5	3.9E-05	-0.6	6.1E-01	0.0	9.6E-01
ENSMUST00000041865	nitric oxide synthase trafficker [Source:MGI Symbol;Acc:MGI:3606242]		Q6WKZ7	1.6	1.1E-01	-0.5	6.1E-01	-2.8	7.6E-03	-0.7	4.3E-01
ENSMUST00000042390	mannosidase, alpha, class 1B, member 1 [Source:MGI Symbol;Acc:MGI:2684954]		A2AJ15	-3.1	2.2E-04	-2.5	2.2E-01	0.9	4.6E-01	-0.6	7.8E-01
ENSMUST00000042391	ferredoxin-fold anticodon binding domain containing 1 [Source:MGI Symbol;Acc:MGI:3584513]		Q3UY23	4.9	1.9E-06	7.5	7.7E-05	-0.6	5.9E-01	-0.6	3.4E-01
ENSMUST00000041874	N-acetylneuraminate pyruvate lyase [Source:MGI Symbol;Acc:MGI:1921341]		Q9DCJ9	0.1	8.4E-01	-1.4	9.0E-02	-2.0	5.9E-03	-0.5	5.0E-01
ENSMUST00000041882	RIKEN cDNA 1600002K03 gene [Source:MGI Symbol;Acc:MGI:1917020]		Q9DAZ5	-1.2	1.3E-01	-0.7	4.4E-01	0.1	8.5E-01	-0.4	6.7E-01
ENSMUST00000042412	hairy/enhancer-of-split related with YRPW motif 1 [Source:MGI Symbol;Acc:MGI:1341800]	Q9QUM5		6.3	1.1E-04	-5.3	9.6E-04	1.9	1.9E-03	0.5	6.8E-01
ENSMUST00000041892	WD repeat domain 19 [Source:MGI Symbol;Acc:MGI:2443231]		Q3UGF1	0.9	7.3E-02	1.4	4.9E-02	0.2	6.6E-01	-0.2	6.8E-01
ENSMUST00000042438	in homology domain containing, family G (with RhoGef domain) member 1 [Source:MGI Symbol;Acc:MGI:2(	Q3UX37		5.3	1.4E-02	-2.5	2.9E-03	0.7	7.9E-02	0.0	9.5E-01
ENSMUST00000042470	zinc finger with KRAB and SCAN domains 2 [Source:MGI Symbol;Acc:MGI:2444060]	G3X952		8.0	1.2E-05	-2.3	2.6E-03	0.2	5.8E-01	0.5	4.2E-01
ENSMUST00000041913	family with sequence similarity 189, member B [Source:MGI Symbol;Acc:MGI:1915771]		Q5HZJ5	0.5	8.3E-01	1.0	7.8E-01	0.4	8.6E-01	-0.1	9.8E-01
ENSMUST00000041944	potassium inwardly-rectifying channel, subfamily J, member 12 [Source:MGI Symbol;Acc:MGI:108495]	B1ATI1		4.6	9.4E-02	6.9	3.0E-02	-0.2	9.4E-01	-2.5	1.3E-01
ENSMUST00000042477	vacuolar protein sorting 25 (yeast) [Source:MGI Symbol;Acc:MGI:106354]		Q9CQ80	-7.0	2.9E-05	-6.5	1.3E-04	0.0	9.2E-01	-1.0	4.1E-01
ENSMUST00000042493	coiled-coil domain containing 115 [Source:MGI Symbol;Acc:MGI:1916918]		Q8VE99	-2.2	6.8E-04	-6.3	1.3E-04	0.6	8.4E-02	-0.6	5.9E-01
ENSMUST00000042497	NADH dehydrogenase (ubiquinone) flavoprotein 1 [Source:MGI Symbol;Acc:MGI:107851]		Q91YT0	-3.9	1.4E-02	1.5	2.9E-02	-0.1	8.3E-01	0.1	8.6E-01
ENSMUST00000042498	high density lipoprotein (HDL) binding protein [Source:MGI Symbol;Acc:MGI:99256]	Q3U4Z7	Q8VDJ3	-8.2	3.0E-06	-0.2	8.0E-01	1.3	5.9E-02	-0.6	5.4E-01
ENSMUST00000042503	USP6 N-terminal like [Source:MGI Symbol;Acc:MGI:2138893]		Q80XC3	4.0	3.3E-02	2.6	5.5E-03	-0.7	3.2E-01	0.9	1.4E-01
ENSMUST00000041984	A kinase (PRKA) anchor protein 7 [Source:MGI Symbol;Acc:MGI:1859150]		Q7TN79	-1.2	3.0E-01	-1.4	3.2E-01	-0.8	4.2E-01	-0.6	6.4E-01
ENSMUST00000041987	dicer 1, ribonuclease type III [Source:MGI Symbol;Acc:MGI:2177178]	F8VQ54		0.2	6.4E-01	1.1	4.8E-02	0.6	1.4E-01	-0.3	4.8E-01
ENSMUST00000042512	antigenic determinant of rec-A protein [Source:MGI Symbol;Acc:MGI:96676]		Q8K339	-4.6	7.5E-05	-2.5	1.2E-01	-4.6	1.4E-03	5.2	4.4E-03
ENSMUST00000042517	family with sequence similarity 169, member A [Source:MGI Symbol;Acc:MGI:2444268]		Q5XG69	6.3	2.1E-02	-1.7	2.3E-02	0.4	3.2E-01	0.2	7.7E-01
ENSMUST00000042530	guanylate cyclase 2f [Source:MGI Symbol;Acc:MGI:105119]		Q5SDA5	6.3	7.8E-05	7.0	6.2E-05	-0.5	6.3E-01	0.1	9.0E-01
ENSMUST00000042546	anoctamin 10 [Source:MGI Symbol;Acc:MGI:2143103]		Q8BH79	-3.5	9.1E-05	2.5	1.3E-03	-5.9	4.4E-05	-0.3	5.7E-01
ENSMUST00000042035	adhesion G protein-coupled receptor B1 [Source:MGI Symbol;Acc:MGI:1933736]		Q3UHD1	3.8	6.9E-02	4.9	3.5E-02	-0.5	8.0E-01	-1.6	2.8E-01
ENSMUST00000042553	alpha-1,4-N-acetylglucosaminyltransferase [Source:MGI Symbol;Acc:MGI:2143261]	Q14BT6		6.9	7.7E-05	6.1	4.0E-04	-1.5	2.5E-01	-0.7	3.3E-01
ENSMUST00000042556	PWP2 periodic tryptophan protein homolog (yeast) [Source:MGI Symbol;Acc:MGI:1341200]	Q2M1K2	Q8BU03	1.4	2.6E-02	2.2	8.1E-03	-6.4	1.2E-04	-0.2	7.2E-01
ENSMUST00000042575	topoisomerase I binding, arginine/serine-rich [Source:MGI Symbol;Acc:MGI:2146189]		Q80Z37	-2.3	3.6E-03	-7.0	1.3E-02	0.5	5.9E-01	1.9	4.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000042581	RIKEN cDNA 6430571L13 gene [Source:MGI Symbol;Acc:MGI:2445137]	Q14AT3	Q8BGK9	6.3	2.1E-05	5.5	1.2E-03	0.0	9.8E-01	0.9	2.5E-01
ENSMUST00000042587	paired-like homeodomain transcription factor 2 [Source:MGI Symbol;Acc:MGI:109340]	Q6DIA6	P97474	6.8	3.2E-03	-6.4	5.4E-03	1.3	1.2E-01	0.1	9.6E-01
ENSMUST00000042601	DEAH (Asp-Glu-Ala-His) box polypeptide 38 [Source:MGI Symbol;Acc:MGI:1927617]	Q80X98		-3.5	8.5E-05	-2.1	1.4E-01	1.0	2.0E-01	-3.8	3.5E-02
ENSMUST00000042603	inhibin beta-A [Source:MGI Symbol;Acc:MGI:96570]	Q3UY39	Q04998	4.9	1.0E-03	8.0	9.3E-06	-1.2	2.5E-01	0.0	9.8E-01
ENSMUST00000042608	adrenocortical dysplasia [Source:MGI Symbol;Acc:MGI:87873]	B2RS36	Q5EE38	-2.0	9.3E-03	3.0	8.8E-03	-0.4	6.6E-01	-0.1	9.1E-01
ENSMUST00000042614	predicted gene 15800 [Source:MGI Symbol;Acc:MGI:3647820]	E9Q2E4		1.3	8.0E-03	8.6	2.5E-05	-0.4	7.1E-01	-0.4	3.9E-01
ENSMUST00000042081	complement component 3a receptor 1 [Source:MGI Symbol;Acc:MGI:1097680]	Q5U7A4	O09047	2.1	3.5E-02	-1.4	2.0E-01	-3.0	4.1E-03	0.5	6.1E-01
ENSMUST00000042084	G elongation factor, mitochondrial 2 [Source:MGI Symbol;Acc:MGI:2444783]		Q8R2Q4	-4.2	1.1E-01	-1.3	6.9E-01	1.8	4.1E-01	-1.1	7.3E-01
ENSMUST00000042092	cadherin-like 26 [Source:MGI Symbol;Acc:MGI:2685856]		P59862	1.9	2.0E-01	5.7	3.4E-03	-0.3	8.3E-01	-4.1	4.3E-03
ENSMUST00000042646	atonal homolog 8 (Drosophila) [Source:MGI Symbol;Acc:MGI:1918343]		Q99NA2	6.0	2.4E-04	5.2	6.6E-04	5.4	2.6E-04	-1.4	4.3E-02
ENSMUST00000042647	in homology domain containing, family G (with RhoGef domain) member 6 [Source:MGI Symbol;Acc:MGI:2(		Q8R0J1	2.0	1.9E-02	9.4	5.5E-05	-0.3	8.6E-01	-0.5	3.9E-01
ENSMUST00000042661	tweety homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925589]		Q6P5F7	-4.0	1.5E-04	-2.6	2.2E-01	0.6	6.2E-01	-0.6	7.7E-01
ENSMUST00000042664	olute carrier family 16 (monocarboxylic acid transporters), member 2 [Source:MGI Symbol;Acc:MGI:1203732	Q05BA2	O70324	5.7	7.4E-04	6.7	5.8E-04	-0.7	6.1E-01	-0.8	3.1E-01
ENSMUST00000042121	histocompatibility 2, class II, locus DMa [Source:MGI Symbol;Acc:MGI:95921]	Q31621		-1.4	1.7E-01	-1.0	3.8E-01	-0.2	7.8E-01	-0.5	6.5E-01
ENSMUST00000042665	poly (ADP-ribose) polymerase family, member 14 [Source:MGI Symbol;Acc:MGI:1919489]		Q2EMV9	-1.7	2.6E-02	-5.4	2.2E-03	-0.3	6.2E-01	0.8	5.8E-01
ENSMUST00000042675	capping protein (actin filament) muscle Z-line, beta [Source:MGI Symbol;Acc:MGI:104652]	A2AMW0		-8.2	2.1E-02	4.6	2.2E-04	0.0	9.5E-01	0.4	4.9E-01
ENSMUST00000042135	RAS p21 protein activator 4 [Source:MGI Symbol;Acc:MGI:1858600]		Q6PFQ7	0.4	8.2E-01	-2.3	3.8E-01	-2.1	2.4E-01	0.6	8.0E-01
ENSMUST00000042699	aldehyde dehydrogenase 8 family, member A1 [Source:MGI Symbol;Acc:MGI:2653900]		Q8BH00	7.2	2.2E-03	-4.5	1.9E-02	-0.3	6.6E-01	-1.0	5.6E-01
ENSMUST00000042701	Max dimerization protein 4 [Source:MGI Symbol;Acc:MGI:104991]	Q91VN7		-2.3	3.1E-04	-3.9	6.6E-03	1.1	6.4E-02	-1.1	4.0E-01
ENSMUST00000042147	nucleolar complex associated 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2140843]		Q8BHY2	-0.6	1.9E-01	-0.6	3.3E-01	0.4	3.2E-01	0.4	5.0E-01
ENSMUST00000042702	family with sequence similarity 173, member B [Source:MGI Symbol;Acc:MGI:1915323]		Q9D1Z3	-3.1	1.5E-02	-2.6	1.8E-03	-1.3	8.5E-03	-0.4	5.4E-01
ENSMUST00000042706	nuclear receptor subfamily 0, group B, member 2 [Source:MGI Symbol;Acc:MGI:1346344]		Q62227	6.2	1.5E-04	6.3	1.7E-03	-0.1	9.6E-01	-0.1	8.7E-01
ENSMUST00000042161	mannoside acetylglucosaminyltransferase 4, isoenzyme A [Source:MGI Symbol;Acc:MGI:2662992]		Q812G0	-2.2	1.8E-01	-2.4	2.6E-01	0.0	9.7E-01	0.2	9.3E-01
ENSMUST00000042163	N(alpha)-acetyltransferase 25, NatB auxiliary subunit [Source:MGI Symbol;Acc:MGI:2442563]	B2RQV1	Q8BWZ3	0.4	5.2E-01	0.7	3.8E-01	-0.9	2.0E-01	-1.2	1.5E-01
ENSMUST00000042710	small integral membrane protein 3 [Source:MGI Symbol;Acc:MGI:1917088]	Q3U1M0	Q99PE5	-4.4	4.8E-06	-4.8	6.7E-05	-0.1	7.1E-01	0.4	5.9E-01
ENSMUST00000042167	carboxypeptidase Q [Source:MGI Symbol;Acc:MGI:1889205]		Q9WVJ3	-0.5	4.5E-01	-4.0	2.7E-03	-2.1	3.9E-03	1.3	1.9E-01
ENSMUST00000042717	tripartite motif-containing 39 [Source:MGI Symbol;Acc:MGI:1890659]	E9QLN4		-5.4	1.6E-02	5.9	5.0E-02	-0.6	8.3E-01	2.0	2.1E-01
ENSMUST00000042724	ubiquitin specific peptidase 38 [Source:MGI Symbol;Acc:MGI:1922091]		Q8BW70	-2.3	5.8E-04	-5.1	9.9E-04	0.6	2.3E-01	-0.9	4.3E-01
ENSMUST00000042726	RNA binding motif protein 42 [Source:MGI Symbol;Acc:MGI:1915285]		Q91V81	-4.8	1.4E-03	-0.2	7.7E-01	1.0	2.7E-02	0.1	9.2E-01
ENSMUST00000042740	ATP-binding cassette, sub-family A (ABC1), member 13 [Source:MGI Symbol;Acc:MGI:2388707]		Q5SSE9	-2.5	3.9E-05	5.8	8.0E-05	-1.8	8.2E-02	0.4	4.8E-01
ENSMUST00000042203	WD repeat domain 5B [Source:MGI Symbol;Acc:MGI:1916794]		Q9D7H2	-1.3	4.8E-02	-0.6	4.0E-01	0.2	6.6E-01	-0.5	5.2E-01
ENSMUST00000042747	neuropeptide Y receptor Y6 [Source:MGI Symbol;Acc:MGI:1098590]		Q61212	5.8	8.8E-04	7.3	5.1E-05	-0.6	6.0E-01	-0.6	3.2E-01
ENSMUST00000042220	NLR family, apoptosis inhibitory protein 6 [Source:MGI Symbol;Acc:MGI:1298222]		Q9JIB6	4.2	1.9E-01	3.9	1.4E-01	-4.1	2.0E-01	-3.8	7.8E-02
ENSMUST00000042750	transmembrane protein 246 [Source:MGI Symbol;Acc:MGI:1914313]		Q91YV9	5.2	5.9E-05	-4.2	4.3E-03	0.6	2.6E-01	0.2	8.7E-01
ENSMUST00000042754	parathyroid hormone 2 [Source:MGI Symbol;Acc:MGI:2152297]		Q91W27	5.5	9.7E-03	-7.0	3.8E-08	-0.5	3.7E-02	0.1	8.3E-01
ENSMUST00000042766	protein phosphatase 1K (PP2C domain containing) [Source:MGI Symbol;Acc:MGI:2442111]	B9EHW0	Q8BXN7	3.2	1.8E-04	6.9	1.1E-03	-0.6	6.9E-01	1.2	1.7E-01
ENSMUST00000042767	SLIT and NTRK-like family, member 5 [Source:MGI Symbol;Acc:MGI:2679448]		Q810B7	8.6	9.9E-06	1.2	1.4E-01	-0.3	6.4E-01	0.3	6.5E-01
ENSMUST00000042771	strawberry notch homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2448490]		Q7TNB8	-5.2	6.3E-05	6.4	9.3E-04	-0.4	7.6E-01	0.0	9.9E-01
ENSMUST00000042775	neuralized E3 ubiquitin protein ligase 2 [Source:MGI Symbol;Acc:MGI:3043305]	A2A5J5		2.8	3.4E-03	-4.8	1.1E-02	0.6	4.9E-01	-2.4	2.6E-01
ENSMUST00000042790	heat shock protein 2 [Source:MGI Symbol;Acc:MGI:1916503]		Q99PR8	5.9	1.2E-04	-4.8	4.0E-03	-0.3	5.4E-01	-0.1	9.5E-01
ENSMUST00000042792	sodium channel, voltage-gated, type VII, alpha [Source:MGI Symbol;Acc:MGI:102965]	B1AYL1		8.6	2.0E-05	-5.5	1.2E-03	1.5	1.8E-02	-2.9	8.9E-02
ENSMUST00000042808	scavenger receptor class F, member 1 [Source:MGI Symbol;Acc:MGI:2449455]		Q5ND28	7.3	1.9E-02	4.0	5.9E-04	-1.2	1.6E-01	-0.3	5.3E-01
ENSMUST00000042824	the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 [Source:MGI Symbo	E9PZP8		-2.2	8.1E-04	3.8	1.0E-03	-3.9	3.9E-03	-0.9	1.6E-01
ENSMUST00000042296	quaking [Source:MGI Symbol;Acc:MGI:97837]		Q9QYS9	0.0	9.9E-01	1.1	1.2E-01	1.2	3.5E-02	0.1	8.1E-01
ENSMUST00000042834	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Source:MGI Symbol;Acc:MGI:1913944]		Q9CR68	-4.4	9.8E-06	5.6	2.0E-04	-1.2	2.6E-01	-0.4	4.9E-01
ENSMUST00000042302	CD84 antigen [Source:MGI Symbol;Acc:MGI:1336885]			-3.0	4.9E-01	-4.6	4.0E-01	-1.9	4.5E-01	-0.3	9.6E-01
ENSMUST00000042844	neuroblastoma, suppression of tumorigenicity 1 [Source:MGI Symbol;Acc:MGI:104591]		Q61477	3.7	5.8E-04	-5.8	4.7E-03	0.9	1.2E-01	0.2	9.1E-01
ENSMUST00000042850	i, von Willebrand factor type A, EGF and pentraxin domain containing 1 [Source:MGI Symbol;Acc:MGI:1928		A2AVA0	3.2	3.8E-04	7.7	3.3E-05	-0.5	6.5E-01	-0.3	5.2E-01
ENSMUST00000042852	family with sequence similarity 210, member A [Source:MGI Symbol;Acc:MGI:1914000]		Q8BGY7	1.8	3.0E-03	-5.9	7.1E-03	-1.0	2.4E-01	-0.6	7.3E-01
ENSMUST00000042857	special AT-rich sequence binding protein 2 [Source:MGI Symbol;Acc:MGI:2679336]		Q8VI24	7.9	2.8E-04	5.8	1.1E-03	0.7	5.7E-01	0.3	6.9E-01
ENSMUST00000042861	syntaxin 11 [Source:MGI Symbol;Acc:MGI:1921982]	Q3U5V8		-5.4	6.9E-05	-2.2	2.9E-03	0.4	2.0E-01	-0.5	3.9E-01
ENSMUST00000042868	calcium/calmodulin-dependent protein kinase IV [Source:MGI Symbol;Acc:MGI:88258]	Q8BGR3		4.9	4.8E-06	6.9	1.5E-04	-0.5	6.8E-01	-0.7	2.5E-01
ENSMUST00000042901	structural maintenance of chromosomes 4 [Source:MGI Symbol;Acc:MGI:1917349]		Q8CG47	-5.2	1.5E-02	-1.5	6.6E-02	1.0	4.6E-02	0.6	4.2E-01
ENSMUST00000042917	regulating synaptic membrane exocytosis 2 [Source:MGI Symbol;Acc:MGI:2152972]	D9HP81		6.6	2.5E-02	3.6	6.2E-03	-1.1	3.3E-01	-1.2	1.5E-01
ENSMUST00000042942	Sec23 interacting protein [Source:MGI Symbol;Acc:MGI:2450915]	G3X928		-1.7	3.2E-03	-1.8	2.2E-02	0.9	3.9E-02	-0.4	5.8E-01
ENSMUST00000042944	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3 [Source:MGI Symbol;Acc:MGI:2147274]		Q8R5G7	-4.1	3.8E-04	5.1	6.4E-06	0.2	7.1E-01	0.0	9.6E-01
ENSMUST00000042399				0.8	1.5E-01	1.3	1.0E-01	0.6	3.3E-01	0.1	9.0E-01
ENSMUST00000042402	pogo transposable element with ZNF domain [Source:MGI Symbol;Acc:MGI:2442117]	Q0VGT3		-2.2	1.6E-01	-1.3	5.3E-01	0.4	7.8E-01	-0.5	7.8E-01
ENSMUST00000042405	fibrillarin [Source:MGI Symbol;Acc:MGI:95486]		P35550	-0.6	3.6E-01	-0.5	5.0E-01	-0.4	4.9E-01	-0.4	5.5E-01
ENSMUST00000042953	neuroblastoma amplified sequence [Source:MGI Symbol;Acc:MGI:1918419]	E9Q411		1.7	4.4E-03	5.2	7.2E-04	-0.9	4.2E-01	0.2	7.4E-01
ENSMUST00000042954	DNA polymerase N [Source:MGI Symbol;Acc:MGI:2675617]			4.5	4.6E-04	5.6	1.7E-02	-1.3	5.1E-01	-1.7	2.4E-01
ENSMUST00000042450	RMI1, RecQ mediated genome instability 1 [Source:MGI Symbol;Acc:MGI:1921636]		Q9D4G9	-1.0	5.4E-02	-0.3	5.6E-01	0.6	1.7E-01	0.0	9.4E-01
ENSMUST00000042452	proteasome (prosome, macropain) inhibitor subunit 1 [Source:MGI Symbol;Acc:MGI:1346072]	A2AU35	Q8BHL8	1.9	3.6E-01	3.7	1.6E-01	-0.2	9.3E-01	-2.1	2.7E-01
ENSMUST00000042468	RIKEN cDNA 1110032A03 gene [Source:MGI Symbol;Acc:MGI:1915971]		Q9D131	1.5	9.1E-02	0.3	8.0E-01	-0.3	6.7E-01	0.9	3.8E-01
ENSMUST00000042957	keratin 75 [Source:MGI Symbol;Acc:MGI:1923500]		Q8BGZ7	5.3	2.4E-04	7.4	4.7E-05	-0.6	6.2E-01	0.0	1.0E+00
ENSMUST00000042471	DIS3 mitotic control homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919912]		Q9CSH3	0.3	6.1E-01	0.6	4.0E-01	-0.4	4.7E-01	-0.7	3.0E-01
ENSMUST00000042970	potassium inwardly-rectifying channel, subfamily J, member 2 [Source:MGI Symbol;Acc:MGI:104744]	Q543W5	P35561	-1.3	1.2E-02	-7.7	6.9E-04	0.5	3.0E-01	1.1	4.8E-01
ENSMUST00000042485	expressed sequence AW551984 [Source:MGI Symbol;Acc:MGI:2143322]	Q8BGF0		5.7	5.2E-02	5.2	1.0E-01	-0.7	8.3E-01	-0.1	9.5E-01
ENSMUST00000042972	Rab interacting lysosomal protein [Source:MGI Symbol;Acc:MGI:2144271]	Q14AQ2	Q5ND29	8.0	3.1E-04	-1.9	8.5E-03	0.3	3.2E-01	0.0	9.6E-01
ENSMUST00000042974	eva-1 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:2385247]		Q91WM6	6.2	1.7E-04	-6.0	2.2E-02	0.0	9.7E-01	2.0	3.9E-01
ENSMUST00000042975	transmembrane protein 30B [Source:MGI Symbol;Acc:MGI:2442082]	Q0VEI2	Q8BHG3	7.0	1.7E-04	-8.5	2.1E-05	-0.1	6.2E-01	0.2	8.4E-01
ENSMUST00000042986	phospholipase C-like 1 [Source:MGI Symbol;Acc:MGI:3036262]		Q3USB7	6.7	2.7E-04	1.6	4.6E-01	-1.3	4.6E-01	1.2	5.2E-01
ENSMUST00000042506	small G protein signaling modulator 3 [Source:MGI Symbol;Acc:MGI:1916329]	F8WIA4		2.7	2.5E-01	3.6	3.9E-01	3.2	3.2E-01	2.2	5.0E-01
ENSMUST00000042509	diphosphoinositol pentakisphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:2142810]		Q6ZQB6	-0.2	8.5E-01	0.0	9.9E-01	0.9	4.6E-01	0.6	6.9E-01
ENSMUST00000042990	serpine1 mRNA binding protein 1 [Source:MGI Symbol;Acc:MGI:1914120]		Q9CY58	-4.3	4.4E-05	-4.1	7.0E-04	-0.4	3.8E-01	-0.9	3.1E-01
ENSMUST00000042993	galectin-related inter-fiber protein [Source:MGI Symbol;Acc:MGI:1925248]		Q9D1U0	7.3	2.9E-05	2.9	3.4E-01	-0.9	7.5E-01	2.5	3.0E-01
ENSMUST00000043011	family with sequence similarity 198, member A [Source:MGI Symbol;Acc:MGI:3041196]		Q3UY90	8.0	2.4E-05	6.8	3.6E-04	0.6	6.4E-01	0.1	9.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000042534	coiled-coil domain containing 85A [Source:MGI Symbol;Acc:MGI:2445069]		Q5SP85	4.4	9.6E-02	3.4	2.1E-01	-0.6	8.4E-01	0.5	7.7E-01
ENSMUST00000043045	WD repeat domain 45 [Source:MGI Symbol;Acc:MGI:1859606]		Q91VM3	-7.7	7.9E-06	-2.0	1.9E-02	1.6	3.4E-03	0.1	9.3E-01
ENSMUST00000043050	carbohydrate sulfotransferase 12 [Source:MGI Symbol;Acc:MGI:1929064]		Q99LL3	-3.8	8.6E-04	6.6	2.1E-04	-0.6	6.4E-01	-0.3	6.7E-01
ENSMUST00000043056	bile acid-Coenzyme A: amino acid N-acyltransferase [Source:MGI Symbol;Acc:MGI:106642]		Q91X34	5.0	2.2E-02	2.0	1.5E-02	0.1	8.5E-01	-0.5	3.9E-01
ENSMUST00000042561	solute carrier family 43, member 2 [Source:MGI Symbol;Acc:MGI:2442746]		Q8CGA3	-2.7	1.8E-01	-0.7	7.3E-01	0.5	7.2E-01	-1.4	5.1E-01
ENSMUST00000042564	growth hormone inducible transmembrane protein [Source:MGI Symbol;Acc:MGI:1913342]		Q91VC9	2.5	3.2E-01	0.9	7.2E-01	-3.0	2.2E-01	-1.4	5.5E-01
ENSMUST00000043058	serine (or cysteine) peptidase inhibitor, clade A, member 3K [Source:MGI Symbol;Acc:MGI:98377]			4.8	1.2E-02	-1.7	5.1E-02	0.4	3.9E-01	-0.2	7.7E-01
ENSMUST00000043059	in, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A [Source:MGI Symbol;Acc:MG		Q9QUR8	2.3	5.6E-03	6.7	1.1E-04	0.3	7.5E-01	0.0	9.5E-01
ENSMUST00000042586	thymocyte expressed, positive selection associated 1 [Source:MGI Symbol;Acc:MGI:1914846]		Q3U132	0.8	3.3E-01	-1.2	2.2E-01	-1.7	3.7E-02	0.2	8.0E-01
ENSMUST00000043061	family with sequence similarity 159, member B [Source:MGI Symbol;Acc:MGI:1925053]		Q9D1Y9	4.7	8.9E-04	3.5	8.6E-02	-1.6	3.9E-01	1.6	2.7E-01
ENSMUST00000042594	encephalic leukoencephalopathy with subcortical cysts 1 homolog (human) [Source:MGI Symbol;Acc:MGI:215		Q8VHK5	4.5	2.0E-01	4.9	2.0E-01	-0.3	9.5E-01	-0.7	7.6E-01
ENSMUST00000043062	acyl-CoA synthetase bubblegum family member 2 [Source:MGI Symbol;Acc:MGI:3587728]		Q2XU92	6.7	3.2E-05	-2.1	7.5E-03	0.8	5.0E-02	-0.5	4.5E-01
ENSMUST00000043069	cytohesin 4 [Source:MGI Symbol;Acc:MGI:2441702]	Q3U0C0	Q80YW0	-5.1	5.2E-06	4.0	6.5E-03	-0.9	4.1E-01	0.0	1.0E+00
ENSMUST00000043074	is-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) [Source:MGI Symbol;Acc:M	Q642K5		-5.0	4.2E-03	-0.3	6.7E-01	1.3	3.5E-02	-0.3	6.6E-01
ENSMUST00000042610	expressed sequence AI607873 [Source:MGI Symbol;Acc:MGI:2138302]	E9Q3L4		-2.8	7.5E-02	-5.3	2.0E-02	-1.3	2.1E-01	1.2	5.4E-01
ENSMUST00000043077	thyroid hormone responsive [Source:MGI Symbol;Acc:MGI:109126]	Q543J4	Q62264	5.6	3.1E-04	2.1	3.3E-03	0.6	1.5E-01	-0.1	7.8E-01
ENSMUST00000042615	Ral GEF with PH domain and SH3 binding motif 1 [Source:MGI Symbol;Acc:MGI:1922008]		A2AR50	0.2	9.3E-01	2.7	3.0E-01	0.7	7.6E-01	-1.8	3.2E-01
ENSMUST00000042617	chloride channel, voltage-sensitive Ka [Source:MGI Symbol;Acc:MGI:1329026]		Q9WUB7	2.1	8.5E-02	6.3	1.7E-04	-0.5	6.4E-01	-4.8	2.4E-04
ENSMUST00000043081	olfactory receptor 11 [Source:MGI Symbol;Acc:MGI:104715]		Q60890	5.8	7.1E-04	6.5	7.1E-04	-0.2	9.1E-01	-0.7	3.7E-01
ENSMUST00000043082	patatin-like phospholipase domain containing 8 [Source:MGI Symbol;Acc:MGI:1914702]		Q8K1N1	-7.4	4.4E-05	2.7	1.7E-02	0.7	3.8E-01	0.0	1.0E+00
ENSMUST00000042658	enoyl Coenzyme A hydratase domain containing 3 [Source:MGI Symbol;Acc:MGI:1915106]		Q9D7J9	-0.3	7.1E-01	0.7	4.7E-01	0.9	2.3E-01	0.0	9.7E-01
ENSMUST00000043089	scleraxis [Source:MGI Symbol;Acc:MGI:102934]	Q53ZC3	Q64124	5.0	1.7E-04	-3.0	4.8E-03	0.9	8.5E-02	-0.2	8.3E-01
ENSMUST00000042662	mitotic spindle organizing protein 1 [Source:MGI Symbol;Acc:MGI:1924039]		Q8BUR9	0.8	3.6E-02	1.1	3.7E-02	0.4	2.6E-01	0.1	7.1E-01
ENSMUST00000043098	growth arrest and DNA-damage-inducible 45 alpha [Source:MGI Symbol;Acc:MGI:107799]	Q3UMH6	P48316	-6.5	4.2E-04	5.3	2.2E-03	-1.6	2.4E-01	-1.2	1.8E-01
ENSMUST00000043108	zinc finger, GRF-type containing 1 [Source:MGI Symbol;Acc:MGI:1918893]		Q0VGT4	3.1	1.3E-04	-1.5	1.2E-01	0.5	4.2E-01	0.3	7.7E-01
ENSMUST00000042666	solute carrier family 39 (metal ion transporter), member 5 [Source:MGI Symbol;Acc:MGI:1919336]		Q9D856	4.8	8.1E-02	5.1	8.0E-02	-1.3	6.7E-01	-1.6	3.3E-01
ENSMUST00000043111	EGF-like repeats and discoidin I-like domains 3 [Source:MGI Symbol;Acc:MGI:1329025]	Q8C4U8		5.0	4.1E-03	4.2	3.9E-01	11.1	1.8E-02	-1.3	7.3E-01
ENSMUST00000042692	t-complex protein 11 [Source:MGI Symbol;Acc:MGI:98544]	B2KF25		0.7	7.4E-01	7.3	1.8E-02	2.8	2.9E-01	-3.9	4.9E-02
ENSMUST00000043126	nuclear receptor coactivator 6 [Source:MGI Symbol;Acc:MGI:1929915]	Q5XJV5		-2.5	7.3E-03	5.4	9.1E-03	-1.2	5.0E-01	0.6	6.3E-01
ENSMUST00000043138	inositol polyphosphate-5-phosphatase F [Source:MGI Symbol;Acc:MGI:2141867]	B2RQ14	Q8CDA1	-3.3	5.6E-03	-1.7	8.5E-03	0.5	1.4E-01	-0.1	8.9E-01
ENSMUST00000043141	HYDIN, axonemal central pair apparatus protein [Source:MGI Symbol;Acc:MGI:2389007]		Q80W93	10.6	1.3E-06	-1.4	2.3E-01	0.1	9.5E-01	-1.7	1.8E-01
ENSMUST00000043148	guanine nucleotide binding protein (G protein), gamma 12 [Source:MGI Symbol;Acc:MGI:1336171]		Q9DAS9	-3.2	1.6E-03	6.8	2.1E-04	0.0	9.8E-01	-0.6	3.8E-01
ENSMUST00000043149	GRB2-related adaptor protein 2 [Source:MGI Symbol;Acc:MGI:1333842]	Q3U0E8	O89100	4.0	4.8E-04	-3.2	2.2E-04	0.5	1.2E-01	-0.7	2.2E-01
ENSMUST00000043150	acyl-CoA synthetase long-chain family member 5 [Source:MGI Symbol;Acc:MGI:1919129]	Q3UC67	Q8JZR0	-3.2	1.5E-03	-5.4	8.3E-02	0.8	4.7E-01	0.8	7.9E-01
ENSMUST00000043160	aquarius [Source:MGI Symbol;Acc:MGI:1276102]		Q8CFQ3	-2.8	8.3E-04	-1.8	1.3E-02	0.7	6.1E-02	0.2	6.8E-01
ENSMUST00000043169	apoptosis resistant E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1915747]		Q8CHG5	-4.7	7.2E-04	-2.2	5.2E-02	0.5	4.4E-01	-2.1	1.1E-01
ENSMUST00000042732	F-box protein 45 [Source:MGI Symbol;Acc:MGI:2447775]		Q8K3B1	-1.2	6.7E-02	0.1	9.3E-01	1.1	7.3E-02	-0.2	8.1E-01
ENSMUST00000043183	carboxylesterase 2G [Source:MGI Symbol;Acc:MGI:1919611]	E9PV38		4.7	1.0E-03	-1.1	3.7E-02	1.4	1.0E-03	-0.1	7.8E-01
ENSMUST00000042744	nephronectin [Source:MGI Symbol;Acc:MGI:2148811]		Q91V88	3.8	1.5E-01	-1.3	4.2E-01	-7.7	4.6E-03	-2.6	1.7E-01
ENSMUST00000043200	small ArfGAP 2 [Source:MGI Symbol;Acc:MGI:1917030]		Q7TN29	-5.7	1.2E-05	7.2	3.1E-04	-0.7	6.4E-01	-2.1	2.1E-02
ENSMUST00000043204	F-box protein 33 [Source:MGI Symbol;Acc:MGI:1917861]		Q8VE08	-4.3	3.6E-04	6.5	8.5E-05	0.5	6.3E-01	-0.9	1.4E-01
ENSMUST00000042753	RNA binding motif protein 48 [Source:MGI Symbol;Acc:MGI:2442653]	H9H9R8		-0.1	8.7E-01	-0.4	6.1E-01	-0.4	4.5E-01	-0.2	8.2E-01
ENSMUST00000043208	sine oculis-related homeobox 4 [Source:MGI Symbol;Acc:MGI:106034]		Q61321	8.2	1.9E-05	4.6	3.5E-02	-0.7	7.4E-01	0.2	8.5E-01
ENSMUST00000043209	carboxylesterase 2D, pseudogene [Source:MGI Symbol;Acc:MGI:3704319]			7.7	4.8E-05	3.3	6.7E-04	0.1	9.0E-01	0.0	9.9E-01
ENSMUST00000043214	RAS-related C3 botulinum substrate 2 [Source:MGI Symbol;Acc:MGI:97846]		Q05144	-5.6	2.5E-06	8.2	2.9E-05	-0.6	6.1E-01	-0.2	7.4E-01
ENSMUST00000043235	TIP41, TOR signalling pathway regulator-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915087]		Q8BH58	-1.1	2.7E-02	-3.7	2.8E-03	1.1	4.7E-02	-0.4	7.1E-01
ENSMUST00000043237	transformation related protein 53 inducible nuclear protein 2 [Source:MGI Symbol;Acc:MGI:1915978]		Q8CFU8	-4.0	4.9E-04	2.5	1.1E-02	-0.7	3.3E-01	-0.4	5.2E-01
ENSMUST00000042779	zinc finger and BTB domain containing 1 [Source:MGI Symbol;Acc:MGI:2442326]	Q5YB37	Q91VL9	0.2	4.8E-01	1.3	1.5E-02	0.6	9.7E-02	-0.4	3.2E-01
ENSMUST00000042780	testis expressed gene 2 [Source:MGI Symbol;Acc:MGI:102465]		Q6ZPJ0	-0.3	6.3E-01	0.5	5.0E-01	0.5	3.8E-01	-0.3	6.8E-01
ENSMUST00000043249	mast cell protease 4 [Source:MGI Symbol;Acc:MGI:96940]	Q3UN88		6.3	2.8E-04	4.3	1.1E-03	-1.5	1.4E-01	0.1	8.7E-01
ENSMUST00000043259	phosphodiesterase 3A, cGMP inhibited [Source:MGI Symbol;Acc:MGI:1860764]	B2RR84	Q9Z0X4	8.6	1.4E-06	6.8	1.7E-04	-1.5	2.4E-01	0.3	5.8E-01
ENSMUST00000043266	RIKEN cDNA 4930596D02 gene [Source:MGI Symbol;Acc:MGI:3588288]	Q3V0H9		6.7	1.2E-04	3.4	2.0E-01	-4.6	1.3E-01	-0.7	7.1E-01
ENSMUST00000042818	proviral integration site 3 [Source:MGI Symbol;Acc:MGI:1355297]	Q3TX64	P58750	0.6	3.3E-01	0.6	4.4E-01	0.2	7.0E-01	0.2	7.4E-01
ENSMUST00000043269	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]		P61979	-10.3	1.5E-05	-1.7	1.5E-02	0.3	3.4E-01	-0.1	8.6E-01
ENSMUST00000043273	U2 small nuclear RNA auxiliary factor 1-like 4 [Source:MGI Symbol;Acc:MGI:2678374]		Q8BGJ9	-4.5	4.2E-03	-3.9	2.4E-04	0.8	3.0E-02	0.3	6.2E-01
ENSMUST00000042842	cell adhesion molecule-related/down-regulated by oncogenes [Source:MGI Symbol;Acc:MGI:1926387]		Q32MD9	2.5	1.5E-01	-1.2	4.9E-01	-2.8	9.0E-02	1.0	5.6E-01
ENSMUST00000043283	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]	Q80XR8		-6.2	1.4E-04	0.9	2.4E-01	-3.5	5.0E-04	-0.7	3.2E-01
ENSMUST00000043285	predicted gene 11992 [Source:MGI Symbol;Acc:MGI:3651127]	B2RVL0	Q5SS90	2.7	1.1E-02	5.9	4.2E-05	2.0	2.1E-02	-0.7	2.1E-01
ENSMUST00000043294	ankyrin repeat and SOCS box-containing 4 [Source:MGI Symbol;Acc:MGI:1929751]		Q9WV71	4.2	2.0E-03	1.4	3.3E-02	-0.7	1.8E-01	-0.2	7.2E-01
ENSMUST00000043305	WD and tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGI:2685541]		Q80ZK9	-5.5	4.1E-03	4.5	1.0E-02	-2.5	1.3E-01	0.9	3.2E-01
ENSMUST00000043311	histocompatibility (minor) HA-1 [Source:MGI Symbol;Acc:MGI:1917969]		Q3TBD2	-7.3	2.0E-04	-7.2	1.3E-03	0.6	2.4E-01	2.3	1.6E-01
ENSMUST00000043314	cytochrome P450, family 2, subfamily s, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1921384]		Q9DBX6	-4.3	4.3E-03	4.2	5.5E-05	-0.5	4.2E-01	0.2	6.3E-01
ENSMUST00000042889	SET domain containing 5 [Source:MGI Symbol;Acc:MGI:1920145]		Q5XJV7	1.9	3.6E-01	2.1	2.6E-01	-2.7	1.6E-01	-3.0	1.2E-01
ENSMUST00000043315	serine (or cysteine) peptidase inhibitor, clade A, member 3G [Source:MGI Symbol;Acc:MGI:105046]	F2Z405		-1.9	1.6E-02	-4.2	2.6E-02	-1.6	9.1E-02	-2.7	2.1E-01
ENSMUST00000043333	transcriptional adaptor 3 [Source:MGI Symbol;Acc:MGI:1915724]		Q8R0L9	-6.4	2.3E-04	4.8	1.0E-01	-1.4	6.2E-01	0.4	8.2E-01
ENSMUST00000042923	sirtuin 6 [Source:MGI Symbol;Acc:MGI:1354161]		P59941	-0.5	4.8E-01	-0.2	8.1E-01	1.2	1.1E-01	0.9	3.1E-01
ENSMUST00000043336	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4 [Source:MGI Symbol;Acc:MGI:106018]	Q53WR7	Q64692	-5.9	1.1E-06	-0.8	1.7E-01	0.8	6.7E-02	-0.1	7.9E-01
ENSMUST00000043338	SFT2 domain containing 2 [Source:MGI Symbol;Acc:MGI:1917362]		Q8VD57	-3.8	3.3E-04	-2.7	1.9E-02	1.3	4.5E-02	-0.1	9.0E-01
ENSMUST00000043342	DPH5 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916990]		Q9CWQ0	4.0	1.9E-04	2.6	2.4E-03	0.5	3.4E-01	-0.3	5.4E-01
ENSMUST00000043349	glutamate receptor, ionotropic, delta 1 [Source:MGI Symbol;Acc:MGI:95812]		Q61627	9.6	1.4E-06	5.7	3.7E-04	0.2	8.1E-01	-0.9	1.9E-01
ENSMUST00000043352	transmembrane protein 156 [Source:MGI Symbol;Acc:MGI:2685292]	D3Z447		-4.9	4.0E-04	7.9	5.0E-04	2.5	1.1E-01	-0.1	9.1E-01
ENSMUST00000043359	d, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 [Source:MGI Symbol;Acc		Q91ZW3	-1.8	5.0E-03	-0.5	2.9E-01	0.2	5.1E-01	-0.5	3.3E-01
ENSMUST00000042971	ADP-ribosylation factor-like 5C [Source:MGI Symbol;Acc:MGI:3028577]		Q6P068	0.8	4.9E-01	0.2	8.8E-01	-1.1	3.1E-01	-0.5	6.9E-01
ENSMUST00000043374	protein phosphatase 1, regulatory (inhibitor) subunit 14c [Source:MGI Symbol;Acc:MGI:1923392]		Q8R4S0	4.9	2.4E-05	3.7	2.8E-02	-3.1	7.2E-02	1.2	2.4E-01
ENSMUST00000043378	transmembrane protein 120A [Source:MGI Symbol;Acc:MGI:2686991]		Q8C1E7	-6.1	1.6E-04	5.8	4.9E-04	-0.5	6.9E-01	-0.1	8.5E-01
ENSMUST00000043380	cation channel, sperm associated 1 [Source:MGI Symbol;Acc:MGI:2179947]		Q91ZR5	8.2	2.7E-05	5.7	1.4E-03	-0.5	7.2E-01	0.8	2.7E-01
ENSMUST00000042985	CCAAT/enhancer binding protein (C/EBP), alpha [Source:MGI Symbol;Acc:MGI:99480]		P53566	-1.3	9.0E-02	-1.7	1.2E-01	0.5	4.4E-01	0.8	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000043382	RIKEN cDNA 4930544G11 gene [Source:MGI Symbol;Acc:MGI:1914903]	Q9CR99		4.9	2.8E-03	6.8	7.8E-04	0.2	8.8E-01	0.1	9.3E-01
ENSMUST00000042988	autophagy related 14 [Source:MGI Symbol;Acc:MGI:1261775]		Q8CDJ3	-0.1	7.2E-01	0.6	2.6E-01	1.2	1.3E-02	0.4	4.2E-01
ENSMUST00000043396	yc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) [Source:MGI Symbol;Acc:MGI:97	Q3UII1	P03966	2.9	3.0E-02	-5.2	8.5E-05	-0.8	5.5E-02	0.1	8.6E-01
ENSMUST00000043400	aspartic peptidase, retroviral-like 1 [Source:MGI Symbol;Acc:MGI:1915105]		Q09PK2	-8.4	6.4E-06	5.3	3.1E-04	-2.0	8.5E-02	0.1	9.1E-01
ENSMUST00000043409	zinc finger protein 503 [Source:MGI Symbol;Acc:MGI:1353644]		Q7TMA2	2.8	3.7E-04	8.3	1.9E-04	0.4	7.7E-01	0.1	8.9E-01
ENSMUST00000043042	transmembrane and coiled-coil domains 4 [Source:MGI Symbol;Acc:MGI:1924306]		Q91WU4	-0.8	2.5E-01	0.4	6.4E-01	1.0	1.5E-01	-0.2	7.7E-01
ENSMUST00000043414	DENN/MADD domain containing 3 [Source:MGI Symbol;Acc:MGI:2146009]		A2RT67	-8.4	1.9E-05	-5.9	2.2E-04	0.2	6.0E-01	-1.6	1.7E-01
ENSMUST00000043415	tektin 5 [Source:MGI Symbol;Acc:MGI:1917676]	G5E8A8		6.7	2.9E-04	-1.9	7.7E-02	1.5	2.5E-02	-0.3	7.6E-01
ENSMUST00000043429	nuclear transcription factor-Y gamma [Source:MGI Symbol;Acc:MGI:107901]		P70353	-7.8	3.4E-06	4.4	2.9E-02	-2.2	2.9E-01	-1.5	2.5E-01
ENSMUST00000043440	immunoglobulin superfamily, member 23 [Source:MGI Symbol;Acc:MGI:1917330]	B2RTN2		4.4	5.5E-04	-0.3	8.4E-01	-6.1	2.8E-03	-1.1	3.8E-01
ENSMUST00000043447	endo-beta-N-acetylglucosaminidase [Source:MGI Symbol;Acc:MGI:2443788]		Q8BX80	6.2	9.7E-05	2.6	1.2E-02	0.4	5.7E-01	0.1	8.6E-01
ENSMUST00000043458	steroid 5 alpha-reductase 2 [Source:MGI Symbol;Acc:MGI:2150380]		Q99N99	6.9	8.2E-05	5.6	9.9E-04	-0.4	7.5E-01	-1.3	1.0E-01
ENSMUST00000043475	urocortin [Source:MGI Symbol;Acc:MGI:1276123]		P81615	4.2	2.8E-03	5.8	2.7E-04	-0.1	9.1E-01	0.8	2.3E-01
ENSMUST00000043484	receptor accessory protein 2 [Source:MGI Symbol;Acc:MGI:2385070]		Q8VCD6	4.0	8.4E-04	-3.9	2.1E-04	0.6	9.0E-02	-0.6	4.1E-01
ENSMUST00000043493	interactor of little elongation complex ELL subunit 1 [Source:MGI Symbol;Acc:MGI:2385865]		E9Q286	-2.0	2.1E-03	-7.1	1.1E-02	-0.5	4.9E-01	1.5	5.2E-01
ENSMUST00000043498	histone deacetylase 3 [Source:MGI Symbol;Acc:MGI:1343091]	Q3UM33		-3.8	2.6E-04	4.2	1.2E-03	-2.1	7.0E-02	-0.7	3.1E-01
ENSMUST00000043503	signal peptide, CUB domain, EGF-like 3 [Source:MGI Symbol;Acc:MGI:3045253]		Q66PY1	8.4	7.4E-05	6.6	5.3E-04	-0.6	6.4E-01	-1.4	1.0E-01
ENSMUST00000043517	poliovirus receptor [Source:MGI Symbol;Acc:MGI:107741]	Q8K094		4.1	8.6E-04	-6.0	3.1E-04	0.1	8.5E-01	-1.3	3.2E-01
ENSMUST00000043087	asparagine-linked glycosylation 12 (alpha-1,6-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:2385025]	Q8VCA2		-1.5	3.4E-01	-2.8	2.7E-01	0.2	9.0E-01	1.4	5.5E-01
ENSMUST00000043550	TRAF3 interacting protein 3 [Source:MGI Symbol;Acc:MGI:2441706]	G3X949		-8.0	8.5E-05	1.1	1.4E-01	-3.7	1.1E-03	0.2	7.2E-01
ENSMUST00000043094	intelectin 1 (galactofuranose binding) [Source:MGI Symbol;Acc:MGI:1333831]	D9J349	O88310	-0.7	3.8E-01	-0.7	5.0E-01	-0.5	4.4E-01	-0.6	5.6E-01
ENSMUST00000043560	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans) [Source:MGI Symbol;Acc:MGI:2682334		Q5RJH6	-1.9	9.4E-03	-6.0	1.7E-02	1.1	1.6E-01	0.6	7.6E-01
ENSMUST00000043577	claudin 5 [Source:MGI Symbol;Acc:MGI:1276112]		O54942	7.4	6.1E-05	2.4	2.8E-03	-0.8	1.6E-01	0.0	9.9E-01
ENSMUST00000043584	tubulin, beta 4B class IVB [Source:MGI Symbol;Acc:MGI:1915472]		P68372	-5.0	1.4E-05	3.2	1.2E-02	-2.8	5.0E-02	-1.1	2.1E-01
ENSMUST00000043112	F-box protein 34 [Source:MGI Symbol;Acc:MGI:1926188]	E9QM55		-4.8	1.2E-01	1.4	7.7E-01	5.7	1.3E-01	-0.5	9.1E-01
ENSMUST00000043598	TLC domain containing 2 [Source:MGI Symbol;Acc:MGI:1917141]		Q8VC26	4.1	8.2E-05	-1.0	2.5E-01	0.7	2.4E-01	-0.8	3.6E-01
ENSMUST00000043605	kinesin family member 27 [Source:MGI Symbol;Acc:MGI:1922300]		Q7M6Z4	6.7	5.9E-05	-4.4	1.7E-02	-0.2	7.4E-01	0.9	5.6E-01
ENSMUST00000043612	phospholipase A2, group IVC (cytosolic, calcium-independent) [Source:MGI Symbol;Acc:MGI:1196403]	Q64GA5		5.3	3.6E-04	10.1	4.3E-06	-0.7	5.7E-01	-0.1	8.2E-01
ENSMUST00000043616	zyg-11 family member B, cell cycle regulator [Source:MGI Symbol;Acc:MGI:2685277]		Q3UFS0	-2.3	4.0E-04	-1.6	1.0E-01	0.7	2.3E-01	-1.0	3.2E-01
ENSMUST00000043624	mediator complex subunit 13 [Source:MGI Symbol;Acc:MGI:3029632]		Q5SWW4	-2.1	3.3E-04	2.4	2.0E-02	-1.5	9.3E-02	0.1	8.6E-01
ENSMUST00000043627	mitochondrial ribosomal protein L12 [Source:MGI Symbol;Acc:MGI:1926273]		Q9DB15	-1.4	3.3E-02	-2.9	1.5E-02	0.5	3.7E-01	0.2	8.6E-01
ENSMUST00000043152	UTP6, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:2445193]		Q8VCY6	-1.0	1.1E-01	-0.5	4.8E-01	-0.3	5.1E-01	-0.8	2.5E-01
ENSMUST00000043628	microphthalmia-associated transcription factor [Source:MGI Symbol;Acc:MGI:104554]	Q32MU7	Q08874	7.7	3.2E-05	-2.3	9.5E-03	0.3	4.8E-01	-0.1	8.4E-01
ENSMUST00000043637	microphthalmia-associated transcription factor [Source:MGI Symbol;Acc:MGI:104554]	Q3U2D2		-1.9	1.0E-02	-5.5	2.7E-03	0.2	6.6E-01	3.7	2.1E-02
ENSMUST00000043650	family with sequence similarity 222, member A [Source:MGI Symbol;Acc:MGI:3605543]		Q6PGH4	4.1	5.9E-05	-2.1	7.5E-02	0.8	2.3E-01	-1.8	1.5E-01
ENSMUST00000043170				1.2	1.5E-01	1.2	2.1E-01	-0.8	3.3E-01	-0.7	3.8E-01
ENSMUST00000043172	retinoic acid receptor, gamma [Source:MGI Symbol;Acc:MGI:97858]		P18911	1.6	4.7E-01	2.3	3.1E-01	-1.7	4.4E-01	-2.3	2.6E-01
ENSMUST00000043654	tubulin, gamma 2 [Source:MGI Symbol;Acc:MGI:2144208]	Q6F4J0	Q8VCK3	7.3	3.5E-05	5.1	2.8E-03	0.5	6.6E-01	0.2	8.2E-01
ENSMUST00000043189	neurofascin [Source:MGI Symbol;Acc:MGI:104753]	E9Q171		6.3	6.6E-02	5.8	6.3E-02	-3.0	3.9E-01	-2.6	1.6E-01
ENSMUST00000043675	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G [Source:MGI Symbol;Acc:MGI:1351597		Q9CPQ8	-5.1	1.6E-04	-4.2	5.8E-04	1.2	1.6E-02	-0.3	6.9E-01
ENSMUST00000043676	SCO-spondin [Source:MGI Symbol;Acc:MGI:2674311]		Q8CG65	7.2	6.9E-04	-2.6	2.4E-02	1.0	9.9E-02	-0.7	4.7E-01
ENSMUST00000043718	RIKEN cDNA 2310007B03 gene [Source:MGI Symbol;Acc:MGI:1919124]		Q8CEZ4	7.5	4.9E-04	6.7	5.8E-04	-1.0	4.7E-01	0.6	4.1E-01
ENSMUST00000043725	contactin associated protein-like 5A [Source:MGI Symbol;Acc:MGI:3643623]		Q0V8T9	8.8	8.6E-07	5.9	5.2E-04	-1.4	2.7E-01	0.4	5.2E-01
ENSMUST00000043211	coenzyme Q10 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:2684847]	E9Q3H6		-1.1	4.6E-02	-0.5	3.9E-01	0.7	1.1E-01	0.2	7.1E-01
ENSMUST00000043726	angiopoietin-like 6 [Source:MGI Symbol;Acc:MGI:1917976]		Q8R0Z6	4.7	5.6E-04	-4.9	5.2E-05	0.8	5.0E-02	0.1	8.6E-01
ENSMUST00000043227	chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 [Source:MGI Symbol;Acc:M			1.1	2.7E-01	3.7	3.5E-02	1.8	2.2E-01	-0.8	4.5E-01
ENSMUST00000043754	cathepsin L-like 3 [Source:MGI Symbol;Acc:MGI:1917452]	Q3ULP7		6.1	2.3E-04	-1.3	5.2E-02	0.0	9.0E-01	0.2	7.2E-01
ENSMUST00000043757	ATP-binding cassette, sub-family F (GCN20), member 1 [Source:MGI Symbol;Acc:MGI:1351658]		Q6P542	-1.9	3.1E-03	-1.4	1.7E-01	2.1	6.2E-03	-0.5	6.0E-01
ENSMUST00000043760	mevalonate kinase [Source:MGI Symbol;Acc:MGI:107624]		Q9R008	-4.7	4.7E-04	5.1	9.7E-04	-1.7	1.9E-01	-0.4	5.5E-01
ENSMUST00000043765	heterogeneous nuclear ribonucleoprotein U-like 1 [Source:MGI Symbol;Acc:MGI:2443517]		Q8VDM6	-4.0	8.9E-06	6.6	1.7E-05	-1.5	1.1E-01	0.5	2.3E-01
ENSMUST00000043767	UPF3 regulator of nonsense transcripts homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1914281]	Q3ULJ3		-4.0	9.0E-05	4.0	1.0E-02	-0.6	6.3E-01	2.1	3.7E-02
ENSMUST00000043775	KDM3B lysine (K)-specific demethylase 3B [Source:MGI Symbol;Acc:MGI:1923356]	B9EKS2		-2.6	2.2E-04	-8.2	4.9E-04	1.1	3.6E-02	-0.9	5.9E-01
ENSMUST00000043812	protein kinase N2 [Source:MGI Symbol;Acc:MGI:109211]		Q8BWW9	-2.6	2.4E-03	-3.7	3.5E-02	0.2	7.8E-01	-0.6	7.2E-01
ENSMUST00000043813	nudix (nucleoside diphosphate linked moiety X)-type motif 15 [Source:MGI Symbol;Acc:MGI:2443366]		Q8BG93	2.4	3.5E-04	-5.6	1.6E-03	0.0	9.8E-01	-0.5	7.0E-01
ENSMUST00000043814	FIG4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143585]		Q91WF7	-3.3	3.4E-05	2.9	1.8E-02	0.0	9.9E-01	-0.2	8.0E-01
ENSMUST00000043286	polymerase (DNA directed), iota [Source:MGI Symbol;Acc:MGI:1347081]			-3.2	2.5E-01	-1.2	6.4E-01	-0.8	6.5E-01	-2.8	3.6E-01
ENSMUST00000043843	LIM and SH3 protein 1 [Source:MGI Symbol;Acc:MGI:109656]	Q543N3	Q61792	-4.6	5.5E-05	6.2	1.7E-03	1.6	2.5E-01	-0.5	5.8E-01
ENSMUST00000043296	discs, large (Drosophila) homolog-associated protein 5 [Source:MGI Symbol;Acc:MGI:2183453]			-0.7	3.1E-01	-1.2	1.7E-01	-0.5	3.5E-01	0.0	9.9E-01
ENSMUST00000043301	activation-induced cytidine deaminase [Source:MGI Symbol;Acc:MGI:1342279]		Q9WVE0	1.0	1.8E-01	2.6	1.3E-02	0.5	5.4E-01	-1.2	1.4E-01
ENSMUST00000043845	proline rich 5 like [Source:MGI Symbol;Acc:MGI:1919696]		A2AVJ5	-7.6	1.3E-03	-1.7	2.3E-01	1.1	2.4E-01	-2.7	1.2E-01
ENSMUST00000043848	non-SMC condensin I complex, subunit D2 [Source:MGI Symbol;Acc:MGI:1915548]			-1.5	3.3E-02	-4.6	1.1E-02	1.2	1.2E-01	-1.6	3.5E-01
ENSMUST00000043313	nicotinamide nucleotide adenylyltransferase 2 [Source:MGI Symbol;Acc:MGI:2444155]	Q5HZI3	Q8BNJ3	3.9	8.8E-02	4.0	1.7E-01	0.2	9.5E-01	0.1	9.6E-01
ENSMUST00000043870	polymerase (RNA) II (DNA directed) polypeptide L [Source:MGI Symbol;Acc:MGI:1913741]		P62876	1.1	2.7E-02	-3.4	4.5E-02	0.4	5.6E-01	-0.5	7.7E-01
ENSMUST00000043884	leucine rich repeat protein 3, neuronal [Source:MGI Symbol;Acc:MGI:106036]		Q8CBC6	3.7	3.2E-03	-1.7	6.0E-02	-0.1	7.7E-01	-0.3	6.7E-01
ENSMUST00000043317	DnaJ (Hsp40) homolog, subfamily C, member 12 [Source:MGI Symbol;Acc:MGI:1353428]		Q9R022	-3.0	6.7E-02	-3.4	1.6E-01	0.1	9.4E-01	0.5	8.2E-01
ENSMUST00000043325	heparan sulfate 2-O-sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1346049]		Q8R3H7	-0.1	8.8E-01	0.3	5.9E-01	0.4	3.4E-01	0.0	9.5E-01
ENSMUST00000043893	TBC1 domain family, member 1 [Source:MGI Symbol;Acc:MGI:1889508]		Q60949	2.0	4.1E-03	-4.0	1.9E-02	1.8	2.0E-02	-0.6	6.8E-01
ENSMUST00000043896	zinc finger homeobox 3 [Source:MGI Symbol;Acc:MGI:99948]	E9QMD3		1.9	6.8E-04	-5.5	1.5E-05	-0.1	7.7E-01	-0.5	5.0E-01
ENSMUST00000043897	ras homolog gene family, member T2 [Source:MGI Symbol;Acc:MGI:2384892]		Q8JZN7	-2.2	4.1E-03	-3.0	8.5E-03	0.9	8.3E-02	0.1	8.8E-01
ENSMUST00000043898	presenilin enhancer 2 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1913590]		Q9CQR7	-5.7	7.1E-06	3.2	1.3E-03	-1.5	5.7E-02	-0.6	2.4E-01
ENSMUST00000043907	mitochondrial ribosomal protein S34 [Source:MGI Symbol;Acc:MGI:1930188]		Q9JIK9	-4.6	1.6E-03	8.0	1.0E-05	-1.4	1.8E-01	0.2	6.3E-01
ENSMUST00000043914	integrator complex subunit 9 [Source:MGI Symbol;Acc:MGI:1098533]			-2.3	9.5E-04	-4.7	2.1E-03	-0.2	7.4E-01	-0.4	7.6E-01
ENSMUST00000043356	RIKEN cDNA 0610010F05 gene [Source:MGI Symbol;Acc:MGI:1918925]		Q68FF0	1.6	2.7E-01	0.8	5.4E-01	-2.4	7.6E-02	-1.7	2.1E-01
ENSMUST00000043915	eine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12 [Source:MGI Symbol;Acc:M		Q7TMF5	8.2	1.5E-05	0.1	8.4E-01	1.5	8.9E-03	-0.5	4.5E-01
ENSMUST00000043368	zinc finger, CCHC domain containing 11 [Source:MGI Symbol;Acc:MGI:2445126]		B2RX14	-2.2	7.1E-02	2.4	1.2E-01	3.5	8.4E-03	-1.0	4.3E-01
ENSMUST00000043931	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D [Source:MGI Symbol;Acc:MGI:1918929		Q9DCX2	-9.4	1.5E-06	5.0	3.2E-05	-0.3	6.3E-01	-0.5	3.2E-01
ENSMUST00000043937	oligosaccharyltransferase complex subunit [Source:MGI Symbol;Acc:MGI:1913607]		Q78XF5	-7.0	1.6E-05	-3.8	9.1E-03	1.0	1.1E-01	-1.3	3.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000043938	phospholipase C-like 2 [Source:MGI Symbol;Acc:MGI:1352756]		Q8K394	-4.4	2.2E-05	7.8	8.1E-05	-0.7	6.0E-01	-0.3	6.6E-01
ENSMUST00000043944	anoctamin 5 [Source:MGI Symbol;Acc:MGI:3576659]		Q75UR0	8.0	1.6E-05	5.9	1.5E-03	-0.4	7.9E-01	-1.4	9.3E-02
ENSMUST00000043951	ARP1 actin-related protein 1B, centractin beta [Source:MGI Symbol;Acc:MGI:1917446]		Q8R5C5	-2.9	1.3E-03	6.0	4.3E-04	-0.5	6.5E-01	-3.6	2.0E-03
ENSMUST00000043397	in homology domain containing, family H (with MyTH4 domain) member 3 [Source:MGI Symbol;Acc:MGI:2		Q8VCE9	6.3	3.6E-02	5.9	6.4E-02	-0.7	8.1E-01	-0.3	8.8E-01
ENSMUST00000043961	ATP-binding cassette, sub-family A (ABC1), member 5 [Source:MGI Symbol;Acc:MGI:2386607]		Q8K448	3.1	3.2E-03	-6.9	1.2E-04	0.8	1.2E-01	-0.7	5.5E-01
ENSMUST00000043962	CDC16 cell division cycle 16 [Source:MGI Symbol;Acc:MGI:1917207]	Q3TI84	Q8R349	-3.0	7.0E-04	2.7	1.2E-03	-0.6	2.6E-01	-0.5	3.0E-01
ENSMUST00000043964	Wolfram syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:1328355]	Q3TDI2	P56695	7.5	4.5E-03	-4.8	6.4E-04	1.2	1.7E-02	-2.5	6.4E-02
ENSMUST00000043970	NUT midline carcinoma, family member 1 [Source:MGI Symbol;Acc:MGI:2661384]		Q8BHP2	6.4	1.1E-05	6.3	8.0E-04	-0.7	6.4E-01	-0.2	7.4E-01
ENSMUST00000043419	eukaryotic translation initiation factor 5A [Source:MGI Symbol;Acc:MGI:106248]		P63242	-1.8	2.2E-01	-2.8	8.3E-02	-0.5	6.1E-01	0.5	7.4E-01
ENSMUST00000043422	TAP binding protein-like [Source:MGI Symbol;Acc:MGI:2384853]		Q8VD31	0.6	2.5E-01	0.9	1.6E-01	0.0	9.4E-01	-0.3	5.9E-01
ENSMUST00000043975	lin-37 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1922910]		Q9D8N6	-5.1	2.5E-04	-7.3	4.9E-05	0.0	8.8E-01	-0.5	6.6E-01
ENSMUST00000043437	FCH and double SH3 domains 1 [Source:MGI Symbol;Acc:MGI:2441771]		Q6PFY1	-1.3	6.4E-02	-0.3	7.3E-01	0.6	2.9E-01	-0.4	6.1E-01
ENSMUST00000043983	immunoglobulin superfamily, member 3 [Source:MGI Symbol;Acc:MGI:1926158]		Q6ZQA6	8.7	7.9E-06	4.4	1.3E-03	-0.4	6.3E-01	-0.5	5.3E-01
ENSMUST00000043441	BCL6 interacting corepressor [Source:MGI Symbol;Acc:MGI:1918708]		Q8CGN4	-0.1	8.6E-01	-1.5	1.7E-01	0.6	4.2E-01	2.0	7.5E-02
ENSMUST00000043990	enhancer of mRNA decapping 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2142951]	A0ELI5	Q8K2D3	-1.8	3.8E-03	7.0	7.0E-05	-0.5	6.5E-01	-1.3	3.9E-02
ENSMUST00000044002	transmembrane protein 184a [Source:MGI Symbol;Acc:MGI:2385897]	G3X923		6.6	9.4E-03	6.2	3.7E-04	-0.6	6.1E-01	0.2	8.1E-01
ENSMUST00000043459	ankyrin repeat domain 9 [Source:MGI Symbol;Acc:MGI:1921501]		Q8BH83	1.2	5.7E-01	1.3	6.4E-01	0.0	1.0E+00	-0.1	9.5E-01
ENSMUST00000043464	cullin 7 [Source:MGI Symbol;Acc:MGI:1913765]	A9C491	Q8VE73	2.6	2.4E-01	6.5	2.3E-02	-0.1	9.8E-01	-4.0	4.5E-02
ENSMUST00000044003	ATP-binding cassette, sub-family A (ABC1), member 6 [Source:MGI Symbol;Acc:MGI:1923434]		Q8K441	2.6	7.3E-03	5.4	1.0E-03	-0.5	6.8E-01	-1.6	4.8E-02
ENSMUST00000044005	activating transcription factor 7 interacting protein 2 [Source:MGI Symbol;Acc:MGI:1922579]		Q3UL97	7.2	2.5E-04	4.9	2.0E-03	0.6	6.2E-01	-0.3	6.5E-01
ENSMUST00000044011	FK506 binding protein 1a [Source:MGI Symbol;Acc:MGI:95541]		P26883	-4.9	2.9E-03	-1.3	5.7E-02	0.5	2.0E-01	-0.1	8.1E-01
ENSMUST00000044018	NADPH oxidase activator 1 [Source:MGI Symbol;Acc:MGI:2449980]		Q8CJ00	5.2	2.5E-02	-2.8	6.6E-03	0.5	3.2E-01	-0.5	5.8E-01
ENSMUST00000044031	recombination activating gene 2 [Source:MGI Symbol;Acc:MGI:97849]	Q542D1	P21784	6.6	2.0E-04	8.3	1.5E-04	-0.6	6.8E-01	-0.5	4.3E-01
ENSMUST00000044036	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	D3Z764		-6.2	3.1E-02	2.7	1.7E-02	-1.0	2.6E-01	0.3	6.7E-01
ENSMUST00000043520	F-box protein 25 [Source:MGI Symbol;Acc:MGI:1914072]		Q9D2Y6	-1.0	5.8E-02	-1.2	5.8E-02	-0.2	5.6E-01	0.0	9.7E-01
ENSMUST00000043521	SEC22 homolog A, vesicle trafficking protein [Source:MGI Symbol;Acc:MGI:2447876]	B2RSR2	Q8BH47	-0.6	3.4E-01	-1.1	1.5E-01	-0.4	4.7E-01	0.2	7.7E-01
ENSMUST00000043526	cylindromatosis (turban tumor syndrome) [Source:MGI Symbol;Acc:MGI:1921506]	Z4YJJ5		-2.6	1.5E-01	-3.2	3.4E-01	1.7	3.8E-01	2.3	4.6E-01
ENSMUST00000043531	family with sequence similarity 65, member A [Source:MGI Symbol;Acc:MGI:1922937]		Q68FE6	0.8	1.7E-01	1.6	5.6E-02	0.8	1.8E-01	0.0	9.8E-01
ENSMUST00000044039	leucine rich repeats and death domain containing 1 [Source:MGI Symbol;Acc:MGI:3045299]		Q8C0R9	3.5	2.3E-03	-6.0	8.7E-04	-0.1	8.2E-01	-2.1	1.8E-01
ENSMUST00000043551	ankyrin repeat and IBR domain containing 1 [Source:MGI Symbol;Acc:MGI:1918047]		Q6ZPS6	-0.4	3.1E-01	0.2	6.4E-01	0.6	1.3E-01	0.0	9.4E-01
ENSMUST00000043552	serine (or cysteine) peptidase inhibitor, clade B, member 6a [Source:MGI Symbol;Acc:MGI:103123]	Q4FJQ6	Q60854	-0.5	7.7E-01	-8.5	1.6E-03	-7.3	6.8E-05	0.8	7.1E-01
ENSMUST00000044048	heat shock protein, alpha-crystallin-related, B6 [Source:MGI Symbol;Acc:MGI:2685325]		Q5EBG6	6.6	3.2E-03	6.3	1.6E-04	-0.6	6.1E-01	-0.7	2.4E-01
ENSMUST00000044051	translocase of inner mitochondrial membrane 8B [Source:MGI Symbol;Acc:MGI:1353424]		P62077	-5.0	1.3E-04	-0.8	2.9E-01	1.0	5.3E-02	0.0	9.6E-01
ENSMUST00000044058	mitochondrial ubiquitin ligase activator of NFKB 1 [Source:MGI Symbol;Acc:MGI:1915600]		Q8VCM5	-3.0	3.3E-02	6.8	2.0E-04	-0.6	6.4E-01	0.0	9.6E-01
ENSMUST00000043578	suppression of tumorigenicity 18 [Source:MGI Symbol;Acc:MGI:2446700]	Q148A0	Q80TY4	3.0	2.4E-01	3.8	1.8E-01	-0.4	8.7E-01	-1.2	5.3E-01
ENSMUST00000044060	CD209c antigen [Source:MGI Symbol;Acc:MGI:2157945]		Q91ZW9	5.5	2.2E-05	-3.9	4.8E-04	0.8	5.5E-02	-0.3	7.0E-01
ENSMUST00000043589	kinesin family member 16B [Source:MGI Symbol;Acc:MGI:1098240]		B1AVY7	0.2	5.5E-01	0.3	6.0E-01	0.3	4.6E-01	0.2	6.3E-01
ENSMUST00000043596	phosphorylase kinase alpha 1 [Source:MGI Symbol;Acc:MGI:97576]	A2AI91		0.5	8.1E-01	5.1	7.8E-02	2.0	4.2E-01	-2.6	2.0E-01
ENSMUST00000044068	microrchidia 3 [Source:MGI Symbol;Acc:MGI:2136841]	F7BJB9		-4.8	6.3E-06	2.6	5.2E-03	-1.0	1.6E-01	0.6	3.3E-01
ENSMUST00000043599	ribosomal protein S6 kinase, polypeptide 5 [Source:MGI Symbol;Acc:MGI:1920336]		Q8C050	0.2	6.7E-01	-0.4	4.7E-01	0.0	9.5E-01	0.7	2.7E-01
ENSMUST00000043604	guanine nucleotide binding protein, alpha 11 [Source:MGI Symbol;Acc:MGI:95766]	Q3UPA1	P21278	-0.1	9.2E-01	0.5	5.7E-01	0.4	4.5E-01	-0.1	9.3E-01
ENSMUST00000044081	PAP associated domain containing 7 [Source:MGI Symbol;Acc:MGI:2682295]		Q6PB75	1.7	1.3E-02	5.7	9.2E-05	-1.9	8.3E-02	-0.8	1.8E-01
ENSMUST00000043610	RAB6A GEF complex partner 1 [Source:MGI Symbol;Acc:MGI:1924893]	E9QPA1		-0.4	4.3E-01	0.7	4.0E-01	1.4	3.1E-02	0.3	6.7E-01
ENSMUST00000044083	death associated protein kinase 1 [Source:MGI Symbol;Acc:MGI:1916885]		Q80YE7	4.7	2.1E-03	6.3	3.0E-04	0.1	9.0E-01	-0.9	2.0E-01
ENSMUST00000044089	ankyrin repeat and SOCS box-containing 17 [Source:MGI Symbol;Acc:MGI:1914022]		Q8VHP9	4.7	3.9E-04	-0.8	1.6E-01	1.1	1.2E-02	-0.4	4.6E-01
ENSMUST00000044094	roxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5 [Source:MGI Symbol;Acc:MGI:1046		Q61694	6.7	4.0E-04	-1.0	6.4E-02	0.8	2.5E-02	-0.3	5.3E-01
ENSMUST00000044105	tetraspanin 10 [Source:MGI Symbol;Acc:MGI:2384781]	Q3UGA5		7.1	6.9E-05	-1.4	8.3E-02	-0.2	7.0E-01	-0.2	7.4E-01
ENSMUST00000044106	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 [Source:MGI Symbol;Acc:MGI:1351511]	A1L3B8	P26516	-2.7	1.5E-04	1.9	1.6E-01	-1.5	2.2E-01	4.3	2.2E-03
ENSMUST00000044113	argonaute RISC catalytic subunit 2 [Source:MGI Symbol;Acc:MGI:2446632]		Q8CJG0	-1.0	1.4E-02	-0.4	6.2E-01	0.9	1.2E-01	-0.7	3.9E-01
ENSMUST00000044115	zinc finger and SCAN domain containing 2 [Source:MGI Symbol;Acc:MGI:99176]		Q07230	2.6	1.6E-03	3.8	2.6E-04	-0.2	7.8E-01	0.2	7.6E-01
ENSMUST00000044123	thyrotropin releasing hormone receptor 2 [Source:MGI Symbol;Acc:MGI:2177284]	Q9ERT2		7.1	5.4E-05	5.4	1.7E-04	-2.0	7.7E-02	-0.1	9.2E-01
ENSMUST00000043674	valyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:1916165]		Q3U2A8	-1.0	4.8E-01	1.1	5.4E-01	0.4	7.9E-01	-1.7	2.9E-01
ENSMUST00000044125	NK6 homeobox 1 [Source:MGI Symbol;Acc:MGI:1206039]		Q99MA9	6.5	4.8E-04	-6.1	2.6E-04	-1.1	3.7E-02	-0.2	8.8E-01
ENSMUST00000044138	carbohydrate (N-acetylglucosamino) sulfotransferase 7 [Source:MGI Symbol;Acc:MGI:1891767]		Q9EP78	6.8	1.2E-04	9.1	1.0E-03	0.4	8.3E-01	-1.5	1.2E-01
ENSMUST00000043680	tubulin, gamma 1 [Source:MGI Symbol;Acc:MGI:101834]	Q6F4J1	P83887	-0.1	8.7E-01	0.5	5.6E-01	0.5	4.4E-01	-0.1	8.8E-01
ENSMUST00000043707	rhomboid domain containing 2 [Source:MGI Symbol;Acc:MGI:1915612]		Q8VEK2	1.1	3.9E-02	0.7	2.9E-01	0.1	8.2E-01	0.5	3.7E-01
ENSMUST00000043709	guanine nucleotide binding protein, alpha 15 [Source:MGI Symbol;Acc:MGI:95770]		P30678	-1.2	1.0E-01	0.5	5.9E-01	1.4	5.8E-02	-0.3	7.3E-01
ENSMUST00000043716	cyclin-dependent kinase 2 interacting protein [Source:MGI Symbol;Acc:MGI:1914486]		Q9D0V8	-0.7	1.8E-01	-1.1	9.1E-02	-0.9	5.0E-02	-0.5	4.0E-01
ENSMUST00000044158	glioma tumor suppressor candidate region gene 2 [Source:MGI Symbol;Acc:MGI:2154441]	Q8BK35		-4.4	1.4E-04	7.5	8.8E-04	-0.7	6.8E-01	-0.7	4.2E-01
ENSMUST00000043722	lectin, galactoside-binding, soluble, 3 binding protein [Source:MGI Symbol;Acc:MGI:99554]		Q07797	-0.1	8.9E-01	-2.0	3.3E-02	-2.5	1.2E-03	-0.7	4.4E-01
ENSMUST00000044159	serine (or cysteine) peptidase inhibitor, clade A, member 6 [Source:MGI Symbol;Acc:MGI:88278]		Q06770	7.6	3.3E-05	7.9	7.5E-06	-0.8	3.6E-01	0.1	8.7E-01
ENSMUST00000044165	integrin alpha 9 [Source:MGI Symbol;Acc:MGI:104756]		B8JK39	8.1	7.5E-06	3.6	3.0E-03	-1.3	1.9E-01	-0.1	8.4E-01
ENSMUST00000043735	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like [Source:MGI Symbol;Acc:MGI:1924836		Q3V3R1	-0.7	7.9E-01	-0.8	8.2E-01	-0.6	8.0E-01	-0.5	8.9E-01
ENSMUST00000043739	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3 [Source:MGI Symbol;Acc:MGI:119		O35949	1.3	9.7E-02	3.0	1.2E-02	2.2	2.8E-02	0.5	4.9E-01
ENSMUST00000044166	cell division cycle 40 [Source:MGI Symbol;Acc:MGI:1918963]		Q9DC48	-2.5	1.2E-02	6.1	4.1E-04	-0.5	6.8E-01	-0.6	4.0E-01
ENSMUST00000043755				3.4	1.1E-01	1.7	4.1E-01	-2.6	1.8E-01	-0.8	6.5E-01
ENSMUST00000044179	testis expressed gene 13 [Source:MGI Symbol;Acc:MGI:1890544]	Q99MW5		6.6	5.0E-05	-1.4	5.9E-02	0.6	1.5E-01	0.1	9.1E-01
ENSMUST00000044180	neuropeptides B/W receptor 1 [Source:MGI Symbol;Acc:MGI:891989]		P49681	8.7	6.5E-05	-3.2	1.9E-02	0.9	1.2E-01	-0.6	6.4E-01
ENSMUST00000044190	hedgehog acyltransferase [Source:MGI Symbol;Acc:MGI:2444681]		Q8BMT9	4.8	1.9E-03	-2.9	4.4E-04	0.8	2.8E-02	-0.3	6.4E-01
ENSMUST00000044195	transmembrane channel-like gene family 7 [Source:MGI Symbol;Acc:MGI:2443317]		Q8C428	5.1	3.6E-05	-2.2	1.0E-02	0.1	8.3E-01	-1.7	3.7E-02
ENSMUST00000044204	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2141161]			5.5	1.8E-04	-1.3	3.4E-02	0.7	5.7E-02	-0.5	3.3E-01
ENSMUST00000043785	signal transducing adaptor family member 2 [Source:MGI Symbol;Acc:MGI:2147039]		Q8R0L1	1.2	8.5E-02	2.4	1.2E-02	0.4	5.3E-01	-0.8	2.5E-01
ENSMUST00000043794	janus kinase and microtubule interacting protein 1 [Source:MGI Symbol;Acc:MGI:1923321]		Q8BVL9	2.2	4.1E-02	1.8	1.3E-01	-0.7	4.9E-01	-0.2	8.0E-01
ENSMUST00000044207	squamous cell carcinoma antigen recognized by T cells 1 [Source:MGI Symbol;Acc:MGI:1309453]		Q9Z315	-2.0	1.4E-03	-0.6	4.5E-01	1.3	3.6E-02	-0.7	3.7E-01
ENSMUST00000044216	src homology 2 domain-containing transforming protein D [Source:MGI Symbol;Acc:MGI:1099461]		O88834	6.5	1.1E-04	2.6	8.8E-04	0.0	9.4E-01	-0.2	5.9E-01
ENSMUST00000044217	spectrin repeat containing, nuclear envelope 2 [Source:MGI Symbol;Acc:MGI:2449316]		Q6ZWQ0	6.1	3.8E-04	-2.4	1.3E-03	0.2	4.2E-01	-0.7	2.4E-01
ENSMUST00000043815	nucleoporin 205 [Source:MGI Symbol;Acc:MGI:2141625]	B9EJ54		-0.2	7.1E-01	-0.4	4.7E-01	-0.6	1.2E-01	-0.4	4.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000043839	F11 receptor [Source:MGI Symbol;Acc:MGI:1321398]		O88792	0.3	5.4E-01	1.0	2.3E-01	0.8	2.1E-01	0.1	8.5E-01
ENSMUST00000044220	COX assembly mitochondrial protein 1 [Source:MGI Symbol;Acc:MGI:1915149]		Q9CPZ8	-3.3	4.9E-03	-2.7	7.2E-03	1.6	8.5E-03	-0.3	7.6E-01
ENSMUST00000044224	2'-5' oligoadenylate synthetase 1D [Source:MGI Symbol;Acc:MGI:2140770]	Q8VI95		6.1	8.9E-05	-6.1	1.9E-02	0.7	4.0E-01	-0.9	7.2E-01
ENSMUST00000044228	CD79B antigen [Source:MGI Symbol;Acc:MGI:96431]	B1ARJ9		2.3	1.6E-02	-0.2	7.8E-01	1.3	3.5E-02	0.1	9.1E-01
ENSMUST00000043864	cell division cycle 123 [Source:MGI Symbol;Acc:MGI:2138811]		Q8CII2	0.0	9.2E-01	0.3	5.8E-01	-0.5	2.0E-01	-0.8	9.7E-02
ENSMUST00000043865	mercaptopyruvate sulfurtransferase [Source:MGI Symbol;Acc:MGI:2179733]	Q3UW66		1.2	6.4E-02	2.6	5.2E-03	0.6	3.2E-01	-0.8	2.1E-01
ENSMUST00000044231	eine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 [Source:MGI Symbol;Acc:M		Q8R121	6.8	4.9E-07	1.4	2.3E-02	-0.4	4.1E-01	-0.6	2.0E-01
ENSMUST00000043881	BCL2-associated transcription factor 1 [Source:MGI Symbol;Acc:MGI:1917580]		Q8K019	-1.0	8.1E-01	0.4	9.3E-01	-0.5	8.8E-01	-1.8	6.5E-01
ENSMUST00000044248	podocan [Source:MGI Symbol;Acc:MGI:2674939]		Q7TQ62	8.9	2.6E-04	0.8	3.7E-01	-3.4	3.4E-03	-0.5	5.2E-01
ENSMUST00000044252	nucleotide binding protein 2 [Source:MGI Symbol;Acc:MGI:1347072]		Q9R061	-3.3	6.5E-04	2.2	9.3E-03	0.3	6.2E-01	0.1	8.4E-01
ENSMUST00000044271	nuclear protein localization 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2679787]		P60670	-8.0	1.2E-03	2.6	8.0E-04	1.2	2.4E-02	0.5	2.5E-01
ENSMUST00000044277	charged multivesicular body protein 4B [Source:MGI Symbol;Acc:MGI:1922858]		Q9D8B3	-7.0	5.4E-06	-0.4	5.8E-01	1.1	4.4E-02	-0.7	3.7E-01
ENSMUST00000044278	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5 [Source:MGI Symbo	Q6GTI0		9.0	1.6E-05	-5.0	1.1E-04	0.0	9.0E-01	-0.8	3.3E-01
ENSMUST00000044286	zinc finger, DHHC domain containing 1 [Source:MGI Symbol;Acc:MGI:1918046]		Q8R0N9	2.9	2.4E-03	-4.8	1.2E-02	0.7	2.6E-01	0.9	5.9E-01
ENSMUST00000043911	RIKEN cDNA A230050P20 gene [Source:MGI Symbol;Acc:MGI:2441788]		Q8CAK3	1.9	2.9E-01	3.2	8.2E-02	-1.5	4.0E-01	-2.7	8.1E-02
ENSMUST00000044297	insulin-like growth factor binding protein-like 1 [Source:MGI Symbol;Acc:MGI:1933198]		Q80W15	8.1	3.1E-05	-0.5	3.8E-01	0.9	3.4E-02	-0.8	2.0E-01
ENSMUST00000044299	somatostatin receptor 1 [Source:MGI Symbol;Acc:MGI:98327]	Q543T0	P30873	6.2	1.8E-03	8.2	1.8E-05	-0.5	6.5E-01	-0.6	2.9E-01
ENSMUST00000043922	zinc finger protein 653 [Source:MGI Symbol;Acc:MGI:2442362]		Q6YND2	2.8	9.8E-02	7.2	1.9E-02	3.6	1.7E-01	-0.8	5.5E-01
ENSMUST00000044306	glutamate receptor, metabotropic 1 [Source:MGI Symbol;Acc:MGI:1351338]		P97772	5.2	3.4E-04	-9.3	1.3E-05	-0.7	4.1E-02	-0.8	4.9E-01
ENSMUST00000044311	collagen beta(1-O)galactosyltransferase 2 [Source:MGI Symbol;Acc:MGI:2138232]		Q6NVG7	8.6	1.3E-05	-6.2	7.4E-05	-0.5	2.8E-01	-1.2	2.5E-01
ENSMUST00000044338	Rho GTPase activating protein 33 [Source:MGI Symbol;Acc:MGI:2673998]		Q80YF9	4.8	1.7E-05	-3.0	1.3E-03	0.8	5.0E-02	-0.6	4.1E-01
ENSMUST00000044352	pecanex-like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1914958]	E9QN69		2.0	2.2E-03	8.1	3.0E-05	-0.5	6.7E-01	-0.6	2.7E-01
ENSMUST00000044355	selenoprotein W, muscle 1 [Source:MGI Symbol;Acc:MGI:1100878]		P63300	-2.7	3.1E-02	-1.4	1.0E-01	0.8	1.2E-01	-0.7	3.9E-01
ENSMUST00000044369	ATPase, H+ transporting, lysosomal V1 subunit H [Source:MGI Symbol;Acc:MGI:1914864]		Q8BVE3	-5.8	4.1E-05	5.9	6.7E-04	2.2	6.8E-02	-0.6	4.0E-01
ENSMUST00000044373	regulatory factor X-associated protein [Source:MGI Symbol;Acc:MGI:2180854]	F7DBT7		-2.4	1.2E-02	-1.8	3.2E-02	0.7	1.8E-01	-0.5	5.5E-01
ENSMUST00000044380	forkhead box A1 [Source:MGI Symbol;Acc:MGI:1347472]		P35582	9.4	8.9E-06	2.5	2.8E-01	-3.5	1.5E-01	1.5	3.6E-01
ENSMUST00000043966	mitochondrial ribosomal protein L47 [Source:MGI Symbol;Acc:MGI:1921850]		Q8K2Y7	0.1	8.8E-01	-0.2	8.3E-01	-0.5	4.3E-01	-0.2	7.7E-01
ENSMUST00000044385	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta [Source:MGI Symbol;Acc:MGI:2444615]		Q8VD33	2.4	1.5E-02	7.2	3.6E-05	0.5	6.2E-01	-0.3	5.8E-01
ENSMUST00000044387	RIKEN cDNA 2010107G12 gene [Source:MGI Symbol;Acc:MGI:1917272]	E9PW54		5.4	3.5E-04	-5.6	1.3E-03	-0.1	8.3E-01	0.3	8.0E-01
ENSMUST00000044392	cysteine conjugate-beta lyase 2 [Source:MGI Symbol;Acc:MGI:2677849]		Q71RI9	5.4	8.5E-03	5.2	1.6E-04	-3.5	5.5E-03	0.0	9.9E-01
ENSMUST00000044423	BRCA1 interacting protein C-terminal helicase 1 [Source:MGI Symbol;Acc:MGI:2442836]		Q5SXJ3	4.2	1.8E-05	-1.1	1.1E-01	0.6	1.4E-01	-0.1	8.9E-01
ENSMUST00000044426	guanylate cyclase activator 2b (retina) [Source:MGI Symbol;Acc:MGI:1270851]	Q9QUQ3	O09051	6.3	1.8E-04	6.7	1.3E-02	-0.9	7.3E-01	-1.0	4.7E-01
ENSMUST00000044434	cone-rod homeobox [Source:MGI Symbol;Acc:MGI:1194883]	Q543C9	O54751	8.2	1.5E-02	2.5	2.0E-02	-0.7	4.0E-01	-0.5	4.9E-01
ENSMUST00000044441	transmembrane protein 132D [Source:MGI Symbol;Acc:MGI:3044963]			8.9	1.2E-05	5.4	3.3E-03	-0.6	6.7E-01	1.2	1.7E-01
ENSMUST00000044007	oxidoreductase like domain containing 1 [Source:MGI Symbol;Acc:MGI:1913681]	B2RVP3	Q9CR10	-0.1	8.2E-01	0.3	6.5E-01	0.2	7.3E-01	-0.3	6.8E-01
ENSMUST00000044009	calcium/calmodulin-dependent protein kinase ID [Source:MGI Symbol;Acc:MGI:2442190]	B1AW58	Q8BW96	-0.8	1.9E-01	-0.6	4.3E-01	0.5	4.0E-01	0.3	6.9E-01
ENSMUST00000044442	PTK7 protein tyrosine kinase 7 [Source:MGI Symbol;Acc:MGI:1918711]		Q8BKG3	5.3	5.2E-05	-1.6	1.8E-01	0.1	8.7E-01	-3.2	4.1E-02
ENSMUST00000044451	N-acetylated alpha-linked acidic dipeptidase-like 1 [Source:MGI Symbol;Acc:MGI:2685810]		Q7M758	6.1	5.3E-05	7.0	7.1E-03	-0.7	7.6E-01	-2.5	8.0E-02
ENSMUST00000044019	solute carrier family 41, member 3 [Source:MGI Symbol;Acc:MGI:1918949]	G3X937		-0.8	2.4E-01	0.6	4.8E-01	1.2	7.3E-02	-0.2	8.4E-01
ENSMUST00000044021	solute carrier family 19 (thiamine transporter), member 2 [Source:MGI Symbol;Acc:MGI:1928761]	Q9EQN9		-1.1	4.2E-01	3.3	1.1E-01	4.0	3.2E-02	-0.4	8.0E-01
ENSMUST00000044454	5-azacytidine induced gene 2 [Source:MGI Symbol;Acc:MGI:1351332]		Q9QYP6	-5.4	1.9E-05	6.6	7.7E-04	-0.8	5.9E-01	-0.8	2.9E-01
ENSMUST00000044455	zinc finger protein 451 [Source:MGI Symbol;Acc:MGI:2137896]	Q8VCL4		2.9	5.6E-05	-2.7	3.0E-01	1.1	4.7E-01	-2.4	4.3E-01
ENSMUST00000044462	testicular cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1923120]	Q99NB3		6.2	6.3E-05	3.7	2.5E-03	-1.1	2.5E-01	-1.2	1.2E-01
ENSMUST00000044043	predicted gene 11273 [Source:MGI Symbol;Acc:MGI:3649411]	Q9D881		-0.5	7.7E-01	2.1	3.9E-01	1.4	5.1E-01	-1.2	5.2E-01
ENSMUST00000044466	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative) [Source:MGI Symbol;Acc:MGI:2142075]		Q8BGV0	-2.2	7.5E-03	5.7	2.5E-02	0.1	9.5E-01	1.0	4.5E-01
ENSMUST00000044475	e (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) [Source:MG		Q8CGY8	-6.6	1.9E-03	-6.9	5.2E-04	-0.6	2.6E-01	1.3	3.3E-01
ENSMUST00000044053	SNF2 histone linker PHD RING helicase [Source:MGI Symbol;Acc:MGI:1917581]		Q7TPQ3	0.8	1.5E-01	1.3	6.7E-02	0.0	9.7E-01	-0.5	3.7E-01
ENSMUST00000044478	3-hydroxyisobutyryl-Coenzyme A hydrolase [Source:MGI Symbol;Acc:MGI:1923792]		Q8QZS1	-6.9	1.0E-04	0.2	8.6E-01	1.3	2.2E-01	-2.0	1.9E-01
ENSMUST00000044484	lysine (K)-specific demethylase 6A [Source:MGI Symbol;Acc:MGI:1095419]		O70546	-5.7	2.5E-05	5.8	3.2E-05	-0.4	5.7E-01	-0.7	1.6E-01
ENSMUST00000044491	cDNA sequence AF529169 [Source:MGI Symbol;Acc:MGI:2667167]	Q14CG5	Q8K3V7	8.3	2.0E-06	-4.6	4.8E-05	-0.4	2.1E-01	-0.6	3.6E-01
ENSMUST00000044505	phosphodiesterase 1C [Source:MGI Symbol;Acc:MGI:108413]		Q64338	5.7	4.0E-04	2.2	1.7E-02	0.4	5.4E-01	-0.1	9.1E-01
ENSMUST00000044524	death-associated protein [Source:MGI Symbol;Acc:MGI:1918190]	Q3U706	Q91XC8	-4.6	4.9E-06	0.8	5.6E-01	-1.5	2.2E-01	2.4	7.4E-02
ENSMUST00000044527	testis specific 10 interacting protein [Source:MGI Symbol;Acc:MGI:1925556]	F7A1F0		3.3	8.7E-03	4.5	1.4E-03	-0.3	7.8E-01	-0.1	8.7E-01
ENSMUST00000044530	SET and MYND domain containing 4 [Source:MGI Symbol;Acc:MGI:2442796]		Q8BTK5	5.1	9.2E-06	6.9	5.9E-04	-0.7	6.4E-01	-0.9	2.8E-01
ENSMUST00000044532	dedicator of cyto-kinesis 3 [Source:MGI Symbol;Acc:MGI:2429763]	F8VPQ1		7.8	2.9E-05	5.4	2.3E-05	-0.4	5.0E-01	0.0	9.7E-01
ENSMUST00000044533	protease, serine 56 [Source:MGI Symbol;Acc:MGI:1916703]		F2YMG0	7.8	7.7E-05	7.3	9.7E-05	-0.6	6.3E-01	-0.9	1.8E-01
ENSMUST00000044547	carcinoembryonic antigen-related cell adhesion molecule 2 [Source:MGI Symbol;Acc:MGI:1347246]		Q925P2	8.5	4.2E-05	-3.6	1.5E-04	0.0	9.3E-01	0.9	1.3E-01
ENSMUST00000044111	Harvey rat sarcoma oncogene, subgroup R [Source:MGI Symbol;Acc:MGI:98179]	Q3U1N3	P10833	-1.6	7.1E-02	-1.7	1.2E-01	0.1	8.6E-01	0.2	8.2E-01
ENSMUST00000044551	intestinal cell kinase [Source:MGI Symbol;Acc:MGI:1934157]		Q9JKV2	3.3	6.8E-03	-0.1	7.4E-01	0.9	1.7E-02	0.1	8.7E-01
ENSMUST00000044554	leukotriene B4 receptor 2 [Source:MGI Symbol;Acc:MGI:1888501]		Q9JJL9	3.7	6.5E-03	3.2	1.7E-03	0.9	1.8E-01	0.3	6.5E-01
ENSMUST00000044116	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human) [Source:MGI Symbol;Acc:MGI:2139806]	Q3TVW1	Q8R1X6	-2.2	1.7E-01	-2.8	1.6E-01	-0.1	9.3E-01	0.5	8.1E-01
ENSMUST00000044565	collagen, type XVI, alpha 1 [Source:MGI Symbol;Acc:MGI:1095396]		Q8BLX7	7.2	9.5E-04	7.2	9.4E-05	-0.6	6.1E-01	-0.7	2.7E-01
ENSMUST00000044567	agine-linked glycosylation 5 (dolichyl-phosphate beta-glucosyltransferase) [Source:MGI Symbol;Acc:MGI:191		Q9DB25	-6.0	1.0E-04	6.3	1.4E-03	-0.2	8.7E-01	0.0	9.9E-01
ENSMUST00000044579	cytokine receptor-like factor 2 [Source:MGI Symbol;Acc:MGI:1889506]			-5.0	2.7E-06	3.7	5.8E-03	-2.6	5.1E-02	0.6	4.2E-01
ENSMUST00000044148	asparagine-linked glycosylation 2 (alpha-1,3-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:1914731]		Q9DBE8	-0.6	2.7E-01	0.6	3.8E-01	0.9	1.3E-01	-0.4	5.7E-01
ENSMUST00000044152	HID1 domain containing [Source:MGI Symbol;Acc:MGI:2445087]	Q3UU20	Q8R1F6	2.8	2.1E-01	1.6	5.1E-01	-0.9	6.6E-01	0.2	9.1E-01
ENSMUST00000044155	ubiquitin associated and SH3 domain containing, B [Source:MGI Symbol;Acc:MGI:1920078]		Q8BGG7	-1.3	4.8E-02	-0.4	6.1E-01	0.7	1.7E-01	-0.2	8.1E-01
ENSMUST00000044581	RIKEN cDNA 1700025G04 gene [Source:MGI Symbol;Acc:MGI:1916649]	Q3TJL3	Q8K207	5.1	4.4E-05	-2.7	9.8E-03	1.1	3.5E-02	-0.6	5.2E-01
ENSMUST00000044602	carboxylesterase 1G [Source:MGI Symbol;Acc:MGI:88378]	Q3UW56	Q8VCC2	6.9	2.4E-05	6.1	3.3E-04	-0.6	6.0E-01	0.8	2.1E-01
ENSMUST00000044163	CCR4-NOT transcription complex, subunit 4 [Source:MGI Symbol;Acc:MGI:1859026]		Q8BT14	1.1	9.0E-02	0.6	4.7E-01	-0.5	3.6E-01	0.0	9.6E-01
ENSMUST00000044604	beta-gamma crystallin domain containing 3 [Source:MGI Symbol;Acc:MGI:2676311]		Q80W49	-2.8	5.4E-04	2.7	2.8E-03	-5.3	1.8E-04	0.1	8.3E-01
ENSMUST00000044620	breast cancer 2, early onset [Source:MGI Symbol;Acc:MGI:109337]		P97929	3.1	1.2E-04	-3.7	1.1E-02	-0.5	4.4E-01	0.7	5.5E-01
ENSMUST00000044624	potassium channel, subfamily K, member 9 [Source:MGI Symbol;Acc:MGI:3521816]		Q3LS21	6.0	1.5E-04	5.8	3.2E-04	-1.4	2.3E-01	-0.5	4.3E-01
ENSMUST00000044634	te carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 [Source:MGI Symbol;Acc:MGI:2445		Q8BZ09	9.3	2.6E-04	8.8	6.9E-04	1.0	5.9E-01	0.9	2.8E-01
ENSMUST00000044189	SUMO1/sentrin specific peptidase 1 [Source:MGI Symbol;Acc:MGI:2445054]		P59110	-1.1	5.3E-02	0.6	3.6E-01	1.0	5.7E-02	-0.7	2.6E-01
ENSMUST00000044672	cyclin-dependent kinase 19 [Source:MGI Symbol;Acc:MGI:1925584]	B7ZMT1	Q8BWD8	-3.3	3.9E-03	4.2	6.1E-03	-1.2	3.2E-01	-0.5	5.5E-01
ENSMUST00000044681	ADP-ribosylation factor-like 6 interacting protein 5 [Source:MGI Symbol;Acc:MGI:1929501]		Q8R5J9	-5.4	7.0E-07	5.2	1.5E-04	-0.1	9.2E-01	-0.2	7.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000044200	NOP2 nucleolar protein [Source:MGI Symbol;Acc:MGI:107891]	E9QN31		-0.2	6.3E-01	0.1	9.0E-01	0.2	6.0E-01	-0.1	8.9E-01
ENSMUST00000044687	interferon, alpha-inducible protein 27 like 2B [Source:MGI Symbol;Acc:MGI:1916390]		Q8VC49	5.5	1.8E-03	6.1	1.0E-03	0.9	4.8E-01	0.3	7.0E-01
ENSMUST00000044691	BCL2-associated athanogene 2 [Source:MGI Symbol;Acc:MGI:1891254]		Q91YN9	2.4	2.2E-02	-1.0	1.1E-01	0.9	4.3E-02	-0.2	7.8E-01
ENSMUST00000044694	tetratricopeptide repeat domain 36 [Source:MGI Symbol;Acc:MGI:2384760]		Q8VBW8	3.6	1.6E-02	5.1	1.3E-03	-1.1	3.5E-01	0.3	6.6E-01
ENSMUST00000044702	FERM and PDZ domain containing 3 [Source:MGI Symbol;Acc:MGI:3646547]	Q8BXG0		5.3	5.0E-04	6.7	1.3E-03	0.2	8.8E-01	-0.4	6.2E-01
ENSMUST00000044705	V-set and transmembrane domain containing 2B [Source:MGI Symbol;Acc:MGI:1914525]		Q9JME9	6.9	7.3E-05	-3.7	5.2E-03	-0.9	1.6E-01	-0.5	6.4E-01
ENSMUST00000044711	sorting nexin 22 [Source:MGI Symbol;Acc:MGI:2685966]	Q8C084		3.2	4.6E-04	7.0	1.2E-04	0.4	7.0E-01	-0.5	4.5E-01
ENSMUST00000044725	T cell leukemia translocation altered gene [Source:MGI Symbol;Acc:MGI:1918829]		Q8VEA7	-4.1	1.2E-04	2.1	3.8E-02	-1.0	2.1E-01	-0.8	2.8E-01
ENSMUST00000044729	coiled-coil domain containing 129 [Source:MGI Symbol;Acc:MGI:2685304]		Q14B48	7.2	1.2E-04	8.4	3.8E-07	0.9	1.9E-01	-0.7	3.8E-02
ENSMUST00000044234	transforming growth factor, beta receptor I [Source:MGI Symbol;Acc:MGI:98728]		Q64729	0.9	6.2E-01	2.3	3.7E-01	1.1	5.1E-01	-0.2	9.2E-01
ENSMUST00000044730	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6 [Source:MGI Symbol;Acc:M	B1AR09		6.0	1.5E-02	6.2	1.9E-03	-2.3	2.0E-01	0.4	6.8E-01
ENSMUST00000044250	alkB, alkylation repair homolog 5 (E. coli) [Source:MGI Symbol;Acc:MGI:2144489]		Q3TSG4	-1.0	8.1E-02	-0.6	4.3E-01	1.2	3.6E-02	0.8	2.5E-01
ENSMUST00000044734	regulating synaptic membrane exocytosis 4 [Source:MGI Symbol;Acc:MGI:2674366]		P60191	8.9	7.3E-06	-2.6	1.2E-02	0.5	2.5E-01	-0.2	8.4E-01
ENSMUST00000044260	ubiquitin specific peptidase 37 [Source:MGI Symbol;Acc:MGI:2442483]		Q8C0R0	-0.1	8.7E-01	1.6	2.4E-02	0.9	1.1E-01	-0.9	1.4E-01
ENSMUST00000044746	mitochondrial transcription termination factor 1a [Source:MGI Symbol;Acc:MGI:1918240]		Q8CHZ9	-5.3	3.0E-04	-3.6	3.8E-02	1.2	1.8E-01	-3.2	1.3E-01
ENSMUST00000044766	RIKEN cDNA 4930402H24 gene [Source:MGI Symbol;Acc:MGI:1923029]		Q7TT23	1.8	1.7E-02	-6.8	1.0E-04	0.7	1.2E-01	0.5	6.6E-01
ENSMUST00000044767	neurogenic differentiation 6 [Source:MGI Symbol;Acc:MGI:106593]	Q5M8T7	P48986	7.0	9.6E-06	8.2	7.3E-05	-0.5	7.1E-01	0.3	6.1E-01
ENSMUST00000044773	FERM and PDZ domain containing 1 [Source:MGI Symbol;Acc:MGI:2446274]		A2AKB4	6.9	2.8E-03	2.7	8.1E-03	-0.6	4.5E-01	-0.4	5.8E-01
ENSMUST00000044790	forkhead box N4 [Source:MGI Symbol;Acc:MGI:2151057]		Q8K3Q3	7.5	3.9E-05	7.9	9.2E-05	-0.2	8.7E-01	0.0	9.6E-01
ENSMUST00000044792	regulator of calcineurin 2 [Source:MGI Symbol;Acc:MGI:1858219]	Q543P2	Q9JHG2	8.1	4.2E-06	5.8	4.7E-03	-0.5	7.6E-01	-0.1	9.4E-01
ENSMUST00000044795	nucleoporin 133 [Source:MGI Symbol;Acc:MGI:2442620]		Q8R0G9	2.7	3.0E-04	4.9	4.1E-03	-0.1	9.2E-01	0.2	8.2E-01
ENSMUST00000044798	potassium channel, subfamily K, member 15 [Source:MGI Symbol;Acc:MGI:2675209]	B2RVL1		6.2	1.4E-03	7.6	7.4E-05	-0.7	5.9E-01	0.3	5.5E-01
ENSMUST00000044324	ankyrin repeat domain 33B [Source:MGI Symbol;Acc:MGI:1917904]	H7BX04		2.4	1.7E-01	0.7	7.1E-01	-0.8	6.3E-01	0.9	6.0E-01
ENSMUST00000044331	K(lysine) acetyltransferase 6A [Source:MGI Symbol;Acc:MGI:2442415]	G3X940		-0.8	3.9E-01	-4.2	2.6E-02	0.1	9.0E-01	3.5	4.9E-02
ENSMUST00000044332	ceramide kinase [Source:MGI Symbol;Acc:MGI:2386052]		Q8K4Q7	0.3	5.9E-01	0.4	5.1E-01	0.1	8.9E-01	-0.1	8.8E-01
ENSMUST00000044804	corneodesmosin [Source:MGI Symbol;Acc:MGI:3505689]		Q7TPC1	8.0	2.2E-05	6.5	2.8E-05	1.5	8.1E-02	-0.2	6.3E-01
ENSMUST00000044823	zinc finger SWIM-type containing 5 [Source:MGI Symbol;Acc:MGI:1921714]		Q80TC6	7.0	4.4E-06	2.0	4.9E-03	-0.8	1.4E-01	-0.7	1.4E-01
ENSMUST00000044828	leucine-rich repeat-containing G protein-coupled receptor 6 [Source:MGI Symbol;Acc:MGI:2441805]		Q3UVD5	8.1	6.8E-07	-1.7	2.0E-01	-0.7	3.9E-01	-1.7	2.1E-01
ENSMUST00000044857	trafficking protein particle complex 5 [Source:MGI Symbol;Acc:MGI:1913932]		Q9CQA1	-1.8	9.7E-03	-5.0	8.4E-04	0.3	4.3E-01	-0.5	6.7E-01
ENSMUST00000044858	retinoid X receptor beta [Source:MGI Symbol;Acc:MGI:98215]	Q3TWJ1		-5.7	4.3E-05	-0.6	5.0E-01	0.4	5.4E-01	-1.3	1.6E-01
ENSMUST00000044878	alkaline phosphatase 3, intestine, not Mn requiring [Source:MGI Symbol;Acc:MGI:87984]	F8VQM0		8.2	2.3E-05	4.8	5.0E-04	-3.3	1.4E-02	1.3	6.0E-02
ENSMUST00000044384	aldehyde dehydrogenase 1 family, member B1 [Source:MGI Symbol;Acc:MGI:1919785]		Q9CZS1	1.5	5.0E-02	2.0	3.6E-02	-0.1	8.8E-01	-0.6	4.1E-01
ENSMUST00000044895	regulator of calcineurin 2 [Source:MGI Symbol;Acc:MGI:1858219]	Q8VIP4		6.7	1.9E-04	1.7	8.7E-02	-0.6	4.7E-01	0.0	9.9E-01
ENSMUST00000044911	STIP1 homology and U-Box containing protein 1 [Source:MGI Symbol;Acc:MGI:1891731]		Q9WUD1	-3.1	3.5E-04	4.5	1.7E-03	-1.4	1.9E-01	-0.6	4.8E-01
ENSMUST00000044922	heparan sulfate (glucosamine) 3-O-sulfotransferase 6 [Source:MGI Symbol;Acc:MGI:3580487]	A2RTI7	Q5GFD5	5.9	4.3E-04	4.9	1.1E-02	-2.6	1.7E-01	-2.0	8.3E-02
ENSMUST00000044405	lysophosphatidic acid receptor 6 [Source:MGI Symbol;Acc:MGI:1914418]		Q8BMC0	1.7	4.3E-02	0.6	4.7E-01	-1.0	1.8E-01	0.1	9.5E-01
ENSMUST00000044415	aminopeptidase-like 1 [Source:MGI Symbol;Acc:MGI:2448523]		Q6NSR8	0.4	4.6E-01	1.4	6.3E-02	-0.2	7.3E-01	-1.2	9.4E-02
ENSMUST00000044923	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 [Source:MGI Symbol;Acc:MGI:1351337]		Q9ESV0	-7.2	1.3E-03	4.4	4.0E-05	-0.2	7.0E-01	-0.5	2.8E-01
ENSMUST00000044926	coiled-coil domain containing 151 [Source:MGI Symbol;Acc:MGI:1924859]	G3X951		7.5	1.9E-03	2.4	1.1E-01	-0.6	6.4E-01	3.4	9.3E-03
ENSMUST00000044970	mannoside acetylglucosaminyltransferase 3 [Source:MGI Symbol;Acc:MGI:104532]	Q5RKT9		7.5	1.8E-06	8.6	1.6E-02	-0.9	7.8E-01	-1.3	4.3E-01
ENSMUST00000044972	FK506 binding protein 6 [Source:MGI Symbol;Acc:MGI:2137612]		Q91XW8	9.7	3.0E-04	6.6	9.0E-05	-2.2	8.1E-02	0.2	7.8E-01
ENSMUST00000044977	rier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16 [Source:MGI Symbol;Acc:MGI:		Q8C0K5	-1.9	9.9E-03	2.2	1.2E-02	-3.4	1.0E-03	-0.4	5.2E-01
ENSMUST00000044443	ankyrin 2, brain [Source:MGI Symbol;Acc:MGI:88025]		Q8C8R3	0.7	7.1E-01	1.4	5.0E-01	-1.6	3.7E-01	-2.2	2.8E-01
ENSMUST00000044989	family with sequence similarity 90, member A1B [Source:MGI Symbol;Acc:MGI:1921682]	Q9D4F3		6.3	1.4E-04	5.6	3.1E-04	-1.3	2.2E-01	-0.7	2.4E-01
ENSMUST00000045004	dopey family member 2 [Source:MGI Symbol;Acc:MGI:1917278]		Q3UHQ6	-1.8	2.3E-03	-3.1	2.5E-03	0.9	4.9E-02	-1.3	1.3E-01
ENSMUST00000045008	camello-like 2 [Source:MGI Symbol;Acc:MGI:2136446]		Q8CHQ9	6.1	1.4E-04	3.1	2.4E-04	0.4	3.8E-01	0.2	6.6E-01
ENSMUST00000045016	chaperonin containing TCP1, subunit 8 (theta)-like 1 [Source:MGI Symbol;Acc:MGI:2685289]	Q80YT3		7.6	6.8E-05	4.1	8.3E-04	-1.9	5.6E-02	0.2	7.7E-01
ENSMUST00000045022	NLR family, pyrin domain containing 2 [Source:MGI Symbol;Acc:MGI:3041206]	Q4PLS0		6.0	1.4E-04	-3.1	3.9E-03	-0.7	1.7E-01	0.2	7.8E-01
ENSMUST00000045029	phosphatidylinositol glycan anchor biosynthesis, class K [Source:MGI Symbol;Acc:MGI:1913863]	Q8BL63		-5.8	3.0E-03	-6.6	2.4E-02	1.3	2.1E-01	1.3	6.1E-01
ENSMUST00000045054	TRPM8 channel-associated factor 1 [Source:MGI Symbol;Acc:MGI:1914665]		Q8BNE1	6.7	1.6E-04	-4.2	2.8E-03	0.4	4.2E-01	-2.3	1.0E-01
ENSMUST00000045066	olfactory receptor 1509 [Source:MGI Symbol;Acc:MGI:3031343]	Q7TQQ0		5.7	2.7E-04	-5.2	7.7E-04	1.2	2.1E-02	0.8	4.6E-01
ENSMUST00000045068	complexin 3 [Source:MGI Symbol;Acc:MGI:2384571]		Q8R1B5	7.4	8.7E-05	6.5	1.8E-05	-1.5	1.1E-01	0.3	5.2E-01
ENSMUST00000044492	A kinase (PRKA) anchor protein (yotiao) 9 [Source:MGI Symbol;Acc:MGI:2178217]	E9QQ10		-0.2	7.6E-01	-0.7	3.3E-01	-0.6	2.0E-01	-0.1	8.9E-01
ENSMUST00000044503	raftlin lipid raft linker 1 [Source:MGI Symbol;Acc:MGI:1923688]		Q6A0D4	3.2	1.3E-01	3.4	1.8E-01	-0.3	9.0E-01	-0.4	8.1E-01
ENSMUST00000045075	CD300 molecule-like family member d [Source:MGI Symbol;Acc:MGI:2442358]		Q8VCH2	-2.8	4.4E-03	6.9	5.3E-04	0.7	6.0E-01	-0.5	5.2E-01
ENSMUST00000044507	inositol polyphosphate 5-phosphatase J [Source:MGI Symbol;Acc:MGI:2158663]		P59644	-0.9	4.9E-01	2.7	1.8E-01	3.2	6.8E-02	-0.4	7.9E-01
ENSMUST00000044509	TSPY-like 2 [Source:MGI Symbol;Acc:MGI:106244]		Q7TQI8	-3.2	5.5E-02	-2.3	1.9E-01	-0.1	9.1E-01	-1.0	5.8E-01
ENSMUST00000045085	glutamate receptor, ionotropic, NMDA3B [Source:MGI Symbol;Acc:MGI:2150393]		Q91ZU9	4.3	3.3E-04	-2.9	7.7E-04	1.3	3.1E-03	-0.5	4.5E-01
ENSMUST00000045091	kin of IRRE like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1914953]	G5E8B6		7.7	4.9E-04	5.0	7.3E-03	1.0	4.7E-01	-0.7	4.3E-01
ENSMUST00000045096	protein phosphatase 1, regulatory (inhibitor) subunit 3A [Source:MGI Symbol;Acc:MGI:2153588]		Q99MR9	6.9	7.8E-05	3.6	2.5E-04	-1.4	4.4E-02	0.1	8.2E-01
ENSMUST00000045102	GIPC PDZ domain containing family, member 3 [Source:MGI Symbol;Acc:MGI:2387006]		Q8R5M0	5.8	5.5E-05	6.7	1.2E-04	-1.4	2.5E-01	-0.4	5.3E-01
ENSMUST00000045105	spire homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1915416]	D3YTL8		8.9	1.6E-05	7.6	1.8E-04	-0.7	6.3E-01	-0.4	5.2E-01
ENSMUST00000044535	family with sequence similarity 175, member A [Source:MGI Symbol;Acc:MGI:1917931]		Q8BPZ8	6.2	3.7E-02	2.7	4.4E-01	-0.7	8.3E-01	2.8	2.9E-01
ENSMUST00000045108	DNA segment, Chr 1, Pasteur Institute 1 [Source:MGI Symbol;Acc:MGI:91842]	B9EIA2	P16381	7.1	5.1E-05	7.9	1.4E-04	-0.7	6.1E-01	-0.2	8.2E-01
ENSMUST00000045110	dual serine/threonine and tyrosine protein kinase [Source:MGI Symbol;Acc:MGI:1925064]		Q6XUX1	-1.5	2.5E-02	5.0	1.2E-03	0.7	4.9E-01	-1.0	2.3E-01
ENSMUST00000045114	ribosome production factor 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914489]	G3X926		5.2	2.8E-04	3.5	2.6E-02	-0.2	8.6E-01	0.0	9.7E-01
ENSMUST00000044556	TBC1 domain family, member 13 [Source:MGI Symbol;Acc:MGI:2385326]	Q3TZ63	Q8R3D1	0.4	5.1E-01	0.0	9.6E-01	0.4	5.5E-01	0.8	3.6E-01
ENSMUST00000044564	forkhead box J3 [Source:MGI Symbol;Acc:MGI:2443432]		Q8BUR3	-3.1	4.2E-02	-5.1	6.5E-02	-0.1	9.1E-01	1.8	4.7E-01
ENSMUST00000045127	WAP four-disulfide core domain 5 [Source:MGI Symbol;Acc:MGI:2384800]	Q4KXB6		7.9	2.5E-05	-0.4	8.1E-01	-4.9	1.0E-02	2.7	1.1E-01
ENSMUST00000045140	TRPM8 channel-associated factor 1 [Source:MGI Symbol;Acc:MGI:1914665]		Q8BNE1	7.8	1.6E-04	-6.1	1.0E-04	-1.4	6.8E-03	-1.3	2.8E-01
ENSMUST00000045142	catenin (cadherin associated protein), alpha-like 1 [Source:MGI Symbol;Acc:MGI:1859649]		O88327	2.6	2.8E-03	-5.4	2.2E-05	0.2	4.3E-01	0.6	3.7E-01
ENSMUST00000045153	phosphoinositide-3-kinase interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917016]		Q7TMJ8	-3.7	2.1E-03	4.3	3.5E-04	-0.8	2.9E-01	-0.1	8.6E-01
ENSMUST00000045154	thymocyte selection associated family member 2 [Source:MGI Symbol;Acc:MGI:2446213]		Q91YX0	-5.2	1.3E-04	5.3	1.5E-04	-1.4	1.4E-01	0.1	7.9E-01
ENSMUST00000045173	transforming growth factor, beta induced [Source:MGI Symbol;Acc:MGI:99959]	A1L353	P82198	-7.3	1.1E-05	-1.8	2.6E-02	0.9	5.1E-02	0.0	9.5E-01
ENSMUST00000044608	jumonji, AT rich interactive domain 2 [Source:MGI Symbol;Acc:MGI:104813]		Q62315	2.4	3.0E-01	1.5	5.7E-01	-0.7	7.2E-01	0.2	9.4E-01
ENSMUST00000045174	yippee-like 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:1916937]		P62700	-6.7	3.3E-07	3.3	4.2E-04	0.2	7.5E-01	0.0	1.0E+00
ENSMUST00000044622	ectopic P-granules autophagy protein 5 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1918673]		Q80TA9	0.8	3.7E-02	1.4	1.2E-02	0.7	7.3E-02	0.1	7.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000045186	ribosomal protein L3-like [Source:MGI Symbol;Acc:MGI:1913461]	Q9CQ09		-4.4	7.8E-04	6.2	2.1E-04	-0.5	6.4E-01	-0.7	2.5E-01
ENSMUST00000045196	K+ voltage-gated channel, subfamily S, 1 [Source:MGI Symbol;Acc:MGI:1197019]		O35173	6.3	1.7E-05	7.9	1.6E-03	-0.6	7.6E-01	0.8	3.8E-01
ENSMUST00000044638	syntaxin 16 [Source:MGI Symbol;Acc:MGI:1923396]	F6X4N5		-2.7	1.4E-01	-5.3	1.7E-01	0.5	7.0E-01	3.1	4.0E-01
ENSMUST00000044642	MICAL-like 2 [Source:MGI Symbol;Acc:MGI:2444818]		Q3TN34	2.1	3.9E-01	4.1	2.1E-01	0.1	9.8E-01	-1.9	3.9E-01
ENSMUST00000044660	armadillo repeat containing 5 [Source:MGI Symbol;Acc:MGI:2384586]		Q5EBP3	0.2	7.5E-01	0.9	3.2E-01	1.0	1.5E-01	0.3	6.7E-01
ENSMUST00000045215	ret finger protein-like 4 [Source:MGI Symbol;Acc:MGI:2149590]		Q8VH31	6.4	1.1E-02	-4.3	1.1E-02	1.0	1.6E-01	2.0	1.7E-01
ENSMUST00000044673	tRNA methyltransferase 10B [Source:MGI Symbol;Acc:MGI:1917184]		Q9D075	-1.4	4.3E-02	-0.9	2.3E-01	-0.3	5.2E-01	-0.8	2.5E-01
ENSMUST00000045218	pericentriolar material 1 [Source:MGI Symbol;Acc:MGI:1277958]		Q9R0L6	-3.1	2.8E-04	-5.4	6.7E-06	0.4	1.3E-01	0.4	5.0E-01
ENSMUST00000045228	zinc finger with KRAB and SCAN domains 8 [Source:MGI Symbol;Acc:MGI:1913815]	Q8BSL0		2.5	7.9E-04	6.4	1.6E-03	-0.2	9.0E-01	-1.0	2.4E-01
ENSMUST00000045245	tudor and KH domain containing protein [Source:MGI Symbol;Acc:MGI:1919884]		Q80VL1	5.0	2.1E-03	1.2	2.6E-01	-0.8	4.0E-01	0.4	6.3E-01
ENSMUST00000045262	adenylate kinase 5 [Source:MGI Symbol;Acc:MGI:2677491]		Q920P5	4.7	6.0E-05	3.7	2.8E-02	-0.6	6.9E-01	-0.7	5.2E-01
ENSMUST00000045270	-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human) [Source:MGI Symbol;Acc:MGI:1333		O70374	-5.2	1.1E-04	5.6	6.9E-04	-0.6	6.3E-01	-0.9	2.3E-01
ENSMUST00000045277	epsin 1 [Source:MGI Symbol;Acc:MGI:1333763]		Q80VP1	-9.6	2.5E-06	6.1	3.6E-04	-0.5	6.8E-01	0.3	6.2E-01
ENSMUST00000045286	transmembrane protein 59-like [Source:MGI Symbol;Acc:MGI:1915187]		Q7TNI2	8.6	1.0E-04	3.1	1.5E-03	-0.2	7.6E-01	-0.1	8.1E-01
ENSMUST00000044721	ATPase, H+ transporting, lysosomal V0 subunit A1 [Source:MGI Symbol;Acc:MGI:103286]		Q9Z1G4	-2.0	5.0E-01	-1.5	7.0E-01	0.7	8.0E-01	0.2	9.5E-01
ENSMUST00000045288	transforming growth factor, beta 2 [Source:MGI Symbol;Acc:MGI:98726]		P27090	9.8	8.9E-06	-3.1	3.7E-03	1.0	4.4E-02	0.0	9.7E-01
ENSMUST00000045289	patatin-like phospholipase domain containing 3 [Source:MGI Symbol;Acc:MGI:2151796]	E9QNZ9		6.4	4.2E-06	7.1	2.6E-04	-0.6	6.7E-01	-0.4	5.3E-01
ENSMUST00000045295	patatin-like phospholipase domain containing 7 [Source:MGI Symbol;Acc:MGI:2385325]		A2AJ88	-5.6	2.7E-03	0.9	7.4E-01	-1.3	5.6E-01	3.8	1.4E-01
ENSMUST00000045301	histone cluster 1, H1d [Source:MGI Symbol;Acc:MGI:107502]	Q149Z9	P43277	5.1	4.5E-04	8.8	2.7E-05	-0.3	8.1E-01	-0.2	6.7E-01
ENSMUST00000045312	structural maintenance of chromosomes 1A [Source:MGI Symbol;Acc:MGI:1344345]		Q9CU62	-5.2	5.9E-05	-5.2	1.9E-03	-0.3	5.9E-01	-0.4	7.7E-01
ENSMUST00000044749	myosin IIIA [Source:MGI Symbol;Acc:MGI:2183924]	F6QNG5		4.1	8.3E-02	5.2	5.5E-02	-0.3	9.2E-01	-1.3	3.7E-01
ENSMUST00000044751	zyg-11 related, cell cycle regulator [Source:MGI Symbol;Acc:MGI:2442511]		Q80ZJ6	-1.3	1.6E-01	0.1	9.0E-01	0.2	7.6E-01	-1.2	2.6E-01
ENSMUST00000045319	G protein-coupled receptor 142 [Source:MGI Symbol;Acc:MGI:2668437]		Q7TQN9	6.0	4.1E-04	2.3	2.2E-02	0.7	3.4E-01	0.1	8.6E-01
ENSMUST00000045351	autophagy related 2A [Source:MGI Symbol;Acc:MGI:1916291]		Q6P4T0	-1.8	2.2E-02	7.8	3.1E-05	0.0	9.9E-01	-0.8	1.2E-01
ENSMUST00000045356	ribosomal protein L37 [Source:MGI Symbol;Acc:MGI:1914531]		Q9D823	-5.9	7.5E-05	3.7	6.5E-02	-1.6	4.2E-01	1.7	2.1E-01
ENSMUST00000044776	glutaminase 2 (liver, mitochondrial) [Source:MGI Symbol;Acc:MGI:2143539]		Q571F8	3.6	1.8E-01	3.0	2.8E-01	-0.4	8.7E-01	0.1	9.4E-01
ENSMUST00000044781	coiled-coil domain containing 30 [Source:MGI Symbol;Acc:MGI:1920582]		Q8BVF4	2.8	9.6E-02	6.3	2.4E-03	-0.5	7.6E-01	-4.0	5.3E-03
ENSMUST00000045376	adenosine kinase [Source:MGI Symbol;Acc:MGI:87930]		P55264	-3.8	1.6E-04	7.0	1.3E-04	-0.6	6.1E-01	-0.1	8.3E-01
ENSMUST00000045450	integrator complex subunit 7 [Source:MGI Symbol;Acc:MGI:1924315]			3.2	6.6E-05	8.1	2.4E-05	0.2	8.8E-01	0.1	8.2E-01
ENSMUST00000045454	family with sequence similarity 207, member A [Source:MGI Symbol;Acc:MGI:1916334]		P58468	-1.9	3.3E-03	2.9	1.0E-03	0.2	6.9E-01	0.0	9.7E-01
ENSMUST00000045466	zinc finger protein 644 [Source:MGI Symbol;Acc:MGI:1277212]	E9Q624		-5.4	4.5E-05	5.0	1.0E-02	-0.5	7.5E-01	0.7	4.9E-01
ENSMUST00000045467	H2-K region expressed gene 6 [Source:MGI Symbol;Acc:MGI:95911]		P50171	-5.6	7.2E-05	8.1	3.6E-05	-0.6	5.9E-01	-0.8	1.6E-01
ENSMUST00000044812	G patch domain containing 2 [Source:MGI Symbol;Acc:MGI:1915019]	E9PY25		0.8	3.3E-01	-0.3	7.2E-01	-0.5	4.8E-01	0.6	5.1E-01
ENSMUST00000045473	transmembrane and coiled-coil domains 2 [Source:MGI Symbol;Acc:MGI:1916125]		Q80W04	5.2	4.3E-03	6.6	5.7E-05	-0.2	8.4E-01	0.1	7.9E-01
ENSMUST00000044825	NADH dehydrogenase (ubiquinone) complex I, assembly factor 5 [Source:MGI Symbol;Acc:MGI:1916737]		A2APY7	0.0	9.5E-01	-3.5	6.7E-03	-0.6	3.1E-01	2.9	1.4E-02
ENSMUST00000045477	serine/threonine kinase 32A [Source:MGI Symbol;Acc:MGI:2442403]		Q8BGW6	8.5	1.1E-05	4.5	4.8E-05	-3.8	3.9E-04	-0.2	6.8E-01
ENSMUST00000044833	2'-5' oligoadenylate synthetase 3 [Source:MGI Symbol;Acc:MGI:2180850]		Q8VI93	-0.3	7.0E-01	0.5	5.8E-01	0.9	2.3E-01	0.1	9.0E-01
ENSMUST00000044844	major facilitator superfamily domain containing 12 [Source:MGI Symbol;Acc:MGI:3604804]		Q3U481	0.2	7.3E-01	1.0	1.9E-01	0.6	2.9E-01	-0.2	7.7E-01
ENSMUST00000044850	ATP-binding cassette, sub-family A (ABC1), member 9 [Source:MGI Symbol;Acc:MGI:2386796]		Q8K449	1.3	1.1E-01	0.3	7.1E-01	-1.8	2.9E-02	-0.8	3.8E-01
ENSMUST00000045487	ras homolog gene family, member U [Source:MGI Symbol;Acc:MGI:1916831]		Q9EQT3	-2.3	3.9E-03	-0.8	2.9E-01	1.2	3.5E-02	0.2	7.7E-01
ENSMUST00000045512	DENN/MADD domain containing 4C [Source:MGI Symbol;Acc:MGI:1914769]	E9Q449		9.6	4.7E-06	-4.8	1.1E-03	1.3	1.2E-02	0.4	7.3E-01
ENSMUST00000045517	FLYWCH-type zinc finger 1 [Source:MGI Symbol;Acc:MGI:2442638]		Q8CI03	4.9	5.3E-03	6.1	2.6E-04	-1.4	2.4E-01	0.7	2.8E-01
ENSMUST00000045521	deltex 4 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2672905]		Q6PDK8	-2.4	1.9E-03	7.8	1.1E-04	-0.5	7.3E-01	-1.6	2.8E-02
ENSMUST00000045526	RIKEN cDNA 2010001E11 gene [Source:MGI Symbol;Acc:MGI:1919295]	G5E8A5		7.4	7.4E-05	-1.7	3.5E-02	0.9	5.1E-02	-0.5	5.2E-01
ENSMUST00000045537	cholinergic receptor, muscarinic 4 [Source:MGI Symbol;Acc:MGI:88399]	Q0VBU3	P32211	6.7	2.0E-04	5.9	1.5E-03	-0.2	8.9E-01	-0.2	8.3E-01
ENSMUST00000045540	suppressor of cytokine signaling 7 [Source:MGI Symbol;Acc:MGI:2651588]		Q8VHQ2	1.3	3.3E-02	-5.9	4.4E-03	0.4	5.6E-01	-0.8	6.7E-01
ENSMUST00000045542	testis-specific kinase 2 [Source:MGI Symbol;Acc:MGI:2385204]		Q8VCT9	-6.0	4.4E-05	5.5	1.8E-02	-0.7	7.5E-01	1.3	2.9E-01
ENSMUST00000044937	lectin, mannose-binding 1 like [Source:MGI Symbol;Acc:MGI:2667537]		Q8VCD3	4.0	3.9E-02	5.5	2.1E-02	-0.6	7.6E-01	-2.1	1.6E-01
ENSMUST00000044949	DPH1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2151233]		Q5NCQ5	-0.2	8.3E-01	-0.1	9.2E-01	-0.7	3.2E-01	-0.8	3.6E-01
ENSMUST00000044954	solute carrier family 30 (zinc transporter), member 1 [Source:MGI Symbol;Acc:MGI:1345281]	Q3UM63	Q60738	-1.1	6.6E-02	0.0	9.8E-01	1.3	3.6E-02	0.1	8.8E-01
ENSMUST00000045550	X Kell blood group precursor related family member 8 homolog [Source:MGI Symbol;Acc:MGI:2685877]		Q8C0T0	2.1	1.1E-03	3.5	2.1E-04	-4.3	1.7E-04	-0.3	5.6E-01
ENSMUST00000045557	e carrier family 7 (cationic amino acid transporter, y+ system), member 5 [Source:MGI Symbol;Acc:MGI:1298		Q9Z127	-2.2	1.1E-02	8.3	2.1E-03	-0.4	8.7E-01	1.0	2.9E-01
ENSMUST00000045560	solute carrier family 19, member 3 [Source:MGI Symbol;Acc:MGI:1931307]		Q99PL8	6.2	1.1E-03	-1.3	1.3E-01	0.8	1.2E-01	0.2	7.6E-01
ENSMUST00000044985	BAH domain and coiled-coil containing 1 [Source:MGI Symbol;Acc:MGI:2679272]	E9Q7G4		6.3	4.9E-02	6.0	8.1E-02	-0.3	9.2E-01	-0.1	9.7E-01
ENSMUST00000045583	corticotropin releasing hormone binding protein [Source:MGI Symbol;Acc:MGI:88497]	Q3UY07	Q60571	6.9	1.0E-04	5.7	5.5E-04	-0.6	6.2E-01	0.0	9.5E-01
ENSMUST00000045586	ligand dependent nuclear receptor corepressor-like [Source:MGI Symbol;Acc:MGI:2651932]		Q3U285	-3.1	7.8E-04	-1.0	1.1E-01	0.8	6.7E-02	-0.1	9.3E-01
ENSMUST00000045593	diacylglycerol lipase, beta [Source:MGI Symbol;Acc:MGI:2442032]		Q91WC9	-2.8	3.4E-02	3.5	5.8E-03	-2.3	4.3E-02	0.3	7.2E-01
ENSMUST00000045602	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 [Source:MGI Symbol;Acc:MGI:1915592]		Q9DCS9	-7.6	1.4E-05	7.9	9.3E-05	-0.7	6.1E-01	-1.0	1.5E-01
ENSMUST00000045604	mitochondrial ribosomal protein L41 [Source:MGI Symbol;Acc:MGI:1333816]		Q9CQN7	-3.2	1.3E-03	7.0	2.1E-04	0.5	6.5E-01	-0.4	5.3E-01
ENSMUST00000045026	sperm associated antigen 5 [Source:MGI Symbol;Acc:MGI:1927470]		Q7TME2	-0.8	1.7E-01	-1.0	1.8E-01	0.1	8.7E-01	0.3	6.8E-01
ENSMUST00000045617	heparanase [Source:MGI Symbol;Acc:MGI:1343124]		Q6YGZ1	-1.7	1.1E-02	-4.4	4.5E-02	0.3	7.7E-01	-1.1	5.8E-01
ENSMUST00000045041	:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 [Source:MGI Symbol;Acc:MGI	Q60GT3	Q8BGT9	1.8	2.0E-01	2.6	1.1E-01	-0.2	8.6E-01	-1.1	4.3E-01
ENSMUST00000045621	bromodomain adjacent to zinc finger domain, 2A [Source:MGI Symbol;Acc:MGI:2151152]	F8VPM0		-2.2	4.6E-04	2.6	1.0E-02	-3.7	5.6E-03	0.3	6.3E-01
ENSMUST00000045628	R3H domain containing 4 [Source:MGI Symbol;Acc:MGI:1924814]	B2RRK4	Q4VBF2	-6.0	5.5E-05	6.2	2.5E-04	-0.5	6.5E-01	-1.1	1.1E-01
ENSMUST00000045644	ARP5 actin-related protein 5 [Source:MGI Symbol;Acc:MGI:1924748]	A0A0A0MQ89		-2.8	1.0E-03	7.2	5.2E-04	-0.3	8.2E-01	-0.2	8.0E-01
ENSMUST00000045652	BTB (POZ) domain containing 7 [Source:MGI Symbol;Acc:MGI:1917858]		Q8CFE5	-1.8	3.2E-03	-2.7	2.5E-02	0.2	7.5E-01	0.1	9.5E-01
ENSMUST00000045078	glyoxylate reductase/hydroxypyruvate reductase [Source:MGI Symbol;Acc:MGI:1923488]	Q3T9Z2	Q91Z53	-1.0	8.3E-02	0.6	3.6E-01	0.3	5.2E-01	-1.2	6.0E-02
ENSMUST00000045664	ATPase family, AAA domain containing 2B [Source:MGI Symbol;Acc:MGI:2444798]	E9Q166		-1.3	1.6E-02	5.0	1.2E-03	0.7	4.8E-01	0.1	9.0E-01
ENSMUST00000045665	protein phosphatase 1, regulatory (inhibitor) subunit 12B [Source:MGI Symbol;Acc:MGI:1916417]		Q8BG95	2.3	1.3E-03	4.5	2.6E-02	-0.7	6.9E-01	2.5	5.4E-02
ENSMUST00000045674	phosphatidic acid phosphatase type 2 domain containing 2 [Source:MGI Symbol;Acc:MGI:1921661]		Q9D4F2	-1.6	6.9E-03	6.5	2.2E-04	-0.5	7.0E-01	-0.1	8.2E-01
ENSMUST00000045097	guanylate binding protein 7 [Source:MGI Symbol;Acc:MGI:2444421]	Q91Z40		3.7	4.1E-02	1.6	4.6E-01	-0.9	5.7E-01	1.3	5.0E-01
ENSMUST00000045689	mitochondrial ribosomal protein L15 [Source:MGI Symbol;Acc:MGI:1351639]	F8WHN1		-3.9	4.1E-03	6.6	1.1E-04	0.5	6.2E-01	-0.2	6.7E-01
ENSMUST00000045692	F-box and leucine-rich repeat protein 16 [Source:MGI Symbol;Acc:MGI:2448488]	B2RPY3	A2RT62	8.4	3.6E-06	5.4	4.5E-04	-3.6	1.2E-02	-0.2	8.0E-01
ENSMUST00000045699	autophagy/beclin 1 regulator 1 [Source:MGI Symbol;Acc:MGI:2443564]		A2AH22	-7.8	2.5E-04	6.0	2.5E-04	-1.3	2.6E-01	-0.2	6.8E-01
ENSMUST00000045702	solute carrier family 2 (facilitated glucose transporter), member 6 [Source:MGI Symbol;Acc:MGI:2443286]	Q3UDF0		-8.2	1.5E-04	-0.6	4.1E-01	0.8	1.5E-01	-0.1	9.2E-01
ENSMUST00000045706	cystic fibrosis transmembrane conductance regulator [Source:MGI Symbol;Acc:MGI:88388]		P26361	6.0	9.8E-05	5.0	1.6E-03	-0.1	9.3E-01	0.1	9.2E-01
ENSMUST00000045713	NAC alpha domain containing [Source:MGI Symbol;Acc:MGI:3603030]		Q5SWP3	3.3	9.5E-04	7.2	1.1E-04	-0.6	6.0E-01	0.1	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000045138	golgin, RAB6-interacting [Source:MGI Symbol;Acc:MGI:2138271]		Q8BRM2	0.2	6.8E-01	-0.3	6.0E-01	-1.2	1.9E-02	-0.7	2.0E-01
ENSMUST00000045714	ATP-binding cassette, sub-family G (WHITE), member 8 [Source:MGI Symbol;Acc:MGI:1914720]		Q9DBM0	8.3	8.5E-05	7.6	1.1E-03	0.3	8.7E-01	0.4	6.6E-01
ENSMUST00000045717	tudor domain containing 6 [Source:MGI Symbol;Acc:MGI:2679727]	F2Z429		6.4	2.9E-02	0.6	3.2E-01	-3.2	4.3E-04	-1.3	5.2E-02
ENSMUST00000045151	CD300A antigen [Source:MGI Symbol;Acc:MGI:2443411]		Q6SJQ0	0.8	3.0E-01	0.5	6.6E-01	0.3	7.2E-01	0.7	4.7E-01
ENSMUST00000045726	ral guanine nucleotide dissociation stimulator-like 3 [Source:MGI Symbol;Acc:MGI:1918996]		Q3UYI5	7.7	4.6E-05	-2.6	3.1E-02	0.1	8.5E-01	-1.0	4.0E-01
ENSMUST00000045730	A kinase (PRKA) anchor protein (gravin) 12 [Source:MGI Symbol;Acc:MGI:1932576]	B2RRE0	Q9WTQ5	5.9	2.7E-05	-3.8	4.0E-03	0.8	1.5E-01	-0.6	5.8E-01
ENSMUST00000045167	EH domain binding protein 1 [Source:MGI Symbol;Acc:MGI:2667252]		Q69ZW3	3.9	1.7E-01	0.0	1.0E+00	-1.4	6.6E-01	2.5	4.6E-01
ENSMUST00000045736	maestro heat-like repeat family member 2B [Source:MGI Symbol;Acc:MGI:1921905]		Q7M6Y6	8.0	2.6E-05	-5.5	4.0E-04	1.1	3.6E-02	-0.7	5.2E-01
ENSMUST00000045738	solute carrier family 32 (GABA vesicular transporter), member 1 [Source:MGI Symbol;Acc:MGI:1194488]	Q49S98	O35633	1.6	7.0E-03	-5.5	7.3E-06	0.1	6.1E-01	-1.0	1.4E-01
ENSMUST00000045747	wingless-type MMTV integration site family, member 4 [Source:MGI Symbol;Acc:MGI:98957]	Q3ZB23	P22724	7.3	8.6E-06	-2.1	5.0E-02	0.0	9.4E-01	-2.3	5.3E-02
ENSMUST00000045748	pyruvate dehydrogenase kinase, isoenzyme 3 [Source:MGI Symbol;Acc:MGI:2384308]	Q4FJR4	Q922H2	-5.0	2.7E-05	7.2	1.1E-04	0.8	4.5E-01	-0.1	8.5E-01
ENSMUST00000045756	S100 calcium binding protein A10 (calpactin) [Source:MGI Symbol;Acc:MGI:1339468]	Q3TC45	P08207	-7.0	2.7E-06	6.5	1.6E-02	-0.8	7.3E-01	-0.9	5.0E-01
ENSMUST00000045766	WD repeat domain 70 [Source:MGI Symbol;Acc:MGI:1921020]	G3X934		-1.4	7.9E-03	-2.4	7.3E-03	0.8	8.0E-02	0.1	9.2E-01
ENSMUST00000045771	sperm maturation 1 [Source:MGI Symbol;Acc:MGI:1921538]		Q5F289	6.3	9.7E-05	3.1	6.4E-04	0.0	9.9E-01	-0.6	2.1E-01
ENSMUST00000045229	transmembrane and coiled-coil domains 3 [Source:MGI Symbol;Acc:MGI:2444946]		Q8BH01	-0.5	2.0E-01	0.2	6.5E-01	0.5	2.1E-01	-0.3	5.6E-01
ENSMUST00000045235	RIKEN cDNA B630005N14 gene [Source:MGI Symbol;Acc:MGI:2141466]		Q8BXK4	1.2	7.9E-02	1.1	2.1E-01	0.7	3.3E-01	0.7	3.3E-01
ENSMUST00000045243	phosphodiesterase 4D interacting protein (myomegalin) [Source:MGI Symbol;Acc:MGI:1891434]		Q80YT7	0.1	9.3E-01	0.8	3.5E-01	0.5	4.3E-01	-0.2	7.6E-01
ENSMUST00000045779	tweety homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2157091]		Q3TH73	1.4	1.5E-02	2.6	1.8E-02	-4.2	4.9E-03	-1.8	4.5E-02
ENSMUST00000045246	protein kinase N3 [Source:MGI Symbol;Acc:MGI:2388285]		Q8K045	2.8	2.2E-01	4.8	1.2E-01	0.2	9.4E-01	-1.8	3.7E-01
ENSMUST00000045247	WD repeat domain 18 [Source:MGI Symbol;Acc:MGI:2158400]		Q4VBE8	0.3	5.9E-01	0.6	4.0E-01	-0.1	8.9E-01	-0.4	5.9E-01
ENSMUST00000045788	H2A histone family, member Y [Source:MGI Symbol;Acc:MGI:1349392]		Q9QZQ8	-2.8	1.2E-02	4.6	2.0E-04	-0.5	4.6E-01	-0.5	4.3E-01
ENSMUST00000045791	secretory carrier membrane protein 2 [Source:MGI Symbol;Acc:MGI:1346518]	Q3TAL2	Q9ERN0	-4.2	7.7E-05	-3.3	9.8E-03	1.3	2.4E-02	-0.6	6.3E-01
ENSMUST00000045793	ring finger protein 38 [Source:MGI Symbol;Acc:MGI:1920719]	Q3UH35		-6.4	2.5E-03	-6.9	2.2E-04	1.9	6.1E-04	-0.7	5.7E-01
ENSMUST00000045279	jumonji domain containing 4 [Source:MGI Symbol;Acc:MGI:2144404]		Q8BFT6	1.7	5.6E-01	2.6	6.6E-01	4.5	3.3E-01	3.6	4.3E-01
ENSMUST00000045281	5mg-6 homolog, nonsense mediated mRNA decay factor (C. elegans) [Source:MGI Symbol;Acc:MGI:2144117		P61406	0.0	9.7E-01	0.8	1.7E-01	0.7	1.1E-01	-0.1	8.9E-01
ENSMUST00000045807	TSR1 20S rRNA accumulation [Source:MGI Symbol;Acc:MGI:2144566]		Q5SWD9	-3.1	6.9E-03	7.7	4.7E-04	-0.8	6.3E-01	0.2	8.4E-01
ENSMUST00000045827	5-methyltetrahydrofolate-homocysteine methyltransferase reductase [Source:MGI Symbol;Acc:MGI:1891037]			3.9	6.9E-05	6.0	2.6E-04	-3.6	1.5E-02	0.1	8.5E-01
ENSMUST00000045840	G protein-coupled receptor 26 [Source:MGI Symbol;Acc:MGI:2441758]	Q0VBG4	Q8BZA7	8.7	9.8E-08	6.6	2.8E-05	0.4	6.0E-01	0.2	6.7E-01
ENSMUST00000045291	lysine (K)-specific methyltransferase 2C [Source:MGI Symbol;Acc:MGI:2444959]	F8WI37		0.3	4.0E-01	1.1	3.6E-02	0.7	6.2E-02	-0.1	8.3E-01
ENSMUST00000045846	sideroflexin 5 [Source:MGI Symbol;Acc:MGI:2137681]		Q925N0	-3.6	1.4E-03	-6.8	2.7E-02	1.5	1.2E-01	2.7	3.3E-01
ENSMUST00000045296	seven in absentia 1A [Source:MGI Symbol;Acc:MGI:108064]		P61092	-1.9	3.9E-02	-0.5	6.4E-01	0.9	2.2E-01	-0.5	6.1E-01
ENSMUST00000045847	Ets2 repressor factor [Source:MGI Symbol;Acc:MGI:109637]			-1.6	2.2E-02	4.3	2.5E-03	-0.8	4.5E-01	0.0	9.5E-01
ENSMUST00000045303	spinster homolog 2 [Source:MGI Symbol;Acc:MGI:2384936]		Q91VM4	0.3	6.6E-01	1.6	5.9E-02	0.8	2.2E-01	-0.6	4.1E-01
ENSMUST00000045855	heme binding protein 1 [Source:MGI Symbol;Acc:MGI:1333880]			-6.0	1.6E-06	-5.4	2.9E-04	-0.3	4.5E-01	-0.1	8.9E-01
ENSMUST00000045864	TBC1 domain family, member 10c [Source:MGI Symbol;Acc:MGI:1922072]		Q8C9V1	-4.3	3.5E-05	6.5	4.0E-04	-0.6	6.7E-01	-1.0	1.7E-01
ENSMUST00000045325		F8WH01		-4.0	1.6E-01	-5.5	1.1E-01	-2.5	1.3E-01	-0.9	7.9E-01
ENSMUST00000045329	family with sequence similarity 53, member A [Source:MGI Symbol;Acc:MGI:1919225]	E9PV82		2.5	1.8E-01	3.3	1.6E-01	-0.2	9.3E-01	-1.0	5.3E-01
ENSMUST00000045870	ring finger protein 225 [Source:MGI Symbol;Acc:MGI:1924198]		Q9D7D1	4.1	1.3E-04	-0.9	3.6E-01	1.1	9.2E-02	0.1	8.9E-01
ENSMUST00000045884	kelch domain containing 4 [Source:MGI Symbol;Acc:MGI:2384569]	G3X961		-6.1	6.3E-04	-6.4	1.8E-04	-1.5	1.2E-02	-0.9	4.2E-01
ENSMUST00000045366	1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2142		Q8BZJ7	-1.8	5.1E-01	-0.1	9.7E-01	1.1	6.8E-01	-0.6	8.6E-01
ENSMUST00000045368	family with sequence similarity 206, member A [Source:MGI Symbol;Acc:MGI:2677850]		Q80ZQ9	2.1	3.7E-02	3.3	4.6E-02	1.8	1.9E-01	0.6	5.1E-01
ENSMUST00000045372	2,3-bisphosphoglycerate mutase [Source:MGI Symbol;Acc:MGI:1098242]		P15327	-0.4	3.7E-01	-1.4	2.0E-02	-2.1	2.9E-04	-1.1	6.4E-02
ENSMUST00000045374	receptor (calcitonin) activity modifying protein 3 [Source:MGI Symbol;Acc:MGI:1860292]		Q9WUP1	0.4	8.0E-01	2.2	1.3E-01	-2.2	1.2E-01	-4.0	2.0E-02
ENSMUST00000045887	CDGSH iron sulfur domain 1 [Source:MGI Symbol;Acc:MGI:1261855]		Q91WS0	-1.8	1.7E-02	-3.8	6.6E-04	-1.0	3.5E-02	-1.1	1.9E-01
ENSMUST00000045396	RIKEN cDNA 9130011E15 gene [Source:MGI Symbol;Acc:MGI:1918867]		Q6PD19	-0.4	3.3E-01	0.9	1.7E-01	1.2	2.0E-02	-0.1	8.9E-01
ENSMUST00000045402	solute carrier family 38, member 10 [Source:MGI Symbol;Acc:MGI:1919305]		Q5I012	0.5	7.3E-01	0.6	7.9E-01	1.4	4.2E-01	1.3	4.3E-01
ENSMUST00000045441	brain glycogen phosphorylase [Source:MGI Symbol;Acc:MGI:97828]		Q8CI94	0.2	6.2E-01	0.5	3.9E-01	0.2	6.6E-01	-0.1	8.6E-01
ENSMUST00000045892	RIKEN cDNA 4921530L21 gene [Source:MGI Symbol;Acc:MGI:1913982]	Q9CQ47		6.3	2.9E-04	3.7	1.2E-04	0.1	7.9E-01	-0.3	4.1E-01
ENSMUST00000045896	protein kinase C and casein kinase substrate in neurons 1 [Source:MGI Symbol;Acc:MGI:1345181]	Q543Y7	Q61644	4.1	1.2E-04	-1.1	1.2E-01	0.7	1.0E-01	-0.1	8.4E-01
ENSMUST00000045897	prothymosin alpha [Source:MGI Symbol;Acc:MGI:97803]	Q0VGU2	P26350	-4.8	4.9E-03	-4.6	7.3E-04	0.1	8.2E-01	-0.7	5.2E-01
ENSMUST00000045905	fermitin family homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2385001]	Q3TLE2	Q8CIB5	7.3	1.4E-05	-3.5	7.3E-03	1.3	2.7E-02	-0.8	4.9E-01
ENSMUST00000045469	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Source:MGI Symbol;Acc:MGI:1298224]	F8WHW6		-0.1	9.5E-01	-2.8	1.7E-01	-0.5	6.5E-01	2.2	2.5E-01
ENSMUST00000045907	RIKEN cDNA 2700049A03 gene [Source:MGI Symbol;Acc:MGI:1924217]	E9Q0E2		4.9	1.1E-02	3.8	4.2E-02	-1.7	3.0E-01	-0.3	8.2E-01
ENSMUST00000045909	zinc finger, BED type containing 3 [Source:MGI Symbol;Acc:MGI:1919364]		Q9D0L1	2.7	1.2E-02	7.8	4.6E-05	-0.6	6.0E-01	0.1	8.1E-01
ENSMUST00000045912	repetin [Source:MGI Symbol;Acc:MGI:1099055]		P97347	9.3	3.4E-05	-1.4	1.4E-01	1.4	2.5E-02	0.4	6.1E-01
ENSMUST00000045503	protein phosphatase 1, regulatory (inhibitor) subunit 16B [Source:MGI Symbol;Acc:MGI:2151841]	Q544H9	Q8VHQ3	5.8	4.0E-02	5.7	5.2E-02	-0.7	8.0E-01	-0.5	7.9E-01
ENSMUST00000045919	ecrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) [Source:MGI Symbol;Acc:MGI:2(	Q80WM9		-4.2	4.5E-03	5.9	1.2E-04	-3.9	6.2E-03	-0.2	7.6E-01
ENSMUST00000045923	LIM domain containing 2 [Source:MGI Symbol;Acc:MGI:1915053]		Q8BGB5	-4.9	3.9E-05	5.5	1.5E-02	-0.3	8.7E-01	-0.8	4.8E-01
ENSMUST00000045931	zinc finger protein 410 [Source:MGI Symbol;Acc:MGI:1289280]		Q8BKX7	-1.3	7.6E-03	-0.7	3.1E-01	1.5	1.3E-02	-0.2	7.9E-01
ENSMUST00000045942	empty spiracles homeobox 1 [Source:MGI Symbol;Acc:MGI:95387]		Q04742	5.1	2.7E-03	6.4	3.9E-04	-0.8	5.2E-01	0.2	8.0E-01
ENSMUST00000045529	KISS1 receptor [Source:MGI Symbol;Acc:MGI:2148793]	B2CP06	Q91V45	0.7	1.7E-01	1.7	2.0E-02	1.1	4.5E-02	0.1	8.8E-01
ENSMUST00000045959	BPI fold containing family B, member 5 [Source:MGI Symbol;Acc:MGI:2385160]	Q3UQ05		7.7	6.5E-05	5.9	7.5E-04	-1.2	3.5E-01	-0.4	5.7E-01
ENSMUST00000045971	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle) [Source:MGI Symbol;Acc:MGI:87890]		P09690	3.0	1.5E-03	1.4	7.4E-02	0.5	3.9E-01	0.4	5.1E-01
ENSMUST00000045972	solute carrier family 5 (sodium/glucose cotransporter), member 12 [Source:MGI Symbol;Acc:MGI:2138890]		Q49B93	4.4	2.0E-05	-0.8	2.5E-01	1.1	2.7E-02	-4.2	9.4E-04
ENSMUST00000045976	translocase of inner mitochondrial membrane 8A2 [Source:MGI Symbol;Acc:MGI:3615492]		Q4FZG7	5.8	1.4E-03	3.3	4.6E-04	1.1	7.1E-02	-0.1	7.9E-01
ENSMUST00000045993	(constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	Q14AI7	O88544	-6.6	3.6E-05	-0.8	3.9E-01	1.7	2.1E-02	0.3	7.4E-01
ENSMUST00000046004	RIKEN cDNA 1700019O17 gene [Source:MGI Symbol;Acc:MGI:1919113]		Q9DA60	7.9	2.6E-05	5.4	4.0E-03	-0.5	7.3E-01	0.2	8.2E-01
ENSMUST00000045562	cytochrome c oxidase assembly protein 15 [Source:MGI Symbol;Acc:MGI:1920112]		Q8BJ03	-0.2	6.9E-01	0.7	2.6E-01	0.9	5.4E-02	0.1	8.9E-01
ENSMUST00000045566	forkhead box P3 [Source:MGI Symbol;Acc:MGI:1891436]	Q53Z59	Q99JB6	0.4	8.3E-01	-0.1	9.9E-01	2.6	2.9E-01	3.0	3.4E-01
ENSMUST00000046011	nucleolar protein 10 [Source:MGI Symbol;Acc:MGI:2684913]	Q3TUB5	Q5RJG1	3.0	4.4E-05	3.4	3.5E-03	-2.8	2.2E-02	0.6	3.4E-01
ENSMUST00000046022	superkiller viralicidic activity 2-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1099835]	Q6NZR5		-8.4	2.5E-05	-3.2	9.3E-03	0.0	9.5E-01	0.1	9.1E-01
ENSMUST00000046038	solute carrier family 25, member 28 [Source:MGI Symbol;Acc:MGI:2180509]		Q8R0Z5	-3.6	8.7E-04	-0.2	8.7E-01	1.1	2.7E-01	-1.6	2.8E-01
ENSMUST00000046045	nexilin [Source:MGI Symbol;Acc:MGI:1916060]		Q7TPW1	5.9	7.2E-05	-6.1	2.8E-05	-0.6	1.3E-01	-2.2	5.8E-02
ENSMUST00000046071	kelch domain containing 8A [Source:MGI Symbol;Acc:MGI:2442630]		Q91XA8	8.8	1.5E-05	-3.3	3.0E-03	-0.8	1.3E-01	-0.6	4.8E-01
ENSMUST00000045607	maternal embryonic leucine zipper kinase [Source:MGI Symbol;Acc:MGI:106924]		Q61846	0.3	5.9E-01	0.6	3.5E-01	-0.3	4.8E-01	-0.7	2.9E-01
ENSMUST00000046091	elastase, neutrophil expressed [Source:MGI Symbol;Acc:MGI:2679229]		Q3UP87	-3.7	4.5E-03	-0.7	3.4E-01	0.6	1.9E-01	-0.4	5.7E-01
ENSMUST00000046093	H6 homeobox 3 [Source:MGI Symbol;Acc:MGI:107160]		P42581	6.8	9.2E-05	-1.8	1.1E-02	0.8	3.6E-02	0.4	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000046094	protein phosphatase 1, catalytic subunit, alpha isoform [Source:MGI Symbol;Acc:MGI:103016]		P62137	-7.1	1.6E-05	-4.6	2.6E-03	1.4	2.5E-02	0.0	9.8E-01
ENSMUST00000045633	MYB binding protein (P160) 1a [Source:MGI Symbol;Acc:MGI:106181]	Q3U2W2	Q7TPV4	-3.4	5.1E-02	-6.0	5.2E-02	-0.5	6.2E-01	2.1	4.5E-01
ENSMUST00000046095	visual system homeobox 1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1890816]	A2AQX5	Q91V10	7.8	2.7E-05	-2.5	3.5E-02	1.4	2.1E-02	1.1	2.8E-01
ENSMUST00000046114	mitochondrial ribosomal protein L54 [Source:MGI Symbol;Acc:MGI:1913297]		Q9CPW3	-2.9	2.2E-03	-1.2	7.5E-02	0.6	1.3E-01	0.0	9.7E-01
ENSMUST00000046144	tensin 2 [Source:MGI Symbol;Acc:MGI:2387586]		Q8CGB6	8.6	1.5E-03	-0.7	2.5E-01	0.9	6.2E-02	0.3	6.8E-01
ENSMUST00000046154	lin-54 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2140902]		Q571G4	-7.1	7.7E-05	2.4	4.0E-03	-0.3	6.2E-01	-0.4	4.7E-01
ENSMUST00000046157	fibronectin type III domain containing 3B [Source:MGI Symbol;Acc:MGI:1919257]			-3.3	3.5E-02	0.1	9.0E-01	1.3	1.2E-02	-0.4	5.3E-01
ENSMUST00000045682	GRAM domain containing 1B [Source:MGI Symbol;Acc:MGI:1925037]		Q80TI0	-0.2	8.6E-01	0.7	6.8E-01	0.3	7.8E-01	-0.6	7.1E-01
ENSMUST00000046174	claudin 11 [Source:MGI Symbol;Acc:MGI:106925]		Q60771	7.3	2.5E-05	-3.7	1.6E-02	-0.7	3.2E-01	-0.9	5.2E-01
ENSMUST00000046186	spondin 2, extracellular matrix protein [Source:MGI Symbol;Acc:MGI:1923724]		Q8BMS2	8.1	3.3E-05	8.8	1.3E-05	0.3	8.1E-01	-0.1	7.4E-01
ENSMUST00000045693	SET and MYND domain containing 5 [Source:MGI Symbol;Acc:MGI:108048]		Q3TYX3	0.2	6.9E-01	1.0	2.2E-01	0.2	7.3E-01	-0.5	4.4E-01
ENSMUST00000045694	methyltransferase like 18 [Source:MGI Symbol;Acc:MGI:1917212]		Q9CZ09	2.5	7.9E-02	0.5	7.2E-01	-1.3	3.5E-01	0.7	5.9E-01
ENSMUST00000046207	splicing factor 3B, subunit 6 [Source:MGI Symbol;Acc:MGI:1913305]		P59708	-2.8	5.2E-05	-5.7	8.2E-03	1.4	5.0E-02	-0.7	7.1E-01
ENSMUST00000046233	ne (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase) [Source:MGI Symbol;Acc:MG		Q924Y0	5.7	4.1E-04	-7.8	4.3E-03	1.2	1.1E-01	0.7	7.3E-01
ENSMUST00000045705	autophagy/beclin 1 regulator 1 [Source:MGI Symbol;Acc:MGI:2443564]		A2AH22	-1.9	2.7E-01	-3.8	2.7E-01	0.8	6.4E-01	2.8	3.8E-01
ENSMUST00000046245	zinc finger and SCAN domain containing 18 [Source:MGI Symbol;Acc:MGI:3643810]	E9PUD6		7.1	5.1E-05	6.8	1.6E-04	0.5	6.6E-01	-0.3	5.9E-01
ENSMUST00000046246	PDZ and LIM domain 7 [Source:MGI Symbol;Acc:MGI:1914649]		Q3TJD7	-8.4	4.9E-05	3.1	5.1E-03	0.0	9.6E-01	0.1	8.3E-01
ENSMUST00000046254	leucine rich repeat and fibronectin type III domain containing 2 [Source:MGI Symbol;Acc:MGI:1917780]		Q80TG9	8.3	2.3E-05	6.8	4.5E-04	-1.5	3.2E-01	0.0	9.6E-01
ENSMUST00000046257	spectrin alpha, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98386]		P16546	-3.4	9.9E-03	7.5	1.7E-02	-0.9	7.7E-01	-2.0	1.9E-01
ENSMUST00000046259	Sad1 and UNC84 domain containing 2 [Source:MGI Symbol;Acc:MGI:2443011]		Q8BJS4	-8.2	4.1E-04	6.0	1.8E-04	-2.1	8.9E-02	-0.3	5.8E-01
ENSMUST00000046266	ELM2 and Myb/SANT-like domain containing 1 [Source:MGI Symbol;Acc:MGI:2685106]	E9Q2I4		-4.7	1.9E-03	3.9	7.8E-04	-1.9	4.0E-02	0.1	8.7E-01
ENSMUST00000046274	Ral GTPase activating protein, beta subunit (non-catalytic) [Source:MGI Symbol;Acc:MGI:2444531]	F8WHN4		-5.6	1.9E-03	8.1	5.0E-05	-0.5	6.9E-01	-0.6	3.0E-01
ENSMUST00000045737	:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 [Source:MGI Symbol;Acc:MGI		Q921L8	-0.9	7.0E-01	-4.0	1.9E-01	-3.5	5.4E-02	-0.5	8.8E-01
ENSMUST00000046283	heat shock protein 70 family, member 13 [Source:MGI Symbol;Acc:MGI:1309463]		Q8BM72	-2.0	2.0E-02	2.9	1.3E-03	1.3	3.0E-02	0.1	9.0E-01
ENSMUST00000045740	ZXD family zinc finger C [Source:MGI Symbol;Acc:MGI:1933108]		Q8C8V1	-1.2	4.5E-01	5.0	7.6E-02	4.7	6.1E-02	-1.5	4.0E-01
ENSMUST00000045743	protein kinase, AMP-activated, beta 2 non-catalytic subunit [Source:MGI Symbol;Acc:MGI:1336185]		Q6PAM0	0.8	5.8E-01	1.1	5.4E-01	-0.1	9.3E-01	-0.4	7.8E-01
ENSMUST00000045744	tight junction protein 3 [Source:MGI Symbol;Acc:MGI:1351650]	Q921G9		0.6	4.0E-01	2.0	4.4E-02	1.3	8.8E-02	-0.1	8.5E-01
ENSMUST00000046288	NADH dehydrogenase (ubiquinone) flavoprotein 3 [Source:MGI Symbol;Acc:MGI:1890894]	Q3U422		-2.0	2.4E-02	5.4	1.4E-04	-1.5	1.3E-01	0.4	4.1E-01
ENSMUST00000046290	lysophosphatidylcholine acyltransferase 2 [Source:MGI Symbol;Acc:MGI:3606214]		Q8BYI6	-7.2	9.6E-07	-2.7	8.4E-03	1.8	3.7E-03	-0.5	5.4E-01
ENSMUST00000046303	cAMP responsive element binding protein-like 2 [Source:MGI Symbol;Acc:MGI:1889385]			-3.1	2.4E-04	-7.7	1.8E-06	-2.3	4.3E-05	-1.6	7.7E-02
ENSMUST00000045761	leucine zipper, putative tumor suppressor family member 3 [Source:MGI Symbol;Acc:MGI:2656976]		A2AHG0	3.9	1.7E-01	5.1	7.9E-02	-1.3	6.7E-01	-2.4	2.4E-01
ENSMUST00000046305	AT rich interactive domain 4A (RBP1-like) [Source:MGI Symbol;Acc:MGI:2444354]	F8VPQ2		-3.2	8.6E-04	-0.3	5.5E-01	0.3	3.8E-01	-0.8	1.4E-01
ENSMUST00000046306	IKAROS family zinc finger 5 [Source:MGI Symbol;Acc:MGI:1914393]		Q8BU00	-1.9	5.8E-03	6.5	1.4E-04	-0.6	6.2E-01	-0.8	1.9E-01
ENSMUST00000046331	WD repeat domain 20, retrogene [Source:MGI Symbol;Acc:MGI:1918198]		Q9D5R2	6.9	9.0E-05	1.6	2.6E-02	0.5	3.3E-01	0.2	7.0E-01
ENSMUST00000046351	leucine rich repeat and fibronectin type III domain containing 3 [Source:MGI Symbol;Acc:MGI:2442512]		Q8BLY3	8.9	9.4E-06	-1.1	3.2E-01	-0.1	9.0E-01	-1.9	1.1E-01
ENSMUST00000046383	tumor necrosis factor (ligand) superfamily, member 10 [Source:MGI Symbol;Acc:MGI:107414]	Q3U5H0	P50592	5.6	4.3E-05	-2.8	5.1E-03	1.0	3.9E-02	-0.4	6.2E-01
ENSMUST00000046386	zinc finger, CCHC domain containing 14 [Source:MGI Symbol;Acc:MGI:2159407]	A2RTC2	Q8VIG0	5.2	3.4E-05	-7.7	2.5E-02	1.0	2.8E-01	2.3	4.6E-01
ENSMUST00000045802	RIKEN cDNA 2810417H13 gene [Source:MGI Symbol;Acc:MGI:1915276]		Q9CQX4	0.3	6.7E-01	0.7	4.8E-01	0.6	4.2E-01	0.2	8.1E-01
ENSMUST00000046389	RNA binding motif protein 45 [Source:MGI Symbol;Acc:MGI:2387367]		Q8BHN5	-2.0	1.0E-03	-3.6	1.2E-02	-1.3	5.6E-02	-0.8	5.2E-01
ENSMUST00000046399	adipocyte plasma membrane associated protein [Source:MGI Symbol;Acc:MGI:1919131]		Q9D7N9	-4.3	7.7E-05	3.1	1.5E-03	-0.6	3.6E-01	0.3	5.6E-01
ENSMUST00000046404	ubiquitin protein ligase E3 component n-recognin 7 (putative) [Source:MGI Symbol;Acc:MGI:1913872]	Q52KC0	Q8BU04	-2.5	6.5E-04	7.6	7.2E-07	-0.8	2.3E-01	0.4	2.8E-01
ENSMUST00000046418	RIKEN cDNA E130309D02 gene [Source:MGI Symbol;Acc:MGI:2442621]		Q8BGA7	-5.7	2.1E-03	-3.0	2.1E-02	0.7	2.7E-01	0.1	9.5E-01
ENSMUST00000046425	taxilin alpha [Source:MGI Symbol;Acc:MGI:105968]	Q3UD58	Q6PAM1	-5.1	5.1E-04	-0.8	2.9E-01	0.7	1.6E-01	-0.1	9.4E-01
ENSMUST00000046433	ring finger protein 113A1 [Source:MGI Symbol;Acc:MGI:1917192]	Q8R3P8		-1.5	7.9E-03	-6.6	6.2E-06	-0.2	4.5E-01	0.4	5.5E-01
ENSMUST00000046461	docking protein 4 [Source:MGI Symbol;Acc:MGI:2148865]		Q99KE3	2.0	4.2E-03	-4.2	2.8E-04	0.2	5.7E-01	0.1	8.7E-01
ENSMUST00000045866	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 [Source:MGI Symbol;Acc:MGI:1860494]		Q9JIK5	-0.4	4.1E-01	-2.0	7.4E-03	-1.0	1.8E-02	0.6	3.2E-01
ENSMUST00000046463	GTP binding protein 1 [Source:MGI Symbol;Acc:MGI:109443]		O08582	-2.6	1.1E-03	4.0	4.6E-04	-0.1	9.0E-01	0.0	9.5E-01
ENSMUST00000046470	methyltransferase like 22 [Source:MGI Symbol;Acc:MGI:2384301]		Q8R1C6	3.6	5.4E-03	-4.3	1.6E-02	1.4	5.8E-02	-0.5	7.7E-01
ENSMUST00000046490	ornithine decarboxylase antizyme 2 [Source:MGI Symbol;Acc:MGI:109492]	J3QNN0		-9.0	1.1E-05	-0.6	4.3E-01	-0.3	5.3E-01	-1.6	5.8E-02
ENSMUST00000046497	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 [Source:MGI Symbol;Acc:MGI:3039376]		Q80VJ3	4.4	1.8E-05	6.1	6.4E-04	-0.7	6.2E-01	-0.5	5.1E-01
ENSMUST00000046498	gap junction protein, beta 5 [Source:MGI Symbol;Acc:MGI:95723]	Q542M8	Q02739	6.8	1.7E-04	4.7	3.2E-04	0.4	5.8E-01	-0.1	8.3E-01
ENSMUST00000046502	RAD54 like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1933196]	E9QKL0		2.3	2.7E-04	-6.7	6.9E-03	-0.7	3.7E-01	1.2	5.6E-01
ENSMUST00000045898	phosphate cytidylyltransferase 1, choline, beta isoform [Source:MGI Symbol;Acc:MGI:2147987]		Q811Q9	6.3	5.1E-02	4.1	2.3E-01	-0.2	9.6E-01	2.0	3.1E-01
ENSMUST00000045903	trafficking protein, kinesin binding 1 [Source:MGI Symbol;Acc:MGI:1914345]		Q6PD31	0.7	1.0E-01	1.5	1.5E-02	0.6	1.3E-01	-0.2	7.0E-01
ENSMUST00000046514	glutamyl-prolyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:97838]		Q8CGC7	-1.9	4.5E-03	0.9	1.3E-01	-6.9	1.3E-05	-0.5	3.3E-01
ENSMUST00000046515	neutral cholesterol ester hydrolase 1 [Source:MGI Symbol;Acc:MGI:2443191]		Q8BLF1	-1.4	1.2E-02	4.9	3.4E-02	-0.2	9.0E-01	-0.2	8.9E-01
ENSMUST00000046522	butyrophilin-like 9 [Source:MGI Symbol;Acc:MGI:2442439]		Q8BJE2	5.1	2.1E-05	2.9	1.5E-02	-0.2	7.8E-01	-0.5	5.8E-01
ENSMUST00000046525	kringle containing transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1920266]		Q8K1S7	8.7	4.7E-05	7.9	2.5E-04	-0.8	6.1E-01	0.6	3.8E-01
ENSMUST00000045918	asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:1098592]		Q8K2A8	-3.1	6.4E-02	-0.1	9.2E-01	-0.3	7.5E-01	-3.3	6.4E-02
ENSMUST00000046532	gap junction protein, beta 3 [Source:MGI Symbol;Acc:MGI:95721]		P28231	5.8	3.2E-02	-4.1	3.6E-02	0.3	7.0E-01	0.2	9.1E-01
ENSMUST00000046533	proline rich 7 (synaptic) [Source:MGI Symbol;Acc:MGI:3487246]	B2RSG4	Q3V0I2	-2.2	1.5E-03	-3.4	2.6E-03	1.1	3.0E-02	-0.4	6.1E-01
ENSMUST00000045924				-1.5	4.5E-01	2.6	1.2E-01	-1.0	4.9E-01	-5.1	1.9E-02
ENSMUST00000046549	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2 [Source:MGI Symbol;Acc:MGI:1343178]		Q9WV35	6.2	2.5E-04	-1.3	3.2E-02	0.2	5.5E-01	0.1	7.8E-01
ENSMUST00000046557	A kinase (PRKA) anchor protein 14 [Source:MGI Symbol;Acc:MGI:3618288]	Q3V0I7		4.4	5.8E-03	6.1	1.3E-03	-0.6	6.8E-01	-1.6	7.8E-02
ENSMUST00000045956	coiled-coil alpha-helical rod protein 1 [Source:MGI Symbol;Acc:MGI:2385321]		Q8K2I2	3.5	1.3E-01	3.6	2.8E-01	0.7	8.1E-01	0.6	7.7E-01
ENSMUST00000046565	aristaless related homeobox [Source:MGI Symbol;Acc:MGI:1097716]		O35085	5.6	1.3E-02	7.4	1.6E-04	-0.7	6.1E-01	-0.4	5.2E-01
ENSMUST00000045970	glypican 1 [Source:MGI Symbol;Acc:MGI:1194891]	Q3U379	Q9QZF2	-1.2	8.3E-02	-1.4	1.2E-01	-0.1	7.9E-01	0.0	9.8E-01
ENSMUST00000046575	prostate tumor over expressed gene 1 [Source:MGI Symbol;Acc:MGI:1933946]		Q91VU8	-3.9	3.3E-03	0.3	7.2E-01	-2.4	4.4E-03	0.3	6.3E-01
ENSMUST00000046587	secretory carrier membrane protein 5 [Source:MGI Symbol;Acc:MGI:1928948]		Q9JKD3	6.1	4.8E-04	5.0	2.3E-05	0.1	9.2E-01	-0.5	2.4E-01
ENSMUST00000046603	cyclin G associated kinase [Source:MGI Symbol;Acc:MGI:2442153]			-8.4	8.2E-05	4.5	9.7E-03	-0.8	5.8E-01	0.4	6.7E-01
ENSMUST00000045986	sepiapterin reductase [Source:MGI Symbol;Acc:MGI:103078]	Q91XH5		-1.9	7.7E-02	-0.1	9.2E-01	0.3	7.1E-01	-1.4	2.3E-01
ENSMUST00000046611	CUB and zona pellucida-like domains 1 [Source:MGI Symbol;Acc:MGI:1202881]	B2RU69		6.4	1.7E-04	-3.8	4.2E-04	-0.5	2.0E-01	-3.3	6.3E-03
ENSMUST00000045994	RNA binding motif protein 34 [Source:MGI Symbol;Acc:MGI:1098653]	B2RUP0		0.7	1.8E-01	0.8	1.6E-01	-0.6	2.3E-01	-0.7	1.9E-01
ENSMUST00000046633	expressed sequence AW549877 [Source:MGI Symbol;Acc:MGI:2146232]		Q8BR90	-3.3	4.1E-05	7.2	1.1E-04	-0.6	6.0E-01	0.1	8.9E-01
ENSMUST00000046005	GLIS family zinc finger 1 [Source:MGI Symbol;Acc:MGI:2386723]		Q8K1M4	3.8	3.7E-02	6.7	2.0E-03	-0.5	7.7E-01	-3.5	9.4E-03
ENSMUST00000046644	tubulin cofactor A [Source:MGI Symbol;Acc:MGI:107549]	Q5I0U7	P48428	-6.3	1.3E-06	2.9	4.3E-04	0.3	5.8E-01	0.4	3.4E-01
ENSMUST00000046651	O-acyl-ADP-ribose deacylase 1 [Source:MGI Symbol;Acc:MGI:2146818]		Q8R5F3	-6.2	5.7E-04	-6.9	8.8E-04	1.1	3.5E-02	-0.3	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000046030	SF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913830	A2APY6	Q3V1V3	-0.5	4.7E-01	-1.9	4.7E-02	-0.8	2.0E-01	0.6	5.0E-01
ENSMUST00000046658	major facilitator superfamily domain containing 4 [Source:MGI Symbol;Acc:MGI:2442786]		Q6PDC8	6.4	2.5E-06	-1.3	1.7E-01	0.7	2.5E-01	-1.7	9.3E-02
ENSMUST00000046659	discs, large (Drosophila) homolog-associated protein 3 [Source:MGI Symbol;Acc:MGI:3039563]	Q3TY61	Q6PFD5	6.5	1.1E-02	2.7	4.6E-03	-2.8	7.0E-03	0.4	5.5E-01
ENSMUST00000046064	zinc finger protein 384 [Source:MGI Symbol;Acc:MGI:2443203]	E9QAR1		0.4	7.9E-01	1.3	5.4E-01	1.3	4.1E-01	0.4	8.1E-01
ENSMUST00000046662	predicted gene 4847 [Source:MGI Symbol;Acc:MGI:3643320]	G3X946		10.8	1.1E-04	6.3	7.6E-05	-2.5	5.0E-02	0.0	9.3E-01
ENSMUST00000046663	discoidin, CUB and LCCL domain containing 2 [Source:MGI Symbol;Acc:MGI:1920629]		Q91ZV3	5.1	9.4E-04	-2.1	1.3E-01	1.5	8.7E-02	-0.2	9.0E-01
ENSMUST00000046687	spondin 1, (f-spondin) extracellular matrix protein [Source:MGI Symbol;Acc:MGI:2385287]		Q8VCC9	5.3	1.2E-03	5.6	7.3E-04	-0.6	6.2E-01	0.6	3.5E-01
ENSMUST00000046689	RIKEN cDNA 2810474O19 gene [Source:MGI Symbol;Acc:MGI:1914496]	B2KFD2	Q5DTW7	-8.6	4.3E-04	-4.9	1.2E-03	1.5	1.2E-02	-0.8	5.1E-01
ENSMUST00000046704	interferon gamma inducible protein 47 [Source:MGI Symbol;Acc:MGI:99448]	Q61635		-5.2	1.5E-03	6.6	2.4E-04	-1.0	4.2E-01	0.3	6.7E-01
ENSMUST00000046110	astrotactin 1 [Source:MGI Symbol;Acc:MGI:1098567]	Q3UHD7	Q61137	6.1	9.1E-02	6.4	8.9E-02	-0.9	8.1E-01	-1.2	6.0E-01
ENSMUST00000046709	suppressor of Ty 16 [Source:MGI Symbol;Acc:MGI:1890948]	G3X956		-2.9	4.6E-04	-3.0	8.3E-03	-0.2	6.5E-01	-0.2	8.3E-01
ENSMUST00000046717	MAX gene associated [Source:MGI Symbol;Acc:MGI:1352483]		A2AWL7	-7.3	3.8E-06	6.2	3.4E-04	0.2	8.5E-01	0.2	7.8E-01
ENSMUST00000046122	leucine aminopeptidase 3 [Source:MGI Symbol;Acc:MGI:1914238]		Q9CPY7	0.9	1.2E-01	-1.5	4.1E-02	-2.3	9.7E-04	0.2	8.1E-01
ENSMUST00000046128	urocanase domain containing 1 [Source:MGI Symbol;Acc:MGI:2385332]		Q8VC12	2.2	4.3E-01	2.8	3.6E-01	-0.4	8.9E-01	-1.1	6.1E-01
ENSMUST00000046748	G protein-coupled receptor 160 [Source:MGI Symbol;Acc:MGI:1919112]		Q3U3F9	-6.3	2.2E-05	3.3	8.9E-02	-4.6	4.3E-02	0.7	6.2E-01
ENSMUST00000046765	potassium channel, subfamily K, member 1 [Source:MGI Symbol;Acc:MGI:109322]		O08581	7.9	1.1E-05	-3.5	2.3E-03	0.1	8.4E-01	-1.6	1.5E-01
ENSMUST00000046792	olfactomedin-like 2B [Source:MGI Symbol;Acc:MGI:2443310]		Q3V1G4	-3.4	1.5E-04	1.7	3.2E-01	7.8	1.6E-04	-1.0	4.9E-01
ENSMUST00000046807	olute carrier family 16 (monocarboxylic acid transporters), member 9 [Source:MGI Symbol;Acc:MGI:1914109		Q7TM99	5.8	4.5E-05	-5.3	2.2E-02	0.3	7.6E-01	2.4	2.6E-01
ENSMUST00000046833	mitotic spindle positioning [Source:MGI Symbol;Acc:MGI:1926156]		Q9D279	3.6	5.5E-03	6.3	1.5E-04	-0.5	6.2E-01	0.4	4.5E-01
ENSMUST00000046177	r factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta [Source:MGI Symbol;Acc:MGI:304		Q2TB02	-1.9	2.5E-01	-0.6	8.1E-01	1.0	6.1E-01	-0.4	8.4E-01
ENSMUST00000046835	folliculin interacting protein 1 [Source:MGI Symbol;Acc:MGI:2444668]		Q68FD7	-3.5	4.4E-05	4.1	4.6E-04	-4.8	1.2E-03	-0.7	2.4E-01
ENSMUST00000046846	lysine (K)-specific demethylase 1A [Source:MGI Symbol;Acc:MGI:1196256]	G8JL40		-6.2	5.5E-04	2.9	6.8E-03	-1.0	2.3E-01	-0.5	4.4E-01
ENSMUST00000046191	glucosamine-phosphate N-acetyltransferase 1 [Source:MGI Symbol;Acc:MGI:1858963]		Q9JK38	-1.1	1.1E-01	-1.2	1.3E-01	-0.7	1.9E-01	-0.6	4.3E-01
ENSMUST00000046206	regulation of nuclear pre-mRNA domain containing 1A [Source:MGI Symbol;Acc:MGI:2385066]		Q8VDS4	-0.4	4.6E-01	0.8	2.2E-01	0.3	5.7E-01	-0.9	1.5E-01
ENSMUST00000046863	roxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 [Source:MGI Symbol;Acc:MGI:2141		Q9EQC1	-6.1	5.7E-04	-3.1	1.8E-04	-0.4	1.5E-01	-0.1	7.9E-01
ENSMUST00000046212	solute carrier family 16 (monocarboxylic acid transporters), member 1 [Source:MGI Symbol;Acc:MGI:106013]	Q544N9	P53986	1.1	3.8E-02	-0.8	1.7E-01	-1.8	1.4E-03	0.1	8.9E-01
ENSMUST00000046223	ATP-binding cassette, sub-family A (ABC1), member 8a [Source:MGI Symbol;Acc:MGI:2386846]	F8WGE3		3.3	1.3E-01	3.8	8.9E-02	-1.4	5.2E-01	-1.9	2.3E-01
ENSMUST00000046864	vav 3 oncogene [Source:MGI Symbol;Acc:MGI:1888518]		Q9R0C8	-6.9	5.1E-05	6.6	2.8E-04	-0.5	6.7E-01	-1.4	6.4E-02
ENSMUST00000046244	decapping exoribonuclease [Source:MGI Symbol;Acc:MGI:1890444]			-2.5	1.1E-01	-2.3	3.2E-01	2.0	2.5E-01	1.8	3.7E-01
ENSMUST00000046869	F-box and WD-40 domain protein 4 [Source:MGI Symbol;Acc:MGI:1354698]		Q9JMJ2	-4.2	5.5E-04	6.5	6.5E-04	-0.1	9.6E-01	0.5	5.1E-01
ENSMUST00000046870	LIM homeobox protein 9 [Source:MGI Symbol;Acc:MGI:1316721]		Q9WUH2	9.0	2.7E-05	-7.2	1.1E-03	1.5	1.3E-02	0.3	8.4E-01
ENSMUST00000046891	prostaglandin E receptor 2 (subtype EP2) [Source:MGI Symbol;Acc:MGI:97794]	Q543A9	Q62053	-1.9	2.1E-02	7.8	7.1E-05	-0.6	6.1E-01	-0.2	7.8E-01
ENSMUST00000046892	complexin 1 [Source:MGI Symbol;Acc:MGI:104727]		P63040	5.4	1.7E-04	-5.0	7.1E-03	0.1	8.6E-01	1.7	2.8E-01
ENSMUST00000046893	G protein-coupled receptor 162 [Source:MGI Symbol;Acc:MGI:1315214]		Q3UN16	6.2	1.1E-05	-6.1	7.3E-03	1.2	1.6E-01	-0.8	6.8E-01
ENSMUST00000046898	regulatory factor X, 3 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:106582]	G5E890		9.5	9.5E-04	-2.6	8.4E-02	1.1	1.9E-01	-1.1	4.5E-01
ENSMUST00000046901	platelet derived growth factor, alpha [Source:MGI Symbol;Acc:MGI:97527]	G5E891		7.3	3.9E-04	-5.8	2.5E-02	0.4	6.3E-01	0.5	8.3E-01
ENSMUST00000046908	oxidative stress responsive serine rich 1 [Source:MGI Symbol;Acc:MGI:1913930]		Q9D722	-3.6	2.7E-05	-1.6	9.2E-02	0.2	7.8E-01	-0.2	8.4E-01
ENSMUST00000046285	complement component 1, q subcomponent, alpha polypeptide [Source:MGI Symbol;Acc:MGI:88223]		P98086	2.2	1.2E-01	-5.5	1.6E-03	-8.1	3.5E-05	-0.4	7.5E-01
ENSMUST00000046929	ubiquitin specific peptidase 31 [Source:MGI Symbol;Acc:MGI:1923429]	E9Q6Y8		4.1	1.3E-05	-1.5	1.3E-01	0.1	8.9E-01	-0.4	6.8E-01
ENSMUST00000046937	testis-specific serine kinase 1 [Source:MGI Symbol;Acc:MGI:1347557]		Q61241	8.8	1.6E-05	-6.0	3.0E-05	0.7	5.0E-02	-0.5	5.7E-01
ENSMUST00000046941	ring finger protein 122 [Source:MGI Symbol;Acc:MGI:1916117]			2.6	3.1E-03	-2.6	3.5E-03	0.3	4.6E-01	-0.2	7.7E-01
ENSMUST00000046944	RIKEN cDNA D630003M21 gene [Source:MGI Symbol;Acc:MGI:3606579]		Q8BWG4	7.7	1.1E-04	-2.7	7.5E-03	-0.2	6.9E-01	-0.7	4.0E-01
ENSMUST00000046945	paralemmin [Source:MGI Symbol;Acc:MGI:1261814]		Q9Z0P4	-4.5	6.3E-04	-1.8	2.4E-02	-0.2	6.6E-01	-0.3	7.0E-01
ENSMUST00000046316	leucine-rich repeats and immunoglobulin-like domains 2 [Source:MGI Symbol;Acc:MGI:2443718]		Q52KR2	-0.4	4.3E-01	0.5	4.3E-01	0.7	1.8E-01	-0.2	6.9E-01
ENSMUST00000046950	PHD finger protein 8 [Source:MGI Symbol;Acc:MGI:2444341]		Q80TJ7	-7.8	1.6E-05	7.3	1.4E-04	-0.1	9.5E-01	-0.5	4.3E-01
ENSMUST00000046332	complement component 1, q subcomponent, C chain [Source:MGI Symbol;Acc:MGI:88225]		Q02105	3.9	4.9E-02	-5.9	5.1E-03	-9.6	9.8E-05	0.2	9.1E-01
ENSMUST00000046951	PAK1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1915333]		Q9DCE5	-8.0	1.1E-05	2.4	3.3E-03	0.1	8.6E-01	0.2	6.6E-01
ENSMUST00000046955	WD repeat domain 92 [Source:MGI Symbol;Acc:MGI:2144224]		Q8BGF3	-2.4	5.3E-03	6.9	5.2E-05	-1.9	1.2E-01	0.1	8.6E-01
ENSMUST00000046371	lipid phosphate phosphatase-related protein type 2 [Source:MGI Symbol;Acc:MGI:2384575]		Q8VCY8	0.3	8.6E-01	4.5	1.5E-01	3.4	2.4E-01	-0.8	6.6E-01
ENSMUST00000046373	IQ motif and Sec7 domain 3 [Source:MGI Symbol;Acc:MGI:2677208]		Q3TES0	3.0	8.4E-02	4.1	2.6E-02	-0.5	7.5E-01	-1.6	2.1E-01
ENSMUST00000046959	solute carrier family 22 (organic cation transporter), member 2 [Source:MGI Symbol;Acc:MGI:1335072]		O70577	5.9	1.9E-04	4.9	3.0E-04	-0.5	5.2E-01	0.2	7.5E-01
ENSMUST00000046384	complement component 1, q subcomponent, beta polypeptide [Source:MGI Symbol;Acc:MGI:88224]		P14106	2.4	4.5E-02	-5.2	5.1E-04	-8.0	7.6E-06	-0.4	7.4E-01
ENSMUST00000046963	mitogen-activated protein kinase kinase 4 [Source:MGI Symbol;Acc:MGI:1346869]	Q543X6	P47809	-4.6	2.0E-05	3.2	2.1E-03	-1.6	5.0E-02	0.4	4.8E-01
ENSMUST00000046972	RNA binding motif protein 27 [Source:MGI Symbol;Acc:MGI:2147194]		Q5SFM8	-4.1	6.1E-03	-0.9	1.2E-01	0.9	2.1E-02	-0.1	8.1E-01
ENSMUST00000046974	F-box and WD-40 domain protein 17 [Source:MGI Symbol;Acc:MGI:1923584]	Q8CFE8		-2.4	1.9E-02	-3.3	2.3E-03	0.6	1.7E-01	-0.4	6.0E-01
ENSMUST00000046975	polycomb group ring finger 3 [Source:MGI Symbol;Acc:MGI:1916837]		Q8BTQ0	2.4	5.7E-04	-1.7	2.4E-02	0.4	2.7E-01	-0.4	5.0E-01
ENSMUST00000046993	dynein, axonemal, heavy chain 3 [Source:MGI Symbol;Acc:MGI:2683040]		Q8BW94	6.5	3.0E-05	-4.8	2.3E-02	1.0	1.7E-01	0.2	9.0E-01
ENSMUST00000046422	acyl-CoA thioesterase 5 [Source:MGI Symbol;Acc:MGI:2384969]		Q6Q2Z6	3.7	7.4E-02	6.0	1.4E-02	-0.3	8.8E-01	-2.7	5.3E-02
ENSMUST00000047005	spermatogenesis associated 16 [Source:MGI Symbol;Acc:MGI:1918112]		Q8C636	5.5	3.1E-02	-1.5	1.4E-01	1.1	7.6E-02	-2.5	4.6E-02
ENSMUST00000046426	two pore channel 1 [Source:MGI Symbol;Acc:MGI:2182472]		Q9EQJ0	-0.6	3.1E-01	0.0	9.7E-01	0.5	3.3E-01	-0.1	9.1E-01
ENSMUST00000047013	CKLF-like MARVEL transmembrane domain containing 8 [Source:MGI Symbol;Acc:MGI:2447167]		Q9CZR4	3.4	3.0E-04	-1.2	6.5E-02	0.3	4.7E-01	0.0	9.9E-01
ENSMUST00000047025	otoancorin [Source:MGI Symbol;Acc:MGI:2149209]		Q8K561	5.6	4.8E-05	3.1	8.2E-04	-0.1	9.3E-01	-1.1	5.2E-02
ENSMUST00000047028	lectin, galactoside binding-like [Source:MGI Symbol;Acc:MGI:1916114]		Q8VED9	1.6	1.9E-02	-1.5	6.3E-02	1.2	2.6E-02	0.1	8.8E-01
ENSMUST00000047034	tau tubulin kinase 1 [Source:MGI Symbol;Acc:MGI:2147036]		Q6PCN3	8.5	7.2E-07	2.9	1.7E-02	-2.0	6.9E-02	-1.3	1.6E-01
ENSMUST00000046485	EF-hand calcium binding domain 11 [Source:MGI Symbol;Acc:MGI:1926017]		Q9D0E5	1.4	4.7E-02	1.6	5.8E-02	0.4	4.9E-01	0.2	7.7E-01
ENSMUST00000047037	THO complex 2 [Source:MGI Symbol;Acc:MGI:2442413]		B1AZI6	-6.5	5.2E-05	-3.2	4.1E-03	1.9	2.2E-03	-3.8	8.0E-03
ENSMUST00000047040	protein kinase C, delta binding protein [Source:MGI Symbol;Acc:MGI:1923422]		Q91VJ2	4.7	2.2E-04	4.7	4.0E-05	-0.1	9.1E-01	-0.4	3.8E-01
ENSMUST00000047045	acyl-CoA synthetase medium-chain family member 4 [Source:MGI Symbol;Acc:MGI:2681844]		Q80W40	6.4	1.1E-04	3.2	3.8E-03	-4.1	4.0E-03	-0.5	4.3E-01
ENSMUST00000047057	deleted in primary ciliary dyskinesia [Source:MGI Symbol;Acc:MGI:1924407]		Q8BPA8	-3.3	4.6E-05	3.1	2.3E-04	0.7	1.8E-01	-0.2	6.2E-01
ENSMUST00000046506	cardiotrophin-like cytokine factor 1 [Source:MGI Symbol;Acc:MGI:1930088]		Q9QZM3	-0.2	8.1E-01	-2.5	8.7E-02	-1.7	5.9E-02	0.6	6.8E-01
ENSMUST00000047085	TBC1 domain family, member 17 [Source:MGI Symbol;Acc:MGI:2449973]		Q8BYH7	-6.8	2.8E-04	-2.8	1.9E-03	-1.2	9.0E-03	-0.4	5.6E-01
ENSMUST00000047091	BTB (POZ) domain containing 10 [Source:MGI Symbol;Acc:MGI:1916065]		Q80X66	-4.0	1.2E-02	-1.1	9.8E-02	0.2	5.7E-01	-0.1	8.3E-01
ENSMUST00000047098	mesothelin-like [Source:MGI Symbol;Acc:MGI:3607710]		Q8C160	8.0	1.6E-05	4.7	2.2E-02	-0.5	8.0E-01	-0.7	5.4E-01
ENSMUST00000046518	inositol 1,3,4-triphosphate 5/6 kinase [Source:MGI Symbol;Acc:MGI:2446159]		Q8BYN3	-0.2	7.7E-01	0.1	9.4E-01	0.8	2.0E-01	0.6	4.8E-01
ENSMUST00000046521	B cell CLL/lymphoma 9 [Source:MGI Symbol;Acc:MGI:1924828]		Q9D219	0.1	8.5E-01	1.4	1.7E-01	0.2	7.4E-01	-1.0	2.7E-01
ENSMUST00000047104	peripherin [Source:MGI Symbol;Acc:MGI:97774]	G3X981		7.2	1.3E-03	5.9	3.5E-05	0.7	3.5E-01	0.0	9.9E-01
ENSMUST00000047111	pyruvate kinase liver and red blood cell [Source:MGI Symbol;Acc:MGI:97604]	G3X925		6.0	1.1E-02	7.0	3.0E-04	-1.0	4.6E-01	0.7	3.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000047115	WD repeat domain 25 [Source:MGI Symbol;Acc:MGI:3045255]		E9Q349	6.0	6.5E-05	5.6	4.7E-02	-0.8	7.8E-01	-0.6	7.3E-01
ENSMUST00000047131	importin 4 [Source:MGI Symbol;Acc:MGI:1923001]		Q8VI75	4.6	1.8E-02	-1.2	6.8E-02	0.3	4.2E-01	-0.6	3.2E-01
ENSMUST00000046534				0.7	4.0E-01	0.2	8.2E-01	0.0	9.7E-01	0.5	6.2E-01
ENSMUST00000046548	leucine-rich repeat-containing G protein-coupled receptor 4 [Source:MGI Symbol;Acc:MGI:1891468]		A2ARI4	3.4	1.7E-01	5.7	6.6E-02	0.5	8.4E-01	-1.7	3.8E-01
ENSMUST00000047134	4short chain dehydrogenase/reductase family 9C, member 7 [Source:MGI Symbol;Acc:MGI:1917311]		Q8K3P0	7.1	7.4E-05	3.2	4.3E-03	-3.3	9.5E-03	-0.3	6.2E-01
ENSMUST00000047144	RIKEN cDNA 5031439G07 gene [Source:MGI Symbol;Acc:MGI:2444899]		Q3UE31	-4.8	5.7E-05	2.5	9.6E-02	-1.4	3.1E-01	0.5	6.3E-01
ENSMUST00000047145	tripartite motif-containing 41 [Source:MGI Symbol;Acc:MGI:2384814]		Q5NCC3	-2.9	4.0E-04	2.2	3.9E-01	-0.6	7.7E-01	2.8	1.6E-01
ENSMUST00000047173	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils [Source:MGI Symbol;Acc:MGI:1925350]		Q91YU3	-3.1	4.6E-04	-2.3	8.2E-02	1.1	1.7E-01	-0.5	6.9E-01
ENSMUST00000047177	NTF2-related export protein 1 [Source:MGI Symbol;Acc:MGI:1929619]		Q9QZV9	-3.5	2.2E-04	1.7	1.4E-01	-4.5	2.7E-03	-0.1	9.3E-01
ENSMUST00000047179	zinc finger protein 598 [Source:MGI Symbol;Acc:MGI:2670965]		Q80YR4	-1.4	2.4E-02	-4.1	4.0E-03	1.3	2.9E-02	-3.0	6.4E-02
ENSMUST00000047194	immunoglobulin superfamily, member 6 [Source:MGI Symbol;Acc:MGI:1891393]		P0C6B7	-5.3	9.4E-05	6.4	3.0E-04	-0.6	6.0E-01	-0.7	3.4E-01
ENSMUST00000047196	Williams Beuren syndrome chromosome region 27 (human) [Source:MGI Symbol;Acc:MGI:1933146]	Q8BGM4		6.7	1.5E-04	-2.2	3.3E-03	0.9	1.6E-02	-0.1	8.1E-01
ENSMUST00000046638	methyltransferase like 25 [Source:MGI Symbol;Acc:MGI:3041259]			-2.1	3.6E-02	-2.3	1.3E-01	1.0	2.6E-01	1.2	3.8E-01
ENSMUST00000047199	retinol dehydrogenase 7 [Source:MGI Symbol;Acc:MGI:1860517]		O88451	5.3	7.0E-04	-5.9	1.6E-05	-0.3	3.1E-01	-0.8	2.9E-01
ENSMUST00000047203	ring finger protein 126 [Source:MGI Symbol;Acc:MGI:1917544]	Q3U3G2	Q91YL2	-1.8	1.1E-02	-5.1	4.0E-03	-0.1	8.8E-01	-1.3	4.2E-01
ENSMUST00000046656	taspase, threonine aspartase 1 [Source:MGI Symbol;Acc:MGI:1923062]		Q8R1G1	4.0	6.2E-02	5.9	4.0E-02	1.3	6.1E-01	-0.7	6.6E-01
ENSMUST00000047206	in homology domain containing, family H (with MyTH4 domain) member 2 [Source:MGI Symbol;Acc:MGI:2		Q8C115	7.3	9.9E-06	4.3	1.0E-04	-1.9	1.5E-02	0.2	6.4E-01
ENSMUST00000047207	coiled-coil domain containing 27 [Source:MGI Symbol;Acc:MGI:2685881]	B1AX94	Q3V036	7.8	1.8E-05	6.7	6.4E-03	-1.7	4.7E-01	-1.8	1.8E-01
ENSMUST00000047208	DAZ interacting protein 1 [Source:MGI Symbol;Acc:MGI:1914311]		Q8BMD2	7.0	8.8E-04	7.4	1.4E-03	-1.7	3.9E-01	1.7	1.0E-01
ENSMUST00000047226	lon peptidase 1, mitochondrial [Source:MGI Symbol;Acc:MGI:1921392]		Q8CGK3	-1.6	8.4E-03	0.3	7.5E-01	-4.1	2.6E-03	0.6	5.4E-01
ENSMUST00000046675	IQ motif containing C [Source:MGI Symbol;Acc:MGI:2446212]		A2ADZ8	1.0	3.5E-02	0.8	1.4E-01	0.0	1.0E+00	0.2	7.3E-01
ENSMUST00000047232	alkylglycerone phosphate synthase [Source:MGI Symbol;Acc:MGI:2443065]	A2AL50		-3.4	6.4E-05	2.5	4.5E-02	-3.3	1.9E-02	-0.5	5.5E-01
ENSMUST00000047257	katanin p60 subunit A-like 1 [Source:MGI Symbol;Acc:MGI:2387638]		Q8K0T4	4.9	8.4E-05	-4.7	7.0E-03	0.3	6.5E-01	-3.6	7.5E-02
ENSMUST00000047265	RIKEN cDNA 1700019B03 gene [Source:MGI Symbol;Acc:MGI:1923656]	G3XA23		7.8	4.6E-03	-7.2	2.3E-03	-1.7	3.1E-02	0.3	8.5E-01
ENSMUST00000047275	beta-site APP-cleaving enzyme 2 [Source:MGI Symbol;Acc:MGI:1860440]			6.7	9.5E-06	-2.5	4.7E-03	0.1	8.5E-01	-0.3	6.6E-01
ENSMUST00000047281	RIKEN cDNA 2310036O22 gene [Source:MGI Symbol;Acc:MGI:1922833]		Q9D735	-5.1	9.0E-06	-6.6	6.0E-05	0.1	7.0E-01	-0.6	5.4E-01
ENSMUST00000046719	nuclear transcription factor-Y alpha [Source:MGI Symbol;Acc:MGI:97316]	Q9DBV7		0.2	9.1E-01	-3.2	2.9E-01	-1.0	5.8E-01	2.4	4.1E-01
ENSMUST00000046735	testis expressed gene 264 [Source:MGI Symbol;Acc:MGI:1096570]	E9Q137		-2.5	4.5E-02	-4.4	2.4E-02	-0.9	2.5E-01	1.0	5.8E-01
ENSMUST00000046743	cDNA sequence BC026585 [Source:MGI Symbol;Acc:MGI:2448516]		Q3UNZ8	3.0	1.6E-01	0.1	9.7E-01	-2.4	2.4E-01	0.5	8.0E-01
ENSMUST00000046745	T cell specific GTPase 2 [Source:MGI Symbol;Acc:MGI:3710083]	Q62293		0.4	7.4E-01	-3.1	5.4E-02	-2.4	3.6E-02	1.1	4.5E-01
ENSMUST00000047285	adaptor-related protein complex AP-4, beta 1 [Source:MGI Symbol;Acc:MGI:1337130]		Q9WV76	-6.6	4.6E-03	-4.6	1.3E-03	1.0	4.0E-02	-0.8	4.8E-01
ENSMUST00000046750	tetraspanin 33 [Source:MGI Symbol;Acc:MGI:1919012]		Q8R3S2	3.4	1.1E-01	4.8	4.6E-02	-0.5	8.3E-01	-1.9	2.3E-01
ENSMUST00000046751	zinc finger, MYM-type 6 [Source:MGI Symbol;Acc:MGI:106505]	Q8BS54		0.7	4.7E-01	-0.4	7.6E-01	-0.6	5.5E-01	0.5	6.5E-01
ENSMUST00000047286	methionine adenosyltransferase I, alpha [Source:MGI Symbol;Acc:MGI:88017]		Q91X83	6.1	1.1E-03	5.3	2.6E-05	-3.2	5.5E-03	-0.7	1.9E-01
ENSMUST00000046769	cytoskeleton associated protein 5 [Source:MGI Symbol;Acc:MGI:1923036]			1.6	4.5E-01	1.8	4.9E-01	-0.1	9.4E-01	-0.3	8.9E-01
ENSMUST00000046770	neuron derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:1913458]		Q9CQ45	0.5	5.0E-01	-2.4	2.6E-02	-2.2	9.9E-03	0.7	4.2E-01
ENSMUST00000046777	intraflagellar transport 57 [Source:MGI Symbol;Acc:MGI:1921166]	B2RQZ0	Q8BXG3	-0.6	2.4E-01	0.0	9.4E-01	0.2	6.9E-01	-0.5	4.3E-01
ENSMUST00000047305	Williams-Beuren syndrome chromosome region 28 (human) [Source:MGI Symbol;Acc:MGI:1923879]		Q6UJB9	7.6	1.7E-04	-1.6	6.3E-02	2.1	9.8E-04	0.3	7.2E-01
ENSMUST00000047309	N-acetyltransferase 14 [Source:MGI Symbol;Acc:MGI:3039561]		Q8BVG8	5.5	6.8E-05	5.0	2.5E-04	-0.7	4.3E-01	0.1	8.8E-01
ENSMUST00000047315	forkhead box A2 [Source:MGI Symbol;Acc:MGI:1347476]		P35583	6.2	1.2E-04	4.4	5.3E-04	-1.4	1.4E-01	-0.6	3.4E-01
ENSMUST00000046831	transmembrane protein 205 [Source:MGI Symbol;Acc:MGI:3045495]		Q91XE8	-1.1	1.1E-01	-1.7	4.8E-02	-0.6	2.5E-01	0.0	1.0E+00
ENSMUST00000047328	insulin-like growth factor binding protein 2 [Source:MGI Symbol;Acc:MGI:96437]		P47877	4.1	2.6E-02	5.1	2.4E-03	1.0	4.2E-01	-0.5	5.2E-01
ENSMUST00000047331	leucine-rich repeat LGI family, member 3 [Source:MGI Symbol;Acc:MGI:2182619]		Q8K406	8.3	1.4E-05	-3.5	2.8E-04	0.2	5.5E-01	0.2	7.2E-01
ENSMUST00000046839	rowth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration) [Source:MGI Symbol;Acc:MGI:10775		P56213	0.8	2.6E-01	0.8	3.4E-01	-0.4	5.3E-01	-0.4	5.9E-01
ENSMUST00000047334	potassium inwardly-rectifying channel, subfamily J, member 1 [Source:MGI Symbol;Acc:MGI:1927248]		O88335	6.6	8.1E-03	-2.4	5.7E-02	0.8	2.5E-01	-3.0	5.5E-02
ENSMUST00000046859	forkhead box N3 [Source:MGI Symbol;Acc:MGI:1918625]		Q499D0	-1.4	3.8E-01	7.5	2.4E-02	6.8	2.5E-02	-2.1	2.3E-01
ENSMUST00000047348	sperm associated antigen 1 [Source:MGI Symbol;Acc:MGI:1349387]		Q80ZX8	3.3	2.5E-02	-5.1	7.3E-03	0.2	7.4E-01	-0.8	6.4E-01
ENSMUST00000047356	activating transcription factor 5 [Source:MGI Symbol;Acc:MGI:2141857]	Q3UJF3	O70191	-4.0	5.2E-03	-7.0	1.0E-03	0.7	1.6E-01	0.8	6.0E-01
ENSMUST00000047357	cleavage and polyadenylation specific factor 2 [Source:MGI Symbol;Acc:MGI:1861601]		O35218	-2.6	6.1E-04	-1.4	1.1E-01	0.6	2.5E-01	-2.2	3.8E-02
ENSMUST00000047373	SRY (sex determining region Y)-box 15 [Source:MGI Symbol;Acc:MGI:98363]	Q5F2B2	P43267	3.4	1.5E-02	9.7	3.8E-04	1.7	3.6E-01	1.0	1.9E-01
ENSMUST00000046875	UDP-glucose glycoprotein glucosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2443162]		Q6P5E4	-1.0	1.8E-01	0.3	6.9E-01	0.1	8.3E-01	-1.2	1.6E-01
ENSMUST00000046890	as association (RalGDS/AF-6) domain family (N-terminal) member 7 [Source:MGI Symbol;Acc:MGI:191423		Q9DD19	-0.3	7.3E-01	0.0	9.6E-01	0.4	6.2E-01	0.2	8.6E-01
ENSMUST00000047393	cardiotrophin 1 [Source:MGI Symbol;Acc:MGI:105115]	Q541U3	Q60753	5.5	3.9E-04	-0.5	5.3E-01	0.6	2.8E-01	-0.7	4.2E-01
ENSMUST00000047399	adhesion G protein-coupled receptor F1 [Source:MGI Symbol;Acc:MGI:1924846]		Q8VEC3	7.5	3.1E-05	6.8	4.0E-04	1.4	2.6E-01	0.0	9.6E-01
ENSMUST00000047404	dynein cytoplasmic 1 light intermediate chain 1 [Source:MGI Symbol;Acc:MGI:2135610]	Q3TWG5	Q8R1Q8	-1.6	3.3E-02	6.7	5.4E-05	0.5	5.6E-01	0.0	9.8E-01
ENSMUST00000046897	tripartite motif-containing 14 [Source:MGI Symbol;Acc:MGI:1921985]	Q14AR3	Q8BVW3	-0.7	3.0E-01	-1.0	2.4E-01	-0.1	8.5E-01	0.2	8.1E-01
ENSMUST00000047405	NCK associated protein 1 like [Source:MGI Symbol;Acc:MGI:1926063]	Q8K1X4		-5.2	1.2E-06	5.7	3.1E-02	-1.0	6.9E-01	2.9	7.5E-02
ENSMUST00000047409	vasohibin 2 [Source:MGI Symbol;Acc:MGI:2444826]		Q8C5G2	6.3	3.1E-02	1.2	2.4E-01	-5.4	2.0E-03	0.6	4.7E-01
ENSMUST00000046903	tripartite motif-containing 7 [Source:MGI Symbol;Acc:MGI:2137353]	Q5NCB7		3.6	4.0E-02	5.1	1.1E-02	0.3	8.6E-01	-1.2	3.3E-01
ENSMUST00000047413	methyl-CpG binding domain protein 5 [Source:MGI Symbol;Acc:MGI:2138934]	B1AYB5		7.3	3.1E-02	-3.5	2.9E-04	0.1	7.7E-01	0.0	1.0E+00
ENSMUST00000046916	cytoskeleton associated protein 2 [Source:MGI Symbol;Acc:MGI:1931797]		Q3V1H1	-1.0	2.1E-01	-1.3	1.7E-01	-0.7	2.8E-01	-0.4	6.4E-01
ENSMUST00000046924	family with sequence similarity 102, member B [Source:MGI Symbol;Acc:MGI:3036259]		Q8BQS4	-1.6	9.5E-02	-0.4	6.7E-01	-0.1	8.4E-01	-1.3	2.2E-01
ENSMUST00000047419	translocator protein [Source:MGI Symbol;Acc:MGI:88222]	Q541E3	P50637	-7.8	1.8E-06	3.6	2.5E-04	0.3	5.9E-01	0.7	1.2E-01
ENSMUST00000047421	tyrosine kinase with immunoglobulin-like and EGF-like domains 1 [Source:MGI Symbol;Acc:MGI:99906]		Q06806	2.9	1.0E-02	7.1	8.5E-05	-1.5	2.4E-01	0.2	7.6E-01
ENSMUST00000047425	syntrophin, basic 2 [Source:MGI Symbol;Acc:MGI:101771]	Q542S9	Q61235	-1.8	1.3E-02	1.6	6.3E-02	-0.9	2.1E-01	0.2	8.2E-01
ENSMUST00000047431	expressed sequence AU040320 [Source:MGI Symbol;Acc:MGI:2140475]		Q8K135	-3.0	1.3E-03	7.7	2.0E-04	-0.7	6.2E-01	-0.7	3.3E-01
ENSMUST00000047441	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF [Source:MGI Symbol;Acc:MGI:2681862]	H7BX05		10.4	2.4E-04	-2.3	5.1E-02	1.2	6.6E-02	-1.0	3.7E-01
ENSMUST00000047443	MANSC domain containing 1 [Source:MGI Symbol;Acc:MGI:1914979]		Q9CR33	3.6	2.3E-03	-6.1	6.7E-04	1.1	3.2E-02	-0.6	6.6E-01
ENSMUST00000047446	SID1 transmembrane family, member 1 [Source:MGI Symbol;Acc:MGI:2443155]	E9Q247		7.4	6.3E-04	-8.0	1.3E-04	0.4	2.9E-01	0.4	7.5E-01
ENSMUST00000047450	cAMP responsive element binding protein 5 [Source:MGI Symbol;Acc:MGI:2443973]			4.9	5.0E-05	-2.7	8.8E-03	-0.4	4.2E-01	-0.2	8.3E-01
ENSMUST00000047477	small proline-rich protein 2D [Source:MGI Symbol;Acc:MGI:1330347]		O70555	6.3	1.7E-04	6.9	3.1E-04	0.7	5.6E-01	-0.2	7.5E-01
ENSMUST00000046962	PHD finger protein 8 [Source:MGI Symbol;Acc:MGI:2444341]	A2ABV3	Q80TJ7	-1.3	2.1E-01	-0.9	5.1E-01	0.0	9.7E-01	-0.5	7.3E-01
ENSMUST00000047479	protocadherin alpha subfamily C, 2 [Source:MGI Symbol;Acc:MGI:1891443]	Q91Y09		7.8	1.5E-05	-4.0	4.5E-04	0.8	5.1E-02	0.2	7.8E-01
ENSMUST00000047480	piezo-type mechanosensitive ion channel component 2 [Source:MGI Symbol;Acc:MGI:1918781]	E9QNW4		9.4	6.7E-05	-1.5	2.6E-01	0.8	3.1E-01	-1.8	2.3E-01
ENSMUST00000047485	RUN domain containing 3B [Source:MGI Symbol;Acc:MGI:2685286]		Q6PDC0	3.1	7.4E-03	-2.6	3.9E-02	0.2	7.1E-01	0.4	7.1E-01
ENSMUST00000047488	RAP1 GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:3028623]		Q5SVL6	-3.7	4.6E-03	2.1	7.3E-03	0.2	6.3E-01	0.5	2.9E-01
ENSMUST00000046977	adhesion G protein-coupled receptor L4 [Source:MGI Symbol;Acc:MGI:2655562]		Q923X1	-0.7	2.0E-01	0.6	4.7E-01	1.8	1.3E-02	0.5	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000046983	sphingomyelin phosphodiesterase 1, acid lysosomal [Source:MGI Symbol;Acc:MGI:98325]		Q04519	-1.5	4.3E-02	-0.8	3.8E-01	1.1	9.2E-02	0.4	6.7E-01
ENSMUST00000047490	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 [Source:MGI Symbol;Acc:MGI:97040]		P52850	-1.8	1.7E-02	8.0	1.8E-05	0.8	4.4E-01	-0.7	1.6E-01
ENSMUST00000046999	abhydrolase domain containing 11 [Source:MGI Symbol;Acc:MGI:1916008]		Q8K4F5	-0.6	5.4E-01	0.0	9.9E-01	-0.2	8.4E-01	-0.8	4.8E-01
ENSMUST00000047498	expressed sequence AA467197 [Source:MGI Symbol;Acc:MGI:3034182]	Q3UCF3	Q810Q5	-7.8	1.4E-06	7.0	1.4E-02	-0.6	8.0E-01	-2.1	1.6E-01
ENSMUST00000047502	myoneurin [Source:MGI Symbol;Acc:MGI:1931415]		Q99MD8	-5.7	1.1E-04	4.0	3.9E-04	0.7	3.1E-01	0.1	8.5E-01
ENSMUST00000047023	centlein, centrosomal protein [Source:MGI Symbol;Acc:MGI:2443104]		A2AM05	5.9	3.7E-02	5.8	5.2E-02	-0.8	7.9E-01	-0.7	7.0E-01
ENSMUST00000047503	ral guanine nucleotide dissociation stimulator-like 2 [Source:MGI Symbol;Acc:MGI:107483]		Q61193	-4.0	9.8E-04	6.6	1.4E-04	0.2	8.6E-01	-0.8	2.2E-01
ENSMUST00000047511	shootin 1 [Source:MGI Symbol;Acc:MGI:1918903]		Q8K2Q9	-3.9	2.3E-02	1.4	6.0E-02	-0.7	2.3E-01	-0.5	4.0E-01
ENSMUST00000047521	cerebral endothelial cell adhesion molecule [Source:MGI Symbol;Acc:MGI:2139134]	B2RSF7	A3KGW5	4.5	1.1E-05	7.5	1.0E-05	-0.7	4.2E-01	0.4	4.0E-01
ENSMUST00000047036	CD3E antigen, epsilon polypeptide associated protein [Source:MGI Symbol;Acc:MGI:1917583]		Q76KJ5	1.1	4.7E-02	0.7	2.7E-01	-0.2	7.2E-01	0.2	7.2E-01
ENSMUST00000047524	thyroid adenoma associated [Source:MGI Symbol;Acc:MGI:3039623]		A8C756	1.4	3.6E-03	-6.3	3.8E-04	0.1	8.2E-01	-0.1	9.4E-01
ENSMUST00000047526	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 [Source:MGI Symbol;Acc:MGI:2684986]		Q5U464	8.0	1.2E-05	-0.5	4.3E-01	-5.4	3.6E-05	-0.2	7.3E-01
ENSMUST00000047527	zinc finger protein 804A [Source:MGI Symbol;Acc:MGI:2442949]		A2AKY4	8.1	2.9E-05	6.3	2.3E-04	-0.5	6.6E-01	-0.5	4.6E-01
ENSMUST00000047531	methyltransferase like 20 [Source:MGI Symbol;Acc:MGI:2443575]		Q80ZM3	-3.3	5.3E-03	-2.7	7.4E-04	0.0	9.3E-01	-0.6	3.2E-01
ENSMUST00000047075	SET domain containing 1A [Source:MGI Symbol;Acc:MGI:2446244]	E9PYH6		1.5	3.4E-01	3.7	1.1E-01	1.3	5.2E-01	-0.9	5.6E-01
ENSMUST00000047534	family with sequence similarity 168, member B [Source:MGI Symbol;Acc:MGI:2448487]		Q80XQ8	-6.1	1.4E-03	-6.0	6.6E-03	0.9	1.5E-01	0.1	9.6E-01
ENSMUST00000047086	WD repeat domain 43 [Source:MGI Symbol;Acc:MGI:1919765]		Q6ZQL4	-0.7	1.7E-01	-1.4	2.8E-02	-1.5	3.6E-03	-0.8	2.0E-01
ENSMUST00000047577	PR domain containing 14 [Source:MGI Symbol;Acc:MGI:3588194]		E9Q3T6	7.0	7.1E-05	-4.1	2.9E-02	-0.4	6.3E-01	-0.4	8.3E-01
ENSMUST00000047093	leucine rich repeat containing 56 [Source:MGI Symbol;Acc:MGI:1917802]		Q8K375	-0.8	7.2E-01	3.0	4.0E-01	4.4	1.7E-01	0.7	7.8E-01
ENSMUST00000047611	nth (endonuclease III)-like 1 (E.coli) [Source:MGI Symbol;Acc:MGI:1313275]		O35980	2.7	1.5E-03	7.8	3.9E-05	-0.6	5.9E-01	-0.4	4.4E-01
ENSMUST00000047614	protocadherin alpha 12 [Source:MGI Symbol;Acc:MGI:1298370]	Q91Y18		8.1	1.8E-05	5.3	1.4E-02	-0.6	7.6E-01	1.3	2.4E-01
ENSMUST00000047615	ated matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 [Source:MGI Symbol;Acc:M		Q8BJL0	-6.1	4.6E-05	4.1	1.3E-01	0.4	8.8E-01	2.3	1.6E-01
ENSMUST00000047616	jumonji domain containing 6 [Source:MGI Symbol;Acc:MGI:1858910]		Q9ER15	-5.4	1.6E-04	8.6	1.8E-04	2.6	8.4E-02	-0.1	9.1E-01
ENSMUST00000047620	family with sequence simliarity 151, member A [Source:MGI Symbol;Acc:MGI:2657115]		Q8QZW3	6.4	1.8E-03	3.8	9.1E-02	-0.2	9.0E-01	0.5	7.5E-01
ENSMUST00000047621	protein phosphatase 1, regulatory (inhibitor) subunit 13 like [Source:MGI Symbol;Acc:MGI:3525053]	Q3TCU2	Q5I1X5	2.4	2.6E-03	7.6	7.4E-05	-0.6	6.0E-01	-1.2	8.4E-02
ENSMUST00000047627	GC-rich promoter binding protein 1 [Source:MGI Symbol;Acc:MGI:1920524]		Q6NXH3	-4.5	2.5E-03	-2.3	1.4E-02	1.3	2.0E-02	-1.2	1.7E-01
ENSMUST00000047629	cirrhosis, autosomal recessive 1A (human) [Source:MGI Symbol;Acc:MGI:1096573]		Q8R2N2	-2.2	3.0E-03	-1.9	1.7E-02	0.9	5.0E-02	0.0	9.5E-01
ENSMUST00000047157	SET domain containing 1A [Source:MGI Symbol;Acc:MGI:2446244]	E9PYH6		-0.8	2.9E-01	0.3	7.8E-01	0.8	2.5E-01	-0.3	7.5E-01
ENSMUST00000047630	actin related protein T3 [Source:MGI Symbol;Acc:MGI:1923902]		Q8BXF8	6.9	1.3E-05	-4.3	3.1E-04	-0.5	2.6E-01	0.8	3.3E-01
ENSMUST00000047652	tetraspanin 14 [Source:MGI Symbol;Acc:MGI:1196325]		Q8QZY6	-5.3	7.8E-06	-2.4	4.9E-03	-0.2	6.5E-01	-1.2	1.1E-01
ENSMUST00000047664	Rho guanine nucleotide exchange factor (GEF) 4 [Source:MGI Symbol;Acc:MGI:2442507]	Q3TQN9	Q7TNR9	-3.0	1.3E-04	-0.5	4.6E-01	0.7	1.8E-01	-0.2	7.3E-01
ENSMUST00000047186	WD repeat domain, phosphoinositide interacting 1 [Source:MGI Symbol;Acc:MGI:1261864]		Q8R3E3	0.6	1.9E-01	1.6	2.4E-02	1.6	8.3E-03	0.5	3.5E-01
ENSMUST00000047665	death-associated protein kinase 3 [Source:MGI Symbol;Acc:MGI:1203520]	Q05A21	O54784	6.5	7.5E-05	-5.4	7.4E-04	-0.1	7.8E-01	-0.1	9.3E-01
ENSMUST00000047666	phosphoglucomutase 5 [Source:MGI Symbol;Acc:MGI:1925668]		Q8BZF8	7.3	3.6E-05	6.6	7.7E-04	-0.1	9.6E-01	0.0	9.7E-01
ENSMUST00000047672	chaperonin containing Tcp1, subunit 2 (beta) [Source:MGI Symbol;Acc:MGI:107186]	Q542X7	P80314	-5.0	1.8E-06	2.9	1.5E-02	-3.6	9.2E-03	-1.2	1.4E-01
ENSMUST00000047677	coiled-coil domain containing 18 [Source:MGI Symbol;Acc:MGI:1922974]		Q640L5	2.2	6.6E-03	-0.6	4.4E-01	1.0	8.3E-02	-0.2	7.3E-01
ENSMUST00000047687	ectonucleoside triphosphate diphosphohydrolase 3 [Source:MGI Symbol;Acc:MGI:1321386]	Q8BFW6		-3.9	4.8E-06	4.0	4.2E-04	-3.5	2.4E-03	-0.2	6.5E-01
ENSMUST00000047698	syntaxin 3 [Source:MGI Symbol;Acc:MGI:103077]	Q8R1B7		5.9	7.5E-03	7.5	5.0E-05	-0.6	5.9E-01	-0.3	5.8E-01
ENSMUST00000047720	patched domain containing 2 [Source:MGI Symbol;Acc:MGI:2444403]	E9QL24		9.4	1.0E-05	7.1	1.4E-03	-0.7	6.9E-01	-0.8	3.9E-01
ENSMUST00000047218	receptor accessory protein 4 [Source:MGI Symbol;Acc:MGI:1919799]		Q8K072	-0.8	1.9E-01	0.1	8.9E-01	1.0	1.1E-01	0.0	9.5E-01
ENSMUST00000047721	RRP9, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:2384313]		Q91WM3	-3.0	1.9E-02	-0.8	2.4E-01	0.7	1.2E-01	-0.1	8.1E-01
ENSMUST00000047734	zinc finger protein 281 [Source:MGI Symbol;Acc:MGI:3029290]		Q99LI5	-2.9	8.6E-03	-2.6	3.2E-03	1.1	1.3E-02	0.4	6.0E-01
ENSMUST00000047242	TRAF3 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1921269]		Q149C2	0.4	7.7E-01	0.2	9.1E-01	0.2	9.0E-01	0.4	8.4E-01
ENSMUST00000047737	interferon regulatory factor 8 [Source:MGI Symbol;Acc:MGI:96395]	Q544J7	P23611	-1.9	3.4E-02	4.8	9.5E-04	-0.1	9.1E-01	0.0	9.6E-01
ENSMUST00000047740	uroplakin 2 [Source:MGI Symbol;Acc:MGI:98913]	Q3SXK0		6.8	4.5E-05	1.7	5.4E-01	-2.9	2.3E-01	3.2	1.8E-01
ENSMUST00000047273	RNA pseudouridylate synthase domain containing 1 [Source:MGI Symbol;Acc:MGI:1919186]		Q8VCZ8	0.5	3.1E-01	1.8	2.2E-02	0.8	1.7E-01	-0.5	4.0E-01
ENSMUST00000047746	ring finger protein 123 [Source:MGI Symbol;Acc:MGI:2148796]		Q5XPI3	5.3	3.4E-03	7.3	6.0E-05	0.9	4.0E-01	0.3	5.8E-01
ENSMUST00000047749	RIKEN cDNA 4921524J17 gene [Source:MGI Symbol;Acc:MGI:1913964]		Q9CR55	-2.0	3.0E-03	-4.1	3.2E-04	0.9	3.5E-02	-0.1	8.9E-01
ENSMUST00000047753	ATP-binding cassette, sub-family B (MDR/TAP), member 1A [Source:MGI Symbol;Acc:MGI:97570]		P21447	3.7	1.1E-04	-2.4	1.7E-01	0.9	3.3E-01	-3.3	1.4E-01
ENSMUST00000047760	splA/ryanodine receptor domain and SOCS box containing 2 [Source:MGI Symbol;Acc:MGI:1315199]		O88838	7.1	4.0E-04	2.0	1.1E-01	-4.9	5.1E-03	-0.8	4.0E-01
ENSMUST00000047762	GATA binding protein 6 [Source:MGI Symbol;Acc:MGI:107516]		Q61169	7.3	5.5E-05	7.1	5.3E-04	-0.7	6.4E-01	-0.2	8.0E-01
ENSMUST00000047768	nei like 3 (E. coli) [Source:MGI Symbol;Acc:MGI:2384588]		Q8K203	-2.8	2.9E-03	5.9	3.9E-04	0.1	9.3E-01	-0.3	5.8E-01
ENSMUST00000047311	membrane bound O-acyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:2387184]		Q8BH98	0.6	2.6E-01	1.8	3.2E-02	0.8	2.0E-01	-0.4	5.5E-01
ENSMUST00000047786	membrane-associated ring finger (C3HC4) 4 [Source:MGI Symbol;Acc:MGI:2683550]		Q80TE3	9.1	5.0E-06	5.9	3.3E-04	-0.5	6.5E-01	-0.3	6.8E-01
ENSMUST00000047321	aryl hydrocarbon receptor nuclear translocator-like [Source:MGI Symbol;Acc:MGI:1096381]	Q3UHZ2	Q9WTL8	-0.4	4.6E-01	0.3	6.2E-01	0.5	2.8E-01	-0.2	7.7E-01
ENSMUST00000047322	retinoblastoma binding protein 8 [Source:MGI Symbol;Acc:MGI:2442995]		Q80YR6	-2.3	6.4E-02	-3.2	5.4E-02	-0.9	2.8E-01	0.0	9.9E-01
ENSMUST00000047793	homeobox D1 [Source:MGI Symbol;Acc:MGI:96201]		Q01822	6.9	5.7E-05	5.5	6.6E-03	-0.6	7.5E-01	-1.9	1.2E-01
ENSMUST00000047835	SR-related CTD-associated factor 11 [Source:MGI Symbol;Acc:MGI:1919443]	E9PZM7		-2.5	3.6E-04	8.3	2.7E-05	-0.6	6.1E-01	-0.6	2.5E-01
ENSMUST00000047864	eukaryotic translation elongation factor 2 [Source:MGI Symbol;Acc:MGI:95288]		P58252	-3.8	2.4E-04	2.8	2.8E-01	0.0	9.9E-01	3.7	5.4E-02
ENSMUST00000047873	Rho guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:1353510]		Q61210	-10.0	4.2E-05	6.0	8.1E-03	2.3	2.2E-01	-0.4	6.8E-01
ENSMUST00000047349	ubiquitin specific peptidase 28 [Source:MGI Symbol;Acc:MGI:2442293]		Q5I043	-0.6	3.2E-01	0.2	7.5E-01	0.3	5.4E-01	-0.5	4.8E-01
ENSMUST00000047875	eukaryotic elongation factor-2 kinase [Source:MGI Symbol;Acc:MGI:1195261]		O08796	2.9	1.2E-03	-1.5	2.2E-01	0.9	2.3E-01	-1.6	2.3E-01
ENSMUST00000047877	docking protein 3 [Source:MGI Symbol;Acc:MGI:1351490]	Q14AA1	Q9QZK7	-5.9	6.2E-06	-2.2	7.7E-03	0.2	6.8E-01	-0.3	6.6E-01
ENSMUST00000047363	isoleucine-tRNA synthetase [Source:MGI Symbol;Acc:MGI:2145219]		Q8BU30	-1.2	5.0E-01	-1.4	5.4E-01	0.2	8.9E-01	0.4	8.5E-01
ENSMUST00000047368	meiotic nuclear divisions 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924165]		Q8K396	0.3	6.8E-01	-0.8	2.5E-01	-1.8	1.0E-02	-0.7	3.1E-01
ENSMUST00000047883	tetraspanin 15 [Source:MGI Symbol;Acc:MGI:1917673]		F7BWT7	5.1	1.2E-05	2.7	5.8E-02	-0.6	6.0E-01	0.1	9.3E-01
ENSMUST00000047379	prostaglandin E receptor 4 (subtype EP4) [Source:MGI Symbol;Acc:MGI:104311]		P32240	1.0	2.9E-01	-0.5	6.8E-01	0.4	6.4E-01	1.9	1.2E-01
ENSMUST00000047885	5'-nucleotidase domain containing 1 [Source:MGI Symbol;Acc:MGI:2442446]	Q05AG7	Q8C5P5	-6.8	1.0E-03	3.3	1.3E-02	-1.1	2.9E-01	1.0	2.6E-01
ENSMUST00000047898	lysine (K)-specific demethylase 2A [Source:MGI Symbol;Acc:MGI:1354736]	F6YRW4		3.0	1.8E-04	7.4	1.0E-04	-0.1	9.4E-01	0.0	9.7E-01
ENSMUST00000047904	homeobox D4 [Source:MGI Symbol;Acc:MGI:96208]		P10628	4.5	3.0E-02	-1.5	1.5E-01	1.0	9.7E-02	0.9	3.2E-01
ENSMUST00000047906	TCDD-inducible poly(ADP-ribose) polymerase [Source:MGI Symbol;Acc:MGI:2159210]		Q8C1B2	-4.7	2.4E-04	-4.5	2.9E-05	0.4	2.1E-01	-0.3	6.0E-01
ENSMUST00000047408	ataxia, cerebellar, Cayman type homolog (human) [Source:MGI Symbol;Acc:MGI:2448730]		Q8BHE3	5.1	5.4E-02	3.3	2.2E-01	-0.7	8.0E-01	1.1	5.4E-01
ENSMUST00000047922	tetratricopeptide repeat domain 22 [Source:MGI Symbol;Acc:MGI:3045307]	A2AVQ6	Q8C159	3.2	3.2E-03	7.3	2.2E-02	-0.5	8.7E-01	-1.5	3.3E-01
ENSMUST00000047412	mesoderm induction early response 1, family member 3 [Source:MGI Symbol;Acc:MGI:2442317]		Q3UHF3	-1.0	7.6E-01	-2.0	6.1E-01	-1.0	6.8E-01	0.0	9.9E-01
ENSMUST00000047929	acyl-CoA synthetase medium-chain family member 1 [Source:MGI Symbol;Acc:MGI:2152200]		Q91VA0	5.4	8.8E-03	6.1	8.7E-02	-0.9	8.0E-01	0.3	8.6E-01
ENSMUST00000047935	TSPY-like 4 [Source:MGI Symbol;Acc:MGI:106393]		Q8VD63	3.3	2.6E-04	-6.5	4.7E-05	0.9	3.7E-02	-0.4	6.4E-01
ENSMUST00000047936	chemokine-like receptor 1 [Source:MGI Symbol;Acc:MGI:109603]	Q497D3	P97468	2.2	1.9E-03	5.3	9.5E-04	1.0	3.5E-01	-1.3	1.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000047947	GDP-mannose pyrophosphorylase B [Source:MGI Symbol;Acc:MGI:2660880]		Q8BTZ7	-4.8	1.8E-03	-1.8	4.9E-02	0.5	3.4E-01	0.5	5.5E-01
ENSMUST00000047429	mitochondrial ribosomal protein S6 [Source:MGI Symbol;Acc:MGI:2153111]	Q3TLQ4	P58064	-0.7	5.3E-01	-3.1	4.2E-02	-1.4	1.5E-01	1.1	4.4E-01
ENSMUST00000047951	F-box protein 2 [Source:MGI Symbol;Acc:MGI:2446216]	Q3USR5	Q80UW2	6.5	9.9E-05	-1.0	2.1E-01	1.3	3.0E-02	-0.6	4.4E-01
ENSMUST00000047978	RAB interacting factor [Source:MGI Symbol;Acc:MGI:2138605]		Q91X96	-2.9	7.1E-05	9.2	1.1E-03	-0.8	7.3E-01	0.4	6.2E-01
ENSMUST00000047997	trans-acting transcription factor 6 [Source:MGI Symbol;Acc:MGI:1932575]	A2A708	Q9ESX2	9.1	6.9E-06	3.6	8.2E-03	0.2	8.4E-01	0.2	7.9E-01
ENSMUST00000048001	dimethylglycine dehydrogenase precursor [Source:MGI Symbol;Acc:MGI:1921379]		Q9DBT9	6.7	1.1E-04	6.0	7.1E-03	-0.7	6.8E-01	0.7	5.0E-01
ENSMUST00000048012	RIKEN cDNA 5330417C22 gene [Source:MGI Symbol;Acc:MGI:1923930]		A2AFS3	4.7	2.1E-03	3.9	8.7E-04	-0.4	5.9E-01	0.5	3.7E-01
ENSMUST00000047463	Rho GTPase activating protein 44 [Source:MGI Symbol;Acc:MGI:2144423]		Q5SSM3	3.2	2.7E-01	3.4	2.5E-01	-0.5	8.8E-01	-0.7	7.6E-01
ENSMUST00000048026	homeobox A11 [Source:MGI Symbol;Acc:MGI:96172]		P31311	7.7	3.4E-04	5.9	4.8E-04	-0.6	6.2E-01	-0.2	7.3E-01
ENSMUST00000048043	coronin, actin binding protein, 2B [Source:MGI Symbol;Acc:MGI:2444283]		Q8BH44	6.4	1.1E-04	7.2	5.4E-05	-0.5	6.2E-01	0.0	9.4E-01
ENSMUST00000048044	TruB pseudouridine (psi) synthase homolog 2 (E. coli) [Source:MGI Symbol;Acc:MGI:2442186]		Q91WG3	-5.5	1.4E-04	4.8	1.2E-03	-5.0	5.1E-03	-0.4	5.6E-01
ENSMUST00000048050	transmembrane protein 45b [Source:MGI Symbol;Acc:MGI:2384574]		Q8VCZ2	8.4	9.2E-06	2.7	2.0E-02	-0.6	5.2E-01	-0.3	7.5E-01
ENSMUST00000047486	RIKEN cDNA C330007P06 gene [Source:MGI Symbol;Acc:MGI:1924894]		Q8VDP2	3.4	1.5E-01	8.1	6.4E-03	-0.3	9.0E-01	-5.0	5.2E-03
ENSMUST00000048052	family with sequence similarity 26, member D [Source:MGI Symbol;Acc:MGI:2685489]		Q8CE93	4.8	1.6E-04	-2.0	1.6E-01	1.3	1.0E-01	-0.4	7.5E-01
ENSMUST00000048064	gene regulated by estrogen in breast cancer protein [Source:MGI Symbol;Acc:MGI:2149712]		Q3UHK3	9.0	5.6E-03	-0.3	7.3E-01	0.7	1.8E-01	-0.8	3.2E-01
ENSMUST00000047497	centrosomal protein 104 [Source:MGI Symbol;Acc:MGI:2687282]		Q80V31	0.0	9.9E-01	0.9	1.8E-01	1.1	4.0E-02	0.2	7.0E-01
ENSMUST00000048065	triggering receptor expressed on myeloid cells 3 [Source:MGI Symbol;Acc:MGI:1930003]	Q9JKE1		-7.2	7.8E-07	-6.9	3.7E-05	0.9	3.3E-02	0.0	9.9E-01
ENSMUST00000048068	arrestin domain containing 4 [Source:MGI Symbol;Acc:MGI:1913662]	A0A0B4J1F4		-3.0	2.0E-02	-6.2	4.3E-04	-0.7	1.3E-01	-0.2	9.0E-01
ENSMUST00000048073	phosphatidylinositol glycan anchor biosynthesis, class S [Source:MGI Symbol;Acc:MGI:2687325]	Q3V307	Q6PD26	-2.5	1.8E-03	-3.1	1.9E-02	0.7	2.3E-01	-0.2	8.8E-01
ENSMUST00000047510	ubiquitin specific peptidase 5 (isopeptidase T) [Source:MGI Symbol;Acc:MGI:1347343]		P56399	0.2	7.1E-01	1.6	9.4E-02	1.1	1.3E-01	-0.2	7.5E-01
ENSMUST00000048077	Lck interacting transmembrane adaptor 1 [Source:MGI Symbol;Acc:MGI:1919949]		Q9EQR5	-5.4	4.3E-03	-3.3	9.4E-02	-0.5	5.8E-01	-1.2	5.3E-01
ENSMUST00000048079	family with sequence similarity 160, member A2 [Source:MGI Symbol;Acc:MGI:1921599]		Q3U2I3	-5.6	3.7E-03	4.9	2.3E-05	0.2	6.9E-01	-0.2	7.2E-01
ENSMUST00000048096	toll-like receptor 4 [Source:MGI Symbol;Acc:MGI:96824]	L0CL36	Q9QUK6	-4.9	9.1E-06	2.2	1.3E-03	0.7	7.8E-02	-0.1	8.9E-01
ENSMUST00000048116	te carrier family 7 (cationic amino acid transporter, y+ system), member 1 [Source:MGI Symbol;Acc:MGI:881	Q3UGD6	Q09143	4.6	3.2E-05	5.7	6.6E-05	-2.4	3.0E-02	-0.1	8.6E-01
ENSMUST00000048118	hydroxysteroid (17-beta) dehydrogenase 13 [Source:MGI Symbol;Acc:MGI:2140804]		Q8VCR2	6.7	6.0E-05	5.9	4.0E-04	-1.5	2.4E-01	0.8	2.6E-01
ENSMUST00000048121	myosin VIIA and Rab interacting protein [Source:MGI Symbol;Acc:MGI:2384407]		Q8K3I4	8.6	7.7E-06	-4.4	2.0E-03	-2.1	3.7E-03	-1.0	4.2E-01
ENSMUST00000048138	S100 calcium binding protein A13 [Source:MGI Symbol;Acc:MGI:109581]	A0A0A0MQ90		-6.2	4.6E-06	-2.7	8.4E-02	1.0	2.3E-01	-2.3	1.8E-01
ENSMUST00000047560	dehydrogenase/reductase (SDR family) member 11 [Source:MGI Symbol;Acc:MGI:2652816]		Q3U0B3	-1.6	8.4E-02	0.9	4.4E-01	1.6	8.9E-02	-0.9	3.8E-01
ENSMUST00000048147	anaphase promoting complex subunit 10 [Source:MGI Symbol;Acc:MGI:1916249]		Q8K2H6	2.8	4.7E-04	6.1	4.1E-04	-1.3	2.9E-01	-0.4	5.4E-01
ENSMUST00000048150	coiled-coil and C2 domain containing 2A [Source:MGI Symbol;Acc:MGI:1924487]		Q8CFW7	7.3	1.4E-03	1.2	1.2E-01	-1.3	6.1E-02	0.3	6.4E-01
ENSMUST00000048155	RNA binding motif protein 25 [Source:MGI Symbol;Acc:MGI:1914289]		B2RY56	-5.5	4.1E-04	7.2	8.8E-05	-0.6	6.1E-01	0.3	6.5E-01
ENSMUST00000048162	BSD domain containing 1 [Source:MGI Symbol;Acc:MGI:1913466]		Q80Y55	-4.2	3.6E-05	-4.6	1.6E-03	0.7	1.6E-01	-0.8	5.1E-01
ENSMUST00000048183	fibromodulin [Source:MGI Symbol;Acc:MGI:1328364]	Q543D2	P50608	8.7	1.3E-05	-5.5	9.8E-04	0.1	8.7E-01	0.2	9.0E-01
ENSMUST00000048184	programmed cell death 7 [Source:MGI Symbol;Acc:MGI:1859170]	Q3U2X6		-2.1	9.7E-04	6.7	2.4E-03	-0.7	6.9E-01	-1.0	3.2E-01
ENSMUST00000048188	PHD finger protein 20-like 1 [Source:MGI Symbol;Acc:MGI:2444412]		Q8CCJ9	-3.7	2.9E-05	2.9	3.6E-03	0.7	3.1E-01	0.1	8.0E-01
ENSMUST00000048194	transcription factor AP-2, epsilon [Source:MGI Symbol;Acc:MGI:2679630]		Q6VUP9	7.3	1.3E-04	-3.5	2.0E-02	-0.7	3.1E-01	-1.6	2.5E-01
ENSMUST00000048207	aryl hydrocarbon receptor-interacting protein-like 1 [Source:MGI Symbol;Acc:MGI:2148800]		Q924K1	4.5	3.6E-05	-1.9	2.3E-02	0.0	9.2E-01	-0.4	6.0E-01
ENSMUST00000048209	lactate dehydrogenase A [Source:MGI Symbol;Acc:MGI:96759]	Q564E2	P06151	-8.3	6.0E-07	6.5	5.4E-05	-0.4	7.1E-01	0.0	9.4E-01
ENSMUST00000047632	surfeit gene 6 [Source:MGI Symbol;Acc:MGI:98447]	Q3V1X4	P70279	0.2	7.2E-01	1.0	2.3E-01	0.2	7.0E-01	-0.6	4.7E-01
ENSMUST00000048216	abhydrolase domain containing 13 [Source:MGI Symbol;Acc:MGI:1916154]		Q80UX8	-7.4	6.7E-06	-4.1	3.5E-04	0.9	2.6E-02	-0.2	7.6E-01
ENSMUST00000048222	zinc finger with UFM1-specific peptidase domain [Source:MGI Symbol;Acc:MGI:1919830]		Q3T9Z9	-2.2	3.5E-02	-1.0	1.1E-01	1.1	1.6E-02	-0.9	1.4E-01
ENSMUST00000048229	myelin regulatory factor-like [Source:MGI Symbol;Acc:MGI:2685085]		Q3UN70	6.1	5.3E-05	1.4	6.8E-02	-5.6	1.7E-04	-0.4	5.2E-01
ENSMUST00000048246	fibrinogen beta chain [Source:MGI Symbol;Acc:MGI:99501]	Q3TGR2	Q8K0E8	5.2	4.3E-03	7.4	5.9E-05	-0.5	6.8E-01	-0.6	2.8E-01
ENSMUST00000048249	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) [Source:MGI Symbol;Acc:MGI:1913666]		Q9Z1P6	-6.4	2.9E-04	-4.2	3.0E-05	-0.2	3.9E-01	-1.0	1.1E-01
ENSMUST00000048250	TGF-beta activated kinase 1/MAP3K7 binding protein 3 [Source:MGI Symbol;Acc:MGI:1913974]	B1ASY9	Q571K4	-1.5	1.4E-02	2.4	9.4E-03	0.0	9.6E-01	-0.2	7.4E-01
ENSMUST00000048252	branched chain aminotransferase 1, cytosolic [Source:MGI Symbol;Acc:MGI:104861]	E9Q4K3		6.9	9.3E-04	-3.0	1.8E-04	0.4	1.5E-01	-0.5	3.8E-01
ENSMUST00000047697	tripartite motif-containing 17 [Source:MGI Symbol;Acc:MGI:1861440]	A2AB81		1.5	2.0E-01	4.6	3.6E-03	0.4	7.5E-01	-2.7	1.8E-02
ENSMUST00000048260	lectin, mannose-binding, 1 [Source:MGI Symbol;Acc:MGI:1917611]		Q9D0F3	-1.5	1.7E-02	6.4	7.5E-03	-0.7	7.3E-01	-1.2	3.0E-01
ENSMUST00000047704	centrosomal protein 78 [Source:MGI Symbol;Acc:MGI:1924386]		Q6IRU7	0.4	4.8E-01	0.5	4.8E-01	0.1	7.9E-01	0.0	9.5E-01
ENSMUST00000047711	vezatin, adherens junctions transmembrane protein [Source:MGI Symbol;Acc:MGI:2143698]		Q3ZK22	-1.3	4.3E-01	-0.6	7.1E-01	-0.8	5.3E-01	-1.5	3.9E-01
ENSMUST00000047714	lysine (K)-specific demethylase 5B [Source:MGI Symbol;Acc:MGI:1922855]		Q80Y84	-1.6	5.1E-02	-0.4	6.8E-01	0.9	1.9E-01	-0.3	7.3E-01
ENSMUST00000048263	WAPL cohesin release factor [Source:MGI Symbol;Acc:MGI:2675859]		Q65Z40	-2.6	2.9E-03	7.0	3.4E-05	-2.5	5.2E-02	-0.1	8.2E-01
ENSMUST00000048274	tetratricopeptide repeat domain 39B [Source:MGI Symbol;Acc:MGI:1917113]		Q8BYY4	-3.5	1.0E-02	-0.1	9.0E-01	-0.6	3.7E-01	-3.6	9.7E-03
ENSMUST00000048302	ankyrin repeat and SOCS box-containing 10 [Source:MGI Symbol;Acc:MGI:2152836]		Q91ZT7	5.2	6.1E-03	-4.7	7.0E-03	1.0	1.6E-01	2.8	6.9E-02
ENSMUST00000048308	RIKEN cDNA C130074G19 gene [Source:MGI Symbol;Acc:MGI:2444831]		Q8BGN9	8.3	1.6E-05	-1.2	2.5E-01	0.1	8.9E-01	-0.7	4.9E-01
ENSMUST00000048319	zinc finger, FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:3026685]		Q810J8	-2.2	3.7E-04	7.0	6.7E-05	-0.6	5.9E-01	-0.8	1.8E-01
ENSMUST00000048359	transport and golgi organization 6 [Source:MGI Symbol;Acc:MGI:2142786]		Q8C3S2	2.9	4.7E-04	3.3	2.4E-02	-3.0	5.5E-02	-1.0	3.0E-01
ENSMUST00000048371	TSC22 domain family, member 1 [Source:MGI Symbol;Acc:MGI:109127]	E9QLZ1		4.4	1.3E-03	-1.5	3.4E-02	-0.4	3.6E-01	-0.9	1.6E-01
ENSMUST00000048372	transmembrane protein 71 [Source:MGI Symbol;Acc:MGI:2146049]			-3.7	3.5E-05	2.3	4.9E-03	-1.8	1.2E-02	-0.3	5.3E-01
ENSMUST00000048374	RIKEN cDNA C330027C09 gene [Source:MGI Symbol;Acc:MGI:2146335]		Q8BWY9	-4.5	1.1E-03	2.5	1.8E-01	-0.7	6.5E-01	3.9	1.5E-02
ENSMUST00000048375	family with sequence similarity 102, member A [Source:MGI Symbol;Acc:MGI:2138935]		Q78T81	-5.7	2.7E-03	2.6	5.8E-03	-5.1	5.1E-04	-0.4	5.1E-01
ENSMUST00000048377	SUN domain containing ossification factor [Source:MGI Symbol;Acc:MGI:2138346]	B2RRF3	Q8C341	-3.3	1.2E-04	-1.3	1.8E-01	0.9	1.8E-01	-0.6	4.8E-01
ENSMUST00000047783	Rpgrip1-like [Source:MGI Symbol;Acc:MGI:1920563]		Q8CG73	0.9	2.8E-01	2.8	2.1E-02	1.0	2.5E-01	-0.9	3.1E-01
ENSMUST00000048391	claspin [Source:MGI Symbol;Acc:MGI:2445153]		Q80YR7	1.8	1.7E-03	9.2	5.7E-05	0.5	7.1E-01	0.4	5.1E-01
ENSMUST00000048393	autophagy related 101 [Source:MGI Symbol;Acc:MGI:1915368]		Q9D8Z6	-4.9	3.6E-04	6.7	1.4E-04	-0.5	6.7E-01	-0.3	6.0E-01
ENSMUST00000047799	acyl-Coenzyme A dehydrogenase family, member 11 [Source:MGI Symbol;Acc:MGI:2143169]			-2.0	4.9E-02	-3.4	3.4E-02	0.0	9.5E-01	1.3	3.6E-01
ENSMUST00000047812	dipeptidylpeptidase 4 [Source:MGI Symbol;Acc:MGI:94919]		P28843	1.3	8.5E-02	-0.4	5.8E-01	-1.9	9.0E-03	-0.3	7.2E-01
ENSMUST00000047815	solute carrier family 9 (sodium/hydrogen exchanger), member 8 [Source:MGI Symbol;Acc:MGI:1924281]		Q8R4D1	-3.1	3.8E-02	-1.9	2.8E-01	1.0	3.2E-01	-0.2	9.1E-01
ENSMUST00000047816	phospholipase A2, group VI [Source:MGI Symbol;Acc:MGI:1859152]	Q3UN31	P97819	-2.0	4.6E-01	3.3	3.2E-01	3.6	2.5E-01	-1.7	5.1E-01
ENSMUST00000047817	kinesin family member 14 [Source:MGI Symbol;Acc:MGI:1098226]	E9Q3T3		6.3	1.3E-01	2.7	4.4E-01	-3.9	3.4E-01	-0.3	9.1E-01
ENSMUST00000048400	tankyrase 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:2446193]	Z4YJL4		-3.3	2.1E-02	-1.5	3.1E-02	0.7	8.4E-02	-0.4	5.0E-01
ENSMUST00000047852	family with sequence similarity 199, X-linked [Source:MGI Symbol;Acc:MGI:2384304]		Q8K2D0	0.5	2.7E-01	1.1	8.7E-02	0.3	4.7E-01	-0.2	6.5E-01
ENSMUST00000047857	F-box and leucine-rich repeat protein 5 [Source:MGI Symbol;Acc:MGI:2152883]		Q8C2S5	-2.2	5.4E-01	-7.2	3.8E-02	-5.3	2.2E-02	-0.2	9.5E-01
ENSMUST00000047860	nitric oxide associated 1 [Source:MGI Symbol;Acc:MGI:1914306]		Q9JJG9	-1.3	5.2E-02	-2.0	6.2E-02	1.0	1.1E-01	1.8	8.4E-02
ENSMUST00000048409	ELMO/CED-12 domain containing 1 [Source:MGI Symbol;Acc:MGI:3583900]		Q3V1U8	5.6	1.2E-02	-2.6	1.2E-02	1.0	7.5E-02	-0.2	7.7E-01
ENSMUST00000047865	myelin basic protein [Source:MGI Symbol;Acc:MGI:96925]		P04370	2.4	3.1E-01	1.3	5.9E-01	-0.8	7.5E-01	0.3	8.7E-01
ENSMUST00000048418	importin 8 [Source:MGI Symbol;Acc:MGI:2444611]		Q7TMY7	-3.1	9.1E-03	-8.7	7.3E-04	0.5	3.3E-01	-0.8	6.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000048421	cDNA sequence BC037034 [Source:MGI Symbol;Acc:MGI:2385896]	E9Q2V5		-6.0	1.4E-04	3.1	4.5E-03	0.5	5.3E-01	0.3	6.8E-01
ENSMUST00000048427	ankyrin repeat domain 35 [Source:MGI Symbol;Acc:MGI:2442590]	E9Q9D8		8.6	4.8E-05	-4.4	2.6E-04	1.1	1.3E-02	-0.4	6.6E-01
ENSMUST00000048430	cerberus 1 homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1201414]	A2ADM9	O55233	8.1	2.9E-06	2.5	2.0E-03	-2.9	9.4E-04	-0.2	6.1E-01
ENSMUST00000048432	proline arginine-rich end leucine-rich repeat [Source:MGI Symbol;Acc:MGI:2151110]	Q543S0	Q9JK53	8.7	6.3E-06	-0.1	9.7E-01	4.1	6.7E-03	-2.7	1.3E-01
ENSMUST00000047889	ATPase, Na+/K+ transporting, beta 2 polypeptide [Source:MGI Symbol;Acc:MGI:88109]	Q3UR55	P14231	3.5	5.3E-02	1.3	6.1E-01	0.5	8.1E-01	2.6	2.5E-01
ENSMUST00000048444	kallikrein related-peptidase 5 [Source:MGI Symbol;Acc:MGI:1915918]	Q9D140		6.7	5.2E-05	3.0	4.9E-04	-0.5	3.9E-01	-0.5	2.9E-01
ENSMUST00000047903	collagen beta(1-O)galactosyltransferase 1 [Source:MGI Symbol;Acc:MGI:1924348]		Q8K297	-0.9	1.6E-01	-0.9	2.8E-01	0.0	9.9E-01	0.0	9.8E-01
ENSMUST00000048452	plasmalemma vesicle associated protein [Source:MGI Symbol;Acc:MGI:1890497]	G3X924		5.8	7.5E-05	6.7	9.9E-03	0.3	8.8E-01	-1.9	1.5E-01
ENSMUST00000048453	BTB (POZ) domain containing 16 [Source:MGI Symbol;Acc:MGI:3045247]		E9Q173	4.2	4.8E-05	-3.1	1.0E-02	0.8	1.6E-01	-0.7	4.8E-01
ENSMUST00000047910	methionine aminopeptidase 2 [Source:MGI Symbol;Acc:MGI:1929701]	Q58E65	O08663	0.6	3.3E-01	0.8	2.8E-01	-0.1	8.1E-01	-0.4	5.9E-01
ENSMUST00000048455	netrin G2 [Source:MGI Symbol;Acc:MGI:2159341]		Q8R4F1	-5.8	1.1E-03	4.3	1.1E-03	0.5	5.6E-01	-0.6	3.8E-01
ENSMUST00000047923	Sec24 related gene family, member D (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916858]	Q6NXL1		0.6	1.7E-01	0.4	4.1E-01	-0.5	2.5E-01	-0.3	5.5E-01
ENSMUST00000048478	olfactory receptor 750 [Source:MGI Symbol;Acc:MGI:3030584]	E9Q0Z1		6.6	1.9E-04	3.1	8.6E-02	-1.9	3.1E-01	0.5	6.7E-01
ENSMUST00000048482	RIKEN cDNA 2010003K11 gene [Source:MGI Symbol;Acc:MGI:1917111]		Q8VC23	6.3	2.0E-03	2.6	4.1E-03	-0.3	6.7E-01	0.4	4.7E-01
ENSMUST00000048486	fibrinogen gamma chain [Source:MGI Symbol;Acc:MGI:95526]	Q3UEM7	Q8VCM7	4.9	6.7E-03	0.5	4.6E-01	-1.3	2.8E-02	0.4	4.6E-01
ENSMUST00000048490	La ribonucleoprotein domain family, member 1B [Source:MGI Symbol;Acc:MGI:1914604]	Q8R3F0		-4.8	3.4E-04	-3.8	2.2E-02	0.4	5.9E-01	-0.6	7.0E-01
ENSMUST00000047950	zinc finger protein 292 [Source:MGI Symbol;Acc:MGI:1353423]		Q9Z2U2	-2.6	1.1E-01	-0.2	9.1E-01	1.7	2.1E-01	-0.7	7.1E-01
ENSMUST00000048502	echinoderm microtubule associated protein like 2 [Source:MGI Symbol;Acc:MGI:1919455]		Q7TNG5	-3.8	1.7E-02	3.2	2.5E-03	-3.7	3.7E-03	-0.4	5.6E-01
ENSMUST00000047973	24-dehydrocholesterol reductase [Source:MGI Symbol;Acc:MGI:1922004]		Q8VCH6	-0.9	1.5E-01	0.7	3.5E-01	1.0	8.3E-02	-0.5	4.2E-01
ENSMUST00000048514	NLR family, pyrin domain containing 1A [Source:MGI Symbol;Acc:MGI:2684861]	Q67EY4		7.8	5.3E-05	-1.9	6.2E-03	0.8	3.1E-02	-0.2	6.5E-01
ENSMUST00000048519	sorting nexin 13 [Source:MGI Symbol;Acc:MGI:2661416]	E9QNG6		-4.1	1.8E-04	5.7	8.7E-05	-3.2	1.0E-02	0.2	7.1E-01
ENSMUST00000048527	abhydrolase domain containing 14b [Source:MGI Symbol;Acc:MGI:1923741]	E9QN99		3.9	4.3E-03	5.5	3.1E-04	-2.1	9.0E-02	-0.8	2.2E-01
ENSMUST00000048002	beta-1,4-N-acetyl-galactosaminyl transferase 4 [Source:MGI Symbol;Acc:MGI:2652891]		Q766D5	1.0	8.1E-02	3.3	1.9E-03	2.3	4.9E-03	0.0	9.4E-01
ENSMUST00000048010	dermatan sulfate epimerase [Source:MGI Symbol;Acc:MGI:2443455]		Q8BLI4	-0.7	4.1E-01	-0.8	4.4E-01	-1.1	1.6E-01	-1.0	3.4E-01
ENSMUST00000048544	bicaudal D homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1924145]		Q921C5	3.0	6.8E-05	5.2	4.8E-03	0.8	5.6E-01	0.3	7.6E-01
ENSMUST00000048015	zinc finger protein 715 [Source:MGI Symbol;Acc:MGI:1917180]	G3X9T1		-1.4	6.9E-01	0.4	9.3E-01	0.5	8.8E-01	-1.3	7.5E-01
ENSMUST00000048016	fucosyltransferase 11 [Source:MGI Symbol;Acc:MGI:1920318]	B2RRR9	Q8BHC9	-0.1	8.3E-01	0.2	7.3E-01	0.1	8.3E-01	-0.2	7.1E-01
ENSMUST00000048545	arginine and glutamate rich 1 [Source:MGI Symbol;Acc:MGI:2442985]		Q3UL36	-3.3	7.8E-03	7.1	1.0E-03	-0.6	7.2E-01	0.0	9.9E-01
ENSMUST00000048565	tripartite motif-containing 60 [Source:MGI Symbol;Acc:MGI:2387430]		Q8VI40	6.3	7.3E-04	6.6	3.7E-04	-0.2	9.0E-01	-0.3	6.0E-01
ENSMUST00000048572	H2.0-like homeobox [Source:MGI Symbol;Acc:MGI:96109]	Q549B7	Q61670	-2.8	8.7E-04	-5.8	4.3E-03	1.3	3.5E-02	1.6	3.2E-01
ENSMUST00000048578	tetratricopeptide repeat domain 1 [Source:MGI Symbol;Acc:MGI:1914077]		Q91Z38	-6.6	5.2E-04	7.3	3.3E-05	-1.5	1.9E-01	-0.4	4.0E-01
ENSMUST00000048603	dynein, axonemal, heavy chain 1 [Source:MGI Symbol;Acc:MGI:107721]	E9Q8T7		8.5	3.1E-06	5.3	4.4E-04	0.2	8.3E-01	-0.3	6.1E-01
ENSMUST00000048054	CTF18, chromosome transmission fidelity factor 18 [Source:MGI Symbol;Acc:MGI:2384887]			-2.1	1.4E-01	-1.2	5.5E-01	1.2	3.6E-01	0.2	8.9E-01
ENSMUST00000048606	RIKEN cDNA 4921522P10 gene [Source:MGI Symbol;Acc:MGI:1913969]	Q9D5T6		6.6	1.2E-04	5.0	1.1E-01	-0.5	8.7E-01	3.4	5.8E-02
ENSMUST00000048615	purine-nucleoside phosphorylase [Source:MGI Symbol;Acc:MGI:97365]	Q543K9		-3.8	5.0E-05	-5.8	2.4E-05	0.0	9.9E-01	-1.5	8.5E-02
ENSMUST00000048630	cartilage acidic protein 1 [Source:MGI Symbol;Acc:MGI:1920082]		Q8R555	2.6	9.8E-04	-2.3	1.4E-01	0.6	4.6E-01	-0.1	9.2E-01
ENSMUST00000048642	presenilin associated, rhomboid-like [Source:MGI Symbol;Acc:MGI:1277152]		Q5XJY4	-4.5	1.9E-04	-1.3	1.2E-01	1.2	3.2E-02	0.0	9.6E-01
ENSMUST00000048644	pancreatic lipase related protein 1 [Source:MGI Symbol;Acc:MGI:97723]		Q5BKQ4	7.0	3.4E-05	-2.9	8.8E-02	0.9	3.1E-01	-1.5	4.1E-01
ENSMUST00000048646	vacuolar protein sorting 13B (yeast) [Source:MGI Symbol;Acc:MGI:1916380]	E9QKX5		-1.3	9.9E-03	-5.6	1.9E-02	0.9	2.4E-01	0.8	7.0E-01
ENSMUST00000048653	copine II [Source:MGI Symbol;Acc:MGI:2387578]		P59108	-5.9	1.9E-03	7.2	8.5E-05	0.1	9.6E-01	0.3	5.9E-01
ENSMUST00000048657	Sec24 related gene family, member C (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919746]	G3X972		-2.8	4.4E-04	-6.2	1.5E-05	-0.5	1.6E-01	0.8	3.2E-01
ENSMUST00000048099	transmembrane protein 194 [Source:MGI Symbol;Acc:MGI:2446113]		Q6ZQE4	-0.2	6.7E-01	1.1	1.2E-01	0.8	1.5E-01	-0.5	3.7E-01
ENSMUST00000048112	small G protein signaling modulator 1 [Source:MGI Symbol;Acc:MGI:107320]	B2RQR5		1.4	3.6E-01	7.3	2.6E-03	1.4	4.5E-01	-4.5	3.8E-03
ENSMUST00000048670	solute carrier family 35, member F2 [Source:MGI Symbol;Acc:MGI:1919272]		Q7TML3	4.9	2.2E-04	3.6	7.8E-04	-0.7	3.2E-01	0.3	5.1E-01
ENSMUST00000048678	lanosterol synthase [Source:MGI Symbol;Acc:MGI:1336155]		Q8BLN5	-3.2	9.3E-03	5.7	2.3E-04	-1.5	1.8E-01	-0.5	4.4E-01
ENSMUST00000048680	homeobox A9 [Source:MGI Symbol;Acc:MGI:96180]		P09631	4.6	4.8E-04	8.0	2.8E-05	-0.6	6.0E-01	0.0	9.5E-01
ENSMUST00000048128	zinc finger and BTB domain containing 7a [Source:MGI Symbol;Acc:MGI:1335091]		O88939	-0.4	5.0E-01	-0.4	6.2E-01	1.0	1.3E-01	1.0	2.4E-01
ENSMUST00000048129	piwi-like RNA-mediated gene silencing 2 [Source:MGI Symbol;Acc:MGI:1930036]		Q8CDG1	-0.3	6.8E-01	-0.1	9.1E-01	-0.1	8.7E-01	-0.3	7.3E-01
ENSMUST00000048686	proline-rich protein MP5 [Source:MGI Symbol;Acc:MGI:1927478]	E9PXN1		9.0	1.2E-04	-4.6	1.9E-04	0.0	9.9E-01	-1.6	7.8E-02
ENSMUST00000048139	WD repeat containing, antisense to Trp53 [Source:MGI Symbol;Acc:MGI:2384933]		Q8VC51	-1.3	5.1E-02	0.8	2.9E-01	1.0	9.1E-02	-1.1	1.4E-01
ENSMUST00000048145	RNA binding protein, fox-1 homolog (C. elegans) 2 [Source:MGI Symbol;Acc:MGI:1933973]		Q8BP71	3.5	2.3E-01	3.3	3.0E-01	-0.4	8.9E-01	-0.2	9.4E-01
ENSMUST00000048687	WW domain binding protein 5 [Source:MGI Symbol;Acc:MGI:109567]		Q9DD24	-5.1	3.0E-03	2.6	1.5E-03	-0.6	3.0E-01	-0.4	4.0E-01
ENSMUST00000048688	F-box protein 38 [Source:MGI Symbol;Acc:MGI:2444639]		Q8BMI0	-3.6	1.1E-05	5.1	8.0E-03	-3.6	6.8E-02	-1.5	1.7E-01
ENSMUST00000048691	patched domain containing 4 [Source:MGI Symbol;Acc:MGI:1920485]	E9QMK6		8.0	8.8E-06	-2.7	4.2E-02	0.8	2.5E-01	-2.0	1.4E-01
ENSMUST00000048698	'6 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:109		Q62311	-5.7	1.5E-03	-3.1	1.7E-03	0.8	4.9E-02	-0.2	7.4E-01
ENSMUST00000048180	nology domain containing, family A (phosphoinositide binding specific) member 1 [Source:MGI Symbol;Acc:M		Q8BUL6	-1.3	2.5E-01	-2.3	1.9E-01	0.6	5.4E-01	1.5	3.5E-01
ENSMUST00000048702	PAP associated domain containing 4 [Source:MGI Symbol;Acc:MGI:2140950]		Q91YI6	-4.1	4.0E-05	8.0	4.8E-05	-0.6	6.1E-01	0.0	9.9E-01
ENSMUST00000048706	origin recognition complex, subunit 3 [Source:MGI Symbol;Acc:MGI:1354944]		Q9JK30	-6.5	4.4E-05	-1.3	4.1E-02	0.7	7.5E-02	-0.1	8.3E-01
ENSMUST00000048715	homeobox A7 [Source:MGI Symbol;Acc:MGI:96179]		P02830	5.5	2.4E-04	-2.6	1.5E-03	0.4	2.7E-01	-0.7	2.4E-01
ENSMUST00000048192	HAUS augmin-like complex, subunit 1 [Source:MGI Symbol;Acc:MGI:2385076]		Q8BHX1	-1.5	8.0E-02	-1.5	1.1E-01	-1.1	1.3E-01	-1.1	2.3E-01
ENSMUST00000048731	actin-related protein 2/3 complex inhibitor [Source:MGI Symbol;Acc:MGI:1917670]		Q9D0A3	4.5	2.6E-05	7.1	2.7E-04	-0.6	6.7E-01	-0.4	5.2E-01
ENSMUST00000048762	:artilage intermediate layer protein, nucleotide pyrophosphohydrolase [Source:MGI Symbol;Acc:MGI:2444507			8.0	3.7E-05	5.0	5.4E-05	0.2	7.7E-01	-0.3	5.4E-01
ENSMUST00000048770	SH3-binding domain glutamic acid-rich protein [Source:MGI Symbol;Acc:MGI:1354740]		Q9WUZ7	6.5	1.1E-02	-6.6	1.0E-05	0.4	2.2E-01	-1.3	1.5E-01
ENSMUST00000048774	coatomer protein complex, subunit gamma 2 [Source:MGI Symbol;Acc:MGI:1858683]		Q9QXK3	-6.0	1.9E-06	-6.3	2.0E-04	1.2	1.0E-02	0.0	9.8E-01
ENSMUST00000048782	triggering receptor expressed on myeloid cells 1 [Source:MGI Symbol;Acc:MGI:1930005]		Q9JKE2	-5.0	3.7E-05	-1.8	1.5E-01	0.5	5.1E-01	0.0	9.7E-01
ENSMUST00000048786	family with sequence similarity 92, member B [Source:MGI Symbol;Acc:MGI:3588213]		Q3V2J0	3.5	2.5E-02	5.1	1.9E-04	-1.3	1.7E-01	-0.3	6.2E-01
ENSMUST00000048790	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane) [Source:MGI Symbol;Acc:MGI:2685214]		Q6PAQ9	8.2	2.1E-06	1.2	3.0E-01	-5.9	2.1E-03	-1.9	8.2E-02
ENSMUST00000048248	BR serine/threonine kinase 1 [Source:MGI Symbol;Acc:MGI:2685946]		Q5RJI5	5.9	9.6E-02	4.3	2.5E-01	-0.7	8.5E-01	0.9	6.9E-01
ENSMUST00000048792	RIKEN cDNA 1110008P14 gene [Source:MGI Symbol;Acc:MGI:1920987]		P58686	-7.3	5.7E-04	-6.3	1.7E-03	-0.9	1.5E-01	-0.9	5.7E-01
ENSMUST00000048794	homeobox A5 [Source:MGI Symbol;Acc:MGI:96177]		P09021	5.5	4.3E-04	-1.9	1.7E-02	0.5	2.5E-01	0.9	1.7E-01
ENSMUST00000048807	MIS12 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914389]		Q9CY25	-2.7	1.2E-03	3.9	2.7E-02	-2.1	2.0E-01	0.9	4.0E-01
ENSMUST00000048824	predicted gene 5617 [Source:MGI Symbol;Acc:MGI:3643566]		Q91VN2	-3.2	4.8E-04	-1.4	4.6E-02	-0.3	5.4E-01	-0.3	6.5E-01
ENSMUST00000048854	zinc finger protein 647 [Source:MGI Symbol;Acc:MGI:3052806]		Q7TNU6	5.9	2.6E-05	-2.1	3.8E-02	0.8	1.4E-01	0.3	7.6E-01
ENSMUST00000048269				-1.3	2.7E-01	-1.0	5.3E-01	0.2	8.3E-01	-0.1	9.6E-01
ENSMUST00000048880	metastasis associated in colon cancer 1 [Source:MGI Symbol;Acc:MGI:2685113]	E9PXX8		6.4	7.9E-05	-4.4	1.5E-02	-0.9	1.9E-01	0.0	9.9E-01
ENSMUST00000048289	early growth response 2 [Source:MGI Symbol;Acc:MGI:95296]	Q3U207	P08152	2.2	3.9E-01	2.6	3.4E-01	-1.3	6.3E-01	-1.7	4.5E-01
ENSMUST00000048893	RIKEN cDNA 1700013G24 gene [Source:MGI Symbol;Acc:MGI:1916630]	Q9DAC6		8.2	9.5E-05	6.7	2.4E-03	-0.4	8.2E-01	-1.8	7.6E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000048305	SMEK homolog 1, suppressor of mek1 (Dictyostelium) [Source:MGI Symbol;Acc:MGI:1915984]		Q6P2K6	-2.2	5.2E-02	-4.9	1.5E-02	1.3	1.6E-01	3.9	3.5E-02
ENSMUST00000048896	fibrosin [Source:MGI Symbol;Acc:MGI:104648]		Q8R089	-2.6	4.6E-03	6.9	1.4E-04	-1.2	3.3E-01	0.1	8.1E-01
ENSMUST00000048309	calmodulin regulated spectrin-associated protein family, member 2 [Source:MGI Symbol;Acc:MGI:1922434]	H7BX08		4.2	8.2E-02	-0.1	9.8E-01	-3.0	1.7E-01	1.2	5.9E-01
ENSMUST00000048914	mitochondrial ribosomal protein L34 [Source:MGI Symbol;Acc:MGI:2137227]		Q99N91	-2.9	3.8E-04	-1.2	4.1E-02	0.8	3.0E-02	-0.2	7.1E-01
ENSMUST00000048915	RNA binding motif protein 8a [Source:MGI Symbol;Acc:MGI:1913129]	A0A067XG47	Q9CWZ3	-2.9	1.8E-04	3.2	1.4E-03	0.5	4.3E-01	0.2	7.5E-01
ENSMUST00000048363	cytochrome c oxidase assembly protein 18 [Source:MGI Symbol;Acc:MGI:2448532]		Q8VC74	-2.4	2.5E-01	3.8	1.7E-01	3.6	1.5E-01	-2.7	2.2E-01
ENSMUST00000048923	sprouty-related, EVH1 domain containing 3 [Source:MGI Symbol;Acc:MGI:2142186]			6.2	9.2E-05	4.4	7.6E-03	-0.3	8.3E-01	-0.3	7.5E-01
ENSMUST00000048934	T-box brain gene 1 [Source:MGI Symbol;Acc:MGI:107404]		Q64336	6.6	2.1E-05	-3.6	3.2E-04	-0.1	6.9E-01	-0.3	6.7E-01
ENSMUST00000048937	1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2685(		Q5XJE5	-4.0	5.2E-05	-4.5	9.9E-03	0.2	7.1E-01	0.2	8.9E-01
ENSMUST00000048941	calpain 8 [Source:MGI Symbol;Acc:MGI:2181366]			6.8	1.5E-03	-6.2	6.5E-03	0.9	2.5E-01	1.4	4.8E-01
ENSMUST00000048945	kallikrein 1-related petidase b26 [Source:MGI Symbol;Acc:MGI:891981]		P36369	4.5	4.6E-03	-3.3	1.1E-03	0.5	1.7E-01	0.5	5.1E-01
ENSMUST00000048946	RIKEN cDNA 1110007C09 gene [Source:MGI Symbol;Acc:MGI:1915730]	B2RV71	Q9D1I2	-6.2	6.5E-06	2.2	2.9E-03	0.2	6.8E-01	-0.1	7.6E-01
ENSMUST00000048957	protein tyrosine phosphatase, non-receptor type 13 [Source:MGI Symbol;Acc:MGI:103293]	G5E8B1		6.3	1.7E-06	-3.6	8.7E-03	0.7	2.3E-01	-0.6	6.3E-01
ENSMUST00000048966	transcription factor 20 [Source:MGI Symbol;Acc:MGI:108399]		Q9EPQ8	-3.5	2.3E-02	-5.1	4.4E-02	0.1	9.0E-01	1.9	4.0E-01
ENSMUST00000048967	carboxypeptidase E [Source:MGI Symbol;Acc:MGI:101932]	Q543R4	Q00493	6.6	4.4E-04	5.2	2.9E-02	-0.7	7.5E-01	-0.3	8.4E-01
ENSMUST00000048977	growth regulation by estrogen in breast cancer-like [Source:MGI Symbol;Acc:MGI:3576497]		B9EJV3	6.1	4.8E-05	-2.4	1.0E-01	0.8	3.3E-01	0.1	9.6E-01
ENSMUST00000048982	prickle homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1916034]		Q3U5C7	4.7	7.5E-05	-3.4	1.1E-02	0.7	2.1E-01	-1.9	1.4E-01
ENSMUST00000048988	zinc finger, NFX1-type containing 1 [Source:MGI Symbol;Acc:MGI:2138982]		Q8R151	-3.2	9.1E-03	5.4	2.6E-04	-3.3	2.0E-02	-0.2	7.7E-01
ENSMUST00000048994	r factor of kappa light polypeptide gene enhancer in B cells inhibitor like 1 [Source:MGI Symbol;Acc:MGI:13		O88995	-3.2	8.9E-04	7.9	3.0E-05	0.0	1.0E+00	0.3	5.9E-01
ENSMUST00000048431	nuclear apoptosis inducing factor 1 [Source:MGI Symbol;Acc:MGI:1918504]		Q6PFD7	-0.2	7.9E-01	0.9	2.2E-01	0.9	1.3E-01	-0.2	7.8E-01
ENSMUST00000049005	bone morphogenetic protein receptor, type 1A [Source:MGI Symbol;Acc:MGI:1338938]	Q53Z43	P36895	-2.5	1.5E-03	5.0	4.2E-05	-3.9	1.8E-03	-0.2	6.6E-01
ENSMUST00000049009	RAD9 homolog B [Source:MGI Symbol;Acc:MGI:2385231]	Q8VC54	Q6WBX7	4.7	1.1E-02	6.6	1.1E-04	-0.6	6.1E-01	-0.5	4.2E-01
ENSMUST00000049016	zinc finger protein 532 [Source:MGI Symbol;Acc:MGI:3036282]		Q6NXK2	7.4	3.2E-05	5.5	6.2E-04	-0.2	8.5E-01	0.1	8.7E-01
ENSMUST00000049020	immunity-related GTPase family, Q [Source:MGI Symbol;Acc:MGI:2667176]		Q8VIM9	1.5	9.8E-03	4.5	1.1E-04	0.1	8.6E-01	-0.2	6.4E-01
ENSMUST00000049022	ninjurin 1 [Source:MGI Symbol;Acc:MGI:1196617]	Q3TXT8	O70131	-7.2	4.4E-06	-4.3	2.6E-02	0.9	2.2E-01	-0.6	7.4E-01
ENSMUST00000049027	solute carrier family 26, member 9 [Source:MGI Symbol;Acc:MGI:2444594]			8.0	9.0E-07	5.5	1.2E-03	-0.6	6.3E-01	0.5	5.0E-01
ENSMUST00000049031	family with sequence similarity 63, member B [Source:MGI Symbol;Acc:MGI:2443086]		Q6PDI6	-3.2	6.6E-05	6.2	3.5E-03	-0.7	6.9E-01	-0.6	5.1E-01
ENSMUST00000049032	glucocorticoid modulatory element binding protein 2 [Source:MGI Symbol;Acc:MGI:2652836]		P58929	-2.4	5.9E-03	-0.2	8.5E-01	-5.7	2.6E-03	-0.6	6.1E-01
ENSMUST00000049038	SRY (sex determining region Y)-box 30 [Source:MGI Symbol;Acc:MGI:1341157]		Q8CGW4	7.7	3.9E-05	-3.3	1.1E-02	0.7	1.8E-01	-0.8	5.1E-01
ENSMUST00000049052	RIKEN cDNA 9130019O22 gene [Source:MGI Symbol;Acc:MGI:1926171]	G3X941		2.7	3.7E-04	-1.6	3.6E-01	1.6	1.6E-01	-0.6	7.5E-01
ENSMUST00000049055	LysM, putative peptidoglycan-binding, domain containing 3 [Source:MGI Symbol;Acc:MGI:1915906]		Q99LE3	-2.4	1.9E-03	7.3	1.8E-04	-0.6	6.5E-01	-0.1	8.8E-01
ENSMUST00000048518	PARP1 binding protein [Source:MGI Symbol;Acc:MGI:1922567]			0.0	9.5E-01	0.4	6.0E-01	0.4	5.3E-01	0.0	9.7E-01
ENSMUST00000049057	family with sequence similarity 171, member A2 [Source:MGI Symbol;Acc:MGI:2448496]		A2A699	6.5	2.0E-04	-2.7	9.6E-03	1.0	4.6E-02	-0.3	7.6E-01
ENSMUST00000049064	RAP2B, member of RAS oncogene family [Source:MGI Symbol;Acc:MGI:1921262]	Q6ZWR0	P61226	-1.6	1.2E-02	2.1	6.9E-02	-2.4	4.6E-02	-0.6	5.3E-01
ENSMUST00000049074	protein tyrosine phosphatase, receptor type, F [Source:MGI Symbol;Acc:MGI:102695]		A2A8L5	5.4	4.2E-06	3.3	2.7E-04	0.6	2.2E-01	0.3	4.7E-01
ENSMUST00000049089	twist basic helix-loop-helix transcription factor 1 [Source:MGI Symbol;Acc:MGI:98872]		P26687	6.9	5.1E-05	-3.1	3.6E-02	0.6	4.1E-01	0.4	7.5E-01
ENSMUST00000048560	KN motif and ankyrin repeat domains 3 [Source:MGI Symbol;Acc:MGI:1098615]		Q9Z1P7	1.0	1.1E-01	-0.1	8.9E-01	-0.6	3.5E-01	0.6	4.2E-01
ENSMUST00000049091	cytochrome c oxidase assembly protein 10 [Source:MGI Symbol;Acc:MGI:1917633]	Q3U3N1	Q8CFY5	2.5	1.2E-03	6.2	3.1E-03	-0.1	9.6E-01	0.1	9.5E-01
ENSMUST00000048568	family with sequence similarity 212, member A [Source:MGI Symbol;Acc:MGI:1915426]		Q9CX62	1.7	3.9E-02	0.8	3.5E-01	-1.1	1.4E-01	-0.3	7.0E-01
ENSMUST00000049093	thioredoxin interacting protein [Source:MGI Symbol;Acc:MGI:1889549]		Q8BG60	-8.4	5.6E-04	-2.3	1.3E-02	1.0	4.8E-02	0.5	4.9E-01
ENSMUST00000049124	complement component 1, r subcomponent-like [Source:MGI Symbol;Acc:MGI:2660692]		Q3UZ09	-2.4	7.4E-05	-6.1	2.0E-03	-0.6	3.1E-01	-1.2	4.9E-01
ENSMUST00000049126	delta/notch-like EGF repeat containing [Source:MGI Symbol;Acc:MGI:2152889]		Q8JZM4	6.6	6.7E-05	8.4	2.2E-05	-0.2	8.8E-01	-0.1	8.2E-01
ENSMUST00000048604	Myb/SANT-like DNA-binding domain containing 2 [Source:MGI Symbol;Acc:MGI:2384579]		Q6NZR2	0.1	8.2E-01	0.0	1.0E+00	-0.2	7.5E-01	0.0	9.5E-01
ENSMUST00000049149	low density lipoprotein receptor-related protein 1 [Source:MGI Symbol;Acc:MGI:96828]			-1.1	5.2E-03	6.5	2.5E-04	-0.5	7.0E-01	-0.4	5.6E-01
ENSMUST00000049150	serine/threonine/tyrosine kinase 1 [Source:MGI Symbol;Acc:MGI:2141396]		Q6J9G1	5.1	5.2E-05	-0.7	2.9E-01	1.7	2.8E-03	-1.4	4.7E-02
ENSMUST00000049152	sorting nexin 10 [Source:MGI Symbol;Acc:MGI:1919232]	Q4FJX6	Q9CWT3	-5.9	2.6E-05	3.2	9.5E-04	0.1	9.0E-01	-0.4	3.9E-01
ENSMUST00000049166	blocked early in transport 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1343104]		O35623	-2.4	3.8E-03	-4.1	2.4E-03	0.4	4.5E-01	0.0	1.0E+00
ENSMUST00000049167	PHD finger protein 12 [Source:MGI Symbol;Acc:MGI:1924057]	Q3U2C9	Q5SPL2	-3.8	2.7E-04	6.3	1.5E-04	-0.5	6.1E-01	0.1	8.4E-01
ENSMUST00000049168	component of oligomeric golgi complex 3 [Source:MGI Symbol;Acc:MGI:2450151]	E9QL65		-1.7	8.2E-03	-0.1	7.7E-01	0.5	1.5E-01	-0.6	2.3E-01
ENSMUST00000049169	transcriptional regulator, SIN3A (yeast) [Source:MGI Symbol;Acc:MGI:107157]		Q60520	-6.9	2.5E-03	-6.1	1.4E-02	1.5	1.2E-01	1.7	4.3E-01
ENSMUST00000048655	dual specificity phosphatase 10 [Source:MGI Symbol;Acc:MGI:1927070]		Q9ESS0	1.1	1.1E-01	1.3	1.4E-01	-0.1	8.7E-01	-0.3	7.0E-01
ENSMUST00000048656	ubiquitin associated and SH3 domain containing, A [Source:MGI Symbol;Acc:MGI:1926074]		Q3V3E1	-1.5	7.8E-02	0.9	3.8E-01	2.0	2.7E-02	-0.4	6.6E-01
ENSMUST00000049184	Usher syndrome 1C binding protein 1 [Source:MGI Symbol;Acc:MGI:1922920]		Q8R370	7.5	6.7E-06	-2.0	1.8E-02	0.8	6.7E-02	0.0	9.8E-01
ENSMUST00000048665	chromodomain helicase DNA binding protein 9 [Source:MGI Symbol;Acc:MGI:1924001]		Q8BYH8	2.2	4.7E-01	-2.0	6.8E-01	-1.5	6.4E-01	2.7	5.3E-01
ENSMUST00000049185	ybeY metallopeptidase [Source:MGI Symbol;Acc:MGI:2656825]		Q8CAV0	5.0	1.6E-06	5.6	8.5E-04	0.5	6.4E-01	-0.2	8.3E-01
ENSMUST00000048677	TBC1 domain family, member 22B [Source:MGI Symbol;Acc:MGI:2681867]	Q80VE5		-0.3	6.2E-01	1.3	1.7E-01	1.3	9.1E-02	-0.4	6.6E-01
ENSMUST00000049206	Rho guanine nucleotide exchange factor (GEF) 3 [Source:MGI Symbol;Acc:MGI:1918954]		Q91X46	-5.1	1.8E-06	-1.9	1.7E-01	0.8	2.5E-01	-0.5	7.0E-01
ENSMUST00000049208	hemochromatosis type 2 (juvenile) (human homolog) [Source:MGI Symbol;Acc:MGI:1916835]		Q7TQ32	5.8	5.0E-04	6.6	1.1E-03	2.1	1.4E-01	0.1	8.5E-01
ENSMUST00000049209	group specific component [Source:MGI Symbol;Acc:MGI:95669]		P21614	4.3	1.5E-02	8.1	1.4E-03	0.2	9.2E-01	1.1	2.4E-01
ENSMUST00000049242	leucine rich repeat containing 20 [Source:MGI Symbol;Acc:MGI:2387182]		Q8CI70	1.8	8.6E-03	-3.7	2.2E-02	-1.3	1.4E-01	-2.6	1.2E-01
ENSMUST00000049245	RNA binding motif protein, X-linked like-1 [Source:MGI Symbol;Acc:MGI:1343045]		Q91VM5	-1.8	1.7E-03	-3.2	2.0E-04	0.2	4.7E-01	-0.3	6.2E-01
ENSMUST00000049246	SET domain without mariner transposase fusion [Source:MGI Symbol;Acc:MGI:1921979]		Q80UJ9	-1.8	1.4E-02	7.6	4.4E-05	0.0	9.7E-01	0.4	5.0E-01
ENSMUST00000049251	carboxypeptidase A4 [Source:MGI Symbol;Acc:MGI:1919041]		Q6P8K8	7.7	2.5E-05	-0.8	4.9E-01	1.2	1.5E-01	-3.6	3.0E-02
ENSMUST00000049257	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52 [Source:MGI Symbol;Acc:MGI:1925644]		Q8K301	-3.6	2.3E-04	-3.0	2.5E-03	1.1	1.9E-02	0.1	9.0E-01
ENSMUST00000049260	GRB2 associated, regulator of MAPK1 [Source:MGI Symbol;Acc:MGI:2685790]		Q3UFT3	6.1	7.1E-06	-6.2	4.4E-04	0.0	9.3E-01	-0.2	8.7E-01
ENSMUST00000049262	signal-regulatory protein alpha [Source:MGI Symbol;Acc:MGI:108563]	E0CYM8		-6.7	1.5E-03	6.8	2.2E-04	0.5	7.0E-01	-0.8	2.3E-01
ENSMUST00000048716	FYVE, RhoGEF and PH domain containing 3 [Source:MGI Symbol;Acc:MGI:1353657]	Q3TNB8		1.8	6.3E-02	4.7	5.0E-03	2.1	9.4E-02	-0.8	3.6E-01
ENSMUST00000048718	methylmalonic aciduria (cobalamin deficiency) type A [Source:MGI Symbol;Acc:MGI:1923805]		Q8C7H1	0.5	2.6E-01	0.3	6.2E-01	-0.5	2.4E-01	-0.3	6.3E-01
ENSMUST00000049263	SAFB-like, transcription modulator [Source:MGI Symbol;Acc:MGI:1913910]	B9EI57	Q8CH25	-2.8	3.2E-03	2.1	6.5E-03	-2.6	1.5E-03	-0.1	7.7E-01
ENSMUST00000049271	RIKEN cDNA 4930427A07 gene [Source:MGI Symbol;Acc:MGI:2144738]		Q3UK37	4.6	4.4E-04	2.4	1.3E-01	-0.6	6.2E-01	5.0	1.2E-03
ENSMUST00000049285	leucine rich repeat protein 1, neuronal [Source:MGI Symbol;Acc:MGI:106038]		Q61809	8.2	9.9E-06	6.9	1.3E-02	-0.9	7.3E-01	-1.2	3.8E-01
ENSMUST00000049289	UDP glucuronosyltransferase 1 family, polypeptide A2 [Source:MGI Symbol;Acc:MGI:3576049]		P70691	4.9	7.4E-03	-4.6	7.7E-05	0.5	1.4E-01	-0.9	2.5E-01
ENSMUST00000048781	phosphoenolpyruvate carboxykinase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1860456]			1.0	1.4E-01	0.7	4.3E-01	0.3	6.7E-01	0.6	4.7E-01
ENSMUST00000049294	small nuclear ribonucleoprotein D2 [Source:MGI Symbol;Acc:MGI:98345]	Q14AF6	P62317	-3.2	3.0E-03	-5.1	3.9E-04	0.3	5.0E-01	0.4	6.9E-01
ENSMUST00000049295	EH domain binding protein 1-like 1 [Source:MGI Symbol;Acc:MGI:3612340]	E9QP49		-3.0	2.5E-04	3.2	9.1E-02	0.5	7.5E-01	0.8	5.3E-01
ENSMUST00000048788	cDNA sequence BC027231 [Source:MGI Symbol;Acc:MGI:2384836]	Q8R2U2		1.0	1.2E-01	1.9	3.5E-02	0.3	6.2E-01	-0.5	4.2E-01
ENSMUST00000049298	tryptophan hydroxylase 1 [Source:MGI Symbol;Acc:MGI:98796]	Q3UK52	P17532	6.9	8.8E-05	7.1	2.4E-05	-0.6	5.4E-01	0.5	3.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000049305	espin [Source:MGI Symbol;Acc:MGI:1861630]	Q9DD12		5.9	9.5E-04	-5.6	1.5E-03	0.0	9.6E-01	-1.6	3.3E-01
ENSMUST00000049308	inositol 1,4,5-triphosphate receptor 3 [Source:MGI Symbol;Acc:MGI:96624]		P70227	1.4	7.0E-03	1.4	1.3E-01	-3.8	3.5E-03	0.3	7.2E-01
ENSMUST00000049312	transmembrane protein 55b [Source:MGI Symbol;Acc:MGI:2448501]	F8WHW3		-6.7	3.2E-04	-0.8	2.3E-01	0.4	3.3E-01	-1.4	6.2E-02
ENSMUST00000049324	FMS-like tyrosine kinase 3 [Source:MGI Symbol;Acc:MGI:95559]	Q3UEW6		-3.9	1.3E-02	-1.9	2.2E-02	0.1	8.4E-01	-1.2	1.2E-01
ENSMUST00000049339	nodal [Source:MGI Symbol;Acc:MGI:97359]		P43021	6.1	2.5E-04	5.7	3.0E-04	0.1	9.0E-01	0.4	5.7E-01
ENSMUST00000048860	melanoregulin [Source:MGI Symbol;Acc:MGI:2151839]		Q6NVG5	0.2	6.6E-01	2.0	2.0E-02	1.8	1.1E-02	0.0	9.5E-01
ENSMUST00000049344	chondroitin sulfate N-acetylgalactosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI:1926002]		Q8C1F4	-8.4	3.4E-06	4.8	5.0E-04	-1.6	1.3E-01	-0.1	9.1E-01
ENSMUST00000048892	isoprenylcysteine carboxyl methyltransferase [Source:MGI Symbol;Acc:MGI:1888594]	Q3U4N2		-2.6	8.7E-02	-2.9	1.4E-01	0.3	7.9E-01	0.5	7.9E-01
ENSMUST00000049346	acid-sensing (proton-gated) ion channel 3 [Source:MGI Symbol;Acc:MGI:2159339]		Q6X1Y6	6.1	3.1E-05	7.1	5.9E-04	-0.7	6.2E-01	0.4	5.8E-01
ENSMUST00000049352	homeobox B7 [Source:MGI Symbol;Acc:MGI:96188]		P09024	7.0	2.5E-04	-2.0	6.6E-02	1.0	1.2E-01	0.4	7.0E-01
ENSMUST00000049355	mitogen-activated protein kinase 6 [Source:MGI Symbol;Acc:MGI:1354946]		Q61532	-7.7	1.4E-04	-0.9	1.7E-01	0.7	1.3E-01	-1.2	7.4E-02
ENSMUST00000049357	proline-rich nuclear receptor coactivator 1 [Source:MGI Symbol;Acc:MGI:1917838]	Q3TWH3		-6.2	1.5E-04	-3.4	3.3E-04	-0.9	2.4E-02	-0.4	5.1E-01
ENSMUST00000049369	oligonucleotide/oligosaccharide-binding fold containing 1 [Source:MGI Symbol;Acc:MGI:1915581]		Q8K2X3	-1.9	8.6E-03	3.4	7.6E-03	-2.2	5.1E-02	0.6	4.5E-01
ENSMUST00000049378	actin binding LIM protein family, member 3 [Source:MGI Symbol;Acc:MGI:2442582]		Q69ZX8	7.0	5.1E-05	7.1	4.2E-05	0.1	9.1E-01	-0.4	4.9E-01
ENSMUST00000048935	doublesex and mab-3 related transcription factor 3 [Source:MGI Symbol;Acc:MGI:2449470]		Q80WT2	0.6	1.8E-01	1.6	2.2E-02	0.7	1.3E-01	-0.2	7.0E-01
ENSMUST00000049382	GATA zinc finger domain containing 2B [Source:MGI Symbol;Acc:MGI:2443225]		Q8VHR5	-1.6	9.3E-03	-2.5	4.9E-03	0.5	2.1E-01	-1.0	1.8E-01
ENSMUST00000049385	eukaryotic translation initiation factor 1 [Source:MGI Symbol;Acc:MGI:105125]	Q4V9T8	P48024	-5.1	7.5E-06	4.3	3.8E-02	-0.6	7.2E-01	1.9	1.5E-01
ENSMUST00000049389	zinc finger, DHHC domain containing 2 [Source:MGI Symbol;Acc:MGI:1923452]		P59267	2.4	3.6E-03	5.8	1.6E-03	-0.4	7.6E-01	-1.8	4.9E-02
ENSMUST00000049393	zinc finger protein 113 [Source:MGI Symbol;Acc:MGI:1929116]	Q8C689		5.2	4.0E-06	-4.7	2.4E-04	0.3	4.2E-01	-1.2	2.0E-01
ENSMUST00000049400	KN motif and ankyrin repeat domains 1 [Source:MGI Symbol;Acc:MGI:2147707]	E9Q238		7.8	2.8E-05	5.2	1.3E-05	-1.6	2.3E-02	-0.5	2.2E-01
ENSMUST00000048962	kinesin family member 4 [Source:MGI Symbol;Acc:MGI:108389]		P33174	-0.2	5.8E-01	-0.3	5.9E-01	0.1	8.8E-01	0.1	8.2E-01
ENSMUST00000048964	CDKN1A interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1920234]	Q8VEH2		3.2	5.2E-02	0.5	8.1E-01	-0.8	6.2E-01	1.9	3.6E-01
ENSMUST00000049411	apurinic/apyrimidinic endonuclease 1 [Source:MGI Symbol;Acc:MGI:88042]	Q544Z7	P28352	-3.3	1.6E-02	-2.8	1.1E-01	0.6	5.1E-01	-0.1	9.4E-01
ENSMUST00000049435	RAB9, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1890695]	A2AFP5		2.2	1.2E-02	-0.1	8.7E-01	-7.5	1.0E-04	-0.7	3.5E-01
ENSMUST00000049452	transmembrane protein 108 [Source:MGI Symbol;Acc:MGI:1932411]		Q8BHE4	5.4	1.8E-04	6.1	1.4E-04	-0.8	4.2E-01	-0.9	1.8E-01
ENSMUST00000049453	ubiquitin protein ligase E3C [Source:MGI Symbol;Acc:MGI:2140998]		Q80U95	-1.5	2.3E-03	-2.0	1.3E-01	-1.7	3.9E-02	5.0	1.5E-03
ENSMUST00000049454	sine oculis-related homeobox 5 [Source:MGI Symbol;Acc:MGI:106220]		P70178	6.0	9.1E-06	-1.1	3.7E-01	0.9	2.6E-01	-1.2	3.1E-01
ENSMUST00000048993	polymerase (RNA) III (DNA directed) polypeptide G [Source:MGI Symbol;Acc:MGI:1914736]		Q6NXY9	-1.5	3.3E-01	2.9	1.3E-01	1.6	3.4E-01	-2.8	8.3E-02
ENSMUST00000049457	melanocortin 2 receptor accessory protein 2 [Source:MGI Symbol;Acc:MGI:3609239]		D3Z1Q2	6.4	3.4E-04	-2.0	3.9E-02	1.1	4.3E-02	-0.1	9.5E-01
ENSMUST00000049004	alanyl (membrane) aminopeptidase [Source:MGI Symbol;Acc:MGI:5000466]		P97449	3.7	4.7E-02	1.1	5.2E-01	-3.4	5.3E-02	-0.8	5.9E-01
ENSMUST00000049460	granulin [Source:MGI Symbol;Acc:MGI:95832]	Q3U9N4		-10.7	5.8E-05	-1.6	4.7E-02	0.9	7.8E-02	0.0	9.8E-01
ENSMUST00000049469	exocyst complex component 1 [Source:MGI Symbol;Acc:MGI:2445020]	Q5PPR2		-7.6	1.6E-04	5.4	8.8E-03	-0.2	9.2E-01	-0.9	4.8E-01
ENSMUST00000049470	transmembrane protein 183A [Source:MGI Symbol;Acc:MGI:1914729]		Q9JJB9	-2.8	1.9E-03	3.1	1.5E-03	-4.7	7.2E-04	-0.4	4.5E-01
ENSMUST00000049476	RIKEN cDNA C130079G13 gene [Source:MGI Symbol;Acc:MGI:3028051]	Q8BUY2		4.7	1.6E-04	2.4	4.8E-03	1.2	5.3E-02	0.3	5.5E-01
ENSMUST00000049483	formin-like 2 [Source:MGI Symbol;Acc:MGI:1918659]	F8VPR2		6.1	1.1E-02	-8.3	1.3E-05	-1.0	8.3E-03	0.2	8.6E-01
ENSMUST00000049488	serine incorporator 5 [Source:MGI Symbol;Acc:MGI:2444223]		Q8BHJ6	-1.6	1.2E-02	7.2	1.0E-05	-0.6	4.9E-01	0.2	7.1E-01
ENSMUST00000049501	oral-facial-digital syndrome 1 gene homolog (human) [Source:MGI Symbol;Acc:MGI:1350328]	A2AEG2		-1.9	3.2E-02	-2.2	5.4E-03	0.9	2.4E-02	-0.1	8.3E-01
ENSMUST00000049506	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1 [Source:MGI Symbol;Acc:MGI:98885	Q793C9	Q64707	-1.7	1.8E-02	-1.1	2.5E-01	1.2	7.2E-02	-0.2	8.4E-01
ENSMUST00000049507	proprotein convertase subtilisin/kexin type 9 [Source:MGI Symbol;Acc:MGI:2140260]		Q80W65	6.8	3.5E-05	7.3	1.1E-04	-0.6	6.2E-01	-0.2	7.0E-01
ENSMUST00000049040	Bri3 binding protein [Source:MGI Symbol;Acc:MGI:1924059]		Q8BXV2	0.6	1.9E-01	1.4	3.6E-02	0.9	8.4E-02	0.1	9.0E-01
ENSMUST00000049509	vesicle amine transport protein 1 homolog-like (T. californica) [Source:MGI Symbol;Acc:MGI:2142534]		Q80TB8	6.0	2.7E-04	4.2	8.3E-05	1.1	8.0E-02	-0.4	3.8E-01
ENSMUST00000049053	family with sequence similarity 168, member A [Source:MGI Symbol;Acc:MGI:2442372]	Q68FE1	Q8BGZ2	-3.1	4.8E-02	-1.7	4.1E-01	1.6	2.2E-01	0.2	9.4E-01
ENSMUST00000049519	immunity-related GTPase family M member 1 [Source:MGI Symbol;Acc:MGI:107567]		Q60766	-3.0	1.9E-02	-3.8	8.3E-04	-0.2	6.8E-01	1.2	1.7E-01
ENSMUST00000049527	protein kinase, cAMP dependent regulatory, type I, alpha [Source:MGI Symbol;Acc:MGI:104878]		Q9DBC7	-10.1	2.2E-06	4.8	1.7E-03	-1.5	2.2E-01	0.2	8.1E-01
ENSMUST00000049060	centrosomal protein 135 [Source:MGI Symbol;Acc:MGI:2681869]		Q6P5D4	-2.3	5.2E-02	-4.2	3.9E-02	-0.4	6.1E-01	1.5	4.2E-01
ENSMUST00000049530	alpha 1,4-galactosyltransferase [Source:MGI Symbol;Acc:MGI:3512453]	Q3UF00	Q67BJ4	6.5	2.6E-02	-0.7	3.2E-01	0.9	9.1E-02	-0.1	9.4E-01
ENSMUST00000049531	monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Source:MGI Symbol;Acc:M	A3KML3	P68254	-3.3	3.0E-04	4.4	2.9E-05	-1.4	3.1E-02	-0.4	2.9E-01
ENSMUST00000049537	phosphatidylinositol binding clathrin assembly protein [Source:MGI Symbol;Acc:MGI:2385902]		Q7M6Y3	-7.7	3.1E-06	0.9	2.2E-01	-5.9	1.3E-04	0.2	7.4E-01
ENSMUST00000049544	coiled-coil domain containing 141 [Source:MGI Symbol;Acc:MGI:1919735]	A2AST1		8.9	4.6E-05	2.5	3.8E-03	-0.2	7.6E-01	-0.2	6.9E-01
ENSMUST00000049545	adrenergic receptor, alpha 2c [Source:MGI Symbol;Acc:MGI:87936]		Q01337	6.8	3.9E-04	-9.1	3.3E-03	0.4	6.6E-01	1.0	6.9E-01
ENSMUST00000049113	protein tyrosine phosphatase, receptor type, H [Source:MGI Symbol;Acc:MGI:3026877]	E9Q0N2		4.7	6.5E-02	6.6	3.0E-02	0.4	8.8E-01	-1.5	3.6E-01
ENSMUST00000049122	periphilin 1 [Source:MGI Symbol;Acc:MGI:1917029]	G3X959		-1.2	3.6E-01	-0.5	7.4E-01	-0.8	4.6E-01	-1.5	3.3E-01
ENSMUST00000049567	kelch-like ECH-associated protein 1 [Source:MGI Symbol;Acc:MGI:1858732]		Q9Z2X8	-3.1	2.5E-02	-1.5	7.9E-03	0.7	3.8E-02	-0.2	6.1E-01
ENSMUST00000049572	lysosomal acid lipase A [Source:MGI Symbol;Acc:MGI:96789]		Q9Z0M5	-3.3	1.3E-03	6.0	1.9E-04	-1.3	2.6E-01	-0.7	2.6E-01
ENSMUST00000049128	SUMO1/sentrin specific peptidase 7 [Source:MGI Symbol;Acc:MGI:1913565]	Q9CQN9		-1.7	1.2E-01	-1.5	2.1E-01	-0.8	3.2E-01	-1.1	3.7E-01
ENSMUST00000049138	RIKEN cDNA 2410131K14 gene [Source:MGI Symbol;Acc:MGI:1924042]		Q8BTG6	1.4	3.6E-02	1.3	1.3E-01	0.7	3.0E-01	0.8	2.8E-01
ENSMUST00000049575	clathrin, light polypeptide (Lcb) [Source:MGI Symbol;Acc:MGI:1921575]		Q6IRU5	-3.4	1.8E-02	-0.6	1.9E-01	0.5	1.1E-01	-0.1	8.3E-01
ENSMUST00000049583	zinc finger and BTB domain containing 40 [Source:MGI Symbol;Acc:MGI:2682254]	Q6PCS8		2.5	5.5E-03	5.5	3.8E-04	0.6	5.1E-01	0.2	7.7E-01
ENSMUST00000049151	pseudouridylate synthase 7 homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:1926145]		Q8CE46	0.8	1.3E-01	1.4	4.9E-02	0.2	6.4E-01	-0.4	5.0E-01
ENSMUST00000049614	RIKEN cDNA B430306N03 gene [Source:MGI Symbol;Acc:MGI:2443478]	Q6QX36		-2.9	1.1E-03	-6.2	1.5E-04	-0.3	4.2E-01	0.0	9.7E-01
ENSMUST00000049156	TBC/LysM associated domain containing 1 [Source:MGI Symbol;Acc:MGI:1921597]		Q8K0P3	0.0	9.7E-01	1.1	2.7E-01	1.3	7.6E-02	0.3	7.2E-01
ENSMUST00000049618	GTPase activating RANGAP domain-like 3 [Source:MGI Symbol;Acc:MGI:2139309]	A2AHW8		6.7	6.7E-05	-2.1	2.3E-02	-0.2	7.2E-01	-0.5	5.0E-01
ENSMUST00000049621	hairy and enhancer of split 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:104876]	Q499J8	P70120	7.6	1.0E-04	-1.4	1.1E-01	1.0	5.8E-02	-1.4	1.1E-01
ENSMUST00000049625	zinc finger protein 879 [Source:MGI Symbol;Acc:MGI:3053099]		Q8BI99	6.1	2.6E-02	-1.6	4.5E-02	0.5	2.7E-01	0.4	5.9E-01
ENSMUST00000049628	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit E [Source:MGI Symbol;Acc:MGI:10663(		Q06185	-6.8	7.9E-05	-7.0	3.4E-02	0.5	5.9E-01	0.6	8.4E-01
ENSMUST00000049655	transmembrane protein 215 [Source:MGI Symbol;Acc:MGI:2444167]	B7ZN35	A7E1Z1	7.0	2.3E-04	7.3	2.9E-05	-0.4	6.6E-01	-0.2	7.1E-01
ENSMUST00000049658	phosphatidylinositol transfer protein, membrane-associated 1 [Source:MGI Symbol;Acc:MGI:1197524]		O35954	-6.7	1.0E-03	6.3	2.3E-06	0.7	2.1E-01	-0.5	1.5E-01
ENSMUST00000049676	transient receptor potential cation channel, subfamily V, member 3 [Source:MGI Symbol;Acc:MGI:2181407]		Q8K424	9.6	8.5E-06	-4.3	3.8E-05	0.2	4.7E-01	-0.5	3.8E-01
ENSMUST00000049680	zinc finger protein 710 [Source:MGI Symbol;Acc:MGI:1921747]		Q3U288	-4.4	7.8E-03	5.5	9.9E-04	-1.2	3.6E-01	-0.8	2.6E-01
ENSMUST00000049681	integrin, beta-like 1 [Source:MGI Symbol;Acc:MGI:2443439]		Q8VDV0	4.5	1.0E-02	-1.6	3.0E-01	-5.2	5.4E-03	0.6	6.3E-01
ENSMUST00000049239	mitogen-activated protein kinase kinase kinase kinase 5 [Source:MGI Symbol;Acc:MGI:1925503]	E9PX30		2.3	3.2E-01	0.5	8.7E-01	-1.7	4.6E-01	0.1	9.8E-01
ENSMUST00000049241	homeobox B4 [Source:MGI Symbol;Acc:MGI:96185]		P10284	0.1	8.5E-01	2.6	1.8E-02	1.8	3.7E-02	-0.6	4.0E-01
ENSMUST00000049697	claudin 8 [Source:MGI Symbol;Acc:MGI:1859286]	Q3UZK2	Q9Z260	6.6	1.0E-04	3.6	9.0E-04	1.4	5.3E-02	-0.4	4.5E-01
ENSMUST00000049705	zinc finger protein 457 [Source:MGI Symbol;Acc:MGI:2664334]	L7N1X4		7.7	5.1E-05	-2.4	1.8E-03	-0.5	1.5E-01	0.1	9.1E-01
ENSMUST00000049706	Fc receptor, IgE, high affinity I, alpha polypeptide [Source:MGI Symbol;Acc:MGI:95494]		P20489	-3.8	5.8E-03	-1.1	1.5E-01	-0.2	7.1E-01	-0.9	2.3E-01
ENSMUST00000049248	MALT1 paracaspase [Source:MGI Symbol;Acc:MGI:2445027]		Q2TBA3	-1.3	4.5E-02	-0.2	8.0E-01	0.7	1.8E-01	-0.4	5.8E-01
ENSMUST00000049724	olfactory receptor 1443 [Source:MGI Symbol;Acc:MGI:3031277]	Q8VFW8		8.7	1.4E-05	7.3	7.3E-05	-0.6	6.3E-01	-0.2	6.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000049255	armadillo repeat containing 3 [Source:MGI Symbol;Acc:MGI:1918132]	A2AU71		-2.0	2.1E-01	-4.1	6.8E-02	-1.0	4.1E-01	1.0	6.1E-01
ENSMUST00000049729	olfactory receptor 735 [Source:MGI Symbol;Acc:MGI:3030569]	Q7TRM4		6.5	5.1E-04	-3.9	8.2E-04	-0.1	7.3E-01	0.2	8.3E-01
ENSMUST00000049732	small integral membrane protein 4 [Source:MGI Symbol;Acc:MGI:1913737]		Q8C1Q6	-6.4	2.9E-04	6.8	3.3E-05	0.6	4.6E-01	0.0	9.8E-01
ENSMUST00000049740	zinc finger and BTB domain containing 33 [Source:MGI Symbol;Acc:MGI:1927290]	A2A3Z3	Q8BN78	-3.2	1.7E-03	-7.4	9.2E-03	0.6	4.5E-01	1.3	5.8E-01
ENSMUST00000049743	olfactory receptor 462 [Source:MGI Symbol;Acc:MGI:3030296]	Q5SW50		6.4	9.7E-05	-4.3	1.8E-03	-0.7	2.1E-01	0.8	4.2E-01
ENSMUST00000049744	M-phase specific PLK1 intereacting protein [Source:MGI Symbol;Acc:MGI:1913558]	B2RTG9	Q9D011	3.4	2.8E-04	4.8	3.1E-03	1.0	3.5E-01	0.9	3.0E-01
ENSMUST00000049272	homeobox B5 [Source:MGI Symbol;Acc:MGI:96186]		P09079	3.5	7.1E-02	4.5	3.9E-02	-0.5	8.0E-01	-1.5	2.9E-01
ENSMUST00000049281	family with sequence similarity 53, member C [Source:MGI Symbol;Acc:MGI:1913556]		Q8BXQ8	4.2	8.7E-02	4.5	1.1E-01	-0.9	7.2E-01	-1.2	5.2E-01
ENSMUST00000049778	zinc finger protein 11 [Source:MGI Symbol;Acc:MGI:99156]		P10751	4.3	5.7E-06	7.1	6.6E-05	-0.6	6.1E-01	0.5	3.3E-01
ENSMUST00000049784	myelin transcription factor 1-like [Source:MGI Symbol;Acc:MGI:1100511]	D3Z1P7		8.4	2.4E-05	3.1	1.3E-01	-1.1	5.5E-01	0.7	5.9E-01
ENSMUST00000049787	leucine rich repeat neuronal 4 [Source:MGI Symbol;Acc:MGI:2445154]		P59383	5.9	5.1E-06	-3.6	5.7E-03	-0.8	1.6E-01	-0.4	6.7E-01
ENSMUST00000049788	potassium channel, subfamily K, member 13 [Source:MGI Symbol;Acc:MGI:2384976]	Q3TYG8	Q8R1P5	6.2	2.6E-02	-1.6	3.1E-02	1.0	3.7E-02	-0.4	5.2E-01
ENSMUST00000049793	double homeobox B-like 1 [Source:MGI Symbol;Acc:MGI:1916048]	Q7TNE6		7.9	3.3E-05	7.2	1.2E-04	-0.6	6.0E-01	-0.9	1.9E-01
ENSMUST00000049810	chemokine (C-X-C motif) receptor 6 [Source:MGI Symbol;Acc:MGI:1934582]		Q9EQ16	2.9	1.1E-02	5.2	2.2E-03	-1.6	2.5E-01	-1.0	2.5E-01
ENSMUST00000049811	centrosomal protein 120 [Source:MGI Symbol;Acc:MGI:2147298]		Q7TSG1	-2.2	8.6E-04	1.8	9.0E-03	0.4	3.5E-01	0.0	9.3E-01
ENSMUST00000049813	YOD1 OTU deubiquitinating enzyme 1 homologue (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2442596]		Q8CB27	2.0	2.9E-03	-5.6	5.8E-03	0.7	2.5E-01	-0.4	8.4E-01
ENSMUST00000049323	WD repeat domain 55 [Source:MGI Symbol;Acc:MGI:1915186]		Q9CX97	-0.9	8.8E-02	-1.6	3.6E-02	0.0	9.6E-01	0.6	3.5E-01
ENSMUST00000049845	plexin A1 [Source:MGI Symbol;Acc:MGI:107685]		P70206	8.0	5.3E-04	-2.9	1.1E-01	0.4	6.1E-01	-0.6	7.2E-01
ENSMUST00000049863	protein O-fucosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2153207]		Q91ZW2	1.1	3.4E-02	5.5	1.8E-03	0.4	7.6E-01	1.0	2.0E-01
ENSMUST00000049343	polymerase (DNA directed), delta 1, catalytic subunit [Source:MGI Symbol;Acc:MGI:97741]		P52431	-2.0	1.6E-01	-0.9	6.3E-01	1.0	4.4E-01	-0.2	9.3E-01
ENSMUST00000049887	nucleoporin like 2 [Source:MGI Symbol;Acc:MGI:2387631]	E9QL43		1.8	1.0E-02	-8.4	3.4E-05	-0.1	8.6E-01	0.0	1.0E+00
ENSMUST00000049896	G patch domain and KOW motifs [Source:MGI Symbol;Acc:MGI:1859610]		Q56A08	-3.1	3.1E-05	6.3	2.4E-04	0.1	8.9E-01	0.0	9.9E-01
ENSMUST00000049348	TRAF-interacting protein [Source:MGI Symbol;Acc:MGI:1096377]		Q8VIG6	0.6	3.6E-01	0.9	3.0E-01	0.0	9.4E-01	-0.3	6.9E-01
ENSMUST00000049908	single stranded DNA binding protein 4 [Source:MGI Symbol;Acc:MGI:1924150]	Q3U4B1		-3.2	2.9E-04	5.7	1.9E-03	-0.6	6.8E-01	0.8	3.4E-01
ENSMUST00000049353	zinc finger protein 692 [Source:MGI Symbol;Acc:MGI:2144276]		Q3U381	0.4	8.0E-01	-1.8	5.2E-01	0.8	7.0E-01	3.0	1.9E-01
ENSMUST00000049911	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]		P63280	-4.9	2.0E-05	-8.2	4.2E-03	1.0	1.1E-01	1.5	5.0E-01
ENSMUST00000049930	transcription factor 21 [Source:MGI Symbol;Acc:MGI:1202715]		O35437	5.0	3.8E-04	-4.4	5.7E-03	1.3	5.7E-02	-0.6	6.7E-01
ENSMUST00000049931	sialophorin [Source:MGI Symbol;Acc:MGI:98384]	Q544C5	P15702	-2.2	8.7E-04	-1.2	1.2E-01	0.3	5.0E-01	-0.3	6.3E-01
ENSMUST00000049937	chromatin target of PRMT1 [Source:MGI Symbol;Acc:MGI:1913761]		Q9CY57	-3.9	3.8E-03	7.9	3.7E-05	-0.5	6.9E-01	-1.3	3.3E-02
ENSMUST00000049948	asparaginase like 1 [Source:MGI Symbol;Acc:MGI:1913764]		Q8C0M9	4.9	3.4E-04	-0.3	6.1E-01	0.7	1.1E-01	-0.5	4.3E-01
ENSMUST00000049956	leucine rich repeat containing 24 [Source:MGI Symbol;Acc:MGI:3605040]		Q8BHA1	7.7	1.9E-04	-4.6	2.5E-04	1.1	1.2E-02	0.5	5.0E-01
ENSMUST00000049388	COMM domain containing 10 [Source:MGI Symbol;Acc:MGI:1916706]	Q3TKN7	Q8JZY2	-0.6	2.1E-01	-0.4	5.3E-01	-0.2	6.2E-01	-0.4	4.4E-01
ENSMUST00000049968	outer dense fiber of sperm tails 3B [Source:MGI Symbol;Acc:MGI:1917363]		Q5M8M2	6.0	1.1E-04	1.1	1.6E-01	-0.5	4.1E-01	0.7	2.7E-01
ENSMUST00000049972	secretogranin II [Source:MGI Symbol;Acc:MGI:103033]		Q03517	7.4	3.1E-05	4.8	3.6E-05	0.0	9.4E-01	0.4	3.5E-01
ENSMUST00000049985	HEPACAM family member 2 [Source:MGI Symbol;Acc:MGI:2141520]		Q4VAH7	5.7	4.5E-04	3.4	9.1E-04	-4.8	8.7E-04	-0.4	4.9E-01
ENSMUST00000049404	CLIP associating protein 1 [Source:MGI Symbol;Acc:MGI:1923957]	E9QKH0		1.4	4.6E-01	5.3	2.0E-02	0.5	8.0E-01	-3.5	6.8E-02
ENSMUST00000049994	ribosomal modification protein rimK-like family member A [Source:MGI Symbol;Acc:MGI:3040686]		Q6PFX8	6.1	1.5E-05	-3.0	1.7E-02	-1.9	2.1E-02	-2.2	1.1E-01
ENSMUST00000049412	staufen (RNA binding protein) homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1338864]	A2A5R8		-3.5	3.1E-01	-2.8	5.1E-01	-0.1	9.5E-01	-0.9	8.5E-01
ENSMUST00000049424	WD repeat domain 74 [Source:MGI Symbol;Acc:MGI:2147427]		Q8VCG3	-0.1	8.1E-01	-0.7	3.5E-01	-0.1	8.4E-01	0.4	5.2E-01
ENSMUST00000050000	syntaxin binding protein 1 [Source:MGI Symbol;Acc:MGI:107363]		O08599	6.7	3.6E-04	1.4	1.4E-01	-0.2	7.7E-01	0.5	5.2E-01
ENSMUST00000049449	protein tyrosine phosphatase, non-receptor type 7 [Source:MGI Symbol;Acc:MGI:2156893]		Q8BUM3	0.2	6.8E-01	1.6	6.9E-02	1.5	3.4E-02	0.2	8.1E-01
ENSMUST00000050003	RIKEN cDNA 1700001O22 gene [Source:MGI Symbol;Acc:MGI:1923631]	A2APZ1		5.4	1.1E-02	6.1	2.7E-04	0.5	6.5E-01	-0.3	6.6E-01
ENSMUST00000050004	ring finger protein 125 [Source:MGI Symbol;Acc:MGI:1914914]		Q9D9R0	-1.7	1.2E-02	-1.0	6.6E-02	0.5	1.4E-01	-0.1	9.1E-01
ENSMUST00000050011	guanylate binding protein 6 [Source:MGI Symbol;Acc:MGI:2140937]	L7N1X8		2.0	9.7E-03	6.1	4.6E-05	-0.1	9.2E-01	-0.2	7.1E-01
ENSMUST00000050020	adhesion molecule, interacts with CXADR antigen 1 [Source:MGI Symbol;Acc:MGI:2685484]		Q80UL9	-5.3	2.0E-04	5.1	4.4E-03	-0.1	9.5E-01	1.2	2.2E-01
ENSMUST00000050026	cDNA sequence BC051628 [Source:MGI Symbol;Acc:MGI:3051572]		Q80WB0	6.0	7.6E-03	-6.7	5.5E-04	1.3	3.7E-02	-2.8	1.3E-01
ENSMUST00000049461	cysteinyl-tRNA synthetase 2 (mitochondrial)(putative) [Source:MGI Symbol;Acc:MGI:1919191]	G3X975		-1.0	1.3E-01	0.2	7.7E-01	0.4	4.9E-01	-0.8	2.7E-01
ENSMUST00000050027	nephroblastoma overexpressed gene [Source:MGI Symbol;Acc:MGI:109185]		Q64299	6.5	1.4E-04	-6.8	3.5E-03	0.8	2.0E-01	-0.1	9.6E-01
ENSMUST00000050029	sine oculis-related homeobox 1 [Source:MGI Symbol;Acc:MGI:102780]	Q3V2C3	Q62231	7.1	3.7E-05	-1.2	1.5E-01	0.7	1.9E-01	-0.9	2.9E-01
ENSMUST00000049474	F-box and WD-40 domain protein 8 [Source:MGI Symbol;Acc:MGI:1923041]		Q8BIA4	-0.6	2.4E-01	0.2	7.3E-01	0.7	1.7E-01	-0.2	8.0E-01
ENSMUST00000050034	protocadherin beta 15 [Source:MGI Symbol;Acc:MGI:2136750]	Q91Y04		7.8	2.1E-05	4.5	1.2E-03	-0.3	7.3E-01	-0.1	8.8E-01
ENSMUST00000050047	RIKEN cDNA D630023F18 gene [Source:MGI Symbol;Acc:MGI:2138198]		Q8C3M9	8.8	1.7E-04	6.8	9.2E-03	-0.8	7.2E-01	-1.5	2.4E-01
ENSMUST00000049484	glucoside xylosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2684933]		Q3UHH8	0.3	5.3E-01	0.3	6.3E-01	0.6	2.7E-01	0.6	3.7E-01
ENSMUST00000050063	ADP-ribosylation factor 6 [Source:MGI Symbol;Acc:MGI:99435]	Q3U0D7	P62331	-3.9	1.8E-04	-1.2	1.2E-01	0.6	2.0E-01	0.2	8.1E-01
ENSMUST00000050067	HECT domain containing 3 [Source:MGI Symbol;Acc:MGI:1923858]		Q3U487	-2.7	3.8E-04	-2.0	8.2E-02	0.5	4.4E-01	0.7	5.3E-01
ENSMUST00000049503	echinoderm microtubule associated protein like 4 [Source:MGI Symbol;Acc:MGI:1926048]			3.6	1.2E-01	-2.0	3.7E-01	-4.7	2.9E-02	0.9	6.7E-01
ENSMUST00000050083	cullin 4B [Source:MGI Symbol;Acc:MGI:1919834]		A2A432	-6.0	2.0E-04	-2.0	2.4E-02	-0.7	1.9E-01	-0.4	6.5E-01
ENSMUST00000050092	zinc finger protein 518A [Source:MGI Symbol;Acc:MGI:1919922]		B2RRF6	-2.7	3.2E-04	7.2	1.2E-04	0.2	8.7E-01	-0.3	6.3E-01
ENSMUST00000050096	adducin 3 (gamma) [Source:MGI Symbol;Acc:MGI:1351615]	Q3UNK1	Q9QYB5	-7.1	5.7E-04	5.4	7.0E-04	-1.2	3.2E-01	-0.6	3.8E-01
ENSMUST00000050103	neurogenin 3 [Source:MGI Symbol;Acc:MGI:893591]	Q548G3	P70661	7.5	7.6E-05	-3.7	1.9E-02	-1.3	1.1E-01	-0.5	7.0E-01
ENSMUST00000050104	G protein-coupled receptor, family C, group 5, member A [Source:MGI Symbol;Acc:MGI:1891250]	G5E8C3		7.2	1.0E-04	6.3	7.8E-04	-0.7	6.3E-01	-0.4	6.0E-01
ENSMUST00000050106	keratin associated protein 4-13 [Source:MGI Symbol;Acc:MGI:1916714]	Q9D7P3		7.0	5.3E-05	-9.5	3.6E-05	0.9	2.0E-02	0.4	7.9E-01
ENSMUST00000050120	potassium channel tetramerisation domain containing 4 [Source:MGI Symbol;Acc:MGI:1914766]		Q9D7X1	6.2	1.5E-04	5.4	5.3E-02	-2.2	4.3E-01	-1.2	4.7E-01
ENSMUST00000050125	RIKEN cDNA 2900026A02 gene [Source:MGI Symbol;Acc:MGI:1920194]		Q8BRV5	7.7	1.9E-07	-2.8	1.8E-03	-0.7	9.5E-02	-1.2	1.1E-01
ENSMUST00000050140	transmembrane protein 88 [Source:MGI Symbol;Acc:MGI:1914270]		Q9D0N8	2.1	3.1E-02	-6.5	7.1E-05	0.7	8.8E-02	-0.4	6.6E-01
ENSMUST00000050148	cell division cycle 37-like 1 [Source:MGI Symbol;Acc:MGI:1914322]		Q9CZP7	-1.8	7.9E-03	6.4	6.3E-04	-2.1	1.7E-01	0.5	4.8E-01
ENSMUST00000050149	tubule associated monooxygenase, calponin and LIM domain containing 2 [Source:MGI Symbol;Acc:MGI:244		Q8BML1	4.3	4.0E-05	5.8	2.0E-03	-0.6	6.7E-01	0.3	6.8E-01
ENSMUST00000050160	expressed sequence AU021092 [Source:MGI Symbol;Acc:MGI:2146559]		Q3UST5	7.8	1.3E-05	-1.4	4.2E-01	2.4	6.1E-02	0.7	6.9E-01
ENSMUST00000050178	coiled-coil domain containing 60 [Source:MGI Symbol;Acc:MGI:2141043]		Q8C4J0	8.6	1.8E-05	-3.9	3.3E-03	0.3	5.1E-01	1.0	3.6E-01
ENSMUST00000050183	uveal autoantigen with coiled-coil domains and ankyrin repeats [Source:MGI Symbol;Acc:MGI:1919815]			3.3	3.8E-04	-4.0	2.9E-02	0.1	9.3E-01	0.7	6.9E-01
ENSMUST00000050205	nudix (nucleoside diphosphate linked moiety X)-type motif 1 [Source:MGI Symbol;Acc:MGI:109280]		P53368	-4.3	7.9E-04	4.2	1.4E-03	1.2	1.7E-01	-0.5	4.5E-01
ENSMUST00000050211	thymidine kinase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1913266]	Q8BN51		-3.4	2.1E-04	-2.7	1.3E-02	0.9	1.2E-01	0.7	4.7E-01
ENSMUST00000050214	A kinase (PRKA) anchor protein 8-like [Source:MGI Symbol;Acc:MGI:1860606]	Q5RL57		-2.2	2.3E-02	7.7	1.8E-04	0.6	6.2E-01	-0.3	6.1E-01
ENSMUST00000050220	tetratricopeptide repeat domain 34 [Source:MGI Symbol;Acc:MGI:2445205]		Q8C0Q3	9.4	4.8E-06	5.1	1.3E-03	-2.4	9.1E-02	0.2	7.9E-01
ENSMUST00000050226	smoothelin-like 2 [Source:MGI Symbol;Acc:MGI:2442764]		Q8CI12	6.2	8.8E-06	7.2	1.8E-02	-0.6	8.3E-01	-1.7	2.7E-01
ENSMUST00000050234	jerky [Source:MGI Symbol;Acc:MGI:106214]	Q543Z9	Q60976	6.6	1.9E-05	-5.8	2.8E-04	-0.7	1.9E-01	-1.7	1.9E-01
ENSMUST00000049630	cytochrome c oxidase assembly protein 19 [Source:MGI Symbol;Acc:MGI:1915283]		Q8K0C8	0.4	5.3E-01	-0.4	6.2E-01	-0.3	6.0E-01	0.5	5.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000049642	fumarylacetoacetate hydrolase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915886]		Q8R0F8	1.2	1.0E-01	0.0	1.0E+00	-1.1	1.0E-01	0.1	9.1E-01
ENSMUST00000049648	kelch repeat and BTB (POZ) domain containing 3 [Source:MGI Symbol;Acc:MGI:1916399]		Q8BHI4	-1.1	8.0E-02	0.1	9.2E-01	0.7	2.4E-01	-0.5	4.4E-01
ENSMUST00000050236	thioredoxin domain containing 2 (spermatozoa) [Source:MGI Symbol;Acc:MGI:2389312]	H7BX21		6.6	2.4E-03	7.8	3.6E-04	0.0	9.8E-01	-0.7	3.3E-01
ENSMUST00000050248	zinc finger and BTB domain containing 11 [Source:MGI Symbol;Acc:MGI:2443876]	G5E8B9		-3.2	1.0E-04	-5.7	7.5E-03	1.4	6.1E-02	0.4	8.3E-01
ENSMUST00000050258	tetratricopeptide repeat domain 24 [Source:MGI Symbol;Acc:MGI:2443841]	B9EJT8	Q8BYG0	7.1	5.3E-05	-3.3	9.7E-03	-0.2	6.5E-01	-1.7	1.7E-01
ENSMUST00000050273	cytochrome c oxidase assembly protein 17 [Source:MGI Symbol;Acc:MGI:1333806]	Q54AC6	P56394	-7.3	6.1E-05	8.9	3.2E-05	-0.7	5.9E-01	0.0	9.4E-01
ENSMUST00000050309	RIKEN cDNA F830045P16 gene [Source:MGI Symbol;Acc:MGI:3045317]	Q8BJ95		2.1	1.8E-02	-2.9	1.5E-01	1.7	1.2E-01	0.1	9.4E-01
ENSMUST00000050312	mitogen-activated protein kinase 8 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1309464]		Q9WVI9	5.8	7.8E-05	6.5	1.8E-03	-0.5	7.5E-01	-2.6	2.0E-02
ENSMUST00000050325	histocompatibility 2, class II antigen E beta2 [Source:MGI Symbol;Acc:MGI:95902]	Q3UUV9		7.3	1.4E-05	6.4	2.4E-04	-0.6	6.3E-01	-0.4	5.5E-01
ENSMUST00000049699	protein serine kinase H1 [Source:MGI Symbol;Acc:MGI:3528383]		Q91YA2	-1.3	5.2E-02	0.1	9.3E-01	0.8	1.6E-01	-0.6	4.3E-01
ENSMUST00000050327	atypical chemokine receptor 2 [Source:MGI Symbol;Acc:MGI:1891697]		O08707	7.8	1.8E-05	9.6	3.7E-05	0.8	5.5E-01	-1.1	9.2E-02
ENSMUST00000050328	aryotic translation initiation factor 2, subunit 3, structural gene X-linked [Source:MGI Symbol;Acc:MGI:1349	Q3TML6	Q9Z0N1	-2.8	2.5E-03	-3.5	3.2E-02	0.1	9.0E-01	-0.1	9.2E-01
ENSMUST00000050331	heterogeneous nuclear ribonucleoprotein H2 [Source:MGI Symbol;Acc:MGI:1201779]		P70333	-9.0	8.2E-03	8.3	4.2E-05	-0.7	6.0E-01	-0.2	6.6E-01
ENSMUST00000050342	a disintegrin and metallopeptidase domain 30 [Source:MGI Symbol;Acc:MGI:1918328]	Q811Q3		4.1	1.3E-03	5.6	2.5E-03	-0.7	6.5E-01	0.3	7.4E-01
ENSMUST00000050360	purinergic receptor P2Y, G-protein coupled 12 [Source:MGI Symbol;Acc:MGI:1918089]	Q546L4	Q9CPV9	-3.2	4.8E-03	-5.2	2.3E-03	-0.5	3.4E-01	-1.7	2.6E-01
ENSMUST00000050372	crumbs family member 2 [Source:MGI Symbol;Acc:MGI:2679260]		Q80YA8	10.6	1.1E-06	-3.3	1.1E-02	0.7	2.4E-01	0.7	4.8E-01
ENSMUST00000050383	zinc finger protein 646 [Source:MGI Symbol;Acc:MGI:3665412]	Q6NV66		-1.9	2.9E-03	6.4	1.9E-04	-0.6	6.0E-01	-0.6	3.5E-01
ENSMUST00000050385	killer cell lectin-like receptor family I member 2 [Source:MGI Symbol;Acc:MGI:2443965]	Q5DT36		4.2	4.0E-03	3.4	7.8E-04	-0.1	8.1E-01	-0.2	7.4E-01
ENSMUST00000049768	eosinophil peroxidase [Source:MGI Symbol;Acc:MGI:107569]		P49290	2.4	4.1E-02	4.4	6.0E-03	1.1	3.2E-01	-0.8	4.0E-01
ENSMUST00000050389	transmembrane protein 174 [Source:MGI Symbol;Acc:MGI:1915594]		Q9DCX7	7.0	1.1E-04	4.5	2.0E-05	0.2	6.7E-01	0.0	9.8E-01
ENSMUST00000050398	RFad1, flavin adenine dinucleotide synthetase, homolog (yeast) [Source:MGI Symbol;Acc:MGI:2443030]		Q8R123	-3.3	9.1E-03	7.2	1.8E-04	-0.6	6.1E-01	0.6	3.8E-01
ENSMUST00000050401	src homology 2 domain-containing transforming protein E [Source:MGI Symbol;Acc:MGI:1099462]		Q8BSD5	6.0	2.1E-05	4.2	1.1E-04	-1.6	2.9E-02	0.0	1.0E+00
ENSMUST00000050433	transient receptor potential cation channel, subfamily C, member 6 [Source:MGI Symbol;Acc:MGI:109523]		Q61143	4.8	4.1E-04	7.8	1.1E-02	-0.8	7.7E-01	-2.4	1.3E-01
ENSMUST00000049789	NLR family, apoptosis inhibitory protein 5 [Source:MGI Symbol;Acc:MGI:1298220]	Q8CGT2		0.4	5.5E-01	1.0	2.9E-01	0.0	9.5E-01	-0.5	5.4E-01
ENSMUST00000050434	nyctalopin [Source:MGI Symbol;Acc:MGI:2448607]		P83503	6.2	9.7E-07	7.3	1.5E-04	-0.2	8.8E-01	0.4	5.7E-01
ENSMUST00000050451	olfactory receptor 279 [Source:MGI Symbol;Acc:MGI:3030113]	Q8VFD8		6.7	4.2E-04	1.9	7.8E-02	-1.9	6.7E-02	-0.8	3.4E-01
ENSMUST00000050471	phosphatidylethanolamine binding protein 2 [Source:MGI Symbol;Acc:MGI:1923650]	E9QLE5		6.5	2.0E-04	-1.5	2.2E-02	0.2	5.4E-01	-0.4	4.7E-01
ENSMUST00000050476	solute carrier family 35, member A4 [Source:MGI Symbol;Acc:MGI:1915093]		Q9D321	-3.0	3.1E-02	2.8	2.7E-03	1.1	9.0E-02	0.3	5.7E-01
ENSMUST00000049822	thioesterase superfamily member 4 [Source:MGI Symbol;Acc:MGI:1923028]		Q3UUI3	-0.1	8.7E-01	-0.8	3.3E-01	-1.0	1.3E-01	-0.3	6.4E-01
ENSMUST00000049836	sperm antigen with calponin homology and coiled-coil domains 1 [Source:MGI Symbol;Acc:MGI:2442356]		Q5SXY1	-0.4	4.9E-01	0.9	2.7E-01	1.0	1.2E-01	-0.3	6.4E-01
ENSMUST00000050483	poly (ADP-ribose) polymerase family, member 6 [Source:MGI Symbol;Acc:MGI:1914537]			-4.1	1.4E-02	0.7	7.3E-01	-2.3	2.0E-01	4.9	2.1E-02
ENSMUST00000049861	RB-associated KRAB zinc finger [Source:MGI Symbol;Acc:MGI:1927369]		Q8BQC8	4.2	1.0E-01	0.4	8.7E-01	-4.1	9.6E-02	-0.3	8.8E-01
ENSMUST00000050484	neurotrophin 3 [Source:MGI Symbol;Acc:MGI:97380]		P20181	-5.5	2.7E-04	2.2	4.9E-03	1.1	4.5E-02	0.0	9.5E-01
ENSMUST00000049872	G protein-coupled receptor 183 [Source:MGI Symbol;Acc:MGI:2442034]		Q3U6B2	0.9	1.2E-01	-0.8	2.3E-01	-1.6	8.4E-03	0.1	8.3E-01
ENSMUST00000050487	invariant polypeptide of major histocompatibility complex, class II antigen-associated) [Source:MGI Symbol;A	Q545Y5	P04441	-5.3	1.3E-03	2.5	8.0E-03	0.4	5.0E-01	-0.2	7.0E-01
ENSMUST00000050511	kynureninase (L-kynurenine hydrolase) [Source:MGI Symbol;Acc:MGI:1918039]	A2ARD7		7.7	4.7E-05	-3.1	2.5E-04	-0.1	7.7E-01	-0.1	8.0E-01
ENSMUST00000050516	activating signal cointegrator 1 complex subunit 1 [Source:MGI Symbol;Acc:MGI:1916340]		Q9D8Z1	-4.3	3.6E-03	-3.0	2.6E-03	0.6	1.8E-01	0.3	6.5E-01
ENSMUST00000050519	leucine rich repeat and fibronectin type III, extracellular 1 [Source:MGI Symbol;Acc:MGI:2442479]		Q8C8T7	10.9	1.7E-05	-3.2	1.8E-03	0.6	1.7E-01	-1.2	1.5E-01
ENSMUST00000049912	avian reticuloendotheliosis viral (v-rel) oncogene related B [Source:MGI Symbol;Acc:MGI:103289]	Q8K220		-1.5	5.0E-01	-3.9	1.5E-01	-2.5	1.3E-01	-0.1	9.7E-01
ENSMUST00000049920	INO80 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915392]		Q6ZPV2	0.1	8.7E-01	0.3	7.0E-01	0.5	3.0E-01	0.3	6.1E-01
ENSMUST00000049927				0.8	1.9E-01	0.0	9.5E-01	0.3	5.4E-01	1.0	1.3E-01
ENSMUST00000050535	Myb/SANT-like DNA-binding domain containing 1 [Source:MGI Symbol;Acc:MGI:2684990]		Q8BIL2	7.3	4.8E-05	5.6	8.0E-04	-0.2	8.8E-01	-0.8	2.7E-01
ENSMUST00000050544	hyaluronan synthase 2 [Source:MGI Symbol;Acc:MGI:107821]		P70312	5.5	3.7E-05	-1.2	6.2E-02	0.7	1.1E-01	-0.4	5.4E-01
ENSMUST00000049932	cAMP responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:88494]	Q547S9	Q01147	-0.8	7.8E-01	-1.8	5.8E-01	-1.3	5.7E-01	-0.3	9.3E-01
ENSMUST00000050551	300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1 [Source:MGI Symbol;Acc:MGI:1(	Q3UGA1	P97769	7.3	7.1E-05	-2.2	8.8E-02	-0.1	9.3E-01	-1.7	2.0E-01
ENSMUST00000050552	basic leucine zipper and W2 domains 1 [Source:MGI Symbol;Acc:MGI:1914132]		Q9CQC6	-3.8	2.4E-06	3.8	7.5E-03	0.1	9.2E-01	1.2	1.7E-01
ENSMUST00000050562	cholesterol 25-hydroxylase [Source:MGI Symbol;Acc:MGI:1333869]		Q9Z0F5	6.7	1.9E-04	6.1	7.8E-04	-1.8	2.2E-01	-0.2	8.0E-01
ENSMUST00000050567	RIKEN cDNA 1700019D03 gene [Source:MGI Symbol;Acc:MGI:1914330]		Q9CPS8	4.5	3.2E-03	5.9	2.3E-04	-0.9	4.3E-01	-0.7	2.5E-01
ENSMUST00000050575	thiamine triphosphatase [Source:MGI Symbol;Acc:MGI:2446078]		Q8JZL3	1.5	2.6E-02	7.1	8.1E-05	-0.6	6.1E-01	-0.3	5.8E-01
ENSMUST00000050584	cysteine-rich transmembrane module containing 1 [Source:MGI Symbol;Acc:MGI:1913310]		Q8K353	-3.4	9.5E-04	6.6	3.2E-04	-0.1	9.2E-01	-1.0	2.0E-01
ENSMUST00000050585	olfactory receptor 522 [Source:MGI Symbol;Acc:MGI:3030356]	Q8VGL1		6.9	1.4E-04	5.4	9.9E-05	-0.9	3.0E-01	-0.2	7.1E-01
ENSMUST00000049995	membrane-associated ring finger (C3HC4) 10 [Source:MGI Symbol;Acc:MGI:2443469]	E9PX79		3.7	6.7E-02	6.5	9.2E-03	-0.3	8.8E-01	-3.1	2.7E-02
ENSMUST00000050586	RIKEN cDNA 5430419D17 gene [Source:MGI Symbol;Acc:MGI:1918645]		Q8BZE1	7.3	3.1E-05	4.3	1.7E-02	-2.3	1.6E-01	0.2	8.5E-01
ENSMUST00000050595	zinc finger protein 454 [Source:MGI Symbol;Acc:MGI:2679253]	Q80Y34		6.3	1.9E-03	5.3	2.0E-02	-0.6	7.7E-01	-0.5	6.9E-01
ENSMUST00000050611	centrosomal protein 68 [Source:MGI Symbol;Acc:MGI:2667663]		Q8C0D9	1.7	5.3E-03	-0.5	4.6E-01	0.6	2.0E-01	-0.5	4.6E-01
ENSMUST00000050010	vesicle-associated membrane protein 4 [Source:MGI Symbol;Acc:MGI:1858730]	Q8BSN6		-0.4	7.0E-01	1.8	5.7E-01	7.5	9.5E-03	5.2	4.6E-02
ENSMUST00000050623	signal-regulatory protein beta 1C [Source:MGI Symbol;Acc:MGI:3807521]	Q1AN90		-11.1	2.7E-05	0.2	7.4E-01	-2.7	9.2E-04	-0.9	1.8E-01
ENSMUST00000050625	peats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B [		Q60519	7.3	2.3E-03	-6.0	6.4E-04	-0.5	3.6E-01	0.2	8.5E-01
ENSMUST00000050649	G protein-coupled receptor 135 [Source:MGI Symbol;Acc:MGI:2676315]	A7E1Z8	Q7TQP2	6.5	3.7E-04	5.4	2.0E-02	-0.8	7.1E-01	-0.2	8.6E-01
ENSMUST00000050658	spermatogenic leucine zipper 1 [Source:MGI Symbol;Acc:MGI:1930801]		Q99MY0	7.0	4.6E-05	6.3	2.0E-04	-1.5	2.2E-01	-1.2	7.8E-02
ENSMUST00000050660	transmembrane epididymal protein 1A [Source:MGI Symbol;Acc:MGI:2668439]	E9QLK8		7.1	2.1E-05	3.9	5.7E-04	-3.1	8.2E-03	0.1	8.2E-01
ENSMUST00000050687	Jun dimerization protein 2 [Source:MGI Symbol;Acc:MGI:1932093]		P97875	-5.8	7.6E-05	7.4	6.1E-05	-0.6	5.9E-01	-0.3	6.4E-01
ENSMUST00000050702	protein tyrosine phosphatase, receptor type, Q [Source:MGI Symbol;Acc:MGI:1096349]		P0C5E4	7.0	6.9E-05	6.2	2.8E-03	-1.1	5.1E-01	1.5	1.4E-01
ENSMUST00000050705	developmental pluripotency associated 4 [Source:MGI Symbol;Acc:MGI:2157525]	E9PUG8		7.4	2.3E-05	-2.6	1.1E-02	1.4	1.4E-02	0.2	8.4E-01
ENSMUST00000050707	V-set and immunoglobulin domain containing 4 [Source:MGI Symbol;Acc:MGI:2679720]	Q80WA3		3.0	3.0E-02	-1.0	1.2E-01	1.3	1.1E-02	-0.4	5.2E-01
ENSMUST00000050069	RNA binding motif protein 12 B1 [Source:MGI Symbol;Acc:MGI:1919647]		Q80YR9	-2.1	1.2E-01	-4.0	6.7E-02	-1.0	3.1E-01	0.9	6.4E-01
ENSMUST00000050073	DnaJ (Hsp40) homolog, subfamily B, member 4 [Source:MGI Symbol;Acc:MGI:1914285]		Q9D832	-0.5	4.3E-01	-0.6	5.0E-01	-0.5	3.9E-01	-0.5	5.2E-01
ENSMUST00000050077	LanC (bacterial lantibiotic synthetase component C)-like 2 [Source:MGI Symbol;Acc:MGI:1919085]		Q9JJK2	0.2	7.0E-01	-1.3	1.8E-01	0.1	9.0E-01	1.7	8.4E-02
ENSMUST00000050078	stromal cell derived factor 4 [Source:MGI Symbol;Acc:MGI:108079]		Q61112	-0.5	3.5E-01	0.1	9.1E-01	0.7	1.9E-01	0.1	8.7E-01
ENSMUST00000050709	docking protein 7 [Source:MGI Symbol;Acc:MGI:3584043]			8.6	1.5E-05	-4.0	6.8E-03	0.6	2.8E-01	-1.4	3.0E-01
ENSMUST00000050714	insulin-like growth factor binding protein, acid labile subunit [Source:MGI Symbol;Acc:MGI:107973]			7.2	7.2E-05	-1.9	1.1E-02	0.3	4.7E-01	-0.6	3.6E-01
ENSMUST00000050715	proprotein convertase subtilisin/kexin type 5 [Source:MGI Symbol;Acc:MGI:97515]	Q91VK0	Q04592	5.9	4.5E-04	-7.6	7.4E-04	0.3	6.1E-01	0.9	6.2E-01
ENSMUST00000050101	zinc finger protein 322A [Source:MGI Symbol;Acc:MGI:2442566]		Q8BZ89	0.2	6.0E-01	0.9	1.3E-01	0.5	2.0E-01	-0.1	8.3E-01
ENSMUST00000050717	predicted pseudogene 5422 [Source:MGI Symbol;Acc:MGI:3643411]	J3KMQ2		7.2	1.5E-04	6.7	3.3E-04	-0.6	6.2E-01	0.2	8.1E-01
ENSMUST00000050719	formin-like 2 [Source:MGI Symbol;Acc:MGI:1918659]	E9PXE6		5.0	1.6E-02	2.9	5.3E-03	-5.1	9.3E-04	-0.7	3.1E-01
ENSMUST00000050729	olfactory receptor 449 [Source:MGI Symbol;Acc:MGI:3030283]	Q8VGW8		5.1	3.1E-03	6.1	3.0E-04	-0.6	6.1E-01	0.4	5.6E-01
ENSMUST00000050732	potassium channel tetramerisation domain containing 14 [Source:MGI Symbol;Acc:MGI:1289222]	Q5EER8		4.5	3.9E-04	5.3	5.0E-04	-1.4	2.2E-01	-0.5	4.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000050754	RIKEN cDNA A730018C14 gene [Source:MGI Symbol;Acc:MGI:2442339]	Q8C987		8.1	2.5E-05	4.9	8.4E-06	-2.6	1.4E-03	0.2	5.1E-01
ENSMUST00000050756	family with sequence similarity 19, member A2 [Source:MGI Symbol;Acc:MGI:2143691]			8.3	5.7E-05	7.5	4.7E-04	-0.7	6.3E-01	0.1	9.2E-01
ENSMUST00000050758	filaggrin [Source:MGI Symbol;Acc:MGI:95553]	A0A0A6YY62		8.2	1.0E-04	6.9	9.2E-05	-0.5	6.4E-01	-1.9	1.1E-02
ENSMUST00000050770	complement component 5a receptor 1 [Source:MGI Symbol;Acc:MGI:88232]		P30993	-10.7	1.6E-05	7.0	1.7E-04	0.1	9.0E-01	-0.9	1.6E-01
ENSMUST00000050771	predicted gene 11437 [Source:MGI Symbol;Acc:MGI:3650287]		Q5QR91	6.7	1.4E-04	1.8	9.9E-02	0.6	5.2E-01	0.8	3.6E-01
ENSMUST00000050772	solute carrier family 22 (organic cation transporter), member 17 [Source:MGI Symbol;Acc:MGI:1926225]		Q9D9E0	6.5	1.6E-04	-1.2	9.6E-02	0.2	7.1E-01	-0.4	5.4E-01
ENSMUST00000050776	BarH-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1859288]		P63157	6.2	2.3E-02	3.9	1.9E-04	-0.6	3.1E-01	-0.2	6.3E-01
ENSMUST00000050780	camello-like 3 [Source:MGI Symbol;Acc:MGI:2136449]			8.0	5.1E-05	5.9	1.2E-04	-2.0	7.8E-02	0.0	9.8E-01
ENSMUST00000050171	NIMA (never in mitosis gene a)-related expressed kinase 4 [Source:MGI Symbol;Acc:MGI:1344404]	Q6GTE9		0.5	4.1E-01	0.6	4.0E-01	0.0	9.8E-01	-0.1	8.6E-01
ENSMUST00000050785	lipocalin 2 [Source:MGI Symbol;Acc:MGI:96757]		P11672	-10.8	8.2E-07	6.5	2.1E-04	-1.3	2.8E-01	0.7	2.6E-01
ENSMUST00000050833	INO80 complex subunit E [Source:MGI Symbol;Acc:MGI:2141881]	Q8R359		6.6	1.6E-03	2.3	7.2E-03	-1.2	8.4E-02	-0.2	7.7E-01
ENSMUST00000050859	cytidine monophospho-N-acetylneuraminic acid hydroxylase [Source:MGI Symbol;Acc:MGI:103227]		Q61419	-6.0	1.6E-04	-4.3	3.0E-03	-0.8	1.4E-01	-0.8	4.9E-01
ENSMUST00000050207	transcription elongation factor, mitochondrial [Source:MGI Symbol;Acc:MGI:1915800]		Q5SSK3	-0.3	8.1E-01	0.5	7.0E-01	-1.4	2.4E-01	-2.3	1.0E-01
ENSMUST00000050867	cactin, spliceosome C complex subunit [Source:MGI Symbol;Acc:MGI:1917562]	A1L013	Q9CS00	-1.5	2.1E-02	-2.6	6.9E-03	0.8	9.3E-02	-0.1	9.1E-01
ENSMUST00000050872	nuclear factor I/B [Source:MGI Symbol;Acc:MGI:103188]		P97863	8.9	1.4E-05	-1.6	1.5E-01	0.3	6.0E-01	-0.3	7.8E-01
ENSMUST00000050874	transmembrane channel-like gene family 8 [Source:MGI Symbol;Acc:MGI:2669037]	B1ATC0	Q7TN58	-3.3	2.3E-03	6.4	6.8E-05	-2.9	2.2E-02	0.1	9.1E-01
ENSMUST00000050881	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1 [Source:MGI Symbol;Acc:MGI:1914161]		Q8VHN8	-2.2	1.3E-02	4.8	2.1E-04	-0.3	7.1E-01	1.1	7.1E-02
ENSMUST00000050228	transmembrane protein 241 [Source:MGI Symbol;Acc:MGI:2442435]	H7BX28		-1.9	2.0E-01	-3.0	1.1E-01	-0.8	4.8E-01	0.3	8.9E-01
ENSMUST00000050884	high mobility group nucleosomal binding domain 1 [Source:MGI Symbol;Acc:MGI:96120]		P18608	2.0	4.8E-03	6.6	2.4E-04	0.2	8.3E-01	0.3	6.7E-01
ENSMUST00000050887	prokineticin receptor 1 [Source:MGI Symbol;Acc:MGI:1929676]		Q9JKL1	8.2	1.0E-05	6.0	1.6E-02	0.1	9.8E-01	0.7	6.1E-01
ENSMUST00000050890	sialidase 4 [Source:MGI Symbol;Acc:MGI:2661364]		Q8BZL1	8.1	7.0E-05	-1.6	2.0E-02	0.5	1.9E-01	-1.1	1.0E-01
ENSMUST00000050897	spindle and centriole associated protein 1 [Source:MGI Symbol;Acc:MGI:1196252]		Q8C804	5.7	5.2E-05	7.3	8.5E-05	-0.5	6.4E-01	-0.7	2.4E-01
ENSMUST00000050899	transmembrane protein 198 [Source:MGI Symbol;Acc:MGI:2443133]		Q8BG75	8.1	8.3E-05	-8.8	1.5E-04	-0.9	5.2E-02	0.5	7.2E-01
ENSMUST00000050288	lysine (K)-specific demethylase 4A [Source:MGI Symbol;Acc:MGI:2446210]	A2A8L9		0.3	7.8E-01	0.9	5.6E-01	0.2	8.5E-01	-0.3	8.2E-01
ENSMUST00000050306	RIKEN cDNA 1700056E22 gene [Source:MGI Symbol;Acc:MGI:1920613]	F7CNM6		0.2	8.8E-01	0.9	5.7E-01	0.3	8.4E-01	-0.4	8.0E-01
ENSMUST00000050901	apolipoprotein F [Source:MGI Symbol;Acc:MGI:104539]			4.5	1.5E-04	3.3	7.7E-03	0.9	3.0E-01	-0.3	7.0E-01
ENSMUST00000050916	sorting nexin 33 [Source:MGI Symbol;Acc:MGI:2443239]		Q4VAA7	1.8	5.5E-03	3.5	1.6E-03	-3.2	4.3E-03	-0.9	1.8E-01
ENSMUST00000050918	calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:MGI Symbol;Acc:MGI:1913509]		Q6QWF9	7.3	2.6E-05	5.1	1.1E-04	-2.3	3.0E-02	0.0	9.9E-01
ENSMUST00000050921	RIKEN cDNA A230052G05 gene [Source:MGI Symbol;Acc:MGI:3045239]	Q8C546		7.4	8.0E-05	5.7	2.3E-04	-2.3	5.3E-02	-0.2	7.0E-01
ENSMUST00000050933	oogenesin 3 [Source:MGI Symbol;Acc:MGI:2684047]	Q3UWY1		5.6	1.1E-03	-2.7	1.9E-02	0.5	3.6E-01	0.4	6.6E-01
ENSMUST00000050937	cDNA sequence BC053393 [Source:MGI Symbol;Acc:MGI:3039605]	A0A0B4J1F6		5.7	2.9E-04	-9.0	2.8E-02	-1.1	3.1E-01	-1.1	7.8E-01
ENSMUST00000050940	forkhead box E3 [Source:MGI Symbol;Acc:MGI:1353569]		Q9QY14	3.6	2.5E-02	4.9	9.7E-04	-0.3	7.9E-01	-1.1	1.8E-01
ENSMUST00000050349	family with sequence similarity 109, member B [Source:MGI Symbol;Acc:MGI:2443609]			-1.1	4.4E-01	2.7	2.1E-01	1.9	2.8E-01	-1.9	2.5E-01
ENSMUST00000050952	starch binding domain 1 [Source:MGI Symbol;Acc:MGI:1261768]		Q8C7E7	5.2	6.7E-05	-3.2	9.1E-03	-1.1	8.7E-02	-1.2	2.8E-01
ENSMUST00000050958	transmembrane inner ear [Source:MGI Symbol;Acc:MGI:2159400]	B2RSF0	Q8K467	6.3	2.5E-05	7.2	1.6E-05	-3.0	1.6E-02	0.4	3.2E-01
ENSMUST00000050373	testis-specific serine kinase 6 [Source:MGI Symbol;Acc:MGI:2148775]		Q925K9	1.2	1.5E-01	1.9	7.5E-02	0.8	3.2E-01	0.1	8.8E-01
ENSMUST00000050962	claudin 14 [Source:MGI Symbol;Acc:MGI:1860425]	A2RSP0	Q9Z0S3	5.5	1.1E-03	-0.4	5.0E-01	1.0	3.5E-02	-0.5	4.2E-01
ENSMUST00000050963	interleukin 17C [Source:MGI Symbol;Acc:MGI:2446486]			3.6	1.6E-03	3.5	1.3E-02	-1.6	1.8E-01	-0.9	3.6E-01
ENSMUST00000050970	polymerase (RNA) I polypeptide D [Source:MGI Symbol;Acc:MGI:108403]	Q545W2	P97304	-3.2	4.3E-05	7.4	1.4E-04	-0.5	6.8E-01	-0.9	1.9E-01
ENSMUST00000050975	leucine rich repeat and Ig domain containing 4 [Source:MGI Symbol;Acc:MGI:2444651]			6.4	6.8E-06	-1.9	1.4E-01	1.0	2.1E-01	-0.5	7.1E-01
ENSMUST00000050983	RIKEN cDNA 4932411E22 gene [Source:MGI Symbol;Acc:MGI:3045332]	Q8CDJ6		7.7	1.9E-05	5.0	2.1E-04	-0.9	3.1E-01	0.1	9.2E-01
ENSMUST00000050410	SWI5 recombination repair homolog (yeast) [Source:MGI Symbol;Acc:MGI:1920181]	A0A0A0MQ99		2.4	2.2E-01	-3.6	1.3E-01	-5.0	1.2E-02	0.9	6.7E-01
ENSMUST00000050993	eukaryotic translation initiation factor 5 [Source:MGI Symbol;Acc:MGI:95309]	Q3TQR3	P59325	-6.1	7.7E-05	4.4	1.1E-03	-0.8	4.2E-01	-0.3	6.2E-01
ENSMUST00000050997	Rieske (Fe-S) domain containing [Source:MGI Symbol;Acc:MGI:2145198]		Q8K2P6	-4.8	3.5E-03	6.1	3.2E-06	-0.3	6.3E-01	-0.2	5.8E-01
ENSMUST00000050446	MMS22-like, DNA repair protein [Source:MGI Symbol;Acc:MGI:2684980]	G8JL47		3.6	5.9E-02	0.8	6.5E-01	-2.2	2.2E-01	0.6	7.2E-01
ENSMUST00000051011	transmembrane protein 198b [Source:MGI Symbol;Acc:MGI:1921077]	Q8CFU0		-4.8	1.6E-03	6.6	8.5E-04	-0.6	6.7E-01	-0.5	5.1E-01
ENSMUST00000050467	transducer of ERBB2, 2 [Source:MGI Symbol;Acc:MGI:1888525]	Q543X9	Q9JM55	-0.4	4.0E-01	0.0	9.5E-01	0.8	9.7E-02	0.4	5.3E-01
ENSMUST00000051014	exophilin 5 [Source:MGI Symbol;Acc:MGI:2443248]		Q0VAV2	8.8	6.3E-06	5.5	6.8E-04	-1.5	2.5E-01	-0.5	4.5E-01
ENSMUST00000050472	ubiquitin specific peptidase like 1 [Source:MGI Symbol;Acc:MGI:2442342]	E9QLC6		-0.8	5.4E-01	1.8	1.7E-01	-0.7	5.3E-01	-3.3	3.3E-02
ENSMUST00000051016	ORAI calcium release-activated calcium modulator 1 [Source:MGI Symbol;Acc:MGI:1925542]	A3KCG1	Q8BWG9	-8.8	1.9E-04	-0.2	8.5E-01	0.4	6.2E-01	-2.3	1.1E-01
ENSMUST00000050480	coiled-coil domain containing 66 [Source:MGI Symbol;Acc:MGI:2443639]		Q6NS45	0.9	2.1E-01	0.3	7.0E-01	-0.9	1.7E-01	-0.3	6.5E-01
ENSMUST00000051025	transmembrane protein 102 [Source:MGI Symbol;Acc:MGI:1921591]		Q3UPR7	5.9	2.0E-05	-0.3	8.2E-01	0.6	5.8E-01	-3.2	6.9E-02
ENSMUST00000051039	SUMO/sentrin specific peptidase 8 [Source:MGI Symbol;Acc:MGI:1918849]		Q9D2Z4	2.8	3.6E-03	0.2	8.1E-01	0.6	2.9E-01	-5.0	6.0E-04
ENSMUST00000051064	zinc finger, C2HC-type containing 1A [Source:MGI Symbol;Acc:MGI:1914556]		Q8BJH1	4.1	6.4E-04	-9.4	2.6E-03	-1.9	1.3E-02	2.2	3.7E-01
ENSMUST00000050493	expressed sequence BB014433 [Source:MGI Symbol;Acc:MGI:2142823]	Q8C5R5		4.3	1.3E-01	5.2	1.1E-01	-0.2	9.6E-01	-1.0	5.7E-01
ENSMUST00000050497	expressed sequence C87436 [Source:MGI Symbol;Acc:MGI:2141787]		Q8R3C1	1.0	6.2E-01	-3.1	3.5E-01	-1.5	4.2E-01	2.6	4.2E-01
ENSMUST00000051065	GPRIN family member 3 [Source:MGI Symbol;Acc:MGI:1924785]	B2RQZ6	Q8BWS5	7.5	1.6E-05	5.9	3.5E-04	-1.2	3.1E-01	0.5	4.3E-01
ENSMUST00000051079	glycoprotein hormone beta 5 [Source:MGI Symbol;Acc:MGI:2156540]	B2RTN6	Q812B2	7.2	8.2E-05	2.0	4.0E-01	7.4	1.7E-03	1.1	5.3E-01
ENSMUST00000051091	histone cluster 1, H2be [Source:MGI Symbol;Acc:MGI:2448380]		Q6ZWY9	-4.9	2.0E-02	8.7	1.0E-04	-1.4	3.8E-01	0.8	2.3E-01
ENSMUST00000051094	golgi autoantigen, golgin subfamily a, 7 [Source:MGI Symbol;Acc:MGI:1931029]		Q91W53	-3.9	1.3E-05	6.8	1.1E-04	-1.3	2.7E-01	-0.8	2.1E-01
ENSMUST00000051097	protease, serine 50 [Source:MGI Symbol;Acc:MGI:2447303]		Q8BLH5	6.6	8.5E-05	1.7	3.2E-02	-4.0	2.9E-04	-0.2	6.9E-01
ENSMUST00000051100	vesicle-associated membrane protein 7 [Source:MGI Symbol;Acc:MGI:1096399]		P70280	-4.5	1.2E-04	6.7	2.5E-04	-0.6	6.3E-01	0.0	9.4E-01
ENSMUST00000051117	predicted gene 6583 [Source:MGI Symbol;Acc:MGI:3648511]	E9Q8Z1		3.8	1.2E-03	-3.0	6.0E-05	0.1	6.1E-01	-0.6	1.8E-01
ENSMUST00000050555	potassium channel tetramerisation domain containing 11 [Source:MGI Symbol;Acc:MGI:2448712]		Q8K485	-0.7	2.7E-01	0.3	7.3E-01	1.1	8.3E-02	0.2	8.3E-01
ENSMUST00000050556	biorientation of chromosomes in cell division 1-like [Source:MGI Symbol;Acc:MGI:2444804]	E9Q6J5	E9Q6J5	-0.6	1.6E-01	-0.6	2.8E-01	0.3	4.2E-01	0.3	5.5E-01
ENSMUST00000050561	MAU2 chromatid cohesion factor homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1921799]		Q9D2X5	-2.9	4.6E-02	-7.8	3.2E-02	0.3	7.5E-01	5.2	1.2E-01
ENSMUST00000051118	trans-golgi network vesicle protein 23A [Source:MGI Symbol;Acc:MGI:3665441]	Q6NVH0		5.5	4.1E-05	5.1	1.2E-03	-1.6	2.3E-01	0.1	8.8E-01
ENSMUST00000051126	protocadherin beta 10 [Source:MGI Symbol;Acc:MGI:2136745]	Q91VE5		8.2	2.3E-05	5.7	1.0E-03	-0.6	6.5E-01	-1.7	4.8E-02
ENSMUST00000050574	cyclin J-like [Source:MGI Symbol;Acc:MGI:2685723]		Q5SRT8	0.6	3.4E-01	1.0	2.0E-01	0.2	7.0E-01	-0.2	7.5E-01
ENSMUST00000051129	leucine rich repeat containing 75B [Source:MGI Symbol;Acc:MGI:2143657]		Q7TPD7	1.7	3.4E-03	2.8	3.3E-03	0.6	3.7E-01	-0.7	2.2E-01
ENSMUST00000050581				3.9	3.7E-02	4.0	6.1E-02	-0.1	9.7E-01	-0.2	9.1E-01
ENSMUST00000051133	trace amine-associated receptor 8A [Source:MGI Symbol;Acc:MGI:2685076]		Q5QD07	6.6	1.6E-03	-1.7	7.9E-02	0.7	2.2E-01	-1.0	2.5E-01
ENSMUST00000051137	RIKEN cDNA E030002O03 gene [Source:MGI Symbol;Acc:MGI:2443346]	Q8BU90		5.5	3.0E-03	6.6	3.8E-04	-0.6	6.7E-01	-0.3	7.1E-01
ENSMUST00000051163	protocadherin beta 8 [Source:MGI Symbol;Acc:MGI:2136742]	Q91XZ2		8.9	5.5E-06	6.6	1.4E-04	-0.6	6.2E-01	0.2	7.9E-01
ENSMUST00000051176	family with sequence similarity 180, member A [Source:MGI Symbol;Acc:MGI:3039626]		Q8BR21	5.3	2.0E-04	5.2	1.1E-02	-0.6	7.4E-01	0.6	5.7E-01
ENSMUST00000051186	protein kinase, AMP-activated, alpha 1 catalytic subunit [Source:MGI Symbol;Acc:MGI:2145955]		Q5EG47	-4.4	1.2E-06	2.4	2.3E-03	0.0	9.2E-01	-0.7	1.8E-01
ENSMUST00000051201	olfactory receptor 544 [Source:MGI Symbol;Acc:MGI:3030378]	E9PX47		6.8	1.8E-04	-8.3	1.4E-04	-0.5	3.2E-01	-3.3	7.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000051209	paternally expressed 3 [Source:MGI Symbol;Acc:MGI:104748]		Q3URU2	10.5	1.7E-06	5.1	5.3E-02	0.4	8.7E-01	2.6	1.1E-01
ENSMUST00000050646	tetratricopeptide repeat domain 19 [Source:MGI Symbol;Acc:MGI:1920045]		Q8CC21	-0.2	7.5E-01	0.0	9.9E-01	0.3	5.7E-01	0.1	8.7E-01
ENSMUST00000051221	ankyrin repeat domain 40 [Source:MGI Symbol;Acc:MGI:1918702]		Q5SUE8	-2.9	2.9E-02	5.6	1.1E-03	-1.4	3.1E-01	-0.5	4.8E-01
ENSMUST00000051226	phosphofructokinase, muscle [Source:MGI Symbol;Acc:MGI:97548]		P47857	4.9	3.1E-02	7.5	4.9E-05	-0.6	6.0E-01	-1.1	7.8E-02
ENSMUST00000051234	CUE domain containing 2 [Source:MGI Symbol;Acc:MGI:1914366]		Q9CXX9	-6.5	4.6E-04	5.8	1.0E-04	-1.3	2.0E-01	0.0	9.8E-01
ENSMUST00000050668	zinc finger protein 770 [Source:MGI Symbol;Acc:MGI:2445100]		Q8BIQ8	1.3	1.3E-01	1.5	1.3E-01	-0.1	9.1E-01	-0.4	6.6E-01
ENSMUST00000051236	ADP-ribosylation factor-like 4C [Source:MGI Symbol;Acc:MGI:2445172]		P61208	4.3	4.1E-04	-5.7	6.3E-04	0.4	3.8E-01	0.3	8.4E-01
ENSMUST00000051241	zinc finger protein 36 [Source:MGI Symbol;Acc:MGI:99180]	Q3U3D2	P22893	-6.7	1.6E-03	6.2	2.1E-04	-1.2	3.1E-01	-0.4	5.0E-01
ENSMUST00000051249	aarF domain containing kinase 2 [Source:MGI Symbol;Acc:MGI:1889336]	E9QL72		-3.5	9.1E-04	7.0	7.7E-05	-0.6	5.9E-01	-0.2	7.6E-01
ENSMUST00000051259	adhesion G protein-coupled receptor G3 [Source:MGI Symbol;Acc:MGI:1859670]		Q8R0T6	-3.8	3.4E-04	6.6	3.3E-04	-0.6	6.5E-01	-1.0	1.9E-01
ENSMUST00000051264	CD300 antigen like family member F [Source:MGI Symbol;Acc:MGI:2442359]		Q6SJQ7	-9.4	8.9E-05	-3.2	2.0E-03	-8.4	2.0E-05	-2.2	2.8E-02
ENSMUST00000051272	WAP four-disulfide core domain 12 [Source:MGI Symbol;Acc:MGI:2183434]	Q3V469	Q9JHY3	8.2	8.9E-05	7.9	5.8E-05	-0.6	6.0E-01	0.0	9.4E-01
ENSMUST00000051277	prolactin releasing hormone receptor [Source:MGI Symbol;Acc:MGI:2135956]		Q6VMN6	7.5	4.2E-05	7.9	1.4E-04	0.3	8.5E-01	-0.5	4.2E-01
ENSMUST00000051293	G protein-coupled receptor 146 [Source:MGI Symbol;Acc:MGI:1933113]		Q99LE2	-7.9	1.5E-04	5.4	2.8E-03	0.0	9.9E-01	0.4	5.9E-01
ENSMUST00000051297	transition protein 2 [Source:MGI Symbol;Acc:MGI:98785]	Q91XK4		6.5	1.1E-03	7.5	2.5E-04	-0.2	9.0E-01	-0.5	5.1E-01
ENSMUST00000051301	purine rich element binding protein A [Source:MGI Symbol;Acc:MGI:103079]		P42669	1.7	3.7E-03	4.2	9.6E-02	-0.2	9.4E-01	0.7	6.7E-01
ENSMUST00000051308	MICAL C-terminal like [Source:MGI Symbol;Acc:MGI:1918127]		Q9D5U9	6.9	1.3E-02	5.7	2.8E-03	-0.4	8.0E-01	-1.0	2.6E-01
ENSMUST00000051330	RIKEN cDNA D830039M14 gene [Source:MGI Symbol;Acc:MGI:2445111]	Q8BG14		5.3	2.0E-04	5.4	1.2E-03	0.9	4.3E-01	0.0	9.7E-01
ENSMUST00000050735	zinc finger protein 260 [Source:MGI Symbol;Acc:MGI:1347071]		Q62513	3.3	1.7E-01	1.7	5.5E-01	-0.4	8.8E-01	1.2	6.1E-01
ENSMUST00000050753	RIKEN cDNA A930002H24 gene [Source:MGI Symbol;Acc:MGI:2443151]	Q8C8Y3		1.7	8.7E-02	1.7	9.5E-02	-1.2	1.9E-01	-1.2	1.9E-01
ENSMUST00000051341	major facilitator superfamily domain containing 5 [Source:MGI Symbol;Acc:MGI:2145901]		Q921Y4	-3.6	6.8E-04	8.0	5.5E-05	-0.6	6.0E-01	-0.5	3.7E-01
ENSMUST00000051356	thymoma viral proto-oncogene 2 [Source:MGI Symbol;Acc:MGI:104874]	Q3TY95	Q60823	-6.7	1.0E-03	6.7	4.4E-04	-1.4	3.2E-01	0.2	7.7E-01
ENSMUST00000051358	F-box and leucine-rich repeat protein 13 [Source:MGI Symbol;Acc:MGI:2443416]		Q8CDU4	5.7	4.4E-04	7.4	4.0E-04	-0.7	6.7E-01	0.2	8.0E-01
ENSMUST00000051364	gem (nuclear organelle) associated protein 7 [Source:MGI Symbol;Acc:MGI:1916981]		Q9CWY4	-7.7	1.6E-05	-10.3	1.1E-03	1.5	1.6E-02	1.1	6.3E-01
ENSMUST00000051377	dpy-19-like 3 (C. elegans) [Source:MGI Symbol;Acc:MGI:2443952]		Q71B07	1.4	1.9E-02	6.6	3.0E-04	-0.6	6.2E-01	-0.5	4.5E-01
ENSMUST00000051379	mitochondrial tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2142572]			-8.8	4.4E-06	4.7	8.1E-04	-2.0	8.1E-02	-0.2	7.4E-01
ENSMUST00000051390	zinc finger and BTB domain containing 45 [Source:MGI Symbol;Acc:MGI:2685003]	Q52KG4		-3.6	1.4E-02	7.7	9.6E-03	-0.7	7.8E-01	-2.2	1.4E-01
ENSMUST00000051395	proline rich 11 [Source:MGI Symbol;Acc:MGI:2444496]		Q8BHE0	1.8	3.8E-03	7.3	2.2E-04	-0.5	7.0E-01	0.2	7.8E-01
ENSMUST00000051396	sterol O-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:104665]		Q61263	-9.7	8.0E-05	-10.0	6.0E-06	0.1	8.6E-01	-0.7	5.5E-01
ENSMUST00000050797	E26 avian leukemia oncogene 1, 5' domain [Source:MGI Symbol;Acc:MGI:95455]	E9PWI8		1.0	6.1E-01	-2.9	2.2E-01	-3.0	7.4E-02	0.9	7.1E-01
ENSMUST00000050826	tet methylcytosine dioxygenase 1 [Source:MGI Symbol;Acc:MGI:1098693]		Q3URK3	1.4	5.2E-01	1.7	5.3E-01	-0.3	8.9E-01	-0.6	8.0E-01
ENSMUST00000051401	claudin 4 [Source:MGI Symbol;Acc:MGI:1313314]	Q3UM35	O35054	8.0	3.2E-05	5.1	1.4E-02	-0.6	7.5E-01	1.0	3.7E-01
ENSMUST00000051430	MARVEL (membrane-associating) domain containing 3 [Source:MGI Symbol;Acc:MGI:1920858]	G3X9A4		7.1	8.1E-05	-4.5	9.9E-03	1.5	3.0E-02	0.0	9.9E-01
ENSMUST00000051431	F-box protein 28 [Source:MGI Symbol;Acc:MGI:1261890]		Q8BIG4	-2.1	4.1E-03	-0.6	3.9E-01	0.8	1.3E-01	-0.1	8.8E-01
ENSMUST00000051435	zinc finger protein 418 [Source:MGI Symbol;Acc:MGI:2444763]	Q8BFS8		4.1	2.1E-03	4.2	1.4E-04	-6.2	1.6E-04	-1.5	1.7E-02
ENSMUST00000051442	protocadherin beta 16 [Source:MGI Symbol;Acc:MGI:2136752]	Q91Y03		9.0	8.1E-06	-0.3	7.6E-01	1.6	3.5E-02	-1.4	1.6E-01
ENSMUST00000050880	solute carrier family 26, member 11 [Source:MGI Symbol;Acc:MGI:2444589]		Q80ZD3	-1.6	6.0E-02	-0.3	7.3E-01	0.6	3.8E-01	-0.7	4.6E-01
ENSMUST00000051443	synaptopodin 2 [Source:MGI Symbol;Acc:MGI:2153070]		Q91YE8	8.4	1.3E-05	-0.9	3.3E-01	1.0	1.0E-01	-0.2	7.9E-01
ENSMUST00000051454	family with sequence similarity 171, member B [Source:MGI Symbol;Acc:MGI:2444579]		Q14CH0	7.7	3.5E-05	0.4	5.3E-01	-1.3	3.7E-02	0.3	5.7E-01
ENSMUST00000051477	cell division cycle 42 [Source:MGI Symbol;Acc:MGI:106211]		P60766	-7.5	4.3E-07	7.7	2.6E-05	-0.9	4.1E-01	-0.4	4.0E-01
ENSMUST00000051482	potassium voltage-gated channel, subfamily G, member 3 [Source:MGI Symbol;Acc:MGI:2663923]		P59053	7.9	4.7E-05	6.3	6.8E-04	-1.5	2.9E-01	0.4	6.0E-01
ENSMUST00000051484	melanoma antigen, family H, 1 [Source:MGI Symbol;Acc:MGI:1922875]	Q3UKU3	Q9NWG9	4.9	9.5E-03	4.2	4.2E-03	-0.6	5.6E-01	0.8	2.5E-01
ENSMUST00000051504	extracellular matrix protein 2, female organ and adipocyte specific [Source:MGI Symbol;Acc:MGI:3039578]		Q5FW85	6.0	5.9E-06	6.4	9.3E-04	-0.7	6.5E-01	1.1	1.7E-01
ENSMUST00000051509	tubulin tyrosine ligase-like family, member 10 [Source:MGI Symbol;Acc:MGI:1921855]	B1ASM0		7.0	1.1E-03	7.4	2.6E-04	-1.3	3.6E-01	-0.6	3.6E-01
ENSMUST00000051558	chromodomain helicase DNA binding protein 7 [Source:MGI Symbol;Acc:MGI:2444748]		A2AJK6	-3.7	1.4E-03	2.9	6.0E-03	-1.4	1.0E-01	0.2	7.3E-01
ENSMUST00000050909	adhesion molecule with Ig like domain 1 [Source:MGI Symbol;Acc:MGI:2653612]		Q80ZD8	1.9	2.8E-01	4.2	4.7E-02	-0.2	9.2E-01	-2.4	1.5E-01
ENSMUST00000051565	unc-51-like kinase 4 [Source:MGI Symbol;Acc:MGI:1921622]	H7BX20		6.7	4.1E-04	2.1	9.9E-03	0.2	6.7E-01	-0.1	8.8E-01
ENSMUST00000051569	paraneoplastic antigen family 5 [Source:MGI Symbol;Acc:MGI:2180566]		Q5DTT8	6.6	3.7E-04	5.8	9.5E-05	-1.8	1.0E-01	-0.3	6.5E-01
ENSMUST00000051572	serum deprivation response [Source:MGI Symbol;Acc:MGI:99513]		Q63918	4.8	7.0E-04	7.2	1.7E-04	-0.6	6.4E-01	-0.4	5.2E-01
ENSMUST00000051589	noadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase [Source:MGI Symbol;Acc:MGI:1914		Q9CQF6	1.3	8.8E-03	6.3	9.2E-04	-0.4	7.7E-01	-1.1	1.7E-01
ENSMUST00000051594	DEP domain containing 1B [Source:MGI Symbol;Acc:MGI:2145425]		Q8BH88	-2.0	3.7E-03	5.6	1.0E-03	-0.5	6.6E-01	-0.4	5.5E-01
ENSMUST00000051605	deoxyuridine triphosphatase [Source:MGI Symbol;Acc:MGI:1346051]	Q9CQ43		2.5	1.2E-02	5.3	4.5E-03	-0.5	7.5E-01	-2.2	5.1E-02
ENSMUST00000050949	transmembrane and coiled-coil domains 4 [Source:MGI Symbol;Acc:MGI:1924306]		Q91WU4	-2.4	1.7E-01	-0.7	7.2E-01	1.6	2.9E-01	-0.1	9.7E-01
ENSMUST00000051614	a disintegrin and metallopeptidase domain 24 (testase 1) [Source:MGI Symbol;Acc:MGI:105984]		Q9R160	7.4	2.2E-04	2.3	8.3E-03	-3.0	2.4E-03	-0.1	8.2E-01
ENSMUST00000051620	cytochrome b5 domain containing 1 [Source:MGI Symbol;Acc:MGI:2685586]		Q5NCY3	-2.7	2.4E-02	4.9	3.0E-04	-1.6	9.5E-02	-0.2	7.6E-01
ENSMUST00000051667	zinc finger protein 105 [Source:MGI Symbol;Acc:MGI:1277119]	G3X9I0		4.2	5.3E-04	5.6	1.8E-03	-0.5	7.4E-01	-0.5	5.0E-01
ENSMUST00000051674	lin-28 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:1890546]		Q8K3Y3	-3.3	7.7E-04	3.7	4.1E-03	-0.7	4.2E-01	-0.9	2.7E-01
ENSMUST00000051676	family with sequence similarity 46, member B [Source:MGI Symbol;Acc:MGI:2140500]		Q8C152	7.1	1.0E-04	-2.9	3.2E-04	-0.5	1.2E-01	-0.7	1.9E-01
ENSMUST00000051687	predicted gene 1840 [Source:MGI Symbol;Acc:MGI:3037698]	F6SAC3		-3.2	1.2E-03	7.0	4.2E-05	0.3	7.9E-01	-0.3	5.7E-01
ENSMUST00000051691	STE20-like kinase [Source:MGI Symbol;Acc:MGI:103241]		O54988	-6.6	1.3E-03	7.6	3.8E-05	-0.6	5.9E-01	-0.6	2.8E-01
ENSMUST00000051704	citron [Source:MGI Symbol;Acc:MGI:105313]	E9QL53		4.2	5.6E-05	-4.7	4.3E-03	1.3	4.3E-02	-0.1	9.4E-01
ENSMUST00000051705	potassium voltage-gated channel, Isk-related subfamily, member 1 [Source:MGI Symbol;Acc:MGI:96673]	Q545H6	P23299	7.6	4.5E-05	0.2	8.2E-01	0.2	7.8E-01	-4.8	3.7E-03
ENSMUST00000051706	DDI1, DNA-damage inducible 1, homolog 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919079]		Q9DAF3	6.9	6.5E-05	-3.9	4.5E-02	0.8	3.1E-01	-0.2	9.3E-01
ENSMUST00000051714	cDNA sequence BC049730 [Source:MGI Symbol;Acc:MGI:2681843]	Q810N3		4.6	4.0E-04	8.8	1.3E-05	-0.6	5.9E-01	-0.6	2.4E-01
ENSMUST00000051720	SH3 domain and tetratricopeptide repeats 2 [Source:MGI Symbol;Acc:MGI:2444417]		Q80VA5	8.1	3.0E-05	-7.4	3.2E-03	0.8	1.7E-01	-0.5	8.0E-01
ENSMUST00000051754	protocadherin beta 3 [Source:MGI Symbol;Acc:MGI:2136737]	Q91XZ7		8.1	2.6E-05	5.3	2.0E-04	-0.8	3.8E-01	-0.2	7.7E-01
ENSMUST00000051756	interleukin 31 receptor A [Source:MGI Symbol;Acc:MGI:2180511]		Q8K5B1	7.1	3.3E-05	4.4	2.9E-03	1.7	1.2E-01	0.2	8.3E-01
ENSMUST00000051053	ubiquitin domain containing 2 [Source:MGI Symbol;Acc:MGI:2444752]		Q6PGH0	2.2	3.9E-02	1.7	1.6E-01	-0.5	5.9E-01	0.0	9.8E-01
ENSMUST00000051757	solute carrier family 26 (sulfate transporter), member 1 [Source:MGI Symbol;Acc:MGI:2385894]	Q3UPH6	P58735	7.3	5.1E-03	0.9	1.9E-01	-4.0	5.0E-04	-0.8	1.8E-01
ENSMUST00000051765	glucagon-like peptide 2 receptor [Source:MGI Symbol;Acc:MGI:2136733]		Q5IXF8	8.6	2.3E-05	5.3	7.7E-04	-1.2	2.7E-01	1.0	1.6E-01
ENSMUST00000051772	MORN repeat containing 4 [Source:MGI Symbol;Acc:MGI:2449568]		Q6PGF2	7.2	1.7E-04	7.6	1.3E-04	-0.2	9.0E-01	-0.5	4.3E-01
ENSMUST00000051773	one cut domain, family member 3 [Source:MGI Symbol;Acc:MGI:1891409]		Q8K557	7.0	3.2E-06	4.0	7.3E-03	-1.5	2.5E-01	-2.3	4.3E-02
ENSMUST00000051089				-0.6	4.0E-01	0.8	3.6E-01	0.6	3.7E-01	-0.8	3.3E-01
ENSMUST00000051777	C2 calcium-dependent domain containing 3 [Source:MGI Symbol;Acc:MGI:2142166]		Q52KB6	-1.9	2.1E-03	-1.2	5.0E-01	1.0	3.9E-01	-2.7	2.0E-01
ENSMUST00000051803	aldehyde dehydrogenase 3 family, member B1 [Source:MGI Symbol;Acc:MGI:1914939]	Q3TX25	Q80VQ0	-6.1	4.3E-06	-6.2	3.6E-05	0.1	7.7E-01	2.3	1.8E-02
ENSMUST00000051806	deoxynucleotidyltransferase, terminal [Source:MGI Symbol;Acc:MGI:98659]		P09838	7.5	2.3E-05	6.6	1.5E-04	-0.5	6.5E-01	-0.6	3.5E-01
ENSMUST00000051809	myc target 1 [Source:MGI Symbol;Acc:MGI:1915882]		Q8R411	2.0	7.4E-03	-2.8	4.6E-03	0.1	9.0E-01	-1.7	6.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000051822	WD repeat domain 61 [Source:MGI Symbol;Acc:MGI:1917493]	A0MNP4	Q9ERF3	-6.6	4.4E-04	4.1	2.0E-03	0.0	9.8E-01	-0.3	7.2E-01
ENSMUST00000051839	hepatocyte cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1920177]	B2RSY3	Q640R3	8.9	6.2E-06	5.1	2.6E-04	-0.7	4.4E-01	-0.3	6.5E-01
ENSMUST00000051857	insulinoma-associated 2 [Source:MGI Symbol;Acc:MGI:1930787]		Q9JMC2	7.4	2.4E-05	7.7	7.3E-05	-0.6	6.1E-01	-0.2	7.5E-01
ENSMUST00000051864	somatostatin receptor 5 [Source:MGI Symbol;Acc:MGI:894282]		O08858	7.4	4.9E-03	2.9	6.3E-04	0.9	8.1E-02	-0.3	4.6E-01
ENSMUST00000051867	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925901]	Q542U7	P62313	-3.9	7.3E-04	4.8	1.9E-02	-0.6	7.5E-01	1.2	2.7E-01
ENSMUST00000051873	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 [Source:MGI Symbol;Acc:MGI:2687284]		Q6DTY7	-5.4	3.8E-06	6.6	1.6E-03	-0.4	8.1E-01	-1.5	1.1E-01
ENSMUST00000051139	rosbin, round spermatid basic protein 1 [Source:MGI Symbol;Acc:MGI:2444993]		Q80T69	-2.0	3.7E-02	-1.6	1.9E-01	0.4	5.9E-01	0.0	9.7E-01
ENSMUST00000051145	WD repeat domain 47 [Source:MGI Symbol;Acc:MGI:2139593]		Q8CGF6	-0.5	4.1E-01	0.2	7.3E-01	0.2	6.6E-01	-0.5	4.8E-01
ENSMUST00000051153	RIKEN cDNA 3300002I08 gene [Source:MGI Symbol;Acc:MGI:1916527]	Q9CXH3		3.0	1.1E-01	5.1	1.7E-02	-0.4	8.4E-01	-2.5	8.5E-02
ENSMUST00000051160	glycoprotein Ib, beta polypeptide [Source:MGI Symbol;Acc:MGI:107852]	B2RR03		1.4	1.8E-01	4.8	1.5E-03	0.5	6.5E-01	-2.9	6.6E-03
ENSMUST00000051888	BLOC-1 related complex subunit 6 [Source:MGI Symbol;Acc:MGI:1919173]		Q9D6W8	-3.0	1.3E-03	6.9	4.0E-05	-1.9	9.3E-02	0.1	7.9E-01
ENSMUST00000051169	erythroid differentiation regulatory factor 1 [Source:MGI Symbol;Acc:MGI:1919831]	E9Q9F9		1.4	3.6E-02	1.2	1.5E-01	0.5	4.5E-01	0.7	3.4E-01
ENSMUST00000051171				-3.3	4.6E-02	-1.9	3.0E-01	0.7	5.2E-01	-0.7	7.3E-01
ENSMUST00000051906	A kinase (PRKA) anchor protein 17B [Source:MGI Symbol;Acc:MGI:2443758]		A2A3V1	2.0	6.3E-03	5.1	2.6E-04	-1.3	1.8E-01	-1.0	1.2E-01
ENSMUST00000051907	spermatogenesis associated 21 [Source:MGI Symbol;Acc:MGI:3607787]		Q8BHW6	8.1	2.7E-05	6.1	1.6E-04	0.6	5.3E-01	0.6	2.7E-01
ENSMUST00000051925	peroxiredoxin 6 [Source:MGI Symbol;Acc:MGI:894320]	D3Z0Y2		-3.5	1.0E-02	-3.5	4.6E-05	0.5	7.5E-02	-0.4	4.0E-01
ENSMUST00000051934	GSK3B interacting protein [Source:MGI Symbol;Acc:MGI:1914037]	Q3TBR1	Q8BGR8	-2.5	6.8E-04	6.4	5.0E-04	-0.6	6.2E-01	-0.3	7.0E-01
ENSMUST00000051207	solute carrier family 35, member E4 [Source:MGI Symbol;Acc:MGI:2144150]			-1.5	2.6E-01	-5.6	8.1E-02	0.5	6.8E-01	4.5	1.4E-01
ENSMUST00000051937	RAS-like, family 11, member B [Source:MGI Symbol;Acc:MGI:1916189]		Q922H7	4.1	3.2E-04	7.9	1.1E-05	-2.2	6.7E-02	0.4	4.2E-01
ENSMUST00000051943	olfactory receptor 524 [Source:MGI Symbol;Acc:MGI:3030358]	Q7TRU0		6.5	1.5E-04	-1.8	3.6E-01	2.5	5.6E-02	1.3	4.7E-01
ENSMUST00000051950	ataxin 2 [Source:MGI Symbol;Acc:MGI:1277223]	E9QM77		-3.5	1.2E-02	8.6	2.8E-05	-0.6	6.0E-01	-0.3	5.9E-01
ENSMUST00000051955	ribosomal protein S23 [Source:MGI Symbol;Acc:MGI:1913725]		P62267	-7.9	1.7E-04	6.6	1.9E-02	0.2	9.2E-01	-1.5	3.7E-01
ENSMUST00000051973	pregnancy-specific glycoprotein 22 [Source:MGI Symbol;Acc:MGI:1891354]	Q810J1		5.6	6.7E-04	-6.6	7.8E-03	1.0	1.5E-01	1.1	5.9E-01
ENSMUST00000051982	olfactory receptor 1349 [Source:MGI Symbol;Acc:MGI:3031183]	Q7TQV1		7.0	2.8E-04	4.2	1.3E-03	-0.5	6.2E-01	-0.3	6.2E-01
ENSMUST00000051995	Janus kinase 3 [Source:MGI Symbol;Acc:MGI:99928]			-5.4	2.3E-03	-4.4	4.3E-02	1.7	9.5E-02	-0.6	7.6E-01
ENSMUST00000052011	transducin-like enhancer of split 4, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104633]		Q62441	-3.8	6.9E-03	-4.4	9.6E-03	1.1	9.4E-02	1.9	1.7E-01
ENSMUST00000052027	predicted gene 12794 [Source:MGI Symbol;Acc:MGI:3795847]	L7MTS5		6.8	9.2E-05	-2.5	1.7E-02	0.9	9.0E-02	-0.4	6.6E-01
ENSMUST00000052060	mannan-binding lectin serine peptidase 2 [Source:MGI Symbol;Acc:MGI:1330832]		Q91WP0	7.4	8.4E-05	-9.8	1.8E-03	0.8	1.9E-01	1.1	6.4E-01
ENSMUST00000052068	retinol binding protein 1, cellular [Source:MGI Symbol;Acc:MGI:97876]	Q58EU7	Q00915	5.1	8.4E-04	5.8	9.5E-04	-1.8	2.1E-01	0.6	4.6E-01
ENSMUST00000052069	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 [Source:MGI Symbol;Acc:MGI:		Q8C7U7	-4.7	7.1E-05	6.8	1.8E-04	-0.6	6.2E-01	0.2	7.6E-01
ENSMUST00000052072	transmembrane protein 221 [Source:MGI Symbol;Acc:MGI:3525074]		Q8K071	4.8	6.6E-05	-8.3	5.3E-03	1.2	8.3E-02	1.6	5.1E-01
ENSMUST00000052079	PML-RAR alpha-regulated adaptor molecule 1 [Source:MGI Symbol;Acc:MGI:3576625]		Q6BCL1	-7.4	6.8E-04	6.0	3.3E-03	-0.7	6.7E-01	-0.2	8.4E-01
ENSMUST00000052104	a disintegrin and metalloppeptidase domain 33 [Source:MGI Symbol;Acc:MGI:1341813]	A2AP51	Q923W9	6.6	3.3E-04	1.5	3.7E-02	0.5	3.6E-01	0.7	1.8E-01
ENSMUST00000052120	WD repeat domain 3 [Source:MGI Symbol;Acc:MGI:2443143]		Q8BHB4	-4.5	5.4E-05	6.9	1.9E-02	-0.9	7.4E-01	-0.9	5.6E-01
ENSMUST00000051310	DDHD domain containing 1 [Source:MGI Symbol;Acc:MGI:2150302]	F8WHP5		-0.4	6.4E-01	0.8	4.5E-01	-0.3	7.1E-01	-1.5	1.5E-01
ENSMUST00000052124	NLR family, CARD domain containing 4 [Source:MGI Symbol;Acc:MGI:3036243]		Q3UP24	2.6	1.2E-03	7.1	3.7E-04	1.4	2.8E-01	-0.4	5.5E-01
ENSMUST00000052125	par-6 family cell polarity regulator beta [Source:MGI Symbol;Acc:MGI:2135605]		Q9JK83	8.2	6.1E-06	-2.1	3.5E-02	0.8	1.2E-01	-0.7	4.7E-01
ENSMUST00000052135	retinoblastoma binding protein 6 [Source:MGI Symbol;Acc:MGI:894835]		P97868	-1.7	1.3E-03	-4.2	2.6E-02	1.0	2.5E-01	-1.4	4.3E-01
ENSMUST00000052138	telomeric repeat binding factor 2, interacting protein [Source:MGI Symbol;Acc:MGI:1929871]		Q91VL8	1.7	9.1E-03	4.8	1.1E-03	-1.7	1.7E-01	-0.8	3.0E-01
ENSMUST00000051363				0.5	4.9E-01	1.7	1.8E-01	2.1	4.7E-02	0.9	3.6E-01
ENSMUST00000052164	neuropeptide Y receptor Y4 [Source:MGI Symbol;Acc:MGI:105374]		Q61041	8.4	2.1E-05	-5.9	7.2E-04	1.1	2.9E-02	-0.8	5.7E-01
ENSMUST00000052167	G patch domain and ankyrin repeats 1 [Source:MGI Symbol;Acc:MGI:2148975]		Q61858	-5.3	1.1E-03	2.3	5.2E-03	0.2	7.3E-01	-0.7	2.0E-01
ENSMUST00000052172	chemokine (C-X-C motif) receptor 4 [Source:MGI Symbol;Acc:MGI:109563]			-5.6	3.3E-04	-6.6	1.1E-04	0.4	3.9E-01	-1.9	1.2E-01
ENSMUST00000051389	synemin, intermediate filament protein [Source:MGI Symbol;Acc:MGI:2661187]		Q70IV5	-0.7	7.4E-01	1.5	5.7E-01	1.9	4.0E-01	-0.3	9.0E-01
ENSMUST00000052174	phosphatidylinositol glycan anchor biosynthesis, class Z [Source:MGI Symbol;Acc:MGI:2443822]		Q8BTP0	6.0	2.4E-04	-3.1	1.2E-01	1.7	8.6E-02	1.2	5.1E-01
ENSMUST00000052179	protocadherin beta 20 [Source:MGI Symbol;Acc:MGI:2136758]	Q91XZ9		8.0	1.5E-04	3.8	2.9E-04	1.9	9.3E-03	-0.2	6.8E-01
ENSMUST00000052183	Smad nuclear interacting protein 1 [Source:MGI Symbol;Acc:MGI:2156003]		Q8BIZ6	-2.1	2.5E-03	-6.8	4.7E-03	2.2	5.7E-03	-0.7	7.2E-01
ENSMUST00000052185	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6 [Source:MGI Symbol;Acc:MGI:2152819]		Q91Z92	4.0	9.8E-05	6.0	2.4E-04	-1.9	1.3E-01	0.1	8.7E-01
ENSMUST00000051416	histamine N-methyltransferase [Source:MGI Symbol;Acc:MGI:2153181]	A2AQK4	Q91VF2	-5.8	4.3E-02	-2.5	4.5E-01	1.9	3.4E-01	-1.4	6.8E-01
ENSMUST00000052201	MIS18 binding protein 1 [Source:MGI Symbol;Acc:MGI:2145099]		Q80WQ8	-3.0	1.8E-02	7.7	1.0E-04	-0.1	9.2E-01	-0.7	2.6E-01
ENSMUST00000052204	on imprinted in Prader-Willi/Angelman syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:244205		Q8BHK1	6.2	5.1E-06	-0.7	3.0E-01	0.9	8.4E-02	-0.5	5.1E-01
ENSMUST00000052211	zinc and ring finger 4 [Source:MGI Symbol;Acc:MGI:1341258]	Q9DAH2		5.5	1.2E-03	3.5	8.5E-03	-1.3	2.1E-01	-0.7	4.4E-01
ENSMUST00000052224	prosaposin-like 1 [Source:MGI Symbol;Acc:MGI:1924193]			8.4	9.2E-06	8.1	2.8E-05	-0.5	6.8E-01	0.5	3.5E-01
ENSMUST00000052248	eukaryotic translation elongation factor 1 gamma [Source:MGI Symbol;Acc:MGI:1914410]	Q4FZK2	Q9D8N0	-5.6	1.2E-03	7.0	2.7E-05	-1.9	1.0E-01	-0.4	4.1E-01
ENSMUST00000052254	olfactory receptor 410 [Source:MGI Symbol;Acc:MGI:3030244]	Q8VFX7		6.0	3.5E-04	6.0	2.1E-04	-1.7	1.6E-01	0.1	9.3E-01
ENSMUST00000052258	serine dehydratase-like [Source:MGI Symbol;Acc:MGI:2182607]		Q8R238	2.2	2.2E-02	-6.4	1.1E-05	0.6	7.9E-02	-0.5	5.4E-01
ENSMUST00000052277	IQ motif and ubiquitin domain containing [Source:MGI Symbol;Acc:MGI:3041159]		Q8CDK3	6.7	6.9E-05	6.3	2.2E-04	-2.0	1.3E-01	-0.3	5.7E-01
ENSMUST00000052281	RIKEN cDNA E130012A19 gene [Source:MGI Symbol;Acc:MGI:2143991]		Q7TNS8	2.4	5.9E-03	3.6	4.4E-02	-1.7	3.2E-01	-0.4	7.1E-01
ENSMUST00000051490	idnK gluconokinase homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1922981]		Q8R0J8	-3.0	7.6E-02	-2.5	2.1E-01	0.1	9.4E-01	-0.4	8.5E-01
ENSMUST00000052283	melanoma antigen family B, 16 [Source:MGI Symbol;Acc:MGI:1919217]		Q9CWV4	5.9	1.1E-02	5.7	5.2E-04	-1.2	3.3E-01	-0.7	3.1E-01
ENSMUST00000052296	parathyroid hormone-like peptide [Source:MGI Symbol;Acc:MGI:97800]	Q924X4		8.5	9.9E-05	5.2	6.6E-05	-0.2	8.2E-01	0.6	2.3E-01
ENSMUST00000052325	RAN binding protein 1 [Source:MGI Symbol;Acc:MGI:96269]	H7BX22		-2.3	8.9E-03	5.8	5.9E-03	-0.5	7.7E-01	0.6	5.2E-01
ENSMUST00000051540	olfactory receptor 460 [Source:MGI Symbol;Acc:MGI:3030294]	Q8VF31		4.8	4.4E-02	6.5	2.9E-02	0.5	8.4E-01	-1.1	4.7E-01
ENSMUST00000052342	RIKEN cDNA D930015E06 gene [Source:MGI Symbol;Acc:MGI:2443399]	A0A0B4J1F5		-7.2	8.5E-04	-2.1	5.8E-02	0.8	2.1E-01	-0.7	4.9E-01
ENSMUST00000052346	lethal giant larvae homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:102682]			-4.8	1.5E-03	6.7	7.9E-04	-0.4	7.7E-01	-0.4	5.7E-01
ENSMUST00000052366	protocadherin beta 1 [Source:MGI Symbol;Acc:MGI:2136730]	Q91Y08		7.7	4.0E-05	6.6	6.8E-04	-0.6	6.7E-01	-0.6	4.4E-01
ENSMUST00000052374	RAN GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:103071]		P46061	-4.0	3.2E-02	-0.7	4.1E-01	-5.6	1.3E-04	0.0	9.9E-01
ENSMUST00000052387	protocadherin beta 14 [Source:MGI Symbol;Acc:MGI:2136749]		Q6PB90	9.2	2.2E-07	1.6	7.3E-03	-0.2	5.8E-01	-0.5	2.3E-01
ENSMUST00000052396	ring finger protein 138 [Source:MGI Symbol;Acc:MGI:1929211]		Q9CQE0	-5.4	1.7E-04	-0.1	8.8E-01	1.8	4.7E-03	-0.2	8.2E-01
ENSMUST00000052404	erythrocyte membrane protein band 4.1 like 5 [Source:MGI Symbol;Acc:MGI:103006]		Q8BGS1	9.5	3.1E-06	2.2	4.1E-02	-0.5	5.8E-01	-0.1	8.6E-01
ENSMUST00000052413	lymphocyte cytosolic protein 2 [Source:MGI Symbol;Acc:MGI:1321402]	B1ATD2		2.7	4.9E-05	5.5	2.9E-03	-0.7	6.4E-01	1.2	1.8E-01
ENSMUST00000052416	LKAAEAR motif containing 1 (IKAAEAR murine motif) [Source:MGI Symbol;Acc:MGI:2685538]		Q8BIG2	6.4	4.8E-04	-1.4	2.9E-01	0.6	4.3E-01	-0.7	5.8E-01
ENSMUST00000051633	UbiA prenyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:1918957]		Q9DC60	-0.4	5.3E-01	0.5	5.4E-01	1.1	7.9E-02	0.2	7.4E-01
ENSMUST00000051665	zinc finger protein 316 [Source:MGI Symbol;Acc:MGI:1860402]	G3XA34		7.3	5.7E-02	3.4	4.2E-01	0.2	9.6E-01	4.1	1.8E-01
ENSMUST00000052437	leucine rich repeat containing 25 [Source:MGI Symbol;Acc:MGI:2445284]	B9EHD0	Q8K1T1	-4.7	4.0E-04	3.3	3.8E-03	-0.7	4.1E-01	0.2	7.3E-01
ENSMUST00000051672	bone marrow stromal cell antigen 2 [Source:MGI Symbol;Acc:MGI:1916800]		Q8R2Q8	-1.2	7.1E-02	-3.5	1.0E-03	-1.9	2.7E-03	0.4	5.6E-01
ENSMUST00000052438	cytochrome b5 reductase 2 [Source:MGI Symbol;Acc:MGI:2444415]		Q3KNK3	7.3	5.7E-05	-1.3	1.7E-01	1.9	6.5E-03	-0.1	9.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000052441	solute carrier family 17 (anion/sugar transporter), member 5 [Source:MGI Symbol;Acc:MGI:1924105]		Q8BN82	-4.1	8.7E-03	5.4	8.9E-04	-1.9	1.6E-01	-0.1	9.1E-01
ENSMUST00000052448	potassium channel, subfamily K, member 7 [Source:MGI Symbol;Acc:MGI:1341841]	Q9JJ14		2.9	8.1E-03	-0.9	3.0E-01	1.3	3.1E-02	-1.0	2.7E-01
ENSMUST00000052449	ubinuclein 1 [Source:MGI Symbol;Acc:MGI:1891307]		Q4G0F8	-2.3	6.5E-04	-5.4	8.0E-03	0.4	6.3E-01	-0.9	6.5E-01
ENSMUST00000051698	lymphocyte antigen 6 complex, locus E [Source:MGI Symbol;Acc:MGI:106651]	Q99JA5		3.4	1.4E-01	-0.2	9.6E-01	-1.1	6.3E-01	2.5	4.2E-01
ENSMUST00000052457	metastasis suppressor 1-like [Source:MGI Symbol;Acc:MGI:3039591]		Q6P9S0	6.4	3.7E-04	6.0	1.1E-04	2.5	1.5E-02	0.7	2.4E-01
ENSMUST00000052458	leucine rich repeat containing 38 [Source:MGI Symbol;Acc:MGI:2442845]		A2VDH3	6.1	2.1E-04	7.1	1.5E-04	-0.6	6.3E-01	-0.1	8.4E-01
ENSMUST00000052472	gephyrin [Source:MGI Symbol;Acc:MGI:109602]		Q8BUV3	6.8	1.6E-03	6.7	1.7E-04	-0.6	6.1E-01	-0.3	5.9E-01
ENSMUST00000052478	doublesex and mab-3 related transcription factor like family A1 [Source:MGI Symbol;Acc:MGI:2653627]		Q8CFG4	7.8	1.1E-04	5.3	2.4E-04	-0.7	4.7E-01	-1.4	4.6E-02
ENSMUST00000052501	family with sequence similarity 69, member C [Source:MGI Symbol;Acc:MGI:3041188]		Q8BQT2	8.7	8.3E-05	4.7	1.8E-04	-3.8	4.8E-03	-0.4	4.9E-01
ENSMUST00000051737	adaptor-related protein complex 1 associated regulatory protein [Source:MGI Symbol;Acc:MGI:2384822]	E9PYF7		1.0	1.1E-01	-0.4	6.2E-01	-0.6	2.6E-01	0.7	3.1E-01
ENSMUST00000052505	transmembrane protein 186 [Source:MGI Symbol;Acc:MGI:1913940]	Q78HW2	Q9CR76	1.3	3.2E-02	7.6	8.2E-05	-0.6	6.1E-01	-0.2	7.3E-01
ENSMUST00000052521	growth arrest-specific 2 like 2 [Source:MGI Symbol;Acc:MGI:3652048]		Q5SSG4	8.8	1.6E-03	5.8	2.6E-04	-1.3	2.6E-01	0.0	9.7E-01
ENSMUST00000052529	protein phosphatase 1, regulatory (inhibitor) subunit 15b [Source:MGI Symbol;Acc:MGI:2444211]		Q8BFW3	-3.8	2.1E-06	7.3	5.5E-03	-1.3	5.8E-01	-1.3	3.4E-01
ENSMUST00000051758	vitamin K epoxide reductase complex, subunit 1-like 1 [Source:MGI Symbol;Acc:MGI:1916818]	Q0VGU5	Q6TEK5	-0.9	1.7E-01	0.4	6.6E-01	1.3	5.3E-02	0.1	9.5E-01
ENSMUST00000052550	low density lipoprotein-related protein 1B (deleted in tumors) [Source:MGI Symbol;Acc:MGI:2151136]	A2API5		7.9	2.2E-05	8.0	7.8E-05	-0.7	6.0E-01	-0.1	8.0E-01
ENSMUST00000052556	abhydrolase domain containing 17B [Source:MGI Symbol;Acc:MGI:1917816]		Q7M759	-4.5	2.2E-04	6.9	3.7E-04	-0.8	5.5E-01	-0.6	4.1E-01
ENSMUST00000052560	olfactory receptor 221 [Source:MGI Symbol;Acc:MGI:3030055]	B2RVX8		5.5	3.5E-04	5.4	5.0E-05	-1.0	2.0E-01	0.5	2.8E-01
ENSMUST00000052566	transmembrane protein 199 [Source:MGI Symbol;Acc:MGI:2144113]	B2RV69	Q5SYH2	-2.3	4.9E-03	-0.6	3.1E-01	0.8	5.4E-02	-0.5	4.1E-01
ENSMUST00000051784	FAST kinase domains 3 [Source:MGI Symbol;Acc:MGI:1916827]		Q8BSN9	0.1	8.0E-01	0.7	2.7E-01	0.1	9.2E-01	-0.6	3.6E-01
ENSMUST00000052580	piggyBac transposable element derived 5 [Source:MGI Symbol;Acc:MGI:2429955]	D3Z077		-2.8	2.6E-02	-4.8	1.6E-04	0.8	4.5E-02	-0.5	5.4E-01
ENSMUST00000052588	zinc finger protein 654 [Source:MGI Symbol;Acc:MGI:1919270]		Q9DAU9	-3.3	8.7E-04	2.3	8.9E-02	-0.6	6.1E-01	4.6	8.6E-04
ENSMUST00000052590	endoplasmic reticulum protein 29 [Source:MGI Symbol;Acc:MGI:1914647]	F8WJI4		-8.5	5.3E-06	0.2	7.7E-01	-1.3	3.8E-02	0.4	4.6E-01
ENSMUST00000052596	chibby homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1923903]	Z4YJN4		5.4	1.2E-02	-6.9	1.5E-03	-1.3	5.2E-02	-0.9	6.0E-01
ENSMUST00000052602	expressed sequence C77080 [Source:MGI Symbol;Acc:MGI:2140651]		A2A7S8	4.8	1.3E-02	6.6	4.0E-04	-0.1	9.2E-01	-0.3	6.3E-01
ENSMUST00000052605	carcinoembryonic antigen-related cell adhesion molecule 19 [Source:MGI Symbol;Acc:MGI:2443001]	Q3TQ88		6.3	9.2E-05	6.4	5.6E-05	-2.5	3.7E-02	0.0	9.8E-01
ENSMUST00000052609	distal-less homeobox 5 [Source:MGI Symbol;Acc:MGI:101926]	Q3TYA7	P70396	5.4	2.3E-02	7.3	5.3E-05	-0.5	6.3E-01	-0.4	4.5E-01
ENSMUST00000052622	RIKEN cDNA 1810011O10 gene [Source:MGI Symbol;Acc:MGI:1916318]		Q9D915	5.8	2.4E-04	5.6	3.3E-02	-0.6	8.1E-01	1.2	3.6E-01
ENSMUST00000052631	snail family zinc finger 1 [Source:MGI Symbol;Acc:MGI:98330]	Q4FK48	Q02085	-2.3	6.8E-03	-3.7	4.5E-03	0.0	9.2E-01	-0.1	8.9E-01
ENSMUST00000051870	chromosome alignment maintaining phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:1196398]		Q8K327	0.5	3.8E-01	1.3	8.3E-02	0.5	3.8E-01	-0.4	5.7E-01
ENSMUST00000052648	coiled-coil domain containing 28A [Source:MGI Symbol;Acc:MGI:2443508]	Q8CEI3		-2.1	1.1E-02	-4.1	1.7E-04	0.7	5.0E-02	-0.6	4.0E-01
ENSMUST00000052650	homeobox B8 [Source:MGI Symbol;Acc:MGI:96189]	A2A9Z8	P09632	6.5	2.4E-04	-2.7	1.6E-02	1.1	6.0E-02	0.7	4.8E-01
ENSMUST00000052652	retinol dehydrogenase 9 [Source:MGI Symbol;Acc:MGI:2143528]	Q8K5C8		7.7	1.4E-03	4.4	1.0E-04	1.0	1.3E-01	-1.3	2.9E-02
ENSMUST00000052659	olfactory receptor 648 [Source:MGI Symbol;Acc:MGI:3030482]	Q8VG19		5.5	3.6E-03	6.1	2.1E-04	-1.8	1.4E-01	0.1	8.4E-01
ENSMUST00000052668	olfactory receptor 1394 [Source:MGI Symbol;Acc:MGI:3031228]	Q8VET2		7.4	3.5E-04	-1.3	4.1E-01	1.6	1.3E-01	-0.6	7.0E-01
ENSMUST00000051929	Bmi1 polycomb ring finger oncogene [Source:MGI Symbol;Acc:MGI:88174]	Q2LC58	P25916	0.5	4.5E-01	-1.3	1.1E-01	-1.4	3.5E-02	0.4	6.0E-01
ENSMUST00000052670	APC membrane recruitment 3 [Source:MGI Symbol;Acc:MGI:3026939]		Q6NS69	8.1	2.0E-05	-2.4	4.3E-03	0.0	9.8E-01	0.0	9.7E-01
ENSMUST00000052678	filamin, beta [Source:MGI Symbol;Acc:MGI:2446089]		Q80X90	2.2	3.5E-04	2.9	4.9E-03	-1.0	1.9E-01	0.1	8.7E-01
ENSMUST00000052686	H2A histone family, member X [Source:MGI Symbol;Acc:MGI:102688]		P27661	-2.0	3.8E-03	6.6	2.4E-04	-0.5	6.6E-01	-0.7	3.1E-01
ENSMUST00000051947	NFKB inhibitor interacting Ras-like protein 2 [Source:MGI Symbol;Acc:MGI:1919216]		Q9CR56	-2.6	2.5E-01	-0.9	7.7E-01	1.7	3.7E-01	0.0	9.9E-01
ENSMUST00000052690	protease, serine 54 [Source:MGI Symbol;Acc:MGI:1918243]	A6H685		7.1	1.4E-04	0.8	4.2E-01	0.9	3.0E-01	-3.5	1.6E-02
ENSMUST00000052691	RIKEN cDNA 1600012H06 gene [Source:MGI Symbol;Acc:MGI:1915162]		Q9DAY5	-5.4	4.1E-04	-9.1	3.4E-04	-0.3	6.3E-01	0.9	6.1E-01
ENSMUST00000052699	suppressor of variegation 4-20 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444557]		Q3U8K7	8.6	1.1E-05	6.7	3.5E-04	-0.5	6.9E-01	-1.6	4.5E-02
ENSMUST00000052700	free fatty acid receptor 1 [Source:MGI Symbol;Acc:MGI:2684079]		Q76JU9	6.6	1.5E-04	6.6	7.9E-04	-0.7	6.5E-01	-0.2	7.6E-01
ENSMUST00000052702	cDNA sequence BC049715 [Source:MGI Symbol;Acc:MGI:3605234]		Q810N5	5.2	1.9E-04	-5.8	4.0E-02	1.2	2.0E-01	1.5	5.5E-01
ENSMUST00000051996	RAB11 family interacting protein 2 (class I) [Source:MGI Symbol;Acc:MGI:1922248]		G3XA57	2.3	1.1E-01	3.9	5.2E-02	1.3	4.1E-01	-0.3	8.2E-01
ENSMUST00000051997	H6 homeobox 2 [Source:MGI Symbol;Acc:MGI:107159]		P43687	3.6	5.6E-02	4.5	1.1E-02	-2.2	1.9E-01	-3.1	2.9E-02
ENSMUST00000052718	potassium voltage-gated channel, shaker-related subfamily, member 3 [Source:MGI Symbol;Acc:MGI:96660]		P16390	4.3	1.1E-04	-0.8	5.5E-01	2.1	5.5E-02	-0.9	5.2E-01
ENSMUST00000052018	nuclear factor I/A [Source:MGI Symbol;Acc:MGI:108056]	B1AUB9		5.8	1.0E-01	-0.6	8.3E-01	-5.8	8.5E-02	0.5	8.2E-01
ENSMUST00000052724	urocortin 2 [Source:MGI Symbol;Acc:MGI:2176375]		Q99ML8	5.8	3.3E-04	6.7	2.1E-04	-0.5	6.8E-01	-0.4	5.6E-01
ENSMUST00000052725	l-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae) [Source:MGI Symbol;Acc:MGI:135		O88822	-1.2	1.8E-02	3.0	2.0E-02	-3.6	1.2E-02	0.8	3.4E-01
ENSMUST00000052727	splA/ryanodine receptor domain and SOCS box containing 2 [Source:MGI Symbol;Acc:MGI:1315199]		O88838	-3.0	2.2E-04	-0.2	8.2E-01	-5.3	4.3E-04	0.1	9.2E-01
ENSMUST00000052747	NHL repeat containing 1 [Source:MGI Symbol;Acc:MGI:2145264]	Q0VF71	Q8BR37	4.7	4.5E-04	-3.0	5.7E-03	1.1	3.4E-02	-0.6	4.9E-01
ENSMUST00000052761	isocitrate dehydrogenase 3 (NAD+), gamma [Source:MGI Symbol;Acc:MGI:1099463]	Q3TGZ3	P70404	-8.7	1.1E-06	3.9	4.4E-04	-1.5	5.5E-02	-0.6	3.3E-01
ENSMUST00000052774	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2445040]		Q8BSA9	-4.4	9.6E-03	-4.5	2.2E-02	1.3	1.3E-01	-1.5	4.3E-01
ENSMUST00000052089	zinc finger and BTB domain containing 21 [Source:MGI Symbol;Acc:MGI:1927240]	G3X9A3		0.1	9.6E-01	-2.0	4.6E-01	0.7	7.0E-01	2.8	2.8E-01
ENSMUST00000052776	histone cluster 1, H2ba [Source:MGI Symbol;Acc:MGI:2448375]		P70696	6.2	1.5E-04	6.0	1.2E-03	-0.7	6.4E-01	0.0	9.8E-01
ENSMUST00000052107	zinc finger SWIM-type containing 3 [Source:MGI Symbol;Acc:MGI:1914788]		Q8CFL8	-0.3	6.4E-01	0.8	3.2E-01	1.1	6.6E-02	0.1	8.7E-01
ENSMUST00000052119	e carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 [Source:MGI Symbol;Acc:MGI:1915		A2ASZ8	4.7	6.3E-02	4.2	7.2E-02	-3.6	1.7E-01	-3.0	7.4E-02
ENSMUST00000052778	zinc finger and BTB domain containing 12 [Source:MGI Symbol;Acc:MGI:88133]	Q9Z150		2.4	2.5E-02	-3.7	5.1E-04	-0.5	1.9E-01	-1.3	1.2E-01
ENSMUST00000052806	RIKEN cDNA 9230106D20 gene [Source:MGI Symbol;Acc:MGI:3045371]	Q8CC72		6.6	1.6E-04	3.2	1.4E-03	0.2	7.0E-01	-0.3	5.3E-01
ENSMUST00000052827	protein phosphatase 1, regulatory subunit 17 [Source:MGI Symbol;Acc:MGI:1333876]		Q9Z2E4	7.8	1.6E-05	7.7	8.2E-05	0.3	8.0E-01	0.8	2.0E-01
ENSMUST00000052829	family with sequence similarity 166, member B [Source:MGI Symbol;Acc:MGI:2445194]		A2AIP0	6.4	1.2E-02	-0.9	7.4E-02	0.3	4.2E-01	-0.6	2.2E-01
ENSMUST00000052832	RIKEN cDNA 2410015M20 gene [Source:MGI Symbol;Acc:MGI:2442174]		Q8R404	-4.3	2.4E-04	2.6	3.2E-03	0.7	2.5E-01	-0.3	6.1E-01
ENSMUST00000052140	germ cell-specific gene 2 [Source:MGI Symbol;Acc:MGI:1194498]			0.4	4.2E-01	1.2	6.5E-02	0.3	5.5E-01	-0.5	3.4E-01
ENSMUST00000052835	family with sequence similarity 167, member B [Source:MGI Symbol;Acc:MGI:2668032]		P17257	7.0	1.1E-04	-5.8	8.2E-04	-0.9	8.6E-02	-0.9	4.9E-01
ENSMUST00000052837	androgen receptor [Source:MGI Symbol;Acc:MGI:88064]		P19091	6.0	8.0E-05	7.7	9.2E-05	-0.6	6.4E-01	0.2	7.8E-01
ENSMUST00000052838	mindbomb homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443157]		Q80SY4	5.0	2.2E-05	-2.7	6.8E-02	0.5	4.9E-01	-2.2	1.6E-01
ENSMUST00000052168	OTU domain containing 1 [Source:MGI Symbol;Acc:MGI:1918448]		Q9CUB6	0.4	4.9E-01	1.4	1.1E-01	0.8	2.2E-01	-0.2	8.1E-01
ENSMUST00000052843	minichromosome maintenance domain containing 2 [Source:MGI Symbol;Acc:MGI:3045334]		E9Q956	6.5	3.6E-04	-4.7	4.2E-03	0.3	6.7E-01	-0.7	6.2E-01
ENSMUST00000052853	ubiquitin-like 4B [Source:MGI Symbol;Acc:MGI:1914841]		Q9CQ84	7.2	2.6E-05	4.0	1.4E-03	-2.3	4.7E-02	-0.3	6.7E-01
ENSMUST00000052176	RIKEN cDNA C130050O18 gene [Source:MGI Symbol;Acc:MGI:2442694]	Q497Y9		-3.0	3.9E-02	-3.7	7.9E-02	-0.5	6.1E-01	0.2	9.2E-01
ENSMUST00000052865	transmembrane protein 123 [Source:MGI Symbol;Acc:MGI:1919179]		Q91Z22	-5.3	1.6E-03	6.4	8.6E-04	-1.5	3.4E-01	0.1	8.5E-01
ENSMUST00000052867	predicted gene 9843 [Source:MGI Symbol;Acc:MGI:3708621]	Q642K5		-9.5	1.5E-06	-0.8	2.4E-01	0.8	8.4E-02	-0.5	4.3E-01
ENSMUST00000052872	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF [Source:MGI Symbol;Acc:MGI:2681862]	E9QQ96		10.4	1.4E-04	3.4	8.8E-04	-0.1	8.8E-01	0.5	4.0E-01
ENSMUST00000052876	eva-1 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:1922063]		Q8K2Y3	4.1	2.6E-02	-3.1	1.1E-01	0.8	4.0E-01	0.8	6.4E-01
ENSMUST00000052885	transmembrane protein 259 [Source:MGI Symbol;Acc:MGI:2177957]		Q8CIV2	-5.6	3.2E-04	5.1	5.1E-05	-1.0	1.7E-01	0.1	8.9E-01
ENSMUST00000052209	core binding factor beta [Source:MGI Symbol;Acc:MGI:99851]		Q08024	2.2	3.7E-01	3.4	1.8E-01	-1.2	5.9E-01	-2.4	2.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000052904	coiled-coil domain containing 169 [Source:MGI Symbol;Acc:MGI:2444356]		Q8BXX9	7.0	4.0E-04	6.4	1.3E-03	-0.2	9.1E-01	-1.0	2.2E-01
ENSMUST00000052907	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19 [Source:MGI Symbol;Acc:M		P59509	7.9	1.4E-05	7.7	4.1E-05	-0.6	5.9E-01	0.1	8.4E-01
ENSMUST00000052236	F-box protein 10 [Source:MGI Symbol;Acc:MGI:2686937]		Q7TQF2	0.8	1.2E-01	1.0	1.7E-01	0.5	3.2E-01	0.3	5.8E-01
ENSMUST00000052910	acyl-CoA thioesterase 10 [Source:MGI Symbol;Acc:MGI:1928940]		Q32MW3	3.9	1.2E-02	-3.3	3.5E-02	0.5	4.8E-01	-1.7	2.7E-01
ENSMUST00000052249	mitochondrial ribosomal protein S27 [Source:MGI Symbol;Acc:MGI:1919064]		Q8BK72	0.8	2.4E-01	1.5	7.9E-02	-0.1	8.1E-01	-0.9	2.3E-01
ENSMUST00000052250	zinc finger protein 423 [Source:MGI Symbol;Acc:MGI:1891217]		Q80TS5	4.7	1.2E-01	7.8	2.6E-02	-0.2	9.6E-01	-3.2	7.5E-02
ENSMUST00000052915	axin2 [Source:MGI Symbol;Acc:MGI:1270862]		O88566	6.1	4.2E-03	5.9	6.7E-04	-0.5	7.0E-01	-0.5	5.1E-01
ENSMUST00000052927	protein phosphatase 1, regulatory (inhibitor) subunit 16B [Source:MGI Symbol;Acc:MGI:2151841]	Q544H9	Q8VHQ3	-5.0	1.9E-03	4.9	9.4E-04	1.2	2.3E-01	-1.5	7.5E-02
ENSMUST00000052266	exocyst complex component 4 [Source:MGI Symbol;Acc:MGI:1096376]		O35382	-0.8	9.4E-02	-0.2	7.7E-01	0.3	4.5E-01	-0.3	5.3E-01
ENSMUST00000052946	T-box 20 [Source:MGI Symbol;Acc:MGI:1888496]		Q9ES03	9.5	5.4E-07	6.5	1.7E-04	-0.5	6.4E-01	-0.3	5.9E-01
ENSMUST00000052949	hexokinase 3 [Source:MGI Symbol;Acc:MGI:2670962]		Q3TRM8	-4.9	1.5E-03	1.4	1.1E-01	-0.7	3.2E-01	0.3	6.4E-01
ENSMUST00000052965	Nipped-B homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913976]		Q6KCD5	-2.5	2.5E-04	6.7	8.4E-03	-0.7	7.4E-01	-1.6	2.1E-01
ENSMUST00000052290	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914974	Q8K205		4.8	1.3E-01	5.0	1.6E-01	-0.3	9.3E-01	-0.4	8.4E-01
ENSMUST00000052975	olfactory receptor 433 [Source:MGI Symbol;Acc:MGI:3030267]	Q7TRV9		5.2	3.2E-04	5.1	1.4E-03	-3.3	3.5E-02	0.1	8.6E-01
ENSMUST00000052315				-2.7	3.0E-01	-3.2	3.0E-01	-1.3	4.5E-01	-0.8	8.0E-01
ENSMUST00000052978	spermatogenesis associated 31 subfamily D, member 1D [Source:MGI Symbol;Acc:MGI:3045260]	E9Q5W2		9.8	3.5E-05	-4.1	1.2E-02	0.0	9.5E-01	1.8	1.8E-01
ENSMUST00000053013	otolin 1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2685260]		Q4ZJM7	7.4	2.4E-05	-5.9	2.8E-02	1.5	8.9E-02	0.2	9.3E-01
ENSMUST00000053015	poly(rC) binding protein 1 [Source:MGI Symbol;Acc:MGI:1345635]		P60335	-4.3	3.0E-05	-5.3	4.4E-03	0.2	6.8E-01	0.7	6.5E-01
ENSMUST00000052355	nucleoporin 37 [Source:MGI Symbol;Acc:MGI:1919964]		Q9CWU9	-1.6	2.3E-01	-1.9	2.7E-01	-0.7	5.5E-01	-0.4	8.1E-01
ENSMUST00000053016	POU domain, class 4, transcription factor 1 [Source:MGI Symbol;Acc:MGI:102525]		P17208	9.2	1.6E-05	6.6	2.7E-04	-0.6	6.1E-01	0.5	4.4E-01
ENSMUST00000053020	neuralized E3 ubiquitin protein ligase 1B [Source:MGI Symbol;Acc:MGI:3643092]		Q0MW30	6.2	6.8E-06	-3.4	1.2E-01	0.6	5.9E-01	0.0	9.8E-01
ENSMUST00000053024	phosphoglycolate phosphatase [Source:MGI Symbol;Acc:MGI:1914328]		Q8CHP8	-3.4	1.5E-03	9.2	1.9E-06	0.2	8.3E-01	0.2	6.7E-01
ENSMUST00000053033	DNA segment, Chr 1, ERATO Doi 622, expressed [Source:MGI Symbol;Acc:MGI:1277184]		Q8VEB3	4.3	8.4E-06	-3.8	7.3E-03	0.7	1.8E-01	-0.9	4.9E-01
ENSMUST00000053034	cDNA sequence BC068281 [Source:MGI Symbol;Acc:MGI:3040699]		Q6NV72	4.4	5.1E-04	8.0	2.2E-05	-0.7	5.1E-01	0.8	1.3E-01
ENSMUST00000053035	leucine rich repeat containing 8 family, member E [Source:MGI Symbol;Acc:MGI:1919517]		Q66JT1	6.7	7.8E-07	3.3	5.0E-05	0.4	3.4E-01	-0.3	4.5E-01
ENSMUST00000053037	protocadherin beta 7 [Source:MGI Symbol;Acc:MGI:2136741]	Q8CDY9		7.7	1.2E-04	6.6	9.3E-04	-0.2	9.1E-01	-0.4	6.5E-01
ENSMUST00000052420	RIKEN cDNA E130308A19 gene [Source:MGI Symbol;Acc:MGI:2442164]		Q8C4P0	0.6	4.8E-01	3.1	1.9E-02	0.6	5.9E-01	-1.9	5.3E-02
ENSMUST00000052431	armadillo repeat containing, X-linked 6 [Source:MGI Symbol;Acc:MGI:2147993]		Q8K3A6	3.8	6.1E-02	0.3	9.1E-01	-0.5	8.0E-01	3.0	2.5E-01
ENSMUST00000053042	zinc finger and BTB domain containing 8b [Source:MGI Symbol;Acc:MGI:2387181]			6.9	1.7E-02	-3.6	1.1E-02	1.1	7.9E-02	0.0	9.9E-01
ENSMUST00000053043	interleukin 1 receptor-like 1 [Source:MGI Symbol;Acc:MGI:98427]		P14719	2.4	8.6E-04	7.3	1.2E-04	-0.5	6.8E-01	-0.5	4.6E-01
ENSMUST00000053063	hexamethylene bis-acetamide inducible 1 [Source:MGI Symbol;Acc:MGI:2385923]		Q8R409	-3.8	3.1E-05	-5.3	3.7E-02	0.4	6.2E-01	1.7	4.6E-01
ENSMUST00000053068	doublesex and mab-3 related transcription factor 2 [Source:MGI Symbol;Acc:MGI:1330307]		Q8BG36	7.7	3.6E-05	3.3	6.2E-03	-0.7	4.4E-01	-1.1	1.9E-01
ENSMUST00000053073	protocadherin beta 11 [Source:MGI Symbol;Acc:MGI:2136746]	Q91UZ8		7.3	5.3E-05	-1.7	1.9E-02	0.9	4.1E-02	0.3	6.1E-01
ENSMUST00000052455	phosphatidylinositol glycan anchor biosynthesis, class M [Source:MGI Symbol;Acc:MGI:1914806]		Q8C2R7	-0.6	3.1E-01	0.6	3.9E-01	1.1	6.1E-02	-0.1	9.3E-01
ENSMUST00000053086	a disintegrin and metallopeptidase domain 6A [Source:MGI Symbol;Acc:MGI:2676316]	B2RSY5		7.0	3.9E-05	3.3	1.6E-02	-3.2	2.2E-02	0.0	9.6E-01
ENSMUST00000053087	kelch-like 23 [Source:MGI Symbol;Acc:MGI:2683536]		Q6GQU2	3.1	6.9E-04	6.3	3.1E-04	-0.5	6.7E-01	-0.7	2.8E-01
ENSMUST00000053094	family with sequence similarity 188, member B [Source:MGI Symbol;Acc:MGI:3583959]		Q3UQI9	5.8	1.1E-05	4.3	3.1E-02	-2.4	2.0E-01	0.1	9.6E-01
ENSMUST00000053106	adhesion molecule with Ig like domain 2 [Source:MGI Symbol;Acc:MGI:2145995]	Q4VBE6	Q80ZD9	3.5	2.5E-04	5.8	3.0E-03	-0.9	5.6E-01	1.1	2.2E-01
ENSMUST00000052499	ribosomal protein S19 binding protein 1 [Source:MGI Symbol;Acc:MGI:1913788]		Q8C6B9	-1.3	3.5E-02	-1.5	4.8E-02	-0.4	3.7E-01	-0.3	7.0E-01
ENSMUST00000053107	involucrin [Source:MGI Symbol;Acc:MGI:96626]	G3X9D9		8.2	7.8E-04	6.2	6.1E-04	-2.1	1.6E-01	0.3	6.6E-01
ENSMUST00000052503	GTPase, IMAP family member 7 [Source:MGI Symbol;Acc:MGI:1349657]	Q8R379		0.4	4.7E-01	-0.5	3.5E-01	-1.9	2.3E-03	-1.0	1.1E-01
ENSMUST00000053150	ribosomal protein S27, retrogene [Source:MGI Symbol;Acc:MGI:3704345]		Q6ZWU9	-7.7	2.6E-07	1.4	6.1E-02	0.0	9.4E-01	-0.1	9.3E-01
ENSMUST00000052509	zinc finger protein 771 [Source:MGI Symbol;Acc:MGI:2442050]		Q8BJ90	-0.7	2.2E-01	0.0	9.7E-01	0.2	6.6E-01	-0.5	4.9E-01
ENSMUST00000052514	solute carrier family 38, member 9 [Source:MGI Symbol;Acc:MGI:1918839]		Q8BGD6	-0.2	7.4E-01	0.3	6.6E-01	0.0	9.4E-01	-0.5	4.2E-01
ENSMUST00000053157	family with sequence similarity 159, member A [Source:MGI Symbol;Acc:MGI:3651644]		A2A9G7	6.8	2.6E-04	5.7	3.0E-02	-0.7	7.9E-01	2.4	8.4E-02
ENSMUST00000053175	V-set and transmembrane domain containing 4 [Source:MGI Symbol;Acc:MGI:2444633]		T1NXB5	5.0	1.2E-02	-2.9	1.4E-04	1.1	1.8E-03	0.3	5.4E-01
ENSMUST00000052539	RUN and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919546]		Q8BG26	0.4	6.1E-01	2.7	1.5E-01	5.4	2.7E-03	3.1	4.3E-02
ENSMUST00000053177	WD repeat and FYVE domain containing 3 [Source:MGI Symbol;Acc:MGI:1096875]		Q6VNB8	-3.5	3.7E-04	7.7	5.9E-05	-0.5	6.8E-01	-0.3	6.5E-01
ENSMUST00000053211	major facilitator superfamily domain containing 6-like [Source:MGI Symbol;Acc:MGI:2384904]		Q8R3N2	2.6	7.5E-03	-1.9	5.9E-02	1.1	7.7E-02	-1.5	1.4E-01
ENSMUST00000053215	phosphoinositide-3-kinase, catalytic, gamma polypeptide [Source:MGI Symbol;Acc:MGI:1353576]		Q9JHG7	-5.4	9.6E-05	6.1	4.8E-04	0.1	9.5E-01	-0.5	4.8E-01
ENSMUST00000053218	dapper homolog 2, antagonist of beta-catenin (xenopus) [Source:MGI Symbol;Acc:MGI:1920347]		Q7TN08	8.4	2.7E-05	-0.6	4.5E-01	0.6	3.0E-01	-1.1	1.7E-01
ENSMUST00000053225	oligodendrocyte transcription factor 3 [Source:MGI Symbol;Acc:MGI:2149955]		Q6PFG8	6.2	1.1E-05	-2.1	2.3E-01	1.1	2.5E-01	0.4	8.1E-01
ENSMUST00000053230	unc-51-like kinase 3 [Source:MGI Symbol;Acc:MGI:1918992]		Q3U3Q1	2.3	1.3E-02	-3.2	1.6E-02	1.3	4.1E-02	1.2	2.8E-01
ENSMUST00000053232	protein tyrosine phosphatase 4a3 [Source:MGI Symbol;Acc:MGI:1277098]		Q9D658	4.7	1.9E-02	-8.5	5.4E-05	0.2	5.2E-01	0.2	8.8E-01
ENSMUST00000053239	somatostatin receptor 3 [Source:MGI Symbol;Acc:MGI:98329]		P30935	9.0	7.7E-06	2.8	1.9E-01	-0.6	7.8E-01	2.1	1.4E-01
ENSMUST00000053250	clarin 2 [Source:MGI Symbol;Acc:MGI:3646230]	B2RVW2		6.5	1.6E-04	2.2	1.3E-01	-5.1	7.8E-03	-2.5	6.5E-02
ENSMUST00000053257	spermatogenesis associated glutamate (E)-rich protein 4B [Source:MGI Symbol;Acc:MGI:1920776]	Q9D9F7		6.3	4.7E-04	5.9	4.4E-04	0.0	9.8E-01	0.4	5.6E-01
ENSMUST00000053266	minichromosome maintenance deficient 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:101845]	Q3UI57	P25206	-4.8	2.6E-03	6.2	1.9E-02	-0.5	8.3E-01	-1.3	3.4E-01
ENSMUST00000052615				-1.3	6.2E-01	6.2	1.2E-01	6.7	7.8E-02	-0.8	7.6E-01
ENSMUST00000053273	inositol 1,4,5-triphosphate receptor 2 [Source:MGI Symbol;Acc:MGI:99418]		Q9Z329	-6.2	1.7E-02	-1.2	8.4E-02	-7.4	1.9E-05	-0.4	5.6E-01
ENSMUST00000053286	coiled-coil domain containing 84 [Source:MGI Symbol;Acc:MGI:2685960]		Q4VA36	-1.7	3.4E-02	-1.0	2.5E-01	0.5	3.5E-01	-0.8	3.5E-01
ENSMUST00000053288	cerebellar degeneration-related protein 2-like [Source:MGI Symbol;Acc:MGI:2684867]		A2A6T1	8.9	6.1E-05	-1.1	1.9E-01	-0.1	9.0E-01	-1.1	2.2E-01
ENSMUST00000053293	zinc finger and SCAN domain containing 12 [Source:MGI Symbol;Acc:MGI:1099444]		Q9Z1D7	1.7	1.2E-02	6.8	3.5E-04	-0.4	7.5E-01	-0.7	3.4E-01
ENSMUST00000053306	oxytocin receptor [Source:MGI Symbol;Acc:MGI:109147]		P97926	8.5	1.6E-05	6.3	1.6E-03	-2.5	1.9E-01	-1.1	2.4E-01
ENSMUST00000053336	RIKEN cDNA 2510009E07 gene [Source:MGI Symbol;Acc:MGI:1919440]		Q6GQU0	3.3	4.7E-04	5.3	7.5E-03	-0.5	7.9E-01	-0.3	7.8E-01
ENSMUST00000053355	cellular repressor of E1A-stimulated genes 2 [Source:MGI Symbol;Acc:MGI:1928333]		Q8BGC9	5.7	2.6E-05	7.1	8.0E-04	-0.7	6.5E-01	-0.5	5.7E-01
ENSMUST00000053361	G protein-coupled receptor, family C, group 5, member C [Source:MGI Symbol;Acc:MGI:1917605]	I7HPW4		6.4	1.1E-04	8.3	5.2E-05	0.0	9.9E-01	-0.2	6.9E-01
ENSMUST00000053364	asp (abnormal spindle)-like, microcephaly associated (Drosophila) [Source:MGI Symbol;Acc:MGI:1334448]		Q8CJ27	1.2	2.6E-02	0.9	7.7E-02	-1.3	7.2E-03	0.0	9.2E-01
ENSMUST00000053373	pyrimidinergic receptor P2Y, G-protein coupled, 4 [Source:MGI Symbol;Acc:MGI:1926594]	Q0VBT7	Q9JIS7	7.1	2.5E-06	-0.2	7.8E-01	1.4	1.4E-02	-0.5	4.6E-01
ENSMUST00000053375	purinergic receptor P2Y, G-protein coupled 10 [Source:MGI Symbol;Acc:MGI:1926076]		Q8BFU7	-2.7	1.3E-02	6.8	3.6E-04	-0.7	6.2E-01	-0.4	5.7E-01
ENSMUST00000053386	Pigy upstream reading frame [Source:MGI Symbol;Acc:MGI:1913709]		Q9D1C3	1.2	2.2E-02	-4.1	4.7E-03	0.1	8.3E-01	-1.3	3.4E-01
ENSMUST00000053389	chemokine (C-X-C motif) receptor 1 [Source:MGI Symbol;Acc:MGI:2448715]		Q810W6	-8.0	2.4E-04	8.2	3.1E-05	-0.6	6.2E-01	-0.2	7.2E-01
ENSMUST00000053392	zinc finger protein 689 [Source:MGI Symbol;Acc:MGI:1918381]		Q8BKK5	2.7	2.8E-03	5.4	4.9E-04	-1.8	1.4E-01	-0.6	3.7E-01
ENSMUST00000053407	alkB, alkylation repair homolog 8 (E. coli) [Source:MGI Symbol;Acc:MGI:1914917]		Q80Y20	3.6	7.1E-05	4.3	6.6E-04	-1.3	1.7E-01	-0.4	5.2E-01
ENSMUST00000052708	cytoskeleton associated protein 2-like [Source:MGI Symbol;Acc:MGI:1917716]		Q7TS74	-0.3	6.6E-01	-1.1	2.1E-01	-0.5	3.4E-01	0.3	7.4E-01
ENSMUST00000052712	trimethylguanosine synthase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2151797]		Q923W1	-0.8	2.1E-01	-0.9	2.4E-01	-0.2	6.2E-01	-0.1	8.9E-01
ENSMUST00000052715	zinc finger protein 691 [Source:MGI Symbol;Acc:MGI:3041163]	A2A7P4		1.2	3.0E-01	0.9	5.9E-01	1.1	4.1E-01	1.4	3.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000053414	coiled-coil domain containing 171 [Source:MGI Symbol;Acc:MGI:1922152]		E9Q1U1	5.3	4.9E-03	3.5	9.5E-04	-0.8	2.4E-01	-0.1	9.2E-01
ENSMUST00000053419	leucine rich repeat containing 19 [Source:MGI Symbol;Acc:MGI:2140219]		Q8BZT5	7.4	6.0E-05	5.1	2.6E-03	0.1	9.5E-01	0.7	4.0E-01
ENSMUST00000053426	PTC7 protein phosphatase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2444593]		Q6NVE9	-3.2	1.4E-04	-0.9	1.2E-01	0.2	5.2E-01	0.0	9.5E-01
ENSMUST00000053429	zinc finger and BTB domain containing 22 [Source:MGI Symbol;Acc:MGI:1931870]	Q3TXW4	Q9Z0G7	-3.2	5.6E-04	-1.8	1.8E-02	1.1	1.6E-02	0.0	1.0E+00
ENSMUST00000052740	T cell activation inhibitor, mitochondrial [Source:MGI Symbol;Acc:MGI:1196217]	G3X983		-3.0	1.1E-01	-0.3	8.8E-01	2.3	1.8E-01	-0.4	8.4E-01
ENSMUST00000053434	tripartite motif-containing 26 [Source:MGI Symbol;Acc:MGI:1337056]		Q99PN3	-5.2	3.5E-02	4.8	8.6E-04	-0.1	9.1E-01	-0.2	7.5E-01
ENSMUST00000053440	coiled-coil domain containing 40 [Source:MGI Symbol;Acc:MGI:2443893]		Q8BI79	7.4	1.5E-03	-8.4	9.9E-06	-0.6	5.0E-02	-0.9	4.2E-01
ENSMUST00000053445	kinase non-catalytic C-lobe domain (KIND) containing 1 [Source:MGI Symbol;Acc:MGI:1923734]		Q0KK55	6.3	2.9E-02	-0.8	5.0E-01	0.4	6.5E-01	-3.1	5.8E-02
ENSMUST00000053456	septin 6 [Source:MGI Symbol;Acc:MGI:1888939]		Q9R1T4	-3.2	9.0E-04	5.6	5.5E-04	-0.6	6.3E-01	0.0	9.6E-01
ENSMUST00000053458	family with sequence similarity 228, member B [Source:MGI Symbol;Acc:MGI:2442121]		Q497Q6	7.0	5.4E-05	2.7	3.0E-02	0.1	9.3E-01	-0.2	8.1E-01
ENSMUST00000052798	prostaglandin E synthase 3 (cytosolic) [Source:MGI Symbol;Acc:MGI:1929282]		Q9R0Q7	-1.1	7.4E-02	-0.9	2.7E-01	1.2	3.8E-02	1.0	1.7E-01
ENSMUST00000053464	ubiquitin specific peptidase 17-like E [Source:MGI Symbol;Acc:MGI:107697]			7.4	6.0E-05	6.2	3.7E-04	-0.9	4.5E-01	-0.6	4.3E-01
ENSMUST00000052825	UFM1-specific peptidase 1 [Source:MGI Symbol;Acc:MGI:1917490]		Q9CZP0	1.6	6.1E-02	2.6	1.3E-02	0.0	9.9E-01	-1.1	1.6E-01
ENSMUST00000053467	zinc finger protein, multitype 2 [Source:MGI Symbol;Acc:MGI:1334444]		Q8CCH7	9.1	5.1E-06	7.2	3.4E-05	-1.4	2.1E-01	-0.8	1.4E-01
ENSMUST00000053469	methyltransferase like 21A [Source:MGI Symbol;Acc:MGI:1914349]		Q9CQL0	3.3	3.4E-02	3.8	1.2E-01	-0.5	8.4E-01	2.1	1.8E-01
ENSMUST00000053491	POU domain, class 3, transcription factor 1 [Source:MGI Symbol;Acc:MGI:101896]		P21952	7.3	7.7E-05	-4.8	4.5E-04	-1.1	4.0E-02	-0.6	5.1E-01
ENSMUST00000053498	ring finger protein 216 [Source:MGI Symbol;Acc:MGI:1344349]		P58283	-2.8	1.2E-04	6.7	2.7E-04	-0.7	6.1E-01	-0.4	5.7E-01
ENSMUST00000052836	adducin 1 (alpha) [Source:MGI Symbol;Acc:MGI:87918]	F8WHZ9		0.9	6.4E-01	1.7	5.7E-01	1.0	6.2E-01	0.2	9.5E-01
ENSMUST00000053499	ankyrin and armadillo repeat containing [Source:MGI Symbol;Acc:MGI:2442559]		A2RT91	6.2	3.6E-04	6.1	6.5E-04	0.3	8.1E-01	0.1	8.7E-01
ENSMUST00000053506	Bardet-Biedl syndrome 1 (human) [Source:MGI Symbol;Acc:MGI:1277215]	Q3V3N7		4.9	1.8E-06	4.6	3.1E-04	0.8	2.7E-01	1.2	5.1E-02
ENSMUST00000052839	ephrin B1 [Source:MGI Symbol;Acc:MGI:102708]	Q544L9	P52795	1.3	1.0E-01	2.0	5.9E-02	0.8	2.9E-01	0.1	8.6E-01
ENSMUST00000053536	CDC42 effector protein (Rho GTPase binding) 4 [Source:MGI Symbol;Acc:MGI:1929760]		Q9JM96	-6.9	3.6E-04	6.1	3.9E-03	-0.2	9.0E-01	0.2	8.3E-01
ENSMUST00000053558	ankyrin repeat domain 37 [Source:MGI Symbol;Acc:MGI:3603344]		Q569N2	-5.5	1.0E-03	7.2	5.4E-05	-0.5	6.5E-01	-0.5	3.9E-01
ENSMUST00000053568	leucine rich repeat and Ig domain containing 1 [Source:MGI Symbol;Acc:MGI:1915522]		Q9D1T0	8.0	4.3E-05	-5.4	1.2E-02	0.0	9.6E-01	0.1	9.6E-01
ENSMUST00000053575	predicted gene 8186 [Source:MGI Symbol;Acc:MGI:3643110]		P62309	-4.2	2.5E-03	-7.2	2.2E-05	-0.4	3.0E-01	-2.7	2.3E-02
ENSMUST00000053577	epithelial cell adhesion molecule [Source:MGI Symbol;Acc:MGI:106653]		Q99JW5	4.3	1.4E-03	7.3	3.3E-03	-0.9	6.7E-01	2.2	4.4E-02
ENSMUST00000053593	RAP2C, member of RAS oncogene family [Source:MGI Symbol;Acc:MGI:1919315]		Q8BU31	-6.5	6.9E-06	4.8	4.0E-02	0.0	9.8E-01	-0.7	6.3E-01
ENSMUST00000053597	leucine rich repeat and fibronectin type III domain containing 4 [Source:MGI Symbol;Acc:MGI:2385612]		Q80XU8	7.4	1.2E-04	-7.5	1.6E-04	-1.0	6.7E-02	-1.4	3.1E-01
ENSMUST00000053612	RIKEN cDNA A530064D06 gene [Source:MGI Symbol;Acc:MGI:2443476]	Q8BNV8		-4.4	4.0E-04	-6.6	6.2E-03	1.0	1.4E-01	1.9	3.2E-01
ENSMUST00000052888				0.3	9.1E-01	-3.7	1.9E-01	-5.4	2.1E-02	-1.4	6.6E-01
ENSMUST00000052902	predicted pseudogene 9797 [Source:MGI Symbol;Acc:MGI:3704349]		Q9WVA2	-0.4	6.3E-01	0.4	6.5E-01	-0.7	3.9E-01	-1.5	1.3E-01
ENSMUST00000053640	adrenergic receptor, beta 2 [Source:MGI Symbol;Acc:MGI:87938]		P18762	-3.3	4.0E-03	4.6	1.2E-02	-0.5	7.3E-01	1.8	8.4E-02
ENSMUST00000053646	sphingosine-1-phosphate receptor 4 [Source:MGI Symbol;Acc:MGI:1333809]		Q9Z0L1	-2.1	5.4E-03	7.6	3.5E-05	-0.6	6.2E-01	-0.3	5.7E-01
ENSMUST00000053657	alkB, alkylation repair homolog 2 (E. coli) [Source:MGI Symbol;Acc:MGI:2141032]		Q6P6J4	5.3	5.4E-03	6.0	3.0E-03	0.5	7.3E-01	-1.6	9.9E-02
ENSMUST00000053661	GTPase, IMAP family member 6 [Source:MGI Symbol;Acc:MGI:1918876]		Q8K349	-4.6	1.4E-03	3.9	7.9E-02	-2.2	2.8E-01	0.0	9.9E-01
ENSMUST00000052919	ORM1-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913862]		Q9CPZ6	-0.6	3.1E-01	-0.7	3.3E-01	0.2	7.4E-01	0.3	6.5E-01
ENSMUST00000053664	thioredoxin-related transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1914208]		Q9D710	-3.9	9.5E-03	-2.5	1.3E-01	1.8	4.4E-02	-0.7	6.8E-01
ENSMUST00000052932	phosphodiesterase 12 [Source:MGI Symbol;Acc:MGI:2443226]		Q3TIU4	-0.5	1.7E-01	-0.2	6.7E-01	0.7	4.2E-02	0.4	3.1E-01
ENSMUST00000052939	calcium/calmodulin-dependent protein kinase II inhibitor 2 [Source:MGI Symbol;Acc:MGI:1920297]	B2RXL5	Q78WH7	0.3	7.1E-01	1.3	2.1E-01	0.7	4.2E-01	-0.3	6.9E-01
ENSMUST00000053668	G protein-coupled receptor 68 [Source:MGI Symbol;Acc:MGI:2441763]		Q8BFQ3	9.4	4.0E-04	9.3	3.7E-06	0.4	6.6E-01	0.6	2.1E-01
ENSMUST00000053681	ferric-chelate reductase 1 like [Source:MGI Symbol;Acc:MGI:2442704]		B1AXV0	7.0	6.6E-05	-7.2	3.4E-03	1.2	1.2E-01	3.5	8.5E-02
ENSMUST00000053692	solute carrier family 38, member 10 [Source:MGI Symbol;Acc:MGI:1919305]		Q5I012	3.9	1.9E-03	-2.4	2.6E-03	0.5	1.4E-01	0.4	4.7E-01
ENSMUST00000052969	stonin 2 [Source:MGI Symbol;Acc:MGI:1918272]		Q8BZ60	0.8	1.7E-01	2.4	8.0E-03	0.8	1.9E-01	-0.8	2.2E-01
ENSMUST00000053699	SECIS binding protein 2-like [Source:MGI Symbol;Acc:MGI:1917604]	A2AQE2		-1.5	3.9E-03	5.9	3.9E-04	-0.1	9.2E-01	-0.9	2.1E-01
ENSMUST00000053708	killer cell lectin-like receptor family E member 1 [Source:MGI Symbol;Acc:MGI:2662547]	Q8CJC7		7.9	4.7E-04	8.6	2.0E-04	-0.8	6.1E-01	0.4	5.8E-01
ENSMUST00000053716	clarin 3 [Source:MGI Symbol;Acc:MGI:2142022]		Q8BHH8	5.5	1.6E-04	7.5	3.9E-05	-0.6	6.0E-01	-0.8	1.8E-01
ENSMUST00000053718	retinaldehyde binding protein 1 [Source:MGI Symbol;Acc:MGI:97930]	Q544Y3	Q9Z275	7.5	2.1E-05	-3.6	7.5E-04	0.9	3.5E-02	0.2	7.9E-01
ENSMUST00000053734	dual oxidase 2 [Source:MGI Symbol;Acc:MGI:3036280]	A2AQ99		9.6	8.2E-06	7.4	1.0E-04	-1.4	2.7E-01	0.3	5.6E-01
ENSMUST00000053737	splicing factor, suppressor of white-apricot homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:101760]		Q3USH5	-1.7	5.8E-03	5.2	6.2E-05	-0.6	4.2E-01	0.4	4.7E-01
ENSMUST00000053740	zinc finger protein 207 [Source:MGI Symbol;Acc:MGI:1340045]		Q9JMD0	-6.4	1.8E-02	-1.5	1.2E-01	1.0	1.2E-01	-1.0	3.3E-01
ENSMUST00000053743	RIKEN cDNA 4931431F19 gene [Source:MGI Symbol;Acc:MGI:1918230]	Q9D4I8		7.3	3.5E-05	3.6	1.2E-04	-0.5	3.3E-01	0.2	5.8E-01
ENSMUST00000053744	RIKEN cDNA 2410016O06 gene [Source:MGI Symbol;Acc:MGI:1919202]		Q9JJF3	-2.6	3.5E-04	3.5	6.8E-03	-0.3	7.6E-01	0.6	4.3E-01
ENSMUST00000053748	erythrocyte membrane protein band 4.1 like 2 [Source:MGI Symbol;Acc:MGI:103009]		O70318	-4.4	2.6E-03	5.4	7.4E-06	-1.7	1.8E-02	-0.4	2.7E-01
ENSMUST00000053753	gap junction protein, alpha 4 [Source:MGI Symbol;Acc:MGI:95715]	Q3UPZ2	P28235	8.2	4.5E-05	5.9	1.6E-03	-0.8	5.5E-01	1.0	2.3E-01
ENSMUST00000053760	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast) [Source:MGI Symbol;Acc:MGI:2445092]	E9Q9S3		4.3	1.0E-03	2.4	4.8E-01	-0.7	7.8E-01	3.7	2.0E-01
ENSMUST00000053764	forkhead box O1 [Source:MGI Symbol;Acc:MGI:1890077]		Q9R1E0	1.6	7.8E-03	2.0	1.4E-02	0.0	9.9E-01	0.4	4.1E-01
ENSMUST00000053766	autocrine motility factor receptor [Source:MGI Symbol;Acc:MGI:1345634]	Q3TCI2	Q9R049	-4.4	6.2E-05	-3.2	6.3E-04	0.5	1.6E-01	-0.1	8.6E-01
ENSMUST00000053768	syntaxin binding protein 6 (amisyn) [Source:MGI Symbol;Acc:MGI:2384963]	Q3TYA4		6.3	1.4E-04	7.3	1.0E-04	-0.6	6.3E-01	-0.2	7.1E-01
ENSMUST00000053792	RIKEN cDNA 9030612E09 gene [Source:MGI Symbol;Acc:MGI:1921780]	Q8CE20		6.0	2.8E-05	6.9	1.8E-04	-0.6	6.4E-01	-0.2	7.3E-01
ENSMUST00000053811	lipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Source:MGI Symbol;Acc:MGI:19		Q9D2G2	-4.0	1.1E-05	6.2	1.6E-04	-0.5	6.2E-01	0.2	7.6E-01
ENSMUST00000053078	microtubule-associated protein 10 [Source:MGI Symbol;Acc:MGI:1921643]		Q8BJS7	0.5	3.4E-01	2.3	6.3E-03	1.3	3.4E-02	-0.5	3.8E-01
ENSMUST00000053085	NLR family, CARD domain containing 5 [Source:MGI Symbol;Acc:MGI:3612191]		C3VPR6	1.2	9.8E-02	1.1	1.8E-01	-0.8	2.6E-01	-0.7	3.5E-01
ENSMUST00000053819	serine/arginine-rich splicing factor 4 [Source:MGI Symbol;Acc:MGI:1890577]	Q542V3		-4.9	1.7E-03	6.7	1.1E-04	-0.5	6.2E-01	-0.3	6.4E-01
ENSMUST00000053821	cDNA sequence AY358078 [Source:MGI Symbol;Acc:MGI:2682312]	Q6UY53		6.9	1.1E-04	3.9	5.7E-04	0.8	2.6E-01	0.0	9.9E-01
ENSMUST00000053830	high-mobility group box 4 [Source:MGI Symbol;Acc:MGI:1916567]		Q6P8W9	6.1	3.7E-04	5.9	4.1E-05	-0.3	6.8E-01	-0.4	4.5E-01
ENSMUST00000053098	zinc finger and BTB domain containing 6 [Source:MGI Symbol;Acc:MGI:2442998]		Q8K088	0.0	9.5E-01	1.1	2.2E-01	0.2	7.3E-01	-0.8	3.5E-01
ENSMUST00000053855	DNA-damage-inducible transcript 4-like [Source:MGI Symbol;Acc:MGI:1920534]	B2RVG4	Q8VHZ5	7.4	6.2E-05	1.1	9.9E-02	-2.3	3.4E-03	0.1	8.9E-01
ENSMUST00000053856	protocadherin beta 17 [Source:MGI Symbol;Acc:MGI:2136754]	Q91VD8		8.2	1.0E-05	5.6	7.7E-03	-2.2	2.6E-01	0.4	6.9E-01
ENSMUST00000053109	F-box protein 46 [Source:MGI Symbol;Acc:MGI:2444918]		Q8BG80	-0.8	2.7E-01	0.1	8.8E-01	1.2	1.0E-01	0.3	7.5E-01
ENSMUST00000053862	PQ loop repeat containing 2 [Source:MGI Symbol;Acc:MGI:2384837]		Q8C4N4	-3.3	1.7E-02	-8.4	1.2E-06	-0.7	2.7E-02	0.0	9.5E-01
ENSMUST00000053156	free fatty acid receptor 2 [Source:MGI Symbol;Acc:MGI:2441731]		Q8VCK6	-0.5	3.9E-01	1.8	4.8E-02	1.5	3.7E-02	-0.8	2.7E-01
ENSMUST00000053865	predicted gene 5424 [Source:MGI Symbol;Acc:MGI:3643173]	J3QNG0		7.8	4.9E-04	6.0	1.1E-03	-0.7	6.3E-01	0.1	8.6E-01
ENSMUST00000053871	cytoskeleton-associated protein 4 [Source:MGI Symbol;Acc:MGI:2444926]		Q8BMK4	-6.2	1.4E-04	6.6	3.9E-03	-0.5	7.8E-01	-2.2	5.9E-02
ENSMUST00000053872	CDC42 small effector 1 [Source:MGI Symbol;Acc:MGI:1889510]		Q8BHL7	-5.8	9.2E-06	-1.1	1.4E-01	1.1	3.6E-02	-1.2	1.3E-01
ENSMUST00000053183	ADP-ribosylation factor 3 [Source:MGI Symbol;Acc:MGI:99432]	Q3U344	P61205	-0.1	8.7E-01	-0.6	4.8E-01	1.0	1.3E-01	1.5	7.9E-02
ENSMUST00000053876	glucose-6-phosphate dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:105977]	G3UWD6		3.0	2.2E-03	2.3	3.2E-02	-0.6	4.8E-01	-0.2	8.0E-01
ENSMUST00000053880	glutamate receptor, ionotropic, NMDA2B (epsilon 2) [Source:MGI Symbol;Acc:MGI:95821]	G3X9V4		9.7	7.9E-06	-3.8	4.9E-03	1.5	1.9E-02	-0.1	9.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000053896	microrchidia 2B [Source:MGI Symbol;Acc:MGI:3045293]		Q8C5W4	6.2	3.2E-02	4.9	1.8E-04	-3.6	7.1E-03	-0.1	8.4E-01
ENSMUST00000053902	ELMO/CED-12 domain containing 2 [Source:MGI Symbol;Acc:MGI:2445165]		Q8BGF6	-3.6	2.4E-03	7.9	3.0E-05	1.1	2.8E-01	-0.6	2.5E-01
ENSMUST00000053906	serine/threonine/tyrosine interacting-like 1 [Source:MGI Symbol;Acc:MGI:1923821]	Q9DAR2		6.7	2.3E-04	2.3	5.3E-02	0.9	3.4E-01	0.9	3.1E-01
ENSMUST00000053909	2'-5' oligoadenylate synthetase 2 [Source:MGI Symbol;Acc:MGI:2180852]		E9Q9A9	-6.6	2.2E-02	8.2	8.1E-03	2.7	2.9E-01	-0.8	5.1E-01
ENSMUST00000053913	diacylglycerol kinase, theta [Source:MGI Symbol;Acc:MGI:102918]		Q6P5E8	-4.6	7.7E-03	8.3	1.6E-05	-0.8	4.7E-01	-0.1	8.2E-01
ENSMUST00000053249	RIKEN cDNA E330017A01 gene [Source:MGI Symbol;Acc:MGI:3045360]	Q8BU47		3.9	1.0E-01	5.7	4.1E-02	-0.2	9.3E-01	-2.0	2.0E-01
ENSMUST00000053917	cyclin Y [Source:MGI Symbol;Acc:MGI:1915224]		Q8BGU5	-3.4	1.7E-05	6.4	3.4E-04	-0.5	6.8E-01	-0.4	5.3E-01
ENSMUST00000053251	RNA binding protein gene with multiple splicing [Source:MGI Symbol;Acc:MGI:1334446]		Q9WVB0	-0.2	9.0E-01	2.6	4.2E-01	3.6	2.0E-01	0.8	7.0E-01
ENSMUST00000053252	cortexin 1 [Source:MGI Symbol;Acc:MGI:88566]	Q3TYB7	Q8K129	0.7	2.7E-01	1.4	9.1E-02	0.7	2.6E-01	0.0	1.0E+00
ENSMUST00000053922	von Willebrand factor C domain-containing protein 2-like [Source:MGI Symbol;Acc:MGI:2444069]		Q505H4	5.9	1.3E-03	6.0	1.2E-03	-0.5	7.4E-01	-0.2	8.3E-01
ENSMUST00000053265	LYR motif containing 4 [Source:MGI Symbol;Acc:MGI:2683538]		Q8K215	0.7	2.4E-01	-0.1	9.0E-01	0.0	9.4E-01	0.8	2.6E-01
ENSMUST00000053932	predicted gene 28230 [Source:MGI Symbol;Acc:MGI:5578936]	A0A0A0MQ91		7.1	6.2E-05	-6.3	1.1E-02	0.0	9.7E-01	1.5	4.6E-01
ENSMUST00000053949	shisa family member 2 [Source:MGI Symbol;Acc:MGI:2444716]		Q8QZV2	5.1	3.6E-05	-1.5	1.0E-01	0.9	1.3E-01	-0.3	7.6E-01
ENSMUST00000053950	leucine rich repeat containing 28 [Source:MGI Symbol;Acc:MGI:1915689]		Q3TX51	-3.9	8.9E-04	-1.4	4.7E-01	-0.1	9.3E-01	-4.9	6.8E-02
ENSMUST00000053969	signal-induced proliferation-associated 1 like 1 [Source:MGI Symbol;Acc:MGI:2443679]		Q8C0T5	-7.3	3.4E-04	-1.5	1.2E-01	0.4	5.0E-01	0.2	7.9E-01
ENSMUST00000053287	ubiquitin specific peptidase 42 [Source:MGI Symbol;Acc:MGI:1924050]		B2RQC2	-0.6	2.5E-01	-0.1	8.4E-01	1.0	8.0E-02	0.5	4.8E-01
ENSMUST00000053970	G-protein coupled receptor 119 [Source:MGI Symbol;Acc:MGI:2668412]		Q7TQP3	5.7	8.1E-04	5.9	2.1E-03	-2.6	1.1E-01	0.3	6.6E-01
ENSMUST00000053981	RIKEN cDNA 1110012L19 gene [Source:MGI Symbol;Acc:MGI:1915868]		Q9D1F3	-3.3	1.0E-04	0.6	2.9E-01	-1.4	1.9E-02	-0.4	4.7E-01
ENSMUST00000053986	leucine rich repeat and Ig domain containing 3 [Source:MGI Symbol;Acc:MGI:3609246]		Q6GQU6	8.6	1.4E-05	-9.6	4.0E-04	-1.1	4.2E-02	1.1	5.5E-01
ENSMUST00000053990	olfactory receptor 368 [Source:MGI Symbol;Acc:MGI:3030202]	Q8VF22		5.4	3.5E-03	7.8	3.5E-04	0.3	8.4E-01	0.9	2.0E-01
ENSMUST00000054002	suppressor of cytokine signaling 3 [Source:MGI Symbol;Acc:MGI:1201791]		O35718	-5.8	2.7E-05	6.3	1.5E-04	1.3	2.1E-01	0.2	7.3E-01
ENSMUST00000054014	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 [Source:MGI Symbol;Acc:MGI:1914290]	Q3U741		-4.1	1.9E-04	1.5	4.4E-02	-1.7	1.9E-02	0.0	9.5E-01
ENSMUST00000054018	cDNA sequence AY074887 [Source:MGI Symbol;Acc:MGI:3575512]	Q8R5F9		9.7	6.9E-06	4.9	2.9E-04	0.2	8.2E-01	0.9	1.4E-01
ENSMUST00000054030	aspartoacylase (aminoacylase) 3 [Source:MGI Symbol;Acc:MGI:1918920]		Q91XE4	6.0	8.2E-04	5.7	1.1E-03	-0.6	6.2E-01	0.1	8.8E-01
ENSMUST00000054034	polymerase (DNA directed), theta [Source:MGI Symbol;Acc:MGI:2155399]	Q80XB7	Q8CGS6	6.3	6.7E-04	1.2	5.4E-02	0.0	9.6E-01	-0.1	9.1E-01
ENSMUST00000054048	MAS-related GPR, member E [Source:MGI Symbol;Acc:MGI:2441884]	Q4V9R2	Q91ZB7	8.6	1.2E-06	7.2	2.4E-05	0.3	7.4E-01	0.2	7.2E-01
ENSMUST00000054050	GTPase, IMAP family member 9 [Source:MGI Symbol;Acc:MGI:3511744]	G3X987		-3.0	2.6E-03	-5.3	5.0E-03	-1.5	3.9E-02	1.2	4.4E-01
ENSMUST00000054052	zinc finger protein, multitype 1 [Source:MGI Symbol;Acc:MGI:1095400]		O35615	3.8	1.3E-03	1.3	3.1E-02	-0.4	3.8E-01	-0.5	3.1E-01
ENSMUST00000054055	ubiquitin specific peptidase 29 [Source:MGI Symbol;Acc:MGI:1888998]		Q9ES63	8.0	3.9E-04	-5.3	1.3E-02	1.4	8.0E-02	-1.3	5.2E-01
ENSMUST00000054072	zinc finger protein 81 [Source:MGI Symbol;Acc:MGI:1890752]	B8JJZ7		2.6	3.7E-04	3.3	2.3E-03	0.3	7.2E-01	-0.4	5.8E-01
ENSMUST00000054083	endoplasmic reticulum metallopeptidase 1 [Source:MGI Symbol;Acc:MGI:106250]	G8JL46		-7.0	1.8E-04	3.0	8.5E-04	-0.7	2.7E-01	0.0	9.9E-01
ENSMUST00000053410	zinc finger protein 574 [Source:MGI Symbol;Acc:MGI:2442951]		Q8BY46	-4.3	4.2E-02	-1.4	3.9E-01	-0.2	8.6E-01	-3.1	1.6E-01
ENSMUST00000053413	cyclin-dependent kinase 5, regulatory subunit 1 (p35) [Source:MGI Symbol;Acc:MGI:101764]	Q542T9	P61809	0.2	7.0E-01	1.5	4.1E-02	1.4	2.0E-02	0.1	9.0E-01
ENSMUST00000054095	potassium channel tetramerisation domain containing 8 [Source:MGI Symbol;Acc:MGI:2443804]		Q50H33	7.3	4.9E-05	3.8	5.0E-02	-1.7	3.3E-01	-0.2	8.4E-01
ENSMUST00000054098	solute carrier family 35, member G1 [Source:MGI Symbol;Acc:MGI:2444789]		Q8BY79	4.0	7.4E-04	5.8	6.0E-04	-1.4	2.7E-01	0.1	8.4E-01
ENSMUST00000054099	LIM homeobox protein 3 [Source:MGI Symbol;Acc:MGI:102673]	A2ALD9	P50481	6.8	3.8E-04	-1.8	1.6E-02	0.7	8.1E-02	-0.7	2.9E-01
ENSMUST00000053427	upregulator of cell proliferation [Source:MGI Symbol;Acc:MGI:1919296]		Q5NCI0	2.9	1.5E-01	6.9	4.9E-03	-0.4	8.6E-01	-4.4	7.0E-03
ENSMUST00000054125	premelanosome protein [Source:MGI Symbol;Acc:MGI:98301]	Q9CZB2		1.9	2.3E-02	-1.9	3.2E-02	0.8	1.1E-01	-0.5	5.0E-01
ENSMUST00000054128	desmoglein 1 gamma [Source:MGI Symbol;Acc:MGI:2664358]		Q7TSF0	7.3	4.0E-05	-4.5	1.6E-01	0.0	9.9E-01	-0.7	8.2E-01
ENSMUST00000054145	DDB1 and CUL4 associated factor 5 [Source:MGI Symbol;Acc:MGI:2444785]	Q3UV57	Q80T85	-1.4	1.5E-02	7.1	2.4E-03	-1.0	6.1E-01	-0.7	5.3E-01
ENSMUST00000054173	phosphatase, orphan 1 [Source:MGI Symbol;Acc:MGI:2447348]		Q8R2H9	-10.5	4.7E-05	2.6	4.3E-01	-0.8	7.8E-01	2.9	2.7E-01
ENSMUST00000053451	predicted gene 9887 [Source:MGI Symbol;Acc:MGI:3642578]	F6RFI0		-0.1	9.5E-01	3.8	1.9E-02	0.2	8.6E-01	-3.6	2.2E-02
ENSMUST00000054174	cytochrome P450, family 4, subfamily f, polypeptide 14 [Source:MGI Symbol;Acc:MGI:1927669]		Q9EP75	6.2	9.7E-03	-2.9	6.7E-03	0.7	1.9E-01	0.4	6.2E-01
ENSMUST00000054178	nuclear receptor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1315213]		Q8CBD1	7.2	6.1E-05	6.6	2.8E-04	0.1	9.5E-01	0.5	4.7E-01
ENSMUST00000054202	vomeronasal 1 receptor 45 [Source:MGI Symbol;Acc:MGI:1333762]		Q8VIC7	7.4	3.7E-05	7.2	1.4E-04	-0.6	6.4E-01	-0.4	5.1E-01
ENSMUST00000054212	RAB11 family interacting protein 1 (class I) [Source:MGI Symbol;Acc:MGI:1923017]	E9Q8L9		-2.7	4.8E-04	7.3	3.9E-05	-1.5	2.0E-01	0.4	4.3E-01
ENSMUST00000054220	ribosomal protein L18A [Source:MGI Symbol;Acc:MGI:1924058]		P62717	-5.8	2.2E-04	4.0	1.5E-02	-0.6	6.7E-01	-1.2	2.7E-01
ENSMUST00000053484	early endosome antigen 1 [Source:MGI Symbol;Acc:MGI:2442192]		Q8BL66	-0.8	9.8E-02	-1.4	2.9E-02	-0.5	2.0E-01	0.2	7.4E-01
ENSMUST00000054223	RIKEN cDNA 2310057N15 gene [Source:MGI Symbol;Acc:MGI:1916946]	Q9D6T8		4.8	1.1E-02	7.4	1.1E-04	-0.6	6.3E-01	-0.8	2.3E-01
ENSMUST00000054237	doublecortin-like kinase 1 [Source:MGI Symbol;Acc:MGI:1330861]		Q9JLM8	10.0	2.3E-06	-1.4	3.2E-02	1.1	1.2E-02	-0.4	4.7E-01
ENSMUST00000054244	developing brain homeobox 2 [Source:MGI Symbol;Acc:MGI:107445]	F8VQH7		7.3	5.9E-05	6.8	3.3E-04	-0.5	7.3E-01	-1.1	1.5E-01
ENSMUST00000054254	proline and serine rich 2 [Source:MGI Symbol;Acc:MGI:2442238]		Q8C5R2	6.1	4.2E-04	5.1	5.6E-06	0.0	9.9E-01	-0.2	5.0E-01
ENSMUST00000054260	lipase, family member K [Source:MGI Symbol;Acc:MGI:2679259]		Q8BM14	6.8	9.6E-05	-1.8	6.8E-02	1.0	1.0E-01	-4.1	1.2E-02
ENSMUST00000054280	enolase 4 [Source:MGI Symbol;Acc:MGI:2441717]		Q8C042	5.9	1.4E-04	-4.0	5.0E-03	-0.7	2.5E-01	-2.2	1.3E-01
ENSMUST00000054294	frizzled homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1196625]		O70421	8.0	1.0E-05	8.3	6.0E-05	-0.7	6.2E-01	-1.0	1.3E-01
ENSMUST00000053569	interleukin 17 receptor E [Source:MGI Symbol;Acc:MGI:1889371]		Q8BH06	2.2	2.0E-01	5.3	1.2E-02	0.0	9.9E-01	-3.0	4.7E-02
ENSMUST00000054301	lipase, hormone sensitive [Source:MGI Symbol;Acc:MGI:96790]		P54310	-8.3	2.8E-05	-4.3	6.5E-03	-1.0	1.6E-01	-0.9	5.1E-01
ENSMUST00000054310	cytochrome c oxidase assembly factor 4 [Source:MGI Symbol;Acc:MGI:1915435]		Q8BT51	-2.3	1.3E-03	2.0	8.7E-02	-1.8	8.7E-02	0.5	5.8E-01
ENSMUST00000053583	SWIM type zinc finger 7 associated protein 1 [Source:MGI Symbol;Acc:MGI:1914212]		Q8VCI7	0.8	1.4E-01	2.1	8.7E-03	0.5	3.3E-01	-0.8	1.8E-01
ENSMUST00000054343	AKT1 substrate 1 (proline-rich) [Source:MGI Symbol;Acc:MGI:1914855]		Q9D1F4	-3.5	6.2E-03	-6.2	8.6E-05	0.1	8.1E-01	-0.2	8.0E-01
ENSMUST00000053594	CASP2 and RIPK1 domain containing adaptor with death domain [Source:MGI Symbol;Acc:MGI:1336168]	Q549T4	O88843	1.3	5.2E-02	0.6	4.5E-01	0.0	9.5E-01	0.7	3.6E-01
ENSMUST00000054344	iF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase [Source:MGI Symbol;Acc:MGI:21416		Q8BYW9	2.7	8.9E-04	5.4	1.1E-03	-2.5	8.0E-02	-0.4	5.4E-01
ENSMUST00000054351	neuron-derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:1915419]		Q8C119	5.8	3.3E-04	-7.3	5.5E-04	0.3	5.4E-01	3.2	4.5E-02
ENSMUST00000054368	GTPase, IMAP family member 1 [Source:MGI Symbol;Acc:MGI:109368]	Q3TFI6		5.0	4.3E-06	-2.6	5.4E-02	1.1	1.4E-01	0.4	7.3E-01
ENSMUST00000054387	RAB33B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1330805]	Q0PD21	O35963	-1.6	3.3E-02	-1.2	1.6E-01	1.5	2.0E-02	0.6	4.6E-01
ENSMUST00000054395	predicted gene 9817 [Source:MGI Symbol;Acc:MGI:3809102]	Q9D2M0		5.2	4.1E-05	4.0	2.6E-02	-2.0	2.5E-01	-0.7	5.4E-01
ENSMUST00000054399	inhibitor of growth family, member 1 [Source:MGI Symbol;Acc:MGI:1349481]		Q9QXV3	-3.3	1.7E-04	-5.2	1.4E-03	-2.2	4.0E-03	-1.6	2.3E-01
ENSMUST00000053663	WD repeat domain 36 [Source:MGI Symbol;Acc:MGI:1917819]	Q3TAQ9		-2.1	4.0E-01	1.0	6.4E-01	-0.9	6.2E-01	-3.9	1.2E-01
ENSMUST00000054414	chemokine (C-C motif) receptor 4 [Source:MGI Symbol;Acc:MGI:107824]		P51680	5.8	1.2E-05	-5.1	3.6E-02	-0.1	9.0E-01	1.1	6.0E-01
ENSMUST00000053666	solute carrier family 12, member 6 [Source:MGI Symbol;Acc:MGI:2135960]		Q924N4	3.4	1.8E-01	4.4	1.1E-01	-1.2	6.4E-01	-2.3	2.4E-01
ENSMUST00000054418	reticulon 4 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2178759]			2.3	6.1E-03	7.1	2.4E-03	-2.7	1.9E-01	-0.4	6.8E-01
ENSMUST00000053670	calcium release activated channel regulator 2B [Source:MGI Symbol;Acc:MGI:2446129]		Q80ZJ8	1.8	4.4E-01	2.5	4.5E-01	0.3	9.1E-01	-0.3	9.0E-01
ENSMUST00000054426	late cornified envelope 1L [Source:MGI Symbol;Acc:MGI:1920980]	Q9D1G7		6.5	1.6E-03	6.2	7.5E-05	-1.3	2.4E-01	-0.5	3.8E-01
ENSMUST00000053686	uridine-cytidine kinase 2 [Source:MGI Symbol;Acc:MGI:1931744]	Q543C2	Q99PM9	0.3	4.9E-01	0.4	4.6E-01	-0.5	2.2E-01	-0.5	2.6E-01
ENSMUST00000054450	programmed cell death 2 [Source:MGI Symbol;Acc:MGI:104643]			-4.2	6.8E-04	2.4	5.6E-02	0.0	9.7E-01	1.5	1.2E-01
ENSMUST00000054459	transmembrane protein 201 [Source:MGI Symbol;Acc:MGI:1196277]		A2A8U2	6.3	1.5E-05	-0.6	2.4E-01	0.8	4.4E-02	-0.1	8.7E-01
ENSMUST00000053705	beta-1,4-glucuronyltransferase 1 [Source:MGI Symbol;Acc:MGI:1919680]		Q8BWP8	-0.2	7.5E-01	1.1	9.6E-02	0.8	1.5E-01	-0.5	3.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000054462	TBC1 domain family, member 8 [Source:MGI Symbol;Acc:MGI:1927225]		Q9Z1A9	-4.5	2.0E-05	5.4	9.8E-03	-1.2	5.0E-01	1.3	2.5E-01
ENSMUST00000053713	interferon regulatory factor 2 binding protein 1 [Source:MGI Symbol;Acc:MGI:2442159]		Q8R3Y8	-1.8	5.5E-02	-1.0	3.9E-01	1.2	1.2E-01	0.3	7.5E-01
ENSMUST00000054472	Bartter syndrome, infantile, with sensorineural deafness (Barttin) [Source:MGI Symbol;Acc:MGI:2153465]		Q8VIM4	8.2	2.8E-05	5.4	4.6E-04	0.0	9.7E-01	0.2	8.1E-01
ENSMUST00000054487	ajuba LIM protein [Source:MGI Symbol;Acc:MGI:1341886]		Q91XC0	6.7	2.1E-05	2.3	9.1E-02	-0.6	6.1E-01	4.7	7.7E-04
ENSMUST00000053722	zinc finger protein 607 [Source:MGI Symbol;Acc:MGI:3584526]	Q3TQG9		1.6	4.8E-02	0.9	3.0E-01	-1.3	9.5E-02	-0.5	4.7E-01
ENSMUST00000053729	prenyl (solanesyl) diphosphate synthase, subunit 1 [Source:MGI Symbol;Acc:MGI:1889278]		Q33DR2	-0.4	5.2E-01	-2.6	3.5E-02	-1.2	7.3E-02	0.9	3.9E-01
ENSMUST00000054491	SRY (sex determining region Y)-box 18 [Source:MGI Symbol;Acc:MGI:103559]		P43680	5.8	9.8E-05	9.0	2.9E-05	-0.7	5.9E-01	-0.1	9.1E-01
ENSMUST00000054500	C2 calcium-dependent domain containing 4A [Source:MGI Symbol;Acc:MGI:3645763]	E9Q861		6.2	1.4E-04	-1.6	4.1E-02	0.8	8.8E-02	0.7	3.4E-01
ENSMUST00000054523	IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3041174]		Q8CAK1	2.9	1.8E-03	-8.1	1.8E-02	-2.5	3.1E-02	-0.7	8.2E-01
ENSMUST00000054530	von Willebrand factor D and EGF domains [Source:MGI Symbol;Acc:MGI:2685313]		Q6DFV8	6.9	4.8E-05	7.2	7.6E-05	-0.6	6.0E-01	-0.5	3.9E-01
ENSMUST00000054532	keratin associated protein 1-5 [Source:MGI Symbol;Acc:MGI:1916914]	A2A590		6.8	4.2E-04	-1.3	4.8E-02	1.3	6.7E-03	0.1	9.3E-01
ENSMUST00000054536	PQ loop repeat containing [Source:MGI Symbol;Acc:MGI:2444067]		Q8C6U2	-8.3	1.5E-06	-6.1	5.6E-03	-0.3	6.5E-01	1.4	4.6E-01
ENSMUST00000054544	ribosomal protein L36A-like [Source:MGI Symbol;Acc:MGI:1913733]	Q5M9P1	P83882	-6.7	2.3E-05	7.9	1.1E-04	-0.7	6.1E-01	-0.4	5.1E-01
ENSMUST00000054547	protein tyrosine phosphatase, non-receptor type 11 [Source:MGI Symbol;Acc:MGI:99511]		P35235	-6.4	3.6E-05	4.9	5.2E-03	0.7	5.8E-01	0.2	8.5E-01
ENSMUST00000054551	RIKEN cDNA 1110032F04 gene [Source:MGI Symbol;Acc:MGI:1915975]		E9Q0B3	4.5	7.3E-04	1.7	2.4E-02	0.5	4.1E-01	0.3	5.4E-01
ENSMUST00000054553	zinc finger protein 384 [Source:MGI Symbol;Acc:MGI:2443203]	D3YX49		-3.3	3.2E-02	-3.2	3.7E-03	1.3	1.4E-02	0.1	9.5E-01
ENSMUST00000054555	zinc finger protein 41 [Source:MGI Symbol;Acc:MGI:99186]		Q02526	6.6	2.7E-03	4.5	3.1E-03	-0.8	4.8E-01	1.0	2.1E-01
ENSMUST00000053771	phosphorylase kinase beta [Source:MGI Symbol;Acc:MGI:97578]		Q7TSH2	-1.0	1.2E-01	-2.6	1.1E-02	0.2	7.2E-01	1.8	5.1E-02
ENSMUST00000054562	NK1 transcription factor related, locus 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:104806]		P42580	9.4	1.3E-05	5.7	1.2E-04	-0.5	6.1E-01	-0.1	8.1E-01
ENSMUST00000054565	intraflagellar transport 43 [Source:MGI Symbol;Acc:MGI:1923661]		Q9DA69	2.2	1.9E-02	-3.2	3.9E-04	0.7	5.0E-02	-0.1	9.3E-01
ENSMUST00000054588	collagen, type IX, alpha 1 [Source:MGI Symbol;Acc:MGI:88465]	G3X995		6.2	3.3E-03	-7.0	9.0E-03	1.0	1.8E-01	3.0	1.9E-01
ENSMUST00000054599	small proline-rich protein 1A [Source:MGI Symbol;Acc:MGI:106660]		Q62266	6.5	1.7E-03	6.8	2.4E-04	-0.5	7.0E-01	-0.4	5.4E-01
ENSMUST00000054622	regulator of telomere elongation helicase 1 [Source:MGI Symbol;Acc:MGI:2139369]		Q0VGM9	-2.6	2.8E-02	5.8	9.2E-04	-0.6	6.5E-01	-0.3	6.8E-01
ENSMUST00000054635	orofacial cleft 1 candidate 1 [Source:MGI Symbol;Acc:MGI:2658851]	C3S7Q5		4.2	3.6E-04	8.0	2.0E-04	0.4	7.7E-01	-0.2	7.6E-01
ENSMUST00000054636	BCL2-associated athanogene 5 [Source:MGI Symbol;Acc:MGI:1917619]		Q8CI32	-3.1	1.5E-02	6.2	8.9E-05	-1.8	1.1E-01	0.2	7.4E-01
ENSMUST00000054650	heat shock protein 3 [Source:MGI Symbol;Acc:MGI:1928479]		Q9QZ57	6.0	2.1E-04	-4.5	3.9E-02	0.9	3.0E-01	2.0	3.0E-01
ENSMUST00000054651	phospholipase A2, group IVF [Source:MGI Symbol;Acc:MGI:2685493]		Q50L41	8.0	2.0E-04	7.5	1.2E-03	-0.8	6.6E-01	-0.5	6.1E-01
ENSMUST00000054654	zinc finger protein 286 [Source:MGI Symbol;Acc:MGI:2384758]	Q8C0E6		4.6	2.4E-04	-3.7	1.0E-02	1.8	1.3E-02	-0.6	6.3E-01
ENSMUST00000054661	adrenergic receptor, alpha 1a [Source:MGI Symbol;Acc:MGI:104773]		P97718	6.6	6.7E-05	-4.3	4.7E-04	1.1	1.8E-02	-0.3	7.1E-01
ENSMUST00000054666	cold inducible RNA binding protein [Source:MGI Symbol;Acc:MGI:893588]	K4DI65		-4.0	2.2E-03	3.8	2.5E-03	0.6	4.6E-01	-0.1	8.3E-01
ENSMUST00000054680	zinc finger protein 444 [Source:MGI Symbol;Acc:MGI:1923365]	Q3TDV8		2.5	3.4E-03	8.9	7.2E-05	-0.8	5.7E-01	0.0	9.9E-01
ENSMUST00000054684	ring finger protein 130 [Source:MGI Symbol;Acc:MGI:1891717]	Q5SVR5		-3.8	4.0E-03	5.9	5.3E-02	-0.6	8.5E-01	-0.3	8.4E-01
ENSMUST00000054691	forkhead box C2 [Source:MGI Symbol;Acc:MGI:1347481]	B9EI61	Q61850	8.2	5.0E-05	-5.8	9.7E-03	0.4	5.0E-01	2.6	1.7E-01
ENSMUST00000054697	Yip1 domain family, member 6 [Source:MGI Symbol;Acc:MGI:1925179]		Q8BR70	2.6	9.9E-03	7.5	2.0E-04	-0.5	7.3E-01	-1.2	1.1E-01
ENSMUST00000054716	actin, beta-like 2 [Source:MGI Symbol;Acc:MGI:2444552]		Q8BFZ3	6.5	9.4E-05	-4.9	1.0E-01	0.5	7.2E-01	-1.1	7.2E-01
ENSMUST00000054730	hippocampus abundant transcript-like 1 [Source:MGI Symbol;Acc:MGI:1913881]		Q8C1A9	-5.0	5.4E-06	-1.1	5.6E-01	2.8	4.2E-02	-0.7	7.2E-01
ENSMUST00000054738	G protein-coupled receptor 151 [Source:MGI Symbol;Acc:MGI:2441887]		Q7TSN6	5.9	2.3E-04	-1.8	4.2E-03	0.8	1.9E-02	-0.8	1.5E-01
ENSMUST00000053918	pyrroline-5-carboxylate reductase-like [Source:MGI Symbol;Acc:MGI:1913444]		Q9DCC4	0.9	2.4E-01	0.6	5.0E-01	0.1	9.3E-01	0.3	7.0E-01
ENSMUST00000054742	actin-binding Rho activating protein [Source:MGI Symbol;Acc:MGI:2444891]		Q8BUZ1	6.5	3.8E-04	7.3	5.3E-04	-0.4	8.1E-01	-1.7	4.9E-02
ENSMUST00000054776	rin homology domain containing, family F (with FYVE domain) member 2 [Source:MGI Symbol;Acc:MGI:19		Q91WB4	-4.9	5.9E-05	5.5	8.1E-04	-0.6	6.4E-01	1.1	1.2E-01
ENSMUST00000054781	predicted gene 20715 [Source:MGI Symbol;Acc:MGI:5313162]	E9Q3L7		10.4	1.7E-05	5.5	1.7E-04	0.5	5.5E-01	0.1	7.9E-01
ENSMUST00000054786	immunoglobulin (CD79A) binding protein 1b [Source:MGI Symbol;Acc:MGI:1354380]	A0A0B4J1F7		6.6	3.1E-04	-4.3	4.6E-03	0.5	3.0E-01	0.9	4.4E-01
ENSMUST00000053959	integrator complex subunit 6 [Source:MGI Symbol;Acc:MGI:1202397]		Q6PCM2	0.5	3.2E-01	1.5	7.0E-02	1.1	7.9E-02	0.2	7.6E-01
ENSMUST00000054791	V-set domain containing T cell activation inhibitor 1 [Source:MGI Symbol;Acc:MGI:3039619]		Q7TSP5	6.3	1.0E-04	-1.8	1.3E-01	0.7	3.3E-01	-4.9	7.5E-03
ENSMUST00000054799	cDNA sequence BC048671 [Source:MGI Symbol;Acc:MGI:2679261]		Q8C5S3	4.5	2.2E-04	6.4	7.0E-04	-0.4	7.6E-01	-1.1	1.7E-01
ENSMUST00000054801	methyltransferase like 21E [Source:MGI Symbol;Acc:MGI:2685837]		Q8CDZ2	8.2	4.8E-04	-3.1	5.9E-04	-0.7	6.7E-02	-0.9	1.8E-01
ENSMUST00000054815	protein phosphatase 1, regulatory (inhibitor) subunit 13B [Source:MGI Symbol;Acc:MGI:1336199]		Q62415	1.7	1.7E-02	7.5	6.5E-05	-1.4	2.6E-01	-0.3	5.8E-01
ENSMUST00000054819	SRY (sex determining region Y)-box 14 [Source:MGI Symbol;Acc:MGI:98362]	Q3UUP3	Q04892	5.8	2.9E-03	5.4	6.4E-03	-0.5	7.8E-01	-0.4	6.7E-01
ENSMUST00000054825	retinoic acid receptor responder (tazarotene induced) 1 [Source:MGI Symbol;Acc:MGI:1924461]	F6ZIS7		5.1	9.5E-04	-4.7	6.3E-04	1.0	5.6E-02	-0.1	9.2E-01
ENSMUST00000054836	harakiri, BCL2 interacting protein (contains only BH3 domain) [Source:MGI Symbol;Acc:MGI:1201608]		P62816	9.2	4.7E-05	-3.6	2.8E-03	0.5	2.8E-01	-0.1	9.5E-01
ENSMUST00000054865	cilia and flagella associated protein 69 [Source:MGI Symbol;Acc:MGI:2443778]		Q8BH53	7.3	3.2E-05	7.2	2.1E-04	-1.2	3.6E-01	1.3	6.6E-02
ENSMUST00000054022	cDNA sequence BC024139 [Source:MGI Symbol;Acc:MGI:2442591]	Q8BVJ3		3.6	1.0E-01	0.4	9.0E-01	-0.4	8.9E-01	2.8	3.1E-01
ENSMUST00000054867	G protein-coupled receptor 37 [Source:MGI Symbol;Acc:MGI:1313297]		Q9QY42	7.7	2.3E-05	4.9	8.7E-03	-1.0	4.9E-01	0.0	9.6E-01
ENSMUST00000054883	POU domain, class 3, transcription factor 3 [Source:MGI Symbol;Acc:MGI:102564]		P31361	9.1	4.5E-05	5.5	1.0E-02	0.6	7.3E-01	1.3	2.5E-01
ENSMUST00000054889	claudin 2 [Source:MGI Symbol;Acc:MGI:1276110]		O88552	5.7	7.3E-04	7.3	1.6E-05	-0.1	9.2E-01	1.1	3.2E-02
ENSMUST00000054895	scavenger receptor cysteine rich family, 4 domains [Source:MGI Symbol;Acc:MGI:1924709]	G3X988		-5.9	2.2E-04	-2.8	1.0E-02	-0.5	3.7E-01	-0.7	4.9E-01
ENSMUST00000054908	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915205]		Q9CX34	-5.6	2.3E-05	3.0	1.1E-02	-0.5	5.3E-01	0.3	7.4E-01
ENSMUST00000054917	erythrocyte membrane protein band 4.1 [Source:MGI Symbol;Acc:MGI:95401]		P48193	-9.4	6.7E-05	7.5	1.0E-03	-0.8	6.6E-01	-0.4	6.9E-01
ENSMUST00000054920	expressed sequence AI464131 [Source:MGI Symbol;Acc:MGI:2140300]		Q69ZQ1	7.0	5.5E-06	2.2	2.2E-03	-0.6	2.0E-01	-0.3	4.6E-01
ENSMUST00000054080	family with sequence similarity 60, member A [Source:MGI Symbol;Acc:MGI:1929091]		Q8C8M1	0.8	1.7E-01	1.2	1.1E-01	0.6	2.6E-01	0.1	8.1E-01
ENSMUST00000054925	F-box and WD-40 domain protein 21 [Source:MGI Symbol;Acc:MGI:2443323]	Q8BI38		6.1	8.4E-04	-4.2	2.1E-02	2.2	8.5E-03	-0.6	7.4E-01
ENSMUST00000054930	pentraxin 4 [Source:MGI Symbol;Acc:MGI:1915759]	E9QNW3		7.5	2.0E-05	6.7	1.8E-04	-0.6	6.2E-01	0.0	1.0E+00
ENSMUST00000054096	mannosidase, alpha, class 1C, member 1 [Source:MGI Symbol;Acc:MGI:2446214]	Q6NXK9		-3.3	8.3E-02	-0.4	7.7E-01	-0.5	6.6E-01	-3.3	1.0E-01
ENSMUST00000054945	aquaporin 7 [Source:MGI Symbol;Acc:MGI:1314647]	Q5DX24	O54794	6.5	1.2E-06	3.9	4.0E-03	0.3	7.5E-01	0.4	6.1E-01
ENSMUST00000054952	ER membrane protein complex subunit 6 [Source:MGI Symbol;Acc:MGI:1913298]		Q9CQW0	-4.0	4.8E-05	6.2	1.3E-03	-0.6	7.0E-01	0.0	9.9E-01
ENSMUST00000054107	potassium channel tetramerisation domain containing 21 [Source:MGI Symbol;Acc:MGI:3643121]	B2RTJ2		0.5	3.8E-01	2.6	7.6E-03	1.8	1.7E-02	-0.3	6.3E-01
ENSMUST00000054955	echinoderm microtubule associated protein like 1 [Source:MGI Symbol;Acc:MGI:1915769]		Q05BC3	5.2	1.5E-02	2.4	2.6E-02	0.4	5.8E-01	0.0	9.5E-01
ENSMUST00000054956	STAM binding protein like 1 [Source:MGI Symbol;Acc:MGI:1923880]		Q76N33	-1.9	4.8E-03	7.5	6.9E-05	-0.5	6.7E-01	-0.7	2.7E-01
ENSMUST00000054963	farnesyl diphosphate farnesyl transferase 1 [Source:MGI Symbol;Acc:MGI:102706]		P53798	-1.7	1.4E-03	-0.6	3.5E-01	0.8	8.0E-02	0.0	9.5E-01
ENSMUST00000054973	chitinase-like 5 [Source:MGI Symbol;Acc:MGI:2676649]	F7D8T8		-6.8	1.5E-04	-5.5	8.9E-04	-0.4	4.0E-01	-0.4	7.7E-01
ENSMUST00000054979	AF4/FMR2 family, member 1 [Source:MGI Symbol;Acc:MGI:1100819]	A3KMF4		-7.1	6.4E-05	-9.8	6.4E-04	1.4	1.9E-02	0.7	7.6E-01
ENSMUST00000055013	zinc finger, MYM domain containing 1 [Source:MGI Symbol;Acc:MGI:1915560]	Q3TJB1		-4.4	2.7E-04	7.2	6.3E-03	-0.8	7.3E-01	-1.8	1.5E-01
ENSMUST00000055014	selection and upkeep of intraepithelial T cells 7 [Source:MGI Symbol;Acc:MGI:3041190]		A7XV04	6.0	1.1E-03	4.9	2.8E-03	-1.6	2.0E-01	0.7	3.8E-01
ENSMUST00000054197	sphingosine-1-phosphate receptor 2 [Source:MGI Symbol;Acc:MGI:99569]		P52592	-0.5	2.9E-01	1.0	1.3E-01	1.1	3.5E-02	-0.4	5.1E-01
ENSMUST00000055022	transmembrane protein, adipocyte asscociated 1 [Source:MGI Symbol;Acc:MGI:1345190]		Q99MU1	-4.5	2.9E-03	6.9	1.3E-04	-0.5	6.4E-01	-0.1	9.0E-01
ENSMUST00000055032	lysine (K)-specific demethylase 5D [Source:MGI Symbol;Acc:MGI:99780]		Q62240	4.9	8.8E-08	-1.7	2.7E-02	0.7	9.7E-02	-0.3	6.7E-01
ENSMUST00000054213	translocase of inner mitochondrial membrane 8A1 [Source:MGI Symbol;Acc:MGI:1353433]		Q9WVA2	-1.3	2.2E-01	-1.9	2.0E-01	-0.4	6.4E-01	0.1	9.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000055036	outer dense fiber of sperm tails 3-like 1 [Source:MGI Symbol;Acc:MGI:2681875]		Q810P2	6.4	1.7E-04	-6.3	6.3E-04	-1.0	9.6E-02	-0.5	7.1E-01
ENSMUST00000055052	carboxylesterase 2C [Source:MGI Symbol;Acc:MGI:2385905]		Q91WG0	5.2	3.3E-02	6.1	4.0E-03	-0.6	7.4E-01	-1.9	8.2E-02
ENSMUST00000054230	Scm-like with four mbt domains 1 [Source:MGI Symbol;Acc:MGI:1859609]		Q9JMD1	0.2	7.8E-01	0.8	2.8E-01	0.4	5.0E-01	-0.3	6.7E-01
ENSMUST00000054234	NIMA (never in mitosis gene a)-related expressed kinase 6 [Source:MGI Symbol;Acc:MGI:1891638]		Q9ES70	-1.4	2.8E-01	2.9	1.4E-01	2.6	1.3E-01	-1.6	2.4E-01
ENSMUST00000055056	ras homolog gene family, member T1 [Source:MGI Symbol;Acc:MGI:1926078]		Q8BG51	5.9	7.7E-04	6.1	8.0E-05	-3.5	8.7E-03	0.4	3.6E-01
ENSMUST00000055064	otassium voltage-gated channel, shaker-related subfamily, member 10 [Source:MGI Symbol;Acc:MGI:303782(	B2RQA1		6.7	1.3E-04	7.0	2.2E-04	-0.2	8.9E-01	0.1	9.0E-01
ENSMUST00000054245	transmembrane protein 132E [Source:MGI Symbol;Acc:MGI:2685490]	A0A0A0MQ93		3.7	1.0E-01	4.7	7.1E-02	-0.5	8.4E-01	-1.4	3.9E-01
ENSMUST00000055071	interferon, alpha-inducible protein 27 like 2A [Source:MGI Symbol;Acc:MGI:1924183]		Q8R412	-3.9	1.5E-03	3.8	2.2E-03	-2.9	2.4E-02	-0.7	3.7E-01
ENSMUST00000055077	paralemmin 3 [Source:MGI Symbol;Acc:MGI:1921587]		A2TJV2	8.0	2.5E-05	6.8	1.7E-04	-0.6	6.1E-01	-0.7	3.0E-01
ENSMUST00000054274	lipoma HMGIC fusion partner-like 2 [Source:MGI Symbol;Acc:MGI:2145236]		Q8BGA2	-1.4	5.1E-01	2.0	5.3E-01	3.5	1.7E-01	0.1	9.7E-01
ENSMUST00000054279	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	E9Q4Y0		0.2	6.3E-01	0.3	6.7E-01	0.0	1.0E+00	0.0	9.6E-01
ENSMUST00000055083	hypocretin [Source:MGI Symbol;Acc:MGI:1202306]	Q547R2	O55241	7.1	8.3E-05	7.0	1.6E-04	0.5	6.9E-01	-0.6	3.2E-01
ENSMUST00000054287	zinc finger and BTB domain containing 39 [Source:MGI Symbol;Acc:MGI:2443316]	Q6PDK0		-0.8	2.2E-01	0.4	6.6E-01	0.9	1.8E-01	-0.3	6.9E-01
ENSMUST00000054289	ribosomal protein S2 [Source:MGI Symbol;Acc:MGI:105110]	Q58EU3	P25444	1.0	3.7E-01	-0.4	8.4E-01	1.4	3.0E-01	2.7	1.1E-01
ENSMUST00000055087	spleen tyrosine kinase [Source:MGI Symbol;Acc:MGI:99515]	Q3UPF7	P48025	-7.3	1.5E-03	2.8	2.5E-03	-4.9	3.6E-04	0.3	6.3E-01
ENSMUST00000055096	tetratricopeptide repeat domain 12 [Source:MGI Symbol;Acc:MGI:2444588]		Q8BW49	1.9	9.3E-03	-6.9	8.9E-04	1.1	3.6E-02	-0.3	8.3E-01
ENSMUST00000054308	G2/M-phase specific E3 ubiquitin ligase [Source:MGI Symbol;Acc:MGI:2444298]		Q5RJY2	-0.4	4.8E-01	0.7	2.8E-01	0.3	4.6E-01	-0.7	2.5E-01
ENSMUST00000055100	guanine nucleotide binding protein (G protein), gamma 2 [Source:MGI Symbol;Acc:MGI:102705]		P63213	-6.5	2.2E-05	-1.3	6.4E-02	0.0	9.1E-01	-1.0	1.3E-01
ENSMUST00000054324	nucleotide-binding oligomerization domain containing 2 [Source:MGI Symbol;Acc:MGI:2429397]		Q8K3Z0	2.3	3.4E-01	3.3	3.3E-01	1.9	4.6E-01	0.9	7.6E-01
ENSMUST00000055104	transcription elongation factor A (SII)-like 1 [Source:MGI Symbol;Acc:MGI:2385317]		Q921P9	5.3	9.7E-05	-3.3	4.7E-02	1.1	1.6E-01	0.9	5.6E-01
ENSMUST00000055107	predicted gene 4922 [Source:MGI Symbol;Acc:MGI:3644318]		Q8C0N0	7.3	6.6E-05	1.6	4.2E-02	-0.4	4.9E-01	0.7	2.8E-01
ENSMUST00000055115	von Willebrand factor C and EGF domains [Source:MGI Symbol;Acc:MGI:1919018]		Q3U515	9.2	4.3E-06	5.2	2.0E-03	-1.1	4.0E-01	-0.5	5.2E-01
ENSMUST00000055117	LEM domain containing 2 [Source:MGI Symbol;Acc:MGI:2385045]		Q6DVA0	-2.7	3.3E-03	4.3	3.6E-05	-0.9	1.4E-01	-0.2	6.7E-01
ENSMUST00000054384	tripartite motif-containing 56 [Source:MGI Symbol;Acc:MGI:2685298]			-0.3	5.7E-01	-0.1	9.3E-01	0.6	3.5E-01	0.3	6.9E-01
ENSMUST00000055121	keratin associated protein 4-7 [Source:MGI Symbol;Acc:MGI:1923694]	Q9D732		7.3	6.5E-05	-1.1	2.2E-01	0.4	4.2E-01	-0.1	9.5E-01
ENSMUST00000055125	DIRAS family, GTP-binding RAS-like 1 [Source:MGI Symbol;Acc:MGI:2183442]		Q91Z61	9.7	1.9E-04	6.4	1.6E-04	1.1	2.8E-01	-0.1	8.7E-01
ENSMUST00000055128	transmembrane anterior posterior transformation 1 [Source:MGI Symbol;Acc:MGI:2683537]		Q4VBD2	-3.6	2.0E-04	-3.6	7.0E-04	0.2	6.7E-01	0.4	5.6E-01
ENSMUST00000055131	ubiquitin specific peptidase 48 [Source:MGI Symbol;Acc:MGI:2158502]		Q3V0C5	-4.5	2.7E-02	4.0	5.2E-04	-1.1	1.4E-01	0.7	2.3E-01
ENSMUST00000054415	zinc finger protein 668 [Source:MGI Symbol;Acc:MGI:2442943]		Q8K2R5	1.4	1.8E-01	1.9	2.5E-01	1.5	3.0E-01	1.0	4.0E-01
ENSMUST00000055156	catsper channel auxiliary subunit beta [Source:MGI Symbol;Acc:MGI:2443988]		A2RTF1	6.4	1.3E-04	2.3	2.5E-02	0.4	5.8E-01	0.4	5.8E-01
ENSMUST00000055159	ADP-ribosylation factor-like 11 [Source:MGI Symbol;Acc:MGI:2444054]		Q6P3A9	-4.9	4.2E-06	5.7	5.6E-03	-0.7	6.7E-01	0.0	9.8E-01
ENSMUST00000054442	N-6 adenine-specific DNA methyltransferase 1 (putative) [Source:MGI Symbol;Acc:MGI:1915018]	Q6SKR2		-1.3	5.0E-01	-0.1	9.5E-01	-2.0	1.7E-01	-3.3	1.2E-01
ENSMUST00000054445	hypoxia inducible lipid droplet associated [Source:MGI Symbol;Acc:MGI:1916823]		Q9JLS0	-0.1	9.2E-01	-2.1	4.1E-02	-1.7	2.9E-02	0.3	7.3E-01
ENSMUST00000055168	potassium voltage-gated channel, shaker-related subfamily, member 1 [Source:MGI Symbol;Acc:MGI:96654]		P16388	10.1	1.1E-05	-4.4	3.1E-03	0.0	9.4E-01	0.2	8.9E-01
ENSMUST00000055190	BAI1-associated protein 2-like 1 [Source:MGI Symbol;Acc:MGI:1914148]		Q9DBJ3	3.4	4.7E-03	5.7	4.2E-04	-0.2	8.2E-01	0.4	5.2E-01
ENSMUST00000055195	limb region 1 [Source:MGI Symbol;Acc:MGI:1861746]		Q9JIT0	6.7	2.4E-02	-2.1	9.3E-03	1.4	4.7E-03	-1.0	1.8E-01
ENSMUST00000055204	olfactory receptor 30 [Source:MGI Symbol;Acc:MGI:109305]	Q8VGD8		6.8	6.7E-05	5.3	1.7E-04	-1.3	1.8E-01	1.1	6.2E-02
ENSMUST00000054471	RIKEN cDNA 4930430F08 gene [Source:MGI Symbol;Acc:MGI:1921197]		Q8BHN7	0.3	6.1E-01	-0.5	5.0E-01	-1.0	1.1E-01	-0.2	8.0E-01
ENSMUST00000055211	leucine rich repeat containing 3B [Source:MGI Symbol;Acc:MGI:2384996]	Q543Z7	Q8VCH9	5.8	6.4E-03	8.5	4.2E-05	-0.7	6.1E-01	-0.9	1.4E-01
ENSMUST00000054477				-1.5	3.2E-01	-2.0	4.4E-01	1.5	3.2E-01	2.0	4.1E-01
ENSMUST00000054483	TRAF-interacting protein with forkhead-associated domain [Source:MGI Symbol;Acc:MGI:2182965]	I3PQW8	Q793I8	1.8	4.2E-01	1.1	6.0E-01	-2.0	3.3E-01	-1.4	5.0E-01
ENSMUST00000055213	MYST/Esa1-associated factor 6 [Source:MGI Symbol;Acc:MGI:1917338]		Q2VPQ9	-4.4	2.2E-03	4.6	4.6E-04	-2.1	3.7E-02	0.0	9.6E-01
ENSMUST00000055221	potassium channel, subfamily K, member 12 [Source:MGI Symbol;Acc:MGI:2684043]	Q76M80		3.8	3.9E-03	5.2	4.8E-04	-0.7	4.8E-01	-0.1	8.5E-01
ENSMUST00000055223	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:MGI Symbol;Acc:MGI:1928739]		Q9QYI5	3.2	2.8E-02	5.4	7.3E-04	-0.6	6.2E-01	0.2	7.1E-01
ENSMUST00000055241	zinc finger protein 106 [Source:MGI Symbol;Acc:MGI:1270153]	R4GML0		-2.8	3.8E-04	4.0	1.2E-03	0.9	2.7E-01	-0.2	7.1E-01
ENSMUST00000055242	cleft lip and palate associated transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1927155]		Q8VBZ3	-2.9	6.4E-04	7.2	6.9E-05	-0.5	6.4E-01	-0.8	1.7E-01
ENSMUST00000055257	family with sequence similarity 89, member A [Source:MGI Symbol;Acc:MGI:1916877]		Q14BJ1	2.9	4.3E-03	5.6	2.5E-03	-0.7	6.6E-01	0.5	5.5E-01
ENSMUST00000055261	MOB kinase activator 1A [Source:MGI Symbol;Acc:MGI:2442631]		Q921Y0	-7.6	2.2E-05	-6.6	6.5E-06	0.5	1.3E-01	-1.2	1.7E-01
ENSMUST00000054538	Rho guanine nucleotide exchange factor (GEF) 39 [Source:MGI Symbol;Acc:MGI:3036286]		Q66JY6	-0.4	8.0E-01	3.4	1.3E-01	2.6	1.8E-01	-1.2	4.5E-01
ENSMUST00000055262	vesicle transport through interaction with t-SNAREs 1B [Source:MGI Symbol;Acc:MGI:1855688]	Q91XH6		-5.8	2.5E-04	-9.9	1.6E-04	-1.4	8.2E-03	1.8	2.9E-01
ENSMUST00000055281	SKI family transcriptional corepressor 1 [Source:MGI Symbol;Acc:MGI:2443473]		Q8BX46	7.4	1.9E-02	-6.0	8.3E-04	0.9	6.1E-02	0.5	7.1E-01
ENSMUST00000055294	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1344367]	Q3TST1	O88273	7.8	2.2E-05	5.5	1.6E-03	1.3	2.8E-01	0.3	7.3E-01
ENSMUST00000055303	methyltransferase like 6 [Source:MGI Symbol;Acc:MGI:1914261]		Q8BVH9	-2.0	3.1E-03	-1.5	3.6E-01	0.6	5.7E-01	-1.1	5.0E-01
ENSMUST00000055304	phosphatidylinositol-4-phosphate 5-kinase-like 1 [Source:MGI Symbol;Acc:MGI:2448520]		Q6U7H8	5.3	5.2E-03	6.7	4.5E-03	-0.3	8.8E-01	-0.4	6.9E-01
ENSMUST00000055314	transmembrane epididymal protein 1B [Source:MGI Symbol;Acc:MGI:3646829]	Q8CC62		5.3	8.3E-04	8.7	1.5E-04	0.1	9.4E-01	0.8	2.4E-01
ENSMUST00000055322	immediate early response 5 [Source:MGI Symbol;Acc:MGI:1337072]	Q3UJ54	O89113	-5.7	2.0E-04	-0.7	3.9E-01	-3.2	2.2E-03	-0.2	8.0E-01
ENSMUST00000055327	aquaporin 3 [Source:MGI Symbol;Acc:MGI:1333777]		Q8R2N1	7.5	8.2E-06	3.4	9.2E-02	-0.5	7.8E-01	2.3	9.6E-02
ENSMUST00000054591	threonine synthase-like 1 (bacterial) [Source:MGI Symbol;Acc:MGI:2139347]	Q149D1	Q8BH55	0.7	2.4E-01	0.4	6.4E-01	-0.2	7.8E-01	0.2	7.6E-01
ENSMUST00000054598	actin-binding LIM protein 2 [Source:MGI Symbol;Acc:MGI:2385758]		Q8BL65	5.6	9.2E-02	4.0	2.5E-01	-0.5	8.9E-01	1.0	6.2E-01
ENSMUST00000055334	homeobox B3 [Source:MGI Symbol;Acc:MGI:96184]		P09026	7.6	1.3E-03	4.0	9.8E-03	-2.7	9.8E-02	-0.2	7.9E-01
ENSMUST00000054607	S-adenosylhomocysteine hydrolase [Source:MGI Symbol;Acc:MGI:87968]	Q3TF14	P50247	1.4	1.8E-01	2.0	1.3E-01	1.1	3.0E-01	0.5	6.5E-01
ENSMUST00000055341	glucose-fructose oxidoreductase domain containing 1 [Source:MGI Symbol;Acc:MGI:2145304]		Q3UHD2	-1.2	1.3E-02	-1.3	3.7E-01	0.8	3.9E-01	-0.5	7.1E-01
ENSMUST00000055345	transmembrane protein 202 [Source:MGI Symbol;Acc:MGI:1921143]	B9EHM8	Q80W35	-2.4	9.0E-03	3.9	1.1E-03	-1.0	2.1E-01	-0.7	2.8E-01
ENSMUST00000055349	zinc finger prtoein 943 [Source:MGI Symbol;Acc:MGI:1921920]	Q6NZP4		-3.0	1.1E-03	-1.3	2.1E-01	-0.4	5.5E-01	-2.3	7.4E-02
ENSMUST00000055353	msh homeobox 3 [Source:MGI Symbol;Acc:MGI:106587]	G3X9C7		5.8	2.3E-02	6.2	4.5E-04	0.1	9.6E-01	-0.1	8.6E-01
ENSMUST00000055355	.as association (RalGDS/AF-6) domain family (N-terminal) member 9 [Source:MGI Symbol;Acc:MGI:238430]		Q8K342	6.4	1.1E-04	7.5	6.2E-04	-0.7	6.5E-01	-0.2	8.1E-01
ENSMUST00000055369	cDNA sequence BC106179 [Source:MGI Symbol;Acc:MGI:3702726]	Q8C9L1		6.1	9.0E-06	6.9	2.0E-04	1.5	2.0E-01	-0.8	2.5E-01
ENSMUST00000055374	testis-specific serine kinase 2 [Source:MGI Symbol;Acc:MGI:1347559]		O54863	5.1	4.8E-05	2.2	1.0E-01	-0.5	6.5E-01	3.8	2.8E-03
ENSMUST00000055389	xyloside xylosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2146443]		Q3U4G3	-2.5	1.9E-03	4.2	2.4E-02	0.1	9.4E-01	-0.3	7.6E-01
ENSMUST00000054665	ankyrin repeat domain 23 [Source:MGI Symbol;Acc:MGI:1925571]	A2RT50	Q812A3	4.1	5.4E-02	7.4	2.4E-02	2.0	4.6E-01	-1.3	4.5E-01
ENSMUST00000055390	ras homolog gene family, member J [Source:MGI Symbol;Acc:MGI:1931551]		Q9ER71	2.6	3.3E-03	-1.5	2.1E-01	1.0	1.7E-01	-1.5	2.4E-01
ENSMUST00000054674	Holliday junction recognition protein [Source:MGI Symbol;Acc:MGI:2685821]	E9QKG8		-0.9	8.8E-02	0.5	4.0E-01	1.3	2.2E-02	-0.1	8.2E-01
ENSMUST00000055404	RIKEN cDNA 9930022D16 gene [Source:MGI Symbol;Acc:MGI:2444178]	Q8BG27		7.7	2.0E-05	3.5	2.0E-03	1.0	1.7E-01	0.0	9.6E-01
ENSMUST00000055406	serine/threonine kinase-like domain containing 1 [Source:MGI Symbol;Acc:MGI:2685557]		Q80YS9	3.2	6.6E-04	-3.5	1.7E-02	-0.4	5.9E-01	-0.6	6.3E-01
ENSMUST00000055408	coiled-coil domain containing 64 [Source:MGI Symbol;Acc:MGI:1922915]		A0JNT9	-3.6	5.2E-03	4.4	1.1E-03	-3.7	9.8E-03	0.0	9.7E-01
ENSMUST00000055421	transmembrane 239 [Source:MGI Symbol;Acc:MGI:1914016]		Q9DA47	8.7	1.2E-03	1.6	1.5E-01	-0.1	9.3E-01	0.9	3.4E-01
ENSMUST00000054708	)P-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase) [Source:MGI Syml		P42867	-0.9	1.9E-01	-0.5	5.5E-01	0.0	9.3E-01	-0.5	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000055424	stimulated by retinoic acid 13 [Source:MGI Symbol;Acc:MGI:894324]		Q8C4X1	-6.6	3.6E-04	4.2	4.0E-02	-1.4	4.6E-01	0.5	6.6E-01
ENSMUST00000055436	4-hydroxyphenylpyruvate dioxygenase-like [Source:MGI Symbol;Acc:MGI:2444646]		Q8K248	7.0	4.9E-05	6.7	1.5E-04	-0.6	6.3E-01	-0.7	2.6E-01
ENSMUST00000055438	protein phosphatase 1E (PP2C domain containing) [Source:MGI Symbol;Acc:MGI:2444096]	B2KGP3	Q80TL0	3.0	7.0E-04	-4.9	6.3E-05	0.6	7.8E-02	0.6	4.4E-01
ENSMUST00000055458	CDC42 effector protein (Rho GTPase binding) 2 [Source:MGI Symbol;Acc:MGI:1929744]		Q8JZX9	-4.1	7.1E-04	4.4	8.7E-04	-1.9	8.9E-02	-0.4	5.3E-01
ENSMUST00000055483	X-linked inhibitor of apoptosis [Source:MGI Symbol;Acc:MGI:107572]		Q60989	-7.3	1.6E-02	6.3	1.2E-03	0.0	9.8E-01	0.2	8.0E-01
ENSMUST00000054764	sulfite oxidase [Source:MGI Symbol;Acc:MGI:2446117]		Q8R086	1.0	1.4E-01	1.9	4.8E-02	0.9	2.1E-01	0.0	9.8E-01
ENSMUST00000055485	LSM14 homolog B (SCD6, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3040677]		Q8CGC4	-6.0	9.5E-05	-3.3	4.7E-03	1.5	9.6E-03	-0.1	9.3E-01
ENSMUST00000054780	zinc finger protein 959 [Source:MGI Symbol;Acc:MGI:2385058]	Q91VM8		-0.1	9.0E-01	0.5	5.7E-01	0.5	5.0E-01	-0.1	8.6E-01
ENSMUST00000055490	otopetrin 2 [Source:MGI Symbol;Acc:MGI:2388365]		Q80SX5	7.8	1.5E-04	8.1	1.3E-04	-1.4	3.4E-01	0.9	1.8E-01
ENSMUST00000055495	protocadherin beta 12 [Source:MGI Symbol;Acc:MGI:2136747]	Q91Y07		7.8	3.6E-05	5.4	2.2E-03	-0.6	6.8E-01	0.6	4.2E-01
ENSMUST00000055502	keratin associated protein 3-1 [Source:MGI Symbol;Acc:MGI:1916723]		A2AS91	7.0	2.5E-04	4.5	9.2E-04	-1.7	1.2E-01	0.0	9.7E-01
ENSMUST00000055528	zinc finger and SCAN domain containing 22 [Source:MGI Symbol;Acc:MGI:2443312]	Q8BGS5		4.7	7.2E-03	5.2	6.4E-04	0.4	6.7E-01	-0.3	6.9E-01
ENSMUST00000055535	protogenin homolog (Gallus gallus) [Source:MGI Symbol;Acc:MGI:2444710]		Q2EY15	9.1	3.5E-06	6.0	1.5E-03	-2.6	1.5E-01	-0.4	6.5E-01
ENSMUST00000055545	olfactory receptor 70 [Source:MGI Symbol;Acc:MGI:1860079]	Q80ZX9		7.7	1.8E-05	2.1	3.2E-02	0.5	4.2E-01	0.2	7.6E-01
ENSMUST00000055549	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI:1889505]	Q3TVJ9	Q9Z222	-2.5	1.8E-03	7.0	1.4E-03	-0.7	6.9E-01	-1.8	7.1E-02
ENSMUST00000055557	syntaxin 19 [Source:MGI Symbol;Acc:MGI:1915409]		Q8R1Q0	4.2	5.0E-04	3.0	8.5E-03	-2.8	2.3E-02	-0.7	3.4E-01
ENSMUST00000055558	GTPase, IMAP family member 5 [Source:MGI Symbol;Acc:MGI:2442232]		Q8BWF2	2.1	1.3E-02	7.6	3.2E-04	-1.4	3.6E-01	0.2	8.0E-01
ENSMUST00000054855	Leber congenital amaurosis 5-like [Source:MGI Symbol;Acc:MGI:3041157]	E9QN53		6.2	3.7E-02	2.8	3.7E-01	-0.8	8.0E-01	2.6	2.3E-01
ENSMUST00000054857	family with sequence similarity 110, member B [Source:MGI Symbol;Acc:MGI:1916593]		Q8C739	3.3	1.7E-01	5.2	5.2E-02	-0.5	8.3E-01	-2.4	1.7E-01
ENSMUST00000055559	coiled-coil domain containing 126 [Source:MGI Symbol;Acc:MGI:1889376]		Q8BIS8	-3.2	8.6E-05	5.9	1.1E-03	-0.9	5.0E-01	-0.6	4.3E-01
ENSMUST00000055562	homeobox C12 [Source:MGI Symbol;Acc:MGI:96194]		Q8K5B8	6.5	1.6E-04	6.6	8.3E-05	-1.5	1.9E-01	-0.8	1.8E-01
ENSMUST00000055575	U7 snRNP-specific Sm-like protein LSM10 [Source:MGI Symbol;Acc:MGI:2151045]	Q3UPL7	Q8QZX5	-2.9	1.9E-03	7.9	4.9E-05	-0.1	9.1E-01	-0.3	5.3E-01
ENSMUST00000055615	olfactory receptor 1361 [Source:MGI Symbol;Acc:MGI:3031195]	Q8VFH0		5.9	2.2E-04	7.8	1.7E-04	-0.9	5.5E-01	0.4	5.6E-01
ENSMUST00000055619	hypermethylated in cancer 1 [Source:MGI Symbol;Acc:MGI:1338010]	Z4YJP0		7.1	2.0E-05	4.4	2.0E-03	-2.5	6.4E-02	-1.2	1.4E-01
ENSMUST00000055636	clarin 1 [Source:MGI Symbol;Acc:MGI:2388124]		Q8K445	7.2	4.7E-07	-2.0	4.7E-02	0.7	2.4E-01	-3.2	1.6E-02
ENSMUST00000055655	fatty acid synthase [Source:MGI Symbol;Acc:MGI:95485]		P19096	2.3	4.9E-03	-6.0	8.5E-05	-0.3	4.5E-01	0.1	9.0E-01
ENSMUST00000054910	proline rich 33 [Source:MGI Symbol;Acc:MGI:3642289]		Q8C494	-1.9	4.8E-02	-0.9	4.0E-01	0.3	7.0E-01	-0.7	4.9E-01
ENSMUST00000055662	leucine-rich repeats and transmembrane domains 1 [Source:MGI Symbol;Acc:MGI:2442106]	A6H6T2	Q8BXQ3	8.1	9.9E-06	-3.0	1.2E-01	5.6	1.4E-04	-0.8	6.8E-01
ENSMUST00000055693	cytochrome P450, family 2, subfamily j, polypeptide 9 [Source:MGI Symbol;Acc:MGI:1921769]	Q924D1		3.0	1.0E-02	5.6	8.7E-05	-1.0	2.4E-01	0.5	3.9E-01
ENSMUST00000055698	gap junction protein, beta 2 [Source:MGI Symbol;Acc:MGI:95720]	Q3UJE9	Q00977	7.2	5.7E-05	5.2	3.8E-03	-0.5	7.5E-01	0.4	6.6E-01
ENSMUST00000055704	guanine nucleotide binding protein (G protein), alpha inhibiting 2 [Source:MGI Symbol;Acc:MGI:95772]		P08752	-9.0	2.0E-06	6.5	1.2E-04	-0.6	5.9E-01	0.4	5.2E-01
ENSMUST00000055719	cDNA sequence BC025446 [Source:MGI Symbol;Acc:MGI:2385015]	Q8R155		4.2	4.2E-04	5.0	2.1E-05	-1.1	9.6E-02	0.4	3.6E-01
ENSMUST00000055721	cytochrome P450, family 2, subfamily d, polypeptide 40 [Source:MGI Symbol;Acc:MGI:1919004]	Q6P8N9		6.7	2.4E-04	-2.6	5.4E-03	1.2	2.0E-02	-0.2	7.8E-01
ENSMUST00000055735	olfactory receptor 374 [Source:MGI Symbol;Acc:MGI:3030208]	Q7TRY0		5.1	2.3E-04	1.3	3.4E-01	-5.3	9.8E-03	-1.4	2.6E-01
ENSMUST00000055738	TSC22 domain family, member 3 [Source:MGI Symbol;Acc:MGI:1196284]		Q9Z2S7	-9.4	3.1E-05	-1.1	7.6E-02	-0.2	6.0E-01	-0.9	1.6E-01
ENSMUST00000054960	interferon regulatory factor 2 binding protein 2 [Source:MGI Symbol;Acc:MGI:2443921]		E9Q1P8	-1.2	7.2E-02	-0.8	3.4E-01	0.7	2.3E-01	0.3	7.3E-01
ENSMUST00000055745	NLR family, pyrin domain containing 10 [Source:MGI Symbol;Acc:MGI:2444084]	Q6JGS9	Q8CCN1	4.4	2.2E-05	-1.5	1.4E-02	0.1	6.7E-01	-0.1	8.8E-01
ENSMUST00000055770	histone cluster 1, H1a [Source:MGI Symbol;Acc:MGI:1931523]		P43275	5.7	7.2E-04	-6.9	1.2E-03	-0.3	5.3E-01	-0.3	8.8E-01
ENSMUST00000055776	Rho GTPase activating protein 15 [Source:MGI Symbol;Acc:MGI:1923367]		Q811M1	-7.7	8.6E-05	-1.6	5.3E-02	0.9	1.0E-01	-4.6	1.7E-03
ENSMUST00000054984	SFT2 domain containing 3 [Source:MGI Symbol;Acc:MGI:1914408]	E9QJT3		0.6	3.0E-01	1.5	7.0E-02	0.3	6.4E-01	-0.5	4.1E-01
ENSMUST00000055001	Kruppel-like factor 7 (ubiquitous) [Source:MGI Symbol;Acc:MGI:1935151]	Q3UES6		1.1	1.2E-01	1.2	1.1E-01	-1.4	3.9E-02	-1.5	3.6E-02
ENSMUST00000055006	tripartite motif-containing 16 [Source:MGI Symbol;Acc:MGI:2137356]	Q5SVT2		1.4	3.7E-01	3.4	1.5E-01	1.0	6.1E-01	-0.9	5.4E-01
ENSMUST00000055009	Vpr (HIV-1) binding protein [Source:MGI Symbol;Acc:MGI:2445220]		Q80TR8	-2.8	3.4E-01	-0.3	9.0E-01	-0.5	8.0E-01	-3.0	3.5E-01
ENSMUST00000055012	INO80 complex subunit C [Source:MGI Symbol;Acc:MGI:2443014]	F8WIA0		-0.4	8.1E-01	0.3	8.5E-01	-0.9	5.4E-01	-1.6	3.5E-01
ENSMUST00000055792	RIKEN cDNA D030056L22 gene [Source:MGI Symbol;Acc:MGI:3583960]	Q3U2A5		4.9	2.5E-02	-2.9	1.3E-02	0.7	2.2E-01	-0.8	4.5E-01
ENSMUST00000055808	ɔnooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide [Source:MGI Symbol;Acc:I	A8IP69	P61982	-1.5	9.0E-03	5.8	7.0E-03	0.9	5.9E-01	1.0	3.3E-01
ENSMUST00000055843	RNA binding motif protein 15B [Source:MGI Symbol;Acc:MGI:1923598]		Q6PHZ5	-1.0	3.4E-02	-4.3	7.8E-03	0.9	1.9E-01	0.7	6.0E-01
ENSMUST00000055028	zinc finger and BTB domain containing 5 [Source:MGI Symbol;Acc:MGI:1924601]		Q7TQG0	-0.8	3.9E-01	-1.6	2.6E-01	0.6	5.0E-01	1.4	3.1E-01
ENSMUST00000055872	galanin receptor 2 [Source:MGI Symbol;Acc:MGI:1337018]		O88854	6.2	4.5E-05	4.7	5.3E-07	-0.2	5.9E-01	0.1	7.9E-01
ENSMUST00000055879	WD repeat domain 72 [Source:MGI Symbol;Acc:MGI:3583957]	D3YYM4		7.7	2.6E-05	5.9	5.8E-04	-0.5	6.9E-01	0.0	9.9E-01
ENSMUST00000055040	coiled-coil domain containing 69 [Source:MGI Symbol;Acc:MGI:1196234]		Q3TCJ8	-0.5	5.9E-01	-1.4	1.8E-01	-1.2	1.2E-01	-0.3	7.5E-01
ENSMUST00000055884	5-hydroxytryptamine (serotonin) receptor 5B [Source:MGI Symbol;Acc:MGI:96284]	G3X9C6		7.7	2.6E-05	7.5	7.6E-03	-0.6	8.1E-01	-2.9	5.2E-02
ENSMUST00000055890	olfactory receptor 523 [Source:MGI Symbol;Acc:MGI:3030357]	Q8VFE7		6.7	7.2E-05	6.3	2.3E-03	0.3	8.3E-01	-0.1	9.3E-01
ENSMUST00000055892	cation channel, sperm associated 4 [Source:MGI Symbol;Acc:MGI:3043288]		Q8BVN3	5.4	2.0E-02	6.6	2.7E-04	-0.5	6.8E-01	-0.4	5.2E-01
ENSMUST00000055911	tigger transposable element derived 3 [Source:MGI Symbol;Acc:MGI:2681860]		Q7TM95	4.0	4.0E-05	-4.6	1.4E-03	-1.9	8.6E-03	-1.2	2.7E-01
ENSMUST00000055915	hepatoma derived growth factor-like 1 [Source:MGI Symbol;Acc:MGI:1194493]	Q2VPR5		7.4	7.7E-05	7.8	5.9E-05	-0.7	5.9E-01	-0.5	4.1E-01
ENSMUST00000055081	tetratricopeptide repeat domain 17 [Source:MGI Symbol;Acc:MGI:1921819]	A2AGG1		-3.7	6.9E-02	-1.4	5.1E-01	0.8	5.9E-01	-1.5	4.9E-01
ENSMUST00000055922	leucine rich adaptor protein 1-like [Source:MGI Symbol;Acc:MGI:106510]		Q8K2P1	6.2	7.7E-05	6.0	4.9E-04	-0.6	6.2E-01	0.4	5.2E-01
ENSMUST00000055085	transmembrane protein 86B [Source:MGI Symbol;Acc:MGI:1915505]		Q497J1	0.2	8.1E-01	1.1	2.6E-01	0.3	6.6E-01	-0.6	4.8E-01
ENSMUST00000055931	dual specificity phosphatase 18 [Source:MGI Symbol;Acc:MGI:1922469]		Q8VE01	2.5	1.4E-03	-8.1	9.4E-03	1.0	3.0E-01	1.8	5.0E-01
ENSMUST00000055941	ATPase, Cu++ transporting, alpha polypeptide [Source:MGI Symbol;Acc:MGI:99400]	A2AG68		-4.9	2.1E-03	0.8	2.3E-01	-1.2	5.1E-02	-0.2	7.9E-01
ENSMUST00000055097	RIKEN cDNA 3110062M04 gene [Source:MGI Symbol;Acc:MGI:1925662]		Q8BHZ5	-1.8	1.4E-01	0.2	8.7E-01	0.6	5.3E-01	-1.4	3.3E-01
ENSMUST00000055946	G protein-coupled receptor 158 [Source:MGI Symbol;Acc:MGI:2441697]		Q8C419	9.0	1.2E-05	-6.9	1.1E-04	-0.6	1.2E-01	-0.2	8.7E-01
ENSMUST00000055947	sterile alpha motif domain containing 14 [Source:MGI Symbol;Acc:MGI:2384945]		Q8K070	3.3	1.8E-03	4.2	2.0E-04	-2.0	3.0E-02	-1.0	9.7E-02
ENSMUST00000055949	protocadherin beta 18 [Source:MGI Symbol;Acc:MGI:2136756]		Q91Y02	8.3	7.6E-06	6.3	4.0E-04	-0.6	6.4E-01	0.4	5.2E-01
ENSMUST00000055966	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3 [Source:MGI Symbol;Acc:MGI:95615]		P26049	6.3	9.5E-05	7.1	1.2E-05	-2.5	3.0E-02	-0.4	4.4E-01
ENSMUST00000055990	eukaryotic translation elongation factor 1 alpha 2 [Source:MGI Symbol;Acc:MGI:1096317]		P62631	7.5	8.0E-05	-1.0	2.7E-01	1.2	5.2E-02	-0.5	5.7E-01
ENSMUST00000056006	one cut domain, family member 1 [Source:MGI Symbol;Acc:MGI:1196423]		O08755	9.0	1.4E-05	6.6	2.5E-04	-0.6	6.5E-01	0.1	8.7E-01
ENSMUST00000056032	E4F transcription factor 1 [Source:MGI Symbol;Acc:MGI:109530]		Q8CCE9	-1.1	3.4E-02	8.2	1.2E-03	-0.9	6.6E-01	0.7	4.5E-01
ENSMUST00000056045	family with sequence similarity 185, member A [Source:MGI Symbol;Acc:MGI:2140983]		Q7TPD2	1.5	1.5E-02	-2.8	6.2E-03	0.8	7.9E-02	0.0	9.5E-01
ENSMUST00000056078	mitochondrial ribosomal protein S12 [Source:MGI Symbol;Acc:MGI:1346333]		O35680	-4.2	2.2E-03	-2.0	2.5E-01	-0.3	8.1E-01	-2.7	1.9E-01
ENSMUST00000055144	diphthamine biosynthesis 6 [Source:MGI Symbol;Acc:MGI:1913882]		Q9CQ28	2.3	2.1E-01	3.3	4.1E-02	-3.3	6.0E-02	-4.3	1.2E-02
ENSMUST00000056085	citrate synthase like [Source:MGI Symbol;Acc:MGI:1919082]	Q80X68		7.1	6.7E-05	5.9	4.2E-04	-0.5	6.5E-01	-0.1	9.1E-01
ENSMUST00000056086	RIKEN cDNA 4930442H23 gene [Source:MGI Symbol;Acc:MGI:1922144]	Q9D5G7		4.8	3.1E-04	-3.6	1.9E-04	0.2	4.8E-01	-1.1	1.1E-01
ENSMUST00000056089	transmembrane protein 37 [Source:MGI Symbol;Acc:MGI:2157899]		Q9JJV3	2.6	1.3E-02	9.3	4.0E-05	-0.7	6.2E-01	0.1	9.1E-01
ENSMUST00000055184	glycoprotein 1b, alpha polypeptide [Source:MGI Symbol;Acc:MGI:1333744]	A2CFB8	O35930	1.6	3.3E-01	-0.7	7.5E-01	-1.5	3.5E-01	0.8	6.8E-01
ENSMUST00000056102	Down syndrome cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1196281]		Q9ERC8	9.0	6.8E-06	0.5	6.3E-01	-2.3	2.7E-02	0.6	5.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000056110	delta-like 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:94900]	Q925U3		6.4	1.2E-02	0.5	9.0E-01	-3.1	2.8E-01	3.1	3.0E-01
ENSMUST00000056113	alkaline ceramidase 1 [Source:MGI Symbol;Acc:MGI:2181962]		Q8R4X1	8.2	2.4E-06	7.0	1.0E-04	-0.6	6.0E-01	-0.8	1.9E-01
ENSMUST00000056117	integrin alpha 2 [Source:MGI Symbol;Acc:MGI:96600]		Q62469	3.9	4.1E-04	6.7	4.3E-03	-0.7	7.2E-01	-1.6	1.5E-01
ENSMUST00000056120	olfactory receptor 1336 [Source:MGI Symbol;Acc:MGI:3031170]	Q8VGH5		6.1	1.6E-04	-1.9	1.7E-01	1.7	4.3E-02	-0.7	6.1E-01
ENSMUST00000056129	neuronal PAS domain protein 4 [Source:MGI Symbol;Acc:MGI:2664186]		Q8BGD7	8.5	2.4E-05	4.7	9.8E-03	-0.5	7.2E-01	-0.6	5.5E-01
ENSMUST00000056130	G protein-coupled receptor 150 [Source:MGI Symbol;Acc:MGI:2441872]		Q8BL07	6.9	8.0E-05	4.8	6.5E-03	1.4	2.9E-01	0.4	6.7E-01
ENSMUST00000056136	potassium inwardly-rectifying channel, subfamily J, member 10 [Source:MGI Symbol;Acc:MGI:1194504]	Q56VN0	Q9JM63	7.2	1.1E-06	4.1	4.5E-03	-1.8	1.6E-01	-2.8	1.5E-02
ENSMUST00000055224	mbrane associated guanylate kinase, WW and PDZ domain containing 1 [Source:MGI Symbol;Acc:MGI:12035			3.8	1.0E-01	7.0	1.7E-02	0.1	9.7E-01	-3.2	5.9E-02
ENSMUST00000055226	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]		P11276	5.4	1.7E-01	0.7	8.6E-01	-5.7	1.6E-01	-0.9	7.7E-01
ENSMUST00000056144	olfactory receptor 1346 [Source:MGI Symbol;Acc:MGI:3031180]	Q8VGH6		9.7	2.2E-05	-2.7	3.4E-03	0.4	3.4E-01	0.3	6.9E-01
ENSMUST00000056146	RIKEN cDNA 1810024B03 gene [Source:MGI Symbol;Acc:MGI:1925560]	Q8BWE1		4.3	1.0E-03	-1.6	4.8E-02	1.0	4.1E-02	-0.2	8.0E-01
ENSMUST00000055245	family with sequence similarity 175, member A [Source:MGI Symbol;Acc:MGI:1917931]		Q8BPZ8	2.4	2.3E-01	2.5	2.7E-01	-0.9	6.6E-01	-0.9	6.1E-01
ENSMUST00000055256	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]	E9Q701		1.2	5.4E-01	4.0	2.3E-01	4.1	1.6E-01	1.3	5.7E-01
ENSMUST00000056147	zinc finger protein 119b [Source:MGI Symbol;Acc:MGI:2385323]	Q8K0G9		-5.4	7.7E-05	2.8	1.9E-02	0.3	7.6E-01	0.4	5.8E-01
ENSMUST00000056149	abhydrolase domain containing 12 [Source:MGI Symbol;Acc:MGI:1923442]		Q99LR1	-6.1	2.4E-04	-6.8	6.7E-04	0.8	1.5E-01	0.0	9.8E-01
ENSMUST00000056153	fatty acid desaturase domain family, member 6 [Source:MGI Symbol;Acc:MGI:3039592]		Q80UG1	4.7	5.0E-05	-4.2	1.7E-03	-0.8	1.6E-01	-2.3	7.2E-02
ENSMUST00000056157	mixed lineage kinase domain-like [Source:MGI Symbol;Acc:MGI:1921818]		Q9D2Y4	4.2	2.5E-02	5.9	7.0E-02	-0.8	7.9E-01	0.7	7.0E-01
ENSMUST00000056184	basic helix-loop-helix family, member a9 [Source:MGI Symbol;Acc:MGI:2444198]		Q5RJB0	6.4	1.5E-04	6.0	1.2E-04	-2.3	5.4E-02	-0.6	3.4E-01
ENSMUST00000055296	polymerase (RNA) I polypeptide A [Source:MGI Symbol;Acc:MGI:1096397]		O35134	-0.8	5.6E-02	0.2	6.6E-01	0.4	2.4E-01	-0.6	2.1E-01
ENSMUST00000056198	protein phosphatase 2C-like domain containing 1 [Source:MGI Symbol;Acc:MGI:3612067]		Q8BVT6	4.8	4.1E-04	-1.9	1.8E-02	-0.2	6.5E-01	-0.4	5.7E-01
ENSMUST00000056228	serine palmitoyltransferase, small subunit A [Source:MGI Symbol;Acc:MGI:1913399]		Q8R207	-4.4	6.3E-04	5.2	6.1E-03	-1.4	4.0E-01	-1.3	2.0E-01
ENSMUST00000056235	olfactory receptor 578 [Source:MGI Symbol;Acc:MGI:3030412]	Q8VH17		5.7	2.3E-04	4.1	8.1E-03	-1.1	3.4E-01	0.1	9.5E-01
ENSMUST00000056237	protein arginine methyltransferase 10 (putative) [Source:MGI Symbol;Acc:MGI:2142651]	F8WIU7		-6.6	6.4E-05	-3.4	1.3E-02	1.5	3.2E-02	-0.8	5.1E-01
ENSMUST00000056256	RIKEN cDNA 4933415A04 gene [Source:MGI Symbol;Acc:MGI:1922977]	Q9D443		5.3	6.2E-05	7.5	1.7E-05	-0.8	3.8E-01	-0.8	1.2E-01
ENSMUST00000056288	expressed sequence AI467606 [Source:MGI Symbol;Acc:MGI:2141979]		Q8C708	-5.7	4.2E-05	3.7	6.1E-02	-1.4	4.7E-01	2.5	5.5E-02
ENSMUST00000056290	neurofibromatosis 2 [Source:MGI Symbol;Acc:MGI:97307]		P46662	6.7	9.9E-04	0.0	9.6E-01	1.0	2.4E-02	-0.2	6.6E-01
ENSMUST00000056329	kallikrein related-peptidase 14 [Source:MGI Symbol;Acc:MGI:2447564]	A0A0B6VSR0	Q8CGR5	6.0	1.0E-05	-0.2	8.4E-01	0.2	7.0E-01	-2.0	3.1E-02
ENSMUST00000056331	a disintegrin and metalloppeptidase domain 20 [Source:MGI Symbol;Acc:MGI:2152342]	Q7M763		5.7	5.2E-04	-1.7	5.6E-02	0.6	2.9E-01	-0.7	3.8E-01
ENSMUST00000055352	family with sequence similarity 120, member B [Source:MGI Symbol;Acc:MGI:1914794]		Q6RI63	-1.4	4.4E-02	-0.8	3.2E-01	0.1	7.9E-01	-0.5	5.4E-01
ENSMUST00000056336	opioid receptor, delta 1 [Source:MGI Symbol;Acc:MGI:97438]	A2AD37	P32300	6.9	3.2E-05	7.1	1.3E-02	-0.5	8.4E-01	-1.8	1.8E-01
ENSMUST00000056338	zinc finger protein 536 [Source:MGI Symbol;Acc:MGI:1926102]		Q8K083	6.2	2.8E-02	5.5	6.3E-04	-0.5	6.5E-01	0.4	5.1E-01
ENSMUST00000056355	N-acetyltransferase 8-like [Source:MGI Symbol;Acc:MGI:2447776]			2.5	5.8E-03	4.9	7.5E-05	-1.8	4.0E-02	-0.6	2.6E-01
ENSMUST00000055372	RIKEN cDNA 1110037F02 gene [Source:MGI Symbol;Acc:MGI:1913435]		A2AIV2	-0.8	4.7E-01	-0.9	4.7E-01	-1.0	2.9E-01	-0.9	4.5E-01
ENSMUST00000056362	keratin 34 [Source:MGI Symbol;Acc:MGI:1309994]		Q9D646	6.5	1.3E-04	6.3	8.9E-05	0.6	5.2E-01	-0.6	3.0E-01
ENSMUST00000056365	Ellis van Creveld syndrome 2 [Source:MGI Symbol;Acc:MGI:1915775]		Q8K1G2	8.0	9.4E-05	-1.3	1.1E-01	0.8	1.2E-01	-0.5	5.0E-01
ENSMUST00000056370	polyamine-modulated factor 1 [Source:MGI Symbol;Acc:MGI:1914287]		Q9CPV5	-5.3	2.5E-03	2.5	6.4E-03	-1.3	6.8E-02	-1.3	5.9E-02
ENSMUST00000056398	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923772]		Q6ZWM4	-4.8	1.5E-04	6.7	6.8E-05	-1.5	1.9E-01	-0.5	3.9E-01
ENSMUST00000056403	H1 histone family, member X [Source:MGI Symbol;Acc:MGI:2685307]	Q80ZM5		3.5	2.8E-02	4.3	2.8E-04	0.5	4.7E-01	-0.6	3.3E-01
ENSMUST00000056410	gem (nuclear organelle) associated protein 8 [Source:MGI Symbol;Acc:MGI:2384300]		Q8BHE1	5.1	4.9E-06	-1.1	4.5E-01	2.1	3.5E-02	-0.5	7.4E-01
ENSMUST00000055413	RIKEN cDNA 2510002D24 gene [Source:MGI Symbol;Acc:MGI:1919557]		Q3U595	1.0	6.1E-01	-3.4	2.5E-01	-2.5	1.5E-01	1.9	5.0E-01
ENSMUST00000056416	RNA binding protein, fox-1 homolog (C. elegans) 1 [Source:MGI Symbol;Acc:MGI:1926224]		Q9JJ43	7.0	3.6E-05	8.0	5.9E-03	0.2	9.5E-01	0.8	4.8E-01
ENSMUST00000056442	olute carrier family 6 (neurotransmitter transporter, glycine), member 5 [Source:MGI Symbol;Acc:MGI:10509(	B2RQX9		8.0	4.4E-07	-6.9	1.7E-03	-0.5	3.7E-01	-0.2	9.3E-01
ENSMUST00000055433	splA/ryanodine receptor domain and SOCS box containing 4 [Source:MGI Symbol;Acc:MGI:2183445]		Q8R5B6	0.9	4.9E-01	2.9	7.4E-02	-0.5	7.0E-01	-2.4	8.9E-02
ENSMUST00000056449	Rho GTPase activating protein 30 [Source:MGI Symbol;Acc:MGI:2684948]	E9QMX7		-11.9	1.1E-05	7.0	1.5E-04	0.0	9.9E-01	-0.1	9.1E-01
ENSMUST00000056467	zinc finger protein 445 [Source:MGI Symbol;Acc:MGI:2143340]		Q8R2V3	-1.8	5.6E-03	3.6	6.0E-04	0.4	5.4E-01	-0.2	6.5E-01
ENSMUST00000055439				5.8	4.8E-02	0.8	7.0E-01	-5.6	4.8E-02	-0.5	7.8E-01
ENSMUST00000055447	transmembrane protein 241 [Source:MGI Symbol;Acc:MGI:2442435]	Z4YJM6		-0.5	8.2E-01	2.0	5.5E-01	1.9	4.8E-01	-0.6	8.3E-01
ENSMUST00000055454	proline-rich polypeptide 3 [Source:MGI Symbol;Acc:MGI:1922460]		Q811B5	1.5	4.2E-01	5.2	6.5E-02	2.6	2.9E-01	-1.2	5.1E-01
ENSMUST00000056470	zinc finger protein 459 [Source:MGI Symbol;Acc:MGI:3040701]	Q8BZ17		6.3	1.6E-06	-1.8	1.0E-01	1.6	2.3E-02	-0.7	5.3E-01
ENSMUST00000055475	G protein-coupled receptor 18 [Source:MGI Symbol;Acc:MGI:107859]		Q8K1Z6	0.1	8.5E-01	-1.3	1.2E-01	-1.6	1.5E-02	-0.2	7.9E-01
ENSMUST00000056474	family with sequence similarity 221, member B [Source:MGI Symbol;Acc:MGI:2441678]		Q8C627	8.1	2.7E-04	-4.5	2.3E-01	2.1	2.9E-01	-0.8	8.4E-01
ENSMUST00000056480	histamine receptor H3 [Source:MGI Symbol;Acc:MGI:2139279]	Q540P3	P58406	7.3	1.3E-04	-1.0	1.9E-01	1.5	1.3E-02	-3.5	5.6E-03
ENSMUST00000056482	intersectin 1 (SH3 domain protein 1A) [Source:MGI Symbol;Acc:MGI:1338069]		Q9Z0R4	-5.8	4.2E-04	4.8	9.2E-03	-0.7	6.7E-01	2.4	2.7E-02
ENSMUST00000056484	neuroligin 2 [Source:MGI Symbol;Acc:MGI:2681835]		Q69ZK9	4.2	2.4E-02	8.0	6.6E-05	-0.2	8.7E-01	-0.4	4.9E-01
ENSMUST00000055497	B RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:303		Q6NZA9	1.9	3.0E-01	5.1	7.2E-02	2.4	3.5E-01	-0.8	5.9E-01
ENSMUST00000056512	WD repeat domain 41 [Source:MGI Symbol;Acc:MGI:2445123]		Q3UDP0	-1.6	3.4E-02	6.2	1.1E-03	-0.7	6.5E-01	0.2	8.4E-01
ENSMUST00000055503	X Kell blood group precursor-related family, member 5 [Source:MGI Symbol;Acc:MGI:2442327]	Q8BG78		2.5	5.5E-02	5.4	5.9E-04	-1.4	2.5E-01	-4.3	6.8E-04
ENSMUST00000055506	general transcription factor III C 1 [Source:MGI Symbol;Acc:MGI:107887]		Q8K284	-0.5	3.0E-01	0.6	2.8E-01	0.9	7.0E-02	-0.2	6.5E-01
ENSMUST00000055518	osphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) [Source:MGI Symbol;Acc:MGI:9758		P26450	-1.3	4.8E-02	-0.8	3.5E-01	1.0	9.6E-02	0.4	5.6E-01
ENSMUST00000056517	gap junction protein, alpha 10 [Source:MGI Symbol;Acc:MGI:1339969]		Q9WUS4	6.8	5.3E-05	6.9	1.0E-02	1.8	3.9E-01	-0.3	8.1E-01
ENSMUST00000056518	family with sequence similarity 131, member A [Source:MGI Symbol;Acc:MGI:1925658]		Q8BWU3	5.7	1.8E-03	7.5	1.7E-05	-1.4	2.0E-01	0.2	7.3E-01
ENSMUST00000056521	RIKEN cDNA 2900011O08 gene [Source:MGI Symbol;Acc:MGI:1914504]		Q8R1Y2	6.7	5.6E-05	7.6	4.0E-05	-0.6	6.0E-01	-0.5	3.5E-01
ENSMUST00000056522	protocadherin beta 2 [Source:MGI Symbol;Acc:MGI:2136735]	Q91Y00		7.0	7.1E-05	-1.3	6.8E-02	-0.1	8.8E-01	-1.2	1.2E-01
ENSMUST00000056533	myozenin 3 [Source:MGI Symbol;Acc:MGI:2179296]	E9QJU4		6.2	8.6E-04	5.0	5.8E-04	0.3	7.3E-01	-0.5	4.2E-01
ENSMUST00000056549	zinc finger protein 235 [Source:MGI Symbol;Acc:MGI:1929117]	Q499D5		2.5	2.3E-03	2.2	1.6E-02	-0.8	2.3E-01	-1.0	1.5E-01
ENSMUST00000056558	zinc finger protein 366 [Source:MGI Symbol;Acc:MGI:2178429]	Q6NS86		8.3	3.7E-06	-2.4	2.6E-03	0.7	7.8E-02	0.0	9.7E-01
ENSMUST00000056578	brain protein I3 [Source:MGI Symbol;Acc:MGI:1933174]		P28662	-4.5	2.5E-03	6.5	3.0E-04	-0.6	6.3E-01	-0.5	4.3E-01
ENSMUST00000056617	adhesion G protein-coupled receptor D1 [Source:MGI Symbol;Acc:MGI:3041203]		Q80T32	8.1	1.4E-05	-3.5	3.1E-03	-0.1	8.2E-01	0.5	6.1E-01
ENSMUST00000055604	zinc finger protein 526 [Source:MGI Symbol;Acc:MGI:2445181]		Q8BI66	1.0	9.6E-02	1.6	5.7E-02	1.1	8.6E-02	0.5	4.9E-01
ENSMUST00000056623	transmembrane protein 72 [Source:MGI Symbol;Acc:MGI:2442707]		Q8C3K5	9.2	4.8E-04	5.6	5.6E-04	-0.5	6.6E-01	-0.2	7.1E-01
ENSMUST00000056635	rearranged L-myc fusion sequence [Source:MGI Symbol;Acc:MGI:1924705]	A2A7F4		-7.0	3.7E-04	6.1	1.7E-04	-1.0	3.3E-01	0.0	9.8E-01
ENSMUST00000056641	pleckstrin and Sec7 domain containing 4 [Source:MGI Symbol;Acc:MGI:2674093]		Q8BLR5	-6.9	4.1E-04	5.9	4.5E-06	-1.1	9.2E-02	0.1	7.6E-01
ENSMUST00000055647	kinesin family member 1B [Source:MGI Symbol;Acc:MGI:108426]		Q60575	2.1	3.5E-01	0.6	8.4E-01	-1.7	4.3E-01	-0.2	9.4E-01
ENSMUST00000056677	zinc finger protein 830 [Source:MGI Symbol;Acc:MGI:1914233]		Q8R1N0	-2.1	4.4E-03	2.9	6.8E-03	0.1	8.8E-01	-0.4	5.0E-01
ENSMUST00000056683	zinc finger protein 111 [Source:MGI Symbol;Acc:MGI:1929114]	Q9R164		7.0	1.1E-03	7.3	3.7E-05	-0.9	4.3E-01	-0.1	9.0E-01
ENSMUST00000055676	sphingosine-1-phosphate receptor 1 [Source:MGI Symbol;Acc:MGI:1096355]		O08530	0.1	9.2E-01	-0.2	7.7E-01	-0.7	1.7E-01	-0.5	5.1E-01
ENSMUST00000055688	PHD finger protein 13 [Source:MGI Symbol;Acc:MGI:2446217]	Q3V230	Q8K2W6	-0.3	6.0E-01	1.2	1.3E-01	1.2	5.8E-02	-0.3	6.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000056708	potassium channel, subfamily V, member 2 [Source:MGI Symbol;Acc:MGI:2670981]		Q8CFS6	8.6	8.7E-06	4.1	5.2E-03	0.6	5.7E-01	-0.5	5.8E-01
ENSMUST00000056712	protocadherin beta 4 [Source:MGI Symbol;Acc:MGI:2136738]	Q91XZ6		7.6	2.2E-05	6.8	1.6E-04	-0.5	6.9E-01	-0.1	8.5E-01
ENSMUST00000056728	stablizer of axonemal microtubules 2 [Source:MGI Symbol;Acc:MGI:1914618]		Q8BQB6	6.1	1.5E-04	-6.4	7.6E-05	1.2	1.4E-02	-1.4	1.8E-01
ENSMUST00000056732	microfibrillar-associated protein 1B [Source:MGI Symbol;Acc:MGI:3694697]		Q9CQU1	-4.0	4.7E-05	2.8	1.1E-02	-1.5	8.7E-02	0.0	9.4E-01
ENSMUST00000056740	gliomedin [Source:MGI Symbol;Acc:MGI:2388361]		Q8BMF8	6.1	9.4E-05	7.5	1.7E-04	-0.7	6.3E-01	-1.5	5.1E-02
ENSMUST00000055723	tumor necrosis factor receptor superfamily, member 26 [Source:MGI Symbol;Acc:MGI:2651928]	Q3U3N2	P83626	1.6	6.2E-02	1.7	1.3E-01	0.6	4.6E-01	0.5	5.5E-01
ENSMUST00000056745	F-box and WD-40 domain protein 15 [Source:MGI Symbol;Acc:MGI:3505701]	L7N1X6		2.9	4.8E-03	4.8	1.4E-03	-0.4	6.8E-01	-0.1	8.6E-01
ENSMUST00000056749	NHL repeat containing 3 [Source:MGI Symbol;Acc:MGI:2444520]		Q8CCH2	-1.5	1.6E-02	-5.3	1.6E-03	0.8	2.0E-01	-3.4	4.0E-02
ENSMUST00000056755	pannexin 1 [Source:MGI Symbol;Acc:MGI:1860055]	B1PL19		-3.2	4.2E-03	6.4	6.3E-06	1.2	9.4E-02	-0.8	7.3E-02
ENSMUST00000055754	G protein-coupled receptor 153 [Source:MGI Symbol;Acc:MGI:1916157]		Q8K0Z9	4.0	6.5E-02	5.5	2.1E-02	-1.1	6.2E-01	-2.6	9.1E-02
ENSMUST00000055758	ubiquitin protein ligase E3 component n-recognin 3 [Source:MGI Symbol;Acc:MGI:1861100]		Q5U430	-1.5	1.1E-01	0.7	5.8E-01	1.8	1.2E-01	-0.5	6.4E-01
ENSMUST00000056758	protein phosphatase 3, catalytic subunit, alpha isoform [Source:MGI Symbol;Acc:MGI:107164]	B2RRX2	P63328	-4.4	2.2E-03	2.7	1.6E-02	-3.0	2.3E-02	0.0	1.0E+00
ENSMUST00000056759	olfactory receptor 56 [Source:MGI Symbol;Acc:MGI:1333785]		Q8VGD6	5.4	1.4E-03	-7.4	7.4E-04	-0.1	8.6E-01	-0.4	7.9E-01
ENSMUST00000056773	serologically defined colon cancer antigen 8 [Source:MGI Symbol;Acc:MGI:1924066]	E9Q2E2		4.2	7.7E-05	6.1	3.6E-02	1.6	5.3E-01	0.4	7.9E-01
ENSMUST00000056815	neuronal PAS domain protein 2 [Source:MGI Symbol;Acc:MGI:109232]	G3X9B7		8.5	6.7E-06	0.3	6.4E-01	1.2	1.6E-02	-0.5	3.5E-01
ENSMUST00000056822	acyl-CoA thioesterase 6 [Source:MGI Symbol;Acc:MGI:1921287]	B2RTE4	Q32Q92	7.3	1.5E-04	0.3	6.2E-01	1.1	2.1E-02	-0.2	6.9E-01
ENSMUST00000055858	RIKEN cDNA 2410002F23 gene [Source:MGI Symbol;Acc:MGI:1914226]	Q3TE80		0.3	9.2E-01	-2.5	4.7E-01	-1.5	4.7E-01	1.3	7.2E-01
ENSMUST00000056866	patatin-like phospholipase domain containing 1 [Source:MGI Symbol;Acc:MGI:3617850]	B2KF06	Q3V1D5	1.3	6.9E-03	5.3	5.7E-04	-0.2	8.5E-01	0.7	3.0E-01
ENSMUST00000056882	oligodendrocyte transcription factor 1 [Source:MGI Symbol;Acc:MGI:1355334]	Q3UN59	Q9JKN5	5.9	4.9E-03	7.2	9.2E-05	-0.6	6.2E-01	-0.1	8.9E-01
ENSMUST00000056888	ankyrin repeat domain 13 family, member D [Source:MGI Symbol;Acc:MGI:1915673]		Q6PD24	-5.6	3.4E-02	5.6	2.5E-04	-1.9	1.0E-01	0.1	8.2E-01
ENSMUST00000056904	air cross-complementing rodent repair deficiency complementation group 6 like [Source:MGI Symbol;Acc:MC		Q8BHK9	2.6	4.3E-04	6.9	1.0E-04	-0.6	6.1E-01	-0.8	1.9E-01
ENSMUST00000056907	h-Magenis syndrome chromosome region, candidate 8 homolog (human) [Source:MGI Symbol;Acc:MGI:2444		Q3UMB5	-1.5	7.5E-03	7.0	8.4E-03	-0.6	8.0E-01	-2.2	1.0E-01
ENSMUST00000056915	protocadherin beta 13 [Source:MGI Symbol;Acc:MGI:2136748]	Q91Y06		7.8	2.0E-05	4.8	6.3E-05	1.2	8.4E-02	0.3	4.6E-01
ENSMUST00000056924	pleiomorphic adenoma gene-like 2 [Source:MGI Symbol;Acc:MGI:1933165]	Q925T4		-2.7	1.1E-03	7.3	1.6E-04	-0.6	6.3E-01	-0.5	4.3E-01
ENSMUST00000055918	chemokine (C-C motif) receptor 2 [Source:MGI Symbol;Acc:MGI:106185]	Q543S8	P51683	-3.8	4.5E-01	-8.6	1.9E-01	-5.0	6.6E-02	-0.2	9.7E-01
ENSMUST00000056925	collagen, type VI, alpha 3 [Source:MGI Symbol;Acc:MGI:88461]	E9PWQ3		11.3	7.1E-07	4.2	4.4E-04	-2.4	2.5E-02	-0.5	4.1E-01
ENSMUST00000056932	RIKEN cDNA 4933408B17 gene [Source:MGI Symbol;Acc:MGI:3045347]	G3X9B4		-5.1	7.5E-03	2.5	1.1E-02	0.7	3.2E-01	0.7	2.9E-01
ENSMUST00000056937	HscB iron-sulfur cluster co-chaperone homolog (E. coli) [Source:MGI Symbol;Acc:MGI:2141135]			-3.9	6.4E-04	-2.9	1.1E-01	2.1	4.0E-02	0.0	9.8E-01
ENSMUST00000056941	RIKEN cDNA 4933402P03 gene [Source:MGI Symbol;Acc:MGI:1918293]		Q8C5U4	8.7	1.7E-04	8.1	6.0E-05	-0.7	6.0E-01	0.2	7.3E-01
ENSMUST00000056949	sperm equatorial segment protein 1 [Source:MGI Symbol;Acc:MGI:1913962]		Q9D5A0	7.5	2.5E-05	2.2	1.9E-02	-1.9	3.1E-02	-0.8	2.6E-01
ENSMUST00000056950	Ras and Rab interactor 3 [Source:MGI Symbol;Acc:MGI:2385708]		P59729	-3.2	9.7E-03	6.6	5.7E-05	-1.5	1.8E-01	0.2	7.2E-01
ENSMUST00000056955	RIKEN cDNA 4933428G20 gene [Source:MGI Symbol;Acc:MGI:1918475]	Q9D3X4		4.8	4.7E-04	3.2	1.6E-03	-3.8	2.2E-03	-0.7	2.6E-01
ENSMUST00000055984	interferon stimulated exonuclease gene 20-like 2 [Source:MGI Symbol;Acc:MGI:2140076]			-0.3	4.8E-01	0.1	9.0E-01	0.8	1.0E-01	0.4	5.3E-01
ENSMUST00000056962	coiled-coil domain containing 74A [Source:MGI Symbol;Acc:MGI:1919565]	E9Q9U8		7.0	7.2E-05	7.4	1.6E-04	-0.6	6.5E-01	-0.5	4.4E-01
ENSMUST00000056965	F-box protein 6 [Source:MGI Symbol;Acc:MGI:1354743]		Q9QZN4	-5.4	8.9E-04	8.0	7.1E-05	-0.6	6.3E-01	0.3	5.5E-01
ENSMUST00000056028	SH3-binding kinase 1 [Source:MGI Symbol;Acc:MGI:2135937]		Q8QZX0	0.3	6.3E-01	1.1	1.7E-01	0.6	3.0E-01	-0.2	7.8E-01
ENSMUST00000056977	runt related transcription factor 3 [Source:MGI Symbol;Acc:MGI:102672]	Q3U1Q3		3.2	1.5E-03	-0.4	4.8E-01	0.3	4.3E-01	-0.4	4.8E-01
ENSMUST00000056978	kinesin family member 13A [Source:MGI Symbol;Acc:MGI:1098264]	F8VQ75		2.3	1.2E-03	2.4	3.8E-03	0.0	9.6E-01	-0.8	1.4E-01
ENSMUST00000056050	pyruvate dehyrogenase phosphatase catalytic subunit 1 [Source:MGI Symbol;Acc:MGI:2685870]	A8Y5Q1	Q3UV70	1.5	5.0E-01	1.3	5.3E-01	-2.5	2.2E-01	-2.3	2.7E-01
ENSMUST00000056053	SET domain containing 1B [Source:MGI Symbol;Acc:MGI:2652820]		Q8CFT2	-1.4	9.1E-02	0.7	4.5E-01	1.2	1.0E-01	-0.9	3.2E-01
ENSMUST00000056071	pyrin and HIN domain family, member 1 [Source:MGI Symbol;Acc:MGI:2138243]		Q8BV49	1.8	6.4E-02	0.6	6.1E-01	-0.5	5.9E-01	0.7	4.6E-01
ENSMUST00000056994	RIKEN cDNA 4921513I03 gene [Source:MGI Symbol;Acc:MGI:1918124]	Q9D5W2		5.9	5.1E-06	-3.9	2.4E-02	0.9	1.9E-01	0.7	6.5E-01
ENSMUST00000056997	cytidine and dCMP deaminase domain containing 1 [Source:MGI Symbol;Acc:MGI:1919141]		Q8BMD5	-6.3	2.1E-04	6.9	1.5E-04	-0.6	6.5E-01	-0.4	5.2E-01
ENSMUST00000057019	apelin receptor [Source:MGI Symbol;Acc:MGI:1346086]		Q9WV08	3.3	3.1E-03	5.1	1.1E-03	-0.1	9.5E-01	-0.4	5.6E-01
ENSMUST00000057021	odd-skipped related 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1344424]		Q9WVG7	9.3	5.2E-05	-0.6	5.4E-01	-2.7	6.5E-03	0.5	6.1E-01
ENSMUST00000056096	zinc finger protein 697 [Source:MGI Symbol;Acc:MGI:2139736]	G5E8C0		6.6	5.3E-02	4.7	2.1E-01	0.5	9.0E-01	2.3	3.2E-01
ENSMUST00000056097	thymocyte selection associated [Source:MGI Symbol;Acc:MGI:2443552]		Q8BGW0	1.9	3.2E-01	1.0	5.9E-01	-3.0	1.2E-01	-2.0	2.5E-01
ENSMUST00000057026	solute carrier family 25, member 47 [Source:MGI Symbol;Acc:MGI:2144766]		Q6IS41	3.7	7.1E-04	8.4	1.4E-05	-0.6	5.9E-01	0.1	9.2E-01
ENSMUST00000057029	zinc finger protein 13 [Source:MGI Symbol;Acc:MGI:99159]		P10754	6.1	3.5E-03	5.5	3.9E-03	-0.5	7.3E-01	-0.1	8.8E-01
ENSMUST00000056108	ankyrin repeat domain 16 [Source:MGI Symbol;Acc:MGI:2444796]		A2AS55	-2.0	7.6E-02	-3.2	6.0E-02	-0.2	7.8E-01	1.0	5.4E-01
ENSMUST00000057043	iption elongation factor A (SII) N-terminal and central domain containing 2 [Source:MGI Symbol;Acc:MGI:19		Q8R2M0	1.7	1.0E-03	7.1	1.0E-02	-0.8	7.4E-01	-1.5	2.6E-01
ENSMUST00000057054	mesenchyme homeobox 1 [Source:MGI Symbol;Acc:MGI:103220]		P32442	6.3	1.0E-04	8.0	2.0E-05	0.6	5.5E-01	0.8	1.2E-01
ENSMUST00000057062	BRO1 domain and CAAX motif containing [Source:MGI Symbol;Acc:MGI:1918928]		Q8K2Q7	-4.7	1.0E-02	3.5	2.2E-03	-0.7	3.8E-01	-0.3	6.6E-01
ENSMUST00000057067	meiosis-specific, MEI4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1922283]		Q8BRM6	8.9	1.0E-05	6.3	2.3E-04	-0.6	6.2E-01	-0.8	2.2E-01
ENSMUST00000056124	fibrosin-like 1 [Source:MGI Symbol;Acc:MGI:1920907]	E9PUB6		0.1	9.7E-01	-2.7	2.5E-01	0.2	8.5E-01	3.0	1.9E-01
ENSMUST00000057072	peroxiredoxin 6B [Source:MGI Symbol;Acc:MGI:1336888]	Q8BG37		6.3	1.3E-04	7.6	1.5E-04	-0.2	8.6E-01	0.6	3.2E-01
ENSMUST00000057080	trace amine-associated receptor 6 [Source:MGI Symbol;Acc:MGI:2685074]		Q5QD13	5.9	4.5E-04	7.3	1.6E-04	0.0	9.7E-01	-0.4	5.4E-01
ENSMUST00000057110	eukaryotic translation initiation factor 3, subunit J2 [Source:MGI Symbol;Acc:MGI:3704486]		Q66JS6	-5.7	2.3E-04	7.1	6.4E-06	-0.2	8.2E-01	0.0	9.7E-01
ENSMUST00000057115	iron-sulfur cluster assembly 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916296]		Q9D924	-2.3	1.7E-03	9.5	3.0E-05	-0.9	5.3E-01	-0.7	2.0E-01
ENSMUST00000057151	transmembrane protein 18 [Source:MGI Symbol;Acc:MGI:2387176]		Q3TUD9	-2.6	1.5E-03	4.3	2.3E-03	-1.1	3.0E-01	-1.1	1.7E-01
ENSMUST00000057161	olfactory receptor 978 [Source:MGI Symbol;Acc:MGI:3030812]	E9Q985		5.7	3.6E-04	-5.2	7.5E-04	0.6	1.6E-01	0.5	6.8E-01
ENSMUST00000057167	solute carrier family 34 (sodium phosphate), member 1 [Source:MGI Symbol;Acc:MGI:1345284]	Q9D2V6		8.6	4.9E-05	-2.4	3.6E-02	1.2	5.6E-02	-2.6	5.6E-02
ENSMUST00000057169	elastin microfibril interfacer 3 [Source:MGI Symbol;Acc:MGI:2389142]		P59900	7.2	2.8E-02	4.6	1.4E-04	-0.3	7.0E-01	-0.2	6.7E-01
ENSMUST00000057174	potassium channel tetramerisation domain containing 20 [Source:MGI Symbol;Acc:MGI:1914239]		Q8CDD8	-5.2	8.7E-03	-2.7	2.5E-01	-3.1	6.2E-02	3.8	1.1E-01
ENSMUST00000056159	glutathione S-transferase omega 2 [Source:MGI Symbol;Acc:MGI:1915464]		Q8K2Q2	4.8	4.5E-02	3.2	1.9E-01	-0.7	7.8E-01	0.9	5.8E-01
ENSMUST00000056176	vav 2 oncogene [Source:MGI Symbol;Acc:MGI:102718]		Q60992	0.3	8.6E-01	1.9	2.7E-01	-0.9	5.6E-01	-2.5	1.4E-01
ENSMUST00000056177	protein kinase C and casein kinase substrate in neurons 2 [Source:MGI Symbol;Acc:MGI:1345153]	Q3TDA7	Q9WVE8	-0.8	2.3E-01	-1.1	2.8E-01	0.9	1.5E-01	1.2	2.1E-01
ENSMUST00000057176	ucine-rich repeat, immunoglobulin-like and transmembrane domains 2 [Source:MGI Symbol;Acc:MGI:244488		Q6PFC5	8.4	1.2E-05	5.7	8.2E-04	-0.5	6.7E-01	0.2	7.6E-01
ENSMUST00000057177	polymerase (RNA) II (DNA directed) polypeptide K [Source:MGI Symbol;Acc:MGI:102725]	Q8BFX0		-4.4	3.6E-03	2.2	1.0E-01	-2.8	6.5E-02	1.7	8.7E-02
ENSMUST00000057178	NK2 homeobox 3 [Source:MGI Symbol;Acc:MGI:97348]		P97334	6.8	7.8E-05	5.4	5.2E-04	-0.2	8.8E-01	-0.8	2.9E-01
ENSMUST00000057185	protocadherin 1 [Source:MGI Symbol;Acc:MGI:104692]	Q8CFX3		7.0	2.7E-04	-3.7	5.4E-03	-0.2	7.5E-01	-0.9	4.5E-01
ENSMUST00000056232	zinc finger protein 553 [Source:MGI Symbol;Acc:MGI:2384725]		Q3US17	1.0	3.0E-01	2.5	7.7E-02	1.1	2.9E-01	-0.3	7.6E-01
ENSMUST00000057186	growth hormone secretagogue receptor [Source:MGI Symbol;Acc:MGI:2441906]	Q0VBE5	Q99P50	8.4	6.8E-06	6.2	2.4E-04	-0.6	6.1E-01	-1.0	1.2E-01
ENSMUST00000057190	poly(A) binding protein, cytoplasmic 6 [Source:MGI Symbol;Acc:MGI:1914793]	Q9D4E6		7.5	2.7E-05	-6.4	6.1E-04	0.0	9.7E-01	-0.2	8.9E-01
ENSMUST00000056246	zinc finger protein 954 [Source:MGI Symbol;Acc:MGI:1917764]	Q7TNU5		-1.2	4.2E-02	-1.0	1.6E-01	0.3	5.7E-01	0.1	9.4E-01
ENSMUST00000057194	leucine rich repeat containing 75A [Source:MGI Symbol;Acc:MGI:2682293]		Q7TSF4	2.4	6.4E-03	4.2	1.9E-03	0.1	9.2E-01	1.2	1.2E-01
ENSMUST00000057195	interleukin 4 induced 1 [Source:MGI Symbol;Acc:MGI:109552]	Q5FWJ9	Q63850	-6.1	2.4E-04	-4.4	1.4E-03	1.0	6.0E-02	-0.3	7.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000057198	RIKEN cDNA 5730508B09 gene [Source:MGI Symbol;Acc:MGI:1917867]	A0A0H2UKC2		-5.2	8.7E-05	6.0	2.7E-03	-1.3	4.4E-01	-0.5	5.9E-01
ENSMUST00000057208	mitochondrial ribosomal protein S9 [Source:MGI Symbol;Acc:MGI:1916777]		Q9D7N3	-3.4	2.9E-04	-3.9	1.4E-03	0.3	5.9E-01	-0.1	8.9E-01
ENSMUST00000056328	ring finger protein 26 [Source:MGI Symbol;Acc:MGI:2388131]		Q8BUH7	1.1	9.2E-02	2.6	1.1E-02	1.1	1.3E-01	-0.3	6.1E-01
ENSMUST00000057209	small G protein signaling modulator 1 [Source:MGI Symbol;Acc:MGI:107320]		Q8BPQ7	6.3	9.2E-05	6.8	4.9E-05	0.6	5.5E-01	-0.2	6.6E-01
ENSMUST00000057224	RIKEN cDNA 4932418E24 gene [Source:MGI Symbol;Acc:MGI:3045295]	Q8C5V8		7.9	4.3E-05	6.0	6.5E-04	-0.5	7.2E-01	-0.8	2.9E-01
ENSMUST00000057228	protocadherin beta 9 [Source:MGI Symbol;Acc:MGI:2136744]	E9Q5G2		7.6	1.6E-05	7.2	1.8E-04	0.5	6.9E-01	0.2	7.5E-01
ENSMUST00000057241	zinc finger protein 874a [Source:MGI Symbol;Acc:MGI:3040703]	Q3UWF5		5.3	5.6E-05	5.3	7.8E-02	-0.7	8.1E-01	0.2	9.1E-01
ENSMUST00000057243	transmembrane protein 252 [Source:MGI Symbol;Acc:MGI:3583948]		Q8C353	8.1	1.7E-05	2.9	1.4E-02	0.6	4.7E-01	0.2	7.3E-01
ENSMUST00000057254	ubiquilin 3 [Source:MGI Symbol;Acc:MGI:3045291]	Q497R3	Q8C5U9	7.6	6.5E-05	5.6	7.4E-04	-0.5	6.7E-01	0.5	4.9E-01
ENSMUST00000057256	RIKEN cDNA 6030458C11 gene [Source:MGI Symbol;Acc:MGI:1925127]		Q8BGC1	2.2	8.8E-03	5.3	4.7E-04	-3.5	1.8E-02	-0.8	2.3E-01
ENSMUST00000057258	zinc finger protein 518B [Source:MGI Symbol;Acc:MGI:2140750]	J3QPN0		3.4	4.1E-03	-1.7	2.5E-01	1.6	8.0E-02	-1.9	2.4E-01
ENSMUST00000056391	multiple endocrine neoplasia 1 [Source:MGI Symbol;Acc:MGI:1316736]		O88559	2.4	3.4E-01	3.8	2.4E-01	0.8	7.8E-01	-0.6	8.0E-01
ENSMUST00000056396	predicted pseudogene 6563 [Source:MGI Symbol;Acc:MGI:3646907]	B2RXM7	Q9D1J3	-3.6	2.5E-01	-3.8	2.3E-01	-1.6	3.9E-01	-1.4	6.9E-01
ENSMUST00000057261	anterior pharynx defective 1c homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1915568]	Q4R1J7		-4.9	4.1E-03	-7.5	5.2E-04	-0.8	1.1E-01	1.9	2.1E-01
ENSMUST00000057262	potassium voltage-gated channel, Isk-related subfamily, gene 4 [Source:MGI Symbol;Acc:MGI:1891125]		Q9WTW3	7.1	3.3E-03	4.6	3.9E-02	0.7	7.0E-01	-0.4	7.6E-01
ENSMUST00000056406	family with sequence similarity 78, member A [Source:MGI Symbol;Acc:MGI:2443569]	A2ATN4	Q8C552	1.0	1.3E-01	0.9	2.8E-01	-0.2	8.0E-01	0.0	9.6E-01
ENSMUST00000057270	pancreatic lipase [Source:MGI Symbol;Acc:MGI:97722]		Q6P8U6	6.1	3.2E-04	4.9	1.9E-05	-0.3	6.3E-01	-0.1	7.2E-01
ENSMUST00000057272	RIKEN cDNA 4932438A13 gene [Source:MGI Symbol;Acc:MGI:2444631]		A2AAE1	-3.6	2.5E-02	7.1	6.7E-05	-0.5	6.4E-01	-0.6	3.1E-01
ENSMUST00000056427	tubulin, beta 2A class IIA [Source:MGI Symbol;Acc:MGI:107861]		Q7TMM9	0.5	3.5E-01	-1.7	1.9E-02	-1.9	1.5E-03	0.3	5.8E-01
ENSMUST00000056433	G protein-coupled receptor 107 [Source:MGI Symbol;Acc:MGI:2139054]	Q148Z6	Q8BUV8	-0.7	9.1E-02	0.0	9.8E-01	0.8	4.3E-02	0.1	7.8E-01
ENSMUST00000057279	olfactomedin-like 2A [Source:MGI Symbol;Acc:MGI:2444741]	B2RQD8	Q8BHP7	5.7	7.0E-06	7.1	1.9E-06	-1.0	1.5E-01	-0.2	6.4E-01
ENSMUST00000057288	protein disulfide isomerase associated 6 [Source:MGI Symbol;Acc:MGI:1919103]	Q3TML0		-5.7	2.2E-05	-10.1	2.5E-04	0.9	6.4E-02	-0.9	6.5E-01
ENSMUST00000057293	proline rich 12 [Source:MGI Symbol;Acc:MGI:2679002]	E9PYL2		1.6	9.1E-03	-1.1	1.1E-01	0.5	2.3E-01	-0.1	8.4E-01
ENSMUST00000057311	stratifin [Source:MGI Symbol;Acc:MGI:1891831]		O70456	1.4	2.3E-02	5.5	1.0E-05	-0.7	3.1E-01	0.1	8.4E-01
ENSMUST00000057314	insulin receptor substrate 3 [Source:MGI Symbol;Acc:MGI:1194882]	O54718		5.5	5.4E-05	7.4	9.5E-04	-0.8	6.5E-01	0.0	9.6E-01
ENSMUST00000057320	transmembrane channel-like gene family 5 [Source:MGI Symbol;Acc:MGI:1921674]		Q32NZ6	6.5	1.1E-04	7.3	2.4E-04	-0.6	6.5E-01	-0.6	4.0E-01
ENSMUST00000057324	fibronectin leucine rich transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:3603594]	Q8BLU0	Q8BLU0	6.9	2.3E-05	-5.6	2.6E-03	-0.5	3.6E-01	-0.7	6.3E-01
ENSMUST00000057325	coiled-coil domain containing 125 [Source:MGI Symbol;Acc:MGI:1923291]		Q5U465	-3.5	3.5E-03	2.3	3.5E-01	0.3	8.8E-01	2.2	2.1E-01
ENSMUST00000057337	fibroblast growth factor binding protein 3 [Source:MGI Symbol;Acc:MGI:1919764]			4.8	2.3E-04	0.5	5.1E-01	0.7	2.4E-01	-1.4	9.7E-02
ENSMUST00000057343	polypyrimidine tract binding protein 1 [Source:MGI Symbol;Acc:MGI:97791]	E9QMW9		-4.5	1.9E-02	6.2	1.9E-04	-0.6	6.0E-01	0.0	9.4E-01
ENSMUST00000057373	RAB11B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:99425]	Q78ZJ8	P46638	-1.6	1.1E-02	5.2	1.2E-02	-0.3	8.5E-01	0.1	8.9E-01
ENSMUST00000057386	olfactory receptor 283 [Source:MGI Symbol;Acc:MGI:3030117]	Q8VGU2		6.3	3.3E-04	7.0	8.1E-05	-0.6	6.2E-01	-0.8	1.8E-01
ENSMUST00000057405	cDNA sequence BC027072 [Source:MGI Symbol;Acc:MGI:2385061]		Q6PAC4	9.0	1.3E-05	7.6	6.8E-05	-0.6	6.1E-01	-1.2	6.8E-02
ENSMUST00000057407	pyroglutamylated RFamide peptide [Source:MGI Symbol;Acc:MGI:3630329]		Q8CE23	5.1	4.4E-05	6.5	1.2E-03	-0.7	6.6E-01	-0.9	2.8E-01
ENSMUST00000057410	fibulin 1 [Source:MGI Symbol;Acc:MGI:95487]	B2CQD6	Q08879	9.2	4.6E-06	2.3	1.2E-02	0.2	7.3E-01	0.3	5.8E-01
ENSMUST00000057416	transmembrane protein 251 [Source:MGI Symbol;Acc:MGI:2443862]		Q8BH26	-1.8	9.2E-03	6.2	4.8E-05	-1.6	1.2E-01	0.5	3.5E-01
ENSMUST00000057423	phosphatidic acid phosphatase type 2 domain containing 3 [Source:MGI Symbol;Acc:MGI:2445183]		Q91WB2	7.5	1.5E-04	-1.8	1.2E-01	1.5	6.5E-02	-1.2	3.7E-01
ENSMUST00000056601	vacuolar protein sorting 53 (yeast) [Source:MGI Symbol;Acc:MGI:1915549]		Q8CCB4	-2.3	9.3E-02	-0.3	8.8E-01	2.0	1.8E-01	-0.1	9.7E-01
ENSMUST00000056614	chemokine (C-X-C motif) receptor 3 [Source:MGI Symbol;Acc:MGI:1277207]		O88410	0.4	4.9E-01	0.2	7.9E-01	0.0	1.0E+00	0.2	7.5E-01
ENSMUST00000057428	myosin light chain kinase family, member 4 [Source:MGI Symbol;Acc:MGI:3643758]	F8WIP5		6.2	3.6E-05	3.3	9.5E-04	-5.2	3.5E-04	-0.5	3.9E-01
ENSMUST00000057431	lens epithelial protein [Source:MGI Symbol;Acc:MGI:1930020]	Q543C4	Q9WVB6	6.5	2.4E-04	9.1	4.4E-03	0.9	7.1E-01	1.0	4.0E-01
ENSMUST00000057442	DIRAS family, GTP-binding RAS-like 2 [Source:MGI Symbol;Acc:MGI:1915453]	Q3UWU7	Q5PR73	7.6	8.5E-06	-4.3	5.7E-03	0.2	6.9E-01	-2.5	1.2E-01
ENSMUST00000057465	RIKEN cDNA A530016L24 gene [Source:MGI Symbol;Acc:MGI:2443020]			7.8	4.1E-05	-5.5	5.1E-03	0.9	1.9E-01	-0.5	7.7E-01
ENSMUST00000056649	growth arrest-specific 2 like 1 [Source:MGI Symbol;Acc:MGI:1926176]		Q8JZP9	4.3	8.5E-02	-2.0	3.6E-01	-4.8	4.3E-02	1.4	4.8E-01
ENSMUST00000056654	family with sequence similarity 109, member A [Source:MGI Symbol;Acc:MGI:2442708]		Q8BH49	-0.2	7.3E-01	1.7	5.8E-02	1.3	6.0E-02	-0.6	4.2E-01
ENSMUST00000056660	transmembrane protein 229B [Source:MGI Symbol;Acc:MGI:2444389]		Q8BFQ2	2.3	3.1E-01	5.9	3.9E-02	0.1	9.7E-01	-3.5	9.1E-02
ENSMUST00000056665	kelch-like 11 [Source:MGI Symbol;Acc:MGI:2388648]	Q14DU1	Q8CE33	0.7	3.8E-01	1.1	2.9E-01	0.7	3.7E-01	0.3	7.5E-01
ENSMUST00000057486	ankyrin repeat domain 46 [Source:MGI Symbol;Acc:MGI:1916089]		Q8BTZ5	-2.9	6.6E-05	6.3	3.1E-04	-0.2	9.0E-01	-0.1	9.3E-01
ENSMUST00000057488	CD200 receptor 1 [Source:MGI Symbol;Acc:MGI:1889024]		Q9ES57	-4.1	1.4E-05	-1.6	4.2E-02	0.1	8.7E-01	-0.4	5.8E-01
ENSMUST00000057497	collagen, type XXVI, alpha 1 [Source:MGI Symbol;Acc:MGI:2155345]		Q91VF6	4.6	2.2E-02	2.4	1.8E-01	-3.0	9.8E-02	1.5	2.3E-01
ENSMUST00000057500	ring finger protein 7 [Source:MGI Symbol;Acc:MGI:1337096]		Q9WTZ1	-2.7	7.3E-05	8.0	3.4E-05	-0.6	6.1E-01	0.1	9.2E-01
ENSMUST00000056710	anterior pharynx defective 1a homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2385110]		Q8BVF7	3.9	7.9E-02	-3.1	2.7E-01	-3.8	6.6E-02	3.1	2.4E-01
ENSMUST00000057540	zinc finger protein 422 [Source:MGI Symbol;Acc:MGI:1914505]		Q9ERU3	-4.0	1.4E-03	7.3	5.8E-05	-0.5	6.4E-01	-0.3	5.9E-01
ENSMUST00000057557	MCM (minichromosome maintenance deficient) binding protein [Source:MGI Symbol;Acc:MGI:1920977]		Q8R3C0	-3.4	2.9E-04	6.8	1.4E-04	-0.5	6.7E-01	-1.1	9.1E-02
ENSMUST00000057561	WW, C2 and coiled-coil domain containing 2 [Source:MGI Symbol;Acc:MGI:1261872]		Q6NXJ0	2.1	5.2E-04	-4.7	7.9E-05	-1.1	1.0E-02	-0.3	6.5E-01
ENSMUST00000057567	interleukin 1 family, member 9 [Source:MGI Symbol;Acc:MGI:2449929]	Q3U0P4		-2.1	1.0E-03	7.4	1.8E-04	1.3	3.0E-01	0.0	9.5E-01
ENSMUST00000057569	leukotriene B4 receptor 1 [Source:MGI Symbol;Acc:MGI:1309472]	A7VJD3	O88855	-5.2	4.8E-05	6.3	7.2E-04	2.6	5.3E-02	-0.8	3.0E-01
ENSMUST00000057576	component of oligomeric golgi complex 7 [Source:MGI Symbol;Acc:MGI:2685013]			2.8	3.8E-05	-5.5	1.0E-03	0.6	1.9E-01	4.6	2.9E-03
ENSMUST00000057578	tRNA nucleotidyl transferase, CCA-adding, 1 [Source:MGI Symbol;Acc:MGI:1917297]		Q8K1J6	-4.2	1.9E-04	-3.0	1.3E-02	0.2	7.3E-01	0.0	9.9E-01
ENSMUST00000057580	mechanistic target of rapamycin (serine/threonine kinase) [Source:MGI Symbol;Acc:MGI:1928394]		Q9JLN9	-3.8	8.0E-03	-4.1	1.6E-02	0.8	2.6E-01	0.6	7.0E-01
ENSMUST00000057598	metallo-beta-lactamase domain containing 2 [Source:MGI Symbol;Acc:MGI:1920102]		Q8BL86	1.3	2.9E-02	8.3	1.8E-03	2.4	2.1E-01	-0.5	6.1E-01
ENSMUST00000056760	fibronectin leucine rich transmembrane protein 3 [Source:MGI Symbol;Acc:MGI:1918686]	Q8BGT1	Q8BGT1	4.0	9.1E-02	5.6	3.9E-02	-0.3	9.1E-01	-1.9	2.0E-01
ENSMUST00000057608	leucine rich repeat containing 3 [Source:MGI Symbol;Acc:MGI:2447899]	Q543Z4	P59034	8.7	6.0E-05	8.2	6.2E-05	-0.7	5.9E-01	0.3	5.4E-01
ENSMUST00000057610	dishevelled associated activator of morphogenesis 2 [Source:MGI Symbol;Acc:MGI:1923691]		Q80U19	3.8	5.8E-05	6.5	2.5E-05	1.5	8.9E-02	-0.8	1.1E-01
ENSMUST00000056781	coiled-coil domain containing 57 [Source:MGI Symbol;Acc:MGI:1918526]		Q6PHN1	1.2	1.2E-01	2.5	1.8E-02	0.7	3.7E-01	-0.7	3.7E-01
ENSMUST00000057612	scavenger receptor cysteine rich family, 5 domains [Source:MGI Symbol;Acc:MGI:3606211]		Q8BV57	8.5	9.4E-05	7.2	2.8E-05	-1.5	1.8E-01	-0.2	7.4E-01
ENSMUST00000057613	growth differentiation factor 6 [Source:MGI Symbol;Acc:MGI:95689]	A2AII0	P43028	8.4	8.9E-06	6.5	8.7E-04	-0.5	7.4E-01	0.3	6.5E-01
ENSMUST00000057623	lamin B2 [Source:MGI Symbol;Acc:MGI:96796]			4.2	1.2E-02	3.4	1.5E-04	1.4	1.4E-02	-0.6	1.3E-01
ENSMUST00000057627	spermatogenesis associated 2 [Source:MGI Symbol;Acc:MGI:2146885]	Q8K004		-1.3	2.5E-02	6.5	4.3E-03	-0.7	7.3E-01	-1.3	2.3E-01
ENSMUST00000057645	G protein-coupled receptor 101 [Source:MGI Symbol;Acc:MGI:2685211]	Q1WKE2	Q80T62	6.6	1.6E-04	-2.8	2.7E-01	1.0	5.8E-01	-1.8	4.8E-01
ENSMUST00000056889	chromodomain helicase DNA binding protein 4 [Source:MGI Symbol;Acc:MGI:1344380]		Q6PDQ2	3.7	8.7E-02	-0.7	8.1E-01	-2.0	3.1E-01	2.4	3.7E-01
ENSMUST00000056890	F-box and leucine-rich repeat protein 22 [Source:MGI Symbol;Acc:MGI:1921415]		Q8C7B6	0.7	2.0E-01	2.2	8.2E-03	1.0	9.9E-02	-0.5	3.3E-01
ENSMUST00000057649	predicted gene 9803 [Source:MGI Symbol;Acc:MGI:3704359]		Q9CQV1	-3.3	1.2E-02	6.2	1.1E-04	-1.4	1.8E-01	0.1	8.6E-01
ENSMUST00000057653	carbonic anhydrase 5a, mitochondrial [Source:MGI Symbol;Acc:MGI:101946]		P23589	6.4	1.6E-06	2.9	6.3E-04	-0.2	6.6E-01	-0.5	2.7E-01
ENSMUST00000057659	GRIP and coiled-coil domain containing 2 [Source:MGI Symbol;Acc:MGI:1917547]	B2RSU7		-4.3	4.9E-03	-0.4	4.5E-01	0.8	8.0E-02	-0.3	5.8E-01
ENSMUST00000057669	mitogen-activated protein kinase 3 [Source:MGI Symbol;Acc:MGI:1346859]		Q63844	-9.7	3.8E-04	8.0	1.0E-04	0.6	6.3E-01	0.3	5.9E-01
ENSMUST00000056919	casein kinase 2, alpha prime polypeptide [Source:MGI Symbol;Acc:MGI:88547]	Q545V8	O54833	-0.6	2.2E-01	0.8	2.4E-01	1.2	3.0E-02	-0.2	7.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000057676	UBA-like domain containing 2 [Source:MGI Symbol;Acc:MGI:1914635]		Q8BQH4	-6.5	1.0E-05	-0.2	7.8E-01	1.4	1.6E-02	-1.1	1.3E-01
ENSMUST00000057685	glycolipid transfer protein domain containing 2 [Source:MGI Symbol;Acc:MGI:2444527]		Q8K0R6	6.0	6.1E-03	6.8	2.3E-05	-4.3	2.5E-03	0.2	5.8E-01
ENSMUST00000056931	LIM domain binding 1 [Source:MGI Symbol;Acc:MGI:894762]		P70662	0.9	2.2E-01	0.6	5.2E-01	0.3	7.1E-01	0.6	4.7E-01
ENSMUST00000057718	proline rich 30 [Source:MGI Symbol;Acc:MGI:1923877]		Q9D9B7	5.2	1.9E-03	-2.4	1.8E-01	1.4	1.8E-01	-1.2	5.1E-01
ENSMUST00000057722	predicted gene 9837 [Source:MGI Symbol;Acc:MGI:3642517]	Q8C607		6.8	7.7E-05	-1.5	5.5E-02	0.4	4.5E-01	-2.1	3.4E-02
ENSMUST00000057725	SAM domain and HD domain, 1 [Source:MGI Symbol;Acc:MGI:1927468]	F8WJE0		-4.5	1.0E-04	7.5	9.1E-04	-0.8	6.5E-01	0.3	7.0E-01
ENSMUST00000056946	neuralized E3 ubiquitin protein ligase 3 [Source:MGI Symbol;Acc:MGI:2429944]		Q8CJC5	0.0	9.6E-01	1.0	2.2E-01	1.2	6.7E-02	0.2	7.3E-01
ENSMUST00000056948				-0.5	8.8E-01	-3.8	2.9E-01	-4.1	8.0E-02	-0.8	8.4E-01
ENSMUST00000057742	copine IV [Source:MGI Symbol;Acc:MGI:1921270]		Q8BLR2	5.6	7.0E-03	7.4	6.0E-05	-0.6	6.1E-01	-0.4	4.6E-01
ENSMUST00000057767	uroplakin 1B [Source:MGI Symbol;Acc:MGI:98912]		Q9Z2C6	6.6	2.9E-03	-1.9	2.0E-01	2.3	2.1E-02	1.0	4.7E-01
ENSMUST00000057773	metallo-beta-lactamase domain containing 1 [Source:MGI Symbol;Acc:MGI:2679717]		Q8BWY4	1.8	2.1E-02	4.8	1.9E-03	-0.9	4.5E-01	-0.8	2.7E-01
ENSMUST00000057781	kelch-like 31 [Source:MGI Symbol;Acc:MGI:3045305]	G3X9D8		6.3	5.5E-06	4.8	9.0E-04	-1.9	1.1E-01	0.2	7.2E-01
ENSMUST00000057784	ıte carrier family 7 (cationic amino acid transporter, y+ system), member 2 [Source:MGI Symbol;Acc:MGI:998		P18581	8.2	1.9E-04	-5.8	4.8E-03	0.5	4.4E-01	0.9	5.9E-01
ENSMUST00000056972	cap methyltransferase 2 [Source:MGI Symbol;Acc:MGI:2384580]		Q8BWQ4	1.0	7.8E-02	1.0	1.6E-01	-0.2	7.3E-01	-0.1	8.0E-01
ENSMUST00000057795	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]		A2RTL5	-5.6	1.5E-02	3.3	6.3E-03	0.4	6.5E-01	0.2	7.4E-01
ENSMUST00000057798	amyloid beta (A4) precursor protein-binding, family A, member 3 [Source:MGI Symbol;Acc:MGI:1888527]		O88888	-1.6	2.5E-02	2.3	3.0E-03	-0.5	3.5E-01	-0.6	2.4E-01
ENSMUST00000057801	potassium inwardly-rectifying channel, subfamily J, member 4 [Source:MGI Symbol;Acc:MGI:104743]	Q8R435		7.4	2.6E-05	5.8	1.9E-05	0.1	8.6E-01	0.3	5.7E-01
ENSMUST00000057810	pregnancy-specific glycoprotein 23 [Source:MGI Symbol;Acc:MGI:1891355]	Q9D2U0		7.1	1.2E-06	-6.5	1.5E-03	-0.3	5.5E-01	0.0	9.8E-01
ENSMUST00000057000	zinc finger CCCH type containing 14 [Source:MGI Symbol;Acc:MGI:1919824]		Q8BJ05	3.6	1.3E-01	0.3	9.3E-01	-1.1	6.5E-01	2.2	4.2E-01
ENSMUST00000057015	solute carrier family 4, sodium bicarbonate cotransporter, member 7 [Source:MGI Symbol;Acc:MGI:2443878]	F8VQC9		-0.9	9.7E-02	-0.1	8.5E-01	0.7	1.3E-01	0.0	9.7E-01
ENSMUST00000057814	2'-5' oligoadenylate synthetase 1F [Source:MGI Symbol;Acc:MGI:2180855]	Q14AZ4		7.5	9.6E-04	5.9	1.2E-03	2.2	9.0E-02	-0.3	6.3E-01
ENSMUST00000057831	cartilage intermediate layer protein 2 [Source:MGI Symbol;Acc:MGI:1915959]	D3Z7H8		7.8	5.4E-05	5.2	1.7E-03	-2.8	6.6E-02	1.2	1.4E-01
ENSMUST00000057836	zinc finger protein 672 [Source:MGI Symbol;Acc:MGI:2442105]		Q99LH4	-5.5	5.6E-04	2.8	7.7E-03	-1.1	1.7E-01	-0.2	7.3E-01
ENSMUST00000057028	calmodulin regulated spectrin-associated protein family, member 3 [Source:MGI Symbol;Acc:MGI:1916947]	U5LK19	Q80VC9	2.5	1.9E-01	4.9	6.9E-03	-1.5	3.7E-01	-4.0	1.4E-02
ENSMUST00000057844	RIKEN cDNA B230219D22 gene [Source:MGI Symbol;Acc:MGI:1925771]		Q80X32	-1.1	2.8E-02	5.2	1.5E-02	-0.6	7.7E-01	0.4	7.2E-01
ENSMUST00000057846	NCK-associated protein 5 [Source:MGI Symbol;Acc:MGI:2686394]	Q29SA9		7.9	3.5E-03	2.3	7.4E-04	0.3	3.7E-01	-0.2	6.1E-01
ENSMUST00000057849	complement component 1, q subcomponent-like 1 [Source:MGI Symbol;Acc:MGI:1344400]		O88992	6.6	1.4E-04	5.3	5.4E-04	-0.9	4.0E-01	0.1	9.1E-01
ENSMUST00000057855	exocyst complex component 3-like [Source:MGI Symbol;Acc:MGI:3041195]		Q8BI71	3.9	6.5E-04	-6.8	4.1E-02	0.3	7.5E-01	2.4	4.3E-01
ENSMUST00000057870	reprimo-like [Source:MGI Symbol;Acc:MGI:2144486]	B2RV63	Q3URD2	6.4	2.0E-04	7.0	7.1E-05	-1.4	2.5E-01	0.5	3.5E-01
ENSMUST00000057070	zinc finger protein 456 [Source:MGI Symbol;Acc:MGI:3040694]	B2RUK9		0.9	2.8E-01	3.9	3.7E-03	2.1	3.8E-02	-0.9	2.6E-01
ENSMUST00000057885	ribosomal protein L9 [Source:MGI Symbol;Acc:MGI:1298373]	Q5EBQ6	P51410	-6.6	2.3E-07	6.1	2.9E-04	-0.5	6.8E-01	-0.3	5.9E-01
ENSMUST00000057892	bromodomain PHD finger transcription factor [Source:MGI Symbol;Acc:MGI:2444008]	E9Q6A7		-1.8	7.7E-03	6.2	5.7E-04	-0.7	6.2E-01	-1.0	1.9E-01
ENSMUST00000057089	POZ (BTB) and AT hook containing zinc finger 1 [Source:MGI Symbol;Acc:MGI:1891832]	Q9JMG9		-1.6	4.5E-01	-2.6	4.4E-01	0.2	9.2E-01	1.2	6.8E-01
ENSMUST00000057090	synaptopodin 2-like [Source:MGI Symbol;Acc:MGI:1916010]		Q8BWB1	4.5	1.6E-01	8.0	2.6E-02	-0.2	9.6E-01	-3.8	5.8E-02
ENSMUST00000057893	frizzled homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1888513]		Q9JIP6	8.1	7.2E-05	-2.9	1.5E-02	1.1	7.3E-02	-1.6	1.8E-01
ENSMUST00000057897	zinc finger, AN1-type domain 3 [Source:MGI Symbol;Acc:MGI:1096572]		Q497H0	-4.3	2.2E-05	-2.2	6.9E-03	-0.8	6.2E-02	-0.9	1.8E-01
ENSMUST00000057135	tau tubulin kinase 2 [Source:MGI Symbol;Acc:MGI:2155779]		Q3UVR3	-1.6	5.8E-01	1.7	2.8E-01	-4.1	4.1E-02	-7.4	1.1E-02
ENSMUST00000057145	hydroxycarboxylic acid receptor 2 [Source:MGI Symbol;Acc:MGI:1933383]	Q0VBA6	Q9EP66	-1.9	5.3E-02	-2.7	4.4E-02	-0.2	7.8E-01	0.6	6.4E-01
ENSMUST00000057907	F-box protein 44 [Source:MGI Symbol;Acc:MGI:1354744]	A2A7H5		5.9	3.9E-04	-1.8	4.1E-02	0.7	1.5E-01	-0.2	8.1E-01
ENSMUST00000057921	ADP-ribosylation factor 2 [Source:MGI Symbol;Acc:MGI:99595]		Q8BSL7	-4.2	3.9E-04	6.2	3.7E-04	-0.5	7.1E-01	-1.0	1.7E-01
ENSMUST00000057927	Ras interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917153]		Q3U0S6	3.4	3.0E-03	6.7	3.3E-04	-1.9	1.9E-01	0.1	9.1E-01
ENSMUST00000057934	transcription factor 25 (basic helix-loop-helix) [Source:MGI Symbol;Acc:MGI:1914105]		Q8R3L2	-4.3	3.9E-05	8.2	2.0E-02	-0.6	8.5E-01	-1.7	3.1E-01
ENSMUST00000057942	melanocortin 4 receptor [Source:MGI Symbol;Acc:MGI:99457]		P56450	7.6	1.8E-05	-4.8	5.2E-02	0.8	3.7E-01	0.4	8.6E-01
ENSMUST00000057944	UDP galactosyltransferase 8A [Source:MGI Symbol;Acc:MGI:109522]		Q64676	-3.3	3.0E-04	7.6	3.3E-05	-1.5	2.0E-01	-0.7	2.1E-01
ENSMUST00000057950	sal-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:109295]		Q62255	9.8	3.9E-06	-2.5	6.8E-02	0.1	8.9E-01	-1.8	2.1E-01
ENSMUST00000057977	RIKEN cDNA A730049H05 gene [Source:MGI Symbol;Acc:MGI:1921766]	Q8C940		6.2	1.3E-03	6.7	2.5E-04	-0.3	8.2E-01	-0.2	7.1E-01
ENSMUST00000057180	RIKEN cDNA A830080D01 gene [Source:MGI Symbol;Acc:MGI:2685992]		A2AG58	-2.1	1.9E-01	-0.5	7.1E-01	-0.2	8.2E-01	-1.8	2.8E-01
ENSMUST00000058007	relaxin family peptide receptor 3 [Source:MGI Symbol;Acc:MGI:2441827]	Q5Y988	Q8BGE9	8.5	1.4E-05	7.1	4.3E-04	-0.6	6.6E-01	-0.7	3.4E-01
ENSMUST00000058016	purinergic receptor P2X, ligand-gated ion channel, 2 [Source:MGI Symbol;Acc:MGI:2665170]		Q8K3P1	7.2	3.8E-03	6.8	4.2E-05	-1.5	1.8E-01	0.1	8.1E-01
ENSMUST00000057188	cannabinoid receptor 1 (brain) [Source:MGI Symbol;Acc:MGI:104615]		P47746	6.0	4.6E-02	8.0	1.7E-02	-0.9	7.6E-01	-2.9	1.2E-01
ENSMUST00000058022	two pore segment channel 2 [Source:MGI Symbol;Acc:MGI:2385297]		Q8BWC0	-2.9	1.4E-03	7.1	8.8E-05	-0.5	6.4E-01	-0.1	8.4E-01
ENSMUST00000058030	methylthioadenosine phosphorylase [Source:MGI Symbol;Acc:MGI:1914152]		Q9CQ65	1.7	1.3E-02	2.7	9.0E-03	0.2	7.8E-01	-0.1	9.1E-01
ENSMUST00000058033	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2 [Source:MGI Symbol;Acc:MGI:1925868]		Q6ZQK5	-3.4	2.9E-05	-6.2	1.3E-03	0.8	1.3E-01	0.9	5.5E-01
ENSMUST00000058038	zinc finger protein 629 [Source:MGI Symbol;Acc:MGI:2444524]		Q6A085	6.7	6.1E-04	-2.7	3.0E-02	2.1	4.7E-03	-0.5	6.6E-01
ENSMUST00000057207	teneurin transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1345184]	A0A0A0MQ92		3.4	9.2E-02	1.8	4.6E-01	-0.4	8.4E-01	1.2	5.4E-01
ENSMUST00000058045	GRB2 associated, regulator of MAPK1-like [Source:MGI Symbol;Acc:MGI:2685290]		Q6PAJ3	8.4	1.5E-05	-3.9	6.7E-04	-0.5	2.4E-01	0.0	9.8E-01
ENSMUST00000058060	biorientation of chromosomes in cell division 1 [Source:MGI Symbol;Acc:MGI:1916806]		Q5SQY2	1.4	2.8E-02	-0.2	8.3E-01	-2.8	1.1E-02	3.7	4.4E-03
ENSMUST00000058089	hnRNP-associated with lethal yellow [Source:MGI Symbol;Acc:MGI:97850]	Q3U3F6	Q64012	-6.9	1.9E-04	-5.7	6.8E-04	0.2	6.8E-01	-0.9	4.6E-01
ENSMUST00000058092	MAS-related GPR, member G [Source:MGI Symbol;Acc:MGI:3033145]		Q91ZB5	7.6	2.3E-05	8.0	7.0E-05	-0.7	6.1E-01	-0.8	2.1E-01
ENSMUST00000058093	family with sequence similarity 187, member B [Source:MGI Symbol;Acc:MGI:1923665]		Q0VAY3	6.2	6.4E-04	7.4	4.1E-05	-0.6	6.0E-01	-0.4	5.0E-01
ENSMUST00000058098	membrane-bound transcription factor peptidase, site 2 [Source:MGI Symbol;Acc:MGI:2444506]		Q8CHX6	2.9	2.2E-02	5.5	9.1E-05	-0.6	4.6E-01	-0.8	1.4E-01
ENSMUST00000058099	coagulation factor II (thrombin) receptor-like 3 [Source:MGI Symbol;Acc:MGI:1298207]		O88634	4.1	3.6E-04	7.3	1.3E-04	0.2	8.5E-01	1.0	1.5E-01
ENSMUST00000057251	olfactory receptor 456 [Source:MGI Symbol;Acc:MGI:3030290]	B2RT27		1.5	5.1E-02	0.5	5.1E-01	-1.2	8.2E-02	-0.2	7.3E-01
ENSMUST00000058104	zinc finger protein 719 [Source:MGI Symbol;Acc:MGI:2444708]	Q8BIV1		-1.8	7.1E-03	7.5	1.3E-04	-0.6	6.4E-01	-0.5	4.0E-01
ENSMUST00000058133	eukaryotic translation initiation factor 4 gamma, 3 [Source:MGI Symbol;Acc:MGI:1923935]	Q8BQR8		3.0	4.0E-03	2.4	2.1E-02	0.4	5.7E-01	0.2	8.1E-01
ENSMUST00000057257	JNK1/MAPK8-associated membrane protein [Source:MGI Symbol;Acc:MGI:1915057]		Q8BI36	-0.6	5.8E-01	-2.2	1.2E-01	-1.1	2.4E-01	0.6	6.5E-01
ENSMUST00000058137	RAB, member RAS oncogene family-like 6 [Source:MGI Symbol;Acc:MGI:2442633]		Q5U3K5	-2.1	3.0E-03	5.0	2.9E-03	0.9	4.6E-01	-0.7	3.9E-01
ENSMUST00000058142	small proline-rich protein 3 [Source:MGI Symbol;Acc:MGI:1330237]		O09116	7.7	1.1E-04	-5.3	3.4E-02	1.0	2.5E-01	1.3	5.6E-01
ENSMUST00000058150	loricrin [Source:MGI Symbol;Acc:MGI:96816]		P18165	7.1	1.3E-04	5.6	2.1E-02	-0.8	7.2E-01	0.8	5.3E-01
ENSMUST00000058154	transmembrane and tetratricopeptide repeat containing 3 [Source:MGI Symbol;Acc:MGI:3036255]	G5E8C4		2.2	6.4E-03	6.9	2.4E-04	-0.6	6.4E-01	-1.4	6.5E-02
ENSMUST00000058159	cannabinoid receptor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917505]		Q5M8N0	4.5	2.7E-04	-0.8	5.1E-01	-0.4	6.1E-01	-3.2	5.4E-02
ENSMUST00000058162	naf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian) [Source:MGI Symbol;Acc:MGI:9691		O54790	-2.0	7.3E-03	6.2	2.5E-05	0.7	3.8E-01	0.1	8.0E-01
ENSMUST00000058178	tumor-associated calcium signal transducer 2 [Source:MGI Symbol;Acc:MGI:1861606]		Q8BGV3	-3.3	5.5E-05	-7.2	6.9E-05	-1.5	4.3E-03	0.1	9.6E-01
ENSMUST00000058196	sushi domain containing 3 [Source:MGI Symbol;Acc:MGI:1913579]		Q9D176	-4.2	7.0E-05	2.1	9.5E-03	0.7	1.9E-01	0.2	6.9E-01
ENSMUST00000058213	oxoglutarate (alpha-ketoglutarate) receptor 1 [Source:MGI Symbol;Acc:MGI:2685145]		Q6IYF8	7.8	2.5E-05	2.6	3.8E-03	0.7	2.5E-01	-0.5	3.5E-01
ENSMUST00000058229	retinitis pigmentosa 1 homolog (human)-like 1 [Source:MGI Symbol;Acc:MGI:2384303]	A1L340	Q8CGM2	9.9	1.2E-06	6.0	2.8E-04	0.7	5.1E-01	0.2	7.2E-01
ENSMUST00000058230	endosulfine alpha [Source:MGI Symbol;Acc:MGI:1891189]		P60840	-3.9	4.9E-05	5.8	4.6E-04	-0.5	6.4E-01	0.1	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000058237	UDP glucuronosyltransferase 1 family, polypeptide A7C [Source:MGI Symbol;Acc:MGI:3032636]		Q6ZQM8	-5.0	6.2E-05	3.9	1.4E-04	-4.6	3.5E-04	-1.6	9.7E-03
ENSMUST00000058265	C1GALT1-specific chaperone 1 [Source:MGI Symbol;Acc:MGI:1913493]		Q9JMG2	-6.1	4.6E-05	-5.3	3.8E-03	0.1	8.8E-01	1.9	2.1E-01
ENSMUST00000057330	kinesin family member 3A [Source:MGI Symbol;Acc:MGI:107689]	Q3UI47		0.2	9.0E-01	-4.5	7.5E-02	-3.3	2.7E-02	1.5	5.5E-01
ENSMUST00000058280	proline dehydrogenase (oxidase) 2 [Source:MGI Symbol;Acc:MGI:1929093]		Q8VCZ9	5.2	5.1E-03	4.2	3.0E-03	-0.5	6.0E-01	0.1	8.4E-01
ENSMUST00000058286	ribosomal protein S6 kinase, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1270849]	Q8C3J7		3.0	7.8E-03	-3.3	1.6E-01	0.9	3.5E-01	-0.3	9.1E-01
ENSMUST00000057344	polycystic kidney disease 1 like 3 [Source:MGI Symbol;Acc:MGI:2664670]	A2A258	Q2EG98	0.1	9.5E-01	1.4	5.3E-01	-0.6	7.3E-01	-1.9	3.7E-01
ENSMUST00000058292	RAS and EF hand domain containing [Source:MGI Symbol;Acc:MGI:2448565]		Q5RI75	6.2	8.9E-04	-0.3	6.1E-01	1.2	3.1E-02	-0.1	9.0E-01
ENSMUST00000058295	c leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) [Source:MGI Syn		P70424	8.7	7.4E-05	6.4	5.6E-04	-0.6	6.5E-01	-0.7	3.7E-01
ENSMUST00000058326	sal-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1354373]		Q9QX96	8.1	1.2E-05	8.8	3.1E-05	-0.7	5.9E-01	-0.5	3.8E-01
ENSMUST00000058333	translocase of inner mitochondrial membrane 10B [Source:MGI Symbol;Acc:MGI:1315196]		Q9WV96	-7.9	7.2E-06	4.7	4.2E-04	-0.3	7.3E-01	0.1	8.1E-01
ENSMUST00000058347	vestigial like 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2447460]			4.5	1.1E-02	7.2	4.0E-05	-1.6	1.7E-01	0.4	4.3E-01
ENSMUST00000058351	phosphoglucomutase 2 [Source:MGI Symbol;Acc:MGI:97565]		Q9D0F9	-7.1	7.8E-05	-1.2	1.1E-01	0.4	3.9E-01	-0.2	7.7E-01
ENSMUST00000057421	RAD9-HUS1-RAD1 interacting nuclear orphan 1 [Source:MGI Symbol;Acc:MGI:1915315]	E9Q1D4		-0.9	4.7E-01	-1.0	6.0E-01	1.0	4.3E-01	1.1	5.1E-01
ENSMUST00000058383	poly(A) binding protein interacting protein 2B [Source:MGI Symbol;Acc:MGI:2386865]		Q91W45	1.6	6.4E-03	5.5	1.5E-03	-1.6	2.6E-01	0.4	5.8E-01
ENSMUST00000057427				0.1	8.3E-01	2.0	3.0E-02	1.2	9.1E-02	-0.6	3.5E-01
ENSMUST00000058393	RIKEN cDNA A430005L14 gene [Source:MGI Symbol;Acc:MGI:2140680]		Q80WR5	-4.3	1.0E-03	7.0	4.2E-05	0.6	5.1E-01	-0.2	7.7E-01
ENSMUST00000058404	myc-like oncogene, s-myc protein [Source:MGI Symbol;Acc:MGI:1332242]		Q9Z304	6.4	4.3E-04	6.2	5.7E-04	-0.7	6.2E-01	-0.4	5.4E-01
ENSMUST00000057438	valosin containing protein (p97)/p47 complex interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917925]			-1.0	3.9E-02	-0.1	7.9E-01	0.8	5.6E-02	0.0	9.8E-01
ENSMUST00000058407	ubiquinol-cytochrome c reductase, complex III subunit X [Source:MGI Symbol;Acc:MGI:1913402]	Q5NCJ9	Q8R1I1	-4.6	2.0E-03	6.3	9.8E-05	-0.6	5.3E-01	0.7	2.1E-01
ENSMUST00000058418	solute carrier family 29 (nucleoside transporters), member 4 [Source:MGI Symbol;Acc:MGI:2385330]		Q8R139	4.8	9.0E-05	8.2	8.1E-05	0.0	9.8E-01	-0.5	4.5E-01
ENSMUST00000057481	nucleoporin 160 [Source:MGI Symbol;Acc:MGI:1926227]		Q9Z0W3	-0.3	5.1E-01	1.2	5.8E-02	0.6	2.1E-01	-1.0	1.0E-01
ENSMUST00000058429	interleukin 27 [Source:MGI Symbol;Acc:MGI:2384409]		Q8K3I6	-2.2	1.9E-02	-1.9	6.8E-03	0.9	1.5E-02	-0.1	8.4E-01
ENSMUST00000058437	ribosomal protein L7 [Source:MGI Symbol;Acc:MGI:98073]	Q5M9N8	P14148	-6.0	7.4E-06	-3.2	3.9E-04	0.0	9.1E-01	-0.9	1.8E-01
ENSMUST00000057495	transmembrane protein 161B [Source:MGI Symbol;Acc:MGI:1919995]		Q8C2L6	-1.6	3.6E-02	-1.6	7.8E-02	0.1	8.6E-01	0.1	9.1E-01
ENSMUST00000058438	DDB1 and CUL4 associated factor 7 [Source:MGI Symbol;Acc:MGI:1919083]		P61963	-2.4	5.5E-04	7.4	1.9E-03	-0.7	7.0E-01	-3.5	1.3E-02
ENSMUST00000058440	dynein, axonemal, heavy chain 10 [Source:MGI Symbol;Acc:MGI:1860299]	D3YYQ8		10.2	1.7E-05	-2.8	3.5E-04	-0.1	8.0E-01	0.0	9.3E-01
ENSMUST00000057501	zinc finger protein 871 [Source:MGI Symbol;Acc:MGI:1921793]	Q80XN4		0.3	6.1E-01	-0.1	9.3E-01	0.0	9.7E-01	0.4	5.7E-01
ENSMUST00000057502	histocompatibility 2, M region locus 10.4 [Source:MGI Symbol;Acc:MGI:1276527]	Q85ZW8		3.3	1.4E-01	4.8	5.5E-02	-0.5	8.3E-01	-2.0	2.3E-01
ENSMUST00000058464	teine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9 [Source:MGI Symbol;Acc:M		Q9D7D2	6.9	2.5E-05	6.6	1.1E-04	-2.6	5.2E-02	0.1	9.2E-01
ENSMUST00000057525	tripartite motif-containing 3 [Source:MGI Symbol;Acc:MGI:1860040]		Q9R1R2	-1.1	7.0E-01	0.0	9.9E-01	0.5	8.3E-01	-0.5	8.6E-01
ENSMUST00000058470	polymerase (RNA) II (DNA directed) polypeptide A [Source:MGI Symbol;Acc:MGI:98086]		P08775	-3.5	2.2E-03	-4.9	4.2E-03	0.3	6.3E-01	1.2	4.1E-01
ENSMUST00000057551	stem-loop binding protein [Source:MGI Symbol;Acc:MGI:108402]	Q3U4T7	P97440	-1.4	6.4E-01	1.8	5.5E-01	0.9	7.5E-01	-2.4	4.2E-01
ENSMUST00000058472	SV2 related protein [Source:MGI Symbol;Acc:MGI:1915916]		Q8BFT9	7.8	6.0E-05	-2.0	2.6E-02	1.0	3.7E-02	-0.3	6.8E-01
ENSMUST00000058475	neurogenin 1 [Source:MGI Symbol;Acc:MGI:107754]		P70660	6.8	7.4E-05	2.0	3.2E-03	-0.1	7.3E-01	0.0	9.2E-01
ENSMUST00000058476	OTU domain containing 7A [Source:MGI Symbol;Acc:MGI:2158505]		Q8R554	4.7	1.0E-02	-1.2	4.6E-02	0.5	2.5E-01	-0.4	4.1E-01
ENSMUST00000058479	dynein regulatory complex subunit 7 [Source:MGI Symbol;Acc:MGI:2685616]		Q6V3W6	5.0	2.4E-04	-3.4	5.8E-03	1.9	3.7E-03	0.0	9.7E-01
ENSMUST00000058488	transmembrane emp24 domain containing 3 [Source:MGI Symbol;Acc:MGI:1913361]		Q78IS1	-3.3	1.6E-04	3.2	1.1E-04	0.8	9.0E-02	0.3	3.7E-01
ENSMUST00000058491	transmembrane protein 121 [Source:MGI Symbol;Acc:MGI:1916445]		Q80XA0	6.0	9.3E-04	-3.0	1.3E-02	1.1	6.4E-02	-0.1	9.4E-01
ENSMUST00000058524	zinc finger CCCH-type, antiviral 1-like [Source:MGI Symbol;Acc:MGI:2443387]	B9EHM1	Q8BFR1	4.5	1.6E-04	-3.4	4.5E-02	0.2	7.6E-01	-0.2	9.1E-01
ENSMUST00000058535	G protein-coupled receptor 149 [Source:MGI Symbol;Acc:MGI:2443628]		Q3UVY1	9.0	5.8E-06	2.3	5.9E-03	0.8	1.4E-01	-0.2	7.6E-01
ENSMUST00000058548	interleukin 17 receptor E [Source:MGI Symbol;Acc:MGI:1889371]		Q8BH06	6.3	3.2E-05	7.9	3.4E-04	-0.1	9.4E-01	0.7	3.7E-01
ENSMUST00000058550	cyclin I [Source:MGI Symbol;Acc:MGI:1341077]		Q9Z2V9	-4.3	7.6E-06	4.7	9.0E-05	0.9	1.8E-01	0.0	9.5E-01
ENSMUST00000057611	predicted pseudogene 7367 [Source:MGI Symbol;Acc:MGI:3646404]	D3YZA3		-2.0	4.4E-01	3.3	3.5E-01	4.4	1.6E-01	-0.9	7.4E-01
ENSMUST00000058578	progesterone receptor membrane component 2 [Source:MGI Symbol;Acc:MGI:1918054]		Q80UU9	-2.5	2.0E-03	8.4	8.2E-04	0.2	9.2E-01	0.2	7.7E-01
ENSMUST00000058579	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28 [Source:MGI Symbol;Acc:MGI:1919236]		Q9CWT6	-2.4	3.1E-04	6.3	1.0E-04	-1.5	1.9E-01	0.6	2.6E-01
ENSMUST00000058585	iption elongation factor A (SII) N-terminal and central domain containing 2 [Source:MGI Symbol;Acc:MGI:19		Q8R2M0	-5.8	3.1E-04	7.2	4.9E-03	2.4	2.4E-01	-0.7	5.2E-01
ENSMUST00000058593	EGF-like, fibronectin type III and laminin G domains [Source:MGI Symbol;Acc:MGI:2146149]		Q4VBE4	7.6	5.5E-05	0.5	4.8E-01	1.2	2.7E-02	-0.6	3.6E-01
ENSMUST00000057631	small G protein signaling modulator 2 [Source:MGI Symbol;Acc:MGI:2144695]		Q80U12	2.1	2.2E-01	0.4	8.5E-01	-0.5	7.6E-01	1.2	5.4E-01
ENSMUST00000058600	forkhead box D4 [Source:MGI Symbol;Acc:MGI:1347467]		Q60688	7.2	2.8E-05	6.2	5.2E-04	-0.5	7.1E-01	0.0	9.9E-01
ENSMUST00000058609	olfactory receptor 370 [Source:MGI Symbol;Acc:MGI:3030204]	E9Q848		6.2	6.6E-04	-1.3	2.7E-01	0.2	8.1E-01	-1.8	1.8E-01
ENSMUST00000058610	urocortin 3 [Source:MGI Symbol;Acc:MGI:1932970]	Q3UFJ9	Q924A4	7.7	2.4E-04	6.8	4.7E-03	-0.8	6.9E-01	-0.7	5.2E-01
ENSMUST00000058615	corepressor interacting with RBPJ, 1 [Source:MGI Symbol;Acc:MGI:1914185]		Q9DA19	-2.2	4.3E-03	5.6	1.7E-05	-0.5	4.8E-01	0.3	5.2E-01
ENSMUST00000058635	carrier family 25 (mitochondrial carrier, ornithine transporter) member 2 [Source:MGI Symbol;Acc:MGI:213		Q99ML6	4.8	7.7E-04	-3.8	2.1E-02	0.1	8.3E-01	-0.3	8.2E-01
ENSMUST00000058636	helt bHLH transcription factor [Source:MGI Symbol;Acc:MGI:3040955]		Q7TS99	7.7	3.8E-05	-6.7	3.4E-03	1.4	5.2E-02	-1.7	4.5E-01
ENSMUST00000058643	F-box protein 43 [Source:MGI Symbol;Acc:MGI:1926053]	G3X9B2		5.9	1.1E-05	-5.7	2.5E-04	1.1	3.2E-02	0.3	8.0E-01
ENSMUST00000058644	transmembrane protein 196 [Source:MGI Symbol;Acc:MGI:2685374]	D3YWQ9		6.1	1.3E-04	6.6	5.4E-03	-0.7	7.3E-01	-1.3	2.4E-01
ENSMUST00000057692	LUC7-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2183260]		Q7TNC4	-0.5	8.6E-01	-3.7	3.0E-01	-2.1	2.9E-01	1.1	7.6E-01
ENSMUST00000057717	zinc finger protein 319 [Source:MGI Symbol;Acc:MGI:1890618]		Q9ERR8	-0.6	2.4E-01	0.3	6.7E-01	1.0	4.6E-02	0.2	7.4E-01
ENSMUST00000058651	L-amino acid oxidase 1 [Source:MGI Symbol;Acc:MGI:2140628]	B1ARV3		7.6	1.0E-04	5.4	2.0E-03	-1.2	4.1E-01	-1.3	1.4E-01
ENSMUST00000058652	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 [Source:MGI Symbol;Acc:MGI:1333861]	Q52KJ0	Q8BKN6	7.3	6.1E-05	5.9	4.3E-04	-0.6	6.2E-01	0.4	5.8E-01
ENSMUST00000058659	thiosulfate sulfurtransferase, mitochondrial [Source:MGI Symbol;Acc:MGI:98852]	Q545S0	P52196	-2.4	9.9E-03	-2.8	6.5E-03	1.1	4.5E-02	-0.6	5.1E-01
ENSMUST00000058667	leucine rich repeat containing 4B [Source:MGI Symbol;Acc:MGI:3027390]		P0C192	8.1	5.3E-05	-5.3	4.9E-05	-0.2	5.6E-01	-1.3	1.3E-01
ENSMUST00000058678	protein phosphatase 1, regulatory subunit 3D [Source:MGI Symbol;Acc:MGI:1917664]	A2AJW4		-4.4	1.1E-05	6.1	6.8E-03	-0.7	7.2E-01	-1.2	2.8E-01
ENSMUST00000058679	myotubularin related protein 9 [Source:MGI Symbol;Acc:MGI:2442842]		Q9Z2D0	-1.5	6.2E-03	0.5	7.2E-01	-5.4	7.2E-03	0.8	5.1E-01
ENSMUST00000058682	anoctamin 7 [Source:MGI Symbol;Acc:MGI:3052714]		Q14AT5	7.4	8.6E-05	2.7	1.0E-02	1.0	1.8E-01	0.2	7.6E-01
ENSMUST00000058688	ring finger protein 152 [Source:MGI Symbol;Acc:MGI:2443787]		Q8BG47	11.4	2.3E-05	6.2	3.8E-05	0.0	1.0E+00	0.0	9.2E-01
ENSMUST00000058702	death effector domain-containing DNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1914629]		Q8QZV0	-5.3	1.4E-04	2.7	2.0E-02	-5.1	3.7E-03	0.4	5.8E-01
ENSMUST00000057792	paraoxonase 2 [Source:MGI Symbol;Acc:MGI:106687]		Q62086	-1.3	1.0E-01	-1.8	1.3E-01	0.3	6.1E-01	0.7	4.8E-01
ENSMUST00000057793	activity-dependent neuroprotective protein [Source:MGI Symbol;Acc:MGI:1338758]	A2BDX0	Q9Z103	0.9	6.4E-01	-0.6	8.2E-01	0.1	9.6E-01	1.6	5.0E-01
ENSMUST00000058704	immunity-related GTPase family M member 2 [Source:MGI Symbol;Acc:MGI:1926262]	Q9Z1M2		-3.7	9.5E-03	-4.8	7.6E-02	0.4	7.2E-01	-0.5	8.7E-01
ENSMUST00000058714	CD24a antigen [Source:MGI Symbol;Acc:MGI:88323]	Q3THW4	P24807	-6.9	4.9E-08	-1.1	2.2E-01	1.1	5.6E-02	0.6	4.7E-01
ENSMUST00000057799	zinc finger protein 867 [Source:MGI Symbol;Acc:MGI:2681848]	E9Q2M4		1.0	8.0E-02	0.9	1.6E-01	-0.6	2.3E-01	-0.5	3.4E-01
ENSMUST00000058716	Sad1 and UNC84 domain containing 1 [Source:MGI Symbol;Acc:MGI:1924303]		Q9D666	-2.9	2.9E-02	7.3	5.7E-05	-0.6	6.1E-01	-0.5	4.2E-01
ENSMUST00000058725	anthrax toxin receptor-like [Source:MGI Symbol;Acc:MGI:1925726]		Q8BVM2	7.8	3.5E-05	6.5	5.9E-06	-0.6	4.0E-01	0.0	9.3E-01
ENSMUST00000058733	small integral membrane protein 7 [Source:MGI Symbol;Acc:MGI:1914068]	F8WIU9		-5.1	4.9E-05	4.7	1.9E-02	-1.5	4.2E-01	1.3	2.3E-01
ENSMUST00000057816	uridine-cytidine kinase 1-like 1 [Source:MGI Symbol;Acc:MGI:1915806]		Q91YL3	-4.8	1.9E-01	-5.9	2.0E-01	-1.4	4.6E-01	-0.3	9.5E-01
ENSMUST00000057829	mitochondrial ribosomal protein L50 [Source:MGI Symbol;Acc:MGI:107329]		Q8VDT9	-1.3	4.0E-02	-1.6	4.0E-02	-0.8	9.7E-02	-0.5	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000058735	ubiquilin 1 [Source:MGI Symbol;Acc:MGI:1860276]		Q8R317	-8.1	1.5E-04	7.8	1.8E-04	0.0	9.9E-01	0.0	9.7E-01
ENSMUST00000058747	methyltransferase like 24 [Source:MGI Symbol;Acc:MGI:3045338]		Q8CCB5	5.6	6.6E-04	-4.2	2.3E-02	1.4	5.6E-02	0.0	9.8E-01
ENSMUST00000058748	family with sequence similarity 124, member B [Source:MGI Symbol;Acc:MGI:3026880]		Q8BLQ0	7.3	3.9E-06	-0.6	3.1E-01	0.9	4.0E-02	0.5	4.3E-01
ENSMUST00000058754	zinc metallopeptidase, STE24 [Source:MGI Symbol;Acc:MGI:1890508]	B9EHY2	Q80W54	-3.5	2.0E-05	5.3	4.3E-02	-0.7	7.8E-01	1.9	1.9E-01
ENSMUST00000058755	frizzled homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:108520]	Q3V1B2	Q61088	4.6	3.6E-05	6.2	3.9E-04	-0.6	6.4E-01	-0.2	7.6E-01
ENSMUST00000058777	predicted gene 6484 [Source:MGI Symbol;Acc:MGI:3643534]	A0A0A0R784	Q8R1L8	5.2	7.6E-04	5.1	5.5E-04	0.9	3.2E-01	-0.2	7.4E-01
ENSMUST00000057859	FERM domain containing 6 [Source:MGI Symbol;Acc:MGI:2442579]		Q8C0V9	0.6	1.9E-01	0.8	1.7E-01	0.1	8.6E-01	-0.1	7.7E-01
ENSMUST00000057866	neurensin 1 [Source:MGI Symbol;Acc:MGI:894662]		P97799	4.3	9.7E-02	4.8	9.8E-02	-0.3	9.3E-01	-0.8	6.4E-01
ENSMUST00000058785	cytochrome P450, family 4, subfamily a, polypeptide 10 [Source:MGI Symbol;Acc:MGI:88611]		O88833	6.6	6.6E-04	6.0	5.9E-04	-0.5	7.0E-01	-0.1	8.5E-01
ENSMUST00000057884	G protein pathway suppressor 2 [Source:MGI Symbol;Acc:MGI:1891751]	Q921N8		-1.3	2.2E-01	-1.1	5.3E-01	1.8	1.8E-01	1.5	3.0E-01
ENSMUST00000058787	glycine receptor, alpha 2 subunit [Source:MGI Symbol;Acc:MGI:95748]	Q3UTL8	Q7TNC8	5.6	4.6E-04	-7.2	1.5E-06	-0.6	3.6E-02	0.0	9.8E-01
ENSMUST00000058793	polymerase (DNA-directed), delta interacting protein 3 [Source:MGI Symbol;Acc:MGI:1921076]		Q8BG81	-8.1	2.2E-04	0.4	5.3E-01	0.9	7.4E-02	-1.3	6.5E-02
ENSMUST00000058796	lysine (K)-specific demethylase 4D [Source:MGI Symbol;Acc:MGI:3606484]		Q3U2K5	7.6	1.8E-05	3.7	1.7E-03	-4.5	3.5E-03	-0.1	9.1E-01
ENSMUST00000057896	glucoside xylosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2684933]	D3Z6W7		-0.3	6.5E-01	-0.2	8.7E-01	2.3	1.9E-02	2.1	7.5E-02
ENSMUST00000058804	zinc finger protein 612 [Source:MGI Symbol;Acc:MGI:2443465]	G5E8C8		7.8	1.8E-05	-3.1	1.5E-03	1.1	1.4E-02	-0.1	8.7E-01
ENSMUST00000058806	Grb2-binding adaptor, transmembrane [Source:MGI Symbol;Acc:MGI:3608341]		Q8CB93	-3.0	9.6E-04	6.7	3.0E-04	-0.6	6.7E-01	-1.3	7.6E-02
ENSMUST00000057910	REX1, RNA exonuclease 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914182]		Q7TT28	-0.2	7.3E-01	0.6	5.0E-01	1.0	1.3E-01	0.2	7.5E-01
ENSMUST00000058814	RAB9B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2442454]	Q3KNA5	Q8BHH2	10.9	3.1E-05	-5.8	1.1E-03	0.1	9.1E-01	1.7	2.0E-01
ENSMUST00000058825	coiled-coil domain containing 121 [Source:MGI Symbol;Acc:MGI:2685601]	E9Q6D3		7.0	7.2E-05	3.5	8.0E-03	0.3	7.8E-01	0.2	8.4E-01
ENSMUST00000058829	neuropilin (NRP) and tolloid (TLL)-like 1 [Source:MGI Symbol;Acc:MGI:2180216]		Q8R4I7	7.3	6.0E-05	-3.9	4.2E-04	0.2	5.4E-01	-0.1	8.8E-01
ENSMUST00000057935	solute carrier family 25, member 44 [Source:MGI Symbol;Acc:MGI:2444391]	Q3TMC4		1.5	5.9E-01	-0.2	9.6E-01	-0.4	8.8E-01	1.3	7.2E-01
ENSMUST00000058839	kelch-like 6 [Source:MGI Symbol;Acc:MGI:2686922]		Q6V595	-6.4	4.9E-05	6.8	9.8E-05	-0.6	6.0E-01	0.3	6.1E-01
ENSMUST00000058844	zinc finger protein 786 [Source:MGI Symbol;Acc:MGI:3026883]	B2RSK4	Q8BV42	7.7	6.5E-05	-1.4	8.2E-02	1.4	1.5E-02	-0.5	5.3E-01
ENSMUST00000058845	brain abundant, membrane attached signal protein 1 [Source:MGI Symbol;Acc:MGI:1917600]		Q91XV3	-3.8	1.2E-03	9.1	1.5E-05	-0.7	5.8E-01	0.0	9.7E-01
ENSMUST00000057974	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2685009]	A0A0A0MQ97		1.4	4.2E-02	3.8	1.6E-03	2.0	2.3E-02	-0.4	5.7E-01
ENSMUST00000058856	stearoyl-coenzyme A desaturase 4 [Source:MGI Symbol;Acc:MGI:2670997]		Q6T707	6.5	3.2E-06	6.6	1.5E-03	-0.6	7.1E-01	-1.0	2.7E-01
ENSMUST00000058860	upstream transcription factor 2 [Source:MGI Symbol;Acc:MGI:99961]		Q64705	-8.5	1.8E-05	8.3	3.2E-05	-0.6	6.5E-01	-0.4	4.7E-01
ENSMUST00000058009	family with sequence similarity 65, member B [Source:MGI Symbol;Acc:MGI:2444879]		Q80U16	2.1	6.6E-02	3.1	4.5E-02	0.0	9.7E-01	-1.0	3.4E-01
ENSMUST00000058011	minichromosome maintenance deficient 2 mitotin (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:105380]		P97310	-0.1	7.9E-01	0.4	5.5E-01	0.4	4.1E-01	-0.1	8.4E-01
ENSMUST00000058866	neurexophilin 3 [Source:MGI Symbol;Acc:MGI:1336188]	Q544G3	Q91VX5	7.2	1.9E-04	5.6	2.5E-02	-0.7	7.7E-01	1.0	4.3E-01
ENSMUST00000058879	neurotrophin 5 [Source:MGI Symbol;Acc:MGI:97381]		Q80VU4	6.2	1.7E-04	-2.1	2.7E-02	0.6	2.3E-01	-0.1	8.8E-01
ENSMUST00000058884	poly(A)-specific ribonuclease (deadenylation nuclease) [Source:MGI Symbol;Acc:MGI:1921358]			3.5	2.2E-04	-1.4	5.6E-02	-2.9	2.5E-04	0.2	7.8E-01
ENSMUST00000058889	Fanconi anemia, complementation group M [Source:MGI Symbol;Acc:MGI:2442306]		Q8BGE5	3.2	3.0E-04	-2.4	2.3E-03	1.0	1.1E-02	0.0	1.0E+00
ENSMUST00000058897	paired immunoglobin-like type 2 receptor alpha [Source:MGI Symbol;Acc:MGI:2450529]		Q2YFS3	-5.1	5.9E-05	8.4	1.3E-03	1.7	3.7E-01	0.0	9.8E-01
ENSMUST00000058899	nuclear receptor subfamily 1, group H, member 5 [Source:MGI Symbol;Acc:MGI:3026618]	E9Q5A6		5.9	1.7E-05	7.6	3.5E-05	-0.9	4.5E-01	-0.1	8.0E-01
ENSMUST00000058902	echinoderm microtubule associated protein like 6 [Source:MGI Symbol;Acc:MGI:2442895]		Q5SQM0	9.0	3.7E-06	0.8	2.5E-01	-0.4	4.8E-01	0.2	7.6E-01
ENSMUST00000058912	lipocalin 10 [Source:MGI Symbol;Acc:MGI:1925000]	Q0VBF7	Q810Z1	6.8	6.8E-05	-7.9	4.4E-03	0.7	2.8E-01	1.7	4.3E-01
ENSMUST00000058914	tubulin, alpha 1C [Source:MGI Symbol;Acc:MGI:1095409]	Q52L87	P68373	-4.1	1.1E-04	8.3	2.1E-05	-0.6	6.0E-01	-1.3	3.6E-02
ENSMUST00000058918	predicted gene 7461 [Source:MGI Symbol;Acc:MGI:3645338]	Q8C5X8		5.6	5.9E-04	6.0	1.3E-03	-0.7	6.4E-01	-0.5	5.1E-01
ENSMUST00000058096	Wolf-Hirschhorn syndrome candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1276574]		Q8BVE8	-3.3	4.1E-02	-1.5	4.2E-01	1.1	3.5E-01	-0.7	6.9E-01
ENSMUST00000058943	ankyrin repeat domain 34A [Source:MGI Symbol;Acc:MGI:3617846]	B2RW11		8.2	2.2E-05	2.1	1.9E-01	0.7	6.0E-01	1.4	2.7E-01
ENSMUST00000058981	latexin [Source:MGI Symbol;Acc:MGI:107633]	Q14BZ3	P70202	-3.2	3.8E-04	4.5	7.2E-04	0.5	5.4E-01	0.1	8.7E-01
ENSMUST00000058987	keratin associated protein 4-2 [Source:MGI Symbol;Acc:MGI:1915923]	B1AQ85		6.1	2.4E-04	-1.5	3.8E-02	-0.5	2.1E-01	-0.8	2.3E-01
ENSMUST00000058109	mitchondrial ribosomal protein S7 [Source:MGI Symbol;Acc:MGI:1354367]		Q80X85	-1.2	3.6E-02	-0.7	2.5E-01	-0.2	5.8E-01	-0.7	2.5E-01
ENSMUST00000058119	adipocyte-related X-chromosome expressed sequence 2 [Source:MGI Symbol;Acc:MGI:1924226]		Q9D365	3.7	5.2E-02	0.4	8.2E-01	-1.7	3.1E-01	1.5	3.4E-01
ENSMUST00000058994	translocation associated membrane protein 1-like 1 [Source:MGI Symbol;Acc:MGI:2443503]		Q8QZR0	5.0	4.8E-05	3.0	1.6E-02	0.3	7.8E-01	0.3	6.9E-01
ENSMUST00000058136	toll-like receptor adaptor molecule 1 [Source:MGI Symbol;Acc:MGI:2147032]		Q80UF7	-0.8	1.1E-01	0.8	2.0E-01	1.2	2.2E-02	-0.4	4.8E-01
ENSMUST00000058997	zinc finger and BTB domain containing 7C [Source:MGI Symbol;Acc:MGI:2443302]		Q8VCZ7	9.0	4.7E-06	-1.3	8.2E-02	0.3	5.0E-01	-0.6	4.1E-01
ENSMUST00000058139	solute carrier family 38, member 6 [Source:MGI Symbol;Acc:MGI:3648156]	Q3USV8		-0.6	7.6E-01	-3.7	1.7E-01	-2.2	2.5E-01	0.9	6.9E-01
ENSMUST00000059018	F-box protein 31 [Source:MGI Symbol;Acc:MGI:1354708]		Q3TQF0	-2.6	4.3E-03	5.9	1.3E-03	-0.7	6.1E-01	1.0	1.9E-01
ENSMUST00000059021	peroxisomal biogenesis factor 2 [Source:MGI Symbol;Acc:MGI:107486]	Q91YZ5		-6.1	5.2E-05	7.2	2.1E-04	-0.6	6.6E-01	-0.7	3.2E-01
ENSMUST00000059026	ABI gene family, member 3 [Source:MGI Symbol;Acc:MGI:1913860]		Q8BYZ1	-2.3	1.3E-02	-0.3	6.4E-01	-1.7	2.1E-02	0.9	2.1E-01
ENSMUST00000059033	olfactory receptor 1441 [Source:MGI Symbol;Acc:MGI:3031275]	Q8VFV3		7.3	1.0E-03	4.2	7.3E-04	-0.6	5.0E-01	-0.3	6.3E-01
ENSMUST00000059049	leucine rich repeat containing 4C [Source:MGI Symbol;Acc:MGI:2442636]		Q8C031	5.7	1.5E-04	-1.1	1.8E-01	1.0	8.9E-02	0.1	9.4E-01
ENSMUST00000058163	pseudouridylate synthase 10 [Source:MGI Symbol;Acc:MGI:1921717]		Q9D3U0	0.0	9.9E-01	-0.9	3.4E-01	-1.3	7.0E-02	-0.4	6.5E-01
ENSMUST00000058167	transmembrane protein 81 [Source:MGI Symbol;Acc:MGI:1921876]		Q9D5K1	0.6	6.4E-01	1.2	4.1E-01	-0.3	7.9E-01	-0.9	4.7E-01
ENSMUST00000059056	solute carrier family 12 (potassium/chloride transporters), member 8 [Source:MGI Symbol;Acc:MGI:2443672]		Q8VI23	8.0	2.0E-04	-2.7	1.1E-03	0.4	2.6E-01	-0.2	7.0E-01
ENSMUST00000059057	family with sequence similarity 118, member B [Source:MGI Symbol;Acc:MGI:1924483]		Q8C569	-6.7	2.6E-05	-3.8	1.5E-03	1.0	4.9E-02	0.5	5.3E-01
ENSMUST00000058210	epidermal growth factor receptor pathway substrate 8 [Source:MGI Symbol;Acc:MGI:104684]		Q08509	0.2	8.8E-01	-0.2	8.7E-01	0.0	1.0E+00	0.4	7.6E-01
ENSMUST00000059072	bestrophin 2 [Source:MGI Symbol;Acc:MGI:2387588]			7.2	1.3E-04	7.2	5.3E-05	-0.9	4.3E-01	-0.4	5.3E-01
ENSMUST00000059080	ribosomal protein S21 [Source:MGI Symbol;Acc:MGI:1913731]		Q9CQR2	-7.8	5.9E-05	8.7	4.1E-06	-1.5	1.6E-01	-0.3	4.8E-01
ENSMUST00000059082	aryl hydrocarbon receptor-interacting protein-like 1 [Source:MGI Symbol;Acc:MGI:2148800]	I6L993		4.6	2.8E-03	-3.6	3.9E-04	-0.2	6.0E-01	-0.5	4.8E-01
ENSMUST00000059091	chloride channel accessory 3A1 [Source:MGI Symbol;Acc:MGI:1316732]	Q9QX15		3.2	1.8E-03	-3.5	4.9E-03	1.3	2.4E-02	-0.3	7.9E-01
ENSMUST00000058240	RIKEN cDNA 9930012K11 gene [Source:MGI Symbol;Acc:MGI:2145726]		Q66JV7	-0.8	7.4E-01	-2.0	4.1E-01	-2.1	2.6E-01	-0.9	7.3E-01
ENSMUST00000058245	FGFR1 oncogene partner 2 [Source:MGI Symbol;Acc:MGI:1914779]	F8WGG1		-1.5	6.5E-01	-5.5	2.0E-01	-3.2	1.5E-01	0.8	8.7E-01
ENSMUST00000059093	cytochrome c oxidase assembly factor 6 [Source:MGI Symbol;Acc:MGI:1915142]		Q8BGD8	-3.4	5.8E-04	-5.2	7.7E-04	0.2	7.2E-01	-0.7	5.5E-01
ENSMUST00000058266	tubulin tyrosine ligase-like family, member 13 [Source:MGI Symbol;Acc:MGI:1920845]		A4Q9F6	1.7	5.5E-02	2.4	3.5E-02	0.5	6.0E-01	-0.2	8.2E-01
ENSMUST00000058269	family with sequence similarity 161, member A [Source:MGI Symbol;Acc:MGI:1921123]	B1AVK0		4.2	6.6E-02	5.4	6.0E-02	0.4	8.8E-01	-0.7	6.5E-01
ENSMUST00000059099	PDZ domain containing 11 [Source:MGI Symbol;Acc:MGI:1919871]		Q9CZG9	-6.7	2.7E-05	4.3	1.2E-02	-1.9	2.6E-01	-1.0	3.1E-01
ENSMUST00000059102	uridine phosphorylase 2 [Source:MGI Symbol;Acc:MGI:1923904]	Q8R093		6.1	1.0E-04	4.4	5.4E-03	0.3	8.1E-01	-1.1	2.0E-01
ENSMUST00000059115	mitochondrial tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2142572]			4.5	6.8E-03	4.4	1.6E-02	-0.6	7.1E-01	1.3	2.2E-01
ENSMUST00000059121	ubiquilin-like [Source:MGI Symbol;Acc:MGI:2685336]		Q14DL0	8.0	1.6E-05	8.7	1.8E-04	-0.3	8.7E-01	-0.3	6.7E-01
ENSMUST00000058300	interleukin 17 receptor C [Source:MGI Symbol;Acc:MGI:2159336]		Q8K4C2	3.9	5.4E-02	4.3	1.8E-02	-2.6	1.7E-01	-3.0	3.8E-02
ENSMUST00000058307	inositol polyphosphate-4-phosphatase, type I [Source:MGI Symbol;Acc:MGI:1931123]			-1.3	4.2E-01	-1.7	4.6E-01	0.4	7.8E-01	0.8	7.4E-01
ENSMUST00000059138	proline rich 15 [Source:MGI Symbol;Acc:MGI:1925254]	A2RT92	Q9D1T5	5.4	6.6E-04	7.7	4.1E-05	-0.6	5.8E-01	-0.2	7.4E-01
ENSMUST00000059145	transforming, acidic coiled-coil containing protein 2 [Source:MGI Symbol;Acc:MGI:1928899]	E9Q9Z4		-2.2	1.5E-02	-6.5	2.0E-04	0.5	1.8E-01	-0.9	4.8E-01
ENSMUST00000059155	insulin induced gene 1 [Source:MGI Symbol;Acc:MGI:1916289]		Q8BGI3	-1.5	7.6E-03	6.5	1.2E-03	-0.6	6.9E-01	-2.7	1.9E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000059193	coagulation factor II (thrombin) receptor [Source:MGI Symbol;Acc:MGI:101802]		P30558	1.9	3.5E-03	-7.4	1.5E-03	1.0	6.2E-02	1.3	4.6E-01
ENSMUST00000058358	leukocyte receptor cluster (LRC) member 9 [Source:MGI Symbol;Acc:MGI:2444509]		Q8BTN6	0.1	9.3E-01	2.1	1.3E-02	1.0	1.0E-01	-1.0	1.1E-01
ENSMUST00000058370	coiled-coil domain containing 137 [Source:MGI Symbol;Acc:MGI:1914541]		Q8R0K4	0.2	7.9E-01	0.9	2.2E-01	0.1	8.7E-01	-0.7	3.2E-01
ENSMUST00000059199	zinc finger protein 764 [Source:MGI Symbol;Acc:MGI:2443580]	E9QAP1		7.0	1.8E-03	1.6	2.2E-02	-0.1	8.0E-01	-0.1	8.5E-01
ENSMUST00000059204	F-box and leucine-rich repeat protein 7 [Source:MGI Symbol;Acc:MGI:3052506]		Q5BJ29	6.9	5.2E-05	-5.8	1.4E-03	-0.6	2.2E-01	0.9	5.3E-01
ENSMUST00000059206	proline-serine-threonine phosphatase-interacting protein 1 [Source:MGI Symbol;Acc:MGI:1321396]			-8.5	4.2E-05	5.0	3.9E-03	-0.6	6.9E-01	0.8	3.1E-01
ENSMUST00000059241	shadow of prion protein [Source:MGI Symbol;Acc:MGI:3582583]		Q8BWU1	7.6	1.8E-05	-6.3	3.1E-03	-0.8	2.4E-01	0.9	5.9E-01
ENSMUST00000059272	homeobox D9 [Source:MGI Symbol;Acc:MGI:96210]		P28357	8.9	1.4E-03	5.9	2.5E-04	1.0	3.1E-01	-0.1	8.7E-01
ENSMUST00000059279	predicted gene 884 [Source:MGI Symbol;Acc:MGI:2685730]	A2A9H6		9.0	4.5E-06	0.1	8.8E-01	1.7	4.4E-02	-0.6	5.1E-01
ENSMUST00000059287	Eph receptor B2 [Source:MGI Symbol;Acc:MGI:99611]	A3KG02		7.3	1.3E-04	-6.5	3.1E-05	-0.9	3.0E-02	-0.5	5.5E-01
ENSMUST00000059295	synaptotagmin XII [Source:MGI Symbol;Acc:MGI:2159601]	Q14AG7	Q920N7	8.1	2.6E-06	-1.3	4.9E-02	1.0	2.3E-02	0.0	9.8E-01
ENSMUST00000059318	RIKEN cDNA 4930590J08 gene [Source:MGI Symbol;Acc:MGI:2685917]		Q8CDN1	6.2	1.9E-04	9.8	4.7E-05	-0.7	6.4E-01	-0.3	5.6E-01
ENSMUST00000058444	protein phosphatase 1, regulatory subunit 37 [Source:MGI Symbol;Acc:MGI:2687042]		Q8BKR5	-1.2	8.9E-02	-0.7	4.3E-01	0.8	2.1E-01	0.3	7.5E-01
ENSMUST00000059319	transmembrane protein 17 [Source:MGI Symbol;Acc:MGI:2144205]		Q8K0U3	5.6	9.4E-05	7.0	4.7E-05	-0.5	6.1E-01	-0.6	2.8E-01
ENSMUST00000059339	preprononiceptin [Source:MGI Symbol;Acc:MGI:105308]	Q543U6	Q64387	6.6	1.9E-05	-1.9	9.9E-02	1.1	1.1E-01	-0.6	6.1E-01
ENSMUST00000059341	zinc finger, C2HC-type containing 1C [Source:MGI Symbol;Acc:MGI:1919600]		Q8CCG1	4.5	1.1E-03	7.9	9.7E-05	-0.6	6.6E-01	-0.7	2.8E-01
ENSMUST00000059343	Eph receptor A10 [Source:MGI Symbol;Acc:MGI:3586824]		Q8BYG9	10.3	1.8E-05	6.3	2.5E-04	-0.5	6.6E-01	0.0	9.6E-01
ENSMUST00000059349	toll-like receptor 1 [Source:MGI Symbol;Acc:MGI:1341295]	B9EJ46	Q9EPQ1	-6.3	7.0E-05	5.7	5.4E-03	-0.5	7.5E-01	-1.5	1.5E-01
ENSMUST00000059352	leiomodin 1 (smooth muscle) [Source:MGI Symbol;Acc:MGI:2135671]	F8VPR1		9.1	5.4E-06	7.5	3.5E-04	2.2	1.2E-01	-0.3	6.6E-01
ENSMUST00000059354	sigma non-opioid intracellular receptor 1 [Source:MGI Symbol;Acc:MGI:1195268]		O55242	-4.5	6.7E-03	-2.7	2.0E-03	0.0	9.3E-01	-0.6	3.9E-01
ENSMUST00000059362	syncytin b [Source:MGI Symbol;Acc:MGI:3045308]	Q8BI41		4.6	4.3E-05	3.1	1.3E-02	-3.0	3.3E-02	-0.1	8.8E-01
ENSMUST00000058496	TAO kinase 1 [Source:MGI Symbol;Acc:MGI:1914490]	B2RX66	Q5F2E8	-2.8	1.6E-01	-0.9	6.6E-01	-0.1	9.5E-01	-2.0	3.9E-01
ENSMUST00000059374	pleckstrin and Sec7 domain containing 3 [Source:MGI Symbol;Acc:MGI:1918215]	Q8C0E9		6.5	1.1E-04	4.8	6.7E-04	0.8	3.8E-01	0.5	4.2E-01
ENSMUST00000058534	mediator complex subunit 26 [Source:MGI Symbol;Acc:MGI:1917875]		Q7TN02	0.0	1.0E+00	0.6	4.0E-01	0.8	1.2E-01	0.3	6.8E-01
ENSMUST00000059379	olfactory receptor 1395 [Source:MGI Symbol;Acc:MGI:3031229]	Q8VGD7		6.3	5.1E-04	8.9	1.2E-05	-0.6	6.2E-01	-0.5	2.9E-01
ENSMUST00000059383	four and a half LIM domains 4 [Source:MGI Symbol;Acc:MGI:1338765]	Q8CDC8		5.7	1.5E-04	5.8	4.0E-05	-1.4	1.2E-01	-1.0	9.3E-02
ENSMUST00000059390	RIKEN cDNA 9030624J02 gene [Source:MGI Symbol;Acc:MGI:1918767]	1I1E4X5		2.5	1.7E-03	-3.1	5.8E-04	1.1	7.9E-03	-0.1	9.2E-01
ENSMUST00000058577	proline and serine rich 1 [Source:MGI Symbol;Acc:MGI:1919933]		Q5PRE5	-0.3	5.3E-01	0.6	3.8E-01	1.0	8.3E-02	0.0	9.5E-01
ENSMUST00000059401	autophagy related 9B [Source:MGI Symbol;Acc:MGI:2685420]		Q6EBV9	5.2	3.7E-05	-0.7	3.4E-01	1.0	6.1E-02	-0.7	3.1E-01
ENSMUST00000059407	SLIT and NTRK-like family, member 3 [Source:MGI Symbol;Acc:MGI:2679447]		Q810B9	5.7	2.1E-02	-1.4	2.9E-02	1.0	1.2E-02	0.0	9.6E-01
ENSMUST00000059424	transmembrane protease, serine 11c [Source:MGI Symbol;Acc:MGI:3521861]	Q1JRP2		5.4	1.8E-03	-3.3	3.4E-02	1.8	2.1E-02	-0.7	6.1E-01
ENSMUST00000059428	coiled-coil domain containing 149 [Source:MGI Symbol;Acc:MGI:2685293]	F6V035		6.4	5.4E-06	7.0	2.0E-04	-0.7	6.0E-01	-0.1	9.0E-01
ENSMUST00000059438	RIKEN cDNA 2310057M21 gene [Source:MGI Symbol;Acc:MGI:1915527]		Q9D2Q3	1.2	2.7E-02	6.8	1.0E-04	-0.3	7.7E-01	0.1	9.3E-01
ENSMUST00000059448	signal peptide peptidase 2C [Source:MGI Symbol;Acc:MGI:3045264]		A2A6C4	6.5	9.4E-05	6.0	1.6E-03	-0.7	6.5E-01	-0.4	6.3E-01
ENSMUST00000059449	carboxyesterase 2B [Source:MGI Symbol;Acc:MGI:2448547]	Q6PDB7		7.7	1.5E-06	7.0	8.7E-04	-0.7	6.4E-01	-0.1	9.5E-01
ENSMUST00000059458	mastermind like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1890504]		Q6T264	-4.7	5.1E-04	-2.5	6.4E-03	-0.6	2.2E-01	-0.2	8.0E-01
ENSMUST00000058626	PDZ and LIM domain 5 [Source:MGI Symbol;Acc:MGI:1927489]	F8WJI6		2.7	6.6E-02	0.2	8.9E-01	-1.9	1.6E-01	0.6	6.9E-01
ENSMUST00000059462	charged multivesicular body protein 3 [Source:MGI Symbol;Acc:MGI:1913950]		Q9CQ10	-4.1	1.5E-05	5.2	1.7E-03	0.8	5.4E-01	0.3	6.8E-01
ENSMUST00000059472	methionine adenosyltransferase II, alpha [Source:MGI Symbol;Acc:MGI:2443731]	Q99J57	Q3THS6	-1.9	4.9E-03	6.7	2.2E-04	-0.6	6.4E-01	0.4	5.1E-01
ENSMUST00000058639	valosin containing protein lysine (K) methyltransferase [Source:MGI Symbol;Acc:MGI:2684917]		Q8C436	-0.2	6.7E-01	-0.6	4.3E-01	-0.6	2.9E-01	-0.3	6.7E-01
ENSMUST00000059482	protease, serine 27 [Source:MGI Symbol;Acc:MGI:2450123]		Q8BJR6	4.7	1.3E-03	7.1	4.1E-05	0.9	3.4E-01	-0.3	5.6E-01
ENSMUST00000059486	olfactory receptor 266 [Source:MGI Symbol;Acc:MGI:3030100]	Q8VFC3		5.7	1.5E-02	6.4	1.6E-04	-0.5	6.4E-01	-0.8	1.8E-01
ENSMUST00000059498	ER degradation enhancer, mannosidase alpha-like 3 [Source:MGI Symbol;Acc:MGI:1914217]		Q2HXL6	-2.0	6.7E-04	7.2	2.9E-04	-0.7	6.2E-01	-0.3	6.7E-01
ENSMUST00000059512	olfactory receptor 13 [Source:MGI Symbol;Acc:MGI:104812]	Q0VAZ7	P34984	5.6	1.5E-03	6.9	1.7E-04	-0.5	6.6E-01	-0.2	7.8E-01
ENSMUST00000059515	guanosine diphosphate (GDP) dissociation inhibitor 2 [Source:MGI Symbol;Acc:MGI:99845]		Q61598	-5.9	8.2E-06	-1.0	3.1E-01	1.3	6.4E-02	-0.1	9.3E-01
ENSMUST00000059524	predicted gene 4737 [Source:MGI Symbol;Acc:MGI:3643647]	Q3TF14	P50247	-1.7	8.6E-03	7.1	4.0E-04	-0.2	8.6E-01	0.8	2.5E-01
ENSMUST00000058669	guanine nucleotide binding protein, alpha transducing 2 [Source:MGI Symbol;Acc:MGI:95779]	A2AE33	P50149	1.6	3.9E-01	2.5	3.2E-01	-0.2	9.3E-01	-1.1	5.4E-01
ENSMUST00000059534	taste receptor, type 2, member 126 [Source:MGI Symbol;Acc:MGI:2681273]		P59532	7.2	1.7E-04	-3.3	6.0E-04	1.2	7.5E-03	0.1	9.1E-01
ENSMUST00000059539	nucleosome assembly protein 1-like 5 [Source:MGI Symbol;Acc:MGI:1923555]		Q9JJF0	5.2	9.5E-04	-0.2	7.3E-01	1.2	1.1E-02	-0.1	8.7E-01
ENSMUST00000059551	solute carrier family 39 (zinc transporter), member 3 [Source:MGI Symbol;Acc:MGI:2147269]		Q99K24	-5.5	4.6E-03	5.9	6.9E-04	-1.4	2.9E-01	0.1	8.3E-01
ENSMUST00000059555	ubiquitin-conjugating enzyme E2Q (putative) 2 [Source:MGI Symbol;Acc:MGI:2388672]		Q8K2Z8	-3.8	4.4E-03	10.2	1.1E-04	-0.8	6.5E-01	0.3	6.0E-01
ENSMUST00000059571	protocadherin beta 19 [Source:MGI Symbol;Acc:MGI:2136757]	Q91Y01		6.2	2.6E-05	-3.7	5.1E-03	1.0	7.4E-02	-0.6	6.1E-01
ENSMUST00000059579	family with sequence similarity 76, member B [Source:MGI Symbol;Acc:MGI:1920076]		Q80XP8	-4.0	5.6E-05	-3.8	3.1E-02	0.2	7.6E-01	0.3	8.5E-01
ENSMUST00000059580	SET domain containing (lysine methyltransferase) 8 [Source:MGI Symbol;Acc:MGI:1915206]	E9QNB8		-2.1	5.2E-03	-6.6	8.1E-07	0.1	5.3E-01	-0.1	8.0E-01
ENSMUST00000059582	transmembrane protein 216 [Source:MGI Symbol;Acc:MGI:1920020]		Q9CQC4	-3.0	2.1E-02	-1.9	2.5E-01	0.8	3.8E-01	-0.2	9.0E-01
ENSMUST00000059588	pyruvate dehyrogenase phosphatase catalytic subunit 2 [Source:MGI Symbol;Acc:MGI:1918878]	Q504M2		4.6	6.4E-05	7.4	1.0E-04	-0.6	6.0E-01	-0.3	6.4E-01
ENSMUST00000058728	predicted gene 10681 [Source:MGI Symbol;Acc:MGI:3711284]		Q61767	3.2	1.3E-01	4.6	5.2E-02	-0.5	8.4E-01	-1.9	2.4E-01
ENSMUST00000059589	reticulon 4 receptor [Source:MGI Symbol;Acc:MGI:2136886]		Q99PI8	7.0	9.0E-05	-5.9	5.3E-04	0.1	7.4E-01	0.9	4.3E-01
ENSMUST00000059595	protein kinase C, alpha [Source:MGI Symbol;Acc:MGI:97595]	Q4VA93		4.1	3.8E-05	-3.6	7.4E-03	0.7	2.1E-01	-3.8	2.5E-02
ENSMUST00000058745	E2F transcription factor 8 [Source:MGI Symbol;Acc:MGI:1922038]		Q58FA4	1.4	1.3E-01	3.3	3.0E-02	1.7	1.7E-01	-0.2	7.8E-01
ENSMUST00000058746	CD151 antigen [Source:MGI Symbol;Acc:MGI:1096360]		O35566	0.1	9.4E-01	-2.8	3.9E-02	-1.1	1.4E-01	1.8	1.5E-01
ENSMUST00000059598	predicted gene 9776 [Source:MGI Symbol;Acc:MGI:3641792]	Q8BRW6		5.9	1.2E-05	2.9	1.5E-02	-2.7	3.5E-02	0.0	9.7E-01
ENSMUST00000059607	transmembrane epididymal family member 2 [Source:MGI Symbol;Acc:MGI:1923273]	Q208S0		8.5	9.7E-05	6.3	6.6E-05	-0.5	5.8E-01	0.5	3.5E-01
ENSMUST00000059617	olfactory receptor 518 [Source:MGI Symbol;Acc:MGI:3030352]	Q8VEW1		6.2	6.6E-04	-3.4	1.7E-04	-0.2	4.4E-01	-0.4	5.3E-01
ENSMUST00000059619	CDC42 effector protein (Rho GTPase binding) 1 [Source:MGI Symbol;Acc:MGI:1929763]			7.4	2.0E-05	4.3	1.9E-04	-0.2	8.0E-01	0.1	8.4E-01
ENSMUST00000058762	peptidylglycine alpha-amidating monooxygenase [Source:MGI Symbol;Acc:MGI:97475]		P97467	3.3	1.5E-01	1.6	5.2E-01	-2.0	3.8E-01	-0.3	8.7E-01
ENSMUST00000058764	LSM14 homolog B (SCD6, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3040677]	Q8BM41		1.5	3.7E-01	0.6	8.0E-01	-0.3	8.9E-01	0.6	7.3E-01
ENSMUST00000058771	LysM, putative peptidoglycan-binding, domain containing 4 [Source:MGI Symbol;Acc:MGI:1922349]		Q8CC84	-0.1	9.4E-01	-0.7	5.5E-01	0.3	7.5E-01	0.9	4.2E-01
ENSMUST00000059637	serine (or cysteine) peptidase inhibitor, clade B, member 6d [Source:MGI Symbol;Acc:MGI:2667783]	Q3UWK8		5.7	8.0E-04	4.3	2.9E-03	-1.3	2.5E-01	-0.4	6.4E-01
ENSMUST00000059644	RNA binding motif protein 33 [Source:MGI Symbol;Acc:MGI:1919670]		Q9CXK9	-4.5	2.4E-03	6.7	9.6E-04	-0.6	6.9E-01	-0.8	3.8E-01
ENSMUST00000059647	RNA binding motif protein 12 [Source:MGI Symbol;Acc:MGI:1922960]		Q8R4X3	-5.8	7.5E-03	6.7	6.7E-04	0.9	5.3E-01	-0.3	6.9E-01
ENSMUST00000058790	low density lipoprotein receptor class A domain containing 3 [Source:MGI Symbol;Acc:MGI:2138856]	B2RR20	A2AR95	2.5	1.2E-01	0.5	7.9E-01	-1.3	3.6E-01	0.7	6.6E-01
ENSMUST00000059650	neuropeptide S receptor 1 [Source:MGI Symbol;Acc:MGI:2441738]	A1KXK3	Q8BZP8	5.7	4.4E-04	-7.8	1.9E-03	0.9	1.3E-01	0.6	7.7E-01
ENSMUST00000059657	glycerol kinase 2 [Source:MGI Symbol;Acc:MGI:1329027]		Q9WU65	6.2	1.5E-04	7.7	3.2E-05	-0.6	5.9E-01	-0.7	2.0E-01
ENSMUST00000059662	OTU deubiquitinase with linear linkage specificity [Source:MGI Symbol;Acc:MGI:3577015]		Q3UCV8	-4.1	1.4E-05	6.3	9.9E-05	-1.4	2.1E-01	0.0	9.4E-01
ENSMUST00000059666	SAYSVFN motif domain containing 1 [Source:MGI Symbol;Acc:MGI:1914759]		Q8K190	2.2	5.6E-03	-3.0	6.4E-03	0.9	7.9E-02	0.9	3.0E-01
ENSMUST00000059667	hippocalcin-like 4 [Source:MGI Symbol;Acc:MGI:2157521]	B2RRY8	Q8BGZ1	8.7	1.9E-05	9.7	2.3E-04	-0.1	9.6E-01	1.1	1.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000059672	phosphoinositide-3-kinase adaptor protein 1 [Source:MGI Symbol;Acc:MGI:1933177]		Q9EQ32	-2.4	9.1E-04	7.0	1.4E-04	-0.6	6.1E-01	-0.6	3.6E-01
ENSMUST00000059676	aquaporin 12 [Source:MGI Symbol;Acc:MGI:2664636]		Q8CHJ2	6.4	3.1E-04	6.9	1.8E-04	-0.6	6.3E-01	-0.2	7.6E-01
ENSMUST00000059680	golgi phosphoprotein 3 [Source:MGI Symbol;Acc:MGI:1913879]		Q9CRA5	-4.9	4.7E-06	-5.8	4.1E-04	-0.3	5.4E-01	-0.9	4.7E-01
ENSMUST00000059692	tripartite motif family-like 1 [Source:MGI Symbol;Acc:MGI:2687279]		Q8BVP1	6.4	1.7E-04	7.3	2.8E-04	-0.2	8.9E-01	0.2	7.5E-01
ENSMUST00000059693	lipocalin 6 [Source:MGI Symbol;Acc:MGI:3045364]	A2AJC0		7.1	7.8E-05	-2.4	4.2E-02	0.8	2.4E-01	-0.6	5.6E-01
ENSMUST00000059707	keratin 9 [Source:MGI Symbol;Acc:MGI:96696]		Q6RHW0	8.7	3.3E-05	6.7	8.2E-06	0.0	9.9E-01	-0.2	6.7E-01
ENSMUST00000059718	inhibin beta E [Source:MGI Symbol;Acc:MGI:109269]		O08717	6.9	6.8E-05	-7.4	4.5E-04	1.3	1.3E-02	0.1	9.3E-01
ENSMUST00000059743	ubiquitin-conjugating enzyme E2F (putative) [Source:MGI Symbol;Acc:MGI:1915171]		Q9CY34	-4.2	2.3E-03	7.2	3.1E-04	-0.6	6.6E-01	-0.6	3.7E-01
ENSMUST00000058868	RIKEN cDNA 9530077C05 gene [Source:MGI Symbol;Acc:MGI:1915533]		Q7TQE7	-0.1	9.0E-01	-1.0	2.1E-01	-0.3	6.2E-01	0.7	3.8E-01
ENSMUST00000059754	olfactory receptor 418 [Source:MGI Symbol;Acc:MGI:3030252]			6.8	8.7E-05	5.6	1.6E-03	-0.3	8.3E-01	0.3	6.8E-01
ENSMUST00000059775	TGFB-induced factor homeobox 1 [Source:MGI Symbol;Acc:MGI:1194497]		P70284	-2.6	3.0E-02	2.3	1.4E-02	-0.1	8.5E-01	1.1	9.9E-02
ENSMUST00000059787	desmoglein 2 [Source:MGI Symbol;Acc:MGI:1196466]		O55111	8.2	9.3E-06	4.0	3.1E-04	0.5	4.3E-01	-0.3	5.8E-01
ENSMUST00000059794	nescient helix loop helix 1 [Source:MGI Symbol;Acc:MGI:98481]		Q02576	7.3	7.9E-05	-4.9	6.6E-04	0.2	6.5E-01	0.0	1.0E+00
ENSMUST00000059805	solute carrier family 35, member D3 [Source:MGI Symbol;Acc:MGI:1923407]	B9EI54	Q8BGF8	4.8	7.2E-05	7.2	4.3E-05	0.4	6.7E-01	-0.9	1.2E-01
ENSMUST00000059808	H2B histone family, member M [Source:MGI Symbol;Acc:MGI:1916639]	Q9DAB5		6.8	6.4E-04	6.9	2.7E-05	-2.0	7.7E-02	0.1	7.6E-01
ENSMUST00000058905	prolyl-tRNA synthetase (mitochondrial)(putative) [Source:MGI Symbol;Acc:MGI:2386296]		Q8CFI5	0.4	7.9E-01	1.9	2.7E-01	0.1	9.5E-01	-1.4	3.5E-01
ENSMUST00000058906	coiled-coil-helix-coiled-coil-helix domain containing 10 [Source:MGI Symbol;Acc:MGI:2143558]	Q7TNL9		1.1	1.4E-01	0.7	4.3E-01	0.0	9.8E-01	0.4	5.8E-01
ENSMUST00000059825	crumbs family member 1, photoreceptor morphogenesis associated [Source:MGI Symbol;Acc:MGI:2136343]		Q8VHS2	8.1	1.3E-05	6.0	3.2E-04	-0.5	6.4E-01	0.2	7.1E-01
ENSMUST00000059826	potassium voltage gated channel, Shab-related subfamily, member 1 [Source:MGI Symbol;Acc:MGI:96666]		Q03717	7.1	2.1E-05	-2.4	7.9E-03	0.9	6.0E-02	-0.8	3.0E-01
ENSMUST00000059833	fibrous sheath CABYR binding protein [Source:MGI Symbol;Acc:MGI:3646964]	E9QJV1		8.6	4.3E-05	5.5	1.4E-03	-0.5	6.8E-01	-0.4	6.1E-01
ENSMUST00000059839	astacin-like metalloendopeptidase (M12 family) [Source:MGI Symbol;Acc:MGI:3046414]		Q6HA09	6.9	3.3E-04	6.7	1.1E-04	-1.4	2.4E-01	0.1	8.7E-01
ENSMUST00000058960	coiled-coil domain containing 63 [Source:MGI Symbol;Acc:MGI:3607777]			0.5	6.0E-01	0.7	4.5E-01	-1.0	2.1E-01	-1.3	1.7E-01
ENSMUST00000058978	NAD(P)H dehydrogenase, quinone 2 [Source:MGI Symbol;Acc:MGI:104513]		Q9JI75	0.0	9.8E-01	-3.4	7.1E-02	-0.6	5.9E-01	2.8	1.1E-01
ENSMUST00000059844	canopy 3 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1919279]		Q9DAU1	-3.1	1.8E-03	-3.2	1.6E-03	-0.3	4.6E-01	-0.3	6.8E-01
ENSMUST00000059849	negative elongation factor complex member B [Source:MGI Symbol;Acc:MGI:1931035]		Q8C4Y3	-4.9	7.8E-05	5.7	7.1E-04	-0.5	7.0E-01	-0.1	8.7E-01
ENSMUST00000059851	٧1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2679		Q8K0V2	-1.6	3.2E-02	3.3	3.5E-03	-0.3	7.1E-01	1.4	5.4E-02
ENSMUST00000059857	Ras and Rab interactor-like [Source:MGI Symbol;Acc:MGI:2444024]		Q80UW3	-3.8	2.2E-04	7.4	1.9E-05	-1.9	9.0E-02	-0.3	5.2E-01
ENSMUST00000059882	RIKEN cDNA 5830411N06 gene [Source:MGI Symbol;Acc:MGI:2443685]	Q8C9T4		8.3	2.8E-05	-1.4	1.4E-01	1.1	8.8E-02	-0.2	8.5E-01
ENSMUST00000059888	integrin beta 6 [Source:MGI Symbol;Acc:MGI:96615]		Q9Z0T9	6.9	2.7E-06	-4.3	2.9E-04	0.0	9.8E-01	-1.8	8.6E-02
ENSMUST00000059893	solute carrier family 2 (facilitated glucose transporter), member 7 [Source:MGI Symbol;Acc:MGI:3650865]	B1ARZ3		7.1	1.1E-04	-2.0	7.8E-02	0.6	3.4E-01	0.3	7.9E-01
ENSMUST00000059899	membrane magnesium transporter 1 [Source:MGI Symbol;Acc:MGI:2384305]		Q8K273	-2.2	2.9E-03	6.4	4.2E-03	-0.7	6.9E-01	0.2	8.5E-01
ENSMUST00000059037	tripartite motif-containing 12C [Source:MGI Symbol;Acc:MGI:4821183]	E9Q987		0.8	1.3E-01	1.0	9.5E-02	-0.1	7.4E-01	-0.4	4.4E-01
ENSMUST00000059042	general transcription factor II I [Source:MGI Symbol;Acc:MGI:1202722]		Q9ESZ8	3.7	1.2E-01	5.5	8.2E-02	0.4	8.9E-01	-1.4	5.0E-01
ENSMUST00000059045	exosome component 4 [Source:MGI Symbol;Acc:MGI:1923576]	Q542B0	Q921I9	-1.1	8.9E-02	-1.0	2.8E-01	1.0	9.6E-02	0.9	3.2E-01
ENSMUST00000059906	protease, serine 33 [Source:MGI Symbol;Acc:MGI:2661234]		Q80WM7	7.0	9.6E-05	6.1	2.5E-04	0.1	9.4E-01	-0.3	5.7E-01
ENSMUST00000059052	tRNA methyltransferase 10C [Source:MGI Symbol;Acc:MGI:1196261]		Q3UFY8	-1.2	1.0E-01	-1.3	1.2E-01	-0.6	3.0E-01	-0.4	6.1E-01
ENSMUST00000059914	RIKEN cDNA 1110037F02 gene [Source:MGI Symbol;Acc:MGI:1913435]		A2AIV2	-3.0	1.7E-03	8.4	2.4E-04	-0.7	6.7E-01	-1.1	1.7E-01
ENSMUST00000059937	predicted gene 597 [Source:MGI Symbol;Acc:MGI:2685443]	E9Q8J5		7.5	2.5E-05	-4.7	2.4E-04	-0.7	1.1E-01	-2.7	2.3E-02
ENSMUST00000059970	gulonolactone (L-) oxidase [Source:MGI Symbol;Acc:MGI:1353434]		P58710	7.1	3.6E-04	6.8	4.7E-04	-1.0	4.9E-01	-0.5	4.5E-01
ENSMUST00000059078	family with sequence similarity 43, member A [Source:MGI Symbol;Acc:MGI:2676309]		Q8BUP8	0.0	1.0E+00	1.1	1.5E-01	0.7	2.3E-01	-0.4	5.3E-01
ENSMUST00000059975	family with sequence similarity 174, member A [Source:MGI Symbol;Acc:MGI:1914948]		Q9D3L0	-7.4	2.4E-04	-7.1	4.9E-04	-0.9	1.2E-01	-1.7	2.8E-01
ENSMUST00000059980	ribosomal protein L37a [Source:MGI Symbol;Acc:MGI:98068]	Q4VAF2	P61514	-6.1	9.1E-05	5.7	4.3E-03	1.3	3.9E-01	0.3	7.4E-01
ENSMUST00000059983	vesicle-associated membrane protein 8 [Source:MGI Symbol;Acc:MGI:1336882]			-7.9	2.9E-06	4.0	1.0E-03	-0.2	7.9E-01	-1.0	1.7E-01
ENSMUST00000059986	ring finger protein 182 [Source:MGI Symbol;Acc:MGI:3045355]		Q8C432	8.1	8.3E-05	-3.4	1.8E-03	-0.6	2.3E-01	-0.6	4.6E-01
ENSMUST00000059997	RIKEN cDNA A430105I19 gene [Source:MGI Symbol;Acc:MGI:2685199]		A3KGF9	8.5	2.5E-06	-6.0	2.5E-04	-0.4	3.5E-01	-1.1	3.7E-01
ENSMUST00000060005	regulator of calcineurin 1 [Source:MGI Symbol;Acc:MGI:1890564]	Q7TNY3		-4.0	2.7E-03	5.4	3.3E-04	-1.2	2.7E-01	-0.5	4.5E-01
ENSMUST00000059112	ankyrin repeat and SOCS box-containing 8 [Source:MGI Symbol;Acc:MGI:1925791]			-3.1	4.9E-02	-3.2	8.7E-02	-0.7	4.4E-01	-0.6	7.6E-01
ENSMUST00000060009	exonuclease 3'-5' domain containing 1 [Source:MGI Symbol;Acc:MGI:3045306]		Q8CDF7	4.8	3.0E-03	-1.0	5.0E-01	-4.9	3.1E-03	0.5	7.0E-01
ENSMUST00000060010	olute carrier family 16 (monocarboxylic acid transporters), member 13 [Source:MGI Symbol;Acc:MGI:191655		Q8CE94	3.2	4.2E-03	8.0	3.7E-05	0.5	6.5E-01	-0.5	3.7E-01
ENSMUST00000060041	coiled-coil domain containing 185 [Source:MGI Symbol;Acc:MGI:3618292]	Q3V118		7.5	2.1E-05	7.3	7.3E-05	-0.6	6.0E-01	0.1	8.2E-01
ENSMUST00000060043	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]		P83741	-3.3	4.0E-03	3.7	5.6E-03	-1.5	1.9E-01	0.2	8.0E-01
ENSMUST00000060049	HAUS augmin-like complex, subunit 3 [Source:MGI Symbol;Acc:MGI:2387633]		Q8QZX2	-2.4	3.6E-03	-2.9	2.1E-02	-0.2	7.4E-01	0.5	6.7E-01
ENSMUST00000060050	glycine/arginine rich protein 1 [Source:MGI Symbol;Acc:MGI:1919940]		Q80X91	5.5	4.8E-03	-1.0	8.6E-02	0.0	9.2E-01	-0.5	3.6E-01
ENSMUST00000060057	sosondowah ankyrin repeat domain family member D [Source:MGI Symbol;Acc:MGI:3045274]		Q8BY98	7.2	1.8E-04	6.4	1.6E-04	-0.4	7.1E-01	-1.4	5.4E-02
ENSMUST00000060061	pygopus 2 [Source:MGI Symbol;Acc:MGI:1916161]	Q80V76		-3.2	2.6E-02	1.5	3.8E-02	-0.3	5.6E-01	0.1	8.3E-01
ENSMUST00000060062	actin-related protein T2 [Source:MGI Symbol;Acc:MGI:1920603]		Q9D9L5	6.9	3.7E-04	4.9	5.6E-02	0.4	8.4E-01	2.5	1.4E-01
ENSMUST00000060077	coproporphyrinogen oxidase [Source:MGI Symbol;Acc:MGI:104841]		P36552	3.2	1.1E-04	6.9	1.0E-04	-0.5	6.6E-01	-0.5	4.0E-01
ENSMUST00000060092	UPF2 regulator of nonsense transcripts homolog (yeast) [Source:MGI Symbol;Acc:MGI:2449307]	A2AT37		-3.0	3.4E-04	-4.8	7.0E-04	0.7	1.4E-01	-2.9	4.2E-02
ENSMUST00000059229	phosphoglycerate mutase family member 5 [Source:MGI Symbol;Acc:MGI:1919792]		Q8BX10	-1.6	2.4E-01	2.6	2.3E-01	3.6	6.5E-02	-0.6	7.0E-01
ENSMUST00000059231	frequently rearranged in advanced T cell lymphomas 2 [Source:MGI Symbol;Acc:MGI:2673967]		Q8K025	1.2	1.7E-01	0.7	5.6E-01	0.6	5.2E-01	1.1	2.9E-01
ENSMUST00000060095	transmembrane and tetratricopeptide repeat containing 1 [Source:MGI Symbol;Acc:MGI:3039590]		Q3UV71	7.7	2.5E-02	7.4	4.3E-05	-0.6	6.1E-01	-0.4	4.8E-01
ENSMUST00000059250	breast cancer metastasis-suppressor 1-like [Source:MGI Symbol;Acc:MGI:1196337]		Q3U1T3	0.1	8.7E-01	-0.3	6.0E-01	-0.5	2.8E-01	-0.1	8.7E-01
ENSMUST00000059270	HEAT repeat containing 1 [Source:MGI Symbol;Acc:MGI:2442524]	G3X9B1		0.1	8.8E-01	-0.4	4.9E-01	-0.3	4.3E-01	0.1	7.8E-01
ENSMUST00000059271	suppression of tumorigenicity 7-like [Source:MGI Symbol;Acc:MGI:2386964]		Q8K4P7	-6.8	1.1E-01	-2.0	7.0E-01	2.7	3.9E-01	-2.0	7.0E-01
ENSMUST00000060100	coiled-coil domain containing 96 [Source:MGI Symbol;Acc:MGI:1913967]		Q9CR92	5.6	2.3E-05	6.8	1.3E-02	-1.1	6.5E-01	1.1	3.9E-01
ENSMUST00000060108	RIKEN cDNA 1810030O07 gene [Source:MGI Symbol;Acc:MGI:1916405]	A2BDN9	Q8C5K5	1.3	1.7E-02	8.5	1.6E-05	-0.6	5.9E-01	-0.1	9.1E-01
ENSMUST00000059286	interleukin-1 receptor-associated kinase 2 [Source:MGI Symbol;Acc:MGI:2429603]		Q8CFA1	-1.4	1.5E-01	-2.5	1.1E-01	1.0	2.3E-01	2.1	1.5E-01
ENSMUST00000060125	sodium channel, type IV, beta [Source:MGI Symbol;Acc:MGI:2687406]	Q1MXF9	Q7M729	6.6	1.4E-05	7.3	3.3E-04	-0.5	7.2E-01	-0.5	4.2E-01
ENSMUST00000060128	claudin 23 [Source:MGI Symbol;Acc:MGI:1919158]		Q9D7D7	5.0	1.4E-04	7.9	4.7E-05	0.0	9.9E-01	0.3	6.1E-01
ENSMUST00000059305	small nuclear ribonucleoprotein N [Source:MGI Symbol;Acc:MGI:98347]	Q3UN87	P63163	4.0	5.4E-02	1.2	6.0E-01	-1.3	5.3E-01	1.6	4.0E-01
ENSMUST00000060174	pyrimidinergic receptor P2Y, G-protein coupled, 6 [Source:MGI Symbol;Acc:MGI:2673874]	Q3UQ86	Q9ERK9	-1.6	1.6E-02	6.7	4.9E-04	-0.4	7.7E-01	-0.8	2.6E-01
ENSMUST00000060187	olfactory receptor 78 [Source:MGI Symbol;Acc:MGI:2157548]		Q8VBV9	6.0	7.5E-03	3.2	1.4E-03	-2.4	1.4E-02	-0.1	8.6E-01
ENSMUST00000059331	Myb-related transcription factor, partner of profilin [Source:MGI Symbol;Acc:MGI:2446472]		Q8R4U1	1.9	5.2E-02	4.5	3.1E-03	1.1	2.9E-01	-1.5	9.6E-02
ENSMUST00000060188	protein phosphatase 1, regulatory (inhibitor) subunit 2 [Source:MGI Symbol;Acc:MGI:1914099]		Q9DCL8	-2.5	1.4E-03	5.7	2.6E-05	-1.7	7.0E-02	-0.7	2.0E-01
ENSMUST00000060196	transmembrane protein 74B [Source:MGI Symbol;Acc:MGI:1918629]	A2AU34		6.6	1.5E-03	5.4	1.0E-03	0.4	6.9E-01	-0.5	5.1E-01
ENSMUST00000060204	olfactory receptor 214 [Source:MGI Symbol;Acc:MGI:3030048]	Q8VG27		6.2	8.9E-04	8.8	1.3E-04	-0.8	6.3E-01	0.7	2.6E-01
ENSMUST00000059348	guanylate cyclase activator 1a (retina) [Source:MGI Symbol;Acc:MGI:102770]		P43081	-1.6	6.4E-02	-0.7	4.6E-01	-0.1	9.0E-01	-1.0	2.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000060212	fucosidase, alpha-L- 2, plasma [Source:MGI Symbol;Acc:MGI:1914098]	Q505Q3	Q99KR8	-9.5	5.0E-06	-4.9	1.2E-03	0.2	6.9E-01	-1.2	3.3E-01
ENSMUST00000060214	transmembrane protein 125 [Source:MGI Symbol;Acc:MGI:1923409]		Q8CHQ6	5.4	1.4E-04	8.3	2.4E-05	-0.7	5.7E-01	0.1	8.0E-01
ENSMUST00000060225	G protein-coupled receptor 4 [Source:MGI Symbol;Acc:MGI:2441992]		Q8BUD0	4.9	2.5E-04	-5.6	1.7E-02	-0.1	8.7E-01	1.0	6.3E-01
ENSMUST00000060232	RAB2A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1928750]	Q0PD65	P53994	-5.6	4.5E-06	3.5	7.1E-04	-0.7	3.0E-01	0.3	5.0E-01
ENSMUST00000059372	ring finger protein 24 [Source:MGI Symbol;Acc:MGI:1261771]	Q4VA59	Q8BGI1	0.0	1.0E+00	-1.3	6.6E-01	-0.9	6.7E-01	0.4	8.8E-01
ENSMUST00000060242	SH2 domain containing 7 [Source:MGI Symbol;Acc:MGI:2441692]		Q8BI17	5.8	1.0E-03	6.9	1.3E-04	-0.5	6.8E-01	-0.9	1.7E-01
ENSMUST00000060251	HIG1 domain family, member 1A [Source:MGI Symbol;Acc:MGI:1930666]	Q1XG81	Q9JLR9	-2.6	1.0E-03	6.3	9.0E-04	-0.7	6.5E-01	-0.7	3.9E-01
ENSMUST00000060255	ring finger protein 112 [Source:MGI Symbol;Acc:MGI:106611]		Q96DY5	7.4	3.2E-05	3.9	2.4E-03	-1.2	2.6E-01	0.7	3.2E-01
ENSMUST00000060265	N(alpha)-acetyltransferase 11, NatA catalytic subunit [Source:MGI Symbol;Acc:MGI:2141314]	A8W660	Q3UX61	7.5	2.8E-05	3.0	4.3E-03	1.0	1.8E-01	0.5	4.4E-01
ENSMUST00000060271	forkhead box I1 [Source:MGI Symbol;Acc:MGI:1096329]		Q922I5	8.4	2.1E-05	5.9	1.5E-04	0.8	3.5E-01	0.1	8.1E-01
ENSMUST00000060311	huntingtin interacting protein 1 [Source:MGI Symbol;Acc:MGI:1099804]		Q8VD75	-1.7	3.5E-03	6.3	1.9E-02	-0.6	8.2E-01	-1.2	3.7E-01
ENSMUST00000059410				1.3	2.8E-01	-1.0	5.5E-01	0.2	8.6E-01	2.5	1.2E-01
ENSMUST00000060315	tripartite motif-containing 34A [Source:MGI Symbol;Acc:MGI:2137359]	E9PYZ4		-3.0	2.4E-02	6.0	1.5E-03	-0.4	7.7E-01	-1.1	2.0E-01
ENSMUST00000060336	fibroblast growth factor 4 [Source:MGI Symbol;Acc:MGI:95518]		P11403	7.5	2.2E-05	4.7	1.5E-04	-1.8	3.8E-02	-0.1	9.1E-01
ENSMUST00000059433	PC-esterase domain containing 1B [Source:MGI Symbol;Acc:MGI:2446270]		Q8BGX1	-0.7	1.8E-01	0.6	3.9E-01	1.1	5.7E-02	-0.3	6.7E-01
ENSMUST00000060345	olfactory receptor 985 [Source:MGI Symbol;Acc:MGI:3030819]	Q8VGB4		7.0	5.7E-05	1.8	1.7E-02	0.8	1.4E-01	0.2	6.8E-01
ENSMUST00000060348	RIKEN cDNA 5330417H12 gene [Source:MGI Symbol;Acc:MGI:1923929]	Q9D3P2		6.0	4.0E-04	5.9	2.2E-04	-1.5	2.0E-01	-0.9	1.5E-01
ENSMUST00000060356	forkhead box I2 [Source:MGI Symbol;Acc:MGI:3028075]	A2RTG9		7.4	2.6E-05	7.7	7.2E-06	-0.2	8.0E-01	-0.2	6.6E-01
ENSMUST00000059452	zinc finger protein 831 [Source:MGI Symbol;Acc:MGI:3641861]	A2ADM8		1.0	4.5E-02	1.4	3.4E-02	0.2	6.6E-01	-0.2	7.0E-01
ENSMUST00000060360	predicted gene 11492 [Source:MGI Symbol;Acc:MGI:3651136]		Q5ND19	9.0	1.3E-04	-2.3	2.6E-02	0.6	2.7E-01	-1.8	1.0E-01
ENSMUST00000060366	zinc finger protein 36, C3H type-like 2 [Source:MGI Symbol;Acc:MGI:107945]		P23949	-6.3	2.0E-04	-4.0	1.6E-04	0.1	8.1E-01	-0.1	9.1E-01
ENSMUST00000059468	family with sequence similarity 58, member B [Source:MGI Symbol;Acc:MGI:1916359]		Q8QZR8	1.0	6.2E-02	1.6	2.4E-02	0.2	6.2E-01	-0.4	4.9E-01
ENSMUST00000060369	neurexophilin 1 [Source:MGI Symbol;Acc:MGI:107492]		Q61200	7.2	4.2E-05	-1.4	6.0E-02	0.2	6.6E-01	-0.4	6.0E-01
ENSMUST00000060389	ring finger and SPRY domain containing 1 [Source:MGI Symbol;Acc:MGI:1914860]		Q8BVR6	-3.3	4.2E-05	1.6	1.7E-01	-0.6	5.4E-01	0.5	5.9E-01
ENSMUST00000060396	solute carrier family 25, member 46 [Source:MGI Symbol;Acc:MGI:1914703]		Q9CQS4	1.3	1.4E-02	5.9	1.7E-03	0.4	7.4E-01	-0.8	3.2E-01
ENSMUST00000060397	regulatory factor X, 4 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:1918387]		Q7TNK1	7.5	2.1E-04	5.7	2.3E-02	-0.8	7.4E-01	-0.7	5.7E-01
ENSMUST00000060398	olfactory receptor 1396 [Source:MGI Symbol;Acc:MGI:3031230]	Q8VEY7		5.8	2.0E-02	-1.0	7.5E-02	0.5	1.2E-01	-0.5	3.5E-01
ENSMUST00000060402	transmembrane protease, serine 15 [Source:MGI Symbol;Acc:MGI:1197523]	E9Q6Y6		6.4	3.0E-03	5.7	2.2E-03	-0.5	7.5E-01	-0.6	4.9E-01
ENSMUST00000060418	paraneoplastic antigen MA3 [Source:MGI Symbol;Acc:MGI:2180565]		Q8JZW8	8.2	4.3E-05	-4.5	3.6E-04	1.0	2.9E-02	-0.4	6.4E-01
ENSMUST00000060427	immediate early response 2 [Source:MGI Symbol;Acc:MGI:104815]		P17950	-5.6	5.8E-04	-1.0	1.2E-01	0.0	9.3E-01	-0.6	3.7E-01
ENSMUST00000060435	selenoprotein N, 1 [Source:MGI Symbol;Acc:MGI:2151208]	D3Z2R5		-3.3	1.1E-03	5.4	1.2E-03	-1.8	1.9E-01	0.1	9.1E-01
ENSMUST00000060441	phosphoinositide-3-kinase, regulatory subunit 6 [Source:MGI Symbol;Acc:MGI:2144613]		Q3U6Q4	-4.0	3.4E-02	4.7	1.5E-03	-1.5	2.1E-01	-1.1	1.5E-01
ENSMUST00000060444	zinc finger protein 3 [Source:MGI Symbol;Acc:MGI:99177]		Q8BLB0	2.2	1.8E-03	-1.7	2.2E-01	0.7	4.2E-01	-3.1	8.6E-02
ENSMUST00000060447	methyltransferase like 5 [Source:MGI Symbol;Acc:MGI:1922672]		Q8K1A0	-4.2	1.3E-03	-1.1	3.8E-01	1.1	2.1E-01	-1.7	2.0E-01
ENSMUST00000059562	lipoma HMGIC fusion partner [Source:MGI Symbol;Acc:MGI:1920048]		Q8BM86	3.6	7.6E-02	0.1	9.5E-01	-5.7	5.1E-03	-2.2	1.4E-01
ENSMUST00000060455	cyclin D-type binding-protein 1 [Source:MGI Symbol;Acc:MGI:109595]		Q3TVC7	-8.9	4.8E-06	4.5	1.8E-04	-1.9	3.8E-02	-0.2	6.9E-01
ENSMUST00000060479	Usher syndrome 2A (autosomal recessive, mild) [Source:MGI Symbol;Acc:MGI:1341292]		Q2QI47	10.2	2.8E-06	-2.8	2.6E-03	0.4	3.2E-01	-0.8	3.1E-01
ENSMUST00000060484	C-type lectin domain family 4, member a1 [Source:MGI Symbol;Acc:MGI:3036291]	Q80UI7		-3.6	1.1E-03	-0.5	5.3E-01	1.3	2.9E-02	-0.3	6.6E-01
ENSMUST00000060500	eukaryotic translation initiation factor 5A2 [Source:MGI Symbol;Acc:MGI:1933735]		Q8BGY2	2.3	1.9E-03	-4.1	2.0E-02	-0.6	4.1E-01	0.5	7.7E-01
ENSMUST00000060513	acyl-Coenzyme A dehydrogenase family, member 8 [Source:MGI Symbol;Acc:MGI:1914198]			-5.0	3.2E-04	3.5	1.7E-03	-0.3	6.5E-01	0.8	2.1E-01
ENSMUST00000060524	tripartite motif-containing 10 [Source:MGI Symbol;Acc:MGI:1338757]		Q9WUH5	5.8	2.3E-04	6.7	5.4E-04	-0.1	9.6E-01	0.3	7.0E-01
ENSMUST00000060537	kinesin family member 1B [Source:MGI Symbol;Acc:MGI:108426]		Q60575	-2.1	3.4E-03	2.7	1.7E-03	-1.2	5.5E-02	0.2	7.5E-01
ENSMUST00000059596	EP300 interacting inhibitor of differentiation 2 [Source:MGI Symbol;Acc:MGI:2681174]		Q6X7S9	1.2	1.8E-01	3.1	1.1E-02	0.6	4.9E-01	-1.3	1.3E-01
ENSMUST00000060551	apolipoprotein L 10A [Source:MGI Symbol;Acc:MGI:3036238]	Q8CCA5		7.5	6.1E-05	6.3	3.0E-05	0.2	7.8E-01	-0.2	6.5E-01
ENSMUST00000060561	family with sequence similarity 221, member A [Source:MGI Symbol;Acc:MGI:2442161]		Q8C790	5.4	4.9E-03	8.2	3.4E-04	-0.2	9.2E-01	0.2	8.4E-01
ENSMUST00000060574	cDNA sequence BC048546 [Source:MGI Symbol;Acc:MGI:3039594]		Q3UU35	8.2	1.3E-05	5.7	2.0E-03	-0.6	6.7E-01	-0.1	8.8E-01
ENSMUST00000060576	lysophosphatidic acid receptor 4 [Source:MGI Symbol;Acc:MGI:1925384]		Q8BLG2	8.6	1.1E-04	0.9	1.5E-01	-7.2	1.5E-05	-0.7	2.3E-01
ENSMUST00000060579	mannoside acetylglucosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI:2384966]		Q921V5	-3.6	3.6E-05	6.0	9.9E-04	-0.4	7.4E-01	-0.8	3.1E-01
ENSMUST00000059642	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 [Source:MGI Symbol;Acc:MGI:1888669]		Q9CX56	2.4	2.5E-01	0.9	6.5E-01	-0.9	6.5E-01	0.6	7.6E-01
ENSMUST00000060603	vomeronasal 1 receptor 235 [Source:MGI Symbol;Acc:MGI:2159636]	Q8R297		6.3	2.1E-04	-0.9	3.6E-01	0.2	7.2E-01	-3.4	1.6E-02
ENSMUST00000060642	leucine-rich repeat kinase 2 [Source:MGI Symbol;Acc:MGI:1913975]		Q5S006	-4.1	9.0E-06	-3.4	1.9E-01	1.7	2.2E-01	-0.7	7.7E-01
ENSMUST00000060645	ubiquitin-conjugating enzyme E2 variant 1 [Source:MGI Symbol;Acc:MGI:1913839]		Q9CZY3	-2.2	2.6E-02	6.3	4.0E-04	-0.4	7.2E-01	-1.1	1.4E-01
ENSMUST00000060651	claudin 7 [Source:MGI Symbol;Acc:MGI:1859285]	B1AR46		5.7	9.8E-04	6.0	3.4E-04	-0.5	6.6E-01	-0.4	5.5E-01
ENSMUST00000060652	enhancer of yellow 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1919286]		Q9JIX0	-2.1	1.3E-03	-2.7	1.2E-03	0.5	1.9E-01	-0.9	1.5E-01
ENSMUST00000060703	coiled coil glutamate rich protein 1 [Source:MGI Symbol;Acc:MGI:1913966]		Q9CQL2	7.1	4.3E-05	2.2	1.3E-02	-0.3	6.3E-01	-0.3	5.9E-01
ENSMUST00000060705	predicted gene 5084 [Source:MGI Symbol;Acc:MGI:3647835]	Q8CAZ1		6.6	4.2E-04	8.4	5.1E-05	-0.7	6.0E-01	-0.4	5.0E-01
ENSMUST00000060714	ubiquilin 2 [Source:MGI Symbol;Acc:MGI:1860283]		Q9QZM0	-1.6	2.1E-02	-0.9	1.5E-01	0.7	1.1E-01	-0.8	2.3E-01
ENSMUST00000060716	sterile alpha motif domain containing 3 [Source:MGI Symbol;Acc:MGI:2685469]	E9Q3G4		3.5	4.7E-03	6.3	8.9E-04	-0.2	8.9E-01	0.0	9.8E-01
ENSMUST00000060719	toll-like receptor 7 [Source:MGI Symbol;Acc:MGI:2176882]	Q548J0	P58681	-7.3	1.5E-05	-4.5	6.4E-05	0.7	4.6E-02	0.3	6.3E-01
ENSMUST00000060722	CXXC finger 5 [Source:MGI Symbol;Acc:MGI:1914643]		Q91WA4	3.5	7.6E-04	6.9	2.0E-04	-0.6	6.3E-01	-1.0	1.4E-01
ENSMUST00000060728	olfactory receptor 95 [Source:MGI Symbol;Acc:MGI:2177478]	Q8VFE2		6.9	1.1E-04	7.2	1.2E-04	-0.6	6.0E-01	-0.8	2.1E-01
ENSMUST00000060738	S100 calcium binding protein A1 [Source:MGI Symbol;Acc:MGI:1338917]	Q91V77		-5.8	4.7E-04	3.6	5.4E-04	0.1	8.5E-01	-0.1	8.2E-01
ENSMUST00000060747	basic helix-loop-helix family, member a15 [Source:MGI Symbol;Acc:MGI:891976]		Q9QYC3	6.4	1.2E-05	7.7	1.9E-04	-0.7	6.0E-01	0.3	6.1E-01
ENSMUST00000060761	per-hexamer repeat gene 2 [Source:MGI Symbol;Acc:MGI:104524]		P15972	6.2	8.5E-05	6.1	2.2E-04	-1.3	2.8E-01	-0.5	4.3E-01
ENSMUST00000060766	clathrin, heavy polypeptide (Hc) [Source:MGI Symbol;Acc:MGI:2388633]	Q5SXR6		-5.3	7.2E-05	-2.3	2.4E-02	-1.2	6.3E-02	-3.1	1.9E-02
ENSMUST00000060782	apolipoprotein N [Source:MGI Symbol;Acc:MGI:88931]	G3X9D6		3.8	5.2E-04	6.2	3.3E-04	-0.6	6.2E-01	0.0	9.9E-01
ENSMUST00000060792	polymerase I and transcript release factor [Source:MGI Symbol;Acc:MGI:1277968]		O54724	4.7	6.2E-05	-0.2	8.4E-01	0.7	3.6E-01	-1.6	1.7E-01
ENSMUST00000060798	unc-119 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:2147162]		Q8C4B4	-1.9	5.6E-03	5.5	5.3E-05	-2.8	1.4E-02	-0.1	8.3E-01
ENSMUST00000059790	PRAME family member 8 [Source:MGI Symbol;Acc:MGI:2140473]	Q8CE24		1.1	1.4E-01	0.3	6.9E-01	-1.1	1.2E-01	-0.3	7.0E-01
ENSMUST00000060805	family with sequence similarity 120, member A [Source:MGI Symbol;Acc:MGI:2446163]		Q6A0A9	-2.1	4.0E-04	6.4	2.7E-04	-1.4	2.7E-01	-0.6	3.7E-01
ENSMUST00000060808	plexin B2 [Source:MGI Symbol;Acc:MGI:2154239]		B2RXS4	6.1	2.9E-03	5.5	2.4E-04	0.7	4.6E-01	-0.1	9.3E-01
ENSMUST00000060820	NK3 homeobox 2 [Source:MGI Symbol;Acc:MGI:108015]		P97503	6.7	6.8E-05	5.6	3.9E-03	-0.7	6.6E-01	0.5	5.8E-01
ENSMUST00000059817	zinc finger protein 367 [Source:MGI Symbol;Acc:MGI:2442266]		Q0VDT2	0.7	4.3E-01	0.2	8.5E-01	0.4	6.9E-01	0.8	4.4E-01
ENSMUST00000060833	glycoprotein A33 (transmembrane) [Source:MGI Symbol;Acc:MGI:1891703]			9.1	1.8E-05	7.3	4.0E-05	-1.3	2.5E-01	-0.4	4.0E-01
ENSMUST00000060835	testis expressed gene 14 [Source:MGI Symbol;Acc:MGI:1933227]		Q7M6U3	4.1	5.0E-03	7.4	4.9E-05	0.0	9.8E-01	-0.4	4.9E-01
ENSMUST00000060847	ssu-2 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2443733]		Q8C3L1	6.5	7.3E-05	7.3	3.2E-04	-0.7	6.3E-01	0.6	3.8E-01
ENSMUST00000060855	H1 histone family, member N, testis-specific [Source:MGI Symbol;Acc:MGI:1917319]		Q8CJI4	7.7	5.1E-05	7.8	2.3E-04	-0.5	7.6E-01	-1.4	7.2E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000060864	testis specific protein kinase 1 [Source:MGI Symbol;Acc:MGI:1201675]		O70146	2.5	1.2E-02	-1.5	1.1E-01	0.8	1.5E-01	-0.7	4.2E-01
ENSMUST00000060894	glutamate rich 5 [Source:MGI Symbol;Acc:MGI:2447772]		Q8K0S2	6.5	1.6E-05	-5.0	1.7E-03	1.3	2.3E-02	1.4	2.5E-01
ENSMUST00000060895	UDP-glucose pyrophosphorylase 2 [Source:MGI Symbol;Acc:MGI:2183447]	Q3U548	Q91ZJ5	-9.2	2.1E-05	0.2	8.2E-01	1.6	3.2E-02	-0.2	7.7E-01
ENSMUST00000060917	aquaporin 9 [Source:MGI Symbol;Acc:MGI:1891066]	D3YYD6		4.4	1.1E-02	-2.3	1.8E-02	1.2	2.5E-02	-0.2	7.6E-01
ENSMUST00000059873	triggering receptor expressed on myeloid cells-like 4 [Source:MGI Symbol;Acc:MGI:1923239]		Q3LRV9	-0.9	4.7E-01	-2.9	1.2E-01	-0.5	6.3E-01	1.5	4.0E-01
ENSMUST00000060918	archaelysin family metallopeptidase 1 [Source:MGI Symbol;Acc:MGI:2442258]	A1L312	Q8BVF9	-5.2	1.1E-02	5.2	3.1E-04	-3.4	1.3E-02	-0.2	7.0E-01
ENSMUST00000060930	coiled-coil domain containing 158 [Source:MGI Symbol;Acc:MGI:2444555]		Q8CDI6	7.0	3.3E-05	8.4	2.4E-05	1.9	8.3E-02	0.4	4.1E-01
ENSMUST00000060945	AF4/FMR2 family, member 4 [Source:MGI Symbol;Acc:MGI:2136171]		Q9ESC8	-1.9	2.8E-03	7.5	1.3E-04	-0.6	6.2E-01	-1.1	1.2E-01
ENSMUST00000060955	lycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:10489		Q8C0L9	-10.9	2.6E-07	-1.3	9.4E-02	1.0	5.4E-02	0.1	8.4E-01
ENSMUST00000060972	potassium voltage-gated channel, shaker-related subfamily, member 5 [Source:MGI Symbol;Acc:MGI:96662]		Q61762	7.8	2.8E-05	6.6	3.0E-04	-0.6	6.1E-01	-0.2	7.9E-01
ENSMUST00000060989	sortilin-related receptor, LDLR class A repeats-containing [Source:MGI Symbol;Acc:MGI:1202296]		O88307	-5.4	6.6E-06	-4.2	3.7E-03	0.7	2.0E-01	1.9	1.1E-01
ENSMUST00000059930	predicted gene 12185 [Source:MGI Symbol;Acc:MGI:3652173]	Q5NCB2		-0.3	8.5E-01	4.2	2.1E-02	-1.1	5.1E-01	-5.6	3.5E-03
ENSMUST00000060991	tetraspanin 31 [Source:MGI Symbol;Acc:MGI:1914375]		Q9CQ88	-1.8	4.8E-03	7.3	6.4E-05	-0.6	6.1E-01	-0.4	5.2E-01
ENSMUST00000059946	HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1913965]		Q8CAE2	5.1	4.3E-02	4.9	7.3E-02	-0.6	8.1E-01	-0.4	7.9E-01
ENSMUST00000059954	phospholipid transfer protein [Source:MGI Symbol;Acc:MGI:103151]	Q3UFS5	P55065	-2.8	1.1E-01	-5.0	1.3E-02	-3.4	3.2E-03	-1.2	5.4E-01
ENSMUST00000060992	reticulon 4 [Source:MGI Symbol;Acc:MGI:1915835]	Q78NS1	Q99P72	-8.5	1.9E-03	5.3	1.5E-03	-2.6	9.0E-02	-0.7	3.7E-01
ENSMUST00000061013	maestro heat-like repeat family member 2A [Source:MGI Symbol;Acc:MGI:3705228]		D3Z750	9.6	1.9E-04	-4.1	2.1E-03	0.3	5.2E-01	-3.0	5.3E-02
ENSMUST00000061019	kinesin family member 2B [Source:MGI Symbol;Acc:MGI:1920720]	A2RSC8	Q8C0N1	7.3	2.5E-05	-7.1	2.1E-04	-1.0	7.1E-02	0.1	9.5E-01
ENSMUST00000061030	receptor transporter protein 2 [Source:MGI Symbol;Acc:MGI:2685451]		Q80ZI2	7.0	4.9E-05	-6.9	2.4E-05	-0.4	3.1E-01	-1.4	1.6E-01
ENSMUST00000061035	Fer3-like (Drosophila) [Source:MGI Symbol;Acc:MGI:2150010]		Q923Z4	6.4	2.0E-04	7.6	2.5E-04	-0.7	6.4E-01	-0.2	8.0E-01
ENSMUST00000061038	small proline-rich protein 2B [Source:MGI Symbol;Acc:MGI:1330352]	A9JTY7		6.6	6.9E-05	4.3	8.6E-05	-3.8	9.6E-04	0.4	4.2E-01
ENSMUST00000061047	PH domain and leucine rich repeat protein phosphatase 1 [Source:MGI Symbol;Acc:MGI:2138327]		Q8CHE4	2.3	5.2E-04	-1.4	1.3E-01	0.3	6.3E-01	-2.3	5.7E-02
ENSMUST00000061071	lipid phosphate phosphatase-related protein type 4 [Source:MGI Symbol;Acc:MGI:106530]		Q7TME0	9.5	9.6E-06	5.0	1.6E-02	0.6	7.1E-01	0.4	7.1E-01
ENSMUST00000061093	solute carrier family 30, member 10 [Source:MGI Symbol;Acc:MGI:2685058]		Q3UVU3	9.5	2.3E-06	3.1	1.2E-02	-0.5	5.7E-01	-0.4	6.2E-01
ENSMUST00000061096	olfactory receptor 564 [Source:MGI Symbol;Acc:MGI:3030398]	E9PWA8		6.6	6.6E-05	7.3	4.9E-05	-0.5	6.4E-01	-0.3	5.2E-01
ENSMUST00000061099	coiled-coil domain containing 169 [Source:MGI Symbol;Acc:MGI:2444356]		Q8BXX9	5.6	6.0E-04	-3.1	3.8E-02	1.1	1.2E-01	0.9	4.7E-01
ENSMUST00000061101	transforming growth factor, beta receptor II [Source:MGI Symbol;Acc:MGI:98729]	Q543C0	Q62312	-7.5	2.6E-05	-2.1	2.7E-02	0.2	6.9E-01	-0.1	8.9E-01
ENSMUST00000061103	collagen and calcium binding EGF domains 1 [Source:MGI Symbol;Acc:MGI:2445053]		Q3MI99	8.7	6.3E-06	6.7	2.3E-03	-0.6	7.3E-01	-1.8	7.9E-02
ENSMUST00000061111	MARVEL (membrane-associating) domain containing 1 [Source:MGI Symbol;Acc:MGI:2147570]		Q7TQJ1	-1.6	2.1E-02	5.4	1.5E-03	-1.4	3.0E-01	0.4	6.1E-01
ENSMUST00000061118	e carrier family 25 (mitochondrial carrier, phosphate carrier), member 26 [Source:MGI Symbol;Acc:MGI:1914		Q5U680	1.9	9.0E-03	-0.8	5.3E-01	0.2	8.2E-01	-2.3	1.3E-01
ENSMUST00000061156	3-hydroxyacyl-CoA dehydratase 2 [Source:MGI Symbol;Acc:MGI:1918007]		Q9D3B1	-2.8	3.9E-04	6.7	8.1E-04	-0.6	7.1E-01	-0.4	6.0E-01
ENSMUST00000060067	DnaJ (Hsp40) homolog, subfamily A, member 3 [Source:MGI Symbol;Acc:MGI:1933786]		Q99M87	-1.6	2.8E-01	-0.6	7.0E-01	-0.7	5.3E-01	-1.7	2.9E-01
ENSMUST00000061158	COMM domain containing 3 [Source:MGI Symbol;Acc:MGI:88218]		Q63829	-4.5	2.1E-04	4.3	9.9E-05	0.8	2.1E-01	-0.3	4.8E-01
ENSMUST00000061169	galactose-3-O-sulfotransferase 3 [Source:MGI Symbol;Acc:MGI:3617843]		P61315	7.0	1.2E-05	-3.2	1.3E-03	-0.3	3.9E-01	-0.2	8.1E-01
ENSMUST00000061174	sterile alpha and HEAT/Armadillo motif containing 1 [Source:MGI Symbol;Acc:MGI:2136419]		Q6PDS3	7.6	4.3E-05	3.2	4.2E-01	-1.0	7.7E-01	3.5	2.5E-01
ENSMUST00000061185	keratin 81 [Source:MGI Symbol;Acc:MGI:1928858]		Q9ERE2	6.7	1.4E-04	5.2	1.6E-04	-0.3	7.1E-01	0.1	9.1E-01
ENSMUST00000061187	doublesex and mab-3 related transcription factor like family A2 [Source:MGI Symbol;Acc:MGI:2653629]		A2A9A2	5.6	5.8E-04	2.1	4.9E-03	0.3	5.0E-01	-0.4	3.7E-01
ENSMUST00000061190	glycoprotein 5 (platelet) [Source:MGI Symbol;Acc:MGI:1096363]	Q9QZU3		3.6	1.7E-04	7.1	7.6E-05	0.3	7.9E-01	-0.3	6.0E-01
ENSMUST00000061193	catsper channel auxiliary subunit gamma 2 [Source:MGI Symbol;Acc:MGI:1923968]		C6KI89	7.2	1.9E-05	7.6	2.0E-04	2.5	6.9E-02	-0.1	8.7E-01
ENSMUST00000060148	human immunodeficiency virus type I enhancer binding protein 1 [Source:MGI Symbol;Acc:MGI:96100]	F8VPM9		0.2	5.4E-01	0.9	8.9E-02	1.0	2.0E-02	0.3	4.3E-01
ENSMUST00000060173	sterile alpha motif domain containing 10 [Source:MGI Symbol;Acc:MGI:2443872]	Q3TBN2	Q7TST3	3.6	1.1E-01	0.0	9.9E-01	-2.9	1.7E-01	0.7	7.6E-01
ENSMUST00000061203	transmembrane emp24 protein transport domain containing 5 [Source:MGI Symbol;Acc:MGI:1921586]	E9Q2J2		3.5	8.2E-05	-0.7	3.4E-01	0.5	2.9E-01	-0.4	5.6E-01
ENSMUST00000060175	cDNA sequence BC030336 [Source:MGI Symbol;Acc:MGI:2446240]		Q8C784	0.5	2.4E-01	1.2	5.5E-02	0.5	2.3E-01	-0.2	7.6E-01
ENSMUST00000060185	fibronectin type III domain containing 9 [Source:MGI Symbol;Acc:MGI:2443410]		Q8BJN4	-0.1	8.4E-01	1.3	1.4E-01	0.8	2.0E-01	-0.6	4.4E-01
ENSMUST00000061209	coiled-coil domain containing 71 [Source:MGI Symbol;Acc:MGI:1919704]		Q8VEG0	-5.4	1.4E-03	5.0	2.9E-02	-0.5	8.0E-01	0.5	7.0E-01
ENSMUST00000061222	kelch repeat and BTB (POZ) domain containing 7 [Source:MGI Symbol;Acc:MGI:2685141]	G5E8C2		-2.9	1.2E-04	-0.7	3.6E-01	1.4	1.3E-02	-0.5	5.1E-01
ENSMUST00000061235	olfactory receptor 1417 [Source:MGI Symbol;Acc:MGI:3031251]	Q8VGJ6		7.3	1.0E-04	5.7	6.0E-03	-0.6	7.4E-01	0.3	7.7E-01
ENSMUST00000061242	ADP-ribosylation factor 1 [Source:MGI Symbol;Acc:MGI:99431]		P84078	-6.4	2.9E-07	6.2	1.7E-03	-0.6	6.8E-01	-0.6	4.9E-01
ENSMUST00000061244	Eph receptor B4 [Source:MGI Symbol;Acc:MGI:104757]		P54761	4.5	4.3E-03	-8.4	9.7E-05	0.3	4.3E-01	-0.9	5.4E-01
ENSMUST00000061251	RIKEN cDNA 1500011B03 gene [Source:MGI Symbol;Acc:MGI:1913486]	Q3TTH7		-2.5	3.5E-03	4.4	1.2E-03	-0.6	5.2E-01	0.4	5.2E-01
ENSMUST00000061260	FAT tumor suppressor homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:3045256]		Q2PZL6	11.2	6.8E-07	7.3	1.5E-04	-0.9	4.9E-01	0.5	4.4E-01
ENSMUST00000060223	zinc binding alcohol dehydrogenase, domain containing 2 [Source:MGI Symbol;Acc:MGI:2444835]	Q14AZ9	Q8BGC4	-0.2	7.2E-01	-0.3	6.9E-01	0.1	8.7E-01	0.2	8.0E-01
ENSMUST00000061273	dapper homolog 1, antagonist of beta-catenin (xenopus) [Source:MGI Symbol;Acc:MGI:1891740]		Q8R4A3	4.3	5.2E-04	5.2	1.4E-03	0.0	9.8E-01	-0.4	6.2E-01
ENSMUST00000060226	transmembrane emp24 domain trafficking protein 2 [Source:MGI Symbol;Acc:MGI:1929269]	A2RS53	Q9R0Q3	-2.1	5.2E-01	-2.5	4.8E-01	-1.4	5.6E-01	-0.9	8.1E-01
ENSMUST00000061274	G protein-coupled receptor 156 [Source:MGI Symbol;Acc:MGI:2653880]			7.8	2.9E-06	-4.4	1.4E-04	0.4	2.5E-01	-0.8	3.2E-01
ENSMUST00000061279	protocadherin gamma subfamily A, 11 [Source:MGI Symbol;Acc:MGI:1935228]	Q91XY8		5.0	1.7E-04	7.0	1.9E-03	0.7	6.6E-01	-0.4	6.3E-01
ENSMUST00000061280	in-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:2441	Q3TGS5	P59913	-4.3	7.5E-03	-3.2	1.4E-03	-0.6	1.6E-01	-0.1	9.4E-01
ENSMUST00000060253	feminization 1 homolog a (C. elegans) [Source:MGI Symbol;Acc:MGI:1335089]		Q9Z2G1	-0.9	8.4E-02	-0.2	7.6E-01	0.7	1.4E-01	0.0	9.8E-01
ENSMUST00000061283	cytokine receptor-like factor 3 [Source:MGI Symbol;Acc:MGI:1860086]		Q9Z2L7	-4.4	2.6E-04	7.7	4.6E-05	-0.5	6.7E-01	-0.8	1.6E-01
ENSMUST00000061284	olfactory receptor 683 [Source:MGI Symbol;Acc:MGI:3030517]	Q8VGV1		5.9	5.7E-03	6.9	1.1E-04	-0.6	6.2E-01	0.0	9.6E-01
ENSMUST00000061295	DnaJ (Hsp40) homolog, subfamily C, member 22 [Source:MGI Symbol;Acc:MGI:1920028]		Q8CHS2	7.1	2.1E-05	7.5	1.1E-04	-0.7	6.0E-01	0.3	6.4E-01
ENSMUST00000060274	TNF receptor-associated factor 3 [Source:MGI Symbol;Acc:MGI:108041]	Q3UHJ1		1.8	4.9E-01	1.9	3.9E-01	-3.2	1.7E-01	-3.3	1.7E-01
ENSMUST00000060303	teashirt zinc finger family member 1 [Source:MGI Symbol;Acc:MGI:1346031]		Q5DTH5	1.6	2.4E-01	3.2	3.9E-02	-0.8	5.2E-01	-2.5	6.0E-02
ENSMUST00000061299	fibroblast growth factor binding protein 1 [Source:MGI Symbol;Acc:MGI:1096350]		O70514	6.9	1.6E-04	-0.8	1.6E-01	0.4	3.2E-01	-0.5	3.6E-01
ENSMUST00000061318	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 12 [Source:MGI Symbol;Acc:M		Q811B3	9.7	1.3E-05	-3.2	5.8E-02	-0.2	8.0E-01	0.0	9.9E-01
ENSMUST00000060323	golgi phosphoprotein 3-like [Source:MGI Symbol;Acc:MGI:1917129]	K3W4N3		4.0	1.7E-01	4.5	1.8E-01	-0.2	9.4E-01	-0.7	7.4E-01
ENSMUST00000060330	RIKEN cDNA 1700012B09 gene [Source:MGI Symbol;Acc:MGI:1916575]	Q9DAE7		3.7	7.2E-02	0.7	7.2E-01	-2.3	2.4E-01	0.7	6.4E-01
ENSMUST00000061324	predicted pseudogene 9923 [Source:MGI Symbol;Acc:MGI:3704365]	J3KMK0		4.7	1.0E-02	7.1	6.8E-05	-0.5	6.6E-01	-0.1	8.6E-01
ENSMUST00000061327	F-box protein 48 [Source:MGI Symbol;Acc:MGI:2442569]		Q8CAT8	3.7	1.1E-03	6.3	2.3E-04	-0.6	5.8E-01	0.0	9.5E-01
ENSMUST00000061328	sosondowah ankyrin repeat domain family member B [Source:MGI Symbol;Acc:MGI:1925338]		Q8BZW2	10.2	8.2E-06	5.8	8.7E-04	-0.5	7.1E-01	-0.3	6.6E-01
ENSMUST00000061331	heterogeneous nuclear ribonucleoprotein L-like [Source:MGI Symbol;Acc:MGI:1919942]		Q921F4	-4.4	8.3E-04	6.9	8.9E-05	-0.6	6.2E-01	0.0	9.3E-01
ENSMUST00000061334	methionine-tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:2444136]	A2RT28	Q499X9	3.4	6.7E-05	7.9	6.4E-04	-0.8	6.4E-01	0.3	7.4E-01
ENSMUST00000061343	protease, serine 48 [Source:MGI Symbol;Acc:MGI:2685865]		Q14B25	7.6	5.0E-05	-5.0	4.1E-03	1.1	1.1E-01	-0.2	8.7E-01
ENSMUST00000061350	ATPase type 13A3 [Source:MGI Symbol;Acc:MGI:2685387]		Q5XF89	-3.1	1.6E-02	5.9	3.7E-04	-0.5	6.6E-01	0.8	2.1E-01
ENSMUST00000061372	testis-specific protein, Y-encoded-like 1 [Source:MGI Symbol;Acc:MGI:1298395]		O88852	-2.0	2.7E-03	-2.9	6.7E-04	0.3	3.2E-01	-0.1	8.1E-01
ENSMUST00000061391	coiled-coil domain containing 89 [Source:MGI Symbol;Acc:MGI:1917304]		Q9DA73	6.4	1.9E-04	2.9	5.1E-04	0.9	7.5E-02	-0.7	1.4E-01
ENSMUST00000061403	keratin associated protein 5-4 [Source:MGI Symbol;Acc:MGI:1354758]		Q62220	8.1	1.1E-04	6.9	6.8E-04	-0.7	6.5E-01	-0.1	8.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000061405	protocadherin beta 21 [Source:MGI Symbol;Acc:MGI:2136759]	Q91V48		7.6	9.8E-05	4.5	6.0E-02	-1.2	6.0E-01	0.1	9.4E-01
ENSMUST00000061425	paraneoplastic antigen MA1 [Source:MGI Symbol;Acc:MGI:2180564]		Q8C1C8	5.8	1.3E-04	5.3	1.5E-02	-0.6	7.5E-01	0.5	6.4E-01
ENSMUST00000060404	torsin A interacting protein 2 [Source:MGI Symbol;Acc:MGI:3582695]		Q8BYU6	-0.2	8.7E-01	1.0	4.4E-01	0.9	3.8E-01	-0.3	7.9E-01
ENSMUST00000061427	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3 [Source:MGI Symbol;Acc:M	G3X9D2		5.4	5.3E-03	4.2	7.7E-03	-0.7	5.6E-01	0.3	7.6E-01
ENSMUST00000060417	transformation related protein 53 inducible protein 13 [Source:MGI Symbol;Acc:MGI:1915125]	B2RVS3	Q5F267	-0.5	5.0E-01	1.9	6.0E-02	0.8	2.8E-01	-1.5	7.4E-02
ENSMUST00000061437	adhesion regulating molecule 1 [Source:MGI Symbol;Acc:MGI:1929289]		Q9JKV1	-7.5	5.4E-05	7.3	2.2E-04	-0.7	6.1E-01	0.2	7.1E-01
ENSMUST00000060419	gap junction protein, beta 4 [Source:MGI Symbol;Acc:MGI:95722]		Q02738	3.0	2.0E-01	-0.1	9.7E-01	-4.5	4.6E-02	-1.4	4.4E-01
ENSMUST00000061444	mitochondrial ribosomal protein S16 [Source:MGI Symbol;Acc:MGI:1913492]		Q9CPX7	-3.9	3.6E-05	-3.5	2.7E-02	1.6	4.5E-02	-0.5	7.2E-01
ENSMUST00000060433	tumor-suppressing subchromosomal transferable fragment 4 [Source:MGI Symbol;Acc:MGI:1861712]		Q9JHE7	-2.2	4.5E-01	-1.3	6.9E-01	-0.3	8.7E-01	-1.3	7.1E-01
ENSMUST00000061446	transmembrane protein 130 [Source:MGI Symbol;Acc:MGI:3607706]		Q6NXM3	8.2	1.3E-05	-1.9	5.0E-02	0.7	2.0E-01	-0.7	4.5E-01
ENSMUST00000061450	transmembrane protein 104 [Source:MGI Symbol;Acc:MGI:2444222]		Q3TB48	-2.9	2.6E-03	0.2	9.6E-01	5.6	2.4E-02	1.5	6.0E-01
ENSMUST00000061455	family with sequence similarity 46, member C [Source:MGI Symbol;Acc:MGI:1921895]		Q5SSF7	-1.2	9.8E-03	2.1	7.2E-03	-0.3	6.0E-01	-0.1	8.2E-01
ENSMUST00000061456	F-box and WD-40 domain protein 13 [Source:MGI Symbol;Acc:MGI:3505590]	Q8BI57		4.6	2.4E-03	1.4	3.5E-01	5.5	8.1E-04	-0.1	9.3E-01
ENSMUST00000061457	cysteine-serine-rich nuclear protein 2 [Source:MGI Symbol;Acc:MGI:2386852]		Q8BGQ2	2.1	8.7E-04	-5.2	4.6E-05	0.6	1.2E-01	-3.2	1.0E-02
ENSMUST00000060474	septin 6 [Source:MGI Symbol;Acc:MGI:1888939]		Q9R1T4	0.2	8.2E-01	1.6	1.9E-01	0.3	7.8E-01	-1.1	2.9E-01
ENSMUST00000061468	B cell CLL/lymphoma 7C [Source:MGI Symbol;Acc:MGI:1332237]		O08664	-5.1	5.2E-04	9.8	7.8E-06	-0.7	5.8E-01	-0.3	4.3E-01
ENSMUST00000061469	follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 [Source:MGI Symbol;Acc:MGI:266		Q7TQN3	2.0	1.6E-03	-2.2	4.4E-02	0.6	2.7E-01	-0.8	4.2E-01
ENSMUST00000061481	protease, serine 38 [Source:MGI Symbol;Acc:MGI:2685095]		Q3UKY7	6.7	8.4E-05	1.1	1.0E-01	-1.3	3.5E-02	0.0	9.4E-01
ENSMUST00000061482	olfactory receptor 543 [Source:MGI Symbol;Acc:MGI:3030377]	E9PWI5		6.6	2.1E-04	-0.7	3.6E-01	0.9	1.2E-01	-3.4	6.0E-03
ENSMUST00000061491	solute carrier family 27 (fatty acid transporter), member 2 [Source:MGI Symbol;Acc:MGI:1347099]		O35488	4.5	6.3E-05	5.2	2.2E-03	-0.6	6.1E-01	0.0	9.8E-01
ENSMUST00000060531	leucine rich repeat containing 8D [Source:MGI Symbol;Acc:MGI:1922368]		Q8BGR2	-3.6	1.0E-01	1.2	5.6E-01	1.3	4.4E-01	-3.5	1.3E-01
ENSMUST00000061506	transmembrane and tetratricopeptide repeat containing 2 [Source:MGI Symbol;Acc:MGI:1914057]		Q56A06	7.5	7.9E-05	-1.0	1.8E-01	0.8	9.1E-02	-0.3	6.9E-01
ENSMUST00000061512	mitogen-activated protein kinase kinase kinase 19 [Source:MGI Symbol;Acc:MGI:1203481]		E9Q3S4	8.5	7.7E-06	7.7	1.3E-04	-0.1	9.3E-01	-0.4	5.6E-01
ENSMUST00000061514	retinoic acid induced 2 [Source:MGI Symbol;Acc:MGI:1344378]		Q9QVY8	6.5	3.4E-04	5.1	1.8E-02	0.3	8.9E-01	0.6	6.1E-01
ENSMUST00000061516	formyl peptide receptor 1 [Source:MGI Symbol;Acc:MGI:107443]		P33766	-7.8	2.6E-06	7.8	4.0E-05	-0.5	6.6E-01	-0.1	8.1E-01
ENSMUST00000061522	dead end homolog 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:2447763]		Q6VY05	3.4	9.5E-03	6.8	7.8E-04	-1.5	3.6E-01	0.4	6.2E-01
ENSMUST00000061541	olfactory receptor 161 [Source:MGI Symbol;Acc:MGI:3032605]	Q8VGB9		6.3	3.0E-04	-3.6	2.3E-04	0.4	2.2E-01	0.4	5.0E-01
ENSMUST00000061545	C1q-like 3 [Source:MGI Symbol;Acc:MGI:2387350]		Q9ESN4	6.6	6.0E-05	5.6	8.9E-04	-0.5	6.8E-01	0.2	7.8E-01
ENSMUST00000060608	cytochrome P450, family 20, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1925201]		Q8BKE6	0.6	6.9E-01	-4.1	1.2E-01	-2.0	1.3E-01	2.6	2.8E-01
ENSMUST00000060632	2-oxoglutarate and iron-dependent oxygenase domain containing 1 [Source:MGI Symbol;Acc:MGI:2442978]	D3YTU2		-5.0	8.1E-02	0.9	6.9E-01	2.4	2.6E-01	-3.6	1.9E-01
ENSMUST00000061552	pseudopodium-enriched atypical kinase 1 [Source:MGI Symbol;Acc:MGI:2442366]		Q69Z38	3.5	5.7E-05	-3.0	5.4E-04	0.7	4.9E-02	-0.4	4.9E-01
ENSMUST00000061571	neurogenic differentiation 4 [Source:MGI Symbol;Acc:MGI:108055]	Q545C0	O09105	6.6	5.2E-05	-0.1	9.5E-01	0.9	1.9E-01	-1.2	2.4E-01
ENSMUST00000061578	senataxin [Source:MGI Symbol;Acc:MGI:2443480]		A2AKX3	-2.0	1.6E-03	6.2	1.0E-03	-0.6	6.8E-01	-1.1	1.8E-01
ENSMUST00000061586	zinc finger protein 507 [Source:MGI Symbol;Acc:MGI:1916378]		Q6ZPY5	2.3	1.4E-03	-2.2	2.5E-03	-1.3	3.5E-03	-1.2	5.1E-02
ENSMUST00000060655	nucleotide-binding oligomerization domain containing 1 [Source:MGI Symbol;Acc:MGI:1341839]	Q540J8	Q8BHB0	-1.2	2.2E-01	1.0	3.7E-01	0.4	6.0E-01	-1.7	1.2E-01
ENSMUST00000060673	lipase, member H [Source:MGI Symbol;Acc:MGI:2388029]		Q8C1V3	3.5	1.5E-01	4.9	7.9E-02	-0.4	8.7E-01	-1.8	3.1E-01
ENSMUST00000061587	ORAI calcium release-activated calcium modulator 3 [Source:MGI Symbol;Acc:MGI:3039586]	A3KCG3	Q6P8G8	-4.5	6.5E-03	6.9	1.1E-04	-0.6	6.3E-01	-0.3	6.5E-01
ENSMUST00000061590	inturned planar cell polarity effector homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2443752]		Q059U7	7.1	3.5E-05	7.2	4.1E-04	-0.4	7.9E-01	-1.0	1.9E-01
ENSMUST00000060710	cell division cycle 25C [Source:MGI Symbol;Acc:MGI:88350]	Q3UR74	P48967	0.8	1.7E-01	0.7	2.9E-01	-1.1	4.6E-02	-1.0	1.1E-01
ENSMUST00000060711	EPM2A (laforin) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1925031]		Q8VEH5	-0.3	6.4E-01	1.2	9.9E-02	0.5	3.6E-01	-1.0	1.4E-01
ENSMUST00000061597	RIKEN cDNA 4921517D22 gene [Source:MGI Symbol;Acc:MGI:1918150]	Q8CET0		6.8	6.8E-05	-0.8	3.3E-01	1.0	1.0E-01	0.1	8.7E-01
ENSMUST00000061601	uronyl-2-sulfotransferase [Source:MGI Symbol;Acc:MGI:2442406]		Q8BUB6	4.5	7.4E-05	2.7	2.3E-02	-1.2	2.4E-01	-0.3	7.1E-01
ENSMUST00000061611	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:2443419]	E9QMX4		-3.2	1.2E-02	-7.0	1.8E-04	0.1	7.6E-01	-0.2	8.8E-01
ENSMUST00000061614	gap junction protein, alpha 3 [Source:MGI Symbol;Acc:MGI:95714]		Q64448	7.6	9.1E-04	3.0	6.4E-03	0.0	9.8E-01	0.5	4.8E-01
ENSMUST00000061617	zinc finger protein 280B [Source:MGI Symbol;Acc:MGI:1927865]	Q505F4		2.6	1.1E-03	5.8	6.4E-04	-0.6	6.3E-01	0.5	5.0E-01
ENSMUST00000061618	protein associated with topoisomerase II homolog 1 (yeast) [Source:MGI Symbol;Acc:MGI:2147679]		Q3TC46	-2.3	2.1E-03	-4.7	4.3E-03	-0.6	3.9E-01	-1.7	2.4E-01
ENSMUST00000061620	unc-80 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2652882]	B8XCJ6		8.2	2.3E-07	6.2	6.3E-05	-0.3	7.0E-01	-0.1	8.1E-01
ENSMUST00000061632	TRH-degrading enzyme [Source:MGI Symbol;Acc:MGI:2384311]		Q8K093	7.2	9.5E-05	5.7	6.4E-04	-0.3	8.0E-01	0.1	8.4E-01
ENSMUST00000060762	zinc finger protein 397 [Source:MGI Symbol;Acc:MGI:1916506]	Q7TNK4		-0.1	8.9E-01	-0.1	8.2E-01	0.3	4.7E-01	0.3	5.1E-01
ENSMUST00000061653	complement factor D (adipsin) [Source:MGI Symbol;Acc:MGI:87931]	Q3UP47	P03953	5.9	3.9E-04	-8.3	7.3E-04	1.0	5.9E-02	4.0	3.7E-02
ENSMUST00000061669	olfactory receptor 1495 [Source:MGI Symbol;Acc:MGI:3031329]	Q8VEZ4		4.5	1.0E-02	4.0	7.0E-04	-0.7	3.8E-01	-0.8	2.2E-01
ENSMUST00000060783	zinc finger protein 768 [Source:MGI Symbol;Acc:MGI:2384582]		Q8R0T2	-1.1	7.8E-02	0.1	9.2E-01	1.3	3.6E-02	0.1	8.6E-01
ENSMUST00000061673	integrin alpha 1 [Source:MGI Symbol;Acc:MGI:96599]		Q3V3R4	1.8	3.8E-03	-1.0	1.2E-01	-5.5	6.7E-06	0.1	8.5E-01
ENSMUST00000061679	RIKEN cDNA 4921508M14 gene [Source:MGI Symbol;Acc:MGI:1918094]	Q9D5X6		6.3	3.6E-04	-0.9	2.0E-01	1.0	5.4E-02	0.1	9.3E-01
ENSMUST00000061688	ER membrane associated RNA degradation [Source:MGI Symbol;Acc:MGI:1917317]	Q8C5D3		2.3	3.6E-03	-1.6	1.3E-02	0.8	3.6E-02	0.2	6.5E-01
ENSMUST00000060807	family with sequence similarity 83, member H [Source:MGI Symbol;Acc:MGI:2145900]		Q148V8	6.0	6.0E-02	0.4	8.8E-01	-4.4	1.3E-01	1.2	6.1E-01
ENSMUST00000061690	olfactory receptor 509 [Source:MGI Symbol;Acc:MGI:3030343]	Q8VF20		5.9	1.3E-03	-2.6	6.9E-02	-6.9	5.0E-04	1.8	2.0E-01
ENSMUST00000061695	RIKEN cDNA 4930451I11 gene [Source:MGI Symbol;Acc:MGI:1925368]	E9Q9R3		6.4	1.4E-04	6.4	1.8E-04	-0.5	6.6E-01	-0.2	6.8E-01
ENSMUST00000061699	BPI fold containing family C [Source:MGI Symbol;Acc:MGI:3026884]	Q3V1D7		6.1	2.1E-05	4.1	3.0E-03	-5.4	1.4E-03	-0.5	4.9E-01
ENSMUST00000061706	RIKEN cDNA E130311K13 gene [Source:MGI Symbol;Acc:MGI:3607716]		Q8BN57	3.4	5.4E-04	2.6	6.5E-02	-1.7	1.8E-01	-0.1	8.9E-01
ENSMUST00000060837	RAB11 family interacting protein 5 (class I) [Source:MGI Symbol;Acc:MGI:1098586]		Q8R361	-0.7	1.8E-01	-0.3	6.1E-01	0.1	8.3E-01	-0.3	6.3E-01
ENSMUST00000061717	protocadherin beta 6 [Source:MGI Symbol;Acc:MGI:2136740]	Q91XZ4		8.3	1.4E-05	6.6	1.2E-04	-0.6	6.1E-01	-0.7	2.7E-01
ENSMUST00000061720	zinc finger protein 775 [Source:MGI Symbol;Acc:MGI:2683557]		Q8BI73	4.7	3.1E-05	7.4	1.3E-04	-0.7	6.1E-01	-0.4	5.6E-01
ENSMUST00000061721	E2F transcription factor 2 [Source:MGI Symbol;Acc:MGI:1096341]		P56931	-3.7	2.4E-04	3.9	9.5E-03	1.0	3.6E-01	-0.3	7.3E-01
ENSMUST00000061723	olfactory receptor 215 [Source:MGI Symbol;Acc:MGI:3030049]	Q8VF82		5.0	3.8E-03	5.1	3.8E-04	-0.8	3.7E-01	0.6	3.3E-01
ENSMUST00000061725	protease, serine 32 [Source:MGI Symbol;Acc:MGI:1917064]	E9Q409		7.9	1.6E-04	-7.6	1.4E-04	1.2	2.1E-02	-0.3	8.3E-01
ENSMUST00000060899	N-acyl phosphatidylethanolamine phospholipase D [Source:MGI Symbol;Acc:MGI:2140885]		Q8BH82	4.2	7.7E-02	2.3	5.4E-01	2.1	5.3E-01	4.0	1.3E-01
ENSMUST00000060913	dual specificity phosphatase 28 [Source:MGI Symbol;Acc:MGI:1914696]		Q8BTR5	-1.1	1.3E-01	-1.2	1.9E-01	-0.2	7.4E-01	-0.1	9.0E-01
ENSMUST00000061728	noggin [Source:MGI Symbol;Acc:MGI:104327]	A2RTJ4	P97466	6.2	1.1E-04	4.0	5.4E-02	-0.7	7.1E-01	-0.3	7.9E-01
ENSMUST00000061740	transmembrane protein 178B [Source:MGI Symbol;Acc:MGI:3647581]	Q8BNC6		10.4	3.0E-05	-2.8	9.8E-02	0.5	6.2E-01	-1.9	3.4E-01
ENSMUST00000061745	homeobox D10 [Source:MGI Symbol;Acc:MGI:96202]		P28359	7.3	4.3E-04	6.3	8.7E-05	-1.4	1.9E-01	-0.7	2.2E-01
ENSMUST00000061753	WD repeat and FYVE domain containing 4 [Source:MGI Symbol;Acc:MGI:3584510]	E9PV60		-4.6	1.4E-02	-2.0	1.3E-02	0.4	3.1E-01	0.5	4.4E-01
ENSMUST00000060947	claudin 12 [Source:MGI Symbol;Acc:MGI:1929288]		Q9ET43	1.8	4.5E-01	6.3	7.5E-02	3.9	1.8E-01	-0.6	8.2E-01
ENSMUST00000061755	lysosomal-associated membrane protein 2 [Source:MGI Symbol;Acc:MGI:96748]		P17047	-8.3	4.8E-07	-10.8	2.5E-06	-0.5	7.1E-02	-0.7	5.6E-01
ENSMUST00000061766	ankyrin repeat and death domain containing 1A [Source:MGI Symbol;Acc:MGI:2686319]	F8VQ39		7.1	6.8E-05	7.8	5.4E-05	-0.6	6.2E-01	-0.5	3.4E-01
ENSMUST00000060987	ornithine decarboxylase antizyme 1 [Source:MGI Symbol;Acc:MGI:109433]	F8WI29		2.6	3.2E-01	4.6	2.0E-01	0.8	8.0E-01	-1.2	6.3E-01
ENSMUST00000061771	fukutin [Source:MGI Symbol;Acc:MGI:2179507]		Q8R507	10.6	2.1E-05	-4.1	2.9E-04	1.1	2.2E-02	-0.2	7.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000061789	ieuronal tyrosine-phosphorylated phosphoinositide 3-kinase adaptor 1 [Source:MGI Symbol;Acc:MGI:2443880		Q6PFX7	6.1	4.4E-04	-0.4	5.5E-01	1.0	4.6E-02	-0.5	4.6E-01
ENSMUST00000061796	G protein-coupled receptor 6 [Source:MGI Symbol;Acc:MGI:2155249]		Q6YNI2	7.3	3.7E-04	4.3	1.5E-01	10.1	2.2E-03	-2.7	2.4E-01
ENSMUST00000061799	lysyl oxidase-like 1 [Source:MGI Symbol;Acc:MGI:106096]			8.7	6.1E-06	1.9	2.4E-01	-3.3	6.4E-02	0.3	8.0E-01
ENSMUST00000061826	3-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1349		Q920V1	5.6	3.4E-04	11.3	2.4E-04	0.4	8.6E-01	-1.3	1.0E-01
ENSMUST00000061828	potassium voltage-gated channel, subfamily G, member 4 [Source:MGI Symbol;Acc:MGI:1913983]		Q80XM3	9.5	1.6E-05	7.5	4.2E-05	-0.6	5.9E-01	-0.8	1.9E-01
ENSMUST00000061829	CD14 antigen [Source:MGI Symbol;Acc:MGI:88318]	Q4FJP7	P10810	-5.5	1.4E-06	6.5	1.7E-04	-0.6	6.2E-01	-0.1	8.9E-01
ENSMUST00000061831	mab-21-like 3 (C. elegans) [Source:MGI Symbol;Acc:MGI:2446273]		Q8CI17	8.3	1.8E-05	6.1	5.1E-04	-0.5	6.9E-01	-0.2	7.5E-01
ENSMUST00000061833	transmembrane protein 136 [Source:MGI Symbol;Acc:MGI:2685030]		Q3TYE7	7.5	4.8E-06	6.5	1.4E-04	-0.5	6.2E-01	-0.5	4.1E-01
ENSMUST00000061835	V-set and immunoglobulin domain containing 8 [Source:MGI Symbol;Acc:MGI:3642995]		Q6P3A4	3.9	1.3E-02	5.6	5.3E-03	-1.8	2.8E-01	1.4	1.5E-01
ENSMUST00000061850	protein-O-mannose kinase [Source:MGI Symbol;Acc:MGI:1921903]		Q3TUA9	2.7	9.6E-03	2.6	1.3E-03	0.1	8.0E-01	-0.1	7.9E-01
ENSMUST00000061050	coiled-coil domain containing 80 [Source:MGI Symbol;Acc:MGI:1915146]		Q8R2G6	3.9	1.4E-01	3.6	4.0E-01	2.5	5.1E-01	2.8	2.9E-01
ENSMUST00000061070	PWWP domain containing 2A [Source:MGI Symbol;Acc:MGI:1918052]		Q69Z61	3.2	1.8E-01	2.9	2.5E-01	-0.4	8.7E-01	-0.1	9.7E-01
ENSMUST00000061856	glycerol-3-phosphate acyltransferase, mitochondrial [Source:MGI Symbol;Acc:MGI:109162]		Q61586	4.6	4.1E-05	6.4	1.5E-04	-2.8	4.0E-02	0.2	6.9E-01
ENSMUST00000061086	otein tyrosine phosphatase, receptor type, C polypeptide-associated protein [Source:MGI Symbol;Acc:MGI:978	Q542J3	Q64697	-1.4	5.7E-02	-1.2	1.7E-01	-0.2	6.8E-01	-0.4	5.7E-01
ENSMUST00000061866	DnaJ (Hsp40) homolog, subfamily B, member 8 [Source:MGI Symbol;Acc:MGI:1922801]		Q9QYI7	6.9	2.3E-04	8.6	1.2E-05	-0.6	6.0E-01	0.4	3.9E-01
ENSMUST00000061875	zinc finger protein 622 [Source:MGI Symbol;Acc:MGI:1289282]		Q91VY9	-1.2	1.6E-02	6.9	9.0E-05	-0.5	6.5E-01	-0.8	1.8E-01
ENSMUST00000061878	kelch domain containing 9 [Source:MGI Symbol;Acc:MGI:1916124]		Q3USL1	4.5	4.7E-04	4.1	1.0E-02	-0.5	7.1E-01	1.0	2.3E-01
ENSMUST00000061885	RIKEN cDNA 1700001C19 gene [Source:MGI Symbol;Acc:MGI:1922712]	Q8K168		4.5	1.7E-04	-6.9	3.3E-04	0.2	6.7E-01	-0.5	7.3E-01
ENSMUST00000061890	zinc finger protein 282 [Source:MGI Symbol;Acc:MGI:2141413]	E9PVC2		1.4	1.6E-02	4.2	1.4E-04	-4.7	5.1E-04	-0.2	6.5E-01
ENSMUST00000061891	RIKEN cDNA 1110034G24 gene [Source:MGI Symbol;Acc:MGI:1920997]	B2RR16	Q9D112	-4.0	2.6E-03	0.7	3.6E-01	1.9	6.9E-03	-0.4	6.0E-01
ENSMUST00000061895	phosphatidylserine decarboxylase [Source:MGI Symbol;Acc:MGI:2445114]	Q505E1	Q8BSF4	-4.0	3.0E-03	2.5	5.1E-03	0.2	7.2E-01	-0.4	4.5E-01
ENSMUST00000061135	Myb/SANT-like DNA-binding domain containing 3 [Source:MGI Symbol;Acc:MGI:1913915]		Q9CR78	-0.9	3.3E-01	-1.4	5.1E-01	2.7	5.1E-02	3.1	1.1E-01
ENSMUST00000061143	MAP7 domain containing 1 [Source:MGI Symbol;Acc:MGI:2384297]		A2AJI0	2.7	1.4E-01	5.3	1.3E-02	-0.3	8.8E-01	-2.9	5.9E-02
ENSMUST00000061155	kinesin family member 9 [Source:MGI Symbol;Acc:MGI:1098237]	Q8C0X6		-0.8	3.7E-01	-0.1	9.2E-01	-0.6	4.7E-01	-1.3	2.3E-01
ENSMUST00000061920	olfactory receptor 690 [Source:MGI Symbol;Acc:MGI:3030524]	Q8VH18		5.5	2.8E-03	-1.3	6.7E-02	1.0	3.2E-02	-0.5	4.4E-01
ENSMUST00000061923	relaxin 3 [Source:MGI Symbol;Acc:MGI:2158015]		Q8CHK2	5.0	2.7E-03	-6.7	6.9E-04	-0.8	1.3E-01	1.3	3.3E-01
ENSMUST00000061937	chitobiase, di-N-acetyl- [Source:MGI Symbol;Acc:MGI:1921495]	Q102J0	Q8R242	-3.5	1.6E-04	6.4	8.8E-05	-0.5	6.4E-01	0.2	7.2E-01
ENSMUST00000061938	predicted gene 15698 [Source:MGI Symbol;Acc:MGI:3651308]	A6PWE0		6.8	2.4E-04	7.2	1.2E-04	-0.6	6.3E-01	-0.2	7.5E-01
ENSMUST00000061179	RAB GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2385139]	B2RRC5	A2AWA9	-0.7	2.4E-01	-0.7	3.0E-01	-0.3	5.1E-01	-0.2	7.4E-01
ENSMUST00000061990	olfactory receptor 419 [Source:MGI Symbol;Acc:MGI:3030253]	E9Q0Y7		6.7	1.3E-04	5.0	4.1E-04	-2.3	5.9E-02	-0.6	3.8E-01
ENSMUST00000062000	forkhead box O4 [Source:MGI Symbol;Acc:MGI:1891915]	B1AUT3	Q9WVH3	-3.7	1.7E-04	2.5	1.2E-02	-4.3	2.4E-03	-1.2	9.7E-02
ENSMUST00000062009	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]	Q3TVH6	Q9JHC9	-5.0	9.5E-04	2.6	3.1E-03	-1.0	1.2E-01	0.0	9.8E-01
ENSMUST00000062010	zinc finger, CCHC domain containing 5 [Source:MGI Symbol;Acc:MGI:2685221]	Q6P1Y1		8.0	3.9E-04	5.2	9.7E-05	-2.8	1.3E-02	-0.8	1.5E-01
ENSMUST00000062024	tumor suppressor candidate 5 [Source:MGI Symbol;Acc:MGI:3029307]		Q8C838	7.5	6.1E-05	5.8	4.0E-04	0.0	9.7E-01	-0.1	8.2E-01
ENSMUST00000062028	G protein-coupled receptor 61 [Source:MGI Symbol;Acc:MGI:2441719]		Q8C010	4.9	3.4E-03	4.2	7.0E-05	0.0	9.8E-01	-0.7	1.1E-01
ENSMUST00000062041	isoprenoid synthase domain containing [Source:MGI Symbol;Acc:MGI:1923097]		Q5RJG7	3.9	1.8E-03	-3.6	2.7E-02	0.3	6.2E-01	-1.5	3.6E-01
ENSMUST00000061213				2.8	1.0E-01	1.9	4.5E-01	1.6	4.0E-01	2.5	2.6E-01
ENSMUST00000062045	histone cluster 1, H1e [Source:MGI Symbol;Acc:MGI:1931527]		P43274	2.3	3.3E-02	-0.7	2.2E-01	1.4	3.2E-03	-0.8	1.8E-01
ENSMUST00000061234	PDLIM1 interacting kinase 1 like [Source:MGI Symbol;Acc:MGI:2385213]		Q8QZR7	3.2	1.9E-01	-1.6	6.4E-01	-2.5	3.1E-01	2.3	4.7E-01
ENSMUST00000062047	family with sequence similarity 110, member A [Source:MGI Symbol;Acc:MGI:1921097]		Q8R184	-2.2	8.2E-03	6.2	4.2E-04	-1.4	2.8E-01	-0.3	6.2E-01
ENSMUST00000062058	Lix1-like [Source:MGI Symbol;Acc:MGI:3036267]	G3X9C8		4.0	6.6E-05	-6.5	4.2E-06	0.4	1.8E-01	0.5	5.0E-01
ENSMUST00000062067	late endosomal/lysosomal adaptor, MAPK and MTOR activator 4 [Source:MGI Symbol;Acc:MGI:1913346]		Q8CF66	-7.8	2.3E-05	4.1	2.2E-03	-4.3	4.2E-03	-3.9	1.1E-03
ENSMUST00000062069	prostaglandin-endoperoxide synthase 1 [Source:MGI Symbol;Acc:MGI:97797]	Q543T1	P22437	-2.2	7.3E-04	-2.6	8.9E-03	-0.4	3.8E-01	-0.3	7.1E-01
ENSMUST00000062092	cell division cycle associated 4 [Source:MGI Symbol;Acc:MGI:1919213]		Q9CWM2	-2.3	1.3E-03	9.0	2.3E-06	-2.2	5.5E-02	0.0	9.9E-01
ENSMUST00000061262	podocalyxin-like 2 [Source:MGI Symbol;Acc:MGI:2442488]	G3X9D3		6.4	4.7E-02	3.9	2.4E-01	-0.7	8.3E-01	1.8	3.8E-01
ENSMUST00000062108	inhibitor of kappaB kinase epsilon [Source:MGI Symbol;Acc:MGI:1929612]		Q9R0T8	-1.7	5.4E-03	5.1	2.1E-03	1.7	1.7E-01	0.9	2.0E-01
ENSMUST00000062117	RAS related protein 2a [Source:MGI Symbol;Acc:MGI:97855]		Q80ZJ1	-2.3	5.6E-03	7.4	1.4E-05	-0.4	6.3E-01	-0.1	7.9E-01
ENSMUST00000062122	cardiomyopathy associated 5 [Source:MGI Symbol;Acc:MGI:1923719]	E9QLJ0		9.0	2.9E-06	4.4	1.9E-03	-0.4	7.0E-01	0.2	7.5E-01
ENSMUST00000062145	RIKEN cDNA 4933430I17 gene [Source:MGI Symbol;Acc:MGI:3045314]	Q8BHW4		6.7	1.1E-04	-4.0	3.9E-02	-0.3	7.5E-01	-0.5	7.6E-01
ENSMUST00000062147	actin, gamma, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:87906]	B1ATY1		-8.4	3.2E-02	-4.8	1.9E-03	0.7	1.8E-01	1.0	3.7E-01
ENSMUST00000062149	ring finger protein 144A [Source:MGI Symbol;Acc:MGI:1344401]		Q925F3	-4.8	6.6E-03	6.2	6.3E-03	-0.7	7.2E-01	-1.0	3.6E-01
ENSMUST00000062153	Rab interacting lysosomal protein-like 1 [Source:MGI Symbol;Acc:MGI:1922945]		Q9JJC6	3.4	1.8E-04	2.4	4.5E-03	-5.0	2.0E-04	-0.4	5.1E-01
ENSMUST00000062163	MAS-related GPR, member D [Source:MGI Symbol;Acc:MGI:3033142]	Q5UCB4	Q91ZB8	7.9	1.2E-05	1.9	3.8E-02	-5.1	9.3E-04	-0.2	7.8E-01
ENSMUST00000062182	predicted gene 4787 [Source:MGI Symbol;Acc:MGI:3646380]	B2RUD9		4.5	5.9E-04	7.0	5.8E-05	-2.5	6.4E-02	0.1	8.3E-01
ENSMUST00000062202	sushi, nidogen and EGF-like domains 1 [Source:MGI Symbol;Acc:MGI:3045960]			2.7	2.6E-03	0.7	7.7E-01	-0.3	8.8E-01	3.7	1.1E-01
ENSMUST00000061326	ubiquinol-cytochrome c reductase, complex III subunit VII [Source:MGI Symbol;Acc:MGI:107807]		Q9CQ69	-0.9	2.0E-01	0.2	8.1E-01	-0.2	7.2E-01	-1.2	1.0E-01
ENSMUST00000062211	glycerol-3-phosphate acyltransferase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:2684962]		Q14DK4	8.4	6.1E-06	3.7	4.7E-03	-0.4	6.4E-01	-0.3	6.5E-01
ENSMUST00000062213	sideroflexin 3 [Source:MGI Symbol;Acc:MGI:2137679]		Q91V61	-3.9	1.8E-02	8.1	8.8E-05	-1.3	3.5E-01	0.8	2.2E-01
ENSMUST00000062215	chemokine (C-X-C motif) receptor 5 [Source:MGI Symbol;Acc:MGI:103567]		Q04683	-3.6	6.0E-03	-4.5	4.1E-03	0.6	2.4E-01	0.7	5.9E-01
ENSMUST00000062216	empty spiracles homeobox 2 [Source:MGI Symbol;Acc:MGI:95388]		Q04744	7.3	6.2E-05	3.4	4.3E-04	0.4	5.0E-01	0.4	4.2E-01
ENSMUST00000062241	toll-like receptor 9 [Source:MGI Symbol;Acc:MGI:1932389]		Q9EQU3	3.8	9.0E-05	7.0	1.8E-04	-0.6	6.2E-01	0.0	9.4E-01
ENSMUST00000062246	tumor necrosis factor (ligand) superfamily, member 15 [Source:MGI Symbol;Acc:MGI:2180140]	F6VXB8		5.4	2.3E-05	0.3	8.0E-01	1.7	9.9E-02	-1.7	2.0E-01
ENSMUST00000062254	C-type lectin domain family 14, member a [Source:MGI Symbol;Acc:MGI:1914114]		Q8VCP9	7.9	3.2E-05	-1.1	1.2E-01	1.3	1.7E-02	0.4	5.4E-01
ENSMUST00000061390	fukutin related protein [Source:MGI Symbol;Acc:MGI:2447586]		Q8CG64	-0.9	1.0E-01	0.1	9.0E-01	1.0	5.1E-02	0.1	9.3E-01
ENSMUST00000062292	forkhead box C1 [Source:MGI Symbol;Acc:MGI:1347466]		Q61572	6.9	3.9E-05	5.8	4.2E-04	-1.5	2.4E-01	-0.9	2.0E-01
ENSMUST00000062304	leucine rich repeat containing 4 [Source:MGI Symbol;Acc:MGI:2182081]		Q99PH1	9.1	2.0E-05	7.5	3.9E-04	-0.7	6.6E-01	0.0	9.7E-01
ENSMUST00000062307	PHD finger protein 11A [Source:MGI Symbol;Acc:MGI:1918441]		Q8BVM9	1.5	3.3E-02	5.3	4.9E-04	-2.5	6.5E-02	-0.1	8.7E-01
ENSMUST00000062315	toll-like receptor 6 [Source:MGI Symbol;Acc:MGI:1341296]	Q3UV88		-5.0	1.3E-04	6.5	3.1E-04	0.5	6.8E-01	-0.3	7.1E-01
ENSMUST00000062355	RIKEN cDNA 4930470P17 gene [Source:MGI Symbol;Acc:MGI:1914887]	Q9D542		6.2	1.2E-03	3.0	2.0E-01	-0.4	8.4E-01	2.1	1.8E-01
ENSMUST00000062356	MARCKS-like 1 [Source:MGI Symbol;Acc:MGI:97143]		P28667	-3.8	4.0E-04	-4.4	1.5E-03	1.2	3.1E-02	-1.9	1.5E-01
ENSMUST00000062357	RIKEN cDNA 4930539E08 gene [Source:MGI Symbol;Acc:MGI:1925441]		Q8CC96	5.6	3.8E-06	-3.5	2.9E-04	-0.7	8.3E-02	-1.0	1.4E-01
ENSMUST00000062370	WD repeat domain 89 [Source:MGI Symbol;Acc:MGI:1919588]		Q9D0R9	5.5	3.1E-04	7.6	8.6E-05	-0.7	5.6E-01	-0.1	9.0E-01
ENSMUST00000062387	potassium inwardly-rectifying channel, subfamily J, member 9 [Source:MGI Symbol;Acc:MGI:108007]	Q544N3	P48543	5.7	1.1E-03	-1.8	7.2E-02	0.7	2.0E-01	-0.4	6.7E-01
ENSMUST00000062405	RAS, dexamethasone-induced 1 [Source:MGI Symbol;Acc:MGI:1270848]	Q5SWR8	O35626	4.2	2.9E-04	-0.1	8.0E-01	0.7	6.3E-02	-0.4	4.1E-01
ENSMUST00000062437	NK2 homeobox 6 [Source:MGI Symbol;Acc:MGI:97351]		P43688	6.6	1.6E-04	3.8	4.6E-03	-1.7	1.7E-01	-0.8	3.0E-01
ENSMUST00000062474	cytochrome P450, family 8, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1338044]			6.7	2.6E-04	2.4	2.6E-03	0.5	2.9E-01	0.3	5.6E-01
ENSMUST00000062483	GLI-Kruppel family member GLI2 [Source:MGI Symbol;Acc:MGI:95728]		Q0VGT2	9.6	2.1E-05	-3.7	7.1E-03	0.4	4.2E-01	-1.0	4.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000062492	prefoldin 5 [Source:MGI Symbol;Acc:MGI:1928753]	E9PVG3		-7.5	3.7E-05	4.0	1.5E-04	1.4	2.8E-02	-0.5	2.8E-01
ENSMUST00000062495	CUB domain containing protein 2 [Source:MGI Symbol;Acc:MGI:3045328]		Q8BQH6	8.5	1.3E-05	6.4	2.2E-04	-0.6	6.1E-01	-0.3	5.9E-01
ENSMUST00000062519	CREB3 regulatory factor [Source:MGI Symbol;Acc:MGI:1924378]		Q8CDG5	-3.4	2.1E-05	4.6	3.1E-03	-1.5	2.5E-01	0.5	4.7E-01
ENSMUST00000061483	brain expressed myelocytomatosis oncogene [Source:MGI Symbol;Acc:MGI:88184]	A0PJL6	Q6P8Z1	1.7	8.0E-02	0.8	4.3E-01	-0.7	4.2E-01	0.1	8.8E-01
ENSMUST00000062525	ring finger protein 149 [Source:MGI Symbol;Acc:MGI:2677438]		Q3U2C5	-6.4	3.1E-05	6.2	8.7E-05	1.1	2.2E-01	-0.6	3.1E-01
ENSMUST00000061496	transcription factor 7 like 2, T cell specific, HMG box [Source:MGI Symbol;Acc:MGI:1202879]	Q80WT9		-1.0	6.7E-01	3.1	3.1E-01	3.4	2.3E-01	-0.7	7.5E-01
ENSMUST00000061498	fucosyltransferase 4 [Source:MGI Symbol;Acc:MGI:95594]	Q544B8	Q11127	0.6	2.4E-01	0.8	2.4E-01	0.7	2.0E-01	0.5	4.4E-01
ENSMUST00000062528	cadherin 20 [Source:MGI Symbol;Acc:MGI:1346069]		Q9Z0M3	10.5	4.1E-05	5.5	5.2E-04	-2.7	4.6E-02	-0.8	2.8E-01
ENSMUST00000061508	zinc finger protein 358 [Source:MGI Symbol;Acc:MGI:2153740]	E9Q8M1		1.2	1.0E-01	1.6	8.5E-02	0.2	7.9E-01	-0.2	7.9E-01
ENSMUST00000062530	hexamethylene bis-acetamide inducible 2 [Source:MGI Symbol;Acc:MGI:1918309]		Q3TVI4	3.8	6.0E-04	8.1	2.4E-05	-0.6	5.9E-01	-0.2	6.7E-01
ENSMUST00000062560	lengsin, lens protein with glutamine synthetase domain [Source:MGI Symbol;Acc:MGI:2672844]		Q8CIX8	6.2	2.2E-04	4.3	1.0E-02	-0.6	6.7E-01	1.6	1.1E-01
ENSMUST00000062572	frizzled homolog 9 (Drosophila) [Source:MGI Symbol;Acc:MGI:1313278]		Q9R216	8.3	1.2E-05	-7.5	2.4E-05	-0.1	6.9E-01	-0.4	6.6E-01
ENSMUST00000062580	intersectin 2 [Source:MGI Symbol;Acc:MGI:1338049]	E9QNG1		-3.0	1.5E-04	4.9	6.6E-03	0.6	6.6E-01	-0.9	3.3E-01
ENSMUST00000061537				-0.7	3.8E-01	-1.8	5.2E-02	-1.8	1.4E-02	-0.7	4.5E-01
ENSMUST00000062601	ribosomal protein L34 [Source:MGI Symbol;Acc:MGI:1915686]		Q9D1R9	-2.8	1.2E-02	6.3	5.2E-04	-0.5	7.1E-01	-0.5	4.6E-01
ENSMUST00000062606	uroplakin 3B [Source:MGI Symbol;Acc:MGI:2140882]			8.0	9.8E-06	6.6	1.9E-04	0.0	9.7E-01	0.0	9.8E-01
ENSMUST00000062609	zinc finger with KRAB and SCAN domains 4 [Source:MGI Symbol;Acc:MGI:3649412]	Q5SZT6		3.4	8.4E-04	2.6	2.6E-03	-0.6	2.6E-01	0.4	4.7E-01
ENSMUST00000061568	solute carrier family 36 (proton/amino acid symporter), member 4 [Source:MGI Symbol;Acc:MGI:2442595]			-0.5	2.4E-01	1.2	7.1E-02	1.2	2.4E-02	-0.5	3.4E-01
ENSMUST00000062613	testis development related protein [Source:MGI Symbol;Acc:MGI:1919398]		Q8C5P7	2.5	1.7E-02	4.8	3.2E-04	-2.1	5.4E-02	-0.3	6.0E-01
ENSMUST00000062623	tigger transposable element derived 4 [Source:MGI Symbol;Acc:MGI:2685264]		Q8BUZ3	7.0	3.6E-06	-1.2	7.0E-02	0.8	5.1E-02	0.1	9.1E-01
ENSMUST00000062626	tigger transposable element derived 2 [Source:MGI Symbol;Acc:MGI:1915390]		Q0VBL1	-1.6	1.4E-02	2.6	2.5E-03	0.1	8.3E-01	-0.3	6.2E-01
ENSMUST00000062629	nucleophosmin/nucleoplasmin 2 [Source:MGI Symbol;Acc:MGI:1890811]		Q80W85	4.7	4.1E-04	-1.1	4.5E-01	1.4	1.5E-01	-1.9	2.5E-01
ENSMUST00000062638	RIKEN cDNA 4930563D23 gene [Source:MGI Symbol;Acc:MGI:1922578]		Q8CDS7	7.4	2.9E-05	5.0	2.5E-04	-2.3	4.5E-02	-0.1	8.1E-01
ENSMUST00000062654	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1 [Source:MGI Symbol;Acc:MGI:2441705		Q3U129	4.1	2.2E-04	5.2	2.7E-04	-2.1	6.9E-02	-0.5	3.9E-01
ENSMUST00000062657	lymphocyte antigen 6 complex, locus G5B [Source:MGI Symbol;Acc:MGI:2385809]	N0E6I7	Q8K1T4	-4.0	3.1E-02	3.4	8.3E-04	-1.4	5.7E-02	-0.3	5.3E-01
ENSMUST00000062678	ribosomal RNA processing 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1203500]		P56183	-3.1	4.2E-05	-5.9	2.8E-02	0.7	4.1E-01	3.3	1.7E-01
ENSMUST00000062683	keratin associated protein 9-3 [Source:MGI Symbol;Acc:MGI:1922836]		Q3V2C1	6.4	3.5E-04	6.8	3.0E-03	-0.8	6.8E-01	0.0	9.9E-01
ENSMUST00000062709	homeobox B13 [Source:MGI Symbol;Acc:MGI:107730]		P70321	7.5	1.8E-05	3.6	9.4E-04	0.9	2.2E-01	-0.2	7.8E-01
ENSMUST00000062723	acid phosphatase, prostate [Source:MGI Symbol;Acc:MGI:1928480]		Q8CE08	-3.6	6.7E-05	-1.0	1.9E-01	0.9	8.0E-02	-0.5	4.8E-01
ENSMUST00000062747	Kruppel-like factor 17 [Source:MGI Symbol;Acc:MGI:2181068]		Q8CFA7	8.5	7.4E-06	8.3	3.6E-06	0.0	9.9E-01	0.0	9.1E-01
ENSMUST00000062753	RIKEN cDNA D030056L22 gene [Source:MGI Symbol;Acc:MGI:3583960]	Q3UMB2	Q8VCE4	-4.1	2.3E-02	7.0	2.4E-04	-0.6	6.5E-01	-0.4	6.0E-01
ENSMUST00000061639	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2142062]		Q68FG3	0.0	9.7E-01	0.0	9.3E-01	0.7	1.2E-01	0.7	1.8E-01
ENSMUST00000062759	chemokine (C-C motif) receptor 10 [Source:MGI Symbol;Acc:MGI:1096320]		Q9JL21	5.5	1.5E-05	5.5	7.4E-04	-1.5	2.5E-01	-1.0	1.7E-01
ENSMUST00000061656	RPTOR independent companion of MTOR, complex 2 [Source:MGI Symbol;Acc:MGI:1926007]		Q6QI06	0.3	4.3E-01	-0.3	5.8E-01	0.0	9.9E-01	0.6	2.4E-01
ENSMUST00000062769	centrin 1 [Source:MGI Symbol;Acc:MGI:1347086]		P41209	5.8	5.1E-04	5.6	5.6E-03	-0.4	8.3E-01	-1.4	1.5E-01
ENSMUST00000062784	family with sequence similarity 26, member F [Source:MGI Symbol;Acc:MGI:2443082]		Q8C9E8	2.4	8.4E-03	3.0	8.3E-04	0.6	2.6E-01	-0.6	2.8E-01
ENSMUST00000062789	laccase (multicopper oxidoreductase) domain containing 1 [Source:MGI Symbol;Acc:MGI:2445077]		Q8BZT9	3.4	3.4E-03	6.2	7.1E-04	-0.6	6.4E-01	-0.6	4.5E-01
ENSMUST00000061681	predicted gene 7334 [Source:MGI Symbol;Acc:MGI:3647393]	Q52L83	P50615	0.5	8.0E-01	-0.8	7.1E-01	-1.8	3.1E-01	-0.6	7.8E-01
ENSMUST00000062802	LYR motif containing 2 [Source:MGI Symbol;Acc:MGI:1917573]		Q8R033	-6.1	4.3E-05	3.0	1.9E-03	0.1	8.8E-01	-0.7	2.5E-01
ENSMUST00000062806	leukocyte cell-derived chemotaxin 2 [Source:MGI Symbol;Acc:MGI:1278342]			5.3	9.0E-04	5.2	5.0E-03	-0.5	7.6E-01	0.2	7.8E-01
ENSMUST00000062821	EMI domain containing 1 [Source:MGI Symbol;Acc:MGI:2155091]	Q5SUT2	Q91VF5	7.1	2.8E-03	6.2	3.4E-04	-0.6	6.0E-01	-0.4	5.2E-01
ENSMUST00000062844	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI:1889505]	Q3TVJ9	Q9Z222	-2.5	1.0E-02	5.3	3.5E-04	0.5	6.2E-01	1.3	5.3E-02
ENSMUST00000062862	insulin-like growth factor 1 [Source:MGI Symbol;Acc:MGI:96432]	Q8CAR0		7.7	1.4E-04	2.2	1.1E-02	-1.3	7.5E-02	-0.1	8.2E-01
ENSMUST00000062869	olfactory receptor 330 [Source:MGI Symbol;Acc:MGI:3030164]	Q8VGD9		6.0	5.8E-04	6.5	1.1E-04	-1.5	2.0E-01	0.3	6.1E-01
ENSMUST00000062879	predicted gene 5414 [Source:MGI Symbol;Acc:MGI:3646939]	Q6IFZ8		8.2	3.1E-05	5.2	7.1E-05	0.6	3.8E-01	0.1	8.4E-01
ENSMUST00000062904	DnaJ (Hsp40) homolog, subfamily C, member 11 [Source:MGI Symbol;Acc:MGI:2443386]		Q5U458	-2.7	7.5E-03	-1.9	4.4E-02	1.7	5.8E-03	-0.1	9.1E-01
ENSMUST00000062915	GDP-D-glucose phosphorylase 1 [Source:MGI Symbol;Acc:MGI:2443429]		Q3TLS3	2.7	1.5E-03	6.2	1.7E-03	-0.4	8.0E-01	-1.6	8.2E-02
ENSMUST00000062917	IQ motif containing F3 [Source:MGI Symbol;Acc:MGI:1915515]		Q9D498	5.7	1.2E-03	6.9	9.7E-04	-0.3	8.5E-01	0.8	3.6E-01
ENSMUST00000062944	gap junction protein, alpha 8 [Source:MGI Symbol;Acc:MGI:99953]	Q548M7	P28236	7.4	4.3E-05	6.4	1.6E-04	-0.6	6.2E-01	-0.8	1.8E-01
ENSMUST00000062957	tetratricopeptide repeat domain 7B [Source:MGI Symbol;Acc:MGI:2144724]	E9Q6P5		-1.9	3.0E-03	8.8	4.8E-04	-0.4	8.2E-01	1.1	1.7E-01
ENSMUST00000062964	olfactory receptor 1412 [Source:MGI Symbol;Acc:MGI:3031246]	Q8VET3		6.5	3.6E-04	7.0	1.5E-03	-0.1	9.6E-01	0.2	7.9E-01
ENSMUST00000062967	coiled-coil domain containing 64B [Source:MGI Symbol;Acc:MGI:2388267]		Q8CHW5	3.4	2.3E-03	-3.7	7.3E-02	0.8	4.7E-01	-0.1	9.5E-01
ENSMUST00000062978	cDNA sequence BC030500 [Source:MGI Symbol;Acc:MGI:2447770]	Q8K0R8		5.8	5.4E-04	-6.6	1.8E-05	0.8	4.0E-02	-0.9	3.1E-01
ENSMUST00000061757	zinc finger protein 62 [Source:MGI Symbol;Acc:MGI:99662]		Q8C827	-4.9	6.0E-02	-3.5	2.3E-01	0.2	8.8E-01	-1.1	7.2E-01
ENSMUST00000062990	schlafen like 1 [Source:MGI Symbol;Acc:MGI:3045330]		Q8BHW9	6.0	2.5E-05	6.9	8.4E-05	-1.5	2.2E-01	-1.2	6.9E-02
ENSMUST00000061767	CREB/ATF bZIP transcription factor [Source:MGI Symbol;Acc:MGI:2675296]			0.9	3.6E-01	-0.5	6.9E-01	-1.1	2.5E-01	0.3	7.8E-01
ENSMUST00000063004	galactose-3-O-sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1858277]		Q9JHE4	6.2	5.3E-04	7.7	1.6E-04	-2.5	1.2E-01	0.4	5.9E-01
ENSMUST00000061772	RNA binding motif protein 15 [Source:MGI Symbol;Acc:MGI:2443205]	Q0VBL3		0.2	6.4E-01	1.4	3.6E-02	1.0	5.4E-02	-0.2	7.0E-01
ENSMUST00000061786	transmembrane protein 220 [Source:MGI Symbol;Acc:MGI:2443691]		Q8BP07	1.6	4.6E-02	1.4	1.7E-01	0.6	4.6E-01	0.7	3.8E-01
ENSMUST00000063042	galactosidase, beta 1 [Source:MGI Symbol;Acc:MGI:88151]	Q3TAW7	P23780	-1.5	1.0E-02	6.0	9.1E-04	-0.6	6.6E-01	-0.5	4.7E-01
ENSMUST00000063062	chitinase-like 3 [Source:MGI Symbol;Acc:MGI:1330860]		O35744	-9.0	6.1E-06	6.2	1.9E-03	-0.7	6.6E-01	0.4	6.4E-01
ENSMUST00000063063	sex comb on midleg-like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2446140]		Q80VG1	5.2	1.2E-04	5.0	4.0E-05	-3.9	1.8E-03	-0.2	6.5E-01
ENSMUST00000063076	5-hydroxytryptamine (serotonin) receptor 1F [Source:MGI Symbol;Acc:MGI:99842]	Q543V2	Q02284	5.3	2.2E-03	5.6	5.7E-05	0.1	8.6E-01	-0.4	4.4E-01
ENSMUST00000063084	X-box binding protein 1 [Source:MGI Symbol;Acc:MGI:98970]		O35426	-6.3	2.6E-06	2.4	1.3E-02	-4.1	1.9E-03	-0.9	1.8E-01
ENSMUST00000063103	RIKEN cDNA 1700048O20 gene [Source:MGI Symbol;Acc:MGI:1920637]	F6VFT9		6.5	5.5E-07	8.9	5.4E-05	-0.7	6.0E-01	-0.1	8.4E-01
ENSMUST00000063116	msh homeobox 1 [Source:MGI Symbol;Acc:MGI:97168]		P13297	6.6	1.4E-04	-5.5	1.1E-05	-0.1	7.1E-01	-0.1	9.0E-01
ENSMUST00000063117	glutathione transferase zeta 1 (maleylacetoacetate isomerase) [Source:MGI Symbol;Acc:MGI:1341859]		Q9WVL0	1.2	2.3E-02	6.4	1.0E-04	-2.4	6.0E-02	-0.5	4.1E-01
ENSMUST00000063119	relaxin family peptide receptor 4 [Source:MGI Symbol;Acc:MGI:2182926]	Q5Y985	Q7TQP4	7.5	4.9E-05	7.0	1.0E-04	-0.1	9.0E-01	0.4	4.8E-01
ENSMUST00000063136	otopetrin 1 [Source:MGI Symbol;Acc:MGI:2388363]	E9QMU2		5.1	3.0E-02	5.1	1.1E-02	0.0	9.8E-01	-1.1	3.4E-01
ENSMUST00000061837	neuralized E3 ubiquitin protein ligase 4 [Source:MGI Symbol;Acc:MGI:1921092]		Q5NCX5	-1.6	7.1E-02	-2.8	7.7E-02	1.2	1.5E-01	2.4	1.1E-01
ENSMUST00000063138	male-specific lethal 3-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1920640]	G3X992		3.5	1.2E-03	1.9	9.8E-02	-0.3	7.4E-01	0.5	5.8E-01
ENSMUST00000061852	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2441769]		Q8K4J0	1.4	4.0E-02	1.7	5.3E-02	0.2	7.4E-01	-0.1	8.9E-01
ENSMUST00000063140	hypocretin (orexin) receptor 2 [Source:MGI Symbol;Acc:MGI:2680765]		P58308	5.6	3.8E-04	4.3	2.8E-04	-0.3	6.7E-01	0.0	9.3E-01
ENSMUST00000061859	DNA segment, Chr 17, human D6S53E [Source:MGI Symbol;Acc:MGI:90673]	B2RS43	Q9Z1R4	0.2	6.7E-01	0.9	2.2E-01	1.6	1.5E-02	0.8	1.9E-01
ENSMUST00000063166	family with sequence similarity 71, member B [Source:MGI Symbol;Acc:MGI:3650836]		Q5STT6	6.2	3.1E-04	7.1	5.0E-04	-0.1	9.7E-01	-0.2	7.7E-01
ENSMUST00000063192	transmembrane protein 150C [Source:MGI Symbol;Acc:MGI:3041258]		Q8C8S3	7.2	1.1E-04	-0.8	1.8E-01	0.6	1.4E-01	0.1	8.2E-01
ENSMUST00000063216	RIKEN cDNA 5730507C01 gene [Source:MGI Symbol;Acc:MGI:1917882]	Q3UT17		3.3	5.2E-03	4.8	2.2E-03	0.8	4.7E-01	0.5	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000061882	malonyl CoA:ACP acyltransferase (mitochondrial) [Source:MGI Symbol;Acc:MGI:2388651]		Q8R3F5	-0.7	2.2E-01	0.1	8.5E-01	0.6	2.2E-01	-0.2	7.8E-01
ENSMUST00000063219	poly(A) binding protein, cytoplasmic 2 [Source:MGI Symbol;Acc:MGI:1349723]	Q62029		7.3	4.3E-05	4.6	7.1E-04	0.1	9.2E-01	0.0	9.9E-01
ENSMUST00000063232	Ewing sarcoma breakpoint region 1 [Source:MGI Symbol;Acc:MGI:99960]	Q8BQU4		5.5	1.7E-04	1.7	3.0E-02	0.4	4.6E-01	0.2	7.6E-01
ENSMUST00000063262	zinc finger protein 68 [Source:MGI Symbol;Acc:MGI:1344427]	Q9Z116		-3.0	1.6E-03	-3.5	1.5E-02	-0.1	8.3E-01	-0.6	6.3E-01
ENSMUST00000063263	IQ motif containing J [Source:MGI Symbol;Acc:MGI:3644166]		Q8BPW0	7.5	1.6E-04	-4.7	1.2E-02	0.4	5.1E-01	1.1	5.0E-01
ENSMUST00000063272	transmembrane protein 175 [Source:MGI Symbol;Acc:MGI:1919642]		Q9CXY1	-5.3	2.7E-04	4.4	1.4E-02	-1.0	5.4E-01	0.1	9.1E-01
ENSMUST00000063278	angiotensinogen (serpin peptidase inhibitor, clade A, member 8) [Source:MGI Symbol;Acc:MGI:87963]	Q3UTR7		6.3	1.8E-04	6.2	3.4E-03	0.5	7.4E-01	-0.7	4.8E-01
ENSMUST00000061936	bonuclease, RNase A family, 2A (liver, eosinophil-derived neurotoxin) [Source:MGI Symbol;Acc:MGI:189046	Q8K196		-0.1	8.9E-01	-0.9	3.5E-01	-1.7	4.7E-02	-1.0	3.0E-01
ENSMUST00000063289	olfactory receptor 284 [Source:MGI Symbol;Acc:MGI:3030118]	Q8VET7		6.6	1.0E-04	-2.8	3.0E-03	0.4	3.6E-01	-0.3	6.7E-01
ENSMUST00000063292	keratin 73 [Source:MGI Symbol;Acc:MGI:3607712]		Q6NXH9	7.4	3.7E-05	6.9	4.2E-04	-0.6	6.5E-01	-0.7	3.5E-01
ENSMUST00000063317	a disintegrin and metallopeptidase domain 6B [Source:MGI Symbol;Acc:MGI:2444636]	Q6IMH7		6.0	1.5E-04	7.1	1.1E-03	1.3	3.8E-01	-0.4	5.9E-01
ENSMUST00000061973	three prime repair exonuclease 1 [Source:MGI Symbol;Acc:MGI:1328317]		Q91XB0	0.4	7.8E-01	4.1	2.2E-01	5.4	4.9E-02	1.7	4.8E-01
ENSMUST00000061986	src homology 2 domain-containing transforming protein B [Source:MGI Symbol;Acc:MGI:98294]		Q6PD21	1.2	4.2E-01	1.5	3.5E-01	-1.3	3.7E-01	-1.6	3.0E-01
ENSMUST00000063318	olute carrier family 16 (monocarboxylic acid transporters), member 7 [Source:MGI Symbol;Acc:MGI:1330284	Q149G3	O70451	3.3	8.6E-04	5.3	1.2E-03	-0.6	6.3E-01	0.8	2.8E-01
ENSMUST00000061995	SPRY domain containing 4 [Source:MGI Symbol;Acc:MGI:1913951]		Q91WK1	0.3	7.0E-01	2.2	3.3E-02	0.3	7.1E-01	-1.6	6.3E-02
ENSMUST00000063414	TBC1 domain family, member 22a [Source:MGI Symbol;Acc:MGI:1289265]		Q8R5A6	-2.0	1.0E-03	-4.1	1.4E-03	0.7	1.3E-01	1.1	2.6E-01
ENSMUST00000063417	serine/arginine-rich splicing factor 7 [Source:MGI Symbol;Acc:MGI:1926232]	Q3THA6	Q8BL97	-5.2	5.5E-06	-4.2	1.2E-02	0.2	8.0E-01	-0.6	6.7E-01
ENSMUST00000063433	eyes absent 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109341]		O08575	7.1	3.3E-03	7.3	1.3E-03	-0.8	6.5E-01	-0.1	8.7E-01
ENSMUST00000062015	StAR-related lipid transfer (START) domain containing 13 [Source:MGI Symbol;Acc:MGI:2385331]	F8WIY7		3.3	1.2E-01	-0.3	9.0E-01	-2.1	3.0E-01	1.5	4.9E-01
ENSMUST00000063444	RasGEF domain family, member 1C [Source:MGI Symbol;Acc:MGI:1921813]		Q9D300	8.4	2.0E-05	7.4	1.6E-04	-0.9	5.0E-01	-0.8	2.3E-01
ENSMUST00000063465	wingless-type MMTV integration site family, member 5A [Source:MGI Symbol;Acc:MGI:98958]		P22725	10.5	5.8E-05	4.5	1.6E-02	-1.1	4.9E-01	-0.7	5.1E-01
ENSMUST00000062037	C-type lectin domain family 4, member g [Source:MGI Symbol;Acc:MGI:1923113]		Q8BNX1	3.4	4.9E-02	2.7	1.4E-01	-1.8	3.0E-01	-1.1	4.3E-01
ENSMUST00000063481	RIKEN cDNA 9830107B12 gene [Source:MGI Symbol;Acc:MGI:3608415]	D3Z5D6		-2.6	5.4E-04	1.7	7.8E-02	-2.5	1.8E-02	-0.3	6.6E-01
ENSMUST00000063492	R-spondin 2 [Source:MGI Symbol;Acc:MGI:1922667]		Q8BFU0	7.6	5.5E-05	1.2	3.2E-01	0.0	9.7E-01	1.0	3.1E-01
ENSMUST00000063507	mcf.2 transforming sequence [Source:MGI Symbol;Acc:MGI:96932]	A2AEU1		5.6	8.5E-03	0.5	5.8E-01	2.1	9.6E-03	-0.6	4.5E-01
ENSMUST00000063508	glutamate receptor, ionotropic, AMPA4 (alpha 4) [Source:MGI Symbol;Acc:MGI:95811]		Q9Z2W8	5.7	3.1E-02	2.7	1.4E-03	-2.2	3.8E-03	-0.9	1.1E-01
ENSMUST00000063517	spermatogenesis associated, serine-rich 2 [Source:MGI Symbol;Acc:MGI:1919822]		Q8K1N4	7.3	6.5E-05	-6.4	2.4E-04	-0.1	9.0E-01	-1.4	2.6E-01
ENSMUST00000063520	N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source:MGI Symbol;Acc:MGI:1919367]		Q6PGB6	-2.1	8.3E-03	-1.9	7.9E-03	0.3	3.6E-01	0.0	9.4E-01
ENSMUST00000063523	protease, serine 58 [Source:MGI Symbol;Acc:MGI:3608323]		Q8BW11	6.0	3.5E-04	-1.5	3.1E-02	0.4	2.6E-01	-0.3	6.5E-01
ENSMUST00000063524	RIKEN cDNA 5031410I06 gene [Source:MGI Symbol;Acc:MGI:3036277]	E9Q4E0		9.0	1.8E-05	-0.6	3.6E-01	0.6	1.2E-01	-0.5	4.1E-01
ENSMUST00000063531	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) [Source:MGI Symbol;Acc:MGI:105388]		Q60772	-4.0	5.9E-03	-2.6	2.2E-02	0.8	1.4E-01	1.2	2.4E-01
ENSMUST00000062118	phosphatidylinositol glycan anchor biosynthesis, class V [Source:MGI Symbol;Acc:MGI:2442480]		Q7TPN3	0.0	9.8E-01	1.5	3.1E-02	1.3	2.4E-02	-0.2	6.7E-01
ENSMUST00000063542	N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source:MGI Symbol;Acc:MGI:1919367]		Q6PGB6	-5.2	5.9E-05	7.1	1.1E-05	-1.9	6.6E-02	0.0	9.9E-01
ENSMUST00000062125	RIKEN cDNA 1810026J23 gene [Source:MGI Symbol;Acc:MGI:1917023]		Q8BGX2	-0.6	1.8E-01	0.1	8.7E-01	1.1	2.9E-02	0.4	5.2E-01
ENSMUST00000063551	regulator of G-protein signalling 7 binding protein [Source:MGI Symbol;Acc:MGI:106334]		Q8BQP9	6.0	6.1E-06	6.3	2.9E-04	-0.5	6.9E-01	-0.8	2.6E-01
ENSMUST00000063563	nanos homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2676627]	I6ZHM2	P60322	7.7	7.9E-05	5.9	3.6E-04	-0.9	4.4E-01	-0.1	8.7E-01
ENSMUST00000063570	toll-like receptor 11 [Source:MGI Symbol;Acc:MGI:3045226]		Q6R5P0	5.2	1.1E-03	-1.4	8.0E-01	6.9	5.4E-02	-0.1	9.8E-01
ENSMUST00000062148	malignant T cell amplified sequence 2 [Source:MGI Symbol;Acc:MGI:1913655]		Q9CQ21	0.4	5.7E-01	1.0	2.9E-01	-0.4	6.0E-01	-0.9	2.7E-01
ENSMUST00000063578	growth hormone releasing hormone receptor [Source:MGI Symbol;Acc:MGI:95710]		P32082	7.3	3.6E-05	-1.7	3.0E-01	1.7	1.1E-01	-1.4	4.4E-01
ENSMUST00000063594	neuropilin 2 [Source:MGI Symbol;Acc:MGI:1100492]	Q8QZY7	O35375	4.2	1.5E-02	2.8	1.0E-03	-1.2	5.5E-02	-0.7	1.8E-01
ENSMUST00000062161	transmembrane protein 232 [Source:MGI Symbol;Acc:MGI:2685786]		Q5K6N0	4.7	4.5E-02	4.9	5.9E-02	-0.6	8.2E-01	-0.7	6.4E-01
ENSMUST00000063641	small integral membrane protein 11 [Source:MGI Symbol;Acc:MGI:1916186]		Q99J19	-4.1	4.2E-05	7.8	2.7E-05	-0.6	6.0E-01	-0.5	3.7E-01
ENSMUST00000062181	zinc finger protein 146 [Source:MGI Symbol;Acc:MGI:1347092]		Q8BQN6	-1.0	1.0E-01	-1.3	5.6E-02	-1.5	6.3E-03	-1.2	9.1E-02
ENSMUST00000063642	coiled-coil domain containing 30 [Source:MGI Symbol;Acc:MGI:1920582]		Q8BVF4	7.2	2.4E-04	5.6	5.5E-04	0.4	7.4E-01	-0.8	2.7E-01
ENSMUST00000063645	mbt domain containing 1 [Source:MGI Symbol;Acc:MGI:2143977]	A2ABG6		5.1	1.9E-03	1.9	5.3E-02	-0.4	5.5E-01	0.4	6.1E-01
ENSMUST00000063661	ATPase, H+ transporting, lysosomal V1 subunit A [Source:MGI Symbol;Acc:MGI:1201780]		P50516	-8.5	1.0E-04	6.2	2.4E-05	-2.5	2.1E-02	-0.4	4.4E-01
ENSMUST00000063672	whirlin [Source:MGI Symbol;Acc:MGI:2682003]		Q80VW5	7.7	6.9E-05	-5.8	3.8E-02	0.0	9.8E-01	2.0	4.4E-01
ENSMUST00000063690	dehydrogenase/reductase (SDR family) member 9 [Source:MGI Symbol;Acc:MGI:2442798]	Q148Q4	Q58NB6	-5.3	1.7E-06	-1.5	1.5E-01	-0.3	6.0E-01	-2.5	5.4E-02
ENSMUST00000063694	Kruppel-like factor 13 [Source:MGI Symbol;Acc:MGI:1354948]		Q9JJZ6	-3.8	5.5E-06	7.2	1.2E-04	-0.6	6.5E-01	-0.5	4.5E-01
ENSMUST00000062232	neural retina leucine zipper gene [Source:MGI Symbol;Acc:MGI:102567]	Q543Y0	P54846	3.1	1.6E-01	6.6	1.1E-02	-0.5	8.4E-01	-4.0	2.0E-02
ENSMUST00000063707	sperm tail PG rich repeat containing 1 [Source:MGI Symbol;Acc:MGI:1926056]		Q9D2F5	4.7	3.2E-04	3.3	7.7E-04	-0.4	5.3E-01	0.1	8.5E-01
ENSMUST00000063710	zinc finger protein 217 [Source:MGI Symbol;Acc:MGI:2685408]	Q3U0X6		-7.3	1.2E-03	6.3	1.0E-04	1.1	2.7E-01	0.1	8.0E-01
ENSMUST00000063747	scribbled homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2145950]		Q80U72	-6.6	2.8E-04	8.0	5.7E-05	-0.6	6.6E-01	-0.6	2.8E-01
ENSMUST00000062264	nuclear casein kinase and cyclin-dependent kinase substrate 1 [Source:MGI Symbol;Acc:MGI:1934811]		Q80XU3	-0.8	1.8E-01	0.4	5.4E-01	0.7	2.1E-01	-0.6	4.2E-01
ENSMUST00000063750	retinoic acid receptor, beta [Source:MGI Symbol;Acc:MGI:97857]	Q6DFX0	P22605	3.3	5.6E-04	2.5	1.1E-02	-3.3	5.3E-03	1.1	1.1E-01
ENSMUST00000063761	carnitine palmitoyltransferase 1c [Source:MGI Symbol;Acc:MGI:2446526]		Q8BGD5	8.0	1.5E-05	8.1	5.4E-05	-1.5	2.8E-01	-0.4	4.6E-01
ENSMUST00000063771	regulator of G-protein signaling 14 [Source:MGI Symbol;Acc:MGI:1859709]		P97492	-4.6	6.1E-04	-1.1	1.1E-01	-3.6	1.1E-04	-1.0	1.5E-01
ENSMUST00000063775	low density lipoprotein receptor class A domain containing 4 [Source:MGI Symbol;Acc:MGI:1277150]	Q4VAH9	Q8BWJ4	3.8	1.4E-04	-4.0	1.9E-03	0.0	9.6E-01	-1.0	3.4E-01
ENSMUST00000062322	roxisome proliferative activated receptor, gamma, coactivator-related 1 [Source:MGI Symbol;Acc:MGI:238509		Q6NZN1	-1.0	7.5E-01	-0.5	8.4E-01	-2.5	2.8E-01	-3.0	3.3E-01
ENSMUST00000063788	solute carrier family 25, member 42 [Source:MGI Symbol;Acc:MGI:1920345]		Q8R0Y8	5.6	4.7E-03	6.3	2.0E-03	-0.2	9.1E-01	-0.3	7.1E-01
ENSMUST00000063814	glucosamine-6-phosphate deaminase 1 [Source:MGI Symbol;Acc:MGI:1347054]		O88958	-4.8	3.5E-05	-2.1	3.5E-02	1.4	2.2E-02	-0.3	7.6E-01
ENSMUST00000063816	RIKEN cDNA D630039A03 gene [Source:MGI Symbol;Acc:MGI:2442889]	Q8K0M7		6.1	3.5E-05	6.3	8.4E-06	0.3	6.7E-01	-0.4	3.5E-01
ENSMUST00000062368	DEAH (Asp-Glu-Ala-His) box polypeptide 30 [Source:MGI Symbol;Acc:MGI:1920081]		Q99PU8	2.6	7.3E-02	3.5	6.4E-02	-0.6	6.9E-01	-1.5	2.4E-01
ENSMUST00000062369	zinc finger and BTB domain containing 14 [Source:MGI Symbol;Acc:MGI:1195345]	Q544H8	Q08376	-0.8	8.2E-01	-1.8	7.6E-01	1.1	7.7E-01	2.1	6.9E-01
ENSMUST00000063824	RAS protein activator like 3 [Source:MGI Symbol;Acc:MGI:2444128]		Q8C2K5	-4.7	2.1E-04	5.0	1.6E-03	-0.2	8.7E-01	0.3	6.9E-01
ENSMUST00000062372	reelin [Source:MGI Symbol;Acc:MGI:103022]		Q60841	4.6	1.1E-01	5.4	5.9E-02	-3.1	3.2E-01	-3.8	5.3E-02
ENSMUST00000063854	protein phosphatase 4, regulatory subunit 2 [Source:MGI Symbol;Acc:MGI:3027896]			-3.3	5.9E-05	5.0	8.6E-03	-0.7	6.2E-01	0.0	9.8E-01
ENSMUST00000062389	polycomb group ring finger 5 [Source:MGI Symbol;Acc:MGI:1923505]		Q3UK78	1.5	4.3E-01	-4.0	2.0E-01	-2.9	1.0E-01	2.6	3.8E-01
ENSMUST00000063871	cerebellin 3 precursor protein [Source:MGI Symbol;Acc:MGI:1889286]		Q9JHG0	5.3	2.0E-05	6.7	1.4E-04	2.1	6.3E-02	-0.4	5.3E-01
ENSMUST00000062428	zinc finger protein 784 [Source:MGI Symbol;Acc:MGI:3606042]	B2RVK6	Q8BI69	-1.0	1.4E-01	1.2	1.7E-01	1.2	1.0E-01	-1.1	1.8E-01
ENSMUST00000063886	activin receptor IIA [Source:MGI Symbol;Acc:MGI:102806]	A2AI38	P27038	1.7	2.2E-02	6.7	2.6E-04	-0.5	6.7E-01	-0.7	3.3E-01
ENSMUST00000062451	mucin 6, gastric [Source:MGI Symbol;Acc:MGI:2663233]	F8WIM6		7.7	4.2E-02	7.5	2.1E-02	-2.5	4.6E-01	-2.4	2.5E-01
ENSMUST00000063888	phospholipase D family, member 4 [Source:MGI Symbol;Acc:MGI:2144765]		Q8BG07	-3.0	9.5E-03	4.7	1.4E-03	-2.6	5.8E-02	-0.7	3.7E-01
ENSMUST00000063918	trans-acting transcription factor 8 [Source:MGI Symbol;Acc:MGI:2443471]	Q5QR90	Q8BMJ8	7.2	1.3E-04	8.9	7.1E-05	-0.7	6.1E-01	-0.1	8.8E-01
ENSMUST00000063956	CD177 antigen [Source:MGI Symbol;Acc:MGI:1916141]		Q8R2S8	-8.3	1.9E-07	-6.1	4.1E-05	-1.0	2.5E-02	-2.4	5.4E-02
ENSMUST00000063977	protein phosphatase 1, regulatory subunit 36 [Source:MGI Symbol;Acc:MGI:2684916]		D3Z0R2	6.9	6.2E-05	7.9	4.6E-05	-0.6	6.0E-01	-0.1	9.0E-01
ENSMUST00000063980	zinc finger with KRAB and SCAN domains 7 [Source:MGI Symbol;Acc:MGI:3040678]	E9PVW1		3.1	3.7E-03	-4.2	9.1E-05	0.1	8.6E-01	0.8	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000063982	frizzled homolog 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:108571]		Q9EQD0	3.8	4.4E-05	-5.7	4.7E-04	0.7	1.6E-01	0.0	1.0E+00
ENSMUST00000063989	zinc finger protein 438 [Source:MGI Symbol;Acc:MGI:2444919]	Q8BFX2		2.5	3.4E-03	8.1	3.0E-04	-1.3	4.4E-01	1.1	1.4E-01
ENSMUST00000064016	G protein-coupled receptor 17 [Source:MGI Symbol;Acc:MGI:3584514]		Q6NS65	9.1	1.3E-05	3.3	3.7E-03	-0.2	8.4E-01	0.3	6.8E-01
ENSMUST00000064035	stonin 1 [Source:MGI Symbol;Acc:MGI:1924307]		Q8CDJ8	4.9	3.2E-02	6.9	2.3E-04	-0.1	9.3E-01	-0.8	2.7E-01
ENSMUST00000062562	apolipoprotein L 7c [Source:MGI Symbol;Acc:MGI:1920912]	Q8C6E1		0.9	1.5E-01	6.9	2.9E-04	5.7	6.1E-04	-0.3	6.9E-01
ENSMUST00000064054	synaptotagmin I [Source:MGI Symbol;Acc:MGI:99667]	H6RXZ1	P46096	6.2	2.5E-02	6.3	7.9E-05	-1.9	1.0E-01	0.1	8.8E-01
ENSMUST00000062574	notif, leucine rich repeats, tropomodulin domain and proline-rich containing [Source:MGI Symbol;Acc:MGI:26		Q3V3V9	0.9	2.7E-01	2.1	6.8E-02	0.6	5.0E-01	-0.6	5.0E-01
ENSMUST00000064061	scratch homolog 2, zinc finger protein (Drosophila) [Source:MGI Symbol;Acc:MGI:2139287]		Q8BTH6	6.8	7.2E-05	-2.3	5.8E-03	0.7	8.2E-02	-0.1	9.3E-01
ENSMUST00000064062	inner membrane protein, mitochondrial [Source:MGI Symbol;Acc:MGI:1923864]		Q8CAQ8	-4.3	9.9E-03	-3.1	2.2E-02	-0.5	4.0E-01	-0.3	8.2E-01
ENSMUST00000064067	single-strand selective monofunctional uracil DNA glycosylase [Source:MGI Symbol;Acc:MGI:1918976]		Q6P5C5	1.6	6.1E-03	2.3	3.9E-03	-6.1	5.5E-05	-0.5	3.5E-01
ENSMUST00000064068	formyl peptide receptor 2 [Source:MGI Symbol;Acc:MGI:1278319]		O88536	-7.3	7.8E-08	3.7	1.1E-03	-0.3	7.0E-01	-0.6	3.1E-01
ENSMUST00000064076	TNNI3 interacting kinase [Source:MGI Symbol;Acc:MGI:2443276]		Q5GIG6	6.9	5.8E-05	2.6	2.8E-02	-0.4	6.7E-01	-0.5	5.8E-01
ENSMUST00000064099	protein phosphatase 6, regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:2442163]		Q7TSI3	-4.3	6.1E-05	6.1	1.8E-05	-1.4	8.9E-02	-0.5	2.6E-01
ENSMUST00000064104	CDC42 small effector 2 [Source:MGI Symbol;Acc:MGI:1919979]		Q8BGH7	-4.0	2.6E-05	-0.9	2.1E-01	0.7	1.5E-01	0.0	9.9E-01
ENSMUST00000064107	TBC1 domain family, member 30 [Source:MGI Symbol;Acc:MGI:1921944]		Q69ZT9	6.5	2.0E-04	5.4	3.3E-04	0.1	8.8E-01	-0.6	3.6E-01
ENSMUST00000064110	double C2, alpha [Source:MGI Symbol;Acc:MGI:109446]		Q7TNF0	5.9	6.6E-03	7.5	5.3E-05	-0.5	6.6E-01	-0.6	2.8E-01
ENSMUST00000062652	Sp2 transcription factor [Source:MGI Symbol;Acc:MGI:1926162]	Q8BNQ4		3.8	1.1E-01	6.0	7.1E-02	1.9	5.1E-01	-0.3	8.8E-01
ENSMUST00000064139	phosphatidic acid phosphatase type 2B [Source:MGI Symbol;Acc:MGI:1915166]		Q99JY8	8.0	1.1E-05	2.9	1.0E-02	-0.3	6.9E-01	0.8	2.3E-01
ENSMUST00000064151	patatin-like phospholipase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914103]		Q8BJ56	-7.7	1.1E-05	-1.3	4.6E-01	1.1	3.6E-01	-1.7	3.9E-01
ENSMUST00000062674	ribosomal protein S15 [Source:MGI Symbol;Acc:MGI:98117]	D3YTQ9		-1.3	3.6E-01	2.5	1.0E-01	0.8	5.7E-01	-3.1	4.1E-02
ENSMUST00000062677	transmembrane protein 11 [Source:MGI Symbol;Acc:MGI:2144726]		Q8BK08	-2.1	5.5E-02	-0.1	9.6E-01	0.5	5.7E-01	-1.6	2.0E-01
ENSMUST00000064162	RIKEN cDNA 1700024B05 gene [Source:MGI Symbol;Acc:MGI:1922768]	E9Q6D7		10.2	1.4E-06	-2.6	8.0E-04	0.2	4.2E-01	-0.3	6.4E-01
ENSMUST00000064165	chemokine (C-X3-C motif) receptor 1 [Source:MGI Symbol;Acc:MGI:1333815]	Q543X3	Q9Z0D9	2.2	2.4E-02	5.4	2.0E-03	-0.5	7.0E-01	0.5	5.3E-01
ENSMUST00000062684	transmembrane protein 64 [Source:MGI Symbol;Acc:MGI:2140359]		Q3U145	1.0	1.2E-01	0.3	6.6E-01	-0.4	5.1E-01	0.3	6.7E-01
ENSMUST00000062686	mitogen-activated protein kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346871]		Q8CE90	-2.3	2.5E-01	-0.6	8.3E-01	1.6	4.5E-01	-0.1	9.5E-01
ENSMUST00000064166	G protein-coupled receptor 20 [Source:MGI Symbol;Acc:MGI:2441803]		Q8BYC4	8.7	2.2E-05	7.1	5.4E-05	-0.5	6.2E-01	-0.2	7.2E-01
ENSMUST00000064167	ring finger protein 11 [Source:MGI Symbol;Acc:MGI:1352759]		Q9QYK7	-9.7	1.3E-04	-1.9	1.5E-02	0.9	3.9E-02	-0.9	1.9E-01
ENSMUST00000062740	acid phosphatase 1, soluble [Source:MGI Symbol;Acc:MGI:87881]	Q4VAI2	Q9D358	-1.1	3.1E-01	-3.6	3.7E-02	-0.5	5.9E-01	2.1	1.9E-01
ENSMUST00000064174	cell migration inducing protein, hyaluronan binding [Source:MGI Symbol;Acc:MGI:2443629]		Q8BI06	7.9	7.1E-06	8.0	2.6E-05	-0.6	5.9E-01	-0.1	8.6E-01
ENSMUST00000064192	zinc finger, DHHC domain containing 19 [Source:MGI Symbol;Acc:MGI:2682948]		Q810M5	7.1	7.9E-05	-3.2	5.2E-02	0.7	5.0E-01	-0.2	9.1E-01
ENSMUST00000062755	BLOC-1 related complex subunit 5 [Source:MGI Symbol;Acc:MGI:1915024]		Q9D920	0.3	7.8E-01	2.7	1.1E-01	1.2	3.8E-01	-1.1	3.3E-01
ENSMUST00000064196	RIKEN cDNA B630019K06 gene [Source:MGI Symbol;Acc:MGI:2147918]	Q7TNS5		3.8	1.8E-03	6.5	5.4E-05	0.9	3.0E-01	-0.1	7.9E-01
ENSMUST00000062765	zinc finger protein 583 [Source:MGI Symbol;Acc:MGI:2682297]		Q3V080	1.5	1.2E-01	4.0	3.8E-03	1.1	2.9E-01	-1.4	1.1E-01
ENSMUST00000064204	actinin alpha 2 [Source:MGI Symbol;Acc:MGI:109192]		Q9JI91	6.1	2.5E-05	6.4	4.7E-04	-0.5	7.1E-01	-1.1	1.5E-01
ENSMUST00000064214	ribonuclease, RNase A family, 9 (non-active) [Source:MGI Symbol;Acc:MGI:3057273]	Q5QJV3	P60154	6.4	7.8E-05	3.2	3.4E-03	0.1	8.7E-01	-0.7	3.1E-01
ENSMUST00000062787	CD300e antigen [Source:MGI Symbol;Acc:MGI:2387602]		Q8K249	0.7	2.1E-01	1.2	9.6E-02	-0.2	7.7E-01	-0.6	3.1E-01
ENSMUST00000064231	monoacylglycerol O-acyltransferase 2 [Source:MGI Symbol;Acc:MGI:2663253]		Q80W94	3.2	4.2E-03	1.1	2.7E-01	-1.7	7.8E-02	0.6	4.9E-01
ENSMUST00000064234	ezrin [Source:MGI Symbol;Acc:MGI:98931]	Q4KML7	P26040	-4.4	6.5E-05	-4.6	1.3E-04	-0.5	2.2E-01	-2.1	4.9E-02
ENSMUST00000062804	fucosyltransferase 8 [Source:MGI Symbol;Acc:MGI:1858901]		Q9WTS2	3.7	4.6E-02	-2.5	2.6E-01	-3.5	3.7E-02	2.6	2.2E-01
ENSMUST00000064257	trichohyalin [Source:MGI Symbol;Acc:MGI:2177944]	A0A0B4J1F9		4.3	4.2E-05	3.7	4.8E-03	-2.8	3.5E-02	-1.2	1.4E-01
ENSMUST00000064272	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1928767]	Q3U260	Q91YY2	-7.4	7.6E-05	4.8	1.8E-02	-3.3	1.2E-01	-1.0	4.0E-01
ENSMUST00000062831	repair cross-complementing rodent repair deficiency, complementation group 2 [Source:MGI Symbol;Acc:MG		O08811	-1.1	5.9E-01	-1.7	5.9E-01	1.2	6.1E-01	1.8	5.1E-01
ENSMUST00000064290	CCAAT/enhancer binding protein (C/EBP), epsilon [Source:MGI Symbol;Acc:MGI:103572]		Q6PZD9	-3.6	1.8E-04	-2.6	2.7E-02	0.0	1.0E+00	0.1	9.2E-01
ENSMUST00000062855	mesoderm induction early response 1, family member 2 [Source:MGI Symbol;Acc:MGI:1917677]		Q3U3N0	0.7	6.0E-01	5.9	7.5E-03	3.1	8.5E-02	-2.1	1.3E-01
ENSMUST00000062861	Rab geranylgeranyl transferase, a subunit [Source:MGI Symbol;Acc:MGI:1860443]		Q9JHK4	-0.6	6.1E-01	-2.8	1.4E-01	0.9	3.9E-01	3.2	8.1E-02
ENSMUST00000064314	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial) [Source:MGI Symbol;Acc:MGI:1928379]		O54984	-4.3	5.7E-05	6.9	6.1E-04	-0.7	6.5E-01	0.2	8.3E-01
ENSMUST00000064341	RIKEN cDNA C130026I21 gene [Source:MGI Symbol;Acc:MGI:3612702]	Q3KNJ6		3.6	1.0E-02	6.4	6.6E-04	-0.5	6.9E-01	-1.0	2.2E-01
ENSMUST00000064347	transmembrane protein 171 [Source:MGI Symbol;Acc:MGI:2685751]		Q4KL18	4.0	9.0E-04	7.5	1.3E-04	-0.7	6.0E-01	0.0	1.0E+00
ENSMUST00000062893	centromere protein E [Source:MGI Symbol;Acc:MGI:1098230]	E9QKK1		0.0	9.7E-01	-0.8	3.0E-01	-0.6	2.9E-01	0.2	7.6E-01
ENSMUST00000064370	ney disease (polycystin) and REJ (sperm receptor for egg jelly homolog, sea urchin) [Source:MGI Symbol;Acc:I	F8VQF3		8.4	1.6E-05	7.8	1.8E-04	-0.2	8.6E-01	0.4	5.6E-01
ENSMUST00000064376	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	Q80Z68		-7.7	2.2E-05	-0.9	3.5E-01	0.1	8.7E-01	-1.7	1.1E-01
ENSMUST00000064377	golgi coiled coil 1 [Source:MGI Symbol;Acc:MGI:1921625]		Q9D4H2	5.5	6.8E-03	3.2	3.7E-03	0.6	3.9E-01	0.2	7.5E-01
ENSMUST00000064391	copine VIII [Source:MGI Symbol;Acc:MGI:1914121]		Q9DC53	-4.9	1.5E-02	6.5	9.1E-04	-0.6	7.0E-01	-1.4	1.1E-01
ENSMUST00000062934	family with sequence similarity 171, member A1 [Source:MGI Symbol;Acc:MGI:2442917]	A2ATL0		0.7	7.1E-01	3.7	1.7E-01	1.5	5.2E-01	-1.4	4.4E-01
ENSMUST00000064392	olfactory receptor 536 [Source:MGI Symbol;Acc:MGI:3030370]	Q8VFE9		7.8	1.2E-06	6.7	1.8E-04	-0.6	6.0E-01	0.1	9.1E-01
ENSMUST00000062945	BCL12-like 15 [Source:MGI Symbol;Acc:MGI:2685412]		Q08ED0	-3.3	1.0E-01	-5.5	6.3E-02	-2.4	6.3E-02	-0.2	9.4E-01
ENSMUST00000062946	mex3 homolog D (C. elegans) [Source:MGI Symbol;Acc:MGI:2681847]	E9PUA0		1.1	8.8E-02	2.3	1.3E-02	1.0	1.5E-01	-0.2	7.0E-01
ENSMUST00000064395	neuron navigator 2 [Source:MGI Symbol;Acc:MGI:2183691]	E9Q842		10.3	2.1E-05	-0.8	2.3E-01	1.1	2.4E-02	0.0	9.9E-01
ENSMUST00000062962	solute carrier family 35, member F6 [Source:MGI Symbol;Acc:MGI:1922169]		Q8VE96	-1.2	8.6E-02	-0.8	3.7E-01	0.5	3.8E-01	0.1	9.0E-01
ENSMUST00000064404	glutaredoxin 3 [Source:MGI Symbol;Acc:MGI:1353653]		Q9CQM9	-3.5	1.8E-04	6.4	6.8E-04	-0.6	6.5E-01	-0.6	4.3E-01
ENSMUST00000064405	Eph receptor A3 [Source:MGI Symbol;Acc:MGI:99612]	Q8BRB1		6.2	3.3E-04	4.5	1.3E-03	0.4	7.0E-01	-0.8	2.8E-01
ENSMUST00000064407	inhibitor of kappaB kinase gamma [Source:MGI Symbol;Acc:MGI:1338074]	Q8VC91		-8.1	6.7E-05	5.3	1.7E-03	-0.6	6.7E-01	-0.1	8.7E-01
ENSMUST00000064444	mannosidase, endo-alpha-like [Source:MGI Symbol;Acc:MGI:2684896]		Q6P1J0	5.9	2.7E-05	6.4	5.1E-05	-0.3	7.1E-01	-0.8	1.6E-01
ENSMUST00000062991	GrpE-like 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1334416]	Q0VB85	O88396	-0.1	7.6E-01	0.6	2.6E-01	0.0	9.5E-01	-0.8	1.7E-01
ENSMUST00000064454	GCN1 general control of amino-acid synthesis 1-like 1 (yeast) [Source:MGI Symbol;Acc:MGI:2444248]	E9PVA8		-5.0	1.3E-02	3.8	2.4E-02	-0.5	7.3E-01	1.9	8.5E-02
ENSMUST00000064462	complement component 1, q subcomponent-like 4 [Source:MGI Symbol;Acc:MGI:3579909]		Q4ZJM9	5.9	5.5E-04	-6.7	8.3E-04	-0.1	8.1E-01	-0.1	9.3E-01
ENSMUST00000064473	adenosine deaminase, RNA-specific, B2 [Source:MGI Symbol;Acc:MGI:2151118]		Q9JI20	7.6	3.8E-05	-1.3	6.2E-02	0.2	6.8E-01	-0.1	8.9E-01
ENSMUST00000064477	discs, large homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:107231]		Q811D0	-7.0	8.4E-06	-7.7	6.6E-05	-0.2	7.2E-01	-1.5	2.5E-01
ENSMUST00000064481	noncompact myelin associated protein [Source:MGI Symbol;Acc:MGI:2444888]		Q99JS0	6.3	6.2E-04	4.4	2.5E-03	0.1	9.6E-01	0.9	2.2E-01
ENSMUST00000063071	potassium channel tetramerisation domain containing 19 [Source:MGI Symbol;Acc:MGI:3045294]		Q562E2	3.4	1.6E-01	1.7	5.6E-01	-0.3	9.0E-01	1.3	5.7E-01
ENSMUST00000064488	giant axonal neuropathy [Source:MGI Symbol;Acc:MGI:1890619]		Q8CA72	4.8	2.8E-02	5.0	5.2E-03	-0.4	7.9E-01	-0.2	8.5E-01
ENSMUST00000064513	endonuclease V [Source:MGI Symbol;Acc:MGI:2444688]	F8WJ25		2.6	8.4E-03	-6.8	4.3E-05	0.8	4.0E-02	1.3	2.0E-01
ENSMUST00000063089	NOL1/NOP2/Sun domain family member 3 [Source:MGI Symbol;Acc:MGI:2146565]		Q8CCT7	-1.9	3.4E-01	-2.1	3.4E-01	-0.5	7.3E-01	-0.2	9.1E-01
ENSMUST00000063091	Fyn proto-oncogene [Source:MGI Symbol;Acc:MGI:95602]		P39688	-2.4	2.4E-01	4.4	1.1E-01	4.6	6.5E-02	-2.2	2.8E-01
ENSMUST00000063093	cholinergic receptor, muscarinic 3, cardiac [Source:MGI Symbol;Acc:MGI:88398]	Q542R4	Q9ERZ3	1.1	1.4E-01	1.1	2.0E-01	-1.4	5.3E-02	-1.4	8.7E-02
ENSMUST00000064517	stress-associated endoplasmic reticulum protein family member 2 [Source:MGI Symbol;Acc:MGI:1919911]		Q6TAW2	4.2	1.2E-03	5.8	2.7E-06	-1.1	8.5E-02	-0.3	3.2E-01
ENSMUST00000064536	a disintegrin and metallopeptidase domain 17 [Source:MGI Symbol;Acc:MGI:1096335]		Q9Z0F8	-5.0	2.3E-02	6.3	3.5E-04	-0.5	6.9E-01	-0.3	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000064545	LIM domain containing 2 [Source:MGI Symbol;Acc:MGI:1915053]		Q8BGB5	-6.7	2.5E-04	0.6	2.4E-01	-0.9	4.7E-02	-0.4	4.5E-01
ENSMUST00000064562	protocadherin 15 [Source:MGI Symbol;Acc:MGI:1891428]	E9Q159		9.2	1.3E-05	6.1	2.6E-04	-1.5	2.3E-01	-0.1	8.9E-01
ENSMUST00000064571	actin filament associated protein 1 [Source:MGI Symbol;Acc:MGI:1917542]		Q80YS6	2.1	6.3E-04	3.2	7.3E-02	-3.1	1.4E-01	-1.2	3.7E-01
ENSMUST00000064580	olute carrier family 6 (neurotransmitter transporter, GABA), member 13 [Source:MGI Symbol;Acc:MGI:9562		P31649	1.6	2.9E-02	5.3	7.5E-04	1.5	1.6E-01	-0.3	6.8E-01
ENSMUST00000064595	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 [Source:MGI Symbol;Acc:MGI:2685438]	E9PX52		8.5	1.3E-02	6.1	3.8E-04	-0.5	6.9E-01	-1.0	1.5E-01
ENSMUST00000064606	leucine rich repeat containing 15 [Source:MGI Symbol;Acc:MGI:1921738]		Q80X72	8.5	4.8E-06	5.2	1.5E-03	-1.0	4.1E-01	0.0	9.6E-01
ENSMUST00000063169	deleted in lymphocytic leukemia, 7 [Source:MGI Symbol;Acc:MGI:2447771]		Q8CHZ8	2.3	3.9E-02	3.2	1.6E-02	-0.2	8.7E-01	-1.0	2.6E-01
ENSMUST00000064646	RIKEN cDNA 5830454E08 gene [Source:MGI Symbol;Acc:MGI:1923350]			2.1	1.3E-02	7.3	2.7E-04	-0.2	9.0E-01	-0.3	6.9E-01
ENSMUST00000064652	RIKEN cDNA 1110051M20 gene [Source:MGI Symbol;Acc:MGI:1915079]		Q8BHR8	4.1	6.6E-03	0.0	9.8E-01	1.1	3.3E-01	4.4	1.4E-02
ENSMUST00000064656	zinc finger protein 365 [Source:MGI Symbol;Acc:MGI:2143676]		Q8BG89	7.9	1.8E-04	6.6	1.8E-04	-0.6	6.1E-01	0.1	9.0E-01
ENSMUST00000064659	zinc finger, matrin type 1 [Source:MGI Symbol;Acc:MGI:2442284]	G5E8E4		-4.0	1.3E-02	5.8	3.5E-04	0.1	9.4E-01	-0.1	8.1E-01
ENSMUST00000063249	X-ray repair complementing defective repair in Chinese hamster cells 1 [Source:MGI Symbol;Acc:MGI:99137		Q60596	-0.2	7.4E-01	0.3	7.1E-01	0.7	2.2E-01	0.2	7.5E-01
ENSMUST00000064667	RAS related protein 1b [Source:MGI Symbol;Acc:MGI:894315]	Q52L50	Q99JI6	-7.8	8.7E-07	-3.2	4.8E-03	-0.1	8.3E-01	0.1	9.3E-01
ENSMUST00000064679	RAB7B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2442295]		Q8VEA8	1.5	2.5E-02	6.3	1.1E-03	-0.7	6.5E-01	0.6	4.7E-01
ENSMUST00000064690	acyl-CoA synthetase long-chain family member 6 [Source:MGI Symbol;Acc:MGI:894291]	Q8C028		5.9	7.5E-04	-2.6	5.7E-02	2.0	1.1E-02	-0.8	5.6E-01
ENSMUST00000064703	protein kinase inhibitor, gamma [Source:MGI Symbol;Acc:MGI:1343086]	Q3TP50	O70139	-4.8	3.3E-02	4.4	1.2E-03	-2.5	4.2E-02	-0.5	4.2E-01
ENSMUST00000064740	succinate-CoA ligase, GDP-forming, alpha subunit [Source:MGI Symbol;Acc:MGI:1927234]		Q9WUM5	-5.0	2.7E-05	6.5	2.2E-04	-0.6	5.9E-01	-0.5	4.2E-01
ENSMUST00000064759	striatin interacting protein 1 [Source:MGI Symbol;Acc:MGI:2443884]		Q8C079	-2.1	1.1E-03	7.8	4.6E-05	-0.6	6.3E-01	-1.0	1.1E-01
ENSMUST00000063307	eroxisome proliferative activated receptor, gamma, coactivator 1 beta [Source:MGI Symbol;Acc:MGI:2444934		Q8VHJ7	3.8	1.2E-01	5.6	7.3E-02	0.0	9.9E-01	-1.8	3.8E-01
ENSMUST00000063314	general transcription factor II A, 1 [Source:MGI Symbol;Acc:MGI:1933277]	Q149E9		0.7	7.7E-01	1.6	5.5E-01	0.2	9.3E-01	-0.8	7.6E-01
ENSMUST00000064762	microtubule-associated protein 1B [Source:MGI Symbol;Acc:MGI:1306778]		P14873	3.5	8.2E-04	4.9	1.1E-03	-0.9	4.4E-01	0.2	7.4E-01
ENSMUST00000064765	syntaxin 17 [Source:MGI Symbol;Acc:MGI:1914977]		Q9D0I4	-5.9	2.3E-04	4.1	6.7E-04	0.5	4.8E-01	-0.3	6.3E-01
ENSMUST00000063339	retinoic acid receptor, gamma [Source:MGI Symbol;Acc:MGI:97858]		P18911	-0.3	7.0E-01	-0.4	6.2E-01	0.0	9.8E-01	0.2	8.4E-01
ENSMUST00000063344	lipase maturation factor 1 [Source:MGI Symbol;Acc:MGI:1923733]	Z4YJR1		4.0	4.2E-02	2.1	3.4E-01	-0.7	7.2E-01	1.1	4.8E-01
ENSMUST00000063347	ADP-ribosylation factor 2 [Source:MGI Symbol;Acc:MGI:99595]		Q8BSL7	3.6	4.2E-02	3.5	1.2E-01	-0.3	8.6E-01	-0.3	8.5E-01
ENSMUST00000063401	inhibitor of kappaB kinase beta [Source:MGI Symbol;Acc:MGI:1338071]			0.5	6.0E-01	1.4	2.7E-01	-0.2	8.6E-01	-1.1	3.6E-01
ENSMUST00000064771	SWT1 RNA endoribonuclease homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914125]		Q9DBQ9	-3.7	1.8E-04	-0.9	1.2E-01	1.0	2.2E-02	-0.1	7.9E-01
ENSMUST00000064775	adenylate cyclase activating polypeptide 1 [Source:MGI Symbol;Acc:MGI:105094]	Q3UYH8	O70176	6.7	1.5E-04	-5.0	3.7E-05	-0.7	5.6E-02	-0.8	2.5E-01
ENSMUST00000064780	gamma-aminobutyric acid (GABA) A receptor, subunit epsilon [Source:MGI Symbol;Acc:MGI:1330235]	A2AMW3		7.3	1.2E-04	0.4	7.9E-01	-5.6	1.0E-02	1.2	3.9E-01
ENSMUST00000064783	microfibrillar-associated protein 4 [Source:MGI Symbol;Acc:MGI:1342276]		Q9D1H9	5.9	1.2E-03	8.0	5.7E-05	-0.6	6.1E-01	-0.3	6.5E-01
ENSMUST00000063445	kelch domain containing 1 [Source:MGI Symbol;Acc:MGI:2672853]		Q80YG3	1.5	6.1E-02	0.3	7.1E-01	-1.3	1.0E-01	0.0	9.5E-01
ENSMUST00000064788	RIKEN cDNA A630001G21 gene [Source:MGI Symbol;Acc:MGI:2443131]	Q3UTB2		-3.5	6.4E-03	7.9	1.5E-03	-1.6	4.1E-01	1.1	2.3E-01
ENSMUST00000064793	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]		Q80TM6	7.9	9.0E-03	-2.0	9.6E-03	0.1	7.8E-01	-0.5	4.6E-01
ENSMUST00000064795	early growth response 1 [Source:MGI Symbol;Acc:MGI:95295]	Q544D6	P08046	4.6	3.4E-02	7.0	2.0E-04	-0.6	6.4E-01	0.0	9.6E-01
ENSMUST00000063496	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]	E9PUA7		-5.8	1.4E-01	-9.0	8.6E-02	-2.8	8.2E-02	0.4	9.4E-01
ENSMUST00000063502	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2156057]		Q8C7W7	0.2	9.5E-01	1.2	6.8E-01	0.6	8.3E-01	-0.4	8.6E-01
ENSMUST00000064798	NADH dehydrogenase (ubiquinone) flavoprotein 3 [Source:MGI Symbol;Acc:MGI:1890894]		Q8BK30	-7.0	4.3E-04	5.8	1.1E-02	-0.7	7.4E-01	-0.8	4.7E-01
ENSMUST00000064806	diencephalon/mesencephalon homeobox 1 [Source:MGI Symbol;Acc:MGI:2153518]		Q91ZK4	9.6	6.5E-06	6.1	3.4E-02	-0.6	8.4E-01	-0.9	5.3E-01
ENSMUST00000064807	Myb/SANT-like DNA-binding domain containing 3 [Source:MGI Symbol;Acc:MGI:1913915]		Q9CR78	6.1	1.8E-03	3.1	2.5E-03	-4.8	1.0E-03	-0.6	3.1E-01
ENSMUST00000064821	integrin alpha M [Source:MGI Symbol;Acc:MGI:96607]	G5E8F1		-9.0	3.2E-05	3.1	1.1E-02	4.0	7.8E-04	-1.1	1.5E-01
ENSMUST00000064846	predicted gene, 21685 [Source:MGI Symbol;Acc:MGI:5435040]	Q80WR8		7.2	6.2E-05	6.3	3.8E-04	-0.7	6.0E-01	-1.0	1.6E-01
ENSMUST00000064856	carboxypeptidase N, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1919006]		Q9DBB9	7.9	2.7E-05	8.3	7.2E-05	-0.6	6.5E-01	0.1	8.6E-01
ENSMUST00000063530	gasdermin C4 [Source:MGI Symbol;Acc:MGI:1921798]		Q3TR54	2.0	5.4E-02	-1.2	3.7E-01	-0.2	8.7E-01	3.1	3.0E-02
ENSMUST00000064873	complement component 8, alpha polypeptide [Source:MGI Symbol;Acc:MGI:2668347]		Q8K182	6.6	3.4E-02	-1.8	5.3E-02	-1.5	4.6E-02	-3.6	1.1E-02
ENSMUST00000064900	protein inhibitor of activated STAT 3 [Source:MGI Symbol;Acc:MGI:1913126]		O54714	-3.0	2.2E-02	-3.7	3.4E-03	0.9	7.0E-02	-0.7	5.2E-01
ENSMUST00000064910	serine/threonine kinase receptor associated protein [Source:MGI Symbol;Acc:MGI:1329037]	B2RUC7	Q9Z1Z2	-4.7	2.6E-05	5.9	3.3E-05	-0.1	8.7E-01	-0.1	8.7E-01
ENSMUST00000063562	mitochondrial intermediate peptidase [Source:MGI Symbol;Acc:MGI:1917728]		A6H611	-0.4	3.5E-01	0.5	4.3E-01	0.8	7.8E-02	-0.1	9.0E-01
ENSMUST00000064921	protein kinase C, beta [Source:MGI Symbol;Acc:MGI:97596]		P68404	-8.3	6.4E-05	7.8	1.3E-04	-0.7	6.2E-01	-0.8	2.4E-01
ENSMUST00000064922	jun B proto-oncogene [Source:MGI Symbol;Acc:MGI:96647]	Q569U6	P09450	-6.9	2.8E-05	4.0	2.4E-03	-2.3	6.1E-02	-1.0	2.3E-01
ENSMUST00000063574	TSR3 20S rRNA accumulation [Source:MGI Symbol;Acc:MGI:1915577]		Q5HZH2	-1.0	9.1E-02	-0.4	6.0E-01	0.6	2.5E-01	0.0	9.5E-01
ENSMUST00000063577	zinc finger, MYM-type 3 [Source:MGI Symbol;Acc:MGI:1927231]	B1AXS5	Q9JLM4	-0.8	7.0E-01	2.5	3.0E-01	2.3	3.1E-01	-1.0	5.9E-01
ENSMUST00000064924	extra spindle pole bodies 1, separase [Source:MGI Symbol;Acc:MGI:2146156]		P60330	1.5	1.6E-02	7.0	1.1E-04	-0.6	6.1E-01	-0.2	7.3E-01
ENSMUST00000064932	taste receptor, type 2, member 137 [Source:MGI Symbol;Acc:MGI:3606604]			6.3	9.1E-05	7.2	6.1E-04	-0.5	7.7E-01	0.4	6.3E-01
ENSMUST00000063587	partner and localizer of BRCA2 [Source:MGI Symbol;Acc:MGI:3040695]		Q3U0P1	4.2	6.3E-02	0.2	9.4E-01	-1.4	5.4E-01	2.5	3.2E-01
ENSMUST00000064941	nuclear receptor subfamily 1, group D, member 1 [Source:MGI Symbol;Acc:MGI:2444210]		Q3UV55	7.1	1.5E-05	0.9	6.1E-01	-1.2	4.3E-01	2.1	2.2E-01
ENSMUST00000063597	calcium-sensing receptor [Source:MGI Symbol;Acc:MGI:1351351]		Q9QY96	2.1	1.3E-01	7.2	1.9E-04	-0.5	7.0E-01	-5.6	2.0E-04
ENSMUST00000063605	zinc finger and BTB domain containing 21 [Source:MGI Symbol;Acc:MGI:1927240]	E9Q3R9		0.8	2.0E-01	4.3	3.2E-03	3.5	5.7E-03	0.0	9.9E-01
ENSMUST00000063632	Sec31 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2685187]		Q3TZ89	3.0	1.1E-01	4.8	5.6E-02	-0.1	9.7E-01	-1.9	2.2E-01
ENSMUST00000064948	dynein, axonemal, heavy chain 6 [Source:MGI Symbol;Acc:MGI:107744]	E9Q0B6		6.1	2.8E-02	-4.9	2.7E-04	-0.6	1.3E-01	0.2	8.6E-01
ENSMUST00000064950	death effector domain-containing [Source:MGI Symbol;Acc:MGI:1333874]	Q3U001	Q9Z1L3	-7.6	1.4E-05	7.0	5.6E-04	-0.7	6.6E-01	-0.4	6.3E-01
ENSMUST00000064989	protein kinase C, beta [Source:MGI Symbol;Acc:MGI:97596]		P68404	-4.1	1.5E-04	3.8	1.3E-02	-1.8	1.7E-01	-0.6	5.7E-01
ENSMUST00000063654	B and T lymphocyte associated [Source:MGI Symbol;Acc:MGI:2658978]	E9QNY6		-1.6	4.6E-01	0.5	7.3E-01	-2.7	1.0E-01	-4.8	3.2E-02
ENSMUST00000065001	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]	A2AUX5		5.8	4.7E-03	-9.1	1.7E-03	0.5	3.9E-01	1.2	6.0E-01
ENSMUST00000063663	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S) [Source:MGI Symbol;Acc:MGI:2389490]		P59270	1.5	4.7E-02	1.4	1.3E-01	-0.4	5.5E-01	-0.2	7.6E-01
ENSMUST00000063669	DEAH (Asp-Glu-Ala-His) box polypeptide 32 [Source:MGI Symbol;Acc:MGI:2141813]		Q8BZS9	-0.1	9.0E-01	0.7	5.6E-01	-0.6	5.0E-01	-1.5	2.1E-01
ENSMUST00000065005	autophagy related 4D, cysteine peptidase [Source:MGI Symbol;Acc:MGI:2444308]		Q8BGV9	-2.0	1.1E-02	7.2	2.1E-04	-0.6	6.5E-01	-0.1	8.8E-01
ENSMUST00000063683	T cell activation GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:1919786]		P0CAX8	-0.5	5.3E-01	-0.5	5.8E-01	0.1	8.9E-01	0.1	8.7E-01
ENSMUST00000065014	laminin, beta 2 [Source:MGI Symbol;Acc:MGI:99916]		Q61292	7.8	6.4E-06	-5.4	1.9E-05	0.1	8.3E-01	0.2	8.0E-01
ENSMUST00000065047	arginine/serine-rich coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1914130]	Q8BR75		7.5	1.9E-05	-3.2	2.1E-04	1.1	6.1E-03	0.5	3.9E-01
ENSMUST00000065049	ribonuclease H2, large subunit [Source:MGI Symbol;Acc:MGI:1916974]	Q05C51		-5.6	2.9E-04	5.2	1.6E-03	0.4	6.9E-01	0.0	9.8E-01
ENSMUST00000065060	transmembrane and coiled coil domains 3 [Source:MGI Symbol;Acc:MGI:2442900]		Q8R310	3.7	1.8E-04	-5.8	3.0E-02	1.8	1.3E-01	0.3	8.8E-01
ENSMUST00000063718	mbt domain containing 1 [Source:MGI Symbol;Acc:MGI:2143977]		Q6P5G3	-1.7	1.1E-01	-0.6	6.5E-01	0.5	5.4E-01	-0.5	6.9E-01
ENSMUST00000063719	transmembrane protein 9 [Source:MGI Symbol;Acc:MGI:1913491]		Q9CR23	2.0	2.0E-01	1.0	5.5E-01	-1.3	3.9E-01	-0.3	8.7E-01
ENSMUST00000065074	arginine/serine-rich coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1914130]		Q9DBU6	-3.3	2.1E-02	0.4	6.1E-01	1.1	9.4E-02	-6.0	6.9E-04
ENSMUST00000065080	C2 calcium-dependent domain containing 2-like [Source:MGI Symbol;Acc:MGI:1919014]		Q80X80	-1.7	3.1E-02	2.1	1.4E-02	-1.5	4.5E-02	-0.3	6.5E-01
ENSMUST00000065086	growth arrest specific 1 [Source:MGI Symbol;Acc:MGI:95655]			6.6	1.9E-04	5.4	3.7E-05	-3.5	4.3E-03	-0.9	8.8E-02
ENSMUST00000065090	filamin C, gamma [Source:MGI Symbol;Acc:MGI:95557]	D3Z576	Q8VHX6	8.4	2.6E-02	-5.1	4.4E-03	0.9	1.4E-01	1.4	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000065103	mitochondrial ribosomal protein L35 [Source:MGI Symbol;Acc:MGI:1913473]		Q9CQL6	3.3	3.6E-04	3.8	3.1E-04	-0.5	3.9E-01	-0.5	3.4E-01
ENSMUST00000065111	ubiquitin specific petidase 45 [Source:MGI Symbol;Acc:MGI:101850]		Q8K387	-5.4	1.9E-03	6.0	4.4E-03	-0.6	7.2E-01	-1.0	3.2E-01
ENSMUST00000065112	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 15 [Source:MGI Symbol;Acc:M		P59384	9.2	3.4E-06	-3.2	2.5E-03	1.1	2.8E-02	-0.5	5.6E-01
ENSMUST00000065118	ubiquitin-conjugating enzyme E2Q family-like 1 [Source:MGI Symbol;Acc:MGI:1924230]	E9QMD2		7.6	2.5E-05	7.3	1.7E-04	1.2	3.1E-01	0.0	9.5E-01
ENSMUST00000063820	coagulation factor X [Source:MGI Symbol;Acc:MGI:103107]	Q3TBR2	O88947	0.8	1.1E-01	1.0	1.1E-01	0.2	6.3E-01	0.0	9.7E-01
ENSMUST00000065119	family with sequence similarity 53, member A [Source:MGI Symbol;Acc:MGI:1919225]	E9PV82		-4.4	1.2E-03	1.3	3.0E-01	6.3	7.5E-05	0.2	8.6E-01
ENSMUST00000063838	family with sequence similarity 49, member B [Source:MGI Symbol;Acc:MGI:1923520]		Q921M7	-1.8	4.7E-02	-2.1	5.7E-02	-0.4	5.7E-01	0.0	9.6E-01
ENSMUST00000063839	RNA binding motif protein 12 B2 [Source:MGI Symbol;Acc:MGI:1924854]		Q66JV4	-3.1	4.4E-02	-1.9	4.1E-01	1.7	2.3E-01	0.5	8.0E-01
ENSMUST00000065125	leucine rich repeat containing 74B [Source:MGI Symbol;Acc:MGI:1921935]		Q14BP6	5.5	2.2E-03	-2.4	3.9E-03	0.9	2.7E-02	-0.1	9.1E-01
ENSMUST00000063869	CD1d1 antigen [Source:MGI Symbol;Acc:MGI:107674]	E9Q395		5.5	1.1E-01	2.6	3.9E-01	-2.7	4.3E-01	0.2	9.3E-01
ENSMUST00000065134	immediate early response 5-like [Source:MGI Symbol;Acc:MGI:1919750]		Q99J55	3.6	1.1E-02	5.5	6.7E-05	0.3	7.3E-01	0.1	8.6E-01
ENSMUST00000063879	phosphatidic acid phosphatase type 2C [Source:MGI Symbol;Acc:MGI:1354945]		Q9DAX2	-1.3	4.3E-01	3.1	1.4E-01	0.6	7.2E-01	-3.7	3.7E-02
ENSMUST00000063882	·1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2140		Q8CCA0	-1.5	2.6E-01	3.5	9.6E-02	2.7	1.3E-01	-2.3	1.3E-01
ENSMUST00000065162	family with sequence similarity 53, member A [Source:MGI Symbol;Acc:MGI:1919225]	E9PV65		5.2	7.1E-05	1.2	1.7E-01	0.3	6.6E-01	0.8	3.0E-01
ENSMUST00000065163	calcium and integrin binding 1 (calmyrin) [Source:MGI Symbol;Acc:MGI:1344418]		Q9Z0F4	-7.3	2.5E-04	-2.3	7.5E-02	0.2	7.4E-01	-0.5	7.1E-01
ENSMUST00000065167	adrenergic receptor kinase, beta 2 [Source:MGI Symbol;Acc:MGI:87941]		Q3UYH7	3.8	2.4E-03	7.3	3.3E-04	0.1	9.7E-01	-0.1	8.7E-01
ENSMUST00000065196	sodium channel, voltage-gated, type V, alpha [Source:MGI Symbol;Acc:MGI:98251]	K3W4N7		10.9	2.8E-03	-5.6	1.3E-05	1.6	6.3E-04	-1.1	1.5E-01
ENSMUST00000063976	optic atrophy 3 [Source:MGI Symbol;Acc:MGI:2686271]		Q505D7	-0.4	4.7E-01	0.9	2.2E-01	1.0	8.6E-02	-0.3	6.5E-01
ENSMUST00000065204	potassium channel, subfamily K, member 18 [Source:MGI Symbol;Acc:MGI:2685627]		Q6VV64	8.1	1.4E-05	6.2	2.5E-04	-0.5	6.4E-01	0.1	8.8E-01
ENSMUST00000065213	ring finger protein 222 [Source:MGI Symbol;Acc:MGI:2443227]		Q8CEF8	7.4	9.9E-06	2.7	1.7E-02	-0.5	5.6E-01	0.0	9.5E-01
ENSMUST00000065224	galanin receptor 1 [Source:MGI Symbol;Acc:MGI:1096364]		P56479	8.6	1.6E-05	4.8	8.1E-05	1.4	5.3E-02	0.4	4.5E-01
ENSMUST00000063988	transducin (beta)-like 1X-linked receptor 1 [Source:MGI Symbol;Acc:MGI:2441730]		Q8BHJ5	-3.3	4.3E-02	0.1	9.3E-01	1.5	2.1E-01	-2.0	2.4E-01
ENSMUST00000065248	CD8 antigen, beta chain 1 [Source:MGI Symbol;Acc:MGI:88347]	Q3TEK8	P10300	1.9	5.6E-03	2.2	1.7E-02	-0.2	7.4E-01	0.0	9.9E-01
ENSMUST00000065263	sno, strawberry notch homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2384298]	B2RRI2		-1.8	3.9E-03	8.9	3.2E-05	-0.7	5.9E-01	-0.4	4.2E-01
ENSMUST00000064019	target of myb1-like 2 (chicken) [Source:MGI Symbol;Acc:MGI:2443306]		Q5SRX1	1.2	9.1E-02	0.9	2.8E-01	-0.5	4.2E-01	-0.2	8.0E-01
ENSMUST00000065286	family with sequence similarity 204, member A [Source:MGI Symbol;Acc:MGI:1289174]		Q8C6C7	-2.1	5.6E-03	4.1	9.7E-02	-0.7	7.7E-01	0.1	9.3E-01
ENSMUST00000065289	C-type lectin domain family 12, member a [Source:MGI Symbol;Acc:MGI:3040968]			-9.0	9.0E-06	6.9	2.4E-02	-0.6	8.3E-01	-1.2	4.2E-01
ENSMUST00000065291	RIKEN cDNA 9230110C19 gene [Source:MGI Symbol;Acc:MGI:3045346]	Q8CC70		4.9	2.6E-04	7.0	1.8E-04	-0.3	8.3E-01	-0.4	5.0E-01
ENSMUST00000065297	LON peptidase N-terminal domain and ring finger 1 [Source:MGI Symbol;Acc:MGI:3609241]	D3YY23		2.3	7.3E-03	-1.5	2.5E-01	-0.3	7.3E-01	-3.0	7.2E-02
ENSMUST00000065323	lines homolog (Drosophila) 1 [Source:MGI Symbol;Acc:MGI:1919885]	D6RFA2		-7.8	7.4E-05	2.6	1.9E-03	0.7	2.0E-01	-0.3	5.4E-01
ENSMUST00000065330	CDC-like kinase 3 [Source:MGI Symbol;Acc:MGI:1098670]		O35492	-3.4	2.4E-05	-7.7	9.5E-07	0.4	1.3E-01	0.8	2.6E-01
ENSMUST00000065335	G protein-coupled receptor 141 [Source:MGI Symbol;Acc:MGI:2672983]		Q7TQP0	-5.3	2.1E-05	7.3	6.8E-05	-0.6	5.9E-01	-1.0	1.1E-01
ENSMUST00000064091	protein tyrosine phosphatase, non-receptor type 4 [Source:MGI Symbol;Acc:MGI:1099792]		Q9WU22	0.9	1.4E-01	1.6	6.5E-02	0.5	4.4E-01	-0.2	8.0E-01
ENSMUST00000064098	LIM domain binding 3 [Source:MGI Symbol;Acc:MGI:1344412]	E9PYJ9		5.8	1.3E-01	5.7	1.7E-01	-0.9	8.3E-01	-0.8	7.6E-01
ENSMUST00000065358	COMM domain containing 4 [Source:MGI Symbol;Acc:MGI:1913449]		Q9CQ02	-2.7	7.0E-04	-3.1	2.3E-03	0.8	7.3E-02	-0.4	6.3E-01
ENSMUST00000064101				-0.4	6.8E-01	0.4	7.9E-01	0.8	4.9E-01	-0.1	9.7E-01
ENSMUST00000065359	fibronectin type 3 and ankyrin repeat domains 1 [Source:MGI Symbol;Acc:MGI:1914180]		Q9DAM9	6.8	6.7E-05	-3.0	1.1E-03	0.7	6.8E-02	-0.3	6.3E-01
ENSMUST00000065364	charged multivesicular body protein 3 [Source:MGI Symbol;Acc:MGI:1913950]		Q9CQ10	-6.7	7.0E-04	5.8	1.5E-03	-0.4	7.3E-01	0.3	7.1E-01
ENSMUST00000065371	family with sequence similarity 53, member B [Source:MGI Symbol;Acc:MGI:1925188]		Q8BGR5	-6.8	1.9E-04	7.2	3.2E-03	-0.7	7.4E-01	-2.0	8.7E-02
ENSMUST00000064129	tetratricopeptide repeat domain 39A [Source:MGI Symbol;Acc:MGI:2444350]		A2ACP1	2.3	1.7E-01	3.3	8.1E-02	-0.9	5.9E-01	-1.8	2.5E-01
ENSMUST00000065379	ring finger protein 26 [Source:MGI Symbol;Acc:MGI:2388131]		Q8BUH7	6.1	8.1E-03	3.6	6.8E-04	-3.7	2.3E-03	0.7	2.3E-01
ENSMUST00000065382	GS homeobox 1 [Source:MGI Symbol;Acc:MGI:95842]	B2RQ55	P31315	6.4	8.3E-05	-7.0	2.1E-04	1.2	9.7E-03	0.5	7.2E-01
ENSMUST00000065422	RNA polymerase II associated protein 2 [Source:MGI Symbol;Acc:MGI:2141142]		Q8VC34	-3.0	3.1E-02	10.0	3.5E-06	-0.6	6.2E-01	-0.4	3.4E-01
ENSMUST00000065433	IKAROS family zinc finger 1 [Source:MGI Symbol;Acc:MGI:1342540]	Q5SWT9		-4.8	4.0E-05	2.4	4.1E-02	0.2	8.1E-01	0.0	9.8E-01
ENSMUST00000065438	cadherin 22 [Source:MGI Symbol;Acc:MGI:1341843]		Q9WTP5	8.1	1.3E-04	8.1	7.9E-05	-0.7	6.0E-01	0.0	9.6E-01
ENSMUST00000065441	G protein-coupled receptor 21 [Source:MGI Symbol;Acc:MGI:2441890]		Q8BX79	5.8	5.8E-04	-6.9	5.6E-03	1.8	1.7E-02	-0.9	6.8E-01
ENSMUST00000065461	ubiquitin specific peptidase 2 [Source:MGI Symbol;Acc:MGI:1858178]		O88623	-2.5	7.4E-03	4.8	3.4E-05	-4.0	9.6E-04	-0.9	8.2E-02
ENSMUST00000064187	thyroid hormone receptor alpha [Source:MGI Symbol;Acc:MGI:98742]		P63058	1.1	7.4E-02	2.0	1.6E-02	0.1	8.9E-01	-0.8	2.1E-01
ENSMUST00000065486	calcium and integrin binding family member 4 [Source:MGI Symbol;Acc:MGI:1920509]		Q9D9N5	6.2	1.7E-04	7.0	1.8E-04	-0.6	6.5E-01	-0.4	5.3E-01
ENSMUST00000065496	Rho GTPase activating protein 20 [Source:MGI Symbol;Acc:MGI:2445175]		Q6IFT4	8.1	1.0E-05	3.9	9.9E-03	0.7	5.5E-01	0.6	5.0E-01
ENSMUST00000064200	transmembrane protein 106C [Source:MGI Symbol;Acc:MGI:1196384]		Q80VP8	0.5	4.1E-01	0.7	3.7E-01	0.0	9.9E-01	-0.2	8.0E-01
ENSMUST00000065504	annexin A7 [Source:MGI Symbol;Acc:MGI:88031]		Q07076	-10.7	1.1E-06	5.1	1.3E-04	-1.6	7.0E-02	-0.6	3.3E-01
ENSMUST00000065509	lysine (K)-specific demethylase 3A [Source:MGI Symbol;Acc:MGI:98847]		Q6PCM1	-4.6	6.3E-03	5.7	3.6E-04	-0.6	6.1E-01	0.2	7.7E-01
ENSMUST00000064230	RFT1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3607791]		Q8C3B8	-4.5	5.2E-02	-1.3	5.6E-01	2.2	2.3E-01	-1.0	6.8E-01
ENSMUST00000065515	Trk-fused gene [Source:MGI Symbol;Acc:MGI:1338041]	Q9Z1A1		-3.5	6.0E-05	4.9	2.4E-03	1.5	2.0E-01	-0.2	7.5E-01
ENSMUST00000065527	retinoic acid early transcript 1E [Source:MGI Symbol;Acc:MGI:2675273]	D7F2B6	Q9CZQ6	-6.4	2.0E-04	-3.7	1.0E-03	0.4	2.9E-01	-0.3	7.2E-01
ENSMUST00000065534	differentially expressed in FDCP 8 [Source:MGI Symbol;Acc:MGI:1346331]		Q99J78	-8.0	5.1E-04	3.8	3.2E-04	-0.3	6.7E-01	0.2	7.2E-01
ENSMUST00000064265	phospholipase A2, group III [Source:MGI Symbol;Acc:MGI:2444945]	Q8BZT7		5.5	3.6E-02	6.1	3.5E-02	-0.6	8.3E-01	-1.2	4.6E-01
ENSMUST00000065536	family with sequence similarity 161, member B [Source:MGI Symbol;Acc:MGI:2443027]		Q8CB59	4.1	1.1E-03	5.4	8.9E-05	-1.5	9.6E-02	0.8	1.4E-01
ENSMUST00000065562	suppressor of cytokine signaling 4 [Source:MGI Symbol;Acc:MGI:1914546]		Q91ZA6	-1.3	7.7E-03	-5.1	4.9E-04	0.6	2.0E-01	-1.7	1.9E-01
ENSMUST00000064285	glucocorticoid induced transcript 1 [Source:MGI Symbol;Acc:MGI:2179717]	E9QKK4		4.6	4.3E-02	6.8	2.0E-02	0.7	8.0E-01	-1.5	3.2E-01
ENSMUST00000065573	G patch domain containing 2 [Source:MGI Symbol;Acc:MGI:1915019]		Q7TQC7	-3.5	3.2E-03	-1.8	3.8E-02	1.6	5.7E-03	-0.3	7.3E-01
ENSMUST00000065574	TM2 domain containing 3 [Source:MGI Symbol;Acc:MGI:1915884]		Q8BJ83	6.8	3.3E-04	5.3	4.2E-04	-0.3	7.9E-01	0.8	2.3E-01
ENSMUST00000065587	atypical chemokine receptor 3 [Source:MGI Symbol;Acc:MGI:109562]		P56485	8.4	1.5E-04	-3.5	1.1E-03	0.2	5.7E-01	-0.6	4.7E-01
ENSMUST00000065588	guanylate-binding protein 10 [Source:MGI Symbol;Acc:MGI:4359647]	Q000W5		4.9	4.3E-04	3.1	2.1E-02	-1.6	1.7E-01	-1.1	2.4E-01
ENSMUST00000065600	cDNA sequence BC048403 [Source:MGI Symbol;Acc:MGI:2670984]		Q6P1I3	3.7	1.8E-03	4.2	9.3E-04	-0.3	7.7E-01	-0.5	4.1E-01
ENSMUST00000065629	calpastatin [Source:MGI Symbol;Acc:MGI:1098236]		Q8CE80	-4.7	1.1E-05	5.4	1.9E-03	-0.6	6.8E-01	0.0	9.7E-01
ENSMUST00000064364	ring finger protein 185 [Source:MGI Symbol;Acc:MGI:1922078]		Q91YT2	1.9	4.4E-01	1.8	5.8E-01	-0.9	7.5E-01	-0.7	7.7E-01
ENSMUST00000065664	cytochrome b-561 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919273]	Q3TPE5		-6.8	6.6E-04	8.6	2.7E-05	-0.5	7.0E-01	-0.7	2.1E-01
ENSMUST00000064371	mbrane associated guanylate kinase, WW and PDZ domain containing 3 [Source:MGI Symbol;Acc:MGI:19234		Q9EQJ9	-3.9	3.5E-02	-0.8	5.6E-01	-0.3	7.8E-01	-3.3	8.2E-02
ENSMUST00000065666	resistin like gamma [Source:MGI Symbol;Acc:MGI:2667763]	Q8K426		-9.9	5.2E-08	-5.4	1.9E-03	1.7	5.4E-03	-0.6	6.5E-01
ENSMUST00000065678	Sec61 beta subunit [Source:MGI Symbol;Acc:MGI:1913462]		Q9CQS8	-6.8	8.4E-07	5.8	1.8E-02	0.3	8.9E-01	-0.1	9.4E-01
ENSMUST00000065679	SLAM family member 8 [Source:MGI Symbol;Acc:MGI:1921998]	Q3UQA2		3.7	5.6E-04	7.4	3.4E-04	-0.7	6.2E-01	0.0	9.8E-01
ENSMUST00000065692	adaptor-related protein complex 2, beta 1 subunit [Source:MGI Symbol;Acc:MGI:1919020]		Q9DBG3	-4.1	6.3E-03	-1.9	2.9E-01	1.1	3.2E-01	-1.9	3.5E-01
ENSMUST00000065703	T cell-interacting, activating receptor on myeloid cells 1 [Source:MGI Symbol;Acc:MGI:2442280]		B6A8R8	-6.6	1.8E-07	7.0	8.0E-06	-0.8	3.3E-01	-0.1	8.7E-01
ENSMUST00000064393	RNA terminal phosphate cyclase-like 1 [Source:MGI Symbol;Acc:MGI:1913275]		Q9JJT0	0.5	3.7E-01	0.1	8.9E-01	-0.9	8.6E-02	-0.5	4.0E-01
ENSMUST00000065716	echinoderm microtubule associated protein like 5 [Source:MGI Symbol;Acc:MGI:2442513]		Q8BQM8	2.7	1.2E-03	6.4	3.8E-04	-4.0	2.0E-02	-0.2	7.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000065753	transformation related protein 53 regulating kinase B [Source:MGI Symbol;Acc:MGI:1914050]	A2A5R0		4.7	5.9E-04	-5.4	1.7E-04	-1.0	3.0E-02	0.9	3.2E-01
ENSMUST00000065766	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 6 [Source:MGI Symbol;Acc:M	D3Z1A5		3.1	4.6E-03	5.8	6.1E-04	-1.1	3.8E-01	-0.8	2.9E-01
ENSMUST00000065778	hosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150 [Source:MGI Symbol;Acc:MGI:1922919		Q8VD65	-5.8	6.7E-04	-6.4	1.8E-03	0.8	1.4E-01	-0.9	6.0E-01
ENSMUST00000064433	tropomodulin 2 [Source:MGI Symbol;Acc:MGI:1355335]		Q9JKK7	3.8	1.1E-01	3.6	2.4E-01	-0.2	9.3E-01	0.0	9.9E-01
ENSMUST00000065785	tripartite motif-containing 50 [Source:MGI Symbol;Acc:MGI:2664992]		Q810I2	7.9	4.8E-05	5.9	2.0E-04	0.0	9.9E-01	0.0	9.5E-01
ENSMUST00000065788	m large conductance calcium-activated channel, subfamily M, alpha member 1 [Source:MGI Symbol;Acc:MGI	F6ZSN2		9.7	3.4E-02	7.1	3.4E-04	0.0	9.9E-01	0.2	8.0E-01
ENSMUST00000064447	nucleoporin 188 [Source:MGI Symbol;Acc:MGI:2446190]		Q6ZQH8	0.6	2.3E-01	0.9	2.0E-01	0.5	3.5E-01	0.2	7.6E-01
ENSMUST00000065796	Janus kinase 2 [Source:MGI Symbol;Acc:MGI:96629]	G5E852		-4.8	4.1E-03	-1.4	4.7E-01	1.3	2.7E-01	-2.3	2.8E-01
ENSMUST00000065797	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1924219]	Q3UY35	Q9EQC0	4.2	4.7E-05	5.4	1.9E-03	-0.6	6.5E-01	-0.1	8.9E-01
ENSMUST00000065815	glycosyltransferase 8 domain containing 2 [Source:MGI Symbol;Acc:MGI:1922032]	E9PWN8		2.5	3.5E-02	7.8	5.6E-05	-0.6	6.2E-01	-0.8	1.6E-01
ENSMUST00000065841	butyrophilin-like 4 [Source:MGI Symbol;Acc:MGI:1932036]	A2CG29		8.1	4.1E-05	-4.4	5.2E-04	0.6	1.4E-01	-2.0	7.0E-02
ENSMUST00000064480	G protein-coupled receptor 35 [Source:MGI Symbol;Acc:MGI:1929509]	Q3TBY9	Q9ES90	2.3	3.3E-01	1.4	6.1E-01	-1.0	7.0E-01	0.0	9.9E-01
ENSMUST00000065856	hormonally upregulated Neu-associated kinase [Source:MGI Symbol;Acc:MGI:1347352]		O88866	3.6	1.4E-03	4.6	4.8E-03	-1.3	3.6E-01	0.4	6.4E-01
ENSMUST00000065865	THO complex 7 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913481]		Q7TMY4	-6.1	4.4E-05	2.2	2.2E-01	-3.3	9.9E-02	-0.6	6.8E-01
ENSMUST00000064495	hook homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2181664]		Q7TMK6	0.6	3.0E-01	1.4	7.4E-02	0.4	5.0E-01	-0.4	4.9E-01
ENSMUST00000064503	limb and neural patterns [Source:MGI Symbol;Acc:MGI:1918115]		Q7TQ95	-2.4	3.6E-01	-2.6	4.2E-01	-0.3	8.5E-01	-0.1	9.8E-01
ENSMUST00000065870	regulator of G-protein signaling 3 [Source:MGI Symbol;Acc:MGI:1354734]	Z4YJQ4		7.3	2.6E-04	3.3	5.2E-03	0.0	1.0E+00	-0.7	3.6E-01
ENSMUST00000065871	zinc finger protein 229 [Source:MGI Symbol;Acc:MGI:2679295]	E9PWT2		8.7	1.6E-04	2.4	1.7E-02	-2.3	2.6E-02	-0.5	4.6E-01
ENSMUST00000065887	KIF1 binding protein [Source:MGI Symbol;Acc:MGI:1919570]		Q6ZPU9	-4.0	4.1E-04	-1.0	6.5E-01	2.5	1.1E-01	-1.5	5.1E-01
ENSMUST00000065904	heparan sulfate 6-O-sulfotransferase 3 [Source:MGI Symbol;Acc:MGI:1354960]		Q9QYK4	6.8	1.9E-04	-3.8	4.6E-03	1.0	9.1E-02	-1.9	1.7E-01
ENSMUST00000064547	isochorismatase domain containing 2b [Source:MGI Symbol;Acc:MGI:1914691]		Q9DCC7	-1.0	2.0E-01	1.7	1.3E-01	1.6	9.8E-02	-1.1	2.0E-01
ENSMUST00000065906	gamma-glutamyl carboxylase [Source:MGI Symbol;Acc:MGI:1927655]	B2RS80	Q9QYC7	3.0	6.7E-04	8.1	7.3E-05	-0.7	6.1E-01	0.4	5.3E-01
ENSMUST00000065917	nucleosome assembly protein 1-like 1 [Source:MGI Symbol;Acc:MGI:1855693]		P28656	-7.6	2.2E-05	1.9	6.6E-03	-0.1	7.8E-01	0.1	7.9E-01
ENSMUST00000065928	cyclin C [Source:MGI Symbol;Acc:MGI:1858199]	Q8CAS3		-2.9	1.6E-02	2.6	3.8E-03	-0.5	4.1E-01	-1.5	2.6E-02
ENSMUST00000065932	GRIP1 associated protein 1 [Source:MGI Symbol;Acc:MGI:1859616]		Q8VD04	-5.4	9.8E-03	4.4	1.5E-01	-3.5	2.8E-01	0.6	7.4E-01
ENSMUST00000065938	inositol (myo)-1(or 4)-monophosphatase 1 [Source:MGI Symbol;Acc:MGI:1933158]	Q924B0		2.8	1.9E-03	7.6	3.5E-05	-1.0	3.6E-01	-0.1	9.0E-01
ENSMUST00000064635	eukaryotic elongation factor 2 lysine methyltransferase [Source:MGI Symbol;Acc:MGI:1917761]		Q3UZW7	0.9	1.2E-01	1.3	7.7E-02	0.1	8.9E-01	-0.3	5.8E-01
ENSMUST00000064637	ring finger protein 103 [Source:MGI Symbol;Acc:MGI:109483]		Q9R1W3	-2.0	1.3E-01	-3.1	1.1E-01	0.7	5.5E-01	1.8	3.2E-01
ENSMUST00000064639	ubiquitin-associated protein 2-like [Source:MGI Symbol;Acc:MGI:1921633]		Q80X50	0.8	2.0E-01	0.5	5.9E-01	0.6	3.4E-01	1.0	2.2E-01
ENSMUST00000065941	ubiquitin specific peptidase 21 [Source:MGI Symbol;Acc:MGI:1353665]	E9PUE2		-3.7	7.9E-03	1.8	4.7E-02	0.2	7.9E-01	0.4	5.2E-01
ENSMUST00000065950	cDNA sequence BC049762 [Source:MGI Symbol;Acc:MGI:3039622]	Q8C601		5.2	6.5E-03	5.1	1.4E-02	1.1	5.1E-01	0.1	9.4E-01
ENSMUST00000065956	predicted gene 5444 [Source:MGI Symbol;Acc:MGI:3644242]	Q8CDE5		7.3	4.2E-05	7.3	5.9E-04	-0.5	7.3E-01	0.0	9.6E-01
ENSMUST00000065957	synaptotagmin V [Source:MGI Symbol;Acc:MGI:1926368]		Q9R0N5	7.1	7.2E-05	-1.8	2.2E-01	0.3	7.4E-01	-1.9	2.3E-01
ENSMUST00000064664	RAB7B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2442295]	J9UUF7	Q8VEA8	-2.0	9.9E-02	-0.6	5.6E-01	-1.5	8.8E-02	-3.0	2.8E-02
ENSMUST00000065977	nardilysin, N-arginine dibasic convertase, NRD convertase 1 [Source:MGI Symbol;Acc:MGI:1201386]		Q8BHG1	-7.5	1.5E-03	-6.5	2.6E-05	0.9	1.8E-02	-0.4	6.8E-01
ENSMUST00000065987	4-aminobutyrate aminotransferase [Source:MGI Symbol;Acc:MGI:2443582]		P61922	8.1	3.4E-05	1.8	2.6E-02	0.0	9.4E-01	-0.4	5.3E-01
ENSMUST00000065997	aprataxin and PNKP like factor [Source:MGI Symbol;Acc:MGI:1919353]		Q9D842	4.4	2.7E-02	6.1	1.0E-03	-0.5	7.3E-01	-0.7	3.4E-01
ENSMUST00000064701	protein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I) [Source:MGI Symbol;Acc:MGI:23	Q3TAW1	Q8R087	-0.3	5.9E-01	1.2	1.4E-01	1.3	4.6E-02	-0.2	7.6E-01
ENSMUST00000066003	trans-acting transcription factor 3 [Source:MGI Symbol;Acc:MGI:1277166]		O70494	-5.5	5.6E-06	0.3	8.6E-01	2.0	1.8E-01	-3.1	1.7E-01
ENSMUST00000064709	cDNA sequence BC004004 [Source:MGI Symbol;Acc:MGI:2136782]		Q99KU6	0.0	9.8E-01	-0.3	6.8E-01	-0.2	6.1E-01	0.1	9.4E-01
ENSMUST00000064725	erine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1 [Source:MGI Symbol;Acc:MGI:8809	Q543J5	P32261	-0.7	7.3E-01	-0.8	6.9E-01	-1.4	4.2E-01	-1.3	5.4E-01
ENSMUST00000066039	cleavage stimulation factor, 3' pre-RNA subunit 2, tau [Source:MGI Symbol;Acc:MGI:1932622]		Q8C7E9	-1.9	1.0E-03	-4.6	2.4E-04	-0.4	3.3E-01	-0.8	3.5E-01
ENSMUST00000066049	transmembrane protein 200A [Source:MGI Symbol;Acc:MGI:1924470]	B2RUN2	Q8C817	7.8	1.6E-05	-1.0	1.1E-01	1.1	2.0E-02	0.0	9.7E-01
ENSMUST00000066058	mitogen-activated protein kinase binding protein 1 [Source:MGI Symbol;Acc:MGI:1347004]	A0A0A0MQA2		3.2	3.1E-04	3.0	9.1E-03	-0.3	7.1E-01	0.3	7.1E-01
ENSMUST00000064763	zinc finger protein 608 [Source:MGI Symbol;Acc:MGI:2442338]	B9EKR3	Q56A10	-1.1	7.1E-02	-0.8	2.8E-01	0.5	3.5E-01	0.2	7.8E-01
ENSMUST00000066060	B cell leukemia/lymphoma 11B [Source:MGI Symbol;Acc:MGI:1929913]		Q99PV8	4.2	3.8E-05	-6.4	7.0E-04	-1.2	3.1E-02	-0.7	6.4E-01
ENSMUST00000066070	eukaryotic translation initiation factor 3, subunit K [Source:MGI Symbol;Acc:MGI:1921080]		Q9DBZ5	-6.2	1.4E-05	-3.4	1.4E-03	-0.1	8.0E-01	-0.4	5.8E-01
ENSMUST00000066091	SMAD family member 1 [Source:MGI Symbol;Acc:MGI:109452]		P70340	-2.6	1.2E-03	6.6	3.1E-04	-0.6	6.3E-01	-0.5	4.7E-01
ENSMUST00000066106	RIKEN cDNA A730061H03 gene [Source:MGI Symbol;Acc:MGI:2445099]	Q8BGD2		4.5	4.5E-03	7.1	2.0E-03	0.7	6.5E-01	1.0	2.7E-01
ENSMUST00000066121	membrane-associated ring finger (C3HC4) 2 [Source:MGI Symbol;Acc:MGI:1925915]	Q8CA25		-2.9	9.2E-03	5.5	3.3E-03	-0.4	7.7E-01	0.0	9.8E-01
ENSMUST00000064786	zinc finger protein 672 [Source:MGI Symbol;Acc:MGI:2442105]		Q99LH4	0.8	7.0E-01	2.5	3.6E-01	1.8	4.8E-01	0.1	9.5E-01
ENSMUST00000066134	ribose 5-phosphate isomerase A [Source:MGI Symbol;Acc:MGI:103254]		P47968	-2.9	9.0E-04	-5.1	1.3E-02	-0.5	5.1E-01	1.1	5.2E-01
ENSMUST00000066140	protocadherin gamma subfamily A, 8 [Source:MGI Symbol;Acc:MGI:1935221]	Q91XX0		7.1	1.3E-03	4.8	1.1E-01	-0.6	8.3E-01	2.5	1.5E-01
ENSMUST00000064794	fibroblast growth factor 7 [Source:MGI Symbol;Acc:MGI:95521]	Q544I6	P36363	3.6	6.5E-02	4.6	2.1E-02	-1.5	4.2E-01	-2.5	7.5E-02
ENSMUST00000066149	protocadherin gamma subfamily A, 8 [Source:MGI Symbol;Acc:MGI:1935221]	Q91XY0		8.2	1.0E-05	4.9	7.0E-02	0.6	8.1E-01	0.3	8.3E-01
ENSMUST00000066155	adenosine deaminase-like [Source:MGI Symbol;Acc:MGI:1923144]		Q80SY6	-5.7	2.3E-03	-7.8	1.1E-03	-0.6	2.9E-01	0.2	9.1E-01
ENSMUST00000066157	predicted gene 9913 [Source:MGI Symbol;Acc:MGI:3642395]	Q8BQQ2		7.0	2.0E-04	8.2	1.6E-05	-1.8	1.5E-01	-0.4	3.6E-01
ENSMUST00000066160	checkpoint kinase 2 [Source:MGI Symbol;Acc:MGI:1355321]	Q543W6	Q9Z265	2.3	1.8E-03	0.6	6.6E-01	-4.6	8.8E-03	1.0	4.1E-01
ENSMUST00000066163	RIKEN cDNA A930004D18 gene [Source:MGI Symbol;Acc:MGI:1925190]	Q8C8W7		7.3	1.3E-05	5.4	2.3E-03	0.1	9.2E-01	-0.5	4.9E-01
ENSMUST00000066166	tolloid-like [Source:MGI Symbol;Acc:MGI:106923]	G3X9F5		8.7	3.9E-06	-11.0	1.1E-03	0.7	1.8E-01	2.7	2.7E-01
ENSMUST00000064831	ectonucleoside triphosphate diphosphohydrolase 4 [Source:MGI Symbol;Acc:MGI:1914714]		Q9DBT4	-2.0	1.1E-01	3.0	5.1E-02	1.6	2.2E-01	-3.4	1.5E-02
ENSMUST00000066173	fucosyltransferase 10 [Source:MGI Symbol;Acc:MGI:2384748]		Q5F2L2	4.1	2.8E-02	7.7	5.6E-04	1.3	3.9E-01	0.8	3.3E-01
ENSMUST00000064848	nucleoporin 107 [Source:MGI Symbol;Acc:MGI:2143854]		Q8BH74	-1.2	3.5E-02	-1.4	4.1E-02	-0.6	1.4E-01	-0.4	5.1E-01
ENSMUST00000064853	RIKEN cDNA 1700030K09 gene [Source:MGI Symbol;Acc:MGI:1919504]		Q922C1	-1.9	1.5E-01	1.2	4.1E-01	1.8	1.3E-01	-1.3	3.6E-01
ENSMUST00000066175	ATP-binding cassette, sub-family G (WHITE), member 5 [Source:MGI Symbol;Acc:MGI:1351659]	Q540E8	Q99PE8	7.2	6.7E-05	6.0	7.1E-05	-2.3	5.3E-02	-0.4	5.0E-01
ENSMUST00000066177	catenin (cadherin associated protein), delta 1 [Source:MGI Symbol;Acc:MGI:105100]		P30999	-5.1	2.9E-04	2.2	5.5E-01	-0.6	8.7E-01	3.9	1.8E-01
ENSMUST00000064883	ology domain-containing, family A (phosphoinositide binding specific) member 2 [Source:MGI Symbol;Acc:M		Q9ERS5	-0.5	3.4E-01	1.0	1.7E-01	1.0	8.9E-02	-0.5	4.0E-01
ENSMUST00000064889	solute carrier family 29 (nucleoside transporters), member 1 [Source:MGI Symbol;Acc:MGI:1927073]	Q3TCZ2	Q9JIM1	-2.2	6.3E-02	-4.9	1.3E-02	-1.2	1.2E-01	1.5	3.8E-01
ENSMUST00000066187	nescient helix loop helix 2 [Source:MGI Symbol;Acc:MGI:97324]		Q64221	7.3	1.0E-05	-1.6	3.3E-01	1.3	2.3E-01	-0.1	9.5E-01
ENSMUST00000066197	acid-sensing (proton-gated) ion channel 2 [Source:MGI Symbol;Acc:MGI:1100867]	Q3UYD3	Q925H0	8.4	7.8E-05	-5.3	2.0E-04	0.3	4.4E-01	0.8	3.7E-01
ENSMUST00000064916	serine (or cysteine) peptidase inhibitor, clade B, member 2 [Source:MGI Symbol;Acc:MGI:97609]	Q542A3	P12388	0.3	7.7E-01	-4.8	1.7E-03	-5.9	4.4E-05	-0.8	5.0E-01
ENSMUST00000066207	matrix extracellular phosphoglycoprotein with ASARM motif (bone) [Source:MGI Symbol;Acc:MGI:2137384]	Q8K4L6		7.6	4.2E-04	-6.3	2.5E-03	1.2	4.0E-02	-0.8	6.6E-01
ENSMUST00000066208	aldehyde dehydrogenase family 7, member A1 [Source:MGI Symbol;Acc:MGI:108186]		Q9DBF1	6.3	2.9E-03	-5.6	5.7E-04	1.0	7.4E-02	-0.3	8.1E-01
ENSMUST00000066211	G protein-coupled estrogen receptor 1 [Source:MGI Symbol;Acc:MGI:1924104]		Q8BMP4	5.5	6.6E-04	2.3	4.8E-03	0.2	6.9E-01	-0.7	2.4E-01
ENSMUST00000066257	KH domain containing, RNA binding, signal transduction associated 1 [Source:MGI Symbol;Acc:MGI:893579		Q60749	-3.7	2.2E-03	7.7	6.7E-05	-0.6	6.1E-01	-0.3	6.5E-01
ENSMUST00000066264	enoyl coenzyme A hydratase 1, peroxisomal [Source:MGI Symbol;Acc:MGI:1858208]		O35459	-9.7	1.1E-05	6.2	1.8E-04	-0.6	5.8E-01	-0.5	3.9E-01
ENSMUST00000066272	7 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:134		Q9R1C0	-3.1	1.1E-03	4.8	4.8E-04	-2.1	5.0E-02	0.3	6.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000066277	aldehyde dehydrogenase family 3, subfamily A2 [Source:MGI Symbol;Acc:MGI:1353452]	B1ATI0		4.9	4.2E-03	8.2	7.8E-03	-0.8	7.7E-01	-2.9	6.5E-02
ENSMUST00000066279	SH3-domain binding protein 4 [Source:MGI Symbol;Acc:MGI:2138297]		Q92116	3.9	4.5E-05	-5.9	5.4E-04	0.9	4.8E-02	-0.7	5.6E-01
ENSMUST00000064953	palmitoyl-protein thioesterase 2 [Source:MGI Symbol;Acc:MGI:1860075]		O35448	1.8	3.5E-01	1.8	3.8E-01	-0.9	5.9E-01	-1.0	5.9E-01
ENSMUST00000066285	heat shock protein 12A [Source:MGI Symbol;Acc:MGI:1920692]		Q8K0U4	7.2	6.3E-06	-3.4	6.1E-03	1.1	4.4E-02	0.4	7.0E-01
ENSMUST00000066295	potassium channel, subfamily K, member 3 [Source:MGI Symbol;Acc:MGI:1100509]		O35111	7.8	4.5E-05	7.4	4.2E-03	1.6	4.2E-01	0.0	9.9E-01
ENSMUST00000066298	RIKEN cDNA B430305J03 gene [Source:MGI Symbol;Acc:MGI:3697707]	Q8BQQ8		4.6	3.4E-02	-1.0	2.8E-01	1.0	9.0E-02	-0.1	9.4E-01
ENSMUST00000066308	cilia and flagella associated protein 58 [Source:MGI Symbol;Acc:MGI:2685815]		B2RW38	7.6	2.2E-05	4.2	1.6E-04	-4.1	7.9E-04	-0.5	3.0E-01
ENSMUST00000065028	active BCR-related gene [Source:MGI Symbol;Acc:MGI:107771]		Q5SSL4	-4.6	3.1E-01	-2.5	5.0E-01	-1.8	4.8E-01	-3.9	4.2E-01
ENSMUST00000065039	bactericidal permeablility increasing protein [Source:MGI Symbol;Acc:MGI:3045315]		Q67E05	3.8	1.4E-01	7.2	1.9E-02	-0.2	9.5E-01	-3.6	4.3E-02
ENSMUST00000065040	Rho guanine nucleotide exchange factor (GEF) 15 [Source:MGI Symbol;Acc:MGI:3045246]		Q5FWH6	3.0	1.8E-01	4.6	5.5E-02	-0.8	7.2E-01	-2.4	1.9E-01
ENSMUST00000066330	myosin phosphatase Rho interacting protein [Source:MGI Symbol;Acc:MGI:1349438]	Q5SWZ5		2.5	1.6E-03	6.6	1.2E-04	-0.4	7.4E-01	0.5	3.9E-01
ENSMUST00000066345	C-type lectin domain family 16, member A [Source:MGI Symbol;Acc:MGI:1921624]		Q80U30	5.7	2.2E-02	-4.2	8.5E-03	0.7	2.6E-01	-0.8	5.8E-01
ENSMUST00000066368	MyoD family inhibitor [Source:MGI Symbol;Acc:MGI:107687]		P70331	7.1	5.0E-05	1.4	5.2E-02	-2.2	4.3E-03	0.0	9.5E-01
ENSMUST00000066379	coiled-coil-helix-coiled-coil-helix domain containing 3 [Source:MGI Symbol;Acc:MGI:1913325]		Q9CRB9	-5.8	4.0E-04	-0.8	4.4E-01	-1.7	4.8E-02	-4.2	7.6E-03
ENSMUST00000066384	zinc finger protein of the cerebellum 4 [Source:MGI Symbol;Acc:MGI:107201]		Q61467	6.2	1.7E-04	-0.1	8.8E-01	1.1	9.1E-02	-0.5	5.8E-01
ENSMUST00000066387	retinol dehydrogenase 8 [Source:MGI Symbol;Acc:MGI:2685028]	D3Z6W3		7.5	9.3E-05	3.2	2.8E-03	-4.1	3.2E-03	-0.8	2.4E-01
ENSMUST00000066391	Sfi1 homolog, spindle assembly associated (yeast) [Source:MGI Symbol;Acc:MGI:1926137]		Q3UZY0	3.2	4.8E-04	4.3	1.8E-01	-5.6	1.2E-01	-1.5	5.2E-01
ENSMUST00000066401	cathepsin D [Source:MGI Symbol;Acc:MGI:88562]	F8WIR1		-12.9	1.4E-05	1.6	3.7E-02	-1.2	7.3E-02	0.5	3.9E-01
ENSMUST00000066408	RIKEN cDNA 1700016K19 gene [Source:MGI Symbol;Acc:MGI:1921480]		Q810M6	6.8	1.7E-04	-4.2	5.9E-02	1.5	9.9E-02	0.4	8.5E-01
ENSMUST00000066412	angiotensin II receptor, type 1a [Source:MGI Symbol;Acc:MGI:87964]		P29754	5.7	4.0E-04	6.3	1.7E-05	-3.2	7.6E-03	-0.3	5.5E-01
ENSMUST00000066427	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	Q8C405		-2.4	2.9E-03	5.9	2.0E-04	-1.5	2.1E-01	0.3	6.4E-01
ENSMUST00000066432	sodium channel, voltage-gated, type III, alpha [Source:MGI Symbol;Acc:MGI:98249]	A2ASI5		7.4	4.0E-05	-3.7	1.6E-02	0.7	2.5E-01	0.0	9.9E-01
ENSMUST00000066437	family with sequence similarity 216, member B [Source:MGI Symbol;Acc:MGI:2145738]		Q8CC14	6.1	6.5E-04	5.9	2.3E-03	-0.4	7.8E-01	-0.9	3.2E-01
ENSMUST00000066439	exocyst complex component 6 [Source:MGI Symbol;Acc:MGI:1351611]	Q3U9D6		-4.8	2.0E-05	1.1	2.9E-01	-3.5	8.3E-03	-1.0	3.0E-01
ENSMUST00000065135	nucleoside-triphosphatase, cancer-related [Source:MGI Symbol;Acc:MGI:1913816]	Q8C373		-1.1	8.8E-02	-0.4	6.6E-01	1.3	4.8E-02	0.5	4.8E-01
ENSMUST00000065143	BCL6 interacting corepressor [Source:MGI Symbol;Acc:MGI:1918708]		Q8CGN4	0.5	8.8E-01	6.0	1.1E-01	3.3	3.1E-01	-2.2	4.3E-01
ENSMUST00000066461	predicted gene 9922 [Source:MGI Symbol;Acc:MGI:3642123]	Q8C3P1		4.7	3.2E-03	4.6	5.4E-04	-0.3	7.6E-01	0.3	6.0E-01
ENSMUST00000066465	acyl-CoA synthetase medium-chain family member 5 [Source:MGI Symbol;Acc:MGI:2444086]		Q8BGA8	7.4	3.7E-05	-8.0	9.9E-04	-0.1	8.4E-01	0.6	7.5E-01
ENSMUST00000066466	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]		Q6PHZ2	-5.3	2.0E-03	3.7	1.1E-02	0.0	9.9E-01	0.1	9.0E-01
ENSMUST00000065169	GATA zinc finger domain containing 2A [Source:MGI Symbol;Acc:MGI:2384585]	E9QMN5		-3.1	1.5E-01	-0.6	8.3E-01	1.9	3.4E-01	-0.6	8.0E-01
ENSMUST00000065173	leucine rich repeat and Ig domain containing 2 [Source:MGI Symbol;Acc:MGI:2442298]	B2RQD4	Q3URE9	4.0	9.0E-02	3.9	1.6E-01	-0.3	9.0E-01	-0.2	9.3E-01
ENSMUST00000066469	coatomer protein complex, subunit epsilon [Source:MGI Symbol;Acc:MGI:1891702]		O89079	-4.7	4.2E-05	6.8	2.2E-02	-4.5	1.6E-01	-0.5	7.6E-01
ENSMUST00000066475	ceramide synthase 3 [Source:MGI Symbol;Acc:MGI:2681008]		Q1A3B0	3.0	9.4E-04	7.9	3.7E-05	-0.6	6.2E-01	-0.3	5.2E-01
ENSMUST00000065210	PYM homolog 1, exon junction complex associated factor [Source:MGI Symbol;Acc:MGI:1925678]		Q8CHP5	-0.6	7.9E-01	2.3	3.3E-01	0.3	8.9E-01	-2.6	2.1E-01
ENSMUST00000066489	prolyl 3-hydroxylase family member 4 (non-enzymatic) [Source:MGI Symbol;Acc:MGI:1913430]		Q8K2B0	7.3	2.4E-05	7.7	2.5E-05	0.1	9.3E-01	-0.2	6.7E-01
ENSMUST00000065220	purinergic receptor P2Y, G-protein coupled, 14 [Source:MGI Symbol;Acc:MGI:2155705]	Q544F4	Q9ESG6	-0.8	6.1E-01	-0.2	8.8E-01	-1.5	2.5E-01	-2.1	2.1E-01
ENSMUST00000066497	zinc finger protein 191 [Source:MGI Symbol;Acc:MGI:1929704]		Q91VN1	-1.8	3.8E-03	7.9	6.0E-05	-0.6	6.2E-01	0.0	9.8E-01
ENSMUST00000066510	spermatogenesis associated 31 subfamily D, member 1A [Source:MGI Symbol;Acc:MGI:1919469]	E9QA35		9.1	5.7E-05	0.6	3.4E-01	-1.1	5.7E-02	0.2	7.7E-01
ENSMUST00000065253	acyl-CoA thioesterase 11 [Source:MGI Symbol;Acc:MGI:1913736]	A2AVR6		-0.8	5.7E-01	0.6	7.6E-01	2.1	1.4E-01	0.8	6.8E-01
ENSMUST00000066514	nudix (nucleoside diphosphate linked moiety X)-type motif 7 [Source:MGI Symbol;Acc:MGI:1914778]		Q99P30	-5.3	2.7E-04	-1.2	9.2E-02	0.6	1.4E-01	0.0	9.9E-01
ENSMUST00000066529	natriuretic peptide receptor 3 [Source:MGI Symbol;Acc:MGI:97373]		P70180	7.5	2.0E-06	-2.4	1.1E-02	-0.1	7.8E-01	0.1	8.9E-01
ENSMUST00000066532	lipase, endothelial [Source:MGI Symbol;Acc:MGI:1341803]	C0LQ91	Q9WVG5	-5.3	3.7E-07	-7.1	1.1E-04	0.3	5.3E-01	-1.6	2.3E-01
ENSMUST00000066540	serine dehydratase [Source:MGI Symbol;Acc:MGI:98270]	Q3UEN6	Q8VBT2	5.8	7.7E-04	3.7	1.4E-03	-1.4	1.2E-01	-0.2	7.8E-01
ENSMUST00000066545	SH3/ankyrin domain gene 3 [Source:MGI Symbol;Acc:MGI:1930016]		Q4ACU6	6.1	1.6E-04	1.3	1.8E-01	0.5	4.9E-01	1.5	8.4E-02
ENSMUST00000065302	centromere protein J [Source:MGI Symbol;Acc:MGI:2684927]		Q569L8	-0.6	2.8E-01	-1.0	1.6E-01	-0.2	7.2E-01	0.3	6.8E-01
ENSMUST00000065308	antizyme inhibitor 1 [Source:MGI Symbol;Acc:MGI:1859169]		O35484	-1.0	2.0E-01	1.7	1.2E-01	2.1	3.1E-02	-0.7	4.5E-01
ENSMUST00000066554	uromodulin-like 1 [Source:MGI Symbol;Acc:MGI:1929785]		Q5DID3	9.2	3.0E-05	-6.4	1.5E-03	0.5	3.3E-01	-0.9	6.0E-01
ENSMUST00000065329	transmembrane protein 248 [Source:MGI Symbol;Acc:MGI:1918917]		Q3TBN1	-1.3	4.8E-02	0.5	5.4E-01	1.7	1.6E-02	-0.1	8.6E-01
ENSMUST00000066559	minichromosome maintenance deficient 8 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913884]		Q9CWV1	6.1	2.1E-04	-2.3	1.3E-03	0.6	5.5E-02	-0.5	3.8E-01
ENSMUST00000066560	galactosidase, beta 1-like 2 [Source:MGI Symbol;Acc:MGI:2388283]	E0CYE1		6.5	1.5E-04	-5.1	1.4E-04	-0.2	6.5E-01	-0.3	7.1E-01
ENSMUST00000065353	yes-associated protein 1 [Source:MGI Symbol;Acc:MGI:103262]		P46938	3.5	1.7E-01	5.0	7.9E-02	-0.4	8.7E-01	-1.9	2.9E-01
ENSMUST00000066583	predicted gene 9925 [Source:MGI Symbol;Acc:MGI:3641738]	F6T2U3		5.5	1.3E-02	-3.0	1.5E-03	-0.5	2.6E-01	-0.2	8.1E-01
ENSMUST00000066587	acyl-Coenzyme A oxidase 1, palmitoyl [Source:MGI Symbol;Acc:MGI:1330812]		Q9R0H0	-5.1	3.0E-03	6.1	2.9E-04	-0.5	6.5E-01	0.2	7.7E-01
ENSMUST00000066594	SH2 domain containing 4A [Source:MGI Symbol;Acc:MGI:1919531]		Q9D7V1	9.3	5.2E-05	-6.6	7.7E-04	-1.5	2.0E-02	-1.6	3.3E-01
ENSMUST00000066610	family with sequence similarity 212, member B [Source:MGI Symbol;Acc:MGI:1923497]		Q80VY2	6.0	3.8E-06	-5.8	3.1E-03	0.4	4.1E-01	-0.6	7.2E-01
ENSMUST00000065373	transmembrane protein 70 [Source:MGI Symbol;Acc:MGI:1915068]		Q921N7	-1.4	4.5E-01	-2.0	3.9E-01	-0.2	8.9E-01	0.4	8.7E-01
ENSMUST00000066632	angel homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1196310]		Q8K1C0	-6.7	1.2E-03	3.9	1.1E-01	-0.8	7.2E-01	1.4	3.9E-01
ENSMUST00000066650	debranching enzyme homolog 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1931520]		Q923B1	-2.8	7.6E-03	6.6	1.4E-04	-0.5	6.5E-01	-0.6	2.9E-01
ENSMUST00000065388	suppressor of Ty 7-like [Source:MGI Symbol;Acc:MGI:1919445]		Q9CZV5	0.9	3.4E-01	1.3	3.6E-01	0.7	4.7E-01	0.4	7.5E-01
ENSMUST00000065398	nucleoporin 214 [Source:MGI Symbol;Acc:MGI:1095411]		Q80U93	-1.1	8.0E-02	1.0	1.7E-01	0.9	1.1E-01	-1.2	9.8E-02
ENSMUST00000066652	kinase D-interacting substrate 220 [Source:MGI Symbol;Acc:MGI:1924730]	E9Q9B7		-2.8	1.6E-04	4.7	2.9E-04	-1.2	1.5E-01	0.2	7.2E-01
ENSMUST00000065420	Holliday junction recognition protein [Source:MGI Symbol;Acc:MGI:2685821]	E9Q4T0		1.1	4.5E-01	2.0	4.1E-01	2.4	1.8E-01	1.6	4.5E-01
ENSMUST00000066674	carbonic anhydrase 8 [Source:MGI Symbol;Acc:MGI:88253]		P28651	2.9	1.0E-03	-1.9	1.1E-01	-1.3	1.4E-01	-2.4	8.6E-02
ENSMUST00000066675	mitochondrial translational initiation factor 3 [Source:MGI Symbol;Acc:MGI:1923616]	A4QMQ0	Q9CZD5	4.7	3.8E-05	-7.3	7.1E-04	1.4	1.1E-02	3.9	2.3E-02
ENSMUST00000066701	interferon, alpha-inducible protein 27 [Source:MGI Symbol;Acc:MGI:1277180]	Q9D1E1		-6.3	8.4E-04	7.8	3.0E-04	-0.7	6.7E-01	-0.3	6.5E-01
ENSMUST00000066708	dentin matrix protein 1 [Source:MGI Symbol;Acc:MGI:94910]		O55188	6.1	4.4E-04	6.2	5.5E-04	-0.4	7.5E-01	-0.8	3.2E-01
ENSMUST00000066717	transcription factor 4 [Source:MGI Symbol;Acc:MGI:98506]	E9Q8G4		5.8	8.0E-04	0.6	4.2E-01	0.9	1.8E-01	-2.3	1.9E-02
ENSMUST00000065478	growth factor independent 1 [Source:MGI Symbol;Acc:MGI:103170]	H3BJM0		0.7	3.1E-01	1.2	2.1E-01	0.4	5.9E-01	-0.1	9.4E-01
ENSMUST00000065482	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11 [Source:MGI Symbol;Acc:	Q543U0	P97783	-0.1	9.1E-01	0.9	3.2E-01	0.4	5.8E-01	-0.6	4.7E-01
ENSMUST00000066728	phosphodiesterase 5A, cGMP-specific [Source:MGI Symbol;Acc:MGI:2651499]		Q8CG03	5.2	3.6E-05	6.5	2.4E-04	-0.5	6.7E-01	-0.7	2.7E-01
ENSMUST00000065487	periaxin [Source:MGI Symbol;Acc:MGI:108176]	Q6NVF7		-1.1	4.4E-01	0.0	9.9E-01	1.9	1.8E-01	0.8	6.4E-01
ENSMUST00000066742	predicted gene 9930 [Source:MGI Symbol;Acc:MGI:3642400]	E9Q104		7.5	3.7E-05	7.2	4.1E-05	-1.2	2.7E-01	-0.3	5.6E-01
ENSMUST00000065499	proline rich 5 (renal) [Source:MGI Symbol;Acc:MGI:1924714]		Q812A5	-0.6	6.8E-01	6.4	3.9E-03	2.6	1.4E-01	-4.4	6.6E-03
ENSMUST00000066760	SUMO/sentrin specific peptidase 3 [Source:MGI Symbol;Acc:MGI:2158736]		Q9EP97	-4.6	1.7E-02	-4.4	8.2E-05	1.1	8.6E-03	-5.2	4.4E-04
ENSMUST00000066774	tumor suppressor candidate 1 [Source:MGI Symbol;Acc:MGI:2684283]		Q673H1	-2.8	8.0E-04	-4.6	3.1E-02	0.3	7.0E-01	0.4	8.5E-01
ENSMUST00000065512	rhotekin [Source:MGI Symbol;Acc:MGI:107371]		Q8C6B2	0.8	5.0E-01	0.2	9.1E-01	-0.4	7.6E-01	0.3	8.3E-01
ENSMUST00000066778	phosphatidylinositol 4-kinase type 2 alpha [Source:MGI Symbol;Acc:MGI:1934031]		Q2TBE6	-2.9	1.1E-04	-3.9	2.8E-04	0.1	8.5E-01	0.5	5.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000065523	transformation related protein 63 [Source:MGI Symbol;Acc:MGI:1330810]		O88898	3.4	1.3E-01	5.0	4.3E-02	-0.5	8.2E-01	-2.1	1.9E-01
ENSMUST00000066780	MHC I like leukocyte 1 [Source:MGI Symbol;Acc:MGI:2179988]	Q8HWE7		7.8	5.4E-05	-5.0	2.2E-03	0.1	8.0E-01	-1.3	3.5E-01
ENSMUST00000066791	transmembrane protein 179 [Source:MGI Symbol;Acc:MGI:2144891]		Q8BHH9	8.9	2.3E-05	7.5	6.7E-05	-0.6	6.2E-01	-0.7	2.2E-01
ENSMUST00000066804	sirtuin 5 [Source:MGI Symbol;Acc:MGI:1915596]		Q8K2C6	2.5	4.3E-03	-2.2	1.2E-01	2.2	1.6E-02	-3.6	5.7E-02
ENSMUST00000066807	epair cross-complementing rodent repair deficiency, complementation group 6 [Source:MGI Symbol;Acc:MGI:	F8VPZ5		1.9	2.4E-03	5.2	2.3E-03	0.9	4.6E-01	-0.2	7.9E-01
ENSMUST00000065537	junction-mediating and regulatory protein [Source:MGI Symbol;Acc:MGI:1913096]			-0.2	5.3E-01	1.2	2.7E-02	1.0	2.7E-02	-0.5	2.5E-01
ENSMUST00000065539	DAN domain family, member 5 [Source:MGI Symbol;Acc:MGI:1344365]		Q76LW6	0.7	2.5E-01	2.2	2.8E-02	1.5	5.4E-02	0.0	9.5E-01
ENSMUST00000066814	a disintegrin and metallopeptidase domain 39 [Source:MGI Symbol;Acc:MGI:3045694]	Q7M762		5.6	5.2E-03	-1.2	5.4E-02	0.6	1.2E-01	0.4	4.5E-01
ENSMUST00000066824	SH3-domain GRB2-like (endophilin) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1920344]		Q8VD37	6.3	3.8E-04	8.1	1.8E-05	0.4	7.0E-01	0.4	3.1E-01
ENSMUST00000066852	osteocrin [Source:MGI Symbol;Acc:MGI:2677164]		P61364	5.1	1.4E-04	-3.0	3.1E-02	0.5	4.3E-01	0.0	9.8E-01
ENSMUST00000066854	Wolf-Hirschhorn syndrome candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1276574]		Q8BVE8	5.8	1.5E-02	4.7	3.2E-03	-2.4	1.1E-01	-0.2	7.5E-01
ENSMUST00000066859	complement component factor h [Source:MGI Symbol;Acc:MGI:88385]		P06909	-6.7	8.5E-03	-0.3	7.2E-01	-8.0	1.5E-04	0.8	3.3E-01
ENSMUST00000066873	plakophilin 3 [Source:MGI Symbol;Acc:MGI:1891830]		Q9QY23	4.2	2.6E-02	0.1	8.7E-01	-4.1	1.0E-03	0.7	3.8E-01
ENSMUST00000066880	calpain 12 [Source:MGI Symbol;Acc:MGI:1891369]	E9QL26		6.4	1.3E-04	5.3	1.5E-03	0.8	4.9E-01	-0.8	2.8E-01
ENSMUST00000065601	beta-transducin repeat containing protein [Source:MGI Symbol;Acc:MGI:1338871]		Q3ULA2	0.4	8.7E-01	1.8	5.9E-01	2.0	4.7E-01	0.6	8.1E-01
ENSMUST00000065603	leucine rich repeat containing 49 [Source:MGI Symbol;Acc:MGI:2442689]	E9QM16		2.9	1.3E-01	7.1	1.3E-02	1.8	4.4E-01	-2.4	1.4E-01
ENSMUST00000065625	tRNA methyltransferase 1 like [Source:MGI Symbol;Acc:MGI:1916185]			-1.3	1.6E-01	-4.7	3.2E-02	0.3	7.0E-01	3.6	7.3E-02
ENSMUST00000066885	SKI/DACH domain containing 1 [Source:MGI Symbol;Acc:MGI:1919918]		Q80YR3	5.8	6.5E-05	-4.6	8.0E-05	-0.3	3.4E-01	-0.4	6.1E-01
ENSMUST00000065630	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 [Source:MGI Symbol;Acc:MGI:1924841]		Q80Y44	-0.1	7.7E-01	-1.3	4.9E-02	-1.1	2.3E-02	0.1	9.0E-01
ENSMUST00000065638				2.1	3.8E-01	1.1	6.8E-01	-0.4	8.7E-01	0.6	7.9E-01
ENSMUST00000065648	torsin A interacting protein 2 [Source:MGI Symbol;Acc:MGI:3582695]		Q9ER81	-1.4	6.0E-01	-3.5	3.0E-01	-2.5	1.9E-01	-0.5	8.9E-01
ENSMUST00000066888	JTP18, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1923402	Q3U3Q3	Q5SSI6	-5.8	3.3E-05	-4.7	4.5E-02	2.3	2.3E-02	0.2	9.4E-01
ENSMUST00000066889	G-protein signalling modulator 1 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:1915089]		Q6IR34	7.4	3.1E-03	-9.4	3.5E-07	-0.3	3.7E-01	-0.8	2.8E-01
ENSMUST00000065668	neurogranin [Source:MGI Symbol;Acc:MGI:1927184]		P60761	0.1	7.9E-01	-2.1	4.9E-03	-2.2	2.9E-04	0.0	9.9E-01
ENSMUST00000066905	cell adhesion molecule with homology to L1CAM [Source:MGI Symbol;Acc:MGI:1098266]		P70232	5.9	1.1E-05	-8.2	2.6E-05	-0.2	4.2E-01	1.2	2.8E-01
ENSMUST00000066949	zinc finger, DHHC domain containing 25 [Source:MGI Symbol;Acc:MGI:1917323]	Q810M4		6.3	1.0E-04	4.0	7.7E-04	-0.7	3.4E-01	-1.0	1.6E-01
ENSMUST00000066991	adrenomedullin 2 [Source:MGI Symbol;Acc:MGI:2675256]		Q7TNK8	6.7	1.7E-03	-2.6	1.2E-01	1.1	1.6E-01	-0.3	8.4E-01
ENSMUST00000065694	DIS3 mitotic control homolog (S. cerevisiae)-like 2 [Source:MGI Symbol;Acc:MGI:2442555]		Q8CI75	-2.1	6.6E-02	-3.9	5.7E-02	0.0	9.7E-01	1.9	3.1E-01
ENSMUST00000065698	FIC domain containing [Source:MGI Symbol;Acc:MGI:1098550]		Q8BIX9	0.5	4.2E-01	1.6	6.4E-02	0.9	1.7E-01	-0.2	7.3E-01
ENSMUST00000066997	olfactory receptor 24 [Source:MGI Symbol;Acc:MGI:109311]		Q8VFM9	5.6	7.9E-04	-5.9	2.9E-06	0.3	3.1E-01	-0.5	4.4E-01
ENSMUST00000067020	NK2 homeobox 4 [Source:MGI Symbol;Acc:MGI:97349]		Q9EQM3	6.1	2.0E-04	1.7	2.8E-02	-1.1	9.9E-02	-0.1	8.5E-01
ENSMUST00000065740	predicted gene 9905 [Source:MGI Symbol;Acc:MGI:3642311]	E9PXZ0		-1.5	1.1E-01	0.3	7.9E-01	0.2	8.4E-01	-1.6	1.3E-01
ENSMUST00000067033	serine/threonine kinase 3 [Source:MGI Symbol;Acc:MGI:1928487]		Q9JI10	-5.8	2.1E-03	6.4	3.8E-04	0.8	5.1E-01	-0.9	2.1E-01
ENSMUST00000067036	basigin [Source:MGI Symbol;Acc:MGI:88208]		P18572	-2.6	6.0E-03	2.9	1.1E-02	-0.9	2.8E-01	-0.8	3.2E-01
ENSMUST00000067048	dynein, axonemal, heavy chain 5 [Source:MGI Symbol;Acc:MGI:107718]		Q8VHE6	9.1	8.8E-06	-4.1	2.4E-02	0.8	2.3E-01	-0.8	6.3E-01
ENSMUST00000065784	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b [Source:MGI Symbol;Acc:MGI:2148251]	Q8BZY3		0.1	9.6E-01	-1.3	6.2E-01	-1.1	5.5E-01	0.3	9.1E-01
ENSMUST00000067058	phosphatidylinositol glycan anchor biosynthesis, class W [Source:MGI Symbol;Acc:MGI:1917575]	B7ZN11	Q8C398	4.4	2.6E-04	8.9	4.8E-05	-0.2	9.0E-01	-1.1	7.2E-02
ENSMUST00000067060	Kruppel-like factor 1 (erythroid) [Source:MGI Symbol;Acc:MGI:1342771]	E9QNP6		5.8	6.9E-04	5.3	2.6E-01	-0.1	9.9E-01	4.3	1.7E-01
ENSMUST00000065793	3-phosphoglycerate dehydrogenase [Source:MGI Symbol;Acc:MGI:1355330]		Q61753	1.0	1.3E-01	0.8	3.2E-01	-0.7	2.4E-01	-0.5	5.0E-01
ENSMUST00000067075	NK2 homeobox 2 [Source:MGI Symbol;Acc:MGI:97347]	Q3URZ4	P42586	5.5	1.1E-03	-8.4	7.2E-03	-0.6	3.9E-01	2.9	2.7E-01
ENSMUST00000067077	predicted gene 9938 [Source:MGI Symbol;Acc:MGI:3641836]	Q8C3P5		3.0	1.7E-03	5.7	2.4E-05	1.2	1.1E-01	-0.3	5.5E-01
ENSMUST00000067081	cyclin-dependent kinase 11B [Source:MGI Symbol;Acc:MGI:88353]		P24788	-5.2	2.5E-03	5.9	1.7E-03	1.2	3.8E-01	-2.2	2.3E-02
ENSMUST00000067086	estrogen receptor 1 (alpha) [Source:MGI Symbol;Acc:MGI:1352467]	E7FJU2	P19785	4.6	2.0E-02	7.7	1.2E-04	-0.7	6.1E-01	-0.2	7.0E-01
ENSMUST00000067087	family with sequence similarity 150, member B [Source:MGI Symbol;Acc:MGI:3697448]		Q80UG6	5.4	6.8E-04	3.7	3.9E-03	0.3	7.5E-01	0.1	8.5E-01
ENSMUST00000065858	neuroligin 3 [Source:MGI Symbol;Acc:MGI:2444609]		Q8BYM5	2.6	1.4E-01	7.2	6.3E-04	-1.3	4.3E-01	-5.9	7.6E-04
ENSMUST00000067101	potassium inwardly-rectifying channel, subfamily J, member 3 [Source:MGI Symbol;Acc:MGI:104742]	Q3ZAT1	P63250	8.2	8.0E-06	-4.9	3.2E-04	-0.6	1.9E-01	-1.8	9.2E-02
ENSMUST00000067103	RNA polymerase II, TATA box binding protein (TBP)-associated factorq [Source:MGI Symbol;Acc:MGI:192		Q9EQH4	-2.5	8.9E-04	6.3	1.4E-03	-0.7	6.5E-01	0.4	6.5E-01
ENSMUST00000067120	cholinergic receptor, nicotinic, alpha polypeptide 4 [Source:MGI Symbol;Acc:MGI:87888]	Q53YK0	O70174	9.3	6.9E-06	4.4	1.0E-02	-2.4	1.5E-01	1.9	6.1E-02
ENSMUST00000067124	lipin 1 [Source:MGI Symbol;Acc:MGI:1891340]			5.1	1.6E-02	-3.7	8.1E-03	1.6	1.1E-02	1.3	2.7E-01
ENSMUST00000065896	kinesin family member 2C [Source:MGI Symbol;Acc:MGI:1921054]		Q922S8	-1.4	1.3E-01	-3.9	1.7E-02	-0.1	8.5E-01	2.3	1.1E-01
ENSMUST00000065900	hedgehog interacting protein-like 2 [Source:MGI Symbol;Acc:MGI:1926022]		Q9D2G9	4.2	8.5E-02	6.8	1.8E-02	-0.3	9.1E-01	-3.0	5.7E-02
ENSMUST00000067137	Tp53rk binding protein [Source:MGI Symbol;Acc:MGI:1917036]		Q8QZZ7	2.5	2.0E-03	7.0	3.0E-04	-0.6	6.7E-01	-0.7	3.1E-01
ENSMUST00000067168	musashi RNA-binding protein 1 [Source:MGI Symbol;Acc:MGI:107376]	F8WJA5		4.0	2.4E-02	3.2	1.7E-03	0.3	5.8E-01	0.1	8.1E-01
ENSMUST00000065916	thyroglobulin [Source:MGI Symbol;Acc:MGI:98733]		O08710	1.8	7.7E-02	2.9	3.5E-02	0.8	4.4E-01	-0.3	7.3E-01
ENSMUST00000067176	predicted gene 5082 [Source:MGI Symbol;Acc:MGI:3644232]	B2RV89		6.5	1.5E-04	-6.8	7.3E-05	0.0	9.0E-01	-0.8	5.3E-01
ENSMUST00000065927	tumor necrosis factor alpha induced protein 6 [Source:MGI Symbol;Acc:MGI:1195266]	Q3USX6	O08859	0.7	1.8E-01	0.9	2.1E-01	0.2	7.5E-01	0.0	9.8E-01
ENSMUST00000067178	von Willebrand factor A domain containing 3B [Source:MGI Symbol;Acc:MGI:1918103]	Q8BH17		6.2	1.7E-02	-5.6	1.4E-02	-0.5	4.7E-01	2.2	2.6E-01
ENSMUST00000067205	kinesin family member 21A [Source:MGI Symbol;Acc:MGI:109188]	F8WGN6		2.7	3.3E-02	-3.5	6.4E-02	-0.1	8.6E-01	-2.1	3.2E-01
ENSMUST00000067215	ADP-ribosylation factor GTPase activating protein 3 [Source:MGI Symbol;Acc:MGI:1913501]			-1.3	1.8E-02	2.6	7.9E-03	-0.2	8.0E-01	0.0	9.6E-01
ENSMUST00000067218	poly (ADP-ribose) polymerase family, member 3 [Source:MGI Symbol;Acc:MGI:1891258]	Q8CFB8		3.0	1.9E-02	-1.1	4.3E-01	1.2	1.8E-01	-1.4	3.2E-01
ENSMUST00000067230	SRY (sex determining region Y)-box 4 [Source:MGI Symbol;Acc:MGI:98366]		Q06831	4.2	1.0E-04	2.1	2.2E-01	-2.1	2.2E-01	1.1	4.2E-01
ENSMUST00000067240	lymphocyte protein tyrosine kinase [Source:MGI Symbol;Acc:MGI:96756]		P06240	8.6	1.6E-04	7.4	8.7E-05	-0.2	8.8E-01	-0.3	6.3E-01
ENSMUST00000067246	solute carrier family 30 (zinc transporter), member 5 [Source:MGI Symbol;Acc:MGI:1916298]		Q8R4H9	-2.5	1.5E-03	6.9	2.2E-04	-0.2	8.8E-01	0.0	9.6E-01
ENSMUST00000067268	paxillin [Source:MGI Symbol;Acc:MGI:108295]		Q8VI36	-10.5	1.4E-04	-2.7	7.8E-02	0.8	3.1E-01	-4.0	5.4E-02
ENSMUST00000067284	cleavage and polyadenylation specificity factor 3 [Source:MGI Symbol;Acc:MGI:1859328]		Q9QXK7	-3.9	1.9E-05	7.4	7.9E-05	-1.5	2.5E-01	-0.8	1.9E-01
ENSMUST00000067298	mitochondrial ribosomal protein S21 [Source:MGI Symbol;Acc:MGI:1913542]	Q059G7	P58059	-7.1	3.6E-04	3.8	3.4E-02	-1.8	3.1E-01	-1.2	3.5E-01
ENSMUST00000067305	leucine rich repeat containing 36 [Source:MGI Symbol;Acc:MGI:2448585]		Q3V0M2	6.3	2.1E-04	-4.6	8.3E-05	0.6	1.1E-01	-0.4	6.3E-01
ENSMUST00000066028	protein kinase inhibitor beta, cAMP dependent, testis specific [Source:MGI Symbol;Acc:MGI:101937]	Q3TZU5		-3.2	4.5E-02	-2.8	1.8E-01	0.5	6.3E-01	0.1	9.6E-01
ENSMUST00000066037	bobby sox homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1917758]		Q8VBW5	-0.3	8.5E-01	-1.1	7.3E-01	1.9	3.7E-01	2.7	3.4E-01
ENSMUST00000067327	cyclin-dependent kinase inhibitor 1B [Source:MGI Symbol;Acc:MGI:104565]		P46414	-3.4	5.5E-03	-1.2	4.1E-02	0.4	1.9E-01	-0.2	6.3E-01
ENSMUST00000067328	cytochrome P450, family 2, subfamily c, polypeptide 67 [Source:MGI Symbol;Acc:MGI:3612288]	Q569X9		4.5	1.2E-02	7.4	5.2E-05	-0.6	6.1E-01	-0.1	8.1E-01
ENSMUST00000066052	RIKEN cDNA 3110082I17 gene [Source:MGI Symbol;Acc:MGI:1920462]		Q9CXL3	0.0	9.9E-01	-0.2	7.6E-01	0.2	7.1E-01	0.4	5.6E-01
ENSMUST00000067375	brain specific homeobox [Source:MGI Symbol;Acc:MGI:2669849]		Q810B3	5.8	4.9E-04	3.6	8.5E-04	0.2	7.6E-01	-0.2	7.4E-01
ENSMUST00000067384	ras homolog gene family, member B [Source:MGI Symbol;Acc:MGI:107949]	Q4FJM5	P62746	-4.7	2.8E-04	3.9	3.7E-04	0.1	8.2E-01	0.5	3.2E-01
ENSMUST00000067404	FGFR1 oncogene partner 2 [Source:MGI Symbol;Acc:MGI:1914779]		Q9CRA9	-4.8	8.5E-03	-6.5	5.6E-05	-0.5	2.2E-01	-0.2	8.5E-01
ENSMUST00000066078	TBK1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1920424]		A2A9T0	-1.0	1.8E-01	-0.2	8.4E-01	1.0	1.7E-01	0.2	8.7E-01
ENSMUST00000067410	diacylglycerol kinase kappa [Source:MGI Symbol;Acc:MGI:3580254]	E9Q7N4		7.8	8.3E-04	-2.3	1.5E-02	1.1	3.6E-02	0.8	3.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000067417	GATA binding protein 4 [Source:MGI Symbol;Acc:MGI:95664]	E9PXW9		4.8	2.3E-02	3.4	2.9E-02	-1.6	2.3E-01	-0.6	5.9E-01
ENSMUST00000066107	G protein-coupled receptor 19 [Source:MGI Symbol;Acc:MGI:892973]		Q61121	3.4	1.6E-01	3.0	3.1E-01	0.1	9.8E-01	0.5	8.0E-01
ENSMUST00000067426	cyclin-dependent kinase inhibitor 3 [Source:MGI Symbol;Acc:MGI:1919641]		Q810P3	-3.3	2.3E-03	1.5	5.7E-02	-0.3	6.6E-01	-4.6	4.4E-04
ENSMUST00000067444	glial fibrillary acidic protein [Source:MGI Symbol;Acc:MGI:95697]		P03995	7.5	3.8E-05	-2.4	1.5E-02	1.0	6.3E-02	0.4	6.0E-01
ENSMUST00000067458	peats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A [		Q3UPZ0	10.8	1.4E-06	4.6	1.8E-02	-1.2	5.0E-01	1.2	2.9E-01
ENSMUST00000066148	tubulin folding cofactor E-like [Source:MGI Symbol;Acc:MGI:1925543]		Q8C5W3	0.8	7.4E-01	-1.3	6.5E-01	-2.1	3.1E-01	0.0	1.0E+00
ENSMUST00000067469	transmembrane protein 74 [Source:MGI Symbol;Acc:MGI:2443417]		Q8BQU7	5.5	7.2E-04	7.9	2.8E-05	-0.6	5.9E-01	-0.3	5.0E-01
ENSMUST00000067472	retbindin [Source:MGI Symbol;Acc:MGI:2443686]		Q8QZY4	7.1	1.5E-04	-0.6	7.1E-01	2.1	8.1E-02	-3.0	8.2E-02
ENSMUST00000067476	signal peptidase complex subunit 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923937]	Q6ZWQ7		-4.0	3.9E-05	6.4	6.9E-04	-0.6	6.6E-01	0.0	9.9E-01
ENSMUST00000067479	cytochrome P450, family 3, subfamily a, polypeptide 44 [Source:MGI Symbol;Acc:MGI:2449818]	Q9EQW4		6.2	3.1E-04	2.4	8.3E-03	0.5	4.5E-01	0.4	4.9E-01
ENSMUST00000067485	solute carrier family 30 (zinc transporter), member 7 [Source:MGI Symbol;Acc:MGI:1913750]		Q9JKN1	-1.7	1.8E-03	5.0	1.7E-04	-2.3	2.8E-02	0.0	1.0E+00
ENSMUST00000067495	wingless-type MMTV integration site family, member 11 [Source:MGI Symbol;Acc:MGI:101948]	Q059Y4	P48615	7.2	6.2E-05	6.3	1.4E-04	-1.2	2.7E-01	1.2	6.0E-02
ENSMUST00000067496	ATPase inhibitory factor 1 [Source:MGI Symbol;Acc:MGI:1196457]		O35143	-7.4	2.6E-04	3.6	1.0E-01	-0.8	6.9E-01	-0.3	8.6E-01
ENSMUST00000067505	transmembrane protein 120B [Source:MGI Symbol;Acc:MGI:3603158]		Q3TA38	7.3	4.9E-05	7.3	1.1E-04	-0.5	6.6E-01	-0.7	2.9E-01
ENSMUST00000067512	sphingomyelin phosphodiesterase 3, neutral [Source:MGI Symbol;Acc:MGI:1927578]		Q9JJY3	6.8	3.5E-06	-4.7	2.5E-03	-0.3	5.3E-01	-0.8	5.5E-01
ENSMUST00000067523	predicted gene 9945 [Source:MGI Symbol;Acc:MGI:3641652]	Q8BNZ3		9.3	1.3E-05	7.9	1.9E-05	0.1	9.3E-01	-0.5	3.3E-01
ENSMUST00000067530	vesicle-associated membrane protein, associated protein B and C [Source:MGI Symbol;Acc:MGI:1928744]	Q8BH80		-2.0	8.7E-04	7.9	2.4E-04	-0.7	6.3E-01	-0.3	7.1E-01
ENSMUST00000067538	protein tyrosine phosphatase, receptor type, S [Source:MGI Symbol;Acc:MGI:97815]		B0V2N1	3.5	9.1E-04	8.3	3.6E-04	-0.7	6.6E-01	-1.4	1.0E-01
ENSMUST00000067543	tribbles homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443397]		Q8K4K4	-2.5	2.4E-02	-0.3	8.9E-01	-4.3	3.1E-02	2.3	1.8E-01
ENSMUST00000067563	WDYHV motif containing 1 [Source:MGI Symbol;Acc:MGI:1924023]		Q80WB5	-2.3	9.3E-04	4.2	2.5E-03	-2.0	9.4E-02	-0.7	3.8E-01
ENSMUST00000067567	lysophospholipase 2 [Source:MGI Symbol;Acc:MGI:1347000]		Q9WTL7	-7.5	2.0E-04	-1.0	4.0E-01	2.1	1.4E-02	-0.6	6.2E-01
ENSMUST00000067584	zinc finger, NFX1-type containing 1 [Source:MGI Symbol;Acc:MGI:2138982]	A2A5R6		-1.7	2.9E-02	-9.2	1.1E-04	-0.2	5.3E-01	-0.7	6.7E-01
ENSMUST00000067620	choline dehydrogenase [Source:MGI Symbol;Acc:MGI:1860776]		Q8BJ64	2.7	2.8E-04	-2.7	8.4E-03	-0.3	5.9E-01	-0.7	4.2E-01
ENSMUST00000067625	glutamine repeat protein 1 [Source:MGI Symbol;Acc:MGI:108038]	E9Q9S8		5.7	7.4E-05	5.1	9.5E-03	-1.1	4.8E-01	-1.2	2.4E-01
ENSMUST00000067630	DNA-damage regulated autophagy modulator 2 [Source:MGI Symbol;Acc:MGI:1914421]		Q9CR48	2.8	3.2E-03	2.8	7.7E-04	-1.5	1.8E-02	-0.5	3.1E-01
ENSMUST00000066283	leukemia inhibitory factor [Source:MGI Symbol;Acc:MGI:96787]		P09056	3.4	1.4E-01	5.9	1.7E-02	-2.2	3.3E-01	-4.7	1.8E-02
ENSMUST00000067638	SH3-domain binding protein 2 [Source:MGI Symbol;Acc:MGI:1346349]	Q5U3L0		-4.8	4.1E-04	5.6	6.2E-05	-2.1	3.5E-02	-0.4	4.0E-01
ENSMUST00000067663	proteasome (prosome, macropain) 26S subunit, ATPase 3 [Source:MGI Symbol;Acc:MGI:1098754]		O88685	-7.0	1.1E-04	7.6	3.5E-04	-0.3	8.3E-01	-0.2	7.9E-01
ENSMUST00000066296	family with sequence similarity 179, member B [Source:MGI Symbol;Acc:MGI:2684313]		Q6A070	0.5	1.9E-01	0.9	1.0E-01	0.4	2.8E-01	0.1	8.9E-01
ENSMUST00000067664	nooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Source:MGI Symbol;Acc:M	Q5SS40	P62259	-5.8	6.4E-06	4.6	1.0E-02	-3.0	1.3E-01	-2.9	3.1E-02
ENSMUST00000067670	olfactory receptor 1500 [Source:MGI Symbol;Acc:MGI:3031334]	Q7TQQ3		6.4	9.5E-05	7.4	5.6E-05	-0.5	6.4E-01	-0.3	5.8E-01
ENSMUST00000067680	a disintegrin and metallopeptidase domain 12 (meltrin alpha) [Source:MGI Symbol;Acc:MGI:105378]		Q61824	9.3	6.9E-06	2.5	8.2E-03	0.1	9.3E-01	0.1	9.0E-01
ENSMUST00000066337	aminolevulinic acid synthase 2, erythroid [Source:MGI Symbol;Acc:MGI:87990]	A2AFM0	P08680	-2.6	2.2E-01	-3.5	1.6E-01	-2.6	8.9E-02	-1.7	5.1E-01
ENSMUST00000067692	RAD51 homolog C [Source:MGI Symbol;Acc:MGI:2150020]		Q924H5	7.9	3.7E-04	2.5	3.8E-01	-0.8	7.5E-01	2.5	2.6E-01
ENSMUST00000067695	ubiquitin specific peptidase 17-like A [Source:MGI Symbol;Acc:MGI:107699]		Q61068	7.3	1.7E-05	6.3	2.2E-04	-0.6	6.2E-01	0.2	7.6E-01
ENSMUST00000067700	coiled-coil serine rich 2 [Source:MGI Symbol;Acc:MGI:101859]		Q3UHI0	-5.9	3.5E-04	-4.9	1.3E-03	-0.7	2.0E-01	-1.6	2.2E-01
ENSMUST00000067741	chimerin 2 [Source:MGI Symbol;Acc:MGI:1917243]		Q80XD1	5.9	8.7E-04	6.2	3.0E-04	-0.9	4.5E-01	-0.9	2.0E-01
ENSMUST00000066386	LysM, putative peptidoglycan-binding, domain containing 1 [Source:MGI Symbol;Acc:MGI:1919409]	A6H624	Q9D0E3	-1.0	2.3E-01	0.9	3.7E-01	0.7	3.7E-01	-1.3	2.0E-01
ENSMUST00000067744	CGG triplet repeat binding protein 1 [Source:MGI Symbol;Acc:MGI:2146370]		Q8BHG9	-4.3	4.4E-04	6.5	5.4E-04	-0.6	6.7E-01	0.4	5.5E-01
ENSMUST00000067752	methyltransferase like 7A1 [Source:MGI Symbol;Acc:MGI:1916523]	Q8C6B0		-2.5	1.4E-03	4.5	3.2E-04	0.5	5.0E-01	-0.8	1.6E-01
ENSMUST00000067778	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme [Source:MGI Symbol;Acc:MGI:1100870]	Q7TPQ8		-5.5	1.1E-04	-8.4	1.3E-04	1.3	3.2E-02	-3.2	9.1E-02
ENSMUST00000067782	X-linked lymphocyte-regulated [Source:MGI Symbol;Acc:MGI:98976]	Q8BS74		5.8	5.7E-06	6.7	3.5E-04	-0.6	6.3E-01	-0.5	5.0E-01
ENSMUST00000067784	cadherin-like 24 [Source:MGI Symbol;Acc:MGI:1928330]		Q6PFX6	3.8	4.3E-04	5.0	1.2E-03	-1.2	3.2E-01	-0.5	4.9E-01
ENSMUST00000067790	UDP glucuronosyltransferase 2 family, polypeptide B5 [Source:MGI Symbol;Acc:MGI:98900]	Q8K169		4.7	1.7E-02	-0.5	4.9E-01	0.8	1.5E-01	-1.2	1.1E-01
ENSMUST00000067801	cystathionine beta-synthase [Source:MGI Symbol;Acc:MGI:88285]		Q91WT9	7.9	2.8E-05	6.6	1.8E-04	-0.9	4.6E-01	-0.1	8.9E-01
ENSMUST00000067836	anoctamin 9 [Source:MGI Symbol;Acc:MGI:1918595]		P86044	8.2	1.1E-05	6.2	1.1E-03	-0.5	7.3E-01	-0.6	4.8E-01
ENSMUST00000067841	insulin receptor substrate 4 [Source:MGI Symbol;Acc:MGI:1338009]		Q9Z0Y7	8.0	2.8E-05	-4.3	2.2E-04	-0.1	7.0E-01	-0.6	4.3E-01
ENSMUST00000066452	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]	E9PXV3		-1.7	1.1E-01	-0.3	8.1E-01	1.1	2.3E-01	-0.2	8.8E-01
ENSMUST00000067843	homeobox containing 1 [Source:MGI Symbol;Acc:MGI:2445066]		Q8BJA3	-3.5	2.1E-02	6.0	1.0E-03	-0.6	6.7E-01	-1.8	4.5E-02
ENSMUST00000067853	transmembrane protein 119 [Source:MGI Symbol;Acc:MGI:2385228]		Q8R138	2.8	4.3E-03	6.6	1.2E-04	-1.3	2.7E-01	-0.5	4.2E-01
ENSMUST00000067854	RIKEN cDNA 1600014C10 gene [Source:MGI Symbol;Acc:MGI:1919494]		Q8WUR0	-7.1	1.9E-03	-4.6	4.6E-02	1.6	8.2E-02	1.0	6.4E-01
ENSMUST00000067857	apoptosis-inducing factor, mitochondrion-associated 2 [Source:MGI Symbol;Acc:MGI:1918611]		Q8BUE4	-4.3	6.1E-03	-5.1	1.2E-03	0.6	2.0E-01	0.9	4.2E-01
ENSMUST00000067864	serine/arginine-rich splicing factor 12 [Source:MGI Symbol;Acc:MGI:2661424]		Q8C8K3	8.8	5.2E-05	5.2	1.3E-04	1.9	3.4E-02	-0.4	4.7E-01
ENSMUST00000066478	tetratricopeptide repeat domain 16 [Source:MGI Symbol;Acc:MGI:2443048]	Q3V0B6		3.5	6.4E-02	6.0	6.2E-03	-0.5	8.0E-01	-3.0	2.7E-02
ENSMUST00000067880	a disintegrin and metallopeptidase domain 10 [Source:MGI Symbol;Acc:MGI:109548]		O35598	-5.1	8.6E-05	3.6	4.7E-04	-4.0	1.5E-03	-0.3	6.4E-01
ENSMUST00000066496	NudC domain containing 3 [Source:MGI Symbol;Acc:MGI:2144158]	B0FTY3	Q8R1N4	-0.5	5.4E-01	0.0	9.8E-01	0.4	5.9E-01	-0.1	9.3E-01
ENSMUST00000067902	phosphatidylinositol glycan anchor biosynthesis, class V [Source:MGI Symbol;Acc:MGI:2442480]		Q7TPN3	-4.7	1.4E-04	-1.0	1.3E-01	0.2	6.2E-01	-0.7	2.6E-01
ENSMUST00000067912	Kruppel-like factor 2 (lung) [Source:MGI Symbol;Acc:MGI:1342772]		Q60843	-6.6	4.3E-05	9.2	1.5E-04	-0.1	9.4E-01	-0.2	7.8E-01
ENSMUST00000067924	leucine rich repeat containing 8 family, member C [Source:MGI Symbol;Acc:MGI:2140839]		Q8R502	2.1	1.7E-03	-3.7	8.9E-03	0.5	3.4E-01	-1.0	4.4E-01
ENSMUST00000067925	high mobility group box 2 [Source:MGI Symbol;Acc:MGI:96157]		P30681	-6.5	3.1E-07	5.6	3.4E-05	-1.4	9.7E-02	0.5	3.0E-01
ENSMUST00000067927	methionine sulfoxide reductase A [Source:MGI Symbol;Acc:MGI:106916]		Q9D6Y7	-5.1	9.1E-07	-3.5	8.4E-05	1.6	2.3E-04	-0.2	6.7E-01
ENSMUST00000066537	chitinase-like 5 [Source:MGI Symbol;Acc:MGI:2676649]	F7AQE8		-2.6	4.2E-02	0.3	8.2E-01	0.9	3.6E-01	-1.9	1.4E-01
ENSMUST00000067935	vacuolar protein sorting 37D (yeast) [Source:MGI Symbol;Acc:MGI:2159402]		Q810I0	4.0	1.0E-03	5.8	1.4E-03	-0.5	7.0E-01	-0.5	4.8E-01
ENSMUST00000067947	Rho-associated coiled-coil containing protein kinase 1 [Source:MGI Symbol;Acc:MGI:107927]		P70335	-4.1	1.6E-05	5.0	3.0E-04	-1.8	9.6E-02	-0.7	2.9E-01
ENSMUST00000067955	diphthamine biosynthesis 3 [Source:MGI Symbol;Acc:MGI:1922658]		Q8K0W9	-2.9	2.1E-02	9.0	7.1E-05	-0.7	6.2E-01	-0.5	4.0E-01
ENSMUST00000067972	predicted gene 9956 [Source:MGI Symbol;Acc:MGI:3641872]	Q8C3H7		7.5	4.4E-05	5.6	2.1E-03	-0.3	8.2E-01	0.2	8.0E-01
ENSMUST00000067975	NLR family, apoptosis inhibitory protein 2 [Source:MGI Symbol;Acc:MGI:1298226]		Q9QUK4	-4.7	1.0E-02	4.2	1.5E-03	-2.5	3.7E-02	-0.1	8.5E-01
ENSMUST00000066568	fucose-1-phosphate guanylyltransferase [Source:MGI Symbol;Acc:MGI:1922790]	G5E8F4		-0.4	5.3E-01	-0.4	5.5E-01	-0.7	2.4E-01	-0.7	3.7E-01
ENSMUST00000066576	L1 cell adhesion molecule [Source:MGI Symbol;Acc:MGI:96721]	A2AFG7		-3.4	6.1E-02	-3.0	1.9E-01	0.1	9.5E-01	-0.3	8.9E-01
ENSMUST00000067976	protein phosphatase 2, regulatory subunit B', alpha [Source:MGI Symbol;Acc:MGI:2388479]		Q6PD03	-4.5	5.4E-06	6.0	1.2E-02	-0.7	7.6E-01	-1.2	3.4E-01
ENSMUST00000067984	melatonin receptor 1A [Source:MGI Symbol;Acc:MGI:102967]	Q14AC3	Q61184	6.5	1.6E-04	-0.8	4.5E-01	0.7	3.5E-01	-3.6	2.9E-02
ENSMUST00000067996	SET nuclear oncogene [Source:MGI Symbol;Acc:MGI:1860267]		Q9EQU5	-7.6	1.7E-05	8.6	4.5E-04	-0.3	8.4E-01	0.4	6.2E-01
ENSMUST00000066597	kelch-like 26 [Source:MGI Symbol;Acc:MGI:2443079]		Q8BGY4	0.4	4.3E-01	2.7	4.2E-03	1.5	2.6E-02	-0.7	2.3E-01
ENSMUST00000066601	hypoxia up-regulated 1 [Source:MGI Symbol;Acc:MGI:108030]		Q9JKR6	-1.9	3.9E-02	-1.3	3.3E-01	2.1	2.4E-02	1.6	2.3E-01
ENSMUST00000068006	molybdenum cofactor sulfurase [Source:MGI Symbol;Acc:MGI:1915841]		Q14CH1	-4.3	1.1E-04	6.6	2.8E-05	1.0	2.6E-01	0.3	4.8E-01
ENSMUST00000066617	zinc finger with KRAB and SCAN domains 1 [Source:MGI Symbol;Acc:MGI:1921820]		Q8BGS3	1.5	4.8E-01	1.9	6.1E-01	2.9	3.2E-01	2.5	4.0E-01
ENSMUST00000068021	platelet/endothelial cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97537]	B1ARB3		1.4	1.2E-02	-6.6	5.6E-03	-0.7	3.3E-01	-0.7	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000066640	N-acetylneuraminic acid phosphatase [Source:MGI Symbol;Acc:MGI:1914561]		Q9CPT3	0.5	7.8E-01	1.5	4.6E-01	0.0	9.8E-01	-1.0	5.3E-01
ENSMUST00000066646	REST corepressor 2 [Source:MGI Symbol;Acc:MGI:1859854]		Q8C796	2.9	6.4E-02	4.7	7.8E-03	-0.6	6.9E-01	-2.4	5.4E-02
ENSMUST00000068023	cell adhesion molecule 4 [Source:MGI Symbol;Acc:MGI:2449088]		Q8R464	6.2	7.6E-05	-1.3	2.1E-01	0.6	4.2E-01	-0.9	3.8E-01
ENSMUST00000068025	kelch-like 18 [Source:MGI Symbol;Acc:MGI:2143315]	E9Q4F2		-2.5	4.5E-04	-1.7	1.1E-02	0.5	1.5E-01	-0.5	3.7E-01
ENSMUST00000068031	topoisomerase (DNA) II alpha [Source:MGI Symbol;Acc:MGI:98790]		Q01320	-3.5	5.9E-04	4.0	1.0E-03	-2.7	1.9E-02	-0.2	7.4E-01
ENSMUST00000068044	solute carrier family 39 (zinc transporter), member 14 [Source:MGI Symbol;Acc:MGI:2384851]		Q75N73	1.7	2.0E-02	1.9	3.3E-02	-0.4	5.1E-01	0.6	3.7E-01
ENSMUST00000068045	actinin alpha 4 [Source:MGI Symbol;Acc:MGI:1890773]	Q3ULT2	P57780	-5.9	2.3E-04	5.5	4.6E-05	0.4	5.9E-01	-0.4	4.9E-01
ENSMUST00000068056	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B [Source:MGI Symbol;Acc:MGI:99240]		Q9Z1N5	-8.2	2.0E-05	-4.8	7.6E-03	-0.2	7.4E-01	-1.7	3.3E-01
ENSMUST00000068058	ubiquitin specific peptidase 46 [Source:MGI Symbol;Acc:MGI:1916977]		P62069	-4.6	4.6E-03	5.6	2.7E-03	-0.4	7.5E-01	0.1	9.2E-01
ENSMUST00000066715	zinc finger and BTB domain containing 48 [Source:MGI Symbol;Acc:MGI:2140248]		Q1H9T6	-3.3	1.1E-01	1.3	4.6E-01	1.0	4.9E-01	-3.6	9.0E-02
ENSMUST00000068063	T cell specific GTPase 1 [Source:MGI Symbol;Acc:MGI:98734]	Q62293		-4.2	4.8E-03	6.1	1.0E-03	-0.6	6.5E-01	-0.9	2.3E-01
ENSMUST00000066723	lectin, galactose binding, soluble 4 [Source:MGI Symbol;Acc:MGI:107536]	Q3UL35	Q8K419	-0.9	4.5E-01	1.6	2.2E-01	-0.1	9.6E-01	-2.5	5.8E-02
ENSMUST00000068071	elongator acetyltransferase complex subunit 6 [Source:MGI Symbol;Acc:MGI:1919349]	A0A0H2UH13		2.5	2.2E-03	4.0	7.1E-04	-0.8	3.4E-01	0.4	4.3E-01
ENSMUST00000068079	zinc finger protein 560 [Source:MGI Symbol;Acc:MGI:1915280]	Q3URI6		4.3	3.2E-05	8.2	1.3E-04	0.8	5.7E-01	0.1	9.2E-01
ENSMUST00000066743	ADNP homeobox 2 [Source:MGI Symbol;Acc:MGI:2448562]		Q8CHC8	-0.8	1.2E-01	0.1	8.9E-01	0.8	8.8E-02	-0.1	9.3E-01
ENSMUST00000066747	CD8 antigen, alpha chain [Source:MGI Symbol;Acc:MGI:88346]		P01731	1.4	6.4E-01	0.2	9.5E-01	-2.4	3.9E-01	-1.2	6.9E-01
ENSMUST00000066748	PAP associated domain containing 5 [Source:MGI Symbol;Acc:MGI:1917820]	F8WI26		0.1	9.7E-01	1.1	6.9E-01	-1.1	6.2E-01	-2.1	4.1E-01
ENSMUST00000068088	family with sequence similarity 19, member A5 [Source:MGI Symbol;Acc:MGI:2146182]		Q91WE9	6.8	3.7E-05	-1.6	5.3E-01	2.7	1.2E-01	-0.4	8.8E-01
ENSMUST00000066773	protein phosphatase 2, regulatory subunit B", alpha [Source:MGI Symbol;Acc:MGI:2442104]	G3X9E8		0.7	7.0E-01	1.9	2.6E-01	-2.2	1.8E-01	-3.5	5.3E-02
ENSMUST00000068106	small integral membrane protein 10 like 2A [Source:MGI Symbol;Acc:MGI:2443645]	A0A0B4J1F8		8.0	3.9E-05	-1.5	8.0E-02	1.3	2.6E-02	0.1	9.4E-01
ENSMUST00000068116	leucine rich repeat (in FLII) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1342770]	G5E8E1		-4.5	1.1E-02	-1.9	1.0E-02	1.0	1.5E-02	0.0	9.6E-01
ENSMUST00000068125	aprataxin [Source:MGI Symbol;Acc:MGI:1913658]		Q7TQC5	-4.1	5.7E-04	7.4	3.7E-04	0.4	7.8E-01	0.7	3.1E-01
ENSMUST00000068133	retinoic acid receptor, alpha [Source:MGI Symbol;Acc:MGI:97856]	Q3U3R3	P11416	-4.5	7.7E-03	6.8	1.0E-04	-2.1	1.1E-01	0.0	9.6E-01
ENSMUST00000068135	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8 [Source:MGI Symbol;Acc:M	F8VQ15		6.7	1.0E-04	6.9	6.0E-04	-0.2	9.0E-01	0.2	7.4E-01
ENSMUST00000068150	a disintegrin and metallopeptidase domain 11 [Source:MGI Symbol;Acc:MGI:1098667]	Q7TQG7		9.7	3.4E-05	1.7	5.1E-02	-1.5	5.0E-02	-0.6	3.5E-01
ENSMUST00000068168	KAT8 regulatory NSL complex subunit 1-like [Source:MGI Symbol;Acc:MGI:1915941]		Q5DTI6	-3.7	4.9E-03	2.5	2.4E-03	0.4	4.2E-01	-0.2	6.8E-01
ENSMUST00000068175	Rho guanine nucleotide exchange factor (GEF) 33 [Source:MGI Symbol;Acc:MGI:2685787]		Q8BW86	6.1	1.5E-04	4.9	2.0E-02	-0.5	7.7E-01	0.2	8.7E-01
ENSMUST00000068182	stefin A3 [Source:MGI Symbol;Acc:MGI:106196]		P35173	-10.5	9.2E-06	5.8	1.2E-03	-0.7	6.3E-01	-0.2	8.3E-01
ENSMUST00000066849	lymphoid enhancer binding factor 1 [Source:MGI Symbol;Acc:MGI:96770]	D3Z654		1.5	6.4E-01	1.4	6.0E-01	-2.1	4.5E-01	-2.1	4.6E-01
ENSMUST00000068214	astrotactin 2 [Source:MGI Symbol;Acc:MGI:1889277]		Q80Z10	4.7	2.7E-02	6.9	7.4E-05	0.7	5.1E-01	-1.1	6.9E-02
ENSMUST00000068225	nucleolar and spindle associated protein 1 [Source:MGI Symbol;Acc:MGI:2675669]		Q9ERH4	-4.5	2.1E-03	3.7	2.6E-01	0.7	7.9E-01	2.8	2.6E-01
ENSMUST00000068235	NFKB activating protein-like [Source:MGI Symbol;Acc:MGI:1913957]	Q5SZT7		4.7	1.2E-03	-6.4	9.8E-03	-2.6	1.7E-02	-3.0	2.5E-01
ENSMUST00000068237	MLX interacting protein [Source:MGI Symbol;Acc:MGI:2141183]	G5E8D8		-6.9	7.5E-03	-0.1	9.7E-01	-4.7	1.2E-02	-0.4	7.4E-01
ENSMUST00000068242	ribosomal modification protein rimK-like family member B [Source:MGI Symbol;Acc:MGI:1918325]		Q80WS1	7.7	2.8E-05	8.1	2.1E-04	1.1	4.4E-01	-0.6	4.0E-01
ENSMUST00000068258	RIKEN cDNA 9130008F23 gene [Source:MGI Symbol;Acc:MGI:1918833]	Q9D2Z6		4.7	2.2E-04	6.0	3.7E-04	0.0	9.6E-01	-0.2	7.1E-01
ENSMUST00000068262	5'-nucleotidase, cytosolic IA [Source:MGI Symbol;Acc:MGI:2155700]		A3KFX0	7.0	4.4E-05	-3.6	9.6E-04	0.5	1.8E-01	-1.6	1.0E-01
ENSMUST00000068275	neuronal tyrosine-phophorylated phosphoinositide 3-kinase adaptor 2 [Source:MGI Symbol;Acc:MGI:2443135			6.5	9.4E-04	4.5	5.8E-02	-0.5	8.3E-01	2.3	9.6E-02
ENSMUST00000068282	atlastin GTPase 2 [Source:MGI Symbol;Acc:MGI:1929492]		Q6PA06	-3.9	1.2E-02	4.7	9.4E-05	-1.4	7.2E-02	-0.2	7.1E-01
ENSMUST00000066912	interferon inducible GTPase 1 [Source:MGI Symbol;Acc:MGI:1926259]	J7NNX8	Q9QZ85	0.2	9.1E-01	-4.2	2.7E-02	-4.4	3.9E-03	0.1	9.8E-01
ENSMUST00000066921	solute carrier family 25, member 40 [Source:MGI Symbol;Acc:MGI:2442486]		Q8BGP6	0.3	8.5E-01	2.8	1.9E-01	1.5	4.2E-01	-1.0	5.1E-01
ENSMUST00000066936	G-protein signalling modulator 1 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:1915089]		Q6IR34	0.8	7.5E-01	1.4	6.1E-01	-2.6	2.9E-01	-3.1	2.5E-01
ENSMUST00000068291	histocompatibility 2, Q region locus 10 [Source:MGI Symbol;Acc:MGI:95929]		P01898	-3.3	8.5E-04	6.3	1.9E-04	-0.6	6.1E-01	-0.6	3.7E-01
ENSMUST00000066983	abhydrolase domain containing 10 [Source:MGI Symbol;Acc:MGI:2442422]		Q6PE15	0.2	7.8E-01	1.8	5.9E-02	1.4	7.8E-02	-0.3	7.2E-01
ENSMUST00000066987	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 [Source:MGI Symbol;Acc:MGI	Q5SQF9	Q6P9S7	-0.9	2.3E-01	1.3	2.0E-01	1.2	1.3E-01	-1.0	2.7E-01
ENSMUST00000068301	choline/ethanolaminephosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2139793]		Q8BGS7	-6.8	1.3E-05	6.8	2.5E-03	-0.7	6.9E-01	-0.8	3.9E-01
ENSMUST00000066994	zinc finger protein 395 [Source:MGI Symbol;Acc:MGI:2682318]	E9Q5N9		0.6	1.5E-01	1.5	1.8E-02	0.7	1.1E-01	-0.2	7.2E-01
ENSMUST00000068304	nuclear receptor coactivator 2 [Source:MGI Symbol;Acc:MGI:1276533]	E9PV80		-8.1	1.1E-05	6.7	4.3E-04	-0.6	6.6E-01	-1.7	4.4E-02
ENSMUST00000067005	spectrin repeat containing, nuclear envelope family member 3 [Source:MGI Symbol;Acc:MGI:2442408]		Q4FZC9	-2.5	9.5E-02	-0.4	8.1E-01	1.5	2.4E-01	-0.5	7.6E-01
ENSMUST00000068307	kelch repeat and BTB (POZ) domain containing 13 [Source:MGI Symbol;Acc:MGI:1921742]		Q8C828	6.4	1.8E-05	6.0	4.4E-04	-0.5	6.7E-01	-0.4	5.7E-01
ENSMUST00000068316	angiotensin II receptor, type 1b [Source:MGI Symbol;Acc:MGI:87965]		P29755	8.6	1.1E-05	-0.3	8.0E-01	1.2	1.6E-01	-4.2	1.4E-02
ENSMUST00000068322	SEC14-like lipid binding 3 [Source:MGI Symbol;Acc:MGI:3617848]	Q5SQ27		6.4	4.0E-05	-2.0	5.9E-02	0.2	6.5E-01	-0.4	6.6E-01
ENSMUST00000067043	zinc finger and BTB domain containing 26 [Source:MGI Symbol;Acc:MGI:2444402]	Q6P9Q3		0.9	1.9E-01	1.3	1.5E-01	0.1	9.4E-01	-0.3	6.8E-01
ENSMUST00000068351	leucine-rich repeats and transmembrane domains 2 [Source:MGI Symbol;Acc:MGI:2141485]		Q8BGX3	9.6	4.2E-05	9.0	2.1E-05	-0.5	6.9E-01	-0.4	4.3E-01
ENSMUST00000068355	opsin 5 [Source:MGI Symbol;Acc:MGI:2662912]		Q6VZZ7	6.9	1.2E-04	2.1	1.9E-02	-2.7	5.4E-03	-0.4	5.4E-01
ENSMUST00000068387	E1A binding protein p300 [Source:MGI Symbol;Acc:MGI:1276116]		B2RWS6	-2.9	2.4E-05	3.9	9.3E-03	-1.4	2.7E-01	0.5	5.9E-01
ENSMUST00000068399	small proline-rich protein 2E [Source:MGI Symbol;Acc:MGI:1330346]		O70556	6.0	2.3E-03	6.2	1.0E-03	-0.4	7.6E-01	-1.1	1.6E-01
ENSMUST00000068403	olfactory receptor 420 [Source:MGI Symbol;Acc:MGI:3030254]	E9Q4G0		6.2	4.7E-04	3.4	1.8E-03	0.0	1.0E+00	-0.4	5.1E-01
ENSMUST00000068407	COMM domain containing 5 [Source:MGI Symbol;Acc:MGI:1913648]			-4.6	7.4E-04	-7.8	1.2E-02	-0.1	8.6E-01	2.4	3.5E-01
ENSMUST00000068408	ribosomal protein S15 [Source:MGI Symbol;Acc:MGI:98117]		P62843	-6.5	1.3E-05	5.5	9.7E-03	-0.8	6.8E-01	-1.7	1.7E-01
ENSMUST00000068411	coiled-coil domain containing 88C [Source:MGI Symbol;Acc:MGI:1915589]		Q6VGS5	-4.1	1.3E-02	6.3	5.0E-04	-0.4	7.3E-01	-1.3	8.4E-02
ENSMUST00000068421	telomeric repeat binding factor 2 [Source:MGI Symbol;Acc:MGI:1195972]		O35144	-4.5	1.1E-02	7.6	3.2E-05	-0.5	6.1E-01	0.1	9.1E-01
ENSMUST00000068448	predicted gene 9964 [Source:MGI Symbol;Acc:MGI:3642605]	E9Q9S5		8.5	4.1E-05	-0.9	1.8E-01	0.9	4.6E-02	-0.7	3.2E-01
ENSMUST00000068456	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 5 [Source:MGI Symbol;Acc:MGI:95617]		Q8BHJ7	7.7	2.5E-05	8.9	2.2E-05	-0.7	5.8E-01	-0.2	6.9E-01
ENSMUST00000068457	periphilin 1 [Source:MGI Symbol;Acc:MGI:1917029]	Q3UBL8		-5.7	3.7E-03	3.5	1.9E-01	-0.5	8.3E-01	1.2	4.9E-01
ENSMUST00000068505	calpain 2 [Source:MGI Symbol;Acc:MGI:88264]		O08529	-2.4	8.2E-04	2.7	3.8E-03	-0.1	9.3E-01	-0.3	6.5E-01
ENSMUST00000067145	family with sequence similarity 220, member A [Source:MGI Symbol;Acc:MGI:1914488]		Q3ZN08	-2.2	3.3E-01	-3.7	2.2E-01	-0.1	9.4E-01	1.4	6.5E-01
ENSMUST00000067167	FRA10AC1 homolog (human) [Source:MGI Symbol;Acc:MGI:1917817]		Q8BP78	-0.1	8.7E-01	-0.7	3.2E-01	-0.9	1.0E-01	-0.3	5.8E-01
ENSMUST00000068519	sushi domain containing 6 [Source:MGI Symbol;Acc:MGI:2444661]		Q8BGE4	-3.8	4.3E-05	4.6	1.7E-02	-0.5	7.7E-01	-1.0	3.6E-01
ENSMUST00000067173	transmembrane protein 45A2 [Source:MGI Symbol;Acc:MGI:1916707]	B7ZWJ5		1.2	6.1E-02	1.8	1.9E-02	-0.4	5.2E-01	-1.0	1.2E-01
ENSMUST00000068532	cell growth regulator with ring finger domain 1 [Source:MGI Symbol;Acc:MGI:1916368]		Q8BMJ7	-2.9	8.6E-05	6.7	2.2E-04	-0.6	6.5E-01	-0.7	2.7E-01
ENSMUST00000068551	X-linked lymphocyte-regulated 4C [Source:MGI Symbol;Acc:MGI:3574099]	Q3TKR2		4.7	8.2E-04	5.6	4.3E-02	-0.9	7.4E-01	-0.2	8.9E-01
ENSMUST00000067190	leukemia inhibitory factor receptor [Source:MGI Symbol;Acc:MGI:96788]		P42703	2.0	2.0E-01	0.6	7.4E-01	-0.6	6.7E-01	0.7	6.8E-01
ENSMUST00000068564	Ras association (RalGDS/AF-6) domain family member 5 [Source:MGI Symbol;Acc:MGI:1926375]		Q5EBH1	-5.8	2.8E-06	8.0	3.1E-05	-0.6	6.1E-01	-5.8	4.3E-05
ENSMUST00000068567	nuclear receptor coactivator 7 [Source:MGI Symbol;Acc:MGI:2444847]		Q6DFV7	1.6	6.7E-03	-0.1	8.4E-01	0.8	6.6E-02	-0.3	5.5E-01
ENSMUST00000068580	demilune cell and parotid protein 1 [Source:MGI Symbol;Acc:MGI:105949]	L7N1X9		5.3	7.9E-04	4.4	2.2E-02	1.9	2.3E-01	0.5	6.1E-01
ENSMUST00000068581	gap junction protein, alpha 1 [Source:MGI Symbol;Acc:MGI:95713]		P23242	4.1	6.1E-05	2.4	1.1E-02	-0.9	1.9E-01	0.8	1.8E-01
ENSMUST00000068583	AE binding protein 2 [Source:MGI Symbol;Acc:MGI:1338038]			-3.5	3.4E-03	2.9	6.3E-02	-4.2	2.2E-02	1.5	1.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000068584	CD48 antigen [Source:MGI Symbol;Acc:MGI:88339]		P18181	-4.4	4.2E-04	-2.0	1.7E-02	0.3	4.5E-01	-0.1	8.4E-01
ENSMUST00000067252	piezo-type mechanosensitive ion channel component 1 [Source:MGI Symbol;Acc:MGI:3603204]	E9PUQ9		2.7	4.5E-02	2.4	2.0E-01	-0.5	7.7E-01	-0.1	9.3E-01
ENSMUST00000067258	adrenergic receptor, alpha 1b [Source:MGI Symbol;Acc:MGI:104774]	Q9DBL0		4.7	1.2E-01	7.5	3.3E-02	-0.1	9.7E-01	-3.0	1.1E-01
ENSMUST00000068593	complement component 1, r subcomponent A [Source:MGI Symbol;Acc:MGI:1355313]		Q8CG16	1.8	7.0E-03	-8.8	1.2E-03	1.3	6.9E-02	-0.4	8.6E-01
ENSMUST00000067272	E2F-associated phosphoprotein [Source:MGI Symbol;Acc:MGI:1913516]	F8WGY8		-1.7	4.2E-01	-3.3	2.6E-01	-1.3	4.5E-01	0.2	9.4E-01
ENSMUST00000068603	IQ motif containing GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:2449975]		Q3UQ44	-2.9	1.5E-04	5.3	1.7E-04	-0.2	8.2E-01	0.3	5.5E-01
ENSMUST00000068613	family with sequence similarity 72, member A [Source:MGI Symbol;Acc:MGI:1919669]		Q8BFZ8	1.9	1.0E-02	-3.3	3.4E-04	0.0	8.9E-01	-0.6	3.6E-01
ENSMUST00000067288	oocyte specific homeobox 1 [Source:MGI Symbol;Acc:MGI:1918718]	Q9D350		4.5	1.1E-01	6.2	5.2E-02	-0.2	9.4E-01	-1.9	2.7E-01
ENSMUST00000068625	kallikrein related-peptidase 15 [Source:MGI Symbol;Acc:MGI:2447533]	Q8CGR4		5.1	5.1E-04	-7.4	3.6E-04	-0.4	4.3E-01	-0.1	9.6E-01
ENSMUST00000068631	FEV (ETS oncogene family) [Source:MGI Symbol;Acc:MGI:2449712]		Q8QZW2	5.5	4.8E-04	7.3	1.8E-04	-0.1	9.5E-01	-1.1	1.3E-01
ENSMUST00000068641	SERTA domain containing 3 [Source:MGI Symbol;Acc:MGI:2180697]	Q3UYB0	Q9ERC3	-2.6	2.3E-03	-2.0	1.1E-01	0.4	5.4E-01	-1.0	4.3E-01
ENSMUST00000068654	forkhead box D2 [Source:MGI Symbol;Acc:MGI:1347471]		O35392	3.5	6.8E-04	5.9	5.0E-03	-0.4	8.3E-01	-1.7	1.0E-01
ENSMUST00000068664	neogenin [Source:MGI Symbol;Acc:MGI:1097159]	E9QK04		7.3	1.7E-06	6.1	6.7E-04	-0.6	6.6E-01	-0.8	2.6E-01
ENSMUST00000068681	neuronal guanine nucleotide exchange factor [Source:MGI Symbol;Acc:MGI:1858414]	E9QK62		7.8	2.4E-05	-3.3	1.1E-02	1.3	4.0E-02	-0.2	8.9E-01
ENSMUST00000067386	RIKEN cDNA 2310022A10 gene [Source:MGI Symbol;Acc:MGI:1913617]	G5E8E3		-2.5	1.0E-01	0.4	8.1E-01	1.1	3.7E-01	-1.8	3.0E-01
ENSMUST00000067399	JDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1 [Source:MGI Symbol;Acc:MGI:2441705		Q3U129	-0.7	2.0E-01	-1.1	1.6E-01	-0.1	8.0E-01	0.3	7.3E-01
ENSMUST00000068686	calcium binding and coiled-coil domain 2 [Source:MGI Symbol;Acc:MGI:1343177]		A2A6M5	7.1	1.6E-04	-5.5	2.6E-02	0.7	4.6E-01	1.5	5.0E-01
ENSMUST00000068690	carbohydrate (chondroitin 6/keratan) sulfotransferase 3 [Source:MGI Symbol;Acc:MGI:1858224]		O88199	7.0	1.1E-03	5.4	1.5E-02	-0.6	7.4E-01	1.8	1.2E-01
ENSMUST00000067414	neuron navigator 1 [Source:MGI Symbol;Acc:MGI:2183683]		Q8CH77	5.0	2.5E-01	4.6	3.6E-01	0.0	9.9E-01	0.4	8.8E-01
ENSMUST00000068693	WD repeat domain 86 [Source:MGI Symbol;Acc:MGI:1915466]	D3Z757		6.3	2.8E-04	5.1	2.0E-02	-0.7	7.4E-01	-1.0	4.4E-01
ENSMUST00000067425	zinc finger protein 747 [Source:MGI Symbol;Acc:MGI:2443581]	Q8BHM7		0.1	7.9E-01	0.3	6.6E-01	0.5	3.3E-01	0.3	6.1E-01
ENSMUST00000068697	potassium channel modulatory factor 1 [Source:MGI Symbol;Acc:MGI:1921537]		Q80UY2	-3.9	7.8E-05	-2.1	4.2E-02	-0.5	4.2E-01	-1.6	1.1E-01
ENSMUST00000067443	schlafen 5 [Source:MGI Symbol;Acc:MGI:1329004]		Q8CBA2	1.6	8.3E-02	1.1	3.1E-01	-0.5	5.9E-01	0.0	9.8E-01
ENSMUST00000068698	myelin-associated oligodendrocytic basic protein [Source:MGI Symbol;Acc:MGI:108511]		Q9D2P8	7.6	4.2E-05	7.6	6.1E-05	-0.6	6.1E-01	-0.7	2.2E-01
ENSMUST00000068700	WD repeat domain 6 [Source:MGI Symbol;Acc:MGI:1930140]		Q99ME2	2.7	7.3E-04	5.4	3.0E-05	-4.6	9.6E-04	0.8	9.0E-02
ENSMUST00000068767	NLR family, pyrin domain containing 4A [Source:MGI Symbol;Acc:MGI:2443697]	B2RUQ7	Q8BU40	8.6	1.2E-05	3.9	4.2E-03	-2.1	1.1E-01	-0.4	5.4E-01
ENSMUST00000068783	predicted gene 9881 [Source:MGI Symbol;Acc:MGI:3641832]	Q8BR56		8.4	3.3E-05	5.9	9.4E-04	-0.7	6.3E-01	0.5	5.1E-01
ENSMUST00000068792	transmembrane protein 245 [Source:MGI Symbol;Acc:MGI:2445107]		B1AZA5	5.1	1.4E-07	-3.7	4.0E-04	0.5	2.0E-01	0.2	7.6E-01
ENSMUST00000068795	Morf4 family associated protein 1 [Source:MGI Symbol;Acc:MGI:1914818]		Q9CQL7	-4.1	2.5E-05	6.0	7.8E-04	-0.5	7.2E-01	-0.2	7.8E-01
ENSMUST00000067481	phosphatidylinositol glycan anchor biosynthesis, class O [Source:MGI Symbol;Acc:MGI:1861452]	A2AG36		-1.3	4.1E-01	2.2	2.6E-01	1.1	4.9E-01	-2.4	1.8E-01
ENSMUST00000068797	complement component 1, s subcomponent 2 [Source:MGI Symbol;Acc:MGI:3644269]	W4VSN5	Q8CFG8	6.1	2.2E-03	-1.5	1.2E-02	-0.2	5.7E-01	-0.4	4.5E-01
ENSMUST00000068798	RIKEN cDNA 4933434E20 gene [Source:MGI Symbol;Acc:MGI:1914027]	H7BX33		-7.0	4.7E-05	6.6	2.3E-04	-0.6	6.3E-01	0.0	9.9E-01
ENSMUST00000068805	eukaryotic translation initiation factor 2D [Source:MGI Symbol;Acc:MGI:109342]		Q61211	-5.4	2.0E-03	-7.3	3.7E-04	-1.1	4.3E-02	-1.2	4.5E-01
ENSMUST00000068813	thioesterase superfamily member 7 [Source:MGI Symbol;Acc:MGI:1921338]	Q9DCP4		4.6	6.6E-04	3.1	3.7E-03	-3.7	4.7E-03	0.5	4.0E-01
ENSMUST00000068822	zinc finger protein 37 [Source:MGI Symbol;Acc:MGI:99181]		P17141	8.7	2.1E-05	5.1	5.5E-05	-1.5	5.9E-02	0.1	7.8E-01
ENSMUST00000068825	negative regulator of ubiquitin-like proteins 1 [Source:MGI Symbol;Acc:MGI:1889001]	Q3UYM1	P54729	-4.3	3.4E-06	8.6	2.9E-05	-0.9	4.6E-01	-0.3	6.1E-01
ENSMUST00000068853	FAT tumor suppressor homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685369]		Q5F226	9.4	2.0E-02	-1.2	4.7E-02	0.6	9.3E-02	-0.2	7.7E-01
ENSMUST00000068860	Eph receptor A6 [Source:MGI Symbol;Acc:MGI:108034]	G1K381		6.0	2.7E-04	1.0	1.8E-01	-2.7	3.3E-03	-0.2	7.1E-01
ENSMUST00000067542	membrane-associated ring finger (C3HC4) 7 [Source:MGI Symbol;Acc:MGI:1931053]		Q9WV66	-8.3	8.2E-02	-8.8	1.4E-01	-1.7	3.5E-01	-1.1	8.6E-01
ENSMUST00000068861	cytochrome P450, family 2, subfamily d, polypeptide 12 [Source:MGI Symbol;Acc:MGI:88604]	Q8BVD2		7.0	1.1E-03	-1.6	2.3E-01	1.0	2.4E-01	0.0	1.0E+00
ENSMUST00000067545	lysocardiolipin acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2684937]	B0V2Q7	Q3UN02	0.8	1.7E-01	0.3	6.9E-01	0.3	6.1E-01	0.8	2.7E-01
ENSMUST00000067549	zinc finger protein 219 [Source:MGI Symbol;Acc:MGI:1917140]	Q6IQX8		-0.2	7.4E-01	1.0	2.5E-01	0.4	5.3E-01	-0.8	3.1E-01
ENSMUST00000067556	RIKEN cDNA 4930503L19 gene [Source:MGI Symbol;Acc:MGI:1922045]	G8CZ53	Q8CB14	-0.4	4.7E-01	0.5	5.4E-01	0.7	2.7E-01	-0.2	7.4E-01
ENSMUST00000068875	poprotein B mRNA editing enzyme, catalytic polypeptide-like 4 (putative) [Source:MGI Symbol;Acc:MGI:191		Q497M3	7.1	3.2E-05	-1.5	3.5E-02	0.6	1.3E-01	-0.2	7.3E-01
ENSMUST00000068877	T cell immunoglobulin and mucin domain containing 4 [Source:MGI Symbol;Acc:MGI:2445125]		Q6U7R4	7.0	3.6E-05	-3.4	8.2E-03	0.9	1.3E-01	-3.2	4.2E-02
ENSMUST00000067582	transmembrane protein 62 [Source:MGI Symbol;Acc:MGI:2139461]		Q8BXJ9	-1.6	7.6E-02	1.2	4.0E-01	3.9	3.1E-03	1.1	3.8E-01
ENSMUST00000068891	ring finger protein 144B [Source:MGI Symbol;Acc:MGI:2384986]		Q8BKD6	6.3	2.0E-02	-0.5	5.9E-01	0.9	1.4E-01	-0.3	7.6E-01
ENSMUST00000068892	ash2 (absent, small, or homeotic)-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1344416]		Q91X20	3.6	1.1E-03	3.8	1.5E-04	0.8	1.7E-01	-0.3	5.0E-01
ENSMUST00000068904	keratin 7 [Source:MGI Symbol;Acc:MGI:96704]		Q9DCV7	6.5	3.4E-04	2.3	1.9E-02	-3.2	4.0E-03	0.3	6.9E-01
ENSMUST00000068911	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3 [Source:MGI Symbol;Acc:MGI:95624]		P27681	9.3	1.6E-06	2.2	1.8E-02	-1.0	1.8E-01	-0.4	5.1E-01
ENSMUST00000067631	solute carrier family 35, member C1 [Source:MGI Symbol;Acc:MGI:2443301]		Q8BLX4	-1.5	1.1E-01	-0.1	9.6E-01	0.7	3.2E-01	-0.7	5.1E-01
ENSMUST00000067632	tripartite motif-containing 65 [Source:MGI Symbol;Acc:MGI:2442815]		Q8BFW4	0.5	7.9E-01	0.3	9.0E-01	-0.6	7.0E-01	-0.4	8.5E-01
ENSMUST00000068938	paired related homeobox protein-like 1 [Source:MGI Symbol;Acc:MGI:2148204]		Q8BYH0	6.5	1.3E-03	-6.5	5.6E-03	1.5	2.7E-02	3.2	1.1E-01
ENSMUST00000067646	interleukin enhancer binding factor 3 [Source:MGI Symbol;Acc:MGI:1339973]		Q9Z1X4	0.9	6.0E-02	1.3	3.9E-02	0.3	4.3E-01	-0.1	8.4E-01
ENSMUST00000068944	pleckstrin homology domain containing, family O member 2 [Source:MGI Symbol;Acc:MGI:2143132]		Q8K124	-4.8	1.1E-04	-5.6	2.5E-04	-0.4	3.4E-01	-1.8	1.7E-01
ENSMUST00000068947	acyl-Coenzyme A oxidase 3, pristanoyl [Source:MGI Symbol;Acc:MGI:1933156]		Q9EPL9	-5.3	3.0E-05	-4.9	2.1E-04	1.1	1.8E-02	0.1	9.4E-01
ENSMUST00000068952	wntless homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1915401]		Q6DID7	-3.4	7.5E-04	6.0	2.9E-04	-0.6	6.0E-01	-0.2	7.7E-01
ENSMUST00000068958	CDC42 effector protein (Rho GTPase binding) 3 [Source:MGI Symbol;Acc:MGI:2384718]		Q9CQC5	-4.4	2.3E-04	6.9	5.8E-05	-1.5	1.9E-01	0.9	1.3E-01
ENSMUST00000067689	trinucleotide repeat containing 6b [Source:MGI Symbol;Acc:MGI:2443730]		Q8BKI2	0.4	2.9E-01	0.6	2.8E-01	0.5	2.3E-01	0.4	4.5E-01
ENSMUST00000068967	multiple EGF-like-domains 11 [Source:MGI Symbol;Acc:MGI:1920951]		Q80T91	6.1	2.4E-05	6.7	9.6E-03	0.3	8.7E-01	1.6	1.6E-01
ENSMUST00000068992	protocadherin 9 [Source:MGI Symbol;Acc:MGI:1306801]	F8VPK8		6.5	2.8E-03	7.9	1.5E-04	0.7	5.7E-01	0.2	7.7E-01
ENSMUST00000068996	RIKEN cDNA 9430038I01 gene [Source:MGI Symbol;Acc:MGI:1924502]	Q9CX25		-4.6	1.7E-04	-5.3	1.1E-02	1.0	1.5E-01	0.4	8.3E-01
ENSMUST00000068999	mitochondrial calcium uptake family, member 3 [Source:MGI Symbol;Acc:MGI:1925756]		Q9CTY5	3.3	1.8E-03	5.6	2.1E-02	-0.8	6.9E-01	0.7	5.3E-01
ENSMUST00000067715	poly(A) binding protein, cytoplasmic 1-like [Source:MGI Symbol;Acc:MGI:1922908]	A2A5N3		1.1	1.2E-01	1.9	4.3E-02	0.4	5.5E-01	-0.4	5.8E-01
ENSMUST00000069023	TRPM8 channel-associated factor 3 [Source:MGI Symbol;Acc:MGI:3042585]		Q6QR59	5.6	4.4E-05	4.5	2.9E-03	-1.5	2.5E-01	-0.1	9.1E-01
ENSMUST00000067743	predicted gene 9949 [Source:MGI Symbol;Acc:MGI:3647947]	Q8C9F4		-0.5	3.8E-01	-1.5	6.3E-02	-0.6	2.2E-01	0.4	6.2E-01
ENSMUST00000069025	serine/arginine-rich splicing factor 11 [Source:MGI Symbol;Acc:MGI:1916457]	F6RDI8		-4.2	2.5E-02	-2.7	2.8E-02	1.5	2.3E-02	-0.1	9.4E-01
ENSMUST00000069036	mesencephalic astrocyte-derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:1922090]	Q80ZP8		-6.5	7.3E-06	-0.7	3.2E-01	1.1	3.2E-02	-0.7	3.3E-01
ENSMUST00000067757	phospholipase D1 [Source:MGI Symbol;Acc:MGI:109585]	Q6NVF2		-1.0	7.1E-01	7.2	6.8E-02	5.7	1.1E-01	-2.5	3.5E-01
ENSMUST00000069041	adaptor-related protein complex 1, sigma 2 subunit [Source:MGI Symbol;Acc:MGI:1889383]		Q9DB50	-4.0	2.7E-03	-4.7	1.6E-03	0.6	2.9E-01	-0.2	8.4E-01
ENSMUST00000069057	myosin IC [Source:MGI Symbol;Acc:MGI:106612]		Q9WTI7	-7.8	6.6E-05	5.4	2.3E-05	-0.8	2.3E-01	-0.4	3.8E-01
ENSMUST00000069097	argonaute RISC catalytic subunit 3 [Source:MGI Symbol;Acc:MGI:2446634]		Q8CJF9	1.7	2.3E-03	3.5	1.4E-03	-0.6	4.3E-01	-0.3	6.4E-01
ENSMUST00000067786	solute carrier family 20, member 2 [Source:MGI Symbol;Acc:MGI:97851]		Q80UP8	1.1	4.8E-02	1.0	1.2E-01	-0.6	2.0E-01	-0.5	3.5E-01
ENSMUST00000069098	suppressor of glucose, autophagy associated 1 [Source:MGI Symbol;Acc:MGI:2444575]	A2ACV6		6.3	2.5E-05	1.9	2.4E-01	-2.8	1.3E-01	0.0	9.8E-01
ENSMUST00000067795	ligand dependent nuclear receptor corepressor [Source:MGI Symbol;Acc:MGI:2443930]	A4FTY7	Q6ZPI3	0.5	3.2E-01	0.8	2.9E-01	0.5	3.5E-01	0.3	6.8E-01
ENSMUST00000069106	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha [Source:MGI Symbol;Acc:MGI:1341085]		Q9WUA5	2.4	1.2E-03	7.5	7.9E-05	-0.6	6.3E-01	-0.2	6.8E-01
ENSMUST00000067826	metastasis associated 3 [Source:MGI Symbol;Acc:MGI:2151172]		Q924K8	-0.4	5.1E-01	-0.9	3.2E-01	0.4	4.9E-01	0.9	3.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000069107	mitogen-activated protein kinase 1 [Source:MGI Symbol;Acc:MGI:1346858]		P63085	-3.6	2.6E-04	5.1	7.9E-05	-3.4	5.5E-03	-0.2	6.8E-01
ENSMUST00000067837	ring finger protein (C3H2C3 type) 6 [Source:MGI Symbol;Acc:MGI:1921382]		Q9DBU5	-3.7	1.4E-01	-2.6	2.1E-01	-2.3	1.2E-01	-3.4	2.1E-01
ENSMUST00000069125	family with sequence similarity 26, member E [Source:MGI Symbol;Acc:MGI:2143897]		Q8R100	5.7	1.5E-04	7.5	8.7E-05	-0.6	6.1E-01	-0.1	8.0E-01
ENSMUST00000069174	tripartite motif-containing 23 [Source:MGI Symbol;Acc:MGI:1933161]		Q8BGX0	6.6	5.7E-05	1.3	3.2E-01	0.3	7.3E-01	-4.5	9.4E-03
ENSMUST00000069180	zinc finger, CCHC domain containing 24 [Source:MGI Symbol;Acc:MGI:1919168]		B2RVL6	1.8	1.4E-02	1.3	1.2E-01	-2.0	1.9E-02	-0.5	4.4E-01
ENSMUST00000069183	guanylate cyclase 2g [Source:MGI Symbol;Acc:MGI:106025]		Q6TL19	7.0	3.1E-05	-6.0	2.2E-02	1.1	2.9E-01	0.0	9.9E-01
ENSMUST00000069195	zinc finger protein 46 [Source:MGI Symbol;Acc:MGI:99192]		Q8BPP0	2.0	3.9E-03	-2.5	7.7E-02	0.2	7.8E-01	-1.5	3.2E-01
ENSMUST00000069245	serine peptidase inhibitor, Kazal type 5 [Source:MGI Symbol;Acc:MGI:1919682]	Q148R4		6.7	1.1E-04	6.9	2.9E-04	-1.7	2.4E-01	0.2	7.4E-01
ENSMUST00000069256	TEA domain family member 1 [Source:MGI Symbol;Acc:MGI:101876]	Q6PAQ8		8.0	3.0E-06	-3.3	6.6E-03	1.2	3.0E-02	-0.6	5.6E-01
ENSMUST00000067886	solute carrier family 2 (facilitated glucose transporter), member 9 [Source:MGI Symbol;Acc:MGI:2152844]	Q3T9X0		-0.2	8.6E-01	2.2	1.5E-01	0.0	9.9E-01	-2.5	1.0E-01
ENSMUST00000067896	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 [Source:MGI Symbol;Acc:MGI:185	Q548M4	Q9JLJ5	-2.0	2.5E-01	-1.6	5.1E-01	0.4	8.4E-01	0.0	9.9E-01
ENSMUST00000069271	DMRT-like family B with proline-rich C-terminal, 1 [Source:MGI Symbol;Acc:MGI:1927125]		A2A9I7	7.0	9.1E-05	-4.0	2.2E-03	0.1	8.5E-01	-0.6	5.5E-01
ENSMUST00000069284	FYVE, RhoGEF and PH domain containing 4 [Source:MGI Symbol;Acc:MGI:2183747]	F8WGX0		-7.5	4.8E-05	-4.9	1.5E-03	1.0	7.1E-02	-0.8	5.2E-01
ENSMUST00000067916	phospholipase C, delta 4 [Source:MGI Symbol;Acc:MGI:107469]		Q8K3R3	3.3	9.2E-02	6.5	6.5E-03	-0.5	8.2E-01	-3.6	1.7E-02
ENSMUST00000067918	protein phosphatase 1H (PP2C domain containing) [Source:MGI Symbol;Acc:MGI:2442087]		Q3UYC0	-0.4	5.3E-01	0.9	2.8E-01	1.1	1.2E-01	-0.3	7.3E-01
ENSMUST00000069292	zinc finger protein 248 [Source:MGI Symbol;Acc:MGI:1919970]	Q640N4		6.0	1.9E-05	1.7	1.6E-02	-0.6	2.9E-01	-0.2	7.5E-01
ENSMUST00000069293	dynein, axonemal, heavy chain 7B [Source:MGI Symbol;Acc:MGI:2684953]	L7N1Y0		6.9	7.0E-04	-6.6	1.7E-06	-0.7	3.0E-02	-0.6	3.7E-01
ENSMUST00000069324	zinc finger protein 580 [Source:MGI Symbol;Acc:MGI:1916242]		Q9DB38	2.4	9.6E-03	-3.6	5.0E-05	0.7	1.9E-02	-0.7	1.9E-01
ENSMUST00000067929	fatty acyl CoA reductase 1 [Source:MGI Symbol;Acc:MGI:1914670]		Q922J9	3.2	8.8E-02	1.2	5.0E-01	-3.0	8.7E-02	-1.0	5.6E-01
ENSMUST00000067931	vimentin-type intermediate filament associated coiled-coil protein [Source:MGI Symbol;Acc:MGI:2146912]		Q8BP01	4.2	8.5E-02	0.1	9.5E-01	-4.1	8.7E-02	0.1	9.8E-01
ENSMUST00000069334	dachshund 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1277991]		Q9QYB2	-6.8	6.2E-05	5.1	5.6E-04	0.2	8.1E-01	-0.9	2.1E-01
ENSMUST00000067936	Rho GDP dissociation inhibitor (GDI) alpha [Source:MGI Symbol;Acc:MGI:2178103]		Q99PT1	-0.5	5.2E-01	-0.5	6.8E-01	0.8	3.3E-01	0.7	4.9E-01
ENSMUST00000069360	glypican 3 [Source:MGI Symbol;Acc:MGI:104903]	Q3TWB2	Q8CFZ4	-4.6	8.4E-05	-2.3	3.9E-03	1.4	2.9E-03	-0.5	4.7E-01
ENSMUST00000069399	kelch repeat and BTB (POZ) domain containing 11 [Source:MGI Symbol;Acc:MGI:1922151]		Q8BNW9	3.0	2.5E-03	-0.8	5.2E-01	0.5	5.8E-01	-1.6	2.4E-01
ENSMUST00000069420	transmembrane protein 191C [Source:MGI Symbol;Acc:MGI:107238]		Q9JJB1	5.6	8.9E-03	6.8	1.9E-04	-0.6	6.0E-01	0.1	9.2E-01
ENSMUST00000069431	predicted gene 9978 [Source:MGI Symbol;Acc:MGI:3641806]	Q8C4R4		3.6	1.0E-04	-2.1	2.5E-01	0.5	6.4E-01	-2.1	2.8E-01
ENSMUST00000069456	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	Q8BK32		2.3	2.1E-03	-3.1	5.1E-04	1.3	3.6E-03	-0.1	8.7E-01
ENSMUST00000069457	predicted gene 9979 [Source:MGI Symbol;Acc:MGI:3642885]	G5E8F2		8.4	2.7E-05	6.2	4.4E-04	-0.5	6.6E-01	-0.2	7.8E-01
ENSMUST00000069476	leucine zipper, down-regulated in cancer 1-like [Source:MGI Symbol;Acc:MGI:2675858]		Q505G4	3.5	2.3E-04	-4.6	3.5E-04	0.3	4.6E-01	-2.7	3.1E-02
ENSMUST00000068004	pyruvate carboxylase [Source:MGI Symbol;Acc:MGI:97520]	E9QPD7		2.0	4.3E-01	5.2	1.1E-01	0.5	8.5E-01	-2.7	2.6E-01
ENSMUST00000069507	complement component 4B (Chido blood group) [Source:MGI Symbol;Acc:MGI:88228]		P01029	4.0	1.6E-04	-2.8	6.9E-03	1.2	2.0E-02	-0.2	7.8E-01
ENSMUST00000069509	ubiquitin specific peptidase 26 [Source:MGI Symbol;Acc:MGI:1933247]		Q99MX1	6.6	7.8E-04	1.4	3.5E-02	0.2	7.1E-01	0.1	8.2E-01
ENSMUST00000069511	ATP-binding cassette, sub-family D (ALD), member 2 [Source:MGI Symbol;Acc:MGI:1349467]			-3.3	2.9E-05	3.3	1.6E-03	-3.4	3.7E-03	-0.5	4.6E-01
ENSMUST00000069520	synaptophysin [Source:MGI Symbol;Acc:MGI:98467]		Q62277	-1.4	1.8E-02	-1.3	5.7E-02	1.2	1.3E-02	0.0	9.9E-01
ENSMUST00000069530	X-ray repair complementing defective repair in Chinese hamster cells 6 [Source:MGI Symbol;Acc:MGI:95606]			-5.2	8.4E-05	-4.6	6.2E-04	-0.6	2.0E-01	0.5	6.1E-01
ENSMUST00000068036	5-hydroxytryptamine (serotonin) receptor 6 [Source:MGI Symbol;Acc:MGI:1196627]	Q14AW8	Q9R1C8	2.8	1.3E-01	6.0	5.0E-03	-0.5	7.8E-01	-3.7	1.5E-02
ENSMUST00000069533	CAP, adenylate cyclase-associated protein 1 (yeast) [Source:MGI Symbol;Acc:MGI:88262]		P40124	-8.5	6.5E-06	1.1	1.4E-01	-1.0	1.3E-01	-0.4	5.0E-01
ENSMUST00000069536	transcription factor 7 like 1 (T cell specific, HMG box) [Source:MGI Symbol;Acc:MGI:1202876]	A1A550		6.9	2.2E-04	-2.9	1.1E-02	0.5	3.1E-01	-2.5	5.0E-02
ENSMUST00000068054	STAM binding protein [Source:MGI Symbol;Acc:MGI:1917777]		Q9CQ26	-0.5	4.5E-01	-0.6	4.5E-01	0.3	6.3E-01	0.5	5.8E-01
ENSMUST00000069548	Rho GTPase activating protein 9 [Source:MGI Symbol;Acc:MGI:2143764]	Q8QZW8		-6.6	3.5E-06	-3.5	1.1E-03	0.7	1.2E-01	-4.0	4.6E-03
ENSMUST00000069549	claudin 17 [Source:MGI Symbol;Acc:MGI:2652030]		Q8BXA6	6.0	2.6E-03	-3.4	6.9E-02	0.8	3.6E-01	-0.5	7.9E-01
ENSMUST00000069556	melanoma antigen, family A, 5 [Source:MGI Symbol;Acc:MGI:1333838]	O89009		5.7	2.6E-02	-2.2	4.7E-02	-1.2	8.7E-02	-3.2	2.6E-02
ENSMUST00000069562	tescalcin-like [Source:MGI Symbol;Acc:MGI:1916551]	Q9DAJ7		6.7	5.3E-05	2.6	5.4E-03	0.0	9.8E-01	-0.1	8.3E-01
ENSMUST00000069579	transcription elongation factor B (SIII), polypeptide 2 [Source:MGI Symbol;Acc:MGI:1914923]		P62869	-5.8	1.8E-04	5.2	2.5E-05	0.1	9.4E-01	-0.8	7.9E-02
ENSMUST00000069580	ring finger protein 181 [Source:MGI Symbol;Acc:MGI:1913760]		Q9CY62	-5.2	5.7E-04	5.1	1.1E-04	-2.4	2.6E-02	-0.7	2.2E-01
ENSMUST00000069597	casein kinase 1, gamma 3 [Source:MGI Symbol;Acc:MGI:1917675]		Q8C4X2	-2.8	9.1E-04	6.5	1.8E-04	-1.7	1.8E-01	-0.2	7.9E-01
ENSMUST00000068110	protocadherin 7 [Source:MGI Symbol;Acc:MGI:1860487]	A2RS43		1.5	3.2E-01	5.6	2.2E-02	2.3	2.7E-01	-1.8	1.8E-01
ENSMUST00000069614	doublecortin domain containing 2a [Source:MGI Symbol;Acc:MGI:2652818]	R4GML1		6.9	5.1E-05	-2.3	1.5E-01	-0.3	7.8E-01	-2.5	1.8E-01
ENSMUST00000069616	tryptase beta 2 [Source:MGI Symbol;Acc:MGI:96942]	E9QJW9		6.2	1.6E-04	-3.5	6.3E-03	-0.1	8.8E-01	-0.7	5.3E-01
ENSMUST00000069619	stromal antigen 2 [Source:MGI Symbol;Acc:MGI:1098583]		O35638	-8.1	4.6E-06	-2.2	2.7E-01	2.0	1.2E-01	-0.3	8.8E-01
ENSMUST00000069623	Rho guanine nucleotide exchange factor (GEF) 10-like [Source:MGI Symbol;Acc:MGI:1920004]		A2AWP8	8.7	2.2E-05	6.1	2.3E-04	-1.4	2.4E-01	-0.8	2.2E-01
ENSMUST00000068137	breast carcinoma amplified sequence 1 [Source:MGI Symbol;Acc:MGI:1924210]	A2AVX1		5.7	7.6E-02	3.7	2.8E-01	-0.5	8.9E-01	1.5	4.6E-01
ENSMUST00000069634	forkhead box I3 [Source:MGI Symbol;Acc:MGI:3511278]	D3Z120		6.5	4.2E-03	6.6	5.2E-04	-2.8	8.3E-02	0.3	6.3E-01
ENSMUST00000068156	vacuolar protein sorting 13A (yeast) [Source:MGI Symbol;Acc:MGI:2444304]		Q5H8C4	-0.5	3.2E-01	-0.1	9.4E-01	0.1	8.4E-01	-0.4	5.5E-01
ENSMUST00000068167	leucine rich repeat (in FLII) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1342770]	E9Q9T1		-0.5	7.0E-01	-0.3	8.5E-01	0.4	7.1E-01	0.2	8.9E-01
ENSMUST00000069649	abhydrolase domain containing 16B [Source:MGI Symbol;Acc:MGI:3607711]		Q80YU0	6.1	2.5E-04	-3.0	7.0E-02	0.7	3.9E-01	-0.1	9.7E-01
ENSMUST00000068169	pecanex-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1861733]		Q8VI59	-2.5	1.6E-01	-3.8	2.8E-01	1.8	3.4E-01	3.0	3.4E-01
ENSMUST00000069651	glutamate decarboxylase-like 1 [Source:MGI Symbol;Acc:MGI:1920998]	E9QP13		6.3	1.7E-05	6.9	2.0E-04	0.1	9.0E-01	-0.7	2.8E-01
ENSMUST00000069686	ring finger protein 180 [Source:MGI Symbol;Acc:MGI:1919066]		Q3U827	3.4	1.8E-04	-10.0	7.2E-05	-0.7	2.1E-01	-1.2	4.7E-01
ENSMUST00000069692	zinc finger protein 277 [Source:MGI Symbol;Acc:MGI:1890393]	E9Q6D6		5.0	1.0E-06	5.3	1.1E-01	2.5	3.9E-01	2.0	2.6E-01
ENSMUST00000069705	ATP/GTP binding protein-like 5 [Source:MGI Symbol;Acc:MGI:2441745]		Q09M02	5.0	7.6E-04	-6.5	8.3E-03	-0.5	4.7E-01	1.6	4.4E-01
ENSMUST00000069711	predicted gene 14137 [Source:MGI Symbol;Acc:MGI:3651144]	B2RX56		5.2	6.7E-05	3.1	1.8E-02	-1.5	1.9E-01	0.1	8.8E-01
ENSMUST00000069712	tumor protein D52-like 2 [Source:MGI Symbol;Acc:MGI:1913564]	Q8BKP1		-6.4	1.4E-04	-5.0	2.7E-02	1.1	2.8E-01	-0.9	7.2E-01
ENSMUST00000068240	kelch domain containing 10 [Source:MGI Symbol;Acc:MGI:1924038]		Q6PAR0	4.5	5.2E-02	1.9	5.4E-01	0.1	9.5E-01	2.7	3.0E-01
ENSMUST00000069722	tafazzin [Source:MGI Symbol;Acc:MGI:109626]	Q91WF0		-5.3	1.6E-04	7.1	1.0E-04	-0.6	6.1E-01	0.0	9.5E-01
ENSMUST00000069742	proline rich 18 [Source:MGI Symbol;Acc:MGI:2443403]		Q6PAN7	8.2	7.4E-03	3.7	3.5E-03	-0.2	8.0E-01	0.8	2.7E-01
ENSMUST00000068259	kelch domain containing 10 [Source:MGI Symbol;Acc:MGI:1924038]		Q6PAR0	-1.0	6.0E-02	-0.1	8.3E-01	0.9	6.8E-02	0.0	9.5E-01
ENSMUST00000068261	ATPase, H+ transporting, lysosomal V1 subunit G2 [Source:MGI Symbol;Acc:MGI:1913487]	Q54A87	Q9WTT4	-1.9	1.7E-01	1.3	4.6E-01	1.7	2.9E-01	-1.5	2.9E-01
ENSMUST00000069747	ER membrane protein complex subunit 7 [Source:MGI Symbol;Acc:MGI:1920274]	Q14C26	Q9EP72	-1.5	1.7E-03	6.3	2.0E-04	-0.6	6.1E-01	0.2	7.8E-01
ENSMUST00000069756	occludin [Source:MGI Symbol;Acc:MGI:106183]	B2RS24	Q61146	6.4	5.4E-04	6.0	2.6E-03	-0.5	7.5E-01	-0.1	9.5E-01
ENSMUST00000069763	LanC lantibiotic synthetase component C-like 3 (bacterial) [Source:MGI Symbol;Acc:MGI:2443335]		Q8CD19	6.4	1.3E-04	-6.7	2.2E-02	-0.1	8.8E-01	2.6	3.1E-01
ENSMUST00000069789	leptin [Source:MGI Symbol;Acc:MGI:104663]	Q544U0	P41160	7.8	6.5E-05	-4.6	9.0E-03	1.3	4.3E-02	2.6	8.7E-02
ENSMUST00000069792	Ngfi-A binding protein 1 [Source:MGI Symbol;Acc:MGI:107564]		Q61122	-4.0	3.4E-02	-4.4	2.1E-03	1.8	3.2E-03	-0.6	5.9E-01
ENSMUST00000069799	insulin receptor substrate 1 [Source:MGI Symbol;Acc:MGI:99454]	Q543V3		10.4	2.2E-06	-6.7	2.9E-04	0.7	1.1E-01	-0.7	6.2E-01
ENSMUST00000069800	fucosyltransferase 2 [Source:MGI Symbol;Acc:MGI:109374]	A6H6C9	Q9JL27	8.3	2.7E-05	7.3	7.6E-05	0.9	4.2E-01	0.0	1.0E+00
ENSMUST00000069817	proline-rich coiled-coil 2B [Source:MGI Symbol;Acc:MGI:1923304]	F8WHT3		1.2	3.1E-02	6.9	8.5E-05	-1.5	2.1E-01	0.2	7.1E-01
ENSMUST00000069828	thrombospondin, type I, domain 1 [Source:MGI Symbol;Acc:MGI:1929096]			5.4	5.1E-03	7.2	6.1E-05	0.0	9.6E-01	-0.8	1.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000068326	olute carrier family 8 (sodium/lithium/calcium exchanger), member B1 [Source:MGI Symbol;Acc:MGI:218078		Q925Q3	-2.2	6.2E-02	-3.1	6.9E-02	0.7	4.0E-01	1.7	3.0E-01
ENSMUST00000068333	phenylalanyl-tRNA synthetase, beta subunit [Source:MGI Symbol;Acc:MGI:1346035]		Q9WUA2	-0.9	4.8E-01	-1.2	5.4E-01	0.6	6.7E-01	0.9	5.9E-01
ENSMUST00000069837	slit homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1315202]		Q9WVB4	8.3	1.0E-05	8.6	2.1E-04	-0.8	6.3E-01	0.3	6.7E-01
ENSMUST00000069852	predicted gene 11541 [Source:MGI Symbol;Acc:MGI:3650066]	Q8C4D8		6.2	2.5E-04	5.8	7.1E-04	-0.6	6.2E-01	0.4	5.2E-01
ENSMUST00000068367	DIS3 mitotic control homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:2143272]		Q8C0S1	2.6	2.2E-01	5.4	1.9E-02	-0.6	7.8E-01	-3.4	4.7E-02
ENSMUST00000068378	contactin 1 [Source:MGI Symbol;Acc:MGI:105980]		P12960	3.9	1.4E-01	3.0	3.3E-01	-0.2	9.4E-01	0.7	7.1E-01
ENSMUST00000069861	catsper channel auxiliary subunit gamma 1 [Source:MGI Symbol;Acc:MGI:2443617]		E9Q355	5.8	2.7E-03	-2.1	2.1E-03	1.0	7.6E-03	0.1	7.9E-01
ENSMUST00000069862	RIKEN cDNA A430033K04 gene [Source:MGI Symbol;Acc:MGI:3583896]	E9Q8G5		4.8	1.9E-05	6.2	3.0E-03	-0.7	6.8E-01	-0.9	3.3E-01
ENSMUST00000069870	ADP-ribosylation factor-like 5B [Source:MGI Symbol;Acc:MGI:1923119]	Q6NXZ5		-4.3	9.5E-03	5.7	1.4E-03	-0.6	6.5E-01	-0.2	8.1E-01
ENSMUST00000069877	dynein, axonemal, light chain 4 [Source:MGI Symbol;Acc:MGI:1859217]	Q8CDT8		-4.2	5.4E-03	-3.5	1.4E-02	0.1	8.8E-01	-1.0	4.2E-01
ENSMUST00000069902	nicotinamide nucleotide transhydrogenase [Source:MGI Symbol;Acc:MGI:109279]	Q8C9V5		-2.9	2.3E-02	-7.2	5.1E-05	-1.0	4.0E-02	-0.3	7.6E-01
ENSMUST00000069912	regulator of G-protein signalling 9 binding protein [Source:MGI Symbol;Acc:MGI:2384418]		Q148R9	7.7	3.8E-06	-3.8	7.1E-02	1.1	2.8E-01	0.8	7.0E-01
ENSMUST00000068415	zinc finger E-box binding homeobox 2 [Source:MGI Symbol;Acc:MGI:1344407]		Q9R0G7	-3.5	6.8E-02	-4.6	9.0E-02	-0.3	8.1E-01	0.8	7.6E-01
ENSMUST00000069926	SLIT and NTRK-like family, member 4 [Source:MGI Symbol;Acc:MGI:2442509]	Q149A4	Q810B8	7.9	1.2E-05	-4.6	3.0E-02	-0.6	4.9E-01	-0.4	8.3E-01
ENSMUST00000068439	PDZ and LIM domain 1 (elfin) [Source:MGI Symbol;Acc:MGI:1860611]		O70400	0.7	3.0E-01	1.7	6.3E-02	0.3	6.3E-01	-0.7	3.6E-01
ENSMUST00000069927	S100 calcium binding protein A8 (calgranulin A) [Source:MGI Symbol;Acc:MGI:88244]	Q53X15	P27005	-11.0	2.0E-07	6.7	3.6E-04	-1.4	3.0E-01	0.4	5.4E-01
ENSMUST00000068449	RAB39, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2442855]	Q0PD15	Q8BHD0	0.6	2.6E-01	1.3	7.2E-02	-0.2	7.4E-01	-0.8	1.7E-01
ENSMUST00000068452	CCR4-NOT transcription complex, subunit 1 [Source:MGI Symbol;Acc:MGI:2442402]	B7ZWL1		-0.1	9.2E-01	-0.8	3.2E-01	-1.2	4.0E-02	-0.6	4.6E-01
ENSMUST00000069929	PDZ and LIM domain 7 [Source:MGI Symbol;Acc:MGI:1914649]		Q3TJD7	-3.8	2.9E-02	7.0	1.1E-04	-0.6	6.0E-01	0.1	8.6E-01
ENSMUST00000069936	interphotoreceptor matrix proteoglycan 2 [Source:MGI Symbol;Acc:MGI:3044955]		Q80XH2	4.7	1.9E-04	-5.8	4.9E-02	0.7	4.7E-01	0.7	7.8E-01
ENSMUST00000069941	butyrophilin-like 10 [Source:MGI Symbol;Acc:MGI:2182073]		Q9JK39	9.7	1.3E-05	6.2	1.8E-04	-0.5	6.3E-01	-0.4	5.5E-01
ENSMUST00000069949	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:MGI Symbol;Acc:MGI:104819]		O88569	-8.2	3.4E-05	-2.4	3.7E-03	-0.2	6.1E-01	-0.2	7.9E-01
ENSMUST00000069958	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme [Source:MGI Symbol;Acc:MGI:1100870]		P97402	-2.1	1.0E-03	-2.5	3.7E-03	1.2	1.1E-02	-0.1	8.5E-01
ENSMUST00000069960	S100 calcium binding protein A9 (calgranulin B) [Source:MGI Symbol;Acc:MGI:1338947]	Q3UP42	P31725	-11.1	2.9E-07	6.8	2.7E-04	-0.6	6.3E-01	-1.1	1.5E-01
ENSMUST00000069968	PDZ and LIM domain 7 [Source:MGI Symbol;Acc:MGI:1914649]	Q8BVJ7		-6.3	3.6E-03	-2.8	5.7E-04	-0.1	7.9E-01	-0.2	6.9E-01
ENSMUST00000069992	predicted gene 5468 [Source:MGI Symbol;Acc:MGI:3648948]	Q8C3D3		6.0	5.9E-04	4.4	2.3E-03	-0.7	5.1E-01	-0.4	6.5E-01
ENSMUST00000068563	acyl-Coenzyme A oxidase 3, pristanoyl [Source:MGI Symbol;Acc:MGI:1933156]	Q8C178		-1.0	1.2E-01	-0.5	5.5E-01	0.7	2.8E-01	0.1	8.5E-01
ENSMUST00000069994	ST3 beta-galactoside alpha-2,3-sialyltransferase 5 [Source:MGI Symbol;Acc:MGI:1339963]		O88829	-1.8	1.3E-02	-4.9	7.9E-05	0.7	5.1E-02	-0.1	8.5E-01
ENSMUST00000070000	Rho GTPase activating protein 24 [Source:MGI Symbol;Acc:MGI:1922647]	D3Z5T4		7.0	1.2E-04	1.0	9.9E-02	-0.4	3.7E-01	0.1	7.9E-01
ENSMUST00000068569	B cell leukemia/lymphoma 2 related protein A1b [Source:MGI Symbol;Acc:MGI:1278326]	Q497M6		-1.1	2.3E-01	-5.2	1.7E-03	-3.8	3.4E-04	0.3	7.9E-01
ENSMUST00000070004	lactate dehydrogenase D [Source:MGI Symbol;Acc:MGI:106428]		Q7TNG8	2.4	9.0E-03	6.3	4.0E-04	-0.5	7.1E-01	-1.5	5.1E-02
ENSMUST00000070039	fasciculation and elongation protein zeta 2 (zygin II) [Source:MGI Symbol;Acc:MGI:2675856]	Q3U049	Q6TYB5	-4.3	3.2E-03	-1.5	1.4E-02	-6.1	9.3E-07	-0.5	3.8E-01
ENSMUST00000070059	predicted gene 9992 [Source:MGI Symbol;Acc:MGI:3712668]	B2RWK3		6.4	5.5E-04	-2.5	5.7E-02	0.5	3.9E-01	-0.5	6.9E-01
ENSMUST00000070102	nanos homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2675387]		P60324	5.4	4.1E-04	-5.9	1.5E-03	-0.9	1.0E-01	0.6	6.7E-01
ENSMUST00000070112	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 [Source:MGI Symbol;Acc:MGI:1915625]		Q9DCJ5	-5.0	1.1E-05	0.3	5.6E-01	-1.8	4.9E-03	-0.3	5.7E-01
ENSMUST00000070116	suppressor of cytokine signaling 6 [Source:MGI Symbol;Acc:MGI:1924885]		Q9JLY0	3.0	3.4E-03	-2.9	1.1E-03	0.3	4.3E-01	0.3	6.1E-01
ENSMUST00000070117	CCR4-NOT transcription complex, subunit 10 [Source:MGI Symbol;Acc:MGI:1926143]		Q8BH15	-1.9	3.1E-03	3.0	2.6E-03	0.8	2.1E-01	-0.2	7.1E-01
ENSMUST00000068617	Williams Beuren syndrome chromosome region 27 (human) [Source:MGI Symbol;Acc:MGI:1933146]	Q8BY07		4.7	5.1E-02	4.1	1.1E-01	-0.7	7.6E-01	-0.1	9.5E-01
ENSMUST00000070124	histone cluster 1, H2ai [Source:MGI Symbol;Acc:MGI:2448457]	B2RVF0	P22752	2.4	2.2E-02	6.1	2.7E-04	-0.5	6.7E-01	-1.5	3.7E-02
ENSMUST00000070125	choline acetyltransferase [Source:MGI Symbol;Acc:MGI:88392]	Q8BQV2		8.9	4.9E-06	5.8	6.9E-04	-0.5	7.0E-01	-0.7	2.9E-01
ENSMUST00000070132	collagen, type VIII, alpha 2 [Source:MGI Symbol;Acc:MGI:88464]		P25318	7.8	3.8E-05	-2.0	4.6E-02	1.2	4.2E-02	0.5	5.4E-01
ENSMUST00000070135	PQ loop repeat containing 1 [Source:MGI Symbol;Acc:MGI:1914193]		Q80XM9	-8.1	1.4E-04	5.2	2.1E-04	0.9	3.0E-01	-0.8	1.8E-01
ENSMUST00000070139	carnosine dipeptidase 1 (metallopeptidase M20 family) [Source:MGI Symbol;Acc:MGI:2451097]			6.2	7.1E-04	3.8	2.1E-03	0.1	9.5E-01	0.0	9.5E-01
ENSMUST00000070143	zinc fingers and homeoboxes 1 [Source:MGI Symbol;Acc:MGI:109271]		P70121	-5.3	1.1E-03	2.6	1.1E-03	-4.9	3.5E-05	-0.2	6.1E-01
ENSMUST00000070150	RIKEN cDNA E130308A19 gene [Source:MGI Symbol;Acc:MGI:2442164]	Q0P6E2	Q8C4P0	6.0	9.6E-06	8.1	3.5E-05	-0.6	6.0E-01	-0.9	1.2E-01
ENSMUST00000070152	olute carrier family 16 (monocarboxylic acid transporters), member 6 [Source:MGI Symbol;Acc:MGI:2144585		B1AT66	-4.1	7.9E-04	4.5	8.5E-03	-0.6	6.5E-01	2.0	4.4E-02
ENSMUST00000070165	nucleoporin 98 [Source:MGI Symbol;Acc:MGI:109404]			-2.0	4.2E-03	3.2	4.3E-02	-3.8	3.2E-02	0.1	9.6E-01
ENSMUST00000070173	pyroglutamyl-peptidase I [Source:MGI Symbol;Acc:MGI:1913772]		Q9ESW8	2.6	4.4E-03	3.9	2.6E-03	-2.5	4.5E-02	-0.1	8.8E-01
ENSMUST00000070174	transmembrane protein 229B [Source:MGI Symbol;Acc:MGI:2444389]		Q8BFQ2	5.6	2.5E-02	-2.4	7.2E-03	1.0	3.6E-02	-0.5	5.1E-01
ENSMUST00000070181	inositol 1,4,5-trisphosphate 3-kinase B [Source:MGI Symbol;Acc:MGI:109235]	B2RXC2		-1.6	2.3E-02	6.3	3.2E-04	-0.6	6.1E-01	0.7	3.1E-01
ENSMUST00000070189	leucine-rich repeats and guanylate kinase domain containing [Source:MGI Symbol;Acc:MGI:1921604]		Q9D5S7	6.3	1.8E-03	2.3	6.7E-03	-0.4	4.9E-01	-0.1	9.2E-01
ENSMUST00000068702	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	A2AHG3		0.4	8.7E-01	6.8	2.8E-02	2.1	4.4E-01	-4.4	4.7E-02
ENSMUST00000068714	son of sevenless homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:98354]		Q62245	0.1	8.2E-01	0.8	2.5E-01	1.0	6.8E-02	0.3	6.0E-01
ENSMUST00000068726	CUGBP, Elav-like family member 1 [Source:MGI Symbol;Acc:MGI:1342295]			-1.3	6.7E-01	-1.6	5.6E-01	-3.2	1.8E-01	-2.9	3.6E-01
ENSMUST00000068747	CUGBP, Elav-like family member 1 [Source:MGI Symbol;Acc:MGI:1342295]		P28659	-3.2	9.5E-02	-3.0	2.4E-01	1.0	4.1E-01	0.8	7.7E-01
ENSMUST00000068755	basic helix-loop-helix domain containing, class B9 [Source:MGI Symbol;Acc:MGI:1917487]		Q6PB60	2.6	1.1E-01	4.5	1.1E-02	-0.5	7.5E-01	-2.4	5.7E-02
ENSMUST00000070198	protein phosphatase 3, catalytic subunit, alpha isoform [Source:MGI Symbol;Acc:MGI:107164]		P63328	-3.5	1.1E-03	6.6	1.3E-04	-1.5	2.1E-01	0.6	3.4E-01
ENSMUST00000070200	phospholipase A2, group IVA (cytosolic, calcium-dependent) [Source:MGI Symbol;Acc:MGI:1195256]	Q3UMQ1	P47713	-2.7	3.5E-03	6.4	2.9E-04	-1.9	1.6E-01	0.1	8.3E-01
ENSMUST00000068791	eukaryotic translation initiation factor 2D [Source:MGI Symbol;Acc:MGI:109342]	Q8C8I3		-1.3	5.9E-02	-0.8	3.4E-01	0.0	9.6E-01	-0.5	5.1E-01
ENSMUST00000070210	ATPase family, AAA domain containing 1 [Source:MGI Symbol;Acc:MGI:1915229]		Q9D5T0	-4.3	6.3E-05	4.8	1.0E-06	-0.3	4.8E-01	0.1	8.4E-01
ENSMUST00000070215	nucleoplasmin 3 [Source:MGI Symbol;Acc:MGI:894653]		Q9CPP0	-2.2	9.6E-03	-3.2	9.2E-04	0.9	3.3E-02	0.1	9.3E-01
ENSMUST00000070216	spermatogenesis associated 31 [Source:MGI Symbol;Acc:MGI:1925374]		E9QAF0	8.1	6.9E-05	3.3	1.4E-02	-4.0	1.9E-02	-1.2	2.3E-01
ENSMUST00000070219	par-6 family cell polarity regulator gamma [Source:MGI Symbol;Acc:MGI:2135606]		Q9JK84	5.7	5.5E-06	-6.5	4.5E-04	-0.4	3.4E-01	-0.9	5.0E-01
ENSMUST00000070246	UBX domain protein 11 [Source:MGI Symbol;Acc:MGI:1914836]	I7HIQ5		5.3	2.2E-03	-4.0	3.6E-02	1.1	1.9E-01	-0.3	8.6E-01
ENSMUST00000070256	potassium voltage-gated channel, subfamily Q, member 3 [Source:MGI Symbol;Acc:MGI:1336181]		Q8K3F6	8.1	1.5E-07	5.8	5.6E-04	0.5	6.7E-01	-0.8	2.7E-01
ENSMUST00000070257	activating signal cointegrator 1 complex subunit 2 [Source:MGI Symbol;Acc:MGI:1922702]		Q91WR3	-2.9	2.6E-02	6.7	3.8E-04	-0.4	7.6E-01	1.6	4.8E-02
ENSMUST00000070258	predicted gene 5447 [Source:MGI Symbol;Acc:MGI:3644017]	Q8BPB2		4.9	9.2E-04	-3.9	4.0E-05	-0.2	5.4E-01	-0.5	3.6E-01
ENSMUST00000068830	cannabinoid receptor 2 (macrophage) [Source:MGI Symbol;Acc:MGI:104650]		P47936	0.5	9.0E-01	-0.8	9.0E-01	0.7	8.5E-01	2.0	7.4E-01
ENSMUST00000068836				0.6	4.8E-01	1.7	1.4E-01	0.3	7.7E-01	-0.8	4.0E-01
ENSMUST00000070300	F-box protein 30 [Source:MGI Symbol;Acc:MGI:1919115]		Q8BJL1	-5.5	4.4E-04	10.9	1.2E-02	-1.0	8.2E-01	-2.4	1.7E-01
ENSMUST00000068856	snurportin 1 [Source:MGI Symbol;Acc:MGI:1913319]		Q80W37	1.0	1.3E-01	0.0	9.9E-01	-0.7	2.5E-01	0.3	6.7E-01
ENSMUST00000070316	G-protein coupled receptor 173 [Source:MGI Symbol;Acc:MGI:1918021]		Q6PI62	9.4	1.1E-05	6.5	2.6E-04	-0.5	7.0E-01	-1.1	1.3E-01
ENSMUST00000070323	synaptoporin [Source:MGI Symbol;Acc:MGI:1919253]		Q8BGN8	5.7	1.6E-02	7.3	1.5E-03	-0.7	7.0E-01	-1.0	3.1E-01
ENSMUST00000068865	leukocyte-associated Ig-like receptor 1 [Source:MGI Symbol;Acc:MGI:105492]		Q8BG84	-1.6	9.1E-02	-3.9	1.5E-02	-0.6	3.9E-01	1.8	2.0E-01
ENSMUST00000070326	Ttk protein kinase [Source:MGI Symbol;Acc:MGI:1194921]		P35761	-5.0	3.0E-03	6.2	1.9E-04	-0.6	5.9E-01	0.4	5.2E-01
ENSMUST00000070328	SH2 domain containing 4B [Source:MGI Symbol;Acc:MGI:1925182]		A6X942	2.5	4.1E-03	-1.2	8.8E-02	-7.4	1.2E-05	0.7	2.6E-01
ENSMUST00000068878	lymphocyte antigen 9 [Source:MGI Symbol;Acc:MGI:96885]		Q01965	-0.1	9.5E-01	-0.8	5.8E-01	-1.7	1.6E-01	-1.0	5.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000068880	progestin and adipoQ receptor family member VIII [Source:MGI Symbol;Acc:MGI:1921479]		Q80ZE5	-0.5	5.6E-01	3.0	9.5E-03	1.0	2.4E-01	-2.5	1.4E-02
ENSMUST00000070330	dynamin 3 [Source:MGI Symbol;Acc:MGI:1341299]		Q8BZ98	5.7	3.1E-02	7.6	1.2E-02	-0.7	8.0E-01	-1.9	1.8E-01
ENSMUST00000070340	purine-rich element binding protein G [Source:MGI Symbol;Acc:MGI:1922279]		Q8R4E6	4.5	1.7E-04	3.6	1.4E-02	0.9	4.1E-01	0.9	2.4E-01
ENSMUST00000070342	serine rich and transmembrane domain containing 1 [Source:MGI Symbol;Acc:MGI:3607715]		Q8CD78	5.0	1.5E-02	6.0	4.6E-03	-0.1	9.5E-01	0.5	5.9E-01
ENSMUST00000070345	ubiquitin specific peptidase 39 [Source:MGI Symbol;Acc:MGI:107622]		Q3TIX9	-3.2	8.4E-05	8.0	1.4E-05	-0.5	6.0E-01	0.8	1.2E-01
ENSMUST00000070359	predicted gene 9996 [Source:MGI Symbol;Acc:MGI:3642549]	Q8CDX6		5.7	5.4E-03	3.1	9.0E-02	-0.5	7.5E-01	2.8	3.3E-02
ENSMUST00000070375	preproenkephalin [Source:MGI Symbol;Acc:MGI:104629]		P22005	3.6	9.5E-04	-3.2	5.4E-03	1.0	6.7E-02	-0.7	4.7E-01
ENSMUST00000070418	doublecortin-like kinase 1 [Source:MGI Symbol;Acc:MGI:1330861]	H7BX36		5.6	4.2E-03	-3.2	3.7E-03	1.2	2.1E-02	-1.0	2.8E-01
ENSMUST00000070449	G-protein-coupled receptor 50 [Source:MGI Symbol;Acc:MGI:1333877]		O88495	6.8	4.7E-05	-3.1	6.0E-03	0.3	5.0E-01	0.1	9.4E-01
ENSMUST00000070458	leucine rich repeat containing 56 [Source:MGI Symbol;Acc:MGI:1917802]		Q8K375	-4.6	2.1E-03	-2.7	1.8E-02	1.3	2.9E-02	-0.4	6.7E-01
ENSMUST00000070478	syndecan 3 [Source:MGI Symbol;Acc:MGI:1349163]		Q64519	2.7	4.6E-03	5.6	3.6E-04	-0.7	4.9E-01	-0.2	7.7E-01
ENSMUST00000068975	zinc finger protein 180 [Source:MGI Symbol;Acc:MGI:1923701]	Q6NZI9		0.4	4.1E-01	0.1	8.3E-01	0.0	9.2E-01	0.3	6.0E-01
ENSMUST00000068980	ankyrin repeat and SOCS box-containing 7 [Source:MGI Symbol;Acc:MGI:2152835]	Q8BQC5		-1.0	1.2E-01	0.7	3.4E-01	1.0	1.1E-01	-0.8	2.9E-01
ENSMUST00000070481	protein phosphatase 1, regulatory (inhibitor) subunit 3B [Source:MGI Symbol;Acc:MGI:2177268]		Q8C767	-2.3	7.0E-03	6.3	5.2E-03	-0.7	7.3E-01	-0.5	6.6E-01
ENSMUST00000070515	epoxide hydrolase 2, cytoplasmic [Source:MGI Symbol;Acc:MGI:99500]		P34914	6.1	4.9E-05	-4.4	1.2E-03	-0.1	7.8E-01	-0.2	8.2E-01
ENSMUST00000070524	trans-golgi network protein [Source:MGI Symbol;Acc:MGI:105080]	Q4FJY3	Q62313	-3.6	2.4E-05	3.7	1.2E-03	-1.3	1.4E-01	-1.6	2.7E-02
ENSMUST00000069000	poly (ADP-ribose) polymerase family, member 16 [Source:MGI Symbol;Acc:MGI:2446133]		Q7TMM8	0.8	1.6E-01	2.0	2.0E-02	1.0	1.1E-01	-0.2	8.0E-01
ENSMUST00000069005	family with sequence similarity 49, member A [Source:MGI Symbol;Acc:MGI:1261783]		Q8BHZ0	-1.0	5.3E-01	-3.4	1.4E-01	-0.7	5.9E-01	1.7	4.3E-01
ENSMUST00000069009	vian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog [Source:MGI Symbol;Acc:MGI:9690		P54843	1.7	4.3E-02	-0.1	8.8E-01	-2.3	6.6E-03	-0.5	5.1E-01
ENSMUST00000070532	fatty acid binding protein 3, muscle and heart [Source:MGI Symbol;Acc:MGI:95476]	Q5EBJ0	P11404	5.3	1.1E-03	5.5	4.3E-04	-0.2	8.5E-01	-0.1	8.6E-01
ENSMUST00000070533	X Kell blood group precursor related family member 4 [Source:MGI Symbol;Acc:MGI:3528744]		Q5GH67	7.2	3.5E-05	-4.3	1.2E-01	0.3	7.6E-01	0.4	8.8E-01
ENSMUST00000070575	casein kinase 1, delta [Source:MGI Symbol;Acc:MGI:1355272]	Q3UBT6	Q9DC28	-3.5	7.2E-03	-7.8	5.7E-05	-0.6	1.1E-01	0.7	5.3E-01
ENSMUST00000070577	RIKEN cDNA 1700030J22 gene [Source:MGI Symbol;Acc:MGI:1916778]	B9EHE0	Q8BHB7	2.4	2.4E-03	-0.3	7.2E-01	0.8	2.8E-01	-2.9	1.9E-02
ENSMUST00000070587	RIKEN cDNA 5730596B20 gene [Source:MGI Symbol;Acc:MGI:1924830]	Q8BQ08		7.8	1.4E-05	7.5	1.1E-04	-0.6	6.2E-01	-0.8	2.3E-01
ENSMUST00000070617	sodium channel, voltage-gated, type XI, alpha [Source:MGI Symbol;Acc:MGI:1345149]		Q9R053	5.9	1.4E-05	-4.7	1.3E-03	0.7	1.4E-01	-2.4	9.8E-02
ENSMUST00000069066	family with sequence similarity 49, member A [Source:MGI Symbol;Acc:MGI:1261783]		Q8BHZ0	2.4	4.2E-01	2.4	4.2E-01	-3.1	2.9E-01	-3.1	2.6E-01
ENSMUST00000070630	CD248 antigen, endosialin [Source:MGI Symbol;Acc:MGI:1917695]		Q91V98	9.2	4.4E-06	1.8	5.9E-03	-0.2	6.3E-01	-0.3	4.6E-01
ENSMUST00000070631	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:MGI Symbol;Acc:MGI:2384570]	G3X9F7		-3.3	2.8E-02	3.1	3.2E-03	-3.1	4.8E-03	0.1	8.4E-01
ENSMUST00000069103	X-linked lymphocyte-regulated 4B [Source:MGI Symbol;Acc:MGI:1350975]	Q9JJQ7		2.8	7.1E-02	1.4	3.7E-01	-1.7	2.4E-01	-0.3	8.1E-01
ENSMUST00000070635	zyxin [Source:MGI Symbol;Acc:MGI:103072]	Q7TQE2	Q62523	-8.1	1.4E-05	2.8	1.4E-03	0.0	9.8E-01	-0.4	4.4E-01
ENSMUST00000070639	predicted gene 14548 [Source:MGI Symbol;Acc:MGI:3709645]	E9Q1Z6		-7.2	5.5E-08	-2.6	1.0E-02	1.1	3.0E-02	0.2	8.0E-01
ENSMUST00000070642	CCAAT/enhancer binding protein (C/EBP), beta [Source:MGI Symbol;Acc:MGI:88373]	Q3UPN9	P28033	-4.9	1.5E-04	6.5	2.1E-04	0.4	7.0E-01	-0.4	5.6E-01
ENSMUST00000069168	cleavage and polyadenylation specific factor 6 [Source:MGI Symbol;Acc:MGI:1913948]		Q6NVF9	-1.2	1.7E-01	-0.5	6.7E-01	0.0	9.9E-01	-0.8	4.7E-01
ENSMUST00000070653	olute carrier family 16 (monocarboxylic acid transporters), member 3 [Source:MGI Symbol;Acc:MGI:1933438	Q3UDP9	P57787	-9.6	4.8E-05	-4.4	1.1E-01	2.1	7.7E-02	3.4	2.0E-01
ENSMUST00000070656	transforming growth factor beta 1 induced transcript 1 [Source:MGI Symbol;Acc:MGI:102784]		Q62219	5.9	1.4E-03	5.8	2.8E-04	-0.6	6.1E-01	0.2	6.7E-01
ENSMUST00000070658	mahogunin, ring finger 1 [Source:MGI Symbol;Acc:MGI:2447670]		Q9D074	-3.3	2.3E-04	0.0	9.9E-01	-1.4	2.9E-02	0.4	5.8E-01
ENSMUST00000070663	protein phosphatase 1, regulatory (inhibitor) subunit 12A [Source:MGI Symbol;Acc:MGI:1309528]		Q9DBR7	-4.8	3.6E-05	7.9	6.8E-05	0.5	6.7E-01	-0.4	5.4E-01
ENSMUST00000069188				1.3	5.5E-01	-2.1	3.2E-01	-3.8	4.3E-02	-0.4	8.5E-01
ENSMUST00000070673	RAB31, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1914603]	Q3TXV4		-5.7	3.4E-07	2.1	1.9E-02	1.0	1.3E-01	0.9	1.5E-01
ENSMUST00000069221	synaptotagmin binding, cytoplasmic RNA interacting protein [Source:MGI Symbol;Acc:MGI:1891690]		Q7TMK9	0.3	6.8E-01	0.9	3.7E-01	-0.6	4.0E-01	-1.2	2.2E-01
ENSMUST00000070681	GID complex subunit 4, VID24 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914021]		Q9CPY6	1.5	1.7E-02	6.5	2.6E-04	-0.5	6.8E-01	-0.3	5.9E-01
ENSMUST00000070690	platelet-activating factor receptor [Source:MGI Symbol;Acc:MGI:106066]		Q62035	-3.3	1.2E-04	4.5	1.1E-04	-4.2	5.2E-04	-0.7	1.5E-01
ENSMUST00000070705	ring finger protein, LIM domain interacting [Source:MGI Symbol;Acc:MGI:1342291]		Q9WTV7	-3.8	5.2E-04	6.5	3.1E-04	-0.6	6.6E-01	0.0	1.0E+00
ENSMUST00000069281	bifunctional apoptosis regulator [Source:MGI Symbol;Acc:MGI:1914368]		Q8R079	-1.6	5.7E-01	-2.4	3.9E-01	-2.3	2.7E-01	-1.5	6.2E-01
ENSMUST00000070720	sortilin-related VPS10 domain containing receptor 2 [Source:MGI Symbol;Acc:MGI:1932289]	Q8BI74		7.0	3.3E-05	-6.6	7.1E-04	0.2	6.0E-01	-0.6	6.7E-01
ENSMUST00000069285	syntaxin 3 [Source:MGI Symbol;Acc:MGI:103077]	Q3TBP0	Q64704	-1.6	7.1E-02	-0.9	4.0E-01	0.0	1.0E+00	-0.8	4.4E-01
ENSMUST00000069289	myeloid zinc finger 1 [Source:MGI Symbol;Acc:MGI:107457]	F6VC78		4.2	5.2E-02	2.8	2.9E-01	-1.1	6.5E-01	0.4	8.2E-01
ENSMUST00000070731	interleukin 6 signal transducer [Source:MGI Symbol;Acc:MGI:96560]		Q00560	-5.0	3.0E-04	5.9	3.9E-05	-0.6	4.7E-01	-0.5	3.7E-01
ENSMUST00000070733	protein tyrosine phosphatase, receptor type, N polypeptide 2 [Source:MGI Symbol;Acc:MGI:107418]		P80560	5.7	5.3E-03	8.1	4.3E-04	-0.3	8.6E-01	-1.4	7.9E-02
ENSMUST00000069298	Hermansky-Pudlak syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:2177763]	E9Q045		1.5	2.6E-01	1.9	2.9E-01	0.1	9.6E-01	-0.3	7.9E-01
ENSMUST00000069304	heterogeneous nuclear ribonucleoprotein H1 [Source:MGI Symbol;Acc:MGI:1891925]	Q811L7	O35737	-1.4	4.3E-01	-2.8	3.5E-01	0.5	7.9E-01	1.9	4.9E-01
ENSMUST00000070742	Mab-21 domain containing 1 [Source:MGI Symbol;Acc:MGI:2442261]		Q8C6L5	2.9	3.9E-03	3.6	3.7E-03	0.9	3.1E-01	-0.3	6.5E-01
ENSMUST00000069330	acid phosphatase 5, tartrate resistant [Source:MGI Symbol;Acc:MGI:87883]		Q05117	-2.0	1.1E-01	-1.2	3.6E-01	-1.1	2.3E-01	-1.9	1.6E-01
ENSMUST00000069333	CASP8 and FADD-like apoptosis regulator [Source:MGI Symbol;Acc:MGI:1336166]	Q812G4		0.4	8.4E-01	2.3	4.3E-01	1.7	3.8E-01	-0.2	9.4E-01
ENSMUST00000070748	LIM domain binding 2 [Source:MGI Symbol;Acc:MGI:894670]		O55203	7.4	4.2E-05	-1.3	1.3E-01	1.7	7.6E-03	-3.9	4.5E-03
ENSMUST00000069345	integrin beta 5 [Source:MGI Symbol;Acc:MGI:96614]	G5E8F8		-0.5	8.3E-01	4.5	1.4E-01	3.1	2.7E-01	-1.9	4.0E-01
ENSMUST00000070755	RAD54 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3605986]		Q6PFE3	2.2	2.0E-02	-3.7	8.9E-03	1.5	1.4E-02	0.6	6.0E-01
ENSMUST00000069372	RIKEN cDNA E030030I06 gene [Source:MGI Symbol;Acc:MGI:2442914]	F6UW72		1.7	5.5E-01	0.8	7.8E-01	-1.3	6.2E-01	-0.5	8.5E-01
ENSMUST00000069395	zinc finger, ZZ-type with EF hand domain 1 [Source:MGI Symbol;Acc:MGI:2444286]		Q5SSH7	5.7	3.6E-02	-0.1	9.6E-01	-4.6	6.1E-02	1.1	5.9E-01
ENSMUST00000070756	adenylate cyclase activating polypeptide 1 receptor 1 [Source:MGI Symbol;Acc:MGI:108449]	Q6NXJ9		8.7	5.5E-06	1.7	1.1E-01	-0.2	8.1E-01	1.2	1.7E-01
ENSMUST00000070758	myelin protein zero [Source:MGI Symbol;Acc:MGI:103177]	E9QK82		4.7	1.2E-03	3.1	1.2E-01	-2.8	1.6E-01	-0.3	8.3E-01
ENSMUST00000070782	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]		B1AZP2	5.8	3.2E-02	5.0	6.9E-05	0.9	1.9E-01	-0.4	3.4E-01
ENSMUST00000069449	related RAS viral (r-ras) oncogene homolog 2 [Source:MGI Symbol;Acc:MGI:1914172]		P62071	-0.1	7.9E-01	-1.0	8.1E-02	-0.7	8.8E-02	0.2	6.8E-01
ENSMUST00000070785	zinc finger with KRAB and SCAN domains 3 [Source:MGI Symbol;Acc:MGI:1919989]			-3.3	1.0E-02	2.8	3.1E-03	0.3	5.9E-01	-0.2	7.0E-01
ENSMUST00000070805	leucine rich repeat containing 48 [Source:MGI Symbol;Acc:MGI:1921915]	Q5SX99		5.5	3.5E-04	7.5	1.4E-04	-0.6	6.5E-01	0.2	6.9E-01
ENSMUST00000070808	olfactory receptor 90 [Source:MGI Symbol;Acc:MGI:2177473]	Q0VEL5		5.9	2.2E-03	3.7	7.4E-04	0.1	8.3E-01	0.0	1.0E+00
ENSMUST00000069477	melanoma antigen, family A, 2 [Source:MGI Symbol;Acc:MGI:1333793]	Q9R2A2		3.7	1.6E-01	3.2	2.8E-01	-0.2	9.3E-01	0.3	8.9E-01
ENSMUST00000069483	fibrosin-like 1 [Source:MGI Symbol;Acc:MGI:1920907]	E9Q9T0		-0.1	8.3E-01	1.0	1.2E-01	0.5	2.6E-01	-0.6	3.1E-01
ENSMUST00000069503	tubulin, delta 1 [Source:MGI Symbol;Acc:MGI:1891826]	Q5SWF8	Q9R1K7	-2.2	8.2E-02	-3.7	9.6E-02	0.0	1.0E+00	1.5	4.7E-01
ENSMUST00000070810	neuropeptide Y receptor Y5 [Source:MGI Symbol;Acc:MGI:108082]	Q543U8	O70342	7.1	3.0E-04	-0.9	1.5E-01	-5.1	1.3E-05	-0.1	8.2E-01
ENSMUST00000070814	predicted gene 10000 [Source:MGI Symbol;Acc:MGI:3641968]	Q8BR97		7.5	5.4E-05	5.8	3.2E-03	-0.7	6.9E-01	0.2	8.3E-01
ENSMUST00000070816	artemin [Source:MGI Symbol;Acc:MGI:1333791]		Q9Z0L2	7.6	1.4E-05	-2.9	3.7E-04	-0.1	7.3E-01	-0.5	3.7E-01
ENSMUST00000070820	DC-STAMP domain containing 1 [Source:MGI Symbol;Acc:MGI:1925022]		Q059Y8	3.6	5.6E-04	-0.1	9.2E-01	0.6	2.1E-01	-0.8	2.2E-01
ENSMUST00000070832	WAP four-disulfide core domain 21 [Source:MGI Symbol;Acc:MGI:1913357]	Q8BTE6		-9.2	3.3E-06	-5.5	2.8E-04	-1.1	1.9E-02	-0.8	4.5E-01
ENSMUST00000070864	calcium channel, voltage-dependent, N type, alpha 1B subunit [Source:MGI Symbol;Acc:MGI:88296]	A2AIS0		9.4	9.6E-04	-8.8	9.4E-05	0.9	6.3E-02	1.2	3.8E-01
ENSMUST00000070875	ankyrin repeat domain 33 [Source:MGI Symbol;Acc:MGI:2443398]		Q8BXP5	7.3	1.1E-04	4.4	7.1E-04	-3.5	1.3E-02	-1.0	1.7E-01
ENSMUST00000069537	zinc finger, AN1-type domain 6 [Source:MGI Symbol;Acc:MGI:1929510]		Q9DCH6	-3.7	3.8E-02	-1.5	4.1E-01	0.3	7.9E-01	-1.9	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000070878	FK506 binding protein 2 [Source:MGI Symbol;Acc:MGI:95542]	Q3TND1	P45878	-4.6	3.0E-04	-4.6	1.9E-04	1.1	1.6E-02	-0.9	2.8E-01
ENSMUST00000070886	zinc finger, CCHC domain containing 9 [Source:MGI Symbol;Acc:MGI:1916335]	F7A6K2		5.0	2.9E-02	4.9	1.5E-02	-0.6	7.3E-01	0.5	6.5E-01
ENSMUST00000070888	MTOR associated protein, LST8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1929514]		Q9DCJ1	-1.9	5.7E-03	4.3	1.6E-03	-1.2	2.5E-01	-1.1	1.4E-01
ENSMUST00000070892	desmoglein 3 [Source:MGI Symbol;Acc:MGI:99499]	Q3UFC6		10.5	1.0E-04	5.4	5.1E-02	-0.9	7.4E-01	-0.5	7.7E-01
ENSMUST00000069557	SMAD family member 5 [Source:MGI Symbol;Acc:MGI:1328787]		P97454	-0.7	1.9E-01	0.1	8.8E-01	-0.1	7.4E-01	-0.9	1.4E-01
ENSMUST00000070911	apolipoprotein L 8 [Source:MGI Symbol;Acc:MGI:2444921]	A2VDH7		5.6	3.9E-03	6.3	1.5E-04	-0.5	6.3E-01	-0.2	7.3E-01
ENSMUST00000070980	RIKEN cDNA 4933402N03 gene [Source:MGI Symbol;Acc:MGI:1914681]	Q8CDT9		6.1	9.3E-05	-5.5	9.3E-04	-0.8	1.7E-01	-1.1	4.1E-01
ENSMUST00000071006	U1 small nuclear ribonucleoprotein C [Source:MGI Symbol;Acc:MGI:109489]	Q569X3	Q62241	-4.5	5.2E-05	-6.3	2.3E-03	0.2	7.7E-01	1.3	4.3E-01
ENSMUST00000071024	Rho GTPase activating protein 25 [Source:MGI Symbol;Acc:MGI:2443687]		Q8BYW1	-4.0	1.3E-02	-1.6	5.0E-02	0.7	1.7E-01	-0.5	4.7E-01
ENSMUST00000069600	N-myc downstream regulated gene 3 [Source:MGI Symbol;Acc:MGI:1352499]	Q8VCV2		4.2	1.6E-01	1.5	5.8E-01	-4.2	1.8E-01	-1.4	5.0E-01
ENSMUST00000069604	5,10-methylenetetrahydrofolate reductase [Source:MGI Symbol;Acc:MGI:106639]	A2A7F7		0.4	4.7E-01	1.4	1.1E-01	1.0	1.5E-01	0.0	9.8E-01
ENSMUST00000071044	capping protein (actin filament), gelsolin-like [Source:MGI Symbol;Acc:MGI:1098259]	Q99LB4		-7.4	5.2E-06	5.9	5.2E-04	-0.4	7.0E-01	0.5	4.8E-01
ENSMUST00000071057	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 [Source:MGI Symbol;Acc:MGI:1915098]		Q6ZPL9	-4.8	1.5E-04	3.3	1.6E-03	-3.8	2.7E-03	-1.0	1.5E-01
ENSMUST00000071065	nuclear factor, interleukin 3, regulated [Source:MGI Symbol;Acc:MGI:109495]		O08750	-6.0	1.4E-04	-9.3	6.6E-05	0.2	6.2E-01	1.3	3.6E-01
ENSMUST00000069620	period circadian clock 2 [Source:MGI Symbol;Acc:MGI:1195265]			-0.3	5.8E-01	-0.3	6.7E-01	0.2	6.1E-01	0.2	7.0E-01
ENSMUST00000071067	RIKEN cDNA C330011M18 gene [Source:MGI Symbol;Acc:MGI:3045248]	Q8C7V4		2.3	4.6E-03	4.7	1.4E-03	-4.3	5.4E-03	-0.2	7.5E-01
ENSMUST00000071068	COMM domain containing 1 [Source:MGI Symbol;Acc:MGI:109474]	G8JL54		-4.4	9.7E-04	4.6	4.0E-02	-0.7	7.5E-01	1.2	3.5E-01
ENSMUST00000069648	K(lysine) acetyltransferase 6B [Source:MGI Symbol;Acc:MGI:1858746]		Q8BRB7	0.4	8.8E-01	4.3	2.4E-01	3.0	3.7E-01	-1.0	6.9E-01
ENSMUST00000071069	tripartite motif-containing 30D [Source:MGI Symbol;Acc:MGI:3035181]	Q3TNW3		3.2	9.4E-03	6.4	2.3E-04	-0.5	6.6E-01	-0.8	2.3E-01
ENSMUST00000071087	centrosome and spindle pole associated protein 1 [Source:MGI Symbol;Acc:MGI:2681832]		B2RX88	-5.8	8.6E-04	7.0	2.1E-05	0.5	5.6E-01	-0.2	7.4E-01
ENSMUST00000069652	RAB3 GTPase activating protein subunit 2 [Source:MGI Symbol;Acc:MGI:1916043]	E9QKE4		-2.9	8.7E-02	-1.1	5.7E-01	0.6	6.6E-01	-1.3	5.2E-01
ENSMUST00000069660	RIKEN cDNA D430042O09 gene [Source:MGI Symbol;Acc:MGI:2442760]		Q8C753	0.2	8.2E-01	-3.3	4.8E-02	0.6	5.2E-01	4.0	1.6E-02
ENSMUST00000069673				0.7	2.1E-01	0.8	3.1E-01	0.3	5.4E-01	0.3	7.1E-01
ENSMUST00000071095	SET domain containing 3 [Source:MGI Symbol;Acc:MGI:1289184]		Q91WC0	-3.6	8.7E-05	3.2	7.3E-04	-0.5	3.9E-01	-0.3	6.0E-01
ENSMUST00000069690	metastasis associated 1 [Source:MGI Symbol;Acc:MGI:2150037]	F8WHY8		-1.5	3.2E-01	-1.9	4.3E-01	1.7	2.5E-01	2.2	3.5E-01
ENSMUST00000071103	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [Source:MGI Symbol;Acc:MGI:2144727]		Q91VR5	-1.9	9.3E-03	4.9	3.8E-06	0.0	9.8E-01	0.1	8.7E-01
ENSMUST00000071104	keratin 72 [Source:MGI Symbol;Acc:MGI:2146034]		Q6IME9	7.6	8.6E-05	3.0	3.9E-02	-1.2	3.3E-01	0.8	3.9E-01
ENSMUST00000071106	G patch domain containing 2 like [Source:MGI Symbol;Acc:MGI:1917623]		Q6PE65	-2.4	2.0E-04	3.6	2.2E-03	-0.9	2.8E-01	0.6	3.1E-01
ENSMUST00000071118	predicted gene 6169 [Source:MGI Symbol;Acc:MGI:3646298]	Q0VEW4	Q9R1Q7	6.5	1.1E-02	-6.5	6.9E-04	-0.8	1.2E-01	-0.7	6.5E-01
ENSMUST00000069718	fat mass and obesity associated [Source:MGI Symbol;Acc:MGI:1347093]		Q8BGW1	-1.0	1.0E-01	0.3	6.8E-01	0.4	4.1E-01	-0.8	2.3E-01
ENSMUST00000071130	arachidonate 5-lipoxygenase activating protein [Source:MGI Symbol;Acc:MGI:107505]		P30355	-8.3	4.8E-08	2.4	1.6E-01	8.2	6.8E-05	0.5	6.8E-01
ENSMUST00000071134	tubulin, beta 3 class III [Source:MGI Symbol;Acc:MGI:107813]		Q9ERD7	7.2	1.2E-05	5.3	6.9E-02	-2.8	3.3E-01	0.1	9.8E-01
ENSMUST00000071135	tubulin, beta 4A class IVA [Source:MGI Symbol;Acc:MGI:107848]		Q9D6F9	5.5	1.7E-05	-1.2	2.2E-02	0.2	5.2E-01	-0.1	8.0E-01
ENSMUST00000071152	ring finger and FYVE like domain containing protein [Source:MGI Symbol;Acc:MGI:1914588]	Q3UCG9		-5.6	8.1E-04	5.6	2.3E-03	-0.7	6.6E-01	0.2	8.3E-01
ENSMUST00000071182	RIKEN cDNA E330014E10 gene [Source:MGI Symbol;Acc:MGI:3615333]	Q3UL33		7.7	2.4E-05	6.5	2.1E-04	-0.5	6.7E-01	-0.7	2.9E-01
ENSMUST00000071215	coiled-coil-helix-coiled-coil-helix domain containing 1 [Source:MGI Symbol;Acc:MGI:1913371]		Q9CQA6	-3.1	2.6E-04	6.5	1.5E-03	-0.7	6.5E-01	0.9	2.9E-01
ENSMUST00000071219	trehalase (brush-border membrane glycoprotein) [Source:MGI Symbol;Acc:MGI:1926230]	E9PYP7		7.3	3.9E-03	5.6	1.7E-03	-0.1	9.4E-01	-0.7	3.4E-01
ENSMUST00000069782	RIKEN cDNA 9030617O03 gene [Source:MGI Symbol;Acc:MGI:2444813]		Q8BH86	1.5	5.2E-01	6.9	5.2E-02	2.5	4.2E-01	-2.9	1.5E-01
ENSMUST00000071221	olfactory receptor 1512 [Source:MGI Symbol;Acc:MGI:3031346]	Q8VF72		6.6	1.4E-04	5.7	4.2E-03	-0.5	7.8E-01	-2.5	3.2E-02
ENSMUST00000071230	eukaryotic translation initiation factor 2, subunit 1 alpha [Source:MGI Symbol;Acc:MGI:95299]		Q6ZWX6	-2.8	1.5E-03	6.8	3.6E-04	-0.7	6.3E-01	0.3	6.3E-01
ENSMUST00000071248	agrin [Source:MGI Symbol;Acc:MGI:87961]	Z4YJS5		5.8	1.1E-03	-3.8	2.1E-01	1.5	3.8E-01	1.3	6.4E-01
ENSMUST00000069794	Rap1 interacting factor 1 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1098622]		Q6PR54	0.9	1.8E-01	2.1	2.7E-02	0.7	3.1E-01	-0.5	4.8E-01
ENSMUST00000071250	liver glycogen phosphorylase [Source:MGI Symbol;Acc:MGI:97829]		Q9ET01	-8.3	1.1E-07	6.0	2.7E-05	-4.4	1.8E-03	0.0	9.2E-01
ENSMUST00000071254	per-hexamer repeat gene 4 [Source:MGI Symbol;Acc:MGI:104522]	Q3KNH0	P15974	6.5	1.9E-05	5.4	5.5E-04	-2.6	4.9E-02	0.2	7.4E-01
ENSMUST00000069805	ATPase, class I, type 8B, member 2 [Source:MGI Symbol;Acc:MGI:1859660]		P98199	2.2	4.0E-01	8.3	1.4E-02	2.7	3.4E-01	-3.4	1.5E-01
ENSMUST00000069808	nuclear respiratory factor 1 [Source:MGI Symbol;Acc:MGI:1332235]	Q99K73		-4.1	1.3E-01	-4.2	1.9E-01	-1.1	4.8E-01	-1.0	7.6E-01
ENSMUST00000071263	DnaJ (Hsp40) homolog, subfamily C, member 30 [Source:MGI Symbol;Acc:MGI:1913364]		P59041	-1.3	3.1E-02	1.7	3.5E-02	0.8	2.0E-01	0.3	5.8E-01
ENSMUST00000071267	polycomb group ring finger 5 [Source:MGI Symbol;Acc:MGI:1923505]		Q3UK78	-5.7	9.4E-04	8.1	8.4E-03	2.8	2.6E-01	0.0	1.0E+00
ENSMUST00000071268	TAO kinase 2 [Source:MGI Symbol;Acc:MGI:1915919]		Q6ZQ29	-2.1	2.3E-03	3.5	4.7E-04	-5.1	3.5E-04	-0.3	5.1E-01
ENSMUST00000071281	forkhead box B1 [Source:MGI Symbol;Acc:MGI:1927549]		Q64732	10.1	5.5E-05	6.4	3.7E-04	-0.6	6.4E-01	-0.8	2.7E-01
ENSMUST00000071308	cDNA sequence AF366264 [Source:MGI Symbol;Acc:MGI:2667157]	G3X9P9		9.0	2.1E-05	5.4	6.8E-03	-1.2	4.9E-01	-0.8	4.6E-01
ENSMUST00000071329	branched chain ketoacid dehydrogenase E1, alpha polypeptide [Source:MGI Symbol;Acc:MGI:107701]	Q3U3J1		-3.5	4.2E-04	4.7	7.3E-05	-0.4	5.9E-01	-0.2	6.1E-01
ENSMUST00000071370	protocadherin 17 [Source:MGI Symbol;Acc:MGI:2684924]	E9PXF0		8.1	1.6E-05	-4.7	8.0E-02	1.1	2.8E-01	1.5	5.4E-01
ENSMUST00000071378	interferon alpha B [Source:MGI Symbol;Acc:MGI:1097683]	L7MTU6		6.6	1.5E-03	-1.0	5.4E-01	2.9	2.1E-02	-0.3	8.4E-01
ENSMUST00000071399	pregnancy specific glycoprotein 16 [Source:MGI Symbol;Acc:MGI:1347249]	Q8K0U8		4.1	5.1E-06	-3.4	1.2E-01	1.3	1.9E-01	1.9	3.5E-01
ENSMUST00000071402	ELOVL family member 6, elongation of long chain fatty acids (yeast) [Source:MGI Symbol;Acc:MGI:2156528		Q920L5	4.2	4.1E-04	6.4	9.7E-05	-0.5	6.3E-01	0.8	1.5E-01
ENSMUST00000069922	melanoma inhibitory activity 3 [Source:MGI Symbol;Acc:MGI:2443183]	J3KMG3		-2.4	4.9E-02	-2.7	6.4E-02	0.3	7.5E-01	0.6	6.6E-01
ENSMUST00000071404	chemokine (C-C motif) receptor 1-like 1 [Source:MGI Symbol;Acc:MGI:104617]		P51676	6.0	5.1E-04	7.2	1.7E-04	0.3	7.9E-01	1.0	1.5E-01
ENSMUST00000071410	olfactory receptor 516 [Source:MGI Symbol;Acc:MGI:3030350]	Q8VFZ5		5.8	1.1E-03	-9.1	3.8E-06	1.3	2.6E-02	-0.6	5.3E-01
ENSMUST00000071419	maestro heat-like repeat family member 5 [Source:MGI Symbol;Acc:MGI:2685474]	Q3TY91		6.4	2.7E-04	-1.7	3.9E-01	0.9	4.7E-01	-1.2	5.5E-01
ENSMUST00000071423	NHL repeat containing 2 [Source:MGI Symbol;Acc:MGI:1914116]	B2RR26	Q8BZW8	-1.3	2.9E-02	4.1	1.9E-03	-0.1	8.7E-01	0.5	4.7E-01
ENSMUST00000069937	cyclin-dependent kinase-like 2 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1858227]		Q9QUK0	0.0	1.0E+00	3.7	2.1E-01	5.0	6.2E-02	1.3	4.7E-01
ENSMUST00000071457	calcium and integrin binding 1 (calmyrin) [Source:MGI Symbol;Acc:MGI:1344418]	Q8C2K4		-6.2	4.7E-04	8.8	3.2E-04	0.0	9.8E-01	0.8	2.4E-01
ENSMUST00000071465	zinc finger with KRAB and SCAN domains 6 [Source:MGI Symbol;Acc:MGI:1289293]		Q810A1	-3.9	1.3E-02	-6.3	9.0E-05	-0.4	3.1E-01	-2.3	8.1E-02
ENSMUST00000071487	La ribonucleoprotein domain family, member 1 [Source:MGI Symbol;Acc:MGI:1890165]	Z4YJT3		10.1	3.7E-05	-1.1	8.4E-02	0.7	9.1E-02	-0.4	5.2E-01
ENSMUST00000071521	olfactory receptor 1415 [Source:MGI Symbol;Acc:MGI:3031249]	Q7TQS4		6.3	1.5E-03	-10.2	1.3E-06	-0.5	3.3E-01	-1.4	1.4E-01
ENSMUST00000069965	cyclin-dependent kinase 17 [Source:MGI Symbol;Acc:MGI:97517]		Q8K0D0	-1.1	1.4E-01	-1.0	3.3E-01	0.8	2.5E-01	0.7	4.9E-01
ENSMUST00000071522	predicted gene 10032 [Source:MGI Symbol;Acc:MGI:3642901]	Q8BS28		7.0	6.1E-07	-2.3	3.5E-01	3.4	3.1E-02	-0.6	7.9E-01
ENSMUST00000071533	dachshund 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1277991]		Q9QYB2	-2.3	3.9E-03	5.8	1.4E-03	-0.6	6.5E-01	-0.4	6.0E-01
ENSMUST00000071535	maltase-glucoamylase [Source:MGI Symbol;Acc:MGI:1203495]	B5THE2		-3.3	4.3E-04	-1.7	6.9E-02	0.4	4.5E-01	0.2	7.7E-01
ENSMUST00000071543	uridine phosphorylase 2 [Source:MGI Symbol;Acc:MGI:1923904]	A2APN2		5.3	1.1E-03	8.0	4.4E-04	0.9	5.4E-01	-0.2	8.4E-01
ENSMUST00000071544	small nuclear RNA activating complex, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1916338]	Q9CQB0		4.6	1.2E-02	-0.8	5.5E-01	1.0	2.2E-01	4.1	6.0E-03
ENSMUST00000071555	actin, gamma, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:87906]	Q4KL81	P63260	-10.2	1.8E-04	6.3	6.6E-04	-0.3	8.3E-01	0.8	3.2E-01
ENSMUST00000071564	F-box protein 18 [Source:MGI Symbol;Acc:MGI:1354699]		Q8K2I9	-6.4	1.9E-05	-1.0	3.4E-01	0.3	6.4E-01	-3.0	3.6E-02
ENSMUST00000071565	predicted gene 4978 [Source:MGI Symbol;Acc:MGI:3645765]	F6VBB8		7.1	6.7E-05	7.1	4.8E-04	-0.6	6.7E-01	-1.3	1.1E-01
ENSMUST00000070080	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 [Source:MGI Symbol;Acc:MGI:1928380]	Q3UUA9	Q9WVK5	-0.4	5.0E-01	0.7	3.8E-01	1.4	4.0E-02	0.3	6.6E-01
ENSMUST00000070084	toll-like receptor adaptor molecule 2 [Source:MGI Symbol;Acc:MGI:3040056]		Q8BJQ4	0.2	8.1E-01	1.4	1.1E-01	0.5	4.2E-01	-0.7	3.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000071580	predicted gene 10436 [Source:MGI Symbol;Acc:MGI:3704393]	L7N1Y3		5.8	1.7E-03	5.7	4.5E-04	-0.9	4.4E-01	-1.2	9.0E-02
ENSMUST00000071588	NK6 homeobox 3 [Source:MGI Symbol;Acc:MGI:1921811]	B2RU70	Q3UHX8	7.6	3.7E-05	-3.7	4.4E-04	0.4	3.0E-01	-0.9	2.3E-01
ENSMUST00000071646	retinol dehydrogenase 16 [Source:MGI Symbol;Acc:MGI:1201375]	O54909		6.5	3.6E-03	3.5	7.8E-03	0.8	4.0E-01	0.3	7.0E-01
ENSMUST00000071648	vascular endothelial growth factor A [Source:MGI Symbol;Acc:MGI:103178]	F8WH10		-6.2	2.4E-03	-2.0	8.6E-03	-0.3	4.2E-01	-0.2	7.6E-01
ENSMUST00000070118	ermal growth factor-containing fibulin-like extracellular matrix protein 2 [Source:MGI Symbol;Acc:MGI:1891	G5E8D6		-1.7	1.6E-01	6.5	2.5E-03	4.9	8.1E-03	-3.3	1.3E-02
ENSMUST00000071650	iduronidase, alpha-L- [Source:MGI Symbol;Acc:MGI:96418]	Q8BMG0		7.1	2.7E-02	6.7	3.4E-04	1.5	2.2E-01	-2.7	3.4E-03
ENSMUST00000071652	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like [Source:MGI Symbol;Acc:MGI:1915871		D3YZG8	2.0	3.2E-02	7.8	1.7E-05	-1.5	1.9E-01	-0.3	5.2E-01
ENSMUST00000071664	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 [Source:MGI Symbol;Acc:MGI:1201670]	Q3ULG4	O35226	-8.3	3.4E-06	6.4	1.9E-04	-1.3	2.6E-01	0.1	9.3E-01
ENSMUST00000071677	Williams Beuren syndrome chromosome region 22 [Source:MGI Symbol;Acc:MGI:1913388]	Q9DCT4		-5.3	5.9E-04	-6.0	4.8E-03	1.3	4.1E-02	-0.7	7.2E-01
ENSMUST00000071691	trace amine-associated receptor 7F [Source:MGI Symbol;Acc:MGI:3527447]		Q5QD08	6.5	2.3E-04	6.8	6.9E-04	-0.4	7.6E-01	-1.0	2.0E-01
ENSMUST00000071703	zinc finger, CCHC domain containing 6 [Source:MGI Symbol;Acc:MGI:2387179]	E9PUA2		-4.7	9.4E-05	-7.4	7.2E-03	-0.3	7.0E-01	1.8	4.1E-01
ENSMUST00000071704	proteasome (prosome, macropain) subunit, alpha type 3 [Source:MGI Symbol;Acc:MGI:104883]	F8WH02		-7.7	7.9E-06	5.6	4.7E-05	0.1	9.1E-01	0.4	4.3E-01
ENSMUST00000071708	Fras1 related extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:2670972]		Q684R7	3.1	1.4E-02	-2.4	3.5E-02	0.5	3.7E-01	-1.2	2.8E-01
ENSMUST00000071711	zinc finger protein 36, C3H type-like 3 [Source:MGI Symbol;Acc:MGI:3525151]		Q5ISE2	7.0	6.8E-05	-0.3	7.2E-01	1.0	5.1E-02	-0.8	2.8E-01
ENSMUST00000070166	GRAM domain containing 3 [Source:MGI Symbol;Acc:MGI:1914815]	Q9D2W5		0.1	9.2E-01	-0.5	4.1E-01	-1.3	2.5E-02	-0.7	3.2E-01
ENSMUST00000070172	sorting nexin 32 [Source:MGI Symbol;Acc:MGI:2444704]		Q80ZJ7	-0.4	5.3E-01	1.1	2.1E-01	0.7	3.0E-01	-0.8	3.0E-01
ENSMUST00000071732	predicted gene 6793 [Source:MGI Symbol;Acc:MGI:3643578]	B2RXM2		4.0	7.2E-04	3.3	4.6E-03	0.3	7.3E-01	-0.4	5.7E-01
ENSMUST00000071739	glycogen synthase kinase 3 alpha [Source:MGI Symbol;Acc:MGI:2152453]		Q2NL51	-8.9	1.8E-04	4.8	5.8E-02	-1.2	5.9E-01	-0.3	8.6E-01
ENSMUST00000071750	collagen, type XII, alpha 1 [Source:MGI Symbol;Acc:MGI:88448]		Q60847	7.9	9.2E-04	-0.7	3.9E-01	0.9	1.2E-01	0.0	9.5E-01
ENSMUST00000071782	neuronal pentraxin 2 [Source:MGI Symbol;Acc:MGI:1858209]		O70340	7.7	8.0E-05	5.8	4.1E-03	-1.4	4.0E-01	-0.9	3.6E-01
ENSMUST00000070191	CCAAT/enhancer binding protein (C/EBP), gamma [Source:MGI Symbol;Acc:MGI:104982]	Q54AJ1	P53568	-0.6	5.0E-01	-4.1	2.8E-02	-0.7	3.3E-01	2.8	1.0E-01
ENSMUST00000070193	male germ cell-associated kinase [Source:MGI Symbol;Acc:MGI:96913]		Q04859	0.5	8.2E-01	5.1	1.1E-01	1.3	6.3E-01	-3.2	1.8E-01
ENSMUST00000071804	expressed sequence AI987944 [Source:MGI Symbol;Acc:MGI:2142079]	Q7TPX5		-5.1	2.7E-04	-1.9	7.6E-02	1.3	4.6E-02	-0.4	6.9E-01
ENSMUST00000071805	small proline-rich protein 2A2 [Source:MGI Symbol;Acc:MGI:3845026]		Q4KL71	6.2	5.3E-03	-3.0	6.5E-03	-0.3	5.4E-01	0.0	1.0E+00
ENSMUST00000070203	SH3 domain and tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGI:2678949]	G3X9F6		0.0	1.0E+00	-1.4	4.1E-01	0.4	6.9E-01	1.8	2.7E-01
ENSMUST00000071825	predicted gene 5434 [Source:MGI Symbol;Acc:MGI:3646221]		Q3UWQ3	6.4	3.0E-04	-4.8	1.5E-04	-0.5	2.4E-01	0.0	9.9E-01
ENSMUST00000071826	crumbs family member 3 [Source:MGI Symbol;Acc:MGI:2670904]		Q8QZT4	4.1	3.1E-02	-5.1	1.8E-03	-0.4	4.6E-01	2.5	6.1E-02
ENSMUST00000071841	kelch domain containing 3 [Source:MGI Symbol;Acc:MGI:2651568]			-4.1	2.2E-04	7.1	3.8E-04	-0.7	6.3E-01	0.3	6.6E-01
ENSMUST00000071857	signal-induced proliferation associated gene 1 [Source:MGI Symbol;Acc:MGI:107576]	E9Q0Y4		-4.4	8.3E-03	5.0	9.6E-05	-0.6	3.9E-01	0.1	8.2E-01
ENSMUST00000070223	KH domain containing 1C [Source:MGI Symbol;Acc:MGI:3583007]		Q4KL78	2.9	1.5E-01	5.4	2.2E-02	-0.5	8.1E-01	-3.0	5.8E-02
ENSMUST00000071858	hippocalcin-like 1 [Source:MGI Symbol;Acc:MGI:1855689]		P62748	-3.2	3.7E-04	7.5	2.6E-03	1.8	3.4E-01	-0.5	5.9E-01
ENSMUST00000071874	anoctamin 6 [Source:MGI Symbol;Acc:MGI:2145890]		Q6P9J9	-1.4	6.1E-03	7.8	5.4E-07	-0.5	4.8E-01	-0.1	6.8E-01
ENSMUST00000071885	reproductive homeobox 8 [Source:MGI Symbol;Acc:MGI:3579898]	Q6VSS7		5.7	6.6E-04	-1.2	3.6E-01	0.8	3.3E-01	-0.9	5.1E-01
ENSMUST00000071889	carbonic anyhydrase 12 [Source:MGI Symbol;Acc:MGI:1923709]			7.3	3.9E-05	5.1	9.4E-04	-1.2	3.0E-01	-1.4	6.0E-02
ENSMUST00000071902	adrenergic receptor, alpha 2b [Source:MGI Symbol;Acc:MGI:87935]	F8VQ23		9.0	6.3E-04	-4.5	1.2E-02	1.5	3.6E-02	0.5	7.5E-01
ENSMUST00000070313	PR domain containing 16 [Source:MGI Symbol;Acc:MGI:1917923]		A2A935	2.6	4.2E-01	4.2	2.2E-01	-0.8	8.1E-01	-2.5	3.0E-01
ENSMUST00000071917	F-box and WD-40 domain protein 26 [Source:MGI Symbol;Acc:MGI:3646662]	Q8BI58		6.5	1.2E-03	8.9	3.8E-05	-0.6	6.3E-01	0.0	9.2E-01
ENSMUST00000071926	nucleolar protein 7 [Source:MGI Symbol;Acc:MGI:1917328]	A1L3B6	Q9D7Z3	-5.1	1.2E-04	5.0	3.9E-02	-1.5	5.3E-01	-0.8	5.5E-01
ENSMUST00000071935	myosin IXb [Source:MGI Symbol;Acc:MGI:106624]	E9QKV6		-9.4	1.8E-03	-2.6	1.6E-01	1.6	1.5E-01	-0.9	6.1E-01
ENSMUST00000071937	potassium inwardly-rectifying channel, subfamily J, member 14 [Source:MGI Symbol;Acc:MGI:2384820]		Q8JZN3	5.7	7.3E-05	3.9	8.1E-04	0.9	2.2E-01	-0.5	4.1E-01
ENSMUST00000071943	olfactory receptor 222 [Source:MGI Symbol;Acc:MGI:3030056]	Q7TS30		6.8	2.9E-04	5.4	5.8E-02	-0.6	8.1E-01	-0.3	8.3E-01
ENSMUST00000070334	glucose 6 phosphatase, catalytic, 3 [Source:MGI Symbol;Acc:MGI:1915651]		Q6NSQ9	-2.1	7.7E-02	-3.1	1.3E-01	0.6	5.1E-01	1.6	3.9E-01
ENSMUST00000071949	biogenesis of lysosomal organelles complex-1, subunit 4, cappuccino [Source:MGI Symbol;Acc:MGI:1929230]		Q8VED2	-3.0	4.1E-04	4.5	1.1E-03	0.1	8.8E-01	0.1	9.2E-01
ENSMUST00000071968	transient receptor potential cation channel, subfamily V, member 4 [Source:MGI Symbol;Acc:MGI:1926945]		Q9EPK8	6.0	1.4E-03	6.2	8.0E-03	-0.5	8.0E-01	-1.7	1.5E-01
ENSMUST00000071979	olfactory receptor 1329 [Source:MGI Symbol;Acc:MGI:3031163]	L7MTV4		6.8	9.4E-05	-2.2	4.7E-03	0.7	8.6E-02	-0.3	5.7E-01
ENSMUST00000071982	BMP-binding endothelial regulator [Source:MGI Symbol;Acc:MGI:1920480]		Q8CJ69	7.9	1.0E-05	5.0	1.9E-02	-0.6	7.6E-01	0.1	9.1E-01
ENSMUST00000070368	seven in absentia 2 [Source:MGI Symbol;Acc:MGI:108062]	Q3UEV2	Q06986	0.1	8.5E-01	0.9	2.6E-01	0.7	2.2E-01	0.0	9.7E-01
ENSMUST00000071985	solute carrier organic anion transporter family, member 4C1 [Source:MGI Symbol;Acc:MGI:2442784]		Q8BGD4	-3.3	1.4E-05	3.9	1.4E-03	0.0	9.9E-01	-0.3	6.5E-01
ENSMUST00000070395	alanyl-tRNA synthetase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916934]		Q3THG9	-0.7	2.9E-01	0.1	8.6E-01	0.1	8.9E-01	-0.8	3.2E-01
ENSMUST00000071991	developmental pluripotency associated 5A [Source:MGI Symbol;Acc:MGI:101800]		Q9CQS7	6.8	5.2E-05	4.5	1.3E-02	-2.2	2.0E-01	-1.1	3.1E-01
ENSMUST00000070420	START domain containing 9 [Source:MGI Symbol;Acc:MGI:3045258]	A2AKI0		-2.3	1.6E-01	-0.6	8.0E-01	1.9	2.6E-01	0.2	9.4E-01
ENSMUST00000072008	SH3 domain containing ring finger 2 [Source:MGI Symbol;Acc:MGI:2444628]		Q8BZT2	8.1	1.3E-05	6.4	1.5E-04	-0.6	6.0E-01	-0.1	8.1E-01
ENSMUST00000072014	predicted gene 10330 [Source:MGI Symbol;Acc:MGI:3642221]	Q8BKS1		6.9	9.6E-06	8.0	2.1E-04	0.1	9.2E-01	0.3	6.3E-01
ENSMUST00000072018	Alstrom syndrome 1 [Source:MGI Symbol;Acc:MGI:1934606]		Q8K4E0	3.9	6.7E-05	-1.6	1.4E-01	0.1	9.2E-01	-2.9	3.9E-02
ENSMUST00000072030	olfactory receptor 322 [Source:MGI Symbol;Acc:MGI:3030156]	Q5NCC8		7.7	7.1E-05	-2.5	1.3E-02	-4.8	3.4E-05	0.3	6.7E-01
ENSMUST00000072040	vaccinia related kinase 1 [Source:MGI Symbol;Acc:MGI:1261847]		Q80X41	-7.0	8.3E-05	-2.0	6.6E-02	0.8	1.7E-01	0.5	6.1E-01
ENSMUST00000070508	leucine rich repeat containing 29 [Source:MGI Symbol;Acc:MGI:2443262]	F6SF53		0.1	8.6E-01	0.6	3.7E-01	0.5	3.4E-01	0.0	9.4E-01
ENSMUST00000072061	ectonucleoside triphosphate diphosphohydrolase 5 [Source:MGI Symbol;Acc:MGI:1321385]	Q3TQC7		4.1	2.0E-03	3.7	7.9E-04	-2.2	2.5E-02	0.2	7.5E-01
ENSMUST00000070518	natural killer cell group 7 sequence [Source:MGI Symbol;Acc:MGI:1931250]	Q9CY55		-0.5	5.1E-01	-0.2	8.6E-01	0.7	3.0E-01	0.4	6.4E-01
ENSMUST00000070522	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2 [Source:MGI Symbol;Acc:MGI:1347007]		Q9R0B9	4.6	4.4E-02	6.4	3.1E-02	0.7	7.8E-01	-1.1	4.6E-01
ENSMUST00000072079	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1929721]		Q9CYH6	2.3	1.2E-03	-4.0	1.7E-04	0.1	6.9E-01	0.5	4.4E-01
ENSMUST00000072093	plexin B1 [Source:MGI Symbol;Acc:MGI:2154238]		Q8CJH3	9.6	1.5E-06	0.9	3.2E-01	-4.7	1.8E-03	-0.3	7.0E-01
ENSMUST00000072100	DNA binding protein with his-thr domain [Source:MGI Symbol;Acc:MGI:2679513]	Q8IWX3		9.7	7.3E-05	6.8	1.1E-04	-0.5	6.5E-01	0.0	9.5E-01
ENSMUST00000072111	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 [Source:MGI Symbo		Q9JM95	-5.8	5.9E-04	-4.5	1.0E-02	1.0	2.1E-01	2.0	2.0E-01
ENSMUST00000072141	programmed cell death 11 [Source:MGI Symbol;Acc:MGI:1341788]		Q6NS46	2.5	1.0E-04	3.2	2.6E-03	0.9	2.1E-01	0.1	8.5E-01
ENSMUST00000072154	phosphatidylinositol glycan anchor biosynthesis, class H [Source:MGI Symbol;Acc:MGI:99463]		Q5M9N4	1.9	1.2E-02	6.6	6.2E-05	-1.5	1.8E-01	-0.3	5.6E-01
ENSMUST00000070597	retinol saturase (all trans retinol 13,14 reductase) [Source:MGI Symbol;Acc:MGI:1914692]		Q64FW2	1.8	5.0E-02	2.3	5.0E-02	0.5	5.6E-01	0.0	1.0E+00
ENSMUST00000070607	HAUS augmin-like complex, subunit 6 [Source:MGI Symbol;Acc:MGI:1923389]	Q6NV99		0.4	5.3E-01	1.4	1.0E-01	0.8	2.3E-01	-0.3	7.1E-01
ENSMUST00000072155	predicted gene 166 [Source:MGI Symbol;Acc:MGI:2685012]		Q6NZQ0	-1.5	5.4E-03	6.6	4.2E-05	0.4	6.3E-01	-0.3	6.0E-01
ENSMUST00000072156	T cell lymphoma invasion and metastasis 2 [Source:MGI Symbol;Acc:MGI:1344338]		Q6ZPF3	-5.8	3.2E-03	4.6	7.0E-05	-4.3	1.1E-03	0.3	5.9E-01
ENSMUST00000072177	NUAK family, SNF1-like kinase, 2 [Source:MGI Symbol;Acc:MGI:1921387]		Q8BZN4	-3.4	2.2E-02	-3.6	4.4E-02	-1.0	3.1E-01	-0.7	6.8E-01
ENSMUST00000072182	single-minded homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:98307]		Q61079	7.1	6.8E-06	-6.2	3.6E-04	1.4	2.1E-02	-0.5	6.8E-01
ENSMUST00000072186	spermatid perinuclear RNA binding protein [Source:MGI Symbol;Acc:MGI:104626]		Q91WM1	-5.9	3.9E-05	-6.9	6.5E-07	0.2	3.7E-01	-0.1	8.3E-01
ENSMUST00000072217	gamma-glutamyltransferase 5 [Source:MGI Symbol;Acc:MGI:1346063]		Q9Z2A9	-3.7	1.3E-04	-5.1	1.3E-03	0.7	2.1E-01	0.8	4.9E-01
ENSMUST00000072222	zinc finger protein 329 [Source:MGI Symbol;Acc:MGI:1921283]	B2RSV9	Q6GQR8	3.6	5.8E-05	-5.9	1.4E-03	1.4	3.5E-02	-2.3	1.7E-01
ENSMUST00000072228	glucokinase regulatory protein [Source:MGI Symbol;Acc:MGI:1096345]		Q91X44	7.2	2.0E-04	6.3	3.8E-03	0.2	9.2E-01	-0.2	8.4E-01
ENSMUST00000072232	tropomodulin 3 [Source:MGI Symbol;Acc:MGI:1355315]		Q9JHJ0	-4.0	2.6E-05	-2.0	2.0E-02	0.9	5.7E-02	-0.5	5.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000072239	thymopoietin [Source:MGI Symbol;Acc:MGI:106920]		Q61029	-6.4	4.0E-05	-3.6	1.2E-03	0.6	1.3E-01	-0.5	5.4E-01
ENSMUST00000072271	ethanolamine phosphate phospholyase [Source:MGI Symbol;Acc:MGI:1919010]		Q8BWU8	5.6	2.9E-03	-4.4	2.0E-05	1.0	3.0E-03	-0.3	6.3E-01
ENSMUST00000072286	predicted gene 5862 [Source:MGI Symbol;Acc:MGI:3645135]	K7N5V5		6.5	3.1E-04	1.2	1.2E-01	0.4	5.1E-01	0.6	3.2E-01
ENSMUST00000072289	flotillin 2 [Source:MGI Symbol;Acc:MGI:103309]		Q60634	-8.4	1.3E-04	-3.1	2.2E-03	0.7	1.2E-01	0.4	5.7E-01
ENSMUST00000070699	phosphatidylinositol glycan anchor biosynthesis, class N [Source:MGI Symbol;Acc:MGI:1351629]	G3X9F1		4.1	1.3E-01	3.0	3.6E-01	-0.9	7.6E-01	0.3	9.2E-01
ENSMUST00000072298	N-myc downstream regulated gene 3 [Source:MGI Symbol;Acc:MGI:1352499]	Q544I1	Q9QYF9	-3.4	2.4E-02	-2.5	1.7E-02	0.7	1.8E-01	-0.6	5.0E-01
ENSMUST00000070713	integrator complex subunit 10 [Source:MGI Symbol;Acc:MGI:1918135]			6.3	6.7E-02	-0.9	8.1E-01	-4.8	1.7E-01	2.5	4.5E-01
ENSMUST00000072299	visinin-like 1 [Source:MGI Symbol;Acc:MGI:1349453]	Q4W4C9	P62761	7.8	8.3E-05	5.2	2.6E-04	-1.9	8.6E-02	-0.1	8.4E-01
ENSMUST00000070726	solute carrier family 39 (metal ion transporter), member 6 [Source:MGI Symbol;Acc:MGI:2147279]		Q8C145	-0.4	4.8E-01	0.4	6.4E-01	0.4	4.5E-01	-0.4	6.2E-01
ENSMUST00000072306	predicted gene 11938 [Source:MGI Symbol;Acc:MGI:3651233]	Q9D3H4		7.8	3.7E-05	-4.1	6.4E-03	0.5	3.4E-01	-0.4	7.4E-01
ENSMUST00000072312	ubiquitin specific peptidase 13 (isopeptidase T-3) [Source:MGI Symbol;Acc:MGI:1919857]		Q5BKP2	8.5	9.0E-06	5.9	6.7E-03	-0.3	8.6E-01	-0.6	5.5E-01
ENSMUST00000072329	dystrobrevin binding protein 1 [Source:MGI Symbol;Acc:MGI:2137586]		Q91WZ8	-7.0	1.2E-05	3.7	5.2E-03	0.9	3.3E-01	0.1	8.6E-01
ENSMUST00000072334	DnaJ (Hsp40) homolog, subfamily C, member 5 [Source:MGI Symbol;Acc:MGI:892995]		P60904	-2.5	5.0E-03	6.4	2.8E-04	-0.6	6.1E-01	0.5	4.7E-01
ENSMUST00000072357	hexokinase 1 [Source:MGI Symbol;Acc:MGI:96103]		P17710	-8.0	3.7E-04	3.1	6.7E-03	0.0	1.0E+00	-0.9	2.3E-01
ENSMUST00000072359	tropomyosin 3, related sequence 7 [Source:MGI Symbol;Acc:MGI:99705]	D3Z2H9		-7.2	6.7E-07	5.8	1.2E-04	-2.2	5.0E-02	0.7	2.4E-01
ENSMUST00000072362	dynamin 2 [Source:MGI Symbol;Acc:MGI:109547]	G3X9G4		-7.1	1.4E-03	5.4	1.5E-03	0.5	6.8E-01	-0.2	7.6E-01
ENSMUST00000072363	keratinocyte expressed, proline-rich [Source:MGI Symbol;Acc:MGI:1920981]		B2RUR4	7.9	1.4E-05	6.6	2.3E-02	-0.7	8.0E-01	-1.5	3.4E-01
ENSMUST00000072376	ring finger protein 14 [Source:MGI Symbol;Acc:MGI:1929668]		Q9JI90	-8.5	1.5E-04	-3.3	5.8E-02	1.2	1.5E-01	1.2	4.5E-01
ENSMUST00000070801	asparagine-linked glycosylation 13 [Source:MGI Symbol;Acc:MGI:1914824]		Q9D8C3	-1.0	2.9E-01	0.4	6.9E-01	-0.6	4.3E-01	-2.0	5.7E-02
ENSMUST00000072383	WAS protein family homolog 1 [Source:MGI Symbol;Acc:MGI:1916017]		Q8VDD8	-3.8	8.0E-03	5.6	2.8E-03	-0.3	8.4E-01	-0.3	6.5E-01
ENSMUST00000072415	MHC I like leukocyte 2 [Source:MGI Symbol;Acc:MGI:2179989]	Q8HWE6		6.5	2.2E-04	6.4	2.1E-03	-0.5	7.4E-01	-1.1	2.3E-01
ENSMUST00000072437	predicted gene 10113 [Source:MGI Symbol;Acc:MGI:3642714]	Q8CE57		7.5	2.8E-05	7.1	5.2E-04	-0.7	6.6E-01	-0.7	3.9E-01
ENSMUST00000072452	'S1 Golgi-localized integral membrane protein homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191371		Q78S06	-7.5	7.0E-05	7.7	8.0E-05	-0.6	6.6E-01	-0.8	2.0E-01
ENSMUST00000072453	luteinizing hormone beta [Source:MGI Symbol;Acc:MGI:96782]	G3X9G6		6.3	4.0E-04	4.2	2.1E-04	-3.5	3.1E-03	-0.1	8.9E-01
ENSMUST00000072465	zinc finger protein 809 [Source:MGI Symbol;Acc:MGI:2143362]		G3X9G7	-2.1	1.0E-02	3.0	4.0E-03	-0.4	5.5E-01	0.2	8.1E-01
ENSMUST00000072476	2'-5' oligoadenylate synthetase 1H [Source:MGI Symbol;Acc:MGI:2180853]	Q8VI97		5.6	2.0E-04	-9.5	2.6E-05	-0.2	7.3E-01	0.1	9.2E-01
ENSMUST00000070850	protein phosphatase 1, regulatory (inhibitor) subunit 14B [Source:MGI Symbol;Acc:MGI:107682]		Q62084	-0.8	2.5E-01	-1.6	6.5E-02	-1.5	2.0E-02	-0.7	4.2E-01
ENSMUST00000072482	membrane-associated ring finger (C3HC4) 1 [Source:MGI Symbol;Acc:MGI:1920175]		Q6NZQ8	-7.9	2.1E-04	4.6	1.3E-02	-4.0	7.7E-02	0.8	4.1E-01
ENSMUST00000070872	olute carrier family 16 (monocarboxylic acid transporters), member 6 [Source:MGI Symbol;Acc:MGI:2144585		B1AT66	-1.2	5.1E-02	-2.4	1.0E-02	-0.2	7.2E-01	1.0	2.0E-01
ENSMUST00000072503	ribosomal protein L18 [Source:MGI Symbol;Acc:MGI:98003]	Q58EW0	P35980	-9.2	8.0E-05	4.8	2.0E-03	-1.8	1.8E-01	0.8	3.0E-01
ENSMUST00000070877	alpha-methylacyl-CoA racemase [Source:MGI Symbol;Acc:MGI:1098273]		O09174	0.5	4.5E-01	1.6	6.5E-02	0.6	3.5E-01	-0.5	4.5E-01
ENSMUST00000072513	olfactory receptor 68 [Source:MGI Symbol;Acc:MGI:1341790]	E9PYY2		5.6	5.0E-04	-3.9	3.5E-03	-0.1	8.0E-01	-0.8	4.8E-01
ENSMUST00000072514	myogenic differentiation 1 [Source:MGI Symbol;Acc:MGI:97275]		P10085	7.0	1.1E-04	3.9	9.6E-02	-0.7	7.3E-01	0.3	8.3E-01
ENSMUST00000072519	engulfment and cell motility 1 [Source:MGI Symbol;Acc:MGI:2153044]		Q8BPU7	-3.1	2.5E-04	-0.1	8.9E-01	1.2	2.3E-02	-0.6	4.1E-01
ENSMUST00000070890	carbohydrate (chondroitin 4) sulfotransferase 13 [Source:MGI Symbol;Acc:MGI:1919047]	D3Z6E3		-0.8	2.2E-01	-0.1	8.8E-01	1.1	1.0E-01	0.4	6.3E-01
ENSMUST00000072530	DDB1 and CUL4 associated factor 11 [Source:MGI Symbol;Acc:MGI:90168]		Q91VU6	-8.5	1.6E-05	8.5	9.9E-04	-0.9	6.5E-01	1.1	2.2E-01
ENSMUST00000072566	NME/NM23 nucleoside diphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:97356]	Q5NC82	Q01768	-2.9	2.5E-03	1.8	2.1E-01	-2.8	7.1E-02	0.9	4.3E-01
ENSMUST00000070923	thioesterase superfamily member 6 [Source:MGI Symbol;Acc:MGI:1925301]		Q80ZW2	0.9	2.6E-01	1.8	7.2E-02	-0.1	9.3E-01	-1.0	2.4E-01
ENSMUST00000070949	PRELI domain containing 2 [Source:MGI Symbol;Acc:MGI:1924869]		Q0VBB0	-0.5	3.7E-01	-0.7	2.8E-01	-0.8	1.2E-01	-0.6	3.3E-01
ENSMUST00000070953	pantothenate kinase 4 [Source:MGI Symbol;Acc:MGI:2387466]		Q80YV4	-0.1	9.7E-01	2.0	3.8E-01	0.6	7.9E-01	-1.5	4.4E-01
ENSMUST00000070968	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	Q8C3V4		1.3	5.3E-01	3.1	1.6E-01	-1.5	4.3E-01	-3.3	1.1E-01
ENSMUST00000072576	signal recognition particle 19 [Source:MGI Symbol;Acc:MGI:1913634]	Q9D104		-6.6	8.5E-05	7.2	1.8E-04	0.8	4.9E-01	-0.2	7.1E-01
ENSMUST00000070990	ELMO/CED-12 domain containing 3 [Source:MGI Symbol;Acc:MGI:2445168]		Q91YP6	-0.4	8.4E-01	-1.9	4.9E-01	-0.1	9.4E-01	1.4	6.0E-01
ENSMUST00000070996	eukaryotic translation initiation factor 5A [Source:MGI Symbol;Acc:MGI:106248]		P63242	-2.8	3.6E-02	-4.3	4.0E-02	-0.1	9.4E-01	1.5	4.4E-01
ENSMUST00000072578	ubiquitin-conjugating enzyme E2D 2B [Source:MGI Symbol;Acc:MGI:1920568]		Q6ZWY6	6.5	6.4E-05	-2.7	7.8E-03	1.2	2.2E-02	-0.6	4.9E-01
ENSMUST00000072587	mitochondrial ribosomal protein S21 [Source:MGI Symbol;Acc:MGI:1913542]	Q059G7	P58059	-4.8	2.2E-02	-4.4	8.1E-02	0.8	4.4E-01	1.1	6.2E-01
ENSMUST00000071026	eukaryotic translation initiation factor 5A [Source:MGI Symbol;Acc:MGI:106248]		P63242	0.5	8.1E-01	1.9	4.2E-01	1.6	4.7E-01	0.1	9.6E-01
ENSMUST00000072600	gap junction protein, alpha 5 [Source:MGI Symbol;Acc:MGI:95716]		Q01231	3.4	2.3E-03	-6.2	3.7E-04	1.2	2.1E-02	0.0	9.7E-01
ENSMUST00000071056	branched chain ketoacid dehydrogenase kinase [Source:MGI Symbol;Acc:MGI:1276121]	Q3UCB5	O55028	-0.2	7.3E-01	0.8	2.7E-01	1.0	6.1E-02	0.1	8.7E-01
ENSMUST00000072602	hydrogen voltage-gated channel 1 [Source:MGI Symbol;Acc:MGI:1921346]		Q3U2S8	-4.9	1.7E-03	1.4	3.3E-02	0.7	1.7E-01	-5.5	5.7E-05
ENSMUST00000072612	RIKEN cDNA 4921528I07 gene [Source:MGI Symbol;Acc:MGI:1924299]	Q9D5S6		9.2	6.8E-06	-3.6	9.4E-03	1.2	7.0E-02	-1.2	3.4E-01
ENSMUST00000072631	NK2 homeobox 9 [Source:MGI Symbol;Acc:MGI:1270158]		O70584	10.9	1.0E-04	2.8	4.1E-03	0.6	3.3E-01	0.1	8.6E-01
ENSMUST00000072634	amyloid beta (A4) precursor-like protein 2 [Source:MGI Symbol;Acc:MGI:88047]	Q60709		-3.1	7.3E-05	-5.3	3.7E-03	-0.6	3.4E-01	0.4	8.0E-01
ENSMUST00000072646	exocyst complex component 3-like 4 [Source:MGI Symbol;Acc:MGI:1921363]			3.7	2.4E-04	2.2	3.6E-02	-2.4	2.9E-02	-1.4	1.0E-01
ENSMUST00000071076	glutamate receptor, metabotropic 7 [Source:MGI Symbol;Acc:MGI:1351344]	G5E8D5		5.5	3.8E-02	6.3	2.6E-02	-0.7	8.0E-01	-1.5	3.4E-01
ENSMUST00000072662	zinc finger and SCAN domain containing 5B [Source:MGI Symbol;Acc:MGI:2159640]	B2RTN3		7.2	2.6E-06	-4.5	1.7E-03	0.9	6.3E-02	-0.7	5.3E-01
ENSMUST00000072666	zinc finger protein 474 [Source:MGI Symbol;Acc:MGI:1914008]		Q6V5K9	7.3	2.3E-04	-5.6	1.6E-02	0.7	3.3E-01	0.6	7.7E-01
ENSMUST00000071093	regulating synaptic membrane exocytosis 3 [Source:MGI Symbol;Acc:MGI:2443331]	Q14BY7	Q80U57	2.3	4.9E-01	5.5	1.7E-01	2.0	5.8E-01	-1.1	7.1E-01
ENSMUST00000072685	sortilin-related VPS10 domain containing receptor 1 [Source:MGI Symbol;Acc:MGI:1929666]	E9QQ02		6.3	2.0E-04	-3.1	1.5E-03	0.9	3.3E-02	0.5	5.1E-01
ENSMUST00000071096	hemogen [Source:MGI Symbol;Acc:MGI:2136910]		Q9ERZ0	1.6	3.6E-01	2.9	2.0E-01	0.7	7.1E-01	-0.6	7.4E-01
ENSMUST00000072692	plectin [Source:MGI Symbol;Acc:MGI:1277961]		Q9QXS1	-3.7	1.7E-02	7.2	1.2E-04	-0.5	6.9E-01	0.3	5.8E-01
ENSMUST00000072695	transducin-like enhancer of split 1, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104636]	Q5SQA2		-4.5	3.1E-03	-2.7	3.3E-03	-1.3	1.4E-02	-0.4	5.3E-01
ENSMUST00000072697	acyl-Coenzyme A dehydrogenase, medium chain [Source:MGI Symbol;Acc:MGI:87867]		P45952	-2.8	4.3E-04	6.5	5.6E-04	-0.6	6.7E-01	0.6	4.2E-01
ENSMUST00000072713	zinc finger protein 108 [Source:MGI Symbol;Acc:MGI:1891198]	E9Q8I5		7.0	2.4E-05	-1.3	2.6E-02	0.7	4.8E-02	-0.4	4.5E-01
ENSMUST00000071108	zinc finger protein 362 [Source:MGI Symbol;Acc:MGI:2652839]	B1ASA5		-3.2	6.3E-02	-2.7	9.7E-02	0.1	9.1E-01	-0.4	8.1E-01
ENSMUST00000072727	nucleosome assembly protein 1-like 4 [Source:MGI Symbol;Acc:MGI:1316687]	A2RSB1	Q78ZA7	-3.4	1.1E-04	4.3	6.7E-03	0.3	7.9E-01	-0.6	4.7E-01
ENSMUST00000072729	membrane-spanning 4-domains, subfamily A, member 4C [Source:MGI Symbol;Acc:MGI:1927656]	Q9D3F6		-3.7	3.9E-03	5.7	2.6E-02	-2.2	3.5E-01	-1.4	3.5E-01
ENSMUST00000072735	family with sequence similarity 173, member A [Source:MGI Symbol;Acc:MGI:2384888]		Q501J2	-2.9	1.7E-03	-7.8	6.4E-07	0.2	3.9E-01	-0.3	6.1E-01
ENSMUST00000072740	active BCR-related gene [Source:MGI Symbol;Acc:MGI:107771]		Q5SSL4	7.6	3.6E-05	8.0	6.2E-05	0.4	7.2E-01	-0.3	5.5E-01
ENSMUST00000072744	B interacting protein, apical-basolateral polarity regulator, spe-39 homolog [Source:MGI Symbol;Acc:MGI:21		Q8BGQ1	-9.5	4.8E-06	4.0	2.9E-04	-1.8	2.9E-02	-0.3	5.7E-01
ENSMUST00000072748	membrane-spanning 4-domains, subfamily A, member 10 [Source:MGI Symbol;Acc:MGI:1917076]	B2RWS0	Q99N03	5.7	3.3E-04	-5.1	2.2E-03	0.9	1.6E-01	0.4	8.0E-01
ENSMUST00000071169	regulator of chromosome condensation 2 [Source:MGI Symbol;Acc:MGI:1919784]		Q8BK67	3.3	2.5E-01	1.9	6.1E-01	-1.7	6.0E-01	-0.3	9.1E-01
ENSMUST00000072750	heterogeneous nuclear ribonucleoprotein D [Source:MGI Symbol;Acc:MGI:101947]	G5E8G0		-4.3	2.5E-03	7.9	3.8E-05	-0.5	6.7E-01	-0.7	2.0E-01
ENSMUST00000072751	deoxyhypusine hydroxylase/monooxygenase [Source:MGI Symbol;Acc:MGI:1915964]		Q99LN9	-2.3	1.3E-02	5.8	8.8E-04	-0.6	6.5E-01	-0.3	6.9E-01
ENSMUST00000071201	netrin G2 [Source:MGI Symbol;Acc:MGI:2159341]	A2AKX2		-0.6	4.7E-01	0.0	9.7E-01	1.0	2.1E-01	0.5	6.4E-01
ENSMUST00000071213	polymerase (RNA) II (DNA directed) polypeptide A [Source:MGI Symbol;Acc:MGI:98086]			2.8	2.8E-01	1.7	6.4E-01	1.3	6.5E-01	2.4	4.1E-01
ENSMUST00000072753	single-stranded DNA binding protein 3 [Source:MGI Symbol;Acc:MGI:1919725]		Q9D032	-3.5	5.9E-03	-3.0	1.2E-03	-0.8	4.9E-02	-1.0	1.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000072755	collagen, type XVIII, alpha 1 [Source:MGI Symbol;Acc:MGI:88451]	E9QPX1		8.3	2.9E-04	5.1	4.1E-02	-0.6	7.9E-01	1.6	2.3E-01
ENSMUST00000072767	Rho guanine nucleotide exchange factor (GEF) 12 [Source:MGI Symbol;Acc:MGI:1916882]		Q8R4H2	3.3	3.1E-04	6.3	3.8E-04	-0.6	6.2E-01	-0.3	6.6E-01
ENSMUST00000072776	cytochrome P450, family 2, subfamily d, polypeptide 10 [Source:MGI Symbol;Acc:MGI:88602]		P24456	5.9	2.3E-03	-3.3	1.7E-03	-1.1	3.0E-02	-0.5	5.1E-01
ENSMUST00000071233	zinc finger protein 516 [Source:MGI Symbol;Acc:MGI:2443957]		Q7TSH3	-0.9	4.7E-01	-4.3	2.2E-01	3.0	1.1E-01	6.5	5.5E-02
ENSMUST00000072857	Sec1 family domain containing 2 [Source:MGI Symbol;Acc:MGI:2443446]		Q8BTY8	3.0	2.7E-03	1.8	2.9E-01	-2.0	2.5E-01	0.2	9.1E-01
ENSMUST00000072863	pre B cell leukemia homeobox 1 [Source:MGI Symbol;Acc:MGI:97495]	Q71VB4	P41778	-4.1	4.3E-03	1.6	3.2E-01	-1.4	3.2E-01	2.8	4.7E-02
ENSMUST00000072868	K+ voltage-gated channel, subfamily S, 2 [Source:MGI Symbol;Acc:MGI:1197011]		O35174	7.6	3.8E-05	-7.7	1.9E-06	0.5	9.6E-02	-0.1	8.5E-01
ENSMUST00000072875	serine/arginine-rich splicing factor 11 [Source:MGI Symbol;Acc:MGI:1916457]	Q3UIX4		-4.8	1.5E-04	6.3	5.3E-05	-1.1	2.6E-01	-0.8	1.4E-01
ENSMUST00000072876	serine (or cysteine) peptidase inhibitor, clade A, member 1A [Source:MGI Symbol;Acc:MGI:891971]	A0A0A0MQA3		5.6	2.6E-03	-0.1	9.4E-01	1.2	3.4E-02	-0.1	9.1E-01
ENSMUST00000072886	secretin receptor [Source:MGI Symbol;Acc:MGI:2441720]	H7BX37		6.8	2.0E-04	0.9	5.4E-01	4.4	3.5E-03	-2.1	1.3E-01
ENSMUST00000072899	cingulin-like 1 [Source:MGI Symbol;Acc:MGI:1915428]	B2RSU6		5.6	9.4E-03	-1.1	9.6E-02	0.6	1.7E-01	-0.4	5.7E-01
ENSMUST00000071280	peroxisomal biogenesis factor 2 [Source:MGI Symbol;Acc:MGI:107486]	Q91YZ5		0.3	9.1E-01	0.6	8.6E-01	0.7	7.8E-01	0.4	9.0E-01
ENSMUST00000072910	chondroadherin-like [Source:MGI Symbol;Acc:MGI:3036284]		E9Q7T7	6.4	8.6E-04	7.9	6.6E-04	-0.7	6.8E-01	1.4	8.7E-02
ENSMUST00000071282				-0.9	3.5E-01	-0.4	7.2E-01	-0.9	3.3E-01	-1.4	2.1E-01
ENSMUST00000071296	RIKEN cDNA 2410002F23 gene [Source:MGI Symbol;Acc:MGI:1914226]	Q3TE80		2.6	4.6E-02	3.3	2.6E-02	-0.5	6.4E-01	-1.2	2.6E-01
ENSMUST00000072915	forkhead box B2 [Source:MGI Symbol;Acc:MGI:1347468]	B9EII5	Q64733	6.6	1.3E-04	8.4	1.1E-04	0.0	9.9E-01	0.6	3.3E-01
ENSMUST00000071325	neurofibromatosis 1 [Source:MGI Symbol;Acc:MGI:97306]		Q04690	-0.4	4.8E-01	0.4	6.4E-01	0.6	3.4E-01	-0.2	7.5E-01
ENSMUST00000072916	zinc finger SWIM-type containing 7 [Source:MGI Symbol;Acc:MGI:1916997]		Q9CWQ2	-2.7	3.8E-03	-2.5	1.5E-02	0.9	9.2E-02	-0.2	8.3E-01
ENSMUST00000072933	transmembrane protein 40 [Source:MGI Symbol;Acc:MGI:2137870]		Q4FJU9	-9.8	2.4E-06	8.7	1.3E-04	1.0	4.6E-01	0.4	5.2E-01
ENSMUST00000072939	e carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 [Source:MGI Symbol;Acc:MGI:1270		O55192	6.6	3.9E-06	5.0	1.5E-02	-0.7	6.9E-01	0.9	4.1E-01
ENSMUST00000072943	prolactin family 7, subfamily c, member 1 [Source:MGI Symbol;Acc:MGI:1914755]		Q9CRB5	6.0	3.2E-04	3.7	2.4E-05	-0.6	1.6E-01	-0.3	3.8E-01
ENSMUST00000072955	family with sequence similarity 171, member A1 [Source:MGI Symbol;Acc:MGI:2442917]	A2ATL1		7.9	5.4E-04	3.3	5.6E-03	-0.6	4.9E-01	0.3	6.3E-01
ENSMUST00000072961	vacuolar protein sorting 41 (yeast) [Source:MGI Symbol;Acc:MGI:1929215]		Q5KU39	-2.9	1.4E-03	5.7	9.4E-04	-0.4	7.3E-01	-0.1	8.7E-01
ENSMUST00000072965	sirtuin 2 [Source:MGI Symbol;Acc:MGI:1927664]		Q8VDQ8	-8.0	4.4E-06	6.1	1.4E-03	-0.5	7.4E-01	-0.8	3.4E-01
ENSMUST00000072971	ase, aminophospholipid transporter (APLT), class I, type 8A, member 1 [Source:MGI Symbol;Acc:MGI:1330			-2.7	2.5E-02	6.9	3.1E-04	-0.5	7.3E-01	-0.9	2.1E-01
ENSMUST00000073001	lectin, galactose binding, soluble 9 [Source:MGI Symbol;Acc:MGI:109496]	B1AQR8		-6.0	1.3E-04	-0.4	5.4E-01	0.6	2.2E-01	-0.3	6.1E-01
ENSMUST00000071430	RIKEN cDNA 2310039H08 gene [Source:MGI Symbol;Acc:MGI:1914351]		Q9D727	-0.1	8.7E-01	0.3	7.5E-01	-0.6	4.0E-01	-0.9	2.6E-01
ENSMUST00000071452	polymerase (DNA directed), theta [Source:MGI Symbol;Acc:MGI:2155399]		Q8CGS6	-0.3	8.8E-01	2.4	1.9E-01	0.2	9.2E-01	-2.5	1.7E-01
ENSMUST00000071455	protein-tyrosine sulfotransferase 2 [Source:MGI Symbol;Acc:MGI:1309516]	Q3TQN1		-3.8	3.8E-02	-2.8	2.6E-01	1.9	2.0E-01	0.9	6.8E-01
ENSMUST00000073029	Fanconi anemia, complementation group C [Source:MGI Symbol;Acc:MGI:95480]	Q8CBR3		3.8	2.0E-04	-3.5	2.7E-02	1.4	6.3E-02	-1.3	3.9E-01
ENSMUST00000073043	chemokine (C-X-C motif) ligand 12 [Source:MGI Symbol;Acc:MGI:103556]	H7BX38		9.4	4.4E-06	6.1	1.6E-04	-0.5	6.3E-01	-0.7	2.8E-01
ENSMUST00000073049	UDP glucuronosyltransferase 1 family, polypeptide A1 [Source:MGI Symbol;Acc:MGI:98898]		Q63886	3.2	5.2E-03	-5.4	1.9E-02	0.4	6.8E-01	1.9	3.6E-01
ENSMUST00000073054	metallophosphoesterase 1 [Source:MGI Symbol;Acc:MGI:2661311]		Q80XL7	-3.0	1.4E-04	9.7	9.7E-05	-0.8	6.1E-01	-0.5	4.7E-01
ENSMUST00000071488	integrator complex subunit 3 [Source:MGI Symbol;Acc:MGI:2140050]		Q7TPD0	-0.1	9.7E-01	1.0	8.1E-01	-0.7	8.6E-01	-1.8	6.2E-01
ENSMUST00000071492	family with sequence similarity 136, member A [Source:MGI Symbol;Acc:MGI:1913738]		Q9CR98	0.9	6.4E-02	-0.5	3.7E-01	-1.2	1.8E-02	0.2	6.3E-01
ENSMUST00000071510	src family associated phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:1925723]		Q3UUV5	-2.6	1.4E-01	-1.7	4.9E-01	1.1	5.1E-01	0.2	9.4E-01
ENSMUST00000073062	zinc finger protein 663 [Source:MGI Symbol;Acc:MGI:2685854]	Q6NXM6		9.7	5.9E-05	5.6	5.6E-03	-0.6	7.3E-01	0.2	8.4E-01
ENSMUST00000073080	predicted gene 10053 [Source:MGI Symbol;Acc:MGI:3704493]	Q56A15	P62897	-7.0	5.6E-05	6.1	3.4E-06	-1.2	7.3E-02	-0.4	3.1E-01
ENSMUST00000073081	RIKEN cDNA 1700010B08 gene [Source:MGI Symbol;Acc:MGI:1922735]	Q9DAI7		6.1	1.0E-04	-10.6	6.6E-04	-0.8	1.8E-01	0.4	8.7E-01
ENSMUST00000073089	family with sequence similarity 73, member A [Source:MGI Symbol;Acc:MGI:1924567]	B2RRB9	Q4QQM5	2.4	1.8E-03	-4.2	8.1E-03	1.8	6.1E-03	3.7	1.3E-02
ENSMUST00000073094	SH3-domain kinase binding protein 1 [Source:MGI Symbol;Acc:MGI:1889583]		Q8R550	-5.7	3.2E-04	-1.9	3.5E-02	1.2	3.2E-02	-0.1	8.6E-01
ENSMUST00000071537	neighbor of Brca1 gene 1 [Source:MGI Symbol;Acc:MGI:108498]	K3W4P1		0.4	8.4E-01	1.5	6.0E-01	0.8	6.4E-01	-0.2	9.3E-01
ENSMUST00000071539	solute carrier family 39 (metal ion transporter), member 11 [Source:MGI Symbol;Acc:MGI:1917056]		Q8BWY7	-4.1	3.8E-02	-3.0	1.8E-01	0.9	4.9E-01	-0.2	9.4E-01
ENSMUST00000073104	protein phosphatase 4, regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1917601]	E9QPR5		-5.6	3.4E-02	6.4	5.1E-04	-0.5	7.3E-01	-1.6	4.8E-02
ENSMUST00000073115	histone cluster 2, H2ab [Source:MGI Symbol;Acc:MGI:2448314]		Q64522	5.5	5.7E-04	0.4	8.1E-01	-3.2	4.5E-02	1.0	4.6E-01
ENSMUST00000073116	ear factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100 [Source:MGI Symbol;Acc:MGI:109	Q3UG25	Q9WTK5	-3.3	6.0E-04	-5.9	3.0E-03	1.2	1.0E-01	-3.1	1.4E-01
ENSMUST00000071561	sigma non-opioid intracellular receptor 1 [Source:MGI Symbol;Acc:MGI:1195268]	A2AMS0	O55242	-0.9	6.6E-01	4.0	1.5E-01	2.7	2.8E-01	-2.2	2.9E-01
ENSMUST00000071562	candidate tumor suppressor in ovarian cancer 2 [Source:MGI Symbol;Acc:MGI:2179725]		Q9D7E3	-1.1	8.6E-02	1.1	1.9E-01	1.7	1.6E-02	-0.4	5.4E-01
ENSMUST00000071563	calcium release activated channel regulator 2A [Source:MGI Symbol;Acc:MGI:2685919]		Q3UP38	1.1	9.3E-02	1.1	1.9E-01	0.7	2.4E-01	0.7	3.0E-01
ENSMUST00000073120	protoporphyrinogen oxidase [Source:MGI Symbol;Acc:MGI:104968]		P51175	-5.4	2.1E-04	-4.2	7.3E-04	0.3	4.2E-01	-1.8	8.2E-02
ENSMUST00000073124	zinc finger protein 746 [Source:MGI Symbol;Acc:MGI:1916478]		Q3U133	-1.6	6.5E-03	5.6	6.3E-04	-0.6	6.1E-01	0.8	2.4E-01
ENSMUST00000073128	SH3 binding domain protein 5 like [Source:MGI Symbol;Acc:MGI:1933124]		Q99LH9	-8.2	6.0E-05	1.8	3.1E-01	-0.6	7.1E-01	1.4	3.2E-01
ENSMUST00000073139	N-myc downstream regulated gene 4 [Source:MGI Symbol;Acc:MGI:2384590]		Q8BTG7	8.1	1.7E-05	6.2	1.9E-03	-0.4	7.8E-01	-0.9	3.1E-01
ENSMUST00000071585	opioid receptor-like 1 [Source:MGI Symbol;Acc:MGI:97440]	Q542U1	P35377	3.3	1.2E-01	6.4	1.3E-02	-0.3	8.9E-01	-3.4	2.8E-02
ENSMUST00000073149	solute carrier family 9 (sodium/hydrogen exchanger), member 5 [Source:MGI Symbol;Acc:MGI:2685542]	B2RXE2		6.0	2.8E-06	7.2	1.1E-04	-0.6	6.3E-01	-0.2	7.3E-01
ENSMUST00000071590	retinoblastoma binding protein 6 [Source:MGI Symbol;Acc:MGI:894835]		P97868	-2.2	2.1E-01	-4.1	1.8E-01	-0.2	8.6E-01	1.7	5.8E-01
ENSMUST00000071592	protein arginine N-methyltransferase 7 [Source:MGI Symbol;Acc:MGI:2384879]		Q922X9	0.7	2.4E-01	0.5	5.2E-01	-0.4	4.6E-01	-0.2	8.0E-01
ENSMUST00000073150	pellino 2 [Source:MGI Symbol;Acc:MGI:1891445]	E9QPQ6		-2.1	5.5E-04	-6.3	6.6E-04	-1.3	4.7E-02	-2.1	1.6E-01
ENSMUST00000071642	midasin homolog (yeast) [Source:MGI Symbol;Acc:MGI:1926159]	A2ANY6		-2.4	1.6E-01	1.9	2.5E-01	0.3	8.3E-01	-4.0	3.4E-02
ENSMUST00000073151	NLR family, pyrin domain containing 9B [Source:MGI Symbol;Acc:MGI:2675377]		Q66X22	5.8	1.8E-03	4.3	5.6E-02	-0.1	9.5E-01	2.0	1.4E-01
ENSMUST00000073152	FAST kinase domains 1 [Source:MGI Symbol;Acc:MGI:2444596]		Q6DI86	1.8	1.0E-02	0.0	9.9E-01	1.7	9.2E-02	-4.4	2.1E-02
ENSMUST00000073157	zinc finger protein 65 [Source:MGI Symbol;Acc:MGI:107769]	Q91W94		6.2	1.1E-05	8.0	2.2E-02	-0.7	8.5E-01	-1.5	3.7E-01
ENSMUST00000073179	RIKEN cDNA 4933415F23 gene [Source:MGI Symbol;Acc:MGI:1914005]	Q14BX6		6.5	1.3E-04	1.5	1.3E-01	-1.2	1.6E-01	-0.7	4.1E-01
ENSMUST00000073192	endoplasmic reticulum lectin 1 [Source:MGI Symbol;Acc:MGI:1914003]		Q8VEH8	-3.9	1.0E-03	-7.2	7.7E-05	0.4	2.5E-01	-0.8	5.1E-01
ENSMUST00000073201	zinc finger protein 958 [Source:MGI Symbol;Acc:MGI:2385298]	F6R9A8		-2.6	1.8E-03	-3.7	1.8E-02	1.0	1.4E-01	-0.6	6.9E-01
ENSMUST00000073211	myomesin 1 [Source:MGI Symbol;Acc:MGI:1341430]		Q62234	8.6	1.1E-04	5.9	8.0E-04	-0.6	6.4E-01	0.0	9.9E-01
ENSMUST00000071698	ER lipid raft associated 1 [Source:MGI Symbol;Acc:MGI:2387613]			-1.1	6.7E-01	-4.9	2.4E-01	-2.5	2.2E-01	1.3	7.6E-01
ENSMUST00000071699	engulfment and cell motility 2 [Source:MGI Symbol;Acc:MGI:2153045]		Q8BHL5	3.7	1.3E-01	7.5	1.1E-02	-0.4	8.7E-01	-4.2	1.7E-02
ENSMUST00000073238	predicted gene 10076 [Source:MGI Symbol;Acc:MGI:3704451]		P62947	-2.6	1.7E-03	-3.3	2.8E-03	0.4	4.2E-01	-1.1	2.5E-01
ENSMUST00000073251	coiled-coil domain containing 177 [Source:MGI Symbol;Acc:MGI:2686414]		Q3UHB8	9.1	6.6E-06	-6.4	2.1E-04	0.4	3.6E-01	-1.0	4.1E-01
ENSMUST00000073252	cholinergic receptor, nicotinic, delta polypeptide [Source:MGI Symbol;Acc:MGI:87893]	Q80VZ5	P02716	4.2	1.8E-02	6.9	4.5E-05	-1.5	1.8E-01	-5.3	6.8E-05
ENSMUST00000073308	Ewing sarcoma breakpoint region 1 [Source:MGI Symbol;Acc:MGI:99960]	Q5SUT0		-6.1	1.7E-03	6.8	2.0E-04	-0.2	8.7E-01	0.0	9.8E-01
ENSMUST00000071718	peroxiredoxin 6 [Source:MGI Symbol;Acc:MGI:894320]	Q6GT24		-1.5	1.1E-01	-2.0	1.4E-01	0.6	4.5E-01	1.0	4.1E-01
ENSMUST00000073339	progesterone receptor membrane component 1 [Source:MGI Symbol;Acc:MGI:1858305]	Q3TXU8	O55022	-3.5	4.3E-04	4.7	1.1E-03	1.2	1.9E-01	0.5	5.1E-01
ENSMUST00000073350	cathepsin E [Source:MGI Symbol;Acc:MGI:107361]		P70269	-6.5	7.8E-07	-3.8	1.4E-02	1.2	9.7E-02	-3.9	3.9E-02
ENSMUST00000073371	calcineurin-like phosphoesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:2443300]		Q8BFS6	4.1	9.8E-04	2.4	2.7E-02	0.6	4.8E-01	0.3	6.8E-01
ENSMUST00000073388	arylformamidase [Source:MGI Symbol;Acc:MGI:2448704]		Q8K4H1	-3.7	8.0E-03	7.3	3.5E-03	0.0	9.8E-01	0.5	5.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000073391	cytochrome P450, family 26, subfamily c, polypeptide 1 [Source:MGI Symbol;Acc:MGI:2679699]	B2RXA7		4.7	5.9E-05	7.6	2.2E-04	-0.2	8.8E-01	-0.2	7.9E-01
ENSMUST00000071792	RIKEN cDNA 1110038F14 gene [Source:MGI Symbol;Acc:MGI:2152337]		Q3U6N9	-0.8	2.8E-01	0.3	7.4E-01	0.7	3.0E-01	-0.4	6.6E-01
ENSMUST00000073394	ubiquitin specific peptidase 17-like D [Source:MGI Symbol;Acc:MGI:3051372]	G5E8G2		8.1	1.2E-03	-2.6	1.8E-02	0.4	4.7E-01	-2.1	6.9E-02
ENSMUST00000073410	predicted gene 6871 [Source:MGI Symbol;Acc:MGI:3643456]	L7N1Z0		3.1	3.2E-02	5.0	3.1E-02	-0.1	9.7E-01	1.1	4.2E-01
ENSMUST00000071812	IQ motif containing GTPase activating protein 3 [Source:MGI Symbol;Acc:MGI:3028642]	F8VQ29		-1.7	2.9E-01	-0.7	7.4E-01	1.8	2.3E-01	0.8	7.0E-01
ENSMUST00000073415	vomeronasal 1 receptor 48 [Source:MGI Symbol;Acc:MGI:2148508]		Q9EQ52	4.0	1.2E-02	5.6	1.3E-03	-0.5	7.1E-01	0.3	7.0E-01
ENSMUST00000073428	solute carrier family 39 (zinc transporter), member 4 [Source:MGI Symbol;Acc:MGI:1919277]		Q78IQ7	1.6	2.1E-02	4.4	1.9E-02	-2.3	2.1E-01	-2.6	4.3E-02
ENSMUST00000071829	phosphatidylserine decarboxylase [Source:MGI Symbol;Acc:MGI:2445114]	D3YY63		-2.9	8.2E-02	-1.5	4.3E-01	0.6	5.9E-01	-0.8	6.8E-01
ENSMUST00000073430	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]		Q8K1E0	-7.7	9.5E-06	-7.1	1.4E-03	0.8	1.2E-01	3.8	3.7E-02
ENSMUST00000073447	protocadherin gamma subfamily A, 3 [Source:MGI Symbol;Acc:MGI:1935215]	Q91XY5		7.8	2.0E-05	2.8	1.8E-02	0.6	4.8E-01	0.1	8.9E-01
ENSMUST00000073456	NSA2 ribosome biogenesis homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913883]		Q9CR47	-3.6	1.3E-04	4.9	2.9E-03	-1.9	1.8E-01	0.6	4.4E-01
ENSMUST00000071852	COMM domain containing 7 [Source:MGI Symbol;Acc:MGI:1914197]	Q56A13	Q8BG94	0.3	5.3E-01	1.6	2.3E-02	0.8	1.1E-01	-0.5	3.7E-01
ENSMUST00000073459	synaptotagmin IX [Source:MGI Symbol;Acc:MGI:1926373]		Q9R0N9	7.2	1.9E-03	-2.3	1.3E-01	0.7	4.2E-01	-1.5	3.7E-01
ENSMUST00000073471	ribosomal protein L26 [Source:MGI Symbol;Acc:MGI:106022]	Q4FZH2	P61255	-5.8	2.2E-06	-1.9	3.0E-02	1.2	3.0E-02	-0.1	8.7E-01
ENSMUST00000073490	lactase [Source:MGI Symbol;Acc:MGI:104576]	F8VPT3		5.4	1.2E-05	-0.9	1.2E-01	0.3	3.9E-01	-0.3	6.1E-01
ENSMUST00000071876	cysteine rich, DPF motif domain containing 1 [Source:MGI Symbol;Acc:MGI:1919605]		Q8R3A2	0.3	7.4E-01	0.0	9.7E-01	-0.9	3.4E-01	-0.6	6.0E-01
ENSMUST00000071880	myosin XV [Source:MGI Symbol;Acc:MGI:1261811]		Q9QZZ4	7.8	4.8E-02	8.5	4.2E-02	-0.8	8.5E-01	-1.5	5.0E-01
ENSMUST00000073521	nudix (nucleoside diphosphate linked moiety X)-type motif 7 [Source:MGI Symbol;Acc:MGI:1914778]		Q99P30	1.8	3.2E-02	6.1	2.9E-03	0.9	5.8E-01	0.4	6.0E-01
ENSMUST00000073528	zygote arrest 1 [Source:MGI Symbol;Acc:MGI:2180337]		Q80SU3	5.8	2.1E-04	7.1	9.2E-05	-0.6	6.0E-01	-0.4	4.6E-01
ENSMUST00000071898	cleavage and polyadenylation specific factor 1 [Source:MGI Symbol;Acc:MGI:2679722]		Q9EPU4	-0.6	2.3E-01	0.2	7.3E-01	0.8	1.4E-01	-0.1	8.9E-01
ENSMUST00000073543	olfactory receptor 1375 [Source:MGI Symbol;Acc:MGI:3031209]			6.1	9.2E-05	6.1	1.8E-02	-1.3	5.6E-01	1.7	2.4E-01
ENSMUST00000073546	histocompatibility 2, M region locus 10.3 [Source:MGI Symbol;Acc:MGI:1276524]	Q85ZW6		7.3	3.0E-05	5.8	4.6E-03	-0.1	9.4E-01	0.5	5.7E-01
ENSMUST00000071921	cyclin D binding myb-like transcription factor 1 [Source:MGI Symbol;Acc:MGI:1344415]		Q8CE22	-5.1	1.1E-01	-6.2	1.2E-01	-1.6	3.3E-01	-0.5	9.0E-01
ENSMUST00000073551	zinc finger protein 386 (Kruppel-like) [Source:MGI Symbol;Acc:MGI:1930708]	Q3TN43		-2.3	6.1E-03	-3.7	1.3E-03	-0.1	8.9E-01	-1.4	1.6E-01
ENSMUST00000073556	MAM domain containing glycosylphosphatidylinositol anchor 1 [Source:MGI Symbol;Acc:MGI:1922012]	D3Z499		4.9	5.4E-04	-5.1	1.4E-02	0.9	3.1E-01	-3.4	1.8E-01
ENSMUST00000073571	olfactory receptor 1507 [Source:MGI Symbol;Acc:MGI:3031341]	Q0VEP0		6.2	1.6E-04	6.0	7.3E-04	0.8	4.9E-01	0.5	4.6E-01
ENSMUST00000073575	solute carrier family 39 (metal ion transporter), member 13 [Source:MGI Symbol;Acc:MGI:1915677]	B2RQ45	Q8BZH0	-3.6	1.6E-03	7.3	2.9E-04	-0.7	6.2E-01	-1.2	1.2E-01
ENSMUST00000071944	tec protein tyrosine kinase [Source:MGI Symbol;Acc:MGI:98662]	Q3U436		-0.3	9.0E-01	2.4	5.0E-01	2.5	3.0E-01	-0.2	9.5E-01
ENSMUST00000073581	protein kinase, cGMP-dependent, type I [Source:MGI Symbol;Acc:MGI:108174]		P0C605	5.6	3.4E-04	-0.9	1.8E-01	0.7	1.5E-01	-1.4	5.9E-02
ENSMUST00000071951	histocompatibility 2, Q region locus 7 [Source:MGI Symbol;Acc:MGI:95936]		P14429	-2.5	1.3E-01	-2.1	3.4E-01	-0.2	9.1E-01	-0.6	7.9E-01
ENSMUST00000073600	ERBB receptor feedback inhibitor 1 [Source:MGI Symbol;Acc:MGI:1921405]	Q3TK48	Q99JZ7	7.1	4.0E-03	0.6	6.1E-01	-5.2	2.5E-03	0.2	8.1E-01
ENSMUST00000071972	cilia and flagella associated protein 57 [Source:MGI Symbol;Acc:MGI:2686209]		Q9D180	3.5	5.4E-02	2.5	2.4E-01	0.2	9.2E-01	1.2	4.5E-01
ENSMUST00000071973	ERO1-like beta (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914725]		Q8R2E9	-0.5	3.3E-01	-0.4	4.9E-01	0.4	3.8E-01	0.4	5.5E-01
ENSMUST00000071977	microfibrillar-associated protein 2 [Source:MGI Symbol;Acc:MGI:99559]	Q99PM0		1.5	3.5E-01	3.3	2.9E-02	-1.5	2.8E-01	-3.3	3.3E-02
ENSMUST00000073605	glyceraldehyde-3-phosphate dehydrogenase [Source:MGI Symbol;Acc:MGI:95640]	D2KHZ9	P16858	-11.0	7.3E-06	5.9	4.4E-04	-0.6	6.0E-01	0.2	7.5E-01
ENSMUST00000073618	cDNA sequence BC021785 [Source:MGI Symbol;Acc:MGI:2446139]	Q3TN71		3.2	9.9E-04	5.1	4.2E-05	-3.3	4.0E-03	-0.5	2.8E-01
ENSMUST00000073625	inhibitor of CDK, cyclin A1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2144284]		Q6PKN7	5.9	2.3E-02	-2.0	2.4E-03	0.9	8.6E-03	-0.4	4.5E-01
ENSMUST00000073639	retinol dehydrogenase 1 (all trans) [Source:MGI Symbol;Acc:MGI:1195275]	Q8CGV4		8.8	7.0E-06	5.6	2.6E-04	-1.5	1.9E-01	-0.3	6.3E-01
ENSMUST00000071993	myotubularin related protein 12 [Source:MGI Symbol;Acc:MGI:2443034]		Q80TA6	-0.3	8.9E-01	0.5	8.9E-01	2.4	3.7E-01	1.6	5.8E-01
ENSMUST00000073705	family with sequence similarity 222, member B [Source:MGI Symbol;Acc:MGI:2384939]		Q6P539	-5.3	1.5E-03	8.2	2.4E-05	-0.5	6.6E-01	-0.6	2.6E-01
ENSMUST00000072012	androgen dependent TFPI regulating protein [Source:MGI Symbol;Acc:MGI:1924596]			0.5	4.8E-01	2.7	1.4E-02	0.5	5.5E-01	-1.7	5.2E-02
ENSMUST00000073724	PHD finger protein 1 [Source:MGI Symbol;Acc:MGI:98647]		Q9Z1B8	-3.9	1.7E-03	8.6	2.2E-05	1.2	2.9E-01	-0.5	3.4E-01
ENSMUST00000073781	E2F transcription factor 7 [Source:MGI Symbol;Acc:MGI:1289147]		Q6S7F2	2.6	2.8E-03	3.2	8.9E-04	-0.5	4.4E-01	0.2	6.6E-01
ENSMUST00000073782	zinc finger protein 937 [Source:MGI Symbol;Acc:MGI:3644476]	A2ANU7		6.6	8.9E-06	6.9	3.3E-04	-0.6	6.4E-01	0.2	7.7E-01
ENSMUST00000072031	myosin phosphatase Rho interacting protein [Source:MGI Symbol;Acc:MGI:1349438]		P97434	3.0	1.6E-01	4.3	8.2E-02	-0.1	9.5E-01	-1.4	4.4E-01
ENSMUST00000073783	choline phosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2384841]		Q8C025	5.0	1.2E-05	-9.1	4.6E-04	-0.4	3.4E-01	1.7	3.6E-01
ENSMUST00000073792	MON2 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914324]		Q80TL7	-6.0	3.0E-05	1.8	3.4E-01	2.6	9.9E-02	4.8	6.9E-03
ENSMUST00000073822	opioid binding protein/cell adhesion molecule-like [Source:MGI Symbol;Acc:MGI:97397]	G5E8G3		7.6	1.5E-05	2.2	6.0E-03	-0.1	8.5E-01	0.0	1.0E+00
ENSMUST00000072080	leucine rich repeat containing 40 [Source:MGI Symbol;Acc:MGI:1914394]			0.7	4.0E-01	1.1	2.7E-01	-0.1	8.6E-01	-0.6	5.3E-01
ENSMUST00000073834	leucine rich repeat containing 10 [Source:MGI Symbol;Acc:MGI:2448063]		Q8K3W2	8.1	9.4E-06	5.5	1.1E-05	-4.3	6.3E-04	-0.2	5.7E-01
ENSMUST00000072097	hematopoietic SH2 domain containing [Source:MGI Symbol;Acc:MGI:2676364]		Q6VYH9	-1.1	3.2E-01	0.6	6.0E-01	-0.4	6.3E-01	-2.2	9.7E-02
ENSMUST00000073840	eukaryotic translation initiation factor 4, gamma 1 [Source:MGI Symbol;Acc:MGI:2384784]	E9Q9E1		-7.4	4.3E-03	8.8	6.2E-04	0.0	1.0E+00	0.9	2.7E-01
ENSMUST00000073853	predicted gene 11562 [Source:MGI Symbol;Acc:MGI:3652059]	A0PK51		6.7	8.2E-05	-3.4	4.1E-02	1.6	4.8E-02	-0.8	6.1E-01
ENSMUST00000072113	transmembrane protein 65 [Source:MGI Symbol;Acc:MGI:1922118]		Q4VAE3	-0.2	8.0E-01	-0.2	7.9E-01	0.6	3.8E-01	0.7	4.6E-01
ENSMUST00000072119	cyclin B1 [Source:MGI Symbol;Acc:MGI:88302]	Q3TQW9	P24860	-0.6	5.3E-01	-0.2	8.8E-01	-0.3	7.0E-01	-0.7	5.1E-01
ENSMUST00000073868	nascent polypeptide-associated complex alpha polypeptide [Source:MGI Symbol;Acc:MGI:106095]		Q60817	-8.6	3.7E-06	4.9	2.7E-03	0.1	9.7E-01	0.5	5.1E-01
ENSMUST00000073870	dual specificity phosphatase and pro isomerase domain containing 1 [Source:MGI Symbol;Acc:MGI:3647127]		Q8BK84	6.5	1.8E-04	1.9	2.0E-03	-0.6	1.5E-01	-0.1	8.4E-01
ENSMUST00000073890	keratin 33B [Source:MGI Symbol;Acc:MGI:1309991]		Q61897	5.7	9.4E-04	2.1	1.5E-02	-0.1	8.9E-01	-0.4	5.6E-01
ENSMUST00000073926	ribosomal protein S12 [Source:MGI Symbol;Acc:MGI:98105]	Q6ZWZ6		-10.2	1.6E-04	-0.4	4.1E-01	0.0	9.6E-01	-1.1	5.8E-02
ENSMUST00000073935	GSG1-like [Source:MGI Symbol;Acc:MGI:2685483]		D3Z7H4	6.6	3.9E-05	-2.2	1.2E-01	-0.3	6.7E-01	-3.9	3.6E-02
ENSMUST00000073945	vitamin K epoxide reductase complex, subunit 1-like 1 [Source:MGI Symbol;Acc:MGI:1916818]			-2.6	2.0E-02	-1.9	2.1E-01	0.5	5.6E-01	-0.9	5.6E-01
ENSMUST00000073948	vomeronasal 2, receptor 19 [Source:MGI Symbol;Acc:MGI:3647444]	G5E8G4		6.8	6.1E-05	6.3	1.4E-04	0.0	9.9E-01	0.8	1.9E-01
ENSMUST00000073957	in, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E [Source:MGI Symbol;Acc:MC		P70275	7.4	1.7E-05	-5.4	4.3E-04	-0.3	4.9E-01	-0.8	4.6E-01
ENSMUST00000072187	kinesin family member 1C [Source:MGI Symbol;Acc:MGI:1098260]	E9Q9B0		-0.8	6.5E-01	0.3	9.0E-01	1.6	3.9E-01	0.5	8.3E-01
ENSMUST00000072206	POC1 centriolar protein homolog A (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1917485]		Q8JZX3	-0.5	6.0E-01	2.0	3.4E-01	4.8	7.9E-03	2.2	2.0E-01
ENSMUST00000073961	protein tyrosine phosphatase, receptor type, E [Source:MGI Symbol;Acc:MGI:97813]		P49446	-1.4	2.2E-02	-3.1	4.3E-03	1.0	4.1E-02	0.4	6.6E-01
ENSMUST00000073962	F-box and WD-40 domain protein 24 [Source:MGI Symbol;Acc:MGI:3646659]	E9PXM9		3.9	4.5E-03	2.6	2.7E-03	-0.1	8.1E-01	0.9	1.1E-01
ENSMUST00000074002	ubiquitin protein ligase E3B [Source:MGI Symbol;Acc:MGI:1891295]		Q9ES34	-3.0	3.2E-02	6.2	8.0E-04	-1.4	3.1E-01	-0.4	5.7E-01
ENSMUST00000074015	neuronal growth regulator 1 [Source:MGI Symbol;Acc:MGI:2444846]		Q80Z24	6.7	5.7E-05	-4.3	9.6E-05	-0.4	2.2E-01	0.0	9.6E-01
ENSMUST00000072237	misshapen-like kinase 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1355329]	G3X9G2		2.3	3.3E-01	3.3	3.0E-01	2.0	4.1E-01	1.0	7.0E-01
ENSMUST00000074043	Kruppel-like factor 10 [Source:MGI Symbol;Acc:MGI:1101353]		O89091	-3.4	2.7E-04	-5.8	1.1E-03	1.0	8.0E-02	0.4	7.6E-01
ENSMUST00000072249	carnitine deficiency-associated gene expressed in ventricle 3 [Source:MGI Symbol;Acc:MGI:2448759]		Q4VAA2	-3.0	6.1E-02	-5.6	8.2E-02	0.7	5.0E-01	3.3	2.8E-01
ENSMUST00000074051	serine (or cysteine) peptidase inhibitor, clade A, member 1C [Source:MGI Symbol;Acc:MGI:891969]			5.0	2.5E-02	5.2	5.8E-03	-1.2	4.5E-01	-0.7	4.3E-01
ENSMUST00000074053	predicted gene 10094 [Source:MGI Symbol;Acc:MGI:3704317]	E9Q317		-7.7	2.1E-05	5.7	1.0E-03	-1.3	3.5E-01	-0.5	4.8E-01
ENSMUST00000072287	phosphatidylinositol 4-kinase, catalytic, beta polypeptide [Source:MGI Symbol;Acc:MGI:1334433]		Q8BKC8	-1.9	7.7E-02	0.9	4.1E-01	0.5	5.9E-01	-2.3	5.3E-02
ENSMUST00000074058	methyl-CpG binding domain protein 2 [Source:MGI Symbol;Acc:MGI:1333813]		Q9Z2E1	-10.0	3.0E-06	-6.3	6.4E-03	1.6	4.8E-02	-0.5	8.1E-01
ENSMUST00000072292	zinc finger protein 280C [Source:MGI Symbol;Acc:MGI:2387585]		Q6P3Y5	0.0	9.9E-01	0.3	9.0E-01	-2.5	2.7E-01	-2.9	3.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000074072	predicted gene 10260 [Source:MGI Symbol;Acc:MGI:3642298]	F6YVP7		-6.6	8.4E-05	-2.9	1.3E-01	0.7	4.7E-01	0.2	9.0E-01
ENSMUST00000074077	bone morphogenetic protein 4 [Source:MGI Symbol;Acc:MGI:88180]	Q3ULR1	P21275	9.2	4.7E-05	6.9	6.9E-04	-0.1	9.7E-01	0.8	3.0E-01
ENSMUST00000074082	aminolevulinic acid synthase 1 [Source:MGI Symbol;Acc:MGI:87989]			-8.6	5.0E-06	6.8	2.3E-04	-0.6	6.2E-01	0.4	4.8E-01
ENSMUST00000072311	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1 [Source:MGI Symbol;Acc:MGI:99147]	Q3TJI7	Q04736	1.0	2.2E-01	1.2	2.6E-01	0.7	3.7E-01	0.5	5.3E-01
ENSMUST00000074085	ribosomal protein L10 [Source:MGI Symbol;Acc:MGI:105943]		Q6ZWV3	-5.6	1.6E-03	8.5	3.0E-05	0.0	1.0E+00	0.0	9.9E-01
ENSMUST00000074114	general transcription factor II I repeat domain-containing 1 [Source:MGI Symbol;Acc:MGI:1861942]		Q9JI57	6.4	2.4E-04	-5.9	2.7E-04	0.4	2.8E-01	-0.7	5.4E-01
ENSMUST00000074127	aldehyde dehydrogenase family 3, subfamily A2 [Source:MGI Symbol;Acc:MGI:1353452]		P47740	-5.1	1.1E-05	-1.5	1.4E-01	1.2	6.2E-02	0.2	8.3E-01
ENSMUST00000074132	vomeronasal 1 receptor 59 [Source:MGI Symbol;Acc:MGI:3033479]	Q8R2B9		6.1	1.8E-04	-6.5	1.6E-02	1.6	5.5E-02	0.1	9.5E-01
ENSMUST00000074142	late cornified envelope 1A1 [Source:MGI Symbol;Acc:MGI:1914377]	Q9CQH5		5.9	1.8E-04	-5.5	3.2E-05	0.9	1.7E-02	-0.8	2.9E-01
ENSMUST00000074148	predicted gene 7361 [Source:MGI Symbol;Acc:MGI:3805965]	D3Z6R1		7.8	1.9E-05	-5.9	1.2E-02	1.6	8.9E-02	0.5	8.3E-01
ENSMUST00000074156	adenylate kinase 8 [Source:MGI Symbol;Acc:MGI:1916120]		Q32M07	3.4	5.9E-04	7.6	3.8E-05	-0.6	6.1E-01	-0.3	6.0E-01
ENSMUST00000074171	otoferlin [Source:MGI Symbol;Acc:MGI:1891247]	E9PYR6		8.7	1.3E-05	-4.3	3.3E-03	0.3	5.6E-01	-3.9	2.7E-02
ENSMUST00000074173	spermatogenesis and centriole associated 1 [Source:MGI Symbol;Acc:MGI:1921531]			-4.0	3.9E-05	4.9	1.3E-02	-0.5	7.6E-01	0.7	5.3E-01
ENSMUST00000074230	lipase, member H [Source:MGI Symbol;Acc:MGI:2388029]		Q8CIV3	6.8	4.3E-05	-3.0	7.3E-02	0.4	5.9E-01	-0.3	8.3E-01
ENSMUST00000072391	histone cluster 1, H2aa [Source:MGI Symbol;Acc:MGI:2448285]	Q8CGP4		0.7	3.2E-01	1.9	4.4E-02	0.8	2.7E-01	-0.4	5.8E-01
ENSMUST00000072406	prolyl endopeptidase-like [Source:MGI Symbol;Acc:MGI:2441932]		Q8C167	-2.2	2.5E-01	-3.1	1.4E-01	-1.5	3.0E-01	-0.6	7.9E-01
ENSMUST00000074231	vesicle-associated membrane protein 5 [Source:MGI Symbol;Acc:MGI:1858622]	Q791P0	Q9Z2P8	3.3	3.4E-03	7.3	1.8E-04	-0.6	6.5E-01	-1.4	7.0E-02
ENSMUST00000072431	S100P binding protein [Source:MGI Symbol;Acc:MGI:1921898]		Q9D5K4	-0.7	8.2E-01	2.2	5.1E-01	0.7	8.1E-01	-2.2	4.9E-01
ENSMUST00000074233	synemin, intermediate filament protein [Source:MGI Symbol;Acc:MGI:2661187]		Q70IV5	10.3	1.1E-05	7.2	7.3E-05	-0.5	6.8E-01	-0.2	6.9E-01
ENSMUST00000074240	family with sequence similarity 69, member B [Source:MGI Symbol;Acc:MGI:1927576]		Q99ML4	2.8	1.8E-02	-5.4	8.9E-04	0.7	1.7E-01	-1.4	3.0E-01
ENSMUST00000074246	baculoviral IAP repeat-containing 2 [Source:MGI Symbol;Acc:MGI:1197009]		Q62210	-3.8	2.8E-02	5.4	2.0E-03	-0.6	6.6E-01	0.3	7.1E-01
ENSMUST00000072460	myocyte enhancer factor 2A [Source:MGI Symbol;Acc:MGI:99532]	S4R2H4		-0.8	4.7E-01	0.7	6.3E-01	1.8	1.0E-01	0.4	7.9E-01
ENSMUST00000074248	SH2 domain containing 3C [Source:MGI Symbol;Acc:MGI:1351631]		Q9QZS8	-4.6	3.9E-04	-1.3	1.5E-01	0.0	9.5E-01	-0.8	3.2E-01
ENSMUST00000074259	nurim (nuclear envelope membrane protein) [Source:MGI Symbol;Acc:MGI:2146855]		Q8VC65	-2.6	2.4E-03	6.9	1.7E-04	0.5	6.5E-01	-0.8	2.3E-01
ENSMUST00000074262	calcitonin receptor-like [Source:MGI Symbol;Acc:MGI:1926944]	A2AR99	Q9R1W5	4.8	1.3E-05	-5.5	1.3E-03	-0.4	5.3E-01	-2.8	9.9E-02
ENSMUST00000074267	ribosomal protein S7 [Source:MGI Symbol;Acc:MGI:1333818]	Q4FZE6	P62082	-5.3	1.0E-03	-9.2	8.4E-04	-0.7	3.2E-01	-0.7	7.2E-01
ENSMUST00000074285	Meis homeobox 2 [Source:MGI Symbol;Acc:MGI:108564]	Q3TYM2		7.4	4.6E-04	6.6	2.7E-04	-0.5	7.0E-01	-1.5	4.4E-02
ENSMUST00000074298	solute carrier family 4, sodium bicarbonate cotransporter, member 9 [Source:MGI Symbol;Acc:MGI:2443384]	Q8BUG8		4.1	1.8E-02	7.6	1.0E-04	-0.6	6.6E-01	-1.2	8.9E-02
ENSMUST00000074301	SET and MYND domain containing 1 [Source:MGI Symbol;Acc:MGI:104790]		P97443	8.0	3.5E-04	-1.5	4.6E-02	1.2	1.7E-02	-0.4	5.3E-01
ENSMUST00000074357	arginyl aminopeptidase (aminopeptidase B) [Source:MGI Symbol;Acc:MGI:2384902]	E9PYF1		-4.3	2.6E-04	-6.9	5.0E-04	0.9	6.6E-02	-0.8	5.9E-01
ENSMUST00000072554	RIKEN cDNA 9430015G10 gene [Source:MGI Symbol;Acc:MGI:2444364]	A2ASP7		0.1	9.2E-01	-1.0	7.2E-01	1.3	4.6E-01	2.4	3.1E-01
ENSMUST00000074359	kallikrein 1-related peptidase b5 [Source:MGI Symbol;Acc:MGI:892020]		P15945	6.5	1.7E-04	-5.0	6.8E-04	-1.4	1.8E-02	0.7	5.1E-01
ENSMUST00000074366	eyes absent 4 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1337104]		Q9Z191	4.9	3.0E-02	6.0	1.1E-03	-0.4	7.6E-01	-0.4	6.4E-01
ENSMUST00000072572	asparagine-linked glycosylation 11 (alpha-1,2-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:2142632]	A0A077K846	Q3TZM9	-0.6	7.3E-01	1.9	2.7E-01	-0.5	7.4E-01	-2.9	1.1E-01
ENSMUST00000074369	zinc finger protein 825 [Source:MGI Symbol;Acc:MGI:2385315]	K7N5X2		-3.2	6.1E-03	-6.4	5.7E-04	-0.7	1.6E-01	-0.9	5.2E-01
ENSMUST00000074370	axin 1 [Source:MGI Symbol;Acc:MGI:1096327]	E9QMJ8		-1.5	2.9E-02	6.6	1.0E-04	-0.6	6.1E-01	-0.7	2.5E-01
ENSMUST00000072580	lemur tyrosine kinase 3 [Source:MGI Symbol;Acc:MGI:3039582]			4.6	6.1E-02	2.4	4.4E-01	0.3	9.2E-01	2.4	3.2E-01
ENSMUST00000074371	programmed cell death 4 [Source:MGI Symbol;Acc:MGI:107490]		Q61823	8.0	8.4E-04	-6.2	1.9E-02	-1.8	7.7E-02	-0.4	8.7E-01
ENSMUST00000074372	Iroquois related homeobox 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1197526]		P81066	7.1	2.3E-04	4.6	3.6E-03	2.0	8.2E-02	0.8	3.5E-01
ENSMUST00000074380	testis expressed 33 [Source:MGI Symbol;Acc:MGI:1920626]	Q3KNN2	Q9D9J2	6.6	6.3E-05	-1.4	2.5E-01	0.2	7.9E-01	-3.4	3.0E-02
ENSMUST00000072607	integrator complex subunit 1 [Source:MGI Symbol;Acc:MGI:1915760]	K3W4P2		0.9	9.1E-02	1.8	1.9E-02	0.8	1.3E-01	-0.1	8.9E-01
ENSMUST00000074403	carboxylesterase 3B [Source:MGI Symbol;Acc:MGI:3644960]		Q8VCU1	6.6	5.5E-04	7.2	4.0E-05	-1.9	1.2E-01	0.1	8.4E-01
ENSMUST00000072621	K(lysine) acetyltransferase 7 [Source:MGI Symbol;Acc:MGI:2182799]		Q5SVQ0	0.2	9.2E-01	0.2	9.5E-01	-1.6	4.0E-01	-1.5	5.3E-01
ENSMUST00000074416	proline rich membrane anchor 1 [Source:MGI Symbol;Acc:MGI:1926097]	F8VQJ2		6.9	1.2E-04	8.6	9.8E-04	-0.8	6.9E-01	1.5	1.0E-01
ENSMUST00000074425	EF-hand calcium binding domain 14 [Source:MGI Symbol;Acc:MGI:2442397]	Q6PCQ6		-2.0	1.0E-02	-7.9	9.9E-05	0.5	1.2E-01	5.4	1.3E-03
ENSMUST00000072639	tripartite motif-containing 16 [Source:MGI Symbol;Acc:MGI:2137356]	Q5SVT1		3.1	8.2E-02	2.4	3.3E-01	0.7	6.8E-01	1.4	5.1E-01
ENSMUST00000074455	zinc finger protein 772 [Source:MGI Symbol;Acc:MGI:2385265]	Q3UQL6		4.4	3.8E-05	2.3	4.5E-03	-2.1	8.6E-03	-0.7	1.9E-01
ENSMUST00000074465	aquaporin 9 [Source:MGI Symbol;Acc:MGI:1891066]	Q4FK77	Q9JJJ3	-6.1	1.7E-04	7.2	1.7E-05	0.1	9.5E-01	0.1	8.7E-01
ENSMUST00000074466	predicted gene 10083 [Source:MGI Symbol;Acc:MGI:3642418]	F6WB82		7.6	5.9E-05	7.6	3.1E-04	-0.7	6.5E-01	-1.0	2.1E-01
ENSMUST00000074510	PR domain containing 10 [Source:MGI Symbol;Acc:MGI:2682952]	D3YYD1		2.3	4.6E-04	5.9	7.4E-04	-0.5	6.6E-01	-0.1	8.6E-01
ENSMUST00000074519	thioredoxin interacting protein [Source:MGI Symbol;Acc:MGI:1889549]		Q8BG60	-10.8	2.7E-06	-1.0	4.9E-01	1.1	2.5E-01	-1.6	3.0E-01
ENSMUST00000074525	GULP, engulfment adaptor PTB domain containing 1 [Source:MGI Symbol;Acc:MGI:1920407]		Q8K2A1	5.6	6.2E-03	-2.6	8.7E-02	0.6	4.7E-01	-1.4	3.5E-01
ENSMUST00000074540	olfactory receptor 373 [Source:MGI Symbol;Acc:MGI:3030207]	E9Q4J3		6.5	1.9E-04	-2.9	1.4E-03	-0.5	2.2E-01	-0.4	6.0E-01
ENSMUST00000072699	high mobility group box 3 [Source:MGI Symbol;Acc:MGI:1098219]	Q544R9	O54879	-1.6	3.3E-01	-5.6	1.2E-01	-0.2	8.5E-01	3.8	2.6E-01
ENSMUST00000074543	olfactory receptor 1382 [Source:MGI Symbol;Acc:MGI:3031216]	Q7TQT3		5.8	1.1E-03	5.6	1.1E-04	-1.5	1.3E-01	-0.1	8.7E-01
ENSMUST00000072726	WD repeat domain 7 [Source:MGI Symbol;Acc:MGI:1860197]		Q920I9	-0.9	9.4E-02	0.3	6.2E-01	1.4	1.7E-02	0.2	7.9E-01
ENSMUST00000074546	sidekick homolog 1 (chicken) [Source:MGI Symbol;Acc:MGI:2444413]		Q3UH53	6.7	2.8E-03	-3.2	1.3E-03	0.5	1.8E-01	0.3	6.3E-01
ENSMUST00000074552	non-SMC condensin II complex, subunit H2 [Source:MGI Symbol;Acc:MGI:1289164]		Q8BSP2	-4.3	4.5E-03	-4.6	2.1E-02	-0.2	7.7E-01	0.7	6.7E-01
ENSMUST00000074555	olfactory receptor 121 [Source:MGI Symbol;Acc:MGI:2177504]	Q5CZY0		6.0	3.3E-04	-2.3	2.3E-02	0.2	6.3E-01	-0.4	6.2E-01
ENSMUST00000072739	predicted gene 10146 [Source:MGI Symbol;Acc:MGI:3704367]		Q9CQQ8	-2.7	6.3E-02	-2.1	2.8E-01	0.6	6.6E-01	0.0	9.8E-01
ENSMUST00000074556	H2A histone family, member J [Source:MGI Symbol;Acc:MGI:3606192]		Q8R1M2	-3.0	9.2E-05	7.0	1.4E-04	-0.5	6.6E-01	0.1	8.7E-01
ENSMUST00000074574	unc-5 homolog C (C. elegans)-like [Source:MGI Symbol;Acc:MGI:1923839]	E9QLC2		4.6	1.0E-03	-8.0	1.2E-04	0.6	1.1E-01	-0.9	5.5E-01
ENSMUST00000074575	small nuclear ribonucleoprotein 70 (U1) [Source:MGI Symbol;Acc:MGI:98341]	A2RS68	Q62376	-4.3	7.1E-04	6.6	2.1E-04	-0.6	6.3E-01	-1.5	4.1E-02
ENSMUST00000074606	CD302 antigen [Source:MGI Symbol;Acc:MGI:1913455]		Q9DCG2	-4.6	4.4E-03	-3.1	7.5E-03	-0.7	2.3E-01	-1.9	1.3E-01
ENSMUST00000074608	RIKEN cDNA 1700029P11 gene [Source:MGI Symbol;Acc:MGI:1913596]	Q9CQ68		6.0	9.6E-04	-1.9	6.9E-02	-0.1	8.2E-01	-0.6	5.6E-01
ENSMUST00000074622	bone morphogenetic protein/retinoic acid inducible neural specific 3 [Source:MGI Symbol;Acc:MGI:2443035]		Q499E0	6.0	6.5E-04	-1.6	2.6E-01	1.4	1.2E-01	-0.5	7.2E-01
ENSMUST00000074628	WW domain binding protein 2 [Source:MGI Symbol;Acc:MGI:104709]	Q544A1	P97765	-5.5	1.0E-04	6.7	2.3E-03	-0.8	6.7E-01	0.8	3.8E-01
ENSMUST00000074651	G protein-coupled receptor kinase 4 [Source:MGI Symbol;Acc:MGI:95801]	Q8BP13		8.2	8.8E-07	2.3	3.9E-03	-1.7	1.4E-02	-0.7	2.2E-01
ENSMUST00000074653	RIKEN cDNA 8030462N17 gene [Source:MGI Symbol;Acc:MGI:2444951]	Q0VAW6		-1.5	3.9E-03	3.9	1.3E-02	-3.1	5.9E-02	-1.1	2.4E-01
ENSMUST00000072777	high mobility group AT-hook 2 [Source:MGI Symbol;Acc:MGI:101761]		P52927	-0.7	4.7E-01	0.4	6.1E-01	-1.7	4.7E-02	-2.8	1.6E-02
ENSMUST00000072796				2.3	3.5E-01	0.3	9.1E-01	-2.5	2.7E-01	-0.5	8.5E-01
ENSMUST00000074662	leucine rich repeat transmembrane neuronal 4 [Source:MGI Symbol;Acc:MGI:2389180]		Q80XG9	6.6	3.7E-03	8.0	1.0E-04	-0.6	6.4E-01	0.1	9.0E-01
ENSMUST00000072836	sphingosine kinase 2 [Source:MGI Symbol;Acc:MGI:1861380]	Q58E38	Q9JIA7	-0.2	8.4E-01	1.3	3.0E-01	1.4	1.4E-01	0.0	9.8E-01
ENSMUST00000072837	forkhead box K1 [Source:MGI Symbol;Acc:MGI:1347488]		P42128	0.1	9.0E-01	0.4	5.2E-01	1.1	4.1E-02	0.7	2.1E-01
ENSMUST00000072838	heat shock factor 1 [Source:MGI Symbol;Acc:MGI:96238]	A0A075F882	P38532	-0.5	4.0E-01	0.2	8.0E-01	0.5	4.0E-01	-0.2	7.6E-01
ENSMUST00000072841	enolase 3, beta muscle [Source:MGI Symbol;Acc:MGI:95395]		P21550	-0.4	4.9E-01	-1.5	5.7E-02	-1.7	9.1E-03	-0.6	3.8E-01
ENSMUST00000072847	ring finger protein 138 [Source:MGI Symbol;Acc:MGI:1929211]		Q9CQE0	-0.5	6.5E-01	2.3	1.7E-01	2.0	1.7E-01	-0.7	5.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000074667	brachyury [Source:MGI Symbol;Acc:MGI:98472]	Q78ZW9	P20293	6.2	2.2E-03	3.3	6.2E-03	0.5	5.6E-01	0.2	7.2E-01
ENSMUST00000074669	heterogeneous nuclear ribonucleoprotein A/B [Source:MGI Symbol;Acc:MGI:1330294]	Q544Z3	Q99020	-3.1	1.2E-03	-3.6	2.9E-02	0.0	9.6E-01	-0.4	7.7E-01
ENSMUST00000072866	ubiquitin-associated protein 1 [Source:MGI Symbol;Acc:MGI:2149543]		Q8BH48	-0.6	4.2E-01	0.4	6.9E-01	1.0	1.7E-01	0.0	9.6E-01
ENSMUST00000074690	UBX domain protein 11 [Source:MGI Symbol;Acc:MGI:1914836]		Q9D572	-4.9	7.7E-04	7.4	8.5E-05	-0.5	7.0E-01	-0.4	5.4E-01
ENSMUST00000072873	misshapen-like kinase 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1355329]	Q5SXG3		1.1	6.1E-01	-2.6	4.0E-01	-2.1	2.5E-01	1.6	6.0E-01
ENSMUST00000074694	guanine nucleotide binding protein (G protein), alpha inhibiting 1 [Source:MGI Symbol;Acc:MGI:95771]		B2RSH2	6.7	7.1E-05	-4.0	1.3E-03	0.1	8.0E-01	-0.7	4.9E-01
ENSMUST00000074698	extraembryonic, spermatogenesis, homeobox 1 [Source:MGI Symbol;Acc:MGI:1096388]	O88933		5.4	1.3E-02	4.0	9.9E-03	-2.9	7.3E-02	-1.2	2.0E-01
ENSMUST00000074713	olfactory receptor 802 [Source:MGI Symbol;Acc:MGI:3030636]	Q8VGJ2		5.6	5.9E-04	6.5	5.3E-04	-0.6	6.5E-01	-0.3	6.8E-01
ENSMUST00000072889	leucine rich repeat containing 16A [Source:MGI Symbol;Acc:MGI:1915982]		Q6EDY6	2.4	1.7E-01	0.6	6.5E-01	-4.0	1.5E-02	-2.2	1.3E-01
ENSMUST00000072896	armadillo repeat containing 10 [Source:MGI Symbol;Acc:MGI:1914461]		Q9D0L7	-0.7	2.7E-01	0.1	8.7E-01	0.5	4.4E-01	-0.4	6.0E-01
ENSMUST00000074733	septin 11 [Source:MGI Symbol;Acc:MGI:1277214]		Q8C1B7	1.1	1.8E-02	1.2	4.0E-01	-5.6	6.7E-03	-1.3	3.5E-01
ENSMUST00000072904				-1.6	5.0E-01	3.3	2.9E-01	3.5	2.0E-01	-1.4	5.8E-01
ENSMUST00000074752	histone cluster 1, H2ak [Source:MGI Symbol;Acc:MGI:2448297]		Q8CGP7	5.2	3.5E-03	6.7	1.2E-03	-0.6	7.3E-01	-0.8	3.3E-01
ENSMUST00000074761	predicted gene 10134 [Source:MGI Symbol;Acc:MGI:3642322]	F6ZQC6		8.5	3.7E-06	6.8	2.0E-04	-0.6	6.4E-01	-0.8	2.4E-01
ENSMUST00000074783	hemicentin 1 [Source:MGI Symbol;Acc:MGI:2685047]	D3YXG0		8.1	4.7E-05	-2.6	1.2E-02	-0.8	1.7E-01	-0.9	2.9E-01
ENSMUST00000074792	mitochondrial methionyl-tRNA formyltransferase [Source:MGI Symbol;Acc:MGI:1916856]		Q9D799	2.3	8.8E-04	-8.1	7.4E-05	0.9	2.1E-02	-0.7	5.9E-01
ENSMUST00000074802	sex comb on midleg-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1340042]	B1AVB4		5.0	1.4E-03	5.0	5.0E-05	-1.7	4.2E-02	-0.2	7.5E-01
ENSMUST00000074805	GLI pathogenesis-related 1 (glioma) [Source:MGI Symbol;Acc:MGI:1920940]	Q4QQK5	Q9CWG1	-11.1	4.0E-06	7.0	1.9E-04	-0.5	7.0E-01	-1.5	4.6E-02
ENSMUST00000072948	acyl-Coenzyme A oxidase 1, palmitoyl [Source:MGI Symbol;Acc:MGI:1330812]		Q9R0H0	-2.4	2.4E-01	-2.6	4.6E-01	1.5	4.5E-01	1.6	6.1E-01
ENSMUST00000072954	LanC (bacterial lantibiotic synthetase component C)-like 2 [Source:MGI Symbol;Acc:MGI:1919085]		Q9JJK2	2.9	1.9E-01	4.4	7.9E-02	-0.7	7.7E-01	-2.2	1.9E-01
ENSMUST00000074806	histocompatibility 2, Q region locus 2 [Source:MGI Symbol;Acc:MGI:95931]	Q4KN81		-5.5	2.1E-04	6.9	8.5E-04	-2.0	2.5E-01	-1.0	2.6E-01
ENSMUST00000074807	leucine-rich repeats and immunoglobulin-like domains 3 [Source:MGI Symbol;Acc:MGI:2443955]		Q6P1C6	6.3	4.2E-05	-3.2	3.4E-03	-0.6	1.7E-01	-0.4	6.5E-01
ENSMUST00000074829	toll-like receptor 12 [Source:MGI Symbol;Acc:MGI:3045221]	A2RRZ9	Q6QNU9	5.1	5.7E-05	-6.7	1.2E-04	0.7	6.4E-02	-0.6	6.2E-01
ENSMUST00000074839	eosinophil-associated, ribonuclease A family, member 2 [Source:MGI Symbol;Acc:MGI:108020]	W0UVF7	P97425	-1.5	3.5E-02	-1.3	4.3E-01	2.2	3.9E-02	0.8	6.3E-01
ENSMUST00000074840	prolactin regulatory element binding [Source:MGI Symbol;Acc:MGI:1355326]	Q3UAP1	Q9WUQ2	-7.0	4.0E-04	5.2	3.7E-03	0.4	8.0E-01	-0.9	3.2E-01
ENSMUST00000074856	Rho guanine nucleotide exchange factor (GEF7) [Source:MGI Symbol;Acc:MGI:1860493]			-7.2	9.3E-06	-5.8	1.2E-03	0.1	9.1E-01	-0.1	9.5E-01
ENSMUST00000073014				4.7	6.0E-02	3.8	8.7E-02	-2.4	3.2E-01	-1.4	3.6E-01
ENSMUST00000074859	olfactory receptor 1413 [Source:MGI Symbol;Acc:MGI:3031247]	Q8VGU3		5.9	6.7E-04	2.6	4.3E-03	-1.1	1.0E-01	0.0	9.9E-01
ENSMUST00000074874	olfactory receptor 464 [Source:MGI Symbol;Acc:MGI:3030298]	Q5SW48		6.1	4.7E-04	9.0	1.3E-05	-0.7	5.7E-01	-0.3	5.3E-01
ENSMUST00000074898	haptoglobin [Source:MGI Symbol;Acc:MGI:96211]	Q3UBS3	Q61646	-9.2	2.9E-07	2.3	5.7E-02	-0.8	4.3E-01	0.1	8.9E-01
ENSMUST00000074912	BLOC-1 related complex subunit 7 [Source:MGI Symbol;Acc:MGI:1913689]		Q9CRC6	1.6	7.2E-03	-2.3	4.6E-03	0.7	7.3E-02	0.0	9.5E-01
ENSMUST00000074919	WW domain containing adaptor with coiled-coil [Source:MGI Symbol;Acc:MGI:2387357]		Q924H7	-7.0	8.6E-04	8.6	4.1E-04	-0.2	9.1E-01	0.9	2.5E-01
ENSMUST00000073067	olute carrier family 10 (sodium/bile acid cotransporter family), member 3 [Source:MGI Symbol;Acc:MGI:9504		P21129	-3.9	1.4E-01	-3.5	2.9E-01	-0.2	9.0E-01	-0.7	8.4E-01
ENSMUST00000073076	ATP-binding cassette, sub-family B (MDR/TAP), member 8 [Source:MGI Symbol;Acc:MGI:1351667]		Q9CXJ4	-1.2	3.2E-01	-1.6	4.3E-01	1.3	3.3E-01	1.7	3.8E-01
ENSMUST00000074936	interleukin-1 receptor-associated kinase 4 [Source:MGI Symbol;Acc:MGI:2182474]		Q8R4K2	-4.0	2.8E-04	-6.6	7.2E-04	-0.5	3.2E-01	-0.9	5.4E-01
ENSMUST00000074941	zinc finger protein 35 [Source:MGI Symbol;Acc:MGI:99179]	Q3V142	P15620	-2.2	3.6E-03	7.0	1.8E-04	0.5	6.9E-01	-0.4	5.7E-01
ENSMUST00000074945	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:2653690]	E9Q3K3		-6.0	2.5E-05	2.0	9.2E-03	-0.9	1.3E-01	-0.6	3.1E-01
ENSMUST00000074948	nuclear transcription factor, X-box binding-like 1 [Source:MGI Symbol;Acc:MGI:1923646]	E9Q3K1		4.7	1.6E-02	-5.6	2.0E-03	-0.4	4.7E-01	-0.5	7.5E-01
ENSMUST00000074949	transmembrane protein 140 [Source:MGI Symbol;Acc:MGI:1915737]		Q8BGY5	-3.3	4.2E-03	-5.8	7.4E-02	-0.5	6.6E-01	-0.2	9.4E-01
ENSMUST00000073109	xy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like [Source:MGI Symbol;Acc:MC		P58465	-0.5	2.5E-01	1.1	9.9E-02	1.3	1.7E-02	-0.3	5.6E-01
ENSMUST00000074950	heterogeneous nuclear ribonucleoprotein H2 [Source:MGI Symbol;Acc:MGI:1201779]		P70333	-7.9	8.9E-05	5.4	1.2E-03	-0.5	7.0E-01	-0.4	5.3E-01
ENSMUST00000074957	BUD13 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2443443]		Q8R149	-6.4	2.9E-04	-2.1	2.5E-02	0.9	7.1E-02	-0.2	8.2E-01
ENSMUST00000074976	histone cluster 2, H2aa2 [Source:MGI Symbol;Acc:MGI:2448283]	B2RWH3	Q6GSS7	-5.4	2.1E-03	-4.3	5.9E-03	1.0	8.3E-02	-0.1	9.3E-01
ENSMUST00000074991	transmembrane protein 184b [Source:MGI Symbol;Acc:MGI:2445179]		Q8BG09	-7.5	1.0E-03	-0.3	6.3E-01	0.9	4.5E-02	-0.4	4.7E-01
ENSMUST00000073127	non-SMC condensin II complex, subunit D3 [Source:MGI Symbol;Acc:MGI:2142989]	K4DI67		-1.0	4.0E-02	-0.4	4.2E-01	0.3	3.8E-01	-0.2	6.8E-01
ENSMUST00000075010	lethal, Chr 7, Rinchik 6 [Source:MGI Symbol;Acc:MGI:96738]		Q9DD02	-3.1	2.0E-02	-6.0	3.0E-03	1.6	1.2E-02	-0.6	7.1E-01
ENSMUST00000075012	helicase with zinc finger domain [Source:MGI Symbol;Acc:MGI:1925705]			-4.8	3.0E-04	4.5	9.3E-04	-2.8	2.5E-02	0.8	2.4E-01
ENSMUST00000075017	pre-B lymphocyte gene 1 [Source:MGI Symbol;Acc:MGI:98936]	Q545E0	P13372	6.4	1.1E-04	5.6	2.2E-05	-0.6	3.5E-01	-0.2	6.6E-01
ENSMUST00000075052	otassium voltage-gated channel, subfamily H (eag-related), member 7 [Source:MGI Symbol;Acc:MGI:215956		Q9ER47	1.9	8.7E-04	-1.7	1.6E-02	1.1	1.0E-02	0.7	2.6E-01
ENSMUST00000075062	hematopoietic cell signal transducer [Source:MGI Symbol;Acc:MGI:1344360]		Q9QUJ0	-5.7	4.5E-05	6.7	1.2E-03	-0.4	8.2E-01	-1.3	1.5E-01
ENSMUST00000075068	peptidase D [Source:MGI Symbol;Acc:MGI:97542]	A2RS23	Q11136	-1.8	8.8E-03	2.1	1.6E-02	0.0	1.0E+00	-0.3	6.7E-01
ENSMUST00000075069	neurotrimin [Source:MGI Symbol;Acc:MGI:2446259]	Q8BG33		7.3	7.7E-05	5.7	3.2E-05	-0.8	3.0E-01	-0.3	5.0E-01
ENSMUST00000073173	ATP-binding cassette, sub-family C (CFTR/MRP), member 9 [Source:MGI Symbol;Acc:MGI:1352630]		P70170	6.8	4.5E-02	2.8	4.9E-01	-0.8	8.1E-01	3.1	3.1E-01
ENSMUST00000075072	G-protein coupled receptor 65 [Source:MGI Symbol;Acc:MGI:108031]			-5.0	1.1E-04	6.2	3.7E-04	-0.5	6.5E-01	-0.2	8.0E-01
ENSMUST00000075076	DNA segment, Chr 17, Wayne State University 92, expressed [Source:MGI Symbol;Acc:MGI:106281]	B2KF52		2.6	2.8E-02	-2.4	7.4E-02	1.2	8.6E-02	-0.2	8.9E-01
ENSMUST00000075080	family with sequence similarity 19, member A1 [Source:MGI Symbol;Acc:MGI:2443695]		Q7TPG8	8.9	7.7E-05	-0.6	3.7E-01	0.3	6.2E-01	-1.7	3.0E-02
ENSMUST00000075084	tripartite motif-containing 58 [Source:MGI Symbol;Acc:MGI:2684862]		Q5NCC9	5.7	2.7E-04	8.8	1.7E-04	-0.7	6.4E-01	-0.9	2.2E-01
ENSMUST00000073228	solute carrier protein family 52, member 3 [Source:MGI Symbol;Acc:MGI:1916948]		Q9D6X5	-1.8	5.6E-01	2.2	4.0E-01	-1.2	6.1E-01	-5.2	1.0E-01
ENSMUST00000073234	ataxin 7-like 3 [Source:MGI Symbol;Acc:MGI:3036270]		A2AWT3	-1.5	6.8E-01	-1.3	7.3E-01	-0.6	8.5E-01	-0.8	8.4E-01
ENSMUST00000075085	vomeronasal 1 receptor 63 [Source:MGI Symbol;Acc:MGI:3033470]	Q9EPT1		8.3	7.9E-05	2.5	1.1E-02	2.7	3.0E-03	-2.5	4.4E-03
ENSMUST00000073242	cadherin 23 (otocadherin) [Source:MGI Symbol;Acc:MGI:1890219]	F8WIF5		-2.1	5.1E-01	-1.1	7.8E-01	0.2	9.3E-01	-0.8	8.5E-01
ENSMUST00000075092	NADH dehydrogenase (ubiquinone) Fe-S protein 8 [Source:MGI Symbol;Acc:MGI:2385079]	Q5M9P5	Q8K3J1	-3.5	1.6E-03	8.3	2.8E-05	-0.6	6.2E-01	0.2	6.5E-01
ENSMUST00000075095	vomeronasal 2, receptor 24 [Source:MGI Symbol;Acc:MGI:3647530]	D3YUI0		6.4	1.2E-04	6.8	9.7E-03	1.1	5.9E-01	-1.4	2.5E-01
ENSMUST00000073261	histone cluster 1, H2af [Source:MGI Symbol;Acc:MGI:2448309]		Q8CGP5	1.4	1.7E-01	2.2	9.4E-02	0.4	7.4E-01	-0.4	6.8E-01
ENSMUST00000073302	Rho GTPase activating protein 24 [Source:MGI Symbol;Acc:MGI:1922647]		Q8C4V1	2.2	2.2E-01	-0.2	9.1E-01	-4.6	6.9E-03	-2.3	1.6E-01
ENSMUST00000075108	vomeronasal 2, receptor 31 [Source:MGI Symbol;Acc:MGI:3757688]	L7N1Z4		5.3	1.7E-03	-5.0	1.5E-02	0.4	5.7E-01	-0.7	7.2E-01
ENSMUST00000073312	zinc finger protein 760 [Source:MGI Symbol;Acc:MGI:2679257]	E9QAF5		0.1	8.3E-01	1.1	2.1E-01	0.7	3.0E-01	-0.3	7.0E-01
ENSMUST00000073316	forkhead box M1 [Source:MGI Symbol;Acc:MGI:1347487]	Q6P1H7		0.7	2.2E-01	2.1	2.0E-02	1.2	6.7E-02	-0.2	7.7E-01
ENSMUST00000073325	pleckstrin homology-like domain, family B, member 3 [Source:MGI Symbol;Acc:MGI:3642959]	E9QAF4		0.9	1.5E-01	1.5	8.5E-02	0.8	2.1E-01	0.2	7.7E-01
ENSMUST00000073337	Crm, cramped-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1930190]		Q6PG95	0.4	4.4E-01	0.6	3.4E-01	0.8	1.4E-01	0.5	3.9E-01
ENSMUST00000075132	cadherin 12 [Source:MGI Symbol;Acc:MGI:109503]		Q5RJH3	8.4	3.3E-05	-2.7	1.1E-02	0.8	1.5E-01	0.0	9.9E-01
ENSMUST00000075141	tripartite motif-containing 17 [Source:MGI Symbol;Acc:MGI:1861440]		Q7TPM3	7.1	9.6E-05	5.7	1.0E-03	-0.5	6.8E-01	-0.3	6.7E-01
ENSMUST00000075162	kallikrein 1 [Source:MGI Symbol;Acc:MGI:102850]	A0A0B6VSQ6	P15947	4.7	1.6E-04	-5.9	1.1E-05	0.1	8.0E-01	-0.5	4.9E-01
ENSMUST00000073352	TGFB-induced factor homeobox 2 [Source:MGI Symbol;Acc:MGI:1915299]	Q3TZS1		-1.1	6.2E-01	1.0	7.1E-01	2.3	2.8E-01	0.3	9.1E-01
ENSMUST00000073364	family with sequence similarity 120, member C [Source:MGI Symbol;Acc:MGI:2387687]		Q8C3F2	0.5	6.9E-01	2.9	3.8E-02	-0.8	5.2E-01	-3.2	2.6E-02
ENSMUST00000075164	kinesin family member 21B [Source:MGI Symbol;Acc:MGI:109234]	F8VQE2		-4.7	3.9E-03	3.7	5.1E-03	-0.2	8.1E-01	0.2	8.0E-01
ENSMUST00000073379	deleted in colorectal carcinoma [Source:MGI Symbol;Acc:MGI:94869]		P70211	3.5	5.9E-02	5.2	1.1E-02	-0.6	7.3E-01	-2.3	9.6E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000073387	Eph receptor A1 [Source:MGI Symbol;Acc:MGI:107381]		Q60750	-0.5	3.4E-01	-0.4	5.7E-01	0.1	7.8E-01	0.0	9.8E-01
ENSMUST00000075175	RIKEN cDNA 2810428I15 gene [Source:MGI Symbol;Acc:MGI:1913712]		Q9CYZ6	-4.6	8.5E-04	-3.4	5.8E-02	0.5	5.0E-01	0.2	8.9E-01
ENSMUST00000075177	olfactory receptor 1377 [Source:MGI Symbol;Acc:MGI:3031211]	Q8VGH1		6.1	1.0E-04	4.8	2.1E-04	-0.6	4.6E-01	-0.6	2.9E-01
ENSMUST00000075178	ribosomal protein L18 [Source:MGI Symbol;Acc:MGI:98003]	Q58EW0	P35980	-1.3	2.1E-02	5.3	2.3E-02	-0.8	7.0E-01	1.9	1.5E-01
ENSMUST00000075190	cadherin 11 [Source:MGI Symbol;Acc:MGI:99217]		P55288	5.5	1.9E-04	1.1	5.5E-01	0.3	8.4E-01	2.3	1.4E-01
ENSMUST00000075192	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]			-7.4	4.3E-06	6.7	1.1E-03	-0.2	9.1E-01	-2.9	1.1E-02
ENSMUST00000073418	plectin [Source:MGI Symbol;Acc:MGI:1277961]		Q9QXS1	2.7	3.0E-01	2.3	3.3E-01	-2.5	3.2E-01	-2.1	3.0E-01
ENSMUST00000075221	oncostatin M [Source:MGI Symbol;Acc:MGI:104749]		P53347	-3.3	7.4E-03	1.6	5.2E-02	0.0	9.6E-01	0.0	9.7E-01
ENSMUST00000075242	heat shock protein 1 (chaperonin 10) [Source:MGI Symbol;Acc:MGI:104680]	Q4KL76	Q64433	-3.3	1.2E-04	-6.5	2.3E-04	0.5	1.8E-01	-0.7	5.8E-01
ENSMUST00000073441	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans) [Source:MGI Symbol;Acc:MGI:2682334		Q5RJH6	-2.7	6.8E-02	-1.2	4.5E-01	0.6	5.5E-01	-0.8	6.2E-01
ENSMUST00000075245	unc-13 homolog C (C. elegans) [Source:MGI Symbol;Acc:MGI:2149021]		Q8K0T7	7.6	2.5E-05	6.6	8.6E-05	-0.9	4.3E-01	0.3	5.9E-01
ENSMUST00000075253	cytochrome P450, family 4, subfamily f, polypeptide 13 [Source:MGI Symbol;Acc:MGI:2158641]	Q99N19		-1.8	1.9E-02	-4.2	2.6E-04	-1.0	2.6E-02	-0.4	5.5E-01
ENSMUST00000075255	zinc finger protein 874a [Source:MGI Symbol;Acc:MGI:3040703]	Q8BX23		-4.1	7.4E-04	5.5	1.6E-02	-0.7	7.4E-01	1.1	3.7E-01
ENSMUST00000073466	crystallin, zeta (quinone reductase)-like 1 [Source:MGI Symbol;Acc:MGI:1913859]		Q921W4	-1.7	1.9E-01	-1.3	3.9E-01	0.0	9.9E-01	-0.4	7.8E-01
ENSMUST00000075281	MAP/microtubule affinity regulating kinase 3 [Source:MGI Symbol;Acc:MGI:1341865]		Q03141	-2.8	8.2E-05	-7.7	4.0E-06	-0.8	1.9E-02	1.0	2.1E-01
ENSMUST00000073488	nuclear receptor subfamily 1, group H, member 2 [Source:MGI Symbol;Acc:MGI:1352463]		Q60644	-2.7	5.3E-01	-5.3	3.7E-01	-1.3	5.7E-01	1.2	8.5E-01
ENSMUST00000075290	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 [Source:MGI Symbol;Acc:MGI:109243]		P70126	5.1	2.1E-02	8.1	1.4E-05	2.1	4.2E-02	-0.6	2.0E-01
ENSMUST00000075296	MAS-related GPR, member H [Source:MGI Symbol;Acc:MGI:1934134]	W8W3M0	Q99MT8	6.2	3.3E-04	2.3	2.9E-02	0.5	5.7E-01	-0.1	9.3E-01
ENSMUST00000075299	eroxisome proliferative activated receptor, gamma, coactivator 1 beta [Source:MGI Symbol;Acc:MGI:2444934		Q8VHJ7	5.9	6.4E-03	6.0	3.5E-04	-0.5	6.6E-01	-0.7	3.0E-01
ENSMUST00000073534	zinc finger protein 523 [Source:MGI Symbol;Acc:MGI:2687278]		Q8BMU0	-2.4	5.1E-02	-2.7	1.5E-01	1.2	2.3E-01	1.5	4.1E-01
ENSMUST00000073536	nebulin-related anchoring protein [Source:MGI Symbol;Acc:MGI:1098765]		Q80XB4	3.2	2.0E-01	6.0	7.9E-02	1.6	6.2E-01	-1.2	5.2E-01
ENSMUST00000075312	transthyretin [Source:MGI Symbol;Acc:MGI:98865]	Q5M9K1	P07309	3.8	2.8E-02	6.6	1.0E-04	-0.5	6.2E-01	-1.0	1.2E-01
ENSMUST00000075316	glutamate receptor, ionotropic, AMPA2 (alpha 2) [Source:MGI Symbol;Acc:MGI:95809]	G5E8H1		6.2	6.1E-04	6.2	1.2E-04	-1.5	1.9E-01	-0.4	5.1E-01
ENSMUST00000075317	PDZ domain containing 2 [Source:MGI Symbol;Acc:MGI:1922394]	E9Q1M1		5.2	2.4E-05	-2.7	2.4E-02	0.4	4.9E-01	0.8	4.3E-01
ENSMUST00000075363	acyl-CoA thioesterase 7 [Source:MGI Symbol;Acc:MGI:1917275]		Q91V12	-3.8	3.4E-03	9.0	4.2E-04	4.4	1.9E-02	0.3	6.6E-01
ENSMUST00000073570	zinc finger protein 414 [Source:MGI Symbol;Acc:MGI:1915641]	Q14A93	Q9DCK4	2.2	2.8E-01	6.1	5.3E-02	3.2	2.5E-01	-0.8	6.8E-01
ENSMUST00000075387	seizure related 6 homolog like [Source:MGI Symbol;Acc:MGI:1935121]			8.8	1.3E-05	5.9	4.1E-04	-0.5	6.7E-01	-0.2	7.3E-01
ENSMUST00000073572	metaxin 1 [Source:MGI Symbol;Acc:MGI:103025]	F7C846		-2.0	6.7E-02	0.2	8.5E-01	-0.2	8.0E-01	-2.3	4.8E-02
ENSMUST00000075410	BTB (POZ) domain containing 3 [Source:MGI Symbol;Acc:MGI:2385155]		P58545	8.8	2.2E-03	-0.1	8.9E-01	-0.3	4.8E-01	-3.8	1.3E-03
ENSMUST00000075414	olfactory receptor 701 [Source:MGI Symbol;Acc:MGI:3030535]	Q9D3U9		7.8	1.2E-05	5.9	4.7E-04	-0.5	6.9E-01	-0.8	2.5E-01
ENSMUST00000075418	StAR-related lipid transfer (START) domain containing 5 [Source:MGI Symbol;Acc:MGI:2156765]		Q9EPQ7	-2.0	2.1E-03	5.1	3.9E-02	-0.1	9.7E-01	1.9	1.6E-01
ENSMUST00000075420	methyltransferase like 7A3 [Source:MGI Symbol;Acc:MGI:3710670]	G3X9G9		5.2	1.9E-04	-10.7	6.9E-05	-0.2	5.5E-01	-0.6	7.4E-01
ENSMUST00000075422	mab-21-like 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1333773]		O70299	8.1	1.5E-05	3.5	1.6E-03	0.6	4.1E-01	0.2	7.3E-01
ENSMUST00000075444	dendrin [Source:MGI Symbol;Acc:MGI:108101]		Q80TS7	7.9	2.4E-05	2.4	4.0E-01	-0.8	7.6E-01	2.7	2.4E-01
ENSMUST00000075447	poliovirus receptor-related 2 [Source:MGI Symbol;Acc:MGI:97822]		P32507	-2.2	9.5E-04	7.9	5.0E-05	-0.4	7.1E-01	0.5	4.1E-01
ENSMUST00000073660	flotillin 2 [Source:MGI Symbol;Acc:MGI:103309]	Q5SS83		-3.3	6.2E-02	-1.5	5.0E-01	1.5	2.8E-01	-0.2	9.3E-01
ENSMUST00000073687	discs, large homolog 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:1918478]	E9Q9I2		7.2	5.4E-02	-1.4	7.0E-01	-5.3	1.5E-01	3.3	2.8E-01
ENSMUST00000073691	LIM domain and actin binding 1 [Source:MGI Symbol;Acc:MGI:1920992]		Q9ERG0	2.6	1.1E-01	5.0	9.1E-03	-0.6	7.2E-01	-2.9	3.6E-02
ENSMUST00000075451	complement component (3b/4b) receptor 1-like [Source:MGI Symbol;Acc:MGI:88513]		Q64735	-8.1	1.1E-05	-2.3	1.3E-01	2.2	2.0E-02	-0.8	5.9E-01
ENSMUST00000073722	predicted pseudogene 10073 [Source:MGI Symbol;Acc:MGI:3641908]	E9Q3T0		0.5	5.4E-01	-1.3	3.0E-01	-1.1	1.9E-01	0.7	5.6E-01
ENSMUST00000075452	cysteine-rich hydrophobic domain 2 [Source:MGI Symbol;Acc:MGI:1921527]		Q9D9G3	-2.0	2.2E-03	-2.2	5.5E-02	0.7	2.4E-01	-0.9	4.1E-01
ENSMUST00000075453	ribosomal protein L21 [Source:MGI Symbol;Acc:MGI:1278340]	Q9CQM8		-3.3	8.6E-03	5.2	4.3E-04	1.8	6.9E-02	-0.8	2.1E-01
ENSMUST00000075468	olfactory receptor 452 [Source:MGI Symbol;Acc:MGI:3030286]	Q7TRV8		6.3	2.0E-04	6.4	2.1E-05	-0.9	3.2E-01	-0.7	1.4E-01
ENSMUST00000075477	caveolin 3 [Source:MGI Symbol;Acc:MGI:107570]		P51637	7.1	8.7E-05	4.1	1.2E-04	-1.0	1.5E-01	-0.1	8.9E-01
ENSMUST00000073787	ldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase) [Source:MGI Symbol;Acc:MGI:10779(		Q8CG76	0.0	9.9E-01	0.9	3.0E-01	0.2	7.5E-01	-0.7	3.8E-01
ENSMUST00000075491	FK506 binding protein 8 [Source:MGI Symbol;Acc:MGI:1341070]		O35465	-9.9	4.0E-05	-5.7	8.9E-04	0.9	7.1E-02	0.5	6.6E-01
ENSMUST00000075510	scaffold attachment factor B2 [Source:MGI Symbol;Acc:MGI:2146808]		Q80YR5	-7.9	7.4E-05	7.3	3.5E-04	0.9	4.9E-01	1.2	1.2E-01
ENSMUST00000073833	zinc finger protein 111 [Source:MGI Symbol;Acc:MGI:1929114]	Q99K53		4.6	6.1E-02	3.9	8.8E-02	-2.2	3.5E-01	-1.6	3.5E-01
ENSMUST00000075523	bone gamma-carboxyglutamate protein 3 [Source:MGI Symbol;Acc:MGI:88155]		P54615	8.0	2.5E-04	6.7	4.9E-05	-1.5	1.8E-01	-0.1	8.3E-01
ENSMUST00000073837	POU domain, class 6, transcription factor 1 [Source:MGI Symbol;Acc:MGI:102935]	Q5U4D4		1.9	2.9E-01	1.5	5.4E-01	0.6	7.3E-01	1.0	6.5E-01
ENSMUST00000075552	cytochrome P450, family 2, subfamily a, polypeptide 12 [Source:MGI Symbol;Acc:MGI:105055]		P56593	6.3	7.7E-04	-5.0	1.0E-01	1.7	2.3E-01	-0.6	8.3E-01
ENSMUST00000073843	tec protein tyrosine kinase [Source:MGI Symbol;Acc:MGI:98662]	Q8CFK4		-3.6	1.3E-01	-1.8	6.1E-01	2.2	3.2E-01	0.5	8.9E-01
ENSMUST00000075571	sulfotransferase family, cytosolic, 2B, member 1 [Source:MGI Symbol;Acc:MGI:1926342]		O35400	3.7	8.5E-03	6.4	2.1E-04	-0.5	6.7E-01	-0.2	7.2E-01
ENSMUST00000075573	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	D3Z1I8		14.4	4.6E-08	-9.9	1.9E-05	-0.9	1.9E-02	0.3	7.9E-01
ENSMUST00000075578	ATP-binding cassette, sub-family B (MDR/TAP), member 10 [Source:MGI Symbol;Acc:MGI:1860508]		Q9JI39	1.4	1.8E-02	6.6	2.7E-04	-0.5	6.7E-01	-0.7	3.1E-01
ENSMUST00000073879	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]	A2AQ43		-1.0	6.7E-02	-0.3	7.1E-01	0.8	1.4E-01	0.0	9.7E-01
ENSMUST00000073884	neuregulin 1 [Source:MGI Symbol;Acc:MGI:96083]	Q6DR99		0.5	4.1E-01	1.1	1.5E-01	0.4	4.6E-01	-0.2	7.4E-01
ENSMUST00000073889	polymerase (DNA directed), gamma [Source:MGI Symbol;Acc:MGI:1196389]	Q75WC0		-1.6	1.1E-01	-0.9	5.4E-01	1.8	7.3E-02	1.1	4.0E-01
ENSMUST00000075606	EH domain binding protein 1-like 1 [Source:MGI Symbol;Acc:MGI:3612340]	G5E8Y6		-3.4	3.4E-04	4.2	4.1E-03	-2.4	7.9E-02	-0.9	2.5E-01
ENSMUST00000073899	synaptotagmin VII [Source:MGI Symbol;Acc:MGI:1859545]		Q9R0N7	7.5	9.2E-02	5.8	2.0E-01	-1.1	8.1E-01	0.5	8.4E-01
ENSMUST00000073909	DCP1 decapping enzyme homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2442404]		Q3U564	-2.3	4.7E-02	0.8	4.2E-01	0.9	2.6E-01	-2.3	6.7E-02
ENSMUST00000073924	RIKEN cDNA 2810021J22 gene [Source:MGI Symbol;Acc:MGI:1917194]	Q8BIB6		0.0	9.6E-01	0.3	6.8E-01	0.1	9.1E-01	-0.3	7.0E-01
ENSMUST00000075607	olfactory receptor 317 [Source:MGI Symbol;Acc:MGI:3030151]	Q5NCD6		4.6	1.1E-02	-11.7	2.2E-03	-0.7	3.2E-01	0.9	7.7E-01
ENSMUST00000075630	nthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9) [Source:MGI Symbol;Acc:MGI:19		P56383	-3.7	1.9E-02	6.4	2.5E-04	0.3	7.6E-01	0.5	4.1E-01
ENSMUST00000073939	endothelial-specific receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:98664]	Q80YS4		4.2	1.3E-01	3.7	3.2E-01	0.7	8.4E-01	1.2	5.9E-01
ENSMUST00000073942	cyclic nucleotide binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1918123]	A2AV95		-0.8	9.1E-02	-0.1	9.2E-01	0.7	9.7E-02	0.0	1.0E+00
ENSMUST00000075632	tetratricopeptide repeat domain 41 [Source:MGI Symbol;Acc:MGI:2387653]	F8VPV8		5.4	1.1E-05	-0.4	6.1E-01	-0.1	8.9E-01	-2.3	4.7E-02
ENSMUST00000075657	adaptor-related protein complex 3, sigma 2 subunit [Source:MGI Symbol;Acc:MGI:1337060]		Q8BSZ2	0.9	3.1E-02	5.9	3.3E-04	-0.6	6.2E-01	0.3	5.9E-01
ENSMUST00000075667	mitogen-activated protein kinase 1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1916796]		Q9D7G9	-6.2	2.2E-03	5.6	9.6E-04	-1.4	2.6E-01	0.4	5.4E-01
ENSMUST00000075671	tor of activated T cells, cytoplasmic, calcineurin dependent 2 interacting protein [Source:MGI Symbol;Acc:MG		O09130	1.9	2.4E-02	-1.5	6.4E-02	0.5	2.6E-01	0.6	3.8E-01
ENSMUST00000075686	2-aminoethanethiol (cysteamine) dioxygenase [Source:MGI Symbol;Acc:MGI:2685083]		Q6PDY2	1.6	2.2E-02	3.5	1.6E-02	-0.5	6.3E-01	-0.2	8.3E-01
ENSMUST00000075689	poly (ADP-ribose) polymerase family, member 10 [Source:MGI Symbol;Acc:MGI:3712326]	Q8CIE4		-5.1	2.5E-03	0.2	9.0E-01	1.0	3.2E-01	-2.2	1.4E-01
ENSMUST00000075693	Yip1 domain family, member 1 [Source:MGI Symbol;Acc:MGI:1915532]		Q91VU1	-8.8	1.4E-06	6.3	1.7E-04	-0.5	6.6E-01	-0.2	7.9E-01
ENSMUST00000074038	acid phosphatase 1, soluble [Source:MGI Symbol;Acc:MGI:87881]	Q561M1		-1.4	1.6E-01	-1.4	1.9E-01	-1.9	2.2E-02	-2.0	9.3E-02
ENSMUST00000074042	proline rich protein HaeIII subfamily 1 [Source:MGI Symbol;Acc:MGI:97773]	E9QMX6		3.0	8.8E-02	6.7	2.3E-03	-0.4	8.1E-01	-4.1	4.5E-03
ENSMUST00000075738	cytochrome c oxidase, subunit VIb polypeptide 1 [Source:MGI Symbol;Acc:MGI:107460]		P56391	-6.7	1.1E-05	-2.4	8.3E-03	0.5	2.6E-01	-0.5	5.6E-01
ENSMUST00000074046	engulfment and cell motility 2 [Source:MGI Symbol;Acc:MGI:2153045]		Q8BHL5	1.7	4.1E-01	4.4	4.3E-02	-0.6	7.5E-01	-3.3	7.9E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000075756	olfactory receptor 212 [Source:MGI Symbol;Acc:MGI:3030046]	Q7TS33		5.8	7.3E-05	-0.3	8.4E-01	-5.8	1.1E-02	-0.5	7.2E-01
ENSMUST00000075759	c-abl oncogene 1, non-receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:87859]	Q3SYK5	P00520	-7.3	1.9E-04	-8.3	1.1E-04	-0.6	1.6E-01	0.0	9.9E-01
ENSMUST00000075764	dopamine receptor D2 [Source:MGI Symbol;Acc:MGI:94924]		P61168	4.5	5.6E-04	-7.3	1.4E-05	0.5	1.6E-01	-2.2	7.5E-02
ENSMUST00000075767	FERM domain containing 4A [Source:MGI Symbol;Acc:MGI:1919850]		Q8BIE6	8.2	1.4E-05	-8.3	2.5E-04	-0.9	1.1E-01	0.9	5.6E-01
ENSMUST00000075770	multiple EGF-like-domains 10 [Source:MGI Symbol;Acc:MGI:2685177]		Q6DIB5	8.1	8.9E-06	8.6	1.5E-04	-0.7	6.5E-01	-0.2	8.2E-01
ENSMUST00000075774	tubulin, beta 2B class IIB [Source:MGI Symbol;Acc:MGI:1920960]	B2RSN3	Q9CWF2	5.6	2.8E-05	-6.7	2.1E-04	1.2	8.8E-03	-0.6	6.2E-01
ENSMUST00000075775	reduced expression 2 [Source:MGI Symbol;Acc:MGI:1328322]	A2AWF2		7.5	2.6E-05	-5.1	6.9E-03	-0.6	3.7E-01	-1.1	5.0E-01
ENSMUST00000074113	prominin 1 [Source:MGI Symbol;Acc:MGI:1100886]	G5E8G5		0.7	7.4E-01	1.5	5.9E-01	0.5	7.8E-01	-0.3	9.1E-01
ENSMUST00000075827	jagged 2 [Source:MGI Symbol;Acc:MGI:1098270]		Q9QYE5	5.5	1.7E-05	6.8	6.0E-04	-0.1	9.6E-01	-0.5	5.4E-01
ENSMUST00000075829	mitochondrial ribosomal protein L42 [Source:MGI Symbol;Acc:MGI:1333774]		Q9CPV3	-2.5	7.2E-03	-3.4	8.2E-04	0.6	9.7E-02	-1.1	1.7E-01
ENSMUST00000075838	APOBEC1 complementation factor [Source:MGI Symbol;Acc:MGI:1917115]		Q5YD48	6.9	3.3E-05	6.9	1.4E-04	-0.6	6.2E-01	-1.4	5.6E-02
ENSMUST00000075843	adhesion G protein-coupled receptor E5 [Source:MGI Symbol;Acc:MGI:1347095]	E9QJS7		-7.7	8.8E-05	6.7	1.3E-04	-0.6	6.2E-01	-1.4	4.9E-02
ENSMUST00000074144	DDB1 and CUL4 associated factor 8 [Source:MGI Symbol;Acc:MGI:91860]		Q8N7N5	-0.9	2.4E-01	-0.8	3.9E-01	0.2	7.6E-01	0.2	8.7E-01
ENSMUST00000075844	olfactory receptor 1371 [Source:MGI Symbol;Acc:MGI:3031205]	Q7TQT7		6.5	8.5E-03	7.8	3.8E-05	-0.5	6.6E-01	-0.5	3.5E-01
ENSMUST00000075845	Rho GTPase activating protein 35 [Source:MGI Symbol;Acc:MGI:1929494]	B2RTN5	Q91YM2	4.6	1.3E-05	2.4	1.1E-02	-1.4	6.0E-02	-0.3	6.1E-01
ENSMUST00000074157	myosin VB [Source:MGI Symbol;Acc:MGI:106598]	G5E8G6		4.4	1.1E-01	4.9	1.1E-01	-0.3	9.1E-01	-0.9	6.2E-01
ENSMUST00000075851	olfactory receptor 282 [Source:MGI Symbol;Acc:MGI:3030116]	A1L1B4		6.7	8.2E-05	2.4	1.1E-01	-0.6	6.1E-01	5.7	4.0E-04
ENSMUST00000075853	CDC28 protein kinase regulatory subunit 2 [Source:MGI Symbol;Acc:MGI:1913447]	Q545R9	P56390	-2.6	7.9E-04	-2.8	1.4E-03	0.0	9.5E-01	-1.2	1.0E-01
ENSMUST00000074204	solute carrier family 6 (neurotransmitter transporter), member 15 [Source:MGI Symbol;Acc:MGI:2143484]		Q8BG16	3.1	2.7E-01	3.9	2.2E-01	-0.4	8.9E-01	-1.2	5.7E-01
ENSMUST00000075856	lysine (K)-specific demethylase 2A [Source:MGI Symbol;Acc:MGI:1354736]	F6YRW4		-9.8	2.5E-05	-2.3	7.6E-03	-6.2	1.9E-05	-0.3	6.4E-01
ENSMUST00000074208	DH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3 [Source:MGI Symbol;Acc:MGI:19139		Q9JKL4	-1.2	6.9E-02	-0.8	2.8E-01	-0.2	6.9E-01	-0.6	4.0E-01
ENSMUST00000075869	F-box protein 40 [Source:MGI Symbol;Acc:MGI:2443753]	Q3KN92	P62932	6.1	1.5E-04	6.6	1.9E-04	-0.6	5.7E-01	-0.5	4.5E-01
ENSMUST00000075872	myb-like, SWIRM and MPN domains 1 [Source:MGI Symbol;Acc:MGI:2444584]		Q69Z66	-5.6	2.7E-04	3.9	2.7E-03	-0.1	9.2E-01	-0.7	3.8E-01
ENSMUST00000075884	mesothelin [Source:MGI Symbol;Acc:MGI:1888992]		Q61468	7.8	1.0E-05	6.9	1.6E-04	-2.7	7.1E-02	0.7	2.7E-01
ENSMUST00000075888	zinc finger protein of the cerebellum 2 [Source:MGI Symbol;Acc:MGI:106679]	F8VPV3		7.2	1.9E-04	3.5	1.2E-02	0.3	8.0E-01	-0.4	6.3E-01
ENSMUST00000075895	peroxisomal biogenesis factor 19 [Source:MGI Symbol;Acc:MGI:1334458]		Q8VCI5	-5.8	2.5E-04	-6.0	3.5E-06	-1.0	3.3E-03	-0.6	3.2E-01
ENSMUST00000075916	zinc finger protein 12 [Source:MGI Symbol;Acc:MGI:99157]	M0QWS1		6.6	5.3E-03	-3.6	7.3E-02	-0.5	6.1E-01	-0.7	7.1E-01
ENSMUST00000075934	pregnancy-specific glycoprotein 29 [Source:MGI Symbol;Acc:MGI:1891361]	Q3URN6		6.0	1.6E-05	-2.9	1.6E-02	0.8	1.7E-01	-0.8	4.5E-01
ENSMUST00000075941	protein phosphatase 2, regulatory subunit B", alpha [Source:MGI Symbol;Acc:MGI:2442104]	B2RXC8		3.9	1.4E-03	-1.1	2.0E-01	1.0	7.5E-02	-0.5	5.2E-01
ENSMUST00000075946	ELL associated factor 2 [Source:MGI Symbol;Acc:MGI:2146616]		Q91ZD6	5.7	1.8E-06	4.8	2.1E-05	-0.9	1.5E-01	-0.9	4.0E-02
ENSMUST00000075953	TD and POZ domain containing 4 [Source:MGI Symbol;Acc:MGI:3027904]		Q6YCH2	5.9	1.4E-03	-6.0	1.5E-03	-1.6	3.0E-02	-0.9	5.3E-01
ENSMUST00000075954	ATA box binding protein (Tbp)-associated factor, RNA polymerase I, B [Source:MGI Symbol;Acc:MGI:10957		P97358	-2.2	7.6E-03	5.1	3.8E-03	-2.2	1.5E-01	0.1	9.4E-01
ENSMUST00000075992	protein kinase inhibitor beta, cAMP dependent, testis specific [Source:MGI Symbol;Acc:MGI:101937]	Q3TZU5		5.5	4.5E-05	6.7	1.0E-03	-0.6	7.1E-01	-3.2	8.6E-03
ENSMUST00000074300				3.2	1.0E-01	0.0	9.9E-01	-0.8	6.8E-01	2.5	2.9E-01
ENSMUST00000075994	PDZ domain containing RING finger 3 [Source:MGI Symbol;Acc:MGI:1933157]		Q69ZS0	9.5	9.8E-06	7.7	8.2E-04	-0.8	6.5E-01	-0.5	5.8E-01
ENSMUST00000075995	cullin-associated and neddylation-dissociated 2 (putative) [Source:MGI Symbol;Acc:MGI:1914338]		Q6ZQ73	6.8	1.4E-06	7.0	8.2E-05	-0.6	5.9E-01	-1.2	5.9E-02
ENSMUST00000076022	exosome component 10 [Source:MGI Symbol;Acc:MGI:1355322]	Q8K366		7.1	1.4E-02	-1.9	5.4E-02	1.4	2.2E-02	-1.0	3.0E-01
ENSMUST00000076038	contactin associated protein-like 5C [Source:MGI Symbol;Acc:MGI:3646013]		Q0V8T7	6.8	5.3E-05	6.2	5.5E-04	-0.2	8.9E-01	0.2	7.6E-01
ENSMUST00000076043	ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A [Source:MGI Symbol;Acc:MGI		O35464	9.3	4.0E-05	4.0	6.8E-02	-1.1	6.0E-01	-0.2	8.7E-01
ENSMUST00000076070	zinc finger CCHC-type and RNA binding motif 1 [Source:MGI Symbol;Acc:MGI:1914447]		Q9CZ96	-6.7	2.4E-05	-2.7	6.8E-02	0.8	2.9E-01	0.4	7.9E-01
ENSMUST00000076091	cardiotrophin 2 [Source:MGI Symbol;Acc:MGI:2684607]	Q0VB69	P83714	4.4	5.0E-05	-0.4	5.8E-01	0.7	2.0E-01	-0.4	5.8E-01
ENSMUST00000076099	spermatogenesis associated glutamate (E)-rich protein 4F1 [Source:MGI Symbol;Acc:MGI:1918185]	Q9D5Q6		6.2	1.7E-04	4.0	6.4E-02	-0.6	7.7E-01	3.5	1.8E-02
ENSMUST00000076110	ring finger protein 2 [Source:MGI Symbol;Acc:MGI:1101759]		Q9CQJ4	-6.7	8.6E-06	1.6	9.9E-02	-5.5	1.0E-03	0.1	8.9E-01
ENSMUST00000076124	serine/arginine repetitive matrix 4 [Source:MGI Symbol;Acc:MGI:1916205]	J9QHX6	Q8BKA3	9.4	2.1E-04	2.4	8.3E-02	-0.6	6.0E-01	3.7	3.5E-03
ENSMUST00000076147	atypical chemokine receptor 4 [Source:MGI Symbol;Acc:MGI:2181676]		Q924I3	8.0	5.7E-05	6.9	6.8E-04	-0.6	6.9E-01	-1.0	2.4E-01
ENSMUST00000074408	interferon lambda receptor 1 [Source:MGI Symbol;Acc:MGI:2429859]	Q3URN4	Q8CGK5	-0.6	3.2E-01	0.2	8.4E-01	1.2	6.4E-02	0.5	5.5E-01
ENSMUST00000076155	enolase 1B, retrotransposed [Source:MGI Symbol;Acc:MGI:3648653]	Q5FW97	P17182	-5.9	3.1E-07	6.6	3.2E-04	-0.6	6.2E-01	-0.3	6.5E-01
ENSMUST00000076169	metaxin 3 [Source:MGI Symbol;Acc:MGI:2686040]	D3YTP3		5.5	3.7E-04	-1.1	2.5E-01	1.3	4.2E-02	0.3	7.1E-01
ENSMUST00000074449	small proline-rich protein 2A1 [Source:MGI Symbol;Acc:MGI:1330350]		Q4KL71	3.0	1.4E-01	2.8	1.9E-01	-0.4	8.3E-01	-0.3	8.7E-01
ENSMUST00000076183	ring finger protein 207 [Source:MGI Symbol;Acc:MGI:2684989]		Q3V3A7	6.6	2.5E-04	4.4	1.9E-04	0.2	7.9E-01	0.2	7.2E-01
ENSMUST00000076195	zinc finger protein 935 [Source:MGI Symbol;Acc:MGI:1918758]	Q14DI0		-2.4	1.2E-03	-3.0	1.6E-02	0.6	2.6E-01	-2.4	7.3E-02
ENSMUST00000076212	ankyrin repeat and BTB (POZ) domain containing 2 [Source:MGI Symbol;Acc:MGI:2139365]	Q3T9J9	Q7TQI7	-2.5	6.0E-04	7.0	2.3E-04	-1.2	3.9E-01	-0.6	3.2E-01
ENSMUST00000076224	solute carrier family 45, member 4 [Source:MGI Symbol;Acc:MGI:2146236]		Q0P5V9	-6.7	5.6E-03	2.6	1.0E-03	0.3	4.8E-01	0.0	9.5E-01
ENSMUST00000074515	ring finger and FYVE like domain containing protein [Source:MGI Symbol;Acc:MGI:1914588]	Q3UD78	Q6ZQM0	-3.1	1.1E-01	-3.1	3.1E-01	0.7	6.3E-01	0.7	8.1E-01
ENSMUST00000076236	leucine rich repeat containing 16B [Source:MGI Symbol;Acc:MGI:2448573]		Q3UFQ8	8.0	2.5E-05	-6.3	3.3E-05	0.1	7.8E-01	-4.4	3.4E-03
ENSMUST00000076249	interferon-induced protein with tetratricopeptide repeats 3B [Source:MGI Symbol;Acc:MGI:3698419]	E9PV48		3.5	1.0E-02	5.6	9.2E-03	-0.7	7.1E-01	-0.7	4.9E-01
ENSMUST00000076251	zinc finger protein 865 [Source:MGI Symbol;Acc:MGI:2442656]		Q3U3I9	-1.7	9.8E-03	4.2	1.1E-02	-0.2	8.9E-01	2.1	3.9E-02
ENSMUST00000074541	JAZF zinc finger 1 [Source:MGI Symbol;Acc:MGI:2141450]		Q80ZQ5	0.6	7.8E-01	2.0	4.8E-01	0.5	8.2E-01	-0.9	7.1E-01
ENSMUST00000076258	protein phosphatase 1M [Source:MGI Symbol;Acc:MGI:1915155]	F8WGF9		-2.1	3.0E-03	5.7	1.5E-03	-1.5	3.2E-01	-1.4	1.1E-01
ENSMUST00000076265	UPF3 regulator of nonsense transcripts homolog B (yeast) [Source:MGI Symbol;Acc:MGI:1915384]	Q3ULL6		-3.2	1.5E-03	6.9	4.0E-03	-0.6	7.5E-01	-0.8	4.5E-01
ENSMUST00000076270	rabaptin, RAB GTPase binding effector protein 1 [Source:MGI Symbol;Acc:MGI:1860236]		O35551	-2.1	2.0E-02	-6.4	2.9E-02	0.9	3.1E-01	2.9	2.6E-01
ENSMUST00000076272	ATP-binding cassette, sub-family A (ABC1), member 15 [Source:MGI Symbol;Acc:MGI:2388709]	Q6XBG2		5.9	2.3E-04	5.7	8.4E-04	-0.5	6.8E-01	-0.2	7.4E-01
ENSMUST00000076306	protein kinase, AMP-activated, gamma 2 non-catalytic subunit [Source:MGI Symbol;Acc:MGI:1336153]	Q8BIQ9		5.5	2.2E-03	-2.6	1.2E-03	0.3	3.6E-01	-0.1	8.5E-01
ENSMUST00000074557	histocompatibility 2, class II antigen E beta [Source:MGI Symbol;Acc:MGI:95901]	O78196		-1.8	5.0E-02	-4.7	1.2E-03	-2.5	1.3E-03	0.4	7.3E-01
ENSMUST00000076313	PRP40 pre-mRNA processing factor 40 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1860512]		Q9R1C7	-3.7	1.5E-05	4.0	7.7E-03	-0.1	9.4E-01	0.6	5.4E-01
ENSMUST00000076316	Rho GTPase activating protein 10 [Source:MGI Symbol;Acc:MGI:1925764]		Q6Y5D8	1.1	3.2E-02	-3.2	9.4E-03	0.3	5.9E-01	-0.8	4.8E-01
ENSMUST00000074582	a disintegrin and metallopeptidase domain 15 (metargidin) [Source:MGI Symbol;Acc:MGI:1333882]		O88839	0.2	9.4E-01	-0.6	8.8E-01	-1.1	6.2E-01	-0.3	9.3E-01
ENSMUST00000076326	cDNA sequence AB124611 [Source:MGI Symbol;Acc:MGI:3043001]	G8JL59		-3.6	2.6E-02	-5.2	1.7E-02	0.2	8.4E-01	0.7	6.9E-01
ENSMUST00000076331	olfactory receptor 127 [Source:MGI Symbol;Acc:MGI:2177510]	Q8VF25		6.1	2.4E-04	4.9	2.3E-03	-2.0	1.6E-01	-0.9	2.9E-01
ENSMUST00000074613	acylphosphatase 2, muscle type [Source:MGI Symbol;Acc:MGI:1922822]		P56375	-0.1	8.8E-01	0.2	8.3E-01	-1.5	5.4E-02	-1.8	4.5E-02
ENSMUST00000074616	splicing regulatory glutamine/lysine-rich protein 1 [Source:MGI Symbol;Acc:MGI:2145245]		Q8BZX4	0.6	3.6E-01	0.0	9.9E-01	0.0	9.4E-01	0.7	4.3E-01
ENSMUST00000074618	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 [Source:MGI Symbol;Acc:MGI:102463		Q60591	-1.6	2.0E-01	2.6	1.4E-01	3.3	2.8E-02	-0.8	5.5E-01
ENSMUST00000076352	serine (or cysteine) peptidase inhibitor, clade B, member 1a [Source:MGI Symbol;Acc:MGI:1913472]		Q9D154	-11.3	1.9E-05	6.4	7.9E-04	-0.5	7.5E-01	-0.8	3.0E-01
ENSMUST00000076364	ribosomal protein L10, pseudogene 3 [Source:MGI Symbol;Acc:MGI:3704336]		Q6ZWV3	-7.7	5.0E-04	-3.2	1.2E-02	1.4	2.5E-02	-0.9	4.0E-01
ENSMUST00000076372	splicing factor 3b, subunit 4 [Source:MGI Symbol;Acc:MGI:109580]		Q8QZY9	-3.2	8.6E-04	8.2	7.0E-06	0.4	6.1E-01	0.5	3.0E-01
ENSMUST00000076373	predicted pseudogene 8730 [Source:MGI Symbol;Acc:MGI:3644565]	E9Q070		-6.0	9.0E-06	-0.9	9.5E-02	0.5	1.7E-01	-0.1	8.9E-01
ENSMUST00000076383	F-box and WD-40 domain protein 11 [Source:MGI Symbol;Acc:MGI:2144023]		Q5SRY7	4.5	2.7E-02	4.6	7.0E-02	0.1	9.5E-01	2.1	1.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000076384	carboxylesterase 2F [Source:MGI Symbol;Acc:MGI:1919153]	Q08ED5		7.5	7.9E-05	6.0	3.3E-03	-1.4	4.2E-01	-1.2	2.2E-01
ENSMUST00000076393	olfactory receptor 314 [Source:MGI Symbol;Acc:MGI:3030148]	Q7TRZ7		7.1	6.1E-05	-1.4	1.0E-01	0.6	2.6E-01	-1.1	2.0E-01
ENSMUST00000074680				1.9	1.5E-01	2.5	1.2E-01	-0.6	6.8E-01	-1.1	3.3E-01
ENSMUST00000074686	family with sequence similarity 160, member A2 [Source:MGI Symbol;Acc:MGI:1921599]	F8WHJ1		-4.2	5.1E-02	-0.1	9.5E-01	0.2	8.8E-01	-3.9	8.5E-02
ENSMUST00000076431	peptidase (mitochondrial processing) alpha [Source:MGI Symbol;Acc:MGI:1918568]		Q9DC61	-3.6	1.9E-04	-3.3	3.5E-02	1.4	6.1E-02	-0.3	8.4E-01
ENSMUST00000076443	gamma-glutamyltransferase 6 [Source:MGI Symbol;Acc:MGI:1918772]		Q6PDE7	6.8	5.9E-03	4.5	8.2E-04	-2.1	7.2E-02	0.2	7.3E-01
ENSMUST00000076470	NLR family, pyrin domain containing 4E [Source:MGI Symbol;Acc:MGI:3056600]		Q66X19	7.8	1.3E-05	5.9	1.2E-02	-0.6	7.9E-01	-1.1	3.4E-01
ENSMUST00000076493	solute carrier family 22 (organic cation transporter), member 21 [Source:MGI Symbol;Acc:MGI:1929481]	A2RSK7	Q9WTN6	4.3	8.6E-05	6.0	6.8E-04	-0.5	6.9E-01	-0.9	2.2E-01
ENSMUST00000074729	diacylglycerol kinase, eta [Source:MGI Symbol;Acc:MGI:2444188]	D3YXJ0		0.2	6.7E-01	1.3	5.7E-02	1.0	5.9E-02	-0.1	8.3E-01
ENSMUST00000076500	spermatogenesis associated glutamate (E)-rich protein 2 [Source:MGI Symbol;Acc:MGI:2668488]	E9Q9U2		5.7	6.5E-04	0.9	7.3E-02	-0.5	1.9E-01	-0.3	4.2E-01
ENSMUST00000076501	ubiquitin specific peptidase 17-like B [Source:MGI Symbol;Acc:MGI:3051498]	E9Q9U0		5.7	3.4E-02	2.8	6.4E-02	-2.1	1.8E-01	0.3	8.0E-01
ENSMUST00000074758	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Source:MGI Symbol;Acc:MGI:95653]			2.3	1.5E-01	3.7	9.4E-02	0.3	8.6E-01	-1.1	4.4E-01
ENSMUST00000076505	pyridine nucleotide-disulphide oxidoreductase domain 2 [Source:MGI Symbol;Acc:MGI:1921830]		Q3U4I7	1.8	2.5E-02	6.2	6.4E-05	-1.7	9.6E-02	0.5	3.3E-01
ENSMUST00000074770	transient receptor potential cation channel, subfamily M, member 3 [Source:MGI Symbol;Acc:MGI:2443101]	Q5F4S8		4.1	7.3E-02	4.3	6.6E-02	-1.4	5.3E-01	-1.6	3.2E-01
ENSMUST00000076514	olfactory receptor 51 [Source:MGI Symbol;Acc:MGI:1333747]	Q8VGG9		6.1	3.2E-04	8.3	7.7E-05	-0.5	7.4E-01	-0.7	2.5E-01
ENSMUST00000076521	interferon regulatory factor 6 [Source:MGI Symbol;Acc:MGI:1859211]		P97431	5.5	7.8E-05	2.2	4.3E-03	0.0	9.6E-01	0.1	8.6E-01
ENSMUST00000076532	serine (or cysteine) peptidase inhibitor, clade B, member 6a [Source:MGI Symbol;Acc:MGI:103123]	Q4FJQ6	Q60854	-5.5	3.5E-04	5.3	9.4E-04	-2.0	1.4E-01	-2.2	1.3E-02
ENSMUST00000076541	CDK5 regulatory subunit associated protein 2 [Source:MGI Symbol;Acc:MGI:2384875]	H7BX43		-4.0	3.5E-04	-7.9	1.5E-05	-0.3	4.0E-01	-3.6	1.7E-02
ENSMUST00000076587	protein tyrosine phosphatase 4a1 [Source:MGI Symbol;Acc:MGI:1277096]	B9EKL6	Q63739	-4.8	5.4E-04	-4.2	3.7E-03	0.5	4.2E-01	-0.9	4.5E-01
ENSMUST00000076592	coiled-coil domain containing 36 [Source:MGI Symbol;Acc:MGI:3612242]		Q6PDM4	5.8	1.4E-04	4.9	1.6E-04	-1.7	7.8E-02	-0.2	6.9E-01
ENSMUST00000074813	zinc finger protein 616 [Source:MGI Symbol;Acc:MGI:3650906]	A7DTG8		3.9	1.0E-01	4.5	9.5E-02	-0.2	9.3E-01	-0.8	6.0E-01
ENSMUST00000076599	adaptor-related protein complex AP-4, beta 1 [Source:MGI Symbol;Acc:MGI:1337130]		Q9WV76	-5.1	1.1E-03	5.7	8.1E-05	0.0	9.8E-01	-0.6	3.0E-01
ENSMUST00000074834	plectin [Source:MGI Symbol;Acc:MGI:1277961]		Q9QXS1	-3.0	1.1E-01	4.8	5.6E-02	4.7	4.1E-02	-3.1	1.1E-01
ENSMUST00000076617	F-box and WD-40 domain protein 19 [Source:MGI Symbol;Acc:MGI:3505706]	Q8C2W8		6.8	6.2E-05	-3.7	3.9E-03	-1.0	6.2E-02	1.2	2.4E-01
ENSMUST00000076622	stathmin domain containing 1 [Source:MGI Symbol;Acc:MGI:2686420]		Q6P3A1	6.0	6.1E-04	-7.7	5.9E-03	0.5	4.8E-01	1.2	6.0E-01
ENSMUST00000074846	heat shock 105kDa/110kDa protein 1 [Source:MGI Symbol;Acc:MGI:105053]		Q61699	-1.1	3.9E-01	2.5	1.7E-01	1.6	3.3E-01	-2.1	1.4E-01
ENSMUST00000074849	transforming, acidic coiled-coil containing protein 3 [Source:MGI Symbol;Acc:MGI:1341163]	Q99LH8		0.5	7.8E-01	-2.1	3.5E-01	-1.5	3.1E-01	1.1	6.2E-01
ENSMUST00000076623	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2 [Source:MGI Symbol;Acc:MGI:2684416]	E9QP44		1.9	4.7E-03	-1.7	1.4E-02	0.9	3.3E-02	-4.6	3.9E-04
ENSMUST00000076648	Fc fragment of IgG binding protein [Source:MGI Symbol;Acc:MGI:2444336]	E9Q9C6		8.0	5.4E-05	6.1	9.8E-04	-0.6	6.9E-01	-0.7	3.5E-01
ENSMUST00000074863				0.4	8.5E-01	-3.7	4.2E-02	-6.3	2.0E-03	-2.2	2.9E-01
ENSMUST00000076657	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 [Source:MGI Symbol;Acc:MGI:1913341]		Q9CQ91	-8.0	2.1E-05	5.6	1.4E-03	-0.5	7.2E-01	-0.1	9.4E-01
ENSMUST00000074876	zinc finger protein 420 [Source:MGI Symbol;Acc:MGI:2444666]	Q7TMN8		-1.0	6.4E-01	1.2	6.1E-01	0.3	9.0E-01	-1.9	3.7E-01
ENSMUST00000076664	zinc finger protein 53 [Source:MGI Symbol;Acc:MGI:99200]	Q9Z117		-2.3	2.3E-02	-8.3	3.4E-06	0.3	3.5E-01	-0.6	4.6E-01
ENSMUST00000076670	lipid phosphate phosphatase-related protein type 1 [Source:MGI Symbol;Acc:MGI:2445015]		Q8BFZ2	7.7	3.7E-05	1.3	3.7E-02	-0.3	5.1E-01	-0.1	9.0E-01
ENSMUST00000076675	olfactory receptor 403 [Source:MGI Symbol;Acc:MGI:3030237]	Q7TRX2		6.6	1.7E-04	-4.1	2.4E-02	1.2	1.7E-01	-1.7	3.5E-01
ENSMUST00000076700	IKAROS family zinc finger 1 [Source:MGI Symbol;Acc:MGI:1342540]	G5E8H3		-4.5	4.0E-04	-2.8	1.3E-02	1.0	6.6E-02	-0.3	7.7E-01
ENSMUST00000076713	WNT1 inducible signaling pathway protein 3 [Source:MGI Symbol;Acc:MGI:2685581]		D3Z5L9	3.1	5.4E-04	-1.8	2.6E-02	-0.2	5.8E-01	-0.6	4.1E-01
ENSMUST00000076730	predicted gene 1123 [Source:MGI Symbol;Acc:MGI:2685969]	Q1RME4		3.5	5.6E-04	-0.3	5.2E-01	0.7	8.1E-02	-5.0	1.2E-04
ENSMUST00000076734	SR-related CTD-associated factor 8 [Source:MGI Symbol;Acc:MGI:1925212]		Q6DID3	-2.2	3.0E-03	4.9	2.7E-02	-0.6	7.6E-01	-0.8	5.2E-01
ENSMUST00000076737	desmoglein 1 beta [Source:MGI Symbol;Acc:MGI:2664357]	B2RQH0	Q7TSF1	8.5	7.7E-06	-2.1	7.0E-02	0.4	5.7E-01	-0.8	4.9E-01
ENSMUST00000076791	RIKEN cDNA 4632433K11 gene [Source:MGI Symbol;Acc:MGI:1924293]	Q9D656		4.5	7.4E-04	-6.3	2.9E-04	-0.4	3.6E-01	-2.0	1.7E-01
ENSMUST00000076803	autophagy related 13 [Source:MGI Symbol;Acc:MGI:1196429]		Q91YI1	-4.9	3.0E-03	-4.7	9.4E-03	1.0	1.2E-01	-0.7	6.7E-01
ENSMUST00000076813	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914982]		Q9DB29	-3.5	2.7E-03	-0.8	5.5E-01	1.4	1.4E-01	-3.2	5.7E-02
ENSMUST00000074989	B cell CLL/lymphoma 9-like [Source:MGI Symbol;Acc:MGI:1933114]		Q67FY2	1.2	8.6E-02	1.5	1.2E-01	0.4	5.4E-01	0.2	8.2E-01
ENSMUST00000076831	CDC42 effector protein (Rho GTPase binding) 5 [Source:MGI Symbol;Acc:MGI:1929745]		Q9Z0X0	3.7	2.0E-03	-7.6	6.0E-03	0.0	9.5E-01	0.0	9.9E-01
ENSMUST00000076840	ephrin A5 [Source:MGI Symbol;Acc:MGI:107444]		O08543	7.7	1.0E-04	-3.9	4.4E-02	-0.3	7.3E-01	0.5	7.9E-01
ENSMUST00000076846	interleukin 34 [Source:MGI Symbol;Acc:MGI:1923777]		Q8R1R4	5.9	2.3E-02	-4.5	3.7E-03	1.2	4.3E-02	0.8	5.4E-01
ENSMUST00000076887	radial spoke head 6 homolog A (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1927643]	Q99MM9		6.9	1.3E-04	6.4	2.0E-04	-0.6	5.8E-01	-0.6	3.2E-01
ENSMUST00000075036	unc-13 homolog D (C. elegans) [Source:MGI Symbol;Acc:MGI:1917700]		B2RUP2	0.4	9.1E-01	-1.6	7.5E-01	-2.0	5.2E-01	0.1	9.9E-01
ENSMUST00000076889	guanine nucleotide binding protein (G protein), beta 5 [Source:MGI Symbol;Acc:MGI:101848]		P62881	-1.6	9.8E-03	1.9	3.0E-03	0.0	9.4E-01	0.0	9.1E-01
ENSMUST00000076891	zinc finger, DHHC domain containing 6 [Source:MGI Symbol;Acc:MGI:1914230]		Q9CPV7	-2.4	3.0E-04	-5.4	2.9E-04	-0.6	1.7E-01	-0.9	3.8E-01
ENSMUST00000076894	ring finger and WD repeat domain 2 [Source:MGI Symbol;Acc:MGI:1347046]		Q9R1A8	-3.9	1.3E-03	-1.9	1.5E-02	-1.3	9.9E-03	-1.3	8.3E-02
ENSMUST00000076896	CDC28 protein kinase 1b, retrogene [Source:MGI Symbol;Acc:MGI:3643620]	Q3UNC9		6.6	1.7E-04	6.9	2.0E-04	-0.5	6.9E-01	-0.2	7.4E-01
ENSMUST00000076922	tripartite motif-containing 30A [Source:MGI Symbol;Acc:MGI:98178]		P15533	-6.2	1.3E-05	-4.7	6.8E-04	-0.6	1.8E-01	-1.0	3.4E-01
ENSMUST00000076939	C1q and tumor necrosis factor related protein 7 [Source:MGI Symbol;Acc:MGI:1925911]	E9PVG1		9.3	6.8E-06	4.0	1.7E-02	0.9	4.7E-01	-0.5	5.9E-01
ENSMUST00000076942	ankyrin repeat domain 33B [Source:MGI Symbol;Acc:MGI:1917904]		Q3U0L2	-2.5	1.0E-03	7.5	9.9E-04	0.0	9.9E-01	1.4	1.4E-01
ENSMUST00000076949	GPN-loop GTPase 1 [Source:MGI Symbol;Acc:MGI:1921504]	Q4VAB2	Q8VCE2	2.4	8.9E-04	1.7	2.5E-01	9.0	1.9E-05	-1.0	4.3E-01
ENSMUST00000076957	zinc finger, DHHC domain containing 8 [Source:MGI Symbol;Acc:MGI:1338012]		Q5Y5T5	3.1	2.1E-03	5.5	1.5E-03	-0.6	6.5E-01	-0.4	5.7E-01
ENSMUST00000076958	olfactory receptor 715 [Source:MGI Symbol;Acc:MGI:3030549]	Q8VG49		5.8	1.9E-04	6.5	1.8E-03	-0.4	7.8E-01	1.3	1.4E-01
ENSMUST00000076961	Rab acceptor 1 (prenylated) [Source:MGI Symbol;Acc:MGI:1201692]		Q9Z0S9	-5.7	1.4E-04	-4.2	2.1E-03	-0.8	1.3E-01	-0.1	9.1E-01
ENSMUST00000076965	olfactory receptor 319 [Source:MGI Symbol;Acc:MGI:3030153]	L7MTY4		6.7	5.1E-04	6.3	2.6E-04	-0.5	6.8E-01	-0.4	5.2E-01
ENSMUST00000076989	spermatogenesis and oogenesis specific basic helix-loop-helix 1 [Source:MGI Symbol;Acc:MGI:2684956]		Q6IUP1	6.5	2.6E-03	6.3	8.9E-04	-0.5	7.4E-01	-1.5	9.0E-02
ENSMUST00000075117	ZXD family zinc finger C [Source:MGI Symbol;Acc:MGI:1933108]		Q8C8V1	-0.1	9.0E-01	0.7	4.3E-01	1.2	8.2E-02	0.5	5.5E-01
ENSMUST00000075118	smoothelin [Source:MGI Symbol;Acc:MGI:1354727]		Q921U8	2.1	1.0E-01	-1.1	4.9E-01	-1.0	4.0E-01	2.2	1.7E-01
ENSMUST00000076997	UDP-glucuronate decarboxylase 1 [Source:MGI Symbol;Acc:MGI:1915133]	G5E8H4		-5.0	4.8E-04	5.8	6.6E-04	-1.5	2.6E-01	1.1	1.3E-01
ENSMUST00000077037	poly(rC) binding protein 2 [Source:MGI Symbol;Acc:MGI:108202]		Q61990	-6.6	1.2E-03	2.6	1.2E-01	0.3	8.5E-01	4.7	2.7E-03
ENSMUST00000075144	neuropilin 2 [Source:MGI Symbol;Acc:MGI:1100492]		O35375	2.0	2.0E-01	5.3	1.1E-02	0.1	9.7E-01	-3.3	2.5E-02
ENSMUST00000077066	transmembrane protein 151A [Source:MGI Symbol;Acc:MGI:2147713]		Q6GQT5	7.4	4.6E-06	4.9	6.4E-02	0.3	8.8E-01	0.7	6.8E-01
ENSMUST00000077078	ring finger protein 185 [Source:MGI Symbol;Acc:MGI:1922078]		Q91YT2	-5.2	2.8E-03	4.6	9.9E-03	-0.5	7.3E-01	-0.3	8.0E-01
ENSMUST00000075159	circadian locomotor output cycles kaput [Source:MGI Symbol;Acc:MGI:99698]		O08785	-0.7	1.5E-01	-0.9	1.3E-01	0.1	8.9E-01	0.3	5.6E-01
ENSMUST00000077093	KRAB-A domain containing 1 [Source:MGI Symbol;Acc:MGI:1925077]	D3Z4B8		7.7	4.5E-05	0.2	8.1E-01	-4.5	1.3E-04	0.0	9.4E-01
ENSMUST00000077119	gap junction protein, gamma 3 [Source:MGI Symbol;Acc:MGI:2153041]		Q921C1	8.4	2.5E-06	-2.2	1.2E-01	1.2	1.6E-01	-1.2	4.3E-01
ENSMUST00000077142	RIKEN cDNA C230062I16 gene [Source:MGI Symbol;Acc:MGI:2442417]	F7D818		6.8	9.8E-05	-5.8	1.4E-03	-0.5	3.0E-01	0.7	6.0E-01
ENSMUST00000077143	olfactory receptor 1383 [Source:MGI Symbol;Acc:MGI:3031217]	Q7TQT2		6.3	1.3E-03	6.2	1.6E-04	-0.6	5.9E-01	-0.7	2.3E-01
ENSMUST00000077146	desmoglein 1 alpha [Source:MGI Symbol;Acc:MGI:94930]		Q61495	7.9	1.5E-05	-1.0	1.3E-01	0.2	5.3E-01	0.0	9.7E-01
ENSMUST00000075180	brain-specific angiogenesis inhibitor 1-associated protein 2 [Source:MGI Symbol;Acc:MGI:2137336]	Q3UKP6	Q8BKX1	-1.4	3.3E-01	2.2	2.9E-01	3.8	2.5E-02	0.2	9.0E-01
ENSMUST00000075181	nology domain containing, family A (phosphoinositide binding specific) member 1 [Source:MGI Symbol;Acc:M		Q8BUL6	1.3	3.5E-01	1.0	5.6E-01	-0.6	6.3E-01	-0.3	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000077159	tubule associated monooxygenase, calponin and LIM domain containing 3 [Source:MGI Symbol;Acc:MGI:244		Q8CJ19	4.6	1.1E-04	2.6	1.0E-02	-3.4	3.9E-03	-0.5	4.3E-01
ENSMUST00000077173	developmental pluripotency associated 1 [Source:MGI Symbol;Acc:MGI:2157522]	Q810Y7		5.7	2.7E-04	-4.9	4.0E-04	1.4	8.6E-03	-1.2	2.4E-01
ENSMUST00000075220	chromodomain protein, Y chromosome-like [Source:MGI Symbol;Acc:MGI:1339956]		Q9WTK2	-0.8	1.2E-01	0.8	2.2E-01	0.8	1.0E-01	-0.8	2.0E-01
ENSMUST00000077182	neurexin II [Source:MGI Symbol;Acc:MGI:1096362]	E9Q5N7		6.7	6.4E-03	-2.2	8.9E-02	0.6	4.3E-01	-0.5	7.1E-01
ENSMUST00000077191	ethylmalonic encephalopathy 1 [Source:MGI Symbol;Acc:MGI:1913321]		Q9DCM0	-4.0	3.3E-04	-4.8	5.6E-05	-1.4	3.1E-03	0.1	8.6E-01
ENSMUST00000077194	transmembrane phosphatase with tensin homology [Source:MGI Symbol;Acc:MGI:2446460]	G5E8H5		5.9	2.4E-04	5.6	5.2E-04	-0.5	6.4E-01	1.5	3.5E-02
ENSMUST00000075249	in homology domain containing, family G (with RhoGef domain) member 3 [Source:MGI Symbol;Acc:MGI:2		Q4VAC9	0.2	6.7E-01	0.5	5.6E-01	1.1	1.1E-01	0.8	2.7E-01
ENSMUST00000077200	p21 protein (Cdc42/Rac)-activated kinase 7 [Source:MGI Symbol;Acc:MGI:1920334]		Q8C015	7.7	8.4E-05	-2.1	5.4E-02	0.8	1.7E-01	1.1	2.5E-01
ENSMUST00000077220	GTP binding protein 6 (putative) [Source:MGI Symbol;Acc:MGI:1306825]			-5.0	3.6E-04	-4.7	6.8E-03	0.4	4.7E-01	1.1	4.4E-01
ENSMUST00000075258	PITPNM family member 3 [Source:MGI Symbol;Acc:MGI:2685726]		Q3UHE1	5.2	4.3E-02	7.9	6.7E-03	-0.8	7.6E-01	-3.5	3.5E-02
ENSMUST00000075263				-0.2	9.4E-01	-4.6	1.7E-01	-3.1	9.5E-02	1.3	6.9E-01
ENSMUST00000075269	MAP-kinase activating death domain [Source:MGI Symbol;Acc:MGI:2444672]	A2AGQ2		4.3	2.6E-01	5.8	2.6E-01	0.7	8.9E-01	-0.8	7.9E-01
ENSMUST00000075275	NEL-like 2 [Source:MGI Symbol;Acc:MGI:1858510]		Q61220	2.9	5.7E-02	6.6	6.4E-04	-0.5	7.3E-01	-4.2	1.7E-03
ENSMUST00000075280	exosome component 1 [Source:MGI Symbol;Acc:MGI:1913833]		Q9DAA6	-1.8	1.8E-01	-0.1	9.5E-01	-0.9	3.9E-01	-2.7	9.2E-02
ENSMUST00000077221	sarcoglycan, delta (dystrophin-associated glycoprotein) [Source:MGI Symbol;Acc:MGI:1346525]	Q544D4	P82347	6.1	6.4E-04	-1.9	3.9E-03	0.4	1.7E-01	-0.5	3.9E-01
ENSMUST00000077247	olfactory receptor 1337 [Source:MGI Symbol;Acc:MGI:3031171]	A2ACY8		6.8	5.7E-05	6.6	7.2E-03	-0.8	7.2E-01	-2.3	9.9E-02
ENSMUST00000077273	exostoses (multiple) 1 [Source:MGI Symbol;Acc:MGI:894663]	Q3V1P4	P97464	2.3	4.3E-03	6.5	4.5E-04	-0.4	7.4E-01	-0.7	3.1E-01
ENSMUST00000077282	attractin like 1 [Source:MGI Symbol;Acc:MGI:2147749]		Q6A051	-2.5	2.5E-04	4.0	1.1E-01	-1.0	6.3E-01	0.9	5.7E-01
ENSMUST00000075301	nebulin [Source:MGI Symbol;Acc:MGI:97292]	A2AQA9		4.1	1.3E-01	8.3	1.8E-02	0.8	7.8E-01	-3.4	1.1E-01
ENSMUST00000075303	cat eye syndrome chromosome region, candidate 5 [Source:MGI Symbol;Acc:MGI:2136976]		Q91WM2	1.5	7.5E-02	2.0	6.7E-02	0.5	5.3E-01	0.0	9.9E-01
ENSMUST00000077290	protein disulfide isomerase associated 4 [Source:MGI Symbol;Acc:MGI:104864]			-2.1	1.2E-03	-1.2	3.0E-01	-6.3	1.3E-03	-1.2	2.8E-01
ENSMUST00000077301	vomeronasal 1 receptor 237 [Source:MGI Symbol;Acc:MGI:2159637]	Q8R296		4.6	3.5E-03	6.8	6.1E-04	-0.4	7.9E-01	-1.0	2.2E-01
ENSMUST00000077303	protein tyrosine phosphatase, receptor type, A [Source:MGI Symbol;Acc:MGI:97808]		P18052	-3.0	1.1E-02	5.3	6.7E-05	-0.1	8.9E-01	-0.2	7.5E-01
ENSMUST00000075326	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]	A2AQ42		0.9	6.1E-01	1.3	6.0E-01	0.1	9.4E-01	-0.3	9.1E-01
ENSMUST00000075341	orosomucoid 2 [Source:MGI Symbol;Acc:MGI:97444]		P07361	0.9	1.9E-01	-0.1	8.5E-01	-1.3	5.1E-02	-0.3	6.8E-01
ENSMUST00000077337	Iroquois related homeobox 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1197515]		P81068	8.0	4.9E-05	-1.8	1.3E-01	0.7	3.0E-01	-1.3	2.9E-01
ENSMUST00000075374	par-3 family cell polarity regulator beta [Source:MGI Symbol;Acc:MGI:1919301]		Q9CSB4	5.3	1.5E-01	4.8	2.5E-01	-0.2	9.6E-01	0.3	9.0E-01
ENSMUST00000077338	ATP5S-like [Source:MGI Symbol;Acc:MGI:1913599]		Q9D7K5	-3.8	2.3E-03	7.4	5.3E-05	-1.5	2.3E-01	-0.1	8.3E-01
ENSMUST00000075406	seizure threshold 2 [Source:MGI Symbol;Acc:MGI:3033336]		A2A9C3	0.5	3.5E-01	2.0	1.9E-02	1.2	7.9E-02	-0.4	5.4E-01
ENSMUST00000077340	arginyl aminopeptidase (aminopeptidase B) [Source:MGI Symbol;Acc:MGI:2384902]		Q8VCT3	-7.1	5.0E-05	3.5	1.3E-01	-3.5	1.6E-01	1.9	2.0E-01
ENSMUST00000077353	hydroxymethylbilane synthase [Source:MGI Symbol;Acc:MGI:96112]		P22907	-5.1	1.2E-04	7.0	3.5E-05	-1.5	1.7E-01	-0.6	2.3E-01
ENSMUST00000077354	kallikrein 1-related pepidase b4 [Source:MGI Symbol;Acc:MGI:97320]		P00757	6.7	4.9E-05	-1.1	1.1E-01	0.8	6.5E-02	-0.1	8.9E-01
ENSMUST00000077356	cytochrome P450, family 2, subfamily b, polypeptide 23 [Source:MGI Symbol;Acc:MGI:3646735]	E9Q593		8.1	4.1E-05	4.6	6.7E-04	-0.8	4.1E-01	-0.2	7.6E-01
ENSMUST00000077367	glucosidase, beta, acid [Source:MGI Symbol;Acc:MGI:95665]		P17439	-7.4	4.1E-05	7.5	6.0E-05	-0.6	5.9E-01	0.0	9.5E-01
ENSMUST00000075433	chemokine (C-X-C motif) ligand 2 [Source:MGI Symbol;Acc:MGI:1340094]	Q3U1J5	P10889	-2.3	2.5E-01	-1.9	4.0E-01	-0.6	6.7E-01	-1.0	6.8E-01
ENSMUST00000077376	RIKEN cDNA 2810006K23 gene [Source:MGI Symbol;Acc:MGI:1919900]		Q80VP5	2.6	3.9E-04	6.5	2.1E-04	-1.4	2.6E-01	0.1	8.9E-01
ENSMUST00000077385	Flt3 interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1344336]	Q3TRV0	Q9WTJ4	-5.9	1.0E-03	0.7	2.3E-01	2.0	1.0E-03	-0.9	1.3E-01
ENSMUST00000077407	dynactin 1 [Source:MGI Symbol;Acc:MGI:107745]	E9Q586		-9.0	4.5E-05	-6.7	1.4E-04	-0.1	8.8E-01	-1.5	2.5E-01
ENSMUST00000077417	olfactory receptor 644 [Source:MGI Symbol;Acc:MGI:3030478]	Q8VH21		6.8	7.1E-05	-0.7	2.8E-01	1.2	1.7E-02	-0.1	8.8E-01
ENSMUST00000077458	syntaxin binding protein 1 [Source:MGI Symbol;Acc:MGI:107363]		O08599	6.4	7.0E-03	-3.0	1.9E-02	-1.4	5.8E-02	-1.8	1.5E-01
ENSMUST00000077460	olfactory receptor 763 [Source:MGI Symbol;Acc:MGI:3030597]	Q8VGC1		7.3	2.2E-03	5.9	5.6E-04	-0.6	6.1E-01	-0.2	7.1E-01
ENSMUST00000077462	SRA stem-loop interacting RNA binding protein [Source:MGI Symbol;Acc:MGI:1916394]	F8WHU8		-4.8	2.3E-04	6.9	2.1E-04	-0.6	6.1E-01	-0.4	5.4E-01
ENSMUST00000077472	arbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15 [Source:MGI Symbol;Acc:MGI:192484(		Q91XQ5	5.8	7.4E-03	-8.7	6.6E-04	0.6	2.0E-01	-0.6	7.6E-01
ENSMUST00000077477	serine/threonine kinase 19 [Source:MGI Symbol;Acc:MGI:1860085]	Q3TG64	Q9JHN8	-4.0	1.0E-03	4.7	9.6E-03	-0.6	6.9E-01	1.9	7.2E-02
ENSMUST00000077502	DEAQ RNA-dependent ATPase [Source:MGI Symbol;Acc:MGI:2136388]		Q924H9	3.5	3.3E-03	-7.3	1.0E-03	0.6	2.4E-01	0.0	9.8E-01
ENSMUST00000077517	transmembrane protein 236 [Source:MGI Symbol;Acc:MGI:1919309]		A2ARJ3	5.2	4.8E-05	4.9	1.3E-02	-0.7	6.8E-01	2.4	3.7E-02
ENSMUST00000075540	minichromosome maintenance complex component 9 [Source:MGI Symbol;Acc:MGI:1918817]		Q2KHI9	0.5	3.7E-01	0.7	3.8E-01	0.5	4.4E-01	0.3	6.9E-01
ENSMUST00000075550	centromere protein H [Source:MGI Symbol;Acc:MGI:1349448]		Q9QYM8	-0.3	6.1E-01	-0.7	3.2E-01	-0.2	6.7E-01	0.2	7.5E-01
ENSMUST00000077523	serine (or cysteine) peptidase inhibitor, clade E, member 1 [Source:MGI Symbol;Acc:MGI:97608]	G5E899		5.0	2.8E-02	4.4	4.8E-03	-2.4	1.0E-01	-0.4	6.0E-01
ENSMUST00000077528	kallikrein 1-related peptidase b22 [Source:MGI Symbol;Acc:MGI:95291]	Q540N3	P15948	6.7	1.8E-04	4.4	1.1E-03	-2.9	2.3E-02	-3.6	1.5E-03
ENSMUST00000077530	retinol dehydrogenase 19 [Source:MGI Symbol;Acc:MGI:2678390]	G5E8H9		8.9	2.2E-05	16.9	6.4E-07	1.6	2.5E-01	-0.9	1.6E-02
ENSMUST00000077549	protease, serine 43 [Source:MGI Symbol;Acc:MGI:2684822]	Q76HL1		7.8	6.6E-05	1.9	1.5E-02	0.4	4.2E-01	-0.1	9.0E-01
ENSMUST00000075588	tumor necrosis factor receptor superfamily, member 22 [Source:MGI Symbol;Acc:MGI:1930270]		Q9ER62	0.3	8.7E-01	-0.1	9.8E-01	-0.3	8.5E-01	0.0	9.8E-01
ENSMUST00000075602	predicted pseudogene 10282 [Source:MGI Symbol;Acc:MGI:3704312]	Q5BL14	P09602	0.1	8.8E-01	-1.7	2.0E-01	1.1	1.6E-01	2.8	3.4E-02
ENSMUST00000077577	tubulin, alpha 1B [Source:MGI Symbol;Acc:MGI:107804]		P05213	-4.4	8.8E-05	-2.4	1.5E-02	1.3	1.6E-02	0.4	6.6E-01
ENSMUST00000077605	eukaryotic translation initiation factor 4A2 [Source:MGI Symbol;Acc:MGI:106906]	Q8BTU6		-6.6	1.2E-03	7.0	1.7E-03	-0.2	9.0E-01	-2.6	2.4E-02
ENSMUST00000077609	fused in sarcoma [Source:MGI Symbol;Acc:MGI:1353633]	Q8CFQ9		-8.9	2.3E-05	-4.5	1.7E-02	-1.7	4.3E-02	-0.9	6.1E-01
ENSMUST00000077636	linker for activation of T cells family, member 2 [Source:MGI Symbol;Acc:MGI:1926479]		Q9JHL0	-3.8	1.0E-02	6.5	2.0E-05	0.3	6.7E-01	-0.8	1.2E-01
ENSMUST00000075637	protein tyrosine phosphatase, non-receptor type 3 [Source:MGI Symbol;Acc:MGI:105307]		A2ALK8	0.6	1.3E-01	1.8	6.8E-03	1.2	1.4E-02	0.0	9.4E-01
ENSMUST00000075639	RIKEN cDNA 1700112E06 gene [Source:MGI Symbol;Acc:MGI:1923883]		Q9D9B4	-3.2	4.3E-02	-1.6	3.3E-01	0.4	7.5E-01	-1.2	4.7E-01
ENSMUST00000075650				-1.7	1.1E-01	-4.9	1.1E-02	-2.6	6.0E-03	0.6	7.1E-01
ENSMUST00000077639	cytochrome P450, family 4, subfamily f, polypeptide 37 [Source:MGI Symbol;Acc:MGI:3780112]	Q3V1F1		6.1	8.6E-05	2.0	1.6E-03	0.6	1.4E-01	-0.5	2.1E-01
ENSMUST00000075666	UPF1 regulator of nonsense transcripts homolog (yeast) [Source:MGI Symbol;Acc:MGI:107995]		Q9EPU0	-1.1	4.8E-02	-0.2	7.5E-01	1.2	3.1E-02	0.3	6.2E-01
ENSMUST00000077659	ATPase, class V, type 10B [Source:MGI Symbol;Acc:MGI:2442688]	B1AWN4		7.7	6.5E-06	-2.2	3.2E-01	3.7	1.4E-02	-0.3	8.8E-01
ENSMUST00000075670	stem-loop binding protein [Source:MGI Symbol;Acc:MGI:108402]	Q3V2L1		0.2	8.0E-01	-0.6	4.5E-01	-1.3	5.5E-02	-0.5	5.2E-01
ENSMUST00000077666	cyclin M2 [Source:MGI Symbol;Acc:MGI:2151054]		Q3TWN3	-4.4	4.6E-03	2.1	6.6E-02	0.9	3.0E-01	0.7	3.8E-01
ENSMUST00000077672	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein [Source:MGI Symbol;Acc:MGI:1915268]		Q9EQG9	-4.5	4.9E-03	2.0	2.3E-02	0.6	3.8E-01	0.1	8.9E-01
ENSMUST00000077680	transcription factor E3 [Source:MGI Symbol;Acc:MGI:98511]	A2AEW1		-5.9	8.7E-05	-6.7	2.5E-02	1.0	2.7E-01	2.6	3.2E-01
ENSMUST00000077687	coiled-coil domain containing 148 [Source:MGI Symbol;Acc:MGI:3039583]		Q6P5U8	7.8	5.2E-05	-6.6	3.2E-05	0.1	8.6E-01	-2.1	5.7E-02
ENSMUST00000077693	eukaryotic translation initiation factor 2B, subunit 4 delta [Source:MGI Symbol;Acc:MGI:95300]		Q61749	-3.5	2.5E-02	-11.5	1.4E-03	-1.3	6.6E-02	1.5	5.8E-01
ENSMUST00000075724	regulatory factor X-associated ankyrin-containing protein [Source:MGI Symbol;Acc:MGI:1333865]	Q53X17	Q9Z205	0.3	5.6E-01	0.4	5.1E-01	0.1	7.9E-01	0.0	9.9E-01
ENSMUST00000077696	immunoglobulin superfamily, DCC subclass, member 4 [Source:MGI Symbol;Acc:MGI:1858497]	E9QAQ0		9.2	8.2E-06	-7.1	3.9E-05	-0.8	6.5E-02	-0.4	6.9E-01
ENSMUST00000077698	calmodulin-like 3 [Source:MGI Symbol;Acc:MGI:1917655]		Q9D6P8	7.1	3.4E-05	6.6	2.2E-04	0.9	4.4E-01	0.1	8.5E-01
ENSMUST00000077705	cytochrome P450, family 26, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:2176159]		Q811W2	7.2	1.6E-02	-5.2	8.8E-03	1.5	3.8E-02	-0.6	7.5E-01
ENSMUST00000077706	lysozyme-like 4 [Source:MGI Symbol;Acc:MGI:1916282]	Q78ID0	Q9D925	3.4	1.0E-02	3.9	1.0E-02	0.1	9.0E-01	0.7	3.6E-01
ENSMUST00000077709	RIKEN cDNA 6330416G13 gene [Source:MGI Symbol;Acc:MGI:1913920]		Q8R239	-5.8	1.4E-02	8.0	3.3E-05	-0.6	6.1E-01	-0.4	4.8E-01
ENSMUST00000077730	phosphoinositide-3-kinase, class 2, beta polypeptide [Source:MGI Symbol;Acc:MGI:2685045]	E9QAN8		1.7	1.2E-02	7.5	3.5E-05	-0.5	6.3E-01	0.1	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000077741	solute carrier family 9 (sodium/hydrogen exchanger), member 6 [Source:MGI Symbol;Acc:MGI:2443511]	A1L3P4		-3.4	2.2E-02	1.7	3.1E-02	-3.8	4.3E-04	0.1	9.1E-01
ENSMUST00000077755	actin related protein 2/3 complex, subunit 5 [Source:MGI Symbol;Acc:MGI:1915021]		Q9CPW4	-9.7	7.2E-05	2.3	9.2E-02	-0.6	6.0E-01	4.6	1.0E-03
ENSMUST00000075806	ATPase type 13A5 [Source:MGI Symbol;Acc:MGI:2444068]		Q3TYU2	6.0	4.6E-02	4.4	1.7E-01	-0.8	8.0E-01	0.8	7.0E-01
ENSMUST00000077775	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound [Source:MGI Symbol;Acc:MGI:2180001]	B1AVD1		6.5	6.4E-04	7.0	7.3E-05	-0.5	6.4E-01	-0.8	1.7E-01
ENSMUST00000075812	Wolf-Hirschhorn syndrome candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1276574]		Q8BVE8	-2.2	3.3E-01	1.1	6.5E-01	2.3	2.9E-01	-1.0	6.7E-01
ENSMUST00000077787	zinc finger protein 14 [Source:MGI Symbol;Acc:MGI:99160]		P10755	4.7	4.9E-04	5.1	6.1E-05	-0.7	3.2E-01	-0.3	5.0E-01
ENSMUST00000077788	tumor necrosis factor, alpha-induced protein 8-like 1 [Source:MGI Symbol;Acc:MGI:1913693]		Q8K288	1.6	2.1E-02	-4.0	1.3E-03	-1.7	1.2E-02	-0.1	8.8E-01
ENSMUST00000075836	dedicator of cytokinesis 7 [Source:MGI Symbol;Acc:MGI:1914549]	E9PX48		0.9	5.0E-01	0.2	9.1E-01	1.8	3.2E-01	2.4	1.6E-01
ENSMUST00000077798	structure specific recognition protein 1 [Source:MGI Symbol;Acc:MGI:107912]		Q08943	-7.3	8.3E-05	6.9	1.0E-04	0.0	9.8E-01	0.0	9.5E-01
ENSMUST00000077839	nuclear receptor binding factor 2 [Source:MGI Symbol;Acc:MGI:1354950]		Q8VCQ3	-4.0	1.8E-04	-7.1	9.8E-04	0.5	3.6E-01	-0.1	9.5E-01
ENSMUST00000077843	olfactory receptor 1359 [Source:MGI Symbol;Acc:MGI:3031193]	Q5SZZ5		5.5	2.5E-02	4.0	1.0E-01	-0.6	8.0E-01	1.9	2.0E-01
ENSMUST00000077853	PRP4 pre-mRNA processing factor 4 homolog B (yeast) [Source:MGI Symbol;Acc:MGI:109584]		Q61136	-2.0	2.7E-03	2.9	5.7E-04	-1.9	7.9E-03	-0.1	7.6E-01
ENSMUST00000077855	cytochrome P450, family 2, subfamily b, polypeptide 19 [Source:MGI Symbol;Acc:MGI:107303]		O55071	7.7	2.5E-05	6.4	2.5E-04	-0.5	6.5E-01	-0.2	8.0E-01
ENSMUST00000077876	sorting nexin 12 [Source:MGI Symbol;Acc:MGI:1919331]	Q3TGS7		-4.0	4.7E-03	-3.4	6.9E-04	-0.3	4.1E-01	0.5	4.7E-01
ENSMUST00000077879	vacuolar protein sorting 13C (yeast) [Source:MGI Symbol;Acc:MGI:2444207]	A1ILG8	Q8BX70	-1.4	1.2E-02	-8.1	6.6E-04	0.9	8.0E-02	-0.8	6.8E-01
ENSMUST00000077886	predicted gene 8994 [Source:MGI Symbol;Acc:MGI:3644226]	E9PV04		8.1	1.2E-05	5.0	9.5E-04	-1.5	1.9E-01	-0.4	6.0E-01
ENSMUST00000077890	IQ motif containing E [Source:MGI Symbol;Acc:MGI:1921489]		Q6PCQ0	-3.1	9.2E-03	-3.2	1.3E-02	-0.1	8.6E-01	-2.5	6.4E-02
ENSMUST00000077902	glial fibrillary acidic protein [Source:MGI Symbol;Acc:MGI:95697]		P03995	7.7	4.8E-04	0.5	3.4E-01	-8.4	3.1E-06	-1.0	4.6E-02
ENSMUST00000077909	suppression of tumorigenicity 5 [Source:MGI Symbol;Acc:MGI:108517]		Q924W7	8.0	8.7E-05	7.1	3.6E-04	-0.6	6.5E-01	-0.5	4.5E-01
ENSMUST00000077915	ribosomal protein L38 [Source:MGI Symbol;Acc:MGI:1914921]	Q52KP0	Q9JJI8	-5.7	1.2E-03	-4.1	4.3E-03	0.4	5.1E-01	-1.3	3.1E-01
ENSMUST00000075896	translin-associated factor X [Source:MGI Symbol;Acc:MGI:1855672]		Q9QZE7	0.0	9.9E-01	-0.2	7.3E-01	0.2	6.0E-01	0.4	4.7E-01
ENSMUST00000077918	complement component factor i [Source:MGI Symbol;Acc:MGI:105937]		Q61129	5.7	4.1E-04	4.9	2.0E-03	0.2	8.7E-01	0.5	4.5E-01
ENSMUST00000077925	unc-5 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:894703]		Q8K1S3	10.5	8.4E-06	4.0	1.3E-01	-0.6	8.1E-01	2.1	2.5E-01
ENSMUST00000077946	dedicator of cytokinesis 10 [Source:MGI Symbol;Acc:MGI:2146320]	E9QM99		-5.5	2.9E-03	-5.7	4.9E-03	-0.4	5.1E-01	-1.5	4.2E-01
ENSMUST00000077960	histocompatibility 2, T region locus 22 [Source:MGI Symbol;Acc:MGI:95956]	Q31615		-4.7	1.2E-03	4.7	1.9E-04	-1.5	8.3E-02	-0.2	7.0E-01
ENSMUST00000077962	potassium voltage-gated channel, subfamily G, member 2 [Source:MGI Symbol;Acc:MGI:3694646]	F7A6P6		7.2	1.9E-05	3.6	4.1E-03	-0.9	3.0E-01	-0.6	4.3E-01
ENSMUST00000077967	lines homolog (Drosophila) 1 [Source:MGI Symbol;Acc:MGI:1919885]		Q3U1D0	-6.8	5.8E-05	5.9	3.8E-06	-0.4	5.2E-01	-0.6	1.1E-01
ENSMUST00000077983	serologically defined colon cancer antigen 3 [Source:MGI Symbol;Acc:MGI:1915362]		A2AIW0	-7.0	5.1E-04	6.6	1.1E-03	-0.7	6.6E-01	-1.4	1.1E-01
ENSMUST00000077985	G protein-coupled bile acid receptor 1 [Source:MGI Symbol;Acc:MGI:2653863]	Q14AA9	Q80SS6	6.1	1.0E-04	-2.7	9.3E-03	-0.4	3.8E-01	0.1	9.4E-01
ENSMUST00000075968				0.2	7.6E-01	-0.9	2.5E-01	-0.7	2.0E-01	0.4	6.0E-01
ENSMUST00000075982	serum amyloid A 2 [Source:MGI Symbol;Acc:MGI:98222]		P05367	-1.2	4.5E-01	0.2	9.2E-01	-0.8	5.9E-01	-2.2	1.9E-01
ENSMUST00000077988	transmembrane channel-like gene family 2 [Source:MGI Symbol;Acc:MGI:2151017]		Q8R4P4	8.4	2.5E-05	4.5	5.7E-04	-0.5	5.5E-01	0.5	3.8E-01
ENSMUST00000078001	testis expressed gene 101 [Source:MGI Symbol;Acc:MGI:1930791]		Q9JMI7	5.7	1.4E-03	4.6	2.7E-04	-4.5	2.2E-03	0.4	4.4E-01
ENSMUST00000078049	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 1 [Source:MGI Symbol;Acc:MGI:102469	Q6P7T9		-5.7	9.3E-05	4.8	3.4E-05	-1.7	2.6E-02	0.3	5.2E-01
ENSMUST00000076016	mediator complex subunit 14 [Source:MGI Symbol;Acc:MGI:1349442]	A2BDN7		-0.3	7.7E-01	-1.0	4.0E-01	-0.6	4.7E-01	0.1	9.5E-01
ENSMUST00000078050	ring finger protein 114 [Source:MGI Symbol;Acc:MGI:1933159]		Q9ET26	-4.3	2.5E-03	2.3	3.2E-01	-5.0	7.5E-02	-0.2	8.9E-01
ENSMUST00000076034	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8 [Source:MGI Symbol;Acc:MGI:2385269]		Q8R3I9	0.3	6.3E-01	2.6	2.1E-02	1.5	7.7E-02	-0.7	3.6E-01
ENSMUST00000078057	olfactory receptor 47 [Source:MGI Symbol;Acc:MGI:1333821]	Q8VF18		5.3	2.7E-03	7.1	7.5E-05	-0.5	6.3E-01	-0.8	1.7E-01
ENSMUST00000078070	interaction protein for cytohesin exchange factors 1 [Source:MGI Symbol;Acc:MGI:2444159]		Q5DU31	-2.3	2.4E-02	6.5	1.0E-03	-1.4	3.5E-01	1.3	1.3E-01
ENSMUST00000076046	stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) [Source:MGI Symbol;Acc:MGI:13		Q00941	-1.7	7.0E-02	-2.2	9.5E-02	0.7	4.0E-01	1.2	3.3E-01
ENSMUST00000076051	olute carrier family 8 (sodium/lithium/calcium exchanger), member B1 [Source:MGI Symbol;Acc:MGI:218078		Q925Q3	-1.8	1.3E-01	0.1	9.3E-01	1.6	1.4E-01	-0.3	8.2E-01
ENSMUST00000076052	prolylcarboxypeptidase (angiotensinase C) [Source:MGI Symbol;Acc:MGI:1919711]		Q7TMR0	-0.8	1.2E-01	-0.8	2.1E-01	-0.3	5.3E-01	-0.3	6.6E-01
ENSMUST00000076069	crystallin, beta B3 [Source:MGI Symbol;Acc:MGI:102717]		Q9JJU9	3.3	1.3E-01	2.6	2.3E-01	-0.5	8.3E-01	0.2	9.2E-01
ENSMUST00000078079	eukaryotic translation initiation factor 1A [Source:MGI Symbol;Acc:MGI:95298]	Q4FJR7	Q60872	-3.5	8.6E-04	-6.5	2.3E-04	-0.1	7.8E-01	-0.2	8.5E-01
ENSMUST00000076085	coiled-coil domain containing 186 [Source:MGI Symbol;Acc:MGI:2445022]		Q8C9S4	0.4	8.3E-01	1.7	5.4E-01	1.1	5.7E-01	-0.2	9.3E-01
ENSMUST00000078084	arginine/serine rich protein 1 [Source:MGI Symbol;Acc:MGI:106498]		Q3UC65	-8.1	1.4E-04	5.7	3.6E-05	1.1	1.4E-01	-0.1	8.0E-01
ENSMUST00000078090	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 [Source:MGI Symbol;Acc:I		A2AM29	2.7	1.0E-02	6.3	2.5E-04	-0.5	6.8E-01	-0.7	3.0E-01
ENSMUST00000078103	olfactory receptor 525 [Source:MGI Symbol;Acc:MGI:3030359]	Q8VGL5		4.6	1.8E-02	-7.4	3.4E-05	-0.3	3.3E-01	0.4	7.1E-01
ENSMUST00000076123	zinc finger protein 58 [Source:MGI Symbol;Acc:MGI:99205]		P16372	3.8	9.2E-02	0.6	8.4E-01	-1.3	5.4E-01	1.9	5.0E-01
ENSMUST00000078124	cofilin 2, muscle [Source:MGI Symbol;Acc:MGI:101763]	Q3UHW9	P45591	-2.7	1.4E-03	8.8	6.1E-04	-0.8	6.7E-01	-0.2	8.2E-01
ENSMUST00000076136	folliculin interacting protein 2 [Source:MGI Symbol;Acc:MGI:2683054]		Q80TD3	-2.9	3.6E-02	0.2	8.8E-01	2.2	5.6E-02	-1.0	5.3E-01
ENSMUST00000078182	guanine nucleotide binding protein (G protein), gamma 8 [Source:MGI Symbol;Acc:MGI:109163]	Q3UMY0	P63078	4.7	6.0E-03	5.6	3.2E-04	-2.6	5.6E-02	-0.2	8.1E-01
ENSMUST00000078185	nuclear factor I/C [Source:MGI Symbol;Acc:MGI:109591]		P70255	-4.0	2.2E-02	-4.6	1.2E-05	0.5	7.1E-02	-0.8	1.7E-01
ENSMUST00000078209	olfactory receptor 96 [Source:MGI Symbol;Acc:MGI:2177479]	Q8VFE3		7.1	1.3E-04	3.3	1.4E-02	-1.7	1.4E-01	0.5	5.4E-01
ENSMUST00000078214	src family associated phosphoprotein 2 [Source:MGI Symbol;Acc:MGI:1889206]		Q3UND0	-7.9	7.7E-07	5.1	2.4E-03	-0.8	5.3E-01	0.7	3.9E-01
ENSMUST00000078217	olfactory receptor 312 [Source:MGI Symbol;Acc:MGI:3030146]	Q7TRZ9		6.7	1.1E-04	-0.8	2.7E-01	0.9	7.6E-02	-0.7	2.6E-01
ENSMUST00000078218	serine hydrolase-like [Source:MGI Symbol;Acc:MGI:1890404]	Q80XK9	Q9EPB5	-5.7	1.4E-03	-1.2	7.4E-02	1.1	2.1E-02	-0.2	7.2E-01
ENSMUST00000076219	pumilio RNA-binding family member 3 [Source:MGI Symbol;Acc:MGI:106253]			-0.1	7.9E-01	-1.4	4.8E-02	-1.4	9.7E-03	-0.1	8.6E-01
ENSMUST00000078223	GTPase, IMAP family member 8 [Source:MGI Symbol;Acc:MGI:2685303]		Q75N62	2.2	2.9E-03	-4.5	1.2E-01	1.6	2.6E-01	-0.6	8.2E-01
ENSMUST00000076226	the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 [Source:MGI Symb		Q4U2R1	-1.2	4.3E-01	-2.7	2.4E-01	0.5	6.9E-01	2.0	3.8E-01
ENSMUST00000076228	Williams-Beuren syndrome chromosome region 16 homolog (human) [Source:MGI Symbol;Acc:MGI:2137600	Q548B0	Q9CYF5	1.6	5.6E-02	1.5	1.2E-01	-0.4	5.8E-01	-0.3	6.8E-01
ENSMUST00000078229	POU domain, class 3, transcription factor 4 [Source:MGI Symbol;Acc:MGI:101894]	A6H6L6	P62515	10.1	2.1E-05	8.0	7.8E-05	-0.3	7.9E-01	-0.3	5.5E-01
ENSMUST00000078259	SL1, MIND kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:268583	E9QME3		5.6	4.9E-06	2.3	7.8E-02	-1.1	3.5E-01	0.1	9.5E-01
ENSMUST00000078264	olfactory receptor 1373 [Source:MGI Symbol;Acc:MGI:3031207]	Q7TQT6		5.8	2.0E-03	0.2	7.9E-01	0.9	7.4E-02	-1.0	1.5E-01
ENSMUST00000078267	histone cluster 3, H2ba [Source:MGI Symbol;Acc:MGI:1925553]		Q9D2U9	6.4	3.0E-04	-0.1	8.6E-01	1.6	6.5E-03	-0.3	6.2E-01
ENSMUST00000076260	integrin beta 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1306802]		O35671	-4.1	1.5E-01	-6.4	7.4E-02	-2.8	8.2E-02	-0.5	9.0E-01
ENSMUST00000076264	zinc finger protein 512 [Source:MGI Symbol;Acc:MGI:1917345]		Q69Z99	0.7	2.0E-01	0.6	4.4E-01	0.0	9.4E-01	0.2	7.7E-01
ENSMUST00000078271	protocadherin beta 5 [Source:MGI Symbol;Acc:MGI:2136739]	Q91XZ5		8.2	1.8E-04	-3.2	6.7E-03	-0.4	5.1E-01	-0.4	6.8E-01
ENSMUST00000078272	calcium channel, voltage-dependent, alpha2/delta subunit 1 [Source:MGI Symbol;Acc:MGI:88295]		O08532	6.0	1.2E-02	-1.5	1.4E-01	0.6	3.4E-01	0.0	9.7E-01
ENSMUST00000078286	ribosomal protein L7-like 1 [Source:MGI Symbol;Acc:MGI:1913479]		Q9D8M4	-2.3	5.2E-05	6.2	3.3E-04	-0.5	6.7E-01	-0.7	2.7E-01
ENSMUST00000076275	nuclear receptor subfamily 6, group A, member 1 [Source:MGI Symbol;Acc:MGI:1352459]		Q64249	-1.8	5.4E-01	-0.9	8.2E-01	0.3	9.1E-01	-0.6	8.7E-01
ENSMUST00000078307	lysozyme G-like 2 [Source:MGI Symbol;Acc:MGI:2685622]		Q3V1I0	6.5	4.3E-04	7.1	1.9E-03	0.3	8.5E-01	-1.3	1.9E-01
ENSMUST00000078308	RAS protein activator like 2 [Source:MGI Symbol;Acc:MGI:2443881]	E9PW37		4.9	1.3E-05	-3.1	3.7E-04	0.2	4.1E-01	-0.4	5.1E-01
ENSMUST00000078314	solute carrier family 22 (organic cation transporter), member 16 [Source:MGI Symbol;Acc:MGI:1918090]	B2RRB7	Q497L8	7.0	1.2E-02	0.5	3.6E-01	-0.3	4.7E-01	0.2	6.4E-01
ENSMUST00000078324	calcium channel, voltage-dependent, beta 4 subunit [Source:MGI Symbol;Acc:MGI:103301]	A2ATZ8	Q8R0S4	8.9	2.4E-05	-2.5	2.2E-01	0.9	4.0E-01	-0.1	9.6E-01
ENSMUST00000078350	chondroitin sulfate N-acetylgalactosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI:2442354]		Q8BJQ9	3.6	1.8E-03	6.1	4.4E-04	-0.6	6.3E-01	-0.6	4.0E-01
ENSMUST00000078357	epithelial membrane protein 2 [Source:MGI Symbol;Acc:MGI:1098726]	Q548I4	O88662	8.8	3.9E-06	-9.1	1.1E-04	0.1	8.4E-01	-2.1	2.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000076362	eukaryotic translation initiation factor 4E member 2 [Source:MGI Symbol;Acc:MGI:1914440]	G3X9H1		1.6	2.8E-01	2.2	2.8E-01	1.0	5.2E-01	0.5	7.7E-01
ENSMUST00000078362	vaccinia related kinase 2 [Source:MGI Symbol;Acc:MGI:1917172]		Q8BN21	-3.5	8.0E-03	-9.9	9.9E-04	-0.6	4.0E-01	1.5	5.0E-01
ENSMUST00000078364	interferon lambda 3 [Source:MGI Symbol;Acc:MGI:2450574]		Q8CGK6	5.4	1.1E-03	-1.1	1.8E-01	0.9	9.1E-02	-1.2	1.8E-01
ENSMUST00000078374	U2 snRNP-associated SURP domain containing [Source:MGI Symbol;Acc:MGI:1915208]		Q6NV83	-2.0	6.0E-03	-5.4	1.3E-04	0.2	6.6E-01	-0.4	6.9E-01
ENSMUST00000078386	SLIT and NTRK-like family, member 6 [Source:MGI Symbol;Acc:MGI:2443198]	A6H6M2	Q8C110	6.8	6.0E-05	7.0	1.3E-02	1.0	6.5E-01	-1.4	3.6E-01
ENSMUST00000078404	poly(rC) binding protein 2 [Source:MGI Symbol;Acc:MGI:108202]		Q61990	-5.4	1.7E-03	6.8	3.4E-04	-0.6	6.3E-01	0.1	8.9E-01
ENSMUST00000078409	apelin receptor early endogenous ligand [Source:MGI Symbol;Acc:MGI:3642370]	Q8JZK6		6.9	1.2E-04	6.4	2.5E-04	-0.6	6.1E-01	0.1	9.2E-01
ENSMUST00000078432	ribosomal protein L28 [Source:MGI Symbol;Acc:MGI:101839]	Q5M9J8	P41105	2.0	3.4E-02	-2.9	3.7E-03	0.7	1.2E-01	0.0	9.7E-01
ENSMUST00000076442	plectin [Source:MGI Symbol;Acc:MGI:1277961]		Q9QXS1	1.7	5.7E-01	0.0	1.0E+00	-1.4	5.9E-01	0.2	9.4E-01
ENSMUST00000078438	tripartite motif-containing 31 [Source:MGI Symbol;Acc:MGI:2385051]		Q8R0K2	6.9	5.8E-05	5.6	2.5E-02	-0.7	7.6E-01	0.5	7.0E-01
ENSMUST00000076454	ubiquilin 1 [Source:MGI Symbol;Acc:MGI:1860276]		Q8R317	-1.8	2.4E-01	-3.4	2.0E-01	1.5	4.0E-01	3.1	1.7E-01
ENSMUST00000076463	G protein-coupled receptor 155 [Source:MGI Symbol;Acc:MGI:1915776]	A2AWR3		3.7	3.6E-02	1.8	3.6E-01	-0.5	7.5E-01	1.4	3.9E-01
ENSMUST00000078442	predicted gene 11567 [Source:MGI Symbol;Acc:MGI:3649436]	Q9D141		5.8	1.7E-02	7.3	4.8E-05	-0.6	6.0E-01	-0.1	8.5E-01
ENSMUST00000078459	mediator of cell motility 1 [Source:MGI Symbol;Acc:MGI:1924140]		Q91VH6	-2.4	3.7E-03	4.1	3.7E-04	-0.4	5.4E-01	-0.2	7.8E-01
ENSMUST00000078470	otassium voltage-gated channel, subfamily H (eag-related), member 1 [Source:MGI Symbol;Acc:MGI:1341721	Q3USQ9	Q60603	8.1	4.5E-05	5.9	9.7E-04	-0.5	7.2E-01	-0.6	3.9E-01
ENSMUST00000078478	2-phosphoxylose phosphatase 1 [Source:MGI Symbol;Acc:MGI:2442444]		Q8BHA9	-5.8	5.6E-04	5.4	6.3E-02	-0.7	8.1E-01	-0.3	8.3E-01
ENSMUST00000078481	scinderin [Source:MGI Symbol;Acc:MGI:1306794]		Q60604	7.3	2.2E-03	1.6	9.3E-02	-0.2	8.2E-01	0.0	9.8E-01
ENSMUST00000078482	dachsous 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685011]		E9PVD3	9.7	9.1E-03	6.2	5.4E-04	-0.5	6.9E-01	-0.6	4.1E-01
ENSMUST00000078494	recombination activating gene 1 [Source:MGI Symbol;Acc:MGI:97848]		P15919	6.4	1.6E-05	4.4	2.7E-04	-1.7	6.7E-02	-0.6	3.1E-01
ENSMUST00000078496	calcium channel, voltage-dependent, T type, alpha 1H subunit [Source:MGI Symbol;Acc:MGI:1928842]	E9Q6P9		8.5	1.5E-02	-5.7	3.3E-03	-0.2	7.1E-01	0.0	1.0E+00
ENSMUST00000078505	reticulon 1 [Source:MGI Symbol;Acc:MGI:1933947]	Q4FJL2	Q8K0T0	8.3	2.4E-05	6.7	1.7E-03	-0.7	6.7E-01	-0.1	8.8E-01
ENSMUST00000078508	Sp7 transcription factor 7 [Source:MGI Symbol;Acc:MGI:2153568]	Q2KHK9	Q8VI67	9.1	9.8E-06	-2.8	5.9E-03	0.3	4.5E-01	-0.9	3.4E-01
ENSMUST00000078521	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4 [Source:MGI Symbol;Acc:MGI:1330292]		Q8BI55	7.3	1.6E-04	4.5	7.8E-03	-1.2	4.1E-01	-0.1	9.5E-01
ENSMUST00000078525	ring finger protein 150 [Source:MGI Symbol;Acc:MGI:2443860]		Q5DTZ6	3.9	9.8E-05	-2.7	4.4E-02	1.5	4.0E-02	-0.7	5.7E-01
ENSMUST00000078527	relaxin/insulin-like family peptide receptor 1 [Source:MGI Symbol;Acc:MGI:2682211]		Q6R6I7	8.4	3.5E-06	5.1	6.7E-04	-1.1	3.0E-01	-0.3	6.4E-01
ENSMUST00000078528	complement component 1, q subcomponent binding protein [Source:MGI Symbol;Acc:MGI:1194505]	Q8R5L1		-2.8	1.0E-02	-5.8	1.7E-02	1.1	1.7E-01	1.7	4.1E-01
ENSMUST00000076605	guanine nucleotide binding protein, alpha stimulating, olfactory type [Source:MGI Symbol;Acc:MGI:95774]		Q8CGK7	-0.4	5.7E-01	-0.1	9.1E-01	1.2	9.9E-02	0.9	3.1E-01
ENSMUST00000076615	CREB regulated transcription coactivator 1 [Source:MGI Symbol;Acc:MGI:2142523]		Q68ED7	-0.7	5.0E-01	-2.3	1.7E-01	1.0	3.6E-01	2.6	1.1E-01
ENSMUST00000078532	trace amine-associated receptor 7A [Source:MGI Symbol;Acc:MGI:2685075]		Q5QD12	6.2	6.4E-04	5.3	7.0E-04	-0.6	6.2E-01	0.9	1.7E-01
ENSMUST00000078547	SEC22 homolog C, vesicle trafficking protein [Source:MGI Symbol;Acc:MGI:2447871]		Q8BXT9	1.4	5.5E-03	6.5	6.1E-04	-0.7	6.1E-01	-1.2	1.6E-01
ENSMUST00000078572	Yip1 domain family, member 2 [Source:MGI Symbol;Acc:MGI:1922016]		Q99LP8	-5.3	4.4E-03	0.8	2.2E-01	-1.3	2.3E-02	-0.2	7.7E-01
ENSMUST00000078615	cDNA sequence BC051142 [Source:MGI Symbol;Acc:MGI:3039565]	A2CG24		6.3	2.7E-02	5.4	5.1E-04	0.3	8.0E-01	-1.5	7.6E-02
ENSMUST00000076634	estrogen receptor 2 (beta) [Source:MGI Symbol;Acc:MGI:109392]			6.5	3.8E-02	2.8	4.5E-01	-0.9	7.9E-01	2.9	3.1E-01
ENSMUST00000076639	chromatin target of PRMT1 [Source:MGI Symbol;Acc:MGI:1913761]		Q9CY57	-5.2	7.3E-02	2.2	5.9E-01	7.3	2.2E-02	-0.1	9.8E-01
ENSMUST00000078616	G-protein signalling modulator 1 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:1915089]		Q6IR34	-2.7	2.3E-02	8.2	8.3E-05	-0.7	6.3E-01	-0.9	1.8E-01
ENSMUST00000076654	testis derived transcript [Source:MGI Symbol;Acc:MGI:105081]	Q3ULB1		5.1	1.1E-01	3.2	2.8E-01	-3.3	3.2E-01	-1.3	5.0E-01
ENSMUST00000078626	tetratricopeptide repeat and ankyrin repeat containing 1 [Source:MGI Symbol;Acc:MGI:1341834]		Q8BV79	9.4	3.6E-06	-8.1	1.3E-04	-0.8	6.4E-02	-0.8	5.9E-01
ENSMUST00000076661	Ewing tumor-associated antigen 1 [Source:MGI Symbol;Acc:MGI:1915395]		Q5SVT3	-1.3	4.5E-02	-1.1	1.7E-01	0.6	2.8E-01	0.3	6.5E-01
ENSMUST00000078647	RAB43, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1917084]	Q0PD10	Q8CG50	-3.8	1.5E-04	-2.2	1.2E-01	1.1	1.7E-01	1.0	4.4E-01
ENSMUST00000078665	deoxyhypusine synthase [Source:MGI Symbol;Acc:MGI:2683592]		Q3TXU5	-5.1	9.8E-04	7.7	7.5E-05	-0.5	7.1E-01	-0.4	4.6E-01
ENSMUST00000076674	glutamate receptor ionotropic, NMDA3A [Source:MGI Symbol;Acc:MGI:1933206]	A2AIR4		0.9	7.0E-01	2.0	5.3E-01	2.8	3.2E-01	1.7	4.9E-01
ENSMUST00000078676	ubiquinol-cytochrome c reductase hinge protein [Source:MGI Symbol;Acc:MGI:1913826]		P99028	-6.9	1.2E-07	5.6	9.9E-04	-0.5	6.8E-01	0.5	4.9E-01
ENSMUST00000076694	te carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Source:MGI Symbol;Acc:MGI:1353		Q8VEM8	-3.5	2.2E-01	-1.4	7.1E-01	1.3	5.7E-01	-0.8	8.2E-01
ENSMUST00000076697	solute carrier family 38, member 10 [Source:MGI Symbol;Acc:MGI:1919305]		Q5I012	-0.3	7.9E-01	1.5	2.8E-01	1.1	3.2E-01	-0.7	5.7E-01
ENSMUST00000076698	synaptophysin-like protein [Source:MGI Symbol;Acc:MGI:108081]		O09117	-0.4	3.1E-01	0.6	2.4E-01	0.9	5.1E-02	-0.2	6.8E-01
ENSMUST00000078680	Usher syndrome 1C [Source:MGI Symbol;Acc:MGI:1919338]			-4.7	1.3E-03	-1.6	1.3E-01	1.7	1.6E-02	-1.2	2.8E-01
ENSMUST00000076702	interferon, alpha-inducible protein 27 [Source:MGI Symbol;Acc:MGI:1277180]	Q70LN0		1.9	3.7E-01	0.7	6.8E-01	-3.9	6.6E-02	-2.7	1.3E-01
ENSMUST00000078686	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 [Source:MGI Symbol;Acc:MGI:1916197]		Q8BQ86	7.3	4.1E-05	3.8	3.5E-04	0.0	9.4E-01	-0.7	2.1E-01
ENSMUST00000076715	nuclear factor I/X [Source:MGI Symbol;Acc:MGI:97311]		P70257	1.8	2.1E-01	-1.2	4.5E-01	-2.6	4.0E-02	0.4	8.2E-01
ENSMUST00000078687	GID complex subunit 8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923675]		Q9D7M1	4.2	3.6E-04	5.8	3.4E-04	2.0	6.3E-02	-0.2	6.9E-01
ENSMUST00000078691	BCL2-antagonist/killer 1 [Source:MGI Symbol;Acc:MGI:1097161]		O08734	-2.4	9.9E-03	-1.2	1.2E-01	0.7	1.4E-01	-0.3	6.7E-01
ENSMUST00000078694	protein phosphatase 1, regulatory (inhibitor) subunit 1B [Source:MGI Symbol;Acc:MGI:94860]		Q60829	5.9	1.2E-03	7.7	2.9E-05	-0.9	4.2E-01	-0.1	8.1E-01
ENSMUST00000076757	DiGeorge syndrome critical region gene 6 [Source:MGI Symbol;Acc:MGI:1202877]	Q3TV71		-3.0	4.0E-02	-0.8	5.9E-01	1.1	3.0E-01	-1.1	5.0E-01
ENSMUST00000078695	predicted gene 13078 [Source:MGI Symbol;Acc:MGI:3650231]	A2AGW8		6.5	1.3E-04	3.6	8.9E-03	-0.2	8.1E-01	0.7	4.1E-01
ENSMUST00000078734	poly(A) binding protein, cytoplasmic 4 [Source:MGI Symbol;Acc:MGI:2385206]	Q91YZ8		-3.8	1.4E-03	-2.2	1.5E-01	1.0	2.5E-01	-1.7	3.0E-01
ENSMUST00000078748	ute carrier family 10 (sodium/bile acid cotransporter family), member 5 [Source:MGI Symbol;Acc:MGI:26852		Q5PT54	6.4	2.7E-04	-1.6	1.2E-01	0.0	9.4E-01	-1.9	8.7E-02
ENSMUST00000076817	utrophin [Source:MGI Symbol;Acc:MGI:104631]	E9Q6R7		0.0	9.5E-01	0.8	2.4E-01	0.2	7.1E-01	-0.6	3.4E-01
ENSMUST00000078752	cancer susceptibility candidate 4 [Source:MGI Symbol;Acc:MGI:2443129]		Q6P2L7	5.8	2.4E-02	1.3	1.7E-01	-2.5	1.7E-02	-0.1	9.0E-01
ENSMUST00000078757	galactose-3-O-sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1858277]		Q9JHE4	5.5	2.4E-02	3.0	1.0E-02	-4.4	3.9E-03	0.3	6.8E-01
ENSMUST00000078778	leukocyte immunoglobulin-like receptor, subfamily B, member 4A [Source:MGI Symbol;Acc:MGI:102701]		Q64281	-13.0	6.8E-03	-7.8	2.6E-03	0.9	1.4E-01	-0.9	6.7E-01
ENSMUST00000078800	nuclear transcription factor-Y alpha [Source:MGI Symbol;Acc:MGI:97316]		P23708	-3.8	2.8E-03	2.2	3.5E-01	-2.9	2.5E-01	0.9	6.1E-01
ENSMUST00000076859	polo-like kinase 3 [Source:MGI Symbol;Acc:MGI:109604]	Q6P571		0.1	9.8E-01	-2.9	4.5E-01	-1.6	4.6E-01	1.3	7.2E-01
ENSMUST00000078803	tonsoku-like, DNA repair protein [Source:MGI Symbol;Acc:MGI:1919999]		Q9D1C8	-6.3	1.6E-06	3.7	2.1E-02	-0.6	6.3E-01	2.6	2.5E-02
ENSMUST00000078804	ribosomal protein L35A [Source:MGI Symbol;Acc:MGI:1928894]	Q6ZWX1	O55142	-6.8	2.6E-04	-1.1	1.3E-01	0.7	1.0E-01	0.2	7.4E-01
ENSMUST00000078825	Fc receptor, IgG, low affinity IV [Source:MGI Symbol;Acc:MGI:2179523]	A0A0B4J1G0		-5.9	5.4E-07	-1.9	6.8E-03	0.6	9.3E-02	0.1	8.0E-01
ENSMUST00000078827	component of Sp100-rs [Source:MGI Symbol;Acc:MGI:1891441]	Q8BYZ8		1.8	5.6E-03	-2.0	8.5E-02	0.6	3.2E-01	-1.3	2.5E-01
ENSMUST00000078835	kallikrein 1-related peptidase b1 [Source:MGI Symbol;Acc:MGI:892019]		P00755	6.7	1.7E-04	6.8	4.3E-04	-0.4	7.6E-01	-0.5	4.4E-01
ENSMUST00000078845	glia maturation factor, gamma [Source:MGI Symbol;Acc:MGI:1927135]	A7VJA4	Q9ERL7	-10.4	1.3E-06	-5.7	1.2E-04	-0.2	5.3E-01	-0.7	4.6E-01
ENSMUST00000078849	glypican 6 [Source:MGI Symbol;Acc:MGI:1346322]	Q3V1C9	Q9R087	7.4	8.9E-05	7.4	5.3E-05	-1.5	2.2E-01	0.4	4.6E-01
ENSMUST00000076941	transcription termination factor, RNA polymerase II [Source:MGI Symbol;Acc:MGI:1921294]		Q5NC05	0.1	9.7E-01	-0.3	8.7E-01	0.1	9.6E-01	0.4	8.0E-01
ENSMUST00000078856	klotho [Source:MGI Symbol;Acc:MGI:1101771]		O35082	8.7	2.4E-05	-2.1	1.1E-02	0.2	6.7E-01	-0.2	7.2E-01
ENSMUST00000078873	limbic system-associated membrane protein [Source:MGI Symbol;Acc:MGI:1261760]		Q8BLK3	6.5	1.3E-04	1.6	2.4E-02	-0.6	2.6E-01	0.2	6.8E-01
ENSMUST00000078878	mitochondrial ribosomal protein S14 [Source:MGI Symbol;Acc:MGI:1928141]	M0QWY3		-7.5	2.1E-05	2.6	1.8E-02	-0.2	8.4E-01	0.3	6.5E-01
ENSMUST00000078880	sortilin-related VPS10 domain containing receptor 3 [Source:MGI Symbol;Acc:MGI:1913923]	Q1HL22	Q8VI51	8.0	2.1E-05	6.3	2.0E-04	-0.5	6.6E-01	-1.0	1.4E-01
ENSMUST00000078908	NTPase, KAP family P-loop domain containing 1 [Source:MGI Symbol;Acc:MGI:1916797]	H7BX48		6.0	1.7E-04	-4.3	2.3E-03	0.3	6.2E-01	-1.1	3.5E-01
ENSMUST00000078912	adenosine monophosphate deaminase 2 [Source:MGI Symbol;Acc:MGI:88016]	A2AE27		-2.7	6.1E-03	5.6	2.9E-03	-0.7	6.6E-01	0.5	5.9E-01
ENSMUST00000078918	lethal, Chr 7, Rinchik 6 [Source:MGI Symbol;Acc:MGI:96738]	G5E8I4		-4.3	4.8E-04	5.1	8.8E-03	-2.0	2.7E-01	-0.7	5.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000076991	RIKEN cDNA 4930453N24 gene [Source:MGI Symbol;Acc:MGI:1914859]		Q3TTL0	0.2	4.9E-01	0.3	4.3E-01	0.0	9.4E-01	-0.1	8.3E-01
ENSMUST00000078933	olfactory receptor 502 [Source:MGI Symbol;Acc:MGI:3030336]		Q8VG09	5.9	1.8E-04	-6.5	1.6E-03	-0.5	3.7E-01	1.1	4.8E-01
ENSMUST00000078944	PHD finger protein 6 [Source:MGI Symbol;Acc:MGI:1918248]		Q9D4J7	-3.5	3.3E-03	-5.2	1.3E-02	0.7	4.1E-01	-0.7	7.0E-01
ENSMUST00000078945	G-rich RNA sequence binding factor 1 [Source:MGI Symbol;Acc:MGI:106479]		Q8C5Q4	-3.6	5.4E-03	5.0	1.0E-04	-2.5	1.3E-02	-0.1	8.8E-01
ENSMUST00000078953	DENN/MADD domain containing 6B [Source:MGI Symbol;Acc:MGI:1916690]		Q9D9V7	3.6	1.3E-03	-6.1	1.1E-02	0.9	3.1E-01	1.8	3.8E-01
ENSMUST00000077083				0.4	4.0E-01	0.9	1.2E-01	0.0	9.4E-01	-0.5	3.3E-01
ENSMUST00000077088	RAD18 E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1890476]		Q9QXK2	3.7	1.0E-01	0.6	7.9E-01	-2.3	3.2E-01	0.9	6.1E-01
ENSMUST00000078988	LIM domain containing preferred translocation partner in lipoma [Source:MGI Symbol;Acc:MGI:2441849]		Q8BFW7	10.3	1.4E-04	6.2	4.3E-04	-1.9	1.6E-01	-0.4	5.5E-01
ENSMUST00000079009	tudor domain containing 9 [Source:MGI Symbol;Acc:MGI:1921941]		Q14BI7	7.7	2.0E-05	7.8	1.3E-05	-0.3	7.4E-01	0.4	4.3E-01
ENSMUST00000079012	membrane-associated ring finger (C3HC4) 8 [Source:MGI Symbol;Acc:MGI:1919029]		Q9DBD2	-4.5	3.3E-03	5.5	9.4E-04	-1.1	3.5E-01	0.2	7.5E-01
ENSMUST00000079033	biogenesis of lysosomal organelles complex-1, subunit 2 [Source:MGI Symbol;Acc:MGI:1920939]		Q9CWG9	-4.0	1.6E-04	5.7	4.2E-03	-0.7	6.6E-01	-0.1	9.1E-01
ENSMUST00000079038	Hedgehog-interacting protein [Source:MGI Symbol;Acc:MGI:1341847]		Q7TN16	7.7	2.5E-05	7.5	4.8E-05	-0.6	6.1E-01	-0.1	7.8E-01
ENSMUST00000079045	fused in sarcoma [Source:MGI Symbol;Acc:MGI:1353633]	Q8BNR3		2.7	7.4E-03	5.2	2.4E-04	0.2	8.4E-01	-0.5	4.5E-01
ENSMUST00000077160	SRY (sex determining region Y)-box 5 [Source:MGI Symbol;Acc:MGI:98367]	Q2TBA9		4.8	8.4E-02	4.3	1.6E-01	-0.5	8.7E-01	0.0	9.9E-01
ENSMUST00000077163				-3.3	3.2E-01	-8.4	6.6E-02	-5.1	1.2E-02	-0.1	9.9E-01
ENSMUST00000079063	SRY (sex determining region Y)-box 11 [Source:MGI Symbol;Acc:MGI:98359]		Q7M6Y2	8.2	2.5E-05	6.9	1.9E-04	0.1	9.4E-01	-1.1	1.2E-01
ENSMUST00000077175	polymerase (RNA) III (DNA directed) polypeptide B [Source:MGI Symbol;Acc:MGI:1917678]		P59470	-0.6	2.0E-01	0.9	1.6E-01	0.8	9.3E-02	-0.7	2.3E-01
ENSMUST00000079080	mitogen-activated protein kinase 7 [Source:MGI Symbol;Acc:MGI:1346347]		Q9WVS8	-6.4	2.1E-03	2.8	2.9E-01	-0.7	7.5E-01	3.2	1.2E-01
ENSMUST00000079081	aquaporin 4 [Source:MGI Symbol;Acc:MGI:107387]			6.9	2.3E-04	-3.2	7.5E-03	1.3	2.8E-02	0.5	6.2E-01
ENSMUST00000079085	ribosomal protein L34 [Source:MGI Symbol;Acc:MGI:1915686]		Q9D1R9	-6.9	5.9E-05	5.5	7.3E-04	-0.5	6.6E-01	-0.1	8.9E-01
ENSMUST00000077196	keratin 80 [Source:MGI Symbol;Acc:MGI:1921377]		Q0VBK2	-1.1	1.2E-01	-0.4	6.6E-01	0.9	1.8E-01	0.2	8.4E-01
ENSMUST00000079117	olfactory receptor 66 [Source:MGI Symbol;Acc:MGI:1341906]	F8VQ01		4.6	1.6E-02	6.9	3.7E-04	-0.7	6.1E-01	0.1	8.8E-01
ENSMUST00000079121	mitochondrial ribosomal protein L18 [Source:MGI Symbol;Acc:MGI:1914931]		Q9CQL5	-4.0	5.0E-05	-4.0	8.6E-03	1.3	4.8E-02	0.2	8.6E-01
ENSMUST00000079125	SCAN domain-containing 1 [Source:MGI Symbol;Acc:MGI:1343132]	Q2M4I6		-6.4	1.3E-03	6.5	7.7E-04	-0.4	7.6E-01	-0.8	2.9E-01
ENSMUST00000077225	zinc finger and BTB domain containing 18 [Source:MGI Symbol;Acc:MGI:1353609]		Q9WUK6	0.7	2.2E-01	2.0	2.0E-02	1.1	8.7E-02	-0.2	7.1E-01
ENSMUST00000079132	chitinase, acidic 1 [Source:MGI Symbol;Acc:MGI:1932052]		Q91XA9	6.1	4.3E-04	6.8	6.2E-05	0.1	8.9E-01	0.3	5.9E-01
ENSMUST00000077235	dehydrogenase/reductase (SDR family) X-linked [Source:HGNC Symbol;Acc:HGNC:18399]			-0.7	2.3E-01	-1.2	1.5E-01	0.6	2.4E-01	1.1	1.7E-01
ENSMUST00000079184	stefin A2 like 1 [Source:MGI Symbol;Acc:MGI:3524944]	Q8BWM3		-9.3	2.1E-06	5.7	4.0E-04	-0.6	5.9E-01	0.5	4.2E-01
ENSMUST00000077257	retinoid X receptor alpha [Source:MGI Symbol;Acc:MGI:98214]	A2AJP1	P28700	-0.6	2.4E-01	-0.5	4.7E-01	0.3	4.6E-01	0.2	7.4E-01
ENSMUST00000077271	G elongation factor, mitochondrial 1 [Source:MGI Symbol;Acc:MGI:107339]		Q8K0D5	-0.4	6.1E-01	-0.1	8.8E-01	-0.4	5.0E-01	-0.6	4.4E-01
ENSMUST00000079195	storkhead box 2 [Source:MGI Symbol;Acc:MGI:1918319]		Q499E5	7.8	6.0E-04	1.0	2.0E-01	-1.3	5.4E-02	0.0	9.6E-01
ENSMUST00000079204	rabphilin 3A [Source:MGI Symbol;Acc:MGI:102788]		P47708	4.3	2.6E-05	-1.5	2.0E-02	1.0	1.7E-02	0.0	9.5E-01
ENSMUST00000079213	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A [Source:MGI Symbol;Acc:MGI:1916962]	B2RTE3	Q4FK66	-4.7	2.1E-05	-2.9	5.5E-04	-1.1	8.4E-03	-0.3	6.7E-01
ENSMUST00000079234	olfactory receptor 157 [Source:MGI Symbol;Acc:MGI:1352684]	Q9QZ20		6.5	2.0E-04	6.5	6.7E-04	-0.5	7.3E-01	-2.4	1.2E-02
ENSMUST00000079237	zinc finger protein 125 [Source:MGI Symbol;Acc:MGI:1336211]	F6SU29		2.9	2.3E-03	4.0	8.2E-02	7.9	1.7E-03	0.9	4.8E-01
ENSMUST00000079242	zinc finger protein 52 [Source:MGI Symbol;Acc:MGI:99199]	Q8BJ45		-2.1	8.3E-03	6.4	6.4E-04	-0.6	6.4E-01	-0.3	6.7E-01
ENSMUST00000079252	inositol polyphosphate multikinase [Source:MGI Symbol;Acc:MGI:1916968]		Q7TT16	-3.5	5.3E-04	4.7	8.6E-04	-3.2	2.1E-02	0.2	7.8E-01
ENSMUST00000079278	neurensin 2 [Source:MGI Symbol;Acc:MGI:2684969]		Q5HZK2	6.6	5.9E-05	-2.7	5.1E-02	0.8	2.3E-01	-0.3	8.0E-01
ENSMUST00000079279	predicted gene 10118 [Source:MGI Symbol;Acc:MGI:3642340]	Q8C8J5		7.0	5.1E-04	-5.4	2.3E-03	1.5	2.2E-02	-0.3	8.4E-01
ENSMUST00000079282	suppression of tumorigenicity 5 [Source:MGI Symbol;Acc:MGI:108517]		Q924W7	7.0	1.2E-04	-0.5	3.9E-01	0.0	9.7E-01	-4.6	3.4E-04
ENSMUST00000079300	Rho guanine nucleotide exchange factor (GEF) 26 [Source:MGI Symbol;Acc:MGI:1918053]	D3YYY8		3.6	2.1E-04	6.1	2.0E-04	-0.6	6.0E-01	0.1	9.3E-01
ENSMUST00000079306	Ly6/Plaur domain containing 4 [Source:MGI Symbol;Acc:MGI:2687054]		Q8BVP6	6.4	1.3E-03	7.1	2.6E-04	-0.7	6.2E-01	0.4	5.3E-01
ENSMUST00000079323	multiple C2 domains, transmembrane 2 [Source:MGI Symbol;Acc:MGI:2685335]		Q5RJH2	-3.8	4.2E-05	-8.0	7.1E-04	0.2	5.9E-01	0.8	6.3E-01
ENSMUST00000079324	ubiquitin-like 3 [Source:MGI Symbol;Acc:MGI:1344373]		Q9Z2M6	-5.4	2.0E-04	2.6	1.8E-03	0.1	7.9E-01	0.1	7.6E-01
ENSMUST00000079360	actin-binding LIM protein 1 [Source:MGI Symbol;Acc:MGI:1194500]	E9QK41		6.2	2.4E-04	0.5	6.0E-01	1.2	1.4E-01	-5.3	2.9E-03
ENSMUST00000079368	a disintegrin and metallopeptidase domain 1b [Source:MGI Symbol;Acc:MGI:2429506]		Q8R534	7.6	3.0E-05	-10.6	2.5E-05	-1.0	1.7E-02	0.8	5.5E-01
ENSMUST00000079390	lin-28 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:3584032]		Q45KJ6	8.3	1.4E-05	-5.4	1.1E-03	1.3	2.3E-02	-2.3	1.4E-01
ENSMUST00000077408	biogenesis of lysosomal organelles complex-1, subunit 3 [Source:MGI Symbol;Acc:MGI:2678952]		Q5U5M8	-0.6	2.3E-01	0.4	5.6E-01	1.4	1.8E-02	0.4	5.3E-01
ENSMUST00000079400	asparaginase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2144822]		A0JNU3	7.5	1.2E-04	5.3	8.5E-04	-0.6	6.0E-01	0.9	1.8E-01
ENSMUST00000079403	ATH1, acid trehalase-like 1 (yeast) [Source:MGI Symbol;Acc:MGI:2444047]		Q8BP56	-5.5	1.3E-03	2.4	4.5E-02	-3.5	2.5E-02	1.0	2.5E-01
ENSMUST00000079405	zinc finger protein 239 [Source:MGI Symbol;Acc:MGI:1306812]		P24399	6.5	3.1E-04	6.0	2.2E-03	-0.9	5.5E-01	-1.2	2.0E-01
ENSMUST00000077440	nuclear factor of activated T cells 5 [Source:MGI Symbol;Acc:MGI:1859333]		Q9WV30	0.1	8.9E-01	1.2	3.0E-01	0.5	5.7E-01	-0.5	6.3E-01
ENSMUST00000077451	ras homolog gene family, member T1 [Source:MGI Symbol;Acc:MGI:1926078]		Q8BG51	-3.5	6.4E-02	-0.9	6.9E-01	2.5	1.2E-01	-0.1	9.8E-01
ENSMUST00000077453	death associated protein kinase 1 [Source:MGI Symbol;Acc:MGI:1916885]		Q80YE7	1.2	4.6E-01	1.2	4.4E-01	-2.2	1.6E-01	-2.2	1.7E-01
ENSMUST00000077456	ataxin 7-like 1 [Source:MGI Symbol;Acc:MGI:3584458]		Q9CZ05	-1.4	3.9E-02	-3.6	1.2E-02	0.7	2.0E-01	2.9	2.9E-02
ENSMUST00000079413	FK506 binding protein 5 [Source:MGI Symbol;Acc:MGI:104670]	Q4FJN2	Q64378	-6.3	4.3E-06	2.0	2.8E-01	-3.4	9.5E-02	1.0	5.3E-01
ENSMUST00000079421	Fas death domain-associated protein [Source:MGI Symbol;Acc:MGI:1197015]	Q3UKR0		-3.4	1.1E-03	5.4	1.9E-02	-0.7	7.5E-01	1.1	3.4E-01
ENSMUST00000079423	family with sequence similarity 57, member B [Source:MGI Symbol;Acc:MGI:1916202]		Q7TNV1	5.7	2.6E-04	-4.8	9.6E-04	-0.9	7.8E-02	-0.9	4.3E-01
ENSMUST00000079424	glycoprotein galactosyltransferase alpha 1, 3 [Source:MGI Symbol;Acc:MGI:95704]	Q91W00		-7.1	3.1E-03	3.1	8.6E-02	-2.8	1.4E-01	-0.2	8.8E-01
ENSMUST00000079443	midline 1 [Source:MGI Symbol;Acc:MGI:1100537]	Q6PD02		18.1	7.7E-05	-3.1	1.9E-02	0.5	3.5E-01	-0.3	7.8E-01
ENSMUST00000077485	zinc finger protein 12 [Source:MGI Symbol;Acc:MGI:99157]		Q7TSI0	-3.6	2.6E-01	0.4	9.1E-01	1.8	5.0E-01	-2.1	5.0E-01
ENSMUST00000079447	spermatogenesis associated glutamate (E)-rich protein 4A [Source:MGI Symbol;Acc:MGI:1922907]	F8VPX6		8.6	6.2E-06	3.2	4.0E-02	-1.5	3.0E-01	0.0	1.0E+00
ENSMUST00000079451	potassium channel, subfamily K, member 2 [Source:MGI Symbol;Acc:MGI:109366]	Q6P6P9		7.0	1.0E-04	3.8	8.7E-03	0.2	8.7E-01	-0.1	8.8E-01
ENSMUST00000079463	cholinergic receptor, nicotinic, beta polypeptide 3 [Source:MGI Symbol;Acc:MGI:106212]		Q8BMN3	7.8	6.8E-05	5.6	4.3E-04	1.0	3.1E-01	0.6	3.2E-01
ENSMUST00000079464	tubulin, alpha 4A [Source:MGI Symbol;Acc:MGI:1095410]	A0A0A0MQA5		-7.0	4.4E-05	0.8	5.9E-01	-4.6	3.0E-02	-0.5	7.4E-01
ENSMUST00000079465	olfactory receptor 156 [Source:MGI Symbol;Acc:MGI:1352683]	Q8VGA9		6.6	1.5E-04	6.1	6.7E-04	-0.7	6.2E-01	0.0	9.9E-01
ENSMUST00000079469	nuclear GTPase, germinal center associated [Source:MGI Symbol;Acc:MGI:2685446]	D3YY21		4.6	1.5E-02	9.0	4.0E-05	-0.4	7.5E-01	-0.6	2.9E-01
ENSMUST00000077548	CTTNBP2 N-terminal like [Source:MGI Symbol;Acc:MGI:1933137]		Q99LJ0	6.6	3.8E-02	8.3	1.7E-02	-0.8	8.0E-01	-2.5	1.6E-01
ENSMUST00000079476	NLR family, pyrin domain containing 3 [Source:MGI Symbol;Acc:MGI:2653833]		Q8R4B8	-4.6	3.4E-03	7.0	3.8E-04	-0.2	8.8E-01	0.5	4.4E-01
ENSMUST00000079490	nucleosome assembly protein 1-like 3 [Source:MGI Symbol;Acc:MGI:1859565]		Q794H2	4.2	9.0E-04	-3.2	2.4E-03	0.4	3.4E-01	-0.7	4.2E-01
ENSMUST00000079491	seizure related 6 homolog like [Source:MGI Symbol;Acc:MGI:1935121]		Q6P1D5	7.7	4.9E-05	-5.1	1.6E-02	0.1	9.0E-01	-1.5	4.5E-01
ENSMUST00000079496	ubiquitin-conjugating enzyme E2S [Source:MGI Symbol;Acc:MGI:1925141]		Q921J4	-2.9	1.6E-03	-7.5	5.2E-04	0.6	2.0E-01	-0.8	6.1E-01
ENSMUST00000077610	sushi domain containing 2 [Source:MGI Symbol;Acc:MGI:1918983]		Q9DBX3	3.2	9.0E-02	-0.1	9.8E-01	-1.0	6.2E-01	2.3	3.1E-01
ENSMUST00000077626	phosphatidylinositol glycan anchor biosynthesis, class U [Source:MGI Symbol;Acc:MGI:3039607]	Q3TAA8		-2.6	1.0E-01	0.1	9.5E-01	2.1	2.5E-01	-0.7	7.1E-01
ENSMUST00000079510	calcium homeostasis endoplasmic reticulum protein [Source:MGI Symbol;Acc:MGI:106417]	G5E8I8		-1.2	2.5E-02	-1.8	2.3E-01	0.6	4.9E-01	-1.4	3.6E-01
ENSMUST00000079534	transforming, acidic coiled-coil containing protein 3 [Source:MGI Symbol;Acc:MGI:1341163]	Q6NV52		4.4	2.1E-02	6.9	2.1E-04	0.8	4.7E-01	0.0	1.0E+00
ENSMUST00000077642	kinesin-associated protein 3 [Source:MGI Symbol;Acc:MGI:107566]		P70188	4.6	1.1E-01	0.3	9.0E-01	-4.9	8.1E-02	-0.6	7.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000079545	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 [Source:MGI Symb		P70277	6.9	7.5E-04	8.0	1.4E-05	-0.3	7.5E-01	-0.7	1.7E-01
ENSMUST00000079548	F-box and WD-40 domain protein 20 [Source:MGI Symbol;Acc:MGI:3584372]	Q5U467		6.1	6.4E-04	-0.7	6.1E-01	1.8	7.3E-02	-2.0	2.0E-01
ENSMUST00000079582	ELKS/RAB6-interacting/CAST family member 1 [Source:MGI Symbol;Acc:MGI:2151013]		Q99MI1	6.4	2.5E-05	-2.2	1.9E-01	1.8	7.7E-02	-0.4	7.9E-01
ENSMUST00000079590	myosin IA [Source:MGI Symbol;Acc:MGI:107732]		O88329	3.8	2.8E-03	-5.9	6.9E-04	0.4	3.3E-01	0.4	7.4E-01
ENSMUST00000079597	progestin and adipoQ receptor family member IX [Source:MGI Symbol;Acc:MGI:1922802]		Q6TCG2	7.5	6.1E-05	7.1	1.5E-04	-1.0	4.5E-01	-0.2	7.6E-01
ENSMUST00000077689	slingshot homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2686240]	F8WHT2		0.7	7.8E-01	-1.1	7.3E-01	-1.6	5.0E-01	0.3	9.3E-01
ENSMUST00000079605	zinc finger protein 462 [Source:MGI Symbol;Acc:MGI:107690]	B1AWL5		6.2	7.1E-03	-3.5	4.8E-02	-0.9	2.8E-01	-0.9	6.2E-01
ENSMUST00000079611	expressed sequence AA415398 [Source:MGI Symbol;Acc:MGI:3035485]	Q6P3A2		2.6	3.1E-03	9.1	1.9E-05	-0.7	5.8E-01	-0.6	2.6E-01
ENSMUST00000079618	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 [Source:MGI Symbol;Acc:MGI:109243]	Q3TRR3	P70126	7.0	5.5E-05	6.7	1.1E-04	-0.6	6.0E-01	-0.2	7.8E-01
ENSMUST00000079624	ankyrin repeat domain 61 [Source:MGI Symbol;Acc:MGI:1913979]		Q9CQM6	7.0	3.5E-04	8.6	8.9E-03	-0.2	9.4E-01	-1.6	2.8E-01
ENSMUST00000079625	torsin family 3, member A [Source:MGI Symbol;Acc:MGI:1353652]		Q9ER38	-5.8	1.7E-03	4.4	1.3E-03	-2.0	8.6E-02	-3.0	2.9E-03
ENSMUST00000079634	exosome component 5 [Source:MGI Symbol;Acc:MGI:107889]		Q9CRA8	-2.7	7.4E-03	-4.4	3.3E-02	0.5	5.8E-01	-0.8	7.1E-01
ENSMUST00000079639	claudin 24 [Source:MGI Symbol;Acc:MGI:3712484]	D3YXJ9		7.4	3.8E-04	2.6	7.9E-03	1.3	6.3E-02	0.5	4.5E-01
ENSMUST00000077737	bromodomain containing 3 [Source:MGI Symbol;Acc:MGI:1914632]	Q3TUI3	Q8K2F0	-1.0	1.8E-01	-1.6	1.6E-01	0.8	2.3E-01	1.4	1.9E-01
ENSMUST00000079642	zinc finger protein 119a [Source:MGI Symbol;Acc:MGI:1345189]	Q9JIC0		-1.7	2.1E-02	-1.6	3.8E-01	1.3	2.5E-01	-0.5	7.7E-01
ENSMUST00000079644	Y box protein 1 [Source:MGI Symbol;Acc:MGI:99146]	Q3UBT1	P62960	-5.9	2.3E-04	-9.9	8.6E-04	0.8	2.5E-01	1.1	6.2E-01
ENSMUST00000079652	SRY (sex determining region Y)-box 7 [Source:MGI Symbol;Acc:MGI:98369]	Q3U1W5	P40646	8.7	3.2E-05	6.4	1.3E-03	-0.6	6.7E-01	-0.5	5.4E-01
ENSMUST00000077776				1.4	1.5E-01	-4.2	3.5E-03	-4.8	1.3E-04	0.8	4.6E-01
ENSMUST00000077780	zinc finger protein 61 [Source:MGI Symbol;Acc:MGI:99663]	Q923D1		3.1	3.5E-02	6.7	5.4E-03	2.3	2.3E-01	-1.2	2.6E-01
ENSMUST00000077783	RIKEN cDNA 0610030E20 gene [Source:MGI Symbol;Acc:MGI:1915614]		Q149G0	-0.9	5.9E-02	0.3	5.7E-01	1.3	1.2E-02	0.1	8.8E-01
ENSMUST00000079692	G protein-coupled receptor 182 [Source:MGI Symbol;Acc:MGI:109545]	G3X9R9		5.5	3.1E-04	4.0	9.0E-04	-1.8	6.6E-02	-1.2	1.0E-01
ENSMUST00000079702	chromobox 1 [Source:MGI Symbol;Acc:MGI:105369]	Q9CYJ8		-3.7	2.1E-02	2.6	8.3E-03	0.6	3.5E-01	-0.3	6.2E-01
ENSMUST00000077791	zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:99154]	Q3UI68		0.4	3.6E-01	0.2	6.6E-01	-1.1	3.1E-02	-0.9	1.3E-01
ENSMUST00000079703	non-SMC element 2 homolog (MMS21, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915751]		Q91VT1	-3.1	1.3E-04	-4.3	1.3E-03	0.0	9.5E-01	-3.1	3.2E-02
ENSMUST00000077817	heterogeneous nuclear ribonucleoprotein H1 [Source:MGI Symbol;Acc:MGI:1891925]	Q8C2Q7		-3.8	2.0E-01	-5.0	1.6E-01	-2.2	2.1E-01	-1.0	8.0E-01
ENSMUST00000077821	Rho GTPase activating protein 39 [Source:MGI Symbol;Acc:MGI:107858]	H7BX46		3.7	1.6E-01	-0.6	8.4E-01	-1.7	4.9E-01	2.6	3.5E-01
ENSMUST00000079716	ribosomal protein L17 [Source:MGI Symbol;Acc:MGI:2448270]	Q6ZWZ7		-8.2	6.0E-05	-4.3	3.1E-03	0.9	7.7E-02	1.3	2.6E-01
ENSMUST00000079719	T-box 3 [Source:MGI Symbol;Acc:MGI:98495]	Q4VA43	P70324	7.0	1.2E-02	6.2	2.2E-02	-0.6	8.2E-01	-1.3	3.5E-01
ENSMUST00000077851	lysine (K)-specific demethylase 4C [Source:MGI Symbol;Acc:MGI:1924054]		Q8VCD7	4.9	9.0E-02	4.5	1.5E-01	-0.5	8.7E-01	-0.1	9.6E-01
ENSMUST00000079721	engrailed 1 [Source:MGI Symbol;Acc:MGI:95389]		P09065	7.5	3.0E-05	-2.5	3.1E-03	-0.5	1.7E-01	0.0	9.5E-01
ENSMUST00000079724	HCLS1 associated X-1 [Source:MGI Symbol;Acc:MGI:1346319]	B9EJR4	O35387	-2.5	6.3E-03	7.4	7.1E-05	-0.6	5.8E-01	-0.4	5.5E-01
ENSMUST00000077856	ribosomal protein L27 [Source:MGI Symbol;Acc:MGI:98036]	Q5BLJ9	P61358	-1.4	2.2E-01	-0.9	5.1E-01	-0.9	3.7E-01	-1.5	2.6E-01
ENSMUST00000077867	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 [Source:MGI Symbol;Acc:MGI:1351644]	F8WJ10		0.2	7.8E-01	2.9	2.6E-02	1.1	3.0E-01	-1.6	9.2E-02
ENSMUST00000079746	C-terminal binding protein 1 [Source:MGI Symbol;Acc:MGI:1201685]		O88712	-4.8	1.2E-04	5.3	9.3E-03	0.4	8.2E-01	0.5	6.1E-01
ENSMUST00000079749	zinc finger protein 422 [Source:MGI Symbol;Acc:MGI:1914505]		Q9ERU3	6.2	1.4E-03	-3.5	2.2E-02	0.2	8.1E-01	-0.3	8.1E-01
ENSMUST00000079759	predicted gene 5591 [Source:MGI Symbol;Acc:MGI:3648692]	Q8CDK1		7.6	2.8E-04	-0.2	7.6E-01	0.6	1.5E-01	-0.6	2.9E-01
ENSMUST00000079764	WD repeat domain 83 opposite strand [Source:MGI Symbol;Acc:MGI:3041257]	Q3UI07	Q6ZWX0	-4.4	1.8E-03	8.4	1.7E-05	-0.5	6.6E-01	-0.8	1.3E-01
ENSMUST00000079772	mor necrosis factor receptor superfamily, member 11b (osteoprotegerin) [Source:MGI Symbol;Acc:MGI:10958	Q3UK97	O08712	6.2	2.9E-03	-2.6	6.3E-02	0.1	8.7E-01	-0.5	7.3E-01
ENSMUST00000079788	mohawk homeobox [Source:MGI Symbol;Acc:MGI:2687286]	B2RQ30		7.3	5.4E-04	6.3	3.3E-03	-0.8	6.6E-01	0.7	4.8E-01
ENSMUST00000079791	phosphate cytidylyltransferase 1, choline, alpha isoform [Source:MGI Symbol;Acc:MGI:88557]		P49586	-8.8	3.5E-06	8.1	1.3E-04	-0.7	6.3E-01	-0.9	2.2E-01
ENSMUST00000079812	notch 2 [Source:MGI Symbol;Acc:MGI:97364]	G5E8J0		-3.6	2.7E-05	-8.3	2.9E-03	-1.2	9.6E-02	1.4	5.1E-01
ENSMUST00000079817	serine/threonine kinase 24 [Source:MGI Symbol;Acc:MGI:2385007]	Q3U335	Q99KH8	-6.1	3.4E-06	3.5	6.4E-03	-2.8	3.3E-02	-0.5	5.1E-01
ENSMUST00000079818	predicted gene 8973 [Source:MGI Symbol;Acc:MGI:3648534]	D3YX71		6.1	6.2E-04	5.3	9.8E-05	-4.9	1.9E-03	0.3	6.3E-01
ENSMUST00000077930	dystrobrevin, beta [Source:MGI Symbol;Acc:MGI:1203728]	Q8K0N0		4.2	6.0E-02	4.7	1.6E-01	0.9	7.6E-01	0.4	8.3E-01
ENSMUST00000077935	trichorhinophalangeal syndrome I (human) [Source:MGI Symbol;Acc:MGI:1927616]	G3UW90		1.1	5.1E-02	1.6	3.5E-02	0.3	5.3E-01	-0.2	7.9E-01
ENSMUST00000077938	hydroxyacylglutathione hydrolase-like [Source:MGI Symbol;Acc:MGI:1919877]		Q9DB32	-1.8	4.2E-02	-1.7	2.1E-01	1.2	1.2E-01	1.1	3.6E-01
ENSMUST00000079824	G protein-coupled receptor 84 [Source:MGI Symbol;Acc:MGI:1934129]			-2.3	7.9E-03	-2.6	6.0E-02	0.1	9.4E-01	-2.9	9.7E-02
ENSMUST00000077955	coiled-coil domain containing 102A [Source:MGI Symbol;Acc:MGI:2686927]	B2RTE5	Q3TMW1	1.9	5.1E-02	2.1	8.6E-02	0.5	6.0E-01	0.3	7.6E-01
ENSMUST00000079828	neurotrophic tyrosine kinase, receptor, type 2 [Source:MGI Symbol;Acc:MGI:97384]		P15209	7.1	2.2E-05	-6.6	6.4E-03	-0.1	8.1E-01	1.7	3.8E-01
ENSMUST00000079857	cell division cycle 25B [Source:MGI Symbol;Acc:MGI:99701]	Q9DBN8		-3.2	1.2E-03	5.9	1.6E-04	-0.9	4.0E-01	0.4	4.3E-01
ENSMUST00000079866	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]		Q6PDM2	-5.0	5.9E-04	-6.2	6.6E-04	-0.2	7.1E-01	-0.8	5.6E-01
ENSMUST00000077977	family with sequence similarity 73, member B [Source:MGI Symbol;Acc:MGI:1922035]		Q8BK03	-2.0	2.3E-01	1.1	4.7E-01	0.2	8.9E-01	-2.9	1.0E-01
ENSMUST00000079875	olfactory receptor 1418 [Source:MGI Symbol;Acc:MGI:3031252]	Q7TQS3		6.1	8.7E-04	-5.7	9.2E-03	0.8	2.4E-01	-0.4	8.2E-01
ENSMUST00000079883	secretory carrier membrane protein 4 [Source:MGI Symbol;Acc:MGI:1928947]	Q3TGX0	Q9JKV5	-4.3	2.1E-02	5.9	2.7E-04	-0.3	7.5E-01	-0.2	7.4E-01
ENSMUST00000079945	phosphate regulating endopeptidase homolog, X-linked [Source:MGI Symbol;Acc:MGI:107489]	Q3TYM9	P70669	6.0	2.3E-04	7.7	2.0E-04	-0.2	9.0E-01	0.5	4.0E-01
ENSMUST00000079957	Fc receptor, IgE, high affinity I, gamma polypeptide [Source:MGI Symbol;Acc:MGI:95496]		P20491	-9.7	4.7E-06	3.7	6.9E-03	-2.9	3.6E-02	-1.0	2.7E-01
ENSMUST00000079960	ribosomal protein L13, pseudogene 3 [Source:MGI Symbol;Acc:MGI:3646682]			4.6	1.6E-03	5.4	5.8E-04	0.8	4.1E-01	-0.3	7.0E-01
ENSMUST00000079961	nucleoporin 93 [Source:MGI Symbol;Acc:MGI:1919055]		Q8BJ71	-3.1	2.7E-02	5.5	4.2E-03	-0.2	9.1E-01	0.1	9.3E-01
ENSMUST00000079978	unc-13 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:1342278]		Q9Z1N9	5.7	1.8E-04	4.1	3.2E-02	-1.8	3.3E-01	-0.7	6.0E-01
ENSMUST00000080001	ubiquitin-fold modifier conjugating enzyme 1 [Source:MGI Symbol;Acc:MGI:1913405]		Q9CR09	-8.5	2.8E-06	0.4	6.1E-01	1.4	2.1E-02	-4.7	5.7E-04
ENSMUST00000080030	G1 to S phase transition 1 [Source:MGI Symbol;Acc:MGI:1316728]		Q8R050	-6.5	4.3E-04	-2.6	6.2E-02	0.6	4.5E-01	-1.1	4.4E-01
ENSMUST00000078053	potassium channel tetramerisation domain containing 9 [Source:MGI Symbol;Acc:MGI:2145579]		Q80UN1	2.8	1.2E-01	0.7	7.2E-01	-1.4	3.9E-01	0.7	6.9E-01
ENSMUST00000080058	egl-9 family hypoxia-inducible factor 2 [Source:MGI Symbol;Acc:MGI:1932287]	Q80X29	Q91YE2	-4.0	7.4E-04	4.9	6.8E-03	-0.4	7.9E-01	-0.1	9.4E-01
ENSMUST00000078058	purine-rich element binding protein G [Source:MGI Symbol;Acc:MGI:1922279]		Q8R4E6	-2.3	1.2E-01	1.2	4.5E-01	1.3	3.3E-01	-2.2	1.5E-01
ENSMUST00000078061	euchromatic histone lysine N-methyltransferase 2 [Source:MGI Symbol;Acc:MGI:2148922]		Q9Z148	-1.5	5.0E-01	-0.5	8.6E-01	0.0	9.9E-01	-0.9	7.1E-01
ENSMUST00000080062	predicted gene, 17541 [Source:MGI Symbol;Acc:MGI:4937175]	F6YJW4		4.7	6.1E-03	0.3	7.9E-01	2.2	2.0E-02	-0.4	7.2E-01
ENSMUST00000080065	solute carrier family 27 (fatty acid transporter), member 4 [Source:MGI Symbol;Acc:MGI:1347347]		Q91VE0	-4.1	6.8E-04	-3.9	1.4E-03	-0.9	7.6E-02	-0.5	6.0E-01
ENSMUST00000080067	solute carrier family 4 (anion exchanger), member 2 [Source:MGI Symbol;Acc:MGI:109351]			-4.2	1.5E-02	-3.9	1.3E-02	2.2	5.8E-03	-1.9	2.3E-01
ENSMUST00000080085	KRIT1, ankyrin repeat containing [Source:MGI Symbol;Acc:MGI:1930618]	B2RUA8	Q6S5J6	-6.8	3.0E-04	1.8	8.2E-02	-1.6	9.0E-02	-0.6	4.4E-01
ENSMUST00000080089	cullin 2 [Source:MGI Symbol;Acc:MGI:1918995]	H7BX52		-2.3	2.1E-02	3.3	5.6E-03	-0.7	4.5E-01	0.1	8.9E-01
ENSMUST00000080106	olfactory receptor 493 [Source:MGI Symbol;Acc:MGI:3030327]		Q8VEW5	5.5	1.3E-03	6.1	9.4E-03	0.0	9.9E-01	-1.5	1.9E-01
ENSMUST00000078111	beta-site APP cleaving enzyme 1 [Source:MGI Symbol;Acc:MGI:1346542]	Q8C4F4		2.4	2.3E-01	3.2	9.1E-02	-2.2	2.1E-01	-3.0	9.8E-02
ENSMUST00000080123	aldolase 1 A, retrogene 2 [Source:MGI Symbol;Acc:MGI:1931052]	A6ZI47		6.8	1.5E-04	-1.8	2.9E-02	-0.1	7.5E-01	-1.0	1.8E-01
ENSMUST00000078137	multiple endocrine neoplasia 1 [Source:MGI Symbol;Acc:MGI:1316736]		O88559	5.1	9.5E-02	2.4	4.3E-01	-3.7	2.4E-01	-1.1	6.4E-01
ENSMUST00000078139	aspartate-beta-hydroxylase [Source:MGI Symbol;Acc:MGI:1914186]		Q8BSY0	-0.4	8.8E-01	-0.4	8.9E-01	-1.8	4.3E-01	-1.8	5.0E-01
ENSMUST00000078155	inosine 5'-phosphate dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:96567]		P50096	-2.7	1.7E-01	-1.6	5.4E-01	1.6	4.2E-01	0.5	8.4E-01
ENSMUST00000080126	ribonuclease, RNase A family, 1 (pancreatic) [Source:MGI Symbol;Acc:MGI:97919]	Q8C6G3		5.1	1.0E-03	6.9	1.9E-03	0.4	8.0E-01	-1.7	8.9E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000080132	RIKEN cDNA 4921509C19 gene [Source:MGI Symbol;Acc:MGI:2685851]		Q8C0X8	9.3	7.2E-05	-0.1	9.7E-01	2.7	4.2E-02	-1.2	5.0E-01
ENSMUST00000080135	a disintegrin and metallopeptidase domain 26B [Source:MGI Symbol;Acc:MGI:3588304]	Q6IMH6		5.4	3.6E-03	7.2	2.4E-04	-0.7	6.1E-01	-0.7	3.3E-01
ENSMUST00000080138	acyl-Coenzyme A binding domain containing 6 [Source:MGI Symbol;Acc:MGI:1919732]		Q9D061	-4.0	3.8E-03	-8.8	3.5E-06	-0.3	4.0E-01	0.6	5.1E-01
ENSMUST00000080141	transmembrane protein 117 [Source:MGI Symbol;Acc:MGI:2444580]		Q8BH18	5.7	1.5E-03	5.7	6.2E-04	-0.6	6.3E-01	0.3	6.0E-01
ENSMUST00000080145	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16 [Source:MGI Symbol;Acc:M		Q69Z28	6.0	3.0E-02	-3.3	2.3E-02	1.1	1.5E-01	-1.4	3.7E-01
ENSMUST00000080164	FIP1 like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914149]		Q9D824	-2.5	1.2E-02	1.4	4.1E-02	-1.6	1.3E-02	-0.8	1.7E-01
ENSMUST00000080167	RUN and FYVE domain containing 4 [Source:MGI Symbol;Acc:MGI:3588214]		Q3TYX8	-3.4	3.5E-04	8.1	2.7E-04	-0.8	6.2E-01	1.3	8.1E-02
ENSMUST00000080190	expressed sequence AI413582 [Source:MGI Symbol;Acc:MGI:2146839]	D6RHA8		-4.7	2.9E-02	-4.8	1.3E-03	-1.4	2.8E-02	-1.7	2.0E-01
ENSMUST00000080202	sirtuin 7 [Source:MGI Symbol;Acc:MGI:2385849]		Q8BKJ9	-9.7	4.2E-06	5.8	3.0E-05	0.9	2.2E-01	0.6	1.7E-01
ENSMUST00000080204	Sp140 nuclear body protein [Source:MGI Symbol;Acc:MGI:3702467]	Q6NSQ5		-4.7	8.0E-05	4.6	2.0E-02	-0.1	9.6E-01	1.2	2.9E-01
ENSMUST00000080208	erythrocyte membrane protein band 4.1 like 3 [Source:MGI Symbol;Acc:MGI:103008]		Q9WV92	7.6	2.6E-03	3.3	6.8E-03	-2.7	3.8E-02	0.4	5.7E-01
ENSMUST00000080210	ute carrier family 1 (glial high affinity glutamate transporter), member 2 [Source:MGI Symbol;Acc:MGI:1019	Q3UYK6	P43006	9.9	5.9E-05	6.7	1.3E-03	-0.7	6.5E-01	0.8	4.0E-01
ENSMUST00000080211	kallikrein related-peptidase 11 [Source:MGI Symbol;Acc:MGI:1929977]	A0A0B6VLT0	Q9QYN3	5.4	1.9E-02	5.1	3.0E-02	-1.4	5.3E-01	-0.4	7.5E-01
ENSMUST00000080217	protein phosphatase 1B, magnesium dependent, beta isoform [Source:MGI Symbol;Acc:MGI:101841]	Q99NF7		-3.3	7.3E-03	-2.1	6.6E-04	0.0	9.6E-01	-0.2	5.5E-01
ENSMUST00000080249	zinc finger protein 947 [Source:MGI Symbol;Acc:MGI:3646759]	Q8BIQ6		1.9	2.4E-02	7.4	3.1E-04	-0.4	7.6E-01	-1.3	9.2E-02
ENSMUST00000080254	butyrophilin-like 1 [Source:MGI Symbol;Acc:MGI:1932027]		Q7TST0	7.1	1.3E-04	4.0	1.7E-04	-0.7	2.9E-01	0.2	6.9E-01
ENSMUST00000080281	ribosomal protein L15 [Source:MGI Symbol;Acc:MGI:1913730]	Q5M8Q0	Q9CZM2	-3.2	2.2E-03	6.6	2.3E-02	-0.9	7.5E-01	-0.4	7.6E-01
ENSMUST00000078323	transmembrane protein 175 [Source:MGI Symbol;Acc:MGI:1919642]		Q9CXY1	-3.3	2.6E-01	-2.0	4.6E-01	-0.8	6.5E-01	-2.1	5.0E-01
ENSMUST00000080288	proline rich 19 [Source:MGI Symbol;Acc:MGI:3648539]	B2RW88		6.5	1.3E-04	7.7	1.7E-04	-0.6	6.6E-01	0.7	3.0E-01
ENSMUST00000078332	mitochondrial fission factor [Source:MGI Symbol;Acc:MGI:1922984]		Q6PCP5	-2.7	2.4E-01	-5.7	5.4E-02	-3.1	4.1E-02	-0.1	9.8E-01
ENSMUST00000080299	YY1 associated factor 2 [Source:MGI Symbol;Acc:MGI:1914307]		Q99LW6	-5.7	6.6E-05	0.5	6.4E-01	-1.2	1.7E-01	1.8	5.2E-02
ENSMUST00000080300	ribosomal protein S25 [Source:MGI Symbol;Acc:MGI:1922867]	Q58EA6	P62852	-7.1	2.6E-06	2.6	7.3E-04	-7.0	1.7E-05	-0.8	8.5E-02
ENSMUST00000080316	Tctex1 domain containing 2 [Source:MGI Symbol;Acc:MGI:1913311]	Q9CQJ9		-5.5	4.8E-05	-3.2	1.2E-02	-2.2	6.4E-03	-2.4	7.6E-02
ENSMUST00000080322	2'-5' oligoadenylate synthetase 1A [Source:MGI Symbol;Acc:MGI:2180860]		P11928	-3.5	6.7E-03	6.0	1.0E-03	-0.5	7.1E-01	-1.1	1.7E-01
ENSMUST00000080324	DNA segment, Chr X, Baylor 18 [Source:MGI Symbol;Acc:MGI:99870]	Q52KH6		6.8	1.5E-02	-2.9	7.5E-03	0.3	5.7E-01	1.3	1.7E-01
ENSMUST00000080336	RIKEN cDNA 6330416G13 gene [Source:MGI Symbol;Acc:MGI:1913920]		Q8R239	-4.6	5.5E-03	7.1	8.3E-05	-0.5	6.8E-01	-0.8	1.9E-01
ENSMUST00000080348	zinc fingr protein 551 [Source:MGI Symbol;Acc:MGI:3588205]		B2RUI1	7.5	8.0E-05	-4.8	4.0E-02	1.8	5.8E-02	1.2	5.9E-01
ENSMUST00000080356	small nuclear ribonucleoprotein polypeptide A [Source:MGI Symbol;Acc:MGI:1855690]		Q62189	-3.5	2.0E-02	6.7	2.8E-04	-0.5	7.1E-01	-0.4	5.9E-01
ENSMUST00000080368	TPase, aminophospholipid transporter-like, class I, type 8A, member 2 [Source:MGI Symbol;Acc:MGI:135471		P98200	4.1	1.1E-04	6.1	3.2E-03	-0.4	8.0E-01	-1.4	1.4E-01
ENSMUST00000080371	metastasis suppressor 1 [Source:MGI Symbol;Acc:MGI:2384818]	G3X9H7		2.4	3.4E-04	2.2	4.8E-02	0.4	6.3E-01	0.1	8.6E-01
ENSMUST00000078434	protein phosphatase 3, catalytic subunit, gamma isoform [Source:MGI Symbol;Acc:MGI:107162]	Q3V074	P48455	-0.5	3.2E-01	-0.2	7.3E-01	-0.1	8.9E-01	-0.4	5.5E-01
ENSMUST00000080391	carboxylesterase 5A [Source:MGI Symbol;Acc:MGI:1915185]	Q9D998		14.5	3.6E-05	7.1	8.9E-05	-0.6	6.3E-01	-0.7	2.2E-01
ENSMUST00000080394	SH3-domain kinase binding protein 1 [Source:MGI Symbol;Acc:MGI:1889583]		Q8R550	-9.1	1.8E-06	6.4	1.5E-02	-0.7	7.8E-01	-1.3	3.2E-01
ENSMUST00000078451	paired Ig-like receptor B [Source:MGI Symbol;Acc:MGI:894311]		P97484	-1.6	4.4E-02	-1.3	2.0E-01	0.8	2.4E-01	0.5	6.1E-01
ENSMUST00000080403	melanoma antigen, family L, 2 [Source:MGI Symbol;Acc:MGI:1351648]		Q9QZ04	9.5	1.6E-05	-2.2	1.8E-02	-0.3	5.7E-01	-0.5	5.4E-01
ENSMUST00000080405	oogenesin 2 [Source:MGI Symbol;Acc:MGI:2684035]	Q7TPX8		5.8	9.5E-04	8.9	3.7E-05	-0.7	6.2E-01	-1.5	3.3E-02
ENSMUST00000080406	zinc finger protein 251 [Source:MGI Symbol;Acc:MGI:1918841]	Q6PCX8		2.9	3.9E-04	-4.4	1.2E-02	0.7	3.0E-01	-0.7	6.6E-01
ENSMUST00000080411	mortality factor 4 like 2 [Source:MGI Symbol;Acc:MGI:1927167]		Q9R0Q4	-8.4	1.2E-06	5.5	7.0E-03	-3.2	1.1E-01	-1.4	2.1E-01
ENSMUST00000080418	al precursor cell expressed, developmentally down-regulated gene 4-like [Source:MGI Symbol;Acc:MGI:1933	G3X9H8		6.3	4.0E-03	6.9	6.5E-02	-0.8	8.3E-01	2.0	3.1E-01
ENSMUST00000078486	transcription factor 4 [Source:MGI Symbol;Acc:MGI:98506]		Q60722	0.2	7.5E-01	2.1	2.0E-02	0.6	3.8E-01	-1.3	7.4E-02
ENSMUST00000080428	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan) [Source:MGI Symbol;Acc:MGI:99438]		P51491	7.3	8.5E-05	6.2	5.0E-05	-0.4	6.3E-01	-0.2	6.5E-01
ENSMUST00000080437	DENN/MADD domain containing 5A [Source:MGI Symbol;Acc:MGI:1201681]		Q6PAL8	-8.9	3.2E-04	8.2	2.3E-02	-0.9	8.0E-01	-0.6	7.2E-01
ENSMUST00000080440	calcium/calmodulin-dependent protein kinase II gamma [Source:MGI Symbol;Acc:MGI:88259]		Q923T9	-7.6	2.4E-03	7.4	1.0E-04	-0.9	4.9E-01	0.1	9.0E-01
ENSMUST00000080443	ribosomal protein S18, pseudogene 3 [Source:MGI Symbol;Acc:MGI:3642474]			-7.5	4.8E-04	8.2	4.5E-05	-0.7	6.0E-01	0.2	6.8E-01
ENSMUST00000080474	olfactory receptor 601 [Source:MGI Symbol;Acc:MGI:3030435]	A2RS33		6.4	8.9E-05	2.5	1.4E-01	-0.7	6.4E-01	4.2	6.5E-03
ENSMUST00000080492	ribosomal protein L36 [Source:MGI Symbol;Acc:MGI:1860603]	Q6ZWZ4		-5.3	4.6E-04	3.4	1.6E-03	0.1	8.4E-01	0.6	2.7E-01
ENSMUST00000080493	AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		Q6R0H7	6.2	9.2E-03	7.1	1.4E-04	-0.4	7.2E-01	0.9	1.5E-01
ENSMUST00000080511	histone cluster 1, H1b [Source:MGI Symbol;Acc:MGI:1861461]		P43276	6.0	9.1E-04	-2.0	5.9E-02	-0.2	7.3E-01	-1.0	3.6E-01
ENSMUST00000080514	ribonuclease P/MRP 25 subunit [Source:MGI Symbol;Acc:MGI:2143151]		Q91WE3	5.9	2.0E-04	5.2	3.7E-03	-0.5	7.5E-01	0.6	4.7E-01
ENSMUST00000080518	suprabasin [Source:MGI Symbol;Acc:MGI:2446326]	E9QPB2		5.8	5.9E-05	2.9	4.2E-04	1.4	1.1E-02	-0.1	8.4E-01
ENSMUST00000080536	ATP-binding cassette, sub-family E (OABP), member 1 [Source:MGI Symbol;Acc:MGI:1195458]	Q3UHY8	P61222	-2.3	1.3E-03	-2.5	8.2E-02	0.6	5.1E-01	-2.3	1.7E-01
ENSMUST00000078573	mitochondrial ribosomal protein S36 [Source:MGI Symbol;Acc:MGI:1913378]	Q9D6T9		-2.7	8.0E-02	-3.4	4.4E-02	-0.8	3.9E-01	-0.1	9.6E-01
ENSMUST00000080537	RAS-related C3 botulinum substrate 1 [Source:MGI Symbol;Acc:MGI:97845]	K7Q7T7	P63001	-5.8	1.6E-05	6.9	2.6E-02	-0.7	8.0E-01	-1.3	4.0E-01
ENSMUST00000080557	peroxisomal biogenesis factor 5 [Source:MGI Symbol;Acc:MGI:1098808]		O09012	-7.7	4.1E-05	0.0	9.9E-01	2.2	4.5E-02	-0.5	6.9E-01
ENSMUST00000078621	ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D [Source:MGI Symbol;Acc:MGI:		Q76KF0	7.1	3.6E-02	9.7	1.0E-02	-0.8	8.2E-01	-3.4	6.6E-02
ENSMUST00000080559	membrane metallo-endopeptidase-like 1 [Source:MGI Symbol;Acc:MGI:1351603]	E9QPA9		9.0	1.9E-05	8.4	1.3E-05	-1.1	3.2E-01	-0.2	7.0E-01
ENSMUST00000080560	in, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F [Source:MGI Symbol;Acc:MG		O88632	7.3	4.9E-05	-2.2	1.4E-02	1.0	4.9E-02	-0.6	4.0E-01
ENSMUST00000080594	immunity-related GTPase family, cinema 1 [Source:MGI Symbol;Acc:MGI:2685948]	D3Z720		7.6	3.2E-05	-3.0	1.7E-02	0.1	8.3E-01	-2.0	1.3E-01
ENSMUST00000080622	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:893586]		Q9D0T1	-2.4	1.7E-02	-7.6	4.5E-07	-0.5	4.2E-02	0.2	7.2E-01
ENSMUST00000080647	sperm motility kinase 2A [Source:MGI Symbol;Acc:MGI:1351487]	G5E8M0		5.7	7.3E-04	-3.2	1.5E-02	-0.4	4.9E-01	-2.0	1.4E-01
ENSMUST00000080664	eyes absent 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109344]	Q8C9D0		6.2	1.7E-04	7.3	8.7E-05	-0.6	5.9E-01	-0.5	3.7E-01
ENSMUST00000080665	dynein, axonemal, heavy chain 9 [Source:MGI Symbol;Acc:MGI:1289279]	B1AR51		7.2	5.2E-05	4.9	1.1E-03	0.3	8.0E-01	-0.5	4.8E-01
ENSMUST00000078690	Sad1 and UNC84 domain containing 1 [Source:MGI Symbol;Acc:MGI:1924303]		Q9D666	3.8	5.0E-02	2.0	1.8E-01	-4.5	2.0E-02	-2.7	6.0E-02
ENSMUST00000080669	predicted gene 4559 [Source:MGI Symbol;Acc:MGI:3782743]	A4IF42		5.9	3.2E-04	-0.7	4.4E-01	1.2	8.0E-02	-0.4	6.4E-01
ENSMUST00000080673	ryanodine receptor 3 [Source:MGI Symbol;Acc:MGI:99684]		A2AGL3	7.3	2.2E-02	5.9	2.1E-03	-0.6	7.0E-01	-0.6	4.7E-01
ENSMUST00000080713	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1919804]		Q640M1	-5.7	3.6E-05	6.8	1.8E-04	-0.5	6.8E-01	-0.8	2.2E-01
ENSMUST00000078717	leucine rich repeat containing 58 [Source:MGI Symbol;Acc:MGI:2443542]		Q3UGP9	0.6	1.2E-01	1.3	3.1E-02	1.0	2.4E-02	0.4	4.0E-01
ENSMUST00000078729				3.2	6.7E-02	0.9	6.5E-01	-0.9	5.9E-01	1.3	4.3E-01
ENSMUST00000080718	Ly6/Plaur domain containing 3 [Source:MGI Symbol;Acc:MGI:1919684]		Q91YK8	8.6	1.2E-04	-3.5	9.8E-03	-0.2	6.8E-01	-0.5	6.7E-01
ENSMUST00000080721	chondroitin sulfate synthase 3 [Source:MGI Symbol;Acc:MGI:1926173]		Q5DTK1	7.9	1.5E-05	6.5	3.4E-02	0.7	8.1E-01	1.4	4.1E-01
ENSMUST00000080723	Tax1 (human T cell leukemia virus type I) binding protein 1 [Source:MGI Symbol;Acc:MGI:1289308]		Q3UKC1	-6.8	1.1E-05	4.9	1.1E-03	-1.3	2.7E-01	0.2	8.0E-01
ENSMUST00000080728	SH3-domain GRB2-like (endophilin) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1920344]		Q8VD37	6.5	6.9E-04	-1.8	4.6E-01	-5.6	1.9E-02	2.0	3.9E-01
ENSMUST00000078756	histone cluster 2, H2aa1 [Source:MGI Symbol;Acc:MGI:96097]	B2RWH3	Q6GSS7	-4.1	3.8E-02	-3.8	6.8E-02	-1.2	2.4E-01	-1.6	4.8E-01
ENSMUST00000080751	RIKEN cDNA 1810041L15 gene [Source:MGI Symbol;Acc:MGI:1919551]	H7BX53		7.4	1.3E-04	5.6	2.9E-02	-0.7	7.6E-01	-0.8	5.8E-01
ENSMUST00000078764	cytochrome c oxidase subunit VIIc [Source:MGI Symbol;Acc:MGI:103226]	B8JJB0		1.8	6.2E-02	1.5	1.5E-01	-1.9	5.7E-02	-1.5	9.7E-02
ENSMUST00000078766				-5.9	9.1E-02	-9.0	3.5E-02	-4.2	1.6E-02	-1.1	7.9E-01
ENSMUST00000080759	olfactory receptor 98 [Source:MGI Symbol;Acc:MGI:2177481]		Q8VFD9	7.6	1.6E-05	7.4	1.3E-01	14.6	4.3E-03	-5.8	1.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000080771	zinc finger and BTB domain containing 24 [Source:MGI Symbol;Acc:MGI:3039618]		Q80X44	-2.0	2.8E-03	1.2	3.5E-01	3.2	5.2E-03	-1.7	1.6E-01
ENSMUST00000080780	lipoma HMGIC fusion partner-like 5 [Source:MGI Symbol;Acc:MGI:1915382]		Q4KL25	6.0	3.2E-04	-5.5	2.3E-05	-0.3	2.8E-01	-1.2	1.3E-01
ENSMUST00000080797	cadherin 3 [Source:MGI Symbol;Acc:MGI:88356]		P10287	8.8	4.0E-06	-6.0	2.2E-03	-0.7	3.0E-01	-1.5	3.6E-01
ENSMUST00000078816	RIKEN cDNA 9130023H24 gene [Source:MGI Symbol;Acc:MGI:2442738]	Q8BG98		-1.0	9.6E-02	0.9	1.9E-01	1.0	7.2E-02	-0.9	1.9E-01
ENSMUST00000080801	olfactory receptor 1475 [Source:MGI Symbol;Acc:MGI:3031309]	Q8VEV6		5.5	1.7E-03	-6.4	3.8E-06	-0.5	6.9E-02	-0.1	9.2E-01
ENSMUST00000080806	sideroflexin 4 [Source:MGI Symbol;Acc:MGI:2137680]	F8WI63		4.3	3.7E-05	2.6	2.7E-03	0.3	5.9E-01	-0.4	4.2E-01
ENSMUST00000080812	zinc finger, C3HC type 1 [Source:MGI Symbol;Acc:MGI:1916023]		Q80YV2	-2.8	9.9E-03	6.4	4.5E-04	-0.6	6.3E-01	-0.3	6.5E-01
ENSMUST00000080813	ribosomal protein S17 [Source:MGI Symbol;Acc:MGI:1309526]	Q5M9L7	P63276	-9.0	1.1E-04	-8.6	5.2E-06	-0.8	6.2E-02	-2.6	3.4E-02
ENSMUST00000078847	target of myb1 homolog (chicken) [Source:MGI Symbol;Acc:MGI:1338026]	Q3UDC3		1.6	3.1E-01	0.0	1.0E+00	1.2	5.7E-01	2.8	1.6E-01
ENSMUST00000080817	ring finger protein 169 [Source:MGI Symbol;Acc:MGI:1920257]		E9Q7F2	-2.1	3.9E-04	6.2	3.1E-04	-0.8	5.1E-01	0.3	6.5E-01
ENSMUST00000080849	predicted gene 8882 [Source:MGI Symbol;Acc:MGI:3645847]	E9Q7E4		8.7	8.6E-04	8.7	1.2E-04	0.4	7.7E-01	0.4	5.2E-01
ENSMUST00000080853	platelet/endothelial cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97537]		Q08481	-6.4	1.3E-03	6.0	4.4E-04	-0.5	6.9E-01	0.0	9.9E-01
ENSMUST00000080856	importin 11 [Source:MGI Symbol;Acc:MGI:2442377]		Q8K2V6	-3.2	2.3E-03	-7.6	1.3E-04	-0.9	5.6E-02	-0.8	5.4E-01
ENSMUST00000080860	coiled-coil domain containing 28A [Source:MGI Symbol;Acc:MGI:2443508]	Q3UFK1		-6.1	4.4E-05	7.5	7.0E-05	-0.4	7.1E-01	0.0	9.4E-01
ENSMUST00000078886	SPEN homolog, transcriptional regulator (Drosophila) [Source:MGI Symbol;Acc:MGI:1891706]	A2ADB1		-0.1	8.4E-01	-0.9	2.4E-01	0.8	1.2E-01	1.7	3.8E-02
ENSMUST00000078902	membrane bound O-acyltransferase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914466]		Q8R3I2	1.6	3.8E-01	6.1	1.4E-02	1.7	4.2E-01	-2.8	8.7E-02
ENSMUST00000080880	disabled 2, mitogen-responsive phosphoprotein [Source:MGI Symbol;Acc:MGI:109175]			6.7	8.0E-04	5.5	9.0E-04	-0.8	5.1E-01	-0.4	6.1E-01
ENSMUST00000080882	ATPase, Na+/K+ transporting, alpha 3 polypeptide [Source:MGI Symbol;Acc:MGI:88107]		Q6PIC6	-9.2	1.1E-04	-2.2	7.0E-02	1.4	5.2E-02	0.8	4.4E-01
ENSMUST00000080885	D site albumin promoter binding protein [Source:MGI Symbol;Acc:MGI:94866]		Q60925	3.6	8.6E-04	-2.0	3.9E-02	0.4	4.9E-01	-2.0	6.4E-02
ENSMUST00000080893	keratin 17 [Source:MGI Symbol;Acc:MGI:96691]		Q9QWL7	7.2	3.9E-05	6.2	2.2E-04	-0.5	6.5E-01	-0.9	1.8E-01
ENSMUST00000080905	zinc finger protein 811 [Source:MGI Symbol;Acc:MGI:2682944]	F7CTH4		2.9	1.7E-02	8.7	5.0E-04	0.1	9.6E-01	1.1	2.2E-01
ENSMUST00000080917	olfactory receptor 15 [Source:MGI Symbol;Acc:MGI:106182]		P23275	6.8	1.9E-04	-2.1	6.9E-02	0.3	6.2E-01	-1.1	3.5E-01
ENSMUST00000080919	thyroid hormone receptor associated protein 3 [Source:MGI Symbol;Acc:MGI:2442637]		Q569Z6	-4.4	4.6E-05	-1.2	2.1E-01	-0.1	9.0E-01	-2.5	4.7E-02
ENSMUST00000080926	enolase 1, alpha non-neuron [Source:MGI Symbol;Acc:MGI:95393]	Q5FW97	P17182	-7.7	4.5E-06	3.4	4.9E-03	-0.1	9.1E-01	0.0	9.8E-01
ENSMUST00000078961	kinesin family member C5B [Source:MGI Symbol;Acc:MGI:2137414]	E9PUA5		1.0	1.1E-01	1.6	4.5E-02	0.3	5.9E-01	-0.3	6.0E-01
ENSMUST00000078975	glucose 6 phosphatase, catalytic, 3 [Source:MGI Symbol;Acc:MGI:1915651]		Q6NSQ9	2.9	1.6E-01	0.7	8.0E-01	-0.7	7.6E-01	1.5	5.3E-01
ENSMUST00000078976	zinc finger protein 706 [Source:MGI Symbol;Acc:MGI:1915286]	B2RVQ7	Q9D115	0.3	5.6E-01	0.4	4.6E-01	0.9	7.7E-02	0.7	2.3E-01
ENSMUST00000080932	feline sarcoma oncogene [Source:MGI Symbol;Acc:MGI:95514]		P16879	-5.7	2.6E-05	5.2	6.3E-03	-5.6	1.3E-02	-0.5	5.6E-01
ENSMUST00000080949	lysine-rich coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1889377]		Q99JT5	-6.7	3.2E-04	7.6	4.2E-05	-0.5	6.6E-01	-0.5	3.9E-01
ENSMUST00000080953	low density lipoprotein receptor-related protein 2 [Source:MGI Symbol;Acc:MGI:95794]		A2ARV4	8.9	9.2E-06	-5.4	2.7E-02	0.6	4.6E-01	1.6	4.7E-01
ENSMUST00000079028	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914974	Q9D4G5		0.1	9.4E-01	-1.1	5.5E-01	-1.3	3.7E-01	0.0	9.8E-01
ENSMUST00000080975	amplified in osteosarcoma [Source:MGI Symbol;Acc:MGI:1924301]		Q8K2C7	-4.5	1.1E-02	-3.8	1.0E-03	-0.4	3.4E-01	-0.6	4.8E-01
ENSMUST00000080987	zinc finger protein 869 [Source:MGI Symbol;Acc:MGI:1914119]	Q9DC47		-3.0	1.5E-03	4.0	4.2E-04	-3.9	2.5E-03	-0.1	8.1E-01
ENSMUST00000079041	solute carrier family 35, member E3 [Source:MGI Symbol;Acc:MGI:2448489]		Q6PGC7	1.3	5.6E-02	2.1	3.2E-02	0.8	2.7E-01	0.0	9.8E-01
ENSMUST00000079042	zinc finger protein 317 [Source:MGI Symbol;Acc:MGI:107775]	Q8C0Q5		0.0	9.8E-01	-0.9	3.0E-01	-1.0	1.2E-01	-0.1	8.8E-01
ENSMUST00000080995	transmembrane protein 26 [Source:MGI Symbol;Acc:MGI:2143537]		Q3UP23	7.2	1.0E-04	4.0	2.7E-03	0.8	3.6E-01	-0.5	5.1E-01
ENSMUST00000081007	keratin associated protein 4-1 [Source:MGI Symbol;Acc:MGI:3622079]	Q3UUY3		6.1	3.1E-04	7.2	2.1E-04	-0.5	7.2E-01	0.5	4.0E-01
ENSMUST00000081022	zinc finger protein 28 [Source:MGI Symbol;Acc:MGI:99175]		P10078	2.2	1.8E-03	-1.9	1.3E-01	1.3	9.7E-02	-3.1	8.6E-02
ENSMUST00000081026	H3 histone, family 3A [Source:MGI Symbol;Acc:MGI:1097686]	F8WI35		-8.2	9.2E-08	6.9	4.7E-04	-0.4	7.6E-01	-0.4	5.7E-01
ENSMUST00000081028	ets variant 6 [Source:MGI Symbol;Acc:MGI:109336]		P97360	-6.8	5.3E-04	-8.8	1.8E-04	-0.8	1.3E-01	1.1	4.6E-01
ENSMUST00000081035	macrophage expressed gene 1 [Source:MGI Symbol;Acc:MGI:1333743]	E9QN37		-5.5	1.2E-04	5.7	9.0E-03	-0.4	8.5E-01	-1.4	2.0E-01
ENSMUST00000081074	RIKEN cDNA 4932411N23 gene [Source:MGI Symbol;Acc:MGI:3045322]	Q8C0S0		9.1	4.3E-04	-5.0	9.6E-05	-0.1	8.2E-01	1.0	2.3E-01
ENSMUST00000081103	Fc receptor, IgG, low affinity IIb [Source:MGI Symbol;Acc:MGI:95499]	A0A0B4J1G1		-9.9	6.0E-07	-5.4	2.6E-03	-1.0	1.5E-01	-2.0	2.4E-01
ENSMUST00000081104	translocase of inner mitochondrial membrane 17a [Source:MGI Symbol;Acc:MGI:1343131]	Q545U2	Q9Z0V8	3.3	2.1E-05	6.0	9.0E-04	-0.5	7.1E-01	-0.4	6.2E-01
ENSMUST00000079157	eyes absent 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109339]		P97480	4.3	1.5E-01	2.8	5.7E-01	1.2	7.7E-01	2.6	5.0E-01
ENSMUST00000079158	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 [Source:MGI Symbol;Acc:MGI:1351644]		Q9R1X5	-1.4	3.1E-01	-0.4	8.2E-01	0.0	1.0E+00	-1.0	5.3E-01
ENSMUST00000079160	leucine zipper-EF-hand containing transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:2444979]		Q7TNU7	-0.1	8.7E-01	-0.6	5.4E-01	-0.5	4.7E-01	0.0	9.8E-01
ENSMUST00000079163	vomeronasal 2, receptor 10 [Source:MGI Symbol;Acc:MGI:1316730]	K7N621		3.7	7.4E-02	5.9	1.6E-02	-0.3	8.8E-01	-2.5	6.6E-02
ENSMUST00000081111	inosine 5'-phosphate dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:109367]	Q3UAT9	P24547	-1.9	2.6E-02	-9.1	1.3E-05	-0.6	1.6E-01	-0.7	5.2E-01
ENSMUST00000081125	myelin transcription factor 1 [Source:MGI Symbol;Acc:MGI:1100535]	B0R0C1		7.6	1.4E-02	8.7	2.0E-05	-0.1	9.2E-01	-0.9	9.4E-02
ENSMUST00000081134	synaptonemal complex protein 2 [Source:MGI Symbol;Acc:MGI:1933281]		Q9CUU3	-2.5	2.7E-02	5.4	3.9E-03	-3.4	7.3E-02	-0.9	2.9E-01
ENSMUST00000081154	phosphoinositide kinase, FYVE finger containing [Source:MGI Symbol;Acc:MGI:1335106]	D3Z5N5		2.0	2.4E-03	6.1	3.5E-05	1.9	3.1E-02	0.1	8.1E-01
ENSMUST00000079205	chondroitin polymerizing factor [Source:MGI Symbol;Acc:MGI:106576]		Q6IQX7	-2.1	1.7E-01	0.5	6.7E-01	-1.0	3.4E-01	-3.6	3.2E-02
ENSMUST00000081182	nuclear autoantigenic sperm protein (histone-binding) [Source:MGI Symbol;Acc:MGI:1355328]		Q99MD9	-6.7	3.2E-05	-3.6	5.1E-04	-0.6	1.3E-01	-1.7	4.4E-02
ENSMUST00000081202	mannosidase, beta A, lysosomal-like [Source:MGI Symbol;Acc:MGI:1916411]	A2BGN7		-2.4	2.8E-03	7.1	2.0E-04	-0.6	6.3E-01	-1.2	1.0E-01
ENSMUST00000081224	formin-like 3 [Source:MGI Symbol;Acc:MGI:109569]		Q6ZPF4	-4.5	6.3E-03	4.3	1.3E-03	1.6	8.9E-02	0.2	7.8E-01
ENSMUST00000081232	phospholipase C, gamma 2 [Source:MGI Symbol;Acc:MGI:97616]		Q8CIH5	-3.9	2.7E-05	-0.8	3.0E-01	0.9	1.5E-01	-0.4	6.0E-01
ENSMUST00000079244	misshapen-like kinase 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1355329]	Q5SXG1		-2.6	4.3E-01	-3.4	4.8E-01	-0.4	8.6E-01	0.3	9.4E-01
ENSMUST00000079251	histone cluster 1, H2bg [Source:MGI Symbol;Acc:MGI:2448386]		Q6ZWY9	0.5	4.9E-01	0.9	3.2E-01	-0.3	7.0E-01	-0.7	4.1E-01
ENSMUST00000081265	early B cell factor 1 [Source:MGI Symbol;Acc:MGI:95275]	Q5SWK5	Q07802	5.0	1.4E-05	-1.5	9.6E-02	1.4	2.2E-02	-0.6	5.2E-01
ENSMUST00000081274	olfactory receptor 12 [Source:MGI Symbol;Acc:MGI:107863]	Q0VBN7	Q60894	6.9	3.9E-05	3.3	4.0E-02	-2.3	1.4E-01	1.8	9.7E-02
ENSMUST00000081275	armadillo repeat containing 4 [Source:MGI Symbol;Acc:MGI:1922184]		B2RY50	6.2	6.6E-04	5.9	2.5E-04	-0.5	6.3E-01	0.1	8.0E-01
ENSMUST00000081285	synaptic Ras GTPase activating protein 1 homolog (rat) [Source:MGI Symbol;Acc:MGI:3039785]			7.9	2.2E-05	4.8	1.2E-02	-0.6	6.9E-01	1.6	1.3E-01
ENSMUST00000081288	family with sequence similarity 3, member C [Source:MGI Symbol;Acc:MGI:107892]	G3X9I1		-4.8	1.4E-04	3.0	6.1E-03	-4.0	3.8E-03	0.0	9.8E-01
ENSMUST00000079286	S100 calcium binding protein A7A [Source:MGI Symbol;Acc:MGI:2687194]		Q6S5I3	-0.1	9.0E-01	0.4	5.3E-01	0.2	7.7E-01	-0.3	5.9E-01
ENSMUST00000081291	cysteine and histidine rich 1 [Source:MGI Symbol;Acc:MGI:1859320]		Q9QXA1	-2.1	4.5E-03	3.2	1.3E-03	-0.1	8.9E-01	0.3	5.9E-01
ENSMUST00000081309	acylpeptide hydrolase [Source:MGI Symbol;Acc:MGI:88041]			-5.7	1.3E-02	5.1	1.0E-02	-0.6	7.4E-01	0.8	4.3E-01
ENSMUST00000079312	copine I [Source:MGI Symbol;Acc:MGI:2386621]	B7ZCP4		-2.0	5.0E-01	-2.5	5.1E-01	-0.8	6.7E-01	-0.3	9.5E-01
ENSMUST00000079314	glia maturation factor, beta [Source:MGI Symbol;Acc:MGI:1927133]		Q9CQI3	-1.2	3.4E-01	1.1	5.6E-01	1.7	2.6E-01	-0.6	7.1E-01
ENSMUST00000081314	Bloom syndrome, RecQ helicase-like [Source:MGI Symbol;Acc:MGI:1328362]		O88700	-4.3	4.9E-04	-2.8	1.7E-03	0.6	1.2E-01	-0.4	5.7E-01
ENSMUST00000081318	Sfi1 homolog, spindle assembly associated (yeast) [Source:MGI Symbol;Acc:MGI:1926137]		Q3UZY0	-3.6	1.4E-02	-3.2	1.8E-02	1.6	2.5E-02	-0.6	6.4E-01
ENSMUST00000079327	multiple endocrine neoplasia 1 [Source:MGI Symbol;Acc:MGI:1316736]		O88559	-2.5	1.8E-01	-3.0	2.6E-01	-0.2	8.9E-01	0.2	9.3E-01
ENSMUST00000081321	POTE ankyrin domain family, member G [Source:MGI Symbol;Acc:MGI:1918202]	A5H0M4		5.5	2.8E-03	7.9	6.3E-05	-0.5	6.8E-01	-2.3	4.9E-03
ENSMUST00000079362	adenomatosis polyposis coli [Source:MGI Symbol;Acc:MGI:88039]	B2RUG9		-0.7	3.3E-01	-0.2	8.3E-01	-0.1	9.2E-01	-0.6	4.9E-01
ENSMUST00000079363	predicted pseudogene 10093 [Source:MGI Symbol;Acc:MGI:3704479]	D3YYI8		-1.6	1.0E-01	-2.8	7.0E-02	0.6	4.3E-01	1.8	2.1E-01
ENSMUST00000081333	frataxin [Source:MGI Symbol;Acc:MGI:1096879]	Q3TV21	O35943	4.6	1.4E-03	8.0	6.0E-05	0.0	1.0E+00	-0.4	4.6E-01
ENSMUST00000081349	formin 1 [Source:MGI Symbol;Acc:MGI:101815]		Q05860	5.0	4.4E-03	8.4	1.9E-07	-0.7	2.7E-01	0.5	8.2E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000081381	membrane-bound transcription factor peptidase, site 1 [Source:MGI Symbol;Acc:MGI:1927235]		Q9WTZ2	-1.9	5.2E-03	8.3	7.2E-05	0.4	7.4E-01	0.4	4.5E-01
ENSMUST00000081387	baculoviral IAP repeat-containing 5 [Source:MGI Symbol;Acc:MGI:1203517]	Q549P2	O70201	-5.6	2.7E-04	5.5	5.0E-04	-2.7	5.6E-02	-0.7	3.3E-01
ENSMUST00000081393	nephronophthisis 4 (juvenile) homolog (human) [Source:MGI Symbol;Acc:MGI:2384210]		P59240	8.4	1.5E-05	-5.7	1.5E-02	1.0	1.6E-01	1.3	5.3E-01
ENSMUST00000081399	kallikrein 1-related peptidase b9 [Source:MGI Symbol;Acc:MGI:95293]		P15949	7.1	1.2E-04	7.2	2.8E-04	-0.7	6.3E-01	-1.3	1.1E-01
ENSMUST00000081417	olfactory receptor 463 [Source:MGI Symbol;Acc:MGI:3030297]	Q5SW49		6.5	3.7E-04	-4.4	3.1E-04	0.9	3.3E-02	-1.0	2.7E-01
ENSMUST00000079414	centrosomal protein 89 [Source:MGI Symbol;Acc:MGI:1919390]		Q9CZX2	-2.7	5.2E-02	-3.8	4.4E-02	-1.0	2.4E-01	0.1	9.7E-01
ENSMUST00000079419	ribosomal protein L15 [Source:MGI Symbol;Acc:MGI:1913730]	Q5M8Q0	Q9CZM2	-2.2	1.4E-01	-3.3	9.0E-02	-1.3	2.3E-01	-0.2	9.2E-01
ENSMUST00000081435	histocompatibility 2, Q region locus 4 [Source:MGI Symbol;Acc:MGI:95933]	Q8HWB2		2.9	2.1E-04	-3.5	1.0E-02	0.5	4.0E-01	0.6	5.8E-01
ENSMUST00000081438	adrenergic receptor, beta 3 [Source:MGI Symbol;Acc:MGI:87939]	Q3UP63	P25962	8.3	6.0E-05	6.4	2.3E-04	-0.5	6.6E-01	-1.2	9.2E-02
ENSMUST00000081457	lectin, galactose binding, soluble 7 [Source:MGI Symbol;Acc:MGI:1316742]	Q9CRB1		4.8	1.5E-03	-1.5	5.3E-01	4.1	1.2E-02	-1.5	5.5E-01
ENSMUST00000081496	latent transforming growth factor beta binding protein 3 [Source:MGI Symbol;Acc:MGI:1101355]	F8VQ06		4.7	4.1E-04	16.3	9.3E-04	0.0	1.0E+00	1.8	1.5E-01
ENSMUST00000081503	pre B cell leukemia homeobox 4 [Source:MGI Symbol;Acc:MGI:1931321]		Q99NE9	5.8	3.1E-04	8.5	1.3E-05	-0.5	6.2E-01	-0.5	2.7E-01
ENSMUST00000081510	O-6-methylguanine-DNA methyltransferase [Source:MGI Symbol;Acc:MGI:96977]		P26187	2.4	4.8E-03	6.1	5.0E-04	-0.6	6.3E-01	0.3	6.8E-01
ENSMUST00000081525	progestin and adipoQ receptor family member VII [Source:MGI Symbol;Acc:MGI:1919154]		Q80ZE4	-3.2	1.9E-03	7.5	9.6E-05	-1.5	2.5E-01	-1.2	8.3E-02
ENSMUST00000081541	acyl-coenzyme A amino acid N-acyltransferase 2 [Source:MGI Symbol;Acc:MGI:2444345]		Q8BGG9	6.2	1.7E-04	-6.8	6.1E-04	0.9	6.7E-02	0.6	6.7E-01
ENSMUST00000081542	potassium voltage-gated channel, Shal-related family, member 2 [Source:MGI Symbol;Acc:MGI:102663]		Q9Z0V2	7.8	1.7E-05	6.7	2.7E-04	-0.6	6.4E-01	-0.6	3.6E-01
ENSMUST00000081551	transcription elongation factor A (SII) 1 [Source:MGI Symbol;Acc:MGI:1196624]	Q3UWX7	P10711	-3.0	1.8E-04	6.6	2.8E-03	-0.6	7.5E-01	-2.7	2.8E-02
ENSMUST00000081554	purinergic receptor P2X, ligand-gated ion channel 4 [Source:MGI Symbol;Acc:MGI:1338859]	Q9Z256		-6.1	1.4E-05	-1.7	2.0E-01	0.4	6.0E-01	-2.5	1.1E-01
ENSMUST00000081560	ecinate dehydrogenase complex, subunit C, integral membrane protein [Source:MGI Symbol;Acc:MGI:191330	F8WGB3		-7.3	1.6E-05	4.0	2.2E-03	-1.1	2.6E-01	-0.9	2.3E-01
ENSMUST00000081574	synaptotagmin XVII [Source:MGI Symbol;Acc:MGI:104966]		Q920M7	7.3	7.3E-05	7.4	1.2E-04	-0.6	6.5E-01	-0.3	6.1E-01
ENSMUST00000081580	predicted gene 5089 [Source:MGI Symbol;Acc:MGI:3644731]	A1L3C8		6.8	1.9E-04	-2.1	3.1E-02	0.8	1.3E-01	0.0	9.9E-01
ENSMUST00000081591	zinc finger CCCH-type containing 15 [Source:MGI Symbol;Acc:MGI:1919747]		Q3TIV5	-7.7	5.0E-05	-0.5	4.1E-01	1.0	3.8E-02	0.3	5.9E-01
ENSMUST00000081593	phosphoglycerate kinase 1 [Source:MGI Symbol;Acc:MGI:97555]		P09411	-8.0	3.7E-05	6.8	8.0E-03	1.2	5.7E-01	-1.2	3.0E-01
ENSMUST00000081619	SH3 and PX domains 2A [Source:MGI Symbol;Acc:MGI:1298393]		O89032	10.5	1.7E-02	1.7	1.5E-01	-4.4	8.7E-03	0.8	3.7E-01
ENSMUST00000081636	protein kinase, AMP-activated, gamma 3 non-catatlytic subunit [Source:MGI Symbol;Acc:MGI:1891343]		Q8BGM7	6.2	7.8E-04	6.1	1.2E-03	-0.4	7.6E-01	-0.4	5.8E-01
ENSMUST00000081640	tetratricopeptide repeat domain 33 [Source:MGI Symbol;Acc:MGI:1914765]		Q9D6K7	-3.5	4.2E-03	7.8	8.3E-05	-0.4	7.1E-01	-0.1	8.6E-01
ENSMUST00000079573	inositol 1,4,5-triphosphate receptor 2 [Source:MGI Symbol;Acc:MGI:99418]		Q9Z329	-1.4	3.9E-01	-1.5	5.6E-01	2.5	1.8E-01	2.6	2.8E-01
ENSMUST00000081645	PRAME family member 6 [Source:MGI Symbol;Acc:MGI:3649940]	E9Q2S4		6.0	2.0E-03	4.8	6.2E-04	-0.3	7.2E-01	1.2	7.9E-02
ENSMUST00000081649	interferon induced transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1933382]		Q99J93	-8.6	4.2E-07	4.7	2.6E-03	0.2	8.8E-01	-0.7	4.1E-01
ENSMUST00000079594	ATP-binding cassette, sub-family A (ABC1), member 3 [Source:MGI Symbol;Acc:MGI:1351617]		Q8R420	-1.7	7.7E-02	-1.6	2.0E-01	0.1	8.7E-01	0.0	9.7E-01
ENSMUST00000081650	ribosomal protein L3 [Source:MGI Symbol;Acc:MGI:1351605]		P27659	-9.3	7.3E-06	4.5	1.7E-03	-2.7	3.4E-02	0.3	7.2E-01
ENSMUST00000079601	ets variant 5 [Source:MGI Symbol;Acc:MGI:1096867]		Q9CXC9	4.2	1.8E-01	-1.8	5.8E-01	-4.2	1.6E-01	1.8	5.6E-01
ENSMUST00000081670	golgi autoantigen, golgin subfamily a, 2 [Source:MGI Symbol;Acc:MGI:2139395]	Z4YJU8		-7.9	7.8E-06	8.3	1.8E-03	-0.7	7.4E-01	-2.8	3.0E-02
ENSMUST00000081684	interferon lambda 2 [Source:MGI Symbol;Acc:MGI:3647279]		Q4VK74	7.0	3.5E-05	2.8	9.7E-03	0.8	2.8E-01	0.6	4.2E-01
ENSMUST00000081695	gon-4-like (C.elegans) [Source:MGI Symbol;Acc:MGI:1917579]	E9Q507		-4.6	6.9E-03	2.2	1.2E-01	-0.5	6.5E-01	4.3	1.8E-03
ENSMUST00000081702	TraB domain containing [Source:MGI Symbol;Acc:MGI:1915226]		Q99JY4	-6.3	9.2E-05	4.3	1.5E-02	-1.3	3.8E-01	1.3	2.0E-01
ENSMUST00000081713	nuclear receptor coactivator 2 [Source:MGI Symbol;Acc:MGI:1276533]	E9PV80		5.6	8.6E-03	-1.3	2.2E-01	0.8	2.7E-01	-3.7	2.6E-02
ENSMUST00000081714	4-hydroxy-2-oxoglutarate aldolase 1 [Source:MGI Symbol;Acc:MGI:1914682]		Q9DCU9	6.5	5.9E-06	-1.1	3.1E-01	1.2	8.8E-02	-0.4	7.2E-01
ENSMUST00000081726	eyes absent 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109339]	Q6P4T3		-8.0	4.2E-05	7.2	1.5E-03	0.1	9.6E-01	0.3	7.7E-01
ENSMUST00000081728	catenin (cadherin associated protein), delta 2 [Source:MGI Symbol;Acc:MGI:1195966]	E9QKH8		7.5	6.9E-06	-1.4	1.0E-01	0.3	6.2E-01	0.0	9.7E-01
ENSMUST00000081735	predicted gene 5152 [Source:MGI Symbol;Acc:MGI:3643407]	L7N200		5.1	1.9E-02	-3.3	1.2E-02	0.1	8.6E-01	-2.5	6.4E-02
ENSMUST00000079648	RIKEN cDNA 1190007I07 gene [Source:MGI Symbol;Acc:MGI:3698433]		Q8BTC1	-0.5	6.5E-01	2.5	9.9E-02	1.2	3.7E-01	-1.9	1.2E-01
ENSMUST00000081746	family with sequence similarity 214, member A [Source:MGI Symbol;Acc:MGI:2387648]		Q69ZK7	8.6	2.8E-05	6.7	2.6E-04	-1.2	3.7E-01	0.8	2.5E-01
ENSMUST00000079659	U2 snRNP-associated SURP domain containing [Source:MGI Symbol;Acc:MGI:1915208]		Q6NV83	-0.6	4.0E-01	-0.2	7.9E-01	-0.2	7.4E-01	-0.5	5.0E-01
ENSMUST00000079681	cytochrome b5 domain containing 2 [Source:MGI Symbol;Acc:MGI:2684848]		Q5SSH8	3.2	1.5E-01	1.7	4.9E-01	-0.6	7.8E-01	0.9	6.7E-01
ENSMUST00000079691	glutathione synthetase [Source:MGI Symbol;Acc:MGI:95852]	Q541E2	P51855	-1.9	1.5E-01	-1.6	2.2E-01	-1.4	1.4E-01	-1.7	2.4E-01
ENSMUST00000081747	RIKEN cDNA 0610040J01 gene [Source:MGI Symbol;Acc:MGI:1923511]		Q99K99	-3.3	2.2E-04	4.3	5.6E-03	-0.3	8.2E-01	0.9	2.8E-01
ENSMUST00000079693	G patch domain containing 1 [Source:MGI Symbol;Acc:MGI:1914721]		Q9DBM1	-2.8	1.3E-01	0.2	9.1E-01	1.1	5.2E-01	-1.9	3.4E-01
ENSMUST00000081752	olfactomedin 3 [Source:MGI Symbol;Acc:MGI:2387329]	Q3UVC5	P63056	6.5	8.5E-04	-1.6	2.5E-01	0.4	6.6E-01	-1.6	3.1E-01
ENSMUST00000081775	nuclear factor, erythroid derived 2,-like 1 [Source:MGI Symbol;Acc:MGI:99421]	Q6GTN8	Q61985	-4.8	3.3E-03	-2.8	9.6E-04	-0.4	3.2E-01	-0.6	3.2E-01
ENSMUST00000081776	apolipoprotein L 9a [Source:MGI Symbol;Acc:MGI:3606001]	Q8VDU3		5.3	1.5E-02	-6.9	3.0E-04	-1.1	6.7E-02	-2.5	1.1E-01
ENSMUST00000081777	murinoglobulin 2 [Source:MGI Symbol;Acc:MGI:99836]		P28666	7.0	6.2E-05	8.4	6.2E-03	-0.8	7.8E-01	-2.2	1.2E-01
ENSMUST00000081790	CDK2 associated, cullin domain 1 [Source:MGI Symbol;Acc:MGI:1926082]		Q8R0X2	-6.3	1.0E-02	6.7	1.4E-04	-0.6	6.2E-01	0.2	6.8E-01
ENSMUST00000081794	mannoside acetylglucosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI:96973]	Q544F0	P27808	-6.0	5.8E-03	-2.6	2.1E-02	0.0	9.5E-01	0.2	8.7E-01
ENSMUST00000079735	ribosomal protein L30 [Source:MGI Symbol;Acc:MGI:98037]	Q58DZ3	P62889	0.1	8.8E-01	1.3	1.0E-01	-0.7	2.9E-01	-1.8	2.2E-02
ENSMUST00000081828	coiled-coil domain containing 176 [Source:MGI Symbol;Acc:MGI:1920123]		Q3V079	3.7	4.2E-04	-2.8	1.2E-02	1.2	3.1E-02	-0.7	4.6E-01
ENSMUST00000081840	ribosomal protein L32 [Source:MGI Symbol;Acc:MGI:98038]		P62911	-6.1	7.8E-06	3.0	7.1E-02	-2.5	1.2E-01	0.7	5.3E-01
ENSMUST00000079758	amyloid beta (A4) precursor-like protein 2 [Source:MGI Symbol;Acc:MGI:88047]		Q06335	-4.8	4.1E-02	2.4	2.2E-01	1.0	5.6E-01	-6.2	1.2E-02
ENSMUST00000081848	farnesyl diphosphate synthetase [Source:MGI Symbol;Acc:MGI:104888]	Q4FJN9	Q920E5	-4.2	1.2E-04	6.9	1.0E-03	-0.7	6.5E-01	0.0	9.9E-01
ENSMUST00000081851	ansmembrane protein with EGF-like and two follistatin-like domains 2 [Source:MGI Symbol;Acc:MGI:186173		Q9QYM9	7.6	5.9E-05	6.5	1.2E-03	1.1	4.7E-01	-1.2	1.9E-01
ENSMUST00000081857	myosin, heavy polypeptide 6, cardiac muscle, alpha [Source:MGI Symbol;Acc:MGI:97255]	B2RQQ1	Q02566	9.3	8.1E-06	-4.0	7.2E-03	-0.1	9.0E-01	-0.5	7.3E-01
ENSMUST00000081869	torsin family 4, member A [Source:MGI Symbol;Acc:MGI:2442720]		Q8BH02	-3.7	2.5E-04	2.1	1.6E-01	-3.3	6.2E-02	0.7	5.0E-01
ENSMUST00000079773	casein kinase 1, gamma 2 [Source:MGI Symbol;Acc:MGI:1920014]	Q99K78		-0.2	6.9E-01	-0.2	7.9E-01	1.2	8.3E-02	1.2	1.6E-01
ENSMUST00000081872	NEL-like 1 [Source:MGI Symbol;Acc:MGI:2443902]		Q2VWQ2	7.7	1.8E-04	4.0	1.1E-02	-2.5	1.2E-01	0.8	4.0E-01
ENSMUST00000081880	lysosomal-associated membrane protein 3 [Source:MGI Symbol;Acc:MGI:2441659]		Q7TST5	5.6	3.1E-04	-3.2	7.4E-04	1.1	9.1E-03	-4.4	1.0E-03
ENSMUST00000081894	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) [Source:MGI Symbol;Acc:MGI:1098267]	Z4YJV4		-4.5	2.4E-02	-2.5	1.8E-03	0.9	3.0E-02	-0.2	7.1E-01
ENSMUST00000081896	RIKEN cDNA 4930512M02 gene [Source:MGI Symbol;Acc:MGI:1922360]	Q5SQK8		10.0	3.7E-03	-4.3	2.6E-04	1.3	5.5E-03	-0.6	4.6E-01
ENSMUST00000081907	carcinoembryonic antigen-related cell adhesion molecule 5 [Source:MGI Symbol;Acc:MGI:1920500]		Q3UKK2	6.6	4.5E-04	4.7	3.8E-03	-1.5	3.0E-01	-0.1	8.7E-01
ENSMUST00000081908	ribosomal protein L10-like [Source:MGI Symbol;Acc:MGI:3647985]		P86048	6.6	3.5E-04	0.1	9.1E-01	1.9	1.1E-02	-0.4	6.1E-01
ENSMUST00000081911	myosin, heavy polypeptide 13, skeletal muscle [Source:MGI Symbol;Acc:MGI:1339967]	B1AR69		7.1	7.5E-04	7.3	6.0E-05	-0.4	7.1E-01	-0.6	2.4E-01
ENSMUST00000079833	heat shock factor 2 [Source:MGI Symbol;Acc:MGI:96239]		P38533	0.2	6.9E-01	0.9	2.1E-01	0.3	5.4E-01	-0.4	5.7E-01
ENSMUST00000079847	succinate-Coenzyme A ligase, GDP-forming, beta subunit [Source:MGI Symbol;Acc:MGI:1306824]		Q9Z2I8	-0.2	6.6E-01	-0.5	4.8E-01	-0.3	4.6E-01	-0.1	8.6E-01
ENSMUST00000081914	ankyrin repeat domain 17 [Source:MGI Symbol;Acc:MGI:1932101]	E9QKG6		-6.3	3.1E-04	-1.3	1.9E-01	1.6	1.7E-02	-0.4	6.9E-01
ENSMUST00000081924	interferon induced transmembrane protein 6 [Source:MGI Symbol;Acc:MGI:2686976]	Q3SXF0		-10.8	3.2E-08	-3.9	2.6E-02	1.2	8.9E-02	0.2	9.0E-01
ENSMUST00000079869	zinc and ring finger 2 [Source:MGI Symbol;Acc:MGI:1196246]		Q71FD5	-0.7	1.8E-01	-0.5	4.5E-01	0.8	1.0E-01	0.7	3.2E-01
ENSMUST00000081940	ubiquitin A-52 residue ribosomal protein fusion product 1 [Source:MGI Symbol;Acc:MGI:98887]	Q66JP1	P62984	-7.8	4.4E-04	6.4	1.1E-03	-0.6	6.9E-01	-0.9	2.9E-01
ENSMUST00000081945	keratin 83 [Source:MGI Symbol;Acc:MGI:3665486]		Q6IMF0	7.3	1.8E-05	-4.2	4.4E-02	0.3	7.4E-01	0.2	9.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000079902	lectin, galactose binding, soluble 12 [Source:MGI Symbol;Acc:MGI:1929094]		Q91VD1	2.6	9.3E-02	4.7	7.5E-03	-0.6	7.0E-01	-2.7	3.5E-02
ENSMUST00000079924	BTB (POZ) domain containing 9 [Source:MGI Symbol;Acc:MGI:1916625]		Q8C726	-0.4	8.7E-01	-4.1	3.1E-01	-2.3	2.8E-01	1.4	7.3E-01
ENSMUST00000079934	MAX gene associated [Source:MGI Symbol;Acc:MGI:1352483]	H7BX50		0.5	8.2E-01	-4.7	2.4E-01	-2.8	1.8E-01	2.5	5.2E-01
ENSMUST00000081956	family with sequence similarity 60, member A [Source:MGI Symbol;Acc:MGI:1929091]		Q8C8M1	4.2	2.7E-02	5.5	3.1E-04	-1.7	1.6E-01	-1.2	9.6E-02
ENSMUST00000079949	Ewing sarcoma breakpoint region 1 [Source:MGI Symbol;Acc:MGI:99960]		Q61545	-2.4	1.1E-01	-1.3	5.4E-01	1.8	2.3E-01	0.6	7.3E-01
ENSMUST00000081960	olfactory receptor 1328 [Source:MGI Symbol;Acc:MGI:3031162]	B1ARV2		6.5	6.3E-04	-8.6	6.7E-05	-0.3	5.8E-01	-1.3	3.4E-01
ENSMUST00000081966	outer dense fiber of sperm tails 1 [Source:MGI Symbol;Acc:MGI:97424]	A6H656		6.2	6.6E-04	3.6	2.0E-02	-0.3	7.9E-01	0.7	4.6E-01
ENSMUST00000081978	solute carrier family 39 (metal ion transporter), member 8 [Source:MGI Symbol;Acc:MGI:1914797]		Q91W10	7.0	5.8E-04	-5.0	9.9E-03	-1.6	4.6E-02	0.3	8.6E-01
ENSMUST00000079970	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1 [Source:MGI Symbol;Acc:MGI:1913495		Q99P31	-0.4	5.3E-01	-0.8	3.4E-01	-0.5	3.7E-01	-0.1	8.7E-01
ENSMUST00000079976	solute carrier family 39 (metal ion transporter), member 13 [Source:MGI Symbol;Acc:MGI:1915677]		Q8BZH0	-1.4	4.2E-01	0.9	7.7E-01	3.7	8.8E-02	1.5	5.5E-01
ENSMUST00000081982	double zinc ribbon and ankyrin repeat domains 1 [Source:MGI Symbol;Acc:MGI:2139080]		Q8C008	9.2	1.4E-03	4.4	1.6E-03	-1.5	1.5E-01	-0.3	7.4E-01
ENSMUST00000079987	LAS1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923380]		A2BE28	-1.1	8.9E-02	-1.4	8.5E-02	-0.6	2.6E-01	-0.3	7.0E-01
ENSMUST00000079996	zinc finger, AN1-type domain 2A [Source:MGI Symbol;Acc:MGI:2140729]		Q9JII7	-2.9	2.3E-01	-1.5	6.5E-01	1.1	6.4E-01	-0.3	9.2E-01
ENSMUST00000081989	ring finger protein 217 [Source:MGI Symbol;Acc:MGI:3610311]		D3YYI7	2.0	6.9E-03	-7.3	5.9E-05	0.3	4.5E-01	-0.9	4.4E-01
ENSMUST00000080008	ADP-ribosylation factor GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:1924288]		Q99K28	-3.1	4.1E-02	-0.5	7.7E-01	0.9	3.9E-01	-1.7	3.1E-01
ENSMUST00000082024	embrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) [Source:MGI Symbol;Acc:MGI:192733	B2RRY4	Q9JLB2	-2.5	3.6E-04	-5.7	1.1E-03	0.8	1.8E-01	0.1	9.5E-01
ENSMUST00000080035	CD99 antigen-like 2 [Source:MGI Symbol;Acc:MGI:2177151]		Q8BIF0	-0.2	9.1E-01	-4.1	1.4E-01	-3.2	4.7E-02	0.6	8.3E-01
ENSMUST00000080036	huntingtin [Source:MGI Symbol;Acc:MGI:96067]	G3X9H5		0.8	5.1E-02	1.6	1.1E-02	0.6	1.4E-01	-0.1	7.5E-01
ENSMUST00000082026	DENN/MADD domain containing 4C [Source:MGI Symbol;Acc:MGI:1914769]		A6H8H2	-3.8	1.5E-02	-2.7	2.4E-02	0.9	1.3E-01	-0.4	6.9E-01
ENSMUST00000082027	olfactory receptor 149 [Source:MGI Symbol;Acc:MGI:2660716]		Q60888	5.7	1.1E-03	2.3	9.6E-02	-2.9	5.5E-02	-0.5	6.6E-01
ENSMUST00000082059	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) [Source:MGI Symbol;Acc:MGI:95411]		Q61526	2.2	2.0E-03	-2.3	5.0E-02	1.6	2.7E-02	-0.2	8.2E-01
ENSMUST00000082060	chitinase-like 1 [Source:MGI Symbol;Acc:MGI:1340899]		Q61362	-8.8	4.4E-06	-4.2	1.3E-01	1.9	1.6E-01	1.9	4.5E-01
ENSMUST00000082088	mastermind-like domain containing 1 [Source:MGI Symbol;Acc:MGI:3045303]		P0C6A2	6.9	2.3E-05	-2.6	3.2E-02	0.9	1.6E-01	-3.3	3.4E-02
ENSMUST00000082090	adaptor-related protein complex 3, beta 2 subunit [Source:MGI Symbol;Acc:MGI:1100869]		Q9JME5	7.1	6.0E-05	-1.8	1.4E-01	0.5	5.2E-01	0.0	9.7E-01
ENSMUST00000082093	granzyme D [Source:MGI Symbol;Acc:MGI:109255]		P11033	5.7	2.7E-04	6.0	1.3E-03	-0.4	7.5E-01	-1.0	2.4E-01
ENSMUST00000082094	pentatricopeptide repeat domain 3 [Source:MGI Symbol;Acc:MGI:1917206]		Q14C51	-2.0	8.3E-03	7.0	1.9E-04	-0.8	5.2E-01	-1.1	1.2E-01
ENSMUST00000082104	CUB and Sushi multiple domains 1 [Source:MGI Symbol;Acc:MGI:2137383]		Q923L3	9.1	1.4E-05	6.3	7.3E-04	0.4	7.4E-01	-0.8	2.7E-01
ENSMUST00000080127	homer homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1347345]		Q9Z2Y3	0.2	8.6E-01	-0.2	9.2E-01	1.2	2.8E-01	1.5	2.8E-01
ENSMUST00000082120	zinc finger protein 42 [Source:MGI Symbol;Acc:MGI:99187]	E9QK22		7.3	3.1E-05	7.8	5.6E-04	-0.8	6.3E-01	0.7	3.7E-01
ENSMUST00000082122	deoxyuridine triphosphatase [Source:MGI Symbol;Acc:MGI:1346051]	Q8VCG1		-3.6	1.4E-03	6.1	2.8E-03	-0.4	8.0E-01	-1.2	2.2E-01
ENSMUST00000082125	NUAK family, SNF1-like kinase, 2 [Source:MGI Symbol;Acc:MGI:1921387]		Q8BZN4	-4.2	1.5E-02	-4.5	5.1E-03	0.2	7.1E-01	0.7	6.1E-01
ENSMUST00000082134	ribosomal protein S16 [Source:MGI Symbol;Acc:MGI:98118]	A4FUS1	P14131	-8.5	5.9E-05	5.1	3.6E-03	-1.1	4.6E-01	-0.4	6.2E-01
ENSMUST00000082136	Max protein [Source:MGI Symbol;Acc:MGI:96921]	Q8C4Y1		-7.3	2.9E-04	6.2	2.3E-02	-2.0	4.7E-01	-2.2	1.5E-01
ENSMUST00000080149	enolase 1, alpha non-neuron [Source:MGI Symbol;Acc:MGI:95393]	Q6PHC1		-2.1	8.2E-02	-2.6	1.8E-01	0.6	5.1E-01	1.2	5.1E-01
ENSMUST00000082170	FAT tumor suppressor homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444314]	E9QK16		8.7	8.5E-06	-5.1	1.4E-03	-0.2	6.9E-01	-2.3	1.2E-01
ENSMUST00000082177	lysine (K)-specific demethylase 5C [Source:MGI Symbol;Acc:MGI:99781]		P41230	-6.3	4.4E-04	-0.6	5.7E-01	1.1	1.4E-01	-0.8	4.1E-01
ENSMUST00000082209	sodium channel, voltage-gated, type VIII, alpha [Source:MGI Symbol;Acc:MGI:103169]	F6U329		8.6	1.5E-02	-2.9	5.1E-03	0.3	4.4E-01	-0.1	8.7E-01
ENSMUST00000080178	poly(A) binding protein, cytoplasmic 4 [Source:MGI Symbol;Acc:MGI:2385206]	Q6PHQ9		-2.7	1.5E-01	-1.2	6.0E-01	1.7	3.5E-01	0.2	9.3E-01
ENSMUST00000082214	cytochrome P450, family 2, subfamily b, polypeptide 9 [Source:MGI Symbol;Acc:MGI:88600]		P12790	3.4	1.3E-02	-3.9	1.1E-01	-0.6	5.6E-01	-1.4	5.7E-01
ENSMUST00000082235	meprin 1 beta [Source:MGI Symbol;Acc:MGI:96964]		Q61847	6.5	2.1E-04	-8.0	1.3E-04	1.0	2.8E-02	-0.7	6.0E-01
ENSMUST00000082237	mex3 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:1918252]	F8WJD6		4.1	1.0E-04	-4.2	1.0E-03	0.2	6.6E-01	-0.3	7.4E-01
ENSMUST00000082254	janus kinase and microtubule interacting protein 2 [Source:MGI Symbol;Acc:MGI:1923467]	D3YXK0		8.0	1.1E-05	2.4	1.5E-01	-3.3	1.0E-01	1.9	1.5E-01
ENSMUST00000082262	ER membrane protein complex subunit 1 [Source:MGI Symbol;Acc:MGI:2443696]	Z4YJW0		6.2	2.0E-04	7.5	1.7E-04	-2.0	2.1E-01	0.5	5.1E-01
ENSMUST00000082269	RIKEN cDNA 3110018I06 gene [Source:MGI Symbol;Acc:MGI:1920410]	Q9CXS0		6.3	4.9E-04	6.3	1.3E-02	-0.6	7.9E-01	-1.5	2.3E-01
ENSMUST00000080215	arbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15 [Source:MGI Symbol;Acc:MGI:192484(		Q91XQ5	-2.4	5.2E-02	-3.7	6.3E-02	1.0	2.9E-01	2.2	2.2E-01
ENSMUST00000082303	collagen, type XV, alpha 1 [Source:MGI Symbol;Acc:MGI:88449]	A2AJY2		7.8	1.4E-02	-1.4	2.0E-01	0.1	9.2E-01	-1.8	1.3E-01
ENSMUST00000080233	testis-specific serine kinase substrate [Source:MGI Symbol;Acc:MGI:1347560]	Q147V4		2.6	5.0E-02	5.4	1.3E-03	-0.2	8.6E-01	-3.0	8.9E-03
ENSMUST00000082337	mediator of DNA damage checkpoint 1 [Source:MGI Symbol;Acc:MGI:3525201]	E9QK89		1.7	1.3E-03	2.0	2.8E-02	-0.9	2.0E-01	-1.1	1.6E-01
ENSMUST00000082365	sulfotransferase family 4A, member 1 [Source:MGI Symbol;Acc:MGI:1888971]		P63046	5.7	1.7E-04	6.7	3.8E-04	-0.6	6.5E-01	-0.2	8.1E-01
ENSMUST00000082392	mitochondrially encoded NADH dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:101787]	Q4JFN6	P03888	-7.8	2.1E-07	-3.8	2.7E-03	-1.1	5.6E-02	-0.5	6.1E-01
ENSMUST00000082396	mitochondrially encoded NADH dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:102500]	Q9MD59	P03893	-5.9	1.3E-04	7.2	1.6E-04	0.1	9.5E-01	-0.6	3.5E-01
ENSMUST00000080292	CD6 antigen [Source:MGI Symbol;Acc:MGI:103566]		Q61003	-0.1	9.3E-01	2.8	1.9E-01	0.2	9.2E-01	-2.8	1.1E-01
ENSMUST00000082402	mitochondrially encoded cytochrome c oxidase I [Source:MGI Symbol;Acc:MGI:102504]	Q9MD68	P00397	-8.6	8.4E-08	-2.6	6.6E-03	0.5	2.6E-01	-2.6	1.7E-02
ENSMUST00000082405	mitochondrially encoded cytochrome c oxidase II [Source:MGI Symbol;Acc:MGI:102503]	Q7JCZ1	P00405	-8.6	6.1E-06	-7.5	1.1E-05	-0.9	2.6E-02	-0.6	5.3E-01
ENSMUST00000082407	mitochondrially encoded ATP synthase 8 [Source:MGI Symbol;Acc:MGI:99926]	Q7JCZ0	P03930	-7.9	2.8E-06	-3.4	5.6E-03	1.2	3.3E-02	-1.0	3.6E-01
ENSMUST00000082408	mitochondrially encoded ATP synthase 6 [Source:MGI Symbol;Acc:MGI:99927]	Q7JCY9	P00848	-12.1	4.9E-05	-2.1	1.2E-01	0.7	3.5E-01	-0.7	6.0E-01
ENSMUST00000082409	mitochondrially encoded cytochrome c oxidase III [Source:MGI Symbol;Acc:MGI:102502]	Q7JCX7	P00416	-9.0	2.6E-05	5.4	6.0E-02	-0.5	8.6E-01	1.0	5.3E-01
ENSMUST00000082411	mitochondrially encoded NADH dehydrogenase 3 [Source:MGI Symbol;Acc:MGI:102499]	Q7GIP5	P03899	-5.8	3.3E-03	-5.1	1.2E-02	0.8	3.3E-01	1.4	4.4E-01
ENSMUST00000082414	mitochondrially encoded NADH dehydrogenase 4 [Source:MGI Symbol;Acc:MGI:102498]	Q7JCY6	P03911	-6.4	6.3E-07	4.8	5.4E-04	-2.6	3.9E-02	0.1	8.4E-01
ENSMUST00000080353	inhibitor of growth family, member 2 [Source:MGI Symbol;Acc:MGI:1916510]		Q9ESK4	-2.5	7.9E-02	-3.2	1.1E-01	1.0	3.9E-01	1.7	3.4E-01
ENSMUST00000082418	mitochondrially encoded NADH dehydrogenase 5 [Source:MGI Symbol;Acc:MGI:102496]	Q9MD82	P03921	-4.9	4.7E-06	-4.8	4.2E-02	0.4	6.7E-01	1.6	4.6E-01
ENSMUST00000080359	RE1-silencing transcription factor [Source:MGI Symbol;Acc:MGI:104897]		Q8VIG1	-2.1	1.5E-01	-3.0	1.6E-01	0.3	7.7E-01	1.1	5.8E-01
ENSMUST00000082419	mitochondrially encoded NADH dehydrogenase 6 [Source:MGI Symbol;Acc:MGI:102495]	Q7JCY4	P03925	-5.7	7.6E-04	5.4	4.0E-05	0.3	6.9E-01	-1.0	7.1E-02
ENSMUST00000082421	mitochondrially encoded cytochrome b [Source:MGI Symbol;Acc:MGI:102501]	Q7JCZ3	P00158	-7.6	1.0E-05	-0.2	7.5E-01	-2.2	4.4E-04	0.4	3.9E-01
ENSMUST00000080379	ADP-ribosylation factor-like 1 [Source:MGI Symbol;Acc:MGI:99436]	F8WIB1		0.5	5.2E-01	6.3	2.9E-03	6.0	2.2E-03	0.2	8.0E-01
ENSMUST00000082424	selenoprotein P, plasma, 1 [Source:MGI Symbol;Acc:MGI:894288]		P70274	-6.1	9.0E-05	13.7	6.1E-04	0.7	8.0E-01	1.5	1.4E-01
ENSMUST00000082426	deiodinase, iodothyronine, type I [Source:MGI Symbol;Acc:MGI:94896]			6.6	4.9E-05	-7.3	7.0E-05	1.0	1.2E-02	-0.8	5.2E-01
ENSMUST00000082428	selenophosphate synthetase 2 [Source:MGI Symbol;Acc:MGI:108388]		P97364	-5.5	4.5E-06	9.1	6.0E-05	-0.3	8.3E-01	0.2	7.7E-01
ENSMUST00000082429	glutathione peroxidase 1 [Source:MGI Symbol;Acc:MGI:104887]		P11352	-6.4	9.5E-06	7.2	3.7E-04	-0.4	7.8E-01	-1.8	3.5E-02
ENSMUST00000082430	glutathione peroxidase 3 [Source:MGI Symbol;Acc:MGI:105102]		P46412	-2.3	5.5E-03	3.8	2.1E-04	0.4	4.5E-01	-0.5	3.4E-01
ENSMUST00000082431	glutathione peroxidase 2 [Source:MGI Symbol;Acc:MGI:106609]			7.3	3.1E-05	-8.0	1.4E-05	-0.5	1.5E-01	-0.9	3.8E-01
ENSMUST00000082432	deiodinase, iodothyronine, type II [Source:MGI Symbol;Acc:MGI:1338833]		Q9Z1Y9	2.9	5.8E-04	9.9	7.1E-03	3.3	2.7E-01	-0.2	8.6E-01
ENSMUST00000082437	selenoprotein [Source:MGI Symbol;Acc:MGI:1927947]			-2.7	2.3E-02	7.1	1.9E-04	-0.7	6.1E-01	-0.5	4.4E-01
ENSMUST00000080431	ute carrier family 5 (sodium-dependent vitamin transporter), member 6 [Source:MGI Symbol;Acc:MGI:26608		Q5U4D8	2.5	1.9E-01	5.5	1.2E-01	4.2	1.8E-01	1.2	5.5E-01
ENSMUST00000082439	selenoprotein O [Source:MGI Symbol;Acc:MGI:1919007]		Q9DBC0	-5.8	5.5E-05	-7.4	7.9E-04	1.2	8.4E-02	-0.2	9.0E-01
ENSMUST00000084013	mitochondrially encoded NADH dehydrogenase 4L [Source:MGI Symbol;Acc:MGI:102497]	Q9MD77	P03903	-7.3	6.4E-05	-2.8	1.0E-01	1.3	1.8E-01	-3.4	1.2E-01
ENSMUST00000084030	transforming, acidic coiled-coil containing protein 1 [Source:MGI Symbol;Acc:MGI:2443510]	F8VQ95		-1.5	2.4E-03	-4.0	9.2E-03	-0.3	6.2E-01	-3.8	3.8E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000080449	heat shock protein 2 [Source:MGI Symbol;Acc:MGI:96243]		P17156	-0.2	7.0E-01	1.1	1.7E-01	1.2	5.8E-02	-0.1	9.0E-01
ENSMUST00000084031	HtrA serine peptidase 4 [Source:MGI Symbol;Acc:MGI:3036260]		A2RT60	5.9	8.1E-04	5.8	3.7E-04	-0.6	6.0E-01	0.1	8.9E-01
ENSMUST00000084032	a disintegrin and metallopeptidase domain 9 (meltrin gamma) [Source:MGI Symbol;Acc:MGI:105376]	E9Q638		-4.0	1.8E-03	-5.2	1.3E-03	-1.0	1.1E-01	-1.0	4.1E-01
ENSMUST00000084046	predicted gene 15319 [Source:MGI Symbol;Acc:MGI:3796981]	E9Q637		9.4	9.0E-05	2.3	2.9E-01	-1.4	5.3E-01	2.5	1.1E-01
ENSMUST00000084086	CD209b antigen [Source:MGI Symbol;Acc:MGI:1916415]	Q3UTX5	Q8CJ91	6.4	1.1E-03	4.1	5.3E-03	-2.0	1.5E-01	0.0	9.6E-01
ENSMUST00000084097	aurora kinase A interacting protein 1 [Source:MGI Symbol;Acc:MGI:1913327]		Q9DCJ7	-2.8	1.8E-02	4.3	7.6E-04	-2.4	3.6E-02	-0.8	2.3E-01
ENSMUST00000080517	RIKEN cDNA 2610301B20 gene [Source:MGI Symbol;Acc:MGI:1914407]		Q3UJP5	-0.9	4.9E-01	-0.5	7.2E-01	-0.8	4.8E-01	-1.1	4.3E-01
ENSMUST00000084103	ski sarcoma viral oncogene homolog (avian) [Source:MGI Symbol;Acc:MGI:98310]	B1AUF2		-1.8	2.4E-02	5.0	9.6E-04	-1.2	2.7E-01	-0.4	5.7E-01
ENSMUST00000084115	in homology domain containing, family G (with RhoGef domain) member 5 [Source:MGI Symbol;Acc:MGI:2(		Q66T02	7.4	1.9E-05	-3.1	7.9E-04	-1.0	2.2E-02	-0.2	7.8E-01
ENSMUST00000084124	phosphogluconate dehydrogenase [Source:MGI Symbol;Acc:MGI:97553]		Q9DCD0	-8.2	9.0E-07	-4.3	1.1E-03	1.5	7.2E-03	0.1	9.5E-01
ENSMUST00000080553	deformed epidermal autoregulatory factor 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1858496]		Q9Z1T5	-1.3	1.0E-01	-0.1	9.2E-01	0.8	2.7E-01	-0.4	6.3E-01
ENSMUST00000084149	predicted gene 13139 [Source:MGI Symbol;Acc:MGI:3701604]	Q8R1N3		-1.8	2.7E-02	-6.4	1.2E-03	1.1	3.9E-02	-0.2	9.1E-01
ENSMUST00000084170	phosphatase and actin regulator 4 [Source:MGI Symbol;Acc:MGI:2140327]		Q501J7	-1.5	3.2E-02	6.4	5.7E-04	-0.7	6.0E-01	1.9	1.9E-02
ENSMUST00000084184	dehydrogenase/reductase (SDR family) member 3 [Source:MGI Symbol;Acc:MGI:1315215]	H7BX54		-4.1	1.1E-02	1.6	5.6E-02	-5.4	3.6E-04	0.4	5.6E-01
ENSMUST00000080583	glutathione S-transferase, C-terminal domain containing [Source:MGI Symbol;Acc:MGI:1914803]		Q5RL51	-2.3	6.0E-02	0.8	5.3E-01	0.3	7.8E-01	-2.8	4.3E-02
ENSMUST00000084203	trin homology domain containing, family M (with RUN domain) member 2 [Source:MGI Symbol;Acc:MGI:19	Z4YJW6		-5.3	2.5E-03	7.1	1.1E-04	-0.5	6.5E-01	0.0	9.7E-01
ENSMUST00000084214	eukaryotic translation initiation factor 4 gamma, 3 [Source:MGI Symbol;Acc:MGI:1923935]			-5.5	1.3E-02	-4.2	2.2E-04	-0.1	6.9E-01	0.1	9.1E-01
ENSMUST00000084238	zinc finger, DHHC domain containing 18 [Source:MGI Symbol;Acc:MGI:3527792]		Q5Y5T2	-4.2	1.6E-04	-4.5	4.0E-03	-0.7	2.7E-01	1.4	2.6E-01
ENSMUST00000084241	WAS protein family, member 2 [Source:MGI Symbol;Acc:MGI:1098641]		Q8BH43	-4.2	1.0E-05	6.2	7.8E-04	-0.5	7.4E-01	-0.9	2.3E-01
ENSMUST00000084250	regulator of chromosome condensation 1 [Source:MGI Symbol;Acc:MGI:1913989]		Q8VE37	-4.4	1.8E-03	5.2	5.5E-03	-0.2	8.7E-01	0.9	3.2E-01
ENSMUST00000084263	SPOC domain containing 1 [Source:MGI Symbol;Acc:MGI:3652045]	B1ASB6		6.6	3.3E-04	9.0	7.0E-05	1.2	4.0E-01	-0.6	2.8E-01
ENSMUST00000084264	taxilin alpha [Source:MGI Symbol;Acc:MGI:105968]	Q3UD58	Q6PAM1	-5.0	2.6E-03	6.1	4.4E-04	-0.6	6.5E-01	-0.8	2.5E-01
ENSMUST00000084275	zinc finger protein 384 [Source:MGI Symbol;Acc:MGI:2443203]	E9Q1A5		-7.5	1.0E-05	3.2	3.8E-01	-1.0	7.5E-01	3.1	2.7E-01
ENSMUST00000084296	cell division cycle associated 8 [Source:MGI Symbol;Acc:MGI:1196274]		Q8BHX3	-1.9	9.2E-03	-6.4	8.6E-05	-0.9	6.1E-02	-0.3	7.9E-01
ENSMUST00000084299	akirin 2 [Source:MGI Symbol;Acc:MGI:1889364]		B1AXD8	-4.4	1.5E-04	3.0	1.1E-02	-5.4	2.2E-03	0.1	9.2E-01
ENSMUST00000084301	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	E9QA63		6.7	1.7E-02	6.9	8.6E-05	-0.6	6.2E-01	0.4	4.3E-01
ENSMUST00000084306	human immunodeficiency virus type I enhancer binding protein 3 [Source:MGI Symbol;Acc:MGI:106589]	F7D7H6		7.3	4.3E-05	-7.7	3.9E-05	-0.3	4.4E-01	0.5	6.2E-01
ENSMUST00000084315	olfactory receptor 1338 [Source:MGI Symbol;Acc:MGI:3031172]	A2ACY7		6.3	1.9E-04	6.0	1.5E-03	-0.1	9.1E-01	0.1	9.2E-01
ENSMUST00000084319	mediator complex subunit 8 [Source:MGI Symbol;Acc:MGI:1915269]	Q9CY05		-5.1	1.9E-04	4.1	8.8E-03	-2.4	1.2E-01	-0.1	9.2E-01
ENSMUST00000080732	zinc finger and SCAN domain containing 21 [Source:MGI Symbol;Acc:MGI:99182]		Q07231	-5.1	3.9E-02	-2.8	3.3E-01	1.1	5.2E-01	-1.1	6.9E-01
ENSMUST00000084325	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1858493]	B1ASJ2	Q9Z2Y2	8.2	1.6E-05	8.7	4.1E-04	1.2	4.8E-01	-0.1	8.7E-01
ENSMUST00000084338	diencephalon/mesencephalon homeobox 1 [Source:MGI Symbol;Acc:MGI:2153518]		Q91ZK4	7.4	5.9E-03	5.1	2.8E-04	-2.3	4.4E-02	0.3	6.2E-01
ENSMUST00000084343	cytochrome P450, family 4, subfamily a, polypeptide 12a [Source:MGI Symbol;Acc:MGI:88612]		Q91WL5	6.0	3.8E-04	-1.6	3.6E-02	0.5	2.5E-01	0.0	9.6E-01
ENSMUST00000084354	spermatogenesis associated 6 [Source:MGI Symbol;Acc:MGI:1915196]	A2AED8		-3.4	1.1E-02	5.6	9.3E-04	-0.5	6.9E-01	-0.1	8.7E-01
ENSMUST00000084368	kinesin family member 19A [Source:MGI Symbol;Acc:MGI:2447024]	A9XMT8	Q99PT9	4.1	8.8E-03	6.1	1.6E-05	-3.3	5.7E-03	-0.5	2.5E-01
ENSMUST00000084383	RNA binding motif protein 10 [Source:MGI Symbol;Acc:MGI:2384310]		Q99KG3	-7.6	2.7E-05	5.4	3.5E-03	-0.5	7.3E-01	-0.4	6.7E-01
ENSMUST00000084415	predicted gene 10153 [Source:MGI Symbol;Acc:MGI:3642359]	D3Z4H5		8.6	2.8E-04	4.2	1.3E-04	-0.3	7.0E-01	-0.1	7.4E-01
ENSMUST00000084418	MOB kinase activator 2 [Source:MGI Symbol;Acc:MGI:1919891]		Q8VI63	-3.2	2.3E-04	-4.6	2.3E-02	0.3	6.6E-01	2.1	2.3E-01
ENSMUST00000084433	alkaline ceramidase 2 [Source:MGI Symbol;Acc:MGI:1920932]		Q8VD53	8.9	4.7E-04	-7.4	2.9E-04	-1.3	4.3E-02	-2.9	1.0E-01
ENSMUST00000084434	ribosomal protein, large P2 [Source:MGI Symbol;Acc:MGI:1914436]		P99027	-4.2	1.4E-04	-1.5	2.1E-02	1.0	1.3E-02	0.4	5.1E-01
ENSMUST00000080824	signal-induced proliferation associated gene 1 [Source:MGI Symbol;Acc:MGI:107576]	E9Q0Y4		-2.7	1.9E-01	-3.5	3.9E-01	1.6	3.9E-01	2.4	5.4E-01
ENSMUST00000084455	olfactory receptor 61 [Source:MGI Symbol;Acc:MGI:1333885]	Q8VGM2		6.1	1.0E-04	5.7	1.8E-02	-0.9	6.9E-01	2.1	9.7E-02
ENSMUST00000084460	CD163 molecule-like 1 [Source:MGI Symbol;Acc:MGI:2443796]	Q8CGY7		8.0	1.2E-05	0.6	6.7E-01	3.3	1.9E-02	-3.8	3.1E-02
ENSMUST00000084474	FERM domain containing 3 [Source:MGI Symbol;Acc:MGI:2442466]		Q8BHD4	6.7	1.0E-04	-3.9	2.9E-03	-0.6	2.4E-01	0.2	8.9E-01
ENSMUST00000084480	predicted gene 11487 [Source:MGI Symbol;Acc:MGI:3650704]	Q5RIS0		5.8	1.7E-04	-6.1	2.7E-04	-0.4	3.4E-01	-0.4	7.6E-01
ENSMUST00000080861	ribosomal protein L35 [Source:MGI Symbol;Acc:MGI:1913739]		Q6ZWV7	-1.0	5.0E-01	-4.4	7.1E-02	-2.6	5.1E-02	0.9	6.9E-01
ENSMUST00000084488	dedicator of cytokinesis 1 [Source:MGI Symbol;Acc:MGI:2429765]		Q8BUR4	2.1	1.2E-03	4.6	9.4E-03	-3.2	6.4E-02	-1.1	2.4E-01
ENSMUST00000084489	predicted gene 11232 [Source:MGI Symbol;Acc:MGI:3651439]	Q5SPI8		7.2	7.3E-05	-8.5	1.5E-03	1.1	7.5E-02	0.3	8.8E-01
ENSMUST00000084496	astrotactin 2 [Source:MGI Symbol;Acc:MGI:1889277]	E9Q8T4		8.0	9.3E-05	3.4	1.7E-03	-1.1	1.6E-01	-1.0	1.6E-01
ENSMUST00000084497	family with sequence similarity 175, member B [Source:MGI Symbol;Acc:MGI:1926116]	Z4YJY0		-8.0	9.2E-06	6.4	1.1E-04	-1.3	2.4E-01	-0.6	3.0E-01
ENSMUST00000080898	S-adenosylmethionine decarboxylase 2 [Source:MGI Symbol;Acc:MGI:1333111]		D3Z6H8	0.0	9.7E-01	1.9	2.4E-02	0.2	7.5E-01	-1.7	2.5E-02
ENSMUST00000084500	ornithine aminotransferase [Source:MGI Symbol;Acc:MGI:97394]	Q3TG75	P29758	-6.5	2.0E-04	4.5	5.9E-03	0.7	5.7E-01	-0.8	3.4E-01
ENSMUST00000084501	pregnancy-associated plasma protein A [Source:MGI Symbol;Acc:MGI:97479]		Q8R4K8	9.5	8.3E-06	6.1	7.4E-04	-0.7	6.1E-01	0.0	9.8E-01
ENSMUST00000084502	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1343463]		Q9WVA3	-3.5	3.2E-05	-3.4	1.5E-03	0.7	9.3E-02	-0.3	6.7E-01
ENSMUST00000084509	deleted in malignant brain tumors 1 [Source:MGI Symbol;Acc:MGI:106210]	E9QPG8		8.6	7.3E-06	-7.4	4.7E-05	0.4	3.0E-01	0.1	9.6E-01
ENSMUST00000084512	transforming, acidic coiled-coil containing protein 1 [Source:MGI Symbol;Acc:MGI:2443510]		Q6Y685	-6.1	7.4E-04	-3.8	1.5E-03	1.0	4.1E-02	-0.8	3.7E-01
ENSMUST00000080933	mitogen-activated protein kinase kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346877]	Q543B5	Q62073	-1.2	3.9E-01	-1.8	3.7E-01	1.5	2.7E-01	2.0	2.9E-01
ENSMUST00000080936	mediator complex subunit 15 [Source:MGI Symbol;Acc:MGI:2137379]	E9Q7C1		-0.1	9.5E-01	-2.1	3.4E-01	1.5	2.3E-01	3.5	1.1E-01
ENSMUST00000084513	transforming, acidic coiled-coil containing protein 2 [Source:MGI Symbol;Acc:MGI:1928899]	E9Q8T1		6.4	1.2E-04	5.0	9.1E-03	-1.4	4.1E-01	0.4	6.9E-01
ENSMUST00000084519	WD repeat domain 11 [Source:MGI Symbol;Acc:MGI:1920230]	G5E8J3		-3.5	9.8E-03	-5.6	6.6E-03	0.6	3.6E-01	-0.5	7.9E-01
ENSMUST00000084521	regulator of G-protein signaling 3 [Source:MGI Symbol;Acc:MGI:1354734]		Q9DC04	4.8	2.4E-02	6.1	3.5E-05	-3.4	9.0E-03	-0.5	2.8E-01
ENSMUST00000084525	cell division cycle 26 [Source:MGI Symbol;Acc:MGI:1913690]		Q99JP4	-8.6	1.2E-06	-5.6	2.2E-02	0.8	4.0E-01	1.9	3.9E-01
ENSMUST00000084526	solute carrier family 31, member 1 [Source:MGI Symbol;Acc:MGI:1333843]		Q8K211	-3.8	1.9E-05	-2.6	1.1E-02	0.0	9.8E-01	-0.4	6.1E-01
ENSMUST00000084527	FK506 binding protein 15 [Source:MGI Symbol;Acc:MGI:2444782]		Q6P9Q6	-7.8	3.9E-04	7.7	2.0E-04	0.1	9.7E-01	-0.5	4.6E-01
ENSMUST00000084528	FK506 binding protein 15 [Source:MGI Symbol;Acc:MGI:2444782]	Q80YW9		2.3	2.2E-03	6.4	4.3E-04	-0.6	6.5E-01	-0.8	2.3E-01
ENSMUST00000084530	solute carrier family 31, member 2 [Source:MGI Symbol;Acc:MGI:1333844]	Q4KL43	Q9CPU9	-2.1	1.4E-02	3.0	1.7E-03	0.7	2.4E-01	0.0	1.0E+00
ENSMUST00000084535	APC membrane recruitment 1 [Source:MGI Symbol;Acc:MGI:1919595]		Q7TS75	3.6	2.6E-05	-6.8	2.4E-06	0.5	7.1E-02	-0.9	1.8E-01
ENSMUST00000084563	transmembrane protein 265 [Source:MGI Symbol;Acc:MGI:5613213]	E9Q8G3		-3.8	1.9E-02	-1.1	3.3E-01	1.0	1.6E-01	-4.8	7.8E-03
ENSMUST00000084593	RIKEN cDNA 6030445D17 gene [Source:MGI Symbol;Acc:MGI:2443447]	E9Q8F9		9.3	5.2E-05	4.3	2.5E-02	-1.3	4.4E-01	0.4	7.3E-01
ENSMUST00000084615	calcium channel, voltage-dependent, gamma subunit 3 [Source:MGI Symbol;Acc:MGI:1859165]		Q9JJV5	8.2	6.0E-06	-5.5	1.2E-03	0.1	9.1E-01	0.0	1.0E+00
ENSMUST00000081042	tripartite motif-containing 72 [Source:MGI Symbol;Acc:MGI:3612190]		Q1XH17	3.4	1.9E-01	2.9	3.6E-01	-1.3	6.7E-01	-0.8	7.1E-01
ENSMUST00000084621	TBC1 domain family, member 2 [Source:MGI Symbol;Acc:MGI:2652885]		B1AVH7	-2.4	1.6E-03	7.3	5.1E-03	-0.4	8.6E-01	1.5	1.7E-01
ENSMUST00000081079	ectonucleoside triphosphate diphosphohydrolase 7 [Source:MGI Symbol;Acc:MGI:2135885]		Q3TCT4	-0.3	6.1E-01	1.1	1.2E-01	1.4	2.0E-02	0.0	9.6E-01
ENSMUST00000084628	heparan sulfate (glucosamine) 3-O-sulfotransferase 2 [Source:MGI Symbol;Acc:MGI:1333802]		Q673U1	7.1	3.3E-05	-9.6	6.1E-06	-0.6	5.5E-02	-0.9	4.2E-01
ENSMUST00000084640	ATP-binding cassette, sub-family A (ABC1), member 14 [Source:MGI Symbol;Acc:MGI:2388708]	E9Q8F8		6.7	1.7E-04	2.2	6.9E-04	-1.3	1.1E-02	-0.2	6.0E-01
ENSMUST00000084650	G protein-coupled receptor 139 [Source:MGI Symbol;Acc:MGI:2685341]		Q80UC8	6.0	2.8E-04	-2.3	5.3E-02	0.8	2.4E-01	1.2	2.7E-01
ENSMUST00000084653	predicted gene 10447 [Source:MGI Symbol;Acc:MGI:3642647]	Q3UQ92		8.4	5.1E-05	8.0	1.4E-02	-0.9	7.6E-01	-1.4	3.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000084662	DnaJ (Hsp40) homolog, subfamily B, member 5 [Source:MGI Symbol;Acc:MGI:1930018]	Q3TY13	O89114	6.1	1.8E-03	-3.7	2.1E-02	0.0	9.6E-01	1.2	4.0E-01
ENSMUST00000084695	galactose-1-phosphate uridyl transferase [Source:MGI Symbol;Acc:MGI:95638]	A2AMS3		-5.2	8.2E-04	2.8	9.7E-04	0.3	6.0E-01	-0.5	2.7E-01
ENSMUST00000081162	homeodomain leucine zipper-encoding gene [Source:MGI Symbol;Acc:MGI:2678023]			2.6	6.3E-02	7.9	2.9E-03	4.1	5.6E-02	-1.2	2.6E-01
ENSMUST00000081170	sarcoglycan, beta (dystrophin-associated glycoprotein) [Source:MGI Symbol;Acc:MGI:1346523]		P82349	1.2	5.7E-02	1.0	1.4E-01	-1.0	9.1E-02	-0.8	2.1E-01
ENSMUST00000084696	spondin 1, (f-spondin) extracellular matrix protein [Source:MGI Symbol;Acc:MGI:2385287]	Q3UYD7		6.7	3.8E-05	-7.1	1.3E-04	-1.2	1.5E-02	-0.8	5.0E-01
ENSMUST00000084701	ciliary neurotrophic factor receptor [Source:MGI Symbol;Acc:MGI:99605]	Q9D586		6.2	1.6E-03	7.9	1.9E-04	0.3	8.0E-01	-0.3	6.3E-01
ENSMUST00000084715	FYVE and coiled-coil domain containing 1 [Source:MGI Symbol;Acc:MGI:107277]		Q8VDC1	15.1	1.3E-06	-0.5	4.9E-01	0.6	1.9E-01	-1.3	1.1E-01
ENSMUST00000081214	WD repeat domain 91 [Source:MGI Symbol;Acc:MGI:2141558]		Q7TMQ7	-0.3	7.8E-01	1.4	4.0E-01	0.5	6.7E-01	-1.2	4.2E-01
ENSMUST00000081216	interferon activated gene 203 [Source:MGI Symbol;Acc:MGI:96428]	E9PUG6		1.9	5.4E-02	3.1	1.3E-02	0.1	9.3E-01	-1.1	2.0E-01
ENSMUST00000084727	zinc finger protein 143 [Source:MGI Symbol;Acc:MGI:1277969]		O70230	-4.2	5.7E-03	-0.1	9.4E-01	1.9	8.2E-02	-2.5	1.2E-01
ENSMUST00000084731	importin 7 [Source:MGI Symbol;Acc:MGI:2152414]		Q9EPL8	-4.3	9.3E-05	-2.2	5.1E-03	1.2	9.2E-03	-0.5	4.5E-01
ENSMUST00000084733	transmembrane protein 42 [Source:MGI Symbol;Acc:MGI:1277176]		Q9CR22	-1.6	2.5E-02	-5.8	9.9E-04	-0.9	8.6E-02	0.3	8.1E-01
ENSMUST00000084743	rotein O-linked mannose beta 1,4-N-acetylglucosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI:2143424		Q8BW41	4.2	1.5E-04	3.2	8.3E-04	-1.8	1.7E-02	0.1	8.4E-01
ENSMUST00000084754	olfactory receptor 514 [Source:MGI Symbol;Acc:MGI:3030348]	Q8VFZ6		7.1	1.5E-04	6.7	9.8E-05	-0.5	6.3E-01	-0.3	5.5E-01
ENSMUST00000084756	olfactory receptor 467 [Source:MGI Symbol;Acc:MGI:3030301]	L7N455		6.8	4.6E-05	7.1	4.5E-04	-0.5	7.2E-01	-1.4	9.2E-02
ENSMUST00000084760	olfactory receptor 472 [Source:MGI Symbol;Acc:MGI:3030306]	A6H654	Q8VG43	6.3	2.2E-04	6.9	1.2E-04	-0.6	6.2E-01	0.4	5.3E-01
ENSMUST00000084763	NLR family, pyrin domain containing 14 [Source:MGI Symbol;Acc:MGI:1924108]		Q6B966	6.2	5.7E-04	-4.0	2.9E-03	0.7	1.4E-01	0.0	9.7E-01
ENSMUST00000084770	fucosyltransferase 9 [Source:MGI Symbol;Acc:MGI:1330859]	Q14AE3	O88819	7.6	4.2E-05	-1.3	1.2E-01	0.7	1.3E-01	-0.1	9.1E-01
ENSMUST00000084771	prostaglandin E synthase 3 (cytosolic) [Source:MGI Symbol;Acc:MGI:1929282]	D3Z7C6		-7.3	9.3E-05	-4.3	1.1E-01	0.7	5.5E-01	-0.7	8.0E-01
ENSMUST00000084782	ADP-ribosylation factor interacting protein 2 [Source:MGI Symbol;Acc:MGI:1924182]		Q8K221	-5.8	1.3E-04	-4.3	2.5E-03	0.0	1.0E+00	0.1	9.5E-01
ENSMUST00000084787	sodium channel, voltage-gated, type X, alpha [Source:MGI Symbol;Acc:MGI:108029]	K3W4P8		9.3	3.2E-06	0.8	6.6E-01	3.8	8.3E-03	-0.5	7.4E-01
ENSMUST00000084797	solute carrier family 22 (organic cation transporter), member 13 [Source:MGI Symbol;Acc:MGI:2143107]		Q6A4L0	3.8	1.3E-04	6.1	2.5E-03	-0.6	7.1E-01	-1.2	2.0E-01
ENSMUST00000084806	dynein, axonemal, heavy chain 11 [Source:MGI Symbol;Acc:MGI:1100864]	E9Q7N9		9.4	2.8E-06	5.2	3.5E-03	0.7	6.2E-01	0.1	8.8E-01
ENSMUST00000081335	TGFB-induced factor homeobox 2 [Source:MGI Symbol;Acc:MGI:1915299]	A2AVY9	Q8C0Y1	1.5	3.3E-01	1.9	3.9E-01	0.7	7.1E-01	0.3	8.6E-01
ENSMUST00000081339	ribosomal RNA processing 1 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919712]		Q91YK2	0.5	4.5E-01	1.8	4.6E-02	0.9	1.8E-01	-0.4	5.4E-01
ENSMUST00000081342	histone cluster 1, H2ap [Source:MGI Symbol;Acc:MGI:3710573]	B2RVF0	P22752	1.2	3.9E-01	2.3	1.7E-01	-0.6	7.1E-01	-1.6	2.1E-01
ENSMUST00000084816	olfactory receptor 559 [Source:MGI Symbol;Acc:MGI:3030393]	Q8VH14		5.9	8.3E-04	4.8	2.4E-02	1.1	5.4E-01	1.4	2.4E-01
ENSMUST00000084830	cholinergic receptor, nicotinic, alpha polypeptide 10 [Source:MGI Symbol;Acc:MGI:3609260]	B2RX82		7.8	1.6E-05	5.8	9.8E-04	0.2	9.0E-01	-0.6	4.5E-01
ENSMUST00000084838	CD47 antigen (Rh-related antigen, integrin-associated signal transducer) [Source:MGI Symbol;Acc:MGI:96617		Q61735	-3.4	5.7E-05	-2.3	1.3E-02	0.7	1.3E-01	1.2	1.5E-01
ENSMUST00000084846	serine/arginine repetitive matrix 1 [Source:MGI Symbol;Acc:MGI:1858303]	A2A8V9		-6.7	1.8E-04	-6.8	6.6E-04	-0.3	4.7E-01	0.9	5.6E-01
ENSMUST00000084852	nuclear mitotic apparatus protein 1 [Source:MGI Symbol;Acc:MGI:2443665]	E9Q7G0		-1.2	7.1E-03	8.6	2.5E-05	-0.5	6.6E-01	-0.7	2.1E-01
ENSMUST00000084867	CKLF-like MARVEL transmembrane domain containing 7 [Source:MGI Symbol;Acc:MGI:2447166]		Q9ESD6	-5.1	4.9E-03	6.3	5.7E-04	-0.7	6.2E-01	0.2	7.7E-01
ENSMUST00000084882	cysteine rich protein 2 [Source:MGI Symbol;Acc:MGI:1915587]	Q4FJU3	Q9DCT8	3.2	1.9E-02	5.5	2.1E-03	-0.6	6.7E-01	0.4	5.8E-01
ENSMUST00000084885	upstream binding protein 1 [Source:MGI Symbol;Acc:MGI:104889]		Q811S7	-7.9	1.1E-03	3.4	2.6E-04	-0.1	8.7E-01	-0.5	2.7E-01
ENSMUST00000084892	dpy-19-like 4 (C. elegans) [Source:MGI Symbol;Acc:MGI:2685869]		A2AJQ3	-4.5	1.4E-04	7.6	2.2E-04	-0.6	6.5E-01	0.0	9.8E-01
ENSMUST00000081440	sodium channel, nonvoltage-gated 1 alpha [Source:MGI Symbol;Acc:MGI:101782]	Q3USG4		-0.2	8.9E-01	1.6	3.0E-01	1.3	3.0E-01	-0.5	7.1E-01
ENSMUST00000084894	phosphodiesterase 2A, cGMP-stimulated [Source:MGI Symbol;Acc:MGI:2446107]	Q5PR72		-5.0	5.8E-04	-0.6	4.7E-01	-6.2	1.6E-04	-0.8	3.0E-01
ENSMUST00000081491	2'-5' oligoadenylate synthetase 2 [Source:MGI Symbol;Acc:MGI:2180852]		E9Q9A9	-2.7	2.1E-01	-2.9	2.9E-01	-0.1	9.4E-01	0.1	9.6E-01
ENSMUST00000084896	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:1916960]		Q4LDD4	-5.5	2.1E-04	1.2	1.5E-01	-3.8	1.0E-03	-0.3	6.3E-01
ENSMUST00000084922	receptor transporter protein 3 [Source:MGI Symbol;Acc:MGI:2446841]		Q5QGU6	4.4	3.9E-03	6.8	1.9E-04	-0.5	7.0E-01	-1.4	4.6E-02
ENSMUST00000081506	short coiled-coil protein [Source:MGI Symbol;Acc:MGI:1927654]		Q78YZ6	2.2	2.1E-01	6.2	3.6E-02	2.3	3.5E-01	-1.6	3.1E-01
ENSMUST00000084926	ALS2 C-terminal like [Source:MGI Symbol;Acc:MGI:2447532]			6.4	2.9E-02	1.2	1.1E-01	-1.8	1.9E-02	-0.7	3.0E-01
ENSMUST00000084935	phosphoglucomutase 2-like 1 [Source:MGI Symbol;Acc:MGI:1918224]		Q8CAA7	3.1	2.2E-03	-2.2	6.1E-02	1.8	1.8E-02	0.7	4.8E-01
ENSMUST00000081527	Aly/REF export factor 2 [Source:MGI Symbol;Acc:MGI:1913144]	G3X9I4		-0.9	1.1E-01	-1.1	1.3E-01	-0.1	7.7E-01	0.0	9.9E-01
ENSMUST00000084941	kinesin light chain 1 [Source:MGI Symbol;Acc:MGI:107978]	Q8CD76		-4.5	1.6E-03	6.8	1.6E-04	-0.5	6.6E-01	-1.1	1.1E-01
ENSMUST00000084947	tRNA methyltransferase 61A [Source:MGI Symbol;Acc:MGI:2443487]		Q80XC2	6.9	7.1E-05	7.0	4.8E-05	-1.5	2.0E-01	-0.6	2.4E-01
ENSMUST00000084949	inositol monophosphatase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915720]		Q80V26	-2.4	1.2E-03	-3.2	8.9E-04	0.1	7.9E-01	0.3	7.0E-01
ENSMUST00000084953	MAP/microtubule affinity regulating kinase 3 [Source:MGI Symbol;Acc:MGI:1341865]		Q03141	-6.6	6.4E-04	-6.3	8.3E-05	-0.3	3.1E-01	0.0	9.7E-01
ENSMUST00000084966	unc-93 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:1933250]		Q710D3	8.6	1.1E-05	-5.9	4.7E-04	0.7	1.1E-01	-0.7	5.9E-01
ENSMUST00000081567	metal response element binding transcription factor 2 [Source:MGI Symbol;Acc:MGI:105050]		Q02395	-2.6	1.6E-01	-3.4	1.5E-01	-1.0	3.9E-01	-0.2	9.2E-01
ENSMUST00000084968	REST corepressor 1 [Source:MGI Symbol;Acc:MGI:106340]	K3W4P9		-1.5	7.1E-03	7.0	2.0E-04	-0.6	6.2E-01	-0.3	6.5E-01
ENSMUST00000084984	F-box and WD-40 domain protein 16 [Source:MGI Symbol;Acc:MGI:2443324]	Q497Z0		5.6	4.1E-04	6.6	2.8E-04	-1.5	2.7E-01	-1.3	8.2E-02
ENSMUST00000081582	zinc finger protein 953 [Source:MGI Symbol;Acc:MGI:3612873]	Q3UPV7		0.6	2.7E-01	2.2	9.4E-03	0.8	2.0E-01	-0.8	1.8E-01
ENSMUST00000084986	aquaporin 11 [Source:MGI Symbol;Acc:MGI:1913583]		Q8BHH1	4.2	3.5E-04	-2.9	5.0E-03	0.5	2.6E-01	-4.2	4.5E-03
ENSMUST00000085026	vaccinia related kinase 1 [Source:MGI Symbol;Acc:MGI:1261847]	Q3UWH3	Q80X41	-3.9	2.7E-02	-10.9	1.4E-03	0.5	3.4E-01	3.5	1.8E-01
ENSMUST00000081618	zinc finger protein 780B [Source:MGI Symbol;Acc:MGI:2444764]	E9Q2S6		0.8	1.3E-01	0.6	3.6E-01	-0.2	6.8E-01	0.0	9.8E-01
ENSMUST00000085027	NHL repeat containing 4 [Source:MGI Symbol;Acc:MGI:3687200]		Q3UP44	8.7	1.9E-05	6.4	9.7E-02	-5.4	2.3E-01	-1.3	5.1E-01
ENSMUST00000081628	DNA methyltransferase 3B [Source:MGI Symbol;Acc:MGI:1261819]		O88509	2.9	3.4E-01	4.5	1.7E-01	-0.4	9.1E-01	-2.0	3.7E-01
ENSMUST00000081631	methyltransferase like 15 [Source:MGI Symbol;Acc:MGI:1924144]		Q9DCL4	0.0	9.9E-01	0.8	6.3E-01	-0.2	8.7E-01	-1.0	4.9E-01
ENSMUST00000085043	T cell leukemia/lymphoma 1B, 1 [Source:MGI Symbol;Acc:MGI:1351601]	Q3UWQ4	P56840	6.8	1.7E-04	4.4	1.4E-02	-0.5	7.4E-01	1.3	1.9E-01
ENSMUST00000085050	serine (or cysteine) peptidase inhibitor, clade A, member 3C [Source:MGI Symbol;Acc:MGI:102848]		P29621	6.3	1.4E-03	-6.2	7.7E-04	-2.5	1.1E-03	0.3	8.5E-01
ENSMUST00000085052	serine (or cysteine) peptidase inhibitor, clade A, member 3B [Source:MGI Symbol;Acc:MGI:2182835]	Q05A44	Q8BYY9	6.3	9.1E-05	5.9	3.9E-03	-0.7	6.9E-01	-0.5	5.7E-01
ENSMUST00000085060	adhesion molecule with Ig like domain 3 [Source:MGI Symbol;Acc:MGI:2444854]		Q8C2S7	2.6	2.2E-02	-7.4	7.5E-06	0.4	2.2E-01	-0.8	3.7E-01
ENSMUST00000085065	interferon, alpha-inducible protein 27 [Source:MGI Symbol;Acc:MGI:1277180]	Q8C6G0		-6.4	1.9E-04	-5.4	4.9E-05	-0.6	1.2E-01	-4.5	2.3E-03
ENSMUST00000081654	collagen, type XVIII, alpha 1 [Source:MGI Symbol;Acc:MGI:88451]		P39061	4.2	6.4E-02	1.1	5.0E-01	-5.7	1.1E-02	-2.5	1.3E-01
ENSMUST00000085073	actin-like 11 [Source:MGI Symbol;Acc:MGI:1914972]	Q9D5V1		9.4	2.3E-05	-7.1	1.3E-04	0.2	6.2E-01	-0.6	6.0E-01
ENSMUST00000081677	peptidylprolyl isomerase (cyclophilin)-like 3 [Source:MGI Symbol;Acc:MGI:1917475]		Q9D6L8	-3.8	5.2E-02	-2.2	3.4E-01	0.8	6.0E-01	-0.9	6.8E-01
ENSMUST00000085077	aryl hydrocarbon receptor nuclear translocator 2 [Source:MGI Symbol;Acc:MGI:107188]		Q61324	9.0	3.8E-06	7.1	5.5E-05	-0.6	6.0E-01	-0.8	1.9E-01
ENSMUST00000081688	SLIT-ROBO Rho GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2152936]	D3YZW1		-1.7	3.3E-01	4.7	5.5E-02	2.2	3.0E-01	-4.2	2.6E-02
ENSMUST00000085092	calcium channel, voltage-dependent, alpha 2/delta subunit 2 [Source:MGI Symbol;Acc:MGI:1929813]		Q6PHS9	8.7	1.3E-02	-4.7	9.9E-02	1.9	9.7E-02	1.9	4.7E-01
ENSMUST00000085094	predicted gene 10160 [Source:MGI Symbol;Acc:MGI:3642884]	F6Y577		7.3	2.4E-05	-6.2	1.3E-03	0.6	1.9E-01	0.5	7.2E-01
ENSMUST00000081710	dynein cytoplasmic 1 intermediate chain 2 [Source:MGI Symbol;Acc:MGI:107750]	A2BFF7	O88487	-2.4	1.7E-01	-0.8	6.1E-01	-0.2	8.5E-01	-1.8	3.2E-01
ENSMUST00000085116	protein tyrosine phosphatase, non-receptor type 21 [Source:MGI Symbol;Acc:MGI:1344406]	G5E8J4		7.1	9.4E-03	9.1	7.3E-03	3.1	2.5E-01	-0.4	7.7E-01
ENSMUST00000085133	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]	Q3UZR5		-4.8	1.8E-03	5.8	8.8E-05	-0.7	4.4E-01	0.1	8.3E-01
ENSMUST00000081721	enhancer of zeste homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:107940]		Q61188	0.0	9.9E-01	-2.2	5.1E-01	-2.8	2.1E-01	-0.7	8.5E-01
ENSMUST00000085164	synaptic vesicle glycoprotein 2 b [Source:MGI Symbol;Acc:MGI:1927338]		Q8BG39	8.0	8.0E-04	-5.3	1.6E-03	0.6	2.2E-01	-2.1	1.6E-01
ENSMUST00000085177	male-specific lethal 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1925103]		Q69ZF8	-3.8	1.6E-03	6.7	5.6E-05	-0.8	4.1E-01	-0.1	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000085222	transient receptor potential cation channel, subfamily M, member 1 [Source:MGI Symbol;Acc:MGI:1330305]		Q2TV84	5.8	1.7E-02	5.8	1.3E-02	-0.7	7.2E-01	-1.4	2.7E-01
ENSMUST00000085238	solute carrier family 8 (sodium/calcium exchanger), member 3 [Source:MGI Symbol;Acc:MGI:107976]	Q7TS90		10.6	2.4E-05	5.6	4.1E-04	-4.0	8.7E-03	-1.1	1.2E-01
ENSMUST00000085240	gamma-aminobutyric acid (GABA) A receptor, subunit beta 3 [Source:MGI Symbol;Acc:MGI:95621]	F6ZYH6		7.9	2.6E-05	-2.2	1.4E-02	0.9	4.4E-02	-0.2	7.7E-01
ENSMUST00000085248	mortality factor 4 like 1 [Source:MGI Symbol;Acc:MGI:1096551]		P60762	-6.9	2.6E-05	4.8	1.1E-02	-0.6	7.0E-01	1.1	2.9E-01
ENSMUST00000085255	cytoplasmic FMR1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1338801]			-6.4	5.4E-03	-6.7	1.5E-02	0.0	1.0E+00	1.9	4.3E-01
ENSMUST00000085256	5, 10-methenyltetrahydrofolate synthetase [Source:MGI Symbol;Acc:MGI:1340032]		Q9D110	-6.9	5.8E-06	3.9	3.3E-02	-3.3	8.9E-02	-1.9	1.6E-01
ENSMUST00000085272	HIV-1 tat interactive protein 2, homolog (human) [Source:MGI Symbol;Acc:MGI:1859271]		Q9Z2G9	-3.6	1.3E-05	6.1	2.2E-04	-1.3	2.9E-01	-0.4	5.5E-01
ENSMUST00000081780	TD and POZ domain containing 3 [Source:MGI Symbol;Acc:MGI:3027903]		Q717B4	3.6	7.6E-02	5.3	2.5E-02	-0.3	8.9E-01	-2.0	1.3E-01
ENSMUST00000085289	interphotoreceptor matrix proteoglycan 1 [Source:MGI Symbol;Acc:MGI:1926876]		Q8R1W8	8.2	6.0E-05	-0.9	7.3E-01	3.0	1.4E-01	-2.4	3.4E-01
ENSMUST00000085311	f-box protein 9 [Source:MGI Symbol;Acc:MGI:1918788]		Q8BK06	-4.3	4.1E-03	-3.0	7.1E-02	-0.4	6.1E-01	-3.4	9.9E-02
ENSMUST00000081799	small G protein signaling modulator 2 [Source:MGI Symbol;Acc:MGI:2144695]		Q80U12	3.5	1.1E-01	7.3	6.7E-03	-0.4	8.7E-01	-4.2	1.1E-02
ENSMUST00000085314	ninein [Source:MGI Symbol;Acc:MGI:105108]	E9Q4S3		-3.8	1.7E-05	3.3	2.3E-03	-0.1	8.7E-01	0.3	6.5E-01
ENSMUST00000081834	armadillo repeat containing, X-linked 3 [Source:MGI Symbol;Acc:MGI:1918953]		Q8BHS6	-1.1	2.9E-01	0.6	6.4E-01	0.7	4.6E-01	-1.0	4.0E-01
ENSMUST00000081838	zinc finger, DHHC domain containing 12 [Source:MGI Symbol;Acc:MGI:1913470]		Q8VC90	-2.8	5.1E-02	-3.1	4.2E-02	-0.9	3.0E-01	-0.5	7.3E-01
ENSMUST00000085319	a disintegrin and metalloeptidase domain 4 [Source:MGI Symbol;Acc:MGI:104731]	Q8CGQ2		3.5	5.7E-03	-6.1	3.3E-05	-1.0	1.9E-02	-1.0	2.4E-01
ENSMUST00000085330	predicted gene 10491 [Source:MGI Symbol;Acc:MGI:3642000]	D3YU47		6.3	1.2E-02	-3.0	4.6E-03	0.7	1.4E-01	-0.5	5.4E-01
ENSMUST00000081849	polyhomeotic-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:103248]	Q3V116		0.6	8.1E-01	-2.9	4.9E-01	-1.3	6.2E-01	2.2	5.7E-01
ENSMUST00000085350	cell cycle progression 1 [Source:MGI Symbol;Acc:MGI:1196419]		Q640L3	-11.5	2.0E-05	6.4	4.0E-04	-0.6	6.3E-01	0.6	3.9E-01
ENSMUST00000085351	histidine rich calcium binding protein [Source:MGI Symbol;Acc:MGI:96226]	G5E8J6		8.3	8.9E-06	8.8	2.7E-05	-0.6	6.1E-01	-0.1	8.1E-01
ENSMUST00000085358	testis expressed gene 9 [Source:MGI Symbol;Acc:MGI:1201610]	Z4YJY6		5.0	3.4E-05	-1.8	4.3E-02	1.3	1.8E-02	-0.6	4.9E-01
ENSMUST00000085368	predicted pseudogene 5786 [Source:MGI Symbol;Acc:MGI:3645003]	J3QMG5		4.2	9.8E-04	6.9	8.2E-04	-0.7	6.3E-01	0.1	9.0E-01
ENSMUST00000085374	ier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 [Source:MGI Symbol;Acc:MG		Q3TXX4	4.6	1.1E-04	4.7	8.8E-04	-1.7	1.4E-01	-0.8	2.6E-01
ENSMUST00000081891				0.9	5.4E-01	3.8	4.5E-02	1.3	3.9E-01	-1.6	2.5E-01
ENSMUST00000081893	synapsin I [Source:MGI Symbol;Acc:MGI:98460]		O88935	-2.4	1.2E-01	2.6	1.4E-01	1.6	2.6E-01	-3.4	5.3E-02
ENSMUST00000085375	PIH1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1916095]		Q9CQJ2	-6.7	5.9E-05	1.1	5.8E-01	1.7	3.1E-01	-4.0	5.9E-02
ENSMUST00000085385	Ral GTPase activating protein, alpha subunit 1 [Source:MGI Symbol;Acc:MGI:1931050]		Q6GYP7	-4.9	1.8E-03	6.5	9.5E-02	-1.0	7.9E-01	2.6	2.0E-01
ENSMUST00000085393	BCL2/adenovirus E1B interacting protein 2 [Source:MGI Symbol;Acc:MGI:109327]	Q91VL0		-6.0	1.5E-03	6.7	7.9E-04	-0.4	7.9E-01	-0.5	5.4E-01
ENSMUST00000085399	adaptor-related protein complex 2, alpha 1 subunit [Source:MGI Symbol;Acc:MGI:101921]		P17426	8.4	2.7E-03	5.4	2.5E-03	-0.6	6.5E-01	0.6	4.7E-01
ENSMUST00000085422	IZUMO family member 2 [Source:MGI Symbol;Acc:MGI:1922760]		Q9DA16	5.5	9.6E-04	2.4	2.1E-01	-1.5	3.6E-01	3.3	4.6E-02
ENSMUST00000085435	casein kinase 1, gamma 2 [Source:MGI Symbol;Acc:MGI:1920014]		Q8BVP5	-6.0	2.5E-04	-6.8	2.2E-03	0.3	6.0E-01	0.8	6.4E-01
ENSMUST00000081921	cilia and flagella associated protein 57 [Source:MGI Symbol;Acc:MGI:2686209]		Q9D180	3.4	1.8E-01	1.3	6.9E-01	-1.3	6.6E-01	0.9	7.1E-01
ENSMUST00000085450	kallikrein 1-related peptidase b3 [Source:MGI Symbol;Acc:MGI:97322]		P00756	6.7	7.7E-05	-9.4	4.7E-07	0.3	2.3E-01	-1.1	1.7E-01
ENSMUST00000081926	zinc finger protein 341 [Source:MGI Symbol;Acc:MGI:2682937]	Q6PGC9		2.9	2.5E-01	9.0	2.2E-02	3.9	2.3E-01	-2.1	3.4E-01
ENSMUST00000085453	RAS-like, family 12 [Source:MGI Symbol;Acc:MGI:1918034]		Q08AT1	4.8	1.9E-04	11.7	5.0E-04	1.8	4.3E-01	1.5	1.2E-01
ENSMUST00000081932	N-myristoyltransferase 2 [Source:MGI Symbol;Acc:MGI:1202298]	Q3THR4	O70311	0.3	6.5E-01	0.4	6.4E-01	0.0	9.8E-01	-0.1	8.8E-01
ENSMUST00000081933	deltex 3-like (Drosophila) [Source:MGI Symbol;Acc:MGI:2656973]		Q3UIR3	-0.5	3.8E-01	-0.5	5.4E-01	0.7	2.4E-01	0.7	3.9E-01
ENSMUST00000085455	kallikrein 1-related peptidase b21 [Source:MGI Symbol;Acc:MGI:892022]	Q3UNG6	Q61759	6.3	1.6E-04	-9.1	1.3E-03	-1.1	8.3E-02	0.2	9.4E-01
ENSMUST00000085519	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A [Source:MGI Symbol;Acc:MGI:108447]		O35381	-5.4	1.3E-05	6.5	1.0E-04	-1.0	3.6E-01	-0.2	7.4E-01
ENSMUST00000081946	translocase of inner mitochondrial membrane 50 [Source:MGI Symbol;Acc:MGI:1913775]		Q9D880	-1.4	5.3E-02	-1.0	2.5E-01	0.3	5.6E-01	-0.1	9.1E-01
ENSMUST00000085546	high mobility group box 1 [Source:MGI Symbol;Acc:MGI:96113]	Q58EV5	P63158	-1.7	2.1E-03	2.9	6.7E-02	-4.1	2.5E-02	-2.8	4.8E-02
ENSMUST00000085553	grainyhead-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2182540]		Q921D9	7.1	2.4E-04	6.4	1.2E-03	-0.7	6.5E-01	-0.6	4.9E-01
ENSMUST00000085555	digestive organ expansion factor homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2138080]			6.4	1.2E-02	6.8	6.2E-04	-0.5	7.5E-01	-1.0	1.9E-01
ENSMUST00000085558	microtubule associated tumor suppressor candidate 2 [Source:MGI Symbol;Acc:MGI:1915388]		Q3UHD3	3.6	1.1E-03	5.0	1.0E-02	-0.6	7.0E-01	1.4	1.7E-01
ENSMUST00000081980	mediator complex subunit 9 [Source:MGI Symbol;Acc:MGI:2183151]		Q8VCS6	0.7	2.0E-01	0.9	2.4E-01	0.7	2.2E-01	0.5	4.4E-01
ENSMUST00000085585	LSM14 homolog A (SCD6, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914320]		Q8K2F8	-4.6	8.7E-05	7.0	1.3E-02	-0.2	9.3E-01	2.0	1.7E-01
ENSMUST00000085591	pancreatic and duodenal homeobox 1 [Source:MGI Symbol;Acc:MGI:102851]		P52946	7.6	4.0E-05	2.2	1.3E-02	0.0	9.5E-01	-0.2	7.9E-01
ENSMUST00000081993	predicted pseudogene 10020 [Source:MGI Symbol;Acc:MGI:3642192]	E9QAZ2		-0.2	7.0E-01	-3.4	8.5E-03	-0.7	2.0E-01	2.4	3.5E-02
ENSMUST00000081998	dipeptidase 2 [Source:MGI Symbol;Acc:MGI:2442042]		Q8C255	0.3	7.3E-01	3.1	2.1E-02	1.2	2.4E-01	-1.6	1.2E-01
ENSMUST00000085614	ubiquitin specific peptidase 12 [Source:MGI Symbol;Acc:MGI:1270128]		Q9D9M2	-5.7	1.3E-03	-3.3	4.6E-04	-0.4	2.1E-01	0.4	5.7E-01
ENSMUST00000085635	major facilitator superfamily domain containing 7B [Source:MGI Symbol;Acc:MGI:2444881]		B2RXV4	-5.7	5.2E-05	-1.3	3.9E-01	0.4	7.1E-01	-2.0	2.2E-01
ENSMUST00000085651	neuroplastin [Source:MGI Symbol;Acc:MGI:108077]		P97300	-8.9	1.1E-06	5.8	1.6E-03	-0.6	6.8E-01	-0.7	3.9E-01
ENSMUST00000082054	regulating synaptic membrane exocytosis 2 [Source:MGI Symbol;Acc:MGI:2152972]		Q9EQZ7	5.6	3.8E-02	7.0	2.1E-02	-0.4	8.8E-01	-1.8	2.2E-01
ENSMUST00000085658	RIKEN cDNA 6030419C18 gene [Source:MGI Symbol;Acc:MGI:2442108]		Q8CD60	8.2	1.1E-05	3.6	3.6E-04	0.5	3.9E-01	-0.9	1.0E-01
ENSMUST00000085661	zinc finger protein 655 [Source:MGI Symbol;Acc:MGI:1919861]	F7AFH2		-2.7	1.1E-02	-9.5	3.4E-05	0.0	9.8E-01	0.7	5.8E-01
ENSMUST00000085668	predicted gene 5113 [Source:MGI Symbol;Acc:MGI:3644651]	Q3UGK8		6.3	5.0E-04	4.0	2.5E-04	-3.4	3.1E-03	-0.4	4.2E-01
ENSMUST00000082089	RNA binding motif protein 10 [Source:MGI Symbol;Acc:MGI:2384310]		Q99KG3	2.1	5.0E-01	-1.9	6.0E-01	-4.5	1.3E-01	-0.5	9.0E-01
ENSMUST00000085679	actin related protein 2/3 complex, subunit 1B [Source:MGI Symbol;Acc:MGI:1343142]		Q9WV32	-4.2	2.6E-05	6.8	1.6E-04	-0.6	6.3E-01	-0.3	6.7E-01
ENSMUST00000085708	signal transducer and activator of transcription 2 [Source:MGI Symbol;Acc:MGI:103039]	Q9QXJ2		-2.4	6.5E-03	2.8	6.6E-03	-3.7	3.9E-03	-0.8	2.5E-01
ENSMUST00000085709	phosphopantothenoylcysteine decarboxylase [Source:MGI Symbol;Acc:MGI:1914062]		Q8BZB2	-2.3	5.1E-03	-2.2	1.6E-02	-0.6	2.0E-01	-0.5	5.4E-01
ENSMUST00000085724	sushi domain containing 4 [Source:MGI Symbol;Acc:MGI:2138351]		Q8BH32	7.6	3.8E-05	9.0	3.0E-05	-0.6	6.3E-01	-0.5	3.2E-01
ENSMUST00000085733	speedy/RINGO cell cycle regulator family, member E4A [Source:MGI Symbol;Acc:MGI:1921923]		Q5IBH6	6.9	8.3E-05	7.8	3.4E-05	-0.6	6.2E-01	-1.1	6.9E-02
ENSMUST00000085741	tetratricopeptide repeat domain 32 [Source:MGI Symbol;Acc:MGI:1922766]		Q9DAC7	-3.1	4.5E-04	-3.2	6.3E-03	0.1	8.3E-01	-0.2	8.0E-01
ENSMUST00000085745	WD repeat domain 35 [Source:MGI Symbol;Acc:MGI:1921932]		Q8BND3	6.8	1.5E-02	-2.4	2.0E-01	1.2	2.7E-01	-0.6	7.5E-01
ENSMUST00000085754	expressed sequence AI118078 [Source:MGI Symbol;Acc:MGI:2142980]		Q8BZB3	8.0	4.6E-06	-11.9	1.2E-03	-0.9	1.3E-01	2.5	3.5E-01
ENSMUST00000085758	Ras association and DIL domains [Source:MGI Symbol;Acc:MGI:2443088]		Q69Z89	7.7	2.2E-03	-4.2	7.5E-03	0.5	4.2E-01	-2.5	1.2E-01
ENSMUST00000082152	ubiquitin-conjugating enzyme E2O [Source:MGI Symbol;Acc:MGI:2444266]		Q6ZPJ3	1.2	9.1E-02	1.3	1.6E-01	0.2	7.4E-01	0.1	8.7E-01
ENSMUST00000085774	sidekick homolog 1 (chicken) [Source:MGI Symbol;Acc:MGI:2444413]		Q3UH53	7.5	3.9E-05	9.6	2.1E-05	0.7	5.9E-01	-0.2	6.2E-01
ENSMUST00000082175	tripartite motif-containing 68 [Source:MGI Symbol;Acc:MGI:2142077]	G3X9I6		0.8	2.8E-01	1.3	1.7E-01	-0.3	7.0E-01	-0.7	3.8E-01
ENSMUST00000085786	caspase recruitment domain family, member 11 [Source:MGI Symbol;Acc:MGI:1916978]		Q8CIS0	3.2	4.8E-04	-5.3	5.2E-03	1.3	7.5E-02	0.2	9.0E-01
ENSMUST00000082197	histone deacetylase 10 [Source:MGI Symbol;Acc:MGI:2158340]		Q6P3E7	-0.4	7.8E-01	3.3	9.9E-02	1.3	4.4E-01	-2.4	1.3E-01
ENSMUST00000085797	left-right determination factor 2 [Source:MGI Symbol;Acc:MGI:2443573]		P57785	5.6	1.1E-05	9.8	9.4E-03	-1.0	7.9E-01	-2.2	1.9E-01
ENSMUST00000085814	nuclear receptor coactivator 1 [Source:MGI Symbol;Acc:MGI:1276523]		P70365	-1.7	3.1E-03	2.1	1.1E-01	-1.4	2.3E-01	-0.1	9.1E-01
ENSMUST00000082223	ribosomal protein L5 [Source:MGI Symbol;Acc:MGI:102854]	Q58EU6	P47962	-1.6	4.0E-01	-1.5	3.4E-01	-2.9	4.2E-02	-3.0	1.2E-01
ENSMUST00000085835	mitogen-activated protein kinase kinase kinase kinase 1 [Source:MGI Symbol;Acc:MGI:1346882]		P70218	-2.5	7.2E-04	6.9	2.7E-04	-0.5	7.1E-01	-0.9	2.2E-01
ENSMUST00000085851	ar factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta [Source:MGI Symbol;Acc:MGI:10		Q60778	-4.4	4.2E-03	4.0	3.6E-04	0.1	9.0E-01	0.2	7.0E-01
ENSMUST00000082243	spire homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1915416]		Q52KF3	5.5	7.6E-02	2.0	4.6E-01	-4.1	1.9E-01	-0.7	7.5E-01
ENSMUST00000085876	pyrin domain containing 3 [Source:MGI Symbol;Acc:MGI:2442822]		Q3V3Q4	6.6	3.1E-06	7.7	3.4E-05	-0.6	5.8E-01	-0.3	6.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000085886	sperm motility kinase 3A [Source:MGI Symbol;Acc:MGI:3693943]		Q9QYZ5	10.1	5.0E-05	-0.6	6.5E-01	-2.9	2.1E-02	3.8	6.4E-03
ENSMUST00000085901	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b [Source:MGI Symbol;Acc:MGI:1330302]		Q9Z188	-5.2	7.0E-03	5.7	1.7E-03	-0.6	6.9E-01	0.1	9.3E-01
ENSMUST00000082300				0.1	9.1E-01	2.8	5.9E-02	0.4	7.5E-01	-2.3	7.4E-02
ENSMUST00000085912	immunoglobulin superfamily, member 8 [Source:MGI Symbol;Acc:MGI:2154090]			-4.3	3.1E-02	7.8	2.0E-02	-0.9	7.8E-01	-0.9	5.7E-01
ENSMUST00000082319	WD repeat domain 33 [Source:MGI Symbol;Acc:MGI:1921570]	D3YX80		0.9	2.5E-01	0.1	9.4E-01	-0.7	2.9E-01	0.1	9.4E-01
ENSMUST00000082321	complement receptor 2 [Source:MGI Symbol;Acc:MGI:88489]	Q9DC83		3.6	1.0E-01	1.1	6.3E-01	-1.7	4.1E-01	0.8	7.1E-01
ENSMUST00000085913	ATPase, Na+/K+ transporting, alpha 2 polypeptide [Source:MGI Symbol;Acc:MGI:88106]	Q3UHK5	Q6PIE5	8.6	7.6E-06	1.8	5.3E-03	0.3	5.3E-01	0.2	6.3E-01
ENSMUST00000085939	FXYD domain-containing ion transport regulator 6 [Source:MGI Symbol;Acc:MGI:1890226]		Q9D164	7.6	5.6E-05	6.9	6.2E-04	1.1	4.0E-01	-0.1	9.3E-01
ENSMUST00000085941	zinc finger, HIT domain containing 1 [Source:MGI Symbol;Acc:MGI:1917353]		Q8R331	-5.8	1.3E-05	-5.9	2.4E-06	-1.2	1.6E-03	-3.1	9.5E-04
ENSMUST00000085984	Williams Beuren syndrome chromosome region 22 [Source:MGI Symbol;Acc:MGI:1913388]	Q148S9	Q9CY21	-5.2	1.7E-03	-4.8	1.4E-03	-0.7	2.0E-01	-1.8	1.6E-01
ENSMUST00000085989	claudin 9 [Source:MGI Symbol;Acc:MGI:1913100]		Q9Z0S7	7.7	2.7E-05	-6.6	1.1E-06	0.0	8.8E-01	-2.0	7.0E-03
ENSMUST00000085992	dual specificity phosphatase 27 (putative) [Source:MGI Symbol;Acc:MGI:2685055]		Q148W8	9.2	3.7E-03	-8.4	5.4E-04	2.6	1.1E-03	2.4	1.6E-01
ENSMUST00000086006	zinc finger protein 111 [Source:MGI Symbol;Acc:MGI:1929114]	Q99K53		6.5	1.8E-04	-7.0	1.3E-05	-0.8	5.5E-02	-1.6	1.0E-01
ENSMUST00000086010	zinc finger protein 114 [Source:MGI Symbol;Acc:MGI:3037815]	Q3UTF4		7.1	1.7E-04	-10.6	5.3E-04	-0.2	6.8E-01	-1.7	4.6E-01
ENSMUST00000086013	predicted gene 10175 [Source:MGI Symbol;Acc:MGI:3704287]		P56383	-5.3	1.6E-03	-7.8	5.7E-04	1.0	1.1E-01	-0.1	9.5E-01
ENSMUST00000086023	Williams-Beuren syndrome chromosome region 17 homolog (human) [Source:MGI Symbol;Acc:MGI:2137594	Q59J92	Q7TT15	7.8	2.6E-06	-7.1	4.7E-03	-1.7	3.6E-02	-0.4	8.6E-01
ENSMUST00000086029	calneuron 1 [Source:MGI Symbol;Acc:MGI:2155987]	F8WHE1		6.4	9.0E-05	-5.8	5.4E-06	-0.5	1.1E-01	-1.0	1.4E-01
ENSMUST00000086032	basic leucine zipper nuclear factor 1 [Source:MGI Symbol;Acc:MGI:1201607]		Q8R2X8	-4.0	9.8E-03	-4.1	7.4E-05	0.0	9.7E-01	-0.8	2.2E-01
ENSMUST00000086040	coagulation factor V [Source:MGI Symbol;Acc:MGI:88382]		O88783	-3.0	1.1E-04	-5.1	6.4E-03	0.2	7.9E-01	-0.5	7.5E-01
ENSMUST00000086046	glioblastoma amplified sequence [Source:MGI Symbol;Acc:MGI:1278343]	Q7TMG8		-4.0	5.3E-05	-5.4	1.2E-04	-0.3	5.4E-01	-2.5	2.8E-02
ENSMUST00000086056	piwi-like RNA-mediated gene silencing 1 [Source:MGI Symbol;Acc:MGI:1928897]		Q9JMB7	9.0	7.1E-06	-5.0	8.0E-04	-1.5	1.6E-02	-2.6	4.3E-02
ENSMUST00000086058	Berardinelli-Seip congenital lipodystrophy 2 homolog (seipin) [Source:MGI Symbol;Acc:MGI:1298392]		Q9Z2E9	-7.5	5.5E-05	5.1	6.4E-04	-0.6	6.0E-01	1.0	1.3E-01
ENSMUST00000086074	dynamin 3 [Source:MGI Symbol;Acc:MGI:1341299]	E9QLL2		7.1	8.2E-04	-4.4	1.7E-04	1.1	8.9E-03	0.1	9.4E-01
ENSMUST00000086075	scavenger receptor class B, member 1 [Source:MGI Symbol;Acc:MGI:893578]	Q4FK30	Q61009	-5.1	2.6E-03	-5.3	2.3E-04	0.8	6.9E-02	-0.3	7.7E-01
ENSMUST00000086101	prostaglandin I receptor (IP) [Source:MGI Symbol;Acc:MGI:99535]	E9PY53		-5.4	2.6E-03	-1.8	6.0E-02	0.5	3.3E-01	-0.1	9.2E-01
ENSMUST00000086112	adaptor-related protein complex 2, sigma 1 subunit [Source:MGI Symbol;Acc:MGI:2141861]	Q3UJ76	P62743	-6.6	2.0E-06	7.7	3.9E-05	-0.6	6.1E-01	-1.0	1.0E-01
ENSMUST00000086122	oocyte specific homeobox 3 [Source:MGI Symbol;Acc:MGI:2149032]	Q3UT54		7.6	1.7E-04	0.8	1.8E-01	-2.1	3.7E-03	0.0	9.8E-01
ENSMUST00000086123	phosphatidylinositol transfer protein, membrane-associated 2 [Source:MGI Symbol;Acc:MGI:1336192]		Q6ZPQ6	2.9	3.4E-03	-4.0	7.8E-03	-2.4	9.2E-03	-1.1	4.0E-01
ENSMUST00000086130	SEC16 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2148802]		Q91XT4	6.9	1.8E-04	-4.3	6.5E-04	0.6	1.7E-01	-0.9	3.6E-01
ENSMUST00000086167	nuclear factor related to kappa B binding protein [Source:MGI Symbol;Acc:MGI:2442410]		Q6PIJ4	-5.4	4.6E-05	-7.9	2.5E-04	-0.7	1.7E-01	0.0	9.9E-01
ENSMUST00000084026	Wolf-Hirschhorn syndrome candidate 1-like 1 (human) [Source:MGI Symbol;Acc:MGI:2142581]	D3Z357		0.7	8.6E-01	-1.3	8.4E-01	1.2	8.1E-01	3.2	5.5E-01
ENSMUST00000084027	fibroblast growth factor receptor 1 [Source:MGI Symbol;Acc:MGI:95522]		P16092	3.7	1.2E-01	0.0	9.9E-01	-5.6	1.9E-02	-2.0	2.5E-01
ENSMUST00000086195	zinc finger protein 648 [Source:MGI Symbol;Acc:MGI:2685049]	D3Z0W3		8.0	1.5E-05	-0.1	8.2E-01	0.9	2.3E-02	-0.6	2.4E-01
ENSMUST00000086199	glutamate-ammonia ligase (glutamine synthetase) [Source:MGI Symbol;Acc:MGI:95739]		P15105	-4.6	9.7E-06	4.4	3.9E-03	-1.8	1.8E-01	-0.3	6.8E-01
ENSMUST00000086210	vomeronasal 2, receptor 54 [Source:MGI Symbol;Acc:MGI:3704110]	K7N649		7.2	3.3E-04	-5.3	3.7E-03	0.6	3.2E-01	1.9	2.0E-01
ENSMUST00000084035	a disintegrin and metallopeptidase domain 9 (meltrin gamma) [Source:MGI Symbol;Acc:MGI:105376]		Q61072	-3.3	2.6E-01	0.2	9.4E-01	0.1	9.6E-01	-3.4	2.7E-01
ENSMUST00000086216	anaphase-promoting complex subunit 5 [Source:MGI Symbol;Acc:MGI:1929722]		Q8BTZ4	-3.1	1.5E-05	10.5	1.8E-04	0.5	8.0E-01	-0.6	3.5E-01
ENSMUST00000086238	predicted gene 10181 [Source:MGI Symbol;Acc:MGI:3642432]	F6VC88		11.2	8.2E-06	6.3	2.2E-03	-0.4	8.2E-01	-0.3	7.4E-01
ENSMUST00000086248	aurora kinase C [Source:MGI Symbol;Acc:MGI:1321119]	E9QL04		6.9	5.7E-03	-4.5	1.8E-02	0.2	8.4E-01	1.9	2.3E-01
ENSMUST00000086274	predicted gene 10490 [Source:MGI Symbol;Acc:MGI:3642001]	F6VBM2		4.3	1.9E-03	1.6	4.1E-02	0.7	2.0E-01	-2.7	4.5E-03
ENSMUST00000086281	zinc finger protein 599 [Source:MGI Symbol;Acc:MGI:2679006]	E9PWP1		4.4	2.8E-05	7.1	5.7E-05	-0.5	6.2E-01	-0.2	7.1E-01
ENSMUST00000084116	nucleolar protein 9 [Source:MGI Symbol;Acc:MGI:1921285]		Q3TZX8	-3.3	1.3E-01	-0.6	8.1E-01	0.7	7.1E-01	-1.9	4.4E-01
ENSMUST00000084117	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) [Source:MGI Symbol;Acc:MGI:2140356]		Q8CFX1	-1.5	4.2E-02	0.1	9.4E-01	1.2	5.6E-02	-0.3	7.4E-01
ENSMUST00000086282	vomeronasal 2, receptor 42 [Source:MGI Symbol;Acc:MGI:1316666]	O35192		8.6	9.9E-06	-6.1	4.7E-05	1.4	2.5E-03	-0.6	4.9E-01
ENSMUST00000084125	TAR DNA binding protein [Source:MGI Symbol;Acc:MGI:2387629]	Q544R5	Q921F2	-2.8	3.6E-02	-1.4	2.9E-01	-1.0	2.3E-01	-2.5	1.0E-01
ENSMUST00000084129	MAD2 mitotic arrest deficient-like 2 [Source:MGI Symbol;Acc:MGI:1919140]		Q9D752	0.5	6.5E-01	1.5	3.4E-01	0.7	6.1E-01	-0.3	8.1E-01
ENSMUST00000086297	vomeronasal 2, receptor 28 [Source:MGI Symbol;Acc:MGI:3645468]	L7N203		5.8	7.0E-04	-1.3	1.3E-01	-0.4	5.1E-01	-0.8	3.2E-01
ENSMUST00000086310	SH2B adaptor protein 3 [Source:MGI Symbol;Acc:MGI:893598]		O09039	-3.9	8.1E-03	0.6	4.5E-01	1.0	8.8E-02	-1.1	1.5E-01
ENSMUST00000086325	FLYWCH-type zinc finger 1 [Source:MGI Symbol;Acc:MGI:2442638]		Q8CI03	-3.1	2.2E-02	-4.2	1.6E-02	0.4	6.0E-01	0.6	7.1E-01
ENSMUST00000084191	preferentially expressed antigen in melanoma like 4 [Source:MGI Symbol;Acc:MGI:2156377]	Q810Z0		2.9	1.5E-01	6.1	1.0E-02	-0.4	8.6E-01	-3.6	2.2E-02
ENSMUST00000086338	vomeronasal 1 receptor 65 [Source:MGI Symbol;Acc:MGI:3033475]	Q9EPS7		6.7	2.9E-06	6.0	4.6E-04	-0.2	8.9E-01	-0.5	4.1E-01
ENSMUST00000086341	NLR family, pyrin domain containing 5 [Source:MGI Symbol;Acc:MGI:1345193]		Q9R1M5	5.5	3.2E-02	0.1	9.6E-01	0.8	3.0E-01	-4.5	9.3E-03
ENSMUST00000084207	Rho guanine nucleotide exchange factor (GEF) 10 [Source:MGI Symbol;Acc:MGI:2444453]		Q8C033	4.1	1.3E-01	8.0	1.3E-02	-0.5	8.8E-01	-4.4	1.9E-02
ENSMUST00000086349	zinc finger protein 524 [Source:MGI Symbol;Acc:MGI:1916740]		Q9D0B1	-3.6	3.1E-04	-3.8	1.3E-01	2.0	1.2E-01	0.3	9.0E-01
ENSMUST00000084215	eukaryotic translation initiation factor 4 gamma, 3 [Source:MGI Symbol;Acc:MGI:1923935]	A2AMI2		-1.5	4.0E-01	2.0	3.6E-01	1.3	4.9E-01	-2.2	2.5E-01
ENSMUST00000086353	mast cell immunoglobulin like receptor 1 [Source:MGI Symbol;Acc:MGI:2685731]		Q3TB92	-9.1	1.9E-04	-2.4	1.8E-02	1.3	2.5E-02	-0.5	5.7E-01
ENSMUST00000086361	cDNA sequence AB124611 [Source:MGI Symbol;Acc:MGI:3043001]	A0A0B4J1G2		-8.5	2.0E-05	-2.8	1.1E-03	1.0	1.4E-02	-0.4	4.8E-01
ENSMUST00000086364	transmembrane protein 150B [Source:MGI Symbol;Acc:MGI:2679718]		Q8R218	4.5	9.5E-04	1.5	3.8E-01	6.2	7.9E-04	0.2	8.5E-01
ENSMUST00000086374	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) [Source:MGI Symbol;Acc:MGI:105387]		Q60773	-6.0	8.6E-06	5.8	1.8E-03	-0.8	5.9E-01	0.0	9.6E-01
ENSMUST00000086377	2'-5' oligoadenylate synthetase 1B [Source:MGI Symbol;Acc:MGI:97430]	V5IRT6		9.2	1.2E-03	-4.8	2.1E-02	0.2	7.3E-01	0.1	9.8E-01
ENSMUST00000086395	G protein-coupled receptor 25 [Source:MGI Symbol;Acc:MGI:2686146]		P0C5I1	4.2	2.5E-03	-5.0	1.2E-03	1.8	1.7E-03	-0.7	5.9E-01
ENSMUST00000084289	argonaute RISC catalytic subunit 4 [Source:MGI Symbol;Acc:MGI:1924100]		Q8CJF8	0.1	8.8E-01	0.4	6.8E-01	0.3	6.7E-01	0.0	9.8E-01
ENSMUST00000086401	leukocyte-associated Ig-like receptor 1 [Source:MGI Symbol;Acc:MGI:105492]		Q8BG84	-5.4	8.8E-03	-0.4	6.3E-01	1.1	5.4E-02	-0.4	5.7E-01
ENSMUST00000086421	non-catalytic region of tyrosine kinase adaptor protein 2 [Source:MGI Symbol;Acc:MGI:1306821]		O55033	3.5	1.6E-03	-1.4	1.4E-01	2.1	4.4E-03	-0.9	3.6E-01
ENSMUST00000086423	predicted pseudogene 10184 [Source:MGI Symbol;Acc:MGI:3704480]	Q52L97	P52293	-2.8	2.1E-03	0.4	8.5E-01	-6.4	2.2E-02	-0.2	9.3E-01
ENSMUST00000086430	collagen, type V, alpha 2 [Source:MGI Symbol;Acc:MGI:88458]		Q3U962	7.1	8.6E-05	7.4	8.3E-05	-0.5	7.1E-01	-0.5	4.1E-01
ENSMUST00000086451	nitric oxide synthase 1, neuronal [Source:MGI Symbol;Acc:MGI:97360]	S4R255		5.9	3.6E-04	6.0	4.7E-04	-0.6	6.2E-01	-0.3	6.3E-01
ENSMUST00000086458	F-box and leucine-rich repeat protein 12 [Source:MGI Symbol;Acc:MGI:1354738]			-6.4	3.5E-05	-4.5	2.1E-03	-0.1	7.5E-01	-0.8	5.2E-01
ENSMUST00000086459	F-box and leucine-rich repeat protein 12 [Source:MGI Symbol;Acc:MGI:1354738]		Q9EPX5	-5.5	3.9E-03	7.5	7.3E-05	-0.6	5.9E-01	0.1	8.5E-01
ENSMUST00000086465	adenosine A1 receptor [Source:MGI Symbol;Acc:MGI:99401]		Q60612	7.0	3.5E-04	4.7	7.4E-02	-0.6	8.0E-01	2.1	1.7E-01
ENSMUST00000086471	suppressor of defective silencing 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919204]		Q8BR65	-5.4	8.5E-04	4.6	2.7E-03	-1.2	3.5E-01	0.2	7.4E-01
ENSMUST00000086479	RIKEN cDNA C330021F23 gene [Source:MGI Symbol;Acc:MGI:3612471]	Q8C7T0		7.6	1.5E-03	7.0	1.1E-03	1.1	4.3E-01	1.1	1.9E-01
ENSMUST00000086483	coiled-coil domain containing 60 [Source:MGI Symbol;Acc:MGI:2141043]			7.4	5.8E-06	3.3	1.6E-01	6.9	3.0E-03	0.2	8.8E-01
ENSMUST00000086519	ribosomal protein, large, P0 [Source:MGI Symbol;Acc:MGI:1927636]	Q5M8R8	P14869	-7.0	6.1E-06	7.9	1.7E-03	1.9	2.9E-01	-1.9	9.4E-02
ENSMUST00000086523	paxillin [Source:MGI Symbol;Acc:MGI:108295]	F8VQ28		-4.4	1.0E-02	-6.2	7.0E-04	0.6	1.9E-01	-0.8	5.8E-01
ENSMUST00000084412	interferon induced transmembrane protein 10 [Source:MGI Symbol;Acc:MGI:2444776]		Q8BR26	1.4	7.1E-02	2.1	3.6E-02	0.3	7.2E-01	-0.4	6.0E-01
ENSMUST00000086535	ribosomal protein L31 [Source:MGI Symbol;Acc:MGI:2149632]	Q5M9K9	P62900	-3.3	9.7E-05	5.7	7.6E-03	-0.8	6.7E-01	2.1	5.2E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000086564	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]	E9PVA6		-7.2	4.4E-05	-2.7	3.0E-03	0.3	3.7E-01	-0.1	9.1E-01
ENSMUST00000086615	transmembrane protein 211 [Source:MGI Symbol;Acc:MGI:2685700]		Q3UUA0	8.7	4.8E-05	5.5	1.5E-02	-3.3	1.3E-01	0.1	9.2E-01
ENSMUST00000086617	myosin XVIIIb [Source:MGI Symbol;Acc:MGI:1921626]	E9PV66		9.3	1.4E-05	-3.0	4.7E-03	0.5	2.3E-01	-0.6	4.8E-01
ENSMUST00000084446	leucine rich repeat containing 56 [Source:MGI Symbol;Acc:MGI:1917802]	Q8BMW2		0.6	5.6E-01	-0.2	8.9E-01	0.5	6.5E-01	1.2	3.2E-01
ENSMUST00000086635	phosphatidylinositol transfer protein, beta [Source:MGI Symbol;Acc:MGI:1927542]		P53811	-2.4	7.6E-04	6.9	3.0E-04	0.3	7.8E-01	-0.7	2.7E-01
ENSMUST00000086639	anaplastic lymphoma kinase [Source:MGI Symbol;Acc:MGI:103305]		P97793	8.4	9.7E-06	7.0	7.2E-05	-0.5	6.3E-01	-1.4	3.8E-02
ENSMUST00000086672	predicted gene 10192 [Source:MGI Symbol;Acc:MGI:3642867]	Q3V0S1		8.1	1.7E-05	4.1	4.5E-04	-3.4	4.7E-03	0.5	4.2E-01
ENSMUST00000086675	RIKEN cDNA A330017A19 gene [Source:MGI Symbol;Acc:MGI:3045380]	Q8CA87		5.3	8.3E-05	7.2	2.2E-04	-0.2	8.7E-01	-0.6	3.0E-01
ENSMUST00000084479	predicted gene 11238 [Source:MGI Symbol;Acc:MGI:3702316]	F2Z478		3.0	1.8E-01	5.3	2.8E-02	-0.5	8.0E-01	-2.9	9.3E-02
ENSMUST00000086721	RIKEN cDNA 2310035C23 gene [Source:MGI Symbol;Acc:MGI:1922832]	G3X9J4		-6.7	5.1E-05	6.4	1.7E-04	-0.5	6.4E-01	-1.1	1.1E-01
ENSMUST00000086723	mannosidase 2, alpha 1 [Source:MGI Symbol;Acc:MGI:104669]		P27046	-4.0	4.1E-06	2.6	1.2E-03	-0.1	8.7E-01	-0.6	2.0E-01
ENSMUST00000086738	contactin associated protein-like 5B [Source:MGI Symbol;Acc:MGI:3664583]		Q0V8T8	6.4	2.4E-04	7.4	1.2E-04	-0.6	6.1E-01	-0.8	2.5E-01
ENSMUST00000084493	sideroflexin 3 [Source:MGI Symbol;Acc:MGI:2137679]	Q3U4F0		2.6	2.6E-01	8.2	2.0E-02	2.7	3.9E-01	-3.0	8.5E-02
ENSMUST00000086763	adhesion G protein-coupled receptor E1 [Source:MGI Symbol;Acc:MGI:106912]	Q3U9R0	Q61549	-4.7	7.5E-03	7.5	1.0E-03	-0.4	8.0E-01	0.0	9.6E-01
ENSMUST00000086764	ribosomal protein S12, pseudogene 3 [Source:MGI Symbol;Acc:MGI:3704503]	Q6ZWZ6		-7.3	1.8E-04	-7.8	1.0E-04	0.4	2.4E-01	0.3	8.4E-01
ENSMUST00000086787	t-complex protein 10b [Source:MGI Symbol;Acc:MGI:98542]	E9PYJ0		5.5	3.4E-02	-5.6	1.8E-03	-0.7	2.8E-01	-1.5	3.0E-01
ENSMUST00000086795	BarH-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1859314]		Q8VIB5	8.8	2.8E-04	6.4	3.8E-05	-3.3	1.4E-02	-0.2	7.4E-01
ENSMUST00000086828	protein tyrosine phosphatase, receptor type, S [Source:MGI Symbol;Acc:MGI:97815]		B0V2N1	3.8	1.1E-04	-2.9	7.7E-04	0.3	3.2E-01	-0.3	6.2E-01
ENSMUST00000086829	bicaudal D homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1101760]		Q8BR07	4.8	1.9E-04	7.9	2.6E-05	-0.9	4.3E-01	-0.2	7.3E-01
ENSMUST00000086831	polycystic kidney disease 2 [Source:MGI Symbol;Acc:MGI:1099818]		O35245	3.2	5.1E-04	-4.4	9.2E-03	0.6	3.5E-01	-1.1	4.9E-01
ENSMUST00000086837	olfactory receptor 1416 [Source:MGI Symbol;Acc:MGI:3031250]	Q8VGU4		6.1	1.4E-04	5.7	6.4E-04	-0.6	6.3E-01	0.1	8.5E-01
ENSMUST00000086851	hairy and enhancer of split 6 [Source:MGI Symbol;Acc:MGI:1859852]		Q9JHE6	-5.3	5.8E-04	-0.7	6.0E-01	0.8	3.7E-01	-2.0	1.4E-01
ENSMUST00000086861	family with sequence similarity 132, member B [Source:MGI Symbol;Acc:MGI:3606476]		Q6PGN1	8.3	1.6E-05	7.7	2.9E-03	0.4	8.5E-01	-2.5	6.7E-02
ENSMUST00000084524	PRP4 pre-mRNA processing factor 4 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1917302]	Q059T9	Q9DAW6	0.7	1.2E-01	1.2	5.1E-02	0.4	3.7E-01	-0.1	8.3E-01
ENSMUST00000086876	protection of telomeres 1B [Source:MGI Symbol;Acc:MGI:1920086]	H7BX60		6.1	1.0E-06	-7.8	2.0E-05	-0.1	8.0E-01	-0.9	4.1E-01
ENSMUST00000086882	ankyrin repeat and SOCS box-containing 18 [Source:MGI Symbol;Acc:MGI:2655109]		Q8VHA6	3.8	1.0E-04	-3.5	3.5E-04	0.7	4.2E-02	0.5	4.8E-01
ENSMUST00000086887	predicted gene 10197 [Source:MGI Symbol;Acc:MGI:3704501]	F6QEY5		-4.3	1.1E-03	-7.0	5.3E-04	0.6	3.3E-01	-0.2	9.1E-01
ENSMUST00000086909	RIKEN cDNA C530008M17 gene [Source:MGI Symbol;Acc:MGI:2444817]	Q3UP88		7.1	7.4E-05	1.1	1.5E-01	0.0	9.6E-01	1.1	1.0E-01
ENSMUST00000086932	transcription factor EB [Source:MGI Symbol;Acc:MGI:103270]		Q9R210	-6.0	7.9E-05	-2.4	3.9E-02	0.5	3.9E-01	0.8	4.1E-01
ENSMUST00000086961	5'-nucleotidase, cytosolic II [Source:MGI Symbol;Acc:MGI:2178563]	G3X9J6		7.0	6.9E-05	3.4	2.5E-04	0.3	5.9E-01	0.5	2.8E-01
ENSMUST00000087012	solute carrier family 22 (organic anion transporter), member 7 [Source:MGI Symbol;Acc:MGI:1859559]			7.2	4.2E-04	-5.5	5.6E-02	0.4	7.2E-01	2.0	4.4E-01
ENSMUST00000084564	zinc finger protein 629 [Source:MGI Symbol;Acc:MGI:2444524]		Q6A085	-0.7	6.0E-01	3.1	6.3E-02	0.6	6.2E-01	-3.1	4.1E-02
ENSMUST00000084586				0.2	8.9E-01	1.7	3.2E-01	1.4	3.7E-01	-0.2	8.6E-01
ENSMUST00000084589	oid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) [Source:MGI Symbol;Acc:MGI:1075		Q61124	-0.7	3.7E-01	-0.1	9.6E-01	1.4	8.9E-02	0.8	4.3E-01
ENSMUST00000087026	polymerase (RNA) I polypeptide C [Source:MGI Symbol;Acc:MGI:103288]		P52432	-1.8	1.6E-02	8.2	2.9E-04	-0.3	8.6E-01	0.8	2.8E-01
ENSMUST00000087050	collagen, type IV, alpha 4 [Source:MGI Symbol;Acc:MGI:104687]		Q9QZR9	7.2	1.7E-05	2.8	1.9E-02	0.2	8.1E-01	0.6	4.1E-01
ENSMUST00000087085	Nance-Horan syndrome (human) [Source:MGI Symbol;Acc:MGI:2684894]	B1AV60		7.8	1.8E-04	-10.8	1.4E-05	-1.0	1.5E-02	-0.3	8.6E-01
ENSMUST00000087086	paired box 3 [Source:MGI Symbol;Acc:MGI:97487]		P24610	7.7	2.5E-02	7.8	3.3E-05	0.0	9.8E-01	0.5	3.7E-01
ENSMUST00000084616	ankyrin repeat and sterile alpha motif domain containing 6 [Source:MGI Symbol;Acc:MGI:1922941]	E9PUD3		-2.1	6.8E-02	4.7	2.8E-03	2.7	2.7E-02	-4.1	3.0E-03
ENSMUST00000087104	cyclin-dependent kinase-like 5 [Source:MGI Symbol;Acc:MGI:1278336]		Q3UTQ8	5.5	4.0E-04	-1.0	1.7E-01	1.5	9.8E-03	0.1	9.0E-01
ENSMUST00000087114	centromere protein Q [Source:MGI Symbol;Acc:MGI:1933744]		Q9CPQ5	-3.1	4.4E-04	7.2	6.1E-05	-0.5	6.4E-01	-0.5	3.3E-01
ENSMUST00000087122	SPEG complex locus [Source:MGI Symbol;Acc:MGI:109282]	E9QQ25		10.5	3.0E-06	5.8	8.5E-04	-0.6	6.6E-01	0.3	6.6E-01
ENSMUST00000087143	eukaryotic translation initiation factor 1A, X-linked [Source:MGI Symbol;Acc:MGI:1913485]		Q8BMJ3	-2.2	2.1E-03	5.6	8.4E-04	-0.5	6.7E-01	-0.1	8.5E-01
ENSMUST00000087157	kelch-like 34 [Source:MGI Symbol;Acc:MGI:2685234]	A2AI76		7.0	7.1E-05	7.1	1.5E-03	-0.5	7.5E-01	0.8	3.1E-01
ENSMUST00000087158	tripartite motif-containing 40 [Source:MGI Symbol;Acc:MGI:2684881]		Q3UWA4	4.9	1.7E-02	3.4	1.4E-01	1.3	4.5E-01	4.0	3.5E-02
ENSMUST00000087176	oligodendrocytic myelin paranodal and inner loop protein [Source:MGI Symbol;Acc:MGI:2657025]	Q3USW3	Q7M750	6.8	4.2E-05	-3.6	2.8E-02	1.3	7.5E-02	-0.3	8.4E-01
ENSMUST00000087177	leucine rich repeat containing 66 [Source:MGI Symbol;Acc:MGI:2387634]		Q8K0B3	7.7	1.1E-04	5.8	2.1E-04	-0.9	4.1E-01	0.0	9.6E-01
ENSMUST00000087186	serine/threonine kinase 36 [Source:MGI Symbol;Acc:MGI:1920831]		Q69ZM6	5.5	1.7E-03	6.5	2.0E-03	-0.7	6.6E-01	-1.1	2.5E-01
ENSMUST00000087195	OCIA domain containing 2 [Source:MGI Symbol;Acc:MGI:1916377]		Q9D8W7	3.6	1.1E-04	12.6	1.3E-05	-0.9	5.7E-01	1.5	8.3E-03
ENSMUST00000084724	RIKEN cDNA 3110043O21 gene [Source:MGI Symbol;Acc:MGI:1920455]		Q6DFW0	-1.1	4.3E-01	1.5	3.7E-01	0.3	8.5E-01	-2.4	1.4E-01
ENSMUST00000087200	guanine nucleotide binding protein-like 1 [Source:MGI Symbol;Acc:MGI:95764]		P36916	-2.1	1.6E-02	-4.8	1.6E-02	-0.4	5.7E-01	0.2	9.3E-01
ENSMUST00000087204	furry homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2443895]		E9Q8I9	-1.0	6.6E-03	-4.4	5.8E-04	-0.1	8.9E-01	0.0	9.6E-01
ENSMUST00000087212	NIPA-like domain containing 1 [Source:MGI Symbol;Acc:MGI:1917951]		Q8BMW7	5.6	3.6E-04	0.0	1.0E+00	1.2	4.6E-02	-0.3	6.6E-01
ENSMUST00000084736	cannabinoid receptor 1 (brain) [Source:MGI Symbol;Acc:MGI:104615]		P47746	5.1	1.1E-01	5.9	8.4E-02	-1.1	7.5E-01	-1.9	3.0E-01
ENSMUST00000084738	suppression of tumorigenicity 5 [Source:MGI Symbol;Acc:MGI:108517]		Q924W7	3.6	9.6E-02	5.8	2.4E-02	-0.3	9.0E-01	-2.5	9.1E-02
ENSMUST00000087215	rcd1 (required for cell differentiation) homolog 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:1928902]		Q9JKY0	-1.8	1.1E-03	4.1	4.9E-04	0.0	9.7E-01	0.1	8.4E-01
ENSMUST00000084748	ankyrin repeat domain 6 [Source:MGI Symbol;Acc:MGI:2154278]		Q69ZU8	1.6	3.2E-01	3.7	7.4E-02	0.2	9.0E-01	-1.8	2.3E-01
ENSMUST00000084749	ankyrin repeat domain 6 [Source:MGI Symbol;Acc:MGI:2154278]		Q69ZU8	5.1	5.4E-02	7.4	1.5E-02	-0.5	8.6E-01	-2.8	8.8E-02
ENSMUST00000087216	nuclear transcription factor, X-box binding-like 1 [Source:MGI Symbol;Acc:MGI:1923646]	E9Q8I7		-4.7	3.6E-03	6.0	8.8E-04	-0.6	6.5E-01	0.5	5.2E-01
ENSMUST00000087225	paroxysmal nonkinesiogenic dyskinesia [Source:MGI Symbol;Acc:MGI:1930773]		Q69ZP3	8.1	2.1E-02	6.0	2.4E-04	-0.6	5.9E-01	0.2	6.8E-01
ENSMUST00000087236	cytochrome P450, family 2, subfamily c, polypeptide 65 [Source:MGI Symbol;Acc:MGI:1919553]	Q148B1		5.1	2.5E-03	5.0	1.8E-03	-0.6	6.1E-01	0.6	4.1E-01
ENSMUST00000087241	shisa family member 3 [Source:MGI Symbol;Acc:MGI:3041225]		Q3UPR0	8.9	5.4E-06	5.6	1.9E-03	-0.5	7.3E-01	0.1	9.0E-01
ENSMUST00000087252	leucine-rich repeat LGI family, member 1 [Source:MGI Symbol;Acc:MGI:1861691]	A0A0G2JEY8		6.9	2.2E-05	7.2	1.4E-04	-0.6	6.1E-01	-0.2	8.0E-01
ENSMUST00000087268	ATP-binding cassette, sub-family A (ABC1), member 12 [Source:MGI Symbol;Acc:MGI:2676312]	E9Q876		8.4	2.2E-05	-3.5	8.3E-03	1.5	1.8E-02	-2.3	1.1E-01
ENSMUST00000087285	forkhead box D3 [Source:MGI Symbol;Acc:MGI:1347473]	A2BDY3		6.8	9.6E-05	-4.9	2.0E-03	0.2	6.3E-01	-0.6	6.2E-01
ENSMUST00000087313	doublecortin [Source:MGI Symbol;Acc:MGI:1277171]		O88809	7.5	7.4E-05	9.1	8.2E-06	-0.6	6.0E-01	-0.4	3.9E-01
ENSMUST00000087315	valyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:90675]	Q790I0	Q9Z1Q9	-4.9	4.7E-03	4.1	1.7E-04	-0.4	5.1E-01	-0.7	1.9E-01
ENSMUST00000084803	dynein, axonemal, heavy chain 17 [Source:MGI Symbol;Acc:MGI:1917176]	E9Q7P0		0.6	7.2E-01	-2.4	4.6E-01	1.5	3.7E-01	4.5	1.6E-01
ENSMUST00000087321	protein phosphatase 1, regulatory (inhibitor) subunit 3C [Source:MGI Symbol;Acc:MGI:1858229]		Q7TMB3	8.0	3.0E-05	9.2	6.8E-06	-0.5	6.4E-01	-0.4	3.8E-01
ENSMUST00000087324	phosphoglucomutase 1 [Source:MGI Symbol;Acc:MGI:97564]		Q7TSV4	-5.4	1.2E-06	5.7	1.8E-03	-0.7	6.4E-01	-0.5	5.4E-01
ENSMUST00000084820	golgi autoantigen, golgin subfamily a, 4 [Source:MGI Symbol;Acc:MGI:1859646]		Q91VW5	-0.1	7.2E-01	-0.2	7.3E-01	0.3	4.0E-01	0.4	4.7E-01
ENSMUST00000087327	RELT-like 1 [Source:MGI Symbol;Acc:MGI:2140767]	H7BX61		-3.0	1.5E-03	6.0	5.2E-04	-0.5	7.1E-01	-0.6	4.1E-01
ENSMUST00000084828	non-SMC condensin II complex, subunit G2 [Source:MGI Symbol;Acc:MGI:1923294]		Q6DFV1	0.5	3.4E-01	0.2	8.0E-01	-0.1	7.4E-01	0.2	7.8E-01
ENSMUST00000087328	heat shock protein 1A [Source:MGI Symbol;Acc:MGI:96244]	Q3TU85	Q61696	2.2	1.0E-02	7.5	3.4E-05	-0.9	4.3E-01	-0.6	2.7E-01
ENSMUST00000087332	predicted gene 16223 [Source:MGI Symbol;Acc:MGI:3648966]	Q8CBM3		11.4	4.3E-06	-2.3	6.8E-03	1.6	2.1E-03	0.5	4.3E-01
ENSMUST00000087333	transmembrane protein 164 [Source:MGI Symbol;Acc:MGI:2148020]		Q6PHN7	-2.4	7.5E-03	-0.5	5.4E-01	1.2	6.8E-02	-5.0	2.0E-03
ENSMUST00000087342	ribosomal protein S28 [Source:MGI Symbol;Acc:MGI:1859516]	Q059I1	P62858	-6.0	7.1E-04	-0.6	2.0E-01	0.5	1.3E-01	-0.1	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000084853	glycerol-3-phosphate dehydrogenase 1-like [Source:MGI Symbol;Acc:MGI:1289257]		Q3ULJ0	3.4	8.3E-02	-1.7	4.0E-01	-4.1	3.6E-02	1.0	5.6E-01
ENSMUST00000087348	predicted gene 10203 [Source:MGI Symbol;Acc:MGI:3642365]	F6QJ09		9.7	3.8E-05	-2.3	1.2E-01	0.8	3.8E-01	-2.0	2.3E-01
ENSMUST00000084881	cartilage associated protein [Source:MGI Symbol;Acc:MGI:1891221]		Q9CYD3	0.1	9.6E-01	-0.9	4.4E-01	-1.9	4.9E-02	-1.0	3.7E-01
ENSMUST00000087351	heterogeneous nuclear ribonucleoprotein A1 [Source:MGI Symbol;Acc:MGI:104820]		P49312	-5.4	6.5E-03	2.4	7.6E-02	-1.5	2.1E-01	-0.7	4.9E-01
ENSMUST00000087366	cAMP responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:88494]	Q543W0	Q01147	-2.7	1.5E-03	-7.2	2.6E-02	1.0	2.7E-01	0.3	9.1E-01
ENSMUST00000084891	phosphofurin acidic cluster sorting protein 2 [Source:MGI Symbol;Acc:MGI:1924399]	E9Q7E9		0.1	8.9E-01	0.6	3.2E-01	0.6	1.6E-01	0.1	8.4E-01
ENSMUST00000087399	tenascin XB [Source:MGI Symbol;Acc:MGI:1932137]	O35452		8.7	1.5E-06	0.3	5.8E-01	0.4	3.3E-01	-4.4	2.2E-04
ENSMUST00000087409	zinc finger and BTB domain containing 46 [Source:MGI Symbol;Acc:MGI:1919397]		Q8BID6	5.0	6.7E-04	-8.5	4.6E-03	1.3	6.4E-02	4.8	6.2E-02
ENSMUST00000084895	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:1916960]		Q4LDD4	-2.4	6.7E-02	-0.9	5.1E-01	-0.4	6.7E-01	-1.9	2.0E-01
ENSMUST00000087435	one morphogenetic protein receptor, type II (serine/threonine kinase) [Source:MGI Symbol;Acc:MGI:1095407		O35607	-0.9	3.2E-02	-2.5	4.0E-02	1.5	3.3E-02	-1.5	2.1E-01
ENSMUST00000087441	prominin 1 [Source:MGI Symbol;Acc:MGI:1100886]	G3X9J8		-6.0	3.4E-03	5.6	6.4E-03	1.5	3.4E-01	0.2	8.3E-01
ENSMUST00000087445	tubulin, alpha 3B [Source:MGI Symbol;Acc:MGI:1095408]	Q5FW91	P05214	8.2	4.9E-05	3.4	2.9E-01	-0.8	7.9E-01	2.2	3.5E-01
ENSMUST00000087511	transmembrane protein 128 [Source:MGI Symbol;Acc:MGI:1913559]		Q9CZB9	-4.4	9.3E-05	4.0	1.2E-03	0.4	5.9E-01	-0.5	4.6E-01
ENSMUST00000084937	RIKEN cDNA 2410002F23 gene [Source:MGI Symbol;Acc:MGI:1914226]	Q3TE80		-3.2	2.5E-01	-2.9	3.8E-01	-0.2	8.9E-01	-0.5	8.8E-01
ENSMUST00000087517	death inducer-obliterator 1 [Source:MGI Symbol;Acc:MGI:1344352]		Q8C9B9	-1.1	1.5E-02	-2.5	1.7E-02	-0.5	4.1E-01	-2.4	5.5E-02
ENSMUST00000087521	Ngg1 interacting factor 3-like 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:1929485]		Q9EQ80	3.5	9.2E-04	6.0	2.0E-03	0.4	7.5E-01	1.4	1.2E-01
ENSMUST00000087543	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4 [Source:MGI Symbol;Acc:MGI:1859517]	A0A068BIS6	Q9Z0F0	-2.2	2.4E-03	-1.6	3.5E-02	0.9	4.7E-02	0.1	8.3E-01
ENSMUST00000084952	kinesin family member 9 [Source:MGI Symbol;Acc:MGI:1098237]		Q9WV04	0.1	8.3E-01	-1.4	1.0E-01	-0.9	1.5E-01	0.7	3.7E-01
ENSMUST00000087566	aldolase A, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:87994]	A6ZI44		-7.8	3.9E-04	-5.5	8.3E-03	0.2	7.0E-01	-0.8	6.5E-01
ENSMUST00000087582	heterogeneous nuclear ribonucleoprotein M [Source:MGI Symbol;Acc:MGI:1926465]	Q3THB3	Q9D0E1	-7.8	1.7E-04	8.2	2.1E-04	0.5	7.2E-01	0.9	1.9E-01
ENSMUST00000087600	guanine deaminase [Source:MGI Symbol;Acc:MGI:95678]	Q548F2	Q9R111	-5.8	7.3E-07	-0.6	3.6E-01	1.3	1.1E-02	0.3	5.6E-01
ENSMUST00000084979	myosin VIIA [Source:MGI Symbol;Acc:MGI:104510]			2.5	2.2E-01	4.8	5.4E-02	-1.0	6.6E-01	-3.2	7.6E-02
ENSMUST00000087605	myosin IF [Source:MGI Symbol;Acc:MGI:107711]	Q8CG29		-6.4	1.1E-05	6.5	2.5E-04	-0.5	7.0E-01	-1.4	5.5E-02
ENSMUST00000084985	protein phosphatase 2, regulatory subunit B', gamma [Source:MGI Symbol;Acc:MGI:1349475]		Q60996	-3.8	6.2E-02	-2.6	2.7E-01	1.0	4.6E-01	-0.3	9.1E-01
ENSMUST00000087614	AE binding protein 2 [Source:MGI Symbol;Acc:MGI:1338038]		Q9Z248	-2.6	3.0E-02	3.1	2.9E-03	-1.4	1.0E-01	-0.3	6.6E-01
ENSMUST00000085018	inositol hexaphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:1923750]		Q80V72	-0.6	7.7E-01	2.3	5.4E-01	4.1	1.5E-01	1.2	6.8E-01
ENSMUST00000087622	pleckstrin homology domain containing, family A member 5 [Source:MGI Symbol;Acc:MGI:1923802]	E9Q6H8		3.9	1.1E-04	-4.6	3.6E-02	-1.0	3.5E-01	-0.3	8.8E-01
ENSMUST00000087623	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10 [Source:MGI Symbol;Acc:M		P58459	-6.1	1.2E-03	7.6	1.1E-04	-0.4	7.7E-01	0.7	2.9E-01
ENSMUST00000085040	G protein-coupled receptor 171 [Source:MGI Symbol;Acc:MGI:2442043]		Q8BG55	0.0	9.6E-01	-1.4	1.1E-01	-1.6	3.3E-02	-0.1	8.8E-01
ENSMUST00000087629	HtrA serine peptidase 3 [Source:MGI Symbol;Acc:MGI:1925808]		Q9D236	7.2	2.7E-05	6.1	6.4E-04	-0.6	6.5E-01	0.1	9.4E-01
ENSMUST00000085044	ubiquitin specific peptidase 19 [Source:MGI Symbol;Acc:MGI:1918722]		Q3UJD6	-1.6	1.5E-01	0.3	8.5E-01	1.5	1.6E-01	-0.4	7.7E-01
ENSMUST00000087638	aldehyde dehydrogenase family 1, subfamily A1 [Source:MGI Symbol;Acc:MGI:1353450]		P24549	2.0	3.4E-02	2.6	4.3E-02	-4.1	1.3E-02	-0.5	6.2E-01
ENSMUST00000087654	zinc finger protein 763 [Source:MGI Symbol;Acc:MGI:1920701]	Q8BIC7		3.0	2.1E-03	6.6	1.2E-04	-0.6	6.2E-01	-0.9	1.5E-01
ENSMUST00000087674	H6 homeobox 1 [Source:MGI Symbol;Acc:MGI:107178]		O70218	5.9	3.9E-04	3.4	3.9E-02	1.0	4.5E-01	0.2	8.3E-01
ENSMUST00000087675	2-deoxyribose-5-phosphate aldolase homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1913762]		Q91YP3	-2.6	4.5E-04	-6.6	7.7E-04	-1.1	4.5E-02	-0.9	5.4E-01
ENSMUST00000087689	prune homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925004]		Q52KR3	4.7	3.4E-06	8.8	8.0E-05	-0.7	6.2E-01	-0.1	8.8E-01
ENSMUST00000087714	histone cluster 1, H4j [Source:MGI Symbol;Acc:MGI:2448436]	B2RTM0	P62806	4.2	2.6E-03	7.7	1.5E-05	-1.4	2.0E-01	-0.1	8.7E-01
ENSMUST00000087721	epoxide hydrolase 3 [Source:MGI Symbol;Acc:MGI:1919182]			9.1	1.9E-05	8.3	2.5E-02	-0.8	8.1E-01	-0.4	8.3E-01
ENSMUST00000087723	notch 3 [Source:MGI Symbol;Acc:MGI:99460]		Q61982	10.0	1.4E-06	7.0	5.6E-04	1.2	3.5E-01	1.5	7.9E-02
ENSMUST00000085096	coiled-coil domain containing 88C [Source:MGI Symbol;Acc:MGI:1915589]		Q6VGS5	6.2	6.3E-02	7.1	9.7E-02	2.7	4.9E-01	1.7	5.0E-01
ENSMUST00000085102	cytokine inducible SH2-containing protein [Source:MGI Symbol;Acc:MGI:103159]		Q62225	-0.5	6.0E-01	3.1	3.4E-02	2.8	2.6E-02	-0.8	4.3E-01
ENSMUST00000085108	forkhead box N3 [Source:MGI Symbol;Acc:MGI:1918625]		Q499D0	-0.7	6.9E-01	-1.1	5.9E-01	-0.9	5.4E-01	-0.5	8.1E-01
ENSMUST00000085109	tetratricopeptide repeat domain 8 [Source:MGI Symbol;Acc:MGI:1923510]		Q8VD72	3.3	1.1E-01	-1.0	5.7E-01	-5.1	1.5E-02	-0.8	6.2E-01
ENSMUST00000087729	germ cell-specific gene 1 [Source:MGI Symbol;Acc:MGI:1194499]		Q8R1W2	4.6	7.2E-03	5.7	8.1E-02	0.3	9.2E-01	1.7	3.3E-01
ENSMUST00000087737	TNFAIP3 interacting protein 2 [Source:MGI Symbol;Acc:MGI:2386643]		Q99JG7	-4.1	1.0E-03	-2.5	1.1E-01	1.7	6.9E-02	-0.5	7.2E-01
ENSMUST00000087824	olfactory receptor 1428 [Source:MGI Symbol;Acc:MGI:3031262]	Q0VDY1		6.0	1.7E-04	4.1	3.9E-02	-2.0	2.9E-01	1.9	1.2E-01
ENSMUST00000087828	olfactory receptor 1425 [Source:MGI Symbol;Acc:MGI:3031259]	K7N659		7.3	2.9E-04	-2.1	9.9E-02	1.6	3.2E-02	0.0	9.8E-01
ENSMUST00000085181	YTH domain family 2 [Source:MGI Symbol;Acc:MGI:2444233]	E9PW90		-1.4	2.6E-01	-0.4	8.1E-01	1.0	4.2E-01	0.0	1.0E+00
ENSMUST00000085192	aldehyde dehydrogenase family 6, subfamily A1 [Source:MGI Symbol;Acc:MGI:1915077]		Q9EQ20	-0.3	5.4E-01	0.7	2.5E-01	-0.2	6.4E-01	-1.2	5.4E-02
ENSMUST00000085206	solute carrier family 25, member 36 [Source:MGI Symbol;Acc:MGI:1924909]		Q922G0	-0.1	8.5E-01	0.1	9.2E-01	-0.3	6.0E-01	-0.5	5.1E-01
ENSMUST00000085217	glycerol kinase 5 (putative) [Source:MGI Symbol;Acc:MGI:2443336]		Q8BX05	0.9	2.5E-01	2.2	4.6E-02	0.7	3.8E-01	-0.6	5.0E-01
ENSMUST00000087853	proline-rich protein BstNI subfamily 1 [Source:MGI Symbol;Acc:MGI:2681872]	Q91X93		9.8	5.9E-04	7.9	4.7E-03	-0.8	7.2E-01	-2.9	4.8E-02
ENSMUST00000087857	olfactory receptor 1419 [Source:MGI Symbol;Acc:MGI:3031253]	Q7TQS2		6.6	2.7E-04	8.9	1.8E-04	-0.8	6.2E-01	0.8	2.3E-01
ENSMUST00000087865	Y box protein 3 [Source:MGI Symbol;Acc:MGI:2137670]		Q9JKB3	-3.9	3.5E-03	7.5	1.3E-04	0.0	1.0E+00	0.4	5.4E-01
ENSMUST00000085245	solute carrier family 39 (zinc transporter), member 9 [Source:MGI Symbol;Acc:MGI:1914820]		Q8BFU1	-0.6	1.7E-01	0.5	3.9E-01	0.5	2.0E-01	-0.6	2.9E-01
ENSMUST00000087867	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2685620]		B1AVZ0	5.5	2.1E-05	-3.5	3.7E-03	0.7	1.3E-01	-2.6	3.5E-02
ENSMUST00000085254	retinol dehydrogenase 11 [Source:MGI Symbol;Acc:MGI:102581]	Q9R1R8		-2.5	4.0E-02	-1.3	2.9E-01	-0.2	8.2E-01	-1.4	2.9E-01
ENSMUST00000087871	AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		P63094	5.3	6.2E-05	-6.7	1.6E-02	-1.0	2.6E-01	-0.7	7.9E-01
ENSMUST00000087877	AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		Q6R0H7	7.1	5.0E-05	-7.4	3.3E-05	-0.7	4.2E-02	-0.3	7.7E-01
ENSMUST00000087879	expressed sequence C77370 [Source:MGI Symbol;Acc:MGI:2148050]		Q5DTT1	5.8	4.7E-03	-3.0	2.3E-04	0.3	3.6E-01	-0.3	6.1E-01
ENSMUST00000085280	spectrin repeat containing, nuclear envelope 2 [Source:MGI Symbol;Acc:MGI:2449316]	Q6DFZ2		-0.6	6.6E-01	-1.2	5.9E-01	1.3	3.9E-01	1.9	3.4E-01
ENSMUST00000087883	collagen, type III, alpha 1 [Source:MGI Symbol;Acc:MGI:88453]	Q3TVI5	P08121	6.9	2.6E-05	7.5	1.3E-04	-1.5	3.0E-01	-0.8	2.1E-01
ENSMUST00000087897	DEP domain containing 5 [Source:MGI Symbol;Acc:MGI:2141101]	Q6GQV2		2.5	1.2E-03	4.9	9.8E-04	-2.4	6.1E-02	-0.3	6.3E-01
ENSMUST00000085299	dishevelled associated activator of morphogenesis 1 [Source:MGI Symbol;Acc:MGI:1914596]		Q8BPM0	-0.6	1.4E-01	1.1	7.0E-02	1.5	6.3E-03	-0.3	5.5E-01
ENSMUST00000087916	histone deacetylase 8 [Source:MGI Symbol;Acc:MGI:1917565]		Q8VH37	-3.1	1.6E-02	-2.1	1.0E-01	0.6	4.3E-01	-1.6	2.5E-01
ENSMUST00000087923	membrane-spanning 4-domains, subfamily A, member 15 [Source:MGI Symbol;Acc:MGI:3617853]		Q3UPL6	6.6	3.5E-04	-3.1	5.6E-04	0.6	7.6E-02	0.0	9.5E-01
ENSMUST00000087927	zinc finger protein 827 [Source:MGI Symbol;Acc:MGI:2444807]		Q505G8	7.1	6.3E-07	4.9	6.6E-03	1.0	4.5E-01	-0.4	6.3E-01
ENSMUST00000087933	tripeptidyl peptidase II [Source:MGI Symbol;Acc:MGI:102724]		Q64514	-7.4	2.8E-06	5.0	5.6E-02	-0.8	7.3E-01	0.4	7.8E-01
ENSMUST00000085340				3.4	6.9E-02	2.1	1.9E-01	-2.7	1.3E-01	-1.4	3.0E-01
ENSMUST00000087938	rhotekin [Source:MGI Symbol;Acc:MGI:107371]		Q8C6B2	7.2	6.8E-05	-10.1	3.5E-04	0.5	3.4E-01	-1.0	6.4E-01
ENSMUST00000087942	RAB44, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:3045302]		Q8CB87	-2.6	6.5E-03	8.7	5.5E-05	0.8	5.3E-01	0.4	5.1E-01
ENSMUST00000087950	cerebellin 4 precursor protein [Source:MGI Symbol;Acc:MGI:2154433]		Q8BME9	8.3	1.5E-05	3.8	6.9E-04	-0.9	2.5E-01	0.3	5.6E-01
ENSMUST00000087951	vacuolar protein sorting 37C (yeast) [Source:MGI Symbol;Acc:MGI:2147661]		Q8R105	-2.5	2.2E-03	6.8	7.8E-04	2.0	1.5E-01	-0.6	4.8E-01
ENSMUST00000087965	m large conductance calcium-activated channel, subfamily M, beta member 4 [Source:MGI Symbol;Acc:MGI:1	F7C7W9		5.2	2.5E-04	6.3	1.5E-04	1.4	1.6E-01	-0.2	7.3E-01
ENSMUST00000087971	zinc finger protein 64 [Source:MGI Symbol;Acc:MGI:107342]	A2AQR4		2.1	1.0E-02	-6.0	9.6E-04	0.7	1.4E-01	0.0	9.8E-01
ENSMUST00000085377				-1.9	1.3E-01	-3.0	8.5E-02	-0.4	6.3E-01	0.7	6.5E-01
ENSMUST00000085383	SR-related CTD-associated factor 1 [Source:MGI Symbol;Acc:MGI:2141980]		Q5U4C3	-2.0	1.3E-01	1.6	2.8E-01	1.5	2.5E-01	-2.1	1.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000087978	sphingosine-1-phosphate receptor 3 [Source:MGI Symbol;Acc:MGI:1339365]		Q9Z0U9	7.7	4.3E-05	-4.3	1.8E-02	0.2	8.2E-01	-0.4	8.0E-01
ENSMUST00000087996	keratin 77 [Source:MGI Symbol;Acc:MGI:3588209]	Q08EK5	Q6IFZ6	9.0	8.2E-06	-4.2	5.5E-03	-0.1	8.9E-01	-0.7	5.7E-01
ENSMUST00000088010	general transcription factor IIIC, polypeptide 2, beta [Source:MGI Symbol;Acc:MGI:1919002]		Q8BL74	-6.4	2.3E-05	-5.7	1.5E-02	0.4	6.4E-01	0.1	9.5E-01
ENSMUST00000088013	myelin regulatory factor [Source:MGI Symbol;Acc:MGI:2684944]		Q3UR85	4.4	7.7E-04	3.4	1.2E-01	-4.3	8.4E-02	0.7	6.1E-01
ENSMUST00000088018	keratin 74 [Source:MGI Symbol;Acc:MGI:3629975]		Q6IFZ9	6.4	1.6E-04	5.7	1.3E-03	-0.5	7.2E-01	-0.7	3.5E-01
ENSMUST00000085425	ISG15 ubiquitin-like modifier [Source:MGI Symbol;Acc:MGI:1855694]	Q4FJR9	Q64339	-1.1	1.1E-01	-1.3	8.7E-02	-1.4	2.3E-02	-1.1	1.5E-01
ENSMUST00000085427	zinc finger protein 865 [Source:MGI Symbol;Acc:MGI:2442656]	H9KUY5		-1.2	2.7E-01	-1.5	2.7E-01	0.2	8.0E-01	0.6	6.6E-01
ENSMUST00000088041	prostaglandin I2 (prostacyclin) synthase [Source:MGI Symbol;Acc:MGI:1097156]	Q8BXC0		5.4	1.1E-03	-3.0	2.4E-02	1.0	1.5E-01	-2.0	1.4E-01
ENSMUST00000088072	testis specific 10 [Source:MGI Symbol;Acc:MGI:2685063]		Q6NY15	3.7	6.6E-03	6.4	2.0E-04	-0.6	6.0E-01	-0.3	6.0E-01
ENSMUST00000088080	predicted gene 10217 [Source:MGI Symbol;Acc:MGI:3642099]	F7BLD2		10.7	2.0E-05	6.4	2.5E-04	0.7	5.1E-01	-0.9	1.7E-01
ENSMUST00000088092	tetratricopeptide repeat domain 9C [Source:MGI Symbol;Acc:MGI:1917637]		Q810A3	-3.3	2.6E-02	6.7	1.9E-04	-0.6	6.5E-01	-1.0	1.5E-01
ENSMUST00000085461	kallikrein related-peptidase 8 [Source:MGI Symbol;Acc:MGI:1343327]	A0A0B6VRH9	Q61955	1.4	4.5E-02	0.1	9.4E-01	-1.5	2.6E-02	-0.1	8.5E-01
ENSMUST00000085469	phosphoinositide-3-kinase, catalytic, gamma polypeptide [Source:MGI Symbol;Acc:MGI:1353576]		Q9JHG7	-1.8	9.6E-02	-1.3	2.8E-01	-0.4	5.6E-01	-0.9	4.7E-01
ENSMUST00000085487	Casitas B-lineage lymphoma-like 1 [Source:MGI Symbol;Acc:MGI:2144842]	E9QM14		-1.0	4.0E-01	-1.5	4.1E-01	1.1	3.0E-01	1.6	3.7E-01
ENSMUST00000085513	URI1, prefoldin-like chaperone [Source:MGI Symbol;Acc:MGI:1342294]		Q3TLD5	-0.4	4.0E-01	-0.2	6.8E-01	-0.3	3.9E-01	-0.5	3.6E-01
ENSMUST00000088095	nuclear receptor coactivator 3 [Source:MGI Symbol;Acc:MGI:1276535]	Q05BA5		-2.6	4.7E-03	-6.2	3.0E-05	-0.6	1.3E-01	0.2	7.8E-01
ENSMUST00000088169	reticulon 3 [Source:MGI Symbol;Acc:MGI:1339970]		Q9ES97	-5.1	5.7E-03	-0.1	8.2E-01	0.7	7.8E-02	-0.9	8.3E-02
ENSMUST00000088171	reticulon 3 [Source:MGI Symbol;Acc:MGI:1339970]		Q9ES97	2.9	2.4E-03	4.7	4.0E-03	-2.4	8.8E-02	-0.1	9.2E-01
ENSMUST00000088172	heparan sulfate 6-O-sulfotransferase 2 [Source:MGI Symbol;Acc:MGI:1354959]		Q80UW0	6.0	8.2E-04	1.9	5.3E-01	-1.5	5.7E-01	3.0	1.7E-01
ENSMUST00000088194	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Source:MGI Symbol;Acc:MGI:1913358]		Q9DC69	-3.8	5.6E-04	5.6	3.9E-04	1.7	1.2E-01	-0.3	6.6E-01
ENSMUST00000085573	TNF receptor-associated factor 5 [Source:MGI Symbol;Acc:MGI:107548]	E9QMA6		0.7	2.7E-01	2.2	1.5E-02	0.8	2.2E-01	-0.7	2.8E-01
ENSMUST00000088217	transducin (beta)-like 1 X-linked [Source:MGI Symbol;Acc:MGI:1336172]		Q9QXE7	-3.1	2.3E-04	-3.7	2.2E-03	0.9	5.8E-02	0.0	9.7E-01
ENSMUST00000088223	tRNA phosphotransferase 1 [Source:MGI Symbol;Acc:MGI:1333115]		Q8K3A2	2.3	5.0E-03	8.0	1.2E-04	0.4	7.6E-01	0.0	9.6E-01
ENSMUST00000085592	RIKEN cDNA 4931406P16 gene [Source:MGI Symbol;Acc:MGI:1924311]	Q8C5X1		1.1	3.6E-01	-1.3	3.9E-01	-0.7	5.1E-01	1.7	2.6E-01
ENSMUST00000088246	tubulin, alpha 3A [Source:MGI Symbol;Acc:MGI:1095406]	Q5FW91	P05214	7.1	1.4E-04	-1.7	1.8E-01	0.6	4.4E-01	-3.4	4.4E-02
ENSMUST00000088260	WAP four-disulfide core domain 13 [Source:MGI Symbol;Acc:MGI:3582777]		Q5DQQ6	8.0	9.4E-06	-5.8	3.6E-04	0.5	1.9E-01	0.6	5.9E-01
ENSMUST00000088287	RAB23, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:99833]	Q9D4I9		-6.1	2.5E-04	-7.7	2.5E-05	0.3	3.2E-01	-0.9	4.1E-01
ENSMUST00000088292	lysophosphatidic acid receptor 5 [Source:MGI Symbol;Acc:MGI:2685918]	G3X9K0		4.7	2.1E-02	6.7	4.4E-05	-1.9	9.1E-02	-0.4	4.2E-01
ENSMUST00000088302	RIKEN cDNA 4931409K22 gene [Source:MGI Symbol;Acc:MGI:3045319]		A6H690	8.5	1.1E-05	-2.0	6.3E-02	-0.4	5.8E-01	-1.1	3.1E-01
ENSMUST00000088310	PHD finger protein 3 [Source:MGI Symbol;Acc:MGI:2446126]	B2RQG2		-3.6	4.6E-05	5.4	4.1E-03	-0.2	9.1E-01	0.7	4.7E-01
ENSMUST00000085671	zinc finger with KRAB and SCAN domains 5 [Source:MGI Symbol;Acc:MGI:107533]		Q9Z1D8	0.6	3.4E-01	1.0	2.0E-01	0.3	6.6E-01	-0.2	7.5E-01
ENSMUST00000085673	promyelocytic leukemia [Source:MGI Symbol;Acc:MGI:104662]	A0A068EW80	Q60953	2.0	2.3E-01	0.4	8.4E-01	-0.8	5.9E-01	0.8	7.0E-01
ENSMUST00000085678	potassium channel tetramerisation domain containing 3 [Source:MGI Symbol;Acc:MGI:2444629]		Q8BFX3	-0.3	8.3E-01	1.4	5.2E-01	1.3	4.6E-01	-0.4	8.2E-01
ENSMUST00000088311	gastrulation brain homeobox 1 [Source:MGI Symbol;Acc:MGI:95667]		P82976	7.4	1.7E-05	-3.6	8.2E-04	1.1	2.4E-02	0.5	4.9E-01
ENSMUST00000085684	SMAD specific E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1923038]		Q9CUN6	-3.0	5.4E-02	-2.4	2.3E-01	0.9	4.2E-01	0.2	9.0E-01
ENSMUST00000085701	tectonin beta-propeller repeat containing 1 [Source:MGI Symbol;Acc:MGI:1917631]		Q80VP0	-0.1	9.3E-01	1.4	1.1E-01	1.0	1.2E-01	-0.4	5.8E-01
ENSMUST00000088313	emerin [Source:MGI Symbol;Acc:MGI:108117]	Q3THM8		-3.6	4.9E-03	-2.5	2.5E-02	0.4	4.4E-01	0.6	5.5E-01
ENSMUST00000088349	collagen, type IX, alpha 1 [Source:MGI Symbol;Acc:MGI:88465]	Q9D0D2		7.3	1.2E-04	-1.9	3.6E-02	0.1	8.2E-01	-0.3	7.6E-01
ENSMUST00000085715	MAP/microtubule affinity regulating kinase 4 [Source:MGI Symbol;Acc:MGI:1920955]		Q8CIP4	-1.2	7.1E-02	-0.1	8.6E-01	1.3	4.7E-02	0.3	7.4E-01
ENSMUST00000088355	collagen, type II, alpha 1 [Source:MGI Symbol;Acc:MGI:88452]		P28481	8.3	5.9E-04	6.8	1.7E-04	-0.6	6.2E-01	0.2	7.9E-01
ENSMUST00000088373	SLIT-ROBO Rho GTPase activating protein 3 [Source:MGI Symbol;Acc:MGI:2152938]	F8VPQ4		7.3	1.7E-05	6.8	1.9E-04	-0.6	6.2E-01	-0.4	5.1E-01
ENSMUST00000085735	phosphoglycerate kinase-1, related sequence-7 [Source:MGI Symbol;Acc:MGI:97562]		P09411	1.4	6.4E-01	6.9	1.0E-01	2.4	5.2E-01	-3.2	2.6E-01
ENSMUST00000088386	solute carrier family 15 (oligopeptide transporter), member 1 [Source:MGI Symbol;Acc:MGI:1861376]		Q9JIP7	6.9	7.7E-06	-2.0	2.2E-02	0.2	6.7E-01	-1.0	2.0E-01
ENSMUST00000088392	serine/arginine-rich protein specific kinase 2 [Source:MGI Symbol;Acc:MGI:1201408]			-3.2	7.5E-05	7.2	1.7E-02	-0.8	7.7E-01	-1.2	4.4E-01
ENSMUST00000088419	muscleblind-like 2 [Source:MGI Symbol;Acc:MGI:2145597]		Q8C181	-4.9	3.1E-03	7.5	3.1E-05	0.0	9.7E-01	0.4	4.0E-01
ENSMUST00000088429	ATPase, Ca++ transporting, plasma membrane 3 [Source:MGI Symbol;Acc:MGI:1347353]	Q0VF55		9.6	1.6E-04	4.0	9.0E-02	-0.8	7.3E-01	2.9	7.1E-02
ENSMUST00000088448	polycystic kidney and hepatic disease 1 [Source:MGI Symbol;Acc:MGI:2155808]	E9PZ36		8.9	5.7E-06	7.4	2.7E-04	-0.5	7.3E-01	-0.3	6.4E-01
ENSMUST00000088454	solute carrier family 38, member 1 [Source:MGI Symbol;Acc:MGI:2145895]		Q8K2P7	-2.1	1.5E-02	2.6	5.7E-03	-0.8	2.3E-01	-0.2	7.3E-01
ENSMUST00000085790	major facilitator superfamily domain containing 2B [Source:MGI Symbol;Acc:MGI:3583946]		Q3T9M1	-0.7	6.3E-01	-3.0	2.4E-01	-0.3	8.1E-01	2.0	4.1E-01
ENSMUST00000085792	zinc finger protein 940 [Source:MGI Symbol;Acc:MGI:2446235]	Q8R2Q3		1.5	3.6E-01	2.8	1.4E-01	-0.3	8.8E-01	-1.5	3.0E-01
ENSMUST00000088459	predicted gene 14685 [Source:MGI Symbol;Acc:MGI:3710618]	Q52KH6		6.5	2.4E-02	6.9	3.6E-05	1.0	2.6E-01	-0.2	6.7E-01
ENSMUST00000085803				1.6	5.0E-01	-3.1	3.2E-01	-3.8	9.4E-02	0.9	7.6E-01
ENSMUST00000085809	signal-induced proliferation-associated 1 like 3 [Source:MGI Symbol;Acc:MGI:1921456]	G3X9J0		-1.3	8.8E-02	0.2	8.6E-01	1.1	1.1E-01	-0.3	7.0E-01
ENSMUST00000088464	TNF receptor-associated factor 7 [Source:MGI Symbol;Acc:MGI:3042141]	F8WJF7		-8.0	2.7E-05	-0.7	2.2E-01	0.8	5.9E-02	-0.2	7.2E-01
ENSMUST00000085818	potassium inwardly-rectifying channel, subfamily K, member 6 [Source:MGI Symbol;Acc:MGI:1891291]	Q3TBV4		1.0	5.8E-02	2.3	3.3E-03	0.9	9.0E-02	-0.4	3.7E-01
ENSMUST00000088468	C-type lectin domain family 4, member a3 [Source:MGI Symbol;Acc:MGI:1920399]	Q8JZX6		-5.0	5.1E-03	6.1	1.1E-04	-0.3	7.0E-01	-0.4	4.4E-01
ENSMUST00000088476	peptidase inhibitor 15 [Source:MGI Symbol;Acc:MGI:1934659]			9.3	5.6E-06	-1.2	9.6E-02	1.0	3.1E-02	-0.3	6.1E-01
ENSMUST00000088516	mbrane associated guanylate kinase, WW and PDZ domain containing 2 [Source:MGI Symbol;Acc:MGI:13549		Q9WVQ1	8.7	7.4E-05	-5.0	1.4E-02	1.1	2.3E-01	1.6	3.5E-01
ENSMUST00000085852	zinc finger protein 68 [Source:MGI Symbol;Acc:MGI:1344427]	Q8BLK6		-2.9	8.8E-02	-2.9	2.4E-01	0.4	7.6E-01	0.4	8.6E-01
ENSMUST00000085856	zinc finger protein 157 [Source:MGI Symbol;Acc:MGI:1919404]	Q6PCM4		1.9	3.7E-02	1.4	1.8E-01	-0.3	7.3E-01	0.2	7.9E-01
ENSMUST00000088538	Kv channel interacting protein 3, calsenilin [Source:MGI Symbol;Acc:MGI:1929258]	Q3YAA9		7.2	1.1E-02	4.7	7.2E-05	-1.7	3.9E-02	0.3	5.4E-01
ENSMUST00000088561	peroxisomal biogenesis factor 26 [Source:MGI Symbol;Acc:MGI:1921293]		Q8BGI5	5.9	1.3E-02	9.2	1.9E-04	-0.8	6.3E-01	0.0	9.9E-01
ENSMUST00000085894	cilia and flagella associated protein 45 [Source:MGI Symbol;Acc:MGI:1919120]	Q9D9U9		1.5	3.9E-02	2.1	1.7E-02	-0.3	5.9E-01	-0.9	1.5E-01
ENSMUST00000088592	leucine rich repeat and fibronectin type III, extracellular 2 [Source:MGI Symbol;Acc:MGI:3608416]		Q68FM6	9.5	6.6E-06	-3.7	1.1E-01	2.1	1.1E-01	0.7	7.6E-01
ENSMUST00000088610	reactive oxygen species modulator 1 [Source:MGI Symbol;Acc:MGI:1914317]		P60603	-5.1	1.6E-03	-1.3	5.0E-01	0.5	7.0E-01	-2.5	2.3E-01
ENSMUST00000088614	kinesin family member 21A [Source:MGI Symbol;Acc:MGI:109188]		Q9QXL2	6.0	1.9E-02	7.1	6.9E-05	-1.2	3.1E-01	0.4	4.9E-01
ENSMUST00000085917	thymoma viral proto-oncogene 2 [Source:MGI Symbol;Acc:MGI:104874]	F8WHG5		0.8	8.2E-01	-1.0	8.2E-01	-2.3	4.9E-01	-0.5	9.1E-01
ENSMUST00000088615	osylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited) [Source:MGI Symbol;Acc:MGI:2		G3X9K3	-4.3	1.9E-05	8.2	1.0E-04	-0.7	6.4E-01	0.0	9.4E-01
ENSMUST00000085934	acetylcholinesterase [Source:MGI Symbol;Acc:MGI:87876]	Q543Z1	P21836	0.8	6.4E-01	0.2	9.2E-01	-1.1	4.9E-01	-0.5	7.8E-01
ENSMUST00000088621	serine/arginine repetitive matrix 2 [Source:MGI Symbol;Acc:MGI:1923206]		Q8BTI8	-2.5	2.2E-02	5.0	7.1E-04	-2.1	9.6E-02	0.4	5.0E-01
ENSMUST00000088625	predicted gene 5152 [Source:MGI Symbol;Acc:MGI:3643407]	G3XA03		6.5	9.1E-04	-6.6	4.4E-04	0.5	2.2E-01	1.3	3.1E-01
ENSMUST00000085948	AXL receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:1347244]	Q6PE80		3.9	5.3E-02	6.9	2.4E-02	3.0	2.3E-01	-0.1	9.7E-01
ENSMUST00000085953	ATP5S-like [Source:MGI Symbol;Acc:MGI:1913599]	Q8CA44		-0.4	5.7E-01	0.0	9.9E-01	0.2	7.3E-01	-0.2	8.5E-01
ENSMUST00000088627	zinc finger protein of the cerebellum 3 [Source:MGI Symbol;Acc:MGI:106676]		Q62521	7.0	2.1E-03	-2.1	2.5E-01	3.0	1.7E-02	-0.1	9.8E-01
ENSMUST00000088646	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]		P83741	-7.3	3.1E-04	7.5	6.5E-05	-0.6	6.0E-01	-0.4	5.0E-01
ENSMUST00000088652	HIV TAT specific factor 1 [Source:MGI Symbol;Acc:MGI:1919709]		Q8BGC0	-2.8	2.4E-03	0.1	9.4E-01	-5.9	3.2E-02	3.1	7.2E-02
ENSMUST00000088653	coiled-coil domain containing 87 [Source:MGI Symbol;Acc:MGI:3026882]		Q8CDL9	8.4	2.6E-05	5.7	2.4E-03	-0.5	6.9E-01	0.2	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000088666	RIKEN cDNA 3110035E14 gene [Source:MGI Symbol;Acc:MGI:1924232]		Q8BG31	8.3	8.5E-06	6.5	8.1E-04	0.0	9.7E-01	0.6	4.4E-01
ENSMUST00000088677	5-hydroxytryptamine (serotonin) receptor 1D [Source:MGI Symbol;Acc:MGI:96276]		Q61224	6.2	2.8E-04	-5.9	1.3E-02	0.4	6.0E-01	0.9	6.5E-01
ENSMUST00000088687	olfactory receptor 707 [Source:MGI Symbol;Acc:MGI:3030541]	K7N662		5.6	5.5E-03	8.6	3.0E-05	1.4	2.2E-01	0.5	2.8E-01
ENSMUST00000088717	non-SMC condensin II complex, subunit H2 [Source:MGI Symbol;Acc:MGI:1289164]		Q8BSP2	-3.4	3.8E-03	6.4	1.7E-04	-0.5	6.2E-01	-0.6	3.4E-01
ENSMUST00000088735	olfactomedin 4 [Source:MGI Symbol;Acc:MGI:2685142]	D3YYD0		-7.8	1.5E-06	-4.8	2.0E-02	-0.8	3.3E-01	0.0	9.9E-01
ENSMUST00000088737	adrenergic receptor kinase, beta 1 [Source:MGI Symbol;Acc:MGI:87940]	Q3U1V3	Q99MK8	-10.0	3.3E-06	-2.4	3.0E-03	0.5	1.8E-01	-0.2	7.9E-01
ENSMUST00000086041	CLK4-associating serine/arginine rich protein [Source:MGI Symbol;Acc:MGI:1855695]		Q8CFC7	-1.3	4.1E-02	-0.7	3.4E-01	0.6	2.6E-01	0.0	9.6E-01
ENSMUST00000088786	sorcin [Source:MGI Symbol;Acc:MGI:98419]		Q6P069	-4.4	3.5E-02	-2.5	5.9E-03	1.0	3.8E-02	-0.5	5.0E-01
ENSMUST00000088790	ret proto-oncogene [Source:MGI Symbol;Acc:MGI:97902]		P35546	5.9	8.3E-05	9.4	1.4E-05	0.1	9.1E-01	-0.3	5.8E-01
ENSMUST00000088809	predicted gene 7168 [Source:MGI Symbol;Acc:MGI:3643198]			8.3	3.2E-05	-6.0	1.6E-03	0.9	1.0E-01	-0.7	6.4E-01
ENSMUST00000088811	zinc finger protein 160 [Source:MGI Symbol;Acc:MGI:108187]	E9Q459		-2.2	3.5E-03	5.7	4.5E-03	-1.5	4.0E-01	0.0	9.8E-01
ENSMUST00000088823	mitogen-activated protein kinase 11 [Source:MGI Symbol;Acc:MGI:1338024]		Q9WUI1	4.7	4.6E-04	-1.7	2.2E-01	1.5	9.6E-02	-2.0	2.0E-01
ENSMUST00000086083	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]	E9PY55		-3.4	4.8E-02	2.2	1.5E-01	0.1	9.2E-01	-5.5	6.5E-03
ENSMUST00000088827	mitogen-activated protein kinase 12 [Source:MGI Symbol;Acc:MGI:1353438]		O08911	4.5	1.7E-04	-3.4	7.3E-02	1.6	1.1E-01	-0.4	8.3E-01
ENSMUST00000086104	protein kinase D2 [Source:MGI Symbol;Acc:MGI:2141917]		Q8BZ03	-0.8	1.4E-01	0.6	4.5E-01	1.4	2.8E-02	0.0	9.6E-01
ENSMUST00000088867	killer cell lectin-like receptor, subfamily A, member 2 [Source:MGI Symbol;Acc:MGI:101906]	E9Q433		-8.0	8.9E-04	-5.5	6.4E-05	0.9	2.9E-02	-0.2	8.3E-01
ENSMUST00000088896	transmembrane and coiled coil domains 1 [Source:MGI Symbol;Acc:MGI:2442368]		Q69ZZ6	-2.8	2.2E-03	8.3	2.3E-04	-0.1	9.6E-01	-0.8	2.7E-01
ENSMUST00000088904	espin-like [Source:MGI Symbol;Acc:MGI:2685402]		Q3UYR4	6.1	2.4E-05	2.1	5.3E-02	0.1	9.1E-01	0.9	2.8E-01
ENSMUST00000088911	bromodomain containing 1 [Source:MGI Symbol;Acc:MGI:1924161]	E9Q412		5.0	3.2E-06	6.0	8.6E-04	-0.5	7.1E-01	0.3	6.3E-01
ENSMUST00000086153	family with sequence similarity 20, member B [Source:MGI Symbol;Acc:MGI:2443990]		Q8VCS3	0.2	8.9E-01	1.9	3.6E-01	1.4	4.1E-01	-0.3	8.7E-01
ENSMUST00000088921	BPI fold containing family B, member 9B [Source:MGI Symbol;Acc:MGI:1918675]	A2AJD1		7.2	3.1E-05	-5.0	6.3E-04	0.7	8.8E-02	0.3	7.7E-01
ENSMUST00000088922	general transcription factor IIF, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1915955]	Q3UMJ4	Q8R0A0	-2.8	3.1E-03	7.2	6.6E-05	-0.6	6.1E-01	0.2	7.1E-01
ENSMUST00000088924	BPI fold containing family B, member 9A [Source:MGI Symbol;Acc:MGI:3767993]		Q80XI7	6.0	2.0E-02	-3.1	6.8E-04	0.7	7.2E-02	-0.9	2.0E-01
ENSMUST00000086209	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent) [Source:MGI Symbol;Acc:MGI:1098272]	B2RQP1	Q05921	3.4	1.9E-01	3.3	3.2E-01	-0.5	8.6E-01	-0.4	8.7E-01
ENSMUST00000088935	zinc finger, DHHC domain containing 9 [Source:MGI Symbol;Acc:MGI:2444393]		P59268	-4.7	8.3E-03	6.3	1.5E-03	-0.7	6.6E-01	0.2	7.7E-01
ENSMUST00000088950	BPI fold containing family B, member 3 [Source:MGI Symbol;Acc:MGI:2675077]		Q80ZU7	7.0	3.5E-05	-2.3	8.3E-04	0.6	4.1E-02	-0.2	6.7E-01
ENSMUST00000088955	BPI fold containing family B, member 6 [Source:MGI Symbol;Acc:MGI:2684965]		Q8BU51	6.7	7.3E-05	11.7	1.4E-05	-0.5	7.6E-01	-0.9	6.9E-02
ENSMUST00000088962	makorin, ring finger protein 2, opposite strand [Source:MGI Symbol;Acc:MGI:1917541]	D3YX48		7.9	1.8E-06	5.6	2.5E-02	-0.7	7.8E-01	0.6	6.4E-01
ENSMUST00000086267				1.5	5.8E-01	-1.2	7.1E-01	-2.3	3.4E-01	0.4	9.0E-01
ENSMUST00000088987	histamine receptor H1 [Source:MGI Symbol;Acc:MGI:107619]	B3Y5T0	P70174	4.5	6.8E-04	3.3	3.9E-02	-0.1	9.3E-01	0.9	3.7E-01
ENSMUST00000086278	zinc finger protein 810 [Source:MGI Symbol;Acc:MGI:2384563]		Q99K45	-0.7	1.8E-01	-0.6	3.0E-01	0.0	9.9E-01	0.0	9.6E-01
ENSMUST00000089015	MAS1 oncogene [Source:MGI Symbol;Acc:MGI:96918]	Q0VB49	P30554	6.6	1.2E-04	4.6	6.8E-05	0.3	6.5E-01	0.1	8.7E-01
ENSMUST00000089024	t-complex protein 1 [Source:MGI Symbol;Acc:MGI:98535]		P11983	-6.9	9.9E-05	8.8	1.6E-05	-0.6	5.9E-01	-0.8	1.2E-01
ENSMUST00000086294	protein phosphatase 1, catalytic subunit, gamma isoform [Source:MGI Symbol;Acc:MGI:104872]		P63087	1.9	4.8E-01	4.2	2.8E-01	2.8	3.4E-01	0.6	8.6E-01
ENSMUST00000089027	transmembrane 9 superfamily protein member 4 [Source:MGI Symbol;Acc:MGI:2139220]		Q8BH24	-3.4	4.0E-04	6.5	6.2E-04	-0.5	7.4E-01	-1.1	1.6E-01
ENSMUST00000086298	vomeronasal 2, receptor 50 [Source:MGI Symbol;Acc:MGI:3643086]	K7N652		4.1	1.2E-01	4.5	1.3E-01	-0.3	9.2E-01	-0.7	6.9E-01
ENSMUST00000089042	interferon (alpha and beta) receptor 2 [Source:MGI Symbol;Acc:MGI:1098243]	Q923Z6	O35664	-5.3	1.7E-04	-3.6	6.1E-02	0.9	3.0E-01	0.6	7.2E-01
ENSMUST00000086319	olfactory receptor 1348 [Source:MGI Symbol;Acc:MGI:3031182]	F6VB59		3.9	9.5E-02	5.6	3.9E-02	-0.3	9.0E-01	-2.0	1.9E-01
ENSMUST00000089052	ring finger protein 121 [Source:MGI Symbol;Acc:MGI:1922462]	K4DI70		6.4	3.1E-02	0.2	8.1E-01	0.5	5.4E-01	-2.9	3.8E-02
ENSMUST00000086327	zinc finger protein 667 [Source:MGI Symbol;Acc:MGI:2442757]		Q2TL60	5.3	4.9E-02	1.7	5.3E-01	-2.3	4.1E-01	1.4	4.9E-01
ENSMUST00000089058	mitogen-activated protein kinase kinase kinase 4 [Source:MGI Symbol;Acc:MGI:1346875]		O08648	1.2	1.4E-02	6.2	8.1E-06	-1.1	1.5E-01	-0.7	1.2E-01
ENSMUST00000089059	histocompatibility 13 [Source:MGI Symbol;Acc:MGI:95886]		Q9D8V0	-8.8	2.6E-05	7.0	1.2E-02	-0.8	7.4E-01	-2.4	1.3E-01
ENSMUST00000089104	RIKEN cDNA 1110025L11 gene [Source:MGI Symbol;Acc:MGI:1915887]	O09048		5.9	1.1E-02	-1.5	8.2E-02	1.1	5.4E-02	-1.0	2.3E-01
ENSMUST00000089111	RIKEN cDNA 2310034C09 gene [Source:MGI Symbol;Acc:MGI:2152338]	Q9D746		6.3	1.4E-04	-5.4	2.4E-03	0.1	8.6E-01	-3.6	6.1E-02
ENSMUST00000089112	transcription factor 15 [Source:MGI Symbol;Acc:MGI:104664]		Q60756	7.1	5.1E-04	-6.0	8.8E-04	0.8	1.5E-01	-1.7	2.3E-01
ENSMUST00000089119	ribonuclease T2B [Source:MGI Symbol;Acc:MGI:3702087]	Q5FWA0	Q9CQ01	-10.2	4.5E-06	4.6	6.5E-03	0.3	8.0E-01	0.2	7.8E-01
ENSMUST00000086368	2'-5' oligoadenylate synthetase 1G [Source:MGI Symbol;Acc:MGI:97429]	Q8K469		0.5	5.2E-01	2.4	3.8E-02	1.2	1.9E-01	-0.7	4.0E-01
ENSMUST00000089120	predicted gene 1604b [Source:MGI Symbol;Acc:MGI:2686450]	Q3TRG0		-4.0	2.9E-03	-5.5	1.6E-04	0.9	4.4E-02	0.3	7.1E-01
ENSMUST00000089129	cytochrome P450, family 2, subfamily d, polypeptide 9 [Source:MGI Symbol;Acc:MGI:88606]		P11714	6.8	5.7E-05	10.0	1.1E-03	-0.5	8.5E-01	-1.4	1.5E-01
ENSMUST00000089161	tumor necrosis factor receptor superfamily, member 13c [Source:MGI Symbol;Acc:MGI:1919299]	Q3SXS6	Q9D8D0	6.1	2.2E-03	5.0	5.4E-04	-1.4	2.1E-01	-2.2	1.4E-02
ENSMUST00000086399	intercellular adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:96392]	Q3U8M7	P13597	-1.0	8.9E-02	0.2	7.7E-01	0.6	2.5E-01	-0.6	3.6E-01
ENSMUST00000089162	ER degradation enhancer, mannosidase alpha-like 1 [Source:MGI Symbol;Acc:MGI:2180139]		Q925U4	-3.6	2.8E-05	-4.2	3.5E-02	0.2	8.6E-01	-1.1	5.9E-01
ENSMUST00000089178	meiosis defective 1 [Source:MGI Symbol;Acc:MGI:3028590]	F8WHB9		7.4	5.1E-05	1.9	6.1E-02	-1.4	1.2E-01	0.2	8.0E-01
ENSMUST00000089185	zinc finger, DHHC domain containing 14 [Source:MGI Symbol;Acc:MGI:2653229]		Q8BQQ1	2.7	5.3E-03	-2.8	5.6E-03	-0.9	7.6E-02	-0.8	3.2E-01
ENSMUST00000089200	cystatin F (leukocystatin) [Source:MGI Symbol;Acc:MGI:1298217]		O89098	-1.5	2.0E-02	1.0	1.8E-01	-6.7	7.8E-05	-0.6	3.3E-01
ENSMUST00000089207	zinc finger protein 120 [Source:MGI Symbol;Acc:MGI:1345179]		Q8BZW4	-6.5	1.7E-04	7.1	1.5E-04	-0.4	7.2E-01	-1.7	2.4E-02
ENSMUST00000089230	protein phosphatase 2, regulatory subunit B, alpha [Source:MGI Symbol;Acc:MGI:1919228]	Q3TT94	Q6P1F6	-2.1	3.7E-03	-4.6	1.9E-03	1.0	5.1E-02	-0.8	5.1E-01
ENSMUST00000089236	paraneoplastic antigen MA2 [Source:MGI Symbol;Acc:MGI:2444129]		Q8BHK0	8.1	1.7E-05	-4.0	4.5E-02	0.1	8.6E-01	-1.4	4.7E-01
ENSMUST00000086461	replication factor C (activator 1) 5 [Source:MGI Symbol;Acc:MGI:1919401]	Q5HZI8	Q9D0F6	-0.2	6.9E-01	0.0	1.0E+00	0.5	2.1E-01	0.3	5.2E-01
ENSMUST00000089250	PTK2 protein tyrosine kinase 2 beta [Source:MGI Symbol;Acc:MGI:104908]	E9Q2A6		-8.7	8.9E-06	6.4	4.2E-03	0.0	9.9E-01	0.5	5.9E-01
ENSMUST00000089257	insulinoma-associated 1 [Source:MGI Symbol;Acc:MGI:1859980]	Q05BD7	Q63ZV0	7.4	6.4E-05	-2.7	5.1E-02	0.6	3.7E-01	-2.0	1.6E-01
ENSMUST00000089279	casein kinase 2, alpha prime interacting protein [Source:MGI Symbol;Acc:MGI:2676295]	Q8CH19		6.5	6.7E-05	7.2	3.6E-03	-0.8	6.9E-01	-0.4	7.3E-01
ENSMUST00000089287	ubiquitin-like modifier activating enzyme 3 [Source:MGI Symbol;Acc:MGI:1341217]		Q8C878	-4.8	4.0E-05	7.4	1.1E-05	-0.8	4.0E-01	-0.8	1.0E-01
ENSMUST00000089289	ADP-ribosylation factor-like 13B [Source:MGI Symbol;Acc:MGI:1915396]		Q640N2	-2.5	1.6E-03	4.8	6.7E-03	0.3	8.1E-01	1.1	3.0E-01
ENSMUST00000089295	family with sequence similarity 19, member A4 [Source:MGI Symbol;Acc:MGI:2444563]		Q7TPG5	6.3	4.9E-04	6.0	3.1E-02	-1.5	5.7E-01	-1.5	3.2E-01
ENSMUST00000089296	olfactory receptor 658 [Source:MGI Symbol;Acc:MGI:3030492]	Q8VGV5		7.7	1.5E-05	-6.9	5.5E-05	0.1	8.0E-01	0.0	9.7E-01
ENSMUST00000089302	ubiquitin specific peptidase 9, X chromosome [Source:MGI Symbol;Acc:MGI:894681]	Q4FE56		-3.5	9.0E-05	-3.0	9.0E-02	1.1	2.2E-01	-0.3	8.8E-01
ENSMUST00000089311	Sad1 and UNC84 domain containing 2 [Source:MGI Symbol;Acc:MGI:2443011]		Q8BJS4	-8.3	9.8E-03	-2.3	5.6E-03	0.9	5.2E-02	-0.1	8.2E-01
ENSMUST00000086545	cyclin-dependent kinase-like 4 [Source:MGI Symbol;Acc:MGI:3587025]		Q3TZA2	1.1	1.2E-01	2.2	1.9E-02	0.5	4.6E-01	-0.6	3.6E-01
ENSMUST00000086555	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 [Source:MGI Symbol;Acc:MGI:2147067]		Q6P5D3	1.1	3.3E-01	2.6	9.5E-02	0.6	6.6E-01	-1.0	3.7E-01
ENSMUST00000086556	ELK4, member of ETS oncogene family [Source:MGI Symbol;Acc:MGI:102853]		P41158	-0.2	5.9E-01	-0.4	4.8E-01	0.5	2.0E-01	0.7	2.2E-01
ENSMUST00000086559	solute carrier family 41, member 1 [Source:MGI Symbol;Acc:MGI:2444823]		Q8BJA2	-0.8	9.1E-02	-0.2	7.3E-01	0.5	2.3E-01	-0.1	8.5E-01
ENSMUST00000089317	nbrane associated guanylate kinase, WW and PDZ domain containing 1 [Source:MGI Symbol;Acc:MGI:12035		Q6RHR9	7.8	7.6E-03	-6.5	5.3E-04	0.1	8.0E-01	-0.5	7.1E-01
ENSMUST00000086580	yes-associated protein 1 [Source:MGI Symbol;Acc:MGI:103262]		P46938	5.4	5.9E-02	-1.2	5.7E-01	-5.9	3.1E-02	0.7	7.3E-01
ENSMUST00000086596				1.9	1.7E-01	2.9	6.8E-02	0.0	9.8E-01	-1.1	3.5E-01
ENSMUST00000086614	zinc finger, RAN-binding domain containing 3 [Source:MGI Symbol;Acc:MGI:1918362]		Q6NZP1	0.4	7.9E-01	1.5	3.4E-01	-1.3	3.7E-01	-2.4	1.3E-01
ENSMUST00000089318	G protein-coupled receptor 15 [Source:MGI Symbol;Acc:MGI:1918473]		Q0VDU3	-4.0	1.5E-03	7.1	2.8E-04	-1.5	3.0E-01	0.1	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000089332	collagen, type VIII, alpha 1 [Source:MGI Symbol;Acc:MGI:88463]		Q00780	9.0	1.4E-06	9.0	3.5E-05	-0.7	6.0E-01	-0.4	4.8E-01
ENSMUST00000089334	FYVE, RhoGEF and PH domain containing 5 [Source:MGI Symbol;Acc:MGI:2443369]	E9QKY4		8.4	1.4E-02	-1.9	1.7E-02	0.8	6.4E-02	0.3	6.7E-01
ENSMUST00000089360	SUMO1/sentrin specific peptidase 7 [Source:MGI Symbol;Acc:MGI:1913565]	E9Q1L5		-2.3	2.7E-02	8.6	1.5E-05	-0.5	6.7E-01	-0.7	1.4E-01
ENSMUST00000089362	SUMO1/sentrin specific peptidase 7 [Source:MGI Symbol;Acc:MGI:1913565]		Q8BUH8	-6.4	7.9E-04	8.2	1.3E-04	0.4	7.8E-01	0.3	5.7E-01
ENSMUST00000089377	lectin, galactose binding, soluble 1 [Source:MGI Symbol;Acc:MGI:96777]		P16045	-5.5	1.6E-04	6.4	1.2E-04	0.7	4.9E-01	-0.4	5.4E-01
ENSMUST00000086693	microtubule crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:1915867]		Q3UHU5	5.4	3.5E-02	4.5	5.4E-02	-3.2	2.1E-01	-2.4	1.1E-01
ENSMUST00000089404	bobby sox homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1917758]		Q8VBW5	5.5	2.8E-02	-5.8	7.5E-04	0.1	8.5E-01	-0.7	5.7E-01
ENSMUST00000086722	transmembrane protein 232 [Source:MGI Symbol;Acc:MGI:2685786]		Q5K6N0	3.3	1.6E-01	3.1	2.3E-01	-0.4	8.6E-01	-0.2	9.2E-01
ENSMUST00000089418	vomeronasal 1 receptor 43 [Source:MGI Symbol;Acc:MGI:2148510]		Q8VIC9	6.0	3.3E-04	-2.8	3.6E-04	1.2	2.7E-03	-0.1	8.5E-01
ENSMUST00000089430	predicted gene 11808 [Source:MGI Symbol;Acc:MGI:3649356]	Q66JP1	P62984	-9.1	1.9E-04	-2.9	1.9E-01	0.1	9.1E-01	-1.4	5.5E-01
ENSMUST00000089450	apolipoprotein L 8 [Source:MGI Symbol;Acc:MGI:2444921]	F6VS49		3.9	1.3E-02	6.6	3.4E-04	-0.5	7.2E-01	-0.7	2.9E-01
ENSMUST00000089461	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 [Source:MGI Symbol;Acc:MGI:1332236]	A2AMQ5		-3.0	7.0E-03	-4.6	1.4E-02	-1.0	2.0E-01	-1.0	5.6E-01
ENSMUST00000089465	apolipoprotein L 10B [Source:MGI Symbol;Acc:MGI:3043522]	G3X9K7		5.4	1.5E-04	-6.3	1.7E-03	-0.7	2.9E-01	-1.7	3.0E-01
ENSMUST00000089469	apolipoprotein L 7b [Source:MGI Symbol;Acc:MGI:3583950]	B1AQP7		9.3	1.2E-04	4.5	6.7E-02	-2.1	4.2E-01	-1.1	4.8E-01
ENSMUST00000089494	interleukin 17D [Source:MGI Symbol;Acc:MGI:2446510]	A0A0B4J1G4		4.4	7.3E-03	8.3	2.4E-03	0.6	7.9E-01	1.1	2.6E-01
ENSMUST00000086801	regulatory factor X, 2 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:106583]		P48379	-3.0	6.2E-02	-2.8	1.8E-01	0.7	5.6E-01	0.5	8.1E-01
ENSMUST00000089497	ISY1 splicing factor homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923310]		Q69ZQ2	-2.9	5.9E-05	2.2	9.9E-03	-1.5	4.0E-02	0.2	7.4E-01
ENSMUST00000089510	centromere protein B [Source:MGI Symbol;Acc:MGI:88376]		P27790	-3.7	2.8E-04	7.0	1.0E-04	1.2	2.8E-01	-1.0	1.2E-01
ENSMUST00000089519	AP2 associated kinase 1 [Source:MGI Symbol;Acc:MGI:1098687]		Q3UHJ0	1.6	2.0E-02	1.4	7.8E-02	-1.1	1.0E-01	0.6	3.2E-01
ENSMUST00000089520	shroom family member 4 [Source:MGI Symbol;Acc:MGI:2685570]		Q1W617	8.6	3.0E-06	6.7	1.3E-04	-0.5	6.5E-01	-1.1	9.8E-02
ENSMUST00000086843	ankyrin repeat and SOCS box-containing 1 [Source:MGI Symbol;Acc:MGI:1929735]	Q3U5A0	Q9WV74	0.7	5.9E-01	3.3	1.1E-01	2.8	1.1E-01	0.2	8.7E-01
ENSMUST00000086844	transcription factor 7, T cell specific [Source:MGI Symbol;Acc:MGI:98507]	Q80UF1	Q00417	-0.8	4.2E-01	-1.2	3.5E-01	-0.3	7.4E-01	0.2	8.9E-01
ENSMUST00000089534	predicted gene 7293 [Source:MGI Symbol;Acc:MGI:3779717]	D3YYI5		-3.0	5.2E-04	-5.4	1.1E-02	0.7	2.6E-01	0.8	6.3E-01
ENSMUST00000089549	granzyme E [Source:MGI Symbol;Acc:MGI:109265]		P08884	6.2	4.3E-04	6.0	2.3E-04	-1.4	2.4E-01	0.9	1.5E-01
ENSMUST00000086869	coiled-coil domain containing 94 [Source:MGI Symbol;Acc:MGI:1920136]		Q9D6J3	-0.6	3.0E-01	0.0	9.6E-01	0.4	4.0E-01	-0.1	8.6E-01
ENSMUST00000089558	small nuclear ribonucleoprotein polypeptide G [Source:MGI Symbol;Acc:MGI:1915261]		P62309	-4.8	1.0E-03	5.9	3.2E-06	-0.5	3.6E-01	-0.4	3.1E-01
ENSMUST00000086880	armadillo repeat containing, X-linked 3 [Source:MGI Symbol;Acc:MGI:1918953]		Q8BHS6	-0.6	3.2E-01	-0.2	7.4E-01	-0.1	8.5E-01	-0.4	5.3E-01
ENSMUST00000089559	DDRGK domain containing 1 [Source:MGI Symbol;Acc:MGI:1924256]		Q80WW9	-3.2	1.4E-04	4.8	1.1E-04	0.5	4.4E-01	-0.4	3.8E-01
ENSMUST00000086884	armadillo repeat containing, X-linked 3 [Source:MGI Symbol;Acc:MGI:1918953]		Q8BHS6	2.9	1.2E-01	3.2	1.6E-01	-0.7	7.3E-01	-1.0	5.8E-01
ENSMUST00000089565	nuclear receptor subfamily 2, group F, member 2 [Source:MGI Symbol;Acc:MGI:1352452]	D3YYP4		6.3	2.9E-03	-3.3	1.5E-02	-0.1	8.6E-01	-1.1	4.0E-01
ENSMUST00000086900	heterogeneous nuclear ribonucleoprotein D-like [Source:MGI Symbol;Acc:MGI:1355299]	D3YTQ3		1.9	2.7E-01	0.5	6.9E-01	-4.9	4.5E-03	-3.4	3.3E-02
ENSMUST00000089578	notochord homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:3053002]		Q5TIS6	6.1	3.5E-04	5.4	2.5E-03	-0.4	7.7E-01	1.3	1.4E-01
ENSMUST00000086923	collagen, type XVII, alpha 1 [Source:MGI Symbol;Acc:MGI:88450]		Q07563	0.9	6.3E-01	5.6	5.2E-02	1.1	6.6E-01	-3.6	6.3E-02
ENSMUST00000089595	dysferlin [Source:MGI Symbol;Acc:MGI:1349385]	E9PXU9		6.2	1.9E-02	-3.2	3.2E-03	0.9	6.0E-02	-1.9	9.0E-02
ENSMUST00000089610	plectin [Source:MGI Symbol;Acc:MGI:1277961]		Q9QXS1	-6.5	5.0E-03	5.0	3.0E-04	-0.5	5.7E-01	-1.1	9.6E-02
ENSMUST00000089614	predicted gene 6899 [Source:MGI Symbol;Acc:MGI:3648261]	Q3USS0		4.4	1.0E-03	8.0	4.1E-05	-0.6	6.0E-01	-1.6	2.0E-02
ENSMUST00000086969	transmembrane protein 180 [Source:MGI Symbol;Acc:MGI:1922396]		Q6PDE8	-4.0	6.5E-02	0.0	9.8E-01	1.9	1.7E-01	-2.2	3.2E-01
ENSMUST00000086975	G protein-coupled receptor 55 [Source:MGI Symbol;Acc:MGI:2685064]		Q3UJF0	-1.0	3.8E-02	0.7	1.8E-01	0.7	9.5E-02	-1.0	6.1E-02
ENSMUST00000086978	cyclin-dependent kinase-like 2 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1858227]	Q149A0	Q9QUK0	0.2	9.4E-01	-1.5	4.5E-01	-2.9	1.1E-01	-1.2	5.7E-01
ENSMUST00000089618	immunoglobulin-like domain containing receptor 1 [Source:MGI Symbol;Acc:MGI:2146574]		Q8CBR1	5.3	9.2E-03	5.7	1.7E-03	-2.0	2.0E-01	-0.5	5.2E-01
ENSMUST00000089619	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) [Source:MGI Symbol;Acc:MGI:1096367]	G3X9K9		-5.5	2.8E-02	-2.8	5.9E-03	-0.6	2.6E-01	0.4	6.0E-01
ENSMUST00000087031	exportin 5 [Source:MGI Symbol;Acc:MGI:1913789]		Q924C1	-0.1	8.7E-01	0.2	7.2E-01	0.5	2.0E-01	0.2	6.2E-01
ENSMUST00000087033	immunoglobulin joining chain [Source:MGI Symbol;Acc:MGI:96493]		P01592	0.1	9.6E-01	-4.7	3.4E-03	-5.9	1.3E-04	-1.1	4.2E-01
ENSMUST00000089620	CD86 antigen [Source:MGI Symbol;Acc:MGI:101773]	Q549Q9	P42082	-3.4	3.2E-03	7.4	5.1E-05	-0.6	5.8E-01	-0.8	1.6E-01
ENSMUST00000089628	predicted gene 5416 [Source:MGI Symbol;Acc:MGI:3644688]	Q6IE28		-5.8	4.6E-05	6.2	8.2E-04	-2.1	1.8E-01	-0.5	4.7E-01
ENSMUST00000089641	T cell leukemia, homeobox 2 [Source:MGI Symbol;Acc:MGI:1350935]		Q61663	3.2	3.2E-02	6.3	7.5E-02	-0.8	8.1E-01	0.6	7.6E-01
ENSMUST00000089645	HtrA serine peptidase 2 [Source:MGI Symbol;Acc:MGI:1928676]		Q9JIY5	-6.4	2.2E-04	5.1	3.8E-03	0.3	8.4E-01	0.7	4.3E-01
ENSMUST00000089651	docking protein 1 [Source:MGI Symbol;Acc:MGI:893587]		P97465	-6.1	4.3E-04	-1.6	4.6E-02	-0.1	8.5E-01	-1.7	4.2E-02
ENSMUST00000089669	mitogen-activated protein kinase 15 [Source:MGI Symbol;Acc:MGI:2652894]		Q80Y86	7.0	4.8E-04	9.9	1.0E-05	-0.7	5.9E-01	-0.1	8.9E-01
ENSMUST00000087123	golgi autoantigen, golgin subfamily a, 7B [Source:MGI Symbol;Acc:MGI:1918396]		Q9D428	5.2	6.8E-02	6.2	6.6E-02	0.4	9.0E-01	-0.6	7.5E-01
ENSMUST00000087133	exocyst complex component 1 [Source:MGI Symbol;Acc:MGI:2445020]		Q8R3S6	-2.1	8.6E-02	-4.5	5.2E-02	-0.4	6.8E-01	2.0	3.5E-01
ENSMUST00000089677	zinc finger protein 148 [Source:MGI Symbol;Acc:MGI:1332234]	Q548L0	Q61624	-4.5	4.1E-04	-2.1	1.4E-02	0.3	4.2E-01	0.2	7.3E-01
ENSMUST00000087155				-2.1	5.0E-02	-0.6	6.0E-01	0.5	5.1E-01	-1.0	3.9E-01
ENSMUST00000089684	RIKEN cDNA 1700021K19 gene [Source:MGI Symbol;Acc:MGI:1915160]		Q80U62	6.0	1.4E-02	6.9	1.6E-04	-0.6	6.0E-01	-0.5	4.6E-01
ENSMUST00000089688	matrix metallopeptidase 14 (membrane-inserted) [Source:MGI Symbol;Acc:MGI:101900]		P53690	4.7	5.0E-05	6.8	5.1E-03	-0.5	8.0E-01	-2.4	5.8E-02
ENSMUST00000087164	ligand dependent nuclear receptor corepressor-like [Source:MGI Symbol;Acc:MGI:2651932]		Q3U285	0.9	6.0E-01	5.8	3.2E-02	3.0	2.1E-01	-1.9	2.0E-01
ENSMUST00000089745	GA repeat binding protein, beta 1 [Source:MGI Symbol;Acc:MGI:95611]		Q00420	2.7	7.9E-03	7.0	6.3E-05	-0.5	6.3E-01	-0.8	2.0E-01
ENSMUST00000089752	chromodomain helicase DNA binding protein 8 [Source:MGI Symbol;Acc:MGI:1915022]		Q09XV5	-2.3	1.2E-03	6.7	3.7E-04	-1.5	3.0E-01	-0.5	4.8E-01
ENSMUST00000087183	serine/threonine kinase 36 [Source:MGI Symbol;Acc:MGI:1920831]		Q69ZM6	-3.0	1.3E-01	1.5	4.9E-01	2.9	1.2E-01	-1.6	4.4E-01
ENSMUST00000089765	chromatin accessibility complex 1 [Source:MGI Symbol;Acc:MGI:2135796]		Q9JKP8	-7.5	1.9E-05	5.9	4.3E-03	-0.2	9.1E-01	-0.6	5.5E-01
ENSMUST00000089770	trafficking protein particle complex 9 [Source:MGI Symbol;Acc:MGI:1923760]		Q3U0M1	-6.0	1.7E-03	1.8	1.2E-02	-1.8	1.1E-02	0.1	8.9E-01
ENSMUST00000089771	ribonuclease, RNase A family, 13 (non-active) [Source:MGI Symbol;Acc:MGI:3528592]		Q5GAM7	6.9	1.5E-04	-0.5	5.7E-01	0.9	1.6E-01	-0.7	4.6E-01
ENSMUST00000089824	HRAS-like suppressor [Source:MGI Symbol;Acc:MGI:1351473]			6.3	6.0E-04	0.5	1.8E-01	1.0	5.3E-03	-0.5	1.4E-01
ENSMUST00000087205				1.8	1.6E-01	2.8	8.5E-02	0.3	8.0E-01	-0.6	6.0E-01
ENSMUST00000087210	protein phosphatase 1, regulatory subunit 10 [Source:MGI Symbol;Acc:MGI:1289273]		Q80W00	-3.2	4.7E-02	-1.3	4.5E-01	1.2	2.9E-01	-0.7	7.0E-01
ENSMUST00000087211	protein phosphatase 1, regulatory subunit 10 [Source:MGI Symbol;Acc:MGI:1289273]		Q80W00	3.6	3.0E-01	5.5	1.4E-01	-0.5	8.9E-01	-2.4	3.1E-01
ENSMUST00000089825	myelin basic protein expression factor 2, repressor [Source:MGI Symbol;Acc:MGI:104592]	G8JL68		-2.6	2.5E-02	3.6	9.9E-03	-1.8	1.3E-01	0.2	8.0E-01
ENSMUST00000089840	cancer antigen 1 [Source:MGI Symbol;Acc:MGI:1918463]		Q5IR70	4.3	4.8E-05	-1.1	5.1E-02	0.8	3.1E-02	0.1	8.1E-01
ENSMUST00000089860	family with sequence similarity 13, member A [Source:MGI Symbol;Acc:MGI:1889842]		Q8BGI4	7.2	5.5E-05	-4.7	3.4E-03	-0.4	5.4E-01	-0.4	7.9E-01
ENSMUST00000087222				1.2	1.2E-01	2.1	3.1E-02	0.4	5.7E-01	-0.5	4.6E-01
ENSMUST00000089874	mutated in colorectal cancers [Source:MGI Symbol;Acc:MGI:96930]	E9PWI3		9.7	5.3E-06	6.9	5.4E-02	-0.9	8.0E-01	0.3	8.9E-01
ENSMUST00000089883	mannan-binding lectin serine peptidase 1 [Source:MGI Symbol;Acc:MGI:88492]		P98064	7.7	3.4E-05	5.8	1.9E-03	-0.4	7.9E-01	-1.1	1.9E-01
ENSMUST00000089926	microfibrillar-associated protein 1A [Source:MGI Symbol;Acc:MGI:1914782]		Q9CQU1	-2.4	1.2E-03	8.4	2.1E-05	-0.5	6.6E-01	0.0	9.5E-01
ENSMUST00000089948	solute carrier family 44, member 5 [Source:MGI Symbol;Acc:MGI:3035141]		Q5RJI2	5.9	1.4E-04	7.8	2.6E-05	0.1	9.4E-01	-0.8	1.5E-01
ENSMUST00000087258	trophinin [Source:MGI Symbol;Acc:MGI:1928994]	Q6DIC6		6.3	4.8E-02	5.0	1.0E-01	-1.9	5.5E-01	-0.5	7.9E-01
ENSMUST00000087264	NEDD4 binding protein 2 [Source:MGI Symbol;Acc:MGI:2684414]	F8VQG7		0.5	8.0E-01	1.7	5.4E-01	1.0	5.9E-01	-0.2	9.3E-01
ENSMUST00000089959	GTP cyclohydrolase 1 [Source:MGI Symbol;Acc:MGI:95675]	Q3U7P6	Q05915	-2.6	6.2E-04	8.2	6.2E-05	-0.7	5.9E-01	-0.5	3.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000089982	zinc finger, ZZ domain containing 3 [Source:MGI Symbol;Acc:MGI:1920453]	D3YTT9		-7.4	5.5E-05	6.4	3.0E-04	-0.6	6.3E-01	-0.1	8.4E-01
ENSMUST00000090002	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:MGI Symbol;Acc:MGI:104819]		O88569	-6.4	5.3E-04	1.9	2.1E-01	-1.1	3.7E-01	4.4	5.2E-03
ENSMUST00000090006	integrin beta 1 (fibronectin receptor beta) [Source:MGI Symbol;Acc:MGI:96610]		P09055	-5.6	2.3E-04	-6.0	6.3E-03	-0.7	3.3E-01	0.4	8.3E-01
ENSMUST00000090023	adaptor-related protein complex 2, mu 1 subunit [Source:MGI Symbol;Acc:MGI:1298405]	Q3TWV4		-9.9	2.1E-05	7.6	8.7E-05	-0.6	6.1E-01	-0.2	7.0E-01
ENSMUST00000090024	coiled-coil serine rich 2 [Source:MGI Symbol;Acc:MGI:101859]		Q3UHI0	9.4	1.5E-05	-3.3	1.9E-04	0.8	2.0E-02	-1.3	5.0E-02
ENSMUST00000090025	alanine and arginine rich domain containing protein [Source:MGI Symbol;Acc:MGI:2181621]		Q811W1	6.1	7.7E-04	-2.0	4.1E-02	0.9	1.3E-01	-0.1	8.7E-01
ENSMUST00000090027	WAPL cohesin release factor [Source:MGI Symbol;Acc:MGI:2675859]	B7ZP47		-6.4	2.0E-05	2.2	3.7E-02	0.5	5.4E-01	0.5	4.7E-01
ENSMUST00000090031	guanine nucleotide binding protein (G protein), gamma 5 [Source:MGI Symbol;Acc:MGI:109164]	Q3UKC8	Q80SZ7	-5.6	1.9E-05	10.1	7.1E-06	-2.0	1.5E-01	-0.7	1.2E-01
ENSMUST00000090042	transmembrane protein 87A [Source:MGI Symbol;Acc:MGI:2441844]	A2AQJ5		-4.9	1.0E-02	-1.0	2.7E-01	0.8	1.7E-01	-0.7	4.6E-01
ENSMUST00000087341	kinesin family member 20B [Source:MGI Symbol;Acc:MGI:2444576]		Q80WE4	-0.2	7.0E-01	-0.7	3.7E-01	-0.6	2.8E-01	-0.1	8.5E-01
ENSMUST00000090046	transmembrane protein 87A [Source:MGI Symbol;Acc:MGI:2441844]	A2AQJ6		-5.0	6.5E-03	-4.0	4.6E-03	-1.2	7.3E-02	-3.2	4.3E-02
ENSMUST00000090061	RIKEN cDNA 1700123L14 gene [Source:MGI Symbol;Acc:MGI:1925732]	Q3V2K7		6.9	2.0E-04	9.5	3.1E-05	-1.3	3.7E-01	-1.2	6.5E-02
ENSMUST00000090063	diamine oxidase-like protein 2 [Source:MGI Symbol;Acc:MGI:3618290]	F6TPL1		8.3	8.4E-05	-4.7	2.2E-02	-1.0	2.8E-01	-1.7	4.1E-01
ENSMUST00000087357	interferon induced protein with tetratricopeptide repeats 1B like 2 [Source:MGI Symbol;Acc:MGI:2148249]	Q3U687		1.6	6.0E-01	-1.4	6.4E-01	-2.7	2.9E-01	0.2	9.4E-01
ENSMUST00000087360	ecombination signal binding protein for immunoglobulin kappa J region [Source:MGI Symbol;Acc:MGI:96522	E9Q7W0		2.1	4.6E-01	3.3	2.7E-01	-1.7	5.4E-01	-2.8	2.6E-01
ENSMUST00000090070	GTPase, IMAP family member 4 [Source:MGI Symbol;Acc:MGI:1349656]	D3YTN4		-4.8	5.6E-03	-1.7	5.9E-02	0.8	1.1E-01	-0.2	8.2E-01
ENSMUST00000090071	phospholipase A2, group IVE [Source:MGI Symbol;Acc:MGI:1919144]		Q50L42	8.1	2.4E-05	5.9	1.4E-05	-2.9	5.1E-03	-0.2	6.4E-01
ENSMUST00000090095	oxidation resistance 1 [Source:MGI Symbol;Acc:MGI:2179326]		Q4KMM3	-5.9	3.8E-03	5.8	1.5E-03	0.1	9.1E-01	-0.6	4.4E-01
ENSMUST00000090127	guanylate binding protein 5 [Source:MGI Symbol;Acc:MGI:2429943]		Q8CFB4	2.6	4.5E-03	5.7	7.7E-04	-0.5	7.1E-01	0.0	9.7E-01
ENSMUST00000090150	neurocalcin delta [Source:MGI Symbol;Acc:MGI:1196326]		Q91X97	5.2	1.9E-02	-0.4	4.7E-01	0.9	1.9E-02	0.4	3.7E-01
ENSMUST00000090156	olfactory receptor 458 [Source:MGI Symbol;Acc:MGI:3030292]	Q8VF80		5.9	8.4E-04	0.1	9.5E-01	3.4	2.5E-02	-2.7	1.3E-01
ENSMUST00000090170	ribosomal protein L7A, pseudogene 3 [Source:MGI Symbol;Acc:MGI:3643413]			5.4	2.8E-02	7.7	8.4E-05	-1.5	2.8E-01	-0.9	1.6E-01
ENSMUST00000087465	F-box and leucine-rich repeat protein 5 [Source:MGI Symbol;Acc:MGI:2152883]		Q8C2S5	-1.3	1.4E-01	-2.7	4.0E-02	-0.3	7.0E-01	1.1	3.4E-01
ENSMUST00000087475	transmembrane protein 237 [Source:MGI Symbol;Acc:MGI:2138365]		Q3V0J1	1.0	5.7E-01	1.7	4.1E-01	-0.7	7.1E-01	-1.4	3.8E-01
ENSMUST00000087485	C2 calcium-dependent domain containing 5 [Source:MGI Symbol;Acc:MGI:1921991]		Q7TPS5	3.4	7.2E-02	3.5	1.5E-01	-0.5	8.3E-01	-0.5	7.3E-01
ENSMUST00000090171	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide [Source:MGI Symbol;Acc:MGI:87926]	Q9D748	Q64437	6.2	7.3E-05	5.2	6.8E-02	-0.8	7.7E-01	0.2	8.8E-01
ENSMUST00000087497	collagen, type XI, alpha 2 [Source:MGI Symbol;Acc:MGI:88447]	I7HJS8	Q64739	0.1	9.4E-01	0.3	8.0E-01	0.3	7.1E-01	0.1	9.4E-01
ENSMUST00000090174	zinc finger, FYVE domain containing 19 [Source:MGI Symbol;Acc:MGI:1919258]		Q9DAZ9	-4.0	2.5E-02	-3.5	1.6E-03	0.2	6.5E-01	-0.7	3.9E-01
ENSMUST00000087514	Ly1 antibody reactive clone [Source:MGI Symbol;Acc:MGI:107470]		Q08288	-3.1	2.1E-01	-3.2	1.3E-01	-3.3	4.1E-02	-3.2	2.2E-01
ENSMUST00000090178	DnaJ (Hsp40) homolog, subfamily B, member 14 [Source:MGI Symbol;Acc:MGI:1917854]		Q149L6	2.6	2.4E-04	-0.7	2.3E-01	0.7	7.2E-02	0.2	6.8E-01
ENSMUST00000090180	in, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G [Source:MGI Symbol;Acc:MC		Q4LFA9	9.1	1.0E-05	3.3	3.2E-03	-0.5	5.3E-01	-0.3	6.3E-01
ENSMUST00000087540	TRM2 tRNA methyltransferase 2B [Source:MGI Symbol;Acc:MGI:2442530]	Q8C8J3		0.2	8.3E-01	-0.6	5.7E-01	-0.6	4.6E-01	0.2	8.6E-01
ENSMUST00000090190	hypermethylated in cancer 2 [Source:MGI Symbol;Acc:MGI:1929869]		Q9JLZ6	7.4	3.4E-06	-0.8	2.7E-01	1.2	2.1E-02	-0.2	7.8E-01
ENSMUST00000087556	structural maintenance of chromosomes 5 [Source:MGI Symbol;Acc:MGI:2385088]		Q8CG46	0.4	4.3E-01	-0.2	7.5E-01	0.1	7.5E-01	0.8	2.5E-01
ENSMUST00000090192	ubiquitin-conjugating enzyme E2L 3 [Source:MGI Symbol;Acc:MGI:109240]	Q561N4	P68037	-7.7	7.5E-05	6.7	2.4E-04	0.3	7.8E-01	0.3	6.6E-01
ENSMUST00000090195	predicted gene 11027 [Source:MGI Symbol;Acc:MGI:3779250]	G8JL69		7.2	1.9E-06	-4.9	9.0E-03	1.3	6.5E-02	-1.5	4.2E-01
ENSMUST00000090205	small integral membrane protein 4 [Source:MGI Symbol;Acc:MGI:1913737]		Q8C1Q6	-4.0	9.8E-03	-7.5	3.5E-04	0.6	3.0E-01	0.3	8.5E-01
ENSMUST00000090227	membrane-associated ring finger (C3HC4) 6 [Source:MGI Symbol;Acc:MGI:2442773]		Q6ZQ89	-3.6	1.8E-05	-4.6	2.7E-05	0.9	1.8E-02	-0.4	5.5E-01
ENSMUST00000090243	olute carrier family 37 (glycerol-3-phosphate transporter), member 3 [Source:MGI Symbol;Acc:MGI:1919394			-2.4	1.1E-03	-4.5	7.0E-04	1.4	1.1E-02	-0.6	5.5E-01
ENSMUST00000090246	sphingomyelin synthase 2 [Source:MGI Symbol;Acc:MGI:1921692]		Q9D4B1	-1.7	3.2E-03	-2.6	3.5E-02	-0.8	2.5E-01	-0.8	5.4E-01
ENSMUST00000087617	coenzyme Q10 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915126]	G5E8J7		-2.1	1.8E-01	1.3	5.4E-01	2.2	2.3E-01	-1.2	4.8E-01
ENSMUST00000090247	triple functional domain (PTPRF interacting) [Source:MGI Symbol;Acc:MGI:1927230]		Q0KL02	2.0	3.6E-04	3.5	5.8E-04	-0.7	3.1E-01	-0.3	6.1E-01
ENSMUST00000090257	predicted gene 8225 [Source:MGI Symbol;Acc:MGI:3643826]	D3Z536		4.8	2.1E-04	1.6	4.6E-01	6.6	2.1E-03	-1.1	5.5E-01
ENSMUST00000090260	predicted gene 4841 [Source:MGI Symbol;Acc:MGI:3643814]	E9QAA8		8.2	1.1E-05	4.0	6.6E-04	-3.1	9.1E-03	0.1	8.4E-01
ENSMUST00000090269	actin, alpha, cardiac muscle 1 [Source:MGI Symbol;Acc:MGI:87905]	Q497E4	P68033	7.5	9.6E-05	-0.2	8.1E-01	-3.7	5.5E-04	-1.5	8.2E-02
ENSMUST00000090275	gap junction protein, delta 2 [Source:MGI Symbol;Acc:MGI:1334209]		O54851	6.5	3.1E-04	2.5	1.4E-02	-0.6	4.5E-01	0.0	9.8E-01
ENSMUST00000090277	EF hand calcium binding domain 1 [Source:MGI Symbol;Acc:MGI:1914043]		Q9D3N2	6.6	9.6E-04	4.3	6.3E-04	1.0	2.1E-01	0.0	9.4E-01
ENSMUST00000087659	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 [Source:MGI Symbol;Acc:MGI:2685817]		Q6I6G8	2.0	2.1E-01	0.2	9.1E-01	-0.2	9.1E-01	1.6	3.6E-01
ENSMUST00000087666	zinc finger protein 952 [Source:MGI Symbol;Acc:MGI:2441928]	B0V2W4		1.0	6.3E-01	-2.7	3.1E-01	-2.2	2.3E-01	1.4	5.8E-01
ENSMUST00000090287	myosin, heavy polypeptide 11, smooth muscle [Source:MGI Symbol;Acc:MGI:102643]	E9QPE7		7.6	5.9E-06	5.9	6.9E-04	-0.6	6.6E-01	-0.6	3.8E-01
ENSMUST00000090292	drosha, ribonuclease type III [Source:MGI Symbol;Acc:MGI:1261425]		Q5HZJ0	-5.2	2.0E-03	-2.2	4.8E-03	0.0	9.1E-01	-0.3	5.9E-01
ENSMUST00000087684	regulator of G-protein signaling 12 [Source:MGI Symbol;Acc:MGI:1918979]	E9Q652		4.3	1.4E-01	1.3	6.3E-01	-3.2	3.0E-01	-0.1	9.5E-01
ENSMUST00000090302	ELKS/RAB6-interacting/CAST family member 2 [Source:MGI Symbol;Acc:MGI:1098749]		Q6PH08	6.0	3.4E-05	3.5	8.4E-05	-1.0	6.2E-02	0.1	6.9E-01
ENSMUST00000090313	dystrotelin [Source:MGI Symbol;Acc:MGI:2685061]		A2CI98	7.0	3.3E-05	3.6	6.4E-04	-0.5	4.8E-01	-0.7	2.0E-01
ENSMUST00000087703	widely-interspaced zinc finger motifs [Source:MGI Symbol;Acc:MGI:1332638]	G5E8J8		-0.4	7.8E-01	7.1	1.9E-02	5.2	4.9E-02	-2.3	1.6E-01
ENSMUST00000090339	retinoic acid induced 14 [Source:MGI Symbol;Acc:MGI:1922896]		Q9EP71	7.9	8.4E-04	4.2	1.2E-02	0.0	1.0E+00	0.0	9.9E-01
ENSMUST00000090371	methyltransferase like 14 [Source:MGI Symbol;Acc:MGI:2442926]	E9QPC5		5.8	1.7E-03	8.4	4.4E-04	0.3	8.4E-01	1.1	1.4E-01
ENSMUST00000090379	ubiquitin specific peptidase 53 [Source:MGI Symbol;Acc:MGI:2139607]		P15975	-1.0	3.0E-02	7.0	3.8E-05	-2.7	2.9E-02	0.3	5.0E-01
ENSMUST00000090380	LMBR1 domain containing 2 [Source:MGI Symbol;Acc:MGI:2444173]		Q8C561	1.4	1.6E-02	6.4	1.6E-03	-0.5	7.4E-01	-2.3	2.7E-02
ENSMUST00000090391	paired box 6 [Source:MGI Symbol;Acc:MGI:97490]		P63015	5.9	1.7E-04	-1.6	9.9E-02	0.3	6.1E-01	-2.2	5.3E-02
ENSMUST00000090413	P3, small subunit (SSU) processome component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:19192		Q9JI13	-3.8	2.8E-04	6.3	2.2E-04	-0.6	6.0E-01	-0.9	1.6E-01
ENSMUST00000090433	SEC14-like lipid binding 1 [Source:MGI Symbol;Acc:MGI:1921386]	A8Y5H7		-4.3	7.4E-05	6.3	1.4E-03	-0.7	6.4E-01	0.2	7.9E-01
ENSMUST00000090453	rogdi homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913299]		Q3TDK6	-4.4	1.9E-03	8.0	3.9E-03	-0.9	7.0E-01	0.9	4.3E-01
ENSMUST00000090461	FYN binding protein [Source:MGI Symbol;Acc:MGI:1346327]	B2RUR0	O35601	-5.7	6.8E-06	5.9	1.0E-03	-0.7	6.3E-01	0.0	9.7E-01
ENSMUST00000087864	UV stimulated scaffold protein A [Source:MGI Symbol;Acc:MGI:1918351]		Q9D479	1.4	5.9E-01	-3.1	4.8E-01	-1.2	6.0E-01	3.3	4.4E-01
ENSMUST00000090464	CDC14 cell division cycle 14A [Source:MGI Symbol;Acc:MGI:2442676]		Q6GQT0	-6.5	3.4E-04	-2.0	8.3E-02	0.0	1.0E+00	-2.0	1.2E-01
ENSMUST00000090473	G-protein coupled receptor 88 [Source:MGI Symbol;Acc:MGI:1927653]	B2RXU4	Q9EPB7	7.7	3.7E-05	5.2	2.1E-04	0.3	7.3E-01	0.6	3.1E-01
ENSMUST00000090475	ets homologous factor [Source:MGI Symbol;Acc:MGI:1270840]		O70273	5.9	2.5E-02	5.7	3.9E-04	0.7	4.7E-01	0.3	6.4E-01
ENSMUST00000090481	calumenin [Source:MGI Symbol;Acc:MGI:1097158]	Q6XLQ8		-3.2	3.1E-02	7.0	1.1E-04	-0.6	6.3E-01	-0.4	4.7E-01
ENSMUST00000090499	family with sequence similarity 149, member B [Source:MGI Symbol;Acc:MGI:2145567]		Q6NSV7	-5.3	2.6E-04	4.1	4.8E-02	-0.4	8.3E-01	1.3	3.0E-01
ENSMUST00000090511	golgi coiled coil 1 [Source:MGI Symbol;Acc:MGI:1921625]		Q9D4H2	-2.4	1.9E-04	-2.0	4.5E-03	-9.6	8.4E-07	-0.7	2.1E-01
ENSMUST00000090522	zinc finger protein 597 [Source:MGI Symbol;Acc:MGI:1918313]	E9Q6S0		-2.3	2.2E-04	3.3	1.3E-03	0.4	5.0E-01	-0.3	5.8E-01
ENSMUST00000087908	syntaxin 16 [Source:MGI Symbol;Acc:MGI:1923396]		Q8BVI5	0.0	9.9E-01	1.8	4.4E-01	0.2	9.1E-01	-1.6	3.9E-01
ENSMUST00000090543	nuclear receptor subfamily 1, group D, member 2 [Source:MGI Symbol;Acc:MGI:2449205]	Q4VAB7	Q60674	1.9	1.4E-02	-1.7	2.1E-01	0.3	7.5E-01	-1.1	4.2E-01
ENSMUST00000090546	transmembrane protein 167B [Source:MGI Symbol;Acc:MGI:1914745]		Q80X45	-4.6	1.2E-03	6.3	8.3E-04	-1.2	4.2E-01	-0.9	2.8E-01
ENSMUST00000090558	n, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila) [Source:MGI Symbol;Acc:MGI:18	A2AEE7		7.0	1.3E-06	5.0	2.6E-05	-1.7	2.0E-02	0.3	4.3E-01
ENSMUST00000090559	cryptochrome 2 (photolyase-like) [Source:MGI Symbol;Acc:MGI:1270859]		Q9R194	3.4	4.5E-04	-7.6	2.3E-05	-0.1	7.9E-01	0.1	9.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000090563	myosin binding protein H-like [Source:MGI Symbol;Acc:MGI:1916003]		Q5FW53	7.8	2.1E-05	6.3	3.4E-04	-0.5	7.1E-01	0.4	5.7E-01
ENSMUST00000090568	protein tyrosine phosphatase, receptor type Z, polypeptide 1 [Source:MGI Symbol;Acc:MGI:97816]		B9EKR1	8.6	7.2E-06	-1.5	1.3E-01	0.6	3.3E-01	-0.4	6.4E-01
ENSMUST00000087948	mediator complex subunit 12 [Source:MGI Symbol;Acc:MGI:1926212]		A2AGH6	-2.8	4.9E-02	-5.1	6.7E-02	0.5	6.4E-01	2.8	2.9E-01
ENSMUST00000090569	proteasome (prosome, macropain) subunit, alpha type 5 [Source:MGI Symbol;Acc:MGI:1347009]	Q3UPK6	Q9Z2U1	-4.4	8.2E-05	7.4	7.4E-05	-0.6	6.1E-01	0.3	6.5E-01
ENSMUST00000090597	ataxin 7-like 1 [Source:MGI Symbol;Acc:MGI:3584458]	B2RW07		-3.7	2.1E-03	-1.1	1.6E-01	1.2	3.8E-02	-0.2	7.9E-01
ENSMUST00000087956	mediator complex subunit 12 [Source:MGI Symbol;Acc:MGI:1926212]		A2AGH6	-4.1	1.2E-01	-1.2	6.9E-01	1.2	6.0E-01	-1.6	5.6E-01
ENSMUST00000090614	Rho GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2445003]		Q5FWK3	-9.5	3.8E-06	6.8	5.1E-04	1.6	2.2E-01	0.0	9.5E-01
ENSMUST00000090678	RAS-related protein-1a [Source:MGI Symbol;Acc:MGI:97852]		P62835	-6.4	7.5E-06	1.4	1.1E-01	-0.3	6.2E-01	0.3	6.5E-01
ENSMUST00000090697	synaptotagmin VI [Source:MGI Symbol;Acc:MGI:1859544]		Q9R0N8	7.3	4.0E-03	6.5	1.0E-03	-0.9	5.4E-01	0.4	6.2E-01
ENSMUST00000090746	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Source:MGI Symbol;Acc:MGI:101939]		P54869	7.0	1.3E-04	8.1	4.3E-05	-0.7	5.9E-01	0.3	5.9E-01
ENSMUST00000088001	activity-dependent neuroprotective protein [Source:MGI Symbol;Acc:MGI:1338758]	A2BDX0	Q9Z103	0.3	8.7E-01	3.0	2.1E-01	0.9	6.4E-01	-1.8	3.5E-01
ENSMUST00000088007	Fanconi anemia, complementation group E [Source:MGI Symbol;Acc:MGI:1920025]	B8JJD6		-1.6	1.8E-01	-0.1	9.2E-01	0.1	9.3E-01	-1.4	2.8E-01
ENSMUST00000090750	phosphodiesterase 4D interacting protein (myomegalin) [Source:MGI Symbol;Acc:MGI:1891434]	G3X9L9		8.1	8.7E-03	0.9	4.8E-01	7.5	2.6E-05	0.2	8.7E-01
ENSMUST00000090760	protein phosphatase 1, regulatory (inhibitor) subunit 1C [Source:MGI Symbol;Acc:MGI:1923185]		Q8BKK4	8.3	1.2E-05	2.7	2.3E-02	-1.8	7.9E-02	0.0	1.0E+00
ENSMUST00000090781	histone cluster 2, H2be [Source:MGI Symbol;Acc:MGI:2448415]		Q64524	2.6	1.1E-03	7.0	1.6E-04	-0.6	6.1E-01	-1.2	9.4E-02
ENSMUST00000088027	ankyrin repeat and SAM domain containing 1 [Source:MGI Symbol;Acc:MGI:2446180]		P59672	-1.5	3.0E-01	-5.3	1.3E-01	0.9	4.8E-01	4.6	1.7E-01
ENSMUST00000090782	histone cluster 2, H2ac [Source:MGI Symbol;Acc:MGI:2448316]	Q149V4	Q64523	5.3	1.9E-03	6.0	9.1E-04	-0.5	7.4E-01	-1.1	1.6E-01
ENSMUST00000088049	keratin 86 [Source:MGI Symbol;Acc:MGI:109362]	B2RTB6	P97861	0.8	3.3E-01	1.4	1.7E-01	0.2	8.1E-01	-0.4	6.0E-01
ENSMUST00000090804	aryl hydrocarbon receptor nuclear translocator [Source:MGI Symbol;Acc:MGI:88071]	Q3ULM2		-5.2	8.7E-03	-4.9	2.0E-03	0.8	1.6E-01	-3.0	6.6E-02
ENSMUST00000090806	retinoic acid induced 1 [Source:MGI Symbol;Acc:MGI:103291]		Q61818	4.1	6.2E-04	4.1	8.7E-03	-0.3	8.0E-01	-0.7	4.2E-01
ENSMUST00000090813	trans-acting transcription factor 9 [Source:MGI Symbol;Acc:MGI:3574660]		Q64HY3	9.9	5.5E-05	9.4	5.1E-04	0.2	9.1E-01	1.5	8.4E-02
ENSMUST00000088081	dihydropyrimidinase-like 5 [Source:MGI Symbol;Acc:MGI:1929772]		Q9EQF6	5.5	7.8E-02	5.2	9.2E-02	-2.0	5.5E-01	-1.7	3.3E-01
ENSMUST00000088086	sulfatase 2 [Source:MGI Symbol;Acc:MGI:1919293]		Q8CFG0	0.3	7.9E-01	-1.0	5.4E-01	-1.1	3.8E-01	0.3	8.5E-01
ENSMUST00000090815	predicted gene 128 [Source:MGI Symbol;Acc:MGI:2684974]	G9MDF2	Q569E4	3.6	5.7E-04	-2.2	7.5E-02	-0.9	2.7E-01	-1.9	1.8E-01
ENSMUST00000090824	sterile alpha motif and leucine zipper containing kinase AZK [Source:MGI Symbol;Acc:MGI:2443258]		Q9ESL4	1.9	1.1E-02	-0.8	3.6E-01	0.9	1.3E-01	-0.9	3.4E-01
ENSMUST00000088102	zinc finger protein X-linked [Source:MGI Symbol;Acc:MGI:99211]	B1ASD1	P17012	-3.9	2.2E-01	-5.7	1.4E-01	-2.7	1.4E-01	-0.9	8.3E-01
ENSMUST00000088113	zinc finger, MYND-type containing 8 [Source:MGI Symbol;Acc:MGI:1918025]	A2A485		2.4	3.7E-01	2.0	4.4E-01	-3.8	1.7E-01	-3.4	1.5E-01
ENSMUST00000088132	eyes absent 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109341]		O08575	0.3	8.9E-01	2.8	2.3E-01	1.6	4.6E-01	-1.0	5.8E-01
ENSMUST00000090839	selenium binding protein 1 [Source:MGI Symbol;Acc:MGI:96825]		P17563	-4.1	2.0E-02	1.2	5.0E-01	4.7	6.4E-03	-1.5	3.7E-01
ENSMUST00000090848	selenium binding protein 2 [Source:MGI Symbol;Acc:MGI:104859]			5.9	4.6E-04	3.3	2.8E-03	0.0	9.5E-01	-0.5	5.0E-01
ENSMUST00000090849	methyltransferase like 8 [Source:MGI Symbol;Acc:MGI:2385142]	Q8CA70		7.9	5.6E-06	3.0	1.1E-01	0.2	9.1E-01	3.2	2.2E-02
ENSMUST00000088174	heparan sulfate 6-O-sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1354958]		Q9QYK5	0.9	1.7E-01	1.1	2.1E-01	0.1	8.5E-01	0.0	9.5E-01
ENSMUST00000090852	Sjogren syndrome antigen B [Source:MGI Symbol;Acc:MGI:98423]	Q564E6	P32067	-6.7	1.5E-05	-4.4	9.5E-04	-0.4	4.3E-01	0.2	8.2E-01
ENSMUST00000088200	aquaporin 5 [Source:MGI Symbol;Acc:MGI:106215]		Q9WTY4	3.7	7.6E-02	3.9	5.1E-02	-1.8	3.6E-01	-2.0	1.5E-01
ENSMUST00000090856	hornerin [Source:MGI Symbol;Acc:MGI:3046938]	E9QNP3		9.7	5.8E-06	-1.8	2.3E-02	1.3	1.2E-02	0.0	9.7E-01
ENSMUST00000090858	peptidyl-prolyl isomerase G (cyclophilin G) [Source:MGI Symbol;Acc:MGI:2445173]		A2AR02	-5.8	4.5E-03	3.2	3.3E-03	0.5	5.3E-01	-0.4	5.4E-01
ENSMUST00000088233	formin-like 3 [Source:MGI Symbol;Acc:MGI:109569]		Q6ZPF4	-1.1	3.3E-01	-0.2	8.7E-01	0.1	8.8E-01	-0.7	5.8E-01
ENSMUST00000088237	nanos homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2669254]		Q80WY3	0.9	9.0E-02	2.0	1.4E-02	1.1	6.2E-02	0.1	9.3E-01
ENSMUST00000088244	ARP3 actin-related protein 3B [Source:MGI Symbol;Acc:MGI:2661120]		Q641P0	4.2	1.0E-01	1.7	6.1E-01	-0.2	9.5E-01	2.4	3.5E-01
ENSMUST00000090860	predicted pseudogene 10116 [Source:MGI Symbol;Acc:MGI:3779109]	Q9CPX4		3.2	2.7E-02	5.0	1.5E-03	-1.8	1.7E-01	0.3	7.1E-01
ENSMUST00000088248	ubiquitin-conjugating enzyme E2C [Source:MGI Symbol;Acc:MGI:1915862]	A2A4Z0	Q9D1C1	0.0	9.9E-01	0.8	2.3E-01	0.9	8.2E-02	0.1	8.7E-01
ENSMUST00000088257	tRNA methyltransferase 11-2 [Source:MGI Symbol;Acc:MGI:1914924]		Q9DCG9	-3.8	1.1E-01	-4.1	2.8E-01	0.6	7.2E-01	0.9	8.2E-01
ENSMUST00000090866	late cornified envelope 1I [Source:MGI Symbol;Acc:MGI:1923835]	Q9D6P5		5.9	7.6E-03	7.3	2.1E-05	-0.9	4.0E-01	-0.2	6.1E-01
ENSMUST00000090908	ubiquitin-associated protein 2-like [Source:MGI Symbol;Acc:MGI:1921633]	A0A0H2UH17		-4.7	4.7E-04	5.3	5.0E-02	-0.8	7.7E-01	-0.7	6.6E-01
ENSMUST00000090927	CDC-like kinase 2 [Source:MGI Symbol;Acc:MGI:1098669]	F8WHX0		-4.6	2.3E-02	-4.2	1.1E-02	1.0	1.1E-01	-0.8	5.7E-01
ENSMUST00000088291	serine/threonine kinase 4 [Source:MGI Symbol;Acc:MGI:1929004]	Q8CDG4		-5.5	6.3E-02	5.7	1.8E-01	10.3	1.1E-02	-0.9	7.7E-01
ENSMUST00000090929	RUN and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919546]		Q8BG26	4.9	3.1E-02	2.5	1.3E-01	-3.7	5.0E-02	-1.5	2.9E-01
ENSMUST00000088294	proacrosin binding protein [Source:MGI Symbol;Acc:MGI:1859515]		Q3V140	-1.1	1.8E-01	-0.1	9.4E-01	0.2	8.3E-01	-0.9	3.4E-01
ENSMUST00000088295	chondroitin polymerizing factor 2 [Source:MGI Symbol;Acc:MGI:1917522]	Q3UU43		0.9	5.5E-01	2.8	1.1E-01	-0.1	9.4E-01	-2.0	1.9E-01
ENSMUST00000090933	ash1 (absent, small, or homeotic)-like (Drosophila) [Source:MGI Symbol;Acc:MGI:2183158]		Q99MY8	-6.6	5.8E-03	-7.5	2.5E-05	1.6	4.3E-04	-1.0	3.7E-01
ENSMUST00000090935	activin A receptor, type 1 [Source:MGI Symbol;Acc:MGI:87911]		P37172	9.0	1.8E-04	6.9	7.8E-05	-1.5	2.1E-01	0.2	7.6E-01
ENSMUST00000088307	cDNA sequence BC003965 [Source:MGI Symbol;Acc:MGI:2670966]		Q6RUT7	0.5	2.5E-01	1.3	2.1E-02	0.3	4.9E-01	-0.6	2.1E-01
ENSMUST00000090938	death associated protein 3 [Source:MGI Symbol;Acc:MGI:1929538]	G3X9M0		3.0	2.2E-04	-2.5	3.0E-03	0.7	6.3E-02	-0.4	5.5E-01
ENSMUST00000090940	ermin, ERM-like protein [Source:MGI Symbol;Acc:MGI:1925017]		Q5EBJ4	7.4	6.2E-05	6.4	9.1E-05	-0.9	4.1E-01	0.1	8.7E-01
ENSMUST00000090942	gon-4-like (C.elegans) [Source:MGI Symbol;Acc:MGI:1917579]	K4DI71		-5.1	3.5E-03	-2.0	1.3E-01	1.4	8.1E-02	-0.2	8.8E-01
ENSMUST00000090971	brevican [Source:MGI Symbol;Acc:MGI:1096385]		Q61361	8.6	2.6E-05	7.2	2.4E-04	-0.7	6.2E-01	-0.6	3.9E-01
ENSMUST00000090981	platelet endothelial aggregation receptor 1 [Source:MGI Symbol;Acc:MGI:1920432]		Q8VIK5	6.1	1.3E-02	5.9	9.7E-03	-1.1	5.7E-01	1.2	2.5E-01
ENSMUST00000088357	atrophin 1 [Source:MGI Symbol;Acc:MGI:104725]		O35126	-0.8	5.0E-01	-1.6	4.0E-01	1.4	2.7E-01	2.2	2.2E-01
ENSMUST00000090986	Fc receptor-like S, scavenger receptor [Source:MGI Symbol;Acc:MGI:1933397]	Q9EQY5		6.7	3.0E-04	6.4	4.3E-04	-0.6	6.1E-01	0.2	6.7E-01
ENSMUST00000090993	actin related protein 2/3 complex, subunit 5-like [Source:MGI Symbol;Acc:MGI:1921442]		Q9D898	-7.8	7.4E-06	6.7	5.3E-05	0.2	8.7E-01	0.3	5.3E-01
ENSMUST00000091014	microtubule-associated protein 9 [Source:MGI Symbol;Acc:MGI:2442208]		Q3TRR0	7.4	5.4E-04	-2.6	1.9E-03	0.3	3.9E-01	-0.3	5.9E-01
ENSMUST00000091037	zinc finger and BTB domain containing 34 [Source:MGI Symbol;Acc:MGI:2685195]	A2ATY4		2.4	2.1E-02	-6.6	7.0E-03	-1.3	9.5E-02	0.5	8.2E-01
ENSMUST00000091064	Ras-related GTP binding A [Source:MGI Symbol;Acc:MGI:1915691]		Q80X95	-3.7	1.4E-04	1.4	4.9E-01	-1.7	3.5E-01	6.5	3.3E-03
ENSMUST00000091087	dynamin 2 [Source:MGI Symbol;Acc:MGI:109547]		P39054	-5.3	8.0E-03	8.7	1.5E-05	-0.5	6.7E-01	-0.3	5.4E-01
ENSMUST00000088452	solute carrier family 38, member 1 [Source:MGI Symbol;Acc:MGI:2145895]		Q8K2P7	2.1	3.9E-01	6.1	4.0E-02	1.1	6.6E-01	-2.9	1.9E-01
ENSMUST00000091137	Fras1 related extracellular matrix protein 2 [Source:MGI Symbol;Acc:MGI:2444465]		Q6NVD0	10.1	1.6E-06	-0.9	3.0E-01	0.5	4.2E-01	-0.7	4.3E-01
ENSMUST00000091144	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]	A0A0B4J1G5		-6.2	7.1E-03	8.6	7.8E-03	-0.7	8.1E-01	-2.8	6.9E-02
ENSMUST00000091178	sex determining region of Chr Y [Source:MGI Symbol;Acc:MGI:98660]	Q53WV7	Q05738	7.9	1.8E-04	-6.3	9.5E-04	1.1	3.9E-02	-0.6	6.8E-01
ENSMUST00000091184	r family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31 [Source:MGI Symbol;Acc:MC	B2RTC8	Q3V132	3.9	3.3E-02	-4.8	2.4E-02	-0.6	4.6E-01	-0.8	6.6E-01
ENSMUST00000091186	inturned planar cell polarity effector homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2443752]		Q059U7	5.7	2.1E-05	8.1	4.2E-05	-0.6	6.1E-01	0.6	2.9E-01
ENSMUST00000091201	ADP-ribosylation factor-like 15 [Source:MGI Symbol;Acc:MGI:2442308]		Q8BGR6	-1.2	2.2E-02	-8.3	2.8E-04	-0.5	2.9E-01	-2.3	2.1E-01
ENSMUST00000088494	bladder cancer associated protein homolog (human) [Source:MGI Symbol;Acc:MGI:1858907]		P62951	-0.2	9.5E-01	-2.0	4.7E-01	-1.6	4.6E-01	0.3	9.3E-01
ENSMUST00000088512	ribonucleic acid binding protein S1 [Source:MGI Symbol;Acc:MGI:97960]		Q99M28	0.2	9.3E-01	0.1	9.8E-01	-1.2	5.8E-01	-1.0	7.0E-01
ENSMUST00000091227	pyroglutamylated RFamide peptide receptor [Source:MGI Symbol;Acc:MGI:2677633]	Q4VA00	P83861	6.9	2.4E-04	7.8	3.3E-04	-0.7	6.5E-01	0.2	7.7E-01
ENSMUST00000088523	SAM domain and HD domain, 1 [Source:MGI Symbol;Acc:MGI:1927468]	E9Q0K6		-2.1	6.9E-01	-3.4	5.9E-01	-2.0	5.8E-01	-0.7	9.1E-01
ENSMUST00000091233	ADAMTS-like 2 [Source:MGI Symbol;Acc:MGI:1925044]	A1A5B7	Q7TSK7	7.4	5.0E-05	6.4	2.8E-02	-0.9	7.5E-01	-0.1	9.7E-01
ENSMUST00000088546	fragile X mental retardation syndrome 1 [Source:MGI Symbol;Acc:MGI:95564]	Q6AXB7		-0.4	8.7E-01	0.0	9.9E-01	0.6	8.2E-01	0.2	9.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000088552	myosin, light polypeptide 9, regulatory [Source:MGI Symbol;Acc:MGI:2138915]		Q9CQ19	0.3	7.5E-01	-2.5	3.7E-02	-3.2	2.9E-03	-0.3	7.9E-01
ENSMUST00000091246	folliculin [Source:MGI Symbol;Acc:MGI:2442184]		Q8QZS3	-8.1	1.1E-04	5.9	1.8E-02	-2.2	3.5E-01	-2.1	1.3E-01
ENSMUST00000091259	carrier family 7 (cationic amino acid transporter, y+ system), member 14 [Source:MGI Symbol;Acc:MGI:304		Q8BXR1	6.4	2.9E-06	8.6	2.8E-05	-0.6	6.0E-01	0.2	7.4E-01
ENSMUST00000091263	quiescin Q6 sulfhydryl oxidase 2 [Source:MGI Symbol;Acc:MGI:2387194]		Q3TMX7	2.6	7.0E-04	-5.2	1.3E-03	-1.3	3.7E-02	-1.1	4.2E-01
ENSMUST00000091268	calmodulin regulated spectrin-associated protein 1 [Source:MGI Symbol;Acc:MGI:3036242]		A2AHC3	7.7	1.1E-02	2.9	3.2E-01	-0.9	7.4E-01	2.3	3.1E-01
ENSMUST00000091269	Erbb2 interacting protein [Source:MGI Symbol;Acc:MGI:1890169]		Q80TH2	-6.3	1.9E-03	-2.3	5.4E-03	1.3	5.5E-03	-0.7	3.5E-01
ENSMUST00000091288	prion protein [Source:MGI Symbol;Acc:MGI:97769]	Q4FJQ7	P04925	-5.2	6.0E-04	-3.1	7.0E-02	1.2	1.7E-01	1.8	2.6E-01
ENSMUST00000091299	cyclin-dependent kinase 7 [Source:MGI Symbol;Acc:MGI:102956]	Q3THG5	Q03147	0.9	2.7E-02	4.4	2.1E-02	-0.7	6.7E-01	1.4	2.2E-01
ENSMUST00000091309	ceruloplasmin [Source:MGI Symbol;Acc:MGI:88476]		Q61147	6.3	8.1E-05	5.4	1.7E-02	-0.7	7.4E-01	1.0	3.9E-01
ENSMUST00000088644	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]		P83741	1.7	4.9E-01	1.0	7.5E-01	-2.2	4.2E-01	-1.5	5.5E-01
ENSMUST00000091314	phosphodiesterase 7A [Source:MGI Symbol;Acc:MGI:1202402]		P70453	-2.6	2.8E-02	-6.3	1.5E-02	1.2	1.2E-01	0.2	9.2E-01
ENSMUST00000088649	copine VIII [Source:MGI Symbol;Acc:MGI:1914121]	Q9CYR4		-2.5	2.0E-01	-0.3	9.2E-01	2.7	2.4E-01	0.5	8.2E-01
ENSMUST00000091318	ring finger protein 224 [Source:MGI Symbol;Acc:MGI:2685603]		Q3UIW8	7.0	1.8E-04	-3.4	4.0E-03	-0.4	4.2E-01	0.2	8.3E-01
ENSMUST00000091319	signal-regulatory protein beta 1B [Source:MGI Symbol;Acc:MGI:3779828]	Q3U390		-9.4	2.2E-05	7.7	1.1E-04	-0.7	6.1E-01	0.1	8.7E-01
ENSMUST00000088658	myeloblastosis oncogene-like 1 [Source:MGI Symbol;Acc:MGI:99925]			3.6	4.8E-02	3.1	1.2E-01	-1.6	4.0E-01	-1.1	4.2E-01
ENSMUST00000091328	mitogen-activated protein kinase 3 [Source:MGI Symbol;Acc:MGI:1346859]	D3Z6D8		-3.8	5.8E-03	6.3	7.4E-05	-2.0	8.3E-02	0.1	8.4E-01
ENSMUST00000091348	euchromatic histone methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1924933]	Z4YJZ7		-3.6	1.8E-02	6.1	6.2E-04	-0.4	7.3E-01	-0.3	6.6E-01
ENSMUST00000091354	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]		Q62393	-10.4	2.4E-05	5.3	1.3E-02	-0.6	7.5E-01	-0.3	8.1E-01
ENSMUST00000088716	d, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 [Source:MGI Symbol;Acc		P97496	0.7	8.9E-02	0.9	1.1E-01	0.1	7.4E-01	0.0	9.4E-01
ENSMUST00000091355	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]		Q62393	-9.3	2.5E-05	-4.2	3.8E-02	1.3	1.1E-01	2.0	2.5E-01
ENSMUST00000091356	ankyrin repeat, family A (RFXANK-like), 2 [Source:MGI Symbol;Acc:MGI:1915808]	Q8C4M9		5.9	5.4E-03	-6.5	2.7E-05	-0.3	3.8E-01	-1.6	9.7E-02
ENSMUST00000091358	ubiquitin specific peptidase 1 [Source:MGI Symbol;Acc:MGI:2385198]		Q8BJQ2	-5.0	2.0E-03	-6.7	5.3E-05	0.8	4.8E-02	-2.6	5.1E-02
ENSMUST00000088744	a disintegrin and metalloppeptidase domain 22 [Source:MGI Symbol;Acc:MGI:1340046]		Q9R1V6	4.3	1.5E-01	1.9	6.1E-01	-0.2	9.6E-01	2.2	4.4E-01
ENSMUST00000088761	a disintegrin and metalloppeptidase domain 22 [Source:MGI Symbol;Acc:MGI:1340046]	D6QSS8	Q9R1V6	2.1	9.7E-02	7.6	5.8E-05	-0.6	6.4E-01	-6.1	5.2E-05
ENSMUST00000088778	CAAX box 1B [Source:MGI Symbol;Acc:MGI:3576504]	Q9D1F0		0.2	8.9E-01	-0.3	8.5E-01	0.4	7.4E-01	0.9	5.8E-01
ENSMUST00000088779	CAAX box 1A [Source:MGI Symbol;Acc:MGI:1913408]	Q9D1F0		0.2	8.2E-01	1.8	1.1E-01	-0.8	4.0E-01	-2.3	4.0E-02
ENSMUST00000088785	zinc finger protein 566 [Source:MGI Symbol;Acc:MGI:1919806]	Q8VCI1		1.0	1.5E-01	0.0	1.0E+00	-0.4	5.3E-01	0.6	4.1E-01
ENSMUST00000091374	small ubiquitin-like modifier 1 [Source:MGI Symbol;Acc:MGI:1197010]		P63166	-5.6	1.5E-05	1.3	5.5E-01	3.6	5.3E-02	-2.2	3.3E-01
ENSMUST00000088788	protein phosphatase 6, regulatory subunit 2 [Source:MGI Symbol;Acc:MGI:1918724]	G3X9K4		-1.0	5.1E-02	-0.2	7.2E-01	0.5	2.2E-01	-0.3	6.5E-01
ENSMUST00000091377	RIKEN cDNA 1700029F12 gene [Source:MGI Symbol;Acc:MGI:1913729]	Q9CRB4		6.4	9.5E-05	7.7	3.0E-04	1.8	1.9E-01	0.1	8.9E-01
ENSMUST00000091391	kielin/chordin-like protein [Source:MGI Symbol;Acc:MGI:2141640]	E9QNB3		7.7	5.3E-04	7.5	1.5E-04	-0.7	6.1E-01	0.1	8.4E-01
ENSMUST00000091403	arylsulfatase B [Source:MGI Symbol;Acc:MGI:88075]			-1.3	1.6E-03	-1.4	7.4E-02	0.4	4.2E-01	-0.4	5.4E-01
ENSMUST00000091418	DnaJ (Hsp40) homolog, subfamily C, member 1 [Source:MGI Symbol;Acc:MGI:103268]		Q61712	3.4	2.6E-05	3.4	8.2E-03	-1.0	3.1E-01	0.3	6.9E-01
ENSMUST00000091420	SKI/DACH domain containing 1 [Source:MGI Symbol;Acc:MGI:1919918]	G3X9M2		7.7	1.5E-04	1.6	5.7E-02	-3.0	2.3E-03	-0.1	9.0E-01
ENSMUST00000091436	cubilin (intrinsic factor-cobalamin receptor) [Source:MGI Symbol;Acc:MGI:1931256]		Q9JLB4	4.6	6.5E-06	-7.3	6.8E-03	-0.3	6.8E-01	-1.0	6.8E-01
ENSMUST00000088874	high mobility group box 3 [Source:MGI Symbol;Acc:MGI:1098219]	Q544R9	O54879	4.0	8.4E-02	7.2	4.4E-02	3.0	3.2E-01	-0.2	9.1E-01
ENSMUST00000091440	zinc finger and SCAN domain containing 4F [Source:MGI Symbol;Acc:MGI:3708485]		Q3URS2	5.7	4.4E-04	-2.1	4.4E-02	0.8	1.7E-01	0.0	9.9E-01
ENSMUST00000088898	zinc finger protein 280C [Source:MGI Symbol;Acc:MGI:2387585]		Q6P3Y5	-3.7	7.6E-02	-2.1	4.3E-01	1.1	5.0E-01	-0.4	8.8E-01
ENSMUST00000091458	nuclear receptor subfamily 2, group F, member 1 [Source:MGI Symbol;Acc:MGI:1352451]	Q32NY6		6.1	1.2E-04	5.8	6.4E-05	-0.7	4.1E-01	-0.4	4.7E-01
ENSMUST00000091459	family with sequence similarity 172, member A [Source:MGI Symbol;Acc:MGI:1915925]	E9QMA2		-2.9	1.4E-03	4.5	2.7E-05	-0.2	6.8E-01	0.2	5.8E-01
ENSMUST00000091477	m large conductance calcium-activated channel, subfamily M, beta member 4 [Source:MGI Symbol;Acc:MGI:1	F6TD25		7.6	2.4E-04	7.3	6.2E-05	-0.5	6.4E-01	-0.5	3.4E-01
ENSMUST00000091493	zinc finger, DHHC domain containing 11 [Source:MGI Symbol;Acc:MGI:1918414]		Q14AK4	6.8	4.3E-05	-3.3	3.4E-03	-1.2	4.0E-02	-0.7	4.7E-01
ENSMUST00000091514	steroid 5 alpha-reductase 1 [Source:MGI Symbol;Acc:MGI:98400]			4.0	4.6E-04	2.9	3.2E-01	-0.8	7.4E-01	2.3	3.1E-01
ENSMUST00000088931	GRAM domain containing 4 [Source:MGI Symbol;Acc:MGI:2676308]		Q8CB44	-1.0	2.7E-01	-3.4	5.9E-02	0.8	3.4E-01	3.3	5.9E-02
ENSMUST00000091526	regulator of sex-limitation candidate 18 [Source:MGI Symbol;Acc:MGI:5433745]	Q7M6X5		6.3	1.1E-04	-0.2	9.0E-01	2.4	5.1E-02	-2.1	2.2E-01
ENSMUST00000088940	transmembrane protein 181A [Source:MGI Symbol;Acc:MGI:1924356]	Q3U3W2		-0.7	1.0E-01	0.3	5.3E-01	-0.1	8.3E-01	-1.1	4.0E-02
ENSMUST00000091554	contactin associated protein-like 3 [Source:MGI Symbol;Acc:MGI:3588199]	E9PY62		6.7	4.7E-05	7.0	6.7E-05	-0.5	6.2E-01	-0.6	3.3E-01
ENSMUST00000091565	zinc finger protein 652 [Source:MGI Symbol;Acc:MGI:2442221]		Q5DU09	-3.2	9.3E-03	6.6	1.5E-04	-0.6	6.1E-01	-0.5	4.0E-01
ENSMUST00000091609	clathrin, light polypeptide (Lcb) [Source:MGI Symbol;Acc:MGI:1921575]	Q3TWZ9	Q6IRU5	1.5	2.5E-02	7.9	1.1E-05	0.1	9.0E-01	0.2	7.4E-01
ENSMUST00000088970	ucine-rich repeats and calponin homology (CH) domain containing 1 [Source:MGI Symbol;Acc:MGI:244339(		P62046	-0.8	1.1E-01	0.3	5.5E-01	0.7	1.3E-01	-0.4	4.2E-01
ENSMUST00000091623	WNK lysine deficient protein kinase 2 [Source:MGI Symbol;Acc:MGI:1922857]	E9QM73		8.1	2.2E-02	5.6	2.8E-03	1.8	1.9E-01	0.7	3.8E-01
ENSMUST00000089011	stannin [Source:MGI Symbol;Acc:MGI:1276549]	Q5M8P0	P61807	1.2	4.3E-02	-0.1	8.4E-01	-1.6	7.2E-03	-0.3	6.6E-01
ENSMUST00000091628	ataxin 1 [Source:MGI Symbol;Acc:MGI:104783]		P54254	-7.3	6.7E-06	7.1	1.3E-04	-0.6	6.3E-01	-1.1	9.9E-02
ENSMUST00000089017	fibronectin type III domain containing 3A [Source:MGI Symbol;Acc:MGI:1196463]		Q8BX90	-1.0	5.6E-02	-0.5	4.3E-01	1.0	4.5E-02	0.5	4.1E-01
ENSMUST00000089018	TatD DNase domain containing 2 [Source:MGI Symbol;Acc:MGI:3576210]	F8VQE6		-1.4	1.6E-01	-0.1	9.2E-01	-0.1	9.3E-01	-1.4	2.4E-01
ENSMUST00000089022	interleukin-1 receptor-associated kinase 2 [Source:MGI Symbol;Acc:MGI:2429603]		Q8CFA1	0.5	7.0E-01	2.9	8.9E-02	1.1	4.4E-01	-1.3	3.5E-01
ENSMUST00000091636	leucine rich repeat transmembrane neuronal 2 [Source:MGI Symbol;Acc:MGI:2389174]		Q8BGA3	7.2	5.3E-05	-7.1	2.0E-04	-0.9	6.7E-02	-0.7	6.1E-01
ENSMUST00000091641	small nuclear ribonucleoprotein 48 (U11/U12) [Source:MGI Symbol;Acc:MGI:1915047]		Q9D361	-3.5	2.6E-03	-1.6	5.5E-02	0.8	8.8E-02	-1.0	2.2E-01
ENSMUST00000091648	G protein-coupled receptor 31, D17Leh66b region [Source:MGI Symbol;Acc:MGI:1354372]		F8VQN3	8.8	6.7E-06	-2.6	1.5E-02	0.0	9.6E-01	-2.7	2.3E-02
ENSMUST00000089049	nudix (nucleoside diphosphate linked moiety X)-type motif 18 [Source:MGI Symbol;Acc:MGI:2385853]		Q3U2V3	-0.9	1.7E-01	-0.6	5.0E-01	0.9	1.6E-01	0.6	4.9E-01
ENSMUST00000091672	dual specificity phosphatase 22 [Source:MGI Symbol;Acc:MGI:1915926]		Q99N11	-3.5	2.7E-03	5.0	1.1E-01	-0.7	8.2E-01	0.7	7.1E-01
ENSMUST00000091674	CDK5 regulatory subunit associated protein 1-like 1 [Source:MGI Symbol;Acc:MGI:1921765]		Q91WE6	6.4	1.3E-04	2.1	2.5E-03	0.3	5.0E-01	-0.6	1.8E-01
ENSMUST00000091694	family with sequence similarity 65, member B [Source:MGI Symbol;Acc:MGI:2444879]		Q80U16	-7.3	2.7E-04	-6.8	2.5E-04	0.9	6.0E-02	-1.1	4.3E-01
ENSMUST00000089084				1.9	3.3E-01	0.4	8.8E-01	-1.3	5.1E-01	0.2	9.0E-01
ENSMUST00000091703	histone cluster 1, H3b [Source:MGI Symbol;Acc:MGI:2448319]	B9EI85	P84228	5.8	2.7E-04	6.5	1.0E-02	-0.8	7.2E-01	-1.4	2.7E-01
ENSMUST00000091708	histone cluster 1, H2al [Source:MGI Symbol;Acc:MGI:3646032]	F8WIX8		-3.6	1.2E-02	7.0	1.1E-04	-0.6	6.2E-01	-1.3	5.7E-02
ENSMUST00000091709	histone cluster 1, H2bn [Source:MGI Symbol;Acc:MGI:2448407]		P10853	6.1	5.2E-03	5.5	4.7E-03	-0.7	6.8E-01	0.9	3.2E-01
ENSMUST00000091741	histone cluster 1, H2ag [Source:MGI Symbol;Acc:MGI:2448293]	B2RVF0	P22752	3.9	1.8E-02	-8.9	9.0E-05	0.4	3.4E-01	-0.9	5.5E-01
ENSMUST00000091789	myelin basic protein [Source:MGI Symbol;Acc:MGI:96925]	Q5D096	P04370	-2.1	2.4E-03	-2.3	8.1E-02	0.4	5.9E-01	-1.3	3.1E-01
ENSMUST00000091790	ATPase, class II, type 9B [Source:MGI Symbol;Acc:MGI:1354757]	D3YV00		-1.5	1.2E-02	4.5	6.6E-04	-2.4	4.1E-02	0.0	9.6E-01
ENSMUST00000089140	NSFL1 (p97) cofactor (p47) [Source:MGI Symbol;Acc:MGI:3042273]	Q3UVN5	Q9CZ44	1.4	3.9E-01	-4.0	8.9E-02	-3.3	3.3E-02	2.0	3.5E-01
ENSMUST00000089157	centromere protein M [Source:MGI Symbol;Acc:MGI:1913820]		Q9CQA0	1.0	5.1E-01	3.3	1.3E-01	1.3	5.0E-01	-1.0	4.8E-01
ENSMUST00000091813	solute carrier family 14 (urea transporter), member 1 [Source:MGI Symbol;Acc:MGI:1351654]		Q8VHL0	4.9	4.0E-03	3.7	4.8E-02	-1.2	4.5E-01	1.2	3.5E-01
ENSMUST00000091818	ryanodine receptor 3 [Source:MGI Symbol;Acc:MGI:99684]	E9PW34		7.4	2.1E-04	-2.7	1.9E-03	1.3	5.2E-03	0.4	5.6E-01
ENSMUST00000089174	coiled-coil domain containing 134 [Source:MGI Symbol;Acc:MGI:1923707]		Q8C7V8	-0.1	9.0E-01	1.5	5.4E-02	0.7	2.5E-01	-0.9	1.6E-01
ENSMUST00000091829	La ribonucleoprotein domain family, member 4B [Source:MGI Symbol;Acc:MGI:106330]		Q6A0A2	-3.8	2.3E-05	7.4	1.1E-04	-0.5	6.8E-01	-0.4	4.6E-01
ENSMUST00000089184	potassium inwardly-rectifying channel, subfamily J, member 12 [Source:MGI Symbol;Acc:MGI:108495]		P52187	2.6	9.0E-02	4.7	7.7E-03	-0.6	7.0E-01	-2.7	3.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000091831	SMAD family member 2 [Source:MGI Symbol;Acc:MGI:108051]		Q62432	-5.5	9.4E-04	3.6	2.1E-03	0.3	7.0E-01	-0.6	3.8E-01
ENSMUST00000091852	mex3 homolog C (C. elegans) [Source:MGI Symbol;Acc:MGI:2652843]		Q05A36	-3.7	1.6E-03	-0.6	3.8E-01	0.5	3.2E-01	-0.4	5.4E-01
ENSMUST00000091853	neuroepithelial cell transforming gene 1 [Source:MGI Symbol;Acc:MGI:1927138]		Q9Z206	-2.6	1.8E-02	-2.3	3.5E-02	0.9	1.2E-01	-3.4	1.9E-02
ENSMUST00000089217	ubiquitin-like modifier activating enzyme 1 [Source:MGI Symbol;Acc:MGI:98890]	B9EHN0	Q02053	4.5	8.5E-02	3.3	3.2E-01	0.2	9.5E-01	1.4	5.6E-01
ENSMUST00000091879	zinc finger protein 942 [Source:MGI Symbol;Acc:MGI:1920483]	B8JJA7		-2.9	2.4E-03	5.0	1.1E-02	-0.6	7.1E-01	1.5	1.7E-01
ENSMUST00000091903	SH3-domain binding protein 5 (BTK-associated) [Source:MGI Symbol;Acc:MGI:1344391]		Q9Z131	-6.3	1.4E-04	-0.6	4.0E-01	1.0	4.9E-02	-0.5	4.6E-01
ENSMUST00000091920	RNA binding motif protein 27 [Source:MGI Symbol;Acc:MGI:2147194]		Q5SFM8	-2.3	2.4E-03	7.6	6.0E-05	-0.6	6.2E-01	-0.1	9.0E-01
ENSMUST00000089245	SHQ1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919421]		Q7TMX5	4.5	3.7E-02	3.1	7.0E-02	-3.7	6.5E-02	-2.2	1.3E-01
ENSMUST00000091927	potassium channel tetramerisation domain containing 16 [Source:MGI Symbol;Acc:MGI:1914659]		Q5DTY9	6.4	8.1E-05	-7.9	1.8E-04	1.4	5.6E-03	0.5	7.1E-01
ENSMUST00000091996	olfactory receptor 9 [Source:MGI Symbol;Acc:MGI:107600]	Q14A42	Q60885	6.6	1.4E-04	8.1	1.0E-04	0.0	9.9E-01	-0.6	3.1E-01
ENSMUST00000092003	additional sex combs like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1922552]	D3Z112		5.5	1.3E-05	6.4	1.5E-04	-0.5	6.3E-01	-0.5	4.4E-01
ENSMUST00000092015	nucleolar protein 4 [Source:MGI Symbol;Acc:MGI:2441684]	F6XSA1		5.7	6.7E-04	-3.6	1.2E-03	0.1	8.5E-01	-1.1	2.1E-01
ENSMUST00000092033	RNA binding motif, single stranded interacting protein 2 [Source:MGI Symbol;Acc:MGI:1861776]		Q8VC70	-1.5	1.2E-02	-1.9	2.5E-02	0.2	6.0E-01	-0.4	5.8E-01
ENSMUST00000092041	synovial sarcoma translocation, Chromosome 18 [Source:MGI Symbol;Acc:MGI:107708]	Q8BJJ6		-4.2	2.9E-03	5.9	1.8E-03	-0.7	6.2E-01	-0.4	6.6E-01
ENSMUST00000092048	nascent polypeptide-associated complex alpha polypeptide [Source:MGI Symbol;Acc:MGI:106095]		P70670	7.7	1.3E-04	6.5	6.8E-05	-1.5	1.8E-01	-0.3	5.8E-01
ENSMUST00000092058	cDNA sequence BC089597 [Source:MGI Symbol;Acc:MGI:3583955]	Q8K3M1		6.9	1.4E-04	-1.4	4.2E-02	1.0	2.4E-02	-1.0	1.4E-01
ENSMUST00000092070	laminin, alpha 3 [Source:MGI Symbol;Acc:MGI:99909]		Q61789	9.6	2.2E-06	-5.2	9.9E-02	2.5	2.0E-01	-0.7	8.4E-01
ENSMUST00000092074	signal transducer and activator of transcription 6 [Source:MGI Symbol;Acc:MGI:103034]		P52633	-4.8	5.7E-06	5.1	4.0E-02	-3.8	1.5E-01	-1.2	4.5E-01
ENSMUST00000092075	transmembrane protein 241 [Source:MGI Symbol;Acc:MGI:2442435]		Q3UME2	2.7	2.5E-03	-2.6	3.6E-02	0.3	6.9E-01	-1.1	3.4E-01
ENSMUST00000092089	lticiliate differentiation and DNA synthesis associated cell cycle protein [Source:MGI Symbol;Acc:MGI:36488		Q3UZ45	8.3	6.3E-06	4.6	3.4E-05	-4.3	4.3E-04	0.2	6.0E-01
ENSMUST00000092096	ubiquitin specific peptidase 14 [Source:MGI Symbol;Acc:MGI:1928898]		Q9JMA1	-2.9	7.2E-04	8.6	1.6E-02	-0.9	7.8E-01	-1.2	4.7E-01
ENSMUST00000092112	WW domain containing adaptor with coiled-coil [Source:MGI Symbol;Acc:MGI:2387357]		Q924H7	-6.7	7.4E-03	-0.8	4.6E-01	0.4	5.7E-01	-1.1	3.5E-01
ENSMUST00000092123	enhancer of polycomb homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1278321]		Q8C0I4	-2.3	2.4E-03	-5.9	1.4E-02	0.7	3.6E-01	0.2	9.3E-01
ENSMUST00000092143	methionine sulfoxide reductase B3 [Source:MGI Symbol;Acc:MGI:2443538]			4.8	5.0E-05	-7.3	5.3E-05	-3.5	5.4E-05	-1.7	1.6E-01
ENSMUST00000089378	SH3-domain binding protein 1 [Source:MGI Symbol;Acc:MGI:104603]		P60487	1.9	3.9E-02	3.2	8.4E-03	0.5	5.6E-01	-0.8	3.2E-01
ENSMUST00000089398	interleukin 2 receptor, beta chain [Source:MGI Symbol;Acc:MGI:96550]		P16297	0.7	3.8E-01	0.2	8.8E-01	-0.5	5.5E-01	0.1	9.1E-01
ENSMUST00000092155	collagen, type XI, alpha 1 [Source:MGI Symbol;Acc:MGI:88446]		Q61245	6.4	7.9E-05	8.0	1.2E-02	0.6	8.2E-01	-1.9	2.0E-01
ENSMUST00000089414	potassium channel tetramerisation domain containing 17 [Source:MGI Symbol;Acc:MGI:1920094]	E0CYQ0		-1.9	2.7E-01	0.2	8.9E-01	0.0	9.7E-01	-2.2	2.6E-01
ENSMUST00000092162	lysozyme 1 [Source:MGI Symbol;Acc:MGI:96902]	A0A077S9N1	P17897	-1.3	2.4E-02	5.9	6.6E-04	-0.6	6.6E-01	-0.5	5.0E-01
ENSMUST00000092163	lysozyme 2 [Source:MGI Symbol;Acc:MGI:96897]	A0A077S2U6	P08905	-9.9	9.7E-09	-8.0	1.2E-03	-0.9	2.2E-01	-2.1	3.0E-01
ENSMUST00000089449	monoglyceride lipase [Source:MGI Symbol;Acc:MGI:1346042]		O35678	0.8	6.7E-01	1.5	5.6E-01	0.4	8.0E-01	-0.3	9.1E-01
ENSMUST00000092167	protein tyrosine phosphatase, receptor type, B [Source:MGI Symbol;Acc:MGI:97809]		B2RU80	8.1	1.7E-05	5.6	5.0E-03	0.1	9.3E-01	-1.5	1.3E-01
ENSMUST00000092170	transmembrane protein 19 [Source:MGI Symbol;Acc:MGI:1914476]		Q91W52	-3.0	9.5E-04	-1.6	1.1E-01	1.1	1.2E-01	-0.2	8.2E-01
ENSMUST00000092175	potassium voltage gated channel, Shaw-related subfamily, member 2 [Source:MGI Symbol;Acc:MGI:96668]	E9QLW0		8.1	1.1E-05	2.1	1.2E-02	-3.9	9.8E-04	-0.7	2.6E-01
ENSMUST00000092215	coiled-coil domain containing 38 [Source:MGI Symbol;Acc:MGI:2444738]		Q8CDN8	4.2	2.4E-02	9.2	4.2E-04	-0.9	6.4E-01	-0.7	3.3E-01
ENSMUST00000089473	zinc finger, DHHC domain containing 20 [Source:MGI Symbol;Acc:MGI:1923215]		Q5Y5T1	-0.5	1.8E-01	-0.8	1.5E-01	0.1	8.3E-01	0.3	5.2E-01
ENSMUST00000089485	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2 [Source:MGI Symbol;Acc:MGI:2444121]	F6VCI2		3.3	4.2E-02	6.0	2.2E-03	-0.5	7.5E-01	-3.2	1.1E-02
ENSMUST00000092227	SCY1-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1289172]	G5E8J9		-7.2	2.0E-04	5.5	3.4E-03	-0.4	7.8E-01	-1.6	9.4E-02
ENSMUST00000092266	thymine DNA glycosylase [Source:MGI Symbol;Acc:MGI:108247]		P56581	-3.3	1.7E-02	-3.5	1.1E-04	0.1	8.4E-01	0.7	2.6E-01
ENSMUST00000092279	centrosomal protein 170B [Source:MGI Symbol;Acc:MGI:2145043]		Q80U49	4.6	3.5E-03	-2.6	1.0E-02	1.1	4.9E-02	0.0	9.9E-01
ENSMUST00000092298	zinc finger protein 750 [Source:MGI Symbol;Acc:MGI:2442210]		Q8BH05	4.7	1.7E-03	2.0	1.8E-02	0.4	5.2E-01	-0.1	8.6E-01
ENSMUST00000092305	DAZ associated protein 1 [Source:MGI Symbol;Acc:MGI:1917498]		Q9JII5	-2.7	2.6E-03	6.6	5.1E-06	-2.6	1.5E-02	-0.6	1.5E-01
ENSMUST00000092366	thrombospondin type laminin G domain and EAR repeats [Source:MGI Symbol;Acc:MGI:2671932]		J3S6Y1	6.3	1.1E-04	-2.7	4.5E-03	-0.1	8.8E-01	-0.4	6.3E-01
ENSMUST00000092368	thrombospondin type laminin G domain and EAR repeats [Source:MGI Symbol;Acc:MGI:2671932]			6.9	2.2E-03	4.3	2.5E-03	-2.5	6.4E-02	-0.6	4.3E-01
ENSMUST00000092369	keratin associated protein 10-4 [Source:MGI Symbol;Acc:MGI:1925013]	Q08EG8		8.4	2.1E-05	-6.3	3.8E-03	-1.1	1.1E-01	0.3	8.4E-01
ENSMUST00000092370	keratin associated protein 12-1 [Source:MGI Symbol;Acc:MGI:1328315]		Q9Z287	6.8	9.5E-05	-2.7	2.5E-03	0.3	4.4E-01	-0.2	7.5E-01
ENSMUST00000092373	ectonucleotide pyrophosphatase/phosphodiesterase 7 [Source:MGI Symbol;Acc:MGI:3027917]	D3Z6V6		7.2	1.2E-04	5.2	1.6E-02	-0.7	7.1E-01	0.4	7.3E-01
ENSMUST00000092378	calcium activated nucleotidase 1 [Source:MGI Symbol;Acc:MGI:1923275]		Q8VCF1	-6.8	6.1E-05	5.0	2.8E-03	-1.0	4.4E-01	0.1	9.2E-01
ENSMUST00000092394	predicted gene 11733 [Source:MGI Symbol;Acc:MGI:3650737]	Q8BQP1		6.7	2.1E-04	6.6	2.3E-03	-0.8	6.5E-01	0.9	3.5E-01
ENSMUST00000092404	serine/arginine-rich splicing factor 2 [Source:MGI Symbol;Acc:MGI:98284]		Q62093	-4.4	6.0E-04	2.9	3.3E-01	-0.9	7.4E-01	2.4	3.0E-01
ENSMUST00000092406	RIKEN cDNA 2610028H24 gene [Source:MGI Symbol;Acc:MGI:1924214]	G5E8K1		6.8	1.9E-04	-4.9	6.3E-02	1.4	1.4E-01	-0.2	9.4E-01
ENSMUST00000092426	coiled-coil domain containing 153 [Source:MGI Symbol;Acc:MGI:2448587]		P0C7Q1	5.4	2.6E-05	5.4	8.1E-04	-0.2	8.5E-01	-1.2	9.0E-02
ENSMUST00000092464	cDNA sequence AF251705 [Source:MGI Symbol;Acc:MGI:2153249]		Q7TSN2	-8.0	2.5E-04	4.1	5.7E-02	-0.1	9.4E-01	1.1	4.1E-01
ENSMUST00000092469	dynein, axonemal, intermediate chain 2 [Source:MGI Symbol;Acc:MGI:2685574]		A2AC93	5.8	8.3E-04	-3.8	1.7E-01	0.1	9.4E-01	-1.6	5.6E-01
ENSMUST00000092486	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 14 [Source:MGI Symbol;Acc:M	B2RXX5		6.6	7.8E-05	-3.4	9.3E-03	-0.5	4.0E-01	-0.5	6.3E-01
ENSMUST00000089622	tet methylcytosine dioxygenase 3 [Source:MGI Symbol;Acc:MGI:2446229]		Q8BG87	0.1	8.7E-01	0.8	1.6E-01	0.6	1.6E-01	-0.1	8.0E-01
ENSMUST00000092491	vomeronasal 2, receptor 111 [Source:MGI Symbol;Acc:MGI:3647034]	K7N674		6.1	1.3E-03	-7.6	1.3E-04	-1.3	8.4E-03	0.4	7.5E-01
ENSMUST00000089634	BCL2-like 11 (apoptosis facilitator) [Source:MGI Symbol;Acc:MGI:1197519]	Q6PEB3		-0.3	7.1E-01	1.1	3.6E-01	1.1	2.6E-01	-0.3	7.4E-01
ENSMUST00000092498	sphingosine phosphate lyase 1 [Source:MGI Symbol;Acc:MGI:1261415]		Q8R0X7	-4.2	1.6E-04	5.0	3.8E-03	-0.5	7.2E-01	-2.3	3.8E-02
ENSMUST00000092508	mitochondrial calcium uptake 1 [Source:MGI Symbol;Acc:MGI:2384909]		Q8VCX5	-8.9	5.7E-06	-4.2	1.5E-02	1.5	3.5E-02	-0.7	6.4E-01
ENSMUST00000092512	-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide [Source:MGI Symbol;Acc:	E9Q7B0		-7.3	1.3E-04	-3.4	2.2E-02	1.3	5.7E-02	-1.4	3.6E-01
ENSMUST00000089654	cDNA sequence BC024139 [Source:MGI Symbol;Acc:MGI:2442591]	E9PXU3		2.1	1.1E-01	7.8	5.5E-05	-0.5	6.7E-01	-6.3	4.6E-05
ENSMUST00000089655	kalirin, RhoGEF kinase [Source:MGI Symbol;Acc:MGI:2685385]		A2CG49	3.6	1.1E-01	6.8	1.1E-02	-0.4	8.5E-01	-3.6	2.8E-02
ENSMUST00000092528	predicted gene 10324 [Source:MGI Symbol;Acc:MGI:3642406]	L7N208		7.9	1.2E-05	5.7	3.2E-03	-0.6	6.9E-01	0.7	4.4E-01
ENSMUST00000089673	astacin-like metalloendopeptidase (M12 family) [Source:MGI Symbol;Acc:MGI:3046414]		Q6HA09	6.4	3.6E-02	5.3	9.8E-02	-0.8	7.9E-01	0.3	8.9E-01
ENSMUST00000092537	tousled-like kinase 2 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1346023]		O55047	-3.9	4.9E-03	-3.3	8.9E-03	0.3	6.2E-01	-1.0	3.6E-01
ENSMUST00000092551	low density lipoprotein receptor-related protein 2 [Source:MGI Symbol;Acc:MGI:95794]	Q3V346		6.6	8.2E-06	5.3	1.0E-01	2.2	4.3E-01	3.0	1.5E-01
ENSMUST00000092566	olute carrier family 16 (monocarboxylic acid transporters), member 10 [Source:MGI Symbol;Acc:MGI:191972		Q3U9N9	-2.6	1.5E-04	0.4	4.8E-01	-4.7	2.8E-05	-0.4	4.7E-01
ENSMUST00000089726	RIKEN cDNA D430041D05 gene [Source:MGI Symbol;Acc:MGI:2181743]	D3YZ21		5.4	6.9E-02	7.2	1.6E-02	-0.6	8.4E-01	-2.3	1.8E-01
ENSMUST00000092567	gap junction protein, gamma 1 [Source:MGI Symbol;Acc:MGI:95718]		P28229	6.2	3.5E-03	0.5	5.9E-01	-0.6	4.6E-01	1.5	1.0E-01
ENSMUST00000092584	myristoylated alanine rich protein kinase C substrate [Source:MGI Symbol;Acc:MGI:96907]		P26645	-5.8	2.5E-04	-1.8	1.9E-02	0.2	6.1E-01	-0.4	5.8E-01
ENSMUST00000092595	maestro heat-like repeat family member 1 [Source:MGI Symbol;Acc:MGI:2442558]	D3Z624		3.5	5.5E-04	-7.6	1.1E-04	-0.9	4.4E-02	-0.8	5.4E-01
ENSMUST00000092602	Na+/K+ transporting ATPase interacting 2 [Source:MGI Symbol;Acc:MGI:1923447]	F7C7C4		5.2	1.8E-02	-2.2	8.5E-02	1.0	1.6E-01	-2.8	9.4E-02
ENSMUST00000092618	ancient ubiquitous protein 1 [Source:MGI Symbol;Acc:MGI:107789]	Q3U3K9		-4.2	3.1E-04	5.9	8.5E-04	-0.7	6.2E-01	0.4	6.0E-01
ENSMUST00000089775	transmembrane protein 44 [Source:MGI Symbol;Acc:MGI:1924489]	F6SF18		1.6	1.4E-01	3.8	6.2E-04	-2.3	2.1E-02	-4.5	4.0E-04
ENSMUST00000089776	centrosomal protein 152 [Source:MGI Symbol;Acc:MGI:2139083]		A2AUM9	0.9	5.6E-02	0.9	1.1E-01	0.3	5.3E-01	0.2	6.9E-01
ENSMUST00000089785				-4.4	1.2E-01	-6.9	5.9E-02	-3.0	4.5E-02	-0.5	8.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000092623	R-spondin 3 [Source:MGI Symbol;Acc:MGI:1920030]		Q2TJ95	6.6	8.5E-05	6.4	9.0E-04	-0.5	7.4E-01	-0.6	4.1E-01
ENSMUST00000092627	RIKEN cDNA 9330159F19 gene [Source:MGI Symbol;Acc:MGI:3036239]	D3Z623		8.5	1.1E-05	-4.4	5.6E-03	-2.1	8.7E-03	-0.3	8.2E-01
ENSMUST00000092629	SOGA family member 3 [Source:MGI Symbol;Acc:MGI:1914662]		Q6NZL0	8.7	1.4E-05	4.6	1.3E-04	0.6	4.0E-01	0.3	6.1E-01
ENSMUST00000092639	laminin, alpha 2 [Source:MGI Symbol;Acc:MGI:99912]		Q60675	8.5	4.0E-05	4.7	2.8E-04	-2.8	2.0E-02	-0.3	5.9E-01
ENSMUST00000092640	ST3 beta-galactoside alpha-2,3-sialyltransferase 1 [Source:MGI Symbol;Acc:MGI:98304]	Q544T4	P54751	-1.6	1.2E-02	9.1	1.9E-05	-0.6	6.3E-01	0.0	9.9E-01
ENSMUST00000092645	erythrocyte membrane protein band 4.1 like 2 [Source:MGI Symbol;Acc:MGI:103009]		O70318	-2.1	2.9E-02	4.2	3.8E-04	-3.9	3.4E-03	-0.3	6.1E-01
ENSMUST00000089922				-1.1	1.7E-01	-1.7	2.0E-01	0.8	3.1E-01	1.4	2.6E-01
ENSMUST00000089925	diacylglycerol kinase, gamma [Source:MGI Symbol;Acc:MGI:105060]		Q91WG7	-2.7	5.2E-02	-1.7	2.9E-01	0.5	5.8E-01	-0.5	7.7E-01
ENSMUST00000092654	trace amine-associated receptor 8B [Source:MGI Symbol;Acc:MGI:2685995]		Q5QD06	6.6	1.3E-03	-2.4	6.1E-03	-0.1	8.6E-01	-0.1	8.9E-01
ENSMUST00000092657	trace amine-associated receptor 7D [Source:MGI Symbol;Acc:MGI:3527443]		Q5QD10	6.9	1.1E-04	5.6	6.6E-04	0.1	9.6E-01	0.4	5.5E-01
ENSMUST00000089950	Rab geranylgeranyl transferase, b subunit [Source:MGI Symbol;Acc:MGI:99537]	Q3TVF4		-2.9	3.9E-02	-3.8	3.9E-02	-1.2	2.0E-01	-0.3	8.5E-01
ENSMUST00000092659	trace amine-associated receptor 5 [Source:MGI Symbol;Acc:MGI:2685073]	B2RTA0	Q5QD14	6.1	9.3E-05	-1.1	1.1E-01	1.2	1.7E-02	-0.3	6.1E-01
ENSMUST00000092663	ATPase, H+ transporting, lysosomal V0 subunit A1 [Source:MGI Symbol;Acc:MGI:103286]		Q9Z1G4	-4.1	5.3E-03	-7.4	3.3E-04	-0.7	1.1E-01	-0.8	6.2E-01
ENSMUST00000092671	signal transducer and activator of transcription 3 [Source:MGI Symbol;Acc:MGI:103038]		P42227	-5.1	1.8E-02	-5.2	7.1E-03	0.1	9.0E-01	-1.2	4.8E-01
ENSMUST00000092672	RIKEN cDNA 4930444G20 gene [Source:MGI Symbol;Acc:MGI:2149738]	D3Z741		6.3	5.9E-05	-4.4	2.8E-03	-0.6	3.0E-01	-1.8	1.5E-01
ENSMUST00000090020	oxysterol binding protein-like 7 [Source:MGI Symbol;Acc:MGI:1918490]	A2A716		0.2	8.3E-01	1.8	2.5E-01	1.7	2.0E-01	0.1	9.2E-01
ENSMUST00000092674	Hbs1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1891704]	L7N209		-5.0	1.8E-04	-6.9	1.4E-04	0.4	3.4E-01	-2.6	8.9E-02
ENSMUST00000092678	BCL2-associated transcription factor 1 [Source:MGI Symbol;Acc:MGI:1917580]	F8WI22		-5.0	1.1E-03	4.8	1.3E-03	-4.6	4.4E-03	0.0	9.5E-01
ENSMUST00000092680	RIKEN cDNA 4933406P04 gene [Source:MGI Symbol;Acc:MGI:1921670]	Q9D488		3.1	2.4E-03	6.3	1.1E-03	-0.7	6.6E-01	-0.8	3.2E-01
ENSMUST00000092689	5'-nucleotidase, cytosolic IIIB [Source:MGI Symbol;Acc:MGI:1915356]			6.9	3.1E-03	-4.7	1.3E-03	1.2	1.7E-02	-0.6	6.0E-01
ENSMUST00000092694	predicted gene 11559 [Source:MGI Symbol;Acc:MGI:3652067]	Q9D3H7		7.6	2.5E-05	-6.2	7.4E-05	-0.1	7.1E-01	0.5	6.3E-01
ENSMUST00000090040	LIM domain binding 3 [Source:MGI Symbol;Acc:MGI:1344412]		Q9JKS4	4.7	1.7E-01	5.1	1.9E-01	-0.3	9.5E-01	-0.6	7.9E-01
ENSMUST00000092695	predicted gene 11563 [Source:MGI Symbol;Acc:MGI:3650330]	B1AQ90		6.2	4.1E-03	-2.6	1.3E-01	-0.3	7.4E-01	-2.7	1.7E-01
ENSMUST00000092699	keratin associated protein 3-2 [Source:MGI Symbol;Acc:MGI:1913958]		Q9D638	5.0	3.7E-03	4.6	1.0E-03	-0.4	6.4E-01	0.1	9.3E-01
ENSMUST00000092700	keratin associated protein 3-3 [Source:MGI Symbol;Acc:MGI:1913630]		Q9D638	7.2	5.1E-04	-3.3	6.4E-02	0.0	9.6E-01	-1.8	3.4E-01
ENSMUST00000090052	YEATS domain containing 2 [Source:MGI Symbol;Acc:MGI:2447762]		Q3TUF7	-0.3	8.6E-01	0.7	7.9E-01	2.6	2.1E-01	1.7	3.9E-01
ENSMUST00000090057	syntabulin (syntaxin-interacting) [Source:MGI Symbol;Acc:MGI:2442392]		Q8BHS8	3.9	6.4E-02	1.8	4.7E-01	-0.5	8.2E-01	1.6	4.0E-01
ENSMUST00000092706	cell division cycle 6 [Source:MGI Symbol;Acc:MGI:1345150]		O89033	3.6	6.9E-03	7.1	2.8E-04	-0.7	6.3E-01	-0.9	2.3E-01
ENSMUST00000092720	RIKEN cDNA 5430403G16 gene [Source:MGI Symbol;Acc:MGI:1924450]	D3Z5L4		4.1	6.1E-05	8.9	8.4E-05	-0.8	6.0E-01	-1.4	6.7E-02
ENSMUST00000092730	ubiquitin-conjugating enzyme E2U (putative) [Source:MGI Symbol;Acc:MGI:3588216]	Q3V081		6.7	1.3E-02	-4.2	1.0E-02	-1.8	3.5E-02	-2.4	1.5E-01
ENSMUST00000092750	zinc finger protein 600 [Source:MGI Symbol;Acc:MGI:3705222]	A2A7V0		7.1	3.2E-05	2.4	1.1E-01	-0.6	6.0E-01	5.1	8.2E-04
ENSMUST00000092766	K(lysine) acetyltransferase 7 [Source:MGI Symbol;Acc:MGI:2182799]		Q5SVQ0	-7.6	1.4E-02	-2.6	2.1E-01	3.1	2.3E-02	-0.2	9.4E-01
ENSMUST00000092768	distal-less homeobox 3 [Source:MGI Symbol;Acc:MGI:94903]	Q78ZZ8	Q64205	8.7	6.0E-06	1.4	1.0E-01	-1.4	6.5E-02	-0.1	8.2E-01
ENSMUST00000090147	biotinidase [Source:MGI Symbol;Acc:MGI:1347001]			-1.5	3.6E-02	0.0	9.9E-01	0.6	2.7E-01	-0.9	2.6E-01
ENSMUST00000092788	transmembrane protein 100 [Source:MGI Symbol;Acc:MGI:1915138]		Q9CQG9	6.0	2.5E-04	2.2	3.8E-01	-0.6	7.9E-01	2.4	2.3E-01
ENSMUST00000092800	ring finger protein 43 [Source:MGI Symbol;Acc:MGI:2442609]		Q5NCP0	3.8	1.1E-02	4.1	8.0E-03	-1.8	2.0E-01	0.0	9.8E-01
ENSMUST00000092834	synergin, gamma [Source:MGI Symbol;Acc:MGI:1354742]		Q5SV85	1.8	1.2E-02	8.1	5.3E-04	1.0	5.4E-01	0.7	3.9E-01
ENSMUST00000092836	WAP four-disulfide core domain 17 [Source:MGI Symbol;Acc:MGI:3649773]	Q5SSJ1		-10.7	1.1E-07	7.7	1.3E-02	0.7	8.0E-01	-1.6	3.2E-01
ENSMUST00000092852	transmembrane protein 132E [Source:MGI Symbol;Acc:MGI:2685490]		Q6IEE6	7.4	7.2E-04	6.8	1.1E-04	0.1	9.1E-01	-0.4	4.4E-01
ENSMUST00000092883	predicted gene 10277 [Source:MGI Symbol;Acc:MGI:3641921]	Q6R5C6		9.1	3.4E-06	-1.5	3.1E-01	0.0	9.6E-01	-2.5	1.7E-01
ENSMUST00000092887	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]		Q9JMH9	-3.5	3.3E-02	2.8	7.0E-04	0.4	3.9E-01	0.2	6.5E-01
ENSMUST00000092891	calcium channel, voltage-dependent, gamma subunit 7 [Source:MGI Symbol;Acc:MGI:1932374]	B9EJ14	P62956	6.0	1.8E-04	7.8	2.8E-05	-1.7	1.6E-01	-0.4	4.8E-01
ENSMUST00000092892	ankyrin repeat domain 13b [Source:MGI Symbol;Acc:MGI:2144501]		Q5F259	5.6	2.1E-02	5.4	7.9E-05	-1.3	1.3E-01	0.7	1.8E-01
ENSMUST00000092907	replication protein A1 [Source:MGI Symbol;Acc:MGI:1915525]		Q8VEE4	6.4	9.0E-04	-5.0	2.8E-03	0.0	9.5E-01	-2.7	8.1E-02
ENSMUST00000092931	predicted gene 4952 [Source:MGI Symbol;Acc:MGI:3643569]		Q5FW57	6.0	1.3E-04	8.4	3.6E-06	0.5	5.4E-01	-0.7	9.6E-02
ENSMUST00000092956	AHNAK nucleoprotein (desmoyokin) [Source:MGI Symbol;Acc:MGI:1316648]	E9Q616		-1.4	3.6E-03	-3.9	2.2E-02	-0.7	3.5E-01	-0.8	6.4E-01
ENSMUST00000090212	5'-nucleotidase domain containing 2 [Source:MGI Symbol;Acc:MGI:1917271]	Q91X76		-1.1	1.3E-01	0.0	9.6E-01	0.4	4.8E-01	-0.7	4.0E-01
ENSMUST00000090219	BCL2 modifying factor [Source:MGI Symbol;Acc:MGI:2176433]	A2AV75		-1.3	5.2E-02	0.8	2.7E-01	1.1	6.3E-02	-1.0	1.8E-01
ENSMUST00000092966	dynein light chain Tctex-type 1C [Source:MGI Symbol;Acc:MGI:3807476]		P51807	7.5	1.4E-03	-2.1	5.3E-03	1.4	2.0E-03	-0.2	8.0E-01
ENSMUST00000092984	myosin, heavy polypeptide 10, non-muscle [Source:MGI Symbol;Acc:MGI:1930780]	Q3UH59		10.3	1.2E-05	4.8	4.2E-03	0.1	9.6E-01	-1.1	2.8E-01
ENSMUST00000092990	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:MGI Symbol;Acc:MGI:3603816]		Q8C0N2	-3.7	6.1E-03	-1.1	1.1E-01	0.9	5.8E-02	-0.4	5.5E-01
ENSMUST00000092995	myosin, heavy chain 7B, cardiac muscle, beta [Source:MGI Symbol;Acc:MGI:3710243]		A2AQP0	7.0	6.7E-06	-1.3	5.2E-02	0.8	7.0E-02	0.4	5.3E-01
ENSMUST00000093001	Rho GTPase activating protein 44 [Source:MGI Symbol;Acc:MGI:2144423]		Q5SSM3	6.5	2.5E-04	2.1	1.4E-03	0.0	9.5E-01	-0.1	7.4E-01
ENSMUST00000093002	Rho GTPase activating protein 44 [Source:MGI Symbol;Acc:MGI:2144423]		Q5SSM3	7.1	3.5E-02	5.5	2.5E-04	0.4	7.0E-01	-0.3	6.8E-01
ENSMUST00000093019	family with sequence similarity 83, member G [Source:MGI Symbol;Acc:MGI:1916890]		Q5SWY7	9.1	2.4E-05	7.7	4.2E-05	-0.3	8.1E-01	0.3	5.7E-01
ENSMUST00000093029	solute carrier family 47, member 2 [Source:MGI Symbol;Acc:MGI:3588190]		Q3V050	7.4	2.7E-04	7.0	2.9E-04	-0.7	6.1E-01	-0.2	7.4E-01
ENSMUST00000093033	calpain 9 [Source:MGI Symbol;Acc:MGI:1920897]		Q9D805	7.6	2.0E-05	6.3	7.1E-04	-0.4	7.6E-01	-0.2	7.3E-01
ENSMUST00000093040	RAB4B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105071]	Q4V9W8	Q91ZR1	-7.9	2.3E-05	5.4	4.6E-03	-1.5	3.7E-01	-0.2	7.9E-01
ENSMUST00000093049	differentially expressed in FDCP 8 [Source:MGI Symbol;Acc:MGI:1346331]		Q99J78	3.5	1.0E-03	6.3	1.5E-05	-1.7	6.6E-02	-0.4	4.1E-01
ENSMUST00000093059	poly(A)binding protein nuclear 1-like [Source:MGI Symbol;Acc:MGI:2685954]		Q5XFR0	6.9	1.4E-04	-1.4	1.9E-01	0.2	8.0E-01	-3.6	2.3E-02
ENSMUST00000090300	meiosis arrest female 1 [Source:MGI Symbol;Acc:MGI:2444505]		Q8BJ34	-1.3	4.1E-02	-0.7	4.0E-01	1.2	4.8E-02	0.6	4.5E-01
ENSMUST00000093061	tripartite motif-containing 11 [Source:MGI Symbol;Acc:MGI:2137355]		Q99PQ2	-7.6	8.3E-05	5.0	1.5E-04	-1.9	4.5E-02	-0.8	1.8E-01
ENSMUST00000093073	zinc finger CCCH-type containing 18 [Source:MGI Symbol;Acc:MGI:1923264]		Q0P678	-6.2	7.9E-04	5.8	2.7E-04	-0.6	6.1E-01	0.7	2.6E-01
ENSMUST00000093078	BTG3 associated nuclear protein [Source:MGI Symbol;Acc:MGI:1889023]		Q8VBU8	-3.3	1.9E-02	5.2	1.8E-02	-0.6	7.6E-01	2.0	9.0E-02
ENSMUST00000090355	RNA binding motif protein 33 [Source:MGI Symbol;Acc:MGI:1919670]	D3YV48		-0.1	9.7E-01	0.0	9.9E-01	0.1	9.6E-01	0.1	9.9E-01
ENSMUST00000093099	ATA box binding protein (Tbp)-associated factor, RNA polymerase I, C [Source:MGI Symbol;Acc:MGI:10957		Q6PDZ2	-7.3	1.3E-04	4.0	3.7E-02	-0.2	8.8E-01	1.5	2.3E-01
ENSMUST00000093100	dynein, axonemal assembly factor 1 [Source:MGI Symbol;Acc:MGI:1915520]		Q9D2H9	7.8	1.5E-05	-1.3	3.1E-02	-0.3	4.3E-01	0.0	9.6E-01
ENSMUST00000093106	acyl-CoA synthetase long-chain family member 6 [Source:MGI Symbol;Acc:MGI:894291]	Q5ICG4	Q91WC3	5.1	1.5E-03	0.8	2.5E-01	0.1	7.9E-01	0.8	2.0E-01
ENSMUST00000093113	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 18 [Source:MGI Symbol;Acc:M		Q4VC17	8.3	6.8E-06	6.3	2.3E-04	-0.5	6.6E-01	-0.8	1.9E-01
ENSMUST00000090398	discs, large homolog 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:1918478]	E9Q9R9		5.8	3.6E-02	9.5	3.1E-03	-0.9	7.4E-01	-4.6	9.6E-03
ENSMUST00000090406	cDNA sequence BC094916 [Source:MGI Symbol;Acc:MGI:3584522]	E9PVL3		1.7	4.3E-01	-0.7	7.9E-01	-1.9	3.4E-01	0.4	8.6E-01
ENSMUST00000093115	v-crk sarcoma virus CT10 oncogene homolog (avian) [Source:MGI Symbol;Acc:MGI:88508]	Q5ND50		-4.1	5.5E-04	-2.9	4.5E-03	-0.1	7.5E-01	-1.0	2.5E-01
ENSMUST00000093126	cDNA sequence BC107364 [Source:MGI Symbol;Acc:MGI:3618860]	E9Q5A2		8.4	2.2E-03	-3.7	2.0E-03	1.1	3.6E-02	0.5	5.8E-01
ENSMUST00000090443	calcium/calmodulin-dependent protein kinase II, beta [Source:MGI Symbol;Acc:MGI:88257]	Q68EG2		3.2	6.5E-02	6.7	2.1E-03	-0.4	8.0E-01	-3.9	5.4E-03
ENSMUST00000093132	CDC like kinase 4 [Source:MGI Symbol;Acc:MGI:1098551]	Q4FJV9	O35493	-6.8	6.0E-05	-3.6	2.1E-02	0.8	2.2E-01	0.1	9.6E-01
ENSMUST00000090457	RIKEN cDNA 4930451G09 gene [Source:MGI Symbol;Acc:MGI:1921934]	Q8C5G4		1.1	7.0E-02	2.3	9.1E-03	0.5	4.2E-01	-0.7	2.6E-01
ENSMUST00000093138	TBC1 domain family, member 9B [Source:MGI Symbol;Acc:MGI:1924045]		Q5SVR0	-3.4	1.5E-02	-6.0	4.0E-05	-0.3	4.1E-01	0.0	9.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000093140	anaphase promoting complex subunit 11 [Source:MGI Symbol;Acc:MGI:1913406]		Q9CPX9	-4.4	2.4E-04	-0.9	3.7E-01	1.4	5.5E-02	-4.2	9.0E-03
ENSMUST00000093152	RIKEN cDNA 9930111J21 gene 2 [Source:MGI Symbol;Acc:MGI:3711310]	Q8CB10		-3.6	5.8E-03	6.9	1.7E-04	-0.5	6.6E-01	0.3	6.8E-01
ENSMUST00000090474				7.9	5.5E-02	8.4	5.5E-02	-0.6	9.0E-01	-1.1	5.8E-01
ENSMUST00000093153	RIKEN cDNA 9930111J21 gene 1 [Source:MGI Symbol;Acc:MGI:3041173]	Q8CB10		7.8	2.7E-03	7.1	1.6E-02	-0.7	8.0E-01	-1.9	2.1E-01
ENSMUST00000090476	cDNA sequence BC028528 [Source:MGI Symbol;Acc:MGI:2385885]		Q8R2K8	1.5	4.5E-01	4.8	2.2E-02	-2.1	2.7E-01	-5.3	1.1E-02
ENSMUST00000090480	coronin 7 [Source:MGI Symbol;Acc:MGI:1926135]	G3X9L5		1.3	1.9E-01	-0.2	8.8E-01	0.1	9.0E-01	1.6	2.4E-01
ENSMUST00000093157	adaptor protein complex AP-1, gamma 1 subunit [Source:MGI Symbol;Acc:MGI:101919]	Q8CBB7		-3.1	1.9E-04	-5.2	5.0E-02	-0.4	6.5E-01	1.6	5.2E-01
ENSMUST00000093162	ataxin 1-like [Source:MGI Symbol;Acc:MGI:3694797]		P0C7T6	-1.1	1.2E-02	-4.7	2.5E-03	-0.2	6.9E-01	-0.7	5.7E-01
ENSMUST00000090503	family with sequence similarity 149, member B [Source:MGI Symbol;Acc:MGI:2145567]		Q6NSV7	3.6	9.3E-02	4.2	1.2E-01	0.2	9.2E-01	-0.4	8.5E-01
ENSMUST00000093165	cytoplasmic FMR1 interacting protein 2 [Source:MGI Symbol;Acc:MGI:1924134]		Q5SQX6	8.9	3.8E-06	-0.8	1.1E-01	1.0	8.9E-03	-0.5	3.1E-01
ENSMUST00000093166	cytoplasmic FMR1 interacting protein 2 [Source:MGI Symbol;Acc:MGI:1924134]		Q5SQX6	-10.1	6.1E-05	-1.7	6.8E-03	0.2	4.1E-01	-0.4	4.4E-01
ENSMUST00000090541	ynthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9) [Source:MGI Symbol;Acc:MGI:1(		Q9CR84	-1.6	3.4E-01	-4.3	1.5E-01	-0.8	5.6E-01	1.9	5.0E-01
ENSMUST00000093171	abl-interactor 1 [Source:MGI Symbol;Acc:MGI:104913]	B7ZCU4		-7.3	1.1E-05	1.0	2.3E-01	-0.9	1.8E-01	0.1	9.0E-01
ENSMUST00000093183	single-pass membrane protein with coiled-coil domains 1 [Source:MGI Symbol;Acc:MGI:1916826]		Q8CEZ1	7.2	7.0E-07	-7.6	6.4E-03	0.1	8.7E-01	3.2	1.7E-01
ENSMUST00000090553	seryl-aminoacyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:102809]		P26638	1.0	1.1E-01	1.4	1.2E-01	0.5	4.2E-01	0.2	7.8E-01
ENSMUST00000090554	transformation related protein 53 inducible protein 11 [Source:MGI Symbol;Acc:MGI:2670995]		Q4QQM4	3.2	2.5E-01	-2.1	6.4E-01	-2.8	3.4E-01	2.4	5.4E-01
ENSMUST00000093193	dedicator of cyto-kinesis 2 [Source:MGI Symbol;Acc:MGI:2149010]		Q8C3J5	-4.7	6.3E-06	7.0	7.9E-06	-0.2	7.7E-01	-0.2	6.1E-01
ENSMUST00000093201	nucleophosmin 1 [Source:MGI Symbol;Acc:MGI:106184]	Q5SQB0		-8.6	4.8E-06	3.0	6.6E-03	0.5	5.3E-01	0.9	1.9E-01
ENSMUST00000093205	F-box and WD-40 domain protein 11 [Source:MGI Symbol;Acc:MGI:2144023]		Q5SRY7	-6.3	3.1E-02	6.4	1.2E-04	-1.5	2.0E-01	-0.1	9.0E-01
ENSMUST00000093209	hemoglobin alpha, adult chain 1 [Source:MGI Symbol;Acc:MGI:96015]	Q91VB8		-3.0	9.3E-03	8.1	1.3E-05	-0.9	4.1E-01	-0.3	4.8E-01
ENSMUST00000093219	neuron specific gene family member 2 [Source:MGI Symbol;Acc:MGI:1202070]	Q5SS03		5.9	1.3E-03	-5.5	9.4E-05	-0.9	4.0E-02	0.2	8.3E-01
ENSMUST00000090586	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	A2AHG2		3.4	4.0E-02	0.3	9.1E-01	0.5	7.6E-01	3.6	1.2E-01
ENSMUST00000090591	interleukin 3 receptor, alpha chain [Source:MGI Symbol;Acc:MGI:96553]		P26952	-1.2	1.2E-01	0.2	7.9E-01	1.3	9.7E-02	-0.1	8.6E-01
ENSMUST00000093268	cyclic nucleotide gated channel beta 1 [Source:MGI Symbol;Acc:MGI:2664102]	Q91WA8		9.0	5.7E-04	-5.3	1.4E-02	1.1	1.3E-01	2.7	1.5E-01
ENSMUST00000090601	cortactin binding protein 2 [Source:MGI Symbol;Acc:MGI:1353467]		B9EJA2	3.7	5.4E-02	6.5	4.6E-03	-0.5	7.9E-01	-3.3	2.0E-02
ENSMUST00000090608	harbinger transposase derived 1 [Source:MGI Symbol;Acc:MGI:2443194]		Q8BR93	-0.6	2.3E-01	-0.1	8.2E-01	0.0	9.3E-01	-0.4	4.6E-01
ENSMUST00000093270	COMM domain containing 1 [Source:MGI Symbol;Acc:MGI:109474]	F7BZY0		-5.5	1.2E-03	-7.6	1.4E-04	1.1	1.1E-02	-0.7	6.2E-01
ENSMUST00000093290	pellino 1 [Source:MGI Symbol;Acc:MGI:1914495]	Q5SRW7	Q8C669	-6.0	6.8E-04	-6.7	1.1E-04	0.0	9.3E-01	0.3	7.5E-01
ENSMUST00000090680	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 [Source:MGI Symbol;Acc:MGI:1858415]		Q9JJY4	-0.5	4.4E-01	-1.2	2.0E-01	0.5	3.8E-01	1.3	1.7E-01
ENSMUST00000090682	kelch repeat and BTB (POZ) domain containing 4 [Source:MGI Symbol;Acc:MGI:1914386]		Q8R179	-3.4	4.1E-02	-2.6	1.9E-01	0.6	5.8E-01	-0.2	9.2E-01
ENSMUST00000093299	sprouty-related, EVH1 domain containing 2 [Source:MGI Symbol;Acc:MGI:2150019]	Q5SRF8		1.7	1.2E-02	5.4	3.0E-02	-0.7	7.8E-01	1.3	3.4E-01
ENSMUST00000093312	Iroquois related homeobox 3 [Source:MGI Symbol;Acc:MGI:1197522]		P81067	5.8	2.0E-02	5.8	5.4E-04	-0.9	4.9E-01	-0.8	2.7E-01
ENSMUST00000090726	solute carrier family 43, member 3 [Source:MGI Symbol;Acc:MGI:1931054]		A2AVZ9	1.0	9.7E-02	1.9	2.7E-02	1.1	8.6E-02	0.1	8.3E-01
ENSMUST00000090732	tissue factor pathway inhibitor [Source:MGI Symbol;Acc:MGI:1095418]	Q8BSB7		3.9	1.4E-01	1.9	5.6E-01	-0.2	9.5E-01	1.8	4.7E-01
ENSMUST00000093336	RIKEN cDNA 2610318N02 gene [Source:MGI Symbol;Acc:MGI:1917708]	Q80VT5		2.4	8.7E-03	3.9	3.6E-03	-3.4	1.7E-02	-0.3	6.2E-01
ENSMUST00000093342	RIKEN cDNA 4933402J07 gene [Source:MGI Symbol;Acc:MGI:3607717]	Q8BHX0		6.7	5.9E-05	-6.3	6.6E-04	-0.9	1.5E-01	-3.6	3.5E-02
ENSMUST00000093346	H2A histone family, member V [Source:MGI Symbol;Acc:MGI:1924855]	Q8R029		-4.8	2.7E-04	5.8	6.3E-02	-0.5	8.7E-01	1.8	2.7E-01
ENSMUST00000090759	acid phosphatase 6, lysophosphatidic [Source:MGI Symbol;Acc:MGI:1931010]		Q8BP40	0.8	2.5E-01	0.7	4.1E-01	-0.3	7.0E-01	-0.1	8.6E-01
ENSMUST00000093355	calcium/calmodulin-dependent protein kinase II, beta [Source:MGI Symbol;Acc:MGI:88257]	Q5SVI1		6.0	2.2E-02	6.7	1.2E-04	-0.9	4.1E-01	0.7	2.2E-01
ENSMUST00000093357	WD repeat domain containing 83 [Source:MGI Symbol;Acc:MGI:1915086]		Q9DAJ4	-4.5	3.5E-04	3.7	5.5E-04	0.7	2.7E-01	-0.4	4.7E-01
ENSMUST00000093360	transportin 2 (importin 3, karyopherin beta 2b) [Source:MGI Symbol;Acc:MGI:2384849]	E9PV58		-1.2	2.9E-02	6.1	1.9E-03	-0.1	9.3E-01	-1.0	2.4E-01
ENSMUST00000090785	OTU domain containing 7B [Source:MGI Symbol;Acc:MGI:2654703]		B2RUR8	-0.7	7.2E-01	-1.9	5.7E-01	1.3	5.1E-01	2.5	4.2E-01
ENSMUST00000090791	regulation of nuclear pre-mRNA domain containing 2 [Source:MGI Symbol;Acc:MGI:1922387]		Q6NXI6	-0.3	4.6E-01	0.3	6.1E-01	0.9	6.9E-02	0.3	6.5E-01
ENSMUST00000090802	activating transcription factor 2 [Source:MGI Symbol;Acc:MGI:109349]	Q543G2	P16951	-0.2	9.3E-01	3.9	3.4E-01	4.0	2.1E-01	-0.2	9.5E-01
ENSMUST00000093369	neurofilament, heavy polypeptide [Source:MGI Symbol;Acc:MGI:97309]		P19246	7.0	1.1E-04	-4.0	8.2E-02	1.0	3.5E-01	-0.2	9.2E-01
ENSMUST00000093380	podocan-like 1 [Source:MGI Symbol;Acc:MGI:2685352]			4.3	5.9E-03	5.3	1.3E-03	0.8	4.8E-01	-0.4	5.7E-01
ENSMUST00000090811	secernin 3 [Source:MGI Symbol;Acc:MGI:1921866]		Q3TMH2	0.4	4.4E-01	0.5	3.9E-01	-0.2	6.9E-01	-0.3	5.6E-01
ENSMUST00000093389	microrchidia 2A [Source:MGI Symbol;Acc:MGI:1921772]		Q69ZX6	1.8	1.4E-03	7.5	2.3E-04	-2.1	2.1E-01	0.3	6.4E-01
ENSMUST00000093427	NACHT and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:2442268]		A6H603	10.2	4.8E-04	2.5	1.0E-02	-1.2	1.1E-01	-0.1	8.3E-01
ENSMUST00000093434	olfactory receptor 372 [Source:MGI Symbol;Acc:MGI:3030206]	Q7TRY2		6.7	3.3E-06	1.6	3.9E-02	-0.7	2.7E-01	-0.4	4.7E-01
ENSMUST00000090834	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 [Source:MGI Symbol;Acc:MGI:2685438]		Q7SIG6	-0.6	7.0E-01	-0.7	7.1E-01	-0.8	5.7E-01	-0.7	6.9E-01
ENSMUST00000093444	FCH domain only 1 [Source:MGI Symbol;Acc:MGI:1921265]		Q8K285	-2.9	6.8E-03	-3.1	6.9E-02	-0.1	9.5E-01	-1.1	5.3E-01
ENSMUST00000090840	inc finger (CCCH type), RNA binding motif and serine/arginine rich 2 [Source:MGI Symbol;Acc:MGI:103287	B1B0E9		-0.2	8.2E-01	0.2	8.6E-01	0.2	8.0E-01	-0.2	8.5E-01
ENSMUST00000093450	anoctamin 8 [Source:MGI Symbol;Acc:MGI:2687327]		Q6PB70	2.5	1.2E-03	3.2	1.1E-02	-3.1	2.4E-02	-0.4	5.7E-01
ENSMUST00000093454	elongation factor RNA polymerase II [Source:MGI Symbol;Acc:MGI:109377]		O08856	-2.3	3.7E-03	6.3	3.5E-04	-0.6	5.7E-01	1.0	1.1E-01
ENSMUST00000093456	KxDL motif containing 1 [Source:MGI Symbol;Acc:MGI:1922870]		Q80XH1	-4.4	4.0E-06	-4.2	1.7E-04	0.0	9.4E-01	-2.5	1.8E-02
ENSMUST00000093470	N-acetyltransferase 2 (arylamine N-acetyltransferase) [Source:MGI Symbol;Acc:MGI:109201]	Q78ZC4	P50295	-5.5	2.9E-04	9.3	1.9E-05	-0.6	6.4E-01	-0.1	8.0E-01
ENSMUST00000093490	chloride channel, voltage-sensitive 3 [Source:MGI Symbol;Acc:MGI:103555]	Q790S0	P51791	-4.3	4.2E-03	-6.4	4.1E-02	0.8	3.9E-01	1.4	6.3E-01
ENSMUST00000093506	RIKEN cDNA C130026I21 gene [Source:MGI Symbol;Acc:MGI:3612702]	Q8C898		2.7	1.1E-03	6.0	1.3E-02	2.1	3.0E-01	-0.7	4.8E-01
ENSMUST00000093508	Sp110 nuclear body protein [Source:MGI Symbol;Acc:MGI:1923364]		Q8BVK9	-3.8	4.3E-04	6.0	9.9E-03	-0.8	7.1E-01	-0.9	4.2E-01
ENSMUST00000090896	Cobl-like 1 [Source:MGI Symbol;Acc:MGI:2442894]		Q3UMF0	0.0	9.9E-01	2.0	2.2E-01	-0.8	5.4E-01	-2.8	8.3E-02
ENSMUST00000093517	caspase 3 [Source:MGI Symbol;Acc:MGI:107739]		P70677	-5.0	2.4E-05	-2.6	3.0E-02	1.1	1.0E-01	-1.0	3.7E-01
ENSMUST00000090925	bromodomain adjacent to zinc finger domain, 2B [Source:MGI Symbol;Acc:MGI:2442782]	A2AUY4		-2.4	1.7E-01	-2.8	2.2E-01	1.0	4.4E-01	1.5	5.0E-01
ENSMUST00000093526	family with sequence similarity 149, member A [Source:MGI Symbol;Acc:MGI:2387177]		Q8CFV2	8.4	1.3E-05	-2.5	2.9E-01	1.5	2.2E-01	-0.6	7.9E-01
ENSMUST00000093527	predicted gene 10608 [Source:MGI Symbol;Acc:MGI:3642009]	E9PZ13		9.7	4.6E-05	9.4	4.1E-03	2.7	2.9E-01	-1.9	2.5E-01
ENSMUST00000093534	mitochondrial tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2142572]			-9.9	1.5E-03	-3.8	4.7E-02	0.5	6.1E-01	-2.4	2.8E-01
ENSMUST00000093552	translocase of outer mitochondrial membrane 40 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1858259]		Q9QYA2	-1.3	2.2E-02	3.0	7.1E-02	-4.3	2.6E-02	1.7	1.2E-01
ENSMUST00000093769	nbrane associated guanylate kinase, WW and PDZ domain containing 1 [Source:MGI Symbol;Acc:MGI:12035	E9PZ12		7.6	7.4E-05	2.5	3.9E-03	0.1	8.7E-01	0.6	3.0E-01
ENSMUST00000093772	zinc finger protein 651 [Source:MGI Symbol;Acc:MGI:2670992]	E9PZ11		5.4	4.1E-05	6.0	4.2E-04	-1.6	2.3E-01	-0.1	8.9E-01
ENSMUST00000093775	solute carrier family 22 (organic cation transporter), member 14 [Source:MGI Symbol;Acc:MGI:2685974]	Q497L9		7.6	1.1E-04	-1.8	1.4E-01	-0.2	7.9E-01	-3.5	3.6E-02
ENSMUST00000090945	synaptotagmin XI [Source:MGI Symbol;Acc:MGI:1859547]		Q9R0N3	-1.2	1.7E-01	-0.8	4.2E-01	-0.3	6.8E-01	-0.7	4.9E-01
ENSMUST00000090952	formin-like 2 [Source:MGI Symbol;Acc:MGI:1918659]		A2APV2	-2.4	6.7E-02	-3.0	7.5E-02	-0.6	4.5E-01	0.0	9.9E-01
ENSMUST00000093785	N-acetyltransferase 6 [Source:MGI Symbol;Acc:MGI:1888902]	Q3UVC9	Q9R123	-1.8	1.0E-02	7.9	1.0E-04	-0.7	6.2E-01	0.1	9.3E-01
ENSMUST00000093800	plastin 1 (I-isoform) [Source:MGI Symbol;Acc:MGI:104809]		Q3V0K9	4.8	2.9E-04	7.1	9.6E-03	-0.8	7.4E-01	-1.8	2.0E-01
ENSMUST00000093801	phospholipid scramblase 1 [Source:MGI Symbol;Acc:MGI:893575]		Q9JJ00	-4.9	2.1E-03	1.6	9.1E-02	-5.7	7.2E-04	-0.5	5.1E-01
ENSMUST00000093802	centrosomal protein 162 [Source:MGI Symbol;Acc:MGI:1925343]		Q6ZQ06	3.6	5.2E-05	-6.3	2.3E-04	0.6	1.3E-01	-0.9	4.8E-01
ENSMUST00000091002	FH2 domain containing 1 [Source:MGI Symbol;Acc:MGI:2684972]		Q3ULZ2	1.4	1.2E-01	1.9	9.3E-02	0.0	9.6E-01	-0.5	5.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000093811	filamin A interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917848]	Q059P4		8.1	3.0E-05	4.4	2.5E-02	-0.6	7.4E-01	2.4	5.2E-02
ENSMUST00000091020	F-box and WD-40 domain protein 2 [Source:MGI Symbol;Acc:MGI:1353435]	A2AUF9		-4.4	1.6E-01	-2.9	3.9E-01	0.5	8.1E-01	-1.0	7.9E-01
ENSMUST00000093812	CD109 antigen [Source:MGI Symbol;Acc:MGI:2445221]	A6MDD3	Q8R422	3.4	9.7E-04	3.6	3.1E-02	1.6	2.4E-01	0.4	6.1E-01
ENSMUST00000091039	Ral GEF with PH domain and SH3 binding motif 1 [Source:MGI Symbol;Acc:MGI:1922008]		A2AR50	1.0	6.0E-01	0.4	8.9E-01	-0.5	7.7E-01	0.1	9.6E-01
ENSMUST00000093813	Rho guanine nucleotide exchange factor (GEF) 40 [Source:MGI Symbol;Acc:MGI:2685515]		Q3UPH7	6.5	1.4E-04	-1.9	2.2E-02	0.7	1.1E-01	-1.0	1.9E-01
ENSMUST00000093819	phosphatidylinositol glycan anchor biosynthesis, class B [Source:MGI Symbol;Acc:MGI:1891825]	Q8BSC4		-5.1	2.1E-02	-3.3	8.9E-02	0.0	9.8E-01	-2.0	3.2E-01
ENSMUST00000093829	multiple EGF-like-domains 11 [Source:MGI Symbol;Acc:MGI:1920951]		Q80T91	6.4	1.9E-04	2.9	6.4E-03	-0.6	4.4E-01	-0.1	8.3E-01
ENSMUST00000091112	purinergic receptor P2Y, G-protein coupled, 14 [Source:MGI Symbol;Acc:MGI:2155705]	Q544F4	Q9ESG6	1.2	5.5E-01	-3.4	3.0E-01	-2.6	1.8E-01	2.1	5.1E-01
ENSMUST00000093837	taste receptor cell gene 1 [Source:MGI Symbol;Acc:MGI:3576664]	F8VPJ5		6.8	1.5E-05	-7.2	8.8E-03	0.6	5.1E-01	1.1	6.5E-01
ENSMUST00000093844	cholinergic receptor, nicotinic, alpha polypeptide 5 [Source:MGI Symbol;Acc:MGI:87889]		Q2MKA5	6.6	3.6E-05	-3.6	2.7E-02	-1.2	1.9E-01	-4.0	4.4E-02
ENSMUST00000093852	zinc finger and BTB domain containing 16 [Source:MGI Symbol;Acc:MGI:103222]	Q3UQ17		3.7	2.1E-05	9.6	4.9E-06	-0.6	6.0E-01	-0.1	7.1E-01
ENSMUST00000091142	ubiquitin related modifier 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915455]		Q9D2P4	-0.9	1.4E-01	-0.1	9.1E-01	0.7	2.4E-01	-0.2	8.1E-01
ENSMUST00000093853	neurexophilin and PC-esterase domain family, member 4 [Source:MGI Symbol;Acc:MGI:1924792]		Q52KP5	5.6	4.3E-05	-1.8	4.7E-01	3.4	3.7E-02	-1.0	7.0E-01
ENSMUST00000091146	Rap guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:104580]	Q3UGX8		-2.2	1.8E-01	2.4	2.4E-01	1.4	4.3E-01	-3.2	6.9E-02
ENSMUST00000093855	sodium channel, voltage-gated, type II, beta [Source:MGI Symbol;Acc:MGI:106921]	Q1MXF8	Q56A07	5.4	8.9E-03	3.9	6.8E-03	-2.5	8.6E-02	1.4	1.1E-01
ENSMUST00000093883	ADP-ribosylation factor-like 14 effector protein [Source:MGI Symbol;Acc:MGI:1926020]		Q8BIX3	-4.0	1.3E-03	3.5	9.1E-02	-0.2	9.1E-01	0.2	8.9E-01
ENSMUST00000093893	Rho GTPase activating protein 42 [Source:MGI Symbol;Acc:MGI:1918794]		B2RQE8	6.1	1.7E-04	5.4	1.2E-04	-0.3	7.4E-01	0.1	8.8E-01
ENSMUST00000091190	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked [Source:MGI Symbol;Acc:MGI:1349406]		Q62095	0.9	7.1E-01	-4.4	2.6E-01	-3.5	1.1E-01	1.9	6.3E-01
ENSMUST00000091197	aryotic translation initiation factor 2, subunit 3, structural gene Y-linked [Source:MGI Symbol;Acc:MGI:1349		Q9Z0N2	-3.0	4.6E-01	-5.7	2.4E-01	-3.7	1.3E-01	-0.9	8.6E-01
ENSMUST00000093901	ENTH domain containing 2 [Source:MGI Symbol;Acc:MGI:1926027]	B2RPS6	Q3U3N6	-6.7	5.3E-03	-1.3	4.3E-02	0.1	8.7E-01	0.2	7.5E-01
ENSMUST00000093905	transmembrane protein 235 [Source:MGI Symbol;Acc:MGI:3651706]		B1AQL3	7.7	3.0E-05	5.7	1.6E-03	-0.6	6.7E-01	0.6	4.5E-01
ENSMUST00000093906	baculoviral IAP repeat-containing 5 [Source:MGI Symbol;Acc:MGI:1203517]		O70201	5.2	5.4E-06	7.8	8.9E-05	-0.1	9.1E-01	-0.5	3.9E-01
ENSMUST00000091236	GC-rich promoter binding protein 1 [Source:MGI Symbol;Acc:MGI:1920524]		Q6NXH3	3.9	2.4E-01	2.6	5.6E-01	-1.4	7.3E-01	-0.1	9.9E-01
ENSMUST00000091237	ATPase, class VI, type 11A [Source:MGI Symbol;Acc:MGI:1354735]		P98197	-1.2	4.6E-01	-0.3	8.9E-01	2.6	1.6E-01	1.7	4.1E-01
ENSMUST00000093911	myosin XVB [Source:MGI Symbol;Acc:MGI:2685534]	I7HPW8		9.0	6.2E-06	-6.6	3.2E-03	1.3	4.2E-02	-0.3	8.9E-01
ENSMUST00000091252	SEC16 homolog A, endoplasmic reticulum export factor [Source:MGI Symbol;Acc:MGI:2139207]	E9QAT4		-3.3	1.3E-01	-3.8	2.0E-01	0.8	6.0E-01	1.4	6.5E-01
ENSMUST00000091257	mitofusin 1 [Source:MGI Symbol;Acc:MGI:1914664]		Q811U4	0.7	2.4E-01	1.0	2.8E-01	0.9	1.9E-01	0.7	3.8E-01
ENSMUST00000093914	tripartite motif-containing 80 [Source:MGI Symbol;Acc:MGI:3588186]	Q3V061		7.4	1.6E-04	5.9	1.0E-05	-1.1	1.6E-01	-0.5	2.2E-01
ENSMUST00000093923	cell division cycle 27 [Source:MGI Symbol;Acc:MGI:102685]		A2A6Q5	-3.3	2.0E-04	2.4	5.7E-03	-0.2	7.8E-01	0.1	8.5E-01
ENSMUST00000093925	corticotropin releasing hormone receptor 1 [Source:MGI Symbol;Acc:MGI:88498]	Q3ZAT0	P35347	8.1	1.8E-05	4.3	1.6E-01	-1.1	7.0E-01	2.3	2.5E-01
ENSMUST00000093933	prostaglandin E synthase 3 (cytosolic)-like [Source:MGI Symbol;Acc:MGI:1916146]		Q9D9A7	6.1	3.4E-05	-6.2	9.1E-03	0.2	7.6E-01	0.1	9.5E-01
ENSMUST00000093936	keratin associated protein 9-1 [Source:MGI Symbol;Acc:MGI:1309997]	Q64526		6.5	1.0E-02	-3.7	1.2E-02	0.8	2.0E-01	-0.7	6.2E-01
ENSMUST00000091289				-4.2	2.3E-01	-0.8	7.8E-01	-0.5	8.2E-01	-3.9	2.8E-01
ENSMUST00000091291	insulin receptor [Source:MGI Symbol;Acc:MGI:96575]		P15208	-0.7	9.9E-02	-0.1	8.3E-01	1.1	2.4E-02	0.5	3.8E-01
ENSMUST00000091295	cyclin B1 [Source:MGI Symbol;Acc:MGI:88302]	Q68EM3		-3.6	1.2E-01	-3.9	1.5E-01	-1.3	3.5E-01	-1.0	7.2E-01
ENSMUST00000093937	cell division cycle 6 [Source:MGI Symbol;Acc:MGI:1345150]			-3.9	8.2E-03	0.9	5.5E-02	0.1	7.4E-01	0.1	8.6E-01
ENSMUST00000093942	G protein-coupled receptor 179 [Source:MGI Symbol;Acc:MGI:2443409]	E9PY61		9.6	3.6E-06	-1.1	7.5E-02	-8.3	4.8E-06	-0.9	1.4E-01
ENSMUST00000093943	chromobox 1 [Source:MGI Symbol;Acc:MGI:105369]		P83917	-4.8	1.4E-03	-0.1	9.6E-01	0.8	3.5E-01	-1.7	1.6E-01
ENSMUST00000093944	homeobox B3 [Source:MGI Symbol;Acc:MGI:96184]		P09026	2.7	2.8E-03	7.4	2.2E-04	-0.6	6.8E-01	-1.0	1.8E-01
ENSMUST00000093951	spermatogenesis associated 1 [Source:MGI Symbol;Acc:MGI:1918201]		Q9D5R4	5.1	6.8E-06	-8.3	3.3E-04	-0.1	8.9E-01	-1.1	5.1E-01
ENSMUST00000093955	suppressor of Ty 4A [Source:MGI Symbol;Acc:MGI:107416]		P63271	-9.6	1.5E-05	-1.2	3.5E-01	1.4	1.2E-01	-1.2	3.8E-01
ENSMUST00000093956	heat shock transcription factor family member 5 [Source:MGI Symbol;Acc:MGI:2685585]		Q5ND04	6.9	1.6E-04	-2.7	1.5E-01	0.3	7.6E-01	-0.5	7.6E-01
ENSMUST00000093962	cyclin D1 [Source:MGI Symbol;Acc:MGI:88313]	Q790L7	P25322	3.7	3.0E-04	-10.3	5.8E-04	0.8	1.3E-01	0.7	7.3E-01
ENSMUST00000093976	arylsulfatase J [Source:MGI Symbol;Acc:MGI:2443513]	Q32KI8	Q8BM89	7.9	1.0E-05	-8.4	4.9E-04	0.6	2.1E-01	-0.3	8.7E-01
ENSMUST00000093983	predicted gene 21975 [Source:MGI Symbol;Acc:MGI:5439444]	L7N211		-2.3	3.0E-03	4.9	2.5E-02	-0.5	8.0E-01	0.5	6.5E-01
ENSMUST00000093991	cilia and flagella associated protein 46 [Source:MGI Symbol;Acc:MGI:2444387]	Q14AD7		6.0	3.5E-03	-3.5	6.2E-02	1.4	1.1E-01	-0.1	9.4E-01
ENSMUST00000093995	seizure related gene 6 [Source:MGI Symbol;Acc:MGI:104745]		Q7TSK2	5.3	1.7E-02	-5.1	1.8E-04	0.6	1.7E-01	0.1	9.1E-01
ENSMUST00000094002	DNA segment, Chr 7, ERATO Doi 443, expressed [Source:MGI Symbol;Acc:MGI:1196431]		D2J0Y4	6.5	4.2E-03	7.7	9.5E-05	0.5	6.9E-01	-0.8	1.9E-01
ENSMUST00000091387	polymerase (DNA directed), kappa [Source:MGI Symbol;Acc:MGI:1349767]	Q5Q9H7		-1.4	7.1E-01	-0.2	9.7E-01	0.9	7.7E-01	-0.3	9.4E-01
ENSMUST00000094017	arginyltransferase 1 [Source:MGI Symbol;Acc:MGI:1333870]	Q4FCQ7		-3.5	3.3E-02	8.1	7.1E-04	-0.7	7.0E-01	-1.0	2.5E-01
ENSMUST00000094018	phosphatidic acid phosphatase type 2 domain containing 1A [Source:MGI Symbol;Acc:MGI:2685936]		Q0VBU9	6.5	8.2E-05	-0.6	1.4E-01	1.1	2.5E-03	0.5	2.5E-01
ENSMUST00000094028	capping protein (actin filament) muscle Z-line, alpha 1 [Source:MGI Symbol;Acc:MGI:106227]	Q5RKN9		-7.1	7.1E-07	3.1	2.2E-04	-0.3	5.9E-01	0.0	9.8E-01
ENSMUST00000094050	droxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3 [Source:MGI Symbol;Acc:MGI:962	E9PXG7		6.9	4.3E-04	6.1	8.0E-04	-1.4	3.3E-01	0.2	8.2E-01
ENSMUST00000094053	trinucleotide repeat containing 6a [Source:MGI Symbol;Acc:MGI:2385292]	F6ZMJ4		-1.5	1.5E-02	3.8	8.5E-05	-0.9	1.3E-01	0.0	9.9E-01
ENSMUST00000094065	transmembrane protein 256 [Source:MGI Symbol;Acc:MGI:1916436]		Q5F285	-8.4	9.0E-06	5.8	6.6E-04	-0.5	7.1E-01	-0.6	3.8E-01
ENSMUST00000094077	KDM1 lysine (K)-specific demethylase 6B [Source:MGI Symbol;Acc:MGI:2448492]		Q5NCY0	-3.1	8.0E-04	2.6	5.3E-03	-4.2	1.1E-03	-0.7	2.5E-01
ENSMUST00000094103	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 [Source:MGI Symbol;Acc:MGI:1333853]		Q9QZS6	3.9	3.1E-04	-4.8	3.9E-03	1.1	4.6E-02	3.1	3.4E-02
ENSMUST00000091466	tetratricopeptide repeat domain 37 [Source:MGI Symbol;Acc:MGI:2679923]	F8VPK0		0.8	1.9E-01	0.2	8.1E-01	-0.8	1.4E-01	-0.2	7.6E-01
ENSMUST00000094109	olfactory receptor 2 [Source:MGI Symbol;Acc:MGI:97432]	Q9QWU6		6.9	6.2E-05	5.9	6.3E-03	-1.4	4.3E-01	0.2	7.8E-01
ENSMUST00000094111	cytochrome P450, family 3, subfamily a, polypeptide 41A [Source:MGI Symbol;Acc:MGI:1858451]		Q9JMA7	8.3	2.5E-05	6.6	1.0E-04	-0.6	6.1E-01	-0.4	4.7E-01
ENSMUST00000091497	FERM domain containing 4A [Source:MGI Symbol;Acc:MGI:1919850]		Q8BIE6	-1.8	4.7E-01	-3.5	2.3E-01	-2.5	1.5E-01	-0.8	8.1E-01
ENSMUST00000094124	olfactory receptor 558 [Source:MGI Symbol;Acc:MGI:3030392]	Q8VGZ7		6.6	6.5E-05	4.8	5.1E-04	0.3	7.0E-01	-0.5	4.4E-01
ENSMUST00000094134	interleukin 18 binding protein [Source:MGI Symbol;Acc:MGI:1333800]		Q9Z0M9	-4.1	8.5E-06	4.4	1.6E-03	-1.6	1.4E-01	0.3	7.0E-01
ENSMUST00000094135	myosin XV [Source:MGI Symbol;Acc:MGI:1261811]		Q9QZZ4	8.9	1.3E-03	7.5	6.4E-05	0.1	9.5E-01	-0.6	2.7E-01
ENSMUST00000091556	BTB (POZ) domain containing 3 [Source:MGI Symbol;Acc:MGI:2385155]	Q3TSN9		2.2	2.4E-01	6.2	3.9E-02	1.7	5.0E-01	-2.2	1.9E-01
ENSMUST00000091560	RIKEN cDNA 2010111I01 gene [Source:MGI Symbol;Acc:MGI:1919311]	Q3UQZ7		1.1	6.6E-02	1.7	2.0E-02	-0.2	7.3E-01	-0.8	1.6E-01
ENSMUST00000094140	leucine rich repeat containing 48 [Source:MGI Symbol;Acc:MGI:1921915]	Q8BWX4		4.3	8.8E-04	-2.6	6.7E-02	0.7	3.6E-01	0.1	9.3E-01
ENSMUST00000091579	G kinase anchoring protein 1 [Source:MGI Symbol;Acc:MGI:1891694]		Q9JMB0	1.0	8.8E-02	0.1	9.2E-01	-1.9	5.1E-03	-0.9	1.3E-01
ENSMUST00000094141	folate receptor 2 (fetal) [Source:MGI Symbol;Acc:MGI:95569]		Q05685	4.9	1.9E-04	2.0	1.6E-02	0.1	9.1E-01	-0.5	4.4E-01
ENSMUST00000091614	nuclear transcription factor, X-box binding 1 [Source:MGI Symbol;Acc:MGI:1921414]		B1AY10	-1.7	7.2E-02	-2.2	9.4E-02	0.0	9.9E-01	0.5	6.9E-01
ENSMUST00000094151	ring finger protein 187 [Source:MGI Symbol;Acc:MGI:1914224]			-2.9	2.3E-03	3.5	3.3E-01	-0.9	8.0E-01	3.7	1.3E-01
ENSMUST00000094161	tsukushi, small leucine rich proteoglycan [Source:MGI Symbol;Acc:MGI:2443855]	Q08EE6	Q8CBR6	6.0	6.5E-04	-5.9	3.0E-04	1.8	8.3E-04	0.4	7.2E-01
ENSMUST00000094169	interferon gamma induced GTPase [Source:MGI Symbol;Acc:MGI:107729]	E9PW35		-4.5	3.7E-03	5.4	2.7E-04	-2.1	8.0E-02	-0.3	6.6E-01
ENSMUST00000094190	sucrase isomaltase (alpha-glucosidase) [Source:MGI Symbol;Acc:MGI:1917233]	F8VQM5		4.8	1.3E-02	-3.3	1.7E-02	-0.3	6.6E-01	-0.5	6.8E-01
ENSMUST00000094216	mesoderm development candidate 1 [Source:MGI Symbol;Acc:MGI:1891420]		Q9ERE8	-1.4	2.3E-02	8.2	1.4E-05	-0.9	4.3E-01	-0.2	6.2E-01
ENSMUST00000091668	serine (or cysteine) peptidase inhibitor, clade B, member 1a [Source:MGI Symbol;Acc:MGI:1913472]	Z4YK03		1.6	4.7E-01	4.3	2.3E-01	2.7	4.0E-01	0.0	9.9E-01
ENSMUST00000094218	solute carrier family 17, member 9 [Source:MGI Symbol;Acc:MGI:1919107]		Q8VCL5	-2.9	2.5E-03	-3.8	2.9E-02	0.9	2.3E-01	1.2	4.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000094245	claudin 3 [Source:MGI Symbol;Acc:MGI:1329044]	Q545A5	Q9Z0G9	6.5	8.4E-05	7.0	2.8E-04	0.4	7.6E-01	-0.1	8.4E-01
ENSMUST00000094251	family with sequence similarity 217, member B [Source:MGI Symbol;Acc:MGI:1918782]	A2AJW5		-3.1	6.6E-04	-5.7	7.3E-03	0.6	3.8E-01	-1.0	5.8E-01
ENSMUST00000094273	predicted gene 16432 [Source:MGI Symbol;Acc:MGI:3645414]	B2RW93		8.4	3.4E-05	6.2	3.3E-04	-0.6	6.2E-01	-0.9	1.7E-01
ENSMUST00000091704	histone cluster 1, H2be [Source:MGI Symbol;Acc:MGI:2448380]		Q6ZWY9	0.9	4.9E-01	-0.7	6.2E-01	-2.2	6.9E-02	-0.7	6.3E-01
ENSMUST00000091706	hemochromatosis [Source:MGI Symbol;Acc:MGI:109191]		P70387	-0.8	2.2E-01	-0.3	7.1E-01	0.1	8.6E-01	-0.4	5.8E-01
ENSMUST00000094280	coiled-coil-helix-coiled-coil-helix domain containing 2 [Source:MGI Symbol;Acc:MGI:1261428]		Q9D1L0	-5.0	9.8E-06	-3.5	4.6E-02	-0.1	8.6E-01	-0.3	8.4E-01
ENSMUST00000094287	CCCTC-binding factor (zinc finger protein)-like [Source:MGI Symbol;Acc:MGI:3652571]		A2APF3	7.1	3.5E-04	2.8	9.2E-02	-3.3	8.1E-02	0.0	9.7E-01
ENSMUST00000094303	Fc receptor-like 6 [Source:MGI Symbol;Acc:MGI:3618339]		A1YIY0	4.8	1.1E-04	2.1	2.3E-01	-0.7	6.6E-01	1.1	4.1E-01
ENSMUST00000091742	histone cluster 1, H2ah [Source:MGI Symbol;Acc:MGI:2448295]	A3KPD0	Q8CGP6	3.9	4.1E-02	1.8	2.6E-01	-3.2	8.7E-02	-1.1	3.8E-01
ENSMUST00000091745	histone cluster 1, H2ao [Source:MGI Symbol;Acc:MGI:2448302]	B2RVF0	P22752	3.0	6.8E-02	4.6	6.9E-02	2.4	2.7E-01	0.8	5.9E-01
ENSMUST00000091749	histone cluster 1, H2bq [Source:MGI Symbol;Acc:MGI:3702051]	Q8CBB6		0.7	6.9E-01	6.5	1.8E-02	2.1	3.5E-01	-3.7	3.9E-02
ENSMUST00000091751	histone cluster 1, H2an [Source:MGI Symbol;Acc:MGI:2448300]	B2RVF0	P22752	3.2	5.6E-02	5.7	4.0E-03	-0.5	7.7E-01	-2.9	2.2E-02
ENSMUST00000091752	histone cluster 1, H3c [Source:MGI Symbol;Acc:MGI:2448320]	B9EI85	P84228	2.6	4.7E-02	1.3	3.2E-01	-1.4	2.4E-01	-0.2	8.6E-01
ENSMUST00000091756	histone cluster 1, H2bl [Source:MGI Symbol;Acc:MGI:2448403]		P10853	1.7	3.5E-01	-1.9	3.5E-01	-3.0	8.2E-02	0.6	7.7E-01
ENSMUST00000091759				1.8	1.3E-01	0.4	7.5E-01	-1.2	3.0E-01	0.3	8.2E-01
ENSMUST00000094315	predicted gene 10295 [Source:MGI Symbol;Acc:MGI:3642770]	Q8CCF3		9.0	6.6E-06	-1.6	4.9E-02	0.9	6.2E-02	0.4	6.0E-01
ENSMUST00000094329	engulfment and cell motility 2 [Source:MGI Symbol;Acc:MGI:2153045]		Q8BHL5	-7.4	7.3E-05	-0.9	1.9E-01	0.5	2.2E-01	-0.1	9.2E-01
ENSMUST00000094337	Fc receptor-like B [Source:MGI Symbol;Acc:MGI:3576487]		Q5DRQ8	6.5	3.4E-05	2.4	1.3E-01	-1.6	2.7E-01	0.9	4.5E-01
ENSMUST00000094339	paternally expressed 12 [Source:MGI Symbol;Acc:MGI:1351637]	Q9WVA7		1.7	2.6E-02	8.6	1.0E-04	-0.6	6.9E-01	-1.9	2.0E-02
ENSMUST00000094340	makorin, ring finger protein, 3 [Source:MGI Symbol;Acc:MGI:2181178]		Q60764	7.3	6.9E-05	-2.6	2.0E-03	0.8	3.1E-02	-0.4	5.6E-01
ENSMUST00000094346	WAP four-disulfide core domain 6B [Source:MGI Symbol;Acc:MGI:3575430]		F6ULY1	6.1	5.6E-04	-6.3	1.8E-03	-1.5	2.3E-02	-0.7	6.7E-01
ENSMUST00000091851	mitogen-activated protein kinase 4 [Source:MGI Symbol;Acc:MGI:2444559]		Q6P5G0	-2.4	1.1E-01	-0.4	8.4E-01	1.0	4.4E-01	-1.1	5.4E-01
ENSMUST00000094360	sialic acid binding Ig-like lectin H [Source:MGI Symbol;Acc:MGI:2443256]	G3X9N0		5.0	2.6E-02	-1.6	1.3E-01	0.7	2.5E-01	-1.4	2.1E-01
ENSMUST00000094361	heat shock protein 90, alpha (cytosolic), class A member 1 [Source:MGI Symbol;Acc:MGI:96250]	Q80Y52	P07901	-2.0	1.6E-02	2.3	8.1E-03	-0.1	8.6E-01	-5.0	2.9E-04
ENSMUST00000094363	family with sequence similarity 161, member A [Source:MGI Symbol;Acc:MGI:1921123]	F6XT74		6.2	9.5E-05	-2.6	2.5E-02	0.0	9.7E-01	-0.3	7.4E-01
ENSMUST00000091884	HMG box domain containing 3 [Source:MGI Symbol;Acc:MGI:2441817]	G3X9M3		0.8	9.7E-02	1.4	3.7E-02	0.8	1.1E-01	0.2	7.5E-01
ENSMUST00000091897				2.0	9.1E-02	2.4	8.4E-02	-0.7	5.5E-01	-1.0	3.6E-01
ENSMUST00000091900	PR domain containing 6 [Source:MGI Symbol;Acc:MGI:2684938]		Q3UZD5	2.9	6.1E-02	5.6	2.1E-03	-0.5	7.1E-01	-3.2	1.0E-02
ENSMUST00000094384	MAS-related GPR, member B1 [Source:MGI Symbol;Acc:MGI:3033115]		Q3UG61	6.1	6.2E-05	-7.2	2.8E-03	1.3	4.0E-02	2.1	2.6E-01
ENSMUST00000094390	MAS-related GPR, member X1 [Source:MGI Symbol;Acc:MGI:3033139]		Q8CIP3	7.1	8.3E-05	-0.8	2.5E-01	1.0	5.1E-02	-0.5	5.2E-01
ENSMUST00000091924	polymerase (RNA) III (DNA directed) polypeptide G like [Source:MGI Symbol;Acc:MGI:1917120]		Q8R0C0	0.2	6.6E-01	0.8	2.8E-01	0.4	4.8E-01	-0.2	8.0E-01
ENSMUST00000094391	IQ motif containing D [Source:MGI Symbol;Acc:MGI:1922982]	B2RPX1	Q9D3V1	6.6	1.5E-02	6.3	1.8E-04	-0.6	6.1E-01	-0.4	4.7E-01
ENSMUST00000091967	bridging integrator 1 [Source:MGI Symbol;Acc:MGI:108092]	Q6P1B9		-0.7	5.5E-01	-1.9	1.7E-01	-2.1	4.5E-02	-0.9	5.1E-01
ENSMUST00000091978	phosphoinositide-3-kinase, class 3 [Source:MGI Symbol;Acc:MGI:2445019]	E9QLS6		3.4	1.8E-01	4.5	1.2E-01	-0.7	7.9E-01	-1.9	3.4E-01
ENSMUST00000094398	UEV and lactate/malate dehyrogenase domains [Source:MGI Symbol;Acc:MGI:1860490]		Q3U1V6	-5.1	6.4E-05	6.9	1.9E-04	-0.6	6.1E-01	-0.9	1.9E-01
ENSMUST00000094413	TD and POZ domain containing 1 [Source:MGI Symbol;Acc:MGI:2449436]		P0DMR5	4.5	2.0E-02	4.3	3.2E-04	-0.7	3.7E-01	0.6	2.6E-01
ENSMUST00000094424	sperm acrosome associated 4 [Source:MGI Symbol;Acc:MGI:1916613]		Q80ZQ0	7.2	7.0E-05	6.3	3.7E-03	1.5	3.7E-01	0.9	3.3E-01
ENSMUST00000094434	ferritin light polypeptide 1 [Source:MGI Symbol;Acc:MGI:95589]	Q9CPX4		-7.0	1.9E-06	-0.4	5.2E-01	0.5	2.8E-01	-0.6	3.1E-01
ENSMUST00000094438	hairy and enhancer of split 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:104877]		Q61657	7.4	4.7E-05	-2.7	5.2E-02	0.0	1.0E+00	-1.5	2.9E-01
ENSMUST00000094451	G protein-coupled receptor 157 [Source:MGI Symbol;Acc:MGI:2442046]	Q148S2	Q8C206	4.8	7.4E-06	6.6	9.3E-04	-0.7	6.0E-01	0.4	6.6E-01
ENSMUST00000094452	WSC domain containing 2 [Source:MGI Symbol;Acc:MGI:2445030]		D4PHA7	8.1	4.7E-05	6.3	3.7E-04	-1.4	2.9E-01	-0.8	2.7E-01
ENSMUST00000094460	RIKEN cDNA 2310016G11 gene [Source:MGI Symbol;Acc:MGI:1916828]	Q9D7B4		6.6	3.7E-04	9.2	6.9E-06	-0.6	6.0E-01	-0.2	7.1E-01
ENSMUST00000092073	kelch-like 25 [Source:MGI Symbol;Acc:MGI:2668031]		Q8R2P1	-2.8	1.5E-01	-0.3	9.0E-01	0.6	7.5E-01	-1.9	3.6E-01
ENSMUST00000094463	meningioma 1 [Source:MGI Symbol;Acc:MGI:1261813]	D3YWE6		9.5	1.4E-05	-4.2	1.9E-04	0.9	2.7E-02	0.2	7.7E-01
ENSMUST00000094476	predicted gene 12185 [Source:MGI Symbol;Acc:MGI:3652173]	Q5NCB2		9.4	1.0E-05	2.6	6.3E-03	-0.4	6.0E-01	-0.3	6.3E-01
ENSMUST00000094480	Ras and Rab interactor 2 [Source:MGI Symbol;Acc:MGI:1921280]	F8WGD2		-5.3	3.3E-03	6.7	1.4E-04	-0.9	4.4E-01	0.7	2.6E-01
ENSMUST00000094481	Friend virus susceptibility 1 [Source:MGI Symbol;Acc:MGI:95595]		P70213	2.6	1.0E-03	-1.2	8.7E-02	-0.2	6.5E-01	-1.9	1.8E-02
ENSMUST00000094499	kinesin family member 1C [Source:MGI Symbol;Acc:MGI:1098260]		O35071	-6.1	1.3E-03	-1.3	5.1E-01	3.4	3.6E-02	-2.1	3.7E-01
ENSMUST00000094502	vomeronasal 2, receptor 84 [Source:MGI Symbol;Acc:MGI:3643367]	D3YWE3		3.9	8.5E-03	-2.2	1.1E-02	-0.1	8.1E-01	-0.2	8.3E-01
ENSMUST00000094510	predicted gene 13177 [Source:MGI Symbol;Acc:MGI:3650257]	B1AVU5		6.0	2.7E-04	6.3	1.8E-06	-0.5	4.0E-01	0.1	8.0E-01
ENSMUST00000094532	predicted gene 20449 [Source:MGI Symbol;Acc:MGI:5141914]	E9Q3U2		6.6	3.1E-07	3.0	2.9E-03	-1.4	6.5E-02	0.4	4.8E-01
ENSMUST00000094556	renin 1 structural [Source:MGI Symbol;Acc:MGI:97898]		P06281	8.3	1.3E-05	6.9	9.2E-05	-0.5	6.5E-01	-0.9	1.3E-01
ENSMUST00000094557	golgi transport 1 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915588]		Q9DCQ3	6.9	7.1E-04	-1.9	8.0E-03	-1.7	2.4E-03	-1.1	7.8E-02
ENSMUST00000094559	Rho GTPase activating protein 24 [Source:MGI Symbol;Acc:MGI:1922647]	G3X9N1		-7.6	2.5E-05	-9.5	6.9E-08	-0.4	1.0E-01	-0.8	2.0E-01
ENSMUST00000094569	neurofascin [Source:MGI Symbol;Acc:MGI:104753]		Q810U3	9.2	6.2E-06	7.1	1.3E-04	-0.6	5.8E-01	0.4	5.4E-01
ENSMUST00000094578	Sec31 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916412]		Q3UPL0	-4.1	6.7E-03	-1.3	1.2E-01	1.2	3.6E-02	-0.5	5.4E-01
ENSMUST00000094583	free fatty acid receptor 3 [Source:MGI Symbol;Acc:MGI:2685324]	Q08AU6	Q3UFD7	5.3	7.8E-04	7.7	3.2E-05	-0.5	6.3E-01	-0.1	8.1E-01
ENSMUST00000094587	cDNA sequence BC061212 [Source:MGI Symbol;Acc:MGI:2681870]	Q6P8K3		7.5	1.8E-05	4.4	2.8E-02	-0.8	6.5E-01	-1.1	3.7E-01
ENSMUST00000092219	thymopoietin [Source:MGI Symbol;Acc:MGI:106920]	Q3TNH0	Q61029	-2.9	1.2E-01	-3.2	3.3E-01	1.4	4.5E-01	1.7	5.8E-01
ENSMUST00000094593	DNA segment, Chr 5, ERATO Doi 577, expressed [Source:MGI Symbol;Acc:MGI:1261918]	Q499F0		5.9	1.6E-03	-3.9	1.5E-02	1.2	6.7E-02	-2.0	2.1E-01
ENSMUST00000094604	galactokinase 2 [Source:MGI Symbol;Acc:MGI:1917226]	Q3U3H5	Q68FH4	-3.8	3.3E-03	-2.2	2.3E-01	1.4	1.7E-01	0.3	8.8E-01
ENSMUST00000094615	RIKEN cDNA 5830473C10 gene [Source:MGI Symbol;Acc:MGI:1923342]	F8VQ07		7.3	2.6E-05	5.5	5.5E-03	0.6	7.0E-01	-0.3	7.8E-01
ENSMUST00000094623	chromobox 3 [Source:MGI Symbol;Acc:MGI:108515]	Q9DCC5		5.0	1.6E-02	6.3	1.7E-03	1.6	2.7E-01	0.0	1.0E+00
ENSMUST00000094639	microtubule-associated protein 1 A [Source:MGI Symbol;Acc:MGI:1306776]	A2ARP8		9.3	1.0E-05	-0.2	7.6E-01	0.8	1.5E-01	-1.7	5.8E-02
ENSMUST00000092325	lipid phosphate phosphatase-related protein type 3 [Source:MGI Symbol;Acc:MGI:2388640]			-1.5	3.4E-01	3.2	8.8E-02	0.6	7.0E-01	-4.1	1.8E-02
ENSMUST00000094644	in homology domain containing, family G (with RhoGef domain) member 2 [Source:MGI Symbol;Acc:MGI:2	E9QKB6		-4.4	1.7E-02	6.7	1.2E-04	-0.6	6.1E-01	-1.0	1.1E-01
ENSMUST00000094646	vacuolar protein sorting 4b (yeast) [Source:MGI Symbol;Acc:MGI:1100499]	Q3TN07	P46467	-4.3	6.9E-06	5.3	1.7E-02	-0.6	7.5E-01	1.0	4.0E-01
ENSMUST00000094653	gametocyte specific factor 1-like [Source:MGI Symbol;Acc:MGI:1915486]		Q9CWD0	7.1	6.2E-05	7.3	1.4E-04	-0.6	6.1E-01	0.5	4.2E-01
ENSMUST00000094654	gonadotropin releasing hormone receptor [Source:MGI Symbol;Acc:MGI:95790]	Q6P8H4		6.7	1.8E-04	7.1	1.3E-04	-0.6	6.0E-01	-1.0	1.5E-01
ENSMUST00000094657	DnaJ (Hsp40) homolog, subfamily C, member 8 [Source:MGI Symbol;Acc:MGI:1915848]	A2ALF2	Q6NZB0	-6.2	3.4E-04	7.6	1.4E-04	-0.7	6.2E-01	-1.1	1.3E-01
ENSMUST00000094662	predicted gene 10300 [Source:MGI Symbol;Acc:MGI:3641670]	Q8C8P7		4.2	2.5E-04	-5.6	1.4E-03	0.5	3.1E-01	-0.7	6.0E-01
ENSMUST00000092382	ubiquitin specific peptidase 36 [Source:MGI Symbol;Acc:MGI:1919594]		B1AQJ2	-3.3	1.6E-01	2.1	5.0E-01	4.9	7.0E-02	-0.4	8.8E-01
ENSMUST00000094663	galactose-3-O-sulfotransferase 2 [Source:MGI Symbol;Acc:MGI:2685834]	A2RTS9		7.3	5.9E-03	6.9	3.2E-04	-0.6	6.6E-01	-0.8	2.9E-01
ENSMUST00000094665	phospholipase A2, group IVD [Source:MGI Symbol;Acc:MGI:1925640]		Q50L43	8.3	1.2E-05	-3.9	1.0E-02	0.8	2.2E-01	0.2	8.4E-01
ENSMUST00000094666	transmembrane protein 200B [Source:MGI Symbol;Acc:MGI:3646343]	D3Z0P8		7.3	3.3E-05	6.4	5.7E-04	-0.6	6.3E-01	-0.2	8.0E-01
ENSMUST00000092415	sperm antigen with calponin homology and coiled-coil domains 1 [Source:MGI Symbol;Acc:MGI:2442356]		Q5SXY1	7.0	7.3E-02	1.1	7.4E-01	-3.1	4.2E-01	2.8	3.0E-01
ENSMUST00000092425	ribosomal protein L19 [Source:MGI Symbol;Acc:MGI:98020]	A2A547		-1.8	2.4E-01	-5.1	8.6E-02	-1.0	3.9E-01	2.2	4.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000094681	WAS/WASL interacting protein family, member 1 [Source:MGI Symbol;Acc:MGI:2178801]		Q8K1I7	-6.1	4.9E-03	3.8	3.0E-04	-1.9	1.8E-02	-0.3	5.6E-01
ENSMUST00000092430	transcription factor A, mitochondrial [Source:MGI Symbol;Acc:MGI:107810]		P40630	0.8	1.4E-01	0.1	8.5E-01	0.1	8.3E-01	0.8	2.4E-01
ENSMUST00000092459	CD300 antigen like family member H [Source:MGI Symbol;Acc:MGI:2687214]		Q6SJQ5	-1.3	2.5E-01	-2.8	9.3E-02	-0.2	8.3E-01	1.3	3.9E-01
ENSMUST00000092462	DNA replication helicase 2 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2443732]		Q6ZQJ5	-1.3	6.7E-01	-0.1	9.9E-01	0.8	7.7E-01	-0.4	9.1E-01
ENSMUST00000094693	serine/arginine-rich splicing factor 5 [Source:MGI Symbol;Acc:MGI:98287]		O35326	-5.9	7.2E-05	-8.2	3.6E-04	-0.6	3.5E-01	-0.3	8.6E-01
ENSMUST00000094698	RNA binding motif protein 44 [Source:MGI Symbol;Acc:MGI:2685663]		Q3V089	5.6	2.8E-03	6.9	4.4E-04	-0.6	6.7E-01	-1.6	5.9E-02
ENSMUST00000092473	vacuolar protein sorting 26 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1353654]		P40336	2.6	1.1E-01	4.9	8.2E-03	-0.6	7.2E-01	-2.9	3.3E-02
ENSMUST00000094700	furry homolog-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1919563]	F8VQ05		5.2	5.0E-03	4.2	2.1E-03	-2.2	6.3E-02	0.2	7.8E-01
ENSMUST00000094705	zinc finger protein 575 [Source:MGI Symbol;Acc:MGI:2141921]	B2RX29	Q3TXZ1	6.9	4.0E-06	6.6	1.5E-03	-0.4	8.1E-01	-0.8	3.3E-01
ENSMUST00000094712	predicted gene 12942 [Source:MGI Symbol;Acc:MGI:3758095]		Q3U0Y2	-1.7	2.9E-02	-6.8	1.8E-03	1.4	1.4E-02	4.1	2.7E-02
ENSMUST00000092500	archaelysin family metallopeptidase 2 [Source:MGI Symbol;Acc:MGI:104837]	B1AT59		-0.3	5.7E-01	1.3	8.8E-02	1.3	3.5E-02	-0.3	6.6E-01
ENSMUST00000094753	carcinoembryonic antigen-related cell adhesion molecule 20 [Source:MGI Symbol;Acc:MGI:1918851]	Q9D2Z1		7.2	8.9E-06	-5.2	1.8E-03	3.0	1.4E-04	-0.7	5.8E-01
ENSMUST00000092511	predicted pseudogene 10273 [Source:MGI Symbol;Acc:MGI:3704362]	Q9CXU4		-2.2	2.8E-01	8.4	1.5E-02	7.6	2.0E-02	-3.1	1.2E-01
ENSMUST00000094754	ribosomal protein L7A, pseudogene 8 [Source:MGI Symbol;Acc:MGI:3644288]			5.7	2.2E-03	-6.4	1.6E-03	0.0	9.3E-01	-0.9	5.7E-01
ENSMUST00000094761	serine/threonine kinase 40 [Source:MGI Symbol;Acc:MGI:1921428]		Q7TNL3	-4.5	6.3E-03	7.3	5.1E-05	-0.5	6.5E-01	0.1	8.1E-01
ENSMUST00000092532	nuclear factor I/A [Source:MGI Symbol;Acc:MGI:108056]		Q02780	6.2	6.7E-02	8.1	3.2E-02	-0.4	9.2E-01	-2.2	2.2E-01
ENSMUST00000094782	inositol polyphosphate-5-phosphatase B [Source:MGI Symbol;Acc:MGI:103257]		Q8K337	-7.4	2.1E-04	-2.4	9.1E-02	0.6	4.1E-01	-0.9	5.4E-01
ENSMUST00000094783	protocadherin 7 [Source:MGI Symbol;Acc:MGI:1860487]	E9Q2S0		8.2	8.4E-06	5.9	9.9E-05	-0.7	4.2E-01	-0.1	8.9E-01
ENSMUST00000092557	Rho GTPase activating protein 27 [Source:MGI Symbol;Acc:MGI:1916903]	A2AKN5		1.0	4.6E-01	5.2	2.5E-02	2.3	2.5E-01	-1.9	1.4E-01
ENSMUST00000094787	solute carrier family 34 (sodium phosphate), member 2 [Source:MGI Symbol;Acc:MGI:1342284]		Q9DBP0	7.6	4.9E-05	-1.3	3.6E-02	1.0	9.9E-03	-0.3	6.1E-01
ENSMUST00000094790	gastric inhibitory polypeptide receptor [Source:MGI Symbol;Acc:MGI:1352753]		Q0P543	7.6	8.5E-05	2.8	7.5E-02	-3.3	6.4E-02	0.1	9.1E-01
ENSMUST00000092569	coiled-coil domain containing 43 [Source:MGI Symbol;Acc:MGI:1289318]		Q9CR29	-3.4	1.9E-01	-1.5	4.7E-01	-1.4	3.7E-01	-3.3	2.2E-01
ENSMUST00000092576	Rous sarcoma oncogene [Source:MGI Symbol;Acc:MGI:98397]		P05480	5.7	9.7E-02	5.0	1.7E-01	-0.9	8.1E-01	-0.2	9.4E-01
ENSMUST00000094794	pregnancy-specific glycoprotein 27 [Source:MGI Symbol;Acc:MGI:1891359]	Q497W2		6.5	1.8E-04	-4.3	6.9E-03	1.1	1.0E-01	-0.4	7.4E-01
ENSMUST00000094795	pregnancy-specific glycoprotein 25 [Source:MGI Symbol;Acc:MGI:1891357]	Q497W1		8.7	1.0E-05	3.2	4.5E-03	0.0	9.9E-01	0.2	7.0E-01
ENSMUST00000094798	pregnancy-specific glycoprotein 26 [Source:MGI Symbol;Acc:MGI:1891358]	Q4KL65		6.7	1.0E-04	4.4	4.6E-02	-0.7	7.4E-01	0.1	9.7E-01
ENSMUST00000094801	tetratricopeptide repeat domain 17 [Source:MGI Symbol;Acc:MGI:1921819]	A2AFY7		-4.1	4.7E-05	-3.0	1.1E-02	1.0	7.7E-02	-0.2	8.4E-01
ENSMUST00000094805	coiled-coil domain containing 8 [Source:MGI Symbol;Acc:MGI:3612184]		D3YZV8	6.4	3.9E-06	-8.1	4.5E-04	-1.3	5.3E-02	-0.4	8.2E-01
ENSMUST00000092621	lactate dehydrogenase A [Source:MGI Symbol;Acc:MGI:96759]	D3Z736		-2.5	7.8E-02	-1.9	1.6E-01	-0.5	5.9E-01	-1.1	4.7E-01
ENSMUST00000094807	PNMA-like 2 [Source:MGI Symbol;Acc:MGI:3645856]	G3X9N3		7.8	1.1E-05	6.5	1.8E-04	-0.5	6.6E-01	-0.4	5.3E-01
ENSMUST00000094814	)0-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 [Source:MGI Symbol;Acc:MGI:1	A2A7E7	Q9WUL8	4.6	5.5E-04	8.4	1.1E-04	0.4	7.6E-01	0.5	4.1E-01
ENSMUST00000094815	SUMO1 activating enzyme subunit 1 [Source:MGI Symbol;Acc:MGI:1929264]		Q9R1T2	-2.0	1.1E-03	7.5	9.5E-05	-0.6	6.1E-01	0.6	3.4E-01
ENSMUST00000094823	claudin 19 [Source:MGI Symbol;Acc:MGI:3033992]	Q3UNX6	Q9ET38	8.8	1.2E-05	7.9	8.7E-05	-1.5	2.8E-01	-0.9	1.6E-01
ENSMUST00000094829	vomeronasal 1 receptor 85 [Source:MGI Symbol;Acc:MGI:2182262]	Q8VIB8		6.2	1.1E-04	-0.3	6.0E-01	0.5	3.1E-01	-0.8	2.2E-01
ENSMUST00000094832	olfactory receptor 1339 [Source:MGI Symbol;Acc:MGI:3031173]	Q8VGB1		7.1	4.1E-05	0.0	9.7E-01	0.8	2.4E-01	-1.3	2.1E-01
ENSMUST00000092646	mediator complex subunit 23 [Source:MGI Symbol;Acc:MGI:1917458]	E9QNV2		3.4	6.7E-02	1.7	3.7E-01	-1.9	2.8E-01	-0.1	9.4E-01
ENSMUST00000092648	enhancer of zeste homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:107940]		Q61188	-1.8	4.0E-01	-0.2	9.6E-01	1.4	4.9E-01	-0.2	9.5E-01
ENSMUST00000094833	zinc finger and BTB domain containing 49 [Source:MGI Symbol;Acc:MGI:1922329]		Q8BXX2	6.8	2.0E-03	5.1	1.2E-02	-0.6	7.1E-01	0.9	4.0E-01
ENSMUST00000094836	serine/threonine kinase 32B [Source:MGI Symbol;Acc:MGI:1927552]		Q9JJX8	7.9	2.0E-05	5.9	6.7E-04	-0.6	6.3E-01	0.4	5.3E-01
ENSMUST00000094844	coiled-coil domain containing 108 [Source:MGI Symbol;Acc:MGI:2444274]		Q3V0B4	8.3	1.8E-05	6.2	1.6E-04	-0.5	6.2E-01	-0.6	3.1E-01
ENSMUST00000094868	zinc finger, FYVE domain containing 28 [Source:MGI Symbol;Acc:MGI:2684992]		Q6ZPK7	7.6	6.8E-06	-2.3	1.2E-01	1.4	1.1E-01	-0.4	7.7E-01
ENSMUST00000094870	zinc finger protein 787 [Source:MGI Symbol;Acc:MGI:1914359]		Q8BIF9	-2.1	3.2E-03	-4.8	7.7E-02	0.2	8.7E-01	-0.2	9.4E-01
ENSMUST00000094887	cytochrome P450, family 4, subfamily a, polypeptide 12B [Source:MGI Symbol;Acc:MGI:3611747]	A2A974		7.0	3.0E-05	4.4	1.8E-03	-0.4	7.3E-01	1.5	4.2E-02
ENSMUST00000092673	serum/glucocorticoid regulated kinase 1 [Source:MGI Symbol;Acc:MGI:1340062]		Q9WVC6	0.6	6.2E-01	-1.2	5.9E-01	1.2	4.2E-01	2.9	1.4E-01
ENSMUST00000094892	interleukin 11 [Source:MGI Symbol;Acc:MGI:107613]	A3KPB8	P47873	7.0	3.6E-05	0.6	3.3E-01	0.5	3.2E-01	-5.1	1.7E-04
ENSMUST00000094894	TraB domain containing 2B [Source:MGI Symbol;Acc:MGI:3650152]		B1ATG9	9.1	3.3E-06	-4.4	7.5E-02	2.7	3.0E-02	2.1	3.4E-01
ENSMUST00000094897	dynein, axonemal assembly factor 3 [Source:MGI Symbol;Acc:MGI:3588207]		Q3UYV8	2.2	5.2E-03	3.2	3.3E-03	-0.6	4.3E-01	-0.8	2.9E-01
ENSMUST00000094906	par-3 family cell polarity regulator beta [Source:MGI Symbol;Acc:MGI:1919301]	Q5SV54		7.4	4.1E-04	0.5	7.8E-01	-4.5	4.0E-02	1.9	1.7E-01
ENSMUST00000094916	low density lipoprotein receptor class A domain containing 1 [Source:MGI Symbol;Acc:MGI:3652166]	D3YYZ1		5.9	3.5E-04	6.8	1.3E-04	-0.5	6.5E-01	0.3	6.4E-01
ENSMUST00000094933	ubiquitin specific peptidase 24 [Source:MGI Symbol;Acc:MGI:1919936]		B1AY13	-6.4	1.2E-03	6.1	7.3E-03	-0.6	7.6E-01	-0.5	6.4E-01
ENSMUST00000094946	predicted gene 10471 [Source:MGI Symbol;Acc:MGI:3641900]	E9Q1C7		7.5	8.3E-05	6.8	1.0E-03	-0.4	8.1E-01	-2.1	2.8E-02
ENSMUST00000094962	lysine (K)-specific methyltransferase 2E [Source:MGI Symbol;Acc:MGI:1924825]		Q3UG20	-7.5	1.9E-04	5.4	5.5E-03	-0.7	6.7E-01	1.1	2.6E-01
ENSMUST00000094964	dynein, axonemal, heavy chain 7A [Source:MGI Symbol;Acc:MGI:2685838]	E9Q0T8		6.5	1.3E-04	5.7	3.9E-03	1.6	2.6E-01	-0.5	6.2E-01
ENSMUST00000094977	predicted gene 13288 [Source:MGI Symbol;Acc:MGI:3701985]	Q8CD73		6.9	2.3E-05	3.4	1.0E-03	-0.3	6.4E-01	0.5	3.7E-01
ENSMUST00000092723	AT rich interactive domain 1B (SWI-like) [Source:MGI Symbol;Acc:MGI:1926129]	E9Q6R4		-1.2	1.7E-01	0.5	6.2E-01	0.7	3.7E-01	-1.1	2.9E-01
ENSMUST00000094993	kelch-like 9 [Source:MGI Symbol;Acc:MGI:2180122]		Q6ZPT1	-3.6	1.7E-04	5.1	7.1E-02	-0.8	7.6E-01	0.8	6.3E-01
ENSMUST00000095004	predicted gene 7347 [Source:MGI Symbol;Acc:MGI:3645983]	D3YYI9		8.2	7.5E-06	8.0	2.4E-05	-0.6	6.1E-01	-1.4	2.7E-02
ENSMUST00000095017	cyclin D binding myb-like transcription factor 1 [Source:MGI Symbol;Acc:MGI:1344415]		Q8CE22	-7.3	1.1E-04	-4.2	7.8E-02	0.8	5.0E-01	-2.6	3.7E-01
ENSMUST00000095045	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 [Source:MGI Symbo	E9PUI0		7.8	2.0E-04	6.8	3.8E-05	-1.7	1.2E-01	0.2	7.2E-01
ENSMUST00000095048	RAB7, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105068]	Q4FJQ0	P51150	-8.6	1.2E-05	6.6	2.5E-04	-0.5	6.7E-01	-1.1	1.3E-01
ENSMUST00000092794	musashi RNA-binding protein 2 [Source:MGI Symbol;Acc:MGI:1923876]	Q3TE41	Q920Q6	-1.4	2.8E-01	1.0	5.1E-01	1.5	2.4E-01	-0.9	5.2E-01
ENSMUST00000095070	DnaJ (Hsp40) homolog, subfamily C, member 25 [Source:MGI Symbol;Acc:MGI:1919679]		A2ALW5	2.6	4.4E-03	6.3	4.6E-04	-0.6	6.6E-01	-3.1	5.3E-03
ENSMUST00000092802	myotubularin related protein 4 [Source:MGI Symbol;Acc:MGI:2180699]		Q91XS1	-2.1	2.0E-01	2.5	5.2E-01	7.4	2.4E-02	2.8	3.4E-01
ENSMUST00000092821	breast carcinoma amplified sequence 3 [Source:MGI Symbol;Acc:MGI:2385848]	Q0VF62		-3.5	3.6E-02	-2.6	1.9E-01	0.5	5.7E-01	-0.4	8.6E-01
ENSMUST00000092822	breast carcinoma amplified sequence 3 [Source:MGI Symbol;Acc:MGI:2385848]	B1AR76		-2.6	7.8E-02	0.3	8.0E-01	0.5	6.5E-01	-2.4	1.1E-01
ENSMUST00000095074	progestin and adipoQ receptor family member VII [Source:MGI Symbol;Acc:MGI:1919154]		Q80ZE4	4.5	8.1E-05	1.9	3.6E-02	0.9	1.7E-01	0.8	2.4E-01
ENSMUST00000095075	cysteine-rich secretory protein LCCL domain containing 1 [Source:MGI Symbol;Acc:MGI:1934666]		Q8CGD2	7.6	3.1E-05	-9.8	2.5E-06	0.8	2.9E-02	0.0	9.6E-01
ENSMUST00000092844	RAD51 homolog D [Source:MGI Symbol;Acc:MGI:1261809]	B1ARD4		-0.1	9.6E-01	-0.9	7.2E-01	-2.2	2.4E-01	-1.4	6.0E-01
ENSMUST00000092849	ligase III, DNA, ATP-dependent [Source:MGI Symbol;Acc:MGI:109152]	Q80ZH7		2.3	2.6E-01	-3.4	2.7E-01	-3.3	6.9E-02	2.4	4.3E-01
ENSMUST00000095076	erythrocyte membrane protein band 4.1 like 4b [Source:MGI Symbol;Acc:MGI:1859149]	A2ALK6		7.0	2.3E-05	8.7	3.5E-04	-0.8	6.7E-01	-2.1	3.6E-02
ENSMUST00000092858				-0.8	4.6E-01	-0.9	5.9E-01	0.5	6.8E-01	0.6	7.1E-01
ENSMUST00000095079	actin-like 7a [Source:MGI Symbol;Acc:MGI:1343051]		Q9QY84	6.3	1.3E-04	3.7	9.8E-03	1.3	2.3E-01	0.3	7.5E-01
ENSMUST00000092880	TLC domain containing 1 [Source:MGI Symbol;Acc:MGI:1915572]		Q99JT6	0.4	5.5E-01	2.0	2.1E-02	0.2	7.4E-01	-1.4	5.0E-02
ENSMUST00000095083	spectrin alpha, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98386]		P16546	-8.8	2.0E-05	7.6	1.7E-05	-1.5	1.8E-01	0.0	9.9E-01
ENSMUST00000092884	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]		Q9JMH9	0.0	9.9E-01	1.8	5.8E-01	1.7	4.4E-01	-0.1	9.6E-01
ENSMUST00000095086	acyl-coenzyme A amino acid N-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2140197]		A2AKK5	6.3	2.8E-02	-1.4	4.9E-01	1.7	1.9E-01	-0.4	8.3E-01
ENSMUST00000092888	fructose bisphosphatase 1 [Source:MGI Symbol;Acc:MGI:95492]		Q9QXD6	-1.0	5.8E-02	0.3	5.9E-01	1.0	4.9E-02	-0.3	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000092889	TAO kinase 3 [Source:MGI Symbol;Acc:MGI:3041177]		Q8BYC6	-1.3	5.8E-01	2.8	3.7E-01	1.5	5.9E-01	-2.7	3.0E-01
ENSMUST00000095097	forkhead box E1 [Source:MGI Symbol;Acc:MGI:1353500]		Q8R2I0	6.5	2.9E-04	6.3	2.4E-04	-0.6	6.3E-01	-0.8	2.0E-01
ENSMUST00000095107	calicin [Source:MGI Symbol;Acc:MGI:3045316]	B2RX51	Q8CDE2	2.4	6.4E-03	1.7	4.6E-01	-1.2	6.0E-01	2.7	1.5E-01
ENSMUST00000095109	histidine rich carboxyl terminus 1 [Source:MGI Symbol;Acc:MGI:1917945]		Q9D6B9	7.6	3.9E-05	5.7	5.5E-03	-1.5	3.6E-01	-0.8	3.9E-01
ENSMUST00000092915	clustered mitochondria (cluA/CLU1) homolog [Source:MGI Symbol;Acc:MGI:1921398]			-1.9	1.6E-01	-1.7	3.2E-01	-0.1	9.1E-01	-0.3	8.6E-01
ENSMUST00000095114	chemokine (C-C motif) ligand 21A (serine) [Source:MGI Symbol;Acc:MGI:1349183]		P84444	7.7	4.7E-04	6.3	1.7E-04	-0.5	6.3E-01	-0.8	1.9E-01
ENSMUST00000092937	calcium/calmodulin-dependent protein kinase kinase 1, alpha [Source:MGI Symbol;Acc:MGI:1891766]		Q8VBY2	-3.3	7.3E-02	-1.1	5.5E-01	0.4	7.8E-01	-1.8	3.7E-01
ENSMUST00000092940	spinster homolog 3 [Source:MGI Symbol;Acc:MGI:1924827]		Q9D232	0.8	3.2E-01	4.3	6.0E-03	2.6	3.6E-02	-0.9	3.2E-01
ENSMUST00000092955	AHNAK nucleoprotein (desmoyokin) [Source:MGI Symbol;Acc:MGI:1316648]	G5E8K8		-1.0	2.8E-01	-2.3	4.9E-02	-1.6	4.6E-02	-0.3	7.6E-01
ENSMUST00000095128	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 [Source:MGI Symbol;Acc:MGI:2684983]	A2AP31	Q3UIU2	-5.7	6.5E-04	-1.1	3.2E-02	-0.2	5.4E-01	-0.5	2.6E-01
ENSMUST00000095129	predicted gene 136 [Source:MGI Symbol;Acc:MGI:2684982]	A2AT48	Q3V037	6.7	1.4E-04	8.8	7.6E-04	-0.7	7.3E-01	-1.9	6.5E-02
ENSMUST00000092973	centrobin, centrosomal BRCA2 interacting protein [Source:MGI Symbol;Acc:MGI:2443290]		Q8CB62	0.9	5.9E-01	0.5	8.3E-01	1.8	4.1E-01	2.1	3.0E-01
ENSMUST00000095132	sperm associated antigen 6 like [Source:MGI Symbol;Acc:MGI:3040687]	Q3V0U9		6.0	5.0E-04	4.1	3.8E-03	-6.4	8.8E-04	-0.2	7.4E-01
ENSMUST00000095141	PR domain containing 13 [Source:MGI Symbol;Acc:MGI:2448528]		E9PZZ1	6.8	2.3E-03	-2.3	1.0E-01	0.5	5.3E-01	-0.9	5.1E-01
ENSMUST00000095147	dehydrogenase E1 and transketolase domain containing 1 [Source:MGI Symbol;Acc:MGI:2445096]		A2ATU0	6.4	2.0E-06	7.8	3.0E-05	0.3	7.9E-01	-0.5	3.3E-01
ENSMUST00000095157	PHD finger protein 11D [Source:MGI Symbol;Acc:MGI:1277133]		A6H5X4	7.5	1.4E-05	6.3	5.5E-04	-0.6	6.5E-01	-0.4	5.4E-01
ENSMUST00000095171	ATPase, Ca++ transporting, type 2C, member 2 [Source:MGI Symbol;Acc:MGI:1916297]		A7L9Z8	6.3	5.8E-05	4.8	1.3E-01	-2.1	5.2E-01	0.2	9.0E-01
ENSMUST00000095176	zinc and ring finger 1 [Source:MGI Symbol;Acc:MGI:2177308]		Q91V17	-6.8	5.5E-04	7.6	2.8E-04	-1.3	3.8E-01	0.2	7.4E-01
ENSMUST00000095186	predicted gene 10309 [Source:MGI Symbol;Acc:MGI:3641941]	Q8C648		7.2	1.2E-05	6.8	9.2E-04	-0.7	6.7E-01	0.0	9.6E-01
ENSMUST00000095204	RAS, guanyl releasing protein 3 [Source:MGI Symbol;Acc:MGI:3028579]	Q6NZH9		3.6	1.1E-03	7.6	4.1E-05	-0.6	6.1E-01	-0.6	3.2E-01
ENSMUST00000093039	ke RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor [Source:MGI Symbol;Acc:MGI:1		Q91WQ5	2.2	2.7E-01	4.4	3.9E-02	-0.8	6.6E-01	-3.0	9.6E-02
ENSMUST00000095208	calpain 13 [Source:MGI Symbol;Acc:MGI:2685789]		Q3UW68	6.8	1.9E-04	-5.1	5.8E-04	1.3	1.3E-02	-1.4	2.6E-01
ENSMUST00000093043	growth arrest specific 8 [Source:MGI Symbol;Acc:MGI:1202386]	Q49MD7	Q60779	1.1	4.5E-02	2.2	5.6E-03	0.2	6.9E-01	-0.9	1.3E-01
ENSMUST00000093046	target of myb1-like 2 (chicken) [Source:MGI Symbol;Acc:MGI:2443306]	Q5SXA5		2.7	3.4E-01	4.4	3.0E-01	2.9	4.0E-01	1.1	7.3E-01
ENSMUST00000095211	carboxylesterase 1A [Source:MGI Symbol;Acc:MGI:3648919]	E9PYP1		7.4	5.6E-05	3.2	5.9E-03	-0.2	8.1E-01	0.2	8.1E-01
ENSMUST00000095214	CTD nuclear envelope phosphatase 1 regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1921981]		Q3UJ81	-5.8	2.9E-04	5.3	5.9E-04	-2.1	9.9E-02	-0.5	4.6E-01
ENSMUST00000095218	ribosomal protein L7A, pseudogene 5 [Source:MGI Symbol;Acc:MGI:3643553]			5.3	6.3E-03	-5.2	7.4E-04	1.3	2.5E-02	-1.2	3.8E-01
ENSMUST00000095224	scaffold attachment factor B [Source:MGI Symbol;Acc:MGI:2146974]		D3YXK2	-8.3	5.5E-04	-0.9	4.1E-01	0.6	4.3E-01	-4.8	7.0E-03
ENSMUST00000095259	GTP binding protein 3 [Source:MGI Symbol;Acc:MGI:1917609]		Q923K4	-4.8	8.7E-04	-4.0	6.4E-02	1.1	2.6E-01	1.8	3.7E-01
ENSMUST00000095261	ATP-binding cassette, sub-family C (CFTR/MRP), member 10 [Source:MGI Symbol;Acc:MGI:2386976]		Q8R4P9	3.7	5.2E-04	-2.7	1.0E-01	3.8	6.1E-04	-0.8	6.3E-01
ENSMUST00000095262	leucine rich repeat containing 73 [Source:MGI Symbol;Acc:MGI:2684934]	B2RWC4		4.2	8.7E-04	6.6	6.1E-05	-1.4	2.0E-01	-0.3	6.3E-01
ENSMUST00000095263	Yip1 domain family, member 3 [Source:MGI Symbol;Acc:MGI:106280]		Q3UDR8	-3.4	1.6E-04	6.4	9.4E-04	0.2	9.0E-01	-1.1	1.7E-01
ENSMUST00000093110	mesenteric estrogen dependent adipogenesis [Source:MGI Symbol;Acc:MGI:1917967]		Q14BA6	3.6	8.3E-02	7.2	7.8E-03	0.1	9.7E-01	-3.5	2.0E-02
ENSMUST00000095266	neurexophilin 4 [Source:MGI Symbol;Acc:MGI:1336197]	G3X9N5		6.9	7.0E-05	8.1	1.8E-05	-0.5	6.3E-01	-0.3	5.1E-01
ENSMUST00000095267	jun D proto-oncogene [Source:MGI Symbol;Acc:MGI:96648]		P15066	-4.8	3.5E-05	-4.2	2.5E-03	0.1	8.1E-01	0.2	8.3E-01
ENSMUST00000093120	lysyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1934754]	Q8R2P8		0.8	2.7E-01	0.4	6.7E-01	-0.8	2.5E-01	-0.3	6.9E-01
ENSMUST00000095270	solute carrier family 26, member 10 [Source:MGI Symbol;Acc:MGI:2143920]	F8WGV3		3.3	8.6E-04	5.8	2.8E-02	-0.8	7.4E-01	1.8	2.0E-01
ENSMUST00000095273	nuclear receptor 2C2-associated protein [Source:MGI Symbol;Acc:MGI:1922942]		Q3TV70	-2.0	7.1E-03	-8.4	1.7E-04	-0.9	4.4E-02	0.7	6.4E-01
ENSMUST00000095310	oxysterol binding protein-like 8 [Source:MGI Symbol;Acc:MGI:2443807]	G3X9N6		-3.7	3.3E-02	-1.5	3.3E-01	0.9	3.2E-01	-1.1	4.9E-01
ENSMUST00000095313	PRKC, apoptosis, WT1, regulator [Source:MGI Symbol;Acc:MGI:2149961]		Q925B0	6.0	5.2E-04	-1.6	7.9E-02	0.9	1.1E-01	-1.9	6.8E-02
ENSMUST00000095323	RIKEN cDNA 1700029J07 gene [Source:MGI Symbol;Acc:MGI:1916729]		Q3U1D9	6.5	8.6E-05	9.1	2.6E-04	0.5	7.5E-01	0.8	2.6E-01
ENSMUST00000095326	coiled-coil domain containing 110 [Source:MGI Symbol;Acc:MGI:2685018]		Q3V125	8.8	2.0E-04	2.5	3.5E-02	2.2	2.4E-02	-3.8	5.2E-03
ENSMUST00000095333	ubiquitin specific peptidase 44 [Source:MGI Symbol;Acc:MGI:3045318]	A0A0A0MQB2		7.7	1.9E-05	0.7	6.6E-01	-5.0	2.4E-02	2.1	1.6E-01
ENSMUST00000095345	membrane bound O-acyltransferase domain containing 4 [Source:MGI Symbol;Acc:MGI:2685017]		P0C7A3	7.4	8.9E-06	-2.0	1.4E-02	1.0	2.8E-02	-0.1	8.6E-01
ENSMUST00000095347	bromodomain containing 2 [Source:MGI Symbol;Acc:MGI:99495]	U3KLT0		-7.2	6.2E-05	0.0	9.9E-01	0.9	2.4E-02	-0.2	6.1E-01
ENSMUST00000095350	AE binding protein 2 [Source:MGI Symbol;Acc:MGI:1338038]	F8WGQ1		2.7	2.2E-02	8.6	1.1E-05	-0.6	5.8E-01	-0.3	4.8E-01
ENSMUST00000095360	insulin-like growth factor 1 [Source:MGI Symbol;Acc:MGI:96432]	Q4VJC0	P05017	8.7	6.8E-04	-8.4	3.6E-03	1.7	1.8E-02	0.0	9.9E-01
ENSMUST00000093169	predicted gene 12166 [Source:MGI Symbol;Acc:MGI:3650635]		Q5SSN7	0.4	8.8E-01	0.6	8.6E-01	-0.1	9.7E-01	-0.3	9.2E-01
ENSMUST00000095375	testis expressed gene 24 [Source:MGI Symbol;Acc:MGI:1921539]	Q5DP50		6.9	2.3E-05	-6.8	1.2E-04	-0.1	6.9E-01	-0.6	6.1E-01
ENSMUST00000095383	transmembrane protein 263 [Source:MGI Symbol;Acc:MGI:2143652]		Q9DAM7	2.3	1.5E-03	5.5	1.1E-05	-1.3	6.4E-02	0.3	4.3E-01
ENSMUST00000093191	spindle apparatus coiled-coil protein 1 [Source:MGI Symbol;Acc:MGI:1917635]		Q923A2	0.1	9.3E-01	-1.0	2.7E-01	-1.5	4.4E-02	-0.5	5.6E-01
ENSMUST00000093192	family with sequence similarity 196, member B [Source:MGI Symbol;Acc:MGI:3643491]		Q6GQV1	2.4	3.1E-01	3.0	1.7E-01	-2.9	2.0E-01	-3.5	9.2E-02
ENSMUST00000095410	WD repeat domain 20 [Source:MGI Symbol;Acc:MGI:1916891]	Q3UWE6		-1.4	2.2E-02	-3.8	1.6E-04	0.4	2.0E-01	-0.5	4.6E-01
ENSMUST00000093196	high mobility group box 1 [Source:MGI Symbol;Acc:MGI:96113]	Q58EV5	P63158	-2.6	4.1E-02	-3.9	3.6E-03	-2.7	2.4E-03	-1.3	3.1E-01
ENSMUST00000095412	killer cell lectin-like receptor subfamily K, member 1 [Source:MGI Symbol;Acc:MGI:1196250]		O54709	3.7	1.0E-02	-8.0	5.6E-05	-0.4	2.7E-01	-1.0	4.3E-01
ENSMUST00000095426	IZUMO family member 4 [Source:MGI Symbol;Acc:MGI:1918814]		D3Z690	-1.5	1.9E-02	-2.4	4.8E-01	3.1	1.0E-01	-0.8	8.2E-01
ENSMUST00000093207	hemoglobin alpha, adult chain 2 [Source:MGI Symbol;Acc:MGI:96016]	Q91VB8		-2.6	5.7E-02	-3.1	2.8E-02	-3.1	8.2E-03	-2.6	7.5E-02
ENSMUST00000095427	mitochondrial carrier homolog 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1929261]		Q791T5	-5.1	1.8E-03	-3.8	8.6E-04	-4.4	5.2E-05	-3.6	4.3E-03
ENSMUST00000095440	A kinase (PRKA) anchor protein 3 [Source:MGI Symbol;Acc:MGI:1341149]		O88987	7.8	1.5E-05	5.7	3.1E-03	-0.1	9.5E-01	0.0	9.5E-01
ENSMUST00000093221	carboxylesterase 3B [Source:MGI Symbol;Acc:MGI:3644960]		Q8VCU1	2.7	1.8E-01	0.8	6.6E-01	-2.2	2.3E-01	-0.3	8.6E-01
ENSMUST00000093222	carboxylesterase 3A [Source:MGI Symbol;Acc:MGI:102773]		Q63880	4.8	6.0E-02	3.2	1.8E-01	-2.2	3.9E-01	-0.6	7.0E-01
ENSMUST00000093223	carboxylesterase 3A [Source:MGI Symbol;Acc:MGI:102773]		Q63880	5.9	4.9E-02	4.3	1.7E-01	-0.7	8.1E-01	0.8	6.7E-01
ENSMUST00000095457	polypyrimidine tract binding protein 1 [Source:MGI Symbol;Acc:MGI:97791]	Q8CB58		-8.4	5.5E-06	7.5	2.4E-05	-0.9	4.0E-01	0.1	8.6E-01
ENSMUST00000093239	mitochondrial translational initiation factor 2 [Source:MGI Symbol;Acc:MGI:1924034]		Q91YJ5	0.4	7.8E-01	3.3	5.4E-02	0.1	9.3E-01	-2.8	5.3E-02
ENSMUST00000095458	small integral membrane protein 15 [Source:MGI Symbol;Acc:MGI:1922866]		Q3UTD9	-4.1	2.7E-05	2.8	2.3E-01	-1.5	4.7E-01	4.7	2.4E-02
ENSMUST00000095464	outer dense fiber of sperm tails 3-like 2 [Source:MGI Symbol;Acc:MGI:2686003]		Q3TZ65	7.8	9.7E-05	-5.7	3.0E-03	-1.4	4.1E-02	-1.2	4.6E-01
ENSMUST00000093271	adhesion G protein-coupled receptor G1 [Source:MGI Symbol;Acc:MGI:1340051]		Q8K209	-0.1	9.3E-01	2.0	3.0E-01	0.3	8.5E-01	-1.8	2.9E-01
ENSMUST00000095467	diffuse panbronchiolitis critical region 1 (human) [Source:MGI Symbol;Acc:MGI:2685476]		Q3TNW5	10.6	5.1E-05	-4.2	9.9E-03	0.6	3.2E-01	-1.2	4.6E-01
ENSMUST00000093292	SERTA domain containing 2 [Source:MGI Symbol;Acc:MGI:1931026]	Q3UGZ1	Q9JJG5	-3.4	6.3E-02	3.0	1.5E-01	1.6	3.4E-01	-4.8	2.0E-02
ENSMUST00000093298	sprouty-related, EVH1 domain containing 2 [Source:MGI Symbol;Acc:MGI:2150019]		Q924S7	1.0	5.5E-01	4.5	3.6E-02	0.2	9.1E-01	-3.4	4.1E-02
ENSMUST00000095471	ribosomal protein S2, pseudogene 6 [Source:MGI Symbol;Acc:MGI:3644876]			5.9	2.1E-03	1.0	1.9E-01	0.0	9.6E-01	0.6	3.4E-01
ENSMUST00000093301	2-oxoglutarate and iron-dependent oxygenase domain containing 1 [Source:MGI Symbol;Acc:MGI:2442978]		Q3U0K8	4.7	1.7E-01	4.3	2.7E-01	-0.5	9.0E-01	-0.1	9.7E-01
ENSMUST00000095487	WAP, FS, Ig, KU, and NTR-containing protein 1 [Source:MGI Symbol;Acc:MGI:2670967]		Q8R0S6	3.2	3.8E-03	4.3	1.1E-01	-0.6	8.2E-01	0.9	5.6E-01
ENSMUST00000093321	growth factor receptor bound protein 10 [Source:MGI Symbol;Acc:MGI:103232]		Q60760	1.6	3.9E-01	4.9	4.5E-02	0.9	6.8E-01	-2.4	1.4E-01
ENSMUST00000095491	predicted gene 9507 [Source:MGI Symbol;Acc:MGI:3779917]	D3Z5T3		8.1	8.1E-05	2.7	8.6E-03	-0.3	6.6E-01	-0.6	3.6E-01
ENSMUST00000095500	coiled-coil domain containing 78 [Source:MGI Symbol;Acc:MGI:2685784]		D3Z5T1	5.7	6.1E-04	7.1	7.4E-05	-0.6	6.0E-01	-1.0	1.2E-01
ENSMUST00000095517	component of oligomeric golgi complex 8 [Source:MGI Symbol;Acc:MGI:2142885]		Q9JJA2	1.4	7.1E-03	-4.7	4.6E-03	1.1	5.3E-02	1.0	4.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000093350	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) [Source:MGI Symbol;Acc:MGI:1098267]		Q60597	-1.2	4.2E-01	-2.3	4.4E-01	2.3	2.1E-01	3.4	2.1E-01
ENSMUST00000095521	zinc finger, DHHC-type containing 22 [Source:MGI Symbol;Acc:MGI:2685108]		A0PK84	5.9	1.4E-04	4.7	9.6E-02	-0.9	7.4E-01	0.4	8.1E-01
ENSMUST00000095527	leucine rich repeat containing 74A [Source:MGI Symbol;Acc:MGI:3646959]	F6QBN8		7.9	2.2E-05	-4.3	2.7E-03	0.1	8.3E-01	-0.1	9.5E-01
ENSMUST00000095529	fibroblast growth factor 14 [Source:MGI Symbol;Acc:MGI:109189]	O89096		6.3	1.3E-02	-0.6	3.8E-01	0.8	8.8E-02	0.2	7.6E-01
ENSMUST00000093362	upregulator of cell proliferation [Source:MGI Symbol;Acc:MGI:1919296]		Q5NCI0	0.2	7.5E-01	-2.6	9.6E-02	1.2	1.3E-01	4.1	1.5E-02
ENSMUST00000093365	Ewing sarcoma breakpoint region 1 [Source:MGI Symbol;Acc:MGI:99960]	Q5SUS8		-0.3	7.7E-01	0.5	6.8E-01	0.3	7.6E-01	-0.5	6.6E-01
ENSMUST00000095536	tubulin tyrosine ligase-like family, member 5 [Source:MGI Symbol;Acc:MGI:2443657]	Q8C125		5.9	1.0E-05	7.3	9.2E-04	0.9	5.3E-01	0.6	4.3E-01
ENSMUST00000093374	neurofibromatosis 2 [Source:MGI Symbol;Acc:MGI:97307]	F8WJ43		-0.5	6.5E-01	2.5	5.9E-02	0.9	4.2E-01	-2.1	6.2E-02
ENSMUST00000095541	sushi domain containing 2 [Source:MGI Symbol;Acc:MGI:1918983]		Q9DBX3	8.2	3.6E-05	2.7	5.0E-02	-2.6	5.7E-02	-1.0	3.3E-01
ENSMUST00000093381	coiled-coil domain containing 157 [Source:MGI Symbol;Acc:MGI:3041210]		Q5SPX1	0.5	7.7E-01	0.6	8.1E-01	0.8	6.3E-01	0.8	7.0E-01
ENSMUST00000095544	neuropeptide W [Source:MGI Symbol;Acc:MGI:2685781]	F7B5D6		4.6	1.3E-03	1.9	5.8E-03	0.2	6.8E-01	0.1	8.2E-01
ENSMUST00000093393	TBC1 domain family, member 9 [Source:MGI Symbol;Acc:MGI:1918560]		Q3UYK3	0.1	7.9E-01	1.1	1.5E-01	1.0	9.3E-02	0.0	9.8E-01
ENSMUST00000093402	POZ (BTB) and AT hook containing zinc finger 1 [Source:MGI Symbol;Acc:MGI:1891832]	Q5NBZ1		0.1	9.7E-01	-0.8	7.2E-01	-3.0	1.5E-01	-2.1	4.6E-01
ENSMUST00000095550	synapse differentiation inducing 1 like [Source:MGI Symbol;Acc:MGI:2685107]	B2RRM8	Q3USQ7	5.3	1.4E-04	5.9	2.6E-02	-0.8	7.3E-01	3.5	1.8E-02
ENSMUST00000095551	vertebrae development associated [Source:MGI Symbol;Acc:MGI:3588197]		Q3SYK4	5.9	2.4E-02	-5.2	1.1E-02	-0.2	7.4E-01	-0.2	9.3E-01
ENSMUST00000095576	sciellin [Source:MGI Symbol;Acc:MGI:1891228]	Q14DU0	Q9EQG3	3.2	2.8E-03	6.0	5.4E-05	-0.5	5.5E-01	0.2	7.0E-01
ENSMUST00000095579	THO complex 6 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2677480]		Q5U4D9	-5.8	1.3E-03	1.6	1.1E-01	1.2	1.0E-01	-3.2	6.5E-03
ENSMUST00000095580	myopalladin [Source:MGI Symbol;Acc:MGI:1916052]		Q5DTJ9	8.5	9.0E-06	2.0	1.4E-02	-0.4	4.8E-01	0.1	7.9E-01
ENSMUST00000095585	adhesion G protein-coupled receptor V1 [Source:MGI Symbol;Acc:MGI:1274784]	B8JJE0		8.7	1.4E-05	-1.7	5.3E-02	0.6	2.2E-01	0.1	9.3E-01
ENSMUST00000095606	zinc finger protein 213 [Source:MGI Symbol;Acc:MGI:3053094]	E9QAW0		1.7	1.0E-02	-7.1	3.2E-05	0.2	5.6E-01	2.9	1.0E-02
ENSMUST00000093458	SURP and G patch domain containing 2 [Source:MGI Symbol;Acc:MGI:2678085]		Q8CH09	-2.0	1.4E-01	2.1	1.9E-01	1.1	4.3E-01	-3.0	4.3E-02
ENSMUST00000095610	A kinase (PRKA) anchor protein 5 [Source:MGI Symbol;Acc:MGI:2685104]	H3BIV5		5.4	4.6E-05	-4.8	4.9E-03	0.1	9.2E-01	-0.7	6.4E-01
ENSMUST00000093485	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:MGI Symbol;Acc:MGI:2384570]	E9PZQ1		4.4	5.1E-02	6.0	7.1E-02	1.1	7.1E-01	-0.5	7.8E-01
ENSMUST00000095633	predicted pseudogene 5145 [Source:MGI Symbol;Acc:MGI:3645482]	F8VQ88		6.3	1.3E-03	-3.8	2.1E-02	0.1	8.8E-01	-0.3	8.2E-01
ENSMUST00000095651	formyl peptide receptor, related sequence 4 [Source:MGI Symbol;Acc:MGI:1278317]		A4FUQ5	6.6	3.1E-04	2.9	2.3E-03	-0.3	5.8E-01	-0.5	3.9E-01
ENSMUST00000095655	leiomodin 3 (fetal) [Source:MGI Symbol;Acc:MGI:2444169]	E9QA62		7.7	5.9E-05	-2.0	4.0E-02	0.7	1.7E-01	-1.1	2.2E-01
ENSMUST00000095664	TATA element modulatory factor 1 [Source:MGI Symbol;Acc:MGI:2684999]		B9EKI3	-3.0	4.8E-03	-6.1	6.8E-05	-0.6	1.6E-01	0.4	6.2E-01
ENSMUST00000095712	solute carrier family 5 (choline transporter), member 7 [Source:MGI Symbol;Acc:MGI:1927126]		Q8BGY9	7.3	2.2E-05	7.6	6.0E-05	-0.6	6.0E-01	0.2	7.5E-01
ENSMUST00000095715	blood vessel epicardial substance [Source:MGI Symbol;Acc:MGI:1346013]		Q9ES83	6.2	2.7E-04	9.2	1.6E-04	-0.3	8.4E-01	0.2	7.8E-01
ENSMUST00000095737	A kinase (PRKA) anchor protein 6 [Source:MGI Symbol;Acc:MGI:3050566]	E9Q9K8		7.3	2.1E-06	-7.5	4.6E-02	2.3	4.6E-02	-0.1	9.8E-01
ENSMUST00000095752	cytotoxic granule-associated RNA binding protein 1 [Source:MGI Symbol;Acc:MGI:107914]	G5E8L2		-5.8	2.6E-04	-1.3	6.1E-02	0.2	6.9E-01	0.1	8.0E-01
ENSMUST00000095755	ubiquitin specific protease 51 [Source:MGI Symbol;Acc:MGI:3588217]	B1AY15		6.1	1.4E-03	5.6	5.8E-05	-2.0	4.0E-02	0.0	9.3E-01
ENSMUST00000095757	RIKEN cDNA 1700019G17 gene [Source:MGI Symbol;Acc:MGI:1922791]	G5E8L3		3.4	2.8E-04	4.8	9.4E-04	-2.9	3.6E-02	-0.1	9.1E-01
ENSMUST00000095759	early growth response 4 [Source:MGI Symbol;Acc:MGI:99252]	Q3URA9	Q9WUF2	5.7	1.6E-03	4.5	3.0E-04	-1.2	1.7E-01	-0.3	6.4E-01
ENSMUST00000093773	myelin-associated oligodendrocytic basic protein [Source:MGI Symbol;Acc:MGI:108511]		Q9D2P8	5.2	5.7E-02	9.5	3.9E-03	-0.7	8.2E-01	-4.9	6.0E-03
ENSMUST00000095760	leucine-rich single-pass membrane protein 1 [Source:MGI Symbol;Acc:MGI:2685735]	B2RVW5	Q3UQS2	6.9	2.5E-04	6.8	5.2E-04	-0.7	6.4E-01	0.2	7.8E-01
ENSMUST00000095762	triadin [Source:MGI Symbol;Acc:MGI:1924007]		E9Q9K5	6.1	1.3E-04	0.8	2.6E-01	0.9	8.8E-02	-1.6	3.3E-02
ENSMUST00000093786	Ras association (RalGDS/AF-6) domain family member 1 [Source:MGI Symbol;Acc:MGI:1928386]	A9YZW8	Q99MK9	1.5	5.2E-01	0.8	7.9E-01	-0.2	9.3E-01	0.5	8.7E-01
ENSMUST00000093791	centrosomal protein 63 [Source:MGI Symbol;Acc:MGI:2158560]	F8VPJ7		-1.6	8.2E-02	-2.0	9.1E-02	-0.4	5.8E-01	0.0	9.9E-01
ENSMUST00000093795	centrosomal protein 70 [Source:MGI Symbol;Acc:MGI:1915371]		Q6IQY5	-2.2	1.1E-01	0.0	9.8E-01	1.0	4.1E-01	-1.2	4.3E-01
ENSMUST00000093798	zinc finger and BTB domain containing 38 [Source:MGI Symbol;Acc:MGI:2442866]	Q3LR78		4.1	4.5E-02	4.3	6.7E-02	-0.1	9.8E-01	-0.2	8.9E-01
ENSMUST00000095767	ets variant 1 [Source:MGI Symbol;Acc:MGI:99254]	Q549J8	P41164	6.4	4.1E-03	3.0	2.5E-03	-2.9	6.2E-03	-1.1	1.1E-01
ENSMUST00000095774	cadherin-related family member 3 [Source:MGI Symbol;Acc:MGI:1916014]		Q8BL00	7.3	2.5E-05	-6.9	2.1E-03	-0.2	8.1E-01	1.9	2.9E-01
ENSMUST00000095779	A kinase (PRKA) anchor protein 7 [Source:MGI Symbol;Acc:MGI:1859150]	Q4KL21		3.2	2.1E-02	3.6	1.7E-04	-0.2	6.9E-01	-0.2	5.8E-01
ENSMUST00000095784	monooxygenase, DBH-like 1 [Source:MGI Symbol;Acc:MGI:1921582]		Q9CXI3	5.9	5.3E-05	7.5	1.1E-04	-0.7	6.0E-01	-0.1	9.1E-01
ENSMUST00000095793	ring finger protein 17 [Source:MGI Symbol;Acc:MGI:1353419]		Q99MV7	5.9	5.5E-04	3.6	1.5E-03	-0.4	6.2E-01	-0.6	3.6E-01
ENSMUST00000095794	TATA box binding protein-like 1 [Source:MGI Symbol;Acc:MGI:1339946]		P62340	-5.6	1.6E-05	6.4	3.0E-04	-0.5	6.8E-01	-0.4	5.7E-01
ENSMUST00000095795	retinoic acid early transcript delta [Source:MGI Symbol;Acc:MGI:1861032]		Q9JI58	-6.0	1.7E-03	-5.0	1.2E-01	1.3	3.2E-01	1.2	7.0E-01
ENSMUST00000095797	spindlin 1 [Source:MGI Symbol;Acc:MGI:109242]		Q61142	-2.2	4.0E-04	4.9	1.8E-03	-1.5	2.4E-01	0.0	9.9E-01
ENSMUST00000093832	lectin, mannose-binding 1 like [Source:MGI Symbol;Acc:MGI:2667537]		Q8VCD3	-0.4	7.9E-01	-0.8	7.3E-01	0.7	6.6E-01	1.1	6.0E-01
ENSMUST00000093833	family with sequence similarity 219, member B [Source:MGI Symbol;Acc:MGI:1925573]		Q14DQ1	-3.7	2.2E-01	-0.9	7.0E-01	-0.9	6.1E-01	-3.7	2.3E-01
ENSMUST00000095798	mast cell protease 9 [Source:MGI Symbol;Acc:MGI:1194491]		O35164	7.2	2.8E-05	5.7	1.9E-04	-1.3	2.0E-01	-0.2	7.7E-01
ENSMUST00000095806	mitogen-activated protein kinase kinase kinase 5 [Source:MGI Symbol;Acc:MGI:1346876]		O35099	-4.8	8.2E-04	6.1	1.1E-04	-1.0	3.1E-01	-0.5	3.9E-01
ENSMUST00000095807	hippocalcin [Source:MGI Symbol;Acc:MGI:1336200]		P84075	7.5	2.0E-04	2.6	1.1E-03	-0.8	1.1E-01	0.3	5.4E-01
ENSMUST00000095817	epithelial cell transforming sequence 2 oncogene-like [Source:MGI Symbol;Acc:MGI:3641723]	F7CKP4		6.4	9.2E-05	4.1	6.6E-04	-1.3	1.2E-01	0.1	8.4E-01
ENSMUST00000095823	RIKEN cDNA 2410004P03 gene [Source:MGI Symbol;Acc:MGI:1920917]	D3Z430		7.6	1.1E-06	4.6	5.6E-02	-0.5	8.2E-01	0.3	8.1E-01
ENSMUST00000095852	glutamate receptor, ionotropic, delta 2 [Source:MGI Symbol;Acc:MGI:95813]		Q61625	8.0	1.5E-05	1.2	5.4E-01	-1.4	4.1E-01	2.1	2.4E-01
ENSMUST00000093859	glutamate receptor ionotropic, NMDA3A [Source:MGI Symbol;Acc:MGI:1933206]	A2AIR5		2.9	3.2E-01	3.9	2.0E-01	-1.6	5.9E-01	-2.6	2.7E-01
ENSMUST00000095873	potassium inwardly-rectifying channel, subfamily J, member 6 [Source:MGI Symbol;Acc:MGI:104781]	Q8C4T8		6.6	1.4E-04	-3.5	1.7E-02	0.7	2.3E-01	0.2	8.8E-01
ENSMUST00000095874	RIKEN cDNA 9230019H11 gene [Source:MGI Symbol;Acc:MGI:3588256]	Q3UW27		4.8	1.2E-04	3.7	7.1E-03	-1.8	1.2E-01	0.6	4.8E-01
ENSMUST00000095893	acidic residue methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1920669]		A6H630	-6.4	9.7E-06	-0.9	6.0E-01	1.8	1.2E-01	-4.0	7.6E-02
ENSMUST00000093902	ring finger protein 213 [Source:MGI Symbol;Acc:MGI:1289196]	F7A6H4		-1.1	5.1E-01	0.9	6.2E-01	0.6	6.9E-01	-1.4	4.3E-01
ENSMUST00000095898	corticotropin releasing hormone receptor 2 [Source:MGI Symbol;Acc:MGI:894312]	Q5ERJ2		6.0	1.4E-03	7.3	9.0E-05	-0.6	6.1E-01	-0.2	7.4E-01
ENSMUST00000095909	intersectin 1 (SH3 domain protein 1A) [Source:MGI Symbol;Acc:MGI:1338069]	Q6NZJ5		5.5	1.1E-05	5.6	1.7E-05	0.4	5.0E-01	0.1	8.1E-01
ENSMUST00000093907	septin 9 [Source:MGI Symbol;Acc:MGI:1858222]		Q80UG5	1.1	3.8E-01	0.8	6.7E-01	0.5	7.3E-01	0.8	5.7E-01
ENSMUST00000095922	vomeronasal 2, receptor 12 [Source:MGI Symbol;Acc:MGI:3761377]	L7N217		6.1	1.6E-04	8.7	1.7E-05	-0.6	6.3E-01	-0.3	5.6E-01
ENSMUST00000093912	RIKEN cDNA 2310067B10 gene [Source:MGI Symbol;Acc:MGI:1919197]		Q7TSH8	-3.2	5.2E-02	-0.5	7.6E-01	0.3	8.1E-01	-2.5	1.7E-01
ENSMUST00000095923	ribonuclease, RNase A family, 6 [Source:MGI Symbol;Acc:MGI:1925666]	Q3V3L3		-4.0	4.5E-04	7.4	2.9E-04	-0.6	6.6E-01	-0.6	3.8E-01
ENSMUST00000095925	purine-nucleoside phosphorylase 2 [Source:MGI Symbol;Acc:MGI:3712328]	Q9D8C9		-2.5	1.1E-03	-6.6	3.3E-04	0.2	5.8E-01	3.6	1.3E-02
ENSMUST00000095926	prolactin family 8, subfamily a, member 1 [Source:MGI Symbol;Acc:MGI:1920494]	J3JS25		6.5	5.3E-06	7.4	7.6E-05	-0.6	6.2E-01	0.1	8.5E-01
ENSMUST00000095932	cyclin B1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2685134]		D3Z3K2	4.0	4.4E-04	4.4	8.6E-04	-1.3	1.7E-01	0.4	5.1E-01
ENSMUST00000095948	hyaluronic acid binding protein 2 [Source:MGI Symbol;Acc:MGI:1196378]	Q3V1J8		6.5	2.1E-04	4.7	7.6E-02	-0.8	7.3E-01	1.0	5.5E-01
ENSMUST00000095950	vesicle transport through interaction with t-SNAREs 1A [Source:MGI Symbol;Acc:MGI:1855699]		O89116	-1.8	2.0E-03	-3.7	2.2E-02	0.1	8.4E-01	0.0	9.7E-01
ENSMUST00000093938	gasdermin A2 [Source:MGI Symbol;Acc:MGI:1921490]		Q32M21	5.1	6.7E-02	4.6	1.2E-01	-0.6	8.3E-01	-0.1	9.4E-01
ENSMUST00000093940	Rho GTPase activating protein 23 [Source:MGI Symbol;Acc:MGI:3697726]		Q69ZH9	-4.8	4.2E-02	-1.2	6.5E-01	3.1	9.3E-02	-0.4	8.8E-01
ENSMUST00000095955	olfactory receptor 444 [Source:MGI Symbol;Acc:MGI:3030278]	Q8VFS6		6.4	7.2E-05	8.1	1.3E-05	-1.9	1.0E-01	-0.4	3.7E-01
ENSMUST00000095959	prostaglandin D receptor [Source:MGI Symbol;Acc:MGI:102966]		P70263	5.0	2.2E-04	-5.5	3.8E-03	-0.5	3.8E-01	0.1	9.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000095969	RNA binding motif protein 20 [Source:MGI Symbol;Acc:MGI:1920963]	E9QPB0		6.3	1.8E-02	4.3	5.4E-04	0.7	3.6E-01	-0.9	1.7E-01
ENSMUST00000095974	family with sequence similarity 131, member B [Source:MGI Symbol;Acc:MGI:1923406]		Q3TY60	5.7	1.4E-03	6.2	6.8E-06	0.7	3.0E-01	-0.4	3.5E-01
ENSMUST00000095978	nuclear transport factor 2, pseudogene 1 [Source:MGI Symbol;Acc:MGI:108008]		P61971	-2.6	1.3E-02	-9.1	2.9E-05	-0.2	5.5E-01	-0.7	6.2E-01
ENSMUST00000095987	transmembrane protein 139 [Source:MGI Symbol;Acc:MGI:1924444]	E9PX92		6.2	1.6E-03	6.0	1.2E-03	-0.9	4.9E-01	0.0	9.5E-01
ENSMUST00000095998	cilia and flagella associated protein 43 [Source:MGI Symbol;Acc:MGI:1289258]		Q3TNL8	-4.5	8.1E-05	-1.3	7.0E-02	-4.7	2.2E-05	0.3	6.3E-01
ENSMUST00000093975	ring finger and FYVE like domain containing protein [Source:MGI Symbol;Acc:MGI:1914588]		Q6ZQM0	-0.7	3.5E-01	0.0	9.9E-01	0.5	5.0E-01	-0.2	8.1E-01
ENSMUST00000096000	SH2 domain containing 4B [Source:MGI Symbol;Acc:MGI:1925182]		A6X942	1.7	2.6E-02	6.7	4.4E-05	-1.5	1.7E-01	-0.3	5.7E-01
ENSMUST00000096006	olfactory receptor 263 [Source:MGI Symbol;Acc:MGI:3030097]	Q7TQT8		6.4	1.3E-04	-1.6	4.5E-02	0.0	9.7E-01	-0.7	3.7E-01
ENSMUST00000096014	upregulated during skeletal muscle growth 5 [Source:MGI Symbol;Acc:MGI:1891435]		Q78IK2	-6.6	1.0E-04	5.2	1.4E-02	-0.6	7.6E-01	0.2	8.2E-01
ENSMUST00000093993	PWWP domain containing 2B [Source:MGI Symbol;Acc:MGI:2142008]	Q3TYY8		0.8	6.0E-01	-1.8	4.5E-01	0.4	8.2E-01	2.9	1.9E-01
ENSMUST00000096019	G protein regulated inducer of neurite outgrowth 2 [Source:MGI Symbol;Acc:MGI:2444560]	D3Z1D7		7.6	8.0E-05	2.3	3.3E-01	-0.7	7.3E-01	2.2	2.4E-01
ENSMUST00000096021	PEST proteolytic signal containing nuclear protein [Source:MGI Symbol;Acc:MGI:1923552]	F8WI88		-5.4	2.1E-04	4.2	4.3E-02	-1.3	5.1E-01	0.9	4.4E-01
ENSMUST00000094004	abhydrolase domain containing 15 [Source:MGI Symbol;Acc:MGI:1914727]	B6DQM2	Q5F2F2	0.8	1.5E-01	1.8	2.7E-02	0.5	3.5E-01	-0.4	4.9E-01
ENSMUST00000094012	active BCR-related gene [Source:MGI Symbol;Acc:MGI:107771]		Q5SSL4	2.9	9.6E-02	4.3	1.4E-01	3.1	2.1E-01	1.7	3.6E-01
ENSMUST00000094015	vacuolar protein sorting 53 (yeast) [Source:MGI Symbol;Acc:MGI:1915549]	E9PXG9		0.9	6.3E-01	-4.1	1.6E-01	-3.0	8.8E-02	1.9	4.8E-01
ENSMUST00000096029	pleckstrin and Sec7 domain containing [Source:MGI Symbol;Acc:MGI:1920978]		Q5DTT2	3.6	3.4E-03	-5.0	2.4E-02	-0.9	2.6E-01	0.6	7.6E-01
ENSMUST00000096030	killer cell lectin-like receptor subfamily G, member 2 [Source:MGI Symbol;Acc:MGI:1921503]	G5E8L6		4.0	1.8E-04	4.8	1.4E-03	-0.6	6.1E-01	1.1	1.2E-01
ENSMUST00000096038	RIKEN cDNA 3425401B19 gene [Source:MGI Symbol;Acc:MGI:3588196]	D3Z1D3		10.1	1.9E-05	-6.3	9.2E-06	0.1	7.1E-01	-0.7	3.8E-01
ENSMUST00000094037	T-box 6 [Source:MGI Symbol;Acc:MGI:102539]		P70327	-1.3	3.3E-01	0.0	9.8E-01	-0.2	8.5E-01	-1.5	3.4E-01
ENSMUST00000096040	SV2 related protein homolog (rat)-like [Source:MGI Symbol;Acc:MGI:2444335]		Q6PDF3	7.7	6.8E-05	5.7	2.6E-03	-0.6	6.9E-01	0.6	5.0E-01
ENSMUST00000096057	transgelin 3 [Source:MGI Symbol;Acc:MGI:1926784]		Q9R1Q8	6.1	2.1E-04	6.4	1.5E-03	-0.9	5.4E-01	-2.5	3.1E-02
ENSMUST00000096065	T cell immunoreceptor with Ig and ITIM domains [Source:MGI Symbol;Acc:MGI:3642260]	A0A0B4J1G6		5.6	5.3E-06	-0.9	1.9E-01	0.3	4.8E-01	-0.3	6.3E-01
ENSMUST00000096084	coiled-coil domain containing 136 [Source:MGI Symbol;Acc:MGI:1918128]	E9QP94		6.9	2.3E-04	-8.1	1.2E-04	0.4	3.6E-01	0.0	9.9E-01
ENSMUST00000096089	cDNA sequence BC100530 [Source:MGI Symbol;Acc:MGI:3696883]	Q497J0		-10.3	2.7E-06	-2.1	2.4E-02	1.1	5.4E-02	0.2	8.2E-01
ENSMUST00000094097	transmembrane protein 41B [Source:MGI Symbol;Acc:MGI:1289225]		Q8K1A5	1.4	4.6E-02	1.5	7.5E-02	-0.4	5.1E-01	-0.5	4.9E-01
ENSMUST00000096106	mucin 4 [Source:MGI Symbol;Acc:MGI:2153525]	E9Q7Q0		8.0	7.3E-03	3.1	3.0E-03	-0.7	3.4E-01	0.1	9.3E-01
ENSMUST00000096109	phosphatidylinositol glycan anchor biosynthesis, class X [Source:MGI Symbol;Acc:MGI:1919334]	F7DFD7		-7.8	4.3E-06	5.3	8.1E-04	-0.6	6.0E-01	1.0	1.4E-01
ENSMUST00000096119	N-acylsphingosine amidohydrolase 2 [Source:MGI Symbol;Acc:MGI:1859310]	B9EHG7	Q9JHE3	5.0	1.9E-04	7.1	1.8E-04	-0.6	6.5E-01	0.6	3.6E-01
ENSMUST00000094116	zinc finger and SCAN domain containing 25 [Source:MGI Symbol;Acc:MGI:3647079]	B2RX31		-0.8	1.1E-01	0.5	4.4E-01	0.8	1.0E-01	-0.5	3.8E-01
ENSMUST00000094120	transformation/transcription domain-associated protein [Source:MGI Symbol;Acc:MGI:2153272]	E9PWT1		1.4	6.1E-01	5.0	2.5E-01	3.0	4.6E-01	-0.6	8.1E-01
ENSMUST00000096129	interleukin 1 receptor accessory protein [Source:MGI Symbol;Acc:MGI:104975]	Q3UVZ1		3.4	4.1E-04	6.3	1.7E-04	-0.5	6.4E-01	-0.3	6.6E-01
ENSMUST00000094128	ADP-ribosyltransferase 5 [Source:MGI Symbol;Acc:MGI:107948]		P70352	6.1	4.8E-02	6.0	7.8E-02	-0.3	9.2E-01	-0.2	9.1E-01
ENSMUST00000096164	family with sequence similarity 189, member A2 [Source:MGI Symbol;Acc:MGI:2685813]	E9QP68		7.6	7.0E-05	-3.7	9.5E-05	-0.4	1.9E-01	-0.9	1.6E-01
ENSMUST00000096168	predicted gene 10408 [Source:MGI Symbol;Acc:MGI:3704423]	K7N693		8.0	1.1E-04	7.6	6.7E-03	-0.3	9.0E-01	1.0	3.2E-01
ENSMUST00000096170	predicted gene 5622 [Source:MGI Symbol;Acc:MGI:3646060]	Q810Q0		5.2	6.9E-03	5.3	6.5E-04	-0.1	9.1E-01	-1.1	1.6E-01
ENSMUST00000096171	predicted gene 3383 [Source:MGI Symbol;Acc:MGI:3781561]	E9Q7N2		7.1	1.0E-04	-3.2	2.9E-04	-9.1	6.1E-07	-1.0	1.3E-01
ENSMUST00000094148	family with sequence similarity 160, member A1 [Source:MGI Symbol;Acc:MGI:2444746]		Q505K2	0.2	9.1E-01	4.3	5.0E-02	0.0	9.9E-01	-4.1	2.1E-02
ENSMUST00000096191	vacuolar protein sorting 8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2146407]		Q0P5W1	4.0	2.2E-04	-2.6	2.0E-02	0.9	1.1E-01	0.6	5.3E-01
ENSMUST00000094154	serine (or cysteine) peptidase inhibitor, clade H, member 1 [Source:MGI Symbol;Acc:MGI:88283]		P19324	1.9	2.2E-01	-1.2	2.4E-01	-6.9	1.9E-04	-3.8	1.1E-02
ENSMUST00000096198	sodium channel, voltage-gated, type VIII, alpha [Source:MGI Symbol;Acc:MGI:103169]	Q4KL32		6.0	1.4E-04	3.9	5.3E-03	-2.9	4.0E-02	-0.8	3.2E-01
ENSMUST00000096200	transmembrane (C-terminal) protease, serine 12 [Source:MGI Symbol;Acc:MGI:1922252]		Q3V0Q7	5.9	2.1E-04	-7.6	2.6E-03	-2.0	1.2E-02	1.2	5.6E-01
ENSMUST00000094179	glutamate receptor, ionotropic, AMPA1 (alpha 1) [Source:MGI Symbol;Acc:MGI:95808]	Q7TNB5		3.3	2.4E-01	5.3	7.8E-02	-0.6	8.5E-01	-2.6	2.0E-01
ENSMUST00000096224	adenylate cyclase 6 [Source:MGI Symbol;Acc:MGI:87917]	F8VQ52		6.1	2.7E-06	3.8	6.3E-02	-0.4	8.3E-01	0.6	6.2E-01
ENSMUST00000094203	helicase with zinc finger 2, transcriptional coactivator [Source:MGI Symbol;Acc:MGI:2385169]	A2AS03		3.2	3.2E-01	4.0	2.6E-01	-0.4	9.1E-01	-1.2	6.2E-01
ENSMUST00000094215	mesoderm development candidate 2 [Source:MGI Symbol;Acc:MGI:1891421]		Q9ERE7	0.2	7.4E-01	0.1	8.5E-01	0.1	8.1E-01	0.2	8.1E-01
ENSMUST00000096240	metastasis-associated gene family, member 2 [Source:MGI Symbol;Acc:MGI:1346340]		Q9R190	-4.4	1.6E-05	0.5	4.7E-01	1.2	2.4E-02	-0.6	3.2E-01
ENSMUST00000096241	echinoderm microtubule associated protein like 3 [Source:MGI Symbol;Acc:MGI:2387612]		Q8VC03	-2.8	3.1E-03	-1.5	1.4E-01	1.5	2.6E-02	0.1	9.5E-01
ENSMUST00000096243	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) [Source:MGI Symbol;Acc:MGI:1919977]		P58158	-3.6	1.1E-03	5.1	3.6E-03	0.2	8.8E-01	0.1	9.2E-01
ENSMUST00000096246	alpha glucosidase 2 alpha neutral subunit [Source:MGI Symbol;Acc:MGI:1097667]	A1A4T2	Q8BHN3	-3.3	1.9E-04	5.7	1.3E-04	-1.9	8.7E-02	0.1	8.6E-01
ENSMUST00000096250	AT rich interactive domain 2 (ARID, RFX-like) [Source:MGI Symbol;Acc:MGI:1924294]	E9Q7E2		-1.2	6.3E-03	2.6	7.0E-03	-3.3	5.7E-03	0.6	3.9E-01
ENSMUST00000096251	RIKEN cDNA 1810009A15 gene [Source:MGI Symbol;Acc:MGI:1913526]		Q9D937	-5.5	1.0E-04	-2.6	1.8E-02	1.3	2.5E-02	0.8	4.2E-01
ENSMUST00000096253	ubiquinol-cytochrome c reductase complex assembly factor 3 [Source:MGI Symbol;Acc:MGI:2147553]	Q3V2E3	Q8K2T4	-2.7	2.5E-03	7.7	1.3E-04	-0.7	6.0E-01	-0.1	8.9E-01
ENSMUST00000094276	zinc finger and BTB domain containing 18 [Source:MGI Symbol;Acc:MGI:1353609]	H7BX69		0.2	8.6E-01	2.3	2.9E-01	2.4	2.1E-01	0.3	8.6E-01
ENSMUST00000096255	UBX domain protein 1 [Source:MGI Symbol;Acc:MGI:1289301]		Q922Y1	-6.9	4.3E-04	-4.5	1.5E-04	0.4	2.7E-01	-0.1	8.8E-01
ENSMUST00000096257	LRRN4 C-terminal like [Source:MGI Symbol;Acc:MGI:1916102]		Q3TYX2	8.1	4.8E-06	7.4	1.8E-03	0.0	9.9E-01	-0.3	7.2E-01
ENSMUST00000094294	PWWP domain containing 2A [Source:MGI Symbol;Acc:MGI:1918052]		Q69Z61	1.4	1.9E-01	3.7	2.2E-02	1.6	2.1E-01	-0.7	5.1E-01
ENSMUST00000094300	ankyrin repeat domain 50 [Source:MGI Symbol;Acc:MGI:2139777]	A6H6J9		-0.6	5.8E-01	0.6	6.5E-01	-0.2	8.6E-01	-1.4	2.6E-01
ENSMUST00000096259	guanine nucleotide binding protein (G protein), gamma 3 [Source:MGI Symbol;Acc:MGI:102704]		P63216	6.2	1.6E-05	3.9	5.6E-04	-0.9	2.5E-01	-0.1	8.8E-01
ENSMUST00000096261	polymerase (RNA) II (DNA directed) polypeptide G [Source:MGI Symbol;Acc:MGI:1914960]		P62488	-4.7	2.2E-06	-4.4	5.7E-02	1.4	2.0E-01	1.1	5.9E-01
ENSMUST00000094312	repulsive guidance molecule family member A [Source:MGI Symbol;Acc:MGI:2679262]		Q6PCX7	3.0	2.8E-01	3.0	2.7E-01	-0.5	8.5E-01	-0.5	8.1E-01
ENSMUST00000096273	sorting nexin 29 [Source:MGI Symbol;Acc:MGI:1921728]		Q9D3S3	5.7	2.7E-03	8.4	3.0E-05	-0.1	9.6E-01	0.6	3.1E-01
ENSMUST00000094324	cell division cycle 25A [Source:MGI Symbol;Acc:MGI:103198]		P48964	-0.1	7.6E-01	0.9	1.4E-01	1.6	4.3E-03	0.6	2.8E-01
ENSMUST00000094325	poliovirus receptor-related 4 [Source:MGI Symbol;Acc:MGI:1918990]		Q8R007	2.3	4.1E-01	2.4	5.0E-01	0.7	8.1E-01	0.6	8.3E-01
ENSMUST00000094327	leucine rich repeat containing 43 [Source:MGI Symbol;Acc:MGI:2685907]		Q3V0L5	4.8	9.5E-02	6.4	5.3E-02	-0.2	9.5E-01	-1.8	3.1E-01
ENSMUST00000096301	zinc finger, CCHC domain containing 16 [Source:MGI Symbol;Acc:MGI:3588192]		Q3URY0	6.9	2.7E-05	-6.1	1.7E-03	0.8	1.4E-01	-0.5	7.3E-01
ENSMUST00000094331	necdin-like 2 [Source:MGI Symbol;Acc:MGI:1913897]		Q9CPR8	0.4	3.0E-01	0.7	2.6E-01	0.7	1.2E-01	0.5	3.6E-01
ENSMUST00000096313	TBC1 domain family, member 8B [Source:MGI Symbol;Acc:MGI:1918101]		A3KGB4	2.1	6.8E-04	5.9	2.2E-04	-0.6	5.9E-01	0.0	9.7E-01
ENSMUST00000096318	adaptor-related protein complex 5, beta 1 subunit [Source:MGI Symbol;Acc:MGI:2685808]		Q3TAP4	-2.1	9.0E-03	2.4	2.3E-02	0.8	3.0E-01	0.1	8.5E-01
ENSMUST00000096321	armadillo repeat containing, X-linked 5 [Source:MGI Symbol;Acc:MGI:2148026]		Q3UZB0	-2.6	1.9E-03	6.2	4.3E-04	-0.6	6.2E-01	0.5	4.8E-01
ENSMUST00000096325	predicted gene 960 [Source:MGI Symbol;Acc:MGI:2685806]	Q3UY62		7.0	8.2E-05	6.7	5.0E-04	-0.6	6.5E-01	-1.3	1.1E-01
ENSMUST00000096338	G protein-coupled receptor 152 [Source:MGI Symbol;Acc:MGI:2685519]		Q8BXS7	7.4	4.0E-05	2.6	3.0E-01	-1.0	6.6E-01	1.4	4.6E-01
ENSMUST00000096347	ENTH domain containing 1 [Source:MGI Symbol;Acc:MGI:2686088]	E9Q1Z2		6.9	1.6E-04	-3.6	1.5E-03	-2.2	1.0E-03	-0.6	4.8E-01
ENSMUST00000096350	maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian) [Source:MGI Symbol;Acc:MGI:9691	Q3U0G5	O54791	4.5	8.3E-03	5.9	3.9E-04	-0.1	9.3E-01	0.2	8.1E-01
ENSMUST00000094378	src homology 2 domain-containing transforming protein C1 [Source:MGI Symbol;Acc:MGI:98296]		P98083	-1.9	3.1E-01	2.6	1.2E-01	1.1	4.1E-01	-3.4	9.0E-02
ENSMUST00000094381	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]	F8WHQ1		0.0	9.9E-01	3.5	6.0E-02	1.6	2.9E-01	-1.9	1.8E-01
ENSMUST00000096355	r stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) [Source:MGI Symbol;Acc:MGI:133		P26955	-5.6	6.8E-06	7.2	3.3E-04	1.5	2.6E-01	0.3	6.4E-01
ENSMUST00000096356	stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage) [Source:MGI Symbol;Acc:MGI:13		P26954	-2.4	1.4E-03	5.8	6.6E-04	-0.6	6.4E-01	0.7	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000096357	neutrophil cytosolic factor 4 [Source:MGI Symbol;Acc:MGI:109186]		P97369	-7.9	1.8E-06	7.9	8.4E-03	-0.8	7.7E-01	-2.1	1.4E-01
ENSMUST00000096358	apolipoprotein L 7e [Source:MGI Symbol;Acc:MGI:3704456]	Q3UZ24		6.5	8.8E-04	-5.1	4.3E-04	0.0	9.7E-01	0.0	9.8E-01
ENSMUST00000096363	transmembrane protein 28 [Source:MGI Symbol;Acc:MGI:3648377]		A2BDP1	7.7	3.0E-05	6.5	3.4E-03	-0.7	6.9E-01	-2.7	3.8E-02
ENSMUST00000094421	centrosomal protein 250 [Source:MGI Symbol;Acc:MGI:108084]		Q60952	-2.2	6.4E-01	2.6	5.5E-01	1.5	6.7E-01	-3.3	4.9E-01
ENSMUST00000096365	scratch homolog 1, zinc finger protein (Drosophila) [Source:MGI Symbol;Acc:MGI:2176606]		Q99M85	7.0	2.9E-05	6.4	3.1E-04	-0.6	6.2E-01	0.2	8.1E-01
ENSMUST00000094427				-1.3	6.1E-02	0.4	6.4E-01	1.4	4.2E-02	-0.3	6.8E-01
ENSMUST00000096367	spindlin family, member 4 [Source:MGI Symbol;Acc:MGI:2444925]		Q8K1L2	5.8	2.4E-04	-6.0	4.4E-05	0.7	1.2E-01	-0.3	6.8E-01
ENSMUST00000096385	maestro heat-like repeat family member 1 [Source:MGI Symbol;Acc:MGI:2442558]	E0CZ22		-8.4	2.2E-05	5.8	1.5E-04	-2.1	8.5E-02	-0.5	4.1E-01
ENSMUST00000096386	ring finger protein 41 [Source:MGI Symbol;Acc:MGI:1914838]		Q8BH75	-2.3	2.4E-03	5.2	3.1E-05	0.5	4.6E-01	0.1	8.6E-01
ENSMUST00000096418	alpha-1-B glycoprotein [Source:MGI Symbol;Acc:MGI:2152878]		Q19LI2	7.1	4.1E-05	6.2	3.2E-04	-2.3	9.6E-02	-0.3	6.1E-01
ENSMUST00000096421	RIKEN cDNA 4933412E24 gene [Source:MGI Symbol;Acc:MGI:1918338]		Q9D454	7.8	1.3E-04	6.8	6.4E-04	-0.2	9.0E-01	-0.4	6.3E-01
ENSMUST00000096430	zinc fingers and homeoboxes 2 [Source:MGI Symbol;Acc:MGI:2683087]		Q8C0C0	3.3	2.1E-04	7.6	7.6E-05	-1.4	3.0E-01	0.5	4.4E-01
ENSMUST00000094464	castor zinc finger 1 [Source:MGI Symbol;Acc:MGI:1196251]		Q9CWL2	1.2	9.3E-02	2.7	1.3E-02	1.0	1.9E-01	-0.5	5.4E-01
ENSMUST00000094467	ectonucleoside triphosphate diphosphohydrolase 6 [Source:MGI Symbol;Acc:MGI:1202295]	Q3U0P5		0.5	4.0E-01	1.7	5.1E-02	0.7	2.8E-01	-0.5	4.6E-01
ENSMUST00000094469	selenoprotein M [Source:MGI Symbol;Acc:MGI:2149786]		Q8VHC3	-2.1	8.8E-02	-0.8	5.0E-01	-0.9	3.1E-01	-2.2	9.6E-02
ENSMUST00000094471	POZ (BTB) and AT hook containing zinc finger 1 [Source:MGI Symbol;Acc:MGI:1891832]	Q5NBZ2		1.4	4.8E-02	2.8	7.0E-03	1.1	1.2E-01	-0.3	7.0E-01
ENSMUST00000096431	adhesion G protein-coupled receptor G4 [Source:MGI Symbol;Acc:MGI:2685213]	Q3UNS7		6.6	2.4E-04	2.3	1.5E-01	-0.5	6.8E-01	6.6	2.2E-04
ENSMUST00000096433	DEP domain containing MTOR-interacting protein [Source:MGI Symbol;Acc:MGI:2146322]	B2ZRS3	Q570Y9	3.7	2.7E-05	-5.5	3.6E-02	1.2	1.7E-01	1.4	5.4E-01
ENSMUST00000096447	motile sperm domain containing 1 [Source:MGI Symbol;Acc:MGI:1917630]		Q8VEL0	-7.5	1.1E-04	3.4	5.6E-04	0.1	9.1E-01	-0.7	2.1E-01
ENSMUST00000096452	cDNA sequence BC005561 [Source:MGI Symbol;Acc:MGI:3040669]	E9Q5E2		2.6	2.7E-03	6.2	2.8E-03	-0.8	6.4E-01	0.3	7.3E-01
ENSMUST00000096495	mediator complex subunit 14 [Source:MGI Symbol;Acc:MGI:1349442]		A2ABV5	-4.3	5.4E-04	-5.5	1.9E-02	0.9	2.7E-01	0.3	8.9E-01
ENSMUST00000096514	solute carrier family 35 (UDP-galactose transporter), member A2 [Source:MGI Symbol;Acc:MGI:1345297]	A2AER3		-3.9	5.4E-03	5.6	4.3E-03	1.2	4.4E-01	-0.6	5.4E-01
ENSMUST00000094505	DENN/MADD domain containing 1B [Source:MGI Symbol;Acc:MGI:2447812]		Q3U1T9	-0.8	3.2E-01	2.4	8.4E-02	3.1	1.1E-02	-0.1	9.3E-01
ENSMUST00000096547	lipoxygenase homology domains 1 [Source:MGI Symbol;Acc:MGI:1914609]		C8YR32	7.2	1.5E-04	6.3	3.6E-04	-0.5	6.6E-01	-0.8	2.5E-01
ENSMUST00000096554	adenomatosis polyposis coli down-regulated 1 [Source:MGI Symbol;Acc:MGI:3513977]		Q3U128	6.0	1.9E-04	6.0	2.6E-06	-0.4	5.0E-01	0.3	4.4E-01
ENSMUST00000096575	mitogen-activated protein kinase kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346873]	G5E8L8		-1.8	3.4E-03	-5.5	1.3E-02	0.9	2.1E-01	0.4	8.3E-01
ENSMUST00000096608	maestro heat-like repeat family member 9 [Source:MGI Symbol;Acc:MGI:1925508]	G5E8L9		5.9	5.9E-04	8.5	2.5E-05	-0.2	8.9E-01	-0.4	4.7E-01
ENSMUST00000096633	NUT family member 2 [Source:MGI Symbol;Acc:MGI:2685652]		Q3V0C3	8.3	7.4E-05	7.1	1.0E-03	-0.7	6.7E-01	-0.9	3.1E-01
ENSMUST00000096639	ring finger protein 121 [Source:MGI Symbol;Acc:MGI:1922462]		Q8R1Z9	-3.5	1.7E-02	-6.9	3.4E-04	0.1	8.9E-01	-0.7	6.1E-01
ENSMUST00000096744	myeloid-associated differentiation marker [Source:MGI Symbol;Acc:MGI:1355332]	Q0VE46	O35682	-7.3	4.4E-04	8.2	8.5E-05	-0.9	4.8E-01	0.0	9.4E-01
ENSMUST00000096753	heterogeneous nuclear ribonucleoprotein U-like 2 [Source:MGI Symbol;Acc:MGI:1915943]		Q00PI9	-4.0	8.1E-05	-1.2	3.7E-01	0.7	4.2E-01	-2.2	1.6E-01
ENSMUST00000096862			Q3TR44	2.4	1.1E-03	6.5	6.2E-04	0.4	7.7E-01	-0.8	2.9E-01
ENSMUST00000096953	predicted gene 10354 [Source:MGI Symbol;Acc:MGI:3809109]		K7N6A0	7.7	2.8E-05	6.4	1.2E-04	-0.5	6.2E-01	0.5	3.8E-01
ENSMUST00000096987	septin 5 [Source:MGI Symbol;Acc:MGI:1195461]		Q9Z2Q6	-3.8	6.6E-04	5.6	3.7E-03	-0.4	7.9E-01	-0.1	8.7E-01
ENSMUST00000096990	cell division cycle 45 [Source:MGI Symbol;Acc:MGI:1338073]	F8WJ72		-3.0	7.9E-03	-2.8	2.6E-02	-1.0	1.7E-01	-2.0	1.2E-01
ENSMUST00000097014	tubulin, alpha 1A [Source:MGI Symbol;Acc:MGI:98869]		P68369	-5.8	1.1E-05	7.3	4.8E-05	-0.6	6.0E-01	-0.6	2.6E-01
ENSMUST00000094617	RAS guanyl releasing protein 4 [Source:MGI Symbol;Acc:MGI:2386851]	E9QKB7		-2.3	4.4E-01	-0.6	8.7E-01	0.5	8.6E-01	-1.2	7.4E-01
ENSMUST00000097044	predicted gene 5592 [Source:MGI Symbol;Acc:MGI:3648691]		Q3V0A6	11.5	2.0E-04	2.4	2.9E-01	-0.7	7.2E-01	1.9	2.7E-01
ENSMUST00000094632	seryl-aminoacyl-tRNA synthetase 2 [Source:MGI Symbol;Acc:MGI:1919234]		Q9JJL8	1.2	8.0E-02	1.9	3.0E-02	0.3	6.1E-01	-0.4	5.2E-01
ENSMUST00000097079	Kruppel-like factor 12 [Source:MGI Symbol;Acc:MGI:1333796]		O35738	7.4	7.6E-05	7.1	7.2E-05	-2.5	5.9E-02	-0.3	6.0E-01
ENSMUST00000097080	ophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11 (human) [Source:MGI Symbol;Acc:MGI:1		E9Q152	6.6	6.4E-04	-4.4	5.8E-02	0.1	9.0E-01	0.1	9.6E-01
ENSMUST00000097162	calcium binding and coiled-coil domain 2 [Source:MGI Symbol;Acc:MGI:1343177]		G8JL78	6.2	1.0E-04	-3.9	1.2E-04	0.4	1.6E-01	0.0	9.8E-01
ENSMUST00000094651	EP300 interacting inhibitor of differentiation 2B [Source:MGI Symbol;Acc:MGI:1924095]		E9Q2Y0	1.3	3.6E-02	2.0	3.0E-02	1.1	1.1E-01	0.5	4.6E-01
ENSMUST00000097175	developmental pluripotency associated 2 [Source:MGI Symbol;Acc:MGI:2157523]	B2RQ54	Q9CWH0	7.3	6.9E-05	6.5	2.5E-04	-0.6	6.0E-01	0.0	9.6E-01
ENSMUST00000097177	proteasome (prosome, macropain) subunit, beta type, 11 [Source:MGI Symbol;Acc:MGI:1921152]		Q8BG41	8.4	1.3E-04	6.9	2.5E-04	-0.5	6.7E-01	-0.8	2.4E-01
ENSMUST00000097218	predicted pseudogene 9008 [Source:MGI Symbol;Acc:MGI:3644000]		E9PVG0	6.5	6.1E-04	-7.9	1.7E-03	-0.7	3.2E-01	1.0	5.9E-01
ENSMUST00000097271	immunity-related GTPase family M member 1 [Source:MGI Symbol;Acc:MGI:107567]	Q5NCB5		-4.5	4.6E-03	4.7	4.8E-04	0.0	9.5E-01	-0.4	5.2E-01
ENSMUST00000097275	protein kinase C, epsilon [Source:MGI Symbol;Acc:MGI:97599]		P16054	2.1	3.2E-03	5.6	3.5E-02	-0.6	8.1E-01	1.1	4.2E-01
ENSMUST00000097278	predicted pseudogene 6594 [Source:MGI Symbol;Acc:MGI:3643873]	J3QM43		-4.3	1.9E-03	7.9	3.8E-05	-0.6	5.9E-01	-0.2	7.0E-01
ENSMUST00000097290	leucine rich repeat containing 30 [Source:MGI Symbol;Acc:MGI:2685172]	B2RVX0		7.2	1.4E-04	6.0	1.5E-04	-1.4	2.0E-01	-0.2	7.5E-01
ENSMUST00000097303	arrestin domain containing 5 [Source:MGI Symbol;Acc:MGI:1924170]		Q497K5	6.2	9.8E-04	-1.0	6.1E-01	2.8	5.4E-02	-2.3	2.8E-01
ENSMUST00000097324	exocrine gland secreted peptide 6 [Source:MGI Symbol;Acc:MGI:3643294]	A8R0U0		8.7	2.0E-05	-8.9	5.8E-04	-0.8	1.3E-01	2.2	2.2E-01
ENSMUST00000094695	regulator of microtubule dynamics 3 [Source:MGI Symbol;Acc:MGI:1915059]		Q3UJU9	0.6	3.6E-01	0.4	6.0E-01	0.1	8.4E-01	0.3	7.0E-01
ENSMUST00000097331	predicted gene 6034 [Source:MGI Symbol;Acc:MGI:3646212]	E9Q101		4.7	8.3E-04	5.0	1.1E-02	-0.6	7.0E-01	0.0	9.9E-01
ENSMUST00000097335	predicted gene 8909 [Source:MGI Symbol;Acc:MGI:3704134]	E9Q0G4		-2.2	1.8E-02	1.7	5.1E-01	0.8	6.3E-01	4.3	7.8E-02
ENSMUST00000097336	leukocyte specific transcript 1 [Source:MGI Symbol;Acc:MGI:1096324]	B8JJ61		-7.9	1.5E-05	6.6	3.0E-05	0.2	7.8E-01	0.6	2.6E-01
ENSMUST00000097337	oreceptor tyrosine-based inhibitory motif (ITIM) containing platelet receptor [Source:MGI Symbol;Acc:MGI:21	D3YVS6		4.0	2.8E-04	-0.9	3.2E-01	0.6	2.9E-01	-0.2	8.1E-01
ENSMUST00000097381	vomeronasal 2, receptor 112 [Source:MGI Symbol;Acc:MGI:3644292]	L7N221		6.6	9.1E-04	7.4	3.9E-05	0.1	9.1E-01	-0.1	8.7E-01
ENSMUST00000097393	ER membrane associated RNA degradation [Source:MGI Symbol;Acc:MGI:1917317]	E9Q048		-6.9	1.2E-04	4.5	1.9E-02	-1.2	4.6E-01	0.1	9.5E-01
ENSMUST00000094756	RNA binding motif protein 47 [Source:MGI Symbol;Acc:MGI:2384294]	D3YXZ5		-1.7	5.4E-01	-1.8	6.2E-01	-0.3	8.7E-01	-0.3	9.5E-01
ENSMUST00000097398	t-complex-associated testis expressed 3 [Source:MGI Symbol;Acc:MGI:98642]		P11985	4.0	3.4E-02	-2.7	1.1E-01	0.9	3.4E-01	-1.0	5.5E-01
ENSMUST00000094774				4.1	3.8E-02	1.9	2.9E-01	-2.5	1.5E-01	-0.3	8.3E-01
ENSMUST00000097403	t-complex protein 10c [Source:MGI Symbol;Acc:MGI:98543]	E9Q046		8.7	1.3E-05	-3.3	1.6E-02	0.7	3.0E-01	-3.5	3.3E-02
ENSMUST00000097414	quaking [Source:MGI Symbol;Acc:MGI:97837]		Q9QYS9	-4.2	2.6E-05	6.2	7.7E-05	-2.0	7.7E-02	0.0	9.7E-01
ENSMUST00000097419	Fgfr1 oncogene partner [Source:MGI Symbol;Acc:MGI:1922546]		Q66JX5	4.5	7.1E-03	7.5	1.1E-04	-0.6	6.5E-01	-0.5	4.3E-01
ENSMUST00000097420	ribonuclease T2A [Source:MGI Symbol;Acc:MGI:1915445]	Q5FWA0	Q9CQ01	-1.4	2.0E-02	6.2	2.2E-04	-2.1	1.1E-01	-0.7	3.0E-01
ENSMUST00000097423	radial spoke 3A homolog (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1914082]		Q3UFY4	-2.3	3.7E-03	6.3	4.4E-04	-0.5	6.9E-01	-0.3	6.7E-01
ENSMUST00000097425	fibronectin type III domain containing 1 [Source:MGI Symbol;Acc:MGI:1915905]	E9Q043		10.0	3.0E-06	8.7	6.4E-05	0.3	7.9E-01	0.3	6.4E-01
ENSMUST00000097432	serine active site containing 1 [Source:MGI Symbol;Acc:MGI:2447813]		Q3U213	3.4	5.8E-04	6.6	2.2E-04	-0.6	6.2E-01	-0.5	4.5E-01
ENSMUST00000097437	placenta-specific 8 [Source:MGI Symbol;Acc:MGI:2445289]		Q9JI48	-5.0	3.4E-04	-2.0	1.3E-02	0.4	2.8E-01	-1.7	3.3E-02
ENSMUST00000097442	protein tyrosine phosphatase, non-receptor type 14 [Source:MGI Symbol;Acc:MGI:102467]		Q62130	7.6	1.1E-06	6.2	1.8E-05	0.2	7.4E-01	0.4	4.1E-01
ENSMUST00000097453	CDC42 binding protein kinase alpha [Source:MGI Symbol;Acc:MGI:2441841]	D3YYN8		5.3	2.6E-03	6.8	6.5E-05	-0.8	4.7E-01	0.2	7.4E-01
ENSMUST00000097454	predicted gene 10518 [Source:MGI Symbol;Acc:MGI:3704205]	F6UQQ9		5.8	1.1E-03	5.8	7.5E-04	0.4	7.3E-01	-0.8	2.2E-01
ENSMUST00000097458	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) [Source:MGI Symbol;Acc:MGI:2138151]		Q91WN4	4.1	6.5E-04	-1.0	9.3E-02	0.5	1.7E-01	-0.5	3.3E-01
ENSMUST00000094816	DEAH (Asp-Glu-Ala-His) box polypeptide 34 [Source:MGI Symbol;Acc:MGI:1918973]			3.4	1.6E-01	3.1	2.2E-01	-1.7	5.0E-01	-1.4	4.8E-01
ENSMUST00000094818	chondroitin polymerizing factor [Source:MGI Symbol;Acc:MGI:106576]		Q6IQX7	2.4	2.7E-01	5.9	2.5E-02	1.3	5.5E-01	-2.3	2.3E-01
ENSMUST00000094821	glioma tumor suppressor candidate region gene 1 [Source:MGI Symbol;Acc:MGI:2154263]	F8VPZ9		-0.4	4.6E-01	-0.2	8.3E-01	0.9	1.2E-01	0.7	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000097462	pyrin domain containing 4 [Source:MGI Symbol;Acc:MGI:3695276]	Q3UPZ5		8.2	2.6E-05	8.5	3.3E-05	-0.7	5.9E-01	-0.4	4.9E-01
ENSMUST00000097466	predicted gene 10521 [Source:MGI Symbol;Acc:MGI:3642358]	E9PZK0		2.9	1.1E-03	6.3	2.0E-04	-0.5	6.3E-01	-0.6	3.6E-01
ENSMUST00000097473	transmembrane and coiled-coil domains 1 [Source:MGI Symbol;Acc:MGI:1921173]		Q921L3	8.2	1.3E-04	6.2	2.2E-04	-0.6	5.9E-01	0.3	6.5E-01
ENSMUST00000097474	RCSD domain containing 1 [Source:MGI Symbol;Acc:MGI:2676394]		Q3UZA1	2.9	2.8E-04	3.9	3.5E-02	-3.5	6.8E-02	-0.6	6.1E-01
ENSMUST00000097477	expressed sequence AA792892 [Source:MGI Symbol;Acc:MGI:2140789]	Q8C6S1		6.1	4.4E-04	5.1	1.8E-04	-2.5	3.4E-02	0.3	6.0E-01
ENSMUST00000097479	predicted gene, 16522 [Source:MGI Symbol;Acc:MGI:4360987]	Q8C9W1		8.6	3.0E-05	7.2	5.5E-05	0.6	5.6E-01	-0.6	2.9E-01
ENSMUST00000097494	RIKEN cDNA 9930111J21 gene 1 [Source:MGI Symbol;Acc:MGI:3041173]	Q5SVP0		3.3	6.5E-05	8.6	3.3E-05	-0.2	8.7E-01	-0.5	3.8E-01
ENSMUST00000094853	ring finger protein 220 [Source:MGI Symbol;Acc:MGI:1913993]	Q9D4L6		2.5	1.6E-01	3.0	1.3E-01	-1.4	4.2E-01	-2.0	2.3E-01
ENSMUST00000094866	vomeronasal 2, receptor 32 [Source:MGI Symbol;Acc:MGI:1316696]	K7N686		2.9	2.0E-01	3.6	1.5E-01	-0.5	8.5E-01	-1.2	5.1E-01
ENSMUST00000094867	family with sequence similarity 193, member A [Source:MGI Symbol;Acc:MGI:2447768]		Q8CGI1	-0.4	6.1E-01	-1.5	2.7E-01	1.1	1.7E-01	2.2	1.0E-01
ENSMUST00000097520	predicted gene 7276 [Source:MGI Symbol;Acc:MGI:3646549]	Q3TYW4		5.3	4.5E-04	6.1	7.7E-05	-1.7	9.3E-02	-0.3	5.6E-01
ENSMUST00000097527	torsin A interacting protein 1 [Source:MGI Symbol;Acc:MGI:3582693]		Q921T2	4.9	2.8E-02	-1.6	3.7E-02	0.3	4.1E-01	-0.2	7.8E-01
ENSMUST00000097530	methyl-CpG binding domain protein 1 [Source:MGI Symbol;Acc:MGI:1333811]			-1.5	1.1E-02	6.9	6.5E-05	-0.6	6.0E-01	-0.5	3.7E-01
ENSMUST00000097542	centrosomal protein 76 [Source:MGI Symbol;Acc:MGI:1923401]		Q0VEJ0	1.8	2.8E-03	3.9	2.0E-03	-2.9	1.5E-02	0.2	7.5E-01
ENSMUST00000097546	cDNA sequence BC003331 [Source:MGI Symbol;Acc:MGI:2385108]		Q4PJX1	5.5	3.5E-02	6.8	4.1E-05	-2.0	7.2E-02	0.2	6.7E-01
ENSMUST00000097547	cDNA sequence BC003331 [Source:MGI Symbol;Acc:MGI:2385108]		Q4PJX1	-5.6	2.3E-03	4.9	3.9E-04	2.3	1.7E-02	-0.4	5.5E-01
ENSMUST00000094898	cyclin Y-like 1 [Source:MGI Symbol;Acc:MGI:2138614]	E9Q226		-2.1	2.9E-01	-1.6	6.5E-01	1.8	3.9E-01	1.3	6.7E-01
ENSMUST00000097561	cysteine and glycine-rich protein 1 [Source:MGI Symbol;Acc:MGI:88549]	Q4FJX4	P97315	7.7	5.7E-04	5.8	3.0E-03	-1.6	2.8E-01	0.0	9.7E-01
ENSMUST00000097580	ADP-ribosylation factor-like 14 effector protein-like [Source:MGI Symbol;Acc:MGI:2685795]		Q3UKZ7	4.8	2.0E-05	3.7	3.3E-03	-2.7	3.1E-02	-0.5	4.7E-01
ENSMUST00000097590	leucyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1913808]	Q7TSZ3	Q8BMJ2	-2.0	5.3E-03	-0.4	7.6E-01	1.0	2.5E-01	-5.0	8.5E-03
ENSMUST00000097592	nuclear receptor subfamily 3, group C, member 1 [Source:MGI Symbol;Acc:MGI:95824]	E9PYV1		4.0	2.6E-02	6.7	4.1E-04	-0.5	6.9E-01	0.3	6.7E-01
ENSMUST00000094953	DnaJ (Hsp40) homolog, subfamily C, member 6 [Source:MGI Symbol;Acc:MGI:1919935]		Q80TZ3	6.4	3.7E-02	5.3	1.0E-01	-0.6	8.4E-01	0.5	8.1E-01
ENSMUST00000094955	predicted gene 12689 [Source:MGI Symbol;Acc:MGI:3650433]	Q8BQU9		0.7	5.6E-01	2.0	1.5E-01	-0.2	8.9E-01	-1.5	2.0E-01
ENSMUST00000097617	RIKEN cDNA 1700066B19 gene [Source:MGI Symbol;Acc:MGI:1920699]	Q3TS39		6.9	8.8E-06	-7.7	7.8E-03	1.1	1.3E-01	1.3	5.8E-01
ENSMUST00000097622	family with sequence similarity 53, member C [Source:MGI Symbol;Acc:MGI:1913556]		Q8BXQ8	-5.5	2.7E-03	5.5	5.9E-04	-1.3	2.7E-01	-0.3	6.5E-01
ENSMUST00000097626	bromodomain containing 8 [Source:MGI Symbol;Acc:MGI:1925906]		Q8R3B7	-7.4	1.1E-04	6.0	2.6E-04	-1.0	3.5E-01	-0.1	9.2E-01
ENSMUST00000097632	predicted gene 6086 [Source:MGI Symbol;Acc:MGI:3646771]	Q3ULK5		7.4	1.9E-05	-3.1	3.0E-03	0.9	5.2E-02	0.4	5.9E-01
ENSMUST00000097633	D-2-hydroxyglutarate dehydrogenase [Source:MGI Symbol;Acc:MGI:2138209]		Q8CIM3	-2.1	1.6E-02	8.2	1.5E-05	-0.6	6.0E-01	-0.6	2.2E-01
ENSMUST00000095014	transforming growth factor, beta receptor associated protein 1 [Source:MGI Symbol;Acc:MGI:2447427]		Q3UR70	2.7	3.9E-02	3.7	4.1E-02	0.6	6.9E-01	-0.4	7.1E-01
ENSMUST00000097642	myeloma overexpressed 2 [Source:MGI Symbol;Acc:MGI:1914165]	B2RVT1	Q3U898	-8.9	1.0E-06	3.8	1.1E-01	-0.5	8.4E-01	1.3	3.7E-01
ENSMUST00000097644	histone deacetylase 4 [Source:MGI Symbol;Acc:MGI:3036234]		Q6NZM9	-3.1	2.3E-04	-5.5	3.5E-03	0.8	1.4E-01	-0.9	5.9E-01
ENSMUST00000095027	AF4/FMR2 family, member 3 [Source:MGI Symbol;Acc:MGI:106927]	D3YYI6		1.9	4.4E-01	2.6	2.5E-01	-2.4	3.0E-01	-3.1	1.6E-01
ENSMUST00000095035	zinc finger and BTB domain containing 43 [Source:MGI Symbol;Acc:MGI:1919084]	G3X9N4		-0.1	9.5E-01	-2.8	2.1E-01	-0.4	7.4E-01	2.2	2.9E-01
ENSMUST00000095044	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 [Source:MGI Symbc		Q9JM95	1.8	2.9E-01	1.1	6.0E-01	-1.1	4.8E-01	-0.4	8.5E-01
ENSMUST00000097649	leucine rich repeat (in FLII) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1342770]		Q3UZ39	-9.0	1.5E-05	6.8	9.9E-04	-0.7	6.4E-01	0.3	7.4E-01
ENSMUST00000097651	nucleolar protein 4 [Source:MGI Symbol;Acc:MGI:2441684]		P60954	6.5	2.9E-04	-5.9	7.1E-05	0.0	9.6E-01	-2.7	3.8E-02
ENSMUST00000097659	UDP glucuronosyltransferase 1 family, polypeptide A5 [Source:MGI Symbol;Acc:MGI:3032634]	B2RT14		4.4	4.6E-03	6.6	1.4E-03	-0.6	7.3E-01	-2.6	1.6E-02
ENSMUST00000095062	LMBR1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1915671]		Q8K0B2	-0.4	4.7E-01	-0.8	3.5E-01	0.1	8.7E-01	0.5	5.7E-01
ENSMUST00000095063	INTS3 and NABP interacting protein [Source:MGI Symbol;Acc:MGI:1913459]		Q3TXT3	0.0	9.9E-01	0.6	4.7E-01	0.6	3.4E-01	0.0	9.9E-01
ENSMUST00000097680	RAB18, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:102790]	Q0PD38	P35293	-4.5	2.7E-05	3.0	9.8E-03	0.6	4.7E-01	0.2	7.8E-01
ENSMUST00000097682	ribosomal protein L27, pseudogene 3 [Source:MGI Symbol;Acc:MGI:3646174]	Q5BLJ9	P61358	-8.6	7.2E-05	4.9	3.1E-04	0.5	5.1E-01	0.1	8.3E-01
ENSMUST00000097694	family with sequence similarity 134, member A [Source:MGI Symbol;Acc:MGI:2388278]		Q6NS82	-5.1	3.0E-04	8.3	3.0E-05	-0.5	6.5E-01	-1.2	4.8E-02
ENSMUST00000097709	isocitrate dehydrogenase 1 (NADP+), soluble [Source:MGI Symbol;Acc:MGI:96413]		O88844	-5.7	1.7E-06	7.5	4.4E-05	0.2	8.9E-01	-0.4	4.6E-01
ENSMUST00000095078	leucine rich repeat containing 8A [Source:MGI Symbol;Acc:MGI:2652847]		Q80WG5	-1.8	2.9E-01	0.4	8.4E-01	1.4	4.2E-01	-0.9	6.5E-01
ENSMUST00000097713	pleckstrin homology domain containing, family M, member 3 [Source:MGI Symbol;Acc:MGI:2443627]		Q8BM47	-1.5	1.6E-02	5.8	6.4E-04	-0.8	4.8E-01	-0.4	5.9E-01
ENSMUST00000095080	actin-like 7b [Source:MGI Symbol;Acc:MGI:1343053]		Q9QY83	1.5	5.3E-01	2.6	3.1E-01	-1.5	5.3E-01	-2.6	2.3E-01
ENSMUST00000097715	mitochondrial ribosomal protein L43 [Source:MGI Symbol;Acc:MGI:2137229]	Q5RL20		-3.1	1.4E-04	-4.5	9.2E-04	0.9	6.0E-02	-3.3	2.3E-02
ENSMUST00000097739	post-GPI attachment to proteins 1 [Source:MGI Symbol;Acc:MGI:2443342]		Q3UUQ7	3.0	1.8E-04	6.8	2.8E-02	-0.7	8.2E-01	-1.2	4.7E-01
ENSMUST00000097742	transmembrane protein 88B [Source:MGI Symbol;Acc:MGI:2444329]		Q3TYP4	5.5	5.5E-06	6.8	4.2E-04	-0.5	7.3E-01	-0.7	3.0E-01
ENSMUST00000097773	kelch-like 21 [Source:MGI Symbol;Acc:MGI:1919288]		Q3U410	2.7	6.0E-03	3.8	1.1E-03	0.2	8.2E-01	-1.2	9.6E-02
ENSMUST00000097778	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	D3Z0W0		-7.0	9.8E-04	7.2	1.1E-04	-0.6	6.1E-01	-0.2	6.9E-01
ENSMUST00000097788	5,10-methylenetetrahydrofolate reductase [Source:MGI Symbol;Acc:MGI:106639]		Q9WU20	5.0	3.2E-02	6.7	2.1E-03	-0.7	6.9E-01	0.2	7.9E-01
ENSMUST00000095117	MAM domain containing 4 [Source:MGI Symbol;Acc:MGI:2685841]	D3YY20		5.2	4.0E-02	5.4	2.7E-02	-2.2	3.8E-01	-2.3	1.3E-01
ENSMUST00000097801	RIKEN cDNA 4931408C20 gene [Source:MGI Symbol;Acc:MGI:3588222]	E9PWP9		5.9	1.1E-05	-1.8	6.2E-02	0.4	5.2E-01	-3.5	1.6E-02
ENSMUST00000097808	regulating synaptic membrane exocytosis 1 [Source:MGI Symbol;Acc:MGI:2152971]	E9PWP6		6.4	1.4E-04	6.6	2.7E-04	-0.6	6.1E-01	-0.6	3.9E-01
ENSMUST00000097813	REM2 and RAB-like small GTPase 1 [Source:MGI Symbol;Acc:MGI:1923416]	B2RWG6	A2A825	5.2	4.0E-03	6.7	3.8E-04	-0.5	7.0E-01	-1.3	9.3E-02
ENSMUST00000097822	ubiquitin protein ligase E3 component n-recognin 4 [Source:MGI Symbol;Acc:MGI:1916366]		A2AN08	-2.5	1.6E-03	2.7	1.8E-01	-0.5	7.8E-01	3.6	1.9E-02
ENSMUST00000095143	RNA binding motif protein 12 B2 [Source:MGI Symbol;Acc:MGI:1924854]		Q66JV4	-1.8	3.2E-01	-0.3	8.6E-01	-0.5	6.9E-01	-2.0	3.2E-01
ENSMUST00000097826	serum/glucocorticoid regulated kinase 3 [Source:MGI Symbol;Acc:MGI:2182368]		Q9ERE3	-6.8	7.0E-05	6.0	9.1E-06	-0.2	7.5E-01	0.1	7.5E-01
ENSMUST00000097830	OTU domain containing 3 [Source:MGI Symbol;Acc:MGI:1920412]		B1AZ99	-1.7	3.2E-03	3.7	2.2E-04	-4.7	4.1E-04	-0.9	9.5E-02
ENSMUST00000097837	Rap1 GTPase-activating protein [Source:MGI Symbol;Acc:MGI:109338]		A2ALS5	6.6	1.0E-02	4.3	1.4E-03	-2.0	5.8E-02	0.0	1.0E+00
ENSMUST00000095172	c-Maf inducing protein [Source:MGI Symbol;Acc:MGI:1921690]		Q9D486	-4.6	8.5E-02	-1.3	6.6E-01	1.7	4.5E-01	-1.6	5.8E-01
ENSMUST00000097843	cannabinoid receptor 2 (macrophage) [Source:MGI Symbol;Acc:MGI:104650]		P47936	-2.9	1.8E-04	-6.4	7.1E-03	1.3	1.3E-01	0.9	6.6E-01
ENSMUST00000097849	predicted gene 7534 [Source:MGI Symbol;Acc:MGI:3702974]	Q3UU21		10.4	2.4E-04	6.0	7.1E-05	-1.2	2.3E-01	0.0	9.5E-01
ENSMUST00000095187	S1 RNA binding domain 1 [Source:MGI Symbol;Acc:MGI:1925836]	F8WGW3		-0.2	7.2E-01	0.2	8.1E-01	0.5	3.0E-01	0.2	7.9E-01
ENSMUST00000097856	family with sequence similarity 76, member A [Source:MGI Symbol;Acc:MGI:2385211]		Q922G2	-3.5	2.1E-02	1.6	7.9E-02	-2.3	1.3E-02	-0.3	7.2E-01
ENSMUST00000097864	pumilio RNA-binding family member 1 [Source:MGI Symbol;Acc:MGI:1931749]		Q80U78	4.8	2.6E-02	5.9	1.0E-03	-1.0	4.5E-01	-0.1	9.0E-01
ENSMUST00000097868	adhesion G protein-coupled receptor B2 [Source:MGI Symbol;Acc:MGI:2451244]	H7BX74		5.9	3.2E-02	7.1	1.4E-04	-0.6	6.1E-01	-0.4	5.2E-01
ENSMUST00000097874	ring finger protein 19B [Source:MGI Symbol;Acc:MGI:1922484]	B2KG08		-6.4	1.0E-03	-3.3	1.0E-02	0.6	3.0E-01	-1.9	1.6E-01
ENSMUST00000095217	oocyte specific homeobox 3 [Source:MGI Symbol;Acc:MGI:2149032]	Q3UT54		4.4	1.0E-01	6.6	3.5E-02	-0.2	9.5E-01	-2.4	1.6E-01
ENSMUST00000097877	zinc finger and SCAN domains 20 [Source:MGI Symbol;Acc:MGI:2679268]		B2KFW1	3.2	6.2E-04	1.5	2.9E-01	-3.1	6.1E-02	0.8	5.1E-01
ENSMUST00000095220	F-box and WD-40 domain protein 9 [Source:MGI Symbol;Acc:MGI:1915878]	F8VPX2		-2.0	3.4E-01	0.3	9.1E-01	1.6	4.7E-01	-0.7	7.6E-01
ENSMUST00000097891	SH3 domain containing 21 [Source:MGI Symbol;Acc:MGI:1914188]	Z4YK11		5.8	5.7E-04	-6.8	8.9E-03	0.8	2.8E-01	-0.8	7.4E-01
ENSMUST00000095228	sterile alpha motif domain containing 1 [Source:MGI Symbol;Acc:MGI:2142433]		D3YXK1	-1.1	1.5E-01	-1.1	2.7E-01	0.9	2.3E-01	0.9	3.7E-01
ENSMUST00000095254	target of myb1-like 2 (chicken) [Source:MGI Symbol;Acc:MGI:2443306]		Q5SRX1	-4.2	2.1E-01	2.9	3.9E-01	4.2	1.8E-01	-3.0	3.6E-01
ENSMUST00000097896	Riken cDNA 4933427I04 gene [Source:MGI Symbol;Acc:MGI:3613760]	Q3V053		6.2	1.4E-04	-3.6	2.1E-02	1.2	7.4E-02	0.1	9.5E-01
ENSMUST00000097905	predicted gene 12888 [Source:MGI Symbol;Acc:MGI:3652130]	Q3UW77		6.0	2.7E-04	3.6	1.7E-03	-0.6	4.8E-01	-0.5	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000097911	lysine (K)-specific demethylase 4A [Source:MGI Symbol;Acc:MGI:2446210]		Q8BW72	-4.1	1.5E-02	4.0	3.4E-03	-0.2	8.3E-01	0.0	9.6E-01
ENSMUST00000097918	kinocilin [Source:MGI Symbol;Acc:MGI:3614952]		Q307W7	5.8	1.6E-03	-1.0	1.6E-01	1.5	7.9E-03	-0.8	2.4E-01
ENSMUST00000097935	predicted gene 6471 [Source:MGI Symbol;Acc:MGI:3648397]	Q3UTU4		6.7	4.2E-05	6.6	2.0E-04	-0.5	6.5E-01	-0.2	7.9E-01
ENSMUST00000097942	keratin associated protein 5-5 [Source:MGI Symbol;Acc:MGI:2149673]		Q2TA51	8.5	1.1E-04	-4.8	2.9E-04	0.4	3.4E-01	0.4	6.1E-01
ENSMUST00000097957	Harvey rat sarcoma virus oncogene [Source:MGI Symbol;Acc:MGI:96224]		Q61411	-6.7	1.1E-04	5.3	4.5E-04	1.6	1.1E-01	-0.4	5.5E-01
ENSMUST00000097961	asparagine-linked glycosylation 6 (alpha-1,3,-glucosyltransferase) [Source:MGI Symbol;Acc:MGI:2444031]		Q3TAE8	2.1	1.3E-02	-1.2	1.3E-01	0.0	9.2E-01	-0.8	2.8E-01
ENSMUST00000095295	tripartite motif-containing 75 [Source:MGI Symbol;Acc:MGI:2685640]	B2RTB3	Q3UWZ0	1.5	3.7E-02	2.7	7.2E-03	0.8	2.6E-01	-0.4	5.2E-01
ENSMUST00000097964	RIKEN cDNA I0C0044D17 gene [Source:MGI Symbol;Acc:MGI:3588230]	A6PWL3		7.0	4.5E-06	-3.5	1.1E-01	0.9	3.9E-01	0.8	7.1E-01
ENSMUST00000097974	NK6 homeobox 2 [Source:MGI Symbol;Acc:MGI:1352738]	D3Z4R4		7.6	5.3E-05	1.0	2.6E-01	-4.7	1.9E-03	0.2	8.0E-01
ENSMUST00000095319	antagonist of mitotic exit network 1 [Source:MGI Symbol;Acc:MGI:2442933]	B8JKU8		-3.7	3.8E-02	-3.4	1.2E-01	0.0	1.0E+00	-0.3	9.0E-01
ENSMUST00000097975	inositol polyphosphate-5-phosphatase A [Source:MGI Symbol;Acc:MGI:2686961]	Q3TZT4		-2.4	2.0E-03	5.0	1.6E-03	-1.7	1.7E-01	-0.2	7.8E-01
ENSMUST00000097982	RIKEN cDNA 4930544L04 gene [Source:MGI Symbol;Acc:MGI:1926057]	Q3V0D6		8.1	1.2E-05	7.4	1.3E-03	-0.8	6.4E-01	0.5	5.6E-01
ENSMUST00000095328	cytochrome P450, family 4, subfamily v, polypeptide 3 [Source:MGI Symbol;Acc:MGI:2142763]	B2RSR0	Q9DBW0	0.0	9.8E-01	0.4	5.4E-01	0.0	9.3E-01	-0.5	4.7E-01
ENSMUST00000097992	focadhesin [Source:MGI Symbol;Acc:MGI:2676921]		A2AKG8	5.3	5.4E-03	7.7	5.9E-05	0.1	9.0E-01	0.1	8.6E-01
ENSMUST00000095342	histocompatibility 2, O region beta locus [Source:MGI Symbol;Acc:MGI:95925]	O35424		1.4	8.3E-02	-1.4	2.3E-01	-0.9	2.4E-01	1.9	9.0E-02
ENSMUST00000098015	integrin alpha M [Source:MGI Symbol;Acc:MGI:96607]	Q3U1U4		-3.7	7.7E-05	7.2	8.1E-05	-0.1	9.4E-01	0.1	8.7E-01
ENSMUST00000098031	regulator of G-protein signaling 3 [Source:MGI Symbol;Acc:MGI:1354734]	I7HPB2		6.5	3.0E-04	-4.0	5.1E-03	1.1	6.7E-02	-2.2	1.1E-01
ENSMUST00000095349	UBX domain protein 8 [Source:MGI Symbol;Acc:MGI:1337129]	Q3TTF2		-0.7	1.6E-01	-0.2	7.6E-01	0.5	2.8E-01	0.0	9.4E-01
ENSMUST00000098032	family with sequence similarity 57, member B [Source:MGI Symbol;Acc:MGI:1916202]		Q7TNV1	7.7	6.6E-05	3.2	3.6E-02	-0.1	9.1E-01	-0.7	4.7E-01
ENSMUST00000098033	FK506 binding protein 15 [Source:MGI Symbol;Acc:MGI:2444782]	Q80YW7		-4.4	1.8E-03	4.6	8.1E-03	-3.9	5.4E-02	0.2	8.1E-01
ENSMUST00000098036	oid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) [Source:MGI Symbol;Acc:MGI:1075	Q6PAH4		-8.4	3.7E-05	7.6	3.3E-05	0.1	9.3E-01	-0.6	2.5E-01
ENSMUST00000098042	major urinary protein 13 [Source:MGI Symbol;Acc:MGI:3702003]	L7N222		4.6	2.1E-02	2.3	1.2E-02	0.8	2.3E-01	0.8	1.9E-01
ENSMUST00000095385	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:2682307]		Q80XE1	-2.2	1.8E-01	-3.0	2.6E-01	0.4	7.5E-01	1.2	6.5E-01
ENSMUST00000095388	regulatory factor X, 4 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:1918387]		Q7TNK1	3.7	1.8E-01	3.6	2.6E-01	-0.2	9.5E-01	-0.1	9.8E-01
ENSMUST00000098048	Tu translation elongation factor, mitochondrial [Source:MGI Symbol;Acc:MGI:1923686]		Q8BFR5	-4.4	1.1E-03	-0.6	3.2E-01	0.0	9.6E-01	-0.8	2.3E-01
ENSMUST00000098060	Rho GTPase activating protein 17 [Source:MGI Symbol;Acc:MGI:1917747]		Q3UIA2	-7.3	5.6E-04	-0.7	5.8E-01	-2.9	2.4E-02	1.4	2.2E-01
ENSMUST00000098070	zinc finger protein 462 [Source:MGI Symbol;Acc:MGI:107690]	B1AWL2		10.5	3.0E-06	-1.1	1.3E-01	-0.2	7.4E-01	-0.6	3.7E-01
ENSMUST00000098084	acyl-CoA synthetase medium-chain family member 2 [Source:MGI Symbol;Acc:MGI:2385289]		Q8K0L3	9.5	6.8E-05	-6.1	2.2E-02	0.9	2.8E-01	1.9	4.2E-01
ENSMUST00000095439	spectrin repeat containing, nuclear envelope family member 3 [Source:MGI Symbol;Acc:MGI:2442408]		Q4FZC9	0.1	9.2E-01	2.0	2.4E-01	0.8	5.6E-01	-1.1	4.7E-01
ENSMUST00000098106	RUN and SH3 domain containing 2 [Source:MGI Symbol;Acc:MGI:2140371]	Q3V1Z0		5.9	2.7E-02	7.9	2.8E-05	-0.6	6.2E-01	-0.6	2.2E-01
ENSMUST00000098109	phosphatidylinositol glycan anchor biosynthesis, class O [Source:MGI Symbol;Acc:MGI:1861452]	Q562G0		1.5	1.9E-02	-7.2	1.2E-04	0.5	1.6E-01	-0.6	6.1E-01
ENSMUST00000098132	interleukin 11 receptor, alpha chain 1 [Source:MGI Symbol;Acc:MGI:107426]		Q64385	3.1	1.9E-03	-4.4	1.0E-04	-0.5	1.4E-01	-0.3	6.7E-01
ENSMUST00000098134	PTPRF interacting protein, binding protein 2 (liprin beta 2) [Source:MGI Symbol;Acc:MGI:894649]		O35711	7.9	2.7E-05	7.4	2.5E-04	-0.7	6.2E-01	-0.4	6.0E-01
ENSMUST00000098135	RNA binding motif protein, X-linked-like 2 [Source:MGI Symbol;Acc:MGI:1923822]	Q9DAE2		6.5	1.8E-04	9.0	3.5E-04	-0.9	6.3E-01	0.7	3.3E-01
ENSMUST00000098142	olfactory receptor 703 [Source:MGI Symbol;Acc:MGI:3030537]	Q9EPF5		6.4	2.0E-04	5.8	2.6E-03	-1.2	4.3E-01	-1.2	2.4E-01
ENSMUST00000095476	ligase IV, DNA, ATP-dependent [Source:MGI Symbol;Acc:MGI:1335098]		Q8BTF7	0.1	9.1E-01	0.8	5.8E-01	2.1	8.1E-02	1.4	2.7E-01
ENSMUST00000098143	nuclear transcription factor, X-box binding 1 [Source:MGI Symbol;Acc:MGI:1921414]		B1AY10	-1.8	1.3E-02	4.0	4.0E-03	0.5	6.2E-01	-0.3	7.2E-01
ENSMUST00000098180	tripartite motif-containing 6 [Source:MGI Symbol;Acc:MGI:2137352]		Q8BGE7	3.1	9.8E-03	7.9	1.9E-04	-0.7	6.3E-01	-0.5	4.9E-01
ENSMUST00000095495	armadillo repeat containing 10 [Source:MGI Symbol;Acc:MGI:1914461]	D3Z5T2		0.9	2.6E-01	3.3	5.1E-03	1.4	1.0E-01	-1.0	2.1E-01
ENSMUST00000098182	olfactory receptor 646 [Source:MGI Symbol;Acc:MGI:3030480]	Q8VGW2		6.4	1.8E-04	5.9	1.9E-03	0.4	7.8E-01	0.1	8.7E-01
ENSMUST00000098185	olfactory receptor 635 [Source:MGI Symbol;Acc:MGI:3030469]	K7N6B1		6.7	6.4E-05	1.9	5.3E-03	0.6	2.2E-01	0.0	9.2E-01
ENSMUST00000098189	olfactory receptor 632 [Source:MGI Symbol;Acc:MGI:3030466]	Q9EPN9		5.7	6.6E-04	6.9	8.6E-05	-0.6	6.1E-01	-1.5	2.6E-02
ENSMUST00000098224	olfactory receptor 551 [Source:MGI Symbol;Acc:MGI:3030385]	Q8VG23		6.3	2.8E-04	7.1	5.4E-05	-1.5	2.0E-01	-0.8	1.9E-01
ENSMUST00000098227	olfactory receptor 549 [Source:MGI Symbol;Acc:MGI:3030383]	E9Q542		6.6	1.6E-04	4.4	1.1E-01	-0.8	7.3E-01	1.1	5.3E-01
ENSMUST00000098230	ras homolog gene family, member G [Source:MGI Symbol;Acc:MGI:1928370]	Q3UDZ1	P84096	-9.4	2.3E-04	5.3	2.6E-04	0.2	7.9E-01	0.9	1.4E-01
ENSMUST00000098238	PNN interacting serine/arginine-rich [Source:MGI Symbol;Acc:MGI:1913875]		A2AJT4	-6.2	5.8E-04	7.1	9.3E-05	-1.7	2.0E-01	-0.6	3.5E-01
ENSMUST00000098242	gamma-glutamyl hydrolase [Source:MGI Symbol;Acc:MGI:1329035]		Q9Z0L8	-3.8	1.6E-05	5.5	1.2E-03	0.1	9.6E-01	-0.8	2.6E-01
ENSMUST00000098243	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:1916960]	E9PUB0		-4.3	1.5E-04	4.6	6.2E-04	-0.9	3.5E-01	-0.1	8.4E-01
ENSMUST00000098250	FCH and double SH3 domains 2 [Source:MGI Symbol;Acc:MGI:2448475]		Q3USJ8	-3.3	2.1E-02	7.6	5.4E-03	-1.4	5.7E-01	-3.0	6.3E-02
ENSMUST00000095572	olute carrier family 10 (sodium/bile acid cotransporter family), member 1 [Source:MGI Symbol;Acc:MGI:9737		O08705	1.2	6.7E-02	1.9	2.7E-02	0.2	6.9E-01	-0.4	5.1E-01
ENSMUST00000098256	runt-related transcription factor 1; translocated to, 1 (cyclin D-related) [Source:MGI Symbol;Acc:MGI:104793	B1AXH9	Q61909	9.7	3.8E-04	3.2	5.9E-03	-0.6	4.6E-01	-0.6	4.5E-01
ENSMUST00000098260	predicted gene 10604 [Source:MGI Symbol;Acc:MGI:3642593]	Q3V0X7		7.6	1.4E-04	-3.7	5.2E-02	1.5	7.5E-02	-0.7	7.2E-01
ENSMUST00000098266	arrestin, beta 1 [Source:MGI Symbol;Acc:MGI:99473]		Q8BWG8	-2.5	3.2E-03	8.2	2.5E-05	-0.4	7.5E-01	-0.1	7.7E-01
ENSMUST00000098272	kelch-like 40 [Source:MGI Symbol;Acc:MGI:1919580]			8.3	2.2E-05	8.8	2.4E-05	-0.5	6.9E-01	-0.7	2.0E-01
ENSMUST00000095595	zinc finger and SCAN domain containing 10 [Source:MGI Symbol;Acc:MGI:3040700]		Q3URR7	5.9	6.2E-02	5.0	1.3E-01	-0.9	8.0E-01	0.0	9.8E-01
ENSMUST00000098273	family with sequence similarity 212, member B [Source:MGI Symbol;Acc:MGI:1923497]		Q80VY2	9.2	1.3E-04	2.0	1.7E-02	0.2	7.0E-01	0.0	9.5E-01
ENSMUST00000098274	guanylate cyclase 2d [Source:MGI Symbol;Acc:MGI:106030]	F6VFS9		8.1	1.3E-05	5.2	2.2E-04	0.2	8.0E-01	0.4	4.8E-01
ENSMUST00000098278	lcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase) [Source:MGI Symbol;Acc:MGI:3(		Q3USF0	6.3	8.8E-06	6.6	1.7E-03	-0.7	6.6E-01	-1.0	2.6E-01
ENSMUST00000098281	olfactory marker protein [Source:MGI Symbol;Acc:MGI:97436]	A2RT14	Q64288	8.9	4.0E-05	4.2	1.5E-02	-0.7	6.3E-01	1.8	9.7E-02
ENSMUST00000098324	melanocortin 1 receptor [Source:MGI Symbol;Acc:MGI:99456]	A0A0B6VTJ4	Q01727	8.4	4.3E-06	8.0	8.4E-05	-0.6	6.2E-01	-0.9	1.6E-01
ENSMUST00000098326	homer homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1347354]	E9Q4F9		7.7	6.7E-06	-3.5	1.4E-02	0.6	3.3E-01	1.2	3.5E-01
ENSMUST00000095666	ninein [Source:MGI Symbol;Acc:MGI:105108]		Q61043	-2.8	6.2E-02	-3.8	5.8E-02	-0.9	3.8E-01	0.2	9.3E-01
ENSMUST00000095668	protein kinase inhibitor beta, cAMP dependent, testis specific [Source:MGI Symbol;Acc:MGI:101937]	F7D7A9		-2.4	1.1E-01	-1.7	3.0E-01	-0.1	9.0E-01	-0.9	6.1E-01
ENSMUST00000095691	centrosomal protein 85-like [Source:MGI Symbol;Acc:MGI:3642684]	E9QA61		-0.8	1.6E-01	0.4	5.6E-01	0.7	1.6E-01	-0.4	4.9E-01
ENSMUST00000098334	ankyrin repeat domain 11 [Source:MGI Symbol;Acc:MGI:1924337]	E9Q4F7		-5.3	4.6E-03	7.4	4.0E-05	-0.5	6.2E-01	-0.6	2.7E-01
ENSMUST00000098340	leucine rich repeat (in FLII) interacting protein 2 [Source:MGI Symbol;Acc:MGI:1918518]			-4.2	4.6E-05	6.7	2.7E-04	-0.6	6.3E-01	-1.1	1.2E-01
ENSMUST00000098345	protease, serine 44 [Source:MGI Symbol;Acc:MGI:1920586]		Q402U7	7.5	8.6E-05	4.1	2.1E-02	-1.8	2.7E-01	-1.7	1.3E-01
ENSMUST00000095724	ir cross-complementing rodent repair deficiency, complementation group 6 like 2 [Source:MGI Symbol;Acc:M	E9QPI9		2.8	7.9E-02	1.0	5.4E-01	-2.1	1.6E-01	-0.3	8.1E-01
ENSMUST00000095725	prenyl (solanesyl) diphosphate synthase, subunit 2 [Source:MGI Symbol;Acc:MGI:1918615]		Q33DR3	-1.3	1.4E-01	0.2	8.3E-01	0.9	3.0E-01	-0.7	4.8E-01
ENSMUST00000095729	armadillo repeat containing 2 [Source:MGI Symbol;Acc:MGI:1916449]		Q3URY6	9.3	5.8E-02	6.4	2.2E-01	-0.9	8.6E-01	2.0	4.9E-01
ENSMUST00000098355	d, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 [Source:MGI Symbol;Acc	F6SKR9		4.0	1.4E-04	9.1	7.0E-06	1.3	2.2E-01	-0.5	2.3E-01
ENSMUST00000095739	golgi membrane protein 1 [Source:MGI Symbol;Acc:MGI:1917329]		Q91XA2	-1.8	2.5E-01	-4.0	3.6E-02	-1.7	1.3E-01	0.4	8.1E-01
ENSMUST00000095743	cyclin-dependent kinase 19 [Source:MGI Symbol;Acc:MGI:1925584]	G5E8L1		2.8	3.0E-01	-3.4	6.3E-02	-7.1	5.1E-03	-0.9	6.6E-01
ENSMUST00000095749	RIKEN cDNA G630090E17 gene [Source:MGI Symbol;Acc:MGI:3773841]		Q3UN21	0.0	9.8E-01	1.1	3.0E-01	1.1	2.1E-01	-0.1	9.5E-01
ENSMUST00000098359	F-box and WD-40 domain protein 18 [Source:MGI Symbol;Acc:MGI:3505704]	Q3TSA9		6.0	2.9E-04	-5.1	3.0E-03	-0.1	9.0E-01	-0.8	5.7E-01
ENSMUST00000095753	cytotoxic granule-associated RNA binding protein 1 [Source:MGI Symbol;Acc:MGI:107914]	Q564E7	P52912	-1.5	2.2E-01	1.1	4.3E-01	0.8	4.9E-01	-1.8	1.8E-01
ENSMUST00000098361	adenosine deaminase domain containing 2 [Source:MGI Symbol;Acc:MGI:1923023]	B2RQL4		8.0	6.2E-05	5.0	9.3E-03	-0.5	7.4E-01	0.6	5.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000098363	N-terminal EF-hand calcium binding protein 2 [Source:MGI Symbol;Acc:MGI:2152211]		Q91ZP9	4.7	3.4E-03	4.3	2.0E-04	0.6	3.5E-01	-0.3	5.5E-01
ENSMUST00000098367	malonyl-CoA decarboxylase [Source:MGI Symbol;Acc:MGI:1928485]		Q99J39	-5.3	1.7E-03	6.4	1.5E-03	-0.5	7.6E-01	-1.2	1.7E-01
ENSMUST00000098375	polycystic kidney disease 1 like 2 [Source:MGI Symbol;Acc:MGI:2664668]	E9Q4D4		3.7	2.1E-04	5.1	1.8E-03	-2.0	1.6E-01	-0.2	8.1E-01
ENSMUST00000098382	·like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 17 [Source:MGI Symbol;Acc:M	E9Q4D1		9.1	1.4E-04	5.0	1.0E-03	-0.5	6.6E-01	0.6	3.6E-01
ENSMUST00000098391	proprotein convertase subtilisin/kexin type 6 [Source:MGI Symbol;Acc:MGI:102897]	E9Q4D0		7.3	2.5E-02	3.3	1.0E-01	-3.4	1.0E-01	-0.3	7.9E-01
ENSMUST00000098407	junction adhesion molecule 2 [Source:MGI Symbol;Acc:MGI:1933820]	Q9CWD9		7.8	9.0E-05	6.8	1.0E-04	-0.5	6.5E-01	0.1	9.3E-01
ENSMUST00000098414	small VCP/p97-interacting protein [Source:MGI Symbol;Acc:MGI:1922994]		Q3UZP4	-4.9	1.7E-05	3.9	2.3E-02	0.0	9.8E-01	-0.6	5.9E-01
ENSMUST00000098433	MAS-related GPR, member X2 [Source:MGI Symbol;Acc:MGI:3588270]		Q3UG50	7.6	2.1E-04	6.0	8.0E-05	-0.6	5.3E-01	-0.7	1.9E-01
ENSMUST00000095786	polymerase (DNA-directed), epsilon 4 (p12 subunit) [Source:MGI Symbol;Acc:MGI:1914229]		Q9CQ36	-1.7	1.6E-01	0.8	6.2E-01	2.1	9.7E-02	-0.4	7.5E-01
ENSMUST00000098441	collagen, type VI, alpha 6 [Source:MGI Symbol;Acc:MGI:2444259]		Q8C6K9	9.7	4.4E-07	5.4	1.4E-03	-1.3	3.3E-01	-0.7	3.3E-01
ENSMUST00000098443	copine IV [Source:MGI Symbol;Acc:MGI:1921270]	Q8CEQ2		5.9	1.9E-03	-2.6	5.2E-03	1.7	2.6E-03	-1.3	1.3E-01
ENSMUST00000098460	RIKEN cDNA 7420426K07 gene [Source:MGI Symbol;Acc:MGI:3588253]	Q3UX66		7.3	8.6E-05	-3.3	3.5E-02	0.2	7.8E-01	-2.4	1.6E-01
ENSMUST00000098461	CD37 antigen [Source:MGI Symbol;Acc:MGI:88330]	Q4FK35	Q61470	-10.3	8.5E-05	-1.2	4.9E-02	1.1	9.3E-03	0.1	7.9E-01
ENSMUST00000098464	chemokine-like factor [Source:MGI Symbol;Acc:MGI:1922708]		Q9DAS1	2.0	9.1E-03	6.4	1.5E-04	-0.5	6.4E-01	0.3	5.9E-01
ENSMUST00000098473	CCR4-NOT transcription complex, subunit 1 [Source:MGI Symbol;Acc:MGI:2442402]		Q6ZQ08	-7.0	1.0E-05	-3.4	2.3E-02	1.3	7.3E-02	0.0	9.9E-01
ENSMUST00000098478	polynucleotide kinase 3'- phosphatase [Source:MGI Symbol;Acc:MGI:1891698]	E9Q9A5		-9.4	3.4E-05	7.2	5.1E-04	-0.7	6.2E-01	-0.4	5.9E-01
ENSMUST00000098496	glutamate rich 3 [Source:MGI Symbol;Acc:MGI:1919095]	F6QRE9		9.4	2.6E-06	6.5	1.9E-04	-0.5	6.4E-01	-0.7	2.9E-01
ENSMUST00000098508	zinc finger protein 788 [Source:MGI Symbol;Acc:MGI:1914857]	E9Q980		6.8	2.2E-03	6.7	6.2E-06	-0.9	2.6E-01	0.0	9.5E-01
ENSMUST00000095849	PR domain containing 15 [Source:MGI Symbol;Acc:MGI:1930121]	E9Q8T2		2.3	2.5E-01	1.3	5.6E-01	0.3	8.7E-01	1.4	4.4E-01
ENSMUST00000098513	rin homology domain containing, family F (with FYVE domain) member 1 [Source:MGI Symbol;Acc:MGI:19		Q3TB82	1.9	3.9E-03	8.0	3.1E-05	-0.6	5.9E-01	-0.6	2.7E-01
ENSMUST00000098521	adenylate cyclase 7 [Source:MGI Symbol;Acc:MGI:102891]		P51829	-2.9	1.5E-03	6.0	4.9E-04	-0.5	6.7E-01	0.1	9.4E-01
ENSMUST00000098534	zinc finger, HIT type 6 [Source:MGI Symbol;Acc:MGI:1916996]		Q3UFB2	3.5	9.9E-04	7.4	1.4E-04	2.3	6.1E-02	-0.2	7.4E-01
ENSMUST00000098537	glutathione S-transferase, alpha 1 (Ya) [Source:MGI Symbol;Acc:MGI:1095417]		P13745	4.6	2.9E-02	-4.8	6.6E-04	1.5	3.0E-03	0.0	9.7E-01
ENSMUST00000098545	TLC domain containing 1 [Source:MGI Symbol;Acc:MGI:1915572]		Q99JT6	2.2	3.0E-02	5.0	8.4E-03	-0.6	7.1E-01	0.4	6.7E-01
ENSMUST00000095899	spectrin repeat containing, nuclear envelope 1 [Source:MGI Symbol;Acc:MGI:1927152]	Q0VGB8	Q6ZWR6	-0.3	5.9E-01	0.0	9.9E-01	0.7	2.0E-01	0.4	5.1E-01
ENSMUST00000095903				0.2	8.8E-01	1.6	3.8E-01	-0.4	7.9E-01	-1.8	2.9E-01
ENSMUST00000098546	family with sequence similarity 83, member B [Source:MGI Symbol;Acc:MGI:2685362]		Q0VBM2	7.9	1.9E-03	4.4	2.6E-04	-0.4	6.1E-01	0.8	1.5E-01
ENSMUST00000095914	dual specificity phosphatase 22 [Source:MGI Symbol;Acc:MGI:1915926]		Q99N11	0.4	7.7E-01	0.8	5.8E-01	-1.0	3.9E-01	-1.4	2.9E-01
ENSMUST00000098549	chloride channel accessory 4B [Source:MGI Symbol;Acc:MGI:2139790]	Q3UW98		7.1	3.3E-05	6.1	3.0E-04	-0.5	6.7E-01	-0.5	4.2E-01
ENSMUST00000098550	zinc finger protein 791 [Source:MGI Symbol;Acc:MGI:3648473]	Q497V9		4.7	3.4E-04	-2.8	7.2E-03	-1.1	5.1E-02	-2.3	2.6E-02
ENSMUST00000098552	tropomodulin 2 [Source:MGI Symbol;Acc:MGI:1355335]		Q9JKK7	8.4	5.2E-05	-2.9	3.2E-03	-0.4	3.3E-01	0.0	9.6E-01
ENSMUST00000098574	RAP1, GTP-GDP dissociation stimulator 1 [Source:MGI Symbol;Acc:MGI:2385189]	E9Q912		-5.5	3.6E-04	5.2	4.4E-05	-1.2	1.1E-01	0.1	8.8E-01
ENSMUST00000098578	coiled-coil domain containing 130 [Source:MGI Symbol;Acc:MGI:1914986]		Q9D516	1.8	1.1E-02	4.4	2.1E-03	0.5	6.1E-01	0.1	8.6E-01
ENSMUST00000095941	F-box protein 34 [Source:MGI Symbol;Acc:MGI:1926188]		Q80XI1	-0.7	5.3E-01	3.9	9.8E-03	2.0	9.2E-02	-2.6	3.0E-02
ENSMUST00000095944	zinc finger protein 777 [Source:MGI Symbol;Acc:MGI:1919556]	G5E8L5		2.9	4.7E-02	7.2	2.3E-04	-0.5	6.9E-01	-4.8	5.5E-04
ENSMUST00000095947	nebulin-related anchoring protein [Source:MGI Symbol;Acc:MGI:1098765]		Q80XB4	-1.4	2.2E-01	7.5	9.2E-04	4.4	1.5E-02	-4.6	1.7E-03
ENSMUST00000098592	predicted gene 10643 [Source:MGI Symbol;Acc:MGI:3642507]	Q3URG9		3.1	1.4E-03	6.0	1.0E-03	0.0	9.8E-01	0.5	4.7E-01
ENSMUST00000098595	predicted gene 10644 [Source:MGI Symbol;Acc:MGI:3704314]	Q3TZG3		6.1	2.1E-05	-1.2	5.5E-02	0.5	1.5E-01	-0.1	8.5E-01
ENSMUST00000098596	zinc finger protein 382 [Source:MGI Symbol;Acc:MGI:3588204]		B2RXC5	2.0	7.6E-03	6.6	9.9E-05	-0.6	6.0E-01	-0.9	1.6E-01
ENSMUST00000098609	gametogenetin [Source:MGI Symbol;Acc:MGI:2181461]	G5E8M4		6.5	4.2E-05	4.9	1.2E-03	0.1	8.9E-01	0.3	7.0E-01
ENSMUST00000098611	lymphoid enhancer binding factor 1 [Source:MGI Symbol;Acc:MGI:96770]	Q8C402		-4.3	6.8E-03	7.2	1.3E-02	-0.8	7.7E-01	-1.7	2.4E-01
ENSMUST00000098612	predicted gene 10647 [Source:MGI Symbol;Acc:MGI:3642036]	E9Q8X0		4.9	7.8E-05	5.0	3.2E-03	-1.5	2.6E-01	-0.9	3.9E-01
ENSMUST00000098614	zinc finger protein 827 [Source:MGI Symbol;Acc:MGI:2444807]		Q505G8	9.3	7.9E-06	-4.1	4.8E-03	-0.9	1.6E-01	0.6	6.3E-01
ENSMUST00000095981	predicted gene 8165 [Source:MGI Symbol;Acc:MGI:3648126]	L7N218		3.3	1.2E-01	5.3	2.5E-02	-0.4	8.4E-01	-2.5	9.9E-02
ENSMUST00000098634	predicted gene 10935 [Source:MGI Symbol;Acc:MGI:3809041]	E9Q8W4		8.7	2.2E-05	5.5	4.2E-03	-1.4	3.9E-01	-0.8	3.9E-01
ENSMUST00000098639	RIKEN cDNA 1700049G17 gene [Source:MGI Symbol;Acc:MGI:1920680]	Q3UVF6		2.9	3.3E-03	-2.8	6.7E-03	1.2	2.6E-02	-0.5	5.2E-01
ENSMUST00000098651	protein inhibitor of activated STAT 1 [Source:MGI Symbol;Acc:MGI:1913125]	Q2M4G9	O88907	-3.2	1.0E-04	1.9	3.3E-02	-0.4	5.5E-01	-0.6	3.8E-01
ENSMUST00000098653	predicted gene 10654 [Source:MGI Symbol;Acc:MGI:3643366]	Q3USN8		7.2	4.8E-05	6.8	1.6E-04	-0.6	6.1E-01	-1.0	1.4E-01
ENSMUST00000098657	cytochrome P450, family 2, subfamily a, polypeptide 4 [Source:MGI Symbol;Acc:MGI:88596]		P15392	6.6	8.7E-05	-6.9	5.5E-04	0.3	5.7E-01	0.5	7.1E-01
ENSMUST00000098660	thrombospondin, type I, domain containing 4 [Source:MGI Symbol;Acc:MGI:2672033]		Q3UTY6	10.2	2.5E-05	7.4	1.8E-04	-0.6	6.5E-01	-0.4	5.0E-01
ENSMUST00000098666	carcinoembryonic antigen-related cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1347245]		P31809	-6.4	1.8E-03	-6.1	4.5E-04	-1.5	8.9E-03	-0.8	5.1E-01
ENSMUST00000098669	carcinoembryonic antigen-related cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1347245]	Q925P3		5.7	1.7E-02	4.9	2.3E-03	1.0	3.9E-01	-0.4	6.3E-01
ENSMUST00000098674	REC114 meiotic recombination protein [Source:MGI Symbol;Acc:MGI:1920923]		Q9CWH4	5.8	8.1E-03	3.3	9.3E-04	-1.3	7.6E-02	-0.7	2.6E-01
ENSMUST00000098679	POU domain, class 2, transcription factor 2 [Source:MGI Symbol;Acc:MGI:101897]		Q00196	2.8	2.8E-02	8.5	6.4E-05	-1.3	3.6E-01	0.3	6.8E-01
ENSMUST00000098682	coiled-coil domain containing 33 [Source:MGI Symbol;Acc:MGI:1922464]	E9QQ55		7.7	3.4E-03	6.3	6.1E-04	-1.0	4.4E-01	0.4	6.1E-01
ENSMUST00000096053	family with sequence similarity 178, member A [Source:MGI Symbol;Acc:MGI:1924968]	E9Q839		1.2	4.7E-02	1.1	1.4E-01	0.5	3.7E-01	0.6	3.8E-01
ENSMUST00000098683	Rho guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:1353510]		Q61210	-10.1	1.1E-06	7.3	1.0E-04	-0.6	6.4E-01	-1.7	2.0E-02
ENSMUST00000098696	pleckstrin and Sec7 domain containing 3 [Source:MGI Symbol;Acc:MGI:1918215]		Q2PFD7	6.9	2.8E-04	4.7	5.1E-05	-0.9	1.8E-01	0.0	1.0E+00
ENSMUST00000096069	family with sequence similarity 208, member B [Source:MGI Symbol;Acc:MGI:2145274]		Q5DTT3	1.0	4.0E-02	1.5	1.8E-02	0.1	8.8E-01	-0.4	3.8E-01
ENSMUST00000098750	ligand dependent nuclear receptor interacting factor 1 [Source:MGI Symbol;Acc:MGI:2445214]		Q8CDD9	-6.7	4.0E-05	2.7	1.1E-01	-0.6	6.5E-01	3.6	1.2E-02
ENSMUST00000098754	avian reticuloendotheliosis viral (v-rel) oncogene related B [Source:MGI Symbol;Acc:MGI:103289]		Q04863	-5.0	2.4E-02	-9.9	2.2E-05	-0.1	8.6E-01	-0.5	7.3E-01
ENSMUST00000096090	cystatin A1 [Source:MGI Symbol;Acc:MGI:3524930]	B2RT71	P56567	0.9	2.7E-01	1.6	7.1E-02	-0.9	2.3E-01	-1.7	4.9E-02
ENSMUST00000098757	tyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 6 [Source:MGI Symbol;Acc:MC	F6RYQ3		7.0	7.7E-05	6.9	9.9E-05	-0.5	6.6E-01	-0.4	5.1E-01
ENSMUST00000096093				3.6	1.2E-01	5.1	4.3E-02	-0.5	8.2E-01	-2.0	2.1E-01
ENSMUST00000096096	centrosomal protein 55 [Source:MGI Symbol;Acc:MGI:1921357]		Q8BT07	-3.5	1.5E-01	-3.2	2.6E-01	-0.7	6.5E-01	-1.0	7.4E-01
ENSMUST00000098758	RIKEN cDNA I830077J02 gene [Source:MGI Symbol;Acc:MGI:3588284]		Q3U7U4	-5.0	4.0E-05	4.3	1.4E-01	-0.4	9.0E-01	3.3	5.8E-02
ENSMUST00000098760	tumor necrosis factor, alpha-induced protein 8-like 3 [Source:MGI Symbol;Acc:MGI:2685363]		Q3TBL6	5.3	2.7E-04	-7.8	4.2E-05	0.1	8.2E-01	0.1	9.4E-01
ENSMUST00000098761	potassium voltage-gated channel, Shal-related family, member 3 [Source:MGI Symbol;Acc:MGI:1928743]	Q3UH54	Q9Z0V1	7.9	1.2E-05	3.4	5.1E-03	-1.3	1.5E-01	0.3	7.2E-01
ENSMUST00000098768	expressed sequence AI593442 [Source:MGI Symbol;Acc:MGI:2143099]		Q32M26	7.5	1.3E-05	1.9	2.5E-02	-1.3	5.9E-02	0.2	7.3E-01
ENSMUST00000098781	expressed sequence AA386476 [Source:MGI Symbol;Acc:MGI:3034595]	F6RUV8		6.1	3.7E-05	7.3	1.8E-04	-0.7	6.2E-01	-0.4	5.4E-01
ENSMUST00000098782	layilin [Source:MGI Symbol;Acc:MGI:2685357]		Q8C351	3.2	4.2E-04	6.2	1.4E-03	-0.6	7.1E-01	1.2	1.3E-01
ENSMUST00000098783	pregnancy specific glycoprotein 18 [Source:MGI Symbol;Acc:MGI:1347251]	E9Q8L0		6.8	4.3E-05	6.3	3.4E-03	-0.7	7.1E-01	-1.8	9.1E-02
ENSMUST00000098789	zinc finger CCCH-type containing 4 [Source:MGI Symbol;Acc:MGI:2682314]	E9Q8K8		-1.5	6.5E-03	7.5	1.4E-04	-0.4	7.5E-01	-0.8	2.2E-01
ENSMUST00000098796	FAT tumor suppressor homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:109168]	F2Z4A3		8.1	3.6E-05	5.0	1.2E-04	0.2	8.1E-01	-0.8	1.7E-01
ENSMUST00000096194	transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1890373]		Q5FWI3	2.0	4.1E-02	0.6	6.9E-01	1.8	1.7E-01	3.2	2.7E-02
ENSMUST00000098799	EH-domain containing 2 [Source:MGI Symbol;Acc:MGI:2154274]		Q8BH64	5.0	1.6E-05	4.9	2.5E-03	0.0	9.8E-01	1.1	1.8E-01
ENSMUST00000098801	cone-rod homeobox, opposite strand [Source:MGI Symbol;Acc:MGI:2451355]	Q3UL53		5.8	2.5E-03	5.9	3.9E-04	-0.5	6.9E-01	-0.5	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000098802	oocyte specific homeobox 5 [Source:MGI Symbol;Acc:MGI:2149035]	G3X9P6		6.1	2.6E-04	5.9	1.4E-03	-0.3	8.1E-01	-0.2	8.1E-01
ENSMUST00000098814	ligase I, DNA, ATP-dependent [Source:MGI Symbol;Acc:MGI:101789]	Q3U4X8		-3.6	1.4E-02	4.7	5.0E-05	-0.8	2.3E-01	0.6	2.0E-01
ENSMUST00000096229	dynamin 1-like [Source:MGI Symbol;Acc:MGI:1921256]	E9PUD2		-0.3	9.1E-01	0.5	8.8E-01	-0.1	9.8E-01	-0.9	7.6E-01
ENSMUST00000098822	zinc finger protein 606 [Source:MGI Symbol;Acc:MGI:1914620]	Q7TSV0		3.2	2.1E-03	-5.4	6.7E-06	0.3	3.0E-01	-2.0	1.1E-02
ENSMUST00000096239	terminal uridylyl transferase 1, U6 snRNA-specific [Source:MGI Symbol;Acc:MGI:1917294]		Q8R3F9	-0.5	4.1E-01	0.5	5.1E-01	0.6	2.7E-01	-0.4	6.1E-01
ENSMUST00000098826	deleted in liver cancer 1 [Source:MGI Symbol;Acc:MGI:1354949]			9.2	2.6E-02	-2.9	1.5E-03	1.1	9.3E-03	-0.4	5.4E-01
ENSMUST00000098837	forkhead box R1 [Source:MGI Symbol;Acc:MGI:2685961]		Q3UTB7	5.3	2.6E-05	-1.5	1.1E-01	0.9	1.3E-01	-0.4	6.9E-01
ENSMUST00000096242	rod outer segment membrane protein 1 [Source:MGI Symbol;Acc:MGI:97998]		P32958	-0.3	7.0E-01	1.1	2.7E-01	1.4	9.7E-02	-0.1	9.5E-01
ENSMUST00000098843	histone cluster 2, H3b [Source:MGI Symbol;Acc:MGI:2448351]	B9EI85	P84228	4.9	1.2E-03	-2.0	6.0E-02	0.8	1.4E-01	-0.8	4.4E-01
ENSMUST00000098844	vomeronasal 1 receptor 55 [Source:MGI Symbol;Acc:MGI:3033474]	E9Q8I6		6.3	4.0E-04	-2.4	7.5E-03	0.8	6.7E-02	-0.1	9.2E-01
ENSMUST00000096249	integrator complex subunit 5 [Source:MGI Symbol;Acc:MGI:1923578]		Q8CHT3	-0.8	2.1E-01	0.5	5.2E-01	1.0	1.1E-01	-0.3	6.7E-01
ENSMUST00000098845	epsin 1 [Source:MGI Symbol;Acc:MGI:1333763]		Q80VP1	-3.9	7.8E-04	-0.2	7.1E-01	0.9	1.8E-02	-0.1	7.4E-01
ENSMUST00000098851	proline synthetase co-transcribed [Source:MGI Symbol;Acc:MGI:1891207]	Q80ZV3		2.4	2.0E-02	-5.7	7.5E-04	-0.8	9.6E-02	-0.7	5.8E-01
ENSMUST00000098852	melanoma cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1933966]		Q8R2Y2	-2.0	3.8E-03	-2.7	8.1E-03	-0.5	3.1E-01	-0.5	5.4E-01
ENSMUST00000098857	threonyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:1919057]	Q3TP97		3.7	1.0E-04	-7.4	1.6E-03	-0.4	4.4E-01	0.1	9.7E-01
ENSMUST00000098858	potassium channel, subfamily U, member 1 [Source:MGI Symbol;Acc:MGI:1202300]	G3X9P7		7.4	4.1E-05	5.0	2.6E-04	-2.4	2.6E-02	0.7	2.0E-01
ENSMUST00000098874	predicted gene, 21750 [Source:MGI Symbol;Acc:MGI:5433914]	L7N228		10.2	2.8E-05	5.4	2.4E-04	-0.8	3.8E-01	0.0	9.7E-01
ENSMUST00000098884	filaggrin family member 2 [Source:MGI Symbol;Acc:MGI:3645678]	E9QPZ3		9.8	4.9E-06	-4.3	2.3E-05	-0.2	5.3E-01	-0.6	2.9E-01
ENSMUST00000096272	calcineurin-like phosphoesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:2443300]		Q8BFS6	-1.3	6.2E-01	-0.9	8.0E-01	-0.2	9.4E-01	-0.6	8.6E-01
ENSMUST00000098900	predicted gene 5615 [Source:MGI Symbol;Acc:MGI:3647347]	Q3UW02		7.5	3.4E-05	6.5	6.1E-03	0.5	7.8E-01	-0.3	8.1E-01
ENSMUST00000096275	IQ motif and Sec7 domain 2 [Source:MGI Symbol;Acc:MGI:3528396]	D3Z6V7		-0.2	9.0E-01	-2.0	3.4E-01	0.2	8.4E-01	2.0	3.1E-01
ENSMUST00000096285	WNK lysine deficient protein kinase 3 [Source:MGI Symbol;Acc:MGI:2652875]	V9GWU7		3.0	1.8E-01	4.5	1.0E-01	0.7	7.9E-01	-0.9	6.0E-01
ENSMUST00000098906	prostate and testis expressed 2 [Source:MGI Symbol;Acc:MGI:2685692]	D3Z1P9		3.2	8.8E-03	6.6	9.6E-05	-0.4	7.1E-01	0.0	9.5E-01
ENSMUST00000096308				3.5	1.3E-01	5.6	1.2E-01	2.0	5.2E-01	-0.1	9.6E-01
ENSMUST00000098909	RIKEN cDNA 4930467E23 gene [Source:MGI Symbol;Acc:MGI:1923056]	D3Z1P8		8.9	6.4E-05	2.4	8.9E-04	-0.3	4.9E-01	-0.6	1.7E-01
ENSMUST00000098910	S100 calcium binding protein A16 [Source:MGI Symbol;Acc:MGI:1915110]	Q9D708		5.3	2.2E-02	-0.2	8.4E-01	1.5	2.7E-02	-0.5	5.3E-01
ENSMUST00000098911	S100 calcium binding protein A16 [Source:MGI Symbol;Acc:MGI:1915110]	Q9D708		5.0	2.4E-02	-3.0	9.5E-03	0.0	9.5E-01	0.4	6.5E-01
ENSMUST00000098914	DENN/MADD domain containing 4B [Source:MGI Symbol;Acc:MGI:2446201]			-2.8	4.4E-03	6.7	2.4E-04	-0.5	6.7E-01	-0.2	7.6E-01
ENSMUST00000098916	predicted gene 10699 [Source:MGI Symbol;Acc:MGI:3642530]	Q3UYL4		6.7	5.0E-07	7.1	6.3E-05	-0.6	6.0E-01	-0.3	6.2E-01
ENSMUST00000098935	RIKEN cDNA A230072I06 gene [Source:MGI Symbol;Acc:MGI:3588221]	Q3UUJ8		7.1	5.8E-05	7.1	4.4E-04	0.4	8.0E-01	0.1	9.1E-01
ENSMUST00000098942	C24, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:19148		Q9D083	3.9	1.1E-05	2.0	1.2E-01	-4.5	6.5E-03	-2.0	8.0E-02
ENSMUST00000098949	chemokine (C-C motif) ligand 25 [Source:MGI Symbol;Acc:MGI:1099448]	Q3U4J3		6.5	2.4E-04	-4.2	3.7E-04	1.3	1.2E-02	-0.1	9.5E-01
ENSMUST00000098950	ELAV (embryonic lethal, abnormal vision)-like 1 (Hu antigen R) [Source:MGI Symbol;Acc:MGI:1100851]		P70372	-1.9	3.0E-03	-0.9	2.0E-01	1.5	1.2E-02	0.0	9.9E-01
ENSMUST00000098966	RIKEN cDNA A430078G23 gene [Source:MGI Symbol;Acc:MGI:2442135]	E9Q7Y4		2.5	2.6E-03	-6.1	7.5E-05	1.1	1.2E-02	-0.7	4.6E-01
ENSMUST00000098990	ADP-ribosylation factor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1277120]	A2RSX9		-5.2	5.0E-05	6.3	8.5E-03	0.0	9.8E-01	0.2	8.7E-01
ENSMUST00000099002	predicted gene 14420 [Source:MGI Symbol;Acc:MGI:3652255]	B1AYE1		3.5	4.8E-06	7.3	9.3E-05	-0.6	6.1E-01	-0.1	8.0E-01
ENSMUST00000099007	predicted gene 14296 [Source:MGI Symbol;Acc:MGI:3708667]	A2ARL4		3.9	1.1E-05	7.1	8.7E-05	0.1	9.6E-01	-0.1	8.9E-01
ENSMUST00000099009	RIKEN cDNA 2210418O10 gene [Source:MGI Symbol;Acc:MGI:1924208]	A2ARL4		3.9	1.1E-05	3.9	1.8E-03	-2.0	7.7E-02	-0.1	8.4E-01
ENSMUST00000096368	G1 to S phase transition 2 [Source:MGI Symbol;Acc:MGI:1316727]		Q149F3	-2.5	4.8E-02	0.2	9.0E-01	1.0	3.6E-01	-1.7	2.3E-01
ENSMUST00000099028	predicted gene 14391 [Source:MGI Symbol;Acc:MGI:3709324]	A2ARX2		3.0	1.2E-02	-3.8	3.3E-02	1.1	1.2E-01	-1.2	4.7E-01
ENSMUST00000099042	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	F6QHK0		12.7	7.2E-08	-7.2	4.8E-04	0.6	1.6E-01	-0.6	7.1E-01
ENSMUST00000099046	predicted gene 10718 [Source:MGI Symbol;Acc:MGI:3642028]	D3Z1I7		14.3	2.2E-07	-1.1	1.5E-01	0.9	6.0E-02	-0.2	7.3E-01
ENSMUST00000099047	predicted gene 10719 [Source:MGI Symbol;Acc:MGI:3641690]	E9Q7T3		14.7	1.3E-06	6.4	1.9E-04	-0.5	6.5E-01	0.2	7.5E-01
ENSMUST00000096420	predicted gene 14698 [Source:MGI Symbol;Acc:MGI:3709613]		Q60969	-0.5	4.7E-01	0.1	8.8E-01	0.1	8.4E-01	-0.5	5.3E-01
ENSMUST00000099049	predicted gene 10719 [Source:MGI Symbol;Acc:MGI:3641690]	D3Z1I6		14.7	5.8E-09	7.3	3.6E-04	-0.7	6.2E-01	-0.3	6.9E-01
ENSMUST00000099050	predicted gene 10720 [Source:MGI Symbol;Acc:MGI:3641687]	D3Z1I5		12.3	4.3E-07	4.3	2.6E-04	0.9	1.8E-01	0.0	9.9E-01
ENSMUST00000099051	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	F6QDW5		12.2	1.4E-06	5.7	2.4E-03	-0.5	7.1E-01	0.4	6.5E-01
ENSMUST00000099056	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	D3Z1I4		14.1	8.5E-07	2.8	7.3E-04	-0.6	2.7E-01	0.3	5.1E-01
ENSMUST00000096441	microrchidia 2A [Source:MGI Symbol;Acc:MGI:1921772]		Q69ZX6	-3.5	6.2E-02	-3.3	2.3E-01	0.6	6.4E-01	0.4	8.8E-01
ENSMUST00000099058	transcription factor AP-2, gamma [Source:MGI Symbol;Acc:MGI:106032]	A2APA8		7.0	5.6E-05	-6.6	2.0E-03	0.6	3.1E-01	-0.4	8.2E-01
ENSMUST00000099060	glucosaminyl (N-acetyl) transferase family member 7 [Source:MGI Symbol;Acc:MGI:3606143]	F8WK01	Q3V3K7	5.4	7.8E-05	2.1	2.2E-02	-0.1	9.0E-01	0.4	5.3E-01
ENSMUST00000096485				0.0	9.6E-01	0.1	8.9E-01	-0.9	2.2E-01	-1.1	2.7E-01
ENSMUST00000099061	Cas scaffolding protein family member 4 [Source:MGI Symbol;Acc:MGI:2444482]		Q08EC4	5.9	1.0E-05	-5.4	7.4E-03	0.9	1.5E-01	2.0	2.3E-01
ENSMUST00000099069	potassium voltage-gated channel, subfamily G, member 1 [Source:MGI Symbol;Acc:MGI:3616086]	B2RVK9	A2BDX4	8.0	8.1E-05	-3.9	4.3E-02	1.1	2.3E-01	1.1	5.1E-01
ENSMUST00000099072	dolichol-phosphate (beta-D) mannosyltransferase 1 [Source:MGI Symbol;Acc:MGI:1330239]	F8WII3		-5.6	5.3E-04	7.7	1.7E-04	-0.4	7.7E-01	-0.9	1.8E-01
ENSMUST00000099078	osylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited) [Source:MGI Symbol;Acc:MGI:2		A2A5R2	-1.2	7.3E-03	2.5	2.4E-02	-3.2	9.0E-03	0.3	7.0E-01
ENSMUST00000099087	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	G3X9Q0		-6.9	1.8E-05	-1.0	1.1E-01	0.8	5.9E-02	0.1	9.3E-01
ENSMUST00000099091	ankrin repeat and ubiquitin domain containing 1 [Source:MGI Symbol;Acc:MGI:2685256]		Q3UUE9	6.6	1.7E-04	6.6	4.5E-04	-0.5	7.2E-01	-1.3	1.1E-01
ENSMUST00000099092	solute carrier family 12, member 5 [Source:MGI Symbol;Acc:MGI:1862037]	A0A076FSX1	Q91V14	1.7	5.2E-03	8.1	1.6E-04	-0.7	6.2E-01	-0.5	4.3E-01
ENSMUST00000099097	serine peptidase inhibitor, Kunitz type, 3 [Source:MGI Symbol;Acc:MGI:3651470]	Q3UW09		5.9	1.6E-04	-1.5	3.0E-01	0.1	9.1E-01	-1.9	2.4E-01
ENSMUST00000099106	microsomal glutathione S-transferase 2 [Source:MGI Symbol;Acc:MGI:2448481]	A2RST1		-8.5	9.0E-07	-4.8	1.3E-02	1.5	7.7E-02	-1.1	5.4E-01
ENSMUST00000096751	tetratricopeptide repeat domain 9C [Source:MGI Symbol;Acc:MGI:1917637]		Q810A3	-0.2	6.9E-01	0.4	4.9E-01	0.6	2.1E-01	0.0	9.7E-01
ENSMUST00000099110	TOX high mobility group box family member 2 [Source:MGI Symbol;Acc:MGI:3611233]	A2A472		3.9	1.8E-02	-3.4	1.3E-03	0.7	9.1E-02	0.2	8.2E-01
ENSMUST00000096766	echinoderm microtubule associated protein like 4 [Source:MGI Symbol;Acc:MGI:1926048]	F8WJ93		-2.8	6.9E-02	-3.7	8.6E-02	1.0	3.9E-01	1.9	3.4E-01
ENSMUST00000099112	integrin alpha 7 [Source:MGI Symbol;Acc:MGI:102700]	G3X9Q1		5.5	5.3E-05	2.1	5.9E-03	-0.4	4.4E-01	-0.1	8.0E-01
ENSMUST00000099123	RIKEN cDNA 1700034I23 gene [Source:MGI Symbol;Acc:MGI:1920547]	Q9D9Q3		6.4	1.6E-05	7.2	9.8E-05	-0.6	6.2E-01	-0.1	8.6E-01
ENSMUST00000099126	naf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian) [Source:MGI Symbol;Acc:MGI:1045		P54841	2.8	3.6E-03	7.6	4.6E-05	-0.5	6.6E-01	-1.5	2.7E-02
ENSMUST00000099128	predicted gene 5148 [Source:MGI Symbol;Acc:MGI:3646006]	Q8BGG2		7.5	3.2E-03	-1.4	1.5E-01	1.8	1.1E-02	-0.5	5.9E-01
ENSMUST00000099133	Rho GTPase activating protein 40 [Source:MGI Symbol;Acc:MGI:3649852]	A0A0A0MQB4		7.9	2.6E-03	-1.0	3.3E-01	-0.3	6.3E-01	-2.3	4.8E-02
ENSMUST00000099139	RNA binding motif, single stranded interacting protein 2 [Source:MGI Symbol;Acc:MGI:1861776]	E9Q7G6		8.8	2.0E-05	-4.0	4.1E-04	0.4	2.7E-01	-1.3	1.4E-01
ENSMUST00000099145	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]		B1AZP2	-1.7	3.5E-02	9.3	1.7E-03	-1.1	6.6E-01	1.1	2.7E-01
ENSMUST00000099148	RIKEN cDNA 3110070M22 gene [Source:MGI Symbol;Acc:MGI:1914554]	Q9DAQ7		9.9	9.1E-04	6.0	4.4E-04	-1.4	2.9E-01	0.0	9.9E-01
ENSMUST00000099149	nicotinamide nucleotide transhydrogenase [Source:MGI Symbol;Acc:MGI:109279]	Q8BGK0		-3.6	8.3E-03	6.9	8.4E-04	-0.7	6.7E-01	-1.0	2.6E-01
ENSMUST00000099151	SRY (sex determining region Y)-box 2 [Source:MGI Symbol;Acc:MGI:98364]	Q60I23		6.7	1.4E-04	6.8	1.9E-03	2.9	7.2E-02	0.1	8.9E-01
ENSMUST00000099153	tetratricopeptide repeat domain 14 [Source:MGI Symbol;Acc:MGI:1914370]	A6H6N9		-1.7	1.7E-02	7.6	9.1E-05	0.5	6.8E-01	-0.9	1.5E-01
ENSMUST00000099157	Ngfi-A binding protein 2 [Source:MGI Symbol;Acc:MGI:107563]	Q3TYF1		3.9	9.5E-03	7.0	2.8E-04	0.0	9.8E-01	0.3	6.5E-01
ENSMUST00000099162	predicted gene 10735 [Source:MGI Symbol;Acc:MGI:3642476]	Q3US96		7.3	2.6E-05	7.5	7.2E-04	-0.1	9.7E-01	0.8	3.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000097216	TEA domain family member 2 [Source:MGI Symbol;Acc:MGI:104904]	Q80UL2		-3.0	4.6E-02	-1.3	4.7E-01	1.0	4.1E-01	-0.6	7.1E-01
ENSMUST00000099163	polyhomeotic-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2181434]	E9QPT4		8.4	8.8E-06	7.1	7.8E-04	0.0	9.8E-01	-0.7	4.2E-01
ENSMUST00000097227	glutathione peroxidase 4 [Source:MGI Symbol;Acc:MGI:104767]	Q76LV0		-0.4	8.6E-01	1.7	5.3E-01	0.4	8.5E-01	-1.7	5.0E-01
ENSMUST00000099172	kinesin family member 5A [Source:MGI Symbol;Acc:MGI:109564]		P33175	7.1	7.1E-06	3.0	1.7E-01	-0.6	7.8E-01	2.3	1.2E-01
ENSMUST00000099173	eukaryotic translation initiation factor 2, subunit 2 (beta) [Source:MGI Symbol;Acc:MGI:1914454]	Q3ULL5	Q99L45	-4.5	1.8E-02	-5.2	4.5E-03	-1.8	2.1E-02	-1.1	4.9E-01
ENSMUST00000099178	-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human) [Source:MGI Symbol;Acc:MGI:1333	Q3UGB2		3.4	4.4E-03	2.6	4.4E-03	0.2	6.8E-01	-0.3	6.4E-01
ENSMUST00000099194	TSPY-like 3 [Source:MGI Symbol;Acc:MGI:2139328]	Q3UYP3		1.8	8.0E-03	-3.4	2.0E-02	0.0	9.8E-01	-0.9	4.8E-01
ENSMUST00000097281	HEAT repeat containing 5B [Source:MGI Symbol;Acc:MGI:2444098]		Q8C547	-1.1	3.8E-02	-0.1	8.2E-01	0.4	3.6E-01	-0.6	3.2E-01
ENSMUST00000099195	phosphodiesterase 7A [Source:MGI Symbol;Acc:MGI:1202402]	Q3U3Y7	P70453	2.0	1.3E-03	7.2	2.9E-04	-0.6	6.7E-01	-0.5	4.5E-01
ENSMUST00000097293				-3.1	3.2E-01	-2.4	4.8E-01	-0.3	8.9E-01	-1.0	7.7E-01
ENSMUST00000097299	crumbs family member 3 [Source:MGI Symbol;Acc:MGI:2670904]		Q8QZT4	2.6	9.4E-02	2.3	3.3E-01	1.6	4.0E-01	1.9	3.1E-01
ENSMUST00000099200	forkhead box S1 [Source:MGI Symbol;Acc:MGI:95546]	Q4VA05	Q61574	8.0	1.1E-04	6.6	1.2E-03	-0.6	7.1E-01	-1.0	2.7E-01
ENSMUST00000097311	forkhead box P4 [Source:MGI Symbol;Acc:MGI:1921373]			2.8	1.0E-01	4.2	1.4E-02	-2.2	1.8E-01	-3.5	1.6E-02
ENSMUST00000099202	microtubule associated serine/threonine kinase family member 4 [Source:MGI Symbol;Acc:MGI:1918885]	E9QPR4		7.7	2.0E-05	6.4	1.3E-04	-2.8	3.8E-02	-0.6	3.2E-01
ENSMUST00000099207	zinc finger, CCHC domain containing 3 [Source:MGI Symbol;Acc:MGI:1915167]	Q8BPK2		4.5	7.1E-05	1.9	7.9E-02	-2.1	4.9E-02	0.7	4.4E-01
ENSMUST00000097333	discoidin domain receptor family, member 1 [Source:MGI Symbol;Acc:MGI:99216]	Q544T2	Q03146	2.9	1.6E-01	-2.2	3.4E-01	-4.8	1.8E-02	0.3	8.9E-01
ENSMUST00000099224	casein kinase 2, alpha 1 polypeptide [Source:MGI Symbol;Acc:MGI:88543]		Q60737	-3.6	2.3E-05	-3.0	1.5E-02	0.4	4.5E-01	1.3	2.6E-01
ENSMUST00000099241	chemokine (C-C motif) ligand 28 [Source:MGI Symbol;Acc:MGI:1861731]		Q9JIL2	7.4	1.0E-06	-7.3	8.6E-05	-0.6	2.0E-01	-1.2	3.2E-01
ENSMUST00000099245				7.7	2.9E-05	2.6	6.7E-03	-1.9	2.6E-02	-0.5	4.6E-01
ENSMUST00000097338	mutS homolog 5 (E. coli) [Source:MGI Symbol;Acc:MGI:1329021]			-1.4	5.7E-01	-3.1	3.0E-01	-2.6	1.7E-01	-0.9	7.7E-01
ENSMUST00000097342	euchromatic histone lysine N-methyltransferase 2 [Source:MGI Symbol;Acc:MGI:2148922]	A2CG76		3.0	3.0E-01	3.2	2.6E-01	-0.5	8.6E-01	-0.7	7.4E-01
ENSMUST00000099261	RIKEN cDNA 4933416C03 gene [Source:MGI Symbol;Acc:MGI:3588269]	Q3V063		6.6	9.6E-05	6.4	2.8E-04	-0.6	5.9E-01	0.7	2.7E-01
ENSMUST00000097352	Pbx/knotted 1 homeobox [Source:MGI Symbol;Acc:MGI:1201409]		O70477	-3.9	3.7E-02	-4.2	6.4E-02	0.3	7.9E-01	0.6	7.9E-01
ENSMUST00000097368	phosphatidylinositol glycan anchor biosynthesis, class Q [Source:MGI Symbol;Acc:MGI:1333114]	Q3TD14		2.0	3.0E-01	2.0	4.2E-01	-0.8	7.3E-01	-0.8	6.8E-01
ENSMUST00000097373	tuberous sclerosis 2 [Source:MGI Symbol;Acc:MGI:102548]	Q7TT21		-0.8	1.1E-01	0.4	5.2E-01	1.0	5.0E-02	-0.2	7.1E-01
ENSMUST00000097376	TBC1 domain family, member 24 [Source:MGI Symbol;Acc:MGI:2443456]		Q3UUG6	3.0	7.8E-02	5.8	5.3E-02	3.8	1.5E-01	1.0	4.9E-01
ENSMUST00000099264	RIKEN cDNA C530025M09 gene [Source:MGI Symbol;Acc:MGI:2442090]	F6RGA8		4.9	7.8E-04	5.9	3.3E-03	-0.4	7.9E-01	0.2	7.9E-01
ENSMUST00000099265	RIKEN cDNA B930041F14 gene [Source:MGI Symbol;Acc:MGI:2444790]		A2A9Q0	3.7	8.6E-04	-5.6	2.5E-03	0.4	4.2E-01	-0.9	5.7E-01
ENSMUST00000099266	predicted gene 10750 [Source:MGI Symbol;Acc:MGI:3641996]	Q3V0I0		6.6	1.2E-04	4.9	2.6E-02	-0.9	6.6E-01	-1.8	1.6E-01
ENSMUST00000097399	predicted gene 3448 [Source:MGI Symbol;Acc:MGI:3809205]		P11985	2.1	9.1E-02	3.6	5.1E-03	-1.8	1.2E-01	-3.3	4.6E-03
ENSMUST00000099274	PDZ domain containing 8 [Source:MGI Symbol;Acc:MGI:2677270]	B9EJ80		-2.8	1.2E-04	7.5	8.9E-05	-0.6	6.1E-01	0.5	4.1E-01
ENSMUST00000099276	ataxin 7-like 3B [Source:MGI Symbol;Acc:MGI:1914971]		Q3UD01	-3.9	4.6E-04	6.2	1.8E-04	-1.0	3.7E-01	0.8	2.1E-01
ENSMUST00000099278	kizuna centrosomal protein [Source:MGI Symbol;Acc:MGI:2684960]		Q3UXL4	-4.1	3.0E-04	-3.7	4.1E-04	0.8	5.3E-02	0.3	6.4E-01
ENSMUST00000099294	actin-binding LIM protein 1 [Source:MGI Symbol;Acc:MGI:1194500]		Q8K4G5	6.8	2.0E-03	4.1	3.8E-02	-0.7	6.8E-01	-0.3	8.3E-01
ENSMUST00000099307	isthmin 1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2442963]		A2ATD1	6.2	4.3E-04	-1.0	1.3E-01	0.3	4.7E-01	-0.1	8.6E-01
ENSMUST00000097422	predicted gene 1604A [Source:MGI Symbol;Acc:MGI:3807545]	Q3TRG0		0.9	2.6E-01	1.5	1.2E-01	0.3	7.1E-01	-0.4	6.5E-01
ENSMUST00000099309	betaine-homocysteine methyltransferase [Source:MGI Symbol;Acc:MGI:1339972]		O35490	5.8	1.6E-03	-0.8	2.4E-01	0.6	1.8E-01	-0.8	3.0E-01
ENSMUST00000099329	ubiquitin-conjugating enzyme E2N [Source:MGI Symbol;Acc:MGI:1934835]	A2RTT4	P61089	-3.6	4.7E-06	3.2	4.9E-04	-6.9	4.4E-05	-0.1	7.7E-01
ENSMUST00000099337	plexin C1 [Source:MGI Symbol;Acc:MGI:1890127]		Q9QZC2	-3.2	2.2E-05	3.1	5.2E-03	0.2	7.7E-01	0.5	4.8E-01
ENSMUST00000099343	nuclear receptor subfamily 2, group C, member 1 [Source:MGI Symbol;Acc:MGI:1352465]		Q505F1	5.5	2.0E-03	-4.6	4.6E-03	0.2	7.3E-01	-0.3	8.4E-01
ENSMUST00000099349	heat shock protein 12B [Source:MGI Symbol;Acc:MGI:1919880]		Q9CZJ2	3.3	2.9E-03	4.5	7.2E-05	-3.0	2.0E-03	0.1	7.6E-01
ENSMUST00000097443				0.1	8.1E-01	1.2	1.4E-01	0.5	4.2E-01	-0.5	4.2E-01
ENSMUST00000099353	SWI5 dependent recombination repair 1 [Source:MGI Symbol;Acc:MGI:1915038]		Q8BP27	-5.2	8.5E-05	2.9	1.0E-01	-1.3	4.0E-01	1.1	3.6E-01
ENSMUST00000099355	thymopoietin [Source:MGI Symbol;Acc:MGI:106920]		Q61029	-5.5	6.5E-05	4.4	7.9E-03	-1.5	2.9E-01	-0.2	8.5E-01
ENSMUST00000099356	arrestin domain containing 3 [Source:MGI Symbol;Acc:MGI:2145242]		Q7TPQ9	-5.4	7.1E-04	3.3	5.7E-03	-1.2	1.9E-01	-0.3	6.5E-01
ENSMUST00000099358	family with sequence similarity 172, member A [Source:MGI Symbol;Acc:MGI:1915925]		Q3TNH5	2.8	2.8E-02	5.8	3.7E-04	-1.4	2.3E-01	0.9	2.0E-01
ENSMUST00000099373	cyclin M2 [Source:MGI Symbol;Acc:MGI:2151054]		Q3TWN3	-3.4	3.1E-02	2.7	6.7E-03	0.0	9.8E-01	0.1	8.4E-01
ENSMUST00000097471				-1.8	5.1E-01	-2.3	5.5E-01	-0.2	9.3E-01	0.3	9.3E-01
ENSMUST00000099384	bromodomain containing 9 [Source:MGI Symbol;Acc:MGI:2145317]			-2.5	2.5E-03	6.8	1.3E-03	0.1	9.7E-01	1.4	1.3E-01
ENSMUST00000099392	roxisome proliferative activated receptor, gamma, coactivator-related 1 [Source:MGI Symbol;Acc:MGI:238509		Q6NZN1	4.2	3.3E-02	3.7	4.1E-04	0.7	2.5E-01	-0.1	8.8E-01
ENSMUST00000099396	5'-nucleotidase domain containing 3 [Source:MGI Symbol;Acc:MGI:3513266]		Q3UHB1	1.9	2.3E-03	7.2	2.4E-04	-0.5	7.3E-01	-1.6	4.6E-02
ENSMUST00000097478	predicted gene 6502 [Source:MGI Symbol;Acc:MGI:3779601]	L7N458		3.6	1.7E-01	4.6	1.1E-01	-0.4	9.0E-01	-1.4	4.3E-01
ENSMUST00000099400	poly (A) polymerase beta (testis specific) [Source:MGI Symbol;Acc:MGI:1932115]	A1L349		7.3	4.0E-05	8.6	6.0E-05	-0.6	6.5E-01	-0.6	3.0E-01
ENSMUST00000097491	selectin, lymphocyte [Source:MGI Symbol;Acc:MGI:98279]	B1B507		-4.2	3.7E-02	-8.3	4.8E-03	-3.5	6.3E-03	0.6	8.0E-01
ENSMUST00000097493	cDNA sequence BC055324 [Source:MGI Symbol;Acc:MGI:3590554]		Q3TQQ9	3.5	5.6E-02	4.0	9.7E-02	0.6	7.6E-01	0.1	9.6E-01
ENSMUST00000099401	ladybird homeobox homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:104867]		P52955	7.0	4.1E-05	3.1	5.4E-04	-0.2	6.8E-01	0.0	9.6E-01
ENSMUST00000099416	vomeronasal 2, receptor, pseudogene 104 [Source:MGI Symbol;Acc:MGI:3761523]			6.3	2.6E-04	5.3	8.9E-04	-0.6	6.3E-01	-0.6	4.0E-01
ENSMUST00000099423	ubiquitin specific peptidase 50 [Source:MGI Symbol;Acc:MGI:1922333]	E9Q3B5		-5.7	3.2E-04	7.5	1.4E-02	2.4	3.5E-01	-0.2	8.8E-01
ENSMUST00000097529	acyl-Coenzyme A binding domain containing 6 [Source:MGI Symbol;Acc:MGI:1919732]		Q9D061	0.7	3.8E-01	1.8	8.5E-02	0.4	6.5E-01	-0.7	3.9E-01
ENSMUST00000099425	predicted gene 10775 [Source:MGI Symbol;Acc:MGI:3642324]	Q3V290		5.9	1.2E-04	-0.3	6.1E-01	0.9	5.8E-02	-0.3	6.1E-01
ENSMUST00000097536	actin related protein 2/3 complex, subunit 5 [Source:MGI Symbol;Acc:MGI:1915021]	Q3UA72		-3.0	3.8E-02	-1.2	5.0E-01	1.6	1.9E-01	-0.1	9.4E-01
ENSMUST00000097541	family with sequence similarity 129, member A [Source:MGI Symbol;Acc:MGI:2137237]	E9PYV4		-0.9	5.5E-01	3.1	1.3E-01	1.8	2.7E-01	-2.2	2.0E-01
ENSMUST00000099427	spermatogenesis associated 31 subfamily D, member 1C [Source:MGI Symbol;Acc:MGI:3588241]	E9QAF1		8.2	2.9E-05	1.5	3.2E-02	0.5	2.9E-01	0.8	1.5E-01
ENSMUST00000097543	influenza virus NS1A binding protein [Source:MGI Symbol;Acc:MGI:2152389]		Q920Q8	-0.7	8.0E-01	-0.8	8.7E-01	1.3	6.8E-01	1.4	7.3E-01
ENSMUST00000099428	heparanase 2 [Source:MGI Symbol;Acc:MGI:2685814]		B2RY83	6.2	3.0E-04	7.0	2.2E-02	0.1	9.8E-01	-1.5	3.3E-01
ENSMUST00000099441	solute carrier family 35, member D2 [Source:MGI Symbol;Acc:MGI:1917734]			-3.5	3.0E-04	-6.2	1.3E-02	-0.4	6.2E-01	0.1	9.5E-01
ENSMUST00000097558	hydroxymethylbilane synthase [Source:MGI Symbol;Acc:MGI:96112]	Q3UPG1	P22907	1.1	6.9E-01	-1.3	7.8E-01	0.0	1.0E+00	2.4	5.7E-01
ENSMUST00000099442	cDNA sequence BC025920 [Source:MGI Symbol;Acc:MGI:2670983]	Q3US60		6.4	4.6E-05	3.7	3.5E-02	-2.5	1.5E-01	1.4	2.0E-01
ENSMUST00000097563	invariant polypeptide of major histocompatibility complex, class II antigen-associated) [Source:MGI Symbol;A	Q3U4Q8	P04441	-1.8	2.0E-01	-0.7	6.2E-01	-1.6	1.2E-01	-2.7	9.3E-02
ENSMUST00000097566	synaptopodin [Source:MGI Symbol;Acc:MGI:1099446]	Q3U336	Q8CC35	4.1	8.3E-02	4.6	7.5E-02	-0.5	8.3E-01	-1.1	5.2E-01
ENSMUST00000099443	zinc finger, FYVE domain containing 27 [Source:MGI Symbol;Acc:MGI:1919602]		Q3TXX3	-7.7	3.6E-04	6.6	3.3E-05	2.1	2.6E-02	0.4	4.3E-01
ENSMUST00000097588	SLIT-ROBO Rho GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:109605]		Q91Z67	0.7	2.7E-01	1.3	1.4E-01	0.5	4.4E-01	-0.1	9.2E-01
ENSMUST00000099449	zinc finger protein 80 [Source:MGI Symbol;Acc:MGI:3704127]	B8JJZ4		2.2	1.9E-02	-2.3	9.3E-03	-0.6	2.0E-01	-0.2	7.4E-01
ENSMUST00000099457	solute carrier family 30 (zinc transporter), member 4 [Source:MGI Symbol;Acc:MGI:1345282]	A2AK40		7.5	1.8E-02	2.2	3.9E-01	1.0	5.3E-01	2.8	2.2E-01
ENSMUST00000097593	Rho GTPase activating protein 26 [Source:MGI Symbol;Acc:MGI:1918552]		Q6ZQ82	-0.8	3.7E-01	-0.8	5.1E-01	-0.1	8.8E-01	-0.2	8.9E-01
ENSMUST00000099461	dual oxidase 1 [Source:MGI Symbol;Acc:MGI:2139422]	A2AQ92		8.6	6.0E-06	7.6	7.7E-05	1.2	2.8E-01	0.5	3.9E-01
ENSMUST00000099466	sorbin and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:700014]	E9QNA7		-6.7	6.7E-05	-7.2	1.3E-02	1.3	1.6E-01	3.0	2.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000097625	peptidylglycine alpha-amidating monooxygenase [Source:MGI Symbol;Acc:MGI:97475]	F8VQA4		-1.9	6.5E-02	-2.6	6.9E-02	0.2	7.9E-01	1.0	4.6E-01
ENSMUST00000099475	small EDRK-rich factor 2 [Source:MGI Symbol;Acc:MGI:1337041]	A2ARQ4		-8.1	1.9E-04	-5.9	2.7E-03	0.7	2.3E-01	-0.8	6.2E-01
ENSMUST00000099490	nuclear receptor-binding SET-domain protein 1 [Source:MGI Symbol;Acc:MGI:1276545]	E9QAE4		-1.5	7.2E-03	8.4	1.4E-04	0.8	5.6E-01	0.2	7.2E-01
ENSMUST00000099492	midnolin [Source:MGI Symbol;Acc:MGI:1890222]		Q3TPJ7	-6.5	8.4E-04	7.0	1.4E-04	-0.2	8.8E-01	0.2	6.9E-01
ENSMUST00000099494	olymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae) [Source:MGI Symbol;Acc	E9QAE3		-2.0	1.4E-03	0.3	7.4E-01	0.9	1.5E-01	-1.4	1.2E-01
ENSMUST00000099496	ubiquitin interaction motif containing 1 [Source:MGI Symbol;Acc:MGI:103185]			-5.6	1.3E-03	-8.1	1.7E-05	-0.1	7.4E-01	-0.9	4.0E-01
ENSMUST00000097643	expressed sequence AW554918 [Source:MGI Symbol;Acc:MGI:2147376]		Q6NZK5	3.4	1.4E-01	0.8	8.2E-01	0.0	1.0E+00	2.6	4.3E-01
ENSMUST00000099497	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 [Source:MGI Symbol;Acc:MGI:2136878]		Q9JI67	6.1	1.1E-04	-1.6	3.3E-02	0.9	5.4E-02	-0.6	3.4E-01
ENSMUST00000097646	RIKEN cDNA 2700062C07 gene [Source:MGI Symbol;Acc:MGI:1915296]		Q5XFZ0	0.0	9.9E-01	-0.4	5.3E-01	-0.5	3.7E-01	0.0	9.4E-01
ENSMUST00000097648	receptor (calcitonin) activity modifying protein 1 [Source:MGI Symbol;Acc:MGI:1858418]	Q3TNJ3	Q9WTJ5	-0.3	6.1E-01	-0.2	7.8E-01	0.4	4.5E-01	0.3	6.4E-01
ENSMUST00000099501	histocompatibility (minor) HA-1 [Source:MGI Symbol;Acc:MGI:1917969]	G3X9Q3		-5.4	4.5E-04	-8.7	8.7E-05	-0.4	2.9E-01	-0.7	6.4E-01
ENSMUST00000099505	5-hydroxytryptamine (serotonin) receptor 7 [Source:MGI Symbol;Acc:MGI:99841]	B6VJS3		7.4	6.4E-05	6.8	4.1E-04	-0.4	7.6E-01	-0.7	3.1E-01
ENSMUST00000097653	collagen, type VI, alpha 3 [Source:MGI Symbol;Acc:MGI:88461]	J3QQ16		4.7	7.7E-02	1.2	5.4E-01	-5.0	4.6E-02	-1.5	4.1E-01
ENSMUST00000097655	additional sex combs like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685175]		Q8C4A5	4.5	1.9E-01	1.8	6.8E-01	-0.1	9.9E-01	2.6	4.4E-01
ENSMUST00000099506	G protein-regulated inducer of neurite outgrowth 1 [Source:MGI Symbol;Acc:MGI:1349455]		Q3UNH4	8.6	3.1E-05	0.7	5.9E-01	-3.4	1.4E-02	0.3	7.5E-01
ENSMUST00000097666	calcium binding protein 39 [Source:MGI Symbol;Acc:MGI:107438]		Q06138	-2.0	2.2E-01	-2.1	2.9E-01	-0.6	6.0E-01	-0.5	8.1E-01
ENSMUST00000097670	establishment of cohesion 1 homolog 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925055]	Q3UKT9		-6.2	6.2E-02	0.3	9.1E-01	3.0	2.5E-01	-3.5	3.0E-01
ENSMUST00000097671				0.8	2.6E-01	1.1	2.3E-01	0.4	5.4E-01	0.1	8.5E-01
ENSMUST00000097672	F-box protein 36 [Source:MGI Symbol;Acc:MGI:1289192]		Q9CQ24	-0.4	7.0E-01	-1.1	5.2E-01	-0.4	7.8E-01	0.3	8.4E-01
ENSMUST00000099508	potassium inwardly-rectifying channel, subfamily J, member 6 [Source:MGI Symbol;Acc:MGI:104781]	Q0VB45		6.0	5.6E-04	-3.4	9.0E-04	0.2	5.7E-01	-0.9	2.6E-01
ENSMUST00000099512	e synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase) [Source:MGI Symbol;Ac	Q3TZ03	Q920N2	3.8	2.9E-05	-7.7	2.6E-04	-1.1	9.4E-02	-2.0	2.2E-01
ENSMUST00000099514	sphingomyelin synthase 1 [Source:MGI Symbol;Acc:MGI:2444110]		Q8VCQ6	-8.1	7.5E-06	-3.6	2.0E-02	-1.0	1.7E-01	-0.1	9.2E-01
ENSMUST00000099518	predicted gene 8765 [Source:MGI Symbol;Acc:MGI:3704126]	B7ZWJ3		10.1	3.2E-05	-6.8	1.3E-03	0.4	3.8E-01	2.1	1.9E-01
ENSMUST00000097697	ciliogenesis associated TTC17 interacting protein [Source:MGI Symbol;Acc:MGI:2685062]		B9EKE5	4.6	3.9E-02	3.5	8.1E-02	-2.4	2.7E-01	-1.3	3.5E-01
ENSMUST00000097707	phosphoinositide kinase, FYVE finger containing [Source:MGI Symbol;Acc:MGI:1335106]		Q9Z1T6	0.3	8.7E-01	2.0	4.8E-01	1.5	4.5E-01	-0.2	9.4E-01
ENSMUST00000099521	predicted gene 906 [Source:MGI Symbol;Acc:MGI:2685752]	Q3V0M1		9.8	1.8E-05	-5.5	1.4E-05	-0.4	1.6E-01	-0.7	3.3E-01
ENSMUST00000099525	RAN binding protein 6 [Source:MGI Symbol;Acc:MGI:2683212]	A3KMD2	Q8BIV3	-1.6	1.9E-02	-0.7	3.0E-01	0.2	6.2E-01	-0.6	3.6E-01
ENSMUST00000099537	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	E9QAB8		-3.2	1.4E-02	-2.3	5.1E-03	1.0	2.2E-02	0.2	7.6E-01
ENSMUST00000099538	small ubiquitin-like modifier 3 [Source:MGI Symbol;Acc:MGI:1336201]		Q9Z172	-4.5	2.4E-03	5.9	1.2E-04	-2.9	1.8E-02	-0.3	5.7E-01
ENSMUST00000097718	INO80 complex subunit D [Source:MGI Symbol;Acc:MGI:3027003]	B1AT32		0.4	2.3E-01	2.4	8.1E-04	1.6	3.1E-03	-0.3	3.9E-01
ENSMUST00000099547	family with sequence similarity 8, member A1 [Source:MGI Symbol;Acc:MGI:2145496]	Q3URQ4		-3.1	1.1E-03	-3.6	4.6E-03	0.7	1.5E-01	-0.8	4.3E-01
ENSMUST00000099552	predicted gene 10787 [Source:MGI Symbol;Acc:MGI:3642150]	E9QAB7		7.0	4.5E-04	6.1	3.3E-04	-0.6	6.2E-01	-0.4	5.1E-01
ENSMUST00000097734	stromal cell derived factor 4 [Source:MGI Symbol;Acc:MGI:108079]		Q61112	3.4	3.9E-02	2.8	1.4E-01	-0.5	7.3E-01	0.1	9.5E-01
ENSMUST00000097737	pseudouridylate synthase-like 1 [Source:MGI Symbol;Acc:MGI:3047787]		A2ADA5	1.0	5.0E-01	1.0	6.3E-01	0.1	9.7E-01	0.1	9.7E-01
ENSMUST00000099554	MIS18 kinetochore protein homolog A (S. pombe) [Source:MGI Symbol;Acc:MGI:1913828]		Q9CZJ6	-6.3	1.4E-04	2.3	2.9E-03	-0.8	1.3E-01	-0.1	7.7E-01
ENSMUST00000099556	family with sequence similarity 122, member A [Source:MGI Symbol;Acc:MGI:1915284]		Q9DB52	-3.3	1.7E-03	6.3	1.6E-05	1.1	1.6E-01	0.2	5.7E-01
ENSMUST00000097747	Fanconi anemia core complex associated protein 20 [Source:MGI Symbol;Acc:MGI:1914763]		Q3UN58	-0.6	3.7E-01	1.1	1.8E-01	0.9	1.5E-01	-0.7	3.1E-01
ENSMUST00000097772	interleukin 1 receptor-like 1 [Source:MGI Symbol;Acc:MGI:98427]		P14719	2.5	1.8E-01	5.2	1.3E-02	-0.6	7.6E-01	-3.3	3.6E-02
ENSMUST00000099557	p21 protein (Cdc42/Rac)-activated kinase 6 [Source:MGI Symbol;Acc:MGI:2679420]		Q3ULB5	8.3	6.4E-05	2.7	2.7E-02	0.7	4.4E-01	0.7	3.9E-01
ENSMUST00000097776	cyclin M3 [Source:MGI Symbol;Acc:MGI:2151055]		Q32NY4	3.2	3.3E-01	5.0	3.2E-01	2.6	5.8E-01	0.9	7.6E-01
ENSMUST00000099558	tight junction protein 2 [Source:MGI Symbol;Acc:MGI:1341872]		Q9Z0U1	5.1	9.4E-06	-4.6	3.5E-02	1.4	9.9E-02	-1.0	6.4E-01
ENSMUST00000097781	exosome component 10 [Source:MGI Symbol;Acc:MGI:1355322]	F6VYQ6		1.8	3.1E-01	0.8	7.6E-01	1.1	6.1E-01	2.1	2.8E-01
ENSMUST00000097785	dystonin [Source:MGI Symbol;Acc:MGI:104627]		Q91ZU6	9.2	3.5E-02	7.2	1.1E-01	-0.9	8.5E-01	1.1	6.5E-01
ENSMUST00000099569	transient receptor potential cation channel, subfamily M, member 3 [Source:MGI Symbol;Acc:MGI:2443101]	Q5F4T0		8.5	4.3E-05	3.0	2.8E-01	0.2	9.4E-01	2.1	2.6E-01
ENSMUST00000097799	predicted gene 13102 [Source:MGI Symbol;Acc:MGI:3703005]	A2ASJ3		3.4	1.5E-01	4.4	1.1E-01	-0.4	8.8E-01	-1.4	4.4E-01
ENSMUST00000099575	gremlin 1 [Source:MGI Symbol;Acc:MGI:1344337]	Q3TNY7	O70326	9.4	9.5E-05	5.8	3.2E-05	-0.3	7.2E-01	-0.1	7.7E-01
ENSMUST00000097805	caspase 9 [Source:MGI Symbol;Acc:MGI:1277950]	A2AS93		-1.4	6.9E-01	-3.4	4.5E-01	-1.3	5.8E-01	0.7	8.9E-01
ENSMUST00000099576	formin 1 [Source:MGI Symbol;Acc:MGI:101815]		Q05860	4.0	1.6E-04	6.4	2.6E-04	-0.6	6.3E-01	-0.5	3.9E-01
ENSMUST00000099577	predicted gene 5134 [Source:MGI Symbol;Acc:MGI:3646667]	E9QAB5		6.5	1.9E-04	3.6	4.6E-02	-0.4	7.9E-01	1.1	3.6E-01
ENSMUST00000099589	cholinergic receptor, muscarinic 5 [Source:MGI Symbol;Acc:MGI:109248]		Q920H4	7.4	1.3E-04	-0.3	6.5E-01	1.5	1.5E-02	-0.7	3.4E-01
ENSMUST00000099609	olfactory receptor 1303 [Source:MGI Symbol;Acc:MGI:3031137]	A2AVW1		7.0	9.4E-05	-3.9	1.2E-03	0.4	4.4E-01	-2.6	4.1E-02
ENSMUST00000099623	anoctamin 3 [Source:MGI Symbol;Acc:MGI:3613666]		A2AHL1	7.1	5.4E-05	-0.6	3.2E-01	0.7	7.8E-02	-0.4	4.4E-01
ENSMUST00000097836	heterochromatin protein 1, binding protein 3 [Source:MGI Symbol;Acc:MGI:109369]		Q3TEA8	-1.5	6.3E-01	-4.8	1.9E-01	-3.1	1.4E-01	0.2	9.5E-01
ENSMUST00000099626	fin bud initiation factor homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1914856]		Q9CQS3	6.6	6.9E-05	4.2	5.9E-02	-3.2	1.7E-01	-0.8	6.0E-01
ENSMUST00000099646	ADP-ribosylation factor-like 6 [Source:MGI Symbol;Acc:MGI:1927136]		O88848	4.7	1.3E-02	-1.4	3.6E-02	0.8	4.9E-02	-0.7	2.8E-01
ENSMUST00000097844	serine/arginine-rich splicing factor 10 [Source:MGI Symbol;Acc:MGI:1333805]		Q9R0U0	-1.6	3.5E-01	0.8	6.7E-01	1.5	3.9E-01	-0.9	5.9E-01
ENSMUST00000099659	ein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1, retrogene 1 [Source:MGI Symbol;Acc:MGI:3649	Q3ULQ2		3.3	2.6E-04	8.7	1.6E-03	-1.0	6.6E-01	0.7	4.8E-01
ENSMUST00000099661	predicted gene 10797 [Source:MGI Symbol;Acc:MGI:3642860]	Q3V073		7.7	5.5E-04	5.5	6.6E-05	-0.3	6.9E-01	-0.9	1.3E-01
ENSMUST00000099673	CD44 antigen [Source:MGI Symbol;Acc:MGI:88338]	Q3U8S1		-6.7	6.1E-07	-0.7	5.9E-01	0.2	7.7E-01	-2.6	9.3E-02
ENSMUST00000097862	pumilio RNA-binding family member 1 [Source:MGI Symbol;Acc:MGI:1931749]	Q3TQ21	Q80U78	2.5	3.9E-01	1.4	7.1E-01	-0.9	7.6E-01	0.2	9.4E-01
ENSMUST00000099678	four jointed box 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1341907]		Q8BQB4	7.1	5.2E-05	5.6	2.8E-02	1.2	5.3E-01	0.3	8.5E-01
ENSMUST00000099683	predicted gene 10800 [Source:MGI Symbol;Acc:MGI:3641657]	D3Z496		14.6	5.2E-09	3.0	9.7E-02	-3.8	5.8E-02	1.6	1.8E-01
ENSMUST00000099684	predicted gene 10801 [Source:MGI Symbol;Acc:MGI:3641656]	F7C7Q0		14.4	2.7E-09	2.7	3.9E-01	-0.7	8.0E-01	2.5	3.2E-01
ENSMUST00000099690	1-aminocyclopropane-1-carboxylate synthase (non-functional)-like [Source:MGI Symbol;Acc:MGI:3584519]		Q3UX83	6.0	1.9E-02	6.4	1.3E-04	-0.9	4.3E-01	-0.7	2.8E-01
ENSMUST00000097873	expressed sequence C77080 [Source:MGI Symbol;Acc:MGI:2140651]		A2A7S8	1.0	6.3E-01	-2.1	3.1E-01	-2.5	1.5E-01	0.6	7.8E-01
ENSMUST00000099691	hexokinase 1 [Source:MGI Symbol;Acc:MGI:96103]	Q6GQU1	P17710	-2.3	3.0E-03	-5.5	1.2E-02	1.1	2.0E-01	0.2	9.3E-01
ENSMUST00000099692	predicted gene 10803 [Source:MGI Symbol;Acc:MGI:3641754]	Q3TZS6		7.9	1.9E-05	3.7	1.2E-03	0.6	4.4E-01	0.1	9.1E-01
ENSMUST00000097886	RIKEN cDNA 5730409E04Rik gene [Source:MGI Symbol;Acc:MGI:3609248]		Q8BP99	3.3	4.4E-01	4.6	2.7E-01	-0.5	9.1E-01	-1.8	5.6E-01
ENSMUST00000097888	argonaute RISC catalytic subunit 1 [Source:MGI Symbol;Acc:MGI:2446630]		Q8CJG1	-0.1	7.6E-01	0.6	3.3E-01	0.6	1.6E-01	-0.1	8.9E-01
ENSMUST00000099696	CD82 antigen [Source:MGI Symbol;Acc:MGI:104651]	Q3UII2	P40237	-4.9	7.3E-03	5.7	4.0E-04	-2.2	9.9E-02	-2.1	1.3E-02
ENSMUST00000099706	apoptosis-inducing factor, mitochondrion-associated 2 [Source:MGI Symbol;Acc:MGI:1918611]		Q8BUE4	-1.8	4.8E-03	6.1	3.6E-04	-0.5	6.6E-01	-0.4	5.1E-01
ENSMUST00000097897	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	E9PVY8		0.5	8.1E-01	2.1	5.2E-01	1.6	4.8E-01	0.0	1.0E+00
ENSMUST00000097902	palmitoyl-protein thioesterase 1 [Source:MGI Symbol;Acc:MGI:1298204]	B1B0P9		-0.3	7.7E-01	0.4	7.3E-01	0.0	9.9E-01	-0.6	5.5E-01
ENSMUST00000099709	diacylglycerol kinase zeta [Source:MGI Symbol;Acc:MGI:1278339]	A2AHJ7		-5.2	1.6E-02	6.6	2.8E-04	-0.6	6.2E-01	-1.1	1.1E-01
ENSMUST00000097908	coiled-coil domain containing 23 [Source:MGI Symbol;Acc:MGI:1916466]	A2A7P9		0.0	9.7E-01	3.0	1.0E-02	2.4	1.7E-02	-0.6	3.7E-01
ENSMUST00000099716	cytoskeleton associated protein 5 [Source:MGI Symbol;Acc:MGI:1923036]	K3W4R5		-7.2	1.3E-03	-5.3	2.3E-02	0.5	5.8E-01	1.8	4.0E-01
ENSMUST00000099726	predicted gene 4981 [Source:MGI Symbol;Acc:MGI:3645498]	Q3ULJ8		11.8	1.3E-04	6.1	2.4E-03	0.1	9.7E-01	-0.3	7.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000097921	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) [Source:MGI Symbol;Acc:MGI:105388]		Q60772	-0.8	2.2E-01	0.5	4.7E-01	0.5	3.5E-01	-0.8	2.9E-01
ENSMUST00000097925	zinc finger, CCHC domain containing 11 [Source:MGI Symbol;Acc:MGI:2445126]	A2A8R7		-2.4	4.2E-01	-4.8	3.6E-01	-0.5	8.1E-01	1.9	7.2E-01
ENSMUST00000097929	SH3/ankyrin domain gene 2 [Source:MGI Symbol;Acc:MGI:2671987]		Q80Z38	4.7	6.0E-02	6.4	2.8E-02	-0.3	9.1E-01	-2.0	1.8E-01
ENSMUST00000097729	lectin, galactose binding, soluble 12 [Source:MGI Symbol;Acc:MGI:1929094]		Q91VD1	7.6	3.6E-05	6.8	7.9E-05	-0.5	6.1E-01	-0.6	2.8E-01
ENSMUST00000099735	Yae1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1914258]	Q9DAY6		1.7	2.5E-02	7.6	4.9E-04	-0.7	6.4E-01	0.2	8.0E-01
ENSMUST00000099739	TBC1 domain family, member 32 [Source:MGI Symbol;Acc:MGI:2442827]		Q3URV1	2.2	1.7E-03	7.5	4.2E-04	-0.7	6.3E-01	0.5	4.8E-01
ENSMUST00000097945	mesoderm induction early response 1 homolog (Xenopus laevis [Source:MGI Symbol;Acc:MGI:1918398]		Q5UAK0	1.8	4.6E-01	3.9	1.9E-01	0.8	7.7E-01	-1.3	5.4E-01
ENSMUST00000097950	phosphodiesterase 4B, cAMP specific [Source:MGI Symbol;Acc:MGI:99557]	B1AWD0		1.0	9.5E-02	-1.1	1.4E-01	-1.5	1.1E-02	0.5	4.2E-01
ENSMUST00000097952	interferon regulatory factor 7 [Source:MGI Symbol;Acc:MGI:1859212]	Q3TW14		-5.8	4.3E-02	-4.8	2.1E-01	0.4	8.3E-01	-0.6	8.7E-01
ENSMUST00000099757	olfactory receptor 140 [Source:MGI Symbol;Acc:MGI:2177523]		Q60878	5.0	2.3E-02	-5.1	3.2E-03	0.8	1.4E-01	-0.7	6.2E-01
ENSMUST00000097958	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain [Source:MGI Symbol;Acc:MGI:1344402]	Q3UKS3	Q9JLZ8	0.5	3.5E-01	0.3	7.4E-01	0.2	7.0E-01	0.5	4.8E-01
ENSMUST00000099758	olfactory receptor 1264 [Source:MGI Symbol;Acc:MGI:3031098]	Q9R0K2		6.5	1.3E-04	1.3	1.5E-01	-0.7	3.5E-01	0.2	8.2E-01
ENSMUST00000099761	limbic system-associated membrane protein [Source:MGI Symbol;Acc:MGI:1261760]	Q3TYE5		7.7	8.6E-05	6.4	1.2E-04	0.1	8.8E-01	0.8	1.7E-01
ENSMUST00000097967	polyamine oxidase (exo-N4-amino) [Source:MGI Symbol;Acc:MGI:1916983]	Q3TXR6		4.0	5.7E-02	1.3	5.0E-01	-1.7	3.8E-01	1.0	5.6E-01
ENSMUST00000099762	olfactory receptor 48 [Source:MGI Symbol;Acc:MGI:1333765]	Q8VGN4		6.1	8.1E-04	6.0	4.4E-04	-1.0	4.4E-01	0.6	3.3E-01
ENSMUST00000099774	G protein-coupled receptor 137 [Source:MGI Symbol;Acc:MGI:2147529]	Q3TD99		-4.1	7.4E-04	-1.0	1.9E-01	1.1	4.0E-02	-0.3	6.7E-01
ENSMUST00000097981	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) [Source:MGI Symbol;Acc:MGI:104737]	Q549R4	P55271	1.5	4.8E-02	2.5	1.2E-02	1.2	1.1E-01	0.2	7.8E-01
ENSMUST00000099776	G protein-coupled receptor 137 [Source:MGI Symbol;Acc:MGI:2147529]	E9Q9I0		-4.5	2.6E-03	8.2	2.7E-05	-0.2	8.9E-01	-0.3	5.8E-01
ENSMUST00000099786	olfactory receptor 1231 [Source:MGI Symbol;Acc:MGI:3031065]	Q7TQZ8		5.5	3.9E-04	2.1	1.4E-01	-3.2	5.0E-02	-0.1	9.6E-01
ENSMUST00000097998	family with sequence similarity 53, member B [Source:MGI Symbol;Acc:MGI:1925188]	Q3TNT2		-1.4	2.6E-01	0.2	9.2E-01	4.2	4.1E-02	2.5	1.7E-01
ENSMUST00000097999	family with sequence similarity 53, member B [Source:MGI Symbol;Acc:MGI:1925188]		Q8BGR5	2.2	4.7E-02	5.0	2.5E-03	1.1	3.6E-01	-1.7	7.1E-02
ENSMUST00000099820	lectin, galactose binding, soluble 8 [Source:MGI Symbol;Acc:MGI:1928481]	Q542M5	Q9JL15	-4.5	4.7E-03	5.2	1.5E-03	0.8	4.7E-01	0.6	3.6E-01
ENSMUST00000099856	5-methyltetrahydrofolate-homocysteine methyltransferase [Source:MGI Symbol;Acc:MGI:894292]		A6H5Y3	1.0	3.1E-02	-2.8	2.2E-03	0.5	1.7E-01	-0.3	6.9E-01
ENSMUST00000099888	RIKEN cDNA F930017D23 gene [Source:MGI Symbol;Acc:MGI:3822538]	Q3TZ88		3.1	3.2E-03	3.6	1.1E-02	-2.9	4.5E-02	0.0	9.5E-01
ENSMUST00000099894	olfactory receptor 1055 [Source:MGI Symbol;Acc:MGI:3030889]	A2AVX9		5.4	1.8E-03	7.4	2.4E-04	-0.2	8.9E-01	0.1	8.7E-01
ENSMUST00000099923	RIKEN cDNA 4833423E24 gene [Source:MGI Symbol;Acc:MGI:2687041]		Q0VAX3	5.5	7.3E-04	0.8	4.6E-01	3.3	2.6E-03	-2.0	1.2E-01
ENSMUST00000099930	leucine rich repeat containing 55 [Source:MGI Symbol;Acc:MGI:2685197]		Q3UY51	6.5	2.0E-04	-6.6	1.3E-03	1.2	3.6E-02	-0.7	6.6E-01
ENSMUST00000099934	tubule associated monooxygenase, calponin and LIM domain containing 1 [Source:MGI Symbol;Acc:MGI:238		Q8VDP3	-8.4	2.7E-04	6.7	3.2E-03	-0.7	7.0E-01	-2.9	3.3E-02
ENSMUST00000099945	S-adenosylmethionine decarboxylase 1 [Source:MGI Symbol;Acc:MGI:88004]		P0DMN7	-3.2	3.4E-03	-3.3	1.8E-02	0.6	3.6E-01	-0.5	6.7E-01
ENSMUST00000098059	muscle, skeletal, receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:103581]	F6WVU1		4.2	1.5E-01	1.9	5.9E-01	-0.2	9.5E-01	2.0	4.6E-01
ENSMUST00000099946	neuroepithelial cell transforming gene 1 [Source:MGI Symbol;Acc:MGI:1927138]	Q3USZ7	Q9Z206	2.4	8.2E-04	-5.0	1.5E-02	0.7	3.4E-01	-1.7	3.8E-01
ENSMUST00000098062	retinoblastoma binding protein 6 [Source:MGI Symbol;Acc:MGI:894835]			0.5	6.3E-01	2.6	8.1E-02	1.2	3.1E-01	-0.9	4.6E-01
ENSMUST00000098064	A kinase (PRKA) anchor protein 2 [Source:MGI Symbol;Acc:MGI:1306795]		O54931	7.1	5.2E-02	5.9	1.3E-01	-0.7	8.5E-01	0.5	8.1E-01
ENSMUST00000098068	partner and localizer of BRCA2 [Source:MGI Symbol;Acc:MGI:3040695]		Q3U0P1	4.3	3.7E-02	-1.0	7.5E-01	-0.8	7.1E-01	4.5	1.3E-01
ENSMUST00000099947	predicted gene 13691 [Source:MGI Symbol;Acc:MGI:3702053]	A2AK42		6.5	6.6E-05	5.4	2.7E-05	-5.1	6.2E-04	0.0	9.7E-01
ENSMUST00000098080	ч1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2679		Q8K0V2	-2.9	6.0E-02	0.1	9.5E-01	1.3	3.3E-01	-1.7	3.1E-01
ENSMUST00000099948	predicted gene 13697 [Source:MGI Symbol;Acc:MGI:3702070]	A2AK42		6.5	6.6E-05	4.8	1.8E-02	-0.4	7.9E-01	4.3	3.4E-03
ENSMUST00000098098	ring finger protein 38 [Source:MGI Symbol;Acc:MGI:1920719]		Q8BI21	1.0	2.9E-01	-3.0	2.1E-01	2.1	1.0E-01	6.1	1.6E-02
ENSMUST00000098104	CD72 antigen [Source:MGI Symbol;Acc:MGI:88345]	Q3UB58		1.1	5.6E-01	2.4	1.7E-01	-1.6	3.6E-01	-2.9	8.4E-02
ENSMUST00000099955	family with sequence similarity 89, member B [Source:MGI Symbol;Acc:MGI:106595]		Q9QUI1	-8.0	1.3E-05	7.7	1.1E-02	-0.6	8.3E-01	-2.4	1.2E-01
ENSMUST00000099980	titin [Source:MGI Symbol;Acc:MGI:98864]		A2ASS6	9.2	2.7E-06	2.3	1.4E-02	1.1	9.0E-02	0.4	5.5E-01
ENSMUST00000098110	expressed sequence AA474408 [Source:MGI Symbol;Acc:MGI:3034216]	Q3V1U0		-0.1	8.6E-01	1.8	3.0E-02	0.0	9.9E-01	-1.9	1.4E-02
ENSMUST00000098112	DnaJ (Hsp40) homolog, subfamily B, member 5 [Source:MGI Symbol;Acc:MGI:1930018]	Q3TY13	O89114	-1.0	3.0E-01	4.5	1.1E-03	1.0	2.9E-01	-4.6	6.3E-04
ENSMUST00000099981	titin [Source:MGI Symbol;Acc:MGI:98864]		A2ASS6	11.3	6.1E-04	2.9	9.8E-04	0.6	2.4E-01	-0.7	1.8E-01
ENSMUST00000099990	brain expressed gene 6 [Source:MGI Symbol;Acc:MGI:3588247]		Q3TZW7	2.0	2.0E-02	2.1	6.3E-02	0.2	8.2E-01	1.2	1.2E-01
ENSMUST00000099991	negative regulator of reactive oxygen species [Source:MGI Symbol;Acc:MGI:2445095]		Q8BMT4	-9.2	1.4E-05	7.4	9.8E-05	-0.6	6.3E-01	-0.1	9.1E-01
ENSMUST00000099992	phosphodiesterase 11A [Source:MGI Symbol;Acc:MGI:3036251]		P0C1Q2	7.5	1.9E-05	5.9	7.1E-04	-0.6	6.5E-01	0.1	9.2E-01
ENSMUST00000099994	tetratricopeptide repeat domain 30A1 [Source:MGI Symbol;Acc:MGI:1926052]		Q99J38	-1.2	2.0E-02	6.1	5.0E-04	-0.5	6.7E-01	-0.3	6.8E-01
ENSMUST00000100013	ATPase type 13A3 [Source:MGI Symbol;Acc:MGI:2685387]		Q5XF89	-4.3	5.4E-03	-1.2	1.3E-01	0.5	3.5E-01	-0.1	9.1E-01
ENSMUST00000098148	ribosomal RNA processing 8, methyltransferase, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914251]	E9PVA2		0.7	4.1E-01	0.9	4.5E-01	0.3	7.7E-01	0.1	9.2E-01
ENSMUST00000098161	olfactory receptor 677 [Source:MGI Symbol;Acc:MGI:3030511]	Q8VF06		4.1	4.1E-02	4.5	4.3E-02	-0.3	8.9E-01	-0.6	6.0E-01
ENSMUST00000098163	zinc finger protein 292 [Source:MGI Symbol;Acc:MGI:1353423]		Q9Z2U2	-4.6	6.4E-02	-1.7	5.5E-01	2.4	2.2E-01	-0.5	8.5E-01
ENSMUST00000098179	tripartite motif-containing 5 [Source:MGI Symbol;Acc:MGI:3646853]	E9PV98		2.2	3.4E-01	-2.6	4.6E-01	-2.8	1.8E-01	2.0	5.6E-01
ENSMUST00000100016	predicted gene 1968 [Source:MGI Symbol;Acc:MGI:3584525]	Q3T9I3		5.1	4.4E-05	1.9	1.9E-01	0.2	8.4E-01	1.4	2.2E-01
ENSMUST00000100023	Mab-21 domain containing 2 [Source:MGI Symbol;Acc:MGI:1917028]	D3Z742		5.3	1.1E-05	5.4	7.1E-04	-1.3	2.8E-01	-0.4	5.6E-01
ENSMUST00000100024	fibroblast growth factor 12 [Source:MGI Symbol;Acc:MGI:109183]		P61329	5.5	7.3E-04	6.0	3.1E-04	-0.6	6.1E-01	0.2	7.3E-01
ENSMUST00000100026	coiled-coil domain containing 50 [Source:MGI Symbol;Acc:MGI:1914751]	A6H6M8	Q810U5	2.4	3.3E-04	6.4	5.5E-04	-0.6	6.8E-01	-1.3	1.1E-01
ENSMUST00000098190	Ras-related GTP binding D [Source:MGI Symbol;Acc:MGI:1098604]	B1AWT2		1.9	3.3E-01	1.7	4.9E-01	0.5	8.1E-01	0.7	7.2E-01
ENSMUST00000098192	hemoglobin, beta adult t chain [Source:MGI Symbol;Acc:MGI:5474850]	A8DUK4		-2.6	1.4E-01	-4.7	2.3E-02	-3.7	7.8E-03	-1.6	4.4E-01
ENSMUST00000100028	dynein cytoplasmic 1 intermediate chain 2 [Source:MGI Symbol;Acc:MGI:107750]	Q3TPJ8		-7.5	3.3E-04	6.2	5.8E-04	-0.6	6.4E-01	-0.5	4.9E-01
ENSMUST00000100036	serum/glucocorticoid regulated kinase 1 [Source:MGI Symbol;Acc:MGI:1340062]	E9Q1B0		-6.0	1.4E-04	6.9	2.3E-04	-0.6	6.5E-01	-0.8	2.4E-01
ENSMUST00000100041	glutamate rich 2 [Source:MGI Symbol;Acc:MGI:1913998]	E9Q1A6		6.2	5.9E-04	6.8	5.5E-04	-0.5	7.1E-01	-1.6	6.1E-02
ENSMUST00000100043	trans-acting transcription factor 5 [Source:MGI Symbol;Acc:MGI:1927715]		Q9JHX2	7.3	5.6E-05	-7.2	3.2E-03	1.3	7.2E-02	-0.8	7.1E-01
ENSMUST00000100046	kininogen 2 [Source:MGI Symbol;Acc:MGI:3027157]	Q6S9I3		5.7	1.2E-02	-8.4	3.9E-03	-0.8	2.5E-01	1.5	5.2E-01
ENSMUST00000100050	kelch-like 41 [Source:MGI Symbol;Acc:MGI:2683854]		A2AUC9	6.6	7.5E-06	3.8	2.0E-02	-0.7	5.7E-01	-0.9	3.8E-01
ENSMUST00000100052	insulin-like growth factor 2 mRNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1890358]		Q5SF07	7.8	1.8E-04	-2.6	1.0E-03	0.5	1.5E-01	-0.6	2.7E-01
ENSMUST00000100054	NHS-like 1 [Source:MGI Symbol;Acc:MGI:106390]		Q8CAF4	5.9	3.3E-02	-0.7	4.1E-01	2.1	2.6E-03	-1.5	9.5E-02
ENSMUST00000100067	sodium channel, voltage-gated, type II, alpha 1 [Source:MGI Symbol;Acc:MGI:98248]	B1AWN6		8.6	2.6E-04	-0.1	9.1E-01	0.4	6.8E-01	-2.7	6.2E-02
ENSMUST00000098252	RAB6A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:894313]	Q3U4W5	P35279	0.0	9.9E-01	-4.0	3.4E-01	-4.4	9.0E-02	-0.4	9.2E-01
ENSMUST00000100069	sodium channel, voltage-gated, type III, alpha [Source:MGI Symbol;Acc:MGI:98249]	A2ASI5		5.8	1.4E-04	7.8	3.9E-03	-0.4	8.5E-01	1.5	1.8E-01
ENSMUST00000100070	sterile alpha motif domain containing 5 [Source:MGI Symbol;Acc:MGI:2444815]			6.6	7.8E-05	6.6	9.8E-04	-0.8	6.0E-01	0.2	7.8E-01
ENSMUST00000100078	zinc finger and BTB domain containing 2 [Source:MGI Symbol;Acc:MGI:2685949]	Q3V3W4		-4.0	1.4E-02	-1.0	2.3E-01	0.7	1.7E-01	-0.8	3.7E-01
ENSMUST00000100089	reprimo, TP53 dependent G2 arrest mediator candidate [Source:MGI Symbol;Acc:MGI:1915124]		Q9JJ72	7.8	5.1E-05	6.6	1.1E-04	-1.9	1.3E-01	-0.1	8.2E-01
ENSMUST00000100099	TRM2 tRNA methyltransferase 2A [Source:MGI Symbol;Acc:MGI:96270]	E9PUQ7		-2.6	3.3E-02	8.6	2.4E-03	1.0	6.3E-01	1.6	1.3E-01
ENSMUST00000100127	glycosyltransferase-like domain containing 1 [Source:MGI Symbol;Acc:MGI:2444269]		Q8BW56	4.5	9.4E-05	8.3	2.0E-05	-0.6	6.0E-01	-0.8	1.3E-01
ENSMUST00000100130	olute carrier family 16 (monocarboxylic acid transporters), member 3 [Source:MGI Symbol;Acc:MGI:1933438	Q3UDP9	P57787	-7.5	2.5E-03	6.5	8.5E-05	0.6	5.1E-01	0.4	5.1E-01
ENSMUST00000100131	expressed sequence AW554918 [Source:MGI Symbol;Acc:MGI:2147376]	E0CZ24		6.5	2.2E-04	7.4	1.9E-04	-1.4	3.2E-01	0.1	8.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000098300	asparagine-linked glycosylation 8 (alpha-1,3-glucosyltransferase) [Source:MGI Symbol;Acc:MGI:2141959]		Q6P8H8	1.5	8.6E-02	0.1	9.0E-01	-1.0	2.2E-01	0.4	6.6E-01
ENSMUST00000098312	exocyst complex component 8 [Source:MGI Symbol;Acc:MGI:2142527]		Q6PGF7	0.2	5.1E-01	1.4	2.0E-02	1.4	7.0E-03	0.2	6.2E-01
ENSMUST00000098320	AFG3-like AAA ATPase 1 [Source:MGI Symbol;Acc:MGI:1928277]		Q920A7	-0.1	9.5E-01	7.8	1.0E-02	3.0	2.4E-01	-4.9	1.9E-02
ENSMUST00000100143	ring finger and CCCH-type zinc finger domains 2 [Source:MGI Symbol;Acc:MGI:2442789]		P0C090	-2.0	2.5E-02	7.7	7.5E-05	-0.5	6.9E-01	0.2	6.9E-01
ENSMUST00000100144	olfactory receptor 362 [Source:MGI Symbol;Acc:MGI:3030196]	Q8VGV7		7.1	4.3E-05	7.5	4.1E-05	0.0	1.0E+00	0.2	7.5E-01
ENSMUST00000098327	spermatogenesis associated 2-like [Source:MGI Symbol;Acc:MGI:1926029]	B2RTE8	Q8BNN1	-1.7	1.7E-01	0.5	7.3E-01	1.0	3.8E-01	-1.2	3.9E-01
ENSMUST00000098333	ankyrin repeat domain 11 [Source:MGI Symbol;Acc:MGI:1924337]	E9Q4F8		2.4	1.8E-01	0.4	8.6E-01	0.8	7.0E-01	2.8	2.0E-01
ENSMUST00000100146	olfactory receptor 358 [Source:MGI Symbol;Acc:MGI:3030192]	Q7TRY5		6.7	8.3E-05	-1.5	2.8E-01	0.6	5.0E-01	-3.2	7.8E-02
ENSMUST00000100162	coatomer protein complex, subunit zeta 1 [Source:MGI Symbol;Acc:MGI:1929063]	Q542M2	P61924	-5.4	8.1E-07	-3.5	7.3E-04	0.2	6.8E-01	-0.5	5.0E-01
ENSMUST00000100168	TAR (HIV) RNA binding protein 2 [Source:MGI Symbol;Acc:MGI:103027]	Q3UNH9		6.1	2.5E-02	6.9	3.5E-04	-0.6	6.7E-01	0.1	9.1E-01
ENSMUST00000098346	mannosidase 2, alpha 2 [Source:MGI Symbol;Acc:MGI:2150656]	Q197W7	Q8BRK9	0.1	7.9E-01	0.7	2.4E-01	1.1	3.4E-02	0.5	3.5E-01
ENSMUST00000098350	SREBF chaperone [Source:MGI Symbol;Acc:MGI:2135958]		Q6GQT6	-1.0	8.7E-02	0.2	7.2E-01	1.1	6.2E-02	-0.2	7.5E-01
ENSMUST00000100171	heat shock protein 5 [Source:MGI Symbol;Acc:MGI:95835]		P20029	-10.2	9.0E-05	4.3	2.3E-04	-0.4	6.0E-01	-0.6	2.7E-01
ENSMUST00000100179	keratin 76 [Source:MGI Symbol;Acc:MGI:1924305]		Q3UV17	7.8	5.9E-05	6.5	2.8E-04	-0.5	7.2E-01	-1.0	1.5E-01
ENSMUST00000100184	predicted pseudogene 5478 [Source:MGI Symbol;Acc:MGI:3646318]	D3Z6R0		8.5	2.0E-05	7.4	2.1E-04	-0.7	6.2E-01	-0.1	9.2E-01
ENSMUST00000098362	membrane-bound transcription factor peptidase, site 1 [Source:MGI Symbol;Acc:MGI:1927235]		Q9WTZ2	-1.8	3.6E-01	-1.4	4.7E-01	-1.0	4.7E-01	-1.4	5.1E-01
ENSMUST00000100185	phosphatidylglycerophosphate synthase 1 [Source:MGI Symbol;Acc:MGI:1921701]	F2Z427		4.8	3.3E-02	6.0	1.1E-03	-0.6	6.7E-01	-1.8	4.7E-02
ENSMUST00000098365	oxidative stress induced growth inhibitor 1 [Source:MGI Symbol;Acc:MGI:1919089]	D3YWF1		-5.1	1.8E-01	-4.6	3.1E-01	-0.6	7.8E-01	-1.0	8.3E-01
ENSMUST00000100188	phosphatidylinositol-4-phosphate 5-kinase-like 1 [Source:MGI Symbol;Acc:MGI:2448520]		Q6U7H8	6.3	1.5E-04	-2.8	5.1E-02	1.0	1.8E-01	-1.4	3.5E-01
ENSMUST00000100190	RIKEN cDNA 9430097D07 gene [Source:MGI Symbol;Acc:MGI:2441749]	Q8BS47		5.2	4.3E-04	5.9	3.5E-04	0.1	9.5E-01	-0.3	6.8E-01
ENSMUST00000098371	solute carrier organic anion transporter family, member 3a1 [Source:MGI Symbol;Acc:MGI:1351867]		Q8R3L5	0.2	7.8E-01	-0.3	7.3E-01	-0.2	7.7E-01	0.3	7.1E-01
ENSMUST00000098374	adenosine deaminase, RNA-specific, B1 [Source:MGI Symbol;Acc:MGI:891999]		Q91ZS8	4.8	1.9E-01	2.9	3.4E-01	-5.0	1.8E-01	-3.1	2.2E-01
ENSMUST00000100193	septin 9 [Source:MGI Symbol;Acc:MGI:1858222]		Q80UG5	-4.5	1.1E-03	4.6	2.1E-04	0.6	4.3E-01	-0.3	5.5E-01
ENSMUST00000100194	golgi autoantigen, golgin subfamily a, 2 [Source:MGI Symbol;Acc:MGI:2139395]	E9PUQ5		-6.5	7.9E-05	10.2	2.0E-04	-0.1	9.5E-01	-1.2	1.2E-01
ENSMUST00000100196	asparagine-linked glycosylation 1 (beta-1,4-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:2384774]		Q921Q3	-5.3	1.1E-03	5.5	7.4E-02	-1.9	5.4E-01	-0.1	9.6E-01
ENSMUST00000098402	small nuclear ribonucleoprotein N [Source:MGI Symbol;Acc:MGI:98347]	Q3UN87	P63163	6.8	3.7E-02	5.9	8.3E-02	-1.0	7.7E-01	-0.1	9.7E-01
ENSMUST00000100206	La ribonucleoprotein domain family, member 4 [Source:MGI Symbol;Acc:MGI:2443114]	G3X9Q6		-2.0	1.3E-03	6.9	6.2E-04	-0.4	7.8E-01	0.5	4.7E-01
ENSMUST00000100209	family with sequence similarity 186, member A [Source:MGI Symbol;Acc:MGI:2685766]	K3W4Q5		11.9	2.6E-05	-4.3	3.3E-04	0.1	7.6E-01	-0.5	5.2E-01
ENSMUST00000100214	family with sequence similarity 73, member B [Source:MGI Symbol;Acc:MGI:1922035]		Q8BK03	7.5	4.7E-03	6.0	1.9E-03	-0.7	6.4E-01	0.8	3.1E-01
ENSMUST00000100220	DNA segment, Chr 2, Wayne State University 81, expressed [Source:MGI Symbol;Acc:MGI:106544]		Q3UHX9	-4.1	1.3E-03	5.8	6.2E-06	-3.7	9.4E-04	0.3	4.4E-01
ENSMUST00000100222	Mediterranean fever [Source:MGI Symbol;Acc:MGI:1859396]	Q32MT0		-2.7	1.6E-02	5.3	6.4E-03	-0.5	7.6E-01	0.1	9.0E-01
ENSMUST00000098444	par-6 family cell polarity regulator alpha [Source:MGI Symbol;Acc:MGI:1927223]	D3Z2R1		-1.6	1.9E-01	0.5	7.3E-01	1.4	2.8E-01	-0.8	5.6E-01
ENSMUST00000098453	transmembrane protein 208 [Source:MGI Symbol;Acc:MGI:1913570]		Q9CR96	0.1	9.4E-01	1.3	2.0E-01	0.2	8.0E-01	-1.1	2.4E-01
ENSMUST00000100225	spectrin alpha, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98386]	A3KGU7		-5.4	8.8E-03	4.3	8.1E-05	-0.2	6.8E-01	-0.7	1.6E-01
ENSMUST00000098458	interleukin 20 receptor beta [Source:MGI Symbol;Acc:MGI:2143266]	E9Q9A6		1.9	8.6E-02	0.7	5.0E-01	-1.3	2.0E-01	-0.1	8.9E-01
ENSMUST00000100235	transmembrane protein 104 [Source:MGI Symbol;Acc:MGI:2444222]	A2A6S1		5.7	1.6E-02	6.4	4.5E-04	-0.7	6.1E-01	0.3	6.9E-01
ENSMUST00000100237	transcription termination factor, RNA polymerase I [Source:MGI Symbol;Acc:MGI:105044]		Q62187	-3.4	1.5E-02	-8.6	2.5E-03	1.5	2.5E-02	-0.2	9.4E-01
ENSMUST00000100244	olfactomedin 1 [Source:MGI Symbol;Acc:MGI:1860437]	G3X9Q7		-6.5	1.1E-03	2.3	1.7E-02	0.0	9.9E-01	-0.2	7.4E-01
ENSMUST00000098470	RNA binding motif protein, X chromosome [Source:MGI Symbol;Acc:MGI:1343044]	A2AFI3		1.1	3.3E-01	2.2	1.4E-01	1.0	3.8E-01	-0.1	9.3E-01
ENSMUST00000100249	endonuclease, polyU-specific [Source:MGI Symbol;Acc:MGI:97746]		Q3V188	7.6	9.7E-05	-7.0	4.0E-04	1.6	3.4E-03	1.6	2.6E-01
ENSMUST00000100251	retinoid X receptor alpha [Source:MGI Symbol;Acc:MGI:98214]	Q6LC96		6.3	1.1E-02	-7.3	1.2E-03	1.5	1.2E-02	-0.6	7.3E-01
ENSMUST00000098483	Spi-B transcription factor (Spi-1/PU.1 related) [Source:MGI Symbol;Acc:MGI:892986]		O35906	2.6	6.2E-02	6.9	7.5E-05	-2.7	3.9E-02	-7.1	2.7E-05
ENSMUST00000098486	B cell leukemia/lymphoma 2 related protein A1d [Source:MGI Symbol;Acc:MGI:1278325]	O55179		0.7	3.2E-01	-1.0	1.7E-01	-2.9	8.9E-04	-1.2	1.3E-01
ENSMUST00000098489	NLR family, CARD domain containing 5 [Source:MGI Symbol;Acc:MGI:3612191]	Q3U1H4		-1.5	3.1E-01	-1.2	5.4E-01	0.8	5.4E-01	0.6	7.4E-01
ENSMUST00000100262	solute carrier family 38, member 1 [Source:MGI Symbol;Acc:MGI:2145895]		Q8K2P7	2.4	6.2E-03	8.0	1.2E-05	-1.5	1.8E-01	0.0	9.1E-01
ENSMUST00000098500	trophoblast glycoprotein [Source:MGI Symbol;Acc:MGI:1341264]		Q9Z0L0	2.5	2.5E-01	-1.9	2.9E-01	-4.1	3.2E-02	0.3	8.8E-01
ENSMUST00000100287	ATP-binding cassette, sub-family A (ABC1), member 8a [Source:MGI Symbol;Acc:MGI:2386846]		Q8K442	6.3	1.9E-02	4.1	2.3E-02	-2.3	1.9E-01	0.4	7.1E-01
ENSMUST00000098509	expressed sequence AW146154 [Source:MGI Symbol;Acc:MGI:2142212]	Q3TPQ7		0.1	9.3E-01	1.2	1.0E-01	0.1	8.6E-01	-1.1	1.2E-01
ENSMUST00000100294	predicted gene 10837 [Source:MGI Symbol;Acc:MGI:3642026]	Q3UTT8		6.1	2.1E-04	2.1	1.0E-02	0.4	4.5E-01	0.2	7.1E-01
ENSMUST00000100301	protein kinase C, gamma [Source:MGI Symbol;Acc:MGI:97597]	Q3UN66	P63318	2.7	3.8E-03	5.8	2.3E-04	-0.8	4.5E-01	1.2	8.5E-02
ENSMUST00000098519	cylindromatosis (turban tumor syndrome) [Source:MGI Symbol;Acc:MGI:1921506]		Q80TQ2	1.2	5.9E-01	7.2	3.6E-02	3.0	3.3E-01	-3.1	1.3E-01
ENSMUST00000100303	caspase recruitment domain family, member 9 [Source:MGI Symbol;Acc:MGI:2685628]		A2AIV8	-3.0	1.1E-02	-6.4	1.2E-03	0.3	5.0E-01	3.9	1.9E-02
ENSMUST00000098524	mucolipin 2 [Source:MGI Symbol;Acc:MGI:1915529]		Q8K595	2.0	7.9E-02	1.8	1.6E-01	-1.1	3.6E-01	-0.9	3.6E-01
ENSMUST00000098532	predicted gene 10638 [Source:MGI Symbol;Acc:MGI:3704316]	F6QEG2		3.0	4.5E-02	3.6	4.2E-02	-0.3	8.4E-01	-0.8	4.9E-01
ENSMUST00000100304	kinesin family member 21A [Source:MGI Symbol;Acc:MGI:109188]	E9Q0J5		6.0	1.9E-02	1.9	3.3E-02	-1.9	2.4E-02	-0.3	6.6E-01
ENSMUST00000100314	claudin 10 [Source:MGI Symbol;Acc:MGI:1913101]		Q9Z0S6	6.0	4.2E-04	6.5	8.2E-03	-0.6	7.8E-01	-2.5	6.3E-02
ENSMUST00000100322	SLIT and NTRK-like family, member 1 [Source:MGI Symbol;Acc:MGI:2679446]	B2RXM1	Q810C1	8.7	2.3E-05	3.0	1.8E-02	0.5	5.8E-01	-0.3	7.1E-01
ENSMUST00000100327	RNA binding motif protein 26 [Source:MGI Symbol;Acc:MGI:1921463]	E9PUF4		-3.0	1.0E-02	5.4	2.7E-02	-0.7	7.5E-01	1.9	1.6E-01
ENSMUST00000100330	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2 [Source:MGI Symbol;Acc:MGI:2444121]		A2A690	7.6	7.4E-06	6.8	9.1E-05	-0.6	6.0E-01	-0.3	5.9E-01
ENSMUST00000100332	membrane-associated ring finger (C3HC4) 10 [Source:MGI Symbol;Acc:MGI:2443469]	Q497L7		6.2	1.7E-02	0.9	2.1E-01	-4.3	4.4E-04	-0.5	4.2E-01
ENSMUST00000100335	mannose receptor, C type 2 [Source:MGI Symbol;Acc:MGI:107818]		Q64449	6.7	4.1E-06	7.1	7.7E-05	-0.9	4.4E-01	-1.0	1.3E-01
ENSMUST00000100337	LIM domain only 7 [Source:MGI Symbol;Acc:MGI:1353586]	E9PYF4		7.5	1.7E-03	9.6	3.4E-05	-0.4	7.7E-01	-1.6	1.8E-02
ENSMUST00000100338	predicted gene 10842 [Source:MGI Symbol;Acc:MGI:3642916]	Q3U587		7.0	7.1E-05	3.8	6.6E-03	1.0	3.1E-01	0.9	3.3E-01
ENSMUST00000098567	dyslexia susceptibility 1 candidate 1 homolog (human) [Source:MGI Symbol;Acc:MGI:1914935]	E9Q973		-1.7	2.3E-01	2.4	5.3E-02	-0.4	7.1E-01	-4.4	5.5E-03
ENSMUST00000098571	RIKEN cDNA G430095P16 gene [Source:MGI Symbol;Acc:MGI:3588227]	E9Q913		0.7	3.2E-01	-0.8	3.0E-01	-1.3	6.6E-02	0.2	7.4E-01
ENSMUST00000100339	COMM domain containing 6 [Source:MGI Symbol;Acc:MGI:1913450]	B7ZNP2	Q3V4B5	-4.0	9.6E-05	-1.9	9.8E-02	0.8	2.3E-01	-2.8	3.9E-02
ENSMUST00000100340	TBC1 domain family, member 4 [Source:MGI Symbol;Acc:MGI:2429660]	H7BX82		5.3	1.4E-02	2.3	1.1E-02	0.6	3.9E-01	0.1	9.1E-01
ENSMUST00000098580	microsomal triglyceride transfer protein [Source:MGI Symbol;Acc:MGI:106926]		O08601	1.5	4.5E-01	2.1	3.3E-01	-1.3	4.9E-01	-1.9	3.4E-01
ENSMUST00000098586	succinate dehydrogenase complex assembly factor 1 [Source:MGI Symbol;Acc:MGI:1915582]		Q3U276	0.6	2.1E-01	0.7	2.9E-01	-0.1	8.0E-01	-0.2	7.8E-01
ENSMUST00000098589	predicted gene 10642 [Source:MGI Symbol;Acc:MGI:3704338]	Q3TWM1		-0.9	1.5E-01	1.1	1.7E-01	1.3	5.2E-02	-0.7	3.1E-01
ENSMUST00000100359	kelch repeat and BTB (POZ) domain containing 6 [Source:MGI Symbol;Acc:MGI:3643058]	E9PYD7		2.6	2.5E-03	4.4	7.9E-04	0.9	2.6E-01	-0.3	6.0E-01
ENSMUST00000100369	family with sequence similarity 187, member A [Source:MGI Symbol;Acc:MGI:1914034]		Q9D3R5	6.5	2.1E-04	6.7	1.4E-04	0.6	5.9E-01	-0.1	9.3E-01
ENSMUST00000100375	polymerase (DNA-directed), delta interacting protein 3 [Source:MGI Symbol;Acc:MGI:1921076]	Q3UDD3		-2.6	3.0E-03	2.2	1.0E-02	-0.5	4.3E-01	-0.7	2.8E-01
ENSMUST00000098603	tet methylcytosine dioxygenase 2 [Source:MGI Symbol;Acc:MGI:2443298]		Q4JK59	-0.8	1.5E-01	-0.8	2.5E-01	0.2	7.1E-01	0.2	7.7E-01
ENSMUST00000100377	Nfat activating molecule with ITAM motif 1 [Source:MGI Symbol;Acc:MGI:1921289]		Q8R4V1	-6.8	1.3E-05	7.2	2.2E-04	0.9	4.7E-01	0.2	7.5E-01
ENSMUST00000100378	predicted gene 1564 [Source:MGI Symbol;Acc:MGI:2686410]		A2AG06	5.7	1.3E-03	-3.7	4.0E-02	-0.2	8.5E-01	-0.7	6.8E-01
ENSMUST00000100387	transmembrane and ubiquitin-like domain containing 2 [Source:MGI Symbol;Acc:MGI:1919303]	G8JL73		-6.2	4.2E-04	5.5	1.7E-04	0.3	7.5E-01	-0.3	6.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000100396	RIKEN cDNA 4930407I10 gene [Source:MGI Symbol;Acc:MGI:2685593]	D3Z5T8		9.5	3.7E-05	6.2	1.1E-04	-3.7	9.5E-03	-0.6	2.7E-01
ENSMUST00000100399	X-ray repair complementing defective repair in Chinese hamster cells 6 [Source:MGI Symbol;Acc:MGI:95606]			8.3	1.1E-05	6.7	5.0E-04	-0.7	6.3E-01	-0.4	6.1E-01
ENSMUST00000100433	ureidoimidazoline (2-oxo-4-hydroxy-4-carboxy-5) decarboxylase [Source:MGI Symbol;Acc:MGI:3647519]	B9EK13	Q283N4	6.9	4.8E-04	6.6	1.5E-04	-0.6	6.2E-01	-0.4	4.8E-01
ENSMUST00000100439	Sad1 and UNC84 domain containing 2 [Source:MGI Symbol;Acc:MGI:2443011]		Q8BJS4	-11.2	2.6E-05	8.7	5.0E-05	-0.2	8.6E-01	-0.3	6.0E-01
ENSMUST00000100453	predicted gene 5464 [Source:MGI Symbol;Acc:MGI:3643060]	Q3UY29		6.3	3.9E-05	2.7	1.0E-02	-0.5	5.1E-01	-0.3	6.4E-01
ENSMUST00000098644	periaxin [Source:MGI Symbol;Acc:MGI:108176]	E9QQ57		2.6	3.0E-01	3.4	2.9E-01	0.5	8.7E-01	-0.3	9.0E-01
ENSMUST00000098645				-0.7	5.0E-01	-0.2	8.8E-01	1.2	3.0E-01	0.7	6.4E-01
ENSMUST00000100467	transformation/transcription domain-associated protein [Source:MGI Symbol;Acc:MGI:2153272]	E9QLK7		-3.1	3.2E-02	5.2	3.1E-04	-1.7	1.2E-01	-0.7	2.7E-01
ENSMUST00000100479	keratin associated protein 1-4 [Source:MGI Symbol;Acc:MGI:3651229]	Q3V2D6		6.8	6.8E-05	-3.7	2.9E-04	-0.3	3.1E-01	0.2	8.0E-01
ENSMUST00000100484	eukaryotic translation initiation factor 3, subunit D [Source:MGI Symbol;Acc:MGI:1933181]		O70194	-3.3	1.1E-04	7.0	1.1E-04	-0.4	7.0E-01	-0.3	6.2E-01
ENSMUST00000100486	thioredoxin 2 [Source:MGI Symbol;Acc:MGI:1929468]	Q3TUS3		4.4	1.6E-04	6.3	2.3E-04	-0.6	6.0E-01	-0.3	6.0E-01
ENSMUST00000100487	eukaryotic translation initiation factor 2 alpha kinase 1 [Source:MGI Symbol;Acc:MGI:1353448]		Q9Z2R9	-3.6	5.6E-05	9.6	7.8E-05	-0.8	6.3E-01	-0.2	7.1E-01
ENSMUST00000100489	RAS-related C3 botulinum substrate 1 [Source:MGI Symbol;Acc:MGI:97845]	Q3TLP8		-4.6	9.1E-03	-5.0	3.5E-02	1.3	1.6E-01	0.0	9.9E-01
ENSMUST00000098668	carcinoembryonic antigen-related cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1347245]	Q3LFS9		-1.9	4.5E-02	-2.3	1.0E-01	1.1	1.4E-01	1.6	2.3E-01
ENSMUST00000100496	SPRY domain containing 7 [Source:MGI Symbol;Acc:MGI:1913924]	Q3UBW1		-3.3	2.0E-03	6.1	2.2E-02	-1.2	5.9E-01	-1.6	3.1E-01
ENSMUST00000100497	actin, beta [Source:MGI Symbol;Acc:MGI:87904]	B2RRX1	P60710	-8.4	7.0E-07	5.6	1.4E-02	-0.8	7.0E-01	-0.6	5.8E-01
ENSMUST00000100507	eukaryotic translation initiation factor 3, subunit B [Source:MGI Symbol;Acc:MGI:106478]		Q8JZQ9	-2.4	1.1E-03	4.4	2.9E-03	-1.4	2.3E-01	-3.0	8.0E-03
ENSMUST00000100527	poly-U binding splicing factor 60 [Source:MGI Symbol;Acc:MGI:1915209]		Q3UEB3	-4.7	2.4E-03	5.6	2.8E-02	-0.7	7.9E-01	1.4	3.0E-01
ENSMUST00000100528	ubiquitin-conjugating enzyme E2Z (putative) [Source:MGI Symbol;Acc:MGI:1343160]		Q3UE37	-3.2	1.2E-04	-8.0	5.2E-05	1.4	1.6E-03	-0.6	6.1E-01
ENSMUST00000098686	AT rich interactive domain 3B (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1930768]	F8WIN2		-2.8	4.4E-02	0.0	9.7E-01	1.0	2.5E-01	-1.8	2.1E-01
ENSMUST00000100529	NYN domain and retroviral integrase containing [Source:MGI Symbol;Acc:MGI:2652872]		Q5DTZ0	6.8	1.6E-02	-4.6	4.7E-04	-0.1	8.7E-01	-0.1	8.7E-01
ENSMUST00000100534	RIKEN cDNA B130006D01 gene [Source:MGI Symbol;Acc:MGI:2444371]	Q8BRH6		5.5	1.7E-04	6.7	4.6E-04	-1.4	3.3E-01	-1.2	1.1E-01
ENSMUST00000100538	zinc finger CCCH type containing 3 [Source:MGI Symbol;Acc:MGI:2663721]	Q3UUL4	Q8CHP0	-3.1	3.2E-02	-4.7	2.4E-03	1.1	4.6E-02	-0.9	4.8E-01
ENSMUST00000100540	TSC22 domain family, member 4 [Source:MGI Symbol;Acc:MGI:1926079]	Q3U1U6		-5.4	6.6E-04	-3.4	2.0E-01	0.9	4.7E-01	-0.7	7.8E-01
ENSMUST00000100542	lymphocyte antigen 6 complex, locus C2 [Source:MGI Symbol;Acc:MGI:3712069]		P0CW03	-10.0	4.4E-06	6.2	2.6E-04	-1.5	2.2E-01	-0.7	3.1E-01
ENSMUST00000100554	transmembrane protein 92 [Source:MGI Symbol;Acc:MGI:3034723]		B7ZWI3	3.9	6.6E-04	-4.3	6.1E-04	0.0	9.2E-01	-0.8	3.7E-01
ENSMUST00000100572	src-like adaptor [Source:MGI Symbol;Acc:MGI:104295]	Q4FJX0	Q60898	-11.7	7.8E-06	5.7	1.0E-03	0.7	5.9E-01	0.3	7.2E-01
ENSMUST00000100584	HERV-H LTR-associating 1 [Source:MGI Symbol;Acc:MGI:3615329]		Q3TYV2	7.3	3.8E-04	8.3	1.6E-05	-0.5	6.5E-01	-0.9	8.3E-02
ENSMUST00000098763	CTTNBP2 N-terminal like [Source:MGI Symbol;Acc:MGI:1933137]		Q99LJ0	-0.5	7.5E-01	-0.3	8.6E-01	-0.7	6.0E-01	-0.9	6.1E-01
ENSMUST00000100627	tripartite motif-containing 25 [Source:MGI Symbol;Acc:MGI:102749]	Q5SU72		5.4	2.0E-04	7.4	4.8E-05	0.0	9.7E-01	0.1	8.0E-01
ENSMUST00000098773				3.1	6.2E-02	3.1	4.3E-02	-2.5	1.1E-01	-2.5	5.8E-02
ENSMUST00000100638	transmembrane protein 253 [Source:MGI Symbol;Acc:MGI:3588246]		Q3UNB8	6.4	1.5E-04	3.4	1.4E-03	0.7	3.4E-01	0.1	9.1E-01
ENSMUST00000098780	coiled-coil domain containing 61 [Source:MGI Symbol;Acc:MGI:2685005]		Q3UJV1	-0.6	6.2E-01	-0.5	7.4E-01	0.1	9.1E-01	0.1	9.7E-01
ENSMUST00000100645	epididymal protein 3B [Source:MGI Symbol;Acc:MGI:2684921]	Q8K0E4		5.8	1.6E-04	5.8	3.6E-04	0.1	9.1E-01	0.4	5.1E-01
ENSMUST00000100647	CAP-GLY domain containing linker protein 2 [Source:MGI Symbol;Acc:MGI:1313136]		Q9Z0H8	4.2	7.8E-03	2.3	7.5E-03	-1.2	7.7E-02	-0.2	7.0E-01
ENSMUST00000100655	RIKEN cDNA 9130401M01 gene [Source:MGI Symbol;Acc:MGI:1923008]		Q9D2X8	-5.4	1.9E-03	6.7	1.0E-04	-0.5	6.3E-01	-0.4	5.2E-01
ENSMUST00000100659	predicted gene 9920 [Source:MGI Symbol;Acc:MGI:3642228]	D3YXJ2		6.1	1.0E-02	-0.5	4.2E-01	1.2	1.2E-02	0.2	7.1E-01
ENSMUST00000098792	complement component 5a receptor 2 [Source:MGI Symbol;Acc:MGI:2442013]	E9QQ21		1.0	1.9E-01	0.6	6.4E-01	1.5	1.1E-01	2.0	9.2E-02
ENSMUST00000100676	bone morphogenetic protein 4 [Source:MGI Symbol;Acc:MGI:88180]	Q3ULR1	P21275	7.9	1.0E-05	5.1	3.2E-05	-6.6	1.0E-04	-3.6	1.8E-04
ENSMUST00000100694	predicted gene 10376 [Source:MGI Symbol;Acc:MGI:3704432]	D3YXI9		6.9	1.6E-04	0.6	2.4E-01	-4.3	3.3E-05	0.1	8.7E-01
ENSMUST00000100701	tandem duplication of RIKEN cDNA 1700049E17 gene, gene 2 [Source:MGI Symbol;Acc:MGI:3796510]	E9Q430		6.7	9.7E-04	7.4	1.0E-03	0.0	9.8E-01	-1.6	9.7E-02
ENSMUST00000100713	predicted gene 10384 [Source:MGI Symbol;Acc:MGI:3641812]	Q3UQ87		2.3	5.4E-03	7.0	1.8E-04	-0.6	6.5E-01	-1.5	4.9E-02
ENSMUST00000100719	predicted gene 5460 [Source:MGI Symbol;Acc:MGI:3643519]	Q3UQ97		5.7	8.5E-05	-3.1	1.5E-01	2.1	9.3E-02	1.5	4.4E-01
ENSMUST00000098817	vacuolar protein sorting 37A (yeast) [Source:MGI Symbol;Acc:MGI:1261835]		Q8CHS8	1.2	6.8E-02	0.5	5.4E-01	0.6	3.6E-01	1.3	1.2E-01
ENSMUST00000100720	growth differentiation factor 2 [Source:MGI Symbol;Acc:MGI:1321394]		Q9WV56	7.5	2.0E-04	3.5	2.3E-03	-0.7	3.9E-01	-1.0	1.4E-01
ENSMUST00000098825	expressed sequence AI429214 [Source:MGI Symbol;Acc:MGI:2142538]		Q3TTJ4	0.8	2.6E-01	0.5	5.5E-01	-1.1	1.2E-01	-0.8	3.4E-01
ENSMUST00000100721	V-set and transmembrane domain containing 4 [Source:MGI Symbol;Acc:MGI:2444633]	D3YXI4		5.6	9.5E-03	6.6	1.1E-01	-0.9	8.4E-01	1.7	4.7E-01
ENSMUST00000098827	predicted gene 10684 [Source:MGI Symbol;Acc:MGI:3641851]	Q3V379		3.4	3.6E-02	4.0	6.1E-02	-0.2	9.3E-01	-0.8	5.6E-01
ENSMUST00000100722	chaperonin containing Tcp1, subunit 6b (zeta) [Source:MGI Symbol;Acc:MGI:1329013]	B1AT05		5.0	1.3E-02	4.2	3.9E-04	-0.9	2.6E-01	0.2	6.7E-01
ENSMUST00000098842	TELO2 interacting protein 2 [Source:MGI Symbol;Acc:MGI:2384576]		Q8BGV4	0.9	6.8E-02	0.9	1.8E-01	0.6	2.3E-01	0.6	2.9E-01
ENSMUST00000100730	SH3-domain binding protein 5 (BTK-associated) [Source:MGI Symbol;Acc:MGI:1344391]		Q9Z131	6.4	5.2E-03	3.5	6.7E-03	-2.5	5.1E-02	-1.0	1.8E-01
ENSMUST00000100737	purinergic receptor P2X, ligand-gated ion channel, 7 [Source:MGI Symbol;Acc:MGI:1339957]	Q8CHP4	Q9Z1M0	2.2	8.5E-03	6.1	9.9E-04	-0.6	6.5E-01	-0.3	6.5E-01
ENSMUST00000100739	family with sequence similarity 105, member A [Source:MGI Symbol;Acc:MGI:2687281]		Q3TVP5	-3.0	2.7E-03	-3.5	9.4E-03	0.8	1.8E-01	0.4	7.2E-01
ENSMUST00000098849	OTU domain containing 7B [Source:MGI Symbol;Acc:MGI:2654703]		B2RUR8	-1.3	6.7E-01	8.3	9.0E-02	5.5	2.4E-01	-4.2	1.3E-01
ENSMUST00000100755	unc-119 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1328357]	B1AQD7		-8.3	2.6E-05	1.7	1.2E-01	0.1	8.7E-01	0.8	3.9E-01
ENSMUST00000100757	a disintegrin and metalloppeptidase domain 1a [Source:MGI Symbol;Acc:MGI:2429504]	Q3V0H1	Q60813	1.9	1.5E-02	-0.2	7.2E-01	0.9	5.2E-02	-0.8	2.3E-01
ENSMUST00000098853	suppressor of variegation 4-20 homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2385262]		Q6Q783	3.3	1.9E-01	0.4	9.0E-01	-3.7	1.7E-01	-0.7	7.7E-01
ENSMUST00000100763	heat shock protein 12B [Source:MGI Symbol;Acc:MGI:1919880]	H7BX84		5.8	3.0E-04	3.4	5.7E-04	-0.3	6.3E-01	0.0	9.7E-01
ENSMUST00000100764	protein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I) [Source:MGI Symbol;Acc:MGI:23		Q8R087	8.6	1.0E-02	6.5	1.6E-04	-1.5	2.2E-01	-0.5	4.0E-01
ENSMUST00000098866	nology domain-containing, family A (phosphoinositide binding specific) member 2 [Source:MGI Symbol;Acc:M	F8WIK5		0.7	3.9E-01	0.9	3.0E-01	-0.9	2.0E-01	-1.1	1.9E-01
ENSMUST00000098873	GA repeat binding protein, beta 2 [Source:MGI Symbol;Acc:MGI:95612]		P81069	5.6	8.0E-02	3.2	3.4E-01	-2.6	4.1E-01	-0.3	9.2E-01
ENSMUST00000100769	predicted gene 15800 [Source:MGI Symbol;Acc:MGI:3647820]	Q6GQX8		3.4	1.9E-03	9.1	3.6E-04	0.4	8.0E-01	1.5	1.0E-01
ENSMUST00000100770	protein tyrosine phosphatase, non-receptor type 11 [Source:MGI Symbol;Acc:MGI:99511]		P35235	-7.0	7.9E-06	9.0	1.3E-05	-1.4	2.6E-01	-0.6	2.0E-01
ENSMUST00000100775	RAD1 checkpoint DNA exonuclease [Source:MGI Symbol;Acc:MGI:1316678]		Q9QWZ1	4.4	1.7E-05	7.6	4.8E-04	1.5	2.9E-01	1.4	8.0E-02
ENSMUST00000100780	MANSC domain containing 4 [Source:MGI Symbol;Acc:MGI:3645619]		Q3UU94	6.3	1.8E-04	4.3	3.9E-03	-0.1	9.5E-01	-1.1	1.8E-01
ENSMUST00000100785	2'-5' oligoadenylate synthetase 1E [Source:MGI Symbol;Acc:MGI:2180856]	Q8C2W3		5.9	6.3E-05	9.6	6.6E-05	-0.6	6.9E-01	-1.3	5.2E-02
ENSMUST00000100790	NAD kinase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1915896]		Q8C5H8	-4.2	6.0E-04	6.5	9.8E-03	-0.8	7.3E-01	-2.0	1.5E-01
ENSMUST00000100799	ribosomal protein L15 [Source:MGI Symbol;Acc:MGI:1913730]	Q5M8Q0	Q9CZM2	-7.0	4.4E-03	-3.2	1.6E-01	-5.6	1.1E-02	2.6	2.2E-01
ENSMUST00000100806	transmembrane protein 254b [Source:MGI Symbol;Acc:MGI:3710397]	Q9D890		7.6	2.0E-02	-1.6	1.6E-01	1.1	9.7E-02	-0.1	8.9E-01
ENSMUST00000100810	double homeobox B-like 2 [Source:MGI Symbol;Acc:MGI:3710620]	Q7TNE6		6.1	5.8E-03	5.5	4.7E-06	-1.0	9.7E-02	0.1	7.0E-01
ENSMUST00000098924	adenosine deaminase, RNA-specific [Source:MGI Symbol;Acc:MGI:1889575]		Q99MU3	7.3	3.8E-02	6.2	9.2E-02	-0.9	8.1E-01	0.2	9.2E-01
ENSMUST00000100811	transmembrane protein 254a [Source:MGI Symbol;Acc:MGI:1196450]	Q9D890		7.6	2.0E-02	4.9	5.7E-04	0.8	3.9E-01	-1.0	1.4E-01
ENSMUST00000100816	mediator complex subunit 13-like [Source:MGI Symbol;Acc:MGI:2670178]	E9QLJ3		-1.2	9.9E-03	7.2	9.6E-05	-0.6	6.2E-01	-0.7	2.5E-01
ENSMUST00000098937	ECSIT homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1349469]			2.2	3.0E-01	0.7	7.4E-01	-2.2	2.6E-01	-0.7	7.3E-01
ENSMUST00000100841	epidermal growth factor receptor pathway substrate 8 [Source:MGI Symbol;Acc:MGI:104684]		Q08509	-4.1	6.7E-06	4.1	5.5E-05	0.6	2.6E-01	0.4	3.6E-01
ENSMUST00000098948	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 [Source:MGI Symbol;Ac			-2.4	1.1E-01	1.1	5.4E-01	1.1	4.5E-01	-2.4	1.5E-01
ENSMUST00000100844	annexin A7 [Source:MGI Symbol;Acc:MGI:88031]		Q07076	-2.1	5.9E-04	3.2	4.5E-03	-3.5	8.5E-03	-0.2	8.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000100850	RIKEN cDNA 2610524H06 gene [Source:MGI Symbol;Acc:MGI:2447819]	Q9CZU9		3.4	3.3E-05	-1.5	4.6E-02	0.8	6.2E-02	0.5	4.8E-01
ENSMUST00000100857	dual specificity phosphatase 16 [Source:MGI Symbol;Acc:MGI:1917936]	Q6PCP3		-2.7	3.4E-03	3.0	4.2E-03	0.6	3.6E-01	0.1	8.5E-01
ENSMUST00000098970				-2.0	6.3E-02	-4.6	1.8E-02	-0.7	3.7E-01	1.9	2.6E-01
ENSMUST00000098971	regulator of telomere elongation helicase 1 [Source:MGI Symbol;Acc:MGI:2139369]		Q0VGM9	-2.3	1.5E-01	2.9	9.2E-02	1.4	3.2E-01	-3.7	3.1E-02
ENSMUST00000098979	centrosomal protein 295 [Source:MGI Symbol;Acc:MGI:2442521]	E9QPW4		4.7	7.9E-02	0.9	6.3E-01	-5.9	2.6E-02	-2.0	2.6E-01
ENSMUST00000100864	small integral membrane protein 10 like 1 [Source:MGI Symbol;Acc:MGI:1914379]	E9Q3K4		-2.4	3.5E-03	-5.6	2.0E-03	0.3	6.1E-01	-2.5	1.6E-01
ENSMUST00000100866	RIKEN cDNA E130309D14 gene [Source:MGI Symbol;Acc:MGI:3588240]	Q5SUE3		7.6	9.7E-05	-3.8	2.0E-03	0.4	3.5E-01	-1.0	2.9E-01
ENSMUST00000098994	predicted gene 10709 [Source:MGI Symbol;Acc:MGI:3642754]	D3Z1N9		0.6	5.1E-01	0.5	6.6E-01	-0.5	5.3E-01	-0.4	6.9E-01
ENSMUST00000100872	olfactory receptor 31 [Source:MGI Symbol;Acc:MGI:109304]	E9Q3K2		6.4	1.1E-04	3.5	1.5E-05	-0.3	4.8E-01	-0.3	3.6E-01
ENSMUST00000100874	selectin, platelet (p-selectin) ligand [Source:MGI Symbol;Acc:MGI:106689]	Q3TA56		-6.7	8.4E-06	3.9	2.6E-05	-0.5	3.1E-01	-0.5	1.5E-01
ENSMUST00000100882	predicted gene 6588 [Source:MGI Symbol;Acc:MGI:3648937]	E9Q3K0		7.9	1.8E-05	3.9	2.6E-05	-0.5	3.1E-01	-0.5	1.5E-01
ENSMUST00000100924	leucine rich colipase-like 1 [Source:MGI Symbol;Acc:MGI:2686525]		Q3URS3	4.8	6.9E-04	1.9	6.7E-02	-2.7	1.5E-02	-1.6	7.5E-02
ENSMUST00000100926	RIKEN cDNA 4933413G19 gene [Source:MGI Symbol;Acc:MGI:1918399]		Q3TTI8	7.1	3.9E-04	14.2	4.9E-07	1.1	3.3E-01	-0.4	2.2E-01
ENSMUST00000100955	general transcription factor IIH, polypeptide 5 [Source:MGI Symbol;Acc:MGI:107227]		Q8K2X8	-4.0	2.0E-04	14.2	3.1E-07	-0.8	4.8E-01	-0.7	1.2E-01
ENSMUST00000100968	vomeronasal 2, receptor27 [Source:MGI Symbol;Acc:MGI:3761517]	D3YUK6		6.8	8.9E-05	14.7	2.6E-06	-0.7	6.6E-01	-0.7	2.2E-01
ENSMUST00000100986	extended synaptotagmin-like protein 2 [Source:MGI Symbol;Acc:MGI:1261845]		Q3TZZ7	-2.7	1.7E-04	15.3	1.3E-08	0.4	6.6E-01	-0.3	3.4E-01
ENSMUST00000101015	predicted gene 3259 [Source:MGI Symbol;Acc:MGI:3781437]	D3YUK0		7.3	2.6E-05	15.0	1.4E-06	1.6	2.6E-01	-1.1	1.1E-02
ENSMUST00000101017	nuclear distribution gene E-like homolog 1 (A. nidulans) [Source:MGI Symbol;Acc:MGI:1932915]		Q9ERR1	-1.9	1.5E-02	12.8	2.5E-06	-0.4	7.9E-01	-0.9	3.4E-02
ENSMUST00000101023	predicted gene, Gm16513 [Source:MGI Symbol;Acc:MGI:2141041]	D3YUJ6		7.5	8.7E-05	14.3	1.1E-06	-0.2	8.9E-01	-0.4	2.4E-01
ENSMUST00000101044	ATPase, Ca++ transporting, plasma membrane 2 [Source:MGI Symbol;Acc:MGI:105368]	F8WHB1		5.3	2.6E-02	6.8	1.3E-04	-0.5	6.7E-01	-0.3	5.9E-01
ENSMUST00000101045	ATPase, Ca++ transporting, plasma membrane 2 [Source:MGI Symbol;Acc:MGI:105368]	Q3UHJ3	Q9R0K7	7.7	1.4E-02	6.1	3.0E-04	0.2	8.1E-01	-0.4	4.8E-01
ENSMUST00000101055	cyclin K [Source:MGI Symbol;Acc:MGI:1276106]	Q3U3M5		-1.8	2.9E-02	5.2	4.8E-05	-1.2	1.1E-01	-0.5	2.8E-01
ENSMUST00000099067				5.6	5.1E-02	4.8	1.2E-01	0.0	1.0E+00	0.8	7.0E-01
ENSMUST00000101057	casein alpha s2-like B [Source:MGI Symbol;Acc:MGI:105312]	Q8CEJ6		7.8	1.0E-03	5.4	1.2E-03	-1.9	1.7E-01	0.7	3.6E-01
ENSMUST00000099071	molybdenum cofactor synthesis 3 [Source:MGI Symbol;Acc:MGI:1916622]		A2BDX3	-1.4	5.2E-02	0.0	9.6E-01	0.7	2.5E-01	-0.7	3.6E-01
ENSMUST00000101059	proline-rich transmembrane protein 3 [Source:MGI Symbol;Acc:MGI:2444810]		Q6PE13	7.1	7.6E-05	-4.2	1.1E-02	0.3	6.7E-01	-1.1	4.5E-01
ENSMUST00000099073	family with sequence similarity 65, member C [Source:MGI Symbol;Acc:MGI:1916803]		A1L3T7	6.0	1.2E-01	5.3	1.8E-01	-0.9	8.2E-01	-0.3	9.0E-01
ENSMUST00000101065	interleukin 17 receptor E [Source:MGI Symbol;Acc:MGI:1889371]		Q8BH06	7.3	1.6E-03	-0.3	5.2E-01	0.9	1.7E-02	0.1	9.1E-01
ENSMUST00000099080	osphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1 [Source:MGI Symbol;Acc:MGI:30406	I7HPV9		4.5	8.9E-02	10.3	2.2E-02	5.9	1.2E-01	0.1	9.6E-01
ENSMUST00000099084	zinc finger, MYND-type containing 8 [Source:MGI Symbol;Acc:MGI:1918025]	A2A482		0.8	5.2E-01	0.4	8.5E-01	0.5	7.3E-01	1.0	5.3E-01
ENSMUST00000101066	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	Q5RIM6		-3.6	2.0E-02	-7.9	5.4E-05	-0.7	5.3E-02	0.3	8.1E-01
ENSMUST00000099090	TSC22 domain family, member 2 [Source:MGI Symbol;Acc:MGI:1919283]	E9Q7M2		-0.2	6.7E-01	0.8	1.4E-01	0.7	8.7E-02	-0.2	6.1E-01
ENSMUST00000101067	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	E9Q2B2		-4.7	1.4E-03	4.9	3.1E-03	-0.5	6.5E-01	1.1	2.5E-01
ENSMUST00000101070	jagunal homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1915017]		Q5XKN4	-1.6	1.8E-02	2.5	1.9E-03	0.2	6.6E-01	-0.6	2.1E-01
ENSMUST00000101071	T cell lymphoma breakpoint 1 [Source:MGI Symbol;Acc:MGI:1097166]	Q3UES7		6.9	3.1E-04	6.9	1.4E-03	-0.3	8.8E-01	-0.4	6.1E-01
ENSMUST00000101073	transmembrane protease, serine 11a [Source:MGI Symbol;Acc:MGI:2684853]		Q3UQ41	5.6	8.5E-04	6.1	2.4E-04	-0.5	6.6E-01	-0.7	2.7E-01
ENSMUST00000101080	serine (or cysteine) peptidase inhibitor, clade A, member 3F [Source:MGI Symbol;Acc:MGI:2182838]		Q80X76	6.5	1.1E-03	-7.2	2.5E-05	0.4	2.2E-01	-1.0	3.5E-01
ENSMUST00000101087	signal recognition particle 72 [Source:MGI Symbol;Acc:MGI:1333795]	F8VQC1		-7.5	1.4E-05	5.8	4.8E-03	0.1	9.6E-01	-1.8	9.3E-02
ENSMUST00000101094	OTU domain, ubiquitin aldehyde binding 2 [Source:MGI Symbol;Acc:MGI:1915399]	D3Z0Y8		7.1	1.3E-03	4.2	5.9E-04	-1.7	6.2E-02	-0.5	4.3E-01
ENSMUST00000099113	signal-regulatory protein alpha [Source:MGI Symbol;Acc:MGI:108563]	E9QPT7		-6.2	1.2E-01	-4.5	3.4E-01	1.2	5.9E-01	-0.4	9.3E-01
ENSMUST00000101095	cytidine 5'-triphosphate synthase 2 [Source:MGI Symbol;Acc:MGI:1933185]		P70303	-8.0	3.8E-06	6.6	1.1E-04	0.3	7.5E-01	0.1	8.0E-01
ENSMUST00000101099	unc-79 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2684729]		Q0KK59	8.9	2.5E-05	0.6	5.3E-01	-1.3	9.3E-02	0.9	2.8E-01
ENSMUST00000101114	Ras and Rab interactor 3 [Source:MGI Symbol;Acc:MGI:2385708]	Q3UZ87		-2.4	1.3E-03	3.2	1.2E-01	-2.4	2.7E-01	1.9	1.8E-01
ENSMUST00000099131	d, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 [Source:MGI Symbol;Acc	Q3UID0		-1.0	6.0E-01	0.6	7.4E-01	-1.4	3.8E-01	-2.9	1.5E-01
ENSMUST00000101118	RING1 and YY1 binding protein [Source:MGI Symbol;Acc:MGI:1929059]		Q8CCI5	-3.0	2.1E-03	5.7	2.7E-02	-0.7	7.8E-01	1.6	2.3E-01
ENSMUST00000101120	prokineticin 2 [Source:MGI Symbol;Acc:MGI:1354178]		Q9QXU7	-7.5	7.4E-05	1.5	7.9E-02	-6.3	2.1E-04	1.0	1.4E-01
ENSMUST00000099141	RIKEN cDNA 4930518I15 gene [Source:MGI Symbol;Acc:MGI:1921954]	Q3V2W7		1.8	3.6E-02	2.6	1.5E-02	0.0	9.5E-01	-0.8	2.9E-01
ENSMUST00000101127	furry homolog-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1919563]	F8VQ05		-2.1	2.5E-02	-0.2	8.6E-01	1.0	1.3E-01	-0.6	5.3E-01
ENSMUST00000099147	predicted gene 7120 [Source:MGI Symbol;Acc:MGI:3648543]	H3BJ86		2.7	6.3E-02	3.8	7.6E-02	1.9	3.1E-01	0.7	5.8E-01
ENSMUST00000101146	spermatogenesis associated 7 [Source:MGI Symbol;Acc:MGI:2144877]	Q3TTL3		5.6	7.6E-03	9.2	3.7E-03	0.2	9.3E-01	0.9	4.6E-01
ENSMUST00000101148	NLR family, pyrin domain containing 3 [Source:MGI Symbol;Acc:MGI:2653833]		Q8R4B8	-5.5	2.2E-03	-0.7	5.5E-01	0.6	4.9E-01	-2.3	1.1E-01
ENSMUST00000101151	IQ motif and Sec7 domain 1 [Source:MGI Symbol;Acc:MGI:1196356]	E9PUA3		-4.1	6.5E-05	6.4	3.4E-04	-0.6	6.3E-01	-0.3	6.3E-01
ENSMUST00000101197	Rho GTPase activating protein 25 [Source:MGI Symbol;Acc:MGI:2443687]		Q8BYW1	-9.7	2.9E-05	-2.3	1.4E-02	-0.3	5.6E-01	0.4	6.3E-01
ENSMUST00000101198	transmembrane protein 164 [Source:MGI Symbol;Acc:MGI:2148020]	A2AH99		-7.0	7.1E-05	2.2	1.2E-01	-1.7	1.8E-01	0.0	9.9E-01
ENSMUST00000101205	collagen, type IV, alpha 6 [Source:MGI Symbol;Acc:MGI:2152695]	B1AVK5		7.9	3.4E-05	7.1	7.0E-05	-0.5	6.6E-01	-0.3	6.2E-01
ENSMUST00000101208	superoxide dismutase 3, extracellular [Source:MGI Symbol;Acc:MGI:103181]	Q542X9	O09164	8.4	6.1E-06	4.8	4.7E-04	-2.7	2.3E-02	0.8	1.7E-01
ENSMUST00000099166	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4 [Source:MGI Symbol;Acc:MGI:102670]	Q3V086		3.5	1.8E-01	3.4	2.5E-01	-0.2	9.4E-01	-0.1	9.4E-01
ENSMUST00000101217	ripply1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:3614797]		Q2WG77	4.0	7.3E-04	6.0	7.9E-05	-1.2	2.2E-01	-0.1	8.6E-01
ENSMUST00000101225	presenilin 1 [Source:MGI Symbol;Acc:MGI:1202717]	Q3UYK2	P49769	-4.3	5.1E-05	-3.8	2.5E-02	-2.1	3.6E-02	-2.7	1.5E-01
ENSMUST00000101237	bone marrow stromal cell antigen 1 [Source:MGI Symbol;Acc:MGI:105370]			-9.4	5.9E-06	3.8	5.3E-03	-0.2	8.2E-01	-0.6	4.8E-01
ENSMUST00000101270	TBC1 domain family, member 9B [Source:MGI Symbol;Acc:MGI:1924045]		Q5SVR0	-1.6	3.2E-02	2.4	7.4E-03	0.5	4.3E-01	-0.1	8.2E-01
ENSMUST00000101281	predicted gene 10451 [Source:MGI Symbol;Acc:MGI:3641898]	Q3UW49		3.5	1.6E-03	1.0	8.9E-02	-0.8	1.1E-01	0.2	7.1E-01
ENSMUST00000101293	mannoside acetylglucosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI:96973]	Q544F0	P27808	-5.7	2.2E-03	7.5	3.3E-04	-0.7	6.3E-01	-0.2	7.7E-01
ENSMUST00000099201	signal-regulatory protein beta 1A [Source:MGI Symbol;Acc:MGI:2444824]	A0A0A6YYP6		-5.7	1.3E-01	2.3	6.6E-01	6.0	1.7E-01	-2.0	6.4E-01
ENSMUST00000101294	G protein-coupled receptor 174 [Source:MGI Symbol;Acc:MGI:2685222]		Q3U507	5.4	1.1E-05	8.8	1.2E-05	-0.5	6.3E-01	-1.7	7.5E-03
ENSMUST00000101295	RIKEN cDNA 9930111J21 gene 2 [Source:MGI Symbol;Acc:MGI:3711310]	Q5SVP2		5.1	2.6E-05	4.7	1.5E-04	0.2	8.2E-01	0.0	9.9E-01
ENSMUST00000101306	IL2 inducible T cell kinase [Source:MGI Symbol;Acc:MGI:96621]	Q5STT7		4.1	1.8E-03	-2.9	7.0E-04	0.5	1.1E-01	-0.2	7.7E-01
ENSMUST00000101316	SH3-domain binding protein 2 [Source:MGI Symbol;Acc:MGI:1346349]	Q3UD40		-7.7	1.5E-04	8.1	3.5E-06	0.2	7.8E-01	-0.4	2.8E-01
ENSMUST00000101327	ring finger protein 145 [Source:MGI Symbol;Acc:MGI:1921565]	Q8BU61		2.5	2.1E-03	6.5	2.2E-04	-0.6	6.4E-01	0.6	3.2E-01
ENSMUST00000101341	l RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:133(	D3YZK4		5.4	1.2E-02	6.5	2.1E-04	-0.5	6.5E-01	-0.4	5.1E-01
ENSMUST00000099262	e prime 1, subunit of RNA polymerase III transcription initiation factor IIIB [Source:MGI Symbol;Acc:MGI:1:	F8VQC2		-2.7	5.9E-02	-5.0	6.1E-02	-0.4	7.0E-01	1.8	4.5E-01
ENSMUST00000101347	methionine adenosyltransferase II, beta [Source:MGI Symbol;Acc:MGI:1913667]		Q99LB6	-4.8	3.9E-05	5.2	9.7E-04	-0.5	6.4E-01	-0.9	2.2E-01
ENSMUST00000101351	atonal homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:104654]		P48985	7.1	1.3E-03	2.5	1.6E-02	-1.3	1.2E-01	0.0	9.5E-01
ENSMUST00000101354	stem-loop binding protein [Source:MGI Symbol;Acc:MGI:108402]	Q8K2W7		-5.9	3.2E-05	5.3	9.7E-04	-1.6	1.8E-01	-0.3	7.1E-01
ENSMUST00000099269	CD93 antigen [Source:MGI Symbol;Acc:MGI:106664]		O89103	0.2	6.4E-01	0.3	5.7E-01	-0.1	8.8E-01	-0.2	7.3E-01
ENSMUST00000099270	thrombomodulin [Source:MGI Symbol;Acc:MGI:98736]	Q543W3	P15306	0.9	1.9E-01	1.1	2.3E-01	-0.3	6.2E-01	-0.4	5.6E-01
ENSMUST00000099272	ribosomal protein L21 [Source:MGI Symbol;Acc:MGI:1278340]	Q9CQM8		-1.3	2.8E-01	-4.1	7.0E-02	-0.9	3.9E-01	1.9	3.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000101365	dedicator of cyto-kinesis 2 [Source:MGI Symbol;Acc:MGI:2149010]	Q5SRI3		5.8	1.3E-02	-1.7	1.3E-02	1.3	4.3E-03	0.3	6.2E-01
ENSMUST00000101367	5'-nucleotidase, cytosolic III [Source:MGI Symbol;Acc:MGI:1927186]		Q9D020	-9.5	2.7E-05	-1.7	7.8E-02	1.4	2.7E-02	-0.8	4.0E-01
ENSMUST00000101368	Kv channel-interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917607]		Q9JJ57	7.0	4.1E-03	-4.0	1.5E-03	-0.5	2.9E-01	-0.6	5.0E-01
ENSMUST00000101371	RIKEN cDNA D130052B06 gene [Source:MGI Symbol;Acc:MGI:2685092]	Q3UW13		4.6	1.3E-03	1.3	4.3E-01	-3.5	6.1E-02	2.0	1.3E-01
ENSMUST00000099295	POC5 centriolar protein homolog (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1914713]		Q9DBS8	-0.6	3.5E-01	0.2	8.3E-01	0.2	7.4E-01	-0.6	4.5E-01
ENSMUST00000101375	nucleophosmin 1 [Source:MGI Symbol;Acc:MGI:106184]	Q5SQB5		-6.6	1.1E-03	6.9	3.1E-04	-0.7	6.1E-01	-1.5	7.3E-02
ENSMUST00000101376	phospholipase B1 [Source:MGI Symbol;Acc:MGI:1922406]		Q3TTY0	7.4	2.1E-05	2.3	8.1E-02	-3.9	1.4E-02	-0.5	6.3E-01
ENSMUST00000099311	SLX4 interacting protein [Source:MGI Symbol;Acc:MGI:1921493]		Q9D7Y9	-1.3	2.3E-01	-2.9	1.4E-01	0.8	4.0E-01	2.5	1.8E-01
ENSMUST00000101394	ChaC, cation transport regulator 2 [Source:MGI Symbol;Acc:MGI:1915294]		Q9CQG1	-3.4	1.5E-02	-3.1	9.6E-05	0.1	6.1E-01	-0.4	3.9E-01
ENSMUST00000101395	homeobox A4 [Source:MGI Symbol;Acc:MGI:96176]			4.8	5.3E-04	-1.9	3.9E-03	1.1	4.7E-03	-0.2	6.6E-01
ENSMUST00000101426	transmembrane protein 176A [Source:MGI Symbol;Acc:MGI:1913308]		Q9DCS1	-2.9	8.7E-04	6.1	1.8E-03	-0.4	7.8E-01	-1.0	2.4E-01
ENSMUST00000101429	transmembrane protein 176B [Source:MGI Symbol;Acc:MGI:1916348]		Q9R1Q6	-5.6	7.4E-04	5.4	1.2E-03	1.3	2.7E-01	-0.7	3.1E-01
ENSMUST00000101432	neuronal PAS domain protein 3 [Source:MGI Symbol;Acc:MGI:1351610]	F8VQB2		9.4	2.0E-05	-4.9	5.2E-04	-0.6	1.8E-01	-0.9	3.7E-01
ENSMUST00000101442	dihydropyrimidinase-like 5 [Source:MGI Symbol;Acc:MGI:1929772]	Q3SYJ1		6.0	4.3E-04	-2.8	2.7E-02	2.7	8.5E-04	0.0	9.8E-01
ENSMUST00000101445	zinc finger protein 956 [Source:MGI Symbol;Acc:MGI:2141515]	Q3UZY6		6.1	1.2E-02	-7.5	1.1E-03	-0.2	7.6E-01	1.9	2.7E-01
ENSMUST00000101448	dynein regulatory complex subunit 1 [Source:MGI Symbol;Acc:MGI:2685906]		Q3USS3	4.7	4.6E-05	5.2	8.5E-04	-0.6	6.3E-01	-3.0	5.5E-03
ENSMUST00000099368	ankyrin repeat and sterile alpha motif domain containing 1B [Source:MGI Symbol;Acc:MGI:1924781]	K4DI73		4.1	1.8E-01	4.5	1.8E-01	-0.2	9.4E-01	-0.7	7.5E-01
ENSMUST00000101454	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]	B7FAU9		-11.6	2.2E-04	-6.5	1.6E-03	-0.8	2.1E-01	0.1	9.5E-01
ENSMUST00000101472	ADP-ribosylation factor-like 4A [Source:MGI Symbol;Acc:MGI:99437]		P61213	-3.2	1.3E-03	2.6	4.1E-01	7.8	6.6E-03	1.8	4.6E-01
ENSMUST00000099374	growth arrest-specific 2 like 3 [Source:MGI Symbol;Acc:MGI:1918780]			0.8	6.4E-01	2.8	1.7E-01	0.0	9.9E-01	-2.0	2.4E-01
ENSMUST00000099376	WW domain binding protein 1 like [Source:MGI Symbol;Acc:MGI:107577]		Q8BGW2	-4.8	5.4E-02	-4.5	1.9E-01	1.3	5.4E-01	1.0	7.5E-01
ENSMUST00000101491	C-type lectin domain family 5, member a [Source:MGI Symbol;Acc:MGI:1345151]		Q9R007	-3.3	7.5E-05	-2.9	5.1E-03	-0.3	5.2E-01	0.1	8.8E-01
ENSMUST00000099385	predicted gene 10762 [Source:MGI Symbol;Acc:MGI:3704209]	Q9CZN6		0.9	1.8E-01	1.8	4.0E-02	0.0	9.9E-01	-0.9	1.9E-01
ENSMUST00000101492	RIKEN cDNA E330009J07 gene [Source:MGI Symbol;Acc:MGI:2444256]		Q3UHG7	-2.3	7.5E-04	5.7	1.7E-02	-0.5	8.0E-01	-2.0	1.6E-01
ENSMUST00000099393	Hermansky-Pudlak syndrome 6 [Source:MGI Symbol;Acc:MGI:2181763]		Q8BLY7	0.3	6.3E-01	1.4	8.8E-02	1.2	6.1E-02	0.1	9.0E-01
ENSMUST00000101497	Braf transforming gene [Source:MGI Symbol;Acc:MGI:88190]	F6SZ47		-3.3	8.2E-03	2.2	8.9E-03	0.8	1.4E-01	0.6	2.8E-01
ENSMUST00000101506	cDNA sequence BC023829 [Source:MGI Symbol;Acc:MGI:2448555]	Q3TYW3		-1.9	2.5E-03	6.7	1.6E-04	-0.5	6.6E-01	0.1	8.5E-01
ENSMUST00000101525	uridine phosphorylase 1 [Source:MGI Symbol;Acc:MGI:1097668]	Q5SUC8	P52624	-10.3	5.8E-06	6.4	1.5E-04	-0.5	6.3E-01	0.0	9.8E-01
ENSMUST00000101526	PHD finger protein 23 [Source:MGI Symbol;Acc:MGI:1925496]		Q8BSN5	-5.5	4.0E-04	6.4	4.4E-04	-0.5	7.2E-01	-0.6	4.0E-01
ENSMUST00000101532	diacylglycerol kinase, iota [Source:MGI Symbol;Acc:MGI:2443430]	D3YWQ0		7.1	6.6E-05	-6.3	1.1E-03	-0.5	3.3E-01	0.1	9.5E-01
ENSMUST00000101534	pleiotrophin [Source:MGI Symbol;Acc:MGI:97804]		P63089	9.4	2.6E-05	7.3	1.2E-04	0.9	4.6E-01	-0.6	3.4E-01
ENSMUST00000101538	RIKEN cDNA 9030624G23 gene [Source:MGI Symbol;Acc:MGI:1914058]	Q9D308		3.8	3.2E-03	7.4	1.2E-04	-0.6	6.1E-01	0.1	9.2E-01
ENSMUST00000101558	mbrane associated guanylate kinase, WW and PDZ domain containing 2 [Source:MGI Symbol;Acc:MGI:13549		Q9WVQ1	6.2	7.8E-05	6.8	2.6E-04	-0.5	7.0E-01	-1.2	1.1E-01
ENSMUST00000101560	zinc finger protein 449 [Source:MGI Symbol;Acc:MGI:1925869]	Q8CB76		7.4	1.2E-04	-2.7	6.4E-03	0.3	5.1E-01	-0.5	5.1E-01
ENSMUST00000101564	leucine-rich repeats and guanylate kinase domain containing [Source:MGI Symbol;Acc:MGI:1921604]	Q8BR18		6.0	3.0E-04	4.9	6.8E-04	-0.7	5.1E-01	0.8	2.6E-01
ENSMUST00000101582	predicted gene 3944 [Source:MGI Symbol;Acc:MGI:3782118]	L7N237		6.4	8.8E-04	-5.0	1.1E-02	1.0	1.4E-01	-1.7	3.7E-01
ENSMUST00000101587	PHD finger protein 6 [Source:MGI Symbol;Acc:MGI:1918248]	E9QAG2		10.7	5.3E-06	1.6	1.3E-01	0.1	9.1E-01	0.8	3.5E-01
ENSMUST00000099454	expressed sequence AI606181 [Source:MGI Symbol;Acc:MGI:2147586]	Q8C7B9		-0.1	9.4E-01	1.3	2.1E-01	0.7	3.6E-01	-0.6	4.7E-01
ENSMUST00000101589	Kruppel-like factor 14 [Source:MGI Symbol;Acc:MGI:3577024]		Q19A41	8.5	1.7E-05	0.9	8.0E-01	-3.1	3.0E-01	3.5	2.4E-01
ENSMUST00000101626	coiled-coil domain containing 157 [Source:MGI Symbol;Acc:MGI:3041210]		Q5SPX1	7.1	9.2E-05	10.5	4.9E-04	0.0	9.9E-01	0.9	3.5E-01
ENSMUST00000101638	LIM motif-containing protein kinase 2 [Source:MGI Symbol;Acc:MGI:1197517]		O54785	-3.8	1.3E-02	8.8	1.7E-05	0.0	9.9E-01	-0.2	7.1E-01
ENSMUST00000099462	guanine nucleotide binding protein (G protein), gamma 7 [Source:MGI Symbol;Acc:MGI:95787]	G3X9Q2		3.3	2.0E-01	5.2	6.6E-02	-0.5	8.6E-01	-2.4	2.0E-01
ENSMUST00000101670	WD repeat domain 44 [Source:MGI Symbol;Acc:MGI:1919654]		Q6NVE8	-6.1	5.2E-04	-3.1	1.3E-02	1.6	1.2E-02	-1.9	1.4E-01
ENSMUST00000099467	sorbin and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:700014]	D3Z5J3		1.0	9.0E-02	2.0	1.8E-02	0.7	2.4E-01	-0.3	6.4E-01
ENSMUST00000101800	methionine sulfoxide reductase B1 [Source:MGI Symbol;Acc:MGI:1351642]		Q9JLC3	-6.8	2.8E-07	-7.7	7.4E-04	0.5	3.6E-01	0.1	9.5E-01
ENSMUST00000099479	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 [Source:MGI Symbol;Acc:MGI:1920895]	F8WHR6		-1.2	5.3E-01	2.3	3.7E-01	1.2	5.9E-01	-2.3	2.6E-01
ENSMUST00000099482	G protein-coupled receptor kinase 6 [Source:MGI Symbol;Acc:MGI:1347078]	Q9EP84		-1.6	8.6E-02	-2.8	8.0E-02	0.7	3.7E-01	1.8	2.1E-01
ENSMUST00000099484	zinc finger protein 932 [Source:MGI Symbol;Acc:MGI:1916754]	Q8BJ78		4.6	8.1E-02	1.0	6.0E-01	-4.4	8.3E-02	-0.8	6.4E-01
ENSMUST00000099486	leucine carboxyl methyltransferase 2 [Source:MGI Symbol;Acc:MGI:1353659]	A2ARU0		0.0	9.6E-01	0.9	2.7E-01	1.2	5.8E-02	0.4	5.8E-01
ENSMUST00000099489	cyclin D-type binding-protein 1 [Source:MGI Symbol;Acc:MGI:109595]		Q3TVC7	-1.5	1.3E-01	-2.5	8.1E-02	-0.7	3.6E-01	0.2	8.8E-01
ENSMUST00000101801	VCP-interacting membrane protein [Source:MGI Symbol;Acc:MGI:95994]		Q9BCZ4	-4.3	2.0E-05	-1.0	1.1E-01	0.5	1.9E-01	0.0	9.7E-01
ENSMUST00000102476	beta-2 microglobulin [Source:MGI Symbol;Acc:MGI:88127]		P01887	-9.3	2.8E-08	-8.7	1.7E-02	1.3	1.4E-01	3.5	2.7E-01
ENSMUST00000102478	aldolase C, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:101863]		P05063	-3.3	2.8E-02	-1.4	4.0E-02	0.4	2.7E-01	-0.3	6.5E-01
ENSMUST00000102483	ribosomal protein L23A [Source:MGI Symbol;Acc:MGI:3040672]	Q5M9M5	P62751	-7.0	1.2E-05	-5.3	5.3E-03	-0.1	9.4E-01	-0.4	8.1E-01
ENSMUST00000102484	DNA-damage inducible protein 2 [Source:MGI Symbol;Acc:MGI:1917244]		A2ADY9	-4.3	4.1E-05	6.8	7.0E-05	-1.1	3.3E-01	-1.8	1.0E-02
ENSMUST00000099498	coiled-coil domain containing 80 [Source:MGI Symbol;Acc:MGI:1915146]		Q8R2G6	-2.6	1.9E-01	-2.3	1.9E-01	-2.3	9.0E-02	-2.6	2.0E-01
ENSMUST00000102486	heat shock protein family, member 7 (cardiovascular) [Source:MGI Symbol;Acc:MGI:1352494]		P35385	9.5	5.6E-06	-6.3	3.0E-03	1.0	1.3E-01	1.9	2.7E-01
ENSMUST00000099502	bromodomain and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:1890651]		Q921C3	-0.7	7.9E-01	5.2	1.9E-01	4.7	2.0E-01	-1.3	6.3E-01
ENSMUST00000102487	SUZ RNA binding domain containing 1 [Source:MGI Symbol;Acc:MGI:1098672]		Q6NXN1	-7.8	2.8E-04	4.0	3.6E-03	-2.4	5.9E-02	0.9	2.0E-01
ENSMUST00000102490	erythrocyte membrane protein band 4.2 [Source:MGI Symbol;Acc:MGI:95402]		P49222	9.1	3.2E-06	8.2	9.3E-05	-0.7	6.3E-01	-0.3	6.8E-01
ENSMUST00000102493	coronin 6 [Source:MGI Symbol;Acc:MGI:2183448]		Q920M5	6.8	1.2E-03	6.0	9.3E-04	-0.4	7.6E-01	-0.5	5.0E-01
ENSMUST00000102496	leucine rich repeat containing 57 [Source:MGI Symbol;Acc:MGI:1913856]	Q8JZX5		-6.4	1.7E-02	3.4	2.3E-04	-0.4	5.1E-01	0.0	9.7E-01
ENSMUST00000099513	hyperpolarization-activated, cyclic nucleotide-gated K+ 2 [Source:MGI Symbol;Acc:MGI:1298210]		O88703	3.1	2.7E-01	2.9	3.0E-01	-0.5	8.5E-01	-0.3	8.8E-01
ENSMUST00000102497	leucine rich repeat containing 57 [Source:MGI Symbol;Acc:MGI:1913856]	Q8JZX5		-3.1	3.1E-04	-7.4	1.3E-04	0.8	4.9E-02	0.2	9.1E-01
ENSMUST00000102499	leucine rich repeat containing 57 [Source:MGI Symbol;Acc:MGI:1913856]	Q8JZX5		-3.7	1.4E-02	9.2	1.2E-04	-0.8	6.2E-01	0.0	9.9E-01
ENSMUST00000102500	gem (nuclear organelle) associated protein 4 [Source:MGI Symbol;Acc:MGI:2449313]	Q6P6L6		7.9	1.6E-05	8.6	1.0E-04	-0.8	6.1E-01	0.4	5.0E-01
ENSMUST00000102503	mRNA turnover 4, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1917152]	A2AMU9	Q9D0I8	-3.3	4.9E-03	-1.4	9.1E-02	0.4	4.2E-01	0.2	7.9E-01
ENSMUST00000102507	capping protein (actin filament) muscle Z-line, beta [Source:MGI Symbol;Acc:MGI:104652]		P47757	-5.7	2.2E-04	-0.6	5.0E-01	-0.9	1.9E-01	-3.6	9.8E-03
ENSMUST00000102508	capping protein (actin filament) muscle Z-line, beta [Source:MGI Symbol;Acc:MGI:104652]	Q923G3	P47757	-10.0	2.3E-06	-2.1	1.4E-01	0.8	3.1E-01	-1.6	2.6E-01
ENSMUST00000099546	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14 [Source:MGI Symbol;Acc:MGI:1919386]		Q80V53	-2.1	1.3E-01	3.7	5.4E-02	2.8	9.2E-02	-3.0	4.7E-02
ENSMUST00000102509	phosphatidylinositol transfer protein, alpha [Source:MGI Symbol;Acc:MGI:99887]	F8WGG5		-3.8	7.1E-03	-1.9	5.0E-02	1.0	7.4E-02	-0.2	8.1E-01
ENSMUST00000102510	pre-mRNA processing factor 8 [Source:MGI Symbol;Acc:MGI:2179381]		Q99PV0	-3.2	2.5E-03	6.3	1.6E-03	-0.7	6.7E-01	0.0	1.0E+00
ENSMUST00000102513	phospholipase A2, group V [Source:MGI Symbol;Acc:MGI:101899]	Q6GTW1		5.6	1.9E-02	-6.6	1.1E-03	0.0	9.7E-01	0.3	8.5E-01
ENSMUST00000102514	reticulon 4 receptor-like 1 [Source:MGI Symbol;Acc:MGI:2661375]		Q8K0S5	5.7	7.7E-06	-2.3	3.3E-02	0.6	2.9E-01	-0.3	7.3E-01
ENSMUST00000102515	protein kinase, cAMP dependent, catalytic, beta [Source:MGI Symbol;Acc:MGI:97594]		P68181	-3.6	1.3E-02	6.9	6.0E-04	-0.5	7.5E-01	1.0	1.8E-01
ENSMUST00000102517	delta-like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1859388]		Q9JI71	8.7	1.3E-05	4.1	8.9E-05	-1.4	3.8E-02	-0.3	4.6E-01
ENSMUST00000099560	protein prenyltransferase alpha subunit repeat containing 1 [Source:MGI Symbol;Acc:MGI:1921875]	E9QAB6		1.0	9.9E-02	1.3	9.2E-02	0.0	1.0E+00	-0.3	6.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102518	endothelin converting enzyme 1 [Source:MGI Symbol;Acc:MGI:1101357]		Q4PZA2	3.1	1.1E-03	8.5	8.8E-05	-0.7	6.1E-01	-0.7	3.1E-01
ENSMUST00000099572	protein arginine N-methyltransferase 2 [Source:MGI Symbol;Acc:MGI:1316652]	Q3UID4		2.6	1.6E-01	4.7	9.3E-02	2.4	3.3E-01	0.3	8.4E-01
ENSMUST00000102519	zinc finger, FYVE domain containing 19 [Source:MGI Symbol;Acc:MGI:1919258]	Q4KL52		-5.6	7.2E-05	8.0	3.0E-04	-2.0	2.6E-01	-0.6	3.5E-01
ENSMUST00000102520	platelet-activating factor acetylhydrolase, isoform 1b, subunit 1 [Source:MGI Symbol;Acc:MGI:109520]	Q5SW18	P63005	-3.3	4.7E-04	3.6	1.3E-03	-0.3	6.7E-01	0.1	8.2E-01
ENSMUST00000102522	chymotrypsin-like elastase family, member 3B [Source:MGI Symbol;Acc:MGI:1915118]		Q9CQ52	5.7	2.1E-03	7.6	2.0E-04	0.4	7.8E-01	-0.8	2.7E-01
ENSMUST00000099582	phenylalanine-tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1917205]	G3X9Q4		3.8	5.9E-02	5.2	5.1E-02	1.0	6.7E-01	-0.4	7.8E-01
ENSMUST00000102524	phospholipase C, beta 2 [Source:MGI Symbol;Acc:MGI:107465]		A3KGF7	-3.0	1.8E-03	6.7	5.2E-04	-0.7	6.2E-01	0.0	9.9E-01
ENSMUST00000102525	actin related protein 2/3 complex, subunit 3 [Source:MGI Symbol;Acc:MGI:1928375]		Q9JM76	-10.8	5.7E-05	5.8	7.0E-04	-0.6	6.3E-01	0.6	3.6E-01
ENSMUST00000102526	transient receptor potential cation channel, subfamily V, member 1 [Source:MGI Symbol;Acc:MGI:1341787]		Q704Y3	6.6	3.3E-04	7.4	7.1E-05	-0.5	6.9E-01	-0.9	1.6E-01
ENSMUST00000102528	protein phosphatase 1, catalytic subunit, gamma isoform [Source:MGI Symbol;Acc:MGI:104872]	Q6ZWM8	P63087	-6.1	1.3E-03	7.6	4.2E-05	-0.6	6.0E-01	-1.6	1.9E-02
ENSMUST00000099636				1.6	3.9E-02	2.3	2.0E-02	1.0	1.8E-01	0.2	7.3E-01
ENSMUST00000102529	ain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B [Source:MGI Symbol;Acc:M(	M9MMK0		5.2	3.1E-02	5.4	8.3E-03	-0.5	7.6E-01	-1.3	2.2E-01
ENSMUST00000102534	RAS guanyl releasing protein 1 [Source:MGI Symbol;Acc:MGI:1314635]		Q9Z1S3	6.0	1.5E-02	2.6	2.9E-03	-0.4	5.3E-01	0.3	6.4E-01
ENSMUST00000102536	ribosomal protein L11 [Source:MGI Symbol;Acc:MGI:1914275]		Q9CXW4	-3.7	7.9E-03	8.7	4.4E-03	1.8	4.4E-01	0.8	4.5E-01
ENSMUST00000102537	integrin alpha E, epithelial-associated [Source:MGI Symbol;Acc:MGI:1298377]	Q8BS01		3.5	3.1E-03	-6.1	8.7E-06	0.1	7.9E-01	-0.6	4.5E-01
ENSMUST00000102541	galactose-4-epimerase, UDP [Source:MGI Symbol;Acc:MGI:1921496]		Q8R059	-4.0	1.3E-02	-2.7	6.3E-03	-0.1	8.9E-01	-0.3	6.9E-01
ENSMUST00000102544	serine/arginine-rich splicing factor 10 [Source:MGI Symbol;Acc:MGI:1333805]	Q3TFP0		-4.1	2.8E-03	7.0	1.2E-04	-0.5	6.8E-01	-0.4	5.3E-01
ENSMUST00000102545	Rho GTPase activating protein 11A [Source:MGI Symbol;Acc:MGI:2444300]		Q80Y19	-6.2	1.6E-05	14.8	1.2E-08	-0.2	7.8E-01	-0.4	3.3E-01
ENSMUST00000102546	interleukin 22 receptor, alpha 1 [Source:MGI Symbol;Acc:MGI:2663588]		Q80XZ4	9.5	1.1E-05	14.8	9.1E-09	0.1	9.4E-01	-0.3	3.3E-01
ENSMUST00000099689	predicted gene 13889 [Source:MGI Symbol;Acc:MGI:3652053]	A0A087WRN5		2.9	6.9E-02	4.8	8.3E-03	-0.6	7.0E-01	-2.5	5.4E-02
ENSMUST00000102547	formin 1 [Source:MGI Symbol;Acc:MGI:101815]		Q05860	5.9	2.0E-03	7.4	1.0E-02	-0.7	7.7E-01	-2.1	1.5E-01
ENSMUST00000102549	NIPA-like domain containing 3 [Source:MGI Symbol;Acc:MGI:1921802]		Q8BGN5	-1.9	7.8E-03	-2.0	3.3E-02	1.2	3.6E-02	0.8	3.3E-01
ENSMUST00000102553	high mobility group nucleosomal binding domain 2 [Source:MGI Symbol;Acc:MGI:96136]	Q5BL14	P09602	-7.4	1.2E-05	7.5	5.8E-05	-0.6	6.1E-01	-0.3	6.5E-01
ENSMUST00000102555	DnaJ (Hsp40) homolog, subfamily C, member 24 [Source:MGI Symbol;Acc:MGI:1919522]	A2A4A1		-1.8	1.8E-02	-5.3	4.2E-02	0.8	4.6E-01	1.1	6.3E-01
ENSMUST00000099705	neurexophilin and PC-esterase domain family, member 3 [Source:MGI Symbol;Acc:MGI:2686598]	B9EKK6		0.7	2.6E-01	1.3	9.9E-02	0.4	5.2E-01	-0.3	6.8E-01
ENSMUST00000102556	cholinergic receptor, nicotinic, epsilon polypeptide [Source:MGI Symbol;Acc:MGI:87894]		P20782	6.1	1.8E-02	-0.9	2.0E-01	0.7	1.1E-01	-0.2	7.1E-01
ENSMUST00000102563	arrestin, beta 2 [Source:MGI Symbol;Acc:MGI:99474]		Q91YI4	-7.8	1.8E-03	1.0	6.4E-01	3.6	5.8E-02	-2.6	2.2E-01
ENSMUST00000099712	autophagy/beclin 1 regulator 1 [Source:MGI Symbol;Acc:MGI:2443564]		A2AH22	-0.6	4.9E-01	1.5	2.7E-01	1.4	2.3E-01	-0.7	4.9E-01
ENSMUST00000099714	zinc finger protein 408 [Source:MGI Symbol;Acc:MGI:2685857]	H7BX78		-0.9	5.0E-01	-1.7	3.7E-01	1.0	4.2E-01	1.7	3.3E-01
ENSMUST00000102564	arrestin, beta 2 [Source:MGI Symbol;Acc:MGI:99474]		Q91YI4	-9.4	1.6E-05	-4.2	7.8E-02	2.0	9.6E-02	-1.1	6.4E-01
ENSMUST00000102565	F-box protein 3 [Source:MGI Symbol;Acc:MGI:1929084]		Q9DC63	-4.0	2.3E-03	10.3	6.5E-04	-1.0	6.6E-01	0.5	5.8E-01
ENSMUST00000102567	mediator complex subunit 18 [Source:MGI Symbol;Acc:MGI:1914469]		Q9CZ82	3.4	1.2E-03	8.2	3.7E-05	-0.6	6.1E-01	-1.2	6.3E-02
ENSMUST00000102568	phosphatase and actin regulator 4 [Source:MGI Symbol;Acc:MGI:2140327]		Q501J7	-3.2	3.1E-02	1.0	1.7E-01	-1.6	2.1E-02	-0.9	1.6E-01
ENSMUST00000102571	C-type lectin domain family 10, member A [Source:MGI Symbol;Acc:MGI:96975]		P49300	-3.4	2.4E-02	1.8	9.8E-03	-1.1	5.4E-02	-0.6	2.0E-01
ENSMUST00000099747	?-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:2145		Q8BG28	-1.9	3.5E-02	-0.6	5.4E-01	1.1	1.4E-01	-0.2	8.4E-01
ENSMUST00000099751	olfactory receptor 1271 [Source:MGI Symbol;Acc:MGI:3031105]	Q8VG62		3.4	1.2E-01	5.3	3.0E-02	-0.3	8.8E-01	-2.3	1.1E-01
ENSMUST00000102573	tripartite motif-containing 44 [Source:MGI Symbol;Acc:MGI:1931835]	Q4KMS1		2.1	1.8E-03	5.1	2.8E-02	-0.7	7.3E-01	-0.8	5.2E-01
ENSMUST00000102574	acyl-Coenzyme A dehydrogenase, very long chain [Source:MGI Symbol;Acc:MGI:895149]		P50544	-6.7	2.0E-05	6.1	3.7E-04	-0.6	6.0E-01	-0.2	7.4E-01
ENSMUST00000102575	dishevelled 2, dsh homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:106613]		Q60838	1.6	3.5E-02	8.0	1.3E-04	-0.5	7.2E-01	-0.7	2.5E-01
ENSMUST00000102576	matrilin 1, cartilage matrix protein [Source:MGI Symbol;Acc:MGI:106591]		P51942	7.9	4.4E-05	6.1	1.4E-03	-0.7	6.5E-01	-0.7	4.1E-01
ENSMUST00000102578	ankyrin repeat domain 13a [Source:MGI Symbol;Acc:MGI:1915670]		Q80UP5	-5.8	5.7E-05	-2.4	3.4E-02	0.7	2.4E-01	-1.0	3.4E-01
ENSMUST00000102581	potassium channel tetramerisation domain containing 10 [Source:MGI Symbol;Acc:MGI:2141207]		Q922M3	-7.6	1.7E-05	-4.4	7.0E-03	0.3	5.9E-01	0.2	8.6E-01
ENSMUST00000099782	G protein-coupled receptor 137 [Source:MGI Symbol;Acc:MGI:2147529]	Q3UPL3		4.8	5.2E-02	4.4	1.7E-01	0.2	9.4E-01	0.6	7.7E-01
ENSMUST00000102582	acetyl-Coenzyme A carboxylase beta [Source:MGI Symbol;Acc:MGI:2140940]		E9Q4Z2	9.3	1.5E-05	6.2	3.4E-04	-0.5	6.7E-01	-1.1	1.1E-01
ENSMUST00000099816	CD80 antigen [Source:MGI Symbol;Acc:MGI:101775]	Q549R2	Q00609	-0.9	1.3E-01	-1.2	1.1E-01	0.1	8.9E-01	0.4	5.5E-01
ENSMUST00000102585	fibroblast growth factor 11 [Source:MGI Symbol;Acc:MGI:109167]		P70378	8.3	5.7E-04	-3.2	2.2E-02	-1.2	9.9E-02	-2.5	1.0E-01
ENSMUST00000102586	solute carrier family 35, member G3 [Source:MGI Symbol;Acc:MGI:1927128]	B2RQF0		7.8	1.4E-04	1.3	3.8E-02	0.1	7.7E-01	-0.1	8.2E-01
ENSMUST00000099858	prolyl endopeptidase [Source:MGI Symbol;Acc:MGI:1270863]	Q543B9	Q9QUR6	-0.5	2.5E-01	-0.1	8.5E-01	0.0	9.7E-01	-0.4	4.2E-01
ENSMUST00000102590	karyopherin (importin) alpha 6 [Source:MGI Symbol;Acc:MGI:1100836]	Q8BH30	O35345	-1.6	1.7E-02	3.5	4.6E-03	0.6	5.2E-01	0.1	8.6E-01
ENSMUST00000102592	tight junction protein 1 [Source:MGI Symbol;Acc:MGI:98759]		P39447	7.8	1.2E-04	6.0	3.8E-03	0.0	1.0E+00	-0.6	5.0E-01
ENSMUST00000102593	eukaryotic translation initiation factor 3, subunit I [Source:MGI Symbol;Acc:MGI:1860763]		Q9QZD9	-5.9	2.6E-04	6.3	5.5E-04	-0.4	7.4E-01	-1.2	1.1E-01
ENSMUST00000102594	RIKEN cDNA 1110051M20 gene [Source:MGI Symbol;Acc:MGI:1915079]		Q8BHR8	4.6	8.6E-03	6.4	4.3E-04	-0.5	6.8E-01	-0.4	5.8E-01
ENSMUST00000099931	sestrin 1 [Source:MGI Symbol;Acc:MGI:2155278]	E9PXR3		0.9	3.8E-01	0.3	8.2E-01	0.7	5.3E-01	1.2	3.5E-01
ENSMUST00000102597	histone deacetylase 1 [Source:MGI Symbol;Acc:MGI:108086]	Q58E49	O09106	-4.9	1.1E-03	-6.3	7.4E-03	1.1	1.1E-01	-0.9	6.7E-01
ENSMUST00000102598	retinoblastoma binding protein 4 [Source:MGI Symbol;Acc:MGI:1194912]		Q60972	-3.9	1.0E-05	-4.8	2.9E-03	0.0	9.8E-01	1.7	2.0E-01
ENSMUST00000102600	fibronectin type III domain containing 5 [Source:MGI Symbol;Acc:MGI:1917614]		Q8K4Z2	6.1	3.6E-04	0.9	2.0E-01	-0.6	2.6E-01	1.0	1.2E-01
ENSMUST00000102601	trafficking protein particle complex 1 [Source:MGI Symbol;Acc:MGI:1098727]	Q14BF8	Q5NCF2	-6.1	2.0E-04	6.1	1.9E-04	-0.6	5.9E-01	-0.2	7.2E-01
ENSMUST00000102602	trafficking protein particle complex 1 [Source:MGI Symbol;Acc:MGI:1098727]	Q14BF8	Q5NCF2	-5.8	4.4E-04	6.1	1.9E-04	-0.6	5.9E-01	-0.2	7.2E-01
ENSMUST00000102604	adenylate kinase 2 [Source:MGI Symbol;Acc:MGI:87978]		Q9WTP6	-4.8	2.1E-06	-7.0	3.0E-04	1.3	8.8E-03	0.3	8.2E-01
ENSMUST00000099967	Fyn proto-oncogene [Source:MGI Symbol;Acc:MGI:95602]		P39688	0.0	9.8E-01	-2.2	4.4E-01	-1.7	3.3E-01	0.6	8.3E-01
ENSMUST00000099972	integrin alpha 4 [Source:MGI Symbol;Acc:MGI:96603]	Q792F9		0.4	3.4E-01	1.2	3.9E-02	0.5	2.3E-01	-0.3	5.2E-01
ENSMUST00000099973	5'-nucleotidase domain containing 1 [Source:MGI Symbol;Acc:MGI:2442446]	E9QN01		-1.5	2.4E-01	-0.9	4.0E-01	-2.0	4.7E-02	-2.6	6.8E-02
ENSMUST00000102617	ADP-ribosylhydrolase like 2 [Source:MGI Symbol;Acc:MGI:2140364]		Q8CG72	-4.3	3.3E-03	7.9	1.0E-03	3.0	1.2E-01	-1.4	1.6E-01
ENSMUST00000102620	fibronectin type III domain containing 7 [Source:MGI Symbol;Acc:MGI:2443535]		A2AED3	6.0	8.1E-03	8.3	7.0E-06	-1.5	1.7E-01	-0.6	1.6E-01
ENSMUST00000102621	syntaxin binding protein 3 [Source:MGI Symbol;Acc:MGI:107362]		Q60770	-5.0	1.3E-05	12.2	6.4E-04	-0.9	7.5E-01	-1.8	6.7E-02
ENSMUST00000099985	centromere protein W [Source:MGI Symbol;Acc:MGI:1913561]	B2RVH1	Q3URR0	-1.2	1.1E-01	-2.4	3.5E-02	-0.9	1.6E-01	0.3	7.8E-01
ENSMUST00000102625	seryl-aminoacyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:102809]	Q8C483		-6.3	1.2E-04	4.2	1.0E-03	0.8	3.5E-01	-1.4	5.3E-02
ENSMUST00000102626	protein tyrosine phosphatase, non-receptor type 5 [Source:MGI Symbol;Acc:MGI:97807]		P54830	2.3	2.1E-02	-8.2	2.4E-04	0.4	3.1E-01	-0.6	6.9E-01
ENSMUST00000102628	yrdC domain containing (E.coli) [Source:MGI Symbol;Acc:MGI:2387201]		Q3U5F4	-4.2	4.1E-03	7.3	4.4E-05	-0.5	6.4E-01	-0.4	4.8E-01
ENSMUST00000102632	sortilin 1 [Source:MGI Symbol;Acc:MGI:1338015]		Q6PHU5	-3.9	1.6E-05	-0.7	2.0E-01	0.3	3.8E-01	-0.1	8.3E-01
ENSMUST00000099995	tetratricopeptide repeat domain 30A2 [Source:MGI Symbol;Acc:MGI:3700200]	B2RXQ0	A2AKQ8	-0.5	4.2E-01	0.3	7.3E-01	-0.2	7.7E-01	-1.0	2.2E-01
ENSMUST00000099996	tetratricopeptide repeat domain 30B [Source:MGI Symbol;Acc:MGI:1919671]	B2RXA2	Q9CY00	0.0	9.3E-01	0.2	7.7E-01	0.2	7.2E-01	0.0	9.7E-01
ENSMUST00000100012	A kinase (PRKA) anchor protein 7 [Source:MGI Symbol;Acc:MGI:1859150]		O55074	3.5	1.0E-01	0.9	6.1E-01	-4.4	4.0E-02	-1.7	3.0E-01
ENSMUST00000102633	ataxin 7-like 2 [Source:MGI Symbol;Acc:MGI:1919772]	Q8C8K6		5.4	1.1E-02	-5.5	2.1E-02	-0.2	7.9E-01	0.9	6.5E-01
ENSMUST00000100015	Obg-like ATPase 1 [Source:MGI Symbol;Acc:MGI:1914309]		Q9CZ30	-1.4	1.6E-01	-2.1	1.0E-01	-1.0	2.4E-01	-0.2	8.6E-01
ENSMUST00000102636	akirin 1 [Source:MGI Symbol;Acc:MGI:1915300]		Q99LF1	-3.3	9.1E-05	4.7	1.8E-04	-0.9	2.4E-01	-0.4	4.7E-01
ENSMUST00000100022	phosphatidylinositol transfer protein, membrane-associated 1 [Source:MGI Symbol;Acc:MGI:1197524]		O35954	-0.3	7.9E-01	-1.2	3.8E-01	-0.1	8.7E-01	0.8	5.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102640	3-oxoacid CoA transferase 2A [Source:MGI Symbol;Acc:MGI:1891061]		Q9JJN4	5.9	1.7E-05	4.5	5.0E-05	-1.4	4.2E-02	-0.6	2.1E-01
ENSMUST00000102642	ubiquitin-conjugating enzyme E2L 6 [Source:MGI Symbol;Acc:MGI:1914500]		Q9QZU9	1.2	1.9E-02	5.2	2.7E-03	0.1	9.6E-01	0.3	6.9E-01
ENSMUST00000102643	transient receptor potential cation channel, subfamily V, member 2 [Source:MGI Symbol;Acc:MGI:1341836]		Q9WTR1	-5.3	2.2E-04	1.7	7.1E-03	-0.7	1.5E-01	0.0	9.3E-01
ENSMUST00000102645	mediator complex subunit 19 [Source:MGI Symbol;Acc:MGI:1914234]		Q8C1S0	-1.4	2.7E-02	-7.5	1.6E-03	-0.8	1.6E-01	-0.8	6.9E-01
ENSMUST00000102647	RIKEN cDNA 2700094K13 gene [Source:MGI Symbol;Acc:MGI:1919907]		Q3UQA7	-2.9	1.2E-02	-3.3	2.6E-02	2.3	4.1E-03	-0.5	7.1E-01
ENSMUST00000100037	methyltransferase like 8 [Source:MGI Symbol;Acc:MGI:2385142]	B0R0U1		3.6	1.7E-01	2.8	3.3E-01	-1.6	5.6E-01	-0.7	7.2E-01
ENSMUST00000102648	3-oxoacid CoA transferase 2B [Source:MGI Symbol;Acc:MGI:2664115]			7.6	1.3E-04	6.0	1.3E-03	-0.7	6.5E-01	-0.4	5.8E-01
ENSMUST00000102650	A kinase (PRKA) anchor protein 10 [Source:MGI Symbol;Acc:MGI:1890218]		O88845	-3.8	1.6E-04	6.8	1.8E-04	-0.6	6.2E-01	-0.1	8.4E-01
ENSMUST00000102655	phosphodiesterase 1A, calmodulin-dependent [Source:MGI Symbol;Acc:MGI:1201792]	Q8BRR9		9.3	4.4E-06	5.0	3.4E-02	-0.7	7.5E-01	0.0	1.0E+00
ENSMUST00000102656	forkhead box O6 [Source:MGI Symbol;Acc:MGI:2676586]		Q70KY4	7.6	2.1E-04	6.9	2.3E-05	0.8	3.9E-01	0.5	2.7E-01
ENSMUST00000102660	SEC14 and spectrin domains 1 [Source:MGI Symbol;Acc:MGI:1916262]		Q80UK0	3.5	2.3E-03	1.9	8.7E-02	-5.4	1.7E-03	0.5	5.4E-01
ENSMUST00000102665	myelin oligodendrocyte glycoprotein [Source:MGI Symbol;Acc:MGI:97435]	Q3UY21		6.9	1.1E-04	3.2	1.5E-01	-3.8	1.4E-01	-1.0	5.8E-01
ENSMUST00000100063	sodium channel, voltage-gated, type IX, alpha [Source:MGI Symbol;Acc:MGI:107636]	F8VPQ7		4.1	1.1E-01	4.5	1.2E-01	-0.3	9.1E-01	-0.7	6.9E-01
ENSMUST00000100064	sodium channel, voltage-gated, type IX, alpha [Source:MGI Symbol;Acc:MGI:107636]		Q62205	5.1	7.6E-02	4.6	1.3E-01	-0.7	8.2E-01	-0.2	9.0E-01
ENSMUST00000102667	h-Magenis syndrome chromosome region, candidate 8 homolog (human) [Source:MGI Symbol;Acc:MGI:2444		Q3UMB5	5.7	5.4E-03	6.4	1.9E-03	-1.5	4.0E-01	0.8	3.6E-01
ENSMUST00000102668	topoisomerase (DNA) III alpha [Source:MGI Symbol;Acc:MGI:1197527]	Q3V3P1		7.4	8.8E-04	6.7	1.0E-04	0.0	9.6E-01	-0.9	1.8E-01
ENSMUST00000102671	myeloproliferative leukemia virus oncogene [Source:MGI Symbol;Acc:MGI:97076]		Q08351	5.4	2.0E-03	6.1	2.7E-04	-0.5	6.8E-01	0.0	9.9E-01
ENSMUST00000100077	zinc finger and BTB domain containing 2 [Source:MGI Symbol;Acc:MGI:2685949]	Q3V3W4		1.6	2.1E-01	-2.1	2.7E-01	-0.2	8.4E-01	3.4	6.6E-02
ENSMUST00000102672	nuclear factor, erythroid derived 2, like 2 [Source:MGI Symbol;Acc:MGI:108420]		Q60795	-5.7	9.7E-06	-2.3	2.2E-01	0.8	4.2E-01	-0.9	6.3E-01
ENSMUST00000102673	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 [Source:MGI Symbol;Acc:MGI:185	Q4V9V3		-6.6	6.8E-05	6.6	3.5E-04	-0.6	6.2E-01	0.6	3.8E-01
ENSMUST00000102676	limb and neural patterns [Source:MGI Symbol;Acc:MGI:1918115]	A2ASL8		-5.5	1.7E-03	-0.6	6.8E-01	1.4	1.7E-01	-0.6	6.7E-01
ENSMUST00000102677	chimerin 1 [Source:MGI Symbol;Acc:MGI:1915674]		Q91V57	6.7	8.5E-05	-2.5	1.7E-01	1.6	1.1E-01	1.1	5.5E-01
ENSMUST00000100125	THAP domain containing 7 [Source:MGI Symbol;Acc:MGI:1916259]		Q8VCZ3	-1.6	9.4E-02	-1.2	3.6E-01	0.8	3.5E-01	0.4	7.5E-01
ENSMUST00000102678	histocompatibility 2, T region locus 23 [Source:MGI Symbol;Acc:MGI:95957]	Q3V014	P06339	-4.9	3.3E-04	3.6	1.1E-03	-0.7	3.6E-01	0.2	7.9E-01
ENSMUST00000102680	WAS/WASL interacting protein family, member 1 [Source:MGI Symbol;Acc:MGI:2178801]		Q8K1I7	-7.0	8.0E-05	-2.7	2.3E-01	2.7	3.7E-02	-2.2	3.8E-01
ENSMUST00000102682	target of myb1-like 2 (chicken) [Source:MGI Symbol;Acc:MGI:2443306]		Q5SRX1	2.5	8.1E-03	6.2	6.1E-04	-0.6	6.8E-01	-0.2	7.5E-01
ENSMUST00000100134	G protein pathway suppressor 1 [Source:MGI Symbol;Acc:MGI:2384801]	B1ATU4		-0.3	7.0E-01	-0.6	5.2E-01	-1.0	1.1E-01	-0.8	3.8E-01
ENSMUST00000102687	DNA methyltransferase 1-associated protein 1 [Source:MGI Symbol;Acc:MGI:1913483]		Q9JI44	-1.6	3.1E-02	-0.5	6.0E-01	0.8	2.3E-01	-0.7	4.3E-01
ENSMUST00000102688	retinoic acid induced 1 [Source:MGI Symbol;Acc:MGI:103291]		Q61818	4.1	1.3E-03	6.5	1.6E-04	-0.6	5.8E-01	-0.1	9.0E-01
ENSMUST00000102689	trans-acting transcription factor 3 [Source:MGI Symbol;Acc:MGI:1277166]		O70494	-3.7	8.9E-03	5.8	4.3E-04	-0.6	6.0E-01	0.3	6.8E-01
ENSMUST00000102690	ring finger protein 220 [Source:MGI Symbol;Acc:MGI:1913993]		Q6PDX6	-6.9	3.0E-04	-4.8	2.0E-05	0.4	1.3E-01	-0.2	7.2E-01
ENSMUST00000100164	homeobox C4 [Source:MGI Symbol;Acc:MGI:96195]		Q08624	4.6	6.3E-02	4.6	7.3E-02	-1.3	6.2E-01	-1.4	3.5E-01
ENSMUST00000100167	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 [Source:MGI Symbol;Acc:MGI:102676]	A5D6P3	O35379	1.4	1.0E-01	0.3	7.6E-01	-1.3	8.7E-02	-0.2	7.9E-01
ENSMUST00000102694	prostaglandin F2 receptor negative regulator [Source:MGI Symbol;Acc:MGI:1277114]		Q9WV91	2.3	4.4E-03	2.8	2.7E-01	-4.0	1.3E-01	-0.7	6.9E-01
ENSMUST00000102696	ribosomal protein S8 [Source:MGI Symbol;Acc:MGI:98166]	Q497E9	P62242	-7.4	2.5E-04	-10.2	5.9E-05	-0.5	2.9E-01	-0.5	7.9E-01
ENSMUST00000100172	N-sulfoglucosamine sulfohydrolase (sulfamidase) [Source:MGI Symbol;Acc:MGI:1350341]	B1ATE0		-3.8	1.5E-01	-0.5	8.9E-01	4.1	1.5E-01	0.9	8.1E-01
ENSMUST00000102697	folliculin [Source:MGI Symbol;Acc:MGI:2442184]		Q8QZS3	1.9	9.4E-03	5.7	1.2E-04	-2.7	3.4E-02	-0.7	3.0E-01
ENSMUST00000102703	zinc finger protein 39 [Source:MGI Symbol;Acc:MGI:99183]		Q02525	4.2	6.2E-04	7.7	9.1E-05	-0.7	5.9E-01	0.1	8.6E-01
ENSMUST00000102704	RAD54 like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:894697]		P70270	4.7	4.5E-03	-2.6	1.2E-01	-7.1	2.7E-03	0.2	8.8E-01
ENSMUST00000102705	RAD54 like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:894697]		P70270	-3.0	1.1E-02	5.6	1.0E-03	0.0	9.8E-01	0.8	2.7E-01
ENSMUST00000102707	cytochrome P450, family 4, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:103225]	Q3TNA0	Q64462	6.7	1.3E-02	4.6	3.2E-03	-0.1	9.6E-01	0.6	4.2E-01
ENSMUST00000102710	ATP-binding cassette, sub-family B (MDR/TAP), member 11 [Source:MGI Symbol;Acc:MGI:1351619]		Q9QY30	4.3	3.4E-04	-2.9	2.7E-02	0.5	4.3E-01	-1.1	3.8E-01
ENSMUST00000102715	serine/threonine kinase 39 [Source:MGI Symbol;Acc:MGI:1858416]	A2AQL0	Q9Z1W9	6.2	1.3E-03	-5.4	2.3E-03	0.8	1.1E-01	-0.2	8.6E-01
ENSMUST00000102716	glycine receptor, alpha 1 subunit [Source:MGI Symbol;Acc:MGI:95747]	Q5NCT9	Q64018	6.8	2.0E-04	-3.2	2.1E-02	0.7	2.7E-01	-1.4	3.3E-01
ENSMUST00000100203	DIP2 disco-interacting protein 2 homolog B (Drosophila) [Source:MGI Symbol;Acc:MGI:2145977]		Q3UH60	-0.6	3.6E-01	-0.3	7.1E-01	0.3	5.6E-01	0.1	9.4E-01
ENSMUST00000102718	tetratricopeptide repeat domain 21B [Source:MGI Symbol;Acc:MGI:1920918]		Q0HA38	2.6	2.1E-02	-1.9	6.9E-03	-0.1	7.7E-01	-0.3	6.5E-01
ENSMUST00000100207	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]	A2AQ44		-0.4	9.0E-01	5.5	3.1E-01	6.0	1.3E-01	0.0	9.9E-01
ENSMUST00000100208	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]	A2AQ41		-0.2	9.2E-01	-2.2	4.0E-01	-2.4	1.4E-01	-0.4	8.8E-01
ENSMUST00000102721	solute carrier family 5 (sodium/glucose cotransporter), member 9 [Source:MGI Symbol;Acc:MGI:2140201]		Q8VDT1	8.0	1.7E-04	10.3	1.6E-04	-0.9	6.3E-01	0.7	3.0E-01
ENSMUST00000102722	\V (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) [Source:MGI Symbol;Acc:MGI:107	A2A9R6		6.0	3.4E-02	3.7	1.3E-01	-0.6	8.1E-01	3.2	5.1E-02
ENSMUST00000100215	SH3-domain GRB2-like endophilin B2 [Source:MGI Symbol;Acc:MGI:2385131]		Q8R3V5	-1.6	3.8E-01	-0.3	8.4E-01	-1.4	2.6E-01	-2.7	1.8E-01
ENSMUST00000100219	dolichol kinase [Source:MGI Symbol;Acc:MGI:2677836]		Q8R2Y3	1.0	1.7E-01	0.6	5.4E-01	0.5	5.1E-01	0.9	3.1E-01
ENSMUST00000102724	Fas-associated factor 1 [Source:MGI Symbol;Acc:MGI:109419]		P54731	-1.4	1.2E-02	-3.3	1.7E-02	0.2	7.4E-01	-0.6	6.4E-01
ENSMUST00000102727	annexin A6 [Source:MGI Symbol;Acc:MGI:88255]	F8WIT2		-1.5	3.0E-02	-2.2	7.8E-02	-0.2	8.0E-01	-0.7	5.6E-01
ENSMUST00000102729	epidermal growth factor receptor pathway substrate 15 [Source:MGI Symbol;Acc:MGI:104583]	Q80ZL3	P42567	-3.7	1.9E-04	-4.2	9.5E-02	0.5	6.7E-01	-0.6	8.0E-01
ENSMUST00000102736	nardilysin, N-arginine dibasic convertase, NRD convertase 1 [Source:MGI Symbol;Acc:MGI:1201386]	A6PWC3		6.0	5.7E-03	9.4	4.4E-03	2.5	3.4E-01	-1.3	4.0E-01
ENSMUST00000102740	basic transcription factor 3-like 4 [Source:MGI Symbol;Acc:MGI:1915312]	A2A7Z4	Q9CQH7	-6.5	1.1E-04	-1.5	2.8E-01	0.5	5.8E-01	-1.4	3.4E-01
ENSMUST00000100239	predicted gene 11711 [Source:MGI Symbol;Acc:MGI:3702661]	A2A7W1		1.7	4.7E-01	2.7	3.1E-01	-1.2	6.3E-01	-2.2	3.2E-01
ENSMUST00000102742	basic transcription factor 3-like 4 [Source:MGI Symbol;Acc:MGI:1915312]	A2A7Z4	Q9CQH7	-1.1	2.4E-02	-2.6	1.0E-01	1.6	7.5E-02	-2.3	1.9E-01
ENSMUST00000102743	Rap guanine nucleotide exchange factor (GEF) 6 [Source:MGI Symbol;Acc:MGI:2384761]	Q5NCJ0		-3.7	6.1E-05	7.5	2.1E-04	-0.7	6.1E-01	-0.6	4.1E-01
ENSMUST00000102744	origin recognition complex, subunit 1 [Source:MGI Symbol;Acc:MGI:1328337]		Q9Z1N2	2.3	3.5E-03	6.4	1.6E-02	-0.8	7.5E-01	-0.9	4.9E-01
ENSMUST00000102745	tumor necrosis factor, alpha-induced protein 2 [Source:MGI Symbol;Acc:MGI:104960]		Q61333	-6.2	3.4E-05	4.0	5.1E-03	1.7	1.1E-01	0.2	7.8E-01
ENSMUST00000102746	ubiquitin-like modifier activating enzyme 2 [Source:MGI Symbol;Acc:MGI:1858313]		Q9Z1F9	-5.0	2.2E-06	4.4	9.4E-02	-1.4	5.7E-01	0.4	8.2E-01
ENSMUST00000102747	membrane-associated ring finger (C3HC4) 7 [Source:MGI Symbol;Acc:MGI:1931053]		Q9WV66	-5.0	2.1E-03	5.5	7.2E-04	-0.5	6.5E-01	0.0	9.6E-01
ENSMUST00000100299	dedicator of cytokinesis 9 [Source:MGI Symbol;Acc:MGI:106321]	E9QMR2		-1.9	6.2E-02	0.8	5.5E-01	2.5	4.8E-02	-0.3	8.0E-01
ENSMUST00000102748	membrane-associated ring finger (C3HC4) 7 [Source:MGI Symbol;Acc:MGI:1931053]		Q9WV66	-8.1	2.2E-03	2.2	4.3E-02	0.0	1.0E+00	0.5	5.0E-01
ENSMUST00000102749	aryl hydrocarbon receptor nuclear translocator [Source:MGI Symbol;Acc:MGI:88071]		P53762	-4.8	2.0E-03	-1.6	2.1E-01	0.6	4.2E-01	-0.8	5.0E-01
ENSMUST00000102752	homer homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1347345]	Q5D052	Q9Z2Y3	2.7	4.4E-04	2.9	3.2E-01	-0.9	7.4E-01	2.3	3.1E-01
ENSMUST00000100305	helicase with zinc finger domain [Source:MGI Symbol;Acc:MGI:1925705]	A2AAU3		4.7	6.1E-02	4.1	1.3E-01	-0.5	8.5E-01	0.1	9.7E-01
ENSMUST00000102758	voltage-dependent anion channel 1 [Source:MGI Symbol;Acc:MGI:106919]		Q60932	-2.9	7.8E-05	7.9	3.3E-03	1.2	5.9E-01	-1.1	2.7E-01
ENSMUST00000100309	asparagine-linked glycosylation 10B (alpha-1,2-glucosyltransferase) [Source:MGI Symbol;Acc:MGI:2146159]		Q3UGP8	0.1	7.3E-01	0.8	1.9E-01	1.0	4.2E-02	0.4	5.2E-01
ENSMUST00000102759	ignal transducing adaptor molecule (SH3 domain and ITAM motif) 2 [Source:MGI Symbol;Acc:MGI:1929100	Q3TGH8	O88811	-3.1	3.5E-04	2.1	3.3E-02	-4.1	3.7E-03	-0.3	7.1E-01
ENSMUST00000100320	fucosyltransferase 7 [Source:MGI Symbol;Acc:MGI:107692]	E2D0W5	Q11131	-1.6	1.3E-01	1.7	2.0E-01	1.6	1.5E-01	-1.8	1.5E-01
ENSMUST00000102762	acyl-CoA thioesterase 11 [Source:MGI Symbol;Acc:MGI:1913736]	Q543P6	Q8VHQ9	2.8	2.6E-04	7.8	1.1E-04	-0.7	6.0E-01	0.2	7.8E-01
ENSMUST00000102763	CDKN2A interacting protein N-terminal like [Source:MGI Symbol;Acc:MGI:1261797]		Q9D211	-3.3	6.8E-05	-3.4	3.5E-02	0.4	5.5E-01	0.8	6.0E-01
ENSMUST00000100329	NADPH dependent diflavin oxidoreductase 1 [Source:MGI Symbol;Acc:MGI:1926047]		A2AI05	-0.3	5.9E-01	-0.1	8.8E-01	0.4	5.2E-01	0.2	8.3E-01
ENSMUST00000102765	collagen, type XXIII, alpha 1 [Source:MGI Symbol;Acc:MGI:2653243]		Q8K4G2	8.3	2.5E-06	4.1	7.4E-04	-3.0	6.8E-03	0.5	4.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102767	RNA binding motif protein 43 [Source:MGI Symbol;Acc:MGI:1918934]		Q99J64	-4.3	1.6E-04	2.7	2.6E-01	-1.4	5.7E-01	2.1	2.2E-01
ENSMUST00000100334	MDA receptor synaptonuclear signaling and neuronal migration factor [Source:MGI Symbol;Acc:MGI:186175		Q99NF2	1.4	5.9E-01	2.1	5.1E-01	0.7	8.0E-01	-0.1	9.8E-01
ENSMUST00000102769	ylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria [Source:MGI Symbol;Acc:MGI:192		Q99LS1	-7.4	5.9E-06	4.9	5.9E-05	-2.4	7.9E-03	-0.6	2.4E-01
ENSMUST00000102774	sequestosome 1 [Source:MGI Symbol;Acc:MGI:107931]		Q64337	-7.8	5.2E-05	4.6	2.4E-02	-2.2	2.7E-01	0.8	5.2E-01
ENSMUST00000102776	ring finger protein 130 [Source:MGI Symbol;Acc:MGI:1891717]		Q8VEM1	-10.1	1.3E-05	4.8	3.6E-04	-3.1	1.4E-02	-0.8	2.0E-01
ENSMUST00000102780	adenylate kinase 4 [Source:MGI Symbol;Acc:MGI:87979]	Q3U489	Q9WUR9	4.0	1.0E-02	-3.6	3.9E-04	-1.1	2.1E-02	-1.6	4.7E-02
ENSMUST00000102781	Janus kinase 1 [Source:MGI Symbol;Acc:MGI:96628]	B1ASP2		-5.4	5.7E-06	7.3	3.9E-03	-0.5	8.0E-01	-2.6	3.7E-02
ENSMUST00000102782	predicted gene 2000 [Source:MGI Symbol;Acc:MGI:3780170]		Q6ZWV7	-9.3	1.4E-04	3.3	2.3E-03	0.9	2.2E-01	0.2	7.7E-01
ENSMUST00000102783	phosphoglucomutase 2 [Source:MGI Symbol;Acc:MGI:97565]	A2CEK3		6.8	5.7E-05	7.1	2.0E-04	-0.5	6.9E-01	-1.1	1.2E-01
ENSMUST00000102790	KN motif and ankyrin repeat domains 4 [Source:MGI Symbol;Acc:MGI:3043381]		Q6P9J5	7.8	1.4E-05	-0.6	4.6E-01	1.2	4.0E-02	-0.8	3.1E-01
ENSMUST00000102792	InaD-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1277960]		Q63ZW7	4.8	9.5E-04	-8.1	2.5E-04	1.1	3.0E-02	2.3	1.2E-01
ENSMUST00000102793	TM2 domain containing 1 [Source:MGI Symbol;Acc:MGI:2137022]		Q99MB3	-5.3	4.8E-05	6.6	1.7E-03	0.2	8.8E-01	-0.6	4.8E-01
ENSMUST00000102795	ubiquitin-like domain containing CTD phosphatase 1 [Source:MGI Symbol;Acc:MGI:1933105]		Q8BGR9	-5.1	1.2E-03	-4.4	1.2E-02	0.5	4.3E-01	-1.3	4.0E-01
ENSMUST00000102800	GTPase activating protein and VPS9 domains 1 [Source:MGI Symbol;Acc:MGI:1913941]		Q6PAR5	-2.6	7.9E-04	8.8	1.4E-04	-0.8	6.1E-01	-0.1	9.2E-01
ENSMUST00000100398	embrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2) [Source:MGI Symbol;Acc:MGI:185825		Q9WV34	4.1	5.0E-02	6.8	2.1E-02	1.1	6.7E-01	-1.7	2.8E-01
ENSMUST00000102801	teneurin transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1345184]	A0A0A0MQB7		9.1	1.6E-05	6.1	8.2E-05	-2.3	5.4E-02	-0.1	8.9E-01
ENSMUST00000100403	transmembrane protein 106A [Source:MGI Symbol;Acc:MGI:1922056]		Q8VC04	-1.3	5.7E-01	-1.4	4.9E-01	-2.4	1.5E-01	-2.3	3.1E-01
ENSMUST00000100404	beta-3-glucosyltransferase [Source:MGI Symbol;Acc:MGI:2685903]		Q8BHT6	0.4	3.5E-01	0.7	2.3E-01	-0.5	2.7E-01	-0.7	1.8E-01
ENSMUST00000102805	Cd200 receptor 2 [Source:MGI Symbol;Acc:MGI:3042847]		Q6XJV6	9.4	1.2E-05	6.0	1.2E-03	0.9	4.9E-01	0.2	7.8E-01
ENSMUST00000100414	vacuolar protein sorting 25 (yeast) [Source:MGI Symbol;Acc:MGI:106354]	A2A4K0		0.1	9.3E-01	1.7	3.0E-01	0.7	6.0E-01	-0.9	4.7E-01
ENSMUST00000100417	enhancer of zeste homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1097695]		P70351	1.7	5.9E-02	2.9	1.4E-02	0.4	6.4E-01	-0.8	3.3E-01
ENSMUST00000102806	interferon alpha 12 [Source:MGI Symbol;Acc:MGI:2676324]		Q80SS5	6.1	1.6E-04	6.5	1.3E-03	-0.7	6.5E-01	-0.2	7.7E-01
ENSMUST00000102807	interferon alpha 9 [Source:MGI Symbol;Acc:MGI:107659]		P09235	5.9	5.3E-04	-8.9	9.2E-04	1.7	7.6E-03	-0.6	7.6E-01
ENSMUST00000102813	RIKEN cDNA 1700019L03 gene [Source:MGI Symbol;Acc:MGI:2447809]		Q0VFX2	7.0	2.8E-05	6.4	4.7E-04	-0.5	6.5E-01	-0.1	8.3E-01
ENSMUST00000102814	ribosomal protein S6 [Source:MGI Symbol;Acc:MGI:98159]	Q5BLK1	P62754	-4.7	2.9E-05	6.8	1.2E-04	-0.6	6.0E-01	-0.5	4.1E-01
ENSMUST00000102815	RAN binding protein 17 [Source:MGI Symbol;Acc:MGI:1929706]		Q99NF8	7.5	2.7E-05	6.8	3.1E-04	1.1	3.6E-01	0.6	3.5E-01
ENSMUST00000100461	SMAD specific E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1923038]	E9Q4K9		-0.6	7.3E-01	0.1	9.6E-01	1.8	3.6E-01	1.1	5.8E-01
ENSMUST00000102817	growth associated protein 43 [Source:MGI Symbol;Acc:MGI:95639]		P06837	5.6	7.9E-04	8.0	5.7E-05	-0.6	6.3E-01	-0.4	4.4E-01
ENSMUST00000102820	basonuclin 2 [Source:MGI Symbol;Acc:MGI:2443805]		Q8BMQ3	7.3	3.4E-02	-1.6	3.9E-01	2.0	8.7E-02	0.5	7.6E-01
ENSMUST00000100472	high mobility group nucleosomal binding domain 2 [Source:MGI Symbol;Acc:MGI:96136]	Q5XK38		-6.1	6.5E-02	-6.6	1.1E-01	-1.3	3.9E-01	-0.8	8.4E-01
ENSMUST00000100473	kinesin family member 13B [Source:MGI Symbol;Acc:MGI:1098265]	E9Q4K7		0.5	2.6E-01	1.3	3.2E-02	0.5	2.4E-01	-0.3	4.8E-01
ENSMUST00000102821	serine/threonine kinase 10 [Source:MGI Symbol;Acc:MGI:1099439]		O55098	-2.6	6.4E-04	5.8	4.2E-04	-0.6	6.2E-01	0.5	4.7E-01
ENSMUST00000102827	inducible T cell co-stimulator [Source:MGI Symbol;Acc:MGI:1858745]	Q5SUZ7	Q9WVS0	2.0	1.3E-02	-1.8	1.3E-02	0.6	1.2E-01	-0.9	1.8E-01
ENSMUST00000102829	RIKEN cDNA 4930524B15 gene [Source:MGI Symbol;Acc:MGI:1914842]		Q24JP4	6.0	3.6E-04	2.9	3.8E-03	-2.0	2.4E-02	-0.4	4.7E-01
ENSMUST00000102830	multiple PDZ domain protein [Source:MGI Symbol;Acc:MGI:1343489]		Q8VBX6	8.2	1.6E-05	-3.1	1.8E-03	1.0	2.0E-02	0.5	5.2E-01
ENSMUST00000102834	protein tyrosine phosphatase, receptor type, D [Source:MGI Symbol;Acc:MGI:97812]	Q5SPA9		6.3	1.2E-02	-3.9	1.7E-02	0.0	9.6E-01	-0.7	6.8E-01
ENSMUST00000102837	RAS and EF hand domain containing [Source:MGI Symbol;Acc:MGI:2448565]		Q5RI75	4.9	4.1E-04	-3.8	3.4E-03	-0.3	5.0E-01	0.2	8.4E-01
ENSMUST00000102838	spectrin beta, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98388]		Q62261	1.8	8.5E-03	-6.2	2.9E-05	1.6	4.0E-03	-0.7	4.1E-01
ENSMUST00000100500	mediator complex subunit 24 [Source:MGI Symbol;Acc:MGI:1344385]	A6PW47		-0.2	9.5E-01	4.1	3.1E-01	4.1	1.8E-01	-0.2	9.6E-01
ENSMUST00000100505	BRCA1-associated ATM activator 1 [Source:MGI Symbol;Acc:MGI:1891679]	E9QLK3		-2.1	1.1E-01	-3.0	1.3E-01	-0.1	9.0E-01	0.7	6.9E-01
ENSMUST00000102842	reticulon 4 [Source:MGI Symbol;Acc:MGI:1915835]	Q8BHF5		-5.5	4.1E-05	-1.7	2.2E-02	0.4	3.1E-01	-0.3	6.9E-01
ENSMUST00000100510				2.3	4.9E-02	3.0	3.6E-02	-0.7	5.3E-01	-1.4	1.4E-01
ENSMUST00000100514	G protein-coupled receptor 146 [Source:MGI Symbol;Acc:MGI:1933113]		Q99LE2	-0.7	6.4E-01	0.5	7.2E-01	-0.6	6.3E-01	-1.8	2.7E-01
ENSMUST00000100521	src family associated phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:1925723]		Q3UUV5	3.7	1.2E-01	2.2	3.8E-01	-1.6	5.1E-01	-0.1	9.6E-01
ENSMUST00000102844	ribosomal protein S27A [Source:MGI Symbol;Acc:MGI:1925544]	Q642L7	P62983	-6.4	2.1E-06	5.3	1.3E-02	1.4	4.1E-01	-0.8	4.7E-01
ENSMUST00000102845	ribosomal protein S27A [Source:MGI Symbol;Acc:MGI:1925544]	Q642L7	P62983	-6.6	3.7E-05	-5.8	1.3E-02	0.0	9.9E-01	1.1	5.7E-01
ENSMUST00000102852	prostaglandin E synthase [Source:MGI Symbol;Acc:MGI:1927593]		Q9JM51	2.8	2.6E-04	-2.3	6.4E-03	1.1	1.7E-02	0.2	7.6E-01
ENSMUST00000102853	CSA-conditional, T cell activation-dependent protein [Source:MGI Symbol;Acc:MGI:1925867]	Q9D245		6.9	3.0E-04	6.6	3.2E-02	-1.2	6.8E-01	-1.0	5.5E-01
ENSMUST00000102854	carnitine acetyltransferase [Source:MGI Symbol;Acc:MGI:109501]	H7BX88		-5.0	2.6E-03	4.0	8.5E-04	-2.4	2.1E-02	-0.9	1.7E-01
ENSMUST00000102856	SMEK homolog 2, suppressor of mek1 (Dictyostelium) [Source:MGI Symbol;Acc:MGI:2144474]		Q922R5	7.2	3.8E-04	-0.7	6.5E-01	1.1	2.7E-01	-1.3	4.1E-01
ENSMUST00000100539	TSC22 domain family, member 4 [Source:MGI Symbol;Acc:MGI:1926079]		Q9EQN3	-1.2	6.4E-02	-1.1	2.0E-01	1.1	8.0E-02	1.0	2.3E-01
ENSMUST00000102865	zinc finger, DHHC domain containing 12 [Source:MGI Symbol;Acc:MGI:1913470]		Q8VC90	-3.8	7.2E-03	-2.3	9.7E-02	1.8	3.3E-02	-1.3	3.4E-01
ENSMUST00000102866	SET nuclear oncogene [Source:MGI Symbol;Acc:MGI:1860267]	Q3T9S3	Q9EQU5	4.4	1.9E-02	-9.4	5.3E-05	-0.3	4.1E-01	-0.9	5.2E-01
ENSMUST00000100544	ArfGAP with FG repeats 2 [Source:MGI Symbol;Acc:MGI:2443267]	Q3U2K8		2.9	1.1E-01	1.3	6.0E-01	0.1	9.4E-01	1.7	4.8E-01
ENSMUST00000100551	sarcoglycan, alpha (dystrophin-associated glycoprotein) [Source:MGI Symbol;Acc:MGI:894698]		P82350	2.9	2.0E-01	3.6	1.5E-01	-0.5	8.5E-01	-1.2	5.1E-01
ENSMUST00000102870	exportin 1, CRM1 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2144013]		Q6P5F9	-7.8	2.4E-04	5.5	1.9E-04	0.8	3.7E-01	-0.8	2.2E-01
ENSMUST00000102871	L1 cell adhesion molecule [Source:MGI Symbol;Acc:MGI:96721]	Q6PGJ3		7.9	1.9E-03	6.5	7.3E-03	0.1	9.5E-01	0.4	6.9E-01
ENSMUST00000100568	alkB, alkylation repair homolog 4 (E. coli) [Source:MGI Symbol;Acc:MGI:1919291]		Q9D8F1	4.7	5.7E-02	3.4	2.2E-01	-1.2	6.4E-01	0.1	9.5E-01
ENSMUST00000102874	malate dehydrogenase 1, NAD (soluble) [Source:MGI Symbol;Acc:MGI:97051]		P14152	-4.5	2.7E-04	-9.9	3.7E-05	1.0	3.9E-02	-0.8	6.0E-01
ENSMUST00000102875	UDP-glucose pyrophosphorylase 2 [Source:MGI Symbol;Acc:MGI:2183447]		Q91ZJ5	-3.6	1.9E-04	5.8	3.1E-03	-0.6	6.8E-01	0.8	3.4E-01
ENSMUST00000102879	olfactomedin 1 [Source:MGI Symbol;Acc:MGI:1860437]		O88998	-3.0	2.0E-02	3.6	1.9E-02	0.3	7.9E-01	2.1	3.5E-02
ENSMUST00000100631	RAB2B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1923588]	Q3TEG7		3.8	6.1E-02	-0.7	7.8E-01	-0.9	6.4E-01	3.6	1.2E-01
ENSMUST00000100635	family with sequence similarity 84, member B [Source:MGI Symbol;Acc:MGI:3026924]	D3YXJ5		0.4	3.7E-01	1.8	1.1E-02	1.1	4.4E-02	-0.4	4.7E-01
ENSMUST00000102880	n phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I) [Source:MGI Symbol;Acc:MGI:10		Q63810	-5.7	3.2E-06	5.1	8.4E-04	-1.2	2.9E-01	0.1	9.1E-01
ENSMUST00000102881	pleckstrin [Source:MGI Symbol;Acc:MGI:1860485]	Q5F271	Q9JHK5	-5.2	3.1E-05	0.9	2.2E-01	-5.1	2.2E-04	-0.7	2.3E-01
ENSMUST00000100644	benzodiazepine receptor associated protein 1 [Source:MGI Symbol;Acc:MGI:2450877]	Q5NCP6		2.7	1.9E-01	0.5	8.8E-01	0.3	9.0E-01	2.5	3.5E-01
ENSMUST00000102884	epidermal growth factor receptor [Source:MGI Symbol;Acc:MGI:95294]	Q9WVF5		4.8	3.3E-03	6.1	2.0E-04	-0.6	6.2E-01	-0.9	1.6E-01
ENSMUST00000102886	sarcosine dehydrogenase [Source:MGI Symbol;Acc:MGI:2183102]	Q3TWI2	Q99LB7	8.4	1.4E-05	-0.5	6.8E-01	-4.2	6.4E-03	0.5	6.5E-01
ENSMUST00000102888	calcium/calmodulin-dependent protein kinase II alpha [Source:MGI Symbol;Acc:MGI:88256]		P11798	7.4	5.4E-06	-4.6	3.6E-03	-0.7	3.0E-01	-1.4	3.4E-01
ENSMUST00000102889	expressed sequence AI314180 [Source:MGI Symbol;Acc:MGI:2140220]		Q6PDI5	-5.1	1.9E-04	4.2	5.6E-02	-1.8	3.9E-01	0.1	9.6E-01
ENSMUST00000102891	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 13 [Source:MGI Symbol;Acc:M		Q769J6	7.7	1.9E-04	1.1	3.9E-01	-1.6	1.4E-01	5.2	5.0E-04
ENSMUST00000100680	syntaxin 2 [Source:MGI Symbol;Acc:MGI:108059]	Q3TJ55		-4.0	4.4E-02	-0.9	7.3E-01	3.1	1.1E-01	0.0	1.0E+00
ENSMUST00000100691	eosinophil-associated, ribonuclease A family, member 1 [Source:MGI Symbol;Acc:MGI:108021]	Q53ZF0	P97426	2.1	3.2E-01	-1.1	6.2E-01	-3.4	1.0E-01	-0.2	9.4E-01
ENSMUST00000102894	leukocyte immunoglobulin-like receptor, subfamily B, member 4B [Source:MGI Symbol;Acc:MGI:102702]	Q549E3	Q61450	-7.2	1.8E-04	6.6	4.4E-04	-0.5	7.1E-01	-0.2	8.0E-01
ENSMUST00000100695	predicted gene 10377 [Source:MGI Symbol;Acc:MGI:3704431]	D3YXI8		2.9	2.0E-01	4.7	6.3E-02	-0.4	8.6E-01	-2.2	2.0E-01
ENSMUST00000100700	predicted gene 10382 [Source:MGI Symbol;Acc:MGI:3647829]	Q3V0T5		2.3	8.2E-02	3.3	5.7E-02	-0.2	9.1E-01	-1.2	2.9E-01
ENSMUST00000102898	ribosomal protein L7A [Source:MGI Symbol;Acc:MGI:1353472]	Q58ET1	P12970	-4.8	1.6E-05	6.4	2.5E-03	-0.4	8.4E-01	0.0	9.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000100709	SET domain containing (lysine methyltransferase) 8 [Source:MGI Symbol;Acc:MGI:1915206]	D3YXI6		-3.0	7.0E-02	0.0	1.0E+00	1.0	4.5E-01	-2.0	2.7E-01
ENSMUST00000102899	mediator complex subunit 22 [Source:MGI Symbol;Acc:MGI:98446]		Q62276	-2.5	1.1E-03	1.5	7.5E-02	-0.9	1.8E-01	-0.1	9.3E-01
ENSMUST00000102902	A kinase (PRKA) anchor protein 2 [Source:MGI Symbol;Acc:MGI:1306795]		O54931	7.6	6.2E-04	4.1	5.1E-03	0.2	8.8E-01	0.3	7.2E-01
ENSMUST00000100718	RAD51 homolog D [Source:MGI Symbol;Acc:MGI:1261809]	E9Q428		0.7	7.6E-01	-2.7	3.7E-01	-3.1	1.0E-01	0.3	9.3E-01
ENSMUST00000102904	paralemmin 2 [Source:MGI Symbol;Acc:MGI:1934601]		Q8BR92	10.7	3.2E-05	7.7	1.3E-04	1.4	2.7E-01	-0.5	3.9E-01
ENSMUST00000102911	solute carrier family 44, member 1 [Source:MGI Symbol;Acc:MGI:2140592]		Q6X893	-2.8	2.9E-02	6.8	5.1E-04	-1.5	3.3E-01	-0.8	2.8E-01
ENSMUST00000102912	membrane-associated ring finger (C3HC4) 3 [Source:MGI Symbol;Acc:MGI:2443667]		Q8BRX9	6.2	2.3E-05	4.3	5.5E-02	-0.6	7.8E-01	0.8	5.5E-01
ENSMUST00000102920	glucokinase [Source:MGI Symbol;Acc:MGI:1270854]	Q5SVI5	P52792	8.7	1.3E-05	7.2	1.8E-03	-0.7	7.2E-01	-2.8	2.4E-02
ENSMUST00000100729	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 [Source:MGI Symbol;Acc:MGI:1914401]		Q9CR00	-0.1	7.9E-01	1.0	1.3E-01	0.8	9.7E-02	-0.3	6.0E-01
ENSMUST00000102921	myosin, light polypeptide 7, regulatory [Source:MGI Symbol;Acc:MGI:107495]	Q5SVI8	Q9QVP4	6.7	1.2E-04	4.6	4.4E-02	-2.5	2.6E-01	-0.7	5.8E-01
ENSMUST00000102923	AE binding protein 1 [Source:MGI Symbol;Acc:MGI:1197012]		Q640N1	10.2	4.7E-05	8.2	3.0E-04	2.2	1.4E-01	-0.5	5.2E-01
ENSMUST00000102924	tripartite motif-containing 14 [Source:MGI Symbol;Acc:MGI:1921985]		Q8BVW3	4.9	9.5E-04	1.2	1.9E-01	-0.8	2.8E-01	0.3	7.3E-01
ENSMUST00000102926	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B [Source:MGI Symbol;Acc:MGI:1914878]		Q9EST5	-3.9	6.4E-05	-2.0	6.2E-02	0.8	1.8E-01	-0.2	8.0E-01
ENSMUST00000100747	hydrogen voltage-gated channel 1 [Source:MGI Symbol;Acc:MGI:1921346]		Q3U2S8	0.1	9.5E-01	5.8	1.4E-01	6.1	9.2E-02	0.4	8.4E-01
ENSMUST00000102927	3-phosphoinositide dependent protein kinase 1 [Source:MGI Symbol;Acc:MGI:1338068]		Q9Z2A0	-3.2	1.1E-04	-6.0	1.4E-04	0.3	5.1E-01	-2.0	1.2E-01
ENSMUST00000102928	drebrin-like [Source:MGI Symbol;Acc:MGI:700006]		Q62418	-5.9	3.5E-05	2.4	2.0E-02	0.4	5.6E-01	0.0	9.9E-01
ENSMUST00000102929	tudor domain containing 7 [Source:MGI Symbol;Acc:MGI:2140279]		Q8K1H1	-4.6	6.0E-03	6.7	4.9E-04	0.7	5.9E-01	-0.2	7.9E-01
ENSMUST00000102930	Ewing sarcoma breakpoint region 1 [Source:MGI Symbol;Acc:MGI:99960]	Q5SUS9		-5.6	1.0E-03	4.6	1.2E-01	-2.9	3.5E-01	1.1	5.5E-01
ENSMUST00000102938	euchromatic histone methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1924933]	Z4YJZ7		5.4	3.0E-02	6.3	8.9E-04	3.1	2.7E-02	0.3	7.3E-01
ENSMUST00000102944	cAMP responsive element binding protein 3 [Source:MGI Symbol;Acc:MGI:99946]	Q3UNH6		-4.3	3.7E-05	-7.1	6.7E-05	0.4	2.7E-01	0.4	7.0E-01
ENSMUST00000100772	transmembrane and tetratricopeptide repeat containing 1 [Source:MGI Symbol;Acc:MGI:3039590]		Q3UV71	3.7	5.9E-02	4.9	2.2E-02	-0.9	6.3E-01	-2.1	1.6E-01
ENSMUST00000102950	oxysterol binding protein 2 [Source:MGI Symbol;Acc:MGI:1921559]	Q8K0C7		6.9	1.7E-02	5.0	3.1E-05	0.1	9.3E-01	-0.5	2.6E-01
ENSMUST00000102953	ATPase, class I, type 8B, member 5 [Source:MGI Symbol;Acc:MGI:2444287]		A3FIN4	4.8	5.4E-04	6.1	5.0E-04	-0.3	7.8E-01	-0.1	8.5E-01
ENSMUST00000100782	family with sequence similarity 222, member B [Source:MGI Symbol;Acc:MGI:2384939]	E9PXL0		0.8	4.5E-01	-1.5	3.8E-01	0.0	9.8E-01	2.4	1.7E-01
ENSMUST00000102960	ignal transducing adaptor molecule (SH3 domain and ITAM motif) 1 [Source:MGI Symbol;Acc:MGI:1329014	Q3TQ49	P70297	2.0	4.3E-03	4.4	4.5E-04	-1.5	1.2E-01	0.1	8.8E-01
ENSMUST00000102962	ciliary neurotrophic factor receptor [Source:MGI Symbol;Acc:MGI:99605]		O88507	6.3	2.2E-04	-4.2	3.2E-03	0.4	3.8E-01	0.5	6.8E-01
ENSMUST00000100794	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]	E9Q405		-1.9	2.9E-01	0.7	7.4E-01	0.0	1.0E+00	-2.6	2.2E-01
ENSMUST00000102963	dynein, axonemal, intermediate chain 1 [Source:MGI Symbol;Acc:MGI:1916172]	A2ANP4	Q8C0M8	5.2	1.1E-04	6.7	8.4E-05	-0.4	6.7E-01	0.7	2.6E-01
ENSMUST00000102964	histone cluster 1, H4a [Source:MGI Symbol;Acc:MGI:2448419]	B2RTM0	P62806	5.5	4.8E-03	-6.4	7.1E-03	-1.4	1.7E-01	-1.9	4.0E-01
ENSMUST00000100802	nuclear fragile X mental retardation protein interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915814]		Q5F2E7	-0.8	2.7E-01	-0.6	5.1E-01	0.7	2.6E-01	0.6	5.0E-01
ENSMUST00000102965	histone cluster 1, H4b [Source:MGI Symbol;Acc:MGI:2448420]	B2RTM0	P62806	4.1	3.1E-02	6.0	7.7E-02	-0.9	7.9E-01	0.8	6.9E-01
ENSMUST00000100807	predicted gene 10392 [Source:MGI Symbol;Acc:MGI:3704377]	Q3V3I3		0.9	3.6E-01	1.4	2.4E-01	0.2	8.2E-01	-0.3	7.9E-01
ENSMUST00000102971	histone cluster 1, H4f [Source:MGI Symbol;Acc:MGI:2448425]	B2RTM0	P62806	5.5	9.4E-04	2.5	2.1E-01	-1.3	5.0E-01	2.2	1.1E-01
ENSMUST00000102975	MOB kinase activator 3B [Source:MGI Symbol;Acc:MGI:2664539]		Q8VE04	3.8	1.0E-04	6.0	7.7E-02	-0.9	7.9E-01	0.8	6.9E-01
ENSMUST00000100812	G protein-coupled receptor kinase-interactor 1 [Source:MGI Symbol;Acc:MGI:1927140]	Q5F258		-1.3	9.9E-02	-0.5	5.9E-01	0.5	4.2E-01	-0.3	7.3E-01
ENSMUST00000102976	GATA binding protein 3 [Source:MGI Symbol;Acc:MGI:95663]	Q3U0R5	P23772	5.5	1.7E-05	-0.5	3.1E-01	0.8	4.6E-02	0.1	8.3E-01
ENSMUST00000100818	transmembrane protein 254c [Source:MGI Symbol;Acc:MGI:3711260]	Q9D890		2.6	3.5E-01	2.9	2.5E-01	-1.5	5.8E-01	-1.8	3.9E-01
ENSMUST00000100819	transmembrane protein 254c [Source:MGI Symbol;Acc:MGI:3711260]		Q9DCV5	-1.4	8.7E-02	2.5	1.7E-02	0.9	2.3E-01	-3.0	4.3E-03
ENSMUST00000100827	ATP-binding cassette, sub-family C (CFTR/MRP), member 9 [Source:MGI Symbol;Acc:MGI:1352630]		P70170	0.7	8.1E-01	3.2	3.7E-01	0.3	9.3E-01	-2.2	4.2E-01
ENSMUST00000102977	histone cluster 1, H4i [Source:MGI Symbol;Acc:MGI:2448432]	B2RTM0	P62806	-3.5	1.1E-04	2.8	8.5E-02	0.2	8.8E-01	1.0	3.8E-01
ENSMUST00000100837	calcium/calmodulin-dependent protein kinase II gamma [Source:MGI Symbol;Acc:MGI:88259]	Q6ZWS7	Q923T9	-1.7	1.2E-01	-5.5	1.2E-02	0.3	7.3E-01	4.1	4.0E-02
ENSMUST00000102978	zinc finger protein 184 (Kruppel-like) [Source:MGI Symbol;Acc:MGI:1922244]		Q7TSH9	7.1	6.8E-04	-1.5	1.7E-02	1.1	5.1E-03	-1.5	1.9E-02
ENSMUST00000102979	histone cluster 1, H4n [Source:MGI Symbol;Acc:MGI:4843992]	B2RTM0	P62806	2.6	3.1E-02	-5.6	2.2E-04	1.2	6.3E-03	4.8	6.4E-04
ENSMUST00000102980	aldo-keto reductase family 1, member B3 (aldose reductase) [Source:MGI Symbol;Acc:MGI:1353494]	Q3UDY1	P45376	-4.7	9.5E-04	3.0	1.9E-03	0.0	9.5E-01	0.5	3.3E-01
ENSMUST00000102985	minichromosome maintenance deficient 10 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1917274]		Q0VBD2	3.3	4.0E-04	4.1	3.0E-05	0.2	6.3E-01	-0.5	2.4E-01
ENSMUST00000102993	ubiquitin-conjugating enzyme E2H [Source:MGI Symbol;Acc:MGI:104632]	Q3V2N4	P62257	-4.9	9.0E-05	-2.4	2.5E-02	0.2	6.7E-01	-0.1	9.1E-01
ENSMUST00000102994	UFM1 specific ligase 1 [Source:MGI Symbol;Acc:MGI:1914740]		Q8CCJ3	-3.5	2.0E-02	-1.1	1.9E-01	0.9	1.3E-01	-0.4	6.3E-01
ENSMUST00000102996	RIKEN cDNA 4930452B06 gene [Source:MGI Symbol;Acc:MGI:1926154]		Q6P2K3	6.6	1.1E-04	6.3	1.8E-04	-1.9	1.4E-01	-0.6	3.8E-01
ENSMUST00000102997	cyclin C [Source:MGI Symbol;Acc:MGI:1858199]		Q62447	-5.7	6.6E-04	6.5	3.7E-03	-0.8	6.7E-01	0.8	4.4E-01
ENSMUST00000102998	Na+/K+ transporting ATPase interacting 3 [Source:MGI Symbol;Acc:MGI:2444830]		Q3URJ8	9.8	1.1E-06	6.4	2.1E-04	-0.6	6.2E-01	-0.6	3.5E-01
ENSMUST00000102999	cyclic nucleotide gated channel beta 3 [Source:MGI Symbol;Acc:MGI:1353562]		Q9JJZ9	6.1	4.5E-05	-6.0	1.5E-04	0.6	2.3E-01	-0.2	8.6E-01
ENSMUST00000103004	aspartate-beta-hydroxylase [Source:MGI Symbol;Acc:MGI:1914186]	Q9CR06		6.7	5.2E-05	7.6	5.0E-05	-0.6	6.0E-01	-0.3	5.8E-01
ENSMUST00000103005	shroom family member 4 [Source:MGI Symbol;Acc:MGI:2685570]		Q1W617	6.8	5.0E-03	6.2	2.3E-04	-0.5	6.7E-01	-1.9	1.4E-02
ENSMUST00000103007	nudix (nucleoside diphosphate linked moiety X)-type motif 11 [Source:MGI Symbol;Acc:MGI:1930957]		P0C028	6.5	1.4E-04	5.7	3.0E-03	-0.7	6.4E-01	0.7	4.2E-01
ENSMUST00000100928	rabaptin, RAB GTPase binding effector protein 1 [Source:MGI Symbol;Acc:MGI:1860236]		O35551	-1.6	5.0E-01	-0.9	6.6E-01	-1.9	2.6E-01	-2.6	3.0E-01
ENSMUST00000100933	calmodulin binding transcription activator 2 [Source:MGI Symbol;Acc:MGI:2135957]		Q80Y50	-4.6	8.4E-02	1.2	6.4E-01	2.8	1.9E-01	-3.0	2.5E-01
ENSMUST00000100937	RIKEN cDNA 4930522L14 gene [Source:MGI Symbol;Acc:MGI:1925270]	Q8C1G8		0.3	6.2E-01	1.4	1.1E-01	-0.6	3.6E-01	-1.7	3.8E-02
ENSMUST00000100942	vesicle-associated membrane protein 1 [Source:MGI Symbol;Acc:MGI:1313276]		Q62442	0.8	3.2E-01	0.6	6.0E-01	-0.1	9.3E-01	0.2	8.5E-01
ENSMUST00000103008	syndecan binding protein [Source:MGI Symbol;Acc:MGI:1337026]	Q3TMX0		-10.0	1.1E-05	5.9	1.8E-04	-0.4	7.1E-01	-0.5	4.2E-01
ENSMUST00000100950	RIKEN cDNA 0610010K14 gene [Source:MGI Symbol;Acc:MGI:1915609]	F6XN97		-2.0	1.2E-01	-0.4	7.9E-01	1.1	3.5E-01	-0.4	7.8E-01
ENSMUST00000103010	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog [Source:MGI Symbol;Acc:MGI:96892]	Q3U6Q5	P25911	-10.2	1.3E-04	-4.6	3.8E-04	-0.8	9.0E-02	-0.2	8.0E-01
ENSMUST00000100961	guanylate-binding protein 9 [Source:MGI Symbol;Acc:MGI:3605620]	Q8BTS3		-0.2	8.9E-01	-0.3	7.8E-01	-2.3	3.7E-02	-2.2	1.2E-01
ENSMUST00000100962	guanylate binding protein 4 [Source:MGI Symbol;Acc:MGI:97072]	A4UUI3		0.6	3.4E-01	-1.2	1.0E-01	-2.3	1.3E-03	-0.5	4.8E-01
ENSMUST00000103014	fructosamine 3 kinase [Source:MGI Symbol;Acc:MGI:1926834]	Q7TQJ3		6.3	6.5E-05	6.2	3.5E-04	-0.5	6.9E-01	0.1	8.5E-01
ENSMUST00000103015	nuclear prelamin A recognition factor [Source:MGI Symbol;Acc:MGI:1914858]		Q9CYQ7	-3.6	8.2E-06	-1.9	5.9E-03	0.6	9.9E-02	-0.2	7.3E-01
ENSMUST00000100996				-1.8	5.4E-02	-2.4	7.6E-02	0.4	6.0E-01	0.9	4.6E-01
ENSMUST00000101004	period circadian clock 1 [Source:MGI Symbol;Acc:MGI:1098283]	Q8C4K7		1.1	2.7E-01	2.1	1.5E-01	0.4	7.5E-01	-0.6	5.6E-01
ENSMUST00000103017	nuclear protein localization 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2679787]		P60670	7.0	7.6E-03	6.3	1.6E-04	-0.6	5.9E-01	0.4	4.6E-01
ENSMUST00000103019	apoptosis-associated tyrosine kinase [Source:MGI Symbol;Acc:MGI:1197518]	B1AZF9		-7.2	2.5E-04	-3.3	5.9E-03	-0.2	6.4E-01	1.2	2.2E-01
ENSMUST00000101018	centrosomal protein 170B [Source:MGI Symbol;Acc:MGI:2145043]		Q80U49	8.2	3.9E-02	2.5	6.1E-01	-0.7	8.7E-01	5.0	1.9E-01
ENSMUST00000103024	cDNA sequence BC100451 [Source:MGI Symbol;Acc:MGI:1929713]		Q497N6	5.8	3.0E-03	8.0	1.8E-04	0.2	8.8E-01	-0.3	6.3E-01
ENSMUST00000101029	inverted formin, FH2 and WH2 domain containing [Source:MGI Symbol;Acc:MGI:1917685]	E9QLA5		0.4	5.6E-01	1.0	2.9E-01	0.2	8.2E-01	-0.4	6.1E-01
ENSMUST00000101032	membrane-associated ring finger (C3HC4) 8 [Source:MGI Symbol;Acc:MGI:1919029]		Q9DBD2	1.0	5.0E-01	4.2	5.7E-02	1.7	3.6E-01	-1.6	2.8E-01
ENSMUST00000103027	mannoside acetylglucosaminyltransferase 5, isoenzyme B [Source:MGI Symbol;Acc:MGI:3606200]		Q765H6	8.0	5.9E-05	5.3	4.8E-02	-0.1	9.7E-01	-0.1	9.5E-01
ENSMUST00000103029	rhomboid 5 homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2442473]		Q80WQ6	-7.3	2.4E-04	9.5	5.7E-03	-1.0	7.4E-01	-2.8	8.2E-02
ENSMUST00000101049	elaC homolog 2 (E. coli) [Source:MGI Symbol;Acc:MGI:1890496]		Q80Y81	-2.0	1.5E-01	-1.7	2.9E-01	-0.2	8.1E-01	-0.5	7.7E-01
ENSMUST00000103035	potassium channel tetramerisation domain containing 2 [Source:MGI Symbol;Acc:MGI:1917632]	Q4VBE7		-4.3	1.7E-03	3.0	1.9E-01	0.6	7.8E-01	1.6	2.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000103036	immature colon carcinoma transcript 1 [Source:MGI Symbol;Acc:MGI:1915822]		Q8R035	-4.2	1.0E-03	-1.4	2.0E-01	1.1	9.8E-02	0.7	4.9E-01
ENSMUST00000103037	Usher syndrome 1G [Source:MGI Symbol;Acc:MGI:2450757]	Q0VBT9	Q80T11	8.2	9.9E-06	6.8	4.3E-03	-0.3	8.7E-01	0.6	5.6E-01
ENSMUST00000103038	N-acetyltransferase 9 (GCN5-related, putative) [Source:MGI Symbol;Acc:MGI:1913426]		Q3UG98	-2.4	1.0E-02	6.3	4.8E-04	-0.4	7.6E-01	0.3	6.2E-01
ENSMUST00000103040	N-acetyltransferase 9 (GCN5-related, putative) [Source:MGI Symbol;Acc:MGI:1913426]		Q3UG98	-4.4	8.2E-04	2.9	1.7E-01	-0.7	7.3E-01	3.7	2.3E-02
ENSMUST00000103060	WD repeat domain, phosphoinositide interacting 1 [Source:MGI Symbol;Acc:MGI:1261864]		Q8R3E3	-2.7	2.3E-04	-2.3	2.0E-01	2.0	8.9E-02	0.7	6.8E-01
ENSMUST00000103061	archaelysin family metallopeptidase 2 [Source:MGI Symbol;Acc:MGI:104837]	B1AT59		-3.1	3.5E-03	-2.3	1.5E-01	2.0	2.9E-02	-0.4	8.0E-01
ENSMUST00000103062	regulator of G-protein signaling 9 [Source:MGI Symbol;Acc:MGI:1338824]	A2A6V6		7.1	8.8E-04	-0.8	2.4E-01	0.2	7.5E-01	-0.6	3.9E-01
ENSMUST00000103067	SMAD specific E3 ubiquitin protein ligase 2 [Source:MGI Symbol;Acc:MGI:1913563]		A2A5Z6	-3.0	8.1E-05	4.6	9.1E-03	-0.6	6.6E-01	1.6	1.0E-01
ENSMUST00000103069	platelet/endothelial cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97537]		Q08481	-3.3	2.0E-02	6.1	8.9E-04	-0.4	7.5E-01	-0.9	2.4E-01
ENSMUST00000103070	testis expressed gene 2 [Source:MGI Symbol;Acc:MGI:102465]	B1ATR2		5.9	1.6E-02	5.0	1.1E-02	-0.6	7.0E-01	0.9	3.9E-01
ENSMUST00000101085	mitogen-activated protein kinase 7 [Source:MGI Symbol;Acc:MGI:1346347]	Q5NCN8		0.2	9.5E-01	3.8	2.8E-01	3.4	2.1E-01	-0.2	9.3E-01
ENSMUST00000103071	growth hormone [Source:MGI Symbol;Acc:MGI:95707]		P06880	5.0	3.5E-03	-7.9	1.9E-04	0.5	2.3E-01	0.9	5.3E-01
ENSMUST00000103072	STE20-related kinase adaptor alpha [Source:MGI Symbol;Acc:MGI:1919399]		Q3UUJ4	-3.0	2.7E-02	5.3	1.3E-02	-0.6	7.5E-01	1.2	2.8E-01
ENSMUST00000103075	N-ethylmaleimide sensitive fusion protein [Source:MGI Symbol;Acc:MGI:104560]		P46460	-3.4	1.5E-05	-6.6	1.2E-04	0.6	9.1E-02	-0.8	4.8E-01
ENSMUST00000103076	spermatogenesis associated 32 [Source:MGI Symbol;Acc:MGI:3045340]		Q8C5V0	7.5	1.3E-04	8.4	7.6E-05	-0.7	6.1E-01	-0.2	7.6E-01
ENSMUST00000101102	RALBP1 associated Eps domain containing protein 2 [Source:MGI Symbol;Acc:MGI:2663511]	B9EI38		2.5	2.3E-01	7.0	1.0E-02	0.3	8.9E-01	-4.1	1.9E-02
ENSMUST00000103077	phospholipase C, delta 3 [Source:MGI Symbol;Acc:MGI:107451]		Q8K2J0	7.7	8.4E-05	-1.1	1.1E-01	0.6	1.7E-01	-0.7	3.2E-01
ENSMUST00000103079	cortactin [Source:MGI Symbol;Acc:MGI:99695]		Q60598	9.7	1.4E-06	-1.9	6.7E-02	1.0	8.6E-02	0.0	9.7E-01
ENSMUST00000103081	a disintegrin and metallopeptidase domain 11 [Source:MGI Symbol;Acc:MGI:1098667]		Q9R1V4	5.6	6.6E-04	-5.8	4.9E-03	2.3	6.3E-03	0.6	7.1E-01
ENSMUST00000101122	G protein-coupled receptor 27 [Source:MGI Symbol;Acc:MGI:1202299]		O54897	-1.0	1.3E-01	0.0	9.9E-01	0.6	3.3E-01	-0.4	5.6E-01
ENSMUST00000103084	zinc finger protein 334 [Source:MGI Symbol;Acc:MGI:2388656]	A2A4U6		9.6	1.3E-06	0.2	8.0E-01	0.7	3.1E-01	-1.7	1.0E-01
ENSMUST00000101141	shroom family member 2 [Source:MGI Symbol;Acc:MGI:107194]	A7TU71		4.3	1.9E-01	4.8	1.8E-01	-0.3	9.4E-01	-0.8	7.2E-01
ENSMUST00000103085	zinc finger protein 663 [Source:MGI Symbol;Acc:MGI:2685854]	Q6NXM6		8.0	1.5E-02	4.9	5.1E-02	1.2	5.6E-01	1.9	2.2E-01
ENSMUST00000103093	cathepsin A [Source:MGI Symbol;Acc:MGI:97748]	Q544R6	P16675	-11.6	3.3E-06	-6.3	2.3E-02	0.4	6.6E-01	1.1	6.4E-01
ENSMUST00000101150	zinc finger with KRAB and SCAN domains 17 [Source:MGI Symbol;Acc:MGI:2679270]		Q5SXI5	1.4	2.6E-01	5.1	1.5E-02	2.4	1.5E-01	-1.3	2.6E-01
ENSMUST00000103094	acyl-CoA thioesterase 8 [Source:MGI Symbol;Acc:MGI:2158201]	Q3U965	P58137	-4.6	7.9E-04	-2.7	6.1E-03	1.4	1.1E-02	-0.1	9.0E-01
ENSMUST00000101153	IQ motif and Sec7 domain 1 [Source:MGI Symbol;Acc:MGI:1196356]		Q8R0S2	1.4	3.0E-01	1.5	4.2E-01	0.6	6.5E-01	0.6	6.7E-01
ENSMUST00000101165	aarF domain containing kinase 1 [Source:MGI Symbol;Acc:MGI:1919363]		Q9D0L4	-1.2	2.8E-01	0.2	8.9E-01	-0.1	8.9E-01	-1.5	2.3E-01
ENSMUST00000101171	thioredoxin reductase 3 [Source:MGI Symbol;Acc:MGI:2386711]	D3Z0H7		2.7	9.1E-02	5.9	7.9E-03	1.1	5.4E-01	-2.1	1.1E-01
ENSMUST00000101190	predicted gene 15127 [Source:MGI Symbol;Acc:MGI:3711248]	L7N236		2.1	7.9E-02	7.0	7.2E-05	-0.5	6.3E-01	-5.4	8.1E-05
ENSMUST00000101191	kelch-like 5 [Source:MGI Symbol;Acc:MGI:1919028]	Q6PFE1		-0.2	9.2E-01	-2.5	3.6E-01	-1.3	5.0E-01	1.0	7.1E-01
ENSMUST00000103096	WAP four-disulfide core domain 3 [Source:MGI Symbol;Acc:MGI:1923897]		Q14AE4	5.6	1.5E-02	-7.0	1.8E-04	0.7	8.5E-02	0.6	6.3E-01
ENSMUST00000101195	TBC1 domain family, member 1 [Source:MGI Symbol;Acc:MGI:1889508]	Q3U3T9	Q60949	-3.6	2.3E-01	-1.5	7.1E-01	1.5	5.3E-01	-0.6	8.9E-01
ENSMUST00000103100	epididymal peptidase inhibitor [Source:MGI Symbol;Acc:MGI:1922776]		Q9DA01	6.1	1.5E-04	-8.0	2.3E-04	1.0	5.1E-02	-0.8	6.3E-01
ENSMUST00000103101	phosphatidylinositol glycan anchor biosynthesis, class T [Source:MGI Symbol;Acc:MGI:1926178]		Q8BXQ2	-6.3	9.9E-04	-5.2	3.8E-03	1.7	1.0E-02	0.0	9.8E-01
ENSMUST00000103104	matrilin 4 [Source:MGI Symbol;Acc:MGI:1328314]	F2Z3U4		6.4	2.1E-02	7.0	1.1E-04	-1.5	2.3E-01	-0.5	3.8E-01
ENSMUST00000101206	Rap guanine nucleotide exchange factor (GEF) 6 [Source:MGI Symbol;Acc:MGI:2384761]	Q5NCJ1		2.2	3.8E-01	0.4	9.0E-01	-1.8	5.0E-01	0.0	9.9E-01
ENSMUST00000103105	amine oxidase, copper containing 3 [Source:MGI Symbol;Acc:MGI:1306797]		O70423	4.9	8.6E-05	3.7	3.0E-04	-4.2	9.6E-04	0.5	3.1E-01
ENSMUST00000103108	WNK lysine deficient protein kinase 4 [Source:MGI Symbol;Acc:MGI:1917097]		Q80UE6	8.1	1.1E-02	6.1	4.4E-04	-0.7	6.0E-01	-0.6	3.8E-01
ENSMUST00000103109	contactin associated protein-like 1 [Source:MGI Symbol;Acc:MGI:1858201]		O54991	5.8	6.9E-06	4.8	8.0E-04	0.1	9.3E-01	-0.8	2.2E-01
ENSMUST00000103111	zinc fingers and homeoboxes 3 [Source:MGI Symbol;Acc:MGI:2444772]	Q3UPQ8	Q8C0Q2	10.2	5.3E-05	-3.4	2.1E-03	1.2	1.3E-02	0.4	6.4E-01
ENSMUST00000103114	signal transducer and activator of transcription 3 [Source:MGI Symbol;Acc:MGI:103038]	Q6GU23	P42227	1.9	3.4E-03	-5.6	2.3E-04	0.7	1.2E-01	-3.2	2.2E-02
ENSMUST00000101245	MOB kinase activator 1A [Source:MGI Symbol;Acc:MGI:2442631]		Q921Y0	1.1	6.9E-01	-1.2	6.2E-01	-4.4	6.7E-02	-2.1	4.5E-01
ENSMUST00000101249	heterogeneous nuclear ribonucleoprotein A/B [Source:MGI Symbol;Acc:MGI:1330294]	Q80XR6		3.5	7.4E-02	1.7	5.0E-01	-0.9	7.0E-01	0.9	6.3E-01
ENSMUST00000101253	coiled-coil domain containing 142 [Source:MGI Symbol;Acc:MGI:3045292]		Q8CAI1	1.3	4.7E-02	1.7	3.7E-02	0.4	5.5E-01	-0.1	8.6E-01
ENSMUST00000101254	coiled-coil domain containing 142 [Source:MGI Symbol;Acc:MGI:3045292]		Q8CAI1	3.9	8.1E-02	5.1	3.9E-02	-0.6	8.1E-01	-1.7	2.7E-01
ENSMUST00000101257	lysyl oxidase-like 3 [Source:MGI Symbol;Acc:MGI:1337004]	E9Q0X7		2.2	2.7E-01	1.0	6.7E-01	-1.2	5.4E-01	0.1	9.6E-01
ENSMUST00000103115	phospholipase C, gamma 1 [Source:MGI Symbol;Acc:MGI:97615]		Q62077	7.7	2.5E-04	6.1	1.1E-03	-0.6	6.5E-01	0.2	8.0E-01
ENSMUST00000103119	zinc finger protein 385C [Source:MGI Symbol;Acc:MGI:3608347]		A2A5E6	5.9	5.8E-05	-0.1	9.3E-01	1.1	7.6E-02	-0.4	6.6E-01
ENSMUST00000103120	2',3'-cyclic nucleotide 3' phosphodiesterase [Source:MGI Symbol;Acc:MGI:88437]	Q3TYV5	P16330	-3.7	2.0E-02	3.3	6.0E-03	-0.3	7.3E-01	-0.1	8.8E-01
ENSMUST00000101285	vesicle-associated membrane protein 5 [Source:MGI Symbol;Acc:MGI:1858622]	Q791P0	Q9Z2P8	-3.0	4.0E-02	-4.5	4.1E-02	0.2	8.6E-01	1.7	4.1E-01
ENSMUST00000101291	estrogen receptor 2 (beta) [Source:MGI Symbol;Acc:MGI:109392]			2.9	1.8E-01	8.0	2.9E-03	-0.3	8.8E-01	-5.5	2.2E-03
ENSMUST00000103121	RIKEN cDNA D630003M21 gene [Source:MGI Symbol;Acc:MGI:3606579]	A2AC60		3.6	5.6E-04	-6.0	8.6E-03	1.3	1.3E-01	1.6	4.4E-01
ENSMUST00000103124	huntingtin-associated protein 1 [Source:MGI Symbol;Acc:MGI:1261831]		O35668	6.8	8.6E-04	6.1	8.6E-06	-0.3	6.4E-01	-1.1	2.4E-02
ENSMUST00000103129	SN1, MIND kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191418		Q9CYC5	-2.1	2.0E-02	4.3	3.3E-04	0.1	9.0E-01	0.8	1.6E-01
ENSMUST00000101301	inner membrane protein, mitochondrial [Source:MGI Symbol;Acc:MGI:1923864]		Q8CAQ8	-0.2	9.4E-01	-4.4	1.3E-01	-4.8	1.8E-02	-0.5	8.6E-01
ENSMUST00000103131	keratin 10 [Source:MGI Symbol;Acc:MGI:96685]	A2A513		6.0	3.5E-04	2.8	1.2E-02	-2.4	2.6E-02	-1.1	1.7E-01
ENSMUST00000101313	solute carrier family 38, member 6 [Source:MGI Symbol;Acc:MGI:3648156]	F2Z3Y3		2.8	3.3E-01	1.7	4.8E-01	-3.1	2.6E-01	-2.0	3.7E-01
ENSMUST00000103132	keratin 222 [Source:MGI Symbol;Acc:MGI:2442728]		Q8CCX5	4.3	8.0E-04	-6.0	4.0E-03	1.0	1.0E-01	-0.7	7.1E-01
ENSMUST00000103133	d, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 [Source:MGI Symbol;Acc		O54941	-4.0	8.3E-05	2.0	2.0E-02	-0.5	4.4E-01	0.0	9.9E-01
ENSMUST00000101339	NHS-like 2 [Source:MGI Symbol;Acc:MGI:3645090]	E9Q0V6		3.0	2.3E-01	6.8	2.8E-02	2.5	3.3E-01	-1.3	5.6E-01
ENSMUST00000103140	receptor potential cation channel, subfamily C, member 4 associated protein [Source:MGI Symbol;Acc:MGI:1		Q9JLV2	-8.1	1.4E-04	3.7	7.8E-02	-1.3	5.2E-01	0.4	8.0E-01
ENSMUST00000101343	MAD2 mitotic arrest deficient-like 1 [Source:MGI Symbol;Acc:MGI:1860374]	Q5HZH8	Q9Z1B5	-0.7	1.5E-01	1.2	7.6E-02	0.9	8.7E-02	-1.1	8.5E-02
ENSMUST00000103142	acyl-CoA synthetase short-chain family member 2 [Source:MGI Symbol;Acc:MGI:1890410]	A2AQN4		-3.6	1.1E-02	-4.6	4.7E-04	0.1	8.6E-01	-0.2	8.2E-01
ENSMUST00000103143	F-box and leucine-rich repeat protein 20 [Source:MGI Symbol;Acc:MGI:1919444]		Q9CZV8	-2.3	3.1E-03	7.0	2.5E-03	-0.7	6.9E-01	-0.6	5.4E-01
ENSMUST00000103146	ribosomal protein L23 [Source:MGI Symbol;Acc:MGI:1929455]		P62830	-3.1	2.8E-04	-5.3	3.0E-03	1.7	9.4E-03	1.0	4.5E-01
ENSMUST00000103147	proteasome (prosome, macropain) subunit, beta type 3 [Source:MGI Symbol;Acc:MGI:1347014]	Q545G0	Q9R1P1	-6.2	2.8E-05	4.5	3.6E-02	-2.8	2.0E-01	-1.6	2.5E-01
ENSMUST00000103152	CDK5 regulatory subunit associated protein 3 [Source:MGI Symbol;Acc:MGI:1933126]		Q99LM2	-7.7	2.2E-05	-5.0	7.2E-04	1.1	5.9E-02	-3.4	2.8E-02
ENSMUST00000103155	tubulin tyrosine ligase-like family, member 9 [Source:MGI Symbol;Acc:MGI:1913589]		A2APC3	4.8	3.4E-02	5.6	2.1E-02	-0.7	7.5E-01	0.7	5.9E-01
ENSMUST00000103162	sarcoglycan, alpha (dystrophin-associated glycoprotein) [Source:MGI Symbol;Acc:MGI:894698]		P82350	6.2	3.2E-02	6.5	1.7E-03	0.9	5.5E-01	-1.0	2.2E-01
ENSMUST00000103164	acyl-CoA synthetase family member 2 [Source:MGI Symbol;Acc:MGI:2388287]		Q8VCW8	3.4	1.1E-03	-8.3	1.1E-03	-2.3	6.9E-03	-0.5	7.8E-01
ENSMUST00000103171	ovo-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1338039]		Q8CIV7	5.9	7.1E-04	7.5	3.9E-05	-0.6	5.9E-01	-0.7	2.3E-01
ENSMUST00000103172	destrin [Source:MGI Symbol;Acc:MGI:1929270]	Q4FK36	Q9R0P5	-6.9	3.1E-07	7.8	7.3E-05	-0.6	6.0E-01	-0.4	5.3E-01
ENSMUST00000101388	zinc finger, X-linked, duplicated B [Source:MGI Symbol;Acc:MGI:3694898]		A2CE44	-0.7	4.0E-01	-0.1	8.9E-01	1.1	2.0E-01	0.6	5.7E-01
ENSMUST00000103175	ubiquitin-conjugating enzyme E2J 2 [Source:MGI Symbol;Acc:MGI:2153608]		Q6P073	-5.1	1.0E-03	-4.2	2.8E-02	-0.3	7.4E-01	0.6	7.4E-01
ENSMUST00000103177	lactoperoxidase [Source:MGI Symbol;Acc:MGI:1923363]	Q5SW46		8.2	7.3E-06	3.2	1.4E-02	-0.4	6.7E-01	1.2	1.5E-01
ENSMUST00000101405	deafness, autosomal dominant 5 (human) [Source:MGI Symbol;Acc:MGI:1889850]	D3YYP5		1.3	1.2E-01	2.6	1.8E-02	0.2	7.9E-01	-1.1	1.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000101411	predicted gene 29609 [Source:MGI Symbol;Acc:MGI:5580315]	Q3UU56		-0.9	6.2E-01	-0.3	8.9E-01	0.2	8.8E-01	-0.3	8.6E-01
ENSMUST00000103178	protein kinase C, zeta [Source:MGI Symbol;Acc:MGI:97602]	Q3V341		6.6	5.4E-04	-2.5	5.6E-03	-1.0	3.2E-02	-1.4	7.2E-02
ENSMUST00000103179	myotubularin related protein 4 [Source:MGI Symbol;Acc:MGI:2180699]		Q91XS1	-5.0	2.3E-03	-6.1	6.2E-03	-0.6	3.9E-01	-0.1	9.8E-01
ENSMUST00000103181	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 [Source:MGI Symbol;Acc:MGI:1332236]		Q99L43	-7.3	1.4E-03	7.9	1.2E-04	-0.9	5.3E-01	0.6	3.3E-01
ENSMUST00000101434	family with sequence similarity 220, member A [Source:MGI Symbol;Acc:MGI:1914488]	Q91X57		3.6	8.0E-02	5.2	3.3E-02	0.3	8.9E-01	-1.3	4.5E-01
ENSMUST00000101436	leucine rich repeat containing 61 [Source:MGI Symbol;Acc:MGI:2652848]			1.1	5.0E-02	2.2	6.8E-03	1.0	7.1E-02	-0.1	9.1E-01
ENSMUST00000103182	Ras association (RalGDS/AF-6) domain family member 2 [Source:MGI Symbol;Acc:MGI:2442060]		Q8BMS9	-6.1	5.3E-03	6.4	4.9E-04	-0.5	7.0E-01	-0.9	2.1E-01
ENSMUST00000103184	adrenergic receptor, alpha 1d [Source:MGI Symbol;Acc:MGI:106673]	A2ANQ2		7.6	7.4E-05	2.5	1.6E-01	-3.5	9.6E-02	0.2	9.1E-01
ENSMUST00000103186	clathrin, heavy polypeptide (Hc) [Source:MGI Symbol;Acc:MGI:2388633]		Q68FD5	-7.1	4.4E-06	4.3	1.1E-04	-1.3	7.6E-02	-0.9	9.7E-02
ENSMUST00000103188	RIKEN cDNA 1700037H04 gene [Source:MGI Symbol;Acc:MGI:1914576]		Q9D1K7	-6.7	4.2E-04	-7.7	3.4E-03	1.1	1.9E-01	-2.8	2.7E-01
ENSMUST00000103191	ribosomal protein L22 [Source:MGI Symbol;Acc:MGI:99262]	Q4VAG4	P67984	-10.0	4.4E-06	7.7	1.9E-05	0.2	8.0E-01	0.2	7.1E-01
ENSMUST00000101470	arginine vasopressin receptor 2 [Source:MGI Symbol;Acc:MGI:88123]	Q3SWS4		-2.3	6.9E-02	-0.6	6.5E-01	0.8	4.1E-01	-0.8	5.5E-01
ENSMUST00000103193	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) [Source:MGI Symbol;Acc:MGI:96622]	Q60I30	Q9D892	-2.7	4.1E-04	-1.3	1.1E-01	0.4	4.9E-01	-1.4	9.9E-02
ENSMUST00000101477	pellino 1 [Source:MGI Symbol;Acc:MGI:1914495]	Q5SRW7	Q8C669	3.1	2.1E-01	0.6	8.3E-01	-2.3	3.9E-01	0.2	9.3E-01
ENSMUST00000103197	nucleolar protein 9 [Source:MGI Symbol;Acc:MGI:1921285]		Q3TZX8	3.6	1.1E-02	-3.2	5.5E-04	0.4	2.4E-01	0.3	6.1E-01
ENSMUST00000103198	NOP56 ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1914384]		Q9D6Z1	-4.6	1.3E-03	-1.3	5.9E-02	1.1	1.7E-02	0.1	8.1E-01
ENSMUST00000103199	small nuclear ribonucleoprotein B [Source:MGI Symbol;Acc:MGI:98342]		P27048	-7.7	6.8E-05	0.7	5.4E-01	1.4	1.3E-01	-2.7	3.9E-02
ENSMUST00000101499	Casitas B-lineage lymphoma-like 1 [Source:MGI Symbol;Acc:MGI:2144842]		Q9JIY2	-0.3	7.2E-01	0.9	3.8E-01	1.2	1.2E-01	0.1	9.4E-01
ENSMUST00000103201	acetyl-Coenzyme A carboxylase alpha [Source:MGI Symbol;Acc:MGI:108451]		Q5SWU9	5.7	1.3E-03	-1.4	3.4E-02	0.2	5.4E-01	-0.3	6.5E-01
ENSMUST00000101509	iduronate 2-sulfatase [Source:MGI Symbol;Acc:MGI:96417]		Q08890	-0.3	5.8E-01	-1.1	1.4E-01	0.5	2.6E-01	1.4	6.4E-02
ENSMUST00000103203	signal-regulatory protein alpha [Source:MGI Symbol;Acc:MGI:108563]	Q6P6I8		-12.0	4.3E-05	-8.1	2.4E-04	1.2	1.7E-02	-1.0	5.3E-01
ENSMUST00000103205	polymerase (RNA) I polypeptide B [Source:MGI Symbol;Acc:MGI:108014]		P70700	3.4	4.1E-04	-4.6	2.8E-02	1.9	2.4E-02	1.0	5.9E-01
ENSMUST00000101527	ATPase, class VI, type 11C [Source:MGI Symbol;Acc:MGI:1859661]		Q9QZW0	-4.0	5.1E-02	-2.7	3.1E-01	0.8	5.9E-01	-0.4	8.8E-01
ENSMUST00000103209	matrix metallopeptidase 28 (epilysin) [Source:MGI Symbol;Acc:MGI:2153062]	Q8BG29		3.8	8.8E-03	6.9	1.5E-04	-0.6	6.2E-01	-0.5	4.5E-01
ENSMUST00000103210	BCL2-like 11 (apoptosis facilitator) [Source:MGI Symbol;Acc:MGI:1197519]		O54918	8.1	6.4E-04	7.9	1.4E-04	-1.0	5.0E-01	0.6	3.8E-01
ENSMUST00000103212	ubiquitination factor E4B [Source:MGI Symbol;Acc:MGI:1927086]		Q9ES00	-2.0	1.3E-02	5.8	2.9E-03	1.7	2.5E-01	-0.3	6.8E-01
ENSMUST00000101551	a disintegrin and metallopeptidase domain 17 [Source:MGI Symbol;Acc:MGI:1096335]	E9PXU2		4.5	9.2E-02	-1.3	6.5E-01	-5.4	4.2E-02	0.4	8.8E-01
ENSMUST00000101553	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B [Source:MGI Symbol;Acc:MGI:2442593]	E9PXU1		-0.6	6.8E-01	1.6	4.2E-01	1.3	4.3E-01	-0.8	5.9E-01
ENSMUST00000101554	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) [Source:MGI Symbol;Acc:MGI:1098267]		Q60597	2.7	1.1E-01	7.0	8.3E-04	-0.5	7.6E-01	-4.8	1.7E-03
ENSMUST00000103215	Kv channel interacting protein 3, calsenilin [Source:MGI Symbol;Acc:MGI:1929258]	Q3YAB0	Q9QXT8	8.2	4.3E-04	7.3	2.4E-04	0.5	7.0E-01	-0.5	4.0E-01
ENSMUST00000103216	DNA fragmentation factor, alpha subunit [Source:MGI Symbol;Acc:MGI:1196227]	Q8C535	O54786	2.9	1.2E-04	5.9	1.5E-03	-0.3	8.4E-01	1.2	1.7E-01
ENSMUST00000101562	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 [Source:MGI Symbol;Acc:MGI:2685438]		Q7SIG6	2.0	5.6E-01	4.6	2.4E-01	-0.1	9.9E-01	-2.6	3.4E-01
ENSMUST00000103217	peroxisomal biogenesis factor 14 [Source:MGI Symbol;Acc:MGI:1927868]		Q9R0A0	-1.5	2.6E-02	6.0	5.8E-04	-0.4	7.2E-01	-0.4	5.5E-01
ENSMUST00000103220	small nuclear ribonucleoprotein 200 (U5) [Source:MGI Symbol;Acc:MGI:2444401]		Q6P4T2	-3.1	1.7E-05	7.0	1.4E-03	-0.1	9.6E-01	-0.7	4.2E-01
ENSMUST00000103224	transient receptor potential cation channel, subfamily M, member 7 [Source:MGI Symbol;Acc:MGI:1929996]		Q923J1	-4.6	7.9E-04	7.9	4.9E-05	-2.7	5.7E-02	0.0	9.3E-01
ENSMUST00000103225	RIKEN cDNA 5730455P16 gene [Source:MGI Symbol;Acc:MGI:1917841]		Q9CYI0	-4.8	6.8E-03	7.4	9.5E-05	-0.6	6.4E-01	0.4	4.5E-01
ENSMUST00000101610	rhomboid domain containing 3 [Source:MGI Symbol;Acc:MGI:2444684]	B7ZNJ8	Q8BP97	2.6	1.9E-01	4.4	6.4E-02	0.0	9.9E-01	-1.8	3.0E-01
ENSMUST00000101613	adaptor protein complex AP-1, beta 1 subunit [Source:MGI Symbol;Acc:MGI:1096368]	Q5SVG4		-4.1	9.6E-02	-1.3	7.1E-01	3.4	1.3E-01	0.7	8.4E-01
ENSMUST00000101615	THO complex 5 [Source:MGI Symbol;Acc:MGI:1351333]	Q5SVF9		2.9	1.1E-01	5.1	9.0E-02	3.0	2.5E-01	0.8	6.6E-01
ENSMUST00000103226	GA repeat binding protein, beta 1 [Source:MGI Symbol;Acc:MGI:95611]		Q00420	-3.5	5.3E-03	5.5	2.3E-04	-3.1	2.1E-02	-1.6	2.4E-02
ENSMUST00000101632	oxysterol binding protein 2 [Source:MGI Symbol;Acc:MGI:1921559]	Q5QNQ4		5.8	4.9E-02	5.3	9.5E-02	-0.6	8.6E-01	-0.1	9.7E-01
ENSMUST00000103231	natriuretic peptide type B [Source:MGI Symbol;Acc:MGI:97368]	Q54AE9	P40753	6.0	2.0E-04	-4.5	4.5E-02	1.2	2.5E-01	1.9	3.6E-01
ENSMUST00000101642	LIM motif-containing protein kinase 2 [Source:MGI Symbol;Acc:MGI:1197517]		O54785	0.8	7.2E-01	1.4	6.5E-01	1.4	5.0E-01	0.8	7.7E-01
ENSMUST00000103232	RIKEN cDNA 2510039O18 gene [Source:MGI Symbol;Acc:MGI:1924284]		Q91X21	-3.4	5.9E-04	-3.4	5.1E-02	1.9	2.9E-02	-0.9	6.0E-01
ENSMUST00000101695	transcription factor E3 [Source:MGI Symbol;Acc:MGI:98511]		Q64092	-3.2	3.1E-01	4.5	3.2E-01	5.4	1.9E-01	-2.3	4.8E-01
ENSMUST00000103233	cytokine receptor-like factor 3 [Source:MGI Symbol;Acc:MGI:1860086]		Q9Z2L7	-6.7	7.6E-04	-5.9	6.9E-06	0.3	2.5E-01	-0.6	3.5E-01
ENSMUST00000103234	fibrillin 1 [Source:MGI Symbol;Acc:MGI:95489]	A2AQ53		8.7	5.3E-05	-4.1	1.5E-04	-0.3	4.0E-01	-0.4	5.2E-01
ENSMUST00000103236	ecotropic viral integration site 2a [Source:MGI Symbol;Acc:MGI:95458]		P20934	-9.9	1.4E-06	-8.4	2.5E-07	-1.0	2.2E-03	-1.8	1.8E-02
ENSMUST00000103299	T cell receptor beta, constant 2 [Source:MGI Symbol;Acc:MGI:4835227]	A0A075B5J4		-3.4	3.4E-04	-1.2	5.4E-01	2.3	9.6E-02	0.2	9.2E-01
ENSMUST00000103359	immunoglobulin kappa variable 4-55 [Source:MGI Symbol;Acc:MGI:2686370]	A0A0B4J1I9		2.6	9.4E-03	-8.1	2.2E-04	0.1	8.5E-01	-1.5	3.7E-01
ENSMUST00000103410	immunoglobulin kappa constant [Source:MGI Symbol;Acc:MGI:96495]	A0A075B5P2		-3.1	2.2E-03	-7.6	4.7E-05	-0.9	4.7E-02	-0.3	7.8E-01
ENSMUST00000103418	immunoglobulin heavy constant gamma 2B [Source:MGI Symbol;Acc:MGI:96445]	A0A075B5P3		4.3	1.4E-04	-2.4	5.8E-03	1.1	2.2E-02	-0.7	3.2E-01
ENSMUST00000103423	Immunoglobulin heavy constant gamma 3 [Source:MGI Symbol;Acc:MGI:2144790]	A0A075B5P5		3.8	4.3E-04	8.4	2.3E-05	-0.8	5.2E-01	0.4	4.9E-01
ENSMUST00000103446	immunoglobulin heavy variable 5-6 [Source:MGI Symbol;Acc:MGI:4439815]	A0A075B5Q0		4.6	5.4E-03	-5.1	3.2E-03	0.8	1.9E-01	-1.9	2.6E-01
ENSMUST00000103473	immunoglobulin heavy variable V9-3 [Source:MGI Symbol;Acc:MGI:3642720]	A0A0B4J1J5		4.4	1.5E-03	5.1	2.9E-05	-4.0	1.4E-03	0.1	9.0E-01
ENSMUST00000102491	ciliary rootlet coiled-coil, rootletin [Source:MGI Symbol;Acc:MGI:3529431]		Q8CJ40	3.5	4.5E-02	5.7	1.8E-02	1.1	5.7E-01	-1.1	4.3E-01
ENSMUST00000103486	immunoglobulin heavy variable 6-3 [Source:MGI Symbol;Acc:MGI:4439854]	A0A075B5T2		6.5	1.4E-03	5.1	1.1E-02	-1.2	4.9E-01	0.5	6.4E-01
ENSMUST00000102494	coiled-coil domain containing 55 [Source:MGI Symbol;Acc:MGI:2144305]		Q5NCR9	-1.6	6.3E-02	-3.0	1.5E-02	-1.1	8.9E-02	0.3	7.4E-01
ENSMUST00000103493	immunoglobulin heavy variable 1-4 [Source:MGI Symbol;Acc:MGI:4439618]	A0A075B5T4		5.4	4.3E-04	-2.8	3.8E-01	2.6	1.8E-01	-1.0	7.6E-01
ENSMUST00000103521	immunoglobulin heavy variable 1-50 [Source:MGI Symbol;Acc:MGI:4439753]	A0A075B5W1		6.6	8.1E-03	-1.9	1.7E-02	-0.2	5.6E-01	-1.5	5.2E-02
ENSMUST00000103523	immunoglobulin heavy variable 1-53 [Source:MGI Symbol;Acc:MGI:3576502]	A0A075B5W3		7.0	8.8E-04	-4.1	2.3E-02	-1.1	1.8E-01	-0.7	7.0E-01
ENSMUST00000103525	immunoglobulin heavy variable V1-54 [Source:MGI Symbol;Acc:MGI:3647133]	A0A075B5W5		5.3	7.7E-05	7.4	6.0E-05	-0.6	6.1E-01	0.0	9.7E-01
ENSMUST00000102501	vacuolar protein sorting 39 (yeast) [Source:MGI Symbol;Acc:MGI:2443189]	Q3USV9	Q8R5L3	-1.6	2.8E-01	-2.4	2.2E-01	-0.3	8.2E-01	0.6	7.5E-01
ENSMUST00000103526	immunoglobulin heavy variable 1-55 [Source:MGI Symbol;Acc:MGI:4439716]	A0A075B5W6		5.6	2.2E-04	-1.3	2.2E-01	-0.2	8.1E-01	-2.2	6.2E-02
ENSMUST00000102504	myosin IC [Source:MGI Symbol;Acc:MGI:106612]		Q9WTI7	3.8	6.9E-02	0.3	9.0E-01	-1.2	6.0E-01	2.2	3.5E-01
ENSMUST00000102505	myosin IC [Source:MGI Symbol;Acc:MGI:106612]		Q9WTI7	4.9	1.1E-01	3.1	3.2E-01	-3.5	2.8E-01	-1.8	4.4E-01
ENSMUST00000103534	immunoglobulin heavy variable V1-63 [Source:MGI Symbol;Acc:MGI:3642755]	A0A075B5X2		4.8	5.9E-04	-6.2	8.2E-04	-0.6	2.5E-01	-0.1	9.6E-01
ENSMUST00000103535	immunoglobulin heavy variable 1-64 [Source:MGI Symbol;Acc:MGI:4439789]	A0A075B5X3		5.7	4.9E-04	-10.4	6.4E-05	0.8	3.6E-02	1.2	4.4E-01
ENSMUST00000103536	immunoglobulin heavy variable V8-11 [Source:MGI Symbol;Acc:MGI:3644925]	A0A075B5X4		6.3	4.4E-04	-5.9	2.2E-02	0.2	8.1E-01	2.3	3.1E-01
ENSMUST00000103588	T cell receptor alpha variable 13D-1 [Source:MGI Symbol;Acc:MGI:3652171]	A0A075B606		4.8	1.5E-03	-7.1	4.0E-03	1.1	7.9E-02	5.1	2.2E-02
ENSMUST00000103663	T cell receptor alpha variable 4-4-DV10 [Source:MGI Symbol;Acc:MGI:3702138]	A0A075B651		4.9	1.8E-03	6.8	1.0E-02	-0.8	7.3E-01	-2.0	1.5E-01
ENSMUST00000103740	T cell receptor alpha constant [Source:MGI Symbol;Acc:MGI:4439838]	A0A075B662		-2.2	8.4E-03	3.2	8.4E-04	-2.3	5.7E-03	0.2	7.2E-01
ENSMUST00000104875	olfactory receptor 160 [Source:MGI Symbol;Acc:MGI:1931271]	Q8VGE3		7.2	5.5E-05	-0.5	7.2E-01	1.5	1.7E-01	-1.6	2.9E-01
ENSMUST00000104891	predicted gene 10912 [Source:MGI Symbol;Acc:MGI:3809094]	Q3UXH0		6.1	7.6E-05	6.9	9.4E-05	-1.9	1.4E-01	-0.1	8.9E-01
ENSMUST00000104915	predicted gene 16485 [Source:MGI Symbol;Acc:MGI:3642771]	Q8C4B7		7.8	1.2E-05	1.6	7.7E-02	-1.0	1.8E-01	0.6	4.2E-01
ENSMUST00000104917	olfactory receptor 483 [Source:MGI Symbol;Acc:MGI:3030317]	Q14AB1	Q8VG05	5.9	2.6E-04	-5.0	1.0E-03	0.3	4.3E-01	-0.2	8.8E-01
ENSMUST00000104926	family with sequence similarity 170, member B [Source:MGI Symbol;Acc:MGI:2145650]	E9PXT9		5.6	5.1E-05	-1.4	9.0E-02	1.3	2.6E-02	-0.5	5.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102521	RAP1 GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:3028623]		Q5SVL6	-0.4	8.7E-01	-2.6	4.8E-01	-0.7	7.9E-01	1.5	6.5E-01
ENSMUST00000104928	actin-like 10 [Source:MGI Symbol;Acc:MGI:1917612]		A2AKE7	8.1	2.0E-05	6.4	1.3E-03	-1.0	5.4E-01	-1.6	8.4E-02
ENSMUST00000104929	predicted gene 11555 [Source:MGI Symbol;Acc:MGI:3651823]	B1AQ89		5.8	2.4E-03	-1.3	1.7E-01	1.2	5.5E-02	-0.5	5.4E-01
ENSMUST00000104930	keratin associated protein 1-3 [Source:MGI Symbol;Acc:MGI:3650443]	A2A588		6.4	1.2E-03	-12.4	2.2E-04	-0.7	1.5E-01	0.9	7.0E-01
ENSMUST00000104936	melanoma antigen, family B, 3 [Source:MGI Symbol;Acc:MGI:105109]	Q9D2H4		6.3	1.4E-04	7.1	3.4E-04	-0.5	7.2E-01	-1.0	1.7E-01
ENSMUST00000104937	ankyrin repeat domain 63 [Source:MGI Symbol;Acc:MGI:2686183]		A2ARS0	6.8	1.8E-05	-4.9	3.1E-02	1.8	6.3E-02	0.6	7.6E-01
ENSMUST00000104944	predicted gene 2399 [Source:MGI Symbol;Acc:MGI:3780567]	F6SV87		5.5	2.2E-02	5.2	4.9E-02	-1.1	6.6E-01	-1.1	4.4E-01
ENSMUST00000104955	sosondowah ankyrin repeat domain family member A [Source:MGI Symbol;Acc:MGI:2687280]		Q8BLS7	9.0	7.0E-06	7.7	6.5E-03	-0.3	9.2E-01	-1.9	1.2E-01
ENSMUST00000104958	protease (prosome, macropain) activator subunit 2B [Source:MGI Symbol;Acc:MGI:1341073]	Q5SVP3	P97372	-2.0	2.5E-02	-6.4	2.8E-03	-1.7	3.7E-02	1.1	5.3E-01
ENSMUST00000104962	RIKEN cDNA 4931440F15 gene [Source:MGI Symbol;Acc:MGI:2441689]	Z4YK74	Q8C0T1	7.4	1.1E-05	3.7	3.2E-03	-0.9	3.3E-01	-1.1	1.6E-01
ENSMUST00000104964	predicted gene 16503 [Source:MGI Symbol;Acc:MGI:3642127]	Q8C6M9		8.6	1.5E-04	-3.9	7.8E-02	1.5	1.4E-01	1.5	4.9E-01
ENSMUST00000102543	aquarius [Source:MGI Symbol;Acc:MGI:1276102]	A2AQA7		2.1	3.1E-01	4.7	9.6E-02	1.5	5.6E-01	-1.2	5.0E-01
ENSMUST00000104983	RNA binding motif protein 8A2 [Source:MGI Symbol;Acc:MGI:3612447]			4.7	2.1E-04	-1.9	5.3E-02	-0.5	4.2E-01	-2.6	3.8E-02
ENSMUST00000104984	choroideremia-like [Source:MGI Symbol;Acc:MGI:101913]			2.3	5.8E-04	2.3	8.4E-02	7.8	1.4E-05	-0.7	4.8E-01
ENSMUST00000104994	predicted gene, 17374 [Source:MGI Symbol;Acc:MGI:4937008]	F6SNQ2		6.1	5.9E-06	7.5	6.0E-05	-1.8	1.5E-01	0.2	7.5E-01
ENSMUST00000104998	transmembrane protein 203 [Source:MGI Symbol;Acc:MGI:2443597]		Q8R235	-2.2	1.1E-02	4.9	4.0E-03	-1.5	3.0E-01	-0.5	5.9E-01
ENSMUST00000102548				0.1	9.7E-01	1.9	5.3E-01	1.6	4.1E-01	-0.2	9.4E-01
ENSMUST00000104999	Notch-regulated ankyrin repeat protein [Source:MGI Symbol;Acc:MGI:1914372]		Q91ZA8	3.7	3.8E-04	-0.6	4.4E-01	0.8	1.1E-01	-0.5	4.9E-01
ENSMUST00000102550	mitochondrial fission regulator 1-like [Source:MGI Symbol;Acc:MGI:1924074]		Q9CWE0	-2.5	4.5E-02	-1.1	3.2E-01	-0.4	5.9E-01	-1.8	1.6E-01
ENSMUST00000102552	high mobility group nucleosomal binding domain 2 [Source:MGI Symbol;Acc:MGI:96136]	Q5BL14	P09602	-2.6	4.0E-01	-8.9	1.1E-02	-6.4	3.2E-03	-0.2	9.7E-01
ENSMUST00000105020	predicted gene 14346 [Source:MGI Symbol;Acc:MGI:3709280]	A2BFZ7		7.2	1.6E-03	-5.0	1.1E-03	1.4	1.3E-02	-1.0	3.8E-01
ENSMUST00000102554	kinesin family member 1C [Source:MGI Symbol;Acc:MGI:1098260]		O35071	0.3	9.1E-01	-1.9	5.9E-01	-2.8	2.4E-01	-0.7	8.5E-01
ENSMUST00000105031	kelch domain containing 7A [Source:MGI Symbol;Acc:MGI:2444612]		A2APT9	6.5	3.3E-05	-1.6	5.2E-02	-0.8	1.7E-01	-1.0	2.0E-01
ENSMUST00000105032	family with sequence similarity 43, member B [Source:MGI Symbol;Acc:MGI:3651622]	A2AM80		7.4	8.5E-05	6.7	1.6E-02	-0.7	7.8E-01	-1.3	3.9E-01
ENSMUST00000102558	misshapen-like kinase 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1355329]		Q9JM52	-0.4	8.8E-01	1.5	6.5E-01	0.3	9.0E-01	-1.6	6.1E-01
ENSMUST00000102559	misshapen-like kinase 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1355329]		Q9JM52	3.2	2.5E-01	4.7	9.6E-02	-2.6	3.6E-01	-4.0	8.1E-02
ENSMUST00000102561	replication protein A2 [Source:MGI Symbol;Acc:MGI:1339939]	Q3TE40		-0.8	1.4E-01	-0.6	3.8E-01	-0.2	6.1E-01	-0.4	4.9E-01
ENSMUST00000105038	predicted gene 3550 [Source:MGI Symbol;Acc:MGI:3781727]	W4VSN7		4.4	6.8E-05	-5.9	3.0E-02	1.3	1.3E-01	-0.5	8.4E-01
ENSMUST00000105049	keratin associated protein 17-1 [Source:MGI Symbol;Acc:MGI:1925164]	A2A5X6		5.1	1.1E-03	-8.7	5.4E-04	1.6	5.1E-03	0.9	6.1E-01
ENSMUST00000105050	keratin associated protein 16-1 [Source:MGI Symbol;Acc:MGI:3650326]		A2A5X5	8.3	5.4E-05	-1.5	1.7E-01	-0.1	9.0E-01	-2.6	4.1E-02
ENSMUST00000105051	keratin associated protein 29-1 [Source:MGI Symbol;Acc:MGI:3652056]		A2A5X4	5.9	2.7E-04	3.6	6.3E-03	1.2	2.0E-01	0.9	2.3E-01
ENSMUST00000105052	keratin associated protein 9-5 [Source:MGI Symbol;Acc:MGI:3650333]	A2A5X3		7.0	9.6E-05	-4.1	1.2E-01	1.6	2.3E-01	2.5	2.8E-01
ENSMUST00000105054	RIKEN cDNA 2300003K06 gene [Source:MGI Symbol;Acc:MGI:1916701]	A2A4M0		6.7	2.3E-04	-2.9	6.1E-03	0.2	6.8E-01	0.0	9.5E-01
ENSMUST00000105055	predicted gene 11564 [Source:MGI Symbol;Acc:MGI:3650329]	A2A4L9		6.9	9.0E-05	-4.6	1.4E-02	-2.0	2.6E-02	-0.8	6.5E-01
ENSMUST00000105057	predicted gene 11569 [Source:MGI Symbol;Acc:MGI:3709346]	B1AQB1		5.9	2.2E-02	1.5	3.2E-02	-0.5	3.2E-01	0.1	8.5E-01
ENSMUST00000105058	predicted gene 11596 [Source:MGI Symbol;Acc:MGI:3652177]	B1AQB0		6.8	1.1E-03	-7.1	1.9E-04	0.2	6.8E-01	0.6	6.6E-01
ENSMUST00000105097	zinc finger SWIM-type containing 6 [Source:MGI Symbol;Acc:MGI:1914513]		Q80TB7	-1.7	3.8E-03	3.0	4.2E-03	0.2	7.8E-01	-1.1	1.1E-01
ENSMUST00000105098	forkhead box D1 [Source:MGI Symbol;Acc:MGI:1347463]		Q61345	6.6	3.3E-04	7.8	9.5E-05	-0.7	6.1E-01	-0.5	4.0E-01
ENSMUST00000105106	histone cluster 1, H2bf [Source:MGI Symbol;Acc:MGI:2448383]		P10853	3.7	1.6E-02	-4.0	1.6E-03	0.7	1.7E-01	-1.2	2.6E-01
ENSMUST00000105107	histone cluster 1, H3e [Source:MGI Symbol;Acc:MGI:2448326]	B9EI85	P84228	5.0	3.8E-03	-5.1	8.1E-04	1.3	2.1E-02	-1.2	3.3E-01
ENSMUST00000105113	predicted gene 362 [Source:MGI Symbol;Acc:MGI:2685208]	D3YU32		7.1	1.5E-04	9.7	1.9E-05	-0.7	6.0E-01	-1.2	4.9E-02
ENSMUST00000102584	uracil DNA glycosylase [Source:MGI Symbol;Acc:MGI:109352]	Q791V7	P97931	2.3	1.8E-01	6.6	1.2E-02	1.8	4.1E-01	-2.5	6.6E-02
ENSMUST00000105140	expressed sequence AW011738 [Source:MGI Symbol;Acc:MGI:2140540]	F6S7Q2		3.4	1.2E-02	7.8	2.9E-03	-0.1	9.6E-01	0.4	6.9E-01
ENSMUST00000105144	interferon zeta [Source:MGI Symbol;Acc:MGI:2448469]	Q8BQT1		7.4	2.1E-04	7.0	3.3E-04	-0.8	5.6E-01	-0.1	8.9E-01
ENSMUST00000102588	transmembrane protein 39b [Source:MGI Symbol;Acc:MGI:2682939]		Q810L4	1.3	1.4E-01	7.0	1.0E-03	5.1	4.6E-03	-0.7	4.2E-01
ENSMUST00000105148	interferon alpha 16 [Source:MGI Symbol;Acc:MGI:3649260]	Q810G1		6.1	2.2E-04	-1.1	1.6E-01	0.5	3.0E-01	0.0	9.8E-01
ENSMUST00000102591	transmembrane protein 234 [Source:MGI Symbol;Acc:MGI:1924049]		Q8R1E7	-0.1	7.7E-01	0.0	9.4E-01	0.1	8.4E-01	-0.1	8.7E-01
ENSMUST00000105158	Moloney sarcoma oncogene [Source:MGI Symbol;Acc:MGI:97052]	A6H643		7.0	4.4E-05	1.8	6.9E-02	-5.4	1.2E-03	0.6	4.3E-01
ENSMUST00000105159	vomeronasal 1 receptor 3 [Source:MGI Symbol;Acc:MGI:4438436]	A2AMT7		6.5	2.8E-04	-4.5	2.2E-03	-1.0	9.5E-02	-2.3	8.7E-02
ENSMUST00000105172	predicted gene 6096 [Source:MGI Symbol;Acc:MGI:3649053]	D3YTY6		6.1	3.8E-03	2.9	7.5E-02	-2.1	1.5E-01	-0.4	7.4E-01
ENSMUST00000102596	lymphocyte protein tyrosine kinase [Source:MGI Symbol;Acc:MGI:96756]		P06240	-2.5	1.7E-01	-4.0	2.2E-01	0.2	8.9E-01	1.8	5.5E-01
ENSMUST00000105177	lipase, hormone sensitive [Source:MGI Symbol;Acc:MGI:96790]	Q9D4C4		9.1	6.6E-04	-2.7	4.0E-02	0.1	8.9E-01	-2.2	1.1E-01
ENSMUST00000105229	CD63 antigen [Source:MGI Symbol;Acc:MGI:99529]	Q549D0	P41731	-4.5	3.3E-03	-3.1	4.5E-04	0.7	4.5E-02	-0.1	8.7E-01
ENSMUST00000105230	SAP domain containing ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1913368]	B2RXM7	Q9D1J3	-4.9	7.8E-04	6.5	2.9E-04	-0.2	9.0E-01	-0.6	3.9E-01
ENSMUST00000105235	d, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 [Source:MGI Symbol;Acc		Q6PDG5	-3.5	1.3E-02	-2.5	1.5E-02	-0.3	5.2E-01	-3.9	6.3E-03
ENSMUST00000105238	signal transducer and activator of transcription 2 [Source:MGI Symbol;Acc:MGI:103039]	E9QJX9		6.7	2.4E-03	-8.4	4.9E-03	-0.3	6.4E-01	2.3	3.4E-01
ENSMUST00000105249	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]		Q80TM6	-6.5	3.1E-03	-3.4	2.0E-04	1.0	6.2E-03	-0.4	4.9E-01
ENSMUST00000102605	period circadian clock 1 [Source:MGI Symbol;Acc:MGI:1098283]	Q8CHR1		0.4	8.9E-01	-0.7	8.2E-01	-2.3	3.9E-01	-1.2	6.8E-01
ENSMUST00000102606	solute carrier family 25, member 35 [Source:MGI Symbol;Acc:MGI:1919248]		Q5SWT3	1.8	2.3E-01	3.8	8.4E-02	1.0	5.8E-01	-0.9	5.1E-01
ENSMUST00000102611	myosin, heavy polypeptide 10, non-muscle [Source:MGI Symbol;Acc:MGI:1930780]		Q61879	2.1	2.8E-01	6.8	5.1E-02	3.2	3.0E-01	-1.5	4.2E-01
ENSMUST00000102613	phosphoinositide-3-kinase, regulatory subunit 6 [Source:MGI Symbol;Acc:MGI:2144613]		Q3U6Q4	-4.2	6.5E-02	-2.1	3.3E-01	-0.6	6.5E-01	-2.8	2.6E-01
ENSMUST00000102616	tektin 2 [Source:MGI Symbol;Acc:MGI:1346335]		Q922G7	2.5	8.8E-02	6.5	6.8E-04	-0.5	7.3E-01	-4.4	1.5E-03
ENSMUST00000105250	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]		Q80TM6	-7.9	2.4E-05	-0.6	5.2E-01	0.7	3.2E-01	-3.1	2.7E-02
ENSMUST00000105255	oxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 [Source:MGI Symbol;Acc:MGI	Q8R3B3		-4.3	1.3E-03	2.5	3.1E-01	-0.8	7.1E-01	2.7	1.6E-01
ENSMUST00000105256	oxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 [Source:MGI Symbol;Acc:MGI		Q8BX07	-4.4	1.9E-04	-7.0	1.1E-04	-0.8	5.7E-02	1.2	2.9E-01
ENSMUST00000105267	CCR4-NOT transcription complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1919318]		Q8C5L3	-7.3	1.3E-04	-5.2	2.2E-03	0.1	8.1E-01	-0.9	5.1E-01
ENSMUST00000105280	lin-7 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:2135609]	Q3TUM0		7.6	4.1E-05	5.1	2.4E-03	1.3	2.6E-01	-1.4	1.0E-01
ENSMUST00000105283	kit ligand [Source:MGI Symbol;Acc:MGI:96974]		P20826	5.9	1.0E-03	-1.3	2.5E-01	0.7	4.0E-01	-2.2	1.0E-01
ENSMUST00000105286	keratocan [Source:MGI Symbol;Acc:MGI:1202398]	A4FUJ3	O35367	6.2	2.0E-04	-2.4	2.3E-03	1.2	5.9E-03	-0.2	7.3E-01
ENSMUST00000105293	thymopoietin [Source:MGI Symbol;Acc:MGI:106920]		Q61029	-3.4	9.8E-03	4.3	4.8E-02	-1.3	5.1E-01	-0.2	9.0E-01
ENSMUST00000105298	growth arrest-specific 2 like 3 [Source:MGI Symbol;Acc:MGI:1918780]			3.5	3.3E-04	-2.6	3.6E-03	0.8	5.8E-02	0.1	9.2E-01
ENSMUST00000102637	adenosine monophosphate deaminase 2 [Source:MGI Symbol;Acc:MGI:88016]		Q9DBT5	-3.3	4.1E-02	1.3	4.1E-01	1.1	4.0E-01	-3.5	3.8E-02
ENSMUST00000102638	adenosine monophosphate deaminase 2 [Source:MGI Symbol;Acc:MGI:88016]		Q9DBT5	2.3	3.0E-01	6.3	9.6E-02	3.3	3.3E-01	-0.7	7.4E-01
ENSMUST00000105321	nuclear factor I/C [Source:MGI Symbol;Acc:MGI:109591]	Q3UHA6	P70255	-1.3	2.4E-02	5.3	3.7E-04	0.2	8.7E-01	0.7	2.4E-01
ENSMUST00000102641	bone morphogenetic protein 8a [Source:MGI Symbol;Acc:MGI:104515]		P34821	-0.6	5.3E-01	-2.3	2.1E-01	0.5	5.8E-01	2.2	2.3E-01
ENSMUST00000105323	high mobility group 20B [Source:MGI Symbol;Acc:MGI:1341190]	Q3U1L0	Q9Z104	-5.7	8.2E-04	1.4	2.0E-02	-0.6	2.1E-01	-0.7	1.2E-01
ENSMUST00000105325	thromboxane A2 receptor [Source:MGI Symbol;Acc:MGI:98496]	Q5FW61	P30987	3.8	8.6E-04	-2.9	2.7E-02	1.5	3.9E-02	-0.9	4.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000105331	mitogen-activated protein kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346867]	Q91YS7		-6.6	6.6E-05	-0.3	6.7E-01	0.5	3.6E-01	-0.6	3.4E-01
ENSMUST00000105332	lamin B2 [Source:MGI Symbol;Acc:MGI:96796]	Q3V159	P21619	6.4	4.6E-04	-4.4	3.7E-03	-2.2	4.8E-03	-0.7	5.9E-01
ENSMUST00000105333	transmembrane protease, serine 9 [Source:MGI Symbol;Acc:MGI:3612246]	D3YTR8		8.3	8.0E-06	6.3	1.4E-03	-0.7	6.2E-01	0.6	4.8E-01
ENSMUST00000102649	tRNA isopentenyltransferase 1 [Source:MGI Symbol;Acc:MGI:1914216]		Q80UN9	-1.9	4.5E-01	-0.8	7.1E-01	-1.6	3.8E-01	-2.8	2.9E-01
ENSMUST00000105341	transcription factor 3 [Source:MGI Symbol;Acc:MGI:98510]	E9PWE3		-2.8	1.4E-02	-3.7	3.6E-03	1.0	6.1E-02	0.8	3.9E-01
ENSMUST00000105349	methyl-CpG binding domain protein 3 [Source:MGI Symbol;Acc:MGI:1333812]		Q9Z2D8	-4.8	1.3E-03	8.5	1.2E-04	0.8	5.3E-01	1.6	3.5E-02
ENSMUST00000105355	receptor accessory protein 6 [Source:MGI Symbol;Acc:MGI:1917585]		Q9JM62	6.8	1.7E-02	7.2	5.2E-04	-0.7	6.7E-01	-0.2	7.5E-01
ENSMUST00000102659	SEC14 and spectrin domains 1 [Source:MGI Symbol;Acc:MGI:1916262]		Q80UK0	0.5	4.4E-01	0.5	4.8E-01	-1.3	5.7E-02	-1.2	1.1E-01
ENSMUST00000105357	receptor accessory protein 6 [Source:MGI Symbol;Acc:MGI:1917585]	D3YTR2		6.8	1.7E-02	2.4	2.2E-02	-1.7	7.8E-02	-0.6	4.6E-01
ENSMUST00000105359	adenomatosis polyposis coli 2 [Source:MGI Symbol;Acc:MGI:1346052]	D3YTR0		11.5	5.2E-04	6.7	2.4E-04	-0.6	6.1E-01	-0.5	4.7E-01
ENSMUST00000105361	DAZ associated protein 1 [Source:MGI Symbol;Acc:MGI:1917498]	Q3UGB5		-4.1	7.6E-04	5.2	2.5E-02	-0.8	6.8E-01	-0.3	8.3E-01
ENSMUST00000105362	DAZ associated protein 1 [Source:MGI Symbol;Acc:MGI:1917498]		Q9JII5	-5.7	2.7E-02	5.3	8.9E-03	-1.8	3.3E-01	0.4	7.2E-01
ENSMUST00000105365	cold inducible RNA binding protein [Source:MGI Symbol;Acc:MGI:893588]		P60824	-5.1	1.9E-04	-7.9	1.3E-04	-0.6	2.8E-01	-1.8	2.3E-01
ENSMUST00000105370	serine/threonine kinase 11 [Source:MGI Symbol;Acc:MGI:1341870]	E9Q811		-6.8	7.4E-04	4.1	5.1E-02	0.3	8.4E-01	1.7	1.9E-01
ENSMUST00000105371	serine/threonine kinase 11 [Source:MGI Symbol;Acc:MGI:1341870]	D6RGT4		-6.8	5.3E-04	-5.5	7.2E-05	-0.2	5.4E-01	-0.5	5.8E-01
ENSMUST00000105372	glutathione peroxidase 4 [Source:MGI Symbol;Acc:MGI:104767]		O70325	-7.3	9.1E-04	-7.2	1.3E-03	0.8	1.3E-01	1.3	4.4E-01
ENSMUST00000105373	histocompatibility (minor) HA-1 [Source:MGI Symbol;Acc:MGI:1917969]	D3Z7R7		-4.5	7.2E-03	-4.9	1.2E-02	-0.2	7.5E-01	-0.8	6.5E-01
ENSMUST00000105374	calponin 2 [Source:MGI Symbol;Acc:MGI:105093]	D3Z7R6		-7.3	1.7E-03	7.1	1.1E-04	-0.5	6.8E-01	-0.9	1.6E-01
ENSMUST00000105379	paralemmin [Source:MGI Symbol;Acc:MGI:1261814]	Q542N8	Q9Z0P4	-4.4	9.7E-03	-3.5	1.0E-02	0.8	2.1E-01	-0.6	5.9E-01
ENSMUST00000102679	WAS/WASL interacting protein family, member 1 [Source:MGI Symbol;Acc:MGI:2178801]		Q8K1I7	0.6	3.3E-01	1.1	1.8E-01	0.3	6.4E-01	-0.2	7.7E-01
ENSMUST00000105383	coiled-coil domain containing 105 [Source:MGI Symbol;Acc:MGI:1918226]		Q9D4K7	7.8	2.9E-05	-6.8	2.5E-03	0.9	1.5E-01	0.7	6.8E-01
ENSMUST00000105393	icos ligand [Source:MGI Symbol;Acc:MGI:1354701]	Q544C7	Q9JHJ8	-2.5	3.3E-03	3.8	3.8E-03	0.6	5.5E-01	-0.8	2.7E-01
ENSMUST00000102683	target of myb1-like 2 (chicken) [Source:MGI Symbol;Acc:MGI:2443306]		Q5SRX1	0.7	7.5E-01	-0.1	9.8E-01	-1.1	5.9E-01	-0.3	9.1E-01
ENSMUST00000105397	RIKEN cDNA 1810043G02 gene [Source:MGI Symbol;Acc:MGI:1915134]		Q8C6G1	-5.5	2.2E-04	-0.5	5.2E-01	0.6	2.7E-01	-0.5	5.7E-01
ENSMUST00000105408	predicted gene 10941 [Source:MGI Symbol;Acc:MGI:3779151]	Q3TNV0		4.0	4.6E-04	2.1	6.2E-02	-1.5	1.4E-01	0.4	6.0E-01
ENSMUST00000105411	poly(rC) binding protein 3 [Source:MGI Symbol;Acc:MGI:1890470]		P57722	8.4	5.2E-05	-6.0	1.0E-02	-0.3	7.1E-01	2.0	3.1E-01
ENSMUST00000105413	collagen, type VI, alpha 2 [Source:MGI Symbol;Acc:MGI:88460]	D3Z7D5		7.4	1.1E-05	-3.6	1.3E-02	1.1	1.2E-01	-2.3	1.4E-01
ENSMUST00000102691	cell division cycle associated 7 [Source:MGI Symbol;Acc:MGI:1914203]		Q9D0M2	-0.9	2.5E-01	1.0	3.2E-01	1.3	1.0E-01	-0.6	5.3E-01
ENSMUST00000105417	DIP2 disco-interacting protein 2 homolog A (Drosophila) [Source:MGI Symbol;Acc:MGI:2385920]	D3Z7D3		5.6	3.4E-02	1.1	1.5E-01	-1.3	5.1E-02	-0.2	8.1E-01
ENSMUST00000105420	adenosine A2a receptor [Source:MGI Symbol;Acc:MGI:99402]		Q60613	3.0	2.7E-03	-7.5	9.8E-04	-1.3	7.1E-02	-1.2	4.8E-01
ENSMUST00000105436	family with sequence similarity 13, member C [Source:MGI Symbol;Acc:MGI:1918971]	G3X9S1		6.7	1.4E-02	2.6	8.8E-03	0.8	2.5E-01	0.0	9.6E-01
ENSMUST00000105440	catenin (cadherin associated protein), alpha 3 [Source:MGI Symbol;Acc:MGI:2661445]		Q65CL1	7.0	6.4E-05	3.3	8.8E-03	-0.3	7.2E-01	0.6	4.2E-01
ENSMUST00000105447	vacuolar protein sorting 26 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1353654]		P40336	-5.2	1.0E-04	5.8	7.6E-03	0.0	9.9E-01	-1.0	3.4E-01
ENSMUST00000105454	collagen, type XIII, alpha 1 [Source:MGI Symbol;Acc:MGI:1277201]		Q9R1N9	5.8	5.3E-03	-0.9	4.8E-01	1.5	7.0E-02	-0.6	6.6E-01
ENSMUST00000105459	RIKEN cDNA 4632428N05 gene [Source:MGI Symbol;Acc:MGI:1921298]	D3Z7B7		-10.2	3.0E-05	7.6	9.5E-03	-0.8	7.5E-01	-1.8	2.2E-01
ENSMUST00000105465	prosaposin [Source:MGI Symbol;Acc:MGI:97783]	Q8BFQ1		-10.7	5.8E-04	-6.7	3.2E-03	1.6	2.2E-02	-0.3	8.5E-01
ENSMUST00000105466	proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide [Source:MGI Symbol;Acc:		Q60715	-7.0	5.0E-06	3.5	2.3E-03	-1.5	7.3E-02	-0.7	3.6E-01
ENSMUST00000102711	gem (nuclear organelle) associated protein 5 [Source:MGI Symbol;Acc:MGI:2449311]	A2AFQ9		3.4	9.6E-02	0.0	9.8E-01	-1.7	3.7E-01	1.8	4.3E-01
ENSMUST00000105469	mannosidase 1, alpha [Source:MGI Symbol;Acc:MGI:104677]	D3Z799		6.3	2.0E-04	1.5	3.0E-01	-4.5	1.2E-02	0.2	8.6E-01
ENSMUST00000105473	solute carrier family 35, member F1 [Source:MGI Symbol;Acc:MGI:2139810]		Q8BGK5	7.5	1.1E-05	6.7	3.6E-04	-0.5	6.9E-01	-0.5	4.6E-01
ENSMUST00000105476	discoidin, CUB and LCCL domain containing 1 [Source:MGI Symbol;Acc:MGI:1913936]		Q9D4J3	5.8	2.0E-03	-0.4	7.1E-01	-1.6	1.2E-01	1.5	1.8E-01
ENSMUST00000102720	solute carrier family 5 (sodium/glucose cotransporter), member 9 [Source:MGI Symbol;Acc:MGI:2140201]		Q8VDT1	2.3	5.7E-02	7.5	4.6E-05	-0.5	6.4E-01	-5.7	5.1E-05
ENSMUST00000105481	leukocyte immunoglobulin-like receptor, subfamily B, member 4A [Source:MGI Symbol;Acc:MGI:102701]		Q64281	-8.7	4.1E-04	2.5	1.8E-01	-0.7	6.6E-01	4.7	5.5E-03
ENSMUST00000105482	leukocyte immunoglobulin-like receptor, subfamily B, member 4A [Source:MGI Symbol;Acc:MGI:102701]		Q64281	-3.3	2.3E-02	5.4	7.2E-02	-0.8	7.7E-01	-0.2	9.2E-01
ENSMUST00000105483	glutamate receptor, ionotropic, kainate 2 (beta 2) [Source:MGI Symbol;Acc:MGI:95815]	Q6PAQ0		9.6	1.6E-06	-0.8	1.9E-01	0.6	1.4E-01	0.0	9.4E-01
ENSMUST00000105492	reticulon 4 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2178759]	D3Z792		-5.1	5.2E-03	-2.4	1.4E-02	-0.5	2.8E-01	0.4	6.4E-01
ENSMUST00000105499	sorting nexin 3 [Source:MGI Symbol;Acc:MGI:1860188]	D3Z789		-4.8	2.3E-04	-2.7	6.9E-03	0.8	8.9E-02	-0.2	8.0E-01
ENSMUST00000102730	TNFAIP3 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1926194]	D3Z2W0		-3.7	1.1E-01	-4.0	3.6E-01	1.9	3.9E-01	2.2	5.9E-01
ENSMUST00000102735	ute carrier family 4, sodium bicarbonate cotransporter-like, member 10 [Source:MGI Symbol;Acc:MGI:215015		Q5DTL9	3.5	1.6E-01	5.2	5.7E-02	-0.5	8.4E-01	-2.2	2.1E-01
ENSMUST00000105502	forkhead box O3 [Source:MGI Symbol;Acc:MGI:1890081]		Q9WVH4	-3.4	2.9E-04	1.3	3.2E-01	-4.9	1.2E-02	-0.3	8.0E-01
ENSMUST00000102738	KTI12 homolog, chromatin associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923547]		Q9D1R2	-0.2	7.8E-01	0.5	5.6E-01	0.4	4.9E-01	-0.2	7.7E-01
ENSMUST00000105507	peptidylprolyl isomerase (cyclophilin)-like 6 [Source:MGI Symbol;Acc:MGI:1920325]	B2RWF7		2.5	2.2E-02	-6.3	9.8E-04	0.0	9.5E-01	-0.2	8.7E-01
ENSMUST00000102741	basic transcription factor 3-like 4 [Source:MGI Symbol;Acc:MGI:1915312]	A2A7Z4	Q9CQH7	-1.1	2.1E-01	0.8	2.8E-01	-0.4	5.3E-01	-2.3	1.8E-02
ENSMUST00000105510	histone deacetylase 2 [Source:MGI Symbol;Acc:MGI:1097691]	Q8BQ10		4.2	7.6E-04	-1.5	1.9E-02	-0.3	4.7E-01	0.2	7.6E-01
ENSMUST00000105511	collagen, type X, alpha 1 [Source:MGI Symbol;Acc:MGI:88445]		Q05306	6.3	4.7E-05	-2.4	4.3E-03	0.6	1.5E-01	-0.8	2.5E-01
ENSMUST00000105516	thymocyte selection associated [Source:MGI Symbol;Acc:MGI:2443552]		Q8BGW0	6.6	2.5E-04	2.5	4.8E-03	-0.3	5.9E-01	-0.5	3.6E-01
ENSMUST00000105520	ectonucleotide pyrophosphatase/phosphodiesterase 1 [Source:MGI Symbol;Acc:MGI:97370]	G3X9S2		8.0	2.0E-05	-4.9	1.1E-03	1.1	4.7E-02	-0.2	8.3E-01
ENSMUST00000105545	phosphatase and actin regulator 2 [Source:MGI Symbol;Acc:MGI:2446138]	Q3UQ19		1.5	1.8E-02	-3.7	1.2E-04	0.4	2.5E-01	-1.0	1.3E-01
ENSMUST00000105561	glutamate receptor, metabotropic 1 [Source:MGI Symbol;Acc:MGI:1351338]		P97772	6.1	6.0E-04	-1.9	2.8E-01	2.5	3.0E-02	-0.6	7.2E-01
ENSMUST00000105566	runt-related transcription factor 1; translocated to, 1 (cyclin D-related) [Source:MGI Symbol;Acc:MGI:104793	B1AXH8		6.0	7.3E-04	-8.6	8.4E-03	-0.3	7.1E-01	0.2	9.4E-01
ENSMUST00000105574	agrin [Source:MGI Symbol;Acc:MGI:87961]	Z4YK85		-5.1	5.0E-03	-4.2	1.9E-02	0.2	7.5E-01	-0.3	8.4E-01
ENSMUST00000105578	stromal cell derived factor 4 [Source:MGI Symbol;Acc:MGI:108079]		Q61112	-4.4	6.7E-04	1.6	3.5E-02	0.2	6.9E-01	1.3	4.2E-02
ENSMUST00000102754	plakophilin 4 [Source:MGI Symbol;Acc:MGI:109281]		Q68FH0	2.5	9.2E-02	4.6	7.3E-03	-0.6	7.0E-01	-2.7	3.4E-02
ENSMUST00000105579	stromal cell derived factor 4 [Source:MGI Symbol;Acc:MGI:108079]		Q61112	-9.7	2.0E-06	-2.2	2.5E-03	0.5	1.3E-01	-0.1	8.2E-01
ENSMUST00000105583	ubiquitin-conjugating enzyme E2J 2 [Source:MGI Symbol;Acc:MGI:2153608]	B1ASK8		-6.9	1.6E-05	-2.6	4.9E-03	0.2	5.4E-01	-0.2	7.3E-01
ENSMUST00000105584	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3 [Source:MGI Symbol;Acc:MGI:2153589]	Q6NXL5		-4.6	1.1E-03	3.4	9.0E-04	1.5	3.5E-02	0.8	1.3E-01
ENSMUST00000105588	estrogen receptor 1 (alpha) [Source:MGI Symbol;Acc:MGI:1352467]	D3Z6V3		6.4	1.5E-04	-3.7	2.0E-04	0.2	4.5E-01	0.7	3.0E-01
ENSMUST00000105591	aurora kinase A interacting protein 1 [Source:MGI Symbol;Acc:MGI:1913327]		Q9DCJ7	-8.7	8.9E-06	5.9	2.0E-05	-2.1	2.9E-02	0.2	6.1E-01
ENSMUST00000105592	aurora kinase A interacting protein 1 [Source:MGI Symbol;Acc:MGI:1913327]		Q9DCJ7	-3.7	3.6E-03	-5.3	8.0E-04	-0.4	3.5E-01	0.5	6.3E-01
ENSMUST00000102768	RNA binding motif protein 43 [Source:MGI Symbol;Acc:MGI:1918934]		Q99J64	-0.3	7.6E-01	2.1	1.7E-01	0.8	4.9E-01	-1.6	2.2E-01
ENSMUST00000105593	ankyrin repeat domain 65 [Source:MGI Symbol;Acc:MGI:2685285]	A2AD93		5.3	4.7E-03	-5.6	9.0E-05	0.5	2.0E-01	-1.3	1.9E-01
ENSMUST00000102772	leukotriene C4 synthase [Source:MGI Symbol;Acc:MGI:107498]		Q60860	0.0	9.9E-01	-3.4	1.1E-02	-3.9	6.5E-04	-0.5	6.6E-01
ENSMUST00000105595	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916241]		Q9CY97	-7.6	4.8E-06	-5.1	2.1E-03	0.5	3.4E-01	-2.1	1.5E-01
ENSMUST00000105598	cyclin-dependent kinase 11B [Source:MGI Symbol;Acc:MGI:88353]	A2A9P6		-7.7	2.4E-02	-9.0	4.3E-04	1.3	1.4E-02	0.3	8.6E-01
ENSMUST00000102778	mitogen-activated protein kinase 9 [Source:MGI Symbol;Acc:MGI:1346862]		Q9WTU6	0.4	9.0E-01	4.3	2.6E-01	1.2	7.3E-01	-2.7	3.4E-01
ENSMUST00000105608	solute carrier family 35, member E2 [Source:MGI Symbol;Acc:MGI:2444240]		Q8C811	2.6	1.2E-04	6.7	4.2E-04	-0.6	6.7E-01	-3.3	4.3E-03
ENSMUST00000105611	opioid receptor, mu 1 [Source:MGI Symbol;Acc:MGI:97441]		P42866	5.3	1.7E-04	-4.4	1.7E-04	0.6	1.2E-01	-0.5	5.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000105613	NAD kinase [Source:MGI Symbol;Acc:MGI:2183149]		P58058	-4.5	5.0E-03	-9.7	4.6E-04	-1.3	3.6E-02	-0.9	6.7E-01
ENSMUST00000105616	guanine nucleotide binding protein (G protein), beta 1 [Source:MGI Symbol;Acc:MGI:95781]	Q3TQ70	P62874	-6.3	4.8E-04	7.6	4.5E-05	-0.6	6.0E-01	-1.4	3.6E-02
ENSMUST00000102787	DENN/MADD domain containing 1A [Source:MGI Symbol;Acc:MGI:2442794]		Q8K382	1.0	9.3E-02	1.7	4.4E-02	0.5	3.6E-01	-0.1	8.5E-01
ENSMUST00000105617	interaction protein for cytohesin exchange factors 1 [Source:MGI Symbol;Acc:MGI:2444159]		Q5DU31	-4.1	1.6E-04	6.3	2.1E-05	-2.4	2.9E-02	-0.9	1.0E-01
ENSMUST00000105624	protein kinase C, zeta [Source:MGI Symbol;Acc:MGI:97602]	A2AD75		5.0	8.7E-03	6.8	4.4E-04	1.0	4.4E-01	-0.9	2.1E-01
ENSMUST00000105634	membrane metallo-endopeptidase-like 1 [Source:MGI Symbol;Acc:MGI:1351603]	B1AS17		6.0	4.1E-05	-2.6	1.0E-02	1.6	6.8E-03	-1.1	2.4E-01
ENSMUST00000102794	glycoprotein galactosyltransferase alpha 1, 3 [Source:MGI Symbol;Acc:MGI:95704]	Q9DBU1		-1.0	4.4E-01	1.2	3.8E-01	-1.0	3.9E-01	-3.2	4.1E-02
ENSMUST00000105643	transformation related protein 73 [Source:MGI Symbol;Acc:MGI:1336991]		Q9JJP2	5.3	2.4E-02	-4.4	8.8E-03	-0.6	4.0E-01	-1.3	3.7E-01
ENSMUST00000105644	transformation related protein 73 [Source:MGI Symbol;Acc:MGI:1336991]	Z4YK94		5.8	3.1E-02	2.9	1.0E-02	5.4	7.2E-05	-0.2	8.2E-01
ENSMUST00000105646	adherens junction associated protein 1 [Source:MGI Symbol;Acc:MGI:2685419]		A2ALI5	7.8	3.9E-04	9.0	3.8E-05	-0.6	6.3E-01	-0.5	3.9E-01
ENSMUST00000102802	B and T lymphocyte associated [Source:MGI Symbol;Acc:MGI:2658978]			2.5	2.2E-01	-4.0	2.3E-01	-3.0	1.1E-01	3.4	2.8E-01
ENSMUST00000102803	myosin, heavy polypeptide 7, cardiac muscle, beta [Source:MGI Symbol;Acc:MGI:2155600]	B2RXX9	Q91Z83	5.7	4.1E-02	7.1	2.2E-02	-0.4	8.8E-01	-1.9	2.3E-01
ENSMUST00000105650	G protein-coupled receptor 153 [Source:MGI Symbol;Acc:MGI:1916157]	A2A8K5		7.3	4.9E-03	7.4	1.1E-04	-1.5	2.5E-01	0.5	4.2E-01
ENSMUST00000105652	acyl-CoA thioesterase 7 [Source:MGI Symbol;Acc:MGI:1917275]		Q91V12	-4.2	1.2E-03	6.0	3.3E-04	-0.6	6.1E-01	-0.5	4.5E-01
ENSMUST00000105659	espin [Source:MGI Symbol;Acc:MGI:1861630]	B1AWQ4		5.5	4.0E-03	5.6	1.3E-03	-0.5	7.0E-01	-0.3	7.2E-01
ENSMUST00000105662	in homology domain containing, family G (with RhoGef domain) member 5 [Source:MGI Symbol;Acc:MGI:2(	A0A0A0MQC2		6.5	1.5E-02	6.4	8.1E-05	-0.9	3.9E-01	-0.3	5.9E-01
ENSMUST00000105672	tumor necrosis factor receptor superfamily, member 9 [Source:MGI Symbol;Acc:MGI:1101059]	Q8R037		4.5	1.4E-02	-5.5	6.9E-05	-1.1	1.8E-02	-0.3	6.9E-01
ENSMUST00000105675	Parkinson disease (autosomal recessive, early onset) 7 [Source:MGI Symbol;Acc:MGI:2135637]		Q99LX0	-2.2	1.2E-02	6.7	7.9E-05	-1.5	2.0E-01	-0.6	2.6E-01
ENSMUST00000105676	Parkinson disease (autosomal recessive, early onset) 7 [Source:MGI Symbol;Acc:MGI:2135637]	A2A813		-4.4	2.5E-02	5.9	9.4E-04	-0.5	7.0E-01	-0.9	2.5E-01
ENSMUST00000102818	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4 [Source:MGI Symbc	Q8C3J2		-1.3	1.1E-01	-0.6	5.0E-01	0.3	6.3E-01	-0.3	7.4E-01
ENSMUST00000105680	arginine glutamic acid dipeptide (RE) repeats [Source:MGI Symbol;Acc:MGI:2683486]	A2A7T3		-2.2	1.1E-02	6.0	9.2E-02	-1.0	7.8E-01	0.3	8.9E-01
ENSMUST00000105682	arginine glutamic acid dipeptide (RE) repeats [Source:MGI Symbol;Acc:MGI:2683486]		Q80TZ9	2.4	2.4E-02	-2.0	1.8E-02	1.0	3.5E-02	0.4	5.5E-01
ENSMUST00000102822	neuropilin 2 [Source:MGI Symbol;Acc:MGI:1100492]		O35375	2.0	3.8E-01	3.5	1.0E-01	-1.7	4.2E-01	-3.3	9.0E-02
ENSMUST00000102823	tetratricopeptide repeat domain 39B [Source:MGI Symbol;Acc:MGI:1917113]		Q8BYY4	0.2	7.9E-01	-0.2	8.4E-01	0.0	9.9E-01	0.3	6.7E-01
ENSMUST00000102824	interferon-induced protein with tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGI:99450]		Q64282	1.0	3.7E-01	-0.4	7.4E-01	-1.5	1.4E-01	-0.1	9.3E-01
ENSMUST00000102825	interferon-induced protein with tetratricopeptide repeats 3 [Source:MGI Symbol;Acc:MGI:1101055]	Q5FW82	Q64345	2.0	2.3E-01	-0.3	8.5E-01	-3.2	4.3E-02	-0.9	5.6E-01
ENSMUST00000102826	interferon-induced protein with tetratricopeptide repeats 2 [Source:MGI Symbol;Acc:MGI:99449]	Q6GTM0		-0.2	7.1E-01	-1.2	1.5E-01	-0.6	3.1E-01	0.4	6.1E-01
ENSMUST00000105687	transmembrane protein 201 [Source:MGI Symbol;Acc:MGI:1196277]		A2A8U2	5.4	4.0E-04	1.9	2.3E-02	-1.4	5.5E-02	-1.3	7.2E-02
ENSMUST00000105691	calsyntenin 1 [Source:MGI Symbol;Acc:MGI:1929895]		Q9EPL2	2.3	2.8E-03	5.6	1.2E-03	-0.4	7.4E-01	0.0	9.6E-01
ENSMUST00000105692	catenin beta interacting protein 1 [Source:MGI Symbol;Acc:MGI:1915756]		Q9JJN6	-3.8	1.4E-04	5.3	3.2E-04	-3.6	7.4E-03	-0.7	2.5E-01
ENSMUST00000102832	CD3 antigen, epsilon polypeptide [Source:MGI Symbol;Acc:MGI:88332]	A6H6M1	P22646	-0.5	6.1E-01	0.2	8.6E-01	-0.2	7.7E-01	-0.9	4.0E-01
ENSMUST00000105698	predicted gene 572 [Source:MGI Symbol;Acc:MGI:2685418]	B1ARY8		6.4	9.9E-05	4.1	1.2E-01	-0.9	7.0E-01	1.3	4.3E-01
ENSMUST00000105699	TAR DNA binding protein [Source:MGI Symbol;Acc:MGI:2387629]	Q8R0B4		-5.3	1.5E-03	6.8	1.9E-04	0.5	6.3E-01	-1.3	7.3E-02
ENSMUST00000105706	F-box protein 6 [Source:MGI Symbol;Acc:MGI:1354743]		Q9QZN4	2.1	2.1E-02	1.1	1.6E-01	-0.3	6.0E-01	0.4	5.4E-01
ENSMUST00000102840	argininosuccinate synthetase 1 [Source:MGI Symbol;Acc:MGI:88090]	Q3UJ34	P16460	-0.7	3.0E-01	-0.7	4.6E-01	0.4	5.3E-01	0.4	6.8E-01
ENSMUST00000102841	reticulon 4 [Source:MGI Symbol;Acc:MGI:1915835]		Q99P72	-2.8	1.8E-01	4.7	2.0E-01	7.7	3.0E-02	0.2	9.2E-01
ENSMUST00000105715	mitofusin 2 [Source:MGI Symbol;Acc:MGI:2442230]		Q80U63	5.6	2.4E-02	-3.1	4.1E-03	1.1	4.0E-02	-1.4	1.6E-01
ENSMUST00000102843	reticulon 4 [Source:MGI Symbol;Acc:MGI:1915835]		Q99P72	1.9	5.2E-01	0.2	9.3E-01	-4.2	1.2E-01	-2.6	3.5E-01
ENSMUST00000105716	mitofusin 2 [Source:MGI Symbol;Acc:MGI:2442230]		Q80U63	-7.2	1.1E-03	-5.1	8.9E-05	0.9	2.4E-02	-0.5	5.6E-01
ENSMUST00000105718	zinc finger protein 933 [Source:MGI Symbol;Acc:MGI:1922865]	Q6PEE4		3.7	4.1E-05	-7.5	9.1E-05	-1.2	2.9E-02	-0.3	7.8E-01
ENSMUST00000102849	ubiquitin specific peptidase 20 [Source:MGI Symbol;Acc:MGI:1921520]		Q8C6M1	0.9	6.8E-01	5.1	2.3E-01	5.6	1.5E-01	1.3	5.8E-01
ENSMUST00000105721	predicted gene 13152 [Source:MGI Symbol;Acc:MGI:3701121]	A2A8Q4		6.5	1.5E-04	2.5	2.1E-03	-0.2	7.5E-01	0.1	8.3E-01
ENSMUST00000105733	predicted gene 13251 [Source:MGI Symbol;Acc:MGI:3700963]	B1ASD8		2.7	3.9E-04	4.9	5.5E-03	-0.6	6.6E-01	1.4	1.1E-01
ENSMUST00000105734	predicted gene 13157 [Source:MGI Symbol;Acc:MGI:3651978]	A2A7A2		-1.4	1.7E-02	-4.2	5.4E-02	1.3	1.6E-01	0.5	8.2E-01
ENSMUST00000102855	carnitine acetyltransferase [Source:MGI Symbol;Acc:MGI:109501]		P47934	-3.4	1.2E-01	-0.7	7.9E-01	1.2	5.5E-01	-1.5	5.4E-01
ENSMUST00000105735	predicted gene 13247 [Source:MGI Symbol;Acc:MGI:3700965]	A2A8V7		5.5	2.8E-02	4.2	7.1E-03	-4.2	1.5E-02	-1.1	2.1E-01
ENSMUST00000102858	ATPase, Na+/K+ transporting, alpha 3 polypeptide [Source:MGI Symbol;Acc:MGI:88107]	Q8VCE0		2.1	1.2E-01	4.4	3.5E-02	1.2	4.8E-01	-1.1	3.5E-01
ENSMUST00000102864	reticuloendotheliosis oncogene [Source:MGI Symbol;Acc:MGI:97897]	A4QPD3		-1.0	6.8E-02	-0.2	7.4E-01	0.6	1.9E-01	-0.2	7.9E-01
ENSMUST00000105738	predicted gene 13242 [Source:MGI Symbol;Acc:MGI:3712454]	A2A9J5		7.6	1.9E-05	-0.4	7.7E-01	1.7	5.8E-02	-1.7	2.1E-01
ENSMUST00000105742	predicted gene 13225 [Source:MGI Symbol;Acc:MGI:3652161]	B1AVN5		5.3	8.0E-03	1.3	4.1E-01	-2.8	9.6E-02	0.3	8.0E-01
ENSMUST00000102869	exportin 1, CRM1 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2144013]		Q6P5F9	-0.6	6.2E-01	2.9	7.1E-02	1.8	1.9E-01	-1.7	1.7E-01
ENSMUST00000105747	predicted gene 436 [Source:MGI Symbol;Acc:MGI:2685282]	B1AVU6		6.8	7.5E-05	-4.8	2.0E-02	2.2	1.1E-02	-0.8	6.7E-01
ENSMUST00000105748	predicted gene 13124 [Source:MGI Symbol;Acc:MGI:3652194]	A2A752		4.9	5.1E-03	4.9	5.2E-02	-0.7	7.6E-01	2.4	1.5E-01
ENSMUST00000102872	Rap guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:104580]	Q91ZZ2		-0.2	7.0E-01	0.8	3.5E-01	1.1	8.8E-02	0.1	8.5E-01
ENSMUST00000105749	arylacetamide deacetylase-like 3 [Source:MGI Symbol;Acc:MGI:2685281]		A2A7Z8	7.3	2.5E-05	-4.7	8.7E-04	-1.1	4.4E-02	-1.0	3.7E-01
ENSMUST00000105751	predicted gene 13128 [Source:MGI Symbol;Acc:MGI:3651261]	L7MU96		5.3	5.8E-03	-2.2	1.4E-02	0.9	7.5E-02	-0.6	4.7E-01
ENSMUST00000102877	RIKEN cDNA 1700026L06 gene [Source:MGI Symbol;Acc:MGI:1917237]		Q7TPM5	-0.2	9.3E-01	-1.0	7.0E-01	-2.6	1.9E-01	-1.9	4.9E-01
ENSMUST00000105752	preferentially expressed antigen in melanoma like 5 [Source:MGI Symbol;Acc:MGI:2156389]	Q7TPY4		6.5	2.4E-03	-0.4	7.6E-01	1.2	1.8E-01	-1.4	2.7E-01
ENSMUST00000105773	predicted gene 13083 [Source:MGI Symbol;Acc:MGI:3650232]	A2AGW5		7.3	3.4E-05	-3.5	7.3E-04	1.7	1.2E-03	-0.5	5.0E-01
ENSMUST00000105778	PR domain containing 2, with ZNF domain [Source:MGI Symbol;Acc:MGI:107628]	A2A7B5		-1.8	4.1E-03	-6.1	1.1E-04	-0.8	1.0E-01	0.1	8.8E-01
ENSMUST00000102883	polypyrimidine tract binding protein 3 [Source:MGI Symbol;Acc:MGI:1923334]	G8JL74		0.5	8.6E-01	-5.0	1.2E-01	-6.9	4.8E-03	-1.3	7.1E-01
ENSMUST00000105779	forkhead-associated (FHA) phosphopeptide binding domain 1 [Source:MGI Symbol;Acc:MGI:1920323]		A6PWD2	8.6	2.7E-04	5.7	2.0E-03	-0.4	7.6E-01	-1.4	1.2E-01
ENSMUST00000105782	regulatory solute carrier protein, family 1, member 1 [Source:MGI Symbol;Acc:MGI:3526447]		Q9ER99	-7.9	4.9E-05	8.3	3.2E-05	-0.6	6.2E-01	-0.5	3.7E-01
ENSMUST00000105788	chloride channel, voltage-sensitive Kb [Source:MGI Symbol;Acc:MGI:1930643]		Q9WUB6	6.1	2.7E-02	7.7	5.6E-05	0.3	7.8E-01	0.0	9.6E-01
ENSMUST00000105790	chloride channel, voltage-sensitive Ka [Source:MGI Symbol;Acc:MGI:1329026]		Q9WUB7	7.9	1.8E-04	-3.1	1.3E-02	0.6	2.9E-01	-1.4	2.1E-01
ENSMUST00000102890	solute carrier family 2 (facilitated glucose transporter), member 6 [Source:MGI Symbol;Acc:MGI:2443286]	A2AR26		-2.9	3.1E-01	-4.5	2.5E-01	-1.7	3.9E-01	0.0	9.9E-01
ENSMUST00000105802	5-hydroxytryptamine (serotonin) receptor 6 [Source:MGI Symbol;Acc:MGI:1196627]	Q14AW8	Q9R1C8	8.6	8.0E-05	6.1	1.3E-03	-1.4	3.5E-01	0.1	8.8E-01
ENSMUST00000102893	muscle, skeletal, receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:103581]	Q32S49	Q61006	1.6	4.7E-01	2.5	3.0E-01	-0.3	8.8E-01	-1.2	5.6E-01
ENSMUST00000105808	phospholipase A2, group IIC [Source:MGI Symbol;Acc:MGI:106638]	A2APR1		7.2	1.4E-05	-8.5	3.9E-04	-1.0	1.2E-01	0.3	8.4E-01
ENSMUST00000105809	UBX domain protein 10 [Source:MGI Symbol;Acc:MGI:2443123]		Q8BG34	5.6	8.1E-04	-5.5	4.8E-05	-0.9	3.3E-02	-0.1	8.7E-01
ENSMUST00000105811	UBX domain protein 10 [Source:MGI Symbol;Acc:MGI:2443123]		Q8BG34	6.9	2.3E-04	-1.1	1.4E-01	1.3	1.7E-02	-0.1	8.4E-01
ENSMUST00000105818	kinesin family member 17 [Source:MGI Symbol;Acc:MGI:1098229]	A2AM74		2.9	1.8E-03	6.5	4.4E-03	-1.2	5.2E-01	-0.2	8.5E-01
ENSMUST00000105823	SH2 domain containing 5 [Source:MGI Symbol;Acc:MGI:2446215]	A2AM67		-6.5	3.3E-03	7.9	2.7E-04	-1.7	3.1E-01	1.1	1.5E-01
ENSMUST00000102905	paralemmin 2 [Source:MGI Symbol;Acc:MGI:1934601]		Q8BR92	2.7	1.1E-01	5.0	9.5E-03	-0.6	7.2E-01	-2.8	4.1E-02
ENSMUST00000105824	SH2 domain containing 5 [Source:MGI Symbol;Acc:MGI:2446215]	A2AM67		7.2	1.2E-04	-1.9	1.7E-01	-0.4	6.5E-01	-1.3	3.4E-01
ENSMUST00000105831	eukaryotic translation initiation factor 4 gamma, 3 [Source:MGI Symbol;Acc:MGI:1923935]	Z4YKC4		-8.6	4.9E-06	3.9	9.2E-04	-2.2	2.2E-02	0.1	8.2E-01
ENSMUST00000102914	zinc finger, MIZ-type containing 2 [Source:MGI Symbol;Acc:MGI:106374]		Q8CIE2	-3.3	1.4E-01	-3.5	3.7E-01	1.2	5.8E-01	1.4	6.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102915	structural maintenance of chromosomes 2 [Source:MGI Symbol;Acc:MGI:106067]		Q8CG48	-3.8	4.1E-02	-0.6	6.5E-01	-0.7	4.9E-01	-3.9	4.9E-02
ENSMUST00000102917	collagen, type XV, alpha 1 [Source:MGI Symbol;Acc:MGI:88449]		O35206	3.9	2.1E-01	3.6	2.1E-01	-3.0	3.5E-01	-2.7	2.1E-01
ENSMUST00000102919	ATP-binding cassette, sub-family A (ABC1), member 2 [Source:MGI Symbol;Acc:MGI:99606]	A2AJ26		1.1	3.7E-02	1.7	2.0E-02	0.4	4.7E-01	-0.2	6.7E-01
ENSMUST00000105840	ubiquitin specific peptidase 48 [Source:MGI Symbol;Acc:MGI:2158502]	A2ALR9		-4.2	3.4E-03	8.0	5.6E-05	-0.6	6.0E-01	0.1	8.9E-01
ENSMUST00000105845	Eph receptor B2 [Source:MGI Symbol;Acc:MGI:99611]	A3KG01	P54763	9.0	1.7E-05	5.3	1.1E-03	-0.5	6.6E-01	0.8	2.5E-01
ENSMUST00000102922	polymerase (DNA directed), delta 2, regulatory subunit [Source:MGI Symbol;Acc:MGI:1097163]		O35654	0.5	4.7E-01	-0.1	8.9E-01	-0.9	1.9E-01	-0.3	7.4E-01
ENSMUST00000105847	lysine (K)-specific demethylase 1A [Source:MGI Symbol;Acc:MGI:1196256]	A3KG93		-5.2	2.1E-03	4.5	1.2E-03	-5.3	3.5E-03	0.4	5.4E-01
ENSMUST00000105850	heterogeneous nuclear ribonucleoprotein R [Source:MGI Symbol;Acc:MGI:1891692]	Q8VHM5		-4.6	1.6E-04	4.8	1.5E-03	-0.9	4.3E-01	-0.9	2.3E-01
ENSMUST00000102925	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1 [Source:MGI Symbol;Acc:MGI:2443318]		Q3TW96	-1.2	4.7E-02	-0.8	2.8E-01	0.5	2.8E-01	0.1	8.8E-01
ENSMUST00000105851	rminal proteasome-interacting domain of thioredoxin-like) domain containing 1 [Source:MGI Symbol;Acc:MG		Q8BWR2	-5.3	1.2E-04	-3.0	2.4E-03	0.9	4.3E-02	0.0	9.7E-01
ENSMUST00000105853	serine/arginine-rich splicing factor 10 [Source:MGI Symbol;Acc:MGI:1333805]		Q9R0U0	-3.6	2.3E-02	-2.8	2.8E-03	1.2	9.5E-03	0.7	3.0E-01
ENSMUST00000105854	myomesin family, member 3 [Source:MGI Symbol;Acc:MGI:2685280]		A2ABU4	8.7	1.7E-05	-3.6	3.9E-03	1.4	1.5E-02	-0.9	3.7E-01
ENSMUST00000105855	grainyhead-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2655333]		Q5FWH3	8.2	1.8E-04	-3.7	2.7E-02	-0.3	7.1E-01	-1.1	5.0E-01
ENSMUST00000105856	NIPA-like domain containing 3 [Source:MGI Symbol;Acc:MGI:1921802]	A2A987		5.6	1.0E-06	-3.8	1.8E-02	0.0	9.8E-01	-1.8	2.4E-01
ENSMUST00000102934	ring finger protein 38 [Source:MGI Symbol;Acc:MGI:1920719]	Q3UH35		-1.3	7.4E-01	0.1	9.8E-01	-1.6	5.8E-01	-3.0	4.7E-01
ENSMUST00000102935	arrestin domain containing 1 [Source:MGI Symbol;Acc:MGI:2446136]		Q99KN1	1.3	5.5E-01	2.3	4.2E-01	0.9	7.1E-01	-0.2	9.4E-01
ENSMUST00000102936	ucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase [Source:MGI Symbol;Acc:MGI:135495	Q3TCI8	Q91WG8	-1.0	2.9E-01	3.9	2.4E-03	1.1	2.5E-01	-3.8	1.3E-03
ENSMUST00000105860	noncompact myelin associated protein [Source:MGI Symbol;Acc:MGI:2444888]	A2A992		7.0	2.1E-04	4.8	7.5E-02	-0.7	7.7E-01	0.0	9.8E-01
ENSMUST00000102939	calcium channel, voltage-dependent, N type, alpha 1B subunit [Source:MGI Symbol;Acc:MGI:88296]	A2AIR9		-1.8	4.4E-01	6.3	1.6E-01	5.7	1.6E-01	-2.4	3.6E-01
ENSMUST00000102942	pleckstrin and Sec7 domain containing 4 [Source:MGI Symbol;Acc:MGI:2674093]		Q8BLR5	0.9	1.8E-01	1.8	6.0E-02	0.9	2.0E-01	0.0	9.7E-01
ENSMUST00000105863	transmembrane protein 50A [Source:MGI Symbol;Acc:MGI:1919067]	Q52KP1	Q9CXL1	-4.4	2.0E-04	-4.5	1.7E-04	0.0	9.3E-01	0.1	9.1E-01
ENSMUST00000102946	exocyst complex component 2 [Source:MGI Symbol;Acc:MGI:1913732]		Q9D4H1	-2.3	2.1E-01	-0.7	7.5E-01	0.7	6.2E-01	-0.9	6.8E-01
ENSMUST00000102948	E2F transcription factor 3 [Source:MGI Symbol;Acc:MGI:1096340]	Q3UZJ0	O35261	1.0	5.8E-02	1.2	1.0E-01	0.7	2.1E-01	0.5	3.8E-01
ENSMUST00000105867	stathmin 1 [Source:MGI Symbol;Acc:MGI:96739]	D3Z5N2		-2.6	2.2E-02	7.4	1.9E-02	-0.8	7.8E-01	-1.2	4.2E-01
ENSMUST00000105872	solute carrier family 30 (zinc transporter), member 2 [Source:MGI Symbol;Acc:MGI:106637]	D3Z5N1		5.6	3.2E-02	5.2	9.0E-04	0.1	9.6E-01	-0.3	6.6E-01
ENSMUST00000102956	sarcolemma associated protein [Source:MGI Symbol;Acc:MGI:1933549]		Q3URD3	-1.1	2.6E-01	0.5	7.1E-01	1.6	1.9E-01	-0.1	9.6E-01
ENSMUST00000105875	tripartite motif-containing 63 [Source:MGI Symbol;Acc:MGI:2447992]	F8VPZ1		4.6	2.3E-02	1.7	3.5E-02	0.0	9.9E-01	0.3	5.9E-01
ENSMUST00000105876	PDLIM1 interacting kinase 1 like [Source:MGI Symbol;Acc:MGI:2385213]		Q8QZR7	-4.4	1.9E-02	6.9	1.9E-04	-0.6	6.2E-01	-1.3	8.8E-02
ENSMUST00000105878	cation channel, sperm associated 4 [Source:MGI Symbol;Acc:MGI:3043288]	Z4YKD2		7.7	7.8E-05	5.6	2.9E-04	0.1	9.1E-01	-0.3	6.3E-01
ENSMUST00000105879	SH3 domain binding glutamic acid-rich protein-like 3 [Source:MGI Symbol;Acc:MGI:1920973]	I7HPY0		-3.7	4.5E-03	3.1	7.2E-02	-1.9	2.6E-01	0.5	6.6E-01
ENSMUST00000105884	zinc finger protein 683 [Source:MGI Symbol;Acc:MGI:3650254]	I7HJS4		7.6	2.8E-05	2.7	1.6E-01	-2.0	2.8E-01	-0.6	6.8E-01
ENSMUST00000105889	dehydrodolichyl diphosphate synthase [Source:MGI Symbol;Acc:MGI:1914672]	A3KGL3		-2.9	1.2E-02	3.6	9.8E-03	-1.9	1.4E-01	0.0	1.0E+00
ENSMUST00000102972	histone cluster 1, H4h [Source:MGI Symbol;Acc:MGI:2448427]	B2RTM0	P62806	0.2	8.2E-01	0.3	7.1E-01	-0.8	3.0E-01	-1.0	2.5E-01
ENSMUST00000102973	aconitase 1 [Source:MGI Symbol;Acc:MGI:87879]		P28271	-0.6	1.8E-01	-0.3	6.0E-01	0.2	6.7E-01	-0.1	7.8E-01
ENSMUST00000105894	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:104558]	Q505N6		-4.4	4.3E-04	4.9	1.3E-04	1.0	1.8E-01	-0.1	8.0E-01
ENSMUST00000105898	fibroblast growth factor 3 [Source:MGI Symbol;Acc:MGI:95517]	Q0VG15		7.7	1.1E-05	3.7	6.7E-04	-1.4	7.0E-02	0.4	4.5E-01
ENSMUST00000105899	GPN-loop GTPase 2 [Source:MGI Symbol;Acc:MGI:2140368]	A2A9F7		-4.1	3.9E-03	-4.6	1.7E-04	0.2	6.1E-01	1.3	1.2E-01
ENSMUST00000105900	SH3/ankyrin domain gene 2 [Source:MGI Symbol;Acc:MGI:2671987]	D3Z5K9		9.1	1.6E-02	5.1	1.0E-02	-0.6	7.3E-01	1.4	1.7E-01
ENSMUST00000105902	SH3/ankyrin domain gene 2 [Source:MGI Symbol;Acc:MGI:2671987]	D3Z5K8		9.0	7.3E-06	4.3	1.4E-02	0.8	5.5E-01	-0.9	3.5E-01
ENSMUST00000105907	transmembrane protein 222 [Source:MGI Symbol;Acc:MGI:1098568]		Q8BVA2	-3.4	2.5E-04	-7.7	2.7E-03	-0.9	1.8E-01	2.1	2.8E-01
ENSMUST00000102982	histone cluster 1, H2bp [Source:MGI Symbol;Acc:MGI:2448409]		Q8CGP2	2.9	5.7E-02	3.0	9.0E-02	-0.3	8.4E-01	-0.5	7.0E-01
ENSMUST00000102983	histone cluster 1, H4k [Source:MGI Symbol;Acc:MGI:2448439]	B2RTM0	P62806	2.5	1.7E-01	2.9	7.7E-02	-2.1	1.8E-01	-2.5	1.0E-01
ENSMUST00000105909	cysteinyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1351477]	Q3U716	Q9ER72	-3.1	2.1E-02	3.9	6.1E-04	0.8	2.3E-01	0.2	7.2E-01
ENSMUST00000102988	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2441769]		Q8K4J0	-1.4	1.4E-01	-1.8	1.4E-01	-0.7	3.7E-01	-0.3	8.2E-01
ENSMUST00000105910	CD164 sialomucin-like 2 [Source:MGI Symbol;Acc:MGI:1916905]		Q9D6W7	4.8	3.3E-04	-3.6	3.2E-03	0.9	1.0E-01	-0.4	6.9E-01
ENSMUST00000105911	G-protein coupled receptor 3 [Source:MGI Symbol;Acc:MGI:101908]		P35413	7.0	4.1E-05	-0.8	4.6E-01	-0.2	8.4E-01	-2.9	5.1E-02
ENSMUST00000102995	S-adenosylhomocysteine hydrolase-like 2 [Source:MGI Symbol;Acc:MGI:1921590]	F8WGT1		-1.3	7.0E-01	-5.0	2.8E-01	-2.6	2.6E-01	1.1	8.2E-01
ENSMUST00000105914	AT hook, DNA binding motif, containing 1 [Source:MGI Symbol;Acc:MGI:2444218]		Q6PAL7	7.2	1.3E-04	6.5	3.8E-04	0.1	9.6E-01	0.2	8.1E-01
ENSMUST00000105915	AT hook, DNA binding motif, containing 1 [Source:MGI Symbol;Acc:MGI:2444218]		Q6PAL7	3.9	3.5E-04	5.5	4.5E-03	6.9	6.5E-04	-4.3	4.2E-03
ENSMUST00000105916	AT hook, DNA binding motif, containing 1 [Source:MGI Symbol;Acc:MGI:2444218]		Q6PAL7	6.7	8.0E-03	9.1	1.1E-05	-1.4	2.4E-01	-0.6	1.6E-01
ENSMUST00000105917	solute carrier family 22 (organic cation transporter), member 18 [Source:MGI Symbol;Acc:MGI:1336884]			5.8	3.0E-02	6.6	1.1E-04	0.6	6.0E-01	0.0	9.5E-01
ENSMUST00000103002	ıonooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Source:MGI Symbol;Acc:M	A3KML3	P68254	-3.1	2.6E-01	1.7	4.5E-01	0.3	8.8E-01	-4.5	1.0E-01
ENSMUST00000105930	insulin II [Source:MGI Symbol;Acc:MGI:96573]	D3Z596		6.2	5.4E-04	5.8	2.8E-04	-0.6	5.9E-01	0.3	6.1E-01
ENSMUST00000105936	insulin-like growth factor 2 [Source:MGI Symbol;Acc:MGI:96434]		P09535	7.0	1.8E-02	4.6	3.3E-02	-1.6	4.3E-01	0.6	6.6E-01
ENSMUST00000105939	DnaJ (Hsp40) homolog, subfamily C, member 8 [Source:MGI Symbol;Acc:MGI:1915848]	A2ALF0		-7.7	1.1E-04	5.8	5.9E-04	-0.6	6.5E-01	0.1	8.3E-01
ENSMUST00000105963	2 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:191	E9QNT5		-6.5	2.3E-05	-8.8	1.2E-04	0.1	8.6E-01	-1.1	4.8E-01
ENSMUST00000105964	glucocorticoid modulatory element binding protein 1 [Source:MGI Symbol;Acc:MGI:2135604]		Q9JL60	-4.7	2.2E-04	-8.3	5.4E-04	-0.7	2.5E-01	-0.7	6.8E-01
ENSMUST00000105967	lymphocyte specific 1 [Source:MGI Symbol;Acc:MGI:96832]	A2A6J7		-12.1	1.3E-06	-7.5	4.2E-04	-0.4	5.0E-01	-3.1	1.2E-01
ENSMUST00000103013	tubulin-specific chaperone d [Source:MGI Symbol;Acc:MGI:1919686]		Q8BYA0	-0.4	3.4E-01	-0.2	6.7E-01	0.6	1.5E-01	0.4	4.4E-01
ENSMUST00000105968	lymphocyte specific 1 [Source:MGI Symbol;Acc:MGI:96832]		P19973	-5.6	2.1E-05	6.2	1.8E-04	-0.6	5.8E-01	-0.5	4.2E-01
ENSMUST00000105987	protein tyrosine phosphatase, receptor type, U [Source:MGI Symbol;Acc:MGI:1321151]		B1AUH1	8.5	8.5E-05	-2.2	1.0E-03	0.6	5.8E-02	-0.8	1.3E-01
ENSMUST00000105991	pumilio RNA-binding family member 1 [Source:MGI Symbol;Acc:MGI:1931749]	E9Q6M7		-6.2	1.8E-02	2.0	3.2E-01	-3.5	1.4E-01	1.4	3.5E-01
ENSMUST00000105994	small nuclear ribonucleoprotein 40 (U5) [Source:MGI Symbol;Acc:MGI:1913835]		Q6PE01	-2.5	4.3E-04	-4.8	5.8E-03	1.2	8.1E-02	-1.2	4.7E-01
ENSMUST00000105996	serine incorporator 2 [Source:MGI Symbol;Acc:MGI:1919132]		Q8K0E7	3.2	2.6E-02	7.0	3.9E-03	1.1	5.6E-01	-0.1	9.6E-01
ENSMUST00000103025	transmembrane channel-like gene family 6 [Source:MGI Symbol;Acc:MGI:1098686]		Q7TN60	1.7	5.5E-02	0.0	9.7E-01	-0.3	7.1E-01	1.5	1.9E-01
ENSMUST00000103026	SEC14-like lipid binding 1 [Source:MGI Symbol;Acc:MGI:1921386]	Q99J07		-3.4	1.9E-01	-2.6	4.5E-01	0.6	6.9E-01	-0.2	9.5E-01
ENSMUST00000105999	tubulointerstitial nephritis antigen-like 1 [Source:MGI Symbol;Acc:MGI:2137617]		Q99JR5	-6.6	2.0E-04	7.9	1.1E-04	-0.6	6.5E-01	-0.6	3.7E-01
ENSMUST00000103028	rhomboid 5 homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2442473]		Q80WQ6	1.3	2.1E-01	2.9	5.8E-02	0.5	7.1E-01	-1.1	2.8E-01
ENSMUST00000106003	ribosomal protein, large P2 [Source:MGI Symbol;Acc:MGI:1914436]		P99027	-5.2	5.1E-04	-7.8	1.1E-02	1.3	9.8E-02	1.7	5.0E-01
ENSMUST00000103031	Fas (TNFRSF6) binding factor 1 [Source:MGI Symbol;Acc:MGI:1922033]		A2A870	0.3	9.1E-01	4.6	2.6E-01	3.1	3.9E-01	-1.2	6.7E-01
ENSMUST00000103032	lethal giant larvae homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1918843]		Q3TJ91	-2.7	9.0E-02	1.8	2.6E-01	1.0	4.4E-01	-3.5	4.4E-02
ENSMUST00000103033	RIKEN cDNA 2310067B10 gene [Source:MGI Symbol;Acc:MGI:1919197]		Q7TSH8	-2.1	2.0E-01	0.9	6.7E-01	2.1	2.6E-01	-1.0	6.0E-01
ENSMUST00000106004	ribosomal protein, large P2 [Source:MGI Symbol;Acc:MGI:1914436]		P99027	-9.6	2.2E-05	-1.9	1.4E-01	1.3	1.1E-01	-1.1	3.8E-01
ENSMUST00000106008	Parkinson disease 7 domain containing 1 [Source:MGI Symbol;Acc:MGI:2387178]		Q8BFQ8	-4.8	4.8E-04	-4.3	2.9E-03	-1.1	4.5E-02	-1.1	3.9E-01
ENSMUST00000106017	adhesion G protein-coupled receptor B2 [Source:MGI Symbol;Acc:MGI:2451244]		Q8CGM1	7.5	6.5E-03	8.4	2.7E-05	0.0	9.8E-01	-0.2	6.7E-01
ENSMUST00000106033	ribonuclease/angiogenin inhibitor 1 [Source:MGI Symbol;Acc:MGI:1195456]		Q91VI7	-4.5	4.9E-04	-1.2	1.8E-01	-0.1	8.2E-01	-1.3	1.6E-01
ENSMUST00000106039	plakophilin 3 [Source:MGI Symbol;Acc:MGI:1891830]		Q9QY23	7.0	1.8E-02	-2.3	4.1E-02	0.8	1.9E-01	-1.2	2.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000103055	death inducer-obliterator 1 [Source:MGI Symbol;Acc:MGI:1344352]		Q8C9B9	-2.0	1.2E-01	-1.2	4.4E-01	0.0	9.9E-01	-0.8	6.0E-01
ENSMUST00000103057	death inducer-obliterator 1 [Source:MGI Symbol;Acc:MGI:1344352]		Q8C9B9	0.8	6.7E-01	1.5	5.7E-01	0.6	7.5E-01	-0.1	9.6E-01
ENSMUST00000106040	interferon induced transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1915963]		Q9D103	-12.0	3.0E-06	-1.5	3.2E-02	1.0	2.1E-02	-0.3	6.6E-01
ENSMUST00000106041	DEP domain containing 1a [Source:MGI Symbol;Acc:MGI:1923381]		Q8CIG0	-3.7	6.0E-03	-1.8	6.2E-02	-0.1	8.6E-01	-1.4	1.8E-01
ENSMUST00000106042	interferon induced transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1915963]		Q9D103	-5.7	2.5E-03	5.2	1.1E-02	-0.6	7.1E-01	1.3	2.3E-01
ENSMUST00000103064	phosphatidylinositol transfer protein, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:1919045]		Q8K4R4	-0.7	8.5E-02	-0.1	9.0E-01	0.8	5.4E-02	0.1	7.9E-01
ENSMUST00000103066	phosphatase and actin regulator 3 [Source:MGI Symbol;Acc:MGI:1921439]		Q8BYK5	4.2	6.3E-02	5.6	3.2E-02	-0.3	8.9E-01	-1.8	2.2E-01
ENSMUST00000106044	leucine rich repeat containing 7 [Source:MGI Symbol;Acc:MGI:2676665]	E9Q6L9		8.2	1.2E-05	-2.7	9.6E-04	0.2	5.0E-01	-0.1	8.4E-01
ENSMUST00000103068	centrosomal protein 95 [Source:MGI Symbol;Acc:MGI:2443502]	Q14B65		-0.8	1.7E-01	-0.4	5.6E-01	-0.1	9.0E-01	-0.5	4.8E-01
ENSMUST00000106047	zinc finger and BTB domain containing 8 opposite strand [Source:MGI Symbol;Acc:MGI:1914356]	F7BCB7		-6.2	1.6E-05	-4.7	5.0E-02	-0.2	8.2E-01	1.2	5.8E-01
ENSMUST00000106051	expressed sequence C77080 [Source:MGI Symbol;Acc:MGI:2140651]		A2A7S8	9.7	2.4E-06	5.7	3.4E-02	0.7	7.5E-01	0.9	6.0E-01
ENSMUST00000106052	zinc finger protein 941 [Source:MGI Symbol;Acc:MGI:3039601]	Q6NV92		6.3	3.6E-06	5.4	3.5E-03	-1.2	4.5E-01	-1.5	1.1E-01
ENSMUST00000106059	S100P binding protein [Source:MGI Symbol;Acc:MGI:1921898]		Q9D5K4	-4.8	3.6E-04	-1.7	3.1E-01	1.5	1.7E-01	0.3	8.7E-01
ENSMUST00000103073	Cas scaffolding protein family member 4 [Source:MGI Symbol;Acc:MGI:2444482]			0.3	5.3E-01	0.9	1.6E-01	0.0	9.3E-01	-0.6	2.8E-01
ENSMUST00000106063	zinc finger, RAN-binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1858211]	A0A0H2UH20		-6.0	6.5E-05	-2.6	8.6E-04	0.9	8.5E-03	0.2	7.4E-01
ENSMUST00000106068	antizyme inhibitor 2 [Source:MGI Symbol;Acc:MGI:2442093]	B2RSR5	Q8BVM4	5.0	6.8E-03	6.8	4.6E-04	-0.8	5.6E-01	-0.1	9.0E-01
ENSMUST00000106069	a disintegrin and metallopeptidase domain 8 [Source:MGI Symbol;Acc:MGI:107825]	Q3U1J7	Q05910	-8.2	8.3E-05	4.8	1.5E-03	-3.9	1.2E-02	-1.0	1.8E-01
ENSMUST00000106077	alpha 1,3-galactosyltransferase 2 (isoglobotriaosylceramide synthase) [Source:MGI Symbol;Acc:MGI:2685279]		Q3V1N9	5.0	3.9E-03	2.7	1.2E-03	-6.2	4.1E-05	0.8	1.1E-01
ENSMUST00000106079	polyhomeotic-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1860454]		Q9QWH1	-7.6	1.9E-04	8.6	9.5E-05	0.5	7.1E-01	-2.6	6.0E-03
ENSMUST00000106089	meteorin, glial cell differentiation regulator-like [Source:MGI Symbol;Acc:MGI:2384806]		Q8VE43	-6.0	4.0E-04	6.5	1.3E-05	-3.0	8.9E-03	0.1	8.5E-01
ENSMUST00000106090	gap junction protein, beta 4 [Source:MGI Symbol;Acc:MGI:95722]		Q02738	6.7	4.3E-04	7.9	2.0E-02	-0.9	7.8E-01	-0.9	6.0E-01
ENSMUST00000103086	integrin alpha 2b [Source:MGI Symbol;Acc:MGI:96601]		Q9QUM0	-1.7	6.2E-02	-1.5	1.4E-01	-0.7	2.8E-01	-0.9	3.9E-01
ENSMUST00000103088	engulfment and cell motility 2 [Source:MGI Symbol;Acc:MGI:2153045]		Q8BHL5	-0.3	8.5E-01	-3.0	2.5E-01	0.2	8.8E-01	2.9	2.3E-01
ENSMUST00000103091	engulfment and cell motility 2 [Source:MGI Symbol;Acc:MGI:2153045]		Q8BHL5	0.6	5.0E-01	0.3	7.9E-01	0.3	7.5E-01	0.5	5.8E-01
ENSMUST00000103092	cathepsin A [Source:MGI Symbol;Acc:MGI:97748]	Q544R6	P16675	0.6	4.8E-01	1.3	2.6E-01	0.4	6.1E-01	-0.2	8.4E-01
ENSMUST00000106092	discs, large (Drosophila) homolog-associated protein 3 [Source:MGI Symbol;Acc:MGI:3039563]	B1AS06		7.5	1.3E-04	-10.2	6.7E-05	0.6	1.4E-01	-0.8	6.3E-01
ENSMUST00000106094	discs, large (Drosophila) homolog-associated protein 3 [Source:MGI Symbol;Acc:MGI:3039563]	Q3TY61	Q6PFD5	7.3	3.1E-05	-4.8	1.7E-02	1.2	9.0E-02	1.4	4.0E-01
ENSMUST00000106098	inositol polyphosphate-5-phosphatase A [Source:MGI Symbol;Acc:MGI:2686961]	Q7TNC9		-5.6	1.4E-04	6.3	1.2E-02	-0.7	7.5E-01	-1.4	2.6E-01
ENSMUST00000106103	zinc finger, ZZ domain containing 3 [Source:MGI Symbol;Acc:MGI:1920453]		Q6KAQ7	-6.9	1.1E-03	6.3	2.2E-04	-0.6	6.3E-01	-0.8	2.4E-01
ENSMUST00000106107	Rab40B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2183451]	B1ATT4		5.1	1.6E-03	-2.3	8.2E-02	1.0	1.6E-01	-2.9	7.4E-02
ENSMUST00000106112	BCL2/adenovirus E1B interacting protein 3 [Source:MGI Symbol;Acc:MGI:109326]		O55003	-5.0	3.0E-06	6.8	1.3E-02	-2.0	4.5E-01	-2.4	1.2E-01
ENSMUST00000106115	cDNA sequence BC017643 [Source:MGI Symbol;Acc:MGI:2384959]		Q3TYS2	-6.3	1.0E-04	5.1	6.8E-04	0.0	1.0E+00	-0.2	7.5E-01
ENSMUST00000106121	far upstream element (FUSE) binding protein 1 [Source:MGI Symbol;Acc:MGI:1196294]	Q3TUE1		-5.4	1.7E-04	4.8	8.6E-02	-3.2	2.8E-01	0.2	9.2E-01
ENSMUST00000106128	adhesion G protein-coupled receptor L2 [Source:MGI Symbol;Acc:MGI:2139714]		Q8JZZ7	6.1	9.7E-06	6.1	2.1E-05	-0.2	7.6E-01	-0.5	2.6E-01
ENSMUST00000103110	ATPase, H+ transporting, lysosomal V0 subunit A1 [Source:MGI Symbol;Acc:MGI:103286]		Q9Z1G4	-3.7	1.6E-01	-2.3	5.0E-01	1.2	4.4E-01	-0.1	9.7E-01
ENSMUST00000106132	MAP7 domain containing 1 [Source:MGI Symbol;Acc:MGI:2384297]	A2AJI1		-3.6	1.6E-02	5.3	3.2E-03	-4.2	2.7E-02	0.7	3.4E-01
ENSMUST00000103112	zinc fingers and homeoboxes 3 [Source:MGI Symbol;Acc:MGI:2444772]	Q3UPQ8	Q8C0Q2	-0.8	6.9E-01	0.4	8.7E-01	1.1	5.4E-01	-0.1	9.7E-01
ENSMUST00000106137	protein kinase, cAMP dependent, catalytic, beta [Source:MGI Symbol;Acc:MGI:97594]		P68181	4.2	7.1E-03	2.8	1.7E-03	0.7	2.2E-01	-0.2	6.2E-01
ENSMUST00000106149	synovial sarcoma, X breakpoint 2 interacting protein [Source:MGI Symbol;Acc:MGI:2139150]			5.1	4.6E-03	5.7	3.4E-03	-0.7	6.6E-01	1.3	1.5E-01
ENSMUST00000103116	protein phosphatase 1, regulatory (inhibitor) subunit 16B [Source:MGI Symbol;Acc:MGI:2151841]	Q544H9	Q8VHQ3	-1.4	4.4E-01	-2.1	3.5E-01	-0.1	9.5E-01	0.7	7.6E-01
ENSMUST00000103118	K(lysine) acetyltransferase 2A [Source:MGI Symbol;Acc:MGI:1343101]		Q9JHD2	-2.0	2.8E-01	-2.4	2.7E-01	-0.4	8.2E-01	0.1	9.8E-01
ENSMUST00000106150	eva-1 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:1922063]		Q8K2Y3	1.8	3.2E-02	6.3	4.3E-04	0.3	8.3E-01	-0.1	8.1E-01
ENSMUST00000106151	synovial sarcoma, X breakpoint 2 interacting protein [Source:MGI Symbol;Acc:MGI:2139150]			4.9	9.9E-03	-1.7	2.9E-01	0.1	9.1E-01	-1.9	2.8E-01
ENSMUST00000106157	zinc finger, RAN-binding domain containing 1 [Source:MGI Symbol;Acc:MGI:106441]		Q7M760	-1.8	1.1E-02	4.9	3.5E-04	1.0	2.3E-01	-0.2	7.5E-01
ENSMUST00000103122	transglutaminase 2, C polypeptide [Source:MGI Symbol;Acc:MGI:98731]		P21981	0.8	8.1E-02	-1.5	1.4E-02	-2.6	6.8E-05	-0.2	7.0E-01
ENSMUST00000103123	regulation of nuclear pre-mRNA domain containing 1B [Source:MGI Symbol;Acc:MGI:1917720]			3.9	6.0E-02	7.1	6.3E-03	0.9	6.4E-01	-2.3	1.8E-01
ENSMUST00000106158	alveolar soft part sarcoma chromosome region, candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1916188]		Q8VBT9	-6.2	1.9E-04	3.5	4.0E-02	-2.0	2.3E-01	1.3	2.2E-01
ENSMUST00000106159	alveolar soft part sarcoma chromosome region, candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1916188]		Q8VBT9	-5.0	6.0E-03	-3.2	3.3E-02	0.0	9.5E-01	1.2	3.6E-01
ENSMUST00000103130	SN1, MIND kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191418		Q9CYC5	0.4	7.5E-01	4.4	5.8E-02	3.7	6.6E-02	-0.3	8.5E-01
ENSMUST00000106161	family with sequence similarity 175, member B [Source:MGI Symbol;Acc:MGI:1926116]	D3Z4D8		4.1	8.2E-04	3.7	5.2E-03	-2.1	7.8E-02	0.2	8.3E-01
ENSMUST00000106162	colony stimulating factor 3 receptor (granulocyte) [Source:MGI Symbol;Acc:MGI:1339755]		P40223	-5.4	3.0E-04	4.9	2.7E-03	0.1	9.5E-01	-0.5	5.0E-01
ENSMUST00000106166	family with sequence similarity 53, member B [Source:MGI Symbol;Acc:MGI:1925188]	Q3U0R8		7.2	8.0E-04	-4.8	1.4E-04	-0.7	9.9E-02	0.1	9.1E-01
ENSMUST00000103134	chemokine (C-C motif) receptor 7 [Source:MGI Symbol;Acc:MGI:103011]		P47774	0.3	7.4E-01	-0.8	4.6E-01	-0.9	2.4E-01	0.2	8.6E-01
ENSMUST00000103135	erythrocyte membrane protein band 4.1 like 1 [Source:MGI Symbol;Acc:MGI:103010]	A2AUK5		5.9	4.4E-02	5.8	6.6E-02	-0.7	8.1E-01	-0.6	7.2E-01
ENSMUST00000103137	erythrocyte membrane protein band 4.1 like 1 [Source:MGI Symbol;Acc:MGI:103010]	A2AUK5		2.8	1.3E-01	5.2	1.3E-02	-0.6	7.4E-01	-3.0	4.9E-02
ENSMUST00000103139	thyroid hormone receptor alpha [Source:MGI Symbol;Acc:MGI:98742]		P63058	0.5	6.7E-01	1.1	4.3E-01	0.0	9.9E-01	-0.6	6.2E-01
ENSMUST00000106180	maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian) [Source:MGI Symbol;Acc:MGI:9691		O54790	-3.1	7.1E-03	-7.0	3.6E-03	1.5	3.1E-02	0.4	8.3E-01
ENSMUST00000103141	IKAROS family zinc finger 3 [Source:MGI Symbol;Acc:MGI:1342542]		O08900	0.4	6.1E-01	0.9	4.0E-01	-0.2	7.7E-01	-0.7	4.6E-01
ENSMUST00000106182	maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian) [Source:MGI Symbol;Acc:MGI:9691		O54790	-2.0	1.1E-02	-3.2	5.2E-02	-0.1	8.7E-01	-0.5	7.7E-01
ENSMUST00000106193	metal response element binding transcription factor 1 [Source:MGI Symbol;Acc:MGI:101786]		Q07243	11.5	1.9E-04	-1.8	4.0E-02	0.5	3.2E-01	0.0	9.6E-01
ENSMUST00000103145	E2F transcription factor 1 [Source:MGI Symbol;Acc:MGI:101941]	Q547J6	Q61501	1.4	5.3E-01	5.2	1.3E-01	2.0	5.3E-01	-1.9	3.6E-01
ENSMUST00000106197	Rho GDP dissociation inhibitor (GDI) alpha [Source:MGI Symbol;Acc:MGI:2178103]		Q99PT1	-6.7	4.9E-05	-4.0	2.2E-04	-1.4	6.4E-03	-0.4	5.3E-01
ENSMUST00000106204	rhomboid, veinlet-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:3608413]		A2AGA4	5.8	6.1E-05	-5.0	2.9E-04	-0.7	1.4E-01	-1.8	9.0E-02
ENSMUST00000103150	DNA methyltransferase 3B [Source:MGI Symbol;Acc:MGI:1261819]		O88509	1.1	6.1E-01	5.1	1.3E-01	3.0	3.1E-01	-1.0	6.4E-01
ENSMUST00000106205	HGF-regulated tyrosine kinase substrate [Source:MGI Symbol;Acc:MGI:104681]	B1ATZ0		-5.9	4.4E-03	-4.6	8.1E-04	0.4	3.2E-01	-2.6	4.8E-02
ENSMUST00000106211	selenoprotein [Source:MGI Symbol;Acc:MGI:1927947]	D3Z3Y8		-9.3	9.9E-07	5.0	4.1E-02	-0.7	7.7E-01	-0.8	5.5E-01
ENSMUST00000106215	actin, gamma, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:87906]	Q4KL81	P63260	-6.4	1.9E-05	5.0	1.0E-01	-0.7	8.3E-01	0.5	7.7E-01
ENSMUST00000106230	bone morphogenetic protein receptor, type 1B [Source:MGI Symbol;Acc:MGI:107191]	B2RRZ4	P36898	4.9	9.0E-03	2.5	1.8E-02	-0.7	3.8E-01	0.2	7.9E-01
ENSMUST00000103168	sperm associated antigen 9 [Source:MGI Symbol;Acc:MGI:1918084]			-5.3	6.2E-02	0.3	9.0E-01	1.8	3.7E-01	-3.8	1.6E-01
ENSMUST00000106231	brain-specific angiogenesis inhibitor 1-associated protein 2 [Source:MGI Symbol;Acc:MGI:2137336]		Q8BKX1	6.0	1.4E-03	6.0	1.2E-03	-0.4	7.6E-01	-0.5	4.8E-01
ENSMUST00000106236	unc-5 homolog C (C. elegans) [Source:MGI Symbol;Acc:MGI:1095412]		O08747	5.9	4.1E-04	-6.7	4.1E-06	0.1	7.5E-01	-0.1	9.1E-01
ENSMUST00000103173	tumor necrosis factor receptor superfamily, member 18 [Source:MGI Symbol;Acc:MGI:894675]	Q540M6	O35714	0.0	9.5E-01	-0.2	8.1E-01	-0.4	5.8E-01	-0.1	8.7E-01
ENSMUST00000106237	integrin, alpha D [Source:MGI Symbol;Acc:MGI:3578624]		Q3V0T4	7.1	1.5E-04	-3.9	1.7E-02	0.3	6.0E-01	-0.8	5.8E-01
ENSMUST00000103176	mindbomb homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2679684]		Q8R516	-2.0	1.4E-01	1.0	5.6E-01	2.4	1.2E-01	-0.6	6.9E-01
ENSMUST00000106247	alcohol dehydrogenase 6A (class V) [Source:MGI Symbol;Acc:MGI:1916367]	E9Q5Z6		5.1	1.5E-02	7.3	2.4E-05	-1.5	1.7E-01	-0.5	3.1E-01
ENSMUST00000106250	caspase recruitment domain family, member 14 [Source:MGI Symbol;Acc:MGI:2386258]		Q99KF0	6.8	1.5E-02	6.8	4.5E-04	-1.1	4.5E-01	-1.3	1.1E-01
ENSMUST00000106252	myelocytomatosis viral oncogene homolog, lung carcinoma derived (avian) [Source:MGI Symbol;Acc:MGI:9	Q3UIE0	P10166	7.1	4.6E-04	0.2	8.6E-01	1.1	1.9E-01	-4.1	1.1E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000103180	peroxisomal biogenesis factor 10 [Source:MGI Symbol;Acc:MGI:2684988]		B1AUE5	-0.6	6.1E-01	-0.5	7.9E-01	0.8	5.3E-01	0.6	7.0E-01
ENSMUST00000106255	CAP, adenylate cyclase-associated protein 1 (yeast) [Source:MGI Symbol;Acc:MGI:88262]		P40124	-7.9	1.5E-03	-5.0	1.4E-02	-0.1	9.4E-01	-2.4	2.7E-01
ENSMUST00000106257	CAP, adenylate cyclase-associated protein 1 (yeast) [Source:MGI Symbol;Acc:MGI:88262]		P40124	-10.0	1.2E-06	-8.9	3.2E-02	0.9	4.0E-01	3.6	3.3E-01
ENSMUST00000106258	glucosidase, alpha, acid [Source:MGI Symbol;Acc:MGI:95609]	A2AFL3		7.7	1.0E-04	7.0	2.3E-04	-0.6	6.5E-01	-0.1	9.0E-01
ENSMUST00000106266	predicted gene 12886 [Source:MGI Symbol;Acc:MGI:3651888]	B1AZM5		6.7	2.7E-05	-0.9	8.3E-02	1.4	1.8E-03	-4.8	1.3E-04
ENSMUST00000106267	syntaxin 1B [Source:MGI Symbol;Acc:MGI:1930705]		P61264	9.9	1.9E-06	-6.1	7.4E-03	1.2	9.3E-02	0.6	7.7E-01
ENSMUST00000106282	B cell CLL/lymphoma 7C [Source:MGI Symbol;Acc:MGI:1332237]	D3Z3W8		4.1	8.1E-05	-10.1	3.0E-05	-0.9	2.9E-02	-0.8	5.9E-01
ENSMUST00000106286	C1q and tumor necrosis factor related protein 1 [Source:MGI Symbol;Acc:MGI:1919254]		Q9QXP7	6.6	8.5E-03	-2.1	5.5E-03	-0.1	8.5E-01	-0.6	3.7E-01
ENSMUST00000103195	zinc finger, HIT type 3 [Source:MGI Symbol;Acc:MGI:3051596]		Q9CQK1	-2.5	3.7E-02	-3.8	3.4E-02	-1.4	1.0E-01	-0.2	9.1E-01
ENSMUST00000106288	calcium activated nucleotidase 1 [Source:MGI Symbol;Acc:MGI:1923275]		Q8VCF1	-7.1	4.6E-03	4.1	5.0E-02	1.6	3.4E-01	1.1	3.9E-01
ENSMUST00000106289	calcium activated nucleotidase 1 [Source:MGI Symbol;Acc:MGI:1923275]		Q8VCF1	-3.8	3.0E-02	-3.8	1.6E-03	-1.9	5.4E-03	-2.6	4.0E-02
ENSMUST00000106291	ubiquitin-conjugating enzyme E2D 3 [Source:MGI Symbol;Acc:MGI:1913355]	Q4QQL2	P61079	-7.0	3.9E-06	-8.0	8.5E-04	0.9	9.7E-02	1.2	5.1E-01
ENSMUST00000106292	proline rich 14 [Source:MGI Symbol;Acc:MGI:2384565]		Q7TPN9	-8.5	6.7E-05	8.3	1.4E-03	2.2	2.5E-01	-0.4	6.6E-01
ENSMUST00000103202	signal-regulatory protein alpha [Source:MGI Symbol;Acc:MGI:108563]	Q6P6I8		0.4	8.6E-01	4.7	1.1E-01	1.8	4.3E-01	-2.5	3.4E-01
ENSMUST00000106296	ubiquitin specific peptidase 36 [Source:MGI Symbol;Acc:MGI:1919594]		B1AQJ2	6.1	1.2E-02	-9.4	1.5E-03	1.8	1.0E-02	-0.8	7.3E-01
ENSMUST00000103204	period circadian clock 3 [Source:MGI Symbol;Acc:MGI:1277134]		O70361	3.2	1.2E-01	3.8	7.2E-02	-1.7	4.1E-01	-2.3	1.6E-01
ENSMUST00000106302	cytohesin 1 [Source:MGI Symbol;Acc:MGI:1334257]	Q3TZ02		-3.5	2.6E-04	3.5	1.7E-03	0.2	8.1E-01	0.1	9.0E-01
ENSMUST00000106306	integrin alpha L [Source:MGI Symbol;Acc:MGI:96606]	E9Q5M7		-8.0	4.1E-04	4.0	3.0E-02	-0.2	9.1E-01	-0.3	7.6E-01
ENSMUST00000106307	human immunodeficiency virus type I enhancer binding protein 3 [Source:MGI Symbol;Acc:MGI:106589]		A2A884	8.0	4.4E-05	6.3	1.1E-02	-0.5	8.0E-01	1.3	3.1E-01
ENSMUST00000106308	dynein, axonemal, heavy chain 17 [Source:MGI Symbol;Acc:MGI:1917176]	K3W4R0		6.5	2.0E-02	-0.7	4.6E-01	1.1	8.7E-02	-0.3	7.3E-01
ENSMUST00000103214	prominin 2 [Source:MGI Symbol;Acc:MGI:2138997]		Q3UUY6	2.9	1.5E-01	6.0	1.1E-02	-0.4	8.4E-01	-3.5	2.5E-02
ENSMUST00000106312	zinc finger protein 553 [Source:MGI Symbol;Acc:MGI:2384725]		Q3US17	2.9	2.9E-02	9.0	3.6E-04	-0.7	7.0E-01	-1.6	7.9E-02
ENSMUST00000106313	septin 1 [Source:MGI Symbol;Acc:MGI:1858916]	D3Z3V3		-4.3	1.4E-03	2.4	2.9E-03	0.0	9.3E-01	0.5	2.9E-01
ENSMUST00000106314	septin 1 [Source:MGI Symbol;Acc:MGI:1858916]		P42209	-5.9	1.5E-04	-0.7	3.5E-01	0.9	1.1E-01	0.1	8.8E-01
ENSMUST00000106331	RIKEN cDNA 6030468B19 gene [Source:MGI Symbol;Acc:MGI:1924977]		Q9CX63	6.6	1.5E-04	-2.3	7.4E-04	0.4	1.8E-01	-0.4	4.4E-01
ENSMUST00000103221	mechanistic target of rapamycin (serine/threonine kinase) [Source:MGI Symbol;Acc:MGI:1928394]		Q9JLN9	-0.1	7.2E-01	1.0	5.4E-02	0.6	1.1E-01	-0.5	2.4E-01
ENSMUST00000106334	transmembrane channel-like gene family 8 [Source:MGI Symbol;Acc:MGI:2669037]	B0QZP6	Q7TN58	-5.5	7.5E-03	-3.6	1.4E-02	0.6	3.7E-01	-0.4	7.4E-01
ENSMUST00000106335	seizure related 6 homolog like 2 [Source:MGI Symbol;Acc:MGI:2385295]		Q4V9Z5	8.6	1.1E-05	1.6	3.7E-01	3.6	2.9E-02	-2.8	1.0E-01
ENSMUST00000106337	cytochrome P450, family 2, subfamily u, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1918769]		Q9CX98	6.1	3.1E-05	-2.1	7.2E-02	-0.3	6.7E-01	-1.7	1.6E-01
ENSMUST00000103227	GA repeat binding protein, beta 1 [Source:MGI Symbol;Acc:MGI:95611]	Q3US22	Q00420	-2.1	4.1E-01	-4.0	2.0E-01	-2.0	2.5E-01	-0.1	9.8E-01
ENSMUST00000106340	aspartate beta-hydroxylase domain containing 1 [Source:MGI Symbol;Acc:MGI:2685014]		Q2TA57	5.1	1.7E-05	2.9	4.9E-03	-2.8	1.6E-02	0.2	7.7E-01
ENSMUST00000106341	lymphoid enhancer binding factor 1 [Source:MGI Symbol;Acc:MGI:96770]	Q8BGZ9		11.1	9.1E-05	-2.5	1.8E-02	1.1	5.2E-02	0.2	8.6E-01
ENSMUST00000106343	INO80 complex subunit E [Source:MGI Symbol;Acc:MGI:2141881]	D3Z3H0		-6.6	1.1E-04	-1.8	1.2E-01	1.2	1.2E-01	-3.7	3.0E-02
ENSMUST00000106349	septin 9 [Source:MGI Symbol;Acc:MGI:1858222]		Q80UG5	-7.1	2.6E-04	6.7	2.1E-04	-3.0	4.8E-02	-1.1	1.0E-01
ENSMUST00000106353	collagen, type XXV, alpha 1 [Source:MGI Symbol;Acc:MGI:1924268]	E9Q5L6		6.8	4.9E-05	-9.6	1.9E-05	-0.3	3.4E-01	-0.6	6.5E-01
ENSMUST00000103241	ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D [Source:MGI Symbol;Acc:MGI:		Q76KF0	2.6	3.0E-01	7.3	1.7E-02	1.0	7.0E-01	-3.6	7.2E-02
ENSMUST00000103242	transmembrane protein 97 [Source:MGI Symbol;Acc:MGI:1916321]		Q8VD00	0.6	2.7E-01	-0.9	1.5E-01	-1.4	9.7E-03	0.1	9.0E-01
ENSMUST00000103291	T cell receptor beta, constant region 1 [Source:MGI Symbol;Acc:MGI:4439726]	A0A075B5J3		0.1	9.4E-01	-3.0	2.7E-03	-3.2	2.7E-04	-0.2	7.8E-01
ENSMUST00000106354	septin 9 [Source:MGI Symbol;Acc:MGI:1858222]	A2A6U3		5.5	3.1E-02	-5.8	2.6E-04	-2.0	7.9E-04	0.4	7.3E-01
ENSMUST00000103303	immunoglobulin kappa variable 1-135 [Source:MGI Symbol;Acc:MGI:3819952]	A0A0B4J1H7		1.5	1.7E-01	-2.7	4.5E-02	-4.4	6.9E-04	-0.2	8.6E-01
ENSMUST00000103317	immunoglobulin kappa variable 1-117 [Source:MGI Symbol;Acc:MGI:4439721]			-0.7	5.9E-01	-2.4	3.6E-02	-4.4	5.6E-04	-2.7	5.4E-02
ENSMUST00000103321	immunoglobulin kappa variable 1-110 [Source:MGI Symbol;Acc:MGI:4439558]	A0A0B4J1I0		2.1	4.7E-02	-2.7	1.7E-02	-4.7	2.4E-04	0.2	8.7E-01
ENSMUST00000103328	immunoglobulin kappa variable 10-96 [Source:MGI Symbol;Acc:MGI:4439561]			0.6	6.3E-01	-3.3	7.6E-02	-4.0	3.5E-03	0.0	9.9E-01
ENSMUST00000106356	yippee-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913340]		P61237	-9.3	3.5E-04	0.8	2.5E-01	-4.3	2.1E-04	-2.5	3.1E-03
ENSMUST00000103377	immunoglobulin kappa variable 6-32 [Source:MGI Symbol;Acc:MGI:3641634]			0.0	9.8E-01	-3.4	2.7E-02	-3.7	9.4E-04	-0.4	7.9E-01
ENSMUST00000103391	immunoglobulin kappa variable 6-17 [Source:MGI Symbol;Acc:MGI:1330833]			0.0	9.9E-01	-3.4	3.1E-02	-3.4	2.1E-03	0.0	9.9E-01
ENSMUST00000103393	immunoglobulin kappa variable 6-15 [Source:MGI Symbol;Acc:MGI:1330831]			1.5	1.4E-01	-4.0	7.1E-03	-5.0	8.5E-05	0.5	6.7E-01
ENSMUST00000103401	immunoglobulin kappa variable 3-4 [Source:MGI Symbol;Acc:MGI:1330855]			1.3	1.5E-01	-2.2	1.7E-02	-5.0	3.7E-05	-1.5	9.4E-02
ENSMUST00000103403	immunoglobulin kappa variable 3-2 [Source:MGI Symbol;Acc:MGI:1330850]	A0A075B5P0		0.6	6.0E-01	-1.4	1.2E-01	-4.6	2.5E-04	-2.7	1.9E-02
ENSMUST00000103405	immunoglobulin kappa joining 1 [Source:MGI Symbol;Acc:MGI:1316689]	A0A0G2JEZ6		-1.0	3.4E-01	-3.9	8.6E-03	-3.6	4.7E-04	-0.7	5.9E-01
ENSMUST00000103406				-0.7	4.7E-01	-3.3	1.7E-02	-3.4	8.1E-04	-0.9	4.9E-01
ENSMUST00000106357	yippee-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913340]		P61237	-4.1	1.3E-02	-6.4	4.4E-05	-4.2	1.1E-05	-0.9	3.6E-01
ENSMUST00000106359	yippee-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913340]	D3Z3G7		-4.4	5.6E-03	-0.8	2.1E-01	-5.2	1.6E-05	-0.1	9.1E-01
ENSMUST00000103420	immunoglobulin heavy constant gamma 1 (G1m marker) [Source:MGI Symbol;Acc:MGI:96446]	A0A075B5P4		0.7	6.1E-01	-1.5	2.7E-01	-4.3	4.3E-03	-2.1	1.6E-01
ENSMUST00000106364	coronin, actin binding protein 1A [Source:MGI Symbol;Acc:MGI:1345961]	Q3U1N0	O89053	-5.7	2.6E-04	2.0	2.4E-02	-2.3	8.9E-03	-0.5	4.4E-01
ENSMUST00000103426	immunoglobulin heavy constant mu [Source:MGI Symbol;Acc:MGI:96448]	A0A075B5P6		-1.2	3.8E-01	-5.0	1.7E-02	-3.7	3.9E-03	0.2	9.3E-01
ENSMUST00000106367	RIKEN cDNA 2610528J11 gene [Source:MGI Symbol;Acc:MGI:1913701]		Q9CQM1	5.7	1.0E-03	3.5	2.7E-02	-1.3	3.5E-01	-0.3	7.9E-01
ENSMUST00000106370	methyltransferase like 23 [Source:MGI Symbol;Acc:MGI:1921569]		A2AA28	-3.3	3.6E-03	1.3	2.4E-01	-2.7	1.9E-02	0.4	7.1E-01
ENSMUST00000106378	RIKEN cDNA 1810032O08 gene [Source:MGI Symbol;Acc:MGI:1913543]	Q9D8U9		4.0	1.2E-02	3.2	3.1E-02	-2.4	1.4E-01	1.0	3.2E-01
ENSMUST00000106387	sphingosine kinase 1 [Source:MGI Symbol;Acc:MGI:1316649]		Q8CI15	6.0	3.5E-03	3.1	5.1E-03	-3.5	5.0E-03	-1.2	1.1E-01
ENSMUST00000106391	phosphoribosyl pyrophosphate synthetase-associated protein 1 [Source:MGI Symbol;Acc:MGI:1915013]	B1AT82		-6.4	9.0E-05	1.9	2.4E-01	-4.3	4.5E-02	0.4	7.5E-01
ENSMUST00000106407	rabaptin, RAB GTPase binding effector protein 2 [Source:MGI Symbol;Acc:MGI:1917564]		Q91WG2	-6.7	6.1E-05	2.4	1.3E-01	-3.9	3.4E-02	0.8	4.5E-01
ENSMUST00000106411	exocyst complex component 7 [Source:MGI Symbol;Acc:MGI:1859270]	Q542L0	O35250	-7.2	1.7E-03	4.0	4.2E-04	-1.8	3.8E-02	-0.5	4.0E-01
ENSMUST00000106421	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1858493]	B1ASJ2	Q9Z2Y2	4.5	1.9E-03	2.5	1.2E-02	-3.2	6.3E-03	-0.1	8.6E-01
ENSMUST00000106427	synaptopodin 2 [Source:MGI Symbol;Acc:MGI:2153070]	D3YVV9		7.6	6.5E-03	3.0	1.0E-02	-1.4	1.8E-01	0.4	5.9E-01
ENSMUST00000106429	RIKEN cDNA 1810037I17 gene [Source:MGI Symbol;Acc:MGI:1914954]		Q99M08	-4.8	1.5E-05	2.4	3.5E-02	-2.9	2.3E-02	0.5	5.8E-01
ENSMUST00000106436	kinesin family member 2C [Source:MGI Symbol;Acc:MGI:1921054]	Q3TTL2		5.7	1.1E-03	4.9	1.9E-03	-1.9	1.7E-01	-0.5	5.3E-01
ENSMUST00000106437	heparan sulfate (glucosamine) 3-O-sulfotransferase 4 [Source:MGI Symbol;Acc:MGI:1333792]	D3YVV6		8.2	3.6E-06	5.3	6.3E-04	-2.0	1.1E-01	-2.6	5.2E-03
ENSMUST00000106439	mitochondrial ribosomal protein L38 [Source:MGI Symbol;Acc:MGI:1926269]		Q8K2M0	-3.6	5.2E-03	2.2	1.7E-01	-0.9	4.9E-01	1.8	1.5E-01
ENSMUST00000106440	tripartite motif-containing 65 [Source:MGI Symbol;Acc:MGI:2442815]		Q8BFW4	5.3	5.8E-05	-3.6	1.1E-03	-2.1	1.6E-03	-0.8	3.5E-01
ENSMUST00000103746	immunoglobulin lambda variable 1 [Source:MGI Symbol;Acc:MGI:96530]	A0A075B663		0.0	9.7E-01	-4.1	1.6E-03	-4.6	1.8E-05	-0.4	6.6E-01
ENSMUST00000103749	immunoglobulin lambda constant 2 [Source:MGI Symbol;Acc:MGI:99547]		P01844	-0.9	2.7E-01	-4.0	2.6E-03	-2.8	9.5E-04	0.3	7.8E-01
ENSMUST00000106447	eukaryotic translation initiation factor 2B, subunit 3 [Source:MGI Symbol;Acc:MGI:1313286]	Q3UKV0		5.2	1.6E-04	7.3	1.0E-04	-0.6	6.3E-01	-0.7	2.9E-01
ENSMUST00000106448	eukaryotic translation initiation factor 2B, subunit 3 [Source:MGI Symbol;Acc:MGI:1313286]	B1AUN2		-3.0	1.1E-02	4.6	7.5E-04	-1.3	2.1E-01	0.3	6.6E-01
ENSMUST00000104893	phosphate cytidylyltransferase 1, choline, alpha isoform [Source:MGI Symbol;Acc:MGI:88557]		P49586	2.7	1.9E-01	1.4	5.4E-01	-1.3	5.0E-01	0.1	9.7E-01
ENSMUST00000106451	unc-13 homolog D (C. elegans) [Source:MGI Symbol;Acc:MGI:1917700]		B2RUP2	-7.3	1.3E-03	7.9	1.8E-04	1.0	4.5E-01	0.9	2.0E-01
ENSMUST00000106454	H3 histone, family 3B [Source:MGI Symbol;Acc:MGI:1101768]		P84244	3.4	1.2E-02	6.4	2.7E-04	-0.6	6.0E-01	-1.1	1.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000104922				3.2	1.6E-01	5.1	4.6E-02	-0.3	9.0E-01	-2.2	1.5E-01
ENSMUST00000106459	testis-specific kinase 2 [Source:MGI Symbol;Acc:MGI:2385204]	A2AGE0		4.2	4.1E-03	6.5	9.9E-05	0.4	7.1E-01	-0.5	3.9E-01
ENSMUST00000106460	integrin beta 4 [Source:MGI Symbol;Acc:MGI:96613]		A2A863	8.9	3.7E-05	7.7	5.8E-05	-0.6	6.2E-01	-0.2	7.7E-01
ENSMUST00000106470	peroxiredoxin 1 [Source:MGI Symbol;Acc:MGI:99523]		P35700	-7.7	5.4E-06	5.1	9.8E-03	-0.6	7.3E-01	0.1	8.9E-01
ENSMUST00000106475	GC-rich promoter binding protein 1-like 1 [Source:MGI Symbol;Acc:MGI:1924360]		Q6NZP2	-3.3	1.2E-02	4.1	2.3E-02	-0.6	7.2E-01	1.6	1.1E-01
ENSMUST00000104934	adrenergic receptor, alpha 2b [Source:MGI Symbol;Acc:MGI:87935]	Q925K6		2.9	8.8E-02	8.1	3.2E-04	-0.5	7.6E-01	-5.7	5.1E-04
ENSMUST00000106478	transmembrane protein 69 [Source:MGI Symbol;Acc:MGI:3045357]		Q3KQJ0	2.1	2.2E-03	5.6	3.7E-04	-1.4	2.3E-01	-0.7	2.7E-01
ENSMUST00000106481	tRNA splicing endonuclease 54 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923515]		Q8C2A2	6.1	1.3E-02	8.5	6.9E-05	1.6	2.0E-01	-0.1	8.9E-01
ENSMUST00000104942	cDNA sequence AK157302 [Source:MGI Symbol;Acc:MGI:3574096]	I3ITR1		0.0	9.2E-01	0.0	9.8E-01	-0.4	4.3E-01	-0.3	6.1E-01
ENSMUST00000106483	polymerase (RNA) III (DNA directed) polypeptide E [Source:MGI Symbol;Acc:MGI:1349452]		Q9CZT4	8.3	2.0E-05	4.0	1.1E-01	-0.6	8.0E-01	0.9	5.3E-01
ENSMUST00000104947	calpain, small subunit 2 [Source:MGI Symbol;Acc:MGI:1916793]		Q9D7J7	-0.1	9.3E-01	0.6	5.1E-01	-0.5	4.9E-01	-1.1	1.9E-01
ENSMUST00000106489	eukaryotic elongation factor-2 kinase [Source:MGI Symbol;Acc:MGI:1195261]		O08796	-3.7	2.0E-02	7.6	3.0E-05	-1.4	2.2E-01	0.0	9.5E-01
ENSMUST00000106491	CDC14 cell division cycle 14A [Source:MGI Symbol;Acc:MGI:2442676]		Q6GQT0	5.7	8.3E-04	-1.7	9.4E-02	-0.5	4.6E-01	-0.8	3.9E-01
ENSMUST00000106495	growth factor receptor bound protein 2 [Source:MGI Symbol;Acc:MGI:95805]	B1AT92		-7.7	1.8E-03	5.9	5.6E-05	-1.8	8.0E-02	-0.3	6.1E-01
ENSMUST00000106503	arrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 [Source:MGI Symbol;Acc:MGI:1	A2A9V5		-3.8	1.9E-03	9.0	1.6E-04	0.0	9.8E-01	-0.5	4.7E-01
ENSMUST00000106506	MIF4G domain containing [Source:MGI Symbol;Acc:MGI:1916924]	A2A9W3		-3.4	2.0E-02	5.9	1.7E-04	-0.8	4.6E-01	0.2	7.0E-01
ENSMUST00000106518	LYR motif containing 1 [Source:MGI Symbol;Acc:MGI:1921169]		Q9CQB7	-5.5	2.3E-04	6.1	7.5E-04	-1.4	3.2E-01	0.2	8.2E-01
ENSMUST00000106521	testis expressed 38 [Source:MGI Symbol;Acc:MGI:1922423]	D2D552	A2A8T7	5.3	3.5E-04	4.7	4.5E-04	-0.6	4.7E-01	-0.7	3.1E-01
ENSMUST00000106525	EF-hand calcium binding domain 14 [Source:MGI Symbol;Acc:MGI:2442397]		Q8BGQ6	-4.2	3.4E-04	2.4	2.2E-03	0.1	7.6E-01	0.0	9.6E-01
ENSMUST00000106532	olute carrier family 16 (monocarboxylic acid transporters), member 5 [Source:MGI Symbol;Acc:MGI:2443515	A0A0A0MQC4		4.3	1.0E-03	6.3	4.0E-04	0.0	9.9E-01	-0.9	1.9E-01
ENSMUST00000106536	RNA-binding region (RNP1, RRM) containing 3 [Source:MGI Symbol;Acc:MGI:1914475]		Q3UZ01	-5.2	6.5E-04	6.1	9.1E-05	0.6	5.1E-01	0.5	3.5E-01
ENSMUST00000106537	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D [Source:MGI Symbol;Acc:MGI:1918929		Q9DCX2	2.6	9.0E-03	-2.3	3.2E-02	0.5	3.7E-01	0.7	4.6E-01
ENSMUST00000106539	immature colon carcinoma transcript 1 [Source:MGI Symbol;Acc:MGI:1915822]	A2A6T4		5.6	3.3E-04	2.9	3.2E-03	-1.4	7.4E-02	-0.5	4.0E-01
ENSMUST00000105015	predicted gene 14347 [Source:MGI Symbol;Acc:MGI:3709183]	A2CFD5		6.0	6.5E-02	3.9	2.6E-01	-0.5	8.8E-01	1.6	4.5E-01
ENSMUST00000105017	predicted gene, 21951 [Source:MGI Symbol;Acc:MGI:5439402]			3.0	1.9E-01	5.3	3.3E-02	-0.5	8.2E-01	-2.9	1.0E-01
ENSMUST00000105019	predicted gene 14345 [Source:MGI Symbol;Acc:MGI:3709282]	L7MU83		2.1	9.0E-02	7.2	7.2E-05	-0.5	6.5E-01	-5.6	7.6E-05
ENSMUST00000106545	cytochrome P450, family 4, subfamily x, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1932403]	A2A9Y7		7.5	1.7E-06	5.3	1.6E-02	-0.4	8.6E-01	1.5	1.6E-01
ENSMUST00000106549	lysine rich nucleolar protein 1 [Source:MGI Symbol;Acc:MGI:1913606]		Q9Z2Q2	2.6	2.7E-02	6.6	6.4E-05	-0.3	7.8E-01	-0.4	4.6E-01
ENSMUST00000106552	RIKEN cDNA 9030624J02 gene [Source:MGI Symbol;Acc:MGI:1918767]	D3YW20		-6.0	5.7E-05	5.9	8.3E-04	-0.6	6.4E-01	0.9	2.1E-01
ENSMUST00000106553	RIKEN cDNA 9030624J02 gene [Source:MGI Symbol;Acc:MGI:1918767]	D3YW19		-7.2	2.5E-05	3.2	8.4E-04	-1.4	5.3E-02	-0.3	6.1E-01
ENSMUST00000105046	high mobility group AT-hook I, related sequence 1 [Source:MGI Symbol;Acc:MGI:96161]	Q566K0	P17095	-1.3	6.3E-02	-1.5	6.0E-02	-0.9	9.4E-02	-0.6	4.6E-01
ENSMUST00000106554	glutamate receptor, ionotropic, NMDA2C (epsilon 3) [Source:MGI Symbol;Acc:MGI:95822]	A2A6S2	Q01098	9.6	1.8E-05	8.9	3.4E-05	1.1	3.8E-01	0.1	8.2E-01
ENSMUST00000106561	CD300 antigen like family member F [Source:MGI Symbol;Acc:MGI:2442359]		Q6SJQ7	-10.4	9.5E-05	6.0	7.1E-04	-0.5	7.3E-01	-1.4	7.4E-02
ENSMUST00000106564	selection and upkeep of intraepithelial T cells 4 [Source:MGI Symbol;Acc:MGI:2444425]		A7TZF3	8.9	5.0E-06	7.5	2.3E-04	-0.7	6.1E-01	0.1	9.2E-01
ENSMUST00000106565	selection and upkeep of intraepithelial T cells 4 [Source:MGI Symbol;Acc:MGI:2444425]		A7TZF3	7.0	1.6E-04	6.4	2.8E-04	-0.5	6.7E-01	-1.0	1.4E-01
ENSMUST00000106566	selection and upkeep of intraepithelial T cells 4 [Source:MGI Symbol;Acc:MGI:2444425]	E9QLU2		8.9	5.0E-06	6.4	3.5E-04	-0.6	6.2E-01	0.0	9.6E-01
ENSMUST00000106576	vav 3 oncogene [Source:MGI Symbol;Acc:MGI:1888518]		Q9R0C8	-4.6	1.5E-03	6.1	8.1E-04	-0.7	6.3E-01	0.0	9.6E-01
ENSMUST00000106581	CD300 antigen like family member B [Source:MGI Symbol;Acc:MGI:2685099]	F8WJE9	Q3U497	-10.0	3.4E-06	6.4	3.1E-04	-0.6	6.1E-01	-0.1	9.1E-01
ENSMUST00000106588	ribosomal protein S15A [Source:MGI Symbol;Acc:MGI:2389091]	Q5M9M4	P62245	-9.1	1.6E-06	5.3	5.5E-02	-0.7	7.7E-01	-0.1	9.6E-01
ENSMUST00000106592	ATP/GTP binding protein-like 4 [Source:MGI Symbol;Acc:MGI:1918244]	E4W7Y4		7.4	3.3E-05	5.1	1.2E-02	-0.7	6.9E-01	1.0	3.6E-01
ENSMUST00000106602	ribosomal protein L38 [Source:MGI Symbol;Acc:MGI:1914921]	Q52KP0	Q9JJI8	-7.4	2.3E-04	6.4	3.4E-04	-0.6	6.1E-01	-0.1	9.3E-01
ENSMUST00000105082	pleckstrin homology domain containing, family A member 6 [Source:MGI Symbol;Acc:MGI:2388662]	E9PX43		2.1	6.6E-02	1.1	4.7E-01	0.9	4.4E-01	1.9	1.5E-01
ENSMUST00000105087				3.1	8.1E-02	3.2	1.0E-01	-0.6	7.2E-01	-0.8	6.0E-01
ENSMUST00000106608	RIKEN cDNA 1110004F10 gene [Source:MGI Symbol;Acc:MGI:1929274]	D3YVR9		-5.5	2.4E-03	-0.7	2.5E-01	0.5	2.1E-01	-0.5	3.4E-01
ENSMUST00000106609	chloride channel CLIC-like 1 [Source:MGI Symbol;Acc:MGI:2385186]		Q99LI2	-7.2	5.9E-05	6.0	1.1E-03	-0.5	7.1E-01	0.1	9.4E-01
ENSMUST00000106616	CDC42 effector protein (Rho GTPase binding) 4 [Source:MGI Symbol;Acc:MGI:1929760]		Q9JM96	3.5	6.2E-05	1.1	4.4E-01	-1.4	2.8E-01	1.2	3.4E-01
ENSMUST00000106619	tetratricopeptide repeat domain 39A [Source:MGI Symbol;Acc:MGI:2444350]	A0A0A0MQC5		7.7	1.5E-05	3.7	3.3E-02	-1.8	2.6E-01	-0.5	6.7E-01
ENSMUST00000105111	factor 8-associated gene A [Source:MGI Symbol;Acc:MGI:95474]	Q9JJQ6		-1.1	4.7E-02	-0.2	7.8E-01	1.1	4.2E-02	0.1	8.1E-01
ENSMUST00000106625	RIKEN cDNA 5330417C22 gene [Source:MGI Symbol;Acc:MGI:1923930]	A0A0A0MQC6		7.4	3.7E-05	5.0	3.0E-03	-0.6	6.6E-01	1.5	7.3E-02
ENSMUST00000105139	splicing factor 3b, subunit 5 [Source:MGI Symbol;Acc:MGI:1913375]		Q923D4	-0.1	7.5E-01	-0.5	4.1E-01	-0.1	8.8E-01	0.3	6.1E-01
ENSMUST00000106640	parvin, alpha [Source:MGI Symbol;Acc:MGI:1931144]	Q3UF75		7.1	5.4E-04	2.1	1.8E-01	-0.4	7.3E-01	0.9	4.4E-01
ENSMUST00000106644	nardilysin, N-arginine dibasic convertase, NRD convertase 1 [Source:MGI Symbol;Acc:MGI:1201386]	A2A9Q2		-9.1	1.1E-04	6.0	1.7E-03	-0.6	6.9E-01	0.8	3.1E-01
ENSMUST00000106648	tubule associated monooxygenase, calponin and LIM domain containing 2 [Source:MGI Symbol;Acc:MGI:244		Q8BML1	6.4	7.0E-06	5.1	1.9E-03	-0.1	9.4E-01	1.0	1.9E-01
ENSMUST00000106650	RAB3B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1917158]	Q0PD62	Q9CZT8	7.4	2.3E-05	7.5	4.8E-05	-0.6	6.0E-01	-1.1	8.0E-02
ENSMUST00000106653	ubiquitin specific peptidase 47 [Source:MGI Symbol;Acc:MGI:1922246]		Q8BY87	-3.9	3.9E-05	6.6	4.1E-04	-0.6	6.7E-01	-0.7	3.3E-01
ENSMUST00000105160	vomeronasal 1 receptor 2 [Source:MGI Symbol;Acc:MGI:4438400]	A2AMT6		4.1	1.1E-01	5.2	7.2E-02	-0.2	9.4E-01	-1.3	4.1E-01
ENSMUST00000105169				-1.0	7.9E-01	-0.6	8.7E-01	-2.1	4.4E-01	-2.5	5.4E-01
ENSMUST00000106655	cytochrome b-561 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919273]		A2AE42	-5.0	4.1E-03	6.0	9.0E-03	-0.1	9.6E-01	0.1	9.4E-01
ENSMUST00000106656	adhesion molecule with Ig like domain 1 [Source:MGI Symbol;Acc:MGI:2653612]		Q80ZD8	5.6	1.7E-02	6.2	1.2E-02	-0.9	7.0E-01	2.0	1.0E-01
ENSMUST00000106663	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 18 [Source:MGI Symbol;Acc:MGI	Q59J91		8.0	1.8E-05	-0.2	8.7E-01	1.3	1.3E-01	-2.9	4.4E-02
ENSMUST00000106674	RIKEN cDNA 1700012B07 gene [Source:MGI Symbol;Acc:MGI:1916574]	Q3V0S8		6.8	3.0E-04	-4.9	3.4E-03	-0.7	2.9E-01	-0.8	5.5E-01
ENSMUST00000106677	protein kinase, cAMP dependent regulatory, type I, alpha [Source:MGI Symbol;Acc:MGI:104878]		Q9DBC7	1.4	2.3E-02	-1.5	2.9E-01	0.9	3.4E-01	-1.2	4.1E-01
ENSMUST00000106690	zyg-11 family member A, cell cycle regulator [Source:MGI Symbol;Acc:MGI:2446208]		A2BFL2	6.0	3.2E-04	5.0	3.3E-02	-0.8	6.8E-01	0.9	5.2E-01
ENSMUST00000106696	arylsulfatase G [Source:MGI Symbol;Acc:MGI:1921258]		Q3TYD4	2.9	3.2E-02	-2.8	1.0E-01	1.6	1.0E-01	1.4	3.9E-01
ENSMUST00000105242	timeless circadian clock 1 [Source:MGI Symbol;Acc:MGI:1321393]		Q9R1X4	3.1	3.0E-01	5.7	7.6E-02	-0.6	8.5E-01	-3.2	1.5E-01
ENSMUST00000105244	timeless circadian clock 1 [Source:MGI Symbol;Acc:MGI:1321393]	Q3U574	Q9R1X4	-2.9	4.0E-02	-1.5	3.7E-01	0.7	5.0E-01	-0.6	7.2E-01
ENSMUST00000106697	arylsulfatase G [Source:MGI Symbol;Acc:MGI:1921258]		Q3TYD4	-5.5	1.1E-03	-5.8	5.0E-02	1.0	3.2E-01	0.3	9.1E-01
ENSMUST00000106701	sterol carrier protein 2, liver [Source:MGI Symbol;Acc:MGI:98254]		P32020	-6.4	3.0E-06	-5.8	1.4E-03	1.4	1.1E-02	-0.6	6.7E-01
ENSMUST00000106702	guanine nucleotide binding protein, alpha 13 [Source:MGI Symbol;Acc:MGI:95768]	Q9D034		-4.5	4.5E-04	-2.4	6.5E-02	1.1	1.1E-01	-0.8	5.5E-01
ENSMUST00000106704	regulator of G-protein signaling 9 [Source:MGI Symbol;Acc:MGI:1338824]	A2A6V9		8.4	1.2E-06	-3.9	2.9E-03	0.9	8.2E-02	0.4	6.8E-01
ENSMUST00000105263	transformed mouse 3T3 cell double minute 2 [Source:MGI Symbol;Acc:MGI:96952]		P23804	-3.7	1.3E-01	-1.1	7.5E-01	3.3	1.5E-01	0.7	8.4E-01
ENSMUST00000106709	podocan [Source:MGI Symbol;Acc:MGI:2674939]		Q7TQ62	2.7	3.3E-02	-7.4	7.0E-04	-0.9	1.1E-01	-0.8	6.4E-01
ENSMUST00000106710	RIKEN cDNA E030025P04 gene [Source:MGI Symbol;Acc:MGI:2685510]	A2A6V5		5.9	7.4E-04	7.0	8.4E-04	-0.4	7.8E-01	-1.1	2.1E-01
ENSMUST00000105275	oxysterol binding protein-like 8 [Source:MGI Symbol;Acc:MGI:2443807]	B9EJ86	B9EJ86	1.1	3.8E-01	1.7	4.4E-01	2.7	1.4E-01	2.1	2.0E-01
ENSMUST00000106713	solute carrier family 1 (glutamate transporter), member 7 [Source:MGI Symbol;Acc:MGI:2444087]	Z4YKJ7		8.0	2.1E-05	8.1	6.9E-05	0.0	9.9E-01	-0.6	3.5E-01
ENSMUST00000106722	DENN/MADD domain containing 5A [Source:MGI Symbol;Acc:MGI:1201681]			-4.7	6.5E-03	0.3	7.2E-01	-5.4	1.4E-03	0.2	8.0E-01
ENSMUST00000106729	signal peptide, CUB domain, EGF-like 2 [Source:MGI Symbol;Acc:MGI:1928765]	D3YVM9		6.6	2.4E-04	6.4	2.9E-04	-0.6	6.4E-01	-0.8	2.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000105287	decorin [Source:MGI Symbol;Acc:MGI:94872]	Q3UKR1	P28654	3.1	6.8E-02	-3.6	4.6E-03	-8.9	9.7E-05	-2.1	8.0E-02
ENSMUST00000105290	nuclear receptor subfamily 2, group C, member 1 [Source:MGI Symbol;Acc:MGI:1352465]		Q505F1	-1.0	2.4E-01	2.6	2.6E-02	1.7	6.8E-02	-1.9	5.1E-02
ENSMUST00000106731	density lipoprotein receptor-related protein 8, apolipoprotein e receptor [Source:MGI Symbol;Acc:MGI:13400	F6YZZ8		2.9	3.5E-03	-0.7	4.9E-01	0.4	5.9E-01	-2.3	6.8E-02
ENSMUST00000106735	cDNA sequence BC051019 [Source:MGI Symbol;Acc:MGI:1928824]	Q3UQ01	Q9JJR6	7.1	4.6E-05	-4.7	5.8E-02	0.2	8.0E-01	-0.9	7.1E-01
ENSMUST00000105297	nuclear receptor subfamily 1, group H, member 4 [Source:MGI Symbol;Acc:MGI:1352464]	D3YTT2		-0.1	9.6E-01	1.2	6.1E-01	0.0	1.0E+00	-1.3	5.1E-01
ENSMUST00000106736	ligand dependent nuclear receptor interacting factor 1 [Source:MGI Symbol;Acc:MGI:2445214]	G5E8M8		-4.9	2.8E-04	3.0	3.8E-03	-0.1	8.3E-01	0.4	5.4E-01
ENSMUST00000106738	GLIS family zinc finger 1 [Source:MGI Symbol;Acc:MGI:2386723]	B1ASP5		6.6	1.2E-04	-0.5	4.8E-01	1.0	6.1E-02	0.1	8.7E-01
ENSMUST00000106739	tripartite motif-containing 66 [Source:MGI Symbol;Acc:MGI:2152406]	E9PZP2		7.1	2.4E-05	-4.2	2.4E-02	1.4	7.1E-02	-0.1	9.6E-01
ENSMUST00000105324	high mobility group 20B [Source:MGI Symbol;Acc:MGI:1341190]	Q3U1L0	Q9Z104	-0.7	7.8E-01	-1.9	5.7E-01	-1.1	6.1E-01	0.1	9.9E-01
ENSMUST00000106742	calcium channel, voltage-dependent, gamma subunit 5 [Source:MGI Symbol;Acc:MGI:2157946]	Q544Q4	Q8VHW4	7.0	1.2E-02	3.1	8.9E-03	-0.2	8.3E-01	0.6	4.4E-01
ENSMUST00000106750	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 [Source:MGI Symbol;Acc:MGI:1914247]	B1AT36		-7.6	8.2E-05	-5.8	1.1E-03	0.9	7.1E-02	0.1	9.2E-01
ENSMUST00000106755	ovochymase 2 [Source:MGI Symbol;Acc:MGI:3045251]		Q7M761	6.2	5.2E-04	5.0	2.4E-03	-2.1	1.5E-01	-0.7	4.0E-01
ENSMUST00000106766	predicted gene 4070 [Source:MGI Symbol;Acc:MGI:3782245]		Q80SU7	-8.7	1.8E-06	8.2	3.0E-05	0.0	9.7E-01	0.1	8.6E-01
ENSMUST00000105336	DOT1-like, histone H3 methyltransferase (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143886]	Q6XZL8		0.0	9.7E-01	1.0	1.4E-01	0.7	1.8E-01	-0.3	5.6E-01
ENSMUST00000106770	maestro heat-like repeat family member 7 [Source:MGI Symbol;Acc:MGI:2685873]		A2AVR2	8.3	1.3E-05	-4.3	3.6E-02	0.8	3.0E-01	2.3	2.2E-01
ENSMUST00000105344	transcription factor 3 [Source:MGI Symbol;Acc:MGI:98510]	E9PVV1		2.5	3.0E-01	6.7	5.1E-02	0.8	8.0E-01	-3.5	1.1E-01
ENSMUST00000105346	transcription factor 3 [Source:MGI Symbol;Acc:MGI:98510]		P15806	-3.2	2.9E-01	-1.9	6.3E-01	1.1	6.1E-01	-0.2	9.6E-01
ENSMUST00000105347	methyl-CpG binding domain protein 3 [Source:MGI Symbol;Acc:MGI:1333812]	D3YTR5		-2.8	1.2E-01	1.2	5.2E-01	0.7	6.4E-01	-3.3	8.1E-02
ENSMUST00000106781	prolyl-tRNA synthetase (mitochondrial)(putative) [Source:MGI Symbol;Acc:MGI:2386296]	A8Y5T6		6.0	3.8E-03	-4.1	1.4E-02	0.2	7.3E-01	-0.5	7.2E-01
ENSMUST00000105351	polo-like kinase 5 [Source:MGI Symbol;Acc:MGI:3026984]		Q4FZD7	4.2	6.8E-02	6.2	2.3E-02	-0.3	9.0E-01	-2.3	1.2E-01
ENSMUST00000105354	receptor accessory protein 6 [Source:MGI Symbol;Acc:MGI:1917585]		Q9JM62	2.3	5.4E-02	6.3	1.7E-04	-0.5	6.4E-01	-4.5	3.1E-04
ENSMUST00000106788	lymphocyte expansion molecule [Source:MGI Symbol;Acc:MGI:2681853]	A0A0F6T326	A2AVQ5	7.0	4.2E-05	5.2	9.8E-02	-0.2	9.4E-01	1.4	4.7E-01
ENSMUST00000106789	tripartite motif-containing 3 [Source:MGI Symbol;Acc:MGI:1860040]		Q9R1R2	-3.5	5.7E-03	5.2	9.8E-02	-0.2	9.4E-01	1.4	4.7E-01
ENSMUST00000105358	receptor accessory protein 6 [Source:MGI Symbol;Acc:MGI:1917585]	D3YTR1		2.3	5.4E-02	6.3	1.7E-04	-0.5	6.4E-01	-4.5	3.1E-04
ENSMUST00000106791	tripartite motif-containing 3 [Source:MGI Symbol;Acc:MGI:1860040]	Q3TDT0		4.3	8.8E-05	4.5	7.0E-02	-3.5	1.9E-01	3.6	2.6E-02
ENSMUST00000106796	platelet/endothelial cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97537]		Q08481	5.3	2.5E-02	-3.8	2.0E-03	-0.5	2.7E-01	-0.8	4.3E-01
ENSMUST00000106801	endoplasmic reticulum (ER) to nucleus signalling 1 [Source:MGI Symbol;Acc:MGI:1930134]	Q3TBZ5	Q9EQY0	3.6	2.3E-03	-1.9	5.1E-01	3.1	1.0E-01	-0.7	8.1E-01
ENSMUST00000105364	NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Source:MGI Symbol;Acc:MGI:1922656]		Q9DC70	-0.9	2.6E-01	0.2	8.3E-01	0.9	2.7E-01	-0.2	8.0E-01
ENSMUST00000106804	RIKEN cDNA 1700024P16 gene [Source:MGI Symbol;Acc:MGI:2685466]		A2A995	6.0	5.0E-03	-5.3	1.4E-03	0.4	5.2E-01	0.5	6.7E-01
ENSMUST00000105367	TP synthase, H+ transporting, mitochondrial F1 complex, delta subunit [Source:MGI Symbol;Acc:MGI:191329	Q4FK74	Q9D3D9	0.5	6.3E-01	6.0	1.1E-03	1.4	2.9E-01	-4.1	2.2E-03
ENSMUST00000105369	am channel, voltage-dependent, beta subunit associated regulatory protein [Source:MGI Symbol;Acc:MGI:135	E9QP85		4.3	1.5E-01	1.0	7.1E-01	-3.2	2.9E-01	0.1	9.4E-01
ENSMUST00000106822	BCL2-like 15 [Source:MGI Symbol;Acc:MGI:2685412]	B0V3P6		2.8	1.8E-02	-6.3	9.1E-03	0.4	5.2E-01	-0.1	9.5E-01
ENSMUST00000106828	tripartite motif-containing 30C [Source:MGI Symbol;Acc:MGI:4821257]	D3YVI9		2.6	1.4E-02	-4.9	1.2E-02	1.1	1.2E-01	-0.9	6.2E-01
ENSMUST00000106830	disabled 1 [Source:MGI Symbol;Acc:MGI:108554]	B2RRQ8	P97318	8.7	7.8E-05	-6.6	3.0E-03	-0.4	5.5E-01	-1.2	5.5E-01
ENSMUST00000106831	tripartite motif-containing 30B [Source:MGI Symbol;Acc:MGI:4821256]	D3YVI7		-8.5	1.8E-03	-1.6	3.0E-01	1.3	2.2E-01	-1.6	3.4E-01
ENSMUST00000106832	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2156057]		Q8C7W7	8.7	1.4E-05	-7.3	3.0E-03	0.6	4.0E-01	0.5	8.1E-01
ENSMUST00000105376	AT rich interactive domain 3A (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1328360]		Q62431	-3.2	8.5E-02	-4.3	1.0E-01	0.6	6.1E-01	1.7	4.9E-01
ENSMUST00000105377	AT rich interactive domain 3A (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1328360]			5.7	7.8E-02	6.1	6.9E-02	-0.9	7.9E-01	-1.3	5.2E-01
ENSMUST00000105378	mediator complex subunit 16 [Source:MGI Symbol;Acc:MGI:2158394]	E9QP84		0.7	1.7E-01	1.7	2.9E-02	1.1	5.6E-02	0.1	8.1E-01
ENSMUST00000106843	d, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 [Source:MGI Symbol;Acc		Q99JR8	-5.6	1.5E-03	-2.7	1.6E-01	1.7	1.1E-01	0.0	1.0E+00
ENSMUST00000105381	basigin [Source:MGI Symbol;Acc:MGI:88208]	K3W4Q8		-4.8	4.8E-02	-3.1	2.9E-01	2.2	2.0E-01	0.4	8.8E-01
ENSMUST00000106847	tripartite motif-containing 34B [Source:MGI Symbol;Acc:MGI:4821264]	K7N6K2		-3.7	9.9E-03	7.0	1.2E-04	-0.6	6.0E-01	0.1	8.4E-01
ENSMUST00000105384	ilvB (bacterial acetolactate synthase)-like [Source:MGI Symbol;Acc:MGI:1351911]		Q8BU33	-0.3	6.2E-01	0.1	9.0E-01	0.2	6.7E-01	-0.1	8.3E-01
ENSMUST00000105388	1-acylglycerol-3-phosphate O-acyltransferase 3 [Source:MGI Symbol;Acc:MGI:1336186]		Q9D517	2.7	7.4E-02	4.7	7.5E-03	-0.6	7.0E-01	-2.5	4.4E-02
ENSMUST00000105389	1-acylglycerol-3-phosphate O-acyltransferase 3 [Source:MGI Symbol;Acc:MGI:1336186]		Q9D517	1.4	1.3E-01	1.6	1.3E-01	-0.9	2.9E-01	-1.1	2.5E-01
ENSMUST00000106854	tripartite motif-containing 34A [Source:MGI Symbol;Acc:MGI:2137359]		Q99PP6	-4.9	2.7E-04	-1.5	9.3E-02	1.0	8.3E-02	0.0	1.0E+00
ENSMUST00000106855	mesoderm induction early response 1 homolog (Xenopus laevis [Source:MGI Symbol;Acc:MGI:1918398]		Q5UAK0	-5.7	4.9E-03	-2.8	9.8E-03	1.0	8.1E-02	-1.7	1.3E-01
ENSMUST00000105399	transient receptor potential cation channel, subfamily M, member 2 [Source:MGI Symbol;Acc:MGI:1351901]	D3Z7Q7		-1.0	5.6E-02	-2.5	3.9E-03	-1.1	2.2E-02	0.3	6.0E-01
ENSMUST00000106858	mesoderm induction early response 1 homolog (Xenopus laevis [Source:MGI Symbol;Acc:MGI:1918398]		Q5UAK0	-4.6	1.5E-02	-4.1	4.8E-02	-0.5	6.1E-01	-0.6	7.5E-01
ENSMUST00000105401	transient receptor potential cation channel, subfamily M, member 2 [Source:MGI Symbol;Acc:MGI:1351901]	Q5KTC0		1.2	2.4E-01	0.2	8.6E-01	-0.9	3.4E-01	0.1	9.4E-01
ENSMUST00000105406	adenosine deaminase, RNA-specific, B1 [Source:MGI Symbol;Acc:MGI:891999]		Q91ZS8	7.8	7.0E-02	5.7	2.1E-01	-0.8	8.6E-01	1.3	6.1E-01
ENSMUST00000106859	olfactory receptor 649 [Source:MGI Symbol;Acc:MGI:3030483]	Q8VGW1		5.0	1.4E-02	4.3	5.8E-04	-0.2	8.2E-01	-0.5	4.3E-01
ENSMUST00000105410	solute carrier family 19 (folate transporter), member 1 [Source:MGI Symbol;Acc:MGI:103182]	Q542F3	P41438	-2.3	2.4E-01	6.6	1.5E-02	4.5	5.7E-02	-4.3	2.9E-02
ENSMUST00000106865	coiled-coil domain containing 47 [Source:MGI Symbol;Acc:MGI:1914413]		Q9D024	-6.2	4.2E-04	4.5	3.0E-03	-3.0	4.1E-02	0.9	2.6E-01
ENSMUST00000106867	STE20-related kinase adaptor alpha [Source:MGI Symbol;Acc:MGI:1919399]	B1AR89		5.4	5.7E-06	5.3	4.5E-05	-2.6	1.4E-02	-0.4	4.0E-01
ENSMUST00000106875	LIM domain containing 2 [Source:MGI Symbol;Acc:MGI:1915053]		Q8BGB5	1.5	2.4E-02	5.6	4.4E-02	-0.8	7.8E-01	-0.8	6.4E-01
ENSMUST00000106880	olfactory receptor 630 [Source:MGI Symbol;Acc:MGI:3030464]	Q9EQQ7		4.9	6.2E-04	3.2	5.1E-03	0.0	9.9E-01	-0.2	8.1E-01
ENSMUST00000105421	perm antigen with calponin homology and coiled-coil domains 1-like [Source:MGI Symbol;Acc:MGI:1921642		Q2KN98	-0.4	8.8E-01	-1.1	7.3E-01	-0.3	8.9E-01	0.4	8.8E-01
ENSMUST00000105431	ZW10 interactor [Source:MGI Symbol;Acc:MGI:1289227]		Q9CQU5	-1.4	9.6E-02	-1.1	2.6E-01	-0.5	4.5E-01	-0.9	3.4E-01
ENSMUST00000106882	SH3-domain GRB2-like (endophilin) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1920344]		Q8VD37	5.7	8.7E-03	6.4	2.6E-02	-0.8	7.7E-01	-0.5	7.3E-01
ENSMUST00000105437	rhotekin 2 [Source:MGI Symbol;Acc:MGI:2158417]	E9QP76		4.3	9.8E-02	4.3	1.6E-01	0.3	9.2E-01	0.3	9.0E-01
ENSMUST00000106888	olfactory receptor 613 [Source:MGI Symbol;Acc:MGI:3030447]	E9PYB4		8.2	4.7E-07	7.2	1.4E-04	-0.1	9.5E-01	-0.3	6.3E-01
ENSMUST00000106892	ubiquitin specific peptidase 17-like C [Source:MGI Symbol;Acc:MGI:107698]	G5E8I7		6.1	2.5E-05	-6.7	5.2E-04	0.2	6.5E-01	1.8	1.9E-01
ENSMUST00000106899	chemokine (C-X-C motif) receptor 2 [Source:MGI Symbol;Acc:MGI:105303]		P35343	-2.4	4.9E-03	6.7	2.3E-03	-0.7	6.8E-01	0.0	9.6E-01
ENSMUST00000106914	predicted gene 12789 [Source:MGI Symbol;Acc:MGI:3649399]	B1AUV7		4.3	1.1E-04	6.1	6.1E-03	-0.7	7.2E-01	-1.0	3.6E-01
ENSMUST00000105455	apoptosis-inducing factor, mitochondrion-associated 2 [Source:MGI Symbol;Acc:MGI:1918611]		Q8BUE4	-2.6	1.8E-01	-3.0	3.9E-01	1.2	5.1E-01	1.6	6.1E-01
ENSMUST00000106916	predicted gene 12790 [Source:MGI Symbol;Acc:MGI:3649398]	B1AUV6		6.8	1.8E-03	-8.5	1.1E-03	1.5	1.9E-02	-0.1	9.5E-01
ENSMUST00000105460	RIKEN cDNA 4632428N05 gene [Source:MGI Symbol;Acc:MGI:1921298]	E9PUF5		4.2	1.4E-01	8.0	1.7E-02	-0.2	9.6E-01	-4.0	3.2E-02
ENSMUST00000105462	cadherin 23 (otocadherin) [Source:MGI Symbol;Acc:MGI:1890219]	E9Q7M6		3.3	1.9E-01	5.1	1.2E-01	-0.5	8.7E-01	-2.3	2.5E-01
ENSMUST00000105463	cadherin 23 (otocadherin) [Source:MGI Symbol;Acc:MGI:1890219]		Q99PF4	3.4	2.1E-01	7.8	1.5E-02	-0.5	8.7E-01	-4.9	1.5E-02
ENSMUST00000105464	cadherin 23 (otocadherin) [Source:MGI Symbol;Acc:MGI:1890219]	K4DI74		1.3	5.5E-01	1.2	7.3E-01	0.2	9.2E-01	0.4	9.1E-01
ENSMUST00000106919	RIKEN cDNA B020004J07 gene [Source:MGI Symbol;Acc:MGI:3588238]	Q3UTC0		7.7	4.0E-05	-9.3	8.0E-03	2.0	2.1E-02	0.7	8.3E-01
ENSMUST00000106921	leptin receptor [Source:MGI Symbol;Acc:MGI:104993]	Q3US58	P48356	4.7	1.4E-03	-6.6	5.2E-05	-0.3	3.4E-01	-0.7	5.0E-01
ENSMUST00000105468	LIM and senescent cell antigen-like domains 1 [Source:MGI Symbol;Acc:MGI:1195263]	E9QP62		-1.9	5.6E-01	-5.8	1.8E-01	-4.0	7.9E-02	-0.1	9.8E-01
ENSMUST00000106928	olute carrier family 22 (organic anion/cation transporter), member 15 [Source:MGI Symbol;Acc:MGI:3607704		Q504N2	-2.4	9.9E-03	5.6	9.6E-04	-0.5	7.0E-01	0.3	6.8E-01
ENSMUST00000105470	mannosidase 1, alpha [Source:MGI Symbol;Acc:MGI:104677]	Q544T7	P45700	-0.9	1.6E-01	-1.3	1.3E-01	-0.6	3.0E-01	-0.3	7.4E-01
ENSMUST00000106937	ADP-ribosyltransferase 5 [Source:MGI Symbol;Acc:MGI:107948]		P70352	7.1	1.6E-04	7.4	6.2E-05	0.4	6.8E-01	0.5	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000106939	tousled-like kinase 2 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1346023]		O55047	1.9	9.1E-03	7.7	1.2E-03	0.4	8.1E-01	-1.5	1.5E-01
ENSMUST00000106941	tousled-like kinase 2 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1346023]	B1ASU9		6.0	7.2E-04	-12.9	3.3E-03	-1.5	8.4E-02	2.8	4.2E-01
ENSMUST00000106953	ring finger protein 121 [Source:MGI Symbol;Acc:MGI:1922462]		Q8R1Z9	6.8	4.3E-04	-5.7	9.9E-03	-2.1	2.9E-02	0.2	9.0E-01
ENSMUST00000106955	ribonucleoprotein, PTB-binding 2 [Source:MGI Symbol;Acc:MGI:2443623]	B1ASP0		5.4	6.6E-04	8.9	3.3E-06	-0.9	3.8E-01	-0.2	5.9E-01
ENSMUST00000106961	cell division cycle 27 [Source:MGI Symbol;Acc:MGI:102685]	Q8R568		5.1	1.2E-04	-0.9	4.7E-01	0.4	6.5E-01	-3.9	2.6E-02
ENSMUST00000106969	transmembrane O-methyltransferase [Source:MGI Symbol;Acc:MGI:3769724]		A1Y9I9	4.6	1.6E-03	-3.6	8.3E-03	1.2	5.4E-02	0.0	9.9E-01
ENSMUST00000105501	forkhead box O3 [Source:MGI Symbol;Acc:MGI:1890081]	H9KUZ0		0.8	2.0E-01	1.9	3.0E-02	0.6	3.7E-01	-0.5	4.5E-01
ENSMUST00000106971	KAT8 regulatory NSL complex subunit 1 [Source:MGI Symbol;Acc:MGI:1923969]	A2A5Y4		-1.4	2.9E-03	-1.8	3.4E-02	1.0	5.0E-02	-0.6	4.2E-01
ENSMUST00000106972	KAT8 regulatory NSL complex subunit 1 [Source:MGI Symbol;Acc:MGI:1923969]	A2A5Y4		-5.1	6.4E-05	10.2	4.1E-05	0.6	6.8E-01	-0.4	5.0E-01
ENSMUST00000106973	anaphase promoting complex C subunit 15 [Source:MGI Symbol;Acc:MGI:1922680]	H3BIU1		-4.8	7.8E-04	0.1	9.3E-01	-0.8	4.2E-01	1.6	1.2E-01
ENSMUST00000106978	anaphase promoting complex C subunit 15 [Source:MGI Symbol;Acc:MGI:1922680]		P60007	-5.5	7.6E-05	3.5	1.7E-02	0.9	4.2E-01	1.5	1.2E-01
ENSMUST00000106980	tripartite motif-containing 45 [Source:MGI Symbol;Acc:MGI:1918187]		Q6PFY8	3.2	3.4E-02	6.5	1.1E-04	-0.5	6.4E-01	-0.7	2.5E-01
ENSMUST00000105512	5'-nucleotidase domain containing 1 [Source:MGI Symbol;Acc:MGI:2442446]		Q8C5P5	-3.3	2.3E-01	-4.7	1.6E-01	-2.2	1.9E-01	-0.9	8.0E-01
ENSMUST00000106988	microtubule-associated protein tau [Source:MGI Symbol;Acc:MGI:97180]	A0A0A0MQC7		5.5	1.3E-02	5.9	9.7E-04	-0.5	6.8E-01	0.1	8.4E-01
ENSMUST00000105519	l(3)mbt-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2143628]		Q8BLB7	-0.3	9.2E-01	-4.5	2.2E-01	-1.8	4.2E-01	2.3	5.0E-01
ENSMUST00000106989	microtubule-associated protein tau [Source:MGI Symbol;Acc:MGI:97180]	A2A5Y6		6.2	2.7E-02	6.2	1.3E-04	-2.4	5.9E-02	-0.6	3.0E-01
ENSMUST00000105522	histocompatibility 60b [Source:MGI Symbol;Acc:MGI:3649078]	B1B212		-1.3	2.9E-01	-2.0	3.5E-01	1.0	4.1E-01	1.6	4.2E-01
ENSMUST00000105525	Abelson helper integration site 1 [Source:MGI Symbol;Acc:MGI:87971]	E9QP54		1.0	8.7E-02	0.4	5.3E-01	0.2	7.3E-01	0.7	2.9E-01
ENSMUST00000105527	tumor necrosis factor, alpha-induced protein 3 [Source:MGI Symbol;Acc:MGI:1196377]		Q60769	-0.8	5.3E-01	-1.0	5.2E-01	-0.7	4.9E-01	-0.6	7.2E-01
ENSMUST00000105543	phosphatase and actin regulator 2 [Source:MGI Symbol;Acc:MGI:2446138]	A3KGD2		-2.5	3.7E-02	-0.1	9.4E-01	2.1	5.0E-02	-0.3	8.6E-01
ENSMUST00000106992	microtubule-associated protein tau [Source:MGI Symbol;Acc:MGI:97180]	Q547J4	P10637	8.8	1.3E-05	2.0	2.7E-02	0.9	1.5E-01	0.5	3.9E-01
ENSMUST00000105547	phosphatase and actin regulator 2 [Source:MGI Symbol;Acc:MGI:2446138]	B1AVN8		3.9	1.2E-01	1.9	4.4E-01	-4.2	1.2E-01	-2.2	2.7E-01
ENSMUST00000107000	signal peptide peptidase 2C [Source:MGI Symbol;Acc:MGI:3045264]		A2A6C4	7.6	9.8E-05	5.9	1.2E-03	-1.4	3.2E-01	-1.1	1.8E-01
ENSMUST00000107010	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:1916960]		Q4LDD4	-5.0	5.9E-03	7.1	3.8E-04	-0.4	7.6E-01	-1.6	6.4E-02
ENSMUST00000105569	kelch-like 17 [Source:MGI Symbol;Acc:MGI:2678948]	B2RTE7	Q6TDP3	-0.4	5.0E-01	0.4	6.4E-01	0.7	2.9E-01	-0.1	8.4E-01
ENSMUST00000105571	pleckstrin homology domain containing, family N member 1 [Source:MGI Symbol;Acc:MGI:2387630]	E9QP36		-1.2	2.2E-01	0.4	7.8E-01	1.2	2.1E-01	-0.3	7.9E-01
ENSMUST00000105572	PPARGC1 and ESRR induced regulator, muscle 1 [Source:MGI Symbol;Acc:MGI:1921433]		Q149B8	1.9	4.6E-02	2.3	5.8E-02	0.4	6.4E-01	0.0	9.7E-01
ENSMUST00000107022	droxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 [Source:MGI Symbol;Acc:MGI:962		P26149	7.3	1.6E-06	-3.3	1.0E-01	1.1	2.2E-01	-0.6	7.5E-01
ENSMUST00000107027	formin-like 1 [Source:MGI Symbol;Acc:MGI:1888994]	A2AB60		-5.0	2.6E-03	-4.9	3.9E-03	-0.2	7.6E-01	0.3	8.4E-01
ENSMUST00000107030	InaD-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1277960]		Q63ZW7	9.5	1.3E-04	-10.0	1.8E-05	0.1	6.7E-01	0.4	7.4E-01
ENSMUST00000105581	ubiquitin-conjugating enzyme E2J 2 [Source:MGI Symbol;Acc:MGI:2153608]		Q6P073	-3.7	8.2E-02	3.1	4.4E-01	7.5	3.0E-02	0.7	8.0E-01
ENSMUST00000107032	Rho guanine nucleotide exchange factor (GEF) 17 [Source:MGI Symbol;Acc:MGI:2673002]		Q80U35	9.3	1.3E-06	-5.5	5.2E-04	0.7	1.0E-01	-0.7	5.5E-01
ENSMUST00000107042	family with sequence similarity 168, member A [Source:MGI Symbol;Acc:MGI:2442372]	Q68FE1	Q8BGZ2	-2.3	1.0E-03	-0.1	9.2E-01	0.9	1.7E-01	-3.6	6.3E-03
ENSMUST00000107046	leckstrin homology domain containing, family B (evectins) member 1 [Source:MGI Symbol;Acc:MGI:1351469	Q3TP62	Q9QYE9	7.2	3.4E-04	-2.4	1.6E-01	1.5	1.3E-01	-0.1	9.5E-01
ENSMUST00000107048	RAB6A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:894313]	D3YV69		-7.2	2.2E-04	5.0	1.5E-03	-0.5	7.1E-01	0.9	2.0E-01
ENSMUST00000105590	estrogen receptor 1 (alpha) [Source:MGI Symbol;Acc:MGI:1352467]	E7FJU2	P19785	1.2	1.4E-01	2.7	1.7E-02	0.6	4.7E-01	-0.9	2.7E-01
ENSMUST00000107049	flavin containing monooxygenase 5 [Source:MGI Symbol;Acc:MGI:1310004]		P97872	-4.3	2.4E-03	-7.9	1.2E-04	0.0	9.8E-01	-0.8	5.9E-01
ENSMUST00000107057	nuclear factor I/A [Source:MGI Symbol;Acc:MGI:108056]	B1AUB8		6.6	1.3E-02	-2.8	3.1E-02	0.6	3.4E-01	-0.3	8.3E-01
ENSMUST00000107060	elongation factor Tu GTP binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1336880]	Q543F1	O08810	-5.8	6.1E-03	4.8	1.6E-02	-0.5	7.7E-01	0.1	9.6E-01
ENSMUST00000107075	gap junction protein, gamma 1 [Source:MGI Symbol;Acc:MGI:95718]		P28229	5.6	1.9E-04	-6.5	2.2E-05	0.1	8.6E-01	-1.0	3.0E-01
ENSMUST00000107076	protein inhibitor of activated STAT 3 [Source:MGI Symbol;Acc:MGI:1913126]		O54714	-4.8	2.1E-03	-4.0	2.3E-01	2.1	3.4E-01	-1.7	6.3E-01
ENSMUST00000105600	cyclin-dependent kinase 11B [Source:MGI Symbol;Acc:MGI:88353]		P24788	-2.1	1.6E-01	-0.5	7.9E-01	0.0	9.8E-01	-1.7	3.4E-01
ENSMUST00000107086	solute carrier organic anion transporter family, member 2b1 [Source:MGI Symbol;Acc:MGI:1351872]		Q8BXB6	6.7	3.2E-04	2.9	3.4E-04	0.7	1.7E-01	0.3	4.7E-01
ENSMUST00000107088	solute carrier organic anion transporter family, member 2b1 [Source:MGI Symbol;Acc:MGI:1351872]	Q3V1K7		5.9	7.6E-04	2.8	1.5E-02	-1.0	3.1E-01	1.5	6.5E-02
ENSMUST00000105612	NAD kinase [Source:MGI Symbol;Acc:MGI:2183149]	A2A9P2		-2.7	2.1E-01	-1.8	4.7E-01	0.2	8.9E-01	-0.6	8.1E-01
ENSMUST00000107094	jun proto-oncogene [Source:MGI Symbol;Acc:MGI:96646]	Q52L79	P05627	-4.6	2.9E-06	-6.0	4.2E-03	-0.8	2.3E-01	0.8	6.6E-01
ENSMUST00000107096	ribosomal protein S3 [Source:MGI Symbol;Acc:MGI:1350917]	D3YV43		-10.9	5.4E-05	-5.5	1.3E-02	1.0	1.6E-01	0.3	8.9E-01
ENSMUST00000107107	phospholipase A2, activating protein [Source:MGI Symbol;Acc:MGI:104810]		P27612	-4.7	8.6E-04	-3.4	3.8E-03	0.6	2.1E-01	-0.1	8.8E-01
ENSMUST00000107112	calpain 5 [Source:MGI Symbol;Acc:MGI:1100859]	Q3TPL4	O08688	6.5	2.5E-03	4.7	1.6E-02	-1.4	4.3E-01	-1.1	2.9E-01
ENSMUST00000105631	phospholipase C, eta 2 [Source:MGI Symbol;Acc:MGI:2443078]		A2AP18	5.7	3.6E-02	4.6	6.7E-02	-2.4	3.5E-01	-1.3	4.3E-01
ENSMUST00000105632				-0.1	9.0E-01	-2.4	1.9E-01	-1.2	2.8E-01	1.1	5.3E-01
ENSMUST00000107119	upstream binding transcription factor, RNA polymerase I [Source:MGI Symbol;Acc:MGI:98512]	A2AWT6		-7.4	2.5E-06	6.7	1.7E-04	0.1	9.4E-01	-0.7	2.7E-01
ENSMUST00000105638	PR domain containing 16 [Source:MGI Symbol;Acc:MGI:1917923]	A2A933		4.2	1.4E-01	7.9	1.9E-02	-0.4	8.9E-01	-4.1	3.1E-02
ENSMUST00000107123	upstream binding transcription factor, RNA polymerase I [Source:MGI Symbol;Acc:MGI:98512]	A2AWT5		-7.4	1.8E-05	5.2	3.6E-02	-0.7	7.5E-01	-0.6	6.9E-01
ENSMUST00000107128	myosin VIIA [Source:MGI Symbol;Acc:MGI:104510]		P97479	8.5	3.3E-03	4.3	1.4E-01	-0.5	8.5E-01	1.0	5.7E-01
ENSMUST00000107150	histone deacetylase 5 [Source:MGI Symbol;Acc:MGI:1333784]	B7ZDF7		-7.3	3.2E-03	7.1	1.3E-03	-0.7	6.7E-01	0.0	9.8E-01
ENSMUST00000107151	histone deacetylase 5 [Source:MGI Symbol;Acc:MGI:1333784]	A2AWS5		2.5	1.5E-02	0.7	7.7E-01	-3.5	1.3E-01	3.1	1.5E-01
ENSMUST00000107152	histone deacetylase 5 [Source:MGI Symbol;Acc:MGI:1333784]	Q3UJF1		-8.8	1.3E-05	-3.7	1.7E-02	0.6	3.4E-01	0.2	8.9E-01
ENSMUST00000107156	LSM12 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919592]	A0A0A0MQC9		7.9	6.1E-05	7.4	8.8E-04	-0.6	7.2E-01	-2.5	1.7E-02
ENSMUST00000107157	ute carrier family 24 (sodium/potassium/calcium exchanger), member 2 [Source:MGI Symbol;Acc:MGI:19236	Q8BUN9		7.1	4.4E-03	7.2	1.4E-02	-0.8	7.5E-01	-1.5	3.0E-01
ENSMUST00000105665	THAP domain containing, apoptosis associated protein 3 [Source:MGI Symbol;Acc:MGI:1917126]	A2A8D4		-3.4	6.2E-02	-1.5	5.1E-01	1.2	4.2E-01	-0.7	7.3E-01
ENSMUST00000105668	calmodulin binding transcription activator 1 [Source:MGI Symbol;Acc:MGI:2140230]		A2A891	3.5	1.1E-01	5.3	5.2E-02	0.3	9.1E-01	-1.5	3.0E-01
ENSMUST00000105670	calmodulin binding transcription activator 1 [Source:MGI Symbol;Acc:MGI:2140230]		A2A891	1.9	9.2E-02	5.7	4.2E-04	0.1	9.2E-01	-3.7	1.3E-03
ENSMUST00000107159	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative) [Source:MGI Symbol;Acc:MGI:2142075]	D3YV21		-2.7	2.9E-02	3.5	1.8E-01	1.5	4.9E-01	2.5	1.7E-01
ENSMUST00000105673	Parkinson disease (autosomal recessive, early onset) 7 [Source:MGI Symbol;Acc:MGI:2135637]		Q99LX0	3.7	4.9E-02	1.1	3.7E-01	-4.3	1.7E-02	-1.8	1.5E-01
ENSMUST00000107162	teneurin transmembrane protein 4 [Source:MGI Symbol;Acc:MGI:2447063]		Q3UHK6	7.6	7.6E-03	-1.7	8.4E-02	-0.1	8.7E-01	-0.6	4.9E-01
ENSMUST00000107164	CD300 antigen like family member G [Source:MGI Symbol;Acc:MGI:1289168]		Q1ERP8	6.9	2.2E-02	-3.0	1.8E-01	0.6	6.2E-01	-0.9	7.0E-01
ENSMUST00000107165	teneurin transmembrane protein 4 [Source:MGI Symbol;Acc:MGI:2447063]		Q3UHK6	10.0	2.3E-04	-7.4	5.7E-03	1.0	1.2E-01	6.1	1.3E-02
ENSMUST00000107166	teneurin transmembrane protein 4 [Source:MGI Symbol;Acc:MGI:2447063]		Q3UHK6	6.1	3.4E-05	3.6	2.0E-02	0.3	7.9E-01	-0.8	3.3E-01
ENSMUST00000105686	solute carrier family 25, member 33 [Source:MGI Symbol;Acc:MGI:1917806]		Q3TZX3	-0.4	6.9E-01	0.6	6.1E-01	0.7	4.5E-01	-0.3	8.0E-01
ENSMUST00000107167	embrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) [Source:MGI Symbol;Acc:MGI:132835	B1AQF7		7.2	5.4E-06	3.2	1.9E-02	-1.0	3.5E-01	1.2	2.2E-01
ENSMUST00000105688	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]	Q3UDT3		-1.1	6.9E-01	0.2	9.6E-01	1.2	6.6E-01	-0.2	9.6E-01
ENSMUST00000105689	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]		O35904	3.1	2.3E-01	5.4	2.8E-01	6.0	1.1E-01	3.6	3.6E-01
ENSMUST00000105690	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]	Q3T9Y0		1.9	5.5E-01	-4.9	2.1E-01	-4.8	8.3E-02	2.0	6.1E-01
ENSMUST00000107168	embrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) [Source:MGI Symbol;Acc:MGI:132835	Q6XE40		6.9	1.7E-04	1.2	1.3E-01	-1.0	1.2E-01	0.2	7.9E-01
ENSMUST00000107172	al specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) [Source:MGI Symbol;Acc:MGI:191959		Q9D7X3	7.8	2.7E-03	-5.3	2.0E-03	0.9	7.6E-02	2.4	7.8E-02
ENSMUST00000107187	family with sequence similarity 63, member A [Source:MGI Symbol;Acc:MGI:1922257]	B7ZMR0	Q76LS9	-6.6	4.0E-05	5.2	1.2E-02	-0.4	7.9E-01	-0.1	9.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000107188	SH3-domain GRB2-like 2 [Source:MGI Symbol;Acc:MGI:700009]	A2ALV3		5.8	1.5E-03	4.7	3.9E-04	-2.6	2.9E-02	-0.9	1.9E-01
ENSMUST00000107189	SH3-domain GRB2-like 2 [Source:MGI Symbol;Acc:MGI:700009]	Q8BXU5		9.9	1.6E-05	-6.8	6.2E-03	-0.3	6.4E-01	1.2	5.6E-01
ENSMUST00000105700	TAR DNA binding protein [Source:MGI Symbol;Acc:MGI:2387629]	Q6VYI5		-2.7	4.3E-01	-0.8	8.5E-01	1.1	7.1E-01	-0.7	8.8E-01
ENSMUST00000105702	TAR DNA binding protein [Source:MGI Symbol;Acc:MGI:2387629]	Q6VYI5		2.0	4.6E-01	3.7	3.9E-01	3.1	3.3E-01	1.3	7.2E-01
ENSMUST00000107193	discs, large homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1344351]	D3YUZ8		4.9	4.7E-03	2.3	2.4E-02	-0.2	7.9E-01	-0.5	5.2E-01
ENSMUST00000105707	MAD2 mitotic arrest deficient-like 2 [Source:MGI Symbol;Acc:MGI:1919140]	A2A7G7		-1.5	6.1E-01	-1.2	7.4E-01	-0.4	8.5E-01	-0.7	8.5E-01
ENSMUST00000107195	BCL2/adenovirus E1B 19kD interacting protein like [Source:MGI Symbol;Acc:MGI:2384749]	E9QME1		2.8	2.8E-02	7.2	8.7E-03	-0.7	7.6E-01	-2.3	1.1E-01
ENSMUST00000107199	CDC42 small effector 1 [Source:MGI Symbol;Acc:MGI:1889510]	D3YUZ5		-7.6	2.8E-03	-5.2	2.6E-02	1.3	1.7E-01	-0.8	7.2E-01
ENSMUST00000107206	CREB/ATF bZIP transcription factor [Source:MGI Symbol;Acc:MGI:2675296]		Q91ZR3	-3.7	1.8E-02	3.9	1.4E-04	0.1	8.8E-01	-0.1	8.5E-01
ENSMUST00000107208	neighbor of Brca1 gene 1 [Source:MGI Symbol;Acc:MGI:108498]	A2A4N5		-6.8	6.2E-04	5.6	5.0E-04	-1.4	2.7E-01	-0.5	4.3E-01
ENSMUST00000107209	GA repeat binding protein, beta 2 [Source:MGI Symbol;Acc:MGI:95612]		P81069	-6.2	1.2E-03	3.0	5.0E-04	-0.3	6.1E-01	-0.6	2.1E-01
ENSMUST00000107213	neighbor of Brca1 gene 1 [Source:MGI Symbol;Acc:MGI:108498]	A2A4N8		-8.4	1.8E-05	-1.2	8.0E-02	-0.1	8.2E-01	-0.3	6.4E-01
ENSMUST00000107230	Fras1 related extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:2670972]	A2ADN1	Q684R7	7.8	3.5E-04	6.3	2.3E-02	-0.6	8.3E-01	-1.3	3.6E-01
ENSMUST00000107234	embryonic ectoderm development [Source:MGI Symbol;Acc:MGI:95286]		Q921E6	-4.7	9.0E-05	7.3	5.1E-05	-0.5	6.4E-01	-0.3	6.1E-01
ENSMUST00000107237	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 [Source:MGI Symbol;Acc:MGI:1201670]		O35226	-6.1	2.4E-05	4.9	2.2E-02	0.0	9.9E-01	0.4	7.6E-01
ENSMUST00000105744	dehydrogenase/reductase (SDR family) member 3 [Source:MGI Symbol;Acc:MGI:1315215]		O88876	-1.1	4.8E-01	5.7	4.8E-02	5.7	3.6E-02	-1.2	4.7E-01
ENSMUST00000107245	nuclear factor I/B [Source:MGI Symbol;Acc:MGI:103188]	I7HIP8		7.2	2.8E-02	6.8	1.6E-04	-0.6	6.1E-01	-0.6	3.8E-01
ENSMUST00000107262	multiple PDZ domain protein [Source:MGI Symbol;Acc:MGI:1343489]	D3YUX2		6.6	6.1E-05	5.7	3.5E-03	-0.4	8.2E-01	-1.2	2.0E-01
ENSMUST00000107283	sorting nexin family member 27 [Source:MGI Symbol;Acc:MGI:1923992]		Q3UHD6	-2.4	1.5E-02	7.2	5.4E-05	-0.6	6.1E-01	-0.5	3.6E-01
ENSMUST00000107285	enhancer of zeste homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1097695]			-3.2	9.5E-04	5.4	7.7E-03	-0.4	8.2E-01	-0.5	6.1E-01
ENSMUST00000107289	protein tyrosine phosphatase, receptor type, D [Source:MGI Symbol;Acc:MGI:97812]		Q64487	5.5	3.4E-02	4.9	2.0E-02	-0.5	7.8E-01	1.0	3.6E-01
ENSMUST00000105761	predicted gene 13102 [Source:MGI Symbol;Acc:MGI:3703005]	Q3ULC4		3.0	3.1E-01	4.2	2.0E-01	-0.4	9.0E-01	-1.5	4.8E-01
ENSMUST00000107300	cornulin [Source:MGI Symbol;Acc:MGI:2685861]	D3YUU6		8.7	1.1E-04	7.9	5.1E-05	-0.1	9.5E-01	-0.8	1.9E-01
ENSMUST00000107302	MAX-like protein X [Source:MGI Symbol;Acc:MGI:108398]	A2BFB1		-7.3	4.5E-06	-1.0	1.3E-01	0.8	6.9E-02	0.1	9.0E-01
ENSMUST00000107303	MAX-like protein X [Source:MGI Symbol;Acc:MGI:108398]	A2BFB2		-4.1	2.0E-03	8.0	8.1E-04	-0.8	6.4E-01	-0.3	7.6E-01
ENSMUST00000105780	forkhead-associated (FHA) phosphopeptide binding domain 1 [Source:MGI Symbol;Acc:MGI:1920323]		A6PWD2	3.4	1.2E-01	4.9	4.6E-02	-0.5	8.3E-01	-2.0	2.1E-01
ENSMUST00000107304	late cornified envelope 1J [Source:MGI Symbol;Acc:MGI:3702532]	D3YUU5		6.4	3.0E-04	-4.8	1.2E-03	0.5	3.1E-01	-2.6	7.6E-02
ENSMUST00000105784	filamin binding LIM protein 1 [Source:MGI Symbol;Acc:MGI:1921452]		Q71FD7	3.4	1.1E-01	-1.5	4.3E-01	-4.7	2.2E-02	0.2	9.1E-01
ENSMUST00000105785	filamin binding LIM protein 1 [Source:MGI Symbol;Acc:MGI:1921452]		Q71FD7	5.9	3.7E-02	8.0	1.1E-02	-0.9	7.5E-01	-3.1	7.8E-02
ENSMUST00000105786	SPEN homolog, transcriptional regulator (Drosophila) [Source:MGI Symbol;Acc:MGI:1891706]	A2ADB0		-5.1	3.6E-02	0.8	7.1E-01	2.1	2.2E-01	-3.7	1.3E-01
ENSMUST00000107348	alpha-kinase 3 [Source:MGI Symbol;Acc:MGI:2151224]	D3YUT2		6.3	7.5E-06	8.3	7.3E-03	-0.8	7.7E-01	-3.0	5.9E-02
ENSMUST00000107353	zinc finger protein 592 [Source:MGI Symbol;Acc:MGI:2443541]		Q8BHZ4	-1.4	1.3E-02	4.8	1.1E-02	-0.7	6.7E-01	2.4	3.2E-02
ENSMUST00000105797	Rho guanine nucleotide exchange factor (GEF) 10-like [Source:MGI Symbol;Acc:MGI:1920004]		A2AWP8	-1.7	7.4E-02	-4.3	2.9E-02	0.3	7.3E-01	2.9	1.1E-01
ENSMUST00000105798	Rho guanine nucleotide exchange factor (GEF) 10-like [Source:MGI Symbol;Acc:MGI:1920004]	A2AWP6		2.6	2.1E-01	4.8	6.4E-02	-0.3	8.8E-01	-2.5	2.0E-01
ENSMUST00000105801	PQ loop repeat containing 2 [Source:MGI Symbol;Acc:MGI:2384837]	A6PWV7		1.4	2.7E-01	2.3	2.1E-01	0.7	6.4E-01	-0.2	8.8E-01
ENSMUST00000107357	signal transducer and activator of transcription 5A [Source:MGI Symbol;Acc:MGI:103036]	B2C3G8		-4.2	8.8E-03	6.4	1.4E-03	-0.7	6.6E-01	1.6	6.9E-02
ENSMUST00000105804	phospholipase A2, group IIE [Source:MGI Symbol;Acc:MGI:1349660]	Q3UG05	Q9QUL3	2.5	5.6E-02	5.0	1.5E-03	-0.5	6.5E-01	-3.1	6.7E-03
ENSMUST00000107358	signal transducer and activator of transcription 5B [Source:MGI Symbol;Acc:MGI:103035]		P42232	-3.8	2.8E-04	7.6	3.1E-05	0.1	9.3E-01	-0.3	5.3E-01
ENSMUST00000107362	furin (paired basic amino acid cleaving enzyme) [Source:MGI Symbol;Acc:MGI:97513]		P23188	-10.9	3.9E-04	6.3	6.6E-04	-0.4	7.5E-01	-1.1	1.5E-01
ENSMUST00000105810	UBX domain protein 10 [Source:MGI Symbol;Acc:MGI:2443123]		Q8BG34	2.7	8.6E-02	6.9	8.2E-04	-0.5	7.3E-01	-4.7	1.4E-03
ENSMUST00000107363	otassium voltage-gated channel, subfamily H (eag-related), member 4 [Source:MGI Symbol;Acc:MGI:2156184	A2A5F7		8.7	1.7E-03	2.4	1.5E-01	-0.7	6.4E-01	3.9	8.8E-03
ENSMUST00000105813	mitochondrial ubiquitin ligase activator of NFKB 1 [Source:MGI Symbol;Acc:MGI:1915600]		Q8VCM5	0.5	7.4E-01	0.0	1.0E+00	0.3	8.6E-01	0.8	6.8E-01
ENSMUST00000105817	PTEN induced putative kinase 1 [Source:MGI Symbol;Acc:MGI:1916193]	A2AM78		0.6	8.2E-01	-1.7	6.5E-01	-0.9	7.1E-01	1.4	6.9E-01
ENSMUST00000107364	RAB5C, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105306]	Q3TJ39	P35278	-7.9	1.4E-04	6.6	8.7E-05	2.7	1.5E-02	-1.0	1.1E-01
ENSMUST00000107365	toll-like receptor 4 [Source:MGI Symbol;Acc:MGI:96824]	A2BHU8		2.8	1.9E-03	5.1	1.9E-03	-0.3	8.2E-01	0.2	8.3E-01
ENSMUST00000107366	tripartite motif-containing 32 [Source:MGI Symbol;Acc:MGI:1917057]	Q3TLR3	Q8CH72	1.9	9.0E-03	-3.4	1.8E-01	2.4	9.0E-02	-0.7	7.6E-01
ENSMUST00000107371	tenascin C [Source:MGI Symbol;Acc:MGI:101922]	Q80YX0		5.5	4.5E-03	4.0	1.3E-03	-3.8	7.7E-03	-0.6	3.6E-01
ENSMUST00000105825	heterochromatin protein 1, binding protein 3 [Source:MGI Symbol;Acc:MGI:109369]	Z4YKA3		1.1	1.5E-01	1.6	8.8E-02	0.0	9.6E-01	-0.5	5.6E-01
ENSMUST00000105826	heterochromatin protein 1, binding protein 3 [Source:MGI Symbol;Acc:MGI:109369]	Z4YKB8		-0.8	7.8E-01	-1.3	6.5E-01	-1.9	3.3E-01	-1.4	6.5E-01
ENSMUST00000105827	heterochromatin protein 1, binding protein 3 [Source:MGI Symbol;Acc:MGI:109369]	Z4YKB8		-1.3	3.7E-01	1.7	3.1E-01	0.7	6.3E-01	-2.3	1.4E-01
ENSMUST00000105830	eukaryotic translation initiation factor 4 gamma, 3 [Source:MGI Symbol;Acc:MGI:1923935]	A2AMI6		-0.3	8.3E-01	2.0	2.6E-01	1.1	4.5E-01	-1.2	4.3E-01
ENSMUST00000107372	tenascin C [Source:MGI Symbol;Acc:MGI:101922]		Q80YX1	7.3	1.5E-02	-7.7	8.3E-05	0.2	5.8E-01	-0.7	6.1E-01
ENSMUST00000105837	ubiquitin specific peptidase 48 [Source:MGI Symbol;Acc:MGI:2158502]	A2ALS8		0.0	9.7E-01	2.1	1.7E-01	0.9	4.4E-01	-1.2	3.7E-01
ENSMUST00000105839	ubiquitin specific peptidase 48 [Source:MGI Symbol;Acc:MGI:2158502]	A2ALR8		2.1	3.1E-01	-0.7	8.1E-01	-0.7	7.2E-01	2.2	4.6E-01
ENSMUST00000107373	RAB13, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1927232]	D3YUS4		6.0	2.0E-04	-6.2	1.4E-02	0.6	4.5E-01	2.6	2.2E-01
ENSMUST00000107376	NFKB inhibitor interacting Ras-like protein 2 [Source:MGI Symbol;Acc:MGI:1919216]		Q9CR56	2.7	1.9E-02	8.8	1.3E-04	0.0	9.9E-01	0.2	7.5E-01
ENSMUST00000107377	tenascin C [Source:MGI Symbol;Acc:MGI:101922]		Q80YX1	8.5	1.0E-05	-5.7	1.8E-02	0.9	2.6E-01	1.4	5.1E-01
ENSMUST00000105849	leucine zipper protein 1 [Source:MGI Symbol;Acc:MGI:107629]		Q8R4U7	-0.3	9.0E-01	-0.9	7.5E-01	-0.2	9.3E-01	0.5	8.6E-01
ENSMUST00000107384	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Source:MGI Symbol;Acc:MGI:96414]		P54071	-4.6	1.5E-03	-3.8	2.7E-03	0.1	7.7E-01	-0.7	5.2E-01
ENSMUST00000107385	ATP citrate lyase [Source:MGI Symbol;Acc:MGI:103251]	Q3TS02		3.5	5.7E-04	-5.2	5.0E-03	1.2	5.6E-02	1.1	4.6E-01
ENSMUST00000105852	lysophospholipase 2 [Source:MGI Symbol;Acc:MGI:1347000]		Q9WTL7	0.9	7.3E-01	2.6	5.9E-01	4.1	2.8E-01	2.4	5.2E-01
ENSMUST00000107389	ATP citrate lyase [Source:MGI Symbol;Acc:MGI:103251]	Q3V117		-8.4	3.4E-06	-1.8	3.8E-01	1.7	2.5E-01	-0.1	9.4E-01
ENSMUST00000107392	alanyl (membrane) aminopeptidase [Source:MGI Symbol;Acc:MGI:5000466]		P97449	6.0	2.4E-03	8.7	3.5E-05	-0.6	6.3E-01	-0.6	3.0E-01
ENSMUST00000107394	mesoderm posterior 2 [Source:MGI Symbol;Acc:MGI:1096325]	A6H5V4		8.2	1.0E-05	6.4	9.4E-04	-2.1	2.0E-01	-0.2	7.6E-01
ENSMUST00000107405	adenosine deaminase, RNA-specific [Source:MGI Symbol;Acc:MGI:1889575]		Q99MU3	-4.6	1.9E-02	5.1	5.9E-06	-0.5	3.3E-01	-0.1	8.2E-01
ENSMUST00000107409	milk fat globule-EGF factor 8 protein [Source:MGI Symbol;Acc:MGI:102768]		P21956	2.9	3.0E-03	7.1	3.4E-04	-0.7	6.2E-01	-0.8	2.9E-01
ENSMUST00000105861	serine/arginine repetitive matrix 1 [Source:MGI Symbol;Acc:MGI:1858303]	A2A8V8		-3.5	3.7E-02	-6.0	9.0E-02	0.8	4.9E-01	3.3	3.1E-01
ENSMUST00000107411	keratin 15 [Source:MGI Symbol;Acc:MGI:96689]	B1AQ77		7.9	1.2E-05	-5.0	9.1E-04	0.0	1.0E+00	0.5	6.4E-01
ENSMUST00000105866	aurora kinase A and ninein interacting protein [Source:MGI Symbol;Acc:MGI:1917135]		E9Q6Z5	0.8	2.3E-01	1.2	1.6E-01	-0.1	8.5E-01	-0.5	4.8E-01
ENSMUST00000107413	pygopus 2 [Source:MGI Symbol;Acc:MGI:1916161]	Q3V113		-4.8	2.8E-03	-0.9	4.5E-01	0.5	5.1E-01	-1.2	2.9E-01
ENSMUST00000105869	platelet-activating factor acetylhydrolase 2 [Source:MGI Symbol;Acc:MGI:2140321]		Q8VDG7	1.4	5.7E-01	5.6	1.7E-01	3.4	3.2E-01	-0.8	7.7E-01
ENSMUST00000105870	platelet-activating factor acetylhydrolase 2 [Source:MGI Symbol;Acc:MGI:2140321]	E9QNW6		-0.8	3.3E-01	1.5	1.5E-01	1.6	6.4E-02	-0.7	4.4E-01
ENSMUST00000107415	zinc finger protein 618 [Source:MGI Symbol;Acc:MGI:1919950]		Q80YY7	7.7	3.7E-05	6.1	1.5E-02	-1.8	4.6E-01	-2.4	1.2E-01
ENSMUST00000107416	keratin 36 [Source:MGI Symbol;Acc:MGI:109364]		B1AQ75	7.4	4.3E-05	7.6	1.6E-03	-0.7	7.0E-01	-3.7	9.6E-03
ENSMUST00000107417	src homology 2 domain-containing transforming protein C1 [Source:MGI Symbol;Acc:MGI:98296]		P98083	-9.1	4.6E-04	-4.8	3.6E-02	-0.8	3.8E-01	-0.3	8.7E-01
ENSMUST00000105877	PDLIM1 interacting kinase 1 like [Source:MGI Symbol;Acc:MGI:2385213]	A2A9L3		2.4	1.9E-01	7.2	3.4E-02	4.1	1.7E-01	-0.7	6.6E-01
ENSMUST00000107419	keratin 32 [Source:MGI Symbol;Acc:MGI:1309995]	B1ATJ5		6.3	1.3E-04	6.9	2.9E-04	-0.8	5.5E-01	0.0	9.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000107420	regulator of G-protein signaling 3 [Source:MGI Symbol;Acc:MGI:1354734]		Q9DC04	-5.5	1.4E-05	-1.7	1.4E-01	0.5	4.3E-01	-1.5	2.2E-01
ENSMUST00000107424	regulator of G-protein signaling 3 [Source:MGI Symbol;Acc:MGI:1354734]		Q9DC04	5.5	2.7E-02	6.0	2.1E-04	-1.5	2.0E-01	0.1	8.4E-01
ENSMUST00000105885	dehydrodolichyl diphosphate synthase [Source:MGI Symbol;Acc:MGI:1914672]	A3KGL0		0.1	9.7E-01	-3.0	3.3E-01	-3.6	8.4E-02	-0.5	8.8E-01
ENSMUST00000105887	dehydrodolichyl diphosphate synthase [Source:MGI Symbol;Acc:MGI:1914672]		Q99KU1	-3.8	1.1E-01	-2.0	3.6E-01	0.6	6.6E-01	-1.2	6.3E-01
ENSMUST00000107426	RFad1, flavin adenine dinucleotide synthetase, homolog (yeast) [Source:MGI Symbol;Acc:MGI:2443030]		Q8R123	-2.9	2.1E-02	-0.7	6.3E-01	2.0	4.8E-02	-0.2	8.5E-01
ENSMUST00000107432	zinc finger and BTB domain containing 7B [Source:MGI Symbol;Acc:MGI:102755]	Q5BJ24	Q64321	-6.4	2.8E-02	-2.6	4.3E-02	1.9	9.8E-03	0.0	9.8E-01
ENSMUST00000105897	AT rich interactive domain 1A (SWI-like) [Source:MGI Symbol;Acc:MGI:1935147]		A2BH40	-4.1	3.9E-02	-4.5	3.9E-02	-0.5	6.5E-01	0.0	9.8E-01
ENSMUST00000107433	zinc finger and BTB domain containing 7B [Source:MGI Symbol;Acc:MGI:102755]	Q5BJ24	Q64321	-4.7	6.8E-04	7.2	4.2E-05	-0.4	6.7E-01	0.1	8.3E-01
ENSMUST00000107434	predicted gene 11568 [Source:MGI Symbol;Acc:MGI:3650331]	A2A4M2		6.7	5.2E-04	-2.4	1.5E-01	1.7	5.8E-02	0.0	9.9E-01
ENSMUST00000107437	keratin associated protein 4-16 [Source:MGI Symbol;Acc:MGI:3651030]	Q91W93		5.7	2.6E-04	8.1	3.7E-02	-0.9	8.1E-01	0.2	9.3E-01
ENSMUST00000107439	keratin associated protein 4-8 [Source:MGI Symbol;Acc:MGI:3652306]	B1AQA8		6.7	4.7E-04	9.2	1.3E-05	-0.6	5.9E-01	-0.8	1.2E-01
ENSMUST00000105906	WD and tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGI:2685541]	A2AE98		2.9	2.4E-01	1.9	5.8E-01	1.2	6.9E-01	2.1	4.4E-01
ENSMUST00000107440	predicted gene 11595 [Source:MGI Symbol;Acc:MGI:3652308]	B1AQA7		7.6	1.9E-04	-2.0	1.9E-02	0.6	1.5E-01	-0.8	3.2E-01
ENSMUST00000107445	keratin 39 [Source:MGI Symbol;Acc:MGI:3588208]		Q6IFX4	6.4	1.0E-04	-2.2	1.5E-01	0.4	6.1E-01	-0.4	7.9E-01
ENSMUST00000107448	a disintegrin and metallopeptidase domain 15 (metargidin) [Source:MGI Symbol;Acc:MGI:1333882]		O88839	-7.2	6.3E-04	5.5	6.8E-04	0.9	4.4E-01	0.1	8.8E-01
ENSMUST00000107449	B-box and SPRY domain containing [Source:MGI Symbol;Acc:MGI:2177191]		Q80YW5	7.9	3.7E-05	6.5	1.4E-04	-1.1	3.5E-01	-0.6	3.3E-01
ENSMUST00000105912	WAS protein family, member 2 [Source:MGI Symbol;Acc:MGI:1098641]		Q8BH43	-0.1	9.7E-01	2.3	5.2E-01	1.8	5.4E-01	-0.6	8.4E-01
ENSMUST00000107453	solute carrier organic anion transporter family, member 3a1 [Source:MGI Symbol;Acc:MGI:1351867]	D3YXA8		6.3	2.0E-05	3.3	1.0E-02	-4.2	5.9E-03	-0.4	5.9E-01
ENSMUST00000107454	ring finger protein 183 [Source:MGI Symbol;Acc:MGI:1923322]		Q8QZS5	6.6	7.7E-04	3.4	6.6E-03	0.6	4.5E-01	1.1	1.4E-01
ENSMUST00000107456	family with sequence similarity 174, member B [Source:MGI Symbol;Acc:MGI:3698178]		Q8K064	2.2	4.9E-03	6.5	4.5E-03	-4.3	6.6E-02	-4.0	9.7E-03
ENSMUST00000107461	FK506 binding protein 15 [Source:MGI Symbol;Acc:MGI:2444782]	Q80YW6		-3.6	4.1E-03	6.6	2.4E-02	-0.7	8.0E-01	-1.5	3.1E-01
ENSMUST00000105919	protein phosphatase 1, regulatory (inhibitor) subunit 8 [Source:MGI Symbol;Acc:MGI:2140494]	A2ADR8		-1.2	6.5E-01	-2.5	4.1E-01	-2.3	2.2E-01	-1.0	7.5E-01
ENSMUST00000105929	tyrosine hydroxylase [Source:MGI Symbol;Acc:MGI:98735]	Q3UTB3		3.8	1.4E-01	6.3	3.4E-02	-0.2	9.4E-01	-2.7	1.1E-01
ENSMUST00000107462	dolichyl-phosphate mannosyltransferase polypeptide 3 [Source:MGI Symbol;Acc:MGI:1915813]		Q9D1Q4	6.9	3.3E-05	6.2	8.8E-04	-0.7	6.4E-01	-0.7	3.5E-01
ENSMUST00000107464	tripartite motif-containing 46 [Source:MGI Symbol;Acc:MGI:2673000]	D3YXA6		7.1	1.3E-04	5.9	5.2E-02	-0.9	7.6E-01	0.2	9.0E-01
ENSMUST00000107473	retinoic acid receptor, alpha [Source:MGI Symbol;Acc:MGI:97856]		P11416	-3.2	5.0E-04	-8.6	3.6E-04	-1.2	2.7E-02	-0.3	8.6E-01
ENSMUST00000105951	regulator of chromosome condensation 1 [Source:MGI Symbol;Acc:MGI:1913989]		Q8VE37	3.5	1.6E-01	3.8	3.9E-01	3.0	3.6E-01	2.8	4.1E-01
ENSMUST00000107475	retinoic acid receptor, alpha [Source:MGI Symbol;Acc:MGI:97856]	Q3U3R3	P11416	-7.1	1.8E-05	-5.8	1.6E-04	-0.6	1.3E-01	-1.4	2.1E-01
ENSMUST00000107478	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 17 [Source:MGI Symbol;Acc:M	D3YX90		6.4	9.2E-03	-4.0	3.1E-03	0.1	8.5E-01	-0.6	5.9E-01
ENSMUST00000105965	glucocorticoid modulatory element binding protein 1 [Source:MGI Symbol;Acc:MGI:2135604]		Q9JL60	-1.4	5.2E-01	-2.6	5.0E-01	1.3	5.6E-01	2.5	4.8E-01
ENSMUST00000107479	Rap guanine nucleotide exchange factor (GEF)-like 1 [Source:MGI Symbol;Acc:MGI:3611446]		Q68EF8	9.8	4.9E-07	-11.0	5.6E-06	-0.2	4.9E-01	-1.3	3.6E-01
ENSMUST00000107485	male-specific lethal 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1921276]		Q6PDM1	-4.6	8.3E-05	-4.1	5.9E-04	0.4	3.6E-01	-1.1	2.2E-01
ENSMUST00000105970	erythrocyte membrane protein band 4.1 [Source:MGI Symbol;Acc:MGI:95401]	A2A839		4.1	8.8E-02	3.4	1.8E-01	-0.2	9.3E-01	0.5	7.9E-01
ENSMUST00000105971	troponin I, skeletal, fast 2 [Source:MGI Symbol;Acc:MGI:105070]		P13412	-4.2	7.0E-02	-3.8	1.4E-01	-1.5	2.5E-01	-2.0	4.7E-01
ENSMUST00000105972	erythrocyte membrane protein band 4.1 [Source:MGI Symbol;Acc:MGI:95401]		P48193	0.7	7.5E-01	5.2	4.1E-02	1.3	5.1E-01	-3.3	1.5E-01
ENSMUST00000107486	predicted gene 10974 [Source:MGI Symbol;Acc:MGI:3779185]	D3YX89		7.3	7.3E-06	6.2	9.9E-04	-2.0	2.0E-01	0.3	6.9E-01
ENSMUST00000107491	death associated protein 3 [Source:MGI Symbol;Acc:MGI:1929538]			-6.8	1.6E-05	0.1	9.8E-01	3.7	5.5E-02	-2.5	3.6E-01
ENSMUST00000105992	pumilio RNA-binding family member 1 [Source:MGI Symbol;Acc:MGI:1931749]	Q3TTW5		-2.6	1.1E-01	1.5	3.9E-01	1.2	3.9E-01	-2.8	1.0E-01
ENSMUST00000107508	gasdermin A3 [Source:MGI Symbol;Acc:MGI:3044668]	Z4YKL5		5.9	4.7E-03	-1.7	1.4E-02	0.2	5.7E-01	-0.6	3.2E-01
ENSMUST00000107510	rho/rac guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:103264]		Q60875	4.6	6.2E-03	-0.2	7.8E-01	-5.8	2.6E-04	-2.3	3.8E-02
ENSMUST00000107526	INTS3 and NABP interacting protein [Source:MGI Symbol;Acc:MGI:1913459]		Q3TXT3	-4.9	5.6E-04	-5.0	5.8E-03	0.9	1.2E-01	-0.6	6.8E-01
ENSMUST00000106000	CD151 antigen [Source:MGI Symbol;Acc:MGI:1096360]		O35566	-2.3	8.1E-02	-0.9	5.4E-01	0.4	6.8E-01	-0.9	5.3E-01
ENSMUST00000107538	cyclin-dependent kinase 12 [Source:MGI Symbol;Acc:MGI:1098802]		Q14AX6	-5.3	1.9E-03	-3.2	1.2E-02	1.0	1.1E-01	-1.0	4.2E-01
ENSMUST00000107542	bone gamma-carboxyglutamate protein 3 [Source:MGI Symbol;Acc:MGI:88155]		P54615	4.5	5.9E-05	-8.0	5.4E-04	1.0	5.7E-02	-0.7	7.0E-01
ENSMUST00000107547	expressed sequence AI481877 [Source:MGI Symbol;Acc:MGI:2140313]	A2ALV5		7.1	8.0E-05	-5.2	5.9E-03	1.2	8.1E-02	1.7	2.7E-01
ENSMUST00000107552	transmembrane protein 79 [Source:MGI Symbol;Acc:MGI:1919163]		Q9D709	6.1	8.4E-03	2.2	3.5E-01	-2.0	4.3E-01	3.4	5.5E-02
ENSMUST00000106027	PHD and ring finger domains 1 [Source:MGI Symbol;Acc:MGI:2141847]		A6H619	-3.3	6.8E-02	-3.4	1.6E-01	0.9	4.8E-01	1.0	6.8E-01
ENSMUST00000107554	zinc finger with KRAB and SCAN domains 16 [Source:MGI Symbol;Acc:MGI:3510405]	A2ALW2		7.7	3.6E-05	-2.2	5.4E-02	1.2	7.0E-02	-1.2	3.0E-01
ENSMUST00000106035	coiled coil domain containing 28B [Source:MGI Symbol;Acc:MGI:1913514]	Q9D1N8		-2.0	1.2E-01	-2.6	1.4E-01	0.2	8.0E-01	0.9	6.0E-01
ENSMUST00000107557	expressed sequence AI314180 [Source:MGI Symbol;Acc:MGI:2140220]	A2ALV6		5.4	1.1E-04	7.3	2.1E-02	-0.8	7.8E-01	-1.1	4.6E-01
ENSMUST00000107558	myocyte enhancer factor 2D [Source:MGI Symbol;Acc:MGI:99533]	E9QKT0		3.1	1.4E-02	-10.0	5.1E-05	0.0	9.5E-01	-2.0	2.0E-01
ENSMUST00000107561	calcium channel, voltage-dependent, beta 1 subunit [Source:MGI Symbol;Acc:MGI:102522]	A2A542		6.9	9.6E-04	-3.1	4.4E-02	0.2	8.1E-01	-0.4	7.6E-01
ENSMUST00000107563	ADP-ribosylation factor-like 5C [Source:MGI Symbol;Acc:MGI:3028577]	A2A541		2.8	2.7E-03	-5.1	1.7E-02	-0.1	9.0E-01	-0.8	6.8E-01
ENSMUST00000107574	lysophosphatidic acid receptor 1 [Source:MGI Symbol;Acc:MGI:108429]	Q544V2	P61793	7.6	5.2E-04	7.6	4.7E-05	-0.6	6.0E-01	0.0	9.3E-01
ENSMUST00000106046	zinc finger and BTB domain containing 8b [Source:MGI Symbol;Acc:MGI:2387181]	I7HLR7		3.5	1.3E-01	7.6	7.3E-03	-0.4	8.8E-01	-4.5	8.8E-03
ENSMUST00000107576	RIKEN cDNA 1700001P01 gene [Source:MGI Symbol;Acc:MGI:1919465]		Q9DAQ5	4.8	4.1E-04	-6.0	1.6E-04	-0.3	4.8E-01	-0.5	6.2E-01
ENSMUST00000106048	sirtuin 3 [Source:MGI Symbol;Acc:MGI:1927665]	Q4FJK3	Q8R104	-1.9	1.8E-01	-3.3	1.2E-01	0.2	8.6E-01	1.7	4.0E-01
ENSMUST00000107579	CWC25 spliceosome-associated protein homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914730]	A2A6F5		4.5	7.1E-05	7.7	1.9E-05	-1.5	1.9E-01	0.5	3.2E-01
ENSMUST00000107581	SH2 domain containing 2A [Source:MGI Symbol;Acc:MGI:1351596]		Q9QXK9	5.4	1.4E-02	4.5	1.1E-04	-1.7	3.4E-02	0.1	7.9E-01
ENSMUST00000106054	tyrosyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:2147627]	A2A7S7		-1.2	1.3E-01	0.6	5.0E-01	1.1	1.4E-01	-0.7	4.3E-01
ENSMUST00000106057	zinc finger, RAN-binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1858211]	D3Z4U0		-0.6	7.5E-01	-3.7	1.7E-01	-2.6	9.8E-02	0.5	8.5E-01
ENSMUST00000106058	zinc finger, RAN-binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1858211]	B2RRT9	Q9R020	0.5	7.7E-01	0.3	8.6E-01	-2.6	1.1E-01	-2.4	1.9E-01
ENSMUST00000107590	SRC kinase signaling inhibitor 1 [Source:MGI Symbol;Acc:MGI:1933179]	B1AQX7		7.7	1.5E-05	-4.5	3.3E-03	0.3	6.0E-01	-0.1	9.6E-01
ENSMUST00000106061	S100P binding protein [Source:MGI Symbol;Acc:MGI:1921898]		Q9D5K4	-0.8	5.0E-01	0.3	8.4E-01	0.9	4.6E-01	-0.3	8.5E-01
ENSMUST00000107591	growth arrest specific 2 [Source:MGI Symbol;Acc:MGI:95657]		P11862	7.6	1.2E-05	-6.4	2.4E-04	-0.8	6.5E-02	-0.4	7.4E-01
ENSMUST00000107596	SRC kinase signaling inhibitor 1 [Source:MGI Symbol;Acc:MGI:1933179]	B1AQX9		8.3	2.0E-05	1.1	5.1E-01	-2.5	1.4E-01	1.4	3.1E-01
ENSMUST00000107600	A kinase (PRKA) anchor protein 2 [Source:MGI Symbol;Acc:MGI:1306795]	A2API8		5.8	2.3E-03	-7.9	3.1E-03	1.0	1.1E-01	0.7	7.5E-01
ENSMUST00000106072	zinc finger protein 362 [Source:MGI Symbol;Acc:MGI:2652839]	B1ASA5		2.2	1.2E-01	1.8	3.7E-01	1.0	5.3E-01	1.5	3.3E-01
ENSMUST00000107603	NEL-like 1 [Source:MGI Symbol;Acc:MGI:2443902]	D3YWD8		6.0	2.0E-04	6.6	3.2E-03	-0.8	6.6E-01	0.6	5.7E-01
ENSMUST00000107618	kin of IRRE like (Drosophila) [Source:MGI Symbol;Acc:MGI:1891396]		Q80W68	8.6	3.2E-02	6.5	2.6E-03	0.1	9.3E-01	-1.4	1.6E-01
ENSMUST00000107622	trans-acting transcription factor 6 [Source:MGI Symbol;Acc:MGI:1932575]	A2A708	Q9ESX2	3.0	2.2E-02	-3.5	6.6E-03	0.9	1.3E-01	-3.3	3.8E-02
ENSMUST00000106080	polyhomeotic-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1860454]		Q9QWH1	5.8	4.4E-02	6.6	2.2E-02	-2.6	3.6E-01	-3.4	7.3E-02
ENSMUST00000107626	Sp2 transcription factor [Source:MGI Symbol;Acc:MGI:1926162]	Q8C5J0		-5.3	1.4E-02	-3.6	1.6E-02	0.9	2.0E-01	-1.4	3.2E-01
ENSMUST00000107633	proline rich 15-like [Source:MGI Symbol;Acc:MGI:2387599]		Q8JZM2	5.1	5.8E-04	3.8	3.1E-03	-3.4	1.9E-02	-0.5	5.6E-01
ENSMUST00000106091	gap junction protein, beta 3 [Source:MGI Symbol;Acc:MGI:95721]		P28231	4.4	6.1E-02	3.0	8.7E-02	-3.4	1.2E-01	-2.0	1.7E-01
ENSMUST00000107635	LPS-responsive beige-like anchor [Source:MGI Symbol;Acc:MGI:1933162]	E9Q3Y4		-4.0	4.7E-04	2.9	9.6E-02	-0.2	8.9E-01	4.4	4.5E-03
ENSMUST00000107636	proline rich 15-like [Source:MGI Symbol;Acc:MGI:2387599]		Q8JZM2	7.8	9.9E-06	7.2	6.8E-05	-0.5	6.7E-01	-0.4	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000106095	NK6 homeobox 2 [Source:MGI Symbol;Acc:MGI:1352738]	D3Z4R4		2.7	6.7E-02	5.2	3.5E-03	-0.1	9.4E-01	-2.7	2.9E-02
ENSMUST00000107647	solute carrier family 44, member 1 [Source:MGI Symbol;Acc:MGI:2140592]	A2AMH4		5.3	1.4E-02	-5.0	4.0E-03	1.0	1.1E-01	0.3	8.1E-01
ENSMUST00000106100	zinc finger, ZZ domain containing 3 [Source:MGI Symbol;Acc:MGI:1920453]		Q6KAQ7	-4.7	8.3E-02	-3.1	3.8E-01	1.3	5.1E-01	-0.3	9.3E-01
ENSMUST00000106101	zinc finger, ZZ domain containing 3 [Source:MGI Symbol;Acc:MGI:1920453]		Q6KAQ7	2.1	2.0E-01	2.3	2.9E-01	0.2	9.4E-01	-0.1	9.4E-01
ENSMUST00000106102	zinc finger, MYM domain containing 1 [Source:MGI Symbol;Acc:MGI:1915560]	Q3TJB1		1.5	7.0E-02	0.0	9.8E-01	-1.3	9.1E-02	0.2	7.7E-01
ENSMUST00000107651	solute carrier family 44, member 1 [Source:MGI Symbol;Acc:MGI:2140592]	A2AMH5		-3.8	2.2E-03	-5.4	4.7E-03	0.5	4.7E-01	-1.0	5.6E-01
ENSMUST00000106104	leucine rich repeat containing 27 [Source:MGI Symbol;Acc:MGI:1923862]	D3Z4R3		0.8	2.1E-01	2.4	1.2E-02	1.2	9.2E-02	-0.4	5.2E-01
ENSMUST00000107653	Hermansky-Pudlak syndrome 5 homolog (human) [Source:MGI Symbol;Acc:MGI:2180307]	E9Q3X4		-4.1	4.4E-04	4.9	6.1E-03	-0.7	6.2E-01	-0.5	5.7E-01
ENSMUST00000106108	zinc finger, MYM-type 4 [Source:MGI Symbol;Acc:MGI:1915035]		A2A791	-0.4	7.3E-01	2.5	2.3E-01	2.6	1.5E-01	-0.4	8.0E-01
ENSMUST00000106111	janus kinase and microtubule interacting protein 3 [Source:MGI Symbol;Acc:MGI:1921254]		Q5DTN8	3.7	4.9E-02	5.3	1.0E-02	-1.1	5.4E-01	-2.8	3.5E-02
ENSMUST00000107654	Hermansky-Pudlak syndrome 5 homolog (human) [Source:MGI Symbol;Acc:MGI:2180307]		P59438	-7.5	4.7E-05	-4.8	2.6E-05	0.1	7.9E-01	-0.1	8.2E-01
ENSMUST00000106113	forkhead box K2 [Source:MGI Symbol;Acc:MGI:1916087]		Q3UCQ1	-0.6	1.8E-01	0.7	2.5E-01	0.7	1.1E-01	-0.6	2.8E-01
ENSMUST00000107659	nuclear factor, erythroid derived 2,-like 1 [Source:MGI Symbol;Acc:MGI:99421]	A2A6D2		5.6	2.6E-03	-2.1	1.5E-01	5.1	1.6E-04	0.8	5.3E-01
ENSMUST00000107661	sorting nexin 11 [Source:MGI Symbol;Acc:MGI:1921729]		Q91WL6	-4.3	4.6E-03	-5.4	9.2E-04	-0.6	1.8E-01	-0.7	5.8E-01
ENSMUST00000107663	src family associated phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:1925723]	B1AQX5		5.8	3.2E-04	2.6	3.0E-03	-4.0	2.3E-04	-0.6	3.0E-01
ENSMUST00000107665	nipsnap homolog 3B (C. elegans) [Source:MGI Symbol;Acc:MGI:1913786]	B1AWZ5		-5.4	1.0E-03	-5.4	1.8E-02	0.9	3.4E-01	2.7	1.8E-01
ENSMUST00000106135	dihydrouridine synthase 1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915980]	B1ATU5		-2.3	2.2E-01	1.9	3.3E-01	0.6	7.4E-01	-3.7	6.5E-02
ENSMUST00000107679	F-box and WD-40 domain protein 7 [Source:MGI Symbol;Acc:MGI:1354695]	D3YUA5		-2.8	6.4E-03	6.3	8.7E-04	-0.6	6.6E-01	-2.7	1.1E-02
ENSMUST00000106144	uroporphyrinogen III synthase [Source:MGI Symbol;Acc:MGI:98917]	Q3TPL3		1.3	2.2E-01	1.9	1.7E-01	0.2	8.4E-01	-0.4	7.0E-01
ENSMUST00000107680	tubulin tyrosine ligase-like family, member 6 [Source:MGI Symbol;Acc:MGI:2683461]		A4Q9E8	6.0	7.5E-04	4.0	1.8E-02	-1.5	3.3E-01	-0.4	6.8E-01
ENSMUST00000107682	transmembrane protein 154 [Source:MGI Symbol;Acc:MGI:2444725]		Q8C4Q9	-7.0	5.8E-07	2.1	3.2E-02	0.2	7.9E-01	-0.1	8.7E-01
ENSMUST00000107684	ynthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9) [Source:MGI Symbol;Acc:MGI:1(		Q9CR84	-3.5	1.5E-03	5.6	1.5E-02	0.6	7.7E-01	-0.1	9.1E-01
ENSMUST00000106153	synovial sarcoma, X breakpoint 2 interacting protein [Source:MGI Symbol;Acc:MGI:2139150]		Q8VC66	1.1	6.0E-01	1.2	6.6E-01	0.4	8.4E-01	0.2	9.3E-01
ENSMUST00000107687	ADP-ribosylation factor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1277120]	E9Q3G5		-3.0	3.4E-02	-2.0	3.1E-02	0.4	3.8E-01	0.7	4.2E-01
ENSMUST00000107689	FH2 domain containing 1 [Source:MGI Symbol;Acc:MGI:2684972]		Q3ULZ2	6.0	8.5E-04	-3.9	1.5E-02	1.7	1.6E-02	-0.6	7.0E-01
ENSMUST00000107691	tripartite motif-containing 2 [Source:MGI Symbol;Acc:MGI:1933163]		Q9ESN6	9.2	1.2E-05	-4.0	4.5E-02	0.4	6.2E-01	-0.6	7.6E-01
ENSMUST00000107700	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1343161]	A2A6M1		-3.6	1.4E-02	4.7	1.2E-03	0.0	9.8E-01	-0.5	4.8E-01
ENSMUST00000107708	ucleotide binding protein (G protein), gamma transducing activity polypeptide 2 [Source:MGI Symbol;Acc:MG	A2A614	Q61017	-5.2	1.3E-03	-3.7	9.0E-03	0.8	2.1E-01	-0.9	4.7E-01
ENSMUST00000107709	ucleotide binding protein (G protein), gamma transducing activity polypeptide 2 [Source:MGI Symbol;Acc:MG	A2A614	Q61017	-6.9	2.7E-05	5.1	1.3E-02	-0.7	6.9E-01	1.5	1.9E-01
ENSMUST00000106168	family with sequence similarity 53, member B [Source:MGI Symbol;Acc:MGI:1925188]		Q8BGR5	4.0	8.9E-02	6.8	8.8E-02	4.5	1.9E-01	1.8	4.6E-01
ENSMUST00000106178	notum pectinacetylesterase homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1924833]		Q8R116	4.9	5.4E-02	-1.4	4.8E-01	-5.1	3.9E-02	1.2	5.0E-01
ENSMUST00000107711	ucleotide binding protein (G protein), gamma transducing activity polypeptide 2 [Source:MGI Symbol;Acc:MG	A2A614	Q61017	-7.1	1.2E-05	-1.6	2.5E-01	1.5	9.3E-02	-0.1	9.6E-01
ENSMUST00000107716	transmembrane protein 143 [Source:MGI Symbol;Acc:MGI:1917459]			6.2	1.1E-03	-1.3	1.5E-01	0.6	2.6E-01	-0.1	8.9E-01
ENSMUST00000106188	phosphate cytidylyltransferase 2, ethanolamine [Source:MGI Symbol;Acc:MGI:1915921]	A2ABY3		-2.8	4.3E-02	-1.2	4.9E-01	1.1	3.2E-01	-0.5	7.6E-01
ENSMUST00000107718	L (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 [Source:MGI Symbol;Acc:MGI:1915	D3YUA0		-4.7	3.0E-03	2.6	1.9E-01	-5.9	2.1E-02	3.0	4.0E-02
ENSMUST00000107720	syntaxin 17 [Source:MGI Symbol;Acc:MGI:1914977]		Q9D0I4	-1.6	3.0E-02	-4.8	2.3E-03	1.1	5.5E-02	-0.8	5.4E-01
ENSMUST00000107724	speckle-type POZ protein [Source:MGI Symbol;Acc:MGI:1343085]		Q6ZWS8	-8.9	1.9E-05	4.3	9.6E-04	-1.7	7.4E-02	-0.2	7.6E-01
ENSMUST00000107725	transforming growth factor, beta receptor I [Source:MGI Symbol;Acc:MGI:98728]	Q9D5H8		8.1	8.0E-07	-3.7	5.0E-02	0.8	4.0E-01	-1.4	4.9E-01
ENSMUST00000107726	cytohesin 2 [Source:MGI Symbol;Acc:MGI:1334255]	D3YU96		-3.2	6.5E-03	-8.9	1.1E-05	-0.4	2.3E-01	-0.8	4.6E-01
ENSMUST00000106213	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	B1ARU1		0.3	5.2E-01	0.3	5.0E-01	-0.2	6.1E-01	-0.3	5.6E-01
ENSMUST00000107728	cytohesin 2 [Source:MGI Symbol;Acc:MGI:1334255]	D3YU95		-6.6	1.0E-02	-4.9	7.1E-04	1.1	5.2E-02	-0.4	7.2E-01
ENSMUST00000106216	actin, beta [Source:MGI Symbol;Acc:MGI:87904]	E9Q606		-0.7	7.8E-01	1.6	5.6E-01	0.2	9.2E-01	-2.1	4.4E-01
ENSMUST00000106218	cysteine conjugate-beta lyase 2 [Source:MGI Symbol;Acc:MGI:2677849]		Q71RI9	-1.3	2.9E-01	-1.0	4.8E-01	-0.4	7.3E-01	-0.7	6.2E-01
ENSMUST00000106221	guanylate binding protein 3 [Source:MGI Symbol;Acc:MGI:1926263]		Q61107	-0.6	8.1E-01	-4.1	1.3E-01	-3.5	8.4E-02	0.0	1.0E+00
ENSMUST00000106222	guanylate binding protein 3 [Source:MGI Symbol;Acc:MGI:1926263]		Q61107	-1.4	5.8E-01	-4.3	8.7E-02	-3.4	5.8E-02	-0.5	8.6E-01
ENSMUST00000106223	RIKEN cDNA 1810043H04 gene [Source:MGI Symbol;Acc:MGI:1913676]		A2AMZ4	0.9	1.2E-01	1.8	2.1E-02	0.6	3.3E-01	-0.4	4.7E-01
ENSMUST00000106224	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	B1ARU4		3.3	2.1E-01	3.3	3.8E-01	1.7	6.0E-01	1.7	5.3E-01
ENSMUST00000106225	ENTH domain containing 2 [Source:MGI Symbol;Acc:MGI:1926027]	B1AXJ2		-0.2	9.1E-01	-0.4	9.0E-01	1.5	5.6E-01	1.6	5.2E-01
ENSMUST00000106226	Tia1 cytotoxic granule-associated RNA binding protein-like 1 [Source:MGI Symbol;Acc:MGI:107913]	Q545C1	P70318	0.3	7.4E-01	2.2	1.2E-01	2.5	4.0E-02	0.6	5.9E-01
ENSMUST00000106227	centrosomal protein 131 [Source:MGI Symbol;Acc:MGI:107440]	B1AXI9		2.1	3.1E-01	-1.1	7.3E-01	-1.3	4.9E-01	1.9	5.3E-01
ENSMUST00000106229	centrosomal protein 131 [Source:MGI Symbol;Acc:MGI:107440]		Q62036	2.6	1.3E-01	4.5	2.8E-02	-0.2	8.9E-01	-2.1	1.6E-01
ENSMUST00000107731	collagen, type XV, alpha 1 [Source:MGI Symbol;Acc:MGI:88449]	A2AJY5		4.7	5.0E-04	4.9	1.5E-02	-0.6	7.2E-01	-0.6	5.9E-01
ENSMUST00000107737	sphingosine kinase 2 [Source:MGI Symbol;Acc:MGI:1861380]	Q58E38	Q9JIA7	-2.4	3.6E-03	4.2	3.5E-02	-1.6	3.5E-01	0.1	9.1E-01
ENSMUST00000106233	brain-specific angiogenesis inhibitor 1-associated protein 2 [Source:MGI Symbol;Acc:MGI:2137336]	B1AZ46		-0.5	8.1E-01	-1.6	4.3E-01	-3.1	9.3E-02	-2.0	3.9E-01
ENSMUST00000107738	sphingosine kinase 2 [Source:MGI Symbol;Acc:MGI:1861380]	Q58E38	Q9JIA7	-5.9	8.3E-04	6.3	3.0E-03	1.3	4.1E-01	0.8	3.2E-01
ENSMUST00000107742	netrin 5 [Source:MGI Symbol;Acc:MGI:2685330]		Q3UQ22	5.1	2.7E-02	7.6	1.7E-04	-0.5	7.4E-01	-0.9	1.7E-01
ENSMUST00000106239	sperm tail PG rich repeat containing 2 [Source:MGI Symbol;Acc:MGI:2685863]		Q8C8J0	3.9	4.6E-02	5.1	2.1E-02	-0.4	8.3E-01	-1.6	1.9E-01
ENSMUST00000106240	integrin alpha M [Source:MGI Symbol;Acc:MGI:96607]			-6.2	1.8E-01	-7.3	2.5E-01	-0.8	6.5E-01	0.2	9.7E-01
ENSMUST00000106241	poly(A) binding protein, cytoplasmic 4 [Source:MGI Symbol;Acc:MGI:2385206]	A3KFU8		-1.9	3.0E-01	4.0	7.4E-02	2.9	1.5E-01	-3.0	9.8E-02
ENSMUST00000106242	integrin alpha M [Source:MGI Symbol;Acc:MGI:96607]	E9Q604		-1.1	7.2E-01	5.0	9.7E-02	1.5	5.7E-01	-4.6	1.3E-01
ENSMUST00000106243	poly(A) binding protein, cytoplasmic 4 [Source:MGI Symbol;Acc:MGI:2385206]	A3KFU5		-2.8	1.1E-01	0.2	9.4E-01	3.0	1.3E-01	0.0	9.9E-01
ENSMUST00000106244	endonuclease V [Source:MGI Symbol;Acc:MGI:2444688]		Q8C9A2	3.5	4.5E-02	-2.1	4.9E-01	-0.6	7.7E-01	5.0	8.0E-02
ENSMUST00000106245	endonuclease V [Source:MGI Symbol;Acc:MGI:2444688]		Q8C9A2	3.0	2.5E-01	4.2	1.2E-01	-0.9	7.3E-01	-2.1	3.1E-01
ENSMUST00000107745	glutamate receptor, ionotropic, AMPA2 (alpha 2) [Source:MGI Symbol;Acc:MGI:95809]	E9QKC0		8.0	1.6E-04	6.0	9.6E-03	-0.6	7.5E-01	-1.6	1.9E-01
ENSMUST00000106248	tripartite motif-containing 72 [Source:MGI Symbol;Acc:MGI:3612190]		Q1XH17	2.4	3.5E-01	-1.8	5.9E-01	-1.8	4.7E-01	2.3	4.3E-01
ENSMUST00000107747	ankyrin repeat and sterile alpha motif domain containing 6 [Source:MGI Symbol;Acc:MGI:1922941]	A2ANT9		9.8	3.0E-06	4.0	1.5E-01	-0.4	9.0E-01	2.5	1.4E-01
ENSMUST00000106251	fused in sarcoma [Source:MGI Symbol;Acc:MGI:1353633]	Q564D0	P56959	1.1	7.1E-02	1.2	1.0E-01	-0.4	5.0E-01	-0.5	4.5E-01
ENSMUST00000107748	protein phosphatase 1, regulatory subunit 9B [Source:MGI Symbol;Acc:MGI:2387581]		Q6R891	-3.7	7.7E-03	2.1	2.2E-01	-1.2	4.3E-01	3.7	1.3E-02
ENSMUST00000106253	eukaryotic translation initiation factor 4A3 [Source:MGI Symbol;Acc:MGI:1923731]	A2AFK7		2.6	2.0E-01	-2.2	4.7E-01	-2.0	2.9E-01	2.8	3.4E-01
ENSMUST00000107749	gamma-aminobutyric acid (GABA) B receptor, 2 [Source:MGI Symbol;Acc:MGI:2386030]		Q80T41	8.5	2.0E-05	-5.6	1.1E-02	0.2	8.1E-01	-2.1	3.5E-01
ENSMUST00000107750	TBC1 domain family, member 2 [Source:MGI Symbol;Acc:MGI:2652885]		B1AVH7	5.6	6.5E-06	-9.9	1.4E-05	0.7	3.2E-02	0.6	6.4E-01
ENSMUST00000107752	hydroxysteroid (17-beta) dehydrogenase 14 [Source:MGI Symbol;Acc:MGI:1913315]	E9Q3D4		6.5	1.2E-04	6.0	7.0E-04	-2.1	1.4E-01	-0.3	6.3E-01
ENSMUST00000106259	glucosidase, alpha, acid [Source:MGI Symbol;Acc:MGI:95609]		P70699	-3.3	5.8E-02	1.0	6.2E-01	1.6	3.1E-01	-2.6	1.6E-01
ENSMUST00000106262	zinc finger protein 668 [Source:MGI Symbol;Acc:MGI:2442943]		Q8K2R5	1.0	6.0E-01	3.9	8.5E-02	-0.3	8.6E-01	-3.3	7.8E-02
ENSMUST00000106263	zinc finger protein 668 [Source:MGI Symbol;Acc:MGI:2442943]		Q8K2R5	2.1	3.8E-01	1.4	5.8E-01	-1.4	5.3E-01	-0.7	7.8E-01
ENSMUST00000107756	coronin, actin binding protein 2A [Source:MGI Symbol;Acc:MGI:1345966]	B1AVH4	Q8C0P5	-7.6	7.6E-06	7.3	4.0E-05	0.1	9.3E-01	-0.6	3.0E-01
ENSMUST00000107764	hemogen [Source:MGI Symbol;Acc:MGI:2136910]		Q9ERZ0	10.3	1.1E-04	8.1	1.0E-04	-0.5	6.6E-01	1.3	4.6E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000106271	oxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 [Source:MGI Symbol;Acc:MGI:2141	D3Z3X2		3.0	2.0E-01	0.1	9.8E-01	-1.6	4.9E-01	1.3	5.8E-01
ENSMUST00000106280	zinc finger protein 69 [Source:MGI Symbol;Acc:MGI:107794]	A2A761		3.7	5.0E-02	1.7	3.6E-01	-2.2	2.1E-01	-0.2	8.7E-01
ENSMUST00000106281	zinc finger protein 69 [Source:MGI Symbol;Acc:MGI:107794]	A2A761		0.0	1.0E+00	0.3	8.3E-01	-0.2	8.2E-01	-0.5	6.6E-01
ENSMUST00000107771	RuvB-like protein 2 [Source:MGI Symbol;Acc:MGI:1342299]	Q3TXT7	Q9WTM5	-3.5	1.5E-03	4.4	3.0E-04	0.7	3.8E-01	0.3	5.6E-01
ENSMUST00000106283	regulating synaptic membrane exocytosis 3 [Source:MGI Symbol;Acc:MGI:2443331]	Q14BY7	Q80U57	3.7	1.4E-01	2.6	3.1E-01	-1.2	6.0E-01	-0.2	9.4E-01
ENSMUST00000107773	tropomodulin 1 [Source:MGI Symbol;Acc:MGI:98775]		P49813	7.2	2.0E-04	-0.3	8.6E-01	-4.7	3.6E-02	2.2	1.4E-01
ENSMUST00000107774	potassium voltage-gated channel, shaker-related subfamily, member 7 [Source:MGI Symbol;Acc:MGI:96664]		Q17ST2	9.3	1.1E-05	-5.3	5.6E-02	1.0	3.3E-01	-0.8	7.9E-01
ENSMUST00000107777	tudor domain containing 7 [Source:MGI Symbol;Acc:MGI:2140279]	A0A0A0MQD1		-4.4	1.8E-02	-1.3	5.0E-01	0.9	4.0E-01	-1.6	4.2E-01
ENSMUST00000106290	lectin, galactoside-binding, soluble, 3 binding protein [Source:MGI Symbol;Acc:MGI:99554]	E9Q5X5		4.1	4.9E-02	6.5	1.2E-02	0.6	7.7E-01	-1.7	2.2E-01
ENSMUST00000107779	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3 [Source:MGI Symbol;Ac	B8QI35	P60469	7.0	7.1E-03	-4.2	3.5E-04	1.0	2.3E-02	-1.7	6.7E-02
ENSMUST00000107782	STRA6-like [Source:MGI Symbol;Acc:MGI:1921402]	B1AWX8		7.1	1.1E-04	-6.6	9.4E-04	0.9	8.5E-02	-0.9	5.7E-01
ENSMUST00000107789	calcium channel, voltage-dependent, T type, alpha 1G subunit [Source:MGI Symbol;Acc:MGI:1201678]	Q5SUF7		9.0	2.9E-05	1.0	7.0E-01	-1.5	4.9E-01	3.6	1.5E-01
ENSMUST00000106298	sex comb on midleg homolog 1 [Source:MGI Symbol;Acc:MGI:1352762]		Q8K214	-0.2	9.3E-01	3.0	2.7E-01	-0.5	8.4E-01	-3.7	1.3E-01
ENSMUST00000106299	zinc finger protein 689 [Source:MGI Symbol;Acc:MGI:1918381]	D3Z3V5		4.4	4.8E-02	2.9	2.0E-01	-0.6	7.9E-01	0.9	5.5E-01
ENSMUST00000106300	zinc finger protein 688 [Source:MGI Symbol;Acc:MGI:1916484]	E9Q5M9		-2.5	1.5E-01	-1.4	5.4E-01	1.1	4.5E-01	0.0	9.8E-01
ENSMUST00000107797	CD37 antigen [Source:MGI Symbol;Acc:MGI:88330]	E9Q2X8		-4.3	2.8E-03	-2.9	4.0E-03	0.5	2.4E-01	-0.1	8.7E-01
ENSMUST00000106305	cytohesin 1 [Source:MGI Symbol;Acc:MGI:1334257]		Q9QX11	-5.0	1.2E-01	-4.1	3.0E-01	0.8	6.6E-01	-0.1	9.9E-01
ENSMUST00000107801	TEA domain family member 2 [Source:MGI Symbol;Acc:MGI:104904]	Q3UPV9	P48301	9.1	6.3E-06	-7.0	4.3E-03	0.8	2.6E-01	-0.2	9.4E-01
ENSMUST00000107802	tripartite motif-containing 59 [Source:MGI Symbol;Acc:MGI:1914199]		Q922Y2	-3.2	5.5E-03	5.6	6.5E-04	-2.6	5.4E-02	-0.2	8.0E-01
ENSMUST00000107803	structural maintenance of chromosomes 4 [Source:MGI Symbol;Acc:MGI:1917349]	E9Q2X6		-7.6	4.1E-05	8.7	3.7E-03	-0.9	7.4E-01	-3.1	7.0E-02
ENSMUST00000106310	forkhead box J3 [Source:MGI Symbol;Acc:MGI:2443432]		Q8BUR3	0.5	7.7E-01	3.0	2.0E-01	1.5	4.7E-01	-1.1	5.3E-01
ENSMUST00000107804	FERM and PDZ domain containing 1 [Source:MGI Symbol;Acc:MGI:2446274]		A2AKB4	8.8	2.0E-04	4.1	1.4E-02	0.8	5.2E-01	-0.4	7.1E-01
ENSMUST00000107810	translocase of outer mitochondrial membrane 5 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1915762]		B1AXP6	-4.5	1.7E-04	-2.8	6.2E-02	1.1	1.2E-01	-0.4	7.7E-01
ENSMUST00000107811	PIH1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1916095]		Q9CQJ2	-4.8	2.7E-02	-3.0	9.2E-03	0.5	3.1E-01	-2.3	6.1E-02
ENSMUST00000106318	peptidyl prolyl isomerase H [Source:MGI Symbol;Acc:MGI:106499]		Q9D868	-0.6	2.5E-01	-0.9	1.8E-01	-1.1	3.8E-02	-0.8	2.0E-01
ENSMUST00000106321	peptidyl prolyl isomerase H [Source:MGI Symbol;Acc:MGI:106499]		Q9D868	0.3	6.2E-01	0.4	5.2E-01	-0.2	7.5E-01	-0.3	5.9E-01
ENSMUST00000107814	polymerase (RNA) I polypeptide E [Source:MGI Symbol;Acc:MGI:1929022]		Q8K202	4.0	1.4E-02	7.4	1.8E-04	0.1	9.6E-01	-0.7	3.2E-01
ENSMUST00000106332	seizure related 6 homolog like 2 [Source:MGI Symbol;Acc:MGI:2385295]		Q4V9Z5	-0.9	6.6E-01	2.5	1.7E-01	-1.3	4.3E-01	-4.7	4.1E-02
ENSMUST00000106333	seizure related 6 homolog like 2 [Source:MGI Symbol;Acc:MGI:2385295]		Q4V9Z5	-0.7	5.9E-01	2.5	1.7E-01	1.5	3.3E-01	-1.7	2.4E-01
ENSMUST00000107815	aldehyde dehydrogenase 16 family, member A1 [Source:MGI Symbol;Acc:MGI:1916998]	D3Z0B9		-2.8	1.1E-03	-2.4	3.1E-01	2.5	9.4E-02	-0.6	8.0E-01
ENSMUST00000107816	interleukin 12a [Source:MGI Symbol;Acc:MGI:96539]	Q549G3	P43431	-2.7	6.0E-03	7.4	4.3E-05	-1.5	2.1E-01	-0.2	6.4E-01
ENSMUST00000107817	zinc finger and BTB domain containing 5 [Source:MGI Symbol;Acc:MGI:1924601]		Q7TQG0	2.6	8.8E-04	5.9	2.3E-04	-0.1	8.9E-01	0.1	8.5E-01
ENSMUST00000107818	ankyrin repeat domain 40 [Source:MGI Symbol;Acc:MGI:1918702]		Q5SUE8	-2.2	4.9E-03	4.4	1.4E-04	-0.6	3.7E-01	0.1	8.4E-01
ENSMUST00000107820	LUC7-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914934]		Q5SUF2	-7.2	3.2E-04	2.7	2.6E-01	-0.9	6.7E-01	7.5	1.9E-03
ENSMUST00000107821	LUC7-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914934]		Q5SUF2	-6.1	1.2E-04	-4.8	4.6E-03	1.1	6.5E-02	-0.7	6.2E-01
ENSMUST00000106344	trinucleotide repeat containing 6C [Source:MGI Symbol;Acc:MGI:2443265]	B1ATC3		-1.2	3.2E-01	0.3	8.7E-01	2.3	1.3E-01	0.8	6.5E-01
ENSMUST00000106348	aldolase A, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:87994]	Q5FWB7	P05064	-2.7	9.8E-02	-0.9	6.1E-01	0.1	9.6E-01	-1.7	3.4E-01
ENSMUST00000107822	LUC7-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914934]	F8WGA8		-5.3	3.4E-02	-5.5	2.3E-03	1.1	1.0E-01	-0.6	7.2E-01
ENSMUST00000107824	zinc finger, CCHC domain containing 7 [Source:MGI Symbol;Acc:MGI:2442912]		B1AX39	-4.7	9.1E-04	7.9	2.8E-05	-0.6	6.0E-01	-1.6	1.7E-02
ENSMUST00000107829	nitric oxide synthase interacting protein [Source:MGI Symbol;Acc:MGI:1913644]		Q9D6T0	-8.1	1.5E-05	3.8	7.8E-02	-4.5	7.9E-02	-2.9	6.5E-02
ENSMUST00000106355	zinc finger protein 691 [Source:MGI Symbol;Acc:MGI:3041163]	A2A7P4		1.1	2.3E-01	-3.1	1.2E-01	0.6	5.0E-01	4.8	2.1E-02
ENSMUST00000107834	interferon regulatory factor 3 [Source:MGI Symbol;Acc:MGI:1859179]	Q3U9K6	P70671	-5.7	2.1E-02	-6.5	3.7E-03	1.2	9.5E-02	-1.6	4.6E-01
ENSMUST00000107845	clathrin, light polypeptide (Lca) [Source:MGI Symbol;Acc:MGI:894297]	B1AWE0		-7.9	1.2E-03	-4.2	6.5E-02	0.4	6.9E-01	0.5	8.2E-01
ENSMUST00000107846	clathrin, light polypeptide (Lca) [Source:MGI Symbol;Acc:MGI:894297]	Q6PFA2		4.4	9.1E-04	-4.0	2.8E-02	-0.3	6.6E-01	-0.8	6.5E-01
ENSMUST00000107853	mbt domain containing 1 [Source:MGI Symbol;Acc:MGI:2143977]		Q6P5G3	-3.7	1.8E-02	-3.3	1.9E-02	0.8	2.3E-01	-1.7	2.0E-01
ENSMUST00000107855	GLI pathogenesis-related 2 [Source:MGI Symbol;Acc:MGI:1917770]	B1AWD6		-7.6	3.5E-03	6.1	1.1E-03	-0.6	6.5E-01	-1.1	1.8E-01
ENSMUST00000106369	bolA-like 2 (E. coli) [Source:MGI Symbol;Acc:MGI:1913412]		Q8BGS2	-1.7	6.6E-02	-2.2	4.4E-02	-1.3	7.0E-02	-0.8	4.5E-01
ENSMUST00000107857	adaptor-related protein complex 2, alpha 1 subunit [Source:MGI Symbol;Acc:MGI:101921]		P17426	-4.7	2.2E-03	-1.9	5.6E-02	0.5	4.1E-01	-0.9	3.5E-01
ENSMUST00000106373	sulfotransferase family 1A, phenol-preferring, member 1 [Source:MGI Symbol;Acc:MGI:102896]	E9QNL5		2.3	8.7E-02	-2.6	2.1E-02	-6.3	1.9E-04	-1.4	1.8E-01
ENSMUST00000107858	carbonic anhydrase 10 [Source:MGI Symbol;Acc:MGI:1919855]	E9Q2V1		9.0	1.5E-03	3.6	5.7E-02	-0.7	6.5E-01	-0.4	7.4E-01
ENSMUST00000107860	olfactory receptor 155 [Source:MGI Symbol;Acc:MGI:1352681]	Q9QZ22		6.2	4.7E-04	3.2	1.0E-01	-0.6	7.6E-01	2.2	9.2E-02
ENSMUST00000107861	carbonic anhydrase 10 [Source:MGI Symbol;Acc:MGI:1919855]	Q3TRQ4		4.2	1.1E-03	-3.3	6.2E-03	1.0	6.2E-02	-2.1	9.7E-02
ENSMUST00000106392	Tu translation elongation factor, mitochondrial [Source:MGI Symbol;Acc:MGI:1923686]		Q8BFR5	2.7	1.8E-01	3.6	1.8E-01	0.9	6.8E-01	0.1	9.6E-01
ENSMUST00000106398	ring finger protein 157 [Source:MGI Symbol;Acc:MGI:2442484]	A2AAP0		4.8	8.1E-02	6.1	8.5E-02	1.0	7.5E-01	-0.2	9.2E-01
ENSMUST00000106399	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]	E9Q1W0		-2.3	3.3E-01	-3.5	2.1E-01	-2.0	2.1E-01	-0.8	7.8E-01
ENSMUST00000106400	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]		Q6PHZ2	-2.7	1.1E-01	3.8	1.5E-01	5.7	1.4E-02	-0.8	6.8E-01
ENSMUST00000106402	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]		Q6PHZ2	-0.3	8.6E-01	0.8	6.6E-01	-1.1	4.8E-01	-2.3	2.7E-01
ENSMUST00000106403	lysine (K)-specific demethylase 4A [Source:MGI Symbol;Acc:MGI:2446210]		Q8BW72	-0.6	7.7E-01	-0.9	8.1E-01	2.2	3.5E-01	2.6	4.9E-01
ENSMUST00000106406	lysine (K)-specific demethylase 4A [Source:MGI Symbol;Acc:MGI:2446210]		Q8BW72	-3.0	2.3E-01	-0.1	9.7E-01	2.3	3.7E-01	-0.5	8.6E-01
ENSMUST00000107862	olfactory receptor 71 [Source:MGI Symbol;Acc:MGI:1860080]	Q9QZ18		7.3	5.9E-05	-5.4	1.6E-03	0.6	2.2E-01	-0.7	6.1E-01
ENSMUST00000106410	ST3 beta-galactoside alpha-2,3-sialyltransferase 3 [Source:MGI Symbol;Acc:MGI:1316659]		P97325	-2.1	1.1E-01	-2.7	8.3E-02	0.3	7.8E-01	0.8	5.9E-01
ENSMUST00000107863	carbonic anhydrase 10 [Source:MGI Symbol;Acc:MGI:1919855]	Q3V1V7	P61215	9.3	2.5E-03	-4.8	7.7E-03	0.6	4.5E-01	-1.8	3.4E-01
ENSMUST00000107866	transmembrane protein 8B [Source:MGI Symbol;Acc:MGI:2441680]	B1AWJ4		9.6	4.2E-04	4.9	4.1E-03	-0.1	9.7E-01	-0.4	6.4E-01
ENSMUST00000106425	signal recognition particle 68 [Source:MGI Symbol;Acc:MGI:1917447]	A2AAN2		-4.9	1.5E-01	-0.6	8.6E-01	1.2	6.3E-01	-3.1	3.8E-01
ENSMUST00000106426	synaptopodin 2 [Source:MGI Symbol;Acc:MGI:2153070]	E9Q1U2		3.1	3.9E-02	7.3	3.1E-04	-0.5	7.2E-01	-4.7	6.5E-04
ENSMUST00000107870	sperm associated antigen 8 [Source:MGI Symbol;Acc:MGI:3056295]	Q5UAV3		5.5	1.6E-02	4.4	1.0E-01	-0.6	8.1E-01	2.6	1.1E-01
ENSMUST00000107886	RGP1 retrograde golgi transport homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915956]		Q8BHT7	-2.2	1.4E-03	-4.9	7.9E-05	-0.4	3.0E-01	-0.3	7.3E-01
ENSMUST00000106435	Fas (TNFRSF6) binding factor 1 [Source:MGI Symbol;Acc:MGI:1922033]		A2A870	3.8	5.2E-02	2.1	4.3E-01	0.2	9.1E-01	2.0	3.3E-01
ENSMUST00000107887	monocyte to macrophage differentiation-associated [Source:MGI Symbol;Acc:MGI:1914718]	Z4YKP7		6.0	1.7E-04	3.7	8.1E-03	-3.0	3.8E-02	-1.1	2.1E-01
ENSMUST00000107894	diacylglycerol kinase, epsilon [Source:MGI Symbol;Acc:MGI:1889276]		Q9R1C6	6.0	2.0E-04	8.1	3.6E-05	0.0	9.9E-01	0.1	8.9E-01
ENSMUST00000107896	tripartite motif-containing 25 [Source:MGI Symbol;Acc:MGI:102749]		Q61510	-9.4	6.0E-05	-4.7	9.0E-03	-0.7	3.0E-01	0.4	8.1E-01
ENSMUST00000107904	A kinase (PRKA) anchor protein 1 [Source:MGI Symbol;Acc:MGI:104729]		O08715	8.6	9.2E-06	5.4	1.9E-04	-0.3	7.7E-01	-0.4	4.8E-01
ENSMUST00000106442	Rho GTPase activating protein 17 [Source:MGI Symbol;Acc:MGI:1917747]		Q3UIA2	0.2	8.1E-01	0.8	5.9E-01	1.5	2.5E-01	0.9	4.5E-01
ENSMUST00000107907	potassium voltage gated channel, Shaw-related subfamily, member 3 [Source:MGI Symbol;Acc:MGI:96669]	D3YZV2		7.6	4.4E-05	4.7	2.1E-03	-0.6	6.0E-01	-0.1	9.2E-01
ENSMUST00000107911	nuclear receptor subfamily 1, group H, member 2 [Source:MGI Symbol;Acc:MGI:1352463]	Q8BP65		-8.2	1.1E-02	-5.6	1.2E-03	-2.0	5.0E-03	0.6	6.4E-01
ENSMUST00000106450	unc-13 homolog D (C. elegans) [Source:MGI Symbol;Acc:MGI:1917700]		B2RUP2	-2.9	6.0E-02	-2.6	1.4E-01	-0.2	8.4E-01	-0.5	7.8E-01
ENSMUST00000107912	nuclear receptor subfamily 1, group H, member 2 [Source:MGI Symbol;Acc:MGI:1352463]		Q60644	-4.4	3.5E-02	-6.1	5.8E-02	2.0	7.1E-02	0.8	7.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000106452	unkempt homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2442456]	Q3UYU7	Q8BL48	0.6	8.1E-01	-1.3	6.7E-01	-2.0	4.4E-01	0.0	1.0E+00
ENSMUST00000107920	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]	H7BX95		-3.7	8.7E-03	1.4	2.7E-01	-2.4	5.6E-02	-0.3	7.7E-01
ENSMUST00000106456	testis-specific kinase 2 [Source:MGI Symbol;Acc:MGI:2385204]	A2AGD9		-1.9	2.5E-01	-1.4	5.9E-01	1.8	3.3E-01	1.4	5.5E-01
ENSMUST00000106458	integrin beta 4 [Source:MGI Symbol;Acc:MGI:96613]		A2A863	2.8	3.4E-01	4.5	1.4E-01	-0.4	9.0E-01	-2.2	3.0E-01
ENSMUST00000107923	dynein light chain LC8-type 2 [Source:MGI Symbol;Acc:MGI:1915347]		Q9D0M5	6.4	6.5E-03	1.2	3.7E-01	-1.9	1.1E-01	1.1	3.3E-01
ENSMUST00000107924	selenoprotein T [Source:MGI Symbol;Acc:MGI:1916477]		P62342	-2.9	1.5E-04	8.2	1.4E-04	-0.8	5.8E-01	-0.1	8.8E-01
ENSMUST00000106461	integrin beta 4 [Source:MGI Symbol;Acc:MGI:96613]		A2A863	4.0	7.9E-02	4.8	5.5E-02	-0.5	8.2E-01	-1.3	4.0E-01
ENSMUST00000107927	family with sequence similarity 71, member E1 [Source:MGI Symbol;Acc:MGI:1922788]		A1L3C1	3.1	1.7E-03	3.7	3.6E-02	0.1	9.7E-01	2.1	8.0E-02
ENSMUST00000107937	ATPase, class I, type 8B, member 5 [Source:MGI Symbol;Acc:MGI:2444287]	D6RG77		8.2	2.7E-03	-8.5	1.8E-05	-1.7	6.3E-04	-1.0	3.9E-01
ENSMUST00000106473	lipid phosphate phosphatase-related protein type 5 [Source:MGI Symbol;Acc:MGI:1923019]		Q8BJ52	3.7	1.4E-01	2.6	3.2E-01	-0.5	8.6E-01	0.6	7.3E-01
ENSMUST00000107938	SH3/ankyrin domain gene 1 [Source:MGI Symbol;Acc:MGI:3613677]		D3YZU1	7.6	9.8E-06	-5.1	2.7E-02	0.7	3.4E-01	2.5	2.2E-01
ENSMUST00000107945	acid phosphatase, testicular [Source:MGI Symbol;Acc:MGI:3644563]	D3YZU0		7.3	5.7E-03	3.1	7.8E-04	0.5	4.1E-01	-0.5	3.1E-01
ENSMUST00000106479	IAP promoted placental gene [Source:MGI Symbol;Acc:MGI:96581]		P28575	-1.8	7.7E-02	-2.5	5.9E-02	-0.5	4.9E-01	0.2	8.7E-01
ENSMUST00000107956	family with sequence similarity 214, member B [Source:MGI Symbol;Acc:MGI:2441854]		Q8BR27	-3.3	4.4E-03	5.1	4.7E-02	-0.8	7.5E-01	0.2	8.9E-01
ENSMUST00000107967	kallikrein related-peptidase 6 [Source:MGI Symbol;Acc:MGI:1343166]	Q91Y82		5.9	2.7E-02	7.6	8.4E-05	-0.6	6.1E-01	0.1	9.2E-01
ENSMUST00000106484	microtubule associated serine/threonine kinase 2 [Source:MGI Symbol;Acc:MGI:894676]	B1AST7		-2.5	6.7E-02	1.6	5.6E-01	6.1	1.1E-02	2.0	3.7E-01
ENSMUST00000106488	eukaryotic elongation factor-2 kinase [Source:MGI Symbol;Acc:MGI:1195261]		O08796	0.2	9.4E-01	1.2	6.9E-01	0.8	6.9E-01	-0.3	9.3E-01
ENSMUST00000107968	kallikrein related-peptidase 6 [Source:MGI Symbol;Acc:MGI:1343166]	Q91Y82		4.8	2.0E-02	-2.4	1.8E-01	1.0	3.2E-01	-0.3	8.8E-01
ENSMUST00000107971	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human) [Source:MGI Symbol;Acc:MGI:2139806]		Q8R1X6	4.6	3.4E-02	-3.0	1.7E-02	-6.8	1.3E-04	2.0	8.5E-02
ENSMUST00000107972	zinc finger protein 658 [Source:MGI Symbol;Acc:MGI:2652821]	Q5PPQ4		1.9	8.2E-03	-3.8	9.2E-02	1.9	8.4E-02	-2.0	4.0E-01
ENSMUST00000106497	growth factor receptor bound protein 2 [Source:MGI Symbol;Acc:MGI:95805]	Q3U5I5	Q60631	0.9	6.3E-01	-1.4	4.6E-01	-3.3	4.5E-02	-1.0	6.0E-01
ENSMUST00000106498	protein O-linked mannose beta 1,2-N-acetylglucosaminyltransferase [Source:MGI Symbol;Acc:MGI:1915523]		Q91X88	5.1	7.4E-02	-1.5	7.0E-01	-4.0	2.0E-01	2.6	4.3E-01
ENSMUST00000106499	growth factor receptor bound protein 2 [Source:MGI Symbol;Acc:MGI:95805]		Q60631	-7.4	1.1E-01	1.1	8.7E-01	7.1	1.8E-01	-1.5	8.0E-01
ENSMUST00000106501	exostoses (multiple)-like 2 [Source:MGI Symbol;Acc:MGI:1889574]	Q3TSR0		-2.3	1.8E-01	0.8	7.0E-01	2.5	1.7E-01	-0.6	7.5E-01
ENSMUST00000106502	exostoses (multiple)-like 2 [Source:MGI Symbol;Acc:MGI:1889574]		Q9ES89	0.4	8.4E-01	-2.2	3.6E-01	-2.4	1.9E-01	0.2	9.3E-01
ENSMUST00000107973	DnaJ (Hsp40) homolog, subfamily B, member 5 [Source:MGI Symbol;Acc:MGI:1930018]	Q3TY13	O89114	-6.0	2.6E-04	-2.6	5.7E-02	1.3	7.3E-02	0.1	9.4E-01
ENSMUST00000107974	IgLON family member 5 [Source:MGI Symbol;Acc:MGI:2686277]		Q8HW98	5.7	2.1E-04	-3.1	1.0E-01	0.7	4.3E-01	0.3	8.7E-01
ENSMUST00000106507	MIF4G domain containing [Source:MGI Symbol;Acc:MGI:1916924]		Q3UBZ5	-2.3	4.3E-02	-0.5	6.7E-01	0.5	5.8E-01	-1.3	2.7E-01
ENSMUST00000106508	olgi associated, gamma adaptin ear containing, ARF binding protein 3 [Source:MGI Symbol;Acc:MGI:238415	A2A9W7		0.5	8.2E-01	-1.9	5.5E-01	-2.2	2.8E-01	0.2	9.5E-01
ENSMUST00000106513	MAP kinase-interacting serine/threonine kinase 1 [Source:MGI Symbol;Acc:MGI:894316]	A2A8W8		-4.3	1.9E-01	-3.6	3.6E-01	-0.3	8.7E-01	-1.0	8.1E-01
ENSMUST00000106517	LYR motif containing 1 [Source:MGI Symbol;Acc:MGI:1921169]		Q9CQB7	0.2	8.1E-01	1.5	1.7E-01	0.7	4.5E-01	-0.6	4.4E-01
ENSMUST00000107975	PHD finger protein 24 [Source:MGI Symbol;Acc:MGI:2140712]		Q80TL4	8.1	3.6E-05	-4.8	2.5E-03	-0.3	6.2E-01	-1.0	4.7E-01
ENSMUST00000106519	N1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2679		Q8K0V2	0.8	4.3E-01	0.3	7.7E-01	-0.3	7.2E-01	0.1	9.3E-01
ENSMUST00000107976	PHD finger protein 24 [Source:MGI Symbol;Acc:MGI:2140712]		Q80TL4	6.5	3.3E-02	6.2	3.6E-04	0.5	7.0E-01	-0.5	4.2E-01
ENSMUST00000106522	EF-hand calcium binding domain 14 [Source:MGI Symbol;Acc:MGI:2442397]		Q8BGQ6	-0.2	8.4E-01	0.7	6.2E-01	1.4	2.3E-01	0.5	6.8E-01
ENSMUST00000106524	EF-hand calcium binding domain 14 [Source:MGI Symbol;Acc:MGI:2442397]	A2A8T9		-2.1	4.6E-01	-3.2	3.9E-01	-1.3	5.1E-01	-0.3	9.4E-01
ENSMUST00000107978	family with sequence similarity 205, member C [Source:MGI Symbol;Acc:MGI:2679716]		Q80YD3	6.4	4.5E-03	-4.1	2.2E-03	0.6	1.9E-01	0.5	6.3E-01
ENSMUST00000107979	family with sequence similarity 205, member A1 [Source:MGI Symbol;Acc:MGI:3651059]	D3YZF6		8.3	7.5E-05	5.7	2.0E-03	1.6	2.4E-01	0.2	8.3E-01
ENSMUST00000106533	potassium channel tetramerisation domain containing 2 [Source:MGI Symbol;Acc:MGI:1917632]	A2A9V9		0.1	8.2E-01	-0.1	9.2E-01	-0.1	8.4E-01	0.1	9.0E-01
ENSMUST00000107981	predicted gene 12394 [Source:MGI Symbol;Acc:MGI:3649790]	A2AKP6		3.3	2.2E-03	-4.0	7.4E-03	0.3	5.6E-01	-0.8	5.4E-01
ENSMUST00000107986	zinc finger protein 715 [Source:MGI Symbol;Acc:MGI:1917180]	G3X9T1		-8.3	1.3E-06	2.6	2.0E-02	0.0	9.7E-01	0.0	9.9E-01
ENSMUST00000107992	predicted gene 5595 [Source:MGI Symbol;Acc:MGI:3648690]	Q6NVD6		3.1	1.3E-03	4.8	5.1E-04	-1.7	1.2E-01	-0.9	1.9E-01
ENSMUST00000106542	HID1 domain containing [Source:MGI Symbol;Acc:MGI:2445087]		Q8R1F6	3.8	2.6E-01	3.9	3.0E-01	-0.4	9.2E-01	-0.4	8.5E-01
ENSMUST00000106543	otopetrin 3 [Source:MGI Symbol;Acc:MGI:1916852]		Q80UF9	2.9	1.3E-01	6.3	1.0E-02	0.2	9.3E-01	-3.3	2.9E-02
ENSMUST00000106544	otopetrin 2 [Source:MGI Symbol;Acc:MGI:2388365]		Q80SX5	2.6	4.2E-02	6.3	2.0E-04	-0.5	6.5E-01	-4.3	5.0E-04
ENSMUST00000108014	predicted gene 10985 [Source:MGI Symbol;Acc:MGI:3779200]	F6T1P1		5.0	1.9E-04	7.4	5.3E-06	-0.4	5.7E-01	-0.4	3.9E-01
ENSMUST00000108015	zinc finger protein 619 [Source:MGI Symbol;Acc:MGI:1917477]	G3X9T2		1.7	4.4E-03	2.3	6.1E-02	-2.0	9.5E-02	-1.7	7.2E-02
ENSMUST00000108017	predicted gene 5114 [Source:MGI Symbol;Acc:MGI:3647631]	W4VSN8		8.1	1.1E-04	-4.9	1.3E-03	0.4	3.3E-01	-0.6	5.9E-01
ENSMUST00000108021	peptidyl-tRNA hydrolase 2 [Source:MGI Symbol;Acc:MGI:2444848]		Q8R2Y8	2.9	3.0E-03	-5.9	6.4E-04	0.7	1.3E-01	-0.6	6.3E-01
ENSMUST00000108022	peptidyl-tRNA hydrolase 2 [Source:MGI Symbol;Acc:MGI:2444848]		Q8R2Y8	-3.8	3.5E-03	7.8	2.1E-04	-0.7	6.2E-01	1.1	1.0E-01
ENSMUST00000106557	centriolar coiled coil protein 110 [Source:MGI Symbol;Acc:MGI:2141942]		Q7TSH4	1.1	2.8E-01	-0.9	4.8E-01	-0.8	3.8E-01	1.1	3.5E-01
ENSMUST00000108047	T-box 4 [Source:MGI Symbol;Acc:MGI:102556]		P70325	6.7	1.2E-02	-10.4	2.9E-03	0.6	3.7E-01	0.6	8.3E-01
ENSMUST00000106562	CD300 antigen like family member F [Source:MGI Symbol;Acc:MGI:2442359]	A2A6Z2		-0.4	4.9E-01	0.5	4.9E-01	0.3	5.8E-01	-0.6	3.8E-01
ENSMUST00000108051	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]		Q9JHC9	-5.5	4.1E-03	7.6	8.5E-05	-1.0	4.0E-01	0.3	5.5E-01
ENSMUST00000108052	family with sequence similarity 219, member A [Source:MGI Symbol;Acc:MGI:1919151]	A2ANP1		-4.5	6.0E-03	6.8	5.0E-04	-0.8	5.7E-01	-0.6	4.2E-01
ENSMUST00000108055	kinesin family member 24 [Source:MGI Symbol;Acc:MGI:1918345]		Q6NWW5	4.9	1.2E-05	7.6	8.5E-05	-1.0	4.0E-01	0.3	5.5E-01
ENSMUST00000106567	protein arginine N-methyltransferase 6 [Source:MGI Symbol;Acc:MGI:2139971]		Q6NZB1	1.6	3.7E-02	1.0	2.4E-01	-0.3	6.9E-01	0.3	6.4E-01
ENSMUST00000108056	breast carcinoma amplified sequence 3 [Source:MGI Symbol;Acc:MGI:2385848]		Q8CCN5	5.1	1.1E-03	2.4	1.2E-01	5.7	6.9E-04	-1.3	3.1E-01
ENSMUST00000108060	ubiquitin-associated protein 1 [Source:MGI Symbol;Acc:MGI:2149543]		Q8BH48	-7.8	2.2E-05	-8.8	6.9E-05	0.5	1.7E-01	-0.7	6.2E-01
ENSMUST00000106582	CD300A antigen [Source:MGI Symbol;Acc:MGI:2443411]		Q6SJQ0	-2.1	9.7E-02	-1.1	4.7E-01	0.5	5.8E-01	-0.4	7.6E-01
ENSMUST00000106586	HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1913965]		Q8CAE2	2.8	1.1E-01	6.3	5.0E-03	-0.1	9.5E-01	-3.5	1.5E-02
ENSMUST00000108062	breast carcinoma amplified sequence 3 [Source:MGI Symbol;Acc:MGI:2385848]	B1AR74		-5.0	1.7E-03	-7.9	5.2E-06	-0.3	3.6E-01	-1.5	1.4E-01
ENSMUST00000108068	ubiquitin-associated protein 2 [Source:MGI Symbol;Acc:MGI:1916176]	A2AMY5		4.0	2.6E-02	7.0	1.1E-04	-0.6	6.0E-01	-0.2	7.4E-01
ENSMUST00000108070	potassium channel tetramerisation domain containing 15 [Source:MGI Symbol;Acc:MGI:2385276]		Q8K0E1	8.0	1.8E-05	-6.7	1.5E-03	-1.1	1.4E-01	-1.8	3.0E-01
ENSMUST00000108074	RIKEN cDNA 4931406P16 gene [Source:MGI Symbol;Acc:MGI:1924311]	Q8C5X1		-3.7	3.1E-02	-4.0	2.0E-02	0.2	8.4E-01	-1.4	4.3E-01
ENSMUST00000108075	ubiquitin specific peptidase 32 [Source:MGI Symbol;Acc:MGI:2144475]	F8VPZ3		-4.2	1.7E-04	-6.4	3.2E-04	-0.2	7.3E-01	-0.9	5.0E-01
ENSMUST00000106612	SRY (sex determining region Y)-box 6 [Source:MGI Symbol;Acc:MGI:98368]	Q8BSS6		4.8	1.3E-01	4.9	1.7E-01	-0.3	9.4E-01	-0.3	8.7E-01
ENSMUST00000106613	chloride channel CLIC-like 1 [Source:MGI Symbol;Acc:MGI:2385186]	A2AEM2		0.9	2.6E-01	1.2	2.3E-01	-0.4	6.5E-01	-0.6	4.6E-01
ENSMUST00000108081	gametogenetin binding protein 2 [Source:MGI Symbol;Acc:MGI:2387356]		Q5SV77	-4.8	2.6E-02	2.7	1.3E-03	-0.4	3.9E-01	0.4	4.4E-01
ENSMUST00000106618	tetratricopeptide repeat domain 39A [Source:MGI Symbol;Acc:MGI:2444350]		A2ACP1	5.3	6.4E-02	0.5	8.6E-01	-3.2	2.8E-01	1.7	4.6E-01
ENSMUST00000108086	heat shock protein 4 like [Source:MGI Symbol;Acc:MGI:107422]		P48722	-2.4	2.6E-03	6.2	9.6E-05	-1.5	1.9E-01	0.0	9.5E-01
ENSMUST00000106621	DNA segment, Chr 11, Wayne State University 47, expressed [Source:MGI Symbol;Acc:MGI:106356]		Q6PIX9	-1.5	4.4E-02	-0.8	3.3E-01	0.2	6.6E-01	-0.5	5.6E-01
ENSMUST00000106622	transmembrane protein 167B [Source:MGI Symbol;Acc:MGI:1914745]	A2AGC3		-4.2	2.7E-01	-0.9	7.8E-01	-0.6	7.8E-01	-3.9	3.2E-01
ENSMUST00000108107	sprouty homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1345139]	Q53ZU1	Q9QXV9	6.8	4.8E-05	7.9	6.2E-05	-0.1	9.3E-01	-0.6	3.2E-01
ENSMUST00000106633	solute carrier family 39 (metal ion transporter), member 11 [Source:MGI Symbol;Acc:MGI:1917056]		Q8BWY7	-0.4	8.4E-01	5.7	7.7E-02	4.9	8.7E-02	-1.1	5.7E-01
ENSMUST00000106635	potassium inwardly-rectifying channel, subfamily J, member 16 [Source:MGI Symbol;Acc:MGI:1314842]		Q9Z307	4.3	2.0E-01	5.5	1.3E-01	-0.5	8.9E-01	-1.7	4.3E-01
ENSMUST00000106636	potassium inwardly-rectifying channel, subfamily J, member 16 [Source:MGI Symbol;Acc:MGI:1314842]		Q9Z307	4.1	2.7E-01	3.3	4.0E-01	-1.4	7.2E-01	-0.5	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000108112	spermatogenesis associated 5 [Source:MGI Symbol;Acc:MGI:1927170]		Q3UMC0	6.3	1.5E-04	4.6	5.4E-03	-4.0	2.2E-02	-1.5	1.2E-01
ENSMUST00000108119	upstream transcription factor 2 [Source:MGI Symbol;Acc:MGI:99961]		Q64705	-3.5	4.5E-03	-7.6	2.6E-03	1.0	1.2E-01	-0.5	8.3E-01
ENSMUST00000108124	leucine rich repeat and Ig domain containing 2 [Source:MGI Symbol;Acc:MGI:2442298]	B2RQD4	Q3URE9	5.6	3.3E-04	5.6	5.3E-05	-0.4	6.5E-01	0.5	3.3E-01
ENSMUST00000108127	RIKEN cDNA 3110043O21 gene [Source:MGI Symbol;Acc:MGI:1920455]	Q3U3D8		-7.3	7.1E-06	7.2	5.3E-05	-0.5	6.4E-01	-0.4	4.8E-01
ENSMUST00000108141	RNA binding motif protein 42 [Source:MGI Symbol;Acc:MGI:1915285]	D3YYW8		-6.2	1.0E-03	-3.3	6.5E-04	0.2	5.7E-01	-0.4	5.4E-01
ENSMUST00000106654	cytochrome b-561 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919273]	Q3TPE5		0.6	2.8E-01	0.2	7.7E-01	0.8	1.8E-01	1.2	1.1E-01
ENSMUST00000108147	ets variant 2 [Source:MGI Symbol;Acc:MGI:99253]		P41163	6.5	1.6E-04	-2.0	1.2E-01	-0.1	9.4E-01	-3.0	6.9E-02
ENSMUST00000108151	zinc finger and BTB domain containing 32 [Source:MGI Symbol;Acc:MGI:1891838]	B2RQ06		1.9	2.9E-02	1.0	6.8E-01	-1.3	5.7E-01	3.4	8.6E-02
ENSMUST00000106657	zinc finger, FYVE domain containing 9 [Source:MGI Symbol;Acc:MGI:2652838]	A2A8R0		3.8	1.1E-01	-0.5	9.1E-01	-0.4	8.7E-01	3.8	2.7E-01
ENSMUST00000106658	zinc finger, FYVE domain containing 9 [Source:MGI Symbol;Acc:MGI:2652838]	A8Y5G5		-1.6	3.6E-01	3.4	9.1E-02	1.1	5.0E-01	-3.9	4.2E-02
ENSMUST00000106661	adhesion molecule with Ig like domain 1 [Source:MGI Symbol;Acc:MGI:2653612]	A2AE38		3.4	3.9E-02	5.7	1.5E-03	-2.0	2.0E-01	-4.3	2.1E-03
ENSMUST00000108152	schlafen 8 [Source:MGI Symbol;Acc:MGI:2672859]	E9Q0R4		6.6	8.8E-03	5.6	1.8E-04	-2.1	7.1E-02	0.4	5.3E-01
ENSMUST00000106665				2.0	2.1E-01	1.3	5.3E-01	-0.3	8.9E-01	0.4	7.9E-01
ENSMUST00000108154	lysine (K)-specific methyltransferase 2B [Source:MGI Symbol;Acc:MGI:109565]		O08550	5.7	3.5E-02	5.8	1.7E-03	-0.5	7.3E-01	0.5	5.3E-01
ENSMUST00000106676	protein kinase, cAMP dependent regulatory, type I, alpha [Source:MGI Symbol;Acc:MGI:104878]	A2AI69		0.4	7.1E-01	1.4	4.0E-01	1.5	2.5E-01	0.5	7.1E-01
ENSMUST00000108160	unc-45 homolog B (C. elegans) [Source:MGI Symbol;Acc:MGI:2443377]		Q8CGY6	7.9	1.7E-05	0.5	4.5E-01	-1.3	2.1E-02	-0.4	5.1E-01
ENSMUST00000108165	proline and serine rich 3 [Source:MGI Symbol;Acc:MGI:2681861]		Q7TSA6	5.0	8.1E-04	7.5	1.0E-04	-0.6	6.1E-01	-0.4	4.8E-01
ENSMUST00000106682	ring finger protein 141 [Source:MGI Symbol;Acc:MGI:1914400]		Q99MB7	0.3	7.3E-01	-3.8	7.9E-03	-2.7	2.6E-03	1.4	2.4E-01
ENSMUST00000108173	ring finger and FYVE like domain containing protein [Source:MGI Symbol;Acc:MGI:1914588]	Q3UD78	Q6ZQM0	-8.4	7.6E-05	0.3	7.9E-01	-0.6	4.8E-01	1.2	2.5E-01
ENSMUST00000106689	WD repeat domain, phosphoinositide interacting 1 [Source:MGI Symbol;Acc:MGI:1261864]	B1AT64		1.4	2.5E-01	-0.1	9.5E-01	0.2	9.0E-01	1.7	2.9E-01
ENSMUST00000108176	r factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta [Source:MGI Symbol;Acc:MGI:30		Q2TB02	-4.7	1.5E-02	6.7	3.8E-04	-0.1	9.6E-01	-0.8	2.9E-01
ENSMUST00000108183	mitogen-activated protein kinase kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346877]	A2AP93		10.4	2.8E-04	0.9	4.5E-01	-2.8	2.8E-02	-0.8	4.4E-01
ENSMUST00000108187	THAP domain containing 8 [Source:MGI Symbol;Acc:MGI:1922879]	D3YYI4		6.6	1.2E-03	-4.8	1.1E-02	0.2	8.1E-01	-0.5	7.7E-01
ENSMUST00000108192	polymerase (RNA) II (DNA directed) polypeptide I [Source:MGI Symbol;Acc:MGI:1917170]	D3YYI3		-4.7	6.9E-04	-9.0	5.2E-05	-0.6	8.3E-02	1.9	1.4E-01
ENSMUST00000108193	polymerase (RNA) II (DNA directed) polypeptide I [Source:MGI Symbol;Acc:MGI:1917170]	D3YYI2		-4.5	1.9E-03	-2.5	1.3E-02	0.7	1.8E-01	-1.3	2.1E-01
ENSMUST00000108195	DnaJ (Hsp40) homolog, subfamily C, member 19 [Source:MGI Symbol;Acc:MGI:1914963]		Q9CQV7	-3.5	2.3E-02	7.3	3.8E-05	-0.4	7.1E-01	0.8	1.3E-01
ENSMUST00000108196	calpain, small subunit 1 [Source:MGI Symbol;Acc:MGI:88266]			-8.6	3.8E-05	6.5	1.7E-04	-0.5	6.4E-01	-4.3	4.6E-04
ENSMUST00000108199	fucosyltransferase 9 [Source:MGI Symbol;Acc:MGI:1330859]	Q14AE3	O88819	6.5	8.3E-04	5.1	3.4E-03	-0.5	7.3E-01	0.3	7.0E-01
ENSMUST00000108200	zinc finger protein 260 [Source:MGI Symbol;Acc:MGI:1347071]		Q62513	-6.1	2.2E-04	8.3	3.2E-05	-0.5	6.8E-01	-0.8	1.5E-01
ENSMUST00000106720	carnitine palmitoyltransferase 2 [Source:MGI Symbol;Acc:MGI:109176]	A2A8E7		2.0	4.1E-01	1.1	6.3E-01	-2.3	2.9E-01	-1.4	5.2E-01
ENSMUST00000108205	zinc finger protein 74 [Source:MGI Symbol;Acc:MGI:107784]		Q80W31	4.0	2.1E-03	-5.6	1.5E-02	0.5	5.8E-01	1.4	5.0E-01
ENSMUST00000106726	RIKEN cDNA 0610037L13 gene [Source:MGI Symbol;Acc:MGI:1921348]	A2A8E2		-3.3	5.0E-02	-4.8	2.8E-02	-1.7	8.6E-02	-0.2	9.3E-01
ENSMUST00000106728	signal peptide, CUB domain, EGF-like 2 [Source:MGI Symbol;Acc:MGI:1928765]	D3YVN5		3.3	1.9E-01	2.9	3.4E-01	0.3	9.3E-01	0.7	7.3E-01
ENSMUST00000108210	tetratricopeptide repeat domain 14 [Source:MGI Symbol;Acc:MGI:1914370]	G3X9T5		-3.2	1.4E-02	4.3	9.0E-03	-0.5	6.9E-01	1.7	7.6E-02
ENSMUST00000108212	zinc finger protein 74 [Source:MGI Symbol;Acc:MGI:107784]	Q8BIJ3		5.1	4.9E-04	2.9	1.3E-02	0.4	5.9E-01	0.4	6.3E-01
ENSMUST00000108214	kelch-like 32 [Source:MGI Symbol;Acc:MGI:3612790]	A2AJX1		6.0	3.8E-04	6.7	1.4E-04	-0.6	6.1E-01	-0.2	7.7E-01
ENSMUST00000108216	zinc finger protein 207 [Source:MGI Symbol;Acc:MGI:1340045]	Q8CCB2		2.9	7.8E-04	-5.2	7.6E-04	-1.2	2.8E-02	-0.9	4.7E-01
ENSMUST00000108218	kelch-like 32 [Source:MGI Symbol;Acc:MGI:3612790]	A2AJX0		8.7	2.1E-04	6.5	9.1E-04	0.8	5.6E-01	0.9	2.7E-01
ENSMUST00000108223	zinc finger protein 940 [Source:MGI Symbol;Acc:MGI:2446235]	Q3UVK2		5.8	1.6E-05	7.8	2.7E-04	0.8	5.3E-01	0.2	7.4E-01
ENSMUST00000106741	tripartite motif-containing 66 [Source:MGI Symbol;Acc:MGI:2152406]	E9QLR8		3.3	9.4E-02	7.3	3.4E-03	-0.4	8.5E-01	-4.4	5.2E-03
ENSMUST00000108228	ubiquitin specific peptidase 13 (isopeptidase T-3) [Source:MGI Symbol;Acc:MGI:1919857]	J3QSN2		4.9	4.4E-03	5.6	4.7E-02	-0.6	8.2E-01	0.7	6.3E-01
ENSMUST00000106746	helicase with zinc finger domain [Source:MGI Symbol;Acc:MGI:1925705]		Q6DFV5	1.1	6.9E-02	2.3	8.6E-03	0.9	1.7E-01	-0.4	4.8E-01
ENSMUST00000108229	PNN interacting serine/arginine-rich [Source:MGI Symbol;Acc:MGI:1913875]	A2AJT3		-3.4	2.6E-03	-6.8	9.7E-04	-0.2	7.5E-01	-0.9	5.6E-01
ENSMUST00000108234	guanine nucleotide binding protein (G protein), beta 4 [Source:MGI Symbol;Acc:MGI:104581]		P29387	5.9	4.7E-05	5.9	1.4E-03	-0.4	7.5E-01	-0.1	9.1E-01
ENSMUST00000106757	nucleolar protein 11 [Source:MGI Symbol;Acc:MGI:1916229]		Q8BJW5	0.7	6.8E-01	4.2	4.8E-02	1.2	5.2E-01	-2.2	1.6E-01
ENSMUST00000106763	bromodomain PHD finger transcription factor [Source:MGI Symbol;Acc:MGI:2444008]	A2A654		0.5	3.5E-01	-4.7	2.6E-03	0.0	9.5E-01	5.2	1.2E-03
ENSMUST00000108236	serine protease inhibitor, Kunitz type 2 [Source:MGI Symbol;Acc:MGI:1338031]		Q9WU03	-4.3	3.1E-03	-8.7	1.3E-05	-0.8	2.7E-02	-0.8	5.1E-01
ENSMUST00000106769	suppression of tumorigenicity 7-like [Source:MGI Symbol;Acc:MGI:2386964]		Q8K4P7	3.5	6.8E-02	1.6	4.9E-01	-1.6	4.6E-01	0.3	8.7E-01
ENSMUST00000108238	Yip1 interacting factor homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924504]		Q9CX30	-4.1	1.2E-03	8.0	3.6E-05	-0.6	5.9E-01	-0.3	5.3E-01
ENSMUST00000106774	Moloney leukemia virus 10 [Source:MGI Symbol;Acc:MGI:97054]	D3YVL0		0.8	6.9E-01	0.4	9.0E-01	1.2	6.5E-01	1.7	4.9E-01
ENSMUST00000106778				-3.8	9.3E-02	-2.5	4.1E-01	0.9	6.3E-01	-0.4	8.8E-01
ENSMUST00000108239	ATPase family, AAA domain containing 5 [Source:MGI Symbol;Acc:MGI:2442925]	Z4YKQ9		2.6	8.3E-04	5.2	7.9E-03	-2.1	2.5E-01	-1.3	2.3E-01
ENSMUST00000106783	translocase of inner mitochondrial membrane 10B [Source:MGI Symbol;Acc:MGI:1315196]		Q9WV96	1.7	3.6E-02	3.1	9.1E-03	1.1	2.0E-01	-0.3	6.9E-01
ENSMUST00000106785	translocase of inner mitochondrial membrane 10B [Source:MGI Symbol;Acc:MGI:1315196]	D3YVK5		-1.0	6.9E-01	-3.4	2.6E-01	-2.9	1.1E-01	-0.5	8.8E-01
ENSMUST00000106787	ras homolog gene family, member C [Source:MGI Symbol;Acc:MGI:106028]		Q62159	-1.8	4.1E-01	3.9	2.0E-01	3.8	1.6E-01	-1.8	4.1E-01
ENSMUST00000108240	cyclin C [Source:MGI Symbol;Acc:MGI:1858199]	Q8CAS3		-5.2	8.7E-05	7.0	7.7E-05	-0.6	6.1E-01	-0.6	3.0E-01
ENSMUST00000108243	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide [Source:MGI Symbol;Acc:MGI:1206581]		P42337	-4.5	1.1E-05	-1.8	1.7E-01	0.9	2.7E-01	-0.9	5.1E-01
ENSMUST00000108253	regulator of microtubule dynamics 1 [Source:MGI Symbol;Acc:MGI:1913552]	A2AGJ2		1.4	1.9E-02	4.3	1.9E-04	-0.6	3.7E-01	-0.7	1.8E-01
ENSMUST00000106794	mast cell immunoglobulin like receptor 1 [Source:MGI Symbol;Acc:MGI:2685731]			-0.3	5.2E-01	1.7	2.9E-02	1.3	3.1E-02	-0.7	2.4E-01
ENSMUST00000108263	leucine rich repeat containing 31 [Source:MGI Symbol;Acc:MGI:2443864]	D3YY33		8.5	6.0E-06	3.8	1.3E-01	-0.3	9.1E-01	1.3	4.6E-01
ENSMUST00000108264	kinase suppressor of ras 1 [Source:MGI Symbol;Acc:MGI:105051]	Q5SXE4		3.2	2.3E-02	1.0	3.3E-01	-1.5	1.0E-01	1.0	2.7E-01
ENSMUST00000106803	RIKEN cDNA 1700024P16 gene [Source:MGI Symbol;Acc:MGI:2685466]	E9PZ08		2.7	2.0E-01	5.4	1.8E-02	-0.6	7.7E-01	-3.3	4.8E-02
ENSMUST00000108265	leucine-rich repeats and IQ motif containing 4 [Source:MGI Symbol;Acc:MGI:1915557]		A6H6A4	6.2	1.6E-02	3.8	5.4E-02	-0.6	7.3E-01	1.5	2.4E-01
ENSMUST00000108267	leucine-rich repeats and IQ motif containing 4 [Source:MGI Symbol;Acc:MGI:1915557]		A6H6A4	6.1	1.5E-04	-3.5	1.2E-01	0.3	8.1E-01	-0.3	9.1E-01
ENSMUST00000106808	complement component 8, alpha polypeptide [Source:MGI Symbol;Acc:MGI:2668347]	A2A998		2.9	1.5E-01	4.8	2.0E-02	-1.8	3.3E-01	-3.8	2.9E-02
ENSMUST00000108268	lectin, galactose binding, soluble 9 [Source:MGI Symbol;Acc:MGI:109496]		O08573	-5.6	2.0E-06	0.6	5.6E-01	-2.0	6.1E-02	0.2	8.4E-01
ENSMUST00000106823	adaptor-related protein complex AP-4, beta 1 [Source:MGI Symbol;Acc:MGI:1337130]	B0V3P4		2.8	2.4E-01	3.9	1.4E-01	-0.5	8.6E-01	-1.5	4.2E-01
ENSMUST00000106824	adaptor-related protein complex AP-4, beta 1 [Source:MGI Symbol;Acc:MGI:1337130]	B0V3P3		-0.7	3.2E-01	-3.2	9.6E-03	-1.4	3.2E-02	1.0	3.2E-01
ENSMUST00000108269	lectin, galactose binding, soluble 9 [Source:MGI Symbol;Acc:MGI:109496]	G3X9T7		-4.7	3.1E-04	1.1	2.7E-01	-2.6	1.0E-02	-1.1	2.0E-01
ENSMUST00000108270	MDS1 and EVI1 complex locus [Source:MGI Symbol;Acc:MGI:95457]	H9T841	P14404	6.4	1.1E-02	8.1	2.6E-04	-0.8	6.2E-01	-0.2	8.1E-01
ENSMUST00000108273	N-terminal EF-hand calcium binding protein 1 [Source:MGI Symbol;Acc:MGI:1916602]		Q8BG18	4.4	1.0E-03	-8.7	7.8E-03	-0.8	3.0E-01	-0.6	8.3E-01
ENSMUST00000108275	intraflagellar transport 20 [Source:MGI Symbol;Acc:MGI:1915585]		Q61025	-5.5	1.2E-04	6.1	2.6E-04	-2.7	4.6E-02	-0.1	8.1E-01
ENSMUST00000106834	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2156057]		Q8C7W7	-2.5	4.8E-01	-3.7	4.1E-01	-1.5	5.1E-01	-0.3	9.6E-01
ENSMUST00000108281	F-box protein 27 [Source:MGI Symbol;Acc:MGI:2685007]		Q6DIA9	5.0	8.3E-03	-2.7	1.1E-01	1.6	9.4E-02	-1.3	4.2E-01
ENSMUST00000106845	homeodomain interacting protein kinase 1 [Source:MGI Symbol;Acc:MGI:1314873]		O88904	-0.6	8.8E-01	6.6	2.7E-01	5.1	3.1E-01	-2.1	6.4E-01
ENSMUST00000108287	sterile alpha and HEAT/Armadillo motif containing 1 [Source:MGI Symbol;Acc:MGI:2136419]		Q6PDS3	5.9	2.1E-04	-4.5	3.8E-02	0.2	7.6E-01	1.0	6.0E-01
ENSMUST00000108288	leucine rich repeat and fibronectin type III domain containing 1 [Source:MGI Symbol;Acc:MGI:2136810]		Q2WF71	3.9	6.1E-04	-5.5	6.1E-04	-1.3	1.6E-02	-0.7	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000108289	glia maturation factor, gamma [Source:MGI Symbol;Acc:MGI:1927135]	D3YY16		-2.9	3.4E-03	-5.6	1.9E-02	-0.5	5.4E-01	-0.6	7.9E-01
ENSMUST00000106857	mesoderm induction early response 1 homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1918398]	Q32P49	Q5UAK0	-2.8	4.7E-01	-8.0	2.4E-01	-3.0	2.3E-01	2.3	7.4E-01
ENSMUST00000108292	glia maturation factor, gamma [Source:MGI Symbol;Acc:MGI:1927135]	A7VJA4	Q9ERL7	-4.4	1.7E-03	-2.0	3.6E-01	1.8	2.0E-01	-0.7	7.3E-01
ENSMUST00000108293	transmembrane protein 67 [Source:MGI Symbol;Acc:MGI:1923928]	A2AJP5		2.5	5.2E-03	6.3	7.0E-03	-0.6	7.8E-01	-1.8	1.3E-01
ENSMUST00000106860	tripartite motif-containing 33 [Source:MGI Symbol;Acc:MGI:2137357]	E9QME5		0.8	5.4E-02	0.2	6.7E-01	-0.6	1.3E-01	0.0	9.2E-01
ENSMUST00000108294	forkhead box N1 [Source:MGI Symbol;Acc:MGI:102949]	Q5SYK1	Q61575	8.9	1.1E-04	-5.9	2.7E-03	-0.6	3.3E-01	-0.9	5.9E-01
ENSMUST00000108301	pyruvate dehyrogenase phosphatase catalytic subunit 1 [Source:MGI Symbol;Acc:MGI:2685870]	A2AJQ0		6.9	7.4E-05	5.2	2.7E-05	0.1	9.2E-01	0.3	5.7E-01
ENSMUST00000108303	cadherin 17 [Source:MGI Symbol;Acc:MGI:1095414]	A2AKS7		8.4	9.2E-06	2.7	4.6E-03	1.1	8.8E-02	0.0	9.8E-01
ENSMUST00000108313	epithelial splicing regulatory protein 1 [Source:MGI Symbol;Acc:MGI:1917326]		Q3US41	6.4	1.6E-02	6.2	2.1E-04	-0.5	6.5E-01	-1.9	1.4E-02
ENSMUST00000108315	delta-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1096877]	Q3UND5	O88516	4.8	3.4E-05	5.6	2.8E-02	1.0	6.4E-01	1.2	4.1E-01
ENSMUST00000108316	cDNA sequence BC089491 [Source:MGI Symbol;Acc:MGI:3608324]	Q5FWB9		5.4	3.4E-04	8.3	2.1E-06	0.3	7.1E-01	0.2	6.2E-01
ENSMUST00000108318	integrator complex subunit 8 [Source:MGI Symbol;Acc:MGI:1919906]	A2API3		5.6	4.9E-04	5.6	1.1E-04	-0.6	5.1E-01	0.0	9.6E-01
ENSMUST00000108319	integrator complex subunit 8 [Source:MGI Symbol;Acc:MGI:1919906]		Q80V86	-6.8	5.0E-05	-2.0	3.4E-02	0.4	4.8E-01	0.0	9.8E-01
ENSMUST00000106908	phosphodiesterase 4B, cAMP specific [Source:MGI Symbol;Acc:MGI:99557]	Q8VBU5		-2.6	4.2E-02	-1.7	2.4E-01	0.2	8.3E-01	-0.7	6.3E-01
ENSMUST00000106913	tripartite motif-containing 21 [Source:MGI Symbol;Acc:MGI:106657]	Q3U7K7		-4.0	6.2E-02	-1.3	5.9E-01	1.9	2.9E-01	-0.8	7.2E-01
ENSMUST00000108321	Hermansky-Pudlak syndrome 3 homolog (human) [Source:MGI Symbol;Acc:MGI:2153839]	E9PZY1		-6.7	4.0E-05	5.9	4.0E-05	1.1	1.9E-01	-0.6	2.8E-01
ENSMUST00000108322	RAB34, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:104606]	Q0PD20		2.9	3.0E-02	6.8	2.8E-03	-0.8	6.8E-01	-0.8	4.2E-01
ENSMUST00000108328	ceruloplasmin [Source:MGI Symbol;Acc:MGI:88476]	G3X8Q5		4.5	1.6E-02	6.3	8.6E-04	-0.9	5.0E-01	0.6	4.1E-01
ENSMUST00000108331	zinc finger protein 59 [Source:MGI Symbol;Acc:MGI:99206]	F8VPX4		3.1	4.1E-03	2.1	4.2E-02	-3.2	9.5E-03	-0.6	4.2E-01
ENSMUST00000106923	ras homolog gene family, member G [Source:MGI Symbol;Acc:MGI:1928370]	Q3UDZ1	P84096	-0.9	4.0E-01	0.5	7.0E-01	0.6	5.3E-01	-0.8	5.3E-01
ENSMUST00000106927	leptin receptor overlapping transcript [Source:MGI Symbol;Acc:MGI:2687005]		O89013	2.4	3.9E-01	1.5	6.9E-01	0.9	7.7E-01	1.8	5.3E-01
ENSMUST00000108336	zinc finger protein 60 [Source:MGI Symbol;Acc:MGI:99207]	Q8K0D9		3.2	1.5E-03	-2.9	6.6E-02	1.8	2.7E-02	2.3	1.2E-01
ENSMUST00000108339	aspartate-beta-hydroxylase [Source:MGI Symbol;Acc:MGI:1914186]	Q8CBM2		7.6	1.2E-03	5.9	1.1E-03	-0.6	6.8E-01	0.6	4.2E-01
ENSMUST00000108342	thymoma viral proto-oncogene 2 [Source:MGI Symbol;Acc:MGI:104874]	D3YXM7		4.2	4.3E-03	4.2	4.0E-04	1.7	3.5E-02	-0.6	2.9E-01
ENSMUST00000108346	YTH domain family 3 [Source:MGI Symbol;Acc:MGI:1918850]		Q8BYK6	-6.4	1.6E-03	3.6	7.5E-03	-3.8	1.4E-02	-1.4	9.0E-02
ENSMUST00000106945	adenylate kinase 4 [Source:MGI Symbol;Acc:MGI:87979]	Q3U489	Q9WUR9	2.6	1.7E-01	0.7	8.2E-01	1.1	6.1E-01	3.0	2.8E-01
ENSMUST00000106946	adenylate kinase 4 [Source:MGI Symbol;Acc:MGI:87979]	Q3U489	Q9WUR9	5.0	8.1E-02	6.0	6.9E-02	-0.2	9.4E-01	-1.2	5.0E-01
ENSMUST00000108349	signal-regulatory protein beta 1C [Source:MGI Symbol;Acc:MGI:3807521]	E9PZD0		-4.9	1.2E-03	4.2	7.5E-03	-2.3	1.2E-01	0.3	7.3E-01
ENSMUST00000108352	signal-regulatory protein beta 1C [Source:MGI Symbol;Acc:MGI:3807521]	K7N6K7		-3.8	2.4E-02	6.0	8.6E-04	-0.4	7.3E-01	-1.0	1.9E-01
ENSMUST00000108353	homeodomain interacting protein kinase 4 [Source:MGI Symbol;Acc:MGI:2685008]		Q3V016	6.4	1.6E-04	3.6	7.9E-03	-0.8	4.0E-01	0.7	3.4E-01
ENSMUST00000106962	cell division cycle 27 [Source:MGI Symbol;Acc:MGI:102685]		A2A6Q5	-0.8	3.2E-01	0.1	8.9E-01	0.3	6.9E-01	-0.7	4.8E-01
ENSMUST00000108354	signal-regulatory protein beta 1C [Source:MGI Symbol;Acc:MGI:3807521]	D3YXM0		-8.4	7.3E-04	5.6	6.4E-03	2.0	2.1E-01	1.0	2.9E-01
ENSMUST00000108355	periaxin [Source:MGI Symbol;Acc:MGI:108176]		O55103	7.7	1.4E-03	-0.9	1.1E-01	1.1	8.6E-03	0.5	3.1E-01
ENSMUST00000108361	predicted gene 9733 [Source:MGI Symbol;Acc:MGI:3780136]	Q1AN91		-3.6	1.2E-03	-1.5	2.6E-02	0.1	7.0E-01	-3.5	1.7E-03
ENSMUST00000108362	spectrin beta, non-erythrocytic 4 [Source:MGI Symbol;Acc:MGI:1890574]	E9PZC2		7.5	3.4E-05	-4.5	4.6E-03	-0.5	4.1E-01	-0.7	6.0E-01
ENSMUST00000108364	spectrin beta, non-erythrocytic 4 [Source:MGI Symbol;Acc:MGI:1890574]	E9PZC2		7.2	1.7E-02	-5.2	6.9E-04	-0.2	5.9E-01	-0.5	6.5E-01
ENSMUST00000108376	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]		Q9JMH9	6.9	1.7E-03	6.0	1.5E-02	2.9	1.6E-01	0.0	1.0E+00
ENSMUST00000108379	cDNA sequence BC024978 [Source:MGI Symbol;Acc:MGI:3041247]	D3Z7G4		5.3	7.2E-05	6.7	7.0E-03	-0.6	7.8E-01	-1.8	1.4E-01
ENSMUST00000108380	family with sequence similarity 110, member B [Source:MGI Symbol;Acc:MGI:1916593]		Q8C739	5.9	9.6E-03	2.6	4.2E-01	-0.8	7.7E-01	2.8	2.6E-01
ENSMUST00000108382	egl-9 family hypoxia-inducible factor 2 [Source:MGI Symbol;Acc:MGI:1932287]	Q80X29	Q91YE2	5.2	1.3E-02	8.8	3.4E-05	-0.2	8.7E-01	-0.1	7.9E-01
ENSMUST00000106997	ganglioside-induced differentiation-associated-protein 2 [Source:MGI Symbol;Acc:MGI:1338001]		Q9DBL2	-0.3	9.0E-01	-2.8	3.9E-01	-2.7	2.0E-01	-0.2	9.5E-01
ENSMUST00000106998	ClpB caseinolytic peptidase B [Source:MGI Symbol;Acc:MGI:1100517]	E9PY58		-1.4	1.3E-01	-0.1	9.4E-01	0.3	7.2E-01	-1.1	3.2E-01
ENSMUST00000108384	phosphoprotein associated with glycosphingolipid microdomains 1 [Source:MGI Symbol;Acc:MGI:2443160]	A6H659	Q3U1F9	-3.6	3.0E-02	7.3	2.6E-04	-0.7	6.2E-01	-0.4	6.1E-01
ENSMUST00000108393	hepatocyte nuclear factor 4, gamma [Source:MGI Symbol;Acc:MGI:1353604]	Q059V1		5.7	1.5E-02	4.8	3.3E-03	-0.3	7.9E-01	0.7	4.1E-01
ENSMUST00000108395	cytochrome P450, family 2, subfamily s, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1921384]	D3Z7F1		7.7	9.2E-05	-7.1	2.7E-02	1.4	1.4E-01	3.5	2.3E-01
ENSMUST00000107013	golgi SNAP receptor complex member 2 [Source:MGI Symbol;Acc:MGI:1927204]	A2A9I0		-2.3	2.8E-01	-3.5	1.7E-01	-2.0	1.5E-01	-0.8	7.6E-01
ENSMUST00000108403	B9 protein domain 2 [Source:MGI Symbol;Acc:MGI:2387643]		Q3UK10	-3.5	1.1E-04	7.7	4.1E-06	0.3	7.4E-01	-0.2	6.6E-01
ENSMUST00000108407	active BCR-related gene [Source:MGI Symbol;Acc:MGI:107771]	E9PUE7		-9.4	3.5E-05	-2.2	1.3E-01	1.2	1.4E-01	-1.5	3.3E-01
ENSMUST00000108408	active BCR-related gene [Source:MGI Symbol;Acc:MGI:107771]		Q5SSL4	-2.3	1.3E-02	6.9	6.5E-04	-2.4	1.8E-01	0.2	8.0E-01
ENSMUST00000108409	transmembrane protein 145 [Source:MGI Symbol;Acc:MGI:3607779]	E9PUE6		6.1	6.3E-03	5.7	2.2E-05	-3.8	1.5E-03	-0.1	7.5E-01
ENSMUST00000108411	glycogen synthase kinase 3 alpha [Source:MGI Symbol;Acc:MGI:2152453]	D3Z7E5		7.1	1.1E-02	-1.1	1.1E-01	0.8	5.7E-02	-0.4	5.3E-01
ENSMUST00000108415	POU domain, class 2, transcription factor 2 [Source:MGI Symbol;Acc:MGI:101897]		Q00196	9.9	9.3E-04	5.9	1.7E-03	-0.5	7.3E-01	0.8	3.6E-01
ENSMUST00000108428	ribosomal protein S19 [Source:MGI Symbol;Acc:MGI:1333780]	D3Z722		3.5	3.4E-03	-3.5	6.9E-02	4.4	1.4E-03	0.7	6.9E-01
ENSMUST00000108437	serine (or cysteine) peptidase inhibitor, clade F, member 2 [Source:MGI Symbol;Acc:MGI:107173]	Q5ND36	Q61247	4.0	3.3E-03	1.5	1.6E-01	1.7	4.0E-02	-4.0	5.4E-03
ENSMUST00000107050	flavin containing monooxygenase 5 [Source:MGI Symbol;Acc:MGI:1310004]		P97872	-0.6	3.1E-01	1.6	5.7E-02	1.8	1.5E-02	-0.5	4.9E-01
ENSMUST00000107051	TM2 domain containing 1 [Source:MGI Symbol;Acc:MGI:2137022]	A0A0A0MQC8		0.7	5.0E-01	2.4	1.5E-01	1.4	3.1E-01	-0.2	8.4E-01
ENSMUST00000108438	zinc finger protein 93 [Source:MGI Symbol;Acc:MGI:107611]		Q61116	5.1	6.5E-03	-5.0	7.0E-04	-0.7	1.4E-01	-0.4	7.2E-01
ENSMUST00000108450	poliovirus receptor-related 2 [Source:MGI Symbol;Acc:MGI:97822]		P32507	-2.2	5.9E-04	9.6	2.2E-02	3.2	3.7E-01	0.2	9.1E-01
ENSMUST00000108459	kinesin light chain 3 [Source:MGI Symbol;Acc:MGI:1277971]		Q91W40	6.1	2.2E-02	-4.5	8.8E-02	1.7	2.0E-01	0.4	8.8E-01
ENSMUST00000107062	nuclear factor I/A [Source:MGI Symbol;Acc:MGI:108056]	B1AUC0		-3.5	5.9E-02	-1.3	5.7E-01	1.4	3.5E-01	-0.8	7.3E-01
ENSMUST00000107070	PDZ domain containing 1 [Source:MGI Symbol;Acc:MGI:1928901]			2.9	2.8E-01	4.0	1.6E-01	-0.4	8.8E-01	-1.6	4.3E-01
ENSMUST00000108470	transient receptor potential cation channel, subfamily V, member 1 [Source:MGI Symbol;Acc:MGI:1341787]	Z4YKR8		7.5	1.8E-03	4.1	5.9E-04	-2.9	9.1E-03	-1.4	5.7E-02
ENSMUST00000108473	dystrophia myotonica-protein kinase [Source:MGI Symbol;Acc:MGI:94906]		P54265	6.6	6.1E-04	3.1	5.2E-02	5.7	7.2E-04	-2.2	1.2E-01
ENSMUST00000107077	protein inhibitor of activated STAT 3 [Source:MGI Symbol;Acc:MGI:1913126]		O54714	-2.7	6.2E-02	-3.6	7.6E-02	0.6	5.2E-01	1.5	4.2E-01
ENSMUST00000108477	Tax1 (human T cell leukemia virus type I) binding protein 3 [Source:MGI Symbol;Acc:MGI:1923531]	B1AUD9		-8.4	4.4E-05	3.3	6.1E-03	-3.4	1.5E-02	0.0	9.5E-01
ENSMUST00000108482	pregnancy-specific glycoprotein 20 [Source:MGI Symbol;Acc:MGI:1891352]	E9Q6J6		5.1	1.1E-02	6.5	7.5E-04	-0.5	7.0E-01	-1.1	1.8E-01
ENSMUST00000108485	ATPase, Ca++ transporting, ubiquitous [Source:MGI Symbol;Acc:MGI:1194503]	Q8R0X5	Q64518	-6.8	8.3E-03	-2.7	6.3E-04	1.5	8.1E-04	-0.5	4.2E-01
ENSMUST00000108487	carcinoembryonic antigen-related cell adhesion molecule 12 [Source:MGI Symbol;Acc:MGI:1914565]	Q3V2Q3		3.8	8.1E-03	-8.8	6.3E-05	-0.4	3.6E-01	-2.5	1.6E-01
ENSMUST00000107100	microtubule-associated protein 6 [Source:MGI Symbol;Acc:MGI:1201690]		Q7TSJ2	1.6	3.4E-01	1.2	5.3E-01	-0.4	7.9E-01	0.0	9.9E-01
ENSMUST00000108491	carcinoembryonic antigen-related cell adhesion molecule 3 [Source:MGI Symbol;Acc:MGI:3646296]	E9Q6J4		8.5	1.7E-05	-3.2	2.4E-02	0.8	2.4E-01	-0.7	5.9E-01
ENSMUST00000108492	hypoxia inducible factor 3, alpha subunit [Source:MGI Symbol;Acc:MGI:1859778]		Q0VBL6	8.9	8.8E-06	4.5	2.3E-02	-1.9	3.1E-01	0.1	9.0E-01
ENSMUST00000107117	upstream binding transcription factor, RNA polymerase I [Source:MGI Symbol;Acc:MGI:98512]	A2AWT6		-0.6	8.1E-01	-1.1	7.2E-01	-0.4	8.7E-01	0.2	9.5E-01
ENSMUST00000108493	dapper homolog 3, antagonist of beta-catenin (xenopus) [Source:MGI Symbol;Acc:MGI:3654828]		Q0PHV7	6.6	1.3E-04	-6.0	5.0E-05	0.4	2.5E-01	-1.0	2.8E-01
ENSMUST00000108495	striatin, calmodulin binding protein 4 [Source:MGI Symbol;Acc:MGI:2142346]		P58404	-7.4	7.2E-05	-6.3	4.2E-04	0.5	2.1E-01	-0.7	6.1E-01
ENSMUST00000108498	carcinoembryonic antigen-related cell adhesion molecule 15 [Source:MGI Symbol;Acc:MGI:2141810]	A0A0B4J1L0		6.4	3.8E-04	1.4	5.3E-01	-4.4	8.1E-02	2.7	1.7E-01
ENSMUST00000107134	ataxin 7-like 3 [Source:MGI Symbol;Acc:MGI:3036270]		A2AWT3	-2.2	3.8E-02	-3.1	6.2E-02	1.3	1.2E-01	2.3	1.5E-01
ENSMUST00000108500	smoothelin-like 2 [Source:MGI Symbol;Acc:MGI:2442764]	Q5F247		8.5	7.5E-05	6.9	1.2E-03	-0.9	5.8E-01	1.0	2.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000108502	tektin 1 [Source:MGI Symbol;Acc:MGI:1333819]	Q5NBU4	Q9DAJ2	6.6	6.2E-04	-3.7	1.8E-01	3.1	2.1E-02	-0.6	8.4E-01
ENSMUST00000108504	F-box protein 39 [Source:MGI Symbol;Acc:MGI:3505735]		Q5NBU5	6.0	1.4E-04	2.5	3.7E-02	0.4	6.7E-01	0.4	6.6E-01
ENSMUST00000108505	RIKEN cDNA 4933427D14 gene [Source:MGI Symbol;Acc:MGI:1921727]	A6QRF1		4.3	1.3E-02	-7.0	4.7E-04	1.1	2.2E-02	-0.6	6.7E-01
ENSMUST00000107153	remodeling and spacing factor 1 [Source:MGI Symbol;Acc:MGI:2682305]	E9Q4Y2		0.7	2.6E-01	1.1	1.9E-01	0.5	3.8E-01	0.1	8.7E-01
ENSMUST00000108506	RIKEN cDNA 4933427D14 gene [Source:MGI Symbol;Acc:MGI:1921727]			8.2	5.7E-05	7.1	2.6E-04	-0.7	5.9E-01	0.1	9.4E-01
ENSMUST00000108508	PITPNM family member 3 [Source:MGI Symbol;Acc:MGI:2685726]		Q3UHE1	9.1	2.7E-03	5.8	2.1E-02	-0.8	7.2E-01	0.5	6.9E-01
ENSMUST00000107158	ute carrier family 24 (sodium/potassium/calcium exchanger), member 2 [Source:MGI Symbol;Acc:MGI:19236	Q14BI1		4.5	1.7E-01	7.5	4.2E-02	-0.1	9.7E-01	-3.1	1.2E-01
ENSMUST00000108509	zinc finger protein 541 [Source:MGI Symbol;Acc:MGI:3647699]		Q0GGX2	4.3	5.8E-04	-1.1	3.2E-01	-0.5	5.3E-01	-2.1	1.1E-01
ENSMUST00000107161	aryl hydrocarbon receptor nuclear translocator [Source:MGI Symbol;Acc:MGI:88071]	Q8CEC2		4.1	1.8E-01	2.0	6.4E-01	0.1	9.7E-01	2.3	4.5E-01
ENSMUST00000108513	oocyte specific homeobox 6 [Source:MGI Symbol;Acc:MGI:2149036]	G3X9U1		6.1	2.7E-04	5.6	5.0E-02	-0.5	8.5E-01	1.4	3.3E-01
ENSMUST00000107163	CD300 antigen like family member G [Source:MGI Symbol;Acc:MGI:1289168]		Q1ERP8	3.1	1.8E-01	2.1	4.8E-01	0.0	1.0E+00	1.0	6.6E-01
ENSMUST00000108515	NLR family, pyrin domain containing 1B [Source:MGI Symbol;Acc:MGI:3582959]	A1Z198		-3.2	1.2E-02	3.0	3.7E-01	-0.9	7.6E-01	2.9	2.7E-01
ENSMUST00000108530	nucleoporin 88 [Source:MGI Symbol;Acc:MGI:104900]	Q5QNU0	Q8CEC0	-7.5	1.3E-05	9.7	5.0E-04	-0.9	6.5E-01	-0.7	4.3E-01
ENSMUST00000108531	nucleoporin 88 [Source:MGI Symbol;Acc:MGI:104900]		Q8CEC0	-4.8	3.4E-04	3.9	1.2E-03	-2.3	2.3E-02	-0.1	8.9E-01
ENSMUST00000108536	zinc finger protein 446 [Source:MGI Symbol;Acc:MGI:2442185]	G3X9U2		4.5	1.3E-02	6.4	9.2E-06	-1.5	9.7E-02	-0.7	1.6E-01
ENSMUST00000108537	zinc finger protein 446 [Source:MGI Symbol;Acc:MGI:2442185]	Q149D4		8.8	1.1E-04	7.5	2.8E-04	0.1	9.2E-01	-0.5	4.5E-01
ENSMUST00000107170	SET domain, bifurcated 1 [Source:MGI Symbol;Acc:MGI:1934229]	D3YYC3		-2.7	7.7E-02	-4.7	1.2E-01	1.1	4.5E-01	3.1	2.5E-01
ENSMUST00000107171	SET domain, bifurcated 1 [Source:MGI Symbol;Acc:MGI:1934229]	G5E8N3		-4.1	1.6E-01	-5.2	1.4E-01	-2.1	2.2E-01	-1.0	7.8E-01
ENSMUST00000108544	calmodulin binding transcription activator 2 [Source:MGI Symbol;Acc:MGI:2135957]		Q80Y50	2.7	2.3E-02	5.4	2.9E-02	-0.7	7.6E-01	1.6	2.2E-01
ENSMUST00000108545	calmodulin binding transcription activator 2 [Source:MGI Symbol;Acc:MGI:2135957]		Q80Y50	-5.2	4.9E-03	7.4	1.2E-02	-1.5	5.9E-01	-1.6	2.9E-01
ENSMUST00000108550	vomeronasal 2, receptor 49 [Source:MGI Symbol;Acc:MGI:3757933]	D3Z6L3		5.9	2.6E-04	-3.1	8.0E-03	0.8	1.3E-01	-2.6	3.5E-02
ENSMUST00000108551	glycoprotein 1b, alpha polypeptide [Source:MGI Symbol;Acc:MGI:1333744]	A2CFB8	O35930	6.0	2.9E-03	6.3	1.5E-03	-0.6	7.1E-01	-1.1	2.0E-01
ENSMUST00000108554	vomeronasal 2, receptor 38 [Source:MGI Symbol;Acc:MGI:3757869]	G3UYA8		6.1	1.2E-02	7.9	1.1E-04	-1.6	2.6E-01	0.4	5.1E-01
ENSMUST00000108556	phospholipase D2 [Source:MGI Symbol;Acc:MGI:892877]	Q80ZW1		8.0	3.1E-06	6.0	2.3E-03	-0.4	8.0E-01	-1.5	1.2E-01
ENSMUST00000108557	phospholipase D2 [Source:MGI Symbol;Acc:MGI:892877]	Q6NV49		5.1	2.6E-02	3.9	2.4E-02	-0.1	9.6E-01	-1.2	2.4E-01
ENSMUST00000107198	basonuclin 2 [Source:MGI Symbol;Acc:MGI:2443805]	H3BIU2		3.1	2.3E-01	3.0	2.6E-01	-1.3	6.3E-01	-1.3	4.9E-01
ENSMUST00000108560	zinc finger protein 583 [Source:MGI Symbol;Acc:MGI:2682297]		Q3V080	6.1	2.3E-04	-5.5	4.5E-02	1.1	2.7E-01	-1.0	7.2E-01
ENSMUST00000107200	CDC42 small effector 1 [Source:MGI Symbol;Acc:MGI:1889510]	D3YUZ5		0.0	1.0E+00	2.2	4.2E-01	0.3	9.1E-01	-1.9	4.0E-01
ENSMUST00000107201	CDC42 small effector 1 [Source:MGI Symbol;Acc:MGI:1889510]		Q8BHL7	-6.1	5.8E-02	-6.6	6.6E-02	-0.5	6.6E-01	0.0	9.9E-01
ENSMUST00000108563	zinc finger, MYND-type containing 15 [Source:MGI Symbol;Acc:MGI:3603821]		Q8C0R7	6.3	2.3E-03	7.3	2.1E-05	0.6	5.4E-01	-0.7	2.2E-01
ENSMUST00000107205	CREB/ATF bZIP transcription factor [Source:MGI Symbol;Acc:MGI:2675296]	D3YUZ4		-0.8	5.3E-01	1.2	2.8E-01	-0.7	4.8E-01	-2.6	4.8E-02
ENSMUST00000108566	zinc finger protein 444 [Source:MGI Symbol;Acc:MGI:1923365]	Q3TDV8		-5.6	2.9E-04	-1.6	4.1E-01	1.7	1.5E-01	-0.3	8.5E-01
ENSMUST00000108568	arrestin, beta 2 [Source:MGI Symbol;Acc:MGI:99474]	J3JS97	Q91YI4	-8.7	9.7E-05	6.3	2.2E-03	-0.7	6.8E-01	0.0	9.8E-01
ENSMUST00000108569	vomeronasal 1 receptor 58 [Source:MGI Symbol;Acc:MGI:3033473]	G3X9U3		8.3	6.9E-07	-5.1	1.3E-02	0.8	2.8E-01	-0.9	6.3E-01
ENSMUST00000108574	arachidonate 12-lipoxygenase [Source:MGI Symbol;Acc:MGI:87998]	Q8C587		4.9	6.6E-04	-3.5	9.6E-02	2.1	5.8E-02	-0.6	7.6E-01
ENSMUST00000107210	synaptotagmin-like 2 [Source:MGI Symbol;Acc:MGI:1933366]		Q99N50	1.5	2.6E-01	3.6	2.9E-03	-3.0	1.7E-02	-5.1	6.0E-04
ENSMUST00000107211	synaptotagmin-like 2 [Source:MGI Symbol;Acc:MGI:1933366]		Q99N50	4.4	9.9E-02	1.7	6.1E-01	-0.2	9.4E-01	2.5	3.4E-01
ENSMUST00000107212	neighbor of Brca1 gene 1 [Source:MGI Symbol;Acc:MGI:108498]	A2A4N7		-2.0	4.3E-01	2.0	5.9E-01	3.9	1.7E-01	0.0	1.0E+00
ENSMUST00000108578	RIKEN cDNA 0610010K14 gene [Source:MGI Symbol;Acc:MGI:1915609]		Q9DCT6	-4.0	1.9E-02	-7.6	2.5E-04	0.0	9.2E-01	-0.7	6.1E-01
ENSMUST00000107214	PC4 and SFRS1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2142116]	A2BI12		-2.7	4.8E-01	-1.5	7.5E-01	0.3	9.2E-01	-0.8	8.6E-01
ENSMUST00000107215	PC4 and SFRS1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2142116]		Q99JF8	-1.0	6.9E-01	-3.4	3.3E-01	-1.7	4.2E-01	0.7	8.3E-01
ENSMUST00000108583	suppressor of variegation 4-20 homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2385262]		Q6Q783	-5.2	2.4E-03	7.0	1.4E-03	-0.7	6.7E-01	0.1	8.9E-01
ENSMUST00000107233	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha [Source:MGI Symbol;Acc:MGI:107929]		P70182	-2.0	1.5E-01	-4.3	1.0E-01	0.4	6.7E-01	2.8	2.6E-01
ENSMUST00000108585	asialoglycoprotein receptor 1 [Source:MGI Symbol;Acc:MGI:88081]	B1AR34		6.5	4.3E-03	-3.4	3.4E-03	0.8	9.2E-02	-0.4	6.5E-01
ENSMUST00000107236	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha [Source:MGI Symbol;Acc:MGI:107929]		P70182	-3.5	1.3E-01	-0.5	8.4E-01	0.1	9.7E-01	-2.9	2.4E-01
ENSMUST00000108589	discs, large homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1277959]		Q62108	7.6	5.8E-05	-6.0	4.8E-04	0.3	4.4E-01	0.3	8.1E-01
ENSMUST00000108590	glycoprotein 6 (platelet) [Source:MGI Symbol;Acc:MGI:1889810]		P0C191	3.3	4.9E-03	2.5	5.1E-01	-0.8	8.2E-01	3.9	1.9E-01
ENSMUST00000107249	ribosomal protein L27 [Source:MGI Symbol;Acc:MGI:98036]	Q5BLJ9	P61358	-0.7	2.9E-01	-1.4	9.7E-02	-1.4	3.1E-02	-0.7	3.9E-01
ENSMUST00000107256	RAB38, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1919683]	Q5FW76	Q8QZZ8	2.0	3.7E-02	4.3	7.8E-03	2.5	5.3E-02	0.2	7.7E-01
ENSMUST00000108592	gamma-aminobutyric acid receptor associated protein [Source:MGI Symbol;Acc:MGI:1861742]	B1AR50		-11.5	2.7E-06	4.9	4.2E-04	-2.5	3.4E-02	-0.8	2.2E-01
ENSMUST00000107266	pogo transposable element with ZNF domain [Source:MGI Symbol;Acc:MGI:2442117]	D3YUX1		2.2	2.7E-01	4.6	6.4E-02	0.6	7.5E-01	-1.8	3.8E-01
ENSMUST00000107269	pogo transposable element with ZNF domain [Source:MGI Symbol;Acc:MGI:2442117]	D3YUW8		-2.3	1.5E-01	-0.9	7.3E-01	4.4	1.9E-02	3.0	2.5E-01
ENSMUST00000107270	pogo transposable element with ZNF domain [Source:MGI Symbol;Acc:MGI:2442117]	B9EIG6	Q8BZH4	4.2	7.1E-02	5.0	8.5E-02	0.1	9.8E-01	-0.7	7.1E-01
ENSMUST00000107272	cingulin [Source:MGI Symbol;Acc:MGI:1927237]	D3YUW7		6.3	6.9E-02	2.9	3.5E-01	-2.7	4.3E-01	0.7	7.5E-01
ENSMUST00000107273	cingulin [Source:MGI Symbol;Acc:MGI:1927237]	E9QMC1		7.1	5.4E-02	6.2	1.1E-01	-0.8	8.3E-01	0.1	9.7E-01
ENSMUST00000108593	CTD nuclear envelope phosphatase 1 [Source:MGI Symbol;Acc:MGI:1914431]		Q3TP92	-3.4	1.3E-04	-2.1	8.1E-02	1.1	9.5E-02	0.8	5.1E-01
ENSMUST00000107284	enhancer of zeste homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1097695]		P70351	-2.0	3.0E-01	-3.3	1.7E-01	-1.2	4.3E-01	0.2	9.3E-01
ENSMUST00000108594	elongator acetyltransferase complex subunit 5 [Source:MGI Symbol;Acc:MGI:1859017]		Q99L85	-5.7	6.7E-04	-1.7	5.9E-02	0.8	1.2E-01	-0.7	4.0E-01
ENSMUST00000108608	eukaryotic translation initiation factor 5A [Source:MGI Symbol;Acc:MGI:106248]		P63242	-9.0	4.4E-05	6.8	2.0E-02	-0.5	8.6E-01	-1.8	2.3E-01
ENSMUST00000107295	family with sequence similarity 134, member C [Source:MGI Symbol;Acc:MGI:1915248]		Q9CQV4	-1.5	3.7E-01	3.3	1.3E-01	2.6	1.8E-01	-2.3	2.0E-01
ENSMUST00000108613	eukaryotic translation initiation factor 5A [Source:MGI Symbol;Acc:MGI:106248]		P63242	-9.8	1.0E-05	6.3	2.1E-03	-0.8	6.3E-01	1.6	7.9E-02
ENSMUST00000108615	paired-Ig-like receptor A2 [Source:MGI Symbol;Acc:MGI:1195970]	F8VQ94		-7.1	2.1E-06	-0.7	2.0E-01	1.9	6.3E-04	-4.7	2.0E-04
ENSMUST00000108622	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 [Source:MGI Symbol;Acc:MGI:2388270]	Q8CI47		-7.8	3.8E-06	-5.4	1.1E-02	0.2	8.0E-01	1.5	3.8E-01
ENSMUST00000108623	ribosomal protein S9 [Source:MGI Symbol;Acc:MGI:1924096]	Q9CXW7		-4.6	6.5E-04	4.4	8.1E-03	-0.6	6.6E-01	1.4	1.4E-01
ENSMUST00000107305	hepatoma-derived growth factor, related protein 3 [Source:MGI Symbol;Acc:MGI:1352760]		Q9JMG7	-0.6	4.5E-01	1.0	3.1E-01	0.7	3.4E-01	-0.9	3.4E-01
ENSMUST00000107308	Coenzyme A synthase [Source:MGI Symbol;Acc:MGI:1918993]		Q9DBL7	1.5	3.8E-02	1.8	6.9E-02	0.6	3.7E-01	0.4	5.9E-01
ENSMUST00000107337	transducin-like enhancer of split 1, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104636]		Q62440	-0.4	7.7E-01	0.9	5.8E-01	0.8	5.7E-01	-0.5	7.2E-01
ENSMUST00000107342	chromatin target of PRMT1 [Source:MGI Symbol;Acc:MGI:1913761]		Q9CY57	0.5	8.5E-01	-1.9	5.0E-01	-2.1	3.5E-01	0.3	9.1E-01
ENSMUST00000107344	chromatin target of PRMT1 [Source:MGI Symbol;Acc:MGI:1913761]		Q9CY57	-5.5	5.8E-02	1.9	6.3E-01	6.2	4.4E-02	-1.2	7.3E-01
ENSMUST00000108626	tyrosine kinase, non-receptor, 1 [Source:MGI Symbol;Acc:MGI:1930958]		Q99ML2	7.0	1.0E-04	5.5	5.0E-05	-0.7	3.9E-01	0.2	7.2E-01
ENSMUST00000108627	tRNA splicing endonuclease 34 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913328]		Q8BMZ5	-4.6	1.2E-02	-0.4	5.0E-01	0.8	8.6E-02	-0.2	7.3E-01
ENSMUST00000107356	signal transducer and activator of transcription 5A [Source:MGI Symbol;Acc:MGI:103036]	Q9JIA0	P42230	-1.5	3.1E-01	-1.6	5.0E-01	0.9	5.8E-01	1.1	5.9E-01
ENSMUST00000108628	tyrosine kinase, non-receptor, 1 [Source:MGI Symbol;Acc:MGI:1930958]	Q5F2B4		7.2	9.6E-04	-3.9	2.9E-02	0.4	6.0E-01	0.1	9.7E-01
ENSMUST00000108632	phospholipid scramblase 3 [Source:MGI Symbol;Acc:MGI:1917560]	Q5F283	Q9JIZ9	-4.4	1.9E-04	-3.0	7.6E-03	0.7	1.6E-01	-0.1	9.1E-01
ENSMUST00000107359	multiple EGF-like-domains 9 [Source:MGI Symbol;Acc:MGI:1918264]	Q0VGR4	Q8BH27	0.9	1.7E-01	1.4	1.2E-01	1.5	5.2E-02	0.9	2.1E-01
ENSMUST00000108634	neuroligin 2 [Source:MGI Symbol;Acc:MGI:2681835]		Q69ZK9	4.3	3.1E-04	-8.9	6.8E-03	1.3	8.7E-02	-0.6	8.4E-01
ENSMUST00000108636	PRP31 pre-mRNA processing factor 31 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916238]		Q8CCF0	-5.8	5.6E-05	5.7	2.9E-02	-0.7	7.8E-01	2.3	1.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000108639	zinc finger and BTB domain containing 4 [Source:MGI Symbol;Acc:MGI:1922830]	Q5F293	Q5F293	2.3	1.2E-03	-5.1	5.5E-03	0.7	3.1E-01	-2.1	2.1E-01
ENSMUST00000108648	tumor necrosis factor (ligand) superfamily, member 13 [Source:MGI Symbol;Acc:MGI:1916833]	Q5F2A3		4.0	3.1E-02	1.5	7.6E-02	-1.4	6.8E-02	0.0	9.8E-01
ENSMUST00000108653	NLR family, pyrin domain containing 12 [Source:MGI Symbol;Acc:MGI:2676630]		E9Q5R7	-4.4	2.4E-04	2.6	5.5E-03	0.5	3.9E-01	-0.2	6.9E-01
ENSMUST00000107368	unc-45 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:2142246]		Q99KD5	1.5	1.7E-01	2.1	1.9E-01	0.3	8.0E-01	-0.2	8.3E-01
ENSMUST00000107369	cAMP responsive element binding protein 3-like 4 [Source:MGI Symbol;Acc:MGI:1916603]		Q9D2A5	2.5	8.5E-02	2.0	1.9E-01	-1.3	3.5E-01	-0.8	5.5E-01
ENSMUST00000108659	dynein, axonemal, heavy chain 2 [Source:MGI Symbol;Acc:MGI:107731]	D3Z667		10.3	3.8E-03	6.7	2.3E-03	-0.7	6.9E-01	-1.8	8.5E-02
ENSMUST00000108665	guanylate cyclase 2e [Source:MGI Symbol;Acc:MGI:105123]		P52785	5.3	2.2E-02	8.8	7.9E-03	-0.9	7.5E-01	-2.4	1.2E-01
ENSMUST00000108671	Rho guanine nucleotide exchange factor (GEF) 15 [Source:MGI Symbol;Acc:MGI:3045246]		Q5FWH6	10.0	1.7E-03	4.5	3.9E-04	-2.8	1.7E-02	-1.3	6.2E-02
ENSMUST00000108674	netrin 1 [Source:MGI Symbol;Acc:MGI:105088]		O09118	9.1	9.6E-06	1.9	1.2E-01	0.0	1.0E+00	0.8	4.4E-01
ENSMUST00000108677	ubiquitin specific peptidase 43 [Source:MGI Symbol;Acc:MGI:2444541]	A6PWR8		7.2	5.2E-05	7.3	7.4E-05	-0.6	6.1E-01	0.5	3.4E-01
ENSMUST00000108682	growth arrest specific 7 [Source:MGI Symbol;Acc:MGI:1202388]	Q3U432		-1.9	2.7E-04	4.7	1.7E-02	-1.0	5.4E-01	-1.3	2.5E-01
ENSMUST00000108684	myosin, heavy polypeptide 13, skeletal muscle [Source:MGI Symbol;Acc:MGI:1339967]	B1AR69		6.6	2.5E-02	5.7	3.1E-04	1.2	2.3E-01	0.2	7.8E-01
ENSMUST00000108685	myosin, heavy polypeptide 8, skeletal muscle, perinatal [Source:MGI Symbol;Acc:MGI:1339712]	Q8BGE8		6.6	7.7E-05	-2.1	4.1E-02	-0.1	8.0E-01	-2.7	4.0E-02
ENSMUST00000108690	SCO cytochrome oxidase deficient homolog 1 (yeast) [Source:MGI Symbol;Acc:MGI:106362]	Q5SUD5		3.0	8.4E-05	4.5	7.3E-04	0.9	2.5E-01	0.0	9.7E-01
ENSMUST00000108695	myocardin [Source:MGI Symbol;Acc:MGI:2137495]		Q8VIM5	8.8	7.2E-05	-7.6	5.9E-05	0.3	3.2E-01	-0.5	6.9E-01
ENSMUST00000108703	tripartite motif-containing 16 [Source:MGI Symbol;Acc:MGI:2137356]		Q99PP9	-6.7	8.2E-05	5.4	1.3E-02	-1.2	4.9E-01	-0.6	5.7E-01
ENSMUST00000108707	ubiquitin C [Source:MGI Symbol;Acc:MGI:98889]	E9Q5F6		-4.6	5.6E-05	7.6	3.6E-05	-0.6	6.2E-01	0.0	9.8E-01
ENSMUST00000107396	ATPase, class I, type 8B, member 2 [Source:MGI Symbol;Acc:MGI:1859660]	D3YXQ5		1.2	7.4E-01	0.1	9.8E-01	-1.8	6.1E-01	-0.7	8.7E-01
ENSMUST00000107397	5'-nucleotidase, cytosolic IIIB [Source:MGI Symbol;Acc:MGI:1915356]		Q3UFY7	-3.6	1.5E-01	-2.4	2.6E-01	-2.1	1.7E-01	-3.3	2.1E-01
ENSMUST00000107398	5'-nucleotidase, cytosolic IIIB [Source:MGI Symbol;Acc:MGI:1915356]		Q3UFY7	3.3	1.0E-01	5.0	6.3E-02	1.0	6.9E-01	-0.7	6.4E-01
ENSMUST00000107399	5'-nucleotidase, cytosolic IIIB [Source:MGI Symbol;Acc:MGI:1915356]		Q3UFY7	4.8	8.3E-02	4.4	1.5E-01	-0.6	8.3E-01	-0.2	9.1E-01
ENSMUST00000107403	junction plakoglobin [Source:MGI Symbol;Acc:MGI:96650]		Q02257	2.7	2.1E-01	4.5	8.1E-02	0.3	8.7E-01	-1.5	4.6E-01
ENSMUST00000108710	A kinase (PRKA) anchor protein 10 [Source:MGI Symbol;Acc:MGI:1890218]		O88845	3.5	3.1E-04	-1.7	3.5E-01	0.8	4.7E-01	-2.2	2.8E-01
ENSMUST00000108712	epsin 2 [Source:MGI Symbol;Acc:MGI:1333766]	Q5NCM5		6.3	3.3E-02	6.3	1.5E-02	-0.8	7.4E-01	-1.3	3.2E-01
ENSMUST00000108714	mitogen-activated protein kinase 7 [Source:MGI Symbol;Acc:MGI:1346347]		Q9WVS8	-6.1	8.0E-05	1.6	8.9E-02	-1.3	1.1E-01	0.0	9.5E-01
ENSMUST00000108716	aldehyde dehydrogenase family 3, subfamily A1 [Source:MGI Symbol;Acc:MGI:1353451]		P47739	6.0	7.0E-04	3.5	6.9E-04	-3.9	1.6E-03	0.4	4.4E-01
ENSMUST00000108718	dehydrogenase/reductase (SDR family) member 7B [Source:MGI Symbol;Acc:MGI:2384931]	Z4YKT6		4.8	2.6E-05	-4.0	5.0E-02	1.9	5.3E-02	1.1	5.7E-01
ENSMUST00000108722	leucine rich repeat containing 48 [Source:MGI Symbol;Acc:MGI:1921915]	F6Q537		6.0	2.6E-04	8.0	3.6E-04	0.8	5.8E-01	0.5	4.4E-01
ENSMUST00000108747	coiled-coil domain containing 7A [Source:MGI Symbol;Acc:MGI:1921953]	G3X9U4		7.5	2.5E-05	7.2	1.1E-04	-0.6	6.1E-01	-0.4	5.0E-01
ENSMUST00000108751	myosin phosphatase Rho interacting protein [Source:MGI Symbol;Acc:MGI:1349438]		P97434	-4.9	5.3E-04	-5.2	5.2E-03	1.6	4.7E-02	-2.3	2.6E-01
ENSMUST00000108759	solute carrier family 35, member F3 [Source:MGI Symbol;Acc:MGI:2444426]		Q1LZI2	6.3	4.4E-05	6.8	1.4E-04	-0.6	6.0E-01	-1.1	1.1E-01
ENSMUST00000108768	opioid receptor-like 1 [Source:MGI Symbol;Acc:MGI:97440]	Q542U1	P35377	7.6	1.6E-02	-4.6	4.3E-04	1.1	1.7E-02	0.2	7.9E-01
ENSMUST00000107421	apoptosis enhancing nuclease [Source:MGI Symbol;Acc:MGI:1915298]		Q9CZI9	-1.2	4.7E-01	-1.5	4.9E-01	0.0	9.8E-01	0.3	8.8E-01
ENSMUST00000107423	apoptosis enhancing nuclease [Source:MGI Symbol;Acc:MGI:1915298]		Q9CZI9	2.8	2.2E-01	2.0	5.1E-01	-0.5	8.4E-01	0.2	9.3E-01
ENSMUST00000108769	regulator of G-protein signaling 19 [Source:MGI Symbol;Acc:MGI:1915153]	B7ZCT0		-7.5	9.0E-05	3.7	2.0E-01	0.5	8.6E-01	2.3	2.5E-01
ENSMUST00000108772	regulator of G-protein signaling 19 [Source:MGI Symbol;Acc:MGI:1915153]	Q8BFU4		-3.7	3.9E-03	0.1	9.3E-01	0.6	4.7E-01	-2.3	8.5E-02
ENSMUST00000108775	signal-induced proliferation-associated 1 like 2 [Source:MGI Symbol;Acc:MGI:2676970]		Q80TE4	-2.4	4.4E-04	-5.0	1.9E-01	1.7	3.9E-01	0.3	9.5E-01
ENSMUST00000108776	regulator of G-protein signaling 19 [Source:MGI Symbol;Acc:MGI:1915153]	Q78NN4	Q9CX84	-3.6	1.0E-02	-7.6	7.4E-03	1.6	3.3E-02	4.5	7.1E-02
ENSMUST00000108778	regulator of G-protein signaling 19 [Source:MGI Symbol;Acc:MGI:1915153]	B7ZCT1		-5.9	4.3E-06	3.7	3.8E-02	-0.7	6.6E-01	2.3	6.6E-02
ENSMUST00000107435	zinc finger and BTB domain containing 7B [Source:MGI Symbol;Acc:MGI:102755]	Q5BJ24	Q64321	0.6	4.1E-01	1.8	7.4E-02	1.1	1.7E-01	-0.2	8.0E-01
ENSMUST00000108783	wingless-type MMTV integration site family, member 9A [Source:MGI Symbol;Acc:MGI:2446084]		Q8R5M2	7.3	5.4E-03	5.5	6.5E-04	-0.5	6.7E-01	-0.3	6.1E-01
ENSMUST00000108790	gap junction protein, gamma 2 [Source:MGI Symbol;Acc:MGI:2153060]		Q8BQU6	6.7	3.0E-04	6.0	1.6E-03	-0.6	7.0E-01	0.1	9.4E-01
ENSMUST00000108793	gap junction protein, gamma 2 [Source:MGI Symbol;Acc:MGI:2153060]		Q8BQU6	5.1	3.0E-02	6.7	8.1E-04	-0.7	6.4E-01	0.2	8.4E-01
ENSMUST00000107444	aminolevulinate, delta-, dehydratase [Source:MGI Symbol;Acc:MGI:96853]		P10518	4.1	5.1E-02	6.8	8.6E-03	-0.4	8.7E-01	-3.0	3.1E-02
ENSMUST00000108797	DnaJ (Hsp40) homolog, subfamily C, member 5 [Source:MGI Symbol;Acc:MGI:892995]		P60904	-5.5	2.4E-04	6.5	1.6E-04	-0.6	6.0E-01	-0.7	2.5E-01
ENSMUST00000108799	tumor protein D52-like 2 [Source:MGI Symbol;Acc:MGI:1913564]	A2AUD5		-7.5	2.2E-05	-6.3	8.9E-03	0.8	2.5E-01	-0.1	9.6E-01
ENSMUST00000108808	ADP-ribosylation factor related protein 1 [Source:MGI Symbol;Acc:MGI:1923938]		Q8BXL7	-5.8	7.1E-05	6.7	1.6E-04	-2.0	1.3E-01	-0.9	1.7E-01
ENSMUST00000108809	tripartite motif-containing 11 [Source:MGI Symbol;Acc:MGI:2137355]	A2AB83		-3.0	1.6E-03	5.6	2.7E-04	-0.9	3.4E-01	-0.2	7.4E-01
ENSMUST00000108810	tripartite motif-containing 11 [Source:MGI Symbol;Acc:MGI:2137355]		Q99PQ2	-6.0	2.6E-04	3.7	6.9E-03	-3.2	3.4E-02	-0.3	7.2E-01
ENSMUST00000108825	predicted gene 12253 [Source:MGI Symbol;Acc:MGI:3651568]	Q5NC48		4.7	4.9E-05	3.2	2.0E-03	0.6	4.1E-01	-0.5	4.6E-01
ENSMUST00000108826	LY6/PLAUR domain containing 8 [Source:MGI Symbol;Acc:MGI:1917413]		Q9D7S0	6.2	1.6E-02	-2.3	8.3E-02	0.4	5.5E-01	-0.8	5.1E-01
ENSMUST00000108828	activating transcription factor 7 [Source:MGI Symbol;Acc:MGI:2443472]	Q3U2X8	Q8R0S1	6.5	2.3E-04	5.2	2.4E-04	-2.0	7.4E-02	-0.3	6.3E-01
ENSMUST00000108831	helicase with zinc finger 2, transcriptional coactivator [Source:MGI Symbol;Acc:MGI:2385169]		E9QAM5	-7.6	6.0E-04	6.5	4.5E-04	-0.6	6.6E-01	0.0	9.5E-01
ENSMUST00000107467	solute carrier family 31, member 2 [Source:MGI Symbol;Acc:MGI:1333844]	Q9D524		-4.1	5.1E-02	-3.2	1.4E-01	-0.3	7.4E-01	-1.2	6.0E-01
ENSMUST00000108834	RIKEN cDNA 4930438A08 gene [Source:MGI Symbol;Acc:MGI:1921238]	Q5SPH3		-5.7	4.7E-07	-1.7	3.6E-02	0.9	7.0E-02	-0.5	5.1E-01
ENSMUST00000107474	retinoic acid receptor, alpha [Source:MGI Symbol;Acc:MGI:97856]	Q3U3R3	P11416	-4.5	4.0E-02	-4.0	1.5E-01	0.2	8.7E-01	-0.3	9.1E-01
ENSMUST00000108838	poly(rC) binding protein 2 [Source:MGI Symbol;Acc:MGI:108202]		Q61990	-9.3	1.3E-04	-7.0	1.7E-04	0.7	9.2E-02	0.6	6.1E-01
ENSMUST00000107476	myocyte enhancer factor 2A [Source:MGI Symbol;Acc:MGI:99532]		Q60929	-1.3	2.5E-01	-3.0	1.2E-01	-0.2	8.5E-01	1.5	4.0E-01
ENSMUST00000108840	transcription factor 25 (basic helix-loop-helix) [Source:MGI Symbol;Acc:MGI:1914105]		Q8R3L2	-3.3	3.6E-04	4.4	1.3E-01	0.4	8.8E-01	2.4	1.9E-01
ENSMUST00000108841	l differentiation and proliferation factor homolog (zebrafish)RIKEN cDNA 2700038C09 gene [Source:MGI Sy		Q9CR37	-5.6	1.0E-04	8.8	7.7E-06	0.2	8.7E-01	1.1	3.2E-02
ENSMUST00000107482	pyruvate kinase liver and red blood cell [Source:MGI Symbol;Acc:MGI:97604]	E9Q509		2.1	3.4E-01	4.4	5.2E-02	-1.4	5.2E-01	-3.7	4.9E-02
ENSMUST00000108849	microfibrillar-associated protein 3 [Source:MGI Symbol;Acc:MGI:1924068]			-4.5	5.9E-03	-3.6	2.6E-03	1.3	1.7E-02	0.3	7.3E-01
ENSMUST00000108853	glycine receptor, alpha 1 subunit [Source:MGI Symbol;Acc:MGI:95747]	Q5NCU0		4.7	2.8E-03	7.1	8.0E-05	0.1	9.0E-01	0.3	6.3E-01
ENSMUST00000108857	ATX1 (antioxidant protein 1) homolog 1 (yeast) [Source:MGI Symbol;Acc:MGI:1333855]		O08997	-6.3	4.2E-05	-6.6	1.3E-04	-0.2	5.2E-01	-0.4	7.3E-01
ENSMUST00000107495	TM2 domain containing 3 [Source:MGI Symbol;Acc:MGI:1915884]		Q8BJ83	-3.9	1.0E-01	-4.2	1.4E-01	-1.3	3.4E-01	-1.1	7.2E-01
ENSMUST00000107498	gon-4-like (C.elegans) [Source:MGI Symbol;Acc:MGI:1917579]	E9Q507		3.8	1.9E-01	3.0	3.4E-01	-2.6	4.0E-01	-1.8	4.5E-01
ENSMUST00000107503	synaptotagmin XI [Source:MGI Symbol;Acc:MGI:1859547]	D3YWW9		3.2	1.4E-01	3.4	1.7E-01	0.3	9.0E-01	0.1	9.7E-01
ENSMUST00000107505	synaptotagmin XI [Source:MGI Symbol;Acc:MGI:1859547]		Q9R0N3	0.3	8.9E-01	2.1	4.1E-01	1.4	5.5E-01	-0.5	8.0E-01
ENSMUST00000108858	secreted acidic cysteine rich glycoprotein [Source:MGI Symbol;Acc:MGI:98373]	Q5NCU4		2.6	3.4E-02	7.0	9.9E-04	-0.8	6.4E-01	0.5	5.7E-01
ENSMUST00000108859	ADP-ribosylation factor GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2183559]		Q9EPJ9	4.9	3.1E-02	2.6	1.6E-01	-1.2	5.1E-01	2.1	1.2E-01
ENSMUST00000108861	ADP-ribosylation factor GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2183559]	Q3TGS9		-4.2	1.2E-03	-1.1	4.5E-01	-4.7	4.5E-03	1.0	4.4E-01
ENSMUST00000108864	FAT tumor suppressor homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685369]		Q5F226	7.3	2.9E-02	7.5	1.6E-03	-0.1	9.4E-01	0.8	3.3E-01
ENSMUST00000108878	basic helix-loop-helix family, member e23 [Source:MGI Symbol;Acc:MGI:2153710]	Q0VEJ8	Q8BGW3	7.2	4.1E-05	0.2	8.4E-01	4.2	8.6E-04	-1.0	4.2E-01
ENSMUST00000108880	coiled-coil domain containing 69 [Source:MGI Symbol;Acc:MGI:1196234]		Q3TCJ8	2.5	1.3E-02	5.1	9.8E-03	-0.2	8.9E-01	1.2	2.4E-01
ENSMUST00000107528	hydroxysteroid dehydrogenase like 2 [Source:MGI Symbol;Acc:MGI:1919729]	B1AX78		3.3	7.8E-02	2.2	2.0E-01	-3.4	7.8E-02	-2.3	1.0E-01
ENSMUST00000107531	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI	D3YWV5		-3.0	1.3E-01	0.6	8.3E-01	2.5	2.4E-01	-1.0	6.4E-01
ENSMUST00000107537	ubiquitin protein ligase E3A [Source:MGI Symbol;Acc:MGI:105098]		O08759	0.7	2.5E-01	0.5	6.0E-01	0.9	2.0E-01	1.1	1.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000108883	annexin A6 [Source:MGI Symbol;Acc:MGI:88255]		P14824	-8.0	1.3E-05	-3.1	6.1E-02	0.7	3.9E-01	-1.4	3.8E-01
ENSMUST00000107539	cyclin-dependent kinase 12 [Source:MGI Symbol;Acc:MGI:1098802]		Q14AX6	-0.5	4.2E-01	1.1	1.8E-01	1.3	5.0E-02	-0.3	6.9E-01
ENSMUST00000108886	TNFAIP3 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1926194]		Q9WUU8	-4.7	9.9E-03	6.2	6.4E-05	1.6	7.9E-02	-0.1	8.8E-01
ENSMUST00000107544	sushi domain containing 1 [Source:MGI Symbol;Acc:MGI:3651543]	A2AN91		3.7	1.2E-01	-2.1	4.5E-01	-3.9	1.0E-01	1.9	4.6E-01
ENSMUST00000107545	mediator complex subunit 1 [Source:MGI Symbol;Acc:MGI:1100846]		Q925J9	-0.7	1.5E-01	0.1	8.2E-01	0.7	1.3E-01	-0.1	8.1E-01
ENSMUST00000108889	TNFAIP3 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1926194]	E9QM75		-5.6	3.5E-03	6.4	1.6E-04	-1.4	2.6E-01	-0.7	2.8E-01
ENSMUST00000108891	CDK5 and Abl enzyme substrate 2 [Source:MGI Symbol;Acc:MGI:2182335]		Q8K3M5	-2.5	4.9E-03	6.0	1.4E-02	-0.8	7.3E-01	-0.7	5.8E-01
ENSMUST00000108905	acyl-CoA synthetase long-chain family member 6 [Source:MGI Symbol;Acc:MGI:894291]	Q5F2D0	Q91WC3	5.4	4.1E-04	6.9	9.5E-05	-1.5	2.2E-01	-0.7	2.4E-01
ENSMUST00000108908	sodium channel, voltage-gated, type VIII, alpha [Source:MGI Symbol;Acc:MGI:103169]	F7D6K4		5.5	1.2E-02	4.4	3.0E-03	-1.4	2.2E-01	-0.4	5.7E-01
ENSMUST00000108912	cadherin-like 26 [Source:MGI Symbol;Acc:MGI:2685856]	Q3V1P3		7.8	3.4E-05	2.7	8.4E-02	-0.4	7.5E-01	0.0	9.8E-01
ENSMUST00000107559	myocyte enhancer factor 2D [Source:MGI Symbol;Acc:MGI:99533]		Q63943	2.6	2.0E-01	2.1	4.9E-01	1.4	4.9E-01	1.9	4.9E-01
ENSMUST00000108917	phosphatase and actin regulator 3 [Source:MGI Symbol;Acc:MGI:1921439]	A2AHM4		7.2	1.4E-04	6.1	3.5E-03	-0.7	6.7E-01	0.1	9.5E-01
ENSMUST00000108920	interferon regulatory factor 1 [Source:MGI Symbol;Acc:MGI:96590]	Q5SX13	P15314	-9.2	2.7E-06	2.0	3.7E-02	-0.5	5.2E-01	0.2	7.3E-01
ENSMUST00000108922	interferon regulatory factor 1 [Source:MGI Symbol;Acc:MGI:96590]	Q3U5M1		5.0	1.8E-03	5.2	1.1E-02	-0.7	6.9E-01	1.7	1.1E-01
ENSMUST00000108925	ethanol induced 1 [Source:MGI Symbol;Acc:MGI:1261426]	Q3V498		-4.1	1.3E-03	4.6	4.0E-04	-1.5	1.3E-01	-1.4	4.5E-02
ENSMUST00000108926	ethanol induced 1 [Source:MGI Symbol;Acc:MGI:1261426]	A2BFG8		-4.1	3.4E-04	3.4	1.3E-03	-0.7	3.1E-01	0.4	5.5E-01
ENSMUST00000108934	RIKEN cDNA C330013J21 gene [Source:MGI Symbol;Acc:MGI:1925953]	A2AW64		10.0	3.1E-04	2.2	2.8E-01	-3.2	1.3E-01	0.1	9.7E-01
ENSMUST00000107583	CDGSH iron sulfur domain 3 [Source:MGI Symbol;Acc:MGI:101788]		B1AR13	0.8	4.3E-01	0.1	9.1E-01	-1.0	2.9E-01	-0.4	7.2E-01
ENSMUST00000107586	ıoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6 [Source:MGI Symbol;Acc:I	B1AR10		3.6	1.5E-01	2.9	2.0E-01	-1.9	4.0E-01	-1.2	5.4E-01
ENSMUST00000108951	RIKEN cDNA 6430548M08 gene [Source:MGI Symbol;Acc:MGI:2443793]	Q3TA40		-5.9	1.5E-05	7.2	5.4E-05	-0.6	6.1E-01	-0.1	9.1E-01
ENSMUST00000108959	predicted gene 14412 [Source:MGI Symbol;Acc:MGI:3652251]	A2ARR7		6.7	6.5E-04	2.6	2.6E-03	-5.1	2.0E-04	-0.1	8.8E-01
ENSMUST00000108972	cysteine-rich secretory protein LCCL domain containing 2 [Source:MGI Symbol;Acc:MGI:1926142]		Q8BZQ2	7.8	8.6E-03	7.7	1.3E-04	-0.7	5.8E-01	-0.1	8.6E-01
ENSMUST00000109021	ubiquinol-cytochrome c reductase, complex III subunit VII [Source:MGI Symbol;Acc:MGI:107807]		Q9CQ69	-6.6	1.0E-04	6.9	1.6E-03	0.1	9.5E-01	-1.1	2.7E-01
ENSMUST00000107601	Rho GTPase activating protein 23 [Source:MGI Symbol;Acc:MGI:3697726]	F8VQ11		0.5	6.7E-01	2.7	9.4E-02	1.8	1.5E-01	-0.4	7.4E-01
ENSMUST00000109024	LIM domain and actin binding 1 [Source:MGI Symbol;Acc:MGI:1920992]	Q8CD09	Q9ERG0	3.3	4.0E-04	5.9	4.3E-04	-0.5	6.8E-01	-0.4	5.8E-01
ENSMUST00000109054	predicted gene 14443 [Source:MGI Symbol;Acc:MGI:3652324]	A2ARX0		4.9	2.1E-06	-1.2	3.7E-01	0.2	8.4E-01	-2.7	8.7E-02
ENSMUST00000107613	TBK1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1920424]	G3X9S9		1.5	4.3E-02	1.9	4.3E-02	0.5	4.4E-01	0.2	8.3E-01
ENSMUST00000107615	TBK1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1920424]	Z4YKN2		3.3	2.4E-01	3.3	2.7E-01	-0.4	9.1E-01	-0.4	8.5E-01
ENSMUST00000109057	RIKEN cDNA 9530068E07 gene [Source:MGI Symbol;Acc:MGI:2654705]	A0A0A0MQD4		-5.8	7.2E-03	6.6	1.1E-01	-0.9	8.3E-01	1.1	6.2E-01
ENSMUST00000107619	Kruppel-like factor 4 (gut) [Source:MGI Symbol;Acc:MGI:1342287]	F2YID5	Q60793	0.1	9.1E-01	0.2	7.6E-01	0.3	5.8E-01	0.1	8.5E-01
ENSMUST00000107620				3.3	6.0E-02	1.1	5.9E-01	-0.1	9.6E-01	2.1	2.3E-01
ENSMUST00000109075	negative elongation factor complex member C/D, Th1l [Source:MGI Symbol;Acc:MGI:1926424]		Q922L6	-3.8	2.3E-02	7.0	1.0E-04	-0.6	6.2E-01	-4.6	3.1E-04
ENSMUST00000107623	Sp2 transcription factor [Source:MGI Symbol;Acc:MGI:1926162]	Q8BNQ4		-2.4	1.3E-01	-2.3	2.2E-01	-0.6	5.9E-01	-0.7	7.1E-01
ENSMUST00000109077	cyclin-dependent kinase-like 3 [Source:MGI Symbol;Acc:MGI:2388268]		Q8BLF2	4.0	2.9E-02	1.8	4.3E-01	3.4	8.8E-02	-3.7	9.1E-02
ENSMUST00000107629	pyridoxine 5'-phosphate oxidase [Source:MGI Symbol;Acc:MGI:2144151]	A2A6E7		3.5	6.6E-02	5.1	4.2E-02	1.2	6.0E-01	-0.5	7.3E-01
ENSMUST00000109078	cyclin-dependent kinase-like 3 [Source:MGI Symbol;Acc:MGI:2388268]		Q8BLF2	3.8	1.4E-04	3.8	8.3E-03	-1.0	3.6E-01	0.3	7.6E-01
ENSMUST00000109084	'AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957	Z4YKV1		-8.5	7.1E-05	-3.7	5.1E-03	0.5	3.4E-01	0.1	9.1E-01
ENSMUST00000109085	'AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		P63094	-8.1	4.4E-05	7.2	9.0E-05	-0.3	8.0E-01	0.3	6.3E-01
ENSMUST00000109086	ubiquitin-conjugating enzyme E2B [Source:MGI Symbol;Acc:MGI:102944]	A2RSE4	P63147	-9.0	6.5E-05	6.3	1.7E-04	0.1	9.1E-01	-0.5	3.8E-01
ENSMUST00000107644	general transcription factor II H, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1277216]	E9QKD9		1.6	3.1E-01	-3.0	2.4E-01	-2.7	8.6E-02	2.0	4.1E-01
ENSMUST00000109087	'AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		P63094	-8.9	9.8E-07	4.4	6.6E-02	-1.0	6.1E-01	-0.2	9.2E-01
ENSMUST00000109088	'AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		Q6R0H6	6.2	9.2E-03	-3.9	1.1E-02	0.7	3.0E-01	0.8	5.5E-01
ENSMUST00000109090	jade family PHD finger 2 [Source:MGI Symbol;Acc:MGI:1924151]	A2AA59		7.1	3.5E-02	-3.9	2.5E-03	-0.4	3.5E-01	-0.6	5.8E-01
ENSMUST00000109095	'AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		Q9Z0F1	7.5	5.7E-05	-2.3	1.3E-01	4.1	6.6E-04	-1.1	4.7E-01
ENSMUST00000107657	nuclear factor, erythroid derived 2,-like 1 [Source:MGI Symbol;Acc:MGI:99421]	Q6GTN8	Q61985	0.3	8.8E-01	0.6	8.5E-01	0.0	9.9E-01	-0.3	9.3E-01
ENSMUST00000107658	nuclear factor, erythroid derived 2,-like 1 [Source:MGI Symbol;Acc:MGI:99421]	Q6GTN8	Q61985	-0.9	7.4E-01	-0.1	9.7E-01	-3.2	1.3E-01	-4.0	1.5E-01
ENSMUST00000109099	ATM interactor [Source:MGI Symbol;Acc:MGI:2682328]		Q6P9S1	-0.9	3.0E-02	5.2	1.4E-02	-0.8	6.2E-01	-0.4	7.5E-01
ENSMUST00000109100	family with sequence similarity 186, member B [Source:MGI Symbol;Acc:MGI:3647604]	D3Z420		9.2	4.1E-05	4.9	2.3E-03	-1.4	2.6E-01	0.6	4.8E-01
ENSMUST00000109102	chromodomain protein, Y chromosome-like 2 [Source:MGI Symbol;Acc:MGI:1923046]		Q9D5D8	1.2	7.8E-03	-4.3	1.6E-02	0.9	2.4E-01	0.9	5.5E-01
ENSMUST00000109103	heterogeneous nuclear ribonucleoprotein A/B [Source:MGI Symbol;Acc:MGI:1330294]	Q20BD0		-7.4	3.5E-06	4.6	4.0E-03	-0.9	4.7E-01	0.4	6.3E-01
ENSMUST00000107664	SH3 domain protein D19 [Source:MGI Symbol;Acc:MGI:1350923]		Q91X43	1.2	4.5E-01	-1.1	6.6E-01	-0.3	8.6E-01	2.0	3.9E-01
ENSMUST00000109104	vian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog [Source:MGI Symbol;Acc:MGI:9690		P54843	4.5	3.1E-04	-5.3	1.1E-02	-0.3	6.8E-01	-0.4	8.2E-01
ENSMUST00000107675	F-box and WD-40 domain protein 7 [Source:MGI Symbol;Acc:MGI:1354695]	D3YUA8		-2.5	3.4E-01	5.1	9.7E-02	4.3	1.3E-01	-3.2	1.8E-01
ENSMUST00000109107	WW domain-containing oxidoreductase [Source:MGI Symbol;Acc:MGI:1931237]		Q91WL8	7.0	1.6E-04	-0.5	5.9E-01	0.3	6.2E-01	-2.0	4.9E-02
ENSMUST00000109109	nudix (nucleoside diphosphate linked moiety X)-type motif 7 [Source:MGI Symbol;Acc:MGI:1914778]		Q99P30	6.9	1.5E-05	6.9	5.5E-04	-0.5	7.4E-01	-1.3	1.1E-01
ENSMUST00000109111	CDC like kinase 4 [Source:MGI Symbol;Acc:MGI:1098551]		O35493	-6.0	8.4E-05	-6.6	8.0E-06	0.2	4.0E-01	-0.2	7.5E-01
ENSMUST00000109116	Z-DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:1927449]		Q9QY24	-4.8	1.3E-03	-5.2	1.7E-03	-0.9	1.1E-01	0.8	5.2E-01
ENSMUST00000109122	zinc finger protein 354A [Source:MGI Symbol;Acc:MGI:103172]	Q5PPR4		6.0	8.9E-06	-4.9	9.2E-03	-2.2	1.3E-02	-0.3	8.4E-01
ENSMUST00000109123	RIKEN cDNA 4933414I15 gene [Source:MGI Symbol;Acc:MGI:1918374]	Q9D4D5		6.6	7.9E-05	7.0	2.9E-03	0.9	6.1E-01	-0.1	8.9E-01
ENSMUST00000109124	zinc finger protein 354B [Source:MGI Symbol;Acc:MGI:1351476]		Q9QXT9	6.0	1.5E-04	5.4	4.2E-04	-3.8	9.5E-03	0.0	1.0E+00
ENSMUST00000107692	tripartite motif-containing 2 [Source:MGI Symbol;Acc:MGI:1933163]		Q9ESN6	3.8	1.1E-01	5.9	6.1E-02	1.2	6.8E-01	-0.9	6.0E-01
ENSMUST00000107696	zinc finger protein 189 [Source:MGI Symbol;Acc:MGI:2444707]	Q8BKP2		-0.8	2.3E-01	-0.7	3.9E-01	-0.5	3.8E-01	-0.7	3.9E-01
ENSMUST00000107697	acyl-coenzyme A amino acid N-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2140197]		A2AKK5	3.7	7.3E-02	1.8	2.6E-01	-3.0	9.8E-02	-1.2	4.4E-01
ENSMUST00000109125	SPO11 meiotic protein covalently bound to DSB [Source:MGI Symbol;Acc:MGI:1349669]		Q9WTK8	4.6	7.6E-03	-2.1	2.5E-01	0.8	4.2E-01	-0.7	6.9E-01
ENSMUST00000109129	zinc finger protein 2 [Source:MGI Symbol;Acc:MGI:99167]		P08043	6.0	2.7E-03	-5.9	2.0E-03	-1.8	1.8E-02	-1.0	5.1E-01
ENSMUST00000109135	zinc finger protein 354C [Source:MGI Symbol;Acc:MGI:1353621]		Q571J5	4.1	2.4E-03	-5.9	4.3E-04	-0.1	7.5E-01	-1.1	3.8E-01
ENSMUST00000109140	aurora kinase A [Source:MGI Symbol;Acc:MGI:894678]	Q3TEY6	P97477	-4.1	5.5E-03	-6.4	1.5E-04	-0.3	4.2E-01	-1.0	4.0E-01
ENSMUST00000107714	ucleotide binding protein (G protein), gamma transducing activity polypeptide 2 [Source:MGI Symbol;Acc:MG	A2A614	Q61017	-3.3	1.9E-01	-5.4	8.8E-02	-2.5	1.1E-01	-0.5	8.9E-01
ENSMUST00000109142	heterogeneous nuclear ribonucleoprotein H1 [Source:MGI Symbol;Acc:MGI:1891925]	Q811L7	O35737	7.2	5.4E-05	6.7	3.4E-03	0.3	8.5E-01	-0.2	8.5E-01
ENSMUST00000107717	zinc finger protein 652 [Source:MGI Symbol;Acc:MGI:2442221]		Q5DU09	-0.9	5.5E-02	-0.4	5.5E-01	0.9	5.8E-02	0.3	5.9E-01
ENSMUST00000109149	Rho family GTPase 1 [Source:MGI Symbol;Acc:MGI:2444878]		Q8BLR7	-3.5	2.1E-03	-1.3	3.2E-01	1.6	8.6E-02	-1.8	2.1E-01
ENSMUST00000109150	calcium channel, voltage-dependent, beta 3 subunit [Source:MGI Symbol;Acc:MGI:103307]	D3Z3Z3		3.4	4.2E-04	-1.0	2.5E-01	0.4	5.1E-01	-0.3	7.3E-01
ENSMUST00000107721	syntaxin 17 [Source:MGI Symbol;Acc:MGI:1914977]	Q9D614		-1.9	1.6E-01	-3.9	9.3E-02	-0.7	5.3E-01	1.4	5.2E-01
ENSMUST00000107722	speckle-type POZ protein [Source:MGI Symbol;Acc:MGI:1343085]		Q6ZWS8	0.7	1.9E-01	-0.1	8.8E-01	0.2	7.6E-01	1.0	1.4E-01
ENSMUST00000107723	glutamate-rich WD repeat containing 1 [Source:MGI Symbol;Acc:MGI:2141989]		Q810D6	-1.1	5.3E-01	0.8	7.1E-01	0.7	7.1E-01	-1.2	5.3E-01
ENSMUST00000109155	zinc finger protein 217 [Source:MGI Symbol;Acc:MGI:2685408]	Q3U0X6		-3.2	8.4E-04	-7.3	5.4E-04	0.7	1.3E-01	-0.9	5.5E-01
ENSMUST00000109157	teashirt zinc finger family member 2 [Source:MGI Symbol;Acc:MGI:2153084]		Q68FE9	7.7	2.3E-05	7.5	1.1E-05	0.5	5.8E-01	1.1	3.8E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000109158	melanoma inhibitory activity 3 [Source:MGI Symbol;Acc:MGI:2443183]	J3KMH5		-6.3	9.2E-05	-3.1	6.4E-02	0.8	3.2E-01	0.6	6.6E-01
ENSMUST00000109159	teashirt zinc finger family member 2 [Source:MGI Symbol;Acc:MGI:2153084]		Q68FE9	9.7	3.8E-05	-3.4	2.0E-01	1.8	2.6E-01	-1.4	6.0E-01
ENSMUST00000107729	cytohesin 2 [Source:MGI Symbol;Acc:MGI:1334255]	Q99KH2		0.7	4.8E-01	1.3	2.6E-01	0.2	8.2E-01	-0.4	6.8E-01
ENSMUST00000109160	predicted gene 11011 [Source:MGI Symbol;Acc:MGI:3779229]	D3Z3L9		5.7	5.7E-04	6.3	2.0E-04	0.5	6.6E-01	-1.2	8.1E-02
ENSMUST00000107733	K(lysine) acetyltransferase 7 [Source:MGI Symbol;Acc:MGI:2182799]	Q3TD41	Q5SVQ0	1.5	5.2E-01	4.7	1.2E-01	1.8	4.5E-01	-1.4	5.6E-01
ENSMUST00000107734	K(lysine) acetyltransferase 7 [Source:MGI Symbol;Acc:MGI:2182799]	Q1AJD0	Q5SVQ0	-0.4	8.6E-01	1.6	6.3E-01	1.8	4.0E-01	-0.2	9.4E-01
ENSMUST00000109162	zinc finger protein 64 [Source:MGI Symbol;Acc:MGI:107342]	A2AQR3		4.9	5.6E-04	-1.2	1.4E-01	0.8	1.3E-01	-0.3	6.9E-01
ENSMUST00000109163	olfactory receptor 281 [Source:MGI Symbol;Acc:MGI:3030115]	Q8VET6		5.8	5.9E-04	-6.1	2.3E-02	1.6	6.9E-02	1.7	4.6E-01
ENSMUST00000107739	integrin alpha 3 [Source:MGI Symbol;Acc:MGI:96602]		Q62470	5.2	6.3E-02	5.1	5.0E-02	-2.8	3.1E-01	-2.6	1.5E-01
ENSMUST00000109166	axin interactor, dorsalization associated [Source:MGI Symbol;Acc:MGI:1919737]		Q8C4Q6	2.0	6.4E-03	4.2	8.4E-02	-0.6	8.1E-01	0.4	7.8E-01
ENSMUST00000109175	ATPase, class II, type 9A [Source:MGI Symbol;Acc:MGI:1330826]	Q8C288		9.8	2.3E-06	8.6	2.9E-03	2.1	3.4E-01	1.4	1.7E-01
ENSMUST00000109178	mitogen-activated protein kinase 9 [Source:MGI Symbol;Acc:MGI:1346862]		Q9WTU6	-5.0	6.9E-03	5.6	1.8E-04	-3.8	5.5E-03	0.4	4.1E-01
ENSMUST00000109191	potassium voltage-gated channel, subfamily G, member 1 [Source:MGI Symbol;Acc:MGI:3616086]	B2RVK9	A2BDX4	8.5	6.6E-05	-2.1	1.9E-01	1.6	8.0E-02	0.0	9.9E-01
ENSMUST00000109194	mannoside acetylglucosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI:96973]	Q544F0	P27808	-5.2	5.7E-03	7.6	1.8E-04	-0.1	9.6E-01	0.8	2.3E-01
ENSMUST00000109202	interferon gamma inducible protein 47 [Source:MGI Symbol;Acc:MGI:99448]	Q61635		-5.2	1.3E-02	6.3	1.3E-05	0.0	9.7E-01	-0.7	1.4E-01
ENSMUST00000109203	polyadenylate binding protein-interacting protein 1 [Source:MGI Symbol;Acc:MGI:2384993]	D3Z3J6		-4.4	8.8E-04	4.6	2.8E-03	-0.6	6.2E-01	1.4	7.5E-02
ENSMUST00000109204	nicotinamide nucleotide transhydrogenase [Source:MGI Symbol;Acc:MGI:109279]	E9Q8F4		4.7	1.1E-02	-1.7	1.1E-02	1.1	1.2E-02	-4.8	2.9E-04
ENSMUST00000107757	coronin, actin binding protein 2A [Source:MGI Symbol;Acc:MGI:1345966]	B1AVH5		0.0	9.9E-01	-2.1	5.6E-01	-1.2	6.7E-01	0.9	7.8E-01
ENSMUST00000109207	ubiquitin-conjugating enzyme E2 variant 1 [Source:MGI Symbol;Acc:MGI:1913839]	Q569Y6	Q9CZY3	-3.4	2.7E-03	8.3	1.1E-03	-0.9	6.6E-01	1.2	1.9E-01
ENSMUST00000109210	predicted gene 5431 [Source:MGI Symbol;Acc:MGI:3645205]	A6PWD6		3.3	1.2E-04	-3.7	1.8E-02	0.8	2.0E-01	1.0	4.5E-01
ENSMUST00000107772	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2 [Source:MGI Symbol;Acc:MGI:3039624]		Q3U269	-1.0	1.2E-01	0.1	9.3E-01	1.4	4.5E-02	0.3	7.4E-01
ENSMUST00000109214	ring finger protein 114 [Source:MGI Symbol;Acc:MGI:1933159]		Q9ET26	3.8	1.9E-02	5.4	1.1E-03	-2.1	1.2E-01	-0.4	6.3E-01
ENSMUST00000109220	sarcoglycan, delta (dystrophin-associated glycoprotein) [Source:MGI Symbol;Acc:MGI:1346525]	A2ACH6		7.7	2.5E-05	7.2	7.1E-05	-1.8	1.5E-01	0.3	5.8E-01
ENSMUST00000109221	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5 [Source:MGI Symbol;Acc:MGI:1927169]		Q9JMK0	-2.2	7.3E-03	-1.8	3.6E-01	1.2	2.9E-01	-1.4	4.9E-01
ENSMUST00000109222	carbohydrate (chondroitin 6/keratan) sulfotransferase 4 [Source:MGI Symbol;Acc:MGI:1349479]			6.3	2.4E-04	5.2	4.9E-02	-0.4	8.6E-01	1.4	3.2E-01
ENSMUST00000109229	hepatitis A virus cellular receptor 2 [Source:MGI Symbol;Acc:MGI:2159682]	D3Z3I4		3.9	6.2E-03	7.3	1.7E-04	-0.6	6.1E-01	-0.8	2.5E-01
ENSMUST00000109237	IL2 inducible T cell kinase [Source:MGI Symbol;Acc:MGI:96621]		Q03526	7.2	2.1E-04	7.6	2.2E-04	-0.6	6.7E-01	0.8	2.3E-01
ENSMUST00000107796	solute carrier family 25, member 51 [Source:MGI Symbol;Acc:MGI:2684984]	A2AKW0		0.8	2.9E-01	1.5	7.9E-02	0.3	6.9E-01	-0.5	5.0E-01
ENSMUST00000109238	staufen (RNA binding protein) homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1338864]	A2A5S3		-6.1	2.9E-05	-3.5	2.1E-02	0.4	5.9E-01	-0.4	7.8E-01
ENSMUST00000109241	sorting nexin 18 [Source:MGI Symbol;Acc:MGI:2137642]	Q8C788		-4.2	2.2E-05	-2.5	3.3E-02	1.4	2.4E-02	-0.6	5.6E-01
ENSMUST00000107800	tRNA methyltransferase 10B [Source:MGI Symbol;Acc:MGI:1917184]	Z4YKN9		-1.8	2.5E-01	-5.0	2.0E-02	-3.7	4.8E-03	-0.6	7.6E-01
ENSMUST00000109246	osphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1 [Source:MGI Symbol;Acc:MGI:30406		Q69ZK0	-5.2	6.0E-03	5.8	1.7E-04	-2.2	6.8E-02	1.1	6.8E-02
ENSMUST00000109249	sulfatase 2 [Source:MGI Symbol;Acc:MGI:1919293]		Q8CFG0	6.2	4.1E-04	-0.1	9.2E-01	0.9	2.1E-01	-2.2	5.3E-02
ENSMUST00000109256	periphilin 1 [Source:MGI Symbol;Acc:MGI:1917029]	G3UWD4		-3.3	8.9E-03	-0.7	6.7E-01	6.9	8.0E-05	-0.1	9.7E-01
ENSMUST00000109260	clathrin interactor 1 [Source:MGI Symbol;Acc:MGI:2144243]	Q5SUH7		-9.3	1.1E-06	8.8	3.6E-04	-0.8	6.7E-01	-0.7	3.4E-01
ENSMUST00000109268	early B cell factor 1 [Source:MGI Symbol;Acc:MGI:95275]	Q5SWK8		5.9	1.6E-02	-4.6	1.2E-03	-0.4	3.7E-01	-0.3	7.4E-01
ENSMUST00000109269	zinc finger, MYND-type containing 8 [Source:MGI Symbol;Acc:MGI:1918025]	A2A484		7.3	2.2E-05	-2.6	3.4E-01	1.5	3.5E-01	-0.8	7.6E-01
ENSMUST00000109272	mesoderm induction early response 1, family member 3 [Source:MGI Symbol;Acc:MGI:2442317]		Q3UHF3	-5.5	1.1E-03	-5.5	2.9E-02	0.4	6.5E-01	2.1	3.5E-01
ENSMUST00000109275	solute carrier family 26, member 3 [Source:MGI Symbol;Acc:MGI:107181]	F7BFQ2		7.3	1.4E-04	1.0	4.7E-01	-2.9	5.1E-02	0.1	9.6E-01
ENSMUST00000109283	solute carrier family 2 (facilitated glucose transporter), member 13 [Source:MGI Symbol;Acc:MGI:2146030]		Q3UHK1	8.2	2.7E-05	-2.2	2.3E-02	0.9	6.5E-02	0.3	6.8E-01
ENSMUST00000109298	solute carrier family 35, member C2 [Source:MGI Symbol;Acc:MGI:2385166]	Q5GMH2	Q8VCX2	-7.4	4.4E-06	-1.6	1.1E-01	0.3	6.3E-01	-0.8	4.0E-01
ENSMUST00000109304	RIKEN cDNA 1700025C18 gene [Source:MGI Symbol;Acc:MGI:1919461]	A2A580		5.7	3.2E-04	2.2	9.2E-03	0.7	2.7E-01	1.0	8.4E-02
ENSMUST00000109308	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 3 [Source:MGI Symbol;Acc:MGI:10329	Q3UZ64		-3.3	1.3E-05	-0.6	4.4E-01	1.0	6.9E-02	-0.6	4.4E-01
ENSMUST00000109309	SH3/ankyrin domain gene 3 [Source:MGI Symbol;Acc:MGI:1930016]	A0A0A0MQD5		6.0	2.1E-02	-3.6	1.2E-02	0.4	5.6E-01	-3.3	5.0E-02
ENSMUST00000109313	carnitine palmitoyltransferase 1b, muscle [Source:MGI Symbol;Acc:MGI:1098297]		Q924X2	3.0	2.4E-02	-6.3	6.8E-04	0.2	7.1E-01	0.4	7.9E-01
ENSMUST00000109329	lymphocyte cytosolic protein 2 [Source:MGI Symbol;Acc:MGI:1321402]	B1ATD1		-5.4	3.5E-06	-7.0	3.5E-02	-1.9	1.0E-01	-0.2	9.5E-01
ENSMUST00000109339	WAP four-disulfide core domain 8 [Source:MGI Symbol;Acc:MGI:2685552]	A2A5H1		8.2	9.6E-06	-2.9	8.2E-03	-0.7	2.3E-01	-2.5	4.6E-02
ENSMUST00000109349	dysbindin (dystrobrevin binding protein 1) domain containing 2 [Source:MGI Symbol;Acc:MGI:106562]	Q330P7	Q9CRD4	4.8	6.8E-05	-6.6	4.4E-04	0.8	9.4E-02	-0.7	5.9E-01
ENSMUST00000107830				-4.6	8.6E-02	-5.8	8.6E-02	-1.7	2.0E-01	-0.5	9.0E-01
ENSMUST00000109354	nucleophosmin 1 [Source:MGI Symbol;Acc:MGI:106184]	Q9DAY9		-3.2	2.1E-03	2.7	1.9E-01	-2.4	2.2E-01	-0.4	7.9E-01
ENSMUST00000109363	fibroblast growth factor 18 [Source:MGI Symbol;Acc:MGI:1277980]	Q5SQB3		4.9	1.6E-02	-4.1	1.5E-01	0.6	6.0E-01	-0.9	7.5E-01
ENSMUST00000109366	F-box and WD-40 domain protein 11 [Source:MGI Symbol;Acc:MGI:2144023]		Q5SRY7	-4.4	2.3E-03	-4.5	1.1E-02	0.9	1.5E-01	-0.1	9.5E-01
ENSMUST00000109367	secretory leukocyte peptidase inhibitor [Source:MGI Symbol;Acc:MGI:109297]	Q548X8	P97430	-7.6	6.2E-07	-5.4	6.6E-04	-0.1	8.1E-01	-0.7	5.3E-01
ENSMUST00000109371	tubulin tyrosine ligase-like family, member 8 [Source:MGI Symbol;Acc:MGI:1922902]		A4Q9F1	6.4	1.6E-02	2.9	1.4E-03	0.2	6.7E-01	0.9	1.0E-01
ENSMUST00000109381	bromodomain containing 1 [Source:MGI Symbol;Acc:MGI:1924161]	E9PZ26		-4.1	2.4E-04	-5.7	3.5E-02	1.9	4.7E-02	-0.3	9.0E-01
ENSMUST00000109384	translocase of outer mitochondrial membrane 34 [Source:MGI Symbol;Acc:MGI:1914395]		Q9CYG7	-5.0	2.7E-03	4.2	2.2E-03	-0.9	3.9E-01	-0.6	3.9E-01
ENSMUST00000109392	core binding factor beta [Source:MGI Symbol;Acc:MGI:99851]		Q08024	-7.1	1.5E-04	-3.3	9.4E-02	0.3	7.9E-01	-0.2	9.3E-01
ENSMUST00000107854	mbt domain containing 1 [Source:MGI Symbol;Acc:MGI:2143977]		Q6P5G3	-2.8	2.2E-01	0.5	8.2E-01	0.6	7.6E-01	-2.7	2.2E-01
ENSMUST00000109394	core binding factor beta [Source:MGI Symbol;Acc:MGI:99851]		Q08024	-6.9	8.1E-03	-5.2	1.5E-01	3.1	1.4E-01	0.7	8.2E-01
ENSMUST00000109396	potassium channel, subfamily K, member 15 [Source:MGI Symbol;Acc:MGI:2675209]	A2AHD2		5.5	7.0E-04	-4.0	2.8E-02	1.5	8.1E-02	0.8	6.1E-01
ENSMUST00000109400	protein kinase inhibitor, gamma [Source:MGI Symbol;Acc:MGI:1343086]	Q3TP50	O70139	5.5	6.8E-03	5.0	4.8E-02	-0.8	7.2E-01	3.1	6.9E-02
ENSMUST00000109401	transportin 1 [Source:MGI Symbol;Acc:MGI:2681523]		Q8BFY9	-3.6	1.9E-05	6.3	7.4E-04	-0.6	6.4E-01	-0.8	3.1E-01
ENSMUST00000109410	carboxylesterase 2E [Source:MGI Symbol;Acc:MGI:2443170]		Q8BK48	2.6	6.3E-03	6.7	3.8E-04	1.2	3.3E-01	-1.3	8.9E-02
ENSMUST00000109411	hepatic nuclear factor 4, alpha [Source:MGI Symbol;Acc:MGI:109128]	Z4YKX0		6.2	1.5E-03	7.1	1.5E-04	-0.6	6.1E-01	-0.4	5.5E-01
ENSMUST00000109416	R3H domain containing-like [Source:MGI Symbol;Acc:MGI:3650937]		A2A5I3	6.5	8.9E-05	6.0	4.1E-02	-0.7	8.0E-01	2.6	9.9E-02
ENSMUST00000107865	transmembrane protein 8B [Source:MGI Symbol;Acc:MGI:2441680]		B1AWJ5	6.4	5.0E-02	6.1	7.4E-02	-1.0	7.7E-01	-0.7	7.2E-01
ENSMUST00000109418	fat storage-inducing transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:2444508]		P59266	4.6	1.1E-05	7.9	3.1E-03	-0.8	7.1E-01	0.9	3.6E-01
ENSMUST00000109420	ganglioside-induced differentiation-associated protein 1-like 1 [Source:MGI Symbol;Acc:MGI:2385163]	Q3USC7		6.0	2.1E-04	6.4	7.6E-03	-1.0	6.4E-01	-1.9	1.6E-01
ENSMUST00000107880	AKT1 substrate 1 (proline-rich) [Source:MGI Symbol;Acc:MGI:1914855]		Q9D1F4	-1.9	2.2E-01	2.2	2.2E-01	1.1	4.7E-01	-3.0	7.1E-02
ENSMUST00000109422	peroxisome proliferator activated receptor alpha [Source:MGI Symbol;Acc:MGI:104740]	Q542P9	P23204	8.8	5.4E-05	-1.0	1.6E-01	1.2	1.8E-02	0.0	9.4E-01
ENSMUST00000109424	wingless-type MMTV integration site family, member 7B [Source:MGI Symbol;Acc:MGI:98962]	Q6NZR1		7.7	1.1E-03	5.4	7.0E-04	-0.5	6.5E-01	0.1	8.5E-01
ENSMUST00000109426	Rho guanine nucleotide exchange factor (GEF) 28 [Source:MGI Symbol;Acc:MGI:1346016]	G5E8P2		8.6	1.7E-05	5.2	1.2E-03	-3.1	4.6E-02	-1.3	1.1E-01
ENSMUST00000107893	activating transcription factor 5 [Source:MGI Symbol;Acc:MGI:2141857]	Q3UJF3	O70191	0.2	8.9E-01	1.4	3.7E-01	0.4	7.3E-01	-0.8	5.4E-01
ENSMUST00000109428	TOX high mobility group box family member 2 [Source:MGI Symbol;Acc:MGI:3611233]	A2A473		7.0	7.9E-05	5.5	2.9E-03	-0.2	9.1E-01	0.3	6.8E-01
ENSMUST00000109430	G protein-coupled receptor 75 [Source:MGI Symbol;Acc:MGI:2441843]	Q059L0	Q6X632	7.6	2.2E-05	-8.0	3.0E-03	1.2	6.1E-02	-0.2	9.3E-01
ENSMUST00000107899	myosin, heavy polypeptide 14 [Source:MGI Symbol;Acc:MGI:1919210]		Q6URW6	5.7	1.0E-01	5.2	1.1E-01	-1.8	6.0E-01	-1.3	5.7E-01
ENSMUST00000107900	myosin, heavy polypeptide 14 [Source:MGI Symbol;Acc:MGI:1919210]	K3W4R2		5.3	1.4E-01	5.5	1.6E-01	-0.5	9.1E-01	-0.6	7.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000109432	fibulin 1 [Source:MGI Symbol;Acc:MGI:95487]		Q08879	4.2	3.0E-03	4.7	6.4E-04	-4.0	4.3E-03	0.0	9.6E-01
ENSMUST00000107906	potassium voltage gated channel, Shaw-related subfamily, member 3 [Source:MGI Symbol;Acc:MGI:96669]	E9QKI2		2.5	1.7E-01	-0.9	7.4E-01	-1.1	5.4E-01	2.3	3.8E-01
ENSMUST00000109442	protein tyrosine phosphatase, receptor type, T [Source:MGI Symbol;Acc:MGI:1321152]	B1AQN2		6.5	1.2E-03	7.6	7.8E-05	-0.4	7.3E-01	-0.5	3.5E-01
ENSMUST00000107909	musashi RNA-binding protein 2 [Source:MGI Symbol;Acc:MGI:1923876]	Q2M2Q8	Q920Q6	0.5	3.9E-01	0.5	5.5E-01	-0.2	6.9E-01	-0.2	8.1E-01
ENSMUST00000107910	nuclear receptor subfamily 1, group H, member 2 [Source:MGI Symbol;Acc:MGI:1352463]	Q8BP65		-4.6	1.3E-01	-5.0	2.2E-01	-0.1	9.5E-01	0.2	9.6E-01
ENSMUST00000109444	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein [Source:MGI Symbol;Acc:MGI:1915268]		Q9EQG9	-7.9	4.1E-04	-6.6	7.5E-02	0.7	5.4E-01	-0.9	8.2E-01
ENSMUST00000109445	protein tyrosine phosphatase, receptor type, T [Source:MGI Symbol;Acc:MGI:1321152]		Q99M80	7.7	3.4E-02	-1.2	5.9E-01	1.5	3.4E-01	-1.7	4.4E-01
ENSMUST00000107913	tropomyosin 2, beta [Source:MGI Symbol;Acc:MGI:98810]		P58774	2.9	2.9E-01	4.1	1.7E-01	-0.4	8.9E-01	-1.6	4.3E-01
ENSMUST00000109454	elastin microfibril interfacer 3 [Source:MGI Symbol;Acc:MGI:2389142]	A2A4B4		6.9	1.8E-02	-3.1	6.9E-02	0.4	6.0E-01	-0.3	8.6E-01
ENSMUST00000109468	topoisomerase (DNA) I [Source:MGI Symbol;Acc:MGI:98788]		Q04750	-4.0	1.3E-04	6.9	5.7E-03	-0.7	7.4E-01	-1.3	3.5E-01
ENSMUST00000109469	metallophosphoesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:106316]	B1APX5		4.6	1.4E-02	-3.4	7.1E-04	0.3	4.3E-01	0.8	2.7E-01
ENSMUST00000109470	metallophosphoesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:106316]		Q91ZG2	6.4	1.3E-02	2.6	6.0E-03	-0.9	2.4E-01	-0.5	4.6E-01
ENSMUST00000109477	coiled coil domain containing 88A [Source:MGI Symbol;Acc:MGI:1925177]	Z4YKY0		5.6	2.5E-04	3.7	1.3E-01	-1.5	5.4E-01	3.1	4.9E-02
ENSMUST00000109478	DEAH (Asp-Glu-Ala-His) box polypeptide 35 [Source:MGI Symbol;Acc:MGI:1918965]	A2ACQ1		-3.4	2.6E-02	9.7	5.2E-05	1.8	2.1E-01	-0.4	4.7E-01
ENSMUST00000109479	tubulin tyrosine ligase-like 1 [Source:MGI Symbol;Acc:MGI:2443047]	Q8BJG7		8.9	3.6E-05	5.6	3.4E-02	-0.8	7.5E-01	0.9	5.1E-01
ENSMUST00000109488	small nucleolar RNA host gene 11 [Source:MGI Symbol;Acc:MGI:2441845]	Q4G0K9		6.1	1.0E-06	-5.6	8.6E-03	1.2	9.0E-02	3.5	6.7E-02
ENSMUST00000107957	family with sequence similarity 214, member B [Source:MGI Symbol;Acc:MGI:2441854]		Q8BR27	-1.9	3.0E-01	-0.7	7.6E-01	0.6	7.3E-01	-0.5	7.9E-01
ENSMUST00000107958	family with sequence similarity 214, member B [Source:MGI Symbol;Acc:MGI:2441854]		Q8BR27	0.7	5.7E-01	1.4	3.7E-01	-0.3	8.2E-01	-0.9	5.0E-01
ENSMUST00000107959	family with sequence similarity 214, member B [Source:MGI Symbol;Acc:MGI:2441854]		Q8BR27	-2.2	2.1E-01	2.2	5.9E-01	7.5	3.1E-02	3.1	3.3E-01
ENSMUST00000109491	lipopolysaccharide binding protein [Source:MGI Symbol;Acc:MGI:1098776]	A2AC65		-2.0	7.8E-03	5.4	5.6E-02	-0.9	7.4E-01	-0.4	8.2E-01
ENSMUST00000109493	homer homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1347345]	D3Z6A9		-2.8	2.6E-02	5.6	1.1E-02	-0.7	7.3E-01	-1.5	2.3E-01
ENSMUST00000109500	bactericidal permeablility increasing protein [Source:MGI Symbol;Acc:MGI:3045315]		Q67E05	5.1	2.3E-02	0.1	9.7E-01	-5.0	1.2E-02	-0.5	7.4E-01
ENSMUST00000109503	Nfat activating molecule with ITAM motif 1 [Source:MGI Symbol;Acc:MGI:1921289]		Q8R4V1	-4.3	3.4E-04	1.1	1.3E-01	-0.9	1.3E-01	-0.1	8.6E-01
ENSMUST00000109504	vaccinia related kinase 2 [Source:MGI Symbol;Acc:MGI:1917172]		Q8BN21	-5.0	1.5E-03	-4.5	7.1E-03	0.7	2.1E-01	-0.7	6.3E-01
ENSMUST00000109509	Fanconi anemia, complementation group L [Source:MGI Symbol;Acc:MGI:1914280]		Q9CR14	-3.2	3.1E-03	5.6	1.4E-03	0.9	4.3E-01	1.1	2.1E-01
ENSMUST00000109514	B cell CLL/lymphoma 11A (zinc finger protein) [Source:MGI Symbol;Acc:MGI:106190]	Q5STS9		5.1	1.7E-04	8.3	5.6E-05	-0.5	7.2E-01	-0.7	2.1E-01
ENSMUST00000109515	cytochrome P450, family 2, subfamily d, polypeptide 34 [Source:MGI Symbol;Acc:MGI:2385022]	L7N463		6.8	1.9E-04	2.6	4.5E-01	-0.8	7.9E-01	3.0	2.8E-01
ENSMUST00000107977	V-set and immunoglobulin domain containing 10 like [Source:MGI Symbol;Acc:MGI:1922940]		D3YZF7	-1.5	6.9E-02	-0.1	9.5E-01	1.1	1.1E-01	-0.3	7.7E-01
ENSMUST00000109521	polymerase (RNA) II (DNA directed) polypeptide C [Source:MGI Symbol;Acc:MGI:109299]	Q99M46		-1.9	8.8E-03	3.2	1.5E-01	-0.7	7.3E-01	2.5	1.1E-01
ENSMUST00000109522	TELO2 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1922675]		Q91V83	-3.7	2.8E-02	7.2	4.6E-04	-0.7	6.6E-01	0.4	5.4E-01
ENSMUST00000109523	V-set and transmembrane domain containing 2-like [Source:MGI Symbol;Acc:MGI:2685537]	A2ACD2		5.7	5.4E-04	4.7	2.7E-03	1.4	2.3E-01	0.0	9.6E-01
ENSMUST00000109527	ADP-ribosylation factor-like 2 binding protein [Source:MGI Symbol;Acc:MGI:1349429]		Q9D385	-6.2	9.9E-04	-7.3	3.0E-05	0.3	3.3E-01	-0.7	5.3E-01
ENSMUST00000109528	bladder cancer associated protein homolog (human) [Source:MGI Symbol;Acc:MGI:1858907]		P62951	-3.1	7.5E-03	4.1	7.1E-04	0.5	5.0E-01	-0.5	4.6E-01
ENSMUST00000109529	Rous sarcoma oncogene [Source:MGI Symbol;Acc:MGI:98397]		P05480	6.5	2.1E-03	5.6	1.4E-03	-1.5	2.7E-01	0.6	4.7E-01
ENSMUST00000109535	tumor necrosis factor receptor superfamily, member 13c [Source:MGI Symbol;Acc:MGI:1919299]	Q3U106		10.0	6.9E-05	8.5	5.9E-05	-1.8	2.3E-01	0.4	5.5E-01
ENSMUST00000109537	copine II [Source:MGI Symbol;Acc:MGI:2387578]			-7.7	2.7E-04	6.2	2.1E-04	0.8	4.2E-01	-0.3	5.9E-01
ENSMUST00000109543	versican [Source:MGI Symbol;Acc:MGI:102889]	E9QMK3		-3.5	1.8E-03	1.4	3.0E-02	-0.4	3.6E-01	-0.1	7.9E-01
ENSMUST00000109547	nucleoporin 93 [Source:MGI Symbol;Acc:MGI:1919055]		Q8BJ71	6.4	5.2E-03	7.6	3.4E-04	-0.7	6.4E-01	-0.2	7.6E-01
ENSMUST00000109552	RAS p21 protein activator 1 [Source:MGI Symbol;Acc:MGI:97860]	E9PYG6		-2.9	9.1E-04	4.8	1.1E-03	1.4	1.7E-01	-0.5	4.9E-01
ENSMUST00000109553	thyrotroph embryonic factor [Source:MGI Symbol;Acc:MGI:98663]		Q9JLC6	5.0	3.9E-03	-5.5	3.5E-03	-1.1	8.3E-02	0.5	7.2E-01
ENSMUST00000108023	cyclin E1 [Source:MGI Symbol;Acc:MGI:88316]		Q61457	-1.1	1.1E-01	0.3	6.7E-01	0.9	1.4E-01	-0.5	5.3E-01
ENSMUST00000108038	galactose-1-phosphate uridyl transferase [Source:MGI Symbol;Acc:MGI:95638]	A2AMS2		3.7	5.4E-02	2.1	3.8E-01	-0.7	7.4E-01	0.8	6.2E-01
ENSMUST00000108040	interleukin 11 receptor, alpha chain 1 [Source:MGI Symbol;Acc:MGI:107426]		Q64385	1.3	3.3E-01	5.6	1.2E-02	2.8	1.3E-01	-1.5	2.0E-01
ENSMUST00000108044	interleukin 18 receptor 1 [Source:MGI Symbol;Acc:MGI:105383]		Q61098	1.3	8.8E-02	1.1	2.6E-01	0.5	5.2E-01	0.7	4.1E-01
ENSMUST00000108045	T-box 4 [Source:MGI Symbol;Acc:MGI:102556]	Q8BSY3		6.7	3.6E-02	4.2	1.8E-01	-0.8	8.1E-01	1.7	4.2E-01
ENSMUST00000109554	zinc finger CCCH type containing 7B [Source:MGI Symbol;Acc:MGI:1328310]	F8VPP8		2.5	6.3E-04	7.1	1.3E-02	-0.8	7.7E-01	-1.2	4.0E-01
ENSMUST00000108049	family with sequence similarity 219, member A [Source:MGI Symbol;Acc:MGI:1919151]		Q9D772	1.4	2.3E-01	8.6	3.3E-03	6.4	1.2E-02	-0.8	4.6E-01
ENSMUST00000108050	family with sequence similarity 219, member A [Source:MGI Symbol;Acc:MGI:1919151]	A2ANP2		-1.1	5.5E-01	2.9	4.6E-01	6.0	5.8E-02	2.1	4.9E-01
ENSMUST00000109558	N-myc downstream regulated gene 3 [Source:MGI Symbol;Acc:MGI:1352499]	Q8CBD0		4.2	1.6E-04	-1.4	2.5E-01	0.2	7.8E-01	-3.8	3.5E-02
ENSMUST00000109561	Src-like-adaptor 2 [Source:MGI Symbol;Acc:MGI:1925049]		Q8R4L0	4.4	1.6E-02	-5.5	9.4E-03	-0.1	9.1E-01	0.9	6.4E-01
ENSMUST00000109566	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]	E9PUF2		-6.8	3.0E-04	5.0	9.2E-05	0.6	3.6E-01	0.5	2.8E-01
ENSMUST00000109577	erythrocyte membrane protein band 4.1 like 1 [Source:MGI Symbol;Acc:MGI:103010]	A2AUK8		8.6	2.4E-03	3.1	1.4E-02	-2.1	7.4E-02	-0.1	9.0E-01
ENSMUST00000109578	vacuolar protein sorting 54 (yeast) [Source:MGI Symbol;Acc:MGI:2178798]		Q5SPW0	-5.3	6.8E-04	-7.1	3.4E-04	0.8	7.4E-02	0.2	9.1E-01
ENSMUST00000109579	MKL (megakaryoblastic leukemia)/myocardin-like 1 [Source:MGI Symbol;Acc:MGI:2384495]		Q8K4J6	-4.6	2.9E-03	-2.6	5.4E-02	0.3	6.2E-01	-2.1	1.5E-01
ENSMUST00000109582	carboxylesterase 1B [Source:MGI Symbol;Acc:MGI:3779470]	D3Z5G7		5.3	2.3E-03	4.4	5.4E-02	0.8	6.7E-01	0.3	8.1E-01
ENSMUST00000109583	multiple C2 domains, transmembrane 1 [Source:MGI Symbol;Acc:MGI:1926021]	E9PW38		-6.8	6.8E-04	5.1	2.1E-04	-2.8	1.9E-02	0.1	8.6E-01
ENSMUST00000109585	SERTA domain containing 2 [Source:MGI Symbol;Acc:MGI:1931026]	Q3UGZ1	Q9JJG5	5.3	8.5E-03	1.5	4.6E-01	4.1	1.8E-02	-1.1	5.6E-01
ENSMUST00000109597	reactive oxygen species modulator 1 [Source:MGI Symbol;Acc:MGI:1914317]		P60603	4.9	6.1E-03	-3.3	4.8E-03	0.7	1.4E-01	-0.2	8.4E-01
ENSMUST00000109598	reactive oxygen species modulator 1 [Source:MGI Symbol;Acc:MGI:1914317]		P60603	-2.7	2.5E-02	-6.5	4.3E-02	-0.8	4.5E-01	0.9	7.6E-01
ENSMUST00000109601	RAB1A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:97842]	Q5SW86		-6.9	2.0E-03	-1.1	1.8E-01	1.2	4.1E-02	0.0	9.5E-01
ENSMUST00000108089	BCL2-associated athanogene 1 [Source:MGI Symbol;Acc:MGI:108047]		Q60739	-3.1	2.5E-01	-1.1	6.1E-01	-1.8	3.2E-01	-3.8	1.8E-01
ENSMUST00000108096	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 [Source:MGI Symbol;Acc:MGI:95705]	B1AXY5		3.3	7.9E-02	2.4	1.4E-01	-2.9	1.1E-01	-2.1	1.5E-01
ENSMUST00000108105	predicted gene 5148 [Source:MGI Symbol;Acc:MGI:3646006]	Q8BGG2		3.2	1.2E-01	6.1	1.3E-02	-0.4	8.6E-01	-3.3	3.4E-02
ENSMUST00000109602	RAB1A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:97842]	Q5SW87		8.1	1.6E-05	6.7	9.1E-05	-0.5	6.3E-01	-0.5	3.7E-01
ENSMUST00000108108	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 [Source:MGI Symbol;Acc:MGI:2684983]	A2AP32		1.9	1.3E-01	-1.7	2.4E-01	-2.6	3.7E-02	1.0	4.5E-01
ENSMUST00000108109	sprouty homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1345139]	Q53ZU1	Q9QXV9	2.3	1.4E-01	0.3	8.1E-01	-3.7	2.1E-02	-1.7	2.1E-01
ENSMUST00000109604	RNA binding motif protein 12 [Source:MGI Symbol;Acc:MGI:1922960]		Q8R4X3	5.1	7.7E-03	6.7	1.7E-04	-0.6	6.2E-01	-1.0	1.4E-01
ENSMUST00000108114	HNF1 homeobox B [Source:MGI Symbol;Acc:MGI:98505]		P27889	6.7	4.6E-02	6.0	8.6E-02	-1.0	7.9E-01	-0.3	9.0E-01
ENSMUST00000108116	lipolysis stimulated lipoprotein receptor [Source:MGI Symbol;Acc:MGI:1927471]		Q99KG5	-2.8	9.0E-02	-2.0	3.4E-01	0.2	8.8E-01	-0.5	7.9E-01
ENSMUST00000109605	activating transcription factor 4 [Source:MGI Symbol;Acc:MGI:88096]		Q06507	-4.7	8.9E-06	-2.5	5.9E-02	0.3	5.9E-01	-0.6	6.2E-01
ENSMUST00000108121	Bardet-Biedl syndrome 12 (human) [Source:MGI Symbol;Acc:MGI:2686651]	Z4YKQ3		4.4	7.5E-02	1.9	3.9E-01	-3.1	2.1E-01	-0.5	7.5E-01
ENSMUST00000109607	copine I [Source:MGI Symbol;Acc:MGI:2386621]		Q8C166	-7.2	1.4E-03	7.2	7.9E-05	-0.5	6.4E-01	-2.2	6.0E-03
ENSMUST00000108126	RIKEN cDNA 3110043O21 gene [Source:MGI Symbol;Acc:MGI:1920455]	A2ANZ2		-3.4	2.0E-01	-0.3	9.4E-01	3.2	2.4E-01	0.1	9.7E-01
ENSMUST00000109608	copine I [Source:MGI Symbol;Acc:MGI:2386621]		Q8C166	-6.4	2.7E-05	-7.2	8.0E-05	0.1	8.5E-01	-0.1	9.2E-01
ENSMUST00000109611	fer-1-like 4 (C. elegans) [Source:MGI Symbol;Acc:MGI:1921812]	Z4YL23		9.1	7.3E-06	-4.2	2.2E-02	1.0	2.2E-01	-0.9	5.8E-01
ENSMUST00000108142	origin recognition complex, subunit 3 [Source:MGI Symbol;Acc:MGI:1354944]		Q9JK30	-1.6	5.6E-01	-3.7	2.4E-01	-3.2	9.6E-02	-1.1	7.5E-01
ENSMUST00000108146	peroxisomal biogenesis factor 12 [Source:MGI Symbol;Acc:MGI:2144177]	Q5SWQ8	Q8VC48	-2.3	2.1E-01	1.3	5.3E-01	0.8	6.2E-01	-2.7	1.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000109616	chromobox 7 [Source:MGI Symbol;Acc:MGI:1196439]		Q8VDS3	-4.9	1.9E-02	6.4	3.3E-04	-0.5	7.0E-01	-0.4	5.4E-01
ENSMUST00000109617	RIKEN cDNA 6430550D23 gene [Source:MGI Symbol;Acc:MGI:2443361]	E9Q1X6		7.1	8.5E-04	0.9	3.3E-01	-0.9	2.4E-01	0.1	9.2E-01
ENSMUST00000109621	TOX high mobility group box family member 3 [Source:MGI Symbol;Acc:MGI:3039593]		Q80W03	7.8	1.3E-04	9.9	2.2E-02	4.0	2.9E-01	0.7	6.3E-01
ENSMUST00000108153	RNA guanylyltransferase and 5'-phosphatase [Source:MGI Symbol;Acc:MGI:1329041]	Q3UA94	O55236	0.7	1.1E-01	0.7	2.3E-01	0.3	5.2E-01	0.3	5.5E-01
ENSMUST00000109625	chromobox 6 [Source:MGI Symbol;Acc:MGI:3512628]	Q3UK98		5.8	2.1E-02	1.6	6.2E-01	-0.3	9.3E-01	3.9	1.4E-01
ENSMUST00000108156	Bardet-Biedl syndrome 7 (human) [Source:MGI Symbol;Acc:MGI:1918742]		Q8K2G4	2.8	1.9E-01	1.1	5.5E-01	-3.7	7.9E-02	-2.0	2.4E-01
ENSMUST00000109626	cylindromatosis (turban tumor syndrome) [Source:MGI Symbol;Acc:MGI:1921506]		Q80TQ2	-4.4	1.7E-02	7.8	3.8E-05	-0.6	6.1E-01	-0.5	3.8E-01
ENSMUST00000108161	U2 small nuclear RNA auxiliary factor 1-like 4 [Source:MGI Symbol;Acc:MGI:2678374]	F8WH71		4.0	5.7E-02	2.3	4.6E-01	1.1	6.1E-01	2.7	3.3E-01
ENSMUST00000109627	chromobox 6 [Source:MGI Symbol;Acc:MGI:3512628]		Q9DBY5	3.7	1.3E-03	5.4	6.2E-03	1.4	3.6E-01	0.9	3.2E-01
ENSMUST00000109629	predicted gene 15557 [Source:MGI Symbol;Acc:MGI:3783006]	A6PWY0		7.5	9.7E-05	-5.7	5.1E-03	1.9	9.0E-03	-0.8	6.7E-01
ENSMUST00000108175	r factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta [Source:MGI Symbol;Acc:MGI:30		Q2TB02	1.8	4.5E-01	-4.8	1.8E-01	-4.6	3.3E-02	2.0	5.7E-01
ENSMUST00000109638	eukaryotic translation initiation factor 6 [Source:MGI Symbol;Acc:MGI:1196288]	B1AZQ4		2.2	2.2E-03	-0.1	9.4E-01	2.5	1.3E-01	-2.1	2.7E-01
ENSMUST00000108180	BTB and CNC homology 2 [Source:MGI Symbol;Acc:MGI:894679]		P97303	2.8	3.9E-01	2.3	4.4E-01	-1.6	6.0E-01	-1.2	6.5E-01
ENSMUST00000108182	₹1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2150	A0A0B4J1K8	Q9QZ73	-1.6	5.7E-01	-2.8	4.4E-01	-1.3	5.7E-01	-0.1	9.8E-01
ENSMUST00000109641	SEC61, gamma subunit [Source:MGI Symbol;Acc:MGI:1202066]	Q5SWJ8	P60060	5.1	2.7E-03	8.6	8.1E-04	-2.2	3.0E-01	-0.3	7.0E-01
ENSMUST00000108184	mitogen-activated protein kinase kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346877]	A2AP92		1.1	7.0E-01	-4.6	2.5E-01	-4.1	7.7E-02	1.6	7.0E-01
ENSMUST00000109645	V-set and transmembrane domain containing 2A [Source:MGI Symbol;Acc:MGI:2384826]		Q8R0A6	6.9	6.5E-05	4.1	3.1E-02	-0.7	6.9E-01	1.9	1.1E-01
ENSMUST00000108190	WD repeat domain 62 [Source:MGI Symbol;Acc:MGI:1923696]	E9QK36		0.0	1.0E+00	-0.1	9.8E-01	1.7	5.5E-01	1.8	5.2E-01
ENSMUST00000109647	V-set and transmembrane domain containing 2A [Source:MGI Symbol;Acc:MGI:2384826]	F6Y6A6		6.1	9.2E-04	-4.5	3.5E-03	-0.6	2.5E-01	-0.8	5.4E-01
ENSMUST00000109648	family with sequence similarity 227, member A [Source:MGI Symbol;Acc:MGI:1922979]	Q9D3V8		3.3	8.4E-04	-5.1	3.1E-03	-1.6	3.0E-02	-1.0	5.0E-01
ENSMUST00000109679	solute carrier family 6 (neurotransmitter transporter), member 18 [Source:MGI Symbol;Acc:MGI:1336892]		O88576	5.8	4.8E-04	-5.6	4.4E-03	-2.4	7.5E-03	-0.2	8.9E-01
ENSMUST00000109682	dynein light chain roadblock-type 1 [Source:MGI Symbol;Acc:MGI:1914318]		P62627	-7.4	2.4E-05	-6.2	1.1E-03	1.0	9.7E-02	-1.4	3.6E-01
ENSMUST00000109685	itchy, E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1202301]		Q8C863	-4.4	1.4E-02	5.6	3.7E-03	-0.7	6.8E-01	0.2	7.9E-01
ENSMUST00000109686	neuropilin (NRP) and tolloid (TLL)-like 2 [Source:MGI Symbol;Acc:MGI:1921763]		Q8BNJ6	3.4	1.0E-03	-5.2	1.1E-03	-0.2	7.0E-01	-1.1	4.0E-01
ENSMUST00000109687	TRIO and F-actin binding protein [Source:MGI Symbol;Acc:MGI:1349410]		Q99KW3	4.4	7.3E-03	2.6	4.2E-02	-0.9	4.1E-01	0.6	5.0E-01
ENSMUST00000109688	TRIO and F-actin binding protein [Source:MGI Symbol;Acc:MGI:1349410]	E9QMQ3		-5.3	2.6E-04	-2.7	7.3E-02	0.0	9.9E-01	-0.5	7.0E-01
ENSMUST00000109690	TRIO and F-actin binding protein [Source:MGI Symbol;Acc:MGI:1349410]		Q99KW3	9.0	2.1E-02	5.0	2.5E-03	-0.2	9.0E-01	-0.1	9.3E-01
ENSMUST00000109691	Rap guanine nucleotide exchange factor (GEF) 5 [Source:MGI Symbol;Acc:MGI:2444365]		Q8C0Q9	2.4	4.4E-03	6.2	1.2E-03	0.5	7.1E-01	0.3	6.9E-01
ENSMUST00000109698	SH3-domain binding protein 1 [Source:MGI Symbol;Acc:MGI:104603]	A2A5V2		-2.6	1.7E-02	1.4	8.4E-02	-0.2	7.6E-01	1.3	6.4E-02
ENSMUST00000109699	NOL1/NOP2/Sun domain family member 2 [Source:MGI Symbol;Acc:MGI:107252]		Q1HFZ0	-6.1	2.2E-05	8.6	4.2E-04	-0.7	7.1E-01	-0.5	4.8E-01
ENSMUST00000109703	peroxisomal membrane protein 4 [Source:MGI Symbol;Acc:MGI:1891701]	A2AKD6		2.2	5.0E-03	6.8	3.0E-04	-0.7	6.1E-01	0.5	4.6E-01
ENSMUST00000108222	MMS22-like, DNA repair protein [Source:MGI Symbol;Acc:MGI:2684980]		B1AUR6	-2.6	3.2E-01	5.1	1.5E-01	4.4	1.7E-01	-3.3	2.2E-01
ENSMUST00000109716	N-terminal EF-hand calcium binding protein 3 [Source:MGI Symbol;Acc:MGI:1861721]		Q9D6J4	5.1	3.5E-02	6.1	2.6E-05	-0.1	8.6E-01	-0.4	3.9E-01
ENSMUST00000109721	cerebral cavernous malformation 2 [Source:MGI Symbol;Acc:MGI:2384924]	F7AVU1		-7.7	1.1E-04	4.8	8.4E-03	-0.6	7.1E-01	-0.5	5.7E-01
ENSMUST00000109722	cerebral cavernous malformation 2 [Source:MGI Symbol;Acc:MGI:2384924]	F7AVU1		-4.4	2.7E-03	-2.1	2.3E-02	-1.1	6.2E-02	-2.4	2.8E-02
ENSMUST00000108232	ubiquitin specific petidase 45 [Source:MGI Symbol;Acc:MGI:101850]		Q8K387	2.8	1.4E-01	0.0	9.9E-01	-0.9	6.1E-01	1.9	4.7E-01
ENSMUST00000109730	CDK5 regulatory subunit associated protein 1 [Source:MGI Symbol;Acc:MGI:1914221]	Q3UW67		7.2	4.5E-04	4.1	6.0E-04	-2.5	1.6E-02	-0.6	3.0E-01
ENSMUST00000109737	H2A histone family, member V [Source:MGI Symbol;Acc:MGI:1924855]	B2RVP5	Q3THW5	-3.1	4.4E-04	-2.0	1.2E-01	0.8	3.1E-01	-1.5	2.7E-01
ENSMUST00000108237	Yip1 interacting factor homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924504]	D3YY42		-0.8	6.4E-01	1.4	3.8E-01	-0.4	7.8E-01	-2.5	1.6E-01
ENSMUST00000109738	ribonuclease H2, large subunit [Source:MGI Symbol;Acc:MGI:1916974]		Q9CWY8	5.7	5.2E-04	-3.8	9.4E-03	0.3	5.8E-01	0.0	9.9E-01
ENSMUST00000109746	BPI fold containing family A, member 3 [Source:MGI Symbol;Acc:MGI:1920638]		Q9D9J8	6.5	5.6E-03	2.8	2.1E-03	0.3	6.0E-01	0.1	8.0E-01
ENSMUST00000109747	thioredoxin 2 [Source:MGI Symbol;Acc:MGI:1929468]	A2A439		3.6	2.0E-03	-4.6	9.8E-04	-0.3	5.6E-01	-0.8	4.3E-01
ENSMUST00000108241	UTP6, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:2445193]		Q8VCY6	3.9	4.6E-02	-2.5	1.9E-01	-5.2	8.2E-03	1.3	4.9E-01
ENSMUST00000108242	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide [Source:MGI Symbol;Acc:MGI:1206581]	D3YY41		-6.4	1.4E-01	-5.7	2.8E-01	-0.6	7.8E-01	-1.3	8.3E-01
ENSMUST00000109748	thioredoxin 2 [Source:MGI Symbol;Acc:MGI:1929468]		P97493	2.6	2.0E-02	-3.6	4.6E-04	0.9	3.2E-02	0.0	9.9E-01
ENSMUST00000108246	WW domain containing E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1861728]		Q8BZZ3	-2.0	1.6E-01	-3.7	7.4E-02	0.1	9.2E-01	1.9	3.3E-01
ENSMUST00000108249	protein kinase C, iota [Source:MGI Symbol;Acc:MGI:99260]		Q62074	-0.1	9.1E-01	1.1	8.6E-02	0.8	1.1E-01	-0.4	4.8E-01
ENSMUST00000109753	BPI fold containing family A, member 6 [Source:MGI Symbol;Acc:MGI:3647736]	Q0VGU8		6.4	2.9E-04	0.1	8.6E-01	-1.4	1.3E-02	-0.1	8.5E-01
ENSMUST00000109761	RAD23a homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:105126]		P54726	-5.2	1.3E-03	7.4	5.9E-05	-0.5	6.4E-01	-0.7	2.1E-01
ENSMUST00000108258	G protein-coupled receptor 160 [Source:MGI Symbol;Acc:MGI:1919112]		Q3U3F9	1.0	6.9E-01	0.4	8.9E-01	-2.1	3.6E-01	-1.4	5.8E-01
ENSMUST00000108261	G protein-coupled receptor 160 [Source:MGI Symbol;Acc:MGI:1919112]		Q3U3F9	1.9	3.5E-01	5.0	4.2E-02	0.8	6.8E-01	-2.3	2.5E-01
ENSMUST00000109762	nuclear factor I/X [Source:MGI Symbol;Acc:MGI:97311]	Q3TYK3		7.3	5.7E-04	6.7	3.8E-05	-1.9	8.1E-02	-0.1	8.7E-01
ENSMUST00000109764	nuclear factor I/X [Source:MGI Symbol;Acc:MGI:97311]	E9PUH7		2.8	3.1E-03	4.0	2.6E-02	0.0	9.7E-01	-0.7	5.0E-01
ENSMUST00000109768	tRNA methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1289155]	E9PWD4		-3.4	1.6E-02	6.4	2.0E-02	-0.8	7.6E-01	-1.0	4.6E-01
ENSMUST00000109769	CDC14 cell division cycle 14B [Source:MGI Symbol;Acc:MGI:2441808]		Q6PFY9	2.9	5.7E-04	6.6	1.7E-04	-0.5	6.7E-01	-1.0	1.4E-01
ENSMUST00000109775	apolipoprotein L 9b [Source:MGI Symbol;Acc:MGI:1919148]	Q8C7I4		7.6	4.2E-05	-5.1	3.4E-05	0.2	5.4E-01	-0.3	6.4E-01
ENSMUST00000109782	COMM domain containing 7 [Source:MGI Symbol;Acc:MGI:1914197]	A2AU52		-5.5	7.0E-05	-4.6	2.3E-03	-0.1	8.3E-01	-0.3	8.2E-01
ENSMUST00000109784	nucleolar protein 4-like [Source:MGI Symbol;Acc:MGI:1918765]	Q3TZG8		4.1	5.6E-05	4.9	6.4E-02	-0.8	7.3E-01	0.7	6.4E-01
ENSMUST00000109787	zinc finger, MIZ-type containing 2 [Source:MGI Symbol;Acc:MGI:106374]		Q8CIE2	-4.2	2.3E-02	5.3	1.1E-03	-0.3	8.1E-01	-1.2	1.8E-01
ENSMUST00000109790	additional sex combs like 1 [Source:MGI Symbol;Acc:MGI:2684063]	Q24JP2	P59598	-4.1	2.0E-05	-5.9	3.5E-04	-1.2	1.6E-02	-0.8	5.0E-01
ENSMUST00000108277	tumor necrosis factor, alpha-induced protein 1 (endothelial) [Source:MGI Symbol;Acc:MGI:104961]		O70479	3.0	1.7E-01	1.3	6.9E-01	0.9	6.7E-01	2.6	3.8E-01
ENSMUST00000108278	F-box protein 17 [Source:MGI Symbol;Acc:MGI:1354707]	Q3V064	Q9QZM8	-0.3	9.0E-01	2.8	3.0E-01	2.2	3.7E-01	-0.9	6.7E-01
ENSMUST00000108280	F-box protein 27 [Source:MGI Symbol;Acc:MGI:2685007]	Q3TEI7		3.2	1.5E-01	5.8	7.1E-02	1.8	5.5E-01	-0.8	6.3E-01
ENSMUST00000109793	COMM domain containing 5 [Source:MGI Symbol;Acc:MGI:1913648]			-1.8	2.1E-02	6.0	3.5E-03	-1.0	5.8E-01	-2.0	7.2E-02
ENSMUST00000108283	p21 protein (Cdc42/Rac)-activated kinase 4 [Source:MGI Symbol;Acc:MGI:1917834]		Q8BTW9	-1.4	2.1E-01	-3.4	8.4E-02	0.6	5.3E-01	2.6	1.7E-01
ENSMUST00000109799	hemopoietic cell kinase [Source:MGI Symbol;Acc:MGI:96052]		P08103	-6.4	2.7E-06	7.7	2.1E-04	1.2	3.9E-01	-0.6	3.8E-01
ENSMUST00000109802	adhesion G protein-coupled receptor E5 [Source:MGI Symbol;Acc:MGI:1347095]	E9QMJ5		-7.4	8.5E-06	3.9	1.6E-03	0.0	9.6E-01	0.0	9.7E-01
ENSMUST00000109810	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 [Source:MGI Symbol;Acc:MGI:1915528]		Q8VDW0	5.0	7.0E-03	-3.7	8.9E-03	-0.6	2.9E-01	0.2	8.7E-01
ENSMUST00000109816	TPX2, microtubule-associated protein homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1919369]		A2APB8	-6.4	2.6E-04	-3.6	1.0E-02	-0.5	4.8E-01	-1.2	3.5E-01
ENSMUST00000109820	BCL2-like 1 [Source:MGI Symbol;Acc:MGI:88139]	Q5HZH3	Q64373	-4.4	1.1E-02	2.6	9.3E-03	-0.2	8.0E-01	-0.3	6.3E-01
ENSMUST00000109829	AE binding protein 1 [Source:MGI Symbol;Acc:MGI:1197012]		Q640N1	5.1	2.4E-02	7.3	5.9E-04	-1.2	4.6E-01	0.4	5.9E-01
ENSMUST00000108296				-0.8	7.2E-01	-0.6	7.8E-01	-1.7	3.4E-01	-1.8	4.4E-01
ENSMUST00000109831	calmegin [Source:MGI Symbol;Acc:MGI:107472]		P52194	5.4	5.9E-03	6.2	3.2E-04	-0.6	6.4E-01	0.2	8.1E-01
ENSMUST00000109832	protein phosphatase 2, regulatory subunit B', gamma [Source:MGI Symbol;Acc:MGI:1349475]		Q60996	-6.8	1.3E-03	5.9	2.1E-04	-2.0	8.1E-02	0.5	4.5E-01
ENSMUST00000108304	GTP binding protein (gene overexpressed in skeletal muscle) [Source:MGI Symbol;Acc:MGI:99844]	Q3TH76	P55041	5.8	5.9E-02	4.0	2.2E-01	-0.7	8.4E-01	1.2	5.5E-01
ENSMUST00000108305	spermatogenesis associated 16 [Source:MGI Symbol;Acc:MGI:1918112]		Q8C636	3.1	1.8E-01	3.4	1.8E-01	-0.5	8.5E-01	-0.8	6.6E-01
ENSMUST00000108307	RIKEN cDNA 1110037F02 gene [Source:MGI Symbol;Acc:MGI:1913435]	E9PZY8		2.8	1.2E-01	7.0	2.2E-03	-0.4	8.3E-01	-4.6	3.2E-03

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000108308	neuroligin 1 [Source:MGI Symbol;Acc:MGI:2179435]	E9QK34		4.5	9.8E-02	4.3	1.8E-01	0.3	9.3E-01	0.5	8.2E-01
ENSMUST00000108311	epithelial splicing regulatory protein 1 [Source:MGI Symbol;Acc:MGI:1917326]	F8WGU3		5.6	4.8E-02	4.9	1.1E-01	-0.6	8.3E-01	0.1	9.7E-01
ENSMUST00000109837	polymerase (DNA directed), mu [Source:MGI Symbol;Acc:MGI:1860191]	Q5NCI3		-5.4	4.4E-03	5.2	6.2E-02	-0.8	7.7E-01	0.4	7.8E-01
ENSMUST00000108314				-0.3	8.1E-01	1.1	4.3E-01	0.6	5.5E-01	-0.7	5.7E-01
ENSMUST00000109838	neurotrophic tyrosine kinase, receptor, type 2 [Source:MGI Symbol;Acc:MGI:97384]	Q3UHE3	P15209	4.8	1.4E-05	4.9	9.4E-05	0.1	8.9E-01	0.0	9.9E-01
ENSMUST00000109845	drebrin-like [Source:MGI Symbol;Acc:MGI:700006]		Q62418	-7.6	2.7E-05	6.6	1.6E-04	0.0	9.7E-01	-1.2	8.2E-02
ENSMUST00000109847	RanBP-type and C3HC4-type zinc finger containing 1 [Source:MGI Symbol;Acc:MGI:1344372]		Q9WUB0	-7.8	6.2E-05	1.8	6.6E-02	-4.3	2.5E-03	-0.4	5.8E-01
ENSMUST00000109848	tryptophanyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:104630]	Q3U6U7	P32921	-3.7	1.5E-02	-5.4	1.4E-03	0.7	1.7E-01	-0.8	5.8E-01
ENSMUST00000109855	ankyrin repeat domain 36 [Source:MGI Symbol;Acc:MGI:1923639]	Q9EQ29		6.5	9.2E-05	-6.0	5.1E-04	-0.1	8.4E-01	-0.8	5.5E-01
ENSMUST00000109856	ankyrin repeat domain 36 [Source:MGI Symbol;Acc:MGI:1923639]	D3Z4K0		7.4	4.6E-05	6.2	3.4E-04	-0.5	6.5E-01	-3.8	1.4E-03
ENSMUST00000108324	cyclin E2 [Source:MGI Symbol;Acc:MGI:1329034]	Q544H6	Q9Z238	-2.8	8.5E-02	0.0	9.9E-01	0.5	6.8E-01	-2.4	1.6E-01
ENSMUST00000109864	family with sequence similarity 110, member A [Source:MGI Symbol;Acc:MGI:1921097]		Q8R184	6.3	1.3E-03	-1.4	3.9E-01	-4.5	1.3E-02	1.4	3.5E-01
ENSMUST00000109867	zinc and ring finger 3 [Source:MGI Symbol;Acc:MGI:3039616]		Q5SSZ7	5.5	1.3E-04	3.1	8.0E-03	-0.5	5.5E-01	-0.5	5.5E-01
ENSMUST00000109869	proteasome (prosome, macropain) inhibitor subunit 1 [Source:MGI Symbol;Acc:MGI:1346072]	A2AU35	Q8BHL8	-4.2	1.1E-03	3.2	2.8E-02	-0.9	4.4E-01	-0.1	9.3E-01
ENSMUST00000109872	transmembrane protein 74B [Source:MGI Symbol;Acc:MGI:1918629]	A2AU34		5.2	1.1E-03	3.3	5.4E-03	0.5	5.6E-01	0.4	5.7E-01
ENSMUST00000109874	SMAD family member 5 [Source:MGI Symbol;Acc:MGI:1328787]		P97454	7.5	5.8E-05	5.8	2.1E-02	0.8	7.0E-01	2.6	6.0E-02
ENSMUST00000108340	aspartate-beta-hydroxylase [Source:MGI Symbol;Acc:MGI:1914186]	A2AL85		1.8	5.5E-01	3.5	2.2E-01	-1.1	7.0E-01	-2.8	2.6E-01
ENSMUST00000108341	mitogen-activated protein kinase kinase kinase 10 [Source:MGI Symbol;Acc:MGI:1346879]	D3YXM8		0.7	8.0E-01	1.2	6.6E-01	-1.0	6.6E-01	-1.5	5.9E-01
ENSMUST00000109885	SMAD family member 1 [Source:MGI Symbol;Acc:MGI:109452]	Q8C3Y6		3.7	4.0E-04	3.4	3.1E-02	-0.7	5.5E-01	0.1	9.0E-01
ENSMUST00000108343	thymoma viral proto-oncogene 2 [Source:MGI Symbol;Acc:MGI:104874]	Q3TY95	Q60823	1.0	4.8E-01	4.2	4.5E-02	1.9	2.5E-01	-1.2	4.3E-01
ENSMUST00000108344	thymoma viral proto-oncogene 2 [Source:MGI Symbol;Acc:MGI:104874]	Q3TY95	Q60823	0.5	4.4E-01	1.5	1.0E-01	1.2	1.0E-01	0.1	8.4E-01
ENSMUST00000108345	YTH domain family 3 [Source:MGI Symbol;Acc:MGI:1918850]		Q8BYK6	-3.2	6.3E-02	-3.4	1.6E-01	0.1	9.3E-01	0.3	8.9E-01
ENSMUST00000109888	predicted gene 14147 [Source:MGI Symbol;Acc:MGI:3651555]	A2AQX6		9.4	2.6E-04	-5.8	1.8E-02	0.9	2.5E-01	0.4	8.7E-01
ENSMUST00000108347	predicted gene 5150 [Source:MGI Symbol;Acc:MGI:3779469]	Q1AN92		-0.3	9.2E-01	-6.8	4.2E-02	-7.4	5.2E-03	-0.9	8.0E-01
ENSMUST00000108348	clavesin 1 [Source:MGI Symbol;Acc:MGI:1921688]		Q9D4C9	4.6	1.0E-01	3.8	2.3E-01	-0.3	9.3E-01	0.5	8.2E-01
ENSMUST00000109895	growth arrest-specific 2 like 1 [Source:MGI Symbol;Acc:MGI:1926176]		Q8JZP9	-6.0	1.6E-04	-3.9	1.4E-02	0.1	8.3E-01	-0.9	5.5E-01
ENSMUST00000109896	ninein-like [Source:MGI Symbol;Acc:MGI:1925427]		Q6ZQ12	7.6	9.2E-06	-1.9	4.0E-01	2.4	8.7E-02	0.5	8.1E-01
ENSMUST00000109901	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:109301]		Q61183	-6.3	1.6E-04	6.7	4.0E-04	-0.1	9.1E-01	-0.4	6.3E-01
ENSMUST00000109905	transmembrane emp24 protein transport domain containing 9 [Source:MGI Symbol;Acc:MGI:1914761]	Q6PDC2	Q99KF1	-3.6	4.2E-05	-8.5	3.3E-03	-0.8	2.7E-01	-0.7	7.8E-01
ENSMUST00000109910	neurofibromatosis 2 [Source:MGI Symbol;Acc:MGI:97307]		P46662	-1.0	2.7E-02	4.8	5.2E-02	-0.6	7.9E-01	2.4	1.2E-01
ENSMUST00000108358	biliverdin reductase B (flavin reductase (NADPH)) [Source:MGI Symbol;Acc:MGI:2385271]	E9PZC3		-0.7	3.9E-01	2.5	3.8E-02	2.5	1.9E-02	-0.7	4.3E-01
ENSMUST00000108360	PHD finger protein 12 [Source:MGI Symbol;Acc:MGI:1924057]		Q5SPL2	4.5	4.2E-02	1.1	7.0E-01	-1.0	6.6E-01	2.4	2.6E-01
ENSMUST00000109913	nuclear receptor subfamily 3, group C, member 2 [Source:MGI Symbol;Acc:MGI:99459]	A3KN90		8.0	8.9E-05	-3.7	3.6E-03	-0.4	5.2E-01	-0.3	7.8E-01
ENSMUST00000109914	zinc finger protein 345 [Source:MGI Symbol;Acc:MGI:3652219]	A2AQA1		4.9	3.0E-05	8.1	3.4E-05	-0.6	6.1E-01	-1.2	5.3E-02
ENSMUST00000109921	drebrin 1 [Source:MGI Symbol;Acc:MGI:1931838]			5.0	3.0E-02	5.6	7.3E-02	-0.9	7.7E-01	0.7	6.9E-01
ENSMUST00000108374	syndecan binding protein [Source:MGI Symbol;Acc:MGI:1337026]	A2AKJ9		-0.1	9.0E-01	-0.3	7.8E-01	-1.4	1.1E-01	-1.2	2.1E-01
ENSMUST00000108375	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]		Q9JMH9	0.7	7.3E-01	-1.4	6.1E-01	-1.9	3.2E-01	0.2	9.5E-01
ENSMUST00000109923	drebrin 1 [Source:MGI Symbol;Acc:MGI:1931838]	Q3TRK3	Q9QXS6	5.4	4.4E-03	4.2	1.4E-02	-4.5	2.2E-02	-1.8	1.1E-01
ENSMUST00000109934	synapse differentiation inducing 1 [Source:MGI Symbol;Acc:MGI:3702158]		A2ANU3	6.2	2.4E-02	5.9	3.2E-04	1.2	2.7E-01	0.6	3.6E-01
ENSMUST00000109936	calmin [Source:MGI Symbol;Acc:MGI:2136957]		Q8C5W0	6.1	7.3E-03	3.7	9.2E-02	-1.0	6.2E-01	1.1	4.2E-01
ENSMUST00000109937	calmin [Source:MGI Symbol;Acc:MGI:2136957]		Q8C5W0	-5.1	2.9E-02	1.7	3.8E-01	-2.6	1.9E-01	0.9	5.4E-01
ENSMUST00000109941	predicted gene 11032 [Source:MGI Symbol;Acc:MGI:3779255]	F6ZRP0		7.2	7.5E-06	-2.8	1.7E-01	0.5	5.6E-01	-0.2	9.1E-01
ENSMUST00000108385	cytochrome P450, family 2, subfamily t, polypeptide 4 [Source:MGI Symbol;Acc:MGI:2686296]	D3Z7F6		5.2	5.3E-02	3.2	2.4E-01	-2.3	4.0E-01	-0.3	8.9E-01
ENSMUST00000109943	myotubularin related protein 3 [Source:MGI Symbol;Acc:MGI:1921552]	B1ATD5		-6.0	1.6E-03	5.9	1.8E-02	-0.7	7.6E-01	-1.0	4.6E-01
ENSMUST00000109950	transcriptional regulator, SIN3B (yeast) [Source:MGI Symbol;Acc:MGI:107158]	Q3TN09	Q62141	-5.5	1.3E-05	7.0	4.3E-04	-0.2	8.7E-01	0.5	4.8E-01
ENSMUST00000108400	EF-hand calcium binding domain 5 [Source:MGI Symbol;Acc:MGI:2442440]		A0JP43	2.4	3.6E-02	1.0	4.5E-01	0.0	9.8E-01	1.4	2.2E-01
ENSMUST00000108402	)lute carrier family 6 (neurotransmitter transporter, serotonin), member 4 [Source:MGI Symbol;Acc:MGI:9628		Q60857	4.4	1.3E-01	5.0	1.3E-01	-0.3	9.2E-01	-0.9	6.5E-01
ENSMUST00000109957	eine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3J [Source:MGI Symbol;Acc:M	D3Z451		6.9	5.4E-05	-3.4	8.7E-04	0.2	6.0E-01	0.0	9.8E-01
ENSMUST00000109958	serine (or cysteine) peptidase inhibitor, clade A, member 3I [Source:MGI Symbol;Acc:MGI:2182841]	D3Z450		7.0	2.7E-04	-7.9	8.7E-04	0.9	7.6E-02	-0.6	7.5E-01
ENSMUST00000109961	NTF2-related export protein 1 [Source:MGI Symbol;Acc:MGI:1929619]		Q9QZV9	-4.0	6.8E-04	-2.9	2.5E-02	0.0	1.0E+00	0.6	6.0E-01
ENSMUST00000109962	somatostatin receptor 4 [Source:MGI Symbol;Acc:MGI:105372]			6.4	1.1E-05	6.9	4.7E-03	-0.7	7.5E-01	-1.5	1.9E-01
ENSMUST00000109964	forkhead box A2 [Source:MGI Symbol;Acc:MGI:1347476]	G5E8P5		4.1	1.1E-02	2.5	4.1E-01	-0.8	7.6E-01	3.7	1.3E-01
ENSMUST00000109965	serine (or cysteine) peptidase inhibitor, clade A, member 3A [Source:MGI Symbol;Acc:MGI:1921319]		Q6P4P1	6.2	1.2E-04	6.1	2.0E-02	-3.2	2.2E-01	0.7	5.8E-01
ENSMUST00000108425	v-crk sarcoma virus CT10 oncogene homolog (avian) [Source:MGI Symbol;Acc:MGI:88508]	Q8JZR2		-1.4	1.2E-01	-2.3	7.9E-02	-0.1	8.6E-01	0.7	5.4E-01
ENSMUST00000109968	paired box 1 [Source:MGI Symbol;Acc:MGI:97485]		P09084	8.9	1.1E-05	3.5	8.8E-03	-0.3	7.4E-01	-0.4	6.5E-01
ENSMUST00000108429	ribosomal protein S19 [Source:MGI Symbol;Acc:MGI:1333780]		Q9CZX8	-3.0	4.5E-02	-2.6	5.0E-02	-2.2	2.3E-02	-2.6	9.4E-02
ENSMUST00000108430	ribosomal protein S19 [Source:MGI Symbol;Acc:MGI:1333780]		Q9CZX8	-0.1	9.1E-01	-5.0	5.7E-03	-2.2	1.2E-02	2.6	8.5E-02
ENSMUST00000108431	myosin IC [Source:MGI Symbol;Acc:MGI:106612]		Q9WTI7	-2.7	3.3E-01	-1.9	4.9E-01	-0.8	6.7E-01	-1.7	5.9E-01
ENSMUST00000108433	solute carrier family 43, member 2 [Source:MGI Symbol;Acc:MGI:2442746]		Q8CGA3	-3.3	7.3E-02	-1.7	4.5E-01	1.2	2.9E-01	-0.3	8.8E-01
ENSMUST00000108435	TLC domain containing 2 [Source:MGI Symbol;Acc:MGI:1917141]		Q8VC26	-3.5	4.4E-02	-1.6	3.9E-01	0.9	4.7E-01	-0.9	6.2E-01
ENSMUST00000108436	zinc finger protein 94 [Source:MGI Symbol;Acc:MGI:107610]	E9Q6Y4		5.2	8.6E-02	0.2	9.5E-01	-2.8	3.7E-01	2.2	4.5E-01
ENSMUST00000109975	ic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Source:MGI Symbol;Acc:MGI:1			7.1	3.6E-05	4.1	4.0E-03	-1.1	3.2E-01	-1.1	1.7E-01
ENSMUST00000109981	galactose-3-O-sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1858277]		Q9JHE4	5.2	2.5E-04	6.1	1.1E-02	1.2	5.4E-01	0.3	8.2E-01
ENSMUST00000109985	pescadillo homolog 1, containing BRCT domain (zebrafish) [Source:MGI Symbol;Acc:MGI:1890613]	Q5SQ20		5.8	3.2E-02	-0.4	4.9E-01	1.5	2.1E-03	-0.3	6.3E-01
ENSMUST00000108453	zinc finger protein 296 [Source:MGI Symbol;Acc:MGI:1926956]	E9Q6W4		1.0	8.2E-02	1.9	1.7E-02	0.5	3.8E-01	-0.4	4.7E-01
ENSMUST00000108458	kinesin light chain 3 [Source:MGI Symbol;Acc:MGI:1277971]		Q91W40	1.3	4.7E-01	-0.4	7.9E-01	-1.7	2.6E-01	0.1	9.6E-01
ENSMUST00000109986	Ral GTPase activating protein, alpha subunit 2 (catalytic) [Source:MGI Symbol;Acc:MGI:3036245]	A0A0A0MQD7		1.5	1.6E-02	2.4	4.3E-01	-0.7	7.9E-01	3.0	2.2E-01
ENSMUST00000108460	repair cross-complementing rodent repair deficiency, complementation group 2 [Source:MGI Symbol;Acc:MG	E9Q6K1		-0.4	8.8E-01	1.7	5.1E-01	0.3	9.1E-01	-1.8	4.0E-01
ENSMUST00000108461	repair cross-complementing rodent repair deficiency, complementation group 2 [Source:MGI Symbol;Acc:MG	D3Z700		-3.9	1.1E-01	2.2	3.4E-01	2.8	1.8E-01	-3.3	1.7E-01
ENSMUST00000109988	transcobalamin 2 [Source:MGI Symbol;Acc:MGI:98534]		O88968	-3.5	2.8E-02	7.4	3.0E-03	-0.9	6.7E-01	-0.8	4.8E-01
ENSMUST00000109989	transcobalamin 2 [Source:MGI Symbol;Acc:MGI:98534]		O88968	-8.7	6.8E-05	0.7	5.2E-01	-4.5	5.1E-03	1.4	1.8E-01
ENSMUST00000108476	cystinosis, nephropathic [Source:MGI Symbol;Acc:MGI:1932872]	Q542U5	P57757	-1.4	1.3E-01	0.7	5.9E-01	2.2	3.6E-02	0.0	9.7E-01
ENSMUST00000109991	transcobalamin 2 [Source:MGI Symbol;Acc:MGI:98534]		O88968	-6.3	5.0E-03	-6.2	2.0E-03	1.3	2.8E-02	-0.8	6.1E-01
ENSMUST00000108480	ER membrane protein complex subunit 6 [Source:MGI Symbol;Acc:MGI:1913298]		Q9CQW0	-0.4	7.2E-01	-1.3	2.8E-01	-1.2	2.2E-01	-0.3	8.2E-01
ENSMUST00000109993	transcobalamin 2 [Source:MGI Symbol;Acc:MGI:98534]		O88968	-6.0	7.5E-04	6.6	3.9E-03	-0.6	7.5E-01	-2.1	6.6E-02
ENSMUST00000108484	ATPase, Ca++ transporting, ubiquitous [Source:MGI Symbol;Acc:MGI:1194503]	B1ATS4		-0.9	6.9E-01	1.9	5.7E-01	4.1	1.3E-01	1.3	6.6E-01
ENSMUST00000109994	unc-5 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:894682]		Q8K1S4	3.7	4.1E-04	-5.9	1.5E-01	2.3	2.0E-01	1.3	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000108486	ATPase, Ca++ transporting, ubiquitous [Source:MGI Symbol;Acc:MGI:1194503]	B1ATS5		1.0	7.2E-01	4.6	2.7E-01	3.0	4.4E-01	-0.7	7.9E-01
ENSMUST00000109995	solute carrier family 35, member E4 [Source:MGI Symbol;Acc:MGI:2144150]		Q8K3D6	6.8	1.5E-04	5.4	5.6E-03	1.1	4.7E-01	-0.5	6.0E-01
ENSMUST00000110000	N(alpha)-acetyltransferase 20, NatB catalytic subunit [Source:MGI Symbol;Acc:MGI:1915127]		P61600	-4.6	2.0E-04	7.8	1.3E-05	-1.4	2.2E-01	-0.7	2.0E-01
ENSMUST00000110002	zinc finger protein 882 [Source:MGI Symbol;Acc:MGI:3642748]	E9Q4R4		2.6	2.7E-03	8.1	2.3E-05	-1.0	4.1E-01	-0.2	6.6E-01
ENSMUST00000110003	eukaryotic translation initiation factor 4E family member 1B [Source:MGI Symbol;Acc:MGI:2685119]		Q3UTA9	7.1	1.1E-04	7.1	3.4E-04	0.1	9.2E-01	-0.3	6.6E-01
ENSMUST00000110012	Janus kinase 3 [Source:MGI Symbol;Acc:MGI:99928]			-4.0	5.4E-03	-6.6	1.5E-03	0.9	9.0E-02	0.2	9.1E-01
ENSMUST00000108496	solute carrier family 1 (neutral amino acid transporter), member 5 [Source:MGI Symbol;Acc:MGI:105305]	Q9ESU7		-1.6	1.0E-01	-2.5	8.6E-02	0.4	5.5E-01	1.3	3.3E-01
ENSMUST00000110013	Janus kinase 3 [Source:MGI Symbol;Acc:MGI:99928]			5.6	3.3E-04	5.4	2.1E-03	-0.6	6.8E-01	0.4	5.7E-01
ENSMUST00000110017	polymerase (RNA) III (DNA directed) polypeptide F [Source:MGI Symbol;Acc:MGI:1924086]	Q9CZ23		3.7	2.0E-03	8.2	2.0E-04	-0.7	6.2E-01	-0.4	5.7E-01
ENSMUST00000110020	legumain [Source:MGI Symbol;Acc:MGI:1330838]	A2RTI3	O89017	-4.3	2.0E-02	6.7	9.3E-04	-0.7	6.5E-01	-0.8	3.2E-01
ENSMUST00000110021	maestro heat-like repeat family member 5 [Source:MGI Symbol;Acc:MGI:2685474]	B9EKG2		6.4	1.8E-02	7.0	1.2E-04	0.1	9.6E-01	-1.0	1.4E-01
ENSMUST00000110031	AU RNA binding protein/enoyl-coenzyme A hydratase [Source:MGI Symbol;Acc:MGI:1338011]	E9QMT1		1.7	2.3E-02	4.8	9.1E-03	-0.6	6.9E-01	-1.2	2.9E-01
ENSMUST00000110036	PTK2 protein tyrosine kinase 2 [Source:MGI Symbol;Acc:MGI:95481]		P34152	4.6	1.2E-03	8.4	9.5E-05	-0.7	6.1E-01	-0.8	2.1E-01
ENSMUST00000110039	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D [Source:MGI		O09126	-2.8	2.7E-02	6.1	4.9E-02	-0.2	9.6E-01	2.9	7.9E-02
ENSMUST00000110047	tandem C2 domains, nuclear [Source:MGI Symbol;Acc:MGI:1921663]		Q91XT6	12.5	9.8E-09	4.7	8.3E-04	0.2	8.4E-01	-0.3	6.9E-01
ENSMUST00000110049	eukaryotic translation initiation factor 4E nuclear import factor 1 [Source:MGI Symbol;Acc:MGI:1921453]		Q9EST3	-6.3	8.1E-05	6.0	5.3E-04	-0.6	6.2E-01	-0.5	4.4E-01
ENSMUST00000110052	occludin/ELL domain containing 1 [Source:MGI Symbol;Acc:MGI:1924340]	D3Z3P1		3.0	2.2E-03	-5.5	1.1E-02	-0.3	7.0E-01	2.0	2.7E-01
ENSMUST00000108516	NLR family, pyrin domain containing 1B [Source:MGI Symbol;Acc:MGI:3582959]	Q2LKV8		-1.5	6.5E-02	-1.2	1.6E-01	-1.3	4.0E-02	-1.6	8.9E-02
ENSMUST00000108527	DEAH (Asp-Glu-Ala-His) box polypeptide 33 [Source:MGI Symbol;Acc:MGI:2445102]		Q80VY9	0.6	4.0E-01	1.2	2.1E-01	0.2	7.7E-01	-0.4	6.3E-01
ENSMUST00000110069	RIKEN cDNA 9030617O03 gene [Source:MGI Symbol;Acc:MGI:2444813]		Q8BH86	-3.7	8.5E-04	-6.0	4.6E-04	0.7	9.9E-02	-0.8	5.1E-01
ENSMUST00000110070	RIKEN cDNA 9030617O03 gene [Source:MGI Symbol;Acc:MGI:2444813]		Q8BH86	4.0	2.3E-03	-5.7	6.2E-04	-0.7	1.5E-01	0.2	8.4E-01
ENSMUST00000108532	RIKEN cDNA 6330408A02 gene [Source:MGI Symbol;Acc:MGI:2447816]			1.3	3.6E-01	7.4	1.1E-02	4.3	7.6E-02	-1.8	1.9E-01
ENSMUST00000108534	SLP adaptor and CSK interacting membrane protein [Source:MGI Symbol;Acc:MGI:3610314]		Q3UU41	-1.1	3.1E-01	-2.4	1.2E-01	-0.5	5.5E-01	0.7	6.1E-01
ENSMUST00000108535	zinc finger protein 446 [Source:MGI Symbol;Acc:MGI:2442185]	E9Q6F9		4.4	3.7E-02	4.7	3.1E-02	-1.6	4.1E-01	-2.0	1.9E-01
ENSMUST00000110071	4HAUS augmin-like complex, subunit 8 [Source:MGI Symbol;Acc:MGI:1923728]		Q99L00	-6.9	1.8E-04	4.0	8.4E-02	0.6	7.5E-01	1.1	4.5E-01
ENSMUST00000110078	rmediate/small conductance calcium-activated channel, subfamily N, member 1 [Source:MGI Symbol;Acc:M			6.7	2.3E-05	4.7	8.1E-03	-2.7	1.1E-01	1.4	1.2E-01
ENSMUST00000108539	ribosomal protein S5 [Source:MGI Symbol;Acc:MGI:1097682]	Q91V55		-4.7	4.7E-02	-3.6	7.5E-02	-1.1	3.0E-01	-2.2	3.6E-01
ENSMUST00000110081	rmediate/small conductance calcium-activated channel, subfamily N, member 1 [Source:MGI Symbol;Acc:M	Z4YL28		6.9	7.5E-05	3.2	4.3E-02	0.4	7.3E-01	-0.1	9.5E-01
ENSMUST00000110082	calmodulin 1 [Source:MGI Symbol;Acc:MGI:88251]		P62204	-8.8	5.1E-05	-3.0	1.6E-01	1.6	1.8E-01	-0.6	7.7E-01
ENSMUST00000110087	FYVE, RhoGEF and PH domain containing 3 [Source:MGI Symbol;Acc:MGI:1353657]	Q3TNB8		-4.4	2.5E-05	6.0	4.2E-04	-0.5	6.9E-01	-0.6	3.6E-01
ENSMUST00000110092	RAB3A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:97843]	Q0PD63	P63011	3.5	4.0E-03	5.8	1.6E-02	-0.3	8.8E-01	-0.1	9.7E-01
ENSMUST00000110095	phosphodiesterase 4C, cAMP specific [Source:MGI Symbol;Acc:MGI:99556]		Q3UEI1	7.2	4.6E-03	6.7	1.1E-02	-0.8	7.3E-01	-1.5	2.6E-01
ENSMUST00000110098	synaptosomal-associated protein 25 [Source:MGI Symbol;Acc:MGI:98331]		P60879	11.2	5.9E-05	7.0	9.4E-05	-0.3	7.4E-01	0.6	2.8E-01
ENSMUST00000110100	predicted gene, 21961 [Source:MGI Symbol;Acc:MGI:5439430]	F6YUL9		13.0	1.7E-04	1.2	6.0E-01	-2.0	3.5E-01	1.9	3.3E-01
ENSMUST00000108559	zinc finger protein 78 [Source:MGI Symbol;Acc:MGI:107783]	Q5U406		-3.1	3.7E-02	-0.8	5.3E-01	0.1	8.8E-01	-2.1	1.6E-01
ENSMUST00000110104	zinc finger CCCH type containing 14 [Source:MGI Symbol;Acc:MGI:1919824]		Q8BJ05	-6.3	1.0E-04	6.4	4.5E-04	0.1	9.5E-01	-0.1	8.3E-01
ENSMUST00000110105	zinc finger CCCH type containing 14 [Source:MGI Symbol;Acc:MGI:1919824]		Q8BJ05	-3.6	5.1E-05	5.5	3.8E-03	-2.1	2.2E-01	-1.4	1.9E-01
ENSMUST00000110110	zinc finger protein 169 [Source:MGI Symbol;Acc:MGI:1915161]	E9Q3R6		4.5	1.2E-02	-3.5	2.1E-02	1.4	4.7E-02	-0.7	6.0E-01
ENSMUST00000110111	ring finger protein 144B [Source:MGI Symbol;Acc:MGI:2384986]		Q8BKD6	-2.3	9.4E-03	-9.5	2.1E-03	0.8	2.2E-01	1.5	5.2E-01
ENSMUST00000110113	potassium channel, subfamily K, member 10 [Source:MGI Symbol;Acc:MGI:1919508]	Q8BUW1		7.8	4.8E-05	8.5	3.2E-06	0.0	9.6E-01	-0.2	6.5E-01
ENSMUST00000108572	zinc finger protein 579 [Source:MGI Symbol;Acc:MGI:1915740]		Q80VM4	1.5	2.4E-01	2.6	4.6E-02	-1.5	2.1E-01	-2.6	3.9E-02
ENSMUST00000110115	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]		Q9QWY8	-4.0	4.7E-03	5.9	4.6E-04	-0.2	8.7E-01	-1.2	1.1E-01
ENSMUST00000110116	phospholipase C, beta 1 [Source:MGI Symbol;Acc:MGI:97613]		Q9Z1B3	2.7	6.7E-03	-1.6	4.3E-01	1.7	1.9E-01	-0.6	7.5E-01
ENSMUST00000108580				4.2	1.8E-01	3.4	3.5E-01	0.0	9.9E-01	0.9	7.0E-01
ENSMUST00000108582	suppressor of variegation 4-20 homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2385262]		Q6Q783	0.5	6.2E-01	1.4	3.9E-01	0.6	6.5E-01	-0.2	8.6E-01
ENSMUST00000110117	fibronectin leucine rich transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:3603594]	Q8BLU0	Q8BLU0	8.0	1.1E-05	-5.2	3.5E-02	1.5	9.2E-02	1.5	5.0E-01
ENSMUST00000110120	thioredoxin-related transmembrane protein 4 [Source:MGI Symbol;Acc:MGI:106558]	A2ARI0		9.5	2.9E-05	2.8	1.6E-01	-1.5	4.7E-01	2.2	1.1E-01
ENSMUST00000108588	discs, large homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1277959]		Q62108	3.0	1.9E-01	6.1	6.3E-02	2.6	3.3E-01	-0.5	8.1E-01
ENSMUST00000110125	gasdermin C [Source:MGI Symbol;Acc:MGI:1933176]		Q99NB5	7.5	6.2E-05	7.8	8.3E-05	-0.7	6.0E-01	-0.9	1.6E-01
ENSMUST00000110127	solute carrier family 25, member 42 [Source:MGI Symbol;Acc:MGI:1920345]		Q8R0Y8	5.0	2.9E-06	1.8	8.1E-02	-2.5	1.9E-02	-1.0	2.5E-01
ENSMUST00000110128	dystrobrevin binding protein 1 [Source:MGI Symbol;Acc:MGI:2137586]	K3W4R3		5.9	4.1E-04	-8.7	1.5E-05	0.4	3.1E-01	-2.4	8.9E-02
ENSMUST00000110133	neurexin III [Source:MGI Symbol;Acc:MGI:1096389]	E9Q3Q4		7.1	9.8E-05	-2.7	3.3E-03	1.0	2.9E-02	0.4	6.0E-01
ENSMUST00000110139	BLOC-1 related complex subunit 8 [Source:MGI Symbol;Acc:MGI:1919618]	D3Z373		-5.3	4.5E-04	-4.0	2.1E-02	1.0	1.5E-01	-0.7	6.7E-01
ENSMUST00000108601	Y box protein 2 [Source:MGI Symbol;Acc:MGI:1096372]	A0A0A0MQD2		2.7	1.6E-01	5.4	1.0E-02	-0.5	7.9E-01	-3.2	3.4E-02
ENSMUST00000110147	predicted gene 2016 [Source:MGI Symbol;Acc:MGI:3780185]	Q3TQZ4		4.9	7.9E-04	-7.4	1.0E-03	1.0	7.0E-02	-0.6	7.3E-01
ENSMUST00000108610	eukaryotic translation initiation factor 5A [Source:MGI Symbol;Acc:MGI:106248]		P63242	-0.6	5.6E-01	1.8	9.9E-02	0.1	9.3E-01	-2.4	4.5E-02
ENSMUST00000110152	predicted gene 8300 [Source:MGI Symbol;Acc:MGI:3643794]	Q3UTA4		5.7	8.0E-04	-9.2	2.3E-04	0.7	1.4E-01	0.0	9.8E-01
ENSMUST00000110157	prokineticin receptor 2 [Source:MGI Symbol;Acc:MGI:2181363]	A2AMQ7		6.4	2.1E-06	-6.0	4.0E-05	0.3	4.4E-01	-0.8	3.5E-01
ENSMUST00000110158	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 [Source:MGI Symbol;Acc:MGI:1332236]	Q6PBC0		-3.4	8.0E-04	-1.2	3.3E-01	7.1	4.8E-06	0.5	6.7E-01
ENSMUST00000110160	transmembrane 6 superfamily member 2 [Source:MGI Symbol;Acc:MGI:1933210]	E9QM19		4.5	2.5E-02	-4.9	1.1E-02	0.5	4.1E-01	0.8	6.1E-01
ENSMUST00000108625	ribosomal protein S9 [Source:MGI Symbol;Acc:MGI:1924096]		Q6ZWN5	1.5	4.7E-01	-4.9	1.9E-01	-2.7	1.5E-01	3.7	3.1E-01
ENSMUST00000110164	transmembrane protein 230 [Source:MGI Symbol;Acc:MGI:1917862]		Q8CIB6	1.8	2.4E-02	6.0	7.9E-04	-1.2	3.6E-01	-0.3	7.0E-01
ENSMUST00000110167	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 [Source:MGI Symbol;Acc:MGI:1914434]		Q9ERS2	-4.5	5.7E-04	-5.0	7.2E-02	1.0	3.3E-01	1.3	6.0E-01
ENSMUST00000110176	neuroglobin [Source:MGI Symbol;Acc:MGI:2151886]	D3YW07		6.6	7.8E-05	1.2	5.0E-01	-2.8	1.2E-01	3.2	3.4E-02
ENSMUST00000108630	tRNA splicing endonuclease 34 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913328]		Q8BMZ5	-0.5	6.8E-01	1.8	3.2E-01	0.6	7.1E-01	-1.8	2.2E-01
ENSMUST00000110177	neuroglobin [Source:MGI Symbol;Acc:MGI:2151886]	Q3USR6		4.5	2.6E-02	-1.3	1.7E-01	2.0	6.8E-03	-1.1	2.5E-01
ENSMUST00000108633	phospholipid scramblase 3 [Source:MGI Symbol;Acc:MGI:1917560]	Q5F283	Q9JIZ9	0.0	9.6E-01	1.1	2.6E-01	0.8	2.8E-01	-0.2	7.6E-01
ENSMUST00000110186	spermine oxidase [Source:MGI Symbol;Acc:MGI:2445356]		Q99K82	-7.9	1.2E-02	3.3	2.8E-03	-1.0	2.2E-01	-0.1	8.7E-01
ENSMUST00000110191	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme [Source:MGI Symbol;Acc:MGI:1100870]	Q6T5E4		2.1	3.0E-03	-5.9	3.4E-04	-0.4	3.4E-01	-0.3	7.9E-01
ENSMUST00000110193	transcription factor AP-2, alpha [Source:MGI Symbol;Acc:MGI:104671]			6.4	5.1E-03	2.6	2.7E-03	0.1	8.9E-01	-0.2	6.4E-01
ENSMUST00000108640	zinc finger and BTB domain containing 4 [Source:MGI Symbol;Acc:MGI:1922830]	Q5F293	Q5F293	3.5	5.9E-02	2.3	1.8E-01	-2.5	1.4E-01	-1.3	3.7E-01
ENSMUST00000108641	TCF3 (E2A) fusion partner [Source:MGI Symbol;Acc:MGI:1916964]		Q3U1J1	-3.1	2.6E-01	-1.9	4.9E-01	-0.5	7.9E-01	-1.7	5.8E-01
ENSMUST00000110194	ring finger protein 24 [Source:MGI Symbol;Acc:MGI:1261771]	Q4VA59	Q8BGI1	8.2	1.1E-05	3.3	1.4E-01	-1.0	6.3E-01	-0.2	9.0E-01
ENSMUST00000110199	mitochondrial antiviral signaling protein [Source:MGI Symbol;Acc:MGI:2444773]		Q8VCF0	8.0	4.6E-04	-3.9	2.6E-03	0.1	8.1E-01	-0.4	7.1E-01
ENSMUST00000108654	CD68 antigen [Source:MGI Symbol;Acc:MGI:88342]			3.9	9.2E-02	-1.0	8.0E-01	-0.2	9.4E-01	4.7	1.9E-01
ENSMUST00000108657	transformation related protein 53 [Source:MGI Symbol;Acc:MGI:98834]	I7HIK9		-1.7	2.4E-01	3.9	1.7E-01	5.6	3.2E-02	0.0	9.8E-01
ENSMUST00000108658	transformation related protein 53 [Source:MGI Symbol;Acc:MGI:98834]	Q549C9		-0.5	7.6E-01	-0.1	9.6E-01	-0.5	7.0E-01	-0.9	6.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000110203	estrogen related receptor, beta [Source:MGI Symbol;Acc:MGI:1346832]	D3YW03		6.4	1.4E-04	6.8	5.4E-02	-0.7	8.4E-01	2.8	1.2E-01
ENSMUST00000108660	cytochrome b5 domain containing 1 [Source:MGI Symbol;Acc:MGI:2685586]		Q5NCY3	-0.2	7.4E-01	0.0	9.6E-01	0.6	2.5E-01	0.4	5.2E-01
ENSMUST00000108661	chromodomain helicase DNA binding protein 3 [Source:MGI Symbol;Acc:MGI:1344395]	B1AR17		-2.5	1.9E-01	-3.9	2.4E-01	-0.4	8.3E-01	1.0	7.4E-01
ENSMUST00000110208	adaptor-related protein 5 complex, sigma 1 subunit [Source:MGI Symbol;Acc:MGI:1916846]	A2ANC6		-5.5	2.2E-03	5.1	3.5E-02	-0.7	7.4E-01	-0.5	7.3E-01
ENSMUST00000108666	aurora kinase B [Source:MGI Symbol;Acc:MGI:107168]		O70126	-3.1	8.2E-02	3.4	6.9E-02	3.2	5.5E-02	-3.3	6.5E-02
ENSMUST00000110218	sperm flagellar 1 [Source:MGI Symbol;Acc:MGI:3513546]		Q99JL1	1.9	6.4E-03	5.2	3.6E-05	0.2	7.2E-01	0.1	7.6E-01
ENSMUST00000110220	tubulin tyrosine ligase-like family, member 5 [Source:MGI Symbol;Acc:MGI:2443657]	Q8BUF0		7.4	9.0E-05	6.1	4.2E-02	-0.8	7.7E-01	3.1	5.7E-02
ENSMUST00000110227	sialic acid binding Ig-like lectin 1, sialoadhesin [Source:MGI Symbol;Acc:MGI:99668]	H9KUZ3		6.4	6.5E-05	8.1	4.9E-05	-0.6	6.3E-01	0.4	4.9E-01
ENSMUST00000110238	ras responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:2443664]		Q3UH06	5.2	2.1E-05	6.0	1.9E-04	-1.8	1.3E-01	-0.6	3.4E-01
ENSMUST00000108680	growth arrest specific 7 [Source:MGI Symbol;Acc:MGI:1202388]	B1ATI9		-1.6	5.7E-01	-2.3	5.2E-01	-1.0	6.0E-01	-0.3	9.3E-01
ENSMUST00000110241	integrator complex subunit 10 [Source:MGI Symbol;Acc:MGI:1918135]	E9Q361		-4.1	5.5E-04	-0.8	7.5E-02	0.8	1.4E-02	-0.2	5.7E-01
ENSMUST00000110249	prospero homeobox 2 [Source:MGI Symbol;Acc:MGI:1920672]		Q8BII1	2.6	1.0E-02	9.2	5.3E-03	-0.9	7.7E-01	-3.5	3.4E-02
ENSMUST00000110251	enoyl-Coenzyme A delta isomerase 2 [Source:MGI Symbol;Acc:MGI:1346064]	Q3TCD4		-6.6	8.7E-06	6.3	2.1E-04	-0.6	6.2E-01	-0.3	6.8E-01
ENSMUST00000110258	membrane-associated ring finger (C3HC4) 1 [Source:MGI Symbol;Acc:MGI:1920175]		Q6NZQ8	8.2	2.4E-05	2.7	1.2E-03	0.0	9.4E-01	0.4	3.7E-01
ENSMUST00000110260	leucine zipper, putative tumor suppressor family member 3 [Source:MGI Symbol;Acc:MGI:2656976]		A2AHG0	6.7	2.0E-03	7.8	3.4E-04	-0.7	6.7E-01	0.3	6.5E-01
ENSMUST00000110267	syntabulin (syntaxin-interacting) [Source:MGI Symbol;Acc:MGI:2442392]		Q8BHS8	6.1	1.5E-04	-3.2	3.4E-02	2.7	2.0E-03	-0.8	5.6E-01
ENSMUST00000110272	ectonucleoside triphosphate diphosphohydrolase 5 [Source:MGI Symbol;Acc:MGI:1321385]		Q9WUZ9	-6.2	1.0E-03	-3.5	2.8E-03	1.3	2.3E-02	0.2	8.4E-01
ENSMUST00000108709	sperm antigen with calponin homology and coiled-coil domains 1 [Source:MGI Symbol;Acc:MGI:2442356]		Q5SXY1	-0.4	6.9E-01	1.2	2.7E-01	0.3	7.2E-01	-1.3	2.3E-01
ENSMUST00000110277	PC-esterase domain containing 1A [Source:MGI Symbol;Acc:MGI:2442177]		Q6P1Z5	-4.0	1.2E-03	3.5	8.1E-04	-0.3	6.9E-01	-0.3	5.7E-01
ENSMUST00000110293	serine (or cysteine) peptidase inhibitor, clade B, member 6b [Source:MGI Symbol;Acc:MGI:894688]	O08804		6.4	1.5E-04	3.0	3.6E-01	-0.8	7.8E-01	2.4	3.0E-01
ENSMUST00000108713	epsin 2 [Source:MGI Symbol;Acc:MGI:1333766]	Q5NCM7	Q8CHU3	0.1	9.5E-01	-3.1	6.8E-02	-5.3	2.5E-03	-2.1	2.9E-01
ENSMUST00000110294	ELM2 and Myb/SANT-like domain containing 1 [Source:MGI Symbol;Acc:MGI:2685106]	E9Q2I4		1.2	3.1E-02	2.0	2.2E-01	8.1	6.3E-05	0.0	9.8E-01
ENSMUST00000108715	aldehyde dehydrogenase family 3, subfamily A2 [Source:MGI Symbol;Acc:MGI:1353452]	B1AV77		-0.5	4.1E-01	-0.8	3.1E-01	0.2	7.3E-01	0.5	5.1E-01
ENSMUST00000110299	transglutaminase 3, E polypeptide [Source:MGI Symbol;Acc:MGI:98732]		Q08189	3.2	7.5E-04	4.1	5.3E-03	-2.3	9.3E-02	-0.4	6.0E-01
ENSMUST00000110307	interferon regulatory factor 4 [Source:MGI Symbol;Acc:MGI:1096873]	Q5SUZ5	Q64287	1.4	3.0E-02	5.5	5.1E-05	0.5	4.9E-01	-0.1	7.8E-01
ENSMUST00000108719	lethal giant larvae homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:102682]		Q80Y17	-0.8	1.9E-01	0.8	3.0E-01	1.2	5.0E-02	-0.4	6.1E-01
ENSMUST00000108721	ATP synthase mitochondrial F1 complex assembly factor 2 [Source:MGI Symbol;Acc:MGI:2180561]			-0.1	7.9E-01	0.6	3.6E-01	0.7	1.9E-01	-0.1	8.9E-01
ENSMUST00000110319	zinc finger CCCH type containing 6 [Source:MGI Symbol;Acc:MGI:1926001]		Q8BYK8	2.7	9.4E-03	6.2	4.4E-04	-0.2	8.9E-01	-0.4	5.7E-01
ENSMUST00000110329	antizyme inhibitor 1 [Source:MGI Symbol;Acc:MGI:1859169]		O35484	-10.5	6.2E-05	9.3	5.6E-03	-0.1	9.8E-01	1.2	3.5E-01
ENSMUST00000110333	anaphase promoting complex subunit 1 [Source:MGI Symbol;Acc:MGI:103097]	A2ATQ5		4.6	2.0E-02	5.8	2.1E-04	-1.5	1.9E-01	0.2	7.7E-01
ENSMUST00000110336	ubiquitin protein ligase E3 component n-recognin 5 [Source:MGI Symbol;Acc:MGI:1918040]	E9Q2H1		-4.0	2.9E-05	-4.3	6.2E-03	0.1	8.2E-01	-0.6	6.8E-01
ENSMUST00000108754	:in-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 [Source:MGI Symbol;Acc:MGI:1923	B0R0C7		-1.8	5.8E-01	-2.6	5.5E-01	-0.8	7.2E-01	-0.1	9.8E-01
ENSMUST00000110346	teneurin transmembrane protein 3 [Source:MGI Symbol;Acc:MGI:1345183]	D3YW49		8.8	4.4E-05	6.0	3.8E-04	0.2	8.6E-01	0.4	5.1E-01
ENSMUST00000110351	serine/arginine-rich splicing factor 5 [Source:MGI Symbol;Acc:MGI:98287]	Q9D8S5		-9.2	1.0E-05	6.1	5.8E-02	-0.9	7.7E-01	0.6	7.3E-01
ENSMUST00000110352	serine/arginine-rich splicing factor 5 [Source:MGI Symbol;Acc:MGI:98287]		O35326	-9.2	1.1E-04	-6.8	1.3E-03	0.2	7.6E-01	-0.6	7.2E-01
ENSMUST00000110356	serine/arginine-rich splicing factor 5 [Source:MGI Symbol;Acc:MGI:98287]		O35326	-7.5	8.1E-03	-4.1	8.8E-03	-0.8	1.7E-01	-0.5	7.2E-01
ENSMUST00000110361	nonooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Source:MGI Symbol;Acc:M		P63101	5.2	3.0E-03	-1.0	1.0E-01	1.1	1.5E-02	-0.2	6.6E-01
ENSMUST00000110366	zinc finger protein 661 [Source:MGI Symbol;Acc:MGI:1919430]		Q8BIQ3	7.8	4.4E-04	-0.6	6.4E-01	1.6	1.0E-01	-1.4	3.2E-01
ENSMUST00000108777	jumonji domain containing 4 [Source:MGI Symbol;Acc:MGI:2144404]		Q8BFT6	4.1	1.9E-01	-2.1	4.5E-01	-5.9	4.8E-02	0.3	9.2E-01
ENSMUST00000110367	storkhead box 2 [Source:MGI Symbol;Acc:MGI:1918319]		Q499E5	4.5	2.0E-04	-4.0	4.6E-04	1.4	5.3E-03	-0.5	5.4E-01
ENSMUST00000110374	START domain containing 7 [Source:MGI Symbol;Acc:MGI:2139090]	Q8BXP7		4.8	9.4E-05	3.1	9.7E-02	-2.4	2.5E-01	1.7	2.3E-01
ENSMUST00000108789	zinc finger protein 512B [Source:MGI Symbol;Acc:MGI:2685478]	B7ZCR6		-0.7	7.1E-01	-1.3	7.1E-01	2.0	3.4E-01	2.6	3.9E-01
ENSMUST00000110375	START domain containing 7 [Source:MGI Symbol;Acc:MGI:2139090]		Q8R1R3	-4.6	1.0E-03	6.3	5.3E-04	-0.9	5.2E-01	-0.5	5.3E-01
ENSMUST00000110382	geminin [Source:MGI Symbol;Acc:MGI:1927344]	Q3V295	O88513	-5.9	1.4E-04	5.5	2.9E-02	-0.7	7.6E-01	-1.0	4.9E-01
ENSMUST00000108796	DnaJ (Hsp40) homolog, subfamily C, member 5 [Source:MGI Symbol;Acc:MGI:892995]		P60904	-0.5	8.7E-01	-4.9	2.7E-01	-2.8	2.2E-01	1.7	7.1E-01
ENSMUST00000110383	family with sequence similarity 65, member B [Source:MGI Symbol;Acc:MGI:2444879]	A6PW28		-4.5	5.5E-04	-4.3	2.5E-03	0.5	3.2E-01	-0.7	5.7E-01
ENSMUST00000110384	family with sequence similarity 65, member B [Source:MGI Symbol;Acc:MGI:2444879]		Q80U16	7.1	1.4E-02	-7.9	1.1E-04	-0.7	1.1E-01	-0.3	8.4E-01
ENSMUST00000108800	tumor protein D52-like 2 [Source:MGI Symbol;Acc:MGI:1913564]	Q3TUJ9		-0.2	8.5E-01	1.1	4.7E-01	2.3	8.7E-02	1.0	4.0E-01
ENSMUST00000108807	zinc finger, CCCH-type with G patch domain [Source:MGI Symbol;Acc:MGI:2449939]		Q8VDM1	1.1	6.7E-01	5.0	1.2E-01	1.3	6.4E-01	-2.6	3.0E-01
ENSMUST00000110388	gephyrin [Source:MGI Symbol;Acc:MGI:109602]	A0JNY3		-4.7	6.6E-04	-4.7	1.7E-03	0.4	3.3E-01	-0.7	5.6E-01
ENSMUST00000110395	Max protein [Source:MGI Symbol;Acc:MGI:96921]	B2RS19		-5.7	2.7E-03	-2.0	4.5E-02	0.7	1.9E-01	-0.3	7.5E-01
ENSMUST00000110398	leucine rich repeat containing 16A [Source:MGI Symbol;Acc:MGI:1915982]	D3Z030		6.7	1.6E-04	-5.3	3.4E-03	0.8	1.8E-01	0.2	9.1E-01
ENSMUST00000108814	regulator of telomere elongation helicase 1 [Source:MGI Symbol;Acc:MGI:2139369]		Q0VGM9	-0.2	9.5E-01	4.0	3.2E-01	4.0	2.0E-01	-0.2	9.5E-01
ENSMUST00000108817	histone cluster 3, H2a [Source:MGI Symbol;Acc:MGI:2448458]	A2AB79	Q8BFU2	0.7	3.1E-01	-0.6	5.4E-01	-0.1	8.6E-01	1.1	1.9E-01
ENSMUST00000108824	olfactory receptor 328 [Source:MGI Symbol;Acc:MGI:3030162]	Q5NCD3		2.9	6.7E-02	6.1	2.1E-03	-0.4	7.8E-01	-3.6	6.8E-03
ENSMUST00000110399	churchill domain containing 1 [Source:MGI Symbol;Acc:MGI:1923684]		Q6DG52	6.2	1.0E-03	5.6	2.1E-04	1.2	1.9E-01	0.3	6.0E-01
ENSMUST00000110408	ropporin 1-like [Source:MGI Symbol;Acc:MGI:2182357]			-3.1	2.2E-03	6.8	1.5E-02	-0.9	7.3E-01	-1.5	2.9E-01
ENSMUST00000110411	a disintegrin and metallopeptidase domain 34 [Source:MGI Symbol;Acc:MGI:2181992]	A2RSG8		5.5	1.5E-03	4.3	3.6E-03	-1.7	1.8E-01	0.4	5.6E-01
ENSMUST00000108829	zinc finger protein 672 [Source:MGI Symbol;Acc:MGI:2442105]		Q99LH4	-1.1	3.7E-01	1.5	2.9E-01	0.3	8.0E-01	-2.3	9.0E-02
ENSMUST00000108830	differentially expressed in FDCP 8 [Source:MGI Symbol;Acc:MGI:1346331]		Q99J78	-2.0	3.0E-01	-2.5	4.0E-01	1.3	5.3E-01	1.8	4.7E-01
ENSMUST00000110417	N-acylsphingosine amidohydrolase 1 [Source:MGI Symbol;Acc:MGI:1277124]	D3Z015		-6.0	2.9E-05	-6.1	1.2E-02	1.0	2.0E-01	-0.5	8.1E-01
ENSMUST00000110424	GA repeat binding protein, beta 1 [Source:MGI Symbol;Acc:MGI:95611]	Q3US22	Q00420	-7.5	7.2E-05	-4.1	3.8E-05	1.0	3.5E-03	-0.6	3.4E-01
ENSMUST00000108836	immunity-related GTPase family M member 2 [Source:MGI Symbol;Acc:MGI:1926262]	Q9Z1M2		2.8	3.5E-01	4.0	2.2E-01	-0.2	9.5E-01	-1.4	5.1E-01
ENSMUST00000110425	GA repeat binding protein, beta 1 [Source:MGI Symbol;Acc:MGI:95611]		Q00420	4.2	3.8E-03	-6.5	8.6E-04	0.7	2.3E-01	-2.1	2.4E-01
ENSMUST00000110434	butyrophilin, subfamily 1, member A1 [Source:MGI Symbol;Acc:MGI:103118]	Q921X1		5.7	2.0E-03	-2.8	6.6E-03	0.7	1.4E-01	0.2	8.4E-01
ENSMUST00000110441	predicted gene 11042 [Source:MGI Symbol;Acc:MGI:3779266]	F6VZP0		11.6	1.6E-04	-4.8	1.5E-03	0.0	9.2E-01	-0.8	5.2E-01
ENSMUST00000108843	CCR4-NOT transcription complex, subunit 8 [Source:MGI Symbol;Acc:MGI:1916375]		Q9D8X5	3.6	4.5E-02	2.5	1.8E-01	-1.2	4.7E-01	-0.1	9.2E-01
ENSMUST00000108846	:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 [Source:MGI Symbol;Acc:MGI	Q5ST18		1.2	1.2E-01	1.9	6.0E-02	0.5	4.9E-01	-0.1	8.7E-01
ENSMUST00000110442	fibroblast growth factor 7 [Source:MGI Symbol;Acc:MGI:95521]	Q544I6	P36363	5.2	1.7E-03	-6.8	3.2E-02	0.7	4.3E-01	3.0	2.9E-01
ENSMUST00000108850	family with sequence similarity 114, member A2 [Source:MGI Symbol;Acc:MGI:1917629]		Q8VE88	-0.2	9.4E-01	-2.7	3.4E-01	-2.6	1.2E-01	-0.1	9.6E-01
ENSMUST00000110451	synaptotagmin XVI [Source:MGI Symbol;Acc:MGI:2673872]		Q7TN83	6.8	1.9E-04	0.7	5.8E-01	-2.4	5.7E-02	1.6	1.9E-01
ENSMUST00000108856	collagen, type XX, alpha 1 [Source:MGI Symbol;Acc:MGI:1920618]		Q923P0	-0.7	6.6E-01	1.9	2.5E-01	-0.3	8.5E-01	-2.9	9.8E-02
ENSMUST00000110452	histone cluster 1, H2bj [Source:MGI Symbol;Acc:MGI:2448388]		P10853	5.6	4.8E-03	-7.2	3.1E-04	-0.8	1.4E-01	0.2	8.6E-01
ENSMUST00000110457	myosin X [Source:MGI Symbol;Acc:MGI:107716]		F8VQB6	6.2	1.4E-02	-4.5	2.6E-04	-9.0	2.1E-06	-1.8	7.8E-02
ENSMUST00000110461	hypoxia inducible factor 1, alpha subunit [Source:MGI Symbol;Acc:MGI:106918]			-4.7	8.9E-04	4.7	4.3E-02	-2.1	3.5E-01	-1.9	1.9E-01
ENSMUST00000110463	(constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	Q3V3N6	P61202	-3.1	3.1E-04	-3.4	1.7E-02	0.3	6.2E-01	-0.6	6.4E-01
ENSMUST00000108862	ADP-ribosylation factor GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2183559]	Q3TGS9		2.6	7.7E-02	4.6	7.2E-03	-0.6	6.9E-01	-2.5	3.9E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000110483	StAR-related lipid transfer (START) domain containing 13 [Source:MGI Symbol;Acc:MGI:2385331]		Q923Q2	9.2	1.1E-03	0.0	1.0E+00	-3.6	2.5E-01	3.8	2.4E-01
ENSMUST00000108868	spastic paraplegia 7 homolog (human) [Source:MGI Symbol;Acc:MGI:2385906]		Q3ULF4	-3.7	8.8E-02	-1.4	5.2E-01	0.6	7.3E-01	-1.7	4.5E-01
ENSMUST00000108872	solute carrier family 36 (proton/amino acid symporter), member 1 [Source:MGI Symbol;Acc:MGI:2445299]	Q5F227	Q8K4D3	0.7	2.9E-01	0.8	3.5E-01	0.6	3.4E-01	0.5	5.2E-01
ENSMUST00000108876	YTH domain family 1 [Source:MGI Symbol;Acc:MGI:1917431]	A2AWN8		2.5	2.6E-01	0.5	8.5E-01	-1.1	6.0E-01	0.9	7.3E-01
ENSMUST00000110492	DNA segment, Chr 8, ERATO Doi 82, expressed [Source:MGI Symbol;Acc:MGI:1196223]	E9QLH9		4.9	4.5E-05	7.1	8.0E-05	-0.5	6.5E-01	-0.5	3.9E-01
ENSMUST00000110495	solute carrier family 12, member 1 [Source:MGI Symbol;Acc:MGI:103150]	A2AQ51		6.0	8.6E-03	1.5	1.2E-01	-1.5	1.0E-01	-0.5	5.1E-01
ENSMUST00000110496	relaxin/insulin-like family peptide receptor 2 [Source:MGI Symbol;Acc:MGI:2153463]	E9Q0U9		6.7	1.8E-03	-7.5	1.5E-04	-0.1	7.6E-01	-0.7	6.3E-01
ENSMUST00000110504	SUB1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:104811]		P11031	-8.4	2.6E-07	-2.1	2.4E-01	1.4	2.1E-01	-1.3	4.8E-01
ENSMUST00000110510	GLI-Kruppel family member GLI3 [Source:MGI Symbol;Acc:MGI:95729]	B2RUG4	Q61602	9.8	1.3E-06	-3.4	1.2E-01	1.6	1.8E-01	-0.6	7.7E-01
ENSMUST00000110512	expressed sequence AA467197 [Source:MGI Symbol;Acc:MGI:3034182]	Q3UCF3	Q810Q5	-8.1	1.2E-04	-2.4	3.2E-02	1.2	6.3E-02	1.0	3.0E-01
ENSMUST00000110516	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:2444115]		Q8K4P8	7.6	1.3E-05	6.3	2.8E-04	0.0	1.0E+00	-0.9	1.9E-01
ENSMUST00000110521	predicted gene 14085 [Source:MGI Symbol;Acc:MGI:3702173]	A2AWR5		-4.9	1.5E-05	3.1	2.9E-01	1.0	6.6E-01	3.4	1.4E-01
ENSMUST00000108909	sodium channel, voltage-gated, type VIII, alpha [Source:MGI Symbol;Acc:MGI:103169]	F7D6J5		6.2	1.2E-01	-1.1	7.1E-01	-5.5	1.3E-01	1.7	5.2E-01
ENSMUST00000110523	C1q and tumor necrosis factor related protein 3 [Source:MGI Symbol;Acc:MGI:1932136]	D3YZ61		6.9	1.5E-03	7.2	1.4E-04	-0.6	6.1E-01	0.0	9.7E-01
ENSMUST00000110524	ute carrier family 28 (sodium-coupled nucleoside transporter), member 2 [Source:MGI Symbol;Acc:MGI:19131		O88627	-9.1	1.7E-05	8.5	1.6E-03	2.3	2.3E-01	1.0	2.6E-01
ENSMUST00000110529	FMS-like tyrosine kinase 1 [Source:MGI Symbol;Acc:MGI:95558]	O55095		8.2	3.8E-05	-10.0	3.5E-05	0.3	4.0E-01	1.1	4.6E-01
ENSMUST00000110534	AT rich interactive domain 4B (RBP1-like) [Source:MGI Symbol;Acc:MGI:2137512]		A2CG63	-6.8	2.9E-04	4.6	9.2E-03	-0.4	7.9E-01	0.1	9.5E-01
ENSMUST00000110538	dual oxidase maturation factor 1 [Source:MGI Symbol;Acc:MGI:2384861]	A2AQ96		6.2	1.2E-04	-2.6	1.7E-02	-0.7	2.2E-01	-2.2	6.2E-02
ENSMUST00000110551	sorbitol dehydrogenase [Source:MGI Symbol;Acc:MGI:98266]		Q64442	-1.6	2.9E-02	-3.0	2.2E-02	1.4	2.5E-02	0.3	8.2E-01
ENSMUST00000108930	predicted gene 14326 [Source:MGI Symbol;Acc:MGI:3709298]	A2BFG5		-2.4	4.8E-02	-3.4	6.5E-02	0.4	6.6E-01	1.3	4.4E-01
ENSMUST00000108932	predicted gene 14326 [Source:MGI Symbol;Acc:MGI:3709298]	A2BFG4		-2.6	1.3E-01	-2.2	1.6E-01	-1.1	3.1E-01	-1.6	3.6E-01
ENSMUST00000110557	polymerase (RNA) I polypeptide D [Source:MGI Symbol;Acc:MGI:108403]	Q9D1M1		-3.4	1.1E-03	8.2	3.0E-03	-1.0	6.4E-01	0.8	4.6E-01
ENSMUST00000108948	RIKEN cDNA 6430548M08 gene [Source:MGI Symbol;Acc:MGI:2443793]	Q8BQB5		-0.6	3.9E-01	0.4	5.9E-01	-0.1	9.1E-01	-1.1	1.8E-01
ENSMUST00000108950	RIKEN cDNA 6430548M08 gene [Source:MGI Symbol;Acc:MGI:2443793]		Q8R0A7	2.5	3.8E-01	3.3	3.8E-01	1.4	6.7E-01	0.5	8.5E-01
ENSMUST00000110559	lysosomal trafficking regulator [Source:MGI Symbol;Acc:MGI:107448]	G5E8Q0		-4.0	5.6E-07	-3.6	2.2E-03	1.5	7.0E-03	-0.8	3.7E-01
ENSMUST00000110564	mitochondrial translational initiation factor 3 [Source:MGI Symbol;Acc:MGI:1923616]	A4QMQ0	Q9CZD5	-3.5	6.6E-03	4.5	1.5E-02	-0.7	6.6E-01	1.4	1.8E-01
ENSMUST00000108971	DIP2 disco-interacting protein 2 homolog B (Drosophila) [Source:MGI Symbol;Acc:MGI:2145977]	B2RQC7		1.6	1.1E-01	2.9	5.2E-02	1.7	1.5E-01	0.4	7.1E-01
ENSMUST00000110566	mitochondrial translational initiation factor 3 [Source:MGI Symbol;Acc:MGI:1923616]	A4QMQ0	Q9CZD5	-3.6	1.1E-02	0.9	7.7E-01	-4.5	1.0E-01	2.5	3.3E-01
ENSMUST00000108987	septin 8 [Source:MGI Symbol;Acc:MGI:894310]		Q8CHH9	2.5	1.8E-01	-4.0	1.8E-01	-3.6	4.5E-02	2.8	3.2E-01
ENSMUST00000108988	ubiquitin specific peptidase 10 [Source:MGI Symbol;Acc:MGI:894652]		P52479	0.5	6.8E-01	1.7	2.7E-01	-0.3	8.3E-01	-1.5	3.1E-01
ENSMUST00000109013	shroom family member 1 [Source:MGI Symbol;Acc:MGI:1919024]		Q5SX79	2.2	1.2E-01	5.2	6.8E-03	0.5	7.3E-01	-2.4	4.5E-02
ENSMUST00000110572	cy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2 [Source:MGI Symbol;Acc:M		Q8BG15	-4.1	2.6E-03	-7.8	3.2E-04	-0.4	3.7E-01	0.9	5.8E-01
ENSMUST00000110576				5.7	1.1E-02	1.4	4.8E-02	-2.5	1.9E-03	-0.5	3.5E-01
ENSMUST00000109035	ceramide synthase 5 [Source:MGI Symbol;Acc:MGI:1919199]		Q9D6K9	2.2	5.5E-02	2.7	8.3E-02	0.7	6.1E-01	0.1	9.3E-01
ENSMUST00000110578	cy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2 [Source:MGI Symbol;Acc:M		Q8BG15	-4.8	4.1E-04	4.5	1.1E-05	-0.6	2.2E-01	-0.2	6.4E-01
ENSMUST00000110582	Jrk-like [Source:MGI Symbol;Acc:MGI:1924782]		B2RRL2	-3.6	9.6E-04	-3.8	1.4E-01	1.6	2.2E-01	-0.4	8.7E-01
ENSMUST00000109071	transcription factor 7, T cell specific [Source:MGI Symbol;Acc:MGI:98507]	Q80UF1	Q00417	2.7	1.1E-01	1.8	3.9E-01	-0.3	8.7E-01	0.7	7.0E-01
ENSMUST00000109072	S-phase kinase-associated protein 1A [Source:MGI Symbol;Acc:MGI:103575]	Q5SUR3	Q9WTX5	1.6	3.2E-01	3.7	1.0E-01	1.4	4.8E-01	-0.7	6.2E-01
ENSMUST00000110583	coiled-coil domain containing 82 [Source:MGI Symbol;Acc:MGI:1913646]		Q6PG04	-3.2	3.8E-03	-4.7	1.1E-01	1.9	2.1E-01	2.8	2.9E-01
ENSMUST00000110585	S-phase kinase-associated protein 2 (p45) [Source:MGI Symbol;Acc:MGI:1351663]		Q9Z0Z3	5.0	9.6E-05	3.3	4.5E-02	-2.1	2.1E-01	-1.5	2.0E-01
ENSMUST00000110586	cancer susceptibility candidate 4 [Source:MGI Symbol;Acc:MGI:2443129]	E9PZJ6		5.8	2.2E-05	2.6	5.4E-03	-0.5	4.6E-01	0.7	2.5E-01
ENSMUST00000110595	predicted gene 3415 [Source:MGI Symbol;Acc:MGI:3781593]	L7N249		5.3	8.7E-03	-6.6	2.2E-03	1.2	4.9E-02	-0.7	7.1E-01
ENSMUST00000110596	predicted gene 3404 [Source:MGI Symbol;Acc:MGI:3781582]	Q9D506		8.5	9.8E-06	-6.4	1.3E-03	1.1	4.9E-02	-0.6	7.0E-01
ENSMUST00000110598	RIKEN cDNA 4930449I24 gene [Source:MGI Symbol;Acc:MGI:1914660]	Q9D5E3		7.2	8.2E-05	-8.2	3.4E-04	-0.4	4.4E-01	-1.2	4.9E-01
ENSMUST00000110602	WD repeat domain 76 [Source:MGI Symbol;Acc:MGI:1926186]		A6PWY4	2.4	2.6E-03	-7.4	3.4E-05	1.0	8.7E-03	-0.6	5.8E-01
ENSMUST00000110611	predicted gene 6370 [Source:MGI Symbol;Acc:MGI:3779587]	L7N250		8.2	3.2E-03	2.3	2.9E-01	-1.4	5.3E-01	2.5	1.1E-01
ENSMUST00000110612	huntingtin interacting protein K [Source:MGI Symbol;Acc:MGI:1914943]		Q9CR41	4.0	7.6E-05	6.2	7.5E-02	-0.9	7.9E-01	-0.1	9.6E-01
ENSMUST00000109091	jade family PHD finger 2 [Source:MGI Symbol;Acc:MGI:1924151]		Q6ZQF7	-0.9	1.1E-01	-0.8	2.4E-01	0.0	9.2E-01	-0.1	8.6E-01
ENSMUST00000109093	polycystic kidney disease 1 like 2 [Source:MGI Symbol;Acc:MGI:2664668]	E9QPG2		-0.5	7.4E-01	4.4	2.3E-02	0.6	6.7E-01	-4.2	1.7E-02
ENSMUST00000110616	actinin alpha 2 [Source:MGI Symbol;Acc:MGI:109192]	D3YY95		7.3	1.0E-05	6.5	3.1E-04	-0.6	6.1E-01	0.3	6.5E-01
ENSMUST00000109097	Sec24 related gene family, member A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924621]		Q3U2P1	-0.6	2.7E-01	0.9	2.2E-01	0.9	1.2E-01	-0.6	3.5E-01
ENSMUST00000110627	diphosphoinositol pentakisphosphate kinase 1 [Source:MGI Symbol;Acc:MGI:2443281]		A2ARP1	4.9	2.0E-02	0.0	9.7E-01	0.7	4.2E-02	-0.2	7.2E-01
ENSMUST00000110633	zinc finger, MYND domain containing 11 [Source:MGI Symbol;Acc:MGI:1913755]	D3YY86		-4.6	5.4E-04	7.8	1.4E-04	-1.4	3.6E-01	0.0	9.5E-01
ENSMUST00000110634	zinc finger, MYND domain containing 11 [Source:MGI Symbol;Acc:MGI:1913755]		Q8R5C8	-5.4	2.1E-04	2.4	6.1E-04	1.1	1.9E-02	-0.2	6.7E-01
ENSMUST00000110635	zinc finger, MYND domain containing 11 [Source:MGI Symbol;Acc:MGI:1913755]	D3YY85		-6.6	2.5E-02	-7.5	2.9E-05	0.3	3.2E-01	0.4	7.1E-01
ENSMUST00000110636	zinc finger, MYND domain containing 11 [Source:MGI Symbol;Acc:MGI:1913755]		Q8R5C8	5.1	1.6E-02	2.7	1.8E-02	-0.9	3.0E-01	0.9	2.4E-01
ENSMUST00000110637	zinc finger, MYND domain containing 11 [Source:MGI Symbol;Acc:MGI:1913755]	Q8BJZ0		-8.1	2.7E-05	3.3	7.7E-03	-1.4	1.6E-01	0.1	8.6E-01
ENSMUST00000110667	indoleamine 2,3-dioxygenase 1 [Source:MGI Symbol;Acc:MGI:96416]	D3YXV1		6.3	8.3E-05	5.4	9.2E-04	-1.8	1.7E-01	-0.3	7.1E-01
ENSMUST00000110671	somatostatin receptor 1 [Source:MGI Symbol;Acc:MGI:98327]	Q543T0	P30873	6.3	1.2E-03	7.6	1.2E-04	1.5	2.2E-01	0.8	2.0E-01
ENSMUST00000109110	RAB22A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105072]	A2ARZ7		-1.5	1.4E-01	-2.7	1.2E-01	0.5	6.0E-01	1.7	2.9E-01
ENSMUST00000110673	karyopherin alpha 7 (importin alpha 8) [Source:MGI Symbol;Acc:MGI:2141165]		C0LLJ0	6.8	2.2E-02	2.0	1.9E-01	7.1	9.9E-05	-0.9	4.6E-01
ENSMUST00000109113	CDC like kinase 4 [Source:MGI Symbol;Acc:MGI:1098551]		O35493	-5.7	1.9E-01	-6.5	2.2E-01	-1.6	4.6E-01	-0.8	8.9E-01
ENSMUST00000110674	leucine carboxyl methyltransferase 2 [Source:MGI Symbol;Acc:MGI:1353659]		Q8BYR1	2.4	3.1E-02	-6.3	1.0E-03	-1.7	2.3E-02	-0.1	9.2E-01
ENSMUST00000110675	transglutaminase 7 [Source:MGI Symbol;Acc:MGI:2151164]	A2ART8		7.2	5.7E-05	6.1	1.2E-04	0.3	7.7E-01	0.2	6.4E-01
ENSMUST00000110686	transmembrane protein 62 [Source:MGI Symbol;Acc:MGI:2139461]	A2AQ56		-4.0	4.9E-03	7.0	9.4E-05	-0.5	6.6E-01	-0.9	1.4E-01
ENSMUST00000110687	Ral GTPase activating protein, alpha subunit 1 [Source:MGI Symbol;Acc:MGI:1931050]		Q6GYP7	-4.5	2.4E-02	5.9	3.2E-04	-0.6	6.1E-01	-0.5	4.6E-01
ENSMUST00000110689	complement component 7 [Source:MGI Symbol;Acc:MGI:88235]	D3YXF5		7.2	1.3E-04	4.6	1.3E-02	-0.5	7.6E-01	-0.6	5.9E-01
ENSMUST00000109127	limb region 1 like [Source:MGI Symbol;Acc:MGI:1289247]		Q9D1E5	-2.0	7.5E-02	-0.8	5.7E-01	0.7	4.1E-01	-0.5	7.0E-01
ENSMUST00000110690	3-oxoacid CoA transferase 1 [Source:MGI Symbol;Acc:MGI:1914291]		Q9D0K2	-2.9	1.0E-03	3.9	3.2E-02	-1.3	4.5E-01	0.7	4.9E-01
ENSMUST00000109132				-1.3	3.7E-01	-2.5	1.8E-01	-1.5	1.6E-01	-0.3	8.5E-01
ENSMUST00000109133	zinc finger protein 879 [Source:MGI Symbol;Acc:MGI:3053099]	Q147Z4		5.4	5.4E-02	4.4	1.5E-01	-0.7	8.1E-01	0.3	8.6E-01
ENSMUST00000110691	aldo-keto reductase family 1, member E1 [Source:MGI Symbol;Acc:MGI:1914758]	Q8CEB6		8.7	7.8E-06	4.2	3.1E-03	-0.7	4.9E-01	-0.9	3.2E-01
ENSMUST00000109136	Cas scaffolding protein family member 4 [Source:MGI Symbol;Acc:MGI:2444482]		Q08EC4	-2.2	9.2E-02	1.2	3.5E-01	0.2	8.2E-01	-3.2	2.7E-02
ENSMUST00000110695	brain protein I3 [Source:MGI Symbol;Acc:MGI:1933174]	E9PUB2		-3.8	2.5E-03	-1.9	1.5E-01	0.9	2.7E-01	-1.3	3.7E-01
ENSMUST00000110696	K(lysine) acetyltransferase 6A [Source:MGI Symbol;Acc:MGI:2442415]	G3X940		-5.6	8.7E-03	5.3	3.6E-04	-2.9	2.5E-02	-1.0	1.4E-01
ENSMUST00000110701	congenital dyserythropoietic anemia, type I (human) [Source:MGI Symbol;Acc:MGI:1916218]		Q8CC12	3.4	1.8E-03	-3.3	1.6E-02	0.5	3.7E-01	0.3	8.2E-01
ENSMUST00000110711	synaptosomal-associated protein 23 [Source:MGI Symbol;Acc:MGI:109356]	A2AKH4	O09044	-8.3	1.5E-04	3.2	1.5E-03	-0.4	5.7E-01	-0.2	7.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000110713	E2F-associated phosphoprotein [Source:MGI Symbol;Acc:MGI:1913516]		Q5BU09	-8.8	2.5E-06	-0.8	3.3E-01	1.9	7.6E-03	-0.5	5.4E-01
ENSMUST00000110716	calpain 3 [Source:MGI Symbol;Acc:MGI:107437]	A2AVV7		6.1	6.2E-03	5.7	1.8E-04	-2.3	5.4E-02	-0.3	6.0E-01
ENSMUST00000110727	cytohesin 3 [Source:MGI Symbol;Acc:MGI:1335107]	G5E8Q4		6.6	3.4E-04	-2.3	1.9E-02	1.3	3.0E-02	-2.7	2.8E-02
ENSMUST00000110731	L (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 [Source:MGI Symbol;Acc:MGI:1914		Q9CQM2	-2.5	6.3E-04	8.0	1.6E-04	-1.3	4.0E-01	0.4	5.5E-01
ENSMUST00000110733	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1 [Source:MGI Symbol;Acc:MGI:2176213]		Q0QWG9	7.4	3.1E-05	5.6	1.2E-03	-0.5	7.3E-01	-0.3	6.5E-01
ENSMUST00000110737	asparagine-linked glycosylation 11 (alpha-1,2-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:2142632]		Q3TZM9	7.5	1.6E-02	3.7	6.3E-03	-1.0	3.3E-01	0.2	8.4E-01
ENSMUST00000110738	ATPase, Cu++ transporting, beta polypeptide [Source:MGI Symbol;Acc:MGI:103297]	B1AQ57		6.4	3.4E-03	6.8	3.4E-04	-0.6	6.5E-01	-1.6	4.4E-02
ENSMUST00000110741	family with sequence similarity 90, member A1A [Source:MGI Symbol;Acc:MGI:2142877]	A2A4E2		8.4	2.2E-04	2.3	1.1E-02	0.1	9.1E-01	-0.2	7.1E-01
ENSMUST00000110746	RIKEN cDNA 3110039M20 gene [Source:MGI Symbol;Acc:MGI:1914543]	E9PYS1		6.8	9.6E-05	6.6	3.6E-05	-3.6	6.0E-03	-0.4	4.1E-01
ENSMUST00000109177	ATPase, class II, type 9A [Source:MGI Symbol;Acc:MGI:1330826]	Q8C4G3		-0.3	7.8E-01	-4.3	1.1E-02	-3.7	1.2E-03	0.3	8.2E-01
ENSMUST00000110756	spectrin beta, non-erythrocytic 5 [Source:MGI Symbol;Acc:MGI:2685200]	A2AP58		8.7	4.3E-06	-2.7	1.8E-01	1.5	1.7E-01	-0.9	6.6E-01
ENSMUST00000110766	F-box and leucine-rich repeat protein 18 [Source:MGI Symbol;Acc:MGI:2444450]	E9PYR1		3.5	5.1E-04	-1.7	2.8E-01	0.3	7.5E-01	-3.0	1.3E-01
ENSMUST00000109184	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 [Source:MGI Symbol;Acc:MGI:102463	B5B2P7	Q60591	2.6	3.0E-01	2.8	2.7E-01	-1.0	6.9E-01	-1.1	6.0E-01
ENSMUST00000110767	sperm associated antigen 11B [Source:MGI Symbol;Acc:MGI:3647173]	Q3UW43		5.7	6.0E-04	7.8	2.5E-04	-0.7	6.5E-01	0.0	9.7E-01
ENSMUST00000109193	dolichol-phosphate (beta-D) mannosyltransferase 1 [Source:MGI Symbol;Acc:MGI:1330239]	A2BDX2		0.1	9.2E-01	2.4	8.0E-02	0.9	4.0E-01	-1.4	1.7E-01
ENSMUST00000110773	MAX gene associated [Source:MGI Symbol;Acc:MGI:1352483]		A2AWL7	7.8	2.0E-04	2.1	3.7E-01	5.8	1.1E-02	-1.5	4.1E-01
ENSMUST00000109198	zinc finger protein 62 [Source:MGI Symbol;Acc:MGI:99662]		Q8C827	-1.4	5.9E-01	-2.6	3.6E-01	-2.2	3.0E-01	-1.0	7.5E-01
ENSMUST00000110778	WD repeat domain, phosphoinositide interacting 2 [Source:MGI Symbol;Acc:MGI:1923831]	D3YWK1		-5.9	8.8E-04	-1.9	3.1E-01	0.6	6.3E-01	-2.6	2.0E-01
ENSMUST00000110783	TYRO3 protein tyrosine kinase 3 [Source:MGI Symbol;Acc:MGI:104294]		P55144	6.8	4.5E-04	-2.0	1.2E-01	1.6	5.0E-02	-0.9	4.5E-01
ENSMUST00000110784	Ras association and DIL domains [Source:MGI Symbol;Acc:MGI:2443088]		Q69Z89	5.9	2.6E-02	3.9	4.1E-02	-0.8	6.2E-01	-0.1	9.6E-01
ENSMUST00000110793	RNA polymerase II associated protein 1 [Source:MGI Symbol;Acc:MGI:1916175]		Q80TE0	6.1	4.3E-03	0.1	9.5E-01	1.1	1.2E-01	-2.4	3.4E-02
ENSMUST00000110800	Rho guanine nucleotide exchange factor (GEF) 10 [Source:MGI Symbol;Acc:MGI:2444453]		Q8C033	6.4	1.8E-02	3.0	3.2E-04	-1.1	5.7E-02	-0.8	8.3E-02
ENSMUST00000110802	DH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 [Source:MGI Symbol;Acc:MGI:19169	A2AQ17		-5.8	3.2E-05	2.1	1.7E-01	-2.0	1.5E-01	-0.3	7.9E-01
ENSMUST00000110806	BRCA1-associated ATM activator 1 [Source:MGI Symbol;Acc:MGI:1891679]		Q8C3R1	3.7	4.6E-03	6.2	1.5E-04	-1.5	2.0E-01	0.0	9.9E-01
ENSMUST00000110819	histone deacetylase 9 [Source:MGI Symbol;Acc:MGI:1931221]			4.9	3.9E-04	-1.2	1.9E-01	1.3	4.3E-02	0.3	7.0E-01
ENSMUST00000110832	transmembrane protein 184a [Source:MGI Symbol;Acc:MGI:2385897]		Q3UFJ6	9.3	2.5E-06	5.7	6.2E-04	-1.4	2.8E-01	-0.8	2.7E-01
ENSMUST00000109226	pelota homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2145154]		Q80X73	0.7	2.3E-01	2.2	1.8E-02	1.1	9.6E-02	-0.3	6.3E-01
ENSMUST00000110835	E74-like factor 1 [Source:MGI Symbol;Acc:MGI:107180]	Q3V1H4	Q60775	-4.1	1.3E-03	-1.2	4.4E-01	-1.0	4.1E-01	4.1	1.2E-02
ENSMUST00000109235	staufen (RNA binding protein) homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1338864]	Q9DBE7		-2.6	6.2E-02	-1.1	4.3E-01	0.2	8.8E-01	-1.3	3.7E-01
ENSMUST00000109236	staufen (RNA binding protein) homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1338864]		Q9Z108	-0.7	6.6E-01	-0.6	8.0E-01	1.0	6.2E-01	0.8	6.9E-01
ENSMUST00000110836	naf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian) [Source:MGI Symbol;Acc:MGI:9995	Q3UP84	Q61827	5.0	1.1E-02	0.7	3.9E-01	-7.3	9.6E-05	-0.8	3.2E-01
ENSMUST00000110843	dispatched homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2388733]	A3KGG1		10.0	1.4E-04	-5.1	6.2E-04	0.3	4.1E-01	-0.7	5.6E-01
ENSMUST00000110853	p21 protein (Cdc42/Rac)-activated kinase 6 [Source:MGI Symbol;Acc:MGI:2679420]		Q3ULB5	5.6	2.1E-04	-3.9	4.3E-04	1.0	2.2E-02	0.7	3.9E-01
ENSMUST00000109242	polycystic kidney disease 1 like 3 [Source:MGI Symbol;Acc:MGI:2664670]		Q2EG98	4.5	2.0E-01	7.9	4.3E-02	-0.1	9.9E-01	-3.5	1.0E-01
ENSMUST00000110855	lysophosphatidylglycerol acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2446186]		Q91YX5	-2.9	2.1E-04	-3.0	1.2E-01	0.8	4.0E-01	-1.3	5.1E-01
ENSMUST00000109248	interleukin-1 receptor-associated kinase 4 [Source:MGI Symbol;Acc:MGI:2182474]	Q3USX5		0.3	6.4E-01	0.8	3.8E-01	-0.3	6.2E-01	-0.8	3.4E-01
ENSMUST00000110857	dihydrolipoamide dehydrogenase [Source:MGI Symbol;Acc:MGI:107450]		O08749	-4.2	3.7E-05	4.6	9.9E-03	-1.5	3.1E-01	0.1	8.8E-01
ENSMUST00000109252	nuclear receptor coactivator 3 [Source:MGI Symbol;Acc:MGI:1276535]	A2A468		-1.8	1.4E-01	-4.8	7.9E-02	1.0	3.1E-01	4.0	1.3E-01
ENSMUST00000109255	prickle homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1916034]		Q3U5C7	2.8	4.2E-02	7.8	6.9E-05	-0.5	6.8E-01	-5.5	1.1E-04
ENSMUST00000110859	BCL2 modifying factor [Source:MGI Symbol;Acc:MGI:2176433]	A2AV74		3.8	2.0E-03	-1.5	3.3E-01	2.3	3.6E-02	0.5	7.2E-01
ENSMUST00000110865	ArfGAP with dual PH domains 1 [Source:MGI Symbol;Acc:MGI:2442201]	E9PY16		-4.6	3.8E-03	-7.7	3.5E-05	0.9	1.2E-02	-0.7	5.7E-01
ENSMUST00000109261	clathrin interactor 1 [Source:MGI Symbol;Acc:MGI:2144243]	Q5SUH6		-3.1	4.5E-02	-3.1	1.6E-01	1.9	1.9E-01	1.9	3.2E-01
ENSMUST00000109262	zinc finger, MYND-type containing 8 [Source:MGI Symbol;Acc:MGI:1918025]	A2A481		3.1	2.0E-01	-2.5	4.9E-01	-2.4	3.3E-01	3.2	3.3E-01
ENSMUST00000109266	zinc finger, MYND-type containing 8 [Source:MGI Symbol;Acc:MGI:1918025]	E9Q8D1		-1.7	1.7E-01	-2.8	1.1E-01	-0.4	7.0E-01	0.7	6.7E-01
ENSMUST00000109267	mitogen-activated protein kinase kinase kinase 1 [Source:MGI Symbol;Acc:MGI:1346872]	F8VQ72		0.0	1.0E+00	0.6	4.0E-01	0.9	1.1E-01	0.3	6.4E-01
ENSMUST00000110867	mcf.2 transforming sequence-like [Source:MGI Symbol;Acc:MGI:103263]	E9PY12		4.0	1.0E-02	2.9	2.2E-01	-1.5	5.0E-01	1.5	3.6E-01
ENSMUST00000110870	eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427]		Q9QZ05	7.4	1.0E-04	7.0	1.2E-04	-0.4	7.2E-01	-0.1	8.7E-01
ENSMUST00000109271	mesoderm induction early response 1, family member 3 [Source:MGI Symbol;Acc:MGI:2442317]	F7BFR0		-2.0	3.4E-01	0.5	8.1E-01	-0.4	8.0E-01	-2.9	2.1E-01
ENSMUST00000110874	eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427]	A2AUM1		5.0	1.1E-03	-5.3	6.7E-03	0.2	8.0E-01	0.0	9.9E-01
ENSMUST00000110877	eukaryotic translation initiation factor 2 alpha kinase 4 [Source:MGI Symbol;Acc:MGI:1353427]	A2AUL9		5.9	4.5E-03	6.5	1.2E-03	0.5	7.3E-01	1.3	1.4E-01
ENSMUST00000109278	tetratricopeptide repeat domain 1 [Source:MGI Symbol;Acc:MGI:1914077]	A2AJK8		-0.9	2.8E-01	-1.8	1.4E-01	0.1	8.7E-01	1.0	3.5E-01
ENSMUST00000109280	PWWP domain containing 2A [Source:MGI Symbol;Acc:MGI:1918052]	Z4YKW0		-1.7	1.6E-01	-1.3	4.0E-01	0.1	9.2E-01	-0.4	8.0E-01
ENSMUST00000110878	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914854]		Q9D1H7	-5.4	1.4E-04	6.0	5.5E-04	-0.6	6.6E-01	0.4	5.5E-01
ENSMUST00000110894	tumor protein, translationally-controlled 1 [Source:MGI Symbol;Acc:MGI:104890]		P63028	-8.8	7.0E-03	6.2	1.7E-04	-2.4	7.0E-02	-0.3	5.6E-01
ENSMUST00000109288	kinesin family member 21A [Source:MGI Symbol;Acc:MGI:109188]		Q9QXL2	5.0	6.0E-02	1.8	5.9E-01	-0.4	9.0E-01	2.8	2.7E-01
ENSMUST00000110896	platelet derived growth factor, alpha [Source:MGI Symbol;Acc:MGI:97527]	Q99L56		4.9	4.6E-03	2.1	1.2E-01	8.7	7.0E-06	-0.8	4.4E-01
ENSMUST00000109300	solute carrier family 35, member C2 [Source:MGI Symbol;Acc:MGI:2385166]	Q5GMH2	Q8VCX2	-5.0	8.6E-02	-6.8	1.2E-01	-0.2	8.6E-01	1.6	7.3E-01
ENSMUST00000110905	zinc finger protein 68 [Source:MGI Symbol;Acc:MGI:1344427]	Q9Z116		-3.2	1.9E-02	6.9	1.5E-04	-0.5	6.7E-01	-1.7	2.4E-02
ENSMUST00000109307				2.0	3.5E-02	2.1	6.1E-02	0.1	9.3E-01	-0.1	9.4E-01
ENSMUST00000110909	Rho guanine nucleotide exchange factor (GEF7) [Source:MGI Symbol;Acc:MGI:1860493]		Q9ES28	4.2	1.9E-04	-1.7	4.5E-03	1.1	4.1E-03	-0.5	2.7E-01
ENSMUST00000110934	canopy 4 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1913705]		Q8BQ47	-1.9	7.1E-03	2.2	4.4E-01	-0.7	7.7E-01	3.1	1.7E-01
ENSMUST00000110939	estrogen-related receptor gamma [Source:MGI Symbol;Acc:MGI:1347056]		P62509	7.6	2.6E-05	3.2	7.0E-02	-0.1	9.6E-01	-0.2	8.2E-01
ENSMUST00000109315	neurolysin (metallopeptidase M3 family) [Source:MGI Symbol;Acc:MGI:1923055]		Q91YP2	-1.0	4.4E-02	-0.9	1.7E-01	0.3	5.2E-01	0.1	9.0E-01
ENSMUST00000109316	phospholipid transfer protein [Source:MGI Symbol;Acc:MGI:103151]	Q3UFS5	P55065	1.4	3.4E-01	2.6	1.1E-01	-0.7	6.0E-01	-1.9	1.8E-01
ENSMUST00000109317	phospholipid transfer protein [Source:MGI Symbol;Acc:MGI:103151]	A2A5K2		0.8	6.6E-01	-3.8	2.1E-01	-3.0	8.5E-02	1.6	5.7E-01
ENSMUST00000110942	membrane bound O-acyltransferase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914466]		Q8R3I2	4.9	2.7E-02	-5.8	1.5E-05	-0.6	6.5E-02	-0.3	6.5E-01
ENSMUST00000109331	plexin B2 [Source:MGI Symbol;Acc:MGI:2154239]		B2RXS4	-1.2	2.6E-01	-0.1	9.4E-01	0.1	9.4E-01	-1.0	3.8E-01
ENSMUST00000109333	mitochondrial ribosomal protein S36 [Source:MGI Symbol;Acc:MGI:1913378]		Q9CQX8	-0.4	5.3E-01	-1.0	2.0E-01	-0.4	4.4E-01	0.2	8.0E-01
ENSMUST00000110948	Rho GTPase activating protein 11A [Source:MGI Symbol;Acc:MGI:2444300]	A2AL18		2.8	6.8E-04	7.9	2.7E-05	-0.6	5.8E-01	-0.3	5.3E-01
ENSMUST00000110951	(constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	D3Z0F5		-7.6	8.4E-06	3.2	1.5E-03	-1.7	3.4E-02	-0.1	8.3E-01
ENSMUST00000109350	dysbindin (dystrobrevin binding protein 1) domain containing 2 [Source:MGI Symbol;Acc:MGI:106562]	Q330P7	Q9CRD4	0.3	7.4E-01	0.5	7.3E-01	0.3	7.7E-01	0.2	8.6E-01
ENSMUST00000109353	tubulin, gamma complex associated protein 6 [Source:MGI Symbol;Acc:MGI:2146071]	G5E8P0		0.9	4.3E-02	1.5	1.9E-02	0.7	1.2E-01	0.1	8.3E-01
ENSMUST00000110952	chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2 [Source:MGI Symbol;Acc:M	G1EE51	Q99LJ7	-4.6	1.7E-03	-1.4	1.3E-01	0.4	4.9E-01	-1.4	1.6E-01
ENSMUST00000109358	matrilin 4 [Source:MGI Symbol;Acc:MGI:1328314]	F2Z469		2.8	1.1E-01	1.9	4.3E-01	0.9	6.5E-01	1.7	3.7E-01
ENSMUST00000110959	zinc finger and SCAN domain containing 21 [Source:MGI Symbol;Acc:MGI:99182]		Q07231	5.8	2.7E-03	3.3	1.4E-01	-0.1	9.5E-01	1.6	2.8E-01
ENSMUST00000110962	zinc finger with KRAB and SCAN domains 1 [Source:MGI Symbol;Acc:MGI:1921820]		Q8BGS3	7.4	1.2E-04	-6.1	1.9E-02	1.1	1.6E-01	2.8	2.2E-01
ENSMUST00000110967	sperm motility kinase 3C [Source:MGI Symbol;Acc:MGI:3647925]	A0A087WSF2		10.6	7.6E-05	-7.7	4.3E-06	0.0	9.9E-01	0.1	9.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000109368	encephalic leukoencephalopathy with subcortical cysts 1 homolog (human) [Source:MGI Symbol;Acc:MGI:215	E9QP87		6.1	9.8E-02	4.5	2.4E-01	-0.8	8.4E-01	0.8	7.4E-01
ENSMUST00000109370	seminal vesicle secretory protein 3A [Source:MGI Symbol;Acc:MGI:1927635]	F2Z467		2.8	4.0E-02	6.1	4.6E-04	-0.5	6.9E-01	-3.8	1.7E-03
ENSMUST00000110969	family with sequence similarity 155, member A [Source:MGI Symbol;Acc:MGI:2142765]		Q8CCS2	7.7	1.0E-04	5.3	5.7E-02	-0.4	8.7E-01	0.7	6.2E-01
ENSMUST00000109375	engulfment and cell motility 3 [Source:MGI Symbol;Acc:MGI:2679007]		Q8BYZ7	1.5	3.9E-02	1.6	7.3E-02	-0.1	9.3E-01	-0.1	8.4E-01
ENSMUST00000109379	e prime 1, subunit of RNA polymerase III transcription initiation factor IIIB [Source:MGI Symbol;Acc:MGI:1		Q571C7	0.0	9.7E-01	-2.0	2.5E-01	-1.4	2.2E-01	0.7	7.0E-01
ENSMUST00000109380	bromodomain containing 1 [Source:MGI Symbol;Acc:MGI:1924161]	G5E8P1		-1.3	4.8E-01	1.7	4.9E-01	1.6	3.8E-01	-1.4	5.3E-01
ENSMUST00000110973	zinc finger protein 738 [Source:MGI Symbol;Acc:MGI:3040706]	E9PWN4		5.3	1.5E-05	-2.8	9.9E-03	0.6	2.7E-01	-0.8	4.1E-01
ENSMUST00000110975	isoleucine-tRNA synthetase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1919586]	E9PWN2		5.3	1.3E-03	-5.6	2.0E-02	1.0	2.0E-01	1.7	4.3E-01
ENSMUST00000110978	paired immunoglobin-like type 2 receptor beta 1 [Source:MGI Symbol;Acc:MGI:2450532]		Q2YFS2	-5.9	6.2E-07	6.3	1.3E-03	-0.1	9.6E-01	-0.4	6.2E-01
ENSMUST00000110980	paired immunoglobin-like type 2 receptor alpha [Source:MGI Symbol;Acc:MGI:2450529]		Q2YFS3	-4.3	7.9E-05	-6.3	4.4E-03	1.0	1.1E-01	0.2	9.1E-01
ENSMUST00000110984	dematin actin binding protein [Source:MGI Symbol;Acc:MGI:99670]		Q9WV69	6.3	2.9E-02	-2.1	5.4E-01	4.9	2.0E-02	0.0	1.0E+00
ENSMUST00000110987	solute carrier family 12, member 6 [Source:MGI Symbol;Acc:MGI:2135960]	A2AGJ9		2.4	2.0E-03	5.4	1.4E-03	-0.5	7.0E-01	-0.4	5.9E-01
ENSMUST00000109399	transportin 1 [Source:MGI Symbol;Acc:MGI:2681523]		Q8BFY9	0.1	9.7E-01	3.3	1.5E-01	-1.1	6.1E-01	-4.3	5.6E-02
ENSMUST00000110991	solute carrier family 12, member 6 [Source:MGI Symbol;Acc:MGI:2135960]	Q3V0N8		-2.5	3.8E-03	5.4	2.9E-02	1.3	5.2E-01	1.4	3.3E-01
ENSMUST00000110992	mitochondrial amidoxime reducing component 1 [Source:MGI Symbol;Acc:MGI:1913362]	D3YZZ3		6.0	4.6E-04	-2.6	1.3E-03	0.8	2.5E-02	-0.2	7.4E-01
ENSMUST00000109403	FCH domain only 2 [Source:MGI Symbol;Acc:MGI:3505790]		Q3UQN2	-0.4	8.6E-01	2.0	6.1E-01	4.1	1.8E-01	1.8	5.4E-01
ENSMUST00000109405	tocopherol (alpha) transfer protein-like [Source:MGI Symbol;Acc:MGI:1923330]		Q9D3D0	-2.2	9.8E-02	0.3	8.3E-01	0.4	6.8E-01	-2.1	1.6E-01
ENSMUST00000110997	toll-like receptor 5 [Source:MGI Symbol;Acc:MGI:1858171]	E9QL10		-5.7	3.3E-03	4.8	6.3E-04	1.2	1.7E-01	-1.0	1.8E-01
ENSMUST00000110998	mitogen-activated protein kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346871]		Q8CE90	-4.4	8.2E-03	5.4	1.5E-02	0.0	9.8E-01	0.7	5.1E-01
ENSMUST00000109412	cytoplasmic polyadenylation element binding protein 4 [Source:MGI Symbol;Acc:MGI:1914829]	Q5SU48		-0.5	5.9E-01	-0.3	7.8E-01	-0.3	7.2E-01	-0.5	6.9E-01
ENSMUST00000111002	F-box protein 24 [Source:MGI Symbol;Acc:MGI:1918426]	D3YZY9		5.3	3.4E-02	6.6	1.6E-04	-0.6	6.2E-01	-0.6	3.2E-01
ENSMUST00000111007	motile sperm domain containing 3 [Source:MGI Symbol;Acc:MGI:1916179]	Q05DT5	Q8BGG6	-2.8	2.6E-03	4.5	6.9E-05	0.2	7.1E-01	0.3	4.6E-01
ENSMUST00000111016	mucin 15 [Source:MGI Symbol;Acc:MGI:2442110]	Q0VEM9	Q8C6Z1	6.6	5.7E-03	6.5	2.3E-04	-0.5	7.0E-01	-0.9	1.7E-01
ENSMUST00000111017	mucin 15 [Source:MGI Symbol;Acc:MGI:2442110]	A2AHK7		7.3	1.8E-02	8.3	3.1E-04	-0.1	9.6E-01	0.5	5.0E-01
ENSMUST00000111018	signal recognition particle 9 [Source:MGI Symbol;Acc:MGI:1350930]	D3YZX8		-8.2	1.6E-05	5.3	1.7E-02	-0.7	7.1E-01	1.6	1.8E-01
ENSMUST00000109425	junctophilin 2 [Source:MGI Symbol;Acc:MGI:1891496]		Q9ET78	3.1	1.3E-01	1.3	6.5E-01	0.1	9.6E-01	1.9	3.9E-01
ENSMUST00000111020	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	D3YZX3		-8.5	5.3E-06	5.1	1.5E-04	-3.4	9.5E-03	0.2	7.2E-01
ENSMUST00000111027	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	E9QKR0		-9.6	4.3E-05	5.1	6.8E-04	-1.8	1.3E-01	0.1	9.0E-01
ENSMUST00000111045	brain derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:88145]	Q541P3	P21237	6.1	8.2E-04	7.0	1.5E-04	-0.3	8.0E-01	0.3	5.9E-01
ENSMUST00000111046	brain derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:88145]	Q541P3	P21237	5.8	1.4E-02	1.9	1.1E-01	-1.7	1.4E-01	0.7	4.8E-01
ENSMUST00000111051	brain derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:88145]	Q541P3	P21237	8.3	1.2E-03	6.3	2.5E-03	-0.3	8.6E-01	0.0	9.6E-01
ENSMUST00000111054	Eph receptor B4 [Source:MGI Symbol;Acc:MGI:104757]	E9PWK7		6.9	8.1E-05	-7.2	1.7E-03	1.3	8.4E-02	0.6	7.6E-01
ENSMUST00000111063	metallophosphoesterase domain containing 2 [Source:MGI Symbol;Acc:MGI:1924265]	B1APT2	Q9CZJ0	5.2	9.0E-03	7.4	1.9E-02	-2.5	4.7E-01	-2.1	2.1E-01
ENSMUST00000111064	neurotensin receptor 2 [Source:MGI Symbol;Acc:MGI:108018]		P70310	7.3	2.0E-04	5.6	6.2E-02	-0.8	7.8E-01	0.5	7.7E-01
ENSMUST00000109455	lipin 3 [Source:MGI Symbol;Acc:MGI:1891342]	A2A4B3		6.4	4.5E-02	6.8	4.7E-02	-0.5	8.7E-01	-1.0	5.9E-01
ENSMUST00000109456	lipin 3 [Source:MGI Symbol;Acc:MGI:1891342]	Q149B0	Q99PI4	6.6	8.0E-02	6.1	1.2E-01	-0.9	8.3E-01	-0.4	8.6E-01
ENSMUST00000109460	zinc fingers and homeoboxes 3 [Source:MGI Symbol;Acc:MGI:2444772]	Q3UPQ8	Q8C0Q2	3.9	1.7E-01	7.7	5.7E-02	3.0	3.9E-01	-0.8	7.4E-01
ENSMUST00000109462	phospholipase C, gamma 1 [Source:MGI Symbol;Acc:MGI:97615]	A2A4A6		-0.6	3.2E-01	-0.3	6.9E-01	-0.3	5.6E-01	-0.6	4.1E-01
ENSMUST00000109467				-1.5	1.2E-01	-0.1	9.3E-01	0.7	3.7E-01	-0.7	5.3E-01
ENSMUST00000111067	lipin 1 [Source:MGI Symbol;Acc:MGI:1891340]	E9QKQ5		7.8	8.4E-04	-2.4	1.1E-02	1.0	4.5E-02	-0.6	5.0E-01
ENSMUST00000111072	a disintegrin and metallopeptidase domain 28 [Source:MGI Symbol;Acc:MGI:105988]		Q9JLN6	7.5	2.0E-05	5.8	5.6E-03	-0.6	7.5E-01	-1.8	1.2E-01
ENSMUST00000111080	adaptor protein complex AP-1, sigma 1 [Source:MGI Symbol;Acc:MGI:1098244]		P61967	-3.6	1.4E-04	7.9	6.5E-03	-0.9	7.4E-01	-2.3	9.9E-02
ENSMUST00000111088	paired box 6 [Source:MGI Symbol;Acc:MGI:97490]	A2A412		8.4	1.6E-06	5.3	7.1E-04	-0.6	6.3E-01	-0.3	6.5E-01
ENSMUST00000111089	neurofilament, medium polypeptide [Source:MGI Symbol;Acc:MGI:97314]	D3YZ35		9.0	1.1E-05	-0.8	7.3E-01	3.9	2.4E-02	1.3	5.6E-01
ENSMUST00000111090	zinc finger, HIT domain containing 1 [Source:MGI Symbol;Acc:MGI:1917353]	D3YZ34		-4.5	2.0E-04	7.2	1.2E-04	-2.2	1.2E-01	-0.5	4.3E-01
ENSMUST00000109485	Ral GTPase activating protein, beta subunit (non-catalytic) [Source:MGI Symbol;Acc:MGI:2444531]	E9Q0J2		-0.1	9.7E-01	4.2	4.0E-01	4.6	2.3E-01	0.2	9.6E-01
ENSMUST00000109486	Ral GTPase activating protein, beta subunit (non-catalytic) [Source:MGI Symbol;Acc:MGI:2444531]	A2ACC6		-0.5	7.4E-01	0.4	8.3E-01	-1.5	2.7E-01	-2.4	1.7E-01
ENSMUST00000111093	claudin 15 [Source:MGI Symbol;Acc:MGI:1913103]		Q9Z0S5	7.2	4.6E-03	5.5	5.7E-06	-0.4	4.7E-01	0.1	7.1E-01
ENSMUST00000111094	fission 1 (mitochondrial outer membrane) homolog (yeast) [Source:MGI Symbol;Acc:MGI:1913687]	G3X9U9		-2.0	2.6E-03	-1.4	1.0E-01	0.6	2.6E-01	0.0	9.7E-01
ENSMUST00000111104	presenilin 2 [Source:MGI Symbol;Acc:MGI:109284]			-3.5	2.5E-02	-1.1	4.2E-01	0.4	6.3E-01	-1.3	3.4E-01
ENSMUST00000111108	presenilin 2 [Source:MGI Symbol;Acc:MGI:109284]	Q3U4P5		-7.9	5.3E-05	5.0	3.2E-02	-0.7	7.3E-01	-0.7	6.3E-01
ENSMUST00000111114	coiled-coil domain containing 73 [Source:MGI Symbol;Acc:MGI:3606488]		Q8CDM4	5.6	3.0E-04	6.1	1.4E-04	-2.5	5.5E-02	0.7	2.6E-01
ENSMUST00000111121	PTK2 protein tyrosine kinase 2 beta [Source:MGI Symbol;Acc:MGI:104908]	Q3UDE9		6.6	4.2E-03	-1.6	1.1E-01	1.5	2.2E-02	-1.2	2.6E-01
ENSMUST00000111124	homeodomain interacting protein kinase 3 [Source:MGI Symbol;Acc:MGI:1314882]		Q9ERH7	3.9	4.6E-04	-4.8	2.0E-02	0.6	4.6E-01	0.4	8.4E-01
ENSMUST00000111125	homeodomain interacting protein kinase 3 [Source:MGI Symbol;Acc:MGI:1314882]	A2AQH3		-4.1	2.2E-02	-4.4	4.8E-03	-0.7	2.4E-01	0.5	7.1E-01
ENSMUST00000109510	transcription factor 20 [Source:MGI Symbol;Acc:MGI:108399]		Q9EPQ8	-1.3	5.0E-01	-1.7	4.5E-01	-0.6	6.6E-01	-0.2	9.1E-01
ENSMUST00000111131	CD59b antigen [Source:MGI Symbol;Acc:MGI:1888996]	A2BI28		3.6	1.1E-03	5.4	1.2E-03	0.3	7.9E-01	0.0	9.8E-01
ENSMUST00000111132	CD59b antigen [Source:MGI Symbol;Acc:MGI:1888996]	Q6PBG1		7.7	1.5E-04	6.9	2.9E-04	-0.6	6.4E-01	-0.8	2.6E-01
ENSMUST00000109518	regulation of nuclear pre-mRNA domain containing 1B [Source:MGI Symbol;Acc:MGI:1917720]		Q9CSU0	-0.9	7.5E-01	5.3	1.7E-01	5.4	1.3E-01	-0.8	7.7E-01
ENSMUST00000111137	uroplakin 3B-like [Source:MGI Symbol;Acc:MGI:1916915]	D3YZ16		6.3	1.0E-02	4.4	7.6E-03	0.1	9.4E-01	2.0	4.0E-02
ENSMUST00000111142	deltex 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1921448]		Q8R3P2	-4.6	1.8E-02	-0.5	4.9E-01	0.9	9.0E-02	-0.5	5.1E-01
ENSMUST00000111147	cell cycle associated protein 1 [Source:MGI Symbol;Acc:MGI:1858234]		Q60865	-6.1	7.1E-05	-0.3	9.1E-01	6.0	1.0E-02	2.7	3.4E-01
ENSMUST00000111153	scavenger receptor cysteine rich family, 4 domains [Source:MGI Symbol;Acc:MGI:1924709]		A1L0T3	5.1	3.1E-03	5.9	8.2E-04	-0.5	7.3E-01	-0.7	3.6E-01
ENSMUST00000109525	pseudouridylate synthase 10 [Source:MGI Symbol;Acc:MGI:1921717]		Q9D3U0	-3.4	8.3E-02	0.2	9.2E-01	2.5	1.4E-01	-1.2	5.7E-01
ENSMUST00000111154	family with sequence similarity 228, member A [Source:MGI Symbol;Acc:MGI:1922105]		Q8CDW1	6.8	1.3E-05	-6.9	2.4E-02	1.6	7.7E-02	2.3	3.8E-01
ENSMUST00000111155	heat shock protein 1 [Source:MGI Symbol;Acc:MGI:96240]	D3YZ06		5.7	3.2E-04	-3.7	2.9E-02	1.3	1.0E-01	1.9	2.1E-01
ENSMUST00000111176	ets homologous factor [Source:MGI Symbol;Acc:MGI:1270840]	A2BIB5		7.9	2.0E-05	4.6	1.1E-02	-3.0	1.0E-01	-1.1	2.7E-01
ENSMUST00000109533	Rous sarcoma oncogene [Source:MGI Symbol;Acc:MGI:98397]	Q80XU2		5.9	7.3E-02	4.5	9.1E-02	-4.7	1.4E-01	-3.3	1.3E-01
ENSMUST00000111178	EFR3 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2444851]		Q6ZQ18	6.4	8.3E-06	5.9	1.6E-03	-4.2	2.7E-02	-0.2	8.2E-01
ENSMUST00000111183	pyruvate dehydrogenase complex, component X [Source:MGI Symbol;Acc:MGI:1351627]	A2AWH8		8.2	1.5E-06	-4.8	1.3E-02	1.4	7.7E-02	-1.5	4.2E-01
ENSMUST00000109539	AHA1, activator of heat shock protein ATPase 2 [Source:MGI Symbol;Acc:MGI:1916133]		Q8N9S3	-1.5	8.9E-02	-1.4	1.5E-01	-0.8	2.4E-01	-0.9	3.5E-01
ENSMUST00000111194	CD44 antigen [Source:MGI Symbol;Acc:MGI:88338]	E9QKM8		-8.0	4.3E-04	9.6	2.6E-05	0.8	5.0E-01	1.3	6.1E-02
ENSMUST00000111215	additional sex combs like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1922552]	F6WV21		-6.6	3.9E-05	-5.1	5.4E-04	-2.4	6.7E-04	-0.7	5.2E-01
ENSMUST00000109546	versican [Source:MGI Symbol;Acc:MGI:102889]	E9PYH0		-0.9	1.9E-01	0.6	5.4E-01	1.4	5.0E-02	0.0	9.9E-01
ENSMUST00000111216	abhydrolase domain containing 11 [Source:MGI Symbol;Acc:MGI:1916008]	D3YYK0		-5.2	1.1E-04	6.8	2.4E-02	0.9	7.2E-01	0.5	6.9E-01
ENSMUST00000109549	SAM domain and HD domain, 1 [Source:MGI Symbol;Acc:MGI:1927468]	E9PYG9		1.0	1.6E-01	0.8	3.4E-01	-0.4	5.1E-01	-0.2	7.5E-01
ENSMUST00000111220	cell adhesion molecule 3 [Source:MGI Symbol;Acc:MGI:2137858]		Q99N28	8.8	8.2E-06	-1.0	2.0E-01	1.1	5.4E-02	-0.8	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000111230	transgelin 2 [Source:MGI Symbol;Acc:MGI:1312985]		Q9WVA4	-4.1	1.1E-03	2.6	9.6E-02	-2.3	1.3E-01	0.1	9.0E-01
ENSMUST00000111234	tumor necrosis factor receptor superfamily, member 19 [Source:MGI Symbol;Acc:MGI:1352474]		Q9JLL3	7.4	6.8E-05	2.7	1.3E-03	-0.2	6.4E-01	-0.5	2.8E-01
ENSMUST00000109556	2-oxoglutarate and iron-dependent oxygenase domain containing 1 [Source:MGI Symbol;Acc:MGI:2442978]		Q3U0K8	-0.8	6.2E-01	-1.1	6.6E-01	1.2	4.6E-01	1.5	5.2E-01
ENSMUST00000111243	ATPase, Na+/K+ transporting, alpha 4 polypeptide [Source:MGI Symbol;Acc:MGI:1351335]		Q9WV27	8.7	8.3E-06	3.6	6.6E-04	-1.1	1.7E-01	-0.5	3.5E-01
ENSMUST00000111246	1-aminocyclopropane-1-carboxylate synthase (non-functional) [Source:MGI Symbol;Acc:MGI:1919717]		A2AIG8	5.1	1.2E-04	3.5	6.2E-02	-1.7	2.9E-01	-0.7	6.1E-01
ENSMUST00000111252	peroxisomal biogenesis factor 19 [Source:MGI Symbol;Acc:MGI:1334458]		Q8VCI5	-2.6	1.5E-02	-4.2	2.3E-02	1.8	2.4E-02	-0.7	6.7E-01
ENSMUST00000109568	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]	B7ZNS2		6.3	4.1E-02	5.8	7.2E-02	-0.8	7.9E-01	-0.4	8.5E-01
ENSMUST00000109570	AAR2 splicing factor homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915545]		Q9D2V5	-2.9	4.3E-02	-1.7	3.5E-01	0.9	3.9E-01	-0.3	8.6E-01
ENSMUST00000109572	erythrocyte membrane protein band 4.1 like 1 [Source:MGI Symbol;Acc:MGI:103010]	A2AUK6		1.8	4.3E-01	5.0	1.6E-01	2.4	4.6E-01	-0.8	7.1E-01
ENSMUST00000109574	erythrocyte membrane protein band 4.1 like 1 [Source:MGI Symbol;Acc:MGI:103010]	A2AUK7		2.2	4.0E-01	-1.8	3.1E-01	-6.5	7.3E-03	-2.4	2.8E-01
ENSMUST00000111254	aristaless-like homeobox 4 [Source:MGI Symbol;Acc:MGI:108359]	A2AIK5		8.4	3.0E-05	2.1	3.9E-01	-4.7	5.8E-02	1.8	3.8E-01
ENSMUST00000111263	vang-like 2 (van gogh, Drosophila) [Source:MGI Symbol;Acc:MGI:2135272]		Q91ZD4	9.0	8.2E-06	-2.8	5.2E-02	1.9	1.9E-02	-0.6	6.8E-01
ENSMUST00000111265	tetraspanin 18 [Source:MGI Symbol;Acc:MGI:1917186]		Q80WR1	9.4	1.2E-05	-5.1	1.0E-02	1.2	1.4E-01	1.7	3.3E-01
ENSMUST00000111272	PR domain containing 11 [Source:MGI Symbol;Acc:MGI:2685553]	A0A0A0MQD9		1.2	2.5E-02	1.5	2.3E-01	-3.7	2.0E-02	0.1	8.9E-01
ENSMUST00000111274	PR domain containing 11 [Source:MGI Symbol;Acc:MGI:2685553]		A2AGX3	6.2	8.6E-06	-6.3	5.3E-03	-0.2	7.0E-01	-0.7	7.0E-01
ENSMUST00000111275	neutrophil cytosolic factor 1 [Source:MGI Symbol;Acc:MGI:97283]		Q09014	-7.4	1.3E-06	3.0	1.3E-01	-1.0	5.8E-01	1.3	3.6E-01
ENSMUST00000109586	SERTA domain containing 2 [Source:MGI Symbol;Acc:MGI:1931026]	Q3UGZ1	Q9JJG5	-2.6	6.7E-02	-2.6	1.8E-01	0.5	6.5E-01	0.5	8.1E-01
ENSMUST00000109594	te carrier family 1 (glutamate/neutral amino acid transporter), member 4 [Source:MGI Symbol;Acc:MGI:2135(	Q3UTP8	O35874	6.0	9.1E-02	4.0	2.8E-01	-0.7	8.5E-01	1.3	5.8E-01
ENSMUST00000111279	mitogen-activated protein kinase 8 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1309464]		Q9WVI9	6.5	3.0E-02	6.1	2.4E-03	-0.6	7.3E-01	-1.8	7.8E-02
ENSMUST00000111287	calneuron 1 [Source:MGI Symbol;Acc:MGI:2155987]	Q542R1	Q9JJG7	5.0	4.6E-03	-4.1	2.8E-02	-0.6	4.6E-01	0.7	6.5E-01
ENSMUST00000111293	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	A2AHG2		-7.6	5.8E-04	-7.2	6.8E-03	-0.8	2.9E-01	-0.5	8.3E-01
ENSMUST00000111295	nitrilase 1 [Source:MGI Symbol;Acc:MGI:1350916]		Q8VDK1	-5.9	2.4E-04	8.7	1.9E-05	-0.6	5.9E-01	-1.2	4.4E-02
ENSMUST00000111298	transmembrane protein 248 [Source:MGI Symbol;Acc:MGI:1918917]		Q3TBN1	-5.9	1.3E-03	4.2	4.6E-02	-0.6	7.2E-01	0.3	8.2E-01
ENSMUST00000111308	glucuronidase, beta [Source:MGI Symbol;Acc:MGI:95872]	Q99KJ6		2.9	7.6E-03	-4.1	1.8E-04	0.5	1.4E-01	-0.2	8.1E-01
ENSMUST00000111313	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1928767]	Q3U260	Q91YY2	-7.6	5.2E-03	-6.8	2.5E-02	1.7	7.4E-02	1.3	6.5E-01
ENSMUST00000111314	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4 [Source:MGI Symbol;Acc:M(	E9PV91		5.5	3.7E-03	-4.2	6.3E-04	0.5	2.2E-01	-1.7	1.1E-01
ENSMUST00000109609	thymoma viral proto-oncogene 1 interacting protein [Source:MGI Symbol;Acc:MGI:3693832]		Q64362	-2.3	3.0E-01	-4.1	1.3E-01	-2.6	8.7E-02	-0.9	7.6E-01
ENSMUST00000111315	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4 [Source:MGI Symbol;Acc:M(	Q3TNX8		9.3	1.5E-04	8.8	2.0E-05	-0.7	5.9E-01	-0.3	5.2E-01
ENSMUST00000109614	chromodomain helicase DNA binding protein 9 [Source:MGI Symbol;Acc:MGI:1924001]		Q8BYH8	4.6	8.2E-02	5.5	8.4E-02	-0.3	9.3E-01	-1.2	5.3E-01
ENSMUST00000111325	short chain dehydrogenase/reductase family 39U, member 1 [Source:MGI Symbol;Acc:MGI:1916876]		Q5M8N4	-3.0	1.8E-03	-1.5	3.8E-01	0.3	8.1E-01	-3.2	1.3E-01
ENSMUST00000111327	ranslocase of outer mitochondrial membrane 40 homolog-like (yeast) [Source:MGI Symbol;Acc:MGI:3589112		Q9CZR3	-4.1	7.2E-03	4.7	2.0E-02	-0.7	7.0E-01	1.7	1.5E-01
ENSMUST00000109619	centrosomal protein 250 [Source:MGI Symbol;Acc:MGI:108084]	A3KGJ7		1.2	7.6E-01	-2.5	5.9E-01	-4.3	1.5E-01	-0.6	9.1E-01
ENSMUST00000109620	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 [Source:MGI Symbol;Acc:MGI:1933111]	E9QMH1		-2.2	8.8E-02	-3.2	1.2E-01	0.5	5.7E-01	1.5	4.4E-01
ENSMUST00000111333	zinc finger protein 408 [Source:MGI Symbol;Acc:MGI:2685857]	Q3V1D8		7.2	9.1E-04	6.9	6.3E-04	-0.7	6.3E-01	0.2	7.9E-01
ENSMUST00000111334	myelin protein zero [Source:MGI Symbol;Acc:MGI:103177]	E9QK82		5.6	7.3E-03	5.9	4.2E-02	0.3	9.0E-01	0.3	8.5E-01
ENSMUST00000111343	RAN, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1333112]		P62827	-3.4	1.7E-02	-0.9	5.0E-01	0.4	7.1E-01	-3.1	8.9E-02
ENSMUST00000111346	RIMS binding protein 2 [Source:MGI Symbol;Acc:MGI:2443235]	D3YXR8		8.9	5.7E-05	2.7	2.1E-02	-0.8	3.8E-01	0.2	7.8E-01
ENSMUST00000111349	protein kinase C and casein kinase substrate in neurons 3 [Source:MGI Symbol;Acc:MGI:1891410]	Q543N7	Q99JB8	7.2	1.7E-03	6.0	8.9E-04	-0.6	6.3E-01	0.8	2.6E-01
ENSMUST00000109634	nucleotide-binding oligomerization domain containing 2 [Source:MGI Symbol;Acc:MGI:2429397]		Q8K3Z0	1.2	4.8E-02	1.6	3.8E-02	0.2	7.0E-01	-0.2	6.9E-01
ENSMUST00000109636	ubiquinol-cytochrome c reductase complex assembly factor 1 [Source:MGI Symbol;Acc:MGI:1929472]		Q9CWU6	2.1	2.9E-01	5.2	5.5E-02	1.6	5.1E-01	-1.6	3.4E-01
ENSMUST00000111350	UDP-N-acetylglucosamine pyrophosphorylase 1 [Source:MGI Symbol;Acc:MGI:1334459]			-6.8	5.0E-06	1.6	4.1E-02	0.0	9.8E-01	0.6	2.8E-01
ENSMUST00000111352	damage specific DNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1355314]	A2AGR6		-5.5	4.7E-03	5.6	5.5E-03	0.1	9.3E-01	-0.3	7.3E-01
ENSMUST00000111353	hydroxysteroid (17-beta) dehydrogenase 7 [Source:MGI Symbol;Acc:MGI:1330808]	Q8C5N9		5.6	2.1E-04	5.6	5.6E-04	-0.6	6.3E-01	0.7	2.5E-01
ENSMUST00000111360				4.2	1.7E-04	6.4	1.1E-03	-0.6	6.9E-01	-0.9	3.1E-01
ENSMUST00000111368	UF2, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191422		Q99P69	2.8	2.1E-03	3.5	2.1E-03	-0.2	8.0E-01	-0.4	5.4E-01
ENSMUST00000109664	fidgetin-like 1 [Source:MGI Symbol;Acc:MGI:1890648]		Q8BPY9	0.8	7.1E-01	-2.5	3.4E-01	-2.9	1.3E-01	0.4	8.8E-01
ENSMUST00000111372	MAP-kinase activating death domain [Source:MGI Symbol;Acc:MGI:2444672]	A2AGQ7		-5.8	5.1E-03	7.4	4.2E-04	1.0	4.7E-01	-0.6	3.9E-01
ENSMUST00000109680	solute carrier family 6 (neurotransmitter transporter), member 18 [Source:MGI Symbol;Acc:MGI:1336892]		O88576	7.9	7.2E-02	10.1	3.6E-02	-0.5	9.2E-01	-2.7	1.9E-01
ENSMUST00000109681	von Willebrand factor C domain containing 2 [Source:MGI Symbol;Acc:MGI:2442987]		Q8C8N3	3.8	6.6E-02	5.9	1.6E-02	-0.4	8.7E-01	-2.4	7.8E-02
ENSMUST00000111373	MAP-kinase activating death domain [Source:MGI Symbol;Acc:MGI:2444672]	A2AGQ3		-5.7	1.8E-02	-6.1	3.4E-05	-0.9	3.6E-02	-2.2	5.8E-02
ENSMUST00000111377	LIM homeobox transcription factor 1 alpha [Source:MGI Symbol;Acc:MGI:1888519]	Q543W2	Q9JKU8	10.0	1.4E-03	-3.0	1.1E-01	0.1	9.0E-01	-1.2	5.2E-01
ENSMUST00000111378	proteasome (prosome, macropain) activator subunit 2 (PA28 beta) [Source:MGI Symbol;Acc:MGI:1096365]	G3X9V0		-8.3	3.9E-05	4.5	1.1E-03	1.5	1.2E-01	0.4	5.8E-01
ENSMUST00000111398	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]		Q9WU42	8.9	3.5E-03	-2.0	1.8E-01	-5.4	1.6E-03	1.0	4.7E-01
ENSMUST00000111404	neural retina leucine zipper gene [Source:MGI Symbol;Acc:MGI:102567]	Q543Y0	P54846	7.5	5.8E-04	-3.4	1.1E-02	1.3	4.1E-02	-0.5	6.7E-01
ENSMUST00000111416	immunoglobulin-like domain containing receptor 2 [Source:MGI Symbol;Acc:MGI:1196370]		B5TVM2	7.3	7.9E-06	9.7	2.5E-02	-0.4	9.3E-01	-1.0	5.6E-01
ENSMUST00000111423				2.7	4.1E-03	3.3	2.8E-03	0.7	3.5E-01	-0.2	7.1E-01
ENSMUST00000111432	cellular repressor of E1A-stimulated genes 1 [Source:MGI Symbol;Acc:MGI:1344382]		O88668	-6.1	2.0E-03	-0.6	6.4E-01	1.6	8.9E-02	-0.5	6.9E-01
ENSMUST00000111438	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 [Source:MGI Symbol;Acc:MGI:1915098]	E9Q9T6		3.6	7.6E-03	-4.7	2.0E-04	0.0	9.7E-01	-1.4	1.6E-01
ENSMUST00000109701	hnRNP-associated with lethal yellow [Source:MGI Symbol;Acc:MGI:97850]	Q3U3F6	Q64012	-0.7	8.3E-01	-5.3	2.3E-01	-3.4	1.4E-01	1.2	7.8E-01
ENSMUST00000109702	zinc finger protein 341 [Source:MGI Symbol;Acc:MGI:2682937]	A2AVM0		2.2	1.3E-01	-0.5	8.5E-01	0.4	7.9E-01	3.1	1.7E-01
ENSMUST00000111442	chemokine (C-C motif) receptor 5 [Source:MGI Symbol;Acc:MGI:107182]		P51682	-3.3	3.4E-04	1.9	2.3E-02	-0.7	2.9E-01	-0.4	5.6E-01
ENSMUST00000111448	CUGBP, Elav-like family member 1 [Source:MGI Symbol;Acc:MGI:1342295]		P28659	-3.1	2.4E-02	7.5	8.4E-03	-0.2	9.3E-01	-2.6	8.4E-02
ENSMUST00000111450	G protein-coupled receptor 161 [Source:MGI Symbol;Acc:MGI:2685054]			7.2	1.1E-05	-7.4	1.5E-03	0.7	2.2E-01	0.4	8.2E-01
ENSMUST00000111455	CUGBP, Elav-like family member 1 [Source:MGI Symbol;Acc:MGI:1342295]		P28659	-6.9	2.3E-02	-0.6	5.1E-01	-0.3	6.2E-01	-4.1	5.4E-03
ENSMUST00000109723	metastasis associated 1 [Source:MGI Symbol;Acc:MGI:2150037]	E9PX23		3.3	1.5E-01	6.4	5.0E-02	0.4	8.9E-01	-2.7	1.5E-01
ENSMUST00000109726	metastasis associated 1 [Source:MGI Symbol;Acc:MGI:2150037]	F8WHY8		-2.9	2.7E-01	-4.0	2.0E-01	-2.0	2.2E-01	-0.9	7.8E-01
ENSMUST00000109727	metastasis associated 1 [Source:MGI Symbol;Acc:MGI:2150037]	E9PX23		4.0	9.0E-02	2.3	4.1E-01	-0.3	9.1E-01	1.4	4.7E-01
ENSMUST00000109728	syntrophin, acidic 1 [Source:MGI Symbol;Acc:MGI:101772]	A2AKD7		-0.9	4.7E-01	-3.9	1.5E-01	0.5	6.9E-01	3.5	1.8E-01
ENSMUST00000111466	C1q and tumor necrosis factor related protein 4 [Source:MGI Symbol;Acc:MGI:1914695]		Q8R066	5.1	8.4E-04	5.9	3.8E-03	-0.1	9.5E-01	1.2	2.0E-01
ENSMUST00000109731	CDK5 regulatory subunit associated protein 1 [Source:MGI Symbol;Acc:MGI:1914221]		Q8BTW8	4.7	3.5E-02	4.7	5.2E-02	-0.5	8.3E-01	-0.6	6.8E-01
ENSMUST00000109732	zinc finger protein 429 [Source:MGI Symbol;Acc:MGI:1920057]	Q7M6Y0		0.5	4.2E-01	1.1	1.6E-01	0.3	6.1E-01	-0.3	6.2E-01
ENSMUST00000109733	peroxiredoxin 2 [Source:MGI Symbol;Acc:MGI:109486]		Q61171	3.2	9.9E-02	4.1	3.6E-02	-1.8	3.3E-01	-2.8	5.9E-02
ENSMUST00000109735	zinc finger protein 595 [Source:MGI Symbol;Acc:MGI:3040707]	Q8BIN6		-1.6	4.1E-02	-1.5	1.2E-01	0.1	8.3E-01	0.0	9.7E-01
ENSMUST00000109736	ribonuclease H2, large subunit [Source:MGI Symbol;Acc:MGI:1916974]		Q9CWY8	2.6	1.8E-01	5.3	9.5E-02	2.6	3.5E-01	-0.1	9.4E-01
ENSMUST00000111468	mitochondrial carrier homolog 2 (C. elegans) [Source:MGI Symbol;Acc:MGI:1929260]	D6RCZ1		-7.1	3.5E-06	-1.2	1.1E-01	0.8	1.1E-01	-1.1	1.6E-01
ENSMUST00000111472	CDK2 (cyclin-dependent kinase 2)-associated protein 1 [Source:MGI Symbol;Acc:MGI:1202069]	F2Z4B3		-4.6	2.3E-03	5.0	2.4E-03	-0.4	7.4E-01	0.2	7.9E-01
ENSMUST00000109745	glutaryl-Coenzyme A dehydrogenase [Source:MGI Symbol;Acc:MGI:104541]		Q60759	-1.3	5.7E-01	-1.6	4.3E-01	-2.5	1.4E-01	-2.3	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000111474	CDK2 (cyclin-dependent kinase 2)-associated protein 1 [Source:MGI Symbol;Acc:MGI:1202069]	F2Z4B3		4.1	3.9E-03	3.5	1.3E-01	-0.6	7.7E-01	2.4	1.2E-01
ENSMUST00000111477	RIKEN cDNA 2810006K23 gene [Source:MGI Symbol;Acc:MGI:1919900]		Q80VP5	5.7	7.8E-05	3.8	5.5E-03	0.5	6.1E-01	0.3	7.5E-01
ENSMUST00000111490	methyltransferase like 18 [Source:MGI Symbol;Acc:MGI:1917212]		Q9CZ09	-4.1	2.1E-02	3.6	2.0E-02	0.6	6.3E-01	-0.4	6.3E-01
ENSMUST00000111493	protein tyrosine phosphatase, receptor type, J [Source:MGI Symbol;Acc:MGI:104574]	A2AWF8		-2.6	9.3E-03	5.6	1.2E-03	-0.5	7.2E-01	0.3	7.0E-01
ENSMUST00000109755	SIVA1, apoptosis-inducing factor [Source:MGI Symbol;Acc:MGI:1353606]		O54926	2.9	7.2E-02	5.0	4.6E-02	1.9	3.6E-01	-0.2	8.9E-01
ENSMUST00000109759	BPI fold containing family B, member 4 [Source:MGI Symbol;Acc:MGI:2685852]		A2BGH0	2.7	2.5E-01	5.1	5.0E-02	-0.3	9.0E-01	-2.7	1.2E-01
ENSMUST00000111513	bicaudal D homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1101760]		Q8BR07	7.8	2.0E-05	-3.3	3.6E-02	0.4	5.5E-01	-1.5	3.5E-01
ENSMUST00000111525	flavin containing monooxygenase 4 [Source:MGI Symbol;Acc:MGI:2429497]		Q8VHG0	6.2	1.5E-04	5.4	3.8E-03	-2.2	2.0E-01	-0.2	7.9E-01
ENSMUST00000111557	DENN/MADD domain containing 5B [Source:MGI Symbol;Acc:MGI:2444273]		A2RSQ0	4.7	2.7E-05	1.4	1.1E-01	-1.0	1.7E-01	0.3	6.9E-01
ENSMUST00000111558	actin-binding LIM protein 1 [Source:MGI Symbol;Acc:MGI:1194500]	E9Q9C1		6.7	4.6E-04	-2.9	8.2E-02	0.0	9.8E-01	-0.6	7.2E-01
ENSMUST00000111564	CAP-GLY domain containing linker protein 1 [Source:MGI Symbol;Acc:MGI:1928401]		Q922J3	-6.6	2.2E-04	3.4	1.1E-03	0.2	7.1E-01	-0.2	6.8E-01
ENSMUST00000109771	DNA methyltransferase 3B [Source:MGI Symbol;Acc:MGI:1261819]	Q3KR45		2.2	3.7E-01	3.7	1.6E-01	-1.2	6.5E-01	-2.7	1.9E-01
ENSMUST00000111566	CAP-GLY domain containing linker protein 1 [Source:MGI Symbol;Acc:MGI:1928401]		Q922J3	4.2	3.0E-02	1.4	7.4E-02	-6.0	1.9E-04	0.2	7.2E-01
ENSMUST00000111569	caprin family member 2 [Source:MGI Symbol;Acc:MGI:2448541]	E4NKG5	Q05A80	6.3	5.2E-04	3.6	3.3E-02	-0.9	5.3E-01	1.2	2.8E-01
ENSMUST00000111587	diablo homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913843]		Q9JIQ3	-5.0	1.3E-03	-4.6	1.3E-03	0.9	5.7E-02	0.0	9.9E-01
ENSMUST00000111594	phosphatidylinositol glycan anchor biosynthesis, class C [Source:MGI Symbol;Acc:MGI:1914542]		Q9CXR4	-3.6	3.9E-03	2.9	1.6E-03	-1.1	1.1E-01	0.1	8.3E-01
ENSMUST00000109785	zinc finger, MIZ-type containing 2 [Source:MGI Symbol;Acc:MGI:106374]		Q8CIE2	-2.0	1.9E-01	-3.0	1.8E-01	0.0	1.0E+00	1.0	6.2E-01
ENSMUST00000109786	zinc finger, MIZ-type containing 2 [Source:MGI Symbol;Acc:MGI:106374]		Q8CIE2	2.9	3.2E-01	3.7	2.7E-01	-1.8	5.8E-01	-2.6	2.9E-01
ENSMUST00000111596	MLX interacting protein [Source:MGI Symbol;Acc:MGI:2141183]	B2RQ56		7.2	4.5E-05	-4.2	7.4E-02	0.8	3.8E-01	0.9	7.1E-01
ENSMUST00000111601	leucine rich repeat containing 55 [Source:MGI Symbol;Acc:MGI:2685197]		Q3UY51	6.5	4.8E-04	-3.3	6.6E-04	0.7	7.3E-02	-0.1	8.6E-01
ENSMUST00000109792	tumor necrosis factor, alpha-induced protein 2 [Source:MGI Symbol;Acc:MGI:104960]	D3Z4L9		-1.0	6.0E-01	-0.8	7.5E-01	1.0	5.4E-01	0.8	7.2E-01
ENSMUST00000111604	tudor domain containing 1 [Source:MGI Symbol;Acc:MGI:1933218]		Q99MV1	7.4	2.4E-04	-1.9	5.0E-02	0.6	3.3E-01	0.7	4.2E-01
ENSMUST00000111606	tudor domain containing 1 [Source:MGI Symbol;Acc:MGI:1933218]		Q99MV1	6.1	3.0E-02	-4.6	2.0E-04	1.4	3.8E-03	-0.4	6.3E-01
ENSMUST00000109800	cerebral cavernous malformation 2-like [Source:MGI Symbol;Acc:MGI:2385159]		Q8VCC6	-2.6	5.8E-02	-1.2	5.3E-01	2.1	1.2E-01	0.7	7.0E-01
ENSMUST00000111608	ankyrin repeat domain 45 [Source:MGI Symbol;Acc:MGI:1921094]		Q810N6	6.8	4.9E-05	-10.2	2.0E-04	0.4	3.2E-01	3.2	8.6E-02
ENSMUST00000111610	heterogeneous nuclear ribonucleoprotein C [Source:MGI Symbol;Acc:MGI:107795]		Q9Z204	-4.9	8.6E-05	-3.0	1.2E-01	1.6	1.4E-01	1.6	3.6E-01
ENSMUST00000111620	centromere protein L [Source:MGI Symbol;Acc:MGI:1917704]	Q14A61		-5.3	4.6E-04	3.2	7.7E-02	-1.5	3.7E-01	0.2	8.3E-01
ENSMUST00000111624	solute carrier family 43, member 1 [Source:MGI Symbol;Acc:MGI:1931352]		Q8BSM7	7.2	6.7E-04	-6.0	2.0E-03	-0.3	5.9E-01	-0.7	6.7E-01
ENSMUST00000111627	myelin-associated oligodendrocytic basic protein [Source:MGI Symbol;Acc:MGI:108511]		Q9D2P8	8.1	5.6E-04	-5.5	7.5E-02	1.3	2.2E-01	2.4	4.0E-01
ENSMUST00000109824	inhibitor of DNA binding 1 [Source:MGI Symbol;Acc:MGI:96396]	A2AHY3		0.1	8.9E-01	-0.5	5.2E-01	-1.0	1.1E-01	-0.4	5.9E-01
ENSMUST00000111628	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]	E9Q995		3.7	1.9E-03	2.4	1.8E-01	-2.6	1.9E-01	0.1	9.2E-01
ENSMUST00000111635	xin actin-binding repeat containing 1 [Source:MGI Symbol;Acc:MGI:1333878]	E9QQ93		10.7	1.2E-05	4.1	3.6E-02	-1.4	4.4E-01	-0.1	9.2E-01
ENSMUST00000111639	aryl hydrocarbon receptor nuclear translocator-like 2 [Source:MGI Symbol;Acc:MGI:2684845]		Q2VPD4	4.1	8.4E-05	-7.4	3.5E-03	0.4	6.3E-01	1.0	6.4E-01
ENSMUST00000111644	serine/threonine kinase 38 like [Source:MGI Symbol;Acc:MGI:1922250]		Q7TSE6	1.6	6.6E-03	-3.4	3.8E-02	1.2	1.9E-01	-0.8	6.5E-01
ENSMUST00000111651	transcription factor 7 like 2, T cell specific, HMG box [Source:MGI Symbol;Acc:MGI:1202879]			5.7	2.2E-02	4.9	3.1E-05	-0.6	3.9E-01	-0.6	1.8E-01
ENSMUST00000111654	transcription factor 7 like 2, T cell specific, HMG box [Source:MGI Symbol;Acc:MGI:1202879]	Q3V1G9		5.7	3.4E-04	-6.1	1.0E-03	1.5	1.0E-02	0.1	9.7E-01
ENSMUST00000111657	transcription factor 7 like 2, T cell specific, HMG box [Source:MGI Symbol;Acc:MGI:1202879]	E9QQ90		7.5	9.9E-03	-3.2	3.8E-03	0.7	1.6E-01	-4.0	8.2E-03
ENSMUST00000111665	thioredoxin-related transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1914208]		Q9D710	6.6	9.3E-03	-1.8	2.2E-01	0.9	3.3E-01	-1.0	5.3E-01
ENSMUST00000109854	Ena-vasodilator stimulated phosphoprotein [Source:MGI Symbol;Acc:MGI:1194884]	F8WJB9		1.3	3.3E-01	1.0	5.6E-01	0.3	8.3E-01	0.6	7.1E-01
ENSMUST00000111670	catenin (cadherin associated protein), delta 1 [Source:MGI Symbol;Acc:MGI:105100]	E9Q986		-3.8	2.8E-02	6.5	1.6E-04	-0.6	6.0E-01	-0.7	3.0E-01
ENSMUST00000111700	SEC16 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2148802]		Q91XT4	2.6	3.7E-03	6.8	1.8E-04	-0.5	6.8E-01	0.1	9.0E-01
ENSMUST00000109858	solute carrier protein family 52, member 3 [Source:MGI Symbol;Acc:MGI:1916948]		Q9D6X5	-2.7	2.6E-01	1.6	6.8E-01	4.9	1.2E-01	0.5	8.7E-01
ENSMUST00000109859	solute carrier protein family 52, member 3 [Source:MGI Symbol;Acc:MGI:1916948]		Q9D6X5	0.7	7.8E-01	0.6	8.2E-01	-1.5	4.7E-01	-1.5	5.8E-01
ENSMUST00000109861	solute carrier protein family 52, member 3 [Source:MGI Symbol;Acc:MGI:1916948]		Q9D6X5	2.0	3.1E-01	4.3	1.8E-01	3.1	2.7E-01	0.9	6.5E-01
ENSMUST00000111701	sarcospan [Source:MGI Symbol;Acc:MGI:1353511]	E9Q8Y7		6.5	1.6E-04	-0.3	8.3E-01	-4.3	1.5E-02	2.3	1.3E-01
ENSMUST00000109865	family with sequence similarity 110, member A [Source:MGI Symbol;Acc:MGI:1921097]		Q8R184	4.2	4.5E-02	4.2	1.2E-01	0.0	9.9E-01	0.1	9.7E-01
ENSMUST00000111702	sarcospan [Source:MGI Symbol;Acc:MGI:1353511]	E9Q8Y7		4.7	3.5E-04	3.9	3.2E-03	-1.0	3.1E-01	0.6	3.9E-01
ENSMUST00000109868	idnK gluconokinase homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1922981]	D3Z4J6		-1.8	1.3E-01	-0.3	8.3E-01	-0.4	6.1E-01	-2.0	1.4E-01
ENSMUST00000111703	basic helix-loop-helix family, member e41 [Source:MGI Symbol;Acc:MGI:1930704]	D3Z2G6		5.2	3.1E-03	-3.0	3.7E-02	0.8	2.1E-01	-0.5	7.2E-01
ENSMUST00000111704	as association (RalGDS/AF-6) domain family (N-terminal) member 8 [Source:MGI Symbol;Acc:MGI:191857		Q8CJ96	3.4	6.9E-04	7.0	2.6E-04	-0.5	7.3E-01	-2.3	9.4E-03
ENSMUST00000111706	lamin tail domain containing 1 [Source:MGI Symbol;Acc:MGI:1921321]	E9Q8Y6		6.6	5.7E-05	7.4	3.8E-04	0.4	7.8E-01	0.5	4.9E-01
ENSMUST00000109875	syntaphilin [Source:MGI Symbol;Acc:MGI:2139270]		Q80U23	3.9	1.0E-01	6.7	1.7E-02	-0.4	8.6E-01	-3.2	5.3E-02
ENSMUST00000109877	syntaphilin [Source:MGI Symbol;Acc:MGI:2139270]		Q80U23	4.1	7.3E-02	6.1	2.3E-02	-0.3	8.9E-01	-2.3	1.1E-01
ENSMUST00000109878	rhomboid domain containing 3 [Source:MGI Symbol;Acc:MGI:2444684]	B7ZNJ8	Q8BP97	0.1	9.4E-01	0.9	6.3E-01	-2.0	2.4E-01	-2.8	1.5E-01
ENSMUST00000111710	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog [Source:MGI Symbol;Acc:MGI:96680]	Q0VDV7	P32883	-5.7	9.6E-04	4.1	5.7E-04	0.0	9.7E-01	-0.4	5.0E-01
ENSMUST00000109887	B cell leukemia/lymphoma 11B [Source:MGI Symbol;Acc:MGI:1929913]			2.7	1.3E-01	4.0	4.7E-02	-0.7	6.9E-01	-2.0	1.9E-01
ENSMUST00000111726	LYR motif containing 5 [Source:MGI Symbol;Acc:MGI:1914886]		Q91V16	-7.6	2.6E-06	5.8	1.1E-02	-0.7	7.3E-01	2.9	1.8E-02
ENSMUST00000109890	predicted gene 14151 [Source:MGI Symbol;Acc:MGI:3651016]	A2AQX6		5.6	3.9E-02	7.3	1.5E-02	-0.8	7.6E-01	-2.5	1.4E-01
ENSMUST00000111729	vacuolar protein sorting 29 (S. pombe) [Source:MGI Symbol;Acc:MGI:1928344]	H7BXA2		-8.2	2.0E-06	-4.9	2.9E-03	0.4	3.8E-01	-0.6	6.7E-01
ENSMUST00000111735	transmembrane protein 260 [Source:MGI Symbol;Acc:MGI:2443219]		Q8BMD6	-1.7	1.9E-02	4.3	1.8E-04	-3.4	3.0E-03	-0.1	9.2E-01
ENSMUST00000111737	MAX interactor 1, dimerization protein [Source:MGI Symbol;Acc:MGI:97245]		P50540	-3.0	2.5E-02	-2.7	3.0E-02	0.6	3.6E-01	-3.1	3.3E-02
ENSMUST00000111740	integrin alpha V [Source:MGI Symbol;Acc:MGI:96608]	A2AKI5		-3.7	2.9E-02	-4.3	1.1E-04	0.0	9.4E-01	0.7	3.5E-01
ENSMUST00000111741	adducin 3 (gamma) [Source:MGI Symbol;Acc:MGI:1351615]		Q9QYB5	-3.6	5.4E-04	-0.3	6.0E-01	0.7	8.9E-02	-0.1	8.5E-01
ENSMUST00000111748	SRY (sex determining region Y)-box 5 [Source:MGI Symbol;Acc:MGI:98367]	Q3TVF9	P35710	8.1	1.0E-04	7.7	2.1E-04	-0.6	7.0E-01	-0.3	6.0E-01
ENSMUST00000111752	cut-like homeobox 2 [Source:MGI Symbol;Acc:MGI:107321]		P70298	8.3	8.2E-05	4.0	4.6E-04	-0.5	4.9E-01	0.4	4.1E-01
ENSMUST00000111754	torsin A interacting protein 2 [Source:MGI Symbol;Acc:MGI:3582695]		Q9ER81	-7.6	1.4E-05	-0.1	9.6E-01	-2.4	3.1E-01	2.7	2.7E-01
ENSMUST00000111758	C2 calcium-dependent domain containing 5 [Source:MGI Symbol;Acc:MGI:1921991]		Q7TPS5	-5.3	1.1E-02	0.5	6.5E-01	-4.9	5.7E-03	0.0	9.7E-01
ENSMUST00000109930	activating signal cointegrator 1 complex subunit 2 [Source:MGI Symbol;Acc:MGI:1922702]		Q91WR3	1.1	1.0E-01	2.1	4.0E-02	0.8	3.1E-01	-0.2	8.2E-01
ENSMUST00000109931	zinc finger protein 120 [Source:MGI Symbol;Acc:MGI:1345179]	A2ANU5		-2.5	7.5E-02	-0.9	6.1E-01	1.7	2.1E-01	0.1	9.6E-01
ENSMUST00000111763	eomesodermin homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1201683]		O54839	6.3	2.6E-04	2.9	3.6E-01	-0.8	7.6E-01	2.4	3.1E-01
ENSMUST00000109935	synapse differentiation inducing 1 [Source:MGI Symbol;Acc:MGI:3702158]		A2ANU3	3.3	8.2E-02	6.0	6.8E-03	-0.5	8.1E-01	-3.2	2.3E-02
ENSMUST00000111770	acyl-Coenzyme A dehydrogenase family, member 10 [Source:MGI Symbol;Acc:MGI:1919235]		Q8K370	-3.4	1.1E-02	3.2	1.2E-01	-2.1	2.9E-01	0.8	5.8E-01
ENSMUST00000111773	RNA binding motif, single stranded interacting protein [Source:MGI Symbol;Acc:MGI:2444477]		Q8BWL5	7.8	1.1E-05	5.7	7.3E-02	7.2	2.0E-02	-3.7	1.1E-01
ENSMUST00000109940	HMG box domain containing 4 [Source:MGI Symbol;Acc:MGI:1918073]	Q8BTT5		0.1	9.8E-01	5.4	8.2E-02	3.9	1.7E-01	-1.4	4.6E-01
ENSMUST00000111775	xenotropic and polytropic retrovirus receptor 1 [Source:MGI Symbol;Acc:MGI:97932]	D3Z2B4		-4.0	1.1E-02	5.3	1.4E-04	-1.1	2.1E-01	0.8	1.8E-01
ENSMUST00000111776	acyl-Coenzyme A dehydrogenase family, member 12 [Source:MGI Symbol;Acc:MGI:2443320]	D3Z2B3		7.9	6.6E-05	-4.1	6.7E-02	2.1	6.4E-02	0.2	9.4E-01
ENSMUST00000109946	scribbled homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2145950]		Q80U72	-0.1	9.7E-01	-2.0	6.0E-01	-1.6	5.4E-01	0.3	9.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000109948	HORMA domain containing 2 [Source:MGI Symbol;Acc:MGI:1923078]		Q5SQP1	4.0	9.8E-02	6.0	3.4E-02	-0.3	9.2E-01	-2.2	1.5E-01
ENSMUST00000111783	MAP kinase-activated protein kinase 5 [Source:MGI Symbol;Acc:MGI:1333110]		O54992	-6.7	9.3E-06	-5.9	6.1E-05	-0.4	3.4E-01	0.0	9.8E-01
ENSMUST00000111784	sperm specific antigen 2 [Source:MGI Symbol;Acc:MGI:1917849]	A2AQD5		-4.9	2.9E-03	6.6	1.6E-04	-0.6	5.9E-01	-0.2	6.9E-01
ENSMUST00000111786	MAP kinase-activated protein kinase 5 [Source:MGI Symbol;Acc:MGI:1333110]		O54992	-6.9	1.4E-04	4.8	3.0E-03	-1.9	1.9E-01	0.3	6.9E-01
ENSMUST00000111790	WD repeat and HMG-box DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:2443514]		P59328	5.5	1.9E-03	-3.9	3.8E-03	0.2	6.9E-01	0.2	8.8E-01
ENSMUST00000111802	endoplasmic reticulum protein 29 [Source:MGI Symbol;Acc:MGI:1914647]	F8WIM7		-6.0	3.4E-05	5.5	1.6E-04	-0.7	4.6E-01	0.3	6.4E-01
ENSMUST00000111807	neuralized E3 ubiquitin protein ligase 1A [Source:MGI Symbol;Acc:MGI:1334263]		Q923S6	9.0	3.4E-05	6.3	8.8E-04	-0.6	6.6E-01	-2.8	1.2E-02
ENSMUST00000111808	neuralized E3 ubiquitin protein ligase 1A [Source:MGI Symbol;Acc:MGI:1334263]		Q923S6	3.6	2.8E-02	6.1	1.5E-04	-1.2	2.7E-01	-1.2	7.3E-02
ENSMUST00000109966	zinc finger protein 707 [Source:MGI Symbol;Acc:MGI:1916270]	D3Z445		-0.2	8.9E-01	0.8	6.0E-01	-1.0	4.8E-01	-2.1	2.3E-01
ENSMUST00000109967	zinc finger protein 707 [Source:MGI Symbol;Acc:MGI:1916270]	Q8R0U9		-1.8	2.1E-01	0.3	8.6E-01	1.7	2.1E-01	-0.4	8.0E-01
ENSMUST00000111810	regulator of G-protein signaling 8 [Source:MGI Symbol;Acc:MGI:108408]		Q8BXT1	7.3	1.3E-02	8.6	2.6E-05	-0.9	4.9E-01	-0.5	2.8E-01
ENSMUST00000111812	regulator of G-protein signaling 8 [Source:MGI Symbol;Acc:MGI:108408]		Q8BXT1	9.9	8.3E-04	6.9	8.6E-05	-0.6	6.1E-01	-0.4	5.1E-01
ENSMUST00000111813	calcium homeostasis modulator 1 [Source:MGI Symbol;Acc:MGI:3643383]		D3Z291	7.0	2.6E-04	6.5	1.5E-04	0.1	8.9E-01	-1.2	6.4E-02
ENSMUST00000111816	tripartite motif-containing 71 [Source:MGI Symbol;Acc:MGI:2685973]		Q1PSW8	10.1	3.9E-06	2.5	4.2E-01	-0.6	8.3E-01	2.6	2.8E-01
ENSMUST00000111817	glia maturation factor, beta [Source:MGI Symbol;Acc:MGI:1927133]		Q9CQI3	-3.4	8.0E-05	2.2	9.6E-03	1.0	9.8E-02	0.2	6.6E-01
ENSMUST00000111819	CWC22 spliceosome-associated protein homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2136773]	B1AYU7		-6.0	1.3E-03	-1.2	5.2E-01	2.5	1.0E-01	0.2	9.2E-01
ENSMUST00000111820	transmembrane protein with metallophosphoesterase domain [Source:MGI Symbol;Acc:MGI:5317335]	D3Z286		4.0	2.6E-05	-8.0	1.6E-03	0.7	1.9E-01	0.0	9.9E-01
ENSMUST00000111827	solute carrier organic anion transporter family, member 1a6 [Source:MGI Symbol;Acc:MGI:1351906]		Q99J94	5.6	1.0E-03	-3.6	1.7E-01	2.0	1.5E-01	-0.7	7.8E-01
ENSMUST00000109992	transcobalamin 2 [Source:MGI Symbol;Acc:MGI:98534]		O88968	-2.6	6.6E-02	-0.1	9.2E-01	1.1	3.4E-01	-1.4	3.7E-01
ENSMUST00000111829	zinc finger protein 385B [Source:MGI Symbol;Acc:MGI:2444734]	Q8BM98		6.3	2.3E-04	-3.0	6.0E-02	1.2	1.6E-01	-1.9	2.4E-01
ENSMUST00000111830	zinc finger protein 385B [Source:MGI Symbol;Acc:MGI:2444734]		Q8BXJ8	6.8	2.8E-04	4.3	5.4E-04	0.2	8.3E-01	-0.5	4.5E-01
ENSMUST00000111838	CLIP associating protein 2 [Source:MGI Symbol;Acc:MGI:1923749]	E9Q8N5		5.4	1.0E-03	8.3	5.4E-05	-0.4	7.3E-01	-2.0	8.5E-03
ENSMUST00000109996	dual specificity phosphatase 18 [Source:MGI Symbol;Acc:MGI:1922469]		Q8VE01	-0.5	8.4E-01	-2.1	4.7E-01	-2.0	2.4E-01	-0.4	8.9E-01
ENSMUST00000111859	ral guanine nucleotide dissociation stimulator,-like 1 [Source:MGI Symbol;Acc:MGI:107484]	E9Q8M9		7.6	6.1E-04	-3.1	1.9E-03	-0.8	1.0E-01	-2.3	2.5E-02
ENSMUST00000110001	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 [Source:MGI Symbol;Acc:MGI:1351337]	F8WJA0		2.1	7.6E-02	0.1	9.4E-01	-0.3	8.0E-01	1.7	1.9E-01
ENSMUST00000111860	predicted pseudogene 8257 [Source:MGI Symbol;Acc:MGI:3644430]	D3Z260		8.8	8.3E-06	3.4	1.6E-03	0.3	7.1E-01	-0.5	3.9E-01
ENSMUST00000111861	programmed cell death 6 interacting protein [Source:MGI Symbol;Acc:MGI:1333753]		Q9WU78	-5.8	4.8E-05	7.2	3.5E-04	-0.1	9.3E-01	-0.3	6.5E-01
ENSMUST00000110005	Ras and Rab interactor 2 [Source:MGI Symbol;Acc:MGI:1921280]		Q9D684	-1.8	2.2E-01	0.7	6.8E-01	0.3	8.1E-01	-2.2	1.9E-01
ENSMUST00000110009	activity regulated cytoskeletal-associated protein [Source:MGI Symbol;Acc:MGI:88067]		Q9WV31	5.3	6.0E-02	5.6	4.9E-02	-2.0	5.0E-01	-2.3	1.7E-01
ENSMUST00000110011	smoothelin [Source:MGI Symbol;Acc:MGI:1354727]	D3Z3Q3		1.6	4.1E-01	5.7	2.3E-02	0.5	7.8E-01	-3.6	5.8E-02
ENSMUST00000111878	epidermal growth factor receptor pathway substrate 8 [Source:MGI Symbol;Acc:MGI:104684]		Q08509	-6.3	6.7E-03	-2.8	7.6E-02	1.1	2.0E-01	0.0	9.9E-01
ENSMUST00000111879	doublecortin-like kinase 3 [Source:MGI Symbol;Acc:MGI:3039580]		Q8BWQ5	8.0	6.7E-05	6.8	1.6E-04	-0.6	6.5E-01	-1.7	2.0E-02
ENSMUST00000111884	RBPJ interacting and tubulin associated 1 [Source:MGI Symbol;Acc:MGI:1922021]	D3Z228		6.6	6.8E-04	3.0	1.3E-02	-0.6	5.3E-01	0.1	9.4E-01
ENSMUST00000111888	chemokine (C-C motif) receptor-like 2 [Source:MGI Symbol;Acc:MGI:1920904]		O35457	-2.5	2.2E-02	-6.4	1.1E-02	-1.7	9.7E-02	0.3	8.7E-01
ENSMUST00000111891	Rho, GDP dissociation inhibitor (GDI) beta [Source:MGI Symbol;Acc:MGI:101940]		Q61599	-7.0	2.7E-04	6.4	2.7E-02	-0.8	7.6E-01	-0.8	6.0E-01
ENSMUST00000110029	LIM motif-containing protein kinase 2 [Source:MGI Symbol;Acc:MGI:1197517]		O54785	-2.7	2.7E-01	-3.3	2.2E-01	-0.6	7.2E-01	0.0	9.9E-01
ENSMUST00000110030	sorting nexin 5 [Source:MGI Symbol;Acc:MGI:1916428]		Q9D8U8	-2.7	2.7E-01	-2.9	1.4E-01	-3.7	3.4E-02	-3.5	1.5E-01
ENSMUST00000111892	Rho, GDP dissociation inhibitor (GDI) beta [Source:MGI Symbol;Acc:MGI:101940]		Q61599	-11.5	3.1E-06	2.1	3.4E-02	0.5	4.5E-01	0.1	8.5E-01
ENSMUST00000111905	glutamate receptor, ionotropic, NMDA2B (epsilon 2) [Source:MGI Symbol;Acc:MGI:95821]	G3X9V4		11.3	6.5E-05	-0.1	8.9E-01	-5.1	2.9E-04	-0.3	7.1E-01
ENSMUST00000111908	multimerin 2 [Source:MGI Symbol;Acc:MGI:2385618]		A6H6E2	7.3	1.1E-05	-0.3	8.3E-01	1.8	7.6E-02	-0.7	5.8E-01
ENSMUST00000110040	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D [Source:MGI		O09126	-1.0	7.3E-01	-2.6	4.2E-01	-2.2	3.4E-01	-0.6	8.7E-01
ENSMUST00000110042	predicted gene 15440 [Source:MGI Symbol;Acc:MGI:3642353]	D3Z3P4		0.0	9.9E-01	1.0	4.1E-01	-0.3	7.5E-01	-1.3	2.5E-01
ENSMUST00000110043	POZ (BTB) and AT hook containing zinc finger 1 [Source:MGI Symbol;Acc:MGI:1891832]	Q5NBY9		0.4	8.8E-01	5.5	1.3E-01	3.2	3.3E-01	-2.0	4.1E-01
ENSMUST00000111910	germ cell-specific gene 1 [Source:MGI Symbol;Acc:MGI:1194499]		Q8R1W2	6.0	7.0E-03	11.3	1.0E-07	-0.6	4.3E-01	0.6	5.9E-02
ENSMUST00000110048	eukaryotic translation initiation factor 4E nuclear import factor 1 [Source:MGI Symbol;Acc:MGI:1921453]		Q9EST3	1.0	1.4E-01	0.4	7.2E-01	1.8	4.5E-02	2.5	2.6E-02
ENSMUST00000111913	cDNA sequence BC003331 [Source:MGI Symbol;Acc:MGI:2385108]		Q4PJX1	-3.3	1.2E-02	-4.8	4.7E-03	1.4	2.2E-02	-0.1	9.4E-01
ENSMUST00000110051	occludin/ELL domain containing 1 [Source:MGI Symbol;Acc:MGI:1924340]	D3Z3P2		0.2	7.9E-01	-0.2	8.2E-01	0.7	3.9E-01	1.1	2.7E-01
ENSMUST00000111915	family with sequence similarity 234, member B [Source:MGI Symbol;Acc:MGI:1921775]		Q8BYI8	-2.9	3.9E-04	4.7	1.2E-03	1.5	1.3E-01	-0.1	8.7E-01
ENSMUST00000110065	G protein-coupled receptor 68 [Source:MGI Symbol;Acc:MGI:2441763]		Q8BFQ3	-0.9	6.1E-01	0.5	7.8E-01	-0.3	8.3E-01	-1.7	3.6E-01
ENSMUST00000110066	G protein-coupled receptor 68 [Source:MGI Symbol;Acc:MGI:2441763]		Q8BFQ3	0.2	9.0E-01	4.3	1.7E-01	4.3	1.2E-01	0.2	9.1E-01
ENSMUST00000110067	MACRO domain containing 2 [Source:MGI Symbol;Acc:MGI:1920149]	A2AS33		3.5	4.5E-02	5.0	9.3E-03	-0.6	7.1E-01	-2.1	1.0E-01
ENSMUST00000111916	family with sequence similarity 234, member B [Source:MGI Symbol;Acc:MGI:1921775]		Q8BYI8	6.9	4.2E-05	0.8	2.2E-01	0.0	9.3E-01	-4.5	2.5E-04
ENSMUST00000111920	nology domain-containing, family A (phosphoinositide binding specific) member 3 [Source:MGI Symbol;Acc:M		Q9ERS4	-1.6	8.2E-03	2.5	2.5E-02	-1.5	1.4E-01	-0.1	9.5E-01
ENSMUST00000111928	fibroblast growth factor 8 [Source:MGI Symbol;Acc:MGI:99604]	Q3V279	P37237	7.0	3.3E-04	-5.0	7.2E-03	1.1	8.4E-02	-0.8	6.0E-01
ENSMUST00000111929	oxysterol binding protein-like 6 [Source:MGI Symbol;Acc:MGI:2139014]		Q8BXR9	6.6	4.6E-05	6.2	2.6E-04	0.1	9.5E-01	0.6	4.0E-01
ENSMUST00000111943	mitogen-activated protein kinase 8 [Source:MGI Symbol;Acc:MGI:1346861]	A6P3E4		-3.5	3.2E-02	6.2	2.6E-04	-0.2	8.5E-01	0.5	4.8E-01
ENSMUST00000111953	replication factor C (activator 1) 5 [Source:MGI Symbol;Acc:MGI:1919401]	D3Z1Y6		3.3	6.6E-03	-7.5	5.4E-04	-0.3	5.9E-01	-1.6	3.3E-01
ENSMUST00000110084	bicaudal D homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1924145]	D3Z390		-3.8	4.1E-01	-1.9	7.5E-01	1.0	7.7E-01	-1.0	8.7E-01
ENSMUST00000110085	bicaudal D homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1924145]		Q921C5	0.4	9.0E-01	-3.9	2.1E-01	-3.9	1.1E-01	0.4	9.0E-01
ENSMUST00000110086	FYVE, RhoGEF and PH domain containing 3 [Source:MGI Symbol;Acc:MGI:1353657]			1.5	3.6E-02	3.2	5.4E-03	2.1	1.8E-02	0.4	5.4E-01
ENSMUST00000111956	Rho GTPase activating protein 22 [Source:MGI Symbol;Acc:MGI:2443418]		Q8BL80	7.1	1.5E-03	-3.2	1.6E-03	1.0	2.0E-02	-0.2	8.4E-01
ENSMUST00000110089	McKusick-Kaufman syndrome [Source:MGI Symbol;Acc:MGI:1891836]		Q9JI70	-3.0	3.5E-02	-3.1	5.6E-02	-0.9	2.9E-01	-0.9	5.9E-01
ENSMUST00000111957	glutaredoxin 2 (thioltransferase) [Source:MGI Symbol;Acc:MGI:1916617]	Q3UQ95	Q923X4	-6.5	4.4E-05	3.8	1.3E-02	0.3	8.0E-01	0.0	9.7E-01
ENSMUST00000111962	heterogeneous nuclear ribonucleoprotein A3 [Source:MGI Symbol;Acc:MGI:1917171]	Q0VG47	Q8BG05	-2.5	1.6E-03	3.6	8.1E-02	-3.9	8.4E-02	-0.3	8.2E-01
ENSMUST00000111967	V-set and immunoglobulin domain containing 10 [Source:MGI Symbol;Acc:MGI:2448533]		D3YX43	-4.9	4.7E-03	8.7	4.2E-04	-1.4	4.5E-01	1.1	1.9E-01
ENSMUST00000111972	proline rich protein HaeIII subfamily 1 [Source:MGI Symbol;Acc:MGI:97773]	D3Z1V5		7.7	9.9E-03	11.7	2.2E-03	0.9	7.8E-01	2.1	5.3E-02
ENSMUST00000110103	growth differentiation factor 15 [Source:MGI Symbol;Acc:MGI:1346047]		Q9Z0J7	-0.6	6.0E-01	1.3	3.8E-01	0.8	5.0E-01	-1.1	4.1E-01
ENSMUST00000111973	phosphatidylethanolamine binding protein 1 [Source:MGI Symbol;Acc:MGI:1344408]	D3Z1V4		5.1	1.9E-02	-5.1	1.3E-03	-0.4	4.4E-01	-1.5	2.6E-01
ENSMUST00000111976	complement component factor h [Source:MGI Symbol;Acc:MGI:88385]	E9Q8I0		-5.0	9.1E-03	-2.6	1.1E-03	-0.6	1.2E-01	-1.6	2.3E-02
ENSMUST00000110109	phospholipase C, beta 4 [Source:MGI Symbol;Acc:MGI:107464]	Q91UZ1		2.0	1.8E-01	4.2	1.3E-01	4.5	8.5E-02	2.3	1.6E-01
ENSMUST00000111982	homeobox D3 [Source:MGI Symbol;Acc:MGI:96207]	Q3UZR4	P09027	5.9	3.3E-02	5.6	1.2E-02	0.4	7.9E-01	-0.7	6.2E-01
ENSMUST00000111983	homeobox D3 [Source:MGI Symbol;Acc:MGI:96207]	Q3UZR4	P09027	6.0	1.6E-03	-3.3	2.0E-02	1.0	1.1E-01	2.0	1.1E-01
ENSMUST00000111994	nuclear receptor coactivator 4 [Source:MGI Symbol;Acc:MGI:1350932]	Q5U4H9		-8.7	4.5E-05	7.8	8.8E-05	-0.7	6.0E-01	-0.7	2.7E-01
ENSMUST00000111996	nthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9) [Source:MGI Symbol;Acc:MGI:24	Q14BC2	P56384	-7.2	7.6E-04	-1.7	2.8E-01	2.0	5.3E-02	-0.3	8.5E-01
ENSMUST00000111997	transmembrane protein 233 [Source:MGI Symbol;Acc:MGI:3651514]	A0A0A0MQE1		6.2	9.5E-05	3.1	1.6E-02	0.6	5.3E-01	0.2	7.7E-01
ENSMUST00000112000	diphthamine biosynthesis 3 [Source:MGI Symbol;Acc:MGI:1922658]	D3Z1U2		-2.1	7.8E-03	4.7	5.3E-04	-2.3	4.4E-02	0.9	1.4E-01
ENSMUST00000112010	activating transcription factor 2 [Source:MGI Symbol;Acc:MGI:109349]	Q543G2	P16951	-6.9	1.5E-03	7.9	2.3E-04	-1.1	4.5E-01	0.5	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000110124	homer homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1347359]		Q99JP6	0.3	8.9E-01	1.3	4.1E-01	-3.2	7.1E-02	-4.2	4.7E-02
ENSMUST00000112022	cathelicidin antimicrobial peptide [Source:MGI Symbol;Acc:MGI:108443]			-9.7	4.2E-07	6.6	2.0E-04	-1.5	2.5E-01	-0.6	3.8E-01
ENSMUST00000112027	ke tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase [Source:MGI Symbol;Acc:MG		O35348	7.4	4.7E-05	5.7	8.2E-06	0.7	2.3E-01	0.1	8.1E-01
ENSMUST00000112028	ER lipid raft associated 1 [Source:MGI Symbol;Acc:MGI:2387613]			-5.2	4.8E-04	6.4	4.3E-04	-0.6	6.5E-01	-1.1	1.5E-01
ENSMUST00000112040	F-box and WD-40 domain protein 14 [Source:MGI Symbol;Acc:MGI:1354703]	Q3UPQ4		7.4	4.5E-05	7.1	1.8E-04	-0.7	6.0E-01	-0.7	3.3E-01
ENSMUST00000112047	cutC copper transporter homolog (E.coli) [Source:MGI Symbol;Acc:MGI:1913638]		Q9D8X1	-2.6	8.0E-03	3.7	9.8E-02	-0.6	7.7E-01	2.5	9.0E-02
ENSMUST00000112053	three prime repair exonuclease 1 [Source:MGI Symbol;Acc:MGI:1328317]		Q91XB0	-6.6	5.6E-04	-4.2	2.2E-03	-0.3	5.6E-01	-1.4	2.8E-01
ENSMUST00000110143	myocyte enhancer factor 2B [Source:MGI Symbol;Acc:MGI:104526]	Q80VR4		0.8	6.1E-01	2.6	4.1E-01	4.0	1.2E-01	2.2	3.5E-01
ENSMUST00000112059	shisa family member 5 [Source:MGI Symbol;Acc:MGI:1915044]		Q9D7I0	-9.2	6.8E-04	6.2	2.7E-04	-0.5	6.7E-01	-1.9	1.7E-02
ENSMUST00000110149	expressed sequence BB287469 [Source:MGI Symbol;Acc:MGI:3034635]	Q3UT53		3.8	1.3E-01	6.1	3.5E-02	-0.2	9.3E-01	-2.6	1.3E-01
ENSMUST00000112064	calcium channel, voltage-dependent, L type, alpha 1S subunit [Source:MGI Symbol;Acc:MGI:88294]	F8VQE0		8.2	2.2E-05	6.0	1.0E-03	-0.5	7.3E-01	-0.8	3.1E-01
ENSMUST00000110155	TatD DNase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916944]			-1.1	1.4E-01	-1.7	5.8E-02	-0.7	2.5E-01	0.0	9.6E-01
ENSMUST00000112090	dynein light chain LC8-type 1 [Source:MGI Symbol;Acc:MGI:1861457]		P63168	-7.1	2.3E-05	6.1	6.2E-06	-0.7	3.0E-01	-0.4	3.5E-01
ENSMUST00000112091	RAB9, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1890695]	Q0PD48	Q9R0M6	-4.5	1.3E-04	-2.3	1.9E-02	-0.6	2.5E-01	-1.8	6.6E-02
ENSMUST00000112095	polybromo 1 [Source:MGI Symbol;Acc:MGI:1923998]		Q8BSQ9	-3.0	7.4E-05	2.8	2.5E-01	0.4	8.6E-01	2.1	2.7E-01
ENSMUST00000110163	transmembrane protein 230 [Source:MGI Symbol;Acc:MGI:1917862]		Q8CIB6	2.7	3.7E-01	2.1	4.9E-01	-2.1	4.8E-01	-1.5	5.7E-01
ENSMUST00000112096	ring finger protein 10 [Source:MGI Symbol;Acc:MGI:1859162]		Q3UIW5	-9.1	3.1E-06	1.9	4.3E-02	0.1	8.4E-01	0.0	9.5E-01
ENSMUST00000112101	integrin alpha 6 [Source:MGI Symbol;Acc:MGI:96605]		Q61739	6.6	1.9E-03	-5.2	9.2E-04	-1.0	8.0E-02	-0.3	8.0E-01
ENSMUST00000110168	zinc fingers and homeoboxes 1 [Source:MGI Symbol;Acc:MGI:109271]		P70121	-0.8	6.8E-01	0.7	7.5E-01	1.0	5.8E-01	-0.5	8.2E-01
ENSMUST00000110172	prion protein dublet [Source:MGI Symbol;Acc:MGI:1346999]	Q544A3	Q9QUG3	6.8	4.5E-02	4.7	2.4E-01	0.5	9.0E-01	2.6	2.8E-01
ENSMUST00000112123	exosome component 1 [Source:MGI Symbol;Acc:MGI:1913833]		Q9DAA6	6.1	2.4E-02	6.5	1.6E-04	-0.6	6.0E-01	-0.5	3.8E-01
ENSMUST00000112129	Rho GTPase activating protein 6 [Source:MGI Symbol;Acc:MGI:1196332]	A2ALX7		6.3	3.6E-06	5.0	2.3E-02	-1.1	5.9E-01	-1.6	2.1E-01
ENSMUST00000110181	spermine oxidase [Source:MGI Symbol;Acc:MGI:2445356]	Q3TLR8		1.0	4.3E-01	0.9	5.3E-01	-0.6	6.5E-01	-0.5	7.0E-01
ENSMUST00000112132	pregnancy zone protein [Source:MGI Symbol;Acc:MGI:87854]		Q61838	6.4	5.9E-03	-6.4	8.3E-02	0.5	6.6E-01	-1.0	8.0E-01
ENSMUST00000110188	spermine oxidase [Source:MGI Symbol;Acc:MGI:2445356]		Q99K82	1.0	6.4E-01	3.1	2.3E-01	-0.4	8.4E-01	-2.5	2.6E-01
ENSMUST00000112137	male-specific lethal 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1341851]		Q9WVG9	-4.9	1.3E-04	2.9	2.1E-03	0.7	2.5E-01	-0.1	8.2E-01
ENSMUST00000112138	dynein cytoplasmic 1 intermediate chain 2 [Source:MGI Symbol;Acc:MGI:107750]	A2BFF7	O88487	-8.4	3.0E-05	4.4	1.8E-02	-3.2	1.0E-01	-1.3	2.9E-01
ENSMUST00000112139	dynein cytoplasmic 1 intermediate chain 2 [Source:MGI Symbol;Acc:MGI:107750]	A2BFF8		-5.3	3.3E-04	8.7	1.5E-05	-0.5	6.7E-01	-0.9	7.4E-02
ENSMUST00000112149	FERM and PDZ domain containing 4 [Source:MGI Symbol;Acc:MGI:3042378]		A2AFR3	6.1	1.4E-02	3.7	5.2E-02	-2.0	2.7E-01	2.3	7.0E-02
ENSMUST00000112151	RAD9-HUS1-RAD1 interacting nuclear orphan 1 [Source:MGI Symbol;Acc:MGI:1915315]	E9Q1D4		-4.3	1.7E-03	6.1	3.9E-04	-0.5	6.7E-01	-0.2	7.6E-01
ENSMUST00000110204	estrogen related receptor, beta [Source:MGI Symbol;Acc:MGI:1346832]	G5E8P8		2.5	4.7E-02	6.6	1.5E-04	-0.5	6.5E-01	-4.6	3.1E-04
ENSMUST00000112155	glutamine-rich 1 [Source:MGI Symbol;Acc:MGI:1916482]	G3X8R5		-6.7	6.5E-04	-2.5	1.0E-01	1.1	2.0E-01	-1.8	2.7E-01
ENSMUST00000110217	collagen, type XIV, alpha 1 [Source:MGI Symbol;Acc:MGI:1341272]	K3W4R4		4.2	1.3E-01	0.5	7.8E-01	-4.5	7.4E-02	-0.9	6.4E-01
ENSMUST00000112159	DDB1 and CUL4 associated factor 17 [Source:MGI Symbol;Acc:MGI:1923013]		Q3TUL7	4.9	3.8E-04	3.3	1.4E-03	1.4	4.3E-02	0.0	9.7E-01
ENSMUST00000112161	toll-like receptor 7 [Source:MGI Symbol;Acc:MGI:2176882]	Q548J0	P58681	-6.9	4.2E-03	4.6	2.4E-03	-1.9	1.5E-01	0.9	2.3E-01
ENSMUST00000110221	collagen, type XIV, alpha 1 [Source:MGI Symbol;Acc:MGI:1341272]	B7ZNH7		4.5	1.3E-01	3.1	2.9E-01	-1.7	5.6E-01	-0.3	8.8E-01
ENSMUST00000112162	predicted gene 4461 [Source:MGI Symbol;Acc:MGI:3782645]	K7N6V7		6.6	2.8E-04	4.4	1.0E-03	-2.3	4.0E-02	-0.4	5.7E-01
ENSMUST00000110237	ras responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:2443664]		Q3UH06	0.4	7.4E-01	3.6	2.4E-02	0.3	8.3E-01	-2.9	3.3E-02
ENSMUST00000112163	protein phosphatase 1, regulatory (inhibitor) subunit 12B [Source:MGI Symbol;Acc:MGI:1916417]		Q8BG95	5.3	3.6E-03	6.1	9.5E-05	1.0	3.0E-01	0.1	9.0E-01
ENSMUST00000112168	olfactory receptor 55 [Source:MGI Symbol;Acc:MGI:1333751]	K7N6Q1		7.8	3.6E-05	-2.3	1.1E-02	0.1	8.8E-01	-1.7	8.3E-02
ENSMUST00000112170	toll-like receptor 8 [Source:MGI Symbol;Acc:MGI:2176887]		P58682	-9.1	2.1E-06	7.8	1.7E-04	3.6	1.5E-02	-1.7	4.4E-02
ENSMUST00000112171	tetraspanin 9 [Source:MGI Symbol;Acc:MGI:1924558]		Q8BJU2	6.2	3.9E-04	-7.0	3.4E-05	-1.3	3.6E-03	-0.9	4.1E-01
ENSMUST00000110253	membrane-associated ring finger (C3HC4) 1 [Source:MGI Symbol;Acc:MGI:1920175]		Q6NZQ8	-3.3	4.2E-01	-4.8	1.9E-01	-3.3	1.5E-01	-1.8	7.0E-01
ENSMUST00000110255	membrane-associated ring finger (C3HC4) 1 [Source:MGI Symbol;Acc:MGI:1920175]		Q6NZQ8	-3.3	1.3E-01	-4.2	1.2E-01	-1.2	3.7E-01	-0.3	9.3E-01
ENSMUST00000110256	membrane-associated ring finger (C3HC4) 1 [Source:MGI Symbol;Acc:MGI:1920175]	D3YVY0		1.7	1.2E-01	-2.3	1.1E-01	-2.0	5.2E-02	2.1	1.5E-01
ENSMUST00000112172	thymosin, beta 4, X chromosome [Source:MGI Symbol;Acc:MGI:99510]	Q6ZWX2	P20065	-10.9	2.8E-08	8.2	4.6E-05	-0.7	6.0E-01	-0.7	2.6E-01
ENSMUST00000112173	tetraspanin 9 [Source:MGI Symbol;Acc:MGI:1924558]		Q8BJU2	4.4	1.2E-04	9.9	2.6E-03	2.6	2.9E-01	-0.5	6.4E-01
ENSMUST00000112175	thymosin, beta 4, X chromosome [Source:MGI Symbol;Acc:MGI:99510]		P20065	-4.9	6.2E-03	6.1	8.1E-03	-0.8	6.8E-01	0.7	5.3E-01
ENSMUST00000110262	FAST kinase domains 5 [Source:MGI Symbol;Acc:MGI:2139469]			-1.1	4.2E-01	2.1	2.4E-01	1.1	4.3E-01	-2.1	1.8E-01
ENSMUST00000112176	thymosin, beta 4, X chromosome [Source:MGI Symbol;Acc:MGI:99510]		P20065	-8.6	2.8E-04	7.0	8.6E-04	1.0	5.1E-01	0.9	2.9E-01
ENSMUST00000112184	Scm-like with four mbt domains 1 [Source:MGI Symbol;Acc:MGI:1859609]		Q9JMD1	5.0	5.0E-03	6.8	1.3E-04	-0.5	6.6E-01	-1.2	8.0E-02
ENSMUST00000110269	syntabulin (syntaxin-interacting) [Source:MGI Symbol;Acc:MGI:2442392]		Q8BHS8	4.5	4.0E-02	2.7	1.1E-01	-3.4	8.4E-02	-1.6	2.5E-01
ENSMUST00000112185	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]		Q9JLQ2	-4.7	8.7E-03	-5.7	9.0E-03	0.4	5.8E-01	-0.2	9.4E-01
ENSMUST00000112191	poly (ADP-ribose) polymerase family, member 11 [Source:MGI Symbol;Acc:MGI:2141505]		Q8CFF0	6.2	5.1E-03	-2.6	4.1E-02	0.8	2.0E-01	-0.6	6.1E-01
ENSMUST00000110286	early B cell factor 4 [Source:MGI Symbol;Acc:MGI:2385972]	B2RQX3	Q8K4J2	5.9	8.3E-02	6.2	8.0E-02	-0.9	8.0E-01	-1.2	5.7E-01
ENSMUST00000112192	trafficking protein particle complex 2 [Source:MGI Symbol;Acc:MGI:1913476]	A2AFP1		-4.4	2.7E-04	6.2	3.6E-04	-0.5	7.0E-01	-0.3	6.5E-01
ENSMUST00000112198	lysine (K)-specific demethylase 5B [Source:MGI Symbol;Acc:MGI:1922855]		Q80Y84	-3.9	1.5E-04	1.3	7.7E-02	0.7	2.2E-01	0.5	3.4E-01
ENSMUST00000110298	numb gene homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:107423]	F8WJ71		-2.9	2.8E-01	-1.4	7.4E-01	3.0	2.7E-01	1.5	7.0E-01
ENSMUST00000112201	golgi reassembly stacking protein 2 [Source:MGI Symbol;Acc:MGI:2135962]	A2ATI9		-3.5	6.3E-03	3.8	1.3E-03	0.5	5.2E-01	-0.1	9.3E-01
ENSMUST00000110301	chloride channel, voltage-sensitive 3 [Source:MGI Symbol;Acc:MGI:103555]		P51791	-0.5	7.9E-01	-2.4	3.0E-01	-2.5	9.0E-02	-0.6	8.1E-01
ENSMUST00000110305	low density lipoprotein-related protein 12 [Source:MGI Symbol;Acc:MGI:2443132]		Q8BUJ9	1.6	5.3E-01	3.5	2.9E-01	2.1	4.7E-01	0.3	9.0E-01
ENSMUST00000112207	protein kinase C, delta [Source:MGI Symbol;Acc:MGI:97598]	Q1MX43		-8.4	5.4E-04	1.4	7.4E-02	-0.2	7.3E-01	-0.2	7.8E-01
ENSMUST00000110315	solute carrier family 20, member 1 [Source:MGI Symbol;Acc:MGI:108392]		Q61609	-3.8	7.0E-02	-2.2	5.7E-01	5.0	2.5E-02	3.5	3.6E-01
ENSMUST00000110316	cetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7 [Source:MGI Symbol;Acc:MGI:		Q80VA0	-1.4	1.4E-01	-1.1	3.6E-01	-0.1	9.1E-01	-0.4	7.1E-01
ENSMUST00000112208	protein kinase C, delta [Source:MGI Symbol;Acc:MGI:97598]	Q53YN4	P28867	-3.7	2.7E-02	4.1	2.5E-03	0.1	9.3E-01	-1.4	7.1E-02
ENSMUST00000110320	zinc finger CCCH type containing 6 [Source:MGI Symbol;Acc:MGI:1926001]	A2AP88		0.8	1.5E-01	0.4	5.3E-01	-0.4	4.6E-01	0.0	9.8E-01
ENSMUST00000110322	F-box protein 8 [Source:MGI Symbol;Acc:MGI:1354696]	Q921R9		1.0	5.8E-01	-1.8	3.9E-01	-3.3	6.2E-02	-0.5	8.1E-01
ENSMUST00000110324	fibulin 7 [Source:MGI Symbol;Acc:MGI:1917620]		Q501P1	3.4	9.1E-02	6.6	7.0E-03	-0.4	8.4E-01	-3.6	1.8E-02
ENSMUST00000110325	transmembrane protein 87B [Source:MGI Symbol;Acc:MGI:1919727]		Q8BKU8	-1.6	3.8E-02	-2.1	4.3E-02	-0.2	7.7E-01	0.3	7.6E-01
ENSMUST00000110328	antizyme inhibitor 1 [Source:MGI Symbol;Acc:MGI:1859169]	D3YW58		-0.7	8.5E-01	-0.2	9.7E-01	0.2	9.5E-01	-0.3	9.4E-01
ENSMUST00000112210	protein kinase C, delta [Source:MGI Symbol;Acc:MGI:97598]	Q53YN4	P28867	-9.9	6.7E-07	-7.0	5.7E-04	1.3	4.3E-02	-2.2	2.3E-01
ENSMUST00000112219	transient receptor potential cation channel, subfamily V, member 4 [Source:MGI Symbol;Acc:MGI:1926945]	D3Z1H6		5.8	2.1E-02	5.2	3.3E-02	0.6	7.6E-01	-0.1	9.7E-01
ENSMUST00000112231	ectonucleoside triphosphate diphosphohydrolase 1 [Source:MGI Symbol;Acc:MGI:102805]	Q544U5	P55772	-3.2	3.4E-03	-2.5	3.4E-03	1.0	1.7E-02	-0.4	5.4E-01
ENSMUST00000112237	adiponectin receptor 1 [Source:MGI Symbol;Acc:MGI:1919924]	Q53YY4	Q91VH1	-7.6	3.7E-04	-2.7	3.2E-02	-1.4	6.8E-02	-1.9	1.7E-01
ENSMUST00000110340	cytochrome c oxidase assembly protein 16 [Source:MGI Symbol;Acc:MGI:1913522]	Q497I8	Q9CR63	-2.9	2.2E-01	-1.6	3.5E-01	-2.1	1.7E-01	-3.3	1.5E-01
ENSMUST00000110341	BCL2-like 11 (apoptosis facilitator) [Source:MGI Symbol;Acc:MGI:1197519]	Q542N5	O54918	-1.8	5.9E-02	-3.3	4.5E-02	1.0	2.1E-01	2.5	1.1E-01
ENSMUST00000110344	acyl-Coenzyme A oxidase-like [Source:MGI Symbol;Acc:MGI:1921371]		Q9DBS4	3.7	6.2E-02	4.8	2.6E-02	-1.0	6.2E-01	-2.0	1.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000112238	forkhead box N2 [Source:MGI Symbol;Acc:MGI:1347478]	E9Q7L6		-3.9	8.9E-05	6.9	6.1E-04	-0.7	6.4E-01	1.3	1.0E-01
ENSMUST00000110347	SPARC related modular calcium binding 1 [Source:MGI Symbol;Acc:MGI:1929878]			4.6	9.1E-02	5.7	7.1E-02	0.3	9.3E-01	-0.9	6.3E-01
ENSMUST00000112241	myosin IIIB [Source:MGI Symbol;Acc:MGI:2448580]	Q0P645		5.9	7.7E-03	-8.3	1.5E-04	-0.1	7.4E-01	-1.0	5.0E-01
ENSMUST00000112243	myosin IIIB [Source:MGI Symbol;Acc:MGI:2448580]		Q1EG27	7.0	1.7E-04	-8.6	9.7E-04	-0.5	3.7E-01	-1.1	6.0E-01
ENSMUST00000112247	motile sperm domain containing 2 [Source:MGI Symbol;Acc:MGI:1924013]		Q9CWP6	-7.2	4.0E-05	-4.8	1.6E-01	1.9	2.6E-01	-0.8	8.0E-01
ENSMUST00000112250	calcium channel, voltage-dependent, L type, alpha 1D subunit [Source:MGI Symbol;Acc:MGI:88293]		Q99246	2.6	3.2E-02	2.3	8.7E-02	-3.8	1.8E-02	-0.9	3.3E-01
ENSMUST00000110362	nonooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Source:MGI Symbol;Acc:M		P63101	-6.2	9.8E-02	-8.7	9.0E-02	-1.1	4.2E-01	1.4	8.0E-01
ENSMUST00000112251	ubiquitin protein ligase E3 component n-recognin 3 [Source:MGI Symbol;Acc:MGI:1861100]	F6QC57		-3.8	1.7E-04	6.4	2.2E-03	-1.2	5.0E-01	0.3	7.5E-01
ENSMUST00000112253	Von Willebrand factor homolog [Source:MGI Symbol;Acc:MGI:98941]	Q3TPE1		5.3	2.8E-02	7.1	1.6E-04	2.5	4.5E-02	-0.1	9.0E-01
ENSMUST00000110371	acyl-CoA synthetase long-chain family member 1 [Source:MGI Symbol;Acc:MGI:102797]	D3Z041		-3.1	5.5E-02	-1.8	2.9E-01	-0.3	7.8E-01	-1.6	3.9E-01
ENSMUST00000110372	acyl-CoA synthetase long-chain family member 1 [Source:MGI Symbol;Acc:MGI:102797]		P41216	1.6	5.0E-01	0.7	8.0E-01	-1.6	4.4E-01	-0.7	7.7E-01
ENSMUST00000112254	Von Willebrand factor homolog [Source:MGI Symbol;Acc:MGI:98941]	E9QPU1		7.0	6.6E-05	3.9	1.5E-03	0.0	9.8E-01	0.8	2.2E-01
ENSMUST00000112255	phosphatidylinositol glycan anchor biosynthesis, class A [Source:MGI Symbol;Acc:MGI:99461]	A2AIH5	Q64323	7.3	1.5E-02	-3.3	6.9E-03	0.2	6.4E-01	-1.0	3.9E-01
ENSMUST00000110376	cilia and flagella associated protein 97 [Source:MGI Symbol;Acc:MGI:1914006]	E9Q1K1		0.6	7.6E-01	4.2	1.1E-01	1.4	4.8E-01	-2.2	3.3E-01
ENSMUST00000112257	phosphatidylinositol glycan anchor biosynthesis, class A [Source:MGI Symbol;Acc:MGI:99461]	M0QWH5		2.3	5.5E-03	-6.9	3.8E-04	-0.7	1.2E-01	0.2	9.0E-01
ENSMUST00000112265	BMX non-receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:1101778]	B1AUL6		-6.3	2.6E-04	-4.9	3.8E-03	0.5	4.3E-01	0.9	4.9E-01
ENSMUST00000112268	selenoprotein K [Source:MGI Symbol;Acc:MGI:1931466]		Q9JLJ1	-4.7	1.4E-05	8.5	8.5E-03	0.5	8.5E-01	-0.9	5.6E-01
ENSMUST00000110386	inositol 1,4,5-triphosphate receptor interacting protein-like 1 [Source:MGI Symbol;Acc:MGI:1920588]		A2ASA8	-1.1	6.8E-01	-2.0	5.3E-01	-1.3	4.7E-01	-0.4	9.2E-01
ENSMUST00000110387	non-SMC condensin I complex, subunit H [Source:MGI Symbol;Acc:MGI:2444777]		Q8C156	-1.2	2.4E-01	0.3	8.1E-01	1.0	3.0E-01	-0.5	6.7E-01
ENSMUST00000112294	adaptor-related protein complex 1, sigma 2 subunit [Source:MGI Symbol;Acc:MGI:1889383]	Q8BW87		-4.2	5.4E-04	-3.9	7.5E-03	0.4	5.1E-01	-0.4	7.3E-01
ENSMUST00000110391	cytidine monophospho-N-acetylneuraminic acid hydroxylase [Source:MGI Symbol;Acc:MGI:103227]		Q61419	1.5	4.4E-02	3.2	4.4E-03	1.2	1.4E-01	-0.5	4.7E-01
ENSMUST00000112300	cytidine 5'-triphosphate synthase 2 [Source:MGI Symbol;Acc:MGI:1933185]	A2AEQ5		-6.9	1.8E-04	-7.6	2.3E-02	0.6	5.3E-01	2.4	4.1E-01
ENSMUST00000112303	cytidine 5'-triphosphate synthase 2 [Source:MGI Symbol;Acc:MGI:1933185]		P70303	-3.3	4.0E-03	5.7	6.2E-04	-1.7	1.8E-01	-0.7	3.2E-01
ENSMUST00000112308	leucine-rich PPR-motif containing [Source:MGI Symbol;Acc:MGI:1919666]		Q6PB66	3.6	5.3E-04	3.0	3.5E-02	-2.8	6.3E-02	0.3	7.1E-01
ENSMUST00000110407	solute carrier family 17 (sodium phosphate), member 4 [Source:MGI Symbol;Acc:MGI:2442850]		Q5NCM1	5.8	3.8E-02	7.6	1.5E-02	-0.7	8.2E-01	-2.5	1.4E-01
ENSMUST00000112311	IscU iron-sulfur cluster scaffold homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1913633]	D3Z7W0		2.0	1.2E-03	0.2	7.9E-01	1.1	1.2E-01	-2.2	2.6E-02
ENSMUST00000110410	ankyrin repeat domain 33B [Source:MGI Symbol;Acc:MGI:1917904]		Q3U0L2	-1.1	1.4E-01	-2.0	6.8E-02	-0.2	7.8E-01	0.7	4.9E-01
ENSMUST00000112312	IscU iron-sulfur cluster scaffold homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1913633]	D3Z7W0		-6.2	4.3E-03	5.5	2.7E-03	-0.4	7.7E-01	-0.4	6.1E-01
ENSMUST00000112314	taxilin gamma [Source:MGI Symbol;Acc:MGI:3590652]	A2AFJ4		4.7	5.0E-04	-5.0	6.7E-04	0.6	1.7E-01	-0.4	7.3E-01
ENSMUST00000110421	estrogen receptor 2 (beta) [Source:MGI Symbol;Acc:MGI:109392]			4.0	1.0E-01	2.5	3.8E-01	-0.9	7.2E-01	0.6	7.7E-01
ENSMUST00000112326	retinoblastoma binding protein 7 [Source:MGI Symbol;Acc:MGI:1194910]	A2AFI9		-2.7	3.3E-02	-5.4	3.8E-03	1.4	2.9E-02	-0.8	6.1E-01
ENSMUST00000112327	retinoblastoma binding protein 7 [Source:MGI Symbol;Acc:MGI:1194910]	A2AFJ1		-5.2	1.4E-03	3.6	1.4E-02	-1.4	2.4E-01	-0.7	4.6E-01
ENSMUST00000110433	butyrophilin, subfamily 2, member A2 [Source:MGI Symbol;Acc:MGI:3606486]		A4QPC6	4.5	9.0E-02	5.6	6.3E-02	-0.2	9.4E-01	-1.4	4.1E-01
ENSMUST00000112329	phosphodiesterase 6C, cGMP specific, cone, alpha prime [Source:MGI Symbol;Acc:MGI:105956]		Q91ZQ1	5.8	2.6E-02	4.8	1.1E-02	-0.5	7.5E-01	0.4	6.7E-01
ENSMUST00000110438	family with sequence similarity 134, member B [Source:MGI Symbol;Acc:MGI:1913520]		Q8VE91	-0.3	8.8E-01	-3.9	1.5E-01	-2.0	1.7E-01	1.7	5.2E-01
ENSMUST00000112330	sarcolemma associated protein [Source:MGI Symbol;Acc:MGI:1933549]	D3Z7V3		-7.0	2.9E-05	8.5	2.8E-03	-1.0	6.6E-01	2.0	7.3E-02
ENSMUST00000112331	sarcolemma associated protein [Source:MGI Symbol;Acc:MGI:1933549]	F8WIH0		-6.9	6.2E-03	7.5	1.4E-03	1.0	5.6E-01	-1.4	1.2E-01
ENSMUST00000112346	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1349403]	Q505A3	O54904	6.5	4.9E-04	7.0	2.9E-04	-0.5	7.3E-01	-0.7	3.4E-01
ENSMUST00000112349	metastasis associated 3 [Source:MGI Symbol;Acc:MGI:2151172]	E9Q794		-6.5	1.1E-04	5.9	3.1E-02	1.7	4.3E-01	1.4	3.3E-01
ENSMUST00000110455	histone cluster 1, H2bk [Source:MGI Symbol;Acc:MGI:2448399]	B2RVD5	Q8CGP1	1.5	2.4E-01	-0.4	7.7E-01	-2.1	9.1E-02	-0.1	9.3E-01
ENSMUST00000110456	RIKEN cDNA 0610011F06 gene [Source:MGI Symbol;Acc:MGI:1915597]	D3YZM4		3.2	1.4E-01	6.8	1.5E-02	0.6	8.0E-01	-3.0	7.3E-02
ENSMUST00000112352	metastasis associated 3 [Source:MGI Symbol;Acc:MGI:2151172]	Q3UII8		-2.1	3.2E-02	6.1	2.1E-02	-2.0	4.2E-01	-1.9	2.0E-01
ENSMUST00000112354	sodium channel, voltage-gated, type IX, alpha [Source:MGI Symbol;Acc:MGI:107636]	B1AYL0		6.4	1.5E-02	-3.2	2.1E-02	1.1	1.2E-01	-0.5	6.9E-01
ENSMUST00000110462	(constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	A2AQE4		-3.1	8.9E-02	-6.5	7.0E-03	-4.5	1.3E-03	-1.0	6.4E-01
ENSMUST00000112366	sodium channel, voltage-gated, type I, alpha [Source:MGI Symbol;Acc:MGI:98246]	A2APX8		8.4	1.1E-05	-2.0	1.2E-02	0.4	4.2E-01	-0.7	3.2E-01
ENSMUST00000110469	histone cluster 1, H2bq [Source:MGI Symbol;Acc:MGI:3702051]		P10853	1.3	3.9E-01	-0.5	7.9E-01	0.3	8.3E-01	2.1	2.6E-01
ENSMUST00000110480	SHC (Src homology 2 domain containing) family, member 4 [Source:MGI Symbol;Acc:MGI:2655364]	A2AUN0		2.8	2.0E-01	6.4	3.7E-02	1.0	7.1E-01	-2.6	1.3E-01
ENSMUST00000112370	major facilitator superfamily domain containing 4 [Source:MGI Symbol;Acc:MGI:2442786]		Q6PDC8	3.2	1.3E-02	7.7	2.2E-03	-3.3	1.5E-01	-1.8	1.3E-01
ENSMUST00000110485	zinc finger and SCAN domain containing 26 [Source:MGI Symbol;Acc:MGI:3531417]		Q5RJ54	-0.9	2.6E-01	-1.5	1.6E-01	-0.7	3.2E-01	0.0	9.7E-01
ENSMUST00000110491	glutathione peroxidase 5 [Source:MGI Symbol;Acc:MGI:104886]	F2Z3Y2		3.5	1.4E-01	6.2	2.9E-02	-0.2	9.4E-01	-2.8	8.6E-02
ENSMUST00000112377	phosphorylase kinase alpha 2 [Source:MGI Symbol;Acc:MGI:97577]		Q8BWJ3	-5.5	1.9E-04	4.2	2.9E-04	-0.7	3.3E-01	0.0	9.5E-01
ENSMUST00000110494	solute carrier family 12, member 1 [Source:MGI Symbol;Acc:MGI:103150]	A2AQ52		3.8	2.3E-01	4.1	2.5E-01	-0.1	9.8E-01	-0.4	8.6E-01
ENSMUST00000112384	ribosomal protein S24 [Source:MGI Symbol;Acc:MGI:98147]		P62849	-8.3	6.2E-06	5.0	2.6E-02	-1.4	5.1E-01	-0.3	8.1E-01
ENSMUST00000112386	RAB29, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2385107]	E9QLQ7		-2.5	5.4E-03	3.6	7.5E-02	-0.5	7.7E-01	2.6	5.0E-02
ENSMUST00000110498				0.4	7.4E-01	-4.6	2.5E-02	-3.1	1.1E-02	1.9	3.0E-01
ENSMUST00000110502	WD40 repeat domain 95 [Source:MGI Symbol;Acc:MGI:1923042]	E9PUB4		1.1	5.8E-01	0.6	7.8E-01	-0.4	8.0E-01	0.0	9.9E-01
ENSMUST00000112390	chromodomain helicase DNA binding protein 4 [Source:MGI Symbol;Acc:MGI:1344380]	E9QAS5		-3.2	1.6E-02	-5.6	1.2E-05	0.8	2.6E-02	-2.1	1.8E-02
ENSMUST00000110505	high mobility group box 1 [Source:MGI Symbol;Acc:MGI:96113]	Q58EV5	P63158	-1.4	3.5E-02	-1.1	2.0E-01	0.9	1.2E-01	0.6	4.5E-01
ENSMUST00000112392	chromodomain helicase DNA binding protein 4 [Source:MGI Symbol;Acc:MGI:1344380]	E9QAS4		-6.3	4.2E-03	5.6	3.8E-04	-1.8	1.4E-01	-1.2	1.0E-01
ENSMUST00000112393	peptidase M20 domain containing 1 [Source:MGI Symbol;Acc:MGI:2442939]		Q8C165	8.4	3.4E-06	4.5	3.5E-05	-5.3	1.3E-04	0.0	9.5E-01
ENSMUST00000112404	adhesion G protein-coupled receptor G2 [Source:MGI Symbol;Acc:MGI:2446854]		Q8CJ12	5.6	3.9E-03	-7.0	2.4E-03	1.1	7.9E-02	-0.1	9.5E-01
ENSMUST00000112417	inhibitor of growth family, member 4 [Source:MGI Symbol;Acc:MGI:107307]		Q8C0D7	-6.9	1.3E-04	6.4	3.6E-05	-1.5	1.4E-01	-0.2	6.7E-01
ENSMUST00000110520	tripartite motif-containing 9 [Source:MGI Symbol;Acc:MGI:2137354]		Q8C7M3	1.3	4.3E-01	3.2	1.1E-01	0.3	8.7E-01	-1.6	3.1E-01
ENSMUST00000112424	zinc finger protein 384 [Source:MGI Symbol;Acc:MGI:2443203]	E9QAR6		-6.0	7.6E-03	-3.2	1.1E-03	0.6	1.3E-01	-1.1	1.8E-01
ENSMUST00000110522	tripartite motif-containing 9 [Source:MGI Symbol;Acc:MGI:2137354]	E9QLH4		2.5	2.6E-01	6.2	7.3E-02	2.3	4.6E-01	-1.3	4.6E-01
ENSMUST00000112425	zinc finger protein 384 [Source:MGI Symbol;Acc:MGI:2443203]	E9QAR4		-5.4	2.3E-02	6.5	3.6E-03	-0.8	6.8E-01	-0.4	7.2E-01
ENSMUST00000112426	pseudouridine synthase 1 [Source:MGI Symbol;Acc:MGI:1929237]		Q9WU56	8.9	7.2E-05	-9.6	8.3E-04	0.7	2.3E-01	1.1	5.9E-01
ENSMUST00000112433	E1A binding protein p400 [Source:MGI Symbol;Acc:MGI:1276124]	D3Z6R8		4.2	4.4E-03	6.3	6.3E-04	-1.7	2.4E-01	0.2	7.1E-01
ENSMUST00000110533	AT rich interactive domain 4B (RBP1-like) [Source:MGI Symbol;Acc:MGI:2137512]	Z4YL44		4.8	4.5E-02	3.3	1.3E-01	-2.9	2.2E-01	-1.5	3.1E-01
ENSMUST00000112436	E1A binding protein p400 [Source:MGI Symbol;Acc:MGI:1276124]		Q8CHI8	-5.2	5.3E-03	-6.9	2.7E-03	-0.1	8.0E-01	0.0	9.9E-01
ENSMUST00000110536	AT rich interactive domain 4B (RBP1-like) [Source:MGI Symbol;Acc:MGI:2137512]		A2CG63	2.9	2.2E-01	6.6	5.2E-02	2.7	3.5E-01	-1.0	6.2E-01
ENSMUST00000112437	atlastin GTPase 2 [Source:MGI Symbol;Acc:MGI:1929492]	E9QND8		6.5	2.1E-03	6.6	1.3E-04	-0.6	6.2E-01	-1.0	1.1E-01
ENSMUST00000112452	otassium voltage-gated channel, subfamily H (eag-related), member 7 [Source:MGI Symbol;Acc:MGI:215956(	Q8C782		5.2	3.5E-03	5.8	7.7E-05	-1.5	1.2E-01	0.1	8.5E-01
ENSMUST00000112456	SH3-domain kinase binding protein 1 [Source:MGI Symbol;Acc:MGI:1889583]	Q3TA88	Q8R550	3.3	1.8E-05	-0.3	7.3E-01	1.2	5.8E-02	-0.1	9.1E-01
ENSMUST00000112459	interferon induced with helicase C domain 1 [Source:MGI Symbol;Acc:MGI:1918836]		Q8R5F7	-5.0	1.3E-02	-3.9	1.4E-03	-1.1	4.3E-02	-0.6	5.5E-01
ENSMUST00000112460	pantothenate kinase 1 [Source:MGI Symbol;Acc:MGI:1922985]	Q543J7	Q8K4K6	4.2	3.8E-04	-3.2	2.4E-05	0.6	1.7E-02	-0.2	6.4E-01
ENSMUST00000112471	MAP7 domain containing 2 [Source:MGI Symbol;Acc:MGI:1917474]		A2AG50	6.3	1.5E-03	4.4	3.5E-02	6.8	2.0E-03	-1.1	3.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000112477	Fc receptor, IgA, IgM, high affinity [Source:MGI Symbol;Acc:MGI:1927803]		Q2TB54	6.9	1.8E-02	-5.0	1.3E-02	-0.6	3.8E-01	0.8	6.6E-01
ENSMUST00000110567	mitogen-activated protein kinase kinase kinase kinase 5 [Source:MGI Symbol;Acc:MGI:1925503]		Q8BPM2	-2.1	3.8E-01	1.7	6.2E-01	3.7	1.9E-01	-0.2	9.5E-01
ENSMUST00000112484	protein tyrosine phosphatase, non-receptor type 6 [Source:MGI Symbol;Acc:MGI:96055]		P29351	-8.8	4.0E-06	-3.8	1.7E-02	0.1	9.1E-01	-0.2	8.7E-01
ENSMUST00000112493	ribosomal protein S6 kinase polypeptide 3 [Source:MGI Symbol;Acc:MGI:104557]	B1AXN9		-3.1	1.9E-03	5.2	2.7E-02	-0.6	7.8E-01	-0.1	9.5E-01
ENSMUST00000112494	TRAF family member-associated Nf-kappa B activator [Source:MGI Symbol;Acc:MGI:107676]	A2AR78		-1.9	3.3E-03	-5.1	5.6E-03	0.3	6.2E-01	0.6	7.0E-01
ENSMUST00000112495	TRAF family member-associated Nf-kappa B activator [Source:MGI Symbol;Acc:MGI:107676]	Q8C2D3		-7.9	6.2E-05	-2.7	2.6E-02	1.1	8.1E-02	0.3	8.1E-01
ENSMUST00000112498	cysteine rich transmembrane BMP regulator 1 (chordin like) [Source:MGI Symbol;Acc:MGI:1354756]		Q9JLL0	5.4	8.7E-06	-4.3	9.1E-03	0.3	6.6E-01	1.4	3.2E-01
ENSMUST00000112501	TRAF family member-associated Nf-kappa B activator [Source:MGI Symbol;Acc:MGI:107676]		P70347	-2.7	4.7E-04	6.1	3.0E-04	0.9	4.0E-01	-0.2	7.1E-01
ENSMUST00000112505	phosphoglycerate mutase family member 5 [Source:MGI Symbol;Acc:MGI:1919792]		Q8BX10	-4.6	1.2E-03	9.6	6.2E-05	4.4	8.7E-03	0.6	2.8E-01
ENSMUST00000110593	FERM domain containing 5 [Source:MGI Symbol;Acc:MGI:2442557]	B0R0D4		3.2	2.1E-01	5.1	6.5E-02	-0.5	8.4E-01	-2.4	1.9E-01
ENSMUST00000112517	integrin beta 6 [Source:MGI Symbol;Acc:MGI:96615]	B1AYG6		6.4	3.6E-04	6.5	4.4E-03	-0.6	7.4E-01	-1.8	1.1E-01
ENSMUST00000112519	checkpoint with forkhead and ring finger domains [Source:MGI Symbol;Acc:MGI:2444898]		Q810L3	-5.3	3.5E-05	8.4	2.2E-05	-0.6	6.1E-01	-0.5	3.3E-01
ENSMUST00000112523	calsyntenin 3 [Source:MGI Symbol;Acc:MGI:2178323]	D3Z601		4.6	8.7E-04	6.9	2.3E-04	-0.5	6.9E-01	-0.2	7.8E-01
ENSMUST00000112524	aminolevulinic acid synthase 1 [Source:MGI Symbol;Acc:MGI:87989]	Q3V0B2	Q8VC19	4.5	1.1E-02	2.6	8.0E-03	0.3	6.0E-01	0.2	7.7E-01
ENSMUST00000110608	ash2 (absent, small, or homeotic)-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1344416]	D3YYA0		0.9	6.1E-01	0.9	7.1E-01	-0.3	8.5E-01	-0.3	8.9E-01
ENSMUST00000112525	phospholipase A2 receptor 1 [Source:MGI Symbol;Acc:MGI:102468]	A0A0A0MQE3	Q62028	4.7	8.8E-04	4.6	8.4E-02	-0.6	8.0E-01	3.0	5.7E-02
ENSMUST00000112529	spermine synthase [Source:MGI Symbol;Acc:MGI:109490]		P97355	2.2	2.5E-02	3.8	4.5E-04	-0.1	8.3E-01	0.0	9.6E-01
ENSMUST00000110615	small EDRK-rich factor 2 [Source:MGI Symbol;Acc:MGI:1337041]	A2ARQ2		-2.4	3.5E-01	-3.8	2.7E-01	-0.8	6.4E-01	0.6	8.7E-01
ENSMUST00000112533	lymphocyte antigen 75 [Source:MGI Symbol;Acc:MGI:106662]	A2AW86		-2.6	4.1E-03	7.2	1.8E-04	0.9	4.6E-01	1.0	1.1E-01
ENSMUST00000110617	RIKEN cDNA 2410089E03 gene [Source:MGI Symbol;Acc:MGI:1920942]		Q8CE72	1.1	4.7E-02	1.5	3.8E-02	0.3	5.7E-01	-0.1	8.0E-01
ENSMUST00000110619	ribosomal protein L36A-like [Source:MGI Symbol;Acc:MGI:1913733]	Q5M9P1	P83882	2.4	6.0E-02	1.1	3.5E-01	-2.4	5.0E-02	-1.1	2.9E-01
ENSMUST00000110621	leucine rich repeat protein 1 [Source:MGI Symbol;Acc:MGI:1916956]	D3YY91		1.0	3.1E-01	2.4	6.5E-02	0.1	8.9E-01	-1.3	2.3E-01
ENSMUST00000110625	diphosphoinositol pentakisphosphate kinase 1 [Source:MGI Symbol;Acc:MGI:2443281]		A2ARP1	-3.3	1.1E-01	2.1	3.2E-01	2.2	2.0E-01	-3.2	1.4E-01
ENSMUST00000112534	phosphatidylinositol-specific phospholipase C, X domain containing 1 [Source:MGI Symbol;Acc:MGI:2685422	D3Z5Z4		7.5	1.4E-03	3.2	3.8E-01	2.9	2.9E-01	4.6	1.1E-01
ENSMUST00000112536	zinc finger protein 932 [Source:MGI Symbol;Acc:MGI:1916754]	D3Z5Z2		3.0	2.2E-02	-5.9	1.0E-03	-0.8	9.8E-02	0.5	7.1E-01
ENSMUST00000112538	zinc finger, RAN-binding domain containing 3 [Source:MGI Symbol;Acc:MGI:1918362]		Q6NZP1	6.2	6.8E-03	-5.7	8.2E-04	-0.8	8.4E-02	-0.6	6.3E-01
ENSMUST00000112551	spermidine/spermine N1-acetyl transferase 1 [Source:MGI Symbol;Acc:MGI:98233]	A2BES2		-10.0	1.4E-04	2.0	5.8E-01	7.2	1.7E-02	-1.4	6.8E-01
ENSMUST00000112558	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]		Q80XR2	-4.1	1.3E-03	2.3	3.2E-01	-0.7	7.3E-01	2.1	2.4E-01
ENSMUST00000112570	cyclin T2 [Source:MGI Symbol;Acc:MGI:1920199]	E9QAF8		-7.2	2.7E-05	-7.0	4.9E-04	0.3	4.6E-01	-0.8	6.0E-01
ENSMUST00000110639	microtubule-associated protein 1 A [Source:MGI Symbol;Acc:MGI:1306776]		Q9QYR6	6.2	7.2E-02	2.4	4.3E-01	-4.5	2.0E-01	-0.7	7.4E-01
ENSMUST00000110647	transformation related protein 53 binding protein 1 [Source:MGI Symbol;Acc:MGI:1351320]	A2AU89		-0.7	5.9E-01	1.9	3.7E-01	4.0	4.5E-02	1.3	4.0E-01
ENSMUST00000110648	transformation related protein 53 binding protein 1 [Source:MGI Symbol;Acc:MGI:1351320]	A2AU91		0.2	9.4E-01	-0.6	8.4E-01	-1.6	5.5E-01	-0.8	7.8E-01
ENSMUST00000110658	tubulin, gamma complex associated protein 4 [Source:MGI Symbol;Acc:MGI:1196293]	Q8BYN2		-1.6	4.6E-01	-3.7	1.7E-01	-2.2	1.4E-01	-0.1	9.7E-01
ENSMUST00000110661	zinc finger SCAN domains 29 [Source:MGI Symbol;Acc:MGI:2139317]	A2ARU5		0.1	9.0E-01	0.6	5.8E-01	0.9	3.3E-01	0.3	7.4E-01
ENSMUST00000112571	dpy-30 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1913560]		Q99LT0	-2.7	8.3E-04	2.5	6.3E-03	-3.5	3.4E-03	0.3	6.4E-01
ENSMUST00000112572	potassium channel tetramerisation domain containing 12b [Source:MGI Symbol;Acc:MGI:2444667]	Q8C7J6		7.1	3.0E-03	4.6	1.6E-02	-0.6	7.2E-01	1.1	2.9E-01
ENSMUST00000110672	karyopherin alpha 7 (importin alpha 8) [Source:MGI Symbol;Acc:MGI:2141165]		C0LLJ0	2.6	9.7E-02	6.6	1.1E-03	-0.4	7.8E-01	-4.4	2.0E-03
ENSMUST00000112576	programmed cell death 1 ligand 2 [Source:MGI Symbol;Acc:MGI:1930125]	Q3U304	Q9WUL5	4.9	3.9E-04	5.8	6.2E-02	-0.9	7.6E-01	0.1	9.5E-01
ENSMUST00000112577	plakophilin 4 [Source:MGI Symbol;Acc:MGI:109281]	A2AS47		3.6	3.3E-02	3.4	2.9E-02	0.8	5.1E-01	-0.2	8.3E-01
ENSMUST00000112581	Nanog homeobox [Source:MGI Symbol;Acc:MGI:1919200]		Q80Z64	6.8	1.4E-03	8.0	7.1E-05	0.1	9.4E-01	-0.7	2.5E-01
ENSMUST00000110677	SMAD specific E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1923038]	E9PYU8		4.8	6.2E-02	-0.7	7.9E-01	-5.1	5.6E-02	0.4	8.5E-01
ENSMUST00000112584	lysine (K)-specific demethylase 5C [Source:MGI Symbol;Acc:MGI:99781]		P41230	-2.9	3.2E-02	-0.6	6.3E-01	1.4	1.4E-01	-2.0	1.5E-01
ENSMUST00000112585	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 [Source:MGI Symbol;Acc:MGI:103298]	Q3U9G8	P51908	-7.0	1.2E-04	0.8	7.2E-01	3.1	1.0E-01	-2.2	2.9E-01
ENSMUST00000112588	lysine (K)-specific demethylase 5C [Source:MGI Symbol;Acc:MGI:99781]		P41230	-4.8	6.7E-03	6.9	3.2E-04	-0.7	6.1E-01	-0.4	5.3E-01
ENSMUST00000112598	ribosomal protein L15 [Source:MGI Symbol;Acc:MGI:1913730]	Q5M8Q0	Q9CZM2	-3.7	7.6E-03	-2.8	5.1E-03	0.2	7.2E-01	0.1	9.1E-01
ENSMUST00000112604	IQ motif and Sec7 domain 2 [Source:MGI Symbol;Acc:MGI:3528396]	D3Z5I6		7.1	8.9E-03	6.7	9.5E-05	-1.4	2.1E-01	0.5	4.0E-01
ENSMUST00000112606	dipeptidylpeptidase 10 [Source:MGI Symbol;Acc:MGI:2442409]	E9QN98		7.8	1.5E-07	-1.8	1.5E-01	1.7	4.4E-02	-0.3	8.2E-01
ENSMUST00000112616	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 [Source:MGI Symbol;Acc:MGI:		Q8C102	9.6	6.5E-05	-3.1	1.1E-01	1.0	3.5E-01	-1.5	4.9E-01
ENSMUST00000110700	congenital dyserythropoietic anemia, type I (human) [Source:MGI Symbol;Acc:MGI:1916218]	Z4YL55		-1.3	5.5E-01	-2.3	3.8E-01	-1.7	2.9E-01	-0.7	8.1E-01
ENSMUST00000112621	coiled-coil domain containing 93 [Source:MGI Symbol;Acc:MGI:1918079]	E9QAD4		-5.9	3.3E-05	4.6	2.9E-03	1.0	3.6E-01	-0.3	7.1E-01
ENSMUST00000110706	HAUS augmin-like complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1913546]		Q9CQS9	2.2	2.0E-01	2.5	3.3E-01	0.4	8.6E-01	0.1	9.3E-01
ENSMUST00000110708	signal recognition particle 54B [Source:MGI Symbol;Acc:MGI:3714357]		P14576	-0.4	4.1E-01	-1.3	5.6E-02	-0.6	1.8E-01	0.3	5.7E-01
ENSMUST00000112622	HECT, UBA and WWE domain containing 1 [Source:MGI Symbol;Acc:MGI:1926884]		Q7TMY8	-3.9	1.1E-02	-9.1	5.3E-03	0.8	2.5E-01	1.7	5.3E-01
ENSMUST00000112625	3-oxoacyl-ACP synthase, mitochondrial [Source:MGI Symbol;Acc:MGI:1918397]		Q9D404	-2.7	1.1E-02	-8.2	3.1E-05	-0.3	3.1E-01	-0.9	4.3E-01
ENSMUST00000112627	nuclear receptor subfamily 4, group A, member 2 [Source:MGI Symbol;Acc:MGI:1352456]	A2AQQ8		6.9	2.7E-05	5.2	2.3E-02	-0.7	7.5E-01	0.3	8.1E-01
ENSMUST00000110725	Rho GTPase activating protein 5 [Source:MGI Symbol;Acc:MGI:1332637]	E9PYT0		0.6	4.9E-01	1.1	2.7E-01	-0.4	6.4E-01	-0.9	3.2E-01
ENSMUST00000112641	STEAP family member 3 [Source:MGI Symbol;Acc:MGI:1915678]			4.8	2.1E-04	6.4	8.0E-04	-0.6	6.8E-01	-0.4	6.4E-01
ENSMUST00000112643	STEAP family member 3 [Source:MGI Symbol;Acc:MGI:1915678]	E9QN92		5.7	4.5E-03	-3.2	9.4E-04	0.4	3.5E-01	1.1	1.4E-01
ENSMUST00000112668	PHD finger protein 8 [Source:MGI Symbol;Acc:MGI:2444341]	A2ABV1		8.7	1.2E-05	8.0	3.0E-05	-0.5	6.4E-01	-1.1	5.4E-02
ENSMUST00000112671	RIKEN cDNA A830010M20 gene [Source:MGI Symbol;Acc:MGI:2445097]	G3X9V7		7.1	1.2E-03	5.2	1.1E-01	-0.6	8.5E-01	1.8	3.5E-01
ENSMUST00000112673	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta [Source:MGI Symbol;Acc:MGI:107930]		P70181	5.4	2.1E-02	4.5	2.9E-02	-0.9	6.2E-01	0.9	4.6E-01
ENSMUST00000112676	zinc finger and BTB domain containing 14 [Source:MGI Symbol;Acc:MGI:1195345]	Q544H8	Q08376	2.8	2.4E-02	7.3	1.2E-03	-0.8	6.5E-01	0.4	6.7E-01
ENSMUST00000112682	solute carrier family 25 (mitochondrial carrier), member 18 [Source:MGI Symbol;Acc:MGI:1919053]		Q9DB41	4.0	6.7E-04	6.8	1.8E-04	-0.5	6.8E-01	-0.5	4.4E-01
ENSMUST00000110748	neuronal cell adhesion molecule [Source:MGI Symbol;Acc:MGI:104750]		Q810U4	0.7	7.0E-01	3.4	7.0E-02	-1.6	3.5E-01	-4.4	1.9E-02
ENSMUST00000112686	cat eye syndrome chromosome region, candidate 2 [Source:MGI Symbol;Acc:MGI:1923799]	E9QA25		5.7	1.7E-05	7.1	1.7E-05	-2.3	4.3E-02	-0.6	2.4E-01
ENSMUST00000112701	cadherin 7, type 2 [Source:MGI Symbol;Acc:MGI:2442792]		Q8BM92	9.4	3.1E-05	3.5	3.3E-03	0.7	3.6E-01	0.7	2.8E-01
ENSMUST00000112705	N-myc (and STAT) interactor [Source:MGI Symbol;Acc:MGI:1928368]	Q3UJ82	O35309	-4.9	1.1E-03	5.7	1.1E-03	-0.4	7.4E-01	-0.4	5.7E-01
ENSMUST00000112706	serine (or cysteine) peptidase inhibitor, clade B, member 8 [Source:MGI Symbol;Acc:MGI:894657]		O08800	5.3	2.4E-03	9.2	1.0E-04	-0.4	8.2E-01	-1.8	2.4E-02
ENSMUST00000110774	MAX gene associated [Source:MGI Symbol;Acc:MGI:1352483]	E9QLG3		4.8	4.9E-02	7.8	2.7E-02	3.5	2.2E-01	0.5	8.1E-01
ENSMUST00000112707	leucine rich repeat containing 8 family, member B [Source:MGI Symbol;Acc:MGI:2141353]		Q5DU41	1.8	1.3E-02	-4.6	1.5E-02	0.8	2.4E-01	-0.5	7.8E-01
ENSMUST00000112725	apurinic/apyrimidinic endonuclease 2 [Source:MGI Symbol;Acc:MGI:1924872]		Q68G58	5.6	8.6E-07	7.4	4.1E-04	-0.6	6.7E-01	-1.3	1.2E-01
ENSMUST00000112751	B cell leukemia/lymphoma 2 [Source:MGI Symbol;Acc:MGI:88138]		P10417	2.1	1.9E-03	5.8	4.1E-02	-0.7	7.9E-01	-0.6	6.8E-01
ENSMUST00000112754	methyl-CpG binding domain protein 5 [Source:MGI Symbol;Acc:MGI:2138934]		B1AYB6	-5.2	6.5E-03	5.1	3.5E-02	-0.9	6.6E-01	0.1	9.2E-01
ENSMUST00000112755	predicted gene 8334 [Source:MGI Symbol;Acc:MGI:3648921]	F7CD45		10.0	9.0E-06	3.4	1.4E-02	-2.0	1.3E-01	0.1	8.7E-01
ENSMUST00000112771	dentin sialophosphoprotein [Source:MGI Symbol;Acc:MGI:109172]	E9Q9Z9		7.5	2.6E-05	2.9	2.2E-01	6.6	5.1E-03	-1.8	3.4E-01
ENSMUST00000112793	calcium channel, voltage-dependent, L type, alpha 1C subunit [Source:MGI Symbol;Acc:MGI:103013]	F7C376		5.4	1.1E-03	2.4	3.0E-01	-3.6	1.6E-01	0.4	8.1E-01
ENSMUST00000112797	RIKEN cDNA D830030K20 gene [Source:MGI Symbol;Acc:MGI:2443830]	E9PYQ5		5.7	5.2E-04	-4.6	8.6E-04	0.3	4.8E-01	-0.9	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000112822	Rho GTPase activating protein 15 [Source:MGI Symbol;Acc:MGI:1923367]		Q811M1	-6.5	1.3E-03	3.0	2.7E-02	-0.9	3.9E-01	0.1	8.8E-01
ENSMUST00000112830	ankyrin repeat domain 26 [Source:MGI Symbol;Acc:MGI:1917887]	D3Z482		3.8	2.6E-04	3.7	3.2E-02	0.4	7.8E-01	0.5	6.4E-01
ENSMUST00000110811	aryl-hydrocarbon receptor [Source:MGI Symbol;Acc:MGI:105043]	A0A0B4J1L1		0.0	9.8E-01	1.5	4.2E-01	1.1	4.0E-01	-0.3	8.4E-01
ENSMUST00000110813	glutamate rich 1 [Source:MGI Symbol;Acc:MGI:3588201]	E9PY43		0.7	1.7E-01	-0.2	8.0E-01	-0.1	7.8E-01	0.8	2.5E-01
ENSMUST00000110815	CD34 antigen [Source:MGI Symbol;Acc:MGI:88329]	Q543Y2	Q64314	-0.2	8.6E-01	-0.3	8.4E-01	0.5	6.8E-01	0.6	6.8E-01
ENSMUST00000110817	serine protease inhibitor, Kunitz type 1 [Source:MGI Symbol;Acc:MGI:1338033]		Q9R097	5.3	3.6E-02	8.6	1.3E-02	2.9	3.1E-01	-0.4	8.3E-01
ENSMUST00000112832	RAR-related orphan receptor beta [Source:MGI Symbol;Acc:MGI:1343464]		Q8R1B8	10.3	3.1E-03	2.3	2.1E-02	-3.3	4.7E-03	-0.7	3.4E-01
ENSMUST00000112835	angiomotin [Source:MGI Symbol;Acc:MGI:108440]	A0A067XG49		7.1	5.4E-05	4.3	2.4E-04	0.5	4.8E-01	-0.6	3.0E-01
ENSMUST00000110829	MAD1 mitotic arrest deficient 1-like 1 [Source:MGI Symbol;Acc:MGI:1341857]		Q9WTX8	5.6	9.1E-02	4.9	1.6E-01	-0.8	8.1E-01	-0.2	9.4E-01
ENSMUST00000112842	gypsy retrotransposon integrase 1 [Source:MGI Symbol;Acc:MGI:2182036]		Q8K259	3.1	1.4E-02	7.3	1.2E-05	-2.3	4.1E-02	-0.3	5.1E-01
ENSMUST00000112844	gypsy retrotransposon integrase 1 [Source:MGI Symbol;Acc:MGI:2182036]		Q8K259	-5.0	5.3E-03	-3.0	1.5E-02	-0.2	7.9E-01	-1.3	2.5E-01
ENSMUST00000112848	mitogen-activated protein kinase 10 [Source:MGI Symbol;Acc:MGI:1346863]	E9QN59		6.0	9.2E-04	4.2	7.0E-02	-1.2	5.6E-01	-0.4	7.9E-01
ENSMUST00000110837	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14 [Source:MGI Symbol;Acc:MGI:1919386]	A2AQV2		1.9	4.3E-01	-2.5	4.9E-01	-2.3	3.2E-01	2.1	5.4E-01
ENSMUST00000110838	¶1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2142'	G5E8Q5		-2.1	3.9E-01	-4.2	1.8E-01	-2.2	1.8E-01	-0.1	9.8E-01
ENSMUST00000110840	¶1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2142'		Q8BZJ7	0.5	5.2E-01	1.3	2.0E-01	0.0	9.8E-01	-0.8	4.0E-01
ENSMUST00000110842	kinetochore-localized astrin/SPAG5 binding [Source:MGI Symbol;Acc:MGI:1289298]	A3KGG8		3.7	3.6E-02	-1.3	4.3E-01	-4.5	1.0E-02	0.5	7.7E-01
ENSMUST00000112850	golgi autoantigen, golgin subfamily a, 1 [Source:MGI Symbol;Acc:MGI:1924149]		Q9CW79	4.8	1.7E-03	8.8	5.0E-04	-0.8	6.7E-01	0.4	6.5E-01
ENSMUST00000110851	zinc finger, AN1-type domain 2A [Source:MGI Symbol;Acc:MGI:2140729]		Q9JII7	-1.3	4.9E-01	-1.6	4.9E-01	0.4	8.0E-01	0.7	7.7E-01
ENSMUST00000112851	doublecortin [Source:MGI Symbol;Acc:MGI:1277171]	Q6PGI2		7.1	1.6E-04	6.1	3.0E-04	-0.2	8.8E-01	-0.7	3.4E-01
ENSMUST00000112852	Rho GTPase activating protein 24 [Source:MGI Symbol;Acc:MGI:1922647]		Q8C4V1	7.6	6.4E-04	-1.7	2.7E-02	1.1	1.9E-02	-0.2	7.8E-01
ENSMUST00000110856	lysophosphatidylglycerol acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2446186]	E9QL80		-1.4	3.7E-01	1.4	5.5E-01	2.2	1.9E-01	-0.6	7.7E-01
ENSMUST00000112865	p21 protein (Cdc42/Rac)-activated kinase 3 [Source:MGI Symbol;Acc:MGI:1339656]		Q61036	5.4	2.6E-03	-4.4	1.5E-04	-0.3	4.8E-01	0.0	9.9E-01
ENSMUST00000112866	chemokine (C-X-C motif) ligand 12 [Source:MGI Symbol;Acc:MGI:103556]		P40224	4.9	2.4E-03	7.1	1.0E-03	3.8	2.2E-02	0.5	5.7E-01
ENSMUST00000112872	WD repeat domain 38 [Source:MGI Symbol;Acc:MGI:1923896]		Q9D994	5.8	1.2E-03	-5.4	5.2E-02	1.3	1.6E-01	2.1	4.1E-01
ENSMUST00000112874	non-catalytic region of tyrosine kinase adaptor protein 1 [Source:MGI Symbol;Acc:MGI:109601]	Q8BH99		-7.0	1.7E-04	6.1	4.0E-03	1.3	4.2E-01	-0.8	4.0E-01
ENSMUST00000112877	nuclear receptor subfamily 6, group A, member 1 [Source:MGI Symbol;Acc:MGI:1352459]		Q64249	7.7	1.1E-03	7.6	1.6E-04	-0.7	6.1E-01	-0.8	2.5E-01
ENSMUST00000110871	mcf.2 transforming sequence-like [Source:MGI Symbol;Acc:MGI:103263]	D3YUF4		4.0	8.8E-02	6.1	2.7E-02	-0.3	8.9E-01	-2.4	1.1E-01
ENSMUST00000110873	mcf.2 transforming sequence-like [Source:MGI Symbol;Acc:MGI:103263]	D3YUF3		-1.9	2.0E-01	2.3	2.2E-01	2.0	2.1E-01	-2.2	1.7E-01
ENSMUST00000112878	chordin-like 1 [Source:MGI Symbol;Acc:MGI:1933172]		Q920C1	5.8	1.2E-03	3.8	3.3E-03	-2.8	3.1E-02	-1.7	4.2E-02
ENSMUST00000112883	nuclear receptor subfamily 5, group A, member 1 [Source:MGI Symbol;Acc:MGI:1346833]		P33242	5.4	3.1E-02	4.9	2.1E-02	-0.5	8.1E-01	0.5	6.3E-01
ENSMUST00000112885	DAZ interacting protein 1-like [Source:MGI Symbol;Acc:MGI:1919757]	B2RR42	Q499E4	8.1	1.0E-05	-6.2	1.4E-03	0.5	2.7E-01	1.3	3.7E-01
ENSMUST00000110883	Sad1 and UNC84 domain containing 1 [Source:MGI Symbol;Acc:MGI:1924303]		Q9D666	-3.6	2.9E-01	-2.0	4.9E-01	-1.7	4.0E-01	-3.4	3.5E-01
ENSMUST00000110884	Sad1 and UNC84 domain containing 1 [Source:MGI Symbol;Acc:MGI:1924303]		Q9D666	-1.2	4.7E-01	-3.0	3.2E-01	0.2	9.0E-01	2.0	4.9E-01
ENSMUST00000110889	protein kinase, cAMP dependent regulatory, type I beta [Source:MGI Symbol;Acc:MGI:97759]	D3Z0V6		2.4	2.0E-01	6.8	6.6E-03	1.1	5.9E-01	-3.4	3.2E-02
ENSMUST00000110893	TatD DNase domain containing 3 [Source:MGI Symbol;Acc:MGI:1916222]	E9QL22		2.6	2.7E-01	-0.3	8.9E-01	-2.6	2.3E-01	0.3	9.0E-01
ENSMUST00000112886	DAZ interacting protein 1-like [Source:MGI Symbol;Acc:MGI:1919757]		Q499E4	6.7	1.9E-02	-11.4	3.9E-03	-1.5	1.6E-01	1.0	7.7E-01
ENSMUST00000112888	transmembrane protein 164 [Source:MGI Symbol;Acc:MGI:2148020]	A2AHA2		-5.4	1.2E-02	5.8	2.5E-03	-0.6	7.0E-01	-1.5	1.2E-01
ENSMUST00000112890	deoxythymidylate kinase [Source:MGI Symbol;Acc:MGI:108396]	Q6GRA7	P97930	1.7	3.3E-02	4.4	2.8E-02	-1.5	4.1E-01	-1.0	4.2E-01
ENSMUST00000110904	Rho guanine nucleotide exchange factor (GEF7) [Source:MGI Symbol;Acc:MGI:1860493]	D3Z0V2		3.1	1.2E-01	-0.6	8.5E-01	0.2	9.4E-01	3.9	2.1E-01
ENSMUST00000112896	transmembrane protein 164 [Source:MGI Symbol;Acc:MGI:2148020]		Q6PHN7	-5.4	1.5E-02	-2.3	1.5E-01	0.5	6.1E-01	-0.4	8.1E-01
ENSMUST00000110906	Meis homeobox 2 [Source:MGI Symbol;Acc:MGI:108564]	B1AWK4		6.7	5.1E-02	5.5	1.3E-01	-0.6	8.7E-01	0.6	7.7E-01
ENSMUST00000112898	mitochondrial ribosomal protein S18C [Source:MGI Symbol;Acc:MGI:1915985]	D3Z3D3		-3.7	2.0E-02	4.7	8.8E-04	0.6	5.2E-01	0.1	9.2E-01
ENSMUST00000110918	cDNA sequence BC052040 [Source:MGI Symbol;Acc:MGI:3026886]		Q3U4G0	-1.8	4.1E-01	2.1	4.4E-01	1.9	4.2E-01	-2.0	3.8E-01
ENSMUST00000110920	potassium channel, subfamily K, member 2 [Source:MGI Symbol;Acc:MGI:109366]		P97438	2.7	6.8E-02	4.5	7.2E-03	-0.6	6.9E-01	-2.4	4.5E-02
ENSMUST00000112900	zinc finger, AN1-type domain 4 [Source:MGI Symbol;Acc:MGI:1914742]	K3W4R9		-8.2	1.1E-04	-2.9	1.7E-03	-1.0	3.8E-02	0.1	9.2E-01
ENSMUST00000112901	mitochondrial ribosomal protein S18C [Source:MGI Symbol;Acc:MGI:1915985]	Q8BTZ9		5.7	5.7E-03	7.1	8.6E-05	-0.6	6.3E-01	-0.1	8.5E-01
ENSMUST00000112902	NIMA (never in mitosis gene a)-related expressed kinase 6 [Source:MGI Symbol;Acc:MGI:1891638]	A2ATN9		-2.9	8.0E-04	2.8	2.8E-01	0.4	8.6E-01	2.4	2.5E-01
ENSMUST00000110943	G patch domain containing 2 [Source:MGI Symbol;Acc:MGI:1915019]		Q7TQC7	-1.5	5.5E-01	4.7	7.4E-02	0.3	9.0E-01	-5.9	2.5E-02
ENSMUST00000112904	acyl-CoA synthetase long-chain family member 4 [Source:MGI Symbol;Acc:MGI:1354713]	Q91YN3	Q9QUJ7	-4.9	3.6E-03	1.0	1.6E-01	-1.5	2.3E-02	0.4	5.2E-01
ENSMUST00000110949	Rho GTPase activating protein 11A [Source:MGI Symbol;Acc:MGI:2444300]		Q80Y19	-0.7	6.3E-01	0.0	1.0E+00	1.7	3.2E-01	1.0	5.9E-01
ENSMUST00000112905	THAP domain containing 4 [Source:MGI Symbol;Acc:MGI:1914276]		Q6P3Z3	-6.5	2.2E-04	-7.4	9.3E-05	0.0	9.7E-01	-0.2	8.9E-01
ENSMUST00000112910	placenta-specific 8 [Source:MGI Symbol;Acc:MGI:2445289]		Q9JI48	2.5	1.1E-02	-4.0	5.5E-03	-1.6	1.8E-02	-2.1	1.3E-01
ENSMUST00000112915	predicted gene 11110 [Source:MGI Symbol;Acc:MGI:3779362]	Q3U4K9		5.3	3.0E-04	6.2	3.6E-04	-0.5	7.0E-01	-0.3	6.0E-01
ENSMUST00000112920	RAB GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2385139]	B2RRC5	A2AWA9	-9.6	8.4E-05	5.2	1.4E-02	-1.2	4.8E-01	-0.6	6.3E-01
ENSMUST00000110960	zinc finger and SCAN domain containing 21 [Source:MGI Symbol;Acc:MGI:99182]		Q07231	1.0	5.5E-01	-2.7	2.5E-01	-2.3	1.4E-01	1.4	5.3E-01
ENSMUST00000112931	collagen, type IV, alpha 5 [Source:MGI Symbol;Acc:MGI:88456]	Q63ZW6		7.2	6.3E-03	6.5	6.1E-04	-0.8	5.5E-01	0.1	8.5E-01
ENSMUST00000110963	zinc finger with KRAB and SCAN domains 1 [Source:MGI Symbol;Acc:MGI:1921820]		Q8BGS3	0.3	8.4E-01	-1.3	6.5E-01	1.8	3.2E-01	3.4	2.0E-01
ENSMUST00000112932	zinc finger and BTB domain containing 6 [Source:MGI Symbol;Acc:MGI:2442998]		Q8K088	5.1	1.8E-02	7.6	1.0E-03	-1.4	4.5E-01	1.6	1.0E-01
ENSMUST00000112934	ring finger and CCCH-type zinc finger domains 2 [Source:MGI Symbol;Acc:MGI:2442789]	A2AVP4		-4.1	8.4E-03	7.4	3.5E-04	-0.2	8.9E-01	0.1	9.3E-01
ENSMUST00000112939	heterogeneous nuclear ribonucleoprotein D [Source:MGI Symbol;Acc:MGI:101947]	G3X9W0		-7.8	3.1E-04	8.3	4.2E-05	-0.8	5.5E-01	0.1	8.4E-01
ENSMUST00000112946	transmembrane protein 40 [Source:MGI Symbol;Acc:MGI:2137870]	E9QN39		-2.5	2.4E-03	4.5	1.1E-04	-0.8	2.8E-01	0.0	9.3E-01
ENSMUST00000112949	v-raf-leukemia viral oncogene 1 [Source:MGI Symbol;Acc:MGI:97847]		Q99N57	-4.3	5.3E-04	5.4	3.9E-03	0.0	9.8E-01	-0.2	8.6E-01
ENSMUST00000112959	PR domain containing 8 [Source:MGI Symbol;Acc:MGI:1924880]	B2RU90		9.2	3.3E-06	-4.7	1.4E-05	-0.4	1.6E-01	-1.6	2.5E-02
ENSMUST00000112961	LIM homeobox protein 6 [Source:MGI Symbol;Acc:MGI:1306803]		Q9R1R0	8.7	7.6E-06	-4.6	2.0E-04	-1.1	1.7E-02	-0.8	3.5E-01
ENSMUST00000112968	progestin and adipoQ receptor family member III [Source:MGI Symbol;Acc:MGI:2679683]	D3Z181		7.9	1.7E-05	7.8	1.2E-02	-0.8	7.9E-01	-2.3	1.4E-01
ENSMUST00000110985	TSC22 domain family, member 4 [Source:MGI Symbol;Acc:MGI:1926079]	D3YZZ4		-1.6	1.2E-01	-0.4	7.1E-01	0.4	5.7E-01	-0.7	5.3E-01
ENSMUST00000112971	autophagy related 4A, cysteine peptidase [Source:MGI Symbol;Acc:MGI:2147903]	Q5EBK1	Q8C9S8	-3.2	2.3E-03	2.3	1.2E-02	-0.3	6.5E-01	-0.1	8.5E-01
ENSMUST00000110989				0.7	2.8E-01	3.1	7.2E-03	1.4	1.1E-01	-0.9	1.8E-01
ENSMUST00000112974	BMP2 inducible kinase [Source:MGI Symbol;Acc:MGI:2155456]		Q91Z96	-2.7	1.6E-02	-1.5	9.5E-02	0.7	1.9E-01	-0.2	7.8E-01
ENSMUST00000112978	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 [Source:MGI Symbol;Acc:MGI:1858898]	A2AG83		-3.5	2.6E-03	6.8	3.4E-04	-0.6	6.6E-01	-1.4	7.4E-02
ENSMUST00000110993	transforming growth factor, beta receptor III-like [Source:MGI Symbol;Acc:MGI:3833469]	D3YZZ2		1.7	2.4E-01	2.9	1.3E-01	0.4	8.3E-01	-0.9	5.0E-01
ENSMUST00000110994	mitogen-activated protein kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346871]		Q8CE90	-1.8	2.0E-01	-2.9	1.2E-01	-0.9	4.0E-01	0.2	9.2E-01
ENSMUST00000112979	catsper channel auxiliary subunit delta [Source:MGI Symbol;Acc:MGI:2147030]		E9Q9F6	4.6	3.0E-04	-1.5	2.5E-01	0.5	5.5E-01	-3.7	4.2E-02
ENSMUST00000112983	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]		Q3UHC7	-2.8	3.5E-03	-3.6	8.0E-02	1.4	2.3E-01	0.6	7.7E-01
ENSMUST00000112984	membrane-spanning 4-domains, subfamily A, member 3 [Source:MGI Symbol;Acc:MGI:2158468]	Q53ZU3	Q920C4	-3.4	3.2E-02	6.0	2.7E-02	-0.6	8.1E-01	-1.4	3.3E-01
ENSMUST00000112986	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]		Q3UHC7	5.5	3.2E-03	-1.8	7.6E-02	1.2	4.8E-02	0.2	8.3E-01
ENSMUST00000112998	ankyrin repeat and MYND domain containing 1 [Source:MGI Symbol;Acc:MGI:3045261]	E9PUG3		6.9	8.0E-05	5.3	3.0E-02	-0.5	8.3E-01	0.9	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000113001	glycoprotein galactosyltransferase alpha 1, 3 [Source:MGI Symbol;Acc:MGI:95704]	Q8C2H7		5.8	9.3E-03	6.8	2.5E-02	-1.3	6.4E-01	-0.8	6.5E-01
ENSMUST00000113005	CCR4-NOT transcription complex, subunit 6-like [Source:MGI Symbol;Acc:MGI:2443154]		Q8VEG6	-6.6	1.6E-05	-7.3	1.5E-04	0.1	7.3E-01	-0.8	5.8E-01
ENSMUST00000113007	RNA binding motif protein 41 [Source:MGI Symbol;Acc:MGI:2444923]		Q8JZV4	6.9	4.3E-03	-8.2	1.4E-04	0.9	2.7E-02	0.6	6.9E-01
ENSMUST00000113011	RNA binding motif protein 41 [Source:MGI Symbol;Acc:MGI:2444923]	A2AG09		-5.3	1.2E-02	-8.5	6.8E-04	0.6	2.1E-01	-0.6	7.7E-01
ENSMUST00000111035	processing of precursor 7, ribonuclease P family, (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1921347]		Q9DCH2	0.9	3.0E-01	2.5	4.0E-02	0.8	4.1E-01	-0.8	3.9E-01
ENSMUST00000111037	leucine-rich repeat-containing G protein-coupled receptor 4 [Source:MGI Symbol;Acc:MGI:1891468]		A2ARI4	2.0	3.9E-01	0.7	7.9E-01	-1.4	5.2E-01	-0.1	9.6E-01
ENSMUST00000113022	TatD DNase domain containing 2 [Source:MGI Symbol;Acc:MGI:3576210]	B7ZNL9		-2.5	3.9E-03	6.3	1.2E-03	-0.6	7.0E-01	-0.7	3.7E-01
ENSMUST00000113028	RIKEN cDNA 1190002N15 gene [Source:MGI Symbol;Acc:MGI:1916111]		Q3USZ8	-1.4	3.2E-02	3.1	2.1E-01	-0.7	7.5E-01	2.0	2.4E-01
ENSMUST00000113033	centriolin [Source:MGI Symbol;Acc:MGI:1889576]	A2AS42		7.4	2.4E-05	5.6	2.1E-02	-0.8	7.3E-01	1.9	1.3E-01
ENSMUST00000113052	Nik related kinase [Source:MGI Symbol;Acc:MGI:1351326]	B1B0C9		9.2	5.7E-05	5.1	7.8E-04	-2.3	6.4E-02	-0.5	4.8E-01
ENSMUST00000111055	Eph receptor B4 [Source:MGI Symbol;Acc:MGI:104757]	Q8C8K1		4.3	4.9E-02	-1.5	5.6E-01	-3.4	1.2E-01	2.3	3.1E-01
ENSMUST00000113054	shroom family member 3 [Source:MGI Symbol;Acc:MGI:1351655]			8.6	1.2E-02	-4.2	5.7E-02	1.1	2.6E-01	-0.3	8.9E-01
ENSMUST00000111059	cornichon homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925828]	D3YZJ3		1.8	3.2E-01	2.7	2.4E-01	-0.1	9.5E-01	-1.0	5.4E-01
ENSMUST00000113055	shroom family member 3 [Source:MGI Symbol;Acc:MGI:1351655]	E9QMY5		9.5	2.0E-05	5.8	9.1E-03	-0.4	8.5E-01	-1.0	3.7E-01
ENSMUST00000113066	extraembryonic, spermatogenesis, homeobox 1 [Source:MGI Symbol;Acc:MGI:1096388]	A2AG22		5.8	1.2E-02	6.2	1.1E-03	-0.6	6.6E-01	0.4	5.9E-01
ENSMUST00000113078	F-box and WD-40 domain protein 2 [Source:MGI Symbol;Acc:MGI:1353435]	Q9QUH1		-7.0	2.3E-05	5.0	1.0E-02	-3.2	9.2E-02	-0.3	7.7E-01
ENSMUST00000111068	epoxide hydrolase 1, microsomal [Source:MGI Symbol;Acc:MGI:95405]	E9PWK1		1.2	5.4E-01	0.6	7.1E-01	-3.5	4.7E-02	-2.9	1.1E-01
ENSMUST00000111070	patatin-like phospholipase domain containing 6 [Source:MGI Symbol;Acc:MGI:1354723]		Q3TRM4	0.3	8.7E-01	2.9	2.2E-01	1.3	5.3E-01	-1.3	4.3E-01
ENSMUST00000113093	chemokine (C-X-C motif) ligand 9 [Source:MGI Symbol;Acc:MGI:1352449]		P18340	3.9	3.2E-05	6.9	4.7E-04	0.1	9.3E-01	0.7	2.7E-01
ENSMUST00000113094	IQ motif containing with AAA domain [Source:MGI Symbol;Acc:MGI:1922168]	E9QMY8		6.9	4.8E-04	-3.5	1.0E-03	0.3	4.2E-01	0.2	8.2E-01
ENSMUST00000113102	N-acylethanolamine acid amidase [Source:MGI Symbol;Acc:MGI:1914361]		Q9D7V9	-2.0	2.7E-02	8.1	4.8E-06	-1.0	2.7E-01	-0.8	9.4E-02
ENSMUST00000113110	5, 10-methenyltetrahydrofolate synthetase-like [Source:MGI Symbol;Acc:MGI:3780550]	L7N466		-8.1	2.1E-05	6.8	7.0E-05	-2.3	7.9E-02	0.0	9.4E-01
ENSMUST00000113111	GTPase activating protein and VPS9 domains 1 [Source:MGI Symbol;Acc:MGI:1913941]	F7ADQ2		-1.6	2.7E-02	-4.4	1.3E-03	-0.3	5.2E-01	-0.4	6.7E-01
ENSMUST00000113112	nerve growth factor receptor (TNFRSF16) associated protein 1 [Source:MGI Symbol;Acc:MGI:1338016]		Q9WTZ9	-4.6	2.8E-04	-1.1	7.1E-01	-3.6	1.5E-01	4.8	8.6E-02
ENSMUST00000113117	bromodomain and PHD finger containing, 1 [Source:MGI Symbol;Acc:MGI:1926033]	Q80XK2		-2.4	2.7E-02	-1.1	8.1E-02	-0.4	3.4E-01	-1.3	5.4E-02
ENSMUST00000111103	collagen, type XXVI, alpha 1 [Source:MGI Symbol;Acc:MGI:2155345]		Q91VF6	4.0	8.3E-02	1.6	5.8E-01	-0.3	9.2E-01	2.2	3.4E-01
ENSMUST00000113121	bromodomain and PHD finger containing, 1 [Source:MGI Symbol;Acc:MGI:1926033]	E9PXP1		-4.8	3.1E-03	-1.0	6.0E-01	1.9	1.5E-01	-0.6	7.3E-01
ENSMUST00000113123	mitogen-activated protein kinase associated protein 1 [Source:MGI Symbol;Acc:MGI:2444554]		Q8BKH7	-5.0	1.8E-04	-7.1	8.1E-04	1.1	4.4E-02	0.3	8.3E-01
ENSMUST00000113127	GTPase activating protein (SH3 domain) binding protein 2 [Source:MGI Symbol;Acc:MGI:2442040]	Q542W3	P97379	-6.3	9.6E-06	4.3	2.9E-03	-1.4	2.0E-01	-0.1	9.1E-01
ENSMUST00000111117	CDC42 binding protein kinase alpha [Source:MGI Symbol;Acc:MGI:2441841]	E9PVY0		3.8	1.5E-01	2.2	4.2E-01	-1.3	6.4E-01	0.3	8.8E-01
ENSMUST00000111118	t-complex 11 like 1 [Source:MGI Symbol;Acc:MGI:2444263]		Q8BTG3	1.1	8.1E-02	1.6	8.0E-02	0.7	2.7E-01	0.3	7.1E-01
ENSMUST00000113134	UDP glucuronosyltransferase 1 family, polypeptide A6A [Source:MGI Symbol;Acc:MGI:2137698]		Q64435	-4.6	2.4E-04	0.8	7.4E-01	-2.6	2.0E-01	3.2	1.5E-01
ENSMUST00000111122	pumilio RNA-binding family member 2 [Source:MGI Symbol;Acc:MGI:1931751]	Q3UR91		-6.4	1.9E-01	-3.4	3.8E-01	-1.3	5.8E-01	-4.3	4.1E-01
ENSMUST00000113143	cyclin-dependent kinase-like 2 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1858227]		Q9QUK0	6.0	3.1E-02	4.7	1.1E-03	1.0	2.8E-01	0.3	7.2E-01
ENSMUST00000113146	myotubularin related protein 14 [Source:MGI Symbol;Acc:MGI:1916075]		Q8VEL2	-7.1	1.1E-05	-3.9	9.9E-02	0.2	8.3E-01	-0.1	9.8E-01
ENSMUST00000113155	SET domain containing 5 [Source:MGI Symbol;Acc:MGI:1920145]		Q5XJV7	-4.5	2.6E-03	4.3	1.0E-03	-0.1	9.1E-01	-0.8	2.6E-01
ENSMUST00000113183	predicted gene 15023 [Source:MGI Symbol;Acc:MGI:3805552]	L7MUB4		6.3	2.4E-02	7.8	2.5E-04	-1.0	4.9E-01	-1.2	1.2E-01
ENSMUST00000111136	F-box protein 3 [Source:MGI Symbol;Acc:MGI:1929084]	A2BHN6		-0.6	8.3E-01	1.2	6.1E-01	-2.0	3.2E-01	-3.8	1.7E-01
ENSMUST00000113186	autophagy related 16-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1924290]	Q3TDQ5	Q8C0J2	-3.5	3.3E-03	6.4	1.5E-02	-0.8	7.2E-01	-0.9	5.1E-01
ENSMUST00000111139	LIM domain only 2 [Source:MGI Symbol;Acc:MGI:102811]	A2BHP1		-2.3	2.2E-01	3.7	1.0E-01	3.5	9.9E-02	-2.6	1.6E-01
ENSMUST00000113200	leucine rich repeat and sterile alpha motif containing 1 [Source:MGI Symbol;Acc:MGI:2684789]		Q80ZI6	-6.1	1.4E-02	-2.5	1.7E-01	0.3	7.6E-01	-1.9	3.6E-01
ENSMUST00000111143	LIM domain only 2 [Source:MGI Symbol;Acc:MGI:102811]	A2BHP5		-1.1	5.3E-01	-3.5	7.6E-02	-3.1	2.5E-02	-0.7	7.2E-01
ENSMUST00000111145	deltex 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1921448]		Q8R3P2	0.4	8.0E-01	0.5	8.1E-01	1.8	3.1E-01	1.7	3.9E-01
ENSMUST00000113202	heterogeneous nuclear ribonucleoprotein H2 [Source:MGI Symbol;Acc:MGI:1201779]		P70333	2.2	2.0E-03	-7.1	4.6E-04	0.9	1.2E-01	1.9	1.8E-01
ENSMUST00000113211	ribosomal protein L36A [Source:MGI Symbol;Acc:MGI:1201789]	Q5M9P1	P83882	-9.5	5.1E-05	5.2	8.7E-03	0.4	8.0E-01	0.3	7.5E-01
ENSMUST00000113215	SH3 domain binding glutamic acid-rich protein like 2 [Source:MGI Symbol;Acc:MGI:1915350]		Q8BG73	2.0	4.1E-03	6.8	7.1E-05	0.0	9.7E-01	0.1	8.3E-01
ENSMUST00000113216	solute carrier family 4 (anion exchanger), member 4 [Source:MGI Symbol;Acc:MGI:1927555]		O88343	6.6	2.6E-04	6.2	3.1E-04	-0.5	6.8E-01	-1.0	1.3E-01
ENSMUST00000111159	thymoma viral proto-oncogene 3 [Source:MGI Symbol;Acc:MGI:1345147]		Q9WUA6	2.2	4.7E-02	2.2	1.4E-01	0.3	8.0E-01	0.3	7.9E-01
ENSMUST00000111163	serine/threonine/tyrosine interacting-like 1 [Source:MGI Symbol;Acc:MGI:1923821]	Q9DAR2		-0.3	8.0E-01	-0.1	9.5E-01	0.1	9.1E-01	-0.1	9.7E-01
ENSMUST00000111168	catalase [Source:MGI Symbol;Acc:MGI:88271]	A2AL20		0.8	7.0E-01	-0.8	6.5E-01	-3.9	3.4E-02	-2.3	2.6E-01
ENSMUST00000111171	nuclear pore membrane protein 121 [Source:MGI Symbol;Acc:MGI:2137624]	Q3U425	Q8K3Z9	-2.4	2.6E-01	-0.3	9.1E-01	1.8	4.0E-01	-0.4	8.9E-01
ENSMUST00000113224	dystrophin related protein 2 [Source:MGI Symbol;Acc:MGI:107432]	B1AV35		6.3	3.6E-05	7.0	2.0E-04	-0.6	6.4E-01	0.4	5.3E-01
ENSMUST00000113231	eukaryotic translation initiation factor 4E member 2 [Source:MGI Symbol;Acc:MGI:1914440]	Q0P688		-7.3	1.5E-05	6.9	7.7E-05	1.1	3.0E-01	0.5	3.2E-01
ENSMUST00000113232	eukaryotic translation initiation factor 4E member 2 [Source:MGI Symbol;Acc:MGI:1914440]	Q3UUT0		-4.3	2.7E-03	7.6	6.6E-06	-0.8	3.8E-01	-0.1	8.5E-01
ENSMUST00000111192	CD44 antigen [Source:MGI Symbol;Acc:MGI:88338]	A2APM5		-6.2	9.6E-02	-7.2	6.0E-02	-3.0	5.4E-02	-2.1	6.4E-01
ENSMUST00000113233	eukaryotic translation initiation factor 4E member 2 [Source:MGI Symbol;Acc:MGI:1914440]		Q8BMB3	3.4	6.1E-03	-4.5	1.7E-02	1.2	1.3E-01	-2.2	2.5E-01
ENSMUST00000111210	myeloid nuclear differentiation antigen like [Source:MGI Symbol;Acc:MGI:3780953]		D0QMC3	-4.5	2.0E-01	-5.4	2.0E-01	-2.0	3.1E-01	-1.0	8.2E-01
ENSMUST00000111214	interferon activated gene 204 [Source:MGI Symbol;Acc:MGI:96429]	E9QKL6		-2.2	4.9E-02	-3.3	1.4E-02	-2.2	1.2E-02	-1.1	3.7E-01
ENSMUST00000113234	G-rich RNA sequence binding factor 1 [Source:MGI Symbol;Acc:MGI:106479]	E9Q179		-6.0	8.9E-06	-4.9	1.8E-03	0.9	6.4E-02	-0.8	5.4E-01
ENSMUST00000113239	cereblon [Source:MGI Symbol;Acc:MGI:1913277]		Q8C7D2	-7.2	3.7E-05	-6.0	9.7E-04	0.0	1.0E+00	0.8	5.4E-01
ENSMUST00000113242	SH2 domain containing 3C [Source:MGI Symbol;Acc:MGI:1351631]		Q9QZS8	-5.3	2.0E-03	8.0	3.8E-05	-0.6	5.9E-01	0.2	7.6E-01
ENSMUST00000111222	low density lipoprotein receptor class A domain containing 3 [Source:MGI Symbol;Acc:MGI:2138856]		A2AR95	1.6	2.7E-01	3.2	7.7E-02	0.7	6.6E-01	-1.0	4.8E-01
ENSMUST00000111228	transgelin 2 [Source:MGI Symbol;Acc:MGI:1312985]		Q9WVA4	-3.3	3.4E-01	-2.6	4.5E-01	-0.5	8.0E-01	-1.2	7.7E-01
ENSMUST00000113245	interleukin-1 receptor-associated kinase 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1929475]		Q9ESJ7	8.3	4.6E-05	-2.9	1.7E-02	0.5	3.8E-01	-0.6	5.6E-01
ENSMUST00000111233	LIM-domain containing, protein kinase [Source:MGI Symbol;Acc:MGI:104572]	E9PVB6		0.3	8.8E-01	1.1	6.1E-01	-1.3	4.9E-01	-2.2	3.1E-01
ENSMUST00000113248	tRNA nucleotidyl transferase, CCA-adding, 1 [Source:MGI Symbol;Acc:MGI:1917297]		Q8K1J6	-4.1	2.3E-03	2.8	6.9E-03	-4.8	1.3E-03	-0.2	8.1E-01
ENSMUST00000111235	immunoglobulin superfamily, member 9 [Source:MGI Symbol;Acc:MGI:2135283]		Q05BQ1	4.2	1.5E-01	5.2	1.1E-01	-0.5	8.8E-01	-1.5	4.7E-01
ENSMUST00000111236	tumor necrosis factor receptor superfamily, member 19 [Source:MGI Symbol;Acc:MGI:1352474]		Q9JLL3	4.2	5.5E-02	4.0	4.8E-02	-3.4	1.2E-01	-3.2	4.1E-02
ENSMUST00000111237	tetratricopeptide repeat domain 17 [Source:MGI Symbol;Acc:MGI:1921819]		E9PVB5	5.7	7.2E-02	5.7	9.5E-02	-0.7	8.4E-01	-0.6	7.4E-01
ENSMUST00000111238	tetratricopeptide repeat domain 17 [Source:MGI Symbol;Acc:MGI:1921819]		E9PVB5	1.3	6.6E-01	1.5	6.8E-01	1.4	6.5E-01	1.1	7.2E-01
ENSMUST00000111240	alkB, alkylation repair homolog 3 (E. coli) [Source:MGI Symbol;Acc:MGI:1916363]	A2AKV6		0.4	7.5E-01	2.6	1.6E-01	1.1	5.0E-01	-1.1	4.0E-01
ENSMUST00000113251	triggering receptor expressed on myeloid cells 1 [Source:MGI Symbol;Acc:MGI:1930005]	Q14DT9		-3.9	5.3E-05	7.2	4.5E-05	-1.5	2.0E-01	0.0	9.7E-01
ENSMUST00000111244	general transcription factor II I repeat domain-containing 1 [Source:MGI Symbol;Acc:MGI:1861942]	Q6PD35		0.3	7.5E-01	5.8	1.3E-02	5.1	1.7E-02	-0.4	7.2E-01
ENSMUST00000113270	alkaline phosphatase, intestinal [Source:MGI Symbol;Acc:MGI:1924018]	F8VPQ6		7.8	2.3E-04	3.7	2.4E-03	-0.8	3.7E-01	0.5	4.2E-01
ENSMUST00000111247	phosphoprotein enriched in astrocytes 15A [Source:MGI Symbol;Acc:MGI:104799]		Q62048	4.0	6.8E-02	3.4	2.9E-01	2.0	4.3E-01	2.5	3.2E-01
ENSMUST00000113272	endoglin [Source:MGI Symbol;Acc:MGI:95392]	F7A1B4		4.4	2.8E-03	-0.4	7.2E-01	1.8	6.1E-02	-0.4	7.3E-01
ENSMUST00000113277	adenylate kinase 1 [Source:MGI Symbol;Acc:MGI:87977]		Q9R0Y5	6.8	7.0E-03	8.8	4.2E-05	-0.6	6.7E-01	-0.9	1.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000111257	CD82 antigen [Source:MGI Symbol;Acc:MGI:104651]	Q3UII2	P40237	-0.3	9.1E-01	4.1	2.1E-01	1.8	5.1E-01	-2.6	3.7E-01
ENSMUST00000113278	adenylate kinase 1 [Source:MGI Symbol;Acc:MGI:87977]		Q9R0Y5	6.3	5.2E-04	8.7	2.0E-05	-0.6	6.5E-01	-0.3	5.1E-01
ENSMUST00000113284	transcription factor EB [Source:MGI Symbol;Acc:MGI:103270]	D3Z6Q7		4.8	3.1E-04	7.3	2.0E-04	-1.1	4.1E-01	1.0	1.7E-01
ENSMUST00000111266	transformation related protein 53 inducible protein 11 [Source:MGI Symbol;Acc:MGI:2670995]		Q4QQM4	1.9	4.7E-01	-3.0	1.8E-01	-5.2	1.9E-02	-0.3	9.1E-01
ENSMUST00000113288	transcription factor EB [Source:MGI Symbol;Acc:MGI:103270]		Q9R210	6.5	1.1E-03	1.9	1.4E-02	0.7	1.9E-01	0.1	9.1E-01
ENSMUST00000113294	synaptotagmin-like 4 [Source:MGI Symbol;Acc:MGI:1351606]		Q9R0Q1	7.4	2.4E-04	6.0	4.1E-05	0.2	7.6E-01	0.5	3.7E-01
ENSMUST00000113296	fibroblast growth factor receptor substrate 3 [Source:MGI Symbol;Acc:MGI:2135965]		Q91WJ0	6.1	1.0E-03	-4.3	9.3E-05	1.2	7.7E-03	-1.8	3.0E-02
ENSMUST00000113297	synaptotagmin-like 4 [Source:MGI Symbol;Acc:MGI:1351606]		Q9R0Q1	7.2	1.7E-03	5.6	7.7E-02	-0.6	8.5E-01	0.4	8.3E-01
ENSMUST00000113301	translocase of outer mitochondrial membrane 6 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1913369]		Q9CQN3	-6.8	3.1E-05	5.1	1.5E-03	1.8	1.2E-01	0.2	7.2E-01
ENSMUST00000111285	zinc finger, MYM-type 5 [Source:MGI Symbol;Acc:MGI:3041170]		Q3U2E2	0.8	5.6E-01	-1.5	4.3E-01	0.0	9.7E-01	2.3	2.1E-01
ENSMUST00000111286	poliovirus receptor-related 4 [Source:MGI Symbol;Acc:MGI:1918990]		Q8R007	0.4	8.7E-01	4.7	7.3E-02	-0.6	7.8E-01	-5.0	4.2E-02
ENSMUST00000113302	translocase of outer mitochondrial membrane 6 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1913369]		Q9CQN3	-7.3	1.1E-04	5.3	8.6E-03	0.4	8.2E-01	0.1	9.5E-01
ENSMUST00000111288	calneuron 1 [Source:MGI Symbol;Acc:MGI:2155987]	Q542R1	Q9JJG7	4.0	3.9E-02	5.7	1.2E-02	-0.5	8.2E-01	-2.1	9.7E-02
ENSMUST00000111289	nitrilase 1 [Source:MGI Symbol;Acc:MGI:1350916]		Q8VDK1	-3.0	3.5E-02	-1.8	3.1E-01	2.0	9.6E-02	0.9	5.9E-01
ENSMUST00000111291	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	D3Z764		-1.2	6.7E-01	-2.7	4.7E-01	-0.8	7.0E-01	0.7	8.5E-01
ENSMUST00000111292	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	A2AHG3		0.2	9.1E-01	2.0	5.1E-01	1.5	4.6E-01	-0.2	9.3E-01
ENSMUST00000113306	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Source:MGI Symbol;Acc:MGI:2384394]		Q8K0J2	4.4	2.7E-04	-6.8	9.8E-03	0.7	3.1E-01	-0.1	9.6E-01
ENSMUST00000111294	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	A2AHG4		-1.1	4.0E-01	0.6	7.6E-01	1.0	5.1E-01	-0.7	6.5E-01
ENSMUST00000113307	e carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 [Source:MGI Symbol;Acc:MGI:1915		A2ASZ8	6.0	5.7E-03	-3.9	1.0E-02	0.7	1.9E-01	-1.2	4.0E-01
ENSMUST00000111297	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	E9PV92		2.6	4.0E-01	-1.3	7.5E-01	-2.4	4.0E-01	1.5	7.1E-01
ENSMUST00000113322	forkhead box P1 [Source:MGI Symbol;Acc:MGI:1914004]		P58462	-7.1	5.3E-05	-6.0	5.5E-03	-0.2	8.0E-01	0.0	9.9E-01
ENSMUST00000111299	death effector domain-containing [Source:MGI Symbol;Acc:MGI:1333874]	Q3U001	Q9Z1L3	-2.2	5.3E-02	-1.9	1.8E-01	0.2	8.2E-01	-0.2	8.8E-01
ENSMUST00000111300	death effector domain-containing [Source:MGI Symbol;Acc:MGI:1333874]	Q3U001	Q9Z1L3	-0.6	6.9E-01	2.2	1.9E-01	0.4	8.0E-01	-2.4	1.1E-01
ENSMUST00000111303	diacylglycerol kinase zeta [Source:MGI Symbol;Acc:MGI:1278339]	A2AHK0		0.7	4.9E-01	-0.1	9.4E-01	0.6	5.7E-01	1.4	3.2E-01
ENSMUST00000113326	forkhead box P1 [Source:MGI Symbol;Acc:MGI:1914004]			-2.7	1.6E-02	3.4	1.6E-02	0.1	9.3E-01	-0.4	6.0E-01
ENSMUST00000113334	CDKN1A interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1920234]	Q8VEH2		6.5	4.8E-04	-0.3	9.2E-01	5.8	6.4E-03	-1.5	6.0E-01
ENSMUST00000113337	ubiquitin protein ligase E3 component n-recognin 2 [Source:MGI Symbol;Acc:MGI:1861099]		Q6WKZ8	-2.2	6.3E-04	3.7	9.7E-02	0.8	6.9E-01	2.5	8.9E-02
ENSMUST00000113338	CDKN1A interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1920234]	Q8VEH2		-6.6	8.1E-03	6.8	1.5E-03	-2.8	1.3E-01	-0.4	6.5E-01
ENSMUST00000111318	NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Source:MGI Symbol;Acc:MGI:2385112]	D3YXT0		-3.6	6.6E-02	0.3	8.6E-01	2.6	1.2E-01	-1.4	4.8E-01
ENSMUST00000113344	spermatogenesis associated 3 [Source:MGI Symbol;Acc:MGI:1917310]	Q3V2M5	Q9D9T6	5.2	1.9E-02	-1.5	1.2E-01	0.8	1.7E-01	-0.8	4.0E-01
ENSMUST00000113348	claudin 34C1 [Source:MGI Symbol;Acc:MGI:1920311]	Q8K193		8.5	1.6E-05	-3.6	2.9E-02	0.2	7.7E-01	-0.3	8.4E-01
ENSMUST00000111329	Rho GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2445003]		Q5FWK3	0.4	6.7E-01	0.3	8.3E-01	0.6	5.7E-01	0.7	5.8E-01
ENSMUST00000111330	Rho GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2445003]		Q5FWK3	1.3	9.6E-02	1.6	9.4E-02	-0.2	8.0E-01	-0.5	5.4E-01
ENSMUST00000111331	Rho GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:2445003]	A2AH25		-2.3	6.3E-01	-2.9	6.4E-01	-1.4	6.9E-01	-0.8	9.0E-01
ENSMUST00000111332	Purkinje cell protein 4-like 1 [Source:MGI Symbol;Acc:MGI:1913675]		Q6W8Q3	1.1	1.2E-01	0.4	6.3E-01	-1.0	1.2E-01	-0.3	6.9E-01
ENSMUST00000113352	dynamin 1 [Source:MGI Symbol;Acc:MGI:107384]		P39053	8.1	6.3E-06	6.3	7.4E-03	-0.9	6.2E-01	-0.1	9.4E-01
ENSMUST00000113360	calcium binding protein 39 [Source:MGI Symbol;Acc:MGI:107438]		Q06138	-4.9	3.5E-06	6.5	4.8E-03	-0.8	6.9E-01	-1.7	1.4E-01
ENSMUST00000111335	coagulation factor II [Source:MGI Symbol;Acc:MGI:88380]	H7BX99		2.5	2.6E-01	-1.0	6.4E-01	-3.8	7.2E-02	-0.3	8.6E-01
ENSMUST00000111336	ccinate dehydrogenase complex, subunit C, integral membrane protein [Source:MGI Symbol;Acc:MGI:191330		Q9CZB0	-0.5	2.7E-01	1.0	1.1E-01	0.7	1.3E-01	-0.8	1.6E-01
ENSMUST00000111338	cytoskeleton associated protein 5 [Source:MGI Symbol;Acc:MGI:1923036]	K3W4R5		-1.7	2.5E-01	-0.4	8.1E-01	-0.8	4.6E-01	-2.1	2.2E-01
ENSMUST00000113369	REST corepressor 2 [Source:MGI Symbol;Acc:MGI:1859854]			5.6	2.8E-03	-1.8	2.9E-01	2.1	8.2E-02	0.6	7.1E-01
ENSMUST00000113383	fibronectin leucine rich transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:3026647]	Q6RKD8	Q6RKD8	9.6	7.0E-06	9.2	9.7E-05	-0.8	6.2E-01	-1.1	8.2E-02
ENSMUST00000113385	Sp140 nuclear body protein [Source:MGI Symbol;Acc:MGI:3702467]	D3Z054		4.5	2.2E-04	5.4	1.5E-02	-0.7	7.3E-01	1.1	3.3E-01
ENSMUST00000113400	SWI5 recombination repair homolog (yeast) [Source:MGI Symbol;Acc:MGI:1920181]		Q8K3D3	-7.6	9.2E-05	-7.1	3.6E-05	-0.3	3.4E-01	-0.1	9.5E-01
ENSMUST00000113401	Eph receptor A5 [Source:MGI Symbol;Acc:MGI:99654]	Q6PFV6		7.0	4.8E-04	-3.3	1.2E-01	1.3	2.0E-01	-0.9	6.8E-01
ENSMUST00000113423	BCL2-associated agonist of cell death [Source:MGI Symbol;Acc:MGI:1096330]	Q3U9H3		-4.9	2.1E-03	6.6	1.2E-04	-0.5	6.4E-01	-1.5	2.7E-02
ENSMUST00000111356	nuclear receptor subfamily 1, group H, member 3 [Source:MGI Symbol;Acc:MGI:1352462]	Q91X41	Q9Z0Y9	1.8	2.4E-01	6.5	4.0E-03	1.4	4.4E-01	-3.3	1.8E-02
ENSMUST00000113434	predicted gene 15737 [Source:MGI Symbol;Acc:MGI:3783179]	D3YZR0		7.2	7.4E-06	3.4	1.2E-03	-1.2	1.3E-01	-0.4	4.9E-01
ENSMUST00000113438	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9 [Source:MGI Symbol;Acc:M	E9PUN6		8.0	4.0E-05	2.3	1.7E-02	-0.3	7.0E-01	0.2	7.4E-01
ENSMUST00000111369	MAP-kinase activating death domain [Source:MGI Symbol;Acc:MGI:2444672]	A2AGR1		3.3	2.9E-01	-0.9	8.4E-01	-2.6	4.1E-01	1.6	6.9E-01
ENSMUST00000111370	MAP-kinase activating death domain [Source:MGI Symbol;Acc:MGI:2444672]			0.7	8.3E-01	-1.4	6.8E-01	-2.3	4.1E-01	-0.2	9.4E-01
ENSMUST00000113440	coiled-coil domain containing 88B [Source:MGI Symbol;Acc:MGI:1925567]		Q4QRL3	-3.8	1.9E-04	-3.9	1.1E-01	1.3	2.9E-01	-0.6	8.1E-01
ENSMUST00000113445	prickle homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925144]		Q80Y24	6.5	2.9E-05	-2.6	5.0E-01	3.8	9.1E-02	0.7	8.4E-01
ENSMUST00000111375	MAP-kinase activating death domain [Source:MGI Symbol;Acc:MGI:2444672]	A2AGQ8		-3.8	1.7E-01	0.0	9.9E-01	1.1	6.3E-01	-2.7	3.7E-01
ENSMUST00000111376	MAP-kinase activating death domain [Source:MGI Symbol;Acc:MGI:2444672]	A2AGQ6		-1.9	4.5E-01	-1.6	4.2E-01	-2.9	1.1E-01	-3.2	2.2E-01
ENSMUST00000113446	prickle homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925144]		Q80Y24	7.8	3.1E-04	3.3	3.1E-01	-0.5	8.7E-01	6.3	2.2E-02
ENSMUST00000113451	olute carrier family 22 (organic anion/cation transporter), member 12 [Source:MGI Symbol;Acc:MGI:1195269			7.4	2.7E-05	-7.5	4.8E-04	-0.2	6.6E-01	-1.0	5.4E-01
ENSMUST00000113453	HOP homeobox [Source:MGI Symbol;Acc:MGI:1916782]		Q8R1H0	-7.8	9.6E-06	-6.3	3.2E-04	0.1	8.6E-01	-3.8	1.9E-02
ENSMUST00000111390	scavenger receptor class B, member 1 [Source:MGI Symbol;Acc:MGI:893578]	D3Z2V4		1.8	1.0E-01	2.4	1.7E-01	2.3	1.1E-01	1.7	2.1E-01
ENSMUST00000111393	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]	E9Q9V3		-0.7	7.1E-01	0.3	9.1E-01	1.4	4.6E-01	0.4	8.5E-01
ENSMUST00000113457	collagen, type IV, alpha 3 [Source:MGI Symbol;Acc:MGI:104688]		Q9QZS0	6.8	2.9E-05	2.6	2.6E-01	-6.2	2.8E-02	0.0	9.8E-01
ENSMUST00000111402	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]	F8VQL9		2.2	4.5E-01	2.1	6.9E-01	1.4	7.2E-01	1.6	6.9E-01
ENSMUST00000113458	neurexin II [Source:MGI Symbol;Acc:MGI:1096362]	E9PUN2		3.0	2.4E-02	7.5	1.0E-03	-0.7	6.8E-01	-0.7	4.3E-01
ENSMUST00000113459	neurexin II [Source:MGI Symbol;Acc:MGI:1096362]	E9PUN1		8.0	1.3E-05	4.6	3.5E-04	-2.6	1.3E-02	0.0	9.4E-01
ENSMUST00000111417	zinc finger protein 664 [Source:MGI Symbol;Acc:MGI:2442505]	E9QPD3		-3.9	2.6E-01	-3.0	3.1E-01	-1.9	3.1E-01	-2.9	4.4E-01
ENSMUST00000113460	nuclear receptor subfamily 2, group C, member 2 [Source:MGI Symbol;Acc:MGI:1352466]	Q3ZAS1	P49117	-3.6	1.5E-03	3.5	2.7E-03	0.4	6.5E-01	-0.5	4.7E-01
ENSMUST00000111430	myosin binding protein C, cardiac [Source:MGI Symbol;Acc:MGI:102844]	E9Q9T8		3.2	1.4E-01	1.8	5.4E-01	0.1	9.5E-01	1.6	4.8E-01
ENSMUST00000113461	neurexin II [Source:MGI Symbol;Acc:MGI:1096362]	E9PUN0		5.3	2.4E-02	-7.3	2.9E-03	0.2	7.8E-01	1.5	4.6E-01
ENSMUST00000111435	myelin protein zero-like 1 [Source:MGI Symbol;Acc:MGI:1915731]		Q3TEW6	-1.4	4.5E-01	-0.2	9.3E-01	0.3	8.5E-01	-0.8	7.0E-01
ENSMUST00000113463	nuclear receptor subfamily 2, group C, member 2 [Source:MGI Symbol;Acc:MGI:1352466]	G3X9W4		2.8	8.9E-03	2.0	3.9E-01	3.0	1.0E-01	4.7	1.8E-02
ENSMUST00000113466	FYVE, RhoGEF and PH domain containing 5 [Source:MGI Symbol;Acc:MGI:2443369]	E9QLU9		5.6	2.8E-02	-3.3	7.1E-04	-1.6	2.5E-03	-1.5	5.9E-02
ENSMUST00000111445	receptor-associated protein of the synapse [Source:MGI Symbol;Acc:MGI:99422]	A2AFX4		3.8	1.4E-01	2.8	2.7E-01	-1.9	4.7E-01	-0.8	6.6E-01
ENSMUST00000111446	receptor-associated protein of the synapse [Source:MGI Symbol;Acc:MGI:99422]	A2AFX6		2.1	2.7E-01	2.8	1.9E-01	0.0	9.9E-01	-0.7	6.7E-01
ENSMUST00000113470	PR domain containing 12 [Source:MGI Symbol;Acc:MGI:2685844]		A2AJ77	8.4	1.4E-04	-3.2	4.8E-02	-0.8	3.3E-01	-0.6	6.9E-01
ENSMUST00000113471	RAS, guanyl releasing protein 2 [Source:MGI Symbol;Acc:MGI:1333849]		Q9QUG9	-7.1	1.9E-05	5.4	7.8E-05	-2.0	4.0E-02	-0.3	6.4E-01
ENSMUST00000111452	CUGBP, Elav-like family member 1 [Source:MGI Symbol;Acc:MGI:1342295]		P28659	4.0	7.5E-02	-1.6	6.9E-01	-0.3	8.9E-01	5.3	1.7E-01
ENSMUST00000113476	RAS, guanyl releasing protein 2 [Source:MGI Symbol;Acc:MGI:1333849]		Q9QUG9	5.0	6.7E-03	0.9	8.0E-01	5.6	6.9E-02	-2.2	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000111464	kelch repeat and BTB (POZ) domain containing 4 [Source:MGI Symbol;Acc:MGI:1914386]		Q8R179	0.8	6.9E-01	-0.8	7.5E-01	-1.3	5.1E-01	0.3	8.9E-01
ENSMUST00000113480	cysteinyl leukotriene receptor 1 [Source:MGI Symbol;Acc:MGI:1926218]		Q99JA4	2.8	8.1E-04	5.7	7.9E-04	-0.5	6.9E-01	-1.1	1.3E-01
ENSMUST00000111467	mitochondrial carrier homolog 2 (C. elegans) [Source:MGI Symbol;Acc:MGI:1929260]	A2AFW6		-3.1	4.5E-02	2.3	3.9E-01	5.6	1.4E-02	0.2	9.1E-01
ENSMUST00000113481	zinc finger protein 318 [Source:MGI Symbol;Acc:MGI:1889348]	B0V2M3		1.4	2.0E-02	-6.3	7.8E-05	0.4	2.4E-01	-0.4	6.7E-01
ENSMUST00000113482	far upstream element (FUSE) binding protein 3 [Source:MGI Symbol;Acc:MGI:2443699]	A2AJ72		2.7	7.1E-04	-1.4	2.1E-01	0.6	4.3E-01	-2.6	5.7E-02
ENSMUST00000111473	CDK2 (cyclin-dependent kinase 2)-associated protein 1 [Source:MGI Symbol;Acc:MGI:1202069]	F2Z4B3		-0.8	5.7E-01	-0.1	9.6E-01	1.3	4.6E-01	0.6	7.6E-01
ENSMUST00000113485	splicing factor 1 [Source:MGI Symbol;Acc:MGI:1095403]	F8WHF9		-4.8	9.5E-03	5.1	6.4E-03	0.5	7.5E-01	-0.6	5.1E-01
ENSMUST00000113487	splicing factor 1 [Source:MGI Symbol;Acc:MGI:1095403]	E9Q4Q2		-8.5	3.3E-04	6.8	1.7E-04	0.9	4.3E-01	-0.3	6.6E-01
ENSMUST00000111484	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]		Q9JIX8	1.7	5.4E-01	2.3	5.3E-01	0.3	9.1E-01	-0.3	9.4E-01
ENSMUST00000113494	neuronal tyrosine-phophorylated phosphoinositide 3-kinase adaptor 2 [Source:MGI Symbol;Acc:MGI:2443135			6.4	1.0E-04	-2.3	1.0E-01	-0.6	5.1E-01	-2.4	1.6E-01
ENSMUST00000113498	fibulin 2 [Source:MGI Symbol;Acc:MGI:95488]	Q3TGL4	P37889	4.1	5.1E-04	-1.5	1.2E-01	0.6	3.2E-01	-0.5	6.3E-01
ENSMUST00000111495	protein tyrosine phosphatase, receptor type, J [Source:MGI Symbol;Acc:MGI:104574]	A2AWF9		3.0	2.2E-01	4.2	1.8E-01	1.3	6.1E-01	0.0	9.9E-01
ENSMUST00000111497	abhydrolase domain containing 5 [Source:MGI Symbol;Acc:MGI:1914719]		Q9DBL9	-5.1	7.5E-02	4.6	2.0E-01	6.9	4.1E-02	-2.8	3.3E-01
ENSMUST00000113502	multiple endocrine neoplasia 1 [Source:MGI Symbol;Acc:MGI:1316736]			-5.2	4.3E-04	5.9	1.7E-04	-1.8	1.2E-01	0.1	8.0E-01
ENSMUST00000111515	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	Q8BI46		-1.8	4.5E-02	-1.3	2.0E-01	-0.1	9.1E-01	-0.6	5.6E-01
ENSMUST00000111518	flavin containing monooxygenase 1 [Source:MGI Symbol;Acc:MGI:1310002]	Q8C9C1		0.4	3.3E-01	-0.1	9.1E-01	-0.2	6.6E-01	0.3	5.5E-01
ENSMUST00000113516	kinase insert domain protein receptor [Source:MGI Symbol;Acc:MGI:96683]	Q8VCD0		5.7	2.0E-05	7.0	1.2E-04	-0.5	6.5E-01	-1.3	6.1E-02
ENSMUST00000111526	actin-binding LIM protein 1 [Source:MGI Symbol;Acc:MGI:1194500]	E9Q9Q7		1.9	2.4E-01	4.1	2.0E-02	-1.4	3.7E-01	-3.6	2.1E-02
ENSMUST00000111529	actin-binding LIM protein 1 [Source:MGI Symbol;Acc:MGI:1194500]	E9Q9D1		-1.9	8.4E-02	-5.7	1.8E-02	-0.7	3.3E-01	3.0	1.6E-01
ENSMUST00000111535	antagonist of mitotic exit network 1 [Source:MGI Symbol;Acc:MGI:2442933]	B8JKV0		-0.9	3.2E-01	-1.2	3.2E-01	0.2	8.0E-01	0.5	6.4E-01
ENSMUST00000113526	glycoprotein hormone alpha 2 [Source:MGI Symbol;Acc:MGI:2156541]	A2RSW3	Q925Q5	7.1	4.1E-03	4.1	1.2E-04	-1.0	1.4E-01	-0.5	2.9E-01
ENSMUST00000113528	RIKEN cDNA 1700123I01 gene [Source:MGI Symbol;Acc:MGI:1923913]	E9Q4N4		6.6	9.5E-05	7.0	5.8E-04	-0.6	6.9E-01	-1.0	2.4E-01
ENSMUST00000111560	SEC22 homolog C, vesicle trafficking protein [Source:MGI Symbol;Acc:MGI:2447871]		Q8BXT9	2.0	7.3E-02	5.1	2.2E-02	4.5	2.2E-02	1.4	2.4E-01
ENSMUST00000113530	Kruppel-like factor 15 [Source:MGI Symbol;Acc:MGI:1929988]		Q9EPW2	7.5	8.0E-05	-7.1	2.9E-03	0.7	2.2E-01	1.3	5.1E-01
ENSMUST00000113531	ligand of numb-protein X 1 [Source:MGI Symbol;Acc:MGI:1278335]	E9Q4N3		6.4	1.5E-02	4.8	5.0E-02	-0.1	9.6E-01	-0.7	6.2E-01
ENSMUST00000113532	hemicentin 2 [Source:MGI Symbol;Acc:MGI:2677838]		A2AJ76	10.8	1.4E-06	5.8	3.9E-03	0.0	9.9E-01	0.6	5.5E-01
ENSMUST00000111581	RNA binding protein, fox-1 homolog (C. elegans) 2 [Source:MGI Symbol;Acc:MGI:1933973]		Q8BP71	0.9	5.6E-01	1.7	3.5E-01	-0.9	5.5E-01	-1.6	3.4E-01
ENSMUST00000111584	actin filament associated protein 1-like 2 [Source:MGI Symbol;Acc:MGI:2147658]		Q5DTU0	7.1	4.4E-02	6.2	8.8E-02	-1.0	7.8E-01	-0.1	9.5E-01
ENSMUST00000113535	FIP1 like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914149]		Q9D824	-4.8	1.1E-02	-6.8	6.5E-03	0.2	8.0E-01	1.9	3.4E-01
ENSMUST00000113536	FIP1 like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914149]		Q9D824	-4.9	5.9E-03	-1.9	1.4E-01	1.2	1.1E-01	-0.5	7.0E-01
ENSMUST00000113547	t-complex-associated testis expressed 1 [Source:MGI Symbol;Acc:MGI:98640]		A6H639	10.0	3.0E-05	7.1	2.4E-04	-0.2	8.9E-01	0.0	9.5E-01
ENSMUST00000113553	serine/threonine kinase 11 interacting protein [Source:MGI Symbol;Acc:MGI:1918978]		Q3TAA7	-2.4	1.2E-02	6.7	6.8E-04	-0.6	6.6E-01	-0.8	2.9E-01
ENSMUST00000113557	ATPase, Cu++ transporting, alpha polypeptide [Source:MGI Symbol;Acc:MGI:99400]		Q64430	-3.9	2.0E-02	8.4	1.8E-04	-0.5	7.7E-01	-1.5	5.8E-02
ENSMUST00000111605	tankyrase 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:2446193]		P58871	0.8	5.0E-01	4.1	2.1E-02	1.3	3.5E-01	-2.0	1.0E-01
ENSMUST00000113562	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]		Q80TY0	-8.7	4.1E-04	2.7	4.1E-01	-0.9	7.7E-01	2.6	3.0E-01
ENSMUST00000113567	obscurin-like 1 [Source:MGI Symbol;Acc:MGI:2138628]		D3YYU8	8.3	1.6E-04	6.2	1.9E-04	-0.5	6.4E-01	0.1	9.2E-01
ENSMUST00000113573	ha thalassemia/mental retardation syndrome X-linked homolog (human) [Source:MGI Symbol;Acc:MGI:1030		Q61687	-5.8	3.4E-05	-8.7	9.8E-05	-0.2	6.2E-01	3.6	2.0E-02
ENSMUST00000111611	kelch-like 20 [Source:MGI Symbol;Acc:MGI:2444855]		Q8VCK5	-1.1	2.2E-01	-0.6	6.3E-01	0.5	5.3E-01	-0.1	9.5E-01
ENSMUST00000111618	centromere protein L [Source:MGI Symbol;Acc:MGI:1917704]	Q14A61		-2.4	1.6E-01	0.2	9.4E-01	1.4	4.1E-01	-1.2	5.7E-01
ENSMUST00000113577	acid-sensing (proton-gated) ion channel family member 4 [Source:MGI Symbol;Acc:MGI:2652846]	D3YYS9		7.5	1.2E-03	-2.6	7.3E-02	1.6	6.4E-02	-1.1	4.4E-01
ENSMUST00000113584	GDP-mannose pyrophosphorylase A [Source:MGI Symbol;Acc:MGI:1916330]		Q922H4	-5.2	1.6E-04	6.6	2.0E-03	-0.7	6.9E-01	-0.1	9.1E-01
ENSMUST00000111625	solute carrier family 43, member 1 [Source:MGI Symbol;Acc:MGI:1931352]	A2ATS4		1.8	1.6E-01	2.7	1.0E-01	1.0	4.6E-01	0.0	9.8E-01
ENSMUST00000113585	monoglyceride lipase [Source:MGI Symbol;Acc:MGI:1346042]		O35678	-5.1	1.8E-02	4.8	7.6E-02	1.0	6.5E-01	4.3	1.8E-02
ENSMUST00000113589	SPEG complex locus [Source:MGI Symbol;Acc:MGI:109282]			6.3	3.2E-04	4.1	7.4E-03	0.3	8.1E-01	-0.1	9.3E-01
ENSMUST00000111632	N-myc downstream regulated gene 2 [Source:MGI Symbol;Acc:MGI:1352498]		Q9QYG0	-0.4	8.5E-01	2.1	2.8E-01	-1.1	5.3E-01	-3.6	8.4E-02
ENSMUST00000113595	ring finger 111 [Source:MGI Symbol;Acc:MGI:1934919]		Q99ML9	-1.5	2.8E-02	8.7	4.6E-05	-1.8	2.3E-01	0.3	6.6E-01
ENSMUST00000113597	RAB7, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105068]	Q4FJQ0	P51150	-2.3	2.8E-02	3.6	4.3E-04	-1.0	1.4E-01	-0.5	3.3E-01
ENSMUST00000111641	serine (or cysteine) peptidase inhibitor, clade G, member 1 [Source:MGI Symbol;Acc:MGI:894696]	A2ATR8		4.7	5.3E-02	4.6	8.2E-02	-0.4	8.9E-01	-0.3	8.7E-01
ENSMUST00000111643	yippee-like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:3605071]	A2ATR6		3.9	4.0E-02	4.9	1.1E-02	-2.0	2.8E-01	-3.0	2.3E-02
ENSMUST00000113599	adhesion G protein-coupled receptor F5 [Source:MGI Symbol;Acc:MGI:2182928]		G5E8Q8	6.8	3.8E-06	0.3	5.5E-01	-0.8	1.1E-01	0.5	3.5E-01
ENSMUST00000113600	RAB7, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105068]	Q4FJQ0	P51150	-7.0	1.4E-05	7.2	1.4E-02	-0.2	9.5E-01	-1.6	2.6E-01
ENSMUST00000113605	aspartyl aminopeptidase [Source:MGI Symbol;Acc:MGI:1278328]		Q9Z2W0	-7.7	8.3E-05	4.7	4.4E-03	-1.1	4.0E-01	0.0	9.9E-01
ENSMUST00000113607	coatomer protein complex, subunit gamma 1 [Source:MGI Symbol;Acc:MGI:1858696]		Q9QZE5	-3.3	1.1E-04	3.9	1.1E-01	-4.2	1.1E-01	-0.7	7.0E-01
ENSMUST00000111663	FGFR1 oncogene partner 2 [Source:MGI Symbol;Acc:MGI:1914779]		Q9CRA9	-5.4	1.8E-01	-2.3	5.3E-01	0.7	7.8E-01	-2.4	5.7E-01
ENSMUST00000111664	thioredoxin-related transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1914208]	D3Z2J6		3.3	2.1E-01	3.9	2.2E-01	-1.1	7.1E-01	-1.8	4.4E-01
ENSMUST00000113614	adhesion G protein-coupled receptor F2 [Source:MGI Symbol;Acc:MGI:2182728]		E9Q4J9	7.1	5.8E-05	3.8	1.2E-01	-0.5	8.5E-01	2.3	1.2E-01
ENSMUST00000111668	calcium/calmodulin-dependent protein kinase kinase 2, beta [Source:MGI Symbol;Acc:MGI:2444812]		Q8C078	0.2	6.5E-01	0.7	3.5E-01	1.0	7.0E-02	0.6	3.4E-01
ENSMUST00000113619	cellular nucleic acid binding protein [Source:MGI Symbol;Acc:MGI:88431]	Q3U935	P53996	-9.7	6.4E-07	-4.2	1.6E-02	-0.5	6.1E-01	-0.1	9.5E-01
ENSMUST00000111673				-1.9	6.0E-01	-2.8	5.4E-01	-1.2	6.3E-01	-0.4	9.3E-01
ENSMUST00000111675	catenin (cadherin associated protein), delta 1 [Source:MGI Symbol;Acc:MGI:105100]	D3Z2H7		5.4	6.6E-02	3.2	3.8E-01	0.0	1.0E+00	2.3	3.5E-01
ENSMUST00000111691	catenin (cadherin associated protein), delta 1 [Source:MGI Symbol;Acc:MGI:105100]		P30999	-1.2	6.8E-01	0.8	7.5E-01	-1.4	4.6E-01	-3.4	2.5E-01
ENSMUST00000113627	tein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) [Source:MGI Symbol;Acc:MGI:1916		Q9CWW6	-6.4	5.6E-05	2.9	4.1E-03	-0.3	6.3E-01	-0.7	2.9E-01
ENSMUST00000113637	Rho GTPase activating protein 25 [Source:MGI Symbol;Acc:MGI:2443687]		Q8BYW1	-4.3	3.4E-03	6.1	4.7E-04	-0.5	6.6E-01	-0.2	8.0E-01
ENSMUST00000113641	K(lysine) acetyltransferase 5 [Source:MGI Symbol;Acc:MGI:1932051]	Q3UJQ1	Q8CHK4	-3.7	1.3E-05	5.0	6.0E-04	-0.8	4.2E-01	-1.0	1.5E-01
ENSMUST00000113657	glutamine fructose-6-phosphate transaminase 1 [Source:MGI Symbol;Acc:MGI:95698]	D3YYD9		3.0	2.9E-02	4.8	7.5E-03	-1.1	4.9E-01	-0.7	4.7E-01
ENSMUST00000113661	cysteine conjugate-beta lyase 1 [Source:MGI Symbol;Acc:MGI:1917516]	Q05CI8	Q8BTY1	9.3	1.6E-04	4.1	1.1E-03	0.4	6.6E-01	-0.3	6.3E-01
ENSMUST00000113676	solute carrier family 30 (zinc transporter), member 9 [Source:MGI Symbol;Acc:MGI:1923690]	F8WHL1		-7.2	3.5E-05	7.4	4.7E-05	-0.6	5.9E-01	-1.3	3.8E-02
ENSMUST00000113677	zyg-11 related, cell cycle regulator [Source:MGI Symbol;Acc:MGI:2442511]	Q3U297	Q80ZJ6	-5.6	9.2E-03	-4.1	2.2E-02	0.8	2.7E-01	-0.8	6.3E-01
ENSMUST00000111721	LYR motif containing 5 [Source:MGI Symbol;Acc:MGI:1914886]		Q91V16	0.4	8.9E-01	2.4	5.5E-01	1.0	7.7E-01	-0.9	7.7E-01
ENSMUST00000111725	LYR motif containing 5 [Source:MGI Symbol;Acc:MGI:1914886]		Q91V16	-0.9	3.7E-01	-1.3	2.9E-01	-1.1	2.4E-01	-0.7	5.3E-01
ENSMUST00000113690	tropomyosin 1, alpha [Source:MGI Symbol;Acc:MGI:98809]	G5E8R0		4.0	1.7E-04	-6.3	7.7E-05	0.4	2.1E-01	-0.9	3.9E-01
ENSMUST00000113695	tropomyosin 1, alpha [Source:MGI Symbol;Acc:MGI:98809]	G5E8R1		-4.0	9.2E-03	3.6	7.1E-03	-0.1	8.8E-01	-0.7	3.9E-01
ENSMUST00000111728	cancer susceptibility candidate 1 [Source:MGI Symbol;Acc:MGI:2444480]			3.3	9.2E-02	2.2	2.3E-01	-1.8	3.3E-01	-0.7	6.2E-01
ENSMUST00000113698	expressed sequence C87436 [Source:MGI Symbol;Acc:MGI:2141787]		Q8R3C1	-1.9	5.6E-03	-2.0	7.6E-02	5.0	1.3E-05	-1.2	2.8E-01
ENSMUST00000113700	expressed sequence C87436 [Source:MGI Symbol;Acc:MGI:2141787]		Q8R3C1	-4.0	4.1E-03	-0.3	7.0E-01	0.9	1.1E-01	-0.5	5.5E-01
ENSMUST00000113706	tripartite motif-containing 39 [Source:MGI Symbol;Acc:MGI:1890659]	E9QLN4		-4.5	1.2E-02	-1.1	5.7E-01	3.7	1.3E-02	1.7	3.3E-01
ENSMUST00000111738	tectonic family member 1 [Source:MGI Symbol;Acc:MGI:3603820]		Q8BZ64	0.0	9.9E-01	1.1	5.5E-01	1.3	3.7E-01	0.2	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000113710	e carrier family 7 (cationic amino acid transporter, y+ system), member 3 [Source:MGI Symbol;Acc:MGI:1100		P70423	5.8	1.3E-04	-0.9	7.2E-01	4.3	1.7E-02	1.5	5.4E-01
ENSMUST00000113711	WD repeat domain 34 [Source:MGI Symbol;Acc:MGI:1919070]	A2BE91		3.5	3.8E-05	-3.2	5.2E-03	0.1	8.2E-01	-0.2	7.9E-01
ENSMUST00000113721	ring finger protein 25 [Source:MGI Symbol;Acc:MGI:1890215]	E9Q446		-6.1	2.4E-04	6.1	8.9E-04	-2.3	1.3E-01	-0.2	7.6E-01
ENSMUST00000113733	BCS1-like (yeast) [Source:MGI Symbol;Acc:MGI:1914071]		Q9CZP5	-3.3	1.7E-02	8.0	3.2E-04	-0.1	9.7E-01	0.2	7.6E-01
ENSMUST00000113742	predicted gene 11127 [Source:MGI Symbol;Acc:MGI:3779381]	A7VMS2		4.5	2.8E-05	-5.4	1.4E-03	1.7	4.1E-03	-0.6	6.5E-01
ENSMUST00000111756	sortilin-related VPS10 domain containing receptor 1 [Source:MGI Symbol;Acc:MGI:1929666]	E9QQ63		3.4	1.2E-01	4.7	5.4E-02	-0.5	8.4E-01	-1.8	2.6E-01
ENSMUST00000111757	torsin A interacting protein 2 [Source:MGI Symbol;Acc:MGI:3582695]		Q8BYU6	0.6	3.8E-01	1.0	2.7E-01	0.3	6.6E-01	-0.1	9.0E-01
ENSMUST00000113743	receptor-interacting serine-threonine kinase 4 [Source:MGI Symbol;Acc:MGI:1919638]	D3YXY4		7.8	4.8E-05	-3.2	2.8E-01	2.3	1.7E-01	0.2	9.5E-01
ENSMUST00000113755	outer dense fiber of sperm tails 2 [Source:MGI Symbol;Acc:MGI:1098824]		A3KGV1	-2.7	1.0E-02	5.2	4.4E-03	-0.9	5.3E-01	0.2	8.3E-01
ENSMUST00000111764	quiescin Q6 sulfhydryl oxidase 1 [Source:MGI Symbol;Acc:MGI:1330818]		Q8BND5	-2.4	1.6E-01	-1.9	3.7E-01	0.8	5.3E-01	0.3	8.8E-01
ENSMUST00000113756	outer dense fiber of sperm tails 2 [Source:MGI Symbol;Acc:MGI:1098824]		A3KGV1	-4.6	6.1E-03	-2.5	1.0E-01	0.8	2.9E-01	0.0	9.9E-01
ENSMUST00000113759	outer dense fiber of sperm tails 2 [Source:MGI Symbol;Acc:MGI:1098824]		A3KGV1	-5.3	4.8E-03	7.4	2.0E-05	-0.9	3.7E-01	-0.6	2.7E-01
ENSMUST00000111774	xenotropic and polytropic retrovirus receptor 1 [Source:MGI Symbol;Acc:MGI:97932]		Q9Z0U0	1.2	5.7E-01	1.6	5.9E-01	1.4	4.8E-01	1.1	7.0E-01
ENSMUST00000113760	histocompatibility 2, T region locus 24 [Source:MGI Symbol;Acc:MGI:95958]	F8VQG4		-2.9	2.2E-03	-2.0	1.8E-01	0.2	7.7E-01	-1.7	3.0E-01
ENSMUST00000113764	outer dense fiber of sperm tails 2 [Source:MGI Symbol;Acc:MGI:1098824]		A3KGV1	6.1	6.7E-03	7.5	5.5E-04	0.4	8.0E-01	0.8	3.5E-01
ENSMUST00000113773	integrin beta 2-like [Source:MGI Symbol;Acc:MGI:1277979]	D3YXH8		-2.9	3.4E-02	-4.7	7.6E-04	1.2	1.1E-02	-0.8	4.6E-01
ENSMUST00000113782	mitochondrial ribosomal protein S18B [Source:MGI Symbol;Acc:MGI:1914223]	Q542W5	Q99N84	5.0	1.9E-02	-0.8	5.6E-01	2.8	1.2E-02	-1.2	4.3E-01
ENSMUST00000111785	sperm specific antigen 2 [Source:MGI Symbol;Acc:MGI:1917849]		Q922B9	-1.9	5.7E-01	-6.1	1.7E-01	-3.5	1.2E-01	0.8	8.7E-01
ENSMUST00000113793	RNA binding motif protein 14 [Source:MGI Symbol;Acc:MGI:1929092]	E9QL13		3.5	3.0E-03	-5.8	2.6E-03	0.3	5.5E-01	-0.9	5.9E-01
ENSMUST00000111788	sperm specific antigen 2 [Source:MGI Symbol;Acc:MGI:1917849]	A2AQD6		3.6	8.2E-02	2.0	4.2E-01	-0.5	8.2E-01	1.1	5.5E-01
ENSMUST00000113794	immunoglobulin superfamily, member 5 [Source:MGI Symbol;Acc:MGI:1919308]	D3YXH1		4.5	1.8E-04	5.3	1.3E-02	-0.7	6.8E-01	-0.5	6.4E-01
ENSMUST00000111791	WD repeat and HMG-box DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:2443514]	E9QPB3		2.5	2.8E-01	6.4	4.0E-02	2.8	2.7E-01	-1.2	5.8E-01
ENSMUST00000111792	WD repeat and HMG-box DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:2443514]			-0.3	8.9E-01	-3.3	3.4E-01	-2.2	3.0E-01	0.8	8.2E-01
ENSMUST00000111795	transmembrane protein 116 [Source:MGI Symbol;Acc:MGI:1924712]	Q8CA26		3.3	3.6E-02	1.8	2.8E-01	-1.3	3.5E-01	0.2	9.0E-01
ENSMUST00000111800	SH3 and PX domains 2A [Source:MGI Symbol;Acc:MGI:1298393]		O89032	2.0	4.7E-01	0.2	9.6E-01	0.6	8.5E-01	2.4	5.6E-01
ENSMUST00000113796	transmembrane BAX inhibitor motif containing 1 [Source:MGI Symbol;Acc:MGI:1916910]	Q3U717		7.5	4.7E-07	-4.2	4.2E-04	0.3	5.3E-01	-1.5	1.3E-01
ENSMUST00000111803	RecQ protein-like [Source:MGI Symbol;Acc:MGI:103021]		Q9Z129	1.4	5.3E-01	-0.4	9.0E-01	-0.1	9.8E-01	1.7	5.3E-01
ENSMUST00000113797	praja ring finger 1, E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1101765]	B1AXU3		-6.0	1.9E-05	4.5	1.8E-03	-3.3	2.3E-02	1.1	1.3E-01
ENSMUST00000113800	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 [Source:MGI Symbol;Acc:MGI:2136878]		Q9JI67	7.7	2.5E-05	6.3	1.4E-03	-0.5	7.3E-01	-3.2	8.8E-03
ENSMUST00000113802	predicted gene 5878 [Source:MGI Symbol;Acc:MGI:3647625]	E9PUB3		9.2	4.7E-06	5.7	5.5E-02	-0.6	8.3E-01	1.0	5.4E-01
ENSMUST00000113804	Leber congenital amaurosis 5-like [Source:MGI Symbol;Acc:MGI:3041157]	D3YXG9		6.4	8.6E-05	7.1	7.9E-03	-1.4	5.6E-01	1.4	2.8E-01
ENSMUST00000113805	paroxysmal nonkinesiogenic dyskinesia [Source:MGI Symbol;Acc:MGI:1930773]			-3.4	8.6E-03	6.5	7.9E-04	-0.7	6.2E-01	-0.2	7.8E-01
ENSMUST00000113811	Yip1 domain family, member 6 [Source:MGI Symbol;Acc:MGI:1925179]		Q8BR70	-4.9	9.8E-05	6.2	2.2E-05	-3.7	5.7E-03	0.3	5.9E-01
ENSMUST00000113814	protein phosphatase 1, regulatory subunit 18 [Source:MGI Symbol;Acc:MGI:1923698]		Q8BQ30	-7.8	8.3E-04	-3.2	6.0E-04	-0.3	3.6E-01	-0.6	4.0E-01
ENSMUST00000113820	actin related protein 2/3 complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1923959]		Q9CVB6	-8.6	8.0E-07	-5.0	3.1E-03	-0.7	2.7E-01	-1.7	2.8E-01
ENSMUST00000113821	dysferlin [Source:MGI Symbol;Acc:MGI:1349385]	E9QL12		6.8	1.1E-02	3.8	2.8E-04	0.4	5.1E-01	0.6	2.4E-01
ENSMUST00000113822	leucine rich repeat and fibronectin type III domain containing 4 [Source:MGI Symbol;Acc:MGI:2385612]		Q80XU8	4.3	3.5E-03	5.9	1.3E-03	-0.4	7.7E-01	-0.7	3.6E-01
ENSMUST00000111828	DDHD domain containing 1 [Source:MGI Symbol;Acc:MGI:2150302]	E9QQ38		1.6	4.3E-01	2.5	3.2E-01	0.8	6.7E-01	-0.1	9.8E-01
ENSMUST00000113823	dysferlin [Source:MGI Symbol;Acc:MGI:1349385]	E9Q423		7.1	2.7E-05	6.1	5.4E-04	-0.5	7.2E-01	-0.2	7.2E-01
ENSMUST00000113825	pyruvate carboxylase [Source:MGI Symbol;Acc:MGI:97520]	G5E8R3		5.2	4.0E-03	7.0	4.7E-04	-0.2	8.9E-01	-0.4	5.9E-01
ENSMUST00000113830	mediator complex subunit 27 [Source:MGI Symbol;Acc:MGI:1916225]		Q9DB40	8.3	2.2E-05	2.9	1.9E-02	-3.5	1.6E-02	-1.0	2.1E-01
ENSMUST00000111846	titin [Source:MGI Symbol;Acc:MGI:98864]	E9Q8N1		4.9	1.9E-01	6.8	1.3E-01	0.2	9.6E-01	-1.6	4.8E-01
ENSMUST00000111855	WW domain binding protein 1 like [Source:MGI Symbol;Acc:MGI:107577]		Q8BGW2	-3.8	2.3E-01	-5.4	1.6E-01	-2.5	1.7E-01	-1.0	8.1E-01
ENSMUST00000113835	zinc finger protein 638 [Source:MGI Symbol;Acc:MGI:1203484]		Q61464	-6.3	1.9E-04	8.2	1.7E-03	1.1	5.9E-01	0.5	5.9E-01
ENSMUST00000113837	adrenergic receptor kinase, beta 1 [Source:MGI Symbol;Acc:MGI:87940]	E9Q419		-2.2	3.1E-02	8.8	1.8E-05	-0.5	6.6E-01	-0.5	3.0E-01
ENSMUST00000113846	avian erythroblastosis virus E-26 (v-ets) oncogene related [Source:MGI Symbol;Acc:MGI:95415]		P81270	8.5	1.1E-03	-7.5	1.6E-03	1.5	1.4E-02	3.2	8.8E-02
ENSMUST00000113847	BarH-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1859288]		P63157	6.4	1.8E-04	-4.6	3.2E-02	-0.6	4.7E-01	-2.4	3.1E-01
ENSMUST00000113850	N-acetylglucosamine kinase [Source:MGI Symbol;Acc:MGI:1860418]	D3YXG2		4.6	9.1E-05	7.8	1.5E-04	-0.7	6.3E-01	-0.5	4.5E-01
ENSMUST00000111881	ar factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100 [Source:MGI Symbol;Acc:MGI:109	Q3UG25	Q9WTK5	-0.3	8.5E-01	0.0	1.0E+00	0.7	7.3E-01	0.4	8.5E-01
ENSMUST00000113858	potassium inwardly-rectifying channel, subfamily J, member 15 [Source:MGI Symbol;Acc:MGI:1310000]	Q3TNE6		7.8	9.0E-05	4.2	2.3E-02	-0.7	6.5E-01	1.6	1.6E-01
ENSMUST00000113862	potassium inwardly-rectifying channel, subfamily J, member 15 [Source:MGI Symbol;Acc:MGI:1310000]	Q3TNE6		8.8	4.3E-05	-2.6	4.8E-02	-0.3	6.3E-01	-0.2	8.6E-01
ENSMUST00000111890	lute carrier family 8 (sodium/lithium/calcium exchanger), member B1 [Source:MGI Symbol;Acc:MGI:218078		Q925Q3	1.3	4.0E-01	3.5	1.2E-01	1.9	3.4E-01	-0.4	7.8E-01
ENSMUST00000113865	ecombination signal binding protein for immunoglobulin kappa J region [Source:MGI Symbol;Acc:MGI:96522	Q3UM17	P31266	-4.3	6.0E-03	-7.2	8.4E-04	-1.4	4.9E-02	-1.3	4.5E-01
ENSMUST00000113867	tuberous sclerosis 1 [Source:MGI Symbol;Acc:MGI:1929183]		Q9EP53	-5.5	9.7E-03	-11.3	8.7E-05	0.3	4.9E-01	0.1	9.6E-01
ENSMUST00000111894	single-pass membrane protein with coiled-coil domains 3 [Source:MGI Symbol;Acc:MGI:2443451]		Q8BQM7	5.2	4.8E-02	5.0	5.5E-02	-1.8	4.9E-01	-1.6	3.4E-01
ENSMUST00000113879	histocompatibility 2, Q region locus 6 [Source:MGI Symbol;Acc:MGI:95935]	P79568		-7.5	2.4E-04	-4.4	5.2E-02	0.7	4.6E-01	-0.1	9.7E-01
ENSMUST00000111899	roxisome proliferative activated receptor, gamma, coactivator-related 1 [Source:MGI Symbol;Acc:MGI:238509		Q6NZN1	0.3	8.2E-01	-0.2	9.3E-01	2.8	1.3E-01	3.4	1.6E-01
ENSMUST00000113890	DIS3 mitotic control homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:2143272]		Q8C0S1	6.6	9.8E-04	8.3	5.5E-04	-1.7	3.9E-01	1.3	1.2E-01
ENSMUST00000113893	ral guanine nucleotide dissociation stimulator [Source:MGI Symbol;Acc:MGI:107485]	A2AK33		8.2	1.0E-04	7.9	5.0E-04	-0.8	6.3E-01	0.6	4.4E-01
ENSMUST00000113897	apolipoprotein O [Source:MGI Symbol;Acc:MGI:1915566]		Q9DCZ4	5.7	1.4E-02	7.2	3.6E-05	-0.4	6.9E-01	-0.4	5.0E-01
ENSMUST00000113900	solute carrier family 4, sodium bicarbonate cotransporter, member 5 [Source:MGI Symbol;Acc:MGI:2443220]	E9Q3M5		6.7	1.4E-04	5.2	2.2E-02	-0.8	7.1E-01	0.0	9.7E-01
ENSMUST00000113902	family with sequence similarity 90, member A1B [Source:MGI Symbol;Acc:MGI:1921682]	B1ASQ1		7.1	1.3E-04	-0.6	7.1E-01	2.2	5.6E-02	-0.6	6.8E-01
ENSMUST00000113907	dynactin 1 [Source:MGI Symbol;Acc:MGI:107745]	D3YXJ4		4.2	1.7E-04	-1.8	2.7E-02	0.9	4.6E-02	-0.2	7.9E-01
ENSMUST00000113918	dynactin 1 [Source:MGI Symbol;Acc:MGI:107745]		O08788	6.0	2.9E-02	4.1	3.0E-04	-3.3	4.8E-03	-0.5	3.6E-01
ENSMUST00000111917	family with sequence similarity 35, member A [Source:MGI Symbol;Acc:MGI:1922948]		Q3UEN2	-0.5	3.8E-01	-1.0	1.7E-01	-0.1	7.8E-01	0.4	5.7E-01
ENSMUST00000113920	olfactomedin 1 [Source:MGI Symbol;Acc:MGI:1860437]	A3KGE4		6.9	3.5E-03	-0.9	1.7E-01	0.6	1.5E-01	-0.1	9.1E-01
ENSMUST00000111922	G protein-coupled receptor, family C, group 5, member D [Source:MGI Symbol;Acc:MGI:1935037]	Q0VEL2	Q9JIL6	2.0	3.6E-01	1.5	5.6E-01	0.4	8.7E-01	0.9	6.8E-01
ENSMUST00000113926	zinc finger protein X-linked [Source:MGI Symbol;Acc:MGI:99211]	B1ASD1	P17012	-3.3	4.1E-03	5.4	3.0E-03	-0.6	6.9E-01	0.9	2.7E-01
ENSMUST00000113933	phosphate cytidylyltransferase 1, choline, beta isoform [Source:MGI Symbol;Acc:MGI:2147987]		Q811Q9	4.3	1.2E-02	6.0	2.0E-04	-0.6	5.6E-01	-0.1	9.0E-01
ENSMUST00000111936	beta-transducin repeat containing protein [Source:MGI Symbol;Acc:MGI:1338871]		Q3ULA2	8.7	5.2E-02	2.6	2.9E-01	-6.9	9.6E-02	-0.8	7.0E-01
ENSMUST00000113938	mitochondrial ribosomal protein L53 [Source:MGI Symbol;Acc:MGI:1915749]		Q9D1H8	-5.6	1.5E-04	-4.3	3.0E-02	-1.6	9.2E-02	-0.8	6.6E-01
ENSMUST00000111945	mitogen-activated protein kinase 8 [Source:MGI Symbol;Acc:MGI:1346861]	Q544A0	Q91Y86	0.5	4.4E-01	1.3	1.0E-01	0.0	9.9E-01	-0.8	2.4E-01
ENSMUST00000111948	Kazal-type serine peptidase inhibitor domain 1 [Source:MGI Symbol;Acc:MGI:2147606]		Q8BJ66	3.1	1.0E-01	5.4	7.2E-02	2.1	4.2E-01	-0.2	9.0E-01
ENSMUST00000113940	sperm associated antigen 16 [Source:MGI Symbol;Acc:MGI:1913972]		Q8K450	10.6	5.2E-04	5.9	1.5E-03	-0.6	6.9E-01	0.2	8.4E-01
ENSMUST00000113941	bromodomain containing 3 [Source:MGI Symbol;Acc:MGI:1914632]	Q5CCJ9	Q8K2F0	-3.5	2.4E-02	2.5	9.1E-02	0.5	7.1E-01	1.3	2.2E-01
ENSMUST00000111954	sideroflexin 3 [Source:MGI Symbol;Acc:MGI:2137679]		Q91V61	3.7	2.3E-01	-0.9	8.5E-01	-1.9	5.6E-01	2.7	5.3E-01
ENSMUST00000111955	Rho GTPase activating protein 22 [Source:MGI Symbol;Acc:MGI:2443418]	D3Z1Y5		3.1	3.8E-02	2.1	1.1E-01	-2.7	5.8E-02	-1.7	1.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000113952	WD repeat domain 5 [Source:MGI Symbol;Acc:MGI:2155884]		P61965	-3.4	2.8E-04	0.2	8.9E-01	-5.1	8.3E-03	1.8	1.8E-01
ENSMUST00000113955	melanoma antigen family B, 18 [Source:MGI Symbol;Acc:MGI:3045344]	Q8BQR7		7.1	3.5E-05	-4.8	1.7E-03	0.7	1.8E-01	-1.0	4.4E-01
ENSMUST00000111959	WD repeat and SOCS box-containing 2 [Source:MGI Symbol;Acc:MGI:2144041]	E9Q8J9		1.3	5.7E-01	2.2	3.8E-01	-0.7	7.5E-01	-1.6	5.1E-01
ENSMUST00000111961	heterogeneous nuclear ribonucleoprotein A3 [Source:MGI Symbol;Acc:MGI:1917171]	A2AL12		0.3	9.2E-01	-4.7	2.6E-01	-4.6	6.1E-02	0.3	9.4E-01
ENSMUST00000113956	runt related transcription factor 1 [Source:MGI Symbol;Acc:MGI:99852]	G3X9W7		-2.5	3.2E-02	-2.1	1.6E-02	-0.1	9.0E-01	-0.4	5.4E-01
ENSMUST00000111963	ets variant 6 [Source:MGI Symbol;Acc:MGI:109336]	E9Q8J8		0.0	9.7E-01	-1.6	5.0E-01	1.1	5.3E-01	2.6	1.8E-01
ENSMUST00000111964	heterogeneous nuclear ribonucleoprotein A3 [Source:MGI Symbol;Acc:MGI:1917171]	Q5FB19	Q8BG05	2.0	3.2E-01	0.8	6.6E-01	-3.0	1.1E-01	-1.8	3.3E-01
ENSMUST00000113966	interleukin 1 receptor accessory protein-like 1 [Source:MGI Symbol;Acc:MGI:2687319]	B1ASU0		6.7	1.2E-04	-4.8	5.3E-03	0.5	4.9E-01	0.3	8.3E-01
ENSMUST00000113968	suppressor of variegation 4-20 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444557]		Q3U8K7	1.8	3.1E-02	2.4	4.6E-01	-0.8	7.7E-01	4.5	8.7E-02
ENSMUST00000113973	suppressor of variegation 4-20 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444557]		Q3U8K7	-5.9	1.1E-02	4.8	3.5E-02	-0.7	7.3E-01	-0.4	7.8E-01
ENSMUST00000111975	TAO kinase 3 [Source:MGI Symbol;Acc:MGI:3041177]	Q3V3K3		1.1	6.2E-01	-2.4	3.6E-01	-3.4	7.8E-02	0.0	9.9E-01
ENSMUST00000113975	solute carrier family 5 (inositol transporters), member 3 [Source:MGI Symbol;Acc:MGI:1858226]		Q9JKZ2	5.9	4.7E-06	-5.1	1.1E-02	-2.5	1.3E-02	-2.3	2.4E-01
ENSMUST00000111977	complement component factor h [Source:MGI Symbol;Acc:MGI:88385]	E9Q8H9		-1.7	5.9E-01	-4.6	3.1E-01	-2.4	3.2E-01	0.5	9.1E-01
ENSMUST00000111978	TAO kinase 3 [Source:MGI Symbol;Acc:MGI:3041177]		Q8BYC6	-1.8	3.3E-01	-3.6	1.6E-01	-0.1	9.7E-01	1.7	4.9E-01
ENSMUST00000113979	LanC (bacterial lantibiotic synthetase component C)-like 1 [Source:MGI Symbol;Acc:MGI:1336997]		O89112	2.9	5.4E-04	6.0	3.9E-02	-0.8	7.8E-01	-0.9	5.7E-01
ENSMUST00000113991	dystrophin, muscular dystrophy [Source:MGI Symbol;Acc:MGI:94909]	A2A9Z2		7.9	6.6E-05	4.6	1.5E-02	-0.5	7.7E-01	0.9	3.7E-01
ENSMUST00000111985	Sec31 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2685187]		Q3TZ89	2.9	2.3E-01	1.7	6.2E-01	-0.3	8.9E-01	0.9	7.4E-01
ENSMUST00000113997	protein phosphatase 6, regulatory subunit 3 [Source:MGI Symbol;Acc:MGI:1921807]	G5E8R4		-8.5	4.8E-06	-7.1	1.2E-04	-0.4	4.3E-01	-2.0	1.7E-01
ENSMUST00000114000	dystrophin, muscular dystrophy [Source:MGI Symbol;Acc:MGI:94909]		P11531	6.9	8.7E-05	-3.4	2.6E-02	1.1	1.3E-01	-2.6	1.5E-01
ENSMUST00000114002	intersectin 1 (SH3 domain protein 1A) [Source:MGI Symbol;Acc:MGI:1338069]		Q9Z0R4	7.7	9.7E-07	6.4	1.3E-04	-0.6	6.1E-01	-0.8	1.9E-01
ENSMUST00000111999	protein kinase, AMP-activated, beta 1 non-catalytic subunit [Source:MGI Symbol;Acc:MGI:1336167]	Q542K0	Q9R078	-0.1	9.7E-01	5.8	9.2E-03	4.2	2.6E-02	-1.6	2.3E-01
ENSMUST00000114007	calcium channel flower domain containing 1 [Source:MGI Symbol;Acc:MGI:1924317]		Q8BG21	1.8	1.6E-02	-2.2	1.7E-02	-0.4	4.6E-01	-0.3	7.0E-01
ENSMUST00000112001	diphthamine biosynthesis 3 [Source:MGI Symbol;Acc:MGI:1922658]	E9PZC5		-1.6	5.0E-01	-2.5	4.6E-01	-0.6	7.7E-01	0.3	9.2E-01
ENSMUST00000112007	activating transcription factor 2 [Source:MGI Symbol;Acc:MGI:109349]	Q543G2	P16951	-2.4	1.7E-01	-2.4	3.0E-01	-0.6	6.9E-01	-0.6	7.8E-01
ENSMUST00000114011	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:90676]	Q3U9X2	O35900	-4.0	3.3E-02	-3.3	1.2E-01	2.4	2.9E-02	-1.2	5.8E-01
ENSMUST00000112016	activating transcription factor 2 [Source:MGI Symbol;Acc:MGI:109349]	Q640L6	P16951	-3.9	5.0E-02	-3.6	1.7E-01	0.7	6.5E-01	0.3	8.9E-01
ENSMUST00000112017	activating transcription factor 2 [Source:MGI Symbol;Acc:MGI:109349]		P16951	-1.7	5.6E-01	-2.8	4.5E-01	-1.4	4.8E-01	-0.3	9.4E-01
ENSMUST00000114013	microtubule-associated protein 2 [Source:MGI Symbol;Acc:MGI:97175]		P20357	8.1	8.0E-06	-9.1	4.8E-06	0.1	7.2E-01	-0.4	6.5E-01
ENSMUST00000114020	REX4, RNA exonuclease 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2684957]		Q6PAQ4	-1.3	2.4E-02	6.6	9.1E-05	-1.6	1.8E-01	-0.8	1.8E-01
ENSMUST00000114021	predicted gene 7173 [Source:MGI Symbol;Acc:MGI:3645063]	B1AXF0		6.5	3.8E-04	-7.7	5.2E-03	0.3	6.8E-01	2.8	2.1E-01
ENSMUST00000112036				-2.3	7.0E-02	-2.7	1.4E-01	0.8	3.9E-01	1.2	4.8E-01
ENSMUST00000114023	crystallin, zeta (quinone reductase)-like 1 [Source:MGI Symbol;Acc:MGI:1913859]		Q921W4	-2.7	9.9E-03	7.5	9.7E-05	-0.2	9.0E-01	-0.2	6.8E-01
ENSMUST00000112044	G protein-coupled receptor 155 [Source:MGI Symbol;Acc:MGI:1915776]	A2AWR2		3.1	1.2E-01	4.8	1.8E-02	-3.2	1.2E-01	-4.9	6.1E-03
ENSMUST00000112046	zinc finger protein 281 [Source:MGI Symbol;Acc:MGI:3029290]		Q99LI5	0.1	9.7E-01	2.0	3.9E-01	1.0	6.1E-01	-0.9	6.0E-01
ENSMUST00000114033	euchromatic histone lysine N-methyltransferase 2 [Source:MGI Symbol;Acc:MGI:2148922]		Q9Z148	-5.0	1.1E-02	-2.6	4.6E-02	0.2	8.0E-01	0.2	8.7E-01
ENSMUST00000112050	secernin 3 [Source:MGI Symbol;Acc:MGI:1921866]	A2AWQ9		1.4	1.4E-01	-0.1	9.6E-01	0.2	8.0E-01	1.7	1.5E-01
ENSMUST00000114036	Son DNA binding protein [Source:MGI Symbol;Acc:MGI:98353]		Q9QX47	-2.8	1.7E-03	-6.4	5.0E-03	0.1	8.6E-01	-0.1	9.4E-01
ENSMUST00000114040	dynein, axonemal, heavy chain 6 [Source:MGI Symbol;Acc:MGI:107744]	E9Q3H7		4.7	9.4E-04	-6.9	5.9E-03	0.8	3.6E-01	-1.5	5.2E-01
ENSMUST00000114043	surfeit gene 6 [Source:MGI Symbol;Acc:MGI:98447]	A2ALA0		3.6	4.5E-04	7.1	1.5E-04	-0.6	6.6E-01	0.5	3.7E-01
ENSMUST00000112066	sirtuin 4 [Source:MGI Symbol;Acc:MGI:1922637]		Q8R216	2.8	1.9E-01	4.4	1.4E-01	1.0	7.2E-01	-0.6	7.5E-01
ENSMUST00000112068	calcium channel, voltage-dependent, L type, alpha 1S subunit [Source:MGI Symbol;Acc:MGI:88294]	E9QPX8		4.4	1.9E-01	5.2	1.6E-01	-0.3	9.4E-01	-1.1	6.1E-01
ENSMUST00000112070	collagen, type VII, alpha 1 [Source:MGI Symbol;Acc:MGI:88462]		Q63870	4.5	1.5E-01	9.0	1.5E-02	-0.3	9.4E-01	-4.8	1.3E-02
ENSMUST00000114044	protein kinase, X-linked [Source:MGI Symbol;Acc:MGI:1309999]	B1AVU1		2.9	7.6E-03	8.6	3.2E-05	-0.5	7.0E-01	-0.4	3.9E-01
ENSMUST00000112076	C-type lectin domain family 7, member a [Source:MGI Symbol;Acc:MGI:1861431]		Q6QLQ4	0.9	7.0E-01	-0.1	9.7E-01	-0.7	7.6E-01	0.3	9.2E-01
ENSMUST00000114045	e A, alpha 1-3-N-acetylgalactosaminyltransferase, transferase B, alpha 1-3-galactosyltransferase) [Source:MGI	Z4YLB0		5.8	2.1E-04	-6.6	6.6E-05	-0.1	8.4E-01	-0.6	5.7E-01
ENSMUST00000114047	F-box and leucine-rich repeat protein 5 [Source:MGI Symbol;Acc:MGI:2152883]		Q8C2S5	-12.2	2.9E-06	-4.5	2.0E-03	0.0	9.9E-01	0.0	9.7E-01
ENSMUST00000112092	polybromo 1 [Source:MGI Symbol;Acc:MGI:1923998]	D3Z1N4		-1.4	5.3E-01	-1.6	6.3E-01	0.0	9.9E-01	0.2	9.6E-01
ENSMUST00000112094	polybromo 1 [Source:MGI Symbol;Acc:MGI:1923998]		Q8BSQ9	-1.9	1.1E-01	0.8	5.9E-01	2.4	3.8E-02	-0.3	8.2E-01
ENSMUST00000114050	thymosin, beta 10 [Source:MGI Symbol;Acc:MGI:109146]	A6H6H4	Q6ZWY8	-8.9	2.3E-05	-1.8	8.3E-03	0.8	3.8E-02	-0.4	4.7E-01
ENSMUST00000114053	transcription factor 7 like 1 (T cell specific, HMG box) [Source:MGI Symbol;Acc:MGI:1202876]	A1A549		6.1	1.3E-03	-7.8	3.9E-05	1.4	2.4E-03	0.1	9.3E-01
ENSMUST00000112097	ring finger protein 10 [Source:MGI Symbol;Acc:MGI:1859162]	D3Z1N2		0.1	7.2E-01	0.8	1.9E-01	0.8	7.8E-02	0.2	7.4E-01
ENSMUST00000112099				-2.0	5.2E-01	-3.7	3.4E-01	-2.1	3.1E-01	-0.4	9.3E-01
ENSMUST00000114065	cytoplasmic polyadenylation element binding protein 2 [Source:MGI Symbol;Acc:MGI:2442640]	A0A0H2UH22		-7.1	9.4E-04	-0.6	6.8E-01	-6.5	1.3E-03	0.6	6.1E-01
ENSMUST00000112115	holocytochrome c synthetase [Source:MGI Symbol;Acc:MGI:106911]		P53702	-1.5	1.2E-01	-0.3	7.5E-01	-0.3	7.3E-01	-1.4	1.8E-01
ENSMUST00000112121	malectin [Source:MGI Symbol;Acc:MGI:1924015]	D3Z1M3	Q6ZQI3	-0.1	8.3E-01	6.4	6.2E-04	7.3	1.4E-04	0.7	2.9E-01
ENSMUST00000112122	histone aminotransferase 1 [Source:MGI Symbol;Acc:MGI:96013]	A2ATU9		-0.7	7.0E-01	1.8	3.5E-01	0.3	8.4E-01	-2.1	2.3E-01
ENSMUST00000114071	capping protein (actin filament), gelsolin-like [Source:MGI Symbol;Acc:MGI:1098259]	Q99LB4		-5.2	2.7E-04	5.6	4.9E-02	-0.6	8.3E-01	-0.1	9.5E-01
ENSMUST00000114085	coagulation factor VIII [Source:MGI Symbol;Acc:MGI:88383]	B2RRC9		4.3	5.3E-03	6.8	2.8E-05	0.2	8.3E-01	-0.3	5.0E-01
ENSMUST00000114086	Kruppel-like factor 7 (ubiquitous) [Source:MGI Symbol;Acc:MGI:1935151]		Q99JB0	-3.1	3.0E-04	-0.2	9.1E-01	-4.0	6.3E-02	2.6	9.7E-02
ENSMUST00000114091	membrane protein, palmitoylated [Source:MGI Symbol;Acc:MGI:105941]	A2AN84		-8.1	1.9E-04	-6.9	6.3E-04	-0.4	4.5E-01	1.7	2.5E-01
ENSMUST00000114092	membrane protein, palmitoylated [Source:MGI Symbol;Acc:MGI:105941]	B7ZCL8		-9.3	2.8E-06	-7.1	3.6E-04	0.2	6.0E-01	-1.1	4.6E-01
ENSMUST00000114093	peptidase (mitochondrial processing) alpha [Source:MGI Symbol;Acc:MGI:1918568]	A2AIW9		3.2	2.1E-04	-3.9	8.2E-03	0.4	4.8E-01	-0.9	4.7E-01
ENSMUST00000114094	malate dehydrogenase 1B, NAD (soluble) [Source:MGI Symbol;Acc:MGI:1923918]		Q5F204	5.7	1.7E-03	1.9	2.4E-01	-3.1	1.0E-01	0.6	6.3E-01
ENSMUST00000112143	2'-5' oligoadenylate synthetase-like 1 [Source:MGI Symbol;Acc:MGI:2180849]		Q8VI94	-2.7	1.6E-01	-2.8	2.7E-01	-0.4	7.7E-01	-0.3	9.0E-01
ENSMUST00000112146	FERM and PDZ domain containing 4 [Source:MGI Symbol;Acc:MGI:3042378]		A2AFR3	5.7	6.6E-02	5.5	9.5E-02	-0.7	8.3E-01	-0.5	7.9E-01
ENSMUST00000114106	Ly1 antibody reactive clone [Source:MGI Symbol;Acc:MGI:107470]		Q08288	-3.8	2.6E-03	6.5	1.6E-02	-0.7	7.8E-01	-1.1	4.2E-01
ENSMUST00000114109	growth factor receptor bound protein 2-associated protein 3 [Source:MGI Symbol;Acc:MGI:2387324]	Q3V3J9		5.9	8.5E-05	-3.7	1.5E-02	0.2	8.0E-01	-0.4	7.4E-01
ENSMUST00000114113	zinc finger and BTB domain containing 49 [Source:MGI Symbol;Acc:MGI:1922329]	E9Q2Y5		2.3	1.5E-02	7.7	1.2E-04	0.8	5.4E-01	-0.4	4.9E-01
ENSMUST00000114116	predicted gene 5936 [Source:MGI Symbol;Acc:MGI:3645575]	A2BG95		5.3	7.6E-05	-3.3	2.1E-02	0.1	8.8E-01	-3.3	5.1E-02
ENSMUST00000114119	predicted gene 5640 [Source:MGI Symbol;Acc:MGI:3645126]	A3KG49		7.7	5.2E-05	4.4	2.4E-03	-0.7	4.9E-01	-0.2	8.3E-01
ENSMUST00000112160	RIKEN cDNA 1500011B03 gene [Source:MGI Symbol;Acc:MGI:1913486]	Q3V495		-1.4	5.8E-02	-0.2	8.5E-01	0.3	6.0E-01	-1.0	2.5E-01
ENSMUST00000114127	inhibitor of kappaB kinase gamma [Source:MGI Symbol;Acc:MGI:1338074]		O88522	-4.2	4.1E-03	-1.0	6.8E-01	4.5	1.1E-02	-1.5	5.6E-01
ENSMUST00000114143	family with sequence similarity 3, member A [Source:MGI Symbol;Acc:MGI:1913544]		Q9D8T0	-1.6	2.3E-02	6.5	5.8E-04	-0.4	7.5E-01	-0.4	6.2E-01
ENSMUST00000114151	inner membrane protein, mitochondrial [Source:MGI Symbol;Acc:MGI:1923864]		Q8CAQ8	-7.1	7.4E-06	5.9	5.0E-03	0.0	9.9E-01	-0.5	5.7E-01
ENSMUST00000112164	toll-like receptor 7 [Source:MGI Symbol;Acc:MGI:2176882]	Q548J0	P58681	-0.7	7.7E-01	-0.6	8.0E-01	-1.7	3.6E-01	-1.8	4.7E-01
ENSMUST00000114153	L antigen family, member 3 [Source:MGI Symbol;Acc:MGI:1913442]	J3JS94		5.7	1.8E-04	6.9	1.9E-04	-0.6	6.2E-01	0.3	6.4E-01
ENSMUST00000114154	Ellis van Creveld gene syndrome [Source:MGI Symbol;Acc:MGI:1890596]	D3YUJ0		5.9	6.5E-04	-8.0	4.3E-05	0.3	3.5E-01	-0.8	5.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000114155	neuropilin 2 [Source:MGI Symbol;Acc:MGI:1100492]	Q3U5I8	O35375	1.8	4.9E-03	7.1	2.4E-04	-0.7	6.0E-01	-1.6	4.9E-02
ENSMUST00000114157	neuropilin 2 [Source:MGI Symbol;Acc:MGI:1100492]		O35375	6.4	2.1E-03	-9.5	1.7E-07	-0.3	2.9E-01	-1.7	3.3E-02
ENSMUST00000114159	cleus accumbens associated 2, BEN and BTB (POZ) domain containing [Source:MGI Symbol;Acc:MGI:19152		Q9DCM7	8.1	9.1E-04	2.1	1.4E-02	-2.5	5.5E-03	-0.2	7.7E-01
ENSMUST00000114160	family with sequence similarity 50, member A [Source:MGI Symbol;Acc:MGI:1351626]		Q9WV03	-7.1	1.0E-05	-4.6	4.7E-02	0.1	9.0E-01	-0.2	9.1E-01
ENSMUST00000114167	calmodulin regulated spectrin-associated protein 1 [Source:MGI Symbol;Acc:MGI:3036242]	A0A0A0MQE5		3.9	1.5E-03	-6.4	4.2E-03	0.7	3.8E-01	-1.5	4.5E-01
ENSMUST00000112177	Scm-like with four mbt domains 1 [Source:MGI Symbol;Acc:MGI:1859609]		Q9JMD1	1.6	4.9E-01	1.3	5.1E-01	-2.5	2.1E-01	-2.2	3.2E-01
ENSMUST00000114174	cysteine and tyrosine-rich protein 1 [Source:MGI Symbol;Acc:MGI:2152187]		Q8VIH7	6.7	2.4E-05	-0.1	9.7E-01	5.0	8.9E-03	0.4	8.5E-01
ENSMUST00000112183	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]	D3Z1I2		-4.7	6.1E-02	-1.6	6.9E-01	3.9	1.1E-01	0.8	8.3E-01
ENSMUST00000114176	potassium channel, subfamily T, member 1 [Source:MGI Symbol;Acc:MGI:1924627]	A2AHB7		8.7	7.5E-06	3.7	9.6E-02	0.5	7.5E-01	1.8	2.5E-01
ENSMUST00000114179	ring finger protein 103 [Source:MGI Symbol;Acc:MGI:109483]		Q9R1W3	-2.8	1.6E-02	-4.0	6.0E-02	0.9	3.8E-01	0.2	9.3E-01
ENSMUST00000112188	ription elongation factor A (SII) N-terminal and central domain containing [Source:MGI Symbol;Acc:MGI:268		Q3US16	0.1	8.4E-01	0.9	2.8E-01	1.1	9.9E-02	0.3	6.9E-01
ENSMUST00000114180	tafazzin [Source:MGI Symbol;Acc:MGI:109626]	I7HJS2		-4.1	5.0E-03	3.9	7.8E-02	-0.9	6.5E-01	1.4	3.5E-01
ENSMUST00000114184	GA repeat binding protein, alpha [Source:MGI Symbol;Acc:MGI:95610]		Q00422	-5.5	5.6E-04	-4.9	4.9E-04	-1.4	9.3E-03	-0.9	3.9E-01
ENSMUST00000112194	trafficking protein particle complex 2 [Source:MGI Symbol;Acc:MGI:1913476]	Q5J9A9	Q9CQP2	-3.3	1.0E-01	2.4	3.0E-01	3.1	1.4E-01	-2.6	1.9E-01
ENSMUST00000114191	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F [Source:MGI Symbol;Acc:MGI:107777]		P97450	-3.4	9.5E-03	4.5	1.8E-04	-0.6	4.0E-01	0.1	9.1E-01
ENSMUST00000114192	odorant binding protein 2B [Source:MGI Symbol;Acc:MGI:3651927]	A2BHR0		6.3	1.7E-04	-2.7	7.4E-03	0.8	1.0E-01	-0.4	6.0E-01
ENSMUST00000112199				3.0	6.5E-02	2.4	2.6E-01	0.1	9.6E-01	0.8	6.0E-01
ENSMUST00000112200	deoxynucleotidyltransferase, terminal [Source:MGI Symbol;Acc:MGI:98659]	Q3UZ80	P09838	-0.2	8.7E-01	2.7	5.4E-02	-1.9	1.5E-01	-4.8	6.1E-03
ENSMUST00000114195	junction adhesion molecule 2 [Source:MGI Symbol;Acc:MGI:1933820]		Q9JI59	4.6	4.9E-05	-3.5	4.5E-02	0.7	3.6E-01	0.7	6.6E-01
ENSMUST00000112203	protein kinase C, delta [Source:MGI Symbol;Acc:MGI:97598]	Q1MX41		-1.1	1.2E-01	-0.7	4.0E-01	-0.2	7.7E-01	-0.5	5.0E-01
ENSMUST00000112205	golgi reassembly stacking protein 2 [Source:MGI Symbol;Acc:MGI:2135962]	A2ATI6		2.3	2.2E-01	1.5	5.7E-01	-0.4	8.6E-01	0.5	8.2E-01
ENSMUST00000114217	predicted gene 996 [Source:MGI Symbol;Acc:MGI:2685842]		A2AJA9	7.7	1.2E-02	-7.6	1.2E-02	1.6	5.7E-02	0.8	7.7E-01
ENSMUST00000114218	DNA segment, Chr 16, ERATO Doi 472, expressed [Source:MGI Symbol;Acc:MGI:1196400]		Q9D7G4	-3.2	1.7E-02	-2.3	2.2E-01	1.0	4.0E-01	-0.4	8.1E-01
ENSMUST00000114224	guanine nucleotide binding protein (G protein), gamma 12 [Source:MGI Symbol;Acc:MGI:1336171]		Q9DAS9	-6.5	1.4E-04	-8.7	2.4E-05	1.2	2.0E-03	0.0	1.0E+00
ENSMUST00000112212	glycolipid transfer protein [Source:MGI Symbol;Acc:MGI:1929253]	D3Z1H9		3.1	1.5E-01	1.7	5.9E-01	0.7	7.2E-01	2.1	4.6E-01
ENSMUST00000114227	guanine nucleotide binding protein (G protein), gamma 12 [Source:MGI Symbol;Acc:MGI:1336171]		Q9DAS9	-8.0	5.4E-05	6.9	6.7E-04	-0.6	6.8E-01	0.7	3.8E-01
ENSMUST00000114228	guanine nucleotide binding protein (G protein), gamma 12 [Source:MGI Symbol;Acc:MGI:1336171]		Q9DAS9	-7.5	8.0E-06	7.1	1.2E-02	-0.7	7.7E-01	-2.0	1.6E-01
ENSMUST00000112220	RAD51 associated protein 1 [Source:MGI Symbol;Acc:MGI:1098224]			2.0	1.8E-01	1.4	3.8E-01	-1.7	2.5E-01	-1.0	4.6E-01
ENSMUST00000114229	coxsackie virus and adenovirus receptor [Source:MGI Symbol;Acc:MGI:1201679]		P97792	3.8	2.8E-03	-2.0	8.2E-02	0.7	2.9E-01	-0.6	6.0E-01
ENSMUST00000112232	kelch-like 12 [Source:MGI Symbol;Acc:MGI:2385619]		Q8BZM0	0.7	8.4E-01	-1.7	7.2E-01	-1.5	6.1E-01	0.8	8.6E-01
ENSMUST00000114233	HtrA serine peptidase 3 [Source:MGI Symbol;Acc:MGI:1925808]		Q9D236	6.9	9.1E-05	-6.1	6.4E-03	0.6	4.3E-01	-0.9	6.3E-01
ENSMUST00000114234	TNF receptor-associated factor 2 [Source:MGI Symbol;Acc:MGI:101835]		P39429	-6.4	1.6E-04	-3.3	2.3E-03	1.2	1.5E-02	0.6	4.5E-01
ENSMUST00000114239	SAM domain, SH3 domain and nuclear localization signals, 1 [Source:MGI Symbol;Acc:MGI:1914992]		P57725	-9.2	2.7E-05	4.2	3.3E-02	-2.0	3.2E-01	-0.4	7.4E-01
ENSMUST00000114243	predicted gene 973 [Source:MGI Symbol;Acc:MGI:2685819]	E9Q295		6.2	6.2E-05	6.5	8.6E-05	-1.8	1.5E-01	-1.3	7.8E-02
ENSMUST00000112244	neurotrophin 3 [Source:MGI Symbol;Acc:MGI:97380]	Q3V1A4		1.7	7.9E-02	-0.5	7.3E-01	1.4	2.0E-01	3.6	2.7E-02
ENSMUST00000114244	heat shock protein 70 family, member 13 [Source:MGI Symbol;Acc:MGI:1309463]	D3Z0Y0		-4.0	2.9E-02	-4.6	7.9E-04	0.2	7.1E-01	-2.4	6.2E-02
ENSMUST00000112248	motile sperm domain containing 2 [Source:MGI Symbol;Acc:MGI:1924013]		Q9CWP6	-2.0	8.6E-02	-4.1	9.9E-03	-2.4	7.8E-03	-0.2	9.1E-01
ENSMUST00000112249	calcium channel, voltage-dependent, L type, alpha 1D subunit [Source:MGI Symbol;Acc:MGI:88293]		Q99246	2.6	4.4E-01	4.6	1.7E-01	-0.4	9.0E-01	-2.4	3.5E-01
ENSMUST00000114246	frizzled homolog 7 (Drosophila) [Source:MGI Symbol;Acc:MGI:108570]		Q61090	1.5	2.9E-02	0.0	9.8E-01	0.5	6.7E-01	3.1	5.5E-02
ENSMUST00000114247	leucine rich repeat and Ig domain containing 1 [Source:MGI Symbol;Acc:MGI:1915522]		Q9D1T0	6.6	3.3E-04	-2.8	4.1E-03	0.0	9.5E-01	-0.9	2.6E-01
ENSMUST00000114249	RNA binding motif protein 11 [Source:MGI Symbol;Acc:MGI:2447622]	H9KUZ7		6.2	3.0E-02	5.4	3.9E-02	-0.7	7.7E-01	-0.8	5.8E-01
ENSMUST00000114261	cDNA sequence BC029214 [Source:MGI Symbol;Acc:MGI:2442831]		Q8K0Y7	-4.3	1.2E-02	6.0	1.9E-03	0.0	9.8E-01	1.0	2.5E-01
ENSMUST00000114275	embrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4) [Source:MGI Symbol;Acc:MGI:238668	D3Z0G8		4.6	3.5E-03	4.7	1.2E-01	-0.5	8.7E-01	2.1	2.2E-01
ENSMUST00000114276	reticulocalbin 2 [Source:MGI Symbol;Acc:MGI:1349765]		Q8BP92	-5.1	1.9E-03	4.8	8.3E-05	0.3	6.4E-01	0.1	8.6E-01
ENSMUST00000114278	fucosyltransferase 7 [Source:MGI Symbol;Acc:MGI:107692]	Q3SWS0	Q11131	-5.0	2.4E-03	4.0	1.7E-03	1.5	9.3E-02	-0.1	8.1E-01
ENSMUST00000112263	BMX non-receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:1101778]	B1AUL5	P97504	-1.3	6.9E-01	-5.2	3.1E-01	-2.4	3.0E-01	1.5	7.6E-01
ENSMUST00000114284	regulator of G-protein signaling 12 [Source:MGI Symbol;Acc:MGI:1918979]	D3Z0G6		7.7	6.6E-04	-6.1	8.3E-04	-0.6	3.2E-01	-0.8	5.4E-01
ENSMUST00000114292	cell adhesion molecule 2 [Source:MGI Symbol;Acc:MGI:2442722]		Q8BLQ9	9.7	4.2E-06	-4.7	7.6E-05	-0.7	7.3E-02	-0.7	3.2E-01
ENSMUST00000112275	uracil DNA glycosylase [Source:MGI Symbol;Acc:MGI:109352]	D3Z1G1		3.9	6.3E-02	3.6	1.6E-01	0.4	8.5E-01	0.7	6.9E-01
ENSMUST00000112289	inc finger (CCCH type), RNA binding motif and serine/arginine rich 2 [Source:MGI Symbol;Acc:MGI:103287	B1B0E8		1.0	1.0E-01	0.7	3.8E-01	0.4	5.1E-01	0.7	3.3E-01
ENSMUST00000112292	D-amino acid oxidase [Source:MGI Symbol;Acc:MGI:94859]			5.1	4.3E-02	3.2	2.2E-01	-0.7	7.9E-01	1.3	4.6E-01
ENSMUST00000114309	CASP8 and FADD-like apoptosis regulator [Source:MGI Symbol;Acc:MGI:1336166]	Q5U4G3		-3.2	1.4E-02	-2.8	1.6E-02	0.7	2.3E-01	-0.6	5.5E-01
ENSMUST00000112295	GDP-mannose pyrophosphorylase B [Source:MGI Symbol;Acc:MGI:2660880]		Q8BTZ7	1.9	5.1E-02	1.5	1.9E-01	-0.3	7.2E-01	0.1	9.0E-01
ENSMUST00000112298	slingshot homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2686240]		Q76I79	-0.9	7.5E-01	-0.5	9.0E-01	0.9	6.8E-01	0.6	8.9E-01
ENSMUST00000114314	glutamate receptor, ionotropic, NMDA1 (zeta 1) [Source:MGI Symbol;Acc:MGI:95819]	A2AI17		6.0	3.4E-02	-5.7	3.9E-03	0.9	1.3E-01	-0.3	8.5E-01
ENSMUST00000112302	cytidine 5'-triphosphate synthase 2 [Source:MGI Symbol;Acc:MGI:1933185]		P70303	0.0	9.8E-01	1.4	4.2E-01	-0.3	8.5E-01	-1.6	3.1E-01
ENSMUST00000114323	kelch repeat and BTB (POZ) domain containing 2 [Source:MGI Symbol;Acc:MGI:2384811]	G3X9X1		-4.1	1.4E-02	-1.5	8.9E-02	-0.6	3.2E-01	-2.3	3.6E-02
ENSMUST00000112304	protein phosphatase 1B, magnesium dependent, beta isoform [Source:MGI Symbol;Acc:MGI:101841]	Q546R1	P36993	-0.9	1.2E-01	-0.6	4.6E-01	1.0	6.6E-02	0.7	3.4E-01
ENSMUST00000112307	protein phosphatase 1B, magnesium dependent, beta isoform [Source:MGI Symbol;Acc:MGI:101841]		P36993	-2.3	8.5E-02	-2.2	2.2E-01	0.2	8.7E-01	0.0	9.8E-01
ENSMUST00000114327	phosphodiesterase 1C [Source:MGI Symbol;Acc:MGI:108413]		Q64338	4.9	2.4E-02	1.7	6.7E-02	-0.6	4.1E-01	1.2	1.1E-01
ENSMUST00000114329	major facilitator superfamily domain containing 10 [Source:MGI Symbol;Acc:MGI:1915544]		Q9D2V8	-3.9	2.4E-02	2.3	1.8E-03	-0.1	9.0E-01	-0.4	4.1E-01
ENSMUST00000114331	major facilitator superfamily domain containing 10 [Source:MGI Symbol;Acc:MGI:1915544]		Q9D2V8	-4.7	8.5E-04	-3.1	6.1E-02	-0.2	8.1E-01	-3.3	1.1E-01
ENSMUST00000114335	adducin 1 (alpha) [Source:MGI Symbol;Acc:MGI:87918]	E9Q1K3		-1.5	7.8E-03	4.1	1.9E-03	-0.9	3.4E-01	-0.2	7.4E-01
ENSMUST00000112318	ADP-ribosylation factor 4 [Source:MGI Symbol;Acc:MGI:99433]	E9Q798		-2.1	5.1E-01	-0.7	8.8E-01	1.7	5.7E-01	0.3	9.4E-01
ENSMUST00000112320	C25, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:19136		Q3UA16	0.4	7.0E-01	1.3	3.5E-01	1.5	2.2E-01	0.5	6.1E-01
ENSMUST00000114340	adducin 1 (alpha) [Source:MGI Symbol;Acc:MGI:87918]		Q9QYC0	-10.4	1.9E-05	-2.6	4.5E-02	-1.4	5.8E-02	-1.6	2.4E-01
ENSMUST00000114341	gamma-aminobutyric acid (GABA) receptor, rho 3 [Source:MGI Symbol;Acc:MGI:3588203]	B2RXA8		5.8	4.3E-04	-4.8	6.3E-03	0.5	5.0E-01	0.0	9.9E-01
ENSMUST00000114348	peptidylprolyl isomerase (cyclophilin)-like 3 [Source:MGI Symbol;Acc:MGI:1917475]		Q9D6L8	-4.2	7.7E-04	7.1	1.5E-02	-0.6	8.3E-01	-1.8	2.2E-01
ENSMUST00000114354	interleukin-1 receptor-associated kinase 1 [Source:MGI Symbol;Acc:MGI:107420]	Q8BR10		-5.3	7.0E-03	-5.4	1.1E-03	0.9	5.8E-02	-0.7	5.9E-01
ENSMUST00000114355	ring finger protein 208 [Source:MGI Symbol;Acc:MGI:1916096]		Q8K0W3	6.7	5.6E-04	-1.5	5.6E-01	4.0	2.3E-02	-1.4	6.0E-01
ENSMUST00000114358	ST3 beta-galactoside alpha-2,3-sialyltransferase 6 [Source:MGI Symbol;Acc:MGI:1888707]		Q8VIB3	-5.3	2.6E-03	7.3	9.2E-05	-1.3	2.9E-01	-0.7	2.6E-01
ENSMUST00000112338	retinoic acid induced 2 [Source:MGI Symbol;Acc:MGI:1344378]		Q9QVY8	3.1	6.3E-02	5.3	7.4E-03	-0.2	9.1E-01	-2.4	6.0E-02
ENSMUST00000114366	aldehyde oxidase 2 [Source:MGI Symbol;Acc:MGI:3529596]		Q5SGK3	8.5	2.1E-05	6.4	1.0E-03	-0.4	7.7E-01	-0.4	6.5E-01
ENSMUST00000114385	heterogeneous nuclear ribonucleoprotein M [Source:MGI Symbol;Acc:MGI:1926465]	B8JK32		-5.4	1.6E-03	-5.1	4.0E-03	1.0	9.0E-02	-0.5	7.4E-01
ENSMUST00000112350	metastasis associated 3 [Source:MGI Symbol;Acc:MGI:2151172]	Q3U3A7		0.2	9.2E-01	0.0	9.9E-01	-2.0	2.4E-01	-1.8	4.7E-01
ENSMUST00000114387	N(alpha)-acetyltransferase 10, NatA catalytic subunit [Source:MGI Symbol;Acc:MGI:1915255]	B1AUY9		-4.0	1.5E-02	-1.0	3.9E-01	0.3	7.3E-01	-0.9	4.0E-01
ENSMUST00000114389	N(alpha)-acetyltransferase 10, NatA catalytic subunit [Source:MGI Symbol;Acc:MGI:1915255]	Q3V4D5		-4.3	6.4E-03	5.6	3.7E-02	-0.7	8.0E-01	0.1	9.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000112359	Hermansky-Pudlak syndrome 4 homolog (human) [Source:MGI Symbol;Acc:MGI:2177742]	Q541V2	Q99KG7	-1.3	2.3E-01	-3.3	1.8E-01	1.9	1.8E-01	3.8	9.1E-02
ENSMUST00000112364	annexin A11 [Source:MGI Symbol;Acc:MGI:108481]	D3Z7U0		-0.6	6.5E-01	-0.2	9.3E-01	-0.1	9.7E-01	-0.5	7.3E-01
ENSMUST00000114397	Wolf-Hirschhorn syndrome candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1276574]	D3Z3E4		3.0	1.4E-02	7.6	5.4E-05	-0.6	5.8E-01	0.1	8.1E-01
ENSMUST00000114406	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	Q3TE27		-8.1	6.3E-03	5.1	8.3E-03	1.0	5.0E-01	-0.9	3.5E-01
ENSMUST00000114407	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	B1AUX5		-7.8	1.1E-03	-4.7	3.3E-03	0.5	3.6E-01	-0.3	8.4E-01
ENSMUST00000114410	potassium channel tetramerisation domain containing 18 [Source:MGI Symbol;Acc:MGI:3603813]	E0CZ26		-4.1	1.2E-02	-8.3	4.1E-05	-0.6	2.0E-01	-0.6	6.2E-01
ENSMUST00000114415	special AT-rich sequence binding protein 2 [Source:MGI Symbol;Acc:MGI:2679336]	Q546B3	Q8VI24	5.6	5.5E-03	-3.1	7.6E-03	-0.2	7.4E-01	0.4	6.9E-01
ENSMUST00000114426	transforming, acidic coiled-coil containing protein 3 [Source:MGI Symbol;Acc:MGI:1341163]	Q6NV52		-6.7	1.6E-05	-4.1	3.7E-02	1.0	2.6E-01	2.0	2.7E-01
ENSMUST00000112391	membrane-associated ring finger (C3HC4) 5 [Source:MGI Symbol;Acc:MGI:1915207]			-1.0	3.5E-01	-0.4	7.6E-01	0.6	5.4E-01	0.1	9.6E-01
ENSMUST00000114427	predicted gene 684 [Source:MGI Symbol;Acc:MGI:2685530]	F8VPY8		6.3	7.1E-05	-5.3	1.1E-02	0.9	2.8E-01	0.0	9.8E-01
ENSMUST00000114430	L1 cell adhesion molecule [Source:MGI Symbol;Acc:MGI:96721]	A2AFG8		-7.1	4.9E-03	8.3	1.2E-05	0.0	1.0E+00	0.2	7.5E-01
ENSMUST00000114431	B cell translocation gene 4 [Source:MGI Symbol;Acc:MGI:1860140]		O70552	6.3	2.6E-04	3.4	7.3E-02	-0.6	7.4E-01	1.6	2.1E-01
ENSMUST00000112408	adhesion G protein-coupled receptor G2 [Source:MGI Symbol;Acc:MGI:2446854]		Q8CJ12	2.6	1.1E-01	4.9	8.4E-03	-0.6	7.2E-01	-2.8	3.5E-02
ENSMUST00000112411	cathepsin E [Source:MGI Symbol;Acc:MGI:107361]	D3Z6T3		-5.5	1.4E-01	3.3	5.3E-01	6.6	1.6E-01	-2.1	6.0E-01
ENSMUST00000112412				-1.1	4.0E-01	-0.2	8.9E-01	0.3	8.2E-01	-0.6	6.6E-01
ENSMUST00000112414	proacrosin binding protein [Source:MGI Symbol;Acc:MGI:1859515]		Q3V140	-0.2	8.7E-01	0.1	9.4E-01	0.4	7.4E-01	0.1	9.2E-01
ENSMUST00000114432	euchromatic histone methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1924933]		Q5DW34	-4.7	2.8E-03	-5.6	2.6E-03	0.4	4.3E-01	-0.8	6.0E-01
ENSMUST00000114434	homeobox A3 [Source:MGI Symbol;Acc:MGI:96175]		P02831	6.7	5.1E-04	-5.2	4.6E-02	0.0	9.6E-01	-0.8	7.7E-01
ENSMUST00000114437	protein phosphatase 2, regulatory subunit A, beta [Source:MGI Symbol;Acc:MGI:1920949]		Q7TNP2	-1.7	2.6E-02	-2.3	3.4E-01	1.7	3.0E-01	-1.3	5.9E-01
ENSMUST00000114439	sorting nexin 10 [Source:MGI Symbol;Acc:MGI:1919232]	Q4FJX6	Q9CWT3	-2.8	1.1E-02	4.1	9.1E-03	-3.5	3.5E-02	1.3	1.5E-01
ENSMUST00000112429	Cobl-like 1 [Source:MGI Symbol;Acc:MGI:2442894]	B1AZ14		5.6	3.6E-02	2.6	4.1E-01	-0.6	8.3E-01	2.4	3.2E-01
ENSMUST00000112431	Cobl-like 1 [Source:MGI Symbol;Acc:MGI:2442894]	B1AZ14		2.6	2.2E-01	5.4	1.9E-02	-0.6	7.8E-01	-3.4	4.5E-02
ENSMUST00000114444	PEST proteolytic signal containing nuclear protein [Source:MGI Symbol;Acc:MGI:1923552]	Q3UCC5	Q6P8I4	-6.1	5.2E-04	2.3	2.0E-01	1.2	4.4E-01	3.1	3.0E-02
ENSMUST00000112435	E1A binding protein p400 [Source:MGI Symbol;Acc:MGI:1276124]		Q8CHI8	0.7	7.1E-01	-0.3	9.2E-01	0.8	7.2E-01	1.7	4.4E-01
ENSMUST00000114449	macrophage erythroblast attacher [Source:MGI Symbol;Acc:MGI:1891748]		Q4VC33	-4.5	5.2E-06	-0.1	9.2E-01	1.5	1.8E-01	-3.5	5.4E-02
ENSMUST00000114457	ır factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta [Source:MGI Symbol;Acc:MGI:193		Q9EST8	4.1	3.1E-02	3.7	1.7E-02	-3.8	3.6E-02	-1.0	3.2E-01
ENSMUST00000112439	constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13		Q9CZ04	-1.9	7.9E-02	-1.5	2.4E-01	0.0	9.8E-01	-0.4	7.7E-01
ENSMUST00000114458	ır factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta [Source:MGI Symbol;Acc:MGI:193		Q9EST8	-7.7	6.5E-04	6.1	2.0E-03	-0.5	7.7E-01	-1.4	1.4E-01
ENSMUST00000112453	SH3-domain kinase binding protein 1 [Source:MGI Symbol;Acc:MGI:1889583]		Q8R550	-4.7	4.3E-02	-1.0	6.8E-01	1.6	3.3E-01	-2.0	4.3E-01
ENSMUST00000114459	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:MGI Symbol;Acc:MGI:104819]		O88569	-5.4	4.9E-04	3.5	7.9E-05	0.2	6.5E-01	0.1	8.4E-01
ENSMUST00000114461	ATP-binding cassette, sub-family D (ALD), member 1 [Source:MGI Symbol;Acc:MGI:1349215]	A2ALN0		2.9	8.5E-04	-4.1	6.6E-02	0.0	9.7E-01	-0.9	6.9E-01
ENSMUST00000114464	lute carrier family 6 (neurotransmitter transporter, creatine), member 8 [Source:MGI Symbol;Acc:MGI:214783	F7C668		5.7	1.3E-04	5.1	9.9E-04	1.1	2.7E-01	0.2	8.3E-01
ENSMUST00000112463	interferon induced protein with tetratricopeptide repeats 1B like 2 [Source:MGI Symbol;Acc:MGI:2148249]	Q3U687		1.1	9.0E-02	2.6	7.4E-03	1.1	1.4E-01	-0.4	4.8E-01
ENSMUST00000112464	RIKEN cDNA A830080D01 gene [Source:MGI Symbol;Acc:MGI:2685992]		A2AG58	-1.1	2.2E-01	-3.8	3.1E-02	-0.4	6.1E-01	2.3	1.3E-01
ENSMUST00000114468	oxysterol binding protein-like 3 [Source:MGI Symbol;Acc:MGI:1918970]		Q9DBS9	4.2	3.2E-02	5.0	1.2E-02	-0.6	7.4E-01	0.8	4.2E-01
ENSMUST00000112473	splA/ryanodine receptor domain and SOCS box containing 2 [Source:MGI Symbol;Acc:MGI:1315199]		O88838	-0.2	7.5E-01	-0.3	7.2E-01	0.5	3.5E-01	0.6	3.7E-01
ENSMUST00000114473	pregnancy upregulated non-ubiquitously expressed CaM kinase [Source:MGI Symbol;Acc:MGI:1347357]	Q3TYC1	Q9QYK9	6.3	1.0E-03	6.6	3.1E-02	-0.9	7.7E-01	-0.6	7.1E-01
ENSMUST00000112478	purinergic receptor P2X, ligand-gated ion channel, 2 [Source:MGI Symbol;Acc:MGI:2665170]		Q8K3P1	2.5	2.3E-01	1.5	4.4E-01	-1.3	5.1E-01	-0.3	8.5E-01
ENSMUST00000114474	placenta expressed transcript 1 [Source:MGI Symbol;Acc:MGI:1923759]		Q8VEN2	7.0	4.2E-05	-6.8	1.1E-04	1.1	2.5E-02	-0.9	4.5E-01
ENSMUST00000112487	fasciculation and elongation protein zeta 2 (zygin II) [Source:MGI Symbol;Acc:MGI:2675856]	D3Z6D5		4.2	7.8E-02	-0.9	7.3E-01	-3.1	1.8E-01	2.0	4.1E-01
ENSMUST00000114476	neural cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97281]	E9Q589		7.0	2.7E-06	2.7	1.3E-01	7.5	1.8E-04	1.7	1.9E-01
ENSMUST00000114477	bobby sox homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1917758]	B8JK50		4.5	2.5E-04	-2.1	6.6E-03	-0.4	3.7E-01	-0.2	7.4E-01
ENSMUST00000114485	interleukin 1 receptor antagonist [Source:MGI Symbol;Acc:MGI:96547]	Q3TBV5		-5.0	6.9E-05	-7.8	5.5E-04	0.0	9.4E-01	-0.1	9.7E-01
ENSMUST00000114492	RIKEN cDNA 1700019D03 gene [Source:MGI Symbol;Acc:MGI:1914330]		Q9CPS8	3.2	5.7E-03	3.0	9.2E-04	-2.0	9.1E-03	0.3	4.9E-01
ENSMUST00000114493	RIKEN cDNA 1700019D03 gene [Source:MGI Symbol;Acc:MGI:1914330]		Q9CPS8	4.9	8.3E-03	-2.7	1.8E-03	-0.2	6.8E-01	-0.2	7.8E-01
ENSMUST00000114496	D47 antigen (Rh-related antigen, integrin-associated signal transducer) [Source:MGI Symbol;Acc:MGI:96617	D3Z187		-10.8	3.1E-06	4.8	1.3E-02	-0.3	8.3E-01	0.7	4.8E-01
ENSMUST00000114497	histamine N-methyltransferase [Source:MGI Symbol;Acc:MGI:2153181]	A2AQK4	Q91VF2	-6.3	1.6E-03	-5.1	5.0E-03	-0.5	3.9E-01	0.1	9.7E-01
ENSMUST00000112507	family with sequence similarity 98, member A [Source:MGI Symbol;Acc:MGI:1919972]		Q3TJZ6	-0.5	3.3E-01	-0.3	6.5E-01	-0.3	4.9E-01	-0.5	3.9E-01
ENSMUST00000112509	RNA binding motif, single stranded interacting protein 1 [Source:MGI Symbol;Acc:MGI:1861774]	Q3TTX8	Q91W59	1.2	6.8E-01	-2.4	4.6E-01	-3.9	1.2E-01	-0.3	9.4E-01
ENSMUST00000112512	golgi autoantigen, golgin subfamily a, 3 [Source:MGI Symbol;Acc:MGI:96958]			-0.6	2.7E-01	-0.8	3.0E-01	0.5	3.4E-01	0.7	3.5E-01
ENSMUST00000112514	latent transforming growth factor beta binding protein 1 [Source:MGI Symbol;Acc:MGI:109151]		Q8CG19	2.5	1.8E-01	-3.3	3.9E-02	-6.6	9.3E-04	-0.8	6.4E-01
ENSMUST00000112516	latent transforming growth factor beta binding protein 1 [Source:MGI Symbol;Acc:MGI:109151]		Q8CG19	4.6	5.2E-02	-0.9	7.1E-01	-5.4	2.7E-02	0.1	9.6E-01
ENSMUST00000114503	X-linked lymphocyte-regulated 5C [Source:MGI Symbol;Acc:MGI:1350981]	A2AIE6		3.4	3.4E-02	6.5	6.0E-04	-0.5	6.9E-01	-0.7	3.9E-01
ENSMUST00000114510	glutaminase [Source:MGI Symbol;Acc:MGI:95752]		D3Z7P3	6.7	1.9E-04	-4.7	4.8E-04	0.4	3.2E-01	-0.1	9.2E-01
ENSMUST00000114515	brain and reproductive organ-expressed protein [Source:MGI Symbol;Acc:MGI:1333875]	D3Z7P0		-7.4	5.2E-05	5.0	1.4E-03	0.3	8.1E-01	-0.1	9.2E-01
ENSMUST00000114517	spindlin family, member 2D [Source:MGI Symbol;Acc:MGI:1922101]	B1B0R2		9.8	1.3E-05	5.4	9.5E-03	0.0	9.8E-01	-1.0	3.7E-01
ENSMUST00000114523	acyl-Coenzyme A binding domain containing 5 [Source:MGI Symbol;Acc:MGI:1921409]		Q5XG73	-7.6	1.6E-02	6.5	2.6E-04	0.4	7.1E-01	-1.4	7.8E-02
ENSMUST00000112528	zinc finger protein 605 [Source:MGI Symbol;Acc:MGI:2444933]	E9QAH2		1.4	4.5E-02	1.6	5.7E-02	-0.1	8.2E-01	-0.3	6.1E-01
ENSMUST00000114526	acyl-Coenzyme A binding domain containing 5 [Source:MGI Symbol;Acc:MGI:1921409]		Q5XG73	-3.5	3.9E-03	2.1	4.8E-02	-0.3	7.1E-01	-0.3	7.2E-01
ENSMUST00000112530	peroxisomal biogenesis factor 5 [Source:MGI Symbol;Acc:MGI:1098808]	D3Z600		1.7	5.7E-01	1.7	5.8E-01	-2.4	3.9E-01	-2.4	3.9E-01
ENSMUST00000112531	peroxisomal biogenesis factor 5 [Source:MGI Symbol;Acc:MGI:1098808]		O09012	5.5	8.1E-02	6.7	1.5E-01	1.1	8.0E-01	-0.1	9.6E-01
ENSMUST00000114533	solute carrier family 4 (anion exchanger), member 1, adaptor protein [Source:MGI Symbol;Acc:MGI:1196608]	E9Q585		-6.6	4.5E-05	-0.1	8.7E-01	1.7	1.7E-02	-0.7	3.8E-01
ENSMUST00000114541	myosin IB [Source:MGI Symbol;Acc:MGI:107752]	E9Q580		6.9	2.9E-03	8.8	2.2E-03	1.6	4.6E-01	0.3	7.9E-01
ENSMUST00000114544	abl-interactor 1 [Source:MGI Symbol;Acc:MGI:104913]		Q8CBW3	-7.6	7.8E-05	6.0	5.9E-03	2.4	1.6E-01	-0.6	5.3E-01
ENSMUST00000114546	zinc finger protein 185 [Source:MGI Symbol;Acc:MGI:108095]	A2BI37		6.7	2.9E-04	5.4	3.2E-02	0.1	9.6E-01	0.9	4.9E-01
ENSMUST00000112541	CD163 antigen [Source:MGI Symbol;Acc:MGI:2135946]	B7ZMW6	Q2VLH6	-0.1	9.5E-01	-1.9	2.2E-01	-6.0	5.5E-03	-4.2	6.6E-02
ENSMUST00000112543	glycerate kinase [Source:MGI Symbol;Acc:MGI:2444085]			2.2	1.7E-01	1.2	5.4E-01	0.1	9.7E-01	1.1	5.2E-01
ENSMUST00000112544	predicted gene 15446 [Source:MGI Symbol;Acc:MGI:3709333]	D3Z5Y8		1.0	2.5E-01	1.8	1.2E-01	0.3	7.7E-01	-0.5	6.1E-01
ENSMUST00000112550	bromodomain adjacent to zinc finger domain, 2B [Source:MGI Symbol;Acc:MGI:2442782]	A2AUY4		-3.0	8.9E-02	-5.3	4.2E-02	-0.3	8.0E-01	2.0	4.2E-01
ENSMUST00000114547	cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1889272]		Q8R5M8	5.0	1.0E-03	-10.8	4.5E-04	-1.6	1.5E-02	-0.7	7.5E-01
ENSMUST00000112552	ubiquitin-like, containing PHD and RING finger domains 2 [Source:MGI Symbol;Acc:MGI:1923718]	Q3T995		2.0	2.9E-01	6.5	2.9E-02	1.9	4.5E-01	-2.6	1.1E-01
ENSMUST00000112554	C-type lectin domain family 4, member n [Source:MGI Symbol;Acc:MGI:1861231]		Q9JKF4	-4.6	6.3E-02	-3.6	1.8E-01	-0.5	7.3E-01	-1.5	6.1E-01
ENSMUST00000114551	centrin 2 [Source:MGI Symbol;Acc:MGI:1347085]		Q9R1K9	-4.5	7.8E-03	-3.1	8.6E-02	1.9	4.9E-02	-1.8	3.6E-01
ENSMUST00000114552	ZPR1 zinc finger [Source:MGI Symbol;Acc:MGI:1330262]	F8WHU9		-4.7	1.4E-03	-3.9	8.0E-03	-0.2	7.3E-01	-0.4	7.4E-01
ENSMUST00000112568	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 [Source:MGI Symbol;Acc:MGI:1914110]	E9QAF9		0.1	9.6E-01	-0.2	9.4E-01	0.4	8.4E-01	0.7	7.9E-01
ENSMUST00000114553	gamma-aminobutyric acid (GABA) A receptor, subunit theta [Source:MGI Symbol;Acc:MGI:1888498]	B1AUQ5		10.4	1.0E-04	-5.5	1.3E-04	0.2	5.5E-01	-1.5	1.9E-01
ENSMUST00000114562	transmembrane serine protease 7 [Source:MGI Symbol;Acc:MGI:2686594]		Q8BIK6	6.5	1.6E-04	-2.6	3.1E-03	-0.6	2.0E-01	-0.6	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000114565	ansmembrane protein with EGF-like and two follistatin-like domains 2 [Source:MGI Symbol;Acc:MGI:186173			8.2	4.6E-06	5.9	1.5E-02	-1.4	5.2E-01	-0.1	9.0E-01
ENSMUST00000114573	SID1 transmembrane family, member 2 [Source:MGI Symbol;Acc:MGI:2446134]		Q8CIF6	-5.2	4.3E-04	4.8	3.1E-03	0.0	9.7E-01	0.1	9.1E-01
ENSMUST00000114574	glucagon-like peptide 1 receptor [Source:MGI Symbol;Acc:MGI:99571]		O35659	7.7	4.7E-05	5.7	1.7E-02	1.9	3.6E-01	-0.3	8.3E-01
ENSMUST00000114576	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914298]		Q78T54	-4.4	1.5E-03	3.2	1.4E-01	-1.3	4.9E-01	2.3	1.2E-01
ENSMUST00000114577	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914298]	F2Z446		5.6	5.2E-04	-3.2	7.7E-02	0.0	9.9E-01	0.3	8.6E-01
ENSMUST00000114582	high mobility group box 3 [Source:MGI Symbol;Acc:MGI:1098219]	Q544R9	O54879	4.2	1.3E-02	-5.4	5.8E-04	-0.7	1.6E-01	-2.4	8.7E-02
ENSMUST00000112586	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 [Source:MGI Symbol;Acc:MGI:103298]	Q3U9G8	P51908	-0.1	9.7E-01	-2.1	4.2E-01	-3.7	1.0E-01	-1.6	5.7E-01
ENSMUST00000112587	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 [Source:MGI Symbol;Acc:MGI:103298]	Q3U9G8	P51908	-2.7	6.4E-02	-2.8	9.0E-02	-0.8	4.0E-01	-0.6	6.9E-01
ENSMUST00000114586	CD99 antigen-like 2 [Source:MGI Symbol;Acc:MGI:2177151]	I7HJQ8		6.7	1.2E-04	-1.6	3.7E-01	1.6	1.5E-01	-1.5	4.0E-01
ENSMUST00000112590	acid phosphatase, prostate [Source:MGI Symbol;Acc:MGI:1928480]		Q8CE08	0.7	2.9E-01	-1.0	2.1E-01	-0.9	1.2E-01	0.8	3.2E-01
ENSMUST00000114590	zinc finger protein 513 [Source:MGI Symbol;Acc:MGI:2141255]		Q6PD29	-3.8	7.1E-03	-2.7	6.4E-02	-0.5	5.2E-01	-1.5	2.8E-01
ENSMUST00000112600	polyhomeotic-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:103248]	Q3V116		4.1	1.9E-01	-0.4	9.3E-01	-2.6	4.4E-01	2.0	6.1E-01
ENSMUST00000114598	zinc finger protein 398 [Source:MGI Symbol;Acc:MGI:1917856]	E9Q569		4.1	1.1E-04	5.7	1.9E-02	-3.6	1.6E-01	-2.2	1.1E-01
ENSMUST00000114600	solute carrier family 35, member A5 [Source:MGI Symbol;Acc:MGI:1921352]	D3Z784		-5.4	4.3E-05	7.5	4.6E-07	-0.7	2.7E-01	-0.3	3.8E-01
ENSMUST00000112610	mannose-6-phosphate receptor, cation dependent [Source:MGI Symbol;Acc:MGI:96904]	Q3UKQ5	P24668	0.7	7.5E-01	7.0	4.1E-02	3.4	2.6E-01	-2.8	1.9E-01
ENSMUST00000114606	enhancer trap locus 4 [Source:MGI Symbol;Acc:MGI:95454]		A2AQ25	5.4	1.4E-03	8.1	2.6E-04	-1.5	3.7E-01	0.0	1.0E+00
ENSMUST00000112618	glycerol phosphate dehydrogenase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:99778]	A2AQR0		4.0	2.1E-01	3.2	3.5E-01	-0.4	9.1E-01	0.4	8.7E-01
ENSMUST00000114608	enhancer trap locus 4 [Source:MGI Symbol;Acc:MGI:95454]		A2AQ25	3.4	1.7E-03	-5.4	3.3E-04	-0.2	5.7E-01	-0.6	5.6E-01
ENSMUST00000114610	enhancer trap locus 4 [Source:MGI Symbol;Acc:MGI:95454]	Q8BHR1		6.2	1.5E-04	-1.5	2.9E-01	0.3	7.5E-01	-2.1	1.7E-01
ENSMUST00000114626	CD200 receptor 4 [Source:MGI Symbol;Acc:MGI:3036289]		Q6XJV4	-6.0	1.1E-04	-0.9	4.0E-01	1.6	3.3E-02	-0.2	8.7E-01
ENSMUST00000114629	mastermind-like domain containing 1 [Source:MGI Symbol;Acc:MGI:3045303]	D3Z768		8.5	1.6E-03	4.7	8.4E-04	-1.5	1.5E-01	0.7	2.8E-01
ENSMUST00000112630	NIMA (never in mitosis gene a)- related kinase 10 [Source:MGI Symbol;Acc:MGI:2685128]	K3W4R8		4.6	5.0E-02	3.3	1.5E-01	-1.4	5.2E-01	-0.1	9.4E-01
ENSMUST00000112631	NIMA (never in mitosis gene a)- related kinase 10 [Source:MGI Symbol;Acc:MGI:2685128]		Q3UGM2	2.8	2.7E-01	3.7	2.0E-01	-0.3	9.2E-01	-1.1	5.6E-01
ENSMUST00000112634	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 [Source:MGI Symbol;Acc:MGI		Q8CF93	6.4	6.0E-02	8.8	1.9E-02	-1.0	7.9E-01	-3.3	1.0E-01
ENSMUST00000112635	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 [Source:MGI Symbol;Acc:MGI	A2RRI8	Q8CF93	3.9	1.7E-01	1.9	6.0E-01	0.2	9.6E-01	2.1	4.6E-01
ENSMUST00000112636	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 [Source:MGI Symbol;Acc:MGI	A2RRI8	Q8CF93	5.0	5.6E-02	6.8	2.1E-02	-0.7	7.9E-01	-2.5	1.3E-01
ENSMUST00000112640	STEAP family member 3 [Source:MGI Symbol;Acc:MGI:1915678]			-2.0	2.2E-01	-2.8	1.3E-01	-1.4	2.2E-01	-0.6	7.7E-01
ENSMUST00000114641	contactin associated protein-like 2 [Source:MGI Symbol;Acc:MGI:1914047]	E9QNF7		7.9	2.2E-05	3.1	5.0E-03	-2.3	2.2E-02	-0.6	4.1E-01
ENSMUST00000112642	ecotropic viral integration site 5 [Source:MGI Symbol;Acc:MGI:104736]	F8VPT6		-1.4	6.5E-02	-1.2	1.8E-01	0.0	9.9E-01	-0.2	8.4E-01
ENSMUST00000114644	thiamine pyrophosphokinase [Source:MGI Symbol;Acc:MGI:1352500]		Q9R0M5	5.4	1.8E-02	3.0	9.9E-02	-2.4	1.6E-01	0.3	8.4E-01
ENSMUST00000112645	transferrin [Source:MGI Symbol;Acc:MGI:98821]		Q921I1	-2.7	4.4E-02	-1.3	5.1E-01	2.0	2.1E-01	0.6	7.3E-01
ENSMUST00000112650	RNA polymerase II associated protein 2 [Source:MGI Symbol;Acc:MGI:2141142]		Q8VC34	3.6	1.0E-01	5.6	2.3E-02	-0.5	8.4E-01	-2.5	1.0E-01
ENSMUST00000112657	Ca2+-dependent secretion activator [Source:MGI Symbol;Acc:MGI:1350922]	K4DI76		3.3	7.3E-02	4.9	1.2E-02	-1.2	5.0E-01	-2.8	4.2E-02
ENSMUST00000112664				2.5	3.0E-01	0.9	7.9E-01	0.9	7.4E-01	2.5	3.9E-01
ENSMUST00000114653	fragile X mental retardation syndrome 1 [Source:MGI Symbol;Acc:MGI:95564]	E9QAT0		-5.0	1.4E-02	6.3	2.7E-05	-2.3	4.4E-02	0.1	8.2E-01
ENSMUST00000112669	RIKEN cDNA 3830406C13 gene [Source:MGI Symbol;Acc:MGI:1917937]		Q8BGD0	-2.6	2.1E-01	0.8	5.7E-01	-1.8	2.0E-01	-5.3	1.9E-02
ENSMUST00000114657	fragile X mental retardation syndrome 1 [Source:MGI Symbol;Acc:MGI:95564]	E9QNF5		-6.0	9.5E-05	5.7	8.1E-03	-0.5	7.8E-01	0.9	3.9E-01
ENSMUST00000114664	myelin protein zero-like 3 [Source:MGI Symbol;Acc:MGI:2442647]		Q3V3F6	-4.0	3.0E-04	6.8	9.3E-03	-0.8	7.3E-01	-2.2	1.2E-01
ENSMUST00000112674	zinc finger and BTB domain containing 14 [Source:MGI Symbol;Acc:MGI:1195345]	Q544H8	Q08376	-0.7	7.9E-01	1.3	5.6E-01	-1.3	5.3E-01	-3.3	1.8E-01
ENSMUST00000114666	ATPase, H+ transporting, lysosomal V1 subunit A [Source:MGI Symbol;Acc:MGI:1201780]		P50516	-5.2	4.5E-05	0.3	8.4E-01	-0.3	8.0E-01	2.2	1.0E-01
ENSMUST00000114671	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 [Source:MGI Symbol;Acc:	A2AS70		-5.8	5.6E-04	2.5	2.4E-02	-0.8	3.5E-01	0.7	3.7E-01
ENSMUST00000114689	lysine (K)-specific methyltransferase 2A [Source:MGI Symbol;Acc:MGI:96995]		P55200	5.5	5.6E-03	5.2	6.8E-05	-1.4	8.8E-02	-0.9	1.0E-01
ENSMUST00000112688	nucleolar protein interacting with the FHA domain of MKI67 [Source:MGI Symbol;Acc:MGI:1915199]		Q91VE6	1.2	5.7E-01	-2.7	1.1E-01	-5.7	4.5E-03	-1.8	3.6E-01
ENSMUST00000112689	PX domain containing serine/threonine kinase [Source:MGI Symbol;Acc:MGI:1289230]		Q8BX57	2.0	4.6E-01	-0.7	8.5E-01	-2.2	3.7E-01	0.4	9.0E-01
ENSMUST00000112691	guanine nucleotide binding protein-like 3 (nucleolar)-like [Source:MGI Symbol;Acc:MGI:2448557]		Q6PGG6	0.2	5.7E-01	0.2	7.8E-01	0.1	8.9E-01	0.1	8.0E-01
ENSMUST00000112696	zinc finger protein 644 [Source:MGI Symbol;Acc:MGI:1277212]	E9QA22		-0.3	7.9E-01	-1.7	2.4E-01	-0.1	9.0E-01	1.3	3.4E-01
ENSMUST00000112698	zinc finger protein 644 [Source:MGI Symbol;Acc:MGI:1277212]	E9Q624		1.3	6.6E-01	5.4	1.2E-01	2.0	5.1E-01	-2.0	4.4E-01
ENSMUST00000114694	zinc finger and BTB domain containing 20 [Source:MGI Symbol;Acc:MGI:1929213]		Q8K0L9	5.3	4.9E-06	7.5	3.3E-04	-0.9	5.4E-01	1.0	1.7E-01
ENSMUST00000112703	coiled-coil domain containing 77 [Source:MGI Symbol;Acc:MGI:1914450]		Q9CZH8	3.5	1.3E-01	-2.5	4.4E-01	-3.5	1.3E-01	2.5	4.1E-01
ENSMUST00000114699	peptidase inhibitor 16 [Source:MGI Symbol;Acc:MGI:1921366]	D3Z6T6		-7.5	2.9E-04	-4.5	2.5E-03	-1.1	8.6E-02	-1.5	2.4E-01
ENSMUST00000114701	peptidase inhibitor 16 [Source:MGI Symbol;Acc:MGI:1921366]	E9QNE5		-6.5	5.5E-06	3.7	1.4E-02	-2.6	7.1E-02	-1.0	3.3E-01
ENSMUST00000114716	transmembrane protein 214 [Source:MGI Symbol;Acc:MGI:1916046]	D3Z6S1		-5.4	1.4E-03	1.5	7.4E-02	-0.4	5.3E-01	-0.1	9.2E-01
ENSMUST00000112709	trophinin [Source:MGI Symbol;Acc:MGI:1928994]	Q6DIC6		3.5	2.1E-01	3.2	2.8E-01	-0.4	8.9E-01	-0.2	9.4E-01
ENSMUST00000112712	LY6/PLAUR domain containing 6 [Source:MGI Symbol;Acc:MGI:2443848]		Q8BPP5	3.9	6.2E-02	3.0	2.2E-01	0.4	8.5E-01	1.4	4.3E-01
ENSMUST00000112715	aminolevulinic acid synthase 2, erythroid [Source:MGI Symbol;Acc:MGI:87990]	A2AFM1		-1.7	3.6E-01	-4.6	3.5E-02	-3.5	1.3E-02	-0.7	7.5E-01
ENSMUST00000114726	RNA binding motif protein, X chromosome [Source:MGI Symbol;Acc:MGI:1343044]		Q9WV02	-5.9	8.7E-05	5.2	4.5E-06	-0.5	3.9E-01	-0.1	7.9E-01
ENSMUST00000112736	vacuolar protein sorting 4b (yeast) [Source:MGI Symbol;Acc:MGI:1100499]	Q3TN07	P46467	-1.3	1.6E-01	-0.3	7.5E-01	-0.2	7.5E-01	-1.2	2.5E-01
ENSMUST00000112745	methyl-CpG binding domain protein 5 [Source:MGI Symbol;Acc:MGI:2138934]	B1AYB7		-0.4	5.5E-01	3.3	3.6E-03	2.1	1.4E-02	-1.6	5.4E-02
ENSMUST00000112748	secreted phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:98389]	Q547B5	P10923	3.2	4.0E-02	-6.3	2.1E-03	-8.2	7.1E-05	1.4	3.8E-01
ENSMUST00000114729	dihydropyrimidinase-like 5 [Source:MGI Symbol;Acc:MGI:1929772]		Q9EQF6	7.1	2.5E-02	1.1	8.1E-02	-0.9	8.8E-02	0.1	9.0E-01
ENSMUST00000114730	RNA binding motif protein, X chromosome [Source:MGI Symbol;Acc:MGI:1343044]		Q9WV02	-5.2	1.6E-03	-3.7	5.4E-02	0.3	7.0E-01	-1.1	5.6E-01
ENSMUST00000114732	Eph receptor B6 [Source:MGI Symbol;Acc:MGI:1096338]		O08644	5.3	1.3E-04	8.9	4.5E-05	-0.7	6.1E-01	0.4	4.9E-01
ENSMUST00000112770	RIKEN cDNA 4930555G01 gene [Source:MGI Symbol;Acc:MGI:1922055]	L7N253		4.2	1.2E-01	3.8	2.4E-01	-0.2	9.5E-01	0.3	9.0E-01
ENSMUST00000114737	patatin-like phospholipase domain containing 1 [Source:MGI Symbol;Acc:MGI:3617850]	B2KF06	Q3V1D5	1.3	6.9E-03	7.4	5.7E-05	-0.5	6.5E-01	-0.4	4.3E-01
ENSMUST00000112777	DCP1 decapping enzyme homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2442404]	B9EIX0		3.7	3.6E-02	4.0	8.3E-02	0.4	8.2E-01	0.1	9.4E-01
ENSMUST00000114740	MYCBP-associated, testis expressed 1 [Source:MGI Symbol;Acc:MGI:2443598]		Q8BRC6	7.0	6.2E-06	6.1	8.9E-04	-0.7	6.3E-01	-1.3	1.2E-01
ENSMUST00000114741	proline-serine-threonine phosphatase-interacting protein 2 [Source:MGI Symbol;Acc:MGI:1335088]		Q99M15	-3.7	7.5E-05	3.6	6.9E-03	-1.4	2.4E-01	0.8	3.5E-01
ENSMUST00000112810	glycosyltransferase-like domain containing 1 [Source:MGI Symbol;Acc:MGI:2444269]		Q8BW56	0.1	8.7E-01	-0.2	8.5E-01	-0.1	8.9E-01	0.2	8.2E-01
ENSMUST00000114750	glycogen synthase kinase 3 beta [Source:MGI Symbol;Acc:MGI:1861437]	E9QAQ5		-6.4	1.6E-05	-7.6	4.7E-03	-1.0	1.6E-01	0.0	9.9E-01
ENSMUST00000112824	Rho GTPase activating protein 15 [Source:MGI Symbol;Acc:MGI:1923367]	B1AW40		0.3	6.7E-01	0.7	3.4E-01	-0.8	1.9E-01	-1.2	9.7E-02
ENSMUST00000114751	HIV TAT specific factor 1 [Source:MGI Symbol;Acc:MGI:1919709]		Q8BGC0	3.1	1.4E-03	2.2	1.3E-02	-1.6	3.4E-02	0.0	9.5E-01
ENSMUST00000114752	mitogen-activated protein kinase 14 [Source:MGI Symbol;Acc:MGI:1346865]		P47811	-5.0	8.9E-05	6.5	5.3E-02	-1.0	7.7E-01	2.9	1.1E-01
ENSMUST00000114754	mitogen-activated protein kinase 14 [Source:MGI Symbol;Acc:MGI:1346865]		P47811	-5.9	1.6E-04	6.5	1.5E-04	-1.2	3.0E-01	-0.5	4.0E-01
ENSMUST00000112840	F-box and leucine-rich repeat protein 17 [Source:MGI Symbol;Acc:MGI:1354704]	G3X9V9		-1.4	1.1E-01	-1.4	2.6E-01	1.2	1.2E-01	1.2	3.1E-01
ENSMUST00000114763	follistatin-like 1 [Source:MGI Symbol;Acc:MGI:102793]		Q62356	5.5	4.3E-05	0.9	4.1E-01	-2.7	2.4E-02	-0.5	6.0E-01
ENSMUST00000114764	solute carrier family 26, member 8 [Source:MGI Symbol;Acc:MGI:2385046]		Q8R0C3	4.0	9.7E-04	-2.3	1.2E-01	-0.2	8.0E-01	-2.9	9.5E-02
ENSMUST00000112845	diphosphoinositol pentakisphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:2142810]	E9Q9J4		-3.3	8.1E-02	-2.9	1.5E-01	-0.8	5.3E-01	-1.2	5.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000114765	transmembrane protein 182 [Source:MGI Symbol;Acc:MGI:1923725]		B2RVY9	7.8	3.4E-05	6.6	7.9E-04	-0.5	7.2E-01	-1.2	1.5E-01
ENSMUST00000114769	four and a half LIM domains 1 [Source:MGI Symbol;Acc:MGI:1298387]	A2AEY2		7.4	2.5E-05	2.7	1.9E-01	1.7	2.8E-01	3.8	2.5E-02
ENSMUST00000114776	protein inhibitor of activated STAT 2 [Source:MGI Symbol;Acc:MGI:1096566]	F8WHS8		-3.1	2.1E-02	6.7	3.9E-03	1.5	3.8E-01	1.9	7.0E-02
ENSMUST00000114777	protein inhibitor of activated STAT 2 [Source:MGI Symbol;Acc:MGI:1096566]		Q8C5D8	-4.8	6.8E-03	7.5	1.3E-03	-0.8	6.7E-01	-0.6	4.9E-01
ENSMUST00000112854	Rho GTPase activating protein 24 [Source:MGI Symbol;Acc:MGI:1922647]		Q8C4V1	-3.7	2.1E-01	-2.8	4.4E-01	0.5	7.9E-01	-0.4	9.3E-01
ENSMUST00000112862	actin related protein 2/3 complex, subunit 5-like [Source:MGI Symbol;Acc:MGI:1921442]	A3KGQ6		-2.6	2.6E-01	-1.8	4.1E-01	-1.2	4.3E-01	-2.1	4.0E-01
ENSMUST00000114784	solute carrier family 9 (sodium/hydrogen exchanger), member 6 [Source:MGI Symbol;Acc:MGI:2443511]	B0QZV3		-4.8	6.8E-03	5.9	2.4E-03	-0.5	7.7E-01	-1.0	2.9E-01
ENSMUST00000114791	Ras suppressor protein 1 [Source:MGI Symbol;Acc:MGI:103040]	A2AUR7		-5.2	3.3E-03	3.4	5.1E-03	-3.3	1.6E-02	-1.8	4.2E-02
ENSMUST00000112870	vav 1 oncogene [Source:MGI Symbol;Acc:MGI:98923]	Q8VDU4		-0.4	9.0E-01	0.7	8.9E-01	1.3	6.9E-01	0.2	9.6E-01
ENSMUST00000114794	tubby like protein 1 [Source:MGI Symbol;Acc:MGI:109571]	Q8K0Y6		6.3	1.1E-04	6.3	2.0E-03	0.2	8.9E-01	-0.3	7.5E-01
ENSMUST00000114797	mitochondrial ribosomal protein S33 [Source:MGI Symbol;Acc:MGI:1338046]	Q8R2K5		-5.9	7.3E-05	-6.9	6.2E-03	1.0	1.6E-01	0.8	6.8E-01
ENSMUST00000114822	makorin, ring finger protein, 1 [Source:MGI Symbol;Acc:MGI:1859353]	Q8C5B6	Q9QXP6	-5.5	3.1E-04	4.2	4.6E-02	-1.4	4.9E-01	2.1	1.2E-01
ENSMUST00000114839	DnaJ (Hsp40) homolog, subfamily B, member 6 [Source:MGI Symbol;Acc:MGI:1344381]		O54946	-8.9	3.8E-06	4.8	8.1E-03	-0.5	7.2E-01	0.5	5.9E-01
ENSMUST00000112880	zinc finger protein 422 [Source:MGI Symbol;Acc:MGI:1914505]		Q9ERU3	3.0	9.3E-02	5.4	6.7E-02	2.9	2.6E-01	0.5	7.7E-01
ENSMUST00000112881	D-2-hydroxyglutarate dehydrogenase [Source:MGI Symbol;Acc:MGI:2138209]	E9QN44		-0.7	1.2E-01	0.0	9.9E-01	1.1	2.8E-02	0.3	5.6E-01
ENSMUST00000114842	ankyrin repeat and SAM domain containing 1 [Source:MGI Symbol;Acc:MGI:2446180]		P59672	-6.4	1.8E-03	6.0	2.6E-02	-0.7	7.8E-01	-1.2	4.1E-01
ENSMUST00000114846	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:MGI Symbol;Acc:MGI:2181202]	A2AUP1		-7.8	1.4E-03	8.3	1.7E-05	-0.5	6.3E-01	-0.7	1.8E-01
ENSMUST00000114847	calcium-sensing receptor [Source:MGI Symbol;Acc:MGI:1351351]		Q9QY96	6.8	4.7E-04	2.8	4.0E-01	-0.8	7.7E-01	3.1	2.3E-01
ENSMUST00000112887	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:MGI Symbol;Acc:MGI:3603816]		Q8C0N2	-2.2	2.6E-01	5.1	3.1E-02	3.5	1.0E-01	-3.8	4.3E-02
ENSMUST00000114849	UHRF1 (ICBP90) binding protein 1 [Source:MGI Symbol;Acc:MGI:3041238]	B2KF50		3.7	2.7E-05	-4.5	6.4E-02	0.9	4.1E-01	0.1	9.8E-01
ENSMUST00000112889	transmembrane protein 164 [Source:MGI Symbol;Acc:MGI:2148020]	A2AH99		-2.7	2.3E-01	-2.5	3.7E-01	-0.1	9.3E-01	-0.3	9.1E-01
ENSMUST00000114850	cDNA sequence BC1179090 [Source:MGI Symbol;Acc:MGI:3696881]	L7N257		-9.8	1.0E-05	-0.1	8.9E-01	-1.1	1.2E-01	0.7	3.8E-01
ENSMUST00000112895	NIMA (never in mitosis gene a)-related expressed kinase 6 [Source:MGI Symbol;Acc:MGI:1891638]		Q9ES70	-1.1	5.8E-01	-3.8	2.9E-01	0.0	9.9E-01	2.6	4.7E-01
ENSMUST00000114858	predicted gene 5483 [Source:MGI Symbol;Acc:MGI:3645124]	B2RV77		-10.0	4.7E-06	-4.6	1.9E-01	2.1	2.3E-01	1.3	6.8E-01
ENSMUST00000114863	DNA segment, Chr 17, Wayne State University 92, expressed [Source:MGI Symbol;Acc:MGI:106281]		Q3TT38	-5.9	3.1E-03	-5.5	7.4E-03	-2.6	7.8E-03	-0.8	6.5E-01
ENSMUST00000114865	glutamate receptor, ionotropic, kainate 4 [Source:MGI Symbol;Acc:MGI:95817]		Q8BMF5	9.7	2.7E-06	-3.9	4.4E-03	0.7	2.2E-01	-3.6	2.6E-02
ENSMUST00000114870	SAM pointed domain containing ets transcription factor [Source:MGI Symbol;Acc:MGI:1353422]		Q9WTP3	5.3	3.2E-02	5.1	1.0E-02	-1.6	3.9E-01	-1.0	3.8E-01
ENSMUST00000114874	C-type lectin domain family 2, member L [Source:MGI Symbol;Acc:MGI:2141402]		P0C7M9	6.8	1.1E-04	-1.5	5.7E-02	1.2	2.6E-02	-0.2	8.1E-01
ENSMUST00000112903	acyl-CoA synthetase long-chain family member 4 [Source:MGI Symbol;Acc:MGI:1354713]	Q91YN3	Q9QUJ7	0.9	7.6E-01	-2.2	6.3E-01	-1.2	6.7E-01	1.9	6.6E-01
ENSMUST00000114882	ribosomal protein S10 [Source:MGI Symbol;Acc:MGI:1914347]	Q5M9K7	P63325	-8.1	1.9E-04	-6.0	1.7E-02	-0.3	6.5E-01	0.7	7.4E-01
ENSMUST00000114885	deltex 3-like (Drosophila) [Source:MGI Symbol;Acc:MGI:2656973]		Q3UIR3	2.9	2.6E-03	-4.8	8.9E-03	1.6	2.3E-02	-0.1	9.5E-01
ENSMUST00000112908	heparanase [Source:MGI Symbol;Acc:MGI:1343124]	D3Z3C3		1.3	5.5E-01	1.0	6.2E-01	-1.7	3.5E-01	-1.4	5.0E-01
ENSMUST00000114888	high mobility group AT-hook 1 [Source:MGI Symbol;Acc:MGI:96160]	Q3TVP0	P17095	-5.4	1.3E-03	3.2	6.6E-03	-0.4	6.4E-01	-1.0	2.1E-01
ENSMUST00000112913	nuclear transport factor 2-like export factor 2 [Source:MGI Symbol;Acc:MGI:2147914]		Q3UNA4	-1.4	6.5E-02	-0.4	6.9E-01	1.2	9.5E-02	0.2	7.6E-01
ENSMUST00000114890	predicted gene, 17604 [Source:MGI Symbol;Acc:MGI:4937238]	E9QAD7		8.0	2.1E-05	3.1	3.8E-03	-2.7	1.4E-02	-0.5	4.5E-01
ENSMUST00000112916	nuclear transport factor 2-like export factor 2 [Source:MGI Symbol;Acc:MGI:2147914]		Q3UNA4	0.2	9.4E-01	-3.3	3.0E-01	-3.6	8.5E-02	-0.2	9.6E-01
ENSMUST00000114897	ynthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 [Source:MGI Symbol;Acc:MGI:12(	Q3UD06	Q91VR2	-9.1	1.3E-05	-3.5	9.1E-02	4.8	9.2E-04	-1.3	5.3E-01
ENSMUST00000112925	intraflagellar transport 122 [Source:MGI Symbol;Acc:MGI:1932386]		Q6NWV3	4.1	9.5E-02	-1.1	7.2E-01	-3.9	1.4E-01	1.3	6.1E-01
ENSMUST00000112930	collagen, type IV, alpha 5 [Source:MGI Symbol;Acc:MGI:88456]	Q63ZW6		3.2	8.1E-02	2.0	1.1E-01	-5.3	5.8E-03	-4.0	8.2E-03
ENSMUST00000114900	zinc finger CCCH type, antiviral 1 [Source:MGI Symbol;Acc:MGI:1926031]	D3Z5I1		-2.4	9.4E-03	-0.1	9.7E-01	-4.2	8.7E-02	3.0	1.8E-01
ENSMUST00000114904	Rho GTPase activating protein 36 [Source:MGI Symbol;Acc:MGI:1922654]		B1AUC7	5.3	5.8E-03	4.1	5.0E-02	-1.2	5.4E-01	-0.2	8.8E-01
ENSMUST00000114908	ATPase, H+ transporting, lysosomal V0 subunit A4 [Source:MGI Symbol;Acc:MGI:2153480]		Q920R6	6.3	1.3E-02	-2.3	6.5E-02	-0.6	3.8E-01	-2.4	1.1E-01
ENSMUST00000112935	nicotinamide nucleotide adenylyltransferase 3 [Source:MGI Symbol;Acc:MGI:1921330]		Q99JR6	3.9	6.6E-02	2.7	6.8E-02	-4.5	2.8E-02	-3.3	3.0E-02
ENSMUST00000112936	ring finger and CCCH-type zinc finger domains 2 [Source:MGI Symbol;Acc:MGI:2442789]		P0C090	0.8	6.8E-01	2.1	4.2E-01	1.1	5.3E-01	-0.2	9.3E-01
ENSMUST00000112937	nicotinamide nucleotide adenylyltransferase 3 [Source:MGI Symbol;Acc:MGI:1921330]	Q3V3C7		3.5	6.9E-02	3.1	2.9E-01	1.5	5.3E-01	1.9	3.5E-01
ENSMUST00000114909	3 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:2388	A2ASY0		6.0	1.2E-04	-1.5	4.7E-01	5.5	1.6E-03	-0.8	6.7E-01
ENSMUST00000112940	phosducin-like [Source:MGI Symbol;Acc:MGI:1914716]		Q9DBX2	0.7	1.5E-01	0.9	1.6E-01	-0.5	3.2E-01	-0.6	3.0E-01
ENSMUST00000112942	mitochondrial transcription termination factor 4 [Source:MGI Symbol;Acc:MGI:1918355]	D3Z3A4		1.2	5.8E-02	2.6	4.0E-03	0.5	4.2E-01	-0.9	1.4E-01
ENSMUST00000112944	mitochondrial transcription termination factor 4 [Source:MGI Symbol;Acc:MGI:1918355]	D3Z3A2		1.5	2.1E-01	1.3	4.1E-01	0.0	9.7E-01	0.3	8.2E-01
ENSMUST00000114913	adenylate cyclase 5 [Source:MGI Symbol;Acc:MGI:99673]		P84309	6.8	5.6E-06	-2.3	1.4E-02	0.7	1.8E-01	0.5	5.2E-01
ENSMUST00000114925	unc-50 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1914637]		Q9CQ61	-5.4	8.4E-05	-3.4	1.1E-02	0.9	1.4E-01	-0.1	9.3E-01
ENSMUST00000114934	CUGBP, Elav-like family member 2 [Source:MGI Symbol;Acc:MGI:1338822]		Q9Z0H4	-9.1	1.1E-05	8.3	1.9E-05	-0.5	6.8E-01	0.5	3.1E-01
ENSMUST00000114935	cutA divalent cation tolerance homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1914925]	D5MCW4		-3.5	3.5E-03	8.0	3.2E-05	-0.5	6.7E-01	0.2	7.1E-01
ENSMUST00000112966	LIM homeobox protein 6 [Source:MGI Symbol;Acc:MGI:1306803]		Q9R1R0	4.8	1.0E-01	4.8	1.7E-01	-0.4	9.0E-01	-0.5	8.2E-01
ENSMUST00000114937	USP6 N-terminal like [Source:MGI Symbol;Acc:MGI:2138893]		Q80XC3	1.8	6.7E-03	7.2	9.0E-05	-0.4	7.4E-01	0.3	6.4E-01
ENSMUST00000112969	progestin and adipoQ receptor family member III [Source:MGI Symbol;Acc:MGI:2679683]	Q0VAZ2	Q6TCG8	-1.6	2.0E-01	-2.4	1.8E-01	-0.2	8.4E-01	0.6	7.5E-01
ENSMUST00000114942	proline and serine rich 2 [Source:MGI Symbol;Acc:MGI:2442238]		Q8C5R2	5.8	6.6E-04	-3.4	6.6E-03	-0.2	6.8E-01	-0.1	9.4E-01
ENSMUST00000114943	deleted in colorectal carcinoma [Source:MGI Symbol;Acc:MGI:94869]		P70211	7.6	2.2E-03	-4.1	4.2E-02	1.2	1.4E-01	2.6	1.6E-01
ENSMUST00000112976	tubulin tyrosine ligase-like family, member 11 [Source:MGI Symbol;Acc:MGI:1921660]		A4Q9F4	3.5	1.1E-01	2.4	2.4E-01	-3.2	1.4E-01	-2.2	2.3E-01
ENSMUST00000114946	methyl-CpG binding domain protein 2 [Source:MGI Symbol;Acc:MGI:1333813]		Q9Z2E1	5.3	3.9E-04	-2.0	4.2E-02	-0.3	6.4E-01	-1.9	8.0E-02
ENSMUST00000114949	kalirin, RhoGEF kinase [Source:MGI Symbol;Acc:MGI:2685385]	D3Z559		5.7	1.2E-03	4.3	8.2E-04	-0.7	4.6E-01	-0.4	5.5E-01
ENSMUST00000114956	sodium channel, voltage-gated, type III, beta [Source:MGI Symbol;Acc:MGI:1918882]	Q0P666	Q8BHK2	9.2	9.9E-06	-3.0	2.5E-02	1.1	8.1E-02	1.3	2.6E-01
ENSMUST00000114958	E74-like factor 4 (ets domain transcription factor) [Source:MGI Symbol;Acc:MGI:1928377]		Q9Z2U4	-4.9	1.4E-03	-4.4	7.4E-02	0.0	9.7E-01	1.0	6.6E-01
ENSMUST00000114961	kalirin, RhoGEF kinase [Source:MGI Symbol;Acc:MGI:2685385]	A0A0A0MQF1		7.4	1.2E-02	6.4	2.1E-03	-0.5	7.7E-01	-1.4	1.4E-01
ENSMUST00000112987	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]	A2AUX3		1.2	6.4E-01	-2.2	6.4E-01	-0.9	7.4E-01	2.5	5.5E-01
ENSMUST00000112993	midline 2 [Source:MGI Symbol;Acc:MGI:1344333]	B1AVF4		3.2	1.5E-01	4.6	6.0E-02	-0.5	8.2E-01	-1.9	2.4E-01
ENSMUST00000112995				1.8	3.1E-01	-2.1	5.1E-01	-0.1	9.8E-01	3.8	1.9E-01
ENSMUST00000112996	TSC22 domain family, member 3 [Source:MGI Symbol;Acc:MGI:1196284]		Q9Z2S7	-2.0	4.5E-02	-0.4	7.0E-01	0.5	5.5E-01	-1.1	3.0E-01
ENSMUST00000114963	kalirin, RhoGEF kinase [Source:MGI Symbol;Acc:MGI:2685385]	D3Z535		6.1	1.2E-02	8.0	1.5E-04	0.4	7.7E-01	-0.6	3.4E-01
ENSMUST00000114966	kalirin, RhoGEF kinase [Source:MGI Symbol;Acc:MGI:2685385]	D3Z532		7.5	4.3E-05	0.1	9.8E-01	-1.8	3.9E-01	4.0	1.0E-01
ENSMUST00000113002	glycoprotein galactosyltransferase alpha 1, 3 [Source:MGI Symbol;Acc:MGI:95704]	Q3TXW0	P23336	-3.3	2.7E-01	2.6	4.4E-01	3.3	2.5E-01	-2.6	4.1E-01
ENSMUST00000114973	kalirin, RhoGEF kinase [Source:MGI Symbol;Acc:MGI:2685385]	D3Z4R2		8.8	9.9E-06	-5.3	5.0E-04	0.6	1.2E-01	-0.7	5.5E-01
ENSMUST00000114975	protein kinase, AMP-activated, gamma 2 non-catalytic subunit [Source:MGI Symbol;Acc:MGI:1336153]	Q3TMN8	Q91WG5	-7.3	5.7E-06	2.3	2.9E-01	-3.6	1.2E-01	0.9	5.2E-01
ENSMUST00000114981	family with sequence similarity 178, member B [Source:MGI Symbol;Acc:MGI:3026913]	E9PUL8		6.9	2.9E-04	-3.2	1.7E-01	1.1	3.3E-01	-1.0	6.8E-01
ENSMUST00000114993	CCR4-NOT transcription complex, subunit 4 [Source:MGI Symbol;Acc:MGI:1859026]			-2.6	2.8E-02	5.2	5.6E-03	-1.3	3.8E-01	0.5	5.8E-01
ENSMUST00000114996	optineurin [Source:MGI Symbol;Acc:MGI:1918898]		Q8K3K8	-2.6	3.2E-04	-2.7	1.6E-02	1.1	6.8E-02	1.2	2.1E-01
ENSMUST00000113025	RAB14, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1915615]	A2AL34		-3.7	5.6E-02	-1.5	4.6E-01	0.3	8.1E-01	-1.8	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000113026	ring finger protein 128 [Source:MGI Symbol;Acc:MGI:1914139]		Q9D304	1.8	2.3E-01	0.9	5.6E-01	-2.2	1.4E-01	-1.3	3.6E-01
ENSMUST00000114998	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound [Source:MGI Symbol;Acc:MGI:2180001]	Q8BU59		8.0	1.8E-05	-0.3	7.3E-01	1.1	8.2E-02	-0.1	8.9E-01
ENSMUST00000113032	centriolin [Source:MGI Symbol;Acc:MGI:1889576]	R4GML3		-3.3	6.6E-02	1.0	5.7E-01	1.9	2.4E-01	-2.5	1.6E-01
ENSMUST00000115007	RIKEN cDNA 3110062M04 gene [Source:MGI Symbol;Acc:MGI:1925662]		Q8BHZ5	-4.0	2.2E-02	3.2	2.3E-02	-0.6	5.9E-01	3.6	2.5E-03
ENSMUST00000113034	centriolin [Source:MGI Symbol;Acc:MGI:1889576]	R4GML4		2.1	5.6E-01	-0.3	9.5E-01	-2.8	3.9E-01	-0.5	9.0E-01
ENSMUST00000113035	ubiquitin-like, containing PHD and RING finger domains, 1 [Source:MGI Symbol;Acc:MGI:1338889]		Q8VDF2	3.0	3.0E-01	7.7	1.1E-01	3.4	4.3E-01	-1.2	6.3E-01
ENSMUST00000113037	centriolin [Source:MGI Symbol;Acc:MGI:1889576]	E9Q9E7		4.6	1.1E-01	7.6	6.1E-02	3.1	3.8E-01	0.1	9.8E-01
ENSMUST00000113038	ubiquitin-like, containing PHD and RING finger domains, 1 [Source:MGI Symbol;Acc:MGI:1338889]		Q8VDF2	-1.5	4.4E-01	-0.9	7.3E-01	1.3	5.3E-01	0.6	7.8E-01
ENSMUST00000113039	ubiquitin-like, containing PHD and RING finger domains, 1 [Source:MGI Symbol;Acc:MGI:1338889]		Q8VDF2	-3.3	1.8E-01	-3.2	3.0E-01	-0.3	8.5E-01	-0.4	9.1E-01
ENSMUST00000115013	oculocerebrorenal syndrome of Lowe [Source:MGI Symbol;Acc:MGI:109589]	Q7TPR1		-1.9	1.5E-02	7.9	4.2E-04	-0.3	8.3E-01	0.9	2.3E-01
ENSMUST00000115019	selenophosphate synthetase 1 [Source:MGI Symbol;Acc:MGI:1923580]		Q8BH69	-5.6	1.6E-04	7.2	2.4E-02	-2.8	3.9E-01	-1.4	3.9E-01
ENSMUST00000115032	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]		Q3U108	-9.1	2.3E-04	8.1	1.5E-04	-0.7	6.2E-01	0.7	3.0E-01
ENSMUST00000113059	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7 [Source:MGI Symbol;Acc:M		Q68SA9	5.2	1.1E-01	4.6	2.1E-01	-0.3	9.4E-01	0.4	8.7E-01
ENSMUST00000113060	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7 [Source:MGI Symbol;Acc:M		Q68SA9	5.6	1.4E-01	5.9	1.5E-01	-0.8	8.4E-01	-1.1	6.4E-01
ENSMUST00000113063	interleukin 1 receptor accessory protein-like 2 [Source:MGI Symbol;Acc:MGI:1913106]	Q0VBP3	Q9ERS6	3.6	7.0E-02	4.7	3.8E-02	-0.4	8.3E-01	-1.5	2.8E-01
ENSMUST00000113064	TNF receptor-associated factor 1 [Source:MGI Symbol;Acc:MGI:101836]		P39428	1.1	3.6E-01	5.5	9.5E-03	2.5	1.6E-01	-1.9	9.3E-02
ENSMUST00000115036	transmembrane and ubiquitin-like domain containing 1 [Source:MGI Symbol;Acc:MGI:1923764]	E9QN77		-3.1	2.8E-02	4.4	6.8E-02	-0.7	7.6E-01	0.7	6.5E-01
ENSMUST00000113068	cutA divalent cation tolerance homolog-like [Source:MGI Symbol;Acc:MGI:1925246]	Q9D1U5		3.6	9.7E-02	2.0	4.5E-01	-0.5	8.4E-01	1.2	5.6E-01
ENSMUST00000113072	perilipin 5 [Source:MGI Symbol;Acc:MGI:1914218]		Q8BVZ1	3.7	6.1E-02	0.6	7.5E-01	-3.1	8.7E-02	0.1	9.8E-01
ENSMUST00000113075	F-box and WD-40 domain protein 2 [Source:MGI Symbol;Acc:MGI:1353435]	Q8BS25		0.0	1.0E+00	0.1	9.6E-01	0.3	7.5E-01	0.3	8.4E-01
ENSMUST00000113077	F-box and WD-40 domain protein 2 [Source:MGI Symbol;Acc:MGI:1353435]	A2AUG1		-2.8	3.2E-01	-3.8	2.6E-01	-1.9	3.0E-01	-0.9	8.0E-01
ENSMUST00000115038	roundabout homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1343102]	D3Z4M6		6.3	1.1E-02	-5.8	5.8E-04	0.6	1.8E-01	-0.7	6.1E-01
ENSMUST00000113080	F-box and WD-40 domain protein 2 [Source:MGI Symbol;Acc:MGI:1353435]	Q9QUH1		-0.5	8.8E-01	-4.3	2.7E-01	-4.4	6.7E-02	-0.6	8.9E-01
ENSMUST00000115046	roundabout homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1921394]	D3Z4M4		7.7	3.2E-05	1.4	2.0E-02	-2.3	1.2E-03	0.2	6.9E-01
ENSMUST00000115047	solute carrier family 4 (anion exchanger), member 2 [Source:MGI Symbol;Acc:MGI:109351]			7.6	5.3E-05	3.0	9.2E-02	-0.6	7.1E-01	3.3	1.7E-02
ENSMUST00000115049	solute carrier family 4 (anion exchanger), member 2 [Source:MGI Symbol;Acc:MGI:109351]			-6.4	1.3E-03	-1.3	1.9E-01	0.2	7.1E-01	-0.5	6.2E-01
ENSMUST00000113103	GTPase activating protein and VPS9 domains 1 [Source:MGI Symbol;Acc:MGI:1913941]	F7ADS7		1.4	4.8E-01	-1.8	4.9E-01	-2.1	2.0E-01	1.1	6.8E-01
ENSMUST00000113106				1.3	7.2E-02	2.1	3.7E-02	0.7	3.2E-01	0.0	9.7E-01
ENSMUST00000113107				4.3	4.2E-02	2.4	3.5E-01	-0.8	7.2E-01	1.0	5.7E-01
ENSMUST00000115057	DDB1 and CUL4 associated factor 12-like 2 [Source:MGI Symbol;Acc:MGI:2445178]		Q8BGW4	7.2	8.9E-06	-6.3	2.3E-04	-0.2	6.2E-01	-1.9	1.6E-01
ENSMUST00000115058	teneurin transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1345185]	A2ANL9		7.5	7.3E-05	-0.7	3.8E-01	0.3	5.4E-01	-0.6	4.6E-01
ENSMUST00000115066	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2441769]		Q8K4J0	-4.0	2.9E-03	-4.4	1.5E-03	-0.7	1.6E-01	-0.8	4.5E-01
ENSMUST00000113113	nerve growth factor receptor (TNFRSF16) associated protein 1 [Source:MGI Symbol;Acc:MGI:1338016]		Q9WTZ9	-2.6	3.6E-02	-2.4	1.0E-01	-0.1	9.2E-01	-0.3	8.1E-01
ENSMUST00000115071	protease, serine 40 [Source:MGI Symbol;Acc:MGI:1270857]	E9Q9Y0		6.7	1.6E-04	-4.0	3.1E-02	0.8	3.1E-01	2.4	1.5E-01
ENSMUST00000113119	bromodomain and PHD finger containing, 1 [Source:MGI Symbol;Acc:MGI:1926033]	Q3U109		2.1	3.2E-01	3.8	8.1E-02	-1.9	3.5E-01	-3.5	7.4E-02
ENSMUST00000115073	stromal antigen 2 [Source:MGI Symbol;Acc:MGI:1098583]	A2AFF6		-1.8	3.1E-02	-6.3	1.5E-02	0.5	4.8E-01	1.9	3.9E-01
ENSMUST00000113122	bromodomain and PHD finger containing, 1 [Source:MGI Symbol;Acc:MGI:1926033]	B2RRD7		-4.6	1.5E-01	-1.0	6.4E-01	-0.2	9.2E-01	-3.7	2.5E-01
ENSMUST00000115079	ribosomal protein L35A [Source:MGI Symbol;Acc:MGI:1928894]	Q6ZWX1	O55142	-3.3	1.4E-03	-5.1	8.0E-04	-0.8	1.0E-01	-0.7	5.4E-01
ENSMUST00000113124	mitogen-activated protein kinase associated protein 1 [Source:MGI Symbol;Acc:MGI:2444554]		Q8BKH7	-4.2	1.7E-01	1.1	7.9E-01	4.3	1.8E-01	-1.0	7.9E-01
ENSMUST00000113126	mitogen-activated protein kinase associated protein 1 [Source:MGI Symbol;Acc:MGI:2444554]		Q8BKH7	-1.0	7.2E-01	7.6	1.1E-01	5.3	2.4E-01	-3.3	2.1E-01
ENSMUST00000115086	etoposide induced 2.4 mRNA [Source:MGI Symbol;Acc:MGI:108090]			-3.8	6.4E-04	-6.8	1.8E-04	0.5	2.1E-01	1.0	3.8E-01
ENSMUST00000113130	maestro heat-like repeat family member 2A [Source:MGI Symbol;Acc:MGI:3705228]	F5H8M8		0.7	7.5E-01	0.9	7.9E-01	1.2	6.4E-01	1.0	7.5E-01
ENSMUST00000113132	pre B cell leukemia homeobox 3 [Source:MGI Symbol;Acc:MGI:97496]		O35317	-0.6	6.5E-01	2.3	1.5E-01	0.5	6.8E-01	-2.3	1.0E-01
ENSMUST00000115090	nitric oxide synthase 3, endothelial cell [Source:MGI Symbol;Acc:MGI:97362]	E9Q9X4		8.6	6.1E-04	-4.1	2.4E-03	-0.2	7.3E-01	-0.7	5.5E-01
ENSMUST00000113136	G protein-coupled receptor associated sorting protein 2 [Source:MGI Symbol;Acc:MGI:2442071]		Q8BUY8	3.6	1.2E-01	4.0	1.4E-01	0.2	9.3E-01	-0.2	9.2E-01
ENSMUST00000113137	UDP glucuronosyltransferase 1 family, polypeptide A6B [Source:MGI Symbol;Acc:MGI:3580629]	K9J7B2		-1.3	1.5E-01	-4.9	1.9E-02	-0.4	5.6E-01	3.1	9.6E-02
ENSMUST00000113138	UDP glucuronosyltransferase 1 family, polypeptide A6B [Source:MGI Symbol;Acc:MGI:3580629]	K9J7B2		-1.7	1.6E-01	3.6	1.9E-02	2.2	7.5E-02	-3.2	2.5E-02
ENSMUST00000113142	UDP glycosyltransferase 1 family, polypeptide A10 [Source:MGI Symbol;Acc:MGI:3580642]	E9PXN7		3.2	9.4E-02	6.2	7.5E-03	-0.4	8.5E-01	-3.4	1.8E-02
ENSMUST00000115094	X-linked inhibitor of apoptosis [Source:MGI Symbol;Acc:MGI:107572]		Q60989	-5.1	2.3E-03	3.5	2.7E-01	-0.1	9.7E-01	2.4	2.7E-01
ENSMUST00000113144	G protein-coupled receptor associated sorting protein 1 [Source:MGI Symbol;Acc:MGI:1917418]		Q5U4C1	1.0	6.9E-01	8.6	1.4E-02	3.8	1.9E-01	-3.8	1.2E-01
ENSMUST00000115096	plexin A4 [Source:MGI Symbol;Acc:MGI:2179061]		Q80UG2	7.5	1.2E-06	-6.1	3.4E-04	1.3	8.5E-03	0.2	8.8E-01
ENSMUST00000113149	melanocortin 2 receptor accessory protein 2 [Source:MGI Symbol;Acc:MGI:3609239]		D3Z1Q2	3.4	1.6E-01	7.8	8.8E-03	-0.3	9.0E-01	-4.7	8.8E-03
ENSMUST00000115097	O-acyltransferase like [Source:MGI Symbol;Acc:MGI:2442915]	Q8BML2		6.8	7.2E-05	-4.9	5.3E-02	2.7	1.1E-02	3.1	1.9E-01
ENSMUST00000113157	SET domain containing 5 [Source:MGI Symbol;Acc:MGI:1920145]		Q5XJV7	-3.0	2.9E-01	-3.4	2.3E-01	-1.7	3.2E-01	-1.3	6.8E-01
ENSMUST00000113158	zinc finger and BTB domain containing 34 [Source:MGI Symbol;Acc:MGI:2685195]	A2ATY4		-0.3	9.3E-01	-1.6	6.5E-01	-2.2	3.7E-01	-0.8	8.3E-01
ENSMUST00000113161	RAB3A interacting protein (rabin3)-like 1 [Source:MGI Symbol;Acc:MGI:1922010]		Q8VDV3	-0.2	8.7E-01	-2.6	1.3E-01	-2.1	6.8E-02	0.2	8.9E-01
ENSMUST00000115098	otassium voltage-gated channel, subfamily H (eag-related), member 2 [Source:MGI Symbol;Acc:MGI:1341722			6.6	1.9E-04	5.2	4.1E-04	0.3	7.0E-01	0.9	1.6E-01
ENSMUST00000113165	Ral GEF with PH domain and SH3 binding motif 1 [Source:MGI Symbol;Acc:MGI:1922008]	A0A0A0MQE4		-4.0	1.2E-01	4.5	1.5E-01	4.8	9.7E-02	-3.7	1.4E-01
ENSMUST00000115100	IQ motif containing G [Source:MGI Symbol;Acc:MGI:1916957]		Q80W32	7.6	9.5E-05	7.4	1.5E-02	-0.9	7.5E-01	-2.0	2.2E-01
ENSMUST00000113185	zinc finger, matrin type 1 [Source:MGI Symbol;Acc:MGI:2442284]	Z4YL92		-1.2	4.8E-01	1.9	5.5E-01	4.6	8.7E-02	1.5	5.6E-01
ENSMUST00000115105	RIKEN cDNA 1700021K19 gene [Source:MGI Symbol;Acc:MGI:1915160]		Q80U62	7.0	1.1E-02	-1.6	1.3E-01	0.3	5.8E-01	-1.5	1.8E-01
ENSMUST00000113193	armadillo repeat containing, X-linked 2 [Source:MGI Symbol;Acc:MGI:1914666]		Q6A058	-0.2	9.3E-01	2.8	4.0E-01	2.8	3.5E-01	-0.2	9.3E-01
ENSMUST00000113194	armadillo repeat containing, X-linked 6 [Source:MGI Symbol;Acc:MGI:2147993]		Q8K3A6	4.9	4.3E-02	7.4	9.0E-03	-0.5	8.4E-01	-3.0	5.2E-02
ENSMUST00000113195	raftlin lipid raft linker 1 [Source:MGI Symbol;Acc:MGI:1923688]	D3Z731		-0.6	5.4E-01	0.1	9.3E-01	0.2	8.2E-01	-0.5	6.6E-01
ENSMUST00000115109	family with sequence similarity 126, member A [Source:MGI Symbol;Acc:MGI:2149839]	D3Z481		3.6	1.3E-02	-3.4	2.6E-01	1.9	2.6E-01	-0.8	7.7E-01
ENSMUST00000115116	mucin 20 [Source:MGI Symbol;Acc:MGI:2385039]	E9PUF1		7.7	9.6E-05	1.5	5.2E-02	-0.4	4.7E-01	0.3	5.7E-01
ENSMUST00000115123	tyrosine kinase, non-receptor, 2 [Source:MGI Symbol;Acc:MGI:1858308]	D3Z3U6		-4.8	3.6E-04	-6.7	8.3E-05	-1.0	4.8E-02	-3.8	2.4E-02
ENSMUST00000115134	ATPase, (Na+)/K+ transporting, beta 4 polypeptide [Source:MGI Symbol;Acc:MGI:1915071]	B1APX1	Q99ME6	5.5	3.7E-04	-0.4	4.3E-01	-2.8	1.9E-04	-0.4	4.5E-01
ENSMUST00000115139	carboxypeptidase A5 [Source:MGI Symbol;Acc:MGI:1921899]	B2RQW9	Q8R4H4	6.4	4.6E-03	5.9	6.8E-04	-1.4	3.1E-01	-0.7	3.3E-01
ENSMUST00000115140	phosphate cytidylyltransferase 1, choline, alpha isoform [Source:MGI Symbol;Acc:MGI:88557]		P49586	7.1	9.9E-04	2.5	2.6E-01	-3.3	1.6E-01	0.1	9.5E-01
ENSMUST00000115145	one cut domain, family member 2 [Source:MGI Symbol;Acc:MGI:1891408]		Q6XBJ3	8.9	1.4E-04	8.0	8.7E-05	1.3	2.9E-01	-0.4	4.4E-01
ENSMUST00000113229	MOB kinase activator 1B [Source:MGI Symbol;Acc:MGI:1915723]	Q3UDM0		0.3	6.0E-01	0.2	8.5E-01	0.5	4.9E-01	0.6	4.7E-01
ENSMUST00000113230	eukaryotic translation initiation factor 4E member 2 [Source:MGI Symbol;Acc:MGI:1914440]	D3Z730		2.9	6.6E-02	1.6	3.8E-01	-0.8	5.7E-01	0.5	7.6E-01
ENSMUST00000115149	transmembrane 4 L six family member 19 [Source:MGI Symbol;Acc:MGI:3645933]	E9Q9H8		6.5	3.4E-04	-5.2	1.9E-04	0.3	3.8E-01	-1.7	1.2E-01
ENSMUST00000115151	UBX domain protein 7 [Source:MGI Symbol;Acc:MGI:2146388]	G5E8R8		-1.2	1.6E-02	-5.0	6.8E-03	-0.7	2.9E-01	0.0	9.8E-01
ENSMUST00000115160	transmembrane protein 209 [Source:MGI Symbol;Acc:MGI:1919899]		Q8BRG8	1.2	2.5E-02	4.6	8.8E-03	1.6	2.2E-01	0.4	6.6E-01
ENSMUST00000115165	negative regulator of reactive oxygen species [Source:MGI Symbol;Acc:MGI:2445095]		Q8BMT4	-9.9	1.0E-04	-3.6	2.0E-03	1.9	1.9E-03	-0.6	5.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000113235	eukaryotic translation initiation factor 4E member 2 [Source:MGI Symbol;Acc:MGI:1914440]	D3Z729		0.5	8.5E-01	2.6	5.7E-01	2.6	5.1E-01	0.5	8.6E-01
ENSMUST00000115168	centrosomal protein 19 [Source:MGI Symbol;Acc:MGI:1914244]		Q9CQA8	-6.3	1.8E-04	-4.9	4.4E-04	0.0	9.7E-01	-2.3	6.7E-02
ENSMUST00000115176	solute carrier family 26, member 5 [Source:MGI Symbol;Acc:MGI:1933154]	Q32MT6		6.5	3.3E-04	-2.1	1.6E-01	1.0	2.3E-01	-2.2	1.6E-01
ENSMUST00000115195	DnaJ (Hsp40) homolog, subfamily C, member 2 [Source:MGI Symbol;Acc:MGI:99470]	E9Q9H2		-6.1	1.1E-04	7.9	2.1E-04	-0.4	7.7E-01	0.0	9.6E-01
ENSMUST00000115200	nuclear respiratory factor 1 [Source:MGI Symbol;Acc:MGI:1332235]	E9Q7X0		4.7	3.9E-04	-5.3	3.8E-03	-1.1	8.4E-02	0.0	9.9E-01
ENSMUST00000113249	tRNA nucleotidyl transferase, CCA-adding, 1 [Source:MGI Symbol;Acc:MGI:1917297]		Q8K1J6	-2.4	4.0E-01	-4.7	1.0E-01	-4.0	3.5E-02	-1.7	5.9E-01
ENSMUST00000115211	nuclear respiratory factor 1 [Source:MGI Symbol;Acc:MGI:1332235]		Q9WU00	-7.4	4.7E-04	-3.3	8.8E-04	0.1	8.2E-01	-0.6	4.5E-01
ENSMUST00000113252	TRM2 tRNA methyltransferase 2B [Source:MGI Symbol;Acc:MGI:2442530]		Q8BQJ6	1.3	4.5E-01	2.1	3.1E-01	0.5	7.6E-01	-0.3	8.8E-01
ENSMUST00000113262	forkhead box P4 [Source:MGI Symbol;Acc:MGI:1921373]			-2.6	5.9E-02	-1.8	3.3E-01	1.3	1.9E-01	0.4	8.1E-01
ENSMUST00000113265	forkhead box P4 [Source:MGI Symbol;Acc:MGI:1921373]		Q9DBY0	1.2	1.1E-01	3.0	6.6E-03	1.1	1.6E-01	-0.7	3.5E-01
ENSMUST00000113266	myosin VI [Source:MGI Symbol;Acc:MGI:104785]	E9Q175		0.6	4.2E-01	3.1	5.9E-03	1.1	1.8E-01	-1.4	8.8E-02
ENSMUST00000115217	N-acyl phosphatidylethanolamine phospholipase D [Source:MGI Symbol;Acc:MGI:2140885]		Q8BH82	10.3	3.4E-05	8.0	3.1E-04	-0.7	6.7E-01	-0.9	2.4E-01
ENSMUST00000115224	striatin interacting protein 2 [Source:MGI Symbol;Acc:MGI:2444363]	E9QN41		5.4	4.1E-05	2.4	1.2E-01	-1.8	1.9E-01	0.2	8.6E-01
ENSMUST00000115226	3-hydroxybutyrate dehydrogenase, type 1 [Source:MGI Symbol;Acc:MGI:1919161]		Q80XN0	5.8	4.0E-03	3.9	6.9E-02	-3.1	1.6E-01	-0.2	8.7E-01
ENSMUST00000115227	3-hydroxybutyrate dehydrogenase, type 1 [Source:MGI Symbol;Acc:MGI:1919161]		Q80XN0	3.7	1.6E-04	6.8	5.5E-04	-0.6	7.0E-01	-1.1	1.8E-01
ENSMUST00000115228	mitogen-activated protein kinase 8 interacting protein 3 [Source:MGI Symbol;Acc:MGI:1353598]		Q9ESN9	-5.2	1.6E-02	3.8	2.3E-03	-1.3	1.6E-01	-0.4	6.2E-01
ENSMUST00000113286	cleavage stimulation factor, 3' pre-RNA subunit 2 [Source:MGI Symbol;Acc:MGI:1343054]		Q8BIQ5	2.0	4.8E-02	4.4	7.3E-03	1.5	2.5E-01	-1.0	2.5E-01
ENSMUST00000113287	cleavage stimulation factor, 3' pre-RNA subunit 2 [Source:MGI Symbol;Acc:MGI:1343054]	A2AEK1		-0.1	9.7E-01	-2.7	3.9E-01	-1.9	3.0E-01	0.7	8.3E-01
ENSMUST00000115231	ribosomal protein L39 [Source:MGI Symbol;Acc:MGI:1914498]	Q505A8	P62892	-8.5	1.2E-06	0.0	9.9E-01	-5.9	1.5E-03	0.6	5.8E-01
ENSMUST00000115233	protein phosphatase 1, regulatory (inhibitor) subunit 2 [Source:MGI Symbol;Acc:MGI:1914099]	D3Z3A0		-8.6	1.0E-04	6.0	1.9E-03	-0.8	6.1E-01	0.6	4.8E-01
ENSMUST00000115237	neurotrimin [Source:MGI Symbol;Acc:MGI:2446259]		Q99PJ0	6.4	8.3E-03	7.0	1.7E-03	0.8	6.1E-01	-0.1	9.2E-01
ENSMUST00000115238	S-adenosylhomocysteine hydrolase-like 2 [Source:MGI Symbol;Acc:MGI:1921590]		Q68FL4	7.0	6.2E-04	4.4	9.1E-02	0.3	8.9E-01	3.1	5.9E-02
ENSMUST00000115239	septin 6 [Source:MGI Symbol;Acc:MGI:1888939]		Q9R1T4	-4.6	1.1E-02	-3.9	1.9E-03	0.4	3.7E-01	-2.4	4.9E-02
ENSMUST00000115243	opioid binding protein/cell adhesion molecule-like [Source:MGI Symbol;Acc:MGI:97397]	Q6DFY2		7.3	5.3E-05	-6.6	1.8E-03	0.6	2.5E-01	-0.1	9.7E-01
ENSMUST00000115244	collagen, type XIX, alpha 1 [Source:MGI Symbol;Acc:MGI:1095415]		Q0VF58	3.6	1.7E-02	4.3	8.5E-04	-0.5	5.9E-01	-0.4	5.5E-01
ENSMUST00000115247	immunoglobulin superfamily, member 9B [Source:MGI Symbol;Acc:MGI:2685354]	D3Z169		8.7	1.1E-04	4.5	4.0E-02	-0.6	7.6E-01	0.9	4.7E-01
ENSMUST00000113310	e carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 [Source:MGI Symbol;Acc:MGI:1915		A2ASZ8	-2.1	4.0E-01	-4.2	2.1E-01	-1.4	4.2E-01	0.7	8.4E-01
ENSMUST00000113320	diaphanous homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1858500]		O70566	1.7	3.4E-01	0.1	9.6E-01	2.2	3.5E-01	3.8	1.3E-01
ENSMUST00000115258	zinc finger, CCHC domain containing 12 [Source:MGI Symbol;Acc:MGI:1919943]		Q9CZA5	5.5	1.1E-02	-6.4	7.4E-04	0.1	8.6E-01	-0.7	6.4E-01
ENSMUST00000115259	transmembrane protein 60 [Source:MGI Symbol;Acc:MGI:2673965]		Q8K174	-1.4	1.3E-02	1.7	2.6E-01	3.6	1.4E-02	-0.9	4.7E-01
ENSMUST00000113331	CDKN1A interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1920234]	A2AN61		-0.7	8.0E-01	-3.9	2.7E-01	-3.7	7.7E-02	-0.6	8.8E-01
ENSMUST00000113332	CDKN1A interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1920234]	Q3UUV0		-3.2	3.9E-02	2.5	1.0E-01	2.3	8.0E-02	-3.4	3.5E-02
ENSMUST00000115261	predicted gene 1110 [Source:MGI Symbol;Acc:MGI:2685956]	Q0Q237		5.9	1.4E-03	6.3	1.0E-03	-0.6	6.8E-01	-0.4	5.9E-01
ENSMUST00000113335	ubiquitin protein ligase E3 component n-recognin 2 [Source:MGI Symbol;Acc:MGI:1861099]	Q3UPU3	Q6WKZ8	-2.9	1.3E-01	-2.5	3.7E-01	0.7	7.2E-01	0.3	9.0E-01
ENSMUST00000115262	methionine sulfoxide reductase B1 [Source:MGI Symbol;Acc:MGI:1351642]		Q9JLC3	-10.3	3.1E-06	-1.7	1.0E-02	0.5	1.8E-01	0.0	9.5E-01
ENSMUST00000115264	dedicator of cytokinesis 11 [Source:MGI Symbol;Acc:MGI:1923224]	A2AF65		-8.4	2.3E-03	-4.3	1.5E-01	1.6	3.0E-01	-0.7	8.0E-01
ENSMUST00000115266	dedicator of cytokinesis 11 [Source:MGI Symbol;Acc:MGI:1923224]	A2AF67		-7.7	1.5E-04	6.0	1.4E-02	-0.6	7.9E-01	-1.4	2.7E-01
ENSMUST00000115269	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) [Source:MGI Symbol;Acc:MGI:1924148]	Q8R531		6.3	3.1E-03	8.9	3.9E-05	-0.2	8.8E-01	-0.5	3.6E-01
ENSMUST00000115274	platelet derived growth factor receptor, beta polypeptide [Source:MGI Symbol;Acc:MGI:97531]	E9QN12		6.0	2.3E-02	5.2	2.7E-05	-3.7	1.8E-03	-0.8	1.3E-01
ENSMUST00000113355	FERM domain containing 4B [Source:MGI Symbol;Acc:MGI:2141794]		Q920B0	0.1	9.3E-01	1.6	1.2E-01	-2.7	2.0E-02	-4.2	3.7E-03
ENSMUST00000113359	FERM domain containing 4B [Source:MGI Symbol;Acc:MGI:2141794]	Q6ZQ04		2.2	5.8E-02	-5.7	1.8E-04	-8.6	2.1E-06	-0.7	5.0E-01
ENSMUST00000115286	family with sequence similarity 71, member F2 [Source:MGI Symbol;Acc:MGI:2141439]	B2RXB0		5.1	2.4E-02	-4.5	7.0E-05	0.6	7.9E-02	0.2	8.0E-01
ENSMUST00000115295	calcium/calmodulin-dependent protein kinase II alpha [Source:MGI Symbol;Acc:MGI:88256]		P11798	5.5	1.6E-03	4.2	6.6E-03	-2.9	5.4E-02	-1.5	1.6E-01
ENSMUST00000113373	ubiquitin-like modifier activating enzyme 6 [Source:MGI Symbol;Acc:MGI:1913894]	D3Z061		-1.0	2.4E-01	0.6	5.7E-01	0.6	4.2E-01	-0.9	3.3E-01
ENSMUST00000113377	golgi autoantigen, golgin subfamily a, 2 [Source:MGI Symbol;Acc:MGI:2139395]		Q921M4	0.3	6.4E-01	2.8	4.8E-02	3.4	8.7E-03	1.0	2.9E-01
ENSMUST00000115306	transformation related protein 63 [Source:MGI Symbol;Acc:MGI:1330810]	Q3UVI3		7.1	1.3E-04	8.1	1.1E-04	-0.8	5.7E-01	0.7	2.7E-01
ENSMUST00000115321	zinc finger protein 800 [Source:MGI Symbol;Acc:MGI:1889334]	B7ZMR9	Q0VEE6	-3.4	2.4E-02	4.2	1.6E-03	0.3	7.7E-01	0.6	4.2E-01
ENSMUST00000113388	choroideremia (RAB escort protein 1) [Source:MGI Symbol;Acc:MGI:892979]	Q3UR39		-4.2	3.8E-02	0.2	9.3E-01	0.1	9.5E-01	-4.3	3.1E-02
ENSMUST00000115323	glutamate receptor, metabotropic 8 [Source:MGI Symbol;Acc:MGI:1351345]	Q05BD6		6.8	2.0E-04	-4.6	1.4E-03	-0.4	4.7E-01	-3.4	2.6E-02
ENSMUST00000115331	protein kinase C substrate 80K-H [Source:MGI Symbol;Acc:MGI:107877]		O08795	-5.1	4.7E-03	6.1	2.1E-03	-0.6	6.8E-01	0.3	7.4E-01
ENSMUST00000115334	zinc finger protein 182 [Source:MGI Symbol;Acc:MGI:2442220]	A2AE19		-3.3	6.4E-03	5.3	1.1E-05	-0.5	3.7E-01	-0.6	1.2E-01
ENSMUST00000113421	leucine rich repeat containing 1 [Source:MGI Symbol;Acc:MGI:2442313]	G3X9W3		-1.6	4.6E-01	-1.3	6.6E-01	0.1	9.5E-01	-0.2	9.5E-01
ENSMUST00000115335	beta galactoside alpha 2,6 sialyltransferase 1 [Source:MGI Symbol;Acc:MGI:108470]		Q64685	6.2	3.0E-03	-2.6	1.0E-01	1.5	1.0E-01	-0.7	6.5E-01
ENSMUST00000115341	eukaryotic translation initiation factor 4A2 [Source:MGI Symbol;Acc:MGI:106906]		P10630	-7.3	5.1E-06	7.5	3.7E-05	0.0	1.0E+00	-0.3	5.8E-01
ENSMUST00000115344	cysteine-rich secretory protein 4 [Source:MGI Symbol;Acc:MGI:1925331]	E9PVG4		5.7	5.2E-04	9.0	4.7E-05	0.0	9.8E-01	-0.9	1.3E-01
ENSMUST00000115351	RAB3D, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:97844]	Q543Q4	P35276	-6.2	1.1E-03	-2.0	2.6E-02	1.4	1.7E-02	-0.4	5.8E-01
ENSMUST00000113444	ArfGAP with FG repeats 1 [Source:MGI Symbol;Acc:MGI:1333754]		Q8K2K6	-2.6	2.9E-01	-3.4	2.7E-01	-0.9	6.1E-01	-0.1	9.8E-01
ENSMUST00000115354	ring finger protein 133 [Source:MGI Symbol;Acc:MGI:2677436]		Q14B02	6.6	7.9E-05	7.3	5.9E-05	0.5	6.4E-01	-0.2	6.6E-01
ENSMUST00000115356	Ca2+-dependent activator protein for secretion 2 [Source:MGI Symbol;Acc:MGI:2443963]		Q8BYR5	6.4	4.4E-04	6.1	9.5E-04	-3.3	5.7E-02	-1.6	5.5E-02
ENSMUST00000113447	prickle homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925144]		Q80Y24	5.1	7.0E-02	3.0	3.6E-01	-1.2	6.9E-01	0.9	7.1E-01
ENSMUST00000113449	RE1-silencing transcription factor [Source:MGI Symbol;Acc:MGI:104897]		Q8VIG1	-1.3	5.5E-01	8.2	1.0E-01	7.5	1.1E-01	-2.0	4.0E-01
ENSMUST00000115365	transmembrane protein 243, mitochondrial [Source:MGI Symbol;Acc:MGI:3606159]	B2RVB9		-4.4	2.8E-05	7.0	9.5E-05	-0.5	6.5E-01	-0.2	7.3E-01
ENSMUST00000113452				-2.5	1.5E-01	-0.8	7.1E-01	1.2	3.9E-01	-0.5	8.0E-01
ENSMUST00000115366	solute carrier family 12, member 2 [Source:MGI Symbol;Acc:MGI:101924]	E9QM38		4.5	1.5E-04	-8.7	1.0E-04	0.4	3.2E-01	1.2	3.9E-01
ENSMUST00000115367	RIKEN cDNA 4930444P10 gene [Source:MGI Symbol;Acc:MGI:1923049]	D3YUR1		6.7	4.0E-05	6.8	1.1E-04	-0.3	8.0E-01	-0.3	6.6E-01
ENSMUST00000115374	RNA binding motif protein 10 [Source:MGI Symbol;Acc:MGI:2384310]		Q99KG3	7.4	8.8E-03	5.3	8.5E-04	-0.6	6.2E-01	-2.9	6.5E-03
ENSMUST00000115379	insulin-like growth factor 2 mRNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1890358]	A6X8Z3		3.5	4.7E-03	7.0	4.7E-05	-1.5	1.9E-01	-0.4	4.4E-01
ENSMUST00000115388	a disintegrin and metallopeptidase domain 22 [Source:MGI Symbol;Acc:MGI:1340046]		Q9R1V6	6.9	3.5E-02	-3.2	2.2E-02	1.3	6.3E-02	0.8	5.0E-01
ENSMUST00000115389	inhibitor of growth family, member 3 [Source:MGI Symbol;Acc:MGI:1919027]	D3YUP8		-5.7	7.2E-05	4.4	6.7E-02	-1.2	5.8E-01	-0.3	8.2E-01
ENSMUST00000113462	neurexin II [Source:MGI Symbol;Acc:MGI:1096362]	E9PUM9		2.6	1.5E-01	5.2	1.2E-02	-0.6	7.5E-01	-3.2	3.7E-02
ENSMUST00000115391	retinitis pigmentosa 2 homolog (human) [Source:MGI Symbol;Acc:MGI:1277953]		Q9EPK2	-6.5	8.9E-04	6.2	2.9E-03	4.6	9.5E-03	1.2	1.9E-01
ENSMUST00000115393	solute carrier family 9 (sodium/hydrogen exchanger), member 7 [Source:MGI Symbol;Acc:MGI:2444530]		Q8BLV3	5.6	7.7E-06	6.1	1.9E-02	-1.8	4.7E-01	-2.2	1.6E-01
ENSMUST00000115402	solute carrier organic anion transporter family, member 5A1 [Source:MGI Symbol;Acc:MGI:2443431]	E9PVE0		5.0	5.1E-04	7.8	1.1E-03	0.6	7.3E-01	1.2	1.8E-01
ENSMUST00000115409	3-phosphoinositide dependent protein kinase 1 [Source:MGI Symbol;Acc:MGI:1338068]	F2Z3Z9		8.8	1.6E-03	-6.2	3.0E-04	0.1	8.5E-01	-0.8	5.2E-01
ENSMUST00000113472	RAS, guanyl releasing protein 2 [Source:MGI Symbol;Acc:MGI:1333849]		Q9QUG9	0.1	8.9E-01	-0.3	8.3E-01	-0.1	9.4E-01	0.3	7.8E-01
ENSMUST00000115410	synuclein, alpha interacting protein (synphilin) [Source:MGI Symbol;Acc:MGI:1915097]	Q3V1N2		6.4	9.6E-03	4.9	1.1E-02	-1.0	5.4E-01	-0.9	4.4E-01
ENSMUST00000115421	STEAP family member 4 [Source:MGI Symbol;Acc:MGI:1923560]		Q923B6	-7.9	4.0E-06	1.2	6.6E-02	-1.8	7.8E-03	-0.2	6.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000115423	chordin [Source:MGI Symbol;Acc:MGI:1313268]	A2CG33		7.6	1.9E-05	1.3	7.9E-02	0.1	8.5E-01	0.2	7.2E-01
ENSMUST00000115425	six transmembrane epithelial antigen of prostate 2 [Source:MGI Symbol;Acc:MGI:1921301]	B2RX33	Q8BWB6	4.7	7.5E-03	2.0	1.4E-02	-0.5	3.8E-01	0.2	6.9E-01
ENSMUST00000115426	six transmembrane epithelial antigen of prostate 2 [Source:MGI Symbol;Acc:MGI:1921301]	B2RX33	Q8BWB6	7.6	2.2E-05	-4.9	3.5E-02	0.4	6.4E-01	0.5	8.2E-01
ENSMUST00000115437	thrombopoietin [Source:MGI Symbol;Acc:MGI:101875]	Q543R9	P40226	6.3	4.4E-04	-6.0	1.2E-02	1.7	3.9E-02	-0.8	7.2E-01
ENSMUST00000113488	splicing factor 1 [Source:MGI Symbol;Acc:MGI:1095403]	D3YZD0		0.9	6.0E-01	0.0	9.9E-01	-0.5	7.5E-01	0.4	8.7E-01
ENSMUST00000115442	met proto-oncogene [Source:MGI Symbol;Acc:MGI:96969]	F8VQL0		6.9	3.0E-04	6.5	1.8E-04	-0.5	6.3E-01	-0.7	2.9E-01
ENSMUST00000115445	claudin 12 [Source:MGI Symbol;Acc:MGI:1929288]		Q9ET43	5.5	4.4E-03	3.0	3.2E-03	-2.8	4.9E-03	-1.7	2.4E-02
ENSMUST00000113500	multiple endocrine neoplasia 1 [Source:MGI Symbol;Acc:MGI:1316736]		O88559	-1.5	5.0E-01	-2.5	5.6E-01	0.8	7.6E-01	1.7	6.6E-01
ENSMUST00000115449	ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A [Source:MGI Symbol;Acc:MGI:	K3W4S5		6.5	2.5E-02	2.3	2.3E-01	8.4	1.6E-04	0.9	5.6E-01
ENSMUST00000113505	ribosomal L24 domain containing 1 [Source:MGI Symbol;Acc:MGI:2681840]	E9Q4P7		2.1	8.9E-02	-5.1	9.3E-04	-7.6	1.5E-05	-0.4	7.4E-01
ENSMUST00000113506	steroid 5 alpha-reductase 3 [Source:MGI Symbol;Acc:MGI:1930252]	F6WPW1		5.7	4.6E-02	6.9	3.1E-02	0.1	9.9E-01	-1.2	4.8E-01
ENSMUST00000113507	steroid 5 alpha-reductase 3 [Source:MGI Symbol;Acc:MGI:1930252]	F6WPW1		-1.1	2.1E-01	-3.5	3.1E-02	0.6	3.6E-01	3.1	5.0E-02
ENSMUST00000113509	nucleoporin 210 [Source:MGI Symbol;Acc:MGI:1859555]			-2.3	3.6E-01	-0.6	8.7E-01	2.9	2.6E-01	1.2	7.3E-01
ENSMUST00000113512	WD repeat and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:1916618]	E9Q4P1		-0.9	1.7E-01	0.0	9.7E-01	1.1	9.3E-02	0.2	7.7E-01
ENSMUST00000113513	WD repeat and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:1916618]	E9Q4P1		-0.9	1.7E-01	0.0	9.7E-01	1.1	9.3E-02	0.2	7.7E-01
ENSMUST00000113514	WD repeat and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:1916618]	E9Q4P1		-0.9	1.7E-01	0.0	9.7E-01	1.1	9.3E-02	0.2	7.7E-01
ENSMUST00000113515	WD repeat and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:1916618]	E9Q4P1		-0.9	1.7E-01	0.0	9.7E-01	1.1	9.3E-02	0.2	7.7E-01
ENSMUST00000115451	cyclin-dependent kinase 14 [Source:MGI Symbol;Acc:MGI:894318]	Q6NVF8	O35495	7.3	3.6E-03	5.5	7.2E-05	-0.6	4.7E-01	-0.3	5.5E-01
ENSMUST00000113523	transmembrane protein 63b [Source:MGI Symbol;Acc:MGI:2387609]		Q3TWI9	-1.2	7.3E-02	-0.5	5.2E-01	0.5	3.5E-01	-0.2	8.3E-01
ENSMUST00000115453	caveolin 1, caveolae protein [Source:MGI Symbol;Acc:MGI:102709]		P49817	3.5	1.8E-02	3.7	1.2E-01	-0.7	7.5E-01	2.7	9.6E-02
ENSMUST00000115457	eukaryotic translation initiation factor 4, gamma 1 [Source:MGI Symbol;Acc:MGI:2384784]	E9PVC6		-6.4	2.2E-03	5.6	4.1E-04	-1.3	2.5E-01	-0.3	5.8E-01
ENSMUST00000115460	eukaryotic translation initiation factor 4, gamma 1 [Source:MGI Symbol;Acc:MGI:2384784]		Q6NZJ6	3.5	7.5E-04	7.2	2.3E-04	-0.5	6.8E-01	-0.2	7.2E-01
ENSMUST00000115467	testis derived transcript [Source:MGI Symbol;Acc:MGI:105081]		Q921W7	-5.8	8.1E-04	3.1	1.8E-01	-3.8	1.4E-01	-0.4	8.0E-01
ENSMUST00000115470	forkhead box P2 [Source:MGI Symbol;Acc:MGI:2148705]		Q3TPK1	7.1	7.9E-05	10.5	3.8E-06	-0.7	5.8E-01	-0.4	3.4E-01
ENSMUST00000113533	SAC3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1913656]		G5E8Q7	0.0	9.6E-01	2.6	2.4E-02	1.0	2.5E-01	-1.6	1.0E-01
ENSMUST00000115477	forkhead box P2 [Source:MGI Symbol;Acc:MGI:2148705]		P58463	6.3	4.8E-05	-4.6	3.9E-02	-0.6	5.2E-01	-0.9	6.9E-01
ENSMUST00000115487	ribonucleoprotein, PTB-binding 1 [Source:MGI Symbol;Acc:MGI:1919016]		Q9CW46	-1.7	2.7E-02	-3.1	1.7E-01	1.6	2.0E-01	-0.2	9.1E-01
ENSMUST00000113539	ZXD family zinc finger C [Source:MGI Symbol;Acc:MGI:1933108]	E9Q4N0		0.3	8.1E-01	-2.1	2.5E-01	-0.2	8.9E-01	2.2	1.9E-01
ENSMUST00000115494	zinc finger, GATA-like protein 1 [Source:MGI Symbol;Acc:MGI:3696042]		Q1WG82	5.6	2.0E-04	8.6	1.9E-04	-0.8	6.1E-01	0.5	4.4E-01
ENSMUST00000113552	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]		Q80TY0	1.4	9.5E-02	1.3	2.7E-01	0.2	8.1E-01	0.4	6.4E-01
ENSMUST00000115511	PHD finger protein 14 [Source:MGI Symbol;Acc:MGI:1923539]		Q9D4H9	-4.6	3.8E-03	-0.6	5.2E-01	0.6	3.1E-01	-1.1	2.4E-01
ENSMUST00000115513	BCL6 interacting corepressor [Source:MGI Symbol;Acc:MGI:1918708]		Q8CGN4	-4.1	1.4E-02	-3.4	3.3E-02	-1.5	7.5E-02	-2.0	2.6E-01
ENSMUST00000113558	41, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2140	B7ZMU0		-0.9	6.3E-01	-1.6	5.8E-01	-0.5	8.0E-01	0.2	9.4E-01
ENSMUST00000113559	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]		Q80TY0	0.5	8.4E-01	6.0	7.2E-02	2.6	3.8E-01	-2.9	2.3E-01
ENSMUST00000113560	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]		Q80TY0	-1.0	6.1E-01	-0.9	5.8E-01	-2.8	7.0E-02	-2.9	1.4E-01
ENSMUST00000115516	zinc finger protein 13 [Source:MGI Symbol;Acc:MGI:99159]	D7F2B3	P10754	7.0	1.1E-04	-6.5	1.5E-02	1.7	4.7E-02	-0.6	7.9E-01
ENSMUST00000113564	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]		Q80TY0	-2.8	9.3E-02	-1.0	5.5E-01	-0.5	6.5E-01	-2.3	2.3E-01
ENSMUST00000115519	islet cell autoantigen 1 [Source:MGI Symbol;Acc:MGI:96391]	D3Z118		-5.5	3.2E-04	7.2	8.7E-04	-0.7	6.6E-01	0.4	6.4E-01
ENSMUST00000113571	runt related transcription factor 2 [Source:MGI Symbol;Acc:MGI:99829]		Q08775	-1.7	1.4E-01	5.1	6.3E-02	8.5	3.7E-03	1.7	2.4E-01
ENSMUST00000113572	runt related transcription factor 2 [Source:MGI Symbol;Acc:MGI:99829]	F8WHN7		0.9	7.0E-02	1.0	9.8E-02	-0.2	6.1E-01	-0.3	5.3E-01
ENSMUST00000115524	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish)) [Source:MGI Symbol;Acc:MGI:1915291	Q4FK31	Q9CQ20	-4.0	1.0E-03	-5.4	3.1E-04	-0.1	8.1E-01	-0.5	5.9E-01
ENSMUST00000113575	transmembrane protein 198 [Source:MGI Symbol;Acc:MGI:2443133]		Q8BG75	-0.1	9.4E-01	4.1	2.1E-02	1.8	2.2E-01	-2.4	7.6E-02
ENSMUST00000115526	tetraspanin 7 [Source:MGI Symbol;Acc:MGI:1298407]	Q3UHG5		8.1	1.6E-04	5.4	1.4E-02	-0.6	7.5E-01	1.5	2.0E-01
ENSMUST00000115527	family with sequence similarity 133, member B [Source:MGI Symbol;Acc:MGI:1915402]		Q9CVI2	-1.8	1.5E-02	-2.5	4.2E-02	1.9	7.5E-03	-0.7	5.4E-01
ENSMUST00000115535	zinc finger protein 944 [Source:MGI Symbol;Acc:MGI:2442394]	E9PUS4		-2.2	9.4E-04	-1.1	6.7E-01	3.7	3.3E-02	-0.3	8.9E-01
ENSMUST00000115537	collagen, type XXVIII, alpha 1 [Source:MGI Symbol;Acc:MGI:2685312]		Q2UY11	6.6	1.9E-04	4.4	3.2E-03	-1.9	1.6E-01	0.0	9.9E-01
ENSMUST00000113592	paired related homeobox 2 [Source:MGI Symbol;Acc:MGI:98218]	Q9CY80		4.0	7.0E-02	3.4	1.0E-01	-2.4	2.7E-01	-1.8	2.3E-01
ENSMUST00000113594	tec protein tyrosine kinase [Source:MGI Symbol;Acc:MGI:98662]	Q3U436		-0.9	7.4E-01	-1.2	6.5E-01	-2.1	3.0E-01	-1.7	5.6E-01
ENSMUST00000115557	zinc finger protein 846 [Source:MGI Symbol;Acc:MGI:1924012]	G3X996		6.5	3.3E-04	-0.9	2.6E-01	0.8	1.7E-01	0.2	8.2E-01
ENSMUST00000113596	RAB7, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105068]	Q4FJQ0	P51150	0.7	1.6E-01	-0.5	4.0E-01	-1.0	4.3E-02	0.2	7.1E-01
ENSMUST00000115559	dynein cytoplasmic 1 intermediate chain 1 [Source:MGI Symbol;Acc:MGI:107743]		O88485	6.3	2.1E-02	-1.4	3.4E-01	1.2	2.0E-01	0.2	8.8E-01
ENSMUST00000113598	RAB7, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105068]	Q4FJQ0	P51150	-0.9	8.3E-01	1.9	6.4E-01	0.5	8.9E-01	-2.3	5.7E-01
ENSMUST00000115562	zinc finger protein 426 [Source:MGI Symbol;Acc:MGI:1920248]		Q8R1D1	-4.0	2.6E-03	4.1	1.9E-04	-2.9	2.5E-03	-0.3	5.7E-01
ENSMUST00000115567	nuclear receptor subfamily 3, group C, member 1 [Source:MGI Symbol;Acc:MGI:95824]	E9PUR6		-5.2	1.1E-02	-8.7	1.0E-04	0.8	9.2E-02	2.5	8.5E-02
ENSMUST00000113601	protein phosphatase 2A activator, regulatory subunit B [Source:MGI Symbol;Acc:MGI:1346006]	A2AWF0		-2.1	1.9E-01	-1.5	4.5E-01	0.1	9.5E-01	-0.6	7.7E-01
ENSMUST00000113604	TXK tyrosine kinase [Source:MGI Symbol;Acc:MGI:102960]		P42682	-1.0	3.8E-01	-4.2	5.7E-02	-1.3	1.8E-01	1.8	3.6E-01
ENSMUST00000115571	nuclear receptor subfamily 3, group C, member 1 [Source:MGI Symbol;Acc:MGI:95824]	E9PUR6		-5.3	6.8E-04	-6.4	1.8E-03	0.7	1.6E-01	-0.6	7.1E-01
ENSMUST00000113606	5-hydroxymethylcytosine (hmC) binding, ES cell specific [Source:MGI Symbol;Acc:MGI:1914053]		Q8R1M0	1.7	5.5E-02	6.4	1.0E-03	3.8	1.3E-02	-0.8	3.0E-01
ENSMUST00000115576	limb expression 1 homolog (chicken) [Source:MGI Symbol;Acc:MGI:1913893]		Q6P566	8.3	6.8E-06	-2.6	3.0E-03	0.5	1.5E-01	-0.1	8.3E-01
ENSMUST00000113612	dolichyl pyrophosphate phosphatase 1 [Source:MGI Symbol;Acc:MGI:1914093]	A2AWJ3		-2.9	2.6E-01	-3.0	3.3E-01	-1.0	5.5E-01	-0.9	7.8E-01
ENSMUST00000115590	solute carrier family 38, member 5 [Source:MGI Symbol;Acc:MGI:2148066]		Q3U1J0	8.3	1.5E-04	7.1	1.1E-04	-0.6	6.0E-01	-0.6	3.2E-01
ENSMUST00000113615	pecanex-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1861733]		Q8VI59	-3.3	5.6E-02	-0.9	6.4E-01	0.6	5.9E-01	-1.8	3.6E-01
ENSMUST00000115592	coiled-coil domain containing 67 [Source:MGI Symbol;Acc:MGI:2443026]		Q7M6Y5	6.4	7.4E-03	-8.1	3.5E-06	-0.4	1.3E-01	-2.1	5.5E-02
ENSMUST00000113624	RAR-related orphan receptor alpha [Source:MGI Symbol;Acc:MGI:104661]	Q3U1P4	P51448	3.1	4.0E-02	4.5	2.0E-02	0.1	9.6E-01	-1.4	2.4E-01
ENSMUST00000115595	FtsJ homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1859648]	Q8JZY1		-5.2	7.8E-05	-7.6	2.3E-04	-1.2	2.5E-02	0.1	9.6E-01
ENSMUST00000115610	armadillo repeat gene deleted in velo-cardio-facial syndrome [Source:MGI Symbol;Acc:MGI:109620]		P98203	7.5	1.9E-05	0.3	4.5E-01	1.2	5.1E-03	-0.1	7.6E-01
ENSMUST00000113631	retrotransposon gag domain containing 4 [Source:MGI Symbol;Acc:MGI:3045324]	Q8C065	Q5DTT4	1.6	4.8E-01	1.3	6.7E-01	-0.1	9.6E-01	0.1	9.6E-01
ENSMUST00000115614	armadillo repeat gene deleted in velo-cardio-facial syndrome [Source:MGI Symbol;Acc:MGI:109620]		P98203	8.2	3.0E-02	-2.1	1.2E-01	0.5	5.3E-01	-1.7	2.4E-01
ENSMUST00000115615	RNA binding motif protein 3 [Source:MGI Symbol;Acc:MGI:1099460]	Q545K5	O89086	-9.8	1.9E-04	-2.1	2.3E-03	0.8	2.8E-02	-0.8	1.5E-01
ENSMUST00000113654	leucine rich repeat containing 8A [Source:MGI Symbol;Acc:MGI:2652847]		Q80WG5	1.3	4.3E-01	3.9	1.1E-01	2.7	2.1E-01	0.0	1.0E+00
ENSMUST00000115616	RNA binding motif protein 3 [Source:MGI Symbol;Acc:MGI:1099460]	Q8BG13		-9.9	1.0E-05	4.3	2.0E-02	0.2	8.8E-01	-1.0	3.7E-01
ENSMUST00000113658	glutamine fructose-6-phosphate transaminase 1 [Source:MGI Symbol;Acc:MGI:95698]		P47856	0.7	1.6E-01	0.8	2.5E-01	0.7	2.0E-01	0.6	3.5E-01
ENSMUST00000115622	calcitonin receptor [Source:MGI Symbol;Acc:MGI:101950]		Q60755	6.8	1.6E-04	4.3	3.5E-03	-4.6	1.2E-02	0.4	6.1E-01
ENSMUST00000113668				-0.7	6.6E-01	-1.2	6.3E-01	1.3	5.0E-01	1.8	4.0E-01
ENSMUST00000113669	zinc ribbon domain containing, 1 [Source:MGI Symbol;Acc:MGI:1913386]		Q791N7	-2.1	3.6E-01	-0.8	6.5E-01	-1.7	2.7E-01	-3.0	1.9E-01
ENSMUST00000115628	transport and golgi organization 2 [Source:MGI Symbol;Acc:MGI:101825]	Q8BTN3		-4.9	1.5E-04	-6.1	9.0E-04	0.9	6.7E-02	-0.2	8.9E-01
ENSMUST00000115629	diaphanous homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1194490]	D3Z074		-4.4	1.6E-02	-2.0	3.2E-01	1.5	2.7E-01	-2.1	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000113678	tubulin tyrosine ligase-like family, member 4 [Source:MGI Symbol;Acc:MGI:1914784]	D3YY08		-0.1	9.5E-01	-0.5	7.0E-01	-0.3	7.4E-01	0.1	9.1E-01
ENSMUST00000113682	melanocyte proliferating gene 1 [Source:MGI Symbol;Acc:MGI:1929864]		Q9JK81	1.8	8.9E-02	0.0	9.9E-01	-0.9	3.6E-01	0.9	4.3E-01
ENSMUST00000115632	meiotic recombination 11 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1100512]		Q61216	2.4	2.4E-03	3.4	1.8E-03	0.0	9.7E-01	0.6	3.4E-01
ENSMUST00000115633	DiGeorge syndrome critical region gene 8 [Source:MGI Symbol;Acc:MGI:2151114]		Q9EQM6	4.9	1.5E-02	-5.5	4.4E-03	-2.4	7.0E-03	-0.9	6.0E-01
ENSMUST00000113696	tropomyosin 1, alpha [Source:MGI Symbol;Acc:MGI:98809]	G5E8R2		-1.9	7.4E-02	-1.1	4.4E-01	0.8	4.0E-01	-0.1	9.6E-01
ENSMUST00000115634	diaphanous homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1194490]		O08808	-9.0	1.8E-04	-1.9	1.6E-02	-0.6	2.1E-01	-0.6	3.7E-01
ENSMUST00000115636	suppressor of variegation 3-9 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1099440]		O54864	5.2	1.9E-03	-1.1	5.1E-01	2.9	1.9E-02	-0.1	9.5E-01
ENSMUST00000115637	suppressor of variegation 3-9 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1099440]	A2AC19		-3.8	5.2E-03	-3.1	1.6E-01	1.3	2.9E-01	-0.1	9.7E-01
ENSMUST00000115640	TRM2 tRNA methyltransferase 2A [Source:MGI Symbol;Acc:MGI:96270]	Q3UYU2		-2.9	3.1E-02	6.8	5.7E-04	0.9	4.9E-01	0.0	9.7E-01
ENSMUST00000115642	histone deacetylase 6 [Source:MGI Symbol;Acc:MGI:1333752]		Q9Z2V5	-4.7	3.9E-03	3.6	1.3E-04	-0.2	7.0E-01	-0.3	4.9E-01
ENSMUST00000113712	cytotoxic granule-associated RNA binding protein 1 [Source:MGI Symbol;Acc:MGI:107914]	D3YY02		0.1	9.7E-01	-1.0	8.2E-01	-1.0	7.2E-01	0.1	9.8E-01
ENSMUST00000113713	cytotoxic granule-associated RNA binding protein 1 [Source:MGI Symbol;Acc:MGI:107914]	Q80ZW7		0.2	9.4E-01	-3.5	3.1E-01	-2.6	2.0E-01	1.0	7.6E-01
ENSMUST00000115643	piwi-like RNA-mediated gene silencing 4 [Source:MGI Symbol;Acc:MGI:3041167]	Z4YLE4		8.8	1.2E-05	-5.0	6.3E-03	1.3	4.2E-02	0.3	8.7E-01
ENSMUST00000115644	piwi-like RNA-mediated gene silencing 4 [Source:MGI Symbol;Acc:MGI:3041167]		Q8CGT6	5.0	3.3E-02	-0.9	5.4E-01	1.3	1.8E-01	-0.6	6.8E-01
ENSMUST00000113726	RNA binding motif protein 47 [Source:MGI Symbol;Acc:MGI:2384294]		Q91WT8	1.9	4.8E-01	3.4	3.3E-01	-0.2	9.6E-01	-1.6	5.2E-01
ENSMUST00000113728	kinesin light chain 2 [Source:MGI Symbol;Acc:MGI:107953]	D3YXZ3		-5.4	3.8E-02	1.9	5.7E-01	6.0	2.8E-02	-1.3	6.7E-01
ENSMUST00000113730	anterior pharynx defective 1b homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:3522097]	F8WHK7		-0.4	8.0E-01	1.0	5.8E-01	0.6	7.2E-01	-0.9	6.0E-01
ENSMUST00000113732	BCS1-like (yeast) [Source:MGI Symbol;Acc:MGI:1914071]		Q9CZP5	3.1	1.2E-01	4.1	1.1E-01	-0.1	9.6E-01	-1.1	5.1E-01
ENSMUST00000115645	RAN binding protein 1 [Source:MGI Symbol;Acc:MGI:96269]		P34022	-4.0	8.8E-03	-1.9	2.7E-01	1.1	2.6E-01	-0.3	8.8E-01
ENSMUST00000113734	zinc finger and BTB domain containing 21 [Source:MGI Symbol;Acc:MGI:1927240]	E9Q444		1.9	3.2E-01	0.9	7.0E-01	-1.4	4.5E-01	-0.3	8.7E-01
ENSMUST00000113737	zinc finger protein 142 [Source:MGI Symbol;Acc:MGI:1924514]	Q3V1C1		-2.5	7.2E-02	-0.7	7.5E-01	3.1	5.0E-02	1.2	5.2E-01
ENSMUST00000113738				0.3	5.3E-01	0.8	2.0E-01	0.4	3.0E-01	0.0	9.3E-01
ENSMUST00000115654	polyglutamine binding protein 1 [Source:MGI Symbol;Acc:MGI:1859638]	A2AER7	Q91VJ5	8.3	9.7E-04	2.8	1.5E-03	-1.5	2.7E-02	0.2	6.3E-01
ENSMUST00000115655	polyglutamine binding protein 1 [Source:MGI Symbol;Acc:MGI:1859638]	A2AER7	Q91VJ5	-5.1	4.5E-04	7.0	2.1E-04	-0.5	6.8E-01	0.2	7.6E-01
ENSMUST00000113753	Tp53rk binding protein [Source:MGI Symbol;Acc:MGI:1917036]		Q8QZZ7	1.5	4.4E-01	3.8	1.5E-01	0.9	6.8E-01	-1.4	4.7E-01
ENSMUST00000115658	protocadherin alpha 11 [Source:MGI Symbol;Acc:MGI:1298372]		Q91Y20	7.6	6.2E-05	-2.7	3.2E-02	-0.5	4.0E-01	-0.6	6.2E-01
ENSMUST00000115659	protocadherin alpha 9 [Source:MGI Symbol;Acc:MGI:2447322]		Q91Y11	8.1	2.4E-05	-5.1	1.4E-02	0.7	4.2E-01	1.2	5.1E-01
ENSMUST00000113757	outer dense fiber of sperm tails 2 [Source:MGI Symbol;Acc:MGI:1098824]		A3KGV1	0.2	9.4E-01	0.7	8.4E-01	0.2	9.2E-01	-0.3	9.3E-01
ENSMUST00000115663	solute carrier family 35 (UDP-galactose transporter), member A2 [Source:MGI Symbol;Acc:MGI:1345297]	A2AER4		-4.1	2.4E-03	1.6	3.2E-01	3.4	2.1E-02	-3.5	5.0E-02
ENSMUST00000115666	OTU domain containing 5 [Source:MGI Symbol;Acc:MGI:1859615]	A2AES5		-5.8	5.3E-04	-2.2	2.7E-02	0.0	9.4E-01	-0.6	4.7E-01
ENSMUST00000115668	OTU domain containing 5 [Source:MGI Symbol;Acc:MGI:1859615]		Q3U2S4	-7.0	5.8E-04	6.9	5.3E-03	-0.7	7.3E-01	-1.5	2.0E-01
ENSMUST00000113767	outer dense fiber of sperm tails 2 [Source:MGI Symbol;Acc:MGI:1098824]	A3KGW0		3.1	6.8E-02	3.0	1.1E-01	-0.4	8.0E-01	-0.2	8.8E-01
ENSMUST00000115672	baculoviral IAP repeat-containing 3 [Source:MGI Symbol;Acc:MGI:1197007]	A2CGA3		3.1	2.6E-04	-4.9	1.6E-02	0.1	8.6E-01	2.2	2.3E-01
ENSMUST00000113780	ectodysplasin-A [Source:MGI Symbol;Acc:MGI:1195272]		O54693	2.4	2.0E-01	5.7	2.2E-02	0.5	8.1E-01	-2.7	7.5E-02
ENSMUST00000113781	ectodysplasin-A [Source:MGI Symbol;Acc:MGI:1195272]	Q1L2D8		4.6	6.6E-02	3.0	3.3E-01	0.5	8.7E-01	2.0	3.5E-01
ENSMUST00000115673	baculoviral IAP repeat-containing 3 [Source:MGI Symbol;Acc:MGI:1197007]	E0CZ20		-2.2	3.1E-02	0.9	6.6E-01	-3.2	1.3E-01	0.9	6.0E-01
ENSMUST00000113787	sideroflexin 5 [Source:MGI Symbol;Acc:MGI:2137681]	D3YXH6		0.0	9.4E-01	1.0	1.9E-01	0.1	8.8E-01	-0.9	1.7E-01
ENSMUST00000113792	praja ring finger 1, E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1101765]	Q05CG5	O55176	4.2	4.4E-02	1.4	4.6E-01	-3.0	1.4E-01	-0.1	9.2E-01
ENSMUST00000115675	GRIP1 associated protein 1 [Source:MGI Symbol;Acc:MGI:1859616]	A2AEW8		-6.2	6.8E-04	3.5	2.0E-02	0.0	9.9E-01	0.1	9.4E-01
ENSMUST00000115677	transcription factor E3 [Source:MGI Symbol;Acc:MGI:98511]		Q64092	-8.2	3.0E-04	5.2	6.8E-04	0.9	3.5E-01	0.2	7.5E-01
ENSMUST00000115678	transcription factor E3 [Source:MGI Symbol;Acc:MGI:98511]		Q64092	-8.7	1.1E-03	7.2	3.2E-06	-0.1	8.3E-01	0.2	6.6E-01
ENSMUST00000115679	transcription factor E3 [Source:MGI Symbol;Acc:MGI:98511]		Q64092	-6.8	2.7E-03	-4.8	5.7E-04	0.5	2.4E-01	-0.8	4.6E-01
ENSMUST00000115682	Riken cDNA E230025N22 gene [Source:MGI Symbol;Acc:MGI:3687212]	G5E8S3		7.8	1.7E-05	6.7	1.6E-04	-0.5	6.7E-01	0.4	4.5E-01
ENSMUST00000115687	WD repeat domain 45 [Source:MGI Symbol;Acc:MGI:1859606]		Q91VM3	-3.9	1.1E-02	8.3	2.3E-05	-0.6	6.0E-01	0.3	5.9E-01
ENSMUST00000115689	WD repeat domain 45 [Source:MGI Symbol;Acc:MGI:1859606]		Q91VM3	-6.4	4.2E-04	6.5	2.4E-04	0.1	9.5E-01	0.0	9.5E-01
ENSMUST00000115694	solute carrier family 4, sodium bicarbonate cotransporter, member 9 [Source:MGI Symbol;Acc:MGI:2443384]	E9PUP3		8.0	2.2E-05	-3.4	4.8E-02	0.1	9.1E-01	0.1	9.5E-01
ENSMUST00000115699	ubiquitin-conjugating enzyme E2L 3 [Source:MGI Symbol;Acc:MGI:109240]	Q561N4	P68037	8.0	3.5E-05	-4.4	1.0E-03	-0.3	4.5E-01	-0.9	4.1E-01
ENSMUST00000115706	YdjC homolog (bacterial) [Source:MGI Symbol;Acc:MGI:1916351]	D3YZR5		3.0	1.3E-03	-1.4	3.0E-01	1.4	1.4E-01	-5.0	1.8E-02
ENSMUST00000113819	actin related protein 2/3 complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1923959]	D3YXG6		-2.1	3.1E-01	-7.9	4.0E-02	-2.9	5.6E-02	3.0	4.0E-01
ENSMUST00000115712	neuregulin 2 [Source:MGI Symbol;Acc:MGI:1098246]	D3YZR3		5.4	1.0E-04	-9.4	1.4E-05	0.1	8.4E-01	0.9	4.3E-01
ENSMUST00000115713	neuregulin 2 [Source:MGI Symbol;Acc:MGI:1098246]	D3YZR2		3.7	3.3E-02	2.5	4.0E-01	-0.8	7.5E-01	3.5	1.3E-01
ENSMUST00000115715	phosphodiesterase 10A [Source:MGI Symbol;Acc:MGI:1345143]	F8WHK3		6.9	7.5E-05	2.6	6.5E-02	-1.0	3.8E-01	0.7	5.1E-01
ENSMUST00000115717	phosphodiesterase 10A [Source:MGI Symbol;Acc:MGI:1345143]	S4R197		8.1	1.7E-03	7.4	4.3E-05	-0.5	6.2E-01	-0.8	1.9E-01
ENSMUST00000113824	caseinolytic mitochondrial matrix peptidase chaperone subunit [Source:MGI Symbol;Acc:MGI:1346017]	Q6P8N8		-0.1	9.7E-01	-1.0	7.4E-01	-0.6	8.0E-01	0.3	9.1E-01
ENSMUST00000115722	phosphodiesterase 10A [Source:MGI Symbol;Acc:MGI:1345143]	F2Z3Z4		8.0	1.3E-05	4.0	2.4E-02	-1.5	3.1E-01	-0.4	7.5E-01
ENSMUST00000113827	bromodomain and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:1890651]	Q8BPZ1		1.0	1.9E-01	2.2	3.5E-02	1.6	5.8E-02	0.3	6.6E-01
ENSMUST00000113829	bromodomain and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:1890651]		Q921C3	-0.1	9.3E-01	-0.4	6.4E-01	-0.3	6.3E-01	0.1	9.4E-01
ENSMUST00000115724	phosphodiesterase 10A [Source:MGI Symbol;Acc:MGI:1345143]		Q8CA95	5.6	1.4E-03	7.2	2.5E-04	-0.8	5.6E-01	0.4	5.5E-01
ENSMUST00000115728	transmembrane protein 173 [Source:MGI Symbol;Acc:MGI:1919762]		Q3TBT3	-1.8	5.1E-03	-5.1	2.4E-03	-0.1	8.3E-01	-1.3	3.7E-01
ENSMUST00000113836	zinc finger protein 638 [Source:MGI Symbol;Acc:MGI:1203484]	E9QKZ7		0.0	9.9E-01	-4.5	7.1E-02	-5.1	6.0E-03	-0.6	8.2E-01
ENSMUST00000115729	yippee-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913303]	D3YZQ1		4.3	3.1E-04	-1.8	1.6E-01	0.4	5.7E-01	0.0	1.0E+00
ENSMUST00000115731	mitogen-activated protein kinase 1 [Source:MGI Symbol;Acc:MGI:1346858]		P63085	-6.2	1.3E-04	5.6	1.7E-02	-2.9	2.0E-01	0.0	9.8E-01
ENSMUST00000115733	guanylate cyclase 1, soluble, alpha 2 [Source:MGI Symbol;Acc:MGI:2660877]	F8VQK3		6.7	7.6E-05	5.6	8.8E-04	-0.6	6.4E-01	0.3	7.0E-01
ENSMUST00000115735	polyadenylate-binding protein-interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915119]		Q9D6V8	-3.4	1.2E-02	2.6	4.3E-02	0.8	3.4E-01	2.9	1.0E-02
ENSMUST00000113852	slingshot homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2683546]		Q8K330	-1.2	5.3E-01	0.8	7.4E-01	0.5	8.0E-01	-1.5	4.7E-01
ENSMUST00000113853	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31 [Source:MGI Symbol;Acc:MGI:2682639]	Q6NZQ2		0.9	1.4E-01	1.3	8.2E-02	-0.2	7.5E-01	-0.6	3.4E-01
ENSMUST00000113854	potassium inwardly-rectifying channel, subfamily J, member 15 [Source:MGI Symbol;Acc:MGI:1310000]	Q53Z04	O88932	4.7	1.6E-01	6.0	1.2E-01	-0.3	9.3E-01	-1.6	5.0E-01
ENSMUST00000115736	polyadenylate-binding protein-interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915119]		Q9D6V8	-7.1	1.1E-03	8.0	1.4E-04	-0.7	6.3E-01	-0.8	2.3E-01
ENSMUST00000115747	tubulin tyrosine ligase-like family, member 2 [Source:MGI Symbol;Acc:MGI:3644030]		A4Q9E4	6.6	6.9E-05	8.8	9.4E-05	-0.3	8.2E-01	-0.3	5.8E-01
ENSMUST00000115749	dynamin 1-like [Source:MGI Symbol;Acc:MGI:1921256]		Q8K1M6	-6.1	3.3E-04	-3.4	7.7E-02	1.3	1.7E-01	0.4	8.1E-01
ENSMUST00000115752	cyclin B3 [Source:MGI Symbol;Acc:MGI:2183443]	A2AEP2		6.7	3.1E-04	-3.2	2.0E-01	1.5	2.6E-01	-0.7	7.6E-01
ENSMUST00000113869	tuberous sclerosis 1 [Source:MGI Symbol;Acc:MGI:1929183]		Q9EP53	6.4	3.5E-02	4.1	7.7E-02	-6.8	3.0E-02	-4.6	1.6E-02
ENSMUST00000113870	tuberous sclerosis 1 [Source:MGI Symbol;Acc:MGI:1929183]		Q9EP53	-1.9	5.2E-01	4.7	3.4E-01	6.8	1.4E-01	0.2	9.5E-01
ENSMUST00000113876	CDC42 guanine nucleotide exchange factor (GEF) 9 [Source:MGI Symbol;Acc:MGI:2442233]		Q3UTH8	5.6	4.6E-02	5.4	7.3E-02	-0.7	8.0E-01	-0.5	7.7E-01
ENSMUST00000115763	synaptotagmin-like 3 [Source:MGI Symbol;Acc:MGI:1933367]	F8WHG0		7.6	8.2E-05	-7.1	1.8E-03	-0.3	5.4E-01	-0.7	7.1E-01
ENSMUST00000113883	CDC42 guanine nucleotide exchange factor (GEF) 9 [Source:MGI Symbol;Acc:MGI:2442233]		Q3UTH8	3.6	1.1E-01	2.0	4.7E-01	-0.5	8.5E-01	1.2	5.7E-01
ENSMUST00000113889	general transcription factor IIIC, polypeptide 5 [Source:MGI Symbol;Acc:MGI:1917489]		Q8R2T8	1.1	6.1E-01	7.4	2.0E-02	3.7	1.9E-01	-2.6	1.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000115765	bromodomain containing 8 [Source:MGI Symbol;Acc:MGI:1925906]	D3YZC8		-1.9	1.8E-02	5.1	9.1E-03	-0.6	7.2E-01	0.9	3.6E-01
ENSMUST00000115766	bromodomain containing 8 [Source:MGI Symbol;Acc:MGI:1925906]	D3YZC7		-2.4	8.6E-03	2.4	8.8E-02	-4.1	1.4E-02	1.7	8.9E-02
ENSMUST00000115776	ubiquitin-conjugating enzyme E2 variant 2 [Source:MGI Symbol;Acc:MGI:1917870]		Q9D2M8	-4.2	3.2E-03	3.4	1.4E-01	-0.6	7.9E-01	1.7	2.7E-01
ENSMUST00000113899	solute carrier family 4, sodium bicarbonate cotransporter, member 5 [Source:MGI Symbol;Acc:MGI:2443220]	D3YX36		6.5	5.4E-02	4.2	2.4E-01	-0.3	9.3E-01	2.0	3.7E-01
ENSMUST00000115784	synaptojanin 2 [Source:MGI Symbol;Acc:MGI:1201671]		Q9D2G5	4.9	3.0E-02	5.5	1.0E-03	-0.6	6.4E-01	0.6	4.0E-01
ENSMUST00000115786	synaptojanin 2 [Source:MGI Symbol;Acc:MGI:1201671]	D3YZB5		4.5	9.2E-04	6.5	2.7E-04	-1.5	2.7E-01	-0.8	2.2E-01
ENSMUST00000113904	zinc finger, CCHC domain containing 4 [Source:MGI Symbol;Acc:MGI:1926046]		Q8BKW4	0.9	2.6E-01	0.6	4.9E-01	-0.3	6.2E-01	-0.1	8.9E-01
ENSMUST00000115791	synaptojanin 2 [Source:MGI Symbol;Acc:MGI:1201671]	F8WHD8		9.1	1.2E-05	5.0	4.4E-04	0.5	6.1E-01	-0.3	5.6E-01
ENSMUST00000113913	dynactin 1 [Source:MGI Symbol;Acc:MGI:107745]	E9Q3M3		1.1	6.8E-01	-0.9	8.2E-01	-0.5	8.6E-01	1.5	6.7E-01
ENSMUST00000113915	kelch-like 15 [Source:MGI Symbol;Acc:MGI:1923400]	A2AAX3		1.5	6.1E-02	1.6	1.6E-01	1.0	2.6E-01	0.9	3.3E-01
ENSMUST00000115797	AT rich interactive domain 1B (SWI-like) [Source:MGI Symbol;Acc:MGI:1926129]	E9Q4N7		9.8	5.3E-06	5.1	8.6E-02	-0.9	7.6E-01	0.1	9.5E-01
ENSMUST00000113919	dynactin 1 [Source:MGI Symbol;Acc:MGI:107745]		O08788	2.3	3.1E-01	3.8	1.4E-01	-1.0	6.7E-01	-2.5	2.1E-01
ENSMUST00000115799	AT rich interactive domain 1B (SWI-like) [Source:MGI Symbol;Acc:MGI:1926129]	E9Q4N6		-6.3	2.2E-04	5.5	2.2E-02	-0.2	9.1E-01	1.2	3.4E-01
ENSMUST00000115800	NADPH oxidase 3 [Source:MGI Symbol;Acc:MGI:2681162]		Q672J9	6.6	1.7E-04	-4.4	7.7E-03	1.0	1.6E-01	2.1	1.4E-01
ENSMUST00000113927	zinc finger protein X-linked [Source:MGI Symbol;Acc:MGI:99211]	B1ASD1	P17012	-1.3	5.4E-01	-3.0	6.3E-02	-5.2	3.4E-03	-3.5	9.4E-02
ENSMUST00000115802	pyridoxal-dependent decarboxylase domain containing 1 [Source:MGI Symbol;Acc:MGI:1920909]		Q99K01	6.0	7.5E-05	2.1	2.5E-01	-0.4	7.7E-01	1.8	2.3E-01
ENSMUST00000113935	INO80 complex subunit B [Source:MGI Symbol;Acc:MGI:1917270]		Q99PT3	-2.2	6.8E-02	-0.6	6.4E-01	0.6	5.2E-01	-0.9	4.8E-01
ENSMUST00000113936	WW domain binding protein 1 [Source:MGI Symbol;Acc:MGI:104710]		P97764	2.7	2.6E-01	6.2	4.8E-02	2.7	3.0E-01	-0.8	7.0E-01
ENSMUST00000115812	phosphoinositide-3-kinase, class 3 [Source:MGI Symbol;Acc:MGI:2445019]		Q6PF93	-3.4	7.3E-04	-5.7	9.2E-04	0.2	6.1E-01	0.4	7.8E-01
ENSMUST00000115814	sorting nexin 29 [Source:MGI Symbol;Acc:MGI:1921728]	D3YZ90		3.6	1.3E-02	6.5	6.0E-03	-3.3	1.7E-01	0.8	4.1E-01
ENSMUST00000115817	tubulin polyglutamylase complex subunit 2 [Source:MGI Symbol;Acc:MGI:1913898]	E9QLP0		1.5	1.6E-02	0.9	6.4E-01	3.5	2.2E-02	-0.9	6.1E-01
ENSMUST00000113947	aristaless related homeobox [Source:MGI Symbol;Acc:MGI:1097716]		O35085	2.0	1.8E-01	6.5	1.1E-03	0.1	9.4E-01	-4.4	1.9E-03
ENSMUST00000115821	predicted gene 10563 [Source:MGI Symbol;Acc:MGI:3642630]	F6WIE4		7.6	5.4E-06	-2.5	1.3E-02	1.4	1.1E-02	0.5	5.3E-01
ENSMUST00000115822	predicted gene 11172 [Source:MGI Symbol;Acc:MGI:3779427]	F6ZH14		5.6	2.1E-04	8.6	8.2E-04	1.5	3.8E-01	1.2	1.8E-01
ENSMUST00000115824	C-type lectin domain family 16, member A [Source:MGI Symbol;Acc:MGI:1921624]	Z4YLG3		5.7	2.2E-02	6.8	9.2E-05	-0.6	5.9E-01	-0.3	5.6E-01
ENSMUST00000115830	microtubule-associated protein, RP/EB family, member 2 [Source:MGI Symbol;Acc:MGI:106271]		Q8R001	-3.2	4.9E-03	-0.4	7.2E-01	1.8	4.6E-02	-0.3	8.2E-01
ENSMUST00000115832	dystrobrevin alpha [Source:MGI Symbol;Acc:MGI:106039]	Q8CFR5		8.6	2.1E-05	6.3	3.5E-04	-0.6	6.1E-01	-0.2	7.7E-01
ENSMUST00000115835	glutamate receptor, ionotropic, NMDA2A (epsilon 1) [Source:MGI Symbol;Acc:MGI:95820]		P35436	7.3	1.9E-04	1.5	1.1E-01	0.2	8.1E-01	0.5	5.5E-01
ENSMUST00000113970	suppressor of variegation 4-20 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444557]		Q3U8K7	-1.5	3.5E-01	-2.0	3.9E-01	0.4	7.6E-01	0.9	6.7E-01
ENSMUST00000115841	RNA binding protein, fox-1 homolog (C. elegans) 1 [Source:MGI Symbol;Acc:MGI:1926224]		Q9JJ43	6.0	6.7E-03	-2.0	4.3E-01	1.8	3.0E-01	-2.0	4.1E-01
ENSMUST00000113974	suppressor of variegation 4-20 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444557]		Q3U8K7	3.4	4.7E-02	6.3	2.1E-03	-0.5	7.4E-01	-3.4	9.9E-03
ENSMUST00000115844	glyoxylate reductase 1 homolog (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1921272]	D3YYT1		-8.8	2.1E-04	4.2	1.2E-04	-1.8	2.0E-02	0.0	9.4E-01
ENSMUST00000113976	RIKEN cDNA 5430427O19 gene [Source:MGI Symbol;Acc:MGI:1918648]	Q08EG0	Q9D3J9	0.7	3.5E-01	0.7	4.5E-01	-0.4	5.8E-01	-0.4	6.6E-01
ENSMUST00000113977	suppressor of variegation 4-20 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444557]		Q3U8K7	3.1	1.3E-01	-3.1	2.1E-01	-4.4	2.1E-02	1.8	4.5E-01
ENSMUST00000113978	glycerol kinase [Source:MGI Symbol;Acc:MGI:106594]		Q64516	-1.5	5.7E-01	-0.6	8.7E-01	0.3	9.1E-01	-0.6	8.4E-01
ENSMUST00000115848	desmocollin 3 [Source:MGI Symbol;Acc:MGI:1194993]	G5E8S6		7.6	2.4E-05	3.4	5.1E-04	0.0	9.7E-01	-0.5	3.0E-01
ENSMUST00000113980	meiosis 1 associated protein [Source:MGI Symbol;Acc:MGI:1315200]		Q9Z0E1	1.3	4.9E-02	2.1	1.2E-02	0.1	8.5E-01	-0.7	2.4E-01
ENSMUST00000115859	RIKEN cDNA 1700037C18 gene [Source:MGI Symbol;Acc:MGI:1920511]		Q8BT88	4.0	4.2E-05	5.6	6.7E-03	-1.1	5.3E-01	-0.5	6.6E-01
ENSMUST00000115860	N(alpha)-acetyltransferase 60, NatF catalytic subunit [Source:MGI Symbol;Acc:MGI:1922013]		Q9DBU2	-8.0	1.4E-02	7.7	1.4E-03	1.3	4.2E-01	1.5	1.3E-01
ENSMUST00000113993	intersectin 1 (SH3 domain protein 1A) [Source:MGI Symbol;Acc:MGI:1338069]	E9Q3I9		-0.8	7.5E-01	-2.8	3.6E-01	-2.4	1.8E-01	-0.4	9.1E-01
ENSMUST00000115894	ubiquitin-activating enzyme, Chr Y [Source:MGI Symbol;Acc:MGI:98891]		P31254	7.7	4.0E-06	-7.1	1.3E-04	0.7	7.7E-02	-0.7	5.8E-01
ENSMUST00000115924				5.3	9.3E-06	6.7	2.1E-04	-0.6	6.2E-01	-0.4	5.1E-01
ENSMUST00000114001	intersectin 1 (SH3 domain protein 1A) [Source:MGI Symbol;Acc:MGI:1338069]	E9Q3I4		2.7	1.5E-01	2.2	3.0E-01	-0.4	8.4E-01	0.2	9.3E-01
ENSMUST00000115964	trimethyllysine hydroxylase, epsilon [Source:MGI Symbol;Acc:MGI:2180203]		Q91ZE0	6.5	3.5E-05	6.6	5.7E-06	-1.3	9.6E-02	-0.2	5.5E-01
ENSMUST00000114005	calcium channel flower domain containing 1 [Source:MGI Symbol;Acc:MGI:1924317]		Q8BG21	-0.9	5.3E-01	1.5	4.0E-01	2.0	2.0E-01	-0.4	7.9E-01
ENSMUST00000115979	epithelial splicing regulatory protein 2 [Source:MGI Symbol;Acc:MGI:1924661]		Q8K0G8	3.3	2.6E-04	1.5	1.3E-01	0.7	3.4E-01	1.0	2.0E-01
ENSMUST00000115995	fatty acid desaturase 3 [Source:MGI Symbol;Acc:MGI:1928740]	Q3T9H9	Q9JJE7	4.6	3.3E-04	-1.3	5.4E-01	1.1	4.2E-01	-1.6	4.5E-01
ENSMUST00000116094	ring finger protein 186 [Source:MGI Symbol;Acc:MGI:1914075]	A2ALL3		6.6	2.2E-04	7.6	3.0E-05	-0.5	6.2E-01	0.0	9.6E-01
ENSMUST00000116172	predicted gene 11175 [Source:MGI Symbol;Acc:MGI:3809055]	Q3UXY7		-6.9	2.3E-05	-1.1	1.2E-01	0.1	7.5E-01	-0.1	8.5E-01
ENSMUST00000116231	methyltransferase like 21B [Source:MGI Symbol;Acc:MGI:3645330]	D3YWP0		7.2	1.1E-06	4.8	3.0E-03	-1.4	3.1E-01	0.3	6.7E-01
ENSMUST00000116234	ADP-ribosylation factor-like 1 [Source:MGI Symbol;Acc:MGI:99436]	Q14AC7	P61211	-3.4	6.9E-05	-2.9	3.1E-02	-0.6	3.6E-01	-0.4	7.5E-01
ENSMUST00000116238	hexokinase 1 [Source:MGI Symbol;Acc:MGI:96103]		P17710	5.8	2.7E-02	-3.6	2.3E-01	2.8	6.0E-02	1.3	6.5E-01
ENSMUST00000116247	calcium release activated channel regulator 2B [Source:MGI Symbol;Acc:MGI:2446129]	F6VRL7		5.2	1.0E-03	-1.6	7.3E-02	0.8	1.1E-01	-0.3	6.9E-01
ENSMUST00000114037	Son DNA binding protein [Source:MGI Symbol;Acc:MGI:98353]		Q9QX47	-3.4	4.3E-01	-4.2	4.6E-01	-1.0	6.9E-01	-0.1	9.8E-01
ENSMUST00000116259	microtubule-associated protein 7 [Source:MGI Symbol;Acc:MGI:1328328]	D3YWN7		2.6	7.8E-03	4.6	2.0E-03	-1.1	3.4E-01	-0.9	2.6E-01
ENSMUST00000116279	mitochondrial fission regulator 1-like [Source:MGI Symbol;Acc:MGI:1924074]		Q9CWE0	-6.2	2.8E-04	8.7	5.9E-05	4.5	4.1E-03	-0.7	2.4E-01
ENSMUST00000116304	cathepsin S [Source:MGI Symbol;Acc:MGI:107341]		O70370	-7.3	5.0E-07	2.0	1.4E-01	-0.5	6.3E-01	0.4	6.5E-01
ENSMUST00000116305	G protein pathway suppressor 1 [Source:MGI Symbol;Acc:MGI:2384801]	Q3MIA8		-5.1	3.1E-03	6.7	1.4E-04	-0.5	6.3E-01	-1.4	4.2E-02
ENSMUST00000116341	solute carrier family 25, member 51 [Source:MGI Symbol;Acc:MGI:2684984]		Q5HZI9	1.8	1.2E-03	-8.8	2.8E-05	0.4	3.0E-01	-3.0	6.0E-02
ENSMUST00000114049	thymosin, beta 10 [Source:MGI Symbol;Acc:MGI:109146]	A6H6H4	Q6ZWY8	1.0	1.3E-01	0.9	2.2E-01	-0.8	2.2E-01	-0.7	2.9E-01
ENSMUST00000116358	G protein pathway suppressor 2 [Source:MGI Symbol;Acc:MGI:1891751]	Q921N8		-8.1	1.5E-05	-10.5	6.9E-05	-1.0	2.4E-02	0.6	7.1E-01
ENSMUST00000116359	CTS telomere maintenance complex component 1 [Source:MGI Symbol;Acc:MGI:1916214]		Q5SUQ9	-4.1	1.7E-02	6.0	1.8E-03	-0.9	5.5E-01	-0.8	3.6E-01
ENSMUST00000114059	plastin 3 (T-isoform) [Source:MGI Symbol;Acc:MGI:104807]		Q99K51	-2.5	7.0E-02	-3.6	2.2E-02	-2.3	2.6E-02	-1.3	4.0E-01
ENSMUST00000116363	ADP-ribose/CDP-alcohol diphosphatase, manganese dependent [Source:MGI Symbol;Acc:MGI:1913608]		Q99KS6	-8.4	4.7E-06	-4.8	1.7E-02	0.8	2.6E-01	-1.5	4.6E-01
ENSMUST00000114066	cytoplasmic polyadenylation element binding protein 2 [Source:MGI Symbol;Acc:MGI:2442640]	D3YUJ4		-0.7	4.2E-01	-1.2	3.3E-01	0.0	9.6E-01	0.5	6.7E-01
ENSMUST00000114069	ELMO/CED-12 domain containing 3 [Source:MGI Symbol;Acc:MGI:2445168]		Q91YP6	-1.6	4.0E-01	2.1	4.0E-01	1.2	5.8E-01	-2.5	2.2E-01
ENSMUST00000114070	von Hippel-Lindau binding protein 1 [Source:MGI Symbol;Acc:MGI:1333804]	Q3TIR6		3.0	1.6E-01	-2.1	3.5E-01	-4.4	3.6E-02	0.7	7.5E-01
ENSMUST00000116365	DnaJ (Hsp40) homolog, subfamily C, member 5 [Source:MGI Symbol;Acc:MGI:892995]	G5E8T0		-4.5	9.0E-04	-3.9	6.1E-03	0.2	6.7E-01	-1.1	3.9E-01
ENSMUST00000114077	cyclin Y-like 1 [Source:MGI Symbol;Acc:MGI:2138614]	D3YUJ3		-0.5	6.8E-01	1.2	4.4E-01	-0.1	9.0E-01	-1.8	2.0E-01
ENSMUST00000114079	methyltransferase like 21A [Source:MGI Symbol;Acc:MGI:1914349]		Q9CQL0	0.1	9.1E-01	-2.6	7.9E-02	0.8	3.0E-01	3.5	2.1E-02
ENSMUST00000114082	SEC16 homolog A, endoplasmic reticulum export factor [Source:MGI Symbol;Acc:MGI:2139207]	A2AIX1		-1.3	5.3E-01	-0.1	9.8E-01	0.9	6.7E-01	-0.3	8.9E-01
ENSMUST00000116366	zinc finger, CCCH-type with G patch domain [Source:MGI Symbol;Acc:MGI:2449939]		Q8VDM1	-5.6	1.0E-03	2.7	1.3E-01	-0.2	9.1E-01	1.5	2.4E-01
ENSMUST00000116376	SH3 binding domain protein 5 like [Source:MGI Symbol;Acc:MGI:1933124]		Q99LH9	-3.5	2.8E-02	-1.8	3.4E-02	1.3	1.3E-02	0.0	9.6E-01
ENSMUST00000114090	inositol polyphosphate-5-phosphatase E [Source:MGI Symbol;Acc:MGI:1927753]	A2AIX0		1.0	5.1E-01	-0.5	8.4E-01	0.3	8.5E-01	1.7	4.2E-01
ENSMUST00000116380	ribophorin II [Source:MGI Symbol;Acc:MGI:98085]		Q9DBG6	-4.9	1.4E-04	-7.1	1.0E-03	-0.3	6.0E-01	-1.3	4.8E-01
ENSMUST00000116402	estrogen related receptor, beta [Source:MGI Symbol;Acc:MGI:1346832]	E9QKA2		8.6	9.5E-05	-9.1	3.7E-05	0.1	6.9E-01	-0.1	9.5E-01
ENSMUST00000116423	septin 3 [Source:MGI Symbol;Acc:MGI:1345148]		Q9Z1S5	11.3	7.8E-06	2.6	2.6E-03	-0.6	2.7E-01	0.0	9.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000116425	telomeric repeat binding factor 2 [Source:MGI Symbol;Acc:MGI:1195972]		O35144	2.4	9.8E-03	5.9	2.3E-03	-0.6	7.2E-01	-0.8	3.8E-01
ENSMUST00000114099	otopetrin 1 [Source:MGI Symbol;Acc:MGI:2388363]			2.8	2.1E-01	2.5	2.6E-01	-0.5	8.2E-01	-0.1	9.3E-01
ENSMUST00000114100	serologically defined colon cancer antigen 3 [Source:MGI Symbol;Acc:MGI:1915362]	A2AIW3		0.1	9.8E-01	-2.5	3.0E-01	-4.3	5.1E-02	-1.8	5.1E-01
ENSMUST00000116434	zinc finger with KRAB and SCAN domains 3 [Source:MGI Symbol;Acc:MGI:1919989]			-5.5	4.4E-04	5.7	1.7E-03	-0.5	7.1E-01	0.3	6.7E-01
ENSMUST00000114102	serologically defined colon cancer antigen 3 [Source:MGI Symbol;Acc:MGI:1915362]		A2AIW0	-5.6	3.9E-02	1.6	6.6E-01	6.6	2.6E-02	-0.5	8.7E-01
ENSMUST00000114104	growth factor receptor bound protein 2-associated protein 3 [Source:MGI Symbol;Acc:MGI:2387324]	B1AYB9		-0.3	8.8E-01	-2.9	2.9E-01	-3.1	7.2E-02	-0.5	8.6E-01
ENSMUST00000116440	ic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Source:MGI Symbol;Acc:MGI:1			-7.2	3.3E-05	1.8	3.3E-01	6.4	1.0E-03	0.8	5.8E-01
ENSMUST00000116442	hippocalcin [Source:MGI Symbol;Acc:MGI:1336200]		P84075	6.9	3.4E-04	5.1	1.6E-03	0.5	6.2E-01	1.4	1.1E-01
ENSMUST00000114112	ST3 beta-galactoside alpha-2,3-sialyltransferase 5 [Source:MGI Symbol;Acc:MGI:1339963]			4.1	7.1E-02	8.1	7.5E-03	2.0	4.1E-01	-1.9	2.4E-01
ENSMUST00000116444	hippocalcin [Source:MGI Symbol;Acc:MGI:1336200]		P84075	5.8	1.9E-04	2.7	2.6E-02	1.0	2.7E-01	0.7	3.9E-01
ENSMUST00000114115	small nuclear RNA activating complex, polypeptide 4 [Source:MGI Symbol;Acc:MGI:2443935]	A2AIV6		2.9	2.5E-01	6.2	4.9E-02	-0.2	9.4E-01	-3.5	1.1E-01
ENSMUST00000116457	CD82 antigen [Source:MGI Symbol;Acc:MGI:104651]	Q3UII2	P40237	-8.7	2.1E-02	4.8	4.0E-04	-1.0	2.4E-01	-0.5	4.2E-01
ENSMUST00000116463	GATA zinc finger domain containing 2A [Source:MGI Symbol;Acc:MGI:2384585]		Q8CHY6	-2.3	3.4E-02	8.2	6.6E-05	-0.2	8.6E-01	-0.8	2.2E-01
ENSMUST00000114121	neuroplastin [Source:MGI Symbol;Acc:MGI:108077]	Z4YLB7		-2.5	4.1E-01	-7.3	5.3E-02	-5.6	1.0E-02	-0.8	8.4E-01
ENSMUST00000114124	T cell lymphoma invasion and metastasis 1 [Source:MGI Symbol;Acc:MGI:103306]	G3UWG2		7.2	6.1E-02	6.0	1.4E-01	-0.7	8.6E-01	0.5	8.3E-01
ENSMUST00000114126	syntaxin 18 [Source:MGI Symbol;Acc:MGI:1918366]		Q8VDS8	0.0	9.6E-01	1.2	7.3E-02	0.8	9.6E-02	-0.4	4.9E-01
ENSMUST00000116468	M-phase phosphoprotein 8 [Source:MGI Symbol;Acc:MGI:1922589]		Q3TYA6	-1.8	1.4E-02	-0.8	6.4E-01	3.1	1.1E-02	-0.2	8.8E-01
ENSMUST00000114128	inhibitor of kappaB kinase gamma [Source:MGI Symbol;Acc:MGI:1338074]		O88522	-1.9	4.7E-01	-4.8	1.4E-01	-3.5	5.2E-02	-0.6	8.5E-01
ENSMUST00000114130	inhibitor of kappaB kinase gamma [Source:MGI Symbol;Acc:MGI:1338074]	E9Q2Y3		-3.0	1.8E-01	3.7	1.4E-01	1.4	5.2E-01	-5.4	2.7E-02
ENSMUST00000114132	zinc finger, DBF-type containing 2 [Source:MGI Symbol;Acc:MGI:1921134]		Q5SS00	2.8	3.3E-01	3.5	2.2E-01	-0.5	8.7E-01	-1.2	5.9E-01
ENSMUST00000114134	G-protein signalling modulator 1 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:1915089]	A2AIV3		0.0	1.0E+00	4.3	1.7E-01	2.5	3.7E-01	-1.8	4.1E-01
ENSMUST00000114136	promyelocytic leukemia [Source:MGI Symbol;Acc:MGI:104662]		Q60953	-2.0	4.5E-01	0.8	7.1E-01	-1.5	4.1E-01	-4.3	1.2E-01
ENSMUST00000114137	glutamate receptor, ionotropic, kainate 1 [Source:MGI Symbol;Acc:MGI:95814]	E9Q2Y1		4.1	9.4E-02	6.0	3.4E-02	-0.2	9.3E-01	-2.2	1.6E-01
ENSMUST00000114140	ol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) [Source:MGI Symbol;Acc:M			-2.4	5.4E-01	2.9	4.6E-01	0.8	8.1E-01	-4.4	2.6E-01
ENSMUST00000114142	family with sequence similarity 3, member A [Source:MGI Symbol;Acc:MGI:1913544]		Q9D8T0	0.0	9.9E-01	3.7	3.2E-01	3.4	2.3E-01	-0.3	9.4E-01
ENSMUST00000116473	kallikrein B, plasma 1 [Source:MGI Symbol;Acc:MGI:102849]		P26262	5.3	2.4E-02	-0.7	3.3E-01	0.1	8.3E-01	-0.7	3.2E-01
ENSMUST00000114146	olute carrier family 10 (sodium/bile acid cotransporter family), member 3 [Source:MGI Symbol;Acc:MGI:9504		P21129	-1.7	4.0E-01	4.8	1.2E-01	5.1	6.9E-02	-1.4	5.2E-01
ENSMUST00000116514	WW domain binding protein 11 [Source:MGI Symbol;Acc:MGI:1891823]		Q923D5	-2.4	1.1E-03	-6.0	2.3E-04	0.7	8.5E-02	-0.5	6.8E-01
ENSMUST00000116517	carnitine deficiency-associated gene expressed in ventricle 3 [Source:MGI Symbol;Acc:MGI:2448759]	F8WGL9		9.7	1.1E-05	5.3	4.9E-04	-0.9	4.0E-01	-0.5	4.9E-01
ENSMUST00000116528	kelch-like 12 [Source:MGI Symbol;Acc:MGI:2385619]		Q8BZM0	-4.7	2.4E-03	6.2	8.9E-04	-0.5	7.2E-01	-0.8	3.3E-01
ENSMUST00000116542	flap structure specific endonuclease 1 [Source:MGI Symbol;Acc:MGI:102779]	Q91Z50		-5.7	2.4E-03	2.7	2.0E-03	0.7	2.4E-01	-0.3	6.2E-01
ENSMUST00000116547	cysteine-rich hydrophobic domain 1 [Source:MGI Symbol;Acc:MGI:1344694]	A2RT09	Q8CBW7	5.7	3.8E-06	3.9	4.5E-02	-0.9	6.1E-01	1.6	2.0E-01
ENSMUST00000114158	collapsin response mediator protein 1 [Source:MGI Symbol;Acc:MGI:107793]	Q6P1J1		2.7	4.3E-02	6.3	3.3E-04	-0.5	6.7E-01	-4.1	1.0E-03
ENSMUST00000116552	general transcription factor II A, 2 [Source:MGI Symbol;Acc:MGI:1933289]	Q05C74		-6.0	3.1E-04	7.3	2.8E-03	-0.8	6.9E-01	0.0	9.6E-01
ENSMUST00000116553	transmembrane protease, serine 11f [Source:MGI Symbol;Acc:MGI:2442348]		Q8BHM9	5.7	4.2E-04	-7.0	5.7E-05	-0.1	8.2E-01	-0.2	8.6E-01
ENSMUST00000116556	WAS protein family homolog 1 [Source:MGI Symbol;Acc:MGI:1916017]		Q8VDD8	3.0	2.8E-03	5.0	9.1E-04	0.8	4.3E-01	-0.4	6.0E-01
ENSMUST00000116558	family with sequence similarity 89, member B [Source:MGI Symbol;Acc:MGI:106595]	Q05DI7		-4.4	2.9E-02	6.1	2.9E-04	-0.5	6.7E-01	-1.2	7.2E-02
ENSMUST00000114171	ATPase, H+ transporting, lysosomal accessory protein 1 [Source:MGI Symbol;Acc:MGI:109629]	Q3TKX1		-1.1	6.1E-01	2.9	2.7E-01	2.1	3.3E-01	-1.9	4.1E-01
ENSMUST00000116560	cofilin 1, non-muscle [Source:MGI Symbol;Acc:MGI:101757]	F8WGL3		-8.6	9.0E-09	7.5	7.5E-05	1.0	3.8E-01	0.2	6.8E-01
ENSMUST00000116567	breast cancer metastasis-suppressor 1 [Source:MGI Symbol;Acc:MGI:2388804]	Q547N0	Q99N20	-3.8	2.2E-04	8.2	2.4E-05	-0.6	5.9E-01	-0.2	7.0E-01
ENSMUST00000114178	ring finger protein 103 [Source:MGI Symbol;Acc:MGI:109483]	D3Z0Y5		3.3	8.4E-02	2.9	2.0E-01	-0.7	7.2E-01	-0.3	8.5E-01
ENSMUST00000116578	renin binding protein [Source:MGI Symbol;Acc:MGI:105940]		P82343	-5.0	4.7E-03	-3.3	4.7E-02	0.8	2.7E-01	1.3	3.8E-01
ENSMUST00000116586	roundabout homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1890110]	E9PYK2		7.0	8.9E-05	-4.6	8.6E-03	-1.3	7.9E-02	-0.8	6.0E-01
ENSMUST00000114182	tafazzin [Source:MGI Symbol;Acc:MGI:109626]	H3BKZ8		-0.2	9.2E-01	-0.3	9.0E-01	-0.5	8.0E-01	-0.3	9.1E-01
ENSMUST00000116594	Scm-like with four mbt domains 2 [Source:MGI Symbol;Acc:MGI:2447794]	Q3UH07		5.2	2.4E-02	-5.7	3.1E-03	-0.3	5.9E-01	-0.1	9.4E-01
ENSMUST00000116598	histocompatibility 2, Q region locus 7 [Source:MGI Symbol;Acc:MGI:95936]	L7N260		4.5	2.8E-02	5.0	3.6E-04	-0.3	7.4E-01	-0.2	8.0E-01
ENSMUST00000116605	MAD2 mitotic arrest deficient-like 1 [Source:MGI Symbol;Acc:MGI:1860374]	Q5HZH8	Q9Z1B5	-3.5	4.7E-03	-3.5	3.0E-02	-0.7	3.7E-01	-0.6	6.7E-01
ENSMUST00000116612	retinoid X receptor beta [Source:MGI Symbol;Acc:MGI:98215]		P28704	-4.4	1.7E-03	6.8	1.8E-04	-0.6	6.4E-01	-1.0	1.3E-01
ENSMUST00000116615	BarH-like homeobox 2 [Source:MGI Symbol;Acc:MGI:109617]		O08686	6.9	2.0E-05	1.9	1.8E-02	-2.4	4.2E-03	0.2	6.6E-01
ENSMUST00000114200	family with sequence similarity 219, member B [Source:MGI Symbol;Acc:MGI:1925573]		Q14DQ1	1.4	3.0E-01	1.9	4.0E-01	2.8	1.6E-01	2.3	1.6E-01
ENSMUST00000114205	actin-binding LIM protein 2 [Source:MGI Symbol;Acc:MGI:2385758]		Q8BL65	0.7	7.2E-01	3.0	2.1E-01	0.9	6.7E-01	-1.4	4.7E-01
ENSMUST00000114206	actin-binding LIM protein 2 [Source:MGI Symbol;Acc:MGI:2385758]		Q8BL65	6.0	8.5E-02	6.0	1.0E-01	-0.8	8.4E-01	-0.8	7.2E-01
ENSMUST00000116619	PML-RAR alpha-regulated adaptor molecule 1 [Source:MGI Symbol;Acc:MGI:3576625]	E9PYJ5		-3.7	4.4E-05	8.3	1.1E-02	-0.9	7.7E-01	-1.4	3.3E-01
ENSMUST00000116621	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11 [Source:MGI Symbol;Acc:MGI:1349919]		O09111	-6.1	5.7E-05	-1.8	1.7E-01	-0.5	5.3E-01	-1.9	1.7E-01
ENSMUST00000114220	DNA segment, Chr 16, ERATO Doi 472, expressed [Source:MGI Symbol;Acc:MGI:1196400]		Q9D7G4	0.9	1.8E-01	0.9	2.6E-01	0.2	7.0E-01	0.2	7.6E-01
ENSMUST00000114222	guanine nucleotide binding protein (G protein), gamma 12 [Source:MGI Symbol;Acc:MGI:1336171]		Q9DAS9	0.5	5.7E-01	-0.2	8.7E-01	-0.2	8.6E-01	0.5	6.1E-01
ENSMUST00000116625	fetuin beta [Source:MGI Symbol;Acc:MGI:1890221]	Q6YJU1		4.9	2.3E-02	-6.6	6.3E-04	-0.9	7.6E-02	-0.8	6.0E-01
ENSMUST00000114225	guanine nucleotide binding protein (G protein), gamma 12 [Source:MGI Symbol;Acc:MGI:1336171]		Q9DAS9	1.1	5.9E-01	-1.1	6.6E-01	-1.9	2.6E-01	0.3	9.0E-01
ENSMUST00000116629	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	J3KMU9		-9.4	8.2E-05	-6.3	1.6E-03	0.7	1.9E-01	-1.0	5.3E-01
ENSMUST00000116634	WD repeat domain 45 [Source:MGI Symbol;Acc:MGI:1859606]	A2AEV5		-4.7	6.4E-03	-7.9	5.4E-05	-0.4	2.3E-01	-0.1	9.5E-01
ENSMUST00000116639	proline rich 16 [Source:MGI Symbol;Acc:MGI:1918623]		A3KMN5	6.7	1.3E-03	0.5	6.1E-01	-3.4	4.2E-03	-0.1	9.4E-01
ENSMUST00000114230				0.4	6.6E-01	1.6	1.7E-01	0.1	9.0E-01	-1.1	2.9E-01
ENSMUST00000114232	histocompatibility 2, class II, locus Mb1 [Source:MGI Symbol;Acc:MGI:95922]	Q31094		-0.2	7.8E-01	-1.4	1.4E-01	-1.9	1.9E-02	-0.7	4.3E-01
ENSMUST00000116666	t-complex protein 10b [Source:MGI Symbol;Acc:MGI:98542]	E9PYJ0		7.9	9.9E-04	3.6	2.9E-03	-2.8	2.2E-02	0.5	4.9E-01
ENSMUST00000116669	ubiquitin specific peptidase 14 [Source:MGI Symbol;Acc:MGI:1928898]	E9PYI8		-5.1	1.4E-02	-3.6	5.5E-03	1.0	9.0E-02	-1.8	1.6E-01
ENSMUST00000114236	TNFAIP3 interacting protein 3 [Source:MGI Symbol;Acc:MGI:3041165]	Q3SXA6		2.5	7.5E-02	2.3	1.3E-01	-1.1	3.8E-01	-1.0	4.4E-01
ENSMUST00000114237	acyl-Coenzyme A oxidase 3, pristanoyl [Source:MGI Symbol;Acc:MGI:1933156]		Q9EPL9	-1.1	3.5E-01	-1.1	5.8E-01	2.0	1.2E-01	1.9	3.0E-01
ENSMUST00000114238	acyl-Coenzyme A oxidase 3, pristanoyl [Source:MGI Symbol;Acc:MGI:1933156]	E9Q296		-0.4	6.0E-01	-2.0	1.2E-01	-0.7	2.9E-01	0.8	5.1E-01
ENSMUST00000117053	serine (or cysteine) peptidase inhibitor, clade A, member 1F [Source:MGI Symbol;Acc:MGI:1915598]	E9PUC6		7.9	1.1E-05	-9.3	1.7E-04	-0.9	7.3E-02	-0.8	6.5E-01
ENSMUST00000117061	septin 8 [Source:MGI Symbol;Acc:MGI:894310]		Q8CHH9	7.6	1.1E-02	6.6	8.3E-05	-0.6	5.7E-01	-1.0	1.1E-01
ENSMUST00000117064	RIKEN cDNA A730017C20 gene [Source:MGI Symbol;Acc:MGI:2442934]	I1E4Y1		6.4	1.5E-03	-3.8	3.2E-02	-2.0	6.4E-02	-2.2	2.4E-01
ENSMUST00000117069	peptidylprolyl isomerase (cyclophilin)-like 3 [Source:MGI Symbol;Acc:MGI:1917475]		Q9D6L8	3.3	2.2E-03	1.6	6.6E-02	0.3	6.2E-01	0.2	7.3E-01
ENSMUST00000117077	te carrier family 7 (cationic amino acid transporter, y+ system), member 2 [Source:MGI Symbol;Acc:MGI:998		P18581	4.7	4.7E-03	2.7	1.0E-01	-0.7	6.2E-01	3.2	2.2E-02
ENSMUST00000117083	thyroid hormone receptor interactor 4 [Source:MGI Symbol;Acc:MGI:1928469]		Q9QXN3	-7.4	3.0E-05	2.6	4.2E-01	-0.8	7.7E-01	2.8	2.8E-01
ENSMUST00000114252	collagen, type XI, alpha 2 [Source:MGI Symbol;Acc:MGI:88447]		Q64739	-1.8	1.7E-01	2.8	4.8E-02	0.6	5.9E-01	-4.0	1.0E-02
ENSMUST00000114253	RNA binding motif protein 11 [Source:MGI Symbol;Acc:MGI:2447622]		Q80YT9	2.1	8.8E-02	4.2	7.0E-03	0.4	7.0E-01	-1.7	1.3E-01
ENSMUST00000114255	collagen, type XI, alpha 2 [Source:MGI Symbol;Acc:MGI:88447]		Q64739	3.0	1.7E-01	0.1	9.6E-01	-1.8	4.5E-01	1.0	6.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000114256	leucine rich repeat and Ig domain containing 1 [Source:MGI Symbol;Acc:MGI:1915522]	A9DA50		3.7	7.4E-02	5.1	2.3E-02	-0.6	7.8E-01	-2.0	1.7E-01
ENSMUST00000117085	abhydrolase domain containing 17C [Source:MGI Symbol;Acc:MGI:1917428]		Q8VCV1	-1.3	3.5E-02	-3.3	1.1E-01	1.0	3.1E-01	-0.1	9.8E-01
ENSMUST00000114268	synuclein, alpha [Source:MGI Symbol;Acc:MGI:1277151]		O55042	2.2	2.8E-01	-1.5	4.1E-01	-5.2	1.0E-02	-1.5	4.2E-01
ENSMUST00000117093	DIX domain containing 1 [Source:MGI Symbol;Acc:MGI:2679721]		Q80Y83	5.0	7.4E-03	6.1	2.0E-03	0.5	7.2E-01	-1.0	2.7E-01
ENSMUST00000117095	phospholipase D family, member 3 [Source:MGI Symbol;Acc:MGI:1333782]		O35405	-6.5	2.4E-03	-3.2	2.1E-02	0.0	9.5E-01	-1.8	2.1E-01
ENSMUST00000117096	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 [Source:MGI Symbol;Acc:MGI:185			4.6	1.4E-02	-2.5	1.4E-01	1.7	6.4E-02	-0.8	6.5E-01
ENSMUST00000117098	canopy 1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2442451]		Q4VAB4	5.5	2.0E-03	6.6	2.8E-03	-0.8	6.6E-01	0.2	8.1E-01
ENSMUST00000117100	solute carrier family 45, member 2 [Source:MGI Symbol;Acc:MGI:2153040]	Q541S3	P58355	6.1	6.9E-03	7.3	4.7E-05	-1.4	2.3E-01	1.0	8.2E-02
ENSMUST00000114296	STE20-related kinase adaptor beta [Source:MGI Symbol;Acc:MGI:2144047]		Q8K4T3	-0.7	2.4E-01	-2.0	1.1E-01	1.5	3.9E-02	2.8	2.8E-02
ENSMUST00000114297	vesicular, overexpressed in cancer, prosurvival protein 1 [Source:MGI Symbol;Acc:MGI:2141658]		Q8R1C3	-0.9	1.8E-01	-1.2	1.4E-01	-0.2	6.4E-01	0.1	8.8E-01
ENSMUST00000114299	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]	B7FAU9		0.0	9.7E-01	-1.4	5.0E-01	2.1	1.2E-01	3.5	1.0E-01
ENSMUST00000117102	frizzled homolog 10 (Drosophila) [Source:MGI Symbol;Acc:MGI:2136761]	Q149J3	Q8BKG4	8.3	4.0E-05	-1.9	1.9E-01	0.6	4.8E-01	-0.7	6.5E-01
ENSMUST00000117123	serum/glucocorticoid regulated kinase 2 [Source:MGI Symbol;Acc:MGI:1351318]		Q9QZS5	7.8	1.4E-05	-4.4	5.8E-02	0.5	6.1E-01	-1.6	5.2E-01
ENSMUST00000114312	glutamate receptor, ionotropic, NMDA1 (zeta 1) [Source:MGI Symbol;Acc:MGI:95819]		P35438	2.7	1.9E-01	5.4	1.9E-02	-0.6	7.7E-01	-3.3	5.1E-02
ENSMUST00000114313	CASP8 and FADD-like apoptosis regulator [Source:MGI Symbol;Acc:MGI:1336166]	Q812G4		0.1	8.9E-01	0.3	6.1E-01	0.7	2.0E-01	0.4	5.1E-01
ENSMUST00000117138	acylphosphatase 1, erythrocyte (common) type [Source:MGI Symbol;Acc:MGI:1913454]		P56376	3.6	1.0E-02	2.7	4.1E-01	-0.7	8.2E-01	2.7	3.0E-01
ENSMUST00000114317	glutamate receptor, ionotropic, NMDA1 (zeta 1) [Source:MGI Symbol;Acc:MGI:95819]	A2AI16		3.0	3.4E-01	4.4	2.1E-01	-0.4	9.1E-01	-1.7	4.4E-01
ENSMUST00000114321	kelch repeat and BTB (POZ) domain containing 2 [Source:MGI Symbol;Acc:MGI:2384811]	G3X9X1		0.7	8.2E-01	-1.9	7.2E-01	0.2	9.6E-01	2.7	5.6E-01
ENSMUST00000117146	ubiquitin-conjugating enzyme E2W (putative) [Source:MGI Symbol;Acc:MGI:1914049]	A0A0A0MQF3		-4.0	3.7E-05	-1.0	5.1E-01	1.2	2.5E-01	-2.0	2.7E-01
ENSMUST00000117160	cadherin 13 [Source:MGI Symbol;Acc:MGI:99551]		Q9WTR5	6.9	1.3E-04	6.0	1.4E-02	-0.6	7.8E-01	-1.7	1.9E-01
ENSMUST00000117167	S100 calcium binding protein A9 (calgranulin B) [Source:MGI Symbol;Acc:MGI:1338947]	Q3UP42	P31725	-10.4	6.5E-07	-3.7	9.8E-02	0.2	8.6E-01	-0.1	9.8E-01
ENSMUST00000117171	wingless-type MMTV integration site family, member 5B [Source:MGI Symbol;Acc:MGI:98959]		P22726	7.9	1.7E-03	-2.3	1.0E-01	1.7	3.2E-02	-0.7	5.8E-01
ENSMUST00000117173	C-type lectin domain family 4, member a3 [Source:MGI Symbol;Acc:MGI:1920399]	Q8JZX6		-6.5	7.3E-05	0.0	9.6E-01	0.6	1.1E-01	-0.8	1.6E-01
ENSMUST00000114336	taperin [Source:MGI Symbol;Acc:MGI:2139535]		A2AI08	0.7	2.7E-01	2.0	3.5E-02	1.4	6.3E-02	0.1	9.4E-01
ENSMUST00000114337	Ngg1 interacting factor 3-like 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:1929485]	D3Z0G0		-1.3	4.5E-01	-1.3	4.7E-01	-0.9	5.1E-01	-0.9	6.4E-01
ENSMUST00000117192	kelch-like 22 [Source:MGI Symbol;Acc:MGI:1337995]	H9KV05		4.1	1.3E-02	-7.6	4.6E-04	1.5	1.1E-02	-1.3	4.5E-01
ENSMUST00000117202	predicted gene 10600 [Source:MGI Symbol;Acc:MGI:3710628]	Q8BQ57		5.6	3.2E-04	6.7	2.9E-04	-0.5	6.8E-01	-1.4	6.9E-02
ENSMUST00000117217	numb gene homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:107423]		Q9QZS3	-8.4	2.9E-05	-4.1	3.4E-03	-0.7	2.0E-01	-0.8	4.9E-01
ENSMUST00000114349	NADPH dependent diflavin oxidoreductase 1 [Source:MGI Symbol;Acc:MGI:1926047]		A2AI05	0.7	7.4E-01	2.7	2.9E-01	0.7	7.3E-01	-1.3	5.8E-01
ENSMUST00000114352	interleukin-1 receptor-associated kinase 1 [Source:MGI Symbol;Acc:MGI:107420]	Q540G0	Q62406	-1.2	3.1E-01	1.3	4.7E-01	2.3	9.8E-02	-0.2	8.9E-01
ENSMUST00000117236	DDB1 and CUL4 associated factor 11 [Source:MGI Symbol;Acc:MGI:90168]		Q91VU6	-6.6	1.3E-04	-4.1	6.3E-02	0.4	7.1E-01	-0.9	6.7E-01
ENSMUST00000117237	glutamine and serine rich 1 [Source:MGI Symbol;Acc:MGI:2138986]	A2BIE1		2.5	6.7E-04	6.9	8.1E-04	-0.5	7.2E-01	-0.7	3.6E-01
ENSMUST00000114357	ST3 beta-galactoside alpha-2,3-sialyltransferase 6 [Source:MGI Symbol;Acc:MGI:1888707]		Q8VIB3	-1.3	4.3E-01	-0.5	8.4E-01	0.4	8.1E-01	-0.5	8.2E-01
ENSMUST00000117241	zinc finger protein 367 [Source:MGI Symbol;Acc:MGI:2442266]		Q0VDT2	6.3	1.5E-04	-5.8	2.7E-02	0.3	7.3E-01	0.8	7.3E-01
ENSMUST00000117242	golgi integral membrane protein 4 [Source:MGI Symbol;Acc:MGI:1920374]	D3YVW2		-5.6	3.3E-04	8.5	4.4E-05	-0.4	7.3E-01	-0.5	4.0E-01
ENSMUST00000117245	transformation related protein 53 binding protein 2 [Source:MGI Symbol;Acc:MGI:2138319]	E9QJU8		-1.4	7.8E-03	6.4	1.4E-03	0.3	8.5E-01	0.0	9.9E-01
ENSMUST00000114371	cms small ribosomal subunit 1 [Source:MGI Symbol;Acc:MGI:1913747]		Q9CZT6	1.2	1.8E-01	-0.2	8.6E-01	-1.9	2.8E-02	-0.6	4.5E-01
ENSMUST00000114372	host cell factor C1 [Source:MGI Symbol;Acc:MGI:105942]	B1AUX2		-1.0	5.3E-01	-1.0	6.6E-01	0.7	6.5E-01	0.6	7.7E-01
ENSMUST00000117254	high mobility group AT-hook 1 [Source:MGI Symbol;Acc:MGI:96160]	Q566K0	P17095	5.9	5.2E-04	-6.4	1.0E-02	-0.4	5.3E-01	0.6	7.9E-01
ENSMUST00000117282	SR-related CTD-associated factor 1 [Source:MGI Symbol;Acc:MGI:2141980]		Q5U4C3	-8.0	3.7E-04	-2.2	2.8E-01	1.7	1.6E-01	-0.1	9.6E-01
ENSMUST00000117299	RIKEN cDNA 2700094K13 gene [Source:MGI Symbol;Acc:MGI:1919907]		Q3UQA7	-2.8	4.9E-03	-1.8	1.5E-01	0.1	9.0E-01	-2.4	1.2E-01
ENSMUST00000117301	discoidin domain receptor family, member 1 [Source:MGI Symbol;Acc:MGI:99216]		Q03146	7.5	1.3E-02	2.2	1.5E-01	0.3	8.1E-01	1.1	2.9E-01
ENSMUST00000117316	predicted gene 12216 [Source:MGI Symbol;Acc:MGI:3650088]	A8Y5C0		4.4	2.9E-02	4.9	3.0E-05	-1.1	1.1E-01	-0.6	1.8E-01
ENSMUST00000114404	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	B1AUY2		-3.8	1.5E-01	-1.0	7.7E-01	2.4	3.0E-01	-0.4	9.1E-01
ENSMUST00000114405	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	B1AUY3		1.3	8.4E-02	1.4	1.3E-01	0.0	9.5E-01	-0.1	9.0E-01
ENSMUST00000117338	echinoderm microtubule associated protein like 2 [Source:MGI Symbol;Acc:MGI:1919455]	E9QK48		4.7	3.3E-02	-6.1	7.0E-02	1.0	3.6E-01	-1.0	7.6E-01
ENSMUST00000117341	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human) [Source:MGI Symbol;Acc:MGI:2139806]	D3Z3F8		7.1	1.3E-04	-2.9	2.5E-01	4.3	9.7E-03	-0.6	8.0E-01
ENSMUST00000117346	bestrophin 1 [Source:MGI Symbol;Acc:MGI:1346332]		O88870	5.2	3.7E-04	-3.8	8.0E-02	1.4	1.8E-01	1.1	5.8E-01
ENSMUST00000117355	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 [Source:MGI Symbol;Acc:MGI:1201670]		O35226	-4.6	3.1E-02	7.8	2.9E-03	-0.1	9.6E-01	-2.3	5.7E-02
ENSMUST00000114418	euchromatic histone methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1924933]	E9Q5A3		-1.7	4.6E-01	1.9	5.9E-01	4.2	1.5E-01	0.7	8.1E-01
ENSMUST00000117363	large subunit GTPase 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:107236]		Q3UM18	5.4	3.8E-03	-5.1	7.8E-04	1.0	3.4E-02	-0.7	5.6E-01
ENSMUST00000117383	SEC11 homolog A, signal peptidase complex subunit [Source:MGI Symbol;Acc:MGI:1929464]	D3Z569		-4.4	1.9E-04	3.0	1.7E-03	-4.4	6.4E-04	-1.1	8.3E-02
ENSMUST00000117386	synaptopodin 2-like [Source:MGI Symbol;Acc:MGI:1916010]	B2RQK7		7.4	2.9E-02	-4.2	5.9E-02	1.0	3.6E-01	-1.9	4.3E-01
ENSMUST00000117392	WD repeat domain 81 [Source:MGI Symbol;Acc:MGI:2681828]	K4DI77		-4.0	3.5E-02	6.7	2.9E-04	-0.6	6.2E-01	-1.1	1.5E-01
ENSMUST00000117394	TAO kinase 2 [Source:MGI Symbol;Acc:MGI:1915919]		Q6ZQ29	-1.8	5.1E-03	-1.0	5.5E-01	2.9	1.8E-02	-0.8	6.2E-01
ENSMUST00000117396	non-SMC condensin I complex, subunit G [Source:MGI Symbol;Acc:MGI:1930197]	E9PWG6		-2.2	5.3E-03	4.6	5.1E-03	-2.0	1.6E-01	0.1	9.2E-01
ENSMUST00000117399	moesin [Source:MGI Symbol;Acc:MGI:97167]		P26041	-7.8	1.1E-07	-0.9	3.1E-01	1.0	1.1E-01	0.2	8.0E-01
ENSMUST00000117404	RIKEN cDNA 9430038I01 gene [Source:MGI Symbol;Acc:MGI:1924502]	D3YTU4		3.2	4.5E-03	-3.5	2.2E-02	-0.7	3.0E-01	0.0	9.9E-01
ENSMUST00000117411	single-stranded DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:1920040]	Q8R2K3		-6.3	4.7E-05	-5.5	5.7E-03	0.8	2.0E-01	0.2	9.0E-01
ENSMUST00000114445	chromobox 3 [Source:MGI Symbol;Acc:MGI:108515]	D3Z1A9		5.7	3.5E-02	2.6	4.1E-01	-0.6	8.2E-01	2.5	3.1E-01
ENSMUST00000114446	chromobox 3 [Source:MGI Symbol;Acc:MGI:108515]	Q9DCC5		-3.3	4.0E-01	4.8	2.2E-01	2.5	4.8E-01	-5.5	1.4E-01
ENSMUST00000117423	kinesin family member 2A [Source:MGI Symbol;Acc:MGI:108390]		P28740	-7.9	4.1E-05	-3.2	4.0E-04	0.9	1.5E-02	-0.4	4.9E-01
ENSMUST00000114455	peptidoglycan recognition protein 2 [Source:MGI Symbol;Acc:MGI:1928099]		Q8VCS0	0.9	5.0E-01	0.7	6.7E-01	-0.4	7.3E-01	-0.2	8.8E-01
ENSMUST00000117440	choline phosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2384841]	D3YU39		5.1	4.3E-05	-2.0	3.5E-01	-3.4	5.4E-02	2.7	1.9E-01
ENSMUST00000117441	interleukin 12 receptor, beta 2 [Source:MGI Symbol;Acc:MGI:1270861]	D3Z6H5		6.5	3.7E-05	-4.1	6.6E-03	0.4	5.7E-01	-3.2	8.4E-02
ENSMUST00000117442	slowmo homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1913640]	B0QZU2		-4.1	1.2E-02	-4.2	9.0E-03	0.8	2.4E-01	-0.4	7.6E-01
ENSMUST00000117445	spermatogenesis associated 22 [Source:MGI Symbol;Acc:MGI:2685728]	B0QZP0		4.6	7.2E-05	2.4	1.1E-02	-0.1	8.7E-01	0.4	5.6E-01
ENSMUST00000117446	pituitary tumor-transforming gene 1 [Source:MGI Symbol;Acc:MGI:1353578]		Q9CQJ7	4.3	4.8E-03	0.1	9.3E-01	-3.0	7.6E-03	2.6	2.2E-02
ENSMUST00000117449	JNK1/MAPK8-associated membrane protein [Source:MGI Symbol;Acc:MGI:1915057]		Q8BI36	-2.0	9.7E-03	4.0	7.8E-02	-1.3	5.2E-01	-1.1	4.7E-01
ENSMUST00000114471	Casitas B-lineage lymphoma b [Source:MGI Symbol;Acc:MGI:2146430]	B9EKI5		0.5	2.4E-01	1.4	3.8E-02	0.7	1.5E-01	-0.2	7.6E-01
ENSMUST00000117452	shisa family member 7 [Source:MGI Symbol;Acc:MGI:3605641]	F6T9T6		8.4	3.4E-03	4.9	9.6E-03	-0.7	6.8E-01	0.8	4.4E-01
ENSMUST00000117462	ras homolog gene family, member D [Source:MGI Symbol;Acc:MGI:108446]	G3X9Y4		6.8	6.9E-05	3.6	6.2E-03	-2.5	3.4E-02	0.9	2.8E-01
ENSMUST00000114475	bromodomain containing 4 [Source:MGI Symbol;Acc:MGI:1888520]	B2RSE4	Q9ESU6	1.8	1.5E-01	1.0	5.5E-01	1.4	2.9E-01	2.2	1.6E-01
ENSMUST00000117463	mitochondrial transcription termination factor 1a [Source:MGI Symbol;Acc:MGI:1918240]		Q8CHZ9	1.6	3.4E-02	6.8	5.8E-05	0.7	4.7E-01	0.9	1.2E-01
ENSMUST00000117492	ubiquitin specific peptidase 33 [Source:MGI Symbol;Acc:MGI:2159711]		Q8R5K2	-5.0	5.5E-04	4.6	1.8E-03	0.9	3.8E-01	0.7	3.1E-01
ENSMUST00000114479	ATPase, Ca++ transporting, plasma membrane 3 [Source:MGI Symbol;Acc:MGI:1347353]	A2ALL9		2.7	4.3E-02	8.0	4.3E-05	-0.5	6.7E-01	-5.9	5.5E-05
ENSMUST00000114482	interleukin 1 receptor antagonist [Source:MGI Symbol;Acc:MGI:96547]	Q542C7	P25085	-1.7	7.8E-02	-1.9	1.7E-01	0.6	4.1E-01	0.8	5.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000117506	ubiquitination factor E4A [Source:MGI Symbol;Acc:MGI:2154580]		E9Q735	-3.8	1.4E-04	-6.3	9.8E-05	-1.4	2.8E-03	-0.2	8.6E-01
ENSMUST00000117507	extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:103060]		Q61508	-4.1	3.5E-03	6.1	3.3E-04	-0.5	6.4E-01	-0.6	3.9E-01
ENSMUST00000114487	interleukin 1 receptor antagonist [Source:MGI Symbol;Acc:MGI:96547]	Q542W1	P25085	-3.2	4.9E-02	-0.4	8.2E-01	1.3	3.2E-01	-1.5	4.1E-01
ENSMUST00000114488	bobby sox homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1917758]		Q8VBW5	1.1	5.6E-01	1.9	4.3E-01	-0.1	9.7E-01	-0.9	6.7E-01
ENSMUST00000117510	olfactory receptor 398 [Source:MGI Symbol;Acc:MGI:3030232]	Q8VFY0		5.0	2.2E-02	3.7	7.5E-03	0.1	9.0E-01	-0.3	7.0E-01
ENSMUST00000117513	solute carrier family 29 (nucleoside transporters), member 3 [Source:MGI Symbol;Acc:MGI:1918529]		Q99P65	1.9	1.5E-03	2.2	2.7E-01	-0.4	8.3E-01	2.3	1.4E-01
ENSMUST00000117536	azole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase [Source:MGI S		Q9DCL9	-5.1	8.4E-04	-8.5	1.4E-04	1.4	4.6E-03	-0.9	5.6E-01
ENSMUST00000117539	kinesin family member 2A [Source:MGI Symbol;Acc:MGI:108390]	F8VQ42		-2.2	1.7E-02	-5.0	2.3E-02	0.5	5.2E-01	-0.8	6.8E-01
ENSMUST00000114498	histamine N-methyltransferase [Source:MGI Symbol;Acc:MGI:2153181]	A2AQK4	Q91VF2	2.8	2.9E-01	0.8	8.0E-01	-3.4	2.5E-01	-1.4	6.1E-01
ENSMUST00000114499	zinc finger protein 275 [Source:MGI Symbol;Acc:MGI:1350985]	Q3UQ14		-0.7	7.0E-01	0.7	6.9E-01	-0.5	7.5E-01	-1.9	3.1E-01
ENSMUST00000117544	expressed sequence AU022751 [Source:MGI Symbol;Acc:MGI:2147968]	B1B0V2		6.7	8.1E-03	4.7	5.1E-02	2.1	3.0E-01	0.8	5.7E-01
ENSMUST00000114507	brain and reproductive organ-expressed protein [Source:MGI Symbol;Acc:MGI:1333875]		Q8K3W0	-1.0	6.7E-01	3.1	4.8E-01	4.6	1.7E-01	0.5	8.8E-01
ENSMUST00000114509				-1.9	4.6E-01	-4.0	2.0E-01	-2.8	1.1E-01	-0.7	8.2E-01
ENSMUST00000117549	ubiquitination factor E4A [Source:MGI Symbol;Acc:MGI:2154580]	G3X9Y5		-3.5	1.4E-03	5.5	3.3E-03	-1.3	3.7E-01	-0.1	8.9E-01
ENSMUST00000114512	glutaminase [Source:MGI Symbol;Acc:MGI:95752]	D3Z7P4		2.3	3.0E-01	7.1	5.4E-02	4.2	1.9E-01	-0.6	7.9E-01
ENSMUST00000114513	glutaminase [Source:MGI Symbol;Acc:MGI:95752]		D3Z7P3	0.1	8.2E-01	-0.2	7.9E-01	0.6	2.7E-01	1.0	2.1E-01
ENSMUST00000117550	te immunoglobulin-like receptor, subfamily A (with TM domain), member 5 [Source:MGI Symbol;Acc:MGI:3(	D3Z7A9		2.4	5.6E-03	4.2	1.1E-03	-1.0	3.0E-01	-1.6	4.6E-02
ENSMUST00000117551	RAS p21 protein activator 3 [Source:MGI Symbol;Acc:MGI:1197013]		Q60790	-4.1	1.1E-05	-5.3	3.1E-03	1.4	2.4E-02	-0.8	6.1E-01
ENSMUST00000117555	dipeptidase 2 [Source:MGI Symbol;Acc:MGI:2442042]		Q8C255	-6.4	8.5E-05	8.8	5.9E-05	-0.7	6.0E-01	0.2	7.1E-01
ENSMUST00000117556	RIKEN cDNA D630045J12 gene [Source:MGI Symbol;Acc:MGI:2669829]	D3YTS3		5.2	9.3E-04	-1.8	5.2E-01	2.3	2.5E-01	-3.5	2.7E-01
ENSMUST00000117557	heat shock protein 8 [Source:MGI Symbol;Acc:MGI:105384]	Q504P4		-7.1	1.0E-04	-3.3	2.8E-02	0.2	7.2E-01	0.1	9.6E-01
ENSMUST00000114529	acyl-Coenzyme A binding domain containing 5 [Source:MGI Symbol;Acc:MGI:1921409]	E9QNH7		-1.4	2.1E-01	-2.0	2.3E-01	0.2	8.1E-01	0.8	6.1E-01
ENSMUST00000117564	zonadhesin [Source:MGI Symbol;Acc:MGI:106656]	E9PWQ7		9.6	1.9E-04	-5.8	6.4E-04	0.0	9.3E-01	-0.7	5.6E-01
ENSMUST00000114537	myosin IB [Source:MGI Symbol;Acc:MGI:107752]	E9QNH6		4.1	5.1E-02	0.4	8.3E-01	-5.1	1.5E-02	-1.4	3.8E-01
ENSMUST00000117565	adrenergic receptor, beta 3 [Source:MGI Symbol;Acc:MGI:87939]		P25962	6.3	9.5E-04	5.3	2.1E-02	-0.6	7.8E-01	1.0	4.1E-01
ENSMUST00000117583	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913290]		Q9QZ23	-7.0	1.2E-05	-7.8	1.7E-03	0.9	1.2E-01	1.1	5.4E-01
ENSMUST00000114545	leucine rich repeat containing 61 [Source:MGI Symbol;Acc:MGI:2652848]			-0.5	4.3E-01	0.7	3.7E-01	0.9	1.5E-01	-0.3	6.9E-01
ENSMUST00000117597	F-box protein 7 [Source:MGI Symbol;Acc:MGI:1917004]	Q3UGI9		-5.0	3.5E-03	2.4	8.8E-02	-2.2	1.1E-01	2.2	5.5E-02
ENSMUST00000117598	vacuolar protein sorting 8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2146407]		Q0P5W1	-4.8	8.1E-03	3.1	1.9E-02	-1.5	1.7E-01	0.3	7.7E-01
ENSMUST00000114548	cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1889272]		Q8R5M8	2.6	1.5E-01	5.2	1.2E-02	-0.6	7.4E-01	-3.1	3.8E-02
ENSMUST00000117638	zinc finger protein 534 [Source:MGI Symbol;Acc:MGI:3650650]	A2A7A1		6.4	6.0E-04	-5.9	2.4E-03	-1.6	4.6E-02	-0.2	9.0E-01
ENSMUST00000117644	crystallin, zeta (quinone reductase)-like 1 [Source:MGI Symbol;Acc:MGI:1913859]	D3Z6I4		-4.6	3.3E-03	-5.3	6.4E-03	0.0	9.8E-01	0.6	7.3E-01
ENSMUST00000117646	DIX domain containing 1 [Source:MGI Symbol;Acc:MGI:2679721]		Q80Y83	4.1	1.1E-02	8.6	7.0E-04	-0.3	8.8E-01	1.4	1.4E-01
ENSMUST00000114560	zinc finger protein 467 [Source:MGI Symbol;Acc:MGI:1916160]	B2RU53	Q8JZL0	4.8	5.1E-02	4.6	1.2E-01	0.0	1.0E+00	0.3	8.8E-01
ENSMUST00000114561	zinc finger protein 467 [Source:MGI Symbol;Acc:MGI:1916160]	B2RU53	Q8JZL0	2.1	5.7E-02	2.7	1.0E-01	1.3	3.4E-01	0.7	5.1E-01
ENSMUST00000117654	transforming growth factor beta regulated gene 1 [Source:MGI Symbol;Acc:MGI:1100877]		Q3UB74	-5.1	3.1E-04	7.1	1.4E-04	-0.6	6.2E-01	-1.3	8.3E-02
ENSMUST00000117676	regulator of G-protein signaling 17 [Source:MGI Symbol;Acc:MGI:1927469]		Q9QZB0	3.9	2.9E-03	7.0	1.4E-05	-1.2	2.1E-01	0.0	9.6E-01
ENSMUST00000114571	KRAB-A domain containing 1 [Source:MGI Symbol;Acc:MGI:1925077]	D3Z4B8		5.7	4.4E-02	3.2	2.7E-01	-0.8	8.0E-01	1.7	3.8E-01
ENSMUST00000114572	KRAB-A domain containing 1 [Source:MGI Symbol;Acc:MGI:1925077]		Q6NXZ1	2.2	2.1E-01	4.4	2.8E-02	-0.5	7.4E-01	-2.7	9.7E-02
ENSMUST00000117688	ankyrin repeat and SOCS box-containing 15 [Source:MGI Symbol;Acc:MGI:1926160]		Q8VHS6	7.1	3.8E-05	-8.7	3.6E-03	1.2	8.6E-02	4.6	6.5E-02
ENSMUST00000117694	O-acyltransferase like [Source:MGI Symbol;Acc:MGI:2442915]	E9Q6M1		7.4	1.7E-02	7.2	1.5E-04	-0.7	6.1E-01	-0.2	8.0E-01
ENSMUST00000117695	B cell linker [Source:MGI Symbol;Acc:MGI:96878]	D3YWR2		2.4	1.0E-02	-5.0	3.6E-03	-0.6	3.0E-01	0.0	1.0E+00
ENSMUST00000117699	5-hydroxytryptamine (serotonin) receptor 1D [Source:MGI Symbol;Acc:MGI:96276]		Q61224	7.9	1.5E-04	4.1	2.3E-03	-2.6	4.1E-02	-1.2	1.3E-01
ENSMUST00000117706	mediator complex subunit 12 [Source:MGI Symbol;Acc:MGI:1926212]	A2AGH8		-3.4	3.1E-02	7.8	7.2E-04	-0.9	5.9E-01	1.2	1.4E-01
ENSMUST00000117721	zinc finger with KRAB and SCAN domains 3 [Source:MGI Symbol;Acc:MGI:1919989]	D3YTV4		4.3	6.4E-07	2.4	7.5E-02	-4.1	1.2E-02	-2.3	5.7E-02
ENSMUST00000114583	zinc finger protein 777 [Source:MGI Symbol;Acc:MGI:1919556]	B9EKF4		0.5	4.7E-01	-4.2	2.3E-02	0.6	3.8E-01	5.2	6.1E-03
ENSMUST00000117725	FAD-dependent oxidoreductase domain containing 2 [Source:MGI Symbol;Acc:MGI:106315]		Q3USW5	8.1	2.2E-03	7.0	1.6E-04	-0.6	6.3E-01	-0.9	1.9E-01
ENSMUST00000117748	interferon (alpha and beta) receptor 1 [Source:MGI Symbol;Acc:MGI:107658]		P33896	-3.9	4.8E-03	7.5	5.3E-04	-1.6	3.0E-01	-0.5	4.2E-01
ENSMUST00000117757	glyceraldehyde-3-phosphate dehydrogenase [Source:MGI Symbol;Acc:MGI:95640]	A0A0A0MQF6		-9.9	7.4E-04	-2.5	5.5E-02	0.0	9.6E-01	-1.2	3.7E-01
ENSMUST00000117762	integrin alpha L [Source:MGI Symbol;Acc:MGI:96606]	E9QNL8		-7.1	3.1E-03	3.1	2.2E-03	-0.5	4.2E-01	0.5	4.5E-01
ENSMUST00000117783	RAD50 interactor 1 [Source:MGI Symbol;Acc:MGI:1916233]	D3YU07		3.5	2.7E-04	-4.9	4.4E-04	-0.3	4.7E-01	-0.7	4.7E-01
ENSMUST00000114603	eukaryotic translation initiation factor 2B, subunit 4 delta [Source:MGI Symbol;Acc:MGI:95300]		Q61749	0.8	4.2E-01	2.2	8.3E-02	0.2	8.0E-01	-1.1	2.7E-01
ENSMUST00000117784	ataxin 7-like 2 [Source:MGI Symbol;Acc:MGI:1919772]	Q8C8K6		-4.1	2.1E-02	-0.8	6.0E-01	4.7	5.6E-04	-0.8	5.7E-01
ENSMUST00000117785	roundabout homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1890110]	Q19AB2		6.9	5.8E-05	4.8	5.8E-03	-0.8	5.7E-01	-0.2	8.3E-01
ENSMUST00000117796	Rho guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:1353510]	E9PUF7		-4.9	2.6E-02	5.6	5.6E-04	1.6	1.3E-01	-0.6	3.9E-01
ENSMUST00000117803	interferon induced transmembrane protein 7 [Source:MGI Symbol;Acc:MGI:1921732]	G3X9Z2		6.0	1.8E-06	6.6	1.8E-04	-0.5	6.5E-01	-0.9	1.7E-01
ENSMUST00000114614	enhancer trap locus 4 [Source:MGI Symbol;Acc:MGI:95454]		A2AQ25	4.0	4.9E-02	5.2	2.4E-02	-0.4	8.5E-01	-1.7	2.0E-01
ENSMUST00000114616	enhancer of zeste homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:107940]	D3Z774		-2.9	3.9E-01	0.9	7.7E-01	0.4	8.7E-01	-3.4	3.3E-01
ENSMUST00000114617	X-linked myotubular myopathy gene 1 [Source:MGI Symbol;Acc:MGI:1099452]		Q9Z2C5	2.0	2.7E-01	1.1	6.1E-01	-0.7	6.7E-01	0.2	9.4E-01
ENSMUST00000117811	nephronectin [Source:MGI Symbol;Acc:MGI:2148811]	D3Z4D3		7.4	1.2E-02	-2.5	8.3E-02	2.9	3.3E-03	-0.6	6.3E-01
ENSMUST00000117812	on imprinted in Prader-Willi/Angelman syndrome 2 homolog (human) [Source:MGI Symbol;Acc:MGI:191391		Q9JJC8	-5.6	6.3E-05	5.7	2.7E-02	-0.8	7.2E-01	2.0	1.5E-01
ENSMUST00000114637				3.6	1.2E-01	4.7	7.0E-02	-0.5	8.4E-01	-1.6	3.4E-01
ENSMUST00000114640	armadillo repeat containing 3 [Source:MGI Symbol;Acc:MGI:1918132]		A2AU72	3.0	2.5E-01	5.2	6.7E-02	-0.5	8.7E-01	-2.7	1.7E-01
ENSMUST00000117831	aryl-hydrocarbon receptor-interacting protein [Source:MGI Symbol;Acc:MGI:109622]		O08915	-3.3	6.2E-03	8.2	3.1E-05	-0.5	6.8E-01	-0.8	1.3E-01
ENSMUST00000117836	interferon (alpha and beta) receptor 2 [Source:MGI Symbol;Acc:MGI:1098243]	Q9D1R7	O35664	-7.9	5.2E-05	2.3	2.8E-01	-2.5	2.4E-01	0.6	7.0E-01
ENSMUST00000117849	casein kinase 1, gamma 1 [Source:MGI Symbol;Acc:MGI:2660884]	Q6P2B2		5.7	3.8E-03	6.8	1.3E-03	0.4	7.7E-01	0.3	7.4E-01
ENSMUST00000117852	transmembrane protein 135 [Source:MGI Symbol;Acc:MGI:1920009]	Q8C8G3		4.7	3.3E-03	-4.3	7.0E-02	-0.1	9.2E-01	-0.9	7.1E-01
ENSMUST00000117859	RIKEN cDNA D930048N14 gene [Source:MGI Symbol;Acc:MGI:2144709]	B0QZN8		6.7	4.0E-04	-2.6	1.7E-02	0.8	1.4E-01	-2.6	3.7E-02
ENSMUST00000117868	vacuolar protein sorting 29 (S. pombe) [Source:MGI Symbol;Acc:MGI:1928344]	D3Z645		-3.9	4.2E-03	-2.6	1.9E-02	1.3	3.0E-02	-0.1	9.0E-01
ENSMUST00000117872	fibroblast growth factor receptor 2 [Source:MGI Symbol;Acc:MGI:95523]	E9Q5C2		6.1	7.0E-04	8.0	9.1E-05	-0.5	6.9E-01	-1.0	1.4E-01
ENSMUST00000117878	ubiquitin specific peptidase like 1 [Source:MGI Symbol;Acc:MGI:2442342]		Q3ULM6	-8.0	6.7E-06	-3.3	3.7E-03	0.8	9.0E-02	-1.1	2.5E-01
ENSMUST00000114668	ute carrier family 5 (sodium-dependent vitamin transporter), member 6 [Source:MGI Symbol;Acc:MGI:26608		Q5U4D8	0.2	9.0E-01	6.2	9.5E-03	2.3	2.4E-01	-3.7	2.1E-02
ENSMUST00000114669	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 [Source:MGI Symbol;Acc:	A2AS72		-0.7	8.1E-01	-0.8	7.7E-01	-2.0	3.6E-01	-1.9	5.3E-01
ENSMUST00000117880	theg spermatid protein like [Source:MGI Symbol;Acc:MGI:1919118]		Q9DA15	4.1	3.1E-02	-1.7	1.3E-01	1.5	4.2E-02	-2.6	6.3E-02
ENSMUST00000114676	myelin basic protein [Source:MGI Symbol;Acc:MGI:96925]	D3Z6U4		0.3	6.1E-01	-0.3	7.5E-01	0.7	2.2E-01	1.3	9.5E-02
ENSMUST00000114677	GRAM domain containing 1C [Source:MGI Symbol;Acc:MGI:2443024]		Q8CI52	3.3	1.6E-01	4.9	6.2E-02	-0.4	8.6E-01	-2.1	2.3E-01
ENSMUST00000114680	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 [Source:MGI Symbol;Acc:		O54826	0.4	8.3E-01	2.1	4.6E-01	1.5	4.3E-01	-0.2	9.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000117882	POM121 membrane glycoprotein-like 2 (rat) [Source:MGI Symbol;Acc:MGI:2684870]	Q3V0N0		2.3	1.6E-02	4.2	9.6E-04	-1.2	1.8E-01	-0.6	3.7E-01
ENSMUST00000117883	ankyrin repeat and SOCS box-containing 3 [Source:MGI Symbol;Acc:MGI:1929749]	A8Y5I6		1.7	2.7E-02	2.7	9.9E-02	-4.3	1.8E-02	-1.4	2.7E-01
ENSMUST00000117890	splA/ryanodine receptor domain and SOCS box containing 3 [Source:MGI Symbol;Acc:MGI:1891471]		Q571F5	-6.6	4.2E-04	4.1	2.0E-04	-0.4	5.6E-01	0.8	1.0E-01
ENSMUST00000117892	solute carrier family 48 (heme transporter), member 1 [Source:MGI Symbol;Acc:MGI:1914989]		Q9D8M3	-2.8	4.9E-04	-6.3	4.4E-03	0.7	2.5E-01	-0.5	7.8E-01
ENSMUST00000117900	ankyrin repeat and SOCS box-containing 10 [Source:MGI Symbol;Acc:MGI:2152836]	D3YU18		6.4	3.3E-04	-4.7	3.3E-04	1.1	2.0E-02	-0.7	4.4E-01
ENSMUST00000114705	transmembrane protein 25 [Source:MGI Symbol;Acc:MGI:1918937]		Q9DCF1	2.5	2.7E-01	5.3	4.1E-02	-0.5	8.3E-01	-3.4	5.5E-02
ENSMUST00000114712	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 [Source:MGI Symbol;Acc:MGI:1928387]		Q9JJ04	2.7	8.4E-02	4.8	7.8E-03	-0.6	7.0E-01	-2.6	4.1E-02
ENSMUST00000117911	sodium channel, voltage-gated, type V, alpha [Source:MGI Symbol;Acc:MGI:98251]			4.5	1.1E-02	-3.8	3.4E-02	1.1	1.5E-01	-0.5	7.7E-01
ENSMUST00000117913	NLR family, apoptosis inhibitory protein 2 [Source:MGI Symbol;Acc:MGI:1298226]		Q9QUK4	-1.8	2.6E-02	-2.5	2.3E-01	0.9	4.3E-01	-0.7	7.2E-01
ENSMUST00000117915	tetratricopeptide repeat domain 14 [Source:MGI Symbol;Acc:MGI:1914370]	E9PXW3		5.6	1.9E-02	-5.3	9.3E-04	-0.2	6.9E-01	-0.7	5.6E-01
ENSMUST00000117919	RAS-like, estrogen-regulated, growth-inhibitor [Source:MGI Symbol;Acc:MGI:2665139]		Q8R367	3.7	1.2E-02	7.5	2.7E-02	-0.7	8.3E-01	-1.1	5.0E-01
ENSMUST00000117929	transmembrane and coiled coil domains 3 [Source:MGI Symbol;Acc:MGI:2442900]		Q8R310	6.2	2.3E-04	0.7	6.7E-01	5.1	1.4E-03	-0.7	6.5E-01
ENSMUST00000117944	heparan sulfate (glucosamine) 3-O-sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1201606]		O35310	7.8	8.3E-05	4.1	1.6E-03	-1.2	1.8E-01	0.0	9.7E-01
ENSMUST00000117945	DiGeorge syndrome critical region gene 2 [Source:MGI Symbol;Acc:MGI:892866]			-7.3	2.5E-04	3.4	1.5E-04	1.4	1.4E-02	-0.6	1.3E-01
ENSMUST00000117958	nuclear distribution gene E homolog 1 (A nidulans) [Source:MGI Symbol;Acc:MGI:1914453]		Q9CZA6	-3.1	7.6E-03	7.2	1.7E-05	0.1	9.2E-01	-0.1	8.2E-01
ENSMUST00000117966	nuclear factor I/C [Source:MGI Symbol;Acc:MGI:109591]		P70255	5.1	2.7E-03	-2.1	1.2E-02	1.0	3.3E-02	-0.7	3.3E-01
ENSMUST00000114747	otoferlin [Source:MGI Symbol;Acc:MGI:1891247]			1.8	2.0E-01	6.8	1.1E-04	-1.7	1.8E-01	-6.7	6.1E-05
ENSMUST00000114748	ΓP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1 [Source:MGI Symbol;Acc:MGI:8811	D3Z6F5		1.7	5.8E-02	0.0	9.5E-01	-2.0	2.0E-02	-0.3	7.1E-01
ENSMUST00000117971	B cell CLL/lymphoma 7A [Source:MGI Symbol;Acc:MGI:1924295]		Q9CXE2	6.3	9.0E-07	-5.2	5.0E-04	0.6	1.1E-01	-0.6	5.9E-01
ENSMUST00000117989	neugrin, neurite outgrowth associated [Source:MGI Symbol;Acc:MGI:1933212]		Q99KS2	-6.9	7.5E-06	1.9	4.5E-02	-0.6	4.1E-01	0.6	4.2E-01
ENSMUST00000117997	solute carrier family 45, member 1 [Source:MGI Symbol;Acc:MGI:2653235]	B0QZL3		8.7	1.8E-05	-3.6	5.4E-03	1.2	3.5E-02	-0.1	9.0E-01
ENSMUST00000118000	regulator of G-protein signaling 20 [Source:MGI Symbol;Acc:MGI:1929866]	E9Q720		8.6	9.2E-06	-3.9	1.0E-02	1.2	4.8E-02	-0.7	5.9E-01
ENSMUST00000114758	mitogen-activated protein kinase 14 [Source:MGI Symbol;Acc:MGI:1346865]	B2KF35		-0.2	7.9E-01	-0.8	3.9E-01	-0.3	6.2E-01	0.3	7.4E-01
ENSMUST00000118001	TATA box binding protein [Source:MGI Symbol;Acc:MGI:101838]	Q91YM5		-6.6	1.3E-05	1.3	9.6E-02	-3.9	4.5E-04	0.3	6.4E-01
ENSMUST00000118002	cilia and flagella associated protein 61 [Source:MGI Symbol;Acc:MGI:1926024]	B2FDE9		7.0	5.9E-05	4.1	4.2E-03	0.9	3.6E-01	0.8	3.3E-01
ENSMUST00000118009	nuclear assembly factor 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2682306]	E9QJT2		2.0	1.4E-02	6.9	1.9E-04	-0.7	5.9E-01	0.3	6.7E-01
ENSMUST00000118064	small integral membrane protein 11 [Source:MGI Symbol;Acc:MGI:1916186]		Q99J19	4.6	5.3E-03	6.3	8.8E-04	0.2	8.8E-01	1.3	8.6E-02
ENSMUST00000118068	predicted gene 15922 [Source:MGI Symbol;Acc:MGI:3802148]			-8.6	1.1E-06	7.7	1.4E-04	1.3	2.9E-01	-0.7	2.8E-01
ENSMUST00000118075	mastermind like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2389461]	E9Q6E8		4.5	2.6E-02	0.5	7.6E-01	2.1	1.1E-01	-1.5	2.9E-01
ENSMUST00000118076	upregulator of cell proliferation [Source:MGI Symbol;Acc:MGI:1919296]		Q5NCI0	6.3	4.9E-03	-2.4	1.5E-01	0.6	5.2E-01	-1.8	3.0E-01
ENSMUST00000114783	enase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit [Sour		Q99JY0	-0.9	5.4E-01	1.0	5.7E-01	1.4	3.8E-01	-0.5	7.3E-01
ENSMUST00000118100	Rap guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:2659071]		Q8CHG7	5.0	2.5E-02	-4.4	4.3E-02	0.8	3.7E-01	0.5	8.2E-01
ENSMUST00000114786	enase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit [Sour		Q99JY0	-3.0	5.9E-02	-3.8	7.0E-02	-1.1	3.1E-01	-0.3	8.9E-01
ENSMUST00000118111	neuroligin 3 [Source:MGI Symbol;Acc:MGI:2444609]	A2AGI3		6.7	5.1E-03	-4.5	2.7E-02	0.1	8.9E-01	-0.7	7.2E-01
ENSMUST00000114792	FK506 binding protein 5 [Source:MGI Symbol;Acc:MGI:104670]	Q4FJN2	Q64378	-1.1	5.4E-01	-0.2	8.7E-01	-4.8	1.8E-03	-5.7	6.8E-03
ENSMUST00000118115	N-6 adenine-specific DNA methyltransferase 1 (putative) [Source:MGI Symbol;Acc:MGI:1915018]	D3Z6J0		5.9	6.7E-04	6.3	2.2E-04	-0.5	6.4E-01	-0.5	4.0E-01
ENSMUST00000118117	synaptotagmin VI [Source:MGI Symbol;Acc:MGI:1859544]	Q8C8S6		6.4	4.8E-04	-6.0	5.2E-04	-0.2	6.3E-01	-0.1	9.6E-01
ENSMUST00000114812	golgi autoantigen, golgin subfamily b, macrogolgin 1 [Source:MGI Symbol;Acc:MGI:1099447]	E9QAH1		1.2	3.5E-01	-0.2	9.1E-01	0.8	6.1E-01	2.3	2.0E-01
ENSMUST00000118118	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human) [Source:MGI Symbol;Acc:MGI:2139806]	Q3TVW1	Q8R1X6	7.0	1.2E-02	-4.6	2.9E-03	-0.2	7.6E-01	-1.0	4.2E-01
ENSMUST00000114823	makorin, ring finger protein, 1 [Source:MGI Symbol;Acc:MGI:1859353]	E9QAG7		0.3	7.8E-01	1.5	4.2E-01	2.4	1.4E-01	1.2	3.8E-01
ENSMUST00000114836	t-complex protein 11 [Source:MGI Symbol;Acc:MGI:98544]	Q5FWA2		3.2	2.1E-01	-0.6	8.8E-01	-1.7	5.6E-01	2.1	5.3E-01
ENSMUST00000118121	family with sequence similarity 220, member A [Source:MGI Symbol;Acc:MGI:1914488]	Q91X57		-3.0	3.0E-03	-4.0	1.8E-04	0.4	3.2E-01	-4.5	9.1E-04
ENSMUST00000114840	thymus cell antigen 1, theta [Source:MGI Symbol;Acc:MGI:98747]		P01831	-0.9	2.0E-01	-0.6	4.6E-01	-0.3	5.6E-01	-0.6	4.6E-01
ENSMUST00000118134	tetratricopeptide repeat domain 13 [Source:MGI Symbol;Acc:MGI:2384573]	E9Q723		-1.6	3.2E-03	-5.9	1.5E-02	1.7	5.1E-02	1.2	5.9E-01
ENSMUST00000118139	glycosyltransferase 1 domain containing 1 [Source:MGI Symbol;Acc:MGI:2442755]		A4FUP9	5.5	7.7E-05	-5.3	1.4E-02	0.6	4.7E-01	-1.8	4.0E-01
ENSMUST00000118144	von Willebrand factor A domain containing 5A [Source:MGI Symbol;Acc:MGI:1915026]		Q99KC8	-5.2	2.3E-03	4.0	2.1E-02	-0.5	7.6E-01	2.4	2.7E-02
ENSMUST00000114848	1 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:191		Q99JX1	-0.8	1.8E-01	0.7	3.2E-01	0.1	7.9E-01	-1.3	5.4E-02
ENSMUST00000118159	GRAM domain containing 1B [Source:MGI Symbol;Acc:MGI:1925037]		Q80TI0	6.0	2.4E-03	3.5	2.0E-04	-0.2	6.9E-01	0.0	9.3E-01
ENSMUST00000118161	glutamate receptor, metabotropic 4 [Source:MGI Symbol;Acc:MGI:1351341]	G3XA00		8.8	5.8E-05	-12.2	9.3E-05	-1.1	6.3E-02	1.4	4.7E-01
ENSMUST00000118163	Dmx-like 2 [Source:MGI Symbol;Acc:MGI:2444630]	B0V2P5		-6.2	1.7E-03	4.7	1.3E-05	-0.5	3.5E-01	0.0	9.7E-01
ENSMUST00000114855				1.0	2.0E-01	1.7	1.2E-01	0.6	4.7E-01	0.0	9.5E-01
ENSMUST00000114857	glypican 3 [Source:MGI Symbol;Acc:MGI:104903]	B1ATR5		0.6	6.7E-01	2.0	2.2E-01	0.4	7.7E-01	-1.0	4.6E-01
ENSMUST00000118169	solute carrier family 5 (sodium/glucose cotransporter), member 2 [Source:MGI Symbol;Acc:MGI:2181411]		Q923I7	7.6	1.1E-04	-10.5	2.5E-05	-0.6	2.4E-01	0.0	9.9E-01
ENSMUST00000114859	DNA segment, Chr 17, Wayne State University 92, expressed [Source:MGI Symbol;Acc:MGI:106281]	B2KF54		-1.9	8.7E-02	-2.8	9.8E-02	0.9	3.2E-01	1.8	2.7E-01
ENSMUST00000118174	putative homeodomain transcription factor 2 [Source:MGI Symbol;Acc:MGI:1916020]			-2.7	2.3E-02	-4.9	2.5E-02	1.1	2.7E-01	0.1	9.7E-01
ENSMUST00000118186	intraflagellar transport 46 [Source:MGI Symbol;Acc:MGI:1923818]		Q9DB07	-7.2	4.9E-06	9.5	1.9E-05	0.4	7.4E-01	0.7	2.2E-01
ENSMUST00000118192	ubiquitin-conjugating enzyme E2J 2 [Source:MGI Symbol;Acc:MGI:2153608]	B0QZM1		-6.1	1.4E-03	2.6	3.7E-01	-0.6	8.1E-01	2.1	3.3E-01
ENSMUST00000114873	protein kinase C and casein kinase substrate in neurons 1 [Source:MGI Symbol;Acc:MGI:1345181]	Q543Y7	Q61644	2.8	4.5E-02	6.2	4.8E-04	-0.5	6.8E-01	-4.0	1.6E-03
ENSMUST00000118193	tetratricopeptide repeat domain 33 [Source:MGI Symbol;Acc:MGI:1914765]		Q9D6K7	-4.8	3.9E-04	5.2	1.4E-03	-0.6	6.4E-01	1.0	1.6E-01
ENSMUST00000114875	muscleblind-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444912]	Q3TJQ3		-0.6	5.2E-01	0.1	9.3E-01	0.5	5.5E-01	-0.2	8.5E-01
ENSMUST00000114878	poly (ADP-ribose) polymerase family, member 9 [Source:MGI Symbol;Acc:MGI:1933117]		Q8CAS9	-0.4	4.8E-01	-1.2	7.4E-02	-1.1	1.8E-02	-0.3	5.8E-01
ENSMUST00000118194	peroxisomal biogenesis factor 11 gamma [Source:MGI Symbol;Acc:MGI:1920905]	Q3TN90		5.5	1.2E-04	-7.4	1.4E-03	-0.5	5.0E-01	-1.2	5.3E-01
ENSMUST00000114884	RNA binding motif protein 33 [Source:MGI Symbol;Acc:MGI:1919670]	D3Z5I9		0.3	8.8E-01	-1.6	5.7E-01	1.0	6.3E-01	2.8	2.5E-01
ENSMUST00000118195	lipoma HMGIC fusion partner-like 2 [Source:MGI Symbol;Acc:MGI:2145236]		Q8BGA2	7.1	4.4E-05	2.3	2.7E-02	-0.4	5.7E-01	0.2	7.8E-01
ENSMUST00000114886	nudix (nucleotide diphosphate linked moiety X)-type motif 3 [Source:MGI Symbol;Acc:MGI:1928484]	B2KF67		0.9	6.9E-01	3.4	3.0E-01	3.2	1.9E-01	0.7	8.1E-01
ENSMUST00000114887	serine/threonine kinase 26 [Source:MGI Symbol;Acc:MGI:1917665]	A2AD84		-6.8	4.5E-02	2.0	6.5E-01	7.6	3.3E-02	-1.3	7.6E-01
ENSMUST00000118196	zinc finger, CCHC domain containing 2 [Source:MGI Symbol;Acc:MGI:2444114]		Q69ZB8	-4.4	2.4E-02	-5.2	6.9E-03	-0.4	4.8E-01	-0.6	7.1E-01
ENSMUST00000118204	SKI-like [Source:MGI Symbol;Acc:MGI:106203]		Q60665	-4.4	3.4E-04	9.7	8.5E-05	0.7	6.2E-01	-1.0	1.0E-01
ENSMUST00000114896	ynthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 [Source:MGI Symbol;Acc:MGI:12	Q8C2Q8		4.0	8.0E-02	6.7	2.5E-02	1.3	6.1E-01	-1.4	3.9E-01
ENSMUST00000118205	vezatin, adherens junctions transmembrane protein [Source:MGI Symbol;Acc:MGI:2143698]		Q3ZK22	4.2	2.2E-03	-8.8	2.9E-05	0.0	9.3E-01	-0.3	8.3E-01
ENSMUST00000114898	zinc finger CCCH type, antiviral 1 [Source:MGI Symbol;Acc:MGI:1926031]	G3X9X5		0.6	8.2E-01	-2.5	6.5E-01	1.0	7.6E-01	4.2	4.0E-01
ENSMUST00000118209	,TP synthase, H+ transporting, mitochondrial F0 complex, subunit B1 [Source:MGI Symbol;Acc:MGI:110049	Q5I0W0	Q9CQQ7	-6.1	3.1E-05	-0.9	3.9E-01	1.5	4.7E-02	0.0	9.8E-01
ENSMUST00000118216	acid phosphatase, testicular [Source:MGI Symbol;Acc:MGI:3644563]	D3YTS9		5.9	3.1E-02	5.8	5.3E-03	-0.6	7.2E-01	-1.2	2.6E-01
ENSMUST00000118218	DMRT-like family C1c1 [Source:MGI Symbol;Acc:MGI:1918333]	Q9D410		5.6	1.7E-02	6.9	1.2E-02	-0.8	7.5E-01	-1.4	2.9E-01
ENSMUST00000118229	replication initiator 1 [Source:MGI Symbol;Acc:MGI:1889817]		Q5U4E2	4.4	2.5E-02	4.9	2.3E-03	-0.4	7.4E-01	0.8	3.2E-01
ENSMUST00000114911	ecto-NOX disulfide-thiol exchanger 2 [Source:MGI Symbol;Acc:MGI:2384799]		Q8R0Z2	-1.8	1.3E-01	-3.4	6.8E-02	-1.0	2.8E-01	0.6	7.3E-01
ENSMUST00000118242	LIM and calponin homology domains 1 [Source:MGI Symbol;Acc:MGI:1924819]	D3YU22		5.8	1.9E-02	5.8	2.0E-05	-1.5	7.3E-02	-0.5	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000114918	ecto-NOX disulfide-thiol exchanger 2 [Source:MGI Symbol;Acc:MGI:2384799]		Q8R0Z2	-1.8	4.0E-01	-3.9	1.5E-01	-2.6	8.8E-02	-0.5	8.5E-01
ENSMUST00000118261	cell division cycle 7 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1309511]		Q9Z0H0	7.9	9.5E-05	-4.2	1.7E-03	0.5	3.0E-01	-0.6	5.3E-01
ENSMUST00000114927	CUGBP, Elav-like family member 2 [Source:MGI Symbol;Acc:MGI:1338822]		Q9Z0H4	-0.3	9.3E-01	-4.6	3.0E-01	-4.7	7.5E-02	-0.4	9.2E-01
ENSMUST00000114933	inositol polyphosphate-4-phosphatase, type I [Source:MGI Symbol;Acc:MGI:1931123]	E9QAD0		1.4	4.9E-01	6.1	3.2E-02	3.0	1.8E-01	-1.7	4.4E-01
ENSMUST00000118282	ataxia telangiectasia mutated [Source:MGI Symbol;Acc:MGI:107202]		Q62388	2.6	2.6E-04	-7.5	3.1E-04	0.9	5.8E-02	-0.7	6.2E-01
ENSMUST00000118286	mitofusin 1 [Source:MGI Symbol;Acc:MGI:1914664]		Q811U4	2.0	3.5E-03	-4.1	2.1E-02	1.1	1.4E-01	1.7	2.6E-01
ENSMUST00000118310	N-6 adenine-specific DNA methyltransferase 1 (putative) [Source:MGI Symbol;Acc:MGI:1915018]	Q6PRU9		4.6	6.0E-03	2.0	1.4E-02	-0.1	9.2E-01	-0.2	7.0E-01
ENSMUST00000114939	SMAD family member 4 [Source:MGI Symbol;Acc:MGI:894293]		P97471	-1.6	6.6E-02	-1.5	1.7E-01	0.2	7.4E-01	0.0	9.7E-01
ENSMUST00000114940	zinc finger protein 280C [Source:MGI Symbol;Acc:MGI:2387585]		Q6P3Y5	5.2	4.8E-02	4.3	1.3E-01	-0.7	8.1E-01	0.2	9.2E-01
ENSMUST00000118317	homeodomain interacting protein kinase 1 [Source:MGI Symbol;Acc:MGI:1314873]		O88904	-4.5	2.3E-06	5.6	1.1E-03	0.1	9.6E-01	0.1	8.9E-01
ENSMUST00000118326	ıeuronal tyrosine-phosphorylated phosphoinositide 3-kinase adaptor 1 [Source:MGI Symbol;Acc:MGI:2443880		Q6PFX7	5.5	9.7E-04	4.5	7.6E-03	-1.6	2.6E-01	-0.2	8.2E-01
ENSMUST00000118360	potassium voltage-gated channel, Shal-related family, member 3 [Source:MGI Symbol;Acc:MGI:1928743]	B2RUE0	Q9Z0V1	7.1	1.0E-04	5.0	3.6E-02	-0.7	7.6E-01	2.0	1.5E-01
ENSMUST00000118362	thioredoxin domain containing 11 [Source:MGI Symbol;Acc:MGI:1923620]	Q3TWZ5		1.8	2.6E-02	4.5	3.3E-03	-0.4	6.9E-01	0.4	6.4E-01
ENSMUST00000118364	interleukin 23 receptor [Source:MGI Symbol;Acc:MGI:2181693]	G5E8U4		2.7	3.0E-03	6.9	5.8E-04	-0.4	7.9E-01	-1.6	6.2E-02
ENSMUST00000114952	:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 [Source:MGI Symbol;Acc:MGI		Q921L8	-0.8	2.3E-01	4.2	2.4E-03	4.0	1.5E-03	-1.0	1.7E-01
ENSMUST00000118366	mitochondrial carrier homolog 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1929261]		Q791T5	-6.9	2.1E-04	7.9	7.4E-05	-0.6	6.4E-01	0.7	2.2E-01
ENSMUST00000118368	pituitary tumor-transforming gene 1 [Source:MGI Symbol;Acc:MGI:1353578]		Q9CQJ7	-5.8	1.1E-04	-0.7	3.6E-01	0.0	9.7E-01	-4.2	4.6E-03
ENSMUST00000114960	kalirin, RhoGEF kinase [Source:MGI Symbol;Acc:MGI:2685385]		A2CG49	5.7	3.6E-02	2.6	4.1E-01	-0.6	8.2E-01	2.5	3.1E-01
ENSMUST00000118375	TBK1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1920424]	Z4YKN2		-7.0	3.8E-03	7.2	1.9E-02	-0.9	7.6E-01	-0.7	6.3E-01
ENSMUST00000118395	Fanconi anemia, complementation group A [Source:MGI Symbol;Acc:MGI:1341823]	D3Z6Y5		9.1	2.2E-06	6.6	1.2E-02	-0.8	7.4E-01	-1.3	3.4E-01
ENSMUST00000118408	family with sequence similarity 160, member A1 [Source:MGI Symbol;Acc:MGI:2444746]		Q505K2	7.5	8.2E-03	7.5	8.4E-05	-0.5	7.0E-01	-0.4	4.5E-01
ENSMUST00000114972	BCL6 co-repressor-like 1 [Source:MGI Symbol;Acc:MGI:2443910]	F8WJL9		0.9	5.0E-01	1.0	5.9E-01	0.6	6.4E-01	0.5	7.3E-01
ENSMUST00000118410	inositol (myo)-1(or 4)-monophosphatase 1 [Source:MGI Symbol;Acc:MGI:1933158]	Q80ZJ2		-3.6	5.4E-04	8.0	4.6E-05	-0.6	5.9E-01	0.2	7.8E-01
ENSMUST00000118411	mab-21-like 3 (C. elegans) [Source:MGI Symbol;Acc:MGI:2446273]		Q8CI17	5.9	5.4E-03	0.0	1.0E+00	6.2	8.1E-06	-1.1	3.2E-01
ENSMUST00000114976	Luc7 homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:1914228]		Q9CYI4	0.4	4.7E-01	0.3	6.9E-01	0.5	4.4E-01	0.6	4.6E-01
ENSMUST00000114978	transcription factor 4 [Source:MGI Symbol;Acc:MGI:98506]	Q91XK1	Q60722	0.6	5.0E-01	1.0	3.1E-01	-0.6	4.4E-01	-1.1	2.5E-01
ENSMUST00000118422	RIKEN cDNA 1110059G10 gene [Source:MGI Symbol;Acc:MGI:1913452]	D3YWR8		-4.6	3.8E-04	7.0	1.1E-03	0.4	8.1E-01	0.3	7.5E-01
ENSMUST00000114985	transcription factor 4 [Source:MGI Symbol;Acc:MGI:98506]		Q60722	-1.1	6.7E-01	-1.3	7.1E-01	-0.8	7.2E-01	-0.6	8.4E-01
ENSMUST00000114987	calcium/calmodulin-dependent protein kinase ID [Source:MGI Symbol;Acc:MGI:2442190]		Q8BW96	3.2	6.7E-02	3.9	6.6E-02	0.4	8.2E-01	-0.4	8.0E-01
ENSMUST00000114988	family with sequence similarity 234, member A [Source:MGI Symbol;Acc:MGI:2146854]		Q8C0Z1	0.1	8.4E-01	0.8	3.8E-01	0.8	2.0E-01	0.2	8.0E-01
ENSMUST00000114989	CCR4-NOT transcription complex, subunit 4 [Source:MGI Symbol;Acc:MGI:1859026]	E9QA19		-1.9	2.8E-01	-0.1	9.6E-01	-0.5	7.0E-01	-2.4	2.4E-01
ENSMUST00000114991	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C [Source:MGI		Q64151	4.1	1.7E-01	1.2	6.2E-01	-3.5	2.2E-01	-0.7	7.5E-01
ENSMUST00000118429	transmembrane protein 41B [Source:MGI Symbol;Acc:MGI:1289225]		Q8K1A5	5.0	7.6E-03	-5.2	4.0E-02	0.5	5.4E-01	3.0	1.8E-01
ENSMUST00000118432	te carrier family 7 (cationic amino acid transporter, y+ system), member 2 [Source:MGI Symbol;Acc:MGI:998	E9QJY0		4.3	2.1E-03	-1.7	1.4E-02	0.5	2.1E-01	-0.4	5.0E-01
ENSMUST00000118440	suppressor of fused homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1345643]	D3Z7B6		3.0	1.7E-03	6.8	9.7E-05	-1.3	2.6E-01	-0.1	9.0E-01
ENSMUST00000118444	low density lipoprotein receptor-related protein 3 [Source:MGI Symbol;Acc:MGI:3584516]	E9Q711		7.2	1.1E-02	-1.6	2.9E-01	0.3	7.8E-01	-2.1	2.4E-01
ENSMUST00000115011	lectin, mannose-binding 2-like [Source:MGI Symbol;Acc:MGI:2443010]	D3Z4P2		2.0	2.4E-01	1.1	6.4E-01	0.0	9.8E-01	0.8	7.1E-01
ENSMUST00000118455	low density lipoprotein receptor-related protein 1 [Source:MGI Symbol;Acc:MGI:96828]	D3Z5M3		5.5	1.5E-03	3.1	8.1E-03	3.1	3.6E-03	-1.9	2.3E-02
ENSMUST00000118470	SKI-like [Source:MGI Symbol;Acc:MGI:106203]	Q3TB81	Q60665	-6.2	2.3E-03	-4.0	2.3E-03	0.0	9.8E-01	-1.6	1.8E-01
ENSMUST00000115021	caldesmon 1 [Source:MGI Symbol;Acc:MGI:88250]	Q8VCQ8		2.9	4.6E-02	0.2	8.7E-01	-4.9	2.2E-03	-2.1	8.9E-02
ENSMUST00000115028	integrin beta 5 [Source:MGI Symbol;Acc:MGI:96614]	Q6PE70		-1.9	1.7E-01	-2.6	1.7E-01	-0.5	6.6E-01	0.2	9.0E-01
ENSMUST00000115029	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]		Q3U108	-4.0	7.7E-02	1.3	6.3E-01	3.6	1.0E-01	-1.7	4.9E-01
ENSMUST00000115031	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]		Q3U108	0.4	8.3E-01	1.4	6.2E-01	0.7	7.0E-01	-0.3	9.3E-01
ENSMUST00000118487	family with sequence similarity 234, member A [Source:MGI Symbol;Acc:MGI:2146854]		Q8C0Z1	-6.1	7.2E-04	-7.3	5.0E-03	1.0	1.3E-01	-0.7	7.5E-01
ENSMUST00000115033	transmembrane and ubiquitin-like domain containing 1 [Source:MGI Symbol;Acc:MGI:1923764]		Q9JMG3	0.7	4.1E-01	5.3	6.1E-03	5.2	3.7E-03	0.6	4.7E-01
ENSMUST00000118489	glutamate receptor, metabotropic 4 [Source:MGI Symbol;Acc:MGI:1351341]			7.3	1.1E-04	-0.7	6.0E-01	0.9	3.5E-01	-1.4	3.4E-01
ENSMUST00000118498	nicalin homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1926081]	D3YU17		-8.5	3.7E-04	5.0	5.3E-02	-0.7	7.6E-01	0.5	7.1E-01
ENSMUST00000115043	Fas-activated serine/threonine kinase [Source:MGI Symbol;Acc:MGI:1913837]	D3Z4M5		-0.7	4.2E-01	-3.2	7.8E-02	0.0	9.7E-01	2.4	1.5E-01
ENSMUST00000115044	mucin 13, epithelial transmembrane [Source:MGI Symbol;Acc:MGI:103190]	Q3V1S6	P19467	1.1	6.5E-01	3.7	3.1E-01	3.5	2.0E-01	0.9	7.6E-01
ENSMUST00000118500	centrosomal protein 97 [Source:MGI Symbol;Acc:MGI:1921451]		Q9CZ62	8.8	1.1E-05	7.9	5.3E-05	-0.6	6.5E-01	-0.7	2.2E-01
ENSMUST00000118501	programmed cell death 5 [Source:MGI Symbol;Acc:MGI:1913538]	Q564F6	P56812	-5.4	1.9E-04	6.0	5.9E-04	-0.8	5.0E-01	0.8	3.1E-01
ENSMUST00000115048	roundabout homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1921394]	E9QN68		4.4	6.0E-02	5.1	8.7E-02	0.7	8.0E-01	0.1	9.6E-01
ENSMUST00000118515	ER membrane protein complex subunit 10 [Source:MGI Symbol;Acc:MGI:1916933]		Q3TAS6	-6.4	1.3E-03	-3.6	5.0E-02	1.2	1.5E-01	-1.6	3.9E-01
ENSMUST00000115055	family with sequence similarity 107, member B [Source:MGI Symbol;Acc:MGI:1913790]		Q3TGF2	-0.6	8.2E-01	-1.8	5.7E-01	-1.8	3.8E-01	-0.7	8.4E-01
ENSMUST00000118522	PAX3 and PAX7 binding protein 1 [Source:MGI Symbol;Acc:MGI:1914617]		P58501	3.2	1.9E-03	8.7	1.6E-05	0.9	4.0E-01	-0.6	2.3E-01
ENSMUST00000118539	cystathionase (cystathionine gamma-lyase) [Source:MGI Symbol;Acc:MGI:1339968]		Q8VCN5	4.1	1.4E-03	7.3	1.9E-04	-0.5	7.1E-01	-0.3	6.5E-01
ENSMUST00000118544	acidic residue methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1920669]		A6H630	3.8	1.8E-04	-3.4	2.7E-02	0.3	6.1E-01	-0.2	8.7E-01
ENSMUST00000115068	olute carrier family 37 (glycerol-3-phosphate transporter), member 2 [Source:MGI Symbol;Acc:MGI:1929693		Q9WU81	-0.2	6.9E-01	0.9	2.1E-01	0.4	4.1E-01	-0.7	3.0E-01
ENSMUST00000118556	anoctamin 1, calcium activated chloride channel [Source:MGI Symbol;Acc:MGI:2142149]	G8JL82		8.1	5.4E-03	5.6	1.1E-03	-0.5	6.9E-01	0.6	3.8E-01
ENSMUST00000118564	lemur tyrosine kinase 3 [Source:MGI Symbol;Acc:MGI:3039582]	E9QNZ5		7.0	6.8E-04	-1.6	1.1E-01	0.1	9.1E-01	-0.1	8.9E-01
ENSMUST00000118566	tropomyosin 3, gamma [Source:MGI Symbol;Acc:MGI:1890149]	E9Q7Q3		-8.8	1.4E-05	2.1	3.4E-02	-4.3	2.7E-03	0.6	4.3E-01
ENSMUST00000115077	ATP-binding cassette, sub-family B (MDR/TAP), member 8 [Source:MGI Symbol;Acc:MGI:1351667]		Q9CXJ4	2.0	3.5E-01	6.2	2.3E-02	0.4	8.6E-01	-3.8	5.3E-02
ENSMUST00000118576	coiled-coil domain containing 64 [Source:MGI Symbol;Acc:MGI:1922915]	D3YTR9		3.5	1.4E-02	-4.2	2.8E-03	-0.8	1.5E-01	0.1	9.4E-01
ENSMUST00000118578	orthodenticle homolog 2 [Source:MGI Symbol;Acc:MGI:97451]	Q8VD35		6.1	4.0E-04	-3.6	1.3E-02	1.4	2.7E-02	1.2	3.3E-01
ENSMUST00000118587	ephrin A1 [Source:MGI Symbol;Acc:MGI:103236]	D3YTT5		7.6	2.1E-04	5.0	1.3E-02	-2.3	2.4E-01	1.2	2.6E-01
ENSMUST00000118592	coiled-coil domain containing 186 [Source:MGI Symbol;Acc:MGI:2445022]		Q8C9S4	-2.1	1.1E-02	-4.0	2.3E-02	-0.3	7.0E-01	-1.4	4.0E-01
ENSMUST00000115095	X-linked inhibitor of apoptosis [Source:MGI Symbol;Acc:MGI:107572]		Q60989	-0.5	7.3E-01	1.4	5.1E-01	1.6	3.6E-01	-0.3	8.6E-01
ENSMUST00000118593	colony stimulating factor 1 (macrophage) [Source:MGI Symbol;Acc:MGI:1339753]		P07141	-7.8	1.2E-03	4.4	8.0E-05	-2.9	2.5E-03	0.2	7.0E-01
ENSMUST00000118605	inositol polyphosphate-5-phosphatase F [Source:MGI Symbol;Acc:MGI:2141867]		Q8CDA1	4.5	7.1E-03	8.7	1.6E-05	-0.5	6.4E-01	-2.5	1.5E-03
ENSMUST00000118623	D4, zinc and double PHD fingers family 2 [Source:MGI Symbol;Acc:MGI:109529]	D3Z5N6		-7.6	1.2E-04	7.1	3.7E-04	0.0	9.9E-01	-0.5	4.7E-01
ENSMUST00000118627	Sfi1 homolog, spindle assembly associated (yeast) [Source:MGI Symbol;Acc:MGI:1926137]	A8Y5K5		3.4	7.8E-05	6.3	1.0E-03	-0.4	7.8E-01	1.0	2.6E-01
ENSMUST00000118628	Josephin domain containing 2 [Source:MGI Symbol;Acc:MGI:1913374]		Q9CR30	-5.4	5.4E-03	1.8	3.5E-01	-5.3	3.1E-02	-0.1	9.5E-01
ENSMUST00000118679	thioredoxin domain containing 11 [Source:MGI Symbol;Acc:MGI:1923620]	D3YU69		5.2	5.8E-05	3.8	4.2E-02	0.6	6.5E-01	0.5	7.1E-01
ENSMUST00000115110	hydrolethalus syndrome 1 [Source:MGI Symbol;Acc:MGI:1924082]			-0.2	8.0E-01	-1.9	4.0E-02	-1.1	9.0E-02	0.7	4.0E-01
ENSMUST00000118687	EF hand domain containing 1 [Source:MGI Symbol;Acc:MGI:1921607]		Q9D4J1	5.3	2.0E-02	7.7	1.9E-04	-0.7	6.4E-01	-0.6	3.9E-01
ENSMUST00000115118	cullin 4B [Source:MGI Symbol;Acc:MGI:1919834]		A2A432	-1.5	4.1E-01	-2.9	1.1E-01	-2.6	6.5E-02	-1.2	5.3E-01
ENSMUST00000115120	tyrosine kinase, non-receptor, 2 [Source:MGI Symbol;Acc:MGI:1858308]	D3Z3U7		2.3	3.1E-01	0.2	9.5E-01	-2.3	3.2E-01	-0.1	9.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000118707	DIX domain containing 1 [Source:MGI Symbol;Acc:MGI:2679721]	F2Z453		9.8	6.4E-04	-3.5	1.2E-02	0.7	2.3E-01	-0.6	6.2E-01
ENSMUST00000115124	tyrosine kinase, non-receptor, 2 [Source:MGI Symbol;Acc:MGI:1858308]	G3X9X7		0.7	7.7E-01	6.2	1.0E-01	4.6	1.7E-01	-0.8	7.1E-01
ENSMUST00000115125	tyrosine kinase, non-receptor, 2 [Source:MGI Symbol;Acc:MGI:1858308]			3.8	8.3E-02	2.0	5.2E-01	0.1	9.8E-01	2.0	4.0E-01
ENSMUST00000115128	lysine (K)-specific methyltransferase 2E [Source:MGI Symbol;Acc:MGI:1924825]		Q3UG20	-0.3	8.4E-01	1.9	3.6E-01	1.6	3.7E-01	-0.6	7.1E-01
ENSMUST00000118710	membrane bound O-acyltransferase domain containing 7 [Source:MGI Symbol;Acc:MGI:1924832]	D3YU33		3.2	1.3E-02	4.1	4.3E-03	-1.2	3.2E-01	0.2	7.7E-01
ENSMUST00000115137	phosphate cytidylyltransferase 1, choline, alpha isoform [Source:MGI Symbol;Acc:MGI:88557]	D3Z3T5		3.7	1.9E-01	-3.0	3.0E-01	-5.0	6.8E-02	1.7	5.3E-01
ENSMUST00000118729	zinc finger protein 740 [Source:MGI Symbol;Acc:MGI:1915994]		Q6NZQ6	-6.5	1.1E-03	5.5	1.7E-02	-0.7	7.4E-01	0.2	8.4E-01
ENSMUST00000118755	protease, serine 36 [Source:MGI Symbol;Acc:MGI:1924863]	E9QJT0		7.7	6.9E-05	4.8	8.0E-03	-3.0	9.3E-02	-0.7	4.8E-01
ENSMUST00000115142	zinc finger and BTB domain containing 33 [Source:MGI Symbol;Acc:MGI:1927290]	A2A3Z3	Q8BN78	-2.1	1.7E-01	-1.0	6.6E-01	1.3	4.0E-01	0.2	9.1E-01
ENSMUST00000118762	potassium channel tetramerisation domain containing 20 [Source:MGI Symbol;Acc:MGI:1914239]		Q8CDD8	-4.2	9.4E-05	7.7	1.5E-03	-0.2	9.0E-01	1.0	2.7E-01
ENSMUST00000118769	zygote arrest 1-like [Source:MGI Symbol;Acc:MGI:3690051]	C3VD30		6.5	6.8E-05	3.7	1.3E-02	-1.8	1.9E-01	1.0	2.4E-01
ENSMUST00000118771	WD repeat domain 61 [Source:MGI Symbol;Acc:MGI:1917493]	Q8BVQ0		3.3	7.9E-03	-1.0	9.1E-02	0.4	3.3E-01	0.2	7.3E-01
ENSMUST00000115154	N-acetylglucosamine-1-phosphotransferase, gamma subunit [Source:MGI Symbol;Acc:MGI:2147006]			-2.7	3.3E-01	-3.1	4.3E-01	0.3	8.9E-01	0.7	8.5E-01
ENSMUST00000118788	hydroxyacyl glutathione hydrolase [Source:MGI Symbol;Acc:MGI:95745]	G5E8T9		-4.7	1.5E-02	1.4	4.1E-02	0.3	4.9E-01	0.1	8.2E-01
ENSMUST00000115163	negative regulator of reactive oxygen species [Source:MGI Symbol;Acc:MGI:2445095]		Q8BMT4	-2.1	3.0E-01	-1.7	5.2E-01	0.6	6.9E-01	0.2	9.5E-01
ENSMUST00000118793	predicted gene 16181 [Source:MGI Symbol;Acc:MGI:3802038]	B0V2H2		4.3	2.4E-04	-7.5	3.5E-03	1.6	2.7E-02	-0.8	7.1E-01
ENSMUST00000118795	DEAH (Asp-Glu-Ala-His) box polypeptide 34 [Source:MGI Symbol;Acc:MGI:1918973]	D3YTV3		7.4	1.5E-02	-4.6	5.2E-03	0.3	6.0E-01	-1.5	3.0E-01
ENSMUST00000115174	RAB23, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:99833]	Q9D4I9		4.1	8.4E-02	3.8	1.6E-01	-0.9	7.2E-01	-0.6	7.7E-01
ENSMUST00000118808	ER membrane protein complex subunit 10 [Source:MGI Symbol;Acc:MGI:1916933]		Q3TAS6	5.2	1.6E-02	2.6	1.1E-01	-0.6	6.4E-01	3.2	2.0E-02
ENSMUST00000115178	nuclear cap binding protein subunit 2 [Source:MGI Symbol;Acc:MGI:1915342]	D3Z3D2		-3.0	3.9E-02	-4.4	1.4E-02	-1.8	5.2E-02	-0.4	8.1E-01
ENSMUST00000118812	fizzy/cell division cycle 20 related 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1926790]	D3YTV2		-3.7	5.1E-03	-3.9	1.4E-03	-0.3	4.7E-01	-2.6	3.5E-02
ENSMUST00000115196	discs, large homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:107231]	D3Z3B8		0.5	5.7E-01	1.6	1.2E-01	0.1	9.3E-01	-1.0	2.4E-01
ENSMUST00000118826	microtubule-associated protein, RP/EB family, member 2 [Source:MGI Symbol;Acc:MGI:106271]	Q3TG90		8.0	4.7E-05	3.0	1.6E-02	-0.8	4.0E-01	1.0	2.6E-01
ENSMUST00000115205	discs, large homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:107231]		Q811D0	-1.1	3.9E-01	0.4	8.0E-01	1.1	3.8E-01	-0.4	7.8E-01
ENSMUST00000115206	nuclear respiratory factor 1 [Source:MGI Symbol;Acc:MGI:1332235]	Q99K73		-1.4	6.7E-01	-0.9	8.3E-01	0.1	9.8E-01	-0.5	9.1E-01
ENSMUST00000118828	RAB11 family interacting protein 3 (class II) [Source:MGI Symbol;Acc:MGI:2444431]		Q8CHD8	5.1	3.0E-02	-4.6	5.2E-03	0.7	2.7E-01	-2.0	2.3E-01
ENSMUST00000115212	nuclear respiratory factor 1 [Source:MGI Symbol;Acc:MGI:1332235]		Q9WU00	-0.3	7.2E-01	-0.2	9.1E-01	1.8	1.2E-01	1.6	2.4E-01
ENSMUST00000118830	vacuolar protein sorting 29 (S. pombe) [Source:MGI Symbol;Acc:MGI:1928344]		Q9QZ88	-7.3	5.8E-06	6.2	8.6E-04	-3.7	3.8E-02	0.4	6.0E-01
ENSMUST00000115222	zinc finger and BTB domain containing 44 [Source:MGI Symbol;Acc:MGI:1925123]		Q8R0A2	0.4	3.3E-01	1.0	1.2E-01	0.6	2.0E-01	0.1	9.2E-01
ENSMUST00000118831	synaptotagmin III [Source:MGI Symbol;Acc:MGI:99665]	G3X9Y1		6.5	1.0E-02	5.7	2.8E-04	0.8	3.7E-01	0.5	4.1E-01
ENSMUST00000118833	mediator complex subunit 28 [Source:MGI Symbol;Acc:MGI:1914249]	D3Z7D6		-7.1	1.1E-05	6.1	8.5E-03	0.0	9.8E-01	-0.3	7.5E-01
ENSMUST00000118856	RIKEN cDNA 4930432K21 gene [Source:MGI Symbol;Acc:MGI:1921916]	E9QNR8		6.4	1.9E-02	3.5	2.1E-03	0.8	3.0E-01	1.0	1.1E-01
ENSMUST00000118875	glyceraldehyde-3-phosphate dehydrogenase [Source:MGI Symbol;Acc:MGI:95640]	D2KHZ9	P16858	-7.6	1.6E-04	-4.3	1.8E-01	0.9	5.5E-01	0.0	1.0E+00
ENSMUST00000118878	l RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:133(		Q80UV9	-6.2	3.6E-05	-7.3	1.8E-05	-0.1	8.0E-01	-1.3	1.9E-01
ENSMUST00000118896	sarcoglycan zeta [Source:MGI Symbol;Acc:MGI:2388820]		Q8BX51	6.0	2.9E-02	-6.6	3.1E-03	1.1	7.3E-02	-0.9	6.3E-01
ENSMUST00000118927	zinc finger, DHHC domain containing 13 [Source:MGI Symbol;Acc:MGI:1919227]		Q9CWU2	-4.3	3.4E-04	6.4	1.3E-02	-0.8	7.3E-01	-0.8	5.2E-01
ENSMUST00000118936	guanylyl cyclase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916028]	Q05CJ4		-8.8	7.5E-05	7.9	5.8E-04	0.0	1.0E+00	-0.9	2.9E-01
ENSMUST00000118942	disrupted in schizophrenia 1 [Source:MGI Symbol;Acc:MGI:2447658]		Q811T9	5.8	4.3E-03	-5.0	1.1E-02	-1.3	9.0E-02	-0.9	6.3E-01
ENSMUST00000115242	S-adenosylhomocysteine hydrolase-like 2 [Source:MGI Symbol;Acc:MGI:1921590]		Q68FL4	-3.6	2.9E-01	-1.6	7.4E-01	2.1	4.8E-01	0.1	9.9E-01
ENSMUST00000118952	PAP associated domain containing 5 [Source:MGI Symbol;Acc:MGI:1917820]	E9QJT6		-6.3	3.7E-03	7.7	7.3E-05	-0.4	7.3E-01	-0.8	1.9E-01
ENSMUST00000118959	Fanconi anemia, complementation group I [Source:MGI Symbol;Acc:MGI:2384790]	F2Z414		6.8	5.0E-05	5.2	2.1E-03	-0.6	6.6E-01	-2.2	3.7E-02
ENSMUST00000115245	coiled-coil domain containing 146 [Source:MGI Symbol;Acc:MGI:1922422]	E9Q9F7		1.6	5.8E-02	0.3	7.1E-01	-1.8	2.7E-02	-0.5	5.4E-01
ENSMUST00000115246	casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]	H7BXB1		2.3	2.9E-01	3.0	3.0E-01	1.7	4.6E-01	1.0	6.8E-01
ENSMUST00000118961	latent transforming growth factor beta binding protein 4 [Source:MGI Symbol;Acc:MGI:1321395]	E9Q6B8		6.7	1.7E-04	7.2	8.7E-04	-0.8	6.4E-01	0.7	3.9E-01
ENSMUST00000115248	RIKEN cDNA C330007P06 gene [Source:MGI Symbol;Acc:MGI:1924894]		Q8VDP2	-1.6	8.5E-02	-3.9	2.0E-02	0.4	6.1E-01	2.6	8.4E-02
ENSMUST00000115250	tetraspanin 33 [Source:MGI Symbol;Acc:MGI:1919012]		Q8R3S2	3.3	6.2E-02	1.0	6.8E-01	-0.7	6.8E-01	1.6	4.7E-01
ENSMUST00000115251	transportin 3 [Source:MGI Symbol;Acc:MGI:1196412]		Q6P2B1	-5.6	4.3E-02	1.6	7.1E-01	7.1	4.0E-02	-0.1	9.8E-01
ENSMUST00000115256	zinc finger, CCHC domain containing 12 [Source:MGI Symbol;Acc:MGI:1919943]		Q9CZA5	3.4	6.9E-02	5.9	8.8E-03	-0.4	8.6E-01	-2.8	3.1E-02
ENSMUST00000118966	ras homolog gene family, member J [Source:MGI Symbol;Acc:MGI:1931551]	F2Z463		8.9	8.2E-06	5.9	1.2E-02	-0.7	7.3E-01	-1.1	3.5E-01
ENSMUST00000118976	coiled-coil domain containing 9 [Source:MGI Symbol;Acc:MGI:1921443]	D3YW42		-4.6	1.4E-03	-1.5	2.7E-02	0.0	9.1E-01	0.0	9.6E-01
ENSMUST00000118986	T-box 22 [Source:MGI Symbol;Acc:MGI:2389465]		Q8K402	7.2	6.1E-05	6.2	1.8E-03	-0.4	8.0E-01	-0.7	3.9E-01
ENSMUST00000118987	BAH domain and coiled-coil containing 1 [Source:MGI Symbol;Acc:MGI:2679272]		Q3UHR0	4.8	8.0E-03	-7.8	6.3E-05	0.1	8.9E-01	-2.4	8.4E-02
ENSMUST00000118993	protein-tyrosine sulfotransferase 1 [Source:MGI Symbol;Acc:MGI:1298231]	Q4FK50	O70281	1.9	8.8E-03	-0.2	9.4E-01	6.4	3.7E-03	-1.8	5.4E-01
ENSMUST00000119026	transmembrane protein 132C [Source:MGI Symbol;Acc:MGI:2443061]	E9QP73		8.1	1.8E-05	-5.4	1.9E-02	2.8	3.5E-03	0.5	8.0E-01
ENSMUST00000115268	colony stimulating factor 1 receptor [Source:MGI Symbol;Acc:MGI:1339758]	Q0P635	P09581	-0.2	7.7E-01	-0.6	4.8E-01	-0.4	4.9E-01	0.0	9.9E-01
ENSMUST00000119041	on imprinted in Prader-Willi/Angelman syndrome 2 homolog (human) [Source:MGI Symbol;Acc:MGI:191391		Q9JJC8	-7.5	2.8E-02	5.1	1.7E-02	-0.5	7.7E-01	0.6	5.7E-01
ENSMUST00000115273	regulating synaptic membrane exocytosis 1 [Source:MGI Symbol;Acc:MGI:2152971]	F6Y0S3		2.9	2.1E-01	6.9	1.1E-02	-0.3	9.0E-01	-4.4	1.4E-02
ENSMUST00000119060	CUGBP, Elav-like family member 5 [Source:MGI Symbol;Acc:MGI:2442333]	D3Z588		5.3	7.2E-04	2.8	3.8E-01	-0.4	8.9E-01	2.9	2.3E-01
ENSMUST00000115277	dpy-19-like 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1915685]		A6X919	3.5	5.8E-02	2.3	2.2E-01	-1.5	4.0E-01	-0.3	8.6E-01
ENSMUST00000115278				2.3	8.2E-02	1.8	1.9E-01	-0.9	4.3E-01	-0.5	6.9E-01
ENSMUST00000119077	family with sequence similarity 160, member A1 [Source:MGI Symbol;Acc:MGI:2444746]	E9PX40		6.5	1.4E-02	5.9	1.7E-02	-0.6	7.8E-01	-1.4	2.8E-01
ENSMUST00000115289	hypoxia inducible lipid droplet associated [Source:MGI Symbol;Acc:MGI:1916823]		Q9JLS0	3.1	6.2E-02	5.6	2.9E-02	1.5	4.8E-01	-1.0	4.7E-01
ENSMUST00000119078	methyl-CpG binding domain protein 6 [Source:MGI Symbol;Acc:MGI:106378]		Q3TY92	-6.2	6.1E-05	5.9	2.3E-03	-0.1	9.5E-01	-0.5	5.6E-01
ENSMUST00000115299				3.1	4.0E-02	4.6	1.1E-02	0.1	9.4E-01	-1.3	2.1E-01
ENSMUST00000115300	potassium voltage-gated channel, subfamily Q, member 5 [Source:MGI Symbol;Acc:MGI:1924937]	E9Q9F1		4.6	6.4E-02	6.8	2.0E-02	-0.3	9.1E-01	-2.5	9.8E-02
ENSMUST00000119081	MCM (minichromosome maintenance deficient) binding protein [Source:MGI Symbol;Acc:MGI:1920977]	H9KV04		-7.1	9.0E-06	3.5	2.0E-02	-1.5	2.6E-01	2.1	4.4E-02
ENSMUST00000115314	LIM domain containing preferred translocation partner in lipoma [Source:MGI Symbol;Acc:MGI:2441849]		Q8BFW7	9.0	3.8E-02	11.4	1.6E-02	-0.8	8.7E-01	-3.2	1.0E-01
ENSMUST00000115315	acid phosphatase 5, tartrate resistant [Source:MGI Symbol;Acc:MGI:87883]		Q05117	-2.4	1.3E-01	-2.0	2.0E-01	-1.3	2.2E-01	-1.7	3.3E-01
ENSMUST00000115318	synaptopodin [Source:MGI Symbol;Acc:MGI:1099446]	Q3URF1	Q8CC35	7.2	4.5E-02	5.5	1.5E-01	-0.7	8.5E-01	1.0	6.4E-01
ENSMUST00000119083	ıte carrier family 28 (sodium-coupled nucleoside transporter), member 1 [Source:MGI Symbol;Acc:MGI:36050	E9PXX9		7.7	1.6E-02	-2.6	1.4E-01	0.8	4.1E-01	0.0	1.0E+00
ENSMUST00000119092	protein kinase C, eta [Source:MGI Symbol;Acc:MGI:97600]	D3YWQ8		4.6	1.6E-02	7.4	2.1E-04	-0.6	6.7E-01	-1.1	1.2E-01
ENSMUST00000115330	protection of telomeres 1A [Source:MGI Symbol;Acc:MGI:2141503]		Q91WC1	-1.7	3.5E-02	-1.9	7.2E-02	0.2	7.6E-01	0.4	6.9E-01
ENSMUST00000119120	calmodulin binding transcription activator 2 [Source:MGI Symbol;Acc:MGI:2135957]	B0QZH4		-7.7	9.0E-05	-2.6	1.1E-01	0.5	5.3E-01	-2.0	2.6E-01
ENSMUST00000119129	cell adhesion molecule-related/down-regulated by oncogenes [Source:MGI Symbol;Acc:MGI:1926387]		Q32MD9	8.0	8.6E-03	-4.1	6.9E-03	-1.2	7.1E-02	-0.4	7.5E-01
ENSMUST00000119134	RIKEN cDNA 1700026D08 gene [Source:MGI Symbol;Acc:MGI:1922806]	D3YVU5		6.1	3.7E-04	3.4	8.1E-02	-1.9	2.9E-01	1.0	4.6E-01
ENSMUST00000119139	RIKEN cDNA 6330408A02 gene [Source:MGI Symbol;Acc:MGI:2447816]		Q6DI92	6.9	2.8E-03	-6.0	1.5E-04	0.5	1.7E-01	-0.8	4.4E-01
ENSMUST00000115342	tissue inhibitor of metalloproteinase 1 [Source:MGI Symbol;Acc:MGI:98752]		P12032	1.3	5.1E-01	-0.5	7.4E-01	-5.3	1.3E-02	-3.5	5.3E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000119142	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) [Source:MGI Symbol;Acc:MGI:104771]		Q61527	5.6	3.1E-02	6.4	4.2E-04	-0.6	6.4E-01	-1.3	8.7E-02
ENSMUST00000115345	synapsin I [Source:MGI Symbol;Acc:MGI:98460]		O88935	0.9	6.5E-01	1.4	6.7E-01	2.6	3.2E-01	2.1	4.1E-01
ENSMUST00000119161	translocated promoter region, nuclear basket protein [Source:MGI Symbol;Acc:MGI:1922066]	Q7M739		-4.9	1.7E-03	-5.3	2.3E-02	1.6	7.7E-02	0.7	7.4E-01
ENSMUST00000119166	zinc finger, CCHC domain containing 2 [Source:MGI Symbol;Acc:MGI:2444114]		Q69ZB8	-2.5	7.8E-03	6.2	2.2E-04	-0.6	5.8E-01	-0.2	7.5E-01
ENSMUST00000119201	on imprinted in Prader-Willi/Angelman syndrome 2 homolog (human) [Source:MGI Symbol;Acc:MGI:191391		Q9JJC8	3.0	1.3E-02	4.7	6.1E-03	-0.9	4.8E-01	0.8	4.3E-01
ENSMUST00000115364	cyclin-dependent kinase 16 [Source:MGI Symbol;Acc:MGI:97516]	Q3TM24	Q04735	-1.6	1.7E-01	0.8	5.6E-01	1.1	3.5E-01	-1.4	3.0E-01
ENSMUST00000119212	iduronidase, alpha-L- [Source:MGI Symbol;Acc:MGI:96418]	Q8BLF6		-4.0	3.1E-02	-2.6	5.3E-03	1.2	1.6E-02	-0.6	4.2E-01
ENSMUST00000119213	solute carrier family 17 (anion/sugar transporter), member 5 [Source:MGI Symbol;Acc:MGI:1924105]		Q8BN82	6.2	5.6E-04	1.7	4.4E-02	-2.9	2.9E-03	-0.1	8.9E-01
ENSMUST00000119215	SNF related kinase [Source:MGI Symbol;Acc:MGI:108104]	D3Z3V0		-3.6	1.1E-02	6.4	7.9E-05	-0.9	3.8E-01	-0.5	3.7E-01
ENSMUST00000115371	ribonucleic acid binding protein S1 [Source:MGI Symbol;Acc:MGI:97960]		Q99M28	-3.1	3.6E-01	0.4	8.9E-01	-0.3	9.0E-01	-3.8	2.6E-01
ENSMUST00000119222	metaxin 1 [Source:MGI Symbol;Acc:MGI:103025]	D3Z3F4		-4.3	7.2E-04	2.9	2.3E-01	-2.4	3.6E-01	2.1	1.9E-01
ENSMUST00000115375	RNA binding motif protein 10 [Source:MGI Symbol;Acc:MGI:2384310]		Q99KG3	0.4	8.0E-01	0.8	7.0E-01	0.3	8.5E-01	-0.1	9.7E-01
ENSMUST00000119223	E2F transcription factor 8 [Source:MGI Symbol;Acc:MGI:1922038]		Q58FA4	2.2	2.1E-02	2.6	1.8E-02	-2.3	3.1E-02	-1.5	9.5E-02
ENSMUST00000115383	cadherin-like and PC-esterase domain containing 1 [Source:MGI Symbol;Acc:MGI:2444814]	B2RX70		-1.0	3.3E-01	0.2	9.0E-01	1.0	2.9E-01	-0.1	9.2E-01
ENSMUST00000115384	jade family PHD finger 3 [Source:MGI Symbol;Acc:MGI:2148019]			0.1	9.4E-01	1.5	8.3E-02	0.2	7.0E-01	-1.2	1.1E-01
ENSMUST00000115387	retinitis pigmentosa 2 homolog (human) [Source:MGI Symbol;Acc:MGI:1277953]		Q9EPK2	1.4	5.8E-01	0.9	7.5E-01	-1.9	4.3E-01	-1.3	6.1E-01
ENSMUST00000119224	endothelin converting enzyme 2 [Source:MGI Symbol;Acc:MGI:1101356]	F7DDS0		5.9	4.4E-03	5.1	1.4E-01	-0.7	8.4E-01	1.1	5.9E-01
ENSMUST00000119261	enhancer of mRNA decapping 4 [Source:MGI Symbol;Acc:MGI:2446249]			-5.4	5.9E-04	-5.2	6.9E-04	-0.4	4.0E-01	-0.9	4.6E-01
ENSMUST00000115390	cyclin F [Source:MGI Symbol;Acc:MGI:102551]		P51944	0.4	5.1E-01	1.7	1.1E-01	1.4	8.6E-02	0.2	8.5E-01
ENSMUST00000119273	mitochondrial ribosomal protein L40 [Source:MGI Symbol;Acc:MGI:1332635]	D3Z7C0		-6.7	5.2E-05	-6.6	5.5E-03	0.5	4.3E-01	0.6	7.8E-01
ENSMUST00000119278	BTB (POZ) domain containing 10 [Source:MGI Symbol;Acc:MGI:1916065]	E9Q6L8		-3.3	1.5E-02	5.6	1.6E-05	-0.7	3.3E-01	-0.7	9.9E-02
ENSMUST00000115394	coactivator-associated arginine methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1913208]	D3YUP1		4.2	9.6E-02	-1.8	5.7E-01	-3.6	1.4E-01	2.3	4.4E-01
ENSMUST00000115395	coactivator-associated arginine methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1913208]		Q9WVG6	-2.3	5.0E-01	-1.5	7.3E-01	0.1	9.7E-01	-0.6	8.8E-01
ENSMUST00000119284	protein kinase D3 [Source:MGI Symbol;Acc:MGI:1922542]	Q5FWX6		-2.2	3.0E-02	6.3	1.9E-04	-0.5	6.5E-01	-1.8	1.6E-02
ENSMUST00000115403	solute carrier organic anion transporter family, member 5A1 [Source:MGI Symbol;Acc:MGI:2443431]	E9PVD9		4.8	6.0E-02	4.9	7.9E-02	-0.4	8.8E-01	-0.5	7.6E-01
ENSMUST00000115404	dynamin 2 [Source:MGI Symbol;Acc:MGI:109547]	F8WIV5		-2.0	5.4E-01	-0.3	9.5E-01	1.0	7.4E-01	-0.7	8.7E-01
ENSMUST00000119285	predicted gene 4297 [Source:MGI Symbol;Acc:MGI:3782476]	D3YWB7		9.3	6.4E-06	7.3	1.2E-02	-0.8	7.6E-01	0.8	5.5E-01
ENSMUST00000119292	immunoglobulin mu binding protein 2 [Source:MGI Symbol;Acc:MGI:99954]	D3Z5P5		5.6	6.4E-03	5.7	3.3E-02	0.3	9.0E-01	1.0	4.8E-01
ENSMUST00000115414	interleukin enhancer binding factor 3 [Source:MGI Symbol;Acc:MGI:1339973]	Q45VK5		0.2	7.3E-01	1.1	1.6E-01	0.1	8.1E-01	-0.8	2.8E-01
ENSMUST00000119299	e (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) [Source:MG		Q8CGY8	-5.2	2.5E-03	-6.4	9.7E-05	0.7	1.1E-01	-0.9	4.2E-01
ENSMUST00000119310	m large conductance calcium-activated channel, subfamily M, beta member 2 [Source:MGI Symbol;Acc:MGI:1		Q9CZM9	5.0	2.2E-02	5.7	2.1E-04	-1.5	1.9E-01	0.5	4.1E-01
ENSMUST00000119311	AU RNA binding protein/enoyl-coenzyme A hydratase [Source:MGI Symbol;Acc:MGI:1338011]	E9Q6L3		1.6	2.3E-02	3.4	3.9E-02	-1.6	3.3E-01	-0.2	8.4E-01
ENSMUST00000119315	GTPase, IMAP family member 6 [Source:MGI Symbol;Acc:MGI:1918876]	D3Z3H3		3.8	9.2E-05	4.4	8.6E-04	-3.2	1.1E-02	0.0	9.6E-01
ENSMUST00000115436	alcium/calmodulin-dependent serine protein kinase (MAGUK family) [Source:MGI Symbol;Acc:MGI:1309485		O70589	6.3	5.2E-02	8.6	1.8E-02	-0.6	8.6E-01	-2.8	1.3E-01
ENSMUST00000119316	cyclin J [Source:MGI Symbol;Acc:MGI:2443297]		Q3TZI6	4.8	3.0E-05	6.3	8.7E-04	-0.5	7.1E-01	-0.4	5.6E-01
ENSMUST00000115438	alcium/calmodulin-dependent serine protein kinase (MAGUK family) [Source:MGI Symbol;Acc:MGI:1309485		O70589	-3.1	6.0E-02	-5.3	8.0E-02	-0.2	8.5E-01	1.9	4.8E-01
ENSMUST00000115441	GTP-binding protein 10 (putative) [Source:MGI Symbol;Acc:MGI:2385599]		Q8K013	-0.1	8.7E-01	-1.1	1.2E-01	-0.9	1.1E-01	0.1	8.2E-01
ENSMUST00000119329	signal recognition particle 19 [Source:MGI Symbol;Acc:MGI:1913634]	G5E8T3		-5.7	9.6E-05	7.3	3.6E-04	-0.7	6.2E-01	-1.1	1.6E-01
ENSMUST00000115443	met proto-oncogene [Source:MGI Symbol;Acc:MGI:96969]	F8VQL0		-1.5	3.2E-01	0.7	5.7E-01	-1.2	2.8E-01	-3.5	3.5E-02
ENSMUST00000119353	FK506 binding protein 8 [Source:MGI Symbol;Acc:MGI:1341070]		O35465	-5.4	2.5E-04	2.0	1.6E-01	-3.6	3.0E-02	-0.1	9.3E-01
ENSMUST00000119354	antizyme inhibitor 2 [Source:MGI Symbol;Acc:MGI:2442093]	A8Y5E7		7.1	6.8E-05	7.7	1.6E-02	-0.6	8.3E-01	-1.8	2.4E-01
ENSMUST00000119365	integrin, alpha 10 [Source:MGI Symbol;Acc:MGI:2153482]	E9PXZ3		5.9	7.9E-03	0.4	8.0E-01	-5.6	1.1E-02	1.3	3.1E-01
ENSMUST00000119368	Son DNA binding protein [Source:MGI Symbol;Acc:MGI:98353]	H9KV01		-2.6	5.1E-03	6.7	2.9E-04	-0.5	6.7E-01	-3.8	1.7E-03
ENSMUST00000119374	Na+/K+ transporting ATPase interacting 3 [Source:MGI Symbol;Acc:MGI:2444830]		Q3URJ8	7.5	2.3E-05	-5.9	1.4E-02	0.2	8.3E-01	-0.3	9.0E-01
ENSMUST00000119379	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 [Source:MGI Symbol;Acc:MGI:1915448]		Q9CPU2	-5.1	1.1E-03	4.3	1.8E-03	0.8	3.9E-01	0.0	9.5E-01
ENSMUST00000115461	eukaryotic translation initiation factor 4, gamma 1 [Source:MGI Symbol;Acc:MGI:2384784]	E9PVC5		1.6	5.0E-01	1.1	7.3E-01	-0.8	7.2E-01	-0.3	9.3E-01
ENSMUST00000119422	RIKEN cDNA 4930402H24 gene [Source:MGI Symbol;Acc:MGI:1923029]	Q3V0A7		5.2	1.6E-03	-7.4	1.8E-03	-0.5	5.1E-01	1.1	5.6E-01
ENSMUST00000119423	hypocretin (orexin) receptor 1 [Source:MGI Symbol;Acc:MGI:2385650]		P58307	7.5	1.3E-04	6.5	3.5E-04	-0.2	8.8E-01	0.4	5.0E-01
ENSMUST00000119425	FK506 binding protein 8 [Source:MGI Symbol;Acc:MGI:1341070]	D3Z597		3.7	6.3E-04	6.8	5.4E-04	1.6	2.2E-01	1.1	1.4E-01
ENSMUST00000115481	mediator complex subunit 14 [Source:MGI Symbol;Acc:MGI:1349442]	A2BDP0		-0.3	8.5E-01	1.3	5.4E-01	0.2	9.1E-01	-1.4	4.2E-01
ENSMUST00000119437	transmembrane emp24 protein transport domain containing 5 [Source:MGI Symbol;Acc:MGI:1921586]	E9PXY3		4.0	1.3E-04	-0.2	7.6E-01	1.1	8.0E-02	-0.3	6.9E-01
ENSMUST00000115491	G protein-coupled receptor 85 [Source:MGI Symbol;Acc:MGI:1927851]	Q6ZWR2	P60894	1.4	4.0E-01	3.8	4.0E-02	-0.2	9.0E-01	-2.6	8.3E-02
ENSMUST00000119450	suppressor of IKBKE 1 [Source:MGI Symbol;Acc:MGI:1913891]	D3YTU7		-4.2	8.7E-04	4.5	8.4E-04	-1.5	1.5E-01	-0.4	5.4E-01
ENSMUST00000115496	predicted gene, 20815 [Source:MGI Symbol;Acc:MGI:5434171]	J3KMI0		2.1	1.1E-01	6.8	1.8E-04	-0.6	6.5E-01	-5.3	2.1E-04
ENSMUST00000115509	zinc finger and SCAN domain containing 10 [Source:MGI Symbol;Acc:MGI:3040700]		Q3URR7	2.7	1.1E-01	5.0	9.6E-03	-0.6	7.2E-01	-2.9	4.0E-02
ENSMUST00000115510	PHD finger protein 14 [Source:MGI Symbol;Acc:MGI:1923539]	G5E8S0		-1.5	2.5E-01	2.0	1.8E-01	0.6	6.5E-01	-3.0	4.0E-02
ENSMUST00000119480	zinc finger and BTB domain containing 8 opposite strand [Source:MGI Symbol;Acc:MGI:1914356]	A8Y5E9		-6.7	4.0E-05	-5.4	4.0E-02	0.5	5.2E-01	1.3	5.8E-01
ENSMUST00000119483	synaptopodin 2-like [Source:MGI Symbol;Acc:MGI:1916010]	D3YU08		7.3	1.9E-04	-3.3	1.2E-01	0.3	7.6E-01	-0.6	7.8E-01
ENSMUST00000119485	retinol dehydrogenase 13 (all-trans and 9-cis) [Source:MGI Symbol;Acc:MGI:1918732]			6.9	4.9E-05	6.3	7.0E-04	-1.0	4.7E-01	-0.2	7.5E-01
ENSMUST00000119486	high mobility group AT-hook 1 [Source:MGI Symbol;Acc:MGI:96160]	Q566K0	P17095	4.9	1.4E-03	-4.3	6.7E-03	0.4	4.7E-01	-0.8	5.8E-01
ENSMUST00000115522	endothelin converting enzyme 2 [Source:MGI Symbol;Acc:MGI:1101356]		Q80Z60	-2.2	4.0E-02	-0.6	5.8E-01	0.1	8.6E-01	-1.5	1.9E-01
ENSMUST00000119504	ubiquitin specific peptidase 16 [Source:MGI Symbol;Acc:MGI:1921362]	D3YVU1		-4.8	2.0E-04	-2.9	4.1E-02	1.8	2.6E-02	0.7	5.9E-01
ENSMUST00000119509	sacsin [Source:MGI Symbol;Acc:MGI:1354724]	B2RRL5		7.2	4.5E-05	2.7	1.6E-01	-0.6	7.1E-01	4.9	5.1E-03
ENSMUST00000119512	oxysterol binding protein-like 1A [Source:MGI Symbol;Acc:MGI:1927551]	Q3V156		2.7	1.9E-02	-2.1	1.9E-02	-0.5	3.1E-01	-0.2	8.4E-01
ENSMUST00000119543	transmembrane 6 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1933209]	D3YX52		-7.7	2.1E-04	-2.3	3.4E-03	-0.1	7.3E-01	-0.1	8.6E-01
ENSMUST00000119547	megakaryocyte-associated tyrosine kinase [Source:MGI Symbol;Acc:MGI:99259]			6.4	1.8E-04	7.8	1.3E-04	0.0	9.9E-01	-1.2	8.7E-02
ENSMUST00000119557	palmdelphin [Source:MGI Symbol;Acc:MGI:2148896]	Q3UVT7		5.4	5.3E-03	-5.1	5.9E-04	-0.2	6.8E-01	-0.3	7.9E-01
ENSMUST00000115547	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 [Source:MGI Symbol;Acc:MGI:1351644]		Q9R1X5	0.8	7.9E-01	-0.9	8.1E-01	-2.1	4.5E-01	-0.4	9.0E-01
ENSMUST00000115555	dynein cytoplasmic 1 intermediate chain 1 [Source:MGI Symbol;Acc:MGI:107743]	D3Z0M6		3.1	2.8E-01	5.2	9.6E-02	-0.4	8.9E-01	-2.5	2.3E-01
ENSMUST00000119559	LanC (bacterial lantibiotic synthetase component C)-like 1 [Source:MGI Symbol;Acc:MGI:1336997]		O89112	-5.5	1.8E-04	6.6	8.8E-04	0.0	9.8E-01	-0.2	8.4E-01
ENSMUST00000119595	solute carrier family 29 (nucleoside transporters), member 3 [Source:MGI Symbol;Acc:MGI:1918529]	D3YWS9		7.7	2.7E-04	2.9	3.4E-01	-0.9	7.5E-01	2.5	3.0E-01
ENSMUST00000115560	YEATS domain containing 2 [Source:MGI Symbol;Acc:MGI:2447762]		Q3TUF7	-1.5	4.1E-01	3.4	1.2E-01	1.0	6.2E-01	-4.0	4.2E-02
ENSMUST00000119597	solute carrier family 18, subfamily B, member 1 [Source:MGI Symbol;Acc:MGI:1923556]	E9PU92		7.6	3.1E-06	-3.2	2.0E-02	-0.6	3.0E-01	-1.5	2.7E-01
ENSMUST00000119603	STAM binding protein like 1 [Source:MGI Symbol;Acc:MGI:1923880]		Q76N33	-8.0	9.9E-05	-2.8	7.5E-02	-0.5	5.5E-01	-2.9	1.5E-01
ENSMUST00000119633	family with sequence similarity 45, member A [Source:MGI Symbol;Acc:MGI:1915144]	Q3TH34		-5.0	4.1E-04	-5.8	2.6E-03	0.7	3.0E-01	1.2	4.3E-01
ENSMUST00000119657	ankyrin repeat and SOCS box-containing 10 [Source:MGI Symbol;Acc:MGI:2152836]	D3Z651		6.9	7.9E-05	3.6	1.6E-03	-1.5	1.1E-01	-0.9	1.9E-01
ENSMUST00000119670	histone deacetylase 7 [Source:MGI Symbol;Acc:MGI:1891835]	E9PXW1		-4.6	4.2E-04	8.3	1.4E-05	-0.6	6.1E-01	-0.6	2.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000119693	synaptotagmin XV [Source:MGI Symbol;Acc:MGI:2442166]		Q8C6N3	6.7	7.6E-04	7.9	3.2E-05	1.9	8.3E-02	-0.6	2.8E-01
ENSMUST00000115588	solute carrier family 36 (proton/amino acid symporter), member 4 [Source:MGI Symbol;Acc:MGI:2442595]	D3Z0L1		2.2	2.3E-01	1.1	6.8E-01	0.5	7.9E-01	1.6	5.0E-01
ENSMUST00000119694	cathepsin F [Source:MGI Symbol;Acc:MGI:1861434]		Q9R013	3.6	5.5E-03	7.1	3.9E-04	-2.0	2.1E-01	-0.8	2.7E-01
ENSMUST00000119698	FK506 binding protein 8 [Source:MGI Symbol;Acc:MGI:1341070]		O35465	-5.0	1.4E-03	4.1	1.4E-01	0.2	9.4E-01	2.5	1.8E-01
ENSMUST00000115593	coiled-coil domain containing 67 [Source:MGI Symbol;Acc:MGI:2443026]		Q7M6Y5	7.1	4.8E-02	5.6	1.4E-01	-0.7	8.6E-01	0.8	7.1E-01
ENSMUST00000115594	FtsJ homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1859648]	A2ALH2		-3.9	1.4E-01	-0.8	8.1E-01	2.0	3.5E-01	-1.1	7.4E-01
ENSMUST00000119706	nology domain containing, family A (phosphoinositide binding specific) member 8 [Source:MGI Symbol;Acc:M		Q80W71	3.1	6.7E-04	5.9E-04		-0.5	2.7E-01	-0.7	5.0E-01
ENSMUST00000115601	uanine nucleotide binding protein (G protein), beta polypeptide 1-like [Source:MGI Symbol;Acc:MGI:1338057	Q3TM20		3.7	1.9E-01	3.0	2.4E-01	-1.6	5.4E-01	-0.9	6.6E-01
ENSMUST00000115609	catechol-O-methyltransferase [Source:MGI Symbol;Acc:MGI:88470]		O88587	1.5	3.4E-01	3.0	1.3E-01	-0.2	9.0E-01	-1.7	2.5E-01
ENSMUST00000119717	olfactory receptor 59 [Source:MGI Symbol;Acc:MGI:1333755]	B1ARL3		6.2	1.3E-02	6.2	1.6E-04	-1.0	3.3E-01	0.3	5.9E-01
ENSMUST00000119746	predicted gene 608 [Source:MGI Symbol;Acc:MGI:2685454]	B2RUQ2		-4.5	1.5E-02	3.9	3.1E-01	-0.9	8.2E-01	3.5	1.6E-01
ENSMUST00000119783	GATA zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1914460]		Q920S3	-1.9	3.5E-03	-7.7	3.6E-04	-1.3	5.2E-02	-3.4	9.8E-02
ENSMUST00000119792	anaphase promoting complex subunit 7 [Source:MGI Symbol;Acc:MGI:1929711]	D3YU58		3.4	5.9E-05	-10.5	4.6E-05	-1.4	6.4E-03	-0.7	6.6E-01
ENSMUST00000115619	RNA binding motif protein 3 [Source:MGI Symbol;Acc:MGI:1099460]	Q545K5	O89086	-4.8	2.3E-01	-7.4	1.3E-01	-3.5	9.9E-02	-0.9	8.7E-01
ENSMUST00000119797	RAB guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:1929459]		Q9JM13	-2.6	1.5E-02	6.5	4.0E-04	-0.6	6.5E-01	-0.4	6.0E-01
ENSMUST00000119798	MAS-related GPR, member A2B [Source:MGI Symbol;Acc:MGI:3033098]	E9QNZ7		-11.9	2.8E-05	-4.7	1.2E-03	-0.1	7.5E-01	-0.3	7.9E-01
ENSMUST00000119800	zinc finger protein 740 [Source:MGI Symbol;Acc:MGI:1915994]		Q6NZQ6	-5.8	1.5E-03	-7.4	6.5E-02	1.9	1.1E-01	4.9	2.0E-01
ENSMUST00000115631	diaphanous homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1194490]	Q6NS79		3.9	6.6E-02	2.8	1.1E-01	-4.6	2.8E-02	-3.6	3.5E-02
ENSMUST00000119818	vezatin, adherens junctions transmembrane protein [Source:MGI Symbol;Acc:MGI:2143698]	D3Z4E6		4.9	4.7E-05	2.2	1.4E-02	0.1	8.9E-01	0.2	7.1E-01
ENSMUST00000119823	predicted gene 10639 [Source:MGI Symbol;Acc:MGI:3704339]	E9Q6L7		5.3	9.5E-05	7.2	8.8E-03	2.0	3.6E-01	-0.3	8.5E-01
ENSMUST00000119824	RIKEN cDNA 1700016H13 gene [Source:MGI Symbol;Acc:MGI:1921468]		Q9DAA3	5.6	6.1E-04	-2.6	2.4E-02	1.4	4.1E-02	-4.9	9.8E-03
ENSMUST00000119826	like-glycosyltransferase [Source:MGI Symbol;Acc:MGI:1342270]	Q059X9	Q9Z1M7	5.7	1.9E-04	4.2	1.3E-02	-0.9	5.1E-01	0.0	9.7E-01
ENSMUST00000119827	cyclin-dependent kinase 1 [Source:MGI Symbol;Acc:MGI:88351]		P11440	-5.7	2.8E-03	-1.0	3.8E-01	1.1	1.8E-01	-1.6	2.0E-01
ENSMUST00000119865	mitochondrial fission regulator 1 [Source:MGI Symbol;Acc:MGI:1914722]	Q3TTQ5	Q99MB2	-5.8	2.4E-05	-1.8	2.5E-01	0.6	4.8E-01	-0.5	7.3E-01
ENSMUST00000119866	dual specificity phosphatase 13 [Source:MGI Symbol;Acc:MGI:1351599]	Z4YLI2		6.5	3.8E-04	-5.0	2.5E-02	0.8	3.4E-01	1.1	5.8E-01
ENSMUST00000119870	cyclic nucleotide gated channel beta 1 [Source:MGI Symbol;Acc:MGI:2664102]	E1AZ71		7.1	1.5E-04	2.7	5.4E-03	-5.1	5.4E-04	0.9	1.4E-01
ENSMUST00000119878	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a [Source:MGI Symbol;Acc:MGI:1330299]	A9C475	Q61214	-5.9	7.3E-05	5.6	4.5E-02	0.3	9.1E-01	-0.2	8.8E-01
ENSMUST00000119879	TATA box binding protein [Source:MGI Symbol;Acc:MGI:101838]	F8WJ67		-4.3	8.0E-03	-4.2	2.4E-03	-2.7	3.0E-03	-2.4	9.2E-02
ENSMUST00000119891	cDNA sequence BC026585 [Source:MGI Symbol;Acc:MGI:2448516]		Q3UNZ8	6.5	3.7E-06	4.9	9.0E-03	-2.8	1.4E-01	0.6	5.7E-01
ENSMUST00000119921	nicotinamide nucleotide adenylyltransferase 1 [Source:MGI Symbol;Acc:MGI:1913704]	B0QZL2		5.2	1.6E-04	-4.3	7.6E-03	0.7	2.3E-01	-0.2	8.9E-01
ENSMUST00000119929	transmembrane protein 41B [Source:MGI Symbol;Acc:MGI:1289225]		Q8K1A5	-6.2	1.5E-03	6.5	3.8E-04	-0.6	6.3E-01	0.4	5.1E-01
ENSMUST00000119943	sacsin [Source:MGI Symbol;Acc:MGI:1354724]	E9QNY8		2.4	2.7E-04	7.0	1.5E-04	-0.6	6.3E-01	0.5	3.9E-01
ENSMUST00000115660	solute carrier family 35 (UDP-galactose transporter), member A2 [Source:MGI Symbol;Acc:MGI:1345297]	Q3UIP1	Q9R0M8	1.2	9.7E-02	6.3	7.9E-04	5.2	1.6E-03	0.1	8.9E-01
ENSMUST00000115661	predicted gene, 42416 [Source:MGI Symbol;Acc:MGI:5649001]		O88689	6.2	5.9E-02	5.0	1.5E-01	-0.8	8.2E-01	0.4	8.5E-01
ENSMUST00000119944	LEM domain containing 3 [Source:MGI Symbol;Acc:MGI:3580376]	E9QP59		-5.9	6.5E-05	-4.5	1.4E-02	0.5	4.0E-01	0.9	5.5E-01
ENSMUST00000119945	mitochondrial ribosomal protein S10 [Source:MGI Symbol;Acc:MGI:1928139]	G5E8U5		-5.6	1.2E-03	-4.6	2.8E-03	0.2	7.3E-01	-1.0	4.8E-01
ENSMUST00000119953	ribosomal L1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1913659]		Q8BVY0	-2.4	4.4E-03	-5.2	1.5E-02	1.0	1.7E-01	-0.7	7.1E-01
ENSMUST00000119954	cleavage and polyadenylation factor subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919579]	G3X9Z4		-2.9	1.6E-03	2.8	1.8E-03	-0.6	3.1E-01	-0.3	5.8E-01
ENSMUST00000119960	glycine-N-acyltransferase [Source:MGI Symbol;Acc:MGI:2147502]		Q91XE0	4.9	2.4E-04	-3.1	2.9E-02	-0.8	2.6E-01	0.1	9.4E-01
ENSMUST00000119968	mitochondrial ribosomal protein L24 [Source:MGI Symbol;Acc:MGI:1914957]		Q9CQ06	-4.8	1.4E-04	-7.8	3.0E-03	-0.5	4.6E-01	1.1	5.8E-01
ENSMUST00000119972	DnaJ (Hsp40) homolog, subfamily B, member 3 [Source:MGI Symbol;Acc:MGI:1306822]	Q5RL26		5.4	1.7E-03	-4.3	7.0E-03	1.5	4.6E-02	-2.5	1.5E-01
ENSMUST00000119973	X Kell blood group precursor related family member 6 homolog [Source:MGI Symbol;Acc:MGI:2447765]		E9Q6C8	7.7	4.9E-05	-5.9	3.8E-02	2.2	3.3E-02	-0.6	8.2E-01
ENSMUST00000119976	ankyrin repeat and LEM domain containing 1 [Source:MGI Symbol;Acc:MGI:1918775]	A8VU90		7.2	1.8E-04	-3.7	1.4E-01	2.5	3.5E-02	-0.6	8.2E-01
ENSMUST00000115680	transcription factor E3 [Source:MGI Symbol;Acc:MGI:98511]	Z4YLF7		0.2	9.6E-01	-2.6	6.0E-01	-2.3	4.3E-01	0.4	9.3E-01
ENSMUST00000115681	leucine-zipper-like transcriptional regulator, 1 [Source:MGI Symbol;Acc:MGI:1914113]	E9PUQ1		0.8	6.4E-01	0.1	9.6E-01	0.2	9.1E-01	1.0	6.2E-01
ENSMUST00000119990	in homology domain containing, family G (with RhoGef domain) member 2 [Source:MGI Symbol;Acc:MGI:2	G5E8T4		-4.4	4.4E-03	6.9	5.0E-05	-1.5	1.9E-01	-0.6	2.8E-01
ENSMUST00000119997	apolipoprotein L 10A [Source:MGI Symbol;Acc:MGI:3036238]	Q8CCA5		6.3	4.2E-04	-4.2	4.9E-02	0.6	4.6E-01	0.9	6.4E-01
ENSMUST00000115688	WD repeat domain 45 [Source:MGI Symbol;Acc:MGI:1859606]		Q91VM3	-0.7	8.7E-01	-1.2	8.0E-01	-0.6	8.6E-01	0.0	1.0E+00
ENSMUST00000120004	RIKEN cDNA C030039L03 gene [Source:MGI Symbol;Acc:MGI:2148237]	G3X9H3		4.9	9.3E-06	-5.9	4.3E-03	0.2	7.5E-01	-0.2	8.9E-01
ENSMUST00000120007	transmembrane protein 219 [Source:MGI Symbol;Acc:MGI:1915992]	G3X9Z3		-2.5	1.9E-03	7.6	7.6E-05	-0.5	6.5E-01	-0.1	8.8E-01
ENSMUST00000120016	zinc finger and BTB domain containing 9 [Source:MGI Symbol;Acc:MGI:1918022]		Q8CDC7	-4.9	8.8E-03	7.6	1.0E-04	-0.7	6.0E-01	-0.2	7.0E-01
ENSMUST00000115700	ubiquitin-conjugating enzyme E2L 3 [Source:MGI Symbol;Acc:MGI:109240]	D3YZS3		-2.1	3.3E-01	-5.2	6.9E-02	-3.3	3.5E-02	-0.2	9.5E-01
ENSMUST00000120041	transmembrane 9 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1921390]		Q9DBU0	-5.8	2.8E-04	3.4	1.5E-03	-0.3	6.1E-01	-0.7	3.0E-01
ENSMUST00000120049	cilia and flagella associated protein 44 [Source:MGI Symbol;Acc:MGI:1277238]	E9Q5M6		7.9	1.8E-05	7.3	3.6E-04	2.3	9.8E-02	0.4	5.8E-01
ENSMUST00000120052	ucine-rich repeat, immunoglobulin-like and transmembrane domains 1 [Source:MGI Symbol;Acc:MGI:238532		Q8K099	7.6	2.2E-05	3.5	2.5E-02	-2.9	7.5E-02	-2.6	4.6E-02
ENSMUST00000120056	NmrA-like family domain containing 1 [Source:MGI Symbol;Acc:MGI:1915074]	D3YU12		2.9	4.1E-04	5.8	4.9E-04	-0.6	6.0E-01	0.5	4.7E-01
ENSMUST00000115716	pleckstrin and Sec7 domain containing 2 [Source:MGI Symbol;Acc:MGI:1921252]		Q6P1I6	3.1	1.2E-01	6.6	2.5E-02	1.7	5.1E-01	-1.9	2.2E-01
ENSMUST00000120071	pleckstrin and Sec7 domain containing 3 [Source:MGI Symbol;Acc:MGI:1918215]	E9PUC5		5.8	5.2E-06	1.7	3.4E-01	-2.6	2.0E-01	3.8	1.7E-02
ENSMUST00000115721	peptidylprolyl isomerase (cyclophilin)-like 2 [Source:MGI Symbol;Acc:MGI:2447857]		Q9D787	0.4	5.2E-01	1.2	1.6E-01	0.2	8.0E-01	-0.6	4.0E-01
ENSMUST00000120087	sterile alpha motif domain containing 9-like [Source:MGI Symbol;Acc:MGI:1343184]	E9PX59		-6.0	4.1E-05	7.6	2.1E-05	-0.9	4.2E-01	-0.5	3.3E-01
ENSMUST00000120094	ribosomal protein L9 [Source:MGI Symbol;Acc:MGI:1298373]	Q5EBQ6	P51410	-5.2	3.4E-03	6.1	1.4E-03	-0.5	7.4E-01	-1.0	2.3E-01
ENSMUST00000120095	WD repeat domain 31 [Source:MGI Symbol;Acc:MGI:1918604]		Q9JHB4	6.4	6.7E-05	-1.3	7.0E-02	0.0	9.2E-01	-0.5	4.1E-01
ENSMUST00000120102	desmoglein 2 [Source:MGI Symbol;Acc:MGI:1196466]	Q811I1		6.6	5.8E-05	3.6	2.0E-03	-0.9	2.8E-01	-0.2	6.9E-01
ENSMUST00000120105	cyclin-dependent kinase 9 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1328368]		Q99J95	-7.2	1.3E-04	-1.9	1.0E-01	2.3	5.3E-03	-1.9	1.2E-01
ENSMUST00000120107	zinc finger, MYM-type 3 [Source:MGI Symbol;Acc:MGI:1927231]	B1AXS8		8.2	2.6E-03	6.9	1.2E-04	-0.5	6.9E-01	-0.6	3.2E-01
ENSMUST00000115734	polyadenylate-binding protein-interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915119]		Q9D6V8	-0.9	5.5E-01	1.5	4.2E-01	0.2	8.9E-01	-2.1	1.7E-01
ENSMUST00000120112	transmembrane protein 30C [Source:MGI Symbol;Acc:MGI:1918277]	A9C448		7.6	2.6E-04	-4.4	4.7E-02	0.4	6.2E-01	1.4	4.6E-01
ENSMUST00000120119	post-GPI attachment to proteins 2 [Source:MGI Symbol;Acc:MGI:2385286]			2.5	1.8E-02	-5.8	1.4E-02	0.4	5.8E-01	-0.9	6.9E-01
ENSMUST00000115737	polyadenylate-binding protein-interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915119]		Q9D6V8	-3.4	1.7E-01	-3.6	1.8E-01	-1.4	4.3E-01	-1.3	6.4E-01
ENSMUST00000115739	forkhead box P3 [Source:MGI Symbol;Acc:MGI:1891436]	Q53Z59	Q99JB6	2.1	2.9E-01	3.9	5.4E-02	-1.7	3.5E-01	-3.5	5.4E-02
ENSMUST00000115742	protein phosphatase 1, regulatory (inhibitor) subunit 3F [Source:MGI Symbol;Acc:MGI:1859617]		Q9JIG4	-1.2	2.5E-01	-1.2	3.7E-01	0.7	4.3E-01	0.8	5.3E-01
ENSMUST00000120135	spleen tyrosine kinase [Source:MGI Symbol;Acc:MGI:99515]	Q3UPF7	P48025	-4.5	4.8E-05	7.2	2.2E-04	0.2	9.0E-01	-0.5	4.6E-01
ENSMUST00000120143	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]		Q62393	-1.9	3.0E-02	-5.0	5.5E-03	0.3	6.0E-01	-0.8	5.9E-01
ENSMUST00000120154	hypocretin (orexin) receptor 1 [Source:MGI Symbol;Acc:MGI:2385650]		P58307	5.4	3.5E-04	4.5	9.5E-03	-0.6	6.5E-01	1.6	1.2E-01
ENSMUST00000120157	palmitoyl-protein thioesterase 1 [Source:MGI Symbol;Acc:MGI:1298204]	F7CTA8		-2.4	2.8E-03	5.8	6.3E-04	-2.3	9.3E-02	-0.5	4.8E-01
ENSMUST00000120173	SNF related kinase [Source:MGI Symbol;Acc:MGI:108104]		Q8VDU5	-2.3	1.2E-03	-2.2	3.8E-02	0.3	6.0E-01	0.6	4.8E-01
ENSMUST00000120194	family with sequence similarity 104, member A [Source:MGI Symbol;Acc:MGI:106351]	A2A6P4		-3.0	6.6E-05	2.4	5.9E-02	3.5	4.1E-03	-1.3	1.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000120213	thymoma viral proto-oncogene 1 interacting protein [Source:MGI Symbol;Acc:MGI:3693832]		Q64362	-6.2	1.1E-04	2.0	3.8E-02	-0.1	8.7E-01	0.6	3.9E-01
ENSMUST00000120232	heme oxygenase 2 [Source:MGI Symbol;Acc:MGI:109373]	Q544R7	O70252	-6.4	1.6E-04	-2.4	2.8E-02	-1.4	5.3E-02	-3.2	2.2E-02
ENSMUST00000115777	ubiquitin-conjugating enzyme E2 variant 2 [Source:MGI Symbol;Acc:MGI:1917870]	Q4VBX4	Q9D2M8	0.6	3.0E-01	0.5	5.0E-01	0.6	3.5E-01	0.7	3.2E-01
ENSMUST00000115781	adenomatosis polyposis coli [Source:MGI Symbol;Acc:MGI:88039]	E9QLQ9		0.1	8.3E-01	-0.4	6.6E-01	0.5	4.5E-01	1.1	2.6E-01
ENSMUST00000120239	sirtuin 1 [Source:MGI Symbol;Acc:MGI:2135607]	Q53Z05	Q923E4	5.8	7.9E-04	2.1	3.2E-01	-3.3	1.4E-01	-0.5	7.5E-01
ENSMUST00000120247	SIK family kinase 3 [Source:MGI Symbol;Acc:MGI:2446296]	F6U6U5		4.4	2.8E-02	3.6	9.8E-03	-0.5	6.1E-01	0.4	6.2E-01
ENSMUST00000115789	synaptojanin 2 [Source:MGI Symbol;Acc:MGI:1201671]		Q9D2G5	-1.4	2.4E-01	-3.0	1.4E-01	0.1	8.9E-01	1.8	3.4E-01
ENSMUST00000115790	synaptojanin 2 [Source:MGI Symbol;Acc:MGI:1201671]	D3YZB2		0.3	9.0E-01	1.8	5.5E-01	1.3	5.4E-01	-0.3	9.3E-01
ENSMUST00000120267	autophagy related 16-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1920933]	G9M4M8	Q6KAU8	-4.1	2.8E-02	5.3	4.6E-04	-4.1	5.8E-03	-0.3	6.1E-01
ENSMUST00000115795	nuclear distribution gene E homolog 1 (A nidulans) [Source:MGI Symbol;Acc:MGI:1914453]		Q9CZA6	-2.5	4.9E-02	-0.7	5.9E-01	0.6	5.3E-01	-1.1	4.1E-01
ENSMUST00000120279	signal transducer and activator of transcription 6 [Source:MGI Symbol;Acc:MGI:103034]	D3YU28		6.3	2.0E-04	8.9	2.7E-05	-0.6	6.2E-01	0.3	5.0E-01
ENSMUST00000120284	N-6 adenine-specific DNA methyltransferase 1 (putative) [Source:MGI Symbol;Acc:MGI:1915018]	E9PXT7		9.1	1.1E-05	-4.7	8.0E-03	1.0	1.1E-01	-0.6	6.7E-01
ENSMUST00000120296	branched chain aminotransferase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1276534]	O88374		5.8	2.2E-03	6.4	4.1E-04	-0.6	6.4E-01	-0.4	6.1E-01
ENSMUST00000120301	FERM, RhoGEF and pleckstrin domain protein 2 [Source:MGI Symbol;Acc:MGI:2385126]		Q91VS8	4.3	1.3E-04	5.6	1.6E-03	0.5	6.9E-01	0.9	2.1E-01
ENSMUST00000115804	pyridoxal-dependent decarboxylase domain containing 1 [Source:MGI Symbol;Acc:MGI:1920909]		Q99K01	1.7	3.1E-01	1.3	5.2E-01	-0.8	6.1E-01	-0.4	8.4E-01
ENSMUST00000115808	AMME chromosomal region gene 1-like [Source:MGI Symbol;Acc:MGI:2442711]		Q8JZZ6	-0.8	1.2E-01	-0.3	6.3E-01	1.0	3.9E-02	0.6	3.4E-01
ENSMUST00000115811	phosphoinositide-3-kinase, class 3 [Source:MGI Symbol;Acc:MGI:2445019]	D3YZ98		1.5	1.1E-01	3.7	7.8E-03	0.7	5.0E-01	-1.6	7.4E-02
ENSMUST00000120302	microsomal glutathione S-transferase 1 [Source:MGI Symbol;Acc:MGI:1913850]	Q53ZD4	Q91VS7	-8.3	1.5E-05	-4.3	2.8E-03	0.5	2.9E-01	1.4	2.1E-01
ENSMUST00000120314	DMRT-like family C1c2 [Source:MGI Symbol;Acc:MGI:3802967]	Q9D410		5.6	1.7E-02	5.7	6.5E-03	0.7	6.4E-01	-1.3	2.2E-01
ENSMUST00000120339	RIKEN cDNA 5730559C18 gene [Source:MGI Symbol;Acc:MGI:1921579]	G3X9Z8		8.7	1.6E-05	1.8	2.3E-02	0.1	8.4E-01	-0.1	8.1E-01
ENSMUST00000120344	F-box protein 7 [Source:MGI Symbol;Acc:MGI:1917004]	Q3UD93		-3.9	3.1E-03	7.3	3.6E-05	-0.2	8.1E-01	0.0	9.2E-01
ENSMUST00000120346	cDNA sequence BC004004 [Source:MGI Symbol;Acc:MGI:2136782]		Q99KU6	-7.4	1.9E-05	5.5	4.4E-04	-0.9	4.4E-01	-0.7	2.6E-01
ENSMUST00000115823	C-type lectin domain family 16, member A [Source:MGI Symbol;Acc:MGI:1921624]		Q80U30	2.7	1.0E-01	5.5	2.0E-02	1.1	5.5E-01	-1.7	2.3E-01
ENSMUST00000120355	integrin alpha M [Source:MGI Symbol;Acc:MGI:96607]	E9Q5K8		-5.9	1.8E-03	2.5	3.8E-01	-0.8	7.5E-01	2.5	2.6E-01
ENSMUST00000115828	C-type lectin domain family 16, member A [Source:MGI Symbol;Acc:MGI:1921624]	H7BXB6		0.3	9.0E-01	1.7	5.7E-01	1.2	5.6E-01	-0.3	9.3E-01
ENSMUST00000120377	lamin A [Source:MGI Symbol;Acc:MGI:96794]		P48678	-2.9	2.7E-02	-1.5	1.7E-01	1.0	1.6E-01	-0.8	5.0E-01
ENSMUST00000120381	subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1(	Q3U573	P46978	-2.7	2.5E-04	7.4	1.6E-04	-1.0	4.6E-01	0.2	7.6E-01
ENSMUST00000120388	interleukin 33 [Source:MGI Symbol;Acc:MGI:1924375]		Q8BVZ5	4.5	8.9E-03	7.8	2.3E-04	-0.4	8.1E-01	-0.8	2.4E-01
ENSMUST00000115839	4-aminobutyrate aminotransferase [Source:MGI Symbol;Acc:MGI:2443582]		P61922	5.2	5.0E-02	4.7	8.1E-02	-1.5	5.8E-01	-1.0	5.4E-01
ENSMUST00000120411	family with sequence similarity 107, member A [Source:MGI Symbol;Acc:MGI:3041256]	Q78TU8		7.4	1.1E-02	5.5	1.6E-02	-0.8	7.1E-01	-0.3	7.9E-01
ENSMUST00000120428	tripartite motif-containing 24 [Source:MGI Symbol;Acc:MGI:109275]		Q64127	-4.4	2.2E-02	-8.0	9.1E-03	1.2	1.1E-01	0.5	8.5E-01
ENSMUST00000120432	mixed lineage kinase domain-like [Source:MGI Symbol;Acc:MGI:1921818]		Q9D2Y4	-3.2	4.6E-03	7.5	5.6E-05	-0.5	6.4E-01	-0.4	4.5E-01
ENSMUST00000115854	DnaJ (Hsp40) homolog, subfamily A, member 3 [Source:MGI Symbol;Acc:MGI:1933786]	Q3TJA9	Q99M87	-1.7	1.9E-01	-3.0	2.0E-01	0.3	8.2E-01	1.5	4.9E-01
ENSMUST00000120441	nology domain containing, family A (phosphoinositide binding specific) member 1 [Source:MGI Symbol;Acc:M	D3YU01		-4.0	3.3E-02	3.5	5.8E-04	-0.2	7.8E-01	0.3	5.2E-01
ENSMUST00000120447	basic leucine zipper nuclear factor 1 [Source:MGI Symbol;Acc:MGI:1201607]		Q8R2X8	-6.0	9.2E-04	2.1	6.7E-01	10.0	3.5E-02	-0.1	9.7E-01
ENSMUST00000115861	retinoblastoma binding protein 8 [Source:MGI Symbol;Acc:MGI:2442995]		Q80YR6	-2.4	3.7E-01	5.6	8.4E-02	5.0	9.6E-02	-3.0	2.4E-01
ENSMUST00000115869	embrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) [Source:MGI Symbol;Acc:MGI:192298	G5E8S8		0.7	1.1E-01	1.0	1.3E-01	0.8	1.2E-01	0.5	3.6E-01
ENSMUST00000115870	enhancer of polycomb homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1278322]		Q8C9X6	-2.0	2.0E-01	2.9	2.2E-01	3.1	1.3E-01	-1.8	3.0E-01
ENSMUST00000120452	DnaJ (Hsp40) homolog, subfamily A, member 4 [Source:MGI Symbol;Acc:MGI:1927638]		Q9JMC3	7.4	1.2E-04	7.3	1.5E-05	-0.6	5.1E-01	-0.2	7.2E-01
ENSMUST00000120472	actin filament associated protein 1-like 1 [Source:MGI Symbol;Acc:MGI:2147199]	B2RSM5	Q8BZI0	3.1	3.2E-02	4.7	7.6E-05	-0.4	5.9E-01	0.3	5.6E-01
ENSMUST00000120475	pellino 3 [Source:MGI Symbol;Acc:MGI:1924963]	D3Z6V8		8.1	3.5E-05	4.0	1.6E-03	-1.8	8.2E-02	0.6	3.3E-01
ENSMUST00000120488	kelch-like 22 [Source:MGI Symbol;Acc:MGI:1337995]		Q99JN2	2.0	5.2E-03	5.8	7.0E-04	-0.6	6.3E-01	-0.2	7.8E-01
ENSMUST00000120498	YTH domain containing 1 [Source:MGI Symbol;Acc:MGI:2443713]		E9Q5K9	-4.8	7.2E-04	2.7	2.7E-03	-0.3	5.8E-01	0.3	6.2E-01
ENSMUST00000120516	nology domain containing, family A (phosphoinositide binding specific) member 4 [Source:MGI Symbol;Acc:M	D3YW21		5.9	1.0E-02	3.3	3.6E-03	-1.9	5.2E-02	-0.6	3.7E-01
ENSMUST00000116005				1.5	1.1E-01	1.9	8.7E-02	-0.6	4.7E-01	-1.0	2.6E-01
ENSMUST00000120531	syntaxin binding protein 6 (amisyn) [Source:MGI Symbol;Acc:MGI:2384963]	Q3TYA4		3.4	8.0E-04	6.2	6.5E-03	0.1	9.6E-01	0.9	4.2E-01
ENSMUST00000120537	B cell leukemia/lymphoma 3 [Source:MGI Symbol;Acc:MGI:88140]		Q9Z2F6	-4.9	3.5E-04	5.6	9.2E-04	-1.0	4.6E-01	0.1	8.8E-01
ENSMUST00000116102				1.1	6.7E-02	2.0	1.2E-02	-0.1	9.1E-01	-0.9	1.3E-01
ENSMUST00000120539	LIM domain only 4 [Source:MGI Symbol;Acc:MGI:109360]	Q542S1	P61969	-8.4	2.3E-06	5.9	1.5E-03	-1.5	3.3E-01	0.2	8.0E-01
ENSMUST00000120540	solute carrier family 22, member 30 [Source:MGI Symbol;Acc:MGI:2442750]	Q3V3G0		7.0	5.4E-05	-7.4	1.4E-05	-0.8	5.8E-02	-4.0	7.5E-03
ENSMUST00000120555	dipeptidylpeptidase 6 [Source:MGI Symbol;Acc:MGI:94921]	Q5U4C2		9.9	1.5E-05	4.5	6.8E-04	-2.1	5.8E-02	-0.3	6.6E-01
ENSMUST00000120563	prostaglandin E receptor 4 (subtype EP4) [Source:MGI Symbol;Acc:MGI:104311]	Q91VE4		-3.8	3.1E-02	5.6	4.6E-03	-1.0	5.6E-01	0.0	9.8E-01
ENSMUST00000120573	arylsulfatase K [Source:MGI Symbol;Acc:MGI:1924291]			-1.7	7.1E-03	2.8	2.6E-02	-2.9	4.1E-02	-0.5	5.3E-01
ENSMUST00000120580	PRP39 pre-mRNA processing factor 39 homolog (yeast) [Source:MGI Symbol;Acc:MGI:104602]	E9QJV4		-3.6	8.0E-04	6.8	2.2E-04	-0.2	8.8E-01	0.1	8.2E-01
ENSMUST00000120585	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like [Source:MGI Symbol;Acc:MGI:1924836		Q3V3R1	7.3	2.8E-04	-7.0	1.8E-04	-0.1	8.2E-01	0.0	9.8E-01
ENSMUST00000116174				2.7	5.0E-02	2.5	8.1E-02	-1.5	2.2E-01	-1.4	2.4E-01
ENSMUST00000120591	phosphatidylserine decarboxylase [Source:MGI Symbol;Acc:MGI:2445114]	E9PX91		-2.7	1.5E-03	6.7	1.9E-04	-0.6	6.3E-01	-1.0	1.5E-01
ENSMUST00000120592	parvalbumin [Source:MGI Symbol;Acc:MGI:97821]	Q545M7	P32848	6.2	2.8E-04	7.6	2.4E-04	-0.7	6.3E-01	-0.4	6.1E-01
ENSMUST00000120595	echinoderm microtubule associated protein like 2 [Source:MGI Symbol;Acc:MGI:1919455]	D3YWS2		-6.1	2.4E-03	2.4	1.2E-01	-3.9	2.9E-02	0.6	6.2E-01
ENSMUST00000116229	deltex 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2135752]	E9Q3J1		0.4	6.9E-01	1.2	3.1E-01	0.5	6.2E-01	-0.4	7.0E-01
ENSMUST00000120622	DIX domain containing 1 [Source:MGI Symbol;Acc:MGI:2679721]		Q80Y83	5.5	3.1E-03	6.2	8.6E-06	-0.5	4.8E-01	0.4	3.3E-01
ENSMUST00000120630	archaelysin family metallopeptidase 1 [Source:MGI Symbol;Acc:MGI:2442258]	A1L312	Q8BVF9	2.7	1.9E-03	-3.3	3.9E-04	-0.6	1.0E-01	-0.7	2.7E-01
ENSMUST00000120638	synapsin III [Source:MGI Symbol;Acc:MGI:1351334]		Q8JZP2	5.3	7.1E-04	8.3	5.3E-03	-0.8	7.5E-01	-3.3	3.5E-02
ENSMUST00000120643	coiled-coil domain containing 114 [Source:MGI Symbol;Acc:MGI:2446120]	D3Z3W5		4.9	1.5E-06	5.7	9.3E-04	-0.4	7.4E-01	-0.9	3.2E-01
ENSMUST00000116257	tumor necrosis factor receptor superfamily, member 9 [Source:MGI Symbol;Acc:MGI:1101059]	Q3U3R1	P20334	2.6	6.7E-02	6.6	4.0E-04	-0.5	7.0E-01	-4.5	8.9E-04
ENSMUST00000120664	phosphodiesterase 4D, cAMP specific [Source:MGI Symbol;Acc:MGI:99555]	A6XDA6	Q01063	2.3	1.2E-03	4.5	1.4E-03	1.3	1.8E-01	-0.6	4.1E-01
ENSMUST00000120667	myc induced nuclear antigen [Source:MGI Symbol;Acc:MGI:1914264]	Q8CCK9		7.3	3.0E-05	-5.5	7.3E-03	1.0	1.2E-01	0.3	8.6E-01
ENSMUST00000116280	lysine rich nucleolar protein 1 [Source:MGI Symbol;Acc:MGI:1913606]	E9QKQ3		0.7	3.4E-01	1.0	2.1E-01	-0.4	5.3E-01	-0.7	3.4E-01
ENSMUST00000116284	G protein-coupled receptor 61 [Source:MGI Symbol;Acc:MGI:2441719]		Q8C010	1.7	5.2E-01	4.3	2.2E-01	1.3	6.8E-01	-1.3	5.8E-01
ENSMUST00000116286	serine/threonine kinase 40 [Source:MGI Symbol;Acc:MGI:1921428]		Q7TNL3	-0.7	6.7E-01	-0.3	9.1E-01	1.1	5.6E-01	0.7	7.4E-01
ENSMUST00000120691	RAB11 family interacting protein 3 (class II) [Source:MGI Symbol;Acc:MGI:2444431]		Q8CHD8	5.1	2.4E-02	-9.1	6.5E-07	-2.1	5.4E-05	-0.2	7.8E-01
ENSMUST00000120697	secretory carrier membrane protein 3 [Source:MGI Symbol;Acc:MGI:1346346]	Q3UXS0		-4.9	9.5E-04	-4.5	1.8E-02	0.3	6.5E-01	-0.2	9.0E-01
ENSMUST00000120699	translocase of inner mitochondrial membrane 22 [Source:MGI Symbol;Acc:MGI:1929742]	B0QZS8		-2.5	1.7E-02	6.4	5.5E-04	-0.6	6.4E-01	0.0	9.6E-01
ENSMUST00000120704	olfactory receptor 360 [Source:MGI Symbol;Acc:MGI:3030194]	Q8VFP3		5.1	2.9E-02	1.7	8.7E-03	0.4	3.1E-01	0.5	2.7E-01
ENSMUST00000116343	Ets2 repressor factor [Source:MGI Symbol;Acc:MGI:109637]	D3YXK6		1.8	3.8E-01	2.2	4.0E-01	-0.9	6.9E-01	-1.3	5.2E-01
ENSMUST00000116349	xylosyltransferase II [Source:MGI Symbol;Acc:MGI:2444797]		Q9EPL0	1.2	5.1E-02	0.6	4.3E-01	-0.4	4.5E-01	0.2	7.3E-01
ENSMUST00000116354	zinc finger protein 628 [Source:MGI Symbol;Acc:MGI:2665174]		Q8CJ78	0.0	1.0E+00	0.7	5.0E-01	1.2	1.2E-01	0.5	5.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000120705	TBC1 domain family, member 10b [Source:MGI Symbol;Acc:MGI:1915699]		Q8BHL3	-3.7	3.7E-04	-6.5	1.8E-04	0.1	9.0E-01	-1.5	2.5E-01
ENSMUST00000120707	Fgfr1op N-terminal like [Source:MGI Symbol;Acc:MGI:1913336]	D3Z644		6.6	9.0E-03	-3.2	1.5E-01	1.6	2.1E-01	0.7	7.2E-01
ENSMUST00000120717	calpain 11 [Source:MGI Symbol;Acc:MGI:1352490]		Q6J756	7.4	2.6E-05	-7.5	7.8E-05	0.0	9.6E-01	-0.9	4.6E-01
ENSMUST00000120734	predicted gene 5934 [Source:MGI Symbol;Acc:MGI:3643862]	D3Z4U6		8.6	1.4E-05	-4.3	8.2E-03	0.3	6.3E-01	0.1	9.5E-01
ENSMUST00000120754	activin A receptor, type II-like 1 [Source:MGI Symbol;Acc:MGI:1338946]		Q61288	-4.5	9.5E-03	-5.7	9.5E-03	0.7	3.1E-01	0.9	6.5E-01
ENSMUST00000116371	myosin phosphatase Rho interacting protein [Source:MGI Symbol;Acc:MGI:1349438]		P97434	5.5	7.3E-02	2.9	4.3E-01	-0.5	8.9E-01	2.2	4.1E-01
ENSMUST00000116375	cleavage stimulation factor, 3' pre-RNA, subunit 1 [Source:MGI Symbol;Acc:MGI:1914587]		Q99LC2	-0.5	3.4E-01	0.2	7.5E-01	0.4	3.2E-01	-0.2	7.1E-01
ENSMUST00000120756	peats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B [		Q60519	7.6	3.0E-02	-5.0	8.4E-02	0.7	5.0E-01	2.2	4.0E-01
ENSMUST00000120757	e carrier family 5 (neutral amino acid transporters, system A), member 4b [Source:MGI Symbol;Acc:MGI:189(		Q91ZP4	7.5	9.6E-07	0.4	4.7E-01	0.6	2.0E-01	-4.7	2.3E-04
ENSMUST00000116388	REST corepressor 1 [Source:MGI Symbol;Acc:MGI:106340]			0.8	7.0E-01	4.8	7.2E-02	0.8	7.2E-01	-3.2	1.5E-01
ENSMUST00000116400	KAT8 regulatory NSL complex subunit 2 [Source:MGI Symbol;Acc:MGI:1916862]		Q8BQR4	-1.4	4.3E-02	-0.4	6.6E-01	0.9	1.4E-01	-0.2	8.2E-01
ENSMUST00000120760	DIS3 mitotic control homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:2143272]		Q8C0S1	4.6	1.1E-02	7.3	6.9E-04	-0.7	6.7E-01	0.6	4.3E-01
ENSMUST00000116403	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	Q5FWJ5	P61979	3.7	7.9E-02	5.6	3.5E-02	0.7	7.5E-01	-1.3	4.8E-01
ENSMUST00000116409	histone deacetylase 7 [Source:MGI Symbol;Acc:MGI:1891835]		Q8C2B3	-0.8	4.9E-01	5.3	3.8E-02	6.1	1.3E-02	0.0	9.8E-01
ENSMUST00000116412	cytosolic thiouridylase subunit 2 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1914215]		Q3U308	-2.6	4.2E-02	-2.4	1.1E-01	0.3	7.3E-01	0.1	9.4E-01
ENSMUST00000116415	methenyltetrahydrofolate synthetase domain containing [Source:MGI Symbol;Acc:MGI:2679252]		Q3URQ7	-3.1	4.7E-02	-0.7	6.7E-01	1.0	3.5E-01	-1.4	4.0E-01
ENSMUST00000116420	TRM5 tRNA methyltransferase 5 [Source:MGI Symbol;Acc:MGI:1923607]		Q9D0C4	-0.5	3.5E-01	-1.0	1.2E-01	-0.9	8.8E-02	-0.4	5.4E-01
ENSMUST00000120778	suppressor of fused homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1345643]			5.0	4.6E-05	7.7	8.8E-05	-2.4	1.1E-01	1.2	6.3E-02
ENSMUST00000120784	TRAF type zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1923551]		Q3UDK1	-7.4	5.4E-04	5.2	8.3E-04	1.9	8.9E-02	-0.9	1.9E-01
ENSMUST00000116429	solute carrier family 12, member 4 [Source:MGI Symbol;Acc:MGI:1309465]	Q3TWZ6	Q9JIS8	1.8	2.2E-01	0.1	9.7E-01	-0.4	7.9E-01	1.4	4.1E-01
ENSMUST00000120805	DnaJ (Hsp40) homolog, subfamily C, member 19 [Source:MGI Symbol;Acc:MGI:1914963]	D3Z5K6		-4.6	4.0E-04	-4.0	4.3E-03	-0.3	5.7E-01	-1.8	1.8E-01
ENSMUST00000116436	aryl-hydrocarbon receptor [Source:MGI Symbol;Acc:MGI:105043]	Q3U5D9		-0.7	7.5E-02	0.1	8.3E-01	0.8	3.5E-02	0.0	9.9E-01
ENSMUST00000116437	synaptosomal-associated protein 23 [Source:MGI Symbol;Acc:MGI:109356]	Q9D3L3		3.5	1.7E-01	-1.9	5.3E-01	-3.2	1.5E-01	2.1	4.8E-01
ENSMUST00000120820	X Kell blood group precursor related family member 6 homolog [Source:MGI Symbol;Acc:MGI:2447765]		E9Q6C8	6.4	3.6E-04	-7.3	2.0E-04	-0.7	9.8E-02	-0.7	6.2E-01
ENSMUST00000120825	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1 [Source:MGI Symbol;Acc:MGI:2176213]		Q0QWG9	7.6	2.9E-05	6.0	1.5E-03	-0.6	6.8E-01	0.3	7.4E-01
ENSMUST00000120834	phospholipase D1 [Source:MGI Symbol;Acc:MGI:109585]	Q6NVF2		-6.1	1.8E-04	6.5	1.5E-04	-0.6	6.2E-01	-1.3	5.5E-02
ENSMUST00000116456	cytohesin 3 [Source:MGI Symbol;Acc:MGI:1335107]	Q3TXK1	O08967	0.0	9.8E-01	0.0	9.6E-01	0.0	9.3E-01	0.0	9.8E-01
ENSMUST00000120847	leucine rich repeat containing 8D [Source:MGI Symbol;Acc:MGI:1922368]		Q8BGR2	-2.7	9.7E-03	-1.9	6.4E-01	4.8	6.8E-02	-2.0	6.4E-01
ENSMUST00000120854	acyl-Coenzyme A dehydrogenase family, member 11 [Source:MGI Symbol;Acc:MGI:2143169]	D3YTQ5		-5.3	1.9E-02	-4.5	2.2E-02	1.3	1.5E-01	3.5	5.8E-02
ENSMUST00000120856	CUGBP, Elav-like family member 5 [Source:MGI Symbol;Acc:MGI:2442333]	D3Z4C5		8.0	1.3E-04	-1.6	5.7E-02	-0.1	8.0E-01	-0.4	6.3E-01
ENSMUST00000120864	branched chain aminotransferase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:1276534]	D3Z7C8		-4.0	1.5E-02	6.5	1.2E-02	-0.7	7.5E-01	-1.9	1.9E-01
ENSMUST00000116476	poly(A) binding protein, nuclear 1 [Source:MGI Symbol;Acc:MGI:1859158]		Q8CCS6	-1.8	2.4E-01	-1.8	4.5E-01	1.8	2.6E-01	1.7	4.2E-01
ENSMUST00000120866	leucine rich repeat containing 18 [Source:MGI Symbol;Acc:MGI:1914830]		Q9CQ07	5.6	1.8E-02	6.4	7.9E-04	-0.1	9.2E-01	-0.9	2.9E-01
ENSMUST00000116492	upstream binding protein 1 [Source:MGI Symbol;Acc:MGI:104889]		Q811S7	0.3	9.2E-01	1.0	7.6E-01	0.6	7.8E-01	-0.1	9.8E-01
ENSMUST00000116495	trafficking protein particle complex 2 [Source:MGI Symbol;Acc:MGI:1913476]	Q5J9A9	Q9CQP2	-1.3	5.2E-01	-3.8	2.1E-01	-1.3	4.1E-01	1.2	6.9E-01
ENSMUST00000116506	centrosomal protein 55 [Source:MGI Symbol;Acc:MGI:1921357]		Q8BT07	-0.5	8.1E-01	-3.2	2.6E-01	-2.1	2.1E-01	0.6	8.2E-01
ENSMUST00000120869	RAD50 interactor 1 [Source:MGI Symbol;Acc:MGI:1916233]	D3YU54		6.4	9.7E-05	-1.7	3.7E-02	1.0	3.4E-02	0.3	6.7E-01
ENSMUST00000120902	DEP domain containing 5 [Source:MGI Symbol;Acc:MGI:2141101]		P61460	-4.6	1.4E-03	9.1	3.8E-05	-0.6	6.5E-01	0.0	9.4E-01
ENSMUST00000116522	non-catalytic region of tyrosine kinase adaptor protein 1 [Source:MGI Symbol;Acc:MGI:109601]		Q99M51	-1.5	4.4E-02	-0.7	4.0E-01	-0.8	1.8E-01	-1.7	5.6E-02
ENSMUST00000116527	brain expressed gene 4 [Source:MGI Symbol;Acc:MGI:3606746]	Q14BB8	Q9CWT2	3.2	8.3E-02	6.1	1.0E-02	-0.1	9.7E-01	-2.9	3.8E-02
ENSMUST00000120912	zole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase [Source:MGI S		Q9DCL9	-6.2	1.3E-04	-1.0	4.8E-01	1.9	4.9E-02	-1.8	2.1E-01
ENSMUST00000120918	lysozyme-like 4 [Source:MGI Symbol;Acc:MGI:1916282]	Q78ID0	Q9D925	6.1	9.6E-05	-4.9	1.7E-02	-0.1	8.5E-01	-0.9	6.6E-01
ENSMUST00000120927	acyl-CoA thioesterase 3 [Source:MGI Symbol;Acc:MGI:2159619]		Q9QYR7	5.7	1.5E-02	4.7	3.1E-05	-1.2	9.3E-02	-0.1	7.4E-01
ENSMUST00000116551	tRNA methyltransferase 11-2 [Source:MGI Symbol;Acc:MGI:1914924]		Q9DCG9	4.1	1.4E-01	7.6	4.7E-02	3.3	3.0E-01	-0.2	9.5E-01
ENSMUST00000120929	testis-specific serine kinase substrate [Source:MGI Symbol;Acc:MGI:1347560]		O54887	7.6	6.3E-05	-3.5	2.9E-02	1.6	3.7E-02	-0.9	5.5E-01
ENSMUST00000120939	microsomal glutathione S-transferase 1 [Source:MGI Symbol;Acc:MGI:1913850]	D3YU60		-10.1	9.9E-07	4.2	2.2E-03	-1.9	1.2E-01	-0.3	6.5E-01
ENSMUST00000120942	ectonucleoside triphosphate diphosphohydrolase 5 [Source:MGI Symbol;Acc:MGI:1321385]		Q9WUZ9	-6.9	1.8E-05	5.5	1.7E-03	2.3	8.4E-02	-0.2	7.2E-01
ENSMUST00000120967	zinc finger and SCAN domain containing 10 [Source:MGI Symbol;Acc:MGI:3040700]		Q3URR7	7.0	2.1E-04	-0.9	6.5E-01	1.6	3.3E-01	-1.8	3.7E-01
ENSMUST00000120987	trafficking protein particle complex 11 [Source:MGI Symbol;Acc:MGI:2444585]		B2RXC1	4.4	9.8E-05	-7.2	1.8E-07	0.6	1.5E-02	-0.8	1.4E-01
ENSMUST00000116563	kinesin light chain 2 [Source:MGI Symbol;Acc:MGI:107953]	Q91YS4		0.1	8.8E-01	2.6	5.2E-02	1.2	2.8E-01	-1.3	1.6E-01
ENSMUST00000120990	olfactomedin-like 1 [Source:MGI Symbol;Acc:MGI:2679264]	Q8BSH2		6.7	7.3E-05	-2.8	6.2E-03	0.4	4.0E-01	-0.7	4.0E-01
ENSMUST00000120992	electron transferring flavoprotein, dehydrogenase [Source:MGI Symbol;Acc:MGI:106100]	Q6PF96		-4.0	8.6E-03	-3.9	2.8E-02	-0.4	6.1E-01	-1.5	3.8E-01
ENSMUST00000116584	mitochondrial ribosomal protein L39 [Source:MGI Symbol;Acc:MGI:1351620]		Q9JKF7	-0.8	2.0E-01	-0.2	7.3E-01	-0.6	2.3E-01	-1.1	1.0E-01
ENSMUST00000120997	Rho family GTPase 1 [Source:MGI Symbol;Acc:MGI:2444878]		Q8BLR7	4.3	9.1E-04	5.5	6.8E-04	-1.4	2.7E-01	0.1	8.9E-01
ENSMUST00000121006	tripartite motif-containing 35 [Source:MGI Symbol;Acc:MGI:1914104]	F6U6G6		4.5	1.7E-03	3.1	2.2E-01	0.4	8.8E-01	2.5	1.6E-01
ENSMUST00000121010	janus kinase and microtubule interacting protein 1 [Source:MGI Symbol;Acc:MGI:1923321]	D3Z4U5		8.3	1.4E-05	-2.1	3.2E-01	-5.0	1.3E-02	1.6	4.3E-01
ENSMUST00000121017	coiled-coil domain containing 155 [Source:MGI Symbol;Acc:MGI:2687329]		Q80VJ8	7.0	5.5E-05	-5.0	1.1E-02	-0.1	8.5E-01	1.3	4.2E-01
ENSMUST00000121018	cium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2) [Source:MGI Symbol;Acc:MGI:19183	Q3KNH8	Q9D424	3.2	1.7E-02	-2.0	1.0E-01	0.8	2.7E-01	-1.7	2.0E-01
ENSMUST00000121021	T-box 3 [Source:MGI Symbol;Acc:MGI:98495]	Q4VA43	P70324	6.0	2.6E-02	5.2	1.5E-04	-1.5	1.3E-01	0.2	7.2E-01
ENSMUST00000121043	homeobox A10 [Source:MGI Symbol;Acc:MGI:96171]		P31310	7.0	1.2E-04	-2.6	2.6E-03	1.0	1.9E-02	0.0	9.6E-01
ENSMUST00000121044	betacellulin, epidermal growth factor family member [Source:MGI Symbol;Acc:MGI:99439]	Q543J8	Q05928	6.3	5.1E-06	-6.7	1.8E-04	-0.6	2.5E-01	0.0	9.8E-01
ENSMUST00000121047	deoxyhypusine hydroxylase/monooxygenase [Source:MGI Symbol;Acc:MGI:1915964]	D3Z6Y9		5.4	4.0E-03	1.0	5.5E-01	-3.5	8.4E-02	0.3	8.1E-01
ENSMUST00000121085	in homology domain containing, family G (with RhoGef domain) member 2 [Source:MGI Symbol;Acc:MGI:2	D3Z5N8		7.1	9.4E-05	-7.6	2.0E-03	1.1	6.7E-02	-0.7	7.3E-01
ENSMUST00000121091	sacsin [Source:MGI Symbol;Acc:MGI:1354724]	D3Z3H1		7.7	8.3E-05	1.7	4.6E-01	6.3	4.2E-03	-0.1	9.7E-01
ENSMUST00000121094	adenosine deaminase, RNA-specific [Source:MGI Symbol;Acc:MGI:1889575]		Q99MU3	-7.0	2.1E-03	5.3	7.5E-03	-1.5	4.0E-01	-0.1	9.3E-01
ENSMUST00000121101	ring finger and SPRY domain containing 1 [Source:MGI Symbol;Acc:MGI:1914860]		Q8BVR6	4.1	2.2E-03	9.2	9.1E-04	-1.0	6.6E-01	0.2	8.3E-01
ENSMUST00000116648				2.8	6.4E-02	6.7	1.1E-02	2.2	3.0E-01	-1.7	1.9E-01
ENSMUST00000121114	solute carrier family 43, member 1 [Source:MGI Symbol;Acc:MGI:1931352]		Q8BSM7	7.1	3.6E-03	6.4	6.3E-03	-0.7	7.5E-01	0.8	4.5E-01
ENSMUST00000121127	cyclin G2 [Source:MGI Symbol;Acc:MGI:1095734]	Q5HZK4	O08918	-5.9	9.0E-04	0.7	7.4E-01	3.9	2.1E-02	-1.9	3.8E-01
ENSMUST00000121128	insulin-like growth factor 2 [Source:MGI Symbol;Acc:MGI:96434]	E9QLW5		8.7	4.9E-06	6.1	8.3E-04	-0.5	7.1E-01	-0.3	6.7E-01
ENSMUST00000121142	R3H domain and coiled-coil containing 1 [Source:MGI Symbol;Acc:MGI:1919093]	E9PUE1		4.7	1.7E-02	-8.1	9.8E-05	-0.6	1.3E-01	-0.8	5.8E-01
ENSMUST00000121146	tudor domain containing 5 [Source:MGI Symbol;Acc:MGI:2684949]		Q5VCS6	6.6	7.1E-03	8.6	3.8E-04	-0.8	6.7E-01	-0.5	5.2E-01
ENSMUST00000121160	RIKEN cDNA C530008M17 gene [Source:MGI Symbol;Acc:MGI:2444817]	E9Q5L4		2.9	2.0E-03	7.2	2.9E-05	-0.9	3.8E-01	-0.2	6.9E-01
ENSMUST00000117058				0.4	5.7E-01	0.1	9.3E-01	1.8	3.7E-02	2.0	5.0E-02
ENSMUST00000121162	cyclic nucleotide gated channel beta 1 [Source:MGI Symbol;Acc:MGI:2664102]	E9PXX0		7.0	1.9E-02	6.7	1.1E-04	-1.2	3.1E-01	-1.0	1.5E-01
ENSMUST00000121185	small ubiquitin-like modifier 2 [Source:MGI Symbol;Acc:MGI:2158813]	D3YW94		-5.7	1.6E-03	5.8	4.1E-02	-3.5	2.2E-01	-1.7	3.0E-01
ENSMUST00000121200	palladin, cytoskeletal associated protein [Source:MGI Symbol;Acc:MGI:1919583]		Q9ET54	-3.2	2.3E-02	5.0	1.2E-02	-0.6	7.2E-01	0.7	4.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000121219	FERM domain containing 5 [Source:MGI Symbol;Acc:MGI:2442557]		Q6P5H6	5.1	2.4E-02	3.0	7.8E-03	-0.8	3.5E-01	-0.5	5.3E-01
ENSMUST00000121226	ATP-binding cassette, sub-family A (ABC1), member 17 [Source:MGI Symbol;Acc:MGI:3625331]	E9PX95		8.4	1.0E-05	4.1	8.4E-04	-1.6	8.6E-02	0.0	9.5E-01
ENSMUST00000121227	collagen, type XII, alpha 1 [Source:MGI Symbol;Acc:MGI:88448]	E9PX70		7.3	5.9E-03	5.5	2.2E-02	0.6	7.5E-01	1.5	2.2E-01
ENSMUST00000121231	choline/ethanolaminephosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2139793]		Q8BGS7	-9.1	3.9E-06	1.8	2.5E-01	-0.7	5.9E-01	2.1	1.2E-01
ENSMUST00000121265	ATP-binding cassette, sub-family A (ABC1), member 15 [Source:MGI Symbol;Acc:MGI:2388709]	E9PWH4		5.9	2.3E-04	7.9	4.6E-05	-0.6	5.9E-01	0.2	7.3E-01
ENSMUST00000117082	DiGeorge syndrome critical region gene 2 [Source:MGI Symbol;Acc:MGI:892866]	E9QNU3		1.3	6.0E-01	6.2	7.2E-02	1.1	7.1E-01	-3.7	1.3E-01
ENSMUST00000121266	CUGBP, Elav-like family member 6 [Source:MGI Symbol;Acc:MGI:1923433]		Q7TN33	6.7	9.2E-03	-5.6	2.2E-04	-0.5	2.4E-01	-2.3	7.7E-02
ENSMUST00000121270	leukocyte receptor cluster (LRC) member 8 [Source:MGI Symbol;Acc:MGI:2142195]	D3YWS8		-6.2	2.5E-05	-0.3	6.7E-01	1.0	6.0E-02	0.0	9.6E-01
ENSMUST00000121285	bromodomain containing 4 [Source:MGI Symbol;Acc:MGI:1888520]		Q9ESU6	-2.5	9.0E-03	4.5	4.1E-02	0.7	7.0E-01	1.2	3.3E-01
ENSMUST00000121287	rabphilin 3A-like (without C2 domains) [Source:MGI Symbol;Acc:MGI:1923492]		Q768S4	3.9	3.3E-04	-4.5	1.7E-02	0.4	6.1E-01	-1.6	4.1E-01
ENSMUST00000121303	myeloperoxidase [Source:MGI Symbol;Acc:MGI:97137]		P11247	-1.9	1.6E-02	7.4	9.6E-04	-0.6	7.1E-01	-3.4	8.0E-03
ENSMUST00000121304	d, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 [Source:MGI Symbol;Acc	Q3UDA4	Q9Z0H3	-5.3	1.5E-03	4.6	1.1E-02	-0.4	7.8E-01	0.5	5.8E-01
ENSMUST00000117099	chromatin assembly factor 1, subunit B (p60) [Source:MGI Symbol;Acc:MGI:1314881]		Q9D0N7	-0.1	9.7E-01	-0.9	8.3E-01	0.4	8.8E-01	1.2	7.4E-01
ENSMUST00000121312	GATA binding protein 4 [Source:MGI Symbol;Acc:MGI:95664]	Q3UYJ1		7.7	4.8E-04	6.1	1.1E-02	-0.4	8.4E-01	-0.4	7.1E-01
ENSMUST00000121322	cingulin-like 1 [Source:MGI Symbol;Acc:MGI:1915428]	D3Z3H4		-4.1	1.2E-03	7.0	3.1E-04	-0.7	6.3E-01	0.7	3.1E-01
ENSMUST00000121331	vacuolar protein sorting 25 (yeast) [Source:MGI Symbol;Acc:MGI:106354]	A8XY17		5.9	2.8E-03	6.2	8.5E-06	-0.4	5.9E-01	-0.9	7.0E-02
ENSMUST00000121360	single-stranded DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:1920040]	Q8R2K3		-3.1	9.5E-03	6.7	2.9E-03	-0.5	7.8E-01	0.9	3.7E-01
ENSMUST00000117113				-2.1	4.2E-01	-3.6	3.7E-01	-0.3	8.9E-01	1.3	7.4E-01
ENSMUST00000121369	ring finger protein, transmembrane 2 [Source:MGI Symbol;Acc:MGI:2442859]		Q3UF64	8.5	4.1E-05	6.1	7.5E-04	-0.2	9.1E-01	-0.2	7.8E-01
ENSMUST00000121391	absent in melanoma 1-like [Source:MGI Symbol;Acc:MGI:1334463]	B7ZCC2		8.6	2.0E-05	6.2	3.2E-03	-0.3	8.6E-01	0.7	4.3E-01
ENSMUST00000121393	predicted gene 4631 [Source:MGI Symbol;Acc:MGI:3782813]	A2ART4		2.9	1.2E-04	7.3	5.4E-05	-0.5	6.2E-01	0.0	9.8E-01
ENSMUST00000121394	protease, serine 53 [Source:MGI Symbol;Acc:MGI:2652890]	B2RX64	Q571E5	5.3	4.2E-03	7.2	2.6E-03	-0.4	8.4E-01	1.7	9.1E-02
ENSMUST00000117129				-3.2	4.2E-01	-2.6	4.5E-01	-2.2	3.6E-01	-2.9	5.0E-01
ENSMUST00000117137	meprin 1 alpha [Source:MGI Symbol;Acc:MGI:96963]		P28825	4.0	1.5E-01	1.9	5.9E-01	-0.2	9.6E-01	2.0	4.6E-01
ENSMUST00000121402	aryl-hydrocarbon receptor-interacting protein [Source:MGI Symbol;Acc:MGI:109622]	D3YW40		-3.6	1.8E-02	4.5	2.2E-02	1.4	4.0E-01	0.5	6.5E-01
ENSMUST00000121404	androgen dependent TFPI regulating protein [Source:MGI Symbol;Acc:MGI:1924596]		Q8C138	-3.2	4.2E-03	-3.0	1.4E-03	0.8	6.4E-02	-0.2	8.0E-01
ENSMUST00000121412	RIKEN cDNA 6430531B16 gene [Source:MGI Symbol;Acc:MGI:2685939]	Q3TNW9		2.6	6.9E-03	-6.0	8.3E-05	-0.1	6.9E-01	-0.1	8.9E-01
ENSMUST00000117150	putative homeodomain transcription factor 1 [Source:MGI Symbol;Acc:MGI:1332671]	Q5IBN5	Q9QZ09	-1.5	5.0E-02	-0.9	3.0E-01	0.2	7.7E-01	-0.4	6.1E-01
ENSMUST00000121418	RAB3A interacting protein (rabin3)-like 1 [Source:MGI Symbol;Acc:MGI:1922010]		Q8VDV3	9.0	1.3E-05	7.1	2.2E-05	-2.2	6.3E-02	0.1	8.1E-01
ENSMUST00000121433	ubiquitin-conjugating enzyme E2E 3 [Source:MGI Symbol;Acc:MGI:107412]		P52483	-3.5	4.9E-04	-4.2	4.3E-03	-0.1	8.8E-01	-0.4	7.4E-01
ENSMUST00000121440	mastermind like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2389461]	D4QGC2		3.4	8.1E-05	6.4	2.8E-04	-1.0	4.4E-01	-0.5	4.5E-01
ENSMUST00000121442	IQ motif containing C [Source:MGI Symbol;Acc:MGI:2446212]	A8Y5J7		-3.0	1.9E-02	5.8	2.5E-05	-3.0	9.3E-03	0.2	6.1E-01
ENSMUST00000121446	inositol polyphosphate multikinase [Source:MGI Symbol;Acc:MGI:1916968]	D3YWA2		-4.3	8.2E-03	6.2	2.9E-04	-0.6	6.1E-01	0.2	7.0E-01
ENSMUST00000121469	receptor accessory protein 1 [Source:MGI Symbol;Acc:MGI:1098827]		Q8BGH4	8.1	4.5E-05	-10.3	3.5E-06	-0.5	3.2E-01	-0.6	5.8E-01
ENSMUST00000121484	helicase with zinc finger 2, transcriptional coactivator [Source:MGI Symbol;Acc:MGI:2385169]	A2AS05		7.0	1.3E-02	5.6	2.0E-02	-0.7	7.3E-01	1.5	2.3E-01
ENSMUST00000121492	sialic acid binding Ig-like lectin H [Source:MGI Symbol;Acc:MGI:2443256]	B7ZMQ5		5.7	3.2E-03	-1.8	2.3E-01	4.1	4.7E-04	-0.6	6.5E-01
ENSMUST00000117177	ring finger protein, transmembrane 2 [Source:MGI Symbol;Acc:MGI:2442859]		Q3UF64	5.6	4.4E-02	7.3	1.3E-02	-1.3	6.5E-01	-3.0	7.4E-02
ENSMUST00000121520	zinc finger, MYM-type 3 [Source:MGI Symbol;Acc:MGI:1927231]	B1AXS7		-3.7	1.1E-02	5.3	1.6E-02	-0.6	7.7E-01	0.0	1.0E+00
ENSMUST00000121529	heme oxygenase 2 [Source:MGI Symbol;Acc:MGI:109373]	D3YX62		-4.6	1.7E-02	5.1	5.7E-04	-1.3	2.5E-01	-0.6	3.6E-01
ENSMUST00000117189	zinc finger and SCAN domain containing 22 [Source:MGI Symbol;Acc:MGI:2443312]	Q3TQC3		1.4	6.7E-02	1.9	4.1E-02	0.0	9.9E-01	-0.5	4.5E-01
ENSMUST00000121532	transmembrane protein 219 [Source:MGI Symbol;Acc:MGI:1915992]		Q9D123	-7.4	8.7E-06	6.0	6.0E-03	1.0	5.3E-01	-0.9	4.3E-01
ENSMUST00000117193	2'-5' oligoadenylate synthetase 1C [Source:MGI Symbol;Acc:MGI:2149633]	Q924S2		-1.1	5.9E-02	-1.1	1.2E-01	-0.6	2.3E-01	-0.6	3.8E-01
ENSMUST00000117194	centrosomal protein 164 [Source:MGI Symbol;Acc:MGI:2384878]	D3YVU3		0.5	1.7E-01	1.5	7.9E-03	0.7	5.7E-02	-0.3	4.9E-01
ENSMUST00000121534	constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13		Q8BV13	5.6	3.4E-05	5.0	5.0E-03	-1.6	2.9E-01	-1.0	2.8E-01
ENSMUST00000121573	ligand dependent nuclear receptor corepressor-like [Source:MGI Symbol;Acc:MGI:2651932]	E9PXY2		5.2	3.1E-02	4.6	2.2E-03	-0.2	8.5E-01	0.8	3.1E-01
ENSMUST00000121584	PR domain containing 15 [Source:MGI Symbol;Acc:MGI:1930121]	E9Q6A1		-4.8	1.1E-02	5.2	5.0E-03	0.0	9.9E-01	0.4	6.5E-01
ENSMUST00000121598	apolipoprotein A-V [Source:MGI Symbol;Acc:MGI:1913363]		Q8C7G5	6.9	2.1E-04	-2.0	1.8E-02	-0.9	7.9E-02	-0.8	3.2E-01
ENSMUST00000121616	fused in sarcoma [Source:MGI Symbol;Acc:MGI:1353633]	Q91VQ2		-7.2	7.2E-05	6.1	1.0E-02	-1.0	6.5E-01	1.5	2.0E-01
ENSMUST00000121646	pleiomorphic adenoma gene-like 1 [Source:MGI Symbol;Acc:MGI:1100874]	Q9JLQ4		8.6	1.8E-05	6.1	2.0E-03	0.8	5.7E-01	-0.5	5.2E-01
ENSMUST00000121652	ORAI calcium release-activated calcium modulator 1 [Source:MGI Symbol;Acc:MGI:1925542]	A3KCG1	Q8BWG9	-4.1	3.0E-04	-3.7	3.3E-03	1.1	4.0E-02	-3.6	1.5E-02
ENSMUST00000117219				-0.5	4.5E-01	-1.7	3.7E-02	-1.6	1.3E-02	-0.4	5.9E-01
ENSMUST00000117222	gem (nuclear organelle) associated protein 7 [Source:MGI Symbol;Acc:MGI:1916981]		Q9CWY4	-0.4	4.7E-01	-0.1	8.6E-01	0.2	7.6E-01	-0.1	8.6E-01
ENSMUST00000121693	RAB27B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1931295]	Q549X4	Q99P58	4.9	2.7E-04	6.2	3.9E-04	-0.5	6.8E-01	-0.5	4.6E-01
ENSMUST00000117227				4.7	6.2E-02	3.1	2.2E-01	-2.5	3.2E-01	-1.0	6.0E-01
ENSMUST00000121694	cytochrome P450, family 2, subfamily j, polypeptide 12 [Source:MGI Symbol;Acc:MGI:3717097]	G3UZ89		6.1	4.4E-03	-4.5	5.6E-03	0.9	1.1E-01	-1.2	4.0E-01
ENSMUST00000121707	adhesion G protein-coupled receptor L3 [Source:MGI Symbol;Acc:MGI:2441950]	D3YTW7		6.1	7.9E-03	2.2	6.6E-03	-0.1	9.0E-01	0.2	6.8E-01
ENSMUST00000121717	ankyrin repeat and EF-hand domain containing 1 [Source:MGI Symbol;Acc:MGI:2441685]		Q9D2J7	6.2	1.4E-03	6.6	1.1E-04	-0.5	6.2E-01	-0.9	1.4E-01
ENSMUST00000121733	papilin, proteoglycan-like sulfated glycoprotein [Source:MGI Symbol;Acc:MGI:2386139]	B7ZN28		7.2	1.8E-02	3.7	5.0E-03	-2.2	8.0E-02	0.4	5.9E-01
ENSMUST00000121736	F-box and leucine-rich repeat protein 5 [Source:MGI Symbol;Acc:MGI:2152883]		Q8C2S5	-10.4	1.2E-03	-3.4	5.5E-03	0.2	6.9E-01	-2.0	1.1E-01
ENSMUST00000117243	dynactin 6 [Source:MGI Symbol;Acc:MGI:1343154]	D3Z4E5		-4.3	5.5E-02	-4.6	6.7E-02	-1.8	1.2E-01	-1.4	5.9E-01
ENSMUST00000121748	serine/threonine kinase 33 [Source:MGI Symbol;Acc:MGI:2152419]		Q924X7	6.5	8.3E-03	0.3	6.1E-01	0.9	3.2E-02	-0.8	1.6E-01
ENSMUST00000117253	adhesion G protein-coupled receptor L3 [Source:MGI Symbol;Acc:MGI:2441950]	D3YWR3		3.8	1.4E-01	4.4	1.3E-01	-0.3	9.2E-01	-0.9	6.0E-01
ENSMUST00000121750	calcineurin-like phosphoesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:2443300]		Q8BFS6	4.6	1.7E-02	6.0	8.7E-04	-0.5	7.1E-01	-0.6	4.0E-01
ENSMUST00000121759	synaptojanin 1 [Source:MGI Symbol;Acc:MGI:1354961]	D3Z656		-5.1	1.8E-03	6.0	1.5E-04	-2.2	8.2E-02	-0.6	3.6E-01
ENSMUST00000121766	pleiomorphic adenoma gene-like 1 [Source:MGI Symbol;Acc:MGI:1100874]	Q3UQW2		7.6	2.3E-03	5.9	8.4E-04	-0.6	6.3E-01	0.8	2.7E-01
ENSMUST00000121777	lines homolog (Drosophila) 1 [Source:MGI Symbol;Acc:MGI:1919885]		Q3U1D0	-5.2	4.5E-04	-2.7	1.3E-01	0.0	9.8E-01	-0.5	7.7E-01
ENSMUST00000117268	OTU domain containing 6B [Source:MGI Symbol;Acc:MGI:1919451]	A0A0A0MQF5		-1.3	1.2E-01	-2.1	3.6E-02	-1.5	3.1E-02	-0.6	5.0E-01
ENSMUST00000117269	TNF receptor-associated factor 3 [Source:MGI Symbol;Acc:MGI:108041]	Q3UHJ1		-2.3	3.6E-01	1.9	6.3E-01	4.5	1.5E-01	0.3	9.2E-01
ENSMUST00000117270	ankyrin 1, erythroid [Source:MGI Symbol;Acc:MGI:88024]	D3Z5M4		2.3	2.5E-01	7.4	6.5E-03	0.6	8.0E-01	-4.5	1.2E-02
ENSMUST00000117276	solute carrier family 39 (zinc transporter), member 3 [Source:MGI Symbol;Acc:MGI:2147269]		Q99K24	2.3	4.6E-02	3.3	9.0E-02	3.2	5.3E-02	2.2	1.1E-01
ENSMUST00000117280	structural maintenance of chromosomes 2 [Source:MGI Symbol;Acc:MGI:106067]		Q8CG48	-1.9	2.4E-01	-3.9	1.7E-01	-0.1	9.2E-01	1.9	4.8E-01
ENSMUST00000121778	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 [Source:MGI Symbol;Acc:MGI:1913296]	D3Z6W9		-6.6	1.6E-04	1.3	8.4E-02	0.3	6.1E-01	0.5	4.6E-01
ENSMUST00000121782	ring finger protein 43 [Source:MGI Symbol;Acc:MGI:2442609]	E9PWJ5		4.7	1.8E-02	-5.3	5.3E-03	1.1	1.3E-01	-1.6	3.8E-01
ENSMUST00000117286	ectonucleoside triphosphate diphosphohydrolase 5 [Source:MGI Symbol;Acc:MGI:1321385]		Q9WUZ9	-2.7	5.9E-02	0.7	6.0E-01	0.3	7.9E-01	-3.1	4.8E-02
ENSMUST00000121789	synapsin III [Source:MGI Symbol;Acc:MGI:1351334]	D3Z620		6.8	2.6E-05	4.1	5.3E-03	-2.8	6.4E-02	0.7	4.2E-01
ENSMUST00000121796	LIM domain only 4 [Source:MGI Symbol;Acc:MGI:109360]	Q542S1	P61969	-8.9	1.8E-04	-8.5	2.8E-03	-1.0	2.3E-01	-0.2	9.3E-01
ENSMUST00000117291	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like [Source:MGI Symbol;Acc:MGI:1924836		Q3V3R1	-1.3	3.3E-01	0.5	7.7E-01	0.4	7.2E-01	-1.3	3.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000117295				3.6	1.5E-01	2.2	5.4E-01	0.6	8.4E-01	2.0	4.7E-01
ENSMUST00000121797	keratinocyte differentiation factor 1 [Source:MGI Symbol;Acc:MGI:1916323]	A8Y5H9		6.4	3.0E-04	-1.2	2.3E-01	1.2	1.1E-01	-0.4	6.9E-01
ENSMUST00000121805	dihydropyrimidinase-like 3 [Source:MGI Symbol;Acc:MGI:1349762]	E9PWE8		6.5	7.5E-06	8.0	1.3E-02	-0.9	7.6E-01	-1.4	3.5E-01
ENSMUST00000121820	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2 [Source:MGI Symbol;Acc:MGI:1891351]		Q9ER58	7.0	2.3E-04	4.1	3.4E-02	-1.1	5.3E-01	-0.9	5.1E-01
ENSMUST00000121839	kinase non-catalytic C-lobe domain (KIND) containing 1 [Source:MGI Symbol;Acc:MGI:1923734]	D3Z3X0		5.1	1.6E-02	4.2	9.1E-03	0.5	6.6E-01	-0.7	4.3E-01
ENSMUST00000121840	zinc finger and BTB domain containing 7a [Source:MGI Symbol;Acc:MGI:1335091]	D3Z4C3		2.7	2.2E-02	6.1	2.1E-04	-0.6	6.1E-01	-0.7	2.9E-01
ENSMUST00000121862	achaete-scute complex homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:96920]	D3Z7Q6		2.8	2.3E-02	1.9	1.5E-01	0.1	9.4E-01	0.8	3.8E-01
ENSMUST00000117324	Josephin domain containing 2 [Source:MGI Symbol;Acc:MGI:1913374]		Q9CR30	-4.4	4.2E-02	-1.4	6.1E-01	2.3	2.1E-01	-0.8	7.5E-01
ENSMUST00000117337	ATP-binding cassette, sub-family A (ABC1), member 3 [Source:MGI Symbol;Acc:MGI:1351617]	Q6AXE3		-3.8	4.3E-02	-2.5	2.8E-01	0.7	6.0E-01	-0.7	7.7E-01
ENSMUST00000121875	myosin VB [Source:MGI Symbol;Acc:MGI:106598]	G3X9Y9		8.9	7.4E-06	3.3	1.5E-01	-1.8	4.3E-01	-0.4	8.0E-01
ENSMUST00000121886	zinc finger protein 868 [Source:MGI Symbol;Acc:MGI:2142546]	Q3UTQ6		-3.9	5.0E-04	7.8	4.1E-04	-0.6	7.0E-01	-0.5	5.0E-01
ENSMUST00000121887	family with sequence similarity 107, member A [Source:MGI Symbol;Acc:MGI:3041256]	Q78TU8		8.1	1.6E-02	7.7	2.2E-04	0.0	9.9E-01	-0.6	4.1E-01
ENSMUST00000121900	predicted gene 2012 [Source:MGI Symbol;Acc:MGI:3780181]	B1B0R1		4.9	1.6E-02	6.6	2.1E-04	-0.6	6.4E-01	-1.1	1.1E-01
ENSMUST00000121920	mitochondrial ribosomal protein L24 [Source:MGI Symbol;Acc:MGI:1914957]		Q9CQ06	-6.0	3.1E-05	5.2	6.4E-04	-0.3	7.6E-01	-0.3	6.6E-01
ENSMUST00000117354	lethal, Chr 7, Rinchik 6 [Source:MGI Symbol;Acc:MGI:96738]	D3YU13		-1.5	4.7E-02	-3.9	1.1E-02	-0.3	6.2E-01	2.1	1.1E-01
ENSMUST00000121930	acylphosphatase 1, erythrocyte (common) type [Source:MGI Symbol;Acc:MGI:1913454]	E9QJT5		5.2	7.1E-03	-2.2	3.6E-01	1.5	2.7E-01	-0.9	7.2E-01
ENSMUST00000121931	CDC-like kinase 2 [Source:MGI Symbol;Acc:MGI:1098669]	E9Q5Y1		-6.2	2.7E-05	-6.1	2.5E-04	-1.3	1.5E-02	-0.3	7.5E-01
ENSMUST00000117360	LPS-induced TN factor [Source:MGI Symbol;Acc:MGI:1929512]		Q9JLJ0	-2.3	6.1E-02	-3.4	3.7E-02	-1.6	6.1E-02	-0.5	7.3E-01
ENSMUST00000121953	disrupted in schizophrenia 1 [Source:MGI Symbol;Acc:MGI:2447658]		Q811T9	6.2	2.1E-04	5.2	5.2E-03	1.1	4.3E-01	0.9	3.7E-01
ENSMUST00000121958	olfactory receptor 213 [Source:MGI Symbol;Acc:MGI:3030047]	Q7TS32		6.6	1.6E-04	3.7	1.6E-02	-2.6	9.3E-02	-0.8	4.5E-01
ENSMUST00000121963	collagen, type VI, alpha 4 [Source:MGI Symbol;Acc:MGI:1915803]		A2AX52	2.0	6.8E-03	6.0	7.7E-04	0.9	4.8E-01	-0.1	8.7E-01
ENSMUST00000117373	periostin, osteoblast specific factor [Source:MGI Symbol;Acc:MGI:1926321]		Q62009	4.8	6.8E-02	3.8	9.2E-02	-2.8	2.7E-01	-1.8	2.7E-01
ENSMUST00000121964	WD repeat domain 66 [Source:MGI Symbol;Acc:MGI:1918495]	E9Q743		6.7	3.1E-04	6.1	6.8E-04	-0.7	6.1E-01	-0.5	5.1E-01
ENSMUST00000121972	myosin light chain kinase 3 [Source:MGI Symbol;Acc:MGI:2443063]		Q3UIZ8	4.7	3.1E-02	6.0	8.1E-04	0.0	9.9E-01	-0.3	7.1E-01
ENSMUST00000121987	potassium channel tetramerisation domain containing 14 [Source:MGI Symbol;Acc:MGI:1289222]	Q5EER8		5.7	2.0E-03	-5.1	4.0E-04	-0.9	3.8E-02	-0.2	8.3E-01
ENSMUST00000121990	synaptotagmin II [Source:MGI Symbol;Acc:MGI:99666]			8.8	1.9E-05	4.7	1.7E-02	0.5	7.8E-01	-0.7	4.8E-01
ENSMUST00000121992	indoleamine 2,3-dioxygenase 2 [Source:MGI Symbol;Acc:MGI:2142489]	A4UHF3	Q8R0V5	5.1	1.5E-02	6.9	5.1E-02	-0.8	8.1E-01	-0.3	8.5E-01
ENSMUST00000122010	anaphase promoting complex subunit 7 [Source:MGI Symbol;Acc:MGI:1929711]		Q9WVM3	7.0	4.0E-05	5.1	6.1E-03	-1.1	5.0E-01	0.8	4.3E-01
ENSMUST00000117389	PR domain containing 10 [Source:MGI Symbol;Acc:MGI:2682952]		Q3UTQ7	1.2	1.9E-01	2.0	9.6E-02	0.7	4.6E-01	-0.1	9.1E-01
ENSMUST00000122026	lipoic acid synthetase [Source:MGI Symbol;Acc:MGI:1934604]	D3Z6I3	Q99M04	-6.1	3.5E-05	-1.6	5.0E-01	3.3	3.9E-02	0.9	7.0E-01
ENSMUST00000122038	WD repeat domain 12 [Source:MGI Symbol;Acc:MGI:1927241]	Q4V9X1	Q9JJA4	-5.3	3.0E-04	-0.9	1.9E-01	0.7	1.4E-01	-0.3	6.8E-01
ENSMUST00000122053	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit [Source:MGI Symbol;Acc:MGI:109482]	E9Q1R5		8.4	6.8E-05	-1.7	7.4E-02	0.7	2.4E-01	0.1	9.1E-01
ENSMUST00000122065	cingulin-like 1 [Source:MGI Symbol;Acc:MGI:1915428]	B2RSU6		8.4	1.2E-05	5.2	1.6E-03	-0.4	7.3E-01	0.2	8.0E-01
ENSMUST00000117398				1.0	3.3E-01	1.5	2.0E-01	0.0	9.9E-01	-0.5	5.9E-01
ENSMUST00000122078	RIKEN cDNA 4930435E12 gene [Source:MGI Symbol;Acc:MGI:1921913]	A6X8Z9		7.2	2.0E-03	-5.9	3.2E-06	0.8	1.4E-02	-1.1	9.6E-02
ENSMUST00000122079	cerebellin 2 precursor protein [Source:MGI Symbol;Acc:MGI:88282]		Q8BGU2	5.1	3.4E-02	-1.0	4.9E-01	-0.9	3.1E-01	3.3	3.0E-02
ENSMUST00000122088	sphingosine-1-phosphate receptor 5 [Source:MGI Symbol;Acc:MGI:2150641]		Q91X56	6.0	3.1E-03	-5.4	2.9E-05	-0.1	8.0E-01	-2.1	2.3E-02
ENSMUST00000117410	StAR-related lipid transfer (START) domain containing 5 [Source:MGI Symbol;Acc:MGI:2156765]	D3YU00		1.4	1.9E-01	0.7	6.0E-01	-0.4	7.2E-01	0.3	7.7E-01
ENSMUST00000122092	solute carrier family 31, member 1 [Source:MGI Symbol;Acc:MGI:1333843]	A8Y5P1		2.1	1.3E-02	-5.1	6.4E-04	-0.6	1.6E-01	-1.8	1.5E-01
ENSMUST00000122096	predicted pseudogene 5580 [Source:MGI Symbol;Acc:MGI:3646594]			7.8	3.0E-05	6.8	1.1E-02	-1.1	6.3E-01	0.3	8.2E-01
ENSMUST00000117419	Rho guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:1353510]		Q61210	-6.4	2.2E-01	0.2	9.8E-01	6.2	2.3E-01	-0.4	9.6E-01
ENSMUST00000117422	cAMP responsive element binding protein 3-like 3 [Source:MGI Symbol;Acc:MGI:2384786]		Q91XE9	1.4	5.8E-02	1.6	7.3E-02	0.2	7.2E-01	0.0	9.8E-01
ENSMUST00000122110	ubiquitin specific peptidase 5 (isopeptidase T) [Source:MGI Symbol;Acc:MGI:1347343]	Q3U4W8		-7.6	1.0E-04	-6.0	1.8E-03	1.2	3.3E-02	-0.8	6.2E-01
ENSMUST00000117424	coiled-coil and C2 domain containing 1A [Source:MGI Symbol;Acc:MGI:2384831]	E9PX94		1.7	3.1E-01	6.9	1.4E-02	3.0	2.0E-01	-2.2	1.4E-01
ENSMUST00000117435				-2.0	5.5E-01	-3.6	3.8E-01	-2.0	3.7E-01	-0.5	9.2E-01
ENSMUST00000117438	WD repeat domain 12 [Source:MGI Symbol;Acc:MGI:1927241]	Q4V9X1	Q9JJA4	0.9	5.0E-01	-0.3	8.5E-01	-1.9	1.4E-01	-0.7	5.7E-01
ENSMUST00000122128	pleiotropic regulator 1, PRL1 homolog (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1858197]	D3Z4V1		-4.6	4.7E-03	6.5	5.2E-04	-0.2	8.7E-01	0.6	4.1E-01
ENSMUST00000122129	MAP7 domain containing 1 [Source:MGI Symbol;Acc:MGI:2384297]	A8Y5P4		-5.7	1.7E-03	5.1	2.2E-04	0.4	6.2E-01	0.5	4.2E-01
ENSMUST00000122171	dipeptidylpeptidase 6 [Source:MGI Symbol;Acc:MGI:94921]	E9PWX1		5.9	5.7E-04	7.6	1.5E-04	1.4	2.6E-01	0.2	6.9E-01
ENSMUST00000122219	killer cell lectin-like receptor, subfamily A, member 17 [Source:MGI Symbol;Acc:MGI:2180674]	Q8BJS9		-6.9	2.3E-04	-5.1	3.1E-02	-0.3	7.1E-01	0.8	7.2E-01
ENSMUST00000122222	castor zinc finger 1 [Source:MGI Symbol;Acc:MGI:1196251]	B1AS46		1.9	4.2E-03	-6.8	2.0E-05	-0.8	2.7E-02	-0.5	5.5E-01
ENSMUST00000122227	retinol dehydrogenase 12 [Source:MGI Symbol;Acc:MGI:1925224]			-4.6	8.7E-04	4.3	4.3E-04	0.1	9.3E-01	0.4	5.1E-01
ENSMUST00000122232	furin (paired basic amino acid cleaving enzyme) [Source:MGI Symbol;Acc:MGI:97513]		P23188	-8.3	7.8E-06	3.6	2.7E-02	-0.4	7.8E-01	0.3	7.4E-01
ENSMUST00000122235	vacuolar protein sorting 8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2146407]	D3YU67		4.4	2.0E-04	7.8	7.8E-05	-0.8	5.1E-01	-0.5	3.3E-01
ENSMUST00000122254	crystallin, zeta (quinone reductase)-like 1 [Source:MGI Symbol;Acc:MGI:1913859]	D3YU21		-4.8	1.2E-03	-1.6	5.3E-02	-0.4	4.1E-01	-0.8	3.1E-01
ENSMUST00000117450	BCL2/adenovirus E1B interacting protein 2 [Source:MGI Symbol;Acc:MGI:109327]	G5E8U9		-1.8	1.8E-01	-0.6	6.8E-01	-1.1	3.1E-01	-2.3	1.2E-01
ENSMUST00000122259	sphingosine phosphate lyase 1 [Source:MGI Symbol;Acc:MGI:1261415]		Q8R0X7	-7.9	6.8E-04	5.6	4.2E-02	-0.9	7.2E-01	1.8	2.4E-01
ENSMUST00000117456	nephronectin [Source:MGI Symbol;Acc:MGI:2148811]	D3YTX1		3.6	2.2E-01	2.2	4.3E-01	-2.1	4.7E-01	-0.7	7.2E-01
ENSMUST00000122290	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 [Source:MGI Symbol;Acc:MGI:1913296]	D3Z568		-6.5	1.9E-05	6.2	5.2E-04	-0.6	6.2E-01	0.3	6.6E-01
ENSMUST00000122300	kinesin light chain 1 [Source:MGI Symbol;Acc:MGI:107978]	Q7TNF4		-6.4	2.1E-04	6.8	1.5E-04	-1.0	4.2E-01	-0.4	5.7E-01
ENSMUST00000122302	Son DNA binding protein [Source:MGI Symbol;Acc:MGI:98353]	H9KV02		-10.0	1.6E-03	4.9	5.9E-04	-2.3	5.7E-02	-0.4	5.4E-01
ENSMUST00000122327	family with sequence similarity 160, member A2 [Source:MGI Symbol;Acc:MGI:1921599]		Q3U2I3	-3.4	2.3E-04	1.5	8.1E-02	-0.6	3.9E-01	-0.4	5.4E-01
ENSMUST00000122328	peroxidasin homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1916925]		Q3UQ28	8.8	1.2E-05	6.1	5.5E-03	-0.8	6.5E-01	1.5	1.4E-01
ENSMUST00000122333	kelch-like 14 [Source:MGI Symbol;Acc:MGI:1921249]		Q69ZK5	6.5	3.3E-05	-7.2	2.2E-04	0.5	2.2E-01	0.5	7.1E-01
ENSMUST00000122374	serine incorporator 2 [Source:MGI Symbol;Acc:MGI:1919132]	B2KFY0		6.8	6.0E-05	2.0	4.9E-02	-1.4	1.2E-01	-1.4	1.1E-01
ENSMUST00000117481				4.2	1.4E-01	6.3	5.0E-02	-0.2	9.5E-01	-2.3	2.0E-01
ENSMUST00000117483				-1.5	2.3E-01	-0.4	7.7E-01	-0.2	8.1E-01	-1.3	3.9E-01
ENSMUST00000122377	transmembrane protease, serine 11d [Source:MGI Symbol;Acc:MGI:2385221]		Q8VHK8	6.1	2.0E-05	6.9	1.2E-04	-0.6	6.2E-01	-0.6	3.6E-01
ENSMUST00000117486	ficolin B [Source:MGI Symbol;Acc:MGI:1341158]	Q3U9R5		-2.7	1.2E-01	-2.6	1.6E-01	-0.4	7.3E-01	-0.5	8.0E-01
ENSMUST00000122386	insulin-like growth factor 1 [Source:MGI Symbol;Acc:MGI:96432]	Q4VJC0	P05017	7.1	9.0E-05	-5.0	3.8E-03	0.0	9.6E-01	-0.1	9.5E-01
ENSMUST00000122389	disrupted in schizophrenia 1 [Source:MGI Symbol;Acc:MGI:2447658]		Q811T9	6.6	2.0E-06	6.1	1.1E-03	-0.7	6.4E-01	-1.1	1.9E-01
ENSMUST00000122402	FERM, RhoGEF and pleckstrin domain protein 2 [Source:MGI Symbol;Acc:MGI:2385126]	D3Z4C0		6.3	8.1E-05	3.6	3.6E-02	0.2	9.0E-01	1.0	3.3E-01
ENSMUST00000122410	thyroid hormone receptor interactor 4 [Source:MGI Symbol;Acc:MGI:1928469]		Q9QXN3	-7.7	2.6E-05	-2.0	2.5E-02	1.1	2.5E-02	-0.7	3.7E-01
ENSMUST00000122424	family with sequence similarity 20, member B [Source:MGI Symbol;Acc:MGI:2443990]		Q8VCS3	-6.5	1.7E-04	-2.9	3.8E-02	-0.6	3.7E-01	-1.8	2.0E-01
ENSMUST00000122426	SH2B adaptor protein 3 [Source:MGI Symbol;Acc:MGI:893598]		O09039	3.4	1.4E-03	5.9	1.5E-02	-0.5	8.2E-01	-1.4	2.5E-01
ENSMUST00000122432	zinc finger, imprinted 1 [Source:MGI Symbol;Acc:MGI:1341879]	Q8C393		7.1	2.1E-04	5.8	6.8E-04	-0.6	6.2E-01	0.1	8.8E-01
ENSMUST00000122441	ubiquitin-conjugating enzyme E2Q (putative) 2 [Source:MGI Symbol;Acc:MGI:2388672]		Q8K2Z8	-2.2	1.1E-02	4.9	4.7E-04	-0.6	5.6E-01	-1.4	5.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000122464	cerebellin 2 precursor protein [Source:MGI Symbol;Acc:MGI:88282]		Q8BGU2	6.4	1.3E-04	2.9	6.7E-04	1.0	6.8E-02	0.0	1.0E+00
ENSMUST00000122808	chemokine (C-X-C motif) ligand 11 [Source:MGI Symbol;Acc:MGI:1860203]			8.0	3.4E-05	5.0	5.6E-04	-0.9	3.6E-01	-0.1	9.1E-01
ENSMUST00000117516				-1.2	6.3E-01	0.9	7.7E-01	0.6	8.1E-01	-1.5	5.9E-01
ENSMUST00000117518	acyl-Coenzyme A dehydrogenase, short/branched chain [Source:MGI Symbol;Acc:MGI:1914135]	E9Q5L3		0.6	5.5E-01	0.0	1.0E+00	-0.3	7.6E-01	0.3	7.9E-01
ENSMUST00000122865	SIK family kinase 3 [Source:MGI Symbol;Acc:MGI:2446296]	F6U8X4		-2.3	1.8E-03	6.5	2.8E-04	-0.5	7.1E-01	-0.8	2.5E-01
ENSMUST00000117534	ST3 beta-galactoside alpha-2,3-sialyltransferase 2 [Source:MGI Symbol;Acc:MGI:99427]	D3Z3V2		1.0	3.5E-01	1.9	1.4E-01	-0.1	9.1E-01	-1.0	3.7E-01
ENSMUST00000122872	piggyBac transposable element derived 1 [Source:MGI Symbol;Acc:MGI:2441675]	E9Q2C6		6.4	2.1E-02	5.7	2.3E-02	-0.8	7.4E-01	1.9	1.5E-01
ENSMUST00000122876	proline dehydrogenase (oxidase) 2 [Source:MGI Symbol;Acc:MGI:1929093]	F6ZBU4		6.4	2.5E-05	-6.2	2.3E-03	-1.5	3.9E-02	-0.4	8.2E-01
ENSMUST00000117537	F-box and leucine-rich repeat protein 2 [Source:MGI Symbol;Acc:MGI:1919429]	Q4VA21	Q8BH16	2.2	2.8E-01	-2.3	3.1E-01	-4.2	1.9E-02	0.3	9.0E-01
ENSMUST00000122885	, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3 [Source:MGI Symbol;Acc:MGI:135	F6ZFB8		-5.2	2.0E-02	-2.9	1.7E-02	-1.0	1.3E-01	-0.3	7.9E-01
ENSMUST00000117542				-4.4	7.3E-02	1.9	6.2E-01	6.4	3.8E-02	0.2	9.6E-01
ENSMUST00000122899	protein phosphatase 1, regulatory subunit 18 [Source:MGI Symbol;Acc:MGI:1923698]		Q8BQ30	-3.2	8.8E-03	6.5	1.3E-02	-0.8	7.4E-01	-0.7	5.9E-01
ENSMUST00000117546				-0.2	9.0E-01	-3.5	1.2E-01	-2.2	1.6E-01	1.1	5.9E-01
ENSMUST00000122902	patatin-like phospholipase domain containing 8 [Source:MGI Symbol;Acc:MGI:1914702]	E9PXB0		8.0	7.2E-07	-2.6	1.6E-02	0.0	9.8E-01	-0.9	3.6E-01
ENSMUST00000122912	cysteine-serine-rich nuclear protein 3 [Source:MGI Symbol;Acc:MGI:1925021]		P59055	9.7	1.6E-06	-0.2	7.3E-01	-3.4	3.0E-04	-0.8	2.1E-01
ENSMUST00000122922	regulatory factor X, 6 [Source:MGI Symbol;Acc:MGI:2445208]		Q8C7R7	6.5	1.8E-02	-3.6	2.6E-04	0.6	1.1E-01	0.1	9.3E-01
ENSMUST00000122941	zinc finger RNA binding protein [Source:MGI Symbol;Acc:MGI:1341890]		O88532	-3.6	2.4E-05	-5.2	1.8E-03	0.7	1.9E-01	-0.5	7.2E-01
ENSMUST00000122943	porcupine homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1890212]	S4R2F8		5.6	3.3E-02	1.9	2.7E-01	0.8	5.5E-01	4.1	8.6E-03
ENSMUST00000122960	ankyrin repeat domain 35 [Source:MGI Symbol;Acc:MGI:2442590]	D6RGN5		5.4	1.5E-02	-9.0	2.3E-04	-0.8	2.0E-01	1.2	4.7E-01
ENSMUST00000117563				-2.4	2.6E-01	-4.2	1.7E-01	-1.4	4.1E-01	0.4	8.8E-01
ENSMUST00000122965	elongation protein 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925016]		Q9ER73	2.8	6.0E-03	7.7	1.1E-03	-1.4	4.5E-01	0.5	5.6E-01
ENSMUST00000122967	G protein-coupled receptor, family C, group 5, member C [Source:MGI Symbol;Acc:MGI:1917605]	E9PZP1		8.4	1.0E-05	5.9	2.7E-03	-0.7	6.8E-01	-0.2	8.2E-01
ENSMUST00000122970	solute carrier family 2 (facilitated glucose transporter), member 9 [Source:MGI Symbol;Acc:MGI:2152844]	D6REU9		-3.6	7.5E-03	6.5	3.9E-04	0.2	8.4E-01	0.1	9.4E-01
ENSMUST00000122985	N-acetyltransferase 6 [Source:MGI Symbol;Acc:MGI:1888902]	B7ZCE0		8.8	1.9E-05	5.5	9.3E-04	0.6	6.4E-01	0.3	6.5E-01
ENSMUST00000122996	makorin, ring finger protein, 1 [Source:MGI Symbol;Acc:MGI:1859353]	F6S742		-5.8	5.2E-04	-6.8	2.0E-05	-0.8	2.7E-02	-0.5	5.5E-01
ENSMUST00000122999	dystrophia myotonica-protein kinase [Source:MGI Symbol;Acc:MGI:94906]	D3YYG5		5.2	1.1E-02	7.0	1.9E-04	-0.6	6.2E-01	0.3	6.9E-01
ENSMUST00000123006	pleckstrin homology domain containing, family O member 1 [Source:MGI Symbol;Acc:MGI:1914470]	F6XQM2		-4.0	7.7E-03	5.7	2.6E-03	-0.2	9.2E-01	0.6	4.9E-01
ENSMUST00000123015	polynucleotide kinase 3'- phosphatase [Source:MGI Symbol;Acc:MGI:1891698]			-9.8	1.9E-04	8.5	9.7E-06	0.5	6.2E-01	0.2	6.4E-01
ENSMUST00000123027	tumor necrosis factor receptor superfamily, member 8 [Source:MGI Symbol;Acc:MGI:99908]	D6RHK4		4.7	3.3E-02	-6.6	1.2E-04	-0.4	2.9E-01	-0.8	4.7E-01
ENSMUST00000123091	homeobox B3 [Source:MGI Symbol;Acc:MGI:96184]	G3UZC2		7.7	2.6E-05	3.9	2.3E-02	0.0	9.8E-01	0.3	7.6E-01
ENSMUST00000123097	hexokinase 3 [Source:MGI Symbol;Acc:MGI:2670962]	E9Q8S8		-7.4	5.7E-03	8.5	1.2E-04	0.4	7.9E-01	0.5	4.3E-01
ENSMUST00000123123	pleckstrin homology-like domain, family B, member 1 [Source:MGI Symbol;Acc:MGI:2143230]	F7CB18		7.2	6.4E-04	3.6	8.1E-03	0.5	6.3E-01	-0.2	7.7E-01
ENSMUST00000123179	predicted gene 12666 [Source:MGI Symbol;Acc:MGI:3650864]	A2AMD0		3.1	9.1E-03	-1.7	1.9E-01	0.7	3.7E-01	-2.6	9.5E-02
ENSMUST00000123187	adenosine deaminase, RNA-specific, B2 [Source:MGI Symbol;Acc:MGI:2151118]	Q6PB89		8.3	4.6E-03	-3.0	1.6E-01	1.2	3.1E-01	-0.6	7.6E-01
ENSMUST00000117600	high mobility group AT-hook 1 [Source:MGI Symbol;Acc:MGI:96160]	Q566K0	P17095	-0.1	9.6E-01	-2.9	1.5E-01	-1.4	3.1E-01	1.5	4.3E-01
ENSMUST00000123202	dolichyl pyrophosphate phosphatase 1 [Source:MGI Symbol;Acc:MGI:1914093]			5.1	2.0E-02	8.5	1.7E-04	-0.7	6.4E-01	1.0	2.0E-01
ENSMUST00000117611	phospholipase D family, member 3 [Source:MGI Symbol;Acc:MGI:1333782]		O35405	4.1	1.3E-01	5.4	1.8E-01	0.9	8.0E-01	-0.4	8.7E-01
ENSMUST00000123227	abhydrolase domain containing 11 [Source:MGI Symbol;Acc:MGI:1916008]			-2.2	1.0E-02	7.5	4.6E-04	-0.5	7.3E-01	-1.5	8.3E-02
ENSMUST00000123228	ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A [Source:MGI Symbol;Acc:MGI:	F6WLW8		5.7	1.7E-04	3.4	6.3E-03	-1.3	2.0E-01	-0.5	4.9E-01
ENSMUST00000123237	ubiquitin specific peptidase 33 [Source:MGI Symbol;Acc:MGI:2159711]	D6RES0		6.5	1.6E-04	6.1	7.9E-04	-0.6	6.4E-01	-0.2	7.9E-01
ENSMUST00000117624	tetratricopeptide repeat domain 13 [Source:MGI Symbol;Acc:MGI:2384573]	D3YVV0		-2.5	4.7E-02	-3.8	4.6E-02	0.3	7.8E-01	1.6	3.5E-01
ENSMUST00000123256	ethylmalonic aciduria (cobalamin deficiency) type B homolog (human) [Source:MGI Symbol;Acc:MGI:192494		Q9D273	5.7	7.7E-04	7.4	6.7E-04	0.1	9.7E-01	-0.3	7.1E-01
ENSMUST00000117633	Son DNA binding protein [Source:MGI Symbol;Acc:MGI:98353]	H9KV00		-0.4	8.9E-01	-4.0	2.4E-01	-2.8	2.5E-01	0.8	8.2E-01
ENSMUST00000117634	tetraspanin 4 [Source:MGI Symbol;Acc:MGI:1928097]	Q4FJW7	Q9DCK3	-0.9	5.5E-01	-2.2	1.3E-01	-2.4	4.2E-02	-1.1	4.9E-01
ENSMUST00000123260	syntaxin binding protein 4 [Source:MGI Symbol;Acc:MGI:1342296]	F7AX23		5.9	7.8E-04	6.2	1.5E-03	-0.4	7.9E-01	-0.2	8.4E-01
ENSMUST00000123279	calcium and integrin binding 1 (calmyrin) [Source:MGI Symbol;Acc:MGI:1344418]	D3YY46		-4.5	9.6E-04	7.7	2.1E-02	2.5	3.8E-01	1.4	3.0E-01
ENSMUST00000123285	neuronal tyrosine-phophorylated phosphoinositide 3-kinase adaptor 2 [Source:MGI Symbol;Acc:MGI:2443135			9.2	1.1E-04	-4.0	2.6E-02	0.4	5.9E-01	-0.1	9.3E-01
ENSMUST00000117645	solute carrier family 17 (anion/sugar transporter), member 5 [Source:MGI Symbol;Acc:MGI:1924105]		Q8BN82	2.1	3.5E-01	7.9	2.1E-02	3.4	2.5E-01	-2.4	2.1E-01
ENSMUST00000123293	nuclear receptor coactivator 6 [Source:MGI Symbol;Acc:MGI:1929915]	A2AQM9		8.4	3.2E-03	5.6	5.3E-03	-0.3	8.4E-01	-1.8	9.1E-02
ENSMUST00000117648	tetratricopeptide repeat domain 3 [Source:MGI Symbol;Acc:MGI:1276539]	G5E8T2		1.0	2.2E-01	-2.1	7.1E-02	-1.6	4.5E-02	1.5	1.6E-01
ENSMUST00000123296	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 [Source:MGI Symbol;Acc:MGI:1917566]	Q569N0	Q9CR21	6.8	2.7E-06	6.7	2.7E-04	-1.5	2.7E-01	-0.7	3.3E-01
ENSMUST00000123301	STE20-related kinase adaptor beta [Source:MGI Symbol;Acc:MGI:2144047]			-7.4	5.2E-05	-7.2	1.0E-03	0.1	9.2E-01	2.2	1.8E-01
ENSMUST00000117655				4.3	4.8E-02	6.6	4.1E-02	1.7	5.3E-01	-0.6	7.3E-01
ENSMUST00000123311	Yip1 domain family, member 3 [Source:MGI Symbol;Acc:MGI:106280]	D3YXM6		-4.0	1.4E-02	7.2	2.1E-05	0.0	9.8E-01	-0.6	2.4E-01
ENSMUST00000117661	stromal interaction molecule 2 [Source:MGI Symbol;Acc:MGI:2151156]	A5CVE4	P83093	1.6	8.0E-02	3.3	2.5E-02	1.9	1.2E-01	0.2	8.1E-01
ENSMUST00000117662	ankyrin 1, erythroid [Source:MGI Symbol;Acc:MGI:88024]	E9QNT8		5.7	3.8E-02	5.2	7.1E-02	-0.5	8.5E-01	-0.1	9.5E-01
ENSMUST00000117664				-5.3	6.5E-02	-7.5	3.9E-02	-3.1	3.5E-02	-1.0	7.9E-01
ENSMUST00000123316	glutaminyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1915851]	Q8R1V9		-6.7	7.9E-05	7.4	9.9E-06	-1.1	2.5E-01	-0.2	6.3E-01
ENSMUST00000123320	cathepsin H [Source:MGI Symbol;Acc:MGI:107285]	D7UEQ9		-9.0	2.9E-06	6.8	2.5E-04	0.1	9.5E-01	0.6	4.1E-01
ENSMUST00000123325	ankyrin repeat domain 33B [Source:MGI Symbol;Acc:MGI:1917904]		Q3U0L2	-7.3	1.6E-02	5.6	7.0E-04	0.6	5.8E-01	-1.1	1.7E-01
ENSMUST00000123330	glutamate decarboxylase 1 [Source:MGI Symbol;Acc:MGI:95632]	D3Z5S3		6.2	9.8E-04	7.1	1.1E-03	-0.8	6.4E-01	-0.2	8.5E-01
ENSMUST00000123349	GRAM domain containing 4 [Source:MGI Symbol;Acc:MGI:2676308]	D6RET7		5.1	1.3E-02	7.7	3.9E-05	-0.5	6.5E-01	-1.1	6.9E-02
ENSMUST00000123362	methyl CpG binding protein 2 [Source:MGI Symbol;Acc:MGI:99918]	D3YY81		-4.2	6.2E-03	2.2	5.3E-01	-1.0	7.3E-01	4.2	1.5E-01
ENSMUST00000123370	MLX interacting protein-like [Source:MGI Symbol;Acc:MGI:1927999]	F6Q4B6		6.1	5.0E-04	2.9	6.4E-03	-0.3	6.5E-01	-0.9	2.2E-01
ENSMUST00000123372	ansient receptor potential cation channel, subfamily C, member 2 readthrough [Source:MGI Symbol;Acc:MGI:	E9PVR2		5.6	1.9E-02	6.9	8.2E-04	-0.7	6.6E-01	0.4	6.5E-01
ENSMUST00000123387	metallophosphoesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:106316]	F2Z3Z7		7.9	1.2E-03	4.3	2.4E-04	-1.1	1.4E-01	-0.7	2.0E-01
ENSMUST00000123410	lipoxygenase homology domains 1 [Source:MGI Symbol;Acc:MGI:1914609]	F6XPZ0		6.1	1.7E-02	0.5	7.3E-01	0.8	4.9E-01	-3.1	6.1E-02
ENSMUST00000123412	zinc finger, matrin type 4 [Source:MGI Symbol;Acc:MGI:2443497]		Q8BZ94	5.5	1.4E-03	6.7	9.9E-05	-0.6	6.1E-01	-0.8	2.1E-01
ENSMUST00000117713	cell death inducing Trp53 target 1 [Source:MGI Symbol;Acc:MGI:1913876]		Q9DB75	-1.7	2.4E-01	-2.3	1.7E-01	-1.7	1.0E-01	-1.1	5.4E-01
ENSMUST00000117718	MAS-related GPR, member F [Source:MGI Symbol;Acc:MGI:2384823]	D3Z3Y0		5.1	3.7E-02	4.7	1.7E-02	-3.0	1.8E-01	-2.6	7.1E-02
ENSMUST00000123413	eukaryotic translation initiation factor 4A2 [Source:MGI Symbol;Acc:MGI:106906]	Q8BTU6		-7.7	1.2E-03	4.5	3.1E-06	0.4	2.9E-01	0.2	4.5E-01
ENSMUST00000123415	6 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:109	D3Z5H6		6.3	1.4E-03	8.3	1.1E-03	-0.6	7.8E-01	1.3	1.5E-01
ENSMUST00000123418	ankyrin 1, erythroid [Source:MGI Symbol;Acc:MGI:88024]	D6RJ51		7.5	1.7E-04	3.6	8.3E-02	-4.6	5.2E-02	0.0	9.9E-01
ENSMUST00000117728	SKI-like [Source:MGI Symbol;Acc:MGI:106203]	D3Z7C5		0.1	9.3E-01	1.6	4.8E-01	1.4	3.7E-01	-0.1	9.7E-01
ENSMUST00000117731	RNA binding protein, fox-1 homolog (C. elegans) 3 [Source:MGI Symbol;Acc:MGI:106368]		Q8BIF2	4.1	5.4E-02	6.7	9.5E-03	-0.4	8.8E-01	-3.0	3.4E-02
ENSMUST00000117735	mitochondrial tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2142572]	D3Z7B3		-0.9	1.3E-01	-1.5	4.7E-02	-0.7	1.6E-01	-0.1	9.3E-01
ENSMUST00000123434	phoinositide-interacting regulator of transient receptor potential channels [Source:MGI Symbol;Acc:MGI:2443		Q8BFY0	7.4	2.5E-05	6.0	4.9E-03	-0.6	7.2E-01	1.0	3.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000123453	Gem-interacting protein [Source:MGI Symbol;Acc:MGI:1926066]		Q6PGG2	-4.6	4.2E-03	9.0	4.8E-05	-0.7	5.9E-01	0.2	7.4E-01
ENSMUST00000123454	shisa family member 6 [Source:MGI Symbol;Acc:MGI:2685725]	F6VQZ6		9.9	8.6E-06	-5.5	3.8E-02	1.3	1.6E-01	2.8	2.4E-01
ENSMUST00000123460	predicted gene 13235 [Source:MGI Symbol;Acc:MGI:3649925]	L7MUC9		5.3	1.2E-03	5.7	6.9E-04	-1.0	4.4E-01	0.3	6.2E-01
ENSMUST00000123487	protein O-fucosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2153207]	E9PZ15		8.5	4.0E-04	-8.5	5.9E-03	0.3	7.5E-01	-1.0	7.1E-01
ENSMUST00000117759	transmembrane emp24 protein transport domain containing 5 [Source:MGI Symbol;Acc:MGI:1921586]	Q3V440		0.9	6.1E-01	-2.8	1.6E-01	-4.0	1.5E-02	-0.3	8.8E-01
ENSMUST00000123491	dynein, axonemal, light chain 1 [Source:MGI Symbol;Acc:MGI:1921462]		Q05A62	7.0	4.8E-07	-6.5	9.5E-02	2.2	1.1E-01	1.6	6.7E-01
ENSMUST00000123495	4HAUS augmin-like complex, subunit 8 [Source:MGI Symbol;Acc:MGI:1923728]	D6RCV2		6.2	5.8E-05	7.6	4.0E-05	-0.6	6.2E-01	-1.0	8.6E-02
ENSMUST00000117766	mitochondrial ribosomal protein L1 [Source:MGI Symbol;Acc:MGI:2137202]		Q99N96	3.2	2.0E-01	-2.7	3.6E-01	-4.4	7.6E-02	1.5	5.8E-01
ENSMUST00000123506	myotubularin related protein 3 [Source:MGI Symbol;Acc:MGI:1921552]	R4GML8		-7.2	6.8E-04	7.1	6.3E-04	-0.7	6.4E-01	0.0	9.8E-01
ENSMUST00000123519	asparagine synthetase domain containing 1 [Source:MGI Symbol;Acc:MGI:1917646]	Q3TGY6		-6.7	3.9E-05	-4.3	2.5E-02	-1.5	1.1E-01	-0.9	6.3E-01
ENSMUST00000117780	vesicle-associated membrane protein 2 [Source:MGI Symbol;Acc:MGI:1313277]	B0QZN5		-1.2	2.3E-01	-2.1	1.4E-01	0.2	8.2E-01	1.2	3.7E-01
ENSMUST00000117781	transmembrane channel-like gene family 8 [Source:MGI Symbol;Acc:MGI:2669037]	B0QZP7		1.7	3.9E-01	-2.3	3.4E-01	-3.4	5.6E-02	0.6	7.9E-01
ENSMUST00000117782	ADAMTS-like 4 [Source:MGI Symbol;Acc:MGI:2389008]		Q80T21	-0.8	5.1E-01	2.2	1.8E-01	1.3	2.9E-01	-1.7	2.5E-01
ENSMUST00000123534	solute carrier family 35, member F4 [Source:MGI Symbol;Acc:MGI:1922538]		Q8BZK4	6.6	1.7E-04	3.2	1.6E-03	0.0	9.5E-01	0.3	5.8E-01
ENSMUST00000123552	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16 [Source:MGI Symbol;Acc:M	D6RGS8		8.1	1.9E-03	-2.3	2.7E-01	1.1	3.8E-01	-0.6	7.7E-01
ENSMUST00000123555	poly (ADP-ribose) polymerase family, member 3 [Source:MGI Symbol;Acc:MGI:1891258]	Q8CFB8		-4.7	1.0E-03	6.3	2.3E-04	-0.6	6.3E-01	0.0	9.5E-01
ENSMUST00000117786	casein kinase 1, epsilon [Source:MGI Symbol;Acc:MGI:1351660]		Q9JMK2	-1.0	1.3E-01	0.4	6.4E-01	0.7	2.2E-01	-0.6	3.9E-01
ENSMUST00000123557	suppression of tumorigenicity 14 (colon carcinoma) [Source:MGI Symbol;Acc:MGI:1338881]	D6RIN3		6.4	1.6E-03	5.9	8.5E-04	-0.6	6.3E-01	0.0	9.5E-01
ENSMUST00000123558	neighbor of Brca1 gene 1 [Source:MGI Symbol;Acc:MGI:108498]	Q05BC8		-5.9	1.1E-03	4.1	7.0E-03	-0.3	7.9E-01	0.7	3.9E-01
ENSMUST00000123583	lectin, mannose-binding 2-like [Source:MGI Symbol;Acc:MGI:2443010]	J3QPK9		5.8	1.4E-05	6.5	1.4E-04	-0.6	5.9E-01	-1.6	3.0E-02
ENSMUST00000123594	OTU domain, ubiquitin aldehyde binding 1 [Source:MGI Symbol;Acc:MGI:2147616]	D3YWF6		4.2	3.3E-02	-0.6	7.5E-01	1.0	5.2E-01	-3.3	1.5E-01
ENSMUST00000123614	prostaglandin reductase 2 [Source:MGI Symbol;Acc:MGI:1916372]		Q8VDQ1	-1.8	1.4E-02	6.1	8.7E-04	-0.5	6.9E-01	-0.1	9.4E-01
ENSMUST00000117801	adenylate cyclase 9 [Source:MGI Symbol;Acc:MGI:108450]		P51830	6.6	6.0E-02	6.3	8.6E-02	-0.8	8.2E-01	-0.5	8.0E-01
ENSMUST00000123657	repaiross-complementing rodent repair deficiency, complementation group 8 [Source:MGI Symbol;Acc:MGI:1	D6RET0		4.8	9.1E-03	6.7	1.9E-06	0.1	9.0E-01	-0.6	1.2E-01
ENSMUST00000117805	guanine nucleotide binding protein (G protein), gamma 7 [Source:MGI Symbol;Acc:MGI:95787]	Q3UGN1	Q61016	3.9	1.1E-01	1.9	5.3E-01	-0.5	8.6E-01	1.5	5.1E-01
ENSMUST00000123666	Tia1 cytotoxic granule-associated RNA binding protein-like 1 [Source:MGI Symbol;Acc:MGI:107913]	D6RGU1		-2.8	3.0E-02	2.6	4.3E-01	-0.9	7.6E-01	3.9	1.3E-01
ENSMUST00000123680	phosphatidylinositol glycan anchor biosynthesis, class Y-like [Source:MGI Symbol;Acc:MGI:1913518]		P0C1P0	-5.0	7.2E-04	-4.2	2.2E-03	0.7	1.6E-01	-0.7	5.6E-01
ENSMUST00000117814	calpain 10 [Source:MGI Symbol;Acc:MGI:1344392]	Q9CPY2		0.3	7.2E-01	1.3	1.8E-01	-0.4	6.5E-01	-1.4	1.1E-01
ENSMUST00000117818	clustered mitochondria (cluA/CLU1) homolog [Source:MGI Symbol;Acc:MGI:1921398]	Z4YLI8		1.4	4.1E-01	3.6	7.2E-02	-0.7	6.8E-01	-2.8	1.1E-01
ENSMUST00000123682	aminoadipate-semialdehyde dehydrogenase [Source:MGI Symbol;Acc:MGI:2442517]	E9PUJ1		3.5	2.2E-03	7.0	1.9E-04	0.2	8.4E-01	0.4	5.7E-01
ENSMUST00000117828	abhydrolase domain containing 3 [Source:MGI Symbol;Acc:MGI:2147183]	D3Z6Y2		3.7	8.4E-02	5.0	3.5E-02	-0.5	8.0E-01	-1.8	2.4E-01
ENSMUST00000123684	frataxin [Source:MGI Symbol;Acc:MGI:1096879]	E9Q2P9		6.5	7.0E-03	-0.7	5.4E-01	1.5	8.5E-02	-1.1	3.7E-01
ENSMUST00000123690	5-azacytidine induced gene 2 [Source:MGI Symbol;Acc:MGI:1351332]	F6SY96		-3.7	9.2E-03	-4.5	2.6E-03	1.3	2.6E-02	-2.0	1.6E-01
ENSMUST00000123708	interferon activated gene 203 [Source:MGI Symbol;Acc:MGI:96428]	E9PUG6		8.8	7.5E-03	4.0	1.5E-02	-2.2	1.6E-01	-1.9	1.0E-01
ENSMUST00000123709	Dmx-like 2 [Source:MGI Symbol;Acc:MGI:2444630]	F6RYL8		-7.3	2.3E-03	6.1	7.5E-04	-1.0	4.7E-01	-1.1	1.8E-01
ENSMUST00000123716	olute carrier family 16 (monocarboxylic acid transporters), member 11 [Source:MGI Symbol;Acc:MGI:266370	D6RDF0		6.1	1.3E-02	5.8	9.8E-03	-0.2	9.0E-01	-0.4	7.5E-01
ENSMUST00000123726	zinc finger protein 207 [Source:MGI Symbol;Acc:MGI:1340045]	M0QWF0		-1.9	1.5E-02	5.7	9.6E-04	-0.6	6.4E-01	0.0	9.5E-01
ENSMUST00000123727	cytoplasmic polyadenylation element binding protein 3 [Source:MGI Symbol;Acc:MGI:2443075]	D3Z1R6		5.6	2.9E-04	5.0	4.6E-03	-0.6	6.7E-01	-0.9	3.1E-01
ENSMUST00000123731	remodeling and spacing factor 1 [Source:MGI Symbol;Acc:MGI:2682305]			-6.1	3.3E-04	7.2	3.7E-05	-1.3	2.4E-01	0.8	1.6E-01
ENSMUST00000123750	PQ loop repeat containing 1 [Source:MGI Symbol;Acc:MGI:1914193]		Q80XM9	-6.5	1.3E-04	5.2	3.5E-03	-1.3	3.4E-01	0.2	8.2E-01
ENSMUST00000123811	mcf.2 transforming sequence-like [Source:MGI Symbol;Acc:MGI:103263]	F6WPM5		-3.3	5.9E-03	7.2	6.1E-04	1.3	3.7E-01	0.5	4.9E-01
ENSMUST00000123826	suppressor of cytokine signaling 6 [Source:MGI Symbol;Acc:MGI:1924885]		Q9JLY0	-4.2	7.3E-03	-6.3	2.7E-03	-2.3	4.3E-03	0.1	9.5E-01
ENSMUST00000123864	in homology domain containing, family H (with MyTH4 domain) member 3 [Source:MGI Symbol;Acc:MGI:2	A2A4L0		5.2	8.5E-04	5.6	9.1E-03	1.2	4.7E-01	-0.3	7.3E-01
ENSMUST00000123879	thioredoxin domain containing 16 [Source:MGI Symbol;Acc:MGI:1917811]		Q7TN22	6.8	4.4E-05	2.8	9.9E-02	-0.4	7.6E-01	2.8	3.5E-02
ENSMUST00000123914	GRAM domain containing 2 [Source:MGI Symbol;Acc:MGI:3528937]	D3YVC0		4.1	1.4E-02	5.4	6.5E-04	-1.5	2.2E-01	-0.4	5.9E-01
ENSMUST00000123921	Prkr interacting protein 1 (IL11 inducible) [Source:MGI Symbol;Acc:MGI:1914051]	F7ATT9		-3.0	7.7E-03	5.7	3.1E-03	-0.6	6.9E-01	0.3	7.3E-01
ENSMUST00000123924	ankyrin repeat, family A (RFXANK-like), 2 [Source:MGI Symbol;Acc:MGI:1915808]	Q6NZJ1		-6.1	5.1E-03	-6.4	2.4E-04	0.7	9.9E-02	-0.9	4.5E-01
ENSMUST00000123926	in, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B [Source:MGI Symbol;Acc:M(	M0QWQ7		6.5	4.6E-04	2.3	3.2E-01	0.4	8.4E-01	2.2	2.5E-01
ENSMUST00000123932	SAM domain and HD domain, 1 [Source:MGI Symbol;Acc:MGI:1927468]	E0CXZ5		-3.3	4.4E-03	3.2	5.9E-03	0.0	9.7E-01	-0.9	2.6E-01
ENSMUST00000123941	GTF2I repeat domain containing 2 [Source:MGI Symbol;Acc:MGI:2149780]	D6RI26		1.3	2.8E-02	0.8	3.4E-01	-0.8	2.1E-01	0.1	9.2E-01
ENSMUST00000123952	cilia and flagella associated protein 74 [Source:MGI Symbol;Acc:MGI:1917130]	G3UWF6		8.1	1.2E-04	-5.3	9.2E-03	1.3	5.3E-02	0.1	9.7E-01
ENSMUST00000123989	FYVE, RhoGEF and PH domain containing 2 [Source:MGI Symbol;Acc:MGI:1347084]	E9PVB8		5.4	2.5E-03	-1.4	4.7E-02	0.5	2.1E-01	-0.9	2.0E-01
ENSMUST00000123993	ankyrin repeat domain 24 [Source:MGI Symbol;Acc:MGI:1890394]	D6RE46		8.6	1.0E-06	4.4	1.1E-03	-1.7	1.3E-01	-0.7	2.8E-01
ENSMUST00000124024	small ubiquitin-like modifier 3 [Source:MGI Symbol;Acc:MGI:1336201]	G3UXQ9		-2.2	1.6E-02	8.8	1.6E-02	-1.0	7.6E-01	1.5	2.7E-01
ENSMUST00000124035	ribosomal protein S19 [Source:MGI Symbol;Acc:MGI:1333780]	D3Z5R8		4.1	2.4E-02	5.7	1.4E-03	-0.6	6.4E-01	0.1	8.5E-01
ENSMUST00000124051	opticin [Source:MGI Symbol;Acc:MGI:2151113]	G3UVW2		6.7	7.9E-05	4.7	7.7E-04	-0.7	4.8E-01	-1.2	1.1E-01
ENSMUST00000124065	RAD51 associated protein 2 [Source:MGI Symbol;Acc:MGI:3644580]	G3UW63		6.2	5.9E-04	2.3	9.4E-02	-4.5	9.2E-03	-2.3	6.7E-02
ENSMUST00000124077	histone deacetylase 5 [Source:MGI Symbol;Acc:MGI:1333784]	D6RH93		-3.5	2.1E-02	-1.2	1.8E-01	-0.1	8.9E-01	-0.7	4.4E-01
ENSMUST00000124093	synaptonemal complex protein 2-like [Source:MGI Symbol;Acc:MGI:2685114]	D3YWV8		6.3	1.2E-04	6.2	1.4E-02	-0.8	7.4E-01	-1.3	3.3E-01
ENSMUST00000124120	ubiquitin-conjugating enzyme E2E 3 [Source:MGI Symbol;Acc:MGI:107412]	B2FDH7		7.4	8.2E-05	2.2	2.1E-02	-4.4	1.8E-03	-2.9	7.5E-03
ENSMUST00000124189	transient receptor potential cation channel, subfamily C, member 2 [Source:MGI Symbol;Acc:MGI:109527]		Q9R244	4.3	1.1E-03	6.2	2.4E-03	2.0	1.9E-01	-0.5	5.6E-01
ENSMUST00000124200	tafazzin [Source:MGI Symbol;Acc:MGI:109626]	Q810E8		-8.1	5.0E-05	3.3	2.0E-03	-4.8	1.0E-03	-1.8	1.9E-02
ENSMUST00000124221	solute carrier family 22 (organic cation transporter), member 21 [Source:MGI Symbol;Acc:MGI:1929481]	D6RDB6		6.4	1.6E-02	2.6	1.4E-01	-1.5	3.6E-01	0.1	9.1E-01
ENSMUST00000124222	special AT-rich sequence binding protein 1 [Source:MGI Symbol;Acc:MGI:105084]	D3Z4F8		6.2	8.6E-04	5.0	1.7E-04	1.6	5.7E-02	-0.8	1.8E-01
ENSMUST00000124226	armadillo repeat containing, X-linked 4 [Source:MGI Symbol;Acc:MGI:2147887]	E9PWM3		2.8	8.3E-04	0.5	5.3E-01	-0.3	6.9E-01	1.7	4.3E-02
ENSMUST00000124228	fibroblast growth factor receptor 1 [Source:MGI Symbol;Acc:MGI:95522]	D3Z4V6		7.2	2.3E-04	5.7	3.8E-04	0.8	4.4E-01	-0.9	2.4E-01
ENSMUST00000124231	spectrin beta, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98388]	A0A0A0MQG2		6.2	1.3E-02	6.2	7.4E-04	-1.3	3.7E-01	0.3	6.7E-01
ENSMUST00000124239	SH2 domain containing 5 [Source:MGI Symbol;Acc:MGI:2446215]	A2AM66		4.8	2.2E-02	-5.9	5.2E-03	0.8	1.7E-01	-0.6	7.3E-01
ENSMUST00000117952				-0.3	6.8E-01	0.0	9.7E-01	-0.1	9.4E-01	-0.3	7.0E-01
ENSMUST00000124248	protein phosphatase 1, regulatory (inhibitor) subunit 12C [Source:MGI Symbol;Acc:MGI:1924258]	F6XWD4		-6.9	3.5E-04	6.0	3.8E-04	-0.6	6.0E-01	0.3	6.2E-01
ENSMUST00000117956	zinc finger and BTB domain containing 7a [Source:MGI Symbol;Acc:MGI:1335091]		O88939	2.4	2.5E-01	0.8	7.6E-01	-0.7	7.2E-01	0.9	6.8E-01
ENSMUST00000124250	solute carrier family 25, member 36 [Source:MGI Symbol;Acc:MGI:1924909]	F6R114		2.5	2.4E-02	-2.4	5.7E-02	-0.4	5.1E-01	-1.1	3.6E-01
ENSMUST00000124266	olute carrier family 25 (mitochondrial carrier, glutamate), member 22 [Source:MGI Symbol;Acc:MGI:1915517	E9Q579		-4.3	1.5E-02	6.5	2.5E-04	-0.5	6.5E-01	-1.1	1.2E-01
ENSMUST00000124268	ras responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:2443664]	Q3UHQ4		3.5	4.0E-04	5.4	1.1E-02	1.3	4.6E-01	0.2	8.5E-01
ENSMUST00000124270	nebulette [Source:MGI Symbol;Acc:MGI:1921353]	B7ZCI2		6.8	6.3E-04	7.1	7.9E-06	-0.1	8.6E-01	0.2	6.5E-01
ENSMUST00000124282	crystallin, zeta (quinone reductase)-like 1 [Source:MGI Symbol;Acc:MGI:1913859]	D3YZD6		-6.8	4.2E-05	5.1	9.7E-03	0.5	7.7E-01	0.4	7.0E-01
ENSMUST00000124303	diphthamine biosynthesis 3 [Source:MGI Symbol;Acc:MGI:1922658]	D3YXV3		-4.6	1.3E-03	5.9	5.1E-06	-0.5	4.3E-01	-0.1	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000124310	beaded filament structural protein 2, phakinin [Source:MGI Symbol;Acc:MGI:1333828]		Q6NVD9	6.0	1.7E-03	5.1	2.2E-02	-0.8	6.9E-01	1.4	2.4E-01
ENSMUST00000124316	myosin 1H [Source:MGI Symbol;Acc:MGI:1914674]	E9PVB9	Q9D6A1	7.1	3.6E-03	7.2	1.4E-03	1.1	5.0E-01	0.6	4.4E-01
ENSMUST00000117984	activin A receptor, type II-like 1 [Source:MGI Symbol;Acc:MGI:1338946]		Q61288	1.7	3.8E-01	1.4	5.6E-01	-0.7	7.0E-01	-0.3	8.7E-01
ENSMUST00000124317	chromodomain helicase DNA binding protein 4 [Source:MGI Symbol;Acc:MGI:1344380]	F6WR45		-5.6	4.7E-03	-4.3	2.1E-02	0.0	9.8E-01	0.5	7.7E-01
ENSMUST00000124331	heat shock protein 14 [Source:MGI Symbol;Acc:MGI:1354164]	F6QKP8		2.3	1.4E-03	-6.9	8.3E-05	0.3	3.8E-01	0.3	7.9E-01
ENSMUST00000124332	RIKEN cDNA 6330416G13 gene [Source:MGI Symbol;Acc:MGI:1913920]	Z4YMT7		-1.8	3.4E-02	9.3	6.0E-05	0.6	6.5E-01	0.0	9.9E-01
ENSMUST00000124334	MUS81 endonuclease homolog (yeast) [Source:MGI Symbol;Acc:MGI:1918961]		Q91ZJ0	-5.9	3.7E-03	7.9	3.7E-05	-0.6	5.9E-01	0.0	9.9E-01
ENSMUST00000124341	solute carrier family 4 (anion exchanger), member 3 [Source:MGI Symbol;Acc:MGI:109350]		P16283	9.0	1.3E-05	-5.6	2.4E-04	0.1	7.6E-01	-0.8	4.5E-01
ENSMUST00000124342	glioblastoma amplified sequence [Source:MGI Symbol;Acc:MGI:1278343]	Q7TMG8		-3.5	1.6E-02	6.7	1.5E-04	-0.6	6.1E-01	-0.3	6.1E-01
ENSMUST00000118005				0.7	4.5E-01	-3.2	6.9E-02	-0.1	8.6E-01	3.7	3.4E-02
ENSMUST00000124353	ubiquitin-conjugating enzyme E2E 2 [Source:MGI Symbol;Acc:MGI:2384997]	D3YW10		4.3	4.3E-03	2.3	2.0E-02	0.8	2.6E-01	0.5	4.6E-01
ENSMUST00000124444	cell cycle exit and neuronal differentiation 1 [Source:MGI Symbol;Acc:MGI:1929898]		Q9JKC6	6.7	1.8E-04	2.9	6.1E-02	-2.7	7.4E-02	-1.7	1.8E-01
ENSMUST00000118015	glycogenin [Source:MGI Symbol;Acc:MGI:1351614]	K3W4S6		-0.7	7.6E-01	1.5	4.6E-01	-1.1	5.7E-01	-3.3	1.4E-01
ENSMUST00000124470	prolactin receptor [Source:MGI Symbol;Acc:MGI:97763]		Q08501	9.2	2.1E-06	7.0	3.0E-04	0.5	7.1E-01	0.4	5.3E-01
ENSMUST00000124493	junctophilin 4 [Source:MGI Symbol;Acc:MGI:2443113]		Q80WT0	5.9	1.1E-02	6.4	1.8E-04	-0.6	5.9E-01	-0.4	5.6E-01
ENSMUST00000124499	lymphocyte cytosolic protein 1 [Source:MGI Symbol;Acc:MGI:104808]		Q61233	-4.2	2.2E-02	6.2	1.6E-03	-0.4	8.0E-01	-0.8	3.4E-01
ENSMUST00000118027	lysine (K)-specific demethylase 2B [Source:MGI Symbol;Acc:MGI:1354737]	D3YVU4		3.1	4.4E-02	5.9	1.4E-02	2.5	2.1E-01	-0.3	7.6E-01
ENSMUST00000124526	AHNAK nucleoprotein 2 [Source:MGI Symbol;Acc:MGI:2144831]	E9PYB0		8.5	4.9E-05	5.1	1.4E-03	-1.4	2.9E-01	-0.4	6.2E-01
ENSMUST00000124531	EF-hand calcium binding domain 12 [Source:MGI Symbol;Acc:MGI:2681834]	I6L9E6		8.1	1.5E-05	6.2	2.5E-04	-1.0	4.1E-01	0.3	6.7E-01
ENSMUST00000124533	branched chain ketoacid dehydrogenase kinase [Source:MGI Symbol;Acc:MGI:1276121]			-4.5	1.5E-03	6.1	5.6E-03	-0.9	6.3E-01	0.8	4.4E-01
ENSMUST00000124536	transmembrane protein 259 [Source:MGI Symbol;Acc:MGI:2177957]	F6RN19		-4.8	7.8E-04	-3.6	9.5E-02	0.7	5.1E-01	-0.6	7.9E-01
ENSMUST00000124549	catechol-O-methyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916406]		Q8BIG7	2.2	3.2E-03	-7.8	5.2E-04	0.2	6.2E-01	0.6	6.8E-01
ENSMUST00000124556	mitogen-activated protein kinase kinase kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346883]	D6RCZ7		-7.9	4.0E-03	3.8	1.2E-02	0.3	8.1E-01	1.0	2.1E-01
ENSMUST00000124558	regulator of G-protein signaling like 1 [Source:MGI Symbol;Acc:MGI:2685048]	H3BL40		6.0	3.3E-04	8.4	3.1E-05	-1.5	2.7E-01	-0.9	1.1E-01
ENSMUST00000118059	unc-50 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1914637]		Q9CQ61	-1.2	6.3E-01	-2.8	3.4E-01	-2.9	1.2E-01	-1.3	6.8E-01
ENSMUST00000124565	cell cycle progression 1, opposite strand [Source:MGI Symbol;Acc:MGI:3648770]	V9GXK1		-3.0	2.4E-03	6.2	2.5E-04	2.0	6.6E-02	-0.2	7.5E-01
ENSMUST00000124569	solute carrier family 15, member 4 [Source:MGI Symbol;Acc:MGI:2140796]	F6QFB4		-4.4	1.0E-03	4.6	1.3E-02	-0.5	7.4E-01	-0.5	6.6E-01
ENSMUST00000124603	family with sequence similarity 188, member A [Source:MGI Symbol;Acc:MGI:1914210]	D6REU0		-2.9	2.4E-02	-4.7	1.9E-04	0.5	1.9E-01	0.8	3.4E-01
ENSMUST00000124610	F-box and leucine-rich repeat protein 5 [Source:MGI Symbol;Acc:MGI:2152883]	F7BZC4		-4.3	1.4E-03	6.4	2.0E-04	-0.6	6.0E-01	-0.4	4.6E-01
ENSMUST00000124615	RIKEN cDNA 2010107G23 gene [Source:MGI Symbol;Acc:MGI:1917144]		Q9D882	5.2	6.7E-03	-9.4	2.5E-05	-0.1	8.0E-01	0.7	5.6E-01
ENSMUST00000124632	lycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:10489	F6YDB7		-4.1	1.8E-03	4.0	1.1E-01	2.2	3.1E-01	2.8	1.3E-01
ENSMUST00000124640	nitrogen permease regulator-like 3 [Source:MGI Symbol;Acc:MGI:109258]	F2Z3V7		4.8	4.4E-04	1.3	6.0E-01	-1.2	5.3E-01	3.8	8.3E-02
ENSMUST00000124668	major facilitator superfamily domain containing 10 [Source:MGI Symbol;Acc:MGI:1915544]	D3Z2Z9		4.7	5.4E-03	6.0	3.7E-04	-0.6	6.0E-01	-0.4	5.7E-01
ENSMUST00000124677	spermatogenesis associated glutamate (E)-rich protein 3 [Source:MGI Symbol;Acc:MGI:1918276]	W4VSP1		6.0	1.6E-04	7.5	1.1E-04	0.9	4.6E-01	0.1	9.3E-01
ENSMUST00000124714	ATP-binding cassette, sub-family A (ABC1), member 5 [Source:MGI Symbol;Acc:MGI:2386607]	A2AEP5		5.9	2.9E-03	8.8	1.1E-03	-0.8	7.1E-01	-4.6	3.5E-03
ENSMUST00000124717	serine (or cysteine) peptidase inhibitor, clade A, member 1A [Source:MGI Symbol;Acc:MGI:891971]	D3YZL0		6.7	9.5E-05	7.5	1.1E-02	-0.7	7.9E-01	-2.5	1.1E-01
ENSMUST00000118108	Rab9 effector protein with kelch motifs [Source:MGI Symbol;Acc:MGI:2139530]	B0R0S4		1.9	3.9E-01	2.4	3.9E-01	0.6	8.1E-01	0.0	9.9E-01
ENSMUST00000118110	arrestin domain containing 4 [Source:MGI Symbol;Acc:MGI:1913662]	Q8VD69		0.6	8.1E-01	-3.2	1.7E-01	-5.3	1.4E-02	-1.5	5.8E-01
ENSMUST00000124721	asialoglycoprotein receptor 2 [Source:MGI Symbol;Acc:MGI:88082]	B1AR35		5.8	9.4E-03	5.6	1.0E-01	2.3	4.5E-01	3.4	6.9E-02
ENSMUST00000118113	avian erythroblastosis virus E-26 (v-ets) oncogene related [Source:MGI Symbol;Acc:MGI:95415]	D3YU51		-1.4	3.0E-01	-0.5	7.7E-01	1.5	2.5E-01	0.6	7.4E-01
ENSMUST00000124723	phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Source:MGI Symbol;Acc:MGI:1922019]	D3Z2Z7		4.3	1.5E-02	4.8	2.1E-03	-1.9	1.6E-01	-0.8	3.3E-01
ENSMUST00000124737	activating transcription factor 2 [Source:MGI Symbol;Acc:MGI:109349]	F6Z2B2		4.7	3.2E-02	6.3	9.2E-04	-0.7	6.4E-01	-0.6	4.4E-01
ENSMUST00000124745	DET1 and DDB1 associated 1 [Source:MGI Symbol;Acc:MGI:1913748]		Q9D9Z5	-7.2	6.8E-03	7.2	1.5E-02	-0.8	7.7E-01	-1.0	4.9E-01
ENSMUST00000124763	bassoon [Source:MGI Symbol;Acc:MGI:1277955]	V9GX98		4.4	1.1E-02	-0.9	3.3E-01	0.8	2.2E-01	-1.3	1.7E-01
ENSMUST00000124768	osaminidase (glycosyl hydrolase family 20, catalytic domain) containing [Source:MGI Symbol;Acc:MGI:36055	B1AXL0		5.5	2.7E-06	5.7	1.0E-03	-0.6	6.7E-01	0.4	6.1E-01
ENSMUST00000118125	interleukin 4 induced 1 [Source:MGI Symbol;Acc:MGI:109552]	D3Z4E0		3.4	1.8E-01	3.4	3.1E-01	0.7	8.0E-01	0.7	7.8E-01
ENSMUST00000118126				-3.1	1.4E-01	-2.2	3.6E-01	0.1	9.3E-01	-0.7	7.8E-01
ENSMUST00000124783	zinc finger and BTB domain containing 7B [Source:MGI Symbol;Acc:MGI:102755]	D3YXC8		-2.7	2.7E-02	7.4	2.3E-05	-1.9	9.7E-02	0.1	7.6E-01
ENSMUST00000124812	RIKEN cDNA 6430550D23 gene [Source:MGI Symbol;Acc:MGI:2443361]	D6RHS0		4.2	9.0E-04	-0.6	2.4E-01	0.4	2.2E-01	-0.6	3.0E-01
ENSMUST00000118136	genetic suppressor element 1 [Source:MGI Symbol;Acc:MGI:1098275]		Q3U3C9	-3.9	4.9E-02	-0.1	9.5E-01	0.5	6.1E-01	-3.3	9.7E-02
ENSMUST00000124825	phosphodiesterase 11A [Source:MGI Symbol;Acc:MGI:3036251]	F7AAG1		5.1	9.6E-04	5.0	1.3E-03	0.1	8.9E-01	0.6	3.6E-01
ENSMUST00000124826	integrin beta 1 (fibronectin receptor beta) [Source:MGI Symbol;Acc:MGI:96610]	D6RJL5		-3.3	2.9E-02	6.5	1.1E-03	-0.7	6.5E-01	-1.1	2.0E-01
ENSMUST00000124830	desmoplakin [Source:MGI Symbol;Acc:MGI:109611]		E9Q557	5.8	2.9E-06	4.8	1.1E-03	0.7	4.9E-01	0.3	6.3E-01
ENSMUST00000124838	glycoprotein integral membrane 1 [Source:MGI Symbol;Acc:MGI:2384905]	Q3UN36		-6.1	1.2E-04	-3.5	3.2E-02	-1.1	2.0E-01	-2.8	9.7E-02
ENSMUST00000124861	C1q and tumor necrosis factor related protein 1 [Source:MGI Symbol;Acc:MGI:1919254]	A2A4W1		8.7	5.4E-06	6.2	2.5E-04	0.5	6.7E-01	-1.0	1.2E-01
ENSMUST00000124883	centrosomal protein 57 [Source:MGI Symbol;Acc:MGI:1915551]		Q8CEE0	-3.6	2.2E-02	7.4	4.7E-05	-0.6	5.8E-01	0.0	9.7E-01
ENSMUST00000118152	chromobox 5 [Source:MGI Symbol;Acc:MGI:109372]		Q61686	0.7	6.5E-02	1.1	4.2E-02	0.3	4.0E-01	0.0	9.3E-01
ENSMUST00000118157	ankyrin repeat domain 42 [Source:MGI Symbol;Acc:MGI:1921095]			3.4	1.7E-01	2.6	3.3E-01	-0.4	8.8E-01	0.4	8.3E-01
ENSMUST00000124888	lectin, galactose binding, soluble 8 [Source:MGI Symbol;Acc:MGI:1928481]	Q542M5	Q9JL15	8.0	3.8E-04	4.4	5.6E-04	0.7	3.8E-01	0.2	7.3E-01
ENSMUST00000124899	ankyrin repeat and SOCS box-containing 7 [Source:MGI Symbol;Acc:MGI:2152835]		Q91ZU0	-2.9	2.7E-02	4.9	1.3E-02	-0.6	7.1E-01	0.5	6.5E-01
ENSMUST00000118160	rhotekin 2 [Source:MGI Symbol;Acc:MGI:2158417]		Q14B46	4.2	5.5E-02	2.4	2.2E-01	-3.1	1.6E-01	-1.3	4.0E-01
ENSMUST00000124910	microcephaly, primary autosomal recessive 1 [Source:MGI Symbol;Acc:MGI:2443308]	G3UWE9		7.9	3.9E-05	7.7	3.1E-04	-0.7	6.4E-01	0.4	5.8E-01
ENSMUST00000124931	sterile alpha motif domain containing 13 [Source:MGI Symbol;Acc:MGI:2686498]		D3YUG0	8.2	1.6E-05	-5.4	1.2E-02	0.8	3.5E-01	0.0	9.9E-01
ENSMUST00000124956	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]	D3Z2U2		4.3	5.1E-04	7.5	2.2E-04	-0.7	6.4E-01	-0.6	3.9E-01
ENSMUST00000124973	translocated promoter region, nuclear basket protein [Source:MGI Symbol;Acc:MGI:1922066]		F6ZDS4	-3.8	5.1E-04	9.6	1.1E-05	-0.7	5.8E-01	-0.2	5.9E-01
ENSMUST00000124981	F-box and leucine-rich repeat protein 21 [Source:MGI Symbol;Acc:MGI:2442921]	D6RE27		6.5	1.0E-04	0.5	6.4E-01	0.3	7.2E-01	-2.9	2.5E-02
ENSMUST00000118182				-0.3	8.2E-01	0.2	8.9E-01	0.3	8.2E-01	-0.2	8.8E-01
ENSMUST00000124992	ubiquitin-conjugating enzyme E2J 1 [Source:MGI Symbol;Acc:MGI:1926245]		Q9JJZ4	-6.9	7.4E-05	-6.3	8.1E-05	0.0	9.6E-01	-0.8	4.5E-01
ENSMUST00000125009	glutamate receptor, metabotropic 5 [Source:MGI Symbol;Acc:MGI:1351342]	F6WSV0		8.1	1.8E-04	7.0	2.3E-04	0.4	7.4E-01	0.1	8.6E-01
ENSMUST00000118191				-2.2	4.7E-02	-1.9	9.0E-02	-1.0	1.5E-01	-1.4	2.5E-01
ENSMUST00000125038	kinesin family member 2A [Source:MGI Symbol;Acc:MGI:108390]		Q9D481	2.5	1.6E-02	-3.0	7.3E-02	0.8	2.9E-01	-2.2	2.2E-01
ENSMUST00000125040	PEST proteolytic signal containing nuclear protein [Source:MGI Symbol;Acc:MGI:1923552]	D6RDQ3		-3.7	1.7E-03	-5.4	5.2E-03	0.6	3.3E-01	1.1	4.6E-01
ENSMUST00000125049	START domain containing 7 [Source:MGI Symbol;Acc:MGI:2139090]	F7BBA2		-3.2	9.5E-03	4.5	5.3E-04	-1.4	1.5E-01	-0.3	6.3E-01
ENSMUST00000125053	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]	F6Z4B2		-4.9	3.2E-02	7.8	4.5E-05	-0.6	6.1E-01	-1.2	5.7E-02
ENSMUST00000125107	RIKEN cDNA 0610037L13 gene [Source:MGI Symbol;Acc:MGI:1921348]		Q8BHG2	-6.0	2.1E-05	-0.2	8.9E-01	1.0	4.5E-01	-3.2	1.0E-01
ENSMUST00000125127	predicted gene 16286 [Source:MGI Symbol;Acc:MGI:3833940]	Q9CQX6		-9.0	4.5E-05	8.9	2.3E-05	-0.6	6.0E-01	-1.8	8.5E-03
ENSMUST00000118198	general transcription factor II A, 2 [Source:MGI Symbol;Acc:MGI:1933289]	Q3TE88	Q80ZM7	-1.0	7.5E-01	-3.6	3.2E-01	-2.9	2.7E-01	-0.3	9.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000118199	penta-EF hand domain containing 1 [Source:MGI Symbol;Acc:MGI:1915148]		Q8BFY6	3.4	9.6E-02	7.4	2.4E-02	1.7	5.3E-01	-2.3	1.7E-01
ENSMUST00000125135	splA/ryanodine receptor domain and SOCS box containing 1 [Source:MGI Symbol;Acc:MGI:1921896]	A2A7B1		7.3	1.1E-03	6.8	7.0E-05	-2.7	4.1E-02	0.9	1.2E-01
ENSMUST00000125153	erythrocyte membrane protein band 4.1 like 1 [Source:MGI Symbol;Acc:MGI:103010]	E9PV14		7.2	7.8E-06	-5.3	1.4E-03	-0.3	4.8E-01	0.6	6.3E-01
ENSMUST00000125163	retinol dehydrogenase 16 [Source:MGI Symbol;Acc:MGI:1201375]	D6RFT0		3.9	2.0E-04	4.4	2.4E-03	-1.0	3.5E-01	-1.2	1.8E-01
ENSMUST00000118206	small integral membrane protein 24 [Source:MGI Symbol;Acc:MGI:1919523]	D3Z3Y2		-1.1	3.2E-01	2.1	2.3E-01	2.3	1.4E-01	-0.9	4.5E-01
ENSMUST00000125174	RIKEN cDNA B430306N03 gene [Source:MGI Symbol;Acc:MGI:2443478]	D6RJI6		-1.2	2.0E-02	-8.7	2.0E-04	-1.2	2.5E-02	1.4	3.3E-01
ENSMUST00000125184	ubiquitin A-52 residue ribosomal protein fusion product 1 [Source:MGI Symbol;Acc:MGI:98887]	Q66JP1	P62984	-4.5	7.3E-03	5.1	7.8E-02	-0.7	8.2E-01	0.2	9.2E-01
ENSMUST00000125192	ataxin 7-like 1 [Source:MGI Symbol;Acc:MGI:3584458]	F6X2K7		-2.9	3.8E-03	6.2	1.7E-02	-0.7	7.8E-01	-1.2	3.5E-01
ENSMUST00000125200	syntaxin binding protein 5 (tomosyn) [Source:MGI Symbol;Acc:MGI:1926058]	D3Z2Q2		-4.3	3.2E-02	5.7	7.0E-03	-0.7	6.8E-01	-0.3	7.7E-01
ENSMUST00000125209	multiple C2 domains, transmembrane 1 [Source:MGI Symbol;Acc:MGI:1926021]	E9PV86		-2.5	4.1E-04	6.5	1.4E-03	0.9	5.4E-01	0.7	3.6E-01
ENSMUST00000125243	PRP40 pre-mRNA processing factor 40 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1860512]	A2AQW6		-4.4	1.0E-02	6.2	8.2E-04	-0.6	6.8E-01	-1.1	1.8E-01
ENSMUST00000118228	tribbles homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443397]		Q8K4K4	1.6	3.2E-01	3.3	1.1E-01	1.2	4.8E-01	-0.5	7.5E-01
ENSMUST00000125276	solute carrier family 35, member C1 [Source:MGI Symbol;Acc:MGI:2443301]	Q8R2I1		-3.7	9.4E-03	2.9	7.2E-02	-4.3	2.4E-02	-2.8	5.5E-02
ENSMUST00000125291	membrane-spanning 4-domains, subfamily A, member 6D [Source:MGI Symbol;Acc:MGI:1916024]	F6V7U2		11.1	4.1E-07	6.9	1.0E-02	-0.8	7.5E-01	-1.8	1.9E-01
ENSMUST00000118243	scavenger receptor class F, member 1 [Source:MGI Symbol;Acc:MGI:2449455]	B7ZC28		0.7	6.4E-01	-0.5	8.5E-01	0.6	7.5E-01	1.8	3.5E-01
ENSMUST00000125295	sorbin and SH3 domain containing 2 [Source:MGI Symbol;Acc:MGI:1924574]			6.4	2.8E-02	0.6	7.6E-01	4.2	2.1E-02	-1.5	4.4E-01
ENSMUST00000125302	malate dehydrogenase 1, NAD (soluble) [Source:MGI Symbol;Acc:MGI:97051]	B1ATQ3		-5.5	9.2E-04	7.4	1.9E-04	-0.6	6.5E-01	-1.1	1.3E-01
ENSMUST00000125326	MyoD family inhibitor domain containing [Source:MGI Symbol;Acc:MGI:104611]	A0A087WPB2		6.2	1.7E-04	2.3	2.0E-01	-2.7	1.8E-01	0.6	6.8E-01
ENSMUST00000118257				-1.3	7.1E-02	0.5	5.5E-01	1.1	1.0E-01	-0.8	3.7E-01
ENSMUST00000125362	suppressor of cytokine signaling 6 [Source:MGI Symbol;Acc:MGI:1924885]		Q9JLY0	-4.2	4.6E-03	4.5	3.3E-03	-2.8	5.4E-02	0.6	4.7E-01
ENSMUST00000125366	histocompatibility 13 [Source:MGI Symbol;Acc:MGI:95886]		Q9D8V0	-1.8	1.1E-02	6.6	6.0E-05	0.1	9.4E-01	-0.7	2.1E-01
ENSMUST00000125404	phospholipase D family, member 5 [Source:MGI Symbol;Acc:MGI:2442056]	D6RCJ9		8.3	3.6E-05	4.3	4.1E-02	-1.3	5.1E-01	0.7	5.7E-01
ENSMUST00000125434	glucokinase [Source:MGI Symbol;Acc:MGI:1270854]	F6V339		4.6	7.9E-03	7.1	7.7E-04	-0.6	7.3E-01	-0.4	5.9E-01
ENSMUST00000118276	synaptotagmin VIII [Source:MGI Symbol;Acc:MGI:1859867]		Q9R0N6	1.3	4.1E-01	3.2	1.5E-01	0.4	8.2E-01	-1.4	3.5E-01
ENSMUST00000118279	VPS9 domain containing 1 [Source:MGI Symbol;Acc:MGI:1914143]	Q3U280		-3.7	2.4E-01	-2.2	5.7E-01	0.6	7.7E-01	-0.9	8.2E-01
ENSMUST00000125454	translocase of inner mitochondrial membrane 17a [Source:MGI Symbol;Acc:MGI:1343131]	D3Z1K5		6.4	3.2E-04	5.7	1.3E-03	-1.3	3.5E-01	-0.9	3.0E-01
ENSMUST00000125476	phosphatidylinositol 4-kinase, catalytic, beta polypeptide [Source:MGI Symbol;Acc:MGI:1334433]	E9Q8A3		-4.4	3.3E-03	2.2	2.9E-03	-0.7	1.8E-01	-0.2	6.4E-01
ENSMUST00000125512	supervillin [Source:MGI Symbol;Acc:MGI:2147319]	F6R6A4		-9.3	2.5E-03	6.0	1.8E-04	-0.4	7.2E-01	-0.7	2.3E-01
ENSMUST00000125519	RIKEN cDNA 1110004E09 gene [Source:MGI Symbol;Acc:MGI:1915251]	D6REH7		5.3	3.7E-03	2.8	3.7E-03	0.8	2.3E-01	0.1	9.2E-01
ENSMUST00000125536	inhibitor of growth family, member 2 [Source:MGI Symbol;Acc:MGI:1916510]	E0CXA7		-4.1	3.3E-03	6.5	4.3E-04	-0.2	9.0E-01	0.4	5.9E-01
ENSMUST00000118294	histone deacetylase 7 [Source:MGI Symbol;Acc:MGI:1891835]		Q8C2B3	1.6	5.9E-01	-1.3	7.4E-01	-1.1	7.3E-01	1.8	5.8E-01
ENSMUST00000118302				0.6	4.1E-01	2.0	4.0E-02	0.6	4.4E-01	-0.9	2.5E-01
ENSMUST00000125555	leukotriene C4 synthase [Source:MGI Symbol;Acc:MGI:107498]	Q5SVR6		6.6	1.1E-02	5.4	1.1E-03	-1.5	2.6E-01	0.4	6.1E-01
ENSMUST00000125581	homeobox A10 [Source:MGI Symbol;Acc:MGI:96171]		P31310	5.0	2.0E-02	-8.1	4.6E-05	0.7	5.1E-02	-0.8	5.4E-01
ENSMUST00000125621	RIKEN cDNA 4932414N04 gene [Source:MGI Symbol;Acc:MGI:1922971]	A2AQL4		11.3	5.1E-08	3.6	1.5E-02	-2.2	1.1E-01	-1.2	2.6E-01
ENSMUST00000118314	expressed sequence C77370 [Source:MGI Symbol;Acc:MGI:2148050]	Q003Y7	Q5DTT1	2.5	1.6E-01	5.1	1.1E-02	-0.6	7.4E-01	-3.2	3.3E-02
ENSMUST00000118316	NEDD4 binding protein 2-like 2 [Source:MGI Symbol;Acc:MGI:2687207]		Q8JZS6	0.9	7.8E-02	0.6	2.5E-01	-0.6	2.1E-01	-0.3	5.1E-01
ENSMUST00000125625	Shwachman-Bodian-Diamond syndrome homolog (human) [Source:MGI Symbol;Acc:MGI:1913961]	F6TN03		3.3	1.9E-02	-4.1	1.0E-04	1.2	2.6E-03	0.8	2.0E-01
ENSMUST00000125652	diablo homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913843]		Q9JIQ3	3.3	8.2E-04	6.3	1.8E-04	-0.6	5.9E-01	0.6	2.9E-01
ENSMUST00000125674	RIKEN cDNA 1500012F01 gene [Source:MGI Symbol;Acc:MGI:1916199]	Q3V494		-6.9	8.5E-06	5.8	6.5E-04	-0.7	5.3E-01	0.0	9.8E-01
ENSMUST00000125682	cyclin-dependent kinase 4 [Source:MGI Symbol;Acc:MGI:88357]	E9PZX7		3.8	1.5E-03	5.5	2.9E-03	-1.4	3.1E-01	-1.5	1.2E-01
ENSMUST00000125698	adhesion G protein-coupled receptor V1 [Source:MGI Symbol;Acc:MGI:1274784]			7.2	6.8E-05	8.7	7.7E-05	0.6	6.3E-01	0.1	8.3E-01
ENSMUST00000125704	RIKEN cDNA 2010107G23 gene [Source:MGI Symbol;Acc:MGI:1917144]		Q9D882	4.8	4.6E-03	4.8	9.6E-03	-0.7	6.6E-01	0.7	4.5E-01
ENSMUST00000125716	guanine nucleotide binding protein, alpha O [Source:MGI Symbol;Acc:MGI:95775]	Q543S2	P18872	8.9	1.2E-05	9.2	1.1E-04	-0.5	7.7E-01	-1.6	3.1E-02
ENSMUST00000125733	isthmin 2 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2685110]	D3Z6A3		7.2	5.1E-04	4.8	4.3E-03	-0.5	7.2E-01	-0.5	5.6E-01
ENSMUST00000118340	Rap guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:2659071]	E9QNQ4		5.5	5.5E-02	-0.8	8.4E-01	-1.8	5.1E-01	4.5	2.5E-01
ENSMUST00000125782	PRP31 pre-mRNA processing factor 31 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916238]			6.4	2.2E-04	5.0	4.3E-04	-1.9	9.7E-02	-0.6	3.6E-01
ENSMUST00000125819	granulin [Source:MGI Symbol;Acc:MGI:95832]	H3BJE0		-8.1	1.2E-03	6.4	2.4E-05	-1.1	2.5E-01	-0.5	2.8E-01
ENSMUST00000118351				-1.0	4.1E-01	0.3	7.7E-01	-1.2	2.2E-01	-2.5	6.0E-02
ENSMUST00000125833	lymphocyte cytosolic protein 1 [Source:MGI Symbol;Acc:MGI:104808]	D3Z7D9		-4.0	1.7E-03	1.5	4.5E-01	-2.2	2.7E-01	1.6	3.2E-01
ENSMUST00000125875	tetratricopeptide repeat domain 7 [Source:MGI Symbol;Acc:MGI:1920999]	D3Z0R8		4.1	6.7E-05	6.3	1.1E-03	0.2	8.7E-01	0.7	4.6E-01
ENSMUST00000125891	tetratricopeptide repeat domain 16 [Source:MGI Symbol;Acc:MGI:2443048]	E0CXL5		7.8	3.1E-05	4.4	5.2E-03	-2.1	1.6E-01	0.2	8.0E-01
ENSMUST00000125897	ı-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1 [Source:MGI Symbol;Acc:M	E9PY08		6.3	8.5E-04	6.7	3.0E-04	-0.6	6.6E-01	-0.2	8.0E-01
ENSMUST00000125911	S-adenosylhomocysteine hydrolase-like 2 [Source:MGI Symbol;Acc:MGI:1921590]	H3BKT5		5.7	5.0E-04	4.5	1.1E-02	-0.8	6.0E-01	-0.2	8.5E-01
ENSMUST00000125946	predicted gene 42878 [Source:MGI Symbol;Acc:MGI:5663015]	A0A0G2JDU2		4.1	6.1E-04	2.6	1.3E-02	0.3	6.7E-01	-0.5	4.9E-01
ENSMUST00000125964	ubiquitin-conjugating enzyme E2M [Source:MGI Symbol;Acc:MGI:108278]	F7CDT0		-5.0	6.9E-05	6.4	3.7E-05	-1.2	2.2E-01	-0.2	6.7E-01
ENSMUST00000125971	endothelin converting enzyme 2 [Source:MGI Symbol;Acc:MGI:1101356]	F6WM66		8.6	3.8E-05	3.4	1.8E-03	0.5	4.9E-01	-0.3	7.0E-01
ENSMUST00000118365	caspase recruitment domain family, member 6 [Source:MGI Symbol;Acc:MGI:3032959]	E9PWH2		-0.5	4.1E-01	-0.4	6.4E-01	0.7	2.5E-01	0.6	4.6E-01
ENSMUST00000125975	spastic paraplegia 7 homolog (human) [Source:MGI Symbol;Acc:MGI:2385906]	D3YZN4		-6.3	1.0E-04	-4.1	3.7E-03	0.9	1.2E-01	-2.0	1.7E-01
ENSMUST00000125981	MAP7 domain containing 1 [Source:MGI Symbol;Acc:MGI:2384297]	F6WF36		-8.4	1.6E-04	-6.1	3.9E-04	-1.2	2.4E-02	-0.9	4.7E-01
ENSMUST00000118370	nucleotide-binding oligomerization domain containing 2 [Source:MGI Symbol;Acc:MGI:2429397]	Q80SY9		-2.9	9.0E-02	-1.6	5.6E-01	2.1	2.7E-01	0.7	7.7E-01
ENSMUST00000125990	periaxin [Source:MGI Symbol;Acc:MGI:108176]			3.3	2.9E-02	-5.6	4.0E-02	0.7	4.2E-01	-0.7	8.0E-01
ENSMUST00000125993	cone-rod homeobox, opposite strand [Source:MGI Symbol;Acc:MGI:2451355]	V9GXY9		7.2	1.2E-04	7.2	9.7E-05	-0.6	6.3E-01	-0.4	5.1E-01
ENSMUST00000125995	tubulin folding cofactor E-like [Source:MGI Symbol;Acc:MGI:1925543]		Q8C5W3	-3.3	6.1E-04	5.6	6.2E-04	-0.4	7.3E-01	0.4	5.4E-01
ENSMUST00000126008	UDP-glucuronate decarboxylase 1 [Source:MGI Symbol;Acc:MGI:1915133]		Q91XL3	1.6	3.2E-02	5.8	5.4E-04	-0.5	6.8E-01	-0.5	4.4E-01
ENSMUST00000118381	inositol polyphosphate multikinase [Source:MGI Symbol;Acc:MGI:1916968]		Q7TT16	-0.3	7.0E-01	1.4	2.2E-01	0.6	5.4E-01	-1.2	2.4E-01
ENSMUST00000126032	ectonucleotide pyrophosphatase/phosphodiesterase 5 [Source:MGI Symbol;Acc:MGI:1933830]	D6RH39		3.7	2.3E-04	6.7	1.5E-04	-0.6	6.1E-01	-0.7	2.7E-01
ENSMUST00000118390	synaptojanin 1 [Source:MGI Symbol;Acc:MGI:1354961]	F7BQW7		0.2	9.3E-01	1.8	5.6E-01	0.6	8.1E-01	-1.0	7.3E-01
ENSMUST00000126066	zinc finger and BTB domain containing 38 [Source:MGI Symbol;Acc:MGI:2442866]	F6Z595		5.1	2.0E-02	8.7	5.3E-05	0.8	5.2E-01	1.2	5.1E-02
ENSMUST00000126068	paired box 1 [Source:MGI Symbol;Acc:MGI:97485]	A2ALK0		5.8	9.3E-04	8.0	3.0E-05	-0.2	8.6E-01	-0.6	2.3E-01
ENSMUST00000118405	integrin alpha L [Source:MGI Symbol;Acc:MGI:96606]	D3YW95		-5.2	7.3E-02	-2.9	3.0E-01	-0.6	7.2E-01	-2.8	3.7E-01
ENSMUST00000126071	Fas associated factor family member 2 [Source:MGI Symbol;Acc:MGI:1923827]		Q3TDN2	-1.2	9.3E-03	3.6	4.4E-02	-2.7	1.5E-01	1.4	2.3E-01
ENSMUST00000126077	TBC1 domain family, member 14 [Source:MGI Symbol;Acc:MGI:1098708]	E9PYB1		2.3	1.6E-02	5.8	3.9E-02	-0.8	7.7E-01	0.9	5.4E-01
ENSMUST00000126098	phospholipase C, eta 2 [Source:MGI Symbol;Acc:MGI:2443078]	A6PWW4		5.1	3.5E-03	-2.9	6.6E-03	-0.1	8.1E-01	-0.8	3.8E-01
ENSMUST00000126116	calpain, small subunit 1 [Source:MGI Symbol;Acc:MGI:88266]	D3YW48		-6.5	2.3E-04	5.4	2.4E-02	0.4	8.3E-01	0.9	4.7E-01
ENSMUST00000126175	tousled-like kinase 2 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1346023]	D6RHM1		-7.0	1.4E-03	6.9	2.9E-04	-0.6	6.6E-01	0.1	9.3E-01
ENSMUST00000118420	mitochondrial ribosomal protein S17 [Source:MGI Symbol;Acc:MGI:1913508]		Q9CQE3	-1.9	6.6E-01	-3.0	5.7E-01	-1.7	5.7E-01	-0.6	9.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000126188	cytoplasmic polyadenylation element binding protein 3 [Source:MGI Symbol;Acc:MGI:2443075]		Q7TN99	6.0	4.0E-03	-4.7	1.8E-03	-0.2	6.5E-01	-0.1	9.3E-01
ENSMUST00000126198	family with sequence similarity 78, member B [Source:MGI Symbol;Acc:MGI:2443050]		Q8BQN5	6.8	1.7E-03	2.4	1.6E-02	0.5	5.1E-01	0.1	9.4E-01
ENSMUST00000126203	UDP glucuronosyltransferase 1 family, polypeptide A7C [Source:MGI Symbol;Acc:MGI:3032636]	D6RH94		-7.3	4.2E-05	-5.0	3.1E-02	-6.6	7.5E-04	3.4	1.1E-01
ENSMUST00000118430				0.9	4.8E-01	1.1	3.9E-01	-1.3	2.7E-01	-1.5	2.1E-01
ENSMUST00000126207	cytochrome b5 reductase-like [Source:MGI Symbol;Acc:MGI:1919657]	F6RAM1		6.1	1.1E-03	-3.9	4.7E-03	-1.8	1.9E-02	-2.1	1.2E-01
ENSMUST00000126214	coiled-coil serine rich 1 [Source:MGI Symbol;Acc:MGI:3045354]		Q8C0C4	8.9	5.3E-05	6.2	3.2E-04	-0.5	6.5E-01	-2.4	5.9E-03
ENSMUST00000126239	SURP and G patch domain containing 2 [Source:MGI Symbol;Acc:MGI:2678085]	F6X398		4.5	4.5E-04	7.2	2.2E-04	-0.4	7.4E-01	-0.4	5.2E-01
ENSMUST00000126245	misato homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2385175]	E9PUB7		-3.0	1.1E-02	3.0	2.7E-03	-0.9	1.9E-01	-1.0	1.4E-01
ENSMUST00000118441				2.1	4.5E-02	1.1	3.0E-01	-1.9	6.3E-02	-0.8	3.6E-01
ENSMUST00000126305	ankyrin repeat domain 42 [Source:MGI Symbol;Acc:MGI:1921095]	D6RCX7		4.6	2.5E-02	6.7	2.3E-02	-0.8	7.6E-01	-0.3	8.1E-01
ENSMUST00000126307	sphingosine phosphate lyase 1 [Source:MGI Symbol;Acc:MGI:1261415]	D3YY13		4.0	2.2E-03	4.5	6.7E-03	-0.8	5.4E-01	-0.1	9.0E-01
ENSMUST00000126319	transducin (beta)-like 3 [Source:MGI Symbol;Acc:MGI:2384863]		Q8C4J7	5.2	1.1E-03	-5.1	2.1E-03	-0.8	2.1E-01	0.8	5.4E-01
ENSMUST00000126334	transmembrane 6 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1933209]	D6RD09		-2.8	3.0E-02	6.2	2.0E-03	-0.1	9.7E-01	-0.7	4.0E-01
ENSMUST00000126346	cyclin L2 [Source:MGI Symbol;Acc:MGI:1927119]	F6RXL0		-6.9	3.4E-03	4.6	1.1E-02	-1.2	4.3E-01	-0.3	7.3E-01
ENSMUST00000126366	zinc finger protein 473 [Source:MGI Symbol;Acc:MGI:2442697]	E9Q4I9		4.2	1.9E-04	-6.9	2.1E-04	0.2	6.9E-01	-1.0	4.6E-01
ENSMUST00000126390	RalBP1 associated Eps domain containing protein [Source:MGI Symbol;Acc:MGI:1196373]		O54916	-6.5	3.6E-05	7.9	4.9E-05	0.9	4.2E-01	-0.5	3.0E-01
ENSMUST00000118466	family with sequence similarity 213, member A [Source:MGI Symbol;Acc:MGI:1917814]	Q3U125		4.5	8.0E-02	-0.1	9.5E-01	-4.9	5.3E-02	-0.3	8.9E-01
ENSMUST00000126403	sulfide quinone reductase-like (yeast) [Source:MGI Symbol;Acc:MGI:1929899]	F6ZKZ3		-9.2	1.1E-05	-5.5	7.9E-03	0.6	4.8E-01	-0.1	9.7E-01
ENSMUST00000118471	kinesin light chain 1 [Source:MGI Symbol;Acc:MGI:107978]	Q5UE59		0.6	7.9E-01	-1.5	6.1E-01	-1.4	5.2E-01	0.8	7.8E-01
ENSMUST00000126431	methenyltetrahydrofolate synthetase domain containing [Source:MGI Symbol;Acc:MGI:2679252]	D3Z1R2		4.5	1.3E-02	4.8	1.9E-02	0.6	7.4E-01	0.8	4.6E-01
ENSMUST00000126432	SEC11 homolog C, signal peptidase complex subunit [Source:MGI Symbol;Acc:MGI:1913536]	D6RFV4		-4.9	1.7E-04	8.9	2.1E-04	-0.1	9.6E-01	-1.1	1.4E-01
ENSMUST00000126456	Fanconi anemia, complementation group I [Source:MGI Symbol;Acc:MGI:2384790]	D3YVC7		8.3	9.0E-07	-3.3	3.1E-03	-0.9	9.9E-02	-2.2	5.9E-02
ENSMUST00000126532	HEG homolog 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1924696]		E9Q7X6	8.9	7.0E-05	-3.2	2.5E-02	1.0	1.7E-01	-2.0	1.9E-01
ENSMUST00000126534	uncoupling protein 2 (mitochondrial, proton carrier) [Source:MGI Symbol;Acc:MGI:109354]	Q549J5	P70406	-5.3	9.6E-05	7.0	2.8E-04	-0.6	6.6E-01	-0.3	6.3E-01
ENSMUST00000126611	Lck interacting transmembrane adaptor 1 [Source:MGI Symbol;Acc:MGI:1919949]	F6QX71		-6.0	1.7E-02	-6.0	4.1E-04	-0.8	1.1E-01	-1.3	3.3E-01
ENSMUST00000126656	EF-hand calcium binding domain 8 [Source:MGI Symbol;Acc:MGI:3644206]	H3BL58		5.0	3.0E-04	3.8	4.7E-04	-1.2	1.2E-01	0.0	9.8E-01
ENSMUST00000126681	lipin 2 [Source:MGI Symbol;Acc:MGI:1891341]	E9PWN0		5.1	1.8E-02	-6.9	9.0E-03	1.4	7.3E-02	-0.3	9.0E-01
ENSMUST00000126699	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1928767]	A0A0A6YXE7		-9.9	1.9E-06	-11.4	3.9E-05	-0.8	6.2E-02	0.3	8.4E-01
ENSMUST00000126705	transmembrane protein 208 [Source:MGI Symbol;Acc:MGI:1913570]	S4R1H6		-1.9	3.0E-02	4.9	6.7E-04	-3.5	1.0E-02	0.4	5.4E-01
ENSMUST00000126799	cyclic nucleotide gated channel alpha 1 [Source:MGI Symbol;Acc:MGI:88436]	A0A0G2JG06		6.9	7.7E-05	-6.1	2.3E-04	-1.3	1.7E-02	-0.5	6.6E-01
ENSMUST00000126831	thymus, brain and testes associated [Source:MGI Symbol;Acc:MGI:1923820]	F6RYN6		6.8	5.6E-05	5.9	9.9E-04	-0.6	6.6E-01	-0.3	7.0E-01
ENSMUST00000126854	Rap guanine nucleotide exchange factor (GEF) 3 [Source:MGI Symbol;Acc:MGI:2441741]		Q8VCC8	6.4	1.3E-02	11.2	1.7E-06	-0.5	6.5E-01	0.1	6.9E-01
ENSMUST00000126865	SIK family kinase 3 [Source:MGI Symbol;Acc:MGI:2446296]	E9PU87		-2.2	1.8E-02	5.4	2.3E-02	0.0	9.9E-01	0.2	9.1E-01
ENSMUST00000126879	zinc finger protein 369 [Source:MGI Symbol;Acc:MGI:2176229]	F8VQL6		1.5	1.7E-02	4.3	5.5E-03	0.1	9.6E-01	-1.3	1.9E-01
ENSMUST00000126960	multiple C2 domains, transmembrane 1 [Source:MGI Symbol;Acc:MGI:1926021]	E9PYR7		-3.5	5.6E-05	7.8	6.3E-05	-0.5	6.7E-01	-0.1	8.3E-01
ENSMUST00000126969	male-specific lethal 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1921276]	F7CR37		-5.3	5.7E-04	-3.5	3.4E-02	1.1	1.8E-01	-1.8	2.9E-01
ENSMUST00000126977	supervillin [Source:MGI Symbol;Acc:MGI:2147319]		Q8K4L3	-5.2	5.5E-04	5.2	1.7E-03	-0.5	6.9E-01	-0.6	4.7E-01
ENSMUST00000126979	storkhead box 1 [Source:MGI Symbol;Acc:MGI:2684909]	F6YZ72		6.5	1.3E-04	2.2	4.2E-02	-0.5	5.8E-01	0.6	4.7E-01
ENSMUST00000118525	ankyrin repeat domain 29 [Source:MGI Symbol;Acc:MGI:2687055]	D3YVV3		3.6	1.8E-01	4.7	1.1E-01	-0.4	9.0E-01	-1.5	4.1E-01
ENSMUST00000126980	BTB (POZ) domain containing 2 [Source:MGI Symbol;Acc:MGI:1933831]	E9PY28		-5.9	5.7E-03	3.9	3.4E-02	-0.6	7.2E-01	2.4	3.9E-02
ENSMUST00000126992	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	B7ZD61		-4.2	1.6E-02	-6.8	4.5E-05	-1.2	1.4E-02	-0.7	5.1E-01
ENSMUST00000118535	RAB4A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105069]		P56371	1.9	6.6E-02	0.5	7.1E-01	0.0	9.7E-01	1.4	2.2E-01
ENSMUST00000127095	lymphocyte antigen 6 complex, locus H [Source:MGI Symbol;Acc:MGI:1346030]	Q8K356		4.4	6.8E-03	8.9	2.4E-04	0.2	9.0E-01	0.6	3.8E-01
ENSMUST00000127097	zinc finger protein 703 [Source:MGI Symbol;Acc:MGI:2662729]	E9PXD8		2.9	9.8E-03	2.4	1.9E-02	-2.3	2.8E-02	-0.7	3.5E-01
ENSMUST00000127106	membrane bound O-acyltransferase domain containing 7 [Source:MGI Symbol;Acc:MGI:1924832]	D6RHB6		-7.8	1.4E-03	2.0	2.5E-02	-0.8	2.4E-01	1.0	1.2E-01
ENSMUST00000118545	SH3-domain binding protein 2 [Source:MGI Symbol;Acc:MGI:1346349]	E9QJU7		-0.7	7.6E-01	2.8	2.9E-01	0.2	9.4E-01	-3.3	1.7E-01
ENSMUST00000127134	RUN and FYVE domain containing 4 [Source:MGI Symbol;Acc:MGI:3588214]		Q3TYX8	-6.6	4.1E-04	6.2	3.3E-02	-0.9	7.5E-01	1.1	4.5E-01
ENSMUST00000118557	peroxisomal biogenesis factor 11 beta [Source:MGI Symbol;Acc:MGI:1338882]		Q9Z210	0.5	7.7E-01	2.8	1.3E-01	-0.2	8.9E-01	-2.5	8.8E-02
ENSMUST00000127144	FLYWCH family member 2 [Source:MGI Symbol;Acc:MGI:1924167]	D6RJ61		6.2	1.3E-02	4.8	6.5E-03	-1.2	4.4E-01	0.4	6.8E-01
ENSMUST00000127152	annexin A4 [Source:MGI Symbol;Acc:MGI:88030]	S4R1F2		2.1	7.5E-03	7.9	5.0E-04	-0.5	7.6E-01	-1.4	1.1E-01
ENSMUST00000127157	ataxin 7-like 2 [Source:MGI Symbol;Acc:MGI:1919772]	A2AE44		3.0	1.7E-02	-7.1	4.2E-04	0.8	9.3E-02	-0.9	5.7E-01
ENSMUST00000118571	TMEM9 domain family, member B [Source:MGI Symbol;Acc:MGI:1915254]	D3Z6W5		-2.7	4.6E-02	0.2	8.9E-01	1.9	1.3E-01	-1.0	4.9E-01
ENSMUST00000118574	NLR family, apoptosis inhibitory protein 6 [Source:MGI Symbol;Acc:MGI:1298222]		Q9JIB6	-0.1	9.6E-01	-2.3	6.4E-01	0.7	8.0E-01	2.9	5.2E-01
ENSMUST00000127204	2-hydroxyacyl-CoA lyase 1 [Source:MGI Symbol;Acc:MGI:1929657]	D3YZ54		-4.4	4.1E-04	4.3	3.1E-02	1.8	2.5E-01	1.0	4.0E-01
ENSMUST00000127206	regulator of G-protein signaling 2 [Source:MGI Symbol;Acc:MGI:1098271]		O08849	-6.7	4.2E-05	5.4	1.7E-03	-0.6	6.6E-01	0.1	8.6E-01
ENSMUST00000127208	leucine rich repeat containing 14 [Source:MGI Symbol;Acc:MGI:2445060]		Q8VC16	4.4	1.3E-04	5.7	2.7E-03	-0.2	9.0E-01	0.3	7.1E-01
ENSMUST00000127234	predicted gene 16286 [Source:MGI Symbol;Acc:MGI:3833940]	Q9CQX6		-2.8	3.4E-02	6.2	2.5E-04	2.0	6.6E-02	-0.2	7.5E-01
ENSMUST00000127247	transmembrane protein 229A [Source:MGI Symbol;Acc:MGI:2442812]		B9EJI9	6.3	5.7E-05	6.7	9.5E-04	-0.7	6.5E-01	0.2	7.9E-01
ENSMUST00000127260	methyl-CpG binding domain protein 2 [Source:MGI Symbol;Acc:MGI:1333813]	F6UPR7		-6.6	6.1E-04	-1.0	2.5E-01	0.5	3.5E-01	-0.6	5.1E-01
ENSMUST00000127268	ectonucleoside triphosphate diphosphohydrolase 1 [Source:MGI Symbol;Acc:MGI:102805]	F7B9M9		-4.9	1.3E-02	-6.3	3.4E-02	1.7	8.0E-02	0.2	9.5E-01
ENSMUST00000118600	Dmx-like 2 [Source:MGI Symbol;Acc:MGI:2444630]		Q8BPN8	-2.0	7.9E-02	-3.8	2.9E-02	-0.3	6.6E-01	1.5	3.4E-01
ENSMUST00000127281	-ray repair complementing defective repair in Chinese hamster cells 3 [Source:MGI Symbol;Acc:MGI:192158	Q80W51		9.5	1.6E-05	2.0	2.1E-01	-1.7	2.3E-01	0.8	5.2E-01
ENSMUST00000118607	solute carrier family 35, member E2 [Source:MGI Symbol;Acc:MGI:2444240]		Q8C811	-0.7	6.1E-01	0.0	9.9E-01	-0.5	6.5E-01	-1.2	4.5E-01
ENSMUST00000118620				-0.1	9.5E-01	0.0	9.7E-01	0.2	7.9E-01	0.1	9.1E-01
ENSMUST00000127288	SH3 domain and tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGI:2678949]	F6UWL1		-4.5	9.3E-03	-6.1	3.5E-03	1.2	5.1E-02	-0.3	8.7E-01
ENSMUST00000127297	supervillin [Source:MGI Symbol;Acc:MGI:2147319]	E9Q3Z5		5.1	2.5E-02	5.7	3.5E-03	-0.6	7.2E-01	0.4	6.2E-01
ENSMUST00000127298	integrin linked kinase [Source:MGI Symbol;Acc:MGI:1195267]	F6Q5Z1		-5.8	1.9E-04	4.1	6.6E-05	0.1	8.1E-01	-0.6	1.8E-01
ENSMUST00000127305	epsin 3 [Source:MGI Symbol;Acc:MGI:1919139]		Q91W69	7.1	1.8E-05	-3.8	7.4E-02	0.8	4.0E-01	-0.8	7.1E-01
ENSMUST00000127306	energy homeostasis associated [Source:MGI Symbol;Acc:MGI:1916888]		Q8K1D8	4.0	3.0E-03	6.3	2.6E-04	0.8	4.8E-01	-0.7	2.5E-01
ENSMUST00000127316	ignal transducing adaptor molecule (SH3 domain and ITAM motif) 2 [Source:MGI Symbol;Acc:MGI:1929100		O88811	-2.6	2.5E-02	5.8	3.1E-03	0.0	9.9E-01	-0.3	7.2E-01
ENSMUST00000118648	in homology domain containing, family G (with RhoGef domain) member 5 [Source:MGI Symbol;Acc:MGI:2(	B1AS67		-0.2	9.4E-01	-2.3	3.8E-01	-1.8	3.0E-01	0.4	8.8E-01
ENSMUST00000118650				1.7	1.0E-01	2.5	7.4E-02	1.1	3.3E-01	0.3	7.2E-01
ENSMUST00000118655				1.4	1.2E-01	1.2	2.3E-01	-0.8	3.4E-01	-0.6	4.7E-01
ENSMUST00000127348	glutamyl-tRNA(Gln) amidotransferase, subunit B [Source:MGI Symbol;Acc:MGI:2442496]		Q99JT1	3.8	5.4E-04	5.0	6.0E-03	1.0	4.5E-01	-0.1	9.1E-01
ENSMUST00000127378	Yip1 domain family, member 3 [Source:MGI Symbol;Acc:MGI:106280]	F6YIY0		-5.9	4.9E-04	5.4	1.0E-03	-1.5	2.6E-01	0.9	2.3E-01
ENSMUST00000127405	NHP2 ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1098547]		Q9CRB2	-1.6	2.3E-02	5.2	1.5E-04	-0.3	6.8E-01	-0.3	5.4E-01
ENSMUST00000127430	SMC hinge domain containing 1 [Source:MGI Symbol;Acc:MGI:1921605]		Q6P5D8	-2.3	5.1E-03	5.3	1.8E-02	-0.5	7.8E-01	1.4	2.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000127433	predicted gene 4969 [Source:MGI Symbol;Acc:MGI:3647482]	D6RG70		8.6	6.7E-06	-3.3	3.5E-02	-1.1	2.0E-01	-1.3	3.9E-01
ENSMUST00000127437	elongator acetyltransferase complex subunit 5 [Source:MGI Symbol;Acc:MGI:1859017]	J3QN35		6.5	2.7E-04	7.2	3.4E-04	0.0	9.7E-01	1.3	1.2E-01
ENSMUST00000127463	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]	F6Z2C0		-7.2	1.5E-02	0.9	7.1E-01	-1.9	3.6E-01	2.5	2.1E-01
ENSMUST00000127477	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 [Source:MGI Symbol;Acc:MGI:1913296]		Q9CQH3	-2.2	1.9E-02	6.5	7.6E-05	-1.5	1.7E-01	0.5	4.2E-01
ENSMUST00000127481	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Source:MGI Symbol;Acc:MGI:105037]	S4R1E3		-9.4	2.7E-02	5.4	8.6E-03	-0.7	7.0E-01	0.5	6.0E-01
ENSMUST00000118694	chitinase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915288]		Q922Q9	4.1	2.2E-01	5.1	1.6E-01	-0.3	9.3E-01	-1.3	5.4E-01
ENSMUST00000118703	cell death inducing Trp53 target 1 [Source:MGI Symbol;Acc:MGI:1913876]		Q9DB75	-2.5	4.3E-02	-1.9	3.3E-01	2.2	1.0E-01	1.6	3.6E-01
ENSMUST00000118704	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]	Q3TBW3		-1.6	6.5E-01	-1.0	8.0E-01	-0.7	8.4E-01	-1.3	7.4E-01
ENSMUST00000127485	vesicular, overexpressed in cancer, prosurvival protein 1 [Source:MGI Symbol;Acc:MGI:2141658]		Q8R1C3	6.5	2.2E-04	8.6	3.6E-03	-0.3	9.0E-01	0.9	4.3E-01
ENSMUST00000118708				1.1	3.8E-01	-4.3	2.8E-02	-4.3	2.5E-03	1.2	4.9E-01
ENSMUST00000127520	zinc finger E-box binding homeobox 2 [Source:MGI Symbol;Acc:MGI:1344407]	F6X889		-3.4	1.8E-02	-4.1	7.1E-04	-7.6	7.3E-06	-0.3	7.5E-01
ENSMUST00000127569	ubiquitin specific peptidase 3 [Source:MGI Symbol;Acc:MGI:2152450]		Q91W36	1.6	9.2E-03	6.8	3.8E-04	0.0	9.7E-01	0.4	5.5E-01
ENSMUST00000127586	collagen beta(1-O)galactosyltransferase 2 [Source:MGI Symbol;Acc:MGI:2138232]	D6RCH2		5.5	1.9E-02	6.1	8.8E-04	1.5	2.3E-01	0.0	9.7E-01
ENSMUST00000127605	ribosomal protein S6 kinase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1927343]	E9PUN3		-4.7	6.4E-03	5.0	2.1E-03	-1.5	2.5E-01	-0.2	7.7E-01
ENSMUST00000118726	family with sequence similarity 160, member A2 [Source:MGI Symbol;Acc:MGI:1921599]		Q3U2I3	-0.9	7.2E-01	3.4	2.4E-01	2.3	3.8E-01	-1.9	4.1E-01
ENSMUST00000127608	GPN-loop GTPase 3 [Source:MGI Symbol;Acc:MGI:1289326]	A0A0G2JG32		3.3	3.1E-02	-7.0	5.3E-03	0.7	3.7E-01	1.3	5.4E-01
ENSMUST00000127610	ankyrin repeat and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:1337008]		Q810B6	-8.2	1.6E-04	6.5	4.4E-04	-0.6	6.6E-01	-0.8	2.9E-01
ENSMUST00000127638	signal transducer and activator of transcription 3 [Source:MGI Symbol;Acc:MGI:103038]		P42227	-11.1	1.3E-06	6.3	2.5E-04	-0.9	4.7E-01	-0.2	7.2E-01
ENSMUST00000127644	interferon gamma receptor 2 [Source:MGI Symbol;Acc:MGI:107654]	D6RIP6		-4.2	6.2E-04	6.2	4.7E-02	-0.9	7.6E-01	0.4	8.2E-01
ENSMUST00000127664	predicted gene 20388 [Source:MGI Symbol;Acc:MGI:5141853]		Q6PB93	-2.5	4.8E-04	5.1	7.2E-04	-0.3	7.9E-01	-1.6	3.8E-02
ENSMUST00000127680	RIKEN cDNA 2810474O19 gene [Source:MGI Symbol;Acc:MGI:1914496]	B2KFD0		2.6	2.6E-03	7.9	9.7E-05	-0.6	6.3E-01	-0.8	1.9E-01
ENSMUST00000118756	spleen tyrosine kinase [Source:MGI Symbol;Acc:MGI:99515]	E9PWE9		-0.4	5.5E-01	0.6	5.4E-01	0.5	4.9E-01	-0.5	5.4E-01
ENSMUST00000127698	TATA box binding protein-like 1 [Source:MGI Symbol;Acc:MGI:1339946]		P62340	-2.7	1.3E-03	2.2	1.2E-01	-0.5	6.5E-01	4.0	2.6E-03
ENSMUST00000127720	iption elongation factor A (SII) N-terminal and central domain containing 2 [Source:MGI Symbol;Acc:MGI:19	D6RH96		-6.0	2.6E-05	-3.6	3.9E-03	-0.2	6.6E-01	1.2	2.1E-01
ENSMUST00000127730	expressed sequence AI607873 [Source:MGI Symbol;Acc:MGI:2138302]	D3Z2E7		10.6	1.3E-06	-2.6	1.2E-02	1.6	9.1E-03	-0.1	9.5E-01
ENSMUST00000118763	CUGBP, Elav-like family member 5 [Source:MGI Symbol;Acc:MGI:2442333]	D3Z4T1		2.8	1.8E-01	5.4	1.8E-02	-0.6	7.7E-01	-3.2	5.4E-02
ENSMUST00000127737	Y box protein 1 [Source:MGI Symbol;Acc:MGI:99146]	A2BGG7		-4.2	4.1E-05	6.3	2.9E-04	-0.6	6.1E-01	-0.8	2.2E-01
ENSMUST00000118768	protein kinase D3 [Source:MGI Symbol;Acc:MGI:1922542]	D3Z6I0		0.4	8.0E-01	-2.7	1.1E-01	-4.6	5.5E-03	-1.4	4.4E-01
ENSMUST00000127748	TLR4 interactor with leucine-rich repeats [Source:MGI Symbol;Acc:MGI:1914123]		Q9DBY4	9.8	1.2E-05	6.6	1.2E-04	-0.6	6.0E-01	-0.7	2.9E-01
ENSMUST00000127775	RIKEN cDNA 4931428L18 gene [Source:MGI Symbol;Acc:MGI:1918238]	Q9D4J5		7.3	1.3E-05	7.2	1.4E-04	-1.4	2.9E-01	0.2	7.5E-01
ENSMUST00000127785	protein phosphatase 1, regulatory (inhibitor) subunit 13 like [Source:MGI Symbol;Acc:MGI:3525053]	D3Z5Q5		6.7	2.5E-04	6.9	1.2E-03	2.2	1.4E-01	-1.4	1.3E-01
ENSMUST00000127799	predicted gene 6483 [Source:MGI Symbol;Acc:MGI:3644574]	D3Z1Y8		3.3	6.0E-03	3.1	2.9E-02	-2.4	8.7E-02	-0.1	9.2E-01
ENSMUST00000127800	argonaute RISC catalytic subunit 1 [Source:MGI Symbol;Acc:MGI:2446630]	H3BL59		6.6	5.1E-03	6.3	2.4E-03	2.4	1.3E-01	-1.2	1.8E-01
ENSMUST00000127815	RIKEN cDNA 1700001C02 gene [Source:MGI Symbol;Acc:MGI:1922684]		Q9DAS2	6.2	1.7E-03	9.3	7.8E-05	-0.3	8.4E-01	0.3	6.6E-01
ENSMUST00000127820	early growth response 2 [Source:MGI Symbol;Acc:MGI:95296]	D3Z3K7		4.7	2.5E-02	-2.0	7.6E-03	0.2	5.8E-01	0.2	7.9E-01
ENSMUST00000127827	carbonic anhydrase 4 [Source:MGI Symbol;Acc:MGI:1096574]	D6RCZ3		4.6	3.2E-02	-5.3	5.9E-03	-1.0	2.5E-01	-0.4	8.4E-01
ENSMUST00000127833	ATPase type 13A2 [Source:MGI Symbol;Acc:MGI:1922022]	E9Q2A4		-9.2	6.9E-06	4.6	6.9E-04	0.1	9.3E-01	-0.2	7.2E-01
ENSMUST00000127862	heat shock protein 12B [Source:MGI Symbol;Acc:MGI:1919880]	S4R176		6.4	4.6E-03	5.1	1.1E-01	-0.9	7.7E-01	1.4	4.7E-01
ENSMUST00000127874	ribosomal protein L9 [Source:MGI Symbol;Acc:MGI:1298373]	D3YZT0		5.1	6.9E-03	7.0	2.6E-04	-0.6	6.4E-01	-0.7	3.1E-01
ENSMUST00000127886	Fras1 related extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:2670972]	F7D5I3		9.1	6.0E-05	7.8	3.9E-05	-0.6	5.9E-01	0.1	8.9E-01
ENSMUST00000118802	GTPase, IMAP family member 4 [Source:MGI Symbol;Acc:MGI:1349656]	D3YWB5		0.4	8.5E-01	-3.9	9.8E-02	-5.0	4.1E-03	-0.7	7.6E-01
ENSMUST00000118804				-0.5	4.4E-01	-0.2	8.4E-01	0.5	5.0E-01	0.1	9.0E-01
ENSMUST00000127924	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]	F7AVL7		-7.7	5.9E-03	2.3	3.3E-01	-0.7	7.3E-01	2.2	2.2E-01
ENSMUST00000118810	mitogen-activated protein kinase 1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1916796]		Q9D7G9	0.7	7.5E-01	-4.6	2.3E-01	-2.6	1.8E-01	2.6	4.7E-01
ENSMUST00000127939	ring finger protein 114 [Source:MGI Symbol;Acc:MGI:1933159]	S4R1Z0		-5.8	3.7E-04	-3.2	7.7E-02	1.9	3.5E-02	1.3	4.5E-01
ENSMUST00000127956	predicted gene, 28036 [Source:MGI Symbol;Acc:MGI:5547772]	F6YJB6		-5.7	3.1E-03	6.5	8.9E-04	-0.7	6.3E-01	0.0	9.7E-01
ENSMUST00000118816	cytochrome c oxidase assembly protein 18 [Source:MGI Symbol;Acc:MGI:2448532]	G5E8U6		1.0	5.8E-01	-2.5	3.6E-01	-2.2	1.8E-01	1.3	6.1E-01
ENSMUST00000127957	apolipoprotein L 6 [Source:MGI Symbol;Acc:MGI:1919189]	B7ZC55		7.3	5.0E-06	7.2	1.1E-03	-0.2	8.8E-01	0.5	5.2E-01
ENSMUST00000118821	preferentially expressed antigen in melanoma-like 3 [Source:MGI Symbol;Acc:MGI:1890657]	A2AHA7		3.0	2.3E-01	3.7	1.7E-01	-0.5	8.7E-01	-1.2	5.3E-01
ENSMUST00000127975	solute carrier family 26, member 5 [Source:MGI Symbol;Acc:MGI:1933154]	D3Z013		5.3	3.1E-02	6.7	9.6E-04	-0.2	8.9E-01	1.1	2.0E-01
ENSMUST00000127982	family with sequence similarity 189, member B [Source:MGI Symbol;Acc:MGI:1915771]	D6RDQ0		4.6	2.5E-02	1.9	3.4E-01	-2.0	3.2E-01	1.1	5.1E-01
ENSMUST00000127988	ADP-ribosylation factor related protein 1 [Source:MGI Symbol;Acc:MGI:1923938]		Q8BXL7	-6.4	1.9E-02	-6.3	7.9E-04	-1.2	6.4E-02	0.3	8.0E-01
ENSMUST00000127996	FAD-dependent oxidoreductase domain containing 1 [Source:MGI Symbol;Acc:MGI:2446262]		Q3TQB2	-6.5	2.3E-03	-6.3	1.1E-04	0.1	8.2E-01	-0.8	4.4E-01
ENSMUST00000128005	WD repeat domain 77 [Source:MGI Symbol;Acc:MGI:1917715]	F7D5L2		-6.4	2.1E-04	4.2	9.7E-02	-0.4	8.6E-01	1.9	2.0E-01
ENSMUST00000128040	transcription elongation factor A (SII)-like 3 [Source:MGI Symbol;Acc:MGI:1913354]	A2AEC2		5.7	1.3E-02	-6.9	8.7E-05	-0.6	1.1E-01	-0.8	4.7E-01
ENSMUST00000118835	mitochondrial tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2142572]			-1.2	1.0E-01	-5.1	6.3E-03	0.1	8.4E-01	4.0	2.1E-02
ENSMUST00000128042	zinc finger, CCHC domain containing 11 [Source:MGI Symbol;Acc:MGI:2445126]	A2A8R1		-3.5	1.2E-02	5.5	2.9E-03	-2.4	1.5E-01	0.3	7.6E-01
ENSMUST00000128088	serum amyloid A 1 [Source:MGI Symbol;Acc:MGI:98221]	Q5I0U6	P05366	-2.8	2.5E-02	6.0	3.0E-04	-0.3	7.7E-01	-0.5	4.4E-01
ENSMUST00000128095	alcium/calmodulin-dependent serine protein kinase (MAGUK family) [Source:MGI Symbol;Acc:MGI:1309485	F7CD87		-5.4	1.0E-02	5.5	5.7E-03	-0.5	7.9E-01	0.4	6.3E-01
ENSMUST00000118850	KxDL motif containing 1 [Source:MGI Symbol;Acc:MGI:1922870]	G3X9Z9		-2.5	2.0E-01	-3.1	1.1E-01	-1.9	1.3E-01	-1.4	5.2E-01
ENSMUST00000118853	family with sequence similarity 198, member B [Source:MGI Symbol;Acc:MGI:1915909]		Q3UPI1	3.1	2.9E-01	8.3	1.6E-02	-0.2	9.4E-01	-5.5	1.1E-02
ENSMUST00000128115	TRM2 tRNA methyltransferase 2B [Source:MGI Symbol;Acc:MGI:2442530]	S4R2E5		6.3	6.7E-06	6.8	4.1E-03	-0.6	7.5E-01	-2.0	8.2E-02
ENSMUST00000128119	multiple EGF-like-domains 8 [Source:MGI Symbol;Acc:MGI:2446294]		P60882	5.7	9.9E-06	7.7	1.1E-02	-0.4	9.0E-01	-1.7	2.4E-01
ENSMUST00000128136	host cell factor C1 [Source:MGI Symbol;Acc:MGI:105942]	F6SJS2		-6.9	1.4E-03	6.6	1.7E-04	-0.6	6.2E-01	-1.0	1.3E-01
ENSMUST00000118867	interferon-stimulated protein [Source:MGI Symbol;Acc:MGI:1928895]	Q4FK39	Q9JL16	1.1	5.6E-01	-4.6	5.0E-02	-6.0	1.4E-03	-0.4	8.7E-01
ENSMUST00000128150	intraflagellar transport 46 [Source:MGI Symbol;Acc:MGI:1923818]	D3YYR2		2.0	1.8E-03	4.9	1.3E-04	-2.0	4.8E-02	-0.3	5.3E-01
ENSMUST00000128152	diacylglycerol kinase zeta [Source:MGI Symbol;Acc:MGI:1278339]	D6RHK9		-3.7	1.2E-02	5.7	3.2E-03	-0.7	6.4E-01	-0.3	7.5E-01
ENSMUST00000128156	interleukin 15 receptor, alpha chain [Source:MGI Symbol;Acc:MGI:104644]	Q501M1	Q60819	-4.8	7.4E-04	7.5	2.3E-04	0.3	8.4E-01	-0.2	7.9E-01
ENSMUST00000128170	mitogen-activated protein kinase kinase kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346883]	F6RPB0		-5.9	3.2E-04	6.6	3.1E-05	2.3	1.7E-02	0.2	7.1E-01
ENSMUST00000128172	BCL2-like 1 [Source:MGI Symbol;Acc:MGI:88139]	Q9QWX2		2.8	1.9E-02	-7.1	2.1E-03	1.0	1.4E-01	0.5	7.9E-01
ENSMUST00000128184	hematopoietically expressed homeobox [Source:MGI Symbol;Acc:MGI:96086]	G3UXH1		-2.2	1.0E-02	-5.6	4.8E-04	0.1	8.2E-01	-0.5	6.4E-01
ENSMUST00000118882	canopy 1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2442451]		Q4VAB4	3.2	6.6E-02	3.9	2.4E-02	-1.3	4.0E-01	-2.1	1.1E-01
ENSMUST00000118886	SNF related kinase [Source:MGI Symbol;Acc:MGI:108104]		Q8VDU5	-2.3	2.1E-01	-2.5	3.0E-01	1.0	3.9E-01	1.2	6.3E-01
ENSMUST00000118887				0.0	9.8E-01	-0.1	9.1E-01	-0.8	1.6E-01	-0.7	2.6E-01
ENSMUST00000128187	heterogeneous nuclear ribonucleoprotein D-like [Source:MGI Symbol;Acc:MGI:1355299]	D3YTQ3		-6.8	3.3E-03	7.2	2.2E-03	-0.3	8.8E-01	-0.1	9.3E-01
ENSMUST00000128200	UPF2 regulator of nonsense transcripts homolog (yeast) [Source:MGI Symbol;Acc:MGI:2449307]	F6Q3G7		-7.1	1.1E-02	6.0	2.3E-04	0.1	9.5E-01	-0.7	2.5E-01
ENSMUST00000128201	protein arginine N-methyltransferase 7 [Source:MGI Symbol;Acc:MGI:2384879]	F6RXJ8		6.7	5.8E-04	5.0	9.2E-02	-0.7	8.2E-01	0.4	8.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000118898	heterogeneous nuclear ribonucleoprotein H3 [Source:MGI Symbol;Acc:MGI:1926462]	D3YWT1		-0.7	5.7E-01	1.1	5.4E-01	1.0	5.0E-01	-0.8	5.7E-01
ENSMUST00000128219	netrin G1 [Source:MGI Symbol;Acc:MGI:1934028]	F7CVQ1		6.3	9.9E-05	6.1	3.8E-04	-0.5	6.9E-01	-0.8	2.3E-01
ENSMUST00000118902	nuclear transcription factor-Y gamma [Source:MGI Symbol;Acc:MGI:107901]		P70353	2.2	4.5E-01	4.8	2.9E-01	1.5	7.0E-01	-1.1	7.0E-01
ENSMUST00000118904	axin 1 [Source:MGI Symbol;Acc:MGI:1096327]	Q14DJ8		0.9	7.1E-01	1.0	6.8E-01	-1.4	5.4E-01	-1.5	5.2E-01
ENSMUST00000128231	defender against cell death 1 [Source:MGI Symbol;Acc:MGI:101912]		P61804	5.2	5.1E-05	8.4	4.5E-05	-0.7	5.9E-01	-0.2	7.6E-01
ENSMUST00000128245	wingless-type MMTV integration site family, member 16 [Source:MGI Symbol;Acc:MGI:2136018]	H3BJ29		7.7	1.6E-04	-3.3	1.7E-03	1.5	4.9E-03	-4.0	3.9E-03
ENSMUST00000118910	phosphatidylinositol glycan anchor biosynthesis, class G [Source:MGI Symbol;Acc:MGI:3576484]	D3YTQ6		6.3	6.8E-02	2.1	5.3E-01	-2.6	4.5E-01	1.6	5.5E-01
ENSMUST00000128258	AHNAK nucleoprotein 2 [Source:MGI Symbol;Acc:MGI:2144831]	F7DBB3		10.7	1.1E-06	4.6	6.3E-03	0.3	7.9E-01	0.2	8.3E-01
ENSMUST00000118914				6.1	5.0E-02	5.6	8.8E-02	-0.8	7.9E-01	-0.4	8.3E-01
ENSMUST00000128259	RIKEN cDNA 4932414N04 gene [Source:MGI Symbol;Acc:MGI:1922971]	Q8CEQ9		7.5	3.5E-05	6.2	5.1E-04	-0.4	7.3E-01	-0.5	4.4E-01
ENSMUST00000118923	vacuolar protein sorting 8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2146407]		Q0P5W1	-2.8	1.5E-01	-1.9	4.5E-01	0.6	7.2E-01	-0.3	8.9E-01
ENSMUST00000118924				4.8	4.1E-02	0.6	7.9E-01	-3.0	1.6E-01	1.1	5.7E-01
ENSMUST00000128264	neuroblastoma ras oncogene [Source:MGI Symbol;Acc:MGI:97376]	E9PVD5		-6.0	4.4E-05	5.8	1.0E-03	-0.7	6.2E-01	0.5	5.0E-01
ENSMUST00000128270	subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1(	D6RDS9		-3.8	2.9E-03	-4.1	1.9E-03	-0.4	4.6E-01	-0.6	5.7E-01
ENSMUST00000118928				1.0	3.2E-01	0.1	9.0E-01	-1.7	7.6E-02	-0.8	4.1E-01
ENSMUST00000128273	family with sequence similarity 131, member A [Source:MGI Symbol;Acc:MGI:1925658]	D3YXU9		5.6	1.0E-02	-8.3	1.9E-03	1.3	4.6E-02	0.8	6.9E-01
ENSMUST00000128302	SET and MYND domain containing 3 [Source:MGI Symbol;Acc:MGI:1916976]		Q9CWR2	5.2	2.2E-05	5.8	6.8E-04	-0.6	6.5E-01	0.2	7.9E-01
ENSMUST00000128341	myosin IXa [Source:MGI Symbol;Acc:MGI:107735]		Q8C170	-3.7	1.9E-02	7.7	1.1E-03	-0.6	7.3E-01	-2.5	2.7E-02
ENSMUST00000128353	ankyrin repeat domain 9 [Source:MGI Symbol;Acc:MGI:1921501]		Q8BH83	5.1	7.0E-04	5.2	1.8E-02	-0.7	7.3E-01	0.1	9.2E-01
ENSMUST00000118949				2.5	2.4E-01	-4.0	1.6E-01	-5.0	1.7E-02	1.6	5.7E-01
ENSMUST00000128357	family with sequence similarity 45, member A [Source:MGI Symbol;Acc:MGI:1915144]	D3YUG1		-3.4	2.9E-02	8.9	1.7E-04	-0.3	8.7E-01	-0.3	6.2E-01
ENSMUST00000128364	membrane bound O-acyltransferase domain containing 7 [Source:MGI Symbol;Acc:MGI:1924832]	F6UP63		-6.7	4.0E-03	-4.2	7.7E-02	1.3	1.8E-01	-0.8	7.2E-01
ENSMUST00000128370	zinc finger protein 287 [Source:MGI Symbol;Acc:MGI:2176561]	B7ZC81		4.3	6.6E-04	-1.6	1.8E-01	1.4	5.5E-02	-0.7	5.4E-01
ENSMUST00000128373	family with sequence similarity 78, member B [Source:MGI Symbol;Acc:MGI:2443050]	F6ZXE6		8.0	6.5E-03	5.3	8.1E-04	-0.8	4.5E-01	0.6	3.9E-01
ENSMUST00000128402	kinesin family member 26A [Source:MGI Symbol;Acc:MGI:2447072]		Q52KG5	10.1	1.3E-05	6.9	2.5E-04	-0.5	6.8E-01	-0.7	3.0E-01
ENSMUST00000118962	synaptotagmin III [Source:MGI Symbol;Acc:MGI:99665]	G3X9Y1		2.2	2.2E-01	5.1	1.8E-02	0.1	9.6E-01	-2.8	6.9E-02
ENSMUST00000128467	cell division cycle 123 [Source:MGI Symbol;Acc:MGI:2138811]	A0A0A6YVX4		-2.3	2.4E-02	8.2	3.4E-05	-0.7	5.8E-01	0.0	9.7E-01
ENSMUST00000118970				3.2	7.2E-02	3.8	5.0E-02	-1.2	4.8E-01	-1.8	2.3E-01
ENSMUST00000128482	ribosomal protein S15A [Source:MGI Symbol;Acc:MGI:2389091]	D3YVB4		-9.4	5.9E-06	-4.7	1.0E-02	0.9	1.9E-01	0.9	5.7E-01
ENSMUST00000128485	CAP, adenylate cyclase-associated protein 1 (yeast) [Source:MGI Symbol;Acc:MGI:88262]	B1ARS0		-3.7	4.3E-03	5.2	2.0E-02	-0.5	7.9E-01	0.2	8.8E-01
ENSMUST00000128530	membrane-associated ring finger (C3HC4) 5 [Source:MGI Symbol;Acc:MGI:1915207]	F6W8T3		-6.6	2.1E-03	6.8	6.7E-05	-1.6	1.7E-01	-1.2	5.6E-02
ENSMUST00000128533	t-complex protein 10a [Source:MGI Symbol;Acc:MGI:98541]	Q80W76		7.7	3.1E-05	6.5	8.4E-03	0.0	9.8E-01	-1.6	1.3E-01
ENSMUST00000128557	chromosome alignment maintaining phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:1196398]			4.5	1.7E-02	6.8	1.0E-04	-0.6	5.9E-01	-0.8	1.8E-01
ENSMUST00000128565	CDC42 guanine nucleotide exchange factor (GEF) 9 [Source:MGI Symbol;Acc:MGI:2442233]	S4R1K5		6.9	5.0E-04	1.8	2.3E-02	-0.9	1.5E-01	-0.8	2.1E-01
ENSMUST00000128570	ras responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:2443664]		Q3UH06	-5.7	3.7E-03	-4.0	5.2E-03	-0.2	7.6E-01	-1.1	3.8E-01
ENSMUST00000128576	megakaryocyte-associated tyrosine kinase [Source:MGI Symbol;Acc:MGI:99259]	D6RGA0		2.5	7.7E-03	6.1	7.4E-04	-0.5	7.3E-01	-1.1	1.6E-01
ENSMUST00000119003	zinc finger protein 617 [Source:MGI Symbol;Acc:MGI:2684459]	Q91WM0		-0.7	1.0E-01	-0.8	1.7E-01	0.0	9.7E-01	0.1	8.7E-01
ENSMUST00000128590	signal peptide peptidase 3 [Source:MGI Symbol;Acc:MGI:1891433]			-3.8	6.3E-03	2.5	1.5E-01	-1.0	4.8E-01	1.2	3.0E-01
ENSMUST00000128619	hedgehog acyltransferase [Source:MGI Symbol;Acc:MGI:2444681]		Q8BMT9	2.9	2.9E-03	6.2	3.2E-04	-0.6	6.3E-01	0.0	9.6E-01
ENSMUST00000119014	phosphatidylinositol glycan anchor biosynthesis, class G [Source:MGI Symbol;Acc:MGI:3576484]	D3Z3Y1		-1.4	2.9E-01	1.1	4.7E-01	0.1	9.1E-01	-2.3	1.2E-01
ENSMUST00000119015	PTC7 protein phosphatase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2444593]		Q6NVE9	1.8	4.4E-01	0.1	9.8E-01	-1.2	5.8E-01	0.6	8.2E-01
ENSMUST00000128636	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A [Source:MGI Symbol;Acc:MGI:108447]	D3YYE1		-4.2	2.2E-03	6.0	1.9E-04	-0.5	6.2E-01	0.0	9.9E-01
ENSMUST00000128646	phosphatase and actin regulator 1 [Source:MGI Symbol;Acc:MGI:2659021]		Q2M3X8	6.2	3.0E-02	-4.9	2.6E-03	-1.2	7.8E-02	-3.1	5.7E-02
ENSMUST00000119025	hydroxysteroid (17-beta) dehydrogenase 11 [Source:MGI Symbol;Acc:MGI:2149821]		Q9EQ06	1.3	4.3E-02	1.1	1.4E-01	-0.4	4.6E-01	-0.2	7.8E-01
ENSMUST00000128667	fukutin [Source:MGI Symbol;Acc:MGI:2179507]		Q8R507	2.6	3.5E-03	6.8	8.3E-05	-1.5	2.1E-01	-0.2	7.7E-01
ENSMUST00000128676	zinc finger, NFX1-type containing 1 [Source:MGI Symbol;Acc:MGI:2138982]	A2A5R4		-2.6	2.6E-02	6.4	9.5E-04	-0.7	6.2E-01	0.3	6.9E-01
ENSMUST00000119033	PAP associated domain containing 5 [Source:MGI Symbol;Acc:MGI:1917820]	E9QJT6		0.9	7.5E-01	-0.5	9.1E-01	-0.9	7.8E-01	0.6	8.9E-01
ENSMUST00000128684	protein kinase C and casein kinase substrate in neurons 3 [Source:MGI Symbol;Acc:MGI:1891410]	F6W8Y8		6.2	2.4E-04	4.4	5.8E-03	-0.6	6.4E-01	1.5	7.4E-02
ENSMUST00000128706	transcription factor 4 [Source:MGI Symbol;Acc:MGI:98506]	Q8BPX7		3.9	4.3E-03	2.2	6.2E-01	8.3	1.9E-02	-1.4	7.3E-01
ENSMUST00000128715	ology domain-containing, family A (phosphoinositide binding specific) member 2 [Source:MGI Symbol;Acc:M		Q9ERS5	-2.9	2.9E-04	4.9	4.0E-04	-1.3	2.0E-01	-0.2	7.8E-01
ENSMUST00000128717	ankyrin-repeat and fibronectin type III domain containing 1 [Source:MGI Symbol;Acc:MGI:2686021]	F6RWQ6		6.0	2.5E-02	8.8	2.4E-05	0.4	7.2E-01	-1.4	2.5E-02
ENSMUST00000128748	arrestin, beta 2 [Source:MGI Symbol;Acc:MGI:99474]	G3UZS4		-3.6	1.6E-03	7.3	9.2E-05	-0.6	5.9E-01	-1.1	1.1E-01
ENSMUST00000128757	Mpv17 transgene, kidney disease mutant-like [Source:MGI Symbol;Acc:MGI:2135951]		Q99MS3	5.3	5.0E-05	6.1	2.4E-03	0.4	7.7E-01	-0.5	6.0E-01
ENSMUST00000128775	Rap guanine nucleotide exchange factor (GEF) 3 [Source:MGI Symbol;Acc:MGI:2441741]	E9Q2E5		6.1	3.7E-03	2.9	1.7E-01	-1.7	3.9E-01	2.4	1.4E-01
ENSMUST00000119063	activin A receptor, type II-like 1 [Source:MGI Symbol;Acc:MGI:1338946]		Q61288	-2.2	2.4E-01	-2.7	2.6E-01	0.0	9.7E-01	0.5	8.4E-01
ENSMUST00000128787	NADH dehydrogenase (ubiquinone) flavoprotein 1 [Source:MGI Symbol;Acc:MGI:107851]	D3YUM1		-6.6	1.3E-03	-0.9	2.6E-01	1.1	8.8E-02	-1.1	1.6E-01
ENSMUST00000128788	intraflagellar transport 20 [Source:MGI Symbol;Acc:MGI:1915585]		Q61025	-1.8	1.4E-02	5.6	8.3E-04	-1.5	2.6E-01	1.2	1.0E-01
ENSMUST00000119076	retrotransposon gag domain containing 4 [Source:MGI Symbol;Acc:MGI:3045324]	Q8C065	Q5DTT4	2.8	8.6E-02	2.6	1.4E-01	-1.3	3.8E-01	-1.1	4.3E-01
ENSMUST00000128791	cathepsin C [Source:MGI Symbol;Acc:MGI:109553]	D3Z220		-4.9	4.4E-04	4.8	8.4E-02	-0.8	7.6E-01	0.9	5.9E-01
ENSMUST00000128861	pogo transposable element with KRAB domain [Source:MGI Symbol;Acc:MGI:1918842]			9.7	4.2E-06	-6.0	6.1E-04	0.7	1.2E-01	0.5	6.9E-01
ENSMUST00000119080	gap junction protein, beta 1 [Source:MGI Symbol;Acc:MGI:95719]		P28230	2.4	1.6E-01	2.0	1.6E-01	-2.6	9.7E-02	-2.2	1.2E-01
ENSMUST00000128874	TBC1 domain family, member 2B [Source:MGI Symbol;Acc:MGI:1914266]	A0A087WRL5		2.2	6.0E-03	-6.6	1.4E-04	1.1	1.2E-02	0.6	6.2E-01
ENSMUST00000128901	erythroid differentiation regulatory factor 1 [Source:MGI Symbol;Acc:MGI:1919831]	D3YZE7		-6.3	7.8E-04	2.8	4.4E-01	-0.9	7.8E-01	4.0	1.6E-01
ENSMUST00000128921	prolactin receptor [Source:MGI Symbol;Acc:MGI:97763]	G3UVW6		8.1	1.7E-04	4.7	2.6E-02	-0.4	8.2E-01	0.0	9.7E-01
ENSMUST00000128923	acyl-Coenzyme A dehydrogenase family, member 8 [Source:MGI Symbol;Acc:MGI:1914198]	D6RDD5		-3.4	6.1E-03	6.8	7.8E-05	-2.0	1.0E-01	-0.3	6.0E-01
ENSMUST00000128941	torsin A interacting protein 2 [Source:MGI Symbol;Acc:MGI:3582695]		Q9ER81	2.9	1.0E-02	4.7	4.2E-02	-0.4	8.2E-01	-0.5	7.0E-01
ENSMUST00000119093	LEM domain containing 3 [Source:MGI Symbol;Acc:MGI:3580376]	D3YU56		0.1	9.3E-01	0.9	4.1E-01	0.8	3.5E-01	0.0	9.6E-01
ENSMUST00000128944	GRAM domain containing 2 [Source:MGI Symbol;Acc:MGI:3528937]		Q3V3G7	-3.2	1.4E-02	6.6	1.8E-04	-0.6	5.9E-01	-0.1	8.6E-01
ENSMUST00000119102	DEAH (Asp-Glu-Ala-His) box polypeptide 34 [Source:MGI Symbol;Acc:MGI:1918973]	D3YTV3		-1.1	4.4E-01	6.9	1.3E-02	4.7	5.0E-02	-3.3	4.0E-02
ENSMUST00000119103	beta-carotene oxygenase 2 [Source:MGI Symbol;Acc:MGI:2177469]	Q3KNZ2	Q99NF1	0.1	8.6E-01	1.9	9.2E-02	0.8	3.7E-01	-1.0	3.0E-01
ENSMUST00000128970	oid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) [Source:MGI Symbol;Acc:MGI:1075	D3YUU4		-6.6	3.1E-04	6.0	1.8E-03	0.6	6.6E-01	0.6	4.4E-01
ENSMUST00000119109	ets variant 3 [Source:MGI Symbol;Acc:MGI:1350926]		Q8R4Z4	1.7	2.4E-01	0.6	7.9E-01	2.2	2.2E-01	3.3	8.5E-02
ENSMUST00000128981	chromodomain helicase DNA binding protein 3 [Source:MGI Symbol;Acc:MGI:1344395]	F7C528		2.8	1.1E-03	6.5	8.1E-03	-0.8	6.9E-01	0.3	7.7E-01
ENSMUST00000129002	cyclin L1 [Source:MGI Symbol;Acc:MGI:1922664]	F6WYR6		-3.8	4.8E-03	6.8	2.2E-04	-0.5	7.0E-01	-0.5	4.1E-01
ENSMUST00000129020	gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:95706]	F6WUX1		-3.0	7.5E-03	6.2	7.5E-04	-0.7	6.2E-01	-0.2	7.4E-01
ENSMUST00000129021	aprataxin [Source:MGI Symbol;Acc:MGI:1913658]	E0CXB7		-6.4	1.3E-05	6.1	2.5E-04	-0.5	6.6E-01	0.0	9.5E-01
ENSMUST00000129035	RuvB-like protein 1 [Source:MGI Symbol;Acc:MGI:1928760]	D3YW60		5.9	1.0E-02	-5.9	3.3E-03	1.3	3.4E-02	-0.5	7.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000129043	PQ loop repeat containing 1 [Source:MGI Symbol;Acc:MGI:1914193]		Q80XM9	-7.4	4.4E-05	-0.5	7.0E-01	0.1	8.8E-01	-2.5	1.0E-01
ENSMUST00000129049	epair cross-complementing rodent repair deficiency, complementation group 4 [Source:MGI Symbol;Acc:MGI:	F7A043		2.2	1.9E-02	5.6	3.3E-02	-3.8	1.6E-01	-1.4	3.8E-01
ENSMUST00000129081	synovial apoptosis inhibitor 1, synoviolin [Source:MGI Symbol;Acc:MGI:1921376]	D3YZH4		5.8	5.5E-03	6.5	4.1E-04	-0.5	7.3E-01	-0.9	2.2E-01
ENSMUST00000119135				1.5	7.3E-02	1.7	9.3E-02	0.0	9.9E-01	-0.1	8.5E-01
ENSMUST00000129091	coiled-coil domain containing 167 [Source:MGI Symbol;Acc:MGI:1915847]		Q9D162	-3.7	2.6E-02	4.3	3.2E-02	-0.4	8.1E-01	-0.2	8.7E-01
ENSMUST00000129107	glutaminase [Source:MGI Symbol;Acc:MGI:95752]	F6RDM4		-3.9	2.2E-03	5.9	2.0E-02	0.6	7.8E-01	1.7	2.1E-01
ENSMUST00000119141	2-phosphoxylose phosphatase 1 [Source:MGI Symbol;Acc:MGI:2442444]		Q8BHA9	2.8	2.9E-01	2.8	4.1E-01	0.4	8.9E-01	0.5	8.6E-01
ENSMUST00000129116	death effector domain-containing [Source:MGI Symbol;Acc:MGI:1333874]	D3Z0I1		-3.9	2.7E-03	2.7	3.8E-01	-0.7	8.0E-01	2.3	3.2E-01
ENSMUST00000119146	SKI family transcriptional corepressor 1 [Source:MGI Symbol;Acc:MGI:2443473]		Q8BX46	3.9	4.4E-02	6.4	4.3E-03	-0.5	7.9E-01	-3.0	2.5E-02
ENSMUST00000119154	ubiquitin specific peptidase 46 [Source:MGI Symbol;Acc:MGI:1916977]	D3YVU0		5.6	9.1E-02	4.4	3.5E-01	0.8	8.5E-01	2.0	4.7E-01
ENSMUST00000129173	advillin [Source:MGI Symbol;Acc:MGI:1333798]		O88398	2.7	6.5E-03	8.6	3.9E-03	-0.5	8.4E-01	1.6	1.7E-01
ENSMUST00000119158	tropomyosin 3, gamma [Source:MGI Symbol;Acc:MGI:1890149]	D3Z6I8		-3.1	8.1E-02	-1.8	3.3E-01	-0.6	6.4E-01	-1.8	3.5E-01
ENSMUST00000129174	PDZ and LIM domain 2 [Source:MGI Symbol;Acc:MGI:2384850]	A0A087WPL1		-5.5	1.7E-04	6.1	3.0E-04	-1.5	2.3E-01	-0.3	6.9E-01
ENSMUST00000129190	KAT8 regulatory NSL complex subunit 1-like [Source:MGI Symbol;Acc:MGI:1915941]	F6ULJ7		-4.0	7.1E-03	2.6	2.1E-01	8.2	3.2E-04	0.8	6.3E-01
ENSMUST00000129200	canopy 3 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1919279]	D6RI28		-4.2	4.1E-03	5.7	3.1E-03	-0.2	8.9E-01	0.0	9.7E-01
ENSMUST00000129210	solute carrier family 35, member C2 [Source:MGI Symbol;Acc:MGI:2385166]	Q5GMG7		-2.9	7.8E-03	-1.2	2.5E-01	1.0	1.3E-01	-0.3	7.5E-01
ENSMUST00000119168	zinc finger protein 740 [Source:MGI Symbol;Acc:MGI:1915994]	D3Z4S9		-4.1	4.5E-02	-0.3	8.7E-01	0.2	8.8E-01	-3.6	9.1E-02
ENSMUST00000119172	calcineurin-like EF hand protein 1 [Source:MGI Symbol;Acc:MGI:1927185]	B0R091		0.2	9.1E-01	0.3	9.0E-01	-0.2	9.1E-01	-0.3	8.7E-01
ENSMUST00000119175				5.6	4.8E-02	3.9	7.9E-02	-3.0	2.3E-01	-1.3	4.3E-01
ENSMUST00000129213	ethanolamine kinase 2 [Source:MGI Symbol;Acc:MGI:2443760]	H9KV13		5.5	5.0E-04	7.1	5.0E-03	0.8	6.8E-01	0.7	4.7E-01
ENSMUST00000129224	mannose-P-dolichol utilization defect 1 [Source:MGI Symbol;Acc:MGI:1346040]	F6XX36		-5.7	5.7E-03	3.3	2.3E-03	0.1	9.1E-01	-0.6	3.5E-01
ENSMUST00000119185	myosin binding protein C, slow-type [Source:MGI Symbol;Acc:MGI:1336213]	D3YU50		4.7	9.9E-02	4.5	1.4E-01	-0.5	8.8E-01	-0.3	8.6E-01
ENSMUST00000129241	spectrin alpha, non-erythrocytic 1 [Source:MGI Symbol;Acc:MGI:98386]	A3KGU9		-2.8	1.6E-02	6.0	5.3E-04	0.1	9.6E-01	-0.4	5.3E-01
ENSMUST00000129269	stromal antigen 1 [Source:MGI Symbol;Acc:MGI:1098658]		Q9D3E6	-5.0	9.8E-05	6.6	2.4E-04	-0.8	5.2E-01	0.9	2.2E-01
ENSMUST00000129300	anaphase promoting complex subunit 2 [Source:MGI Symbol;Acc:MGI:2139135]	A2AI11		-3.8	1.1E-02	5.8	5.4E-04	-0.5	6.5E-01	0.1	8.9E-01
ENSMUST00000129339	eukaryotic translation elongation factor 1 beta 2 [Source:MGI Symbol;Acc:MGI:1929520]		O70251	1.4	3.4E-02	6.1	5.7E-04	-1.5	2.7E-01	-0.6	3.9E-01
ENSMUST00000129344	paraoxonase 3 [Source:MGI Symbol;Acc:MGI:106686]	D6RJ12		5.1	3.5E-03	2.4	5.1E-02	-1.0	3.2E-01	-0.5	6.1E-01
ENSMUST00000129414	ubiquitin-like 5 [Source:MGI Symbol;Acc:MGI:1913427]		Q9EPV8	-1.7	2.1E-02	-3.1	2.5E-01	1.3	3.3E-01	0.4	8.8E-01
ENSMUST00000129421	histidine ammonia lyase [Source:MGI Symbol;Acc:MGI:96010]	B2RXW1	P35492	2.9	1.1E-04	6.6	8.5E-04	-0.2	9.0E-01	-0.6	4.4E-01
ENSMUST00000119214				3.8	1.3E-01	4.5	1.2E-01	-0.3	9.0E-01	-1.0	5.6E-01
ENSMUST00000129423	tweety homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1889007]		Q9D3A9	7.0	7.1E-06	-1.0	5.3E-01	1.9	1.0E-01	-0.6	6.8E-01
ENSMUST00000129449	transmembrane protein 170B [Source:MGI Symbol;Acc:MGI:3647046]		P86050	-1.9	8.5E-04	6.9	1.2E-03	-0.7	6.5E-01	-0.8	3.8E-01
ENSMUST00000129464	BEN domain containing 6 [Source:MGI Symbol;Acc:MGI:2444572]	A0A087WSH8		3.4	6.8E-03	6.1	3.7E-04	-0.5	6.7E-01	-0.2	7.4E-01
ENSMUST00000129469	uridine-cytidine kinase 1-like 1 [Source:MGI Symbol;Acc:MGI:1915806]	D6RJ84		-6.7	1.3E-04	-1.2	2.7E-01	1.9	1.9E-02	-1.2	2.9E-01
ENSMUST00000129494	carnitine acetyltransferase [Source:MGI Symbol;Acc:MGI:109501]	A2AWE5		3.9	1.0E-03	1.7	2.0E-01	1.1	2.6E-01	1.7	1.4E-01
ENSMUST00000129507	family with sequence similarity 83, member E [Source:MGI Symbol;Acc:MGI:1921063]		Q80XS7	5.4	3.2E-02	3.5	8.2E-02	-0.6	7.5E-01	1.8	1.8E-01
ENSMUST00000129535	STAM binding protein like 1 [Source:MGI Symbol;Acc:MGI:1923880]	D3Z0S7		-2.1	3.1E-02	4.8	7.7E-03	-0.9	5.6E-01	-1.1	2.7E-01
ENSMUST00000119241				2.3	1.1E-01	4.2	2.4E-02	0.5	7.5E-01	-1.5	2.3E-01
ENSMUST00000129589	antizyme inhibitor 1 [Source:MGI Symbol;Acc:MGI:1859169]	D6RE45		-8.2	1.8E-03	6.4	2.7E-04	-0.6	6.3E-01	-0.7	2.7E-01
ENSMUST00000119246				-0.3	7.5E-01	-0.1	9.2E-01	0.4	7.0E-01	0.2	8.6E-01
ENSMUST00000129593	endoplasmic reticulum lectin 1 [Source:MGI Symbol;Acc:MGI:1914003]	F6Z458		-5.5	6.6E-04	6.0	7.9E-04	1.0	4.0E-01	0.0	9.7E-01
ENSMUST00000129603	multimerin 1 [Source:MGI Symbol;Acc:MGI:1918195]	G3UVV6		3.1	2.3E-03	7.1	1.2E-03	-0.8	6.3E-01	1.1	2.2E-01
ENSMUST00000119251	myocyte enhancer factor 2D [Source:MGI Symbol;Acc:MGI:99533]	E9Q5E0		-2.6	5.9E-02	-2.0	2.9E-01	0.9	4.0E-01	0.3	8.7E-01
ENSMUST00000129616	multiple coagulation factor deficiency 2 [Source:MGI Symbol;Acc:MGI:2183439]	D0EW11	Q8K5B2	-2.6	2.2E-02	2.7	1.5E-01	7.5	2.5E-04	-0.5	7.3E-01
ENSMUST00000119262				4.6	6.0E-02	1.6	4.9E-01	-2.1	3.8E-01	0.8	6.4E-01
ENSMUST00000119269	2-oxoglutarate and iron-dependent oxygenase domain containing 2 [Source:MGI Symbol;Acc:MGI:1913877]	D3YU42		-1.2	3.5E-01	6.9	1.3E-02	6.1	1.5E-02	-2.0	1.6E-01
ENSMUST00000129643	RIKEN cDNA A630010A05 gene [Source:MGI Symbol;Acc:MGI:3584518]	A9C474		8.7	3.5E-05	-5.0	6.1E-04	-0.4	4.3E-01	-1.8	1.7E-01
ENSMUST00000129651	cilia and flagella associated protein 126 [Source:MGI Symbol;Acc:MGI:1922722]	F6YI90		6.8	2.6E-04	-6.5	4.2E-04	-0.5	3.2E-01	-0.7	6.2E-01
ENSMUST00000119274	serine/threonine kinase 38 [Source:MGI Symbol;Acc:MGI:2442572]		Q91VJ4	-3.4	6.9E-02	-2.2	3.0E-01	0.3	7.5E-01	-0.9	7.1E-01
ENSMUST00000129653	glutaredoxin 2 (thioltransferase) [Source:MGI Symbol;Acc:MGI:1916617]	Q3UQ95	Q923X4	9.1	2.4E-05	6.4	1.4E-04	-0.5	6.3E-01	-0.6	3.3E-01
ENSMUST00000129667	special AT-rich sequence binding protein 1 [Source:MGI Symbol;Acc:MGI:105084]		Q60611	-7.2	5.1E-03	-3.3	7.4E-02	1.4	1.6E-01	1.5	3.8E-01
ENSMUST00000129670	von Willebrand factor C domain containing 2 [Source:MGI Symbol;Acc:MGI:2442987]		Q8C8N3	6.3	2.5E-04	-0.7	5.6E-01	1.1	1.9E-01	-0.4	7.2E-01
ENSMUST00000129680	receptor (calcitonin) activity modifying protein 2 [Source:MGI Symbol;Acc:MGI:1859650]		Q9WUP0	5.1	8.0E-04	7.4	1.2E-05	-1.9	9.1E-02	0.0	9.5E-01
ENSMUST00000129712	N-terminal Xaa-Pro-Lys N-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1913867]	A0A0A6YVQ9		6.6	4.1E-04	4.9	4.2E-05	-1.1	1.2E-01	0.1	8.8E-01
ENSMUST00000119288				-0.4	6.1E-01	1.9	6.6E-02	0.4	5.6E-01	-1.9	4.9E-02
ENSMUST00000129726	formin-like 1 [Source:MGI Symbol;Acc:MGI:1888994]	G3UWI1		-6.1	6.0E-03	4.1	1.3E-01	1.6	4.6E-01	3.1	1.3E-01
ENSMUST00000129753	aldehyde dehydrogenase 2, mitochondrial [Source:MGI Symbol;Acc:MGI:99600]	A0A0G2JEU1		-8.4	1.1E-05	5.8	2.5E-06	-1.2	5.5E-02	-0.2	4.5E-01
ENSMUST00000129811	lipopolysaccharide binding protein [Source:MGI Symbol;Acc:MGI:1098776]	F6XKX9		-5.8	6.5E-05	-5.4	5.5E-03	-1.4	5.9E-02	-1.2	4.7E-01
ENSMUST00000129815	IQ motif and Sec7 domain 3 [Source:MGI Symbol;Acc:MGI:2677208]	D6RHQ8		10.9	1.5E-04	5.7	5.8E-04	-0.6	6.3E-01	0.3	6.1E-01
ENSMUST00000129820	U7 snRNP-specific Sm-like protein LSM11 [Source:MGI Symbol;Acc:MGI:1919540]	Q5SUH5	Q8BUV6	4.0	5.8E-05	6.7	9.6E-05	-0.6	6.1E-01	0.0	9.8E-01
ENSMUST00000119305				2.6	1.3E-01	3.3	2.4E-01	2.5	3.0E-01	1.9	2.8E-01
ENSMUST00000119306	fibroblast growth factor 13 [Source:MGI Symbol;Acc:MGI:109178]		P70377	3.6	8.3E-02	5.1	4.0E-02	-0.1	9.6E-01	-1.6	3.3E-01
ENSMUST00000129822	surfeit gene 1 [Source:MGI Symbol;Acc:MGI:98443]	A0A0A6YVX3		-6.1	9.3E-05	6.3	9.9E-03	-0.7	7.5E-01	-2.0	1.2E-01
ENSMUST00000129825	RIKEN cDNA B430306N03 gene [Source:MGI Symbol;Acc:MGI:2443478]	A6XA72		-6.1	2.5E-04	2.0	2.6E-02	0.5	4.6E-01	0.0	9.9E-01
ENSMUST00000129827	ELK3, member of ETS oncogene family [Source:MGI Symbol;Acc:MGI:101762]	G3UVX2		-4.7	2.8E-03	5.3	1.3E-03	-1.4	2.7E-01	-0.7	3.8E-01
ENSMUST00000129828	LIM and SH3 protein 1 [Source:MGI Symbol;Acc:MGI:109656]	A2A6G9		4.0	1.0E-03	2.2	6.1E-03	-1.7	1.6E-02	-0.1	9.1E-01
ENSMUST00000129847	ribosomal protein S19 [Source:MGI Symbol;Acc:MGI:1333780]	S4R223		-9.9	2.9E-05	5.6	8.0E-05	0.6	4.8E-01	-0.2	6.8E-01
ENSMUST00000119324	sirtuin 6 [Source:MGI Symbol;Acc:MGI:1354161]	Q3UKP1		-0.7	2.7E-01	0.3	7.2E-01	0.4	4.5E-01	-0.5	4.7E-01
ENSMUST00000129853	family with sequence similarity 57, member A [Source:MGI Symbol;Acc:MGI:2151840]	B7ZC15		4.4	2.0E-02	-6.8	2.1E-04	-1.1	2.6E-02	0.0	9.9E-01
ENSMUST00000129870	acyl-Coenzyme A binding domain containing 4 [Source:MGI Symbol;Acc:MGI:1914381]	E0CXU7		-3.6	1.9E-02	8.0	1.8E-05	0.4	7.0E-01	0.2	6.4E-01
ENSMUST00000119339	YTH domain containing 1 [Source:MGI Symbol;Acc:MGI:2443713]		E9Q5K9	-0.2	8.6E-01	-2.2	2.0E-01	0.6	5.5E-01	2.6	1.2E-01
ENSMUST00000129880	RAS protein activator like 2 [Source:MGI Symbol;Acc:MGI:2443881]	D3YWZ9		7.1	5.8E-05	6.1	3.1E-04	-0.6	6.3E-01	-0.4	5.7E-01
ENSMUST00000119344	profilin 2 [Source:MGI Symbol;Acc:MGI:97550]		Q9JJV2	2.7	4.6E-02	6.0	5.3E-04	-0.5	6.7E-01	-3.8	1.9E-03
ENSMUST00000129898	ATP-binding cassette, sub-family C (CFTR/MRP), member 12 [Source:MGI Symbol;Acc:MGI:2441679]		Q80WJ6	7.6	3.2E-05	6.8	2.9E-04	-0.1	9.1E-01	-0.5	4.8E-01
ENSMUST00000129904	SH3-binding domain glutamic acid-rich protein [Source:MGI Symbol;Acc:MGI:1354740]	D3Z3Z9		6.8	4.9E-05	-2.4	3.5E-02	0.6	3.4E-01	-2.5	4.9E-02
ENSMUST00000129909	ubiquitin A-52 residue ribosomal protein fusion product 1 [Source:MGI Symbol;Acc:MGI:98887]	Q66JP1	P62984	-3.6	3.8E-03	3.2	6.3E-03	-2.7	2.6E-02	1.1	1.2E-01
ENSMUST00000129935	ribosomal protein L10A [Source:MGI Symbol;Acc:MGI:1343877]	D6RE43		-3.3	1.5E-02	5.7	1.0E-03	-0.6	6.6E-01	-0.3	7.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000129948	C-type lectin domain family 5, member a [Source:MGI Symbol;Acc:MGI:1345151]		Q9R007	-6.4	2.6E-04	6.9	3.6E-06	0.5	5.1E-01	-0.5	2.3E-01
ENSMUST00000129956	PRP39 pre-mRNA processing factor 39 homolog (yeast) [Source:MGI Symbol;Acc:MGI:104602]	D6RDR5		-6.4	9.4E-04	5.2	2.9E-02	-1.5	4.7E-01	-0.9	5.3E-01
ENSMUST00000119366	membrane-spanning 4-domains, subfamily A, member 4C [Source:MGI Symbol;Acc:MGI:1927656]	Q3U5N6		-0.5	6.5E-01	-1.2	4.1E-01	0.0	9.7E-01	0.7	6.4E-01
ENSMUST00000130028	RAB, member RAS oncogene family-like 3 [Source:MGI Symbol;Acc:MGI:1914907]		Q9D4V7	5.6	5.9E-03	6.9	1.1E-04	0.5	6.4E-01	-0.9	1.6E-01
ENSMUST00000130033	t-complex-associated testis expressed 2 [Source:MGI Symbol;Acc:MGI:98641]	D3Z5S1		7.4	1.0E-04	-3.3	1.0E-02	0.3	6.1E-01	1.0	3.5E-01
ENSMUST00000130043	pleckstrin homology domain containing, family O member 1 [Source:MGI Symbol;Acc:MGI:1914470]	F6VV25		-2.8	1.6E-02	6.8	1.0E-04	-0.5	6.6E-01	0.2	7.7E-01
ENSMUST00000130059	integrin beta 2 [Source:MGI Symbol;Acc:MGI:96611]	D3YYP8		-4.4	1.4E-03	6.1	7.1E-04	-0.7	6.2E-01	-0.4	5.8E-01
ENSMUST00000130139	tripartite motif-containing 12C [Source:MGI Symbol;Acc:MGI:4821183]	D3Z3L3		-5.7	1.9E-03	-5.8	4.0E-03	-0.6	3.4E-01	0.1	9.4E-01
ENSMUST00000130161	lines homolog (Drosophila) 1 [Source:MGI Symbol;Acc:MGI:1919885]	D6RFA2		5.1	2.3E-02	5.7	1.1E-03	0.8	5.5E-01	-0.6	4.4E-01
ENSMUST00000119383				4.0	5.6E-02	2.0	3.7E-01	-1.6	4.4E-01	0.5	7.9E-01
ENSMUST00000130163	phosphorylated adaptor for RNA export [Source:MGI Symbol;Acc:MGI:1891839]	G5E8V8		-3.2	1.0E-03	6.4	3.8E-04	0.8	5.2E-01	-0.3	6.6E-01
ENSMUST00000130169	ubiquitin protein ligase E3B [Source:MGI Symbol;Acc:MGI:1891295]	S4R2P2		-4.1	3.5E-02	5.8	4.5E-03	-0.1	9.4E-01	-0.5	6.1E-01
ENSMUST00000130188	mitochondrial ribosomal protein L20 [Source:MGI Symbol;Acc:MGI:2137221]	V9GX65		4.3	7.9E-05	5.1	7.0E-03	-0.8	6.1E-01	-1.3	2.2E-01
ENSMUST00000119398	fibroblast growth factor receptor 1 [Source:MGI Symbol;Acc:MGI:95522]		P16092	-0.6	7.2E-01	-2.8	2.1E-01	-2.6	5.4E-02	-0.5	8.4E-01
ENSMUST00000130216	serine/arginine-rich splicing factor 3 [Source:MGI Symbol;Acc:MGI:98285]		P84104	-4.0	5.5E-03	4.7	7.1E-03	-1.1	4.3E-01	0.1	9.0E-01
ENSMUST00000119418				1.4	9.7E-02	2.1	4.8E-02	0.0	9.7E-01	-0.7	3.9E-01
ENSMUST00000130235	receptor tyrosine kinase-like orphan receptor 2 [Source:MGI Symbol;Acc:MGI:1347521]	E9PUN5		8.9	5.0E-06	6.1	1.8E-03	0.4	7.7E-01	-0.4	6.0E-01
ENSMUST00000130310	cytoplasmic polyadenylation element binding protein 1 [Source:MGI Symbol;Acc:MGI:108442]	F6X7Z3		6.0	9.6E-03	7.0	3.8E-04	-0.7	6.3E-01	-0.2	8.0E-01
ENSMUST00000130320	F-box protein 7 [Source:MGI Symbol;Acc:MGI:1917004]		Q3U7U3	2.6	4.7E-03	4.8	7.1E-04	1.0	2.7E-01	-0.1	8.7E-01
ENSMUST00000119430	sterile alpha motif domain containing 8 [Source:MGI Symbol;Acc:MGI:1914880]	Q3UH82		-0.5	2.8E-01	0.4	5.2E-01	1.3	2.8E-02	0.3	6.4E-01
ENSMUST00000119433	shisa family member 7 [Source:MGI Symbol;Acc:MGI:3605641]		Q8C3Q5	3.3	6.6E-02	5.2	4.7E-03	-1.4	3.9E-01	-3.4	1.6E-02
ENSMUST00000130325	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925901]	Q542U7	P62313	3.0	2.3E-05	3.4	1.5E-03	-0.1	8.3E-01	0.4	4.6E-01
ENSMUST00000130326	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914854]	D3Z4J5		-3.5	1.6E-02	-3.7	1.6E-01	3.3	2.3E-02	-0.6	8.1E-01
ENSMUST00000130332	hosphatidylinositol-specific phospholipase C, X domain containing 3 [Source:MGI Symbol;Acc:MGI:2442605	D6RDF3		8.9	9.6E-06	5.6	1.1E-03	-1.5	2.7E-01	-1.9	3.2E-02
ENSMUST00000130360	synaptopodin [Source:MGI Symbol;Acc:MGI:1099446]	E9Q3E2		6.8	2.8E-02	1.9	5.5E-02	-1.0	2.1E-01	0.6	4.1E-01
ENSMUST00000130367	tripartite motif-containing 26 [Source:MGI Symbol;Acc:MGI:1337056]		Q99PN3	-5.4	7.8E-04	6.6	4.2E-04	-0.4	7.4E-01	-1.2	1.2E-01
ENSMUST00000130379	F-box protein 11 [Source:MGI Symbol;Acc:MGI:2147134]	F6T356		-4.5	6.1E-03	6.1	9.0E-04	2.2	9.0E-02	1.1	1.4E-01
ENSMUST00000130405	Rho GTPase activating protein 20 [Source:MGI Symbol;Acc:MGI:2445175]	D3YUH8		6.7	1.1E-04	-3.6	1.1E-02	0.4	4.3E-01	-0.1	9.1E-01
ENSMUST00000130411	serine/arginine-rich splicing factor 6 [Source:MGI Symbol;Acc:MGI:1915246]		Q3TWW8	-3.7	1.4E-03	6.3	2.0E-04	-0.6	6.2E-01	0.0	9.9E-01
ENSMUST00000119455	transmembrane channel-like gene family 8 [Source:MGI Symbol;Acc:MGI:2669037]	B0QZP6	Q7TN58	0.1	9.4E-01	1.3	2.3E-01	1.0	2.4E-01	-0.2	7.9E-01
ENSMUST00000130414	synaptotagmin IX [Source:MGI Symbol;Acc:MGI:1926373]	D6RGS5		6.2	2.6E-02	7.5	8.1E-05	-0.2	8.9E-01	-0.1	8.7E-01
ENSMUST00000130418	aldehyde dehydrogenase 1 family, member L1 [Source:MGI Symbol;Acc:MGI:1340024]		Q8R0Y6	7.3	7.6E-05	5.2	5.8E-03	0.0	9.9E-01	0.2	8.3E-01
ENSMUST00000130420	Rho GTPase activating protein 44 [Source:MGI Symbol;Acc:MGI:2144423]	F6T1Y2		7.4	1.5E-03	8.2	9.0E-05	-0.5	7.2E-01	-0.9	1.4E-01
ENSMUST00000119467				-1.0	2.6E-01	-2.2	4.2E-02	-2.3	8.1E-03	-1.1	2.5E-01
ENSMUST00000119468	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 [Source:MGI Symbol;Acc:MGI:2137302]		Q8BGY6	1.4	2.5E-01	2.4	5.0E-02	-1.7	1.1E-01	-2.7	3.3E-02
ENSMUST00000130451	endoplasmic reticulum protein 29 [Source:MGI Symbol;Acc:MGI:1914647]		P57759	1.2	1.5E-02	6.2	1.0E-03	0.5	7.3E-01	0.4	5.9E-01
ENSMUST00000130459	promyelocytic leukemia [Source:MGI Symbol;Acc:MGI:104662]	F6RQM1		4.3	3.3E-02	5.8	3.9E-03	-0.7	6.7E-01	0.8	4.0E-01
ENSMUST00000119477	polysaccharide biosynthesis domain containing 1 [Source:MGI Symbol;Acc:MGI:1914933]		Q9D0B6	-2.3	3.5E-02	-1.9	2.9E-01	1.2	2.7E-01	0.8	6.1E-01
ENSMUST00000130481	hosphatidylinositol-specific phospholipase C, X domain containing 2 [Source:MGI Symbol;Acc:MGI:3647874	B2RXA1		2.8	3.2E-04	-5.9	3.5E-04	-1.0	3.7E-02	-1.8	1.5E-01
ENSMUST00000130509	WD repeat and FYVE domain containing 4 [Source:MGI Symbol;Acc:MGI:3584510]	E9Q2M9		-2.1	1.2E-03	3.0	8.7E-02	-0.7	6.3E-01	3.6	1.2E-02
ENSMUST00000130541	FGGY carbohydrate kinase domain containing [Source:MGI Symbol;Acc:MGI:1922828]	B7ZCH9		-4.3	2.6E-03	6.0	2.5E-04	-0.6	6.1E-01	0.3	6.3E-01
ENSMUST00000130549	alin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G [Source:MGI		Q9WUH7	6.7	2.8E-04	0.0	9.8E-01	-1.2	3.4E-01	3.6	3.7E-02
ENSMUST00000119488	family with sequence similarity 220, member A [Source:MGI Symbol;Acc:MGI:1914488]	Q5U425		-2.5	1.7E-01	2.7	2.3E-01	1.8	3.1E-01	-3.4	1.0E-01
ENSMUST00000130553	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 [Source:MGI Symbol;Acc:MGI:1918617]	D6RCI1		5.5	1.8E-03	6.3	2.2E-04	1.7	1.2E-01	-0.6	3.5E-01
ENSMUST00000130559	mitochondrial pyruvate carrier 1 [Source:MGI Symbol;Acc:MGI:1915240]	D3Z5S0		-6.8	8.8E-05	4.1	2.3E-03	0.1	8.8E-01	0.6	3.8E-01
ENSMUST00000119499	oxysterol binding protein-like 5 [Source:MGI Symbol;Acc:MGI:1930265]		Q9ER64	0.7	5.0E-01	1.1	3.6E-01	-1.4	2.0E-01	-1.7	1.4E-01
ENSMUST00000130560	apolipoprotein D [Source:MGI Symbol;Acc:MGI:88056]		P51910	4.6	1.1E-03	-4.8	8.5E-04	-0.8	9.6E-02	-0.7	5.2E-01
ENSMUST00000130590	low density lipoprotein receptor-related protein 11 [Source:MGI Symbol;Acc:MGI:2442989]	D3Z2B1		5.4	1.6E-02	6.0	2.0E-04	-1.5	2.0E-01	-0.3	6.5E-01
ENSMUST00000130602	angiomotin-like 2 [Source:MGI Symbol;Acc:MGI:1929286]	B8JK81		-7.8	1.9E-04	5.5	4.4E-03	2.1	1.6E-01	-0.6	4.5E-01
ENSMUST00000130606	capping protein (actin filament) muscle Z-line, alpha 2 [Source:MGI Symbol;Acc:MGI:106222]	D6RCW7		-8.8	1.1E-05	5.5	1.3E-02	-1.8	3.7E-01	-0.2	8.9E-01
ENSMUST00000130697	interferon regulatory factor 9 [Source:MGI Symbol;Acc:MGI:107587]	Q3UKQ7	Q61179	-7.2	3.5E-06	4.4	1.0E-03	-0.8	4.0E-01	-0.1	8.3E-01
ENSMUST00000130700	selenoprotein O [Source:MGI Symbol;Acc:MGI:1919007]	S4R1U9		1.8	1.1E-02	7.2	6.5E-04	1.2	4.1E-01	0.3	6.7E-01
ENSMUST00000130735	5-azacytidine induced gene 2 [Source:MGI Symbol;Acc:MGI:1351332]	F7A092		-5.7	9.9E-05	5.9	4.4E-04	-0.6	6.2E-01	-0.2	7.4E-01
ENSMUST00000130763	transmembrane BAX inhibitor motif containing 1 [Source:MGI Symbol;Acc:MGI:1916910]	D3Z225		6.8	4.8E-05	6.0	2.7E-04	-0.5	6.3E-01	-0.4	5.2E-01
ENSMUST00000119542				3.6	4.6E-02	5.5	2.2E-02	0.6	7.7E-01	-1.3	3.3E-01
ENSMUST00000130778	SEC22 homolog B, vesicle trafficking protein [Source:MGI Symbol;Acc:MGI:1338759]	D6RES2		-7.1	9.8E-06	-6.0	2.5E-03	0.7	2.7E-01	-1.0	5.6E-01
ENSMUST00000130785	RIKEN cDNA 4933413G19 gene [Source:MGI Symbol;Acc:MGI:1918399]			6.0	5.0E-04	5.0	1.9E-03	-0.6	6.2E-01	0.8	2.9E-01
ENSMUST00000130818	PEST proteolytic signal containing nuclear protein [Source:MGI Symbol;Acc:MGI:1923552]	D6RGL8		-6.3	1.7E-05	7.6	4.0E-05	-0.5	6.4E-01	-0.8	1.8E-01
ENSMUST00000119551				3.3	2.0E-01	4.8	8.6E-02	-0.5	8.5E-01	-2.1	2.6E-01
ENSMUST00000130825	predicted gene 13248 [Source:MGI Symbol;Acc:MGI:3713585]	A2A8V4		2.3	2.9E-02	5.9	5.3E-03	-0.3	8.5E-01	-0.8	4.0E-01
ENSMUST00000119558	RIKEN cDNA 6330408A02 gene [Source:MGI Symbol;Acc:MGI:2447816]	D3YTW6		0.1	9.6E-01	-0.6	8.0E-01	-2.1	3.0E-01	-1.4	5.5E-01
ENSMUST00000130864	kinesin family member 21B [Source:MGI Symbol;Acc:MGI:109234]	E9Q0A4		6.4	9.0E-03	-4.4	3.0E-03	0.1	8.2E-01	-1.0	4.2E-01
ENSMUST00000119567	RUN and FYVE domain-containing 2 [Source:MGI Symbol;Acc:MGI:1917682]	B2RQ36	Q8R4C2	0.5	3.4E-01	0.6	3.4E-01	-0.1	8.7E-01	-0.2	7.2E-01
ENSMUST00000130870	predicted gene 14226 [Source:MGI Symbol;Acc:MGI:3649244]	Q3TZL0		6.4	4.3E-05	5.2	3.3E-03	-0.7	6.2E-01	0.3	6.9E-01
ENSMUST00000130876	lysophosphatidylglycerol acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2446186]	D3YVK0		-2.4	1.7E-02	5.8	8.1E-04	-0.6	6.2E-01	0.3	6.7E-01
ENSMUST00000119581	thrombospondin, type I, domain containing 7A [Source:MGI Symbol;Acc:MGI:2685683]	E9Q6P0		2.7	6.5E-02	4.5	7.2E-03	-0.6	6.8E-01	-2.4	4.7E-02
ENSMUST00000130880	gem (nuclear organelle) associated protein 8 [Source:MGI Symbol;Acc:MGI:2384300]		Q8BHE1	5.0	3.2E-04	3.8	9.6E-04	-2.4	2.7E-02	-1.4	6.0E-02
ENSMUST00000130911	nuclear transcription factor-Y beta [Source:MGI Symbol;Acc:MGI:97317]		P63139	-5.6	1.6E-05	6.7	2.8E-03	0.1	9.5E-01	0.1	9.2E-01
ENSMUST00000119591	conserved helix-loop-helix ubiquitous kinase [Source:MGI Symbol;Acc:MGI:99484]	E9Q605		-2.3	4.8E-01	-3.1	4.6E-01	-1.3	5.9E-01	-0.4	9.2E-01
ENSMUST00000130914	ubiquitin-conjugating enzyme E2E 3 [Source:MGI Symbol;Acc:MGI:107412]	B2FDH0		4.8	2.2E-02	8.2	9.0E-04	0.1	9.6E-01	-0.4	6.8E-01
ENSMUST00000130922	cell division cycle associated 2 [Source:MGI Symbol;Acc:MGI:1919787]	F6RTJ7		2.6	1.0E-02	6.6	2.5E-05	-0.6	4.8E-01	0.4	4.2E-01
ENSMUST00000130990	yc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) [Source:MGI Symbol;Acc:MGI:97	Q3UII1	P03966	4.4	6.0E-03	-0.1	9.2E-01	0.6	2.8E-01	-3.3	7.9E-03
ENSMUST00000131002	lysine (K)-specific methyltransferase 2B [Source:MGI Symbol;Acc:MGI:109565]	F6W623		-3.4	2.6E-02	-6.1	3.3E-03	1.0	9.8E-02	-1.0	5.9E-01
ENSMUST00000119606	zinc finger and BTB domain containing 7a [Source:MGI Symbol;Acc:MGI:1335091]		O88939	-0.4	7.8E-01	0.2	9.1E-01	1.9	1.7E-01	1.3	4.9E-01
ENSMUST00000131011	cytochrome c oxidase subunit VIIc [Source:MGI Symbol;Acc:MGI:103226]		P17665	-2.2	2.5E-02	7.3	1.6E-04	0.9	4.7E-01	-0.2	7.2E-01
ENSMUST00000131017	neurobeachin-like 2 [Source:MGI Symbol;Acc:MGI:2448554]	F6ZZB1		-8.7	5.9E-04	5.0	7.6E-04	-0.8	4.5E-01	0.4	5.9E-01
ENSMUST00000119628	myotubularin related protein 4 [Source:MGI Symbol;Acc:MGI:2180699]		Q91XS1	3.8	7.9E-02	5.4	6.0E-02	0.7	7.8E-01	-0.9	6.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000131028	e regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy) [Source:MGI Symbol;Acc:MG	D6RDQ5		9.1	8.6E-06	4.7	1.1E-02	-0.9	6.0E-01	0.4	6.6E-01
ENSMUST00000131056	scaffold attachment factor B2 [Source:MGI Symbol;Acc:MGI:2146808]	F6WIZ2		-5.2	6.7E-03	7.6	3.7E-05	-1.4	2.5E-01	-0.4	4.8E-01
ENSMUST00000131126	leukocyte-associated Ig-like receptor 1 [Source:MGI Symbol;Acc:MGI:105492]	D6RGS7	Q8BG84	-3.8	3.9E-03	-2.1	2.4E-02	0.2	7.1E-01	-2.6	2.5E-02
ENSMUST00000131127	pecanex-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2445010]		Q5DU28	8.9	1.6E-05	5.3	9.3E-03	-0.5	8.0E-01	-0.4	6.9E-01
ENSMUST00000131134	collagen, type XI, alpha 2 [Source:MGI Symbol;Acc:MGI:88447]	I7HPY2		4.4	2.0E-02	3.8	5.0E-02	-0.7	6.8E-01	2.1	9.5E-02
ENSMUST00000131186	-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:13	Q9Z281		4.7	2.3E-02	6.4	1.9E-04	-0.1	9.4E-01	0.2	7.8E-01
ENSMUST00000119647	C2 calcium-dependent domain containing 3 [Source:MGI Symbol;Acc:MGI:2142166]	D3Z640		1.3	4.2E-01	4.5	2.6E-02	-0.3	8.7E-01	-3.5	3.2E-02
ENSMUST00000131193	solute carrier family 35, member B1 [Source:MGI Symbol;Acc:MGI:1343133]	E0CXH1		-6.0	2.1E-04	6.3	7.8E-04	-0.5	7.2E-01	-0.8	2.9E-01
ENSMUST00000131290	CD37 antigen [Source:MGI Symbol;Acc:MGI:88330]	D3Z0N6		-5.2	3.3E-03	4.2	2.8E-02	-1.0	5.7E-01	-0.3	8.0E-01
ENSMUST00000131292	GDNF-inducible zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1921783]	A2ASL5		5.3	6.3E-03	6.1	3.6E-04	-0.6	6.0E-01	0.1	8.3E-01
ENSMUST00000131309	frizzled homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:108476]		Q61086	4.2	4.2E-04	6.0	1.1E-03	-1.5	3.2E-01	-0.1	9.4E-01
ENSMUST00000119664	mitogen-activated protein kinase 1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1916796]		Q9D7G9	-0.2	8.7E-01	1.5	2.1E-01	0.3	7.4E-01	-1.4	2.2E-01
ENSMUST00000131320	ankyrin repeat and SOCS box-containing 7 [Source:MGI Symbol;Acc:MGI:2152835]	Q8BQC5		-6.5	5.1E-03	0.3	7.8E-01	4.3	4.4E-04	-0.6	5.9E-01
ENSMUST00000131323	adaptor protein complex AP-1, gamma 2 subunit [Source:MGI Symbol;Acc:MGI:1328307]	D6RFT7		6.4	1.2E-04	5.9	8.3E-03	-0.8	6.9E-01	-1.1	3.5E-01
ENSMUST00000131338	acyl-Coenzyme A dehydrogenase family, member 12 [Source:MGI Symbol;Acc:MGI:2443320]	F6RGT6		5.3	2.4E-05	5.5	4.9E-03	-0.7	6.9E-01	0.6	5.1E-01
ENSMUST00000131351	expressed sequence AU019823 [Source:MGI Symbol;Acc:MGI:2143205]	E9PUQ3		-2.5	1.5E-03	1.9	1.0E-01	-2.1	5.7E-02	-0.4	6.4E-01
ENSMUST00000131374	ribosomal protein S15A [Source:MGI Symbol;Acc:MGI:2389091]	Q5M9M4	P62245	-7.5	1.8E-04	5.9	3.5E-04	-0.5	6.4E-01	0.0	9.6E-01
ENSMUST00000131390	major facilitator superfamily domain containing 9 [Source:MGI Symbol;Acc:MGI:2443548]	M0QWK7		6.6	1.4E-03	-5.8	4.6E-03	0.1	8.5E-01	0.9	5.9E-01
ENSMUST00000131415	coronin, actin binding protein 1A [Source:MGI Symbol;Acc:MGI:1345961]	D3YW57		-6.4	1.1E-03	4.4	3.2E-04	0.9	2.3E-01	-0.4	4.6E-01
ENSMUST00000119707	family with sequence similarity 189, member B [Source:MGI Symbol;Acc:MGI:1915771]	E9Q6P6		-2.7	1.0E-01	-1.2	5.7E-01	2.1	1.4E-01	0.7	7.6E-01
ENSMUST00000131422	DNA replication helicase 2 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2443732]		Q6ZQJ5	-6.1	3.1E-05	6.0	3.1E-02	-0.6	8.3E-01	-1.0	5.1E-01
ENSMUST00000131446	ADP-ribosylation factor interacting protein 2 [Source:MGI Symbol;Acc:MGI:1924182]		Q8K221	-3.4	1.0E-02	6.1	2.1E-02	-0.8	7.4E-01	-0.7	6.1E-01
ENSMUST00000119718	predicted gene 13212 [Source:MGI Symbol;Acc:MGI:3651014]	B1ASQ6		1.2	8.5E-02	1.1	1.4E-01	-0.4	5.0E-01	-0.4	5.7E-01
ENSMUST00000119721	sushi domain containing 3 [Source:MGI Symbol;Acc:MGI:1913579]		Q9D176	1.0	3.1E-01	1.8	1.6E-01	1.3	2.0E-01	0.5	6.0E-01
ENSMUST00000119722	expressed sequence AW551984 [Source:MGI Symbol;Acc:MGI:2143322]	Q8BGF0		3.3	9.6E-02	6.7	5.4E-03	-0.5	8.3E-01	-3.8	1.3E-02
ENSMUST00000119727				1.8	1.3E-01	5.8	6.8E-03	3.3	6.6E-02	-0.7	4.7E-01
ENSMUST00000131475	gamma-glutamyl cyclotransferase [Source:MGI Symbol;Acc:MGI:95700]		Q9D7X8	2.5	7.0E-03	7.1	3.1E-04	0.7	5.8E-01	-0.6	4.1E-01
ENSMUST00000131487	pogo transposable element with KRAB domain [Source:MGI Symbol;Acc:MGI:1918842]			6.5	7.7E-03	-4.3	1.7E-02	0.4	5.7E-01	0.6	7.2E-01
ENSMUST00000119744				-0.1	8.2E-01	0.5	4.6E-01	0.1	9.2E-01	-0.6	3.7E-01
ENSMUST00000131522	chloride channel, voltage-sensitive 2 [Source:MGI Symbol;Acc:MGI:105061]	D6RFS3		5.6	2.4E-04	3.8	1.3E-01	-1.3	5.7E-01	0.2	8.9E-01
ENSMUST00000131567	integrin beta 2-like [Source:MGI Symbol;Acc:MGI:1277979]		Q3UV74	-8.2	3.8E-04	1.1	4.9E-01	1.9	1.4E-01	-3.7	5.0E-02
ENSMUST00000119756	TBC1 domain family, member 1 [Source:MGI Symbol;Acc:MGI:1889508]	E9Q6L4		-2.2	4.5E-01	-1.4	6.5E-01	-1.1	6.2E-01	-1.9	5.6E-01
ENSMUST00000131601	transcription elongation factor, mitochondrial [Source:MGI Symbol;Acc:MGI:1915800]	B7ZCA9		2.0	1.5E-02	6.1	6.7E-04	-0.6	6.2E-01	-0.4	5.9E-01
ENSMUST00000131610	mannosidase, beta A, lysosomal [Source:MGI Symbol;Acc:MGI:88175]	D6RGR1		2.5	2.6E-02	5.8	4.4E-04	-0.3	8.1E-01	0.3	6.9E-01
ENSMUST00000131615	fidgetin [Source:MGI Symbol;Acc:MGI:1890647]		Q9ERZ6	8.9	2.6E-06	5.7	6.2E-03	0.0	9.8E-01	0.4	6.8E-01
ENSMUST00000119768				-0.9	3.8E-01	0.4	7.6E-01	1.3	2.5E-01	-0.1	9.5E-01
ENSMUST00000131616	COX assembly mitochondrial protein 2 [Source:MGI Symbol;Acc:MGI:1913781]	D6RD08		-4.4	4.6E-03	4.8	4.8E-04	-1.5	1.5E-01	0.6	3.5E-01
ENSMUST00000131631	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 [Source:MGI Symbol;Acc:MGI:1915098]	A0A0G2JG82		3.6	2.1E-04	6.5	2.1E-04	-0.6	5.9E-01	-0.3	6.2E-01
ENSMUST00000131656	cytochrome c oxidase assembly factor 7 [Source:MGI Symbol;Acc:MGI:1917143]		Q921H9	3.8	2.3E-05	-10.9	4.9E-04	-0.2	7.2E-01	0.6	7.8E-01
ENSMUST00000131662	asunder, spermatogenesis regulator [Source:MGI Symbol;Acc:MGI:1918427]	F6W761		-4.8	1.5E-03	-0.1	9.2E-01	1.5	1.1E-02	-0.3	6.0E-01
ENSMUST00000119787	topoisomerase (DNA) III beta [Source:MGI Symbol;Acc:MGI:1333803]	Q3UJF5	Q9Z321	-2.4	5.9E-01	-2.4	6.8E-01	-0.7	8.2E-01	-0.8	9.0E-01
ENSMUST00000131671	heterogeneous nuclear ribonucleoprotein R [Source:MGI Symbol;Acc:MGI:1891692]	F7B5B5		-6.5	1.3E-05	4.0	4.0E-02	-0.9	6.2E-01	-0.5	6.8E-01
ENSMUST00000131716	predicted gene 1305 [Source:MGI Symbol;Acc:MGI:2686151]	R4GML7		5.4	3.0E-05	4.1	1.4E-01	-0.4	8.9E-01	2.9	8.9E-02
ENSMUST00000131717	adhesion G protein-coupled receptor L1 [Source:MGI Symbol;Acc:MGI:1929461]		Q80TR1	4.4	3.2E-02	4.1	7.3E-05	0.5	3.9E-01	-0.3	4.9E-01
ENSMUST00000131723	solute carrier family 47, member 1 [Source:MGI Symbol;Acc:MGI:1914723]	D6RGQ3		7.8	1.8E-05	-1.9	1.3E-01	0.8	3.2E-01	0.0	9.9E-01
ENSMUST00000131728	proliferation-associated 2G4 [Source:MGI Symbol;Acc:MGI:894684]	D3YVH7		-3.8	1.5E-03	-9.1	2.1E-04	0.7	2.0E-01	-2.1	2.9E-01
ENSMUST00000131730	3-hydroxyacyl-CoA dehydratase 1 [Source:MGI Symbol;Acc:MGI:1353592]	A2AQ81		6.9	1.6E-06	8.6	1.1E-06	-2.5	1.4E-02	0.2	5.1E-01
ENSMUST00000131802	lymphocyte cytosolic protein 1 [Source:MGI Symbol;Acc:MGI:104808]		Q61233	-10.8	7.9E-05	-6.4	3.2E-02	1.6	8.2E-02	2.3	3.9E-01
ENSMUST00000131806	ATP-binding cassette, sub-family C (CFTR/MRP), member 12 [Source:MGI Symbol;Acc:MGI:2441679]	D6RGU5		4.8	2.3E-02	4.8	8.1E-03	-2.0	2.4E-01	-0.2	8.3E-01
ENSMUST00000131818	WD repeat and SOCS box-containing 1 [Source:MGI Symbol;Acc:MGI:1926139]	F6ZUJ8		-6.4	4.1E-03	6.3	7.5E-04	-0.6	6.6E-01	-1.4	8.4E-02
ENSMUST00000119810	RIKEN cDNA 1700021K19 gene [Source:MGI Symbol;Acc:MGI:1915160]	D3Z7B1		2.2	8.4E-02	0.8	5.6E-01	-1.2	2.9E-01	0.1	9.1E-01
ENSMUST00000131855	eukaryotic translation initiation factor 2D [Source:MGI Symbol;Acc:MGI:109342]			3.6	2.8E-04	7.1	2.3E-04	-0.7	6.2E-01	-0.9	1.9E-01
ENSMUST00000119814	heterogeneous nuclear ribonucleoprotein H3 [Source:MGI Symbol;Acc:MGI:1926462]	D3Z6Y3		-2.2	3.7E-01	-0.9	6.9E-01	-1.5	3.8E-01	-2.8	2.7E-01
ENSMUST00000131871	eukaryotic translation initiation factor 4A2 [Source:MGI Symbol;Acc:MGI:106906]	D6RJ11		-8.3	1.7E-03	4.8	1.6E-04	0.0	9.5E-01	0.0	9.7E-01
ENSMUST00000119822				2.0	9.1E-02	3.2	2.5E-02	-0.1	9.2E-01	-1.4	1.8E-01
ENSMUST00000131877	glial cell line derived neurotrophic factor family receptor alpha 1 [Source:MGI Symbol;Acc:MGI:1100842]	D3Z3C9		5.9	2.4E-04	5.1	7.1E-04	-0.4	6.6E-01	-0.1	8.2E-01
ENSMUST00000131878	transmembrane protein 63c [Source:MGI Symbol;Acc:MGI:2444386]		Q8CBX0	3.5	3.4E-02	5.6	1.1E-03	-0.5	7.1E-01	-0.5	4.7E-01
ENSMUST00000131919	tenascin N [Source:MGI Symbol;Acc:MGI:2665790]	E9Q1F6		5.7	8.5E-05	4.0	2.2E-03	-2.2	4.3E-02	-0.4	5.4E-01
ENSMUST00000131954	microrchidia 2B [Source:MGI Symbol;Acc:MGI:3045293]		Q8C5W4	8.1	3.3E-04	-6.1	5.1E-03	-0.9	2.1E-01	-0.4	8.2E-01
ENSMUST00000119829	splA/ryanodine receptor domain and SOCS box containing 3 [Source:MGI Symbol;Acc:MGI:1891471]	D3YW96		-0.8	4.5E-01	1.2	4.4E-01	1.8	1.5E-01	-0.3	8.4E-01
ENSMUST00000119830				-2.7	1.6E-01	-2.1	3.5E-01	0.1	9.6E-01	-0.5	8.3E-01
ENSMUST00000131965	mitochondrial tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2142572]	D3Z2H5		-4.3	3.2E-03	6.0	1.1E-03	0.7	6.0E-01	-0.5	4.8E-01
ENSMUST00000119833	fibroblast growth factor 13 [Source:MGI Symbol;Acc:MGI:109178]	B1AU20		4.7	1.1E-01	4.3	2.0E-01	-0.2	9.5E-01	0.1	9.4E-01
ENSMUST00000131966	coiled-coil domain containing 81 [Source:MGI Symbol;Acc:MGI:1918134]	D6REG7		6.7	1.6E-04	1.3	1.6E-01	-1.0	1.8E-01	-0.1	8.5E-01
ENSMUST00000131981	coronin, actin binding protein, 2B [Source:MGI Symbol;Acc:MGI:2444283]	G3UWZ2		4.6	7.8E-04	6.3	6.3E-04	-0.4	7.5E-01	-0.7	3.1E-01
ENSMUST00000119846	spinster homolog 1 [Source:MGI Symbol;Acc:MGI:1920908]	D3YTR6		-3.7	1.8E-01	-4.4	1.9E-01	-0.6	7.1E-01	0.1	9.7E-01
ENSMUST00000119847	decapping enzyme, scavenger [Source:MGI Symbol;Acc:MGI:1916555]	Q3TBW9		-0.3	7.1E-01	-3.9	2.7E-02	-0.4	5.6E-01	3.1	5.5E-02
ENSMUST00000119848	essential meiotic endonuclease 1 homolog 2 (S. pombe) [Source:MGI Symbol;Acc:MGI:1919889]	D3Z6X0		0.4	5.4E-01	1.1	1.8E-01	0.7	2.3E-01	0.0	9.9E-01
ENSMUST00000131996	regulator of G-protein signaling 17 [Source:MGI Symbol;Acc:MGI:1927469]		Q9QZB0	7.9	5.0E-05	6.8	5.6E-04	-0.5	7.5E-01	-1.0	1.9E-01
ENSMUST00000132017	vacuolar protein sorting 54 (yeast) [Source:MGI Symbol;Acc:MGI:2178798]	Q5SRW8		-7.8	1.9E-04	3.4	1.6E-02	-1.7	2.0E-01	-0.1	9.0E-01
ENSMUST00000119851				1.1	2.1E-01	3.0	2.4E-02	0.9	3.7E-01	-1.0	2.7E-01
ENSMUST00000132032	CCR4-NOT transcription complex, subunit 7 [Source:MGI Symbol;Acc:MGI:1298230]	Q543X5	Q60809	-3.7	2.6E-02	4.2	3.7E-04	-0.3	6.6E-01	-0.8	1.6E-01
ENSMUST00000132034	oligosaccharyltransferase 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914945]		Q99LX8	-5.2	4.4E-05	-5.9	1.2E-04	-0.9	2.9E-02	-0.8	4.3E-01
ENSMUST00000132098	gametogenetin binding protein 2 [Source:MGI Symbol;Acc:MGI:2387356]	F6Y247		-3.5	2.6E-02	5.4	2.3E-03	-0.6	6.6E-01	0.5	5.5E-01
ENSMUST00000132102	general transcription factor III A [Source:MGI Symbol;Acc:MGI:1913846]	F6SIJ4		-5.2	1.3E-04	6.7	8.7E-04	-0.8	5.6E-01	-0.5	4.9E-01
ENSMUST00000132119	predicted gene 5475 [Source:MGI Symbol;Acc:MGI:3646320]	D3YV11		5.7	1.9E-04	6.6	2.0E-04	-0.5	6.9E-01	-1.9	1.6E-02
ENSMUST00000132161	spectrin repeat containing, nuclear envelope 2 [Source:MGI Symbol;Acc:MGI:2449316]	F7BX34		-4.7	1.9E-02	-2.8	1.0E-03	-1.1	2.0E-02	-2.9	3.9E-03

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000132169	GUF1 GTPase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2140726]			5.5	2.4E-04	-5.6	2.2E-03	1.7	8.0E-03	1.3	3.5E-01
ENSMUST00000132183	neuralized E3 ubiquitin protein ligase 4 [Source:MGI Symbol;Acc:MGI:1921092]	F6WND1		-3.1	1.1E-02	-4.9	1.3E-02	-1.2	1.3E-01	-0.6	7.4E-01
ENSMUST00000132186	Sjogren syndrome antigen B [Source:MGI Symbol;Acc:MGI:98423]	D6RI87		-7.7	2.1E-03	7.3	1.1E-05	0.2	8.0E-01	0.5	2.6E-01
ENSMUST00000119884				-1.3	7.1E-01	-0.4	9.1E-01	-1.1	6.9E-01	-1.9	6.2E-01
ENSMUST00000132195	zinc finger protein 687 [Source:MGI Symbol;Acc:MGI:1925516]	D3Z524		3.1	1.2E-02	6.5	1.2E-05	-0.2	7.8E-01	-0.3	4.9E-01
ENSMUST00000132235	ubiquitin-associated protein 1 [Source:MGI Symbol;Acc:MGI:2149543]	F6WHE1		-4.7	6.8E-03	2.2	2.2E-03	0.7	1.3E-01	-0.1	7.7E-01
ENSMUST00000132243	transmembrane protein 150A [Source:MGI Symbol;Acc:MGI:2385244]	S4R204		2.9	1.5E-02	5.9	6.9E-04	-0.6	6.3E-01	-0.2	8.1E-01
ENSMUST00000119905	general transcription factor II A, 2 [Source:MGI Symbol;Acc:MGI:1933289]	D3Z7C2		-3.6	1.8E-01	-5.6	8.9E-02	-2.6	1.1E-01	-0.6	8.6E-01
ENSMUST00000132253	oligosaccharyltransferase 4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914945]		Q99LX8	-5.6	1.7E-04	5.7	2.7E-03	0.5	7.5E-01	0.0	9.8E-01
ENSMUST00000119916	transcriptional adaptor 2B [Source:MGI Symbol;Acc:MGI:3035274]	D3YW26		1.1	5.7E-01	2.2	3.9E-01	-0.7	7.2E-01	-1.8	4.1E-01
ENSMUST00000119917	suppressor of cytokine signaling 2 [Source:MGI Symbol;Acc:MGI:1201787]	Q548Q7	O35717	3.0	4.4E-02	2.6	1.9E-02	-3.3	1.5E-02	-2.8	1.7E-02
ENSMUST00000119920				4.0	8.6E-02	6.1	2.6E-02	-0.3	9.2E-01	-2.4	1.1E-01
ENSMUST00000132280	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 [Source:MGI Symbol;Acc:MGI:87874]	F6QCP8		3.1	6.4E-03	3.5	2.5E-03	-1.6	1.1E-01	0.1	8.6E-01
ENSMUST00000132309	hexokinase 3 [Source:MGI Symbol;Acc:MGI:2670962]	D6RFA3		-9.4	6.2E-04	3.0	1.6E-01	7.1	2.0E-03	-2.1	2.2E-01
ENSMUST00000119934				1.0	4.5E-01	1.7	3.4E-01	0.6	7.1E-01	-0.2	9.0E-01
ENSMUST00000132344	CCR4-NOT transcription complex, subunit 3 [Source:MGI Symbol;Acc:MGI:2385261]	F6YBV1		-4.3	1.8E-02	6.3	3.7E-04	-0.6	6.2E-01	0.3	6.4E-01
ENSMUST00000132358	xeroderma pigmentosum, complementation group A [Source:MGI Symbol;Acc:MGI:99135]	S4R260		-3.9	5.0E-03	2.5	1.0E-03	0.0	9.9E-01	-0.1	8.0E-01
ENSMUST00000132367	MORN repeat containing 1 [Source:MGI Symbol;Acc:MGI:1924116]	F2Z475		6.8	4.1E-04	-4.9	1.4E-03	0.4	4.1E-01	-0.7	5.8E-01
ENSMUST00000132374	NFKB inhibitor interacting Ras-like protein 1 [Source:MGI Symbol;Acc:MGI:1916971]		Q8CEC5	4.9	1.6E-05	-3.1	8.5E-02	1.6	1.2E-01	-0.9	5.8E-01
ENSMUST00000119946	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925947]	Q91VU7		-0.7	7.3E-01	4.9	1.4E-01	3.6	2.3E-01	-2.0	3.5E-01
ENSMUST00000119947				1.0	5.3E-01	1.8	4.2E-01	0.5	7.5E-01	-0.3	8.8E-01
ENSMUST00000132401	inositol polyphosphate-4-phosphatase, type I [Source:MGI Symbol;Acc:MGI:1931123]	D3YUL8		-4.3	7.2E-03	-6.9	1.1E-04	-0.9	2.9E-02	0.3	7.9E-01
ENSMUST00000132404	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific) [Source:MGI Symbol;Acc:MGI:107898]	Q8CET7		-2.7	3.2E-02	5.9	6.7E-04	-0.9	4.7E-01	-0.3	7.0E-01
ENSMUST00000132417	RIKEN cDNA 0610037L13 gene [Source:MGI Symbol;Acc:MGI:1921348]	D6REH4		1.9	2.8E-02	-4.2	6.1E-04	-1.3	1.7E-02	0.4	6.3E-01
ENSMUST00000132430	centrosomal protein 164 [Source:MGI Symbol;Acc:MGI:2384878]	F7AUV3		3.2	6.6E-03	-1.5	7.8E-02	0.0	9.5E-01	-1.4	9.8E-02
ENSMUST00000132435	transmembrane and coiled-coil domains 2 [Source:MGI Symbol;Acc:MGI:1916125]	Q3TZY4		6.7	1.5E-03	4.8	6.6E-04	-0.7	4.2E-01	-0.6	3.6E-01
ENSMUST00000119962	tubule associated monooxygenase, calponin and LIM domain containing 1 [Source:MGI Symbol;Acc:MGI:238		Q8VDP3	3.2	7.1E-02	7.8	1.1E-02	4.2	9.5E-02	-0.4	7.9E-01
ENSMUST00000132525	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	D3Z1M1		-6.3	2.3E-02	-4.7	5.2E-04	-0.8	1.2E-01	-0.8	4.1E-01
ENSMUST00000132527	collagen, type IX, alpha 3 [Source:MGI Symbol;Acc:MGI:894686]	A2ACT7		6.6	1.7E-03	4.2	6.7E-03	-2.3	1.2E-01	-1.0	2.5E-01
ENSMUST00000132545	tubulointerstitial nephritis antigen-like 1 [Source:MGI Symbol;Acc:MGI:2137617]	H3BKM8		6.8	6.8E-05	7.7	1.5E-04	0.0	9.9E-01	0.0	9.7E-01
ENSMUST00000119975	migration and invasion inhibitory protein [Source:MGI Symbol;Acc:MGI:106506]		A2A7Y5	0.7	1.8E-01	0.9	1.5E-01	-0.5	3.1E-01	-0.7	2.3E-01
ENSMUST00000132583	cysteine-rich secretory protein LCCL domain containing 2 [Source:MGI Symbol;Acc:MGI:1926142]		Q8BZQ2	-4.3	8.4E-05	6.6	3.6E-03	0.7	6.7E-01	1.3	1.8E-01
ENSMUST00000132603	Sjogren syndrome antigen B [Source:MGI Symbol;Acc:MGI:98423]	F6SXM5		-5.1	4.0E-03	-1.6	3.7E-01	2.4	3.8E-02	-0.5	7.7E-01
ENSMUST00000119993	tetraspanin 5 [Source:MGI Symbol;Acc:MGI:1928096]	D3Z641		-3.1	4.1E-02	0.6	7.2E-01	2.2	1.3E-01	-1.6	3.3E-01
ENSMUST00000132607	solute carrier family 45, member 4 [Source:MGI Symbol;Acc:MGI:2146236]		Q0P5V9	7.5	1.4E-03	7.3	3.5E-05	-1.5	1.9E-01	-0.4	4.4E-01
ENSMUST00000132620	myosin phosphatase Rho interacting protein [Source:MGI Symbol;Acc:MGI:1349438]	F6S5I0		-6.8	4.2E-04	6.4	7.4E-04	-0.7	6.3E-01	-0.7	3.7E-01
ENSMUST00000132628	phosphorylated adaptor for RNA export [Source:MGI Symbol;Acc:MGI:1891839]	F6RPD4		-5.2	2.4E-03	5.8	9.5E-04	-1.4	3.1E-01	-0.3	6.7E-01
ENSMUST00000132631	cAMP responsive element binding protein 3 [Source:MGI Symbol;Acc:MGI:99946]	E0CYW8		-3.9	4.6E-03	6.5	1.5E-04	-0.3	8.2E-01	-0.3	5.8E-01
ENSMUST00000132641	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	F6WL90		-8.2	3.5E-04	4.3	6.9E-05	-0.5	4.4E-01	0.1	8.9E-01
ENSMUST00000120005	lemur tyrosine kinase 3 [Source:MGI Symbol;Acc:MGI:3039582]			4.3	6.8E-02	1.6	5.6E-01	-0.5	8.4E-01	2.2	3.2E-01
ENSMUST00000120006	zinc finger protein 112 [Source:MGI Symbol;Acc:MGI:1929115]		Q0VAW7	1.6	1.2E-01	3.7	1.1E-02	1.7	1.5E-01	-0.4	6.1E-01
ENSMUST00000132661	protein phosphatase 1, regulatory (inhibitor) subunit 3G [Source:MGI Symbol;Acc:MGI:1923737]		Q9CW07	7.7	3.1E-05	-2.3	9.9E-03	-0.3	5.4E-01	-0.5	5.0E-01
ENSMUST00000132668	uclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 [Source:MGI Symbol;Acc:MGI:9731	F6Z9G5		-6.2	2.2E-03	4.4	2.2E-02	-0.7	6.6E-01	1.8	1.2E-01
ENSMUST00000132670	signal peptide, CUB domain, EGF-like 3 [Source:MGI Symbol;Acc:MGI:3045253]	F7A487		8.3	7.0E-06	-2.4	1.4E-01	0.9	3.4E-01	-1.6	3.7E-01
ENSMUST00000132676	phosphatidylglycerophosphate synthase 1 [Source:MGI Symbol;Acc:MGI:1921701]	B9EKS7	Q8BHF7	-1.9	1.4E-02	5.2	1.1E-04	-1.1	1.6E-01	0.0	9.4E-01
ENSMUST00000132682	SET domain containing 3 [Source:MGI Symbol;Acc:MGI:1289184]	D6RCY6		-6.5	1.0E-04	5.9	1.2E-03	0.0	9.7E-01	-0.2	7.9E-01
ENSMUST00000132685	dynein, axonemal, heavy chain 17 [Source:MGI Symbol;Acc:MGI:1917176]	A2A520		8.7	7.7E-06	4.5	2.8E-03	-2.1	1.3E-01	0.2	7.7E-01
ENSMUST00000132717	methyl-CpG binding domain protein 5 [Source:MGI Symbol;Acc:MGI:2138934]	Q3TTF1		2.8	1.5E-02	-0.6	6.9E-01	4.9	6.4E-04	-0.2	8.9E-01
ENSMUST00000132726	methylphosphate capping enzyme [Source:MGI Symbol;Acc:MGI:106477]	F6XIE4		-3.9	6.1E-03	7.7	8.2E-05	-0.6	6.6E-01	-0.4	5.3E-01
ENSMUST00000132734	eroxisome proliferative activated receptor, gamma, coactivator 1 alpha [Source:MGI Symbol;Acc:MGI:134277		O70343	8.2	6.9E-06	5.2	8.2E-03	-0.5	7.7E-01	-0.3	7.8E-01
ENSMUST00000132741	spleen focus forming virus (SFFV) proviral integration oncogene [Source:MGI Symbol;Acc:MGI:98282]	E9QAI9		-5.7	2.9E-03	7.6	5.0E-05	-0.6	6.1E-01	-0.3	5.8E-01
ENSMUST00000132751	Rho guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:1353510]	F6ZN61		-3.8	6.2E-03	4.9	7.7E-05	-1.4	7.7E-02	-0.7	1.9E-01
ENSMUST00000132831	ring finger protein, transmembrane 2 [Source:MGI Symbol;Acc:MGI:2442859]	F6V638		6.7	9.8E-05	7.7	4.1E-05	-0.5	6.7E-01	-0.6	3.1E-01
ENSMUST00000132848	zinc finger protein 961 [Source:MGI Symbol;Acc:MGI:3583954]	D3YV32		6.1	1.5E-04	2.5	3.3E-03	-0.6	2.8E-01	-0.2	6.6E-01
ENSMUST00000120066	peroxisomal biogenesis factor 26 [Source:MGI Symbol;Acc:MGI:1921293]		Q8BGI5	0.2	9.1E-01	0.0	9.9E-01	-0.1	9.2E-01	0.1	9.7E-01
ENSMUST00000132875	nucleobindin 1 [Source:MGI Symbol;Acc:MGI:97388]	D3Z1N1		4.5	6.8E-03	4.2	1.3E-04	-1.5	4.8E-02	0.2	7.2E-01
ENSMUST00000120080	adenylate cyclase 9 [Source:MGI Symbol;Acc:MGI:108450]	E9Q706		3.2	7.1E-02	5.1	8.3E-03	-1.6	3.6E-01	-3.5	1.5E-02
ENSMUST00000132893	Sfi1 homolog, spindle assembly associated (yeast) [Source:MGI Symbol;Acc:MGI:1926137]	E9PY38		9.0	2.1E-05	5.1	4.4E-04	-1.7	1.4E-01	-0.3	6.5E-01
ENSMUST00000132932	glutamic pyruvate transaminase (alanine aminotransferase) 2 [Source:MGI Symbol;Acc:MGI:1915391]	D6RFQ8		9.9	1.9E-05	6.6	9.1E-05	0.1	9.1E-01	-1.2	6.5E-02
ENSMUST00000132948	lymphoid-restricted membrane protein [Source:MGI Symbol;Acc:MGI:108424]	F6WLY0		-7.3	1.5E-02	-4.8	1.0E-03	0.7	1.8E-01	-0.5	6.3E-01
ENSMUST00000132994	calcyphosphine 2 [Source:MGI Symbol;Acc:MGI:2441980]	E9Q7K6		12.2	1.2E-06	4.8	6.8E-03	-0.9	5.2E-01	0.3	7.6E-01
ENSMUST00000133010	dpy-19-like 2 (C. elegans) [Source:MGI Symbol;Acc:MGI:2444662]		P0CW70	6.7	8.4E-05	-3.6	2.0E-02	-0.2	7.9E-01	-1.8	2.5E-01
ENSMUST00000133040	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF [Source:MGI Symbol;Acc:MGI:2681862]	J9JIB2		4.6	2.5E-02	6.3	1.5E-04	-0.5	6.3E-01	-0.4	5.0E-01
ENSMUST00000133041	phosphofructokinase, platelet [Source:MGI Symbol;Acc:MGI:1891833]	F6VP95		-3.6	2.1E-03	3.0	6.7E-03	0.0	9.7E-01	-0.6	4.0E-01
ENSMUST00000133044	uncoupling protein 2 (mitochondrial, proton carrier) [Source:MGI Symbol;Acc:MGI:109354]	D3YZG5		-4.5	3.8E-03	7.2	1.6E-04	0.0	9.8E-01	-0.6	3.6E-01
ENSMUST00000133052	degenerative spermatocyte homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1097711]	F6S3U4		-6.3	7.5E-05	5.2	3.0E-03	-0.7	6.0E-01	-0.3	6.9E-01
ENSMUST00000133066	cytidine monophosphate (UMP-CMP) kinase 1 [Source:MGI Symbol;Acc:MGI:1913838]	D6RIL5		-7.2	8.2E-05	-6.9	1.1E-03	0.8	1.6E-01	0.4	8.1E-01
ENSMUST00000133070	zinc finger protein 652 [Source:MGI Symbol;Acc:MGI:2442221]	F2Z443		1.4	2.9E-02	3.1	8.5E-04	-1.9	1.2E-02	-0.1	8.6E-01
ENSMUST00000133071	hydroxyacylglutathione hydrolase-like [Source:MGI Symbol;Acc:MGI:1919877]	D3YZU6		-5.3	1.5E-02	4.2	6.0E-02	-3.1	1.8E-01	0.8	5.5E-01
ENSMUST00000133078	predicted gene 13145 [Source:MGI Symbol;Acc:MGI:3701123]	A2A7I0		6.2	3.3E-04	3.8	3.7E-02	-2.1	2.2E-01	-0.3	8.0E-01
ENSMUST00000133150	zinc finger protein 62 [Source:MGI Symbol;Acc:MGI:99662]	Q3UGK1		6.1	1.2E-04	5.8	9.9E-04	-1.8	2.1E-01	0.0	9.6E-01
ENSMUST00000133157	polymerase (RNA) I polypeptide E [Source:MGI Symbol;Acc:MGI:1929022]	Q3V1B9	Q8K202	4.8	1.6E-03	6.0	3.1E-04	-0.5	6.6E-01	-0.7	2.5E-01
ENSMUST00000133213	immunoglobulin superfamily, member 9B [Source:MGI Symbol;Acc:MGI:2685354]	E9PZ19		8.8	8.2E-05	3.3	2.4E-02	0.7	5.4E-01	-0.1	9.5E-01
ENSMUST00000120120	er family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3 [Source:MGI Symbol;Acc:MG		Q8R1T4	-2.6	3.6E-02	0.6	6.2E-01	1.7	1.0E-01	-1.5	2.4E-01
ENSMUST00000120122	cullin 5 [Source:MGI Symbol;Acc:MGI:1922967]	E9Q6Z0		-1.2	2.1E-01	1.8	4.2E-01	5.8	5.1E-03	2.8	1.1E-01
ENSMUST00000120123				0.7	2.4E-01	0.0	9.5E-01	0.0	9.4E-01	0.7	4.1E-01
ENSMUST00000120129	proline rich 14-like [Source:MGI Symbol;Acc:MGI:2443658]	E9Q7C4		-0.3	4.8E-01	0.4	4.6E-01	0.9	5.3E-02	0.2	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000133236	INO80 complex subunit D [Source:MGI Symbol;Acc:MGI:3027003]	B1AT32		6.7	1.3E-04	-3.4	1.2E-03	0.5	2.4E-01	-0.6	4.5E-01
ENSMUST00000133242	hydroxysteroid (17-beta) dehydrogenase 14 [Source:MGI Symbol;Acc:MGI:1913315]	D3YTP9		5.6	1.7E-05	-2.1	3.9E-02	-0.7	2.6E-01	-0.4	6.9E-01
ENSMUST00000120149				0.2	9.2E-01	-0.8	7.0E-01	-1.9	3.1E-01	-0.9	7.0E-01
ENSMUST00000133257	gametogenetin binding protein 1 [Source:MGI Symbol;Acc:MGI:3055306]		Q6K1E7	2.6	3.7E-03	6.2	4.8E-04	0.5	7.0E-01	-0.3	6.4E-01
ENSMUST00000133268	netrin G1 [Source:MGI Symbol;Acc:MGI:1934028]		Q8R4G0	6.3	1.6E-04	-5.7	1.8E-03	0.6	2.5E-01	3.9	1.4E-02
ENSMUST00000133272	SH3 domain binding kinase family, member 3 [Source:MGI Symbol;Acc:MGI:2685924]		P0C5K0	6.3	6.7E-04	6.2	9.0E-04	-0.6	6.4E-01	0.9	2.5E-01
ENSMUST00000133279	interleukin 4 induced 1 [Source:MGI Symbol;Acc:MGI:109552]	G3UXA7		3.3	2.6E-03	7.9	1.5E-04	-0.7	6.3E-01	-0.2	7.4E-01
ENSMUST00000133297	phosphatidylinositol 4-kinase, catalytic, beta polypeptide [Source:MGI Symbol;Acc:MGI:1334433]	F6W459		-4.2	6.4E-03	5.9	2.1E-04	-0.4	6.7E-01	-0.6	3.4E-01
ENSMUST00000133298	discs, large (Drosophila) homolog-associated protein 2 [Source:MGI Symbol;Acc:MGI:2443181]		Q8BJ42	6.2	9.8E-05	6.7	2.1E-04	-0.6	6.0E-01	-0.1	9.1E-01
ENSMUST00000133316	centromere protein A [Source:MGI Symbol;Acc:MGI:88375]	D6RCV6		-2.2	2.0E-02	6.3	5.8E-04	0.8	4.9E-01	-0.8	2.7E-01
ENSMUST00000133320	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1 [Source:MGI Symbol;Acc:MGI:110049	D6RGL7		-9.3	5.0E-05	8.9	1.3E-04	2.3	1.3E-01	-1.3	5.5E-02
ENSMUST00000133325	glutamic-oxaloacetic transaminase 1, soluble [Source:MGI Symbol;Acc:MGI:95791]	F7ALS6		-4.6	7.4E-04	4.1	4.6E-03	-1.8	1.6E-01	0.2	7.8E-01
ENSMUST00000133326	lactation elevated 1 [Source:MGI Symbol;Acc:MGI:2148801]	E9Q4K2		5.9	2.3E-03	10.6	2.2E-07	-0.2	7.7E-01	0.0	8.9E-01
ENSMUST00000133342	IKAROS family zinc finger 4 [Source:MGI Symbol;Acc:MGI:1343139]		Q8C208	8.8	9.7E-06	-1.2	9.5E-02	0.8	7.8E-02	-0.3	5.8E-01
ENSMUST00000133353	dihydroorotate dehydrogenase [Source:MGI Symbol;Acc:MGI:1928378]	F6ZQJ5		4.9	1.0E-04	6.2	6.7E-04	0.1	9.7E-01	-1.2	1.1E-01
ENSMUST00000133371	storkhead box 1 [Source:MGI Symbol;Acc:MGI:2684909]		B2RQL2	6.2	3.6E-05	7.1	2.7E-04	-2.0	1.8E-01	1.2	1.2E-01
ENSMUST00000133397	BCL2-like 2 [Source:MGI Symbol;Acc:MGI:108052]		P70345	8.1	9.0E-05	3.3	8.9E-02	0.4	8.1E-01	1.0	4.4E-01
ENSMUST00000133410	tumor-suppressing subchromosomal transferable fragment 4 [Source:MGI Symbol;Acc:MGI:1861712]	D3YYU6		6.0	1.0E-03	6.6	8.5E-04	0.8	5.6E-01	-1.5	8.5E-02
ENSMUST00000133426	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Source:MGI Symbol;Acc:MGI:105037]	S4R1I6		-8.0	7.2E-06	-2.1	3.3E-03	0.6	9.9E-02	-0.4	4.7E-01
ENSMUST00000120196	C2 calcium-dependent domain containing 3 [Source:MGI Symbol;Acc:MGI:2142166]	D3Z4D9		3.7	6.3E-02	-0.1	9.6E-01	-0.5	8.1E-01	3.3	2.2E-01
ENSMUST00000133437	BTB (POZ) domain containing 18 [Source:MGI Symbol;Acc:MGI:3650217]	A0A0A6YY25		8.2	4.1E-05	4.1	4.7E-03	0.2	8.8E-01	-0.1	8.7E-01
ENSMUST00000133454	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 [Source:MGI Symbol;Acc:MGI:102676]	E9Q1I5		6.8	2.0E-02	3.8	1.1E-02	0.0	1.0E+00	-0.5	6.0E-01
ENSMUST00000133464	C2 calcium-dependent domain containing 3 [Source:MGI Symbol;Acc:MGI:2142166]	D6RH58		6.0	8.5E-06	5.2	2.5E-03	-0.4	7.9E-01	-0.2	8.3E-01
ENSMUST00000133533	transformation related protein 73 [Source:MGI Symbol;Acc:MGI:1336991]		Q9JJP2	6.9	2.1E-04	5.6	3.9E-03	-0.7	6.7E-01	0.5	5.9E-01
ENSMUST00000133549	ataxin 7-like 1 [Source:MGI Symbol;Acc:MGI:3584458]	D3YXW3		-2.9	2.9E-02	-3.6	7.8E-03	1.0	6.8E-02	-1.6	2.3E-01
ENSMUST00000133558	C1q and tumor necrosis factor related protein 1 [Source:MGI Symbol;Acc:MGI:1919254]	A2A4W2		6.9	3.8E-04	3.7	4.1E-02	0.0	9.8E-01	1.7	1.5E-01
ENSMUST00000120223	additional sex combs like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685175]		Q8C4A5	6.9	5.3E-02	9.4	1.6E-02	-0.8	8.2E-01	-3.3	8.6E-02
ENSMUST00000133584	phosphatidylinositol glycan anchor biosynthesis, class X [Source:MGI Symbol;Acc:MGI:1919334]	F6QPF7		-6.0	9.4E-05	6.3	1.5E-04	-0.5	6.1E-01	-0.9	1.5E-01
ENSMUST00000133595	jumonji domain containing 8 [Source:MGI Symbol;Acc:MGI:1919356]		Q3TA59	6.1	4.8E-03	-7.1	2.5E-03	-0.3	5.9E-01	0.3	8.5E-01
ENSMUST00000120233				4.0	1.0E-01	6.0	3.4E-02	-0.2	9.3E-01	-2.2	1.5E-01
ENSMUST00000133600	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]	D3Z224		-8.6	2.3E-03	-9.7	1.0E-03	-0.5	3.6E-01	1.3	5.4E-01
ENSMUST00000133604	scaffold attachment factor B2 [Source:MGI Symbol;Acc:MGI:2146808]	D6RJ78		8.3	6.3E-06	6.3	2.2E-03	-0.7	6.6E-01	0.4	6.2E-01
ENSMUST00000120238	tripartite motif-containing 24 [Source:MGI Symbol;Acc:MGI:109275]	E9Q1U8		-0.8	5.4E-01	0.1	9.5E-01	0.7	5.5E-01	-0.2	9.2E-01
ENSMUST00000133618	neutrophil cytosolic factor 4 [Source:MGI Symbol;Acc:MGI:109186]	A8XU21		-8.1	3.3E-05	6.0	1.1E-03	-0.4	7.6E-01	-0.6	4.2E-01
ENSMUST00000120240	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913290]			2.4	5.8E-02	2.6	6.9E-02	-0.3	8.0E-01	-0.5	6.7E-01
ENSMUST00000133655	tyrosinase-related protein 1 [Source:MGI Symbol;Acc:MGI:98881]	A2ADJ4		4.7	1.7E-03	8.3	2.7E-05	-0.1	9.4E-01	-0.5	3.7E-01
ENSMUST00000120243	colony stimulating factor 1 (macrophage) [Source:MGI Symbol;Acc:MGI:1339753]		P07141	-0.8	3.7E-01	0.2	9.1E-01	2.5	4.4E-02	1.5	2.3E-01
ENSMUST00000133676	chloride channel, voltage-sensitive Ka [Source:MGI Symbol;Acc:MGI:1329026]	A2ADB4		3.5	1.4E-02	3.6	4.8E-03	-1.7	1.0E-01	-0.3	7.1E-01
ENSMUST00000133689	catenin (cadherin associated protein), beta 1 [Source:MGI Symbol;Acc:MGI:88276]	F7CRC6		-2.8	2.7E-03	7.9	9.7E-05	-0.9	4.9E-01	0.4	5.3E-01
ENSMUST00000133701	chitinase-like 1 [Source:MGI Symbol;Acc:MGI:1340899]	D3Z2Z5		-4.1	3.6E-04	6.1	1.3E-02	0.2	9.1E-01	-1.5	3.6E-01
ENSMUST00000133739	family with sequence similarity 118, member B [Source:MGI Symbol;Acc:MGI:1924483]	F6Q255		-3.3	1.3E-02	6.2	2.7E-04	-0.6	6.0E-01	-0.3	6.7E-01
ENSMUST00000133820	Ras and Rab interactor 3 [Source:MGI Symbol;Acc:MGI:2385708]	Q3U332		-4.7	1.4E-04	6.1	2.5E-05	-0.8	3.4E-01	0.0	9.3E-01
ENSMUST00000120259	mitogen-activated protein kinase kinase kinase 5 [Source:MGI Symbol;Acc:MGI:1346876]	E9PWG9		0.0	9.8E-01	-0.6	7.2E-01	-1.3	3.1E-01	-0.6	7.2E-01
ENSMUST00000133833	crystallin, beta A2 [Source:MGI Symbol;Acc:MGI:104336]	A0A087WQQ2		7.3	1.6E-04	3.6	1.4E-02	1.0	3.7E-01	0.6	4.7E-01
ENSMUST00000133843	cathepsin D [Source:MGI Symbol;Acc:MGI:88562]	F6Y6L6		-7.4	1.4E-04	8.8	2.0E-03	0.0	9.8E-01	1.1	2.5E-01
ENSMUST00000133847	replication factor C (activator 1) 4 [Source:MGI Symbol;Acc:MGI:2146571]	D6RGM1		4.9	5.5E-03	-2.5	3.0E-01	1.1	4.0E-01	-0.5	8.2E-01
ENSMUST00000133862	helicase with zinc finger domain [Source:MGI Symbol;Acc:MGI:1925705]	A2AAU5		9.4	1.4E-04	6.2	1.8E-04	-0.5	6.4E-01	-0.2	7.9E-01
ENSMUST00000120272	DEP domain containing 1a [Source:MGI Symbol;Acc:MGI:1923381]	D3Z6J1		1.2	3.6E-01	2.1	2.4E-01	1.7	2.7E-01	0.8	5.5E-01
ENSMUST00000120274	in homology domain containing, family G (with RhoGef domain) member 1 [Source:MGI Symbol;Acc:MGI:2(	Q3UX37		-0.2	9.2E-01	2.2	4.6E-01	2.9	2.3E-01	0.4	8.7E-01
ENSMUST00000120276	bromodomain containing 4 [Source:MGI Symbol;Acc:MGI:1888520]	B0V2V8		-0.3	6.3E-01	0.7	4.1E-01	1.2	7.2E-02	0.2	7.6E-01
ENSMUST00000133869	glutathione S-transferase, theta 3 [Source:MGI Symbol;Acc:MGI:2143526]	G3UYL6		11.2	1.9E-04	5.4	1.2E-03	-0.5	6.8E-01	0.4	5.2E-01
ENSMUST00000120282				2.9	6.4E-02	5.3	3.5E-03	-0.5	7.4E-01	-2.9	2.0E-02
ENSMUST00000133898	FERM domain containing 5 [Source:MGI Symbol;Acc:MGI:2442557]	F6XM46		6.1	1.2E-02	7.4	2.4E-04	-1.0	4.7E-01	0.7	2.7E-01
ENSMUST00000133930	cDNA sequence BC030867 [Source:MGI Symbol;Acc:MGI:2387601]		Q32P12	4.3	8.7E-05	5.7	2.2E-02	0.3	8.9E-01	1.2	3.5E-01
ENSMUST00000120291				0.1	8.4E-01	1.8	2.9E-02	0.8	1.7E-01	-0.9	1.9E-01
ENSMUST00000133931	AKNA domain containing 1 [Source:MGI Symbol;Acc:MGI:3584453]	E9Q8N6		5.9	5.9E-04	4.9	1.7E-02	-0.7	7.2E-01	0.8	4.7E-01
ENSMUST00000133947	glutathione S-transferase, mu 7 [Source:MGI Symbol;Acc:MGI:1915562]	E9QAC8		9.1	5.1E-04	1.7	1.4E-01	-3.9	1.5E-02	0.2	8.3E-01
ENSMUST00000133967	transmembrane protein 256 [Source:MGI Symbol;Acc:MGI:1916436]	F6YWB5		-6.7	2.3E-05	6.4	2.6E-04	-0.6	6.2E-01	0.1	8.2E-01
ENSMUST00000133997	ubiquitin specific peptidase 9, X chromosome [Source:MGI Symbol;Acc:MGI:894681]	G3UZS3		-4.3	3.3E-03	4.9	3.0E-04	0.4	6.3E-01	-0.2	6.7E-01
ENSMUST00000134021	T cell lymphoma invasion and metastasis 1 [Source:MGI Symbol;Acc:MGI:103306]	J3QQ55		3.7	3.2E-04	-9.7	2.2E-04	-0.9	6.2E-02	0.5	7.6E-01
ENSMUST00000134055	olfactory receptor 330 [Source:MGI Symbol;Acc:MGI:3030164]			6.9	7.8E-05	7.4	2.5E-03	0.3	8.9E-01	1.1	2.5E-01
ENSMUST00000120306	upregulator of cell proliferation [Source:MGI Symbol;Acc:MGI:1919296]		Q5NCI0	-0.5	4.5E-01	0.3	6.9E-01	0.6	3.2E-01	-0.2	7.8E-01
ENSMUST00000134056	oxysterol binding protein-like 5 [Source:MGI Symbol;Acc:MGI:1930265]	D3YWU9		5.2	2.4E-02	6.1	5.7E-04	-0.9	5.1E-01	-0.3	6.2E-01
ENSMUST00000134063	ectonucleoside triphosphate diphosphohydrolase 1 [Source:MGI Symbol;Acc:MGI:102805]	Q8CDV7		-8.3	1.8E-04	6.2	1.7E-02	-0.7	7.8E-01	-1.2	3.5E-01
ENSMUST00000134078	serine/threonine kinase 4 [Source:MGI Symbol;Acc:MGI:1929004]	A2A5M9		5.0	4.7E-03	5.4	3.3E-03	-0.5	7.0E-01	0.6	5.2E-01
ENSMUST00000120322				0.4	7.0E-01	5.3	1.5E-02	4.5	1.9E-02	-0.4	7.6E-01
ENSMUST00000134093	LIM-domain containing, protein kinase [Source:MGI Symbol;Acc:MGI:104572]	F6PZ73		7.6	6.9E-03	4.1	1.6E-02	-0.6	6.9E-01	1.9	5.5E-02
ENSMUST00000134108	nuclear prelamin A recognition factor-like [Source:MGI Symbol;Acc:MGI:1914813]		Q7TMW6	-7.2	3.2E-04	5.4	9.3E-04	-0.7	5.5E-01	-0.8	3.1E-01
ENSMUST00000120327	transmembrane protein 175 [Source:MGI Symbol;Acc:MGI:1919642]		Q9CXY1	-0.4	7.0E-01	0.8	4.6E-01	-0.5	5.4E-01	-1.7	1.4E-01
ENSMUST00000134115	cornichon homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1925828]		Q9CX13	-6.8	1.1E-04	7.4	5.5E-04	-0.7	6.4E-01	0.3	7.3E-01
ENSMUST00000134159	zinc finger, CCHC domain containing 17 [Source:MGI Symbol;Acc:MGI:1919955]	Q3TG23	Q9ESX4	-1.8	3.9E-03	6.5	1.3E-04	-1.7	1.8E-01	0.5	4.1E-01
ENSMUST00000134179	transmembrane protease, serine 11g [Source:MGI Symbol;Acc:MGI:2444058]		Q8BZ10	8.5	3.6E-05	-1.3	2.1E-01	1.0	1.7E-01	-1.6	1.8E-01
ENSMUST00000134182	glutamine rich 2 [Source:MGI Symbol;Acc:MGI:2684912]	F6UEA3		5.7	3.1E-02	-6.9	2.1E-04	-0.4	3.9E-01	-0.9	4.8E-01
ENSMUST00000134193	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]	D3YUM3		-5.9	3.2E-03	6.0	3.2E-04	-0.6	5.9E-01	0.1	8.2E-01
ENSMUST00000134208	RecQ protein-like 5 [Source:MGI Symbol;Acc:MGI:2156841]	J3QP94		3.1	3.2E-03	-3.6	3.8E-02	0.4	5.7E-01	-1.8	3.2E-01
ENSMUST00000134220	peroxisomal biogenesis factor 7 [Source:MGI Symbol;Acc:MGI:1321392]	F6QU40		-3.7	7.0E-03	5.9	1.0E-03	0.5	7.1E-01	-0.1	9.1E-01
ENSMUST00000134384	lysophospholipase 1 [Source:MGI Symbol;Acc:MGI:1344588]	J3QP56		4.6	1.4E-03	-8.7	4.6E-04	-1.0	1.2E-01	-0.9	6.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000120367	acyl-Coenzyme A dehydrogenase family, member 8 [Source:MGI Symbol;Acc:MGI:1914198]	D3YTT4		4.1	8.7E-02	1.7	5.7E-01	-0.3	9.2E-01	2.1	3.6E-01
ENSMUST00000134404	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]	D3Z2J5		6.6	8.0E-04	6.4	3.8E-04	-0.2	8.8E-01	-0.9	2.0E-01
ENSMUST00000134415	sphingomyelin synthase 1 [Source:MGI Symbol;Acc:MGI:2444110]	E3W996		-5.1	2.1E-02	5.0	1.8E-03	-0.6	5.9E-01	-1.1	1.8E-01
ENSMUST00000120375	integrin alpha 3 [Source:MGI Symbol;Acc:MGI:96602]		Q62470	3.0	1.9E-01	2.8	9.8E-02	-4.8	3.5E-02	-4.5	1.6E-02
ENSMUST00000134433	5-azacytidine induced gene 2 [Source:MGI Symbol;Acc:MGI:1351332]		Q9QYP6	4.2	3.5E-03	5.3	1.9E-03	0.4	7.4E-01	-1.0	2.1E-01
ENSMUST00000134458	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	F6Q750		-6.4	5.1E-03	-6.7	1.0E-02	-1.9	2.6E-02	1.9	3.8E-01
ENSMUST00000134491	interferon (alpha and beta) receptor 2 [Source:MGI Symbol;Acc:MGI:1098243]	H3BJ04		-3.1	7.7E-03	-2.6	2.0E-03	0.0	9.4E-01	0.0	9.6E-01
ENSMUST00000134503	gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:95706]	Q4FK56	Q60928	-8.5	8.4E-05	5.7	1.5E-02	0.4	8.6E-01	-0.1	9.5E-01
ENSMUST00000134532	potassium channel tetramerisation domain containing 10 [Source:MGI Symbol;Acc:MGI:2141207]	S4R2A3		5.3	2.6E-02	-2.6	4.8E-02	-6.5	5.2E-04	0.6	6.3E-01
ENSMUST00000120389	sorting nexin 12 [Source:MGI Symbol;Acc:MGI:1919331]	Q6ZWQ5		-0.5	4.9E-01	0.4	7.0E-01	1.2	1.3E-01	0.3	7.5E-01
ENSMUST00000134534	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]	B1AS27		4.9	4.8E-03	5.9	3.1E-04	-0.6	6.1E-01	0.1	8.6E-01
ENSMUST00000134538	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143057]		Q80SX8	5.5	3.1E-02	5.9	5.7E-02	-0.2	9.5E-01	1.3	4.2E-01
ENSMUST00000134554	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]			-2.0	8.0E-03	4.3	4.2E-03	-0.2	8.6E-01	0.0	9.9E-01
ENSMUST00000134566	acyl-CoA synthetase long-chain family member 3 [Source:MGI Symbol;Acc:MGI:1921455]	E9PUC2		-4.0	1.5E-03	5.8	3.3E-04	-2.2	9.6E-02	-0.2	7.9E-01
ENSMUST00000120420	sodium channel, voltage-gated, type V, alpha [Source:MGI Symbol;Acc:MGI:98251]		Q9JJV9	3.7	1.9E-01	3.2	1.0E-01	-5.1	6.1E-02	-4.6	2.3E-02
ENSMUST00000134578	kinesin light chain 1 [Source:MGI Symbol;Acc:MGI:107978]	F6UYN4		-5.0	3.2E-04	-10.5	1.2E-04	-1.2	2.5E-02	-0.9	6.3E-01
ENSMUST00000120423				1.9	1.4E-01	3.3	5.7E-02	-0.1	9.6E-01	-1.4	2.3E-01
ENSMUST00000134585	chromobox 1 [Source:MGI Symbol;Acc:MGI:105369]	Q7TPM0		-2.6	1.9E-03	-1.4	2.9E-01	-0.7	5.0E-01	-3.6	5.6E-02
ENSMUST00000134625	CD200 receptor 1 [Source:MGI Symbol;Acc:MGI:1889024]	M0QWY6		-5.7	2.1E-02	3.1	3.1E-03	0.5	4.4E-01	-0.6	3.4E-01
ENSMUST00000134652	tetratricopeptide repeat domain 39D [Source:MGI Symbol;Acc:MGI:1914987]	Q0VF76		5.8	3.1E-04	4.7	1.4E-03	-2.1	1.1E-01	-0.5	4.6E-01
ENSMUST00000134655	aldehyde dehydrogenase 16 family, member A1 [Source:MGI Symbol;Acc:MGI:1916998]	F6RQF0		-5.5	4.9E-04	-0.4	5.1E-01	-2.0	4.0E-03	-4.8	3.4E-04
ENSMUST00000134663	myosin VIIB [Source:MGI Symbol;Acc:MGI:107709]		Q99MZ6	9.4	1.1E-05	4.1	2.1E-03	-1.6	1.5E-01	-0.7	3.5E-01
ENSMUST00000134674	myotubularin related protein 2 [Source:MGI Symbol;Acc:MGI:1924366]	B8JJF6		-5.4	1.4E-04	5.3	2.1E-02	-0.6	7.6E-01	0.8	5.3E-01
ENSMUST00000134682	mitogen-activated protein kinase-activated protein kinase 3 [Source:MGI Symbol;Acc:MGI:2143163]	B0QZU6		4.6	5.5E-04	5.4	3.7E-02	-0.8	7.5E-01	-1.0	5.1E-01
ENSMUST00000134694	integrin alpha M [Source:MGI Symbol;Acc:MGI:96607]	F6YXU0		-4.4	1.1E-04	-1.1	5.1E-01	0.7	5.3E-01	-2.2	2.6E-01
ENSMUST00000134719	protein phosphatase 1, catalytic subunit, gamma isoform [Source:MGI Symbol;Acc:MGI:104872]	A0A0G2JEB0		-3.4	1.1E-03	-3.3	1.4E-02	-0.1	8.2E-01	-2.9	6.7E-02
ENSMUST00000134720	titin [Source:MGI Symbol;Acc:MGI:98864]	F7CR78		7.9	7.3E-05	6.0	3.9E-04	-0.5	6.7E-01	-0.6	3.5E-01
ENSMUST00000120450	phosphoribosylglycinamide formyltransferase [Source:MGI Symbol;Acc:MGI:95654]	Q3TH49	Q64737	-0.9	3.6E-01	-0.1	9.3E-01	0.0	9.7E-01	-0.8	4.4E-01
ENSMUST00000134744	MDA receptor synaptonuclear signaling and neuronal migration factor [Source:MGI Symbol;Acc:MGI:186175	F6VTS9		-3.7	2.5E-02	6.5	5.8E-04	-0.7	6.3E-01	0.5	5.0E-01
ENSMUST00000134746	centrosomal protein 57 [Source:MGI Symbol;Acc:MGI:1915551]	D6RH89		-4.2	3.2E-02	6.9	3.4E-04	-0.7	6.3E-01	-0.2	8.3E-01
ENSMUST00000120454	cytochrome c oxidase assembly factor 4 [Source:MGI Symbol;Acc:MGI:1915435]		Q8BT51	1.1	6.5E-01	-1.5	6.2E-01	-2.1	3.8E-01	0.5	8.6E-01
ENSMUST00000134759	N(alpha)-acetyltransferase 20, NatB catalytic subunit [Source:MGI Symbol;Acc:MGI:1915127]	G5E8X4		3.1	2.7E-03	5.2	6.8E-03	-0.4	8.2E-01	-1.2	2.3E-01
ENSMUST00000120461	lectin, mannose-binding, 1 [Source:MGI Symbol;Acc:MGI:1917611]		Q9D0F3	-0.8	4.8E-01	0.1	9.4E-01	-0.4	6.5E-01	-1.2	2.8E-01
ENSMUST00000120463	SIK family kinase 3 [Source:MGI Symbol;Acc:MGI:2446296]	F6S7W6		1.8	4.6E-01	4.1	2.0E-01	1.6	5.2E-01	-0.6	8.0E-01
ENSMUST00000134767	synaptojanin 2 [Source:MGI Symbol;Acc:MGI:1201671]	S4R207		5.6	6.4E-03	2.7	1.8E-01	0.6	7.1E-01	1.1	4.2E-01
ENSMUST00000134788	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]	D3Z7X7		-4.5	5.2E-03	7.2	9.6E-05	-0.8	5.0E-01	0.0	9.8E-01
ENSMUST00000134814	fructose bisphosphatase 1 [Source:MGI Symbol;Acc:MGI:95492]	E9Q0T7		5.7	7.5E-04	5.9	1.7E-03	-0.7	6.3E-01	0.2	8.3E-01
ENSMUST00000134825	ium voltage-gated channel, Isk-related family, member 1-like, pseudogene [Source:MGI Symbol;Acc:MGI:191		Q9QZ26	6.2	1.3E-04	1.9	1.4E-02	-0.7	2.5E-01	-0.6	3.0E-01
ENSMUST00000120493	genetic suppressor element 1 [Source:MGI Symbol;Acc:MGI:1098275]		Q3U3C9	0.0	9.9E-01	4.3	5.5E-02	2.3	2.4E-01	-2.0	2.1E-01
ENSMUST00000120495	cytochrome c oxidase assembly protein 17 [Source:MGI Symbol;Acc:MGI:1333806]	Q54AC6	P56394	1.2	1.4E-01	1.3	1.8E-01	-0.5	4.9E-01	-0.6	4.5E-01
ENSMUST00000134844	coiled-coil and C2 domain containing 1B [Source:MGI Symbol;Acc:MGI:2443076]	F6XC25		-5.8	2.7E-04	-6.4	1.5E-03	-0.7	1.7E-01	0.9	5.7E-01
ENSMUST00000134863	interferon regulatory factor 9 [Source:MGI Symbol;Acc:MGI:107587]	E9PZJ2		-2.2	6.3E-03	6.2	7.3E-04	-0.1	9.3E-01	1.5	6.9E-02
ENSMUST00000134894	ras homolog gene family, member T1 [Source:MGI Symbol;Acc:MGI:1926078]	F7ASU3		-4.6	2.9E-02	5.7	4.3E-04	-0.9	4.3E-01	-0.8	2.6E-01
ENSMUST00000134896	CCR4-NOT transcription complex, subunit 8 [Source:MGI Symbol;Acc:MGI:1916375]	A2AFQ7		4.3	5.2E-04	6.2	1.6E-03	-0.7	6.4E-01	0.2	8.5E-01
ENSMUST00000120509	serum/glucocorticoid regulated kinase 1 [Source:MGI Symbol;Acc:MGI:1340062]		Q9WVC6	0.7	4.4E-01	0.1	9.6E-01	-0.1	9.3E-01	0.6	5.8E-01
ENSMUST00000120512	MyoD family inhibitor domain containing [Source:MGI Symbol;Acc:MGI:104611]		Q8BX65	0.5	6.2E-01	-0.5	6.4E-01	-1.9	5.2E-02	-0.9	3.6E-01
ENSMUST00000134902	BCL2-like 1 [Source:MGI Symbol;Acc:MGI:88139]		Q64373	6.0	6.6E-04	5.0	1.7E-02	-2.2	2.8E-01	-1.3	2.9E-01
ENSMUST00000120520	alkaline ceramidase 3 [Source:MGI Symbol;Acc:MGI:1913440]	D3YTU8		-3.7	6.9E-02	-0.4	9.0E-01	3.8	4.7E-02	0.6	8.4E-01
ENSMUST00000120522	solute carrier family 22 (organic cation transporter), member 26 [Source:MGI Symbol;Acc:MGI:2385316]	E9Q6M5		2.9	1.0E-01	6.8	2.0E-03	-0.5	7.8E-01	-4.5	3.3E-03
ENSMUST00000120524	transmembrane protein 132A [Source:MGI Symbol;Acc:MGI:2147810]	D3Z4S6		1.1	7.6E-02	1.5	6.1E-02	-0.1	9.3E-01	-0.4	4.8E-01
ENSMUST00000134935	spectrin beta, non-erythrocytic 5 [Source:MGI Symbol;Acc:MGI:2685200]	F7BYG3		8.3	9.5E-06	6.3	1.2E-03	1.1	4.3E-01	-0.3	6.6E-01
ENSMUST00000134943	serine/arginine-rich splicing factor 4 [Source:MGI Symbol;Acc:MGI:1890577]	A0A0A6YXU8		-3.6	5.9E-03	2.6	7.2E-03	-1.0	1.7E-01	-0.2	7.0E-01
ENSMUST00000120532	histone cell cycle regulation defective homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:99430]		Q61666	-0.3	8.1E-01	1.8	2.9E-01	2.3	1.2E-01	0.3	8.2E-01
ENSMUST00000134945	myotubularin related protein 14 [Source:MGI Symbol;Acc:MGI:1916075]	F6W741		-5.9	2.2E-04	5.8	2.4E-03	0.4	7.8E-01	-0.6	4.5E-01
ENSMUST00000120535	AU RNA binding protein/enoyl-coenzyme A hydratase [Source:MGI Symbol;Acc:MGI:1338011]			-0.2	8.2E-01	-0.1	8.9E-01	0.3	6.5E-01	0.3	7.5E-01
ENSMUST00000134978	tubulin, beta 5 class I [Source:MGI Symbol;Acc:MGI:107812]	G3UZR1		-3.7	1.3E-03	-3.4	1.6E-02	1.6	2.3E-02	0.1	9.0E-01
ENSMUST00000134982	predicted gene 14296 [Source:MGI Symbol;Acc:MGI:3708667]	E9Q3Y3		7.0	8.9E-07	-8.6	1.9E-05	0.5	1.4E-01	0.6	5.9E-01
ENSMUST00000135038	interleukin 2 receptor, gamma chain [Source:MGI Symbol;Acc:MGI:96551]	B0QZX1		-3.9	5.0E-03	7.5	1.7E-04	0.1	9.5E-01	-0.4	5.2E-01
ENSMUST00000120544	kinesin light chain 1 [Source:MGI Symbol;Acc:MGI:107978]	E9Q7C9		0.0	9.7E-01	-0.8	6.4E-01	-1.0	4.2E-01	-0.3	8.7E-01
ENSMUST00000120550	signal recognition particle 72 [Source:MGI Symbol;Acc:MGI:1333795]	E9Q740		-5.4	4.1E-02	-5.7	3.8E-02	-2.4	4.2E-02	-2.1	4.7E-01
ENSMUST00000135065	growth factor receptor bound protein 2 [Source:MGI Symbol;Acc:MGI:95805]	B1AT95		-5.4	7.9E-04	7.3	1.6E-04	-1.9	1.9E-01	0.8	2.5E-01
ENSMUST00000135071	proprotein convertase subtilisin/kexin type 4 [Source:MGI Symbol;Acc:MGI:97514]	M0QW95		5.6	6.4E-03	-7.1	9.1E-04	-1.3	7.8E-02	-1.9	2.7E-01
ENSMUST00000135075	Kruppel-like factor 7 (ubiquitous) [Source:MGI Symbol;Acc:MGI:1935151]	A2AAB6		4.4	1.7E-02	6.5	1.6E-04	-0.5	6.7E-01	-0.1	8.1E-01
ENSMUST00000120560				1.2	5.5E-01	-0.9	7.1E-01	-2.0	2.4E-01	0.1	9.7E-01
ENSMUST00000135079	protein disulfide isomerase associated 3 [Source:MGI Symbol;Acc:MGI:95834]	F6Q404		-6.6	3.3E-05	3.1	6.5E-02	1.4	3.0E-01	-5.4	4.9E-03
ENSMUST00000135087	coronin, actin binding protein 1A [Source:MGI Symbol;Acc:MGI:1345961]	D3YXM2		-2.2	1.5E-02	-1.8	2.0E-02	0.2	5.8E-01	0.3	6.7E-01
ENSMUST00000135107	SRY (sex determining region Y)-box 3 [Source:MGI Symbol;Acc:MGI:98365]	A2AM37		5.2	4.3E-04	5.5	3.1E-03	0.5	7.1E-01	-0.2	8.3E-01
ENSMUST00000135158	carbohydrate (chondroitin 6/keratan) sulfotransferase 3 [Source:MGI Symbol;Acc:MGI:1858224]	G5E8X5		6.0	2.3E-03	-3.7	1.0E-02	0.6	2.7E-01	0.7	5.5E-01
ENSMUST00000135159	the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 [Source:MGI Symbo	F6RXM1		4.6	2.1E-02	6.2	5.9E-03	-0.7	7.1E-01	-0.1	9.1E-01
ENSMUST00000135166	lectin, galactose binding, soluble 8 [Source:MGI Symbol;Acc:MGI:1928481]	Q8C6H0		-6.5	3.1E-02	-3.0	7.6E-03	-0.6	2.8E-01	-1.0	3.2E-01
ENSMUST00000135184	MX dynamin-like GTPase 1 [Source:MGI Symbol;Acc:MGI:97243]	V9GWS9		5.4	7.3E-06	6.4	1.5E-03	-0.5	7.4E-01	0.5	5.7E-01
ENSMUST00000135192	coatomer protein complex subunit alpha [Source:MGI Symbol;Acc:MGI:1334462]		Q8CIE6	-3.4	4.2E-04	4.9	1.2E-04	-3.9	2.4E-03	-0.1	8.2E-01
ENSMUST00000135193	ucine-rich repeats and calponin homology (CH) domain containing 3 [Source:MGI Symbol;Acc:MGI:1917394	E9QAU9		4.5	1.2E-02	-1.9	2.6E-02	0.6	2.2E-01	-0.3	7.4E-01
ENSMUST00000135218	mutL homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:101938]	A0A0G2JH14		6.3	8.7E-04	6.6	3.2E-04	-0.5	6.8E-01	-1.0	1.8E-01
ENSMUST00000135222	ethanolamine kinase 2 [Source:MGI Symbol;Acc:MGI:2443760]		A7MCT6	6.0	2.8E-04	5.8	1.6E-04	-2.6	3.5E-02	0.0	9.6E-01
ENSMUST00000135233	c-abl oncogene 1, non-receptor tyrosine kinase [Source:MGI Symbol;Acc:MGI:87859]	A0A0A6YVY6		3.9	6.7E-03	-4.2	1.6E-02	0.9	2.6E-01	-1.0	5.7E-01
ENSMUST00000120596				1.8	2.8E-01	1.7	3.6E-01	-0.9	6.1E-01	-0.7	6.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000135241	vesicle-associated membrane protein 4 [Source:MGI Symbol;Acc:MGI:1858730]		O70480	-8.4	3.3E-06	7.1	3.6E-04	-0.4	7.5E-01	-0.8	2.6E-01
ENSMUST00000120613	kinesin family member 3A [Source:MGI Symbol;Acc:MGI:107689]		P28741	0.2	8.0E-01	-0.2	8.1E-01	-1.4	5.5E-02	-1.0	2.5E-01
ENSMUST00000135259	THO complex 6 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2677480]	F6S2T7		5.6	6.2E-04	5.2	5.5E-03	-1.5	3.7E-01	-1.2	2.1E-01
ENSMUST00000135338	sushi domain containing 5 [Source:MGI Symbol;Acc:MGI:2685972]	G3UW60		8.4	5.1E-05	5.3	4.8E-03	-2.0	2.3E-01	-0.5	5.9E-01
ENSMUST00000135365	jumonji domain containing 7 [Source:MGI Symbol;Acc:MGI:3845785]	D6RGQ7		5.4	1.1E-02	6.8	1.2E-03	0.6	7.0E-01	-0.7	4.5E-01
ENSMUST00000135373	RIKEN cDNA 6430573F11 gene [Source:MGI Symbol;Acc:MGI:2442328]	D3YYA2		6.4	1.4E-04	2.4	1.3E-02	-0.3	6.7E-01	0.0	9.8E-01
ENSMUST00000135375	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]	F6ZGN3		5.7	9.7E-04	5.1	3.4E-03	-0.4	7.3E-01	-0.3	7.3E-01
ENSMUST00000120639	RIKEN cDNA C530008M17 gene [Source:MGI Symbol;Acc:MGI:2444817]	E9Q3Y7		4.6	7.7E-02	3.8	3.1E-01	0.4	9.1E-01	1.1	6.3E-01
ENSMUST00000135386	CD84 antigen [Source:MGI Symbol;Acc:MGI:1336885]			1.8	1.1E-02	-2.3	7.7E-03	0.7	1.2E-01	-1.0	2.0E-01
ENSMUST00000135395	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A [Source:MGI Symbol;Acc:MGI:108447]	D3Z7M9		-3.0	1.8E-03	5.2	5.9E-06	0.2	7.0E-01	-0.1	8.4E-01
ENSMUST00000135402	BBSome interacting protein 1 [Source:MGI Symbol;Acc:MGI:1913610]	J3QMK2		-3.2	8.2E-05	3.7	9.4E-03	-1.0	3.8E-01	0.2	8.6E-01
ENSMUST00000135406	golgi autoantigen, golgin subfamily b, macrogolgin 1 [Source:MGI Symbol;Acc:MGI:1099447]	E9Q028		3.7	3.9E-03	6.4	1.4E-04	-0.5	6.2E-01	-0.9	1.5E-01
ENSMUST00000135452	carrier family 7 (cationic amino acid transporter, y+ system), member 10 [Source:MGI Symbol;Acc:MGI:185	E9Q248		5.7	1.5E-02	1.6	2.9E-02	0.3	5.8E-01	0.9	1.3E-01
ENSMUST00000135454	RIKEN cDNA 0610037L13 gene [Source:MGI Symbol;Acc:MGI:1921348]		Q8BHG2	3.6	1.5E-02	7.6	1.2E-04	0.5	6.5E-01	0.3	6.7E-01
ENSMUST00000135464	transmembrane emp24 domain trafficking protein 2 [Source:MGI Symbol;Acc:MGI:1929269]	Q8BPI2		-4.5	4.7E-03	6.1	9.1E-05	0.1	8.7E-01	0.4	4.6E-01
ENSMUST00000135465	leucine rich repeat containing 57 [Source:MGI Symbol;Acc:MGI:1913856]	B0R031		-3.0	2.9E-02	4.2	6.9E-03	-1.0	3.9E-01	-0.2	8.5E-01
ENSMUST00000120683	histone deacetylase 7 [Source:MGI Symbol;Acc:MGI:1891835]	E9PXW8		0.2	7.9E-01	-1.7	1.4E-01	-0.9	1.9E-01	0.9	3.7E-01
ENSMUST00000135466	retinoic acid receptor, gamma [Source:MGI Symbol;Acc:MGI:97858]	D3YZY4		6.1	2.0E-04	8.0	1.1E-05	-2.8	2.9E-02	-0.1	7.6E-01
ENSMUST00000120690	transmembrane protein 30A [Source:MGI Symbol;Acc:MGI:106402]	D3YVV1		0.9	2.0E-01	5.7	7.0E-04	4.8	1.3E-03	0.0	9.5E-01
ENSMUST00000135469	sterile alpha motif and leucine zipper containing kinase AZK [Source:MGI Symbol;Acc:MGI:2443258]	Q3TRG2	Q9ESL4	5.6	8.3E-05	2.1	4.2E-01	0.3	8.7E-01	3.3	1.6E-01
ENSMUST00000135526	SH3 domain containing ring finger 3 [Source:MGI Symbol;Acc:MGI:2444637]		Q8C120	4.4	1.3E-02	6.7	7.2E-04	-0.7	6.3E-01	-0.1	8.6E-01
ENSMUST00000135529	biliverdin reductase A [Source:MGI Symbol;Acc:MGI:88170]	A2ASB7		7.7	6.4E-04	-2.9	2.9E-02	0.5	4.2E-01	-1.5	2.6E-01
ENSMUST00000135573	peroxiredoxin 1 [Source:MGI Symbol;Acc:MGI:99523]		P35700	-2.5	6.5E-04	6.3	9.1E-05	0.6	5.4E-01	0.1	8.5E-01
ENSMUST00000135574	adenosine deaminase, RNA-specific, B2 [Source:MGI Symbol;Acc:MGI:2151118]		Q9JI20	5.0	3.4E-04	-3.1	4.1E-02	0.3	6.5E-01	0.9	4.9E-01
ENSMUST00000120702				2.1	1.0E-01	3.1	4.1E-02	0.1	9.6E-01	-1.0	3.7E-01
ENSMUST00000135607	coiled-coil domain containing 6 [Source:MGI Symbol;Acc:MGI:1923801]	F7B4D5		5.9	7.4E-04	5.6	2.4E-02	-0.7	7.6E-01	-1.3	3.5E-01
ENSMUST00000135609	B cell leukemia/lymphoma 3 [Source:MGI Symbol;Acc:MGI:88140]	F6YNH8		-3.3	1.7E-02	-2.7	1.5E-02	1.5	1.3E-02	0.6	5.5E-01
ENSMUST00000135636	sortilin 1 [Source:MGI Symbol;Acc:MGI:1338015]	A2AEF0	Q6PHU5	-3.4	1.0E-02	2.5	2.0E-01	-5.3	2.7E-02	-1.2	4.0E-01
ENSMUST00000135639	F-box protein 11 [Source:MGI Symbol;Acc:MGI:2147134]	S4R2I0		-3.6	2.8E-02	3.4	5.3E-03	0.1	9.0E-01	0.2	7.3E-01
ENSMUST00000135660	stomatin (Epb7.2)-like 2 [Source:MGI Symbol;Acc:MGI:1913842]	F6WI02		-5.7	9.8E-04	6.1	3.2E-04	-0.5	6.8E-01	-0.6	3.8E-01
ENSMUST00000135671	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 [Source:MGI Symbol;Acc:MGI:1915448]		Q9CPU2	3.1	4.2E-04	8.0	2.8E-05	-0.6	6.2E-01	-1.1	6.5E-02
ENSMUST00000120718				-0.5	5.3E-01	0.6	5.1E-01	0.7	3.2E-01	-0.4	6.8E-01
ENSMUST00000135673	pogo transposable element with KRAB domain [Source:MGI Symbol;Acc:MGI:1918842]	E9Q3B2		6.0	3.8E-04	7.1	3.9E-04	-0.2	9.1E-01	0.5	4.8E-01
ENSMUST00000120722	RIKEN cDNA 2610002M06 gene [Source:MGI Symbol;Acc:MGI:1914278]		Q9CQD4	-0.8	9.3E-02	0.1	8.6E-01	0.7	8.9E-02	-0.1	7.8E-01
ENSMUST00000135680	mitochondrial ribosomal protein S14 [Source:MGI Symbol;Acc:MGI:1928141]		Q9CR88	2.3	7.7E-03	5.1	2.0E-03	-1.5	2.7E-01	-1.5	9.1E-02
ENSMUST00000135686	glia maturation factor, gamma [Source:MGI Symbol;Acc:MGI:1927135]	D3Z2F6		-5.3	3.3E-06	6.1	5.2E-04	-0.5	6.8E-01	0.3	7.0E-01
ENSMUST00000135688	phosphodiesterase 6A, cGMP-specific, rod, alpha [Source:MGI Symbol;Acc:MGI:97524]	F6UDG9		6.7	3.2E-03	9.3	2.1E-04	1.1	4.8E-01	0.4	5.2E-01
ENSMUST00000120737	mitochondrial ribosomal protein S10 [Source:MGI Symbol;Acc:MGI:1928139]	G5E8U8		2.5	7.2E-02	-3.9	4.9E-03	-6.8	7.7E-05	-0.4	7.2E-01
ENSMUST00000120746	neurocalcin delta [Source:MGI Symbol;Acc:MGI:1196326]		Q91X97	6.1	3.6E-02	8.2	1.3E-02	-0.7	8.2E-01	-2.7	1.1E-01
ENSMUST00000120753	furin (paired basic amino acid cleaving enzyme) [Source:MGI Symbol;Acc:MGI:97513]		P23188	2.5	2.5E-01	3.5	2.1E-01	-0.3	9.0E-01	-1.3	5.2E-01
ENSMUST00000135690	ribosomal protein L10 [Source:MGI Symbol;Acc:MGI:105943]	B7FAU6		-5.1	2.2E-04	-2.8	1.4E-01	1.6	1.4E-01	-0.1	9.7E-01
ENSMUST00000135713	phosphate regulating endopeptidase homolog, X-linked [Source:MGI Symbol;Acc:MGI:107489]	F6S0V7		7.3	3.1E-05	6.2	8.7E-02	-0.9	8.1E-01	0.5	7.9E-01
ENSMUST00000135719	cyclin L1 [Source:MGI Symbol;Acc:MGI:1922664]	F6WST0		-7.8	2.2E-03	7.0	7.8E-06	-0.8	3.3E-01	-0.3	4.7E-01
ENSMUST00000135741	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]	B7ZD29		6.3	5.8E-03	8.1	9.3E-04	0.7	7.0E-01	-2.8	2.0E-02
ENSMUST00000135801	coenzyme Q2 homolog, prenyltransferase (yeast) [Source:MGI Symbol;Acc:MGI:1919133]	D3Z296		2.7	2.6E-02	5.2	5.2E-03	0.0	1.0E+00	0.4	6.3E-01
ENSMUST00000135823	coronin 7 [Source:MGI Symbol;Acc:MGI:1926135]	E9PYU1		-3.3	1.9E-02	7.7	8.4E-05	-0.5	6.7E-01	-0.4	4.6E-01
ENSMUST00000135842	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Source:MGI Symbol;Acc:MGI:2136460]	F6T930		-4.5	6.6E-04	-3.0	1.6E-02	-0.9	1.7E-01	-2.4	7.6E-02
ENSMUST00000135846	ectonucleotide pyrophosphatase/phosphodiesterase 1 [Source:MGI Symbol;Acc:MGI:97370]			3.7	2.0E-02	7.2	8.9E-05	0.1	9.6E-01	0.1	8.5E-01
ENSMUST00000135856	protein phosphatase with EF hand calcium-binding domain 1 [Source:MGI Symbol;Acc:MGI:1097157]	Q3UQZ5		5.3	7.3E-05	4.5	2.1E-04	-1.1	1.5E-01	-0.6	3.0E-01
ENSMUST00000135868	mastermind like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1890504]	F6UY95		-2.9	4.4E-03	9.6	1.1E-04	-0.3	8.4E-01	0.6	3.3E-01
ENSMUST00000135869	ferritin light polypeptide 1 [Source:MGI Symbol;Acc:MGI:95589]	H3BKD3		-4.3	1.6E-02	-5.8	5.5E-03	0.4	5.2E-01	-1.1	5.4E-01
ENSMUST00000135876	eukaryotic translation initiation factor 2A [Source:MGI Symbol;Acc:MGI:1098684]	D6RGA6		-4.6	1.5E-03	5.6	1.8E-04	0.9	2.9E-01	-0.6	3.0E-01
ENSMUST00000120794	cleavage and polyadenylation specific factor 3-like [Source:MGI Symbol;Acc:MGI:1919207]	A8Y5J3		-3.0	5.0E-02	-4.9	5.6E-02	0.0	9.6E-01	1.9	4.2E-01
ENSMUST00000135877	eukaryotic translation elongation factor 1 beta 2 [Source:MGI Symbol;Acc:MGI:1929520]	M0QW60		-8.3	9.3E-06	6.1	5.3E-05	-1.4	1.4E-01	-0.4	4.9E-01
ENSMUST00000135884	NME/NM23 nucleoside diphosphate kinase 1 [Source:MGI Symbol;Acc:MGI:97355]	Q5NC81	P15532	-1.8	4.2E-03	-3.3	1.0E-02	0.3	5.6E-01	-1.0	4.0E-01
ENSMUST00000135887	insulin-like growth factor binding protein 3 [Source:MGI Symbol;Acc:MGI:96438]		P47878	5.2	7.3E-03	5.2	9.7E-03	-0.6	7.2E-01	-0.1	9.4E-01
ENSMUST00000135912	family with sequence similarity 149, member A [Source:MGI Symbol;Acc:MGI:2387177]	F6X0J3		5.5	1.2E-02	6.7	5.0E-04	-0.7	6.3E-01	-0.9	2.4E-01
ENSMUST00000135934	subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1(	F6YHG5		-4.9	2.4E-03	5.7	9.3E-04	-0.5	7.2E-01	-0.6	3.7E-01
ENSMUST00000135975	HNF1 homeobox B [Source:MGI Symbol;Acc:MGI:98505]	A0A0A0MQH4		6.1	1.1E-03	7.2	9.2E-05	-0.5	6.7E-01	-0.1	8.7E-01
ENSMUST00000120827	HOP homeobox [Source:MGI Symbol;Acc:MGI:1916782]		Q8R1H0	-0.7	7.3E-01	0.3	8.9E-01	-0.4	8.3E-01	-1.4	5.0E-01
ENSMUST00000135983	hexokinase 3 [Source:MGI Symbol;Acc:MGI:2670962]	D6RCV7		-2.7	2.0E-02	-3.3	8.7E-03	1.2	3.9E-02	-1.6	2.0E-01
ENSMUST00000120836	BR serine/threonine kinase 1 [Source:MGI Symbol;Acc:MGI:2685946]	D3Z5P0		4.8	1.0E-01	2.5	4.0E-01	-2.9	3.6E-01	-0.6	7.8E-01
ENSMUST00000135984	lymphoid-restricted membrane protein [Source:MGI Symbol;Acc:MGI:108424]	D6RIN0		-5.7	7.2E-06	-1.8	1.6E-01	1.5	6.0E-02	0.6	6.3E-01
ENSMUST00000135986	coiled-coil domain containing 13 [Source:MGI Symbol;Acc:MGI:1920144]		D3YV10	8.1	1.3E-05	6.2	1.0E-05	-1.4	8.9E-02	-0.3	4.2E-01
ENSMUST00000136008	ERGIC and golgi 2 [Source:MGI Symbol;Acc:MGI:1914706]		Q9CR89	-1.9	5.1E-03	1.3	5.8E-01	3.2	1.0E-01	-3.4	1.4E-01
ENSMUST00000136012	major facilitator superfamily domain containing 11 [Source:MGI Symbol;Acc:MGI:1917150]	E9PZJ5		2.9	1.2E-02	7.3	4.6E-04	-0.7	6.3E-01	-0.1	9.2E-01
ENSMUST00000120857	integrin alpha L [Source:MGI Symbol;Acc:MGI:96606]	D3Z627		-0.9	1.7E-01	-0.5	5.3E-01	-0.1	9.1E-01	-0.5	5.6E-01
ENSMUST00000120859	casein kinase 1, epsilon [Source:MGI Symbol;Acc:MGI:1351660]		Q9JMK2	-3.8	5.1E-02	-3.0	2.0E-01	0.4	7.0E-01	-0.4	8.8E-01
ENSMUST00000136020	required for meiotic nuclear division 5 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913339]	D6RII5		-7.0	9.6E-04	6.1	1.1E-03	0.6	6.2E-01	0.2	7.8E-01
ENSMUST00000136057	ubiquitin-associated protein 2 [Source:MGI Symbol;Acc:MGI:1916176]	F6WTC8		3.8	3.4E-02	-3.5	6.6E-02	-0.2	7.9E-01	-0.7	7.1E-01
ENSMUST00000136066	tubulin tyrosine ligase-like family, member 12 [Source:MGI Symbol;Acc:MGI:3039573]	F2Z423		6.8	4.9E-04	6.1	1.7E-02	-0.7	7.7E-01	-1.2	3.7E-01
ENSMUST00000136074	actin related protein 2/3 complex, subunit 1B [Source:MGI Symbol;Acc:MGI:1343142]	F6VVE6		-8.4	3.8E-05	5.8	6.3E-04	-0.6	5.8E-01	-0.1	9.2E-01
ENSMUST00000120875	ankyrin repeat domain 50 [Source:MGI Symbol;Acc:MGI:2139777]	D3Z643		0.4	5.1E-01	1.1	1.8E-01	0.9	1.5E-01	0.2	7.3E-01
ENSMUST00000136075	RIKEN cDNA 4930447C04 gene [Source:MGI Symbol;Acc:MGI:1923051]	D3Z202		6.4	3.5E-04	6.9	1.5E-04	-0.3	7.8E-01	-0.1	8.4E-01
ENSMUST00000136090	coiled-coil domain containing 174 [Source:MGI Symbol;Acc:MGI:2444652]			4.2	1.2E-04	9.0	1.0E-03	0.6	7.7E-01	1.3	1.5E-01
ENSMUST00000136129	JTP23, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1925831	G3XA22		-4.1	1.5E-02	2.8	3.9E-02	-1.5	2.0E-01	0.5	6.0E-01
ENSMUST00000136139	GA repeat binding protein, beta 2 [Source:MGI Symbol;Acc:MGI:95612]		P81069	-6.1	1.4E-04	-3.2	4.3E-02	1.0	1.6E-01	-0.5	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000120904	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 [Source:MGI Symbol;Acc:MGI:2685817]		Q6I6G8	2.7	3.8E-01	3.9	2.0E-01	-0.5	8.8E-01	-1.7	4.7E-01
ENSMUST00000136175	coiled-coil domain containing 85C [Source:MGI Symbol;Acc:MGI:3644008]		E9Q6B2	6.5	3.7E-05	6.5	3.2E-04	-0.5	7.0E-01	-1.0	1.5E-01
ENSMUST00000136186	zinc finger, MYM domain containing 1 [Source:MGI Symbol;Acc:MGI:1915560]	A2A7U0		6.3	2.4E-03	6.6	8.3E-04	0.1	9.5E-01	-0.6	4.1E-01
ENSMUST00000136189	TBC1 domain family, member 14 [Source:MGI Symbol;Acc:MGI:1098708]	E9Q2V7		-6.5	1.1E-02	-2.1	1.4E-01	3.1	3.1E-03	-0.9	4.9E-01
ENSMUST00000136197	solute carrier organic anion transporter family, member 5A1 [Source:MGI Symbol;Acc:MGI:2443431]	A0A087WNX4		5.9	1.3E-03	6.0	2.8E-04	0.5	6.8E-01	-1.1	9.3E-02
ENSMUST00000136223	retinol dehydrogenase 9 [Source:MGI Symbol;Acc:MGI:2143528]	Q6PHA1		9.6	3.7E-07	5.9	2.0E-02	-0.8	7.4E-01	-0.5	6.7E-01
ENSMUST00000136265	chondroitin sulfate N-acetylgalactosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI:1926002]	D3Z5Q0		-6.2	5.1E-03	6.8	2.7E-04	-0.7	6.0E-01	0.2	7.3E-01
ENSMUST00000136278	prolyl 3-hydroxylase 1 [Source:MGI Symbol;Acc:MGI:1888921]	F2Z499		4.1	1.3E-02	2.1	1.3E-01	0.1	9.6E-01	4.1	2.6E-03
ENSMUST00000120920				-3.8	2.8E-01	-2.9	4.3E-01	-1.2	5.6E-01	-2.1	6.1E-01
ENSMUST00000136299	DDB1 and CUL4 associated factor 17 [Source:MGI Symbol;Acc:MGI:1923013]	F6XZ79		5.8	4.8E-05	4.9	4.5E-02	-0.7	7.6E-01	0.0	9.8E-01
ENSMUST00000120928	synaptogyrin 2 [Source:MGI Symbol;Acc:MGI:1328324]	B0QZP8		-3.1	2.9E-01	0.5	8.7E-01	1.2	6.2E-01	-2.4	4.5E-01
ENSMUST00000136307	solute carrier family 22 (organic cation transporter), member 5 [Source:MGI Symbol;Acc:MGI:1329012]	D6RH54		6.2	2.3E-03	6.5	3.9E-04	-0.5	6.9E-01	0.5	4.2E-01
ENSMUST00000120935	zinc finger protein 819 [Source:MGI Symbol;Acc:MGI:1921650]	E9Q5X9		-0.5	5.5E-01	3.1	6.1E-03	0.9	2.9E-01	-2.8	8.5E-03
ENSMUST00000136309	predicted gene 13225 [Source:MGI Symbol;Acc:MGI:3652161]	B1AVN4		3.8	1.5E-03	-8.1	1.8E-03	-0.7	2.2E-01	0.2	9.2E-01
ENSMUST00000136312	ubiquitin C [Source:MGI Symbol;Acc:MGI:98889]		P0CG50	-5.4	1.3E-04	-8.4	1.9E-05	0.1	6.3E-01	-1.5	2.2E-01
ENSMUST00000136319	ubiquitin specific peptidase 50 [Source:MGI Symbol;Acc:MGI:1922333]	D6RCG3		4.0	2.3E-04	-4.2	3.2E-03	1.9	2.2E-03	-0.7	5.3E-01
ENSMUST00000136327	high mobility group nucleosomal binding domain 2 [Source:MGI Symbol;Acc:MGI:96136]	B7ZCQ3		-3.6	2.8E-02	4.3	4.8E-02	0.0	9.9E-01	-0.1	9.7E-01
ENSMUST00000136331	torsin A interacting protein 1 [Source:MGI Symbol;Acc:MGI:3582693]	J3QQ40		-6.4	4.7E-05	7.0	2.1E-05	0.1	9.3E-01	-0.5	3.2E-01
ENSMUST00000136390	scribbled homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2145950]	F6RIN9		-5.9	9.5E-03	6.9	1.5E-04	-0.5	6.8E-01	-0.5	4.5E-01
ENSMUST00000120963	aminoadipate-semialdehyde dehydrogenase [Source:MGI Symbol;Acc:MGI:2442517]		Q80WC9	-1.0	6.2E-01	5.2	3.9E-02	1.9	3.8E-01	-4.3	4.1E-02
ENSMUST00000136396	adhesion G protein-coupled receptor G4 [Source:MGI Symbol;Acc:MGI:2685213]	B7ZCD1		6.1	3.3E-02	6.2	8.9E-04	-0.5	7.3E-01	0.3	7.1E-01
ENSMUST00000120969				4.0	9.8E-02	5.6	4.4E-02	-0.3	9.1E-01	-1.9	2.2E-01
ENSMUST00000120977	WW domain containing transcription regulator 1 [Source:MGI Symbol;Acc:MGI:1917649]		Q9EPK5	0.3	8.3E-01	2.8	7.4E-02	-1.6	3.0E-01	-4.0	1.2E-02
ENSMUST00000136397	torsin A interacting protein 1 [Source:MGI Symbol;Acc:MGI:3582693]	D3YZJ9		-4.1	1.8E-02	-2.1	6.3E-02	1.1	7.0E-02	0.3	7.3E-01
ENSMUST00000136398	period circadian clock 3 [Source:MGI Symbol;Acc:MGI:1277134]	E9PV88		6.5	1.6E-04	5.8	4.5E-04	-0.6	6.3E-01	0.1	8.8E-01
ENSMUST00000136431	protein phosphatase 1M [Source:MGI Symbol;Acc:MGI:1915155]	F6V5B0		-5.8	1.4E-04	5.9	3.0E-03	0.7	6.6E-01	-0.4	6.6E-01
ENSMUST00000120985	nology domain containing, family A (phosphoinositide binding specific) member 4 [Source:MGI Symbol;Acc:M	E9QJX8		4.0	6.7E-02	5.3	6.5E-02	1.0	6.9E-01	-0.3	8.6E-01
ENSMUST00000136441	ADP-ribosylation factor-like 4A [Source:MGI Symbol;Acc:MGI:99437]	G3UVX1		7.4	6.6E-05	5.7	6.4E-06	-0.3	6.7E-01	0.4	3.2E-01
ENSMUST00000136465	phospholipase A2, group XVI [Source:MGI Symbol;Acc:MGI:2179715]		Q8R3U1	7.6	6.2E-05	4.9	5.1E-04	0.8	3.6E-01	0.3	6.0E-01
ENSMUST00000120988	CDGSH iron sulfur domain 2 [Source:MGI Symbol;Acc:MGI:1914256]	D3Z3X4		1.1	9.7E-02	-0.4	5.6E-01	-0.9	1.5E-01	0.7	3.5E-01
ENSMUST00000136471	GC-rich promoter binding protein 1 [Source:MGI Symbol;Acc:MGI:1920524]	D6RCY3		-7.3	5.3E-04	5.9	1.1E-04	-2.1	6.7E-02	-1.2	5.9E-02
ENSMUST00000136479	CD84 antigen [Source:MGI Symbol;Acc:MGI:1336885]	E9Q9E8		-10.9	1.3E-04	-2.2	1.2E-01	0.0	9.7E-01	-1.8	2.3E-01
ENSMUST00000136481	PRP6 pre-mRNA splicing factor 6 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1922946]		Q91YR7	-3.6	9.6E-05	7.5	2.0E-04	-0.5	7.0E-01	0.2	7.6E-01
ENSMUST00000136483	pseudouridine synthase 1 [Source:MGI Symbol;Acc:MGI:1929237]	D3YWU8		6.2	4.1E-04	4.0	9.8E-03	1.2	3.1E-01	1.5	1.2E-01
ENSMUST00000136501	bolA-like 3 (E. coli) [Source:MGI Symbol;Acc:MGI:1925903]	Q14A77	Q8CEI1	3.8	1.0E-02	6.0	5.1E-04	0.9	4.3E-01	-0.8	2.8E-01
ENSMUST00000121001				2.8	2.8E-01	1.4	6.3E-01	-2.1	4.6E-01	-0.7	7.7E-01
ENSMUST00000136521	RIKEN cDNA 6330403A02 gene [Source:MGI Symbol;Acc:MGI:2138735]		Q0VBF8	9.6	4.1E-05	3.0	6.2E-02	0.2	8.4E-01	1.7	1.3E-01
ENSMUST00000121007				4.1	7.2E-02	4.9	5.0E-02	-1.3	5.9E-01	-2.1	1.6E-01
ENSMUST00000136539	zinc finger protein 62 [Source:MGI Symbol;Acc:MGI:99662]	J3JS23		-3.6	9.3E-03	4.2	1.5E-03	-3.6	8.0E-03	0.5	4.0E-01
ENSMUST00000136567	small nuclear ribonucleoprotein 35 (U11/U12) [Source:MGI Symbol;Acc:MGI:1923417]	D3YTL6		6.4	3.2E-03	7.0	3.5E-03	-1.6	4.6E-01	0.4	7.1E-01
ENSMUST00000121015				3.8	1.3E-01	5.3	6.4E-02	-0.2	9.5E-01	-1.7	2.9E-01
ENSMUST00000121016				-1.7	1.1E-01	-0.7	5.5E-01	0.3	7.3E-01	-0.7	5.8E-01
ENSMUST00000136579	Dr1 associated protein 1 (negative cofactor 2 alpha) [Source:MGI Symbol;Acc:MGI:1913806]	G3UXH5		-8.9	7.4E-06	8.3	7.1E-05	0.4	7.2E-01	-0.8	2.1E-01
ENSMUST00000136591	DnaJ (Hsp40) homolog, subfamily C, member 21 [Source:MGI Symbol;Acc:MGI:1925371]	E9Q8D0		-2.6	1.5E-02	0.4	7.9E-01	-0.9	4.6E-01	2.0	1.4E-01
ENSMUST00000136613	dual adaptor for phosphotyrosine and 3-phosphoinositides 1 [Source:MGI Symbol;Acc:MGI:1347063]	Q3TEK6		7.4	3.3E-02	2.3	4.6E-01	-0.6	8.2E-01	3.1	2.1E-01
ENSMUST00000136614	Shc SH2-domain binding protein 1-like [Source:MGI Symbol;Acc:MGI:1919086]	J3QQ47		7.0	1.0E-04	6.0	2.5E-03	0.1	9.6E-01	-1.0	3.0E-01
ENSMUST00000121033	IKAROS family zinc finger 5 [Source:MGI Symbol;Acc:MGI:1914393]		Q8BU00	-1.3	3.9E-01	-3.7	9.5E-02	-1.7	1.4E-01	0.7	7.6E-01
ENSMUST00000136635	sarcolemma associated protein [Source:MGI Symbol;Acc:MGI:1933549]	D3YV81		-4.2	2.7E-02	0.9	2.0E-01	-0.1	8.3E-01	0.8	2.0E-01
ENSMUST00000136659	Fyn proto-oncogene [Source:MGI Symbol;Acc:MGI:95602]	D3YZ57		-3.1	3.2E-02	6.1	1.0E-03	-0.1	9.5E-01	-0.2	8.2E-01
ENSMUST00000121038	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]	D3Z637		-2.5	2.4E-01	-7.2	2.6E-02	-4.1	9.1E-03	0.6	8.3E-01
ENSMUST00000136662	regulatory associated protein of MTOR, complex 1 [Source:MGI Symbol;Acc:MGI:1921620]	F7CN67		5.4	4.4E-03	1.7	1.3E-02	0.1	9.0E-01	-0.4	3.7E-01
ENSMUST00000136671	in homology domain containing, family G (with RhoGef domain) member 1 [Source:MGI Symbol;Acc:MGI:2(	F6S200		7.8	6.4E-03	3.5	1.8E-03	-4.0	3.6E-03	-0.6	3.9E-01
ENSMUST00000136687	integrin linked kinase [Source:MGI Symbol;Acc:MGI:1195267]	D3YZA5		3.3	2.9E-03	5.4	5.8E-05	-1.2	1.3E-01	-0.3	5.7E-01
ENSMUST00000136699	downstream neighbor of SON [Source:MGI Symbol;Acc:MGI:1890621]	F7BX63		-4.0	8.1E-03	-7.6	2.6E-05	-0.6	1.3E-01	-2.0	8.6E-02
ENSMUST00000136726	interleukin 17 receptor B [Source:MGI Symbol;Acc:MGI:1355292]	D6REG3		7.0	5.4E-05	4.7	1.5E-02	-1.1	5.2E-01	-0.4	7.0E-01
ENSMUST00000121048	mitochondrial ribosomal protein L24 [Source:MGI Symbol;Acc:MGI:1914957]		Q9CQ06	0.6	4.9E-01	0.2	8.6E-01	-0.1	9.5E-01	0.4	7.5E-01
ENSMUST00000121052	protein O-linked mannose beta 1,2-N-acetylglucosaminyltransferase [Source:MGI Symbol;Acc:MGI:1915523]		Q91X88	-0.2	9.3E-01	2.3	5.8E-01	4.3	1.9E-01	1.8	5.6E-01
ENSMUST00000121060				-4.2	1.6E-01	2.6	5.2E-01	4.9	1.5E-01	-1.9	5.8E-01
ENSMUST00000136731	myosin VA [Source:MGI Symbol;Acc:MGI:105976]	D3YZ62		-6.4	4.3E-05	6.0	3.2E-03	1.1	4.5E-01	1.1	2.4E-01
ENSMUST00000136755	cDNA sequence BC067074 [Source:MGI Symbol;Acc:MGI:3040697]	F6RXI4		9.3	4.6E-06	5.9	5.3E-03	-0.7	6.8E-01	0.4	7.0E-01
ENSMUST00000136756	phospholipase A2, group XVI [Source:MGI Symbol;Acc:MGI:2179715]		Q8R3U1	-3.9	5.3E-04	5.6	2.0E-03	-0.6	6.7E-01	-0.2	8.3E-01
ENSMUST00000136763	guanylyl cyclase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916028]	D6RDT9		-3.7	2.8E-03	4.8	3.1E-03	-1.5	2.9E-01	-1.6	7.5E-02
ENSMUST00000136766	rine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 13 [Source:MGI Symbol;Acc:MGI:304225	D6RHN5		6.7	2.8E-04	5.7	7.3E-04	-0.5	6.8E-01	0.6	3.8E-01
ENSMUST00000121083	TRPM8 channel-associated factor 1 [Source:MGI Symbol;Acc:MGI:1914665]		Q8BNE1	1.3	2.5E-01	2.5	1.4E-02	-2.5	2.3E-02	-3.7	2.4E-03
ENSMUST00000136770	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast) [Source:MGI Symbol;Acc:MGI:106572]	F6VY64		-4.7	7.4E-04	7.2	1.6E-04	-0.6	6.5E-01	-0.7	3.2E-01
ENSMUST00000136783	predicted gene, 28045 [Source:MGI Symbol;Acc:MGI:5547781]	A0A075B668		8.2	6.5E-03	4.2	4.9E-03	-1.1	3.8E-01	0.9	2.5E-01
ENSMUST00000136819	branched chain aminotransferase 1, cytosolic [Source:MGI Symbol;Acc:MGI:104861]	F6YUH3		7.5	1.0E-04	7.6	8.4E-04	-0.8	6.4E-01	1.6	7.5E-02
ENSMUST00000136839	prefoldin 4 [Source:MGI Symbol;Acc:MGI:1923512]	E9Q6U4		-5.3	6.1E-05	5.4	8.1E-04	-2.4	8.9E-02	-0.1	9.0E-01
ENSMUST00000136848	numb gene homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:107423]	D3Z549		-3.6	5.9E-03	-4.8	1.5E-02	0.2	7.6E-01	-2.0	3.3E-01
ENSMUST00000121097	CTD nuclear envelope phosphatase 1 regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1921981]		Q3UJ81	0.7	3.0E-01	2.4	1.5E-02	0.3	6.9E-01	-1.4	7.3E-02
ENSMUST00000136903	nitrogen permease regulator-like 3 [Source:MGI Symbol;Acc:MGI:109258]	F2Z404		2.7	2.2E-02	6.0	4.8E-02	-0.7	8.2E-01	3.5	3.2E-02
ENSMUST00000136907	caldesmon 1 [Source:MGI Symbol;Acc:MGI:88250]	F6T2Z7		6.5	6.1E-05	4.4	7.8E-03	0.5	7.2E-01	0.1	8.7E-01
ENSMUST00000136925	solute carrier family 19 (folate transporter), member 1 [Source:MGI Symbol;Acc:MGI:103182]	E9Q8X6		6.9	4.0E-04	6.0	8.4E-04	-0.4	7.4E-01	-0.1	8.9E-01
ENSMUST00000136936	sequestosome 1 [Source:MGI Symbol;Acc:MGI:107931]	F6VD69		-8.7	4.0E-04	-4.3	1.0E-02	-1.0	1.3E-01	-0.3	8.2E-01
ENSMUST00000121111	prolyl 3-hydroxylase 1 [Source:MGI Symbol;Acc:MGI:1888921]		Q3V1T4	0.8	5.3E-01	2.6	4.7E-02	-0.8	4.9E-01	-2.6	5.3E-02
ENSMUST00000121112	LIM domain only 4 [Source:MGI Symbol;Acc:MGI:109360]	Q542S1	P61969	-1.3	4.8E-02	-0.8	3.2E-01	0.1	7.9E-01	-0.4	5.6E-01
ENSMUST00000136938	ubiquitin B [Source:MGI Symbol;Acc:MGI:98888]	Q5SX22		-7.8	3.4E-04	4.5	3.6E-03	-1.5	2.7E-01	0.9	2.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000136960	SH2B adaptor protein 3 [Source:MGI Symbol;Acc:MGI:893598]	D6RCY9		-7.4	8.6E-04	5.6	9.3E-03	-2.5	2.4E-01	-1.1	3.6E-01
ENSMUST00000136965	phosphatidylinositol 3-kinase, catalytic, beta polypeptide [Source:MGI Symbol;Acc:MGI:1922019]	S4R1S1		-2.8	2.6E-04	4.6	2.1E-02	1.7	2.9E-01	1.5	1.9E-01
ENSMUST00000136983	D4, zinc and double PHD fingers family 2 [Source:MGI Symbol;Acc:MGI:109529]		Q61103	1.7	3.3E-02	-2.0	1.8E-01	1.9	4.5E-02	-2.1	1.9E-01
ENSMUST00000137063	tubby like protein 4 [Source:MGI Symbol;Acc:MGI:1916092]	F6UMF8		7.0	1.5E-07	7.9	2.3E-05	-0.5	6.2E-01	0.3	5.5E-01
ENSMUST00000137079	coiled-coil domain containing 167 [Source:MGI Symbol;Acc:MGI:1915847]	D6RG69		7.7	3.3E-05	5.8	3.3E-04	-0.6	5.9E-01	0.4	5.2E-01
ENSMUST00000137116	JTP23, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1925831		Q9CX11	2.6	1.2E-04	6.6	1.0E-02	0.0	9.8E-01	-1.8	2.0E-01
ENSMUST00000137141	piezo-type mechanosensitive ion channel component 2 [Source:MGI Symbol;Acc:MGI:1918781]	F6YYK4		3.4	2.1E-02	5.2	3.8E-02	-0.4	8.5E-01	1.0	4.4E-01
ENSMUST00000121153	ring finger protein, LIM domain interacting [Source:MGI Symbol;Acc:MGI:1342291]		Q9WTV7	-2.0	3.3E-01	-4.0	1.1E-01	-2.1	1.7E-01	0.0	9.9E-01
ENSMUST00000137145	heat shock protein 5 [Source:MGI Symbol;Acc:MGI:95835]	A0A0A6YXF5		-3.9	9.8E-03	8.6	7.6E-06	-1.1	3.0E-01	-0.9	8.4E-02
ENSMUST00000137158	family with sequence similarity 160, member A2 [Source:MGI Symbol;Acc:MGI:1921599]	D6RCH8		-8.5	1.7E-04	6.7	2.0E-04	-0.6	6.1E-01	-0.5	4.1E-01
ENSMUST00000137195	AHNAK nucleoprotein 2 [Source:MGI Symbol;Acc:MGI:2144831]	F7CVJ5		6.0	3.5E-03	4.5	7.4E-04	1.6	7.3E-02	-0.1	9.4E-01
ENSMUST00000137197	hemicentin 1 [Source:MGI Symbol;Acc:MGI:2685047]	D3Z2Q7		8.8	3.0E-05	5.8	6.1E-02	-0.9	7.7E-01	0.3	8.7E-01
ENSMUST00000137222	cytochrome P450, family 4, subfamily f, polypeptide 13 [Source:MGI Symbol;Acc:MGI:2158641]	E9Q4L9		-3.7	1.4E-02	5.9	8.3E-04	-0.6	6.5E-01	0.1	8.6E-01
ENSMUST00000137245	enhancer of mRNA decapping 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2142951]	D6RCX6		-5.6	1.1E-03	6.6	5.2E-04	-0.5	6.9E-01	-3.3	3.2E-03
ENSMUST00000137246	DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:MGI Symbol;Acc:MGI:1270129]	B1AXY1		-6.9	3.1E-04	1.4	5.2E-01	6.4	2.3E-03	-0.6	7.3E-01
ENSMUST00000137268	mesoderm induction early response 1, family member 3 [Source:MGI Symbol;Acc:MGI:2442317]	D6RET2		-3.8	2.1E-02	4.5	1.4E-03	-0.2	8.2E-01	-0.2	7.6E-01
ENSMUST00000137293	ubiquitin specific petidase 45 [Source:MGI Symbol;Acc:MGI:101850]	F7CLE5		4.9	4.8E-03	4.0	4.2E-02	-0.6	7.3E-01	-0.4	7.5E-01
ENSMUST00000121198	mbrane associated guanylate kinase, WW and PDZ domain containing 3 [Source:MGI Symbol;Acc:MGI:19234	G5E8T6		-0.3	6.9E-01	1.0	2.9E-01	0.8	2.4E-01	-0.4	6.0E-01
ENSMUST00000137296	ring finger protein 31 [Source:MGI Symbol;Acc:MGI:1934704]	D6RFE2		3.8	4.0E-03	5.8	2.4E-04	-1.5	2.0E-01	-0.3	6.0E-01
ENSMUST00000137329	ribosomal protein S5 [Source:MGI Symbol;Acc:MGI:1097682]	D3YYM6		3.2	3.0E-02	0.0	9.8E-01	1.9	6.4E-02	-1.3	3.8E-01
ENSMUST00000137336	Immunoglobulin heavy constant epsilon [Source:MGI Symbol;Acc:MGI:2685746]	F6W6U3		8.2	1.4E-04	4.5	2.4E-03	-1.0	3.9E-01	1.0	1.7E-01
ENSMUST00000121204	WD repeat domain 61 [Source:MGI Symbol;Acc:MGI:1917493]	A0MNP4	Q9ERF3	-0.8	7.2E-01	-2.6	3.4E-01	-1.8	3.1E-01	0.1	9.8E-01
ENSMUST00000137387	ataxin 7-like 3 [Source:MGI Symbol;Acc:MGI:3036270]	Z4YN62		-8.8	3.3E-05	7.1	5.6E-06	-1.2	1.6E-01	-0.1	7.2E-01
ENSMUST00000137400	ribosomal protein S14 [Source:MGI Symbol;Acc:MGI:98107]	D3Z7I1		-8.9	7.1E-05	6.8	7.6E-03	-0.8	7.3E-01	-1.6	2.1E-01
ENSMUST00000137451	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 [Source:MGI Symbol;Acc:MGI:102463	A2AQC8		3.5	3.5E-02	-3.2	4.6E-02	-0.6	4.3E-01	-0.5	7.3E-01
ENSMUST00000137458	RAS protein activator like 3 [Source:MGI Symbol;Acc:MGI:2444128]		Q8C2K5	-1.5	3.1E-02	6.7	9.4E-03	-0.6	7.9E-01	-2.2	1.1E-01
ENSMUST00000137486	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:104558]	F6Q8A4		-2.5	1.7E-02	8.3	2.3E-05	-0.6	6.2E-01	-0.5	3.3E-01
ENSMUST00000137488	cell cycle exit and neuronal differentiation 1 [Source:MGI Symbol;Acc:MGI:1929898]		Q9JKC6	6.1	5.9E-03	6.4	9.0E-03	-2.6	2.6E-01	-1.7	1.9E-01
ENSMUST00000137496	zinc finger protein 738 [Source:MGI Symbol;Acc:MGI:3040706]	B8JJX8		-2.4	3.3E-03	-0.6	3.4E-01	0.4	2.6E-01	-1.1	9.0E-02
ENSMUST00000137497	Rho GTPase activating protein 26 [Source:MGI Symbol;Acc:MGI:1918552]	Q3U860		-7.8	6.6E-04	-7.0	1.9E-04	1.1	1.4E-02	-1.0	4.7E-01
ENSMUST00000137506	major facilitator superfamily domain containing 10 [Source:MGI Symbol;Acc:MGI:1915544]			4.4	4.6E-04	3.7	3.2E-02	1.6	2.7E-01	1.0	3.0E-01
ENSMUST00000137519	ankyrin repeat domain 13a [Source:MGI Symbol;Acc:MGI:1915670]	F7B209		-5.5	2.1E-04	-2.6	2.0E-02	1.4	1.9E-02	-2.0	9.9E-02
ENSMUST00000121249	tudor domain containing 1 [Source:MGI Symbol;Acc:MGI:1933218]		Q99MV1	7.0	3.7E-02	5.5	1.2E-01	-0.7	8.4E-01	0.8	6.9E-01
ENSMUST00000137526	-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human) [Source:MGI Symbol;Acc:MGI:1333	F6WYU8		7.5	7.5E-03	3.5	8.6E-03	-1.8	1.6E-01	-1.1	2.3E-01
ENSMUST00000121257				3.8	1.0E-01	5.2	5.3E-02	-0.2	9.3E-01	-1.6	2.9E-01
ENSMUST00000137536	sal-like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2139360]	A2AUZ7		6.5	1.1E-02	6.2	3.3E-04	-0.5	6.7E-01	-0.7	2.7E-01
ENSMUST00000137542	sorting nexin 1 [Source:MGI Symbol;Acc:MGI:1928395]	D3YWH1		-2.5	5.2E-03	4.3	1.2E-01	0.4	8.7E-01	2.8	9.2E-02
ENSMUST00000137543	sterile alpha motif domain containing 4 [Source:MGI Symbol;Acc:MGI:1921730]		Q8CBY1	8.7	4.7E-05	-5.7	3.6E-04	1.0	2.6E-02	0.5	6.6E-01
ENSMUST00000137564	predicted gene 42957 [Source:MGI Symbol;Acc:MGI:5663094]	D6RFQ2		8.0	1.5E-05	5.7	1.2E-03	0.9	4.7E-01	-0.9	2.3E-01
ENSMUST00000137570	predicted gene 12830 [Source:MGI Symbol;Acc:MGI:3649998]	F6XVH0		7.3	2.9E-05	5.5	7.7E-03	-1.1	5.4E-01	0.3	7.2E-01
ENSMUST00000137573	zinc finger protein 866 [Source:MGI Symbol;Acc:MGI:3584369]	Q6PGD2		1.0	2.6E-02	7.5	1.0E-05	-1.4	1.4E-01	-0.2	7.3E-01
ENSMUST00000137605	mortality factor 4 like 2 [Source:MGI Symbol;Acc:MGI:1927167]	A2AEB4		-4.2	1.6E-02	6.5	2.5E-04	-0.6	6.3E-01	-1.6	3.1E-02
ENSMUST00000137613	exocyst complex component 3-like 2 [Source:MGI Symbol;Acc:MGI:1921713]	D3YUP5		5.3	3.8E-04	-4.2	1.2E-02	1.1	1.3E-01	2.7	6.5E-02
ENSMUST00000137701	ute carrier family 13 (sodium-dependent citrate transporter), member 5 [Source:MGI Symbol;Acc:MGI:30371	Q5NBV0		5.3	5.6E-04	4.0	1.2E-03	0.0	9.6E-01	-0.1	8.6E-01
ENSMUST00000121288	family with sequence similarity 167, member A [Source:MGI Symbol;Acc:MGI:3606565]		Q6P1G6	0.9	6.1E-02	3.5	2.3E-04	1.8	5.1E-03	-0.8	1.1E-01
ENSMUST00000137707	transmembrane protein 57 [Source:MGI Symbol;Acc:MGI:1913396]	E0CY55		6.1	1.7E-02	6.1	6.0E-03	-0.8	6.7E-01	0.6	5.8E-01
ENSMUST00000121291	peroxisomal biogenesis factor 1 [Source:MGI Symbol;Acc:MGI:1918632]		Q5BL07	-2.0	9.1E-02	-4.0	8.8E-02	0.5	6.2E-01	2.5	2.5E-01
ENSMUST00000137716	paxillin [Source:MGI Symbol;Acc:MGI:108295]			-3.5	3.0E-02	6.6	8.8E-05	-1.3	2.1E-01	1.6	1.5E-02
ENSMUST00000137724	chloride channel, voltage-sensitive 6 [Source:MGI Symbol;Acc:MGI:1347049]	A2A7F6		1.2	2.7E-02	4.8	9.6E-05	0.1	8.6E-01	0.1	8.4E-01
ENSMUST00000137768	phosphodiesterase 6H, cGMP-specific, cone, gamma [Source:MGI Symbol;Acc:MGI:1925850]		P61249	7.0	2.6E-06	-0.5	6.3E-01	2.1	8.0E-03	0.7	4.5E-01
ENSMUST00000137769	RIKEN cDNA 1110065P20 gene [Source:MGI Symbol;Acc:MGI:1916170]	E9Q9M4		-3.7	1.1E-03	-5.1	1.6E-02	0.3	6.4E-01	0.1	9.4E-01
ENSMUST00000137771	LIM domain binding 1 [Source:MGI Symbol;Acc:MGI:894762]		P70662	-4.3	6.9E-03	2.3	5.3E-02	-2.9	3.8E-02	0.5	5.8E-01
ENSMUST00000121309				-4.4	1.2E-01	-6.9	5.9E-02	-3.0	4.5E-02	-0.5	8.9E-01
ENSMUST00000137775	mitochondrial ribosomal protein L24 [Source:MGI Symbol;Acc:MGI:1914957]	A0A0A6YXP0		-4.5	1.3E-03	4.7	8.1E-03	-3.0	8.7E-02	0.0	9.7E-01
ENSMUST00000137792	radical S-adenosyl methionine domain containing 2 [Source:MGI Symbol;Acc:MGI:1929628]	D6RJ49		7.3	5.9E-03	5.2	4.3E-04	-1.5	1.9E-01	-0.9	1.6E-01
ENSMUST00000137798	in, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A [Source:MGI Symbol;Acc:M(	E9Q668		8.0	7.1E-06	-2.4	2.2E-02	2.4	1.8E-03	-2.5	4.1E-02
ENSMUST00000137823	ubiquitin specific peptidase 34 [Source:MGI Symbol;Acc:MGI:109473]	F6WJB7		-1.9	1.1E-03	-7.9	1.6E-03	-1.8	3.3E-02	-0.4	8.5E-01
ENSMUST00000137857	protein arginine N-methyltransferase 2 [Source:MGI Symbol;Acc:MGI:1316652]	M0QW88		4.7	1.6E-02	-5.5	1.2E-02	1.0	1.5E-01	2.4	2.0E-01
ENSMUST00000137873	double C2, alpha [Source:MGI Symbol;Acc:MGI:109446]	D3Z1K1		5.3	1.2E-02	-3.2	9.8E-03	0.2	7.3E-01	0.0	9.7E-01
ENSMUST00000121324				-3.0	1.5E-01	-3.0	2.0E-01	0.2	8.6E-01	0.3	9.2E-01
ENSMUST00000121326	serine/arginine-rich splicing factor 11 [Source:MGI Symbol;Acc:MGI:1916457]	E9Q6E5		-0.1	9.5E-01	1.1	4.8E-01	-0.5	7.2E-01	-1.7	2.3E-01
ENSMUST00000137905	androgen dependent TFPI regulating protein [Source:MGI Symbol;Acc:MGI:1924596]	H9KV14		-2.5	1.3E-02	4.3	2.2E-02	-1.1	5.0E-01	0.5	6.7E-01
ENSMUST00000121334	septin 8 [Source:MGI Symbol;Acc:MGI:894310]	B1AQZ0		1.6	6.6E-02	2.7	1.9E-02	0.4	6.2E-01	-0.7	4.3E-01
ENSMUST00000137913	patatin-like phospholipase domain containing 7 [Source:MGI Symbol;Acc:MGI:2385325]	A0A0A6YWJ6		-5.7	1.6E-02	9.8	9.3E-04	0.6	7.8E-01	1.3	1.4E-01
ENSMUST00000121337	serine (or cysteine) peptidase inhibitor, clade A, member 3F [Source:MGI Symbol;Acc:MGI:2182838]		Q80X76	5.0	5.7E-02	4.2	1.3E-01	-0.8	7.7E-01	0.0	1.0E+00
ENSMUST00000121339	mitochondrial ribosomal protein S17 [Source:MGI Symbol;Acc:MGI:1913508]		Q9CQE3	0.7	2.0E-01	1.0	1.4E-01	0.2	7.1E-01	-0.2	7.8E-01
ENSMUST00000137997	neurofibromatosis 1 [Source:MGI Symbol;Acc:MGI:97306]	Q5SYH9		-2.6	1.6E-02	5.5	3.8E-03	-0.4	8.0E-01	0.6	5.1E-01
ENSMUST00000121344	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 [Source:MGI Symbol;Acc:MGI:2137302]		Q8BGY6	1.7	3.8E-02	0.2	7.9E-01	-1.0	1.7E-01	0.4	5.6E-01
ENSMUST00000138012	nucleoporin 214 [Source:MGI Symbol;Acc:MGI:1095411]	A2ATN3		2.9	7.3E-04	4.6	1.0E-03	-1.5	1.6E-01	-0.2	7.9E-01
ENSMUST00000121352				-2.8	2.1E-01	-3.6	1.8E-01	-1.8	2.2E-01	-1.0	7.2E-01
ENSMUST00000121357	GRAM domain containing 1B [Source:MGI Symbol;Acc:MGI:1925037]		Q80TI0	0.3	4.6E-01	2.4	3.0E-03	1.1	6.0E-02	-1.0	7.6E-02
ENSMUST00000138030	stomatin (Epb7.2)-like 2 [Source:MGI Symbol;Acc:MGI:1913842]	A2AG41		-4.6	3.0E-04	5.5	9.6E-06	-0.4	5.0E-01	0.0	9.1E-01
ENSMUST00000138037	interferon regulatory factor 9 [Source:MGI Symbol;Acc:MGI:107587]	E9Q8M6		-9.2	1.2E-03	3.3	1.1E-03	0.6	3.1E-01	0.0	9.9E-01
ENSMUST00000138040	Tax1 (human T cell leukemia virus type I) binding protein 1 [Source:MGI Symbol;Acc:MGI:1289308]	D3Z213		2.8	1.2E-02	-0.7	4.9E-01	0.6	3.9E-01	-1.7	1.2E-01
ENSMUST00000138041	rabenosyn, RAB effector [Source:MGI Symbol;Acc:MGI:1925537]	D3Z0E7		6.8	7.2E-04	6.7	1.2E-04	0.5	6.2E-01	-0.2	6.7E-01
ENSMUST00000138050	N-methylpurine-DNA glycosylase [Source:MGI Symbol;Acc:MGI:97073]	F2Z3Y1		3.9	5.0E-04	-4.4	5.0E-04	-0.9	7.6E-02	-1.6	1.1E-01
ENSMUST00000138091	S-adenosylhomocysteine hydrolase-like 1 [Source:MGI Symbol;Acc:MGI:2385184]	F7ATQ6		-8.1	2.4E-05	2.4	1.5E-01	-0.7	6.4E-01	5.4	1.2E-03

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000121370	TBC1 domain family, member 1 [Source:MGI Symbol;Acc:MGI:1889508]	Q3U3T9	Q60949	-3.8	1.5E-01	-4.0	2.5E-01	-0.5	7.6E-01	-0.3	9.4E-01
ENSMUST00000121377	nuclear receptor coactivator 5 [Source:MGI Symbol;Acc:MGI:2385165]	B7ZC23		-0.5	7.4E-01	-2.1	3.4E-01	-0.6	6.6E-01	1.0	6.3E-01
ENSMUST00000138099	solute carrier organic anion transporter family, member 3a1 [Source:MGI Symbol;Acc:MGI:1351867]	D3YUC4		6.0	1.0E-03	4.4	8.1E-04	-2.6	2.7E-02	0.1	9.2E-01
ENSMUST00000138101	malate dehydrogenase 2, NAD (mitochondrial) [Source:MGI Symbol;Acc:MGI:97050]	J3QMC8		-7.2	5.6E-05	6.4	1.5E-04	-0.5	6.3E-01	-1.3	6.2E-02
ENSMUST00000138112	coiled-coil domain containing 170 [Source:MGI Symbol;Acc:MGI:2685067]	D3YXL0		7.1	3.7E-06	3.4	5.6E-03	-1.3	2.1E-01	0.2	7.8E-01
ENSMUST00000138119	lysine (K)-specific methyltransferase 2A [Source:MGI Symbol;Acc:MGI:96995]	S4R199		6.0	2.3E-04	6.0	9.1E-04	-0.7	6.3E-01	-0.1	8.5E-01
ENSMUST00000121390	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit [Source:MGI Symbol;Acc:MGI:109482]		P97445	1.2	5.2E-01	7.0	1.1E-02	1.7	4.5E-01	-4.1	1.7E-02
ENSMUST00000138127	zinc finger protein 318 [Source:MGI Symbol;Acc:MGI:1889348]	B8JJA0		7.3	2.3E-03	7.3	6.0E-05	-1.5	2.3E-01	-0.2	6.7E-01
ENSMUST00000138166	bobby sox homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1917758]		Q8VBW5	-1.5	1.9E-02	2.6	7.0E-04	-0.6	2.4E-01	-0.2	5.9E-01
ENSMUST00000138243	mitogen-activated protein kinase kinase kinase 10 [Source:MGI Symbol;Acc:MGI:1346879]			-2.8	1.5E-02	5.1	4.9E-03	-2.1	2.0E-01	-1.9	7.2E-02
ENSMUST00000138247	ubiquitin-conjugating enzyme E2G 1 [Source:MGI Symbol;Acc:MGI:1914378]	D6RES1		-5.0	2.2E-04	5.9	2.9E-03	0.6	6.9E-01	-1.7	7.5E-02
ENSMUST00000121401	SUMO-interacting motifs containing 1 [Source:MGI Symbol;Acc:MGI:2442599]	E9Q6E9		1.3	3.6E-02	0.6	4.0E-01	-0.3	5.5E-01	0.4	5.8E-01
ENSMUST00000138283	Nedd4 family interacting protein 2 [Source:MGI Symbol;Acc:MGI:1923523]	F6RT43		-7.0	9.4E-06	-2.4	1.7E-01	0.7	4.5E-01	-0.5	7.7E-01
ENSMUST00000138325	laminin gamma 3 [Source:MGI Symbol;Acc:MGI:1344394]	A2ATM9		6.1	2.7E-02	-0.6	6.2E-01	2.3	1.8E-02	-0.3	7.7E-01
ENSMUST00000138334	DnaJ (Hsp40) homolog, subfamily C, member 8 [Source:MGI Symbol;Acc:MGI:1915848]	F6QIL6		-4.6	1.9E-02	5.7	1.9E-03	-0.1	9.6E-01	0.9	2.8E-01
ENSMUST00000138356	pleckstrin homology-like domain, family B, member 1 [Source:MGI Symbol;Acc:MGI:2143230]	D3Z0X5		6.0	1.6E-03	2.9	2.1E-02	1.1	2.7E-01	0.7	3.4E-01
ENSMUST00000138363	a disintegrin and metallopeptidase domain 12 (meltrin alpha) [Source:MGI Symbol;Acc:MGI:105378]	F6YWH6		2.7	3.2E-02	-2.1	1.0E-02	-0.7	1.7E-01	-1.0	1.5E-01
ENSMUST00000121416	ubiquitin specific peptidase like 1 [Source:MGI Symbol;Acc:MGI:2442342]			-2.2	3.9E-01	-1.5	7.0E-01	1.6	4.8E-01	0.9	8.0E-01
ENSMUST00000138376	DENN/MADD domain containing 4B [Source:MGI Symbol;Acc:MGI:2446201]	F6RXE7		5.5	2.2E-02	6.2	1.7E-04	-2.4	6.0E-02	0.3	6.4E-01
ENSMUST00000138392	Fc fragment of IgG binding protein [Source:MGI Symbol;Acc:MGI:2444336]	E9Q0B5		8.4	4.7E-05	6.1	7.7E-04	-0.1	9.1E-01	-0.4	5.9E-01
ENSMUST00000121422				-2.9	1.5E-01	-4.7	5.8E-02	-2.5	9.2E-02	-0.8	7.4E-01
ENSMUST00000138393	tetraspanin 13 [Source:MGI Symbol;Acc:MGI:1913359]	A7NSI0		-1.8	2.5E-02	6.8	1.9E-04	-1.4	2.8E-01	0.3	6.7E-01
ENSMUST00000121430				0.5	6.3E-01	1.3	4.5E-01	2.2	1.2E-01	1.4	3.1E-01
ENSMUST00000138425	PHD finger protein 24 [Source:MGI Symbol;Acc:MGI:2140712]	F6SBE4		4.9	1.2E-02	6.7	2.3E-04	-0.6	6.4E-01	-0.7	2.8E-01
ENSMUST00000138434	serine/arginine-rich splicing factor 5 [Source:MGI Symbol;Acc:MGI:98287]	S4R2G3		3.5	2.0E-02	-1.9	4.9E-02	1.2	4.3E-02	-0.3	7.2E-01
ENSMUST00000138465	roline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III [Source:MGI Symbol;Acc:M	F6R2A2		6.8	5.9E-05	4.6	1.3E-03	-2.0	1.1E-01	0.6	3.7E-01
ENSMUST00000138488	single-stranded DNA binding protein 2 [Source:MGI Symbol;Acc:MGI:1914220]	D6RG78		4.9	6.7E-04	3.4	4.0E-04	0.2	7.3E-01	0.1	7.9E-01
ENSMUST00000138493	Rho guanine nucleotide exchange factor (GEF) 10-like [Source:MGI Symbol;Acc:MGI:1920004]	F6S3V7		-4.2	1.1E-02	-3.6	3.8E-02	-0.6	4.3E-01	-0.1	9.7E-01
ENSMUST00000138502	ribosomal protein S20 [Source:MGI Symbol;Acc:MGI:1914677]	Q5BLK2	P60867	-3.0	5.5E-03	4.0	5.1E-03	-2.0	1.2E-01	-0.3	7.3E-01
ENSMUST00000138532	synovial apoptosis inhibitor 1, synoviolin [Source:MGI Symbol;Acc:MGI:1921376]			-3.8	9.9E-03	5.2	1.6E-03	-0.9	4.8E-01	0.2	8.1E-01
ENSMUST00000138563	fibroblast growth factor 2 [Source:MGI Symbol;Acc:MGI:95516]	Q541T2	P15655	4.7	2.0E-03	-2.0	1.8E-01	1.1	2.1E-01	-1.2	4.7E-01
ENSMUST00000138587	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF [Source:MGI Symbol;Acc:MGI:2681862]	F6TJX7		8.8	3.2E-05	6.1	1.7E-03	-0.7	6.5E-01	-0.8	3.3E-01
ENSMUST00000121456				0.7	1.9E-01	2.8	2.0E-03	1.4	2.6E-02	-0.7	2.4E-01
ENSMUST00000138595	ciliary rootlet coiled-coil, rootletin family member 2 [Source:MGI Symbol;Acc:MGI:3045962]	F6XLV1		10.3	2.0E-06	5.4	1.9E-02	-0.4	8.3E-01	-1.3	2.9E-01
ENSMUST00000138603	huntingtin-associated protein 1 [Source:MGI Symbol;Acc:MGI:1261831]		O35668	6.0	3.0E-04	6.9	4.9E-04	-0.5	7.0E-01	1.1	1.6E-01
ENSMUST00000138667	predicted gene 20716 [Source:MGI Symbol;Acc:MGI:5313163]		O70152	-9.0	1.4E-05	4.5	4.4E-03	-1.8	1.7E-01	-1.5	1.0E-01
ENSMUST00000121465	fucosidase, alpha-L- 2, plasma [Source:MGI Symbol;Acc:MGI:1914098]	Q505Q3	Q99KR8	1.2	1.2E-01	1.6	1.2E-01	0.4	5.8E-01	0.0	9.6E-01
ENSMUST00000138693	bromodomain containing 3 [Source:MGI Symbol;Acc:MGI:1914632]	A2AKA9		-3.6	1.1E-02	6.8	2.3E-04	-1.4	2.9E-01	-0.2	7.5E-01
ENSMUST00000121473	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) [Source:MGI Symbol;Acc:MGI:104771]		Q61527	4.8	7.4E-02	7.0	2.5E-02	-0.3	9.3E-01	-2.5	1.2E-01
ENSMUST00000138703	phosphofructokinase, platelet [Source:MGI Symbol;Acc:MGI:1891833]		Q9WUA3	-3.9	6.1E-03	6.0	3.8E-03	-0.4	8.0E-01	-0.9	3.4E-01
ENSMUST00000121477	mitochondrial ribosomal protein L1 [Source:MGI Symbol;Acc:MGI:2137202]	Q9D3F3		-0.2	7.6E-01	0.5	6.1E-01	0.6	3.8E-01	-0.1	9.4E-01
ENSMUST00000138753	post-GPI attachment to proteins 2 [Source:MGI Symbol;Acc:MGI:2385286]	D3Z1F0		4.6	2.0E-02	5.6	4.6E-02	-3.6	2.6E-01	-1.6	2.6E-01
ENSMUST00000138762	centrosomal protein 350 [Source:MGI Symbol;Acc:MGI:1921331]	E9Q309		-1.6	4.1E-03	7.4	1.0E-02	-1.7	5.1E-01	-2.1	1.8E-01
ENSMUST00000138774	cilia and flagella associated protein 61 [Source:MGI Symbol;Acc:MGI:1926024]	Q6ZWM9		7.6	2.6E-06	3.0	8.4E-02	-1.9	2.7E-01	-0.6	5.9E-01
ENSMUST00000121489	purinergic receptor P2X, ligand-gated ion channel, 7 [Source:MGI Symbol;Acc:MGI:1339957]	Q3UN00		-0.7	7.2E-01	-0.9	5.3E-01	-2.6	8.8E-02	-2.3	2.1E-01
ENSMUST00000138785	DNA (cytosine-5-)-methyltransferase 3-like [Source:MGI Symbol;Acc:MGI:1859287]	A3EWM2	Q9CWR8	6.2	3.2E-04	3.5	1.2E-01	1.3	5.1E-01	3.5	2.4E-02
ENSMUST00000121494	sialic acid binding Ig-like lectin F [Source:MGI Symbol;Acc:MGI:2681107]	Q80ZE2		-0.7	6.0E-01	-0.3	8.0E-01	-1.2	2.6E-01	-1.6	2.5E-01
ENSMUST00000138796	cDNA sequence BC100530 [Source:MGI Symbol;Acc:MGI:3696883]	D6REU3		-10.5	2.2E-04	-7.0	9.9E-05	-0.3	5.5E-01	-1.8	1.8E-01
ENSMUST00000138843	arrier family 11 (proton-coupled divalent metal ion transporters), member 2 [Source:MGI Symbol;Acc:MGI:13		P49282	5.7	8.0E-05	6.3	1.3E-03	-0.6	6.9E-01	-1.1	2.0E-01
ENSMUST00000121503	tropomyosin 3, gamma [Source:MGI Symbol;Acc:MGI:1890149]			-0.7	3.3E-01	-2.5	2.6E-02	-1.4	3.5E-02	0.4	6.4E-01
ENSMUST00000121504	ORAI calcium release-activated calcium modulator 3 [Source:MGI Symbol;Acc:MGI:3039586]	D3Z6X8		-0.7	6.2E-01	-0.5	7.9E-01	0.6	6.4E-01	0.5	8.0E-01
ENSMUST00000138880	nucleolar protein 12 [Source:MGI Symbol;Acc:MGI:2146285]		Q8BG17	3.3	1.0E-04	5.5	3.8E-03	-0.4	7.8E-01	-0.8	3.6E-01
ENSMUST00000138913	interferon regulatory factor 1 [Source:MGI Symbol;Acc:MGI:96590]	Q5SX16		2.4	2.2E-03	6.6	5.1E-04	-0.7	6.3E-01	-1.7	4.6E-02
ENSMUST00000121514	histone deacetylase 7 [Source:MGI Symbol;Acc:MGI:1891835]	E9PX62		4.1	6.8E-02	1.7	5.2E-01	-1.6	5.0E-01	0.7	7.1E-01
ENSMUST00000138914	threonine synthase-like 1 (bacterial) [Source:MGI Symbol;Acc:MGI:2139347]	A2AUG4		4.6	1.9E-03	5.1	1.4E-04	-1.4	1.0E-01	0.5	3.2E-01
ENSMUST00000138922	actin related protein 2/3 complex, subunit 1B [Source:MGI Symbol;Acc:MGI:1343142]	F6THG2		-6.3	4.4E-05	6.2	1.4E-03	-0.4	7.9E-01	-1.3	1.5E-01
ENSMUST00000138950	RIKEN cDNA 4932438A13 gene [Source:MGI Symbol;Acc:MGI:2444631]	A2AB97		-8.8	2.0E-04	0.4	7.8E-01	1.5	1.8E-01	-2.5	7.2E-02
ENSMUST00000138977	membrane-associated ring finger (C3HC4) 10 [Source:MGI Symbol;Acc:MGI:2443469]	E9PX79		8.3	3.3E-04	5.3	9.3E-04	-0.5	6.8E-01	0.0	9.9E-01
ENSMUST00000121525				-0.7	3.4E-01	-2.5	7.6E-02	0.3	7.1E-01	2.0	1.2E-01
ENSMUST00000139003	polynucleotide kinase 3'- phosphatase [Source:MGI Symbol;Acc:MGI:1891698]			-6.0	2.2E-04	6.8	2.6E-04	-1.1	3.6E-01	-0.1	9.3E-01
ENSMUST00000139049	phosphoribosyl pyrophosphate synthetase 1-like 3 [Source:MGI Symbol;Acc:MGI:3779453]	G3UXL2		-2.1	4.3E-03	-2.6	1.1E-01	-0.3	7.6E-01	-2.3	2.3E-01
ENSMUST00000139064	POU domain, class 6, transcription factor 2 [Source:MGI Symbol;Acc:MGI:2443631]	F6ZW42		10.0	8.2E-06	-6.6	1.3E-04	0.0	9.3E-01	-0.8	5.1E-01
ENSMUST00000139092	cDNA sequence BC094916 [Source:MGI Symbol;Acc:MGI:3584522]			3.5	2.2E-02	6.0	2.8E-04	0.7	4.9E-01	0.2	6.6E-01
ENSMUST00000139115	dynein cytoplasmic 2 heavy chain 1 [Source:MGI Symbol;Acc:MGI:107736]	D3Z025		4.5	5.8E-04	5.1	1.5E-02	1.2	4.5E-01	0.8	4.4E-01
ENSMUST00000139122	small integral membrane protein 14 [Source:MGI Symbol;Acc:MGI:1915802]		Q91VT8	-1.7	8.7E-03	6.4	2.4E-04	-0.5	6.6E-01	-0.7	2.6E-01
ENSMUST00000139123	kinesin family member 1B [Source:MGI Symbol;Acc:MGI:108426]	F6XNB6		7.8	4.1E-04	3.7	6.6E-02	-3.8	7.7E-02	0.0	9.9E-01
ENSMUST00000139210	suppressor of cytokine signaling 2 [Source:MGI Symbol;Acc:MGI:1201787]	F6RVG2		7.7	4.5E-05	7.1	5.6E-05	-0.5	6.1E-01	-1.5	2.7E-02
ENSMUST00000139215	HECT domain containing 2 [Source:MGI Symbol;Acc:MGI:2442663]	D6REW0		4.9	8.6E-04	5.8	2.5E-03	-0.7	6.6E-01	-0.1	9.2E-01
ENSMUST00000139238	dynamin 1 [Source:MGI Symbol;Acc:MGI:107384]	D6RH60		5.3	3.6E-03	7.6	2.4E-06	-0.1	8.8E-01	-0.2	6.8E-01
ENSMUST00000139253	small EDRK-rich factor 2 [Source:MGI Symbol;Acc:MGI:1337041]		P84102	-6.3	2.9E-06	5.8	3.2E-04	-0.5	6.5E-01	0.5	4.0E-01
ENSMUST00000121565	expressed sequence AU015836 [Source:MGI Symbol;Acc:MGI:2147954]	B1ASY6		3.1	2.5E-01	3.3	2.6E-01	-0.3	9.2E-01	-0.5	7.9E-01
ENSMUST00000121566	centrosomal protein 85 [Source:MGI Symbol;Acc:MGI:1917262]	A2A9K3		1.9	4.6E-01	-1.5	7.0E-01	-0.4	8.8E-01	3.0	4.4E-01
ENSMUST00000139263	SAM domain and HD domain, 1 [Source:MGI Symbol;Acc:MGI:1927468]	F6TVP2		-11.8	3.7E-07	8.2	5.8E-05	-0.7	5.9E-01	-0.5	4.2E-01
ENSMUST00000139287	tripartite motif-containing 27 [Source:MGI Symbol;Acc:MGI:97904]	F6U3T5		-4.2	1.1E-03	6.4	1.4E-04	-0.5	6.3E-01	-0.6	3.3E-01
ENSMUST00000139328	prefoldin 4 [Source:MGI Symbol;Acc:MGI:1923512]	E9Q2U7		4.6	3.8E-03	5.4	5.2E-02	0.5	8.6E-01	0.3	8.7E-01
ENSMUST00000139371	UBX domain protein 6 [Source:MGI Symbol;Acc:MGI:1913780]	B8JJA4		-2.3	1.8E-03	5.5	7.7E-04	-0.6	6.2E-01	-0.7	3.2E-01
ENSMUST00000139376	cytohesin 2 [Source:MGI Symbol;Acc:MGI:1334255]	D6RCZ5		-7.1	2.4E-05	6.1	1.5E-02	-0.7	7.7E-01	-1.8	2.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000139383	l(3)mbt-like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444889]	D6REI4		5.8	9.1E-04	8.2	8.0E-05	-0.7	5.8E-01	-0.3	5.6E-01
ENSMUST00000121583	NLR family, pyrin domain containing 4C [Source:MGI Symbol;Acc:MGI:1890518]		Q3TKR3	3.5	7.7E-02	5.1	2.5E-02	-0.4	8.6E-01	-2.0	1.4E-01
ENSMUST00000139385	dpy-19-like 4 (C. elegans) [Source:MGI Symbol;Acc:MGI:2685869]	A2AJQ2		3.9	3.3E-02	0.4	8.2E-01	1.8	1.9E-01	-3.4	7.0E-02
ENSMUST00000139425	serine/arginine repetitive matrix 4 [Source:MGI Symbol;Acc:MGI:1916205]		Q8BKA3	7.7	4.9E-04	-4.3	3.1E-02	0.3	6.7E-01	-0.6	7.4E-01
ENSMUST00000139451	UDP-glucuronate decarboxylase 1 [Source:MGI Symbol;Acc:MGI:1915133]	D3YUF9		-4.6	1.9E-03	5.6	2.5E-02	-0.8	7.3E-01	-0.4	7.4E-01
ENSMUST00000139456	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 [Source:MGI Symbol;Acc:MGI:1917566]	F6ZFT1		-5.6	3.7E-04	-3.3	2.6E-03	1.2	2.0E-02	0.0	9.7E-01
ENSMUST00000139477	GID complex subunit 4, VID24 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914021]		Q9CPY6	7.3	1.0E-03	2.6	5.1E-03	-1.5	5.2E-02	0.2	7.0E-01
ENSMUST00000139486	methyltransferase like 1 [Source:MGI Symbol;Acc:MGI:1339986]	F6WMV8		5.4	4.2E-03	6.1	1.0E-03	-0.4	7.6E-01	0.4	6.1E-01
ENSMUST00000139517	small G protein signaling modulator 3 [Source:MGI Symbol;Acc:MGI:1916329]		Q8VCZ6	5.5	3.5E-03	-6.3	1.1E-03	0.2	6.9E-01	-0.7	6.3E-01
ENSMUST00000121618	lipoma HMGIC fusion partner-like 2 [Source:MGI Symbol;Acc:MGI:2145236]		Q8BGA2	1.3	1.3E-01	0.1	9.0E-01	-0.7	3.6E-01	0.4	6.3E-01
ENSMUST00000121622	DDB1 and CUL4 associated factor 11 [Source:MGI Symbol;Acc:MGI:90168]		Q91VU6	-0.6	8.4E-01	2.0	6.4E-01	2.4	4.4E-01	-0.3	9.5E-01
ENSMUST00000121629	myosin binding protein C, slow-type [Source:MGI Symbol;Acc:MGI:1336213]	Q6P6L5		3.4	1.6E-01	5.3	4.7E-02	-0.5	8.3E-01	-2.4	1.7E-01
ENSMUST00000121635				-4.8	1.2E-01	-1.3	6.0E-01	0.8	6.6E-01	-2.6	4.0E-01
ENSMUST00000139526	thioredoxin domain containing 16 [Source:MGI Symbol;Acc:MGI:1917811]		Q7TN22	-5.4	5.7E-04	5.7	4.1E-03	-0.4	8.2E-01	-0.8	3.8E-01
ENSMUST00000139528	immunoglobulin superfamily, member 8 [Source:MGI Symbol;Acc:MGI:2154090]	G3UYZ1		5.2	1.7E-02	6.5	1.2E-04	-2.2	8.6E-02	-0.1	9.0E-01
ENSMUST00000139541	unconventional SNARE in the ER 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914273]	D3Z6D3		6.0	2.2E-04	-2.1	5.2E-02	1.8	8.5E-03	-0.2	8.0E-01
ENSMUST00000139547	ubiquitin specific peptidase 3 [Source:MGI Symbol;Acc:MGI:2152450]	D6RG67		-7.9	6.2E-05	6.0	1.5E-03	0.5	7.4E-01	-0.2	8.2E-01
ENSMUST00000139565	transducin (beta)-like 2 [Source:MGI Symbol;Acc:MGI:1351652]	D6RI48		3.1	1.4E-02	-8.3	3.6E-05	0.2	5.9E-01	-0.8	5.0E-01
ENSMUST00000139582	ubiquitin specific peptidase 35 [Source:MGI Symbol;Acc:MGI:2685339]	M0QWN7		3.0	2.6E-03	8.5	1.3E-05	1.1	2.8E-01	-0.2	6.1E-01
ENSMUST00000121661	small integral membrane protein 14 [Source:MGI Symbol;Acc:MGI:1915802]		Q91VT8	1.5	2.2E-01	-0.1	9.5E-01	-2.1	8.9E-02	-0.5	6.5E-01
ENSMUST00000121667				4.7	3.6E-02	2.4	3.1E-01	-1.1	6.1E-01	1.2	5.2E-01
ENSMUST00000121671	canopy 3 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:1919279]	B0V2V1		-1.1	3.1E-01	1.0	4.0E-01	0.2	8.7E-01	-1.9	9.9E-02
ENSMUST00000121673	lon peptidase 2, peroxisomal [Source:MGI Symbol;Acc:MGI:1914137]	Q8BK80		-5.9	7.6E-02	-2.2	4.1E-01	0.3	8.5E-01	-3.4	3.1E-01
ENSMUST00000139609	autophagy related 16-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1920933]		Q6KAU8	5.8	2.2E-03	6.0	4.2E-04	-1.3	3.0E-01	0.0	9.4E-01
ENSMUST00000121677	ubiquitin-conjugating enzyme E2Q (putative) 2 [Source:MGI Symbol;Acc:MGI:2388672]	D3Z647		4.1	6.3E-02	2.9	2.3E-01	-0.3	9.0E-01	0.9	6.5E-01
ENSMUST00000139629	family with sequence similarity 78, member A [Source:MGI Symbol;Acc:MGI:2443569]	A2ATN4	Q8C552	4.3	2.3E-04	2.7	1.5E-02	-1.8	5.6E-02	-0.8	2.9E-01
ENSMUST00000139634	transformation related protein 73 [Source:MGI Symbol;Acc:MGI:1336991]	B1AX91		5.9	5.9E-03	5.4	1.5E-03	0.5	6.8E-01	0.0	9.5E-01
ENSMUST00000139640	vestigial like 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2652840]	D3YZY3		5.1	8.4E-04	5.1	2.0E-02	-0.5	7.9E-01	0.5	6.6E-01
ENSMUST00000121695				1.1	8.6E-02	3.2	1.5E-03	1.1	1.0E-01	-0.9	1.4E-01
ENSMUST00000139649	pleckstrin homology domain containing, family M, member 3 [Source:MGI Symbol;Acc:MGI:2443627]		Q8BM47	4.9	5.6E-05	7.0	2.8E-03	-2.3	2.9E-01	1.1	2.9E-01
ENSMUST00000139709	AT rich interactive domain 1A (SWI-like) [Source:MGI Symbol;Acc:MGI:1935147]	E9Q495		7.3	4.3E-05	6.2	5.2E-04	-0.1	9.5E-01	0.1	9.2E-01
ENSMUST00000121705	syntaxin 4A (placental) [Source:MGI Symbol;Acc:MGI:893577]		P70452	-2.2	3.9E-02	-3.3	1.8E-02	-1.2	1.3E-01	-0.1	9.6E-01
ENSMUST00000139720	parvin, alpha [Source:MGI Symbol;Acc:MGI:1931144]	D6RHM9		8.9	5.2E-06	6.1	8.3E-04	-0.2	8.7E-01	0.7	3.7E-01
ENSMUST00000139734	iduronidase, alpha-L- [Source:MGI Symbol;Acc:MGI:96418]	D6REH5		-2.2	2.9E-02	4.7	4.6E-02	-0.8	7.2E-01	0.6	6.6E-01
ENSMUST00000139735	alcium/calmodulin-dependent serine protein kinase (MAGUK family) [Source:MGI Symbol;Acc:MGI:1309485	F6Y9I5		-5.5	3.7E-03	3.3	6.2E-02	-1.5	3.1E-01	0.4	7.3E-01
ENSMUST00000121715	transmembrane channel-like gene family 5 [Source:MGI Symbol;Acc:MGI:1921674]		Q32NZ6	3.7	1.1E-01	2.7	2.9E-01	-0.4	8.9E-01	0.6	7.4E-01
ENSMUST00000139780	repulsive guidance molecule family member A [Source:MGI Symbol;Acc:MGI:2679262]			8.5	1.6E-04	4.1	2.9E-02	-0.5	7.5E-01	1.6	1.8E-01
ENSMUST00000139783	family with sequence similarity 19, member A3 [Source:MGI Symbol;Acc:MGI:3046463]		Q7TPG6	5.5	4.3E-05	5.2	7.0E-03	-0.6	7.0E-01	0.2	8.7E-01
ENSMUST00000121723	mitogen-activated protein kinase 8 interacting protein 3 [Source:MGI Symbol;Acc:MGI:1353598]	E9Q6E0		-1.5	3.0E-01	1.9	1.9E-01	0.2	8.5E-01	-3.1	3.2E-02
ENSMUST00000121725	guanine deaminase [Source:MGI Symbol;Acc:MGI:95678]	D3YU09		-4.3	1.6E-01	-4.3	2.9E-01	-0.4	8.2E-01	-0.4	9.3E-01
ENSMUST00000139801	EGF-like domain 7 [Source:MGI Symbol;Acc:MGI:2449923]	E9Q4M7		6.4	3.2E-03	2.3	1.6E-01	-1.4	3.4E-01	2.1	1.1E-01
ENSMUST00000139806	castor zinc finger 1 [Source:MGI Symbol;Acc:MGI:1196251]	B1AS48		4.8	8.5E-04	2.6	4.8E-01	-0.2	9.4E-01	4.4	1.3E-01
ENSMUST00000139820	adenosine deaminase, tRNA-specific 1 [Source:MGI Symbol;Acc:MGI:1353631]		Q9JHI2	5.0	2.5E-04	-2.1	7.7E-02	1.0	1.6E-01	0.2	8.5E-01
ENSMUST00000139828	predicted gene 6351 [Source:MGI Symbol;Acc:MGI:3647817]	K9J7D1		7.3	7.0E-05	-4.5	1.4E-01	3.8	2.5E-02	-2.1	5.0E-01
ENSMUST00000121738	serine racemase [Source:MGI Symbol;Acc:MGI:1351636]		Q9QZX7	-1.2	4.9E-01	-1.9	2.3E-01	-3.0	4.0E-02	-2.3	2.2E-01
ENSMUST00000121743	transmembrane channel-like gene family 4 [Source:MGI Symbol;Acc:MGI:2669035]	D3YWB3		-3.8	3.6E-02	-4.5	3.8E-02	-0.7	4.9E-01	0.0	1.0E+00
ENSMUST00000121746	coiled-coil domain containing 64 [Source:MGI Symbol;Acc:MGI:1922915]	D3YTR9		-1.9	4.8E-01	-0.4	8.6E-01	-1.1	5.7E-01	-2.6	3.2E-01
ENSMUST00000139848	RASD family, member 2 [Source:MGI Symbol;Acc:MGI:1922391]		P63032	6.9	2.5E-06	5.8	2.2E-02	-0.8	7.3E-01	-0.1	9.1E-01
ENSMUST00000139853	ring finger protein 10 [Source:MGI Symbol;Acc:MGI:1859162]	F7AN16		-9.0	2.1E-04	1.6	3.3E-01	-3.5	4.8E-02	-0.6	6.9E-01
ENSMUST00000139861	proline dehydrogenase [Source:MGI Symbol;Acc:MGI:97770]	E9PUR5		4.0	4.4E-04	4.7	6.4E-03	-0.6	6.5E-01	-0.7	5.0E-01
ENSMUST00000121758	anoctamin 1, calcium activated chloride channel [Source:MGI Symbol;Acc:MGI:2142149]	A0A0A0MQF2		3.2	2.7E-01	2.1	4.5E-01	-2.9	3.4E-01	-1.8	4.1E-01
ENSMUST00000139892	multiple EGF-like-domains 10 [Source:MGI Symbol;Acc:MGI:2685177]			6.9	2.2E-04	-6.5	1.9E-02	1.5	8.5E-02	2.8	2.5E-01
ENSMUST00000139917	endo-beta-N-acetylglucosaminidase [Source:MGI Symbol;Acc:MGI:2443788]	E9PY27		5.6	5.0E-04	7.8	1.5E-04	-0.6	6.6E-01	0.4	5.6E-01
ENSMUST00000139944	SECIS binding protein 2-like [Source:MGI Symbol;Acc:MGI:1917604]	F6QQ13		2.6	7.5E-03	6.0	2.9E-02	0.2	9.2E-01	1.9	1.9E-01
ENSMUST00000139962	coiled-coil and C2 domain containing 1B [Source:MGI Symbol;Acc:MGI:2443076]	H3BKI0		6.0	6.2E-03	6.5	1.9E-02	-0.5	8.3E-01	-1.5	2.8E-01
ENSMUST00000139965	glutamate receptor, ionotropic, AMPA3 (alpha 3) [Source:MGI Symbol;Acc:MGI:95810]	F2Z488		5.7	1.0E-02	7.1	1.7E-06	-0.5	4.2E-01	-0.4	3.4E-01
ENSMUST00000139976	phospholipase C, eta 2 [Source:MGI Symbol;Acc:MGI:2443078]	F7C3A0		5.3	1.9E-02	1.9	2.7E-01	6.8	3.4E-04	-0.3	8.1E-01
ENSMUST00000139979	asunder, spermatogenesis regulator [Source:MGI Symbol;Acc:MGI:1918427]	F7BP94		-6.6	1.2E-04	-7.0	5.7E-04	-1.2	3.5E-02	-0.8	6.0E-01
ENSMUST00000139989	beta-gamma crystallin domain containing 3 [Source:MGI Symbol;Acc:MGI:2676311]	D3Z4M9		7.2	7.0E-06	-6.8	2.0E-05	-0.8	2.7E-02	-0.5	5.5E-01
ENSMUST00000140020	rhomboid domain containing 1 [Source:MGI Symbol;Acc:MGI:1924117]		Q8BHC7	7.2	1.9E-04	7.2	1.1E-02	1.2	6.0E-01	-1.3	3.6E-01
ENSMUST00000121783	golgi autoantigen, golgin subfamily a, 7 [Source:MGI Symbol;Acc:MGI:1931029]		Q91W53	-0.9	4.7E-01	0.2	8.5E-01	-1.3	2.1E-01	-2.4	7.2E-02
ENSMUST00000140061	ankyrin repeat and KH domain containing 1 [Source:MGI Symbol;Acc:MGI:1921733]	F6RUI8		-2.8	2.6E-02	3.6	1.5E-02	-3.0	7.0E-02	-0.3	7.9E-01
ENSMUST00000121785	palladin, cytoskeletal associated protein [Source:MGI Symbol;Acc:MGI:1919583]		Q9ET54	2.2	2.2E-01	2.3	3.3E-01	1.4	4.8E-01	1.3	4.6E-01
ENSMUST00000140075	family with sequence similarity 73, member B [Source:MGI Symbol;Acc:MGI:1922035]		Q8BK03	6.9	8.4E-05	6.4	3.9E-05	-1.7	9.7E-02	-0.9	8.7E-02
ENSMUST00000121787	mitogen-activated protein kinase 8 interacting protein 3 [Source:MGI Symbol;Acc:MGI:1353598]	E9Q6B6		-3.3	1.0E-01	-4.2	2.2E-01	1.4	3.8E-01	2.3	4.8E-01
ENSMUST00000140089	predicted gene 13247 [Source:MGI Symbol;Acc:MGI:3700965]	A2A8V6		7.0	1.9E-04	7.4	4.7E-05	0.1	9.2E-01	-0.4	4.3E-01
ENSMUST00000121791	transmembrane 9 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1921390]		Q9DBU0	-4.6	9.1E-02	2.1	5.7E-01	6.4	3.5E-02	-0.3	9.3E-01
ENSMUST00000140121	zinc finger and BTB domain containing 38 [Source:MGI Symbol;Acc:MGI:2442866]	Q8BW24		4.0	1.8E-02	-6.0	1.0E-02	2.1	1.2E-02	-0.8	6.9E-01
ENSMUST00000140131	inhibitor of growth family, member 4 [Source:MGI Symbol;Acc:MGI:107307]		Q8C0D7	-4.2	5.4E-04	4.7	1.6E-03	-2.1	1.1E-01	-0.4	5.7E-01
ENSMUST00000121799	Rho GTPase activating protein 23 [Source:MGI Symbol;Acc:MGI:3697726]	B1AQY2		0.0	9.5E-01	0.6	5.8E-01	1.4	9.7E-02	0.8	3.5E-01
ENSMUST00000121801				2.3	8.6E-02	0.6	6.8E-01	-0.9	4.7E-01	0.7	5.9E-01
ENSMUST00000140139	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	D3Z1T4		-3.5	3.1E-04	2.5	5.9E-03	-3.6	7.0E-04	0.4	4.3E-01
ENSMUST00000140239	ceramide synthase 1 [Source:MGI Symbol;Acc:MGI:2136690]	A2RT05	P27545	7.2	4.9E-03	6.1	1.6E-04	-0.9	4.2E-01	0.1	9.0E-01
ENSMUST00000121809	avian erythroblastosis virus E-26 (v-ets) oncogene related [Source:MGI Symbol;Acc:MGI:95415]	I1E4Y2		0.4	8.3E-01	-0.9	7.0E-01	-1.7	2.6E-01	-0.4	8.6E-01
ENSMUST00000121813	mitochondrial ribosomal protein S17 [Source:MGI Symbol;Acc:MGI:1913508]		Q9CQE3	-0.9	6.4E-01	-2.0	1.5E-01	-3.9	1.1E-02	-2.7	1.3E-01
ENSMUST00000140299	transmembrane protein 5 [Source:MGI Symbol;Acc:MGI:2384919]		Q8VDX6	4.0	6.2E-04	4.1	2.4E-03	-0.7	4.8E-01	-1.6	6.5E-02
ENSMUST00000140302	syntrophin, gamma 1 [Source:MGI Symbol;Acc:MGI:1918346]	D6REU8		5.7	1.5E-02	5.6	6.2E-02	-0.9	7.6E-01	0.1	9.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000140312	Son DNA binding protein [Source:MGI Symbol;Acc:MGI:98353]	H9KV15		-6.5	8.6E-04	4.8	2.4E-03	-2.8	4.6E-02	-0.6	4.5E-01
ENSMUST00000140326	deleted in lung and esophageal cancer 1 [Source:MGI Symbol;Acc:MGI:2443671]	D3Z6E8		8.2	3.0E-05	6.3	2.1E-03	-1.0	5.7E-01	0.0	9.6E-01
ENSMUST00000121826	tetraspanin 5 [Source:MGI Symbol;Acc:MGI:1928096]	D3Z641		0.6	4.8E-01	3.2	1.4E-02	1.2	2.2E-01	-1.4	1.2E-01
ENSMUST00000140375	F-box protein 22 [Source:MGI Symbol;Acc:MGI:1926014]	D6REV6		4.8	1.5E-03	6.3	1.9E-03	-0.9	5.6E-01	0.7	4.4E-01
ENSMUST00000121834	synaptotagmin VI [Source:MGI Symbol;Acc:MGI:1859544]		Q9R0N8	2.8	4.1E-02	6.2	3.9E-04	-0.5	6.7E-01	-4.0	1.3E-03
ENSMUST00000140384	RNA binding motif protein, X chromosome [Source:MGI Symbol;Acc:MGI:1343044]		Q9WV02	-4.1	2.0E-03	4.6	1.0E-02	-0.5	7.2E-01	1.9	6.8E-02
ENSMUST00000140466	dynein cytoplasmic 2 heavy chain 1 [Source:MGI Symbol;Acc:MGI:107736]		Q45VK7	2.6	4.9E-03	6.0	8.3E-03	-0.7	7.2E-01	-1.6	2.0E-01
ENSMUST00000140485	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 [Source:MGI Symbol;Acc:MGI:1924550]	F2Z3U3		3.2	7.1E-04	2.9	6.8E-02	1.0	4.2E-01	0.8	4.5E-01
ENSMUST00000121843				4.1	3.9E-02	5.0	4.1E-02	0.8	7.2E-01	-0.1	9.2E-01
ENSMUST00000140494	heat shock protein 14 [Source:MGI Symbol;Acc:MGI:1354164]	D6RJ26		4.6	3.3E-02	6.2	8.9E-03	-0.9	6.8E-01	1.5	2.0E-01
ENSMUST00000140497	zinc finger, DHHC domain containing 3 [Source:MGI Symbol;Acc:MGI:1926134]	D6RFV6		-2.1	8.8E-04	5.3	2.6E-03	-0.6	6.7E-01	-0.2	8.3E-01
ENSMUST00000140512	calcium homeostasis modulator 2 [Source:MGI Symbol;Acc:MGI:1919941]	D3Z2E8		8.4	4.8E-05	5.6	1.7E-03	-0.5	7.4E-01	0.0	9.5E-01
ENSMUST00000140516	MyoD family inhibitor domain containing [Source:MGI Symbol;Acc:MGI:104611]	D6RE10		5.4	1.6E-03	2.9	5.0E-02	0.6	6.2E-01	0.5	6.3E-01
ENSMUST00000121863	chondroitin polymerizing factor 2 [Source:MGI Symbol;Acc:MGI:1917522]	Q3UU43		-2.0	3.6E-02	-5.3	5.8E-03	1.2	1.2E-01	4.5	1.2E-02
ENSMUST00000121870	palmitoyl-protein thioesterase 1 [Source:MGI Symbol;Acc:MGI:1298204]	B1B0P8		0.9	1.5E-01	0.1	8.5E-01	-1.1	7.6E-02	-0.3	6.2E-01
ENSMUST00000140523	solute carrier family 38, member 6 [Source:MGI Symbol;Acc:MGI:3648156]	G3UVW3		2.7	1.8E-03	5.5	2.5E-03	-0.7	6.5E-01	0.2	8.3E-01
ENSMUST00000140540	GRIP1 associated protein 1 [Source:MGI Symbol;Acc:MGI:1859616]	A2AEW6		-4.9	4.6E-04	5.9	3.0E-04	-0.6	6.2E-01	0.1	9.3E-01
ENSMUST00000140546	chemokine (C-C motif) ligand 19 [Source:MGI Symbol;Acc:MGI:1346316]			6.6	8.7E-05	6.4	7.3E-05	-2.5	4.2E-02	0.0	9.9E-01
ENSMUST00000121876				3.1	7.6E-02	2.8	2.6E-01	1.6	4.7E-01	1.9	2.8E-01
ENSMUST00000140583	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S) [Source:MGI Symbol;Acc:MGI:2389490]		P59270	4.0	3.4E-02	6.6	2.5E-04	-0.6	6.5E-01	-0.3	6.1E-01
ENSMUST00000140643	nicastrin [Source:MGI Symbol;Acc:MGI:1891700]	D6RCJ2		4.9	2.0E-02	5.3	3.6E-05	-0.5	5.2E-01	-0.1	8.3E-01
ENSMUST00000140675	cell cycle progression 1 [Source:MGI Symbol;Acc:MGI:1196419]	D3Z7R9		-8.3	3.2E-04	-4.2	1.9E-03	0.1	8.7E-01	0.4	6.8E-01
ENSMUST00000140702	F-box and leucine-rich repeat protein 12 [Source:MGI Symbol;Acc:MGI:1354738]			-2.5	1.8E-02	8.7	1.5E-02	-0.9	7.9E-01	-1.6	3.3E-01
ENSMUST00000140703	immunoglobulin-like and fibronectin type III domain containing 1 [Source:MGI Symbol;Acc:MGI:3045352]	A0A087WPK2		5.3	5.3E-03	6.3	1.0E-03	-0.7	6.5E-01	0.0	9.7E-01
ENSMUST00000121895				0.1	8.7E-01	2.1	4.1E-02	0.9	2.7E-01	-1.2	1.7E-01
ENSMUST00000140706	beclin 1, autophagy related [Source:MGI Symbol;Acc:MGI:1891828]	F7DB15		4.9	5.0E-03	4.6	3.4E-02	-0.3	8.7E-01	0.0	9.8E-01
ENSMUST00000140713	hnRNP-associated with lethal yellow [Source:MGI Symbol;Acc:MGI:97850]	A2AU62		-6.5	6.8E-03	5.9	5.1E-04	-0.5	6.7E-01	-0.6	3.4E-01
ENSMUST00000121902	RIKEN cDNA 1700030K09 gene [Source:MGI Symbol;Acc:MGI:1919504]	E9Q7C0		4.8	5.0E-02	0.7	6.7E-01	-5.7	1.8E-02	-1.6	2.8E-01
ENSMUST00000140743	heterogeneous nuclear ribonucleoprotein H3 [Source:MGI Symbol;Acc:MGI:1926462]	D3Z6Y3		-4.7	3.8E-03	3.9	4.5E-02	-2.2	2.5E-01	-0.5	6.8E-01
ENSMUST00000140761	protein phosphatase 1M [Source:MGI Symbol;Acc:MGI:1915155]	E9Q2I3		-8.9	6.2E-05	-5.9	2.0E-04	-0.8	6.3E-02	-1.0	3.6E-01
ENSMUST00000121924				1.1	1.0E-01	1.1	1.7E-01	0.3	6.5E-01	0.2	7.2E-01
ENSMUST00000121927	nuclear receptor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1315213]		Q8CBD1	0.8	4.2E-01	0.2	8.8E-01	-0.8	3.6E-01	-0.2	8.2E-01
ENSMUST00000140770	homology domain containing, family D (with coiled-coil domains) member 1 [Source:MGI Symbol;Acc:MGI:		B2RPU2	7.8	1.2E-05	6.0	1.5E-03	-0.7	6.5E-01	0.2	7.6E-01
ENSMUST00000140802	RIKEN cDNA D930020B18 gene [Source:MGI Symbol;Acc:MGI:2442001]	D6RIN2		7.3	6.5E-05	6.7	2.5E-03	-0.7	6.9E-01	-2.2	5.3E-02
ENSMUST00000140843	START domain containing 9 [Source:MGI Symbol;Acc:MGI:3045258]	A2AKH9		4.5	2.7E-04	-4.0	3.2E-03	1.5	6.9E-03	-0.7	5.6E-01
ENSMUST00000121942				5.9	5.5E-02	-1.4	5.7E-01	-5.1	7.5E-02	2.1	3.4E-01
ENSMUST00000121949	HEAT repeat containing 3 [Source:MGI Symbol;Acc:MGI:2444491]	E9PWH6		-2.3	3.2E-01	1.1	7.6E-01	4.0	1.2E-01	0.6	8.4E-01
ENSMUST00000140846	Sfi1 homolog, spindle assembly associated (yeast) [Source:MGI Symbol;Acc:MGI:1926137]	E9Q799		11.0	3.3E-06	-2.5	1.9E-01	1.0	3.2E-01	-0.3	8.6E-01
ENSMUST00000140869	methyltransferase like 23 [Source:MGI Symbol;Acc:MGI:1921569]	H3BKB2		-4.5	3.2E-04	2.3	1.2E-01	-0.6	6.2E-01	3.3	1.1E-02
ENSMUST00000140898	zinc finger CCCH type containing 7 A [Source:MGI Symbol;Acc:MGI:2445044]	F6X2N3		-4.4	1.3E-02	5.9	6.2E-04	-0.6	6.1E-01	0.0	9.5E-01
ENSMUST00000140914	intraflagellar transport 57 [Source:MGI Symbol;Acc:MGI:1921166]	F7B458		-4.8	7.3E-04	6.1	3.5E-04	-0.6	6.3E-01	-0.4	5.8E-01
ENSMUST00000140920	URB1 ribosome biogenesis 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2146468]	E9PU96		3.6	1.2E-04	2.2	1.5E-02	-0.1	9.1E-01	-0.3	6.2E-01
ENSMUST00000140934	negative elongation factor complex member B [Source:MGI Symbol;Acc:MGI:1931035]	F6SWS9		3.5	2.3E-02	6.8	1.5E-03	-0.2	9.2E-01	-0.2	8.0E-01
ENSMUST00000140956	centrin 4 [Source:MGI Symbol;Acc:MGI:2677454]	A0A0A0MQN3		7.3	2.0E-04	4.4	8.4E-02	-0.2	9.3E-01	0.2	9.1E-01
ENSMUST00000140979	special AT-rich sequence binding protein 1 [Source:MGI Symbol;Acc:MGI:105084]	E9PVB7		-6.1	4.3E-04	7.9	3.7E-04	-1.9	2.7E-01	-1.5	4.7E-02
ENSMUST00000141047	predicted gene 21985 [Source:MGI Symbol;Acc:MGI:5439454]	Q6P6P5		-4.4	2.6E-03	6.5	5.8E-04	-0.7	6.3E-01	-0.5	5.0E-01
ENSMUST00000121979	centrosomal protein 135 [Source:MGI Symbol;Acc:MGI:2681869]		Q6P5D4	1.2	5.9E-01	5.7	3.1E-02	1.1	5.9E-01	-3.4	1.3E-01
ENSMUST00000141062	gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:95706]	D3YWZ7		-4.4	7.5E-04	7.9	4.0E-04	-0.7	6.5E-01	-0.6	4.6E-01
ENSMUST00000141110	glucocorticoid modulatory element binding protein 2 [Source:MGI Symbol;Acc:MGI:2652836]	D6RG43		5.1	4.8E-03	3.6	1.8E-02	-2.5	8.7E-02	-0.4	7.2E-01
ENSMUST00000141112	expressed sequence AU022252 [Source:MGI Symbol;Acc:MGI:2140466]		Q5EBG8	3.3	2.4E-05	9.1	8.6E-05	0.2	8.6E-01	-0.1	8.6E-01
ENSMUST00000141122	predicted gene 14306 [Source:MGI Symbol;Acc:MGI:3805542]	D6RGN8		4.7	3.1E-03	4.2	1.5E-02	-2.8	1.3E-01	-2.0	1.1E-01
ENSMUST00000141135	ATP-binding cassette, sub-family A (ABC1), member 4 [Source:MGI Symbol;Acc:MGI:109424]	A0A0G2JGG8		4.8	6.8E-04	-5.4	6.2E-04	-1.4	1.8E-02	-2.1	1.2E-01
ENSMUST00000122001	tumor necrosis factor receptor superfamily, member 18 [Source:MGI Symbol;Acc:MGI:894675]	B1ASL6		1.0	4.6E-01	-2.2	1.9E-01	-3.4	1.8E-02	-0.2	9.1E-01
ENSMUST00000122003	CCR4-NOT transcription complex, subunit 6-like [Source:MGI Symbol;Acc:MGI:2443154]		Q8VEG6	0.0	1.0E+00	-0.3	8.9E-01	-1.7	3.5E-01	-1.4	5.0E-01
ENSMUST00000141137	dynein, axonemal, heavy chain 10 [Source:MGI Symbol;Acc:MGI:1860299]	F7ABZ6		6.5	1.1E-02	5.6	5.3E-03	-0.6	7.2E-01	0.0	1.0E+00
ENSMUST00000141144	RIKEN cDNA 2010107G23 gene [Source:MGI Symbol;Acc:MGI:1917144]	D3Z7G3		7.3	1.4E-03	6.2	2.0E-04	-0.6	6.1E-01	0.3	6.6E-01
ENSMUST00000141158	adhesion G protein-coupled receptor L1 [Source:MGI Symbol;Acc:MGI:1929461]		Q80TR1	5.1	1.1E-05	6.3	5.1E-04	-0.4	7.3E-01	-1.9	2.2E-02
ENSMUST00000141159	RIKEN cDNA D430041D05 gene [Source:MGI Symbol;Acc:MGI:2181743]	F6ZGR6		9.5	6.4E-05	6.1	1.2E-03	-0.4	7.7E-01	-0.9	2.7E-01
ENSMUST00000141169	suppressor of Ty 4A [Source:MGI Symbol;Acc:MGI:107416]	G3UVU8		1.7	2.0E-02	5.7	4.2E-04	-1.0	4.0E-01	0.8	2.3E-01
ENSMUST00000141171	high mobility group 20B [Source:MGI Symbol;Acc:MGI:1341190]	F7AVN4		-4.3	1.3E-02	-6.0	2.8E-04	-0.2	5.5E-01	-0.4	7.4E-01
ENSMUST00000141188	cDNA sequence AF251705 [Source:MGI Symbol;Acc:MGI:2153249]	E0CYN3		-5.2	1.2E-03	9.1	2.4E-03	-1.0	6.8E-01	1.2	2.7E-01
ENSMUST00000141191	agine-linked glycosylation 5 (dolichyl-phosphate beta-glucosyltransferase) [Source:MGI Symbol;Acc:MGI:191	D6RCG2		10.0	3.9E-05	5.8	7.4E-04	-0.9	4.7E-01	0.3	6.7E-01
ENSMUST00000141206	transmembrane BAX inhibitor motif containing 4 [Source:MGI Symbol;Acc:MGI:1915462]	D6RIR2		-4.9	7.8E-04	-4.9	2.3E-03	-0.5	3.4E-01	-1.0	4.5E-01
ENSMUST00000122044	casein kinase 1, epsilon [Source:MGI Symbol;Acc:MGI:1351660]	Q3TYE1		-0.3	5.0E-01	-0.4	6.1E-01	0.7	1.5E-01	0.7	2.8E-01
ENSMUST00000141228	small ubiquitin-like modifier 3 [Source:MGI Symbol;Acc:MGI:1336201]	G3UWX9		-5.0	9.5E-04	6.4	3.9E-04	-0.7	6.0E-01	-0.2	8.1E-01
ENSMUST00000141235	zinc finger and BTB domain containing 8 opposite strand [Source:MGI Symbol;Acc:MGI:1914356]	B2KGA7		5.6	6.1E-07	5.7	2.0E-03	-2.0	1.8E-01	0.8	3.5E-01
ENSMUST00000122059	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]	B0QZL5		-4.4	6.9E-02	-2.2	4.5E-01	1.3	5.4E-01	-0.9	7.4E-01
ENSMUST00000141250	alpha-kinase 2 [Source:MGI Symbol;Acc:MGI:2449492]	F6ZZL0		7.6	7.2E-05	3.4	9.8E-04	-4.6	8.2E-04	0.4	5.4E-01
ENSMUST00000122066	zinc finger protein 629 [Source:MGI Symbol;Acc:MGI:2444524]		Q6A085	3.7	5.6E-02	3.6	3.7E-02	-3.2	7.7E-02	-3.1	3.7E-02
ENSMUST00000122070	nuclear receptor coactivator 5 [Source:MGI Symbol;Acc:MGI:2385165]	B7ZC24		-3.4	7.9E-02	-2.3	2.8E-01	0.1	9.4E-01	-1.0	6.5E-01
ENSMUST00000141258	proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide [Source:MGI Symbol;Acc:I	F6ULE1		4.8	1.4E-03	5.8	1.0E-03	-0.6	6.5E-01	-0.3	6.7E-01
ENSMUST00000141264	WAS/WASL interacting protein family, member 1 [Source:MGI Symbol;Acc:MGI:2178801]	F6QWW7		-2.2	1.7E-02	5.5	5.7E-04	-0.5	6.9E-01	-0.9	2.1E-01
ENSMUST00000141268	ic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Source:MGI Symbol;Acc:MGI:1	D3YZT9		-6.2	1.7E-05	3.0	2.0E-01	-0.8	6.7E-01	3.4	7.0E-02
ENSMUST00000141281	tectonic family member 1 [Source:MGI Symbol;Acc:MGI:3603820]	D6RDQ2		-4.2	3.4E-03	4.9	6.2E-02	-0.6	8.2E-01	-0.4	8.1E-01
ENSMUST00000122087	general transcription factor II A, 2 [Source:MGI Symbol;Acc:MGI:1933289]	D3Z793		0.6	4.8E-01	0.2	8.3E-01	0.2	7.8E-01	0.6	5.8E-01
ENSMUST00000141290	olute carrier family 16 (monocarboxylic acid transporters), member 13 [Source:MGI Symbol;Acc:MGI:191655	A2CF71		5.4	3.4E-02	5.7	8.4E-03	-0.7	7.1E-01	-0.4	6.9E-01
ENSMUST00000122090				3.8	8.6E-02	6.1	3.4E-02	0.3	9.2E-01	-2.0	1.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000141298	Rho GTPase activating protein 21 [Source:MGI Symbol;Acc:MGI:1918685]	B7ZCJ1		3.8	9.8E-04	3.8	1.1E-03	0.5	5.3E-01	-1.2	9.1E-02
ENSMUST00000141306	Rap1 GTPase-activating protein [Source:MGI Symbol;Acc:MGI:109338]	A2ALS7		6.3	8.6E-04	5.8	9.0E-04	-0.6	6.5E-01	0.4	5.3E-01
ENSMUST00000141360	UBX domain protein 2A [Source:MGI Symbol;Acc:MGI:2442310]	D6RGU9		-2.9	2.8E-02	7.6	7.1E-05	-0.5	7.0E-01	-0.3	5.6E-01
ENSMUST00000122101	microtubule-associated protein 6 [Source:MGI Symbol;Acc:MGI:1201690]	D3Z6W1		4.8	6.2E-02	5.9	5.0E-02	-0.3	9.2E-01	-1.3	4.0E-01
ENSMUST00000122103	RAB11 family interacting protein 3 (class II) [Source:MGI Symbol;Acc:MGI:2444431]		Q8CHD8	1.2	3.7E-01	2.8	6.7E-02	-0.7	5.7E-01	-2.3	8.8E-02
ENSMUST00000141366	PIH1 domain containing 2 [Source:MGI Symbol;Acc:MGI:1919864]	D3Z3T0		3.9	2.3E-04	-4.4	5.1E-03	1.1	6.7E-02	-2.2	1.6E-01
ENSMUST00000122113	P450 (cytochrome) oxidoreductase [Source:MGI Symbol;Acc:MGI:97744]	Q05DV1		-1.2	4.3E-01	0.2	9.2E-01	1.1	5.4E-01	-0.3	8.6E-01
ENSMUST00000141387	synaptophysin-like 2 [Source:MGI Symbol;Acc:MGI:1328311]	A2AE45	O89104	7.5	4.5E-04	-4.7	8.4E-04	-1.1	4.0E-02	-2.1	9.3E-02
ENSMUST00000122120	family with sequence similarity 19, member A1 [Source:MGI Symbol;Acc:MGI:2443695]		Q7TPG8	4.0	1.4E-01	6.3	4.2E-02	-0.2	9.5E-01	-2.5	1.6E-01
ENSMUST00000122125				0.2	7.9E-01	0.8	3.0E-01	-0.7	2.5E-01	-1.3	7.3E-02
ENSMUST00000141398	eukaryotic translation initiation factor 4E family member 1B [Source:MGI Symbol;Acc:MGI:2685119]	Q27ZI7		7.1	6.2E-05	-4.8	2.3E-02	-0.6	5.2E-01	-0.3	8.7E-01
ENSMUST00000141409	kinase suppressor of ras 1 [Source:MGI Symbol;Acc:MGI:105051]	Q5SXE2		6.1	1.4E-03	-6.8	2.5E-02	1.2	1.8E-01	2.3	4.0E-01
ENSMUST00000141410	BCL2-associated agonist of cell death [Source:MGI Symbol;Acc:MGI:1096330]	F7ABX5		-1.4	2.4E-02	6.3	6.5E-04	0.8	5.2E-01	-1.6	5.1E-02
ENSMUST00000141429	centrosomal protein 128 [Source:MGI Symbol;Acc:MGI:1922466]	B7ZNX8	Q8BI22	-3.8	1.7E-02	6.5	6.9E-04	-0.7	6.3E-01	-0.3	7.0E-01
ENSMUST00000122143	PHD and ring finger domains 1 [Source:MGI Symbol;Acc:MGI:2141847]		A6H619	2.5	1.3E-01	1.2	5.7E-01	0.1	9.5E-01	1.4	4.1E-01
ENSMUST00000122148	BAH domain and coiled-coil containing 1 [Source:MGI Symbol;Acc:MGI:2679272]		Q3UHR0	5.8	3.5E-02	1.6	7.2E-01	0.5	8.6E-01	4.8	2.1E-01
ENSMUST00000141446	poly(A) binding protein, nuclear 1 [Source:MGI Symbol;Acc:MGI:1859158]	D3Z055		-3.6	2.3E-03	5.3	3.2E-04	0.3	7.3E-01	-0.5	4.6E-01
ENSMUST00000141487	DDHD domain containing 1 [Source:MGI Symbol;Acc:MGI:2150302]	G3UWN4		-5.7	1.4E-03	5.6	2.1E-04	-1.9	8.8E-02	-0.3	6.3E-01
ENSMUST00000141504	RecQ protein-like [Source:MGI Symbol;Acc:MGI:103021]	F6S4D9		4.1	3.4E-03	-7.5	9.5E-04	-0.6	3.8E-01	-1.9	2.8E-01
ENSMUST00000122160	ubiquitin specific peptidase like 1 [Source:MGI Symbol;Acc:MGI:2442342]	E9QLC6		-2.4	3.9E-01	-3.1	3.9E-01	-0.9	6.7E-01	-0.1	9.7E-01
ENSMUST00000122162				-1.4	1.5E-01	-0.5	6.0E-01	-0.8	3.2E-01	-1.7	1.3E-01
ENSMUST00000122163	potassium channel tetramerisation domain containing 20 [Source:MGI Symbol;Acc:MGI:1914239]		Q8CDD8	1.5	5.3E-01	-2.3	4.1E-01	-2.6	2.5E-01	1.2	6.5E-01
ENSMUST00000141505	te carrier family 7 (cationic amino acid transporter, y+ system), member 2 [Source:MGI Symbol;Acc:MGI:998			4.6	1.4E-03	4.8	5.1E-04	-0.9	3.5E-01	0.2	6.9E-01
ENSMUST00000141507	lysine (K)-specific demethylase 4B [Source:MGI Symbol;Acc:MGI:2442355]	F7BTY2		-4.0	5.7E-03	6.0	3.1E-04	0.0	9.7E-01	-0.6	3.7E-01
ENSMUST00000141516	ataxin 7-like 3 [Source:MGI Symbol;Acc:MGI:3036270]	F6RCN9		-5.6	8.4E-03	-7.7	5.7E-04	-1.2	3.2E-02	0.0	9.8E-01
ENSMUST00000141530	secreted acidic cysteine rich glycoprotein [Source:MGI Symbol;Acc:MGI:98373]	Q5NCU3		6.1	2.1E-02	5.8	1.3E-03	-0.4	7.5E-01	-0.3	6.8E-01
ENSMUST00000141601	canopy 1 homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2442451]	F7C041	Q4VAB4	5.3	3.6E-04	7.3	2.5E-04	0.1	9.3E-01	0.3	6.6E-01
ENSMUST00000122188	lon peptidase 2, peroxisomal [Source:MGI Symbol;Acc:MGI:1914137]		Q9DBN5	2.2	8.2E-02	-4.5	1.3E-03	-8.0	1.0E-05	-1.3	2.6E-01
ENSMUST00000141623	CTD nuclear envelope phosphatase 1 [Source:MGI Symbol;Acc:MGI:1914431]	J3QPC9		-6.0	1.1E-03	6.4	1.6E-03	-0.4	8.0E-01	-1.8	6.7E-02
ENSMUST00000122202	small nuclear ribonucleoprotein polypeptide A [Source:MGI Symbol;Acc:MGI:1855690]		Q62189	-2.2	1.8E-01	-1.3	5.3E-01	0.9	5.4E-01	0.0	9.8E-01
ENSMUST00000122204	predicted pseudogene 7879 [Source:MGI Symbol;Acc:MGI:3645078]	Q4G0C5	Q9D868	-2.3	8.3E-02	-4.9	2.4E-02	-1.4	1.4E-01	1.2	5.2E-01
ENSMUST00000141628	ubiquitin specific peptidase 48 [Source:MGI Symbol;Acc:MGI:2158502]	A2ALR5		-5.5	2.1E-03	6.7	9.9E-05	-0.5	6.3E-01	-1.2	6.3E-02
ENSMUST00000122211	RAB3D, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:97844]	Q543Q4	P35276	0.1	8.3E-01	2.1	2.7E-02	1.1	9.5E-02	-0.8	2.7E-01
ENSMUST00000122214				0.9	4.8E-01	1.1	3.9E-01	-1.3	2.7E-01	-1.5	2.1E-01
ENSMUST00000122216	bolA-like 3 (E. coli) [Source:MGI Symbol;Acc:MGI:1925903]	E9Q705		-1.7	1.7E-01	-2.5	1.0E-01	-0.9	3.5E-01	-0.1	9.4E-01
ENSMUST00000141629	RNA binding motif protein 3 [Source:MGI Symbol;Acc:MGI:1099460]	S4R2M6		-4.5	2.5E-02	-5.4	5.1E-03	0.7	3.4E-01	-0.8	6.3E-01
ENSMUST00000141630	thymidylate synthase [Source:MGI Symbol;Acc:MGI:98878]	D6RCW9		6.7	1.6E-03	2.6	4.0E-03	1.1	7.2E-02	0.4	4.4E-01
ENSMUST00000141635	proline dehydrogenase [Source:MGI Symbol;Acc:MGI:97770]	F6YFQ5		6.0	5.2E-03	-8.2	4.6E-05	-0.7	9.2E-02	-1.8	2.1E-01
ENSMUST00000141695	ring finger protein 167 [Source:MGI Symbol;Acc:MGI:1917760]	D6RCH3		-2.4	7.9E-03	-5.2	1.3E-03	-1.7	7.7E-03	-1.1	4.0E-01
ENSMUST00000141703	LYR motif containing 7 [Source:MGI Symbol;Acc:MGI:1922780]	D6RD13		6.1	7.3E-04	-7.6	1.5E-04	0.7	7.9E-02	0.0	1.0E+00
ENSMUST00000122233	kinesin family member 2A [Source:MGI Symbol;Acc:MGI:108390]		P28740	-0.4	4.4E-01	0.8	1.9E-01	0.6	1.9E-01	-0.6	3.2E-01
ENSMUST00000141709	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	F6Q968		-2.0	9.4E-03	5.2	3.3E-04	0.1	9.0E-01	-0.6	3.2E-01
ENSMUST00000141713	RIKEN cDNA 4932431P20 gene [Source:MGI Symbol;Acc:MGI:2149781]	E9Q1N0		9.8	2.9E-06	5.1	2.0E-03	-0.1	9.2E-01	1.0	2.0E-01
ENSMUST00000122242	torsin family 3, member A [Source:MGI Symbol;Acc:MGI:1353652]		Q9ER38	-0.1	9.6E-01	-2.3	1.8E-01	-1.1	2.7E-01	1.2	4.8E-01
ENSMUST00000141722	syntaxin binding protein 5 (tomosyn) [Source:MGI Symbol;Acc:MGI:1926058]	D3Z079		-5.7	3.3E-04	6.7	2.9E-04	-0.7	6.0E-01	-0.8	2.7E-01
ENSMUST00000122245				-2.1	3.6E-02	-1.6	2.6E-01	1.1	2.1E-01	0.6	6.7E-01
ENSMUST00000122253	PEST proteolytic signal containing nuclear protein [Source:MGI Symbol;Acc:MGI:1923552]	Q3TM89		0.7	3.5E-01	0.2	8.2E-01	-0.6	3.8E-01	-0.2	8.3E-01
ENSMUST00000141733	TSC22 domain family, member 4 [Source:MGI Symbol;Acc:MGI:1926079]	F6VXN4		-8.3	4.9E-05	-5.0	3.7E-03	-0.7	2.6E-01	-0.4	7.7E-01
ENSMUST00000122255	CREB regulated transcription coactivator 3 [Source:MGI Symbol;Acc:MGI:1917711]		Q91X84	-0.8	5.9E-02	0.3	5.3E-01	0.8	5.5E-02	-0.4	4.7E-01
ENSMUST00000141755	methyltransferase like 16 [Source:MGI Symbol;Acc:MGI:1914743]		Q9CQG2	4.6	1.5E-05	5.8	1.1E-02	-1.0	6.3E-01	-1.8	1.6E-01
ENSMUST00000141775	family with sequence similarity 81, member A [Source:MGI Symbol;Acc:MGI:1924136]	D3YVT3		11.5	7.5E-06	-7.0	8.0E-04	0.2	7.8E-01	-0.8	6.6E-01
ENSMUST00000141830	methionine adenosyltransferase II, beta [Source:MGI Symbol;Acc:MGI:1913667]	E0CYU5		-5.4	7.1E-03	5.6	4.4E-03	0.4	8.0E-01	-0.3	7.1E-01
ENSMUST00000122265				-4.4	2.0E-01	-10.4	1.1E-01	-4.4	5.4E-02	1.7	7.9E-01
ENSMUST00000141833	ELMO/CED-12 domain containing 3 [Source:MGI Symbol;Acc:MGI:2445168]			3.3	5.7E-03	5.9	8.5E-04	-0.6	6.4E-01	0.3	7.2E-01
ENSMUST00000141883	matrix-remodelling associated 8 [Source:MGI Symbol;Acc:MGI:1922011]	A2AD97		4.9	1.4E-02	6.4	5.2E-04	-0.5	7.0E-01	-2.6	6.6E-03
ENSMUST00000141902	F-box and leucine-rich repeat protein 5 [Source:MGI Symbol;Acc:MGI:2152883]	F6W6I1		-8.2	9.9E-05	7.5	3.5E-05	-0.6	6.0E-01	-1.2	5.3E-02
ENSMUST00000122284	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a [Source:MGI Symbol;Acc:MGI:1330299]	A1L341		-0.6	3.8E-01	-1.7	1.6E-01	1.1	1.3E-01	2.2	6.6E-02
ENSMUST00000141916	7-dehydrocholesterol reductase [Source:MGI Symbol;Acc:MGI:1298378]		O88455	7.1	1.5E-02	6.0	8.0E-04	-0.4	7.4E-01	-0.8	2.6E-01
ENSMUST00000141933	Scl/Tal1 interrupting locus [Source:MGI Symbol;Acc:MGI:107477]	D6RH61		7.5	7.0E-05	-7.1	1.1E-04	-0.3	4.2E-01	0.3	8.3E-01
ENSMUST00000141957	RIKEN cDNA D230025D16 gene [Source:MGI Symbol;Acc:MGI:2443049]	D6RCI5		-1.8	2.5E-02	8.6	9.1E-05	1.3	3.2E-01	0.9	1.3E-01
ENSMUST00000142003	protein kinase C, epsilon [Source:MGI Symbol;Acc:MGI:97599]	Q8C944		4.2	2.5E-03	7.5	4.7E-04	0.7	6.3E-01	-0.4	5.7E-01
ENSMUST00000142005	dpy-19-like 4 (C. elegans) [Source:MGI Symbol;Acc:MGI:2685869]	D6RI72		6.0	5.0E-05	6.2	3.6E-04	-0.6	6.2E-01	0.3	6.5E-01
ENSMUST00000142011	angiomotin-like 2 [Source:MGI Symbol;Acc:MGI:1929286]	Q3TP05		3.0	5.1E-04	-5.8	4.0E-03	0.6	2.9E-01	0.0	9.8E-01
ENSMUST00000142029	small integral membrane protein 12 [Source:MGI Symbol;Acc:MGI:1933141]		Q78RX3	-2.7	3.9E-03	-1.3	6.8E-01	6.9	2.1E-03	-1.8	5.7E-01
ENSMUST00000122305				1.8	1.0E-01	1.2	3.8E-01	0.5	6.7E-01	1.1	3.8E-01
ENSMUST00000122309	predicted gene 13157 [Source:MGI Symbol;Acc:MGI:3651978]	A2A7A2		-0.9	9.7E-02	2.1	2.1E-02	3.6	3.6E-04	0.6	3.3E-01
ENSMUST00000122312	v-raf murine sarcoma 3611 viral oncogene homolog [Source:MGI Symbol;Acc:MGI:88065]	Q8CAD1		0.2	8.5E-01	1.1	3.6E-01	0.7	4.0E-01	-0.1	8.8E-01
ENSMUST00000122314	solute carrier family 12 (potassium/chloride transporters), member 8 [Source:MGI Symbol;Acc:MGI:2443672]	D3Z3V1		3.3	7.0E-02	2.3	3.5E-01	0.5	8.1E-01	1.5	3.5E-01
ENSMUST00000142064	dpy-19-like 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1915685]		A6X919	-4.8	6.6E-04	6.1	1.1E-03	-0.5	7.0E-01	-2.5	1.7E-02
ENSMUST00000142092	a disintegrin and metallopeptidase domain 17 [Source:MGI Symbol;Acc:MGI:1096335]	J3QMF2		4.6	1.5E-02	-5.6	1.2E-03	1.3	1.2E-02	3.5	1.7E-02
ENSMUST00000142152	glycerol kinase [Source:MGI Symbol;Acc:MGI:106594]	B1ASZ3		-3.6	7.7E-03	2.2	7.3E-03	-6.9	6.0E-05	-0.3	6.1E-01
ENSMUST00000142231	diacylglycerol kinase zeta [Source:MGI Symbol;Acc:MGI:1278339]	D6RDR3		-7.3	1.8E-03	6.5	6.5E-04	-0.7	6.4E-01	-0.9	2.7E-01
ENSMUST00000142234	DNA segment, Chr 1, ERATO Doi 622, expressed [Source:MGI Symbol;Acc:MGI:1277184]	M0QWF6		-7.6	4.0E-05	6.6	1.6E-04	0.5	6.6E-01	0.5	4.2E-01
ENSMUST00000142271	FK506 binding protein 1a [Source:MGI Symbol;Acc:MGI:95541]	F6X9I3		3.4	2.5E-02	-4.7	1.7E-03	-0.9	8.3E-02	-0.5	6.5E-01
ENSMUST00000142278	synaptosomal-associated protein 23 [Source:MGI Symbol;Acc:MGI:109356]	B0R030		-6.2	1.8E-04	5.1	1.1E-02	-2.1	2.5E-01	-1.2	3.0E-01
ENSMUST00000142300	laccase (multicopper oxidoreductase) domain containing 1 [Source:MGI Symbol;Acc:MGI:2445077]	H3BL27		4.5	2.3E-04	7.9	3.7E-05	1.0	3.6E-01	-1.2	4.9E-02
ENSMUST00000142313	Bardet-Biedl syndrome 9 (human) [Source:MGI Symbol;Acc:MGI:2442833]	D3Z6T1		6.5	8.3E-04	6.3	1.0E-03	-0.7	6.6E-01	-0.6	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000142315	Sfi1 homolog, spindle assembly associated (yeast) [Source:MGI Symbol;Acc:MGI:1926137]	A8Y5K4		2.8	1.7E-02	5.9	1.4E-03	-0.4	7.7E-01	-1.5	8.5E-02
ENSMUST00000122352				2.0	4.6E-02	2.8	2.2E-02	-0.3	7.1E-01	-1.1	2.3E-01
ENSMUST00000142316	chromatin assembly factor 1, subunit B (p60) [Source:MGI Symbol;Acc:MGI:1314881]	D3YTP6		5.1	1.7E-03	4.0	5.9E-03	-2.2	1.2E-01	-0.1	9.1E-01
ENSMUST00000122358	transmembrane 9 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1921390]		Q9DBU0	2.2	2.8E-01	3.8	8.2E-02	-0.5	7.8E-01	-2.1	2.7E-01
ENSMUST00000122359	actin filament associated protein 1-like 2 [Source:MGI Symbol;Acc:MGI:2147658]			4.8	7.3E-02	3.2	1.8E-01	-4.2	1.3E-01	-2.6	1.4E-01
ENSMUST00000142324	gelsolin [Source:MGI Symbol;Acc:MGI:95851]	A6PWS5		-5.0	1.4E-03	-3.6	8.0E-04	-0.9	5.2E-02	-1.3	1.3E-01
ENSMUST00000122364				-2.2	8.2E-02	-5.1	2.8E-02	-1.1	3.6E-01	1.9	3.2E-01
ENSMUST00000142331	RIKEN cDNA 0610007P14 gene [Source:MGI Symbol;Acc:MGI:1915571]	D3YUR8		4.1	2.3E-04	-4.8	3.9E-03	0.7	2.6E-01	-1.2	4.1E-01
ENSMUST00000142340	RIKEN cDNA 1110004E09 gene [Source:MGI Symbol;Acc:MGI:1915251]	D3YUI6		3.2	9.6E-03	5.4	4.5E-04	-1.3	2.6E-01	0.1	9.0E-01
ENSMUST00000122375	golgi autoantigen, golgin subfamily a, 7B [Source:MGI Symbol;Acc:MGI:1918396]		Q9D428	4.7	1.9E-01	5.3	1.9E-01	-0.1	9.8E-01	-0.8	7.4E-01
ENSMUST00000142378	RAS protein-specific guanine nucleotide-releasing factor 2 [Source:MGI Symbol;Acc:MGI:109137]	F6TYF8		6.5	6.3E-06	5.1	1.7E-04	-1.3	1.3E-01	-0.3	5.8E-01
ENSMUST00000142385	MLX interacting protein-like [Source:MGI Symbol;Acc:MGI:1927999]			7.8	5.2E-05	4.7	6.7E-03	-0.1	9.7E-01	-0.3	7.7E-01
ENSMUST00000122383	glycerol kinase 5 (putative) [Source:MGI Symbol;Acc:MGI:2443336]		Q8BX05	0.5	3.3E-01	1.5	8.4E-02	1.3	5.9E-02	0.3	6.2E-01
ENSMUST00000122385				-2.3	5.7E-02	-0.1	9.5E-01	1.8	1.2E-01	-0.4	7.9E-01
ENSMUST00000142388	C-type lectin domain family 2, member g [Source:MGI Symbol;Acc:MGI:1918059]	F5CSM6	Q9D676	7.6	1.6E-04	6.9	2.2E-04	-0.6	6.5E-01	-0.4	5.6E-01
ENSMUST00000122387	zinc finger protein 30 [Source:MGI Symbol;Acc:MGI:99178]	D3Z614		3.7	7.4E-02	5.9	1.0E-02	-0.7	7.2E-01	-2.9	4.9E-02
ENSMUST00000142396	interleukin 9 receptor [Source:MGI Symbol;Acc:MGI:96564]	B7ZD65		5.9	5.2E-03	7.8	7.2E-05	-0.1	9.4E-01	-1.1	9.5E-02
ENSMUST00000142407	ubiquitin-conjugating enzyme E2K [Source:MGI Symbol;Acc:MGI:1858216]	Q6ZWQ6	P61087	2.1	4.7E-03	6.6	3.1E-05	0.2	7.9E-01	0.3	5.0E-01
ENSMUST00000142424	mitochondrial ribosomal protein L3 [Source:MGI Symbol;Acc:MGI:2137204]	D6RI16		-5.8	4.5E-05	6.4	2.3E-04	-0.5	6.7E-01	-0.8	2.2E-01
ENSMUST00000142434	matrix metallopeptidase 16 [Source:MGI Symbol;Acc:MGI:1276107]	B1AVG8		10.5	4.1E-05	6.1	1.2E-03	-0.4	7.6E-01	-2.7	9.1E-03
ENSMUST00000142465	Rho GTPase activating protein 23 [Source:MGI Symbol;Acc:MGI:3697726]	D6RDB5		-6.1	2.5E-03	7.8	1.1E-04	0.4	7.5E-01	-0.5	4.5E-01
ENSMUST00000142472	testicular cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1923120]	Q9D4R6		6.9	1.6E-04	4.5	2.4E-03	-1.8	1.3E-01	0.1	9.3E-01
ENSMUST00000142475	cadherin 8 [Source:MGI Symbol;Acc:MGI:107434]	E9PZC1		6.8	6.3E-05	2.4	1.4E-02	-0.3	6.5E-01	-0.2	7.3E-01
ENSMUST00000122409	low density lipoprotein receptor-related protein 3 [Source:MGI Symbol;Acc:MGI:3584516]	E9Q1T6		4.9	7.1E-02	5.3	5.5E-02	-2.0	4.8E-01	-2.4	1.4E-01
ENSMUST00000142500	solute carrier family 2 (facilitated glucose transporter), member 4 [Source:MGI Symbol;Acc:MGI:95758]	A0A0G2JDD0		4.9	8.4E-03	-5.7	1.2E-03	1.0	5.5E-02	-1.0	4.9E-01
ENSMUST00000122412	protein tyrosine phosphatase, non-receptor type 2 [Source:MGI Symbol;Acc:MGI:97806]		Q06180	-1.3	7.9E-02	-0.3	6.9E-01	0.0	9.9E-01	-1.0	2.2E-01
ENSMUST00000122415				2.0	5.0E-02	0.4	7.6E-01	-0.6	5.3E-01	1.1	2.9E-01
ENSMUST00000122421	centriole, cilia and spindle associated protein [Source:MGI Symbol;Acc:MGI:1920670]		Q8QZT2	-0.8	5.9E-01	1.9	3.6E-01	1.1	5.4E-01	-1.6	3.1E-01
ENSMUST00000122422				3.0	2.9E-01	2.2	4.2E-01	-2.4	3.9E-01	-1.6	4.9E-01
ENSMUST00000122423	sialic acid binding Ig-like lectin F [Source:MGI Symbol;Acc:MGI:2681107]		Q920G3	-0.2	9.2E-01	-0.9	7.4E-01	-1.5	4.6E-01	-0.9	7.4E-01
ENSMUST00000142585	proline-rich nuclear receptor coactivator 2 [Source:MGI Symbol;Acc:MGI:106512]	Z4YMU7		-4.9	3.8E-03	-3.7	4.1E-03	0.4	3.9E-01	-2.3	8.8E-02
ENSMUST00000142594	mitochondrial pyruvate carrier 1 [Source:MGI Symbol;Acc:MGI:1915240]	E9Q0V4		2.7	1.8E-02	4.2	2.3E-03	0.4	6.7E-01	-0.4	5.9E-01
ENSMUST00000142597	protein phosphatase 5, catalytic subunit [Source:MGI Symbol;Acc:MGI:102666]	F7BX26		-4.1	1.4E-03	2.8	1.0E-01	-0.7	6.2E-01	3.7	1.3E-02
ENSMUST00000122433				2.2	4.4E-02	2.9	2.2E-02	-0.6	5.6E-01	-1.3	1.7E-01
ENSMUST00000142615	integrin alpha FG-GAP repeat containing 2 [Source:MGI Symbol;Acc:MGI:1915450]	Q3TWL5		6.9	6.2E-04	9.8	1.4E-04	-1.0	5.8E-01	1.2	1.2E-01
ENSMUST00000122440	RIKEN cDNA 2610015P09 gene [Source:MGI Symbol;Acc:MGI:1922661]	F7D3E1		2.2	2.5E-01	2.8	4.2E-01	2.2	4.2E-01	1.6	5.1E-01
ENSMUST00000142618	sphingomyelin synthase 1 [Source:MGI Symbol;Acc:MGI:2444110]		Q8VCQ6	5.1	8.3E-05	-2.0	7.7E-02	0.7	2.4E-01	0.6	5.8E-01
ENSMUST00000142624	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B [Source:MGI Symbol;Acc:MGI:2442593]	F6RIR5		-7.5	5.6E-03	4.8	1.3E-02	-0.6	7.2E-01	0.1	8.8E-01
ENSMUST00000122456	RNA binding motif protein 18 [Source:MGI Symbol;Acc:MGI:1915139]	B0R043		-0.5	7.9E-01	-3.6	2.3E-01	-1.8	2.8E-01	1.3	6.4E-01
ENSMUST00000142659	Gem-interacting protein [Source:MGI Symbol;Acc:MGI:1926066]	F7AIU6		3.1	3.4E-04	6.6	2.0E-04	-0.5	6.8E-01	-0.7	2.6E-01
ENSMUST00000142664	purinergic receptor P2X, ligand-gated ion channel 4 [Source:MGI Symbol;Acc:MGI:1338859]	D3Z5U5		-3.5	3.2E-03	6.1	8.5E-04	-0.7	6.3E-01	-0.5	5.3E-01
ENSMUST00000142679	sarcolemma associated protein [Source:MGI Symbol;Acc:MGI:1933549]	F6UV57		-4.9	1.4E-02	6.9	1.0E-03	-0.7	6.5E-01	-1.5	1.0E-01
ENSMUST00000142680	adaptor-related protein complex 2, beta 1 subunit [Source:MGI Symbol;Acc:MGI:1919020]	Q5SWR0		4.5	1.1E-03	-2.9	3.1E-02	0.6	3.5E-01	0.0	9.9E-01
ENSMUST00000142681	ATPase type 13A5 [Source:MGI Symbol;Acc:MGI:2444068]	D6RHM2		5.6	2.8E-02	7.5	1.0E-04	-0.6	6.1E-01	-0.2	7.2E-01
ENSMUST00000122809				2.2	1.9E-01	3.0	1.5E-01	-0.8	6.6E-01	-1.7	2.7E-01
ENSMUST00000142682	intraflagellar transport 57 [Source:MGI Symbol;Acc:MGI:1921166]			-3.8	2.3E-04	-3.2	9.1E-03	-0.5	3.6E-01	-1.4	2.3E-01
ENSMUST00000142688	low density lipoprotein-related protein 1B (deleted in tumors) [Source:MGI Symbol;Acc:MGI:2151136]			6.8	4.9E-05	-4.7	6.0E-03	1.7	1.2E-02	-0.9	5.6E-01
ENSMUST00000142692	harbinger transposase derived 1 [Source:MGI Symbol;Acc:MGI:2443194]		Q8BR93	4.3	6.3E-05	5.4	5.1E-04	-0.5	5.9E-01	-0.1	8.2E-01
ENSMUST00000142729	myeloblastosis oncogene-like 2 [Source:MGI Symbol;Acc:MGI:101785]	A2A5P3		2.6	4.4E-03	7.3	5.3E-05	2.9	1.4E-02	-0.4	4.7E-01
ENSMUST00000142734	lectin, galactose binding, soluble 3 [Source:MGI Symbol;Acc:MGI:96778]	Q8C253		-5.5	1.1E-03	5.8	3.4E-04	-0.5	6.7E-01	0.8	1.9E-01
ENSMUST00000122828				5.6	8.9E-02	5.4	2.0E-01	0.9	8.2E-01	1.1	6.4E-01
ENSMUST00000142742	nitric oxide synthase 1, neuronal [Source:MGI Symbol;Acc:MGI:97360]		Q9Z0J4	10.9	6.2E-07	5.4	6.2E-04	-1.2	2.9E-01	0.4	5.7E-01
ENSMUST00000142766	prokineticin receptor 2 [Source:MGI Symbol;Acc:MGI:2181363]	E0CY28		8.4	3.1E-05	4.6	8.0E-02	1.1	6.5E-01	2.2	1.8E-01
ENSMUST00000122835	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative) [Source:MGI Symbol;Acc:MGI:2142075]			-1.8	1.2E-01	-3.7	4.7E-02	-1.1	2.1E-01	0.8	6.1E-01
ENSMUST00000122841	methyl-CpG binding domain protein 5 [Source:MGI Symbol;Acc:MGI:2138934]	F6Q8U1		-1.7	2.2E-01	-2.1	2.9E-01	0.7	5.8E-01	1.1	5.4E-01
ENSMUST00000142772	paired box 6 [Source:MGI Symbol;Acc:MGI:97490]	V9GXI6		7.0	8.7E-04	7.1	1.4E-04	-0.6	6.1E-01	-1.0	1.3E-01
ENSMUST00000142783	coiled-coil domain containing 13 [Source:MGI Symbol;Acc:MGI:1920144]	Q8BYN7		5.8	3.6E-04	4.3	2.8E-03	1.0	3.3E-01	-0.5	4.9E-01
ENSMUST00000142788	elongator acetyltransferase complex subunit 5 [Source:MGI Symbol;Acc:MGI:1859017]	J3QJV1		-5.2	1.1E-04	4.8	5.9E-04	0.2	8.0E-01	-0.4	4.9E-01
ENSMUST00000142808	dehydrogenase/reductase (SDR family) member 3 [Source:MGI Symbol;Acc:MGI:1315215]	B1ARS9		-3.0	1.4E-02	-1.7	2.9E-01	0.4	7.1E-01	-1.6	3.3E-01
ENSMUST00000142843	shisa family member 3 [Source:MGI Symbol;Acc:MGI:3041225]	S4R2D4		3.3	5.9E-03	-1.8	3.1E-02	0.8	8.7E-02	0.3	6.8E-01
ENSMUST00000142876	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide [Source:MGI Symbol;Acc:MGI:2448506]	D6RJ66		3.2	2.6E-03	4.9	1.9E-03	0.1	9.3E-01	1.4	1.0E-01
ENSMUST00000142890	tetraspanin 5 [Source:MGI Symbol;Acc:MGI:1928096]	Q05BH2		-2.8	5.9E-04	7.7	1.2E-02	-0.9	7.5E-01	-2.2	1.6E-01
ENSMUST00000142893	chemokine (C-X-C motif) receptor 4 [Source:MGI Symbol;Acc:MGI:109563]	E9Q2D4		-6.7	7.6E-06	3.8	1.5E-02	-0.8	4.8E-01	0.5	6.1E-01
ENSMUST00000142917	protein tyrosine phosphatase, receptor type, G [Source:MGI Symbol;Acc:MGI:97814]	D6RD11		8.0	1.6E-04	4.3	2.8E-04	-2.4	1.6E-02	-0.3	5.7E-01
ENSMUST00000142934	vomeronasal 2, receptor 42 [Source:MGI Symbol;Acc:MGI:1316666]	D3YZ97		7.7	2.0E-05	4.0	1.9E-02	-1.7	2.7E-01	0.0	9.7E-01
ENSMUST00000142957	phosphatidylserine decarboxylase [Source:MGI Symbol;Acc:MGI:2445114]	D6RIN9		-3.9	2.3E-02	-4.9	3.7E-03	0.5	3.9E-01	-2.2	1.7E-01
ENSMUST00000142977	ankyrin repeat and KH domain containing 1 [Source:MGI Symbol;Acc:MGI:1921733]	E9Q1M6		-3.7	3.5E-02	-5.2	8.6E-02	0.5	6.4E-01	0.5	8.6E-01
ENSMUST00000143035	solute carrier family 43, member 2 [Source:MGI Symbol;Acc:MGI:2442746]	Q5ND24		3.5	5.4E-03	2.2	2.6E-03	-2.1	2.2E-03	0.0	9.1E-01
ENSMUST00000122889				-3.1	4.7E-02	-4.3	4.1E-02	-0.8	3.8E-01	0.5	7.9E-01
ENSMUST00000143057	N-acylsphingosine amidohydrolase 1 [Source:MGI Symbol;Acc:MGI:1277124]	D3Z505		4.6	3.3E-03	6.0	1.4E-04	-1.6	1.4E-01	0.3	5.5E-01
ENSMUST00000143074	predicted gene 42669 [Source:MGI Symbol;Acc:MGI:5662806]	F7CG54		10.2	3.7E-07	5.2	7.0E-03	0.9	5.2E-01	-0.3	7.5E-01
ENSMUST00000143082	serum amyloid A-like 1 [Source:MGI Symbol;Acc:MGI:1926185]	G1UCX4	Q9D2C2	2.3	4.4E-03	-0.9	4.9E-01	1.2	1.6E-01	-1.1	3.7E-01
ENSMUST00000143083	predicted gene 10721 [Source:MGI Symbol;Acc:MGI:3641688]	J3QPJ9		16.4	1.2E-06	4.9	2.6E-02	-0.1	9.7E-01	1.3	2.6E-01
ENSMUST00000143101	ATPase, H+ transporting, lysosomal V1 subunit F [Source:MGI Symbol;Acc:MGI:1913394]	F7B2B4		5.0	8.4E-03	6.4	1.1E-05	-0.4	5.8E-01	1.2	2.6E-02
ENSMUST00000122903				0.6	7.9E-01	2.3	4.9E-01	0.4	8.6E-01	-1.2	6.7E-01
ENSMUST00000122905				-1.4	5.2E-01	-1.8	5.4E-01	0.5	8.1E-01	1.0	7.1E-01
ENSMUST00000143107	ribosomal protein L27A [Source:MGI Symbol;Acc:MGI:1347076]		P14115	-3.8	2.0E-04	8.4	9.0E-07	-1.0	2.0E-01	-0.7	8.0E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000143142	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B [Source:MGI Symbol;Acc:MGI:2442593]	F6WNG1		-9.1	2.8E-03	5.7	5.7E-04	-1.4	2.7E-01	-0.8	2.5E-01
ENSMUST00000143154	transmembrane protein 82 [Source:MGI Symbol;Acc:MGI:2384869]	F2Z3W9		6.3	2.3E-05	7.3	1.3E-05	-2.1	5.4E-02	0.2	6.3E-01
ENSMUST00000143170	large subunit GTPase 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:107236]	D6RFS1		-5.8	3.4E-05	-5.1	7.0E-03	0.9	1.5E-01	0.1	9.3E-01
ENSMUST00000122916	transmembrane protein 106B [Source:MGI Symbol;Acc:MGI:1919150]	D3Z191		-1.5	6.2E-02	-1.3	2.2E-01	0.4	5.7E-01	0.2	8.3E-01
ENSMUST00000143176	CDC42 binding protein kinase alpha [Source:MGI Symbol;Acc:MGI:2441841]	F6S5Z6		3.9	3.7E-04	7.0	4.8E-04	-0.5	7.2E-01	0.8	3.0E-01
ENSMUST00000143203	syntaxin binding protein 4 [Source:MGI Symbol;Acc:MGI:1342296]		Q9WV89	6.0	1.9E-05	-3.7	9.9E-02	0.3	7.5E-01	-0.1	9.6E-01
ENSMUST00000143214	peptidylprolyl isomerase (cyclophilin)-like 4 [Source:MGI Symbol;Acc:MGI:1914668]	D6RJ77		5.2	2.2E-04	7.2	1.6E-02	-0.8	7.6E-01	-1.6	2.9E-01
ENSMUST00000122924	nudix (nucleoside diphosphate linked moiety X)-type motif 8 [Source:MGI Symbol;Acc:MGI:1913637]	D3Z5H8		1.3	1.2E-01	0.8	4.7E-01	0.6	4.8E-01	1.1	2.7E-01
ENSMUST00000143219	phosphatidylinositol transfer protein, alpha [Source:MGI Symbol;Acc:MGI:99887]	Q5ND42	P53810	-7.9	7.2E-06	5.8	2.2E-04	0.3	7.3E-01	-2.0	1.0E-02
ENSMUST00000143223	phenylalkylamine Ca2+ antagonist (emopamil) binding protein [Source:MGI Symbol;Acc:MGI:107822]	A2AC29		-4.9	1.8E-04	-1.8	8.9E-02	-0.5	4.4E-01	-0.9	3.7E-01
ENSMUST00000122932				3.5	1.2E-01	5.9	5.2E-02	0.6	8.3E-01	-1.9	3.2E-01
ENSMUST00000143238	RIKEN cDNA 1500009C09 gene [Source:MGI Symbol;Acc:MGI:1923755]	D3YWK9		6.6	8.5E-05	-2.8	7.8E-04	0.5	1.6E-01	-0.3	5.7E-01
ENSMUST00000143251	cytochrome b-561 [Source:MGI Symbol;Acc:MGI:103253]	A2A685		5.7	6.6E-04	2.3	3.5E-01	-2.3	3.9E-01	1.1	5.1E-01
ENSMUST00000122950				-1.2	2.7E-01	-0.7	6.8E-01	0.9	4.3E-01	0.3	8.5E-01
ENSMUST00000143254	supervillin [Source:MGI Symbol;Acc:MGI:2147319]	E9Q983		-6.8	5.9E-05	5.7	1.7E-04	0.7	4.4E-01	0.0	9.6E-01
ENSMUST00000143288	glucosidase, alpha, acid [Source:MGI Symbol;Acc:MGI:95609]	F6R5R5		4.4	8.5E-03	-5.5	7.4E-02	4.3	2.2E-03	0.6	8.4E-01
ENSMUST00000143304	galactose-4-epimerase, UDP [Source:MGI Symbol;Acc:MGI:1921496]	B1AV53		2.5	2.5E-02	1.0	5.3E-01	-3.5	6.9E-02	0.9	5.1E-01
ENSMUST00000143314	NOL1/NOP2/Sun domain family member 3 [Source:MGI Symbol;Acc:MGI:2146565]	D6RDT7		2.6	1.2E-02	5.7	5.3E-03	-0.2	9.2E-01	-0.2	8.7E-01
ENSMUST00000143359	ATPase, class VI, type 11A [Source:MGI Symbol;Acc:MGI:1354735]	F6Z063		-5.2	9.8E-04	6.7	4.3E-04	-0.2	8.8E-01	1.4	7.7E-02
ENSMUST00000143380	aldehyde dehydrogenase 3 family, member B2 [Source:MGI Symbol;Acc:MGI:2147613]	E9Q3E1		5.0	2.5E-05	2.2	3.6E-02	-0.3	7.0E-01	0.3	7.2E-01
ENSMUST00000143393	PDZ and LIM domain 2 [Source:MGI Symbol;Acc:MGI:2384850]	E9Q996		-5.4	3.5E-04	6.2	9.3E-05	-1.9	9.9E-02	0.3	6.1E-01
ENSMUST00000143419	RIKEN cDNA 2310007B03 gene [Source:MGI Symbol;Acc:MGI:1919124]		Q8CEZ4	6.0	2.8E-02	-0.6	5.8E-01	1.3	1.2E-01	-1.7	2.0E-01
ENSMUST00000143424	sirtuin 6 [Source:MGI Symbol;Acc:MGI:1354161]	D3YY89		4.0	5.9E-03	6.8	3.1E-04	-0.7	6.0E-01	1.3	7.8E-02
ENSMUST00000122986				-1.6	1.8E-01	2.1	1.6E-01	1.6	2.2E-01	-2.1	9.2E-02
ENSMUST00000122989				-1.6	3.2E-01	-1.4	4.9E-01	0.3	8.1E-01	0.2	9.3E-01
ENSMUST00000143432	collagen, type XVI, alpha 1 [Source:MGI Symbol;Acc:MGI:1095396]	E9Q0X4		7.1	4.6E-04	1.0	3.2E-01	-4.3	5.0E-03	-0.4	6.9E-01
ENSMUST00000143467	plasminogen receptor, C-terminal lysine transmembrane protein [Source:MGI Symbol;Acc:MGI:1915009]		Q9D3P8	-5.0	6.4E-04	4.8	1.8E-03	-1.2	2.9E-01	1.0	2.1E-01
ENSMUST00000143495	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	E9PWM7		-8.9	3.0E-05	-3.0	1.3E-02	0.7	2.3E-01	-2.1	1.2E-01
ENSMUST00000143514	ADP-ribosylation factor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1277120]	G5E8V9		-4.4	3.7E-03	4.3	3.7E-02	-0.9	6.5E-01	0.1	9.5E-01
ENSMUST00000143521	glucose-6-phosphate dehydrogenase X-linked [Source:MGI Symbol;Acc:MGI:105979]	A3KG36		-6.2	3.4E-02	-3.9	3.2E-02	-0.5	5.6E-01	-0.5	7.4E-01
ENSMUST00000143522	lipase, member O4 [Source:MGI Symbol;Acc:MGI:3779637]	F6RR30		4.3	2.7E-02	-5.4	5.3E-03	1.4	5.8E-02	-3.0	1.4E-01
ENSMUST00000143533	small nuclear RNA activating complex, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1916338]		Q9D2C9	-3.1	7.5E-03	8.6	9.0E-05	-0.8	5.9E-01	0.3	6.3E-01
ENSMUST00000123019				-1.0	1.4E-01	-0.5	5.5E-01	-0.3	6.1E-01	-0.8	3.1E-01
ENSMUST00000143537	N(alpha)-acetyltransferase 60, NatF catalytic subunit [Source:MGI Symbol;Acc:MGI:1922013]	H3BJZ6		-3.2	2.3E-02	3.3	1.4E-03	0.1	9.3E-01	-0.8	2.0E-01
ENSMUST00000143540	dedicator of cyto-kinesis 2 [Source:MGI Symbol;Acc:MGI:2149010]	D6RGU3		3.7	2.7E-03	3.4	3.3E-03	0.3	7.2E-01	-0.9	1.9E-01
ENSMUST00000143561	chitinase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915288]	D3YWG2		-3.0	2.4E-03	4.8	5.2E-03	-0.8	5.5E-01	-1.3	1.6E-01
ENSMUST00000143563	cat eye syndrome chromosome region, candidate 2 [Source:MGI Symbol;Acc:MGI:1923799]	F7B218		7.0	1.0E-03	4.2	3.3E-02	-3.6	9.7E-02	-3.1	3.3E-02
ENSMUST00000123029				3.7	6.4E-02	3.2	1.4E-01	-1.2	5.5E-01	-0.6	7.0E-01
ENSMUST00000143567	ATPase, Ca++ transporting, plasma membrane 4 [Source:MGI Symbol;Acc:MGI:88111]	Q6Q477		5.0	2.3E-06	6.3	1.0E-04	0.6	5.1E-01	-0.4	4.8E-01
ENSMUST00000143600	Sin3-associated polypeptide 18 [Source:MGI Symbol;Acc:MGI:1277978]	D3Z2N9		-6.9	7.9E-04	4.0	1.2E-04	0.0	9.5E-01	0.2	6.0E-01
ENSMUST00000123033				-3.4	2.4E-01	0.4	9.1E-01	2.3	3.1E-01	-1.5	6.3E-01
ENSMUST00000143616	coenzyme Q4 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1098826]	D6RJJ8		5.3	1.1E-04	5.8	2.8E-05	-0.9	2.5E-01	0.4	3.4E-01
ENSMUST00000143637	tripartite motif-containing 46 [Source:MGI Symbol;Acc:MGI:2673000]	E9PUI3		5.6	2.7E-02	-2.6	6.3E-02	-0.5	4.6E-01	-0.2	8.6E-01
ENSMUST00000123052				-1.7	1.2E-01	-1.3	3.7E-01	0.1	9.3E-01	-0.4	7.8E-01
ENSMUST00000123054				-2.3	3.5E-02	-1.5	2.6E-01	0.5	5.1E-01	-0.3	8.0E-01
ENSMUST00000143663	maestro heat-like repeat family member 8 [Source:MGI Symbol;Acc:MGI:3603828]	E9PYI4		6.3	4.6E-05	5.3	2.3E-03	1.2	3.3E-01	-1.3	1.3E-01
ENSMUST00000143682	negative regulator of reactive oxygen species [Source:MGI Symbol;Acc:MGI:2445095]		Q8BMT4	7.6	8.1E-03	7.6	5.1E-04	0.6	6.5E-01	1.1	1.5E-01
ENSMUST00000143693	lectin, galactose binding, soluble 8 [Source:MGI Symbol;Acc:MGI:1928481]	Q8C6H0		-6.2	2.5E-02	6.2	6.2E-03	0.8	6.5E-01	0.0	9.8E-01
ENSMUST00000143700	signal peptide peptidase like 2A [Source:MGI Symbol;Acc:MGI:1913802]	F6RJQ8		-6.8	2.3E-05	6.6	1.6E-02	-0.7	7.8E-01	-1.4	3.2E-01
ENSMUST00000143709	Fanconi anemia core complex associated protein 20 [Source:MGI Symbol;Acc:MGI:1914763]	F6QQ55		-3.8	1.4E-02	6.7	2.2E-04	-0.1	9.2E-01	-0.2	7.8E-01
ENSMUST00000143721	platelet-derived growth factor, C polypeptide [Source:MGI Symbol;Acc:MGI:1859631]	D6RGS6		7.1	1.5E-05	6.0	4.8E-04	-0.2	8.8E-01	-1.6	4.0E-02
ENSMUST00000143764	fibrous sheath-interacting protein 2 [Source:MGI Symbol;Acc:MGI:2664111]		A2ARZ3	8.8	9.8E-06	4.6	6.9E-03	1.6	2.2E-01	-0.7	4.2E-01
ENSMUST00000123080				0.8	2.6E-01	1.8	5.2E-02	0.3	6.5E-01	-0.7	3.4E-01
ENSMUST00000123082	testis specific 10 [Source:MGI Symbol;Acc:MGI:2685063]	Q3TR21		0.6	3.1E-01	2.0	3.2E-02	1.8	2.0E-02	0.5	4.8E-01
ENSMUST00000123085				-2.7	5.1E-02	1.1	5.0E-01	1.7	1.9E-01	-2.1	1.6E-01
ENSMUST00000143780	cathepsin A [Source:MGI Symbol;Acc:MGI:97748]	A2A5J9		-7.5	8.1E-06	3.6	2.3E-03	-0.7	3.9E-01	0.1	8.8E-01
ENSMUST00000143783	LIM homeobox protein 2 [Source:MGI Symbol;Acc:MGI:96785]	F6Z9H5		4.7	5.1E-03	6.7	8.1E-05	-1.5	2.1E-01	-0.5	3.8E-01
ENSMUST00000123093				0.5	5.0E-01	0.3	7.5E-01	-0.2	7.4E-01	0.0	9.8E-01
ENSMUST00000123096				-3.0	7.7E-02	-2.3	2.1E-01	-0.5	6.0E-01	-1.2	5.3E-01
ENSMUST00000143789	predicted gene 21981 [Source:MGI Symbol;Acc:MGI:5439450]	D3Z6Q6		6.3	2.4E-04	-4.9	1.2E-01	1.7	2.6E-01	-0.8	8.0E-01
ENSMUST00000123109				3.2	9.4E-02	1.4	4.4E-01	-1.8	3.2E-01	0.0	1.0E+00
ENSMUST00000123111				-2.5	1.1E-01	-2.2	2.0E-01	-0.8	5.0E-01	-1.1	5.5E-01
ENSMUST00000143791	bicaudal C homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1933388]		Q99MQ1	6.4	1.7E-04	4.3	3.9E-02	-0.8	6.7E-01	2.7	5.7E-02
ENSMUST00000123115				-0.9	2.7E-01	-0.7	5.5E-01	0.5	5.5E-01	0.3	8.1E-01
ENSMUST00000143829	SLAIN motif family, member 2 [Source:MGI Symbol;Acc:MGI:1923241]		Q8CI08	-3.7	8.8E-04	6.1	3.3E-03	-0.6	7.1E-01	0.5	6.0E-01
ENSMUST00000123128	myosin VA [Source:MGI Symbol;Acc:MGI:105976]		Q99104	0.5	1.9E-01	1.2	3.8E-02	0.8	9.4E-02	0.1	9.1E-01
ENSMUST00000143868	lysine (K)-specific demethylase 1B [Source:MGI Symbol;Acc:MGI:2145261]	D3Z353		5.1	2.0E-02	3.2	3.0E-02	-0.3	8.2E-01	0.3	7.2E-01
ENSMUST00000143916	CUGBP, Elav-like family member 6 [Source:MGI Symbol;Acc:MGI:1923433]	D6RHP1		7.6	2.3E-05	4.2	3.4E-02	-1.4	4.6E-01	0.4	7.5E-01
ENSMUST00000143920	discs, large homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1277959]	J3QMR8		9.3	3.3E-04	5.1	7.9E-03	-0.7	6.5E-01	0.3	7.6E-01
ENSMUST00000143971	mitochondrial inner membrane organizing system 1 [Source:MGI Symbol;Acc:MGI:1913628]		Q7TNS2	-2.3	2.6E-04	6.8	6.6E-03	-1.8	4.2E-01	1.3	2.3E-01
ENSMUST00000123154				0.3	7.4E-01	5.5	2.4E-03	4.5	5.3E-03	-0.8	3.5E-01
ENSMUST00000143977	calmodulin regulated spectrin-associated protein 1 [Source:MGI Symbol;Acc:MGI:3036242]	V9GXD7		-3.1	2.3E-02	5.1	6.6E-04	0.1	9.3E-01	-0.8	2.3E-01
ENSMUST00000143984	TBC1 domain family, member 25 [Source:MGI Symbol;Acc:MGI:2444862]	S4R2S6		-5.3	1.3E-04	6.4	4.3E-04	0.9	4.4E-01	-0.3	6.9E-01
ENSMUST00000123170	cyclin-dependent kinase 9 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1328368]	D6RGN3		-1.9	4.1E-01	-2.9	3.1E-01	-1.1	5.1E-01	-0.1	9.8E-01
ENSMUST00000123172				-1.1	3.3E-01	-0.4	8.0E-01	1.0	3.9E-01	0.3	8.5E-01
ENSMUST00000123174				-0.2	8.7E-01	-1.1	3.4E-01	-1.0	2.7E-01	0.0	9.8E-01
ENSMUST00000123176	centrobin, centrosomal BRCA2 interacting protein [Source:MGI Symbol;Acc:MGI:2443290]	D6RGB4		2.8	3.2E-01	0.6	8.2E-01	-2.9	2.9E-01	-0.6	8.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000123177				-1.7	1.3E-01	-4.6	2.2E-03	-4.1	1.6E-04	-1.3	3.3E-01
ENSMUST00000143987	NADH dehydrogenase (ubiquinone) flavoprotein 2 [Source:MGI Symbol;Acc:MGI:1920150]		Q9D6J6	-4.5	2.2E-03	3.1	5.2E-03	0.8	3.1E-01	-0.6	4.4E-01
ENSMUST00000143997	phospholipase C, gamma 1 [Source:MGI Symbol;Acc:MGI:97615]	F6SLL0		3.4	1.7E-03	3.0	8.0E-03	-2.4	2.4E-02	-2.3	1.6E-02
ENSMUST00000123183				-0.9	4.7E-01	1.7	1.7E-01	0.0	9.8E-01	-2.5	6.1E-02
ENSMUST00000144028	dehydrogenase/reductase (SDR family) member 13 [Source:MGI Symbol;Acc:MGI:1917701]	D6RDR9		-4.0	8.5E-03	2.5	3.3E-02	-0.1	9.1E-01	0.2	8.0E-01
ENSMUST00000144041	metastasis suppressor 1-like [Source:MGI Symbol;Acc:MGI:3039591]	D3YWC9		9.0	1.0E-05	5.2	7.8E-02	-0.3	9.1E-01	2.8	1.3E-01
ENSMUST00000144068	solute carrier family 9 (sodium/hydrogen exchanger), member 6 [Source:MGI Symbol;Acc:MGI:2443511]	D3Z0Q9		-2.8	1.2E-02	-1.3	1.2E-01	1.4	1.8E-02	-3.9	4.1E-03
ENSMUST00000144070	mitochondrial ribosomal protein S23 [Source:MGI Symbol;Acc:MGI:1928138]	F7ARZ1		-4.8	1.3E-04	7.7	8.1E-05	0.5	6.8E-01	0.3	6.1E-01
ENSMUST00000144086	neutrophil cytosolic factor 1 [Source:MGI Symbol;Acc:MGI:97283]	S4R293		-3.3	2.8E-02	5.4	6.0E-04	-0.5	6.4E-01	-0.3	6.9E-01
ENSMUST00000123196	interferon (alpha and beta) receptor 1 [Source:MGI Symbol;Acc:MGI:107658]		P33896	-0.6	5.8E-01	-1.6	3.9E-01	0.2	8.3E-01	1.2	5.0E-01
ENSMUST00000144088	acyl-Coenzyme A binding domain containing 5 [Source:MGI Symbol;Acc:MGI:1921409]	Z4YN06		5.0	3.2E-03	5.4	2.2E-03	-1.4	3.4E-01	-1.4	1.3E-01
ENSMUST00000144099	CDK5 regulatory subunit associated protein 2 [Source:MGI Symbol;Acc:MGI:2384875]		Q8K389	4.9	3.4E-05	6.5	1.5E-04	-1.6	2.0E-01	0.1	8.1E-01
ENSMUST00000144120	tubulin tyrosine ligase [Source:MGI Symbol;Acc:MGI:1916987]	F6ZXS5		6.7	7.1E-05	6.4	3.5E-02	0.8	7.5E-01	-0.5	7.3E-01
ENSMUST00000144153	ubiquitin specific peptidase 36 [Source:MGI Symbol;Acc:MGI:1919594]	B0QZF8		6.6	1.3E-02	8.0	8.5E-05	0.8	4.9E-01	0.7	2.4E-01
ENSMUST00000144177	alcohol dehydrogenase, iron containing, 1 [Source:MGI Symbol;Acc:MGI:1923437]		Q8R0N6	6.8	5.6E-05	6.6	1.9E-02	-0.6	8.0E-01	-1.4	3.2E-01
ENSMUST00000123211				-2.4	1.4E-01	-1.9	3.0E-01	-0.2	8.6E-01	-0.7	6.9E-01
ENSMUST00000123219				-0.5	6.5E-01	0.6	6.8E-01	0.6	6.3E-01	-0.5	6.7E-01
ENSMUST00000144195	ubiquitin-like modifier activating enzyme 5 [Source:MGI Symbol;Acc:MGI:1913913]	F6VRI6		-2.3	1.6E-02	5.9	4.7E-04	-0.5	6.7E-01	-0.7	2.7E-01
ENSMUST00000123225	pleckstrin homology domain containing, family M, member 3 [Source:MGI Symbol;Acc:MGI:2443627]	D3Z0F2		2.3	1.2E-01	4.1	1.2E-02	-0.8	5.4E-01	-2.7	3.4E-02
ENSMUST00000144211	serine/arginine repetitive matrix 3 [Source:MGI Symbol;Acc:MGI:1920309]		Q80WV7	8.4	2.1E-05	7.1	1.9E-03	1.6	3.4E-01	0.4	6.7E-01
ENSMUST00000144216	phosphatidylinositol glycan anchor biosynthesis, class X [Source:MGI Symbol;Acc:MGI:1919334]	F7CUX5		2.9	7.6E-03	-0.3	7.2E-01	1.2	1.0E-01	-0.7	4.1E-01
ENSMUST00000144258	protein kinase N1 [Source:MGI Symbol;Acc:MGI:108022]		P70268	-7.4	4.0E-04	6.5	1.3E-04	-0.6	6.1E-01	-1.3	5.0E-02
ENSMUST00000144270	kit oncogene [Source:MGI Symbol;Acc:MGI:96677]	F7DD14	P05532	-7.0	2.3E-03	5.6	2.2E-03	-1.2	3.9E-01	-0.2	7.8E-01
ENSMUST00000123240				1.6	6.2E-02	2.6	2.4E-02	0.4	6.0E-01	-0.5	5.0E-01
ENSMUST00000144275	McKusick-Kaufman syndrome [Source:MGI Symbol;Acc:MGI:1891836]			-5.0	1.2E-03	0.2	9.4E-01	-1.7	3.5E-01	2.9	1.5E-01
ENSMUST00000123255				0.3	5.7E-01	-1.2	1.4E-01	-0.6	2.9E-01	0.9	2.1E-01
ENSMUST00000144276	breast carcinoma amplified sequence 3 [Source:MGI Symbol;Acc:MGI:2385848]	Q5SWI1		3.5	1.6E-02	4.9	3.3E-03	-1.0	4.7E-01	-0.2	8.4E-01
ENSMUST00000144283	lectin, galactose binding, soluble 8 [Source:MGI Symbol;Acc:MGI:1928481]	A8DIL0		-4.4	8.1E-04	6.2	1.9E-03	0.6	6.9E-01	0.3	7.1E-01
ENSMUST00000123262	small nuclear RNA activating complex, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1916338]		Q9D2C9	0.1	9.4E-01	0.7	6.8E-01	0.4	7.6E-01	-0.2	8.9E-01
ENSMUST00000144296	Eph receptor B4 [Source:MGI Symbol;Acc:MGI:104757]		P54761	6.4	9.9E-04	2.7	3.5E-02	-0.7	5.2E-01	0.2	8.2E-01
ENSMUST00000144326	RAN binding protein 9 [Source:MGI Symbol;Acc:MGI:1928741]	E9Q5D6		-4.4	7.0E-05	6.0	2.2E-03	-1.0	4.8E-01	-0.4	6.5E-01
ENSMUST00000144331	special AT-rich sequence binding protein 1 [Source:MGI Symbol;Acc:MGI:105084]		Q60611	-4.8	4.4E-04	-3.7	1.6E-02	0.9	1.6E-01	0.1	9.3E-01
ENSMUST00000123283	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	D6RFT8		2.5	4.9E-02	2.6	7.3E-02	-0.8	4.9E-01	-0.8	4.5E-01
ENSMUST00000144382	protein phosphatase 1, regulatory subunit 18 [Source:MGI Symbol;Acc:MGI:1923698]		Q8BQ30	-8.1	4.4E-05	7.8	9.6E-04	-0.3	8.6E-01	1.1	2.2E-01
ENSMUST00000144386	SRY (sex determining region Y)-box 13 [Source:MGI Symbol;Acc:MGI:98361]	D3Z7I3		2.0	1.2E-02	-3.6	3.0E-02	2.3	5.7E-03	-0.8	6.0E-01
ENSMUST00000144403	lysosomal-associated membrane protein family, member 5 [Source:MGI Symbol;Acc:MGI:1923411]	A2AT95		6.8	5.1E-04	5.8	3.6E-02	-0.8	7.5E-01	1.8	2.1E-01
ENSMUST00000144429	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]	F6XC15		-6.8	1.4E-02	6.8	7.1E-06	-0.2	8.1E-01	-0.2	7.1E-01
ENSMUST00000144472	crystallin, zeta (quinone reductase)-like 1 [Source:MGI Symbol;Acc:MGI:1913859]	F7BGV1		-3.4	9.3E-03	5.7	1.4E-03	-0.9	5.1E-01	-0.3	7.4E-01
ENSMUST00000144479	family with sequence similarity 179, member A [Source:MGI Symbol;Acc:MGI:2443498]	F6YU21		7.8	5.4E-05	-6.4	2.1E-03	1.1	5.2E-02	0.1	9.6E-01
ENSMUST00000123302	stromal antigen 1 [Source:MGI Symbol;Acc:MGI:1098658]	D6REF2		-0.2	9.5E-01	6.7	8.0E-02	4.7	1.4E-01	-2.2	4.7E-01
ENSMUST00000144531	N(alpha)-acetyltransferase 38, NatC auxiliary subunit [Source:MGI Symbol;Acc:MGI:1925554]		Q9D2U5	-5.0	3.3E-03	5.9	4.2E-03	-0.7	6.9E-01	0.1	9.4E-01
ENSMUST00000144550	thymoma viral proto-oncogene 1 [Source:MGI Symbol;Acc:MGI:87986]	D3YXX3		2.0	9.9E-03	-1.3	5.2E-01	2.9	3.6E-02	0.2	9.0E-01
ENSMUST00000123314				-1.7	1.7E-01	-2.7	1.6E-01	0.0	9.6E-01	1.0	5.9E-01
ENSMUST00000144559	speedy/RINGO cell cycle regulator family, member E4C [Source:MGI Symbol;Acc:MGI:2685201]	I6XKQ3		6.9	8.9E-05	-5.7	1.3E-03	0.2	7.1E-01	-0.8	5.5E-01
ENSMUST00000144574	anaphase promoting complex subunit 4 [Source:MGI Symbol;Acc:MGI:1098673]	D6RDT6		-6.2	1.0E-04	6.6	3.6E-05	-1.3	2.0E-01	0.5	3.1E-01
ENSMUST00000144576	ubiquitin-fold modifier conjugating enzyme 1 [Source:MGI Symbol;Acc:MGI:1913405]	M0QWS4		-3.2	1.3E-02	-8.8	2.4E-05	-0.8	3.3E-02	-1.0	4.3E-01
ENSMUST00000144578	zinc finger protein 128 [Source:MGI Symbol;Acc:MGI:2389445]	Q8BGV5		2.4	5.2E-03	7.3	7.1E-05	-0.5	6.7E-01	-1.1	9.3E-02
ENSMUST00000123323				3.3	4.1E-02	3.0	8.5E-02	-0.8	5.9E-01	-0.5	6.9E-01
ENSMUST00000144585	SET binding factor 1 [Source:MGI Symbol;Acc:MGI:1925230]		Q6ZPE2	-5.1	8.3E-03	-2.3	4.1E-01	2.2	2.4E-01	-2.8	3.7E-01
ENSMUST00000144593	syntrophin, gamma 1 [Source:MGI Symbol;Acc:MGI:1918346]	D6RJM3		6.8	2.5E-02	5.3	5.6E-04	-0.1	9.5E-01	0.0	9.4E-01
ENSMUST00000144629	adenosine deaminase domain containing 1 (testis specific) [Source:MGI Symbol;Acc:MGI:103258]		Q5SUE7	4.6	1.2E-02	5.3	4.4E-03	-0.7	6.7E-01	0.2	8.4E-01
ENSMUST00000144668	dehydrodolichyl diphosphate synthase [Source:MGI Symbol;Acc:MGI:1914672]		Q99KU1	-7.4	1.7E-04	4.5	4.5E-03	-0.4	7.8E-01	0.1	8.6E-01
ENSMUST00000123337				-1.8	7.1E-02	-1.2	2.4E-01	-1.1	1.5E-01	-1.7	1.3E-01
ENSMUST00000123339	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Source:MGI Symbol;Acc:MGI:105037]	B1ARC0		-0.8	2.7E-01	-1.2	2.3E-01	-0.8	2.3E-01	-0.5	6.0E-01
ENSMUST00000123344				0.2	7.5E-01	1.0	2.9E-01	0.4	5.9E-01	-0.4	6.5E-01
ENSMUST00000144725	myosin IG [Source:MGI Symbol;Acc:MGI:1927091]	D6RHL4		-3.8	2.6E-02	4.8	5.0E-02	-1.2	5.9E-01	-0.9	5.2E-01
ENSMUST00000144742	centromere protein A [Source:MGI Symbol;Acc:MGI:88375]		O35216	-5.1	9.3E-04	7.0	1.7E-04	0.6	6.2E-01	-0.6	3.6E-01
ENSMUST00000144759	ubiquitin specific peptidase 16 [Source:MGI Symbol;Acc:MGI:1921362]	D6RHQ6		-6.3	8.0E-03	-0.6	5.3E-01	0.6	4.2E-01	-3.0	2.9E-02
ENSMUST00000144768	solute carrier family 25, member 38 [Source:MGI Symbol;Acc:MGI:2384782]	D6RCI6		-3.7	4.8E-03	-3.0	1.7E-02	0.3	6.0E-01	0.3	7.6E-01
ENSMUST00000144810	cyclin L1 [Source:MGI Symbol;Acc:MGI:1922664]	F7BER3		-2.9	2.8E-02	-1.6	2.0E-01	0.9	2.9E-01	-1.7	2.4E-01
ENSMUST00000144826	nocturnin [Source:MGI Symbol;Acc:MGI:109382]		O35710	2.1	3.8E-03	3.4	7.2E-03	-2.4	5.5E-02	0.2	7.6E-01
ENSMUST00000123371				-3.6	1.2E-01	-6.8	6.0E-02	-2.1	1.1E-01	1.2	7.3E-01
ENSMUST00000144827	EF-hand calcium binding domain 8 [Source:MGI Symbol;Acc:MGI:3644206]		Q8C9R9	5.7	2.0E-04	5.8	1.3E-02	-2.8	2.3E-01	-2.9	4.8E-02
ENSMUST00000144834	karyopherin (importin) alpha 2 [Source:MGI Symbol;Acc:MGI:103561]	A2A600		3.8	9.7E-03	5.9	1.2E-04	-0.7	4.3E-01	-0.5	3.7E-01
ENSMUST00000144847	osylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited) [Source:MGI Symbol;Acc:MGI:2	F6YCJ0		4.2	8.2E-03	-0.7	6.9E-01	2.5	7.8E-02	-0.8	6.3E-01
ENSMUST00000123384	angel homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1196310]		Q8K1C0	-2.3	6.6E-02	-1.3	4.1E-01	1.3	1.7E-01	0.3	8.5E-01
ENSMUST00000144863	SH3 domain binding kinase family, member 3 [Source:MGI Symbol;Acc:MGI:2685924]		P0C5K0	6.8	3.2E-05	3.8	6.1E-03	-0.8	4.4E-01	-0.7	3.9E-01
ENSMUST00000144892	phosphodiesterase 11A [Source:MGI Symbol;Acc:MGI:3036251]	F6SXR7		5.1	1.3E-03	4.6	3.1E-02	-1.5	4.6E-01	1.8	1.5E-01
ENSMUST00000144897	LX1 structure-specific endonuclease subunit homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191522		Q8BX32	5.1	2.4E-06	6.8	1.4E-04	-0.1	8.9E-01	0.2	7.6E-01
ENSMUST00000144936	solute carrier family 45, member 4 [Source:MGI Symbol;Acc:MGI:2146236]	F7BEQ1		-4.4	2.9E-03	4.9	5.7E-03	-1.4	3.5E-01	0.1	8.9E-01
ENSMUST00000123399	U2AF homology motif (UHM) kinase 1 [Source:MGI Symbol;Acc:MGI:1341908]	D3YUF5		0.7	7.8E-01	4.6	1.5E-01	-0.2	9.5E-01	-4.0	9.7E-02
ENSMUST00000144988	Meis homeobox 1 [Source:MGI Symbol;Acc:MGI:104717]		Q60954	6.3	6.4E-04	5.5	4.2E-02	-0.8	7.4E-01	-0.3	8.6E-01
ENSMUST00000145001	polymerase (RNA) III (DNA directed) polypeptide G like [Source:MGI Symbol;Acc:MGI:1917120]	D3YXS1		-3.3	3.0E-03	6.1	1.6E-03	-0.1	9.5E-01	-0.7	4.2E-01
ENSMUST00000145013	poly(A) polymerase gamma [Source:MGI Symbol;Acc:MGI:2442119]	F6THF3		6.1	3.7E-07	-2.8	7.7E-02	1.1	2.3E-01	-3.8	6.7E-02
ENSMUST00000145038	solute carrier family 22, member 23 [Source:MGI Symbol;Acc:MGI:1920352]	F7AWS1		6.3	5.5E-04	4.2	4.0E-02	-0.2	9.0E-01	1.9	1.4E-01
ENSMUST00000145070	RIKEN cDNA 4930444P10 gene [Source:MGI Symbol;Acc:MGI:1923049]	F6QJK4		5.7	3.7E-04	8.3	1.3E-04	-0.6	7.0E-01	-1.4	6.4E-02
ENSMUST00000145071	TPase, aminophospholipid transporter-like, class I, type 8A, member 2 [Source:MGI Symbol;Acc:MGI:135471	D6RG72		7.0	4.9E-05	6.6	1.6E-04	-1.2	3.0E-01	-0.4	5.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000145082	lysine (K)-specific demethylase 2B [Source:MGI Symbol;Acc:MGI:1354737]	D3YV31		3.3	2.5E-02	5.4	7.1E-03	-1.4	4.3E-01	-1.4	2.1E-01
ENSMUST00000123437	LIM domain only 2 [Source:MGI Symbol;Acc:MGI:102811]	Q544Z2	P25801	0.8	3.9E-01	-0.1	9.3E-01	-2.3	2.0E-02	-1.4	1.6E-01
ENSMUST00000123440				-1.2	2.4E-01	0.5	6.9E-01	0.9	3.1E-01	-0.7	5.3E-01
ENSMUST00000123442				-1.6	2.2E-01	-2.3	1.9E-01	-0.5	5.9E-01	0.2	9.2E-01
ENSMUST00000145139	expressed sequence AU019823 [Source:MGI Symbol;Acc:MGI:2143205]	D3YWF5		5.9	2.3E-05	6.3	5.5E-04	-0.2	8.6E-01	0.2	7.3E-01
ENSMUST00000145156	interaction protein for cytohesin exchange factors 1 [Source:MGI Symbol;Acc:MGI:2444159]	D3YVQ1		-3.7	6.2E-03	5.5	9.0E-04	-0.1	9.2E-01	0.3	7.1E-01
ENSMUST00000145175	ribonucleotide reductase M2 B (TP53 inducible) [Source:MGI Symbol;Acc:MGI:2155865]	D3YVM0		4.3	1.6E-03	7.4	1.2E-03	-1.2	5.1E-01	0.9	3.0E-01
ENSMUST00000145195	carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2 [Source:MGI Symbol;Acc:MGI:21	D6RDC5		6.7	1.3E-04	-2.9	8.4E-02	0.8	3.7E-01	-0.9	6.0E-01
ENSMUST00000145211	cDNA sequence BC051019 [Source:MGI Symbol;Acc:MGI:1928824]	D3YXQ0		7.7	1.5E-05	7.4	8.2E-05	-1.8	1.8E-01	0.7	2.4E-01
ENSMUST00000145237	zinc finger and SCAN domain containing 4F [Source:MGI Symbol;Acc:MGI:3708485]		Q3URS2	7.4	1.5E-03	6.8	1.3E-03	0.8	6.2E-01	-0.8	3.5E-01
ENSMUST00000123465				-1.5	4.2E-01	-3.8	9.9E-02	-3.2	2.8E-02	-0.8	7.3E-01
ENSMUST00000145239	family with sequence similarity 69, member A [Source:MGI Symbol;Acc:MGI:1914516]	D3YW04		-3.5	1.8E-02	4.4	7.3E-03	-0.5	6.8E-01	0.3	7.3E-01
ENSMUST00000145266	general transcription factor II H, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1345669]	Q91YN8		-2.2	2.4E-02	6.0	2.5E-05	-2.6	1.9E-02	-0.4	4.3E-01
ENSMUST00000145303	lymphocyte cytosolic protein 1 [Source:MGI Symbol;Acc:MGI:104808]		Q61233	-7.6	1.3E-04	6.7	1.4E-03	0.0	1.0E+00	0.1	8.8E-01
ENSMUST00000145345	transmembrane protein 234 [Source:MGI Symbol;Acc:MGI:1924049]	F6YFM0		-4.7	1.4E-03	5.5	7.7E-03	-2.7	1.6E-01	0.2	8.0E-01
ENSMUST00000145347	microtubule crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:1915867]	B8JJI7		6.4	1.5E-02	-7.1	1.9E-04	-0.5	2.6E-01	-0.4	7.6E-01
ENSMUST00000123490	transmembrane epididymal family member 2 [Source:MGI Symbol;Acc:MGI:1923273]	D3YXN9		2.7	1.1E-01	4.5	1.0E-02	-1.2	4.2E-01	-3.0	3.2E-02
ENSMUST00000145352	post-GPI attachment to proteins 2 [Source:MGI Symbol;Acc:MGI:2385286]	D6RCV1		-3.1	7.6E-03	4.8	1.8E-05	-1.9	9.2E-03	0.3	4.0E-01
ENSMUST00000123493	centrosomal protein 44 [Source:MGI Symbol;Acc:MGI:3525111]	F7BA57		-2.0	1.1E-01	-2.4	1.6E-01	-0.8	4.1E-01	-0.4	8.2E-01
ENSMUST00000123494	kelch domain containing 10 [Source:MGI Symbol;Acc:MGI:1924038]			-1.1	5.5E-01	-1.5	4.9E-01	-0.9	4.9E-01	-0.4	8.5E-01
ENSMUST00000145353	CCR4-NOT transcription complex, subunit 6 [Source:MGI Symbol;Acc:MGI:2144529]		Q8K3P5	-3.6	4.6E-04	6.4	3.3E-04	0.7	5.1E-01	0.5	4.8E-01
ENSMUST00000145362	zinc finger CCCH-type containing 12B [Source:MGI Symbol;Acc:MGI:2442133]	S4R1K0		5.9	1.2E-05	8.1	2.0E-02	-0.6	8.5E-01	-1.7	2.9E-01
ENSMUST00000123502	coiled-coil domain containing 167 [Source:MGI Symbol;Acc:MGI:1915847]		Q9D162	1.0	2.2E-01	-0.4	7.5E-01	0.4	6.2E-01	1.8	1.2E-01
ENSMUST00000145391	PDZ domain containing 7 [Source:MGI Symbol;Acc:MGI:3608325]	E9Q9W7		7.7	1.3E-03	4.9	9.4E-04	0.0	9.8E-01	0.2	7.4E-01
ENSMUST00000145401	interleukin 9 receptor [Source:MGI Symbol;Acc:MGI:96564]	Q78PA5	Q01114	5.9	3.7E-04	-5.3	1.1E-02	1.1	1.7E-01	-0.8	6.8E-01
ENSMUST00000145440	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	D6RIJ4		4.0	2.0E-04	3.5	2.1E-02	-0.1	9.5E-01	1.0	2.8E-01
ENSMUST00000145462	guanylate cyclase activator 1B [Source:MGI Symbol;Acc:MGI:1194489]	E9PWU1		10.1	7.9E-06	-2.8	2.1E-02	-0.1	8.8E-01	0.2	8.3E-01
ENSMUST00000123512				0.2	9.2E-01	-2.8	3.3E-01	-2.3	1.9E-01	0.8	7.9E-01
ENSMUST00000123514	ecrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) [Source:MGI Symbol;Acc:MGI:2(	Q80WM9		0.1	9.4E-01	-1.2	4.6E-01	-1.3	2.9E-01	0.1	9.7E-01
ENSMUST00000145481	N-myc (and STAT) interactor [Source:MGI Symbol;Acc:MGI:1928368]	Q3UJ82	O35309	-5.1	7.1E-04	5.1	1.4E-03	0.3	8.2E-01	-0.5	4.9E-01
ENSMUST00000145530	ynthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 [Source:MGI Symbol;Acc:MGI:12(	A2AKV3		4.9	2.3E-02	-8.4	1.6E-04	-1.2	1.8E-02	0.5	7.5E-01
ENSMUST00000145598	cysteine-serine-rich nuclear protein 3 [Source:MGI Symbol;Acc:MGI:1925021]		P59055	5.6	2.3E-02	6.6	3.2E-04	-0.6	6.5E-01	-0.7	3.2E-01
ENSMUST00000145600	autophagy related 2A [Source:MGI Symbol;Acc:MGI:1916291]	F6V3Y9		-3.8	3.5E-03	4.7	5.0E-03	-1.3	3.5E-01	0.5	5.7E-01
ENSMUST00000123526				2.8	9.5E-02	5.0	9.8E-03	-1.0	5.4E-01	-3.2	2.4E-02
ENSMUST00000145608	vesicular, overexpressed in cancer, prosurvival protein 1 [Source:MGI Symbol;Acc:MGI:2141658]			8.7	8.8E-07	3.1	1.2E-02	-0.4	6.5E-01	-0.5	5.1E-01
ENSMUST00000123533				4.1	5.4E-02	5.2	1.2E-01	2.7	3.7E-01	1.6	3.9E-01
ENSMUST00000145614	mitochondrial ribosomal protein S26 [Source:MGI Symbol;Acc:MGI:1333830]		Q80ZS3	2.8	3.9E-05	5.6	1.0E-03	-0.5	7.0E-01	0.5	4.5E-01
ENSMUST00000123539	phospholipase D1 [Source:MGI Symbol;Acc:MGI:109585]	D6RH77		0.4	7.0E-01	3.0	5.0E-02	1.2	3.1E-01	-1.3	2.8E-01
ENSMUST00000145634	haloacid dehalogenase-like hydrolase domain containing 2 [Source:MGI Symbol;Acc:MGI:1924237]		Q3UGR5	-5.5	1.1E-04	4.0	5.2E-03	-0.8	4.6E-01	-0.7	4.1E-01
ENSMUST00000145650	tryptophanyl tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1917810]	Q8BZQ9		5.8	3.6E-04	5.5	2.7E-02	-0.6	7.9E-01	2.0	1.4E-01
ENSMUST00000123553				-0.7	1.4E-01	0.0	9.5E-01	0.7	1.7E-01	-0.1	8.3E-01
ENSMUST00000145662	phospholipase C, eta 2 [Source:MGI Symbol;Acc:MGI:2443078]		A2AP18	6.6	1.6E-04	-0.7	5.0E-01	1.7	3.9E-02	-2.3	6.7E-02
ENSMUST00000145664	AT rich interactive domain 1A (SWI-like) [Source:MGI Symbol;Acc:MGI:1935147]	E9QAQ7		-3.9	1.6E-02	2.4	2.4E-01	-0.3	8.8E-01	3.7	3.3E-02
ENSMUST00000145665	interleukin-1 receptor-associated kinase 3 [Source:MGI Symbol;Acc:MGI:1921164]	D3Z007		-3.9	5.0E-03	-5.4	8.2E-03	-0.2	7.7E-01	-0.7	6.9E-01
ENSMUST00000123563				-3.4	8.9E-02	-1.6	5.0E-01	0.1	9.3E-01	-1.8	4.5E-01
ENSMUST00000145693	F-box and leucine-rich repeat protein 3 [Source:MGI Symbol;Acc:MGI:1354702]	Q5PRF6	Q8C4V4	-8.3	9.7E-06	6.9	1.8E-04	-0.6	6.3E-01	-0.2	7.0E-01
ENSMUST00000123572	lin-54 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2140902]		Q571G4	-1.1	7.3E-01	-0.6	8.3E-01	-1.9	3.8E-01	-2.4	4.5E-01
ENSMUST00000145698	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]	D6RDE3		7.1	5.6E-03	4.8	2.1E-04	-2.0	3.5E-02	-0.9	1.5E-01
ENSMUST00000145727	putative homeodomain transcription factor 1 [Source:MGI Symbol;Acc:MGI:1332671]	Q5IBN5	Q9QZ09	4.7	2.2E-03	-4.0	6.3E-03	-0.1	9.3E-01	0.6	6.1E-01
ENSMUST00000145735	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5 [Source:MGI Symbol;Acc:MGI:1915826]	G3UW70		-4.4	6.7E-06	5.9	2.0E-04	1.1	2.6E-01	1.0	1.2E-01
ENSMUST00000145798	predicted gene 14025 [Source:MGI Symbol;Acc:MGI:3649276]	A2AP89		6.9	1.8E-04	4.4	1.1E-03	-2.5	3.9E-02	-1.1	9.8E-02
ENSMUST00000145823	calmodulin binding transcription activator 2 [Source:MGI Symbol;Acc:MGI:2135957]	D6RCU2		-5.4	9.4E-03	5.1	3.3E-03	-1.0	4.7E-01	0.2	7.7E-01
ENSMUST00000145853	helicase-like transcription factor [Source:MGI Symbol;Acc:MGI:1196437]	E9PVX5		-3.7	4.4E-03	-4.7	1.3E-02	0.6	4.5E-01	-2.3	2.5E-01
ENSMUST00000123591				-0.7	2.8E-01	0.0	9.7E-01	-0.4	5.0E-01	-1.1	1.5E-01
ENSMUST00000145860	mitochondrial tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2142572]	E9Q8N4		6.9	1.7E-04	5.2	1.4E-02	-0.6	7.3E-01	-1.6	2.3E-01
ENSMUST00000123599	AU RNA binding protein/enoyl-coenzyme A hydratase [Source:MGI Symbol;Acc:MGI:1338011]	F6R307		-1.6	2.7E-01	-0.6	6.9E-01	-0.2	8.7E-01	-1.2	4.5E-01
ENSMUST00000123600	interleukin 15 receptor, alpha chain [Source:MGI Symbol;Acc:MGI:104644]	E9QA82		-0.3	8.9E-01	-2.7	3.3E-01	-2.8	9.9E-02	-0.4	8.8E-01
ENSMUST00000123601				0.4	7.5E-01	0.2	9.1E-01	1.2	3.4E-01	1.3	4.1E-01
ENSMUST00000123602				-1.7	2.2E-01	0.0	9.9E-01	0.8	5.2E-01	-0.9	6.0E-01
ENSMUST00000145890	guanylyl cyclase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916028]			3.4	2.9E-03	-1.6	5.7E-02	0.1	8.1E-01	0.0	9.7E-01
ENSMUST00000145895	multiple coagulation factor deficiency 2 [Source:MGI Symbol;Acc:MGI:2183439]	D3Z6A4		3.8	5.5E-04	6.2	1.0E-03	-0.6	6.6E-01	0.6	4.6E-01
ENSMUST00000145903	Rab9 effector protein with kelch motifs [Source:MGI Symbol;Acc:MGI:2139530]		Q8VCH5	2.2	7.2E-03	5.9	1.3E-05	0.3	6.9E-01	0.2	7.0E-01
ENSMUST00000145904	pantothenate kinase 2 [Source:MGI Symbol;Acc:MGI:1921700]	F6VV40		-4.6	1.7E-04	0.9	5.1E-01	3.4	1.6E-02	-4.0	2.7E-02
ENSMUST00000123626	ankyrin repeat and SOCS box-containing 8 [Source:MGI Symbol;Acc:MGI:1925791]			-2.5	7.7E-02	-1.7	2.3E-01	0.0	9.7E-01	-0.7	6.3E-01
ENSMUST00000145905	tumor protein D52 [Source:MGI Symbol;Acc:MGI:107749]	D3Z125		6.2	3.5E-04	7.5	4.4E-04	0.6	6.6E-01	0.9	2.5E-01
ENSMUST00000123636	transmembrane and coiled-coil domains 4 [Source:MGI Symbol;Acc:MGI:1924306]	A2ALL4		-0.8	5.6E-01	2.1	2.4E-01	1.6	2.9E-01	-1.3	3.7E-01
ENSMUST00000145936	early growth response 2 [Source:MGI Symbol;Acc:MGI:95296]	D3YYY2		5.7	6.6E-03	4.6	1.4E-04	-0.6	3.9E-01	-0.6	2.8E-01
ENSMUST00000145959	TBC1 domain family, member 17 [Source:MGI Symbol;Acc:MGI:2449973]	I6L974		-3.7	5.5E-03	-4.6	1.0E-02	0.7	2.5E-01	-1.5	3.8E-01
ENSMUST00000123645				-1.6	2.7E-01	-2.5	1.1E-01	-2.5	3.7E-02	-1.6	3.2E-01
ENSMUST00000145960	importin 8 [Source:MGI Symbol;Acc:MGI:2444611]	B2KGD7		4.6	9.4E-03	6.4	1.3E-03	-0.6	6.7E-01	0.0	9.8E-01
ENSMUST00000145963	thioredoxin-like 4A [Source:MGI Symbol;Acc:MGI:1351613]		P83877	-2.6	2.0E-02	6.1	4.6E-03	-0.7	6.8E-01	0.3	7.4E-01
ENSMUST00000145988	dynein heavy chain domain 1 [Source:MGI Symbol;Acc:MGI:1924755]	D3Z2X2		2.1	1.3E-02	6.3	7.3E-03	0.8	6.9E-01	-0.7	5.2E-01
ENSMUST00000146028	sirtuin 1 [Source:MGI Symbol;Acc:MGI:2135607]	F6YAQ3		-6.1	4.7E-04	4.9	2.6E-04	0.1	8.6E-01	-0.6	3.3E-01
ENSMUST00000146030	ataxia, cerebellar, Cayman type homolog (human) [Source:MGI Symbol;Acc:MGI:2448730]	D6RIJ5		7.3	5.1E-06	-3.9	2.1E-02	0.3	6.9E-01	0.0	9.9E-01
ENSMUST00000146040	ataxin 7-like 1 [Source:MGI Symbol;Acc:MGI:3584458]	F7C0E4		-4.2	1.2E-02	-2.8	7.3E-02	0.3	6.8E-01	0.3	8.6E-01
ENSMUST00000123669				1.9	2.8E-01	3.0	2.3E-01	0.9	6.9E-01	-0.3	8.8E-01
ENSMUST00000146071	protein tyrosine phosphatase, non-receptor type 22 (lymphoid) [Source:MGI Symbol;Acc:MGI:107170]	E9QAS3		-4.9	3.9E-03	6.9	7.2E-04	1.8	2.1E-01	-0.1	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000146074	zinc finger protein 568 [Source:MGI Symbol;Acc:MGI:2142347]	Q0VGV0		1.7	1.4E-03	2.2	2.8E-01	-0.7	6.7E-01	1.5	2.9E-01
ENSMUST00000146078	disabled 1 [Source:MGI Symbol;Acc:MGI:108554]	F2Z465		6.5	1.7E-03	6.0	4.1E-04	0.0	9.7E-01	-0.4	5.6E-01
ENSMUST00000146085	coiled-coil domain containing 9 [Source:MGI Symbol;Acc:MGI:1921443]	G3UYE3		-5.7	1.6E-03	6.5	2.5E-03	0.0	9.8E-01	0.5	5.9E-01
ENSMUST00000146088	tetratricopeptide repeat domain 38 [Source:MGI Symbol;Acc:MGI:2146198]		A3KMP2	2.6	1.3E-03	-6.0	1.8E-03	-0.3	6.2E-01	0.7	6.3E-01
ENSMUST00000146104	Fanconi anemia, complementation group E [Source:MGI Symbol;Acc:MGI:1920025]	B8JJD1		5.4	2.0E-03	4.4	3.5E-03	0.1	9.2E-01	-0.9	2.7E-01
ENSMUST00000146157	cDNA sequence BC024139 [Source:MGI Symbol;Acc:MGI:2442591]	E9Q3A6		8.4	2.5E-02	4.5	6.2E-02	-0.4	8.4E-01	1.5	3.0E-01
ENSMUST00000123686	myosin, light chain 12A, regulatory, non-sarcomeric [Source:MGI Symbol;Acc:MGI:1914518]	Q6ZWQ9		1.8	5.3E-01	-4.9	9.6E-02	-7.6	8.0E-03	-0.9	7.7E-01
ENSMUST00000146174	T cell leukemia/lymphoma 1B, 2 [Source:MGI Symbol;Acc:MGI:1351609]	Q4FZI4	P56841	7.2	9.7E-05	-3.0	1.4E-01	1.5	1.3E-01	0.9	6.5E-01
ENSMUST00000146205	MAM and LDL receptor class A domain containing 1 [Source:MGI Symbol;Acc:MGI:1928271]	A2AJX4		7.7	1.5E-05	5.4	4.5E-04	-2.1	9.3E-02	-0.4	5.5E-01
ENSMUST00000123696				0.7	2.6E-01	2.0	5.1E-02	1.6	5.0E-02	0.4	6.0E-01
ENSMUST00000146220	phosphodiesterase 6D, cGMP-specific, rod, delta [Source:MGI Symbol;Acc:MGI:1270843]	M0QWG6		6.1	1.9E-03	-5.7	6.3E-03	-0.9	1.8E-01	1.0	5.7E-01
ENSMUST00000123702				2.6	5.3E-02	4.6	1.4E-02	-0.1	9.5E-01	-2.1	7.9E-02
ENSMUST00000146233	XIAP associated factor 1 [Source:MGI Symbol;Acc:MGI:3772572]		Q5NBU8	3.6	6.6E-03	1.5	6.8E-01	-1.6	5.9E-01	5.7	9.5E-02
ENSMUST00000146243	zinc finger SCAN domains 29 [Source:MGI Symbol;Acc:MGI:2139317]	B7ZCX1		-1.1	2.9E-02	0.5	8.2E-01	5.6	5.0E-03	-2.2	3.3E-01
ENSMUST00000146261	centromere protein O [Source:MGI Symbol;Acc:MGI:1923800]	F7D1K8		3.5	4.5E-04	6.1	2.0E-02	-0.8	7.3E-01	-0.8	5.5E-01
ENSMUST00000146274	ribosomal modification protein rimK-like family member B [Source:MGI Symbol;Acc:MGI:1918325]		Q80WS1	5.3	6.1E-03	5.0	1.6E-04	1.2	1.4E-01	0.2	6.8E-01
ENSMUST00000146282	cadherin 7, type 2 [Source:MGI Symbol;Acc:MGI:2442792]	Q8BLT5		6.1	1.1E-03	7.7	1.0E-05	-0.3	7.2E-01	-0.6	1.9E-01
ENSMUST00000123723				-0.5	6.9E-01	-0.3	8.9E-01	1.0	4.7E-01	0.8	6.5E-01
ENSMUST00000146292	transmembrane protein 63c [Source:MGI Symbol;Acc:MGI:2444386]		Q8CBX0	7.5	1.2E-03	-1.2	1.8E-01	0.3	6.3E-01	-0.5	5.6E-01
ENSMUST00000146328	WW domain binding protein 1 [Source:MGI Symbol;Acc:MGI:104710]	D3Z168		-4.4	2.2E-02	5.1	7.0E-04	-1.6	1.4E-01	-1.1	1.6E-01
ENSMUST00000146338	ADP-ribose/CDP-alcohol diphosphatase, manganese dependent [Source:MGI Symbol;Acc:MGI:1913608]		Q99KS6	-1.6	9.8E-03	-4.4	3.3E-03	-0.9	1.3E-01	-2.6	8.2E-02
ENSMUST00000123732	annexin A4 [Source:MGI Symbol;Acc:MGI:88030]	D3Z0S1		-1.6	5.5E-01	-5.6	9.5E-02	-4.6	1.9E-02	-0.6	8.7E-01
ENSMUST00000123736	citron [Source:MGI Symbol;Acc:MGI:105313]	H3BJ74		1.7	1.4E-01	3.4	2.0E-02	-0.3	8.0E-01	-1.9	8.6E-02
ENSMUST00000146354	neutrophil cytosolic factor 1 [Source:MGI Symbol;Acc:MGI:97283]		Q09014	-5.5	2.1E-04	2.9	5.9E-03	-0.4	6.1E-01	0.5	4.7E-01
ENSMUST00000146358	transducin-like enhancer of split 2, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104635]		Q9WVB2	6.9	1.2E-04	6.9	6.3E-04	-0.7	6.3E-01	-0.4	6.2E-01
ENSMUST00000146390	somatostatin receptor 2 [Source:MGI Symbol;Acc:MGI:98328]		P30875	6.4	3.8E-04	-3.8	6.9E-03	1.2	7.1E-02	-1.5	2.6E-01
ENSMUST00000146396	RIKEN cDNA A930011G23 gene [Source:MGI Symbol;Acc:MGI:2442790]	F5H8M5		8.9	4.2E-06	3.2	1.3E-01	-1.6	4.2E-01	0.5	7.3E-01
ENSMUST00000146406	translocase of inner mitochondrial membrane 17b [Source:MGI Symbol;Acc:MGI:1343176]	A2AES1		-4.9	2.0E-03	-3.7	7.6E-03	1.2	3.9E-02	0.4	7.2E-01
ENSMUST00000123766	lysophosphatidylcholine acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2384812]	D6RE48		-3.1	3.0E-01	-2.2	5.1E-01	0.0	9.8E-01	-0.8	8.1E-01
ENSMUST00000123774	asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:1098592]	D6RCW8		3.4	1.4E-01	2.5	3.9E-01	-0.7	7.6E-01	0.1	9.5E-01
ENSMUST00000123778				-1.9	2.1E-01	-0.5	7.2E-01	-0.3	8.3E-01	-1.6	3.2E-01
ENSMUST00000146409	solute carrier family 26 (sulfate transporter), member 2 [Source:MGI Symbol;Acc:MGI:892977]		Q62273	1.4	1.1E-02	3.8	1.0E-01	-1.3	5.5E-01	1.5	3.1E-01
ENSMUST00000146412	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]	H3BJW9		-3.4	3.1E-02	6.1	2.8E-04	-0.5	6.5E-01	0.8	2.2E-01
ENSMUST00000146415	UBX domain protein 10 [Source:MGI Symbol;Acc:MGI:2443123]		Q8BG34	6.9	3.2E-04	5.4	7.8E-05	1.0	2.1E-01	0.0	9.5E-01
ENSMUST00000146417	family with sequence similarity 47, member E [Source:MGI Symbol;Acc:MGI:2686227]	D3YWC7		6.6	4.9E-05	3.7	4.7E-02	0.2	8.8E-01	0.9	4.0E-01
ENSMUST00000123791	SET binding factor 1 [Source:MGI Symbol;Acc:MGI:1925230]		Q6ZPE2	3.2	1.7E-01	-3.2	4.1E-01	-2.0	3.5E-01	4.4	2.5E-01
ENSMUST00000146423	RIKEN cDNA 1110008P14 gene [Source:MGI Symbol;Acc:MGI:1920987]	A0A0A6YXJ8		5.4	3.2E-04	-3.2	1.4E-02	1.5	1.8E-02	-1.5	2.3E-01
ENSMUST00000123798				-2.7	8.6E-02	0.0	9.9E-01	-0.2	8.4E-01	-2.9	7.2E-02
ENSMUST00000123803				1.2	1.7E-01	2.2	4.8E-02	0.4	6.2E-01	-0.6	4.9E-01
ENSMUST00000146432	ELK4, member of ETS oncogene family [Source:MGI Symbol;Acc:MGI:102853]	Q8C6Q0		2.8	1.7E-02	5.2	1.3E-02	-0.6	7.5E-01	0.8	4.8E-01
ENSMUST00000146439	T cell specific GTPase 1 [Source:MGI Symbol;Acc:MGI:98734]	Q5SVP4		4.5	1.7E-02	4.0	2.5E-02	0.3	8.3E-01	1.1	2.4E-01
ENSMUST00000146444	TGF-beta activated kinase 1/MAP3K7 binding protein 2 [Source:MGI Symbol;Acc:MGI:1915902]		Q99K90	-5.3	8.9E-05	-2.1	9.5E-02	0.5	4.3E-01	-0.6	6.1E-01
ENSMUST00000123816				-0.5	6.1E-01	-3.2	6.7E-02	-0.8	3.2E-01	1.9	2.4E-01
ENSMUST00000123819	scavenger receptor class F, member 1 [Source:MGI Symbol;Acc:MGI:2449455]	D6RJK6		3.4	1.5E-01	6.5	3.8E-02	0.2	9.5E-01	-3.0	1.1E-01
ENSMUST00000123824				1.4	6.1E-02	1.7	4.7E-02	-0.6	4.1E-01	-0.9	2.3E-01
ENSMUST00000146451	RIKEN cDNA 2310061I04 gene [Source:MGI Symbol;Acc:MGI:1916912]	B8JJ66		3.4	4.0E-03	2.1	4.0E-01	6.8	4.2E-03	0.5	7.9E-01
ENSMUST00000123827	intermediate filament family orphan 2 [Source:MGI Symbol;Acc:MGI:2140675]	B1AZL1		1.5	1.1E-01	3.7	4.7E-03	0.5	5.8E-01	-1.7	6.7E-02
ENSMUST00000146458	E1A binding protein p400 [Source:MGI Symbol;Acc:MGI:1276124]	Q641K9		6.4	1.3E-02	4.1	2.5E-04	0.1	9.3E-01	0.3	5.5E-01
ENSMUST00000146470	nucleoporin 54 [Source:MGI Symbol;Acc:MGI:1920460]	D6RFN7		6.7	4.4E-05	6.3	6.1E-06	0.3	6.6E-01	-0.2	6.8E-01
ENSMUST00000146476	(constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	D3Z1R9		5.8	3.0E-03	6.6	1.3E-04	-0.4	6.7E-01	1.2	8.0E-02
ENSMUST00000123839				1.6	2.4E-01	0.7	7.7E-01	1.5	3.8E-01	2.4	2.1E-01
ENSMUST00000146492	RAS protein-specific guanine nucleotide-releasing factor 2 [Source:MGI Symbol;Acc:MGI:109137]	D3Z685		5.7	3.6E-04	5.9	5.0E-02	-0.6	8.5E-01	0.5	7.6E-01
ENSMUST00000146510	SRR1 domain containing [Source:MGI Symbol;Acc:MGI:1917368]	F6Q7H5		-4.2	7.3E-03	5.2	1.9E-03	0.5	6.4E-01	0.1	8.9E-01
ENSMUST00000123853	A kinase (PRKA) anchor protein 11 [Source:MGI Symbol;Acc:MGI:2684060]	E9Q777		0.7	3.7E-01	2.7	1.4E-02	1.3	1.2E-01	-0.8	3.2E-01
ENSMUST00000146511	general transcription factor III A [Source:MGI Symbol;Acc:MGI:1913846]	F6RCF6		-3.1	1.7E-02	6.1	1.4E-03	-0.1	9.2E-01	-1.0	2.4E-01
ENSMUST00000146590	DnaJ (Hsp40) homolog, subfamily B, member 12 [Source:MGI Symbol;Acc:MGI:1931881]		Q9QYI4	-4.4	1.9E-03	6.0	2.0E-04	-0.6	5.9E-01	0.1	8.3E-01
ENSMUST00000146598	ubiquitin-fold modifier 1 [Source:MGI Symbol;Acc:MGI:1915140]		P61961	-2.5	3.7E-04	8.1	2.0E-05	-0.4	6.9E-01	-0.1	8.2E-01
ENSMUST00000123884	centriolin [Source:MGI Symbol;Acc:MGI:1889576]	F6QP53		0.8	5.1E-01	2.9	9.8E-02	0.2	9.1E-01	-1.9	1.5E-01
ENSMUST00000146601	RAS, guanyl releasing protein 2 [Source:MGI Symbol;Acc:MGI:1333849]	D3Z3N3		-3.4	2.9E-03	-5.3	3.3E-03	-0.2	7.3E-01	1.6	2.5E-01
ENSMUST00000146623	glycerol-3-phosphate dehydrogenase 1-like [Source:MGI Symbol;Acc:MGI:1289257]	B2RSR7	Q3ULJ0	-3.6	1.5E-05	4.0	6.9E-04	-0.3	7.3E-01	0.5	4.4E-01
ENSMUST00000123889				-2.5	6.1E-02	0.4	8.0E-01	1.9	1.5E-01	-1.0	4.8E-01
ENSMUST00000146647	KN motif and ankyrin repeat domains 1 [Source:MGI Symbol;Acc:MGI:2147707]	E9Q944		7.9	5.6E-05	3.4	1.1E-01	-0.6	7.3E-01	0.9	5.1E-01
ENSMUST00000123893				-3.1	4.3E-02	-1.4	3.5E-01	-0.3	7.4E-01	-2.0	2.2E-01
ENSMUST00000146650	myeloperoxidase [Source:MGI Symbol;Acc:MGI:97137]	F7DC05		-4.0	4.6E-03	5.3	2.2E-05	-1.2	9.9E-02	-0.3	5.1E-01
ENSMUST00000123898	TSC22 domain family, member 3 [Source:MGI Symbol;Acc:MGI:1196284]	B1AVF2		-0.7	8.5E-01	-6.8	1.2E-01	-6.7	1.1E-02	-0.6	9.0E-01
ENSMUST00000146673	predicted gene 16314 [Source:MGI Symbol;Acc:MGI:3833934]	D3YWW5		4.5	2.5E-03	4.5	2.2E-02	-1.0	5.8E-01	0.6	6.0E-01
ENSMUST00000146698	GPN-loop GTPase 3 [Source:MGI Symbol;Acc:MGI:1289326]	F6WTD8		4.4	1.3E-03	5.6	2.5E-03	-0.6	7.0E-01	-2.1	5.4E-02
ENSMUST00000146722	aftiphilin [Source:MGI Symbol;Acc:MGI:1923012]		Q80WT5	-6.0	5.1E-03	-2.8	4.0E-02	-0.5	4.7E-01	-0.7	5.8E-01
ENSMUST00000146756	TAR (HIV) RNA binding protein 2 [Source:MGI Symbol;Acc:MGI:103027]	D3Z282		2.2	3.3E-03	-3.8	3.8E-02	0.2	8.2E-01	-2.1	3.0E-01
ENSMUST00000146764	protein inhibitor of activated STAT 4 [Source:MGI Symbol;Acc:MGI:2136940]	D6RGB7		2.2	9.4E-03	-4.1	4.8E-03	0.7	2.4E-01	-1.4	2.7E-01
ENSMUST00000146782	transcription factor EB [Source:MGI Symbol;Acc:MGI:103270]	F6W7D6		-6.7	1.7E-04	6.2	1.7E-03	0.0	9.8E-01	0.4	6.1E-01
ENSMUST00000146809	sirtuin 7 [Source:MGI Symbol;Acc:MGI:2385849]	A2ABY6		-5.5	2.9E-03	-3.3	1.9E-02	-0.1	8.4E-01	-0.1	9.2E-01
ENSMUST00000146865	protein kinase, cAMP dependent regulatory, type II beta [Source:MGI Symbol;Acc:MGI:97760]	H3BK84		-2.9	2.9E-03	1.7	3.5E-02	0.5	3.6E-01	0.2	7.8E-01
ENSMUST00000146873	SEC16 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2148802]	F6Q2Y9		3.5	5.4E-03	2.0	1.8E-01	-4.2	2.3E-02	0.9	4.1E-01
ENSMUST00000123950				-0.5	6.9E-01	-1.1	5.7E-01	0.9	4.5E-01	1.5	4.0E-01
ENSMUST00000146905	ADP-ribosylation factor-like 4A [Source:MGI Symbol;Acc:MGI:99437]		P61213	2.1	6.4E-03	7.6	1.9E-03	-0.1	9.7E-01	0.4	5.9E-01
ENSMUST00000123958				-1.0	6.8E-01	1.9	6.9E-01	5.2	1.7E-01	2.3	5.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000146919	Wolf-Hirschhorn syndrome candidate 1-like 1 (human) [Source:MGI Symbol;Acc:MGI:2142581]		Q6P2L6	-7.4	8.6E-04	-0.1	9.7E-01	-2.7	3.5E-02	0.7	5.8E-01
ENSMUST00000146927	ribosomal protein S9 [Source:MGI Symbol;Acc:MGI:1924096]	F7CJS8		-8.5	1.6E-05	6.7	2.3E-04	1.1	3.4E-01	-1.1	1.6E-01
ENSMUST00000146934	stromal antigen 1 [Source:MGI Symbol;Acc:MGI:1098658]	F6XQW1		-3.8	2.3E-02	7.2	2.9E-03	1.7	3.4E-01	0.7	4.2E-01
ENSMUST00000146993	Moloney leukemia virus 10-like 1 [Source:MGI Symbol;Acc:MGI:1891384]	D3YWG8		7.0	3.4E-02	-5.4	1.2E-02	0.7	2.9E-01	1.3	4.6E-01
ENSMUST00000147003	phosphatidylinositol glycan anchor biosynthesis, class X [Source:MGI Symbol;Acc:MGI:1919334]	F6WL03		-5.5	4.2E-04	-6.3	9.5E-04	-0.4	4.2E-01	2.6	7.4E-02
ENSMUST00000123977				1.4	5.1E-01	-0.6	7.8E-01	-2.3	2.3E-01	-0.3	9.0E-01
ENSMUST00000147024	RIKEN cDNA A630010A05 gene [Source:MGI Symbol;Acc:MGI:3584518]	A9C473		6.0	1.9E-04	5.0	2.3E-03	-1.4	3.1E-01	-0.5	4.8E-01
ENSMUST00000123985				-1.0	1.3E-01	-0.7	2.7E-01	-1.0	7.7E-02	-1.2	8.4E-02
ENSMUST00000147041	Rho guanine nucleotide exchange factor (GEF) 38 [Source:MGI Symbol;Acc:MGI:1924919]		Q80VK6	5.7	8.4E-05	2.5	1.2E-01	-1.5	3.6E-01	1.0	4.1E-01
ENSMUST00000147097	perilipin 2 [Source:MGI Symbol;Acc:MGI:87920]	B1AXR3		-6.3	3.5E-05	6.6	6.5E-04	-0.5	7.5E-01	-1.7	4.5E-02
ENSMUST00000147103	acyl-CoA wax alcohol acyltransferase 2 [Source:MGI Symbol;Acc:MGI:3045345]		Q6E1M8	8.5	1.6E-05	5.6	9.5E-03	-0.7	6.9E-01	-0.8	4.4E-01
ENSMUST00000147110	surfeit gene 1 [Source:MGI Symbol;Acc:MGI:98443]	A0A0A6YVR9		-7.3	1.6E-04	7.0	2.2E-05	-0.9	3.1E-01	0.7	1.7E-01
ENSMUST00000123995				1.2	1.6E-01	0.8	3.6E-01	-0.9	2.1E-01	-0.6	4.7E-01
ENSMUST00000123999				1.2	6.8E-01	4.0	1.8E-01	-0.4	8.8E-01	-3.2	2.1E-01
ENSMUST00000124002				1.3	5.1E-01	-2.9	3.9E-01	-1.6	4.1E-01	2.6	4.1E-01
ENSMUST00000147146	POU domain, class 2, transcription factor 2 [Source:MGI Symbol;Acc:MGI:101897]	F6X6U7		6.2	3.9E-04	2.4	3.9E-02	-1.5	1.3E-01	-1.0	2.5E-01
ENSMUST00000124008	cell cycle progression 1 [Source:MGI Symbol;Acc:MGI:1196419]	G3UVW4		-4.0	4.1E-01	-8.1	3.6E-01	-2.4	4.4E-01	1.7	8.5E-01
ENSMUST00000147148	small integral membrane protein 20 [Source:MGI Symbol;Acc:MGI:1913528]	D3Z7Q2		-7.6	5.7E-06	1.2	1.2E-01	-0.3	6.2E-01	0.5	4.6E-01
ENSMUST00000124020	lactase-like [Source:MGI Symbol;Acc:MGI:2183549]	D6RI22		3.8	1.4E-01	2.9	3.2E-01	-0.3	9.2E-01	0.6	7.3E-01
ENSMUST00000124023	mitochondrial pyruvate carrier 1 [Source:MGI Symbol;Acc:MGI:1915240]	D3YWY6		-4.3	1.1E-01	-4.0	2.1E-01	-1.0	5.9E-01	-1.2	7.1E-01
ENSMUST00000147153	lipase, member O2 [Source:MGI Symbol;Acc:MGI:3644466]	D3YY49		6.3	1.0E-04	-2.5	7.6E-02	0.7	2.8E-01	1.0	4.2E-01
ENSMUST00000147169	RIKEN cDNA 2010107G12 gene [Source:MGI Symbol;Acc:MGI:1917272]	F6S2M6		6.1	1.7E-03	7.1	8.2E-05	-0.6	6.1E-01	-0.7	2.6E-01
ENSMUST00000147185	ubiquitin-associated protein 1-like [Source:MGI Symbol;Acc:MGI:2685360]	G3UW59		5.3	1.2E-05	5.5	1.7E-03	-0.5	7.4E-01	-0.3	7.1E-01
ENSMUST00000124030				0.3	7.6E-01	-0.3	8.4E-01	0.0	9.7E-01	0.6	6.2E-01
ENSMUST00000124033	BCL6 interacting corepressor [Source:MGI Symbol;Acc:MGI:1918708]		Q8CGN4	2.8	1.5E-01	5.3	1.5E-02	-0.6	7.5E-01	-3.1	5.0E-02
ENSMUST00000147213	ATP-binding cassette, sub-family G (WHITE), member 2 [Source:MGI Symbol;Acc:MGI:1347061]	D3YZX5		6.2	1.1E-04	-3.2	1.6E-02	-8.0	2.6E-04	-0.7	5.5E-01
ENSMUST00000147218	ELK4, member of ETS oncogene family [Source:MGI Symbol;Acc:MGI:102853]	F6ZCI1		-2.2	1.5E-02	6.2	1.0E-04	0.4	6.7E-01	-0.8	2.0E-01
ENSMUST00000147225	cell death inducing Trp53 target 1 [Source:MGI Symbol;Acc:MGI:1913876]	F6X7Q6		7.8	3.2E-03	5.9	3.6E-04	-0.6	6.1E-01	0.2	7.7E-01
ENSMUST00000124053				2.0	4.4E-01	2.4	4.8E-01	0.9	7.4E-01	0.5	8.7E-01
ENSMUST00000147228	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	F6SHS0		6.6	6.1E-04	5.4	2.6E-03	-0.6	6.8E-01	0.2	8.1E-01
ENSMUST00000147282	methyl-CpG binding domain protein 4 [Source:MGI Symbol;Acc:MGI:1333850]	Q3TU27		4.1	4.2E-03	-3.7	6.8E-03	-0.5	3.9E-01	-1.6	2.0E-01
ENSMUST00000147326	mast cell immunoglobulin like receptor 1 [Source:MGI Symbol;Acc:MGI:2685731]		Q3TB92	-6.1	5.1E-04	5.9	8.6E-03	-0.7	7.2E-01	-1.5	2.2E-01
ENSMUST00000124071	diencephalon/mesencephalon homeobox 1 [Source:MGI Symbol;Acc:MGI:2153518]		Q91ZK4	2.2	2.6E-01	7.3	6.6E-03	0.6	7.8E-01	-4.5	9.2E-03
ENSMUST00000147332	haloacid dehalogenase-like hydrolase domain containing 2 [Source:MGI Symbol;Acc:MGI:1924237]		Q3UGR5	6.9	1.2E-03	-3.4	1.1E-01	0.7	4.8E-01	0.6	7.5E-01
ENSMUST00000124082	regulator of G-protein signaling 3 [Source:MGI Symbol;Acc:MGI:1354734]	I7HFV2		3.9	2.0E-01	5.0	3.1E-01	1.5	7.2E-01	0.5	8.5E-01
ENSMUST00000147337	mitogen-activated protein kinase associated protein 1 [Source:MGI Symbol;Acc:MGI:2444554]		Q8BKH7	-4.2	7.1E-03	-3.0	1.8E-02	0.1	8.7E-01	-0.9	4.0E-01
ENSMUST00000147363	prostaglandin reductase 2 [Source:MGI Symbol;Acc:MGI:1916372]		Q8VDQ1	4.2	3.5E-04	1.9	3.1E-02	-0.1	9.2E-01	0.0	9.6E-01
ENSMUST00000147380	cyclin A2 [Source:MGI Symbol;Acc:MGI:108069]	D6RIK7		-3.3	1.6E-02	5.4	1.7E-02	-0.9	6.6E-01	-0.7	5.2E-01
ENSMUST00000124087				-2.3	4.0E-02	-1.1	4.9E-01	1.8	8.9E-02	0.5	7.1E-01
ENSMUST00000124092				2.3	5.5E-02	2.3	1.2E-01	-0.3	8.2E-01	-0.4	7.1E-01
ENSMUST00000147399	CD101 antigen [Source:MGI Symbol;Acc:MGI:2685862]		A8E0Y8	-6.0	9.8E-03	5.2	5.5E-04	-1.3	2.6E-01	-0.3	6.7E-01
ENSMUST00000147407	NADH dehydrogenase (ubiquinone) Fe-S protein 6 [Source:MGI Symbol;Acc:MGI:107932]	D6RJ54		-2.7	3.2E-02	4.7	4.8E-03	-0.7	5.9E-01	-0.4	7.1E-01
ENSMUST00000124098	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]	F6RK07		1.3	3.5E-01	4.5	8.4E-03	-1.0	4.6E-01	-4.2	8.3E-03
ENSMUST00000147426	Rho guanine nucleotide exchange factor (GEF) 10-like [Source:MGI Symbol;Acc:MGI:1920004]	A2AWP4		2.6	2.8E-02	-6.0	5.0E-03	0.4	4.6E-01	-0.8	6.7E-01
ENSMUST00000147466	SET domain containing 3 [Source:MGI Symbol;Acc:MGI:1289184]	D6RCY6		6.0	7.2E-03	0.3	7.9E-01	-0.3	6.8E-01	1.5	1.4E-01
ENSMUST00000124102	ATPase, H+ transporting, lysosomal V1 subunit A [Source:MGI Symbol;Acc:MGI:1201780]	D3YWH3		0.3	9.2E-01	-2.7	4.1E-01	-3.4	1.1E-01	-0.4	9.0E-01
ENSMUST00000124107	lycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:10489	A2AMD6		0.1	9.6E-01	-2.0	6.0E-01	-2.6	2.8E-01	-0.4	9.2E-01
ENSMUST00000124111	scaffold attachment factor B2 [Source:MGI Symbol;Acc:MGI:2146808]	F6VRR0		1.5	4.7E-02	2.1	3.0E-02	-0.4	6.0E-01	-0.9	2.4E-01
ENSMUST00000147488	Rap guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:104580]	F6ZDE5		-6.7	2.2E-04	-2.5	8.0E-02	0.1	8.7E-01	0.3	8.2E-01
ENSMUST00000124113	RIKEN cDNA D230025D16 gene [Source:MGI Symbol;Acc:MGI:2443049]	D6RI91		-0.6	7.8E-01	-0.8	6.8E-01	-2.5	1.7E-01	-2.3	2.9E-01
ENSMUST00000147495	pleckstrin homology-like domain, family B, member 1 [Source:MGI Symbol;Acc:MGI:2143230]	D3Z4N0		6.1	9.0E-03	3.4	1.2E-02	-1.7	1.4E-01	-1.0	2.8E-01
ENSMUST00000147525	RIKEN cDNA 6430573F11 gene [Source:MGI Symbol;Acc:MGI:2442328]		Q80WQ4	6.5	5.6E-04	7.6	1.2E-04	-0.5	7.2E-01	-0.7	2.9E-01
ENSMUST00000124123				0.6	7.9E-01	-3.9	2.6E-01	-2.5	1.9E-01	1.9	5.6E-01
ENSMUST00000147552	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	Q6NTA3	O35892	-5.9	3.1E-04	4.5	1.5E-02	-1.4	4.0E-01	-0.8	4.4E-01
ENSMUST00000147556	rhotekin 2 [Source:MGI Symbol;Acc:MGI:2158417]		Q14B46	6.7	3.6E-03	3.5	3.6E-03	-1.9	5.9E-02	0.6	4.4E-01
ENSMUST00000124131				-0.8	2.2E-01	-0.4	5.7E-01	-0.9	1.1E-01	-1.2	1.1E-01
ENSMUST00000124136	tripartite motif-containing 26 [Source:MGI Symbol;Acc:MGI:1337056]	B8JJ53		-1.5	1.7E-01	-1.1	3.8E-01	0.0	9.5E-01	-0.5	6.9E-01
ENSMUST00000147563	zinc finger, DHHC domain containing 3 [Source:MGI Symbol;Acc:MGI:1926134]		Q8R173	-3.3	2.4E-04	4.9	1.2E-04	-0.1	9.4E-01	0.1	9.0E-01
ENSMUST00000124142	carbohydrate sulfotransferase 12 [Source:MGI Symbol;Acc:MGI:1929064]	D3YUY0		-0.1	9.3E-01	-1.2	4.4E-01	0.4	6.3E-01	1.5	2.9E-01
ENSMUST00000147574	adducin 1 (alpha) [Source:MGI Symbol;Acc:MGI:87918]	D3Z0T1		-4.7	7.5E-04	6.8	1.3E-04	-0.5	6.7E-01	-0.2	7.8E-01
ENSMUST00000147580	resistance to inhibitors of cholinesterase 3 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2443887]	F7CE80		5.7	5.1E-04	5.9	2.7E-04	0.4	6.7E-01	-0.3	6.9E-01
ENSMUST00000147595	homeobox A13 [Source:MGI Symbol;Acc:MGI:96173]	E0CXK7		5.7	3.3E-04	6.2	5.2E-04	0.8	4.7E-01	-0.5	5.0E-01
ENSMUST00000124168	polynucleotide kinase 3'- phosphatase [Source:MGI Symbol;Acc:MGI:1891698]			0.4	6.8E-01	0.4	7.8E-01	-0.1	9.4E-01	0.0	9.9E-01
ENSMUST00000124172				-0.7	7.0E-01	1.4	5.5E-01	0.2	9.3E-01	-2.0	3.2E-01
ENSMUST00000147605	nudix (nucleoside diphosphate linked moiety X)-type motif 7 [Source:MGI Symbol;Acc:MGI:1914778]		Q99P30	-5.9	7.0E-05	-3.1	8.7E-02	0.9	3.7E-01	-1.0	5.8E-01
ENSMUST00000147613	hook homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443554]	F6W1A2		-4.5	1.4E-03	4.9	1.7E-04	-0.2	8.2E-01	0.4	4.5E-01
ENSMUST00000147615	KH domain containing 1B [Source:MGI Symbol;Acc:MGI:2138477]		P0C7A0	7.2	3.5E-05	6.5	3.5E-03	-0.7	7.2E-01	-1.2	2.5E-01
ENSMUST00000124187	HAUS augmin-like complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1913546]		Q9CQS9	-2.8	1.5E-01	-3.8	1.5E-01	0.2	9.0E-01	1.2	6.5E-01
ENSMUST00000147632	proteasome (prosome, macropain) assembly chaperone 4 [Source:MGI Symbol;Acc:MGI:1916916]		P0C7N9	-3.0	6.9E-03	6.8	8.5E-04	2.0	1.6E-01	-0.5	4.9E-01
ENSMUST00000147652	tRNA selenocysteine 1 associated protein 1 [Source:MGI Symbol;Acc:MGI:1919037]	E9Q3V7		-3.9	1.8E-03	5.6	7.4E-04	-1.9	1.6E-01	-0.6	4.3E-01
ENSMUST00000147695	LON peptidase N-terminal domain and ring finger 2 [Source:MGI Symbol;Acc:MGI:1920209]	B2RT44		7.6	1.4E-05	6.6	7.2E-04	-2.0	2.3E-01	0.3	6.7E-01
ENSMUST00000147699	transmembrane protein 109 [Source:MGI Symbol;Acc:MGI:1915789]	D3YX08		5.4	7.9E-04	-6.4	1.4E-03	0.8	1.5E-01	-0.9	5.8E-01
ENSMUST00000124204				-0.3	8.3E-01	1.8	4.3E-01	1.8	3.5E-01	-0.3	8.8E-01
ENSMUST00000124205				1.3	6.9E-02	2.6	7.2E-03	0.2	8.0E-01	-1.1	1.1E-01
ENSMUST00000147714	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]	F6RJ39		-3.4	9.2E-04	5.0	2.1E-04	-0.1	9.4E-01	0.2	7.1E-01
ENSMUST00000147730	polo-like kinase 3 [Source:MGI Symbol;Acc:MGI:109604]	F6V5S5		-5.7	8.8E-04	8.6	1.0E-04	-0.6	6.7E-01	1.4	5.0E-02
ENSMUST00000147732	ornithine decarboxylase antizyme 2 [Source:MGI Symbol;Acc:MGI:109492]	J3QND2		-3.1	3.3E-02	1.9	1.4E-02	-0.3	6.4E-01	0.2	7.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000147744	phospholipase C, beta 4 [Source:MGI Symbol;Acc:MGI:107464]	A2AT93		3.8	1.7E-04	4.6	1.1E-04	-1.4	5.7E-02	-0.3	5.3E-01
ENSMUST00000147802	RAB36, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1924127]		Q8CAM5	5.1	8.8E-03	3.6	1.8E-01	-1.4	5.7E-01	1.4	4.7E-01
ENSMUST00000147835	RAS-like, family 2, locus 9 [Source:MGI Symbol;Acc:MGI:104605]	A6H622	Q61820	3.0	1.3E-02	4.0	1.3E-02	-2.1	1.7E-01	0.2	8.6E-01
ENSMUST00000124223	RIKEN cDNA D430042O09 gene [Source:MGI Symbol;Acc:MGI:2442760]	F6XQI1		0.8	7.4E-01	3.1	2.5E-01	0.3	9.0E-01	-2.0	3.7E-01
ENSMUST00000147845	ATPase, H+ transporting, lysosomal V0 subunit B [Source:MGI Symbol;Acc:MGI:1890510]			-3.8	1.5E-02	3.0	1.9E-02	-1.5	1.4E-01	0.0	9.9E-01
ENSMUST00000147852	tripartite motif-containing 62 [Source:MGI Symbol;Acc:MGI:1914775]	D6RJM1		7.2	3.1E-05	3.9	5.0E-04	1.3	7.7E-02	0.2	7.9E-01
ENSMUST00000147875	LYR motif containing 9 [Source:MGI Symbol;Acc:MGI:1913524]		Q3UN90	3.9	5.5E-05	4.4	4.9E-03	-2.1	1.4E-01	0.6	4.5E-01
ENSMUST00000147884	thioredoxin domain containing 11 [Source:MGI Symbol;Acc:MGI:1923620]	D6REU4		3.6	5.0E-05	2.9	1.8E-03	-0.3	6.7E-01	-1.2	5.1E-02
ENSMUST00000147887	in homology domain containing, family G (with RhoGef domain) member 2 [Source:MGI Symbol;Acc:MGI:2	D3Z1B1		5.9	5.9E-04	6.1	3.3E-02	0.2	9.3E-01	0.3	8.4E-01
ENSMUST00000147891	Son DNA binding protein [Source:MGI Symbol;Acc:MGI:98353]	F7CU80		-3.9	4.5E-03	2.1	5.2E-02	-4.3	4.5E-03	0.5	5.2E-01
ENSMUST00000147920	minichromosome maintenance deficient 7 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1298398]			4.1	3.3E-03	6.1	2.0E-02	1.7	4.5E-01	0.3	8.2E-01
ENSMUST00000124240				-1.4	3.9E-01	4.1	3.7E-02	2.3	1.6E-01	-3.2	6.9E-02
ENSMUST00000147936	GTPase, IMAP family member 9 [Source:MGI Symbol;Acc:MGI:3511744]	F7BEI3		-4.4	1.5E-03	8.4	4.5E-04	-0.7	7.1E-01	-2.0	4.0E-02
ENSMUST00000147964	ATA box binding protein (Tbp)-associated factor, RNA polymerase I, C [Source:MGI Symbol;Acc:MGI:10957	D6RI25		2.4	2.2E-02	6.8	3.5E-05	-1.4	1.7E-01	-0.4	4.8E-01
ENSMUST00000147976	Ras and Rab interactor 2 [Source:MGI Symbol;Acc:MGI:1921280]	E0CYG9		-5.3	3.3E-03	-4.7	3.7E-03	0.7	3.0E-01	-1.5	3.3E-01
ENSMUST00000147999	ubiquitin protein ligase E3 component n-recognin 4 [Source:MGI Symbol;Acc:MGI:1916366]	Z4YMA7		-6.5	5.6E-04	1.4	2.4E-01	-0.2	8.6E-01	0.9	3.7E-01
ENSMUST00000148007	predicted gene 11639 [Source:MGI Symbol;Acc:MGI:3651790]	F6RS26		8.7	6.3E-04	5.7	1.1E-03	0.0	9.9E-01	0.5	5.2E-01
ENSMUST00000148011	postmeiotic segregation increased 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:104288]	B9EJ22		7.1	1.8E-03	6.2	1.9E-04	-1.5	2.1E-01	-1.0	1.4E-01
ENSMUST00000148038	ATP/GTP binding protein-like 4 [Source:MGI Symbol;Acc:MGI:1918244]	F6VQN0		7.6	3.7E-05	-1.4	5.0E-01	2.2	1.2E-01	-0.7	7.2E-01
ENSMUST00000148042	zinc finger, MYND domain containing 19 [Source:MGI Symbol;Acc:MGI:1914437]		Q9CQG3	2.3	3.3E-03	4.8	8.1E-04	1.5	1.1E-01	0.3	6.7E-01
ENSMUST00000148049	actin filament associated protein 1-like 2 [Source:MGI Symbol;Acc:MGI:2147658]	D3YYQ6		7.5	4.3E-05	9.3	2.8E-06	0.7	4.7E-01	0.6	1.5E-01
ENSMUST00000148053	CDC like kinase 4 [Source:MGI Symbol;Acc:MGI:1098551]	F2Z3V2		-4.5	6.3E-03	4.9	5.9E-03	-1.5	3.5E-01	0.4	6.5E-01
ENSMUST00000124271				-1.3	2.4E-01	-2.3	2.1E-01	0.8	4.3E-01	1.8	2.8E-01
ENSMUST00000148070	LYR motif containing 7 [Source:MGI Symbol;Acc:MGI:1922780]		Q9DA03	6.3	1.6E-04	4.9	8.2E-04	0.1	9.4E-01	0.5	4.6E-01
ENSMUST00000148106	nuclear receptor subfamily 3, group C, member 2 [Source:MGI Symbol;Acc:MGI:99459]	D6RIL1		6.9	1.1E-02	5.4	2.2E-02	-0.8	7.1E-01	-0.2	8.9E-01
ENSMUST00000124280				1.5	1.1E-01	2.0	1.1E-01	0.0	9.9E-01	-0.4	6.4E-01
ENSMUST00000148159	tumor necrosis factor, alpha-induced protein 8 [Source:MGI Symbol;Acc:MGI:2147191]	D3Z325		-6.8	1.5E-06	-6.4	3.6E-04	-0.5	2.3E-01	-0.9	4.8E-01
ENSMUST00000148194	signal-regulatory protein beta 1C [Source:MGI Symbol;Acc:MGI:3807521]	F6UP26		-4.3	1.6E-03	6.0	1.3E-04	-1.5	1.8E-01	-0.5	3.6E-01
ENSMUST00000148219	Dr1 associated protein 1 (negative cofactor 2 alpha) [Source:MGI Symbol;Acc:MGI:1913806]	F6T9K1		-6.6	5.2E-04	5.6	9.9E-06	0.1	8.3E-01	0.3	4.9E-01
ENSMUST00000148234	coiled-coil domain containing 7B [Source:MGI Symbol;Acc:MGI:1922703]	D6RD02		5.0	6.4E-04	6.7	1.7E-05	1.6	6.6E-02	0.5	3.2E-01
ENSMUST00000148235	COX assembly mitochondrial protein 2 [Source:MGI Symbol;Acc:MGI:1913781]		Q8K199	-5.2	8.3E-05	3.3	1.3E-02	1.0	3.3E-01	0.6	4.5E-01
ENSMUST00000124300				0.6	8.0E-01	-3.9	1.4E-01	-5.2	8.1E-03	-0.7	7.9E-01
ENSMUST00000124302				1.8	3.1E-01	0.1	9.5E-01	-1.2	4.6E-01	0.4	7.8E-01
ENSMUST00000148242	mannose-P-dolichol utilization defect 1 [Source:MGI Symbol;Acc:MGI:1346040]	E9PVP3		-4.6	4.5E-03	-5.0	8.5E-03	-0.7	2.9E-01	-0.3	8.6E-01
ENSMUST00000148246	echinoderm microtubule associated protein like 2 [Source:MGI Symbol;Acc:MGI:1919455]	D6RGM3		-4.4	2.8E-02	1.8	3.6E-01	-0.6	7.0E-01	4.3	2.2E-02
ENSMUST00000124308				1.0	4.7E-02	1.7	2.2E-02	0.8	1.3E-01	0.1	8.3E-01
ENSMUST00000148255	tubulin polyglutamylase complex subunit 2 [Source:MGI Symbol;Acc:MGI:1913898]	E9PUD7		8.3	5.0E-07	5.1	2.7E-03	-2.5	1.1E-01	-1.5	1.1E-01
ENSMUST00000148292	adenosine monophosphate deaminase 3 [Source:MGI Symbol;Acc:MGI:1096344]	D3Z4N3		-4.5	1.4E-03	4.4	9.1E-05	-1.0	1.3E-01	0.1	8.7E-01
ENSMUST00000148330	CDC-like kinase 1 [Source:MGI Symbol;Acc:MGI:107403]		P22518	-10.7	7.7E-04	6.7	6.6E-05	0.8	4.2E-01	-0.2	6.9E-01
ENSMUST00000124314				2.1	2.1E-01	0.3	9.1E-01	0.3	8.6E-01	2.2	3.8E-01
ENSMUST00000124315				0.5	4.9E-01	0.7	4.8E-01	-0.1	9.3E-01	-0.2	8.1E-01
ENSMUST00000148331	polypyrimidine tract binding protein 3 [Source:MGI Symbol;Acc:MGI:1923334]		Q8BHD7	-8.0	1.9E-03	5.7	2.3E-02	0.1	9.8E-01	1.4	2.9E-01
ENSMUST00000148341	lipoxygenase homology domains 1 [Source:MGI Symbol;Acc:MGI:1914609]	D3YUR7		7.1	3.6E-05	-2.5	1.5E-01	0.9	3.3E-01	-2.2	2.5E-01
ENSMUST00000148361	zinc finger and BTB domain containing 7B [Source:MGI Symbol;Acc:MGI:102755]	D3Z2X8		-3.0	3.3E-02	6.1	3.5E-04	-0.6	6.1E-01	-0.2	7.0E-01
ENSMUST00000148390	solute carrier family 22, member 23 [Source:MGI Symbol;Acc:MGI:1920352]	F7BP73		9.0	3.6E-05	6.9	6.2E-05	-1.3	2.4E-01	-0.7	2.5E-01
ENSMUST00000148396	te carrier family 28 (sodium-coupled nucleoside transporter), member 3 [Source:MGI Symbol;Acc:MGI:21373	D6RFS6		3.7	6.4E-04	2.2	1.1E-01	-1.6	2.0E-01	0.9	3.9E-01
ENSMUST00000148408	WD repeat domain 17 [Source:MGI Symbol;Acc:MGI:1924662]	H3BKT9		6.6	1.3E-05	2.6	2.5E-03	0.0	9.5E-01	-0.3	5.1E-01
ENSMUST00000148442	zinc finger protein 568 [Source:MGI Symbol;Acc:MGI:2142347]	E9PYI1		4.5	1.2E-02	0.2	8.5E-01	0.4	5.7E-01	-1.6	9.2E-02
ENSMUST00000148443	cytochrome P450, family 20, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1925201]	J3QPT8		4.9	1.0E-04	-2.9	1.8E-01	2.3	4.3E-02	-0.7	7.6E-01
ENSMUST00000124340	7-dehydrocholesterol reductase [Source:MGI Symbol;Acc:MGI:1298378]		O88455	-1.5	2.6E-01	1.3	4.0E-01	-0.1	9.3E-01	-2.9	6.8E-02
ENSMUST00000148451	leucine zipper-EF-hand containing transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1932557]			6.1	8.5E-06	8.8	3.2E-05	-0.7	6.0E-01	-0.4	4.4E-01
ENSMUST00000148465	N1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2150			-5.0	9.8E-04	-3.7	3.5E-02	-0.6	4.6E-01	-0.4	8.3E-01
ENSMUST00000124346	in-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 [Source:MGI Symbol;Acc:MGI:1923	F6SPX7		-1.7	4.5E-01	-3.5	2.1E-01	-2.3	1.5E-01	-0.5	8.6E-01
ENSMUST00000148483	zinc finger protein 688 [Source:MGI Symbol;Acc:MGI:1916484]			-6.0	2.3E-04	4.6	7.0E-03	0.9	4.9E-01	-0.3	6.7E-01
ENSMUST00000124350	serum/glucocorticoid regulated kinase 1 [Source:MGI Symbol;Acc:MGI:1340062]	D3YV51		-2.4	4.5E-02	2.8	3.5E-02	2.6	1.9E-02	-2.6	4.5E-02
ENSMUST00000148486	discs, large (Drosophila) homolog-associated protein 1 [Source:MGI Symbol;Acc:MGI:1346065]	E9QAR5		6.1	5.0E-04	5.6	2.0E-03	0.0	9.8E-01	-1.3	1.4E-01
ENSMUST00000124356				-0.1	9.6E-01	3.8	1.3E-01	1.8	4.0E-01	-2.0	2.2E-01
ENSMUST00000148517	microfibrillar associated protein 5 [Source:MGI Symbol;Acc:MGI:1354387]		Q9QZJ6	4.8	4.7E-04	8.3	5.3E-05	1.1	3.6E-01	-0.4	4.9E-01
ENSMUST00000124368				-0.7	7.0E-01	-2.5	4.1E-01	-0.2	9.1E-01	1.6	5.8E-01
ENSMUST00000124385	clathrin, heavy polypeptide (Hc) [Source:MGI Symbol;Acc:MGI:2388633]	F6Z1R4		-5.9	4.2E-02	-2.2	5.4E-01	2.8	2.1E-01	-0.9	8.0E-01
ENSMUST00000148550	adenylate cyclase 10 [Source:MGI Symbol;Acc:MGI:2660854]		Q8C0T9	7.9	5.6E-05	-3.2	4.9E-02	0.6	4.6E-01	-1.5	3.7E-01
ENSMUST00000124387	zinc finger protein 324 [Source:MGI Symbol;Acc:MGI:2444641]	E0CYR3		2.1	2.4E-01	5.9	7.2E-02	4.0	1.6E-01	0.2	9.0E-01
ENSMUST00000148575	small EDRK-rich factor 2 [Source:MGI Symbol;Acc:MGI:1337041]	D6RIP7		-8.2	9.0E-06	4.4	1.8E-03	-0.1	9.3E-01	0.5	5.1E-01
ENSMUST00000148596	retinol binding protein 7, cellular [Source:MGI Symbol;Acc:MGI:1890409]	F6R1Y3		6.6	5.9E-05	5.6	8.4E-04	-0.5	6.6E-01	-2.8	8.5E-03
ENSMUST00000124396				2.3	1.3E-01	0.6	7.2E-01	-1.7	2.9E-01	-0.1	9.4E-01
ENSMUST00000124398				1.9	3.4E-01	1.7	4.7E-01	-0.7	7.2E-01	-0.5	8.1E-01
ENSMUST00000148601	acyl-Coenzyme A oxidase 1, palmitoyl [Source:MGI Symbol;Acc:MGI:1330812]	A2A848		-5.1	2.9E-03	6.7	5.6E-04	0.1	9.3E-01	0.0	9.9E-01
ENSMUST00000148604	trophinin [Source:MGI Symbol;Acc:MGI:1928994]	A2AFN3		8.0	1.1E-03	6.4	8.4E-04	-1.0	4.6E-01	1.2	1.3E-01
ENSMUST00000124409				0.0	9.9E-01	1.1	1.7E-01	0.9	1.8E-01	-0.3	7.0E-01
ENSMUST00000148618	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925947]	B7ZNL8		4.3	2.9E-03	4.8	1.6E-03	0.3	7.7E-01	0.5	4.8E-01
ENSMUST00000148633	sorcin [Source:MGI Symbol;Acc:MGI:98419]		Q6P069	-4.8	3.2E-06	6.1	3.9E-04	-0.7	5.4E-01	-1.2	1.4E-01
ENSMUST00000148665	splicing factor 3a, subunit 2 [Source:MGI Symbol;Acc:MGI:104912]	G3UVU2		-1.8	2.6E-02	6.0	3.4E-03	-0.6	7.1E-01	-1.9	9.8E-02
ENSMUST00000148670	a disintegrin and metallopeptidase domain 8 [Source:MGI Symbol;Acc:MGI:107825]	E9Q359		4.7	3.2E-02	5.9	2.6E-03	-1.1	4.6E-01	1.1	2.2E-01
ENSMUST00000124420				1.2	2.1E-01	1.6	1.8E-01	0.1	8.9E-01	-0.3	7.5E-01
ENSMUST00000148686	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3036246]	D6RJK3		9.2	2.9E-05	-5.7	5.2E-05	-0.1	6.7E-01	-0.1	9.2E-01
ENSMUST00000148702	ubiquitin interaction motif containing 1 [Source:MGI Symbol;Acc:MGI:103185]	E9PWM5		-5.2	4.3E-03	2.7	2.4E-01	-1.6	4.1E-01	3.8	6.0E-02
ENSMUST00000148713	zinc finger protein 827 [Source:MGI Symbol;Acc:MGI:2444807]	F6ULU2		6.4	3.1E-05	3.0	1.5E-01	-0.6	7.8E-01	0.9	5.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000148714	eukaryotic translation initiation factor 2B, subunit 5 epsilon [Source:MGI Symbol;Acc:MGI:2446176]	F6T9C3		-4.3	6.6E-03	6.3	3.2E-04	-0.9	4.5E-01	-1.4	5.4E-02
ENSMUST00000124443	mitogen-activated protein kinase associated protein 1 [Source:MGI Symbol;Acc:MGI:2444554]	A2AR15		-3.0	1.7E-01	-2.3	2.9E-01	-0.8	5.6E-01	-1.5	5.4E-01
ENSMUST00000148716	fucose mutarotase [Source:MGI Symbol;Acc:MGI:1916314]		Q8R2K1	7.6	1.7E-04	4.3	7.4E-03	-0.6	6.6E-01	1.8	6.1E-02
ENSMUST00000124445				3.4	5.6E-02	-0.5	7.9E-01	-2.8	9.5E-02	1.1	5.0E-01
ENSMUST00000148721	RIKEN cDNA 2310061I04 gene [Source:MGI Symbol;Acc:MGI:1916912]	B8JJ69		-4.0	1.8E-02	2.7	3.5E-03	0.0	9.6E-01	-0.6	3.0E-01
ENSMUST00000124451				-0.8	5.2E-01	-1.4	4.4E-01	-0.2	8.6E-01	0.4	8.1E-01
ENSMUST00000124466	dedicator of cytokinesis 7 [Source:MGI Symbol;Acc:MGI:1914549]			-0.1	9.6E-01	1.0	5.2E-01	-2.1	1.3E-01	-3.3	9.4E-02
ENSMUST00000148739	lamin tail domain containing 1 [Source:MGI Symbol;Acc:MGI:1921321]	E9PY33		7.4	3.2E-05	3.1	2.4E-02	0.0	9.9E-01	0.4	6.2E-01
ENSMUST00000148748	interleukin 15 receptor, alpha chain [Source:MGI Symbol;Acc:MGI:104644]	Q810T6		-5.1	1.8E-02	9.3	1.2E-05	-0.1	9.1E-01	-0.2	6.5E-01
ENSMUST00000148750	solute carrier family 4 (anion exchanger), member 4 [Source:MGI Symbol;Acc:MGI:1927555]		O88343	8.0	1.4E-05	3.9	6.5E-03	-0.2	8.8E-01	-0.5	5.5E-01
ENSMUST00000124474	solute carrier family 35, member F6 [Source:MGI Symbol;Acc:MGI:1922169]	D6RHL1		-1.0	6.8E-01	-3.0	3.5E-01	-2.4	2.0E-01	-0.4	9.0E-01
ENSMUST00000124482	mitochondrial ribosomal protein L17 [Source:MGI Symbol;Acc:MGI:1351608]		Q9D8P4	0.7	2.6E-01	2.4	1.6E-02	1.0	1.7E-01	-0.6	3.5E-01
ENSMUST00000148794	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	F7AA45		-6.5	3.5E-03	4.0	1.1E-03	-0.5	5.1E-01	0.2	7.2E-01
ENSMUST00000124484	translocated promoter region, nuclear basket protein [Source:MGI Symbol;Acc:MGI:1922066]	F6R5D8		-1.1	6.4E-01	-3.6	2.8E-01	-1.8	3.4E-01	0.8	8.2E-01
ENSMUST00000124485				2.6	3.7E-02	2.0	1.5E-01	-0.8	4.9E-01	-0.1	9.1E-01
ENSMUST00000124488	tRNA aspartic acid methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1274787]	Q5I0V6	O55055	0.3	6.3E-01	-0.9	2.1E-01	-1.1	5.3E-02	0.1	8.8E-01
ENSMUST00000148798	N-acetyltransferase 10 [Source:MGI Symbol;Acc:MGI:2138939]	E9Q498		5.9	5.8E-04	6.6	9.4E-03	-0.7	7.6E-01	-1.4	2.6E-01
ENSMUST00000124494				0.5	7.8E-01	-1.5	4.5E-01	-2.5	1.2E-01	-0.5	7.9E-01
ENSMUST00000124496	testis expressed gene 15 [Source:MGI Symbol;Acc:MGI:1934816]	E9PY31		2.1	2.9E-01	5.9	3.0E-02	1.1	6.2E-01	-2.7	1.5E-01
ENSMUST00000148810	family with sequence similarity 129, member A [Source:MGI Symbol;Acc:MGI:2137237]		Q3UW53	-4.8	6.3E-06	-4.1	9.7E-02	-0.2	8.5E-01	-0.3	9.0E-01
ENSMUST00000124501	testis expressed gene 15 [Source:MGI Symbol;Acc:MGI:1934816]	M0QWY2		-1.8	1.3E-01	-1.8	2.5E-01	0.4	7.2E-01	0.4	8.1E-01
ENSMUST00000124505	adenylate cyclase 3 [Source:MGI Symbol;Acc:MGI:99675]	B8JK56		3.3	3.9E-02	3.1	3.6E-02	-2.9	5.3E-02	-2.7	3.9E-02
ENSMUST00000148834	ATP/GTP binding protein-like 3 [Source:MGI Symbol;Acc:MGI:1923473]	D6RI59		6.6	1.8E-04	7.8	5.3E-04	0.4	8.0E-01	0.1	8.8E-01
ENSMUST00000124516	myosin, heavy polypeptide 1, skeletal muscle, adult [Source:MGI Symbol;Acc:MGI:1339711]		Q5SX40	7.4	5.5E-02	6.4	1.1E-01	-1.0	8.0E-01	0.0	1.0E+00
ENSMUST00000148835	intermediate filament family orphan 1 [Source:MGI Symbol;Acc:MGI:2444516]	F6VMG1		-4.7	1.1E-03	4.1	8.8E-03	-1.3	2.9E-01	-0.6	5.4E-01
ENSMUST00000148843	heterogeneous nuclear ribonucleoprotein R [Source:MGI Symbol;Acc:MGI:1891692]	Q8VHM5		3.0	2.9E-03	9.2	1.0E-05	-0.6	6.0E-01	0.9	5.0E-02
ENSMUST00000148873	armadillo repeat containing 10 [Source:MGI Symbol;Acc:MGI:1914461]		Q9D0L7	5.9	1.2E-03	4.5	3.0E-03	-3.7	1.9E-02	0.4	5.9E-01
ENSMUST00000148891	phosphatase and actin regulator 1 [Source:MGI Symbol;Acc:MGI:2659021]		Q2M3X8	9.1	1.5E-05	6.8	8.3E-05	-1.4	2.2E-01	-0.1	8.7E-01
ENSMUST00000148895	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 [Source:MGI Symbol;Acc:MGI:1916327]	G3UYH2		-5.4	3.1E-04	-1.4	2.5E-01	2.0	1.7E-02	-1.1	4.1E-01
ENSMUST00000148897	GLI pathogenesis-related 1 like 2 [Source:MGI Symbol;Acc:MGI:1914787]		Q9CQ35	5.9	1.8E-04	1.9	6.7E-02	-1.9	4.9E-02	-1.4	1.2E-01
ENSMUST00000148899	choline phosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2384841]	F6X1K1		5.2	1.8E-02	7.3	4.6E-05	-0.6	6.0E-01	-0.5	3.5E-01
ENSMUST00000148928	predicted gene 5475 [Source:MGI Symbol;Acc:MGI:3646320]	Q3TR11		7.1	1.6E-04	-2.1	8.5E-02	1.0	1.4E-01	-1.6	2.0E-01
ENSMUST00000148945	zinc finger protein 652 [Source:MGI Symbol;Acc:MGI:2442221]	F2Z3V9		-5.1	6.0E-03	5.6	6.4E-04	-0.5	6.5E-01	0.0	9.6E-01
ENSMUST00000148950	transmembrane protein 171 [Source:MGI Symbol;Acc:MGI:2685751]	D3Z2U9		5.4	4.0E-03	6.0	1.8E-03	0.2	8.8E-01	0.0	9.5E-01
ENSMUST00000148955	haloacid dehalogenase-like hydrolase domain containing 2 [Source:MGI Symbol;Acc:MGI:1924237]		Q3UGR5	4.8	3.3E-03	2.4	5.6E-03	0.2	7.3E-01	0.0	9.6E-01
ENSMUST00000148960	myosin, light chain 12A, regulatory, non-sarcomeric [Source:MGI Symbol;Acc:MGI:1914518]	Q6ZWQ9		-4.5	1.6E-04	0.6	5.8E-01	1.7	5.3E-02	-1.8	1.2E-01
ENSMUST00000148989	tumor necrosis factor, alpha-induced protein 8 [Source:MGI Symbol;Acc:MGI:2147191]	D3YWJ5		-4.4	2.3E-02	-6.8	3.1E-02	0.2	8.0E-01	-0.8	7.9E-01
ENSMUST00000149011	zinc finger protein 473 [Source:MGI Symbol;Acc:MGI:2442697]	E9QAY2		5.2	6.8E-06	6.0	5.6E-04	-0.5	7.1E-01	-0.5	4.4E-01
ENSMUST00000124559				-0.5	6.6E-01	-0.7	6.6E-01	0.3	7.7E-01	0.6	7.1E-01
ENSMUST00000124563				-0.1	8.7E-01	0.9	3.4E-01	-0.6	4.5E-01	-1.6	9.4E-02
ENSMUST00000149019	neighbor of Brca1 gene 1 [Source:MGI Symbol;Acc:MGI:108498]	F6S397		-5.3	7.0E-03	-2.9	1.2E-02	-0.1	8.9E-01	-0.2	8.4E-01
ENSMUST00000124566	olgi associated, gamma adaptin ear containing, ARF binding protein 2 [Source:MGI Symbol;Acc:MGI:192135:		Q6P5E6	1.3	5.2E-01	4.4	1.8E-01	4.1	1.8E-01	0.9	6.5E-01
ENSMUST00000149023	eva-1 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:2385247]	D3Z511		6.0	5.5E-04	-2.0	8.2E-02	1.1	1.3E-01	-1.4	2.4E-01
ENSMUST00000149026	Tp53rk binding protein [Source:MGI Symbol;Acc:MGI:1917036]	D3Z5E8		3.7	1.4E-02	5.7	1.2E-03	-0.5	7.1E-01	-1.1	1.5E-01
ENSMUST00000124576	SET binding factor 1 [Source:MGI Symbol;Acc:MGI:1925230]	D6RG52		-0.6	8.7E-01	-0.8	8.5E-01	-0.2	9.5E-01	0.0	9.9E-01
ENSMUST00000124584				-0.8	2.2E-01	1.1	2.1E-01	1.9	1.5E-02	0.0	9.9E-01
ENSMUST00000149034	solute carrier family 39 (metal ion transporter), member 11 [Source:MGI Symbol;Acc:MGI:1917056]	B1ARC5		4.2	1.9E-04	6.0	1.0E-03	0.2	8.8E-01	-0.6	4.9E-01
ENSMUST00000124595				1.1	3.0E-01	1.2	4.4E-01	0.9	5.0E-01	0.8	4.8E-01
ENSMUST00000149046	retrotransposon-like 1 [Source:MGI Symbol;Acc:MGI:2656842]	B4YB44	Q7M732	5.7	6.8E-06	-2.2	1.6E-01	-0.1	9.5E-01	-1.9	2.7E-01
ENSMUST00000149052	nology domain containing, family A (phosphoinositide binding specific) member 4 [Source:MGI Symbol;Acc:M	E9PUJ9		7.0	5.2E-05	2.4	1.0E-02	-0.3	6.9E-01	-0.8	2.2E-01
ENSMUST00000149068	lamin A [Source:MGI Symbol;Acc:MGI:96794]	D3YUF7		7.0	8.6E-05	0.2	9.2E-01	3.6	1.0E-02	0.5	7.1E-01
ENSMUST00000149119	eukaryotic translation initiation factor 2D [Source:MGI Symbol;Acc:MGI:109342]	M0QWK9		2.6	4.3E-03	6.8	2.2E-06	0.1	9.3E-01	0.3	4.2E-01
ENSMUST00000149123	transmembrane protein 168 [Source:MGI Symbol;Acc:MGI:1921794]			-3.3	1.8E-02	-5.9	6.2E-04	-2.7	4.1E-04	-1.0	4.3E-01
ENSMUST00000149144	zinc finger, AN1-type domain 5 [Source:MGI Symbol;Acc:MGI:1278334]	D6RFT9		-5.7	1.7E-04	-5.4	1.0E-02	-0.3	7.0E-01	-0.9	6.4E-01
ENSMUST00000149146	Eph receptor A10 [Source:MGI Symbol;Acc:MGI:3586824]	F6WVB0		8.7	2.1E-05	6.1	4.0E-03	-0.6	7.2E-01	-1.5	1.5E-01
ENSMUST00000124616				-0.1	9.2E-01	-0.3	7.7E-01	0.5	5.6E-01	0.7	5.1E-01
ENSMUST00000149150	integrin alpha 9 [Source:MGI Symbol;Acc:MGI:104756]	F7DB81		4.5	5.0E-05	2.6	5.8E-03	-0.5	4.2E-01	-0.4	4.9E-01
ENSMUST00000149154	protocadherin 19 [Source:MGI Symbol;Acc:MGI:2685563]		Q80TF3	6.9	1.0E-04	-4.7	5.1E-03	-0.7	2.6E-01	0.0	9.8E-01
ENSMUST00000149159	X-box binding protein 1 [Source:MGI Symbol;Acc:MGI:98970]	G3UYH6		-2.6	3.8E-03	-2.2	1.4E-01	0.4	6.4E-01	-1.6	3.0E-01
ENSMUST00000124638				0.1	9.0E-01	1.2	2.5E-01	0.7	3.5E-01	-0.4	6.8E-01
ENSMUST00000149168	olute carrier family 6 (neurotransmitter transporter, glycine), member 9 [Source:MGI Symbol;Acc:MGI:95760	E9PWC4		8.8	5.9E-04	5.7	5.6E-04	0.3	8.0E-01	-0.7	3.3E-01
ENSMUST00000149179	collagen, type XX, alpha 1 [Source:MGI Symbol;Acc:MGI:1920618]	F6UFI2		6.1	1.7E-02	-10.4	2.8E-04	-1.3	2.8E-02	-0.6	7.5E-01
ENSMUST00000149243	mitochondrial ribosomal protein L3 [Source:MGI Symbol;Acc:MGI:2137204]	D3Z456		1.8	1.3E-02	6.3	1.1E-03	-1.4	3.5E-01	-0.7	3.3E-01
ENSMUST00000149248	spastic paraplegia 7 homolog (human) [Source:MGI Symbol;Acc:MGI:2385906]	D3Z1Z1		6.9	5.8E-03	6.0	1.8E-04	-0.9	4.0E-01	0.1	9.1E-01
ENSMUST00000149261	peroxiredoxin 5 [Source:MGI Symbol;Acc:MGI:1859821]	H3BJQ7		-9.0	4.9E-06	-1.3	2.7E-01	0.2	7.6E-01	-1.5	2.5E-01
ENSMUST00000149322	propionyl Coenzyme A carboxylase, beta polypeptide [Source:MGI Symbol;Acc:MGI:1914154]	E9Q1J7		5.4	2.6E-03	5.7	4.5E-04	0.8	4.3E-01	-0.2	7.3E-01
ENSMUST00000149353	matrix metallopeptidase 16 [Source:MGI Symbol;Acc:MGI:1276107]	B1AVH0		6.5	2.0E-04	2.5	4.0E-01	-0.7	7.8E-01	2.7	2.3E-01
ENSMUST00000149359	MKL/myocardin-like 2 [Source:MGI Symbol;Acc:MGI:3050795]	Q5DTZ3		3.2	2.1E-05	5.3	1.7E-05	-0.3	6.0E-01	0.0	9.5E-01
ENSMUST00000149384	heterogeneous nuclear ribonucleoprotein D-like [Source:MGI Symbol;Acc:MGI:1355299]	F6ZKM7		-4.8	1.1E-03	5.6	2.6E-03	-0.6	7.1E-01	-1.5	1.1E-01
ENSMUST00000149395	leukocyte-associated Ig-like receptor 1 [Source:MGI Symbol;Acc:MGI:105492]	D6RGS7	Q8BG84	-6.0	1.6E-05	6.3	2.3E-04	-0.5	6.7E-01	-0.7	2.6E-01
ENSMUST00000149405	cDNA sequence BC004004 [Source:MGI Symbol;Acc:MGI:2136782]		Q99KU6	-6.6	1.1E-05	6.1	4.0E-02	5.0	5.9E-02	3.2	4.0E-02
ENSMUST00000124684				1.8	8.4E-02	2.0	1.0E-01	0.3	7.3E-01	0.1	9.3E-01
ENSMUST00000149410	CAP-GLY domain containing linker protein 1 [Source:MGI Symbol;Acc:MGI:1928401]	Q8C0S5		5.1	5.5E-03	6.7	1.4E-04	-0.3	8.1E-01	0.2	7.1E-01
ENSMUST00000149415	required for meiotic nuclear division 5 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915727]	F6V8A7		-4.8	2.4E-03	6.6	1.7E-04	0.5	6.2E-01	0.2	7.6E-01
ENSMUST00000149444	polymerase (DNA directed), gamma [Source:MGI Symbol;Acc:MGI:1196389]	D6RIP1		-6.4	6.8E-05	5.5	5.3E-03	-0.4	8.1E-01	-0.2	8.5E-01
ENSMUST00000149453	cytochrome b5 reductase-like [Source:MGI Symbol;Acc:MGI:1919657]	F2Z4B1		7.5	2.6E-03	3.7	2.3E-03	0.0	9.7E-01	0.9	1.8E-01
ENSMUST00000124699				1.0	2.7E-01	1.4	2.6E-01	0.3	7.5E-01	-0.1	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000149485	Vps20-associated 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913451]	F6W5Q8		-5.8	2.7E-05	6.5	2.4E-04	1.1	3.4E-01	-0.2	7.6E-01
ENSMUST00000124703				3.7	8.9E-02	4.0	5.5E-02	-1.5	4.8E-01	-1.9	2.1E-01
ENSMUST00000124704				0.1	8.9E-01	-0.5	6.6E-01	-0.4	6.4E-01	0.3	8.2E-01
ENSMUST00000124707				-2.3	1.1E-01	0.0	9.8E-01	-0.3	7.6E-01	-2.6	7.5E-02
ENSMUST00000149529	troponin I, skeletal, fast 2 [Source:MGI Symbol;Acc:MGI:105070]		P13412	-2.0	2.6E-02	5.4	7.9E-04	-1.5	2.5E-01	-0.5	4.8E-01
ENSMUST00000124711	mannosidase 2, alpha B2 [Source:MGI Symbol;Acc:MGI:1195262]	F6TMZ3		0.0	9.9E-01	-0.9	7.6E-01	0.1	9.6E-01	1.0	6.9E-01
ENSMUST00000149564	RIKEN cDNA 2700049A03 gene [Source:MGI Symbol;Acc:MGI:1924217]		E9PV87	-4.7	6.6E-03	4.5	1.4E-02	-1.4	4.1E-01	0.0	9.9E-01
ENSMUST00000149565	l-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) [Source:MGI Symbol;Acc:M		Q9D1E8	3.5	1.8E-03	6.4	2.5E-04	-0.5	6.7E-01	-0.2	7.0E-01
ENSMUST00000149566	ribosomal protein L7 [Source:MGI Symbol;Acc:MGI:98073]	F6XI62		-11.2	9.6E-06	-4.6	2.2E-03	-1.2	3.4E-02	-0.1	9.5E-01
ENSMUST00000124720	transmembrane protein 260 [Source:MGI Symbol;Acc:MGI:2443219]		Q8BMD6	0.4	5.2E-01	0.9	2.2E-01	0.9	1.2E-01	0.4	5.7E-01
ENSMUST00000149569	apolipoprotein L 6 [Source:MGI Symbol;Acc:MGI:1919189]	B7ZC54		7.2	4.6E-04	6.8	6.1E-03	-0.8	7.2E-01	-1.8	1.5E-01
ENSMUST00000149578	SET nuclear oncogene [Source:MGI Symbol;Acc:MGI:1860267]	A2BE92		4.6	1.4E-02	6.0	9.0E-03	0.5	7.7E-01	-1.2	2.8E-01
ENSMUST00000149580	nucleolar protein 12 [Source:MGI Symbol;Acc:MGI:2146285]	B7ZBX7		-4.0	1.4E-03	3.4	1.2E-02	-0.5	6.6E-01	0.6	4.7E-01
ENSMUST00000149582	MKL (megakaryoblastic leukemia)/myocardin-like 1 [Source:MGI Symbol;Acc:MGI:2384495]		Q8K4J6	-3.8	1.9E-02	7.8	3.1E-05	-1.5	2.0E-01	0.7	1.7E-01
ENSMUST00000149604	syncytin a [Source:MGI Symbol;Acc:MGI:2684898]	Q5G5D5		6.8	2.3E-05	7.5	2.3E-02	2.6	3.6E-01	-0.2	9.0E-01
ENSMUST00000149644	hexokinase 3 [Source:MGI Symbol;Acc:MGI:2670962]	D6RCV7		-2.6	7.5E-03	-5.0	1.0E-01	1.5	2.3E-01	-0.7	8.1E-01
ENSMUST00000149652	enolase 2, gamma neuronal [Source:MGI Symbol;Acc:MGI:95394]	D3Z2S4		6.5	1.9E-04	6.7	3.2E-03	-0.7	7.2E-01	0.6	5.3E-01
ENSMUST00000124750				0.6	5.1E-01	1.9	1.3E-01	1.0	3.3E-01	-0.3	7.5E-01
ENSMUST00000149663	CD300 antigen like family member B [Source:MGI Symbol;Acc:MGI:2685099]	Q3TEQ8		-5.1	3.0E-05	7.5	2.4E-04	-0.8	5.6E-01	-0.5	5.0E-01
ENSMUST00000149668	arylformamidase [Source:MGI Symbol;Acc:MGI:2448704]	B1AQL0		9.8	4.3E-04	5.9	3.3E-02	3.0	2.1E-01	1.4	3.0E-01
ENSMUST00000149706	prostaglandin E synthase 3 (cytosolic)-like [Source:MGI Symbol;Acc:MGI:1916146]	F7BAN7		6.6	7.0E-05	5.2	9.8E-06	-0.7	2.4E-01	-0.4	3.4E-01
ENSMUST00000124778				-0.1	9.1E-01	0.6	5.6E-01	-0.4	6.3E-01	-1.0	3.0E-01
ENSMUST00000149712	ankyrin repeat and EF-hand domain containing 1 [Source:MGI Symbol;Acc:MGI:2441685]	D6RDT8		5.7	2.0E-02	-1.1	3.6E-01	0.7	4.4E-01	-1.0	4.4E-01
ENSMUST00000149716	hydroxyacyl glutathione hydrolase [Source:MGI Symbol;Acc:MGI:95745]	D3YUX8		5.0	1.4E-02	5.9	1.6E-03	-0.6	6.9E-01	-0.8	2.9E-01
ENSMUST00000124801				-2.3	4.6E-02	-2.6	8.2E-02	-0.1	8.9E-01	0.2	8.8E-01
ENSMUST00000124806				1.7	3.6E-01	1.4	5.4E-01	-0.7	7.0E-01	-0.4	8.6E-01
ENSMUST00000149719	abl-interactor 1 [Source:MGI Symbol;Acc:MGI:104913]	Q3TPY5	Q8CBW3	-3.8	3.3E-02	6.8	7.3E-04	-0.6	6.5E-01	1.3	1.1E-01
ENSMUST00000124808				-0.2	7.1E-01	0.7	3.9E-01	0.4	5.6E-01	-0.6	4.4E-01
ENSMUST00000149744	collagen, type XVIII, alpha 1 [Source:MGI Symbol;Acc:MGI:88451]	D3Z5C2		6.6	7.7E-05	4.0	1.8E-03	-1.0	3.1E-01	-0.8	2.8E-01
ENSMUST00000149747	zinc finger protein 687 [Source:MGI Symbol;Acc:MGI:1925516]	D3Z717		5.2	3.3E-02	5.5	2.0E-05	-0.1	8.7E-01	-0.8	1.3E-01
ENSMUST00000149756	tubby like protein 4 [Source:MGI Symbol;Acc:MGI:1916092]	Q3UH13		5.3	1.4E-06	8.7	5.4E-03	3.2	2.1E-01	0.0	9.8E-01
ENSMUST00000124821	transmembrane protein 41B [Source:MGI Symbol;Acc:MGI:1289225]	D6RIR0		0.6	7.9E-01	-3.2	2.7E-01	-3.4	8.3E-02	0.4	8.8E-01
ENSMUST00000149776	dual specificity phosphatase 16 [Source:MGI Symbol;Acc:MGI:1917936]	Q8BZE4		4.4	7.2E-05	6.1	6.8E-06	-0.5	4.3E-01	-0.1	7.3E-01
ENSMUST00000149800	Eph receptor B1 [Source:MGI Symbol;Acc:MGI:1096337]	Q8CA63		10.2	6.0E-06	5.8	1.8E-03	0.1	9.7E-01	-0.7	4.1E-01
ENSMUST00000149854	lycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:10489	D6RGT7		-4.8	9.4E-03	-7.6	1.2E-02	-2.1	2.6E-02	2.2	3.9E-01
ENSMUST00000149867	ankyrin repeat domain 40 [Source:MGI Symbol;Acc:MGI:1918702]	B7ZC98		3.0	2.8E-02	7.3	8.5E-06	1.4	1.0E-01	-0.1	7.4E-01
ENSMUST00000149868	ATPase, H+ transporting, lysosomal V0 subunit B [Source:MGI Symbol;Acc:MGI:1890510]	M0QWE4		-2.9	2.4E-02	5.4	8.3E-03	-1.5	3.8E-01	0.8	4.3E-01
ENSMUST00000149892	disrupted in renal carcinoma 2 (human) [Source:MGI Symbol;Acc:MGI:2387188]	D6RI31		-6.5	6.4E-05	4.9	1.9E-05	-0.6	3.3E-01	-0.4	3.1E-01
ENSMUST00000149927	DNA segment, Chr 1, ERATO Doi 622, expressed [Source:MGI Symbol;Acc:MGI:1277184]		Q8VEB3	-10.7	1.3E-06	-4.7	9.5E-04	-0.6	2.6E-01	-2.1	8.9E-02
ENSMUST00000149964	potassium voltage-gated channel, subfamily Q, member 2 [Source:MGI Symbol;Acc:MGI:1309503]	B7ZBV9		9.2	1.2E-05	3.8	9.9E-02	2.1	2.8E-01	1.8	2.0E-01
ENSMUST00000149975	chromodomain helicase DNA binding protein 8 [Source:MGI Symbol;Acc:MGI:1915022]	F7AL76		-4.2	1.6E-02	5.0	2.1E-03	-0.1	9.0E-01	0.0	9.7E-01
ENSMUST00000124852				0.5	3.7E-01	0.8	2.4E-01	-0.6	2.9E-01	-0.8	2.0E-01
ENSMUST00000149983	glutamate-cysteine ligase, modifier subunit [Source:MGI Symbol;Acc:MGI:104995]	F6VNW5		-7.1	1.0E-05	3.6	7.9E-03	-3.3	3.0E-02	-1.4	1.5E-01
ENSMUST00000150019	DDB1 and CUL4 associated factor 11 [Source:MGI Symbol;Acc:MGI:90168]	D6REI5		-5.9	1.7E-02	6.5	1.3E-04	-2.8	3.9E-02	-0.1	9.0E-01
ENSMUST00000150029	RalBP1 associated Eps domain containing protein [Source:MGI Symbol;Acc:MGI:1196373]	F6R6F1		-5.1	2.1E-02	8.7	1.4E-05	-1.1	3.2E-01	-1.1	4.4E-02
ENSMUST00000150041	homeobox A7 [Source:MGI Symbol;Acc:MGI:96179]	A0A087WR88		6.0	2.1E-04	6.9	1.2E-03	-0.3	8.5E-01	1.2	1.6E-01
ENSMUST00000150042	mitochondrial ribosomal protein L48 [Source:MGI Symbol;Acc:MGI:1289321]	E9QPQ8		2.9	3.6E-03	5.0	1.8E-03	-0.9	4.5E-01	0.3	7.0E-01
ENSMUST00000150050	cone-rod homeobox, opposite strand [Source:MGI Symbol;Acc:MGI:2451355]	B6ZND8		7.2	2.3E-02	6.1	3.4E-03	0.9	5.8E-01	0.5	5.9E-01
ENSMUST00000150054	ke tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase [Source:MGI Symbol;Acc:MG	E9PVR3		5.7	1.0E-03	-6.2	1.5E-02	-1.7	7.6E-02	1.0	6.6E-01
ENSMUST00000124886	mitogen-activated protein kinase 14 [Source:MGI Symbol;Acc:MGI:1346865]	B2KF34		-0.7	7.9E-01	2.0	5.7E-01	2.0	4.5E-01	-0.8	8.1E-01
ENSMUST00000150060	leucine rich repeat containing 49 [Source:MGI Symbol;Acc:MGI:2442689]	D6RIL3		5.3	5.1E-03	2.3	1.3E-01	-4.9	1.1E-02	0.8	4.8E-01
ENSMUST00000124889				-3.0	8.2E-02	-2.1	2.8E-01	0.1	9.3E-01	-0.7	7.3E-01
ENSMUST00000150063	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	Q3U9V4	P62880	-2.5	9.4E-03	4.3	9.3E-03	-0.8	5.1E-01	0.0	9.9E-01
ENSMUST00000150068	predicted gene 20518 [Source:MGI Symbol;Acc:MGI:5141983]	E9Q548		5.5	6.4E-04	-4.8	2.0E-02	0.3	7.0E-01	-1.0	6.0E-01
ENSMUST00000150076	arrestin, beta 2 [Source:MGI Symbol;Acc:MGI:99474]	J3QN53		-2.3	2.5E-02	-1.8	2.2E-01	0.6	4.6E-01	-0.5	7.3E-01
ENSMUST00000124904				1.9	7.1E-02	1.5	1.8E-01	-1.4	1.4E-01	-1.0	3.0E-01
ENSMUST00000124905				1.7	1.6E-01	1.5	3.9E-01	0.4	7.8E-01	0.6	6.4E-01
ENSMUST00000150106	SV2 related protein [Source:MGI Symbol;Acc:MGI:1915916]	D3Z379		5.8	9.0E-04	4.6	5.4E-03	-0.4	7.6E-01	-0.9	3.1E-01
ENSMUST00000150120	cell division cycle associated 3 [Source:MGI Symbol;Acc:MGI:1315198]	D3Z3H6		-4.8	9.8E-03	7.1	1.7E-04	-0.7	6.1E-01	0.4	5.7E-01
ENSMUST00000150128	COX assembly mitochondrial protein 2 [Source:MGI Symbol;Acc:MGI:1913781]	D6RJ47		4.8	9.2E-03	7.0	2.1E-04	-0.6	6.3E-01	0.3	6.1E-01
ENSMUST00000124922				-1.9	7.0E-02	-1.6	2.5E-01	0.6	4.9E-01	0.2	8.6E-01
ENSMUST00000150134	phosphatase, orphan 1 [Source:MGI Symbol;Acc:MGI:2447348]	F6Y6Q2		-6.0	3.3E-05	5.6	7.1E-06	0.1	8.7E-01	0.1	8.7E-01
ENSMUST00000124926	enhancer of polycomb homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1278322]	D3Z3Q6		1.5	3.4E-01	-3.0	2.5E-01	-2.3	1.3E-01	2.2	3.7E-01
ENSMUST00000150139	regulator of G-protein signaling 12 [Source:MGI Symbol;Acc:MGI:1918979]	F6YRR2		5.4	2.4E-04	7.9	1.0E-04	-0.5	6.8E-01	-0.2	6.7E-01
ENSMUST00000150155	WD repeat domain 66 [Source:MGI Symbol;Acc:MGI:1918495]	F6W2U4		7.7	3.1E-05	5.9	9.4E-04	-0.6	6.5E-01	-0.4	5.4E-01
ENSMUST00000124936				0.4	5.7E-01	6.4	1.1E-03	5.6	1.4E-03	-0.3	6.6E-01
ENSMUST00000150183	coiled-coil domain containing 34 [Source:MGI Symbol;Acc:MGI:1915451]	F6U3Z3		5.6	1.1E-03	5.7	1.1E-03	-0.5	6.9E-01	-0.4	6.2E-01
ENSMUST00000150184	folate receptor 1 (adult) [Source:MGI Symbol;Acc:MGI:95568]	Q9R223		6.8	2.5E-03	6.5	4.9E-04	-0.7	5.7E-01	1.1	1.6E-01
ENSMUST00000124943	arrestin, beta 2 [Source:MGI Symbol;Acc:MGI:99474]	J3QNV6		-1.5	1.5E-01	0.1	9.4E-01	0.2	8.2E-01	-1.4	2.3E-01
ENSMUST00000150268	pleiotropic regulator 1, PRL1 homolog (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1858197]		Q922V4	-5.1	2.4E-03	4.6	3.4E-03	0.6	5.8E-01	-0.7	3.9E-01
ENSMUST00000124945				2.7	2.0E-01	1.3	4.9E-01	-2.8	1.8E-01	-1.4	3.9E-01
ENSMUST00000124946				-1.3	3.1E-01	-0.5	7.5E-01	0.3	7.8E-01	-0.5	7.6E-01
ENSMUST00000150279	xeroderma pigmentosum, complementation group C [Source:MGI Symbol;Acc:MGI:103557]			2.8	2.5E-03	1.7	3.8E-02	-0.7	3.0E-01	-0.3	6.1E-01
ENSMUST00000150285	ly 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 [Source:MGI Symbol;A		Q8BX24	5.6	8.7E-03	-4.2	2.2E-02	-0.3	7.0E-01	0.4	8.0E-01
ENSMUST00000150290	lectin, galactose binding, soluble 3 [Source:MGI Symbol;Acc:MGI:96778]	Q8C253		-11.2	4.5E-06	3.7	2.8E-03	-0.8	3.4E-01	-0.3	6.9E-01
ENSMUST00000124965				-1.4	1.2E-01	0.4	6.7E-01	0.9	2.7E-01	-0.9	3.4E-01
ENSMUST00000124971	Harvey rat sarcoma virus oncogene [Source:MGI Symbol;Acc:MGI:96224]	C0H5X4		-1.6	1.8E-01	1.9	1.8E-01	1.5	2.2E-01	-2.0	1.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000150300	diacylglycerol kinase, iota [Source:MGI Symbol;Acc:MGI:2443430]	S4R215		6.2	6.5E-04	-2.2	2.5E-02	0.4	4.2E-01	-1.3	1.8E-01
ENSMUST00000124974				-3.3	4.3E-02	-3.3	1.2E-01	0.8	5.1E-01	0.9	6.5E-01
ENSMUST00000150311	oid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) [Source:MGI Symbol;Acc:MGI:1075	D3Z6L5		-4.2	4.3E-04	6.9	2.0E-04	0.1	9.6E-01	-0.3	6.4E-01
ENSMUST00000150336	zinc finger protein 287 [Source:MGI Symbol;Acc:MGI:2176561]	Q3UZW0		6.2	3.3E-06	-3.9	2.1E-03	0.3	5.3E-01	-2.7	4.3E-02
ENSMUST00000150350	ribosomal protein L13A [Source:MGI Symbol;Acc:MGI:1351455]	Q5M9M0	P19253	-4.7	1.8E-04	-3.9	1.5E-02	0.2	8.2E-01	-1.7	2.9E-01
ENSMUST00000150359	coiled-coil domain containing 158 [Source:MGI Symbol;Acc:MGI:2444555]		Q8CDI6	6.5	2.0E-04	4.4	3.1E-03	0.3	8.0E-01	0.0	9.6E-01
ENSMUST00000125005				-1.2	4.2E-01	-1.6	2.7E-01	-2.7	3.3E-02	-2.3	1.5E-01
ENSMUST00000150365	S-adenosylhomocysteine hydrolase-like 2 [Source:MGI Symbol;Acc:MGI:1921590]	E9PX77		4.5	1.4E-03	6.3	7.1E-03	-0.1	9.5E-01	0.4	7.2E-01
ENSMUST00000150384	RIKEN cDNA A230065H16 gene [Source:MGI Symbol;Acc:MGI:2685744]	G3UW55		6.3	2.5E-04	7.1	9.1E-04	-0.7	6.5E-01	0.3	7.5E-01
ENSMUST00000150412	paralemmin A kinase anchor protein [Source:MGI Symbol;Acc:MGI:5141924]	F7AA26		6.5	6.0E-04	6.3	3.2E-04	-0.6	6.0E-01	0.1	9.1E-01
ENSMUST00000150434	bromodomain and WD repeat domain containing 3 [Source:MGI Symbol;Acc:MGI:3029414]		A2AHJ4	-2.7	2.2E-02	7.1	1.8E-05	-0.4	6.3E-01	0.3	5.1E-01
ENSMUST00000125024				-3.3	1.2E-01	-3.0	2.5E-01	0.6	6.7E-01	0.3	9.1E-01
ENSMUST00000125025				0.7	4.5E-01	2.6	7.7E-02	0.6	5.9E-01	-1.2	2.4E-01
ENSMUST00000150440	zinc finger protein 326 [Source:MGI Symbol;Acc:MGI:1927246]	D3YXQ7		-2.3	2.2E-02	3.5	6.7E-04	-0.6	3.8E-01	-0.1	8.7E-01
ENSMUST00000125032	synaptojanin 1 [Source:MGI Symbol;Acc:MGI:1354961]	F6VSS8		-2.5	3.8E-02	-1.7	2.2E-01	0.1	9.3E-01	-0.8	5.8E-01
ENSMUST00000125036	src homology 2 domain-containing transforming protein C1 [Source:MGI Symbol;Acc:MGI:98296]	D3YZV5		-2.1	9.5E-02	0.3	8.6E-01	1.9	1.1E-01	-0.5	7.5E-01
ENSMUST00000125037	PX domain containing 1 [Source:MGI Symbol;Acc:MGI:1914145]	D6REG6		2.8	1.6E-01	5.3	1.5E-02	-0.6	7.6E-01	-3.2	5.0E-02
ENSMUST00000150459	RIKEN cDNA 1500009L16 gene [Source:MGI Symbol;Acc:MGI:1917034]		P0C913	5.2	2.8E-04	2.7	4.6E-02	0.1	9.3E-01	0.0	9.7E-01
ENSMUST00000150498	nuclear receptor subfamily 2, group F, member 1 [Source:MGI Symbol;Acc:MGI:1352451]	B8JJI9		7.4	2.6E-04	-2.8	1.8E-02	0.1	8.6E-01	-0.8	4.4E-01
ENSMUST00000150545	p53 and DNA damage regulated 1 [Source:MGI Symbol;Acc:MGI:1915809]	D6RFC3		5.3	3.3E-02	6.9	1.3E-04	-0.2	8.7E-01	-0.1	9.1E-01
ENSMUST00000150557	torsin family 3, member A [Source:MGI Symbol;Acc:MGI:1353652]	M0QWH2		7.9	2.6E-03	6.5	7.1E-03	-1.0	6.0E-01	0.1	8.8E-01
ENSMUST00000150563	cytochrome b-561 [Source:MGI Symbol;Acc:MGI:103253]	V9GWU6		6.2	1.7E-03	-3.4	2.0E-02	0.2	7.6E-01	0.4	7.8E-01
ENSMUST00000150571	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 [Source:MGI Symbol;Acc:MGI:2385884]		Q921N6	5.4	1.1E-05	-1.9	4.7E-01	2.8	1.0E-01	-0.3	9.2E-01
ENSMUST00000125054				0.1	8.2E-01	0.7	3.6E-01	0.0	9.6E-01	-0.5	4.4E-01
ENSMUST00000125058				1.4	5.7E-02	3.0	1.1E-02	1.3	1.4E-01	-0.3	6.9E-01
ENSMUST00000125063				-0.5	6.9E-01	-1.1	4.4E-01	-0.7	5.1E-01	-0.1	9.5E-01
ENSMUST00000150576	ribosomal protein L29 [Source:MGI Symbol;Acc:MGI:99687]	Q5M8M8	P47915	-2.4	8.2E-03	3.5	1.8E-03	0.3	6.6E-01	-0.2	7.3E-01
ENSMUST00000125065				3.4	1.0E-01	3.3	1.2E-01	-1.9	3.3E-01	-1.7	3.4E-01
ENSMUST00000150587	oid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) [Source:MGI Symbol;Acc:MGI:1075	D3YZN0		-4.4	3.9E-03	5.8	1.0E-04	-2.7	2.2E-02	-1.0	9.7E-02
ENSMUST00000125070				-2.2	1.3E-01	-2.1	3.5E-01	0.8	4.9E-01	0.7	7.4E-01
ENSMUST00000150603	adaptor protein complex AP-1, sigma 1 [Source:MGI Symbol;Acc:MGI:1098244]	D3YXN0		5.9	1.3E-03	-4.5	6.5E-03	-0.2	6.8E-01	-1.3	4.1E-01
ENSMUST00000125076				-1.1	3.6E-01	-5.0	2.0E-03	-5.0	1.6E-04	-1.1	4.0E-01
ENSMUST00000125077	coiled-coil domain containing 171 [Source:MGI Symbol;Acc:MGI:1922152]	A2BI14		2.4	3.7E-01	5.7	8.7E-02	1.0	7.5E-01	-2.3	2.8E-01
ENSMUST00000125079				-0.7	6.0E-01	-2.5	2.4E-01	-0.8	5.2E-01	1.1	6.0E-01
ENSMUST00000150611	synaptosomal-associated protein 23 [Source:MGI Symbol;Acc:MGI:109356]	E9Q8A1		-7.0	4.2E-03	7.4	1.2E-03	-0.3	8.4E-01	0.3	7.5E-01
ENSMUST00000125086	/S1 Golgi-localized integral membrane protein homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191371		Q78S06	1.2	2.9E-01	2.7	1.2E-01	0.7	6.1E-01	-0.7	5.4E-01
ENSMUST00000150618	coiled-coil-helix-coiled-coil-helix domain containing 7 [Source:MGI Symbol;Acc:MGI:1913683]		Q8K2Q5	4.3	3.8E-04	5.7	5.9E-04	0.1	9.1E-01	0.2	7.7E-01
ENSMUST00000150624	CUGBP, Elav-like family member 2 [Source:MGI Symbol;Acc:MGI:1338822]		Q9Z0H4	-7.8	5.6E-04	6.2	1.0E-03	-0.6	6.9E-01	0.2	8.0E-01
ENSMUST00000150634	UDP glucuronosyltransferase 1 family, polypeptide A7C [Source:MGI Symbol;Acc:MGI:3032636]	D3YZ96		-5.3	3.0E-03	-2.3	7.4E-02	0.0	9.8E-01	-2.8	8.0E-02
ENSMUST00000125099				-0.5	7.1E-01	0.4	8.2E-01	0.4	7.6E-01	-0.4	7.6E-01
ENSMUST00000150639	dapper homolog 1, antagonist of beta-catenin (xenopus) [Source:MGI Symbol;Acc:MGI:1891740]	D3Z5V0		5.6	1.7E-02	4.3	1.9E-03	0.4	6.4E-01	-1.7	5.8E-02
ENSMUST00000150680	interleukin 34 [Source:MGI Symbol;Acc:MGI:1923777]		Q8R1R4	5.8	2.5E-02	-5.9	1.8E-04	0.0	1.0E+00	-0.1	9.2E-01
ENSMUST00000150681	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative) [Source:MGI Symbol;Acc:MGI:2142075]			-2.9	6.2E-03	2.6	2.4E-02	0.2	7.8E-01	0.3	6.8E-01
ENSMUST00000125114	solute carrier family 25, member 45 [Source:MGI Symbol;Acc:MGI:2147731]		Q8CFJ7	-2.2	8.8E-02	2.1	1.1E-01	1.3	2.3E-01	-3.0	3.2E-02
ENSMUST00000150704	vezatin, adherens junctions transmembrane protein [Source:MGI Symbol;Acc:MGI:2143698]		Q3ZK22	6.4	2.6E-06	5.5	7.5E-03	-0.6	7.4E-01	-1.0	3.4E-01
ENSMUST00000150762	protein phosphatase 1, regulatory (inhibitor) subunit 1B [Source:MGI Symbol;Acc:MGI:94860]		Q60829	8.7	6.6E-05	3.2	9.2E-04	0.2	7.3E-01	-0.8	1.2E-01
ENSMUST00000150779	musashi RNA-binding protein 1 [Source:MGI Symbol;Acc:MGI:107376]		Q61474	6.3	4.8E-04	2.9	5.8E-02	-2.2	1.2E-01	0.4	6.9E-01
ENSMUST00000125122				-0.5	5.8E-01	-0.1	9.3E-01	0.0	1.0E+00	-0.4	7.2E-01
ENSMUST00000150787	protein phosphatase 1, regulatory (inhibitor) subunit 3F [Source:MGI Symbol;Acc:MGI:1859617]		Q9JIG4	5.4	5.7E-03	-7.9	6.8E-04	0.2	6.6E-01	-0.9	6.2E-01
ENSMUST00000150819	expressed sequence AI661453 [Source:MGI Symbol;Acc:MGI:2146908]		Q91Z58	8.0	1.0E-05	5.5	9.8E-03	-0.8	6.7E-01	1.0	3.4E-01
ENSMUST00000150821	U2AF homology motif (UHM) kinase 1 [Source:MGI Symbol;Acc:MGI:1341908]	Q8C0N6		-4.3	1.7E-02	-2.3	5.7E-02	0.0	9.4E-01	0.5	6.2E-01
ENSMUST00000125139	Fancd2 opposite strand [Source:MGI Symbol;Acc:MGI:1918229]			1.2	4.2E-01	4.8	1.3E-02	0.5	7.5E-01	-3.0	3.3E-02
ENSMUST00000150826	cell cycle progression 1 [Source:MGI Symbol;Acc:MGI:1196419]		Q640L3	-9.3	9.2E-04	6.8	2.0E-03	0.6	7.3E-01	-1.0	3.1E-01
ENSMUST00000150838	syntaxin 1A (brain) [Source:MGI Symbol;Acc:MGI:109355]	D6RFB9		8.0	2.0E-03	5.9	3.4E-03	-0.7	6.6E-01	1.0	2.9E-01
ENSMUST00000150843	pantothenate kinase 2 [Source:MGI Symbol;Acc:MGI:1921700]	Q3U4S0		-5.4	1.3E-02	7.0	1.8E-04	-0.4	7.3E-01	-0.9	1.7E-01
ENSMUST00000150857	inositol polyphosphate 5-phosphatase K [Source:MGI Symbol;Acc:MGI:1194899]	D6RI67		-9.9	4.7E-06	5.6	4.1E-05	-1.9	4.6E-02	-0.3	5.0E-01
ENSMUST00000150867	transient receptor potential cation channel, subfamily M, member 5 [Source:MGI Symbol;Acc:MGI:1861718]		Q9JJH7	6.7	2.6E-04	5.4	2.3E-05	0.1	8.2E-01	-0.2	7.3E-01
ENSMUST00000150897	nuclear GTPase, germinal center associated [Source:MGI Symbol;Acc:MGI:2685446]	D3YWJ0		7.6	2.3E-05	5.2	1.6E-04	0.9	2.5E-01	-0.3	5.7E-01
ENSMUST00000125164				-1.0	6.9E-01	-3.1	3.2E-01	-2.5	1.7E-01	-0.4	9.1E-01
ENSMUST00000125165				2.8	1.1E-01	0.0	9.8E-01	-2.5	1.3E-01	0.3	8.5E-01
ENSMUST00000150912	START domain containing 9 [Source:MGI Symbol;Acc:MGI:3045258]	A2AKI2		5.8	1.7E-03	-3.8	1.3E-02	0.6	3.9E-01	-2.2	1.3E-01
ENSMUST00000125172	prohibitin [Source:MGI Symbol;Acc:MGI:97572]		P67778	1.2	1.1E-01	0.6	4.1E-01	-1.2	7.0E-02	-0.7	3.5E-01
ENSMUST00000150924	G-protein signalling modulator 3 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:2146785]	G3UZQ1		-7.8	4.3E-04	-0.8	1.7E-01	0.4	3.3E-01	0.0	9.9E-01
ENSMUST00000150933	rabaptin, RAB GTPase binding effector protein 2 [Source:MGI Symbol;Acc:MGI:1917564]	D6RCU7		3.0	1.1E-02	5.6	7.1E-05	0.2	8.2E-01	-0.6	2.9E-01
ENSMUST00000125180				0.4	8.3E-01	-1.0	6.9E-01	-0.5	7.8E-01	0.9	7.1E-01
ENSMUST00000150948	RIKEN cDNA 9530053A07 gene [Source:MGI Symbol;Acc:MGI:2442118]	E9PVG8		9.5	3.4E-06	-2.8	3.4E-02	-1.2	1.2E-01	-3.0	6.6E-02
ENSMUST00000150967	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	Q3U5P2		-4.7	2.3E-04	-2.3	4.3E-02	0.4	4.9E-01	-0.2	8.2E-01
ENSMUST00000150968	coatomer protein complex, subunit epsilon [Source:MGI Symbol;Acc:MGI:1891702]	D3Z315		-6.5	3.0E-04	6.2	8.1E-04	-0.6	6.4E-01	-0.5	5.3E-01
ENSMUST00000150993	sorting nexin 29 [Source:MGI Symbol;Acc:MGI:1921728]			6.5	1.6E-05	-2.4	2.2E-01	0.7	5.5E-01	-1.3	5.5E-01
ENSMUST00000151029	RIKEN cDNA A530099J19 gene [Source:MGI Symbol;Acc:MGI:2441809]	B9EKH0		4.2	2.0E-03	4.5	4.1E-04	-2.0	5.2E-02	-0.1	8.1E-01
ENSMUST00000125203				0.3	7.9E-01	-0.1	9.3E-01	-0.3	7.4E-01	0.1	9.6E-01
ENSMUST00000151083	cilia and flagella associated protein 74 [Source:MGI Symbol;Acc:MGI:1917130]		Q3UY96	9.3	6.3E-05	-6.2	8.1E-03	-0.9	2.2E-01	-0.8	6.9E-01
ENSMUST00000151120	cathepsin D [Source:MGI Symbol;Acc:MGI:88562]	Q3UCD9	P18242	-8.7	1.7E-04	-1.6	2.3E-02	0.8	6.0E-02	-0.2	7.2E-01
ENSMUST00000151127	F-box protein 44 [Source:MGI Symbol;Acc:MGI:1354744]	G3UYF5		7.7	1.8E-05	5.0	5.1E-03	-0.5	7.6E-01	0.2	8.2E-01
ENSMUST00000151129	peroxiredoxin 1 [Source:MGI Symbol;Acc:MGI:99523]	B1AXW5		-6.5	2.3E-05	5.3	2.0E-03	0.2	8.8E-01	-0.8	2.7E-01
ENSMUST00000151137	aldolase A, fructose-bisphosphate [Source:MGI Symbol;Acc:MGI:87994]	D3YWI1		-6.0	4.0E-03	4.3	1.6E-04	-0.9	1.8E-01	0.5	3.1E-01
ENSMUST00000151152	otassium voltage-gated channel, subfamily H (eag-related), member 1 [Source:MGI Symbol;Acc:MGI:1341721	A0A0A6YVS8		7.1	1.1E-04	0.6	7.4E-01	-4.8	1.1E-02	7.5	7.4E-04

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000151155	multiple coagulation factor deficiency 2 [Source:MGI Symbol;Acc:MGI:2183439]	D3Z1G3		-2.4	2.2E-02	6.9	3.7E-03	-0.3	8.8E-01	0.2	8.8E-01
ENSMUST00000151180	coiled-coil domain containing 158 [Source:MGI Symbol;Acc:MGI:2444555]		Q8CDI6	6.2	1.5E-03	6.7	4.3E-04	-0.9	5.0E-01	0.2	7.7E-01
ENSMUST00000125232				1.5	6.2E-02	1.3	2.0E-01	-0.2	8.1E-01	0.1	9.1E-01
ENSMUST00000151184	protein phosphatase 1, catalytic subunit, gamma isoform [Source:MGI Symbol;Acc:MGI:104872]	A0A0G2JE42		-8.1	1.0E-03	-5.5	1.6E-02	-0.6	4.4E-01	0.6	7.8E-01
ENSMUST00000125245				2.3	3.9E-02	6.4	1.3E-03	1.7	2.4E-01	-2.4	1.9E-02
ENSMUST00000125249	isochorismatase domain containing 2a [Source:MGI Symbol;Acc:MGI:3609243]		P85094	-0.4	6.3E-01	-1.2	2.7E-01	-0.4	5.6E-01	0.4	7.2E-01
ENSMUST00000151187	transmembrane protein 209 [Source:MGI Symbol;Acc:MGI:1919899]	Q8C214		4.7	9.4E-05	8.4	2.3E-04	-0.8	6.1E-01	0.6	3.8E-01
ENSMUST00000125265	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]	B8JJ89		0.4	7.2E-01	2.9	9.0E-02	1.9	1.9E-01	-0.6	5.9E-01
ENSMUST00000151189	transmembrane emp24 protein transport domain containing 7 [Source:MGI Symbol;Acc:MGI:1913926]	D3YZZ5		-6.8	7.7E-06	-2.7	3.4E-02	-1.7	3.1E-02	-2.5	8.0E-02
ENSMUST00000125271	angiomotin [Source:MGI Symbol;Acc:MGI:108440]	F6QYS7		2.7	8.3E-02	2.3	2.3E-01	1.2	4.5E-01	1.6	3.2E-01
ENSMUST00000151201	helicase, POLQ-like [Source:MGI Symbol;Acc:MGI:2176740]	Q8BKT5		6.1	5.0E-04	6.6	1.6E-04	-0.5	6.4E-01	-0.6	3.2E-01
ENSMUST00000151224	family with sequence similarity 163, member B [Source:MGI Symbol;Acc:MGI:1926106]	B2RVN8	Q8BUM6	8.4	4.6E-05	5.3	4.4E-02	-2.1	4.2E-01	0.0	1.0E+00
ENSMUST00000151231	RIKEN cDNA 8030474K03 gene [Source:MGI Symbol;Acc:MGI:2685988]	E9Q4Y8		6.0	1.0E-03	-2.2	2.0E-01	1.7	9.7E-02	0.3	8.5E-01
ENSMUST00000151243	hemochromatosis [Source:MGI Symbol;Acc:MGI:109191]	F7CW53		4.7	3.9E-05	-4.2	1.2E-02	0.8	2.0E-01	-1.3	3.9E-01
ENSMUST00000151280	3-hydroxyacyl-CoA dehydratase 4 [Source:MGI Symbol;Acc:MGI:1914025]	F7CPS1		-6.1	4.5E-05	7.8	8.7E-03	0.3	9.0E-01	0.4	7.4E-01
ENSMUST00000151285	WAPL cohesin release factor [Source:MGI Symbol;Acc:MGI:2675859]	F6YCH1		-6.2	6.7E-05	8.2	6.8E-06	-1.3	2.1E-01	1.6	4.5E-03
ENSMUST00000151287	t-complex protein 1 [Source:MGI Symbol;Acc:MGI:98535]		P11983	-3.2	7.6E-04	6.8	3.2E-02	-0.6	8.4E-01	-1.0	5.4E-01
ENSMUST00000151288	solute carrier family 45, member 4 [Source:MGI Symbol;Acc:MGI:2146236]		Q0P5V9	3.2	2.8E-04	5.1	3.1E-03	0.8	5.1E-01	-0.7	3.9E-01
ENSMUST00000151289	sphingomyelin synthase 1 [Source:MGI Symbol;Acc:MGI:2444110]		Q8VCQ6	-6.4	2.1E-05	-6.5	1.4E-03	-1.6	1.7E-02	-0.5	7.5E-01
ENSMUST00000125304	lectin, mannose-binding 2-like [Source:MGI Symbol;Acc:MGI:2443010]		P59481	-0.3	6.5E-01	0.1	8.6E-01	0.8	2.0E-01	0.4	5.9E-01
ENSMUST00000125316				0.8	4.9E-01	1.5	2.4E-01	-1.0	3.6E-01	-1.7	1.3E-01
ENSMUST00000125325	E1A binding protein p400 [Source:MGI Symbol;Acc:MGI:1276124]	F6R9G0		-0.2	8.4E-01	0.6	6.0E-01	0.6	4.8E-01	-0.2	8.8E-01
ENSMUST00000151319	antizyme inhibitor 1 [Source:MGI Symbol;Acc:MGI:1859169]	D3Z2P3		-6.0	7.9E-04	6.3	3.0E-04	-0.5	6.9E-01	-0.5	4.1E-01
ENSMUST00000125329				3.5	5.0E-02	5.3	1.1E-02	-0.4	8.3E-01	-2.2	6.9E-02
ENSMUST00000151338	CDC-like kinase 1 [Source:MGI Symbol;Acc:MGI:107403]		P22518	-8.1	1.4E-02	5.6	6.1E-03	-0.6	7.1E-01	-0.4	6.6E-01
ENSMUST00000125332				-0.9	5.4E-01	-2.3	3.1E-01	-0.5	6.8E-01	0.9	6.7E-01
ENSMUST00000125339	family with sequence similarity 129, member C [Source:MGI Symbol;Acc:MGI:3686743]	F6QUK2		2.2	8.9E-02	6.2	5.5E-03	3.0	9.2E-02	-0.9	3.7E-01
ENSMUST00000151341	metallothionein-like 5, testis-specific (tesmin) [Source:MGI Symbol;Acc:MGI:1340029]	Q9D571		4.8	2.2E-04	8.1	3.4E-05	-1.0	4.3E-01	-0.8	1.6E-01
ENSMUST00000151346	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	F7ACR9		-5.8	5.6E-04	4.4	3.0E-04	-0.8	2.9E-01	-0.9	1.3E-01
ENSMUST00000151348	uroporphyrinogen III synthase [Source:MGI Symbol;Acc:MGI:98917]	E9Q8N3		5.9	2.6E-06	5.1	1.5E-03	0.3	7.9E-01	0.7	2.9E-01
ENSMUST00000125346	protein kinase N3 [Source:MGI Symbol;Acc:MGI:2388285]	A2BE96		3.8	3.8E-02	4.7	8.4E-03	-1.9	2.5E-01	-2.9	2.8E-02
ENSMUST00000151373	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]	E9PUR2		4.3	7.0E-03	5.0	1.9E-03	-0.6	6.1E-01	0.9	2.2E-01
ENSMUST00000125357				-0.5	6.7E-01	-4.0	2.5E-02	-2.8	7.9E-03	0.7	6.8E-01
ENSMUST00000151376	predicted gene 10722 [Source:MGI Symbol;Acc:MGI:3642024]	F6VLK5		13.5	3.1E-08	-1.0	3.3E-01	0.2	7.7E-01	-3.0	3.5E-02
ENSMUST00000151397	IQ motif and Sec7 domain 3 [Source:MGI Symbol;Acc:MGI:2677208]			9.4	7.2E-06	-1.1	1.5E-01	0.9	8.2E-02	0.3	7.0E-01
ENSMUST00000151408	RAS protein-specific guanine nucleotide-releasing factor 2 [Source:MGI Symbol;Acc:MGI:109137]	F7B9R2		6.0	1.4E-04	-2.0	1.8E-01	1.5	9.7E-02	0.5	7.4E-01
ENSMUST00000151421	kinase non-catalytic C-lobe domain (KIND) containing 1 [Source:MGI Symbol;Acc:MGI:1923734]	D3Z5B8		8.2	1.0E-05	3.0	1.1E-02	0.5	5.3E-01	0.5	4.8E-01
ENSMUST00000125380				3.7	6.8E-02	3.4	3.7E-02	-3.2	9.4E-02	-2.9	4.4E-02
ENSMUST00000151430	THO complex 2 [Source:MGI Symbol;Acc:MGI:2442413]	F6SBF2		-4.7	9.6E-03	7.4	1.1E-04	-0.4	7.4E-01	-0.7	2.9E-01
ENSMUST00000125383	coiled-coil domain containing 47 [Source:MGI Symbol;Acc:MGI:1914413]	F7C265		0.9	2.1E-01	0.5	5.4E-01	-0.3	6.9E-01	0.1	9.0E-01
ENSMUST00000151451	branched chain ketoacid dehydrogenase kinase [Source:MGI Symbol;Acc:MGI:1276121]	D3Z7R0		-2.3	3.1E-02	4.0	4.1E-03	-2.9	3.6E-02	-0.3	7.4E-01
ENSMUST00000151485	ubiquitin associated and SH3 domain containing, B [Source:MGI Symbol;Acc:MGI:1920078]		Q8BGG7	-3.5	1.6E-02	7.7	5.1E-04	1.7	2.6E-01	-0.9	2.5E-01
ENSMUST00000151528	neuroligin 3 [Source:MGI Symbol;Acc:MGI:2444609]	A2AGI2		8.4	1.4E-02	5.9	6.0E-04	-1.5	2.7E-01	1.0	1.5E-01
ENSMUST00000125408				-0.9	5.3E-01	-0.7	5.1E-01	-2.7	2.3E-02	-2.8	6.5E-02
ENSMUST00000125416	collagen, type XIV, alpha 1 [Source:MGI Symbol;Acc:MGI:1341272]	F7D5Y4		4.4	3.9E-02	3.9	5.9E-02	-2.3	2.8E-01	-1.7	2.2E-01
ENSMUST00000151563	translocated promoter region, nuclear basket protein [Source:MGI Symbol;Acc:MGI:1922066]	F6RX08		-7.4	1.0E-03	7.3	9.0E-05	-1.8	1.8E-01	0.3	6.2E-01
ENSMUST00000151568	cyclin I [Source:MGI Symbol;Acc:MGI:1341077]	D3Z680		-3.8	9.7E-03	7.9	5.6E-05	-1.5	2.5E-01	-1.2	4.7E-02
ENSMUST00000151590	phospholipase C, gamma 1 [Source:MGI Symbol;Acc:MGI:97615]	G3UXP4		5.7	2.9E-04	4.2	7.1E-05	-0.4	5.3E-01	0.7	1.4E-01
ENSMUST00000125430				1.9	6.6E-02	5.7	3.0E-03	2.4	1.1E-01	-1.4	1.2E-01
ENSMUST00000151609	RIKEN cDNA 1700010I14 gene [Source:MGI Symbol;Acc:MGI:1914181]	Q3TTN6		-3.4	2.9E-03	3.7	1.5E-03	0.4	5.7E-01	-0.2	8.0E-01
ENSMUST00000151633	RIKEN cDNA C330021F23 gene [Source:MGI Symbol;Acc:MGI:3612471]	D3Z250		6.5	4.8E-04	5.4	4.4E-03	-0.6	7.2E-01	-1.4	1.6E-01
ENSMUST00000151671	C-type lectin domain family 12, member a [Source:MGI Symbol;Acc:MGI:3040968]	D3YXD8		-2.2	6.4E-03	5.7	1.4E-02	-0.7	7.2E-01	-1.5	2.6E-01
ENSMUST00000125442	DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:MGI Symbol;Acc:MGI:1270129]	B1AXY0		2.7	2.1E-01	2.6	2.2E-01	-0.5	8.1E-01	-0.4	7.9E-01
ENSMUST00000125445	transmembrane protein 39b [Source:MGI Symbol;Acc:MGI:2682939]	D6RCH5		-2.9	5.2E-02	0.1	9.4E-01	-0.2	8.4E-01	-3.2	4.6E-02
ENSMUST00000151678	ıal specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) [Source:MGI Symbol;Acc:MGI:191959	Q3V2Y9		6.8	1.5E-02	-3.5	1.2E-01	0.2	8.7E-01	-1.1	6.1E-01
ENSMUST00000151698	lysosomal-associated protein transmembrane 5 [Source:MGI Symbol;Acc:MGI:108046]	Q544S4	Q61168	-6.7	3.2E-05	5.7	4.4E-04	-0.7	5.1E-01	0.6	3.6E-01
ENSMUST00000125451				5.2	1.3E-01	6.2	8.1E-02	-1.1	7.6E-01	-2.1	3.5E-01
ENSMUST00000151702	ribosomal protein L10 [Source:MGI Symbol;Acc:MGI:105943]	I7HLV2		-8.7	4.3E-04	2.3	1.9E-02	-1.3	1.1E-01	-0.4	5.1E-01
ENSMUST00000151786	Prkr interacting protein 1 (IL11 inducible) [Source:MGI Symbol;Acc:MGI:1914051]		Q9CWV6	2.6	2.7E-04	6.5	3.5E-03	1.4	3.8E-01	1.3	2.0E-01
ENSMUST00000151797	protease, serine 41 [Source:MGI Symbol;Acc:MGI:1918253]		Q920S2	3.2	5.6E-03	5.5	5.9E-04	-0.8	4.7E-01	-0.9	2.1E-01
ENSMUST00000151826	transformation related protein 53 regulating kinase B [Source:MGI Symbol;Acc:MGI:1914050]	Q543M9		4.6	9.6E-06	7.7	6.0E-04	0.5	7.2E-01	0.4	5.8E-01
ENSMUST00000125463				2.0	1.8E-01	5.9	1.5E-02	1.7	4.0E-01	-2.2	1.0E-01
ENSMUST00000151852	leucine rich repeat containing 45 [Source:MGI Symbol;Acc:MGI:2387183]	A2AC11		6.2	3.9E-04	6.9	3.4E-04	-0.2	9.0E-01	-0.1	9.1E-01
ENSMUST00000151880	SLU7 splicing factor homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2385598]	Z4YM25		-4.6	3.3E-03	6.0	1.2E-03	-0.7	6.3E-01	-0.8	3.1E-01
ENSMUST00000151903	RIKEN cDNA 5830415F09 gene [Source:MGI Symbol;Acc:MGI:1922003]	F6QNL9		8.3	9.6E-05	-3.6	5.0E-02	0.8	3.4E-01	0.0	9.8E-01
ENSMUST00000151913	regulatory factor X 8 [Source:MGI Symbol;Acc:MGI:3588206]		D3YU81	7.2	2.9E-05	4.7	1.2E-02	0.3	8.6E-01	0.6	5.1E-01
ENSMUST00000151918	transient receptor potential cation channel, subfamily C, member 7 [Source:MGI Symbol;Acc:MGI:1349470]	D6RI84		10.5	1.2E-05	6.2	8.1E-04	-0.4	7.6E-01	-0.9	2.6E-01
ENSMUST00000125487	vacuolar protein sorting 8 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2146407]	F6ZLN8		1.7	1.6E-01	2.5	1.2E-01	0.0	9.8E-01	-0.8	4.8E-01
ENSMUST00000151937	solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Source:MGI Symbol;Acc:MGI:1926080]		Q8BH59	1.7	5.4E-03	6.2	3.7E-04	-0.2	8.9E-01	-0.8	3.0E-01
ENSMUST00000151960	interaction protein for cytohesin exchange factors 1 [Source:MGI Symbol;Acc:MGI:2444159]	D3Z0U6		-2.5	2.3E-02	5.2	6.0E-04	-1.2	2.9E-01	-2.5	5.1E-03
ENSMUST00000125498	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915123]	F6YY88		1.9	3.6E-02	3.7	3.8E-03	0.5	5.3E-01	-1.2	1.3E-01
ENSMUST00000151961	ceramide-1-phosphate transfer protein [Source:MGI Symbol;Acc:MGI:1933107]	Z4YLU2		-2.8	6.5E-03	7.9	1.6E-04	-0.6	6.5E-01	-0.2	7.3E-01
ENSMUST00000151969	transmembrane protein 234 [Source:MGI Symbol;Acc:MGI:1924049]	D6RDC0		-4.7	1.1E-03	5.6	3.1E-04	0.3	7.3E-01	0.5	4.6E-01
ENSMUST00000151978	kringle containing transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1933988]	F6S1T7		4.5	2.6E-05	-7.6	2.7E-02	0.7	4.8E-01	-1.1	7.5E-01
ENSMUST00000125514	cullin 4A [Source:MGI Symbol;Acc:MGI:1914487]	F6UV36		-0.3	5.7E-01	-0.5	5.2E-01	-0.2	7.0E-01	0.0	9.6E-01
ENSMUST00000151986	bromodomain containing 2 [Source:MGI Symbol;Acc:MGI:99495]	I7HPW1		2.3	1.6E-02	5.9	3.0E-03	-0.7	6.8E-01	-1.3	1.9E-01
ENSMUST00000125521				-2.0	1.5E-01	-0.4	8.1E-01	0.3	8.2E-01	-1.3	4.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000151988	N(alpha)-acetyltransferase 60, NatF catalytic subunit [Source:MGI Symbol;Acc:MGI:1922013]	D3YYN1		4.3	1.8E-02	5.5	3.0E-04	-1.0	3.1E-01	0.9	2.0E-01
ENSMUST00000125524				1.0	5.0E-01	0.3	8.8E-01	-0.6	7.3E-01	0.1	9.5E-01
ENSMUST00000125526	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI	D3Z336		-1.5	1.7E-01	0.4	8.0E-01	1.0	3.5E-01	-0.8	5.2E-01
ENSMUST00000151999	maestro heat-like repeat family member 5 [Source:MGI Symbol;Acc:MGI:2685474]	E9PUJ8		8.4	2.0E-05	2.3	7.5E-02	-1.1	3.0E-01	0.0	9.9E-01
ENSMUST00000152012	glutamate receptor, ionotropic, NMDA2B (epsilon 2) [Source:MGI Symbol;Acc:MGI:95821]	A0A0G2JEA7		5.0	2.0E-03	3.3	4.0E-03	0.4	6.3E-01	-0.3	6.2E-01
ENSMUST00000152034	coagulation factor X [Source:MGI Symbol;Acc:MGI:103107]	D3Z521		-6.6	2.8E-04	-4.6	2.1E-02	0.4	5.9E-01	0.9	5.9E-01
ENSMUST00000152054	Ts translation elongation factor, mitochondrial [Source:MGI Symbol;Acc:MGI:1913649]	D3Z4M7		5.1	2.7E-03	5.6	3.2E-04	-0.9	4.1E-01	-0.7	3.0E-01
ENSMUST00000125544	predicted gene 20431 [Source:MGI Symbol;Acc:MGI:5141896]	E9PY39		1.8	4.7E-01	5.1	1.3E-01	3.1	2.3E-01	-0.2	9.5E-01
ENSMUST00000152080	solute carrier family 35, member E1 [Source:MGI Symbol;Acc:MGI:2142403]		Q8CD26	-3.4	2.2E-04	5.7	1.4E-03	-1.5	3.1E-01	-0.2	8.0E-01
ENSMUST00000152098	F-box protein 6 [Source:MGI Symbol;Acc:MGI:1354743]	Z4YN00		-4.4	9.0E-03	-4.0	6.9E-03	1.1	5.6E-02	-0.6	6.1E-01
ENSMUST00000152103	IQ motif and Sec7 domain 3 [Source:MGI Symbol;Acc:MGI:2677208]	D6RHQ8		7.1	9.8E-03	7.7	2.4E-03	0.9	6.2E-01	1.3	2.0E-01
ENSMUST00000125552				-4.0	7.8E-02	-0.1	9.7E-01	3.5	2.1E-01	-0.4	8.8E-01
ENSMUST00000152126	transmembrane protein 234 [Source:MGI Symbol;Acc:MGI:1924049]	D6RDC0		-7.5	5.1E-04	0.9	6.5E-01	-4.1	9.4E-02	1.5	3.4E-01
ENSMUST00000152135	tocopherol (alpha) transfer protein-like [Source:MGI Symbol;Acc:MGI:1923330]	A6PW50		4.5	2.1E-04	7.5	3.8E-03	-0.2	9.1E-01	1.2	2.7E-01
ENSMUST00000152159	multiple EGF-like-domains 6 [Source:MGI Symbol;Acc:MGI:1919351]	B1ASH4		7.7	5.3E-05	6.3	2.0E-03	-0.7	6.7E-01	0.2	7.7E-01
ENSMUST00000152227	desumoylating isopeptidase 1 [Source:MGI Symbol;Acc:MGI:106313]		Q9CQT7	-3.7	1.9E-02	5.4	4.8E-04	-1.8	1.4E-01	0.0	1.0E+00
ENSMUST00000125567	diacylglycerol lipase, alpha [Source:MGI Symbol;Acc:MGI:2677061]	S4R2M3		1.3	5.6E-01	0.5	9.0E-01	1.8	4.9E-01	2.6	4.3E-01
ENSMUST00000152233	ankyrin repeat and zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1098746]	J3QM81		-6.9	2.6E-05	6.4	1.0E-02	-0.6	7.8E-01	-2.0	1.4E-01
ENSMUST00000152247	trinucleotide repeat containing 18 [Source:MGI Symbol;Acc:MGI:3648294]	F6Z7L1		-3.2	3.3E-02	6.4	1.3E-02	0.0	9.9E-01	-1.4	2.7E-01
ENSMUST00000125587	adenylate kinase 3 [Source:MGI Symbol;Acc:MGI:1860835]	F6RP11		-0.8	3.3E-01	0.2	8.7E-01	0.3	6.7E-01	-0.6	4.9E-01
ENSMUST00000152288	emerin [Source:MGI Symbol;Acc:MGI:108117]	D6RFS0		-6.2	8.0E-03	8.0	1.4E-04	-0.8	5.8E-01	0.2	7.3E-01
ENSMUST00000152305	thrombospondin, type I, domain containing 7B [Source:MGI Symbol;Acc:MGI:2443925]	D3Z366		11.5	4.7E-06	2.9	2.0E-03	-0.5	3.8E-01	0.4	4.3E-01
ENSMUST00000152318	STE20-related kinase adaptor beta [Source:MGI Symbol;Acc:MGI:2144047]	M0QWE6		-5.0	2.0E-04	6.0	1.3E-05	-0.9	2.3E-01	-0.7	1.6E-01
ENSMUST00000125596				0.4	8.3E-01	-1.6	5.6E-01	-1.8	3.2E-01	0.2	9.4E-01
ENSMUST00000125597				-2.0	7.5E-02	-2.4	1.2E-01	-0.2	8.5E-01	0.2	8.9E-01
ENSMUST00000152340	sphingomyelin synthase 1 [Source:MGI Symbol;Acc:MGI:2444110]		Q8VCQ6	-4.8	4.6E-03	3.6	5.1E-03	0.0	9.6E-01	-0.5	5.4E-01
ENSMUST00000152362	PRP18 pre-mRNA processing factor 18 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914479]		Q8BM39	-4.5	1.3E-02	6.1	5.4E-03	-1.4	4.7E-01	-2.1	1.1E-01
ENSMUST00000125618				4.0	5.1E-02	4.5	9.6E-02	1.0	6.3E-01	0.5	8.0E-01
ENSMUST00000152378	retbindin [Source:MGI Symbol;Acc:MGI:2443686]	E9PXB4		6.7	6.3E-05	9.0	4.6E-07	-2.0	2.7E-02	0.3	2.9E-01
ENSMUST00000125624				-0.3	6.2E-01	0.8	2.2E-01	-0.1	8.3E-01	-1.1	7.2E-02
ENSMUST00000152383	propionyl-Coenzyme A carboxylase, alpha polypeptide [Source:MGI Symbol;Acc:MGI:97499]	H3BK61		5.9	3.8E-04	3.0	9.5E-02	0.0	9.9E-01	0.4	7.2E-01
ENSMUST00000152386	dynein, axonemal, heavy chain 9 [Source:MGI Symbol;Acc:MGI:1289279]	F7DC70		5.9	2.1E-04	2.5	3.1E-01	0.4	8.3E-01	4.1	4.2E-02
ENSMUST00000125637	eukaryotic translation initiation factor 4E nuclear import factor 1 [Source:MGI Symbol;Acc:MGI:1921453]	Q5NBZ7		-0.8	5.1E-01	-0.6	6.7E-01	-0.4	6.6E-01	-0.6	6.7E-01
ENSMUST00000125645	nardilysin, N-arginine dibasic convertase, NRD convertase 1 [Source:MGI Symbol;Acc:MGI:1201386]	Q3V3G9		-2.4	3.6E-02	0.3	7.9E-01	1.1	2.1E-01	-1.6	1.9E-01
ENSMUST00000125646				0.0	9.9E-01	1.8	5.6E-01	2.3	4.1E-01	0.5	8.3E-01
ENSMUST00000152389	coiled-coil domain containing 63 [Source:MGI Symbol;Acc:MGI:3607777]	D6RE42		-4.8	4.3E-04	6.5	3.1E-04	-2.1	1.3E-01	0.2	7.4E-01
ENSMUST00000152420	oxidative stress induced growth inhibitor 1 [Source:MGI Symbol;Acc:MGI:1919089]	Q8VC10		-6.4	4.9E-04	8.2	4.2E-05	3.5	8.9E-03	-1.4	2.9E-02
ENSMUST00000152422	dynactin 6 [Source:MGI Symbol;Acc:MGI:1343154]	F6XWI6		-6.9	1.1E-04	5.9	3.9E-04	-3.6	1.7E-02	-1.0	1.7E-01
ENSMUST00000125664				4.4	5.4E-02	7.3	2.1E-02	1.1	6.9E-01	-1.8	2.6E-01
ENSMUST00000152426	SH3-domain kinase binding protein 1 [Source:MGI Symbol;Acc:MGI:1889583]	B0R0Y8		-3.2	1.3E-02	0.5	7.1E-01	-4.5	2.2E-02	1.4	2.8E-01
ENSMUST00000152438	ATP-binding cassette, sub-family C (CFTR/MRP), member 12 [Source:MGI Symbol;Acc:MGI:2441679]		Q80WJ6	7.0	1.0E-04	4.3	3.6E-03	0.2	8.4E-01	-0.5	5.5E-01
ENSMUST00000152447	5'-nucleotidase, cytosolic III [Source:MGI Symbol;Acc:MGI:1927186]	S4R2D9		-4.3	2.9E-04	-6.8	5.7E-05	-0.8	3.5E-02	-0.9	4.0E-01
ENSMUST00000152452	regulation of nuclear pre-mRNA domain containing 1B [Source:MGI Symbol;Acc:MGI:1917720]		Q9CSU0	6.9	3.0E-05	-3.7	1.0E-02	-1.1	9.1E-02	-1.8	2.1E-01
ENSMUST00000152459	cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1889272]	E9PYN1		5.4	1.8E-02	4.1	5.1E-03	-0.9	4.6E-01	0.7	3.2E-01
ENSMUST00000125679				-0.4	8.3E-01	-0.9	7.3E-01	0.5	7.6E-01	1.1	6.8E-01
ENSMUST00000152463	spermidine/spermine N1-acetyl transferase 1 [Source:MGI Symbol;Acc:MGI:98233]	S4R2T2		-8.4	3.4E-03	4.2	1.7E-03	0.1	8.8E-01	-0.3	6.7E-01
ENSMUST00000125687				-0.8	5.7E-01	-0.3	8.9E-01	0.5	7.5E-01	0.0	1.0E+00
ENSMUST00000152471	sorting nexin family member 21 [Source:MGI Symbol;Acc:MGI:1917729]	G3UY23		4.4	1.7E-04	7.5	7.1E-05	0.0	9.7E-01	-0.1	7.9E-01
ENSMUST00000125693				0.6	4.2E-01	1.0	3.2E-01	0.2	8.1E-01	-0.2	8.3E-01
ENSMUST00000152511	ankyrin 1, erythroid [Source:MGI Symbol;Acc:MGI:88024]	F7D1P5		6.4	6.6E-04	5.1	1.7E-03	-0.5	6.7E-01	1.6	4.1E-02
ENSMUST00000125699	coiled-coil domain containing 97 [Source:MGI Symbol;Acc:MGI:1196455]			-0.2	7.6E-01	0.5	6.0E-01	0.1	9.3E-01	-0.7	4.5E-01
ENSMUST00000152533	mitogen-activated protein kinase kinase kinase 5 [Source:MGI Symbol;Acc:MGI:1346876]	D3Z5H1		7.0	3.1E-04	-2.9	9.0E-02	0.1	8.9E-01	-0.4	8.0E-01
ENSMUST00000152565	ring finger protein 19B [Source:MGI Symbol;Acc:MGI:1922484]	A2A7Q8		-3.2	1.0E-02	4.4	1.5E-02	-0.6	6.6E-01	-0.2	8.9E-01
ENSMUST00000125705	vaccinia related kinase 3 [Source:MGI Symbol;Acc:MGI:2182465]	D3Z188		-1.3	1.1E-01	-1.4	2.4E-01	0.7	3.7E-01	0.8	4.8E-01
ENSMUST00000152567	Rap1 GTPase-activating protein [Source:MGI Symbol;Acc:MGI:109338]	A2ALS2		5.2	1.5E-03	-4.6	2.0E-03	0.7	1.6E-01	-0.7	5.8E-01
ENSMUST00000125714				-0.2	9.4E-01	0.6	8.0E-01	-1.5	4.4E-01	-2.2	3.6E-01
ENSMUST00000152571	lymphoid-restricted membrane protein [Source:MGI Symbol;Acc:MGI:108424]	E9Q2C8		-2.1	2.9E-02	5.1	2.8E-04	-3.4	1.1E-02	0.5	4.4E-01
ENSMUST00000152592	serine/threonine kinase 11 [Source:MGI Symbol;Acc:MGI:1341870]	F6WNS2		-6.2	3.3E-04	-2.0	8.2E-03	0.6	1.4E-01	-1.7	2.2E-02
ENSMUST00000152693	oculocutaneous albinism II [Source:MGI Symbol;Acc:MGI:97454]	D6RCY7		7.0	1.5E-02	6.5	1.2E-04	-0.3	8.0E-01	-0.1	8.1E-01
ENSMUST00000125726				1.7	1.1E-01	2.1	1.6E-01	0.1	9.5E-01	-0.3	7.9E-01
ENSMUST00000125729				3.8	6.9E-02	4.0	1.0E-01	-0.4	8.7E-01	-0.5	7.3E-01
ENSMUST00000152700	suppressor of Ty 4A [Source:MGI Symbol;Acc:MGI:107416]	D6RHM5		-5.0	1.5E-03	7.6	8.6E-04	-0.2	8.9E-01	-0.5	5.2E-01
ENSMUST00000152704	basic transcription factor 3 [Source:MGI Symbol;Acc:MGI:1202875]	Q3UJR8	Q64152	-8.6	1.3E-05	3.5	4.8E-03	-0.3	7.3E-01	-0.3	6.4E-01
ENSMUST00000152721	cathepsin A [Source:MGI Symbol;Acc:MGI:97748]	A2A5J6		-4.6	1.9E-04	-3.8	5.0E-02	-0.4	6.4E-01	-0.4	8.5E-01
ENSMUST00000152743	motile sperm domain containing 1 [Source:MGI Symbol;Acc:MGI:1917630]		Q8VEL0	-4.2	9.5E-03	2.4	6.6E-02	0.4	6.4E-01	0.6	5.4E-01
ENSMUST00000152748				3.5	1.2E-01	2.5	3.5E-01	0.0	9.9E-01	1.0	6.2E-01
ENSMUST00000125752	ribonuclease, RNase K [Source:MGI Symbol;Acc:MGI:106369]	H3BLR9		-0.7	4.4E-01	1.6	1.5E-01	0.7	4.1E-01	-1.6	1.3E-01
ENSMUST00000152762	adenylate kinase 2 [Source:MGI Symbol;Acc:MGI:87978]	F7BP55		4.1	2.9E-02	3.4	6.0E-02	-0.2	8.7E-01	1.9	1.3E-01
ENSMUST00000125758	MRV integration site 1 [Source:MGI Symbol;Acc:MGI:1338023]	G5E8V5		5.5	6.2E-02	4.8	1.7E-01	1.3	7.0E-01	1.9	3.8E-01
ENSMUST00000152782	HEG homolog 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1924696]	E9Q440		4.2	1.2E-04	5.7	6.3E-04	-0.6	6.3E-01	0.4	5.7E-01
ENSMUST00000152829	zinc finger SWIM-type containing 2 [Source:MGI Symbol;Acc:MGI:1919111]	B2FDH1		5.7	3.2E-03	2.4	4.3E-02	-0.3	7.4E-01	0.4	6.7E-01
ENSMUST00000125763	zinc finger protein 407 [Source:MGI Symbol;Acc:MGI:2685179]	G3UVV3		-0.8	7.1E-02	-0.3	5.3E-01	0.0	9.9E-01	-0.5	3.3E-01
ENSMUST00000152831	ATPase, Ca++ transporting, plasma membrane 2 [Source:MGI Symbol;Acc:MGI:105368]	S4R1C4		8.3	1.3E-05	7.4	2.2E-04	0.1	9.6E-01	-0.4	5.4E-01
ENSMUST00000125774	ADP-ribosylation factor-like 8A [Source:MGI Symbol;Acc:MGI:1915974]	F6QKK2		-2.0	2.4E-01	-0.2	9.5E-01	2.3	2.2E-01	0.4	8.7E-01
ENSMUST00000152855	nonhomologous end-joining factor 1 [Source:MGI Symbol;Acc:MGI:1922820]	F7BTP0		-2.8	6.2E-04	-3.8	2.0E-02	0.8	2.6E-01	-0.9	5.8E-01
ENSMUST00000125780				-0.8	1.8E-01	-0.4	5.9E-01	0.1	8.4E-01	-0.3	6.6E-01
ENSMUST00000152876	mitochondrial ribosomal protein L48 [Source:MGI Symbol;Acc:MGI:1289321]	D3Z6C8		-5.0	1.3E-04	5.0	1.3E-03	-1.7	1.8E-01	-0.3	6.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000125784				1.6	1.9E-01	0.0	9.9E-01	0.2	9.1E-01	1.7	2.5E-01
ENSMUST00000152877	inhibitor of growth family, member 3 [Source:MGI Symbol;Acc:MGI:1919027]	S4R1J3		-2.4	2.9E-02	2.5	5.3E-03	-0.5	4.3E-01	-0.6	2.9E-01
ENSMUST00000152938	YjeF N-terminal domain containing 3 [Source:MGI Symbol;Acc:MGI:2681845]	A0A0A0MQI6		2.9	1.9E-02	6.9	4.1E-04	1.0	4.5E-01	-1.6	5.1E-02
ENSMUST00000125792				-2.7	7.5E-02	-2.8	2.3E-01	0.5	7.3E-01	0.5	8.0E-01
ENSMUST00000152946	LIM domain binding 1 [Source:MGI Symbol;Acc:MGI:894762]	D3Z1C5		-5.6	1.7E-04	3.5	7.4E-04	0.0	9.7E-01	-0.4	5.0E-01
ENSMUST00000152960	methyltransferase like 1 [Source:MGI Symbol;Acc:MGI:1339986]	D3YXU6		6.1	2.0E-04	5.4	2.5E-04	-0.1	9.4E-01	-0.6	3.8E-01
ENSMUST00000152979	CTS telomere maintenance complex component 1 [Source:MGI Symbol;Acc:MGI:1916214]	E0CXT1		6.8	1.3E-03	-7.4	8.1E-04	-1.2	3.7E-02	-0.5	7.5E-01
ENSMUST00000125815				1.7	1.1E-01	-1.8	7.8E-02	-3.9	1.1E-03	-0.5	6.2E-01
ENSMUST00000153009	coiled-coil domain containing 169 [Source:MGI Symbol;Acc:MGI:2444356]	D3Z7W2		6.3	6.4E-04	-6.3	1.9E-02	0.7	3.9E-01	-1.0	6.8E-01
ENSMUST00000125821				0.9	4.6E-01	0.0	9.8E-01	-1.0	4.0E-01	-0.1	9.6E-01
ENSMUST00000153031	SH3 domain containing ring finger 3 [Source:MGI Symbol;Acc:MGI:2444637]		Q8C120	8.7	8.3E-06	6.3	1.7E-02	0.5	8.2E-01	-0.5	6.7E-01
ENSMUST00000125827	deltex 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1921448]		Q8R3P2	4.7	6.4E-02	7.8	2.7E-02	3.1	3.0E-01	0.0	9.9E-01
ENSMUST00000125831				-2.0	8.1E-02	-0.9	4.5E-01	0.9	2.7E-01	-0.2	8.6E-01
ENSMUST00000153073	RAD51 homolog C [Source:MGI Symbol;Acc:MGI:2150020]	F2Z433		-3.8	3.3E-02	-3.3	1.8E-02	0.0	9.7E-01	-0.7	5.8E-01
ENSMUST00000153102	additional sex combs like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1922552]	D6REV1		-5.4	6.4E-05	-3.5	1.9E-02	0.0	9.9E-01	-0.6	6.5E-01
ENSMUST00000153114	colony stimulating factor 1 (macrophage) [Source:MGI Symbol;Acc:MGI:1339753]	D3Z090		-3.6	1.7E-03	-5.0	9.8E-04	-0.6	2.2E-01	-0.9	4.5E-01
ENSMUST00000153115	DNA segment, Chr 1, ERATO Doi 622, expressed [Source:MGI Symbol;Acc:MGI:1277184]		Q8VEB3	-2.9	2.3E-03	4.2	8.6E-03	-3.8	2.6E-02	0.0	9.8E-01
ENSMUST00000125849				0.8	3.1E-01	1.2	1.6E-01	-0.9	2.4E-01	-1.3	1.0E-01
ENSMUST00000153117	'6 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:109	S4R1R2		7.5	2.2E-04	4.8	2.7E-03	0.5	6.8E-01	0.2	8.0E-01
ENSMUST00000125868				-1.3	3.7E-01	-0.3	8.7E-01	0.8	6.4E-01	-0.2	9.1E-01
ENSMUST00000125871	ring finger protein 44 [Source:MGI Symbol;Acc:MGI:2145310]	E9PUC0		-0.6	5.8E-01	2.5	1.6E-01	3.5	2.3E-02	0.4	7.8E-01
ENSMUST00000153125	guanylyl cyclase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916028]	F6ZAY0		7.7	3.3E-06	3.4	1.1E-03	0.0	9.4E-01	0.6	2.9E-01
ENSMUST00000153148	WD repeat domain 54 [Source:MGI Symbol;Acc:MGI:1922909]		Q9R0D8	6.6	5.3E-04	7.0	2.7E-04	0.7	5.6E-01	0.3	6.2E-01
ENSMUST00000125880	tumor necrosis factor receptor superfamily, member 1a [Source:MGI Symbol;Acc:MGI:1314884]	F6R6K0		-1.6	1.8E-01	-0.5	6.9E-01	-0.1	9.2E-01	-1.1	4.1E-01
ENSMUST00000153194	putative homeodomain transcription factor 2 [Source:MGI Symbol;Acc:MGI:1916020]	F6X6S4		5.2	1.1E-02	4.6	5.9E-03	-0.1	9.3E-01	-0.4	6.3E-01
ENSMUST00000153250	paired box 9 [Source:MGI Symbol;Acc:MGI:97493]	Q3V1K1	P47242	6.8	2.9E-02	4.9	2.5E-03	-1.4	3.0E-01	-0.1	9.2E-01
ENSMUST00000153273	leucine rich repeat containing 37A [Source:MGI Symbol;Acc:MGI:2685097]	B1AWG4		10.9	8.2E-06	8.5	3.9E-05	-0.1	9.5E-01	-0.8	1.5E-01
ENSMUST00000153280	homeobox A7 [Source:MGI Symbol;Acc:MGI:96179]	G3UZU9		4.0	1.2E-03	4.3	2.6E-03	-3.1	3.6E-02	-1.2	1.7E-01
ENSMUST00000125899	bromodomain containing 4 [Source:MGI Symbol;Acc:MGI:1888520]	D6RGP2		-1.9	7.2E-02	-1.2	3.8E-01	0.9	3.0E-01	0.2	8.9E-01
ENSMUST00000153281	tetratricopeptide repeat domain 9C [Source:MGI Symbol;Acc:MGI:1917637]	Q6P3Y6		4.9	6.1E-04	7.4	1.3E-04	-0.6	6.4E-01	-0.6	3.6E-01
ENSMUST00000153287	uncoupling protein 2 (mitochondrial, proton carrier) [Source:MGI Symbol;Acc:MGI:109354]	D3YXM5		-8.6	6.5E-04	6.5	3.8E-04	-0.6	6.4E-01	-1.4	7.3E-02
ENSMUST00000153318	membrane protein, palmitoylated [Source:MGI Symbol;Acc:MGI:105941]	B7ZCM0		-3.9	2.2E-03	-0.9	5.8E-01	2.0	6.8E-02	-1.0	5.5E-01
ENSMUST00000153337	zinc finger protein 191 [Source:MGI Symbol;Acc:MGI:1929704]		Q91VN1	-4.0	2.6E-03	1.4	1.4E-01	0.9	2.3E-01	1.4	8.6E-02
ENSMUST00000125923	alkB, alkylation repair homolog 4 (E. coli) [Source:MGI Symbol;Acc:MGI:1919291]	D6RFB6		-1.1	4.4E-01	1.7	1.9E-01	0.0	9.7E-01	-2.8	6.0E-02
ENSMUST00000153348	sushi domain containing 4 [Source:MGI Symbol;Acc:MGI:2138351]		Q8BH32	4.5	7.6E-03	-8.6	2.5E-04	-1.0	6.3E-02	-0.5	7.6E-01
ENSMUST00000125939				0.0	9.8E-01	0.1	9.2E-01	0.1	8.9E-01	0.0	9.8E-01
ENSMUST00000153360	INO80 complex subunit C [Source:MGI Symbol;Acc:MGI:2443014]		Q8BHA0	-5.2	2.3E-03	3.2	5.8E-02	0.2	8.9E-01	0.9	4.3E-01
ENSMUST00000153424	dystrophin related protein 2 [Source:MGI Symbol;Acc:MGI:107432]		Q05AA6	8.4	2.0E-04	4.3	5.3E-03	0.5	6.7E-01	0.3	6.4E-01
ENSMUST00000125950				-1.6	1.0E-01	-0.2	8.1E-01	0.0	9.8E-01	-1.4	2.0E-01
ENSMUST00000153426	PDZ and LIM domain 7 [Source:MGI Symbol;Acc:MGI:1914649]	B8JJB1		5.8	7.7E-04	3.3	3.3E-03	-0.2	7.8E-01	0.2	7.6E-01
ENSMUST00000153442	heterogeneous nuclear ribonucleoprotein D-like [Source:MGI Symbol;Acc:MGI:1355299]	F6VQH5		-5.7	5.8E-04	5.0	1.1E-04	0.1	9.1E-01	-0.3	5.4E-01
ENSMUST00000125958				1.4	1.5E-01	1.3	2.5E-01	-0.3	7.7E-01	-0.2	8.5E-01
ENSMUST00000153488	N(alpha)-acetyltransferase 30, NatC catalytic subunit [Source:MGI Symbol;Acc:MGI:1922259]		Q8CES0	-3.5	8.0E-03	-5.1	3.4E-03	-1.6	4.2E-02	-1.8	2.9E-01
ENSMUST00000153514	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	E9Q999		-8.0	1.4E-03	-6.1	2.3E-03	1.2	3.1E-02	2.4	1.3E-01
ENSMUST00000153527	regulator of G-protein signaling 2 [Source:MGI Symbol;Acc:MGI:1098271]	A0A087WRB0		-5.5	1.4E-03	5.6	5.8E-06	-0.7	2.8E-01	-0.2	5.0E-01
ENSMUST00000153541	integrin beta 2 [Source:MGI Symbol;Acc:MGI:96611]	M0QWA7		-6.5	1.2E-03	8.2	1.2E-04	-0.3	8.5E-01	0.1	9.3E-01
ENSMUST00000153546	membrane-spanning 4-domains, subfamily A, member 4C [Source:MGI Symbol;Acc:MGI:1927656]	D3YZH6		-4.6	2.6E-03	-4.0	9.8E-03	1.7	1.4E-02	-0.7	6.3E-01
ENSMUST00000153560	interleukin 16 [Source:MGI Symbol;Acc:MGI:1270855]	D6RI15		7.1	4.1E-05	6.4	2.9E-04	-0.9	4.6E-01	0.3	6.0E-01
ENSMUST00000125980				2.3	2.2E-01	1.5	4.3E-01	-2.3	2.0E-01	-1.4	3.9E-01
ENSMUST00000153561	zinc finger E-box binding homeobox 2 [Source:MGI Symbol;Acc:MGI:1344407]	H3BKR1		2.7	1.6E-03	-6.5	4.5E-03	1.1	1.0E-01	-0.9	6.5E-01
ENSMUST00000153574	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]	E9QA05		-5.8	4.3E-05	5.6	5.2E-03	0.7	6.5E-01	-1.6	1.6E-01
ENSMUST00000153609	small nuclear ribonucleoprotein polypeptide A' [Source:MGI Symbol;Acc:MGI:1916231]		P57784	-2.5	1.5E-02	6.4	5.3E-04	-0.5	7.2E-01	0.3	7.0E-01
ENSMUST00000153617	opticin [Source:MGI Symbol;Acc:MGI:2151113]	E9PUR1		5.9	2.0E-02	-0.8	3.0E-01	0.8	9.8E-02	-1.7	5.6E-02
ENSMUST00000153623	S-adenosylhomocysteine hydrolase-like 1 [Source:MGI Symbol;Acc:MGI:2385184]	D3Z2Q0		2.9	1.1E-02	7.0	2.7E-05	-0.2	8.5E-01	0.2	6.6E-01
ENSMUST00000153648	izole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase [Source:MGI S	D6RCU8		5.8	6.6E-04	6.6	6.1E-04	-0.4	7.7E-01	-0.7	3.3E-01
ENSMUST00000153661	TatD DNase domain containing 2 [Source:MGI Symbol;Acc:MGI:3576210]	F6W3K2		-3.7	1.9E-04	5.4	2.3E-03	-1.0	5.0E-01	0.2	7.8E-01
ENSMUST00000126000				0.9	3.3E-01	2.3	6.9E-02	1.1	2.9E-01	-0.4	7.0E-01
ENSMUST00000126005	leucine rich repeat transmembrane neuronal 4 [Source:MGI Symbol;Acc:MGI:2389180]		Q80XG9	5.6	9.8E-02	5.2	1.5E-01	-0.6	8.7E-01	-0.1	9.5E-01
ENSMUST00000153664	low density lipoprotein receptor-related protein associated protein 1 [Source:MGI Symbol;Acc:MGI:96829]	F6WMD1		-3.0	1.8E-02	2.2	1.1E-02	-0.5	4.8E-01	-1.1	9.4E-02
ENSMUST00000153665	hexokinase 3 [Source:MGI Symbol;Acc:MGI:2670962]	E9Q3Z4		-8.8	1.3E-03	4.4	1.4E-02	-1.3	3.8E-01	-0.9	3.8E-01
ENSMUST00000126021				0.6	4.9E-01	1.3	2.7E-01	0.3	7.6E-01	-0.4	7.2E-01
ENSMUST00000153687	HECT, UBA and WWE domain containing 1 [Source:MGI Symbol;Acc:MGI:1926884]	D6RDF2		9.8	4.5E-05	5.7	1.5E-03	1.1	3.9E-01	-1.4	9.2E-02
ENSMUST00000126027	zinc finger and BTB domain containing 7B [Source:MGI Symbol;Acc:MGI:102755]	D3YZR6		-1.0	5.4E-01	-0.3	8.9E-01	0.6	6.8E-01	0.0	9.9E-01
ENSMUST00000126028				-3.2	4.9E-02	-2.5	2.2E-01	0.1	9.4E-01	-0.6	7.6E-01
ENSMUST00000153700	ornithine decarboxylase antizyme 2 [Source:MGI Symbol;Acc:MGI:109492]		O08608	-7.6	1.7E-03	6.2	5.2E-04	0.0	9.8E-01	-0.3	6.8E-01
ENSMUST00000126031				-3.9	1.4E-01	-0.8	8.1E-01	2.1	3.4E-01	-1.1	7.4E-01
ENSMUST00000153723	prenylcysteine oxidase 1 [Source:MGI Symbol;Acc:MGI:1914131]	D3Z275		3.3	6.0E-03	4.5	1.4E-04	0.1	9.0E-01	-0.7	2.1E-01
ENSMUST00000153735	PDZ and LIM domain 2 [Source:MGI Symbol;Acc:MGI:2384850]		Q8R1G6	-7.7	1.3E-04	4.0	1.2E-02	-0.5	6.9E-01	1.2	2.0E-01
ENSMUST00000126043				0.3	8.5E-01	0.4	8.5E-01	-1.2	5.0E-01	-1.3	4.7E-01
ENSMUST00000126046				0.4	7.1E-01	-0.4	7.8E-01	-0.3	7.9E-01	0.6	6.9E-01
ENSMUST00000126049				-1.0	2.2E-01	-0.9	4.3E-01	1.2	1.7E-01	1.1	3.1E-01
ENSMUST00000126062				2.9	7.3E-02	-1.4	4.0E-01	-3.2	4.3E-02	1.1	4.8E-01
ENSMUST00000153758	endoplasmic reticulum protein 29 [Source:MGI Symbol;Acc:MGI:1914647]	D6RG87		4.4	2.8E-04	1.8	4.8E-01	-0.6	7.7E-01	2.7	2.4E-01
ENSMUST00000153777	LanC (bacterial lantibiotic synthetase component C)-like 2 [Source:MGI Symbol;Acc:MGI:1919085]	F6RJV6		-3.5	5.6E-03	5.2	3.2E-03	-0.4	7.7E-01	0.2	8.4E-01
ENSMUST00000126069				-1.1	1.5E-01	-1.0	2.2E-01	-0.8	1.9E-01	-0.9	2.6E-01
ENSMUST00000126070	, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3 [Source:MGI Symbol;Acc:MGI:135	Q9JHF5		1.1	2.8E-01	2.2	1.5E-01	0.8	5.3E-01	-0.4	7.4E-01
ENSMUST00000153798	sorbin and SH3 domain containing 2 [Source:MGI Symbol;Acc:MGI:1924574]		Q3UTJ2	5.4	2.7E-04	-0.4	4.1E-01	0.7	5.8E-02	-0.1	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000153820	promyelocytic leukemia [Source:MGI Symbol;Acc:MGI:104662]	D3YXR5		4.1	1.9E-04	2.8	3.6E-02	1.1	3.1E-01	0.5	5.3E-01
ENSMUST00000153838	SET domain containing 2 [Source:MGI Symbol;Acc:MGI:1918177]		E9Q5F9	-3.0	7.5E-05	6.2	1.7E-04	0.5	5.8E-01	1.0	8.9E-02
ENSMUST00000126088				-0.2	8.7E-01	1.1	3.8E-01	0.5	6.4E-01	-0.8	4.7E-01
ENSMUST00000153843	coiled-coil domain containing 37 [Source:MGI Symbol;Acc:MGI:2141635]			4.7	2.0E-04	5.3	4.4E-03	-0.6	7.0E-01	-0.8	3.6E-01
ENSMUST00000126101	capping protein (actin filament), gelsolin-like [Source:MGI Symbol;Acc:MGI:1098259]	D3YTL5		-2.3	1.5E-01	-3.6	1.7E-01	-0.1	9.2E-01	1.2	6.4E-01
ENSMUST00000153875	regulator of G-protein signaling 3 [Source:MGI Symbol;Acc:MGI:1354734]	F6X4A2		3.1	3.5E-03	4.9	8.6E-03	-1.6	3.2E-01	0.7	5.0E-01
ENSMUST00000126114	inhibitor of CDK, cyclin A1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:2144284]		Q6PKN7	1.4	4.3E-01	7.0	7.9E-03	1.6	4.6E-01	-4.0	1.4E-02
ENSMUST00000153892	small ubiquitin-like modifier 2 [Source:MGI Symbol;Acc:MGI:2158813]		P61957	-4.2	3.4E-05	6.7	1.1E-03	1.5	2.9E-01	-1.6	8.5E-02
ENSMUST00000153914	golgi autoantigen, golgin subfamily a, 1 [Source:MGI Symbol;Acc:MGI:1924149]			-5.2	1.2E-04	-5.2	3.1E-03	1.2	5.3E-02	-0.1	9.5E-01
ENSMUST00000153941	solute carrier family 38, member 6 [Source:MGI Symbol;Acc:MGI:3648156]	D3YUW5		2.5	8.3E-03	4.9	9.9E-04	-3.1	2.1E-02	-0.1	9.2E-01
ENSMUST00000126119	small integral membrane protein 1 [Source:MGI Symbol;Acc:MGI:1916109]		P0C8K7	6.3	4.6E-02	6.0	6.9E-02	-1.0	7.7E-01	-0.7	7.1E-01
ENSMUST00000126120				-1.4	8.7E-02	-3.1	3.0E-02	-0.4	5.3E-01	1.3	2.9E-01
ENSMUST00000153970	F-box protein 22 [Source:MGI Symbol;Acc:MGI:1926014]	D6RFT2		-5.6	6.6E-04	5.0	9.3E-06	-0.7	2.6E-01	-0.4	2.9E-01
ENSMUST00000126135				0.3	8.8E-01	1.6	5.8E-01	-0.2	9.4E-01	-1.5	5.1E-01
ENSMUST00000126136				-0.9	4.0E-01	1.0	4.8E-01	1.3	2.4E-01	-0.6	6.3E-01
ENSMUST00000153985	zinc finger prtoein 943 [Source:MGI Symbol;Acc:MGI:1921920]	D3YYH7		3.4	4.7E-04	3.0	9.6E-02	-0.5	7.4E-01	0.6	5.9E-01
ENSMUST00000153990	STE20-related kinase adaptor beta [Source:MGI Symbol;Acc:MGI:2144047]	M0QW98		-5.9	3.5E-02	4.7	1.4E-03	-1.9	1.0E-01	-0.1	9.0E-01
ENSMUST00000126159				0.5	4.3E-01	0.4	6.5E-01	-0.2	7.8E-01	0.0	9.8E-01
ENSMUST00000153997	predicted gene, 20878 [Source:MGI Symbol;Acc:MGI:5434234]	A2APU9		6.5	2.1E-04	3.6	1.1E-02	0.0	9.8E-01	0.8	3.7E-01
ENSMUST00000154007	transmembrane protein 59 [Source:MGI Symbol;Acc:MGI:1929278]	D6RI96		-7.3	2.2E-04	4.8	2.1E-03	-1.8	1.8E-01	1.3	1.0E-01
ENSMUST00000154032	SPRY domain containing 3 [Source:MGI Symbol;Acc:MGI:2446175]	E9Q9B3		-7.8	2.9E-04	6.8	1.3E-04	0.0	9.7E-01	0.0	9.4E-01
ENSMUST00000154078	A kinase (PRKA) anchor protein 5 [Source:MGI Symbol;Acc:MGI:2685104]		D3YVF0	5.2	6.3E-05	-4.0	7.5E-02	0.5	5.9E-01	0.7	7.3E-01
ENSMUST00000126166	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]		Q9JIX8	-5.8	6.0E-02	-1.7	6.6E-01	3.1	2.1E-01	-1.0	8.0E-01
ENSMUST00000126168	ubiquitin specific peptidase like 1 [Source:MGI Symbol;Acc:MGI:2442342]	D6RI24		-4.2	5.7E-02	-1.9	5.3E-01	2.4	1.7E-01	0.1	9.6E-01
ENSMUST00000126169				2.9	8.2E-02	4.7	1.1E-02	-0.5	7.3E-01	-2.3	7.2E-02
ENSMUST00000154115	PAP associated domain containing 5 [Source:MGI Symbol;Acc:MGI:1917820]	F6UPY1		-3.5	8.5E-03	-3.7	9.8E-02	2.5	2.9E-02	-0.8	7.0E-01
ENSMUST00000126178				-3.4	2.2E-01	-3.0	3.8E-01	-0.5	8.0E-01	-0.9	8.0E-01
ENSMUST00000126179				4.2	3.5E-02	4.5	3.4E-02	-1.4	4.9E-01	-1.7	2.0E-01
ENSMUST00000154131	cyclin-dependent kinase 9 (CDC2-related kinase) [Source:MGI Symbol;Acc:MGI:1328368]	D6RHP4		-2.9	1.4E-02	4.9	1.5E-02	0.3	8.6E-01	0.5	6.6E-01
ENSMUST00000154149	DENN/MADD domain containing 2A [Source:MGI Symbol;Acc:MGI:2444961]	D3Z1C6		7.7	3.5E-04	3.6	7.4E-04	-1.1	1.4E-01	-0.5	4.0E-01
ENSMUST00000154153	polycystic kidney disease 1 like 1 [Source:MGI Symbol;Acc:MGI:2156538]	A0A0A0MQK4		9.2	2.3E-05	4.5	2.6E-02	-0.8	6.4E-01	0.6	6.1E-01
ENSMUST00000154169	RELT-like 1 [Source:MGI Symbol;Acc:MGI:2140767]		Q8K2J7	-6.6	3.9E-04	-4.5	2.1E-02	0.4	6.0E-01	1.7	3.1E-01
ENSMUST00000126194				-0.5	5.0E-01	-1.4	1.8E-01	-0.9	2.0E-01	-0.1	9.3E-01
ENSMUST00000126197				2.3	1.9E-01	6.0	2.5E-02	2.5	2.7E-01	-1.2	4.0E-01
ENSMUST00000154193	START domain containing 9 [Source:MGI Symbol;Acc:MGI:3045258]	F7B335		2.7	1.1E-03	2.4	1.6E-01	-3.6	6.3E-02	0.9	4.7E-01
ENSMUST00000154205	solute carrier family 39 (metal ion transporter), member 6 [Source:MGI Symbol;Acc:MGI:2147279]	D3Z7N4		7.4	2.9E-03	-7.2	2.8E-04	-0.7	1.3E-01	-0.8	5.8E-01
ENSMUST00000126206				0.8	6.4E-01	0.3	9.2E-01	-0.9	6.0E-01	-0.3	9.0E-01
ENSMUST00000154213	SN1, MIND kinetochore complex component, homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:191418	B0QZT5		3.6	1.5E-02	5.2	3.7E-03	-1.9	2.0E-01	-0.9	3.3E-01
ENSMUST00000126211	small nuclear ribonucleoprotein polypeptide A [Source:MGI Symbol;Acc:MGI:1855690]	D3Z0S6		3.2	1.5E-01	1.5	6.1E-01	-1.6	5.2E-01	0.1	9.5E-01
ENSMUST00000154219	eukaryotic translation initiation factor 2A [Source:MGI Symbol;Acc:MGI:1098684]	D6RFN2		-7.2	7.8E-06	8.0	3.2E-04	-0.5	7.4E-01	0.4	6.0E-01
ENSMUST00000154232	bromodomain containing 2 [Source:MGI Symbol;Acc:MGI:99495]	Q3TH63		-5.3	5.6E-04	-1.3	2.1E-01	-0.7	3.4E-01	-2.5	5.0E-02
ENSMUST00000126220				-1.4	6.4E-01	-3.9	2.9E-01	-2.5	2.2E-01	0.0	1.0E+00
ENSMUST00000154237	cytochrome b5 reductase 1 [Source:MGI Symbol;Acc:MGI:1919267]		Q9DB73	-3.2	3.5E-02	6.1	3.2E-02	-0.1	9.7E-01	-1.2	4.5E-01
ENSMUST00000126224				1.4	1.1E-01	2.3	4.8E-02	0.3	7.2E-01	-0.6	4.9E-01
ENSMUST00000126230				-2.3	7.4E-02	-2.7	9.2E-02	-0.7	4.3E-01	-0.3	8.2E-01
ENSMUST00000126234	hexokinase 3 [Source:MGI Symbol;Acc:MGI:2670962]		Q3TRM8	-1.0	7.6E-01	-2.1	7.1E-01	1.1	6.7E-01	2.2	7.0E-01
ENSMUST00000154238	glutamate receptor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1921303]	D3Z6R6		7.2	2.7E-03	6.0	6.8E-05	-0.6	4.5E-01	0.6	1.9E-01
ENSMUST00000154256	zinc finger protein 703 [Source:MGI Symbol;Acc:MGI:2662729]	F6M3K1	P0CL69	-6.2	1.9E-04	5.6	1.1E-03	0.9	4.4E-01	-0.2	7.9E-01
ENSMUST00000126243	methyl-CpG binding domain protein 6 [Source:MGI Symbol;Acc:MGI:106378]	F6S711		-2.6	5.0E-02	-4.5	3.2E-02	0.9	3.8E-01	2.8	1.5E-01
ENSMUST00000154270	epithelial membrane protein 1 [Source:MGI Symbol;Acc:MGI:107941]	S4R2U4		7.6	4.3E-05	-4.1	1.1E-02	-0.6	3.6E-01	0.5	7.2E-01
ENSMUST00000126246				-0.9	4.7E-01	-3.6	5.1E-02	-2.3	4.4E-02	0.3	8.4E-01
ENSMUST00000154276	synaptojanin 1 [Source:MGI Symbol;Acc:MGI:1354961]	F7CD11		-4.3	3.0E-02	3.7	1.7E-02	-1.1	3.8E-01	1.5	1.5E-01
ENSMUST00000126248				2.9	1.9E-01	1.4	6.9E-01	0.7	7.5E-01	2.3	4.7E-01
ENSMUST00000126266				-0.7	6.9E-01	4.4	1.2E-01	4.0	9.4E-02	-1.1	5.8E-01
ENSMUST00000154279	LINE-1 type transposase domain containing 1 [Source:MGI Symbol;Acc:MGI:3578435]		Q587J6	5.0	1.5E-02	-3.5	2.9E-02	0.9	1.8E-01	1.9	1.8E-01
ENSMUST00000154287	ubiquitination factor E4A [Source:MGI Symbol;Acc:MGI:2154580]	E9Q442		-3.1	2.5E-02	2.0	2.3E-02	-0.1	9.0E-01	0.5	4.5E-01
ENSMUST00000154330	mitochondrial ribosomal protein S24 [Source:MGI Symbol;Acc:MGI:1928142]		Q9CQV5	4.3	5.2E-03	7.3	8.4E-03	7.7	4.5E-03	-3.0	3.4E-02
ENSMUST00000126280				0.8	2.7E-01	-0.2	8.0E-01	0.5	4.9E-01	1.5	1.1E-01
ENSMUST00000154356	catenin (cadherin associated protein), beta 1 [Source:MGI Symbol;Acc:MGI:88276]	E9Q6A9		-5.8	1.7E-02	7.9	1.5E-05	0.5	6.2E-01	-0.3	5.5E-01
ENSMUST00000154364	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide [Source:MGI Symbol;Acc:MGI:2448506]	E9Q3L2		-5.1	2.4E-03	-0.1	9.2E-01	-3.2	4.2E-02	2.8	6.9E-02
ENSMUST00000154376	cytoplasmic polyadenylation element binding protein 3 [Source:MGI Symbol;Acc:MGI:2443075]			3.9	2.9E-03	5.7	4.3E-04	-0.5	6.4E-01	-0.2	6.9E-01
ENSMUST00000154381	glycosylated lysosomal membrane protein [Source:MGI Symbol;Acc:MGI:1913318]	H3BJ16		-6.7	6.8E-05	5.1	1.9E-02	-0.7	7.3E-01	-1.2	3.7E-01
ENSMUST00000154402	asparagine synthetase domain containing 1 [Source:MGI Symbol;Acc:MGI:1917646]	D3Z0F1		3.4	1.9E-03	7.7	7.1E-04	0.6	7.3E-01	0.5	5.8E-01
ENSMUST00000154412	dual oxidase maturation factor 1 [Source:MGI Symbol;Acc:MGI:2384861]	A2AQ93		6.5	2.5E-04	5.2	7.0E-04	-1.0	3.8E-01	-2.2	1.6E-02
ENSMUST00000154415	ecotropic viral integration site 2a [Source:MGI Symbol;Acc:MGI:95458]	J3QP09		-5.4	3.8E-03	5.3	2.1E-02	-0.7	7.4E-01	-0.1	9.7E-01
ENSMUST00000154424	RALBP1 associated Eps domain containing protein 2 [Source:MGI Symbol;Acc:MGI:2663511]	B1AV20		5.7	3.9E-03	8.1	3.8E-04	-0.5	7.7E-01	-0.1	8.6E-01
ENSMUST00000154440	Rho, GDP dissociation inhibitor (GDI) beta [Source:MGI Symbol;Acc:MGI:101940]	D3YWL7		-5.3	1.0E-04	2.1	1.9E-02	-0.8	2.4E-01	-0.7	2.9E-01
ENSMUST00000154448	forkhead box P2 [Source:MGI Symbol;Acc:MGI:2148705]	D3Z7E9		8.6	2.0E-06	4.4	8.2E-03	-0.4	7.4E-01	-0.5	5.3E-01
ENSMUST00000154460	adaptor-related protein complex 3, mu 1 subunit [Source:MGI Symbol;Acc:MGI:1929212]		Q9JKC8	-4.6	9.6E-05	5.7	3.4E-03	0.0	9.8E-01	-0.5	5.6E-01
ENSMUST00000154464	cerebral endothelial cell adhesion molecule [Source:MGI Symbol;Acc:MGI:2139134]	A3KGW4		5.4	1.0E-03	-2.6	5.4E-02	1.2	8.8E-02	-0.7	5.6E-01
ENSMUST00000154469	abhydrolase domain containing 11 [Source:MGI Symbol;Acc:MGI:1916008]			-4.7	7.3E-04	6.5	2.6E-03	0.6	7.1E-01	1.0	2.7E-01
ENSMUST00000154473	expressed sequence AI413582 [Source:MGI Symbol;Acc:MGI:2146839]	Q3V2N7		-5.5	5.5E-04	-2.1	1.3E-01	0.7	4.2E-01	0.0	9.9E-01
ENSMUST00000126335				2.2	5.3E-02	4.0	1.4E-02	1.7	1.8E-01	-0.1	9.1E-01
ENSMUST00000126341				0.9	2.1E-01	0.8	3.6E-01	-0.3	6.4E-01	-0.2	7.8E-01
ENSMUST00000154483	casein kinase 1, delta [Source:MGI Symbol;Acc:MGI:1355272]	F7A4U8		-4.8	1.4E-02	-5.6	2.8E-05	0.2	5.9E-01	-0.7	3.7E-01
ENSMUST00000154498	ring finger protein 208 [Source:MGI Symbol;Acc:MGI:1916096]	Z4YMD3		4.2	1.9E-02	6.0	7.5E-05	-1.9	7.8E-02	-0.1	8.4E-01
ENSMUST00000154510	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]	D3Z4E8		-4.6	3.7E-04	3.6	2.3E-03	-0.8	3.2E-01	-1.0	1.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000154526	complement factor B [Source:MGI Symbol;Acc:MGI:105975]	F6XQ00		-3.9	6.0E-03	-6.5	2.6E-02	0.1	9.0E-01	-0.2	9.4E-01
ENSMUST00000154537	immunoglobulin mu binding protein 2 [Source:MGI Symbol;Acc:MGI:99954]	D6RFT3		5.9	2.6E-02	6.7	8.9E-04	-0.8	5.6E-01	0.5	5.0E-01
ENSMUST00000154545	Rho family GTPase 3 [Source:MGI Symbol;Acc:MGI:1921444]	E9Q8D7		5.5	2.5E-05	2.2	1.8E-01	-1.3	3.7E-01	1.5	2.4E-01
ENSMUST00000154553	SFT2 domain containing 1 [Source:MGI Symbol;Acc:MGI:1918689]		Q5SSN7	-7.4	5.8E-05	6.5	3.1E-04	0.5	6.7E-01	-0.1	8.5E-01
ENSMUST00000154583	5-azacytidine induced gene 2 [Source:MGI Symbol;Acc:MGI:1351332]		Q9QYP6	-1.7	2.4E-02	4.1	6.2E-04	-0.4	6.1E-01	-0.4	5.6E-01
ENSMUST00000154585	cyclin L1 [Source:MGI Symbol;Acc:MGI:1922664]	F6WYR6		-4.7	1.2E-02	7.6	1.2E-02	-1.0	7.3E-01	-2.3	1.5E-01
ENSMUST00000126373	cullin associated and neddylation disassociated 1 [Source:MGI Symbol;Acc:MGI:1261820]	D3YWC5		3.3	4.5E-02	2.3	2.6E-01	0.0	1.0E+00	1.0	5.6E-01
ENSMUST00000154586	predicted gene 20537 [Source:MGI Symbol;Acc:MGI:5142002]	G3UY67		8.0	1.0E-03	1.2	2.2E-01	-0.6	4.5E-01	0.4	6.6E-01
ENSMUST00000126386				3.3	6.9E-02	0.3	8.7E-01	-3.2	8.0E-02	-0.1	9.5E-01
ENSMUST00000154604	cation channel, sperm associated 2 [Source:MGI Symbol;Acc:MGI:2387404]	D6RCY8		4.8	6.0E-03	-4.1	1.8E-03	0.3	4.4E-01	-2.1	9.0E-02
ENSMUST00000154617	ribosomal protein S6 kinase, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1270849]		Q8BSK8	-1.4	2.5E-02	-7.6	2.8E-04	0.6	1.6E-01	-0.9	5.4E-01
ENSMUST00000126408	churchill domain containing 1 [Source:MGI Symbol;Acc:MGI:1923684]	D3Z553		2.5	1.7E-01	3.2	5.7E-02	-2.2	1.8E-01	-2.9	6.5E-02
ENSMUST00000126413	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]	D3Z085		-3.9	5.6E-02	-3.2	2.5E-01	0.9	5.6E-01	0.2	9.4E-01
ENSMUST00000126417	natural cytotoxicity triggering receptor 1 [Source:MGI Symbol;Acc:MGI:1336212]			0.6	7.8E-01	0.4	8.8E-01	-0.8	7.0E-01	-0.6	8.0E-01
ENSMUST00000126420				3.8	4.8E-02	4.7	3.0E-02	-0.5	8.0E-01	-1.4	2.9E-01
ENSMUST00000126421	zinc finger protein 341 [Source:MGI Symbol;Acc:MGI:2682937]	D6REV2		-0.4	8.5E-01	-0.1	9.7E-01	-0.4	8.4E-01	-0.7	7.7E-01
ENSMUST00000126425				-1.2	1.8E-01	0.5	6.3E-01	1.2	1.5E-01	-0.5	6.3E-01
ENSMUST00000154619	coiled-coil domain containing 136 [Source:MGI Symbol;Acc:MGI:1918128]	F6VCV9		4.7	2.7E-02	5.7	3.5E-03	-0.6	7.1E-01	-1.8	9.7E-02
ENSMUST00000154629	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 [Source:MGI Symbol;Acc:MGI:1916197]	D6RCV4		7.0	3.9E-05	-5.0	5.9E-04	-1.1	3.6E-02	-0.9	4.1E-01
ENSMUST00000154647	phytanoyl-CoA dioxygenase domain containing 1 [Source:MGI Symbol;Acc:MGI:3612860]		Q9DB26	5.7	3.6E-03	7.7	1.9E-05	-0.4	7.1E-01	0.4	4.3E-01
ENSMUST00000154659	dachsous 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685011]	F6PYJ6		6.5	1.6E-03	7.1	7.8E-05	-0.6	6.0E-01	-0.4	5.1E-01
ENSMUST00000126435	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915123]		Q9CQT1	2.4	5.1E-02	4.2	2.1E-02	1.1	4.3E-01	-0.6	5.3E-01
ENSMUST00000154665	katanin p60 subunit A-like 2 [Source:MGI Symbol;Acc:MGI:1924234]		Q9D3R6	8.7	5.0E-05	6.4	5.0E-05	-0.5	6.0E-01	-0.4	4.5E-01
ENSMUST00000154666	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome [Source:MGI Symbol;Acc:MGI:894810]	D6RFT4		6.4	5.1E-04	4.5	1.6E-02	-0.8	6.0E-01	0.7	5.1E-01
ENSMUST00000154672	CAP-GLY domain containing linker protein 1 [Source:MGI Symbol;Acc:MGI:1928401]	F7CB97		4.8	6.7E-03	-5.4	6.7E-03	-0.9	1.8E-01	0.1	9.7E-01
ENSMUST00000154677	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	D6RJ85		-4.2	6.3E-03	7.6	1.7E-05	-0.5	6.0E-01	0.2	5.9E-01
ENSMUST00000154686	vacuolar protein sorting 29 (S. pombe) [Source:MGI Symbol;Acc:MGI:1928344]	D6RH43		-5.2	1.3E-03	-7.1	3.0E-04	-1.0	4.6E-02	-0.9	5.1E-01
ENSMUST00000126473				2.0	3.5E-01	3.2	2.8E-01	0.9	6.9E-01	-0.3	9.0E-01
ENSMUST00000154689	MYST/Esa1-associated factor 6 [Source:MGI Symbol;Acc:MGI:1917338]		Q2VPQ9	3.7	2.9E-04	-4.8	6.7E-04	0.8	1.0E-01	0.6	5.3E-01
ENSMUST00000154704	DDB1 and CUL4 associated factor 17 [Source:MGI Symbol;Acc:MGI:1923013]		Q3TUL7	2.8	1.8E-04	2.9	2.1E-02	-0.4	6.6E-01	0.0	1.0E+00
ENSMUST00000126486	Fyn proto-oncogene [Source:MGI Symbol;Acc:MGI:95602]		P39688	3.4	6.6E-02	4.8	2.0E-02	-0.5	7.6E-01	-1.9	1.6E-01
ENSMUST00000126489				-0.9	4.5E-01	-1.3	3.8E-01	-0.6	5.7E-01	-0.1	9.4E-01
ENSMUST00000154732	oculocerebrorenal syndrome of Lowe [Source:MGI Symbol;Acc:MGI:109589]	F7CAV3		3.4	1.5E-03	-2.4	1.0E-01	1.3	9.1E-02	1.2	3.8E-01
ENSMUST00000126496				1.9	4.9E-02	1.6	1.8E-01	0.3	7.8E-01	0.6	5.1E-01
ENSMUST00000126499				3.7	6.2E-02	3.6	5.0E-02	-2.0	2.8E-01	-1.8	1.9E-01
ENSMUST00000154744	glycosyltransferase-like domain containing 1 [Source:MGI Symbol;Acc:MGI:2444269]	A0A0A0MQI8		5.7	2.0E-05	4.5	2.5E-04	-1.3	1.4E-01	-0.3	5.2E-01
ENSMUST00000154757	proteasome (prosome, macropain) activator subunit 4 [Source:MGI Symbol;Acc:MGI:2143994]	F6R7K9		5.8	9.1E-04	-1.5	3.4E-01	1.9	8.0E-02	0.6	6.5E-01
ENSMUST00000154801	transmembrane protein 63c [Source:MGI Symbol;Acc:MGI:2444386]	D6RI74		6.9	9.4E-05	5.8	8.4E-04	-0.7	6.2E-01	0.0	9.5E-01
ENSMUST00000154812	CUE domain containing 1 [Source:MGI Symbol;Acc:MGI:2144281]	F2Z3X3		5.5	3.1E-03	3.1	1.9E-02	-0.5	6.4E-01	0.3	7.2E-01
ENSMUST00000154835	RIKEN cDNA 4930563I02 gene [Source:MGI Symbol;Acc:MGI:1914909]	D3YXY1		6.8	1.4E-04	3.7	5.1E-04	0.0	9.9E-01	-0.9	1.4E-01
ENSMUST00000126522	myosin XV [Source:MGI Symbol;Acc:MGI:1261811]	F6VXK7		2.9	2.1E-01	6.1	3.4E-02	0.0	1.0E+00	-3.1	7.6E-02
ENSMUST00000126523				-0.9	3.6E-01	0.1	9.0E-01	-0.5	5.9E-01	-1.5	1.8E-01
ENSMUST00000154841	eukaryotic translation initiation factor 6 [Source:MGI Symbol;Acc:MGI:1196288]	D6RG53		-2.7	2.6E-02	-1.0	4.0E-01	0.6	4.6E-01	-2.9	5.2E-02
ENSMUST00000154865	PTK2 protein tyrosine kinase 2 beta [Source:MGI Symbol;Acc:MGI:104908]	F7CCX1		-5.1	1.5E-02	5.2	2.8E-03	-3.8	2.5E-02	-0.1	8.9E-01
ENSMUST00000126533				-1.1	1.2E-01	-1.8	5.9E-02	-0.1	9.1E-01	0.7	4.3E-01
ENSMUST00000154873	TEA domain family member 3 [Source:MGI Symbol;Acc:MGI:109241]	F6TTJ9		5.0	4.1E-03	-3.7	4.7E-03	1.2	5.7E-02	-0.5	6.1E-01
ENSMUST00000154891	phosphorylase kinase, gamma 2 (testis) [Source:MGI Symbol;Acc:MGI:1916211]	D6RGU6		-7.0	2.6E-02	3.9	1.6E-02	-1.4	3.4E-01	0.2	8.7E-01
ENSMUST00000126560				-0.4	8.7E-01	0.6	8.3E-01	-0.7	7.6E-01	-1.7	5.1E-01
ENSMUST00000126561				-3.4	6.1E-02	0.5	8.6E-01	4.7	6.0E-02	0.9	6.7E-01
ENSMUST00000126562	ribosomal protein S9 [Source:MGI Symbol;Acc:MGI:1924096]	D3YWH9		-2.1	6.4E-02	-1.4	2.6E-01	-0.2	8.5E-01	-0.8	5.0E-01
ENSMUST00000154915	gametogenetin binding protein 2 [Source:MGI Symbol;Acc:MGI:2387356]		Q5SV77	-7.9	8.8E-06	6.3	2.5E-03	-0.7	6.7E-01	-1.5	1.4E-01
ENSMUST00000126573	density lipoprotein receptor-related protein 8, apolipoprotein e receptor [Source:MGI Symbol;Acc:MGI:13400	B1AXJ6		5.3	6.3E-02	6.8	5.9E-02	0.5	8.9E-01	-1.1	5.8E-01
ENSMUST00000126583	interleukin-1 receptor-associated kinase 1 [Source:MGI Symbol;Acc:MGI:107420]	F6THK7		2.2	3.7E-01	-0.8	7.9E-01	-3.5	1.5E-01	-0.5	8.4E-01
ENSMUST00000154929	syntaxin 18 [Source:MGI Symbol;Acc:MGI:1918366]	D3YY98		-4.8	4.4E-04	3.1	1.7E-02	-0.7	4.8E-01	-0.3	7.1E-01
ENSMUST00000126586	lysine (K)-specific methyltransferase 2E [Source:MGI Symbol;Acc:MGI:1924825]	A0A087WSN9		-2.3	6.7E-02	-0.4	7.9E-01	1.7	1.3E-01	-0.2	9.1E-01
ENSMUST00000154970	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143057]	D6RFC6		6.7	7.2E-03	4.5	8.6E-02	-0.7	7.8E-01	0.5	7.7E-01
ENSMUST00000126603				2.6	2.0E-01	3.4	2.0E-01	-0.2	9.2E-01	-1.1	5.4E-01
ENSMUST00000126604	on imprinted in Prader-Willi/Angelman syndrome 2 homolog (human) [Source:MGI Symbol;Acc:MGI:191391	D3Z682		-2.0	3.9E-01	-3.4	2.3E-01	-2.2	1.9E-01	-0.7	8.0E-01
ENSMUST00000154975	Ly1 antibody reactive clone [Source:MGI Symbol;Acc:MGI:107470]	D6RDT2		5.1	8.5E-03	3.3	1.5E-01	-1.9	3.6E-01	0.8	6.0E-01
ENSMUST00000154978	SEC22 homolog C, vesicle trafficking protein [Source:MGI Symbol;Acc:MGI:2447871]	D3Z110		3.2	1.4E-02	6.3	5.7E-05	-0.9	3.3E-01	-1.1	8.6E-02
ENSMUST00000126610	ribosomal protein L12 [Source:MGI Symbol;Acc:MGI:98002]	Q5BLK0	P35979	0.3	7.6E-01	-3.3	4.1E-02	-1.4	1.5E-01	2.2	1.2E-01
ENSMUST00000154987				-4.9	5.1E-03	-4.2	1.3E-01	0.7	5.7E-01	-1.1	7.1E-01
ENSMUST00000126614				-2.3	1.5E-01	-0.8	5.9E-01	-1.0	3.6E-01	-2.5	1.5E-01
ENSMUST00000126618				1.1	3.2E-01	1.2	4.5E-01	0.4	7.1E-01	0.3	7.9E-01
ENSMUST00000126619				-0.3	7.2E-01	0.2	8.6E-01	0.5	5.3E-01	0.0	9.7E-01
ENSMUST00000126620				0.5	7.1E-01	-0.4	8.0E-01	-0.7	5.5E-01	0.1	9.3E-01
ENSMUST00000155003	vesicle-associated membrane protein 4 [Source:MGI Symbol;Acc:MGI:1858730]		O70480	-2.6	6.1E-03	6.2	1.9E-04	-0.6	5.9E-01	0.1	8.0E-01
ENSMUST00000155016	discs, large (Drosophila) homolog-associated protein 1 [Source:MGI Symbol;Acc:MGI:1346065]		Q9D415	5.9	1.2E-02	5.3	1.4E-02	-0.9	6.3E-01	-1.6	2.4E-01
ENSMUST00000126637	WAS/WASL interacting protein family, member 3 [Source:MGI Symbol;Acc:MGI:3044681]	D3Z5R4		3.5	6.0E-02	6.8	2.7E-03	-0.5	8.0E-01	-3.8	7.7E-03
ENSMUST00000155020	predicted gene, 37988 [Source:MGI Symbol;Acc:MGI:5611216]	J3QM41		-5.2	1.2E-02	3.7	1.1E-02	-1.3	3.0E-01	0.1	9.4E-01
ENSMUST00000126641	serine/arginine-rich splicing factor 10 [Source:MGI Symbol;Acc:MGI:1333805]	Q3UA07	Q9R0U0	-0.4	6.2E-01	0.4	6.8E-01	0.7	3.8E-01	-0.1	9.0E-01
ENSMUST00000155022	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 [Source:MGI Symbol;Acc:MGI:1915005]			5.4	6.5E-03	4.0	3.3E-04	-0.4	5.4E-01	0.0	9.3E-01
ENSMUST00000155023	kazrin, periplakin interacting protein [Source:MGI Symbol;Acc:MGI:1918779]	F6RLJ7		8.4	2.0E-05	4.4	6.9E-04	-0.6	4.8E-01	-0.1	9.2E-01
ENSMUST00000155034	adenosine monophosphate deaminase 1 [Source:MGI Symbol;Acc:MGI:88015]	A0A0G2JFD4		6.2	1.7E-04	5.8	5.4E-05	-0.4	6.2E-01	-0.2	7.0E-01
ENSMUST00000155075	cilia and flagella associated protein 46 [Source:MGI Symbol;Acc:MGI:2444387]	D6RJ10		5.7	3.5E-04	7.4	3.3E-03	0.9	6.4E-01	-0.4	7.4E-01
ENSMUST00000155084	obscurin-like 1 [Source:MGI Symbol;Acc:MGI:2138628]	A0A0A0MQG1		7.0	1.2E-04	5.6	6.9E-04	0.2	8.7E-01	-0.4	5.8E-01
ENSMUST00000155090	calcium channel, voltage-dependent, alpha 1F subunit [Source:MGI Symbol;Acc:MGI:1859639]	S4R182		6.5	1.5E-04	6.5	2.3E-04	-0.3	7.9E-01	0.8	2.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000126662	predicted gene 21974 [Source:MGI Symbol;Acc:MGI:5439443]	F6W3F3		6.0	3.6E-02	2.9	3.8E-01	-0.3	9.0E-01	2.7	3.0E-01
ENSMUST00000126663				-0.8	3.8E-01	-0.1	8.9E-01	-0.1	8.6E-01	-0.8	4.3E-01
ENSMUST00000155116	poly(A) binding protein, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:1349722]	F6ZAX1		-6.4	5.3E-04	6.6	5.9E-04	0.2	8.6E-01	-0.1	9.4E-01
ENSMUST00000126671				0.6	4.4E-01	-2.1	1.6E-01	-0.2	7.9E-01	2.6	9.0E-02
ENSMUST00000155126	nuclear receptor subfamily 1, group I, member 3 [Source:MGI Symbol;Acc:MGI:1346307]	Q3UEP1		3.7	6.9E-03	6.4	4.8E-04	-0.7	6.2E-01	-0.8	3.1E-01
ENSMUST00000155128	zinc finger and SCAN domain containing 2 [Source:MGI Symbol;Acc:MGI:99176]	D3YW76		9.2	1.5E-04	3.0	3.6E-02	1.0	3.6E-01	1.1	2.1E-01
ENSMUST00000155152	DnaJ (Hsp40) homolog, subfamily C, member 7 [Source:MGI Symbol;Acc:MGI:1928373]	F7BTP8		-6.7	3.3E-04	5.7	1.8E-02	0.1	9.5E-01	-0.5	7.3E-01
ENSMUST00000155186	gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:95706]	F6V328		-6.3	1.2E-03	4.3	3.2E-04	0.2	7.8E-01	0.2	6.3E-01
ENSMUST00000126691				0.9	7.2E-01	-0.4	8.3E-01	-4.0	5.1E-02	-2.7	2.5E-01
ENSMUST00000126692				2.3	4.2E-01	0.6	8.7E-01	0.1	9.9E-01	1.7	6.2E-01
ENSMUST00000126694				1.4	5.2E-02	2.1	4.1E-02	0.7	3.9E-01	0.0	1.0E+00
ENSMUST00000126698	ERGIC and golgi 2 [Source:MGI Symbol;Acc:MGI:1914706]	B2KFC9		-0.9	7.4E-01	-2.5	4.6E-01	-2.2	2.9E-01	-0.7	8.5E-01
ENSMUST00000155202	-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human) [Source:MGI Symbol;Acc:MGI:1333	F6QMQ3		6.8	5.9E-04	-2.4	7.8E-02	6.3	7.2E-06	-1.3	3.4E-01
ENSMUST00000126703	TNFAIP3 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1926194]	D3Z3B6		-1.7	6.6E-02	-0.4	7.0E-01	1.0	2.0E-01	-0.3	7.6E-01
ENSMUST00000155203	zinc finger and BTB domain containing 10 [Source:MGI Symbol;Acc:MGI:2139883]	E9Q8X5		6.3	3.7E-05	-1.7	9.5E-02	0.0	9.9E-01	-0.2	8.7E-01
ENSMUST00000155244	basal cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1929940]	D3YTK7		6.7	4.8E-04	4.0	3.5E-03	-1.0	3.4E-01	-0.4	5.7E-01
ENSMUST00000126716	serine/arginine-rich splicing factor 11 [Source:MGI Symbol;Acc:MGI:1916457]	D6RE22		-1.4	5.6E-01	-1.8	5.3E-01	-1.0	5.3E-01	-0.6	8.4E-01
ENSMUST00000155249	integrin alpha 6 [Source:MGI Symbol;Acc:MGI:96605]	F6VSK8		8.5	4.3E-05	2.0	2.2E-02	-1.8	2.5E-02	-0.1	9.1E-01
ENSMUST00000126729				1.3	3.1E-01	1.5	4.1E-01	1.1	5.1E-01	0.8	5.3E-01
ENSMUST00000126731	exocyst complex component 7 [Source:MGI Symbol;Acc:MGI:1859270]	A2AAN3		-1.3	1.5E-01	0.9	4.1E-01	1.2	1.4E-01	-1.0	3.5E-01
ENSMUST00000126737				0.8	8.0E-01	6.3	2.0E-01	2.3	6.0E-01	-3.1	2.9E-01
ENSMUST00000155256	LSM14 homolog A (SCD6, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914320]	F6X2V9		-6.0	3.0E-05	3.3	2.1E-04	0.7	1.7E-01	0.1	7.4E-01
ENSMUST00000155261	chromodomain helicase DNA binding protein 4 [Source:MGI Symbol;Acc:MGI:1344380]	G5E8V7		3.3	4.7E-04	-2.8	1.2E-02	-0.4	3.8E-01	-2.1	6.7E-02
ENSMUST00000126745				1.7	4.1E-01	-0.6	8.2E-01	-1.8	3.7E-01	0.5	8.2E-01
ENSMUST00000155272	phosphoribosyl pyrophosphate amidotransferase [Source:MGI Symbol;Acc:MGI:2387203]	D6RHB8		5.8	9.7E-03	5.5	2.5E-03	-0.7	6.4E-01	-0.1	8.9E-01
ENSMUST00000155278	cytoplasmic polyadenylation element binding protein 4 [Source:MGI Symbol;Acc:MGI:1914829]	Q5SU47		-5.7	7.8E-03	-2.5	4.3E-01	2.4	2.2E-01	-1.8	5.8E-01
ENSMUST00000155282	myosin VA [Source:MGI Symbol;Acc:MGI:105976]	D3Z4J3		-6.0	8.3E-04	5.5	8.8E-04	-0.6	6.0E-01	0.7	3.1E-01
ENSMUST00000155309	transmembrane protein 56 [Source:MGI Symbol;Acc:MGI:1923195]		Q8CGF5	4.9	1.2E-03	5.3	2.3E-05	0.0	9.7E-01	0.1	8.0E-01
ENSMUST00000155358	glutamate receptor, metabotropic 5 [Source:MGI Symbol;Acc:MGI:1351342]	F6YJ89		4.4	1.1E-02	6.8	1.6E-04	0.1	9.0E-01	-0.5	3.9E-01
ENSMUST00000155364	mitochondrial pyruvate carrier 1 [Source:MGI Symbol;Acc:MGI:1915240]	Q3UX28	P63030	-6.0	3.6E-03	6.3	4.6E-03	-0.8	6.8E-01	-0.4	7.1E-01
ENSMUST00000126780				1.9	2.8E-01	-0.4	8.5E-01	-0.3	8.7E-01	2.0	3.0E-01
ENSMUST00000126786				0.9	2.0E-01	1.8	5.3E-02	0.6	4.0E-01	-0.3	6.5E-01
ENSMUST00000126787				0.9	2.1E-01	-1.4	8.9E-02	-2.2	3.9E-03	0.2	8.4E-01
ENSMUST00000155385	crystallin, zeta [Source:MGI Symbol;Acc:MGI:88527]	D3Z4Q4		5.9	7.2E-04	4.3	4.8E-03	-0.3	8.1E-01	-0.9	2.7E-01
ENSMUST00000155387	DiGeorge syndrome critical region gene 6 [Source:MGI Symbol;Acc:MGI:1202877]	D3YUN0		2.5	1.8E-02	4.3	1.1E-03	-1.2	1.7E-01	0.6	3.3E-01
ENSMUST00000155392	proline rich 14-like [Source:MGI Symbol;Acc:MGI:2443658]	F6RN94		4.9	2.6E-03	6.2	2.0E-04	-0.9	4.3E-01	-0.2	7.0E-01
ENSMUST00000155405	nudix (nucleoside diphosphate linked moiety X)-type motif 8 [Source:MGI Symbol;Acc:MGI:1913637]		Q9CR24	3.9	2.2E-03	5.8	1.0E-03	0.1	9.6E-01	-0.4	5.8E-01
ENSMUST00000126805	protease-associated domain containing 1 [Source:MGI Symbol;Acc:MGI:1920577]			-1.0	6.3E-01	-3.8	1.8E-01	-2.3	1.5E-01	0.5	8.5E-01
ENSMUST00000155413	RELT tumor necrosis factor receptor [Source:MGI Symbol;Acc:MGI:2443373]	D6RIM1		-3.4	9.0E-04	2.3	2.0E-01	1.3	3.4E-01	4.1	9.8E-03
ENSMUST00000155433	lon peptidase 2, peroxisomal [Source:MGI Symbol;Acc:MGI:1914137]		Q9DBN5	3.4	8.0E-05	6.7	6.0E-04	0.7	5.9E-01	-0.6	4.0E-01
ENSMUST00000126810				1.0	2.3E-01	2.5	3.7E-02	1.1	2.4E-01	-0.5	5.8E-01
ENSMUST00000155466	predicted gene 20696 [Source:MGI Symbol;Acc:MGI:5313143]	H3BJN7		6.2	3.4E-05	5.7	3.1E-04	-1.2	2.7E-01	0.4	5.1E-01
ENSMUST00000155478	tripartite motif-containing 7 [Source:MGI Symbol;Acc:MGI:2137353]	B2RR25		6.7	9.8E-04	1.8	3.4E-02	0.4	4.5E-01	0.6	3.2E-01
ENSMUST00000155480	ıonooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Source:MGI Symbol;Acc:M	F6YY69		-7.7	3.0E-05	2.5	7.4E-03	-0.4	5.3E-01	-0.8	2.2E-01
ENSMUST00000155485	cingulin [Source:MGI Symbol;Acc:MGI:1927237]	A0A0G2JEK8		8.1	1.6E-05	6.5	1.7E-04	-0.6	6.1E-01	-0.2	7.3E-01
ENSMUST00000126833				0.8	4.1E-01	1.1	3.9E-01	0.2	8.7E-01	-0.2	8.9E-01
ENSMUST00000155486	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	Q5RIN0		-4.5	1.5E-03	6.5	7.3E-03	-0.8	7.2E-01	-1.6	1.8E-01
ENSMUST00000126839				-3.3	8.1E-02	-2.4	3.3E-01	1.0	4.8E-01	0.1	9.7E-01
ENSMUST00000126841				-0.1	9.3E-01	0.8	6.4E-01	0.3	8.3E-01	-0.6	6.5E-01
ENSMUST00000155487	hippocampus abundant transcript-like 1 [Source:MGI Symbol;Acc:MGI:1913881]		Q8CIA9	-5.7	6.3E-03	7.4	2.1E-05	-0.9	3.5E-01	0.3	5.4E-01
ENSMUST00000155490	dephospho-CoA kinase domain containing [Source:MGI Symbol;Acc:MGI:1915337]	B0QZX9		-3.6	2.7E-02	5.0	2.4E-04	-0.1	9.5E-01	0.1	9.0E-01
ENSMUST00000126853				1.3	5.8E-01	6.1	9.4E-02	4.5	1.1E-01	-0.3	9.1E-01
ENSMUST00000155493	platelet-activating factor acetylhydrolase, isoform 1b, subunit 1 [Source:MGI Symbol;Acc:MGI:109520]	Q5SW16		-4.7	7.1E-03	6.1	1.6E-02	-1.7	4.6E-01	-1.3	3.6E-01
ENSMUST00000155519	epithelial splicing regulatory protein 1 [Source:MGI Symbol;Acc:MGI:1917326]	Z4YMQ5		6.2	1.9E-04	3.8	5.6E-03	-3.1	2.5E-02	-0.9	3.0E-01
ENSMUST00000155520	breast carcinoma amplified sequence 2 [Source:MGI Symbol;Acc:MGI:1915433]	D6RHR7		-6.0	1.5E-04	5.7	3.4E-02	0.6	8.0E-01	0.4	8.1E-01
ENSMUST00000155534	mucin 5, subtypes A and C, tracheobronchial/gastric [Source:MGI Symbol;Acc:MGI:104697]	E9QAQ8		12.7	2.2E-05	5.9	1.9E-03	-3.1	8.1E-02	-0.9	2.5E-01
ENSMUST00000155559	family with sequence similarity 20, member A [Source:MGI Symbol;Acc:MGI:2388266]		Q8CID3	7.9	1.1E-05	-1.3	2.2E-01	0.7	2.7E-01	-0.1	9.0E-01
ENSMUST00000126869	negative regulator of reactive oxygen species [Source:MGI Symbol;Acc:MGI:2445095]		Q8BMT4	-2.9	5.9E-02	-1.1	5.4E-01	0.8	5.8E-01	-0.9	5.7E-01
ENSMUST00000126874				2.2	3.1E-01	5.1	9.2E-02	1.5	5.7E-01	-1.3	4.9E-01
ENSMUST00000155572	transmembrane channel-like gene family 5 [Source:MGI Symbol;Acc:MGI:1921674]	D3Z0S8		6.1	4.5E-04	2.2	8.9E-03	0.2	6.9E-01	-0.4	4.8E-01
ENSMUST00000155573	RAD9-HUS1-RAD1 interacting nuclear orphan 1 [Source:MGI Symbol;Acc:MGI:1915315]	D3YUX9		2.9	4.2E-03	6.9	6.1E-05	-0.6	5.5E-01	-0.2	7.5E-01
ENSMUST00000126885	adaptor-related protein complex AP-1, mu subunit 1 [Source:MGI Symbol;Acc:MGI:102776]	D3YZ71		-0.6	5.1E-01	-0.4	7.3E-01	0.5	5.7E-01	0.3	7.8E-01
ENSMUST00000155575	cDNA sequence BC005537 [Source:MGI Symbol;Acc:MGI:2441726]	B7FAT3		-6.9	1.7E-03	4.1	1.9E-02	-0.5	7.2E-01	-0.4	6.7E-01
ENSMUST00000155576	Rho GTPase activating protein 26 [Source:MGI Symbol;Acc:MGI:1918552]	E9QAQ3		-3.4	1.1E-03	8.4	3.4E-03	-0.3	8.9E-01	1.7	1.2E-01
ENSMUST00000126893				-1.2	6.0E-02	-0.6	4.7E-01	0.3	5.3E-01	-0.3	6.4E-01
ENSMUST00000126907				-3.7	1.1E-01	3.0	4.2E-01	6.2	5.0E-02	-0.5	8.7E-01
ENSMUST00000155587	glutaminase [Source:MGI Symbol;Acc:MGI:95752]	F6U529		-5.8	4.7E-04	-4.1	1.1E-02	0.4	5.0E-01	1.7	2.1E-01
ENSMUST00000155601	patatin-like phospholipase domain containing 7 [Source:MGI Symbol;Acc:MGI:2385325]	F6UDU9		-4.9	3.8E-03	-3.1	4.3E-02	0.4	5.9E-01	-0.5	7.2E-01
ENSMUST00000155628	discoidin domain receptor family, member 1 [Source:MGI Symbol;Acc:MGI:99216]	G3UXE5		6.2	1.1E-02	4.5	5.7E-04	-2.2	3.7E-02	1.0	1.2E-01
ENSMUST00000155633	C-type lectin domain family 16, member A [Source:MGI Symbol;Acc:MGI:1921624]		Q80U30	-4.3	2.3E-02	5.0	4.8E-04	-1.2	2.5E-01	-1.2	8.1E-02
ENSMUST00000126923	F-box and leucine-rich repeat protein 8 [Source:MGI Symbol;Acc:MGI:1354697]	D6RGN0		3.7	7.4E-02	5.4	4.2E-02	0.9	7.0E-01	-0.9	6.0E-01
ENSMUST00000126928				-2.4	8.7E-02	-3.2	1.3E-01	0.0	9.9E-01	0.7	7.1E-01
ENSMUST00000155672	protein phosphatase 2, regulatory subunit B, delta [Source:MGI Symbol;Acc:MGI:1289252]	F6RV17		-3.8	1.6E-03	-3.3	3.9E-02	0.6	3.9E-01	-0.3	8.3E-01
ENSMUST00000155676	ubiquitin-like 4A [Source:MGI Symbol;Acc:MGI:95049]	Q3UK94	P21126	-4.1	3.2E-03	6.7	8.7E-03	-0.7	7.5E-01	-1.9	1.4E-01
ENSMUST00000155697	solute carrier family 25, member 45 [Source:MGI Symbol;Acc:MGI:2147731]		Q8CFJ7	-5.5	1.2E-03	5.3	2.1E-02	-0.5	8.0E-01	-0.7	5.6E-01
ENSMUST00000126947				0.3	8.1E-01	-1.2	5.6E-01	0.5	7.1E-01	2.0	3.2E-01
ENSMUST00000155701	protocadherin 15 [Source:MGI Symbol;Acc:MGI:1891428]		Q99PJ1	5.9	8.5E-03	7.0	1.9E-04	-1.7	2.3E-01	0.3	6.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000155702	TSR1 20S rRNA accumulation [Source:MGI Symbol;Acc:MGI:2144566]	D6RI76		3.5	2.2E-02	-3.5	1.8E-04	-0.4	2.4E-01	-0.4	5.7E-01
ENSMUST00000155707	tissue inhibitor of metalloproteinase 2 [Source:MGI Symbol;Acc:MGI:98753]	B1AQJ3		-4.9	6.0E-04	4.4	3.8E-04	-0.6	4.2E-01	0.0	9.3E-01
ENSMUST00000155712	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	Q8CHB6		-6.7	8.8E-04	-4.2	9.6E-03	0.3	5.6E-01	-0.7	6.2E-01
ENSMUST00000155716	galactosidase, beta 1-like [Source:MGI Symbol;Acc:MGI:1921827]		Q8VC60	-4.2	2.2E-02	6.0	4.0E-05	0.8	3.2E-01	0.2	6.0E-01
ENSMUST00000155721	spermatogenesis associated glutamate (E)-rich protein 4B [Source:MGI Symbol;Acc:MGI:1920776]	K7N6S0		7.6	2.3E-04	7.5	1.6E-04	0.5	7.0E-01	0.0	9.8E-01
ENSMUST00000126976	bone marrow stromal cell antigen 1 [Source:MGI Symbol;Acc:MGI:105370]	A0A0G2JG11		-2.2	6.1E-02	-4.3	2.0E-02	-1.6	5.3E-02	0.5	7.7E-01
ENSMUST00000155737	guanine nucleotide binding protein (G protein), beta 4 [Source:MGI Symbol;Acc:MGI:104581]		P29387	3.2	5.5E-03	-5.9	3.4E-03	0.3	5.3E-01	1.1	5.1E-01
ENSMUST00000155798	ccinate dehydrogenase complex, subunit C, integral membrane protein [Source:MGI Symbol;Acc:MGI:191330	D3Z1A8		-3.0	8.7E-03	6.0	4.6E-04	-0.6	6.2E-01	0.0	9.6E-01
ENSMUST00000155802	CD84 antigen [Source:MGI Symbol;Acc:MGI:1336885]			-1.6	5.9E-03	-2.9	1.2E-01	1.4	1.9E-01	-1.7	4.0E-01
ENSMUST00000155807	predicted gene 10715 [Source:MGI Symbol;Acc:MGI:3642376]	J3QMT9		14.3	1.5E-07	6.2	2.0E-02	-2.5	3.3E-01	1.6	2.6E-01
ENSMUST00000155837	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	D6RCZ8		-8.7	3.3E-03	4.8	3.9E-03	-0.4	7.2E-01	0.0	9.8E-01
ENSMUST00000126986				-1.8	5.6E-02	-2.7	3.9E-02	0.1	8.9E-01	1.0	3.8E-01
ENSMUST00000155856	RIKEN cDNA 2610001J05 gene [Source:MGI Symbol;Acc:MGI:1913770]	F2Z3Y9		-7.8	1.9E-06	6.0	8.4E-04	0.5	6.8E-01	-0.3	7.3E-01
ENSMUST00000155861	Wolf-Hirschhorn syndrome candidate 1-like 1 (human) [Source:MGI Symbol;Acc:MGI:2142581]		Q6P2L6	-3.3	3.0E-03	-4.5	1.6E-02	-1.8	4.7E-02	-1.5	4.2E-01
ENSMUST00000126993				4.2	6.3E-02	3.1	1.9E-01	-1.3	5.7E-01	-0.2	9.1E-01
ENSMUST00000127005				-1.3	3.8E-01	4.3	4.2E-02	1.9	2.9E-01	-3.8	2.6E-02
ENSMUST00000155869	VPS9 domain containing 1 [Source:MGI Symbol;Acc:MGI:1914143]	D6RGB6		-5.4	5.3E-04	5.2	1.5E-03	-2.0	1.4E-01	-0.4	6.0E-01
ENSMUST00000155873	ribosomal protein L11 [Source:MGI Symbol;Acc:MGI:1914275]	A2BH06		-7.1	1.4E-02	-1.4	9.0E-02	0.5	3.8E-01	-1.9	6.0E-02
ENSMUST00000127019				-0.7	7.1E-01	-4.4	1.4E-01	-2.8	8.6E-02	0.9	7.4E-01
ENSMUST00000155901	CCR4-NOT transcription complex, subunit 6-like [Source:MGI Symbol;Acc:MGI:2443154]		Q8VEG6	-2.6	4.0E-03	6.5	2.2E-04	-0.5	6.9E-01	-1.6	3.2E-02
ENSMUST00000127027	zinc finger protein 960 [Source:MGI Symbol;Acc:MGI:3052731]	L7N267		1.8	2.9E-01	1.1	6.0E-01	-0.2	8.9E-01	0.5	7.5E-01
ENSMUST00000127028				-0.3	8.2E-01	1.0	5.6E-01	-0.5	7.2E-01	-1.8	2.2E-01
ENSMUST00000127030				3.4	4.4E-02	1.9	2.7E-01	-1.9	2.3E-01	-0.3	8.3E-01
ENSMUST00000155907	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 20 [Source:MGI Symbol;Acc:M		P59511	7.2	5.0E-05	5.4	1.4E-03	0.9	4.6E-01	-0.3	6.1E-01
ENSMUST00000127032	t-complex-associated testis expressed 2 [Source:MGI Symbol;Acc:MGI:98641]	D3YY45		3.6	1.4E-01	2.6	3.8E-01	-0.2	9.4E-01	0.7	7.4E-01
ENSMUST00000155908	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]	F7BIK4		-6.9	1.0E-03	6.9	2.1E-04	-0.6	6.3E-01	-0.9	1.7E-01
ENSMUST00000127036				1.9	3.6E-02	2.6	2.3E-02	-0.3	6.8E-01	-1.0	2.4E-01
ENSMUST00000155939	proteasome (prosome, macropain) inhibitor subunit 1 [Source:MGI Symbol;Acc:MGI:1346072]	D6REH2		-3.8	1.1E-02	5.5	4.5E-04	-0.9	4.4E-01	-0.8	2.1E-01
ENSMUST00000155957	discoidin domain receptor family, member 1 [Source:MGI Symbol;Acc:MGI:99216]	E9PW79		3.6	2.5E-02	6.3	6.0E-04	-0.7	6.2E-01	-0.3	6.5E-01
ENSMUST00000127056				-2.9	1.0E-01	-1.6	5.0E-01	1.0	5.2E-01	-0.4	8.7E-01
ENSMUST00000155966	phosphatidylinositol glycan anchor biosynthesis, class X [Source:MGI Symbol;Acc:MGI:1919334]	F6YX19		-7.2	2.3E-03	2.6	5.4E-02	-2.5	6.9E-02	0.2	8.5E-01
ENSMUST00000127059				4.8	4.0E-02	6.1	2.1E-02	-0.3	9.1E-01	-1.5	2.8E-01
ENSMUST00000127061	polymerase (DNA directed), gamma 2, accessory subunit [Source:MGI Symbol;Acc:MGI:1354947]	D6REU1		1.5	2.4E-01	1.2	4.8E-01	-0.5	7.4E-01	-0.2	8.8E-01
ENSMUST00000127071				0.8	5.8E-01	2.1	2.4E-01	0.3	8.7E-01	-1.1	4.2E-01
ENSMUST00000155990	erythrocyte membrane protein band 4.1 [Source:MGI Symbol;Acc:MGI:95401]	F7CR30		-4.8	2.7E-02	5.9	7.9E-04	0.5	7.1E-01	-0.8	2.7E-01
ENSMUST00000127079				1.5	5.0E-01	-2.2	3.1E-01	-3.1	9.6E-02	0.6	7.9E-01
ENSMUST00000127081				1.6	1.1E-01	1.9	1.2E-01	0.0	9.8E-01	-0.2	7.9E-01
ENSMUST00000127082				-1.8	4.5E-01	-1.4	6.0E-01	1.0	5.6E-01	0.6	8.4E-01
ENSMUST00000156001	coiled-coil domain containing 6 [Source:MGI Symbol;Acc:MGI:1923801]	F6SXB0		4.0	2.7E-04	6.0	1.4E-03	-0.7	6.4E-01	0.3	7.0E-01
ENSMUST00000156009	collagen, type XVIII, alpha 1 [Source:MGI Symbol;Acc:MGI:88451]	D3Z556		6.0	2.8E-04	-1.4	4.0E-01	1.2	2.7E-01	-1.6	3.5E-01
ENSMUST00000156019	sperm associated antigen 9 [Source:MGI Symbol;Acc:MGI:1918084]	F6SH61		-3.7	7.3E-03	-0.3	7.8E-01	0.1	9.0E-01	-1.9	9.6E-02
ENSMUST00000156038	ankyrin repeat domain 50 [Source:MGI Symbol;Acc:MGI:2139777]	F7BE84		1.1	2.5E-02	3.7	2.5E-02	-2.5	1.4E-01	-0.5	6.6E-01
ENSMUST00000156043	casein kinase 1, epsilon [Source:MGI Symbol;Acc:MGI:1351660]	A9J9D8		10.5	1.5E-05	3.8	2.7E-03	-0.3	7.2E-01	-0.5	5.0E-01
ENSMUST00000156045	histone deacetylase 7 [Source:MGI Symbol;Acc:MGI:1891835]	E9PZG4		6.1	3.4E-03	2.8	1.0E-02	0.0	9.7E-01	0.1	8.3E-01
ENSMUST00000156071	lipoma HMGIC fusion partner-like 2 [Source:MGI Symbol;Acc:MGI:2145236]	D3Z698		6.2	2.6E-03	-0.1	8.9E-01	0.7	3.7E-01	-2.0	1.0E-01
ENSMUST00000156110	cyclin G associated kinase [Source:MGI Symbol;Acc:MGI:2442153]	F6SLK1		-4.5	6.3E-03	6.2	1.1E-03	-0.6	7.0E-01	-2.4	2.1E-02
ENSMUST00000156133	interleukin 10 receptor, beta [Source:MGI Symbol;Acc:MGI:109380]	E9Q294		3.8	8.3E-04	3.6	1.7E-02	0.6	6.2E-01	-0.2	8.3E-01
ENSMUST00000127100	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 [Source:MGI Symbol;Acc:MGI:1347008]	F6W3Q8		-0.7	3.8E-01	0.2	8.1E-01	0.3	7.2E-01	-0.7	4.8E-01
ENSMUST00000156135	syntaxin 1B [Source:MGI Symbol;Acc:MGI:1930705]			8.2	1.4E-05	3.0	9.2E-02	-1.4	3.8E-01	-0.5	6.8E-01
ENSMUST00000156159	spectrin beta, non-erythrocytic 5 [Source:MGI Symbol;Acc:MGI:2685200]	F6UCX4		8.4	8.2E-06	-7.2	1.7E-02	1.4	1.5E-01	0.8	7.6E-01
ENSMUST00000127113				-1.5	1.2E-01	-0.7	4.9E-01	-0.7	3.5E-01	-1.5	1.9E-01
ENSMUST00000127114				-0.1	9.1E-01	1.1	2.2E-01	-0.7	3.6E-01	-1.9	4.5E-02
ENSMUST00000156163	calumenin [Source:MGI Symbol;Acc:MGI:1097158]	G3UXA8		8.3	3.3E-04	0.8	3.1E-01	-2.4	5.6E-03	-1.4	7.1E-02
ENSMUST00000127122	formin-like 2 [Source:MGI Symbol;Acc:MGI:1918659]	F6XR20		-1.7	4.6E-01	-0.2	9.1E-01	-2.0	2.2E-01	-3.5	1.3E-01
ENSMUST00000127123				-2.0	3.5E-02	-2.4	4.3E-02	-0.4	5.8E-01	0.1	9.6E-01
ENSMUST00000156180	NEDD4 binding protein 2-like 2 [Source:MGI Symbol;Acc:MGI:2687207]	F6WBP1		-5.8	2.3E-04	4.7	3.8E-05	0.2	7.2E-01	0.1	8.6E-01
ENSMUST00000156187	EF-hand calcium binding domain 6 [Source:MGI Symbol;Acc:MGI:1924877]		Q6P1E8	7.7	2.0E-05	-5.6	2.9E-03	-0.1	8.8E-01	-1.1	5.1E-01
ENSMUST00000127138				3.7	1.0E-01	5.9	2.7E-02	-0.2	9.2E-01	-2.5	1.0E-01
ENSMUST00000156208	methyl-CpG binding domain protein 6 [Source:MGI Symbol;Acc:MGI:106378]	D3YV97		2.3	2.3E-02	4.3	2.0E-01	-2.0	5.4E-01	2.2	3.0E-01
ENSMUST00000156216	paired box 6 [Source:MGI Symbol;Acc:MGI:97490]	A2A409		7.5	1.5E-04	7.1	9.7E-03	-0.8	7.4E-01	-1.7	2.2E-01
ENSMUST00000127148	scavenger receptor class B, member 1 [Source:MGI Symbol;Acc:MGI:893578]	F7C5U2		-1.3	5.6E-01	-1.0	7.7E-01	0.8	7.4E-01	0.5	8.7E-01
ENSMUST00000156254	transmembrane protein 63b [Source:MGI Symbol;Acc:MGI:2387609]	D3YY83		3.6	1.1E-02	2.9	4.2E-03	0.2	7.8E-01	-0.6	3.2E-01
ENSMUST00000156255	phospholipid transfer protein [Source:MGI Symbol;Acc:MGI:103151]	A2A5K4		5.5	1.2E-02	0.0	9.8E-01	-0.5	6.1E-01	2.9	4.5E-02
ENSMUST00000127156				1.7	4.6E-01	0.6	8.5E-01	-0.7	7.6E-01	0.3	9.1E-01
ENSMUST00000156282	RIKEN cDNA 1700015F17 gene [Source:MGI Symbol;Acc:MGI:2686532]	D6RFV2		4.7	8.3E-04	3.3	3.8E-02	-0.1	9.5E-01	-0.5	6.3E-01
ENSMUST00000156290	tetratricopeptide repeat domain 28 [Source:MGI Symbol;Acc:MGI:2140873]		Q80XJ3	6.6	2.3E-06	5.1	4.1E-04	-1.9	9.5E-02	-0.1	8.8E-01
ENSMUST00000127161				-2.7	2.0E-01	-1.7	5.3E-01	0.5	8.0E-01	-0.5	8.5E-01
ENSMUST00000156306	endoglin [Source:MGI Symbol;Acc:MGI:95392]	F7BZW0		4.7	1.4E-02	3.1	7.4E-03	0.4	6.3E-01	-0.1	8.4E-01
ENSMUST00000127165				1.8	5.7E-02	2.2	5.8E-02	0.2	7.9E-01	-0.1	8.9E-01
ENSMUST00000156314	ring finger protein 20 [Source:MGI Symbol;Acc:MGI:1925927]	A2AIR2		5.3	2.4E-02	2.7	3.2E-03	0.9	1.4E-01	0.0	1.0E+00
ENSMUST00000156326	transmembrane and ubiquitin-like domain containing 2 [Source:MGI Symbol;Acc:MGI:1919303]		Q3V209	-2.8	1.6E-02	4.1	2.5E-02	-0.3	8.3E-01	0.2	8.0E-01
ENSMUST00000156335	tumor susceptibility gene 101 [Source:MGI Symbol;Acc:MGI:106581]	D3Z0S9		5.9	3.9E-03	8.3	5.0E-03	-1.6	5.4E-01	-2.7	9.5E-02
ENSMUST00000127176				0.5	5.8E-01	0.4	7.2E-01	0.1	8.9E-01	0.2	8.2E-01
ENSMUST00000156359	ribosomal protein, large, P0 [Source:MGI Symbol;Acc:MGI:1927636]	S4R1N1		-7.1	1.8E-02	7.7	8.3E-05	0.5	6.7E-01	-0.3	5.7E-01
ENSMUST00000156360	PQ loop repeat containing [Source:MGI Symbol;Acc:MGI:2444067]	Q3UU83		1.9	6.8E-03	-1.5	2.5E-01	0.0	9.5E-01	-1.7	2.4E-01
ENSMUST00000156363	YTH domain containing 1 [Source:MGI Symbol;Acc:MGI:2443713]	D6RG95		-5.3	3.9E-03	2.3	2.2E-01	-3.6	8.1E-02	-0.8	5.6E-01
ENSMUST00000156372	ribosomal protein S19 [Source:MGI Symbol;Acc:MGI:1333780]	D3YUG3		-10.1	5.9E-05	6.2	4.5E-04	-1.9	1.7E-01	0.2	7.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000156380	PET100 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3615306]		P0DJE0	-6.4	3.7E-06	-3.9	3.9E-03	0.1	8.6E-01	-0.4	7.1E-01
ENSMUST00000156389	ubiquitin-conjugating enzyme E2M [Source:MGI Symbol;Acc:MGI:108278]	F6YXS3		-3.3	1.1E-02	7.0	2.8E-04	-0.6	6.7E-01	-0.1	8.3E-01
ENSMUST00000156390	glycerol kinase [Source:MGI Symbol;Acc:MGI:106594]		Q64516	-8.0	9.8E-06	-6.5	4.9E-04	0.1	8.3E-01	-0.1	9.3E-01
ENSMUST00000156408	cDNA sequence BC089491 [Source:MGI Symbol;Acc:MGI:3608324]	F6TYD6		4.3	1.9E-04	5.8	4.1E-04	1.9	8.5E-02	0.5	4.3E-01
ENSMUST00000127210	actinin alpha 4 [Source:MGI Symbol;Acc:MGI:1890773]	E9Q2W9		2.4	2.3E-01	3.1	1.5E-01	-1.0	5.8E-01	-1.7	3.6E-01
ENSMUST00000156431	2-hydroxyacyl-CoA lyase 1 [Source:MGI Symbol;Acc:MGI:1929657]		Q9QXE0	5.5	1.2E-05	3.2	1.1E-04	-1.2	2.8E-02	0.0	9.1E-01
ENSMUST00000156442	SEC16 homolog A, endoplasmic reticulum export factor [Source:MGI Symbol;Acc:MGI:2139207]	F7BPW6		-7.9	4.9E-04	7.3	1.8E-04	-1.2	3.6E-01	0.4	4.8E-01
ENSMUST00000156461	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A [Source:MGI Symbol;Acc:MGI:108447]	F6UFG6		-6.9	1.9E-05	9.0	2.4E-05	-0.7	6.0E-01	-0.2	6.8E-01
ENSMUST00000127215				-2.0	5.5E-02	-0.7	4.7E-01	-0.3	7.3E-01	-1.5	1.5E-01
ENSMUST00000156481	mediator complex subunit 28 [Source:MGI Symbol;Acc:MGI:1914249]		Q920D3	1.9	1.8E-02	7.1	9.0E-06	-0.3	7.5E-01	0.0	9.2E-01
ENSMUST00000127220	intraflagellar transport 81 [Source:MGI Symbol;Acc:MGI:1098597]	D3Z5A8		2.6	5.5E-02	5.8	6.7E-04	-0.5	6.8E-01	-3.7	2.2E-03
ENSMUST00000156486	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog [Source:MGI Symbol;Acc:MGI:96680]	E9Q8V2		-5.2	3.2E-04	-1.8	1.2E-01	-0.2	7.6E-01	-1.8	1.7E-01
ENSMUST00000156520	abhydrolase domain containing 5 [Source:MGI Symbol;Acc:MGI:1914719]		Q9DBL9	-4.8	8.1E-04	5.1	3.3E-02	6.2	7.9E-03	-1.7	2.1E-01
ENSMUST00000127238				-0.3	7.2E-01	0.8	5.2E-01	0.5	6.3E-01	-0.7	5.5E-01
ENSMUST00000127239				1.3	1.6E-01	1.9	1.2E-01	0.5	5.9E-01	0.0	9.9E-01
ENSMUST00000156529	post-GPI attachment to proteins 2 [Source:MGI Symbol;Acc:MGI:2385286]		Q3TQR0	-4.4	2.3E-03	6.2	5.0E-04	0.1	9.1E-01	0.3	7.2E-01
ENSMUST00000127248				0.5	6.4E-01	1.1	4.8E-01	0.7	5.6E-01	0.2	8.8E-01
ENSMUST00000156537	syntaxin 4A (placental) [Source:MGI Symbol;Acc:MGI:893577]	D6RJ29		-3.7	1.4E-02	5.7	7.5E-03	-0.1	9.5E-01	-2.2	6.5E-02
ENSMUST00000127251				4.5	1.3E-01	5.3	1.2E-01	0.3	9.3E-01	-0.6	7.7E-01
ENSMUST00000156542	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:106299]	F6R0R3		3.1	2.0E-03	-7.5	6.4E-04	0.2	6.0E-01	2.7	1.0E-01
ENSMUST00000156570	lipin 2 [Source:MGI Symbol;Acc:MGI:1891341]		Q99PI5	2.6	1.8E-03	11.7	1.5E-04	1.2	5.5E-01	1.0	1.6E-01
ENSMUST00000127254				2.6	1.5E-01	1.9	2.9E-01	-2.4	1.8E-01	-1.8	2.8E-01
ENSMUST00000156597	leucine rich repeat containing 40 [Source:MGI Symbol;Acc:MGI:1914394]	D6RFC5		-5.0	3.7E-03	-5.2	3.5E-03	-0.1	9.1E-01	-1.5	3.6E-01
ENSMUST00000156598	ectonucleoside triphosphate diphosphohydrolase 1 [Source:MGI Symbol;Acc:MGI:102805]	D6RHQ2		-4.7	3.2E-03	6.3	4.8E-03	-0.4	8.2E-01	-1.3	2.0E-01
ENSMUST00000156610	ATP-binding cassette, sub-family C (CFTR/MRP), member 12 [Source:MGI Symbol;Acc:MGI:2441679]	D6RCU5		5.3	2.8E-02	-2.6	2.8E-01	1.6	2.3E-01	-0.7	7.6E-01
ENSMUST00000127269	alveolar soft part sarcoma chromosome region, candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1916188]	A2AC00		3.9	7.2E-02	0.2	9.3E-01	-1.8	3.9E-01	1.8	4.1E-01
ENSMUST00000156613	zinc finger protein 142 [Source:MGI Symbol;Acc:MGI:1924514]	M0QWZ4		2.5	4.2E-03	6.3	2.6E-04	0.1	9.3E-01	-0.6	3.7E-01
ENSMUST00000156629	RIKEN cDNA 1700093K21 gene [Source:MGI Symbol;Acc:MGI:1914608]	A2AF85		6.4	7.9E-05	3.3	2.6E-02	-1.0	3.9E-01	1.2	2.3E-01
ENSMUST00000156637	p21 protein (Cdc42/Rac)-activated kinase 1 [Source:MGI Symbol;Acc:MGI:1339975]	S4R2K7		6.8	1.4E-02	5.4	2.8E-04	-2.6	3.6E-02	0.2	7.0E-01
ENSMUST00000156638	NAD synthetase 1 [Source:MGI Symbol;Acc:MGI:1926164]	D6RDE7		-3.1	2.8E-02	8.4	2.7E-04	0.1	9.5E-01	1.2	1.2E-01
ENSMUST00000156644	integrin beta 2 [Source:MGI Symbol;Acc:MGI:96611]	M0QWJ6		-6.6	2.7E-03	1.9	4.7E-01	6.7	5.1E-03	0.3	9.0E-01
ENSMUST00000127292				-1.3	6.4E-01	-0.8	8.4E-01	1.3	6.6E-01	0.8	8.3E-01
ENSMUST00000156669	disabled 2 interacting protein [Source:MGI Symbol;Acc:MGI:1916851]	F6QQP6		-4.8	6.4E-03	7.5	6.0E-05	-1.8	1.6E-01	0.1	8.1E-01
ENSMUST00000156687	leckstrin homology domain containing, family B (evectins) member 2 [Source:MGI Symbol;Acc:MGI:2385825	Q3UFC9	Q9QZC7	3.8	3.6E-05	-0.6	8.4E-01	-1.9	3.8E-01	3.8	2.1E-01
ENSMUST00000156690	myocyte enhancer factor 2A [Source:MGI Symbol;Acc:MGI:99532]		Q60929	-5.3	8.9E-04	-0.9	5.0E-01	4.0	1.0E-03	-0.8	5.3E-01
ENSMUST00000156700	potassium channel tetramerisation domain containing 9 [Source:MGI Symbol;Acc:MGI:2145579]	D6RH42		-4.9	8.7E-04	-7.4	5.0E-05	-0.8	7.9E-02	-1.0	3.8E-01
ENSMUST00000156711	torsin family 1, member B [Source:MGI Symbol;Acc:MGI:1353605]	F6VK94		-6.8	1.0E-03	4.2	5.6E-03	-1.0	3.8E-01	-0.5	5.2E-01
ENSMUST00000156714	cytochrome P450, family 2, subfamily s, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1921384]	D3Z762		3.9	4.0E-03	9.0	6.8E-05	-0.4	7.9E-01	1.2	8.9E-02
ENSMUST00000156722	RAS protein activator like 1 (GAP1 like) [Source:MGI Symbol;Acc:MGI:1330842]		Q9Z268	8.2	1.3E-02	-1.1	7.9E-02	-4.0	2.9E-05	-1.0	1.1E-01
ENSMUST00000156741	polyglutamine binding protein 1 [Source:MGI Symbol;Acc:MGI:1859638]	A2AER8		-6.0	5.5E-04	6.1	5.8E-05	-1.2	2.1E-01	-0.2	7.5E-01
ENSMUST00000156752	zinc finger RNA binding protein [Source:MGI Symbol;Acc:MGI:1341890]	F6QJP7		-4.8	2.3E-03	3.7	6.3E-03	-0.8	4.4E-01	-0.5	5.6E-01
ENSMUST00000156784	C1D nuclear receptor co-repressor [Source:MGI Symbol;Acc:MGI:1927354]	A0A0A0MQK7		-4.9	1.4E-04	3.4	1.1E-01	-3.1	1.6E-01	-1.2	4.0E-01
ENSMUST00000156816	mitochondrial ribosomal protein L15 [Source:MGI Symbol;Acc:MGI:1351639]		Q9CPR5	4.1	5.4E-05	6.6	7.5E-03	-0.1	9.7E-01	-1.7	1.6E-01
ENSMUST00000127312				-0.3	6.6E-01	-0.1	8.5E-01	0.0	9.5E-01	-0.1	9.1E-01
ENSMUST00000156834	IQ motif and Sec7 domain 1 [Source:MGI Symbol;Acc:MGI:1196356]			5.0	8.2E-03	-5.3	5.7E-03	-1.0	1.7E-01	1.7	2.7E-01
ENSMUST00000127329				-2.2	9.1E-02	-0.2	9.2E-01	1.2	2.8E-01	-0.8	5.7E-01
ENSMUST00000156835	NEDD4 binding protein 3 [Source:MGI Symbol;Acc:MGI:2442218]	A2AA66		5.1	2.5E-02	6.2	5.4E-04	1.4	2.4E-01	-1.0	1.9E-01
ENSMUST00000127346				-3.0	4.1E-02	-4.2	2.3E-02	-1.8	3.9E-02	-0.6	7.3E-01
ENSMUST00000156873	chitinase-like 1 [Source:MGI Symbol;Acc:MGI:1340899]		Q61362	-8.5	8.5E-04	6.5	1.9E-04	2.4	3.9E-02	-0.3	6.5E-01
ENSMUST00000156876	major facilitator superfamily domain containing 6 [Source:MGI Symbol;Acc:MGI:1922925]	D3Z183		-5.2	2.9E-03	6.4	1.6E-04	-0.5	6.3E-01	-0.5	4.3E-01
ENSMUST00000156898	actin related protein 2/3 complex, subunit 4 [Source:MGI Symbol;Acc:MGI:1915339]		P59999	-7.1	2.0E-04	6.4	9.5E-04	-0.7	6.3E-01	-0.6	4.8E-01
ENSMUST00000156904	phosphoinositide-3-kinase, catalytic, gamma polypeptide [Source:MGI Symbol;Acc:MGI:1353576]		Q9JHG7	-3.8	6.1E-04	3.6	1.2E-01	-0.8	7.2E-01	0.8	6.0E-01
ENSMUST00000156927	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]			-7.5	1.9E-02	4.5	9.6E-04	-2.1	6.4E-02	0.4	5.6E-01
ENSMUST00000156951	topoisomerase (DNA) III beta [Source:MGI Symbol;Acc:MGI:1333803]	F6SDD7		3.0	2.8E-02	7.3	5.3E-04	-1.3	4.0E-01	0.7	3.2E-01
ENSMUST00000156968	replication protein A2 [Source:MGI Symbol;Acc:MGI:1339939]	F6V8R7		7.9	2.9E-05	4.7	2.5E-05	-1.2	6.9E-02	0.5	2.5E-01
ENSMUST00000156969	transforming growth factor beta regulated gene 4 [Source:MGI Symbol;Acc:MGI:1100868]		Q91YM4	-2.4	1.4E-02	3.1	6.3E-03	-0.3	6.8E-01	0.2	7.3E-01
ENSMUST00000157005	tubby-like protein 3 [Source:MGI Symbol;Acc:MGI:1329045]			9.6	2.3E-06	5.1	3.1E-04	0.1	8.9E-01	0.1	8.8E-01
ENSMUST00000127375	sorting nexin 11 [Source:MGI Symbol;Acc:MGI:1921729]	A2A880		-0.2	7.4E-01	1.0	2.4E-01	1.1	1.1E-01	-0.1	8.8E-01
ENSMUST00000157019	cell division cycle associated 7 [Source:MGI Symbol;Acc:MGI:1914203]	A2AR39		5.9	4.6E-03	2.2	3.2E-01	8.3	5.6E-04	0.3	8.8E-01
ENSMUST00000127383	septin 9 [Source:MGI Symbol;Acc:MGI:1858222]	A2A6U5		-0.6	5.5E-01	0.6	6.6E-01	0.0	9.8E-01	-1.2	3.5E-01
ENSMUST00000127385				5.2	8.4E-02	4.2	1.3E-01	-3.3	3.0E-01	-2.3	2.2E-01
ENSMUST00000157034	zinc finger RNA binding protein [Source:MGI Symbol;Acc:MGI:1341890]	F6RTK9		-5.8	3.2E-04	6.2	3.9E-04	-0.9	4.7E-01	-1.1	1.6E-01
ENSMUST00000157067	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:104558]	F6RQA2		3.2	5.2E-03	7.3	7.8E-05	-0.6	6.0E-01	-0.7	2.5E-01
ENSMUST00000159004	MAS-related GPR, member A2A [Source:MGI Symbol;Acc:MGI:3821888]			-5.8	1.4E-03	6.9	5.6E-05	-1.5	1.9E-01	-1.6	2.1E-02
ENSMUST00000159018	BUD31 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2141291]	E0CX20		-6.0	1.2E-03	6.4	2.9E-04	-0.8	4.7E-01	-0.9	1.9E-01
ENSMUST00000127401				2.3	3.9E-01	3.7	3.4E-01	2.4	5.1E-01	1.0	6.6E-01
ENSMUST00000127403	lysine (K)-specific demethylase 2B [Source:MGI Symbol;Acc:MGI:1354737]	D6RHM8		4.4	4.2E-02	4.2	9.3E-02	-1.2	6.1E-01	-1.0	5.2E-01
ENSMUST00000159028	guanine nucleotide binding protein (G protein), gamma 2 [Source:MGI Symbol;Acc:MGI:102705]		P63213	-5.5	4.1E-04	-3.1	1.5E-03	-1.6	6.9E-03	0.0	9.8E-01
ENSMUST00000159039	CKLF-like MARVEL transmembrane domain containing 1 [Source:MGI Symbol;Acc:MGI:2447159]	B7ZP21		5.0	1.8E-02	-1.4	1.2E-01	0.5	3.3E-01	-0.5	5.8E-01
ENSMUST00000159055	cyclic AMP-regulated phosphoprotein, 21 [Source:MGI Symbol;Acc:MGI:107562]	E0CYU3		4.6	2.0E-02	7.2	2.6E-05	-0.9	3.9E-01	-0.1	8.4E-01
ENSMUST00000159062	F-box protein 41 [Source:MGI Symbol;Acc:MGI:1261912]	Q3UGY7	Q6NS60	3.0	2.5E-02	8.5	1.4E-05	-0.6	6.0E-01	-0.5	2.7E-01
ENSMUST00000159067	predicted gene 43720 [Source:MGI Symbol;Acc:MGI:5663857]	E0CXM8		7.5	3.5E-04	5.4	3.4E-03	-1.0	4.5E-01	0.1	8.8E-01
ENSMUST00000159068	adrenergic receptor, alpha 1a [Source:MGI Symbol;Acc:MGI:104773]		P97718	7.4	6.5E-05	2.0	8.6E-02	0.2	8.4E-01	0.4	6.3E-01
ENSMUST00000127442	protein phosphatase 1, regulatory subunit 18 [Source:MGI Symbol;Acc:MGI:1923698]		Q8BQ30	-1.5	1.5E-01	-0.7	6.1E-01	0.6	5.1E-01	-0.3	8.4E-01
ENSMUST00000159081	COMM domain containing 1 [Source:MGI Symbol;Acc:MGI:109474]	A2RSF1	Q8K4M5	2.6	5.5E-03	5.9	1.2E-03	-0.5	7.4E-01	-0.4	6.0E-01
ENSMUST00000127449				-1.8	2.5E-01	-3.0	1.5E-01	-1.2	2.8E-01	0.0	9.9E-01
ENSMUST00000159096	argininosuccinate lyase [Source:MGI Symbol;Acc:MGI:88084]	F7D439		-5.5	6.5E-04	5.8	2.3E-04	-1.3	2.5E-01	-0.1	9.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159110	apoptotic peptidase activating factor 1 [Source:MGI Symbol;Acc:MGI:1306796]		O88879	-7.3	4.2E-04	-2.6	3.5E-01	1.8	2.6E-01	-2.8	3.9E-01
ENSMUST00000127464				1.3	5.4E-01	-3.5	2.8E-01	-2.4	1.9E-01	2.4	4.6E-01
ENSMUST00000159122	RIKEN cDNA A630001G21 gene [Source:MGI Symbol;Acc:MGI:2443131]	Q3UTB2		6.9	8.4E-04	5.0	6.7E-03	-0.5	7.5E-01	-1.6	1.1E-01
ENSMUST00000127469				-3.0	3.1E-01	-1.9	5.8E-01	0.0	9.9E-01	-1.1	7.7E-01
ENSMUST00000127471	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	E9Q8K6		-1.4	1.3E-01	-1.6	1.0E-01	-0.6	3.5E-01	-0.5	6.2E-01
ENSMUST00000159124	inosine 5'-phosphate dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:96567]		P50096	5.3	2.0E-02	2.5	7.6E-03	-1.8	3.2E-02	0.3	5.9E-01
ENSMUST00000159152	RIKEN cDNA 2010111I01 gene [Source:MGI Symbol;Acc:MGI:1919311]	F6SS74		6.4	1.0E-04	4.9	1.7E-03	-1.0	4.0E-01	-0.8	3.6E-01
ENSMUST00000159196	WNK lysine deficient protein kinase 2 [Source:MGI Symbol;Acc:MGI:1922857]	F6SRP4		7.6	1.7E-05	-2.9	2.0E-02	-1.1	9.9E-02	-0.4	7.0E-01
ENSMUST00000159199	:-ray repair complementing defective repair in Chinese hamster cells 4 [Source:MGI Symbol;Acc:MGI:133379			7.1	7.5E-06	-3.1	2.2E-02	0.5	3.8E-01	-0.7	5.6E-01
ENSMUST00000159200	proline-rich transmembrane protein 4 [Source:MGI Symbol;Acc:MGI:2141677]		B2RU40	8.6	5.5E-05	6.5	6.3E-04	-0.7	6.3E-01	-0.7	3.4E-01
ENSMUST00000159207	upstream transcription factor 1 [Source:MGI Symbol;Acc:MGI:99542]	E0CYP7		-2.6	1.1E-02	-10.0	7.2E-02	-1.1	4.6E-01	-0.5	9.3E-01
ENSMUST00000127482	immunoglobulin superfamily, member 9 [Source:MGI Symbol;Acc:MGI:2135283]		Q05BQ1	3.6	9.1E-02	7.9	8.2E-03	0.9	7.1E-01	-3.3	3.7E-02
ENSMUST00000159236	TRAF2 and NCK interacting kinase [Source:MGI Symbol;Acc:MGI:1916264]		P83510	5.6	5.3E-04	5.9	7.6E-04	-0.5	7.2E-01	0.1	9.1E-01
ENSMUST00000127487				-0.6	6.8E-01	-0.7	6.8E-01	0.0	1.0E+00	0.2	9.2E-01
ENSMUST00000127490	CTD nuclear envelope phosphatase 1 regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1921981]		Q3UJ81	0.8	7.7E-01	-1.3	7.2E-01	-1.8	4.5E-01	0.2	9.5E-01
ENSMUST00000159283	mesencephalic astrocyte-derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:1922090]	Q3TMX5		2.0	1.8E-02	6.9	4.2E-04	-0.9	4.8E-01	0.5	4.9E-01
ENSMUST00000159286	in homology domain containing, family G (with RhoGef domain) member 4 [Source:MGI Symbol;Acc:MGI:2	E0CZA7		7.6	9.0E-05	4.3	5.7E-02	-1.7	4.3E-01	-0.9	5.5E-01
ENSMUST00000127503				0.0	9.9E-01	1.1	4.4E-01	0.7	5.4E-01	-0.4	7.6E-01
ENSMUST00000159290	WD repeat domain 26 [Source:MGI Symbol;Acc:MGI:1923825]	F6UT94		-3.7	5.1E-04	-2.1	1.1E-02	0.2	7.1E-01	-0.2	7.4E-01
ENSMUST00000159292	O-sialoglycoprotein endopeptidase [Source:MGI Symbol;Acc:MGI:1913496]			1.9	7.7E-03	5.7	7.9E-04	-2.1	1.3E-01	-1.8	3.4E-02
ENSMUST00000159294	mastermind like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2389460]	F6U238		6.9	2.2E-06	3.8	3.0E-02	-0.7	6.3E-01	2.6	3.2E-02
ENSMUST00000159315	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	F6TRR6		-6.3	4.1E-03	-4.3	1.1E-02	-2.3	1.0E-02	-1.4	3.7E-01
ENSMUST00000159329	ute carrier family 24 (sodium/potassium/calcium exchanger), member 4 [Source:MGI Symbol;Acc:MGI:24473	E9PUL6		6.5	2.8E-05	5.1	3.7E-04	0.2	7.8E-01	0.0	9.4E-01
ENSMUST00000159335	UMAP1-MVP12 associated (UMA) domain containing 1 [Source:MGI Symbol;Acc:MGI:3840148]	E0CYZ5		3.9	1.2E-03	4.2	1.9E-04	-0.6	3.6E-01	-0.3	5.0E-01
ENSMUST00000127539				1.5	3.0E-01	4.5	2.4E-02	1.3	4.4E-01	-1.7	2.0E-01
ENSMUST00000159337	versican [Source:MGI Symbol;Acc:MGI:102889]	Q8BS97		5.5	5.4E-04	-3.6	5.6E-03	0.9	1.1E-01	0.0	9.7E-01
ENSMUST00000127545				0.1	9.2E-01	3.4	4.5E-02	1.5	2.9E-01	-1.8	1.2E-01
ENSMUST00000127548				-2.8	7.7E-02	-0.6	7.2E-01	0.2	8.8E-01	-2.0	2.5E-01
ENSMUST00000127552				0.1	8.5E-01	1.3	1.1E-01	1.0	1.1E-01	-0.2	7.9E-01
ENSMUST00000159338	myelocytomatosis oncogene [Source:MGI Symbol;Acc:MGI:97250]	E0CZD1		4.3	1.1E-02	5.6	4.5E-05	-2.5	1.9E-02	0.4	3.7E-01
ENSMUST00000127556				-1.1	5.7E-01	6.1	1.6E-02	3.1	1.6E-01	-4.1	3.4E-02
ENSMUST00000127559				0.7	3.6E-01	1.2	2.2E-01	0.2	7.6E-01	-0.3	6.9E-01
ENSMUST00000159340	MPN domain containing [Source:MGI Symbol;Acc:MGI:1915297]	F7BJW2		-6.0	3.5E-04	6.6	2.1E-04	-0.9	4.8E-01	-0.8	1.9E-01
ENSMUST00000127567	SID1 transmembrane family, member 1 [Source:MGI Symbol;Acc:MGI:2443155]		Q6AXF6	0.0	9.8E-01	-2.1	3.4E-01	0.0	9.7E-01	2.1	3.2E-01
ENSMUST00000159345	N-acylethanolamine acid amidase [Source:MGI Symbol;Acc:MGI:1914361]	G3XA18		-7.8	3.9E-05	1.6	4.8E-02	0.8	1.8E-01	0.8	1.8E-01
ENSMUST00000159348	RIKEN cDNA 2700081O15 gene [Source:MGI Symbol;Acc:MGI:1919667]		Q4VA45	5.8	1.6E-04	5.4	7.7E-05	-0.3	7.4E-01	-0.1	8.7E-01
ENSMUST00000159386	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	E0CXS2		-3.7	2.9E-02	6.8	2.1E-04	0.1	9.0E-01	-1.1	1.1E-01
ENSMUST00000159388	vang-like 1 (van gogh, Drosophila) [Source:MGI Symbol;Acc:MGI:2159344]	A0A0H2UH25		7.1	4.9E-05	5.5	2.4E-02	-0.7	7.6E-01	-0.7	5.9E-01
ENSMUST00000159416	carbonic anhydrase 7 [Source:MGI Symbol;Acc:MGI:103100]	G3XA26		5.2	3.9E-04	4.9	1.4E-03	0.0	9.8E-01	-0.2	7.6E-01
ENSMUST00000159417	Ly6/Plaur domain containing 1 [Source:MGI Symbol;Acc:MGI:1919835]		Q8BLC3	6.7	1.6E-06	7.8	5.1E-05	2.0	8.1E-02	-0.8	1.7E-01
ENSMUST00000159429	SHANK-associated RH domain interacting protein [Source:MGI Symbol;Acc:MGI:1913331]	F6UHH8		-4.1	7.5E-03	-1.1	5.6E-01	3.2	1.5E-02	-0.4	8.1E-01
ENSMUST00000159451	cyclic AMP-regulated phosphoprotein, 21 [Source:MGI Symbol;Acc:MGI:107562]	E9Q4A0		5.9	1.3E-03	3.8	5.7E-02	0.0	9.8E-01	-0.4	7.1E-01
ENSMUST00000159461	caspase 4, apoptosis-related cysteine peptidase [Source:MGI Symbol;Acc:MGI:107700]	F6SUE5		-6.9	2.4E-02	-5.9	8.1E-03	1.7	3.0E-02	-0.6	7.4E-01
ENSMUST00000159462	SMC5-SMC6 complex localization factor 1 [Source:MGI Symbol;Acc:MGI:2145448]			5.6	2.5E-03	6.3	6.0E-04	-0.5	6.9E-01	-1.7	3.9E-02
ENSMUST00000159492	hepatoma-derived growth factor [Source:MGI Symbol;Acc:MGI:1194494]	E0CXA0		5.9	1.6E-02	4.7	4.3E-03	-1.1	3.8E-01	-0.4	6.6E-01
ENSMUST00000127628				-4.0	1.4E-01	-4.4	2.8E-01	0.2	9.3E-01	0.6	8.8E-01
ENSMUST00000159517	predicted gene 4778 [Source:MGI Symbol;Acc:MGI:3643869]	K7N6S3		5.9	4.6E-04	8.4	3.2E-05	-0.6	6.4E-01	-0.9	1.0E-01
ENSMUST00000127635				-2.6	5.5E-02	-3.1	5.9E-02	-1.1	2.0E-01	-0.6	7.2E-01
ENSMUST00000127637				-3.0	5.5E-02	-1.2	5.3E-01	1.9	1.6E-01	0.0	1.0E+00
ENSMUST00000159524	predicted gene 5286 [Source:MGI Symbol;Acc:MGI:3644284]	E0CXI6		7.4	5.2E-05	-10.1	3.0E-05	1.1	6.5E-03	0.1	9.7E-01
ENSMUST00000159527	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) [Source:MGI Symbol;Acc:MGI:1924148]	Q8R1V2		5.8	8.2E-03	5.0	8.8E-05	-0.7	3.3E-01	0.0	9.3E-01
ENSMUST00000159545	oxysterol binding protein-like 9 [Source:MGI Symbol;Acc:MGI:1923784]	F8VQE8		-10.0	7.0E-07	-2.3	4.4E-02	0.6	2.7E-01	-1.2	2.7E-01
ENSMUST00000127645				3.8	4.5E-02	2.4	2.8E-01	-1.7	4.1E-01	-0.2	8.8E-01
ENSMUST00000159551	Wilms tumour 1-associating protein [Source:MGI Symbol;Acc:MGI:1926395]	E0CYH0		-3.6	2.5E-02	-7.8	3.6E-03	1.3	5.2E-02	0.1	9.6E-01
ENSMUST00000159565	RIKEN cDNA 4931429L15 gene [Source:MGI Symbol;Acc:MGI:1921611]	E9PVU2		6.9	6.8E-06	5.2	9.9E-03	-0.2	9.2E-01	0.3	8.0E-01
ENSMUST00000159567	nucleotide binding protein-like [Source:MGI Symbol;Acc:MGI:1924076]	F7D3P0		3.3	1.3E-03	4.3	9.4E-04	-0.1	8.9E-01	-0.3	6.1E-01
ENSMUST00000159569	zinc finger protein 26 [Source:MGI Symbol;Acc:MGI:99173]	G3XA08		-1.8	7.1E-03	5.5	1.4E-02	-0.6	7.7E-01	2.0	8.2E-02
ENSMUST00000159572	nicotinamide riboside kinase 1 [Source:MGI Symbol;Acc:MGI:2147434]		Q91W63	3.4	4.5E-04	4.1	1.1E-02	-0.9	4.7E-01	-1.1	2.4E-01
ENSMUST00000159576	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase) [Source:MGI Symbol;Acc:MGI:1924753]	E0CZ10		8.6	1.1E-06	-0.9	2.0E-01	1.4	5.4E-03	-0.2	7.0E-01
ENSMUST00000127665				-2.4	5.7E-02	-0.5	6.5E-01	-0.2	7.9E-01	-2.1	1.1E-01
ENSMUST00000127666	coiled-coil-helix-coiled-coil-helix domain containing 3 [Source:MGI Symbol;Acc:MGI:1913325]	D3Z0L4		1.6	4.5E-01	-4.7	1.2E-01	-4.9	1.7E-02	1.4	6.3E-01
ENSMUST00000127674				2.1	1.7E-01	6.5	1.0E-02	2.7	1.9E-01	-1.7	2.1E-01
ENSMUST00000159584	NACHT and WD repeat domain containing 2 [Source:MGI Symbol;Acc:MGI:1920464]		Q6P5U7	6.8	4.1E-05	7.2	3.4E-04	0.1	9.2E-01	-1.2	1.4E-01
ENSMUST00000159596	zinc finger protein 558 [Source:MGI Symbol;Acc:MGI:1921681]	Q9D4E2		5.8	7.3E-05	3.3	1.7E-03	0.1	8.2E-01	-0.6	3.4E-01
ENSMUST00000159608	phosphodiesterase 8B [Source:MGI Symbol;Acc:MGI:2443999]	E9PUL4		6.9	2.7E-04	5.4	2.0E-03	-0.8	5.7E-01	-0.4	6.3E-01
ENSMUST00000127694	actin related protein 2/3 complex, subunit 1A [Source:MGI Symbol;Acc:MGI:1928896]	A0A0G2JF52		0.4	5.0E-01	0.4	6.7E-01	-0.2	7.0E-01	-0.1	8.5E-01
ENSMUST00000159610	calcium channel, voltage-dependent, T type, alpha 1H subunit [Source:MGI Symbol;Acc:MGI:1928842]	E9Q6P9		6.8	1.2E-02	-3.0	4.3E-03	0.6	2.3E-01	0.8	3.2E-01
ENSMUST00000159624	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:2443419]		Q8BLK9	7.7	2.2E-05	7.7	3.4E-04	-1.1	4.9E-01	0.6	4.2E-01
ENSMUST00000127703				-2.5	1.3E-01	-1.0	5.9E-01	0.6	6.5E-01	-0.9	6.4E-01
ENSMUST00000159630	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	Q3TY99		-2.7	1.4E-02	6.5	8.4E-04	-0.8	5.5E-01	1.0	2.0E-01
ENSMUST00000159645	Vpr (HIV-1) binding protein [Source:MGI Symbol;Acc:MGI:2445220]		Q80TR8	7.1	8.3E-04	-2.3	1.8E-02	-1.1	4.9E-02	-0.6	5.2E-01
ENSMUST00000127717	protein phosphatase 1D magnesium-dependent, delta isoform [Source:MGI Symbol;Acc:MGI:1858214]	B1B0B1		1.7	8.3E-02	3.0	3.0E-02	0.6	5.9E-01	-0.7	4.1E-01
ENSMUST00000159646	protein phosphatase 4, regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1917601]	F6V294		-3.4	3.5E-03	5.7	5.9E-05	0.0	9.6E-01	0.2	7.4E-01
ENSMUST00000159649	cDNA sequence BC037034 [Source:MGI Symbol;Acc:MGI:2385896]	A0A0G2JDC3		-8.2	6.7E-04	-5.8	2.1E-04	-0.5	1.9E-01	-0.8	4.8E-01
ENSMUST00000127723				0.7	2.9E-01	0.7	4.7E-01	0.0	9.5E-01	0.1	8.8E-01
ENSMUST00000159688	Fc receptor, IgG, low affinity IIb [Source:MGI Symbol;Acc:MGI:95499]	E9Q415		-6.7	2.6E-02	3.4	2.3E-03	0.3	7.1E-01	0.7	3.0E-01
ENSMUST00000159690	arrestin domain containing 3 [Source:MGI Symbol;Acc:MGI:2145242]	E0CY84		-6.5	1.6E-03	5.9	1.5E-04	-4.0	4.1E-03	0.8	1.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159692	endoplasmic reticulum metallopeptidase 1 [Source:MGI Symbol;Acc:MGI:106250]		Q3UVK0	4.6	5.2E-05	7.9	2.6E-05	-0.6	6.1E-01	-0.5	3.6E-01
ENSMUST00000159694	non-SMC element 4 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915122]	E0CY57		-4.0	1.9E-03	-7.1	2.7E-04	0.4	2.7E-01	3.3	2.4E-02
ENSMUST00000127741	GTP binding protein 3 [Source:MGI Symbol;Acc:MGI:1917609]	D6RDC6		0.1	9.4E-01	-0.6	7.9E-01	-0.7	6.9E-01	0.0	1.0E+00
ENSMUST00000159697	acetyl-Coenzyme A acetyltransferase 2 [Source:MGI Symbol;Acc:MGI:87871]	G3XA25		6.0	1.1E-03	4.3	2.4E-04	-0.6	4.3E-01	-0.1	8.2E-01
ENSMUST00000159699	high mobility group AT-hook 2 [Source:MGI Symbol;Acc:MGI:101761]	Q6NSP9		6.4	1.8E-04	5.0	9.8E-05	-0.9	2.6E-01	0.7	2.0E-01
ENSMUST00000159715	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 [Source:MGI Symbol;Acc:MGI:		Q8C7U7	-5.7	1.2E-03	5.5	1.8E-04	0.2	8.2E-01	-0.4	5.2E-01
ENSMUST00000159725	inositol polyphosphate-1-phosphatase [Source:MGI Symbol;Acc:MGI:104848]	E0CYQ4		5.7	9.6E-06	7.8	1.2E-04	-1.5	2.8E-01	0.4	4.3E-01
ENSMUST00000127751				-1.1	2.1E-01	-1.3	3.0E-01	0.7	3.3E-01	0.9	4.4E-01
ENSMUST00000159728	protein kinase, AMP-activated, gamma 3 non-catatlytic subunit [Source:MGI Symbol;Acc:MGI:1891343]	E0CX18		6.3	4.8E-04	-1.9	1.4E-02	0.7	1.5E-01	-3.2	2.9E-03
ENSMUST00000159739	circadian associated repressor of transcription [Source:MGI Symbol;Acc:MGI:2684975]	A2RTE4	Q3TQ03	6.3	6.4E-05	3.6	1.7E-03	-0.7	3.6E-01	0.5	4.2E-01
ENSMUST00000159747	Rho guanine nucleotide exchange factor (GEF) 4 [Source:MGI Symbol;Acc:MGI:2442507]	E9PYK8		9.3	3.9E-05	3.6	2.6E-02	-3.7	5.3E-02	-1.6	1.8E-01
ENSMUST00000159756	phospholipase C, beta 2 [Source:MGI Symbol;Acc:MGI:107465]	E9PYI3		-6.2	1.0E-04	6.4	9.5E-05	-1.1	3.0E-01	-0.2	7.3E-01
ENSMUST00000159759	expressed sequence AI837181 [Source:MGI Symbol;Acc:MGI:2147598]	E9QNR6		-5.7	1.3E-03	6.5	9.5E-04	0.4	7.6E-01	-1.5	9.5E-02
ENSMUST00000159772	kinesin family member 2A [Source:MGI Symbol;Acc:MGI:108390]	E0CZ72		-6.6	7.5E-06	-6.0	3.2E-02	-0.5	6.0E-01	-0.3	9.0E-01
ENSMUST00000159780	von Willebrand factor A domain containing 5B2 [Source:MGI Symbol;Acc:MGI:2681859]	E0CZ01		6.9	4.4E-05	9.8	2.9E-04	-0.7	7.0E-01	1.5	7.7E-02
ENSMUST00000159781	speedy/RINGO cell cycle regulator family, member E4B [Source:MGI Symbol;Acc:MGI:3612701]	Q8CDE8		6.2	3.5E-04	4.2	4.9E-03	-2.2	1.1E-01	0.3	6.7E-01
ENSMUST00000127797				0.2	8.2E-01	-0.4	7.8E-01	0.4	6.3E-01	1.0	4.0E-01
ENSMUST00000159786	amyloid beta (A4) precursor protein-binding, family B, member 2 [Source:MGI Symbol;Acc:MGI:108405]		Q9DBR4	7.0	1.6E-05	5.2	5.3E-03	1.8	2.2E-01	-0.2	8.1E-01
ENSMUST00000159789	H3 histone, family 3A [Source:MGI Symbol;Acc:MGI:1097686]	E0CZ27		-8.2	6.5E-04	4.0	4.6E-02	-3.4	1.1E-01	-0.8	5.3E-01
ENSMUST00000127802				3.4	1.1E-01	0.4	8.8E-01	-1.6	4.7E-01	1.4	4.9E-01
ENSMUST00000127808				3.7	4.5E-02	6.9	2.7E-03	0.6	7.6E-01	-2.6	4.9E-02
ENSMUST00000159813	zinc finger, DHHC domain containing 4 [Source:MGI Symbol;Acc:MGI:1920131]	M0QWP4		-5.8	4.1E-03	-0.6	6.2E-01	1.2	1.8E-01	-1.2	3.6E-01
ENSMUST00000159814	ADP-ribosylation factor-like 4C [Source:MGI Symbol;Acc:MGI:2445172]		P61208	-1.4	1.1E-02	5.0	1.0E-02	-0.6	7.4E-01	0.5	5.8E-01
ENSMUST00000159816	filamin A interacting protein 1-like [Source:MGI Symbol;Acc:MGI:1925999]	E0CYH7		7.1	1.4E-02	7.4	1.6E-02	1.8	4.7E-01	-0.9	5.7E-01
ENSMUST00000159832	vacuolar protein sorting 51 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915755]		Q3UVL4	4.5	3.0E-02	6.9	2.9E-04	-0.5	7.2E-01	-1.1	1.3E-01
ENSMUST00000127824				-1.9	1.1E-01	-0.1	9.2E-01	1.1	2.6E-01	-0.6	6.7E-01
ENSMUST00000159835	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:97502]	E0CYT8		4.8	3.0E-03	9.1	9.7E-06	-1.4	2.7E-01	-0.2	6.7E-01
ENSMUST00000159840	tassium voltage-gated channel, shaker-related subfamily, beta member 2 [Source:MGI Symbol;Acc:MGI:10923	Q3UPV6		-5.7	4.3E-03	4.3	8.4E-02	-0.1	9.8E-01	0.2	8.8E-01
ENSMUST00000127828	ectonucleoside triphosphate diphosphohydrolase 1 [Source:MGI Symbol;Acc:MGI:102805]	D6RFA9		-1.5	2.2E-01	-5.4	3.0E-02	-1.7	7.9E-02	2.2	3.2E-01
ENSMUST00000159861	pappalysin 2 [Source:MGI Symbol;Acc:MGI:3051647]	E9PZ87		9.2	5.2E-06	-3.4	5.6E-02	-0.1	8.6E-01	-0.2	9.0E-01
ENSMUST00000159879	TROVE domain family, member 2 [Source:MGI Symbol;Acc:MGI:106652]	Q3TJ75	O08848	1.7	3.9E-03	-7.4	2.6E-04	1.3	7.6E-03	-0.5	7.3E-01
ENSMUST00000159880	synaptotagmin-like 3 [Source:MGI Symbol;Acc:MGI:1933367]	E9PUK9		6.2	1.2E-03	5.7	6.0E-04	-0.6	6.2E-01	0.2	7.6E-01
ENSMUST00000159891	C-type lectin domain family 4, member a2 [Source:MGI Symbol;Acc:MGI:1349412]	E0CY25		7.0	6.2E-06	4.3	7.1E-03	-0.2	8.7E-01	0.0	9.7E-01
ENSMUST00000127853				-0.4	8.8E-01	2.3	4.6E-01	0.5	8.4E-01	-2.1	4.0E-01
ENSMUST00000159893	tubulin-specific chaperone E [Source:MGI Symbol;Acc:MGI:1917680]	E0CXJ6		-6.0	2.1E-04	4.0	1.5E-02	-1.6	2.7E-01	-1.3	1.7E-01
ENSMUST00000127861	heat shock protein 1 (chaperonin) [Source:MGI Symbol;Acc:MGI:96242]	D3Z2F2		-0.9	5.7E-01	-0.9	5.6E-01	-1.7	1.7E-01	-1.8	3.0E-01
ENSMUST00000159910	versican [Source:MGI Symbol;Acc:MGI:102889]	G3XA35		-6.4	3.2E-04	5.3	2.2E-02	-0.8	7.1E-01	0.4	7.7E-01
ENSMUST00000159916	proline-rich transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1916267]		E9PUL5	5.1	2.2E-02	5.8	1.6E-03	0.6	6.4E-01	0.0	9.9E-01
ENSMUST00000159917	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:97502]	E9PWE0		-7.5	3.1E-05	3.1	4.3E-02	-1.9	1.7E-01	1.3	2.0E-01
ENSMUST00000159939	PHD finger protein 21B [Source:MGI Symbol;Acc:MGI:2443812]		Q8C966	6.5	8.4E-04	4.3	2.1E-02	-1.9	2.7E-01	-1.1	3.4E-01
ENSMUST00000127878				0.8	4.8E-01	1.2	3.5E-01	-0.7	5.1E-01	-1.1	3.3E-01
ENSMUST00000127880	Dmx-like 2 [Source:MGI Symbol;Acc:MGI:2444630]	B0V2P6		-2.9	3.6E-02	-0.6	7.2E-01	1.6	1.8E-01	-0.7	6.8E-01
ENSMUST00000127881				-2.0	1.2E-01	-3.8	1.9E-02	-1.9	4.0E-02	0.0	9.8E-01
ENSMUST00000127882				-1.2	1.6E-01	0.2	8.4E-01	0.5	4.9E-01	-0.9	3.7E-01
ENSMUST00000159955	laminin, beta 3 [Source:MGI Symbol;Acc:MGI:99915]		Q61087	4.6	1.3E-02	5.2	2.0E-03	0.3	8.3E-01	1.3	1.4E-01
ENSMUST00000159961	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	F6URE6		-3.6	2.3E-02	7.8	5.3E-04	-0.6	7.3E-01	0.8	3.1E-01
ENSMUST00000159962	tyrosyl-tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1917370]	E9PX65		4.9	1.8E-03	5.7	4.7E-04	-1.2	2.8E-01	0.2	7.2E-01
ENSMUST00000159963	chitinase 1 (chitotriosidase) [Source:MGI Symbol;Acc:MGI:1919134]	B2RS82	Q9D7Q1	6.0	1.9E-02	6.5	8.5E-05	-1.3	2.3E-01	0.4	4.9E-01
ENSMUST00000127893	bromodomain containing 4 [Source:MGI Symbol;Acc:MGI:1888520]	B0V2V6		1.9	8.6E-02	0.3	8.7E-01	0.7	5.2E-01	2.3	1.4E-01
ENSMUST00000127898				2.6	2.5E-01	0.0	9.8E-01	-2.8	1.9E-01	-0.2	9.2E-01
ENSMUST00000159964	neurexophilin and PC-esterase domain family, member 5 [Source:MGI Symbol;Acc:MGI:3584036]	E0CYW5		5.1	4.2E-05	7.4	6.1E-06	1.0	2.2E-01	-0.1	7.5E-01
ENSMUST00000127906	desmoplakin [Source:MGI Symbol;Acc:MGI:109611]	E9PZW0		2.5	1.4E-01	2.6	1.7E-01	-1.7	3.2E-01	-1.8	2.3E-01
ENSMUST00000159973	spermatogenesis associated glutamate (E)-rich protein 4e [Source:MGI Symbol;Acc:MGI:2668871]	K7N6S8		8.0	5.8E-05	5.3	1.8E-03	-0.9	4.5E-01	0.3	7.6E-01
ENSMUST00000159983	lectin, galactose binding, soluble 12 [Source:MGI Symbol;Acc:MGI:1929094]		Q91VD1	7.5	3.3E-03	4.9	4.3E-04	-2.8	2.3E-02	-0.2	6.8E-01
ENSMUST00000127921	zinc finger protein 142 [Source:MGI Symbol;Acc:MGI:1924514]	M0QWM7		2.7	2.1E-01	1.8	5.7E-01	1.2	5.6E-01	2.1	4.8E-01
ENSMUST00000159985	hephaestin-like 1 [Source:MGI Symbol;Acc:MGI:2685355]		Q3V1H3	7.3	2.9E-05	0.3	9.4E-01	7.1	5.0E-03	-0.8	7.9E-01
ENSMUST00000127925				6.1	4.6E-02	7.7	2.3E-02	-0.6	8.5E-01	-2.2	1.9E-01
ENSMUST00000127935	MRV integration site 1 [Source:MGI Symbol;Acc:MGI:1338023]	Q3UR44		-3.3	7.3E-02	-1.1	5.4E-01	0.0	9.7E-01	-2.2	2.7E-01
ENSMUST00000159989	chloride channel accessory 3B [Source:MGI Symbol;Acc:MGI:2181989]	E9PUL3		7.2	3.4E-05	-7.8	4.6E-03	0.9	1.9E-01	2.9	1.9E-01
ENSMUST00000127944				-0.6	4.4E-01	-0.1	8.9E-01	0.0	9.4E-01	-0.4	6.5E-01
ENSMUST00000127949				1.2	2.4E-01	1.5	2.0E-01	-0.1	9.3E-01	-0.4	6.7E-01
ENSMUST00000127954				-1.7	6.1E-02	-0.4	7.2E-01	1.2	1.3E-01	-0.1	9.4E-01
ENSMUST00000159990	POC1 centriolar protein homolog B (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1918511]	Q9D3W6		-2.8	1.3E-02	-4.6	7.9E-02	1.6	1.1E-01	0.5	8.5E-01
ENSMUST00000159991	guanine nucleotide binding protein, alpha z subunit [Source:MGI Symbol;Acc:MGI:95780]	Q542R8	O70443	8.3	1.8E-07	5.7	1.6E-05	-2.2	1.7E-02	-0.7	1.5E-01
ENSMUST00000159993	collagen, type XXII, alpha 1 [Source:MGI Symbol;Acc:MGI:1916950]	E9Q7P1		7.6	1.3E-06	6.3	5.8E-05	0.2	8.4E-01	-0.5	3.5E-01
ENSMUST00000159994	radial spoke head homolog 14 (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1918486]	E9Q6E1		7.5	3.0E-04	5.0	2.1E-05	-0.1	8.7E-01	0.3	4.6E-01
ENSMUST00000127972	calcineurin-like phosphoesterase domain containing 1 [Source:MGI Symbol;Acc:MGI:2443300]	D3Z7F7		3.6	7.3E-02	4.0	4.1E-02	-2.0	3.2E-01	-2.3	1.0E-01
ENSMUST00000127974	a disintegrin and metallopeptidase domain 17 [Source:MGI Symbol;Acc:MGI:1096335]	J3QNB3		-4.9	1.1E-01	-6.8	1.1E-01	-1.5	3.7E-01	0.4	9.2E-01
ENSMUST00000160013	guanine nucleotide binding protein (G protein), gamma 2 [Source:MGI Symbol;Acc:MGI:102705]		P63213	-1.9	3.2E-03	5.3	4.2E-02	-0.8	7.5E-01	-0.8	6.2E-01
ENSMUST00000127979	zinc finger protein 65 [Source:MGI Symbol;Acc:MGI:107769]	B8JJX9		0.5	8.3E-01	0.9	7.7E-01	0.7	7.7E-01	0.3	9.1E-01
ENSMUST00000160023	RIKEN cDNA 2010300C02 gene [Source:MGI Symbol;Acc:MGI:1919347]	F7B0R9		7.4	9.3E-03	4.3	8.8E-02	-1.0	6.5E-01	-0.7	6.4E-01
ENSMUST00000127984	-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human) [Source:MGI Symbol;Acc:MGI:1338	B7ZP57		1.8	5.9E-02	2.6	4.3E-02	0.8	3.8E-01	0.0	1.0E+00
ENSMUST00000160027	proteasome (prosome, macropain) subunit, alpha type 3 [Source:MGI Symbol;Acc:MGI:104883]	Q58EV4	O70435	3.0	4.0E-04	-3.9	2.2E-01	1.6	2.9E-01	-0.9	7.7E-01
ENSMUST00000160044	mitochondrial fission factor [Source:MGI Symbol;Acc:MGI:1922984]	F7B1A4		-7.2	5.7E-05	-2.2	4.8E-02	-0.2	7.0E-01	-1.1	3.2E-01
ENSMUST00000127994	Trk-fused gene [Source:MGI Symbol;Acc:MGI:1338041]	F6QJV5		0.2	8.5E-01	-1.5	3.1E-01	-1.0	3.1E-01	0.8	5.9E-01
ENSMUST00000160075	BUD31 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2141291]	E0CX20		-3.2	1.1E-02	-1.6	3.8E-01	2.8	4.1E-02	-2.1	2.9E-01
ENSMUST00000160082	mitochondrial ribosomal protein L30 [Source:MGI Symbol;Acc:MGI:1333820]			2.5	3.8E-03	2.7	1.0E-02	0.2	8.3E-01	-0.1	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000128003	coatomer protein complex, subunit epsilon [Source:MGI Symbol;Acc:MGI:1891702]	F6YFR7		-2.5	7.0E-02	-1.6	2.9E-01	0.1	9.0E-01	-0.7	6.4E-01
ENSMUST00000160084	ARP1 actin-related protein 1B, centractin beta [Source:MGI Symbol;Acc:MGI:1917446]	E0CZD4		6.0	1.7E-04	-5.2	4.3E-03	0.5	3.6E-01	-0.7	6.6E-01
ENSMUST00000160104	GS homeobox 2 [Source:MGI Symbol;Acc:MGI:95843]	E0CZ09		6.8	1.7E-04	6.5	1.3E-03	1.1	4.4E-01	-0.9	2.8E-01
ENSMUST00000160107	R3H domain and coiled-coil containing 1 like [Source:MGI Symbol;Acc:MGI:1196316]	E0CYN2		-6.2	4.5E-05	3.6	9.8E-03	1.1	2.6E-01	0.2	7.7E-01
ENSMUST00000128012	alcium/calmodulin-dependent serine protein kinase (MAGUK family) [Source:MGI Symbol;Acc:MGI:1309485	F6ZQR2		0.2	9.3E-01	-3.0	2.2E-01	-3.7	3.6E-02	-0.5	8.3E-01
ENSMUST00000160115	WD repeat domain 41 [Source:MGI Symbol;Acc:MGI:2445123]	S4R290		8.1	1.5E-04	2.4	6.6E-02	-0.8	4.5E-01	0.0	9.8E-01
ENSMUST00000128029				-0.3	8.3E-01	2.6	8.6E-02	0.3	7.7E-01	-2.5	7.2E-02
ENSMUST00000128035	RAD23a homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:105126]	Q3TN85		1.2	5.8E-01	6.8	2.3E-02	2.9	2.3E-01	-2.6	2.3E-01
ENSMUST00000128038				0.4	5.9E-01	-0.3	7.4E-01	-0.2	7.4E-01	0.5	6.0E-01
ENSMUST00000128039				-0.4	5.6E-01	0.5	5.8E-01	0.3	6.4E-01	-0.5	4.8E-01
ENSMUST00000160129	argininosuccinate lyase [Source:MGI Symbol;Acc:MGI:88084]		Q91YI0	7.0	4.3E-04	5.2	1.6E-02	-2.0	3.3E-01	-1.5	2.4E-01
ENSMUST00000128041	transmembrane protein 180 [Source:MGI Symbol;Acc:MGI:1922396]		Q6PDE8	3.1	2.3E-01	-0.6	8.7E-01	-1.2	6.5E-01	2.5	4.4E-01
ENSMUST00000160138	SID1 transmembrane family, member 2 [Source:MGI Symbol;Acc:MGI:2446134]	F6TVH9		-3.1	3.1E-02	-2.9	4.8E-02	-1.0	1.8E-01	-1.6	2.7E-01
ENSMUST00000160143	ribosomal RNA adenine dimethylase domain containing 1 [Source:MGI Symbol;Acc:MGI:2387197]	E0CYK3		7.9	4.8E-05	5.3	2.9E-04	-1.9	9.0E-02	-0.2	7.6E-01
ENSMUST00000128049				-1.7	1.0E-01	-1.8	2.5E-01	0.8	4.2E-01	0.9	5.5E-01
ENSMUST00000128052				0.6	8.0E-01	5.6	8.0E-02	2.6	3.7E-01	-2.5	2.3E-01
ENSMUST00000128055	actin, gamma, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:87906]	G3UZ07		-1.0	3.6E-01	1.0	4.1E-01	0.4	7.1E-01	-1.7	1.8E-01
ENSMUST00000128057	oral cancer overexpressed 1 [Source:MGI Symbol;Acc:MGI:1919534]	Q8BQU0		0.9	1.8E-01	3.4	1.8E-03	1.4	5.2E-02	-1.1	1.2E-01
ENSMUST00000160147	mannosidase, alpha, class 2C, member 1 [Source:MGI Symbol;Acc:MGI:1920994]	Q3ZCX9	Q91W89	5.6	1.3E-02	6.3	1.8E-04	-0.5	6.5E-01	-0.3	6.6E-01
ENSMUST00000160216	contactin 5 [Source:MGI Symbol;Acc:MGI:3042287]		P68500	6.7	3.9E-03	9.9	6.1E-05	-1.7	3.1E-01	-0.7	3.1E-01
ENSMUST00000160218	small integral membrane protein 17 [Source:MGI Symbol;Acc:MGI:4365374]	A0A504		6.6	9.5E-05	6.6	2.5E-04	0.7	5.2E-01	-0.2	7.1E-01
ENSMUST00000160236	sperm flagellar 2 [Source:MGI Symbol;Acc:MGI:2443727]	E0CYG3		3.9	5.2E-03	5.9	9.4E-05	-2.3	4.6E-02	0.3	5.4E-01
ENSMUST00000160247	cilia and flagella associated protein 43 [Source:MGI Symbol;Acc:MGI:1289258]	E9Q7R9		6.1	9.9E-04	7.0	6.7E-04	0.0	9.8E-01	-0.3	6.5E-01
ENSMUST00000160249	ring finger protein 123 [Source:MGI Symbol;Acc:MGI:2148796]		Q5XPI3	-6.3	5.2E-04	-0.6	6.7E-01	0.7	4.9E-01	-1.5	2.5E-01
ENSMUST00000128093				-3.0	3.0E-01	-3.6	3.1E-01	-1.4	4.7E-01	-0.8	8.3E-01
ENSMUST00000160269	cysteine-rich PDZ-binding protein [Source:MGI Symbol;Acc:MGI:1929655]	F6TQQ9		-8.1	1.2E-05	-3.7	1.1E-01	0.6	5.8E-01	-1.1	6.3E-01
ENSMUST00000160271	oxysterol binding protein-like 9 [Source:MGI Symbol;Acc:MGI:1923784]	Q5FWX7		-10.8	1.4E-06	5.7	1.9E-03	-1.3	3.7E-01	1.5	1.1E-01
ENSMUST00000128100	polymerase (DNA directed), epsilon 3 (p17 subunit) [Source:MGI Symbol;Acc:MGI:1933378]	D6RDT4		4.3	4.1E-02	-0.2	9.4E-01	-1.4	4.9E-01	3.1	1.4E-01
ENSMUST00000160285	WD repeat domain 63 [Source:MGI Symbol;Acc:MGI:3045269]	B2RY71		6.9	1.2E-04	6.0	8.5E-04	1.6	1.8E-01	-0.6	3.9E-01
ENSMUST00000160289	non-SMC element 4 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915122]	G3XA30		-5.7	2.0E-04	6.2	5.4E-04	-0.5	7.1E-01	0.6	3.6E-01
ENSMUST00000160298	predicted gene 8113 [Source:MGI Symbol;Acc:MGI:3648791]	E0CXS8		3.5	7.0E-04	5.5	5.4E-05	-0.6	4.3E-01	0.2	6.9E-01
ENSMUST00000160302	TRAF3 interacting protein 3 [Source:MGI Symbol;Acc:MGI:2441706]	A0A0A6YY84		-4.2	1.9E-03	6.3	1.8E-04	-0.5	6.5E-01	-0.4	5.0E-01
ENSMUST00000160326	ubiquitin specific peptidase 7 [Source:MGI Symbol;Acc:MGI:2182061]	E0CY04		-9.2	5.1E-04	4.9	9.6E-05	-0.7	3.6E-01	0.2	7.1E-01
ENSMUST00000160329	WD repeat domain 35 [Source:MGI Symbol;Acc:MGI:1921932]	E0CYD5		4.9	1.1E-02	1.6	5.2E-01	-0.9	6.7E-01	2.2	2.5E-01
ENSMUST00000128135				-2.3	1.4E-01	-0.7	7.3E-01	1.2	4.6E-01	-0.4	8.4E-01
ENSMUST00000160352	transmembrane protein 33 [Source:MGI Symbol;Acc:MGI:1915128]			-4.2	8.7E-03	-4.7	3.7E-02	1.2	1.8E-01	-1.0	6.4E-01
ENSMUST00000160372	ring finger protein 146 [Source:MGI Symbol;Acc:MGI:1915281]		Q9CZW6	-5.9	6.4E-05	8.0	3.2E-05	-0.6	6.3E-01	-0.6	3.0E-01
ENSMUST00000160377	tryptase gamma 1 [Source:MGI Symbol;Acc:MGI:1349391]	G3XA07		5.7	1.0E-02	1.8	1.2E-02	-0.2	6.9E-01	0.0	9.4E-01
ENSMUST00000160379	cyclin-dependent kinase 5, regulatory subunit 2 (p39) [Source:MGI Symbol;Acc:MGI:1330828]		O35926	7.1	4.8E-05	-0.8	6.0E-01	1.4	1.8E-01	-1.5	3.3E-01
ENSMUST00000160390	alkylglycerol monooxygenase [Source:MGI Symbol;Acc:MGI:2442495]		Q8BS35	6.8	1.8E-05	-4.4	5.3E-03	-0.3	6.1E-01	-0.7	6.2E-01
ENSMUST00000160392	heart and neural crest derivatives expressed transcript 1 [Source:MGI Symbol;Acc:MGI:103577]	Q5SQG1	Q64279	6.6	2.0E-02	1.7	3.8E-02	-0.4	4.9E-01	-0.1	9.1E-01
ENSMUST00000160393	O-sialoglycoprotein endopeptidase [Source:MGI Symbol;Acc:MGI:1913496]			6.7	5.1E-04	8.1	7.2E-04	0.0	9.9E-01	-0.9	3.0E-01
ENSMUST00000160405	ubiquitin specific peptidase 7 [Source:MGI Symbol;Acc:MGI:2182061]	E9PXY8		-4.1	3.7E-03	-4.7	6.5E-03	0.6	3.1E-01	-0.6	7.1E-01
ENSMUST00000160422	cleavage and polyadenylation specific factor 4 [Source:MGI Symbol;Acc:MGI:1861602]	E0CXT7		-7.6	1.3E-05	5.2	3.8E-03	1.7	2.0E-01	-0.7	4.4E-01
ENSMUST00000160424	calcium channel, voltage-dependent, alpha 1I subunit [Source:MGI Symbol;Acc:MGI:2178051]	E9Q7P2		6.4	1.2E-05	5.6	8.3E-04	-1.7	1.9E-01	-0.1	8.5E-01
ENSMUST00000128174				0.9	6.1E-01	1.8	4.2E-01	-0.5	8.0E-01	-1.4	4.3E-01
ENSMUST00000160439	zinc finger, AN1 type domain 2B [Source:MGI Symbol;Acc:MGI:1916068]		Q91X58	-7.8	6.0E-05	5.9	5.1E-04	-0.5	6.9E-01	-0.4	5.7E-01
ENSMUST00000128179	myosin, light chain 12A, regulatory, non-sarcomeric [Source:MGI Symbol;Acc:MGI:1914518]	D3Z249		1.7	1.4E-01	4.5	1.3E-02	1.6	2.5E-01	-1.2	3.0E-01
ENSMUST00000160443	NACHT and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:2442268]	E0CY71		6.3	1.5E-03	8.9	6.6E-05	1.0	4.4E-01	0.6	2.7E-01
ENSMUST00000160455	Hermansky-Pudlak syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:2177763]	Q3U309		-2.0	3.3E-02	-0.6	5.4E-01	1.3	5.7E-02	-0.4	6.8E-01
ENSMUST00000160456	nitric oxide synthase 1 (neuronal) adaptor protein [Source:MGI Symbol;Acc:MGI:1917979]		Q9D3A8	5.3	9.1E-03	-6.7	2.1E-02	0.0	9.7E-01	0.0	1.0E+00
ENSMUST00000160457	zinc finger protein 945 [Source:MGI Symbol;Acc:MGI:2445132]	E9PYM8		5.5	5.2E-04	3.4	1.4E-01	-1.4	4.9E-01	0.3	8.2E-01
ENSMUST00000160483	synaptotagmin-like 3 [Source:MGI Symbol;Acc:MGI:1933367]		Q99N48	3.8	2.7E-03	-5.5	4.5E-04	-4.0	8.9E-05	-2.3	9.1E-02
ENSMUST00000160486	upstream transcription factor 1 [Source:MGI Symbol;Acc:MGI:99542]	E9Q722		-5.2	3.7E-03	4.6	9.9E-03	-0.5	7.1E-01	1.9	6.2E-02
ENSMUST00000160488	SRA stem-loop interacting RNA binding protein [Source:MGI Symbol;Acc:MGI:1916394]		Q9D8T7	-1.6	2.8E-02	6.9	3.9E-04	-1.2	3.5E-01	-0.7	2.8E-01
ENSMUST00000160503	mesencephalic astrocyte-derived neurotrophic factor [Source:MGI Symbol;Acc:MGI:1922090]	F6T4L3		-3.9	3.2E-02	-6.7	4.1E-02	-0.7	5.2E-01	-1.2	7.2E-01
ENSMUST00000160507	succinate-Coenzyme A ligase, ADP-forming, beta subunit [Source:MGI Symbol;Acc:MGI:1306775]		Q9Z2I9	-3.8	4.5E-04	3.6	1.9E-02	-3.5	3.3E-02	-0.4	6.5E-01
ENSMUST00000160511	LUC7-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2183260]	E0CZB9		-7.8	7.7E-04	-5.8	3.4E-04	0.2	5.3E-01	0.0	9.6E-01
ENSMUST00000128204				-0.1	9.2E-01	6.6	2.0E-02	4.1	9.8E-02	-2.7	8.2E-02
ENSMUST00000160534	predicted gene 4477 [Source:MGI Symbol;Acc:MGI:3782661]	E0CYR6		7.5	2.4E-04	10.0	1.3E-05	0.9	4.6E-01	0.6	2.7E-01
ENSMUST00000128210				2.9	1.5E-01	-0.6	6.9E-01	-4.7	1.4E-02	-1.1	5.0E-01
ENSMUST00000160536	transmembrane protein 63a [Source:MGI Symbol;Acc:MGI:2384789]	E0CX77		3.5	3.4E-03	5.9	3.5E-04	-0.5	6.8E-01	0.4	5.4E-01
ENSMUST00000160548	ankyrin repeat and MYND domain containing 1 [Source:MGI Symbol;Acc:MGI:3045261]	E0CYY3		6.1	1.6E-04	7.0	8.3E-04	0.5	7.1E-01	-0.8	3.6E-01
ENSMUST00000160565	predicted gene 4955 [Source:MGI Symbol;Acc:MGI:3646410]	G3UZV2		6.0	3.5E-04	6.6	1.3E-04	-0.5	6.3E-01	-0.8	1.9E-01
ENSMUST00000128221				-2.8	1.0E-01	-3.9	9.0E-02	-1.1	3.6E-01	-0.1	9.7E-01
ENSMUST00000160571	myc induced nuclear antigen [Source:MGI Symbol;Acc:MGI:1914264]		Q8CD15	7.2	6.2E-04	4.9	1.1E-03	-0.9	4.3E-01	0.3	6.4E-01
ENSMUST00000160590	vacuolar protein sorting 51 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915755]		Q3UVL4	-3.3	3.7E-04	3.7	8.3E-02	-0.6	7.5E-01	2.4	8.8E-02
ENSMUST00000128227				1.5	4.1E-01	3.5	1.0E-01	-0.3	8.8E-01	-2.3	1.9E-01
ENSMUST00000160596	CKLF-like MARVEL transmembrane domain containing 1 [Source:MGI Symbol;Acc:MGI:2447159]	E0CXA2		4.9	1.8E-03	-2.1	1.1E-01	0.2	8.2E-01	-2.2	1.3E-01
ENSMUST00000160616	transmembrane protein 163 [Source:MGI Symbol;Acc:MGI:1919410]		Q8C996	4.7	1.6E-03	5.4	1.8E-04	0.2	8.3E-01	-0.1	8.8E-01
ENSMUST00000128239				1.3	2.2E-01	1.6	2.2E-01	-0.1	9.1E-01	-0.4	7.3E-01
ENSMUST00000128243				-2.4	6.6E-02	-1.5	3.0E-01	0.6	5.2E-01	-0.3	8.5E-01
ENSMUST00000128244	solute carrier family 36 (proton/amino acid symporter), member 3 [Source:MGI Symbol;Acc:MGI:2665001]	D6RI58		2.3	2.6E-01	0.0	9.9E-01	-1.3	5.1E-01	1.1	6.2E-01
ENSMUST00000160629	cleavage and polyadenylation specific factor 4 [Source:MGI Symbol;Acc:MGI:1861602]	B2LVG5		-5.2	5.2E-03	4.4	8.1E-03	-1.5	3.0E-01	1.8	5.9E-02
ENSMUST00000128246	ADP-ribosyltransferase 3 [Source:MGI Symbol;Acc:MGI:1202729]	E9Q8Z0		3.9	6.1E-02	3.8	9.9E-02	-0.8	7.1E-01	-0.7	6.2E-01
ENSMUST00000128249				0.4	8.7E-01	-0.1	9.3E-01	-4.8	3.2E-02	-4.3	5.2E-02
ENSMUST00000128250	v-raf murine sarcoma 3611 viral oncogene homolog [Source:MGI Symbol;Acc:MGI:88065]	B1AUP0		0.7	7.9E-01	-0.7	8.5E-01	0.1	9.6E-01	1.6	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000160633	cerebral cavernous malformation 2 [Source:MGI Symbol;Acc:MGI:2384924]	E0CXR5		-6.6	3.6E-04	6.2	5.5E-04	-0.5	7.1E-01	0.3	6.9E-01
ENSMUST00000128256	myotubularin related protein 3 [Source:MGI Symbol;Acc:MGI:1921552]	B1ATD4		-1.0	6.2E-01	2.9	2.5E-01	1.2	5.6E-01	-2.7	2.1E-01
ENSMUST00000160635	transmembrane BAX inhibitor motif containing 6 [Source:MGI Symbol;Acc:MGI:99682]		Q9D2C7	-6.3	3.3E-02	4.8	3.6E-05	-5.8	1.3E-04	0.2	6.5E-01
ENSMUST00000160640	RIKEN cDNA 4933434E20 gene [Source:MGI Symbol;Acc:MGI:1914027]		Q8R092	-2.1	1.5E-02	7.0	1.1E-04	-0.6	6.0E-01	-0.2	7.7E-01
ENSMUST00000128260	receptor (calcitonin) activity modifying protein 2 [Source:MGI Symbol;Acc:MGI:1859650]	E9Q0S5		2.9	7.1E-02	3.3	2.3E-02	-2.6	8.7E-02	-3.0	2.0E-02
ENSMUST00000160662	cyclin-dependent kinase 15 [Source:MGI Symbol;Acc:MGI:3583944]	E3W997		5.0	5.2E-05	-6.5	1.5E-04	-1.2	1.2E-02	-0.8	5.2E-01
ENSMUST00000128266				0.9	5.8E-01	2.5	2.4E-01	1.1	5.7E-01	-0.5	7.4E-01
ENSMUST00000160664	protein phosphatase 4, regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1917601]	E9PX53		-2.9	4.0E-03	-4.2	7.4E-03	-0.4	4.9E-01	0.0	9.8E-01
ENSMUST00000160681	host cell factor C2 [Source:MGI Symbol;Acc:MGI:1915183]	F6T088		-2.5	2.7E-03	7.5	5.4E-04	-0.2	8.8E-01	0.7	3.8E-01
ENSMUST00000160682	ubiquitin-like 5 [Source:MGI Symbol;Acc:MGI:1913427]		Q9EPV8	-10.3	7.0E-07	5.7	1.7E-02	-0.3	8.9E-01	-0.4	7.4E-01
ENSMUST00000160684	BH3 interacting domain death agonist [Source:MGI Symbol;Acc:MGI:108093]		P70444	-3.8	2.3E-02	2.8	3.9E-03	-0.5	4.8E-01	-0.5	4.4E-01
ENSMUST00000160685	activation-induced cytidine deaminase [Source:MGI Symbol;Acc:MGI:1342279]	E0CXQ9		5.4	2.6E-03	6.2	3.7E-04	-0.5	6.6E-01	-0.9	2.1E-01
ENSMUST00000160689	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	E0CXM5		-8.1	8.3E-05	6.0	3.0E-04	0.1	9.1E-01	-0.2	6.9E-01
ENSMUST00000128293	zinc finger protein 324 [Source:MGI Symbol;Acc:MGI:2444641]	E0CXY6		2.3	3.7E-01	3.5	1.7E-01	-2.1	3.9E-01	-3.3	1.6E-01
ENSMUST00000128300	thymoma viral proto-oncogene 1 [Source:MGI Symbol;Acc:MGI:87986]	D3Z783		-3.2	4.4E-01	-3.0	6.0E-01	-0.7	8.0E-01	-0.9	8.7E-01
ENSMUST00000160694	nestin [Source:MGI Symbol;Acc:MGI:101784]		Q6P5H2	6.8	1.6E-03	5.0	1.6E-04	0.1	8.8E-01	0.4	4.5E-01
ENSMUST00000128308	adhesion G protein-coupled receptor G5 [Source:MGI Symbol;Acc:MGI:2685955]	D6RJJ2		4.8	6.0E-02	1.6	5.8E-01	-2.6	3.3E-01	0.5	8.1E-01
ENSMUST00000128309	protein phosphatase 1, catalytic subunit, gamma isoform [Source:MGI Symbol;Acc:MGI:104872]	A0A0G2JGC1		-3.3	5.5E-02	-3.3	9.3E-02	-0.5	6.7E-01	-0.5	8.0E-01
ENSMUST00000128318	CDC-like kinase 2 [Source:MGI Symbol;Acc:MGI:1098669]	D6RG48		-4.8	2.4E-01	-5.4	2.8E-01	-1.6	4.6E-01	-1.0	8.6E-01
ENSMUST00000128319	chloride channel, voltage-sensitive 5 [Source:MGI Symbol;Acc:MGI:99486]	B1ATV1		2.2	2.3E-01	1.6	5.7E-01	0.7	7.5E-01	1.3	6.1E-01
ENSMUST00000128332				0.0	9.8E-01	0.9	6.9E-01	-1.2	5.5E-01	-2.1	2.8E-01
ENSMUST00000160696	polyhomeotic-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:103248]	Q7TT35		6.1	7.2E-04	4.1	4.5E-04	-0.8	2.7E-01	-0.5	4.3E-01
ENSMUST00000128336				-1.9	2.2E-01	-2.5	2.9E-01	0.1	9.4E-01	0.6	7.6E-01
ENSMUST00000160699	ring finger protein 214 [Source:MGI Symbol;Acc:MGI:2444451]		Q8BFU3	-5.4	9.5E-05	6.9	1.2E-04	-0.5	6.6E-01	-1.1	9.4E-02
ENSMUST00000160708	syntaxin binding protein 2 [Source:MGI Symbol;Acc:MGI:107370]	Q548T0	Q64324	-1.4	1.3E-02	4.7	1.2E-03	0.0	1.0E+00	-0.6	3.9E-01
ENSMUST00000160713	polymerase (DNA directed), iota [Source:MGI Symbol;Acc:MGI:1347081]	E0CZD6		3.6	7.0E-03	-4.7	8.0E-02	1.0	3.2E-01	2.0	4.1E-01
ENSMUST00000128344				-1.2	1.7E-01	0.3	7.2E-01	0.4	6.1E-01	-1.2	2.3E-01
ENSMUST00000128346	RAS p21 protein activator 2 [Source:MGI Symbol;Acc:MGI:2149960]	D3YZE9		0.3	8.6E-01	-0.8	7.6E-01	-0.6	7.3E-01	0.6	8.3E-01
ENSMUST00000160717	par-3 family cell polarity regulator [Source:MGI Symbol;Acc:MGI:2135608]		Q99NH2	8.0	7.2E-05	4.7	8.4E-03	-0.4	7.5E-01	0.0	1.0E+00
ENSMUST00000128354				-1.8	1.4E-01	-1.9	3.1E-01	0.7	4.8E-01	0.9	6.3E-01
ENSMUST00000128355				-0.2	8.4E-01	2.4	1.7E-01	1.6	2.9E-01	-1.0	4.1E-01
ENSMUST00000160719	microfibrillar-associated protein 3-like [Source:MGI Symbol;Acc:MGI:1918556]		Q9D3X9	2.4	3.4E-02	5.7	7.7E-04	-0.5	7.0E-01	-0.5	4.4E-01
ENSMUST00000160721	protocadherin 1 [Source:MGI Symbol;Acc:MGI:104692]	E0CXD4		7.9	9.4E-05	-4.8	9.7E-03	-2.1	2.1E-02	-0.7	7.0E-01
ENSMUST00000160726	fibrillarin-like 1 [Source:MGI Symbol;Acc:MGI:3034689]		Q80WS3	8.0	1.6E-05	-5.2	2.0E-02	0.3	7.4E-01	-1.2	6.1E-01
ENSMUST00000160732	protein kinase, AMP-activated, gamma 3 non-catatlytic subunit [Source:MGI Symbol;Acc:MGI:1891343]		Q8BGM7	7.3	6.3E-05	6.1	1.2E-03	-0.5	7.0E-01	-1.1	2.4E-01
ENSMUST00000160740	versican [Source:MGI Symbol;Acc:MGI:102889]	F7B603		-4.4	3.0E-02	5.7	9.2E-04	0.7	5.4E-01	-0.7	3.3E-01
ENSMUST00000128372	AHA1, activator of heat shock protein ATPase 2 [Source:MGI Symbol;Acc:MGI:1916133]	F6S1R2		-2.0	6.2E-01	-2.1	7.6E-01	1.4	7.2E-01	1.5	8.2E-01
ENSMUST00000160766	par-3 family cell polarity regulator [Source:MGI Symbol;Acc:MGI:2135608]	E0CY24		6.7	9.6E-05	6.4	1.7E-02	-2.4	3.6E-01	-0.9	5.6E-01
ENSMUST00000160770	angiomotin-like 1 [Source:MGI Symbol;Acc:MGI:1922973]		Q9D4H4	8.4	3.2E-06	-0.4	8.0E-01	2.2	7.5E-02	0.1	9.4E-01
ENSMUST00000128375				4.8	3.9E-02	2.4	4.3E-01	-0.9	7.5E-01	1.6	4.3E-01
ENSMUST00000160774	oxysterol binding protein-like 9 [Source:MGI Symbol;Acc:MGI:1923784]	F6UHR6		-9.8	8.0E-03	-1.4	8.5E-02	1.4	1.8E-02	-1.7	7.4E-02
ENSMUST00000128377	tumor necrosis factor, alpha-induced protein 8 [Source:MGI Symbol;Acc:MGI:2147191]	J3QM73		0.5	7.7E-01	-5.2	1.4E-02	-6.5	5.3E-04	-0.8	6.6E-01
ENSMUST00000128380				0.6	5.1E-01	0.8	5.0E-01	0.6	5.0E-01	0.4	6.9E-01
ENSMUST00000128382				1.7	4.3E-01	-0.1	9.8E-01	-0.4	8.7E-01	1.4	6.0E-01
ENSMUST00000128383	piezo-type mechanosensitive ion channel component 1 [Source:MGI Symbol;Acc:MGI:3603204]	F6QY99		-0.2	9.4E-01	2.3	4.9E-01	2.3	3.1E-01	-0.2	9.4E-01
ENSMUST00000160781	Wilms tumour 1-associating protein [Source:MGI Symbol;Acc:MGI:1926395]		Q9ER69	-2.7	1.2E-03	5.9	2.1E-02	-0.6	7.9E-01	-0.9	4.9E-01
ENSMUST00000128391				-1.5	6.3E-02	-0.3	7.6E-01	1.8	3.6E-02	0.7	5.1E-01
ENSMUST00000128399	protein tyrosine phosphatase, receptor type, R [Source:MGI Symbol;Acc:MGI:109559]		Q62132	2.8	7.8E-02	3.2	8.1E-02	-0.3	8.4E-01	-0.7	6.0E-01
ENSMUST00000128400				-0.8	1.1E-01	-1.1	7.7E-02	0.0	9.9E-01	0.3	5.6E-01
ENSMUST00000160786	mitochondrial fission factor [Source:MGI Symbol;Acc:MGI:1922984]		Q6PCP5	-8.3	4.1E-06	9.3	4.8E-05	-0.7	6.2E-01	0.0	9.5E-01
ENSMUST00000128403				-0.1	9.0E-01	-0.1	9.3E-01	0.4	7.3E-01	0.4	7.8E-01
ENSMUST00000160789	kinesin family member 26B [Source:MGI Symbol;Acc:MGI:2447076]	E9PX64		7.3	7.5E-05	4.9	5.2E-02	-1.9	4.5E-01	0.7	6.7E-01
ENSMUST00000160823	prenyl (solanesyl) diphosphate synthase, subunit 2 [Source:MGI Symbol;Acc:MGI:1918615]	E0CYM9		5.4	2.3E-05	1.1	4.9E-01	-5.0	1.5E-02	-0.4	7.6E-01
ENSMUST00000160826	predicted gene, 28048 [Source:MGI Symbol;Acc:MGI:5547784]	F7BCN0		-7.9	7.9E-04	-5.0	1.4E-02	0.8	2.4E-01	-1.3	5.0E-01
ENSMUST00000160844	neurexin I [Source:MGI Symbol;Acc:MGI:1096391]		Q9CS84	9.1	5.8E-05	5.3	1.0E-04	-2.0	3.5E-02	-0.1	8.5E-01
ENSMUST00000160853	MAF1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916127]		Q9D0U6	-6.9	1.2E-04	-4.4	2.9E-02	0.9	2.3E-01	2.2	2.2E-01
ENSMUST00000128414				0.7	3.3E-01	0.7	4.3E-01	-0.3	6.0E-01	-0.3	6.6E-01
ENSMUST00000160854	GULP, engulfment adaptor PTB domain containing 1 [Source:MGI Symbol;Acc:MGI:1920407]		Q8K2A1	7.8	3.5E-05	-5.1	4.1E-02	-0.3	7.4E-01	-1.1	6.5E-01
ENSMUST00000128418	coagulation factor X [Source:MGI Symbol;Acc:MGI:103107]	D3Z215		-2.9	1.6E-01	-5.1	4.6E-02	-3.3	2.7E-02	-1.1	6.6E-01
ENSMUST00000128426	ring finger protein 38 [Source:MGI Symbol;Acc:MGI:1920719]	B1AWE8		0.5	8.4E-01	-0.6	8.4E-01	-1.5	4.8E-01	-0.4	8.9E-01
ENSMUST00000128427				3.5	5.5E-02	5.0	2.2E-02	-0.6	7.2E-01	-2.2	1.3E-01
ENSMUST00000160855	Rho guanine nucleotide exchange factor (GEF) 4 [Source:MGI Symbol;Acc:MGI:2442507]	E0CYG8		2.0	2.0E-02	6.1	4.0E-03	0.2	8.8E-01	1.3	2.2E-01
ENSMUST00000128444				-1.3	3.3E-01	-4.2	5.2E-02	-1.8	9.5E-02	1.2	5.5E-01
ENSMUST00000128452				-1.8	2.1E-01	1.0	4.9E-01	0.6	6.2E-01	-2.2	1.5E-01
ENSMUST00000128456				2.3	9.8E-02	2.9	1.1E-01	-0.6	7.1E-01	-1.2	3.6E-01
ENSMUST00000128463				3.6	1.3E-01	6.0	3.0E-02	-0.4	8.8E-01	-2.8	9.1E-02
ENSMUST00000128464	desmocollin 2 [Source:MGI Symbol;Acc:MGI:103221]	D6RDD6		5.7	4.2E-02	6.0	4.9E-02	-0.6	8.5E-01	-0.8	6.2E-01
ENSMUST00000160860	kelch-like 3 [Source:MGI Symbol;Acc:MGI:2445185]	J3KMI2		8.1	1.2E-05	-2.6	3.4E-02	-1.2	9.9E-02	-0.8	4.6E-01
ENSMUST00000160874	ubiquitin-like 5 [Source:MGI Symbol;Acc:MGI:1913427]	E0CY91		-5.8	6.6E-03	6.6	1.8E-04	-0.5	6.9E-01	-0.4	5.5E-01
ENSMUST00000160879	aarF domain containing kinase 3 [Source:MGI Symbol;Acc:MGI:1914676]	A0A0A6YXD9		-4.8	2.1E-04	5.7	1.3E-03	-1.1	4.1E-01	0.6	4.5E-01
ENSMUST00000128475	zinc finger RNA binding protein [Source:MGI Symbol;Acc:MGI:1341890]	D3Z5G4		3.1	1.4E-01	-2.2	4.0E-01	-3.0	1.1E-01	2.3	3.7E-01
ENSMUST00000128478				1.2	5.4E-02	2.2	9.1E-03	0.4	4.4E-01	-0.6	2.9E-01
ENSMUST00000160882	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]		Q08122	-7.8	9.9E-04	6.4	1.1E-03	-0.7	6.5E-01	-0.8	3.2E-01
ENSMUST00000160883	solute carrier family 33 (acetyl-CoA transporter), member 1 [Source:MGI Symbol;Acc:MGI:1332247]		Q99J27	-3.3	2.1E-02	-9.5	4.3E-05	-0.8	5.1E-02	-0.8	5.8E-01
ENSMUST00000160884	tassium voltage-gated channel, shaker-related subfamily, beta member 2 [Source:MGI Symbol;Acc:MGI:10923		P62482	7.2	2.9E-03	-3.9	1.4E-02	0.0	9.8E-01	0.2	8.6E-01
ENSMUST00000128486				-0.5	4.6E-01	-1.3	2.0E-01	-0.3	6.1E-01	0.5	6.1E-01
ENSMUST00000128498				-1.9	1.2E-01	0.8	5.8E-01	1.2	2.4E-01	-1.4	3.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000128500	formin binding protein 1 [Source:MGI Symbol;Acc:MGI:109606]	F6VVN1		-1.7	5.6E-01	-2.5	4.9E-01	-1.2	5.6E-01	-0.3	9.3E-01
ENSMUST00000128510				3.0	8.3E-02	1.2	5.3E-01	-1.6	3.4E-01	0.2	9.0E-01
ENSMUST00000160889	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:2443419]	F6VA16		-5.9	2.2E-03	9.0	7.2E-05	-0.2	9.0E-01	0.5	3.8E-01
ENSMUST00000128513				2.0	7.5E-02	2.0	9.8E-02	-1.0	3.6E-01	-1.0	3.0E-01
ENSMUST00000160918	threonine synthase-like 2 (bacterial) [Source:MGI Symbol;Acc:MGI:3041254]		Q80W22	9.2	9.3E-05	4.5	1.1E-03	-3.8	1.1E-02	0.6	4.1E-01
ENSMUST00000160937	distal-less homeobox 6 [Source:MGI Symbol;Acc:MGI:101927]		P70397	9.3	8.9E-05	3.6	2.5E-02	-0.3	8.3E-01	0.2	8.1E-01
ENSMUST00000128517				-2.2	1.4E-01	-1.4	4.5E-01	0.0	9.8E-01	-0.8	6.6E-01
ENSMUST00000128518				-1.2	4.1E-01	-2.1	2.2E-01	-1.7	1.5E-01	-0.9	5.9E-01
ENSMUST00000160942	family with sequence similarity 83, member A [Source:MGI Symbol;Acc:MGI:2447773]		Q8K2P2	5.4	4.9E-06	-6.1	6.1E-03	-1.1	1.4E-01	-0.9	6.3E-01
ENSMUST00000160953	SPHK1 interactor, AKAP domain containing [Source:MGI Symbol;Acc:MGI:1924879]	E9PUC4		8.7	9.4E-06	1.7	8.0E-02	-0.2	7.4E-01	0.2	7.5E-01
ENSMUST00000160972	mitochondrial fission factor [Source:MGI Symbol;Acc:MGI:1922984]		Q6PCP5	-7.6	1.1E-04	-2.7	1.1E-01	1.8	7.7E-02	-2.1	2.8E-01
ENSMUST00000128532				0.5	5.1E-01	1.4	1.5E-01	1.0	1.8E-01	0.1	9.0E-01
ENSMUST00000160973	spermatogenesis associated 13 [Source:MGI Symbol;Acc:MGI:104838]	E9Q3I3		8.7	6.8E-03	7.7	6.5E-05	-0.6	5.9E-01	-0.6	3.3E-01
ENSMUST00000160977	zinc finger like protein 1 [Source:MGI Symbol;Acc:MGI:1891017]	E0CXM9		-3.5	3.1E-02	7.2	2.6E-04	-0.5	7.4E-01	-1.3	9.0E-02
ENSMUST00000161002	endothelin converting enzyme-like 1 [Source:MGI Symbol;Acc:MGI:1343461]		Q9JMI0	6.5	2.9E-02	4.7	8.7E-04	-1.0	3.2E-01	0.1	9.1E-01
ENSMUST00000161008	MYC binding protein 2 [Source:MGI Symbol;Acc:MGI:2179432]	F6T4V9		-5.7	3.2E-03	8.1	3.9E-04	1.2	4.0E-01	1.1	1.6E-01
ENSMUST00000128548				1.3	1.3E-01	1.2	2.2E-01	0.1	9.0E-01	0.2	8.3E-01
ENSMUST00000128553	zinc finger protein 512B [Source:MGI Symbol;Acc:MGI:2685478]	Q6PHP4		-0.3	8.1E-01	1.8	2.8E-01	0.7	6.0E-01	-1.4	3.5E-01
ENSMUST00000161017	kinesin family member 26B [Source:MGI Symbol;Acc:MGI:2447076]		Q7TNC6	5.9	3.1E-06	-4.3	1.1E-02	0.4	5.2E-01	-0.9	5.5E-01
ENSMUST00000161028	fer-1-like 6 (C. elegans) [Source:MGI Symbol;Acc:MGI:3645398]	E0CZ42		8.1	8.2E-05	4.2	3.5E-02	-0.7	6.7E-01	-0.3	7.9E-01
ENSMUST00000161034	serine (or cysteine) peptidase inhibitor, clade D, member 1 [Source:MGI Symbol;Acc:MGI:960051]		P49182	3.8	9.9E-03	5.5	8.9E-04	-0.5	6.8E-01	-1.4	7.7E-02
ENSMUST00000128559	AHA1, activator of heat shock protein ATPase 2 [Source:MGI Symbol;Acc:MGI:1916133]	A2AF82		-1.7	1.6E-01	-0.4	7.4E-01	-0.8	4.0E-01	-2.1	1.1E-01
ENSMUST00000161051	eukaryotic translation initiation factor 4, gamma 2 [Source:MGI Symbol;Acc:MGI:109207]	F7CBP1		-10.1	7.0E-07	2.5	1.8E-01	-0.7	6.5E-01	3.8	1.8E-02
ENSMUST00000161059	transmembrane protein 120B [Source:MGI Symbol;Acc:MGI:3603158]	E0CYA8		5.4	1.7E-02	6.8	2.7E-04	-0.7	6.1E-01	-0.7	3.4E-01
ENSMUST00000161063	Eph receptor B3 [Source:MGI Symbol;Acc:MGI:104770]	E0CYA3		7.9	2.4E-05	-2.9	2.0E-01	2.3	7.6E-02	-0.5	8.0E-01
ENSMUST00000161069	hairless [Source:MGI Symbol;Acc:MGI:96223]		Q61645	5.6	1.9E-02	6.9	1.3E-04	-0.6	6.0E-01	-1.0	1.3E-01
ENSMUST00000161074	histidine triad nucleotide binding protein 3 [Source:MGI Symbol;Acc:MGI:1914097]		Q9CPS6	-2.7	1.8E-02	5.4	7.3E-04	2.2	5.1E-02	-0.7	3.5E-01
ENSMUST00000161075	desumoylating isopeptidase 2 [Source:MGI Symbol;Acc:MGI:1926075]	Q8BIB9		-3.1	1.2E-02	3.2	5.0E-02	-1.6	2.7E-01	-0.6	6.1E-01
ENSMUST00000161110	exocrine gland secreted peptide 1 [Source:MGI Symbol;Acc:MGI:3645915]		Q3LHH8	5.9	2.2E-03	4.2	1.6E-04	0.2	7.6E-01	-0.1	8.9E-01
ENSMUST00000161114	olute carrier family 37 (glycerol-3-phosphate transporter), member 2 [Source:MGI Symbol;Acc:MGI:1929693		Q9WU81	-4.0	1.6E-02	2.0	5.9E-01	7.2	1.9E-02	-1.4	6.9E-01
ENSMUST00000161115	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) [Source:MGI Symbol;Acc:MGI:1924148]	Q6PIG8		7.6	1.2E-02	-1.4	3.0E-01	0.9	3.2E-01	-1.6	2.6E-01
ENSMUST00000161137	programmed cell death 10 [Source:MGI Symbol;Acc:MGI:1928396]		Q8VE70	-5.2	5.4E-04	-3.6	1.6E-01	1.0	3.7E-01	-0.7	7.9E-01
ENSMUST00000161148	RIKEN cDNA A930011G23 gene [Source:MGI Symbol;Acc:MGI:2442790]	E0CXU2		7.0	5.4E-05	5.4	2.0E-03	-0.6	6.4E-01	0.3	7.4E-01
ENSMUST00000128614	transmembrane protein 106A [Source:MGI Symbol;Acc:MGI:1922056]	A2A4M9		0.2	8.5E-01	0.6	6.7E-01	0.2	8.7E-01	-0.2	8.7E-01
ENSMUST00000128615				3.5	6.1E-02	6.0	8.5E-03	-0.4	8.6E-01	-2.8	3.2E-02
ENSMUST00000128617				-1.8	2.0E-01	0.3	8.4E-01	0.6	6.3E-01	-1.5	3.0E-01
ENSMUST00000161152	selectin, platelet [Source:MGI Symbol;Acc:MGI:98280]	F6TL88		-3.9	1.8E-03	3.1	3.7E-03	-0.6	4.4E-01	-0.8	2.2E-01
ENSMUST00000161154	tryptophanyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:104630]		P32921	-3.4	6.7E-03	5.3	3.5E-03	-0.1	9.3E-01	-0.1	8.8E-01
ENSMUST00000128623				-1.6	1.2E-01	-0.5	7.1E-01	1.3	1.8E-01	0.2	8.6E-01
ENSMUST00000161170	zinc finger protein 9 [Source:MGI Symbol;Acc:MGI:99210]	Q8BIS1		6.6	8.1E-07	5.7	7.1E-04	-0.3	8.1E-01	-0.1	8.4E-01
ENSMUST00000161172	eukaryotic translation initiation factor 2, subunit 2 (beta) [Source:MGI Symbol;Acc:MGI:1914454]	E0CXJ3		3.6	2.2E-04	3.0	4.7E-03	0.3	6.8E-01	-1.0	1.7E-01
ENSMUST00000161178	family with sequence similarity 109, member B [Source:MGI Symbol;Acc:MGI:2443609]			7.4	1.6E-02	-2.3	6.1E-02	0.3	5.9E-01	-1.6	2.3E-01
ENSMUST00000161181	cyclin-dependent kinase 8 [Source:MGI Symbol;Acc:MGI:1196224]	E9Q6E2		-4.4	2.1E-02	7.0	6.3E-04	-0.7	6.5E-01	-1.0	2.2E-01
ENSMUST00000128644	tetraspanin 13 [Source:MGI Symbol;Acc:MGI:1913359]	E0CY97		-0.8	5.0E-01	-5.8	9.7E-03	-3.0	6.0E-03	2.0	2.9E-01
ENSMUST00000128645				0.0	9.6E-01	0.2	8.5E-01	0.1	9.4E-01	-0.1	9.2E-01
ENSMUST00000161186	optic atrophy 1 [Source:MGI Symbol;Acc:MGI:1921393]		P58281	-3.6	3.1E-03	7.7	1.5E-02	-0.6	8.5E-01	-2.1	1.8E-01
ENSMUST00000161194	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	E0CZB4		2.6	3.0E-02	-3.0	1.1E-01	1.0	2.6E-01	1.0	5.6E-01
ENSMUST00000161202	sorting nexin 31 [Source:MGI Symbol;Acc:MGI:1913946]		Q6P8Y7	4.6	2.9E-02	5.3	3.4E-03	0.7	5.7E-01	-0.1	9.2E-01
ENSMUST00000128659				1.2	3.2E-01	0.9	6.5E-01	0.6	7.1E-01	1.0	5.2E-01
ENSMUST00000128661				1.7	5.3E-02	0.6	5.5E-01	-0.9	2.9E-01	0.3	7.1E-01
ENSMUST00000128663				3.1	6.6E-02	7.6	9.6E-03	2.8	2.5E-01	-1.7	1.9E-01
ENSMUST00000128664	ornithine decarboxylase antizyme 2 [Source:MGI Symbol;Acc:MGI:109492]	J3QPT5		-0.7	3.7E-01	-0.9	3.6E-01	0.4	6.0E-01	0.6	5.1E-01
ENSMUST00000161203	ring finger protein 214 [Source:MGI Symbol;Acc:MGI:2444451]		Q8BFU3	-5.6	2.0E-04	1.8	5.0E-02	-0.6	3.9E-01	0.2	7.9E-01
ENSMUST00000128670				-1.4	2.5E-01	2.7	2.5E-02	0.1	9.5E-01	-4.1	5.6E-03
ENSMUST00000161204	retinol dehydrogenase 11 [Source:MGI Symbol;Acc:MGI:102581]		Q9QYF1	-1.8	1.1E-02	6.2	4.1E-04	-0.5	6.6E-01	0.0	9.6E-01
ENSMUST00000161211	mediator complex subunit 6 [Source:MGI Symbol;Acc:MGI:1917042]		Q921D4	-3.0	1.6E-02	-1.5	2.8E-01	0.6	4.7E-01	-0.4	7.6E-01
ENSMUST00000128678				1.5	4.4E-02	2.1	3.3E-02	0.2	7.4E-01	-0.4	6.1E-01
ENSMUST00000161233	transmembrane protein 33 [Source:MGI Symbol;Acc:MGI:1915128]	E0CXY5		-4.2	4.7E-04	-5.2	3.3E-03	-1.8	2.0E-02	-1.9	2.6E-01
ENSMUST00000128682	ADP-ribosylation factor-like 5B [Source:MGI Symbol;Acc:MGI:1923119]	D6RJJ6		1.1	4.9E-01	-1.5	5.1E-01	-1.4	3.2E-01	1.2	5.9E-01
ENSMUST00000161243	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]	F6U2S8		-5.2	4.8E-04	6.4	3.5E-04	-0.6	6.2E-01	-0.8	2.4E-01
ENSMUST00000161263	synaptic vesicle glycoprotein 2c [Source:MGI Symbol;Acc:MGI:1922459]		Q69ZS6	8.5	9.6E-06	5.8	3.1E-04	-0.9	4.3E-01	-1.0	1.4E-01
ENSMUST00000161267	RIKEN cDNA C130026I21 gene [Source:MGI Symbol;Acc:MGI:3612702]	E0CY74		-1.9	1.1E-02	6.4	2.9E-04	-0.6	6.0E-01	-0.5	4.5E-01
ENSMUST00000161286	transformer 2 beta homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:106016]		P62996	-2.9	2.8E-04	-0.1	9.4E-01	-6.0	2.0E-04	-1.1	1.7E-01
ENSMUST00000161289	carboxylesterase 4A [Source:MGI Symbol;Acc:MGI:2384581]		Q8R0W5	7.7	1.5E-05	5.4	7.6E-04	-0.6	6.2E-01	0.6	4.0E-01
ENSMUST00000128704				2.5	1.7E-01	-4.4	4.9E-02	-5.8	2.3E-03	1.1	6.0E-01
ENSMUST00000161300	aarF domain containing kinase 3 [Source:MGI Symbol;Acc:MGI:1914676]	F7B1B6		-4.9	7.6E-04	6.2	2.5E-03	1.6	2.7E-01	-0.6	5.0E-01
ENSMUST00000161306	transmembrane protease, serine 11e [Source:MGI Symbol;Acc:MGI:3513175]		Q5S248	6.2	2.9E-04	2.5	9.4E-03	-1.4	7.7E-02	0.6	3.2E-01
ENSMUST00000161327	RB1-inducible coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1341850]	F7CC56		-8.2	5.4E-06	7.9	9.2E-04	-2.0	2.8E-01	0.8	3.7E-01
ENSMUST00000161335	AE binding protein 2 [Source:MGI Symbol;Acc:MGI:1338038]		Q9Z248	-2.2	1.0E-02	-2.3	9.2E-03	1.2	1.7E-02	0.5	4.6E-01
ENSMUST00000161342	plakophilin 2 [Source:MGI Symbol;Acc:MGI:1914701]	E0CXK9		5.4	1.9E-03	7.5	1.2E-02	-0.8	7.6E-01	-2.3	1.4E-01
ENSMUST00000161354	ATP-binding cassette, sub-family G (WHITE), member 4 [Source:MGI Symbol;Acc:MGI:1890594]	Q91WA9		6.8	1.5E-04	6.0	1.3E-04	-1.5	1.8E-01	-0.6	2.7E-01
ENSMUST00000128721	lysophosphatidylcholine acyltransferase 3 [Source:MGI Symbol;Acc:MGI:1315211]			1.0	6.3E-01	-2.3	4.6E-01	-1.7	3.5E-01	1.7	5.9E-01
ENSMUST00000161365	C-type lectin domain family 4, member a2 [Source:MGI Symbol;Acc:MGI:1349412]		Q9QZ15	-10.2	3.7E-06	-0.4	9.1E-01	0.1	9.5E-01	5.3	7.8E-02
ENSMUST00000161368	family with sequence similarity 89, member B [Source:MGI Symbol;Acc:MGI:106595]	Q7TMI7	Q9QUI1	-5.1	1.3E-02	1.7	4.5E-02	-0.5	4.7E-01	-0.3	5.9E-01
ENSMUST00000128727	ARP3 actin-related protein 3B [Source:MGI Symbol;Acc:MGI:2661120]		Q641P0	3.7	4.6E-02	5.0	1.7E-02	-0.7	7.0E-01	-2.0	1.6E-01
ENSMUST00000128729				-1.7	2.6E-01	-3.6	1.2E-01	-1.0	3.6E-01	0.9	6.8E-01
ENSMUST00000161369	transmembrane protein 33 [Source:MGI Symbol;Acc:MGI:1915128]		Q9CR67	-4.6	1.5E-03	6.0	4.5E-04	-0.6	6.1E-01	-0.1	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000161372	pannexin 2 [Source:MGI Symbol;Acc:MGI:1890615]		Q6IMP4	5.3	1.8E-02	-6.0	1.0E-03	-2.5	3.9E-03	-1.3	3.8E-01
ENSMUST00000161374	autism susceptibility candidate 2 [Source:MGI Symbol;Acc:MGI:1919847]	E9PWJ4		5.9	8.9E-04	5.6	1.7E-03	-0.2	8.9E-01	0.3	7.3E-01
ENSMUST00000128744				3.4	4.8E-02	5.1	1.1E-02	-0.1	9.3E-01	-1.9	1.2E-01
ENSMUST00000161386	NACHT and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:2442268]	E0CYZ6		8.6	3.0E-04	6.9	5.5E-05	-0.6	5.3E-01	0.7	1.6E-01
ENSMUST00000161401	cytochrome c, somatic [Source:MGI Symbol;Acc:MGI:88578]	Q56A15	P62897	1.4	1.4E-02	6.4	2.0E-03	-0.7	6.6E-01	-1.0	2.7E-01
ENSMUST00000161405	grainyhead-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2182543]	Q9DCN4		6.8	3.8E-05	-3.7	2.2E-02	0.9	1.8E-01	1.0	4.9E-01
ENSMUST00000128750				-0.1	9.7E-01	-2.3	4.2E-01	-2.7	1.3E-01	-0.5	8.8E-01
ENSMUST00000161421	microfibrillar-associated protein 3-like [Source:MGI Symbol;Acc:MGI:1918556]		Q9D3X9	7.6	1.4E-04	5.2	1.7E-03	0.5	6.7E-01	-0.6	4.0E-01
ENSMUST00000161435	mitochondrial calcium uniporter [Source:MGI Symbol;Acc:MGI:3026965]	E0CYL3		5.3	1.7E-04	6.0	1.3E-03	0.2	8.8E-01	-0.2	7.9E-01
ENSMUST00000161445	protein phosphatase 3, catalytic subunit, beta isoform [Source:MGI Symbol;Acc:MGI:107163]	E0CZ78		-4.8	4.2E-04	3.9	1.3E-03	-1.9	6.3E-02	0.6	4.1E-01
ENSMUST00000128756	leukocyte receptor cluster (LRC) member 8 [Source:MGI Symbol;Acc:MGI:2142195]	D3YY84		-1.1	3.4E-01	-0.2	8.9E-01	0.0	9.8E-01	-1.0	4.5E-01
ENSMUST00000161448	zinc finger protein 316 [Source:MGI Symbol;Acc:MGI:1860402]	G3XA34		6.5	1.4E-04	3.9	8.3E-04	-1.2	1.5E-01	0.3	6.4E-01
ENSMUST00000128758				1.3	5.2E-01	-2.3	3.3E-01	-2.7	8.3E-02	0.8	7.3E-01
ENSMUST00000161475	predicted gene 10696 [Source:MGI Symbol;Acc:MGI:3702972]	Q3UTC4		6.9	3.1E-04	5.3	5.5E-06	-0.5	3.4E-01	-0.3	4.3E-01
ENSMUST00000161485	nitric oxide synthase 1 (neuronal) adaptor protein [Source:MGI Symbol;Acc:MGI:1917979]	E0CYH9		-3.3	7.0E-03	4.3	4.0E-03	-2.2	1.1E-01	0.2	7.5E-01
ENSMUST00000128764	Sin3-associated polypeptide 18 [Source:MGI Symbol;Acc:MGI:1277978]	E9Q317		0.5	4.5E-01	1.4	9.7E-02	0.7	2.9E-01	-0.3	6.8E-01
ENSMUST00000128767	complement factor B [Source:MGI Symbol;Acc:MGI:105975]	Q3UEG8	P04186	2.1	4.1E-01	-1.9	5.1E-01	-3.9	8.6E-02	0.1	9.6E-01
ENSMUST00000128771				-0.7	6.6E-01	-3.1	1.8E-01	-2.1	1.7E-01	0.3	9.0E-01
ENSMUST00000161487	protein phosphatase 1H (PP2C domain containing) [Source:MGI Symbol;Acc:MGI:2442087]		Q3UYC0	3.3	1.5E-03	2.8	4.5E-02	-0.4	7.3E-01	0.0	9.7E-01
ENSMUST00000161490	protein kinase, cGMP-dependent, type II [Source:MGI Symbol;Acc:MGI:108173]	Q8CAH8		7.5	1.2E-04	5.1	6.3E-03	-2.5	1.4E-01	-1.5	2.2E-01
ENSMUST00000161494	glucocorticoid induced transcript 1 [Source:MGI Symbol;Acc:MGI:2179717]			2.1	2.8E-02	6.5	2.6E-04	-0.6	6.1E-01	-0.1	8.9E-01
ENSMUST00000128784				3.0	6.3E-02	4.8	9.6E-03	-1.1	5.0E-01	-2.9	2.3E-02
ENSMUST00000161501	cerebral cavernous malformation 2 [Source:MGI Symbol;Acc:MGI:2384924]	E0CYY2		-1.5	1.7E-02	-4.6	3.4E-02	1.2	1.6E-01	-0.8	6.9E-01
ENSMUST00000161504	exocyst complex component 5 [Source:MGI Symbol;Acc:MGI:2145645]	E9PZ92		-5.3	5.2E-03	-2.6	8.4E-03	-0.7	1.7E-01	0.0	9.5E-01
ENSMUST00000161514	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 [Source:MGI Symbol;Acc:MGI:		Q8C7U7	5.2	2.2E-02	-5.5	2.4E-03	-0.3	5.6E-01	0.3	8.4E-01
ENSMUST00000128802				1.6	1.6E-01	1.6	3.1E-01	0.0	9.9E-01	0.0	9.6E-01
ENSMUST00000161516	RIKEN cDNA A930011G23 gene [Source:MGI Symbol;Acc:MGI:2442790]	E0CXS0		6.8	6.0E-05	1.8	7.5E-02	-0.6	4.6E-01	0.5	5.1E-01
ENSMUST00000161517	predicted gene 21970 [Source:MGI Symbol;Acc:MGI:5439439]	F7BJH9		-6.1	8.6E-05	6.5	4.1E-03	0.3	8.8E-01	0.8	4.6E-01
ENSMUST00000128818				2.8	1.1E-01	1.8	3.5E-01	-1.6	3.7E-01	-0.7	6.6E-01
ENSMUST00000161520	coiled-coil domain containing 79 [Source:MGI Symbol;Acc:MGI:2443187]	E0CZE9		6.3	2.7E-04	3.4	3.9E-03	-0.1	9.0E-01	-1.0	2.0E-01
ENSMUST00000128823				-1.6	3.9E-01	-2.7	1.8E-01	-2.9	3.4E-02	-1.9	3.8E-01
ENSMUST00000161523	transmembrane protein 63a [Source:MGI Symbol;Acc:MGI:2384789]		Q91YT8	-6.7	3.9E-04	4.0	8.3E-03	-1.1	3.9E-01	0.0	9.8E-01
ENSMUST00000161525	arrestin, beta 1 [Source:MGI Symbol;Acc:MGI:99473]	E0CY53		6.6	2.5E-04	7.7	3.1E-04	-0.7	6.4E-01	-0.3	6.5E-01
ENSMUST00000161527	MAF1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916127]		Q9D0U6	-7.1	2.6E-05	5.2	9.0E-04	-0.8	5.0E-01	-0.4	6.0E-01
ENSMUST00000161546	F-box protein 41 [Source:MGI Symbol;Acc:MGI:1261912]	Q3UGY7	Q6NS60	8.1	3.3E-05	4.1	7.1E-03	-0.4	7.6E-01	-0.3	7.3E-01
ENSMUST00000161553	poly (ADP-ribose) polymerase family, member 4 [Source:MGI Symbol;Acc:MGI:2685589]	E9PYK3		-2.3	1.7E-03	5.5	2.7E-03	-0.6	7.1E-01	0.9	2.7E-01
ENSMUST00000161560	stabilin 2 [Source:MGI Symbol;Acc:MGI:2178743]	F7CNH8		7.0	5.7E-03	6.4	6.0E-05	-2.4	4.1E-02	-0.3	6.2E-01
ENSMUST00000161567	peptidylglycine alpha-amidating monooxygenase [Source:MGI Symbol;Acc:MGI:97475]	E9Q704		-2.7	2.1E-02	1.7	7.5E-02	-1.1	1.6E-01	-0.6	4.3E-01
ENSMUST00000128851				-1.8	1.5E-01	-1.0	5.2E-01	0.3	8.0E-01	-0.5	7.1E-01
ENSMUST00000161568	transmembrane protein 167 [Source:MGI Symbol;Acc:MGI:1913324]		Q9CR64	-1.5	2.1E-03	2.2	1.2E-01	-1.7	2.0E-01	0.0	1.0E+00
ENSMUST00000161576	inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 [Source:MGI Symbol;Acc:I	Q3TMN9	Q9JJK5	-6.8	2.6E-04	-2.9	1.9E-02	0.5	4.0E-01	-0.4	7.4E-01
ENSMUST00000128860	cadherin 8 [Source:MGI Symbol;Acc:MGI:107434]		P97291	4.3	1.2E-01	4.8	1.2E-01	-0.3	9.1E-01	-0.8	6.5E-01
ENSMUST00000161592	E2F-associated phosphoprotein [Source:MGI Symbol;Acc:MGI:1913516]		Q5BU09	1.5	3.2E-02	5.4	5.0E-04	-3.2	1.8E-02	1.2	8.6E-02
ENSMUST00000161609	RING CCCH (C3H) domains 1 [Source:MGI Symbol;Acc:MGI:2685397]		Q4VGL6	-2.2	7.3E-04	4.8	6.4E-04	-1.2	2.6E-01	3.2	4.8E-04
ENSMUST00000161611	lycan 4 (megakaryocyte stimulating factor, articular superficial zone protein) [Source:MGI Symbol;Acc:MGI:1	E0CZ58		10.7	4.3E-04	1.4	1.1E-01	-0.4	5.5E-01	0.4	5.1E-01
ENSMUST00000128876				0.2	8.9E-01	1.3	3.1E-01	-0.3	7.5E-01	-1.5	2.2E-01
ENSMUST00000128880	oxidative-stress responsive 1 [Source:MGI Symbol;Acc:MGI:1917378]	D6RFV0		0.3	8.4E-01	-0.4	8.9E-01	1.3	5.4E-01	2.1	4.5E-01
ENSMUST00000161632	aarF domain containing kinase 3 [Source:MGI Symbol;Acc:MGI:1914676]	F6T0A8		-3.1	2.3E-02	6.0	1.0E-05	-0.2	7.1E-01	-0.1	8.0E-01
ENSMUST00000128883				-1.1	6.7E-01	-3.8	2.4E-01	-3.2	9.1E-02	-0.5	8.7E-01
ENSMUST00000128884				-2.3	1.8E-01	0.2	9.1E-01	0.3	8.1E-01	-2.2	2.4E-01
ENSMUST00000128889				-5.4	8.1E-02	-6.9	3.1E-02	-3.7	4.3E-02	-2.2	5.2E-01
ENSMUST00000161640	argininosuccinate lyase [Source:MGI Symbol;Acc:MGI:88084]	E0CY49		-5.2	4.3E-03	6.2	1.7E-03	0.1	9.2E-01	-0.2	7.8E-01
ENSMUST00000161642	baculoviral IAP repeat-containing 3 [Source:MGI Symbol;Acc:MGI:1197007]	F7BQL8		-5.0	2.0E-03	5.6	1.2E-03	0.5	6.5E-01	0.1	8.6E-01
ENSMUST00000161650	histamine receptor H1 [Source:MGI Symbol;Acc:MGI:107619]	B3Y5T0	P70174	4.7	1.5E-02	-5.3	1.3E-02	0.8	2.7E-01	-0.2	9.2E-01
ENSMUST00000128906	transmembrane protein 80 [Source:MGI Symbol;Acc:MGI:1918698]		Q9D3H0	0.5	4.1E-01	1.3	1.1E-01	0.3	6.1E-01	-0.5	4.7E-01
ENSMUST00000161659	solute carrier family 33 (acetyl-CoA transporter), member 1 [Source:MGI Symbol;Acc:MGI:1332247]		Q99J27	4.8	7.6E-03	-3.6	5.8E-02	0.9	2.9E-01	-0.7	6.9E-01
ENSMUST00000161684	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	Q3TDW1	P97808	-4.1	4.7E-04	6.9	3.6E-05	-0.8	3.7E-01	0.0	1.0E+00
ENSMUST00000161685	RIKEN cDNA C130026I21 gene [Source:MGI Symbol;Acc:MGI:3612702]	F7D3Q7		2.1	3.0E-02	5.8	2.6E-03	-1.6	3.1E-01	0.7	4.5E-01
ENSMUST00000161693	topoisomerase (DNA) II beta [Source:MGI Symbol;Acc:MGI:98791]	F6XX57		-5.3	2.2E-02	-2.9	5.6E-02	0.6	4.4E-01	0.0	9.7E-01
ENSMUST00000128930				2.4	1.8E-01	-1.5	5.9E-01	-0.9	6.1E-01	3.1	2.7E-01
ENSMUST00000128933	testis expressed gene 2 [Source:MGI Symbol;Acc:MGI:102465]	B1ATR3		3.9	1.1E-01	1.6	5.0E-01	-2.0	4.4E-01	0.3	8.6E-01
ENSMUST00000161701	protocadherin 1 [Source:MGI Symbol;Acc:MGI:104692]	F7BJK1		8.1	3.8E-05	6.6	4.2E-04	1.0	3.9E-01	1.0	1.4E-01
ENSMUST00000128937				1.9	7.0E-02	1.9	1.3E-01	-0.2	8.3E-01	-0.2	8.8E-01
ENSMUST00000161703	membrane-type frizzled-related protein [Source:MGI Symbol;Acc:MGI:2385957]	E0CXS1		5.7	7.7E-03	6.4	6.1E-04	-0.3	8.0E-01	0.3	6.8E-01
ENSMUST00000161713	dual specificity phosphatase 26 (putative) [Source:MGI Symbol;Acc:MGI:1914209]		Q9D700	6.0	4.0E-03	3.6	1.6E-02	0.3	8.1E-01	-0.5	5.7E-01
ENSMUST00000161737	hydroxysteroid 11-beta dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:103562]	Q4JHD9	P50172	-5.8	6.5E-07	-1.7	2.7E-01	1.3	1.9E-01	-0.2	8.9E-01
ENSMUST00000161738	insulin-like growth factor 2 receptor [Source:MGI Symbol;Acc:MGI:96435]	F6SFP4		6.1	5.9E-04	4.4	9.7E-03	-0.8	5.3E-01	0.8	4.2E-01
ENSMUST00000128954				-1.5	1.6E-01	-1.1	4.4E-01	0.4	6.9E-01	-0.1	9.6E-01
ENSMUST00000128955				0.9	6.6E-01	-1.6	3.3E-01	-4.9	1.0E-02	-2.4	2.3E-01
ENSMUST00000128958				-0.5	8.0E-01	-3.1	3.6E-01	-0.8	6.7E-01	1.8	5.8E-01
ENSMUST00000128961				1.0	4.4E-01	0.9	6.0E-01	-0.1	9.2E-01	-0.1	9.5E-01
ENSMUST00000161739	polyhomeotic-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:103248]	Q7TT35		-4.0	2.2E-03	4.1	8.0E-03	-2.4	1.0E-01	0.5	5.4E-01
ENSMUST00000128968	ha thalassemia/mental retardation syndrome X-linked homolog (human) [Source:MGI Symbol;Acc:MGI:1030	F6RDB7		1.0	2.1E-01	1.1	2.8E-01	1.1	1.9E-01	1.0	2.8E-01
ENSMUST00000161741	TP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 [Source:MGI Symbol;Acc:MGI:1927558		P56135	-5.2	6.0E-04	-4.9	1.0E-02	1.1	1.0E-01	-0.7	7.0E-01
ENSMUST00000128972	ribonuclease H2, large subunit [Source:MGI Symbol;Acc:MGI:1916974]	F6RP29		2.1	2.7E-01	-2.2	3.6E-01	-3.6	4.6E-02	0.8	7.5E-01
ENSMUST00000161762	cytokine induced apoptosis inhibitor 1 [Source:MGI Symbol;Acc:MGI:1922083]	E0CYY1		-4.0	2.2E-02	6.1	4.7E-02	-1.8	5.6E-01	0.2	9.0E-01
ENSMUST00000161764	inhibitor of kappaB kinase epsilon [Source:MGI Symbol;Acc:MGI:1929612]	E9PYL6		-4.5	7.7E-03	2.5	2.1E-03	-1.8	8.5E-03	-1.6	1.5E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000161769	predicted gene 28062 [Source:MGI Symbol;Acc:MGI:5578768]	G3XA10		-8.3	1.9E-05	6.8	8.0E-05	-0.5	6.2E-01	-0.2	6.6E-01
ENSMUST00000128986				0.4	6.6E-01	1.0	3.4E-01	-0.1	8.7E-01	-0.8	4.1E-01
ENSMUST00000128992				-1.4	3.0E-01	-0.8	6.2E-01	0.5	6.9E-01	-0.1	9.5E-01
ENSMUST00000128993				1.2	1.4E-01	2.4	3.6E-02	1.1	1.9E-01	0.0	9.7E-01
ENSMUST00000161779	homeodomain interacting protein kinase 2 [Source:MGI Symbol;Acc:MGI:1314872]		Q9QZR5	2.1	6.8E-04	-2.9	1.4E-01	1.6	1.5E-01	-0.7	7.2E-01
ENSMUST00000161788	fucosyltransferase 10 [Source:MGI Symbol;Acc:MGI:2384748]		Q5F2L2	3.4	5.2E-04	-4.7	1.7E-02	-0.6	3.8E-01	0.3	8.5E-01
ENSMUST00000161792	cytokine induced apoptosis inhibitor 1 [Source:MGI Symbol;Acc:MGI:1922083]	F7BWP1		-5.0	5.5E-04	-2.5	4.7E-02	0.0	9.8E-01	0.1	9.3E-01
ENSMUST00000129005				-2.7	2.6E-01	-5.9	5.2E-02	-3.7	2.2E-02	-0.5	8.7E-01
ENSMUST00000161801	regulator of G-protein signaling 6 [Source:MGI Symbol;Acc:MGI:1354730]	Q3UTM5		6.5	4.8E-04	9.0	7.1E-04	-0.9	6.3E-01	2.0	4.2E-02
ENSMUST00000161802	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]	F6S7V4		-5.4	1.2E-04	6.8	4.3E-04	-0.7	6.2E-01	-0.1	9.1E-01
ENSMUST00000161804	autism susceptibility candidate 2 [Source:MGI Symbol;Acc:MGI:1919847]	E9PZ86		8.7	3.7E-05	-2.4	1.1E-01	1.1	1.4E-01	0.6	6.9E-01
ENSMUST00000161805	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	Q3TDW1	P97808	-5.9	1.4E-05	-6.3	8.5E-05	-0.8	4.7E-02	-0.9	4.1E-01
ENSMUST00000161807	proteasome (prosome, macropain) activator subunit 2 (PA28 beta) [Source:MGI Symbol;Acc:MGI:1096365]	Q5SVP3	P97372	-7.5	8.4E-05	-5.0	7.3E-03	0.3	5.4E-01	2.2	1.6E-01
ENSMUST00000161821	mitochondrial amidoxime reducing component 2 [Source:MGI Symbol;Acc:MGI:1914497]	E0CZH6		-4.8	3.1E-04	4.4	9.0E-03	0.4	7.5E-01	-0.4	6.4E-01
ENSMUST00000161854	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Source:MGI Symbol;Acc:MGI:1298224]	E0CYP4		-7.2	3.3E-05	9.2	7.2E-06	-1.0	3.9E-01	0.0	9.3E-01
ENSMUST00000129031	drosha, ribonuclease type III [Source:MGI Symbol;Acc:MGI:1261425]	F6QX82		-3.1	8.2E-02	-0.6	6.4E-01	-0.7	5.5E-01	-3.1	9.0E-02
ENSMUST00000161856	RNA binding motif protein 20 [Source:MGI Symbol;Acc:MGI:1920963]	F6TAZ4		7.8	2.3E-02	-7.5	7.2E-04	0.1	7.8E-01	1.0	5.4E-01
ENSMUST00000161859	ring finger protein (C3H2C3 type) 6 [Source:MGI Symbol;Acc:MGI:1921382]		Q9DBU5	-5.4	4.2E-04	5.1	3.6E-02	-0.8	7.2E-01	0.1	9.5E-01
ENSMUST00000129041				-1.9	6.3E-02	-1.4	2.4E-01	0.0	9.8E-01	-0.4	7.2E-01
ENSMUST00000161861	FYVE, RhoGEF and PH domain containing 4 [Source:MGI Symbol;Acc:MGI:2183747]		Q91ZT5	-2.4	6.8E-05	-6.4	9.3E-04	1.2	2.4E-02	0.2	8.7E-01
ENSMUST00000161869	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Source:MGI Symbol;Acc:MGI:1298224]	F6TL71		-3.1	3.2E-02	6.4	1.5E-04	-1.8	1.4E-01	0.1	9.0E-01
ENSMUST00000161870	GLI pathogenesis-related 1 (glioma) [Source:MGI Symbol;Acc:MGI:1920940]	G3UYI2		-6.8	6.1E-04	3.4	7.2E-03	0.5	5.5E-01	-0.7	3.5E-01
ENSMUST00000161880	cornichon homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1920228]	Q9D6E1		5.0	5.8E-03	5.6	1.4E-03	-1.4	3.2E-01	0.0	1.0E+00
ENSMUST00000161883	syndecan 1 [Source:MGI Symbol;Acc:MGI:1349162]	E0CYT6		5.9	8.9E-03	-3.9	8.8E-02	1.0	3.4E-01	0.1	9.7E-01
ENSMUST00000161887	ubiquitin-like 5 [Source:MGI Symbol;Acc:MGI:1913427]	E0CYW1		-7.4	6.4E-03	3.1	3.9E-03	-0.6	3.9E-01	0.6	3.5E-01
ENSMUST00000161892	single-pass membrane protein with aspartate rich tail 1 [Source:MGI Symbol;Acc:MGI:1916279]	E0CXP9		-4.1	5.1E-03	5.2	6.5E-04	-1.5	2.1E-01	0.5	4.1E-01
ENSMUST00000161904	zinc finger protein 27 [Source:MGI Symbol;Acc:MGI:99174]		P10077	5.1	5.3E-04	4.7	1.1E-04	-0.3	6.9E-01	-0.4	4.0E-01
ENSMUST00000161908	SCY1-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1921385]		Q9DBQ7	-6.0	1.3E-03	7.1	1.6E-04	-0.6	6.2E-01	0.3	6.8E-01
ENSMUST00000161918	RIKEN cDNA 4933434E20 gene [Source:MGI Symbol;Acc:MGI:1914027]	E0CYZ4		-4.1	1.1E-02	3.6	2.5E-02	0.2	8.8E-01	1.0	3.1E-01
ENSMUST00000161937	von Willebrand factor C domain-containing protein 2-like [Source:MGI Symbol;Acc:MGI:2444069]		Q505H4	5.9	1.8E-02	2.0	3.0E-01	-2.2	2.6E-01	1.7	2.2E-01
ENSMUST00000161938	phosphatidylinositol transfer protein, membrane-associated 2 [Source:MGI Symbol;Acc:MGI:1336192]		Q6ZPQ6	6.5	2.2E-05	4.0	3.3E-04	-0.4	5.1E-01	1.0	7.1E-02
ENSMUST00000161949	phosphoprotein associated with glycosphingolipid microdomains 1 [Source:MGI Symbol;Acc:MGI:2443160]	A6H659	Q3U1F9	-2.4	2.1E-03	6.0	9.0E-05	-3.1	1.3E-02	-0.6	2.6E-01
ENSMUST00000161954	NCK-associated protein 5 [Source:MGI Symbol;Acc:MGI:2686394]	Q6NZK2		7.8	2.7E-02	2.8	8.6E-02	1.9	1.7E-01	-4.5	9.2E-03
ENSMUST00000161978	fasciculation and elongation protein zeta 1 (zygin I) [Source:MGI Symbol;Acc:MGI:2670976]	F7BWM9		7.3	6.5E-05	-5.6	1.3E-02	-0.3	6.2E-01	1.3	4.7E-01
ENSMUST00000129094				1.0	2.4E-01	1.5	1.6E-01	-0.2	7.8E-01	-0.7	4.2E-01
ENSMUST00000129095				0.0	9.9E-01	-0.3	8.6E-01	0.5	6.1E-01	0.7	5.8E-01
ENSMUST00000129096	mitogen-activated protein kinase 13 [Source:MGI Symbol;Acc:MGI:1346864]	D6RG58		2.2	3.7E-01	3.7	2.7E-01	1.4	6.4E-01	0.0	9.8E-01
ENSMUST00000161987	apoptotic peptidase activating factor 1 [Source:MGI Symbol;Acc:MGI:1306796]	Q80VR5		5.1	9.3E-06	5.0	4.0E-04	-0.6	5.4E-01	0.1	8.1E-01
ENSMUST00000162001	interferon regulatory factor 8 [Source:MGI Symbol;Acc:MGI:96395]	Q544J7	P23611	6.5	8.7E-04	4.9	1.1E-03	-1.7	1.6E-01	-0.4	5.5E-01
ENSMUST00000162003	mitochondrial fission factor [Source:MGI Symbol;Acc:MGI:1922984]	E0CYB9		-4.5	7.5E-03	5.8	1.1E-03	-0.1	9.2E-01	0.1	8.9E-01
ENSMUST00000162004	Hermansky-Pudlak syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:2177763]			-3.8	7.6E-03	-3.2	2.2E-02	0.0	9.7E-01	-0.7	5.8E-01
ENSMUST00000162022	GLIS family zinc finger 3 [Source:MGI Symbol;Acc:MGI:2444289]	Q0GE24		3.4	3.8E-05	6.8	1.2E-06	-0.5	4.2E-01	0.1	7.2E-01
ENSMUST00000129113	Rho guanine nucleotide exchange factor (GEF) 11 [Source:MGI Symbol;Acc:MGI:2441869]	E9Q0A3		0.6	6.6E-01	3.5	1.0E-01	2.2	2.0E-01	-0.7	6.7E-01
ENSMUST00000129115	Hus1 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1277962]		Q8BQY8	1.9	3.2E-01	5.2	7.6E-02	1.9	4.4E-01	-1.3	4.5E-01
ENSMUST00000162031	thioredoxin domain containing 9 [Source:MGI Symbol;Acc:MGI:2138153]		Q9CQ79	-1.7	1.2E-02	-2.0	1.3E-01	1.3	7.8E-02	-0.6	6.7E-01
ENSMUST00000129121				0.9	4.3E-01	2.5	1.1E-01	0.6	6.8E-01	-1.1	3.1E-01
ENSMUST00000162034	UMAP1-MVP12 associated (UMA) domain containing 1 [Source:MGI Symbol;Acc:MGI:3840148]	E0CYC9		-3.7	1.6E-03	3.9	1.8E-04	-1.0	1.6E-01	-0.9	8.8E-02
ENSMUST00000162038	RIKEN cDNA A630001G21 gene [Source:MGI Symbol;Acc:MGI:2443131]	Q8C9T1		-3.5	2.0E-03	4.0	9.4E-03	-1.7	2.0E-01	-1.1	2.3E-01
ENSMUST00000129137	hnRNP-associated with lethal yellow [Source:MGI Symbol;Acc:MGI:97850]	A2AU61		-3.2	2.7E-01	3.4	4.7E-01	6.5	8.2E-02	-0.1	9.9E-01
ENSMUST00000129140				-1.0	5.7E-01	-0.8	7.4E-01	0.1	9.5E-01	-0.1	9.7E-01
ENSMUST00000129145				-0.6	5.8E-01	1.0	4.5E-01	0.6	5.6E-01	-0.9	4.2E-01
ENSMUST00000162041	GRIP and coiled-coil domain containing 2 [Source:MGI Symbol;Acc:MGI:1917547]	E9PWI6		-4.6	8.3E-03	5.9	1.3E-04	0.3	6.9E-01	1.3	3.7E-02
ENSMUST00000129152				1.5	4.0E-01	-1.1	5.8E-01	-1.7	3.0E-01	0.9	6.4E-01
ENSMUST00000129153				1.0	3.6E-01	1.3	3.9E-01	0.4	7.1E-01	0.2	8.9E-01
ENSMUST00000162046	vomeronasal 2, receptor 25 [Source:MGI Symbol;Acc:MGI:3644645]	W4VSP2		6.2	1.0E-04	4.3	1.4E-02	-2.1	2.3E-01	1.4	1.9E-01
ENSMUST00000162049	solute carrier family 4 (anion exchanger), member 8 [Source:MGI Symbol;Acc:MGI:1928745]		Q8JZR6	4.4	5.3E-03	4.6	4.3E-03	0.1	9.5E-01	0.2	7.7E-01
ENSMUST00000129162	membrane magnesium transporter 2 [Source:MGI Symbol;Acc:MGI:2448491]		Q8R3L0	-0.4	5.6E-01	0.1	8.4E-01	0.0	9.9E-01	-0.5	4.7E-01
ENSMUST00000162053	phosphoserine aminotransferase 1 [Source:MGI Symbol;Acc:MGI:2183441]	Q3U6K9		6.5	7.4E-04	2.0	1.8E-02	-0.6	3.3E-01	-0.1	9.0E-01
ENSMUST00000129167				1.3	3.1E-01	-0.3	8.4E-01	-1.4	2.4E-01	0.2	8.8E-01
ENSMUST00000162054	zinc finger and AT hook domain containing [Source:MGI Symbol;Acc:MGI:2681865]		Q7TS63	-1.2	3.4E-02	3.0	1.1E-02	0.5	5.9E-01	0.2	8.0E-01
ENSMUST00000162069	PAXIP1 associated glutamate rich protein 1A [Source:MGI Symbol;Acc:MGI:1914528]	F6V0H0		-5.4	2.6E-03	2.1	3.5E-02	-1.0	2.1E-01	-0.4	5.6E-01
ENSMUST00000162075	thioredoxin domain containing 5 [Source:MGI Symbol;Acc:MGI:2145316]			8.1	3.2E-05	-5.3	2.9E-03	0.9	1.1E-01	0.6	6.6E-01
ENSMUST00000162084	H1 histone family, member O, oocyte-specific [Source:MGI Symbol;Acc:MGI:2176207]	E0CYL2		6.9	2.5E-03	4.0	1.4E-02	0.5	6.8E-01	0.4	6.6E-01
ENSMUST00000129178				1.9	1.8E-01	2.1	2.2E-01	0.1	9.2E-01	0.0	1.0E+00
ENSMUST00000129181				-0.1	8.8E-01	0.7	3.1E-01	0.0	9.6E-01	-0.8	2.1E-01
ENSMUST00000129183				3.7	7.6E-02	7.2	1.3E-02	1.1	6.5E-01	-2.4	1.0E-01
ENSMUST00000162087	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	Q3TDW1	P97808	-12.0	3.9E-07	1.6	1.5E-01	-0.6	4.8E-01	1.0	2.9E-01
ENSMUST00000129187	ATPase, class I, type 8B, member 4 [Source:MGI Symbol;Acc:MGI:1859664]	A2ANX2		1.2	2.4E-01	-0.4	7.1E-01	-1.7	9.7E-02	-0.1	9.6E-01
ENSMUST00000162114	RIKEN cDNA 4933434E20 gene [Source:MGI Symbol;Acc:MGI:1914027]		Q8R092	2.8	2.2E-04	-2.7	7.4E-02	0.3	7.7E-01	-1.1	4.7E-01
ENSMUST00000129193	golgi autoantigen, golgin subfamily a, 2 [Source:MGI Symbol;Acc:MGI:2139395]	A2AN48		0.9	6.0E-01	1.2	5.9E-01	0.0	9.9E-01	-0.3	8.8E-01
ENSMUST00000162150	plakophilin 2 [Source:MGI Symbol;Acc:MGI:1914701]	E0CX59		6.9	2.5E-04	-4.1	2.1E-02	0.2	7.6E-01	0.1	9.6E-01
ENSMUST00000162161	serglycin [Source:MGI Symbol;Acc:MGI:97756]		P13609	-12.0	4.8E-03	5.9	2.8E-04	0.2	8.7E-01	1.3	5.3E-02
ENSMUST00000129204				-1.4	1.5E-01	-0.7	5.9E-01	0.4	6.6E-01	-0.4	7.1E-01
ENSMUST00000162173	zinc finger and AT hook domain containing [Source:MGI Symbol;Acc:MGI:2681865]	E0CX30		6.3	1.3E-04	-0.8	3.8E-01	0.6	3.7E-01	-1.4	1.7E-01
ENSMUST00000162175	exocyst complex component 5 [Source:MGI Symbol;Acc:MGI:2145645]		Q3TPX4	-5.0	1.7E-03	3.9	1.0E-03	-3.0	1.5E-02	-1.4	6.9E-02
ENSMUST00000129223	Rap guanine nucleotide exchange factor (GEF) 3 [Source:MGI Symbol;Acc:MGI:2441741]		Q8VCC8	3.5	1.2E-01	2.9	4.5E-01	2.2	4.7E-01	2.8	3.6E-01
ENSMUST00000162178	cytochrome b5 reductase 3 [Source:MGI Symbol;Acc:MGI:94893]	F2Z456		5.8	4.6E-06	0.0	9.9E-01	3.4	3.8E-02	-2.3	2.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000162184	RAB6A GEF complex partner 1 [Source:MGI Symbol;Acc:MGI:1924893]		Q69ZJ7	7.2	2.3E-04	-1.1	4.3E-01	0.9	3.1E-01	-1.5	3.3E-01
ENSMUST00000129239				-2.2	8.6E-02	-2.9	1.2E-01	0.0	9.7E-01	0.8	6.6E-01
ENSMUST00000162187	RIKEN cDNA 4933406M09 gene [Source:MGI Symbol;Acc:MGI:3045320]	G3XA12		4.6	2.5E-03	3.5	3.4E-03	-1.3	1.7E-01	-0.1	8.9E-01
ENSMUST00000162202	thymocyte selection associated [Source:MGI Symbol;Acc:MGI:2443552]	E0CY68		5.8	6.3E-04	-2.2	8.6E-02	-0.3	6.5E-01	-1.0	4.2E-01
ENSMUST00000162221	potassium channel, subfamily K, member 13 [Source:MGI Symbol;Acc:MGI:2384976]	E0CX83		7.0	9.0E-03	5.4	2.1E-05	0.6	3.6E-01	0.1	8.1E-01
ENSMUST00000129249	repair cross-complementing rodent repair deficiency, complementation group 2 [Source:MGI Symbol;Acc:MG	F6YA33		2.9	2.8E-01	3.8	3.6E-01	2.6	4.7E-01	1.7	5.3E-01
ENSMUST00000129254	small ArfGAP 1 [Source:MGI Symbol;Acc:MGI:2138261]	D3YVX4		-0.3	9.1E-01	-3.8	3.0E-01	-3.9	7.4E-02	-0.5	9.0E-01
ENSMUST00000129256	vacuolar protein sorting 53 (yeast) [Source:MGI Symbol;Acc:MGI:1915549]	E9Q124		-1.3	6.2E-02	0.2	7.7E-01	0.8	2.4E-01	-0.8	3.0E-01
ENSMUST00000162226	zinc finger and BTB domain containing 37 [Source:MGI Symbol;Acc:MGI:2444467]	Q8C3U9		3.9	6.9E-05	3.9	9.8E-05	-0.5	3.8E-01	0.6	1.7E-01
ENSMUST00000162234	SCY1-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1921385]		Q9DBQ7	-3.8	8.2E-03	8.3	1.3E-05	0.1	9.4E-01	-0.2	6.1E-01
ENSMUST00000129265				-1.0	2.6E-01	0.4	6.9E-01	0.6	4.1E-01	-0.7	4.6E-01
ENSMUST00000129267	ceramide synthase 2 [Source:MGI Symbol;Acc:MGI:1924143]	D3YTM0		0.3	7.5E-01	-0.1	9.3E-01	0.4	7.2E-01	0.9	5.3E-01
ENSMUST00000162244	cleavage and polyadenylation specific factor 4 [Source:MGI Symbol;Acc:MGI:1861602]	B2LVG6		-3.4	1.1E-02	-5.6	2.5E-04	-1.2	1.1E-02	-0.7	5.4E-01
ENSMUST00000129270				-0.4	5.9E-01	1.2	2.6E-01	1.9	4.4E-02	0.3	7.7E-01
ENSMUST00000162250	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	F6TWM7		-9.7	2.6E-05	4.4	9.0E-05	-1.5	4.1E-02	0.5	2.9E-01
ENSMUST00000129273	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B [Source:MGI Symbol;Acc:MGI:1914171]	A0A0G2JGW4		-2.6	7.2E-02	-0.7	6.4E-01	-0.4	6.9E-01	-2.3	1.6E-01
ENSMUST00000162252	galactosidase, beta 1-like 2 [Source:MGI Symbol;Acc:MGI:2388283]	E0CY86		7.6	3.8E-05	3.8	8.4E-03	-2.1	1.3E-01	0.2	8.0E-01
ENSMUST00000162257	RB1-inducible coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1341850]	F7CCJ3		-5.7	6.3E-04	6.1	3.4E-03	-2.3	2.1E-01	0.2	7.9E-01
ENSMUST00000162273	catenin (cadherin associated protein), alpha 2 [Source:MGI Symbol;Acc:MGI:88275]	Q8BS72		9.9	9.1E-06	-3.5	1.1E-02	0.1	8.3E-01	-1.3	3.0E-01
ENSMUST00000162277	thioredoxin-related transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:1919986]	F6V084		-4.9	2.9E-02	6.0	2.0E-02	-1.4	5.5E-01	0.0	9.9E-01
ENSMUST00000129293				-2.6	6.1E-02	-1.1	5.2E-01	0.5	6.4E-01	-1.0	5.7E-01
ENSMUST00000129294				-1.7	1.5E-01	-1.9	2.8E-01	0.0	9.8E-01	0.1	9.4E-01
ENSMUST00000129295				1.8	1.6E-01	1.0	4.0E-01	-2.1	8.2E-02	-1.3	2.8E-01
ENSMUST00000162280	lipoma HMGIC fusion partner-like protein 4 [Source:MGI Symbol;Acc:MGI:3057108]		Q5U4E0	9.5	3.5E-05	-2.2	9.4E-02	1.1	1.9E-01	-0.6	6.3E-01
ENSMUST00000162293	glutamate receptor interacting protein 2 [Source:MGI Symbol;Acc:MGI:2681173]	E0CXE0		5.0	1.1E-05	3.0	2.9E-03	0.0	1.0E+00	0.1	8.1E-01
ENSMUST00000162295	calsyntenin 2 [Source:MGI Symbol;Acc:MGI:1929897]		Q9ER65	10.6	6.2E-06	-1.1	5.5E-01	2.4	6.1E-02	-0.3	8.6E-01
ENSMUST00000162303	ubiquitin-like 5 [Source:MGI Symbol;Acc:MGI:1913427]		Q9EPV8	-1.9	8.0E-03	-1.6	3.1E-01	0.9	3.8E-01	-0.7	6.5E-01
ENSMUST00000129305	glycerol-3-phosphate dehydrogenase 1-like [Source:MGI Symbol;Acc:MGI:1289257]	D3Z0L6		0.7	7.9E-01	-2.5	5.5E-01	-0.8	7.3E-01	2.4	5.6E-01
ENSMUST00000129307				1.4	2.0E-01	1.5	3.4E-01	0.0	9.7E-01	-0.1	9.5E-01
ENSMUST00000129308	RFad1, flavin adenine dinucleotide synthetase, homolog (yeast) [Source:MGI Symbol;Acc:MGI:2443030]		Q8R123	-2.9	6.7E-02	-1.0	5.7E-01	1.1	3.8E-01	-0.7	6.8E-01
ENSMUST00000162316	apoptogenic, mitochondrial 1 [Source:MGI Symbol;Acc:MGI:1915270]	E9Q6C3		3.8	4.7E-04	3.6	1.3E-03	0.0	9.5E-01	0.0	1.0E+00
ENSMUST00000162335	ring finger protein 146 [Source:MGI Symbol;Acc:MGI:1915281]		Q9CZW6	-4.0	3.5E-03	3.6	3.1E-04	-0.4	4.8E-01	-0.5	2.8E-01
ENSMUST00000129312				1.6	1.0E-01	2.5	5.9E-02	0.8	4.1E-01	0.0	9.7E-01
ENSMUST00000129314				-1.5	3.2E-01	-2.8	2.4E-01	0.9	4.9E-01	2.2	3.4E-01
ENSMUST00000162342	adaptor-related protein complex AP-1, sigma 3 [Source:MGI Symbol;Acc:MGI:1891304]		Q7TN05	6.7	7.8E-06	4.1	3.0E-04	0.1	8.2E-01	-0.3	5.6E-01
ENSMUST00000129324	uncoupling protein 2 (mitochondrial, proton carrier) [Source:MGI Symbol;Acc:MGI:109354]	D3YZE5		-0.9	4.6E-01	1.1	4.8E-01	0.1	9.6E-01	-2.0	1.6E-01
ENSMUST00000162354	diacylglycerol O-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:1333825]	F6UUI9		-4.8	1.2E-02	7.5	4.6E-04	0.0	9.7E-01	0.6	4.0E-01
ENSMUST00000162360	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 [Source:MGI Symbol;Acc:MGI:1927558	M0QWW1		-4.9	2.1E-04	2.9	3.9E-03	1.2	9.5E-02	-0.3	6.5E-01
ENSMUST00000129342	SKH domain containing, RNA binding, signal transduction associated 1 [Source:MGI Symbol;Acc:MGI:893579		Q60749	-1.8	1.9E-01	-3.3	9.9E-02	-1.0	3.4E-01	0.5	7.9E-01
ENSMUST00000162368	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]	F7CBK9		-3.5	3.6E-03	1.2	3.1E-01	-4.1	9.0E-03	-0.2	8.4E-01
ENSMUST00000162374	predicted gene 28374 [Source:MGI Symbol;Acc:MGI:5579080]	F6SG70		6.6	1.4E-04	-6.4	1.5E-02	-0.7	4.0E-01	0.1	9.5E-01
ENSMUST00000129349				-0.1	8.9E-01	-0.2	8.0E-01	-0.3	6.0E-01	-0.2	8.1E-01
ENSMUST00000129352	DEK oncogene (DNA binding) [Source:MGI Symbol;Acc:MGI:1926209]	D3YVJ6		0.0	9.9E-01	1.9	5.3E-01	0.7	7.7E-01	-1.2	6.6E-01
ENSMUST00000162376	coiled-coil domain containing 127 [Source:MGI Symbol;Acc:MGI:1914683]	E0CYX9		-4.8	1.4E-03	6.5	3.2E-04	-1.2	3.7E-01	0.8	2.7E-01
ENSMUST00000129376	RIKEN cDNA 2700049A03 gene [Source:MGI Symbol;Acc:MGI:1924217]	F7BDN4		-1.3	2.4E-01	0.5	7.0E-01	0.4	6.9E-01	-1.4	2.4E-01
ENSMUST00000129380				-0.6	7.2E-01	-2.5	2.4E-01	-1.3	4.1E-01	0.6	7.7E-01
ENSMUST00000129383				-0.2	7.9E-01	0.9	2.8E-01	-0.5	4.7E-01	-1.7	7.9E-02
ENSMUST00000162387	predicted gene, 21671 [Source:MGI Symbol;Acc:MGI:5435026]	G3UY31		6.4	3.9E-04	4.1	2.1E-03	0.0	9.7E-01	0.2	7.4E-01
ENSMUST00000162409	formin binding protein 1-like [Source:MGI Symbol;Acc:MGI:1925642]	E9PUK3		1.7	9.7E-03	7.6	1.9E-04	-0.7	6.4E-01	-0.3	7.0E-01
ENSMUST00000129393				-3.1	3.9E-02	-1.3	5.7E-01	1.9	1.9E-01	0.1	9.4E-01
ENSMUST00000162412	phosphodiesterase 8B [Source:MGI Symbol;Acc:MGI:2443999]	E9PXX4		5.3	4.3E-04	-2.6	1.9E-01	0.8	4.5E-01	0.0	9.9E-01
ENSMUST00000129403				3.3	9.1E-02	5.8	1.1E-02	-0.5	8.2E-01	-2.9	4.5E-02
ENSMUST00000162413	transformer 2 beta homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:106016]			-5.7	2.7E-03	5.6	1.5E-03	-0.3	8.2E-01	0.1	8.4E-01
ENSMUST00000129411	atrophin 1 [Source:MGI Symbol;Acc:MGI:104725]		O35126	-3.1	1.8E-01	-3.3	2.2E-01	0.1	9.6E-01	0.2	9.4E-01
ENSMUST00000162415	eukaryotic translation initiation factor 4, gamma 2 [Source:MGI Symbol;Acc:MGI:109207]	G3XA17		-4.6	6.5E-06	-4.0	7.1E-03	-0.1	8.5E-01	2.2	8.7E-02
ENSMUST00000162420	paired like homeodomain factor 1 [Source:MGI Symbol;Acc:MGI:109330]	E0CZF7		11.2	8.8E-05	2.1	1.8E-03	-1.1	3.7E-02	-0.2	5.4E-01
ENSMUST00000162421	RIKEN cDNA C130026I21 gene [Source:MGI Symbol;Acc:MGI:3612702]	E0CXL1		3.3	1.2E-02	5.4	1.2E-04	-0.9	3.1E-01	0.7	2.3E-01
ENSMUST00000162422	host cell factor C2 [Source:MGI Symbol;Acc:MGI:1915183]	F6T0G2		-2.5	2.2E-02	6.2	1.2E-04	-1.0	3.5E-01	-0.6	3.2E-01
ENSMUST00000162424	pannexin 2 [Source:MGI Symbol;Acc:MGI:1890615]		Q6IMP4	8.4	1.1E-04	-1.8	8.3E-02	-0.1	8.2E-01	-0.7	5.1E-01
ENSMUST00000162425	guanine nucleotide binding protein (G protein), gamma 2 [Source:MGI Symbol;Acc:MGI:102705]		P63213	-7.6	5.0E-05	6.3	4.2E-04	-0.1	9.2E-01	-0.5	4.5E-01
ENSMUST00000162431	RIKEN cDNA A930017K11 gene [Source:MGI Symbol;Acc:MGI:2442713]	E0CXQ2		7.9	4.0E-05	6.9	1.4E-04	-0.5	7.0E-01	-0.6	3.2E-01
ENSMUST00000129447				0.3	6.3E-01	0.8	3.0E-01	0.2	7.0E-01	-0.3	6.5E-01
ENSMUST00000162443	complement component 1, s subcomponent 1 [Source:MGI Symbol;Acc:MGI:1355312]	E9Q6C2		4.6	2.4E-03	-0.7	2.2E-01	1.3	4.0E-03	0.1	8.5E-01
ENSMUST00000162461	RAD52 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:101949]		P43352	-6.6	1.9E-05	3.1	3.0E-03	-0.3	6.1E-01	0.3	6.1E-01
ENSMUST00000162489	T cell acute lymphocytic leukemia 1 [Source:MGI Symbol;Acc:MGI:98480]	Q3TZH7	P22091	6.6	2.7E-03	7.1	6.0E-04	-0.7	6.5E-01	-1.2	1.6E-01
ENSMUST00000129456	F-box protein 30 [Source:MGI Symbol;Acc:MGI:1919115]		Q8BJL1	1.1	7.5E-02	2.5	7.1E-03	1.0	1.4E-01	-0.5	4.3E-01
ENSMUST00000162494	cyclin-dependent kinase 8 [Source:MGI Symbol;Acc:MGI:1196224]	E0CZC3		8.7	2.4E-03	-1.7	1.1E-01	1.0	1.1E-01	-0.6	5.7E-01
ENSMUST00000162505	TATA box binding protein [Source:MGI Symbol;Acc:MGI:101838]	Q6RI65	P29037	4.0	2.9E-05	5.7	3.0E-03	1.5	2.9E-01	-0.8	3.6E-01
ENSMUST00000162508	GLI pathogenesis-related 1 (glioma) [Source:MGI Symbol;Acc:MGI:1920940]	Q4QQK5	Q9CWG1	-2.6	2.2E-02	6.1	8.7E-04	-0.7	6.2E-01	0.2	7.7E-01
ENSMUST00000129467	tumor necrosis factor, alpha-induced protein 2 [Source:MGI Symbol;Acc:MGI:104960]	G3XA62		0.0	9.9E-01	0.8	6.9E-01	0.6	6.5E-01	-0.1	9.5E-01
ENSMUST00000162514	cytochrome P450, family 2, subfamily j, polypeptide 7 [Source:MGI Symbol;Acc:MGI:2449816]			6.0	1.4E-04	-5.5	2.6E-03	0.5	3.7E-01	-0.7	6.5E-01
ENSMUST00000129473	olute carrier family 16 (monocarboxylic acid transporters), member 3 [Source:MGI Symbol;Acc:MGI:1933438	B1ATM2		3.9	4.0E-02	0.1	9.5E-01	-2.6	1.5E-01	1.2	4.5E-01
ENSMUST00000162519	neurexophilin and PC-esterase domain family, member 5 [Source:MGI Symbol;Acc:MGI:3584036]	Q3TBA1		8.6	2.2E-05	0.2	8.9E-01	1.8	1.6E-01	-2.6	1.5E-01
ENSMUST00000129488	AT rich interactive domain 4B (RBP1-like) [Source:MGI Symbol;Acc:MGI:2137512]	Z4YMH1		3.4	9.0E-02	3.6	1.1E-01	0.0	9.9E-01	-0.2	9.2E-01
ENSMUST00000129489	family with sequence similarity 188, member A [Source:MGI Symbol;Acc:MGI:1914210]	D6RG90		2.0	2.5E-01	0.7	7.3E-01	-1.7	3.1E-01	-0.4	8.5E-01
ENSMUST00000162521	thromboxane A synthase 1, platelet [Source:MGI Symbol;Acc:MGI:98497]	Q3TRY5		6.1	9.3E-05	4.9	2.2E-03	-1.6	2.3E-01	0.0	9.8E-01
ENSMUST00000162524	DIP2 disco-interacting protein 2 homolog A (Drosophila) [Source:MGI Symbol;Acc:MGI:2385920]	F7BCF6		5.8	2.3E-03	-6.7	3.2E-04	0.7	1.2E-01	-0.7	6.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000162528	Kv channel-interacting protein 2 [Source:MGI Symbol;Acc:MGI:2135916]	Q3YAB3		3.6	1.6E-02	1.9	1.1E-01	-0.7	4.8E-01	1.3	1.9E-01
ENSMUST00000129495				-3.0	5.2E-02	-3.6	4.9E-02	-1.5	1.1E-01	-0.9	6.1E-01
ENSMUST00000162541	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]	F7CZC4		-3.6	1.8E-02	0.1	9.0E-01	1.6	8.8E-02	-1.5	2.0E-01
ENSMUST00000162553	MOB family member 4, phocein [Source:MGI Symbol;Acc:MGI:104899]	E0CYJ0		-3.8	1.3E-03	5.5	3.5E-02	-0.7	7.6E-01	-0.9	5.7E-01
ENSMUST00000162554	tetratricopeptide repeat domain 26 [Source:MGI Symbol;Acc:MGI:2444853]		Q8BS45	3.7	1.5E-02	5.9	3.5E-04	-1.5	2.2E-01	0.1	9.4E-01
ENSMUST00000129510				1.2	5.8E-01	3.1	1.6E-01	-0.7	7.3E-01	-2.6	1.9E-01
ENSMUST00000129515	transmembrane protein 234 [Source:MGI Symbol;Acc:MGI:1924049]	D6RDC0		3.8	1.9E-01	3.3	4.0E-01	0.0	1.0E+00	0.4	8.9E-01
ENSMUST00000162569	vesicle transport through interaction with t-SNAREs 1B [Source:MGI Symbol;Acc:MGI:1855688]	F6UHS3		-7.3	4.1E-06	6.0	1.2E-04	0.9	3.2E-01	-0.2	6.5E-01
ENSMUST00000129532				0.9	2.3E-01	1.6	7.4E-02	-0.5	4.9E-01	-1.2	1.2E-01
ENSMUST00000162581	WNK lysine deficient protein kinase 2 [Source:MGI Symbol;Acc:MGI:1922857]	E0CZE3		6.2	1.1E-04	-9.9	3.1E-04	-1.4	1.7E-02	-0.4	8.4E-01
ENSMUST00000162583	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]		Q08122	-8.9	1.7E-02	-1.6	2.2E-01	1.0	2.0E-01	0.5	6.9E-01
ENSMUST00000162585	complement component 6 [Source:MGI Symbol;Acc:MGI:88233]	Q91X70		7.2	7.4E-06	8.0	3.6E-04	1.1	4.3E-01	0.5	4.5E-01
ENSMUST00000162594	BUD31 homolog (yeast) [Source:MGI Symbol;Acc:MGI:2141291]	E0CX20		-7.5	1.3E-05	-1.6	1.8E-01	-0.1	8.7E-01	-0.8	4.6E-01
ENSMUST00000129543				-0.9	3.8E-01	0.4	7.3E-01	0.2	8.1E-01	-1.1	3.4E-01
ENSMUST00000162606	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:97502]	E0CYV0		-4.9	1.4E-04	7.0	4.6E-07	0.2	6.8E-01	0.2	5.7E-01
ENSMUST00000162642	phosphatidylinositol glycan anchor biosynthesis, class K [Source:MGI Symbol;Acc:MGI:1913863]	Q8BXX3		5.8	1.6E-04	5.5	7.7E-04	0.2	8.4E-01	-0.3	6.2E-01
ENSMUST00000129552	family with sequence similarity 175, member B [Source:MGI Symbol;Acc:MGI:1926116]	D6RJ39		-2.6	3.1E-01	-6.8	3.6E-02	-5.2	8.1E-03	-1.1	7.4E-01
ENSMUST00000162645	zinc finger, MIZ-type containing 1 [Source:MGI Symbol;Acc:MGI:3040693]		Q6P1E1	-2.9	1.9E-04	6.5	4.7E-04	-1.8	2.2E-01	1.1	1.6E-01
ENSMUST00000162646	NCK-associated protein 5 [Source:MGI Symbol;Acc:MGI:2686394]	E0CYS4		6.4	2.7E-04	3.2	5.9E-04	0.1	8.0E-01	-0.2	6.6E-01
ENSMUST00000129564	DENN/MADD domain containing 4B [Source:MGI Symbol;Acc:MGI:2446201]		Q3U1Y4	0.9	6.4E-01	3.8	4.5E-02	-1.5	3.8E-01	-4.4	2.2E-02
ENSMUST00000162655	centrosomal protein 63 [Source:MGI Symbol;Acc:MGI:2158560]		Q3UPP8	-6.5	8.1E-04	-2.0	1.6E-01	1.3	1.4E-01	-1.6	2.7E-01
ENSMUST00000129566	RIKEN cDNA 4933408B17 gene [Source:MGI Symbol;Acc:MGI:3045347]	D6RFA1		-0.3	9.0E-01	-2.7	3.2E-01	-2.7	1.8E-01	-0.3	9.0E-01
ENSMUST00000162681	peptidylglycine alpha-amidating monooxygenase [Source:MGI Symbol;Acc:MGI:97475]	F7D4K4		-5.6	7.2E-04	6.5	6.0E-04	-0.6	6.5E-01	-0.2	7.5E-01
ENSMUST00000162694	polymerase (RNA) mitochondrial (DNA directed) [Source:MGI Symbol;Acc:MGI:1915843]	E0CY15		4.2	7.0E-03	5.3	8.4E-04	-0.4	7.2E-01	0.7	3.4E-01
ENSMUST00000162695	sine oculis-related homeobox 3 [Source:MGI Symbol;Acc:MGI:102764]	Q52KB8		10.3	3.6E-05	-4.0	9.3E-03	0.7	2.3E-01	0.4	7.5E-01
ENSMUST00000162708	unc-93 homolog B1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1859307]	E9PYK0		-7.6	1.4E-04	-2.7	3.9E-04	-1.4	1.0E-03	-0.5	3.1E-01
ENSMUST00000129581				2.1	9.0E-02	2.9	4.8E-02	-0.1	9.4E-01	-0.9	4.1E-01
ENSMUST00000129582				1.8	2.2E-01	1.7	4.2E-01	0.3	8.5E-01	0.4	7.8E-01
ENSMUST00000129585	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Source:MGI Symbol;Acc:MGI:105037]	B1ARB9		-3.1	1.4E-01	-4.2	3.9E-02	-3.0	2.2E-02	-1.9	4.1E-01
ENSMUST00000162725	aarF domain containing kinase 3 [Source:MGI Symbol;Acc:MGI:1914676]	E0CXT4		5.9	3.4E-03	-4.8	1.1E-01	3.2	1.7E-02	-0.1	9.7E-01
ENSMUST00000162726	zinc finger, HIT domain containing 2 [Source:MGI Symbol;Acc:MGI:1352481]		Q9QY66	-2.8	2.5E-03	5.5	1.8E-03	0.7	5.8E-01	-0.5	4.9E-01
ENSMUST00000162735	tandem C2 domains, nuclear [Source:MGI Symbol;Acc:MGI:1921663]		Q91XT6	6.2	2.7E-04	0.9	1.1E-01	-0.8	1.1E-01	-0.3	5.2E-01
ENSMUST00000162746	selectin, platelet [Source:MGI Symbol;Acc:MGI:98280]		Q01102	-1.9	6.6E-03	-4.1	1.7E-02	1.0	1.4E-01	-0.3	8.5E-01
ENSMUST00000129595				-2.6	1.2E-01	2.5	1.9E-01	1.6	3.2E-01	-3.5	5.4E-02
ENSMUST00000129599				-2.0	1.3E-01	-0.9	6.2E-01	1.4	3.4E-01	0.3	8.5E-01
ENSMUST00000162752	SH2 domain containing 1B2 [Source:MGI Symbol;Acc:MGI:3622649]	Q45HK4		6.6	1.3E-04	2.1	1.9E-01	-2.7	8.9E-02	-0.9	5.2E-01
ENSMUST00000162759	KIF1 binding protein [Source:MGI Symbol;Acc:MGI:1919570]	E0CXJ9		3.9	1.4E-03	-0.1	9.5E-01	-2.5	6.7E-03	0.7	3.5E-01
ENSMUST00000129604	growth arrest specific 2 [Source:MGI Symbol;Acc:MGI:95657]	D6RDR2		0.1	9.1E-01	2.7	8.9E-02	2.3	1.0E-01	-0.3	7.6E-01
ENSMUST00000162761	carbonic anhydrase 7 [Source:MGI Symbol;Acc:MGI:103100]	G3XA26		5.6	1.5E-03	1.5	9.1E-02	-1.2	1.3E-01	0.0	9.9E-01
ENSMUST00000162772	LIM domain only 3 [Source:MGI Symbol;Acc:MGI:102810]		Q8BZL8	6.9	4.6E-05	6.1	2.5E-03	0.6	7.0E-01	1.2	2.1E-01
ENSMUST00000162787	oxysterol binding protein-like 9 [Source:MGI Symbol;Acc:MGI:1923784]	E9PXZ2		-8.9	1.2E-03	-2.0	5.1E-02	-0.7	2.7E-01	-1.3	2.2E-01
ENSMUST00000162789	vesicle transport through interaction with t-SNAREs 1B [Source:MGI Symbol;Acc:MGI:1855688]	E0CYE5		-6.5	3.4E-03	-4.0	1.1E-03	0.0	9.7E-01	0.6	4.8E-01
ENSMUST00000162792	amylo-1,6-glucosidase, 4-alpha-glucanotransferase [Source:MGI Symbol;Acc:MGI:1924809]	F8VPN4		-8.2	6.4E-05	6.5	5.9E-03	-1.2	5.6E-01	1.7	1.5E-01
ENSMUST00000162795	RB1-inducible coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1341850]	E9PX56		-5.3	8.4E-05	6.4	4.2E-04	-0.6	6.7E-01	-1.0	1.8E-01
ENSMUST00000162811	centrosomal protein 68 [Source:MGI Symbol;Acc:MGI:2667663]	Q3TRP8		4.0	2.9E-03	6.9	7.1E-04	-0.7	6.4E-01	-1.8	4.9E-02
ENSMUST00000129625	DnaJ (Hsp40) homolog, subfamily C, member 12 [Source:MGI Symbol;Acc:MGI:1353428]	D3Z0D9		-0.5	5.7E-01	-2.5	9.1E-02	-1.2	1.8E-01	0.8	5.5E-01
ENSMUST00000129628	ankyrin repeat and SOCS box-containing 6 [Source:MGI Symbol;Acc:MGI:1919573]	A0A0A6YY11		-2.9	8.2E-02	-1.3	3.8E-01	-0.3	7.3E-01	-1.9	2.8E-01
ENSMUST00000162816	runt related transcription factor 2 [Source:MGI Symbol;Acc:MGI:99829]	E0CZC6		4.9	2.7E-04	3.3	7.2E-04	0.1	8.8E-01	-0.1	8.7E-01
ENSMUST00000162819	WD repeat domain 26 [Source:MGI Symbol;Acc:MGI:1923825]		Q8C6G8	-4.3	8.7E-03	-0.5	5.8E-01	-0.8	2.8E-01	-3.1	1.4E-02
ENSMUST00000129635	lipin 2 [Source:MGI Symbol;Acc:MGI:1891341]		Q99PI5	-1.5	5.2E-02	-2.0	6.4E-02	0.2	7.3E-01	0.7	4.7E-01
ENSMUST00000162825	fibronectin type III domain containing 3A [Source:MGI Symbol;Acc:MGI:1196463]	F6TLV3		-5.8	1.6E-02	7.3	2.8E-04	-0.7	6.1E-01	0.7	3.3E-01
ENSMUST00000162830	CUB and Sushi multiple domains 3 [Source:MGI Symbol;Acc:MGI:2386403]		Q80T79	6.9	5.7E-05	6.6	1.2E-03	0.3	8.3E-01	-0.2	8.1E-01
ENSMUST00000162844	complement component 1, s subcomponent 1 [Source:MGI Symbol;Acc:MGI:1355312]	E0CYK5		5.9	4.9E-03	4.9	3.1E-03	-1.0	4.5E-01	0.9	3.0E-01
ENSMUST00000162849	ras responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:2443664]	F6UB40		5.5	2.0E-03	9.1	3.4E-04	0.4	7.9E-01	0.3	6.2E-01
ENSMUST00000162861	zinc finger protein 12 [Source:MGI Symbol;Acc:MGI:99157]	E0CYZ8		5.3	1.5E-03	3.4	1.6E-01	-0.7	7.8E-01	1.2	4.5E-01
ENSMUST00000129662	prickle homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1859635]	Q8BNH2		-4.2	5.3E-02	-1.6	5.8E-01	2.0	3.5E-01	-0.5	8.3E-01
ENSMUST00000129664	SH3 domain and tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGI:2678949]	F6QD49		-2.1	1.2E-01	1.7	1.5E-01	-0.9	3.6E-01	-4.7	4.6E-03
ENSMUST00000162863	mitogen-activated protein kinase 4 [Source:MGI Symbol;Acc:MGI:2444559]	E9PXX5		7.3	1.7E-02	-4.1	9.7E-03	1.0	1.0E-01	1.0	4.3E-01
ENSMUST00000162875	RIKEN cDNA 2010300C02 gene [Source:MGI Symbol;Acc:MGI:1919347]	E9Q3M9		9.1	8.3E-06	-6.1	3.8E-02	0.3	7.9E-01	-0.8	7.8E-01
ENSMUST00000162940	sperm motility kinase 2B [Source:MGI Symbol;Acc:MGI:3037705]		Q9QYZ3	8.7	1.1E-04	5.8	7.7E-04	-0.6	6.4E-01	-0.1	8.4E-01
ENSMUST00000162944	SMC5-SMC6 complex localization factor 1 [Source:MGI Symbol;Acc:MGI:2145448]	Q8C211		5.1	3.8E-04	5.1	5.9E-03	-1.4	3.7E-01	1.3	1.7E-01
ENSMUST00000162945	spermatogenesis associated 13 [Source:MGI Symbol;Acc:MGI:104838]	E0CYU0		-5.6	1.9E-05	3.7	5.9E-04	-0.3	6.1E-01	0.5	4.1E-01
ENSMUST00000129673				-0.5	5.8E-01	1.5	1.6E-01	-0.1	8.7E-01	-2.2	4.2E-02
ENSMUST00000162948	amine oxidase, copper-containing 1 [Source:MGI Symbol;Acc:MGI:1923757]	E9PYN9		7.0	2.0E-02	5.8	6.2E-04	-0.6	6.5E-01	-1.2	9.7E-02
ENSMUST00000162957	transmembrane protein 55b [Source:MGI Symbol;Acc:MGI:2448501]	E0CZ18		-5.4	1.4E-02	2.6	5.0E-02	-0.3	7.7E-01	-0.2	8.7E-01
ENSMUST00000162964	expressed sequence C87414 [Source:MGI Symbol;Acc:MGI:2141341]	E9PWI7		6.9	3.8E-05	6.2	4.4E-04	-0.2	8.9E-01	0.0	9.8E-01
ENSMUST00000129690				0.0	1.0E+00	-2.0	4.8E-01	-2.6	2.2E-01	-0.6	8.6E-01
ENSMUST00000162973	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]		Q08122	-9.6	1.3E-03	-3.3	8.2E-02	-0.2	8.2E-01	-0.1	9.4E-01
ENSMUST00000162986	alkB, alkylation repair homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:2384034]	E0CZH7		4.6	5.1E-04	5.6	2.3E-03	-0.7	6.4E-01	0.4	6.6E-01
ENSMUST00000129718				-0.7	7.5E-01	0.6	7.5E-01	-2.0	2.3E-01	-3.2	1.4E-01
ENSMUST00000129722				1.4	1.3E-01	3.1	7.9E-03	-0.8	3.5E-01	-2.5	1.2E-02
ENSMUST00000162998	predicted gene 7247 [Source:MGI Symbol;Acc:MGI:3643454]	Q6UY52		7.1	1.5E-04	6.5	1.1E-03	-0.7	6.4E-01	0.7	4.1E-01
ENSMUST00000163019	vomeronasal 2, receptor 88 [Source:MGI Symbol;Acc:MGI:1316662]	F6U6R2		9.1	9.5E-05	-4.3	1.2E-01	1.1	3.4E-01	-0.8	7.7E-01
ENSMUST00000129727	low density lipoprotein receptor-related protein 1 [Source:MGI Symbol;Acc:MGI:96828]	F6XU19		1.2	5.2E-01	0.8	7.5E-01	-0.1	9.6E-01	0.2	9.1E-01
ENSMUST00000163031	vesicle transport through interaction with t-SNAREs 1B [Source:MGI Symbol;Acc:MGI:1855688]	F6T4B9		-2.5	7.2E-04	4.1	2.5E-02	0.0	9.8E-01	0.4	7.3E-01
ENSMUST00000129741	DEAH (Asp-Glu-Ala-His) box polypeptide 8 [Source:MGI Symbol;Acc:MGI:1306823]	A2A4N9		2.1	2.3E-01	0.6	7.8E-01	-1.9	2.5E-01	-0.4	8.5E-01
ENSMUST00000129748				1.2	4.6E-02	1.7	3.2E-02	0.8	1.6E-01	0.3	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000163037	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8 [Source:MGI Symbol;Acc:M	F6U6K2		7.9	1.1E-05	-9.1	1.0E-03	1.7	6.5E-03	2.4	2.3E-01
ENSMUST00000163041	plakophilin 3 [Source:MGI Symbol;Acc:MGI:1891830]	E0CY75		5.6	1.8E-02	1.8	3.4E-02	0.3	6.2E-01	0.1	9.2E-01
ENSMUST00000129762				0.4	6.6E-01	1.3	2.5E-01	-0.1	9.4E-01	-1.0	3.6E-01
ENSMUST00000163060	hairless [Source:MGI Symbol;Acc:MGI:96223]	E9PZ81		6.8	1.1E-04	4.9	1.5E-03	-1.4	2.7E-01	0.5	5.0E-01
ENSMUST00000163062	Rho guanine nucleotide exchange factor (GEF) 10 [Source:MGI Symbol;Acc:MGI:2444453]	F7BQE4		4.8	1.5E-02	6.9	1.7E-04	-0.6	6.2E-01	-0.1	8.4E-01
ENSMUST00000163073	FYN binding protein [Source:MGI Symbol;Acc:MGI:1346327]	F6V072		-7.5	2.1E-03	2.8	7.7E-02	0.4	7.7E-01	0.0	1.0E+00
ENSMUST00000163075	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Source:MGI Symbol;Acc:MGI:1298224]		O70161	-8.9	1.6E-04	4.1	1.3E-02	1.1	3.9E-01	0.7	5.0E-01
ENSMUST00000129793				-0.8	2.6E-01	-0.1	9.1E-01	0.1	8.4E-01	-0.6	4.8E-01
ENSMUST00000129794				-1.3	4.1E-01	3.8	1.1E-01	4.1	4.0E-02	-0.9	6.1E-01
ENSMUST00000163079	zinc finger and BTB domain containing 37 [Source:MGI Symbol;Acc:MGI:2444467]	Q8C3U9		-5.4	6.1E-04	6.3	4.9E-05	-2.5	3.0E-02	-0.2	7.1E-01
ENSMUST00000163080	RIKEN cDNA 1110002E22 gene [Source:MGI Symbol;Acc:MGI:1915066]	E0CYV9		9.8	3.4E-06	7.4	2.5E-04	-0.7	6.3E-01	-0.2	8.0E-01
ENSMUST00000163083	cytochrome b5 type A (microsomal) [Source:MGI Symbol;Acc:MGI:1926952]	E0CY88		-5.0	7.4E-05	3.8	2.3E-02	0.6	6.4E-01	-0.6	5.3E-01
ENSMUST00000163085	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:97502]	F7D432		-6.3	3.4E-04	-3.3	1.3E-02	1.9	5.2E-03	-0.7	5.8E-01
ENSMUST00000163095	SMEK homolog 1, suppressor of mek1 (Dictyostelium) [Source:MGI Symbol;Acc:MGI:1915984]	E9Q481		-6.9	7.8E-04	9.7	6.8E-04	-1.0	6.6E-01	0.3	7.2E-01
ENSMUST00000129816				-0.4	6.3E-01	1.4	1.6E-01	-0.1	9.1E-01	-1.9	5.1E-02
ENSMUST00000163116	lymphocyte antigen 6 complex, locus H [Source:MGI Symbol;Acc:MGI:1346030]	Q544M1	Q9WUC3	8.7	9.3E-07	5.8	4.1E-04	-0.9	4.3E-01	0.0	9.9E-01
ENSMUST00000129819	nephronophthisis 3 (adolescent) [Source:MGI Symbol;Acc:MGI:1921275]	H9KV07		3.1	2.7E-01	4.1	2.2E-01	0.5	8.9E-01	-0.6	7.9E-01
ENSMUST00000163118	inter-alpha trypsin inhibitor, heavy chain 1 [Source:MGI Symbol;Acc:MGI:96618]		Q61702	2.9	1.5E-02	4.3	2.3E-04	0.4	5.4E-01	0.1	7.8E-01
ENSMUST00000163119	cullin 3 [Source:MGI Symbol;Acc:MGI:1347360]		Q9JLV5	-3.8	2.1E-03	-5.4	1.1E-03	-0.1	8.9E-01	-0.7	5.8E-01
ENSMUST00000163123	solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:MGI Symbol;Acc:MGI:107956]	Q68FL0		2.0	1.5E-02	-2.8	1.3E-02	0.9	1.2E-01	-2.4	6.3E-02
ENSMUST00000129826				-0.6	5.6E-01	1.4	2.9E-01	0.8	4.9E-01	-1.2	2.6E-01
ENSMUST00000163128	RELT-like 2 [Source:MGI Symbol;Acc:MGI:1918044]	E9Q3X7		4.5	2.3E-02	-2.3	1.1E-01	0.5	5.4E-01	-2.0	2.0E-01
ENSMUST00000163137	EPS8-like 1 [Source:MGI Symbol;Acc:MGI:1914675]	E9Q2P3		7.5	3.1E-05	3.4	8.4E-03	-0.8	4.2E-01	-0.1	8.6E-01
ENSMUST00000129829	interferon activated gene 203 [Source:MGI Symbol;Acc:MGI:96428]	E9QAN9		1.7	6.7E-02	-0.5	5.9E-01	-1.9	3.0E-02	0.3	7.5E-01
ENSMUST00000129835				-1.6	2.5E-01	-1.2	4.9E-01	0.0	9.9E-01	-0.4	8.2E-01
ENSMUST00000163139	plexin A1 [Source:MGI Symbol;Acc:MGI:107685]		P70206	6.1	4.0E-05	3.9	5.0E-03	-0.7	4.9E-01	0.9	2.2E-01
ENSMUST00000129845				-0.9	3.9E-01	-1.9	1.8E-01	-1.1	2.2E-01	0.0	9.8E-01
ENSMUST00000163153	radixin [Source:MGI Symbol;Acc:MGI:97887]		P26043	-3.0	8.9E-04	-10.1	1.6E-04	-0.9	5.9E-02	-0.7	7.1E-01
ENSMUST00000129850				-2.0	7.9E-02	-0.9	5.3E-01	0.5	6.0E-01	-0.6	6.3E-01
ENSMUST00000163168	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]		Q9Z2X1	-5.0	6.7E-04	3.4	7.8E-04	0.0	9.7E-01	0.3	5.0E-01
ENSMUST00000163183	nuclear mitotic apparatus protein 1 [Source:MGI Symbol;Acc:MGI:2443665]	F6ZQA3		-4.1	2.0E-03	5.0	3.0E-02	0.0	9.9E-01	-0.5	6.7E-01
ENSMUST00000129854				1.1	3.3E-01	0.2	9.3E-01	1.8	1.3E-01	2.8	1.2E-01
ENSMUST00000129857				0.3	9.1E-01	9.1	3.5E-02	5.8	1.2E-01	-3.0	3.2E-01
ENSMUST00000163190	microtubule-associated protein 4 [Source:MGI Symbol;Acc:MGI:97178]	A0A0G2JFH2		7.8	1.9E-05	5.0	1.2E-04	-0.2	8.2E-01	0.6	2.3E-01
ENSMUST00000163209	cilia and flagella associated protein 54 [Source:MGI Symbol;Acc:MGI:1922208]	F6SXY8		6.6	1.5E-04	-3.2	1.8E-02	-0.8	2.5E-01	0.2	9.0E-01
ENSMUST00000163230	CD200 antigen [Source:MGI Symbol;Acc:MGI:1196990]	Q80VX2		7.8	1.0E-03	0.4	8.1E-01	1.7	1.1E-01	-2.3	1.7E-01
ENSMUST00000163231	apoptosis resistant E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1915747]	E9PZX5		-3.2	9.0E-03	2.3	1.0E-01	0.5	6.5E-01	1.2	2.7E-01
ENSMUST00000163238	transformed mouse 3T3 cell double minute 1 [Source:MGI Symbol;Acc:MGI:96951]	B2RPU6		-6.1	9.7E-05	6.7	1.9E-04	-0.6	5.9E-01	-0.2	8.1E-01
ENSMUST00000163242	ataxin 10 [Source:MGI Symbol;Acc:MGI:1859293]		P28658	-6.9	8.2E-07	5.0	1.3E-03	-1.6	2.2E-01	-0.7	3.6E-01
ENSMUST00000129883	myotubularin related protein 14 [Source:MGI Symbol;Acc:MGI:1916075]	D6RDS6		-0.9	3.4E-01	-0.9	4.7E-01	0.6	4.7E-01	0.7	5.7E-01
ENSMUST00000129888				0.6	6.8E-01	4.5	3.6E-02	2.1	2.5E-01	-1.8	2.1E-01
ENSMUST00000163246	te carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Source:MGI Symbol;Acc:MGI:1353	E9PX16		-8.3	1.7E-04	3.3	1.6E-01	-0.8	6.8E-01	0.3	8.6E-01
ENSMUST00000163255	tripartite motif-containing 43C [Source:MGI Symbol;Acc:MGI:3647365]		P86449	4.9	5.0E-04	7.0	1.4E-04	-0.5	7.1E-01	0.2	7.3E-01
ENSMUST00000129901				0.6	5.5E-01	0.2	9.1E-01	0.6	6.2E-01	1.0	4.4E-01
ENSMUST00000163260	plakophilin 1 [Source:MGI Symbol;Acc:MGI:1328359]		P97350	7.0	1.8E-03	6.2	6.3E-05	0.2	8.2E-01	0.0	9.4E-01
ENSMUST00000163271	monoglyceride lipase [Source:MGI Symbol;Acc:MGI:1346042]	E9Q3B9		4.4	1.3E-02	8.7	1.1E-04	0.9	5.0E-01	-0.9	1.2E-01
ENSMUST00000163279	SH3-domain GRB2-like B1 (endophilin) [Source:MGI Symbol;Acc:MGI:1859730]		Q9JK48	-6.7	2.4E-06	8.2	1.6E-05	-0.3	7.9E-01	-0.2	7.3E-01
ENSMUST00000163287	MMS19 (MET18 S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919449]	F7C9N6		-7.5	1.2E-04	-2.8	5.2E-02	0.8	2.6E-01	-0.1	9.4E-01
ENSMUST00000163300	ADP-ribosylation factor 1 [Source:MGI Symbol;Acc:MGI:99431]		P84078	-3.6	6.8E-03	6.0	2.5E-04	0.7	4.9E-01	0.3	6.8E-01
ENSMUST00000163319	phospholamban [Source:MGI Symbol;Acc:MGI:97622]		P61014	6.6	3.7E-03	7.8	5.1E-05	-0.6	6.1E-01	-1.5	3.2E-02
ENSMUST00000129917				1.6	2.6E-01	2.1	3.3E-01	1.2	5.0E-01	0.7	6.3E-01
ENSMUST00000163320	capicua homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1918972]		Q924A2	-6.7	2.2E-03	3.7	1.6E-02	-2.0	1.7E-01	-0.1	9.5E-01
ENSMUST00000129922				-2.4	4.1E-02	0.1	9.2E-01	0.8	3.1E-01	-1.7	1.9E-01
ENSMUST00000129927				-0.2	8.3E-01	1.3	2.1E-01	-0.1	8.7E-01	-1.6	1.1E-01
ENSMUST00000129928				0.6	4.4E-01	0.0	9.9E-01	0.1	8.8E-01	0.7	4.6E-01
ENSMUST00000163329	ubiquitin-like 7 (bone marrow stromal cell-derived) [Source:MGI Symbol;Acc:MGI:1916709]		Q91W67	-4.2	2.5E-04	-1.2	2.0E-01	-1.1	1.2E-01	-3.2	2.1E-02
ENSMUST00000163333	metadherin [Source:MGI Symbol;Acc:MGI:1914404]	F6QHD1		-3.1	2.8E-03	5.5	2.1E-03	1.6	2.2E-01	-0.5	5.6E-01
ENSMUST00000163367	solute carrier family 14 (urea transporter), member 2 [Source:MGI Symbol;Acc:MGI:1351653]			6.3	4.7E-04	-6.0	2.2E-03	0.3	6.5E-01	-0.2	9.1E-01
ENSMUST00000129949	ubiquitin protein ligase E3 component n-recognin 4 [Source:MGI Symbol;Acc:MGI:1916366]	F6SSP6		2.3	3.3E-01	8.9	1.8E-02	5.4	9.0E-02	-1.2	5.9E-01
ENSMUST00000129951				2.7	8.9E-02	4.0	3.6E-02	0.6	7.0E-01	-0.7	5.7E-01
ENSMUST00000129952				2.6	9.1E-02	4.7	8.6E-03	-0.2	8.8E-01	-2.4	6.0E-02
ENSMUST00000163377	PYM homolog 1, exon junction complex associated factor [Source:MGI Symbol;Acc:MGI:1925678]		Q8CHP5	-2.5	8.5E-03	-4.7	5.9E-03	-0.2	7.6E-01	-1.9	2.6E-01
ENSMUST00000163389	integrin linked kinase [Source:MGI Symbol;Acc:MGI:1195267]		O55222	-8.4	2.7E-06	2.8	1.9E-02	-0.6	5.2E-01	-0.4	5.7E-01
ENSMUST00000163394	poly(A)-specific ribonuclease (PARN)-like domain containing 1 [Source:MGI Symbol;Acc:MGI:2685159]	B2RXZ1		5.4	2.0E-04	3.7	9.8E-03	-3.4	3.9E-02	-0.8	4.1E-01
ENSMUST00000129966	serine/arginine-rich splicing factor 4 [Source:MGI Symbol;Acc:MGI:1890577]	A0A0A6YWA5		-0.4	7.1E-01	3.4	2.8E-02	1.1	3.8E-01	-2.8	3.9E-02
ENSMUST00000163398	MMS19 (MET18 S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919449]	E9PUY8		-5.9	3.0E-03	7.4	9.5E-04	-0.7	6.7E-01	-0.9	3.2E-01
ENSMUST00000163419	SR-related CTD-associated factor 4 [Source:MGI Symbol;Acc:MGI:2146350]	Q7TSH6		-3.5	2.1E-02	7.6	1.4E-04	0.8	5.1E-01	-0.2	7.9E-01
ENSMUST00000129976	constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	D3Z440		2.7	2.2E-01	0.2	9.4E-01	-1.8	4.1E-01	0.8	6.8E-01
ENSMUST00000163421	axin 1 [Source:MGI Symbol;Acc:MGI:1096327]	Q14DJ8		-4.0	3.6E-03	0.7	3.8E-01	0.3	6.5E-01	1.1	1.5E-01
ENSMUST00000129979	transmembrane protein, adipocyte asscociated 1 [Source:MGI Symbol;Acc:MGI:1345190]			-2.0	4.3E-01	-0.5	8.6E-01	0.3	8.8E-01	-1.2	7.0E-01
ENSMUST00000129985				-2.1	1.3E-01	-1.1	5.3E-01	1.0	4.2E-01	0.0	9.8E-01
ENSMUST00000129990	cilia and flagella associated protein 46 [Source:MGI Symbol;Acc:MGI:2444387]	E9Q2C0		3.0	3.1E-01	3.9	2.2E-01	-0.3	9.3E-01	-1.2	5.5E-01
ENSMUST00000163425	syntaxin 11 [Source:MGI Symbol;Acc:MGI:1921982]	Q3U5V8		-4.8	1.4E-06	-6.6	2.1E-04	-0.7	9.8E-02	-0.9	4.6E-01
ENSMUST00000129993	family with sequence similarity 188, member A [Source:MGI Symbol;Acc:MGI:1914210]	A0A0A6YWB5		-1.6	1.8E-01	-2.1	1.1E-01	-0.4	6.0E-01	0.0	9.8E-01
ENSMUST00000129997	granulin [Source:MGI Symbol;Acc:MGI:95832]	H3BLC9		-0.5	5.9E-01	0.1	9.3E-01	0.4	6.9E-01	-0.3	8.1E-01
ENSMUST00000130002				2.8	1.4E-01	3.0	2.3E-01	-0.5	8.3E-01	-0.6	7.2E-01
ENSMUST00000130006				-4.3	6.8E-02	-3.1	2.8E-01	0.7	6.3E-01	-0.5	8.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000130007	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]	B7FAV1		-0.8	7.9E-01	4.2	2.1E-01	3.5	2.1E-01	-1.5	6.3E-01
ENSMUST00000163433	E2F-associated phosphoprotein [Source:MGI Symbol;Acc:MGI:1913516]		Q5BU09	-5.1	2.0E-02	4.1	1.5E-03	-2.4	4.4E-02	-0.6	3.7E-01
ENSMUST00000130023				0.1	8.8E-01	0.5	6.4E-01	0.0	9.6E-01	-0.5	6.6E-01
ENSMUST00000130024	neurobeachin-like 2 [Source:MGI Symbol;Acc:MGI:2448554]	F6VTL9		-1.8	1.4E-01	-1.0	5.4E-01	1.7	1.4E-01	0.8	6.1E-01
ENSMUST00000163439	RIKEN cDNA 2310050C09 gene [Source:MGI Symbol;Acc:MGI:1913783]	G5E8Z3		6.1	1.2E-04	2.5	1.8E-01	-2.6	1.4E-01	0.5	7.5E-01
ENSMUST00000130032	coactivator-associated arginine methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1913208]	D6RFA7		-2.0	4.1E-01	0.8	6.4E-01	-2.8	9.6E-02	-5.7	3.1E-02
ENSMUST00000163446	Treacher Collins Franceschetti syndrome 1, homolog [Source:MGI Symbol;Acc:MGI:892003]	Q05CS0		8.2	8.2E-03	8.8	4.6E-05	-0.3	8.5E-01	-1.7	2.5E-02
ENSMUST00000163448	decorin [Source:MGI Symbol;Acc:MGI:94872]	Q3UKR1	P28654	4.6	1.3E-03	3.9	2.9E-04	-1.5	5.4E-02	-0.7	1.8E-01
ENSMUST00000163459	thyroid hormone receptor associated protein 3 [Source:MGI Symbol;Acc:MGI:2442637]	F6YH92		-3.9	6.5E-03	-5.1	1.1E-02	-0.6	4.0E-01	1.7	3.3E-01
ENSMUST00000130044	synaptopodin [Source:MGI Symbol;Acc:MGI:1099446]	Q3U336	Q8CC35	1.6	1.3E-01	7.0	1.1E-04	1.1	3.3E-01	-4.4	3.8E-04
ENSMUST00000163475	RIKEN cDNA 2610021A01 gene [Source:MGI Symbol;Acc:MGI:1922662]	E9Q0Q3		2.0	8.5E-03	5.9	2.5E-03	0.2	9.1E-01	0.4	6.9E-01
ENSMUST00000163494	interleukin 2 receptor, beta chain [Source:MGI Symbol;Acc:MGI:96550]		P16297	5.2	2.1E-02	3.6	1.3E-02	-1.7	1.7E-01	-0.5	6.1E-01
ENSMUST00000163499	RNA binding motif protein 26 [Source:MGI Symbol;Acc:MGI:1921463]	E9Q640		-3.2	1.3E-02	6.2	5.1E-04	-0.5	7.0E-01	-1.6	4.8E-02
ENSMUST00000163504	free fatty acid receptor 2 [Source:MGI Symbol;Acc:MGI:2441731]		Q8VCK6	-4.5	1.6E-02	-3.4	2.6E-02	0.6	3.5E-01	-0.4	7.6E-01
ENSMUST00000130066	mannosidase, alpha, class 1A, member 2 [Source:MGI Symbol;Acc:MGI:104676]	A2A723		-1.9	1.0E-01	-0.7	6.0E-01	0.8	3.5E-01	-0.4	7.7E-01
ENSMUST00000163506	microsphere protein 1 [Source:MGI Symbol;Acc:MGI:1858420]	Q3TJY1		-4.7	2.1E-03	5.1	9.6E-05	-0.2	7.7E-01	-1.1	8.1E-02
ENSMUST00000130072				-0.4	7.8E-01	0.7	6.8E-01	0.2	8.7E-01	-0.8	5.8E-01
ENSMUST00000163545	RNA binding motif protein 26 [Source:MGI Symbol;Acc:MGI:1921463]	E9PYZ7		-3.9	1.5E-02	6.1	6.4E-03	-0.3	8.8E-01	-0.7	4.7E-01
ENSMUST00000163559	chemokine (C-C motif) receptor 9 [Source:MGI Symbol;Acc:MGI:1341902]		Q9WUT7	6.8	4.5E-04	6.3	9.1E-04	-0.5	7.4E-01	0.1	9.2E-01
ENSMUST00000130081				-1.2	4.8E-01	1.9	4.2E-01	0.7	7.3E-01	-2.4	2.0E-01
ENSMUST00000130098				-1.4	3.1E-01	-1.2	5.7E-01	1.0	4.6E-01	0.8	6.6E-01
ENSMUST00000130112				1.0	6.1E-01	6.2	3.9E-02	3.3	2.2E-01	-1.9	2.8E-01
ENSMUST00000163568	sine oculis-related homeobox 2 [Source:MGI Symbol;Acc:MGI:102778]		Q62232	9.4	7.1E-06	3.6	4.9E-03	-2.7	4.0E-02	-1.0	1.8E-01
ENSMUST00000130118				0.0	9.9E-01	0.1	9.7E-01	-1.2	5.5E-01	-1.2	6.1E-01
ENSMUST00000130120				0.9	2.9E-01	2.1	7.0E-02	0.4	6.1E-01	-0.7	4.2E-01
ENSMUST00000163582	protein tyrosine phosphatase 4a3 [Source:MGI Symbol;Acc:MGI:1277098]		Q9D658	5.8	1.3E-03	-3.8	1.6E-02	1.2	6.4E-02	-0.1	9.5E-01
ENSMUST00000163584	transcription elongation factor A (SII)-like 8 [Source:MGI Symbol;Acc:MGI:1913934]		Q9CZY2	4.3	1.1E-03	6.3	2.2E-04	0.4	7.0E-01	0.0	9.4E-01
ENSMUST00000163588	stonin 1 [Source:MGI Symbol;Acc:MGI:1924307]		Q8CDJ8	8.0	1.6E-05	-2.0	2.2E-01	2.0	3.3E-02	-0.7	6.7E-01
ENSMUST00000130132				0.6	7.6E-01	-0.1	9.7E-01	-1.5	3.9E-01	-0.8	6.7E-01
ENSMUST00000163590	DTW domain containing 2 [Source:MGI Symbol;Acc:MGI:1916107]	B7ZP35		6.9	4.7E-06	6.5	4.9E-05	0.0	9.8E-01	-1.4	3.3E-02
ENSMUST00000130135				0.4	8.1E-01	0.8	6.0E-01	-0.5	7.5E-01	-0.9	5.7E-01
ENSMUST00000163595	chromodomain protein, Y chromosome-like [Source:MGI Symbol;Acc:MGI:1339956]		Q9WTK2	-4.4	6.5E-04	6.8	4.4E-04	-0.7	6.3E-01	0.1	8.7E-01
ENSMUST00000163600	cyclin H [Source:MGI Symbol;Acc:MGI:1913921]	E9PWD3		-4.5	1.6E-03	4.8	1.5E-03	-1.1	3.4E-01	0.4	5.9E-01
ENSMUST00000163605	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11 [Source:MGI Symbol;Acc:MGI:2443590]		Q6AXC6	4.1	1.2E-05	-6.7	3.1E-03	-1.6	2.9E-02	-0.6	7.5E-01
ENSMUST00000130140				2.9	2.1E-01	2.5	4.2E-01	-0.1	9.6E-01	0.2	9.2E-01
ENSMUST00000163610	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 [Source:MGI Symbol;Acc:MGI:1345192]	E9Q5I9		-3.6	9.0E-03	-4.8	1.2E-02	-1.7	3.5E-02	-0.2	9.2E-01
ENSMUST00000130145	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans) [Source:MGI Symbol;Acc:MGI:2144117]	F6WT10		-1.8	3.4E-01	-2.9	3.3E-01	-0.2	9.2E-01	1.0	7.4E-01
ENSMUST00000163636	predicted gene 8356 [Source:MGI Symbol;Acc:MGI:3779798]	L7N297		7.1	9.0E-05	5.8	8.5E-04	-1.4	2.7E-01	0.3	6.9E-01
ENSMUST00000163643	epidermal growth factor receptor pathway substrate 15-like 1 [Source:MGI Symbol;Acc:MGI:104582]		Q60902	-2.1	1.2E-03	5.1	6.0E-04	-1.6	1.7E-01	-0.4	5.5E-01
ENSMUST00000130160	splA/ryanodine receptor domain and SOCS box containing 2 [Source:MGI Symbol;Acc:MGI:1315199]	D3Z7N7		-1.7	5.8E-01	0.3	9.3E-01	1.1	6.8E-01	-0.9	7.7E-01
ENSMUST00000163655	predicted gene 8127 [Source:MGI Symbol;Acc:MGI:3646865]	E9Q0P0		6.8	1.5E-04	4.5	1.3E-01	1.0	7.1E-01	1.6	3.9E-01
ENSMUST00000163659	nucleoredoxin-like 1 [Source:MGI Symbol;Acc:MGI:1924446]		Q8VC33	4.9	1.2E-04	-4.6	1.7E-03	-1.0	7.6E-02	0.5	6.2E-01
ENSMUST00000163661	Fc receptor-like 1 [Source:MGI Symbol;Acc:MGI:2442862]	E9Q958		-4.0	5.6E-03	1.6	3.4E-01	-2.3	1.4E-01	0.2	8.9E-01
ENSMUST00000163666	eukaryotic translation initiation factor 4A1 [Source:MGI Symbol;Acc:MGI:95303]	Q5F2A7	P60843	-10.6	3.4E-07	2.5	3.1E-02	-0.5	5.9E-01	0.1	9.0E-01
ENSMUST00000163694	pyruvate kinase, muscle [Source:MGI Symbol;Acc:MGI:97591]		P52480	-5.6	2.3E-03	3.8	1.4E-04	-0.6	3.4E-01	-0.1	7.3E-01
ENSMUST00000163701	double zinc ribbon and ankyrin repeat domains 1 [Source:MGI Symbol;Acc:MGI:2139080]	E9Q4Z6		5.8	9.7E-05	-4.5	9.0E-02	1.4	2.7E-01	1.7	5.0E-01
ENSMUST00000130170				2.0	5.3E-02	3.7	1.7E-02	1.0	3.8E-01	-0.6	4.7E-01
ENSMUST00000163705	expressed sequence AI317395 [Source:MGI Symbol;Acc:MGI:2143575]		Q8VCV9	7.7	9.8E-05	2.5	6.0E-01	9.7	1.0E-02	-1.6	7.2E-01
ENSMUST00000130179				0.0	9.9E-01	2.5	4.1E-01	1.2	6.2E-01	-1.2	6.1E-01
ENSMUST00000130183				0.0	9.8E-01	-0.4	7.0E-01	-0.8	3.9E-01	-0.3	7.8E-01
ENSMUST00000130186	ankyrin repeat domain 16 [Source:MGI Symbol;Acc:MGI:2444796]	A0A0A6YWT3		1.7	5.9E-02	0.0	9.6E-01	-0.8	3.4E-01	0.9	3.6E-01
ENSMUST00000163710	troponin T1, skeletal, slow [Source:MGI Symbol;Acc:MGI:1333868]		O88346	-4.5	1.4E-03	4.0	6.1E-03	0.5	6.6E-01	0.0	9.8E-01
ENSMUST00000163716	adenomatosis polyposis coli down-regulated 1 [Source:MGI Symbol;Acc:MGI:3513977]		Q3U128	5.4	1.1E-03	3.2	1.4E-03	-0.9	2.3E-01	0.2	7.1E-01
ENSMUST00000163719	predicted gene, 8281 [Source:MGI Symbol;Acc:MGI:3647811]	L7N2D5		4.3	1.6E-02	4.5	5.9E-02	-0.8	7.1E-01	0.7	6.2E-01
ENSMUST00000130198	LLP homolog, long-term synaptic facilitation (Aplysia) [Source:MGI Symbol;Acc:MGI:1913475]	D3YXW1		1.7	3.9E-02	1.5	9.5E-02	-0.7	3.5E-01	-0.5	4.7E-01
ENSMUST00000163746	WAS/WASL interacting protein family, member 3 [Source:MGI Symbol;Acc:MGI:3044681]	D3Z5R4		8.3	1.0E-04	2.7	3.8E-02	0.1	8.9E-01	-0.2	7.7E-01
ENSMUST00000130214	chondroitin sulfate N-acetylgalactosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI:2442354]		Q8BJQ9	4.6	9.0E-02	4.5	8.4E-02	-2.8	3.2E-01	-2.7	1.3E-01
ENSMUST00000163748	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]		Q9JHC9	-4.7	2.0E-03	-5.5	8.4E-03	-1.5	6.4E-02	0.0	9.8E-01
ENSMUST00000163749	predicted gene, 17669 [Source:MGI Symbol;Acc:MGI:4937303]	F6QL70		6.0	1.6E-03	-4.0	3.9E-03	-2.0	9.0E-03	-0.4	7.6E-01
ENSMUST00000130221				2.3	1.7E-01	7.2	1.3E-03	0.4	8.1E-01	-4.5	4.4E-03
ENSMUST00000163751	phosphodiesterase 2A, cGMP-stimulated [Source:MGI Symbol;Acc:MGI:2446107]	Q3TXZ6		-5.1	1.4E-03	-3.9	4.6E-03	0.7	1.3E-01	-0.5	6.4E-01
ENSMUST00000163754	X-prolyl aminopeptidase (aminopeptidase P) 3, putative [Source:MGI Symbol;Acc:MGI:2445217]		B7ZMP1	2.8	1.1E-03	5.5	2.0E-03	1.0	4.0E-01	-0.7	3.9E-01
ENSMUST00000130229				-1.9	3.8E-01	-0.4	8.9E-01	2.0	3.9E-01	0.5	8.4E-01
ENSMUST00000130234				2.1	9.4E-02	1.3	4.5E-01	-0.2	8.6E-01	0.6	7.0E-01
ENSMUST00000163783	cadherin 16 [Source:MGI Symbol;Acc:MGI:106671]	Q546A8	O88338	8.4	1.2E-05	7.4	1.8E-05	-1.9	9.0E-02	-0.4	4.1E-01
ENSMUST00000163785	cholinergic receptor, muscarinic 1, CNS [Source:MGI Symbol;Acc:MGI:88396]		P12657	7.6	1.4E-05	5.3	4.5E-02	-0.7	7.9E-01	-0.2	8.8E-01
ENSMUST00000130243				-0.5	6.6E-01	2.7	6.0E-02	0.4	7.0E-01	-2.8	4.3E-02
ENSMUST00000163790	predicted gene 3558 [Source:MGI Symbol;Acc:MGI:3781735]	Q5FWC9		6.1	8.3E-03	4.5	1.7E-02	-1.4	3.6E-01	-0.7	5.4E-01
ENSMUST00000130269	mitogen-activated protein kinase kinase 3 [Source:MGI Symbol;Acc:MGI:1346868]			3.2	4.7E-02	-2.7	1.7E-01	-4.2	1.6E-02	1.8	3.2E-01
ENSMUST00000163799	START domain containing 10 [Source:MGI Symbol;Acc:MGI:1860093]	E9PVP0		6.1	1.1E-02	5.9	5.4E-04	-0.5	7.1E-01	-0.3	6.4E-01
ENSMUST00000130274				-2.5	4.3E-01	-4.1	1.7E-01	-3.8	7.7E-02	-2.1	5.4E-01
ENSMUST00000130277				1.1	4.5E-01	4.9	2.0E-02	1.5	3.8E-01	-2.3	9.6E-02
ENSMUST00000130279	prohibitin 2 [Source:MGI Symbol;Acc:MGI:102520]	F6QPR1		-4.1	1.9E-01	-1.8	6.3E-01	1.3	5.6E-01	-1.0	8.1E-01
ENSMUST00000163803	vomeronasal 2, receptor 63 [Source:MGI Symbol;Acc:MGI:3647107]	E9Q0K5		5.6	1.3E-03	6.7	3.3E-05	-2.3	4.5E-02	-0.3	5.8E-01
ENSMUST00000163821	shootin 1 [Source:MGI Symbol;Acc:MGI:1918903]		Q8K2Q9	6.9	1.1E-02	3.4	1.4E-03	-0.2	7.7E-01	-0.2	7.1E-01
ENSMUST00000130290				-2.3	1.1E-01	-6.0	5.3E-02	-0.6	5.8E-01	3.1	2.8E-01
ENSMUST00000163832	glucan (1,4-alpha-), branching enzyme 1 [Source:MGI Symbol;Acc:MGI:1921435]		Q9D6Y9	-5.5	5.6E-05	5.1	3.3E-04	-0.1	8.8E-01	-0.1	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000163839	F-box and WD-40 domain protein 25 [Source:MGI Symbol;Acc:MGI:3588266]	F7C9P2		2.8	5.9E-03	5.4	2.1E-03	-1.5	3.1E-01	-0.8	3.3E-01
ENSMUST00000163845	cytoplasmic FMR1 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1338801]		Q7TMB8	-8.6	3.6E-06	5.0	1.9E-03	-0.7	5.8E-01	-0.2	8.5E-01
ENSMUST00000163852	vomeronasal 2, receptor 56 [Source:MGI Symbol;Acc:MGI:3695438]	E9Q4U5		7.2	5.8E-05	-5.5	1.1E-02	-1.2	1.5E-01	-0.4	8.5E-01
ENSMUST00000163867	SHC (Src homology 2 domain containing) transforming protein 2 [Source:MGI Symbol;Acc:MGI:106180]		Q8BMC3	6.7	1.6E-05	4.5	4.6E-02	-1.0	6.5E-01	0.6	6.7E-01
ENSMUST00000163869	tripartite motif family-like 2 [Source:MGI Symbol;Acc:MGI:3642989]	E9PW10		6.4	1.6E-04	5.0	4.1E-03	-2.0	2.0E-01	-0.4	6.8E-01
ENSMUST00000163884	transmembrane protein 39a [Source:MGI Symbol;Acc:MGI:1915096]		Q9CYC3	-5.9	1.0E-04	1.9	6.0E-02	0.4	6.4E-01	1.1	1.8E-01
ENSMUST00000163885	predicted gene 3248 [Source:MGI Symbol;Acc:MGI:3781426]	K7N721		6.6	6.4E-05	3.0	7.4E-05	-0.5	2.2E-01	-0.4	2.1E-01
ENSMUST00000163889	Rab geranylgeranyl transferase, a subunit [Source:MGI Symbol;Acc:MGI:1860443]		Q9JHK4	-5.8	2.2E-04	-2.6	1.2E-01	0.4	6.1E-01	-0.5	7.7E-01
ENSMUST00000163895	CLIP associating protein 2 [Source:MGI Symbol;Acc:MGI:1923749]	F7DCH5		4.4	2.7E-02	6.8	1.5E-04	-0.6	6.2E-01	-0.4	5.6E-01
ENSMUST00000163913	wingless-type MMTV integration site family, member 11 [Source:MGI Symbol;Acc:MGI:101948]	E9PYZ1		4.3	1.1E-02	8.2	2.4E-05	-1.0	4.2E-01	-0.3	5.4E-01
ENSMUST00000163929	ligand dependent nuclear receptor corepressor [Source:MGI Symbol;Acc:MGI:2443930]	A4FTY7	Q6ZPI3	5.1	1.5E-03	4.8	1.3E-03	0.7	4.7E-01	-0.9	2.5E-01
ENSMUST00000163940	RIKEN cDNA C130050O18 gene [Source:MGI Symbol;Acc:MGI:2442694]	Q497Y9		-4.7	3.6E-04	6.8	5.4E-03	-0.8	7.0E-01	-1.9	1.3E-01
ENSMUST00000130346				-0.3	8.7E-01	-1.5	6.0E-01	0.4	8.1E-01	1.6	5.1E-01
ENSMUST00000130348	NHL repeat containing 3 [Source:MGI Symbol;Acc:MGI:2444520]	D6RE41		0.6	8.0E-01	2.5	2.9E-01	-1.0	6.4E-01	-2.9	2.0E-01
ENSMUST00000163946	RIKEN cDNA 1110065P20 gene [Source:MGI Symbol;Acc:MGI:1916170]	E9Q9M4		-4.9	1.4E-04	8.2	1.7E-05	0.9	3.7E-01	-1.1	5.2E-02
ENSMUST00000163961	schlafen 14 [Source:MGI Symbol;Acc:MGI:2684866]	V9GXG1		7.0	9.6E-05	3.5	2.8E-03	-0.2	7.9E-01	0.0	1.0E+00
ENSMUST00000130353	talin 1 [Source:MGI Symbol;Acc:MGI:1099832]	A2AIM2		3.4	6.3E-02	0.1	9.7E-01	-0.7	7.1E-01	2.6	2.9E-01
ENSMUST00000163968	DEAH (Asp-Glu-Ala-His) box polypeptide 34 [Source:MGI Symbol;Acc:MGI:1918973]			-5.8	1.1E-02	-2.4	2.7E-01	0.7	5.9E-01	-1.0	6.6E-01
ENSMUST00000163979	microtubule-associated protein 4 [Source:MGI Symbol;Acc:MGI:97178]			5.1	1.7E-02	-0.3	8.9E-01	-6.4	2.6E-02	0.7	7.4E-01
ENSMUST00000164022	glyoxalase domain containing 4 [Source:MGI Symbol;Acc:MGI:1914451]	F6ZTG3		-7.2	2.4E-03	-2.9	6.9E-02	2.0	1.7E-02	-0.5	7.4E-01
ENSMUST00000130371				-1.0	1.6E-01	-0.8	3.6E-01	0.1	9.3E-01	-0.1	8.6E-01
ENSMUST00000164037	phosphodiesterase 1C [Source:MGI Symbol;Acc:MGI:108413]	E9Q7V6		5.5	1.8E-02	6.0	8.8E-05	-1.7	1.1E-01	0.3	5.9E-01
ENSMUST00000164039	sortilin-related VPS10 domain containing receptor 1 [Source:MGI Symbol;Acc:MGI:1929666]	E9PYT6		5.9	1.2E-04	-3.4	7.7E-02	1.6	1.2E-01	0.5	7.9E-01
ENSMUST00000130383				2.7	1.0E-01	3.2	1.3E-01	-0.4	8.5E-01	-0.9	5.5E-01
ENSMUST00000130386	ALS2 C-terminal like [Source:MGI Symbol;Acc:MGI:2447532]			-1.3	3.9E-01	2.4	1.3E-01	-0.9	5.2E-01	-4.6	1.3E-02
ENSMUST00000164042	predicted gene, 17555 [Source:MGI Symbol;Acc:MGI:4937189]	F6U8B9		11.3	1.1E-06	4.2	8.1E-04	-2.7	2.3E-02	0.4	5.7E-01
ENSMUST00000164044	Fc receptor, IgG, low affinity III [Source:MGI Symbol;Acc:MGI:95500]	A0A0B4J1M6		-12.9	2.6E-07	8.0	2.9E-05	-0.6	6.1E-01	-0.3	5.9E-01
ENSMUST00000130395				3.2	5.2E-02	3.6	7.4E-02	-1.3	4.6E-01	-1.7	2.0E-01
ENSMUST00000130400				-1.2	1.6E-01	-1.3	2.8E-01	0.1	9.2E-01	0.2	8.4E-01
ENSMUST00000130404				2.0	1.1E-01	3.9	2.1E-02	0.8	5.3E-01	-1.1	3.2E-01
ENSMUST00000164047	interferon-related developmental regulator 1 [Source:MGI Symbol;Acc:MGI:1316717]	F6TBT6		-5.7	2.2E-03	5.4	8.6E-04	-0.6	6.4E-01	0.7	3.4E-01
ENSMUST00000164050	hematopoietic cell specific Lyn substrate 1 [Source:MGI Symbol;Acc:MGI:104568]	E9Q4E5		-7.7	7.6E-05	3.9	8.6E-03	-0.4	7.3E-01	0.8	3.8E-01
ENSMUST00000164052	coiled-coil domain containing 132 [Source:MGI Symbol;Acc:MGI:1920538]		Q8CI71	2.6	7.8E-04	4.5	1.1E-01	-0.5	8.6E-01	3.6	3.4E-02
ENSMUST00000130410	negative regulator of reactive oxygen species [Source:MGI Symbol;Acc:MGI:2445095]	D3Z755		-0.3	8.6E-01	1.2	4.1E-01	0.6	6.2E-01	-0.9	5.6E-01
ENSMUST00000164077	transformed mouse 3T3 cell double minute 1 [Source:MGI Symbol;Acc:MGI:96951]	E9PW14		-4.5	1.4E-03	-3.3	1.7E-02	1.3	6.3E-02	0.9	4.7E-01
ENSMUST00000164078	RIKEN cDNA C130050O18 gene [Source:MGI Symbol;Acc:MGI:2442694]	F7AVJ9		-1.6	2.1E-02	-5.4	8.2E-03	0.5	4.5E-01	1.7	3.0E-01
ENSMUST00000164079	\TA box binding protein (Tbp)-associated factor, RNA polymerase I, D [Source:MGI Symbol;Acc:MGI:19225(		Q9D4V4	-4.7	3.6E-03	4.2	1.3E-01	-0.6	8.2E-01	1.3	4.4E-01
ENSMUST00000164097	Indian hedgehog [Source:MGI Symbol;Acc:MGI:96533]	Q80XI9		5.5	3.9E-05	0.8	3.2E-01	0.7	2.5E-01	-1.9	3.0E-02
ENSMUST00000164108	cullin 3 [Source:MGI Symbol;Acc:MGI:1347360]	E9Q4T8		-6.3	2.6E-04	6.3	9.7E-05	-2.4	5.9E-02	-1.4	3.9E-02
ENSMUST00000130419				2.4	3.3E-01	-2.9	3.9E-01	-3.2	1.6E-01	2.1	5.2E-01
ENSMUST00000164111	microtubule associated serine/threonine kinase family member 4 [Source:MGI Symbol;Acc:MGI:1918885]	Q8BGU6		6.2	1.3E-04	5.2	2.0E-02	-0.7	7.2E-01	1.6	2.1E-01
ENSMUST00000130422	hexokinase 1 [Source:MGI Symbol;Acc:MGI:96103]	G3UVV4		-2.7	4.4E-01	1.1	7.3E-01	-0.2	9.5E-01	-4.0	2.9E-01
ENSMUST00000130423	cap methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1921407]	D3Z491		2.3	7.3E-02	2.2	2.2E-01	1.1	4.6E-01	1.2	3.7E-01
ENSMUST00000164139	predicted gene 8206 [Source:MGI Symbol;Acc:MGI:3779788]	E9Q5Q3		4.8	2.7E-02	5.8	3.3E-04	-0.8	4.5E-01	-0.3	6.2E-01
ENSMUST00000130430				-1.2	1.1E-01	0.4	7.1E-01	1.5	5.0E-02	-0.1	9.5E-01
ENSMUST00000164147	RNA binding motif, single stranded interacting protein 1 [Source:MGI Symbol;Acc:MGI:1861774]	E9PZ21		-4.7	2.3E-02	3.7	3.0E-02	-1.8	2.7E-01	-0.8	4.6E-01
ENSMUST00000164148	eine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 16 [Source:MGI Symbol;Acc:M	D3Z660		6.7	3.3E-04	7.4	8.8E-07	-0.7	2.6E-01	0.1	7.8E-01
ENSMUST00000164161	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]	E9Q0F6		-1.6	3.3E-02	4.3	2.0E-02	0.3	8.4E-01	-0.9	4.1E-01
ENSMUST00000164163	src-like adaptor [Source:MGI Symbol;Acc:MGI:104295]	Q4FJX0	Q60898	-4.9	2.2E-06	1.3	3.7E-02	0.2	6.7E-01	0.1	8.1E-01
ENSMUST00000164167	predicted gene 7535 [Source:MGI Symbol;Acc:MGI:3644434]	F7CXE4		5.8	1.5E-04	4.7	9.2E-04	-1.9	1.1E-01	-0.1	8.3E-01
ENSMUST00000130458	zinc finger protein 963 [Source:MGI Symbol;Acc:MGI:4867078]	D3Z2T8		-0.5	5.5E-01	0.5	6.2E-01	0.1	8.9E-01	-0.9	3.6E-01
ENSMUST00000164178	zonadhesin [Source:MGI Symbol;Acc:MGI:106656]	E9PWQ7		9.9	1.1E-06	3.1	1.4E-01	-0.5	8.1E-01	0.7	5.9E-01
ENSMUST00000164179	Fc receptor, IgG, low affinity III [Source:MGI Symbol;Acc:MGI:95500]	E9PVR4		3.2	3.9E-03	-5.2	2.6E-04	-0.4	4.2E-01	-2.1	6.2E-02
ENSMUST00000130462	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 [Source:MGI Symbol;Acc:MGI:1345192]	F6ZQQ3		-2.5	5.1E-02	-2.4	1.3E-01	-0.6	5.1E-01	-0.6	6.7E-01
ENSMUST00000164181	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Source:MGI Symbol;Acc:MGI:109318]	Q642K0	Q60605	-7.8	5.5E-07	2.2	5.7E-02	0.7	4.4E-01	0.8	3.4E-01
ENSMUST00000164192	RAS, guanyl releasing protein 3 [Source:MGI Symbol;Acc:MGI:3028579]	Q6NZH9		5.8	1.2E-03	6.7	2.5E-03	0.2	9.0E-01	-1.8	8.7E-02
ENSMUST00000130480				-0.4	7.3E-01	-2.7	2.3E-01	0.9	4.3E-01	3.2	1.5E-01
ENSMUST00000164195	phosphodiesterase 7B [Source:MGI Symbol;Acc:MGI:1352752]	E9PW23		6.1	1.5E-02	2.7	1.1E-03	-0.7	2.2E-01	-0.6	2.3E-01
ENSMUST00000164209	RNA binding motif protein 4 [Source:MGI Symbol;Acc:MGI:1100865]	Q5CZX8		-4.3	4.4E-04	8.2	1.1E-04	-1.0	5.1E-01	-0.9	1.9E-01
ENSMUST00000164219	six transmembrane epithelial antigen of prostate 2 [Source:MGI Symbol;Acc:MGI:1921301]	B2RX33	Q8BWB6	6.9	6.1E-03	6.5	6.0E-04	-1.8	2.1E-01	-0.1	9.3E-01
ENSMUST00000130491	CCAAT/enhancer binding protein (C/EBP), gamma [Source:MGI Symbol;Acc:MGI:104982]	Q54AJ1	P53568	-1.4	9.5E-02	-0.3	7.7E-01	1.2	1.1E-01	0.2	8.6E-01
ENSMUST00000164225	mediator complex subunit 12-like [Source:MGI Symbol;Acc:MGI:2139916]		Q8BQM9	8.4	3.6E-05	5.0	1.3E-03	-1.4	2.4E-01	0.6	4.3E-01
ENSMUST00000130498	bolA-like 2 (E. coli) [Source:MGI Symbol;Acc:MGI:1913412]		Q8BGS2	-1.6	7.0E-02	-3.8	2.1E-02	-0.6	4.0E-01	1.6	2.4E-01
ENSMUST00000164233	DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:MGI Symbol;Acc:MGI:1270129]	Q5NTY0	P63037	2.6	4.4E-03	-4.3	6.1E-03	-2.1	1.7E-02	-2.6	1.3E-01
ENSMUST00000164243	signal recognition particle 54B [Source:MGI Symbol;Acc:MGI:3714357]	E9PXC0		-6.2	8.0E-05	5.0	3.2E-02	-1.4	4.8E-01	0.1	9.5E-01
ENSMUST00000164259	amplified in osteosarcoma [Source:MGI Symbol;Acc:MGI:1924301]		Q8K2C7	-5.1	5.7E-04	5.8	4.8E-04	-1.5	2.3E-01	0.6	4.2E-01
ENSMUST00000164263	T cell lymphoma invasion and metastasis 1 [Source:MGI Symbol;Acc:MGI:103306]	E9Q1R7		6.7	1.2E-03	-0.6	3.1E-01	1.0	3.7E-02	-0.6	3.3E-01
ENSMUST00000130516				3.0	4.4E-02	2.7	1.4E-01	0.0	1.0E+00	0.3	8.3E-01
ENSMUST00000130519	iduronate 2-sulfatase [Source:MGI Symbol;Acc:MGI:96417]	F6X9C5		0.9	6.4E-01	1.6	4.9E-01	-0.3	8.6E-01	-1.1	6.1E-01
ENSMUST00000164267	hydrocarboxylic acid receptor 1 [Source:MGI Symbol;Acc:MGI:2441671]	E9PZR8		8.4	3.0E-05	5.7	1.2E-04	-0.6	4.9E-01	0.2	7.5E-01
ENSMUST00000164290	growth factor independent 1B [Source:MGI Symbol;Acc:MGI:1276578]	B7ZNH2		7.8	2.2E-05	-1.5	3.8E-01	1.0	3.3E-01	-0.9	6.2E-01
ENSMUST00000164296	bromodomain containing 3 [Source:MGI Symbol;Acc:MGI:1914632]	Q3TUI3	Q8K2F0	-5.6	1.7E-04	-5.8	4.1E-03	-3.3	1.1E-03	-0.6	7.5E-01
ENSMUST00000130534				2.7	4.7E-02	3.0	8.6E-02	0.1	9.5E-01	-0.3	8.1E-01
ENSMUST00000164298	chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2 [Source:MGI Symbol;Acc:M(	F6ZTZ2		-5.3	2.3E-02	6.2	5.3E-04	-0.5	7.0E-01	-0.8	2.8E-01
ENSMUST00000164304	signal-induced proliferation associated gene 1 [Source:MGI Symbol;Acc:MGI:107576]	E9Q0Y4		-8.1	1.8E-04	2.3	5.9E-03	-0.3	5.8E-01	1.2	4.4E-02
ENSMUST00000164345	RIKEN cDNA 9130019O22 gene [Source:MGI Symbol;Acc:MGI:1926171]	E9PX22		-3.6	1.7E-03	-1.7	2.4E-01	1.6	6.3E-02	-1.0	4.8E-01
ENSMUST00000164359	eukaryotic translation initiation factor 5A [Source:MGI Symbol;Acc:MGI:106248]		P63242	-6.4	4.4E-04	7.2	3.1E-04	-0.1	9.7E-01	0.3	6.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000164362	RIKEN cDNA 5730409E04Rik gene [Source:MGI Symbol;Acc:MGI:3609248]		Q8BP99	5.0	5.7E-03	5.4	2.1E-02	-0.6	7.7E-01	-0.8	5.2E-01
ENSMUST00000164373	insulin related protein 2 (islet 2) [Source:MGI Symbol;Acc:MGI:109156]	Q0VAX2		6.4	1.1E-02	7.5	3.4E-04	0.1	9.7E-01	-0.8	3.0E-01
ENSMUST00000130552				2.1	1.7E-01	3.8	6.3E-03	-2.2	1.0E-01	-4.0	5.6E-03
ENSMUST00000164375	zyxin [Source:MGI Symbol;Acc:MGI:103072]		Q62523	-3.5	1.4E-03	5.1	5.3E-03	-0.4	8.0E-01	0.0	9.5E-01
ENSMUST00000164378	GTPase activating protein (SH3 domain) binding protein 2 [Source:MGI Symbol;Acc:MGI:2442040]	Q3U541	P97379	-3.5	1.2E-02	-5.8	1.4E-03	0.5	3.3E-01	-0.5	7.3E-01
ENSMUST00000164399	protein kinase inhibitor, gamma [Source:MGI Symbol;Acc:MGI:1343086]	Q3TP50	O70139	-4.0	1.4E-02	4.3	3.4E-03	-0.4	7.1E-01	-0.1	9.4E-01
ENSMUST00000130565				-2.0	4.1E-01	-0.8	8.1E-01	0.9	7.0E-01	-0.3	9.2E-01
ENSMUST00000130569				0.6	3.3E-01	1.5	7.1E-02	0.5	4.2E-01	-0.4	5.3E-01
ENSMUST00000164410	tripartite motif-containing 30B [Source:MGI Symbol;Acc:MGI:4821256]	E9PVL6		-5.0	2.1E-03	6.5	4.1E-04	-0.6	6.6E-01	0.0	9.8E-01
ENSMUST00000164415	kelch-like 33 [Source:MGI Symbol;Acc:MGI:3644593]	G3UW92		7.7	1.6E-05	7.0	4.2E-05	-0.5	5.9E-01	-0.7	2.2E-01
ENSMUST00000164416	PCI domain containing 2 [Source:MGI Symbol;Acc:MGI:2443003]		Q8BFV2	-3.8	8.2E-03	2.7	3.2E-01	0.0	9.9E-01	2.7	2.3E-01
ENSMUST00000130597	mitochondrial antiviral signaling protein [Source:MGI Symbol;Acc:MGI:2444773]	S4R1W6		4.0	5.4E-02	7.6	8.9E-03	2.2	3.5E-01	-1.3	3.8E-01
ENSMUST00000164422	predicted gene 4884 [Source:MGI Symbol;Acc:MGI:3649090]	E9PVP9		10.2	9.0E-05	5.9	3.7E-03	0.9	5.8E-01	-0.6	5.0E-01
ENSMUST00000164425	RAS-like, family 10, member B [Source:MGI Symbol;Acc:MGI:2685575]		Q5SSG5	8.9	7.6E-06	-4.3	2.8E-02	2.6	4.6E-03	-0.9	6.4E-01
ENSMUST00000164430	uclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 [Source:MGI Symbol;Acc:MGI:9731		P25799	-5.9	5.7E-04	-7.9	1.7E-04	0.1	8.8E-01	-0.9	5.6E-01
ENSMUST00000164431	synaptojanin 2 binding protein [Source:MGI Symbol;Acc:MGI:1344347]	E9PVQ9		-2.6	3.8E-03	-6.0	5.7E-04	0.8	6.7E-02	-0.7	5.7E-01
ENSMUST00000164447	TRAF-interacting protein with forkhead-associated domain [Source:MGI Symbol;Acc:MGI:2182965]	I3PQW8	Q793I8	-3.7	2.1E-02	5.0	6.2E-03	-0.5	7.4E-01	-1.5	1.4E-01
ENSMUST00000130620	SEC22 homolog B, vesicle trafficking protein [Source:MGI Symbol;Acc:MGI:1338759]	A0A0G2JF08		3.0	1.2E-01	-1.1	6.3E-01	-3.3	8.0E-02	0.8	7.2E-01
ENSMUST00000164454	serine (or cysteine) preptidase inhibitor, clade A, member 1B [Source:MGI Symbol;Acc:MGI:891970]		P22599	8.0	2.3E-05	1.2	1.1E-01	-0.5	4.1E-01	0.5	4.3E-01
ENSMUST00000164459	predicted gene 3278 [Source:MGI Symbol;Acc:MGI:3781456]	L7N2D2		5.7	1.4E-02	6.7	3.0E-05	0.9	3.2E-01	0.1	8.0E-01
ENSMUST00000130624				1.1	1.4E-01	0.9	3.6E-01	0.1	8.8E-01	0.3	7.1E-01
ENSMUST00000130632				1.3	7.9E-02	1.0	2.6E-01	-0.1	8.8E-01	0.2	7.8E-01
ENSMUST00000130637	bromodomain adjacent to zinc finger domain, 2B [Source:MGI Symbol;Acc:MGI:2442782]	F6R4Y5		-3.0	4.7E-02	-2.0	1.6E-01	-0.8	3.7E-01	-1.8	2.4E-01
ENSMUST00000164467	cAMP-regulated phosphoprotein 19 [Source:MGI Symbol;Acc:MGI:1891691]		P56212	-5.1	8.4E-04	6.6	1.6E-03	-0.7	6.8E-01	-0.8	4.0E-01
ENSMUST00000130643	serine/arginine-rich protein specific kinase 1 [Source:MGI Symbol;Acc:MGI:106908]	Q3UB06	O70551	0.5	3.8E-01	0.4	5.8E-01	0.2	7.4E-01	0.3	6.8E-01
ENSMUST00000130645	mitochondrial fission regulator 1 [Source:MGI Symbol;Acc:MGI:1914722]	Q3TTQ5	Q99MB2	0.9	1.2E-01	1.8	1.5E-02	-0.1	8.6E-01	-1.0	8.5E-02
ENSMUST00000130649				1.4	2.7E-01	2.3	1.4E-01	0.5	6.7E-01	-0.4	7.4E-01
ENSMUST00000164472	zinc finger protein 637 [Source:MGI Symbol;Acc:MGI:2448537]		Q80V23	-4.9	9.4E-04	1.8	2.1E-02	-0.7	2.0E-01	0.7	2.4E-01
ENSMUST00000164484	predicted gene 8237 [Source:MGI Symbol;Acc:MGI:3644039]	E9Q257		6.1	4.5E-04	6.1	8.3E-07	-0.4	3.9E-01	-0.1	8.2E-01
ENSMUST00000130663	TRIO and F-actin binding protein [Source:MGI Symbol;Acc:MGI:1349410]	G5E8W1		-1.4	1.1E-01	0.0	9.7E-01	1.1	1.7E-01	-0.2	8.3E-01
ENSMUST00000130664	RIKEN cDNA 2810474O19 gene [Source:MGI Symbol;Acc:MGI:1914496]			-1.9	1.6E-01	-1.1	4.4E-01	1.2	2.1E-01	0.5	7.4E-01
ENSMUST00000164495	assium voltage-gated channel, delayed-rectifier, subfamily S, member 3 [Source:MGI Symbol;Acc:MGI:10988		Q8BQZ8	6.0	3.4E-03	3.2	6.2E-03	-0.4	6.4E-01	-0.3	6.7E-01
ENSMUST00000164502	predicted gene 9573 [Source:MGI Symbol;Acc:MGI:3779983]	F7C950		10.3	3.1E-05	-3.2	6.5E-02	1.5	8.2E-02	0.5	7.3E-01
ENSMUST00000130676				0.6	3.5E-01	0.8	2.8E-01	0.1	9.3E-01	-0.2	7.6E-01
ENSMUST00000130687	PHD and ring finger domains 1 [Source:MGI Symbol;Acc:MGI:2141847]	F6WXS6		-2.8	3.4E-01	-2.1	5.1E-01	-0.6	7.5E-01	-1.3	7.0E-01
ENSMUST00000164504	cilia and flagella associated protein 97 [Source:MGI Symbol;Acc:MGI:1914006]		Q6ZPR1	-3.7	8.1E-03	7.4	6.9E-04	-0.3	8.6E-01	0.7	3.7E-01
ENSMUST00000164505	te carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Source:MGI Symbol;Acc:MGI:1353		Q8VEM8	-5.3	1.9E-04	-7.3	3.0E-05	-0.3	2.8E-01	-0.2	8.3E-01
ENSMUST00000130698				2.8	1.1E-01	-0.1	9.4E-01	-2.1	2.2E-01	0.9	6.2E-01
ENSMUST00000164517	predicted gene, 21319 [Source:MGI Symbol;Acc:MGI:5434674]	F6YNI8		6.0	3.1E-05	2.2	1.4E-02	0.0	9.9E-01	-0.3	5.8E-01
ENSMUST00000130704	vacuolar protein sorting 13 D (yeast) [Source:MGI Symbol;Acc:MGI:2448530]	F6XI52		-1.1	6.2E-01	2.9	3.4E-01	3.3	2.2E-01	-0.7	7.8E-01
ENSMUST00000130709				0.7	4.7E-01	-0.5	7.7E-01	0.4	7.1E-01	1.6	2.9E-01
ENSMUST00000130716	myotubularin related protein 3 [Source:MGI Symbol;Acc:MGI:1921552]	M0QW74		2.7	1.1E-01	-0.3	8.6E-01	-2.5	1.3E-01	0.6	7.4E-01
ENSMUST00000130719				-3.0	8.7E-02	-0.2	9.2E-01	0.7	6.1E-01	-2.2	2.2E-01
ENSMUST00000164518	RIKEN cDNA 4933411K16 gene [Source:MGI Symbol;Acc:MGI:1914015]		Q80Y39	8.3	4.3E-04	7.1	1.2E-04	-0.6	6.4E-01	-0.2	7.3E-01
ENSMUST00000164523	predicted gene 5611 [Source:MGI Symbol;Acc:MGI:3647121]	E9Q5T3		5.5	3.1E-03	5.6	5.1E-04	-0.6	6.2E-01	0.4	5.5E-01
ENSMUST00000130727				1.1	2.0E-01	2.4	3.9E-02	0.9	2.9E-01	-0.4	6.2E-01
ENSMUST00000164532	family with sequence similarity 49, member B [Source:MGI Symbol;Acc:MGI:1923520]		Q921M7	-10.7	5.3E-05	6.0	8.3E-04	-0.8	5.3E-01	-0.5	4.7E-01
ENSMUST00000130729	structure specific recognition protein 1 [Source:MGI Symbol;Acc:MGI:107912]	A2AW05		0.7	7.2E-01	0.5	8.6E-01	-0.6	7.7E-01	-0.3	9.1E-01
ENSMUST00000164538	otogelin [Source:MGI Symbol;Acc:MGI:1202064]	G3UWC8		12.1	7.0E-06	-3.1	1.9E-02	1.9	6.5E-03	-0.7	5.8E-01
ENSMUST00000130736				-1.2	1.4E-01	-0.9	3.4E-01	-0.2	7.7E-01	-0.5	6.1E-01
ENSMUST00000164539	sperm associated antigen 17 [Source:MGI Symbol;Acc:MGI:1921612]		Q5S003	8.0	1.7E-05	4.5	1.8E-03	-2.8	4.0E-02	-2.1	1.6E-02
ENSMUST00000164542	mitochondrial ribosomal protein L13 [Source:MGI Symbol;Acc:MGI:2137218]	G5E909		-5.5	3.5E-04	2.6	2.8E-02	-1.1	2.9E-01	0.5	5.5E-01
ENSMUST00000130743				-1.2	2.0E-01	-0.2	8.3E-01	0.1	9.3E-01	-0.9	3.9E-01
ENSMUST00000130747				1.3	1.5E-01	2.9	2.4E-02	1.2	2.2E-01	-0.4	6.5E-01
ENSMUST00000164545	e carrier family 7 (cationic amino acid transporter, y+ system), member 4 [Source:MGI Symbol;Acc:MGI:2146	E9Q6V0		6.4	8.1E-04	6.3	6.0E-05	0.7	4.2E-01	-0.2	7.1E-01
ENSMUST00000164547	arachidonate 5-lipoxygenase [Source:MGI Symbol;Acc:MGI:87999]	E9QA93		-5.8	8.8E-05	-3.4	1.0E-01	0.6	5.2E-01	-1.5	4.8E-01
ENSMUST00000164553	myeloid-associated differentiation marker [Source:MGI Symbol;Acc:MGI:1355332]	Q0VE46	O35682	-7.1	2.3E-04	6.5	1.4E-04	-0.6	6.2E-01	-0.2	7.4E-01
ENSMUST00000130769				1.5	2.1E-01	5.4	1.7E-03	0.8	5.0E-01	-3.1	9.0E-03
ENSMUST00000164566	cDNA sequence BC021785 [Source:MGI Symbol;Acc:MGI:2446139]	Q8C3P4		6.0	6.0E-06	2.5	2.3E-02	-1.1	2.1E-01	-0.4	6.1E-01
ENSMUST00000164580	ATH1, acid trehalase-like 1 (yeast) [Source:MGI Symbol;Acc:MGI:2444047]	F6QM56		-6.0	3.4E-03	-4.9	4.7E-05	-0.2	5.6E-01	-2.3	2.5E-02
ENSMUST00000164582	ankyrin repeat domain 13c [Source:MGI Symbol;Acc:MGI:2139746]		Q3UX43	-4.2	1.5E-03	4.5	1.3E-03	-0.5	6.5E-01	0.4	5.3E-01
ENSMUST00000164583	RIKEN cDNA 5830411N06 gene [Source:MGI Symbol;Acc:MGI:2443685]	B3F5L4		8.7	1.6E-05	5.8	8.1E-04	-0.9	5.0E-01	-0.6	4.2E-01
ENSMUST00000130789				1.9	5.1E-02	1.7	1.2E-01	-0.7	4.3E-01	-0.5	5.6E-01
ENSMUST00000164598	acyl-Coenzyme A oxidase 2, branched chain [Source:MGI Symbol;Acc:MGI:1934852]		Q9QXD1	3.5	3.9E-04	4.2	8.9E-03	-1.7	2.4E-01	-0.2	8.4E-01
ENSMUST00000130799	zinc finger protein 369 [Source:MGI Symbol;Acc:MGI:2176229]	E9Q628		-0.6	4.3E-01	-0.3	7.1E-01	-0.1	9.3E-01	-0.3	7.1E-01
ENSMUST00000164632	ribonuclease, RNase A family, 10 (non-active) [Source:MGI Symbol;Acc:MGI:1922269]	G3UWD1		6.1	1.9E-02	4.8	7.6E-04	-0.8	4.1E-01	0.5	4.1E-01
ENSMUST00000164649	hippocalcin [Source:MGI Symbol;Acc:MGI:1336200]		P84075	8.7	2.1E-03	-4.2	3.0E-02	-0.3	7.2E-01	-1.3	5.2E-01
ENSMUST00000130813	synaptojanin 1 [Source:MGI Symbol;Acc:MGI:1354961]	D3Z1M7		-1.8	5.3E-01	-2.8	4.4E-01	-1.3	5.1E-01	-0.3	9.4E-01
ENSMUST00000164655	heterogeneous nuclear ribonucleoprotein C [Source:MGI Symbol;Acc:MGI:107795]		Q9Z204	7.6	1.3E-02	-5.9	2.0E-04	-0.1	8.1E-01	-0.5	6.6E-01
ENSMUST00000164661	tripartite motif-containing 43A [Source:MGI Symbol;Acc:MGI:3645218]		Q3TL54	5.0	9.7E-04	3.4	1.3E-02	-0.4	6.9E-01	0.1	9.2E-01
ENSMUST00000130822	schlafen 8 [Source:MGI Symbol;Acc:MGI:2672859]	A0A0A0MQG0		-1.1	2.7E-01	-3.1	3.9E-02	-1.2	1.2E-01	0.9	5.3E-01
ENSMUST00000164662	chromodomain helicase DNA binding protein 5 [Source:MGI Symbol;Acc:MGI:3036258]	E9PYU4		6.6	1.6E-02	0.6	5.4E-01	-1.8	6.0E-02	-0.1	8.9E-01
ENSMUST00000164666	mutated in colorectal cancers [Source:MGI Symbol;Acc:MGI:96930]	G3UW40		5.9	4.8E-05	4.1	1.7E-04	-2.7	7.7E-03	-0.5	3.8E-01
ENSMUST00000164667	RIKEN cDNA B930094E09 gene [Source:MGI Symbol;Acc:MGI:3603750]	Q8C4T2		3.8	1.3E-02	5.8	2.4E-03	-0.6	6.9E-01	-0.9	3.1E-01
ENSMUST00000130832	WD repeat domain 13 [Source:MGI Symbol;Acc:MGI:1914661]	S4R225		-2.2	2.2E-01	-1.5	5.6E-01	0.8	6.8E-01	0.2	9.5E-01
ENSMUST00000130843				0.3	7.8E-01	2.3	1.1E-01	0.9	4.6E-01	-1.1	3.3E-01
ENSMUST00000130846	collagen, type VI, alpha 3 [Source:MGI Symbol;Acc:MGI:88461]	D3YWD1		2.9	1.7E-01	6.3	1.3E-02	-0.4	8.7E-01	-3.7	2.5E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000164688	proline rich 13 [Source:MGI Symbol;Acc:MGI:1913401]		Q9CQJ5	-7.8	6.3E-04	4.3	1.9E-03	-0.9	3.6E-01	-0.5	5.1E-01
ENSMUST00000130855	deltex 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2135752]	D3YV13		2.1	2.4E-01	5.6	4.4E-02	2.1	4.0E-01	-1.4	3.5E-01
ENSMUST00000130857				1.5	8.8E-02	1.4	1.8E-01	0.1	8.7E-01	0.3	7.4E-01
ENSMUST00000164697	rad and gem related GTP binding protein 2 [Source:MGI Symbol;Acc:MGI:2155260]	E9PVZ0		5.9	8.0E-04	5.2	8.7E-02	0.9	7.2E-01	2.1	3.0E-01
ENSMUST00000164730	adenosine A3 receptor [Source:MGI Symbol;Acc:MGI:104847]	Q497R5		-7.7	9.6E-05	5.8	6.9E-03	-0.4	8.0E-01	-1.6	2.0E-01
ENSMUST00000164745	fatty acyl CoA reductase 1 [Source:MGI Symbol;Acc:MGI:1914670]		Q922J9	-7.9	6.4E-06	6.4	9.4E-05	-0.9	4.0E-01	-0.8	1.9E-01
ENSMUST00000130871	predicted gene, 28043 [Source:MGI Symbol;Acc:MGI:5547779]	E0CXC2		-0.3	5.9E-01	0.3	7.2E-01	0.6	3.3E-01	0.0	9.8E-01
ENSMUST00000164751	centrosomal protein 290 [Source:MGI Symbol;Acc:MGI:2384917]	E9Q9M0		3.6	6.5E-04	5.7	3.0E-04	-0.6	6.1E-01	0.2	6.9E-01
ENSMUST00000164756	EP300 interacting inhibitor of differentiation 1 [Source:MGI Symbol;Acc:MGI:1889651]		Q9DCR4	-5.9	2.9E-06	1.6	1.1E-01	1.5	6.7E-02	-2.4	2.0E-02
ENSMUST00000164761	urocanase domain containing 1 [Source:MGI Symbol;Acc:MGI:2385332]	Q3UEL5		7.6	3.1E-02	6.9	1.3E-04	0.5	6.3E-01	0.7	2.2E-01
ENSMUST00000164763	-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:13		Q61493	-4.8	1.7E-02	5.5	3.0E-03	-1.3	3.6E-01	0.7	4.2E-01
ENSMUST00000164766	rad and gem related GTP binding protein 2 [Source:MGI Symbol;Acc:MGI:2155260]	E9Q4D5		3.7	1.9E-03	3.6	6.0E-03	-0.7	5.2E-01	0.7	3.4E-01
ENSMUST00000130881	glutathione synthetase [Source:MGI Symbol;Acc:MGI:95852]	Q3UEE2		-2.1	8.1E-02	0.1	9.7E-01	2.1	6.5E-02	-0.1	9.5E-01
ENSMUST00000164772	leucine rich repeat and Ig domain containing 2 [Source:MGI Symbol;Acc:MGI:2442298]	B2RQD4	Q3URE9	5.4	3.1E-02	6.6	1.4E-04	0.5	6.5E-01	-0.1	8.2E-01
ENSMUST00000130886				1.0	1.0E-01	-0.2	8.1E-01	-1.2	3.4E-02	-0.1	8.5E-01
ENSMUST00000164774	tubulin, gamma complex associated protein 3 [Source:MGI Symbol;Acc:MGI:2183752]	E9Q0R3		-4.5	3.9E-03	7.9	6.3E-04	-0.3	8.5E-01	1.1	1.8E-01
ENSMUST00000164784	zinc finger protein 804B [Source:MGI Symbol;Acc:MGI:2685287]	F6QGP8		7.1	8.5E-05	5.2	2.5E-04	-1.2	2.4E-01	-0.7	2.2E-01
ENSMUST00000164786	lysyl oxidase-like 4 [Source:MGI Symbol;Acc:MGI:1914823]	E9Q600		5.5	2.6E-02	-4.1	7.8E-02	0.3	7.8E-01	1.1	6.2E-01
ENSMUST00000164787	cadherin 18 [Source:MGI Symbol;Acc:MGI:1344366]	E9Q9Q6		6.4	7.3E-05	-5.9	3.2E-04	-0.1	8.5E-01	0.2	8.5E-01
ENSMUST00000164791	uridine phosphorylase 1 [Source:MGI Symbol;Acc:MGI:1097668]	Q5SUC8	P52624	-6.5	5.6E-03	-2.1	2.4E-01	-6.3	2.8E-03	0.6	7.2E-01
ENSMUST00000130916	beclin 1, autophagy related [Source:MGI Symbol;Acc:MGI:1891828]		O88597	1.5	6.7E-02	1.8	8.4E-02	0.0	9.6E-01	-0.2	8.0E-01
ENSMUST00000164807	peroxiredoxin 2 [Source:MGI Symbol;Acc:MGI:109486]		Q61171	-5.9	2.5E-04	4.3	2.4E-04	-1.0	2.0E-01	-0.5	3.1E-01
ENSMUST00000164809	testis-specific serine kinase 4 [Source:MGI Symbol;Acc:MGI:1918349]	A9P6P9		4.0	1.7E-02	2.9	1.7E-02	0.1	8.7E-01	-0.1	9.2E-01
ENSMUST00000164812	kelch-like ECH-associated protein 1 [Source:MGI Symbol;Acc:MGI:1858732]		Q9Z2X8	2.1	2.2E-03	5.6	7.3E-04	-1.4	2.7E-01	-2.0	2.5E-02
ENSMUST00000130925	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]	F6SLJ2		0.3	7.9E-01	0.8	6.2E-01	1.4	2.0E-01	0.9	4.9E-01
ENSMUST00000130926				0.9	6.8E-01	1.0	7.4E-01	-0.6	8.0E-01	-0.7	8.0E-01
ENSMUST00000164826	caspase recruitment domain family, member 10 [Source:MGI Symbol;Acc:MGI:2146012]	E9PUV9		-3.6	1.4E-03	2.1	3.7E-02	-0.4	6.2E-01	0.9	2.5E-01
ENSMUST00000164828	peroxisomal biogenesis factor 2 [Source:MGI Symbol;Acc:MGI:107486]	Q91YZ5		-4.9	2.3E-03	4.0	2.8E-02	0.8	5.8E-01	1.9	1.1E-01
ENSMUST00000164833	heterogeneous nuclear ribonucleoprotein D [Source:MGI Symbol;Acc:MGI:101947]	F7A465		-5.9	8.4E-04	5.6	9.1E-03	-0.4	8.1E-01	1.0	3.6E-01
ENSMUST00000164834	G protein-coupled receptor 62 [Source:MGI Symbol;Acc:MGI:3525078]		Q80UC6	5.3	1.4E-03	3.3	8.3E-03	0.7	4.0E-01	-0.1	8.9E-01
ENSMUST00000130976	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	E9PYS6		-0.5	8.3E-01	-4.9	1.4E-01	-3.2	6.9E-02	1.2	7.0E-01
ENSMUST00000164837	RIKEN cDNA 1600012H06 gene [Source:MGI Symbol;Acc:MGI:1915162]		Q9DAY5	-3.6	7.1E-03	4.0	3.2E-03	-1.5	1.4E-01	0.1	8.5E-01
ENSMUST00000130986	death inducer-obliterator 1 [Source:MGI Symbol;Acc:MGI:1344352]		Q8C9B9	3.9	2.0E-01	5.0	1.4E-01	-0.3	9.2E-01	-1.4	4.9E-01
ENSMUST00000164838	predicted gene 4027 [Source:MGI Symbol;Acc:MGI:3782201]	Q3UT53		7.6	4.0E-05	4.0	5.6E-02	0.7	6.8E-01	1.2	3.5E-01
ENSMUST00000130994	WD repeat domain 77 [Source:MGI Symbol;Acc:MGI:1917715]	D6RIL4		1.2	2.5E-01	2.8	5.6E-02	1.0	4.1E-01	-0.7	5.3E-01
ENSMUST00000131000	zinc finger protein 646 [Source:MGI Symbol;Acc:MGI:3665412]	D3Z083		0.7	3.7E-01	1.6	1.2E-01	1.2	1.2E-01	0.3	7.6E-01
ENSMUST00000164843	calpain 1 [Source:MGI Symbol;Acc:MGI:88263]	Q3TI07	O35350	-9.7	1.2E-04	-1.7	3.0E-01	0.5	6.0E-01	-1.3	4.4E-01
ENSMUST00000164845	vomeronasal 2, receptor 45 [Source:MGI Symbol;Acc:MGI:3757883]	L7N2B5		8.5	1.9E-05	-1.5	1.8E-01	0.2	8.1E-01	-0.6	5.8E-01
ENSMUST00000131014				1.8	1.2E-01	-3.3	2.7E-02	-4.3	9.2E-04	0.9	5.2E-01
ENSMUST00000131015				3.0	7.8E-02	1.8	2.0E-01	-2.8	7.0E-02	-1.6	2.2E-01
ENSMUST00000164848	seven in absentia homolog 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685758]	B2RWG3		7.8	1.7E-05	-2.9	4.6E-02	1.1	1.7E-01	-4.7	2.8E-02
ENSMUST00000131024	interferon-induced protein 35 [Source:MGI Symbol;Acc:MGI:1917360]	D6RFB1		-1.9	1.8E-01	-1.4	4.1E-01	0.1	9.1E-01	-0.4	8.2E-01
ENSMUST00000164853	coiled-coil domain containing 24 [Source:MGI Symbol;Acc:MGI:2685874]	Q3V0I8		6.5	3.4E-05	-3.6	1.2E-02	1.1	6.3E-02	-0.8	5.4E-01
ENSMUST00000164856	vomeronasal 2, receptor 116 [Source:MGI Symbol;Acc:MGI:3646674]		E9Q6I0	6.2	3.7E-04	7.2	5.9E-05	-1.8	1.3E-01	0.1	8.0E-01
ENSMUST00000164859	SUMO/sentrin specific peptidase 6 [Source:MGI Symbol;Acc:MGI:1922075]		Q6P7W0	-4.5	7.0E-03	2.5	6.5E-02	-3.1	3.1E-02	1.7	9.9E-02
ENSMUST00000131034				0.0	1.0E+00	-0.5	7.1E-01	-0.8	4.7E-01	-0.3	8.3E-01
ENSMUST00000131035	ring finger protein 213 [Source:MGI Symbol;Acc:MGI:1289196]		E9Q555	2.3	4.4E-01	1.1	6.7E-01	-2.8	3.2E-01	-1.7	4.9E-01
ENSMUST00000164877	regulating synaptic membrane exocytosis 1 [Source:MGI Symbol;Acc:MGI:2152971]	Q7TPL9		5.1	3.3E-02	7.8	7.2E-03	-0.7	7.7E-01	-2.9	5.9E-02
ENSMUST00000164886	paired immunoglobin-like type 2 receptor beta 2 [Source:MGI Symbol;Acc:MGI:2450535]		Q2YFS1	-5.6	3.9E-07	8.3	1.4E-05	-1.1	3.3E-01	0.0	9.9E-01
ENSMUST00000164904	ubiquitin-like 3 [Source:MGI Symbol;Acc:MGI:1344373]		Q9Z2M6	-4.8	3.0E-04	4.2	1.7E-03	-0.9	3.4E-01	0.0	9.4E-01
ENSMUST00000164915	staphylococcal nuclease and tudor domain containing 1 [Source:MGI Symbol;Acc:MGI:1929266]	E9Q3E9		6.7	7.9E-05	7.1	8.5E-05	-0.3	7.9E-01	0.7	1.9E-01
ENSMUST00000131048	: carrier family 7 (cationic amino acid transporter, y+ system), member 10 [Source:MGI Symbol;Acc:MGI:185	D6RII2		3.1	5.2E-02	5.8	2.5E-03	-0.5	7.6E-01	-3.2	1.1E-02
ENSMUST00000164929	hepsin [Source:MGI Symbol;Acc:MGI:1196620]	E9Q3X9		7.0	5.2E-05	4.8	1.9E-03	-0.4	7.4E-01	0.2	8.1E-01
ENSMUST00000164930	microtubule-associated protein 4 [Source:MGI Symbol;Acc:MGI:97178]	E9PZ43		1.8	1.5E-02	5.7	1.0E-03	-0.5	7.2E-01	-0.3	6.4E-01
ENSMUST00000164932	keratin 78 [Source:MGI Symbol;Acc:MGI:1917529]	E9Q0F0		8.2	1.7E-05	-5.0	1.7E-02	-0.1	9.1E-01	-0.3	8.9E-01
ENSMUST00000164935	HEAT repeat containing 4 [Source:MGI Symbol;Acc:MGI:4937307]	E9Q357		5.5	1.4E-04	-0.8	6.4E-01	-0.1	9.6E-01	3.4	3.1E-02
ENSMUST00000164947	heterogeneous nuclear ribonucleoprotein A3 [Source:MGI Symbol;Acc:MGI:1917171]	Q0VG47	Q8BG05	-7.3	2.5E-04	3.0	2.8E-03	-1.8	3.8E-02	-0.1	8.3E-01
ENSMUST00000131070	insulin degrading enzyme [Source:MGI Symbol;Acc:MGI:96412]	F6RPJ9		-0.4	4.4E-01	0.0	9.9E-01	-0.1	8.5E-01	-0.5	4.5E-01
ENSMUST00000131076				-2.6	5.6E-02	-0.3	8.3E-01	1.6	2.2E-01	-0.7	6.4E-01
ENSMUST00000131078				-1.0	7.2E-01	-1.2	7.5E-01	-0.1	9.8E-01	0.1	9.7E-01
ENSMUST00000164948	predicted gene 7945 [Source:MGI Symbol;Acc:MGI:3646596]	F6QI24		8.2	2.1E-05	5.5	4.8E-06	-1.0	1.3E-01	-0.3	3.6E-01
ENSMUST00000131087	Myb-related transcription factor, partner of profilin [Source:MGI Symbol;Acc:MGI:2446472]		Q8R4U1	0.9	5.7E-01	0.8	6.8E-01	-0.1	9.6E-01	0.0	9.9E-01
ENSMUST00000164954	m large conductance calcium-activated channel, subfamily M, beta member 3 [Source:MGI Symbol;Acc:MGI:3	E9Q7U0		7.0	3.0E-05	4.5	4.0E-02	-0.7	7.0E-01	0.8	5.5E-01
ENSMUST00000131097	RFT1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3607791]	E9Q0V1		1.5	5.7E-01	-1.5	7.3E-01	-1.3	6.4E-01	1.6	6.7E-01
ENSMUST00000131101				-3.3	4.3E-02	-4.1	8.0E-02	-0.1	9.6E-01	0.7	7.5E-01
ENSMUST00000164957	proline rich 13 [Source:MGI Symbol;Acc:MGI:1913401]		Q9CQJ5	-11.7	2.5E-05	6.5	4.9E-04	-0.6	6.6E-01	-0.6	4.4E-01
ENSMUST00000131103	actin, gamma, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:87906]	G3UYG0		-2.4	4.4E-01	-2.9	4.9E-01	-0.8	7.2E-01	-0.3	9.5E-01
ENSMUST00000164960	RasGEF domain family, member 1A [Source:MGI Symbol;Acc:MGI:1917977]	A6H650		6.3	1.0E-04	4.7	1.9E-04	-2.0	3.3E-02	-0.4	4.8E-01
ENSMUST00000164993	inhibin beta-A [Source:MGI Symbol;Acc:MGI:96570]	Q3UY39	Q04998	-4.7	8.7E-04	-1.7	2.5E-02	0.4	3.4E-01	-0.1	9.0E-01
ENSMUST00000131118	AT rich interactive domain 3A (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1328360]	D3YVQ2		1.1	3.4E-01	-0.6	7.1E-01	1.0	4.2E-01	2.6	8.1E-02
ENSMUST00000131120				3.6	4.1E-02	5.2	9.3E-03	-0.4	8.2E-01	-2.0	1.0E-01
ENSMUST00000131122				2.4	8.5E-02	2.8	1.6E-01	0.5	7.5E-01	0.1	9.2E-01
ENSMUST00000131124	zinc finger and BTB domain containing 33 [Source:MGI Symbol;Acc:MGI:1927290]	A2A3Z2		0.7	7.4E-01	0.2	9.3E-01	-0.9	6.2E-01	-0.4	8.7E-01
ENSMUST00000165000	ankyrin repeat domain 65 [Source:MGI Symbol;Acc:MGI:2685285]	F6YK91		6.3	2.4E-04	-3.4	1.5E-02	-1.0	1.2E-01	-1.5	2.7E-01
ENSMUST00000165007	kelch domain containing 3 [Source:MGI Symbol;Acc:MGI:2651568]			-4.0	2.4E-02	7.7	1.1E-04	-0.6	6.2E-01	0.6	3.6E-01
ENSMUST00000131128	F-box and leucine-rich repeat protein 12 [Source:MGI Symbol;Acc:MGI:1354738]			1.2	4.6E-01	2.0	2.9E-01	-1.6	3.6E-01	-2.4	1.3E-01
ENSMUST00000131131				-2.0	2.4E-01	-1.1	4.9E-01	-1.4	2.4E-01	-2.3	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000165024	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2 [Source:MGI Symbol;Acc:MGI:1891351]	F6SLR4		8.4	9.0E-05	4.5	4.1E-02	-0.6	7.4E-01	-0.8	5.7E-01
ENSMUST00000131143	G patch domain containing 1 [Source:MGI Symbol;Acc:MGI:1914721]	D6RJ67		2.8	3.3E-01	-1.4	7.1E-01	-2.7	3.1E-01	1.5	6.8E-01
ENSMUST00000165028	mesoderm induction early response 1, family member 2 [Source:MGI Symbol;Acc:MGI:1917677]		Q3U3N0	3.8	1.4E-02	7.7	5.3E-03	-0.8	7.5E-01	-2.7	5.9E-02
ENSMUST00000131157	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]	H3BJD4		-2.4	1.1E-01	-1.8	3.7E-01	0.7	6.0E-01	0.1	9.7E-01
ENSMUST00000165032	sorting nexing 24 [Source:MGI Symbol;Acc:MGI:1916476]		Q9CRB0	-2.4	1.1E-02	2.2	7.0E-02	-2.2	6.4E-02	0.3	7.2E-01
ENSMUST00000131174				0.6	4.8E-01	1.6	1.3E-01	-0.1	9.1E-01	-1.1	2.3E-01
ENSMUST00000165044	activin receptor IIB [Source:MGI Symbol;Acc:MGI:87912]		P27040	4.8	8.1E-05	2.9	6.0E-04	-1.8	1.4E-02	-1.1	3.8E-02
ENSMUST00000131177				2.6	2.5E-01	-1.1	6.7E-01	-2.2	3.3E-01	1.6	5.1E-01
ENSMUST00000131183				4.6	3.5E-02	4.5	4.9E-02	-1.3	5.2E-01	-1.2	4.4E-01
ENSMUST00000131184	TAR (HIV) RNA binding protein 2 [Source:MGI Symbol;Acc:MGI:103027]	D6RE49		-1.4	2.6E-01	-2.7	9.5E-02	-1.1	2.7E-01	0.2	9.0E-01
ENSMUST00000165061	cytochrome P450, family 4, subfamily f, polypeptide 40 [Source:MGI Symbol;Acc:MGI:3645508]	G3UW81		7.4	6.8E-05	0.9	7.4E-01	-0.5	8.0E-01	3.3	2.2E-01
ENSMUST00000131191				0.8	3.7E-01	-2.0	9.7E-02	-2.3	1.6E-02	0.5	6.3E-01
ENSMUST00000165088	transmembrane protease, serine 5 (spinesin) [Source:MGI Symbol;Acc:MGI:1933407]		Q9ER04	7.1	7.2E-05	-5.8	1.8E-03	-0.4	4.4E-01	-0.6	6.8E-01
ENSMUST00000131195				2.1	3.8E-01	1.7	4.9E-01	-1.1	6.2E-01	-0.7	7.7E-01
ENSMUST00000165096	major vault protein [Source:MGI Symbol;Acc:MGI:1925638]	E9Q3X0		-5.3	9.4E-06	-4.2	9.0E-03	-0.9	2.2E-01	-0.1	9.5E-01
ENSMUST00000131204				-1.9	5.2E-02	-1.5	1.8E-01	-0.4	5.6E-01	-0.9	4.1E-01
ENSMUST00000131210				-0.6	2.6E-01	0.1	8.7E-01	0.6	2.3E-01	-0.1	8.7E-01
ENSMUST00000131213	G patch domain containing 1 [Source:MGI Symbol;Acc:MGI:1914721]	D6RET6		4.5	5.7E-02	3.2	1.2E-01	-3.4	1.5E-01	-2.1	1.8E-01
ENSMUST00000165099	deafness, autosomal dominant 5 (human) [Source:MGI Symbol;Acc:MGI:1889850]	E9Q5V3		2.7	9.9E-04	-2.4	3.2E-01	2.4	1.0E-01	0.4	8.6E-01
ENSMUST00000165104	GRAM domain containing 1B [Source:MGI Symbol;Acc:MGI:1925037]		Q80TI0	-4.8	1.5E-02	-5.0	1.8E-03	-2.0	6.0E-03	-1.3	3.6E-01
ENSMUST00000131230				1.9	1.8E-01	3.5	6.9E-02	0.8	6.3E-01	-0.9	4.8E-01
ENSMUST00000131235	MKL (megakaryoblastic leukemia)/myocardin-like 1 [Source:MGI Symbol;Acc:MGI:2384495]	D3YUI2		3.9	5.3E-02	3.5	1.3E-01	-0.6	7.3E-01	-0.3	8.7E-01
ENSMUST00000165109	neuraminidase 2 [Source:MGI Symbol;Acc:MGI:1344417]	Q0VGI4	Q9JMH3	6.5	3.7E-04	5.6	4.2E-04	-1.8	1.4E-01	-0.2	7.5E-01
ENSMUST00000165111	ATP citrate lyase [Source:MGI Symbol;Acc:MGI:103251]		Q91V92	-9.3	2.7E-05	6.8	2.2E-03	-1.7	3.7E-01	1.0	2.4E-01
ENSMUST00000131244				-1.2	2.5E-01	-2.7	1.2E-01	-0.3	7.8E-01	1.3	4.1E-01
ENSMUST00000131245	transformation related protein 53 binding protein 1 [Source:MGI Symbol;Acc:MGI:1351320]	A2AU90		1.9	2.7E-01	1.0	6.3E-01	-1.3	4.3E-01	-0.4	8.4E-01
ENSMUST00000165117	cyclin-dependent kinase 6 [Source:MGI Symbol;Acc:MGI:1277162]	Q0VBK8	Q64261	3.1	6.9E-05	6.6	2.2E-05	-0.3	6.7E-01	-0.3	5.0E-01
ENSMUST00000131252	splicing factor 1 [Source:MGI Symbol;Acc:MGI:1095403]	Q3UI45	Q64213	-1.3	9.9E-02	-0.1	9.1E-01	0.6	3.5E-01	-0.6	5.0E-01
ENSMUST00000165123	casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]	Q6PJ87	Q8BK63	-4.9	1.4E-04	-2.6	2.0E-02	-0.5	3.5E-01	-0.5	6.5E-01
ENSMUST00000165124	hepsin [Source:MGI Symbol;Acc:MGI:1196620]			6.5	3.7E-04	4.1	5.8E-04	-1.3	1.2E-01	-0.8	2.2E-01
ENSMUST00000131264				0.9	6.4E-01	-0.8	7.3E-01	-1.4	4.4E-01	0.3	9.0E-01
ENSMUST00000131265	phosphatidylinositol transfer protein, membrane-associated 1 [Source:MGI Symbol;Acc:MGI:1197524]	D3YXW5		-0.2	8.8E-01	1.1	5.3E-01	-0.4	8.1E-01	-1.7	2.6E-01
ENSMUST00000165126	ubiquitin A-52 residue ribosomal protein fusion product 1 [Source:MGI Symbol;Acc:MGI:98887]	Q66JP1	P62984	-8.9	3.4E-05	3.6	4.0E-02	0.2	8.9E-01	0.7	5.2E-01
ENSMUST00000165133	spermatogenesis associated 31 subfamily D, member 1B [Source:MGI Symbol;Acc:MGI:3646080]	E9QA57		9.4	3.4E-05	4.7	1.7E-03	-1.7	1.3E-01	0.3	6.6E-01
ENSMUST00000131278				0.0	9.6E-01	1.0	3.1E-01	0.0	9.6E-01	-1.0	3.2E-01
ENSMUST00000165134	SEC23 homolog A, COPII coat complex component [Source:MGI Symbol;Acc:MGI:1349635]	E9Q1S3		-6.0	1.6E-03	5.6	1.5E-04	-2.0	7.5E-02	-0.4	4.7E-01
ENSMUST00000131283	pre-mRNA processing factor 8 [Source:MGI Symbol;Acc:MGI:2179381]	B7ZC27		4.3	8.1E-02	3.1	3.6E-01	0.2	9.5E-01	1.4	5.2E-01
ENSMUST00000165143	polymerase (DNA directed), alpha 2 [Source:MGI Symbol;Acc:MGI:99690]	Q8C2T6		2.3	1.2E-02	1.7	5.0E-02	-0.6	3.2E-01	0.2	7.7E-01
ENSMUST00000165147	mucin 5, subtype B, tracheobronchial [Source:MGI Symbol;Acc:MGI:1921430]	E9Q5I3		8.7	6.8E-07	-3.6	1.9E-02	2.0	8.6E-03	0.1	9.3E-01
ENSMUST00000165148	coiled-coil domain containing 62 [Source:MGI Symbol;Acc:MGI:2684996]		E9PVD1	6.6	2.0E-04	-4.2	7.7E-02	1.1	2.3E-01	0.1	9.7E-01
ENSMUST00000131291				-1.9	5.2E-02	-4.1	8.1E-03	-1.0	1.3E-01	1.2	3.7E-01
ENSMUST00000165173	predicted gene 6729 [Source:MGI Symbol;Acc:MGI:3646339]	E9Q4Z5		7.5	4.1E-05	3.8	4.3E-02	-1.4	4.2E-01	0.2	8.8E-01
ENSMUST00000131298	Ral GEF with PH domain and SH3 binding motif 1 [Source:MGI Symbol;Acc:MGI:1922008]		A2AR50	0.2	9.5E-01	-3.2	4.7E-01	-1.9	4.4E-01	1.4	7.4E-01
ENSMUST00000165175	synaptic vesicle glycoprotein 2 b [Source:MGI Symbol;Acc:MGI:1927338]		Q8BG39	4.1	2.5E-02	-5.7	5.0E-02	-0.3	8.0E-01	-1.3	6.6E-01
ENSMUST00000131306	PDZ and LIM domain 7 [Source:MGI Symbol;Acc:MGI:1914649]	B8JJB3		2.5	5.5E-02	2.5	1.4E-01	0.0	1.0E+00	0.0	1.0E+00
ENSMUST00000165180	vomeronasal 2, receptor 16 [Source:MGI Symbol;Acc:MGI:3647194]	E9Q025		6.2	1.4E-03	5.7	7.8E-04	-1.5	2.6E-01	0.2	7.5E-01
ENSMUST00000165190	tonsoku-like, DNA repair protein [Source:MGI Symbol;Acc:MGI:1919999]	E9Q2M2		6.9	1.3E-04	4.1	1.4E-03	-0.1	9.2E-01	0.0	1.0E+00
ENSMUST00000131310				-1.4	1.4E-01	-3.0	4.8E-02	-0.7	3.6E-01	0.9	4.9E-01
ENSMUST00000165196	predicted gene, 38392 [Source:MGI Symbol;Acc:MGI:5613632]	E9Q2A2		6.6	3.9E-04	7.8	1.4E-06	0.0	9.8E-01	0.3	3.5E-01
ENSMUST00000165205	leucine rich repeat containing 32 [Source:MGI Symbol;Acc:MGI:93882]	G3XA59		7.5	8.1E-07	-4.8	5.5E-02	1.1	3.3E-01	-0.5	8.2E-01
ENSMUST00000165208	myosin binding protein C, fast-type [Source:MGI Symbol;Acc:MGI:1336170]		Q5XKE0	7.7	8.3E-06	6.2	2.6E-04	-0.6	6.0E-01	-0.4	4.9E-01
ENSMUST00000165219	CLP1, cleavage and polyadenylation factor I subunit [Source:MGI Symbol;Acc:MGI:2138968]		Q99LI9	3.8	6.1E-03	-2.1	1.8E-01	0.9	3.6E-01	-2.7	1.4E-01
ENSMUST00000165220	predicted gene 9742 [Source:MGI Symbol;Acc:MGI:3780137]	E9Q1C0		10.7	9.5E-05	3.7	2.8E-02	-0.3	8.2E-01	-0.3	7.8E-01
ENSMUST00000131332	acyl-CoA thioesterase 9 [Source:MGI Symbol;Acc:MGI:1928939]	S4R266		-2.0	4.3E-01	-2.0	5.1E-01	-0.8	6.9E-01	-0.8	8.0E-01
ENSMUST00000165223	CLIP associating protein 1 [Source:MGI Symbol;Acc:MGI:1923957]	E9Q6L0		-6.4	4.0E-03	5.6	2.2E-04	0.7	4.7E-01	0.3	5.6E-01
ENSMUST00000165231	deleted in lung and esophageal cancer 1 [Source:MGI Symbol;Acc:MGI:2443671]	E9Q8C0		5.0	1.0E-02	-3.3	1.1E-02	-1.0	1.1E-01	-1.0	4.1E-01
ENSMUST00000131348	fibroblast growth factor 1 [Source:MGI Symbol;Acc:MGI:95515]	D6RCX9		5.2	6.1E-02	4.9	2.7E-02	-2.9	2.5E-01	-2.6	1.2E-01
ENSMUST00000165242	eukaryotic elongation factor, selenocysteine-tRNA-specific [Source:MGI Symbol;Acc:MGI:2137092]		Q9JHW4	2.0	1.4E-03	-1.8	2.8E-02	0.3	5.3E-01	-0.4	5.3E-01
ENSMUST00000165255	vomeronasal 1 receptor, 238 [Source:MGI Symbol;Acc:MGI:3852494]	E9Q373		6.4	1.2E-04	-1.2	3.4E-01	0.4	6.7E-01	-1.1	4.0E-01
ENSMUST00000165269	dynein, axonemal, heavy chain 12 [Source:MGI Symbol;Acc:MGI:107720]	F6QA95		5.5	2.1E-04	3.4	1.3E-02	-0.4	6.7E-01	0.7	4.2E-01
ENSMUST00000165276	immunoglobulin superfamily containing leucine-rich repeat 2 [Source:MGI Symbol;Acc:MGI:2444277]		Q5RKR3	8.5	9.4E-05	-1.2	7.2E-02	1.0	2.5E-02	-0.3	6.5E-01
ENSMUST00000131359				-2.0	1.5E-01	-1.8	1.4E-01	-2.4	1.9E-02	-2.6	8.4E-02
ENSMUST00000131364	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]	D3Z6L9		-1.4	2.5E-01	-1.3	3.9E-01	-0.2	8.5E-01	-0.2	8.8E-01
ENSMUST00000165280	bone morphogenetic protein receptor, type 1A [Source:MGI Symbol;Acc:MGI:1338938]	Q60607		-4.6	2.4E-03	4.2	3.5E-04	-1.1	1.5E-01	0.4	4.8E-01
ENSMUST00000165289	predicted gene 3298 [Source:MGI Symbol;Acc:MGI:3781476]	L7N281		9.7	9.9E-06	-6.8	4.4E-04	-0.8	1.3E-01	-1.5	3.6E-01
ENSMUST00000165307	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Source:MGI Symbol;Acc:MGI:1913721]		P97822	-3.1	2.3E-02	-1.0	4.7E-01	1.9	3.6E-02	-0.5	7.0E-01
ENSMUST00000131376	extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:103060]	D3YV64		-1.5	5.4E-01	-2.6	4.0E-01	-1.8	3.4E-01	-0.7	8.2E-01
ENSMUST00000131377	RNA binding motif protein 12 [Source:MGI Symbol;Acc:MGI:1922960]	B7ZCP9		1.5	4.2E-01	2.7	1.6E-01	-2.1	2.6E-01	-3.3	7.2E-02
ENSMUST00000165311	cyclin M1 [Source:MGI Symbol;Acc:MGI:1891366]		Q0GA42	8.8	5.8E-06	4.9	1.5E-02	-1.5	4.0E-01	-2.4	6.6E-02
ENSMUST00000131384	glutamate-rich WD repeat containing 1 [Source:MGI Symbol;Acc:MGI:2141989]		Q810D6	4.6	8.2E-02	4.4	1.1E-01	-0.7	8.0E-01	-0.6	7.5E-01
ENSMUST00000165313	RNA binding motif protein 43 [Source:MGI Symbol;Acc:MGI:1918934]		Q99J64	-7.3	8.0E-04	6.1	4.3E-03	-0.5	7.8E-01	0.0	9.9E-01
ENSMUST00000165315	sorting nexin 14 [Source:MGI Symbol;Acc:MGI:2155664]		Q8BHY8	-8.1	1.2E-04	8.9	3.7E-03	3.6	1.5E-01	-0.4	7.1E-01
ENSMUST00000165318	RB-associated KRAB zinc finger [Source:MGI Symbol;Acc:MGI:1927369]		Q8BQC8	4.3	1.8E-02	4.9	2.0E-04	-0.8	3.2E-01	-0.2	7.3E-01
ENSMUST00000165322	ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:13	H9KV21		-6.1	8.5E-05	4.2	3.7E-03	0.8	4.5E-01	0.7	3.5E-01
ENSMUST00000131398	onooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Source:MGI Symbol;Acc:M	F6WA09		-2.2	2.7E-01	3.1	2.4E-01	3.5	1.4E-01	-1.9	3.8E-01
ENSMUST00000131399				-0.1	9.8E-01	-1.1	8.0E-01	0.0	9.9E-01	1.0	8.0E-01
ENSMUST00000165324	hematopoietic SH2 domain containing [Source:MGI Symbol;Acc:MGI:2676364]		Q6VYH9	-3.6	3.0E-02	-7.2	2.5E-04	-0.8	7.8E-02	1.7	1.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000165341	otogelin-like [Source:MGI Symbol;Acc:MGI:3647600]		F7A4A7	7.4	5.8E-05	-2.2	1.4E-02	0.4	3.5E-01	-1.5	7.5E-02
ENSMUST00000131405	phosphoinositide-3-kinase, class 3 [Source:MGI Symbol;Acc:MGI:2445019]	E9Q824		2.9	1.7E-01	4.9	5.7E-02	-0.6	7.9E-01	-2.6	1.4E-01
ENSMUST00000165344	growth factor independent 1 [Source:MGI Symbol;Acc:MGI:103170]	A1L3P3		3.6	1.8E-02	3.5	2.9E-03	0.8	3.3E-01	-0.9	2.1E-01
ENSMUST00000165345	predicted gene, 17521 [Source:MGI Symbol;Acc:MGI:4937155]	F6QAC8		7.4	2.3E-05	5.7	3.6E-04	-1.3	2.8E-01	-0.4	5.0E-01
ENSMUST00000165375	homeobox C4 [Source:MGI Symbol;Acc:MGI:96195]	G3UX59		8.8	2.8E-04	-3.8	1.9E-02	0.8	3.0E-01	-1.8	2.9E-01
ENSMUST00000165389	BCL2/adenovirus E1B interacting protein 2 [Source:MGI Symbol;Acc:MGI:109327]	Q91VL0		-6.9	8.0E-06	-5.3	7.0E-04	1.2	1.7E-02	0.3	7.6E-01
ENSMUST00000165390	molybdenum cofactor synthesis 1 [Source:MGI Symbol;Acc:MGI:1928904]	G3UWH1		4.9	1.7E-04	6.4	4.8E-04	-0.4	7.4E-01	-0.6	4.2E-01
ENSMUST00000131433				0.2	8.3E-01	0.5	5.9E-01	-0.4	6.2E-01	-0.7	4.2E-01
ENSMUST00000131435				2.2	2.1E-01	-1.2	5.1E-01	-2.6	1.1E-01	0.8	6.6E-01
ENSMUST00000165394	ubiquitin-conjugating enzyme E2M [Source:MGI Symbol;Acc:MGI:108278]	G5E919		-2.6	1.8E-02	-3.2	1.2E-01	0.2	8.7E-01	-0.9	6.4E-01
ENSMUST00000165399	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 [Source:MGI Symbol;Acc:MGI:98886]	Q3KQM4		-4.9	1.3E-02	-3.8	3.3E-02	0.3	7.1E-01	0.7	6.7E-01
ENSMUST00000131448	oxidative stress induced growth inhibitor 1 [Source:MGI Symbol;Acc:MGI:1919089]	D3YYR6		-1.6	2.5E-01	0.6	7.2E-01	0.8	5.8E-01	-1.4	3.5E-01
ENSMUST00000165408	BAI1-associated protein 2-like 2 [Source:MGI Symbol;Acc:MGI:2652819]		Q80Y61	7.3	2.0E-04	5.6	1.2E-02	-1.6	4.3E-01	0.7	5.6E-01
ENSMUST00000165416	regulator of G-protein signaling 19 [Source:MGI Symbol;Acc:MGI:1915153]	Q78NN4	Q9CX84	-5.9	4.3E-06	4.5	1.5E-02	-1.4	4.1E-01	-1.0	4.3E-01
ENSMUST00000131470				-1.0	2.5E-01	1.7	4.5E-02	-0.9	2.0E-01	-3.6	2.3E-03
ENSMUST00000165420	ring finger protein 24 [Source:MGI Symbol;Acc:MGI:1261771]	Q4VA59	Q8BGI1	-6.1	2.5E-04	1.2	1.9E-01	-1.1	1.6E-01	0.3	7.2E-01
ENSMUST00000131476	protein phosphatase 2A activator, regulatory subunit B [Source:MGI Symbol;Acc:MGI:1346006]	B7ZDE0		0.8	5.1E-01	2.7	7.4E-02	0.5	6.9E-01	-1.4	2.6E-01
ENSMUST00000131477				-1.0	3.6E-01	1.1	4.1E-01	1.0	4.0E-01	-1.2	3.3E-01
ENSMUST00000131483	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143057]		Q80SX8	-1.8	2.0E-01	-0.4	8.0E-01	1.6	1.5E-01	0.3	8.7E-01
ENSMUST00000165430	catechol-O-methyltransferase [Source:MGI Symbol;Acc:MGI:88470]		O88587	1.9	1.4E-02	2.1	2.8E-01	-3.2	1.5E-01	1.3	3.7E-01
ENSMUST00000131489	SURP and G patch domain containing 2 [Source:MGI Symbol;Acc:MGI:2678085]		Q8CH09	1.4	5.8E-01	1.2	7.2E-01	-0.1	9.8E-01	0.1	9.7E-01
ENSMUST00000131495				2.6	9.6E-02	4.8	7.8E-03	-0.6	7.1E-01	-2.7	3.5E-02
ENSMUST00000165443	nucleoporin 50 [Source:MGI Symbol;Acc:MGI:1351502]		Q9JIH2	-1.7	4.0E-03	4.0	9.7E-04	0.3	7.3E-01	-0.4	5.4E-01
ENSMUST00000165453	plectin [Source:MGI Symbol;Acc:MGI:1277961]			5.9	1.2E-03	4.8	8.3E-03	-0.9	5.3E-01	0.6	5.6E-01
ENSMUST00000131511				0.3	6.3E-01	-0.2	8.1E-01	-0.6	3.7E-01	0.0	9.7E-01
ENSMUST00000165466	RIKEN cDNA 2610042L04 gene [Source:MGI Symbol;Acc:MGI:1914305]	Q9D073		6.8	9.2E-05	7.3	1.2E-04	2.0	9.7E-02	-0.3	6.6E-01
ENSMUST00000165469	sorbin and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:700014]	E9Q6A3		-3.3	2.6E-02	6.1	1.8E-03	-0.7	6.7E-01	-1.3	1.6E-01
ENSMUST00000165477	ATP/GTP binding protein 1 [Source:MGI Symbol;Acc:MGI:2159437]	E9PXA7		4.9	1.2E-03	6.2	7.2E-04	0.3	8.0E-01	-0.2	7.5E-01
ENSMUST00000165485	ermal growth factor-containing fibulin-like extracellular matrix protein 2 [Source:MGI Symbol;Acc:MGI:1891	Q542X5	Q9WVJ9	-4.1	3.1E-03	8.3	1.4E-06	-1.2	1.5E-01	0.3	3.4E-01
ENSMUST00000165493	NOL1/NOP2/Sun domain family, member 4 [Source:MGI Symbol;Acc:MGI:1919431]		C4P6S0	8.7	2.5E-05	-1.1	1.7E-01	0.7	2.2E-01	-0.3	7.1E-01
ENSMUST00000165495	RIKEN cDNA E430018J23 gene [Source:MGI Symbol;Acc:MGI:2141981]	E9PZQ8		6.8	2.8E-05	7.8	2.9E-04	-1.2	4.5E-01	1.4	8.0E-02
ENSMUST00000165504	zinc finger protein 414 [Source:MGI Symbol;Acc:MGI:1915641]	E9Q9N0		-3.0	1.1E-03	7.5	5.3E-05	-0.5	6.7E-01	-1.2	5.2E-02
ENSMUST00000131545	GDP-mannose pyrophosphorylase A [Source:MGI Symbol;Acc:MGI:1916330]	D3Z0T7		0.9	2.6E-01	3.4	4.7E-02	4.6	3.4E-03	2.1	9.3E-02
ENSMUST00000131546	RIKEN cDNA 4933427D14 gene [Source:MGI Symbol;Acc:MGI:1921727]	F2Z444		-2.6	3.5E-01	-3.6	3.0E-01	-1.7	3.6E-01	-0.8	8.3E-01
ENSMUST00000131558	histocompatibility 60b [Source:MGI Symbol;Acc:MGI:3649078]	B1B212		3.7	4.1E-02	5.3	8.8E-03	-0.5	7.7E-01	-2.1	8.4E-02
ENSMUST00000131561				3.3	7.3E-02	5.1	7.0E-02	2.2	3.6E-01	0.4	7.8E-01
ENSMUST00000165512	motor neuron and pancreas homeobox 1 [Source:MGI Symbol;Acc:MGI:109160]	A2RSX2		6.7	1.3E-04	2.5	1.1E-02	0.3	6.5E-01	-0.2	7.4E-01
ENSMUST00000165519	zinc finger CCCH type containing 12C [Source:MGI Symbol;Acc:MGI:3026959]	E9Q1I3		3.6	1.2E-04	-3.6	1.4E-02	0.7	3.2E-01	-3.9	3.9E-02
ENSMUST00000165526	fibroblast growth factor 9 [Source:MGI Symbol;Acc:MGI:104723]	E9Q2N2		7.5	4.2E-05	7.5	2.7E-04	0.5	7.2E-01	1.2	5.9E-02
ENSMUST00000165532	ribosomal protein L14 [Source:MGI Symbol;Acc:MGI:1914365]		Q9CR57	-5.9	7.5E-06	5.6	2.8E-03	-0.5	7.2E-01	-0.5	5.1E-01
ENSMUST00000131579				2.9	1.5E-01	2.2	4.3E-01	0.3	9.0E-01	1.0	6.4E-01
ENSMUST00000131589	nucleobindin 1 [Source:MGI Symbol;Acc:MGI:97388]	D3Z7D7		0.3	8.9E-01	1.4	6.6E-01	0.8	7.1E-01	-0.3	9.3E-01
ENSMUST00000165536	Kruppel-like factor 3 (basic) [Source:MGI Symbol;Acc:MGI:1342773]	Q545J5	Q60980	-3.8	3.6E-05	2.8	5.0E-03	0.1	8.4E-01	0.5	4.4E-01
ENSMUST00000165538	potassium inwardly-rectifying channel, subfamily J, member 6 [Source:MGI Symbol;Acc:MGI:104781]			8.0	1.2E-05	4.6	4.5E-04	-1.1	2.1E-01	-0.1	8.3E-01
ENSMUST00000165541	protein tyrosine phosphatase 4a3 [Source:MGI Symbol;Acc:MGI:1277098]		Q9D658	-5.2	2.4E-03	1.7	5.8E-02	-0.5	5.0E-01	-0.1	8.3E-01
ENSMUST00000165549	caspase 8 [Source:MGI Symbol;Acc:MGI:1261423]	Q3U607	O89110	-2.5	3.3E-02	5.8	4.1E-03	-0.6	7.0E-01	-1.5	1.4E-01
ENSMUST00000131606	transmembrane channel-like gene family 6 [Source:MGI Symbol;Acc:MGI:1098686]	D6RCY1		1.3	3.0E-01	1.7	3.7E-01	0.4	8.0E-01	0.0	9.9E-01
ENSMUST00000131607				0.9	4.2E-01	0.7	6.3E-01	-0.1	9.5E-01	0.1	9.4E-01
ENSMUST00000131609	supervillin [Source:MGI Symbol;Acc:MGI:2147319]	Q8K4L2		3.7	2.4E-01	1.8	6.1E-01	-1.4	6.8E-01	0.6	8.4E-01
ENSMUST00000165555	mindbomb homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2443157]		Q80SY4	-4.7	8.8E-04	0.1	9.4E-01	0.0	9.8E-01	2.4	8.2E-02
ENSMUST00000131613	mitochondrial fission regulator 1-like [Source:MGI Symbol;Acc:MGI:1924074]	D6RCX5		-2.2	3.5E-01	1.6	6.2E-01	4.1	1.1E-01	0.4	9.0E-01
ENSMUST00000165559	CBP80/20-dependent translation initiation factor [Source:MGI Symbol;Acc:MGI:2685518]	E9Q1U6		6.9	2.9E-05	8.3	2.4E-05	-0.2	8.2E-01	0.4	4.9E-01
ENSMUST00000165563	mitochondrial calcium uptake 1 [Source:MGI Symbol;Acc:MGI:2384909]		Q8VCX5	-4.5	4.7E-03	-3.5	4.2E-02	0.2	8.4E-01	-0.7	6.5E-01
ENSMUST00000165566	regulatory factor X, 3 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:106582]		P48381	1.4	2.2E-02	5.4	1.8E-03	-0.8	5.6E-01	-0.7	4.0E-01
ENSMUST00000165594	septin 7 [Source:MGI Symbol;Acc:MGI:1335094]	E9Q1G8		-7.9	4.8E-06	-0.8	6.7E-01	1.7	2.2E-01	-0.8	6.4E-01
ENSMUST00000165605	GH regulated TBC protein 1 [Source:MGI Symbol;Acc:MGI:1914040]		Q9D3N8	5.5	1.5E-04	4.7	7.4E-05	-0.3	6.4E-01	0.3	5.0E-01
ENSMUST00000165607	SUMO/sentrin specific peptidase 6 [Source:MGI Symbol;Acc:MGI:1922075]	F6Z9A1		-6.8	4.8E-03	3.2	1.9E-03	-0.3	6.1E-01	0.1	9.0E-01
ENSMUST00000165608	exportin 6 [Source:MGI Symbol;Acc:MGI:2429950]	F7B8F0		-7.1	1.4E-03	1.9	1.0E-01	0.0	9.8E-01	1.1	2.7E-01
ENSMUST00000165649	growth hormone inducible transmembrane protein [Source:MGI Symbol;Acc:MGI:1913342]		Q91VC9	-6.1	3.4E-04	3.3	1.3E-03	0.2	7.0E-01	-0.2	7.8E-01
ENSMUST00000165665	Rho guanine nucleotide exchange factor (GEF) 12 [Source:MGI Symbol;Acc:MGI:1916882]	F8VQN6		8.5	3.5E-03	1.4	1.1E-01	-1.8	3.5E-02	-0.6	4.3E-01
ENSMUST00000165680	predicted gene, 17509 [Source:MGI Symbol;Acc:MGI:4937143]	Q9CZ61		4.5	8.6E-05	4.0	2.0E-03	0.9	3.0E-01	-0.6	4.0E-01
ENSMUST00000165682	RAS-like, family 12 [Source:MGI Symbol;Acc:MGI:1918034]	E9PUV1		8.0	1.6E-06	3.7	1.3E-04	-0.1	8.2E-01	0.0	9.7E-01
ENSMUST00000165687	transmembrane protein 207 [Source:MGI Symbol;Acc:MGI:2685386]		P86045	6.6	7.0E-05	8.5	9.2E-05	-0.2	8.8E-01	-0.7	2.6E-01
ENSMUST00000165717	prefoldin 5 [Source:MGI Symbol;Acc:MGI:1928753]	E9Q093		-9.2	1.1E-06	-4.6	1.5E-02	0.4	5.7E-01	0.2	9.2E-01
ENSMUST00000165720	transcription elongation factor A (SII) 1 [Source:MGI Symbol;Acc:MGI:1196624]	E9PYD5		7.8	3.7E-05	6.4	4.7E-04	-0.6	6.7E-01	-0.7	3.0E-01
ENSMUST00000165721	casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]		Q8BK63	-7.4	1.6E-05	-3.0	5.8E-04	-0.2	6.3E-01	-3.6	1.5E-03
ENSMUST00000165740	trans-2,3-enoyl-CoA reductase [Source:MGI Symbol;Acc:MGI:1915408]	G3UWE1		-7.4	1.5E-05	7.1	7.0E-06	0.5	5.2E-01	-0.3	5.3E-01
ENSMUST00000131680	PHD finger protein 12 [Source:MGI Symbol;Acc:MGI:1924057]	F6U3I4		-1.8	2.4E-01	-2.3	3.0E-01	0.3	7.9E-01	0.7	7.4E-01
ENSMUST00000165744	predicted gene 3739 [Source:MGI Symbol;Acc:MGI:3781914]	L7N296		5.6	4.1E-04	-3.1	3.7E-02	0.8	2.7E-01	-0.7	6.6E-01
ENSMUST00000131684				-1.2	4.5E-01	2.4	2.1E-01	1.2	4.6E-01	-2.4	1.5E-01
ENSMUST00000165774	guanylate binding protein 2 [Source:MGI Symbol;Acc:MGI:102772]		Q9Z0E6	-4.6	7.0E-04	-1.6	6.9E-02	1.1	5.0E-02	-0.4	5.9E-01
ENSMUST00000131691				1.3	4.6E-01	1.5	5.0E-01	-1.3	4.8E-01	-1.4	4.8E-01
ENSMUST00000131696	nucleolar protein 9 [Source:MGI Symbol;Acc:MGI:1921285]			3.0	1.6E-01	2.9	1.8E-01	-1.4	4.9E-01	-1.3	4.8E-01
ENSMUST00000165781	vomeronasal 2, receptor 120 [Source:MGI Symbol;Acc:MGI:3644483]	E9PX34		7.1	3.3E-05	6.5	2.8E-04	-0.9	4.8E-01	0.7	3.0E-01
ENSMUST00000165806	katanin p60 (ATPase-containing) subunit A1 [Source:MGI Symbol;Acc:MGI:1344353]	E9PZI6		-4.5	2.8E-05	5.5	4.3E-03	-0.7	6.6E-01	-0.6	5.4E-01
ENSMUST00000131706	Scm-like with four mbt domains 1 [Source:MGI Symbol;Acc:MGI:1859609]	E9Q354		1.9	3.1E-01	4.4	6.8E-02	-0.1	9.8E-01	-2.5	1.8E-01
ENSMUST00000165810	SEC14-like lipid binding 5 [Source:MGI Symbol;Acc:MGI:3616084]	B2RXM5		7.9	2.1E-05	8.8	3.5E-05	-0.1	9.1E-01	1.0	7.4E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000165824	RIKEN cDNA 2810459M11 gene [Source:MGI Symbol;Acc:MGI:1920042]	B7ZMV2	Q9CYS6	8.5	2.6E-05	-5.9	6.9E-04	-0.5	3.2E-01	0.2	8.7E-01
ENSMUST00000165829	retrotransposon gag domain containing 1 [Source:MGI Symbol;Acc:MGI:2685231]		Q32KG4	8.1	4.9E-04	6.5	9.2E-05	0.5	5.9E-01	-0.6	3.3E-01
ENSMUST00000165830	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:106299]	F7A9G8		4.4	9.3E-03	5.1	1.7E-02	-0.5	7.7E-01	-1.3	3.6E-01
ENSMUST00000165834	vomeronasal 2, receptor 80 [Source:MGI Symbol;Acc:MGI:3646321]	E9Q1L0		5.0	8.9E-03	3.9	1.6E-04	0.1	8.0E-01	-0.1	7.7E-01
ENSMUST00000165839	solute carrier family 37 (glucose-6-phosphate transporter), member 4 [Source:MGI Symbol;Acc:MGI:1316650]	Q9D1F9		-2.1	5.3E-03	4.6	6.8E-04	0.1	9.3E-01	-0.1	8.7E-01
ENSMUST00000165853	protein tyrosine phosphatase 4a2 [Source:MGI Symbol;Acc:MGI:1277117]		O70274	-4.9	1.1E-04	7.3	6.5E-05	-0.6	6.0E-01	-0.1	8.8E-01
ENSMUST00000165855	receptor (calcitonin) activity modifying protein 1 [Source:MGI Symbol;Acc:MGI:1858418]	E9Q915		5.3	2.7E-02	2.9	9.3E-02	-1.7	2.8E-01	-0.3	7.9E-01
ENSMUST00000165859	transmembrane protein 194B [Source:MGI Symbol;Acc:MGI:2444113]		Q8CB65	-4.8	1.6E-02	5.5	3.6E-04	-2.9	2.9E-02	-0.7	2.9E-01
ENSMUST00000165860	ubiquitin protein ligase E3 component n-recognin 4 [Source:MGI Symbol;Acc:MGI:1916366]		A2AN08	-4.4	2.9E-02	-2.3	5.2E-02	0.4	4.8E-01	-1.0	3.6E-01
ENSMUST00000165861	heterochromatin protein 1, binding protein 3 [Source:MGI Symbol;Acc:MGI:109369]		Q3TEA8	-4.6	1.8E-02	4.7	1.8E-04	-1.0	2.0E-01	-0.1	8.1E-01
ENSMUST00000165866	mesoderm induction early response 1, family member 2 [Source:MGI Symbol;Acc:MGI:1917677]	E9Q3D9		7.4	1.0E-04	7.2	6.0E-06	0.3	7.4E-01	-0.1	8.8E-01
ENSMUST00000165867	component of oligomeric golgi complex 4 [Source:MGI Symbol;Acc:MGI:2142808]	Q7TSQ9		7.2	1.0E-03	5.4	1.4E-04	-1.5	1.2E-01	-1.3	5.1E-02
ENSMUST00000131736	RIKEN cDNA 4930404N11 gene [Source:MGI Symbol;Acc:MGI:1921072]	F6UVB2		2.1	1.1E-01	3.0	1.1E-01	0.6	7.3E-01	-0.3	8.1E-01
ENSMUST00000131741				1.6	5.7E-02	2.3	4.5E-02	0.7	3.9E-01	0.0	9.6E-01
ENSMUST00000131743				0.2	7.7E-01	0.7	4.0E-01	0.2	7.9E-01	-0.3	6.6E-01
ENSMUST00000165870	serine/threonine kinase 32C [Source:MGI Symbol;Acc:MGI:2385336]	E9PXK4		5.5	1.2E-02	5.9	2.6E-03	-2.3	1.6E-01	-0.6	4.8E-01
ENSMUST00000165873	Sec24 related gene family, member B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2139764]	F6VJC5		-4.6	1.2E-03	3.3	6.5E-03	-0.3	7.4E-01	-0.9	3.0E-01
ENSMUST00000165878	prosaposin [Source:MGI Symbol;Acc:MGI:97783]	E9PZ00		-8.4	1.9E-04	6.8	1.8E-03	0.9	5.6E-01	0.8	3.8E-01
ENSMUST00000131752				1.2	7.2E-01	4.9	2.5E-01	0.6	8.8E-01	-3.0	3.2E-01
ENSMUST00000165906	predicted gene 4924 [Source:MGI Symbol;Acc:MGI:3643133]	Q3UF22		5.6	4.2E-05	6.3	2.0E-04	-2.4	7.4E-02	0.9	1.8E-01
ENSMUST00000131759				-0.1	9.8E-01	-1.1	7.6E-01	-1.8	4.6E-01	-0.8	8.3E-01
ENSMUST00000165909	prominin 1 [Source:MGI Symbol;Acc:MGI:1100886]	Q8CDK8		8.4	1.1E-04	7.7	6.7E-05	-0.6	5.9E-01	-0.1	8.5E-01
ENSMUST00000131764				2.6	2.2E-01	0.1	9.6E-01	-1.7	4.0E-01	0.8	7.3E-01
ENSMUST00000165922	E2F transcription factor 5 [Source:MGI Symbol;Acc:MGI:105091]	E9Q011		3.6	2.8E-02	4.5	3.4E-05	-0.1	8.9E-01	0.5	2.5E-01
ENSMUST00000131768				-1.7	4.9E-02	-3.3	2.6E-02	0.1	9.2E-01	1.7	2.0E-01
ENSMUST00000131769				2.5	6.0E-02	6.0	4.1E-03	1.4	3.9E-01	-2.1	5.3E-02
ENSMUST00000165924	trans-acting transcription factor 1 [Source:MGI Symbol;Acc:MGI:98372]	G3X8Q0		4.1	2.2E-02	2.6	3.2E-03	0.5	3.4E-01	0.4	4.7E-01
ENSMUST00000165928	vomeronasal 2, receptor 18 [Source:MGI Symbol;Acc:MGI:3645314]	E9Q280		7.6	9.8E-05	6.0	3.2E-02	-0.6	8.2E-01	-0.9	5.5E-01
ENSMUST00000131780	PQ loop repeat containing 1 [Source:MGI Symbol;Acc:MGI:1914193]		Q80XM9	1.7	4.2E-01	-0.3	8.8E-01	-1.8	3.5E-01	0.3	9.0E-01
ENSMUST00000131784	zinc finger protein 866 [Source:MGI Symbol;Acc:MGI:3584369]	E9Q810		0.6	3.8E-01	0.7	3.9E-01	0.2	7.3E-01	0.0	9.5E-01
ENSMUST00000131788				-2.4	1.0E-01	-2.6	1.8E-01	0.6	5.9E-01	0.8	6.6E-01
ENSMUST00000165935	periphilin 1 [Source:MGI Symbol;Acc:MGI:1917029]	G3UWD4		5.8	2.3E-02	5.2	9.7E-05	0.5	5.6E-01	-0.6	2.9E-01
ENSMUST00000165937	TOX high mobility group box family member 2 [Source:MGI Symbol;Acc:MGI:3611233]	E9Q0B9		7.9	2.3E-05	5.7	1.5E-02	-0.6	7.9E-01	-1.0	3.8E-01
ENSMUST00000165951	macrophage galactose N-acetyl-galactosamine specific lectin 2 [Source:MGI Symbol;Acc:MGI:2385729]	A9XX86		8.4	5.4E-06	7.1	1.1E-04	-1.2	3.0E-01	0.4	5.0E-01
ENSMUST00000165953	negative elongation factor complex member E, Rdbp [Source:MGI Symbol;Acc:MGI:102744]	Q3UIA1	P19426	-3.4	2.3E-03	-9.6	1.3E-03	1.1	1.5E-01	-0.1	9.7E-01
ENSMUST00000131803				-2.7	4.1E-01	-3.5	5.5E-01	1.4	6.2E-01	2.2	7.0E-01
ENSMUST00000131804	ATPase, class VI, type 11A [Source:MGI Symbol;Acc:MGI:1354735]	F6QJS5		-0.7	4.0E-01	-0.5	6.2E-01	0.2	7.7E-01	0.1	9.5E-01
ENSMUST00000131805				-1.6	8.0E-02	-0.9	3.5E-01	-0.2	8.0E-01	-0.8	4.0E-01
ENSMUST00000165954	adrenergic receptor kinase, beta 1 [Source:MGI Symbol;Acc:MGI:87940]	F6QY34		-3.8	1.3E-02	6.6	5.4E-03	-0.8	7.0E-01	-2.5	6.3E-02
ENSMUST00000131810	DnaJ (Hsp40) homolog, subfamily B, member 12 [Source:MGI Symbol;Acc:MGI:1931881]	D6RHR9		-1.2	7.3E-01	-3.5	4.3E-01	-1.6	5.0E-01	0.7	8.7E-01
ENSMUST00000165956	DNA segment, Chr 3, ERATO Doi 254, expressed [Source:MGI Symbol;Acc:MGI:1098769]	F7A4H5		3.5	3.7E-05	-2.0	3.1E-02	0.5	3.8E-01	-2.7	2.2E-02
ENSMUST00000165963	family with sequence similarity 196, member B [Source:MGI Symbol;Acc:MGI:3643491]		Q6GQV1	7.0	7.8E-03	-4.0	7.7E-02	1.0	2.9E-01	-1.4	5.4E-01
ENSMUST00000165971	septin 10 [Source:MGI Symbol;Acc:MGI:1918110]			-1.6	7.0E-03	-7.8	1.1E-02	-1.5	9.1E-02	1.4	6.0E-01
ENSMUST00000131823				-1.3	5.4E-01	0.5	8.4E-01	0.0	1.0E+00	-1.8	4.6E-01
ENSMUST00000131828				0.0	9.7E-01	2.5	1.1E-01	0.7	5.7E-01	-1.7	1.7E-01
ENSMUST00000165980	secretory leukocyte peptidase inhibitor [Source:MGI Symbol;Acc:MGI:109297]	E9Q748		-7.7	6.3E-06	6.0	2.4E-04	1.1	3.0E-01	-0.2	7.2E-01
ENSMUST00000165984	chemokine (C-C motif) receptor 2 [Source:MGI Symbol;Acc:MGI:106185]	Q543S8	P51683	-10.4	9.7E-05	-4.0	5.5E-02	1.4	1.2E-01	-0.5	8.0E-01
ENSMUST00000131839				1.0	2.0E-01	2.0	4.4E-02	-0.4	6.4E-01	-1.3	1.2E-01
ENSMUST00000165990	solute carrier organic anion transporter family, member 1a4 [Source:MGI Symbol;Acc:MGI:1351896]		Q9EP96	5.7	1.1E-03	6.1	2.6E-06	-0.4	4.4E-01	0.0	9.6E-01
ENSMUST00000131848	WD repeat and SOCS box-containing 1 [Source:MGI Symbol;Acc:MGI:1926139]	E9Q647		2.7	2.4E-01	5.7	1.2E-01	4.0	1.4E-01	1.0	7.1E-01
ENSMUST00000131850				-1.5	2.5E-01	-0.6	7.0E-01	0.4	7.0E-01	-0.5	7.7E-01
ENSMUST00000166022	wingless-type MMTV integration site family, member 10B [Source:MGI Symbol;Acc:MGI:108061]		P48614	6.9	8.4E-05	6.2	8.3E-04	-0.5	7.4E-01	-1.0	2.0E-01
ENSMUST00000166030	mitochondrial elongation factor 1 [Source:MGI Symbol;Acc:MGI:2146020]	B2RPW2	Q8BGV8	5.3	4.4E-05	2.6	4.2E-03	-1.1	1.1E-01	-0.1	8.4E-01
ENSMUST00000166032	tudor and KH domain containing protein [Source:MGI Symbol;Acc:MGI:1919884]		Q80VL1	3.8	2.5E-02	-5.4	4.0E-02	1.1	2.4E-01	-1.8	5.0E-01
ENSMUST00000166033	ubiquitin-conjugating enzyme E2D 3 [Source:MGI Symbol;Acc:MGI:1913355]	Q4QQL2	P61079	-4.6	1.3E-04	-6.3	1.1E-04	0.4	2.4E-01	0.4	7.3E-01
ENSMUST00000166056	oocyte maturation, alpha [Source:MGI Symbol;Acc:MGI:106620]	G5E8X8		7.3	2.7E-05	5.9	4.7E-04	-0.6	6.5E-01	-0.5	4.4E-01
ENSMUST00000166075	ADP-ribosylation factor 4 [Source:MGI Symbol;Acc:MGI:99433]	E9Q2C2		-7.0	3.5E-05	6.1	5.9E-03	0.5	7.8E-01	-2.1	7.3E-02
ENSMUST00000166078	ash2 (absent, small, or homeotic)-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1344416]	E9PU93		-6.3	3.1E-05	4.6	1.5E-02	-0.5	7.5E-01	1.1	2.8E-01
ENSMUST00000166098	major urinary protein 7 [Source:MGI Symbol;Acc:MGI:3709615]	E9QA79		6.1	1.4E-02	7.2	5.4E-05	-0.6	6.0E-01	-0.1	9.2E-01
ENSMUST00000166099	sin3 associated polypeptide [Source:MGI Symbol;Acc:MGI:3802945]	E9Q529		-7.5	5.4E-03	5.6	4.8E-04	0.7	5.1E-01	0.3	6.2E-01
ENSMUST00000131888	tripartite motif-containing 41 [Source:MGI Symbol;Acc:MGI:2384814]	Q5NCC4		0.9	2.8E-01	1.8	6.2E-02	-0.4	5.7E-01	-1.3	1.3E-01
ENSMUST00000131889				3.4	1.8E-01	-0.1	9.8E-01	-3.1	2.4E-01	0.4	8.9E-01
ENSMUST00000166101	spectrin beta, erythrocytic [Source:MGI Symbol;Acc:MGI:98387]	E9Q397		7.5	2.0E-06	7.6	5.9E-05	-0.6	6.4E-01	-0.6	2.8E-01
ENSMUST00000166104	molybdenum cofactor synthesis 2 [Source:MGI Symbol;Acc:MGI:1336894]	F6ZGI7		-4.4	5.7E-04	3.4	1.0E-02	0.1	9.1E-01	1.1	1.8E-01
ENSMUST00000166105	predicted gene, 17615 [Source:MGI Symbol;Acc:MGI:4937249]	E9Q9P2		10.4	1.6E-05	2.2	3.5E-02	-0.2	8.5E-01	-0.4	5.8E-01
ENSMUST00000131912	capping protein (actin filament) muscle Z-line, beta [Source:MGI Symbol;Acc:MGI:104652]	F6YHZ8		0.0	9.9E-01	-2.1	2.2E-01	-0.9	4.4E-01	1.2	4.4E-01
ENSMUST00000131918				1.0	1.9E-01	2.2	3.1E-02	0.6	4.0E-01	-0.6	4.3E-01
ENSMUST00000166115	G protein-coupled receptor 137 [Source:MGI Symbol;Acc:MGI:2147529]		Q80ZU9	-2.8	3.4E-02	5.1	5.1E-04	0.1	9.6E-01	0.6	3.6E-01
ENSMUST00000131921				1.2	4.5E-01	-0.9	6.0E-01	-2.7	1.0E-01	-0.5	7.5E-01
ENSMUST00000131924				1.0	4.6E-01	-0.1	9.5E-01	0.0	9.9E-01	1.1	4.9E-01
ENSMUST00000131927	sedoheptulokinase [Source:MGI Symbol;Acc:MGI:1921887]	D6RJM2		0.3	9.1E-01	6.6	4.1E-02	3.8	1.9E-01	-2.6	2.0E-01
ENSMUST00000131930	pleckstrin and Sec7 domain containing 4 [Source:MGI Symbol;Acc:MGI:2674093]	A0A0A6YY70		0.3	7.6E-01	-1.0	5.4E-01	0.7	5.0E-01	2.0	1.8E-01
ENSMUST00000131939				-2.7	8.0E-02	-1.2	6.3E-01	2.2	1.8E-01	0.6	7.7E-01
ENSMUST00000166117	Gen homolog 1, endonuclease (Drosophila) [Source:MGI Symbol;Acc:MGI:2443149]		Q8BMI4	2.0	7.5E-03	-3.2	1.1E-02	1.3	4.5E-02	-0.4	7.1E-01
ENSMUST00000166123	eukaryotic translation initiation factor 5 [Source:MGI Symbol;Acc:MGI:95309]	Q3TQR3	P59325	-4.1	2.0E-04	4.1	3.8E-04	-1.0	2.0E-01	-1.1	8.9E-02
ENSMUST00000131950				0.3	7.9E-01	0.7	5.8E-01	0.4	6.6E-01	0.0	9.7E-01
ENSMUST00000166126	protocadherin 10 [Source:MGI Symbol;Acc:MGI:1338042]	E9PXQ7		7.5	4.3E-06	7.5	1.1E-03	-0.8	6.6E-01	-0.2	8.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000166146	Rab40C, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:2183454]	E9Q0X8		3.1	1.3E-03	-3.9	1.4E-02	-3.4	5.4E-03	-3.5	4.9E-02
ENSMUST00000166170	NEL-like 2 [Source:MGI Symbol;Acc:MGI:1858510]		Q61220	7.8	1.9E-04	-5.6	2.9E-03	-1.4	3.5E-02	-0.2	9.0E-01
ENSMUST00000166171	eukaryotic translation initiation factor 2, subunit 2 (beta) [Source:MGI Symbol;Acc:MGI:1914454]	Q3ULL5	Q99L45	-5.1	7.2E-03	5.0	2.4E-03	-0.5	6.7E-01	1.2	1.3E-01
ENSMUST00000166172	abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene) [Source:MGI Symbol;Acc:MGI:878	B2RQ57		2.3	1.3E-04	6.0	5.4E-04	-0.6	6.4E-01	-0.3	6.9E-01
ENSMUST00000166176	molybdenum cofactor synthesis 2 [Source:MGI Symbol;Acc:MGI:1336894]			2.3	1.2E-02	6.1	4.6E-04	0.2	8.9E-01	-0.9	2.0E-01
ENSMUST00000131978				0.3	8.2E-01	1.6	3.6E-01	0.8	5.9E-01	-0.6	6.7E-01
ENSMUST00000131980				3.7	8.3E-02	6.1	1.8E-02	-0.3	9.0E-01	-2.6	6.7E-02
ENSMUST00000166193	immunoglobulin-like and fibronectin type III domain containing 1 [Source:MGI Symbol;Acc:MGI:3045352]		Q3KNY0	9.7	2.0E-06	6.4	1.7E-04	0.1	9.5E-01	-1.7	2.0E-02
ENSMUST00000166207	SRY (sex determining region Y)-box 6 [Source:MGI Symbol;Acc:MGI:98368]	Q3V1J7	P40645	6.2	9.6E-03	4.1	6.8E-04	-2.4	2.1E-02	-0.1	8.9E-01
ENSMUST00000131990	uridine monophosphate synthetase [Source:MGI Symbol;Acc:MGI:1298388]	D6RJ62		-0.5	8.3E-01	-0.4	8.0E-01	-3.4	4.0E-02	-3.5	8.8E-02
ENSMUST00000131992	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1925947]	Q91VU7		6.6	4.5E-02	6.2	7.9E-02	-0.9	7.9E-01	-0.4	8.2E-01
ENSMUST00000131993	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]	F6WV69		2.4	1.6E-01	2.1	3.7E-01	0.6	7.4E-01	0.9	6.7E-01
ENSMUST00000131995	brain and reproductive organ-expressed protein [Source:MGI Symbol;Acc:MGI:1333875]		Q8K3W0	-4.8	1.2E-01	-2.8	4.8E-01	1.2	6.1E-01	-0.8	8.4E-01
ENSMUST00000166219	heat shock factor binding protein 1-like 1 [Source:MGI Symbol;Acc:MGI:1913505]		B2RXB2	2.7	1.6E-02	7.6	1.2E-04	-0.8	5.6E-01	-0.5	4.2E-01
ENSMUST00000166224	hydroxysteroid (17-beta) dehydrogenase 3 [Source:MGI Symbol;Acc:MGI:107177]		P70385	5.0	3.3E-02	8.1	2.6E-05	-0.6	6.0E-01	-0.7	1.9E-01
ENSMUST00000166232	breast cancer anti-estrogen resistance 1 [Source:MGI Symbol;Acc:MGI:108091]		Q61140	9.4	2.7E-05	4.0	3.5E-03	-0.7	4.9E-01	1.2	1.3E-01
ENSMUST00000166233	density-regulated protein [Source:MGI Symbol;Acc:MGI:1915434]	E9Q0G1		-1.8	2.4E-02	3.6	9.3E-03	-0.7	5.0E-01	-0.3	7.2E-01
ENSMUST00000132009	lysine (K)-specific demethylase 5A [Source:MGI Symbol;Acc:MGI:2136980]	Q921T5		-2.1	6.5E-02	0.6	6.7E-01	2.3	3.4E-02	-0.4	7.8E-01
ENSMUST00000166237	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI		Q62178	-10.4	9.4E-05	-9.2	4.3E-03	0.2	8.0E-01	2.5	3.3E-01
ENSMUST00000166239	Eph receptor B4 [Source:MGI Symbol;Acc:MGI:104757]		P54761	6.9	5.5E-03	-5.1	5.5E-03	0.5	3.5E-01	-2.2	2.2E-01
ENSMUST00000132020				6.3	3.5E-02	2.7	4.3E-01	-0.7	8.2E-01	2.8	2.9E-01
ENSMUST00000166240	leucine-rich repeats and IQ motif containing 1 [Source:MGI Symbol;Acc:MGI:1922228]		Q0P5X1	7.4	5.8E-05	3.3	1.5E-03	-0.4	5.5E-01	0.6	2.8E-01
ENSMUST00000166241	SLIT and NTRK-like family, member 2 [Source:MGI Symbol;Acc:MGI:2679449]	Q14DT0	Q810C0	5.7	9.6E-05	4.5	2.4E-03	-3.0	3.5E-02	0.8	2.7E-01
ENSMUST00000166299	DIP2 disco-interacting protein 2 homolog C (Drosophila) [Source:MGI Symbol;Acc:MGI:1920179]	E9PWR4		6.1	6.3E-03	4.3	6.2E-03	-0.3	8.1E-01	0.6	4.7E-01
ENSMUST00000166315	A kinase (PRKA) anchor protein 13 [Source:MGI Symbol;Acc:MGI:2676556]	E9Q394		-4.9	1.8E-02	4.1	2.9E-03	-3.0	2.6E-02	0.0	9.6E-01
ENSMUST00000166328	predicted gene, 17641 [Source:MGI Symbol;Acc:MGI:4937275]	Q8CCI1		6.2	1.7E-04	0.4	6.2E-01	-4.3	1.4E-03	0.3	6.6E-01
ENSMUST00000166339	Wolfram syndrome 1 homolog (human) [Source:MGI Symbol;Acc:MGI:1328355]	Q3UN10		3.6	1.0E-02	3.7	1.9E-01	7.0	8.9E-03	-0.4	8.4E-01
ENSMUST00000166341	B cell CLL/lymphoma 9 [Source:MGI Symbol;Acc:MGI:1924828]		Q9D219	6.4	1.5E-03	-5.6	1.5E-04	-0.5	2.3E-01	-0.2	8.7E-01
ENSMUST00000132046				1.4	1.6E-01	2.1	1.1E-01	0.4	7.1E-01	-0.3	7.9E-01
ENSMUST00000166353	predicted gene, 17402 [Source:MGI Symbol;Acc:MGI:4937036]	F6Z0L5		8.9	9.4E-06	8.5	5.0E-04	-0.8	6.6E-01	0.2	8.0E-01
ENSMUST00000166367	cullin 5 [Source:MGI Symbol;Acc:MGI:1922967]	E9PV12		-4.5	3.0E-04	5.4	5.2E-04	-1.4	2.2E-01	0.7	3.4E-01
ENSMUST00000166373	RIKEN cDNA C030005K15 gene [Source:MGI Symbol;Acc:MGI:3641867]	Q8BQN9		4.6	7.6E-04	4.6	1.9E-03	-1.3	2.5E-01	0.3	7.0E-01
ENSMUST00000166376	microfibrillar-associated protein 2 [Source:MGI Symbol;Acc:MGI:99559]	Q99PM0		6.2	9.5E-04	5.1	5.1E-04	-1.3	2.4E-01	-1.2	8.0E-02
ENSMUST00000166384	serum/glucocorticoid regulated kinase 3 [Source:MGI Symbol;Acc:MGI:2182368]		Q9ERE3	-8.3	9.0E-05	5.0	2.3E-03	-0.3	7.8E-01	-1.2	2.1E-01
ENSMUST00000132066				-0.8	8.0E-01	0.9	7.7E-01	-1.2	6.7E-01	-2.9	3.8E-01
ENSMUST00000132073	ATPase, H+ transporting, lysosomal V0 subunit B [Source:MGI Symbol;Acc:MGI:1890510]	M0QW50		-3.5	7.3E-02	-1.6	5.2E-01	1.2	4.4E-01	-0.7	7.6E-01
ENSMUST00000166388	pleckstrin and Sec7 domain containing 4 [Source:MGI Symbol;Acc:MGI:2674093]		Q8BLR5	-6.7	5.6E-04	3.2	3.8E-03	0.7	3.4E-01	0.7	3.3E-01
ENSMUST00000166395	TGFB-induced factor homeobox 1 [Source:MGI Symbol;Acc:MGI:1194497]	G3UWC5		2.8	3.4E-03	-4.4	2.0E-02	0.7	3.6E-01	-0.5	7.9E-01
ENSMUST00000132084				-0.7	5.8E-01	-0.4	8.0E-01	-0.1	9.6E-01	-0.4	8.0E-01
ENSMUST00000166397	suppressor of defective silencing 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919204]			-5.1	2.1E-02	7.5	1.3E-03	-0.8	6.6E-01	0.1	9.5E-01
ENSMUST00000166407	UBX domain protein 1 [Source:MGI Symbol;Acc:MGI:1289301]		Q922Y1	-5.3	5.4E-06	6.5	8.7E-04	-0.4	7.8E-01	-0.5	5.5E-01
ENSMUST00000132091	Fanconi anemia, complementation group I [Source:MGI Symbol;Acc:MGI:2384790]		Q8K368	1.2	5.9E-01	0.2	9.6E-01	-1.3	6.2E-01	-0.2	9.5E-01
ENSMUST00000166409	Kruppel-like factor 3 (basic) [Source:MGI Symbol;Acc:MGI:1342773]	Q545J5	Q60980	-4.5	2.7E-03	9.1	3.6E-04	0.9	6.0E-01	0.8	3.0E-01
ENSMUST00000166412	transmembrane protein 258 [Source:MGI Symbol;Acc:MGI:1916288]	E9Q853		-7.0	3.7E-05	-3.2	1.3E-01	0.7	4.9E-01	0.4	8.3E-01
ENSMUST00000166427	serine hydrolase-like [Source:MGI Symbol;Acc:MGI:1890404]	Q3U3G8		3.1	1.1E-03	-4.3	2.5E-03	0.3	5.8E-01	-0.7	5.5E-01
ENSMUST00000166439	C-terminal binding protein 2 [Source:MGI Symbol;Acc:MGI:1201686]	Q91YZ2		-6.6	5.4E-05	7.1	1.7E-04	0.5	6.7E-01	-0.9	1.8E-01
ENSMUST00000166445	protection of telomeres 1A [Source:MGI Symbol;Acc:MGI:2141503]		Q91WC1	-4.2	2.9E-03	9.3	5.4E-04	-1.8	4.2E-01	1.5	1.1E-01
ENSMUST00000166468	protein tyrosine phosphatase, receptor type, K [Source:MGI Symbol;Acc:MGI:103310]		P35822	5.1	5.1E-05	-2.8	1.3E-01	0.2	8.1E-01	0.2	9.3E-01
ENSMUST00000166487	DnaJ (Hsp40) homolog, subfamily B, member 11 [Source:MGI Symbol;Acc:MGI:1915088]		Q99KV1	4.2	7.0E-05	8.0	1.5E-04	-1.7	2.6E-01	1.4	5.4E-02
ENSMUST00000166494	predicted gene 2897 [Source:MGI Symbol;Acc:MGI:3781075]	K7N6T7		6.6	4.7E-03	7.3	5.4E-05	-1.8	1.5E-01	0.6	3.3E-01
ENSMUST00000166497	abhydrolase domain containing 6 [Source:MGI Symbol;Acc:MGI:1913332]		Q8R2Y0	5.0	4.9E-03	6.7	7.2E-04	-0.7	6.5E-01	-0.7	3.8E-01
ENSMUST00000166499	vomeronasal 2, receptor 44 [Source:MGI Symbol;Acc:MGI:3643088]	L7N2E1		7.1	4.1E-05	4.3	9.2E-05	-0.3	6.0E-01	0.2	6.7E-01
ENSMUST00000166505	poly(A) binding protein, cytoplasmic 4-like [Source:MGI Symbol;Acc:MGI:3643087]	G5E8X2		5.6	1.4E-02	4.1	3.2E-03	-0.1	9.1E-01	-0.1	9.0E-01
ENSMUST00000132158	vesicle-associated membrane protein 4 [Source:MGI Symbol;Acc:MGI:1858730]	Q8BSN6		-1.0	7.0E-01	-0.9	6.9E-01	-2.6	1.8E-01	-2.8	3.1E-01
ENSMUST00000166518	signal sequence receptor, delta [Source:MGI Symbol;Acc:MGI:1099464]	Q9D8L3		-7.1	5.8E-04	3.5	7.1E-02	4.1	1.9E-02	-4.1	3.9E-02
ENSMUST00000166526	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1 [Source:MGI Symbol;Acc:MGI:98884]	G3UW94		-3.0	4.4E-03	5.9	1.2E-03	-0.5	7.4E-01	-0.1	8.4E-01
ENSMUST00000166540	exportin 6 [Source:MGI Symbol;Acc:MGI:2429950]	F6ZI11		-6.0	1.8E-03	4.2	2.1E-02	-1.4	4.0E-01	0.6	5.3E-01
ENSMUST00000166542	human immunodeficiency virus type I enhancer binding protein 3 [Source:MGI Symbol;Acc:MGI:106589]		A2A884	8.6	3.1E-04	4.6	6.5E-03	-0.6	6.2E-01	0.3	6.8E-01
ENSMUST00000166543	ralA binding protein 1 [Source:MGI Symbol;Acc:MGI:108466]		Q62172	2.5	1.2E-03	8.8	2.3E-04	1.7	2.6E-01	0.0	9.4E-01
ENSMUST00000132176	discs, large homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:107231]	S4R2T8		-2.4	3.8E-01	-0.9	8.0E-01	1.2	6.1E-01	-0.3	9.3E-01
ENSMUST00000166545	carboxypeptidase, vitellogenic-like [Source:MGI Symbol;Acc:MGI:1918537]		Q9D3S9	6.4	1.1E-04	5.2	3.3E-03	-0.3	8.4E-01	-0.3	6.9E-01
ENSMUST00000132179	diacylglycerol kinase, theta [Source:MGI Symbol;Acc:MGI:102918]	D6RI30		2.6	1.9E-01	0.7	7.8E-01	-0.7	7.0E-01	1.2	5.8E-01
ENSMUST00000132181				0.8	2.2E-01	2.3	2.1E-02	1.1	1.6E-01	-0.5	5.2E-01
ENSMUST00000166546	predicted gene, 18025 [Source:MGI Symbol;Acc:MGI:5010210]	E9Q1N8		6.9	4.7E-05	0.3	7.6E-01	1.0	2.0E-01	-2.4	5.0E-02
ENSMUST00000166578	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:893586]	E9PZS4		3.5	5.4E-04	4.9	1.1E-03	-0.2	8.3E-01	-0.5	4.4E-01
ENSMUST00000166581	fibrinogen alpha chain [Source:MGI Symbol;Acc:MGI:1316726]		E9PV24	5.8	3.8E-04	-5.8	1.0E-02	-0.9	2.6E-01	-2.8	2.3E-01
ENSMUST00000166591	BLOC-1 related complex subunit 5 [Source:MGI Symbol;Acc:MGI:1915024]	E9Q2W8		-1.9	2.4E-02	5.2	1.6E-02	-0.7	7.0E-01	-0.6	6.3E-01
ENSMUST00000166592	transportin 2 (importin 3, karyopherin beta 2b) [Source:MGI Symbol;Acc:MGI:2384849]	E9PV58		5.6	1.8E-02	-0.9	5.6E-01	0.7	5.3E-01	-2.3	2.0E-01
ENSMUST00000132193				-3.1	1.1E-01	-4.1	9.6E-02	-1.0	3.9E-01	-0.1	9.6E-01
ENSMUST00000166599	lysophosphatidylcholine acyltransferase 2B [Source:MGI Symbol;Acc:MGI:1918152]	B2RT16	Q9D5U0	6.6	2.5E-05	1.6	2.8E-01	0.2	8.9E-01	1.6	1.6E-01
ENSMUST00000166603	cell division cycle 34 [Source:MGI Symbol;Acc:MGI:102657]		Q8CFI2	-5.4	2.4E-04	7.7	6.3E-05	-0.7	5.9E-01	0.0	9.4E-01
ENSMUST00000132202	WW domain binding protein 1 like [Source:MGI Symbol;Acc:MGI:107577]		Q8BGW2	-2.3	2.2E-01	1.4	4.9E-01	1.0	5.8E-01	-2.8	1.6E-01
ENSMUST00000132205				-2.2	2.6E-01	0.2	9.3E-01	0.4	8.3E-01	-2.1	3.5E-01
ENSMUST00000132212	RAE1 RNA export 1 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1913929]	A2ASC6		-0.4	7.4E-01	1.0	5.1E-01	0.7	5.6E-01	-0.7	6.0E-01
ENSMUST00000166615	WW domain containing E3 ubiquitin protein ligase 2 [Source:MGI Symbol;Acc:MGI:1914144]	I3RSH5	Q9DBH0	-3.3	1.2E-04	6.3	4.5E-04	-0.5	6.7E-01	-0.4	5.5E-01
ENSMUST00000166627	zinc finger protein 414 [Source:MGI Symbol;Acc:MGI:1915641]		Q9DCK4	-6.1	1.4E-03	4.0	2.9E-03	0.8	3.7E-01	0.1	9.1E-01
ENSMUST00000166650	protein tyrosine phosphatase, receptor type, H [Source:MGI Symbol;Acc:MGI:3026877]	E9Q0N2		8.1	1.1E-05	5.7	4.0E-04	-1.4	2.4E-01	-1.2	8.1E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000166668	von Willebrand factor A domain containing 3A [Source:MGI Symbol;Acc:MGI:3041229]		Q3UVV9	10.1	4.3E-05	9.6	1.1E-03	1.3	5.2E-01	0.7	4.5E-01
ENSMUST00000166687	RUN and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919546]	Q3TDG5	Q8BG26	-5.6	1.2E-03	-2.2	2.4E-01	1.2	2.3E-01	-1.3	5.1E-01
ENSMUST00000166731	CD200 receptor 3 [Source:MGI Symbol;Acc:MGI:1921853]	E9Q7T2		5.5	4.4E-06	-3.1	2.3E-02	-0.5	4.3E-01	-0.7	5.8E-01
ENSMUST00000166734	CLIP associating protein 2 [Source:MGI Symbol;Acc:MGI:1923749]	Q08EB6		-1.8	2.2E-02	3.0	1.8E-02	-0.9	3.8E-01	-0.9	3.0E-01
ENSMUST00000166735	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:109301]			-5.5	3.5E-03	4.4	1.4E-03	-2.1	7.8E-02	0.6	3.7E-01
ENSMUST00000132252	obscurin-like 1 [Source:MGI Symbol;Acc:MGI:2138628]	F7AGE9		3.7	4.8E-02	4.5	3.1E-02	-0.5	8.0E-01	-1.3	3.1E-01
ENSMUST00000166737	zinc finger protein 488 [Source:MGI Symbol;Acc:MGI:2686052]		Q5HZG9	8.1	1.8E-06	-7.3	6.9E-04	-0.7	2.3E-01	1.0	5.1E-01
ENSMUST00000166750	c-Maf inducing protein [Source:MGI Symbol;Acc:MGI:1921690]		Q9D486	-3.9	1.4E-05	5.6	1.7E-03	0.1	9.3E-01	-0.3	6.6E-01
ENSMUST00000132270	solute carrier family 35, member C2 [Source:MGI Symbol;Acc:MGI:2385166]	E0CYZ1		-3.9	3.1E-01	-0.7	8.2E-01	-0.8	7.3E-01	-4.0	3.1E-01
ENSMUST00000132274				4.2	1.3E-01	1.8	6.2E-01	-0.4	8.9E-01	2.0	4.5E-01
ENSMUST00000132277				1.4	7.2E-02	0.4	6.9E-01	-0.2	7.6E-01	0.8	3.6E-01
ENSMUST00000132278				1.3	1.1E-01	2.5	3.0E-02	0.8	3.4E-01	-0.4	6.7E-01
ENSMUST00000166766	ribosomal RNA processing 7 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1922028]	F6VVA3		-1.6	2.6E-02	0.6	6.2E-01	-0.7	4.7E-01	1.8	9.8E-02
ENSMUST00000166768	spermatogenesis associated 2-like [Source:MGI Symbol;Acc:MGI:1926029]	B2RTE8	Q8BNN1	2.9	1.7E-03	6.2	3.2E-04	-0.1	9.1E-01	0.4	5.5E-01
ENSMUST00000166772	vertebrae development associated [Source:MGI Symbol;Acc:MGI:3588197]		Q3SYK4	7.6	1.4E-03	-3.4	2.0E-02	0.5	3.7E-01	-0.5	6.9E-01
ENSMUST00000132298	predicted gene 20708 [Source:MGI Symbol;Acc:MGI:5313155]	H3BKF4		3.9	4.6E-02	4.1	1.1E-01	-0.6	7.9E-01	-0.7	6.5E-01
ENSMUST00000132301				3.3	4.5E-02	3.6	9.1E-02	0.0	9.8E-01	-0.3	8.0E-01
ENSMUST00000166773	taste receptor, type 1, member 2 [Source:MGI Symbol;Acc:MGI:1933546]	E9Q0R6		6.5	6.3E-04	5.3	3.9E-03	-0.6	6.6E-01	0.7	4.5E-01
ENSMUST00000166783	actin binding LIM protein family, member 3 [Source:MGI Symbol;Acc:MGI:2442582]		Q69ZX8	7.2	1.1E-03	2.6	3.0E-02	-1.7	9.3E-02	-0.6	5.3E-01
ENSMUST00000132306				1.0	2.4E-01	0.6	5.4E-01	-0.3	7.5E-01	0.1	8.8E-01
ENSMUST00000166791	CD2 antigen (cytoplasmic tail) binding protein 2 [Source:MGI Symbol;Acc:MGI:1917483]		Q9CWK3	-2.3	9.4E-03	-7.9	7.9E-03	0.4	6.0E-01	-1.1	7.0E-01
ENSMUST00000132313				-0.2	8.1E-01	1.5	2.0E-01	1.1	2.3E-01	-0.6	5.3E-01
ENSMUST00000166793	matrin 3 [Source:MGI Symbol;Acc:MGI:1298379]	Q5BL18	Q8K310	1.5	4.4E-03	5.8	2.1E-03	0.1	9.3E-01	0.7	4.2E-01
ENSMUST00000132320				2.4	3.6E-01	-0.3	9.2E-01	-3.2	1.6E-01	-0.6	8.1E-01
ENSMUST00000132324				-0.9	2.3E-01	-1.0	3.4E-01	0.2	8.0E-01	0.3	7.8E-01
ENSMUST00000132329	nuclear factor related to kappa B binding protein [Source:MGI Symbol;Acc:MGI:2442410]	D6RHP5		2.2	5.7E-02	0.7	6.6E-01	0.3	8.4E-01	1.8	1.9E-01
ENSMUST00000132338	transmembrane 9 superfamily member 1 [Source:MGI Symbol;Acc:MGI:1921390]	D3YWH4		4.9	4.1E-02	1.9	4.5E-01	-0.6	8.0E-01	2.4	2.3E-01
ENSMUST00000166802	adhesion G protein-coupled receptor G5 [Source:MGI Symbol;Acc:MGI:2685955]	A6H6A1		-4.2	2.8E-02	2.4	2.3E-02	-1.8	4.1E-02	-0.1	8.7E-01
ENSMUST00000166820	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]		Q80TM6	-3.0	3.2E-02	5.8	1.2E-05	0.4	5.0E-01	-0.4	3.5E-01
ENSMUST00000166837	predicted gene 17067 [Source:MGI Symbol;Acc:MGI:4937894]	E9Q6S4		6.7	9.0E-05	-2.1	3.3E-01	1.5	2.7E-01	-0.7	7.5E-01
ENSMUST00000166847	radial spoke head 10 homolog B (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:1922386]	E9PYQ0		6.4	3.7E-05	5.5	2.8E-04	-1.1	3.2E-01	-0.5	4.7E-01
ENSMUST00000132346				-2.2	2.3E-01	-2.1	3.9E-01	0.3	8.0E-01	0.3	9.1E-01
ENSMUST00000166852	predicted gene 5093 [Source:MGI Symbol;Acc:MGI:3644404]	E9PZB3		3.1	8.4E-03	4.4	9.7E-02	-0.5	8.3E-01	0.0	1.0E+00
ENSMUST00000166855	melanin-concentrating hormone receptor 1 [Source:MGI Symbol;Acc:MGI:2180756]	Q3UY93		8.1	8.1E-06	3.2	1.0E-02	0.1	9.1E-01	-0.5	5.3E-01
ENSMUST00000166877	SRY (sex determining region Y)-box 6 [Source:MGI Symbol;Acc:MGI:98368]	E9PUW0		5.7	4.5E-03	-1.2	2.6E-01	0.4	5.6E-01	-2.3	7.1E-02
ENSMUST00000132364				-0.9	6.1E-01	1.9	3.9E-01	0.6	7.4E-01	-2.1	2.3E-01
ENSMUST00000166889	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 [Source:MGI Symbol;Acc:MGI:1345192]	E9PY93		-8.0	1.5E-05	4.2	7.9E-03	-3.1	5.1E-02	-0.5	5.4E-01
ENSMUST00000166897	translocase of outer mitochondrial membrane 70 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:106295]		Q9CZW5	-3.3	1.2E-04	6.1	3.0E-04	-0.6	6.3E-01	-0.5	4.1E-01
ENSMUST00000132373				-0.3	7.3E-01	1.5	2.4E-01	1.0	3.5E-01	-0.9	4.2E-01
ENSMUST00000166899	predicted gene, 21962 [Source:MGI Symbol;Acc:MGI:5439431]	L7N280		10.0	1.7E-07	4.4	1.5E-04	-0.2	7.4E-01	0.4	4.6E-01
ENSMUST00000132383	DNA segment, Chr 5, ERATO Doi 579, expressed [Source:MGI Symbol;Acc:MGI:1261849]	F7D143		1.5	5.0E-01	3.4	2.1E-01	0.9	7.2E-01	-1.0	6.1E-01
ENSMUST00000132384				1.8	2.2E-01	4.1	1.7E-02	-0.4	7.9E-01	-2.7	4.7E-02
ENSMUST00000132385				0.6	4.3E-01	1.9	7.5E-02	0.6	4.5E-01	-0.6	4.4E-01
ENSMUST00000166912	PHD finger protein 11C [Source:MGI Symbol;Acc:MGI:3648476]	B4XVP9		4.2	4.5E-05	6.2	6.2E-06	-0.9	2.2E-01	-0.4	3.1E-01
ENSMUST00000166915	small nuclear ribonucleoprotein E [Source:MGI Symbol;Acc:MGI:98346]		P62305	-5.1	8.6E-06	7.9	2.8E-05	0.2	8.7E-01	0.5	3.8E-01
ENSMUST00000132396				-2.9	1.7E-01	-1.6	5.6E-01	0.6	7.3E-01	-0.7	8.0E-01
ENSMUST00000166917	oxidation resistance 1 [Source:MGI Symbol;Acc:MGI:2179326]	B1H3M0		-3.9	6.2E-03	0.4	7.9E-01	1.9	8.7E-02	-2.7	8.0E-02
ENSMUST00000166926	kelch domain containing 7B [Source:MGI Symbol;Acc:MGI:3648212]	E9Q9M9		8.3	7.2E-05	-2.5	2.1E-01	1.8	9.4E-02	1.6	3.9E-01
ENSMUST00000166928	predicted gene 3115 [Source:MGI Symbol;Acc:MGI:3781291]	L7N285		6.5	2.1E-04	6.6	5.8E-04	-0.3	8.2E-01	-0.3	6.0E-01
ENSMUST00000166930	mortality factor 4 like 2 [Source:MGI Symbol;Acc:MGI:1927167]		Q9R0Q4	-3.9	3.0E-02	5.8	7.0E-04	-0.1	9.0E-01	0.8	2.3E-01
ENSMUST00000166938	inner membrane protein, mitochondrial [Source:MGI Symbol;Acc:MGI:1923864]	E9Q800		-5.1	1.5E-02	1.0	2.9E-01	0.0	9.8E-01	0.9	2.8E-01
ENSMUST00000132428	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B [Source:MGI Symbol;Acc:MGI:2442593]		Q8BND4	-1.3	3.8E-01	-4.8	9.4E-03	-4.6	4.9E-04	-1.1	5.1E-01
ENSMUST00000166940	aarF domain containing kinase 1 [Source:MGI Symbol;Acc:MGI:1919363]		Q9D0L4	2.6	1.3E-02	3.7	1.6E-02	1.1	3.6E-01	0.6	5.3E-01
ENSMUST00000166950	SEC61, gamma subunit [Source:MGI Symbol;Acc:MGI:1202066]	G3UWH0		-2.4	2.7E-02	3.2	5.8E-04	-0.7	2.3E-01	0.0	9.9E-01
ENSMUST00000166956	SKI family transcriptional corepressor 2 [Source:MGI Symbol;Acc:MGI:3645984]		A7M7C7	7.3	4.4E-05	6.3	9.3E-03	0.3	9.0E-01	0.6	5.7E-01
ENSMUST00000166957	polycystic kidney and hepatic disease 1-like 1 [Source:MGI Symbol;Acc:MGI:2183153]	E9PUU8		6.0	9.7E-03	6.0	2.5E-04	-2.2	8.6E-02	0.8	2.3E-01
ENSMUST00000166964	mediator complex subunit 16 [Source:MGI Symbol;Acc:MGI:2158394]	E9QAH8		4.1	8.7E-04	3.2	3.2E-02	-2.7	8.4E-02	-0.6	5.1E-01
ENSMUST00000132442	WD repeat domain 81 [Source:MGI Symbol;Acc:MGI:2681828]	F6XD87		-3.4	5.9E-02	-2.5	3.3E-01	1.1	4.4E-01	0.2	9.3E-01
ENSMUST00000166968	neuregulin 3 [Source:MGI Symbol;Acc:MGI:1097165]		O35181	9.6	1.2E-04	-2.4	1.5E-01	-0.1	9.5E-01	-1.4	4.1E-01
ENSMUST00000132459	proline-rich coiled-coil 2B [Source:MGI Symbol;Acc:MGI:1923304]	F7AYW2		1.0	6.2E-01	4.0	9.3E-02	0.9	6.2E-01	-2.1	3.1E-01
ENSMUST00000132463				1.3	5.8E-01	-1.6	6.6E-01	-0.9	7.2E-01	2.0	5.5E-01
ENSMUST00000166979	Moloney leukemia virus 10 [Source:MGI Symbol;Acc:MGI:97054]	E9PW39		-5.1	5.5E-03	3.9	8.4E-04	-0.8	3.2E-01	-0.3	6.0E-01
ENSMUST00000166984	far upstream element (FUSE) binding protein 1 [Source:MGI Symbol;Acc:MGI:1196294]	Q3TUE1		1.8	1.4E-02	4.8	6.2E-05	-0.2	7.2E-01	-0.1	7.6E-01
ENSMUST00000132480				0.5	5.4E-01	2.8	4.5E-02	1.9	1.0E-01	-0.4	6.7E-01
ENSMUST00000132484	speckle-type POZ protein-like [Source:MGI Symbol;Acc:MGI:1924107]		Q2M2N2	1.2	3.6E-02	1.8	1.1E-02	-0.4	4.6E-01	-1.0	7.9E-02
ENSMUST00000132486				-2.0	4.3E-02	-2.1	1.1E-01	-0.2	7.5E-01	-0.2	8.9E-01
ENSMUST00000167002	protein tyrosine phosphatase, receptor type, O [Source:MGI Symbol;Acc:MGI:1097152]	E9PVJ6		-2.8	3.6E-03	4.3	1.2E-02	0.1	9.2E-01	0.6	4.8E-01
ENSMUST00000132493	3-hydroxyacyl-CoA dehydratase 4 [Source:MGI Symbol;Acc:MGI:1914025]	Z4YMP4		0.7	4.0E-01	1.4	2.4E-01	0.9	3.3E-01	0.2	8.0E-01
ENSMUST00000132494	predicted gene, 28036 [Source:MGI Symbol;Acc:MGI:5547772]	V9GXJ1		2.3	4.2E-01	4.8	3.0E-01	3.2	4.3E-01	0.7	8.3E-01
ENSMUST00000132501	membrane protein, palmitoylated [Source:MGI Symbol;Acc:MGI:105941]	B7ZCL9		1.1	3.0E-01	-3.6	4.8E-03	-6.2	4.0E-05	-1.4	2.1E-01
ENSMUST00000167004	glycerol-3-phosphate acyltransferase 4 [Source:MGI Symbol;Acc:MGI:2142716]		Q8K2C8	-1.5	5.8E-03	2.3	1.9E-01	-1.5	3.4E-01	0.7	5.5E-01
ENSMUST00000132517	ATP-binding cassette, sub-family A (ABC1), member 7 [Source:MGI Symbol;Acc:MGI:1351646]		Q91V24	-3.3	5.0E-02	-4.0	1.0E-01	0.9	4.5E-01	1.6	4.9E-01
ENSMUST00000132519				1.6	3.8E-01	2.2	3.6E-01	0.4	8.2E-01	-0.2	9.4E-01
ENSMUST00000132520	NAD synthetase 1 [Source:MGI Symbol;Acc:MGI:1926164]	G5E8V4		1.9	1.2E-01	7.8	1.7E-03	4.2	2.9E-02	-1.7	1.3E-01
ENSMUST00000167008	phosphatidylinositol 4-kinase, catalytic, beta polypeptide [Source:MGI Symbol;Acc:MGI:1334433]		Q8BKC8	-2.5	2.0E-02	-3.2	9.1E-02	1.8	6.0E-02	0.1	9.6E-01
ENSMUST00000132522				-0.9	6.8E-01	-2.4	3.7E-01	-2.4	1.7E-01	-0.9	7.5E-01
ENSMUST00000167023	dihydrouridine synthase 1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915980]		Q8C2P3	-6.0	1.1E-04	-2.1	5.6E-01	3.8	8.3E-02	-0.5	8.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000167032	inositol polyphosphate-5-phosphatase D [Source:MGI Symbol;Acc:MGI:107357]		Q9ES52	-4.3	4.0E-03	5.3	1.1E-02	-0.6	7.3E-01	0.7	5.1E-01
ENSMUST00000167036	enoyl-Coenzyme A delta isomerase 2 [Source:MGI Symbol;Acc:MGI:1346064]	E9Q858		-5.3	1.1E-03	5.6	3.6E-04	-0.1	9.6E-01	-0.4	5.1E-01
ENSMUST00000167058	microtubule associated serine/threonine kinase family member 4 [Source:MGI Symbol;Acc:MGI:1918885]		Q811L6	5.4	4.1E-05	6.7	1.6E-03	-0.7	6.8E-01	-0.9	3.1E-01
ENSMUST00000167061	predicted gene 7873 [Source:MGI Symbol;Acc:MGI:3647803]	F6WEU2		7.0	6.3E-05	6.1	7.5E-05	-1.2	2.1E-01	1.3	3.1E-02
ENSMUST00000167074	junction adhesion molecule 3 [Source:MGI Symbol;Acc:MGI:1933825]	E9Q769		4.8	7.5E-04	6.1	1.6E-04	-0.8	4.5E-01	-0.1	8.2E-01
ENSMUST00000132546				2.1	3.5E-01	8.0	2.9E-02	2.5	4.2E-01	-3.4	1.1E-01
ENSMUST00000167078	golgi integral membrane protein 4 [Source:MGI Symbol;Acc:MGI:1920374]		Q8BXA1	-7.3	4.5E-05	7.3	5.8E-05	-0.5	6.4E-01	-0.6	3.0E-01
ENSMUST00000132551				-0.2	8.5E-01	0.2	9.1E-01	0.8	4.2E-01	0.5	7.2E-01
ENSMUST00000167113	tripartite motif-containing 43B [Source:MGI Symbol;Acc:MGI:3648996]		P86448	3.9	1.4E-03	6.8	1.3E-03	-0.7	6.5E-01	0.7	4.4E-01
ENSMUST00000167122	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7 [Source:MGI Symbol;Acc:M	E9PX36		4.4	2.1E-02	-3.1	5.2E-02	-0.1	9.4E-01	-0.2	8.8E-01
ENSMUST00000167140	mercaptopyruvate sulfurtransferase [Source:MGI Symbol;Acc:MGI:2179733]	Q3UW66		-4.5	3.1E-03	7.8	5.8E-05	-0.8	5.0E-01	1.0	1.2E-01
ENSMUST00000132574				-2.1	7.2E-02	-2.7	9.3E-02	0.2	7.8E-01	0.9	5.6E-01
ENSMUST00000167143	CD79B antigen [Source:MGI Symbol;Acc:MGI:96431]		P15530	-4.8	3.2E-03	-3.4	2.7E-03	0.9	6.7E-02	-0.1	9.4E-01
ENSMUST00000132590				0.1	8.3E-01	1.4	7.2E-02	1.5	3.0E-02	0.2	7.9E-01
ENSMUST00000167149	nuclear factor, erythroid derived 2,-like 1 [Source:MGI Symbol;Acc:MGI:99421]	Q6GTN8	Q61985	-6.4	4.3E-03	5.9	9.4E-05	-2.3	4.6E-02	0.3	5.4E-01
ENSMUST00000167153	transmembrane protein 8B [Source:MGI Symbol;Acc:MGI:2441680]		B1AWJ5	5.8	8.7E-06	2.3	1.3E-01	-2.6	1.1E-01	0.3	8.1E-01
ENSMUST00000132599				0.7	2.7E-01	0.8	2.8E-01	-0.5	4.0E-01	-0.6	3.7E-01
ENSMUST00000132600				0.8	1.7E-01	1.3	8.3E-02	0.1	8.4E-01	-0.4	5.4E-01
ENSMUST00000132602				0.8	2.4E-01	1.1	2.1E-01	0.0	9.8E-01	-0.3	7.0E-01
ENSMUST00000167161	kinesin family member 20A [Source:MGI Symbol;Acc:MGI:1201682]		P97329	-6.0	2.2E-03	-5.5	1.8E-02	-0.7	3.8E-01	-0.3	8.8E-01
ENSMUST00000167173	SH3/ankyrin domain gene 3 [Source:MGI Symbol;Acc:MGI:1930016]	E9Q1P5		4.7	5.8E-03	6.9	4.8E-05	0.8	3.6E-01	-0.5	3.1E-01
ENSMUST00000167180	O-acyl-ADP-ribose deacylase 1 [Source:MGI Symbol;Acc:MGI:2146818]		Q8R5F3	-2.8	3.1E-02	3.0	3.9E-03	-1.4	7.9E-02	-0.1	9.0E-01
ENSMUST00000167182	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]		Q9Z2X1	-4.1	1.0E-02	5.2	9.0E-03	-2.4	2.2E-01	-0.1	9.5E-01
ENSMUST00000167190	MAM domain containing glycosylphosphatidylinositol anchor 1 [Source:MGI Symbol;Acc:MGI:1922012]	E9Q6S8		4.9	1.7E-03	-3.1	1.0E-01	-0.1	9.0E-01	-2.0	3.4E-01
ENSMUST00000167201	staphylococcal nuclease and tudor domain containing 1 [Source:MGI Symbol;Acc:MGI:1929266]	Q3TJ56		7.7	4.9E-06	8.3	8.2E-05	-0.7	6.2E-01	-0.3	5.8E-01
ENSMUST00000167204	doublecortin-like kinase 1 [Source:MGI Symbol;Acc:MGI:1330861]	Q80VB6		7.2	6.8E-05	5.1	1.5E-05	0.0	9.9E-01	-0.1	6.9E-01
ENSMUST00000167227	vertebrae development associated [Source:MGI Symbol;Acc:MGI:3588197]		Q3SYK4	6.4	5.2E-03	-1.2	5.9E-01	3.4	4.3E-02	-0.8	7.3E-01
ENSMUST00000167232	phospholipase A2, group IVC (cytosolic, calcium-independent) [Source:MGI Symbol;Acc:MGI:1196403]	Q08EC7		5.2	2.3E-02	-6.0	4.3E-03	0.0	9.5E-01	-0.8	6.5E-01
ENSMUST00000167239	nebulin-related anchoring protein [Source:MGI Symbol;Acc:MGI:1098765]	E9Q641		5.2	3.0E-02	-4.3	8.2E-03	-1.0	1.5E-01	-1.9	2.3E-01
ENSMUST00000167240	RAS, guanyl releasing protein 2 [Source:MGI Symbol;Acc:MGI:1333849]		Q9QUG9	-8.1	1.2E-02	7.1	5.0E-06	-1.6	6.8E-02	-0.2	5.5E-01
ENSMUST00000167242	exportin 7 [Source:MGI Symbol;Acc:MGI:1929705]	E9PUW7		10.5	1.7E-05	-0.1	9.4E-01	2.9	2.0E-02	-0.8	5.6E-01
ENSMUST00000167246	praja ring finger 1, E3 ubiquitin protein ligase [Source:MGI Symbol;Acc:MGI:1101765]	Q05CG5	O55176	-4.1	1.1E-03	-4.6	2.1E-02	0.2	8.3E-01	0.0	9.9E-01
ENSMUST00000167248	olfactory receptor 1381 [Source:MGI Symbol;Acc:MGI:3031215]	Q7TQT4		5.6	2.3E-02	5.6	3.4E-03	-0.6	7.0E-01	-0.3	7.3E-01
ENSMUST00000167258	tubulin tyrosine ligase-like family, member 6 [Source:MGI Symbol;Acc:MGI:2683461]		A4Q9E8	7.9	2.6E-05	-6.8	5.8E-03	0.5	4.1E-01	-0.9	6.7E-01
ENSMUST00000167261	Iroquois related homeobox 6 (Drosophila) [Source:MGI Symbol;Acc:MGI:1927642]		Q9ER75	6.2	2.1E-04	2.3	1.3E-01	-1.5	2.6E-01	0.0	9.9E-01
ENSMUST00000167263	cadherin-related family member 5 [Source:MGI Symbol;Acc:MGI:1919290]	A0PJK7		10.0	2.1E-04	7.7	1.0E-04	0.0	9.9E-01	0.0	9.9E-01
ENSMUST00000132664				-1.6	2.6E-01	0.1	9.8E-01	-0.1	9.5E-01	-1.8	3.0E-01
ENSMUST00000167264	general transcription factor II E, polypeptide 2 (beta subunit) [Source:MGI Symbol;Acc:MGI:1915403]		Q9D902	-5.7	3.3E-05	-3.6	9.2E-02	1.9	7.2E-02	-0.7	7.3E-01
ENSMUST00000167270	low density lipoprotein-related protein 1B (deleted in tumors) [Source:MGI Symbol;Acc:MGI:2151136]	E9Q202		6.4	2.0E-04	7.8	1.1E-05	-0.9	3.6E-01	-0.5	3.4E-01
ENSMUST00000167290	small integral membrane protein 7 [Source:MGI Symbol;Acc:MGI:1914068]		Q5RKS2	-2.4	8.4E-04	2.6	7.2E-02	1.0	3.7E-01	1.7	1.1E-01
ENSMUST00000167293	cullin 3 [Source:MGI Symbol;Acc:MGI:1347360]	F6ZZK0		-3.5	9.3E-03	-0.3	7.0E-01	0.9	1.3E-01	-0.7	3.8E-01
ENSMUST00000167294	potassium channel tetramerisation domain containing 19 [Source:MGI Symbol;Acc:MGI:3045294]		Q562E2	7.2	2.4E-02	6.5	1.5E-03	-0.3	8.7E-01	-0.4	6.2E-01
ENSMUST00000132678				-0.8	6.8E-01	-1.7	3.4E-01	-2.7	9.3E-02	-1.8	3.5E-01
ENSMUST00000167303	wingless-type MMTV integration site family, member 11 [Source:MGI Symbol;Acc:MGI:101948]	Q059Y4	P48615	3.6	1.0E-02	-3.2	2.1E-02	-0.2	6.9E-01	-1.3	3.4E-01
ENSMUST00000167309	Rho GTPase activating protein 17 [Source:MGI Symbol;Acc:MGI:1917747]	E9QAJ9		-6.2	7.1E-05	-4.9	3.6E-03	0.9	1.1E-01	-0.7	6.2E-01
ENSMUST00000167316	zinc finger protein 655 [Source:MGI Symbol;Acc:MGI:1919861]	Q9CZP3		-3.2	1.8E-04	5.2	2.0E-03	-2.1	1.5E-01	0.1	8.8E-01
ENSMUST00000132684				-4.1	1.0E-01	-3.3	3.1E-01	0.1	9.7E-01	-0.7	8.3E-01
ENSMUST00000167323	apolipoprotein L domain containing 1 [Source:MGI Symbol;Acc:MGI:2685921]	E9Q0X2		7.6	7.0E-06	6.9	6.7E-05	-1.5	2.0E-01	0.4	5.0E-01
ENSMUST00000167327	actinin, alpha 1 [Source:MGI Symbol;Acc:MGI:2137706]	A1BN54		-4.4	3.3E-05	6.7	2.5E-03	-0.8	6.6E-01	1.0	2.8E-01
ENSMUST00000132689	family with sequence similarity 65, member B [Source:MGI Symbol;Acc:MGI:2444879]	F2Z3V4		0.1	9.5E-01	0.9	5.6E-01	-0.5	7.0E-01	-1.3	3.7E-01
ENSMUST00000132693				-0.9	2.8E-01	-1.3	2.4E-01	-0.3	6.6E-01	0.0	9.7E-01
ENSMUST00000167346	zinc finger and BTB domain containing 44 [Source:MGI Symbol;Acc:MGI:1925123]		Q8R0A2	-4.8	9.4E-04	6.1	2.0E-06	-0.9	1.4E-01	0.3	3.7E-01
ENSMUST00000167348	ATPase, Ca++ transporting, plasma membrane 4 [Source:MGI Symbol;Acc:MGI:88111]	F6V4K0		7.5	6.2E-05	8.0	2.0E-04	-0.6	6.7E-01	0.8	1.9E-01
ENSMUST00000132703				-0.8	4.5E-01	-2.3	1.4E-01	-1.5	1.3E-01	0.0	9.8E-01
ENSMUST00000167352	ATPase, H+ transporting, lysosomal V0 subunit E [Source:MGI Symbol;Acc:MGI:1328318]		Q9CQD8	3.1	1.6E-03	3.2	2.4E-02	0.1	8.9E-01	-0.2	8.0E-01
ENSMUST00000132708	diacylglycerol kinase, theta [Source:MGI Symbol;Acc:MGI:102918]	D6RFT1		4.5	4.9E-02	3.9	1.6E-01	-0.2	9.4E-01	0.4	8.3E-01
ENSMUST00000167353	Rho guanine nucleotide exchange factor (GEF) 25 [Source:MGI Symbol;Acc:MGI:1277173]			6.7	1.8E-03	8.0	3.0E-05	-1.0	3.9E-01	-0.6	3.0E-01
ENSMUST00000167354	fragile X mental retardation gene 1, autosomal homolog [Source:MGI Symbol;Acc:MGI:104860]	A0A0H2UH27		-7.4	1.8E-04	4.1	1.1E-02	0.2	8.4E-01	-1.0	2.6E-01
ENSMUST00000132718	cathepsin H [Source:MGI Symbol;Acc:MGI:107285]	D3Z437		-2.8	4.7E-02	-4.3	2.5E-02	-2.0	4.2E-02	-0.5	7.7E-01
ENSMUST00000167358	predicted gene 3250 [Source:MGI Symbol;Acc:MGI:3781428]	E9Q1M3		8.0	8.2E-05	3.1	8.0E-02	-1.9	2.2E-01	-0.1	9.4E-01
ENSMUST00000167364	tripartite motif-containing 36 [Source:MGI Symbol;Acc:MGI:106264]	E9Q3A0		6.9	8.4E-06	7.9	3.4E-06	1.1	1.7E-01	0.2	5.5E-01
ENSMUST00000167369	FXYD domain-containing ion transport regulator 3 [Source:MGI Symbol;Acc:MGI:107497]	Q3TLM3	Q61835	6.2	4.3E-04	-1.7	1.5E-01	0.7	3.6E-01	-1.4	2.8E-01
ENSMUST00000167374	receptor (TNFRSF)-interacting serine-threonine kinase 1 [Source:MGI Symbol;Acc:MGI:108212]		Q60855	-3.1	2.9E-03	5.7	3.0E-05	-2.2	3.4E-02	0.4	4.7E-01
ENSMUST00000167377	IQ motif containing GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:1352757]		Q9JKF1	-6.5	6.3E-08	8.0	9.1E-06	-0.3	7.3E-01	0.0	9.5E-01
ENSMUST00000167390	solute carrier family 39 (metal ion transporter), member 8 [Source:MGI Symbol;Acc:MGI:1914797]		Q91W10	4.6	2.5E-02	7.8	8.0E-05	0.2	8.7E-01	-0.2	7.6E-01
ENSMUST00000167391	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9 [Source:MGI Symbol;Acc:M	E9PYV8		8.7	1.4E-04	-3.1	6.6E-02	1.5	1.2E-01	-1.1	5.2E-01
ENSMUST00000132747				1.9	4.0E-02	3.0	1.3E-02	0.7	4.3E-01	-0.4	6.5E-01
ENSMUST00000167423	predicted gene, 17409 [Source:MGI Symbol;Acc:MGI:4937043]	Q3V2J7		7.0	3.9E-05	-1.4	2.7E-01	0.4	5.6E-01	-2.0	1.6E-01
ENSMUST00000132769				-0.2	7.9E-01	-0.3	8.1E-01	0.0	9.7E-01	0.1	9.5E-01
ENSMUST00000132773	inositol 1,4,5-triphosphate receptor interacting protein-like 1 [Source:MGI Symbol;Acc:MGI:1920588]	A2ASB0		0.2	6.6E-01	1.6	4.2E-02	1.2	4.9E-02	-0.2	7.6E-01
ENSMUST00000167427	secretory leukocyte peptidase inhibitor [Source:MGI Symbol;Acc:MGI:109297]	E9Q4A3		6.0	2.1E-03	7.5	1.6E-04	0.6	6.3E-01	-0.6	3.4E-01
ENSMUST00000132777				0.5	6.6E-01	1.9	1.7E-01	-0.1	9.6E-01	-1.4	2.2E-01
ENSMUST00000167430	predicted gene 3020 [Source:MGI Symbol;Acc:MGI:3781198]	Q9CZI1		5.5	6.8E-03	3.8	1.7E-04	-0.1	9.1E-01	0.1	8.7E-01
ENSMUST00000167435	thymoma viral proto-oncogene 2 [Source:MGI Symbol;Acc:MGI:104874]	Q3TY95	Q60823	-6.4	1.3E-03	5.6	4.4E-03	-0.7	6.6E-01	0.9	3.3E-01
ENSMUST00000167457	zinc finger protein 426 [Source:MGI Symbol;Acc:MGI:1920248]	E9Q951		2.6	5.3E-03	-5.6	2.2E-02	1.2	1.6E-01	-1.0	6.7E-01
ENSMUST00000167459	muscleblind-like 2 [Source:MGI Symbol;Acc:MGI:2145597]		Q8C181	-4.8	6.1E-04	5.3	1.6E-03	0.5	6.7E-01	0.3	6.6E-01
ENSMUST00000167460	corin [Source:MGI Symbol;Acc:MGI:1349451]		Q9Z319	4.6	8.4E-03	-2.6	2.4E-01	0.7	5.5E-01	-1.7	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000167484	adenylate cyclase activating polypeptide 1 receptor 1 [Source:MGI Symbol;Acc:MGI:108449]			4.4	3.7E-03	3.9	3.2E-03	1.0	2.6E-01	0.1	9.1E-01
ENSMUST00000132815	solute carrier family 25, member 51 [Source:MGI Symbol;Acc:MGI:2684984]		Q5HZI9	-0.5	8.5E-01	-2.4	4.3E-01	-1.9	2.8E-01	0.0	1.0E+00
ENSMUST00000132819	proline rich 14 [Source:MGI Symbol;Acc:MGI:2384565]			1.0	6.0E-01	0.7	8.0E-01	-0.4	8.3E-01	-0.1	9.6E-01
ENSMUST00000132828				0.6	6.2E-01	2.2	1.7E-01	0.7	6.0E-01	-1.0	4.3E-01
ENSMUST00000167487	very low density lipoprotein receptor [Source:MGI Symbol;Acc:MGI:98935]		P98156	4.1	8.3E-04	6.1	3.4E-04	-0.4	7.2E-01	0.1	8.5E-01
ENSMUST00000132836	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]	D3Z0J1		-2.2	8.1E-02	-1.0	5.3E-01	0.7	5.2E-01	-0.5	7.3E-01
ENSMUST00000132841				-0.7	4.2E-01	0.1	9.1E-01	0.6	4.2E-01	-0.1	8.9E-01
ENSMUST00000167493	ribonuclease/angiogenin inhibitor 1 [Source:MGI Symbol;Acc:MGI:1195456]		Q91VI7	-6.7	2.7E-04	6.5	3.9E-03	1.7	3.1E-01	0.7	4.5E-01
ENSMUST00000132846	peptidylprolyl isomerase A [Source:MGI Symbol;Acc:MGI:97749]	Q5SVY2	P17742	-0.8	5.1E-01	-2.1	1.7E-01	-1.6	1.4E-01	-0.3	8.2E-01
ENSMUST00000167504	translational machinery associated 7 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913417]	Q14A47	Q8K003	-2.8	6.8E-04	5.2	6.3E-04	-1.3	2.4E-01	-0.4	5.8E-01
ENSMUST00000167505	transmembrane protein 255B [Source:MGI Symbol;Acc:MGI:2685533]	G3UWB7		7.7	2.0E-03	6.7	1.7E-04	-0.5	6.7E-01	-0.6	3.7E-01
ENSMUST00000132859	RIKEN cDNA 2610015P09 gene [Source:MGI Symbol;Acc:MGI:1922661]	B8JJH0		2.8	2.4E-01	2.8	2.9E-01	-1.2	6.4E-01	-1.2	5.6E-01
ENSMUST00000132860				0.8	5.0E-01	1.8	2.1E-01	0.4	7.6E-01	-0.7	5.7E-01
ENSMUST00000132863				1.2	3.1E-01	1.2	3.5E-01	-0.3	8.0E-01	-0.3	7.7E-01
ENSMUST00000167513	solute carrier family 35, member B3 [Source:MGI Symbol;Acc:MGI:1913978]		Q922Q5	-5.4	1.9E-04	4.5	1.7E-03	-2.8	4.9E-02	-1.0	2.2E-01
ENSMUST00000167545	ain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B [Source:MGI Symbol;Acc:MGI:	Q3UTK5	O54951	-7.5	1.0E-03	6.8	6.4E-03	-1.8	4.1E-01	-1.6	2.3E-01
ENSMUST00000167546	upstream transcription factor 1 [Source:MGI Symbol;Acc:MGI:99542]	Q3UQH7	Q61069	-3.2	2.6E-02	4.6	3.1E-02	0.9	5.9E-01	0.8	5.1E-01
ENSMUST00000132877				0.4	6.2E-01	2.2	4.3E-02	0.4	6.2E-01	-1.4	1.2E-01
ENSMUST00000167549	endonuclease domain containing 1 [Source:MGI Symbol;Acc:MGI:1919196]		Q8C522	1.6	8.7E-03	-3.4	3.5E-02	0.0	9.8E-01	0.4	7.7E-01
ENSMUST00000132890				-1.0	3.5E-01	0.4	7.8E-01	0.5	5.8E-01	-0.8	5.2E-01
ENSMUST00000167550	cDNA sequence BC048671 [Source:MGI Symbol;Acc:MGI:2679261]		Q8C5S3	8.1	1.6E-04	6.2	1.8E-03	-0.6	6.5E-01	2.1	3.1E-02
ENSMUST00000167569	RAB11A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1858202]	E9Q6B3		-6.3	7.6E-04	8.6	2.0E-04	0.1	9.6E-01	0.8	2.5E-01
ENSMUST00000167574	adrenergic receptor, alpha 1b [Source:MGI Symbol;Acc:MGI:104774]	Q9DBL0		6.8	9.7E-04	7.0	6.4E-03	0.9	6.4E-01	0.1	9.0E-01
ENSMUST00000167582	protein tyrosine phosphatase 4a3 [Source:MGI Symbol;Acc:MGI:1277098]	E9PXS4		8.3	1.4E-05	4.8	3.3E-03	-0.3	8.4E-01	-0.4	6.0E-01
ENSMUST00000132903				-3.3	8.0E-02	-2.3	3.1E-01	0.1	9.5E-01	-0.9	6.8E-01
ENSMUST00000167588	tripartite motif-containing 67 [Source:MGI Symbol;Acc:MGI:3045323]		Q505D9	6.9	1.0E-05	7.9	2.1E-05	-1.6	1.6E-01	-0.6	2.0E-01
ENSMUST00000132918				0.5	6.3E-01	-1.8	2.2E-01	-0.5	6.0E-01	1.8	2.0E-01
ENSMUST00000132925	transformation/transcription domain-associated protein [Source:MGI Symbol;Acc:MGI:2153272]	F7CGG2		-2.7	1.5E-01	0.2	9.3E-01	0.1	9.6E-01	-2.8	1.8E-01
ENSMUST00000167595	FYVE and coiled-coil domain containing 1 [Source:MGI Symbol;Acc:MGI:107277]		Q8VDC1	-6.2	1.4E-03	-0.2	8.2E-01	0.4	6.2E-01	-1.6	1.3E-01
ENSMUST00000167596	schlafen 4 [Source:MGI Symbol;Acc:MGI:1329010]	Q3UV66		-5.4	3.0E-04	7.5	1.4E-04	-2.1	1.5E-01	0.3	6.6E-01
ENSMUST00000167628	embrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) [Source:MGI Symbol;Acc:MGI:192734	E9PWC5		5.8	1.4E-02	6.3	3.8E-04	0.5	6.9E-01	-0.9	1.9E-01
ENSMUST00000167634	cytochrome P450, family 11, subfamily b, polypeptide 2 [Source:MGI Symbol;Acc:MGI:88584]	G3UWE4		7.4	1.2E-04	5.3	3.3E-03	0.3	8.0E-01	-0.8	3.6E-01
ENSMUST00000132945	protein kinase N1 [Source:MGI Symbol;Acc:MGI:108022]	D6RH37		-0.9	6.0E-01	3.8	2.1E-01	4.4	1.1E-01	-0.3	8.8E-01
ENSMUST00000167636	ation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 [Source:MGI Symbol;Acc:MGI:185	Q548M4	Q9JLJ5	-9.1	6.5E-05	-1.6	5.4E-01	2.6	1.4E-01	-3.2	3.0E-01
ENSMUST00000167646	apolipoprotein E [Source:MGI Symbol;Acc:MGI:88057]	E9Q327		-8.5	5.9E-05	2.1	1.8E-02	-0.3	6.1E-01	-0.5	4.9E-01
ENSMUST00000132952				0.7	4.8E-01	1.9	1.4E-01	0.6	5.5E-01	-0.6	5.9E-01
ENSMUST00000167661	surfeit gene 1 [Source:MGI Symbol;Acc:MGI:98443]			-5.6	7.9E-05	1.4	2.2E-01	-2.8	2.1E-02	-0.9	3.6E-01
ENSMUST00000167669	predicted gene 7138 [Source:MGI Symbol;Acc:MGI:3779678]	L7N2C3		8.3	1.4E-03	4.6	2.0E-03	1.6	1.2E-01	1.2	1.3E-01
ENSMUST00000132961	small integral membrane protein 6 [Source:MGI Symbol;Acc:MGI:1915778]	Q3U0I6		1.8	5.0E-02	1.1	2.6E-01	-0.6	4.4E-01	0.0	9.5E-01
ENSMUST00000167679	protein tyrosine phosphatase, receptor type, O [Source:MGI Symbol;Acc:MGI:1097152]	E9Q4I1		4.0	7.5E-03	1.9	9.2E-02	-1.4	1.5E-01	0.0	9.6E-01
ENSMUST00000167691	killer cell lectin-like receptor subfamily B member 1C [Source:MGI Symbol;Acc:MGI:107538]	E9Q3U6		3.9	9.0E-03	2.9	1.2E-02	0.0	9.6E-01	-0.3	6.9E-01
ENSMUST00000132967	fibrous sheath-interacting protein 2 [Source:MGI Symbol;Acc:MGI:2664111]	F7BGZ6		2.9	1.8E-01	5.7	2.1E-02	-0.3	8.8E-01	-3.1	4.9E-02
ENSMUST00000167715	transcriptional regulator, SIN3A (yeast) [Source:MGI Symbol;Acc:MGI:107157]		Q60520	-5.3	1.5E-02	5.4	7.4E-05	-0.7	3.8E-01	0.5	3.5E-01
ENSMUST00000132972				1.9	3.6E-01	-3.3	2.3E-01	-4.5	2.7E-02	0.7	7.8E-01
ENSMUST00000132974	ATPase, class VI, type 11A [Source:MGI Symbol;Acc:MGI:1354735]	F6Z4J2		-0.5	7.2E-01	-0.5	7.9E-01	0.6	6.6E-01	0.6	7.4E-01
ENSMUST00000132976				-2.6	1.3E-01	-1.6	4.6E-01	0.3	8.1E-01	-0.7	7.5E-01
ENSMUST00000132983				-1.7	1.3E-01	-1.4	3.6E-01	0.5	5.5E-01	0.1	9.5E-01
ENSMUST00000167731	myelocytomatosis oncogene [Source:MGI Symbol;Acc:MGI:97250]	F6PX41		2.6	1.8E-02	7.2	1.0E-04	-0.6	6.2E-01	0.1	8.5E-01
ENSMUST00000167751	cAMP responsive element binding protein 3 [Source:MGI Symbol;Acc:MGI:99946]	E9PW77		-7.2	1.2E-04	3.8	5.2E-03	0.3	7.2E-01	0.4	5.6E-01
ENSMUST00000167755	tripartite motif-containing 9 [Source:MGI Symbol;Acc:MGI:2137354]	E9Q524		9.4	4.3E-06	10.3	9.8E-06	-0.9	4.8E-01	1.0	7.1E-02
ENSMUST00000132996				0.9	3.1E-01	2.2	7.9E-02	1.0	3.2E-01	-0.3	7.1E-01
ENSMUST00000167759	ataxin 2-like [Source:MGI Symbol;Acc:MGI:2446242]	Q3TGG2		-3.8	7.9E-03	5.4	1.0E-03	-0.4	7.2E-01	0.2	7.7E-01
ENSMUST00000133001				0.8	2.0E-01	0.5	5.7E-01	-0.1	9.0E-01	0.3	7.1E-01
ENSMUST00000167771	vomeronasal 2, receptor 55 [Source:MGI Symbol;Acc:MGI:3757950]	E9PXC1		13.5	2.7E-05	6.2	2.9E-04	-0.5	6.4E-01	0.0	9.8E-01
ENSMUST00000167787	SMAD specific E3 ubiquitin protein ligase 2 [Source:MGI Symbol;Acc:MGI:1913563]		A2A5Z6	-2.9	1.5E-02	6.3	2.4E-03	-0.7	6.9E-01	0.3	7.6E-01
ENSMUST00000167797	5-phosphohydroxy-L-lysine phospholyase [Source:MGI Symbol;Acc:MGI:1920197]		Q8R1K4	3.3	2.0E-03	6.0	3.5E-02	1.0	6.9E-01	1.7	2.6E-01
ENSMUST00000167816	WD repeat domain 25 [Source:MGI Symbol;Acc:MGI:3045255]		E9Q349	3.0	4.0E-03	3.6	7.7E-03	-1.5	1.6E-01	-0.4	6.3E-01
ENSMUST00000167818	beclin 1, autophagy related [Source:MGI Symbol;Acc:MGI:1891828]	E9PX06		-6.1	2.8E-05	-0.8	5.1E-01	0.4	6.5E-01	-1.8	2.0E-01
ENSMUST00000133023				-3.2	6.2E-02	-2.4	2.2E-01	-0.1	9.0E-01	-1.0	6.4E-01
ENSMUST00000133026	nuclear factor of activated T cells 5 [Source:MGI Symbol;Acc:MGI:1859333]	D6RH97		0.3	8.3E-01	-3.5	2.2E-01	-0.3	8.4E-01	3.5	1.9E-01
ENSMUST00000133032				-1.7	2.0E-01	0.9	6.0E-01	1.4	3.6E-01	-1.2	3.9E-01
ENSMUST00000167824	RAB3C, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1914545]	Q542T7	P62823	9.0	6.3E-05	0.1	9.0E-01	1.0	1.9E-01	-1.2	2.1E-01
ENSMUST00000167856	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]	E9QA74		4.1	4.7E-03	-0.5	7.5E-01	1.8	8.7E-02	-1.1	4.8E-01
ENSMUST00000167859	solute carrier family 39 (metal ion transporter), member 5 [Source:MGI Symbol;Acc:MGI:1919336]		Q9D856	6.3	3.2E-02	6.6	4.6E-03	-0.7	7.1E-01	-2.7	4.6E-02
ENSMUST00000167861	CUE domain containing 2 [Source:MGI Symbol;Acc:MGI:1914366]		Q9CXX9	-3.5	4.8E-04	-0.6	4.3E-01	0.1	8.6E-01	-2.8	1.3E-02
ENSMUST00000167862	serine hydrolase-like [Source:MGI Symbol;Acc:MGI:1890404]	E9Q2Z9		6.5	9.0E-05	-2.8	1.0E-01	1.2	1.4E-01	-0.5	7.5E-01
ENSMUST00000133046	LSM14 homolog A (SCD6, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914320]	A2BH69		0.9	1.6E-01	0.4	6.3E-01	-0.2	6.8E-01	0.3	6.8E-01
ENSMUST00000133048				-1.2	2.2E-01	-1.0	5.0E-01	0.4	6.2E-01	0.2	8.9E-01
ENSMUST00000167866	isocitrate dehydrogenase 3 (NAD+) alpha [Source:MGI Symbol;Acc:MGI:1915084]		Q9D6R2	-1.7	1.2E-02	-4.1	4.9E-03	1.5	1.1E-02	-0.7	5.7E-01
ENSMUST00000133053				-0.4	5.9E-01	0.3	6.9E-01	0.1	8.6E-01	-0.6	4.6E-01
ENSMUST00000167868	solute carrier family 38, member 3 [Source:MGI Symbol;Acc:MGI:1923507]		Q9DCP2	6.6	9.6E-05	4.0	7.2E-03	0.5	6.2E-01	0.0	9.9E-01
ENSMUST00000167876	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Source:MGI Symbol;Acc:MGI:1913721]	E9PZF5		-5.8	3.0E-04	4.1	1.4E-03	-1.0	3.1E-01	-0.8	2.4E-01
ENSMUST00000167899	predicted gene, 17484 [Source:MGI Symbol;Acc:MGI:4937118]	E9Q7H2		4.4	2.5E-03	3.4	5.4E-03	-0.3	7.5E-01	-0.1	8.5E-01
ENSMUST00000167902	predicted gene 3182 [Source:MGI Symbol;Acc:MGI:3781361]	K7N6T8		6.0	4.2E-03	3.8	5.1E-03	1.3	1.8E-01	0.4	5.4E-01
ENSMUST00000167906	predicted gene, 17571 [Source:MGI Symbol;Acc:MGI:4937205]	F6T7Q8		16.2	1.2E-04	6.8	2.1E-03	-0.4	8.1E-01	0.2	8.5E-01
ENSMUST00000167908	predicted gene 17019 [Source:MGI Symbol;Acc:MGI:4868370]	K7N6W5		6.9	7.7E-04	-5.4	3.2E-03	0.9	1.0E-01	-0.9	5.5E-01
ENSMUST00000133067				-4.1	6.1E-02	-3.7	1.5E-01	-0.3	8.3E-01	-0.7	7.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000167921	zinc finger and BTB domain containing 7C [Source:MGI Symbol;Acc:MGI:2443302]		Q8VCZ7	6.3	9.9E-05	1.9	2.5E-02	0.1	8.9E-01	-0.4	5.4E-01
ENSMUST00000167925	interleukin 5 receptor, alpha [Source:MGI Symbol;Acc:MGI:96558]	Q05A81	P21183	7.2	5.7E-05	-0.8	7.2E-01	3.2	5.0E-02	-1.3	6.0E-01
ENSMUST00000167926	acyl-CoA thioesterase 7 [Source:MGI Symbol;Acc:MGI:1917275]	E9PYH2		6.1	2.9E-03	5.0	1.2E-04	-1.2	1.5E-01	0.1	8.1E-01
ENSMUST00000167927	MMS19 (MET18 S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919449]	E9PW47		2.7	7.9E-03	3.4	3.8E-03	-3.2	1.4E-02	-0.3	6.4E-01
ENSMUST00000133089	Tia1 cytotoxic granule-associated RNA binding protein-like 1 [Source:MGI Symbol;Acc:MGI:107913]			-4.0	4.6E-02	-2.1	4.2E-01	1.5	3.5E-01	-0.4	8.7E-01
ENSMUST00000133090				-2.1	3.6E-02	-1.1	3.1E-01	0.5	4.9E-01	-0.4	6.9E-01
ENSMUST00000133093				-0.1	9.2E-01	-0.8	6.6E-01	1.5	2.6E-01	2.2	1.9E-01
ENSMUST00000133095				0.6	3.7E-01	2.1	1.8E-02	-0.6	3.7E-01	-2.1	1.3E-02
ENSMUST00000167951	proline rich 23A, member 3 [Source:MGI Symbol;Acc:MGI:1919229]		Q9CWP9	6.9	7.8E-05	2.2	3.9E-02	-0.3	7.2E-01	-0.5	5.6E-01
ENSMUST00000133103	prolyl-tRNA synthetase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915189]	A0A0A0MQH9		-1.3	8.0E-02	-0.8	2.9E-01	-0.8	2.2E-01	-1.2	1.3E-01
ENSMUST00000167962	RAB12, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:894284]		P35283	-3.0	9.0E-03	4.4	7.9E-06	-0.6	2.2E-01	-0.3	4.5E-01
ENSMUST00000167968	wingless-type MMTV integration site family, member 7B [Source:MGI Symbol;Acc:MGI:98962]	E9Q5E3		7.4	1.1E-04	6.8	2.4E-04	0.3	8.3E-01	-0.1	8.2E-01
ENSMUST00000167974	olfactory receptor 819 [Source:MGI Symbol;Acc:MGI:3030653]	K7N727		5.2	1.7E-02	-1.6	1.2E-01	0.0	9.5E-01	-1.1	2.9E-01
ENSMUST00000133131	protease (prosome, macropain) 26S subunit, ATPase 5 [Source:MGI Symbol;Acc:MGI:105047]	Q8K1K2		2.7	1.7E-01	1.7	5.3E-01	-0.4	8.7E-01	0.7	7.4E-01
ENSMUST00000167977	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 1 [Source:MGI Symbol;Acc:MGI:102469	B5B2N7		-4.8	9.1E-03	5.3	1.3E-03	-0.6	6.2E-01	-0.3	6.9E-01
ENSMUST00000133138				0.4	6.9E-01	0.6	6.7E-01	0.0	9.7E-01	-0.1	9.3E-01
ENSMUST00000133141				2.9	3.6E-02	6.2	6.4E-03	2.2	2.3E-01	-1.2	2.6E-01
ENSMUST00000167978	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase [Source:MGI Symbol;Acc:MGI:1917309]		Q8R2F2	3.7	5.8E-03	7.3	5.3E-05	-0.5	6.4E-01	-0.5	4.1E-01
ENSMUST00000133143				0.5	6.2E-01	1.2	4.4E-01	0.8	4.7E-01	0.2	8.8E-01
ENSMUST00000133148				0.4	8.5E-01	-2.4	4.1E-01	-2.9	1.1E-01	-0.1	9.8E-01
ENSMUST00000167986	NLR family, apoptosis inhibitory protein 2 [Source:MGI Symbol;Acc:MGI:1298226]	A9C471		-6.4	2.5E-04	4.7	1.7E-03	-0.7	5.1E-01	0.7	3.4E-01
ENSMUST00000133154	folliculin interacting protein 2 [Source:MGI Symbol;Acc:MGI:2683054]	D3YUC5		-0.6	2.0E-01	0.9	2.1E-01	1.4	2.0E-02	-0.1	8.3E-01
ENSMUST00000167992	tumor suppressor candidate 3 [Source:MGI Symbol;Acc:MGI:1933134]		Q8BTV1	-1.5	2.8E-02	3.0	3.3E-02	-1.7	1.7E-01	0.1	9.0E-01
ENSMUST00000133158				3.1	7.7E-02	3.3	9.7E-02	-1.0	5.4E-01	-1.2	4.5E-01
ENSMUST00000133159				2.6	1.7E-01	5.1	6.6E-02	1.8	4.8E-01	-0.7	6.3E-01
ENSMUST00000167994	PR domain containing 9 [Source:MGI Symbol;Acc:MGI:2384854]	E9Q4V2		3.1	1.9E-03	5.7	2.5E-03	-0.6	6.8E-01	-0.1	8.6E-01
ENSMUST00000133165				-1.6	8.5E-02	-1.4	2.4E-01	0.5	5.0E-01	0.4	7.5E-01
ENSMUST00000133166				-0.1	9.7E-01	-3.2	3.4E-01	-1.9	3.2E-01	1.2	7.2E-01
ENSMUST00000167995	predicted gene 4781 [Source:MGI Symbol;Acc:MGI:3643164]	L7N2D7		6.7	4.7E-04	4.0	2.1E-03	0.4	6.4E-01	0.6	4.0E-01
ENSMUST00000133170	5 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:191	F6QCI0		-3.4	7.0E-02	-5.2	5.4E-02	-1.2	2.7E-01	0.5	8.4E-01
ENSMUST00000133174				-1.3	3.4E-01	-0.1	9.6E-01	-0.1	9.1E-01	-1.3	3.8E-01
ENSMUST00000133175				-2.4	4.8E-02	-0.6	6.5E-01	1.2	2.4E-01	-0.6	6.5E-01
ENSMUST00000133181	CDC23 cell division cycle 23 [Source:MGI Symbol;Acc:MGI:1098815]			-1.7	1.5E-01	0.3	8.3E-01	0.9	3.9E-01	-1.1	3.9E-01
ENSMUST00000133187				0.7	3.8E-01	-0.4	6.4E-01	-0.9	2.4E-01	0.2	7.8E-01
ENSMUST00000168003	cytochrome P450, family 26, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:2176159]		Q811W2	8.3	2.2E-03	5.8	2.3E-03	-0.1	9.6E-01	-0.1	8.6E-01
ENSMUST00000133191	neurobeachin-like 2 [Source:MGI Symbol;Acc:MGI:2448554]		Q6ZQA0	1.7	3.9E-01	3.6	3.0E-02	-4.6	2.7E-02	-6.5	1.1E-03
ENSMUST00000133195				0.3	7.6E-01	0.3	8.4E-01	0.9	3.6E-01	0.9	4.8E-01
ENSMUST00000133203	neuralized E3 ubiquitin protein ligase 4 [Source:MGI Symbol;Acc:MGI:1921092]	H9H9T3		0.0	9.9E-01	-2.2	4.2E-01	-2.5	2.7E-01	-0.3	9.2E-01
ENSMUST00000168007	olfactory receptor 78 [Source:MGI Symbol;Acc:MGI:2157548]		Q8VBV9	5.9	3.1E-02	6.6	1.5E-03	0.6	7.0E-01	-0.2	8.3E-01
ENSMUST00000168013	MAU2 chromatid cohesion factor homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1921799]	Z4YNA3		-6.0	3.3E-03	4.7	9.2E-04	-1.9	1.1E-01	-0.1	8.3E-01
ENSMUST00000168015	Moloney leukemia virus 10 [Source:MGI Symbol;Acc:MGI:97054]		P23249	-9.2	7.3E-04	8.0	3.0E-04	-0.7	6.4E-01	0.0	9.8E-01
ENSMUST00000133217				2.4	3.2E-01	0.8	8.1E-01	-1.0	6.9E-01	0.6	8.2E-01
ENSMUST00000168018	coatomer protein complex, subunit epsilon [Source:MGI Symbol;Acc:MGI:1891702]	E9Q6I5		-6.9	7.4E-04	7.2	2.8E-04	-0.7	6.2E-01	-0.1	8.8E-01
ENSMUST00000168033	vomeronasal 2, receptor 114 [Source:MGI Symbol;Acc:MGI:3648252]	E9Q281		5.3	5.4E-03	-2.8	1.2E-01	0.9	3.1E-01	-0.9	6.1E-01
ENSMUST00000168049	predicted gene 4553 [Source:MGI Symbol;Acc:MGI:3782737]	A7MAW9		10.2	2.5E-04	4.3	2.9E-03	0.2	8.6E-01	0.2	7.8E-01
ENSMUST00000168064	vestigial like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1920819]	E9Q1Y1		7.1	2.1E-04	-4.3	1.3E-04	-0.5	1.9E-01	-0.7	3.2E-01
ENSMUST00000168071	activated leukocyte cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1313266]	Q5MPX5		5.7	5.9E-03	7.5	1.7E-05	-1.3	2.0E-01	-0.9	7.7E-02
ENSMUST00000168073	tudor domain containing 6 [Source:MGI Symbol;Acc:MGI:2679727]	E9PZ50		7.4	5.8E-04	5.4	7.8E-04	-2.5	5.9E-02	-1.2	1.3E-01
ENSMUST00000168093	protein kinase D2 [Source:MGI Symbol;Acc:MGI:2141917]		Q8BZ03	-3.8	8.5E-04	6.0	1.2E-04	0.7	4.4E-01	0.3	6.1E-01
ENSMUST00000168095	zinc finger protein 426 [Source:MGI Symbol;Acc:MGI:1920248]	E9Q775		-4.6	3.3E-02	-5.8	3.3E-03	-2.5	8.6E-03	-0.6	7.3E-01
ENSMUST00000168099	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Source:MGI Symbol;Acc:MGI:2443241]		Q91VD9	-7.6	5.1E-04	2.8	8.2E-03	0.2	7.8E-01	-0.1	9.4E-01
ENSMUST00000168100	cDNA sequence BC100451 [Source:MGI Symbol;Acc:MGI:1929713]		Q497N6	5.9	9.4E-03	6.1	2.0E-04	-0.9	4.4E-01	0.1	7.9E-01
ENSMUST00000168110	cilia and flagella associated protein 54 [Source:MGI Symbol;Acc:MGI:1922208]		Q8C6S9	3.0	2.0E-02	3.1	2.6E-02	5.1	7.2E-04	-1.4	1.3E-01
ENSMUST00000168115	phosphoribosyl pyrophosphate synthetase-associated protein 2 [Source:MGI Symbol;Acc:MGI:2384838]	Q5SWZ0	Q8R574	-5.6	4.1E-05	6.7	1.9E-04	-0.5	6.7E-01	-0.9	1.6E-01
ENSMUST00000168119	solute carrier organic anion transporter family, member 1a1 [Source:MGI Symbol;Acc:MGI:1351891]	E9Q0W2		5.7	4.9E-05	6.0	1.6E-03	-0.5	7.3E-01	-0.3	7.4E-01
ENSMUST00000168124	bleomycin hydrolase [Source:MGI Symbol;Acc:MGI:1345186]	E9Q6V3		-5.1	6.6E-04	4.6	5.5E-03	-0.8	5.5E-01	-0.1	9.0E-01
ENSMUST00000168126	nuclear receptor subfamily 5, group A, member 2 [Source:MGI Symbol;Acc:MGI:1346834]	Q1WLP7		5.5	1.1E-03	2.3	1.3E-01	1.2	2.8E-01	2.3	5.2E-02
ENSMUST00000168128	predicted gene 6482 [Source:MGI Symbol;Acc:MGI:3644578]	F6YHC1		7.5	2.1E-04	-1.3	1.7E-01	-0.3	6.5E-01	-1.0	2.8E-01
ENSMUST00000168129	trafficking protein particle complex 12 [Source:MGI Symbol;Acc:MGI:2445089]		Q8K2L8	-4.1	1.1E-02	5.5	5.5E-03	0.1	9.4E-01	-0.2	8.2E-01
ENSMUST00000168142	transferrin [Source:MGI Symbol;Acc:MGI:98821]	F7CJN9		-6.9	2.7E-02	-6.3	8.8E-03	-0.7	3.6E-01	0.3	9.0E-01
ENSMUST00000168148	pore forming protein-like [Source:MGI Symbol;Acc:MGI:1860266]	Q5RKV8		5.8	7.9E-04	-2.5	1.3E-01	0.8	3.3E-01	-0.8	6.1E-01
ENSMUST00000168162	platelet derived growth factor receptor, alpha polypeptide [Source:MGI Symbol;Acc:MGI:97530]		P26618	9.0	1.0E-05	7.9	2.4E-05	-0.5	6.2E-01	-2.3	2.8E-03
ENSMUST00000133300				1.9	4.3E-02	2.6	3.0E-02	0.4	6.2E-01	-0.2	8.2E-01
ENSMUST00000168164	PCI domain containing 2 [Source:MGI Symbol;Acc:MGI:2443003]	E9Q5V9		7.2	2.5E-03	7.2	6.3E-04	-0.6	6.9E-01	-3.3	4.3E-03
ENSMUST00000168165	predicted gene 8104 [Source:MGI Symbol;Acc:MGI:3649000]	K7N744		7.4	5.9E-05	6.3	3.1E-04	-0.2	8.8E-01	0.7	3.2E-01
ENSMUST00000168172	nucleotide-binding oligomerization domain containing 1 [Source:MGI Symbol;Acc:MGI:1341839]	Q540J8	Q8BHB0	-3.3	8.5E-04	5.7	3.1E-04	-1.6	1.7E-01	0.3	6.7E-01
ENSMUST00000168175	vomeronasal 2, receptor 115 [Source:MGI Symbol;Acc:MGI:3647235]	E9Q0E7		6.6	6.5E-05	-4.0	2.0E-02	0.3	6.3E-01	2.1	1.7E-01
ENSMUST00000133317	bromodomain PHD finger transcription factor [Source:MGI Symbol;Acc:MGI:2444008]	A2A652		0.3	6.4E-01	1.6	7.1E-02	0.0	1.0E+00	-1.3	1.1E-01
ENSMUST00000168176	CD59a antigen [Source:MGI Symbol;Acc:MGI:109177]	A2BI31	O55186	7.8	2.5E-02	-7.7	7.1E-04	0.6	2.9E-01	-1.1	5.5E-01
ENSMUST00000168184	intelectin 1 (galactofuranose binding) [Source:MGI Symbol;Acc:MGI:1333831]	F6YSS8		5.4	4.2E-04	-2.3	5.9E-02	0.8	2.2E-01	-1.6	2.1E-01
ENSMUST00000168185	tonsoku-like, DNA repair protein [Source:MGI Symbol;Acc:MGI:1919999]	G3UW83		2.7	3.0E-03	4.5	2.1E-02	-0.5	7.8E-01	0.9	4.1E-01
ENSMUST00000168189	exportin 6 [Source:MGI Symbol;Acc:MGI:2429950]		Q924Z6	-8.3	1.0E-04	6.6	4.5E-04	-0.5	7.0E-01	-1.7	4.3E-02
ENSMUST00000168191	trafficking protein particle complex 9 [Source:MGI Symbol;Acc:MGI:1923760]	E9PZ41		8.2	7.5E-05	5.6	6.0E-04	-1.1	3.6E-01	0.1	8.4E-01
ENSMUST00000133338	ATPase, class VI, type 11A [Source:MGI Symbol;Acc:MGI:1354735]	D6RII8		-1.2	2.0E-01	0.2	8.9E-01	1.5	1.6E-01	0.1	9.2E-01
ENSMUST00000168194	zinc finger protein 511 [Source:MGI Symbol;Acc:MGI:1917002]		Q6P0X2	-2.4	1.7E-03	7.9	2.7E-04	0.1	9.6E-01	0.9	1.6E-01
ENSMUST00000168206	nischarin [Source:MGI Symbol;Acc:MGI:1928323]		Q80TM9	-3.1	1.6E-03	5.4	1.7E-04	0.3	7.5E-01	-0.2	7.6E-01
ENSMUST00000168223	family with sequence similarity 63, member A [Source:MGI Symbol;Acc:MGI:1922257]		Q76LS9	-5.8	1.9E-03	0.1	9.5E-01	-4.1	1.3E-02	4.2	8.8E-03

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000168247	zinc finger protein 110 [Source:MGI Symbol;Acc:MGI:1890378]			-7.0	1.4E-04	4.4	3.7E-04	-1.7	7.1E-02	0.1	8.2E-01
ENSMUST00000168288	cut-like homeobox 2 [Source:MGI Symbol;Acc:MGI:107321]		P70298	6.7	3.1E-02	5.1	2.5E-04	-0.6	5.2E-01	-1.0	1.6E-01
ENSMUST00000133362	exostoses (multiple) 1 [Source:MGI Symbol;Acc:MGI:894663]	D6RE56		-2.2	5.5E-02	0.3	6.8E-01	-1.9	2.0E-02	-4.4	1.6E-03
ENSMUST00000168292	predicted gene, 20721 [Source:MGI Symbol;Acc:MGI:5313030]	E9Q2U8		-6.7	1.6E-03	8.1	7.5E-05	1.5	2.3E-01	-0.4	4.4E-01
ENSMUST00000133374				0.6	6.0E-01	0.7	6.9E-01	0.7	6.3E-01	0.6	6.2E-01
ENSMUST00000168295	e carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 [Source:MGI Symbol;Acc:MGI:9	E9PW98		6.0	9.6E-04	7.8	2.8E-05	-0.4	6.9E-01	0.2	7.6E-01
ENSMUST00000168298	predicted gene 3238 [Source:MGI Symbol;Acc:MGI:3781416]	W4VSP7		7.9	5.8E-05	-5.7	9.6E-03	0.3	6.7E-01	-0.1	9.7E-01
ENSMUST00000168302	signal transducer and activator of transcription 4 [Source:MGI Symbol;Acc:MGI:103062]	Q3V157		-3.0	2.1E-03	5.2	3.6E-04	0.4	6.9E-01	0.1	8.8E-01
ENSMUST00000168320	predicted gene 17124 [Source:MGI Symbol;Acc:MGI:4937951]	F6ZIG1		6.6	2.4E-04	7.3	2.3E-04	-0.4	7.6E-01	1.1	1.3E-01
ENSMUST00000133393	cullin 7 [Source:MGI Symbol;Acc:MGI:1913765]	F6Q1R4		0.4	5.9E-01	4.9	8.9E-04	2.3	3.0E-02	-2.2	1.5E-02
ENSMUST00000133396				-0.9	2.9E-01	-0.3	7.7E-01	0.7	3.8E-01	0.2	8.6E-01
ENSMUST00000168332	predicted gene, 17545 [Source:MGI Symbol;Acc:MGI:4937179]	F7A3L5		6.1	1.4E-04	3.9	2.7E-03	-4.4	5.1E-03	-0.2	7.8E-01
ENSMUST00000168345	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3 [Source:MGI Symbol;Acc:MGI:1929467]	Q542I7	O88653	-3.9	8.8E-05	4.4	5.0E-03	-2.4	9.3E-02	0.1	8.9E-01
ENSMUST00000168348	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]	E9QAX2		8.3	6.6E-05	3.9	1.4E-02	-2.4	1.2E-01	-0.2	7.9E-01
ENSMUST00000168360	prolyl 4-hydroxylase, beta polypeptide [Source:MGI Symbol;Acc:MGI:97464]	E9Q8G8		-6.2	7.4E-04	-5.7	7.8E-04	0.0	9.6E-01	-1.5	3.1E-01
ENSMUST00000133423	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:1916960]	D3Z2S2		-1.1	3.6E-01	1.9	2.2E-01	1.6	2.1E-01	-1.3	3.0E-01
ENSMUST00000168366	RAB11A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1858202]	F6R2Z5		-5.3	4.9E-04	-7.4	8.2E-05	0.3	5.2E-01	-0.3	8.1E-01
ENSMUST00000133432	golgi reassembly stacking protein 2 [Source:MGI Symbol;Acc:MGI:2135962]	A2ATI8		0.4	5.9E-01	4.6	6.0E-04	1.1	2.1E-01	-3.0	2.2E-03
ENSMUST00000168382	eukaryotic translation initiation factor 1A [Source:MGI Symbol;Acc:MGI:95298]	Q4FJR7	Q60872	-6.6	5.1E-05	7.7	1.8E-04	-0.2	8.8E-01	0.3	6.7E-01
ENSMUST00000133446				3.3	1.6E-01	4.9	5.8E-02	-0.5	8.5E-01	-2.1	2.2E-01
ENSMUST00000133448				1.0	4.9E-01	2.2	3.2E-01	1.6	3.5E-01	0.4	8.2E-01
ENSMUST00000168383	purinergic receptor P2X, ligand-gated ion channel, 6 [Source:MGI Symbol;Acc:MGI:1337113]	E9Q857		8.5	2.7E-05	3.1	2.4E-01	-4.2	1.4E-01	-0.5	7.8E-01
ENSMUST00000133461				1.4	3.2E-01	2.0	3.5E-01	1.2	4.9E-01	0.7	6.7E-01
ENSMUST00000168386	proline rich 36 [Source:MGI Symbol;Acc:MGI:3605626]	E9PV26		6.8	1.8E-06	6.2	1.1E-04	1.0	3.0E-01	0.8	1.7E-01
ENSMUST00000168387	dysferlin [Source:MGI Symbol;Acc:MGI:1349385]		Q9ESD7	6.6	9.6E-05	8.8	2.5E-05	-1.4	3.0E-01	-0.2	7.5E-01
ENSMUST00000168412	protein arginine N-methyltransferase 6 [Source:MGI Symbol;Acc:MGI:2139971]		Q6NZB1	4.9	2.3E-02	3.1	1.1E-03	-1.1	9.1E-02	0.0	1.0E+00
ENSMUST00000168419	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:MGI Symbol;Acc:MGI:1913304]		Q9D1A2	-7.4	6.0E-05	-3.2	6.0E-02	1.9	4.3E-02	-1.1	5.1E-01
ENSMUST00000133474	NADH dehydrogenase (ubiquinone) flavoprotein 1 [Source:MGI Symbol;Acc:MGI:107851]	D3Z0K1		-0.6	8.4E-01	-2.3	5.1E-01	-1.3	5.4E-01	0.5	9.0E-01
ENSMUST00000168423	SMAD family member 2 [Source:MGI Symbol;Acc:MGI:108051]		Q62432	-3.0	1.3E-02	3.5	1.0E-03	-0.3	6.3E-01	0.2	7.6E-01
ENSMUST00000133485	PHD finger protein 23 [Source:MGI Symbol;Acc:MGI:1925496]		Q8BSN5	0.8	8.0E-01	-0.2	9.5E-01	-0.8	7.6E-01	0.2	9.6E-01
ENSMUST00000133493	ubiquitin-conjugating enzyme E2U (putative) [Source:MGI Symbol;Acc:MGI:3588216]	B1AUC4		2.8	2.8E-01	3.8	1.7E-01	-0.3	9.1E-01	-1.4	4.8E-01
ENSMUST00000133501				2.0	3.0E-01	0.8	7.3E-01	-1.5	3.9E-01	-0.3	8.7E-01
ENSMUST00000133507				1.8	4.3E-01	0.5	8.4E-01	-0.7	7.6E-01	0.6	8.2E-01
ENSMUST00000133511				3.8	8.4E-02	4.7	6.0E-02	-0.4	8.6E-01	-1.3	3.9E-01
ENSMUST00000168431	mitogen-activated protein kinase kinase kinase kinase 4 [Source:MGI Symbol;Acc:MGI:1349394]	F8VPL5		-4.5	6.9E-04	4.1	1.2E-02	0.4	7.4E-01	-1.1	2.3E-01
ENSMUST00000168438	phosphodiesterase 4D interacting protein (myomegalin) [Source:MGI Symbol;Acc:MGI:1891434]	E9Q1A0		6.9	2.7E-02	7.2	1.5E-04	-1.4	2.9E-01	-1.8	2.7E-02
ENSMUST00000133535				0.2	8.0E-01	0.4	7.0E-01	-0.3	6.8E-01	-0.5	5.9E-01
ENSMUST00000133538				-1.3	1.0E-01	-0.6	4.3E-01	-1.1	7.3E-02	-1.8	5.4E-02
ENSMUST00000168444	opsin 4 (melanopsin) [Source:MGI Symbol;Acc:MGI:1353425]		Q9QXZ9	5.9	5.5E-04	5.8	6.5E-03	-0.6	7.4E-01	-0.5	6.5E-01
ENSMUST00000168445	cytochrome b561 family, member A3 [Source:MGI Symbol;Acc:MGI:2686925]		Q6P1H1	-2.6	2.3E-03	5.4	3.3E-05	-0.9	2.1E-01	0.2	6.4E-01
ENSMUST00000133541				2.2	1.3E-01	3.1	1.3E-01	0.3	8.4E-01	-0.5	6.9E-01
ENSMUST00000133544				0.9	2.5E-01	1.0	3.8E-01	0.7	3.8E-01	0.6	5.1E-01
ENSMUST00000168457	undifferentiated embryonic cell transcription factor 1 [Source:MGI Symbol;Acc:MGI:1276125]	B2RSF1	Q6J1H4	7.2	1.2E-04	-4.2	2.3E-02	0.5	4.6E-01	-2.3	2.4E-01
ENSMUST00000168461	ring finger protein 19B [Source:MGI Symbol;Acc:MGI:1922484]	E9Q2L7		-4.8	1.2E-03	-3.5	5.7E-02	-0.1	8.6E-01	0.5	7.9E-01
ENSMUST00000168480	predicted gene, 21560 [Source:MGI Symbol;Acc:MGI:5434915]	D3Z7A4		6.5	2.8E-04	6.3	9.0E-04	0.2	8.9E-01	-1.7	4.5E-02
ENSMUST00000133553	mitochondrial ribosomal protein S11 [Source:MGI Symbol;Acc:MGI:1915244]			-2.6	4.5E-02	-2.5	8.8E-02	-0.3	7.4E-01	-0.3	8.2E-01
ENSMUST00000168485	myosin, heavy polypeptide 7, cardiac muscle, beta [Source:MGI Symbol;Acc:MGI:2155600]	B2RXX9	Q91Z83	8.1	1.5E-02	7.5	5.2E-05	-0.6	6.3E-01	-1.0	1.1E-01
ENSMUST00000133556				4.0	1.1E-01	2.3	3.9E-01	-0.5	8.6E-01	1.2	5.1E-01
ENSMUST00000168489	vomeronasal 2, receptor 59 [Source:MGI Symbol;Acc:MGI:3643747]	E9PUT5		5.2	6.7E-04	5.8	2.2E-03	-0.7	6.3E-01	0.4	6.0E-01
ENSMUST00000133564	estrogen receptor 2 (beta) [Source:MGI Symbol;Acc:MGI:109392]	S4R2G7		5.1	1.6E-01	4.9	2.2E-01	-0.2	9.6E-01	-0.1	9.7E-01
ENSMUST00000133565	tuberous sclerosis 1 [Source:MGI Symbol;Acc:MGI:1929183]	F2Z3X2		2.4	3.4E-01	-0.9	7.7E-01	-3.1	2.2E-01	0.2	9.3E-01
ENSMUST00000133568	protein phosphatase 1, catalytic subunit, gamma isoform [Source:MGI Symbol;Acc:MGI:104872]	A0A0G2JF34		-2.2	1.1E-01	0.4	8.6E-01	2.8	1.1E-01	0.2	9.0E-01
ENSMUST00000168499	NLR family member X1 [Source:MGI Symbol;Acc:MGI:2429611]		Q3TL44	-8.6	2.7E-04	6.5	4.4E-03	-0.7	7.2E-01	-1.5	1.7E-01
ENSMUST00000133574	special AT-rich sequence binding protein 1 [Source:MGI Symbol;Acc:MGI:105084]		Q60611	-0.1	9.8E-01	-3.0	4.9E-01	-1.2	6.2E-01	1.8	6.9E-01
ENSMUST00000168502	transcriptional regulator, SIN3A (yeast) [Source:MGI Symbol;Acc:MGI:107157]		Q60520	-5.4	2.0E-02	6.9	3.2E-03	0.5	7.7E-01	-1.3	2.8E-01
ENSMUST00000168514	calpain 8 [Source:MGI Symbol;Acc:MGI:2181366]		Q91VA3	6.5	1.1E-04	-6.0	5.1E-04	-0.8	9.5E-02	-0.8	5.2E-01
ENSMUST00000133589				2.7	1.9E-01	-1.1	6.0E-01	-3.4	7.3E-02	0.4	8.6E-01
ENSMUST00000168515	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4 [Source:MGI Symbol;Ac	B8QI36		10.0	1.2E-03	5.5	1.8E-03	-0.5	7.1E-01	-2.4	2.5E-02
ENSMUST00000168527	DENN/MADD domain containing 1B [Source:MGI Symbol;Acc:MGI:2447812]	E9Q246		-6.5	1.0E-04	2.9	1.4E-01	-2.0	2.9E-01	1.2	3.8E-01
ENSMUST00000168529	cytochrome b5 reductase 4 [Source:MGI Symbol;Acc:MGI:2386848]		Q3TDX8	-6.7	2.4E-05	5.3	1.9E-03	-1.3	3.0E-01	0.1	8.6E-01
ENSMUST00000168533	tenascin XB [Source:MGI Symbol;Acc:MGI:1932137]	E9Q2T3		7.8	4.4E-03	-1.8	5.2E-01	5.2	6.4E-03	-1.6	5.8E-01
ENSMUST00000133601	polymerase (DNA-directed), delta interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915061]	F6SQH7		3.4	9.7E-02	4.1	1.5E-01	1.4	5.3E-01	0.7	7.4E-01
ENSMUST00000168536	5'-nucleotidase, cytosolic II [Source:MGI Symbol;Acc:MGI:2178563]		Q3V1L4	-8.0	2.8E-06	3.5	2.5E-03	-4.7	8.2E-04	0.1	8.9E-01
ENSMUST00000168553	glucocorticoid modulatory element binding protein 1 [Source:MGI Symbol;Acc:MGI:2135604]		Q9JL60	3.9	3.9E-04	-3.7	5.7E-02	0.5	5.4E-01	-1.7	3.9E-01
ENSMUST00000168554	predicted gene 5423 [Source:MGI Symbol;Acc:MGI:3643175]	F2Z3Z2		6.0	1.5E-03	5.5	1.2E-03	-1.8	2.1E-01	-0.2	8.0E-01
ENSMUST00000133612	leucine rich repeat containing 57 [Source:MGI Symbol;Acc:MGI:1913856]	A2AKH7		-0.2	8.6E-01	-4.5	3.1E-02	-2.0	4.6E-02	2.3	2.2E-01
ENSMUST00000133614				-0.6	8.5E-01	-5.1	1.7E-01	-4.4	4.2E-02	0.1	9.7E-01
ENSMUST00000133615				-3.9	1.3E-01	-3.2	1.7E-01	-1.8	2.2E-01	-2.5	3.7E-01
ENSMUST00000133617	aminolevulinic acid synthase 1 [Source:MGI Symbol;Acc:MGI:87989]	D6RGR8		-1.5	2.9E-01	0.6	7.5E-01	1.9	2.3E-01	-0.3	8.7E-01
ENSMUST00000168561	maestro heat-like repeat family member 3 [Source:MGI Symbol;Acc:MGI:1923672]	E9QAI4		7.6	1.3E-05	-7.0	1.1E-03	1.1	4.0E-02	0.0	9.9E-01
ENSMUST00000133619	retinitis pigmentosa 2 homolog (human) [Source:MGI Symbol;Acc:MGI:1277953]		Q9EPK2	1.6	5.7E-01	1.4	6.9E-01	0.0	9.9E-01	0.2	9.6E-01
ENSMUST00000133621				1.9	6.6E-02	1.5	2.7E-01	0.4	6.7E-01	0.8	4.7E-01
ENSMUST00000168564	exportin 6 [Source:MGI Symbol;Acc:MGI:2429950]	F6Y2I6		-4.4	4.2E-03	-1.0	3.7E-01	0.4	5.4E-01	-4.2	1.2E-02
ENSMUST00000168578	transmembrane protein 238 [Source:MGI Symbol;Acc:MGI:1922935]		A9JSM3	4.1	6.6E-04	8.5	1.2E-04	1.4	2.9E-01	1.2	8.5E-02
ENSMUST00000168579	olute carrier family 16 (monocarboxylic acid transporters), member 3 [Source:MGI Symbol;Acc:MGI:1933438	Q3UDP9	P57787	-2.9	1.7E-02	-4.9	3.2E-05	0.2	5.6E-01	-0.6	4.1E-01
ENSMUST00000133641				-1.2	2.2E-01	0.0	9.7E-01	0.8	4.0E-01	-0.5	6.7E-01
ENSMUST00000133650	phosphatidylinositol glycan anchor biosynthesis, class Q [Source:MGI Symbol;Acc:MGI:1333114]	F6YYP1		1.1	5.6E-01	2.3	3.6E-01	0.0	1.0E+00	-1.1	6.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000168587	COMM domain containing 6 [Source:MGI Symbol;Acc:MGI:1913450]	B7ZNP3		-5.4	3.1E-04	5.1	1.3E-03	0.7	5.1E-01	0.7	3.3E-01
ENSMUST00000133654	acyl-CoA synthetase short-chain family member 2 [Source:MGI Symbol;Acc:MGI:1890410]	D6RHA7		5.2	3.8E-02	-1.1	5.6E-01	-6.2	1.3E-02	0.1	9.4E-01
ENSMUST00000168600	von Willebrand factor A domain containing 3A [Source:MGI Symbol;Acc:MGI:3041229]	E9Q0W9		7.5	4.7E-06	6.6	2.7E-04	-0.6	6.6E-01	-2.5	4.9E-03
ENSMUST00000168630	unc-5 homolog D (C. elegans) [Source:MGI Symbol;Acc:MGI:2389364]		Q8K1S2	8.7	4.2E-05	6.5	1.6E-04	-0.5	6.5E-01	-0.5	4.0E-01
ENSMUST00000133667				-0.2	9.3E-01	-4.6	1.2E-01	-4.3	4.5E-02	0.0	1.0E+00
ENSMUST00000168641	predicted gene 8251 [Source:MGI Symbol;Acc:MGI:3647616]	F6VUT6		4.6	8.3E-05	6.3	3.2E-04	-0.6	6.4E-01	-3.4	2.4E-03
ENSMUST00000168646	RIKEN cDNA C730034F03 gene [Source:MGI Symbol;Acc:MGI:2441921]	Q8BGL5		3.3	2.6E-04	5.6	2.0E-04	-0.4	7.1E-01	-0.4	5.1E-01
ENSMUST00000133686				0.3	6.8E-01	1.3	2.5E-01	0.6	5.0E-01	-0.4	7.1E-01
ENSMUST00000168651	sno, strawberry notch homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2384298]	F7CVW0		-3.2	2.8E-03	-3.2	3.3E-03	-1.2	3.2E-02	-0.8	3.5E-01
ENSMUST00000133695				2.4	6.8E-02	3.4	6.4E-02	0.2	8.9E-01	-0.8	4.8E-01
ENSMUST00000133696				-0.8	6.3E-01	0.2	9.2E-01	0.8	6.8E-01	-0.2	9.0E-01
ENSMUST00000168678	transcriptional regulator, SIN3A (yeast) [Source:MGI Symbol;Acc:MGI:107157]		Q60520	-4.0	9.4E-03	-5.1	8.1E-03	-0.9	2.0E-01	1.6	3.0E-01
ENSMUST00000168680	myosin, heavy chain 15 [Source:MGI Symbol;Acc:MGI:3643515]	E9Q264		7.4	1.2E-05	5.9	8.6E-04	0.4	7.4E-01	-0.7	3.2E-01
ENSMUST00000168691	zinc finger protein 202 [Source:MGI Symbol;Acc:MGI:1933401]	Q99PG8		5.1	1.8E-03	-3.2	7.5E-03	0.8	1.4E-01	-0.1	9.4E-01
ENSMUST00000168693	solute carrier family 8 (sodium/calcium exchanger), member 2 [Source:MGI Symbol;Acc:MGI:107996]	Q8K596		6.5	1.7E-05	6.7	1.8E-04	-1.6	1.9E-01	-1.6	4.5E-02
ENSMUST00000168700	lysine-rich coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1889377]		Q99JT5	-5.5	2.7E-04	5.8	3.7E-04	-1.1	3.3E-01	-0.3	6.5E-01
ENSMUST00000168702	predicted gene 6904 [Source:MGI Symbol;Acc:MGI:3644962]	E9PVF1		5.6	1.3E-04	-3.9	4.0E-02	-1.3	1.5E-01	-0.8	6.7E-01
ENSMUST00000168722	non-SMC element 2 homolog (MMS21, S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915751]		Q91VT1	2.3	8.1E-03	1.6	4.0E-02	0.1	9.1E-01	-0.1	8.7E-01
ENSMUST00000168727	growth differentiation factor 10 [Source:MGI Symbol;Acc:MGI:95684]		P97737	7.8	1.7E-05	7.1	4.0E-04	-0.6	6.7E-01	-0.8	2.9E-01
ENSMUST00000133718				-8.1	3.7E-02	-4.6	3.8E-01	3.4	1.3E-01	-0.1	9.9E-01
ENSMUST00000168746	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	E9PWM7		-6.4	9.3E-04	6.5	4.7E-05	0.6	4.5E-01	0.5	3.2E-01
ENSMUST00000168747	ATPase, class V, type 10A [Source:MGI Symbol;Acc:MGI:1330809]	Q3V1Y7	O54827	2.5	1.0E-03	3.9	4.6E-03	0.1	8.9E-01	0.9	2.2E-01
ENSMUST00000168755	solute carrier family 25, member 44 [Source:MGI Symbol;Acc:MGI:2444391]	Q3TNN4		-4.7	3.7E-03	5.8	3.3E-04	0.3	7.7E-01	-0.1	9.3E-01
ENSMUST00000168757	ATPase, H+ transporting, lysosomal V0 subunit A1 [Source:MGI Symbol;Acc:MGI:103286]	K3W4T3		-6.8	8.9E-04	1.0	5.9E-01	-0.9	5.7E-01	1.4	3.5E-01
ENSMUST00000168767	predicted gene 10767 [Source:MGI Symbol;Acc:MGI:3642136]	Q3TQP0		5.3	5.1E-03	-3.9	6.2E-03	0.1	7.9E-01	-0.5	7.2E-01
ENSMUST00000168769	predicted gene 4302 [Source:MGI Symbol;Acc:MGI:3782482]	E9PX25		8.4	1.3E-05	6.4	5.5E-04	0.4	7.4E-01	-0.9	2.9E-01
ENSMUST00000168779	RIKEN cDNA 2210408I21 gene [Source:MGI Symbol;Acc:MGI:1919621]		Q3UPC7	3.3	2.3E-03	-3.2	4.3E-02	-0.6	4.3E-01	-0.7	6.6E-01
ENSMUST00000168807	vomeronasal 2, receptor 41 [Source:MGI Symbol;Acc:MGI:3757876]	E9Q5C7		8.9	1.4E-05	4.1	3.8E-02	-0.7	6.5E-01	-0.3	7.7E-01
ENSMUST00000168818	complement component 5a receptor 1 [Source:MGI Symbol;Acc:MGI:88232]		P30993	-3.5	1.6E-02	5.5	1.6E-03	-0.5	6.9E-01	-0.8	3.3E-01
ENSMUST00000133748				-1.4	2.0E-01	-1.9	2.9E-01	0.8	4.7E-01	1.3	4.2E-01
ENSMUST00000168825	transforming growth factor beta 1 induced transcript 1 [Source:MGI Symbol;Acc:MGI:102784]	E9PYQ1		7.3	7.4E-05	3.4	1.5E-03	0.4	5.3E-01	-0.4	5.2E-01
ENSMUST00000168828	zinc finger protein 385A [Source:MGI Symbol;Acc:MGI:1352495]		Q8VD12	-1.9	2.2E-02	5.4	2.4E-04	-0.4	6.4E-01	0.1	8.2E-01
ENSMUST00000168837	RIKEN cDNA 4933427D06 gene [Source:MGI Symbol;Acc:MGI:3026922]	Q8CDD1		4.8	2.7E-04	-5.2	1.3E-02	-0.1	9.0E-01	-0.4	8.6E-01
ENSMUST00000168838	cytochrome P450, family 2, subfamily c, polypeptide 69 [Source:MGI Symbol;Acc:MGI:3721049]	E9PXC3		5.2	5.3E-03	4.9	1.1E-02	-0.6	6.8E-01	0.5	5.9E-01
ENSMUST00000133769	serine/threonine kinase 25 (yeast) [Source:MGI Symbol;Acc:MGI:1891699]	D3Z359		-2.1	1.3E-01	-2.4	1.3E-01	0.1	9.4E-01	0.3	8.4E-01
ENSMUST00000168846	protein kinase, AMP-activated, gamma 1 non-catalytic subunit [Source:MGI Symbol;Acc:MGI:108411]	Q3TWR3	O54950	-5.4	1.0E-05	5.3	1.6E-04	-0.2	8.5E-01	-0.7	2.1E-01
ENSMUST00000168864	immunoglobulin superfamily containing leucine-rich repeat [Source:MGI Symbol;Acc:MGI:1349645]		Q6GU68	5.1	1.1E-02	2.5	3.0E-03	-0.4	4.3E-01	-0.6	3.0E-01
ENSMUST00000133779	cell division cycle 6 [Source:MGI Symbol;Acc:MGI:1345150]	E9PY34		4.2	4.3E-02	1.9	4.6E-01	-0.9	6.6E-01	1.4	4.8E-01
ENSMUST00000133783				-1.2	4.0E-01	-2.6	1.8E-01	-0.8	5.2E-01	0.6	7.5E-01
ENSMUST00000133785				1.9	8.6E-02	0.7	5.6E-01	-0.2	8.4E-01	0.9	3.7E-01
ENSMUST00000133786				0.1	9.4E-01	3.7	4.9E-02	3.2	5.4E-02	-0.4	7.1E-01
ENSMUST00000168869	cytochrome P450, family 2, subfamily a, polypeptide 5 [Source:MGI Symbol;Acc:MGI:88597]	E9Q5D4		5.0	2.1E-02	1.7	7.8E-02	-0.6	4.1E-01	-0.1	8.5E-01
ENSMUST00000168871	ankyrin repeat domain 34B [Source:MGI Symbol;Acc:MGI:2443245]		Q3UUF8	6.4	5.7E-05	6.6	3.6E-04	-0.6	6.3E-01	-0.9	2.1E-01
ENSMUST00000133802	ribosomal protein L34 [Source:MGI Symbol;Acc:MGI:1915686]	A0A0G2JEY6		3.0	7.3E-02	3.3	1.4E-01	0.1	9.4E-01	-0.1	9.4E-01
ENSMUST00000133803	taxilin alpha [Source:MGI Symbol;Acc:MGI:105968]	A2ADZ2		3.5	7.2E-02	0.9	6.9E-01	-0.7	7.1E-01	1.9	3.8E-01
ENSMUST00000133804				1.2	2.7E-01	2.2	1.4E-01	0.7	5.0E-01	-0.2	9.0E-01
ENSMUST00000168875	predicted gene 1979 [Source:MGI Symbol;Acc:MGI:3780148]	E9QAN3		5.9	2.5E-03	7.0	3.8E-05	-2.2	6.4E-02	0.5	3.2E-01
ENSMUST00000133813	phosphatidylinositol glycan anchor biosynthesis, class A [Source:MGI Symbol;Acc:MGI:99461]	A2AIH4		-0.1	9.7E-01	-3.1	3.3E-01	-3.8	8.8E-02	-0.7	8.3E-01
ENSMUST00000168882	protein inhibitor of activated STAT 2 [Source:MGI Symbol;Acc:MGI:1096566]	G3UWE3		6.0	2.1E-02	3.5	7.9E-02	-0.7	6.8E-01	1.8	2.0E-01
ENSMUST00000168900	keratinocyte associated protein 2 [Source:MGI Symbol;Acc:MGI:1913309]	A0A0A0MQN1		-3.7	1.2E-03	-3.0	1.0E-02	1.4	2.7E-02	-0.3	7.7E-01
ENSMUST00000133826				-4.4	2.0E-01	-8.6	5.8E-02	-3.3	4.4E-02	0.9	8.5E-01
ENSMUST00000133827				-2.8	5.6E-02	0.3	8.4E-01	1.8	1.0E-01	-1.3	4.5E-01
ENSMUST00000168907	serum/glucocorticoid regulated kinase 3 [Source:MGI Symbol;Acc:MGI:2182368]		Q9ERE3	-6.7	1.8E-05	7.2	1.2E-02	-1.0	7.0E-01	-0.1	9.2E-01
ENSMUST00000168921	leucine zipper transcription factor-like 1 [Source:MGI Symbol;Acc:MGI:1934860]	F6VTH5		-4.4	8.9E-04	6.3	1.2E-03	0.0	9.8E-01	0.9	2.5E-01
ENSMUST00000133836				1.6	4.3E-01	-0.6	7.4E-01	-4.1	4.9E-02	-1.9	3.1E-01
ENSMUST00000133839	enolase 1, alpha non-neuron [Source:MGI Symbol;Acc:MGI:95393]	B0QZL1		-2.9	2.4E-01	-0.3	9.3E-01	2.3	2.7E-01	-0.3	9.3E-01
ENSMUST00000168928	cyclin T1 [Source:MGI Symbol;Acc:MGI:1328363]	E9Q7A7		5.8	2.6E-03	3.4	2.4E-02	-0.9	4.6E-01	-0.8	4.5E-01
ENSMUST00000168954	Rho GTPase activating protein 32 [Source:MGI Symbol;Acc:MGI:2450166]		Q811P8	3.0	1.3E-02	4.0	1.1E-03	-1.1	1.8E-01	0.0	9.7E-01
ENSMUST00000168960	predicted gene, 17546 [Source:MGI Symbol;Acc:MGI:4937180]	E9Q4A1		5.4	1.1E-02	-4.7	8.0E-03	1.8	2.2E-02	-0.9	5.8E-01
ENSMUST00000168974	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:104558]	E9PWV3		-7.5	1.4E-04	5.7	3.4E-03	-0.6	6.9E-01	-1.4	1.6E-01
ENSMUST00000133852				1.6	1.1E-01	3.0	2.0E-02	0.7	4.5E-01	-0.7	4.6E-01
ENSMUST00000168989	potassium channel tetramerisation domain containing 1 [Source:MGI Symbol;Acc:MGI:1918269]	E9Q6T9		3.8	6.2E-05	4.6	9.4E-04	0.9	3.0E-01	0.5	3.9E-01
ENSMUST00000168997	predicted gene 3233 [Source:MGI Symbol;Acc:MGI:3781411]	E9Q2H5		8.0	3.0E-05	5.9	5.2E-03	-0.4	8.3E-01	-0.9	3.7E-01
ENSMUST00000133861	myosin phosphatase Rho interacting protein [Source:MGI Symbol;Acc:MGI:1349438]	F6RND9		-1.3	3.8E-02	-0.7	3.3E-01	0.1	7.7E-01	-0.4	5.1E-01
ENSMUST00000169012	solute carrier family 25, member 41 [Source:MGI Symbol;Acc:MGI:2144215]		Q8BVN7	4.6	2.2E-02	5.8	3.1E-03	-2.8	1.2E-01	0.8	4.0E-01
ENSMUST00000169016	phosphodiesterase 7B [Source:MGI Symbol;Acc:MGI:1352752]	E9Q5I0		7.4	2.2E-03	9.5	1.6E-03	-0.3	8.9E-01	1.4	1.5E-01
ENSMUST00000169017	Fc receptor, IgG, low affinity III [Source:MGI Symbol;Acc:MGI:95500]	E9PUV2		-9.8	4.4E-05	7.7	2.2E-04	-1.8	2.6E-01	0.5	5.1E-01
ENSMUST00000169020	golgi apparatus protein 1 [Source:MGI Symbol;Acc:MGI:104967]	Q53WR6	Q61543	-1.9	1.7E-03	4.9	4.1E-04	-2.1	6.5E-02	0.1	9.0E-01
ENSMUST00000169023	predicted gene 5799 [Source:MGI Symbol;Acc:MGI:3646715]	E9Q2M1		5.8	3.8E-04	6.6	6.7E-06	-3.5	4.9E-03	-0.7	1.3E-01
ENSMUST00000169056	predicted gene 13040 [Source:MGI Symbol;Acc:MGI:3649498]	A2A8C4		4.3	1.9E-02	8.5	2.2E-05	-0.6	5.9E-01	-0.5	3.4E-01
ENSMUST00000169057	von Willebrand factor A domain containing 3B [Source:MGI Symbol;Acc:MGI:1918103]	Q9D5X0		6.1	5.2E-04	5.9	7.2E-03	-0.7	7.0E-01	-1.0	3.6E-01
ENSMUST00000169058	RAB11A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1858202]	E9Q3P9		-8.4	2.9E-05	6.9	4.5E-04	-0.6	6.5E-01	0.1	8.3E-01
ENSMUST00000169061	drosha, ribonuclease type III [Source:MGI Symbol;Acc:MGI:1261425]		Q5HZJ0	7.1	9.1E-03	1.3	2.2E-01	0.7	3.8E-01	1.4	1.2E-01
ENSMUST00000133896				-2.1	3.3E-01	-0.1	9.7E-01	-0.1	9.5E-01	-2.1	3.9E-01
ENSMUST00000169067	palmitoyl-protein thioesterase 2 [Source:MGI Symbol;Acc:MGI:1860075]		O35448	5.2	6.3E-03	5.8	2.9E-03	-0.7	6.5E-01	0.2	7.9E-01
ENSMUST00000169070	eosinophil-associated, ribonuclease A family, member 6 [Source:MGI Symbol;Acc:MGI:1890463]	Q923L7		5.1	4.9E-04	7.4	1.1E-02	0.7	7.9E-01	-0.6	6.4E-01
ENSMUST00000169079	leucine rich repeat and coiled-coil domain containing 1 [Source:MGI Symbol;Acc:MGI:1918960]	G5E8Y2		2.3	8.5E-03	3.5	2.4E-01	2.2	4.1E-01	3.4	8.8E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000169088	laminin B1 [Source:MGI Symbol;Acc:MGI:96743]		P02469	8.5	1.7E-03	-2.4	1.7E-01	1.2	2.2E-01	0.6	7.1E-01
ENSMUST00000169114	endoplasmic reticulum aminopeptidase 1 [Source:MGI Symbol;Acc:MGI:1933403]		Q9EQH2	-2.6	2.0E-03	5.5	4.5E-04	-0.3	7.8E-01	0.5	4.8E-01
ENSMUST00000169121	synaptotagmin VII [Source:MGI Symbol;Acc:MGI:1859545]	E9PZA8		8.0	3.4E-05	4.5	5.0E-03	-0.6	6.2E-01	-0.7	4.2E-01
ENSMUST00000133910				-5.9	3.9E-02	-5.1	2.4E-02	-3.4	1.1E-02	-4.2	1.5E-01
ENSMUST00000133911				-2.5	8.9E-02	-0.9	5.9E-01	0.5	6.4E-01	-1.1	4.9E-01
ENSMUST00000133921	copine I [Source:MGI Symbol;Acc:MGI:2386621]	B7ZCP7		0.5	8.0E-01	0.3	8.8E-01	-1.9	2.0E-01	-1.8	4.1E-01
ENSMUST00000169123	vomeronasal 1 receptor 1 [Source:MGI Symbol;Acc:MGI:3647849]	E9PVR6		6.6	4.3E-04	6.2	4.4E-04	-0.5	7.2E-01	-1.1	1.4E-01
ENSMUST00000169129	SRY (sex determining region Y)-box 6 [Source:MGI Symbol;Acc:MGI:98368]	E9PUW0		6.1	3.0E-04	6.1	9.0E-05	1.5	1.1E-01	-0.3	5.7E-01
ENSMUST00000169130	vomeronasal 2, receptor 62 [Source:MGI Symbol;Acc:MGI:3757994]	K7N712		5.8	5.0E-04	6.1	8.6E-04	-0.4	7.4E-01	-0.6	4.0E-01
ENSMUST00000133934	arrestin domain containing 1 [Source:MGI Symbol;Acc:MGI:2446136]	A2AIS9		-2.2	1.1E-01	-1.0	5.5E-01	1.4	2.9E-01	0.2	8.9E-01
ENSMUST00000169141	slit homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1315203]	E9Q2P0		7.9	1.3E-05	6.8	1.2E-05	0.5	5.2E-01	-0.2	6.0E-01
ENSMUST00000133938	proline rich 14 [Source:MGI Symbol;Acc:MGI:2384565]	D3Z5U4		-0.4	7.8E-01	1.8	3.2E-01	2.4	1.3E-01	0.2	8.9E-01
ENSMUST00000133942	downstream neighbor of SON [Source:MGI Symbol;Acc:MGI:1890621]	F6RJK8		0.0	9.8E-01	-0.9	5.8E-01	0.5	6.5E-01	1.5	3.2E-01
ENSMUST00000169161	apoptosis resistant E3 ubiquitin protein ligase 1 [Source:MGI Symbol;Acc:MGI:1915747]	E9PY98		3.1	2.4E-03	7.6	3.1E-03	-0.9	6.8E-01	0.6	5.6E-01
ENSMUST00000169186	centrosomal protein 19 [Source:MGI Symbol;Acc:MGI:1914244]		Q9CQA8	-9.7	6.2E-06	5.9	5.7E-05	-0.9	2.8E-01	-0.3	5.9E-01
ENSMUST00000169220	vav 1 oncogene [Source:MGI Symbol;Acc:MGI:98923]	E9PXI0		-10.2	2.9E-05	5.0	6.7E-03	-1.0	5.1E-01	-1.2	2.0E-01
ENSMUST00000169226	myoglobin [Source:MGI Symbol;Acc:MGI:96922]	Q3UVB1	P04247	5.7	8.1E-04	6.3	2.6E-03	-0.7	6.7E-01	-2.0	6.9E-02
ENSMUST00000169234	resistin [Source:MGI Symbol;Acc:MGI:1888506]	Q5BMX4	Q99P87	3.0	2.1E-03	5.2	1.9E-03	-1.4	3.2E-01	-1.4	1.1E-01
ENSMUST00000169241	torsin A interacting protein 1 [Source:MGI Symbol;Acc:MGI:3582693]	E9PWW2		-7.9	7.7E-04	-7.1	1.3E-04	-0.3	4.0E-01	0.1	9.3E-01
ENSMUST00000169256	RIKEN cDNA D630045J12 gene [Source:MGI Symbol;Acc:MGI:2669829]		Q68FD9	9.0	7.9E-06	-2.4	2.0E-02	0.5	3.0E-01	-0.5	6.2E-01
ENSMUST00000169273	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 [Source:MGI Symbol;Acc:MGI:104719]		Q3UHN9	-3.4	7.5E-05	7.7	9.1E-06	1.0	2.3E-01	0.1	8.6E-01
ENSMUST00000169289	plectin [Source:MGI Symbol;Acc:MGI:1277961]	E9PW24		6.4	1.7E-03	6.2	1.1E-04	-1.5	1.7E-01	-0.4	4.8E-01
ENSMUST00000169290	chromosome segregation 1-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1339951]	E9QAX7		-4.1	6.8E-03	2.7	1.6E-02	0.4	6.3E-01	-0.2	8.1E-01
ENSMUST00000169295	lymphocyte transmembrane adaptor 1 [Source:MGI Symbol;Acc:MGI:2443362]		Q8BHB3	2.6	3.9E-03	5.6	9.3E-04	-1.3	2.8E-01	0.3	7.3E-01
ENSMUST00000169303	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 [Source:MGI Symbol;Ac			8.5	1.2E-05	-4.8	2.8E-02	0.6	4.3E-01	1.1	5.7E-01
ENSMUST00000169307	olfactory receptor 976 [Source:MGI Symbol;Acc:MGI:3030810]	Q8VF15		7.3	3.4E-05	5.5	5.1E-04	-0.5	6.5E-01	0.1	9.0E-01
ENSMUST00000134010				0.2	8.3E-01	0.3	8.3E-01	0.3	7.3E-01	0.3	8.2E-01
ENSMUST00000169312	CTF8, chromosome transmission fidelity factor 8 [Source:MGI Symbol;Acc:MGI:2443370]		P0CG14	-3.2	8.9E-04	5.1	3.3E-04	-1.2	2.3E-01	-1.1	8.2E-02
ENSMUST00000169324	pogo transposable element with KRAB domain [Source:MGI Symbol;Acc:MGI:1918842]	E9Q3B2		3.1	1.6E-02	3.4	4.6E-03	0.5	5.7E-01	0.8	2.5E-01
ENSMUST00000134023	RIKEN cDNA 1700029H14 gene [Source:MGI Symbol;Acc:MGI:1913751]	Q9D9Y4		3.8	7.2E-02	2.8	1.1E-01	-2.4	2.2E-01	-1.4	3.4E-01
ENSMUST00000134026	metal response element binding transcription factor 2 [Source:MGI Symbol;Acc:MGI:105050]	E9Q8G7		-3.2	2.4E-01	-4.0	2.2E-01	-1.3	4.4E-01	-0.5	8.8E-01
ENSMUST00000134029	polymerase (DNA directed), gamma 2, accessory subunit [Source:MGI Symbol;Acc:MGI:1354947]	D6RFU3		1.3	5.5E-02	1.2	1.4E-01	0.0	9.6E-01	0.1	9.4E-01
ENSMUST00000169345	synapsin II [Source:MGI Symbol;Acc:MGI:103020]		Q64332	8.5	2.6E-05	6.8	8.6E-05	-0.5	6.3E-01	-0.4	4.8E-01
ENSMUST00000169350	SCO-spondin [Source:MGI Symbol;Acc:MGI:2674311]	E9Q0I4		10.0	2.5E-05	4.9	6.3E-05	-0.9	2.2E-01	0.4	4.0E-01
ENSMUST00000169357	Fanconi anemia, complementation group F [Source:MGI Symbol;Acc:MGI:3689889]	E9Q5Z5		2.2	1.9E-02	4.3	1.8E-01	14.4	4.6E-04	-0.4	8.5E-01
ENSMUST00000169367	mitogen-activated protein kinase kinase kinase 12 [Source:MGI Symbol;Acc:MGI:1346881]	E9PUZ1		5.2	6.2E-03	-5.6	4.6E-05	-3.2	3.6E-05	-1.3	1.5E-01
ENSMUST00000134048				1.6	4.2E-01	2.8	2.5E-01	0.2	9.4E-01	-1.0	5.9E-01
ENSMUST00000169378	GPI anchor attachment protein 1 [Source:MGI Symbol;Acc:MGI:1202392]	E9QA52		2.6	1.1E-02	-4.4	1.3E-03	2.2	3.4E-04	-1.7	1.5E-01
ENSMUST00000169381	cation channel, sperm associated 4 [Source:MGI Symbol;Acc:MGI:3043288]	B3VNK5		7.6	2.2E-04	6.1	3.7E-04	-0.6	6.2E-01	0.2	7.5E-01
ENSMUST00000169389	predicted gene 6811 [Source:MGI Symbol;Acc:MGI:3648804]	E9Q3Y8		7.4	8.7E-05	5.2	4.3E-02	-0.2	9.2E-01	-0.2	8.9E-01
ENSMUST00000169397	solute carrier family 39 (zinc transporter), member 7 [Source:MGI Symbol;Acc:MGI:95909]	A0A068BIT0	Q31125	-6.0	3.9E-03	6.8	1.4E-04	-0.6	6.1E-01	-0.3	6.7E-01
ENSMUST00000169398	upstream binding transcription factor, RNA polymerase I-like 1 [Source:MGI Symbol;Acc:MGI:3588290]		Q3USZ2	7.4	1.9E-05	-8.1	1.3E-03	-0.5	4.5E-01	-0.7	7.2E-01
ENSMUST00000134065				0.5	6.2E-01	1.7	2.2E-01	0.7	5.2E-01	-0.5	6.6E-01
ENSMUST00000169404	phosphodiesterase 7B [Source:MGI Symbol;Acc:MGI:1352752]	E9Q0W7		5.2	3.9E-03	5.9	5.5E-04	-1.4	2.9E-01	0.4	5.3E-01
ENSMUST00000169406	predicted gene 1818 [Source:MGI Symbol;Acc:MGI:3037676]	E9Q4A5		4.5	1.1E-03	3.0	9.6E-03	0.0	9.7E-01	-0.4	5.9E-01
ENSMUST00000169415	dynein light chain Tctex-type 1A [Source:MGI Symbol;Acc:MGI:3807506]		P51807	-4.8	2.7E-03	5.3	3.8E-04	-2.0	9.8E-02	-1.6	3.5E-02
ENSMUST00000169423	calmodulin binding transcription activator 1 [Source:MGI Symbol;Acc:MGI:2140230]		A2A891	10.4	1.9E-05	3.9	1.7E-02	-1.7	2.5E-01	-0.7	4.9E-01
ENSMUST00000169433	C2 calcium-dependent domain containing 4D [Source:MGI Symbol;Acc:MGI:2685505]		P0CG09	5.3	5.8E-04	-3.7	8.7E-03	-1.0	1.1E-01	0.2	8.9E-01
ENSMUST00000134086				-0.6	5.0E-01	-2.7	1.3E-01	0.3	7.4E-01	2.3	1.6E-01
ENSMUST00000134088	translocase of inner mitochondrial membrane 17a [Source:MGI Symbol;Acc:MGI:1343131]	D3Z1Z0		0.0	9.8E-01	-2.4	1.4E-02	-2.8	1.5E-03	-0.4	6.5E-01
ENSMUST00000169437	serine (or cysteine) peptidase inhibitor, clade H, member 1 [Source:MGI Symbol;Acc:MGI:88283]		P19324	8.6	6.6E-05	3.1	1.9E-01	-3.6	1.6E-01	0.9	5.6E-01
ENSMUST00000134094				0.2	7.6E-01	-0.3	7.5E-01	0.5	5.3E-01	1.1	2.7E-01
ENSMUST00000134096				2.6	1.7E-01	7.4	2.6E-02	3.4	2.2E-01	-1.4	4.0E-01
ENSMUST00000134102				-1.6	4.1E-01	4.1	1.1E-01	2.0	3.6E-01	-3.6	7.2E-02
ENSMUST00000134103				-1.7	5.2E-01	-2.5	4.1E-01	-1.8	3.3E-01	-1.0	7.7E-01
ENSMUST00000134105	solute carrier family 2 (facilitated glucose transporter), member 1 [Source:MGI Symbol;Acc:MGI:95755]	A2A7P3		-0.4	6.9E-01	-2.1	1.7E-01	-0.8	3.5E-01	0.9	5.6E-01
ENSMUST00000169449	solute carrier family 6 (neurotransmitter transporter), member 17 [Source:MGI Symbol;Acc:MGI:2442535]		Q8BJI1	8.3	9.7E-04	4.8	4.8E-05	0.3	6.2E-01	0.0	9.6E-01
ENSMUST00000169459	PDZ domain containing 7 [Source:MGI Symbol;Acc:MGI:3608325]	E9Q9W7		5.3	2.1E-02	-2.6	4.0E-02	1.2	8.7E-02	-3.5	3.7E-02
ENSMUST00000169464	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]		B1AZP2	6.4	1.7E-02	5.2	1.3E-02	-1.8	3.3E-01	-1.2	3.0E-01
ENSMUST00000169485	DEAH (Asp-Glu-Ala-His) box polypeptide 37 [Source:MGI Symbol;Acc:MGI:3028576]	Q6NZL1		2.0	3.7E-03	6.1	2.6E-05	-0.2	8.3E-01	-0.7	1.6E-01
ENSMUST00000134114	lymphocyte cytosolic protein 1 [Source:MGI Symbol;Acc:MGI:104808]	D3Z311		-1.6	7.0E-02	-2.8	2.5E-02	-1.2	5.7E-02	-0.1	9.6E-01
ENSMUST00000169499	predicted gene 14569 [Source:MGI Symbol;Acc:MGI:3705243]	E9Q0C6		7.0	3.4E-05	-6.0	9.2E-04	-0.7	1.6E-01	-1.5	2.9E-01
ENSMUST00000169503	striatin, calmodulin binding protein 3 [Source:MGI Symbol;Acc:MGI:2151064]	B2RQS1		-3.7	5.7E-03	5.3	1.8E-03	-1.3	3.6E-01	0.4	6.1E-01
ENSMUST00000169504	tudor domain containing 3 [Source:MGI Symbol;Acc:MGI:2444023]		Q91W18	2.9	1.2E-02	6.9	1.6E-04	0.0	9.8E-01	0.6	3.1E-01
ENSMUST00000169531	predicted gene, 17333 [Source:MGI Symbol;Acc:MGI:4936967]	C6EQI3		9.2	6.1E-05	5.6	5.1E-04	-0.5	6.4E-01	0.5	4.5E-01
ENSMUST00000169534	TXK tyrosine kinase [Source:MGI Symbol;Acc:MGI:102960]	B2RQ20		6.7	5.3E-05	7.5	9.8E-06	-2.3	4.2E-02	-1.0	4.3E-02
ENSMUST00000134133				-4.3	6.4E-02	0.4	8.7E-01	2.5	2.2E-01	-2.2	3.8E-01
ENSMUST00000169544	sulfotransferase family, cytosolic, 6B, member 1 [Source:MGI Symbol;Acc:MGI:1920921]		P0CC03	6.1	8.3E-03	-2.7	7.6E-02	1.2	1.3E-01	0.9	5.2E-01
ENSMUST00000169555	predicted gene 3755 [Source:MGI Symbol;Acc:MGI:3781930]	K7N743		8.2	3.1E-05	-1.3	1.6E-01	0.2	6.7E-01	-0.6	4.9E-01
ENSMUST00000169556	vomeronasal 1 receptor 56 [Source:MGI Symbol;Acc:MGI:3033472]	Q9EPS9		6.7	5.5E-05	6.8	3.1E-04	-0.6	6.4E-01	-0.1	9.0E-01
ENSMUST00000134141				1.6	6.2E-02	1.5	1.7E-01	0.0	9.8E-01	0.2	8.3E-01
ENSMUST00000169558	zinc finger protein 426 [Source:MGI Symbol;Acc:MGI:1920248]	G5E8Z9		-7.0	1.2E-03	5.2	6.0E-02	-0.7	7.9E-01	-0.1	9.3E-01
ENSMUST00000169570	C-terminal binding protein 2 [Source:MGI Symbol;Acc:MGI:1201686]		P56546	8.1	4.0E-05	-1.3	4.6E-02	-0.3	4.7E-01	-0.8	2.1E-01
ENSMUST00000134163				3.1	1.1E-01	2.8	1.7E-01	-0.5	8.2E-01	-0.2	9.2E-01
ENSMUST00000169584	T cell immunoglobulin and mucin domain containing 2 [Source:MGI Symbol;Acc:MGI:2159681]	A8C1R4		9.0	4.0E-06	5.6	3.1E-03	0.0	1.0E+00	1.3	1.4E-01
ENSMUST00000169587	predicted gene 8126 [Source:MGI Symbol;Acc:MGI:3646861]	E9Q1N7		7.6	4.8E-04	3.4	1.4E-01	-2.0	4.0E-01	0.2	8.9E-01
ENSMUST00000169591	cytochrome P450, family 4, subfamily f, polypeptide 16 [Source:MGI Symbol;Acc:MGI:1917351]	Q99N17		-4.2	6.1E-03	7.8	1.4E-03	-0.9	6.5E-01	-1.4	1.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000169593	zinc finger and BTB domain containing 42 [Source:MGI Symbol;Acc:MGI:3644133]		Q811H0	-4.2	1.3E-02	7.3	8.9E-05	-2.0	1.4E-01	-0.8	1.7E-01
ENSMUST00000169609	l-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae) [Source:MGI Symbol;Acc:MGI:135		O88822	-6.0	2.7E-03	6.1	3.5E-02	-0.6	8.4E-01	-0.9	5.5E-01
ENSMUST00000169611	methylmalonyl-Coenzyme A mutase [Source:MGI Symbol;Acc:MGI:97239]		P16332	-1.6	9.2E-03	-1.3	4.5E-01	1.6	1.3E-01	-0.6	7.4E-01
ENSMUST00000169613	glutathione S-transferase, pi 1 [Source:MGI Symbol;Acc:MGI:95865]		P19157	-2.4	1.7E-02	4.9	9.6E-04	-2.0	1.1E-01	-0.4	5.1E-01
ENSMUST00000134189				0.1	9.7E-01	-0.9	7.0E-01	-0.3	8.6E-01	0.7	7.5E-01
ENSMUST00000169628	nischarin [Source:MGI Symbol;Acc:MGI:1928323]	F6YR29		-6.1	1.1E-02	-3.7	5.7E-02	1.1	2.2E-01	-1.2	5.6E-01
ENSMUST00000134201				-1.2	4.0E-01	-1.6	3.6E-01	-0.9	3.9E-01	-0.5	8.0E-01
ENSMUST00000169651	NLR family member X1 [Source:MGI Symbol;Acc:MGI:2429611]		Q3TL44	-5.2	2.4E-03	5.6	1.8E-02	-0.7	7.3E-01	-0.2	9.0E-01
ENSMUST00000169652	F-interacting protein with forkhead-associated domain, family member B [Source:MGI Symbol;Acc:MGI:2385		Q8JZM6	-1.7	3.4E-02	3.7	8.4E-03	0.9	4.1E-01	0.3	7.0E-01
ENSMUST00000169656	F-box protein 16 [Source:MGI Symbol;Acc:MGI:1354706]	Q14BG9	Q9QZM9	5.6	1.0E-04	6.0	3.9E-04	0.2	8.1E-01	0.1	9.0E-01
ENSMUST00000134218	transformation related protein 53 inducible nuclear protein 2 [Source:MGI Symbol;Acc:MGI:1915978]	A2ARD0		1.4	9.6E-02	4.8	2.2E-03	2.8	2.3E-02	-0.6	4.4E-01
ENSMUST00000169657	RIKEN cDNA B430203G13 gene [Source:MGI Symbol;Acc:MGI:3642832]	Q8BL23		7.0	2.5E-06	2.2	5.7E-01	7.9	1.3E-02	-1.5	6.8E-01
ENSMUST00000169658	spermatid associated [Source:MGI Symbol;Acc:MGI:1915176]	E9Q4B1		6.0	6.8E-03	-2.5	5.8E-02	-0.2	7.6E-01	-1.4	3.2E-01
ENSMUST00000169659	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Source:MGI Symbol;Acc:MGI:107815]	Q6GTL7		3.0	1.1E-04	3.5	6.4E-04	-0.1	8.9E-01	-0.2	7.2E-01
ENSMUST00000134224	coiled-coil domain containing 37 [Source:MGI Symbol;Acc:MGI:2141635]			2.6	8.5E-02	5.8	1.6E-03	-0.5	7.2E-01	-3.7	4.9E-03
ENSMUST00000169667	Mdm2, transformed 3T3 cell double minute p53 binding protein [Source:MGI Symbol;Acc:MGI:2146005]		Q8BJS8	5.1	9.2E-04	5.5	7.7E-04	-1.2	3.0E-01	-0.5	4.8E-01
ENSMUST00000169670	radial spoke head 4 homolog A (Chlamydomonas) [Source:MGI Symbol;Acc:MGI:3027894]		Q8BYM7	9.0	7.0E-05	-8.2	2.0E-03	-1.4	4.4E-02	-0.9	6.7E-01
ENSMUST00000169678	predicted gene 6576 [Source:MGI Symbol;Acc:MGI:3646644]	F6YTZ4		5.7	2.0E-03	4.0	4.4E-02	-1.4	4.6E-01	0.1	9.6E-01
ENSMUST00000134233				-1.5	4.9E-01	1.2	6.9E-01	1.2	6.2E-01	-1.4	5.6E-01
ENSMUST00000134235				3.1	1.6E-01	3.2	2.6E-01	0.8	7.6E-01	0.7	6.8E-01
ENSMUST00000169681	eukaryotic translation initiation factor 4B [Source:MGI Symbol;Acc:MGI:95304]		Q8BGD9	-4.1	2.2E-06	6.3	1.1E-04	-1.5	1.9E-01	-0.7	2.6E-01
ENSMUST00000169693	cerebellin 1 precursor protein [Source:MGI Symbol;Acc:MGI:88281]	Q7TNF5	Q9R171	6.5	2.8E-03	5.9	2.5E-03	-0.4	7.9E-01	-0.9	3.0E-01
ENSMUST00000169694	holipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) [Source:MGI Symbol;Acc:MGI:135	E9Q330		-4.8	3.8E-04	5.4	2.8E-04	0.6	4.7E-01	-0.7	2.5E-01
ENSMUST00000169695	cancer susceptibility candidate 3 [Source:MGI Symbol;Acc:MGI:2179723]		Q8K3W3	-3.5	6.4E-03	6.5	5.1E-03	-0.6	7.5E-01	-0.6	5.8E-01
ENSMUST00000134259	fucosyltransferase 7 [Source:MGI Symbol;Acc:MGI:107692]	A2AJ24		1.2	2.4E-01	1.4	3.2E-01	1.3	2.3E-01	1.1	3.8E-01
ENSMUST00000169701	glyoxalase domain containing 4 [Source:MGI Symbol;Acc:MGI:1914451]	E9Q197		-4.1	1.0E-03	7.0	2.3E-05	0.1	9.0E-01	-0.1	8.4E-01
ENSMUST00000134291				-1.9	2.0E-01	-1.5	4.8E-01	0.9	4.9E-01	0.5	8.0E-01
ENSMUST00000169707	cyclin T1 [Source:MGI Symbol;Acc:MGI:1328363]		Q9QWV9	-2.0	1.1E-03	3.8	8.7E-02	-0.7	7.1E-01	1.6	2.8E-01
ENSMUST00000169713	phospholipase C, epsilon 1 [Source:MGI Symbol;Acc:MGI:1921305]		Q8K4S1	8.7	5.5E-05	5.4	1.0E-02	-2.3	2.4E-01	-1.5	2.2E-01
ENSMUST00000169721	zinc finger protein 641 [Source:MGI Symbol;Acc:MGI:2442788]		Q8BZ34	8.0	2.9E-04	-1.2	3.2E-01	0.6	5.0E-01	-2.6	7.4E-02
ENSMUST00000169722	nuclear receptor coactivator 4 [Source:MGI Symbol;Acc:MGI:1350932]	E9Q2H3		-4.9	2.9E-02	3.8	2.4E-03	-1.1	2.4E-01	-0.4	5.7E-01
ENSMUST00000169723	patatin-like phospholipase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914103]	E9Q144		-1.8	3.4E-02	4.6	2.7E-03	0.0	9.8E-01	0.8	2.7E-01
ENSMUST00000169744	adiponectin receptor 2 [Source:MGI Symbol;Acc:MGI:93830]	Q53YY3	Q8BQS5	-3.9	1.7E-03	7.7	1.2E-04	-1.0	4.3E-01	1.3	6.6E-02
ENSMUST00000169754	inositol polyphosphate-5-phosphatase D [Source:MGI Symbol;Acc:MGI:107357]		Q9ES52	-6.4	5.4E-04	3.2	3.2E-03	0.0	9.5E-01	0.3	6.3E-01
ENSMUST00000134331				-0.7	5.2E-01	-0.4	7.8E-01	-0.3	7.3E-01	-0.6	6.4E-01
ENSMUST00000134332				4.4	8.8E-02	6.1	4.2E-02	-0.3	9.1E-01	-2.0	2.2E-01
ENSMUST00000134335				0.7	7.6E-01	3.3	2.5E-01	1.0	6.7E-01	-1.5	5.2E-01
ENSMUST00000134342				-2.4	9.1E-02	-4.9	7.8E-03	-3.6	2.4E-03	-1.0	5.3E-01
ENSMUST00000134349	retinitis pigmentosa 2 homolog (human) [Source:MGI Symbol;Acc:MGI:1277953]		Q9EPK2	-0.2	9.4E-01	-0.3	8.7E-01	-2.3	1.9E-01	-2.1	3.4E-01
ENSMUST00000134350				1.8	8.9E-02	1.7	2.5E-01	1.0	4.3E-01	1.1	3.2E-01
ENSMUST00000134358				5.2	1.7E-01	7.4	7.0E-02	-0.9	8.3E-01	-3.1	1.4E-01
ENSMUST00000134370				0.6	5.2E-01	2.2	7.9E-02	1.0	3.0E-01	-0.6	5.3E-01
ENSMUST00000169759	enoyl-Coenzyme A delta isomerase 2 [Source:MGI Symbol;Acc:MGI:1346064]	E9Q7A8		4.8	7.5E-05	1.2	5.2E-01	-2.7	1.4E-01	2.5	1.1E-01
ENSMUST00000169776	myosin binding protein C, cardiac [Source:MGI Symbol;Acc:MGI:102844]	Q3UIK0		6.1	2.4E-02	5.6	6.3E-04	-0.5	6.8E-01	-0.1	8.6E-01
ENSMUST00000169782	ankyrin repeat domain 10 [Source:MGI Symbol;Acc:MGI:1921840]	Q8BG46		2.7	1.7E-03	5.9	1.9E-04	-1.0	3.2E-01	-1.0	1.3E-01
ENSMUST00000134382				-3.3	3.7E-02	-0.9	5.4E-01	0.9	3.9E-01	-1.5	3.6E-01
ENSMUST00000169803	RIMS binding protein 3 [Source:MGI Symbol;Acc:MGI:2685449]	E9PZY2		9.8	8.3E-06	3.5	6.5E-03	-1.5	1.4E-01	-1.5	9.4E-02
ENSMUST00000169826	ribosomal protein S24 [Source:MGI Symbol;Acc:MGI:98147]	Q5M9M7	P62849	-6.6	1.1E-06	5.2	7.7E-03	0.7	6.2E-01	0.2	8.2E-01
ENSMUST00000169834	NIMA (never in mitosis gene a)-related expressed kinase 5 [Source:MGI Symbol;Acc:MGI:2142824]		Q7TSC3	6.7	4.6E-05	4.7	3.8E-04	-1.2	1.8E-01	-0.1	9.2E-01
ENSMUST00000169851	microtubule-associated protein 4 [Source:MGI Symbol;Acc:MGI:97178]	Q78TF3		5.4	3.5E-05	6.5	5.2E-03	0.3	8.8E-01	0.4	7.3E-01
ENSMUST00000134406				0.6	5.9E-01	1.9	1.7E-01	0.6	6.1E-01	-0.7	5.1E-01
ENSMUST00000169852	spleen focus forming virus (SFFV) proviral integration oncogene [Source:MGI Symbol;Acc:MGI:98282]	E9Q6W1		-7.3	4.6E-05	5.3	2.1E-02	-0.2	9.2E-01	0.3	8.4E-01
ENSMUST00000134412				-0.9	4.1E-01	0.0	9.9E-01	0.8	4.5E-01	-0.1	9.3E-01
ENSMUST00000134413				-2.0	1.9E-01	-1.7	4.4E-01	1.5	2.8E-01	1.2	5.6E-01
ENSMUST00000134414				-3.3	3.1E-01	-9.0	5.4E-02	-5.3	1.4E-02	0.3	9.5E-01
ENSMUST00000169860	mortality factor 4 like 1 [Source:MGI Symbol;Acc:MGI:1096551]	Q569V4	P60762	-10.4	5.4E-06	-5.4	5.6E-02	-0.4	7.1E-01	-0.1	9.7E-01
ENSMUST00000134423	solute carrier family 47, member 2 [Source:MGI Symbol;Acc:MGI:3588190]	Z4YMV2		3.4	3.7E-02	5.8	2.4E-03	-0.5	7.4E-01	-2.9	1.6E-02
ENSMUST00000169861	soc-2 (suppressor of clear) homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1927197]		O88520	-4.1	2.8E-03	6.0	1.1E-03	-0.9	5.0E-01	0.6	4.5E-01
ENSMUST00000169862	B RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:215		G5E8Z2	2.1	3.3E-03	1.9	2.3E-01	-0.3	7.9E-01	2.0	1.3E-01
ENSMUST00000134441				-3.0	3.6E-02	0.0	9.9E-01	1.7	1.8E-01	-1.3	3.9E-01
ENSMUST00000134444				-0.7	7.7E-01	-2.5	3.8E-01	-2.5	1.8E-01	-0.7	8.2E-01
ENSMUST00000134449				1.3	4.3E-01	1.6	4.7E-01	0.0	9.9E-01	-0.3	8.6E-01
ENSMUST00000169870	TraB domain containing [Source:MGI Symbol;Acc:MGI:1915226]	E9PXM1		-4.9	1.5E-02	-5.4	4.4E-02	0.3	7.5E-01	-0.7	7.8E-01
ENSMUST00000169878	lymphocyte cytosolic protein 2 [Source:MGI Symbol;Acc:MGI:1321402]		Q60787	-10.3	9.4E-06	6.1	3.0E-04	-0.6	6.1E-01	-0.6	3.7E-01
ENSMUST00000169880	discs, large homolog 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:1918478]	F6Z115		6.6	4.4E-04	-6.3	3.6E-02	-0.1	9.4E-01	2.0	4.7E-01
ENSMUST00000169893	kin of IRRE like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2442334]		Q7TSU7	6.0	8.7E-03	5.3	1.4E-02	-0.9	6.3E-01	-1.6	2.4E-01
ENSMUST00000134473				-0.6	7.1E-01	1.4	5.9E-01	1.2	5.9E-01	-0.8	6.7E-01
ENSMUST00000169897	glucosaminyl (N-acetyl) transferase 1, core 2 [Source:MGI Symbol;Acc:MGI:95676]		Q09324	-4.1	3.6E-03	5.6	6.5E-03	0.9	5.9E-01	-0.4	6.4E-01
ENSMUST00000134487				2.2	4.9E-02	4.3	1.1E-02	1.5	2.7E-01	-0.7	4.7E-01
ENSMUST00000169905	metadherin [Source:MGI Symbol;Acc:MGI:1914404]	F6ZSG0		-3.5	6.7E-03	2.4	2.3E-01	-1.3	4.7E-01	2.4	1.2E-01
ENSMUST00000169909	schwannomin interacting protein 1 [Source:MGI Symbol;Acc:MGI:1353557]		Q3TI53	-6.4	4.5E-04	-4.1	2.4E-03	-1.7	8.3E-03	-0.8	5.0E-01
ENSMUST00000169921	CCR4-NOT transcription complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1919318]		Q8C5L3	-5.9	1.0E-04	6.8	1.0E-04	-0.5	6.5E-01	-0.8	1.9E-01
ENSMUST00000134498				1.8	2.0E-01	2.2	2.6E-01	0.2	9.2E-01	-0.2	8.8E-01
ENSMUST00000169922	chromodomain helicase DNA binding protein 2 [Source:MGI Symbol;Acc:MGI:2448567]		E9PZM4	-1.7	1.3E-02	6.3	2.4E-04	-0.6	6.0E-01	-0.3	6.7E-01
ENSMUST00000169926	interferon-related developmental regulator 1 [Source:MGI Symbol;Acc:MGI:1316717]	E9Q1E6		-3.5	5.7E-04	-8.0	3.9E-03	2.0	9.9E-03	1.4	5.2E-01
ENSMUST00000169942	PDZ domain containing RING finger 4 [Source:MGI Symbol;Acc:MGI:3056996]	E9PUZ9		6.3	3.8E-04	8.8	7.0E-04	1.1	5.2E-01	1.6	8.5E-02
ENSMUST00000134506	progestin and adipoQ receptor family member VII [Source:MGI Symbol;Acc:MGI:1919154]	D3YZW6		1.3	6.4E-02	2.7	1.0E-02	1.3	9.9E-02	-0.2	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000169948	ring finger and CHY zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1915348]	G3UWD8		-1.9	2.6E-03	4.6	3.3E-03	-2.3	9.1E-02	-1.8	5.7E-02
ENSMUST00000169961	coiled-coil domain containing 82 [Source:MGI Symbol;Acc:MGI:1913646]	Q9D6Z7		-3.9	2.0E-02	6.0	9.5E-05	-0.2	8.4E-01	0.3	5.5E-01
ENSMUST00000170000	RNA binding motif protein 7 [Source:MGI Symbol;Acc:MGI:1914260]	Q14A95	Q9CQT2	-4.4	1.5E-05	2.7	1.3E-02	0.7	3.8E-01	1.3	9.6E-02
ENSMUST00000134520				3.1	3.7E-02	3.2	1.0E-01	0.7	6.8E-01	0.6	6.5E-01
ENSMUST00000170017	glyoxalase domain containing 4 [Source:MGI Symbol;Acc:MGI:1914451]	E9Q055		-6.2	6.7E-03	8.1	2.8E-05	0.9	4.1E-01	0.9	8.7E-02
ENSMUST00000170035	activated leukocyte cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1313266]	E9Q3Q6		-5.4	2.4E-03	4.8	3.6E-04	1.2	1.8E-01	-0.1	8.4E-01
ENSMUST00000134531				2.5	7.6E-02	2.3	1.8E-01	0.1	9.1E-01	0.4	7.9E-01
ENSMUST00000170036	ets variant 3 [Source:MGI Symbol;Acc:MGI:1350926]		Q8R4Z4	-4.3	5.8E-03	2.9	3.1E-01	-0.7	7.7E-01	1.7	4.5E-01
ENSMUST00000170046	Mdm2, transformed 3T3 cell double minute p53 binding protein [Source:MGI Symbol;Acc:MGI:2146005]		Q8BJS8	6.0	2.5E-04	3.7	5.0E-02	-0.4	8.1E-01	0.8	5.0E-01
ENSMUST00000170048	RIKEN cDNA A930033H14 gene [Source:MGI Symbol;Acc:MGI:2444562]	G5E8X6		8.0	2.6E-05	5.5	2.0E-04	-0.7	4.2E-01	0.0	9.9E-01
ENSMUST00000170050	metadherin [Source:MGI Symbol;Acc:MGI:1914404]	F6QFT1		-4.8	2.6E-02	8.4	1.6E-04	-0.8	6.2E-01	0.0	9.6E-01
ENSMUST00000170051	CD36 antigen [Source:MGI Symbol;Acc:MGI:107899]	Q3UAI3	Q08857	3.6	2.2E-03	4.2	1.2E-01	-0.8	7.6E-01	0.4	8.1E-01
ENSMUST00000134540				1.8	9.4E-02	2.4	7.9E-02	-0.5	6.5E-01	-1.2	2.3E-01
ENSMUST00000170054	bromodomain adjacent to zinc finger domain, 2A [Source:MGI Symbol;Acc:MGI:2151152]	E9Q374		-4.7	2.2E-02	6.9	1.2E-06	-0.6	3.2E-01	0.0	9.3E-01
ENSMUST00000170060	zinc finger protein 839 [Source:MGI Symbol;Acc:MGI:1920055]	E9PUU5		2.9	1.9E-04	4.0	1.2E-01	-0.7	7.8E-01	1.9	2.3E-01
ENSMUST00000134550	phosphoribosyl pyrophosphate synthetase 1-like 1 [Source:MGI Symbol;Acc:MGI:1922706]	Q8C5R8		-2.5	1.7E-01	1.2	6.1E-01	2.5	1.9E-01	-1.1	5.7E-01
ENSMUST00000134551	Ras suppressor protein 1 [Source:MGI Symbol;Acc:MGI:103040]	E0CXG5		0.3	9.1E-01	-2.0	2.6E-01	-4.9	1.3E-02	-2.7	2.2E-01
ENSMUST00000134553	far upstream element (FUSE) binding protein 3 [Source:MGI Symbol;Acc:MGI:2443699]	A0A0A6YVV5		3.0	4.2E-02	2.7	6.1E-02	-1.9	1.5E-01	-1.7	1.8E-01
ENSMUST00000170068	sirtuin 2 [Source:MGI Symbol;Acc:MGI:1927664]		Q8VDQ8	-4.6	1.2E-02	-5.0	2.6E-03	-0.2	7.4E-01	2.9	3.8E-02
ENSMUST00000170086	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) [Source:MGI Symbol;Acc:MGI:98483]		P21958	-5.4	7.9E-04	7.0	1.1E-04	-0.5	6.7E-01	-0.4	4.6E-01
ENSMUST00000170091	macrophage scavenger receptor 1 [Source:MGI Symbol;Acc:MGI:98257]	Q8CED7	P30204	-1.9	2.6E-02	4.9	2.2E-03	-1.2	3.7E-01	0.0	9.9E-01
ENSMUST00000134560				-0.2	8.1E-01	-1.4	3.6E-01	-0.6	5.5E-01	0.5	7.1E-01
ENSMUST00000170100	RAD1 checkpoint DNA exonuclease [Source:MGI Symbol;Acc:MGI:1316678]	F7CJR1		2.6	6.6E-03	5.6	2.2E-04	-0.6	5.1E-01	0.6	3.0E-01
ENSMUST00000170104	predicted gene 3411 [Source:MGI Symbol;Acc:MGI:3781589]	Q8C7R2		7.6	6.1E-05	6.2	6.3E-04	-0.6	6.7E-01	-0.3	6.3E-01
ENSMUST00000170111	potassium channel tetramerisation domain containing 6 [Source:MGI Symbol;Acc:MGI:1918643]	A2RS47	Q8BNL5	3.5	6.0E-04	-2.1	2.7E-02	-0.1	8.8E-01	-2.0	6.9E-02
ENSMUST00000170123	predicted gene 10409 [Source:MGI Symbol;Acc:MGI:3710610]	Q9CZI1		5.5	6.8E-03	6.1	5.5E-06	-0.8	2.2E-01	0.2	6.4E-01
ENSMUST00000134569	deoxyribonuclease II alpha [Source:MGI Symbol;Acc:MGI:1329019]	D3Z5U3		-3.3	8.4E-02	-1.6	5.2E-01	1.1	4.7E-01	-0.7	7.8E-01
ENSMUST00000134570	WD repeat domain 62 [Source:MGI Symbol;Acc:MGI:1923696]	F6R9F0		-0.3	8.6E-01	-1.2	5.9E-01	0.3	8.4E-01	1.2	5.9E-01
ENSMUST00000134575	RIKEN cDNA 2410004B18 gene [Source:MGI Symbol;Acc:MGI:1913671]	D6RCI4		-4.7	1.6E-01	2.3	5.0E-01	3.6	2.1E-01	-3.4	3.2E-01
ENSMUST00000134576				1.0	4.9E-01	3.1	1.5E-01	1.5	4.0E-01	-0.6	6.7E-01
ENSMUST00000170124	DNA segment, Chr 6, ERATO Doi 527, expressed [Source:MGI Symbol;Acc:MGI:1261919]	F7D6F6		5.8	5.4E-04	-1.3	3.2E-01	3.4	1.7E-03	-0.3	8.2E-01
ENSMUST00000170127	oxidation resistance 1 [Source:MGI Symbol;Acc:MGI:2179326]	E9Q0A7		-4.5	4.3E-03	-0.6	4.0E-01	0.5	3.4E-01	-1.5	6.3E-02
ENSMUST00000134593	nudix (nucleoside diphosphate linked moiety X)-type motif 7 [Source:MGI Symbol;Acc:MGI:1914778]		Q99P30	-0.5	6.0E-01	-2.0	7.5E-02	-1.9	2.6E-02	-0.4	6.9E-01
ENSMUST00000170142	deafness, autosomal dominant 5 (human) [Source:MGI Symbol;Acc:MGI:1889850]		Q9Z2D3	-9.7	1.8E-05	3.4	6.1E-04	-0.6	3.4E-01	0.0	9.8E-01
ENSMUST00000134595				2.6	1.0E-01	5.4	3.4E-03	-0.5	7.4E-01	-3.3	1.3E-02
ENSMUST00000170146	potassium voltage gated channel, Shab-related subfamily, member 2 [Source:MGI Symbol;Acc:MGI:99632]		A6H8H5	7.5	3.6E-06	6.9	4.9E-05	0.1	9.5E-01	-0.6	2.6E-01
ENSMUST00000170156	ryanodine receptor 2, cardiac [Source:MGI Symbol;Acc:MGI:99685]	F6U7V1		6.8	2.4E-02	5.2	8.4E-04	-0.5	6.3E-01	-0.9	2.6E-01
ENSMUST00000170202	guanylate kinase 1 [Source:MGI Symbol;Acc:MGI:95871]	Q564G0		-3.3	2.4E-04	6.6	5.5E-05	-0.6	5.0E-01	-0.1	8.6E-01
ENSMUST00000170207	predicted gene 8108 [Source:MGI Symbol;Acc:MGI:3779783]	K7N734		6.1	3.1E-04	7.6	3.3E-05	-1.4	2.2E-01	0.5	3.3E-01
ENSMUST00000134611	acyl-CoA thioesterase 8 [Source:MGI Symbol;Acc:MGI:2158201]	G3UXJ8		-0.1	9.0E-01	-1.6	2.6E-01	-0.2	8.4E-01	1.3	3.3E-01
ENSMUST00000170225	zinc finger protein 414 [Source:MGI Symbol;Acc:MGI:1915641]	E9Q4H9		-3.3	1.0E-03	-7.2	5.3E-02	-1.0	3.8E-01	0.5	8.8E-01
ENSMUST00000134629				-2.4	7.7E-02	-2.4	1.1E-01	-0.9	3.6E-01	-0.8	5.9E-01
ENSMUST00000134632				1.0	7.0E-01	-2.5	3.3E-01	-4.1	4.7E-02	-0.6	8.2E-01
ENSMUST00000134637				-2.0	6.6E-02	0.7	5.2E-01	1.0	2.9E-01	-1.8	1.3E-01
ENSMUST00000134639				-1.2	1.7E-01	1.4	1.6E-01	0.9	2.9E-01	-1.7	7.1E-02
ENSMUST00000170227	cytochrome P450, family 2, subfamily a, polypeptide 22 [Source:MGI Symbol;Acc:MGI:3648316]	B2RXZ2		6.2	1.3E-04	-4.0	2.2E-03	0.7	1.5E-01	-0.7	5.1E-01
ENSMUST00000170239	ribosomal protein L3-like [Source:MGI Symbol;Acc:MGI:1913461]	E9PWZ3		6.4	1.4E-02	5.6	5.5E-03	-0.1	9.7E-01	-0.1	9.5E-01
ENSMUST00000170241	clathrin, light polypeptide (Lca) [Source:MGI Symbol;Acc:MGI:894297]	Q6PFA2		-9.2	4.6E-07	2.3	1.8E-01	-1.3	3.6E-01	1.5	2.7E-01
ENSMUST00000170259	cytochrome P450, family 11, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88583]	Q3TG86		9.3	1.5E-06	6.4	2.4E-04	-0.9	4.6E-01	-0.9	1.7E-01
ENSMUST00000170267	trace amine-associated receptor 8C [Source:MGI Symbol;Acc:MGI:3527452]		Q5QD05	6.2	1.3E-02	6.0	4.5E-04	-0.5	7.1E-01	-0.7	3.3E-01
ENSMUST00000170271	delta-like 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2146838]	E9Q0Y2		7.4	8.7E-05	-3.3	3.4E-02	1.5	4.8E-02	-0.7	6.3E-01
ENSMUST00000134660	sterol regulatory element binding transcription factor 1 [Source:MGI Symbol;Acc:MGI:107606]	F6XZS9		-2.8	1.8E-01	-2.2	5.4E-01	2.4	2.9E-01	1.9	5.6E-01
ENSMUST00000134661	kinetochore-localized astrin/SPAG5 binding [Source:MGI Symbol;Acc:MGI:1289298]		Q9D9Z1	1.4	4.3E-02	1.5	5.6E-02	-0.3	6.5E-01	-0.4	5.0E-01
ENSMUST00000170280	vomeronasal 2, receptor 4 [Source:MGI Symbol;Acc:MGI:3648229]	E9Q277		5.9	3.9E-04	9.4	2.2E-05	-0.7	6.1E-01	-0.7	2.1E-01
ENSMUST00000134667	synovial apoptosis inhibitor 1, synoviolin [Source:MGI Symbol;Acc:MGI:1921376]			-1.6	6.2E-02	-1.3	2.6E-01	1.0	1.9E-01	0.7	5.0E-01
ENSMUST00000134668	RNA binding motif protein 18 [Source:MGI Symbol;Acc:MGI:1915139]	D6REF9		-2.7	1.3E-01	-3.3	8.0E-02	-2.0	7.1E-02	-1.4	4.9E-01
ENSMUST00000134671				-1.3	2.1E-01	0.1	9.1E-01	0.9	3.7E-01	-0.5	6.3E-01
ENSMUST00000170285	adaptor protein complex AP-1, gamma 2 subunit [Source:MGI Symbol;Acc:MGI:1328307]		O88512	-6.6	5.0E-03	-5.5	7.9E-04	-0.4	3.3E-01	-0.3	7.9E-01
ENSMUST00000170293	guanine nucleotide binding protein (G protein), beta 2 [Source:MGI Symbol;Acc:MGI:95784]	D3YZX3		-8.5	1.8E-03	5.1	4.5E-03	-0.3	8.4E-01	0.0	9.8E-01
ENSMUST00000170303	predicted gene 20390 [Source:MGI Symbol;Acc:MGI:5141855]	E9PZF0		-6.7	3.8E-04	6.2	7.5E-05	-2.1	6.6E-02	-0.1	8.0E-01
ENSMUST00000170304	coiled-coil domain containing 159 [Source:MGI Symbol;Acc:MGI:1914369]		Q8C963	5.4	3.3E-02	5.9	1.1E-03	1.3	3.1E-01	0.0	9.8E-01
ENSMUST00000170308	cAMP-regulated phosphoprotein 19 [Source:MGI Symbol;Acc:MGI:1891691]		P56212	-7.1	1.4E-05	5.2	1.6E-03	-2.1	1.2E-01	-0.1	8.9E-01
ENSMUST00000134686				0.4	6.0E-01	1.2	2.3E-01	0.2	8.0E-01	-0.6	4.9E-01
ENSMUST00000170315	Bloom syndrome, RecQ helicase-like [Source:MGI Symbol;Acc:MGI:1328362]	E9PZ97		7.7	3.2E-05	6.3	2.5E-04	-2.5	7.3E-02	-0.1	8.5E-01
ENSMUST00000170320	ATP/GTP binding protein-like 2 [Source:MGI Symbol;Acc:MGI:2443254]		Q8CDK2	5.2	3.2E-05	-3.5	2.5E-03	0.4	4.0E-01	-0.5	5.6E-01
ENSMUST00000134697				-1.5	2.4E-01	-1.9	3.7E-01	0.8	5.7E-01	1.2	5.4E-01
ENSMUST00000134698				1.0	4.5E-01	1.4	4.2E-01	0.4	8.1E-01	-0.1	9.5E-01
ENSMUST00000170323	septin 12 [Source:MGI Symbol;Acc:MGI:1918339]	Q9D451		6.8	1.1E-04	5.6	9.1E-04	-1.4	2.8E-01	0.0	1.0E+00
ENSMUST00000134702				-0.5	6.4E-01	-3.4	1.0E-01	-0.5	6.1E-01	2.3	2.3E-01
ENSMUST00000134703				-2.2	1.1E-01	-2.9	4.6E-02	-0.4	6.1E-01	0.3	8.1E-01
ENSMUST00000170331	translocase of inner mitochondrial membrane 23 [Source:MGI Symbol;Acc:MGI:1858317]	E9PVF9		4.7	1.3E-02	6.6	4.4E-04	0.7	5.7E-01	0.5	4.8E-01
ENSMUST00000170349	proline rich 23A, member 1 [Source:MGI Symbol;Acc:MGI:3645743]	G3UW32		5.9	1.5E-03	5.1	1.7E-04	-0.7	4.3E-01	-0.3	6.2E-01
ENSMUST00000170356	dpy-19-like 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1915685]		A6X919	-3.0	1.9E-02	3.0	1.9E-02	-0.4	6.9E-01	0.0	1.0E+00
ENSMUST00000170374	adenosine monophosphate deaminase 3 [Source:MGI Symbol;Acc:MGI:1096344]		O08739	-1.8	1.9E-02	6.2	6.6E-04	-0.6	6.4E-01	-0.5	4.7E-01
ENSMUST00000170377	Ras-like without CAAX 1 [Source:MGI Symbol;Acc:MGI:108053]	G5E8W6		-5.7	2.4E-03	-4.0	8.5E-03	1.2	4.7E-02	1.8	1.6E-01
ENSMUST00000170382	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913623]		P62322	-4.1	8.2E-04	5.6	1.5E-03	-0.4	7.5E-01	1.8	3.3E-02
ENSMUST00000134727	cell division cycle 26 [Source:MGI Symbol;Acc:MGI:1913690]		Q99JP4	0.9	4.3E-02	1.3	1.8E-02	-0.1	7.8E-01	-0.5	2.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000134728				3.6	2.4E-01	3.2	3.5E-01	-0.4	9.1E-01	0.1	9.7E-01
ENSMUST00000134732	CDK5 regulatory subunit associated protein 3 [Source:MGI Symbol;Acc:MGI:1933126]	D6RJ46		3.9	7.4E-02	2.6	3.5E-01	-0.7	7.9E-01	0.7	7.1E-01
ENSMUST00000134735				1.7	3.5E-01	-0.6	8.2E-01	-0.9	6.7E-01	1.4	5.2E-01
ENSMUST00000134737				-1.8	7.8E-02	0.9	4.1E-01	0.4	6.5E-01	-2.3	4.7E-02
ENSMUST00000134741				1.3	1.0E-01	0.9	3.7E-01	-0.2	7.8E-01	0.2	8.1E-01
ENSMUST00000134742				3.2	1.1E-01	5.1	1.7E-02	-1.4	4.7E-01	-3.3	2.6E-02
ENSMUST00000170386	WD repeat domain 27 [Source:MGI Symbol;Acc:MGI:1918932]		Q8C5V5	6.1	1.0E-04	6.2	3.1E-03	0.0	9.8E-01	0.0	9.7E-01
ENSMUST00000170388	purinergic receptor P2Y, G-protein coupled 12 [Source:MGI Symbol;Acc:MGI:1918089]	Q546L4	Q9CPV9	-6.9	3.2E-04	0.2	8.7E-01	0.9	4.4E-01	-3.0	8.3E-02
ENSMUST00000134745	onooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Source:MGI Symbol;Acc:M	D6REF3		-4.2	9.5E-02	-5.3	6.0E-02	-1.2	2.8E-01	-0.2	9.6E-01
ENSMUST00000170392	peptidoglycan recognition protein 2 [Source:MGI Symbol;Acc:MGI:1928099]		Q8VCS0	3.1	1.1E-02	-4.9	3.9E-02	-1.5	1.4E-01	-0.8	7.2E-01
ENSMUST00000170396	achaete-scute complex homolog 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1914591]	M0QW46		8.4	5.8E-05	7.7	5.1E-03	0.5	8.3E-01	-2.1	1.2E-01
ENSMUST00000134750				1.5	6.7E-02	-0.3	7.7E-01	-0.7	3.5E-01	1.1	2.3E-01
ENSMUST00000170397	stimulated by retinoic acid gene 6 [Source:MGI Symbol;Acc:MGI:107742]			7.0	2.3E-04	1.7	9.3E-02	-0.7	4.3E-01	0.8	3.0E-01
ENSMUST00000134763	phosphatidylinositol transfer protein, cytoplasmic 1 [Source:MGI Symbol;Acc:MGI:1919045]	X1WI19		-2.5	4.9E-02	2.6	6.5E-02	2.2	7.1E-02	-2.9	3.0E-02
ENSMUST00000170402	vomeronasal 2, receptor 36 [Source:MGI Symbol;Acc:MGI:3757866]	K7N741		4.8	6.3E-03	6.9	8.0E-03	1.9	3.7E-01	0.5	6.8E-01
ENSMUST00000134775	euchromatic histone methyltransferase 1 [Source:MGI Symbol;Acc:MGI:1924933]	A0A0A6YXD1		-1.9	4.2E-01	1.6	3.8E-01	-1.5	3.7E-01	-5.0	4.0E-02
ENSMUST00000170412	vomeronasal 2, receptor 53 [Source:MGI Symbol;Acc:MGI:3644480]	L7N473		6.7	9.4E-05	-5.7	4.9E-03	-1.8	2.0E-02	-0.6	7.3E-01
ENSMUST00000134789				-0.8	7.0E-01	-1.0	6.4E-01	-1.0	5.6E-01	-0.8	7.2E-01
ENSMUST00000170424	vomeronasal 2, receptor 98 [Source:MGI Symbol;Acc:MGI:3647977]	E9PZ56		5.6	9.3E-04	2.3	2.4E-01	-0.1	9.5E-01	1.1	4.0E-01
ENSMUST00000134797	transmembrane BAX inhibitor motif containing 4 [Source:MGI Symbol;Acc:MGI:1915462]	Q8K191		-0.1	9.3E-01	0.1	9.6E-01	-1.4	1.8E-01	-1.6	1.9E-01
ENSMUST00000134802	pleckstrin homology-like domain, family B, member 2 [Source:MGI Symbol;Acc:MGI:2444981]	D3Z069		2.2	1.7E-01	4.1	4.8E-03	-2.8	6.0E-02	-4.6	2.5E-03
ENSMUST00000170426	transmembrane protease, serine 5 (spinesin) [Source:MGI Symbol;Acc:MGI:1933407]	F7C9D1		5.6	1.7E-02	-3.7	9.3E-02	0.9	3.6E-01	-0.5	8.3E-01
ENSMUST00000134804				-0.2	8.6E-01	1.4	4.2E-01	1.5	2.9E-01	-0.1	9.5E-01
ENSMUST00000170430	osphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide [Source:MGI Symbol;Acc:MGI:120372	F8VPL2		-1.4	5.5E-03	5.9	1.3E-03	1.1	3.8E-01	1.0	2.3E-01
ENSMUST00000170444	uridine phosphorylase 1 [Source:MGI Symbol;Acc:MGI:1097668]	E9Q5K7		-9.4	2.0E-05	7.6	2.9E-03	-2.2	3.2E-01	1.5	1.4E-01
ENSMUST00000170448	neurotensin receptor 1 [Source:MGI Symbol;Acc:MGI:97386]	A2ACT4	O88319	6.4	3.1E-02	-2.1	4.6E-01	2.6	1.6E-01	-3.5	3.3E-01
ENSMUST00000170461	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2445040]	E9PYE2		8.1	3.3E-05	6.1	9.4E-04	-0.5	7.0E-01	-0.8	2.7E-01
ENSMUST00000134816				-0.3	9.0E-01	1.9	3.2E-01	-1.7	3.1E-01	-3.9	8.1E-02
ENSMUST00000134817				-2.8	1.3E-01	-2.5	2.7E-01	-0.4	7.4E-01	-0.7	7.4E-01
ENSMUST00000134819	nuclear receptor co-repressor 2 [Source:MGI Symbol;Acc:MGI:1337080]	F6SK53		2.3	5.4E-02	0.4	8.0E-01	1.1	4.1E-01	2.9	8.6E-02
ENSMUST00000170464	glucan (1,4-alpha-), branching enzyme 1 [Source:MGI Symbol;Acc:MGI:1921435]	F6ZHD8		-5.5	2.0E-03	3.5	2.5E-03	-1.8	4.7E-02	-0.1	8.2E-01
ENSMUST00000170472	aarF domain containing kinase 3 [Source:MGI Symbol;Acc:MGI:1914676]		Q60936	-2.8	1.8E-02	3.4	1.5E-02	0.6	5.7E-01	-0.4	6.4E-01
ENSMUST00000134822				-0.6	6.3E-01	1.5	2.9E-01	0.1	9.1E-01	-2.0	1.4E-01
ENSMUST00000170489	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 [Source:MGI Symbol;Acc:MGI:104976]		P54823	-5.0	9.7E-07	7.6	4.1E-05	-1.5	2.2E-01	0.3	5.5E-01
ENSMUST00000134824	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]	F7AI47		-4.5	2.3E-01	-4.9	2.9E-01	-1.3	5.4E-01	-0.9	8.5E-01
ENSMUST00000170504	olfactory receptor 457 [Source:MGI Symbol;Acc:MGI:3030291]	Q8VGP5		7.2	1.0E-04	5.7	4.7E-04	-0.6	6.2E-01	0.0	9.9E-01
ENSMUST00000170505	cDNA sequence BC021785 [Source:MGI Symbol;Acc:MGI:2446139]	F6YK23		5.7	4.8E-04	6.6	2.0E-04	-0.5	6.7E-01	-0.3	6.4E-01
ENSMUST00000170511	cDNA sequence BC035947 [Source:MGI Symbol;Acc:MGI:2652858]	B2RQY6		9.4	1.6E-02	5.7	1.6E-05	-1.7	3.4E-02	0.1	7.6E-01
ENSMUST00000134837				2.2	8.2E-02	2.5	1.3E-01	-0.8	5.8E-01	-1.1	3.4E-01
ENSMUST00000170513	interleukin 12b [Source:MGI Symbol;Acc:MGI:96540]	Q3ZAX5	P43432	5.3	2.9E-02	4.2	7.3E-03	1.0	4.1E-01	0.0	9.7E-01
ENSMUST00000134841				-1.8	4.6E-02	-1.9	4.4E-02	-1.5	3.0E-02	-1.4	1.4E-01
ENSMUST00000170516	ribosomal protein S6 kinase, polypeptide 4 [Source:MGI Symbol;Acc:MGI:1930076]		Q9Z2B9	-2.2	7.8E-03	4.2	9.8E-04	-2.5	3.5E-02	-0.8	2.8E-01
ENSMUST00000170517	von Willebrand factor A domain containing 9 [Source:MGI Symbol;Acc:MGI:1917132]		Q8R3P6	-4.4	7.5E-04	-4.2	5.6E-03	-0.1	8.9E-01	-1.6	2.5E-01
ENSMUST00000134846	centromere protein A [Source:MGI Symbol;Acc:MGI:88375]	D6RJ71		-2.2	5.6E-02	-0.9	4.3E-01	0.3	7.2E-01	-1.0	4.0E-01
ENSMUST00000170518	predicted gene, 17296 [Source:MGI Symbol;Acc:MGI:4936930]	E9Q368		5.2	1.5E-05	3.6	4.6E-02	-1.2	4.3E-01	-0.8	4.9E-01
ENSMUST00000170536	WD repeat domain 66 [Source:MGI Symbol;Acc:MGI:1918495]	B2RR19		7.4	2.8E-04	-3.5	3.1E-01	3.3	7.3E-02	-1.3	7.3E-01
ENSMUST00000170552	suppressor of Ty 20 [Source:MGI Symbol;Acc:MGI:1929651]		Q7TT00	-3.6	2.0E-04	5.0	1.9E-03	-0.2	8.5E-01	0.5	5.1E-01
ENSMUST00000170556	pyrroline-5-carboxylate reductase 1 [Source:MGI Symbol;Acc:MGI:2384795]	Q3UTR5	Q922W5	6.3	1.4E-05	5.5	6.1E-06	-0.8	2.1E-01	0.0	9.8E-01
ENSMUST00000134861				1.2	1.2E-01	0.4	6.9E-01	0.6	4.5E-01	1.4	1.5E-01
ENSMUST00000134862	ring finger protein 44 [Source:MGI Symbol;Acc:MGI:2145310]		Q3UHJ8	-1.6	7.0E-01	-4.2	2.3E-01	-3.6	1.8E-01	-1.0	8.1E-01
ENSMUST00000170573	RIKEN cDNA A530084C06 gene [Source:MGI Symbol;Acc:MGI:3704402]	Q3UTW2		8.1	3.0E-05	-0.2	7.5E-01	0.0	9.8E-01	-2.0	2.6E-02
ENSMUST00000170575	CTF18, chromosome transmission fidelity factor 18 [Source:MGI Symbol;Acc:MGI:2384887]	E9Q2M3		4.5	4.7E-03	6.7	1.7E-04	-1.4	2.7E-01	-0.1	8.3E-01
ENSMUST00000170578	repulsive guidance molecule family member B [Source:MGI Symbol;Acc:MGI:1916049]		Q7TQ33	2.4	1.1E-03	4.9	1.2E-02	-0.6	7.4E-01	0.9	3.8E-01
ENSMUST00000170579	cDNA sequence BC021785 [Source:MGI Symbol;Acc:MGI:2446139]	E9PYY6		5.9	3.9E-04	-1.6	3.7E-01	0.7	5.3E-01	-1.6	4.3E-01
ENSMUST00000170580	potassium voltage-gated channel, subfamily F, member 1 [Source:MGI Symbol;Acc:MGI:2687399]	E9PYC0		7.6	3.0E-06	6.1	6.6E-04	-0.7	6.2E-01	0.2	7.6E-01
ENSMUST00000170596	vomeronasal 2, receptor 82 [Source:MGI Symbol;Acc:MGI:3646522]	G3UWA2		6.5	7.4E-05	4.5	4.8E-04	-1.8	4.7E-02	-0.3	6.8E-01
ENSMUST00000170608	RIKEN cDNA C130060K24 gene [Source:MGI Symbol;Acc:MGI:2441881]	G3UWA8		6.6	2.9E-04	8.1	2.6E-05	2.7	2.0E-02	-0.5	3.1E-01
ENSMUST00000170618	olfactory receptor 287 [Source:MGI Symbol;Acc:MGI:3030121]	E9PZS7		9.3	1.2E-05	3.6	3.6E-03	0.5	5.3E-01	1.0	1.8E-01
ENSMUST00000170629	G two S phase expressed protein 1 [Source:MGI Symbol;Acc:MGI:1352755]	Q542Q3	Q8R080	2.0	5.0E-03	1.9	5.2E-02	-1.7	5.9E-02	-0.9	2.7E-01
ENSMUST00000170633	trafficking protein particle complex 9 [Source:MGI Symbol;Acc:MGI:1923760]	E9Q3T8		4.1	6.2E-04	-3.8	1.2E-01	-0.1	9.3E-01	-0.9	7.1E-01
ENSMUST00000170653	rho/rac guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:103264]		Q60875	-7.2	1.3E-03	3.1	2.8E-02	0.1	9.5E-01	1.3	1.5E-01
ENSMUST00000170662	SRY (sex determining region Y)-box 21 [Source:MGI Symbol;Acc:MGI:2654070]		Q811W0	8.3	4.5E-05	3.2	1.9E-02	-2.3	7.7E-02	0.0	9.9E-01
ENSMUST00000170672	shisa family member 9 [Source:MGI Symbol;Acc:MGI:1919805]		Q9CZN4	8.5	2.9E-04	5.2	4.4E-03	-1.4	3.4E-01	-0.5	5.6E-01
ENSMUST00000134903				-0.2	7.5E-01	0.3	7.8E-01	0.3	7.1E-01	-0.2	7.8E-01
ENSMUST00000170693	ubiquitin-conjugating enzyme E2D 2A [Source:MGI Symbol;Acc:MGI:1930715]	Q3UT95	P62838	-6.8	1.8E-04	4.6	9.2E-05	-0.9	1.9E-01	-0.3	5.6E-01
ENSMUST00000134905				0.4	5.7E-01	0.6	5.2E-01	0.0	9.5E-01	-0.1	8.6E-01
ENSMUST00000134907	annexin A2 [Source:MGI Symbol;Acc:MGI:88246]	B0V2N8		-2.2	6.9E-02	-1.1	4.5E-01	0.8	3.8E-01	-0.3	8.5E-01
ENSMUST00000170705	general transcription factor II E, polypeptide 2 (beta subunit) [Source:MGI Symbol;Acc:MGI:1915403]		Q9D902	-6.0	7.6E-04	2.4	3.8E-03	0.3	5.9E-01	-0.5	3.6E-01
ENSMUST00000170711	jade family PHD finger 1 [Source:MGI Symbol;Acc:MGI:1925835]		Q6ZPI0	4.9	1.1E-02	4.2	7.3E-03	-1.1	3.7E-01	-0.3	7.4E-01
ENSMUST00000134913				-0.3	7.0E-01	1.0	4.8E-01	2.0	6.9E-02	0.7	5.1E-01
ENSMUST00000170719	surfactant associated protein A1 [Source:MGI Symbol;Acc:MGI:109518]	Q9CQI1		5.7	1.1E-03	4.4	9.4E-03	-0.1	9.3E-01	0.6	4.9E-01
ENSMUST00000134919				-2.5	1.1E-01	-0.7	6.0E-01	-0.3	7.8E-01	-2.0	2.1E-01
ENSMUST00000170724	solute carrier family 2 (facilitated glucose transporter), member 3 [Source:MGI Symbol;Acc:MGI:95757]	E9Q6T5		4.5	2.5E-04	6.3	1.7E-04	-0.5	6.5E-01	-0.6	3.3E-01
ENSMUST00000170731	reticulon 4 [Source:MGI Symbol;Acc:MGI:1915835]	Q8BH78		-5.4	6.0E-05	4.6	2.4E-04	-0.3	6.5E-01	-0.1	8.8E-01
ENSMUST00000170737	calcium channel, voltage-dependent, alpha 2/delta subunit 2 [Source:MGI Symbol;Acc:MGI:1929813]		Q6PHS9	7.6	2.6E-02	6.5	6.0E-05	-2.0	8.8E-02	-0.1	8.2E-01
ENSMUST00000170757	C2 calcium-dependent domain containing 2 [Source:MGI Symbol;Acc:MGI:1891883]	E9Q3C1		4.1	5.1E-06	2.5	1.1E-01	-0.7	6.0E-01	4.8	1.8E-03
ENSMUST00000134939	glutaminyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1915851]	D3Z158		-1.3	2.0E-01	-1.4	3.0E-01	0.0	1.0E+00	0.1	9.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000170759	G patch domain containing 11 [Source:MGI Symbol;Acc:MGI:1858435]			-2.4	9.6E-04	-3.5	4.8E-02	0.4	6.2E-01	0.3	8.6E-01
ENSMUST00000170771	fyn-related kinase [Source:MGI Symbol;Acc:MGI:103265]		Q922K9	6.8	7.9E-03	-4.3	8.2E-03	0.8	1.6E-01	-0.8	5.6E-01
ENSMUST00000134949	SNF related kinase [Source:MGI Symbol;Acc:MGI:108104]	D3Z1F6		0.3	8.9E-01	1.6	5.9E-01	1.1	6.1E-01	-0.3	9.3E-01
ENSMUST00000170773	MICAL-like 2 [Source:MGI Symbol;Acc:MGI:2444818]	E9PZD2		5.6	3.9E-03	6.1	1.7E-02	-0.6	8.0E-01	-1.5	2.7E-01
ENSMUST00000134961				1.0	2.1E-01	1.9	6.4E-02	0.6	4.7E-01	-0.3	6.7E-01
ENSMUST00000134962				1.7	3.5E-02	1.7	9.6E-02	0.3	7.3E-01	0.2	7.7E-01
ENSMUST00000170788	schwannomin interacting protein 1 [Source:MGI Symbol;Acc:MGI:1353557]	A0A097PIJ2	Q3TI53	5.1	5.8E-03	-3.5	2.6E-02	-0.4	6.1E-01	-1.1	4.8E-01
ENSMUST00000170792	mitogen-activated protein kinase 10 [Source:MGI Symbol;Acc:MGI:1346863]	Q80W82		8.7	1.4E-05	0.1	8.9E-01	0.4	4.3E-01	-3.4	3.1E-03
ENSMUST00000170795	ıichromosome maintenance deficient 3 (S. cerevisiae) associated protein [Source:MGI Symbol;Acc:MGI:19300		Q9WUU9	-1.9	1.6E-03	5.3	8.3E-03	-0.2	9.0E-01	-0.5	6.2E-01
ENSMUST00000170799	ecotropic viral integration site 2a [Source:MGI Symbol;Acc:MGI:95458]		P20934	-2.7	7.3E-03	6.8	2.4E-06	-0.9	2.1E-01	-0.7	7.7E-02
ENSMUST00000170808	vomeronasal 2, receptor 22 [Source:MGI Symbol;Acc:MGI:3647952]	E9Q7S8		6.6	5.4E-05	5.8	1.2E-03	1.3	3.0E-01	-0.7	3.6E-01
ENSMUST00000134988				0.2	8.5E-01	-0.9	6.1E-01	-0.5	7.1E-01	0.6	6.8E-01
ENSMUST00000170810	te carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Source:MGI Symbol;Acc:MGI:1353	G5E902		-6.3	4.4E-03	7.3	5.5E-04	1.0	4.8E-01	1.0	2.3E-01
ENSMUST00000134996	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7 [Source:MGI Symbol;Acc:M	D6RI90		5.1	5.7E-02	5.7	4.4E-02	-0.8	7.6E-01	-1.4	4.1E-01
ENSMUST00000170811	ring finger protein 14 [Source:MGI Symbol;Acc:MGI:1929668]	G3XA54		-5.2	3.2E-04	6.6	2.3E-03	-0.6	7.2E-01	-0.2	8.6E-01
ENSMUST00000135001	prostaglandin reductase 2 [Source:MGI Symbol;Acc:MGI:1916372]	Q3TXN1		-2.4	1.0E-01	-4.9	1.6E-02	-2.7	1.0E-02	-0.1	9.4E-01
ENSMUST00000170827	ıoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Source:MGI Symbol;Acc:M	E9Q852		-5.7	2.7E-03	4.6	3.9E-03	1.1	3.1E-01	0.7	3.9E-01
ENSMUST00000135003	zinc finger, MYM-type 4 [Source:MGI Symbol;Acc:MGI:1915035]	F6VYE2		1.2	1.7E-01	-0.4	6.8E-01	-1.3	1.0E-01	0.3	7.6E-01
ENSMUST00000170832	proline rich, lacrimal 1 [Source:MGI Symbol;Acc:MGI:107496]	E9PYQ4		9.1	1.5E-04	7.4	1.2E-03	0.2	8.9E-01	-0.3	7.0E-01
ENSMUST00000170833	hexokinase 2 [Source:MGI Symbol;Acc:MGI:1315197]	E9Q5B5		7.0	2.2E-03	3.4	6.2E-03	-2.7	2.9E-02	1.2	8.9E-02
ENSMUST00000135013				1.2	2.8E-01	3.0	3.5E-02	0.6	5.7E-01	-1.2	2.6E-01
ENSMUST00000135014	RIKEN cDNA A830018L16 gene [Source:MGI Symbol;Acc:MGI:2444149]		Q8BZJ8	5.7	1.4E-01	5.1	2.2E-01	-0.4	9.3E-01	0.3	9.1E-01
ENSMUST00000135017	breast carcinoma amplified sequence 2 [Source:MGI Symbol;Acc:MGI:1915433]	D6RGA5		0.0	9.8E-01	0.6	7.7E-01	1.5	4.0E-01	0.8	6.2E-01
ENSMUST00000170836	proteasome (prosome, macropain) subunit, alpha type 2 [Source:MGI Symbol;Acc:MGI:104885]		P49722	-7.0	1.3E-06	4.2	1.4E-03	-0.1	8.9E-01	0.1	8.9E-01
ENSMUST00000170855	RIKEN cDNA A930018M24 gene [Source:MGI Symbol;Acc:MGI:2686053]	B7ZMY3		5.1	4.8E-04	5.8	1.8E-03	-0.5	7.3E-01	-0.2	7.7E-01
ENSMUST00000135025				-2.6	1.8E-01	-0.8	6.9E-01	-0.7	6.0E-01	-2.5	2.5E-01
ENSMUST00000135035	secretion regulating guanine nucleotide exchange factor [Source:MGI Symbol;Acc:MGI:1351630]	D3Z5A9		2.7	7.3E-02	4.6	7.2E-03	-0.6	6.9E-01	-2.5	4.2E-02
ENSMUST00000170872	thrombospondin 2 [Source:MGI Symbol;Acc:MGI:98738]		Q03350	8.8	5.3E-06	-1.9	2.3E-01	1.9	4.3E-02	-0.1	9.5E-01
ENSMUST00000170883	high density lipoprotein (HDL) binding protein [Source:MGI Symbol;Acc:MGI:99256]	Q3U4Z7	Q8VDJ3	-1.6	1.5E-02	1.8	4.6E-01	8.2	1.0E-03	-1.1	5.9E-01
ENSMUST00000135047	MKL (megakaryoblastic leukemia)/myocardin-like 1 [Source:MGI Symbol;Acc:MGI:2384495]	D3YUG5		-1.4	6.2E-02	-0.6	5.4E-01	1.2	7.3E-02	0.4	6.5E-01
ENSMUST00000170893	histocompatibility 60c [Source:MGI Symbol;Acc:MGI:3774845]	B1B213		2.8	1.8E-03	4.7	2.0E-04	0.4	5.7E-01	-0.4	4.6E-01
ENSMUST00000135050				-0.6	7.0E-01	5.8	2.0E-02	3.4	1.2E-01	-3.0	5.2E-02
ENSMUST00000135051				-0.7	5.5E-01	0.7	6.6E-01	0.7	5.7E-01	-0.6	6.3E-01
ENSMUST00000170895	guanylate kinase 1 [Source:MGI Symbol;Acc:MGI:95871]	E9Q7K1		-5.0	5.7E-04	-4.9	1.3E-02	-0.3	7.0E-01	-0.7	7.1E-01
ENSMUST00000135053	vacuolar protein sorting 33B (yeast) [Source:MGI Symbol;Acc:MGI:2446237]	S4R227		6.3	1.3E-01	8.2	5.9E-02	-0.2	9.6E-01	-2.2	4.3E-01
ENSMUST00000170904	transferrin [Source:MGI Symbol;Acc:MGI:98821]	F7BAE9		-7.4	1.4E-02	-1.7	1.4E-01	1.4	6.2E-02	-2.2	1.1E-01
ENSMUST00000135067	family with sequence similarity 214, member B [Source:MGI Symbol;Acc:MGI:2441854]	E9Q9G4		-1.2	6.2E-01	6.6	7.6E-02	4.3	2.0E-01	-3.5	1.4E-01
ENSMUST00000170909	transcription factor Dp 1 [Source:MGI Symbol;Acc:MGI:101934]	Q3V3X3	Q08639	-3.9	2.6E-06	4.3	6.3E-03	-1.4	3.2E-01	0.7	3.7E-01
ENSMUST00000170922	vomeronasal 2, receptor 29 [Source:MGI Symbol;Acc:MGI:1923479]	L7N2D4		6.8	6.4E-05	5.7	8.2E-03	-0.7	7.3E-01	-0.8	4.4E-01
ENSMUST00000135074	glucosidase, alpha; neutral C [Source:MGI Symbol;Acc:MGI:1923301]	A2AQJ8		-0.5	5.5E-01	0.8	5.0E-01	0.8	3.6E-01	-0.5	6.3E-01
ENSMUST00000170926	LIM domain only 2 [Source:MGI Symbol;Acc:MGI:102811]	Q544Z2	P25801	-2.9	1.4E-02	1.8	2.2E-01	-3.1	6.1E-02	-0.5	7.0E-01
ENSMUST00000170939	PTK2 protein tyrosine kinase 2 [Source:MGI Symbol;Acc:MGI:95481]		P34152	4.2	1.0E-02	8.4	3.4E-05	-1.1	3.6E-01	0.8	1.3E-01
ENSMUST00000170941	triggering receptor expressed on myeloid cells-like 2 [Source:MGI Symbol;Acc:MGI:2147038]		Q2LA85	-3.9	2.5E-05	-5.0	1.3E-03	0.8	7.7E-02	-0.7	5.7E-01
ENSMUST00000170953	ribosomal protein S13 [Source:MGI Symbol;Acc:MGI:1915302]	Q5BLJ7	P62301	-6.8	5.8E-05	-2.9	3.8E-02	0.4	5.0E-01	1.2	3.4E-01
ENSMUST00000135088	ıonooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Source:MGI Symbol;Acc:M	F6VW30		1.4	3.9E-01	1.7	5.6E-01	3.7	1.1E-01	3.4	1.6E-01
ENSMUST00000170955	BAI1-associated protein 2-like 2 [Source:MGI Symbol;Acc:MGI:2652819]		Q80Y61	5.5	1.1E-02	3.9	2.7E-02	-0.7	6.1E-01	0.4	6.5E-01
ENSMUST00000135090				0.4	6.0E-01	-0.3	7.2E-01	-0.8	2.6E-01	-0.1	9.0E-01
ENSMUST00000135091	RIKEN cDNA 1500011K16 gene [Source:MGI Symbol;Acc:MGI:1915135]		Q8BT35	0.4	5.9E-01	-1.5	7.4E-02	-2.6	2.1E-03	-0.7	3.6E-01
ENSMUST00000170962	nuclear import 7 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913414]	E9Q109		8.8	8.9E-03	3.8	2.6E-03	-1.2	2.2E-01	0.1	8.6E-01
ENSMUST00000170994	trafficking protein particle complex 12 [Source:MGI Symbol;Acc:MGI:2445089]	Q8C0C3		6.6	6.2E-05	2.9	6.4E-02	0.0	1.0E+00	-0.3	7.9E-01
ENSMUST00000135100				-1.4	3.7E-01	0.6	7.8E-01	1.0	5.1E-01	-1.0	6.1E-01
ENSMUST00000170998	sodium channel, voltage-gated, type II, beta [Source:MGI Symbol;Acc:MGI:106921]	Q1MXF8	Q56A07	5.3	9.0E-06	3.5	5.5E-03	-0.7	4.6E-01	-0.2	8.0E-01
ENSMUST00000135103				-0.9	3.8E-01	0.2	9.0E-01	0.5	6.1E-01	-0.5	6.5E-01
ENSMUST00000135106	interleukin-1 receptor-associated kinase 3 [Source:MGI Symbol;Acc:MGI:1921164]	D6RCU1		-1.3	4.2E-01	-3.1	1.4E-01	-1.8	1.6E-01	-0.1	9.7E-01
ENSMUST00000171001	dehydrogenase/reductase (SDR family) member 3 [Source:MGI Symbol;Acc:MGI:1315215]	G5E8W9		-7.0	5.6E-04	5.2	9.0E-04	-0.5	6.6E-01	-0.5	4.5E-01
ENSMUST00000135117				-0.7	6.6E-01	2.9	1.6E-01	2.0	2.7E-01	-1.7	3.3E-01
ENSMUST00000171024	exonuclease 3'-5' domain containing 1 [Source:MGI Symbol;Acc:MGI:3045306]		Q8CDF7	3.4	4.3E-05	5.0	2.9E-03	1.5	2.1E-01	0.3	7.1E-01
ENSMUST00000135127	prolyl 3-hydroxylase 3 [Source:MGI Symbol;Acc:MGI:1315208]	D6RHQ3		3.8	9.8E-02	6.7	1.2E-02	-0.5	8.5E-01	-3.4	3.3E-02
ENSMUST00000135128				-1.0	9.8E-02	0.0	9.6E-01	0.2	6.0E-01	-0.7	3.0E-01
ENSMUST00000171030	discs, large homolog-associated protein 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:2138865]	F6YMR0		-4.5	1.1E-02	6.2	1.2E-02	-0.8	7.3E-01	-1.0	4.0E-01
ENSMUST00000135140	ring finger protein 25 [Source:MGI Symbol;Acc:MGI:1890215]	M0QWW2		0.2	9.4E-01	0.9	7.3E-01	-1.7	5.0E-01	-2.4	3.8E-01
ENSMUST00000171032	olute carrier family 16 (monocarboxylic acid transporters), member 11 [Source:MGI Symbol;Acc:MGI:266370		Q5NC32	6.6	1.6E-04	9.5	3.3E-03	3.1	2.3E-01	-0.4	6.7E-01
ENSMUST00000171041	Der1-like domain family, member 2 [Source:MGI Symbol;Acc:MGI:2151483]	Q3U957		-5.0	4.9E-04	3.0	1.9E-01	-0.9	6.4E-01	0.6	7.0E-01
ENSMUST00000171042	WW domain containing adaptor with coiled-coil [Source:MGI Symbol;Acc:MGI:2387357]	E9Q4Y9		4.5	2.4E-02	2.1	4.3E-02	0.9	2.7E-01	0.7	3.2E-01
ENSMUST00000171059	predicted gene 6871 [Source:MGI Symbol;Acc:MGI:3643456]	E9Q1W9		5.9	1.7E-04	-1.5	6.5E-01	3.3	1.2E-01	-1.7	6.2E-01
ENSMUST00000171066	tumor necrosis factor receptor superfamily, member 22 [Source:MGI Symbol;Acc:MGI:1930270]	Q78QS6		6.6	9.4E-05	4.9	3.4E-05	-0.9	1.9E-01	-0.4	3.8E-01
ENSMUST00000135188				-2.8	1.2E-01	-3.7	1.4E-01	-0.3	8.2E-01	0.7	7.8E-01
ENSMUST00000135191				0.3	7.3E-01	0.9	4.6E-01	-0.2	8.6E-01	-0.8	5.0E-01
ENSMUST00000171070	chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2 [Source:MGI Symbol;Acc:M	E9PY30		3.9	1.2E-02	-4.2	1.5E-03	0.6	1.9E-01	1.4	1.7E-01
ENSMUST00000171100	RAB11A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1858202]	E9PZB2		-6.5	9.1E-05	1.7	4.5E-01	-1.1	5.4E-01	1.7	3.4E-01
ENSMUST00000171109	CDK5 and Abl enzyme substrate 1 [Source:MGI Symbol;Acc:MGI:1927065]	Q3U148		6.8	2.6E-03	-2.3	1.5E-01	1.0	3.1E-01	0.0	9.9E-01
ENSMUST00000135195				-1.4	1.5E-01	-1.2	2.8E-01	-0.8	3.1E-01	-1.0	3.5E-01
ENSMUST00000135197	predicted gene 21972 [Source:MGI Symbol;Acc:MGI:5439441]	J3QN38		0.8	5.4E-01	4.2	9.2E-03	0.1	9.2E-01	-3.2	2.0E-02
ENSMUST00000171115	RAN GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:103071]		P46061	6.5	1.2E-03	8.3	2.2E-04	-0.8	6.1E-01	0.6	3.6E-01
ENSMUST00000135201				1.7	4.0E-01	1.9	4.6E-01	-0.1	9.8E-01	-0.3	8.6E-01
ENSMUST00000171121	palmitoyl-protein thioesterase 2 [Source:MGI Symbol;Acc:MGI:1860075]		O35448	-5.0	3.6E-03	8.0	3.0E-05	-0.6	5.9E-01	0.0	9.7E-01
ENSMUST00000171129	diphosphoinositol pentakisphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:2142810]		Q6ZQB6	-5.0	4.1E-03	-4.4	6.8E-03	-1.8	2.1E-02	-0.2	9.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000171131	predicted gene 5174 [Source:MGI Symbol;Acc:MGI:3646116]	E9Q1V8		7.6	2.0E-05	6.6	1.1E-05	-0.1	9.2E-01	0.0	9.1E-01
ENSMUST00000171148	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) [Source:MGI Symbol;Acc:MGI:98483]	F6QHF1		-4.4	1.4E-03	-0.9	3.9E-01	0.4	6.3E-01	-1.4	2.1E-01
ENSMUST00000171150	predicted gene 5795 [Source:MGI Symbol;Acc:MGI:3779520]	E9PZN8		6.5	4.8E-04	4.9	4.1E-03	-2.4	1.3E-01	-0.9	2.9E-01
ENSMUST00000135221	importin 4 [Source:MGI Symbol;Acc:MGI:1923001]	Q5U4C5		2.9	3.0E-01	0.7	8.1E-01	-2.7	3.7E-01	-0.4	8.6E-01
ENSMUST00000171153	predicted gene, 17330 [Source:MGI Symbol;Acc:MGI:4936964]	L7N290		5.7	3.0E-04	5.6	8.5E-04	-0.5	7.0E-01	-0.1	8.7E-01
ENSMUST00000135225	cyclin G associated kinase [Source:MGI Symbol;Acc:MGI:2442153]	D6RHK5		2.8	1.4E-01	5.6	9.3E-03	-0.5	7.9E-01	-3.2	3.3E-02
ENSMUST00000135226				-2.0	1.1E-01	-0.3	8.7E-01	1.3	2.4E-01	-0.4	7.8E-01
ENSMUST00000171158	syndecan 1 [Source:MGI Symbol;Acc:MGI:1349162]	Q3V1F2	P18828	5.1	3.8E-04	2.7	5.4E-02	-3.0	5.2E-02	2.8	9.0E-03
ENSMUST00000171172	MAD2L1 binding protein [Source:MGI Symbol;Acc:MGI:1913841]		Q9DCX1	-2.2	6.0E-03	4.2	9.9E-03	1.2	3.3E-01	-0.5	5.1E-01
ENSMUST00000135230				-2.5	1.2E-01	-3.5	6.4E-02	-1.3	2.0E-01	-0.3	8.7E-01
ENSMUST00000171213	vomeronasal 2, receptor 69 [Source:MGI Symbol;Acc:MGI:3761311]	G3XA45		5.3	2.4E-03	4.5	1.4E-02	-0.5	7.1E-01	-1.1	2.8E-01
ENSMUST00000135234				0.0	9.9E-01	0.8	6.4E-01	0.9	5.2E-01	0.1	9.5E-01
ENSMUST00000171223	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog [Source:MGI Symbol;Acc:MGI:95527]		P14234	-4.5	6.9E-03	5.2	3.8E-04	-1.1	2.8E-01	-1.0	1.8E-01
ENSMUST00000171229	enoyl-Coenzyme A delta isomerase 2 [Source:MGI Symbol;Acc:MGI:1346064]		Q9WUR2	-7.2	5.9E-05	5.0	1.6E-03	-2.0	1.5E-01	0.0	9.9E-01
ENSMUST00000171238	zinc finger protein 516 [Source:MGI Symbol;Acc:MGI:2443957]		Q7TSH3	-3.7	7.7E-05	-5.1	2.1E-04	0.8	5.2E-02	-2.5	3.4E-02
ENSMUST00000135242	Fyn proto-oncogene [Source:MGI Symbol;Acc:MGI:95602]		P39688	0.4	8.0E-01	-2.3	4.3E-01	0.1	9.5E-01	2.7	2.9E-01
ENSMUST00000135243				-1.2	2.0E-01	-1.3	3.1E-01	0.1	8.5E-01	0.2	8.5E-01
ENSMUST00000135248	phosphatidylserine decarboxylase [Source:MGI Symbol;Acc:MGI:2445114]	D3Z0X7		-1.8	7.5E-02	-1.1	4.4E-01	1.1	2.0E-01	0.4	7.7E-01
ENSMUST00000171244	melanocyte proliferating gene 1 [Source:MGI Symbol;Acc:MGI:1929864]	F7A3N3		-4.5	2.2E-03	-3.5	1.1E-02	0.4	4.4E-01	1.5	2.1E-01
ENSMUST00000171245	proline rich 13 [Source:MGI Symbol;Acc:MGI:1913401]		Q9CQJ5	-4.3	8.8E-03	8.1	2.2E-05	-1.7	1.8E-01	-0.3	5.5E-01
ENSMUST00000135251	5-azacytidine induced gene 2 [Source:MGI Symbol;Acc:MGI:1351332]	D3Z7S3		2.0	2.4E-01	-1.3	5.4E-01	-2.7	7.5E-02	0.5	7.9E-01
ENSMUST00000171251	AT rich interactive domain 3C (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:3650624]		A6PWV5	6.6	7.9E-04	6.4	2.5E-04	-0.6	6.0E-01	-1.1	1.2E-01
ENSMUST00000171254	RPA interacting protein [Source:MGI Symbol;Acc:MGI:1916973]	Q0PL80		-5.1	6.3E-03	-3.0	3.5E-03	1.5	7.0E-03	-0.6	4.8E-01
ENSMUST00000171258	enoyl-Coenzyme A delta isomerase 2 [Source:MGI Symbol;Acc:MGI:1346064]	E9PYC6		-4.2	1.7E-03	6.7	3.4E-04	-0.5	6.8E-01	-1.6	5.0E-02
ENSMUST00000135260				-2.8	8.5E-02	2.2	2.2E-01	1.7	2.6E-01	-3.2	5.8E-02
ENSMUST00000171297	RIKEN cDNA F830016B08 gene [Source:MGI Symbol;Acc:MGI:3588218]	G3UWE2		10.4	9.0E-06	-0.7	5.0E-01	0.2	7.9E-01	-2.4	4.3E-02
ENSMUST00000171307	olfactory receptor 455 [Source:MGI Symbol;Acc:MGI:3030289]	A0A0B4J1M2		5.7	9.2E-05	6.3	3.9E-04	-0.6	6.1E-01	-1.4	6.2E-02
ENSMUST00000171313	retinal pigment epithelium derived rhodopsin homolog [Source:MGI Symbol;Acc:MGI:1097709]	Q543W9	O35214	6.7	2.5E-04	3.6	7.0E-03	-0.5	6.2E-01	-0.4	6.1E-01
ENSMUST00000171318	transmembrane 9 superfamily member 2 [Source:MGI Symbol;Acc:MGI:1915309]	E9PZ69		-3.6	1.1E-02	5.8	4.4E-04	-0.6	6.1E-01	-0.3	6.0E-01
ENSMUST00000171321	e (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) [Source:MGI Symbol;Acc:MGI	F6QXK7		-5.8	7.1E-04	-3.0	1.1E-01	0.7	4.3E-01	-1.1	5.7E-01
ENSMUST00000135278	DEK oncogene (DNA binding) [Source:MGI Symbol;Acc:MGI:1926209]	E9Q8Y1		1.5	3.1E-01	-2.6	1.2E-01	-4.3	6.1E-03	-0.2	9.2E-01
ENSMUST00000171322	predicted gene 5415 [Source:MGI Symbol;Acc:MGI:3644687]	E9PXF3		9.2	3.3E-05	4.9	2.4E-03	-0.5	6.9E-01	0.8	2.9E-01
ENSMUST00000135298	myosin IXa [Source:MGI Symbol;Acc:MGI:107735]		Q8C170	2.4	4.5E-01	1.3	7.3E-01	-0.6	8.7E-01	0.5	8.6E-01
ENSMUST00000171324	nyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase) [Source:MGI Symbol;Acc:MGI		E9Q649	6.2	1.7E-05	5.8	1.7E-03	1.3	3.4E-01	0.1	9.2E-01
ENSMUST00000135309	zinc finger and SCAN domains 20 [Source:MGI Symbol;Acc:MGI:2679268]	E9Q8Y3		0.9	4.1E-01	6.2	8.1E-04	1.4	2.5E-01	-3.8	4.5E-03
ENSMUST00000171332	perlecan (heparan sulfate proteoglycan 2) [Source:MGI Symbol;Acc:MGI:96257]	E9PZ16		10.6	3.2E-07	-2.9	7.3E-02	-0.6	5.2E-01	-1.9	2.6E-01
ENSMUST00000171342	ring finger protein 41 [Source:MGI Symbol;Acc:MGI:1914838]		Q8BH75	6.7	2.8E-04	3.7	4.6E-02	-0.5	7.6E-01	-0.9	4.4E-01
ENSMUST00000171343	bone morphogenetic protein receptor, type 1A [Source:MGI Symbol;Acc:MGI:1338938]	E9PW65		-2.4	2.5E-02	5.1	4.1E-02	-0.8	7.3E-01	1.5	3.0E-01
ENSMUST00000135326	inhibitor of kappaB kinase beta [Source:MGI Symbol;Acc:MGI:1338071]	Q3U141		-3.8	5.5E-02	-1.5	3.7E-01	-0.8	5.1E-01	-3.0	1.4E-01
ENSMUST00000171368	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Source:MGI Symbol;Acc:MGI:1913721]	E9Q5H9		-3.2	1.6E-02	5.2	2.5E-05	-0.6	3.8E-01	0.3	4.4E-01
ENSMUST00000171384	transmembrane 4 superfamily member 1 [Source:MGI Symbol;Acc:MGI:104678]		Q64302	4.6	2.8E-04	5.6	6.6E-03	-2.1	2.7E-01	0.4	6.8E-01
ENSMUST00000171385	TBC1 domain family, member 14 [Source:MGI Symbol;Acc:MGI:1098708]	E9PYB1		-11.1	8.4E-05	5.8	4.4E-02	-0.7	8.1E-01	2.2	1.4E-01
ENSMUST00000171394	family with sequence similarity 196, member A [Source:MGI Symbol;Acc:MGI:3605068]	E9PZW7		8.2	2.2E-05	7.7	2.4E-04	-1.0	5.0E-01	-0.3	6.8E-01
ENSMUST00000135341	interleukin 15 receptor, alpha chain [Source:MGI Symbol;Acc:MGI:104644]	Q501M1	Q60819	-1.1	6.7E-01	-4.7	1.3E-01	-4.1	2.5E-02	-0.5	8.7E-01
ENSMUST00000135343	G protein-regulated inducer of neurite outgrowth 1 [Source:MGI Symbol;Acc:MGI:1349455]		Q3UNH4	2.9	1.7E-01	2.2	2.8E-01	-0.5	8.0E-01	0.1	9.3E-01
ENSMUST00000135345				-0.6	5.2E-01	-2.0	8.7E-02	-1.5	8.8E-02	-0.2	8.8E-01
ENSMUST00000135346	alveolar soft part sarcoma chromosome region, candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1916188]	A2AC03		-1.4	3.1E-01	2.4	1.4E-01	1.0	4.6E-01	-2.8	6.2E-02
ENSMUST00000171400	leucine rich repeat containing 10B [Source:MGI Symbol;Acc:MGI:2685551]	G3XA50		9.4	6.6E-05	-6.2	1.4E-03	-2.9	1.2E-03	-0.3	8.3E-01
ENSMUST00000135352				1.0	1.7E-01	1.5	8.8E-02	-0.2	8.2E-01	-0.7	3.5E-01
ENSMUST00000171401	RIKEN cDNA 4932415D10 gene [Source:MGI Symbol;Acc:MGI:3045298]	E9Q0G0		8.5	4.1E-05	3.4	1.2E-02	0.2	8.5E-01	-0.3	6.6E-01
ENSMUST00000171403	family with sequence similarity 110, member B [Source:MGI Symbol;Acc:MGI:1916593]		Q8C739	4.7	3.0E-02	5.7	2.6E-03	-0.9	5.4E-01	-1.4	1.3E-01
ENSMUST00000171416	R3H domain containing 4 [Source:MGI Symbol;Acc:MGI:1924814]	B2RRK4	Q4VBF2	9.3	3.4E-04	3.2	2.0E-02	0.4	7.2E-01	0.8	3.2E-01
ENSMUST00000171433	midline 1 [Source:MGI Symbol;Acc:MGI:1100537]		O70583	13.3	1.4E-04	4.6	3.9E-02	-0.6	7.6E-01	0.1	9.1E-01
ENSMUST00000171436	protein kinase C and casein kinase substrate in neurons 2 [Source:MGI Symbol;Acc:MGI:1345153]	Q3TDA7	Q9WVE8	-4.4	2.5E-02	6.9	1.2E-06	-0.4	5.1E-01	-0.3	3.7E-01
ENSMUST00000171438	a disintegrin and metallopeptidase domain 3 (cyritestin) [Source:MGI Symbol;Acc:MGI:102518]	F8VQ03		5.2	2.1E-02	5.9	4.3E-04	-0.6	6.3E-01	-0.1	8.5E-01
ENSMUST00000171460	proline rich 5 (renal) [Source:MGI Symbol;Acc:MGI:1924714]		Q812A5	7.4	1.5E-03	4.2	4.3E-03	-2.1	1.3E-01	-0.6	4.4E-01
ENSMUST00000171473	histone cluster 2, H4 [Source:MGI Symbol;Acc:MGI:2140113]	B2RTM0	P62806	3.4	1.4E-03	8.0	1.9E-04	2.1	1.2E-01	-0.7	2.7E-01
ENSMUST00000171494	nucleic acid binding protein 2 [Source:MGI Symbol;Acc:MGI:1917167]	E9PW70		3.5	1.1E-03	5.3	4.2E-04	-0.9	3.6E-01	0.2	7.7E-01
ENSMUST00000135379				1.0	7.0E-01	-4.8	1.1E-01	-5.8	1.2E-02	0.0	9.9E-01
ENSMUST00000171496	signal peptide, CUB domain, EGF-like 1 [Source:MGI Symbol;Acc:MGI:1890616]		Q6NZL8	8.9	1.4E-05	4.7	1.5E-02	-0.3	8.6E-01	-0.8	4.6E-01
ENSMUST00000171519	cDNA sequence BC028528 [Source:MGI Symbol;Acc:MGI:2385885]		Q8R2K8	-4.8	2.1E-03	0.4	5.9E-01	-0.1	8.4E-01	1.2	1.2E-01
ENSMUST00000171530	interferon-related developmental regulator 1 [Source:MGI Symbol;Acc:MGI:1316717]	E9Q949		-7.9	9.9E-05	4.7	5.3E-04	-1.2	2.3E-01	0.1	8.6E-01
ENSMUST00000171533	neuronal regeneration related protein [Source:MGI Symbol;Acc:MGI:99444]	Q542Q5	Q07475	8.6	5.3E-05	-3.5	2.3E-03	-0.9	7.7E-02	-0.4	6.4E-01
ENSMUST00000171542	keratin associated protein 11-1 [Source:MGI Symbol;Acc:MGI:99447]	E9Q2E9		7.0	2.2E-04	6.0	2.4E-04	-0.6	6.0E-01	0.0	9.8E-01
ENSMUST00000135397	family with sequence similarity 188, member A [Source:MGI Symbol;Acc:MGI:1914210]	F6Z9V3		-2.4	1.9E-01	-2.6	2.2E-01	-0.5	7.0E-01	-0.2	9.2E-01
ENSMUST00000171545	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Source:MGI Symbol;Acc:MGI:1321390]		Q9R1E6	4.6	5.6E-03	7.4	1.2E-02	-1.4	6.1E-01	-1.9	2.4E-01
ENSMUST00000171548	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1858493]	E9PY89		5.8	3.4E-03	2.8	8.2E-03	-0.5	4.9E-01	0.1	9.3E-01
ENSMUST00000171562	plectin [Source:MGI Symbol;Acc:MGI:1277961]	E9Q3W4		10.1	1.2E-03	-3.1	7.1E-04	-0.1	7.1E-01	-0.3	6.7E-01
ENSMUST00000171584	ATP-binding cassette, sub-family C (CFTR/MRP), member 10 [Source:MGI Symbol;Acc:MGI:2386976]	E9PZG1		3.7	3.6E-03	3.5	2.5E-02	0.1	9.6E-01	0.3	7.6E-01
ENSMUST00000171597	Ngg1 interacting factor 3-like 1 (S. pombe) [Source:MGI Symbol;Acc:MGI:1929485]		Q9EQ80	-3.7	2.0E-02	4.4	1.0E-03	-1.1	2.5E-01	0.1	8.6E-01
ENSMUST00000171600	BTB and CNC homology 2 [Source:MGI Symbol;Acc:MGI:894679]		P97303	4.4	2.6E-02	5.4	7.9E-04	-1.3	3.0E-01	-2.0	3.2E-02
ENSMUST00000135429	NAD kinase [Source:MGI Symbol;Acc:MGI:2183149]	A2A9N9		-1.2	3.6E-01	-1.2	5.2E-01	0.6	6.3E-01	0.6	7.1E-01
ENSMUST00000135439	palladin, cytoskeletal associated protein [Source:MGI Symbol;Acc:MGI:1919583]	D3Z1J5		-0.7	5.5E-01	1.5	1.9E-01	-0.5	6.3E-01	-2.7	4.7E-02
ENSMUST00000171634	plectin [Source:MGI Symbol;Acc:MGI:1277961]			7.3	5.7E-05	4.3	3.9E-05	-1.3	5.1E-02	-0.5	1.9E-01
ENSMUST00000135446	ubiquitin A-52 residue ribosomal protein fusion product 1 [Source:MGI Symbol;Acc:MGI:98887]	Q66JP1	P62984	0.9	3.3E-01	2.4	4.1E-02	0.2	8.2E-01	-1.3	1.8E-01
ENSMUST00000171637	ATP-binding cassette, sub-family A (ABC1), member 7 [Source:MGI Symbol;Acc:MGI:1351646]	E9Q6G4		-4.6	1.0E-02	6.0	1.8E-02	-0.7	7.7E-01	-0.9	4.7E-01
ENSMUST00000171640	heterogeneous nuclear ribonucleoprotein D [Source:MGI Symbol;Acc:MGI:101947]	F6SHF3		-7.5	2.4E-04	3.1	3.6E-02	-1.2	3.6E-01	-0.7	5.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000135455	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2151221]		Q9DB28	0.2	7.7E-01	1.2	2.9E-01	0.8	3.4E-01	-0.1	9.3E-01
ENSMUST00000135461				3.2	1.1E-01	6.6	7.9E-03	-0.3	8.8E-01	-3.7	1.5E-02
ENSMUST00000171643	copine VI [Source:MGI Symbol;Acc:MGI:1334445]		Q9Z140	6.4	1.5E-02	2.5	4.5E-02	-2.0	9.4E-02	0.3	7.8E-01
ENSMUST00000171644	peroxisome proliferator activated receptor gamma [Source:MGI Symbol;Acc:MGI:97747]	M1VPI1		3.2	3.3E-02	-5.4	1.3E-02	1.3	1.5E-01	2.2	2.4E-01
ENSMUST00000171658	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:106299]	E9PYE7		2.7	1.0E-02	-3.7	2.7E-02	-1.4	9.5E-02	-0.7	6.6E-01
ENSMUST00000171664	RIKEN cDNA 4930433I11 gene [Source:MGI Symbol;Acc:MGI:2685327]	B2RX47		8.6	1.5E-05	3.6	2.2E-03	-2.7	2.5E-02	-0.1	8.2E-01
ENSMUST00000171666	choline kinase beta [Source:MGI Symbol;Acc:MGI:1328313]	F6SKI6		-6.9	5.1E-03	4.9	1.1E-03	0.2	8.1E-01	1.0	1.8E-01
ENSMUST00000171671	vomeronasal 2, receptor 58 [Source:MGI Symbol;Acc:MGI:3647877]	K7N6V2		5.8	1.3E-03	5.4	1.7E-02	0.2	9.0E-01	0.2	8.6E-01
ENSMUST00000135471				-1.6	1.2E-01	-4.3	1.5E-02	-1.0	1.9E-01	1.7	2.7E-01
ENSMUST00000171686	ribonuclease P 40 subunit [Source:MGI Symbol;Acc:MGI:1346084]		Q8R1F9	6.1	7.3E-05	2.7	1.7E-02	-0.6	4.9E-01	0.3	7.0E-01
ENSMUST00000171687	transmembrane protein 39a [Source:MGI Symbol;Acc:MGI:1915096]		Q9CYC3	6.8	1.4E-03	4.5	2.7E-02	-1.5	4.4E-01	-0.9	4.6E-01
ENSMUST00000135484				-4.6	4.1E-02	-3.5	2.6E-01	1.2	4.8E-01	0.1	9.7E-01
ENSMUST00000171690	RIKEN cDNA A830018L16 gene [Source:MGI Symbol;Acc:MGI:2444149]		Q8BZJ8	6.0	1.5E-02	3.1	1.5E-03	-0.1	8.5E-01	0.1	8.4E-01
ENSMUST00000135493	myocyte enhancer factor 2A [Source:MGI Symbol;Acc:MGI:99532]		Q60929	3.2	2.2E-01	1.1	5.9E-01	-3.4	1.2E-01	-1.4	5.2E-01
ENSMUST00000135495	coiled-coil domain containing 92 [Source:MGI Symbol;Acc:MGI:106485]	D6RJ58		4.1	6.0E-02	3.7	1.7E-01	-0.7	7.7E-01	-0.3	8.7E-01
ENSMUST00000171691	MAM domain containing glycosylphosphatidylinositol anchor 1 [Source:MGI Symbol;Acc:MGI:1922012]	E9PY95		6.8	1.6E-02	-3.8	3.8E-02	1.1	1.4E-01	-0.9	6.0E-01
ENSMUST00000135500	ribosomal protein L18 [Source:MGI Symbol;Acc:MGI:98003]	G3UZK4		0.4	4.7E-01	0.9	2.0E-01	0.1	8.7E-01	-0.4	4.8E-01
ENSMUST00000171696	tocopherol (alpha) transfer protein-like [Source:MGI Symbol;Acc:MGI:1923330]		Q9D3D0	-5.2	1.1E-03	4.1	6.8E-02	-0.7	7.5E-01	0.7	5.9E-01
ENSMUST00000171706	predicted gene 3629 [Source:MGI Symbol;Acc:MGI:3781805]	K7N6Y2		5.8	6.9E-04	3.5	8.1E-04	-1.4	8.1E-02	-0.8	1.9E-01
ENSMUST00000135515				2.5	2.2E-01	5.3	1.2E-01	2.5	4.0E-01	-0.2	9.0E-01
ENSMUST00000135516				2.6	1.4E-01	5.4	7.3E-03	-0.5	7.8E-01	-3.3	2.4E-02
ENSMUST00000135517				1.8	1.7E-01	-1.1	6.0E-01	0.0	9.8E-01	2.9	1.2E-01
ENSMUST00000171714	serine-rich, secreted, X-linked [Source:MGI Symbol;Acc:MGI:3777603]	B2RZI1		6.4	1.6E-04	7.6	2.5E-05	-0.9	4.1E-01	-0.3	5.3E-01
ENSMUST00000171719	chemokine (C-C motif) receptor 2 [Source:MGI Symbol;Acc:MGI:106185]	Q543S8	P51683	-4.7	1.1E-03	6.1	2.3E-02	0.2	9.3E-01	-1.5	3.3E-01
ENSMUST00000171735	nischarin [Source:MGI Symbol;Acc:MGI:1928323]		Q80TM9	4.4	4.5E-04	6.5	3.4E-04	-0.5	7.2E-01	-0.4	5.4E-01
ENSMUST00000171749	expressed sequence AU018091 [Source:MGI Symbol;Acc:MGI:2142124]	E9PWS4		6.3	1.1E-05	5.6	5.4E-03	-0.5	7.7E-01	-1.7	1.1E-01
ENSMUST00000171754	Jun dimerization protein 2 [Source:MGI Symbol;Acc:MGI:1932093]		P97875	-3.5	1.0E-03	5.7	1.4E-04	-0.4	6.2E-01	-0.3	6.4E-01
ENSMUST00000171765	protein C [Source:MGI Symbol;Acc:MGI:97771]		P33587	6.3	5.6E-04	3.4	6.5E-02	-2.6	1.4E-01	1.7	1.9E-01
ENSMUST00000135532				0.9	5.4E-01	-0.6	7.3E-01	-2.0	1.5E-01	-0.4	8.3E-01
ENSMUST00000171770	fucosyltransferase 8 [Source:MGI Symbol;Acc:MGI:1858901]		Q9WTS2	-3.4	6.4E-03	-1.8	5.2E-02	0.8	1.1E-01	0.8	3.2E-01
ENSMUST00000135559				0.1	9.1E-01	1.1	2.8E-01	0.9	2.2E-01	-0.1	9.5E-01
ENSMUST00000171772	interferon gamma receptor 1 [Source:MGI Symbol;Acc:MGI:107655]	E9Q3Y5		-3.5	1.7E-03	-7.6	4.7E-03	-0.3	6.4E-01	1.2	5.7E-01
ENSMUST00000171786	heterogeneous nuclear ribonucleoprotein D [Source:MGI Symbol;Acc:MGI:101947]	E9Q5B6		-7.0	3.1E-04	-2.5	1.7E-03	-0.9	3.7E-02	-0.8	1.8E-01
ENSMUST00000171788	RIKEN cDNA 4931428F04 gene [Source:MGI Symbol;Acc:MGI:1921606]		Q810A5	7.7	6.1E-03	4.1	2.0E-03	-1.4	1.6E-01	-0.6	4.2E-01
ENSMUST00000171789	ubiquitin fusion degradation 1 like [Source:MGI Symbol;Acc:MGI:109353]	E9Q475		-5.8	9.1E-05	3.7	4.0E-03	-1.1	2.5E-01	-0.1	8.8E-01
ENSMUST00000135579	erythrocyte membrane protein band 4.1 [Source:MGI Symbol;Acc:MGI:95401]	F6S4K9		-0.8	5.6E-01	0.7	6.3E-01	-0.9	4.9E-01	-2.4	1.2E-01
ENSMUST00000135582				-1.2	1.5E-01	-2.7	5.7E-02	0.0	9.9E-01	1.6	2.2E-01
ENSMUST00000171791	microtubule associated serine/threonine kinase family member 4 [Source:MGI Symbol;Acc:MGI:1918885]	E9PWX8		7.3	5.0E-03	5.1	1.1E-03	-1.3	2.6E-01	0.6	4.1E-01
ENSMUST00000171796	kinesin family member 1A [Source:MGI Symbol;Acc:MGI:108391]	G3UW47		9.6	9.4E-05	7.2	2.7E-04	1.1	3.8E-01	0.1	8.5E-01
ENSMUST00000135588	GTF2I repeat domain containing 2 [Source:MGI Symbol;Acc:MGI:2149780]	F6XRH9		-3.0	3.9E-02	0.0	9.7E-01	0.5	6.4E-01	-2.5	8.8E-02
ENSMUST00000171797	nucleosome assembly protein 1-like 1 [Source:MGI Symbol;Acc:MGI:1855693]	E9PW66		3.0	3.3E-04	6.2	3.4E-04	-0.5	7.0E-01	-0.4	5.2E-01
ENSMUST00000171798	family with sequence similarity 71, member A [Source:MGI Symbol;Acc:MGI:3588202]	B7XG49		7.4	5.8E-05	2.0	4.6E-01	6.1	1.1E-02	-0.9	6.7E-01
ENSMUST00000171804	solute carrier family 15, member 5 [Source:MGI Symbol;Acc:MGI:3607714]		Q8CBB2	6.2	2.8E-03	4.9	5.4E-04	-2.6	3.0E-02	-1.2	1.0E-01
ENSMUST00000135600				1.9	7.9E-02	2.8	5.2E-02	1.0	3.8E-01	0.2	8.8E-01
ENSMUST00000171830	tripartite motif-containing 30B [Source:MGI Symbol;Acc:MGI:4821256]	Q8BY96		-5.2	9.0E-03	8.1	4.1E-05	-0.6	6.2E-01	0.2	6.7E-01
ENSMUST00000171835	sodium channel, voltage-gated, type III, beta [Source:MGI Symbol;Acc:MGI:1918882]	Q0P666	Q8BHK2	7.6	4.9E-04	6.5	4.8E-05	0.2	8.2E-01	-0.5	3.4E-01
ENSMUST00000171843	janus kinase and microtubule interacting protein 3 [Source:MGI Symbol;Acc:MGI:1921254]	F6TN46		7.9	1.3E-05	8.2	1.6E-04	0.4	7.9E-01	-1.9	2.6E-02
ENSMUST00000171847	solute carrier family 29 (nucleoside transporters), member 1 [Source:MGI Symbol;Acc:MGI:1927073]	Q3TCZ2	Q9JIM1	5.7	2.9E-02	4.4	5.5E-03	-0.3	8.0E-01	-0.9	2.9E-01
ENSMUST00000171853	RIKEN cDNA D030025P21 gene [Source:MGI Symbol;Acc:MGI:3698049]	Q8BQF7		8.5	6.3E-05	-0.5	7.6E-01	1.7	1.4E-01	-1.2	4.0E-01
ENSMUST00000171887	Rhesus blood group-associated B glycoprotein [Source:MGI Symbol;Acc:MGI:1927379]		Q8BUX5	5.3	1.5E-03	5.9	9.7E-04	0.2	8.9E-01	0.7	3.8E-01
ENSMUST00000135614	O-sialoglycoprotein endopeptidase-like 1 [Source:MGI Symbol;Acc:MGI:1919335]		Q6PEB4	-0.1	9.5E-01	1.6	2.9E-01	2.0	1.4E-01	0.3	7.7E-01
ENSMUST00000171904	termediate/small conductance calcium-activated channel, subfamily N, member 4 [Source:MGI Symbol;Acc:M		O89109	2.1	1.9E-02	4.8	1.2E-02	-0.6	6.9E-01	1.4	1.9E-01
ENSMUST00000135618	RAS protein activator like 3 [Source:MGI Symbol;Acc:MGI:2444128]	D3Z6Z7		-0.3	9.0E-01	0.7	8.6E-01	0.7	7.7E-01	-0.3	9.4E-01
ENSMUST00000135622				2.0	4.2E-02	1.9	1.0E-01	-0.3	7.7E-01	-0.1	9.2E-01
ENSMUST00000135625	zinc finger protein 106 [Source:MGI Symbol;Acc:MGI:1270153]	E9PVH6		1.8	1.1E-01	0.8	6.2E-01	0.5	6.9E-01	1.4	3.3E-01
ENSMUST00000135627				-2.3	3.0E-01	1.8	6.0E-01	3.9	1.5E-01	-0.2	9.5E-01
ENSMUST00000135631	NudC domain containing 3 [Source:MGI Symbol;Acc:MGI:2144158]	A0A0A0MQL8		-2.0	1.4E-01	-2.6	2.5E-01	1.4	2.8E-01	2.0	3.4E-01
ENSMUST00000135633				0.1	9.7E-01	-3.0	3.5E-01	-3.1	1.2E-01	0.1	9.9E-01
ENSMUST00000135634				-1.2	2.0E-01	-0.4	7.5E-01	1.6	8.4E-02	0.7	5.6E-01
ENSMUST00000171906	predicted gene 3667 [Source:MGI Symbol;Acc:MGI:3781843]	K7N757		5.5	1.0E-02	1.7	8.9E-02	0.2	7.4E-01	0.4	6.4E-01
ENSMUST00000171915	ATP-binding cassette, sub-family G (WHITE), member 8 [Source:MGI Symbol;Acc:MGI:1914720]	Q7TSR6		5.9	3.1E-04	-1.8	1.7E-01	0.6	4.4E-01	-1.0	4.6E-01
ENSMUST00000171925	abhydrolase domain containing 14A [Source:MGI Symbol;Acc:MGI:1915894]	E9PW22		5.7	1.6E-02	6.0	7.8E-05	-2.3	4.5E-02	-0.1	8.9E-01
ENSMUST00000171939	WD repeat domain 64 [Source:MGI Symbol;Acc:MGI:1923070]		Q9D565	4.8	3.3E-02	0.1	9.4E-01	1.7	2.8E-01	4.5	1.3E-02
ENSMUST00000171947	predicted gene, 21292 [Source:MGI Symbol;Acc:MGI:5434647]	Q78EE2		10.0	9.5E-06	-3.3	2.0E-01	1.7	1.6E-01	1.4	5.6E-01
ENSMUST00000135644				1.0	3.5E-01	0.6	6.7E-01	-0.2	8.8E-01	0.3	8.1E-01
ENSMUST00000171962	calmodulin regulated spectrin-associated protein family, member 3 [Source:MGI Symbol;Acc:MGI:1916947]	E9Q5B0		7.9	3.0E-04	4.0	9.8E-04	-2.3	2.8E-02	-0.4	5.3E-01
ENSMUST00000171970	bone morphogenetic protein 6 [Source:MGI Symbol;Acc:MGI:88182]		P20722	7.0	8.5E-05	-4.1	6.1E-03	-0.3	6.2E-01	-1.9	2.0E-01
ENSMUST00000171975	: ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:13		Q9Z1K5	-4.0	3.0E-04	3.1	1.4E-03	-0.1	8.5E-01	-0.1	8.1E-01
ENSMUST00000171987	predicted gene 8050 [Source:MGI Symbol;Acc:MGI:3779779]	L7N2E3		8.4	1.9E-05	4.0	1.2E-02	-1.1	4.0E-01	1.0	3.0E-01
ENSMUST00000171996	vomeronasal 2, receptor 117 [Source:MGI Symbol;Acc:MGI:3648766]	K7N6V1		6.2	1.3E-03	6.5	2.9E-06	-0.1	9.2E-01	-0.1	7.4E-01
ENSMUST00000171999	ycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase) [Source:MGI Symbol;Acc:MGI:134938	E9PWY6		4.5	1.9E-02	0.7	4.3E-01	-1.0	1.7E-01	0.6	4.0E-01
ENSMUST00000135683	acyl-CoA synthetase medium-chain family member 1 [Source:MGI Symbol;Acc:MGI:2152200]	D3Z106		4.9	4.6E-02	3.7	1.5E-01	-0.7	7.7E-01	0.5	7.8E-01
ENSMUST00000172002	guanine nucleotide binding protein (G protein), gamma 13 [Source:MGI Symbol;Acc:MGI:1925616]		Q9JMF3	6.7	1.0E-03	-4.6	4.1E-05	-0.6	9.0E-02	-1.2	9.4E-02
ENSMUST00000172020	TBC1 domain family, member 25 [Source:MGI Symbol;Acc:MGI:2444862]	E9PWX7		-4.8	9.4E-03	4.9	3.0E-02	-0.9	6.4E-01	0.9	5.2E-01
ENSMUST00000172032	carboxylesterase 2H [Source:MGI Symbol;Acc:MGI:3648740]	F6Z9B9		7.0	1.0E-04	-1.6	2.0E-01	3.2	1.8E-03	-0.3	8.1E-01
ENSMUST00000172057	Ral GEF with PH domain and SH3 binding motif 2 [Source:MGI Symbol;Acc:MGI:1925505]		Q9ERD6	5.0	4.3E-04	2.7	1.2E-01	-0.5	7.5E-01	1.0	4.5E-01
ENSMUST00000172095	myoferlin [Source:MGI Symbol;Acc:MGI:1919192]	E9Q390		7.2	2.7E-05	-4.2	3.8E-03	-1.0	1.3E-01	-2.0	1.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000172098	peptidyl arginine deiminase, type III [Source:MGI Symbol;Acc:MGI:1338891]	E9QAM4		4.2	4.1E-03	7.3	9.0E-03	-0.8	7.4E-01	-1.5	2.6E-01
ENSMUST00000135709	AT rich interactive domain 4A (RBP1-like) [Source:MGI Symbol;Acc:MGI:2444354]	E9Q9V1		3.3	1.2E-01	0.6	8.5E-01	-0.6	7.9E-01	2.1	4.5E-01
ENSMUST00000172107	suppression of tumorigenicity 13 [Source:MGI Symbol;Acc:MGI:1917606]		Q99L47	-3.4	1.4E-04	6.5	1.7E-04	-0.2	8.7E-01	0.6	3.4E-01
ENSMUST00000135714				-2.9	8.3E-02	-1.4	5.3E-01	1.1	4.8E-01	-0.5	8.2E-01
ENSMUST00000172132	triosephosphate isomerase 1 [Source:MGI Symbol;Acc:MGI:98797]		P17751	-5.1	2.9E-05	4.0	5.2E-03	-0.1	9.4E-01	-0.6	4.6E-01
ENSMUST00000172140	vomeronasal 2, receptor 8 [Source:MGI Symbol;Acc:MGI:3642986]	L7N472		5.4	2.9E-03	-7.0	1.9E-02	0.4	6.5E-01	-0.4	8.8E-01
ENSMUST00000172142	nischarin [Source:MGI Symbol;Acc:MGI:1928323]		Q80TM9	-4.2	3.5E-04	5.1	9.8E-04	0.3	7.5E-01	0.3	6.9E-01
ENSMUST00000172159	TNF receptor-associated factor 1 [Source:MGI Symbol;Acc:MGI:101836]		P39428	5.6	1.3E-05	1.5	7.3E-02	-1.4	8.6E-02	-0.1	9.2E-01
ENSMUST00000135732				-3.5	5.3E-02	-1.9	3.2E-01	0.5	6.9E-01	-1.1	5.8E-01
ENSMUST00000172164	e carrier family 7 (cationic amino acid transporter, y+ system), member 4 [Source:MGI Symbol;Acc:MGI:2146		Q8BLQ7	7.8	2.7E-05	4.7	1.4E-04	-0.3	6.9E-01	0.8	1.5E-01
ENSMUST00000172165	septin 2 [Source:MGI Symbol;Acc:MGI:97298]	E9Q3V6		-6.3	1.6E-03	6.1	2.1E-03	-0.4	7.8E-01	-0.4	6.3E-01
ENSMUST00000172175	zinc finger and BTB domain containing 3 [Source:MGI Symbol;Acc:MGI:1922541]		Q91X45	2.2	1.7E-02	-5.5	3.3E-02	-0.6	5.1E-01	-0.9	7.1E-01
ENSMUST00000172178	RIKEN cDNA A230065N10 gene [Source:MGI Symbol;Acc:MGI:3642744]	Q8CAG4		6.1	2.2E-04	2.1	2.4E-01	-4.3	4.9E-02	0.0	9.8E-01
ENSMUST00000172184	serine (or cysteine) peptidase inhibitor, clade B, member 6c [Source:MGI Symbol;Acc:MGI:2145481]	W4VSP4		5.1	2.8E-03	5.3	1.9E-03	1.4	2.5E-01	0.2	8.1E-01
ENSMUST00000172199	vomeronasal 2, receptor 20 [Source:MGI Symbol;Acc:MGI:3646439]	L7N2B1		6.1	1.2E-04	2.5	3.3E-02	-2.9	2.3E-02	-1.1	2.2E-01
ENSMUST00000172220	zinc finger, ZZ-type with EF hand domain 1 [Source:MGI Symbol;Acc:MGI:2444286]	E9Q5W5		-6.8	7.0E-04	-4.0	2.4E-02	0.7	3.7E-01	-1.2	4.7E-01
ENSMUST00000172230	olfactory receptor 527 [Source:MGI Symbol;Acc:MGI:3030361]	Q7TRT9		6.4	2.6E-04	4.8	4.0E-03	0.2	8.7E-01	-1.4	1.6E-01
ENSMUST00000135760				-0.2	7.3E-01	1.2	1.8E-01	0.3	6.7E-01	-1.2	1.5E-01
ENSMUST00000172239	5'-nucleotidase, cytosolic II [Source:MGI Symbol;Acc:MGI:2178563]	E9Q9M1		-5.9	1.1E-03	3.2	2.1E-02	0.6	5.6E-01	0.2	8.0E-01
ENSMUST00000135764	sarcoglycan zeta [Source:MGI Symbol;Acc:MGI:2388820]	D6RFA5		4.1	1.4E-01	6.8	3.5E-02	-0.2	9.4E-01	-2.9	1.1E-01
ENSMUST00000135770				1.5	1.1E-01	-0.6	5.9E-01	-1.0	2.4E-01	1.1	3.1E-01
ENSMUST00000172240	zinc finger and BTB domain containing 45 [Source:MGI Symbol;Acc:MGI:2685003]	Q52KG4		2.2	3.8E-03	5.8	3.0E-04	-0.6	5.3E-01	0.5	4.5E-01
ENSMUST00000172252	Ras-like without CAAX 1 [Source:MGI Symbol;Acc:MGI:108053]	E9Q672		-7.4	2.5E-04	1.3	2.6E-02	-0.7	1.1E-01	0.7	1.2E-01
ENSMUST00000135789				-1.4	7.0E-01	-3.9	3.5E-01	-3.3	2.0E-01	-0.8	8.6E-01
ENSMUST00000135794				-1.3	4.1E-01	0.2	9.0E-01	0.6	6.7E-01	-0.9	5.9E-01
ENSMUST00000172269	spectrin beta, non-erythrocytic 4 [Source:MGI Symbol;Acc:MGI:1890574]	Q91ZE6		6.6	2.0E-02	1.1	3.8E-01	-0.8	4.5E-01	0.8	4.8E-01
ENSMUST00000135802	lysine (K)-specific demethylase 5A [Source:MGI Symbol;Acc:MGI:2136980]			1.8	4.7E-01	1.8	5.7E-01	-0.3	9.0E-01	-0.3	9.2E-01
ENSMUST00000135807	EPM2A (laforin) interacting protein 1 [Source:MGI Symbol;Acc:MGI:1925031]		Q8VEH5	-1.5	2.3E-01	-1.2	3.9E-01	0.2	8.6E-01	-0.1	9.4E-01
ENSMUST00000135814	PHD finger protein 23 [Source:MGI Symbol;Acc:MGI:1925496]		Q8BSN5	-1.8	5.4E-02	0.8	4.4E-01	0.8	3.3E-01	-1.8	7.9E-02
ENSMUST00000172270	predicted gene 5218 [Source:MGI Symbol;Acc:MGI:3646583]	F6YH22		6.3	7.3E-03	-1.6	3.2E-01	1.5	1.2E-01	-0.2	9.2E-01
ENSMUST00000172271	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 4 [Source:MGI Symbol;Acc:MGI:192043		Q8K120	9.0	7.6E-06	-2.8	1.6E-02	0.2	7.3E-01	-1.5	2.0E-01
ENSMUST00000172272	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 [Source:MGI Symbol;Acc:MGI:1920895]		Q569Z5	-4.6	6.3E-04	1.5	4.7E-01	-2.3	2.7E-01	2.1	2.1E-01
ENSMUST00000172278	cholinergic receptor, muscarinic 2, cardiac [Source:MGI Symbol;Acc:MGI:88397]		Q9ERZ4	7.8	1.3E-05	-3.8	8.1E-03	0.3	6.0E-01	-0.4	7.5E-01
ENSMUST00000172281	GPI anchor attachment protein 1 [Source:MGI Symbol;Acc:MGI:1202392]	E9PW03		-5.6	1.3E-02	6.6	1.2E-04	-0.6	6.0E-01	0.0	9.8E-01
ENSMUST00000172282	polypyrimidine tract binding protein 1 [Source:MGI Symbol;Acc:MGI:97791]	Q922I7		-6.7	2.5E-04	-1.9	3.4E-01	-3.2	3.1E-02	2.4	2.1E-01
ENSMUST00000172298	RAB11A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1858202]	Q0PD45	P62492	-3.3	5.5E-03	4.5	8.6E-04	0.2	8.2E-01	-0.3	6.6E-01
ENSMUST00000172299	ring finger protein 152 [Source:MGI Symbol;Acc:MGI:2443787]		Q8BG47	7.0	5.0E-04	0.1	9.7E-01	1.9	1.6E-01	-2.4	2.0E-01
ENSMUST00000172307	Rho GTPase activating protein 8 [Source:MGI Symbol;Acc:MGI:1920417]		Q9CXP4	5.3	1.8E-02	4.5	2.9E-03	-1.5	2.5E-01	0.1	9.3E-01
ENSMUST00000172314	high mobility group box transcription factor 1 [Source:MGI Symbol;Acc:MGI:894659]	E9Q1A8		-6.8	5.3E-07	4.7	5.3E-04	-0.3	6.9E-01	0.3	6.5E-01
ENSMUST00000172332	coiled-coil domain containing 71 like [Source:MGI Symbol;Acc:MGI:1919373]	E9Q4T4		-2.9	6.2E-04	-1.0	2.9E-01	1.1	9.0E-02	-0.8	3.9E-01
ENSMUST00000172333	Ras-like without CAAX 1 [Source:MGI Symbol;Acc:MGI:108053]	G3UWE0		-6.7	1.3E-04	-6.4	5.9E-03	-0.7	4.1E-01	1.4	4.9E-01
ENSMUST00000172338	vomeronasal 2, receptor 71 [Source:MGI Symbol;Acc:MGI:3646472]	L7N2D8		4.6	8.3E-04	7.0	1.3E-04	-0.1	9.0E-01	-0.2	6.6E-01
ENSMUST00000172356	thrombospondin, type I, domain containing 7A [Source:MGI Symbol;Acc:MGI:2685683]	E9PWD2		6.2	2.8E-05	-4.7	4.7E-03	-0.9	1.4E-01	-0.8	5.7E-01
ENSMUST00000172359	vomeronasal 2, receptor 91 [Source:MGI Symbol;Acc:MGI:3645072]	E9Q2U5		5.1	3.1E-03	-8.0	1.4E-04	-0.3	5.4E-01	-0.6	6.5E-01
ENSMUST00000172361	heterogeneous nuclear ribonucleoprotein D [Source:MGI Symbol;Acc:MGI:101947]		Q60668	2.3	4.0E-03	5.9	3.0E-04	2.4	3.1E-02	0.6	3.4E-01
ENSMUST00000172371	predicted gene 340 [Source:MGI Symbol;Acc:MGI:2685186]	F6RGI3		3.1	6.8E-05	-1.9	8.1E-03	-0.9	3.8E-02	-0.8	2.0E-01
ENSMUST00000135886				1.5	1.1E-01	2.0	1.0E-01	0.6	5.1E-01	0.0	9.6E-01
ENSMUST00000172391	vomeronasal 2, receptor 23 [Source:MGI Symbol;Acc:MGI:3646826]	E9PXI5		6.5	1.2E-04	5.3	1.2E-02	-0.6	7.4E-01	-0.7	5.4E-01
ENSMUST00000172396	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 [Source:MGI Symbol;Acc:MGI:1915528]		Q8VDW0	5.0	1.3E-04	5.9	1.7E-05	-1.1	1.5E-01	0.0	9.4E-01
ENSMUST00000172405	gametogenetin binding protein 2 [Source:MGI Symbol;Acc:MGI:2387356]		Q5SV77	-7.0	2.0E-02	7.4	1.3E-04	0.2	8.9E-01	-0.2	8.0E-01
ENSMUST00000172431	predicted gene 3512 [Source:MGI Symbol;Acc:MGI:3781689]	E9Q032		3.4	1.9E-02	6.0	5.3E-04	-0.3	8.2E-01	-0.1	8.5E-01
ENSMUST00000135909				1.8	1.4E-01	2.5	1.2E-01	0.0	9.8E-01	-0.8	4.9E-01
ENSMUST00000172435	fibronectin type III domain containing 4 [Source:MGI Symbol;Acc:MGI:1917195]	B9EI95	Q3TR08	2.8	2.5E-02	3.8	1.7E-03	0.0	9.9E-01	-0.4	5.3E-01
ENSMUST00000172450	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2 [Source:MGI Symbol;Acc:MGI:108415]		Q61206	-2.2	6.9E-04	5.1	2.6E-02	-0.5	8.3E-01	-0.1	9.2E-01
ENSMUST00000135913				0.6	4.5E-01	-0.2	8.9E-01	0.9	2.6E-01	1.6	1.6E-01
ENSMUST00000172457	ribosomal protein S15A [Source:MGI Symbol;Acc:MGI:2389091]	Q5M9M4	P62245	4.9	8.9E-05	-2.3	1.2E-01	0.4	6.7E-01	-1.2	4.1E-01
ENSMUST00000135919				-0.6	7.1E-01	0.6	7.9E-01	0.2	8.6E-01	-0.9	6.6E-01
ENSMUST00000172492	zinc and ring finger 3 [Source:MGI Symbol;Acc:MGI:3039616]		Q5SSZ7	7.5	5.8E-06	5.3	1.1E-03	-1.8	1.8E-01	0.6	4.2E-01
ENSMUST00000135924	ubiquitin-conjugating enzyme E2J 1 [Source:MGI Symbol;Acc:MGI:1926245]	F6SPK0		-2.0	4.0E-02	-0.1	9.2E-01	1.6	6.9E-02	-0.4	7.4E-01
ENSMUST00000135928				0.4	7.1E-01	-0.1	9.3E-01	-0.6	5.5E-01	-0.1	9.3E-01
ENSMUST00000135929				0.8	7.0E-01	1.1	6.7E-01	0.1	9.8E-01	-0.3	9.0E-01
ENSMUST00000135930	ase, aminophospholipid transporter (APLT), class I, type 8A, member 1 [Source:MGI Symbol;Acc:MGI:1330	F6WYQ5	P70704	1.9	3.9E-01	1.9	4.7E-01	-1.2	5.8E-01	-1.1	6.4E-01
ENSMUST00000172499	von Willebrand factor A domain containing 7 [Source:MGI Symbol;Acc:MGI:1306798]	B9EJA5		8.1	1.5E-05	-4.3	1.8E-02	0.2	8.2E-01	-0.5	7.8E-01
ENSMUST00000172503	histocompatibility 2, D region locus 1 [Source:MGI Symbol;Acc:MGI:95896]	G3UZP7		-5.2	1.8E-03	3.6	9.9E-03	-0.1	9.5E-01	-1.3	1.7E-01
ENSMUST00000135941	prefoldin 2 [Source:MGI Symbol;Acc:MGI:1276111]		O70591	1.1	4.4E-02	1.1	9.1E-02	-0.2	6.4E-01	-0.2	6.8E-01
ENSMUST00000172510	transmembrane and coiled coil domains 1 [Source:MGI Symbol;Acc:MGI:2442368]	G3UXF1		-4.7	4.3E-03	3.5	1.8E-04	-1.0	1.0E-01	-0.3	4.1E-01
ENSMUST00000172518	zinc ribbon domain containing, 1 [Source:MGI Symbol;Acc:MGI:1913386]		Q791N7	-6.6	1.6E-04	3.3	2.3E-03	-0.5	5.3E-01	0.4	4.9E-01
ENSMUST00000135948	maestro heat-like repeat family member 2A [Source:MGI Symbol;Acc:MGI:3705228]	F6W219		2.0	2.4E-01	1.1	5.5E-01	-0.7	6.6E-01	0.1	9.4E-01
ENSMUST00000135949	phosphoglycerate kinase 1 [Source:MGI Symbol;Acc:MGI:97555]	S4R2M7		0.9	7.7E-01	-6.6	2.3E-02	-9.8	2.0E-03	-2.3	4.3E-01
ENSMUST00000172529	heterogeneous nuclear ribonucleoprotein L [Source:MGI Symbol;Acc:MGI:104816]	G3UY38		-8.7	2.6E-05	6.2	5.8E-04	-0.4	7.7E-01	-1.0	1.7E-01
ENSMUST00000172530	androglobin [Source:MGI Symbol;Acc:MGI:3605549]		G3UZ78	4.5	8.6E-03	3.8	1.7E-02	-0.6	6.6E-01	1.4	1.6E-01
ENSMUST00000135960	tryptophanyl tRNA synthetase 2 (mitochondrial) [Source:MGI Symbol;Acc:MGI:1917810]	A0A0G2JDR5		-1.0	6.5E-01	1.2	6.9E-01	1.4	5.5E-01	-0.8	7.6E-01
ENSMUST00000135961	MLX interacting protein [Source:MGI Symbol;Acc:MGI:2141183]	F6UPM1		0.9	3.5E-01	0.3	8.4E-01	0.4	7.0E-01	1.0	4.1E-01
ENSMUST00000172556	lysine (K)-specific methyltransferase 2C [Source:MGI Symbol;Acc:MGI:2444959]	G3UY45		-3.3	8.6E-03	5.1	3.4E-04	-0.2	8.4E-01	0.2	6.9E-01
ENSMUST00000135969				0.4	5.4E-01	0.5	5.8E-01	0.2	7.2E-01	0.1	8.6E-01
ENSMUST00000172557	poly(A) binding protein, nuclear 1 [Source:MGI Symbol;Acc:MGI:1859158]	G3UWS5		-5.7	8.5E-04	5.6	8.5E-05	0.2	7.7E-01	0.3	5.4E-01
ENSMUST00000172566	piggyBac transposable element derived 5 [Source:MGI Symbol;Acc:MGI:2429955]	G3UX58		8.7	2.2E-04	4.4	9.9E-04	-1.6	1.3E-01	-0.5	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000172571	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]	G3UYQ2		6.2	2.6E-02	3.6	4.0E-02	-0.7	6.7E-01	1.8	1.1E-01
ENSMUST00000135977	CCR4-NOT transcription complex, subunit 3 [Source:MGI Symbol;Acc:MGI:2385261]	F6WUZ2		3.6	6.7E-02	0.5	7.9E-01	-2.3	2.1E-01	0.8	6.5E-01
ENSMUST00000172572	sodium channel modifier 1 [Source:MGI Symbol;Acc:MGI:1341284]			-4.6	1.9E-05	-0.3	8.0E-01	0.1	9.3E-01	-2.4	5.3E-02
ENSMUST00000172579	RIKEN cDNA 2410141K09 gene [Source:MGI Symbol;Acc:MGI:1924053]	K7N769		9.3	5.5E-06	-6.5	1.9E-04	0.5	2.4E-01	1.2	2.9E-01
ENSMUST00000172594	calmodulin 3 [Source:MGI Symbol;Acc:MGI:103249]	G3UX57		-5.4	5.8E-04	7.5	2.6E-05	-1.5	2.0E-01	-0.8	1.3E-01
ENSMUST00000135988	desumoylating isopeptidase 1 [Source:MGI Symbol;Acc:MGI:106313]	Q3TCG9		0.8	6.5E-01	0.7	7.3E-01	-0.9	5.7E-01	-0.8	6.5E-01
ENSMUST00000172598	dystrobrevin, beta [Source:MGI Symbol;Acc:MGI:1203728]	G3UYK9		-3.7	2.0E-03	6.7	1.5E-03	0.7	6.7E-01	0.1	9.3E-01
ENSMUST00000135999				-1.5	2.4E-01	0.9	6.2E-01	1.5	3.2E-01	-0.9	5.3E-01
ENSMUST00000136003				1.0	6.8E-01	-2.4	4.9E-01	-2.6	2.1E-01	0.8	8.2E-01
ENSMUST00000172614	OTU domain containing 4 [Source:MGI Symbol;Acc:MGI:1098801]	G3UXQ0		5.4	1.1E-05	-2.7	3.7E-03	-0.5	2.6E-01	0.3	6.5E-01
ENSMUST00000136010				0.0	1.0E+00	-3.6	2.5E-01	-2.5	1.9E-01	1.1	7.2E-01
ENSMUST00000172630	START domain containing 10 [Source:MGI Symbol;Acc:MGI:1860093]	G3UYM0		4.9	1.4E-02	5.9	3.0E-04	-0.1	9.6E-01	-0.4	4.5E-01
ENSMUST00000172652	BR serine/threonine kinase 2 [Source:MGI Symbol;Acc:MGI:1923020]	G3UWV4		6.2	4.5E-03	3.4	1.3E-02	-0.1	9.4E-01	-0.6	5.0E-01
ENSMUST00000172680	growth regulation by estrogen in breast cancer-like [Source:MGI Symbol;Acc:MGI:3576497]	G3UZ23		5.1	2.6E-05	-1.2	2.7E-01	0.5	5.3E-01	-2.5	6.4E-02
ENSMUST00000172689	DNA methyltransferase 3A [Source:MGI Symbol;Acc:MGI:1261827]		O88508	5.1	6.0E-04	8.4	2.3E-03	1.4	4.7E-01	1.4	1.7E-01
ENSMUST00000172697	MDS1 and EVI1 complex locus [Source:MGI Symbol;Acc:MGI:95457]	G3UYK2		6.5	2.2E-03	-3.1	1.3E-01	3.3	5.9E-03	-0.6	7.8E-01
ENSMUST00000136026	synaptonemal complex central element protein 2 [Source:MGI Symbol;Acc:MGI:1919096]		Q505B8	1.9	2.2E-01	4.1	4.2E-02	0.4	8.2E-01	-1.8	2.0E-01
ENSMUST00000172699	mex3 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:1919890]	G3UYU0		7.0	8.3E-06	6.5	6.1E-04	-0.5	6.9E-01	0.0	9.5E-01
ENSMUST00000136030	ankyrin repeat and KH domain containing 1 [Source:MGI Symbol;Acc:MGI:1921733]	F6SI14		-1.0	2.9E-01	-0.2	8.4E-01	0.3	7.2E-01	-0.4	7.1E-01
ENSMUST00000172733	praja 2, RING-H2 motif containing [Source:MGI Symbol;Acc:MGI:2159342]		Q80U04	-6.8	1.3E-05	2.8	1.1E-02	-5.0	1.9E-03	0.0	9.9E-01
ENSMUST00000172738	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) [Source:MGI Symbol;Acc:MGI:1096367]	G3UXY0		-7.6	3.0E-06	7.1	8.0E-05	-0.5	6.6E-01	-1.3	5.6E-02
ENSMUST00000172743	vomeronasal 2, receptor 55 [Source:MGI Symbol;Acc:MGI:3757950]	G3UWZ4		6.6	2.6E-02	5.9	1.5E-04	-0.3	7.9E-01	0.2	7.3E-01
ENSMUST00000172753	heat shock protein 1B [Source:MGI Symbol;Acc:MGI:99517]		P17879	2.3	1.2E-03	6.9	1.2E-04	0.9	4.2E-01	-0.1	8.1E-01
ENSMUST00000136048	enhancer of mRNA decapping 4 [Source:MGI Symbol;Acc:MGI:2446249]	D6RE33		2.3	6.9E-02	6.2	6.9E-03	3.1	9.6E-02	-0.8	4.8E-01
ENSMUST00000172754	MDS1 and EVI1 complex locus [Source:MGI Symbol;Acc:MGI:95457]	G3UYN3		6.8	1.3E-04	3.8	3.5E-02	-1.6	3.5E-01	-1.5	2.1E-01
ENSMUST00000136063				-1.5	6.8E-02	0.6	4.7E-01	1.0	1.5E-01	-1.1	2.2E-01
ENSMUST00000172767	membrane-associated ring finger (C3HC4) 2 [Source:MGI Symbol;Acc:MGI:1925915]		Q99M02	-4.9	8.5E-05	6.9	1.8E-04	-0.6	5.8E-01	0.4	5.5E-01
ENSMUST00000172785	histocompatibility 2, D region locus 1 [Source:MGI Symbol;Acc:MGI:95896]	Q792Z7	P01899	-7.3	1.3E-05	5.5	1.0E-03	-0.8	5.3E-01	-0.6	4.2E-01
ENSMUST00000172792	gamma-aminobutyric acid (GABA) B receptor, 1 [Source:MGI Symbol;Acc:MGI:1860139]		Q9WV18	3.4	4.8E-03	7.2	1.3E-03	0.9	5.8E-01	0.5	5.9E-01
ENSMUST00000172821	ventral anterior homeobox 1 [Source:MGI Symbol;Acc:MGI:1277163]		Q2NKI2	5.9	4.2E-04	1.6	3.6E-01	-2.0	1.7E-01	1.3	3.5E-01
ENSMUST00000172826	calcium-sensing receptor [Source:MGI Symbol;Acc:MGI:1351351]		Q9QY96	7.3	2.5E-02	-4.3	9.1E-03	-0.6	3.3E-01	-0.6	6.7E-01
ENSMUST00000172828	synaptotagmin binding, cytoplasmic RNA interacting protein [Source:MGI Symbol;Acc:MGI:1891690]	G3UXU5		-5.9	7.6E-05	-5.8	9.3E-04	0.6	2.2E-01	-2.0	1.7E-01
ENSMUST00000172834	integrin beta 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1306802]	Q3UGH2		-6.2	1.1E-04	5.4	1.5E-03	-1.4	2.9E-01	-0.4	5.7E-01
ENSMUST00000136076				1.1	4.8E-01	2.1	3.3E-01	0.2	9.3E-01	-0.8	6.1E-01
ENSMUST00000172856	zinc and ring finger 1 [Source:MGI Symbol;Acc:MGI:2177308]		Q91V17	-3.1	2.4E-02	2.6	2.0E-01	-1.0	5.7E-01	0.3	8.4E-01
ENSMUST00000172879	DNA methyltransferase 3A [Source:MGI Symbol;Acc:MGI:1261827]	G3UZY8		8.5	1.8E-05	0.7	6.5E-01	-1.2	3.8E-01	2.7	7.3E-02
ENSMUST00000172912	histocompatibility 2, K1, K region [Source:MGI Symbol;Acc:MGI:95904]	Q3TH01		-7.3	5.5E-05	7.0	8.5E-04	-1.4	3.8E-01	1.1	2.2E-01
ENSMUST00000172928	forkhead box A2 [Source:MGI Symbol;Acc:MGI:1347476]	G3UYH0		6.8	9.0E-03	4.2	4.0E-04	0.2	7.6E-01	0.2	7.7E-01
ENSMUST00000136100				-0.2	8.8E-01	3.0	1.1E-01	0.6	6.9E-01	-2.6	7.8E-02
ENSMUST00000172939	RIKEN cDNA 4921506M07 gene [Source:MGI Symbol;Acc:MGI:1918096]	G3UYY4		6.6	4.2E-04	3.4	2.9E-02	0.1	9.4E-01	-0.6	5.4E-01
ENSMUST00000172951	glutamate receptor, metabotropic 7 [Source:MGI Symbol;Acc:MGI:1351344]		Q68ED2	5.6	3.3E-03	-4.7	3.8E-03	0.6	3.5E-01	0.6	6.3E-01
ENSMUST00000172979	histocompatibility 2, Q region locus 5 [Source:MGI Symbol;Acc:MGI:95934]			-2.2	3.2E-02	4.7	1.0E-02	-1.4	3.8E-01	1.6	1.2E-01
ENSMUST00000172992	A kinase (PRKA) anchor protein 5 [Source:MGI Symbol;Acc:MGI:2685104]	H3BIV5		5.1	5.6E-03	7.0	2.6E-04	-0.4	7.5E-01	-0.6	3.9E-01
ENSMUST00000136122				0.6	8.5E-01	-0.8	8.5E-01	-1.5	6.4E-01	-0.2	9.6E-01
ENSMUST00000173002	C1q and tumor necrosis factor related protein 2 [Source:MGI Symbol;Acc:MGI:1916433]	G3V001		6.0	2.9E-03	6.6	3.8E-06	0.1	9.3E-01	0.2	6.3E-01
ENSMUST00000173014	deiodinase, iodothyronine type III [Source:MGI Symbol;Acc:MGI:1306782]		Q91ZI8	6.2	1.1E-03	-2.9	7.6E-02	-0.5	5.8E-01	-1.6	3.5E-01
ENSMUST00000173015	membrane-associated ring finger (C3HC4) 2 [Source:MGI Symbol;Acc:MGI:1925915]	G3UXS1		-5.4	2.6E-03	-8.4	1.5E-05	-2.4	6.3E-05	-1.3	2.5E-01
ENSMUST00000173023	absent in melanoma 2 [Source:MGI Symbol;Acc:MGI:2686159]	G3UZ36		-4.5	4.4E-04	5.8	4.8E-04	-2.7	5.8E-02	-1.2	1.2E-01
ENSMUST00000173043	G patch domain and ankyrin repeats 1 [Source:MGI Symbol;Acc:MGI:2148975]	H3BL77		-3.2	1.2E-02	-7.2	3.4E-04	-0.5	2.6E-01	0.5	7.1E-01
ENSMUST00000173084	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]		P63280	-4.4	2.0E-03	6.5	7.9E-04	-0.1	9.3E-01	-1.5	7.2E-02
ENSMUST00000173091	peroxiredoxin 5 [Source:MGI Symbol;Acc:MGI:1859821]	G3UZJ4		-10.1	1.3E-05	4.7	7.5E-04	-0.3	7.8E-01	-0.3	5.8E-01
ENSMUST00000173098	ribosomal protein L18 [Source:MGI Symbol;Acc:MGI:98003]	G3UZJ6		-4.1	2.0E-02	5.7	1.3E-04	-2.7	2.4E-02	-0.9	1.2E-01
ENSMUST00000136155				-0.5	8.5E-01	-1.9	5.2E-01	-2.0	3.5E-01	-0.6	8.5E-01
ENSMUST00000136158	fatty acyl CoA reductase 1 [Source:MGI Symbol;Acc:MGI:1914670]	D3Z4N9		-3.1	3.7E-02	-4.7	4.0E-02	-1.0	2.6E-01	0.6	7.6E-01
ENSMUST00000173099	mcf.2 transforming sequence-like [Source:MGI Symbol;Acc:MGI:103263]	G3UXP9		7.2	4.5E-05	-1.9	9.7E-02	1.6	1.8E-02	-1.5	2.0E-01
ENSMUST00000136165				-1.9	5.5E-02	-0.3	7.2E-01	0.2	7.4E-01	-1.3	2.1E-01
ENSMUST00000173102	heat shock transcription factor 4 [Source:MGI Symbol;Acc:MGI:1347058]	G3UXZ1		6.0	2.7E-02	5.1	6.3E-05	-0.2	8.2E-01	-0.2	6.6E-01
ENSMUST00000136174				1.9	1.6E-01	3.4	7.9E-02	1.1	5.2E-01	-0.4	7.3E-01
ENSMUST00000173108	coronin, actin binding protein 1A [Source:MGI Symbol;Acc:MGI:1345961]	G3UYK8		-9.2	2.8E-03	3.8	3.1E-03	-1.5	1.5E-01	1.2	7.9E-02
ENSMUST00000173110	transmembrane and coiled coil domains 1 [Source:MGI Symbol;Acc:MGI:2442368]	G3UXR4		-5.9	2.5E-03	8.7	1.1E-05	-0.3	8.0E-01	0.7	1.5E-01
ENSMUST00000173119	phosphodiesterase 4B, cAMP specific [Source:MGI Symbol;Acc:MGI:99557]	G3UWT3		6.3	1.7E-04	5.7	7.8E-04	-0.2	8.4E-01	-1.2	1.4E-01
ENSMUST00000173128	predicted gene, 19684 [Source:MGI Symbol;Acc:MGI:5011869]	G3UZ45		7.5	1.0E-04	4.9	1.5E-02	-0.6	7.5E-01	0.8	4.9E-01
ENSMUST00000173132	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) [Source:MGI Symbol;Acc:MGI:1913666]	G3UXZ4		-4.9	5.7E-03	-4.3	3.9E-02	-1.5	1.4E-01	-3.8	1.4E-01
ENSMUST00000173135	death associated protein 3 [Source:MGI Symbol;Acc:MGI:1929538]		Q9ER88	-2.9	5.0E-03	7.1	2.3E-04	-0.1	9.3E-01	-0.5	4.2E-01
ENSMUST00000173147	flotillin 1 [Source:MGI Symbol;Acc:MGI:1100500]	G3UWW8		-4.6	1.3E-02	5.1	5.7E-03	-0.4	8.1E-01	0.5	5.9E-01
ENSMUST00000173167	histocompatibility 2, D region locus 1 [Source:MGI Symbol;Acc:MGI:95896]	G3UX20		-7.5	1.6E-03	6.8	3.7E-03	-0.4	8.2E-01	1.3	2.0E-01
ENSMUST00000173168	URB2 ribosome biogenesis 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2681124]	G3UX45		5.9	2.2E-03	-3.7	6.5E-02	0.1	9.5E-01	0.0	9.8E-01
ENSMUST00000136200	inhibitor of growth family, member 3 [Source:MGI Symbol;Acc:MGI:1919027]	S4R2I3		-4.0	5.4E-02	-3.8	1.7E-01	0.7	5.5E-01	0.6	8.4E-01
ENSMUST00000173185	e carrier family 22 (organic cation transporter), member 13b, pseudogene [Source:MGI Symbol;Acc:MGI:1924			2.0	2.8E-02	5.5	6.5E-03	0.9	5.4E-01	0.8	4.3E-01
ENSMUST00000136216				-0.4	6.4E-01	-0.8	5.1E-01	-0.4	6.4E-01	0.0	9.9E-01
ENSMUST00000136219				-1.0	5.1E-01	1.0	6.6E-01	1.1	5.7E-01	-0.9	5.8E-01
ENSMUST00000173196	vacuolar protein sorting 52 (yeast) [Source:MGI Symbol;Acc:MGI:1330304]	G3UY33		-6.5	1.6E-04	8.0	1.1E-04	-0.7	6.1E-01	-0.3	6.7E-01
ENSMUST00000173235	GRB10 interacting GYF protein 2 [Source:MGI Symbol;Acc:MGI:2138584]	G3UZX7		7.6	2.5E-04	8.0	5.8E-06	-1.3	1.6E-01	0.3	4.3E-01
ENSMUST00000173246	jumonji, AT rich interactive domain 2 [Source:MGI Symbol;Acc:MGI:104813]		Q62315	-2.4	3.3E-03	-8.9	4.8E-05	0.2	6.4E-01	-1.8	2.4E-01
ENSMUST00000173280	histocompatibility 2, T region locus 22 [Source:MGI Symbol;Acc:MGI:95956]	G3UYB6		-6.8	1.4E-05	3.6	1.5E-03	-1.2	1.6E-01	-0.2	7.4E-01
ENSMUST00000136258				-1.2	1.2E-01	-1.1	2.4E-01	-0.7	2.3E-01	-0.8	4.0E-01
ENSMUST00000136259				1.2	7.3E-02	2.1	2.2E-02	0.7	2.5E-01	-0.1	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000173283	predicted gene 7221 [Source:MGI Symbol;Acc:MGI:3645327]	L7N2E7		5.3	2.9E-03	4.4	2.7E-02	-0.7	6.7E-01	0.9	4.5E-01
ENSMUST00000136263	8-oxoguanine DNA-glycosylase 1 [Source:MGI Symbol;Acc:MGI:1097693]			-1.1	2.6E-01	-2.8	1.2E-01	0.9	3.0E-01	2.7	1.2E-01
ENSMUST00000173284	ral guanine nucleotide dissociation stimulator-like 2 [Source:MGI Symbol;Acc:MGI:107483]	G3UZ21		-6.9	3.1E-03	0.0	9.9E-01	3.3	4.1E-02	-2.8	2.0E-01
ENSMUST00000173287	ADAMTS-like 3 [Source:MGI Symbol;Acc:MGI:3028499]	G3UXC7		9.1	6.4E-06	6.5	7.6E-04	0.9	4.8E-01	-1.1	1.4E-01
ENSMUST00000173297	SET and MYND domain containing 1 [Source:MGI Symbol;Acc:MGI:104790]	G3UXZ0		7.1	4.1E-05	-0.6	5.4E-01	-0.3	6.6E-01	-2.3	6.9E-02
ENSMUST00000136274	T cell activation inhibitor, mitochondrial [Source:MGI Symbol;Acc:MGI:1196217]	D6RHM0		3.8	8.1E-02	-0.8	6.9E-01	-3.1	1.1E-01	1.4	4.6E-01
ENSMUST00000173328	pre B cell leukemia homeobox 2 [Source:MGI Symbol;Acc:MGI:1341793]	Q3UR63		-6.9	1.2E-04	3.2	2.1E-03	-0.2	7.8E-01	0.0	9.6E-01
ENSMUST00000173329	membrane-associated ring finger (C3HC4) 2 [Source:MGI Symbol;Acc:MGI:1925915]	G3UXU1		2.1	9.7E-03	5.1	4.6E-02	2.3	2.7E-01	1.3	3.5E-01
ENSMUST00000173346	paired box 2 [Source:MGI Symbol;Acc:MGI:97486]	G3UZ20		8.1	2.3E-05	6.6	2.7E-04	-0.5	7.1E-01	-1.6	3.6E-02
ENSMUST00000136282	annexin A2 [Source:MGI Symbol;Acc:MGI:88246]	B0V2N5		-0.4	8.6E-01	2.2	4.6E-01	0.0	9.9E-01	-2.7	2.8E-01
ENSMUST00000173357	negative elongation factor complex member E, Rdbp [Source:MGI Symbol;Acc:MGI:102744]	Q3UIA1	P19426	-3.6	1.2E-02	-2.8	3.2E-01	2.0	2.3E-01	-0.3	9.1E-01
ENSMUST00000173372	myosin IF [Source:MGI Symbol;Acc:MGI:107711]	G3V011		-4.4	1.7E-03	4.1	5.6E-04	-0.9	2.7E-01	1.0	1.1E-01
ENSMUST00000136296	copine I [Source:MGI Symbol;Acc:MGI:2386621]	A3KGK7		1.9	4.1E-01	1.2	7.0E-01	-1.1	6.3E-01	-0.3	9.2E-01
ENSMUST00000136298				-0.5	5.8E-01	1.7	2.2E-01	1.8	1.2E-01	-0.3	7.3E-01
ENSMUST00000173395	oocyte specific homeobox 3 [Source:MGI Symbol;Acc:MGI:2149032]	G3UXQ8		6.2	1.3E-02	5.3	3.6E-04	-0.3	7.3E-01	0.2	7.7E-01
ENSMUST00000173397	dynamin 2 [Source:MGI Symbol;Acc:MGI:109547]	Q3TCR7		-7.3	3.5E-05	6.5	4.6E-03	0.8	6.7E-01	0.4	6.8E-01
ENSMUST00000173420	ADP-ribosyltransferase 2a, pseudogene [Source:MGI Symbol;Acc:MGI:107546]			5.8	2.8E-04	4.4	8.7E-04	-0.6	5.0E-01	-1.3	1.1E-01
ENSMUST00000136310				-1.5	2.8E-01	-0.1	9.3E-01	0.9	5.1E-01	-0.5	7.7E-01
ENSMUST00000173432	homeobox B6 [Source:MGI Symbol;Acc:MGI:96187]		P09023	7.4	1.1E-04	-6.0	2.5E-03	1.0	9.0E-02	1.5	3.4E-01
ENSMUST00000136318				2.9	1.9E-01	5.0	1.0E-01	0.8	7.7E-01	-1.4	4.8E-01
ENSMUST00000173433	bromodomain adjacent to zinc finger domain 1A [Source:MGI Symbol;Acc:MGI:1309478]	G3UWZ0		-9.2	3.3E-05	2.6	9.1E-03	-0.9	2.4E-01	0.5	4.3E-01
ENSMUST00000173441	e (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7) [Source:MGI Symbol;Acc:MGI	G3UZW8		-7.4	1.3E-05	7.0	4.6E-05	1.9	6.0E-02	-1.2	4.2E-02
ENSMUST00000173449	ring finger protein 8 [Source:MGI Symbol;Acc:MGI:1929069]	G3UWU4		5.4	3.3E-04	-1.6	4.6E-01	1.8	1.9E-01	-0.2	9.3E-01
ENSMUST00000136329				-4.4	3.0E-01	-1.5	7.8E-01	1.9	5.4E-01	-0.9	8.7E-01
ENSMUST00000173455	oocyte specific homeobox 5 [Source:MGI Symbol;Acc:MGI:2149035]	G3UZE6		6.0	3.3E-04	-4.8	3.3E-04	-0.3	5.2E-01	-1.9	9.6E-02
ENSMUST00000173456	voltage-dependent anion channel 2 [Source:MGI Symbol;Acc:MGI:106915]	G3UX26		-9.7	3.8E-07	4.8	8.1E-03	-0.5	7.4E-01	0.7	4.5E-01
ENSMUST00000136335				-0.3	8.3E-01	1.1	4.4E-01	-0.3	8.2E-01	-1.6	2.4E-01
ENSMUST00000136339				1.5	8.0E-02	4.7	1.7E-03	2.2	5.3E-02	-1.1	1.6E-01
ENSMUST00000136342	serine/arginine repetitive matrix 1 [Source:MGI Symbol;Acc:MGI:1858303]	E9PUK6		3.0	1.5E-01	0.9	8.0E-01	0.8	7.2E-01	2.9	3.5E-01
ENSMUST00000173459	vomeronasal 2, receptor 34 [Source:MGI Symbol;Acc:MGI:3757700]	E9PVI0		7.6	4.5E-05	-5.2	8.5E-04	-0.9	9.1E-02	1.6	1.5E-01
ENSMUST00000136348	BCL6 co-repressor-like 1 [Source:MGI Symbol;Acc:MGI:2443910]		A2AQH4	-0.5	7.4E-01	-2.6	2.8E-01	0.2	8.9E-01	2.3	2.8E-01
ENSMUST00000173462	sodium channel modifier 1 [Source:MGI Symbol;Acc:MGI:1341284]		Q8K136	-5.3	1.7E-04	-5.8	7.8E-03	1.6	7.0E-02	-2.4	3.2E-01
ENSMUST00000173468	platelet endothelial aggregation receptor 1 [Source:MGI Symbol;Acc:MGI:1920432]	G3UY90		7.0	6.4E-05	3.9	5.6E-03	-0.8	4.3E-01	0.3	6.4E-01
ENSMUST00000173471	E2F transcription factor 7 [Source:MGI Symbol;Acc:MGI:1289147]		Q6S7F2	4.5	1.9E-02	5.0	1.0E-02	1.9	2.4E-01	0.5	5.8E-01
ENSMUST00000136370				0.0	9.7E-01	-0.5	7.5E-01	-0.3	7.8E-01	0.2	9.1E-01
ENSMUST00000173478	lymphocyte antigen 6 complex, locus G6C [Source:MGI Symbol;Acc:MGI:2148930]	Q545T2	Q9Z1Q4	10.3	3.4E-05	-3.6	6.5E-02	0.2	7.9E-01	0.5	7.8E-01
ENSMUST00000136375	RAS protein activator like 3 [Source:MGI Symbol;Acc:MGI:2444128]			1.7	5.0E-01	2.0	5.0E-01	-1.0	7.2E-01	-1.2	6.2E-01
ENSMUST00000136378				1.8	7.1E-02	3.0	1.3E-02	-0.3	7.1E-01	-1.6	8.7E-02
ENSMUST00000173482	steroid receptor RNA activator 1 [Source:MGI Symbol;Acc:MGI:1344414]	G3UZQ4		-8.7	7.4E-07	4.8	1.8E-04	0.6	4.2E-01	1.2	3.6E-02
ENSMUST00000136381	SID1 transmembrane family, member 1 [Source:MGI Symbol;Acc:MGI:2443155]		Q6AXF6	-1.9	2.9E-01	1.4	4.6E-01	-0.1	9.6E-01	-3.4	8.1E-02
ENSMUST00000173494	adenylate kinase 9 [Source:MGI Symbol;Acc:MGI:2685080]	G3UYQ4		6.1	6.9E-06	4.6	2.4E-05	-0.2	6.6E-01	0.0	9.7E-01
ENSMUST00000173506	zinc and ring finger 1 [Source:MGI Symbol;Acc:MGI:2177308]		Q91V17	-6.7	3.5E-05	3.6	2.3E-04	0.1	9.1E-01	-0.6	2.0E-01
ENSMUST00000173514	interleukin 1 receptor-like 1 [Source:MGI Symbol;Acc:MGI:98427]	Q5D095	P14719	4.8	1.1E-03	-3.4	8.0E-02	0.4	6.8E-01	-2.1	3.3E-01
ENSMUST00000173517	adenylate kinase 9 [Source:MGI Symbol;Acc:MGI:2685080]	G3UZ50		5.8	6.6E-04	3.8	2.1E-01	-0.8	8.0E-01	1.6	4.0E-01
ENSMUST00000173530	gastrin releasing peptide [Source:MGI Symbol;Acc:MGI:95833]	V9GX72		5.5	1.1E-02	-2.5	2.4E-01	1.3	2.9E-01	-0.3	8.9E-01
ENSMUST00000173539	delta-like 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:94900]	G3UWU8		5.7	1.6E-03	-0.5	7.3E-01	-2.4	5.6E-02	4.6	4.2E-03
ENSMUST00000173550	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]	G3UZT6		-8.1	5.3E-04	-2.8	6.9E-03	-0.9	8.3E-02	0.6	4.6E-01
ENSMUST00000136410				-2.2	1.3E-01	-2.1	3.8E-01	1.3	3.4E-01	1.1	6.2E-01
ENSMUST00000173574	reproductive homeobox 2C [Source:MGI Symbol;Acc:MGI:3770266]	G3UYU2		5.8	1.3E-03	1.7	5.5E-02	0.8	2.3E-01	0.7	3.4E-01
ENSMUST00000136415	microrchidia 4 [Source:MGI Symbol;Acc:MGI:1922996]	F6WD71		2.6	7.3E-02	6.7	4.6E-04	-0.5	7.1E-01	-4.6	9.2E-04
ENSMUST00000173581	tumor necrosis factor, alpha-induced protein 2 [Source:MGI Symbol;Acc:MGI:104960]	G3UXS6		-2.5	1.6E-02	4.8	2.1E-03	-1.8	1.7E-01	-0.4	5.8E-01
ENSMUST00000173583	RIKEN cDNA 2410141K09 gene [Source:MGI Symbol;Acc:MGI:1924053]	Q8C1L2		11.0	2.7E-05	4.1	1.9E-03	-0.7	4.7E-01	-0.6	4.0E-01
ENSMUST00000136430				5.9	4.0E-02	6.0	4.5E-02	-0.9	7.5E-01	-1.0	5.5E-01
ENSMUST00000173598	chondroadherin-like [Source:MGI Symbol;Acc:MGI:3036284]	G3UXV0		7.1	1.1E-04	-3.3	1.1E-02	1.2	7.1E-02	-1.4	2.3E-01
ENSMUST00000136432	cDNA sequence BC048403 [Source:MGI Symbol;Acc:MGI:2670984]	D3Z5F2		-1.8	1.5E-01	4.2	4.1E-02	4.2	2.6E-02	-1.8	1.8E-01
ENSMUST00000173600	lymphotoxin B [Source:MGI Symbol;Acc:MGI:104796]	G3V002		-8.6	1.8E-06	6.1	4.6E-04	0.5	6.8E-01	-0.2	7.7E-01
ENSMUST00000173618	paired-like homeodomain transcription factor 1 [Source:MGI Symbol;Acc:MGI:107374]	G3UZS0		4.5	3.2E-02	7.6	1.5E-04	-0.2	8.8E-01	-0.4	5.6E-01
ENSMUST00000173620	RIKEN cDNA A930009A15 gene [Source:MGI Symbol;Acc:MGI:1925048]	G3UYI6		5.7	4.5E-04	4.6	1.1E-02	-0.4	8.0E-01	-0.1	8.9E-01
ENSMUST00000173623	even skipped homeotic gene 2 homolog [Source:MGI Symbol;Acc:MGI:95462]		P49749	5.7	6.7E-03	5.4	2.1E-05	0.1	9.1E-01	-0.3	5.2E-01
ENSMUST00000136451	v-raf murine sarcoma 3611 viral oncogene homolog [Source:MGI Symbol;Acc:MGI:88065]	E9Q0P8		-2.4	1.6E-01	-2.6	1.8E-01	-1.2	3.0E-01	-1.0	6.3E-01
ENSMUST00000173628	flotillin 1 [Source:MGI Symbol;Acc:MGI:1100500]	G3XA73		-5.2	1.9E-03	3.4	1.4E-02	-0.1	9.2E-01	0.4	6.7E-01
ENSMUST00000173645	paired-like homeodomain transcription factor 2 [Source:MGI Symbol;Acc:MGI:109340]	G3UZ11		4.8	4.7E-03	5.1	1.2E-02	-1.6	3.5E-01	-0.2	8.4E-01
ENSMUST00000173651	general transcription factor II I [Source:MGI Symbol;Acc:MGI:1202722]	G3UY14		4.7	3.7E-03	6.9	2.0E-04	-0.7	6.0E-01	0.0	9.7E-01
ENSMUST00000173659	LINE-1 type transposase domain containing 1 [Source:MGI Symbol;Acc:MGI:3578435]	G3UYN0		6.7	1.4E-04	-6.4	1.1E-02	1.2	1.2E-01	0.2	9.1E-01
ENSMUST00000136474	phosphoinositide-3-kinase interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917016]	Z4YMN3		-1.2	2.7E-01	0.7	6.7E-01	2.1	9.2E-02	0.2	8.9E-01
ENSMUST00000173660	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2 [Source:MGI Symbol;Acc:MGI:1889505]	G3UWI7		-3.3	1.0E-02	5.0	2.2E-03	-1.2	3.8E-01	-0.7	4.0E-01
ENSMUST00000173665	tripartite motif-containing 39 [Source:MGI Symbol;Acc:MGI:1890659]	G3UX29		6.7	1.6E-03	-10.9	7.8E-04	-1.1	8.9E-02	-1.0	6.8E-01
ENSMUST00000173688	integrin beta 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1306802]	G3UX55		-6.8	1.6E-05	-1.7	1.9E-02	0.3	3.5E-01	-1.5	4.4E-02
ENSMUST00000173713	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]		P63280	-6.3	7.3E-05	4.0	3.0E-03	-2.5	6.1E-02	-0.2	7.5E-01
ENSMUST00000136485				1.9	1.5E-01	4.5	1.9E-02	0.7	6.2E-01	-1.9	1.1E-01
ENSMUST00000136494	Rap guanine nucleotide exchange factor (GEF) 6 [Source:MGI Symbol;Acc:MGI:2384761]	F7ACB1		-0.3	6.0E-01	0.2	7.6E-01	-0.2	7.0E-01	-0.7	2.9E-01
ENSMUST00000136495	eukaryotic translation initiation factor 2B, subunit 2 beta [Source:MGI Symbol;Acc:MGI:2145118]	D3Z487		0.2	9.2E-01	1.2	7.0E-01	0.8	7.2E-01	-0.3	9.3E-01
ENSMUST00000136498				2.8	1.0E-01	3.1	1.7E-01	0.7	7.2E-01	0.4	8.1E-01
ENSMUST00000173726	zinc and ring finger 1 [Source:MGI Symbol;Acc:MGI:2177308]	G3UWY5		-3.8	2.9E-03	0.4	7.5E-01	-2.9	3.0E-02	0.5	6.8E-01
ENSMUST00000136506				-2.7	4.5E-02	-3.2	6.1E-02	-0.7	4.2E-01	-0.1	9.4E-01
ENSMUST00000136507	phosphoserine phosphatase [Source:MGI Symbol;Acc:MGI:97788]	D3Z666		-2.8	4.0E-02	-0.9	4.3E-01	-0.4	6.2E-01	-2.3	9.1E-02
ENSMUST00000173754	DNA segment, Chr 7, ERATO Doi 443, expressed [Source:MGI Symbol;Acc:MGI:1196431]	G3UY66		6.0	7.6E-05	-1.8	8.3E-02	0.7	2.0E-01	-0.5	6.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000136513	N-ethylmaleimide sensitive fusion protein attachment protein beta [Source:MGI Symbol;Acc:MGI:104562]	D6RHL2		3.7	1.3E-01	4.4	8.9E-02	-1.0	6.7E-01	-1.7	4.2E-01
ENSMUST00000173762	jumonji domain containing 1C [Source:MGI Symbol;Acc:MGI:1918614]	G3UZX8		-3.0	2.9E-02	9.2	1.1E-04	-0.8	6.2E-01	-0.4	5.4E-01
ENSMUST00000136523	N-sulfoglucosamine sulfohydrolase (sulfamidase) [Source:MGI Symbol;Acc:MGI:1350341]	G3XA02		-1.4	6.3E-01	4.3	2.5E-01	5.1	1.5E-01	-0.6	8.4E-01
ENSMUST00000173769	cDNA sequence AB124611 [Source:MGI Symbol;Acc:MGI:3043001]	Z4YNA9		-9.6	3.0E-04	-1.8	5.1E-02	0.5	3.2E-01	-1.5	1.1E-01
ENSMUST00000136535				-0.9	3.9E-01	-2.3	1.5E-01	-0.3	7.5E-01	1.1	4.7E-01
ENSMUST00000136536	phosphoinositide-3-kinase interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917016]	Z4YN57		0.0	9.9E-01	-2.4	3.5E-01	-2.8	8.0E-02	-0.4	8.8E-01
ENSMUST00000173772	G-protein signalling modulator 3 (AGS3-like, C. elegans) [Source:MGI Symbol;Acc:MGI:2146785]	G3UYL4		-7.2	2.9E-04	4.5	4.7E-05	-1.1	1.2E-01	-0.5	2.5E-01
ENSMUST00000173824	protein regulator of cytokinesis 1 [Source:MGI Symbol;Acc:MGI:1858961]	G3UY19		-5.6	8.9E-03	-1.1	4.1E-01	0.9	3.1E-01	-1.5	2.7E-01
ENSMUST00000173828	ADAMTS-like 3 [Source:MGI Symbol;Acc:MGI:3028499]	G3UWL5		5.5	4.7E-03	2.4	4.8E-02	-0.6	5.2E-01	0.2	8.2E-01
ENSMUST00000136550				-1.1	2.9E-01	-0.3	8.2E-01	1.2	2.4E-01	0.4	7.3E-01
ENSMUST00000173830	protein kinase N2 [Source:MGI Symbol;Acc:MGI:109211]	G3UXH4		-3.4	1.3E-02	5.9	1.6E-05	-1.0	2.1E-01	-0.6	1.6E-01
ENSMUST00000136558				0.9	5.5E-01	0.6	7.3E-01	-0.5	7.6E-01	-0.2	9.1E-01
ENSMUST00000173833	a disintegrin and metallopeptidase domain 18 [Source:MGI Symbol;Acc:MGI:105986]	G3UWP9		4.7	5.9E-03	4.9	2.0E-03	-0.8	5.0E-01	0.4	5.5E-01
ENSMUST00000136562				1.9	1.4E-01	3.8	4.7E-02	0.8	6.0E-01	-1.0	3.8E-01
ENSMUST00000173844	ribosomal protein S28 [Source:MGI Symbol;Acc:MGI:1859516]	Q059I1	P62858	-6.7	5.5E-04	4.3	2.3E-02	-1.7	3.4E-01	0.3	7.8E-01
ENSMUST00000173846	abhydrolase domain containing 16A [Source:MGI Symbol;Acc:MGI:99476]	G3UX11		-4.0	6.6E-03	6.0	5.2E-04	-0.6	6.1E-01	0.9	1.8E-01
ENSMUST00000173860	RAB11B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:99425]	G3UZD3		-4.5	5.8E-03	6.1	3.5E-03	-0.7	6.7E-01	-0.4	6.3E-01
ENSMUST00000173867	chaperonin containing Tcp1, subunit 4 (delta) [Source:MGI Symbol;Acc:MGI:104689]	Q564F4	P80315	-5.4	1.8E-04	7.8	7.7E-05	-0.6	6.3E-01	0.0	1.0E+00
ENSMUST00000173869	angiopoietin-like 4 [Source:MGI Symbol;Acc:MGI:1888999]	G3UWT7		2.3	3.2E-02	-5.9	2.3E-04	0.6	1.7E-01	-2.4	7.0E-02
ENSMUST00000173874	decapping exoribonuclease [Source:MGI Symbol;Acc:MGI:1890444]	G3UZ39		6.5	4.4E-03	2.8	1.0E-02	-0.3	7.2E-01	0.4	5.1E-01
ENSMUST00000136587				-1.1	6.7E-01	-1.2	7.0E-01	-0.5	7.9E-01	-0.4	9.1E-01
ENSMUST00000136590				-5.4	5.0E-02	1.7	6.1E-01	6.3	1.6E-02	-0.8	8.1E-01
ENSMUST00000173878	RNA binding motif protein 38 [Source:MGI Symbol;Acc:MGI:1889294]	G3UWQ8		-2.3	2.2E-02	-3.6	1.4E-02	-0.5	4.8E-01	0.6	6.6E-01
ENSMUST00000173903	coiled-coil alpha-helical rod protein 1 [Source:MGI Symbol;Acc:MGI:2385321]	G3UWS7		8.0	2.2E-05	2.8	2.7E-03	0.4	5.4E-01	-0.8	1.9E-01
ENSMUST00000173912	oocyte specific homeobox 3 [Source:MGI Symbol;Acc:MGI:2149032]	Q3UT54		6.5	1.1E-04	-1.9	4.0E-01	3.9	1.3E-02	-1.3	5.4E-01
ENSMUST00000136605				-0.7	4.5E-01	-0.1	9.2E-01	0.3	7.5E-01	-0.3	8.0E-01
ENSMUST00000173916	trypsin 5 [Source:MGI Symbol;Acc:MGI:102756]	G3UXD0		7.9	1.3E-03	4.4	8.5E-03	-1.0	4.6E-01	0.0	9.7E-01
ENSMUST00000173922	zinc and ring finger 1 [Source:MGI Symbol;Acc:MGI:2177308]	G3UZ70		-4.6	9.5E-04	2.6	5.3E-01	-0.7	8.5E-01	4.1	2.0E-01
ENSMUST00000173930	mitogen-activated protein kinase kinase kinase 8 [Source:MGI Symbol;Acc:MGI:1346878]	G3UWY2		-5.3	4.9E-03	6.9	4.4E-04	-0.2	8.9E-01	-0.1	8.6E-01
ENSMUST00000173931	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10 [Source:MGI Symbol;Acc:M	G3UZ08		-3.5	3.4E-02	-6.5	4.2E-04	0.1	8.7E-01	-0.3	8.4E-01
ENSMUST00000173934	POU domain, class 5, transcription factor 1 [Source:MGI Symbol;Acc:MGI:101893]	E2JL30		6.8	5.7E-05	4.9	2.1E-03	-1.5	2.7E-01	0.9	2.6E-01
ENSMUST00000173938	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 [Source:MGI Symbol;Acc:MGI:1916327]	Q5BKQ9	Q8BG32	-4.8	7.2E-04	4.9	9.0E-04	1.2	2.2E-01	-0.6	4.0E-01
ENSMUST00000173954	zinc finger, MYM-type 5 [Source:MGI Symbol;Acc:MGI:3041170]		Q3U2E2	-7.2	1.3E-05	5.0	1.3E-04	-0.5	5.2E-01	0.1	8.2E-01
ENSMUST00000173979	RNA binding motif protein 38 [Source:MGI Symbol;Acc:MGI:1889294]	G3UXG4		-5.0	4.1E-03	-4.8	3.9E-02	-1.3	1.8E-01	-0.8	7.2E-01
ENSMUST00000136640	FCH domain only 1 [Source:MGI Symbol;Acc:MGI:1921265]	D6RCG0		-1.7	2.3E-01	1.8	3.1E-01	1.6	2.9E-01	-1.9	2.1E-01
ENSMUST00000136644				2.6	2.3E-01	2.8	2.0E-01	-0.5	8.2E-01	-0.7	6.8E-01
ENSMUST00000136646	arginine glutamic acid dipeptide (RE) repeats [Source:MGI Symbol;Acc:MGI:2683486]	A2A7T1		-2.0	1.5E-01	-1.4	4.3E-01	0.9	4.0E-01	0.4	8.2E-01
ENSMUST00000173985	gastrin releasing peptide [Source:MGI Symbol;Acc:MGI:95833]		Q8R1I2	6.4	1.1E-03	7.1	2.3E-05	-1.3	1.9E-01	-0.1	7.7E-01
ENSMUST00000173990	large tumor suppressor 2 [Source:MGI Symbol;Acc:MGI:1354386]	G3UY78		3.7	5.1E-04	5.2	4.6E-03	-0.1	9.2E-01	1.7	9.7E-02
ENSMUST00000174000	glycophorin C [Source:MGI Symbol;Acc:MGI:1098566]	G3UXY6		-3.3	3.3E-02	6.7	3.2E-03	2.0	2.3E-01	0.3	7.1E-01
ENSMUST00000174004	RIKEN cDNA 1600012H06 gene [Source:MGI Symbol;Acc:MGI:1915162]		Q9DAY5	-5.4	2.2E-03	-0.2	8.8E-01	-0.1	8.9E-01	-3.0	4.0E-02
ENSMUST00000174008	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 [Source:MGI Symbol;Ac		Q3TKT4	-7.5	1.1E-05	8.4	4.6E-03	2.5	2.7E-01	-0.5	7.0E-01
ENSMUST00000136663	misshapen-like kinase 1 (zebrafish) [Source:MGI Symbol;Acc:MGI:1355329]	F7AMS7		-1.9	2.0E-01	-2.4	3.9E-01	2.1	1.5E-01	2.6	3.3E-01
ENSMUST00000136664				1.7	3.6E-01	4.0	1.1E-01	-0.1	9.7E-01	-2.4	1.8E-01
ENSMUST00000174018	glutamate receptor, metabotropic 7 [Source:MGI Symbol;Acc:MGI:1351344]	G3UZU3		6.2	3.5E-03	-3.7	6.2E-02	-1.0	2.5E-01	-1.9	3.8E-01
ENSMUST00000174030	cytosolic iron-sulfur protein assembly 1 [Source:MGI Symbol;Acc:MGI:1346998]	G3UYR5		-5.7	6.7E-05	3.8	1.2E-01	-4.0	1.3E-01	0.0	9.8E-01
ENSMUST00000136676				-2.3	4.4E-01	-1.3	7.2E-01	0.5	8.2E-01	-0.5	9.0E-01
ENSMUST00000136678				-0.6	6.0E-01	-0.9	5.9E-01	0.6	6.1E-01	0.9	5.6E-01
ENSMUST00000174031	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]		P63280	-6.4	5.8E-05	3.0	5.4E-03	-0.5	5.5E-01	-0.3	5.9E-01
ENSMUST00000136681				1.2	2.1E-01	1.4	2.1E-01	0.0	9.9E-01	-0.2	8.2E-01
ENSMUST00000174038	cyclin B1 [Source:MGI Symbol;Acc:MGI:88302]	G3UY65		-5.8	1.1E-04	4.7	5.1E-04	-0.3	7.5E-01	-0.2	7.6E-01
ENSMUST00000174040	membrane-associated ring finger (C3HC4) 2 [Source:MGI Symbol;Acc:MGI:1925915]	G3UZC4		-2.9	1.9E-02	1.7	1.0E-01	-0.8	3.3E-01	0.7	4.1E-01
ENSMUST00000136688				-0.3	8.7E-01	-1.0	7.1E-01	-1.0	6.0E-01	-0.3	8.9E-01
ENSMUST00000174041	ol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) [Source:MGI Symbol;Acc:M	G3UWV6		3.6	5.3E-03	6.0	6.6E-05	-0.7	4.6E-01	-1.0	1.0E-01
ENSMUST00000174042	homeobox B9 [Source:MGI Symbol;Acc:MGI:96190]	Q496Q8		7.8	1.2E-04	7.5	4.8E-05	-0.6	5.8E-01	0.2	6.6E-01
ENSMUST00000174048	prefoldin subunit 6 [Source:MGI Symbol;Acc:MGI:95908]	Q792E4	Q03958	-5.7	1.1E-04	-0.9	4.8E-01	0.7	3.9E-01	-2.4	1.1E-01
ENSMUST00000136703				3.0	1.8E-01	-0.1	9.7E-01	-0.5	8.6E-01	2.6	3.8E-01
ENSMUST00000136706				0.6	3.4E-01	1.9	3.1E-02	0.6	3.3E-01	-0.7	2.9E-01
ENSMUST00000174051	protein regulator of cytokinesis 1 [Source:MGI Symbol;Acc:MGI:1858961]	G3UYX6		4.3	2.4E-02	6.8	1.6E-04	0.4	7.1E-01	-0.3	6.3E-01
ENSMUST00000174056	double homeobox family member 3 [Source:MGI Symbol;Acc:MGI:1921649]	G3UY18		13.5	1.2E-05	-3.6	6.2E-02	0.8	3.0E-01	-0.5	8.1E-01
ENSMUST00000174063	histocompatibility 2, T region locus 24 [Source:MGI Symbol;Acc:MGI:95958]	G3UWY8		7.0	1.8E-04	6.1	8.9E-04	-0.4	7.5E-01	0.5	4.8E-01
ENSMUST00000174064	apolipoprotein E [Source:MGI Symbol;Acc:MGI:88057]	Q3TXU4	P08226	-3.6	2.3E-03	-5.8	5.5E-04	0.1	8.8E-01	-0.5	6.8E-01
ENSMUST00000174072	transmembrane protein 229B [Source:MGI Symbol;Acc:MGI:2444389]		Q8BFQ2	-4.6	8.5E-03	6.9	6.6E-04	-1.2	4.5E-01	0.5	5.4E-01
ENSMUST00000174078	intermediate filament family orphan 2 [Source:MGI Symbol;Acc:MGI:2140675]		Q8R2V2	2.7	1.1E-02	5.5	1.6E-03	-1.3	3.4E-01	-0.4	6.3E-01
ENSMUST00000136740	myosin IXa [Source:MGI Symbol;Acc:MGI:107735]	D3Z3A8		4.6	2.0E-01	5.9	1.3E-01	-0.6	8.7E-01	-1.9	4.1E-01
ENSMUST00000136743	mitogen-activated protein kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346867]	D3Z446		1.0	6.3E-01	3.1	2.4E-01	0.2	9.1E-01	-1.8	4.2E-01
ENSMUST00000136746				1.7	8.4E-02	0.0	9.7E-01	-1.7	7.7E-02	0.0	9.8E-01
ENSMUST00000136748	rhomboid domain containing 2 [Source:MGI Symbol;Acc:MGI:1915612]	D6RCZ4		3.0	2.3E-01	3.0	3.6E-01	-0.2	9.4E-01	-0.3	9.1E-01
ENSMUST00000174143	predicted gene 11128 [Source:MGI Symbol;Acc:MGI:3779382]		Q9JIY8	10.2	3.6E-06	9.2	1.1E-05	-0.6	5.9E-01	-0.5	3.2E-01
ENSMUST00000174146	Fas death domain-associated protein [Source:MGI Symbol;Acc:MGI:1197015]	Q3UKR0		-6.8	4.0E-03	-5.8	1.3E-04	-2.8	1.3E-04	-0.9	3.7E-01
ENSMUST00000174189	tet methylcytosine dioxygenase 1 [Source:MGI Symbol;Acc:MGI:1098693]	E9Q9Y4		10.2	4.1E-05	-3.2	1.5E-02	0.3	5.9E-01	-0.2	8.8E-01
ENSMUST00000174192	kelch domain containing 4 [Source:MGI Symbol;Acc:MGI:2384569]	G3UZG5		-4.8	1.5E-03	5.5	7.9E-04	-0.5	6.6E-01	-2.3	1.5E-02
ENSMUST00000174193	myelin-associated oligodendrocytic basic protein [Source:MGI Symbol;Acc:MGI:108511]		Q9D2P8	6.7	2.1E-04	6.1	4.2E-04	-0.9	4.7E-01	-0.6	3.9E-01
ENSMUST00000174202	interleukin 1 receptor accessory protein [Source:MGI Symbol;Acc:MGI:104975]	Q3UEL3	Q61730	-3.4	3.8E-04	6.7	5.8E-04	-0.2	9.1E-01	-0.2	8.3E-01
ENSMUST00000174205	myotubularin related protein 7 [Source:MGI Symbol;Acc:MGI:1891693]	G3V027		6.1	7.5E-05	7.8	1.1E-04	-1.3	3.6E-01	-0.8	2.1E-01
ENSMUST00000174213	large tumor suppressor 2 [Source:MGI Symbol;Acc:MGI:1354386]	G3UZ29		6.0	1.7E-03	-2.8	2.5E-02	0.2	7.2E-01	-1.7	1.9E-01
ENSMUST00000136774				1.6	1.9E-01	2.6	1.6E-01	0.6	7.1E-01	-0.4	7.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000136775				2.5	1.6E-01	5.1	1.1E-02	-0.6	7.5E-01	-3.2	3.2E-02
ENSMUST00000174236	glucosaminyl (N-acetyl) transferase 1, core 2 [Source:MGI Symbol;Acc:MGI:95676]		Q09324	-8.0	4.1E-04	3.7	1.4E-01	-3.4	2.2E-01	1.1	4.7E-01
ENSMUST00000174251	paired-like homeobox 2b [Source:MGI Symbol;Acc:MGI:1100882]	Q8C741		6.2	2.7E-04	5.7	3.1E-02	-0.2	9.3E-01	-0.3	8.2E-01
ENSMUST00000174257	H2.0-like homeobox [Source:MGI Symbol;Acc:MGI:96109]	G3V024		-5.7	2.8E-02	-1.4	3.8E-01	1.3	2.2E-01	-0.5	7.6E-01
ENSMUST00000174259	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) [Source:MGI Symbol;Acc:MGI:1096367]	Q5HZK3	P97371	-7.5	5.3E-05	-5.9	3.2E-02	0.3	7.9E-01	-1.7	5.7E-01
ENSMUST00000174260	valyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:90675]	G3UZ22		2.6	2.2E-02	6.7	2.2E-03	-0.1	9.6E-01	0.7	4.9E-01
ENSMUST00000136799				1.4	9.9E-02	1.8	1.0E-01	0.2	7.7E-01	-0.1	8.8E-01
ENSMUST00000136800				-1.1	6.0E-01	-2.2	3.7E-01	-2.0	2.4E-01	-0.9	7.1E-01
ENSMUST00000136801				-2.4	1.1E-01	-3.1	1.7E-01	-0.1	9.5E-01	0.7	7.5E-01
ENSMUST00000174265	protein tyrosine phosphatase, non-receptor type 6 [Source:MGI Symbol;Acc:MGI:96055]		P29351	-9.0	3.9E-06	5.0	6.4E-04	-1.1	2.7E-01	-0.4	6.1E-01
ENSMUST00000174266	UDP-glucose glycoprotein glucosyltransferase 1 [Source:MGI Symbol;Acc:MGI:2443162]	G3UZU8		-8.2	7.2E-06	-3.5	2.5E-03	-0.3	5.4E-01	-2.4	5.3E-02
ENSMUST00000174267	platelet endothelial aggregation receptor 1 [Source:MGI Symbol;Acc:MGI:1920432]	G3UXB8		5.2	3.2E-03	5.9	1.1E-03	-0.4	7.5E-01	-0.7	3.9E-01
ENSMUST00000174278	dCMP deaminase [Source:MGI Symbol;Acc:MGI:2444529]	G3X908		4.6	5.4E-03	4.1	2.5E-03	-2.2	7.0E-02	0.8	2.7E-01
ENSMUST00000174282	synaptotagmin binding, cytoplasmic RNA interacting protein [Source:MGI Symbol;Acc:MGI:1891690]			-5.6	3.7E-05	4.0	5.6E-04	0.5	4.8E-01	-0.3	5.6E-01
ENSMUST00000174294	cytochrome b5 reductase 4 [Source:MGI Symbol;Acc:MGI:2386848]	G3UY26		-6.9	2.0E-05	3.5	4.1E-04	-0.9	1.5E-01	-0.2	6.8E-01
ENSMUST00000174306	casein kinase 2, beta polypeptide [Source:MGI Symbol;Acc:MGI:88548]	G3UZA4		-4.1	1.3E-03	8.0	1.1E-04	-0.5	7.2E-01	-1.0	1.3E-01
ENSMUST00000136822	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 [Source:MGI Symbol;Acc:MGI:2142841]		Q8VI16	3.4	1.4E-01	4.1	1.4E-01	-0.9	7.2E-01	-1.7	3.7E-01
ENSMUST00000174313	slit homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1315205]	G3UY21		5.7	9.8E-04	7.1	4.2E-04	3.4	2.1E-02	-1.0	2.0E-01
ENSMUST00000136838				1.8	2.0E-01	3.4	8.0E-02	0.2	9.2E-01	-1.4	2.8E-01
ENSMUST00000174318	cone-rod homeobox [Source:MGI Symbol;Acc:MGI:1194883]	A0A0A0MQN6		6.0	6.8E-05	-4.9	4.8E-04	-0.6	1.8E-01	-1.0	3.6E-01
ENSMUST00000174354	general transcription factor II I [Source:MGI Symbol;Acc:MGI:1202722]		Q9ESZ8	-4.3	1.0E-02	4.7	5.1E-03	0.3	8.1E-01	-0.2	8.2E-01
ENSMUST00000174355	apolipoprotein E [Source:MGI Symbol;Acc:MGI:88057]	Q3TXU4	P08226	-9.1	2.4E-06	8.1	4.2E-03	-0.7	7.9E-01	-3.4	2.4E-02
ENSMUST00000174368	vomeronasal 2, receptor 30 [Source:MGI Symbol;Acc:MGI:1316729]	G3UYU1		8.5	3.9E-05	-1.6	2.8E-01	1.5	1.0E-01	-0.5	7.5E-01
ENSMUST00000174370	cilia and flagella associated protein 221 [Source:MGI Symbol;Acc:MGI:2684947]		A9Q751	5.4	3.0E-02	6.5	7.2E-04	1.7	1.9E-01	-1.0	2.0E-01
ENSMUST00000174382	histocompatibility 2, T region locus 10 [Source:MGI Symbol;Acc:MGI:95942]			-4.9	1.4E-03	7.2	1.1E-04	-0.5	6.5E-01	-1.5	3.8E-02
ENSMUST00000174387	ubiquitin specific peptidase 3 [Source:MGI Symbol;Acc:MGI:2152450]	G3UZF0		-6.7	2.7E-03	-4.7	4.0E-03	-0.3	6.1E-01	0.6	6.5E-01
ENSMUST00000136863				-0.4	6.3E-01	-0.8	4.0E-01	-0.2	7.4E-01	0.2	7.9E-01
ENSMUST00000174388	vomeronasal 2, receptor 39 [Source:MGI Symbol;Acc:MGI:3704108]	L7N2E5		7.3	1.3E-04	6.8	2.0E-03	0.5	7.5E-01	-0.3	7.9E-01
ENSMUST00000174395	sterile alpha motif domain containing 7 [Source:MGI Symbol;Acc:MGI:1923203]	G3UXH0		7.7	1.5E-05	-4.3	1.4E-02	0.0	9.9E-01	1.2	4.1E-01
ENSMUST00000174397	paired related homeobox 1 [Source:MGI Symbol;Acc:MGI:97712]	G3UZ44		6.8	1.2E-05	6.9	9.9E-05	-0.6	6.2E-01	-1.0	1.1E-01
ENSMUST00000136878				1.8	4.3E-02	0.4	6.5E-01	-0.6	4.3E-01	0.8	3.9E-01
ENSMUST00000174408	jumonji domain containing 1C [Source:MGI Symbol;Acc:MGI:1918614]	G3UZM1		-8.3	1.0E-03	8.8	1.8E-02	-0.9	8.1E-01	-1.7	3.0E-01
ENSMUST00000174411	SMAD family member 7 [Source:MGI Symbol;Acc:MGI:1100518]	G3UXH8		3.7	1.2E-02	6.1	5.3E-05	1.0	2.4E-01	-0.2	7.0E-01
ENSMUST00000174433	predicted gene 10302 [Source:MGI Symbol;Acc:MGI:3704281]	K7N709		9.4	4.9E-05	4.9	2.9E-05	-0.3	6.5E-01	-0.5	2.4E-01
ENSMUST00000174439	coronin, actin binding protein, 2B [Source:MGI Symbol;Acc:MGI:2444283]	G3UYG8		5.1	1.8E-04	6.5	1.9E-04	3.7	4.6E-03	-1.2	8.3E-02
ENSMUST00000174443	oocyte specific homeobox 3 [Source:MGI Symbol;Acc:MGI:2149032]	Q3UT54		7.4	1.3E-02	4.6	1.1E-02	1.2	3.8E-01	-0.6	5.0E-01
ENSMUST00000174455	solute carrier organic anion transporter family, member 1a6 [Source:MGI Symbol;Acc:MGI:1351906]			6.9	1.8E-04	2.3	8.5E-03	-4.0	1.3E-03	0.2	7.4E-01
ENSMUST00000174477	heterogeneous nuclear ribonucleoprotein L [Source:MGI Symbol;Acc:MGI:104816]	G5E924		-3.2	9.0E-04	-2.5	3.3E-01	2.8	7.1E-02	-2.1	4.7E-01
ENSMUST00000174479	dystrobrevin, beta [Source:MGI Symbol;Acc:MGI:1203728]	G3UXI3		7.8	2.6E-07	4.7	2.8E-03	-0.5	6.9E-01	0.5	4.6E-01
ENSMUST00000174490	paired box 2 [Source:MGI Symbol;Acc:MGI:97486]			6.6	1.9E-05	5.6	1.9E-03	0.3	8.3E-01	-0.9	2.8E-01
ENSMUST00000174499	BR serine/threonine kinase 2 [Source:MGI Symbol;Acc:MGI:1923020]		Q69Z98	9.9	1.6E-05	6.5	2.8E-04	-1.2	3.7E-01	0.3	6.6E-01
ENSMUST00000174510	ubiquitin-conjugating enzyme E2G 2 [Source:MGI Symbol;Acc:MGI:1343188]	Q3U431	P60605	-2.9	1.3E-03	5.9	1.6E-03	-1.4	3.7E-01	-0.4	6.6E-01
ENSMUST00000174512	zinc finger protein 101 [Source:MGI Symbol;Acc:MGI:107547]	G3UXY5		5.3	1.2E-06	6.5	6.4E-05	-0.6	5.1E-01	-0.1	9.1E-01
ENSMUST00000174518	aldehyde dehydrogenase family 7, member A1 [Source:MGI Symbol;Acc:MGI:108186]		Q9DBF1	7.6	2.3E-05	-1.3	5.8E-01	5.6	1.7E-03	-1.8	4.4E-01
ENSMUST00000136937				0.7	2.7E-01	1.0	2.1E-01	-0.2	7.1E-01	-0.5	4.6E-01
ENSMUST00000174521	surfactant associated 2 [Source:MGI Symbol;Acc:MGI:3643293]	G3UYT9		9.0	2.8E-05	-7.7	7.5E-04	-0.3	5.6E-01	-0.4	8.3E-01
ENSMUST00000136942				1.1	6.3E-01	2.5	4.5E-01	1.4	6.2E-01	0.0	9.9E-01
ENSMUST00000174524	zinc finger protein 57 [Source:MGI Symbol;Acc:MGI:99204]		Q8C6P8	5.3	1.4E-02	5.1	1.4E-03	-2.2	1.1E-01	-0.4	5.4E-01
ENSMUST00000174545	exportin 4 [Source:MGI Symbol;Acc:MGI:1888526]			1.2	3.5E-02	1.0	4.1E-01	-3.3	1.9E-02	-0.1	9.5E-01
ENSMUST00000174552	DIP2 disco-interacting protein 2 homolog C (Drosophila) [Source:MGI Symbol;Acc:MGI:1920179]	B2RQ71		2.6	1.4E-03	6.8	5.5E-04	-0.4	7.8E-01	-0.1	9.3E-01
ENSMUST00000136959				0.1	8.9E-01	0.1	9.3E-01	-0.4	6.8E-01	-0.4	7.3E-01
ENSMUST00000174558	predicted gene 2381 [Source:MGI Symbol;Acc:MGI:3780549]	G3UY53		5.4	4.7E-04	-2.5	1.0E-01	1.1	2.1E-01	-3.8	5.7E-02
ENSMUST00000174561	H2A histone family, member Z [Source:MGI Symbol;Acc:MGI:1888388]	Q3UA95		-6.1	2.5E-05	-1.6	3.2E-02	1.3	8.9E-03	0.1	9.2E-01
ENSMUST00000174563	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) [Source:MGI Symbol;Acc:MGI:1096367]	G3UWN9		-7.7	1.0E-05	5.9	1.1E-03	-1.5	3.0E-01	-1.5	7.7E-02
ENSMUST00000174571	death associated protein 3 [Source:MGI Symbol;Acc:MGI:1929538]	G3UWM7		-5.4	5.0E-05	4.7	7.7E-04	0.2	8.3E-01	-0.6	4.1E-01
ENSMUST00000174576	e (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) [Source:MGI Symbol;Acc:MGI			-6.2	4.7E-06	-5.7	4.4E-02	0.9	3.6E-01	2.0	4.3E-01
ENSMUST00000174586	polypyrimidine tract binding protein 3 [Source:MGI Symbol;Acc:MGI:1923334]	G3UXA6		-6.0	5.5E-05	8.9	7.9E-05	-0.2	8.6E-01	1.0	1.6E-01
ENSMUST00000136974				0.8	3.7E-01	1.9	1.5E-01	1.5	1.9E-01	0.3	7.1E-01
ENSMUST00000136976				-0.8	6.1E-01	-2.3	4.0E-01	0.3	8.7E-01	1.8	4.6E-01
ENSMUST00000174595	ol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) [Source:MGI Symbol;Acc:M			-4.4	5.4E-03	2.0	5.1E-02	0.4	6.4E-01	0.8	2.9E-01
ENSMUST00000174609	ribosomal protein S18 [Source:MGI Symbol;Acc:MGI:98146]	S4R1N6		-7.9	1.1E-04	3.5	5.0E-04	0.3	6.3E-01	0.0	9.9E-01
ENSMUST00000174641	Rho GTPase activating protein 32 [Source:MGI Symbol;Acc:MGI:2450166]		Q811P8	8.8	4.2E-05	3.6	8.6E-03	2.0	6.3E-02	0.1	8.7E-01
ENSMUST00000136985				-1.4	7.5E-02	-2.7	5.4E-02	0.6	3.5E-01	1.9	1.3E-01
ENSMUST00000136993				-2.3	3.5E-01	-4.7	1.2E-01	-3.2	6.0E-02	-0.8	7.9E-01
ENSMUST00000136997				-1.2	2.9E-01	-0.3	8.3E-01	0.6	6.0E-01	-0.3	8.0E-01
ENSMUST00000174681	paired box 7 [Source:MGI Symbol;Acc:MGI:97491]	G3UX36		5.0	1.3E-02	3.0	1.9E-03	-0.8	2.1E-01	0.8	1.8E-01
ENSMUST00000174697	transmembrane protein 229B [Source:MGI Symbol;Acc:MGI:2444389]		Q8BFQ2	9.0	1.1E-05	5.7	1.1E-03	0.6	6.4E-01	-0.6	4.3E-01
ENSMUST00000174699	histocompatibility 2, Q region locus 6 [Source:MGI Symbol;Acc:MGI:95935]	P79568		2.5	2.2E-03	2.3	7.8E-03	0.0	9.5E-01	0.9	1.5E-01
ENSMUST00000174711	protein phosphatase 1, regulatory (inhibitor) subunit 11 [Source:MGI Symbol;Acc:MGI:1923747]	A5A4Y9		-6.1	1.0E-04	6.9	3.3E-05	0.1	9.3E-01	0.5	3.0E-01
ENSMUST00000174731	5'-nucleotidase, cytosolic II [Source:MGI Symbol;Acc:MGI:2178563]	G3UZQ5		-6.8	3.7E-05	3.2	1.6E-01	-0.8	7.1E-01	2.1	1.9E-01
ENSMUST00000174734	lysine (K)-specific methyltransferase 2C [Source:MGI Symbol;Acc:MGI:2444959]	G3UWZ3		-1.9	3.0E-02	3.8	4.0E-03	-1.1	2.8E-01	-1.1	2.0E-01
ENSMUST00000137032				-2.3	2.5E-01	0.1	9.8E-01	1.0	5.5E-01	-1.4	5.4E-01
ENSMUST00000137033	G1 to S phase transition 2 [Source:MGI Symbol;Acc:MGI:1316727]	Q8BQF5		-1.1	2.4E-01	-0.1	9.4E-01	0.7	4.3E-01	-0.3	7.8E-01
ENSMUST00000137035	ST3 beta-galactoside alpha-2,3-sialyltransferase 6 [Source:MGI Symbol;Acc:MGI:1888707]		Q8VIB3	-0.1	9.0E-01	1.4	2.5E-01	-0.7	4.7E-01	-2.2	6.1E-02
ENSMUST00000174757	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B [Source:MGI Symbol;Acc:MGI:99240]	G3UXI6		-2.1	2.7E-02	4.6	2.8E-03	-1.8	1.7E-01	-2.4	1.2E-02
ENSMUST00000174780	zinc finger and BTB domain containing 42 [Source:MGI Symbol;Acc:MGI:3644133]	G3UYC4		-4.5	1.1E-02	6.6	1.7E-04	-0.5	6.8E-01	-0.4	5.0E-01
ENSMUST00000174786	tRNA methyltransferase 11-2 [Source:MGI Symbol;Acc:MGI:1914924]	Q8VCR4		-3.0	3.9E-03	6.6	8.0E-03	-0.8	7.1E-01	-1.9	1.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000174792	UNC homeobox [Source:MGI Symbol;Acc:MGI:108013]	V9GXC0		6.5	1.0E-03	7.5	4.0E-04	-0.7	6.4E-01	-0.7	3.5E-01
ENSMUST00000137050				4.7	1.1E-01	2.3	3.8E-01	-2.8	3.3E-01	-0.4	8.4E-01
ENSMUST00000174799	CDK2-associated protein 2 [Source:MGI Symbol;Acc:MGI:1098779]	G3UX88		-8.1	3.3E-04	7.2	1.1E-04	1.1	3.3E-01	-0.2	6.8E-01
ENSMUST00000137052				-1.2	9.9E-02	-2.7	5.2E-02	0.5	4.5E-01	2.0	1.2E-01
ENSMUST00000174818	dCMP deaminase [Source:MGI Symbol;Acc:MGI:2444529]	Q3UUA6		5.5	1.2E-03	3.1	2.5E-02	-0.1	9.3E-01	0.4	6.5E-01
ENSMUST00000174830	chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 [Source:MGI Symbol;Acc:M	G3UWU1		9.4	3.0E-04	5.6	1.3E-06	-1.5	1.5E-02	-0.2	5.9E-01
ENSMUST00000137064	AU RNA binding protein/enoyl-coenzyme A hydratase [Source:MGI Symbol;Acc:MGI:1338011]	F6RT60		-1.1	2.6E-01	-0.5	6.5E-01	-0.3	7.1E-01	-0.9	4.1E-01
ENSMUST00000174840	tumor necrosis factor (ligand) superfamily, member 10 [Source:MGI Symbol;Acc:MGI:107414]	G3UY25		6.6	3.6E-04	5.4	2.9E-04	-1.7	1.3E-01	0.1	9.0E-01
ENSMUST00000174857	E2F transcription factor 7 [Source:MGI Symbol;Acc:MGI:1289147]	Q8BQ55		6.5	2.4E-07	5.8	7.6E-04	-1.7	1.9E-01	1.4	5.9E-02
ENSMUST00000137074	selenocysteine lyase [Source:MGI Symbol;Acc:MGI:1355310]	F7D651		0.6	4.3E-01	1.9	8.2E-02	0.8	3.3E-01	-0.4	6.0E-01
ENSMUST00000174874	cordon-bleu WH2 repeat [Source:MGI Symbol;Acc:MGI:105056]	G3UWY3		8.4	2.2E-03	5.8	7.0E-05	-0.9	2.9E-01	0.0	9.6E-01
ENSMUST00000137078	homeodomain interacting protein kinase 1 [Source:MGI Symbol;Acc:MGI:1314873]			0.0	9.7E-01	1.9	1.3E-01	0.3	7.3E-01	-1.5	2.2E-01
ENSMUST00000174882	heterogeneous nuclear ribonucleoprotein L [Source:MGI Symbol;Acc:MGI:104816]	G3UY56		-8.3	2.9E-04	7.3	3.2E-04	-0.7	6.2E-01	-0.2	7.1E-01
ENSMUST00000174890	eukaryotic translation elongation factor 1 beta 2 [Source:MGI Symbol;Acc:MGI:1929520]	G3UX43		-7.3	8.9E-05	-0.9	7.2E-01	3.0	9.4E-02	-0.4	8.7E-01
ENSMUST00000175646	alkylglycerone phosphate synthase [Source:MGI Symbol;Acc:MGI:2443065]	H3BKN2		-3.7	3.2E-03	6.5	3.4E-04	1.3	2.6E-01	0.7	3.0E-01
ENSMUST00000175665	glypican 5 [Source:MGI Symbol;Acc:MGI:1194894]	H3BLN8		6.7	7.6E-04	7.0	8.7E-05	-0.5	6.6E-01	-0.1	8.1E-01
ENSMUST00000137090	transmembrane protein 234 [Source:MGI Symbol;Acc:MGI:1924049]	D6RDC0		0.5	5.2E-01	0.5	6.5E-01	0.2	7.9E-01	0.3	7.5E-01
ENSMUST00000175669	FERM domain containing 4A [Source:MGI Symbol;Acc:MGI:1919850]	H3BK97		8.0	2.3E-04	2.1	1.2E-01	-0.2	8.7E-01	0.4	7.2E-01
ENSMUST00000137095				-2.5	4.1E-02	-2.9	8.1E-02	0.5	6.1E-01	0.9	5.6E-01
ENSMUST00000137104				-1.1	2.7E-01	-0.1	9.6E-01	0.8	4.1E-01	-0.2	8.3E-01
ENSMUST00000175670	forkhead box P1 [Source:MGI Symbol;Acc:MGI:1914004]	H3BK38		5.7	1.3E-03	5.3	1.4E-03	-1.1	3.9E-01	0.0	1.0E+00
ENSMUST00000175680	retinal degeneration 3 [Source:MGI Symbol;Acc:MGI:1921273]	Q05D96		4.7	5.2E-03	-2.2	9.5E-02	-1.0	2.1E-01	-2.2	1.3E-01
ENSMUST00000175681	potassium voltage gated channel, Shab-related subfamily, member 2 [Source:MGI Symbol;Acc:MGI:99632]		A6H8H5	7.7	1.4E-03	6.7	2.2E-04	-0.6	6.5E-01	-0.8	2.1E-01
ENSMUST00000175693	sine oculis-related homeobox 4 [Source:MGI Symbol;Acc:MGI:106034]	H3BL91		7.6	8.9E-07	3.3	8.9E-05	0.3	5.4E-01	-0.4	2.5E-01
ENSMUST00000137118				-1.2	3.5E-01	-0.1	9.6E-01	-0.3	7.4E-01	-1.4	3.4E-01
ENSMUST00000137119	kinesin family member 1C [Source:MGI Symbol;Acc:MGI:1098260]		O35071	1.5	7.4E-02	3.7	9.4E-03	2.5	3.0E-02	0.3	7.6E-01
ENSMUST00000137122				2.5	7.3E-02	3.3	1.1E-02	-2.2	8.0E-02	-3.0	1.4E-02
ENSMUST00000175712	esterase D/formylglutathione hydrolase [Source:MGI Symbol;Acc:MGI:95421]	H3BJC6		-6.9	1.2E-04	5.3	2.2E-04	-1.7	1.1E-01	-0.4	4.8E-01
ENSMUST00000175714	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 [Source:MGI Symbol;Acc:MGI:1933111]	H3BJL0		-6.0	1.0E-04	-0.9	3.2E-01	-0.2	7.6E-01	-1.7	1.1E-01
ENSMUST00000175731	RIKEN cDNA 1700084C01 gene [Source:MGI Symbol;Acc:MGI:1925715]	H3BLK0		6.2	3.8E-03	3.3	7.0E-02	1.1	4.6E-01	1.2	3.6E-01
ENSMUST00000175751	phosphodiesterase 4D interacting protein (myomegalin) [Source:MGI Symbol;Acc:MGI:1891434]	H3BJ38		4.9	1.0E-02	3.3	2.2E-03	1.4	6.2E-02	-0.3	6.7E-01
ENSMUST00000175765	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein [Source:MGI Symbol;Acc:MGI:2152213]	H3BKL1		-2.5	1.0E-03	-5.7	2.2E-03	-2.2	6.4E-03	-0.4	8.1E-01
ENSMUST00000175769	syndecan binding protein [Source:MGI Symbol;Acc:MGI:1337026]	H3BLG5		-7.1	1.5E-02	4.6	3.5E-03	-0.7	5.7E-01	0.4	6.0E-01
ENSMUST00000137150	major facilitator superfamily domain containing 10 [Source:MGI Symbol;Acc:MGI:1915544]	D6RI23		-4.4	7.0E-02	-2.2	4.4E-01	0.9	6.0E-01	-1.3	6.6E-01
ENSMUST00000175776	epidermal growth factor receptor pathway substrate 15 [Source:MGI Symbol;Acc:MGI:104583]	H3BK65		-6.2	6.4E-03	9.0	6.1E-04	-0.9	6.6E-01	0.3	7.2E-01
ENSMUST00000175778	SET binding factor 1 [Source:MGI Symbol;Acc:MGI:1925230]	H3BKD9		-6.9	8.5E-04	-6.2	6.4E-03	1.6	2.9E-02	-0.7	7.4E-01
ENSMUST00000137166	neurexin II [Source:MGI Symbol;Acc:MGI:1096362]	E9Q7X7		4.9	1.4E-01	5.0	1.6E-01	-0.6	8.7E-01	-0.7	7.4E-01
ENSMUST00000137168				1.6	1.4E-01	0.2	8.9E-01	0.3	7.5E-01	1.8	1.8E-01
ENSMUST00000137169	DEP domain containing 5 [Source:MGI Symbol;Acc:MGI:2141101]	F6TK47		-2.9	2.6E-01	-2.2	3.8E-01	-1.9	2.6E-01	-2.6	3.7E-01
ENSMUST00000137170	lin-52 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:3045391]	B2RQ11	Q8CD94	-0.1	8.2E-01	1.0	1.4E-01	0.1	9.2E-01	-1.1	9.9E-02
ENSMUST00000137172				3.2	6.4E-02	4.8	1.1E-02	-0.5	7.6E-01	-2.1	9.7E-02
ENSMUST00000175793	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]		Q9QWY8	-6.5	7.5E-03	5.7	5.3E-02	-0.8	7.8E-01	-0.4	8.0E-01
ENSMUST00000175795	Iroquois related homeobox 3 [Source:MGI Symbol;Acc:MGI:1197522]		P81067	6.8	5.3E-03	3.3	2.0E-02	-3.0	3.8E-02	0.8	3.4E-01
ENSMUST00000137181				-2.5	2.8E-01	2.4	2.9E-01	2.1	3.2E-01	-2.9	2.0E-01
ENSMUST00000137185				2.2	4.2E-02	3.3	2.8E-02	0.5	6.7E-01	-0.6	5.0E-01
ENSMUST00000137192	plastin 3 (T-isoform) [Source:MGI Symbol;Acc:MGI:104807]			0.9	6.5E-01	-4.8	6.2E-02	-5.9	2.1E-03	-0.3	9.1E-01
ENSMUST00000175799	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]	H3BKE6		-7.5	1.1E-04	9.1	4.2E-04	-0.2	9.0E-01	-3.3	4.8E-03
ENSMUST00000175807	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919837]	H3BLB9		-5.1	6.3E-03	7.7	6.5E-05	-2.4	8.7E-02	-1.2	6.5E-02
ENSMUST00000137201	lipase maturation factor 1 [Source:MGI Symbol;Acc:MGI:1923733]	D6RDS1		1.0	6.6E-01	3.1	2.6E-01	-0.4	8.6E-01	-2.4	2.7E-01
ENSMUST00000175836	RIKEN cDNA 4930562C15 gene [Source:MGI Symbol;Acc:MGI:1926059]	A0A075B687		8.3	9.1E-04	6.2	5.2E-04	0.9	4.8E-01	0.1	9.1E-01
ENSMUST00000175837	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BJ35		-5.3	2.0E-03	5.5	2.0E-04	-1.0	3.2E-01	-1.4	5.3E-02
ENSMUST00000175847	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	H3BJ43		-4.9	2.6E-02	-2.5	1.9E-01	1.2	2.2E-01	0.0	9.9E-01
ENSMUST00000175856	EF-hand calcium binding domain 8 [Source:MGI Symbol;Acc:MGI:3644206]	H3BJ05		5.7	8.9E-05	4.4	8.1E-04	0.4	6.4E-01	0.0	9.5E-01
ENSMUST00000175858	neuronal pentraxin receptor [Source:MGI Symbol;Acc:MGI:1920590]	E9PZM8		8.1	1.6E-06	6.3	8.5E-04	0.2	8.7E-01	-0.4	5.9E-01
ENSMUST00000175866	zinc finger homeodomain 4 [Source:MGI Symbol;Acc:MGI:2137668]	H3BLK8		10.2	8.9E-05	2.9	6.2E-02	-0.9	5.0E-01	1.1	3.2E-01
ENSMUST00000175872	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]	H3BKJ7		-7.0	1.2E-04	-4.3	3.3E-02	1.4	7.6E-02	0.1	9.6E-01
ENSMUST00000175875	metal response element binding transcription factor 1 [Source:MGI Symbol;Acc:MGI:101786]	A0A0G2JDC6		6.5	6.4E-04	-7.5	8.8E-04	-1.4	2.3E-02	-0.8	6.5E-01
ENSMUST00000175877	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BKL6		-4.0	3.3E-02	-2.5	7.8E-02	0.6	4.1E-01	0.2	8.6E-01
ENSMUST00000175887	esterase D/formylglutathione hydrolase [Source:MGI Symbol;Acc:MGI:95421]	H3BK43		-9.3	1.2E-05	-3.9	3.0E-03	1.2	2.2E-02	-0.1	9.0E-01
ENSMUST00000175906	proline rich 36 [Source:MGI Symbol;Acc:MGI:3605626]	H3BLA4		7.1	4.3E-04	4.0	2.0E-03	-0.3	7.1E-01	-0.5	5.0E-01
ENSMUST00000175914	family with sequence similarity 212, member A [Source:MGI Symbol;Acc:MGI:1915426]	H3BJG7		7.5	4.1E-05	1.3	1.3E-01	0.1	8.7E-01	0.3	6.4E-01
ENSMUST00000175916	prospero homeobox 1 [Source:MGI Symbol;Acc:MGI:97772]		P48437	7.5	6.0E-05	-3.4	1.2E-01	0.5	6.4E-01	0.1	9.4E-01
ENSMUST00000175918	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	H3BL09		3.9	3.7E-03	6.6	4.2E-06	-0.3	7.0E-01	-0.3	3.6E-01
ENSMUST00000137277				2.2	7.3E-02	-4.2	5.9E-04	-7.6	1.0E-05	-1.3	2.0E-01
ENSMUST00000137284				-2.2	1.3E-01	2.3	2.8E-01	3.1	9.7E-02	-1.3	4.1E-01
ENSMUST00000175938	Pbx/knotted 1 homeobox 2 [Source:MGI Symbol;Acc:MGI:2445415]	V9GWW7		5.5	2.1E-02	3.7	9.0E-05	-0.7	2.0E-01	-0.6	1.8E-01
ENSMUST00000175940	CTF8, chromosome transmission fidelity factor 8 [Source:MGI Symbol;Acc:MGI:2443370]		P0CG15	-6.9	3.7E-03	4.6	2.0E-03	0.5	6.5E-01	-0.8	2.9E-01
ENSMUST00000175941	zinc finger protein 536 [Source:MGI Symbol;Acc:MGI:1926102]		Q8K083	8.1	1.7E-04	3.1	4.4E-02	-0.5	7.1E-01	0.7	4.8E-01
ENSMUST00000175955	POU domain class 5, transcription factor 2 [Source:MGI Symbol;Acc:MGI:1922757]			6.0	2.0E-04	7.8	3.4E-03	2.6	2.1E-01	-0.3	7.8E-01
ENSMUST00000175962	protein phosphatase 1, regulatory (inhibitor) subunit 9A [Source:MGI Symbol;Acc:MGI:2442401]	H3BKE7		8.7	1.6E-05	6.9	1.1E-02	-0.8	7.5E-01	-1.8	1.8E-01
ENSMUST00000175965	one cut domain, family member 2 [Source:MGI Symbol;Acc:MGI:1891408]	H3BL85		9.1	9.5E-05	3.5	3.5E-02	0.0	1.0E+00	0.3	7.6E-01
ENSMUST00000175973	abhydrolase domain containing 5 [Source:MGI Symbol;Acc:MGI:1914719]	H3BLJ0		-3.9	1.3E-02	1.0	5.1E-01	4.5	1.2E-03	0.4	7.8E-01
ENSMUST00000137299	cDNA sequence BC017643 [Source:MGI Symbol;Acc:MGI:2384959]	A0A0A0MQK0		-0.5	5.1E-01	0.0	9.8E-01	0.2	8.0E-01	-0.3	7.4E-01
ENSMUST00000175974	family with sequence similarity 47, member E [Source:MGI Symbol;Acc:MGI:2686227]	H3BK06		3.3	1.5E-03	6.9	5.2E-04	0.4	7.9E-01	-0.3	6.8E-01
ENSMUST00000175977	chaperonin containing Tcp1, subunit 8 (theta) [Source:MGI Symbol;Acc:MGI:107183]	H3BL49		-7.4	4.6E-05	9.1	1.4E-02	2.4	4.5E-01	1.4	2.9E-01
ENSMUST00000137306	ankyrin repeat and SOCS box-containing 3 [Source:MGI Symbol;Acc:MGI:1929749]	D6RDR7		-2.6	2.9E-01	-1.8	4.4E-01	-1.4	3.8E-01	-2.2	4.1E-01
ENSMUST00000137307				-2.3	1.7E-01	-2.3	3.1E-01	0.5	7.4E-01	0.5	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000137311	diacylglycerol kinase, gamma [Source:MGI Symbol;Acc:MGI:105060]	F2Z409		1.3	1.7E-01	1.6	1.5E-01	-0.4	6.8E-01	-0.7	4.9E-01
ENSMUST00000137314				-2.3	1.7E-01	-4.6	6.1E-02	-2.1	9.4E-02	0.2	9.2E-01
ENSMUST00000175987	hyaluronan synthase 3 [Source:MGI Symbol;Acc:MGI:109599]	H3BL01		5.2	2.8E-02	-6.1	6.9E-03	1.0	1.4E-01	0.4	8.4E-01
ENSMUST00000176010	ribosomal protein L41 [Source:MGI Symbol;Acc:MGI:1915195]		P62947	-10.1	1.5E-04	6.0	8.2E-05	-0.4	6.3E-01	0.3	5.3E-01
ENSMUST00000176012	forkhead box J3 [Source:MGI Symbol;Acc:MGI:2443432]	H3BKK7		4.3	1.1E-02	3.9	7.3E-02	-1.2	5.2E-01	-0.4	7.8E-01
ENSMUST00000137325				-0.4	7.1E-01	2.2	1.3E-01	1.5	2.2E-01	-1.2	3.4E-01
ENSMUST00000137326				2.9	5.3E-02	6.9	7.0E-04	0.0	9.9E-01	-4.0	3.2E-03
ENSMUST00000176013	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]	H3BKP0		-4.7	1.9E-03	6.3	1.0E-03	-0.6	6.7E-01	-2.1	2.8E-02
ENSMUST00000176030	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	H3BLH0		-2.2	1.0E-02	3.9	2.1E-03	0.3	7.6E-01	0.3	6.0E-01
ENSMUST00000176081	sine oculis-related homeobox 3 [Source:MGI Symbol;Acc:MGI:102764]		Q62233	7.2	1.7E-04	-5.8	9.3E-04	-8.6	1.7E-05	0.5	7.2E-01
ENSMUST00000176086	TNF receptor-associated factor 7 [Source:MGI Symbol;Acc:MGI:3042141]	H3BLM6		-5.5	5.5E-03	6.5	1.1E-03	-1.0	5.3E-01	0.8	3.3E-01
ENSMUST00000137339				3.9	4.1E-02	5.7	8.7E-03	-0.5	8.1E-01	-2.3	6.9E-02
ENSMUST00000176102	zinc finger and BTB domain containing 25 [Source:MGI Symbol;Acc:MGI:99197]	G3UW50		4.2	1.0E-03	5.6	2.1E-04	-1.7	1.2E-01	0.1	8.2E-01
ENSMUST00000176103	high mobility group box transcription factor 1 [Source:MGI Symbol;Acc:MGI:894659]	H3BKS6		-3.3	4.5E-03	4.1	1.9E-04	-4.7	5.8E-04	-0.4	4.1E-01
ENSMUST00000137367				1.3	9.1E-02	0.3	7.1E-01	-0.2	8.2E-01	0.8	3.4E-01
ENSMUST00000176114	zinc finger protein 536 [Source:MGI Symbol;Acc:MGI:1926102]		Q8K083	4.4	2.8E-02	4.5	4.9E-03	-2.0	1.6E-01	-1.0	2.4E-01
ENSMUST00000176116	predicted gene 21988 [Source:MGI Symbol;Acc:MGI:5439457]	H3BJV0		-3.0	4.8E-03	6.0	1.1E-02	-0.8	7.2E-01	-0.8	5.1E-01
ENSMUST00000176129	zinc finger protein 536 [Source:MGI Symbol;Acc:MGI:1926102]	Q3TR09		7.9	2.6E-05	8.3	3.1E-05	-0.8	5.1E-01	0.4	4.2E-01
ENSMUST00000137376				-0.4	7.1E-01	-1.2	3.6E-01	-0.2	8.0E-01	0.6	6.3E-01
ENSMUST00000176155	dysbindin (dystrobrevin binding protein 1) domain containing 1 [Source:MGI Symbol;Acc:MGI:1919435]	H3BKU0		5.8	1.0E-03	4.3	2.3E-04	-0.8	2.6E-01	0.8	1.5E-01
ENSMUST00000137378				-3.0	2.7E-01	-2.7	4.1E-01	-0.7	7.2E-01	-1.0	7.8E-01
ENSMUST00000137382				-0.8	5.0E-01	0.5	6.9E-01	0.1	9.4E-01	-1.2	3.2E-01
ENSMUST00000137384	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:1916960]	D3YZJ7		-0.8	4.0E-01	-0.9	5.3E-01	1.1	2.2E-01	1.2	3.8E-01
ENSMUST00000137386	intraflagellar transport 140 [Source:MGI Symbol;Acc:MGI:2146906]	E9Q682		-2.3	1.1E-01	-0.8	6.8E-01	1.0	4.5E-01	-0.6	7.4E-01
ENSMUST00000176158	mitochondrial ribosomal protein L17 [Source:MGI Symbol;Acc:MGI:1351608]	H3BJT9		-5.4	6.4E-04	-2.3	2.0E-02	1.4	1.6E-02	-5.1	2.4E-03
ENSMUST00000176161	early B cell factor 2 [Source:MGI Symbol;Acc:MGI:894332]		O08792	8.3	1.0E-05	2.4	1.8E-02	0.2	7.6E-01	0.5	4.8E-01
ENSMUST00000176179	active BCR-related gene [Source:MGI Symbol;Acc:MGI:107771]	H3BKT3		6.3	2.3E-03	-10.2	4.6E-04	-0.9	9.6E-02	0.3	8.7E-01
ENSMUST00000137403				1.7	2.5E-01	2.1	1.8E-01	-1.7	2.2E-01	-2.1	1.3E-01
ENSMUST00000137404	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 [Source:MGI Symbol;Acc:MGI:1932544]		Q9EQH7	4.6	1.4E-01	2.9	4.1E-01	-0.2	9.6E-01	1.5	4.9E-01
ENSMUST00000137408				-1.7	5.9E-01	2.3	4.8E-01	1.2	6.7E-01	-2.8	3.8E-01
ENSMUST00000176191	Kv channel interacting protein 4 [Source:MGI Symbol;Acc:MGI:1933131]	Q3YAA7	Q6PHZ8	5.6	9.1E-04	5.2	2.6E-02	2.3	2.3E-01	0.5	6.9E-01
ENSMUST00000176194	phospholipase C, eta 2 [Source:MGI Symbol;Acc:MGI:2443078]	H3BIW6		6.9	3.7E-04	6.4	5.9E-05	-0.6	5.1E-01	0.4	4.3E-01
ENSMUST00000137426	ic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Source:MGI Symbol;Acc:MGI:1	F6ZFU0		2.8	1.7E-01	3.5	1.2E-01	-2.0	3.5E-01	-2.7	1.3E-01
ENSMUST00000176200	RIKEN cDNA 1190007I07 gene [Source:MGI Symbol;Acc:MGI:3698433]		Q8BTC1	7.4	8.2E-04	7.3	1.4E-05	-1.4	1.6E-01	-0.1	8.7E-01
ENSMUST00000176203	complement factor B [Source:MGI Symbol;Acc:MGI:105975]	B8JJM6		5.5	3.3E-02	6.6	2.8E-06	-0.5	4.7E-01	0.3	4.5E-01
ENSMUST00000176204	paternally expressed 10 [Source:MGI Symbol;Acc:MGI:2157785]		Q7TN75	7.7	6.9E-05	-0.8	3.7E-01	-0.4	5.3E-01	-1.8	8.4E-02
ENSMUST00000176216	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	H3BJN3		-8.1	3.1E-05	6.4	2.6E-03	1.6	2.9E-01	-1.3	1.8E-01
ENSMUST00000137435				-0.8	3.1E-01	1.1	3.4E-01	2.2	4.2E-02	0.3	7.4E-01
ENSMUST00000176251	epidermal growth factor receptor pathway substrate 15 [Source:MGI Symbol;Acc:MGI:104583]	Q5JC28		-7.8	2.2E-05	7.3	4.1E-04	-0.7	6.3E-01	0.5	4.5E-01
ENSMUST00000176262	suppressor of variegation 4-20 homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2444557]		Q3U8K7	-5.7	1.4E-04	5.7	1.5E-03	-1.5	3.1E-01	-0.6	4.2E-01
ENSMUST00000176271	POU domain, class 6, transcription factor 1 [Source:MGI Symbol;Acc:MGI:102935]		Q07916	2.9	1.2E-03	-4.2	1.6E-04	-0.3	3.6E-01	0.0	9.6E-01
ENSMUST00000137446				1.0	5.5E-01	4.4	8.6E-02	3.0	1.9E-01	-0.4	7.7E-01
ENSMUST00000176274	cysteine and histidine rich 1 [Source:MGI Symbol;Acc:MGI:1859320]	H3BIV6		-2.6	4.0E-03	-2.6	6.8E-02	-0.6	3.9E-01	-0.8	5.8E-01
ENSMUST00000176276	RIKEN cDNA 1700039E15 gene [Source:MGI Symbol;Acc:MGI:1923963]	H3BL98		7.3	3.2E-05	5.3	1.4E-02	-1.1	5.5E-01	-0.7	5.1E-01
ENSMUST00000176285	mediator complex subunit 23 [Source:MGI Symbol;Acc:MGI:1917458]	H3BK33		-3.6	2.8E-03	5.6	3.5E-03	-0.5	7.4E-01	-2.6	3.3E-02
ENSMUST00000137454	GRAM domain containing 1B [Source:MGI Symbol;Acc:MGI:1925037]	F7BFL8		-3.3	2.8E-01	-4.2	2.5E-01	-1.8	3.5E-01	-0.8	8.3E-01
ENSMUST00000176286	dysbindin (dystrobrevin binding protein 1) domain containing 1 [Source:MGI Symbol;Acc:MGI:1919435]	H3BIX2		3.6	1.8E-03	-6.3	7.8E-05	0.2	5.2E-01	-0.8	4.5E-01
ENSMUST00000176300	POU domain, class 6, transcription factor 1 [Source:MGI Symbol;Acc:MGI:102935]	H3BKJ6		6.6	1.2E-03	-1.0	2.2E-01	0.3	5.3E-01	-0.2	8.1E-01
ENSMUST00000176305	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	H3BK96		-5.6	4.8E-04	6.5	5.2E-05	0.6	5.2E-01	-0.3	5.6E-01
ENSMUST00000137464				1.5	4.4E-01	1.2	6.1E-01	0.2	9.3E-01	0.4	8.5E-01
ENSMUST00000176322	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BJS0		-7.2	7.8E-04	3.8	8.8E-03	0.3	7.8E-01	0.0	9.8E-01
ENSMUST00000137467	transcription factor E3 [Source:MGI Symbol;Acc:MGI:98511]		Q64092	3.6	8.0E-02	6.6	3.5E-02	3.3	2.0E-01	0.3	8.6E-01
ENSMUST00000176330	POU domain, class 1, transcription factor 1 [Source:MGI Symbol;Acc:MGI:97588]		Q00286	9.7	6.4E-05	4.6	3.8E-05	-0.1	8.7E-01	-0.2	5.5E-01
ENSMUST00000137474				-0.8	6.2E-01	-0.6	7.6E-01	0.1	9.7E-01	-0.1	9.4E-01
ENSMUST00000176336	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BJ71		-8.6	5.2E-05	-4.9	1.2E-03	-1.7	1.5E-02	-0.7	5.5E-01
ENSMUST00000137480				-1.9	4.7E-02	-4.1	1.0E-02	-0.6	3.1E-01	1.5	2.7E-01
ENSMUST00000176353	TNF receptor-associated factor 7 [Source:MGI Symbol;Acc:MGI:3042141]	Q8C2K8		-7.1	2.6E-05	4.0	1.9E-02	-2.0	2.1E-01	0.9	3.8E-01
ENSMUST00000176369	MAS-related GPR, member A3 [Source:MGI Symbol;Acc:MGI:2684085]	H3BKL3		6.0	1.2E-04	5.8	3.8E-04	0.9	4.0E-01	0.7	2.6E-01
ENSMUST00000176371	Usher syndrome 1C [Source:MGI Symbol;Acc:MGI:1919338]	H3BIZ2		6.4	2.2E-04	-1.0	4.0E-01	1.7	5.3E-02	0.2	8.6E-01
ENSMUST00000176374	peroxisomal biogenesis factor 12 [Source:MGI Symbol;Acc:MGI:2144177]	H3BJF5		3.5	5.7E-03	3.6	1.0E-01	-0.6	7.8E-01	2.0	1.5E-01
ENSMUST00000176383	zinc finger homeodomain 4 [Source:MGI Symbol;Acc:MGI:2137668]	E9Q5A7		5.9	9.3E-04	7.9	8.5E-04	0.4	8.2E-01	1.2	1.4E-01
ENSMUST00000137494				-1.1	2.6E-01	-3.3	4.4E-02	-0.4	6.4E-01	1.8	2.3E-01
ENSMUST00000176394	RIKEN cDNA 4930562C15 gene [Source:MGI Symbol;Acc:MGI:1926059]	H3BJT7		5.9	1.9E-05	7.9	3.9E-04	1.9	2.0E-01	0.2	7.6E-01
ENSMUST00000176418	basonuclin 2 [Source:MGI Symbol;Acc:MGI:2443805]	H3BKX5		3.5	3.2E-02	-0.7	3.7E-01	0.5	3.8E-01	-1.3	1.1E-01
ENSMUST00000176425	glycosylated lysosomal membrane protein [Source:MGI Symbol;Acc:MGI:1913318]	H3BKY1		-5.9	2.8E-02	-6.5	2.3E-02	1.6	7.3E-02	0.3	9.1E-01
ENSMUST00000176430	adaptor-related protein complex 2, beta 1 subunit [Source:MGI Symbol;Acc:MGI:1919020]	H3BIY9		3.1	1.9E-03	2.0	2.7E-02	-0.2	7.8E-01	-0.3	6.6E-01
ENSMUST00000176464	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BKH2		4.9	3.6E-06	6.4	2.1E-04	-0.6	6.0E-01	0.4	4.9E-01
ENSMUST00000176466	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919837]	H3BL68		-2.6	2.7E-02	6.5	2.9E-04	-0.1	9.2E-01	0.2	7.9E-01
ENSMUST00000176483	lysine (K)-specific demethylase 2A [Source:MGI Symbol;Acc:MGI:1354736]	A0A087WQL9		4.6	2.8E-03	3.4	1.2E-02	-0.8	4.1E-01	0.2	7.9E-01
ENSMUST00000137510				-0.2	7.9E-01	-0.5	5.4E-01	-0.4	4.8E-01	-0.1	8.9E-01
ENSMUST00000176500	rho/rac guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:103264]	H3BJ40		6.5	2.2E-04	7.9	2.3E-04	-0.6	6.7E-01	-0.9	2.1E-01
ENSMUST00000176506	Meis homeobox 3 [Source:MGI Symbol;Acc:MGI:108519]		P97368	7.3	5.0E-05	-2.5	8.6E-02	0.9	3.0E-01	-0.9	5.3E-01
ENSMUST00000176510	X Kell blood group precursor related family member 6 homolog [Source:MGI Symbol;Acc:MGI:2447765]	H3BJG3		7.9	1.8E-04	5.5	2.3E-04	-2.8	3.3E-02	-1.3	6.6E-02
ENSMUST00000176550	HNF1 homeobox A [Source:MGI Symbol;Acc:MGI:98504]	H3BL72		6.4	3.4E-04	-3.3	8.2E-03	0.8	1.7E-01	-1.4	2.4E-01
ENSMUST00000137522				-1.6	2.2E-01	-0.1	9.4E-01	0.6	6.0E-01	-0.8	5.7E-01
ENSMUST00000176551	paternally expressed 10 [Source:MGI Symbol;Acc:MGI:2157785]	H3BJQ1		5.3	6.2E-03	3.8	7.8E-02	-3.6	1.4E-01	0.1	9.2E-01
ENSMUST00000137528	GTPase activating protein and VPS9 domains 1 [Source:MGI Symbol;Acc:MGI:1913941]	F6X819		-2.4	7.8E-02	-1.3	4.5E-01	1.1	2.8E-01	0.0	1.0E+00

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000176559	phosphotyrosine interaction domain containing 1 [Source:MGI Symbol;Acc:MGI:2138391]		Q3UBG2	8.2	3.4E-05	5.0	4.2E-04	-1.2	2.4E-01	0.2	8.0E-01
ENSMUST00000176584	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	H3BKD2		6.8	2.0E-03	5.6	3.2E-02	-0.9	7.3E-01	0.0	1.0E+00
ENSMUST00000176594	vomeronasal 2, receptor 10 [Source:MGI Symbol;Acc:MGI:1316730]	O35204		6.7	1.7E-04	-0.7	6.4E-01	0.9	3.7E-01	-1.3	3.6E-01
ENSMUST00000176596	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919837]	H3BKQ1		-6.6	1.2E-02	-0.6	5.3E-01	1.1	9.9E-02	-0.8	3.4E-01
ENSMUST00000176600	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919837]	H3BKF3		-1.8	2.3E-02	8.2	1.4E-04	-0.7	6.4E-01	-0.2	7.7E-01
ENSMUST00000176617	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BJS5		-7.5	1.0E-02	-3.1	5.6E-02	0.4	6.8E-01	-0.9	5.9E-01
ENSMUST00000176624	cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI Symbol;Acc:MGI:103238]	Q3UT49		7.5	1.5E-04	4.4	2.9E-03	1.2	2.4E-01	0.2	7.5E-01
ENSMUST00000137555				-0.1	8.5E-01	-2.9	4.4E-02	-0.3	6.0E-01	2.4	7.3E-02
ENSMUST00000176637	guanine nucleotide binding protein (G protein), beta 1 [Source:MGI Symbol;Acc:MGI:95781]	Q3TQ70	P62874	-5.8	3.1E-03	6.5	5.4E-05	-2.3	4.9E-02	-0.8	1.6E-01
ENSMUST00000176638	FUN14 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919268]	H3BJZ1		-4.1	2.1E-02	6.9	8.7E-05	-0.6	6.1E-01	-0.2	7.4E-01
ENSMUST00000176645	ecotropic viral integration site 5 like [Source:MGI Symbol;Acc:MGI:2442167]	H3BLD3		5.3	2.0E-02	1.1	4.7E-02	0.1	8.6E-01	0.0	9.2E-01
ENSMUST00000137574				2.6	1.4E-01	3.1	1.0E-01	-1.1	5.0E-01	-1.6	2.7E-01
ENSMUST00000176663	salt inducible kinase 2 [Source:MGI Symbol;Acc:MGI:2445031]	H3BKG1		-3.7	7.7E-03	6.2	3.6E-04	-1.5	2.7E-01	-0.6	4.0E-01
ENSMUST00000176667	ucine-rich repeats and calponin homology (CH) domain containing 4 [Source:MGI Symbol;Acc:MGI:1917193	H3BLL3		-10.5	3.0E-05	5.2	9.5E-05	-0.4	6.0E-01	0.1	7.6E-01
ENSMUST00000137585				0.6	7.9E-01	1.5	6.2E-01	0.7	7.6E-01	-0.2	9.4E-01
ENSMUST00000176668	TNF receptor-associated factor 7 [Source:MGI Symbol;Acc:MGI:3042141]	H3BKZ1		-5.5	5.0E-04	-2.0	1.3E-02	0.9	5.2E-02	-2.8	7.3E-03
ENSMUST00000176670	cleavage and polyadenylation specific factor 6 [Source:MGI Symbol;Acc:MGI:1913948]	H3BJW3		-6.7	3.7E-05	7.4	1.0E-03	0.5	7.7E-01	-3.2	1.5E-02
ENSMUST00000176683	ribosomal protein L41 [Source:MGI Symbol;Acc:MGI:1915195]		P62947	-6.3	4.8E-04	6.6	5.4E-05	-0.2	8.0E-01	-0.3	6.0E-01
ENSMUST00000176686	cleavage and polyadenylation specific factor 6 [Source:MGI Symbol;Acc:MGI:1913948]	H3BJ30		-3.2	8.4E-03	5.3	1.3E-02	-0.7	7.2E-01	0.4	7.1E-01
ENSMUST00000137601	myosin X [Source:MGI Symbol;Acc:MGI:107716]	D3YXU7		3.9	1.1E-01	4.6	1.3E-01	0.1	9.8E-01	-0.6	7.4E-01
ENSMUST00000137602				1.2	5.5E-01	-1.8	3.8E-01	-3.2	7.4E-02	-0.3	8.9E-01
ENSMUST00000176731	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	H3BKN5		-6.6	3.9E-03	-6.6	5.1E-03	-2.5	8.8E-03	-0.1	9.7E-01
ENSMUST00000176745	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	H3BKT0		-8.1	3.4E-05	6.5	2.6E-04	0.1	9.3E-01	-1.1	1.0E-01
ENSMUST00000137615				3.1	2.0E-01	1.2	6.3E-01	-2.2	3.2E-01	-0.3	8.9E-01
ENSMUST00000176755	golgi phosphoprotein 3-like [Source:MGI Symbol;Acc:MGI:1917129]	H3BJ12		-5.9	2.2E-03	4.6	8.2E-04	0.6	4.6E-01	-0.2	8.2E-01
ENSMUST00000137627				3.1	3.5E-02	3.1	5.7E-02	-0.3	7.9E-01	-0.4	7.6E-01
ENSMUST00000176770	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]	H3BIX7		-6.4	3.3E-04	-4.0	8.5E-02	1.4	2.3E-01	-0.2	9.2E-01
ENSMUST00000176778	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	H3BLS0		2.9	5.8E-04	-4.5	3.1E-02	0.1	9.3E-01	-0.8	6.9E-01
ENSMUST00000137638				2.5	1.2E-01	0.5	7.8E-01	-1.4	3.4E-01	0.6	6.9E-01
ENSMUST00000176782	aftiphilin [Source:MGI Symbol;Acc:MGI:1923012]	H3BIZ9		-4.9	2.2E-03	6.1	2.3E-04	-0.2	8.5E-01	0.1	8.3E-01
ENSMUST00000137649	leucine rich repeat containing 14 [Source:MGI Symbol;Acc:MGI:2445060]		Q8VC16	0.9	2.6E-01	2.4	2.0E-02	0.3	6.5E-01	-1.2	1.4E-01
ENSMUST00000137657				-2.4	4.1E-02	-1.0	4.6E-01	0.8	4.0E-01	-0.6	6.4E-01
ENSMUST00000137670	Ras suppressor protein 1 [Source:MGI Symbol;Acc:MGI:103040]	B1AYQ0		-2.9	2.6E-01	-5.9	8.6E-02	-3.2	5.1E-02	-0.2	9.5E-01
ENSMUST00000137676				0.8	4.6E-01	0.2	9.2E-01	0.9	5.4E-01	1.5	3.3E-01
ENSMUST00000176790	pre B cell leukemia homeobox 1 [Source:MGI Symbol;Acc:MGI:97495]	Q71VB4	P41778	-4.4	7.2E-03	7.1	5.9E-03	-0.8	7.1E-01	-2.4	8.2E-02
ENSMUST00000176797	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	H3BLP7		-7.1	1.8E-05	4.1	4.0E-05	0.0	9.5E-01	0.2	5.5E-01
ENSMUST00000176822	phosphotyrosine interaction domain containing 1 [Source:MGI Symbol;Acc:MGI:2138391]	H3BKK5		6.2	1.5E-04	-4.0	1.7E-02	-0.6	3.9E-01	0.4	7.8E-01
ENSMUST00000176825	ecotropic viral integration site 5 like [Source:MGI Symbol;Acc:MGI:2442167]	H3BL92		-4.7	6.5E-03	-2.4	2.2E-02	-0.7	2.0E-01	-0.5	5.8E-01
ENSMUST00000137694				0.6	2.4E-01	0.4	4.5E-01	-0.5	3.3E-01	-0.3	5.6E-01
ENSMUST00000137695				0.5	7.7E-01	4.6	9.0E-02	2.9	2.3E-01	-1.2	4.5E-01
ENSMUST00000137696				-0.1	8.7E-01	1.8	2.0E-01	1.2	3.1E-01	-0.7	4.6E-01
ENSMUST00000176826	oncostatin M receptor [Source:MGI Symbol;Acc:MGI:1330819]			6.7	6.3E-03	4.0	1.5E-04	-1.5	3.9E-02	-0.7	1.4E-01
ENSMUST00000176828	FERM domain containing 4A [Source:MGI Symbol;Acc:MGI:1919850]	Q3TB04		5.8	2.3E-03	5.7	6.2E-04	-0.5	6.6E-01	-0.9	1.8E-01
ENSMUST00000176838	vomeronasal 1 receptor 4 [Source:MGI Symbol;Acc:MGI:2159457]	Q8R2D3		4.9	2.6E-02	3.5	1.6E-01	-3.0	2.4E-01	-0.4	8.2E-01
ENSMUST00000137708	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Source:MGI Symbol;Acc:M	E9PYX7		4.0	4.5E-02	2.5	2.3E-01	-1.5	4.0E-01	0.1	9.8E-01
ENSMUST00000176849	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	H3BKD0		-6.9	9.0E-06	-4.1	9.9E-03	0.3	6.0E-01	-0.6	6.7E-01
ENSMUST00000176854	inositol hexaphosphate kinase 1 [Source:MGI Symbol;Acc:MGI:1351633]	A0A0A6YVR5		2.2	2.4E-03	-2.4	2.5E-01	0.9	3.8E-01	-0.2	9.4E-01
ENSMUST00000176855	Rho GTPase activating protein 39 [Source:MGI Symbol;Acc:MGI:107858]	H3BJM3		6.9	1.2E-03	1.7	4.3E-02	-0.5	4.2E-01	0.0	9.9E-01
ENSMUST00000176867	low density lipoprotein receptor-related protein 5 [Source:MGI Symbol;Acc:MGI:1278315]	H3BL52		5.4	4.4E-04	6.0	1.3E-03	-0.3	8.4E-01	-0.2	7.8E-01
ENSMUST00000176871	ucine-rich repeats and calponin homology (CH) domain containing 4 [Source:MGI Symbol;Acc:MGI:1917193	H3BL36		-2.1	2.8E-02	1.6	3.0E-02	0.2	7.6E-01	-0.2	7.3E-01
ENSMUST00000137726				-0.5	6.2E-01	-1.7	3.3E-01	1.0	3.3E-01	2.2	1.7E-01
ENSMUST00000176875	double homeobox family member 3 [Source:MGI Symbol;Acc:MGI:1921649]			12.0	1.5E-06	3.0	2.4E-02	-2.1	8.9E-02	0.6	4.7E-01
ENSMUST00000176878	UDP glycosyltransferases 3 family, polypeptide A1 [Source:MGI Symbol;Acc:MGI:2146055]	H3BLE9		4.9	1.5E-03	1.5	5.1E-01	0.1	9.7E-01	3.4	7.9E-02
ENSMUST00000137753				1.0	6.8E-01	-1.4	5.9E-01	-1.2	5.1E-01	1.1	6.7E-01
ENSMUST00000137758				1.8	9.6E-02	1.3	2.8E-01	-0.2	8.4E-01	0.3	7.7E-01
ENSMUST00000176887	mitochondrial ribosomal protein L17 [Source:MGI Symbol;Acc:MGI:1351608]	H3BIZ3		-3.6	2.7E-03	5.0	7.1E-02	-0.6	8.2E-01	0.1	9.7E-01
ENSMUST00000137766				0.5	7.8E-01	1.7	3.8E-01	-0.2	8.9E-01	-1.4	4.7E-01
ENSMUST00000176892	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BK44		-7.3	2.3E-04	5.7	4.2E-05	-0.4	5.9E-01	0.9	8.6E-02
ENSMUST00000176896	neuroplastin [Source:MGI Symbol;Acc:MGI:108077]	H3BIX4		-7.5	3.9E-05	-2.1	1.2E-02	-0.7	1.9E-01	-2.2	2.7E-02
ENSMUST00000176911	HNF1 homeobox A [Source:MGI Symbol;Acc:MGI:98504]	H3BKV2		6.4	3.0E-04	-3.3	6.9E-02	0.8	4.0E-01	-0.2	9.0E-01
ENSMUST00000176935	predicted gene 29394 [Source:MGI Symbol;Acc:MGI:5580100]	H3BIW7		3.8	1.8E-03	-5.4	1.8E-03	-1.2	4.1E-02	-0.3	8.3E-01
ENSMUST00000137779				1.1	2.4E-01	2.4	7.3E-02	1.5	1.7E-01	0.2	8.0E-01
ENSMUST00000176957	esterase D/formylglutathione hydrolase [Source:MGI Symbol;Acc:MGI:95421]	H3BKH6		-7.7	8.2E-06	3.3	9.9E-02	-0.9	5.9E-01	0.9	5.0E-01
ENSMUST00000137784	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Source:MGI Symbol;Acc:M	E9Q9C3		-2.8	4.4E-02	-4.0	6.1E-02	-0.1	8.8E-01	1.1	5.9E-01
ENSMUST00000137787				-1.9	1.9E-01	1.2	5.2E-01	1.1	4.7E-01	-2.0	2.1E-01
ENSMUST00000176961	Rho GDP dissociation inhibitor (GDI) gamma [Source:MGI Symbol;Acc:MGI:108430]	Q3UNB6	Q62160	7.5	7.6E-05	5.7	3.3E-04	-0.5	6.3E-01	0.0	9.9E-01
ENSMUST00000176971	basonuclin 2 [Source:MGI Symbol;Acc:MGI:2443805]	H3BL10		6.2	1.1E-02	5.7	3.2E-02	-0.7	7.8E-01	0.9	5.0E-01
ENSMUST00000176982	RIKEN cDNA 4930562C15 gene [Source:MGI Symbol;Acc:MGI:1926059]	H3BJT7		6.0	1.4E-02	3.3	1.6E-02	0.1	9.0E-01	0.3	7.2E-01
ENSMUST00000176992	golgi-specific brefeldin A-resistance factor 1 [Source:MGI Symbol;Acc:MGI:1861607]	Q6A099		-2.2	3.4E-02	5.7	3.0E-04	-0.8	4.1E-01	1.5	3.9E-02
ENSMUST00000137799	zinc finger protein 687 [Source:MGI Symbol;Acc:MGI:1925516]		Q9D2D7	1.9	3.8E-01	2.0	4.3E-01	-0.8	6.9E-01	-1.0	6.7E-01
ENSMUST00000177026	Rho GTPase activating protein 39 [Source:MGI Symbol;Acc:MGI:107858]	H3BLS4		4.7	2.5E-04	7.9	1.2E-03	-0.3	8.7E-01	-0.2	8.4E-01
ENSMUST00000177034	microtubule crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:1915867]	H3BL83		7.4	2.3E-04	4.2	1.2E-04	-1.6	2.8E-02	-0.4	3.9E-01
ENSMUST00000177039	ubiquitin-like modifier activating enzyme 7 [Source:MGI Symbol;Acc:MGI:1349462]	H3BKY9		-4.2	4.8E-03	7.6	9.0E-05	-0.6	6.2E-01	-0.3	5.6E-01
ENSMUST00000137811				-3.5	6.5E-02	-3.6	1.7E-01	0.4	8.0E-01	0.5	8.5E-01
ENSMUST00000137813				2.6	1.2E-01	-0.9	6.3E-01	-3.0	5.3E-02	0.6	7.6E-01
ENSMUST00000177042	RIKEN cDNA 4930562C15 gene [Source:MGI Symbol;Acc:MGI:1926059]	A0A075B686		7.4	4.1E-04	6.0	5.4E-04	-1.5	2.6E-01	-1.5	5.1E-02
ENSMUST00000177054	ubiquitin specific peptidase 2 [Source:MGI Symbol;Acc:MGI:1858178]		O88623	5.9	8.0E-04	7.2	8.4E-05	-0.6	6.2E-01	0.0	9.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000137822				-0.2	9.6E-01	-1.8	5.7E-01	-3.1	2.5E-01	-1.5	6.6E-01
ENSMUST00000177064	neuroplastin [Source:MGI Symbol;Acc:MGI:108077]	H3BKA7		-6.2	1.9E-03	-1.8	1.2E-02	0.7	6.7E-02	0.6	3.0E-01
ENSMUST00000137832				-2.2	6.8E-02	-2.5	1.1E-01	0.4	6.5E-01	0.6	6.7E-01
ENSMUST00000177068	CTF8, chromosome transmission fidelity factor 8 [Source:MGI Symbol;Acc:MGI:2443370]		P0CG15	-7.3	7.1E-06	-4.5	4.5E-03	-0.2	7.3E-01	1.7	1.7E-01
ENSMUST00000137841	small ubiquitin-like modifier 3 [Source:MGI Symbol;Acc:MGI:1336201]	G3UWI9		-2.9	9.3E-02	-1.7	4.2E-01	0.4	7.5E-01	-0.7	7.5E-01
ENSMUST00000137843				0.6	5.9E-01	3.2	8.2E-02	2.0	2.1E-01	-0.6	6.1E-01
ENSMUST00000177074	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]	H3BL44		-7.5	5.0E-06	6.4	1.4E-04	0.4	6.6E-01	0.9	1.6E-01
ENSMUST00000177083	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]	E9QMJ1		-7.3	5.7E-04	3.7	1.1E-01	0.9	6.4E-01	1.9	1.8E-01
ENSMUST00000177087	cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI Symbol;Acc:MGI:103238]	H3BLM0		5.0	5.0E-04	5.1	2.5E-02	-0.5	8.0E-01	0.3	8.2E-01
ENSMUST00000177094	guanine nucleotide binding protein (G protein), beta 1 [Source:MGI Symbol;Acc:MGI:95781]	H3BKR2		-4.6	2.6E-03	1.8	6.8E-02	-0.7	3.9E-01	0.9	2.5E-01
ENSMUST00000177101	cilia and flagella associated protein 53 [Source:MGI Symbol;Acc:MGI:1921703]	H3BJA5		8.7	1.1E-04	5.6	1.4E-02	-0.6	7.6E-01	-0.9	4.3E-01
ENSMUST00000137874				-1.9	5.5E-02	-0.3	7.7E-01	0.0	9.8E-01	-1.6	1.4E-01
ENSMUST00000177102	transient receptor potential cation channel, subfamily M, member 1 [Source:MGI Symbol;Acc:MGI:1330305]		Q2TV84	7.6	1.5E-04	5.1	2.8E-03	-0.6	6.9E-01	0.9	2.6E-01
ENSMUST00000137891	rin homology domain containing, family F (with FYVE domain) member 2 [Source:MGI Symbol;Acc:MGI:19	A8Y5N8		3.2	1.0E-01	-0.9	7.4E-01	-1.9	2.9E-01	2.2	3.9E-01
ENSMUST00000137892				-1.1	6.3E-01	-3.2	2.9E-01	-1.9	2.7E-01	0.3	9.3E-01
ENSMUST00000137893				-3.4	5.5E-02	-3.1	6.7E-02	-1.9	6.4E-02	-2.3	2.3E-01
ENSMUST00000177111	integrin, alpha D [Source:MGI Symbol;Acc:MGI:3578624]	H3BKX8		6.0	1.8E-02	6.0	2.0E-04	-1.5	2.0E-01	-0.1	9.1E-01
ENSMUST00000177116	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	Q99KH6		6.7	8.8E-03	-1.4	2.2E-01	0.4	5.5E-01	-0.6	6.2E-01
ENSMUST00000177126	tubulin polymerization-promoting protein family member 3 [Source:MGI Symbol;Acc:MGI:1915221]		Q9CRB6	2.7	5.3E-03	6.2	1.3E-04	-1.0	3.5E-01	-0.1	8.2E-01
ENSMUST00000137899	alkaline ceramidase 3 [Source:MGI Symbol;Acc:MGI:1913440]	D6RJ31		-1.8	2.8E-01	-3.3	7.4E-02	-2.1	6.0E-02	-0.7	7.2E-01
ENSMUST00000137903				-0.3	7.9E-01	0.1	9.7E-01	0.5	6.2E-01	0.2	9.0E-01
ENSMUST00000177143	phospholipase C, eta 1 [Source:MGI Symbol;Acc:MGI:2683547]	H3BKK4		7.6	1.5E-02	-2.7	3.7E-02	-0.5	4.4E-01	-0.2	8.3E-01
ENSMUST00000137906	AT rich interactive domain 5A (MRF1-like) [Source:MGI Symbol;Acc:MGI:2443039]		Q3U108	-0.8	9.3E-02	-0.4	4.4E-01	0.0	9.2E-01	-0.4	4.5E-01
ENSMUST00000177163	ribosomal protein L41 [Source:MGI Symbol;Acc:MGI:1915195]		P62947	-5.3	6.2E-03	5.0	7.9E-04	1.0	3.0E-01	-0.3	6.7E-01
ENSMUST00000177164	predicted gene, 38999 [Source:MGI Symbol;Acc:MGI:5621884]		H3BKT1	5.5	9.4E-03	-0.1	9.6E-01	1.0	5.7E-01	-4.6	5.4E-02
ENSMUST00000177173	cadherin-related family member 4 [Source:MGI Symbol;Acc:MGI:1916648]	H3BJZ2		6.1	1.0E-03	5.4	6.8E-05	0.3	6.5E-01	0.1	7.7E-01
ENSMUST00000137932				0.5	6.6E-01	1.8	2.1E-01	-0.1	9.6E-01	-1.4	2.8E-01
ENSMUST00000177180	tubulin tyrosine ligase-like family, member 8 [Source:MGI Symbol;Acc:MGI:1922902]	H3BKG4		4.7	2.1E-02	5.3	1.7E-04	-0.6	4.6E-01	0.1	8.2E-01
ENSMUST00000137942	myosin binding protein C, cardiac [Source:MGI Symbol;Acc:MGI:102844]	Q3TF37		-4.8	4.7E-02	2.3	3.0E-01	1.4	4.7E-01	-5.7	2.4E-02
ENSMUST00000177192	epidermal growth factor receptor pathway substrate 15 [Source:MGI Symbol;Acc:MGI:104583]	H3BLE4		-5.1	6.8E-03	4.3	1.4E-03	-0.5	6.0E-01	-0.5	4.0E-01
ENSMUST00000137944				0.8	4.2E-01	1.0	3.7E-01	-0.3	7.2E-01	-0.5	5.9E-01
ENSMUST00000177197	cholinergic receptor, muscarinic 1, CNS [Source:MGI Symbol;Acc:MGI:88396]	H3BKE3		8.3	1.3E-04	5.7	3.4E-03	-0.4	8.0E-01	-1.4	1.4E-01
ENSMUST00000177205	zinc finger protein 428 [Source:MGI Symbol;Acc:MGI:1916463]	H3BLD9		4.4	6.0E-03	2.8	2.3E-02	-0.5	6.3E-01	-0.1	9.4E-01
ENSMUST00000137956				0.7	2.8E-01	1.2	1.4E-01	0.2	7.9E-01	-0.3	6.2E-01
ENSMUST00000137959				-1.6	2.2E-01	-1.1	5.6E-01	0.8	4.7E-01	0.2	9.2E-01
ENSMUST00000137960				3.0	4.2E-02	4.0	6.4E-02	1.6	3.9E-01	0.7	5.9E-01
ENSMUST00000177213	FUN14 domain containing 1 [Source:MGI Symbol;Acc:MGI:1919268]	H3BJ77		-5.8	2.1E-04	4.9	5.9E-03	-0.9	5.3E-01	0.2	8.4E-01
ENSMUST00000177225	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BL19		7.1	1.8E-04	6.4	7.4E-04	0.6	6.6E-01	-0.6	3.6E-01
ENSMUST00000177232	mediator complex subunit 23 [Source:MGI Symbol;Acc:MGI:1917458]	H3BJ66		4.7	1.4E-04	1.9	3.5E-01	-3.3	1.2E-01	0.0	1.0E+00
ENSMUST00000177236	ring finger protein 141 [Source:MGI Symbol;Acc:MGI:1914400]		Q99MB7	-3.2	2.1E-04	6.7	1.7E-03	-1.1	5.1E-01	0.9	3.3E-01
ENSMUST00000137982				-0.2	7.8E-01	-0.1	9.5E-01	0.5	4.2E-01	0.4	6.3E-01
ENSMUST00000177279	inositol polyphosphate-1-phosphatase [Source:MGI Symbol;Acc:MGI:104848]	H3BK26		-4.8	1.4E-04	4.6	9.2E-04	-0.3	7.5E-01	-0.3	6.9E-01
ENSMUST00000137987				0.2	8.5E-01	1.3	3.0E-01	-0.2	8.0E-01	-1.3	2.5E-01
ENSMUST00000177283	esterase D/formylglutathione hydrolase [Source:MGI Symbol;Acc:MGI:95421]	H3BJP2		-8.7	8.8E-06	4.4	3.2E-04	0.5	5.0E-01	0.0	9.7E-01
ENSMUST00000177288	prospero homeobox 1 [Source:MGI Symbol;Acc:MGI:97772]		P48437	7.5	5.8E-05	5.9	2.9E-03	-1.0	5.4E-01	0.0	9.6E-01
ENSMUST00000177289	prospero homeobox 2 [Source:MGI Symbol;Acc:MGI:1920672]		Q8BII1	3.7	1.6E-04	-4.0	3.3E-02	0.5	4.9E-01	1.9	2.6E-01
ENSMUST00000138005				0.8	2.0E-01	0.6	4.5E-01	0.4	4.8E-01	0.6	3.6E-01
ENSMUST00000177293	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]	H3BLI6		-6.4	3.8E-03	-5.3	9.9E-02	0.3	7.9E-01	1.5	6.2E-01
ENSMUST00000177307	forkhead box P1 [Source:MGI Symbol;Acc:MGI:1914004]	H3BLF2		-3.6	4.3E-03	-2.4	2.2E-01	1.8	1.6E-01	-0.7	7.4E-01
ENSMUST00000177322	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]	H3BL25		-6.7	2.0E-05	2.4	8.3E-03	-0.3	6.5E-01	0.2	7.2E-01
ENSMUST00000138019	tripartite motif-containing 41 [Source:MGI Symbol;Acc:MGI:2384814]	F6X2H0		0.9	6.7E-01	1.0	7.4E-01	0.0	1.0E+00	-0.1	9.7E-01
ENSMUST00000138022				-0.5	6.8E-01	-3.6	5.3E-02	-2.1	5.3E-02	1.0	5.6E-01
ENSMUST00000177330	low density lipoprotein receptor-related protein 5 [Source:MGI Symbol;Acc:MGI:1278315]	H3BJH0		7.2	3.9E-05	6.9	1.9E-04	1.3	2.5E-01	-0.1	8.4E-01
ENSMUST00000177352	Rap guanine nucleotide exchange factor (GEF) 3 [Source:MGI Symbol;Acc:MGI:2441741]	H3BK39		6.6	3.4E-04	-3.9	3.7E-03	-0.1	8.8E-01	-0.7	5.0E-01
ENSMUST00000138032				-0.4	6.5E-01	0.0	9.8E-01	0.1	9.2E-01	-0.3	7.4E-01
ENSMUST00000177361	predicted gene 7120 [Source:MGI Symbol;Acc:MGI:3648543]	H3BIZ4		9.0	1.8E-05	5.0	2.5E-03	-3.2	4.3E-02	-1.3	1.3E-01
ENSMUST00000177367	C-type lectin domain family 4, member e [Source:MGI Symbol;Acc:MGI:1861232]	H3BJQ5		-9.9	1.6E-04	-6.5	2.9E-02	1.6	9.4E-02	-1.1	7.2E-01
ENSMUST00000177371	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]	H3BL41		-2.2	3.3E-02	3.4	1.2E-02	-1.4	2.1E-01	0.8	3.5E-01
ENSMUST00000177373	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]	H3BJ02		-5.3	1.1E-04	4.5	5.3E-03	1.4	2.6E-01	-0.4	6.5E-01
ENSMUST00000177375	predicted gene, 42419 [Source:MGI Symbol;Acc:MGI:5649026]		H3BKT1	8.4	4.1E-04	6.1	2.4E-03	-0.7	6.6E-01	0.0	9.8E-01
ENSMUST00000138044				1.7	1.3E-01	0.3	8.2E-01	-0.4	7.4E-01	1.0	4.0E-01
ENSMUST00000138045	capping protein (actin filament) muscle Z-line, beta [Source:MGI Symbol;Acc:MGI:104652]	F7CAZ6		-5.3	9.6E-02	-5.5	1.3E-01	-1.3	3.7E-01	-1.2	7.7E-01
ENSMUST00000177376	chaperonin containing Tcp1, subunit 8 (theta) [Source:MGI Symbol;Acc:MGI:107183]	H3BKR8		-7.7	2.5E-05	4.4	1.9E-03	0.3	7.7E-01	-0.2	7.6E-01
ENSMUST00000177390	golgi phosphoprotein 3-like [Source:MGI Symbol;Acc:MGI:1917129]	H3BJ07		-7.6	5.9E-06	2.9	1.1E-02	-0.1	8.7E-01	-0.1	8.8E-01
ENSMUST00000177392	ubiquitin-like modifier activating enzyme 7 [Source:MGI Symbol;Acc:MGI:1349462]	H3BJA7		-2.2	2.7E-02	6.0	4.8E-04	-0.6	6.0E-01	0.3	7.0E-01
ENSMUST00000177428	granulin [Source:MGI Symbol;Acc:MGI:95832]	H3BJ90		2.7	1.7E-02	6.8	1.5E-04	-0.6	6.1E-01	-1.1	1.1E-01
ENSMUST00000177437	forkhead box P1 [Source:MGI Symbol;Acc:MGI:1914004]			-4.1	6.8E-04	5.8	8.0E-04	-2.0	1.6E-01	-0.8	3.0E-01
ENSMUST00000177458	phosphotyrosine interaction domain containing 1 [Source:MGI Symbol;Acc:MGI:2138391]	H3BJT8		12.1	1.1E-04	5.8	1.5E-02	-0.6	7.9E-01	-1.0	3.9E-01
ENSMUST00000177462	ring finger protein 141 [Source:MGI Symbol;Acc:MGI:1914400]	H3BJB4		-4.2	5.5E-04	5.8	5.6E-04	-0.5	6.7E-01	0.3	6.7E-01
ENSMUST00000138078				4.1	3.6E-02	5.8	1.3E-02	0.0	9.9E-01	-1.7	2.1E-01
ENSMUST00000177497	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	H3BLL4		-3.5	2.1E-02	0.3	8.5E-01	-4.3	1.4E-02	1.7	1.9E-01
ENSMUST00000177523	proline rich protein HaeIII subfamily 1 [Source:MGI Symbol;Acc:MGI:97773]	D3Z1V5		5.8	2.3E-02	-0.2	8.5E-01	1.3	1.1E-01	-2.8	4.4E-02
ENSMUST00000177527	catechol-O-methyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916406]	H3BJ37		-3.3	1.2E-02	-4.6	6.2E-03	2.5	1.4E-03	-1.0	4.9E-01
ENSMUST00000177534	OTU domain containing 7A [Source:MGI Symbol;Acc:MGI:2158505]	H3BKW8		6.8	3.0E-04	7.3	4.0E-04	0.4	7.5E-01	1.2	1.5E-01
ENSMUST00000177545	predicted gene 20605 [Source:MGI Symbol;Acc:MGI:5306917]		Q921G6	-4.0	4.3E-03	-3.8	1.0E-02	1.6	2.4E-02	-0.1	9.6E-01
ENSMUST00000177551	NLR family, CARD domain containing 3 [Source:MGI Symbol;Acc:MGI:2444070]	J3QQ49		6.5	1.5E-04	4.5	4.6E-04	-0.1	9.4E-01	0.3	6.2E-01
ENSMUST00000177565				7.6	7.7E-05	6.4	1.4E-03	0.0	9.7E-01	-0.4	6.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000177570	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]	J3QM80		-5.5	1.6E-04	-5.2	1.9E-03	0.7	2.0E-01	-1.2	3.6E-01
ENSMUST00000177594	ELMO/CED-12 domain containing 2 [Source:MGI Symbol;Acc:MGI:2445165]		Q8BGF6	4.5	3.2E-02	7.6	3.4E-05	0.9	3.6E-01	0.4	4.6E-01
ENSMUST00000177601	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	J3QNH6		14.7	2.2E-07	5.0	3.1E-02	-0.3	9.0E-01	1.3	3.1E-01
ENSMUST00000177612	predicted gene, 21746 [Source:MGI Symbol;Acc:MGI:5433910]	J3QMM6		12.3	4.9E-04	4.9	1.8E-03	0.7	5.3E-01	-0.9	2.5E-01
ENSMUST00000177633	zinc finger, MYND-type containing 8 [Source:MGI Symbol;Acc:MGI:1918025]	Q3U1M7		-5.3	8.9E-03	3.5	8.3E-04	-0.9	1.9E-01	-0.1	8.7E-01
ENSMUST00000177638	RIKEN cDNA E030018B13 gene [Source:MGI Symbol;Acc:MGI:2686543]	J3QMS9		3.8	7.3E-03	-3.8	6.0E-02	-0.9	3.5E-01	-0.3	8.9E-01
ENSMUST00000177648	claudin 14 [Source:MGI Symbol;Acc:MGI:1860425]	A2RSP0	Q9Z0S3	5.2	9.2E-03	4.6	4.3E-03	-1.2	3.3E-01	0.3	7.3E-01
ENSMUST00000177654	phosphatidylinositol 3-kinase catalytic delta polypeptide [Source:MGI Symbol;Acc:MGI:1098211]	Q3T9Y0		-10.2	4.9E-03	7.3	2.2E-04	-0.2	8.9E-01	-0.6	3.7E-01
ENSMUST00000177665	predicted gene, 21833 [Source:MGI Symbol;Acc:MGI:5433997]	J3QPK1		11.9	3.2E-06	3.5	8.8E-02	-2.3	2.6E-01	1.4	2.9E-01
ENSMUST00000138131				-2.0	1.5E-01	-0.7	6.4E-01	0.5	6.7E-01	-0.7	6.3E-01
ENSMUST00000138133	uridine-cytidine kinase 1 [Source:MGI Symbol;Acc:MGI:98904]	F7CBX2		0.6	6.3E-01	0.3	8.7E-01	0.6	6.7E-01	0.9	5.9E-01
ENSMUST00000177696	predicted gene 960 [Source:MGI Symbol;Acc:MGI:2685806]	J3QMY9		6.5	3.1E-04	5.7	7.3E-04	-1.3	3.2E-01	-1.5	5.8E-02
ENSMUST00000138139				-2.0	7.9E-02	-0.6	6.5E-01	0.3	7.7E-01	-1.1	3.8E-01
ENSMUST00000177710	solute carrier family 25 (mitochondrial carrier, brain), member 14 [Source:MGI Symbol;Acc:MGI:1330823]		Q9Z2B2	-4.4	1.2E-02	5.8	4.1E-05	-0.4	5.9E-01	0.1	7.5E-01
ENSMUST00000177714	RIKEN cDNA 2010315B03 gene [Source:MGI Symbol;Acc:MGI:1919321]	J3QK55		2.3	4.0E-03	-9.1	1.4E-06	-1.5	1.8E-03	-2.5	3.1E-02
ENSMUST00000177715	immunoglobulin heavy constant mu [Source:MGI Symbol;Acc:MGI:96448]	A0A075B6A0		-3.5	6.8E-03	-4.3	1.4E-02	0.7	2.8E-01	-0.6	7.2E-01
ENSMUST00000138151				-2.9	5.7E-02	-2.5	1.2E-01	-0.2	8.4E-01	-0.6	7.1E-01
ENSMUST00000138157	FERM domain containing 5 [Source:MGI Symbol;Acc:MGI:2442557]		Q6P5H6	5.2	6.7E-02	3.0	3.2E-01	-0.5	8.8E-01	1.8	3.7E-01
ENSMUST00000177722	predicted gene 11168 [Source:MGI Symbol;Acc:MGI:3779420]	J3QN50		8.1	6.8E-04	-4.8	5.1E-04	-0.4	3.8E-01	-3.1	1.9E-02
ENSMUST00000177752	FK506 binding protein 2 [Source:MGI Symbol;Acc:MGI:95542]	Q3TND1	P45878	-1.8	1.8E-02	2.1	5.8E-02	-1.3	1.6E-01	0.8	3.5E-01
ENSMUST00000177766				6.6	1.5E-02	-0.2	7.3E-01	0.7	1.6E-01	-0.6	3.9E-01
ENSMUST00000177814	Ca2+-dependent secretion activator [Source:MGI Symbol;Acc:MGI:1350922]	J3QJW3		7.2	4.1E-04	-4.2	2.3E-02	-0.2	8.0E-01	-0.4	8.0E-01
ENSMUST00000138181	ubiquitination factor E4B [Source:MGI Symbol;Acc:MGI:1927086]	H7BXC2		-2.7	3.5E-01	-3.1	3.8E-01	-0.8	6.7E-01	-0.4	9.2E-01
ENSMUST00000138193				3.1	7.6E-02	0.8	6.1E-01	-2.6	1.1E-01	-0.3	8.3E-01
ENSMUST00000138199				0.6	7.7E-01	1.6	5.6E-01	0.8	6.9E-01	-0.3	9.2E-01
ENSMUST00000177817	predicted gene, 21738 [Source:MGI Symbol;Acc:MGI:5433902]	J3QP72		14.7	4.3E-08	6.1	2.5E-05	-0.9	2.7E-01	0.0	9.2E-01
ENSMUST00000138202				-1.0	2.1E-01	0.7	4.5E-01	0.7	3.1E-01	-1.0	2.9E-01
ENSMUST00000177822	discs, large (Drosophila) homolog-associated protein 5 [Source:MGI Symbol;Acc:MGI:2183453]	J3QPN1		4.7	2.0E-05	5.4	5.4E-03	0.3	8.5E-01	-0.8	4.0E-01
ENSMUST00000177840	CD151 antigen [Source:MGI Symbol;Acc:MGI:1096360]		O35566	-6.7	7.7E-05	2.9	6.7E-02	-1.5	2.7E-01	-0.9	4.4E-01
ENSMUST00000177841	tumor-suppressing subchromosomal transferable fragment 4 [Source:MGI Symbol;Acc:MGI:1861712]		Q9JHE7	-3.9	1.4E-02	-8.1	2.3E-03	0.3	6.5E-01	-1.1	6.2E-01
ENSMUST00000138233				0.0	9.8E-01	1.2	5.0E-01	1.0	5.2E-01	-0.2	8.8E-01
ENSMUST00000177848	RAD17 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1333807]	Q3UYY2	Q6NXW6	-5.5	4.2E-03	-2.6	8.9E-02	0.6	5.3E-01	-0.5	7.2E-01
ENSMUST00000138238				-1.0	5.4E-01	-2.1	3.3E-01	-0.7	6.1E-01	0.4	8.3E-01
ENSMUST00000138242				0.1	9.5E-01	-0.3	8.3E-01	-0.4	7.6E-01	0.0	9.8E-01
ENSMUST00000177850	ornithine decarboxylase antizyme 1 [Source:MGI Symbol;Acc:MGI:109433]	J3QMV2		-4.9	2.2E-04	-0.2	8.4E-01	0.4	6.2E-01	-2.3	6.1E-02
ENSMUST00000177875	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	J3QPP7		14.3	5.1E-08	-0.2	7.3E-01	0.1	7.9E-01	-4.6	4.2E-04
ENSMUST00000177877	predicted gene 8220 [Source:MGI Symbol;Acc:MGI:3643828]	J3QMR5		6.8	3.6E-04	0.3	7.8E-01	3.2	2.1E-03	0.8	4.6E-01
ENSMUST00000177878	predicted gene, 21788 [Source:MGI Symbol;Acc:MGI:5433952]	J3QNH3		12.5	1.7E-04	2.3	6.1E-02	0.2	8.3E-01	0.6	5.2E-01
ENSMUST00000177891	predicted gene 5108 [Source:MGI Symbol;Acc:MGI:3645064]	J3QP01		10.9	2.3E-06	1.3	2.0E-01	0.3	7.4E-01	0.8	3.1E-01
ENSMUST00000138280	constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	D6RH36		-2.9	6.9E-02	-3.3	5.7E-02	-1.8	7.3E-02	-1.4	4.5E-01
ENSMUST00000177908	coiled-coil domain containing 42B [Source:MGI Symbol;Acc:MGI:3779542]	J3QPZ5		6.6	1.3E-04	-4.4	6.3E-02	0.3	7.6E-01	-0.6	8.0E-01
ENSMUST00000177916	zinc finger protein 131 [Source:MGI Symbol;Acc:MGI:1919715]		Q8K3J5	-5.4	9.1E-05	-6.1	1.6E-04	0.2	6.5E-01	-0.7	5.3E-01
ENSMUST00000177921				9.7	8.9E-06	5.6	1.1E-04	0.3	6.9E-01	0.4	4.9E-01
ENSMUST00000138287				1.7	3.8E-01	1.4	5.7E-01	-0.7	7.1E-01	-0.3	8.8E-01
ENSMUST00000138296				2.2	6.7E-02	2.6	9.9E-02	-0.4	7.7E-01	-0.8	4.5E-01
ENSMUST00000177929	predicted gene 10610 [Source:MGI Symbol;Acc:MGI:3642045]	Q8C4H5		6.2	2.3E-04	7.7	1.4E-04	-0.6	6.6E-01	-2.1	1.3E-02
ENSMUST00000138299	trinucleotide repeat containing 6C [Source:MGI Symbol;Acc:MGI:2443265]	B7ZC94		-1.9	2.4E-01	-4.3	1.4E-01	0.0	9.9E-01	2.4	3.9E-01
ENSMUST00000138302	WW domain binding protein 1 like [Source:MGI Symbol;Acc:MGI:107577]		Q8BGW2	-1.2	7.9E-02	-4.4	5.0E-03	0.6	3.2E-01	3.8	9.8E-03
ENSMUST00000138304				3.9	7.5E-02	0.0	9.9E-01	-4.0	6.0E-02	0.0	1.0E+00
ENSMUST00000138306				-1.5	2.6E-01	0.3	8.0E-01	-0.5	6.4E-01	-2.3	1.2E-01
ENSMUST00000138309				0.8	3.3E-01	0.2	8.7E-01	-0.5	5.6E-01	0.2	8.3E-01
ENSMUST00000177946	prominin 1 [Source:MGI Symbol;Acc:MGI:1100886]	Q8CDK8		-4.6	2.7E-03	5.0	1.4E-04	-0.3	7.0E-01	-0.3	5.0E-01
ENSMUST00000177955	carbohydrate kinase domain containing [Source:MGI Symbol;Acc:MGI:1913353]	J3QMM7		-6.1	5.1E-05	1.9	9.2E-02	-0.1	9.1E-01	1.7	8.0E-02
ENSMUST00000138318				0.9	6.7E-01	0.4	8.6E-01	0.1	9.7E-01	0.5	8.1E-01
ENSMUST00000138321	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]	F6Q8C0		1.4	1.5E-01	1.4	2.2E-01	-0.4	6.6E-01	-0.4	6.8E-01
ENSMUST00000177962	B cell receptor associated protein 29 [Source:MGI Symbol;Acc:MGI:101917]	Q542A1	Q61334	-4.0	5.4E-04	6.5	6.1E-04	-0.6	6.6E-01	-0.5	4.9E-01
ENSMUST00000177966	nebulette [Source:MGI Symbol;Acc:MGI:1921353]	Q3TR73		7.1	1.0E-04	-4.9	4.1E-03	-1.1	9.2E-02	-0.2	8.8E-01
ENSMUST00000177967	ECSIT homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1349469]	J3KMM6		4.5	5.6E-03	7.1	1.9E-02	-0.7	8.2E-01	-1.6	2.8E-01
ENSMUST00000138328	ER membrane protein complex subunit 10 [Source:MGI Symbol;Acc:MGI:1916933]	D3Z665		3.0	9.6E-02	5.4	1.3E-02	0.7	6.8E-01	-1.7	2.3E-01
ENSMUST00000177969	predicted gene 10715 [Source:MGI Symbol;Acc:MGI:3642376]	J3QP74		11.9	7.3E-07	6.4	4.2E-04	-0.6	6.4E-01	0.4	5.4E-01
ENSMUST00000177978	RIKEN cDNA 1700047I17 gene 2 [Source:MGI Symbol;Acc:MGI:3714351]		Q8BR63	-4.5	2.8E-04	-2.6	2.3E-01	1.1	3.4E-01	-0.9	7.0E-01
ENSMUST00000177985	RIKEN cDNA 4930474N05 gene [Source:MGI Symbol;Acc:MGI:3586330]	Q8BVR5		5.1	5.7E-04	6.2	2.4E-04	0.7	4.8E-01	-1.4	4.8E-02
ENSMUST00000177999	RIKEN cDNA F930015N05 gene [Source:MGI Symbol;Acc:MGI:3606161]	Q8C3A3		6.1	3.8E-04	5.7	5.9E-04	-0.6	6.4E-01	-0.1	8.9E-01
ENSMUST00000138343				1.6	9.4E-02	2.3	6.7E-02	0.5	5.7E-01	-0.2	8.6E-01
ENSMUST00000178015	pumilio RNA-binding family member 2 [Source:MGI Symbol;Acc:MGI:1931751]		Q80U58	-8.3	5.2E-03	3.8	2.7E-04	-0.3	6.3E-01	-0.2	7.5E-01
ENSMUST00000178021	interferon induced transmembrane protein 7 [Source:MGI Symbol;Acc:MGI:1921732]	Q9D3R8		8.4	1.2E-04	6.5	9.4E-04	-0.7	6.4E-01	-1.0	2.5E-01
ENSMUST00000138353				2.2	3.6E-01	2.4	4.2E-01	0.4	8.8E-01	0.2	9.4E-01
ENSMUST00000178024	RIKEN cDNA G530012D1 gene [Source:MGI Symbol;Acc:MGI:3642025]	J3QK25		16.0	5.8E-06	0.6	7.2E-01	-2.1	1.6E-01	3.3	4.0E-02
ENSMUST00000178034	transglutaminase 1, K polypeptide [Source:MGI Symbol;Acc:MGI:98730]			-7.1	1.6E-04	-1.3	2.6E-01	1.3	9.7E-02	-1.0	3.9E-01
ENSMUST00000178045	expressed sequence AA474331 [Source:MGI Symbol;Acc:MGI:3035041]	J3QNS5		3.7	1.7E-03	6.6	1.4E-04	-0.5	6.3E-01	-4.4	3.6E-04
ENSMUST00000178065	predicted gene 4791 [Source:MGI Symbol;Acc:MGI:3779436]	J3QQ14		9.1	1.2E-05	3.8	1.3E-01	-0.6	8.1E-01	1.2	4.5E-01
ENSMUST00000138381				-0.7	7.0E-01	-4.3	5.4E-02	-4.4	3.8E-03	-0.7	7.4E-01
ENSMUST00000138386				-0.5	7.0E-01	0.3	8.8E-01	1.2	4.2E-01	0.5	7.4E-01
ENSMUST00000178075	ubiquitin specific peptidase 19 [Source:MGI Symbol;Acc:MGI:1918722]	J3KMM1		-8.7	1.9E-04	8.5	7.5E-05	-0.7	6.3E-01	-0.8	1.9E-01
ENSMUST00000178077	predicted gene 11168 [Source:MGI Symbol;Acc:MGI:3779420]	J3QNI2		12.5	8.2E-07	-2.0	2.5E-02	-1.5	1.9E-02	-1.3	1.3E-01
ENSMUST00000138395	erythroblast membrane-associated protein [Source:MGI Symbol;Acc:MGI:1349816]	A2A7P7		3.2	3.2E-01	5.3	1.3E-01	-0.4	9.1E-01	-2.5	2.6E-01
ENSMUST00000138397	interleukin-1 receptor-associated kinase 1 [Source:MGI Symbol;Acc:MGI:107420]	F6TQF4		-0.2	9.1E-01	-1.1	6.8E-01	-1.2	4.5E-01	-0.4	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000178092	purine-nucleoside phosphorylase [Source:MGI Symbol;Acc:MGI:97365]	Q543K9		-5.4	1.3E-05	3.9	1.5E-03	-0.8	3.6E-01	0.3	6.1E-01
ENSMUST00000178096	predicted gene, 18856 [Source:MGI Symbol;Acc:MGI:5011041]	J3QMW8		7.2	4.7E-04	0.1	9.0E-01	1.3	6.7E-02	-0.9	2.4E-01
ENSMUST00000178100	T cell receptor alpha variable 7N-6 [Source:MGI Symbol;Acc:MGI:3704442]	A0A0B4J1N1		4.1	4.6E-04	1.2	3.0E-01	-0.1	8.9E-01	1.5	1.5E-01
ENSMUST00000178110	DNA methyltransferase (cytosine-5) 1 [Source:MGI Symbol;Acc:MGI:94912]		P13864	9.7	7.8E-06	5.9	6.3E-03	-0.6	7.3E-01	-1.6	1.6E-01
ENSMUST00000178124	predicted gene 4980 [Source:MGI Symbol;Acc:MGI:3646425]		Q8C013	6.6	7.3E-05	1.2	4.4E-01	-0.2	8.7E-01	2.0	1.6E-01
ENSMUST00000178140	fidgetin-like 2 [Source:MGI Symbol;Acc:MGI:3646919]	J3QK54		-2.1	9.0E-04	7.9	2.3E-05	0.1	9.5E-01	-0.7	1.5E-01
ENSMUST00000178142	NIM1 serine/threonine protein kinase [Source:MGI Symbol;Acc:MGI:2442399]		Q8BHI9	3.3	1.5E-04	2.2	3.7E-02	-0.7	4.0E-01	-0.8	3.4E-01
ENSMUST00000178149	predicted gene, 20825 [Source:MGI Symbol;Acc:MGI:5434181]	J3QM67		5.8	5.0E-03	5.3	2.5E-04	-1.0	2.9E-01	0.3	5.9E-01
ENSMUST00000138443				1.7	1.5E-01	2.5	9.5E-02	0.7	5.3E-01	-0.1	9.3E-01
ENSMUST00000178156	ankyrin repeat domain 44 [Source:MGI Symbol;Acc:MGI:3045243]	J3QNJ4		-1.7	3.2E-02	6.3	2.3E-04	-0.2	8.8E-01	0.5	4.4E-01
ENSMUST00000178161	RIKEN cDNA B020004C17 gene [Source:MGI Symbol;Acc:MGI:3588236]	J3QP07		5.5	7.3E-06	6.4	1.0E-03	1.0	4.7E-01	-2.1	4.1E-02
ENSMUST00000178174	POU domain, class 3, transcription factor 2 [Source:MGI Symbol;Acc:MGI:101895]		P31360	9.5	1.7E-05	4.6	1.6E-03	-1.5	2.1E-01	1.3	7.3E-02
ENSMUST00000178224	RIKEN cDNA D430019H16 gene [Source:MGI Symbol;Acc:MGI:2443127]	J3QPM6		8.5	2.5E-06	5.8	2.9E-06	-0.7	2.3E-01	0.2	4.7E-01
ENSMUST00000178226	ankyrin repeat domain 44 [Source:MGI Symbol;Acc:MGI:3045243]	J3QK13		-3.8	8.6E-03	5.1	1.1E-03	-0.7	5.4E-01	1.0	2.0E-01
ENSMUST00000178228	C2 calcium-dependent domain containing 4C [Source:MGI Symbol;Acc:MGI:2685084]		Q5HZI2	10.1	3.5E-05	3.4	6.2E-04	0.2	7.6E-01	-0.6	2.6E-01
ENSMUST00000178231	adenosine deaminase, tRNA-specific 3 [Source:MGI Symbol;Acc:MGI:1924344]		Q6PAT0	4.7	2.3E-04	6.0	2.8E-03	-0.6	7.0E-01	0.0	9.6E-01
ENSMUST00000178235	angio-associated migratory protein [Source:MGI Symbol;Acc:MGI:107809]	J3QN89		-4.7	2.6E-03	4.3	7.0E-04	-0.8	3.3E-01	0.3	6.4E-01
ENSMUST00000138478				-1.9	1.9E-01	0.8	7.2E-01	2.6	1.5E-01	-0.1	9.4E-01
ENSMUST00000178241	RIKEN cDNA 8430408G22 gene [Source:MGI Symbol;Acc:MGI:1918730]		Q8K2F3	4.6	3.8E-05	-1.9	2.0E-01	0.9	3.0E-01	0.2	8.8E-01
ENSMUST00000178253	nucleoporin 88 [Source:MGI Symbol;Acc:MGI:104900]	J3QNZ2		3.4	1.2E-03	3.9	1.0E-02	-0.3	7.9E-01	0.7	3.9E-01
ENSMUST00000178254	profilin 1 [Source:MGI Symbol;Acc:MGI:97549]	J3QMC2		-8.9	3.1E-02	-1.1	5.6E-01	2.3	8.2E-02	-0.7	6.9E-01
ENSMUST00000178271	zinc finger protein 131 [Source:MGI Symbol;Acc:MGI:1919715]		Q8K3J5	-3.5	1.0E-03	5.8	1.2E-04	1.6	7.4E-02	-0.1	9.0E-01
ENSMUST00000178293	ubiquitin specific peptidase 27, X chromosome [Source:MGI Symbol;Acc:MGI:1859645]		Q8CEG8	6.4	2.6E-05	5.9	4.0E-04	0.2	8.7E-01	0.7	2.7E-01
ENSMUST00000178310	is-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) [Source:MGI Symbol;Acc:M	Q642K5		-5.8	1.3E-03	-4.2	3.4E-03	-1.4	4.5E-02	-0.2	8.7E-01
ENSMUST00000138505	DOT1-like, histone H3 methyltransferase (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143886]	F6S070		1.8	1.2E-01	1.8	2.3E-01	0.1	9.1E-01	0.1	9.0E-01
ENSMUST00000138506	tubulin folding cofactor E-like [Source:MGI Symbol;Acc:MGI:1925543]		Q8C5W3	2.8	7.0E-02	3.6	6.4E-02	0.5	7.4E-01	-0.4	8.1E-01
ENSMUST00000138507				-3.1	4.1E-02	-2.7	9.8E-02	0.0	9.8E-01	-0.4	8.1E-01
ENSMUST00000178312	predicted gene, 21897 [Source:MGI Symbol;Acc:MGI:5434061]	J3KMP5		12.7	6.5E-06	-2.0	6.2E-02	0.3	6.2E-01	-1.2	3.0E-01
ENSMUST00000138512				1.1	6.3E-01	1.4	6.5E-01	-0.3	9.1E-01	-0.6	8.1E-01
ENSMUST00000178327				6.5	1.0E-03	5.3	2.3E-03	-0.5	7.3E-01	-0.1	9.2E-01
ENSMUST00000178328	glycogenin [Source:MGI Symbol;Acc:MGI:1351614]		Q9R062	-8.4	1.7E-04	7.6	3.8E-03	7.7	2.1E-03	-3.6	1.5E-02
ENSMUST00000138536				-0.7	4.6E-01	-0.2	8.7E-01	0.8	3.8E-01	0.3	7.7E-01
ENSMUST00000138541				0.5	8.3E-01	1.3	7.0E-01	0.5	8.5E-01	-0.3	9.2E-01
ENSMUST00000178332	predicted gene, 21882 [Source:MGI Symbol;Acc:MGI:5434046]	J3QN86		9.0	1.1E-05	6.9	1.3E-04	-0.6	6.1E-01	-1.5	3.5E-02
ENSMUST00000138544				-0.2	8.7E-01	2.0	1.7E-01	1.4	2.0E-01	-0.7	5.6E-01
ENSMUST00000178343	phosphatidylserine decarboxylase [Source:HGNC Symbol;Acc:HGNC:8999]			4.1	4.0E-04	6.2	1.1E-03	-0.7	6.5E-01	0.3	6.9E-01
ENSMUST00000178348	predicted gene 11168 [Source:MGI Symbol;Acc:MGI:3779420]	J3QK61		14.4	5.1E-08	3.7	7.9E-04	0.2	8.1E-01	-0.2	7.6E-01
ENSMUST00000138557	tripartite motif-containing 5 [Source:MGI Symbol;Acc:MGI:3646853]	D6RCJ3		-0.3	8.6E-01	3.7	1.1E-01	2.3	2.6E-01	-1.8	2.9E-01
ENSMUST00000178353	predicted gene 21992 [Source:MGI Symbol;Acc:MGI:5439461]	J3QN51		3.5	9.1E-04	4.3	9.8E-04	0.1	8.9E-01	0.7	2.9E-01
ENSMUST00000138560	downstream neighbor of SON [Source:MGI Symbol;Acc:MGI:1890621]	F6QFE2		0.5	8.4E-01	-1.6	5.1E-01	-3.2	9.5E-02	-1.2	6.5E-01
ENSMUST00000178355	nuclear protein transcriptional regulator 1 like [Source:MGI Symbol;Acc:MGI:1923099]		Q497P3	5.5	1.3E-05	6.1	6.8E-04	-0.5	7.2E-01	-1.8	2.9E-02
ENSMUST00000178372	zinc finger protein 697 [Source:MGI Symbol;Acc:MGI:2139736]	G5E8C0		8.4	2.6E-03	4.9	1.9E-02	-0.3	8.5E-01	-0.4	6.9E-01
ENSMUST00000138567	MMS22-like, DNA repair protein [Source:MGI Symbol;Acc:MGI:2684980]	G5E925		3.4	1.5E-01	0.7	7.5E-01	-2.0	3.9E-01	0.7	7.3E-01
ENSMUST00000178385	zinc finger, AN1-type domain 6 [Source:MGI Symbol;Acc:MGI:1929510]		Q9DCH6	-7.2	3.5E-05	6.0	5.9E-04	-0.5	7.0E-01	0.2	8.2E-01
ENSMUST00000178401	zinc finger protein 870 [Source:MGI Symbol;Acc:MGI:3029586]	J3QMA4		4.0	3.1E-04	6.2	1.4E-04	-1.2	3.0E-01	-0.7	3.1E-01
ENSMUST00000178410	cyclic AMP-regulated phosphoprotein, 21 [Source:MGI Symbol;Acc:MGI:107562]		Q9DCB4	7.5	6.3E-03	7.4	1.1E-05	-2.5	2.9E-02	0.1	8.3E-01
ENSMUST00000178414	predicted gene 3383 [Source:MGI Symbol;Acc:MGI:3781561]	J3QQ59		5.7	7.8E-04	3.7	1.7E-02	-1.8	2.2E-01	0.3	7.2E-01
ENSMUST00000178422	death-associated protein kinase 3 [Source:MGI Symbol;Acc:MGI:1203520]	Q05A21	O54784	-6.6	2.1E-04	8.3	6.2E-05	-1.5	2.8E-01	-0.9	1.4E-01
ENSMUST00000178438	predicted gene, 21119 [Source:MGI Symbol;Acc:MGI:5434474]	Q8C646		6.8	1.6E-03	5.3	1.9E-03	-0.4	7.4E-01	-1.3	1.4E-01
ENSMUST00000138589				-2.2	1.1E-01	-0.6	7.3E-01	0.8	5.0E-01	-0.8	6.1E-01
ENSMUST00000178473	Fanconi anemia core complex associated protein 20 [Source:MGI Symbol;Acc:MGI:1914763]		Q3UN58	-5.6	9.2E-04	5.5	7.9E-04	-0.5	6.6E-01	0.2	8.0E-01
ENSMUST00000178474	ARP3 actin-related protein 3 [Source:MGI Symbol;Acc:MGI:1921367]	Q3ULF7	Q99JY9	-12.0	5.9E-07	9.1	5.9E-06	-1.5	2.1E-01	-0.2	5.8E-01
ENSMUST00000178477	NK2 homeobox 1 [Source:MGI Symbol;Acc:MGI:108067]		P50220	8.0	1.8E-05	4.1	2.7E-04	-0.5	4.4E-01	0.2	7.1E-01
ENSMUST00000178509	predicted gene 9830 [Source:MGI Symbol;Acc:MGI:3704332]		Q9CQY2	-5.3	5.5E-04	3.0	3.3E-04	-0.2	6.2E-01	-0.4	3.8E-01
ENSMUST00000138602				-1.9	1.6E-01	0.2	8.8E-01	0.3	7.3E-01	-1.7	2.4E-01
ENSMUST00000178510	2-cell-stage, variable group, member 1 [Source:MGI Symbol;Acc:MGI:1933437]	O70619		6.0	2.9E-04	4.5	2.6E-03	-2.1	9.1E-02	-0.5	5.5E-01
ENSMUST00000178522	transmembrane protein 184b [Source:MGI Symbol;Acc:MGI:2445179]		Q8BG09	-3.3	1.1E-02	4.4	2.6E-03	-0.6	6.1E-01	-0.1	9.0E-01
ENSMUST00000138605				-1.2	5.5E-01	5.5	6.9E-02	3.5	1.9E-01	-3.2	1.2E-01
ENSMUST00000138615	zinc finger protein 326 [Source:MGI Symbol;Acc:MGI:1927246]	D6RG92		1.0	5.2E-01	1.2	4.7E-01	-0.6	6.8E-01	-0.9	5.6E-01
ENSMUST00000178524	predicted gene, 20946 [Source:MGI Symbol;Acc:MGI:5434301]	J3QN60		8.4	9.9E-03	6.5	4.0E-03	0.5	7.9E-01	-2.1	7.9E-02
ENSMUST00000138622	zinc finger, DHHC domain containing 3 [Source:MGI Symbol;Acc:MGI:1926134]	D6RDS4		1.0	5.7E-02	0.7	3.0E-01	0.7	2.0E-01	1.0	1.1E-01
ENSMUST00000178533	predicted gene 13694 [Source:MGI Symbol;Acc:MGI:3702064]	A2AK42		6.5	6.6E-05	5.4	1.5E-03	0.5	6.6E-01	-0.3	6.8E-01
ENSMUST00000138628	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:1916960]	D3YVS8		2.1	6.5E-02	4.4	1.0E-02	1.2	3.8E-01	-1.1	2.5E-01
ENSMUST00000138629				0.5	4.5E-01	-4.6	1.9E-03	-2.4	1.8E-03	2.7	2.9E-02
ENSMUST00000178539	predicted gene 5627 [Source:MGI Symbol;Acc:MGI:3645308]	Q3V3D0		6.7	7.6E-05	6.4	7.3E-04	-0.4	7.6E-01	-0.9	2.5E-01
ENSMUST00000178545	transmembrane protein 200C [Source:MGI Symbol;Acc:MGI:3646281]	J3QK46		7.9	2.2E-05	6.3	9.7E-04	2.6	6.4E-02	-0.4	6.0E-01
ENSMUST00000178552	predicted gene 7978 [Source:MGI Symbol;Acc:MGI:3704107]	Q6P8K3		5.9	2.2E-03	6.4	9.0E-04	-0.6	6.9E-01	-0.4	5.8E-01
ENSMUST00000138638				0.9	9.7E-02	1.6	4.2E-02	0.6	2.6E-01	0.0	9.4E-01
ENSMUST00000178553	predicted gene, 17467 [Source:MGI Symbol;Acc:MGI:4937101]	J3QNF7		9.0	2.0E-04	-1.6	1.9E-01	1.2	1.3E-01	-0.6	6.1E-01
ENSMUST00000178561	coiled-coil domain containing 180 [Source:MGI Symbol;Acc:MGI:2685871]	J3QNE4		8.6	5.6E-04	-3.9	1.3E-01	0.6	6.2E-01	-0.5	8.4E-01
ENSMUST00000138648				0.6	5.8E-01	2.0	1.3E-01	-0.1	9.0E-01	-1.5	1.8E-01
ENSMUST00000178563	expressed sequence AA474331 [Source:MGI Symbol;Acc:MGI:3035041]	J3QPW5		3.6	3.3E-02	0.3	6.8E-01	-0.6	3.5E-01	-3.3	3.4E-03
ENSMUST00000178569				8.5	8.2E-06	6.5	2.2E-04	-0.6	6.2E-01	-3.4	1.5E-03
ENSMUST00000138657				-2.9	1.0E-01	-3.7	1.2E-01	-0.5	6.8E-01	0.4	8.8E-01
ENSMUST00000178573	WD repeat domain 53 [Source:MGI Symbol;Acc:MGI:1916230]		Q9DB94	-3.0	8.7E-03	4.5	2.8E-04	-3.8	2.9E-03	-0.5	3.4E-01
ENSMUST00000178581	predicted gene, 19668 [Source:MGI Symbol;Acc:MGI:5011853]	J3QMD1		8.2	5.4E-05	3.4	7.9E-03	0.3	7.9E-01	0.1	8.5E-01
ENSMUST00000178594	predicted gene 8237 [Source:MGI Symbol;Acc:MGI:3644039]	J3QN62		6.6	7.3E-05	-7.0	5.7E-04	1.2	2.0E-02	-0.8	6.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000138671	K(lysine) acetyltransferase 7 [Source:MGI Symbol;Acc:MGI:2182799]	F6S4B9		-0.9	4.2E-01	-2.4	1.7E-01	-0.2	8.2E-01	1.4	4.0E-01
ENSMUST00000138673				-0.7	5.6E-01	0.9	5.2E-01	0.1	9.1E-01	-1.5	2.6E-01
ENSMUST00000178605	acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI		O08912	-5.5	7.1E-03	-1.9	6.8E-02	0.6	3.7E-01	0.7	4.8E-01
ENSMUST00000178611	ynthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9) [Source:MGI Symbol;Acc:MGI:1(		Q9CR84	8.1	4.3E-04	-5.2	2.2E-02	0.1	9.1E-01	-1.3	5.5E-01
ENSMUST00000138683	chondroitin polymerizing factor [Source:MGI Symbol;Acc:MGI:106576]	D6RFA4		-1.9	1.4E-01	-3.3	8.7E-02	-0.5	5.8E-01	0.9	6.2E-01
ENSMUST00000138688				2.1	1.1E-01	2.2	2.4E-01	1.3	4.4E-01	1.1	3.9E-01
ENSMUST00000178618	predicted gene, 21188 [Source:MGI Symbol;Acc:MGI:5434543]	Q3T9V6		-3.7	1.6E-03	-1.4	3.8E-01	1.6	1.3E-01	-0.5	7.4E-01
ENSMUST00000178627	ubiquitin-conjugating enzyme E2F (putative) [Source:MGI Symbol;Acc:MGI:1915171]		Q9CY34	-6.4	4.1E-05	3.0	1.4E-03	0.3	5.8E-01	-0.3	6.0E-01
ENSMUST00000178630	calcium homeostasis modulator 3 [Source:MGI Symbol;Acc:MGI:3645665]	J3QMI4		6.8	4.6E-05	-2.5	9.0E-02	0.2	7.7E-01	-1.1	4.5E-01
ENSMUST00000178641	predicted gene, 17535 [Source:MGI Symbol;Acc:MGI:4937169]	J3KMR8		13.0	1.4E-06	5.4	1.7E-03	1.0	4.1E-01	-0.9	2.9E-01
ENSMUST00000178644	predicted gene 21969 [Source:MGI Symbol;Acc:MGI:5439438]	J3QJZ1		6.8	3.4E-04	7.0	1.6E-04	-1.0	4.2E-01	0.1	8.9E-01
ENSMUST00000178646	predicted gene 6367 [Source:MGI Symbol;Acc:MGI:3704106]	Q8C6L9		4.6	2.8E-02	5.9	5.7E-04	1.2	3.0E-01	-1.5	4.8E-02
ENSMUST00000178665	zinc finger protein 207 [Source:MGI Symbol;Acc:MGI:1340045]		Q9JMD0	-2.6	3.1E-02	-6.8	4.6E-03	1.7	1.6E-02	2.4	2.2E-01
ENSMUST00000138728				3.3	2.1E-01	2.0	4.9E-01	-1.9	4.8E-01	-0.6	7.8E-01
ENSMUST00000178679	testis and ovary specific PAZ domain containing 1 [Source:MGI Symbol;Acc:MGI:3779933]		E5FYH1	7.0	3.2E-04	4.1	1.8E-03	-2.1	7.6E-02	0.5	4.3E-01
ENSMUST00000178687	cat eye syndrome chromosome region, candidate 6 [Source:MGI Symbol;Acc:MGI:2136977]	B2RQD1	Q99MX7	6.2	3.9E-05	3.9	2.5E-04	-1.7	3.1E-02	-0.2	7.4E-01
ENSMUST00000138739				1.7	7.1E-02	0.6	5.8E-01	-0.4	6.5E-01	0.7	4.3E-01
ENSMUST00000178691	ubiquitin-like 4A [Source:MGI Symbol;Acc:MGI:95049]	Q3UK94	P21126	-2.9	3.2E-02	-2.4	3.9E-02	0.6	3.1E-01	-0.4	7.1E-01
ENSMUST00000178700	G protein-coupled receptor 161 [Source:MGI Symbol;Acc:MGI:2685054]		B2RPY5	5.4	1.5E-04	-3.6	2.0E-02	-1.4	8.5E-02	-0.8	6.0E-01
ENSMUST00000138746				3.4	1.8E-01	5.5	9.2E-02	0.1	9.7E-01	-2.0	3.4E-01
ENSMUST00000178730	PTK2 protein tyrosine kinase 2 beta [Source:MGI Symbol;Acc:MGI:104908]	K7QD41	Q9QVP9	-8.8	8.2E-04	4.6	9.7E-05	0.6	4.0E-01	0.0	9.5E-01
ENSMUST00000178747	predicted gene, 21645 [Source:MGI Symbol;Acc:MGI:5435000]	J3QN64		5.6	1.3E-03	0.9	5.5E-01	-1.1	3.6E-01	1.3	2.9E-01
ENSMUST00000178752	filaggrin [Source:MGI Symbol;Acc:MGI:95553]	A0A0A6YVU7		8.0	1.2E-04	6.4	7.2E-03	0.5	8.1E-01	-1.3	2.9E-01
ENSMUST00000178756	D4, zinc and double PHD fingers, family 3 [Source:MGI Symbol;Acc:MGI:1917377]		P58269	7.7	2.4E-03	7.6	3.6E-04	-1.4	3.8E-01	0.3	6.3E-01
ENSMUST00000138759	hydroxyacylglutathione hydrolase-like [Source:MGI Symbol;Acc:MGI:1919877]	D3YZU6		-3.7	1.0E-01	-2.0	4.9E-01	1.0	5.8E-01	-0.7	8.0E-01
ENSMUST00000178757	predicted gene 9994 [Source:MGI Symbol;Acc:MGI:3711964]		Q6XQH0	3.8	1.5E-04	-1.0	9.7E-02	0.6	1.2E-01	0.1	9.1E-01
ENSMUST00000138766				1.0	1.5E-01	2.2	2.7E-02	1.1	1.2E-01	-0.1	9.1E-01
ENSMUST00000178759	predicted gene 8247 [Source:MGI Symbol;Acc:MGI:3644638]	J3KMT2		6.2	8.3E-04	10.0	4.5E-05	0.3	8.4E-01	1.9	7.2E-03
ENSMUST00000138773				-0.4	5.7E-01	0.6	5.7E-01	0.9	2.2E-01	-0.1	9.1E-01
ENSMUST00000178767	predicted gene 6537 [Source:MGI Symbol;Acc:MGI:3645242]	J3QPU5		7.1	6.7E-05	7.3	5.6E-05	0.6	5.6E-01	0.8	1.4E-01
ENSMUST00000138779				0.5	5.9E-01	1.3	2.6E-01	0.4	7.0E-01	-0.4	6.7E-01
ENSMUST00000178774	ribosomal protein S10 [Source:MGI Symbol;Acc:MGI:1914347]	Q5M9K7	P63325	-8.7	1.3E-03	5.6	1.2E-03	-0.4	7.4E-01	0.2	8.1E-01
ENSMUST00000138789				-0.1	9.5E-01	-0.1	9.3E-01	-0.6	4.4E-01	-0.5	5.3E-01
ENSMUST00000178785	predicted gene, 21964 [Source:MGI Symbol;Acc:MGI:5439433]	J3QNV0		5.7	5.3E-04	7.0	1.9E-04	-0.2	8.9E-01	0.1	9.3E-01
ENSMUST00000138792				-1.8	6.0E-01	-1.5	7.2E-01	-0.5	8.6E-01	-0.7	8.6E-01
ENSMUST00000138793				3.2	3.6E-02	2.0	1.8E-01	-2.1	1.3E-01	-1.0	4.5E-01
ENSMUST00000178808	glutathione S-transferase, mu 4 [Source:MGI Symbol;Acc:MGI:95862]	A2AE91		-4.9	1.1E-04	-5.7	4.8E-03	1.4	6.8E-02	-3.4	1.3E-01
ENSMUST00000178812	catenin (cadherin associated protein), beta 1 [Source:MGI Symbol;Acc:MGI:88276]		Q02248	-6.6	4.8E-05	-1.4	2.2E-01	-0.3	7.3E-01	-2.1	1.3E-01
ENSMUST00000178817	carbohydrate kinase domain containing [Source:MGI Symbol;Acc:MGI:1913353]	J3QPU6		4.7	6.2E-04	5.6	7.5E-05	0.5	5.4E-01	0.2	7.7E-01
ENSMUST00000138803				2.1	4.2E-02	1.4	2.0E-01	-0.7	4.3E-01	0.0	9.9E-01
ENSMUST00000138822				0.2	8.6E-01	0.5	7.5E-01	0.0	9.9E-01	-0.2	8.5E-01
ENSMUST00000178823	RIKEN cDNA 1700122O11 gene [Source:MGI Symbol;Acc:MGI:1923901]	J3QPW6		7.1	3.4E-04	6.1	3.9E-05	-0.6	4.6E-01	0.9	6.8E-02
ENSMUST00000178826	glutamate-cysteine ligase, modifier subunit [Source:MGI Symbol;Acc:MGI:104995]	Q4FJZ6	O09172	-8.2	1.4E-06	5.7	1.3E-03	0.2	8.8E-01	0.2	7.7E-01
ENSMUST00000138831	WAS protein family, member 2 [Source:MGI Symbol;Acc:MGI:1098641]	B1AUN0		1.8	1.1E-01	2.7	5.6E-02	0.9	4.3E-01	0.0	9.7E-01
ENSMUST00000178843	lactamase, beta-like 1 [Source:MGI Symbol;Acc:MGI:2448566]	S4R213		7.5	2.1E-05	-4.6	4.3E-02	0.0	9.8E-01	0.6	7.7E-01
ENSMUST00000178851	anaphase promoting complex C subunit 15 [Source:MGI Symbol;Acc:MGI:1922680]		P60007	6.6	1.9E-03	6.4	9.8E-05	-0.4	7.2E-01	-0.4	4.7E-01
ENSMUST00000138842	tec protein tyrosine kinase [Source:MGI Symbol;Acc:MGI:98662]			1.0	6.2E-01	-3.0	1.9E-01	-4.5	2.1E-02	-0.5	8.2E-01
ENSMUST00000178855	SEC61, gamma subunit [Source:MGI Symbol;Acc:MGI:1202066]	Q5SWJ8	P60060	-2.7	3.0E-02	5.1	1.8E-03	-0.3	8.2E-01	0.3	6.6E-01
ENSMUST00000138857				-0.9	3.3E-01	-1.2	3.2E-01	0.3	6.7E-01	0.6	5.6E-01
ENSMUST00000138859				-3.8	9.4E-02	-0.9	7.6E-01	2.5	2.4E-01	-0.4	8.9E-01
ENSMUST00000178858	predicted gene 7325 [Source:MGI Symbol;Acc:MGI:3649059]	Q2Q5T5		5.1	1.0E-03	-3.9	1.2E-02	0.5	4.4E-01	-1.4	3.3E-01
ENSMUST00000178876	RIKEN cDNA 1600014C10 gene [Source:MGI Symbol;Acc:MGI:1919494]			2.2	3.2E-02	4.7	7.1E-05	-0.4	5.9E-01	-0.6	2.3E-01
ENSMUST00000178893	cytokine receptor-like factor 3 [Source:MGI Symbol;Acc:MGI:1860086]	J3QPM4		-4.4	2.8E-02	6.1	3.5E-03	2.0	2.3E-01	-1.2	2.3E-01
ENSMUST00000178895	predicted gene 9821 [Source:MGI Symbol;Acc:MGI:3704208]	Q8K076		4.1	9.4E-05	5.2	1.0E-04	-1.5	7.7E-02	0.5	3.1E-01
ENSMUST00000178901	zinc finger protein 872 [Source:MGI Symbol;Acc:MGI:3588272]	Q3UVL3		5.5	1.8E-04	2.3	1.7E-01	-0.4	8.0E-01	0.8	4.8E-01
ENSMUST00000178923	low density lipoprotein receptor A domain containing 2 [Source:MGI Symbol;Acc:MGI:3588210]	Q3V0V0		6.5	1.1E-03	2.0	5.2E-03	-1.2	3.3E-02	0.0	9.5E-01
ENSMUST00000138885	RAB35, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1924657]	S4R1W7		-2.6	1.3E-01	-2.1	3.4E-01	-0.2	8.6E-01	-0.8	7.3E-01
ENSMUST00000178925	caspase 8 associated protein 2 [Source:MGI Symbol;Acc:MGI:1349399]		Q9WUF3	-3.7	2.1E-02	2.5	1.1E-01	-1.0	4.6E-01	-0.4	7.4E-01
ENSMUST00000178942	RIKEN cDNA 7530416G11 gene [Source:MGI Symbol;Acc:MGI:3036279]	J3QJX6		5.0	2.7E-05	5.4	1.6E-03	-0.6	6.5E-01	0.2	7.7E-01
ENSMUST00000178945	C-type lectin domain family 10, member A [Source:MGI Symbol;Acc:MGI:96975]	J3QPR7		5.9	3.8E-03	-9.2	2.0E-05	0.7	4.9E-02	-0.7	5.8E-01
ENSMUST00000178948	predicted gene, 21967 [Source:MGI Symbol;Acc:MGI:5439436]	H3BJ86		2.9	1.6E-02	6.3	2.2E-04	-0.6	6.3E-01	0.4	4.9E-01
ENSMUST00000138904				0.2	8.5E-01	0.0	1.0E+00	0.1	9.2E-01	0.3	8.1E-01
ENSMUST00000138907	phosphoinositide-3-kinase interacting protein 1 [Source:MGI Symbol;Acc:MGI:1917016]	F6S185		-1.8	1.5E-01	-1.8	2.8E-01	-0.2	8.5E-01	-0.2	9.2E-01
ENSMUST00000178952	predicted gene, 17267 [Source:MGI Symbol;Acc:MGI:4936901]	B6ZB74		8.0	1.6E-03	1.1	1.6E-01	-0.3	6.2E-01	1.1	1.1E-01
ENSMUST00000178960	predicted gene 13693 [Source:MGI Symbol;Acc:MGI:3702055]	A2AK42		6.5	6.6E-05	3.3	8.6E-03	-2.2	6.2E-02	-0.9	2.8E-01
ENSMUST00000138918				0.9	7.1E-01	0.9	7.9E-01	0.9	7.5E-01	0.9	7.4E-01
ENSMUST00000178961	proline rich protein 2 [Source:MGI Symbol;Acc:MGI:1932491]	F8VPU9		7.0	9.2E-05	3.6	3.9E-04	-1.2	6.9E-02	-0.3	5.4E-01
ENSMUST00000178962	predicted gene 17174 [Source:MGI Symbol;Acc:MGI:4938001]	M0QWQ9		12.3	1.9E-06	-5.0	7.5E-04	0.5	3.3E-01	-0.8	4.6E-01
ENSMUST00000178973	NIM1 serine/threonine protein kinase [Source:MGI Symbol;Acc:MGI:2442399]	Q3UQ09		6.3	1.2E-04	6.5	1.6E-04	-1.5	2.2E-01	0.0	9.4E-01
ENSMUST00000138927	3-oxoacid CoA transferase 1 [Source:MGI Symbol;Acc:MGI:1914291]	Q3UJQ9		1.6	5.2E-01	-3.2	3.2E-01	-3.7	8.3E-02	1.0	7.4E-01
ENSMUST00000178977	RIKEN cDNA 4931406C07 gene [Source:MGI Symbol;Acc:MGI:1918234]		Q91V76	-5.0	5.7E-04	3.6	1.9E-02	0.1	9.6E-01	0.9	3.6E-01
ENSMUST00000138936				0.0	9.7E-01	-1.4	1.9E-01	-2.8	1.1E-02	-1.4	2.2E-01
ENSMUST00000178988	transmembrane protein 205 [Source:MGI Symbol;Acc:MGI:3045495]		Q91XE8	-4.3	1.2E-02	-7.8	5.3E-04	1.0	4.2E-02	-0.8	6.5E-01
ENSMUST00000178992	RIKEN cDNA 3110021N24 gene [Source:MGI Symbol;Acc:MGI:1920383]	J3QMN2		7.8	3.2E-04	-4.0	5.1E-02	1.6	1.4E-01	-0.5	8.1E-01
ENSMUST00000178999	single-pass membrane protein with coiled-coil domains 4 [Source:MGI Symbol;Acc:MGI:3039636]		Q9JIS3	6.0	3.5E-03	-7.4	3.2E-03	0.4	5.4E-01	-1.1	6.2E-01
ENSMUST00000138957				3.5	4.2E-02	6.0	7.3E-03	0.7	7.0E-01	-1.8	1.8E-01
ENSMUST00000179001	signal-regulatory protein alpha [Source:MGI Symbol;Acc:MGI:108563]	Q6P6I8		-7.9	1.8E-04	-1.0	4.4E-01	0.8	3.4E-01	-1.2	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000179022	lamin B2 [Source:MGI Symbol;Acc:MGI:96796]		P21619	-4.3	8.7E-03	4.7	3.1E-02	-0.2	9.0E-01	0.0	9.8E-01
ENSMUST00000138974				2.4	5.8E-02	0.9	5.2E-01	-0.6	6.4E-01	0.9	4.6E-01
ENSMUST00000179028	predicted gene, 21883 [Source:MGI Symbol;Acc:MGI:5434047]	J3QPV3		5.6	3.2E-04	5.1	1.4E-02	-0.7	6.9E-01	2.4	4.5E-02
ENSMUST00000179030	ankyrin repeat domain 44 [Source:MGI Symbol;Acc:MGI:3045243]		B2RXR6	-7.8	5.3E-05	-3.6	4.0E-03	-0.9	8.2E-02	-0.6	5.9E-01
ENSMUST00000179032	predicted gene 6408 [Source:MGI Symbol;Acc:MGI:3779591]	J3QNG1		8.0	5.4E-05	4.9	2.0E-02	-0.7	6.9E-01	2.5	5.2E-02
ENSMUST00000138981	testis specific protein kinase 1 [Source:MGI Symbol;Acc:MGI:1201675]	D6RFP6		-0.4	7.5E-01	-1.5	3.8E-01	-0.8	5.0E-01	0.3	8.6E-01
ENSMUST00000138982				-2.1	1.2E-01	-2.6	2.2E-01	0.6	6.0E-01	1.1	5.7E-01
ENSMUST00000138986				1.6	1.3E-01	2.6	5.9E-02	0.2	8.6E-01	-0.8	4.7E-01
ENSMUST00000179036	predicted gene 498 [Source:MGI Symbol;Acc:MGI:2685344]	J3QK70		6.0	1.7E-02	2.5	3.2E-01	8.0	2.2E-03	-0.2	9.0E-01
ENSMUST00000179041	centrosomal protein 170B [Source:MGI Symbol;Acc:MGI:2145043]		Q80U49	5.0	2.1E-02	-4.5	9.8E-03	1.6	2.3E-02	0.1	9.7E-01
ENSMUST00000179056	predicted gene, 21820 [Source:MGI Symbol;Acc:MGI:5433984]	J3KMU2		8.0	1.7E-05	7.6	2.9E-03	1.3	4.9E-01	0.5	5.7E-01
ENSMUST00000179077	erythroid differentiation regulator 1 [Source:MGI Symbol;Acc:MGI:2384747]	J3QQ45		2.7	9.8E-03	4.8	2.2E-03	0.1	9.0E-01	0.7	3.6E-01
ENSMUST00000179094	solute carrier family 38, member 10 [Source:MGI Symbol;Acc:MGI:1919305]	J3QNE8		-6.8	6.8E-05	2.6	9.0E-02	-3.2	6.7E-02	1.1	2.7E-01
ENSMUST00000179106	LysM, putative peptidoglycan-binding, domain containing 4 [Source:MGI Symbol;Acc:MGI:1922349]		Q8CC84	5.4	2.2E-02	6.6	1.6E-03	-1.1	4.7E-01	1.1	2.2E-01
ENSMUST00000179116	predicted gene, 16867 [Source:MGI Symbol;Acc:MGI:4439791]		Q920G8	6.4	2.1E-04	4.1	8.4E-02	-1.1	6.3E-01	0.3	8.3E-01
ENSMUST00000179118	DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:MGI Symbol;Acc:MGI:1927346]		Q9D844	-5.7	3.4E-05	5.5	5.2E-04	0.3	7.3E-01	-0.3	7.0E-01
ENSMUST00000179124				3.5	1.4E-03	2.1	2.8E-02	-1.3	1.1E-01	-0.7	3.5E-01
ENSMUST00000139047	Ras association (RalGDS/AF-6) domain family member 2 [Source:MGI Symbol;Acc:MGI:2442060]	A2APB1		-1.5	2.5E-01	-1.2	4.1E-01	-0.2	8.4E-01	-0.4	7.7E-01
ENSMUST00000179127	arginyl aminopeptidase (aminopeptidase B)-like 1 [Source:MGI Symbol;Acc:MGI:1914170]	J3QMP7		-7.3	5.8E-05	-1.9	2.1E-02	-0.4	4.3E-01	-0.6	4.0E-01
ENSMUST00000179142	is-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) [Source:MGI Symbol;Acc:M		Q642K5	-3.6	2.8E-03	8.5	2.0E-05	0.0	9.9E-01	-0.4	3.6E-01
ENSMUST00000179162	fer-1-like 5 (C. elegans) [Source:MGI Symbol;Acc:MGI:3616091]		P0DM40	5.6	5.8E-05	4.7	1.4E-04	-0.1	8.3E-01	0.9	9.3E-02
ENSMUST00000139061	zinc finger protein 715 [Source:MGI Symbol;Acc:MGI:1917180]	D3YV82		1.7	4.3E-01	-1.0	6.5E-01	-2.6	1.8E-01	0.1	9.7E-01
ENSMUST00000179165	frizzled homolog 6 (Drosophila) [Source:MGI Symbol;Acc:MGI:108474]	Q542J1	Q61089	4.8	2.6E-03	8.1	5.0E-05	-1.5	2.7E-01	0.4	4.9E-01
ENSMUST00000179192	predicted gene 13698 [Source:MGI Symbol;Acc:MGI:3702072]	A2AK42		6.5	6.6E-05	-7.9	3.4E-02	0.3	7.5E-01	2.1	5.3E-01
ENSMUST00000179205	predicted gene 5294 [Source:MGI Symbol;Acc:MGI:3646467]	J3QP53		-2.6	2.3E-02	3.7	1.6E-04	0.0	9.5E-01	0.1	8.9E-01
ENSMUST00000139075	sarcolemma associated protein [Source:MGI Symbol;Acc:MGI:1933549]		Q3URD3	5.2	4.6E-02	1.8	4.4E-01	-3.7	1.2E-01	-0.3	8.9E-01
ENSMUST00000179218	golgi autoantigen, golgin subfamily a, 5 [Source:MGI Symbol;Acc:MGI:1351475]		Q9QYE6	-4.7	1.7E-03	2.1	1.9E-02	0.0	9.5E-01	-0.5	4.5E-01
ENSMUST00000139085				3.2	4.2E-02	-1.3	5.7E-01	-1.3	3.7E-01	3.2	1.4E-01
ENSMUST00000139091	DNA-damage inducible transcript 3 [Source:MGI Symbol;Acc:MGI:109247]	D3YX14		-2.7	4.2E-01	-1.8	6.7E-01	0.4	8.6E-01	-0.5	9.1E-01
ENSMUST00000179234	aldolase 1 A, retrogene 1 [Source:MGI Symbol;Acc:MGI:2447811]	Q9CPQ9		6.2	4.7E-04	1.9	1.8E-01	-1.1	4.1E-01	0.5	6.4E-01
ENSMUST00000139094				1.7	4.5E-02	3.8	5.3E-03	1.1	2.7E-01	-0.9	2.2E-01
ENSMUST00000179238	prosaposin [Source:MGI Symbol;Acc:MGI:97783]	Q3UFE8	Q61207	-5.8	7.5E-03	8.5	8.1E-06	0.6	5.3E-01	-0.2	5.8E-01
ENSMUST00000179250	filaggrin [Source:MGI Symbol;Acc:MGI:95553]	A0A0A6YWE2		7.4	2.8E-04	4.8	2.7E-04	-0.3	6.9E-01	-1.4	4.0E-02
ENSMUST00000179264	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	J3QPS1		11.8	2.1E-06	5.4	9.5E-04	0.5	6.3E-01	-0.4	6.3E-01
ENSMUST00000139118				-0.3	9.0E-01	-1.5	4.8E-01	-1.7	3.6E-01	-0.5	8.1E-01
ENSMUST00000139120				1.5	2.2E-01	2.2	1.7E-01	-0.3	8.0E-01	-1.1	3.5E-01
ENSMUST00000179269	shisa family member 8 [Source:MGI Symbol;Acc:MGI:2146080]	J3QNX5		4.7	3.4E-04	-0.6	3.9E-01	0.8	1.0E-01	-0.3	6.1E-01
ENSMUST00000179272	predicted gene 10719 [Source:MGI Symbol;Acc:MGI:3641690]	J3QM83		13.9	1.0E-08	7.8	3.4E-03	0.4	8.4E-01	0.4	7.1E-01
ENSMUST00000179276	TAO kinase 3 [Source:MGI Symbol;Acc:MGI:3041177]		Q8BYC6	-7.3	1.9E-05	4.8	2.3E-03	-1.3	2.6E-01	0.3	7.2E-01
ENSMUST00000179285	histone cluster 4, H4 [Source:MGI Symbol;Acc:MGI:2448443]	B2RTM0	P62806	7.2	1.8E-07	6.1	4.7E-05	0.1	9.1E-01	0.2	7.4E-01
ENSMUST00000139129	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]		Q6PDM2	-1.9	5.3E-02	-2.0	1.4E-01	0.7	4.0E-01	0.8	5.1E-01
ENSMUST00000139143	zinc finger protein 451 [Source:MGI Symbol;Acc:MGI:2137896]	M0QWT6		-0.5	6.9E-01	1.4	4.1E-01	0.7	6.0E-01	-1.3	4.2E-01
ENSMUST00000179292				3.5	1.4E-03	3.9	4.3E-04	1.3	6.5E-02	-0.8	1.8E-01
ENSMUST00000179295	predicted gene 5435 [Source:MGI Symbol;Acc:MGI:3643292]	J3QNT2		5.9	5.4E-04	6.3	2.1E-03	-1.9	2.6E-01	-0.5	5.9E-01
ENSMUST00000179297	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:106247]		Q99KP6	4.7	1.2E-05	-3.2	2.1E-02	-0.7	3.5E-01	-0.5	6.7E-01
ENSMUST00000179301	transportin 1 [Source:MGI Symbol;Acc:MGI:2681523]	Q3TKD0		-3.4	1.1E-02	2.6	5.0E-02	0.1	9.4E-01	-0.2	8.6E-01
ENSMUST00000179308	EDAR (ectodysplasin-A receptor)-associated death domain [Source:MGI Symbol;Acc:MGI:1931001]	Q5D0F1		5.4	1.2E-05	4.2	8.3E-03	1.1	3.8E-01	-0.3	6.7E-01
ENSMUST00000179309	predicted gene, 21732 [Source:MGI Symbol;Acc:MGI:5433896]	J3QM79		9.7	4.4E-06	-1.3	2.5E-01	0.7	3.5E-01	-1.1	3.4E-01
ENSMUST00000139167	glutamyl-tRNA(Gln) amidotransferase, subunit C [Source:MGI Symbol;Acc:MGI:1923776]		Q8CBY0	1.0	8.5E-02	0.9	2.2E-01	0.2	7.6E-01	0.3	6.5E-01
ENSMUST00000139173				-1.6	5.3E-01	-1.8	5.4E-01	-1.1	5.9E-01	-0.9	7.7E-01
ENSMUST00000139176				1.8	5.1E-02	1.7	1.1E-01	-0.3	6.6E-01	-0.3	7.5E-01
ENSMUST00000179313	melanocortin 2 receptor accessory protein 2 [Source:MGI Symbol;Acc:MGI:3609239]		D3Z1Q2	7.7	2.1E-02	-6.9	1.0E-03	0.2	6.4E-01	0.3	8.4E-01
ENSMUST00000139179				0.9	4.0E-01	1.1	4.3E-01	0.3	8.3E-01	0.0	1.0E+00
ENSMUST00000179318	SH3-domain GRB2-like 3 [Source:MGI Symbol;Acc:MGI:700011]	J3QQ44		5.1	3.0E-03	6.0	6.1E-03	-0.7	7.2E-01	-0.9	3.9E-01
ENSMUST00000139188	serine/threonine kinase 40 [Source:MGI Symbol;Acc:MGI:1921428]	B1AW00		0.4	6.4E-01	1.4	2.7E-01	0.5	6.6E-01	-0.5	5.9E-01
ENSMUST00000139204	spectrin repeat containing, nuclear envelope 2 [Source:MGI Symbol;Acc:MGI:2449316]	F6W8R9		-0.9	6.9E-01	-0.7	8.1E-01	-0.2	9.2E-01	-0.4	8.7E-01
ENSMUST00000179321	solute carrier family 18, subfamily B, member 1 [Source:MGI Symbol;Acc:MGI:1923556]		D3Z5L6	7.6	1.0E-06	2.3	1.4E-01	0.5	7.1E-01	4.0	5.7E-03
ENSMUST00000179322	ecotropic viral integration site 2b [Source:MGI Symbol;Acc:MGI:1890682]		Q8VD58	-7.5	3.3E-05	6.3	3.9E-04	-0.6	6.5E-01	0.8	2.6E-01
ENSMUST00000139211	Shwachman-Bodian-Diamond syndrome homolog (human) [Source:MGI Symbol;Acc:MGI:1913961]	D6REV5		-1.3	1.9E-01	-2.1	7.0E-02	-1.7	4.6E-02	-0.9	4.1E-01
ENSMUST00000139212				0.3	6.5E-01	1.5	9.9E-02	0.0	9.8E-01	-1.2	1.5E-01
ENSMUST00000179323	U7 snRNP-specific Sm-like protein LSM10 [Source:MGI Symbol;Acc:MGI:2151045]	Q3UPL7	Q8QZX5	-6.5	1.8E-04	6.6	5.0E-04	1.0	4.6E-01	-0.7	3.2E-01
ENSMUST00000139225				1.8	1.0E-01	3.1	2.5E-02	0.0	9.8E-01	-1.2	2.3E-01
ENSMUST00000139231	RIKEN cDNA 2610001J05 gene [Source:MGI Symbol;Acc:MGI:1913770]	F2Z3Y9		-0.7	1.6E-01	0.5	4.3E-01	0.3	5.1E-01	-0.9	1.3E-01
ENSMUST00000179332	RIKEN cDNA 5730455P16 gene [Source:MGI Symbol;Acc:MGI:1917841]	J3KMQ6		8.3	6.9E-03	5.3	5.7E-03	-0.7	6.8E-01	-0.7	4.9E-01
ENSMUST00000179341	ornithine decarboxylase antizyme 1 [Source:MGI Symbol;Acc:MGI:109433]	J3QME8		-4.2	4.3E-03	5.5	6.5E-04	-1.5	2.4E-01	-1.1	1.4E-01
ENSMUST00000139249				0.2	9.1E-01	-1.7	5.6E-01	0.5	7.7E-01	2.4	3.6E-01
ENSMUST00000179343	purine rich element binding protein B [Source:MGI Symbol;Acc:MGI:1338779]		O35295	-2.9	2.4E-04	-5.4	7.4E-05	0.5	2.3E-01	-0.5	5.7E-01
ENSMUST00000179344	predicted gene 5784 [Source:MGI Symbol;Acc:MGI:3647969]	Q8BME7		10.9	2.1E-07	-1.1	2.8E-01	0.6	3.8E-01	-2.4	5.5E-02
ENSMUST00000179347	predicted gene 3336 [Source:MGI Symbol;Acc:MGI:3781514]	J3QMQ6		6.6	6.3E-05	-11.3	4.5E-06	-0.3	2.7E-01	-0.8	5.2E-01
ENSMUST00000179351	adhesion G protein-coupled receptor A2 [Source:MGI Symbol;Acc:MGI:1925810]	J3QPS6		5.3	1.6E-02	-6.6	2.7E-03	-1.7	1.7E-02	-0.7	7.2E-01
ENSMUST00000179353	septin 2 [Source:MGI Symbol;Acc:MGI:97298]		P42208	-6.2	4.6E-03	5.5	1.5E-03	-3.1	5.5E-02	0.0	9.9E-01
ENSMUST00000179355	predicted gene, 21773 [Source:MGI Symbol;Acc:MGI:5433937]	J3QNB5		6.9	2.4E-03	5.2	3.0E-03	-0.8	5.6E-01	0.3	7.2E-01
ENSMUST00000179363	family with sequence similarity 181, member A [Source:MGI Symbol;Acc:MGI:3647570]	J3QNB7		5.7	2.0E-03	-4.1	1.4E-02	0.7	2.5E-01	0.7	6.4E-01
ENSMUST00000179365	sorting nexin 10 [Source:MGI Symbol;Acc:MGI:1919232]	Q4FJX6	Q9CWT3	-5.3	2.1E-06	5.1	5.1E-04	0.6	4.9E-01	0.2	7.6E-01
ENSMUST00000139297				-2.8	7.0E-02	-3.2	2.2E-01	0.8	5.2E-01	1.2	6.2E-01
ENSMUST00000139302	heterogeneous nuclear ribonucleoprotein M [Source:MGI Symbol;Acc:MGI:1926465]	B8JK33		2.1	3.6E-01	1.0	6.9E-01	-1.2	6.2E-01	-0.2	9.3E-01
ENSMUST00000179367	predicted gene 8674 [Source:MGI Symbol;Acc:MGI:3645762]	J3QK40		8.2	4.5E-05	-2.1	3.1E-02	0.7	1.7E-01	-0.1	8.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000179393	oxidation resistance 1 [Source:MGI Symbol;Acc:MGI:2179326]		Q4KMM3	3.1	1.3E-03	2.2	5.0E-03	-0.1	7.8E-01	-0.3	5.3E-01
ENSMUST00000179395	thyroid hormone receptor interactor 4 [Source:MGI Symbol;Acc:MGI:1928469]		Q9QXN3	2.2	2.7E-03	4.2	1.3E-03	1.8	5.1E-02	-0.5	4.0E-01
ENSMUST00000179412	mucin 3A, cell surface associated [Source:MGI Symbol;Acc:MGI:3588263]	Q3U5A2		3.0	1.4E-03	8.0	1.5E-05	-1.0	3.4E-01	0.2	6.1E-01
ENSMUST00000179425	predicted gene 13272 [Source:MGI Symbol;Acc:MGI:3701968]	B1AYI3		6.1	1.6E-04	-4.5	1.2E-02	0.2	7.6E-01	-0.9	5.9E-01
ENSMUST00000179430	predicted gene 10845 [Source:MGI Symbol;Acc:MGI:3641716]	Q3UNY9		6.6	2.0E-04	5.6	5.0E-04	-1.9	1.3E-01	-0.6	4.1E-01
ENSMUST00000179433	aldehyde dehydrogenase 3 family, member B3 [Source:MGI Symbol;Acc:MGI:1920708]	J3QMK6		5.3	1.5E-02	5.2	8.2E-03	0.6	7.2E-01	0.0	1.0E+00
ENSMUST00000139332				2.7	1.1E-01	5.7	4.7E-02	3.3	1.9E-01	0.3	8.6E-01
ENSMUST00000139333				0.1	9.3E-01	4.7	1.4E-02	-0.6	6.9E-01	-5.2	4.6E-03
ENSMUST00000179434	cytochrome P450, family 4, subfamily f, polypeptide 14 [Source:MGI Symbol;Acc:MGI:1927669]		Q9EP75	2.5	1.7E-02	5.9	3.4E-04	-0.6	6.1E-01	0.4	4.9E-01
ENSMUST00000139337	predicted gene 12258 [Source:MGI Symbol;Acc:MGI:3651534]	Q5NC63		0.7	1.6E-01	0.6	3.0E-01	-0.1	8.4E-01	0.0	9.5E-01
ENSMUST00000139342				-3.7	3.7E-02	-3.8	6.6E-02	-1.1	3.0E-01	-1.0	6.3E-01
ENSMUST00000179436				-6.1	2.2E-03	7.8	9.1E-05	-0.5	7.1E-01	-0.9	1.7E-01
ENSMUST00000139353	cytochrome P450, family 4, subfamily f, polypeptide 13 [Source:MGI Symbol;Acc:MGI:2158641]	B8JK07		-1.7	5.3E-01	-2.9	2.2E-01	-2.2	2.3E-01	-0.9	7.4E-01
ENSMUST00000179443	golgi-associated olfactory signaling regulator [Source:MGI Symbol;Acc:MGI:2685427]		J3KML8	9.7	9.3E-04	6.6	2.9E-03	2.3	1.6E-01	-1.2	2.4E-01
ENSMUST00000179445	phosphatidylinositol transfer protein, alpha [Source:MGI Symbol;Acc:MGI:99887]	J3QQ30		-6.4	1.1E-03	-1.0	1.8E-01	1.2	3.7E-02	-0.2	8.2E-01
ENSMUST00000179472	maestro [Source:MGI Symbol;Acc:MGI:2152817]	E9QNX2		5.9	7.0E-05	5.5	3.1E-03	0.8	5.5E-01	-0.6	4.7E-01
ENSMUST00000179478	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]	J3QMT0		-3.5	7.0E-03	-4.2	3.4E-03	1.5	1.2E-02	-1.5	2.3E-01
ENSMUST00000179488	RIKEN cDNA 2610528A11 gene [Source:MGI Symbol;Acc:MGI:1917295]	A0A0B4J1N3		6.5	4.1E-03	-5.3	7.2E-03	-2.0	3.6E-02	-2.2	3.0E-01
ENSMUST00000179521	phosphatidylinositol transfer protein, alpha [Source:MGI Symbol;Acc:MGI:99887]	J3QPW1		7.3	3.8E-05	6.2	1.1E-03	-0.5	7.3E-01	-0.9	2.7E-01
ENSMUST00000179525	RIKEN cDNA 1600014C10 gene [Source:MGI Symbol;Acc:MGI:1919494]			-8.7	7.1E-05	0.8	7.6E-01	1.6	4.1E-01	4.6	6.3E-02
ENSMUST00000139387				-5.8	4.7E-02	2.1	5.9E-01	7.1	2.3E-02	-0.7	8.4E-01
ENSMUST00000139388				-0.8	3.2E-01	0.2	8.0E-01	-0.5	5.0E-01	-1.6	1.1E-01
ENSMUST00000139389	trehalase (brush-border membrane glycoprotein) [Source:MGI Symbol;Acc:MGI:1926230]	D6RI51		2.5	2.3E-01	5.4	1.9E-02	-0.6	7.8E-01	-3.5	4.3E-02
ENSMUST00000179553	RIKEN cDNA 1110059E24 gene [Source:MGI Symbol;Acc:MGI:1913456]	J3QQ03		-2.9	2.0E-02	-1.4	1.9E-01	0.3	7.0E-01	-1.8	1.5E-01
ENSMUST00000179554	dynein light chain Tctex-type 1F [Source:MGI Symbol;Acc:MGI:3780996]		P51807	-8.2	3.9E-05	4.4	2.0E-03	-1.0	3.5E-01	0.2	7.7E-01
ENSMUST00000139396				2.9	4.7E-02	-0.6	7.3E-01	-2.4	8.0E-02	1.1	5.0E-01
ENSMUST00000179569	dynein light chain Tctex-type 1B [Source:MGI Symbol;Acc:MGI:98643]		P51807	-9.7	2.4E-06	1.3	3.7E-01	-2.0	1.5E-01	0.9	4.5E-01
ENSMUST00000139402				-3.3	2.7E-01	-2.8	2.9E-01	-1.9	3.0E-01	-2.4	4.5E-01
ENSMUST00000139404				2.0	3.6E-02	0.3	7.4E-01	-1.0	2.6E-01	0.7	4.1E-01
ENSMUST00000179584	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:MGI Symbol;Acc:MGI:2181202]	Q3U3S6		-8.9	8.0E-05	6.2	3.8E-04	0.1	9.5E-01	-1.2	9.1E-02
ENSMUST00000179605	zinc finger protein 653 [Source:MGI Symbol;Acc:MGI:2442362]		Q6YND2	-2.8	6.5E-03	3.6	3.7E-02	-2.4	1.4E-01	-0.6	5.9E-01
ENSMUST00000139412				-0.5	6.1E-01	-1.6	2.1E-01	-0.7	4.0E-01	0.4	7.3E-01
ENSMUST00000179612	predicted gene, 21900 [Source:MGI Symbol;Acc:MGI:5434064]	J3QP38		9.6	5.4E-04	5.7	5.5E-04	0.8	5.0E-01	-0.6	3.4E-01
ENSMUST00000139419				1.5	3.5E-01	2.7	1.8E-01	-0.1	9.7E-01	-1.3	3.7E-01
ENSMUST00000179614	coiled-coil domain containing 162 [Source:MGI Symbol;Acc:MGI:1923223]		Q0VG85	6.8	8.3E-05	4.9	1.7E-02	-0.7	6.8E-01	2.1	7.7E-02
ENSMUST00000139428	transmembrane protein 62 [Source:MGI Symbol;Acc:MGI:2139461]	D6RH67		-0.1	9.7E-01	-1.0	6.5E-01	-2.4	2.3E-01	-1.5	5.6E-01
ENSMUST00000179619	adhesion G protein-coupled receptor G1 [Source:MGI Symbol;Acc:MGI:1340051]		Q8K209	4.6	2.9E-02	5.2	1.8E-02	-0.7	7.0E-01	0.8	4.8E-01
ENSMUST00000179620	ornithine decarboxylase antizyme 1 [Source:MGI Symbol;Acc:MGI:109433]	J3QM60		-8.4	2.0E-04	4.2	3.1E-03	0.0	9.7E-01	0.0	9.8E-01
ENSMUST00000139443	high mobility group box 1 [Source:MGI Symbol;Acc:MGI:96113]			-1.6	2.0E-01	-4.1	1.5E-02	-3.5	1.7E-03	-0.9	5.5E-01
ENSMUST00000139446				0.4	8.7E-01	-2.7	3.2E-01	-3.3	7.5E-02	-0.2	9.3E-01
ENSMUST00000179636	solute carrier family 6 (neurotransmitter transporter), member 15 [Source:MGI Symbol;Acc:MGI:2143484]		Q8BG16	7.1	2.6E-02	8.2	9.7E-05	1.3	3.1E-01	-0.9	1.6E-01
ENSMUST00000179657	immunoglobulin heavy variable 2-6 [Source:MGI Symbol;Acc:MGI:4439518]	A0A075B6A7		6.6	1.7E-04	-5.7	2.4E-03	-1.1	7.4E-02	0.0	9.8E-01
ENSMUST00000179693	CCCTC-binding factor (zinc finger protein)-like [Source:MGI Symbol;Acc:MGI:3652571]		A2APF3	5.6	1.2E-03	-0.2	8.8E-01	3.1	5.0E-03	-2.3	1.1E-01
ENSMUST00000179695	zinc finger protein 799 [Source:MGI Symbol;Acc:MGI:2443934]	J3QMI2		5.5	2.6E-05	4.0	6.8E-03	-2.4	9.2E-02	-0.4	5.6E-01
ENSMUST00000179709	mitochondrial calcium uptake 1 [Source:MGI Symbol;Acc:MGI:2384909]		Q8VCX5	-6.1	1.3E-03	6.3	3.0E-06	0.1	8.9E-01	0.4	2.4E-01
ENSMUST00000139476	glutamate-ammonia ligase (glutamine synthetase) [Source:MGI Symbol;Acc:MGI:95739]	D3YVK1		-1.0	7.4E-01	-0.4	8.8E-01	-1.2	5.4E-01	-1.8	5.5E-01
ENSMUST00000179721	PH domain and leucine rich repeat protein phosphatase 2 [Source:MGI Symbol;Acc:MGI:2444928]	J3QM82		3.4	2.2E-04	6.7	7.7E-03	0.7	7.5E-01	1.3	2.3E-01
ENSMUST00000179725	predicted gene 13285 [Source:MGI Symbol;Acc:MGI:3701981]	B1AYI3		9.8	2.8E-07	7.5	2.4E-04	-1.9	2.2E-01	0.7	3.1E-01
ENSMUST00000179728	ribonuclease T2B [Source:MGI Symbol;Acc:MGI:3702087]	Q5FWA0	Q9CQ01	3.4	2.1E-04	3.3	8.5E-03	-0.4	6.7E-01	-0.4	6.0E-01
ENSMUST00000179741	predicted gene 7104 [Source:MGI Symbol;Acc:MGI:3779672]	J3QNS6		8.5	8.2E-06	5.2	2.4E-03	-2.2	1.6E-01	-2.0	5.2E-02
ENSMUST00000179748	nudix (nucleoside diphosphate linked moiety X)-type motif 5 [Source:MGI Symbol;Acc:MGI:1858232]		Q9JKX6	-5.1	8.0E-05	6.3	5.1E-04	-0.7	5.6E-01	0.0	9.7E-01
ENSMUST00000139496				-0.1	9.3E-01	0.8	3.9E-01	0.2	8.2E-01	-0.7	4.2E-01
ENSMUST00000179758	androgen dependent TFPI regulating protein [Source:MGI Symbol;Acc:MGI:1924596]		Q8C138	-5.5	3.0E-04	4.7	2.1E-02	0.6	6.9E-01	-0.8	5.1E-01
ENSMUST00000179760	predicted gene, 21887 [Source:MGI Symbol;Acc:MGI:5434051]	J3QM40		4.2	2.0E-03	-3.6	1.1E-02	0.2	7.5E-01	-1.5	2.6E-01
ENSMUST00000179762	lymphocyte antigen 6 complex, locus C1 [Source:MGI Symbol;Acc:MGI:96882]		P0CW02	-7.0	3.3E-05	5.6	4.0E-04	-1.8	1.3E-01	-0.6	3.6E-01
ENSMUST00000179765	polycomb group ring finger 2 [Source:MGI Symbol;Acc:MGI:99161]		P23798	6.6	2.9E-02	5.5	1.4E-02	-0.2	9.1E-01	-0.2	9.0E-01
ENSMUST00000139522	RAS, guanyl releasing protein 2 [Source:MGI Symbol;Acc:MGI:1333849]	D6RDD3		-0.1	9.6E-01	0.2	8.8E-01	1.3	3.0E-01	1.0	5.0E-01
ENSMUST00000179766	G protein-coupled receptor 45 [Source:MGI Symbol;Acc:MGI:2135882]	Q148B5	Q9EQQ4	8.3	5.1E-05	-4.6	2.6E-03	-0.5	3.3E-01	-1.4	3.2E-01
ENSMUST00000179769	PRP31 pre-mRNA processing factor 31 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1916238]		Q8CCF0	7.2	2.2E-04	1.7	4.2E-01	-1.4	5.1E-01	2.2	1.7E-01
ENSMUST00000179780	tsukushi, small leucine rich proteoglycan [Source:MGI Symbol;Acc:MGI:2443855]	Q08EE6	Q8CBR6	4.6	6.5E-03	1.4	3.0E-01	-0.2	8.5E-01	1.0	3.6E-01
ENSMUST00000179781	basigin [Source:MGI Symbol;Acc:MGI:88208]		P18572	-6.9	5.0E-05	-3.0	2.7E-02	0.2	7.8E-01	-0.2	8.6E-01
ENSMUST00000179784	ER membrane protein complex subunit 1 [Source:MGI Symbol;Acc:MGI:2443696]		Q8C7X2	8.6	1.5E-05	4.3	1.8E-03	-1.6	1.6E-01	0.0	9.7E-01
ENSMUST00000179797	predicted gene, 20594 [Source:MGI Symbol;Acc:MGI:5295700]	J3QJY3		-1.5	1.5E-02	0.8	3.4E-01	0.4	5.7E-01	-3.1	7.4E-03
ENSMUST00000179802	CKLF-like MARVEL transmembrane domain containing 4 [Source:MGI Symbol;Acc:MGI:2142888]		Q8CJ61	3.8	6.8E-05	-5.8	2.7E-03	1.2	4.5E-02	-0.9	5.9E-01
ENSMUST00000179824	predicted gene 16429 [Source:MGI Symbol;Acc:MGI:3704105]	J3QMM8		7.1	3.7E-05	4.3	1.3E-02	0.8	5.6E-01	-0.1	8.7E-01
ENSMUST00000179828	chemokine (C-X-C motif) receptor 5 [Source:MGI Symbol;Acc:MGI:103567]		Q04683	6.6	4.8E-03	3.9	9.2E-04	-0.1	9.4E-01	-0.1	9.0E-01
ENSMUST00000179829	predicted gene, 20821 [Source:MGI Symbol;Acc:MGI:5434177]	J3QPJ2		6.6	1.1E-04	7.6	3.6E-04	-0.7	6.3E-01	0.0	1.0E+00
ENSMUST00000139560	NDC1 transmembrane nucleoporin [Source:MGI Symbol;Acc:MGI:1920037]		Q8VCB1	1.7	1.6E-01	0.0	9.8E-01	0.1	9.3E-01	1.8	2.2E-01
ENSMUST00000139563				-0.9	3.2E-01	0.5	5.9E-01	0.0	9.6E-01	-1.5	1.6E-01
ENSMUST00000179839	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	J3QNK0		11.3	7.3E-06	3.9	1.5E-02	-0.2	8.9E-01	-0.9	3.2E-01
ENSMUST00000179857	translocase of outer mitochondrial membrane 20 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1915202]	Q4KL41	Q9DCC8	-1.1	3.2E-02	5.3	2.5E-02	-0.6	7.9E-01	1.0	4.2E-01
ENSMUST00000139578				1.3	1.4E-01	2.1	6.4E-02	0.2	8.5E-01	-0.7	4.6E-01
ENSMUST00000179862	predicted pseudogene 5900 [Source:MGI Symbol;Acc:MGI:3643907]	Q542I7	O88653	-2.9	2.5E-03	4.6	4.0E-03	1.0	3.7E-01	-0.2	7.6E-01
ENSMUST00000179869	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 [Source:MGI Symbol;Acc:MGI:107592]		Q8JZK9	-2.1	5.6E-04	4.3	2.9E-03	1.0	3.2E-01	-0.2	7.7E-01
ENSMUST00000139585	Wilms tumor 1 homolog [Source:MGI Symbol;Acc:MGI:98968]	F6VXG5		4.2	1.0E-01	3.8	1.3E-01	-2.0	4.5E-01	-1.7	3.2E-01
ENSMUST00000139594				2.3	2.5E-01	4.4	1.1E-01	1.0	6.9E-01	-1.1	5.4E-01
ENSMUST00000139602				-4.3	6.0E-02	5.3	7.7E-02	6.6	2.3E-02	-3.0	1.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000139606				-1.6	3.2E-01	0.3	8.6E-01	0.2	8.8E-01	-1.7	3.5E-01
ENSMUST00000179880	predicted gene, 21913 [Source:MGI Symbol;Acc:MGI:5434077]	J3KML9		8.5	8.2E-06	6.3	2.7E-06	-0.8	2.0E-01	-0.3	4.4E-01
ENSMUST00000179881	predicted gene 11168 [Source:MGI Symbol;Acc:MGI:3779420]	J3QN11		14.3	7.1E-08	6.4	3.9E-03	0.0	9.9E-01	-0.6	5.5E-01
ENSMUST00000179890				5.7	1.1E-03	-6.0	2.3E-05	-0.7	6.8E-02	-1.3	1.5E-01
ENSMUST00000139627				-0.1	9.2E-01	1.8	1.3E-01	0.7	5.0E-01	-1.3	2.1E-01
ENSMUST00000179891	trafficking protein particle complex 13 [Source:MGI Symbol;Acc:MGI:1914225]	J3QNW4		-5.8	3.5E-04	2.8	6.1E-03	-1.4	8.4E-02	0.1	8.9E-01
ENSMUST00000139632	glucosamine-6-phosphate deaminase 2 [Source:MGI Symbol;Acc:MGI:1915230]		Q9CRC9	-0.1	9.7E-01	-3.9	2.1E-01	-4.5	3.5E-02	-0.8	8.1E-01
ENSMUST00000179893	ryanodine receptor 1, skeletal muscle [Source:MGI Symbol;Acc:MGI:99659]		E9PZQ0	4.5	1.7E-04	4.1	6.3E-02	-0.8	7.0E-01	1.0	4.6E-01
ENSMUST00000179900	serine-rich, secreted, Y-linked [Source:MGI Symbol;Acc:MGI:3526567]	A8HG57		10.3	2.4E-05	4.5	1.3E-03	-1.9	1.1E-01	-1.4	6.4E-02
ENSMUST00000179905	cDNA sequence AF067061 [Source:MGI Symbol;Acc:MGI:2681166]	O70616		6.2	1.2E-04	-2.4	2.4E-02	-0.2	7.3E-01	-0.8	4.0E-01
ENSMUST00000179907	RIKEN cDNA G430049J08 gene [Source:MGI Symbol;Acc:MGI:3645649]	Q3TL09		5.4	1.7E-06	4.8	3.1E-04	0.4	6.6E-01	0.4	4.8E-01
ENSMUST00000179909	predicted gene 21992 [Source:MGI Symbol;Acc:MGI:5439461]	B0LM42		-2.7	4.3E-03	5.5	2.8E-05	0.2	7.9E-01	-0.6	2.5E-01
ENSMUST00000179916	predicted gene, 17577 [Source:MGI Symbol;Acc:MGI:4937211]	J3QNF7		9.0	2.0E-04	5.7	5.1E-04	-1.9	1.5E-01	-1.0	1.9E-01
ENSMUST00000139657				-1.1	2.7E-01	-1.0	5.0E-01	1.3	1.9E-01	1.2	3.8E-01
ENSMUST00000139661	NLR family, pyrin domain containing 5 [Source:MGI Symbol;Acc:MGI:1345193]		Q9R1M5	4.5	1.4E-01	4.8	1.6E-01	-0.3	9.4E-01	-0.6	7.6E-01
ENSMUST00000139666	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Source:MGI Symbol;Acc:M		Q9QZQ1	3.6	1.3E-01	6.7	1.8E-02	-0.3	9.2E-01	-3.4	4.2E-02
ENSMUST00000179919	sterile alpha motif domain containing 11 [Source:MGI Symbol;Acc:MGI:2446220]	J3QN61		3.7	2.0E-04	4.5	6.7E-04	-0.2	8.4E-01	0.8	2.1E-01
ENSMUST00000179928	host cell factor C1 regulator 1 (XPO1-dependent) [Source:MGI Symbol;Acc:MGI:2663619]	J3QPD4		-6.8	4.0E-04	6.2	1.6E-05	-0.7	3.7E-01	0.1	8.4E-01
ENSMUST00000179939	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Source:MGI Symbol;Acc:MGI:88110]	J3KMM5	O55143	5.9	1.6E-02	4.9	1.2E-03	0.1	8.9E-01	-0.1	8.8E-01
ENSMUST00000179941	expressed sequence BB014433 [Source:MGI Symbol;Acc:MGI:2142823]		Q8C5R5	5.7	3.3E-02	1.5	8.9E-02	-1.0	1.8E-01	0.5	4.7E-01
ENSMUST00000179944	shugoshin like 2b (S. pombe) [Source:MGI Symbol;Acc:MGI:3644562]	J3QMK1		6.9	6.2E-05	3.8	2.5E-02	2.8	5.1E-02	1.5	1.6E-01
ENSMUST00000179949	predicted gene, 20823 [Source:MGI Symbol;Acc:MGI:5434179]	Q810R8		6.4	3.5E-03	2.8	6.9E-03	-1.3	1.1E-01	-0.8	2.5E-01
ENSMUST00000139702				-3.2	4.4E-02	0.5	7.6E-01	1.1	4.1E-01	-2.6	1.1E-01
ENSMUST00000179953	predicted gene 7903 [Source:MGI Symbol;Acc:MGI:3648697]	Q1RLL5		6.2	2.4E-02	6.8	1.9E-04	-0.8	5.0E-01	-0.3	6.2E-01
ENSMUST00000179973	predicted gene, 21870 [Source:MGI Symbol;Acc:MGI:5434034]	J3QPN2		6.3	8.3E-04	5.9	1.6E-03	-0.6	6.8E-01	-1.7	7.6E-02
ENSMUST00000179981	predicted gene 16505 [Source:MGI Symbol;Acc:MGI:3642261]	J3QPN4		1.8	1.2E-02	3.9	1.4E-04	-0.9	1.6E-01	0.1	8.8E-01
ENSMUST00000179982	predicted gene 10717 [Source:MGI Symbol;Acc:MGI:3642031]	J3QMM9		14.8	2.1E-08	9.0	1.6E-05	-0.4	7.4E-01	-0.5	3.7E-01
ENSMUST00000139721				2.0	4.5E-01	0.1	9.7E-01	-1.9	4.5E-01	0.0	1.0E+00
ENSMUST00000179990	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 [Source:MGI Symbol;Acc:MGI:1913664]			-5.2	2.2E-03	5.2	2.0E-05	0.5	4.5E-01	-0.3	4.0E-01
ENSMUST00000139731				-0.5	8.1E-01	-3.3	3.3E-01	-1.1	5.6E-01	1.7	6.0E-01
ENSMUST00000139732	inositol 1,4,5-triphosphate receptor 2 [Source:MGI Symbol;Acc:MGI:99418]	B2KF92		0.2	9.3E-01	-2.3	4.9E-01	-1.4	4.5E-01	1.1	7.5E-01
ENSMUST00000179996	predicted gene 4944 [Source:MGI Symbol;Acc:MGI:3643318]	J3QM38		3.7	8.5E-05	-1.4	2.9E-01	1.5	8.9E-02	0.8	5.3E-01
ENSMUST00000180023	potassium inwardly-rectifying channel, subfamily J, member 16 [Source:MGI Symbol;Acc:MGI:1314842]		Q9Z307	8.4	2.4E-05	-4.8	2.4E-02	-0.2	8.3E-01	-0.9	6.6E-01
ENSMUST00000139740	topoisomerase (DNA) III beta [Source:MGI Symbol;Acc:MGI:1333803]	D3YWY3		0.2	9.4E-01	2.3	4.6E-01	1.9	3.8E-01	-0.2	9.3E-01
ENSMUST00000180036	ornithine decarboxylase antizyme 1 [Source:MGI Symbol;Acc:MGI:109433]		P54369	-10.9	1.5E-04	6.0	1.0E-03	-0.6	6.4E-01	0.4	6.2E-01
ENSMUST00000180063	fibronectin type III domain containing 7 [Source:MGI Symbol;Acc:MGI:2443535]	J3QMB8		6.6	5.9E-03	7.0	3.1E-04	-1.6	2.8E-01	0.1	9.2E-01
ENSMUST00000139749				-0.9	4.9E-01	1.4	4.6E-01	1.0	5.3E-01	-1.3	3.8E-01
ENSMUST00000180072	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D [Source:MGI Symbol;Acc:MGI:1918929		Q9DCX2	-8.8	1.6E-06	5.9	9.8E-04	1.0	4.5E-01	-0.5	5.3E-01
ENSMUST00000180077	CCAAT/enhancer binding protein (C/EBP), zeta, opposite strand [Source:MGI Symbol;Acc:MGI:1915804]		Q8BTE5	-3.7	6.9E-03	6.1	2.2E-04	-0.5	6.5E-01	-0.1	8.0E-01
ENSMUST00000180081	potassium inwardly rectifying channel, subfamily J, member 11 [Source:MGI Symbol;Acc:MGI:107501]		Q61743	7.2	4.9E-05	5.4	1.2E-05	-2.3	7.3E-03	-0.4	2.7E-01
ENSMUST00000180092	predicted gene 11236 [Source:MGI Symbol;Acc:MGI:3702277]	J3QMS7		6.7	2.0E-02	-3.9	5.2E-03	-1.2	5.7E-02	0.6	6.1E-01
ENSMUST00000139768	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide [Source:MGI Symbol;Acc:MGI:2448506]	F6WIX7		3.9	3.8E-02	1.6	4.8E-01	-0.7	6.8E-01	1.6	4.1E-01
ENSMUST00000139774				1.0	3.1E-01	2.5	1.2E-01	2.5	7.9E-02	0.9	4.1E-01
ENSMUST00000180093	chemokine (C-C motif) receptor 9 [Source:MGI Symbol;Acc:MGI:1341902]		Q9WUT7	9.5	2.0E-05	2.1	1.1E-01	-0.8	4.4E-01	-0.3	7.8E-01
ENSMUST00000180095	myeloid leukemia factor 2 [Source:MGI Symbol;Acc:MGI:1353554]	Q3UNV7	Q99KX1	-5.5	8.3E-04	5.1	3.6E-03	-2.5	1.3E-01	0.9	3.0E-01
ENSMUST00000139782	methenyltetrahydrofolate synthetase domain containing [Source:MGI Symbol;Acc:MGI:2679252]	D3Z0Q4		-1.5	4.8E-01	-3.5	2.1E-01	-2.3	1.5E-01	-0.4	9.0E-01
ENSMUST00000180100	predicted gene 10097 [Source:MGI Symbol;Acc:MGI:3642295]	J3KMK7		5.7	9.6E-05	6.7	1.3E-04	1.5	1.7E-01	0.2	7.6E-01
ENSMUST00000180105	predicted gene, 21798 [Source:MGI Symbol;Acc:MGI:5433962]	J3QNU5		8.9	1.8E-05	6.6	2.5E-04	0.6	6.2E-01	0.7	2.6E-01
ENSMUST00000139788				1.8	4.3E-01	-0.5	8.7E-01	-1.5	4.9E-01	0.8	7.7E-01
ENSMUST00000180119				3.5	1.4E-03	2.8	5.6E-02	-2.0	1.7E-01	0.8	4.3E-01
ENSMUST00000139790	roline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III [Source:MGI Symbol;Acc:M	D6RFD3		4.8	7.7E-02	6.4	4.2E-02	-0.2	9.4E-01	-1.8	2.7E-01
ENSMUST00000139793	abhydrolase domain containing 13 [Source:MGI Symbol;Acc:MGI:1916154]		Q80UX8	-0.3	5.5E-01	0.0	9.9E-01	0.5	3.1E-01	0.2	7.4E-01
ENSMUST00000180139	RIKEN cDNA 1700014D04 gene [Source:MGI Symbol;Acc:MGI:1921474]	J3QMS2		7.0	2.1E-05	-4.6	5.0E-02	-0.2	8.1E-01	-1.6	5.1E-01
ENSMUST00000180143	predicted gene 3194 [Source:MGI Symbol;Acc:MGI:3781373]	J3QQ59		5.7	7.8E-04	5.0	3.7E-03	-1.8	2.3E-01	1.3	1.4E-01
ENSMUST00000180157	predicted gene 9507 [Source:MGI Symbol;Acc:MGI:3779917]	J3QK30		7.4	8.4E-05	5.9	9.3E-03	0.1	9.7E-01	0.5	6.5E-01
ENSMUST00000139803	-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:13	F6T1D2		-3.5	4.0E-02	-2.9	2.0E-01	0.4	7.3E-01	-0.2	9.1E-01
ENSMUST00000180159	polymerase (RNA) II (DNA directed) polypeptide K [Source:MGI Symbol;Acc:MGI:102725]	Q545V5	Q63871	-4.6	3.6E-04	5.9	1.5E-03	1.0	4.4E-01	-0.1	8.9E-01
ENSMUST00000180161	predicted gene 7137 [Source:MGI Symbol;Acc:MGI:3779677]	J3QMW1		8.2	5.2E-04	6.3	1.4E-03	-0.6	7.1E-01	-2.2	3.1E-02
ENSMUST00000180164	fibronectin type III and SPRY domain containing 1-like [Source:MGI Symbol;Acc:MGI:2442443]	J3QM95		4.9	3.8E-05	6.0	9.7E-04	0.9	4.5E-01	0.0	9.4E-01
ENSMUST00000180165	olfactory receptor 332 [Source:MGI Symbol;Acc:MGI:3030166]	Q5NC45		6.4	1.4E-04	6.8	1.3E-04	0.9	4.2E-01	-0.3	6.2E-01
ENSMUST00000180168	predicted gene 7102 [Source:MGI Symbol;Acc:MGI:3648735]	J3QQ10		4.6	5.3E-04	5.8	3.9E-04	-0.5	6.4E-01	0.9	1.4E-01
ENSMUST00000139826	tumor necrosis factor receptor superfamily, member 9 [Source:MGI Symbol;Acc:MGI:1101059]	A2A886		2.8	7.9E-02	3.5	2.6E-02	-2.6	1.0E-01	-3.2	1.4E-02
ENSMUST00000180196	solute carrier family 39 (metal ion transporter), member 8 [Source:MGI Symbol;Acc:MGI:1914797]		Q91W10	2.6	1.1E-02	7.4	1.1E-04	-0.6	6.6E-01	-0.7	2.6E-01
ENSMUST00000139837				3.2	7.8E-02	2.7	2.1E-01	-1.2	5.3E-01	-0.7	6.3E-01
ENSMUST00000139840	PQ loop repeat containing 2 [Source:MGI Symbol;Acc:MGI:2384837]		Q8C4N4	-0.1	8.8E-01	1.4	1.9E-01	0.9	2.7E-01	-0.6	5.1E-01
ENSMUST00000180217	zinc finger and BTB domain containing 5 [Source:MGI Symbol;Acc:MGI:1924601]		Q7TQG0	6.7	6.8E-03	-5.3	2.8E-02	2.5	1.1E-02	0.9	6.7E-01
ENSMUST00000180232	predicted gene 10424 [Source:MGI Symbol;Acc:MGI:3704250]	J3QNN3		7.7	3.9E-04	2.8	2.2E-03	0.1	8.0E-01	-0.4	5.2E-01
ENSMUST00000180233	protein phosphatase 2 (formerly 2A), regulatory subunit B", delta [Source:MGI Symbol;Acc:MGI:1335093]	J3QPX4		-2.6	1.4E-02	9.3	5.8E-06	1.7	1.1E-01	-0.7	1.2E-01
ENSMUST00000180239	fibrinogen silencer binding protein [Source:MGI Symbol;Acc:MGI:5301008]		Q8BKE5	6.2	1.2E-03	-5.7	9.8E-03	1.5	6.5E-02	-1.8	3.9E-01
ENSMUST00000180252	transmembrane protein 151B [Source:MGI Symbol;Acc:MGI:2685169]		Q68FE7	9.5	4.5E-05	5.8	3.0E-04	-0.8	4.4E-01	0.2	7.1E-01
ENSMUST00000139856	inositol polyphosphate 5-phosphatase K [Source:MGI Symbol;Acc:MGI:1194899]	Q5ND44		-3.0	3.6E-02	-2.5	1.9E-01	1.2	2.5E-01	0.6	7.4E-01
ENSMUST00000180278	autophagy related 4C, cysteine peptidase [Source:MGI Symbol;Acc:MGI:2651854]		Q811C2	-6.3	1.1E-04	-1.9	3.0E-01	1.3	2.4E-01	0.3	8.7E-01
ENSMUST00000180288	histone cluster 1 H2br [Source:MGI Symbol;Acc:MGI:3710645]	Q8CBB6		-5.2	1.2E-02	5.6	5.9E-06	-0.7	2.4E-01	0.1	8.7E-01
ENSMUST00000180290	phosphatase, orphan 2 [Source:MGI Symbol;Acc:MGI:1920623]		Q9D9M5	3.6	1.9E-04	3.4	3.3E-03	-0.6	4.2E-01	0.0	9.7E-01
ENSMUST00000139863	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 [Source:MGI Symbol;Acc:MGI:1914110]		Q0VGY8	4.4	1.4E-01	0.7	7.7E-01	-4.7	8.0E-02	-1.0	6.8E-01
ENSMUST00000139868				0.5	6.3E-01	2.5	1.2E-01	0.8	5.3E-01	-1.1	3.3E-01
ENSMUST00000180293	filaggrin [Source:MGI Symbol;Acc:MGI:95553]	A0A0A6YX57		10.0	2.2E-05	6.0	5.9E-04	0.5	6.5E-01	0.3	6.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000180297	predicted gene, 19402 [Source:MGI Symbol;Acc:MGI:5011587]	J3QJV4		8.4	2.6E-05	-1.5	3.2E-01	0.6	5.3E-01	-1.3	4.1E-01
ENSMUST00000139889				5.2	3.6E-02	7.8	7.4E-03	-0.2	9.2E-01	-2.8	6.6E-02
ENSMUST00000180305	tumor necrosis factor, alpha-induced protein 8 [Source:MGI Symbol;Acc:MGI:2147191]	J3QNB8		8.2	3.2E-04	7.3	2.7E-04	-0.7	6.2E-01	-1.1	1.6E-01
ENSMUST00000180308	filaggrin [Source:MGI Symbol;Acc:MGI:95553]	A0A0A6YXI5		6.8	1.2E-03	3.9	9.0E-04	0.7	3.1E-01	-0.6	3.7E-01
ENSMUST00000139902				-2.7	2.2E-01	-0.7	8.4E-01	2.8	2.4E-01	0.9	7.9E-01
ENSMUST00000180336	zinc finger protein 853 [Source:MGI Symbol;Acc:MGI:2685638]	J3QPU9		6.6	1.6E-04	5.6	2.8E-03	1.1	4.2E-01	-0.7	4.7E-01
ENSMUST00000180341	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]		Q9Z2X1	-9.1	4.5E-06	3.9	1.5E-03	0.4	6.4E-01	0.0	9.4E-01
ENSMUST00000180347	predicted gene 13696 [Source:MGI Symbol;Acc:MGI:3702068]	A2AK42		6.5	6.6E-05	7.7	4.7E-04	1.6	3.0E-01	-0.5	4.7E-01
ENSMUST00000180353	SRY (sex determining region Y)-box 1 [Source:MGI Symbol;Acc:MGI:98357]		P53783	8.0	2.3E-05	4.9	6.5E-03	-1.9	2.1E-01	-0.3	7.3E-01
ENSMUST00000180365	Yip1 domain family, member 2 [Source:MGI Symbol;Acc:MGI:1922016]		Q99LP8	-2.3	2.9E-02	4.2	1.2E-03	0.3	6.9E-01	-0.3	6.5E-01
ENSMUST00000180376	family with sequence similarity 193, member A [Source:MGI Symbol;Acc:MGI:2447768]	M0QWZ1		-1.3	1.3E-02	5.5	8.9E-04	0.1	9.6E-01	-0.5	4.7E-01
ENSMUST00000180384	cytotoxic and regulatory T cell molecule [Source:MGI Symbol;Acc:MGI:1859822]	M0QWH9		6.9	7.5E-05	-2.1	1.2E-01	0.7	3.7E-01	-0.3	8.0E-01
ENSMUST00000180393	RIKEN cDNA C130032M10 gene [Source:MGI Symbol;Acc:MGI:3642482]	Q8C888		4.3	1.5E-02	2.5	2.0E-02	-0.2	7.8E-01	-0.1	8.5E-01
ENSMUST00000139947				-0.8	5.1E-01	1.9	3.5E-01	2.2	2.3E-01	-0.6	6.9E-01
ENSMUST00000180430	kinase suppressor of ras 2 [Source:MGI Symbol;Acc:MGI:3610315]	M0QW59		7.8	2.1E-06	8.6	2.0E-04	-0.3	8.3E-01	-1.3	8.0E-02
ENSMUST00000180435	CDK2-associated protein 2 [Source:MGI Symbol;Acc:MGI:1098779]		Q9CPY4	-7.6	2.5E-06	-1.2	3.3E-01	2.0	1.7E-02	-1.2	3.6E-01
ENSMUST00000180436	achaete-scute complex homolog 5 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685043]	M0QWB7		6.1	2.9E-04	6.1	4.6E-04	0.0	9.9E-01	-1.4	1.0E-01
ENSMUST00000139954	major facilitator superfamily domain containing 11 [Source:MGI Symbol;Acc:MGI:1917150]	E9PZJ5		-5.6	4.2E-02	2.4	5.0E-01	6.6	3.0E-02	-1.4	6.5E-01
ENSMUST00000139956				-3.1	1.0E-01	-1.2	4.5E-01	-0.7	5.2E-01	-2.6	1.9E-01
ENSMUST00000180480	glutathione S-transferase, pi 1 [Source:MGI Symbol;Acc:MGI:95865]		P19157	-2.4	1.7E-02	-7.2	4.7E-03	-0.9	1.9E-01	-1.0	6.6E-01
ENSMUST00000180487	RIKEN cDNA 9130213A22 gene [Source:MGI Symbol;Acc:MGI:3642718]	Q3V3T2		8.0	1.5E-04	5.7	6.8E-04	-0.5	6.8E-01	-3.4	3.4E-03
ENSMUST00000180499	predicted gene, 21190 [Source:MGI Symbol;Acc:MGI:5434545]			6.2	9.0E-03	3.7	6.9E-02	-1.8	3.6E-01	0.5	7.2E-01
ENSMUST00000180502	zinc finger protein 850 [Source:MGI Symbol;Acc:MGI:3036281]	A0A087WSI7		1.7	8.7E-03	2.3	3.2E-01	-1.5	4.8E-01	2.0	2.7E-01
ENSMUST00000139966	Wolf-Hirschhorn syndrome candidate 1-like 1 (human) [Source:MGI Symbol;Acc:MGI:2142581]	D3Z197		-2.7	1.3E-01	-1.7	3.5E-01	-0.7	5.3E-01	-1.7	4.1E-01
ENSMUST00000180542	predicted gene, 26620 [Source:MGI Symbol;Acc:MGI:5477114]	Q9CY65		5.7	1.3E-04	4.6	2.5E-02	-0.7	7.2E-01	0.7	5.4E-01
ENSMUST00000180559	predicted gene, 26558 [Source:MGI Symbol;Acc:MGI:5477052]	Q8BLW8		3.9	2.2E-02	4.2	1.9E-03	-1.1	2.5E-01	-0.5	4.7E-01
ENSMUST00000180575	protein phosphatase 1, catalytic subunit, alpha isoform [Source:MGI Symbol;Acc:MGI:103016]		P62137	-7.1	1.6E-05	2.5	1.7E-02	-0.7	4.0E-01	0.3	6.9E-01
ENSMUST00000180611	Dmx-like 1 [Source:MGI Symbol;Acc:MGI:2443926]		Q6PNC0	-2.5	2.9E-02	5.9	1.4E-02	-0.8	7.3E-01	-1.3	3.1E-01
ENSMUST00000180614				-5.4	1.3E-03	-4.2	7.8E-03	0.9	1.3E-01	-1.6	2.8E-01
ENSMUST00000180621	polymerase (DNA-directed), delta 4 [Source:EntrezGene;Acc:69745]	Q547B4	Q9CWP8	-3.4	3.2E-04	-8.1	2.2E-03	-0.5	5.0E-01	-0.4	8.4E-01
ENSMUST00000180642	predicted gene, 21083 [Source:MGI Symbol;Acc:MGI:5434438]			7.7	2.1E-05	7.3	9.9E-05	0.9	3.7E-01	0.9	1.6E-01
ENSMUST00000180648	retinoic acid early transcript 1E [Source:MGI Symbol;Acc:MGI:2675273]	M0QWQ3		7.6	3.1E-05	4.0	6.1E-02	-1.9	3.4E-01	0.7	5.7E-01
ENSMUST00000180649	RIKEN cDNA A130051J0 gene [Source:MGI Symbol;Acc:MGI:3642574]	Q8CAU1		5.1	1.3E-04	5.6	1.6E-04	-2.7	2.8E-02	-0.1	8.9E-01
ENSMUST00000180657	SUMO1/sentrin specific peptidase 1 [Source:MGI Symbol;Acc:MGI:2445054]	M0QWX4		-3.3	7.5E-03	-5.0	1.7E-03	-1.5	1.5E-02	-0.5	6.7E-01
ENSMUST00000180660	phosphatidylinositol transfer protein, membrane-associated 1 [Source:MGI Symbol;Acc:MGI:1197524]		O35954	-6.7	1.0E-03	4.9	2.0E-02	-0.7	7.0E-01	-0.9	4.8E-01
ENSMUST00000139997				-0.9	4.0E-01	-0.1	9.6E-01	0.1	9.1E-01	-0.8	5.7E-01
ENSMUST00000180688	methionine aminopeptidase 2 [Source:MGI Symbol;Acc:MGI:1929701]	M0QW48		-4.8	1.7E-03	0.8	3.4E-01	-2.2	1.3E-02	-0.7	3.8E-01
ENSMUST00000140002	SH3-domain binding protein 5 (BTK-associated) [Source:MGI Symbol;Acc:MGI:1344391]		Q9Z131	3.3	9.4E-02	1.0	6.2E-01	-3.6	8.3E-02	-1.3	4.2E-01
ENSMUST00000180758	aryl-hydrocarbon receptor-interacting protein [Source:MGI Symbol;Acc:MGI:109622]		O08915	-7.0	3.7E-04	7.6	5.1E-04	0.0	9.8E-01	0.4	5.3E-01
ENSMUST00000180768	RIKEN cDNA B020031M17 gene [Source:MGI Symbol;Acc:MGI:3588226]	Q3UT11		6.3	1.5E-04	-4.2	3.5E-02	1.5	6.9E-02	1.5	3.9E-01
ENSMUST00000140012	piggyBac transposable element derived 5 [Source:MGI Symbol;Acc:MGI:2429955]	D3YZI9		2.4	1.6E-01	7.1	2.1E-03	0.7	7.1E-01	-4.0	1.2E-02
ENSMUST00000180817				5.7	6.6E-04	5.0	9.2E-04	-0.7	5.0E-01	0.2	8.1E-01
ENSMUST00000180886	transmembrane protein 178B [Source:MGI Symbol;Acc:MGI:3647581]	M0QWJ9		4.9	7.9E-03	2.7	1.2E-02	1.0	1.9E-01	0.8	2.3E-01
ENSMUST00000180928	RIKEN cDNA E030037K01 gene [Source:MGI Symbol;Acc:MGI:3704310]	M0QWF9		5.1	2.4E-04	8.2	1.1E-04	-0.7	6.3E-01	-1.7	3.2E-02
ENSMUST00000180971	RIKEN cDNA 9230104M06 gene [Source:MGI Symbol;Acc:MGI:3642845]	M0QWX8		4.6	8.5E-05	4.3	9.9E-04	0.2	8.1E-01	-0.4	5.1E-01
ENSMUST00000180998	Myeloid-associated differentiation marker [Source:UniProtKB/Swiss-Prot;Acc:O35682]	Q0VE46	O35682	-1.2	2.8E-02	3.8	4.6E-02	-3.0	1.3E-01	1.2	3.2E-01
ENSMUST00000140030	calmodulin binding transcription activator 1 [Source:MGI Symbol;Acc:MGI:2140230]	Z4YMK8		3.0	9.6E-02	2.2	3.7E-01	0.2	9.3E-01	1.0	6.2E-01
ENSMUST00000140037				-1.6	6.7E-02	-0.5	6.5E-01	0.2	7.5E-01	-0.9	3.5E-01
ENSMUST00000181023	nuclear fragile X mental retardation protein interacting protein 2 [Source:MGI Symbol;Acc:MGI:1915814]		Q5F2E7	-5.8	1.2E-03	5.9	7.2E-04	-0.8	5.1E-01	-0.2	7.6E-01
ENSMUST00000181061	aryl-hydrocarbon receptor-interacting protein [Source:MGI Symbol;Acc:MGI:109622]			-3.6	1.8E-02	-3.3	2.1E-01	1.8	2.0E-01	-0.7	7.8E-01
ENSMUST00000181080	calcium binding protein 4 [Source:MGI Symbol;Acc:MGI:1920910]		Q8VHC5	5.1	3.8E-04	6.0	1.0E-04	0.1	9.5E-01	0.5	3.8E-01
ENSMUST00000181091	methionine aminopeptidase 2 [Source:MGI Symbol;Acc:MGI:1929701]	Q3TMN1		-6.5	1.5E-02	4.5	2.2E-02	-1.3	4.3E-01	0.0	1.0E+00
ENSMUST00000140050	serine/arginine repetitive matrix 1 [Source:MGI Symbol;Acc:MGI:1858303]	F6UK16		3.3	2.1E-01	1.9	4.4E-01	-2.7	2.9E-01	-1.3	5.4E-01
ENSMUST00000181110	RIKEN cDNA 4930507D05 gene [Source:MGI Symbol;Acc:MGI:1921956]	Q8C9C9		5.0	6.7E-04	-6.2	5.1E-04	-0.5	3.0E-01	-0.9	5.1E-01
ENSMUST00000140057	protein tyrosine phosphatase, non-receptor type 12 [Source:MGI Symbol;Acc:MGI:104673]	F6Z0X5		-2.6	8.7E-02	-1.7	3.5E-01	-0.1	9.3E-01	-1.0	5.7E-01
ENSMUST00000181168	RIKEN cDNA B430218F22 gene [Source:MGI Symbol;Acc:MGI:3704413]	Q8BQR5		6.7	2.5E-05	-2.5	7.3E-02	-0.1	8.7E-01	-0.4	7.4E-01
ENSMUST00000181173	predicted pseudogene 3839 [Source:MGI Symbol;Acc:MGI:3782011]	S4R1W1		7.5	2.8E-06	6.1	1.3E-03	-0.5	7.5E-01	-1.2	1.8E-01
ENSMUST00000181174	RIKEN cDNA gene D630044L22 gene [Source:MGI Symbol;Acc:MGI:3709661]	Q8C701		3.9	4.3E-05	7.1	1.0E-04	-0.5	6.7E-01	-0.9	1.6E-01
ENSMUST00000181177	solute carrier family 35, member A5 [Source:MGI Symbol;Acc:MGI:1921352]	M0QWE5		-7.9	5.9E-05	6.7	9.4E-05	-0.8	4.7E-01	0.7	2.7E-01
ENSMUST00000181205	predicted gene, 20909 [Source:MGI Symbol;Acc:MGI:5434265]	Q5FWB5		6.9	1.9E-04	6.5	7.3E-04	-0.6	6.6E-01	-1.7	4.8E-02
ENSMUST00000181217	methionine aminopeptidase 2 [Source:MGI Symbol;Acc:MGI:1929701]	Q3UI33		-7.1	8.3E-04	6.6	2.2E-04	-0.6	6.2E-01	-0.3	6.0E-01
ENSMUST00000140076	phosphoribosyl pyrophosphate amidotransferase [Source:MGI Symbol;Acc:MGI:2387203]	Q8CIH9		-2.5	3.1E-01	-1.9	3.7E-01	-1.1	4.9E-01	-1.8	4.8E-01
ENSMUST00000140079	suppression of tumorigenicity 18 [Source:MGI Symbol;Acc:MGI:2446700]	Q148A0	Q80TY4	4.0	1.4E-01	1.9	5.9E-01	-0.2	9.6E-01	2.0	4.5E-01
ENSMUST00000181228	TBC1 domain family, member 10c [Source:MGI Symbol;Acc:MGI:1922072]		Q8C9V1	-4.3	3.5E-05	6.7	2.9E-03	-1.7	3.8E-01	-1.6	1.7E-01
ENSMUST00000181243	aryl-hydrocarbon receptor-interacting protein [Source:MGI Symbol;Acc:MGI:109622]		O08915	-3.3	6.2E-03	5.6	1.6E-03	-0.6	6.5E-01	0.8	3.0E-01
ENSMUST00000140096				1.1	3.2E-01	0.0	9.9E-01	0.4	7.2E-01	1.5	2.7E-01
ENSMUST00000181313	predicted gene, 21936 [Source:MGI Symbol;Acc:MGI:5439387]	M0QWL1		5.4	1.9E-03	7.3	1.9E-05	-1.1	2.8E-01	-0.2	6.8E-01
ENSMUST00000181319	zinc finger protein 493 [Source:MGI Symbol;Acc:MGI:1920208]	M0QWP5		4.4	5.7E-03	8.2	1.1E-04	-0.7	6.1E-01	0.5	4.4E-01
ENSMUST00000181320	NLR family, pyrin domain containing 12 [Source:MGI Symbol;Acc:MGI:2676630]		E9Q5R7	-4.4	2.4E-04	4.3	4.6E-06	-0.8	9.1E-02	0.1	6.5E-01
ENSMUST00000181324		D3Z081		7.3	6.7E-05	4.6	2.8E-02	0.0	1.0E+00	-0.6	6.5E-01
ENSMUST00000181326	predicted gene 2042 [Source:MGI Symbol;Acc:MGI:3800544]	M0QWA3		6.5	4.8E-04	5.1	7.8E-05	0.6	4.3E-01	0.7	1.7E-01
ENSMUST00000181329	RAD9 homolog A [Source:MGI Symbol;Acc:MGI:1328356]		Q9Z0F6	-2.8	7.4E-03	6.1	1.7E-04	-0.9	4.2E-01	-0.4	5.3E-01
ENSMUST00000181369	RIKEN cDNA 4930519P11 gene [Source:MGI Symbol;Acc:MGI:1921971]	Q9CUJ8		6.2	1.1E-03	-3.4	4.7E-03	-0.1	8.3E-01	-0.9	4.1E-01
ENSMUST00000181375	transmembrane protein 134 [Source:EntrezGene;Acc:66990]			-3.9	4.6E-04	5.3	9.1E-05	-0.6	4.3E-01	0.3	5.5E-01
ENSMUST00000181379	family with sequence similarity 193, member A [Source:MGI Symbol;Acc:MGI:2447768]	M0QWS6		3.6	1.4E-04	6.7	4.0E-04	-0.5	7.0E-01	-1.4	7.8E-02
ENSMUST00000181415	ribosomal protein S6 kinase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1927343]			-4.7	6.4E-03	-2.6	7.3E-03	0.5	2.8E-01	-0.3	6.7E-01
ENSMUST00000181455	Protein kinase C gamma type [Source:UniProtKB/Swiss-Prot;Acc:P63318]	Q3UN66	P63318	2.7	3.8E-03	11.3	1.3E-04	0.4	8.3E-01	-1.3	6.8E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000181467	apolipoprotein L 11b [Source:MGI Symbol;Acc:MGI:3036248]	M0QWU4		5.5	3.6E-03	6.2	6.7E-04	-0.7	6.2E-01	0.0	9.5E-01
ENSMUST00000181494	Coronin-1B [Source:UniProtKB/Swiss-Prot;Acc:Q9WUM3]	A2RS22	Q9WUM3	-6.9	1.5E-05	5.4	2.2E-03	0.6	6.6E-01	-1.0	2.7E-01
ENSMUST00000181504	forkhead box F1 [Source:MGI Symbol;Acc:MGI:1347470]		Q61080	7.2	1.7E-04	6.3	1.0E-03	-0.6	6.6E-01	-0.2	7.9E-01
ENSMUST00000181545	RIKEN cDNA A730071L15Rik gene [Source:MGI Symbol;Acc:MGI:3642498]	Q8C4X0		6.4	1.3E-04	-7.9	3.9E-04	-0.3	5.4E-01	-0.9	5.8E-01
ENSMUST00000181548	G protein-coupled receptor 152 [Source:MGI Symbol;Acc:MGI:2685519]		Q8BXS7	7.4	4.0E-05	4.3	4.3E-05	-1.0	1.2E-01	0.3	5.1E-01
ENSMUST00000181549	predicted gene, 20854 [Source:MGI Symbol;Acc:MGI:5434210]	Q62461		8.2	7.7E-06	6.1	2.1E-03	-0.6	7.2E-01	-1.7	7.8E-02
ENSMUST00000140171				4.8	6.4E-02	3.6	9.8E-02	-1.8	4.4E-01	-0.6	7.1E-01
ENSMUST00000140174	RecQ protein-like 5 [Source:MGI Symbol;Acc:MGI:2156841]	J3QMY1		-0.5	7.8E-01	0.8	7.7E-01	1.2	5.9E-01	-0.1	9.5E-01
ENSMUST00000140178	ring finger protein 31 [Source:MGI Symbol;Acc:MGI:1934704]	F6XVP7		-3.4	4.9E-02	-1.2	4.9E-01	1.0	3.8E-01	-1.1	5.7E-01
ENSMUST00000181564	leucine rich repeat containing 38 [Source:MGI Symbol;Acc:MGI:2442845]		A2VDH3	6.1	2.1E-04	1.2	2.9E-01	-0.6	5.0E-01	0.6	5.4E-01
ENSMUST00000181609	forkhead box L1 [Source:MGI Symbol;Acc:MGI:1347469]		Q64731	8.3	1.3E-05	7.9	1.7E-02	-0.9	7.7E-01	-2.3	1.8E-01
ENSMUST00000181616	predicted gene, 21149 [Source:MGI Symbol;Acc:MGI:5434504]			8.1	2.7E-05	2.3	2.9E-02	0.7	3.9E-01	0.0	9.8E-01
ENSMUST00000181645	retinoic acid early transcript 1E [Source:MGI Symbol;Acc:MGI:2675273]	D7F2B6	Q9CZQ6	3.9	9.6E-03	7.1	2.1E-03	-0.8	6.8E-01	-0.4	7.0E-01
ENSMUST00000181669				6.3	1.1E-05	4.7	3.2E-04	0.4	5.7E-01	0.8	2.1E-01
ENSMUST00000181684	CDK2-associated protein 2 [Source:MGI Symbol;Acc:MGI:1098779]			-8.1	3.3E-04	-3.2	2.9E-02	0.4	5.9E-01	-1.4	3.5E-01
ENSMUST00000181686	Voltage-dependent calcium channel gamma-7 subunit [Source:UniProtKB/Swiss-Prot;Acc:P62956]	B9EJ14	P62956	6.0	1.8E-04	5.6	8.4E-04	-0.5	6.8E-01	-0.1	8.5E-01
ENSMUST00000140205	a disintegrin and metallopeptidase domain 10 [Source:MGI Symbol;Acc:MGI:109548]	E9PYF2		2.8	3.8E-01	-2.9	4.2E-01	-4.2	1.5E-01	1.5	6.7E-01
ENSMUST00000140211	centrosomal protein 41 [Source:MGI Symbol;Acc:MGI:1891414]	S4R2L7		4.5	8.5E-02	4.0	1.1E-01	-2.8	3.0E-01	-2.2	2.0E-01
ENSMUST00000181711	predicted gene, 19426 [Source:MGI Symbol;Acc:MGI:5011611]	M0QWC7		6.8	1.7E-04	-3.4	4.1E-02	0.5	5.6E-01	-0.7	6.6E-01
ENSMUST00000140221				2.8	6.3E-02	-3.4	7.3E-02	-4.2	5.4E-03	2.0	2.6E-01
ENSMUST00000181767	zinc finger protein 87 [Source:MGI Symbol;Acc:MGI:107768]	Q8K2A4		-4.0	1.6E-04	2.8	2.7E-02	-0.5	6.2E-01	-0.4	6.4E-01
ENSMUST00000140227				-3.5	1.5E-01	-1.8	3.3E-01	-1.2	3.9E-01	-2.9	2.3E-01
ENSMUST00000181779	predicted gene 2916 [Source:MGI Symbol;Acc:MGI:3781094]	Q9D9B9		8.4	7.5E-07	6.2	1.8E-03	-2.0	2.5E-01	-0.9	2.9E-01
ENSMUST00000140229				0.9	7.0E-01	0.9	6.9E-01	-1.3	5.5E-01	-1.3	5.5E-01
ENSMUST00000181786	predicted gene 10251 [Source:MGI Symbol;Acc:MGI:3704424]	J3QPM5		6.8	2.5E-04	5.7	1.1E-03	-0.9	5.1E-01	-0.9	2.4E-01
ENSMUST00000181795	cytochrome c oxidase subunit IV isoform 1 [Source:MGI Symbol;Acc:MGI:88473]	M0QWX7		-6.6	2.0E-03	5.8	1.6E-03	-0.5	7.4E-01	-0.8	3.0E-01
ENSMUST00000181835	RIKEN cDNA 4933408J17 gene [Source:MGI Symbol;Acc:MGI:1921704]	Q9D475		6.3	1.9E-04	7.2	1.4E-05	0.3	7.2E-01	-0.5	2.7E-01
ENSMUST00000181836	ER membrane protein complex subunit 8 [Source:MGI Symbol;Acc:MGI:1343095]	M0QWP2		-4.4	2.9E-04	6.7	2.7E-03	-0.7	6.8E-01	-0.3	7.6E-01
ENSMUST00000181843	predicted gene 2042 [Source:MGI Symbol;Acc:MGI:3800544]	M0QW82		5.7	2.4E-03	-3.5	8.8E-03	-0.7	2.1E-01	-2.5	7.5E-02
ENSMUST00000181880	predicted gene 3532 [Source:MGI Symbol;Acc:MGI:3781709]	M0QWL4		5.6	1.5E-03	5.1	2.9E-02	-1.3	5.5E-01	0.8	5.5E-01
ENSMUST00000140247				3.6	6.5E-02	-1.2	5.5E-01	-3.0	9.1E-02	1.8	3.5E-01
ENSMUST00000181892	zinc finger protein 748 [Source:MGI Symbol;Acc:MGI:1916455]	Q7TPL6		-2.4	8.3E-04	3.1	1.0E-01	-0.6	7.5E-01	3.0	2.9E-02
ENSMUST00000140254				-1.0	1.3E-01	-0.8	3.0E-01	-0.6	2.9E-01	-0.8	3.0E-01
ENSMUST00000140255	d, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 [Source:MGI Symbol;Acc	G3UXC0		-3.6	9.0E-02	-3.7	1.6E-01	-0.6	6.2E-01	-0.5	8.4E-01
ENSMUST00000181904	CXXC finger 4 [Source:MGI Symbol;Acc:MGI:2442112]	M0QWU0		7.0	1.2E-04	5.5	9.2E-04	-2.5	8.3E-02	-1.7	4.9E-02
ENSMUST00000140257				-1.7	7.1E-02	-0.3	7.6E-01	0.2	8.1E-01	-1.2	2.6E-01
ENSMUST00000181948	microtubule-associated protein 1 light chain 3 beta [Source:MGI Symbol;Acc:MGI:1914693]	M0QWC2		-11.1	2.1E-06	7.2	1.3E-02	-0.8	7.6E-01	-1.4	3.2E-01
ENSMUST00000181950	ER membrane protein complex subunit 8 [Source:MGI Symbol;Acc:MGI:1343095]	M0QWS0		-4.8	2.2E-04	4.1	9.5E-03	-2.5	1.0E-01	-0.1	9.3E-01
ENSMUST00000140264	inositol polyphosphate-4-phosphatase, type I [Source:MGI Symbol;Acc:MGI:1931123]	Q3UEQ1		0.3	6.7E-01	1.5	1.5E-01	0.8	3.2E-01	-0.4	6.6E-01
ENSMUST00000181956	RIKEN cDNA D330020A13 gene [Source:MGI Symbol;Acc:MGI:3642762]	Q8C799		5.4	1.3E-03	3.3	1.8E-02	0.9	4.3E-01	0.1	8.6E-01
ENSMUST00000140269				2.0	7.4E-02	2.7	8.6E-02	0.3	8.2E-01	-0.3	7.4E-01
ENSMUST00000181969	Nedd4 family interacting protein 2 [Source:MGI Symbol;Acc:MGI:1923523]	M0QWK1		-3.5	1.7E-03	1.9	1.9E-02	-0.5	4.4E-01	0.0	9.7E-01
ENSMUST00000140280				2.9	4.9E-02	2.8	8.6E-02	-0.5	7.1E-01	-0.4	7.6E-01
ENSMUST00000181981	pleckstrin homology domain containing, family A member 7 [Source:MGI Symbol;Acc:MGI:2445094]		Q3UIL6	7.3	4.7E-05	5.6	1.3E-03	-0.3	8.2E-01	-0.6	4.4E-01
ENSMUST00000181986	RNA binding motif protein 6 [Source:MGI Symbol;Acc:MGI:1338037]	S4R1D1		-3.5	2.2E-02	-5.2	3.9E-03	-1.1	6.7E-02	-0.5	7.4E-01
ENSMUST00000181987	CDC42 guanine nucleotide exchange factor (GEF) 9 [Source:MGI Symbol;Acc:MGI:2442233]		Q3UTH8	6.3	5.4E-05	-2.9	9.8E-02	2.2	2.1E-02	-0.7	7.1E-01
ENSMUST00000181998	pleckstrin homology domain containing, family A member 7 [Source:MGI Symbol;Acc:MGI:2445094]		Q3UIL6	6.1	1.5E-02	2.4	2.2E-02	-1.8	5.2E-02	-0.1	8.7E-01
ENSMUST00000182018	dystonin [Source:MGI Symbol;Acc:MGI:104627]	S4R1Y6		6.1	4.5E-04	6.5	1.1E-02	-0.6	7.9E-01	-1.5	2.5E-01
ENSMUST00000182023	mast cell immunoglobulin like receptor 1 [Source:MGI Symbol;Acc:MGI:2685731]	A0A0B4J1N6		-3.0	1.8E-03	4.3	1.6E-02	-1.2	4.0E-01	-0.6	5.6E-01
ENSMUST00000182047	ring finger protein 4 [Source:MGI Symbol;Acc:MGI:1201691]		Q9QZS2	4.4	5.1E-03	-6.0	2.4E-03	0.2	7.7E-01	-0.3	8.8E-01
ENSMUST00000140314				0.8	6.3E-01	3.1	1.7E-01	0.5	8.1E-01	-1.8	2.6E-01
ENSMUST00000182078	ankyrin 2, brain [Source:MGI Symbol;Acc:MGI:88025]	S4R2R5		5.1	1.7E-02	5.0	1.1E-04	-0.7	3.6E-01	-0.1	8.1E-01
ENSMUST00000182128	pregnancy-specific glycoprotein 21 [Source:MGI Symbol;Acc:MGI:1891353]	S4R1D2		6.8	1.0E-04	-0.7	2.4E-01	0.5	2.5E-01	-0.1	8.6E-01
ENSMUST00000182151	small integral membrane protein 1 [Source:MGI Symbol;Acc:MGI:1916109]		P0C8K7	7.3	2.6E-04	7.4	7.6E-05	-1.5	2.6E-01	-0.7	2.5E-01
ENSMUST00000140337				2.5	1.9E-01	6.8	2.8E-02	3.3	2.2E-01	-1.0	5.2E-01
ENSMUST00000140339				-0.5	4.0E-01	-0.9	2.1E-01	-0.5	3.6E-01	0.0	9.9E-01
ENSMUST00000182172	coiled-coil domain containing 166 [Source:MGI Symbol;Acc:MGI:1925902]	Q0P5Z5		2.3	1.1E-02	4.3	1.0E-03	-1.4	1.9E-01	-0.8	2.3E-01
ENSMUST00000140349	jumonji domain containing 6 [Source:MGI Symbol;Acc:MGI:1858910]	F6VRF7		0.2	9.4E-01	-1.7	5.9E-01	-2.7	2.1E-01	-0.9	7.8E-01
ENSMUST00000182183	coiled-coil domain containing 53 [Source:MGI Symbol;Acc:MGI:1914532]	S4R287		-7.3	1.2E-05	3.3	1.6E-03	0.1	8.9E-01	0.1	9.1E-01
ENSMUST00000182198	rine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10 [Source:MGI Symbol;Acc:MGI:213864	G3UYR4		-4.2	1.0E-03	5.6	9.6E-04	-0.6	6.3E-01	0.6	3.6E-01
ENSMUST00000182209	cyclin D3 [Source:MGI Symbol;Acc:MGI:88315]	Q3TSW4	P30282	-10.7	1.8E-05	3.8	1.5E-02	-0.4	7.2E-01	-0.5	5.7E-01
ENSMUST00000140355				2.0	2.7E-01	0.6	7.7E-01	-1.8	3.2E-01	-0.3	8.7E-01
ENSMUST00000182213	Rho GTPase activating protein 12 [Source:MGI Symbol;Acc:MGI:1922665]	S4R221		-4.1	1.7E-02	5.3	5.6E-02	-0.6	8.1E-01	-0.4	7.8E-01
ENSMUST00000182214	SH3-binding domain kinase family, member 2 [Source:MGI Symbol;Acc:MGI:2685925]		P0C5K1	7.9	6.8E-05	6.4	1.8E-04	0.5	6.2E-01	-0.1	8.8E-01
ENSMUST00000140363				-1.6	3.8E-01	-1.4	5.1E-01	-0.1	9.6E-01	-0.3	9.0E-01
ENSMUST00000140364	aarF domain containing kinase 2 [Source:MGI Symbol;Acc:MGI:1889336]			1.5	3.7E-02	2.5	5.1E-03	-0.1	9.1E-01	-1.1	8.1E-02
ENSMUST00000182222	calcium channel, voltage-dependent, gamma subunit 8 [Source:MGI Symbol;Acc:MGI:1932376]	F7CZ64		4.9	1.2E-03	3.4	9.0E-04	0.2	7.3E-01	-0.6	2.8E-01
ENSMUST00000182233	piezo-type mechanosensitive ion channel component 2 [Source:MGI Symbol;Acc:MGI:1918781]	S4R1C9		6.8	3.0E-04	3.2	3.7E-03	-1.6	8.2E-02	-0.8	2.6E-01
ENSMUST00000182260	REX1, RNA exonuclease 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914182]	S4R246		-5.2	2.6E-02	4.4	5.7E-03	-3.3	3.8E-02	-0.5	5.3E-01
ENSMUST00000182267	phospholipase C, epsilon 1 [Source:MGI Symbol;Acc:MGI:1921305]	S4R1Q8		7.2	7.1E-04	-4.6	2.0E-02	-4.7	9.8E-04	4.7	1.6E-02
ENSMUST00000140376	DnaJ (Hsp40) homolog, subfamily B, member 6 [Source:MGI Symbol;Acc:MGI:1344381]	F6YRQ2		0.2	8.3E-01	1.4	1.7E-01	0.8	2.9E-01	-0.4	6.5E-01
ENSMUST00000140382	perilipin 2 [Source:MGI Symbol;Acc:MGI:87920]	B1AXR5		-0.2	9.5E-01	4.2	1.6E-01	1.6	5.2E-01	-2.7	2.8E-01
ENSMUST00000182276	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1930042]	S4R1N2		-2.9	1.1E-02	-1.6	1.3E-01	0.3	5.9E-01	-2.1	7.8E-02
ENSMUST00000182283	protein tyrosine phosphatase, receptor type, C [Source:MGI Symbol;Acc:MGI:97810]	S4R2V1		-12.9	2.0E-06	-5.1	6.1E-03	-0.7	2.5E-01	-0.3	8.6E-01
ENSMUST00000140386				1.8	5.1E-02	0.2	9.0E-01	0.1	9.5E-01	1.7	1.4E-01
ENSMUST00000182309	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	S4R2L4		-7.9	1.9E-03	4.7	1.4E-02	0.3	8.2E-01	0.2	7.9E-01
ENSMUST00000140391				2.8	1.1E-01	3.4	1.2E-01	-0.7	7.0E-01	-1.3	3.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000182328	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 [Source:MGI Symbol;Acc:MGI:1888669]	Q9CPS5		-5.8	1.1E-05	4.0	7.8E-03	-1.5	2.1E-01	-0.4	6.8E-01
ENSMUST00000140393	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	E9Q4R3		-3.4	5.5E-02	-2.8	2.7E-01	0.9	5.5E-01	0.2	9.2E-01
ENSMUST00000140396	WD repeat domain 5 [Source:MGI Symbol;Acc:MGI:2155884]	F6Q3W0		2.5	2.8E-01	0.4	8.6E-01	-4.1	6.2E-02	-2.0	3.5E-01
ENSMUST00000140398				3.2	6.2E-02	4.7	1.4E-02	-0.5	7.5E-01	-2.0	1.1E-01
ENSMUST00000182350	chemokine (C motif) receptor 1 [Source:MGI Symbol;Acc:MGI:1346338]	S4R1K3		7.9	4.5E-05	4.5	1.3E-03	-0.9	3.5E-01	0.5	5.0E-01
ENSMUST00000182356	ankyrin repeat and sterile alpha motif domain containing 1B [Source:MGI Symbol;Acc:MGI:1924781]			9.7	3.2E-06	6.0	2.0E-06	-0.4	5.1E-01	0.0	9.2E-01
ENSMUST00000182371	RNA binding motif protein 5 [Source:MGI Symbol;Acc:MGI:1933204]	S4R184		-9.2	3.6E-04	5.7	2.4E-02	-0.8	7.5E-01	2.1	1.2E-01
ENSMUST00000182384	oxysterol binding protein-like 10 [Source:MGI Symbol;Acc:MGI:1921736]	S4R296		5.7	3.2E-02	3.1	2.2E-03	-1.5	6.9E-02	-0.3	6.0E-01
ENSMUST00000182386	septin 14 [Source:MGI Symbol;Acc:MGI:1921472]	S4R2P6		6.6	4.3E-04	-2.5	9.8E-02	0.0	9.8E-01	-0.3	8.5E-01
ENSMUST00000140423				1.5	7.8E-02	1.6	1.4E-01	0.3	6.7E-01	0.2	8.1E-01
ENSMUST00000182393	proline-rich coiled-coil 2C [Source:MGI Symbol;Acc:MGI:1913754]	S4R209		-3.4	3.1E-02	-9.4	1.4E-03	-0.1	9.2E-01	-1.0	6.8E-01
ENSMUST00000182396	son of sevenless homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:98355]	S4R2C4		-6.5	3.5E-03	6.5	8.1E-04	-0.4	7.6E-01	-1.3	1.3E-01
ENSMUST00000182407	piccolo (presynaptic cytomatrix protein) [Source:MGI Symbol;Acc:MGI:1349390]		Q9QYX7	11.4	7.8E-04	6.2	5.3E-04	-0.1	9.3E-01	0.6	3.9E-01
ENSMUST00000182443	pleckstrin homology domain containing, family A member 7 [Source:MGI Symbol;Acc:MGI:2445094]			7.4	2.1E-06	7.3	1.2E-02	-0.8	7.5E-01	-1.2	3.7E-01
ENSMUST00000182450	RNA binding motif protein 25 [Source:MGI Symbol;Acc:MGI:1914289]	S4R1X9		-6.9	8.1E-03	6.1	4.0E-04	-1.5	2.6E-01	-0.8	2.4E-01
ENSMUST00000140436	BCL2-like 1 [Source:MGI Symbol;Acc:MGI:88139]		Q64373	5.0	4.8E-02	5.4	6.2E-02	-0.9	7.3E-01	-1.3	4.3E-01
ENSMUST00000140438	mitochondrial ribosomal protein S25 [Source:MGI Symbol;Acc:MGI:1928140]		Q9D125	-0.7	3.2E-01	0.4	6.3E-01	0.8	2.0E-01	-0.3	7.4E-01
ENSMUST00000182462	anoctamin 4 [Source:MGI Symbol;Acc:MGI:2443344]	S4R1Z9		6.3	1.6E-02	-5.0	1.6E-02	-1.1	1.7E-01	1.3	4.4E-01
ENSMUST00000182491	relaxin/insulin-like family peptide receptor 1 [Source:MGI Symbol;Acc:MGI:2682211]	S4R2B5		6.3	1.1E-04	6.2	5.7E-04	-1.4	2.8E-01	0.1	8.8E-01
ENSMUST00000182500	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble [Source:MGI Symbol;Acc:MGI:2180003]	S4R167		7.5	7.9E-08	4.0	7.9E-05	-0.9	1.5E-01	0.2	5.9E-01
ENSMUST00000140448	supervillin [Source:MGI Symbol;Acc:MGI:2147319]		Q8K4L3	3.8	7.8E-02	3.2	3.0E-02	-5.2	1.5E-02	-4.7	4.5E-03
ENSMUST00000140452	fer-1-like 5 (C. elegans) [Source:MGI Symbol;Acc:MGI:3616091]			-1.9	1.2E-01	-2.3	1.9E-01	0.6	5.5E-01	1.0	5.6E-01
ENSMUST00000140454				-0.9	7.0E-01	-3.2	7.0E-02	-5.4	3.6E-03	-3.1	1.9E-01
ENSMUST00000182501	signal peptidase complex subunit 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916269]			-9.4	1.8E-06	6.6	3.4E-05	0.7	4.3E-01	-0.4	4.2E-01
ENSMUST00000182510	autophagy related 7 [Source:MGI Symbol;Acc:MGI:1921494]	S4R1N8		-2.5	9.1E-03	4.8	5.2E-03	-0.6	6.5E-01	-1.8	6.9E-02
ENSMUST00000182511	pleckstrin homology domain containing, family A member 7 [Source:MGI Symbol;Acc:MGI:2445094]		Q3UIL6	6.1	1.7E-02	7.5	3.7E-04	0.2	8.6E-01	1.0	1.6E-01
ENSMUST00000140462				1.6	1.3E-01	3.3	1.7E-02	0.4	7.3E-01	-1.4	1.6E-01
ENSMUST00000182533	scaffold attachment factor B [Source:MGI Symbol;Acc:MGI:2146974]	S4R1M2		-7.0	4.9E-05	1.5	1.0E-01	-1.1	1.4E-01	0.0	9.6E-01
ENSMUST00000140467				1.2	1.6E-01	1.0	3.4E-01	-0.2	8.1E-01	0.0	1.0E+00
ENSMUST00000140468				0.2	9.2E-01	-4.9	9.3E-02	-5.0	9.9E-03	0.0	9.9E-01
ENSMUST00000140469				-2.7	4.0E-02	-3.0	8.8E-02	0.0	9.7E-01	0.3	8.8E-01
ENSMUST00000140470				-2.7	1.4E-01	-4.1	6.8E-02	-2.2	7.2E-02	-0.8	7.3E-01
ENSMUST00000140471				0.6	6.8E-01	1.1	5.7E-01	0.1	9.5E-01	-0.4	8.1E-01
ENSMUST00000182539	cyclin D3 [Source:MGI Symbol;Acc:MGI:88315]	S4R216		-6.4	2.2E-03	4.2	7.1E-04	-1.6	8.1E-02	-1.6	4.3E-02
ENSMUST00000182577	suprabasin [Source:MGI Symbol;Acc:MGI:2446326]	S4R1T6		5.6	2.7E-05	6.8	1.4E-06	-0.4	5.6E-01	0.8	4.6E-02
ENSMUST00000140481				-1.0	5.5E-01	-2.2	4.3E-01	0.3	8.2E-01	1.6	5.5E-01
ENSMUST00000140482				0.6	7.5E-01	2.9	2.3E-01	0.2	9.3E-01	-2.2	2.5E-01
ENSMUST00000182584	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	A0A0G2JDD3		-6.2	3.3E-04	2.4	1.5E-02	-0.5	4.9E-01	0.3	6.4E-01
ENSMUST00000140486	E74-like factor 4 (ets domain transcription factor) [Source:MGI Symbol;Acc:MGI:1928377]	Q3U1U8		1.7	4.4E-01	4.0	8.5E-02	-0.5	8.3E-01	-2.8	1.7E-01
ENSMUST00000140487				1.7	1.4E-01	2.2	1.0E-01	-0.3	7.7E-01	-0.8	4.3E-01
ENSMUST00000182597	baculoviral IAP repeat-containing 6 [Source:MGI Symbol;Acc:MGI:1276108]		O88738	-5.1	2.1E-02	3.0	1.8E-01	-0.5	8.1E-01	1.0	4.9E-01
ENSMUST00000182625	SRY (sex determining region Y)-box 12 [Source:MGI Symbol;Acc:MGI:98360]		Q04890	4.4	9.0E-05	-1.2	8.1E-02	1.2	9.3E-03	0.3	6.0E-01
ENSMUST00000140511				-1.5	9.9E-02	-0.2	8.5E-01	0.0	9.5E-01	-1.4	1.6E-01
ENSMUST00000182666	SH3 domain protein D19 [Source:MGI Symbol;Acc:MGI:1350923]		Q91X43	10.6	4.7E-06	8.2	1.0E-04	-0.7	6.3E-01	-0.6	3.8E-01
ENSMUST00000140513	jumonji domain containing 6 [Source:MGI Symbol;Acc:MGI:1858910]	F6VMC4		-3.2	3.9E-01	-1.3	7.8E-01	1.0	7.2E-01	-0.9	8.5E-01
ENSMUST00000182709	ring finger protein 4 [Source:MGI Symbol;Acc:MGI:1201691]		Q9QZS2	-7.4	2.6E-05	4.6	8.7E-03	-0.7	6.5E-01	0.1	8.8E-01
ENSMUST00000182719	schwannomin interacting protein 1 [Source:MGI Symbol;Acc:MGI:1353557]		Q3TI53	5.6	2.7E-02	4.5	3.2E-03	-0.3	7.7E-01	0.1	8.5E-01
ENSMUST00000182722	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent) [Source:MGI Symbol;Acc:MGI:1098272]	S4R1J5		-8.1	1.8E-05	2.4	1.3E-02	0.2	7.5E-01	0.5	4.4E-01
ENSMUST00000182741	cytochrome P450, family 2, subfamily ab, polypeptide 1 [Source:MGI Symbol;Acc:MGI:3644957]	S4R196		4.5	1.7E-03	-8.6	1.9E-04	-1.6	5.5E-03	0.9	5.3E-01
ENSMUST00000182750	netrin 5 [Source:MGI Symbol;Acc:MGI:2685330]	S4R1X6		7.1	9.0E-04	2.4	2.6E-02	-1.3	1.4E-01	-0.7	3.8E-01
ENSMUST00000140530				4.4	7.3E-02	5.6	6.0E-02	0.6	8.3E-01	-0.6	7.2E-01
ENSMUST00000182755	protein tyrosine phosphatase, receptor type, C [Source:MGI Symbol;Acc:MGI:97810]	S4R1M0		-8.1	2.1E-03	6.0	9.7E-05	-2.0	7.6E-02	-1.6	1.9E-02
ENSMUST00000182769	caspase 16, apoptosis-related cysteine peptidase, pseudogene [Source:MGI Symbol;Acc:MGI:3646305]			6.0	4.6E-04	6.6	3.2E-04	-0.6	6.2E-01	-0.7	3.2E-01
ENSMUST00000182780	signal-induced proliferation-associated 1 like 3 [Source:MGI Symbol;Acc:MGI:1921456]	S4R1P8		5.8	8.5E-03	-4.3	4.8E-03	0.0	9.6E-01	-0.6	6.6E-01
ENSMUST00000140543				0.6	6.4E-01	1.6	2.9E-01	0.1	9.4E-01	-0.9	4.7E-01
ENSMUST00000140544				0.3	7.2E-01	-0.5	6.1E-01	-1.2	1.3E-01	-0.4	6.5E-01
ENSMUST00000182793	autophagy related 7 [Source:MGI Symbol;Acc:MGI:1921494]		Q9D906	-6.8	2.7E-03	6.1	3.0E-04	-0.6	6.1E-01	-0.1	9.3E-01
ENSMUST00000182814	bridging integrator 2 [Source:MGI Symbol;Acc:MGI:3611448]	S4R1B8		5.3	9.5E-03	7.0	1.1E-04	0.0	9.8E-01	-0.2	6.8E-01
ENSMUST00000182825	BAI1-associated protein 3 [Source:MGI Symbol;Acc:MGI:2685783]	S4R1K2		7.5	5.4E-05	8.3	1.8E-05	-0.5	6.7E-01	-1.6	9.1E-03
ENSMUST00000182827	zinc finger protein 229 [Source:MGI Symbol;Acc:MGI:2679295]	S4R233		7.4	2.9E-06	4.4	3.9E-02	-0.5	8.0E-01	-0.8	5.2E-01
ENSMUST00000140592	dolichol-phosphate (beta-D) mannosyltransferase 2 [Source:MGI Symbol;Acc:MGI:1330238]	E0CXW3		-0.6	5.7E-01	0.5	6.9E-01	0.3	7.6E-01	-0.8	5.0E-01
ENSMUST00000182831	neuropeptide Y receptor Y2 [Source:MGI Symbol;Acc:MGI:108418]		P97295	6.1	2.4E-03	4.1	4.1E-02	-3.4	1.2E-01	-0.3	7.8E-01
ENSMUST00000140594	PQ loop repeat containing 1 [Source:MGI Symbol;Acc:MGI:1914193]		Q80XM9	-0.4	4.6E-01	0.7	3.4E-01	0.3	5.3E-01	-0.7	2.5E-01
ENSMUST00000140596	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	A0A0A0MQH5		-1.6	2.1E-01	-1.6	3.0E-01	0.0	9.7E-01	0.1	9.5E-01
ENSMUST00000182851	CUGBP, Elav-like family member 2 [Source:MGI Symbol;Acc:MGI:1338822]		Q9Z0H4	-4.1	1.8E-02	4.1	9.0E-02	-0.8	6.9E-01	-0.1	9.6E-01
ENSMUST00000182858	as association (RalGDS/AF-6) domain family (N-terminal) member 10 [Source:MGI Symbol;Acc:MGI:192599		Q8BL43	7.9	7.1E-05	-4.8	1.5E-02	0.1	8.8E-01	0.0	9.8E-01
ENSMUST00000140607	TBC1 domain family, member 14 [Source:MGI Symbol;Acc:MGI:1098708]	E9Q8K4		-0.4	9.3E-01	7.6	3.1E-01	8.4	1.1E-01	0.4	9.6E-01
ENSMUST00000182861	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	A0A0G2JDD3		-7.7	3.1E-02	5.4	4.7E-05	1.3	8.4E-02	0.1	8.3E-01
ENSMUST00000182884	ankyrin 3, epithelial [Source:MGI Symbol;Acc:MGI:88026]		G5E8K5	8.4	1.1E-05	4.4	1.5E-04	-0.1	8.5E-01	0.5	3.4E-01
ENSMUST00000182902	autophagy related 7 [Source:MGI Symbol;Acc:MGI:1921494]		Q9D906	-5.2	8.0E-03	6.3	6.7E-04	-0.5	6.9E-01	-0.8	2.7E-01
ENSMUST00000140620	iduronidase, alpha-L- [Source:MGI Symbol;Acc:MGI:96418]	D6RIN7		4.4	7.9E-02	4.6	6.3E-02	-3.1	2.2E-01	-3.2	9.4E-02
ENSMUST00000140621	WD repeat domain 83 opposite strand [Source:MGI Symbol;Acc:MGI:3041257]	F7AME8		-2.8	4.0E-02	2.2	2.1E-01	2.7	8.2E-02	-2.2	1.1E-01
ENSMUST00000140622	actinin alpha 4 [Source:MGI Symbol;Acc:MGI:1890773]	D3Z0L8		0.7	8.0E-01	2.4	5.2E-01	1.4	6.0E-01	-0.3	9.2E-01
ENSMUST00000182905	Rho guanine nucleotide exchange factor (GEF) 40 [Source:MGI Symbol;Acc:MGI:2685515]	S4R2U9		7.0	1.7E-04	4.2	9.9E-04	-3.0	1.7E-02	0.4	5.4E-01
ENSMUST00000182908	mast cell immunoglobulin like receptor 1 [Source:MGI Symbol;Acc:MGI:2685731]		Q3TB92	-6.6	2.3E-04	-10.5	2.2E-04	-0.6	2.2E-01	0.1	9.4E-01
ENSMUST00000140634	zinc finger, AN1-type domain 1 [Source:MGI Symbol;Acc:MGI:1913611]	F7CFT1		0.3	8.2E-01	-4.1	4.2E-02	-4.7	2.2E-03	-0.3	9.0E-01
ENSMUST00000140638				-3.0	9.5E-02	0.3	8.4E-01	0.9	5.0E-01	-2.5	1.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000140640				-1.9	8.1E-02	-0.2	8.8E-01	0.6	5.2E-01	-1.1	3.3E-01
ENSMUST00000140641				3.7	6.6E-02	2.8	2.6E-01	-0.9	6.9E-01	0.0	9.9E-01
ENSMUST00000182912	anaphase promoting complex subunit 16 [Source:MGI Symbol;Acc:MGI:1289325]	S4R1V1		-3.5	4.0E-03	5.5	2.2E-02	-1.0	6.0E-01	-1.6	3.0E-01
ENSMUST00000182915	piccolo (presynaptic cytomatrix protein) [Source:MGI Symbol;Acc:MGI:1349390]	S4R2E0		5.4	1.1E-02	6.1	1.9E-05	-0.3	7.0E-01	0.2	7.3E-01
ENSMUST00000140653	DNA segment, Chr 5, ERATO Doi 579, expressed [Source:MGI Symbol;Acc:MGI:1261849]		Q80U59	1.1	5.3E-02	1.5	2.5E-02	-0.5	3.2E-01	-0.9	1.0E-01
ENSMUST00000182947	melatonin receptor 1B [Source:MGI Symbol;Acc:MGI:2181726]	Q3SXF8		6.9	1.9E-04	6.0	1.0E-04	-0.4	6.5E-01	-0.2	6.7E-01
ENSMUST00000182955	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	S4R1M5		-8.0	8.8E-06	-2.9	7.8E-02	-0.1	8.8E-01	-1.0	5.4E-01
ENSMUST00000140670				-2.1	4.7E-02	0.3	7.5E-01	0.4	5.8E-01	-2.0	8.8E-02
ENSMUST00000182958	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Source:MGI Symbol;Ac	S4R1D4		-3.4	3.1E-02	-4.3	3.0E-03	-0.7	2.4E-01	-4.7	1.5E-02
ENSMUST00000182980	transmembrane protein 161A [Source:MGI Symbol;Acc:MGI:2384577]		Q8VCA6	-4.6	1.0E-03	5.2	2.9E-03	-0.4	7.3E-01	0.2	8.6E-01
ENSMUST00000182994	ankyrin 2, brain [Source:MGI Symbol;Acc:MGI:88025]		Q8C8R3	6.8	5.5E-05	-2.9	6.6E-02	1.8	2.6E-02	-0.5	7.3E-01
ENSMUST00000183032	RNA binding motif protein 6 [Source:MGI Symbol;Acc:MGI:1338037]	S4R1W5		-7.8	1.7E-04	4.3	2.7E-02	-0.6	7.5E-01	-1.0	3.8E-01
ENSMUST00000183037	glutathione peroxidase 4 [Source:MGI Symbol;Acc:MGI:104767]	S4R1E5		-7.2	6.5E-05	2.5	6.4E-01	10.1	1.6E-02	-1.5	7.6E-01
ENSMUST00000183044	cyclin D3 [Source:MGI Symbol;Acc:MGI:88315]	Q3TSW4	P30282	-8.2	6.3E-05	6.6	1.8E-04	0.5	6.0E-01	1.2	7.1E-02
ENSMUST00000183048	zinc finger protein 236 [Source:MGI Symbol;Acc:MGI:1926950]	S4R1D8		4.6	3.0E-02	5.2	3.0E-04	-0.1	9.3E-01	-0.9	1.6E-01
ENSMUST00000183059	minichromosome maintenance domain containing 2 [Source:MGI Symbol;Acc:MGI:3045334]	S4R1E1		7.4	3.0E-06	-2.0	2.8E-01	0.9	4.0E-01	-1.6	3.8E-01
ENSMUST00000183070	natural killer tumor recognition sequence [Source:MGI Symbol;Acc:MGI:97346]	Q3TQ51		2.0	5.2E-03	-0.3	8.1E-01	0.7	3.8E-01	-1.6	1.7E-01
ENSMUST00000183104	oxysterol binding protein-like 10 [Source:MGI Symbol;Acc:MGI:1921736]	S4R1M9	S4R1M9	6.1	1.5E-03	6.5	2.6E-03	-0.7	7.1E-01	-1.8	8.8E-02
ENSMUST00000183108	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble [Source:MGI Symbol;Acc:MGI:2180003]	Q3UE92		2.7	2.2E-03	5.8	4.3E-03	1.0	5.5E-01	0.0	9.9E-01
ENSMUST00000140712				1.5	5.8E-02	1.4	1.5E-01	0.0	9.9E-01	0.1	9.4E-01
ENSMUST00000183109	ankyrin repeat and sterile alpha motif domain containing 1B [Source:MGI Symbol;Acc:MGI:1924781]	S4R2J3		6.8	7.6E-05	-3.4	8.9E-02	0.2	8.7E-01	-2.9	2.2E-01
ENSMUST00000183126	ADP-ribosylation factor-like 14 [Source:MGI Symbol;Acc:MGI:1918869]	S4R1T9		2.2	9.8E-03	-2.5	1.3E-01	-0.1	8.6E-01	-0.5	7.4E-01
ENSMUST00000140715				2.5	5.2E-02	2.6	1.0E-01	-0.8	5.8E-01	-0.9	4.0E-01
ENSMUST00000140719	zinc finger protein 956 [Source:MGI Symbol;Acc:MGI:2141515]	D6RE39		0.7	7.4E-01	1.7	5.5E-01	0.5	8.3E-01	-0.5	8.2E-01
ENSMUST00000140725				1.1	2.4E-01	-0.1	9.6E-01	-0.2	8.1E-01	1.0	4.2E-01
ENSMUST00000183143	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1930042]	S4R284		4.3	1.4E-04	3.7	1.8E-01	-0.8	7.7E-01	1.3	4.4E-01
ENSMUST00000140732				1.7	8.4E-02	2.9	5.6E-02	1.1	3.9E-01	-0.2	8.7E-01
ENSMUST00000140733				2.0	4.3E-02	2.2	7.3E-02	0.4	6.7E-01	0.2	8.2E-01
ENSMUST00000140734				-2.0	1.5E-01	-1.2	5.4E-01	1.6	2.5E-01	0.8	6.5E-01
ENSMUST00000183146	ring finger protein 113A2 [Source:MGI Symbol;Acc:MGI:1913631]	Q14B01		-4.0	3.1E-04	6.4	2.2E-04	-0.6	5.9E-01	-0.1	8.8E-01
ENSMUST00000183177	cyclin D3 [Source:MGI Symbol;Acc:MGI:88315]	Q3TSW4	P30282	-4.5	4.4E-03	5.8	4.4E-04	-0.2	8.2E-01	-0.5	3.8E-01
ENSMUST00000183178	coiled-coil domain containing 154 [Source:MGI Symbol;Acc:MGI:2685163]	S4R2I6		7.5	2.5E-05	4.3	1.9E-02	-1.9	2.9E-01	-0.1	9.1E-01
ENSMUST00000183187	transketolase-like 2 [Source:MGI Symbol;Acc:MGI:1921669]			6.8	1.1E-04	-2.6	4.4E-02	0.1	8.5E-01	-1.9	1.9E-01
ENSMUST00000183198	calmodulin 5 [Source:MGI Symbol;Acc:MGI:3511177]	A0A087WNL0		7.2	5.2E-05	5.3	3.9E-03	-0.2	9.0E-01	0.1	9.0E-01
ENSMUST00000183211	bridging integrator 2 [Source:MGI Symbol;Acc:MGI:3611448]	S4R270		-10.6	2.7E-04	8.6	5.9E-03	-1.1	6.9E-01	0.6	6.5E-01
ENSMUST00000183219	H6 homeobox 2 [Source:MGI Symbol;Acc:MGI:107159]		P43687	8.6	2.0E-03	-7.9	1.0E-03	1.5	1.3E-02	0.6	7.6E-01
ENSMUST00000183223	proline-rich coiled-coil 2C [Source:MGI Symbol;Acc:MGI:1913754]	S4R2L9		-5.7	6.3E-04	7.2	4.4E-05	-0.8	4.4E-01	0.2	6.7E-01
ENSMUST00000140769	cellular repressor of E1A-stimulated genes 1 [Source:MGI Symbol;Acc:MGI:1344382]	J3QP41		2.5	2.0E-01	2.1	4.2E-01	0.1	9.7E-01	0.5	8.2E-01
ENSMUST00000183241	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent) [Source:MGI Symbol;Acc:MGI:1098272]	S4R2R4		-7.7	3.9E-05	8.1	2.8E-05	0.0	9.8E-01	-0.3	5.4E-01
ENSMUST00000183249	baculoviral IAP repeat-containing 6 [Source:MGI Symbol;Acc:MGI:1276108]	S4R268		-3.9	3.7E-03	-4.0	7.1E-03	-0.6	2.7E-01	-0.6	6.6E-01
ENSMUST00000140775				1.8	9.1E-02	0.5	7.5E-01	0.2	8.3E-01	1.6	2.1E-01
ENSMUST00000140786	e carrier family 25 (mitochondrial carrier, phosphate carrier), member 24 [Source:MGI Symbol;Acc:MGI:1917	A0A0G2JFB9		2.1	2.6E-01	2.9	1.2E-01	-1.1	5.2E-01	-2.0	2.4E-01
ENSMUST00000140788	ankyrin repeat domain 9 [Source:MGI Symbol;Acc:MGI:1921501]		Q8BH83	4.4	5.1E-02	6.4	3.7E-02	2.5	3.2E-01	0.5	7.9E-01
ENSMUST00000183271	DENN/MADD domain containing 2D [Source:MGI Symbol;Acc:MGI:2181193]	S4R219		-4.8	5.6E-05	8.4	8.3E-04	-0.3	8.9E-01	1.3	1.6E-01
ENSMUST00000183273	myosin XVIIIb [Source:MGI Symbol;Acc:MGI:1921626]	S4R2L2		6.5	1.5E-04	7.0	1.6E-04	-1.5	2.8E-01	-1.5	3.5E-02
ENSMUST00000140796	eukaryotic translation initiation factor 4 gamma, 3 [Source:MGI Symbol;Acc:MGI:1923935]	A2AMI7		-1.1	5.5E-01	3.3	1.3E-01	2.3	2.5E-01	-2.1	2.4E-01
ENSMUST00000140800	tripartite motif-containing 41 [Source:MGI Symbol;Acc:MGI:2384814]	Q5NCC2		0.6	7.5E-01	2.0	4.6E-01	1.1	5.4E-01	-0.3	9.2E-01
ENSMUST00000183274	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble [Source:MGI Symbol;Acc:MGI:2180003]	S4R1I3		-2.5	3.2E-02	7.2	3.3E-04	0.2	8.9E-01	0.3	6.4E-01
ENSMUST00000183301	protein tyrosine phosphatase, receptor type, C [Source:MGI Symbol;Acc:MGI:97810]	S4R1S4		-7.8	6.4E-05	3.2	5.0E-04	-0.7	2.3E-01	-0.4	4.4E-01
ENSMUST00000140820	cilia and flagella associated protein 46 [Source:MGI Symbol;Acc:MGI:2444387]	G3UVW5		3.7	1.5E-01	5.4	5.4E-02	-0.5	8.4E-01	-2.3	2.1E-01
ENSMUST00000140829	zinc finger protein 563 [Source:MGI Symbol;Acc:MGI:2677168]	B8JK01		2.0	2.7E-01	1.5	4.9E-01	-0.7	7.1E-01	-0.2	9.1E-01
ENSMUST00000140830	syndecan binding protein [Source:MGI Symbol;Acc:MGI:1337026]	A2AKJ5		-0.4	6.3E-01	-2.5	5.1E-02	-1.3	8.6E-02	0.8	4.9E-01
ENSMUST00000140832				-0.8	4.2E-01	0.5	6.6E-01	0.7	4.7E-01	-0.6	5.7E-01
ENSMUST00000140835				2.3	1.5E-01	3.7	1.3E-01	2.6	2.1E-01	1.2	4.6E-01
ENSMUST00000183302	dystonin [Source:MGI Symbol;Acc:MGI:104627]			7.8	5.4E-05	7.9	6.7E-05	1.0	4.0E-01	0.0	9.5E-01
ENSMUST00000183309	ribosome production factor 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914489]		Q9JJ80	-2.9	1.7E-02	1.4	1.7E-01	-0.6	4.3E-01	0.3	7.5E-01
ENSMUST00000140842	XIAP associated factor 1 [Source:MGI Symbol;Acc:MGI:3772572]		Q5NBU8	0.7	5.0E-01	0.1	9.6E-01	-1.7	7.0E-02	-1.1	2.9E-01
ENSMUST00000183324	zinc finger protein 236 [Source:MGI Symbol;Acc:MGI:1926950]	S4R1Z3		-4.1	8.4E-04	-0.3	7.5E-01	-1.5	9.9E-02	3.3	6.7E-03
ENSMUST00000183367				6.4	1.2E-02	10.4	1.1E-05	-0.8	5.7E-01	-0.1	7.6E-01
ENSMUST00000183368	collagen, type XXV, alpha 1 [Source:MGI Symbol;Acc:MGI:1924268]	V9GWX5		6.8	6.9E-05	3.8	8.2E-03	-1.7	2.0E-01	0.6	4.9E-01
ENSMUST00000183390	coiled-coil domain containing 182 [Source:MGI Symbol;Acc:MGI:1921547]		Q9D9C6	6.2	3.6E-04	5.9	3.4E-04	-0.6	6.3E-01	0.3	6.8E-01
ENSMUST00000140857				0.3	7.1E-01	1.1	2.5E-01	-0.6	4.2E-01	-1.4	1.2E-01
ENSMUST00000183402	seizure threshold 2 [Source:MGI Symbol;Acc:MGI:3033336]	V9GXW1		-4.0	4.4E-03	6.1	2.1E-04	-0.3	8.0E-01	0.5	4.4E-01
ENSMUST00000140861				1.3	5.8E-01	-4.9	1.1E-01	-5.2	1.6E-02	1.0	7.4E-01
ENSMUST00000183404	transcription factor 12 [Source:MGI Symbol;Acc:MGI:101877]		Q61286	4.2	1.3E-04	-4.6	1.3E-03	-0.9	8.2E-02	-0.9	4.2E-01
ENSMUST00000140871	GATA zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1914460]	F7CAN4		-0.6	2.9E-01	0.4	6.2E-01	0.5	3.5E-01	-0.5	5.0E-01
ENSMUST00000183409	GTPase, very large interferon inducible 1 [Source:MGI Symbol;Acc:MGI:1921808]	L7N451		6.8	2.9E-02	7.1	1.0E-04	1.1	3.1E-01	0.3	5.9E-01
ENSMUST00000183416	RIKEN cDNA 1190007I07 gene [Source:MGI Symbol;Acc:MGI:3698433]	V9GX89		5.7	2.2E-02	6.4	4.0E-04	-0.6	6.5E-01	-0.8	2.7E-01
ENSMUST00000140879				2.5	5.7E-02	0.8	5.5E-01	-1.0	4.2E-01	0.7	5.7E-01
ENSMUST00000140883				-0.6	4.8E-01	0.5	6.5E-01	0.1	9.2E-01	-1.1	3.3E-01
ENSMUST00000183421	trichorhinophalangeal syndrome I (human) [Source:MGI Symbol;Acc:MGI:1927616]	Q8BZ62		6.3	3.7E-04	5.9	1.0E-03	-0.6	6.7E-01	-0.1	9.0E-01
ENSMUST00000183425	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 [Source:MGI Symbol;Acc:MGI:2446108]	V9GXD2		5.3	3.1E-03	-2.3	8.4E-02	0.5	5.1E-01	-1.4	3.1E-01
ENSMUST00000183432	ly 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 [Source:MGI Symbol;A	V9GX08		6.5	1.4E-05	-1.9	3.1E-01	1.7	1.5E-01	-0.8	6.9E-01
ENSMUST00000140901	fizzy/cell division cycle 20 related 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1926790]	Q3U3D4	Q9R1K5	-1.4	9.7E-02	0.6	5.4E-01	1.3	1.1E-01	-0.8	4.4E-01
ENSMUST00000183456	synergin, gamma [Source:MGI Symbol;Acc:MGI:1354742]	V9GX40		-4.7	5.0E-04	5.2	3.2E-02	0.3	8.7E-01	-0.4	7.8E-01
ENSMUST00000183463	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]	Q80UM8		-5.0	3.2E-03	-4.4	1.3E-02	0.4	5.2E-01	0.0	9.9E-01
ENSMUST00000183468	zinc finger protein 280D [Source:MGI Symbol;Acc:MGI:2384583]	Q8R2V6		3.1	2.6E-02	5.7	6.6E-04	-1.1	3.5E-01	0.9	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000140917				-2.7	6.3E-02	-1.0	6.3E-01	1.6	2.3E-01	-0.1	9.7E-01
ENSMUST00000183471	kelch repeat and BTB (POZ) domain containing 11 [Source:MGI Symbol;Acc:MGI:1922151]		Q8BNW9	4.4	1.5E-04	3.7	7.2E-03	-1.8	1.2E-01	-0.1	9.0E-01
ENSMUST00000183482	5-hydroxytryptamine (serotonin) receptor 1B [Source:MGI Symbol;Acc:MGI:96274]	Q0VES5	P28334	5.9	6.2E-05	3.5	6.0E-04	-0.2	7.6E-01	-0.1	7.9E-01
ENSMUST00000183520	surfeit gene 1 [Source:MGI Symbol;Acc:MGI:98443]	V9GXE6		-5.8	1.1E-04	7.2	2.2E-04	-1.1	3.9E-01	0.3	5.7E-01
ENSMUST00000183528	RAN binding protein 1 [Source:MGI Symbol;Acc:MGI:96269]		P34022	-4.0	8.8E-03	4.6	5.6E-04	-3.1	1.2E-02	0.3	6.1E-01
ENSMUST00000140931				3.0	2.2E-01	-0.7	8.2E-01	-3.0	2.3E-01	0.6	8.1E-01
ENSMUST00000140932	microsomal glutathione S-transferase 1 [Source:MGI Symbol;Acc:MGI:1913850]			-5.9	1.5E-01	1.9	7.4E-01	6.8	1.2E-01	-1.0	8.4E-01
ENSMUST00000183583	netrin G2 [Source:MGI Symbol;Acc:MGI:2159341]	V9GX85		-3.4	7.5E-03	3.2	8.2E-03	0.0	9.8E-01	0.2	7.3E-01
ENSMUST00000183626	catechol-O-methyltransferase [Source:MGI Symbol;Acc:MGI:88470]		O88587	1.9	1.4E-02	0.5	8.1E-01	-0.7	6.3E-01	2.3	2.3E-01
ENSMUST00000183630				-4.9	1.5E-04	3.8	2.3E-02	-1.0	4.4E-01	-0.1	8.9E-01
ENSMUST00000183662	matrix metallopeptidase 16 [Source:MGI Symbol;Acc:MGI:1276107]	V9GXD8		7.6	2.9E-05	-3.1	4.4E-02	-0.7	3.7E-01	-1.0	5.0E-01
ENSMUST00000140947				5.0	9.8E-02	6.5	5.9E-02	-0.2	9.5E-01	-1.7	3.5E-01
ENSMUST00000140955				-2.8	4.9E-02	0.9	4.6E-01	0.9	3.4E-01	-2.8	5.9E-02
ENSMUST00000183684	inositol polyphosphate 5-phosphatase J [Source:MGI Symbol;Acc:MGI:2158663]	V9GX61		4.4	6.8E-04	6.5	4.4E-03	-0.1	9.7E-01	0.8	3.9E-01
ENSMUST00000183690	spermatid perinuclear RNA binding protein [Source:MGI Symbol;Acc:MGI:104626]		Q91WM1	6.4	1.4E-03	1.2	2.9E-01	2.1	3.3E-02	-4.5	5.7E-03
ENSMUST00000140963				-0.7	5.0E-01	-4.3	1.3E-01	1.3	3.3E-01	4.8	6.6E-02
ENSMUST00000183712	beta galactoside alpha 2,6 sialyltransferase 2 [Source:MGI Symbol;Acc:MGI:2445190]		Q76K27	7.5	4.8E-05	4.4	2.0E-03	-0.2	8.0E-01	-0.4	5.6E-01
ENSMUST00000140973				-1.8	5.3E-01	-2.1	5.5E-01	-0.8	7.1E-01	-0.5	8.9E-01
ENSMUST00000183731	ARP5 actin-related protein 5 [Source:MGI Symbol;Acc:MGI:1924748]	V9GXE4		6.4	1.3E-03	-4.3	1.2E-02	1.1	1.5E-01	-3.3	9.6E-02
ENSMUST00000140975	centromere protein O [Source:MGI Symbol;Acc:MGI:1923800]		Q8K015	1.0	1.4E-01	0.9	2.4E-01	-0.3	6.1E-01	-0.3	7.1E-01
ENSMUST00000183734	leucine rich repeat containing 1 [Source:MGI Symbol;Acc:MGI:2442313]		Q80VQ1	5.0	6.3E-03	-5.0	1.6E-02	1.2	9.5E-02	0.2	9.2E-01
ENSMUST00000183742	mitochondrial ribosomal protein S23 [Source:MGI Symbol;Acc:MGI:1928138]		Q8VE22	-5.0	4.3E-04	4.0	5.9E-03	-0.6	6.3E-01	1.9	2.2E-02
ENSMUST00000140982	NIPA-like domain containing 3 [Source:MGI Symbol;Acc:MGI:1921802]	F6V4P1		0.3	8.8E-01	-0.8	8.1E-01	-1.0	6.0E-01	0.1	9.9E-01
ENSMUST00000140983	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 [Source:MGI Symbc	Z4YLN2		3.4	9.6E-02	1.6	5.2E-01	-0.4	8.4E-01	1.4	4.8E-01
ENSMUST00000183773	DPH2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914978]	V9GX25		-3.8	4.4E-03	3.6	1.0E-02	0.3	7.6E-01	-0.3	6.7E-01
ENSMUST00000140991	SAP30 binding protein [Source:MGI Symbol;Acc:MGI:1927479]		Q02614	-0.4	2.5E-01	-0.4	4.4E-01	0.2	5.5E-01	0.2	7.5E-01
ENSMUST00000183775	phosphodiesterase 1A, calmodulin-dependent [Source:MGI Symbol;Acc:MGI:1201792]	Q8BRR9		6.6	4.8E-03	6.2	3.3E-04	0.1	9.5E-01	-0.1	8.2E-01
ENSMUST00000140996	BRCA1 associated protein [Source:MGI Symbol;Acc:MGI:1919649]	D6RG84		-1.2	6.6E-01	-1.3	6.0E-01	-2.7	1.6E-01	-2.5	3.7E-01
ENSMUST00000183836	sterile alpha motif domain containing 10 [Source:MGI Symbol;Acc:MGI:2443872]	V9GXE8		-5.8	1.7E-03	-0.9	5.8E-01	1.2	3.2E-01	-1.7	3.2E-01
ENSMUST00000183840	predicted gene, 16867 [Source:MGI Symbol;Acc:MGI:4439791]		Q920G8	5.8	5.5E-04	8.0	1.1E-05	0.1	8.8E-01	0.6	1.9E-01
ENSMUST00000183845	NLR family, pyrin domain containing 6 [Source:MGI Symbol;Acc:MGI:2141990]		Q91WS2	9.2	5.6E-05	2.7	6.2E-02	-1.1	3.7E-01	-0.4	7.0E-01
ENSMUST00000141012				-0.5	5.4E-01	1.7	1.2E-01	1.8	3.8E-02	-0.4	6.7E-01
ENSMUST00000183856	testis expressed gene 9 [Source:MGI Symbol;Acc:MGI:1201610]	V9GXN9		7.3	3.8E-05	-7.9	9.4E-04	-0.7	1.7E-01	1.4	4.1E-01
ENSMUST00000141020	caspase recruitment domain family, member 6 [Source:MGI Symbol;Acc:MGI:3032959]	D3YYK3		-1.3	1.8E-01	1.0	4.0E-01	1.5	1.4E-01	-0.8	4.4E-01
ENSMUST00000183869	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:MGI Symbol;Acc:MGI:2181202]	A7UAK4		-3.5	1.3E-02	4.4	1.1E-02	-1.1	4.2E-01	-0.4	6.7E-01
ENSMUST00000183886	interleukin 6 signal transducer [Source:MGI Symbol;Acc:MGI:96560]	Q3TDT5		7.4	8.8E-06	5.4	1.4E-05	-0.4	5.2E-01	-0.3	5.1E-01
ENSMUST00000183914	suppression of tumorigenicity 7-like [Source:MGI Symbol;Acc:MGI:2386964]	V9GXQ4		2.2	1.8E-03	-1.8	4.7E-01	3.0	4.4E-02	0.4	8.5E-01
ENSMUST00000183918	transcription factor 12 [Source:MGI Symbol;Acc:MGI:101877]	V9GX46		6.8	1.2E-04	-4.0	3.5E-03	1.9	2.2E-03	-1.0	4.0E-01
ENSMUST00000141046	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143057]	D3YZ87		3.9	4.0E-02	4.8	2.7E-02	-0.4	8.2E-01	-1.3	2.8E-01
ENSMUST00000183937	predicted gene 4707 [Source:MGI Symbol;Acc:MGI:3782887]	V9GXN5		6.6	1.0E-04	-1.4	2.2E-01	0.8	3.0E-01	-2.2	9.8E-02
ENSMUST00000183940	poly(A) binding protein, cytoplasmic 4 [Source:MGI Symbol;Acc:MGI:2385206]	V9GXG3		7.0	3.7E-04	7.1	1.7E-05	-0.7	4.2E-01	1.0	5.3E-02
ENSMUST00000183946	SWI5 recombination repair homolog (yeast) [Source:MGI Symbol;Acc:MGI:1920181]	E3WH32	Q8K3D3	-8.1	4.3E-05	1.1	2.3E-01	-0.9	2.3E-01	0.5	5.4E-01
ENSMUST00000183952	transmembrane protein 185B [Source:MGI Symbol;Acc:MGI:1917634]		Q8R3R5	-2.5	2.3E-03	3.3	7.1E-03	0.1	9.4E-01	0.1	8.9E-01
ENSMUST00000141052	forkhead box N2 [Source:MGI Symbol;Acc:MGI:1347478]	E9PYQ6		4.7	4.6E-02	4.2	1.0E-01	-1.2	6.1E-01	-0.6	7.3E-01
ENSMUST00000183955	muscular LMNA-interacting protein [Source:MGI Symbol;Acc:MGI:1916892]	V9GWW6		6.2	1.6E-04	4.1	3.9E-03	0.7	5.0E-01	0.1	8.7E-01
ENSMUST00000141055				1.8	1.8E-01	4.9	1.8E-02	1.2	4.8E-01	-1.9	1.4E-01
ENSMUST00000183959				-2.6	1.1E-03	6.6	3.5E-05	-0.9	3.4E-01	-0.4	4.9E-01
ENSMUST00000183969	TRM2 tRNA methyltransferase 2A [Source:MGI Symbol;Acc:MGI:96270]			-2.9	3.1E-02	6.9	3.3E-05	-0.4	7.1E-01	-0.3	6.0E-01
ENSMUST00000183997	trichorhinophalangeal syndrome I (human) [Source:MGI Symbol;Acc:MGI:1927616]	V9GXE9		-3.2	1.0E-02	3.3	6.9E-03	-0.7	4.5E-01	-0.3	6.5E-01
ENSMUST00000184063	CUB and Sushi multiple domains 2 [Source:MGI Symbol;Acc:MGI:2386401]	V9GX34		8.8	1.9E-06	-2.1	9.2E-02	1.7	3.3E-02	-0.6	5.8E-01
ENSMUST00000184067	collagen, type XXVII, alpha 1 [Source:MGI Symbol;Acc:MGI:2672118]	V9GXJ0		7.1	1.5E-04	6.3	2.5E-04	-0.5	6.8E-01	-0.4	5.0E-01
ENSMUST00000184105	pantothenate kinase 2 [Source:MGI Symbol;Acc:MGI:1921700]	V9GX56		-4.1	1.8E-03	5.7	3.3E-03	2.5	9.0E-02	-0.2	8.1E-01
ENSMUST00000141072				1.6	9.8E-02	1.4	3.5E-01	1.3	3.0E-01	1.5	2.1E-01
ENSMUST00000184112	tripartite motif-containing 14 [Source:MGI Symbol;Acc:MGI:1921985]		Q8BVW3	5.6	4.0E-04	3.6	1.0E-03	0.6	4.1E-01	-0.2	7.2E-01
ENSMUST00000141079				-2.5	1.2E-01	-1.3	4.8E-01	0.0	9.7E-01	-1.2	5.3E-01
ENSMUST00000184113	ect2 oncogene [Source:MGI Symbol;Acc:MGI:95281]	V9GXV8		6.9	1.0E-04	6.6	4.4E-04	-0.7	6.1E-01	0.1	9.3E-01
ENSMUST00000141092				0.8	3.4E-01	0.3	8.0E-01	-0.2	8.2E-01	0.4	7.0E-01
ENSMUST00000184117				2.3	4.0E-03	6.5	3.0E-04	0.1	9.5E-01	-0.5	4.3E-01
ENSMUST00000184124	neuron navigator 2 [Source:MGI Symbol;Acc:MGI:2183691]	V9GXT5		8.5	2.0E-05	4.8	1.9E-03	-1.2	3.0E-01	0.7	3.6E-01
ENSMUST00000141108	mindbomb homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2679684]	A2A9P8		0.2	8.9E-01	-1.1	6.3E-01	0.8	6.0E-01	2.1	3.1E-01
ENSMUST00000184132				5.7	1.6E-03	2.8	4.4E-02	-4.4	1.0E-02	-2.1	6.0E-02
ENSMUST00000184137	kinesin family member 7 [Source:MGI Symbol;Acc:MGI:1098239]	E9QMU1		6.2	1.8E-02	3.8	5.6E-05	0.3	5.6E-01	-0.2	5.7E-01
ENSMUST00000184142	placenta specific 9b [Source:MGI Symbol;Acc:MGI:3711222]		Q8K262	5.7	4.0E-03	3.9	2.2E-04	0.1	8.4E-01	-0.9	8.1E-02
ENSMUST00000141116	0 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:134		Q8K0H5	-0.8	3.5E-01	0.1	9.2E-01	1.0	2.5E-01	0.1	9.6E-01
ENSMUST00000141118	aminolevulinic acid synthase 1 [Source:MGI Symbol;Acc:MGI:87989]	Q3V0B2	Q8VC19	0.1	9.3E-01	0.9	3.1E-01	0.2	8.0E-01	-0.7	4.0E-01
ENSMUST00000184146	RAB27A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:1861441]	Q544U7	Q9ERI2	-5.5	2.2E-04	5.5	5.7E-03	0.3	8.4E-01	-0.5	6.3E-01
ENSMUST00000141126	Tia1 cytotoxic granule-associated RNA binding protein-like 1 [Source:MGI Symbol;Acc:MGI:107913]			1.4	3.3E-01	-2.3	1.5E-01	-4.0	7.6E-03	-0.3	8.2E-01
ENSMUST00000141128				2.9	3.1E-01	5.3	1.8E-01	1.2	7.4E-01	-1.3	6.2E-01
ENSMUST00000184152	copine I [Source:MGI Symbol;Acc:MGI:2386621]	V9GX86		7.6	1.1E-03	5.1	2.8E-03	0.5	6.6E-01	0.3	7.6E-01
ENSMUST00000184159	cyclin D binding myb-like transcription factor 1 [Source:MGI Symbol;Acc:MGI:1344415]		Q8CE22	-6.0	3.4E-02	4.2	1.1E-01	-1.0	6.8E-01	1.2	4.5E-01
ENSMUST00000184169	solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Source:MGI Symbol;Acc:MGI:1926080]	V9GXX9		-8.3	4.2E-06	-3.6	1.3E-02	0.9	1.5E-01	0.0	1.0E+00
ENSMUST00000184205	MYST/Esa1-associated factor 6 [Source:MGI Symbol;Acc:MGI:1917338]	V9GX42		-2.2	2.9E-02	5.9	4.9E-03	-1.4	4.5E-01	-0.1	9.5E-01
ENSMUST00000184245	molybdenum cofactor synthesis 2 [Source:MGI Symbol;Acc:MGI:1336894]	F6ZGI7		7.5	1.3E-05	3.6	2.2E-03	-0.7	3.8E-01	-0.5	4.4E-01
ENSMUST00000184261	tyrosine kinase with immunoglobulin-like and EGF-like domains 1 [Source:MGI Symbol;Acc:MGI:99906]	Q6PAP2		7.7	1.6E-05	4.1	2.5E-03	-0.4	6.4E-01	-0.2	8.1E-01
ENSMUST00000184292		Q8CCV7		3.6	1.1E-02	5.8	3.4E-03	0.0	9.9E-01	-0.6	5.1E-01
ENSMUST00000184297	heterogeneous nuclear ribonucleoprotein L-like [Source:MGI Symbol;Acc:MGI:1919942]	V9GXB6		-6.8	4.3E-04	3.8	2.4E-04	-1.0	1.4E-01	0.3	5.4E-01
ENSMUST00000184298				-2.6	1.4E-02	8.9	2.3E-04	-0.6	7.3E-01	0.1	9.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000141161				2.3	5.1E-02	2.3	8.8E-02	0.1	9.6E-01	0.1	9.5E-01
ENSMUST00000184314	ectonucleoside triphosphate diphosphohydrolase 4 [Source:MGI Symbol;Acc:MGI:1914714]	Q80WR8		7.2	6.2E-05	2.4	9.2E-03	0.7	3.1E-01	-0.1	8.5E-01
ENSMUST00000184322	muscular LMNA-interacting protein [Source:MGI Symbol;Acc:MGI:1916892]	V9GXA0		5.3	1.2E-02	0.5	7.6E-01	2.8	5.9E-02	-2.1	2.3E-01
ENSMUST00000184333	neural precursor cell expressed, developmentally down-regulated 4 [Source:MGI Symbol;Acc:MGI:97297]	V9GXK3		4.5	4.1E-04	2.8	1.9E-01	-4.0	9.7E-02	-0.7	6.4E-01
ENSMUST00000141175				-0.4	7.3E-01	-2.1	2.7E-01	0.5	6.7E-01	2.1	2.3E-01
ENSMUST00000184348	tubulin tyrosine ligase-like family, member 10 [Source:MGI Symbol;Acc:MGI:1921855]	V9GXT8		6.7	4.2E-03	7.9	1.2E-02	-0.8	7.8E-01	-2.4	1.4E-01
ENSMUST00000184356	oocyte specific homeobox 8 [Source:MGI Symbol;Acc:MGI:3645855]	V9GWY9		6.8	6.9E-05	7.8	4.1E-06	0.2	8.4E-01	-0.5	2.3E-01
ENSMUST00000184423	retrotransposon-like 1 [Source:EntrezGene;Acc:353326]	B4YB44	Q7M732	5.7	6.8E-06	8.2	3.4E-05	-1.3	3.0E-01	0.2	7.7E-01
ENSMUST00000184450	neural precursor cell expressed, developmentally down-regulated 4 [Source:MGI Symbol;Acc:MGI:97297]	Q3V335		5.7	2.2E-03	-5.8	2.7E-03	-0.5	5.0E-01	0.1	9.6E-01
ENSMUST00000184487	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI	V9GXF5		-4.3	1.3E-03	7.8	5.0E-04	-1.6	3.3E-01	0.6	4.3E-01
ENSMUST00000184517	zinc finger protein 280D [Source:MGI Symbol;Acc:MGI:2384583]		Q68FE8	4.8	1.9E-02	8.2	1.1E-02	-1.8	5.7E-01	-0.9	5.9E-01
ENSMUST00000184550	uclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 [Source:MGI Symbol;Acc:MGI:9731	V9GX90		-5.2	5.2E-03	-4.2	7.3E-03	-0.3	6.4E-01	-1.0	4.5E-01
ENSMUST00000184560	NLR family, pyrin domain containing 6 [Source:MGI Symbol;Acc:MGI:2141990]	F8UKQ6		5.6	1.1E-04	3.5	5.4E-03	-0.6	5.1E-01	0.9	2.3E-01
ENSMUST00000184581	C-type lectin domain family 7, member a [Source:MGI Symbol;Acc:MGI:1861431]	V9GXI5		-7.3	2.1E-04	4.9	1.2E-03	-1.2	2.8E-01	0.8	2.9E-01
ENSMUST00000184588	tumor protein D52-like 2 [Source:MGI Symbol;Acc:MGI:1913564]	V9GXN2		-5.2	7.2E-04	-0.4	5.8E-01	-1.4	4.1E-02	0.7	3.3E-01
ENSMUST00000184590	synaptopodin 2 [Source:MGI Symbol;Acc:MGI:2153070]	A0A0G2JDM5		5.0	2.9E-02	2.0	8.0E-03	-1.7	1.4E-02	-0.5	3.3E-01
ENSMUST00000184616	activating transcription factor 7 [Source:MGI Symbol;Acc:MGI:2443472]	Q3TZR9		1.7	1.5E-02	-5.1	3.9E-03	-0.6	2.7E-01	-0.6	6.8E-01
ENSMUST00000184647	complement component 1, r subcomponent B [Source:MGI Symbol;Acc:MGI:3779804]		Q8CFG9	5.2	2.1E-03	4.8	1.9E-03	-0.9	4.4E-01	0.0	9.9E-01
ENSMUST00000141230				0.7	4.5E-01	2.0	1.7E-01	0.9	4.6E-01	-0.3	7.6E-01
ENSMUST00000184664	kelch repeat and BTB (POZ) domain containing 12 [Source:MGI Symbol;Acc:MGI:1918481]	V9GXB1		6.7	5.4E-05	1.8	4.1E-02	0.1	8.7E-01	0.2	7.4E-01
ENSMUST00000184666	unc-13 homolog C (C. elegans) [Source:MGI Symbol;Acc:MGI:2149021]		Q8K0T7	8.3	1.7E-05	4.5	4.4E-04	1.6	6.2E-02	0.2	7.6E-01
ENSMUST00000141234				-2.4	9.6E-02	-1.3	4.3E-01	0.3	7.6E-01	-0.7	6.6E-01
ENSMUST00000184744	potassium channel tetramerisation domain containing 12 [Source:MGI Symbol;Acc:MGI:2145823]			-4.7	6.1E-05	5.6	2.3E-06	-0.1	9.1E-01	-0.1	8.2E-01
ENSMUST00000141236				3.7	6.0E-02	-2.6	1.2E-01	-6.5	2.4E-03	-0.3	8.6E-01
ENSMUST00000141237				-0.1	9.2E-01	0.8	4.1E-01	0.5	5.5E-01	-0.5	6.1E-01
ENSMUST00000184757	hypocretin (orexin) receptor 2 [Source:MGI Symbol;Acc:MGI:2680765]		P58308	6.1	5.4E-03	3.5	1.1E-01	0.4	8.3E-01	0.9	5.3E-01
ENSMUST00000184775				6.1	1.0E-06	8.1	8.3E-05	-0.6	6.5E-01	-1.1	1.1E-01
ENSMUST00000141251				1.7	9.3E-02	0.4	7.3E-01	-0.7	4.4E-01	0.6	5.8E-01
ENSMUST00000184816	predicted gene, 16867 [Source:MGI Symbol;Acc:MGI:4439791]		Q920G8	6.8	1.1E-04	7.1	6.5E-04	-0.2	8.8E-01	-1.1	1.9E-01
ENSMUST00000184849	tumor protein D52-like 2 [Source:MGI Symbol;Acc:MGI:1913564]	V9GWU5		-4.2	2.7E-03	6.8	2.5E-04	-0.1	9.1E-01	-2.2	1.2E-02
ENSMUST00000184858	maestro heat-like repeat family member 6 [Source:MGI Symbol;Acc:MGI:5011755]	V9GX81		3.6	2.7E-04	-0.9	3.5E-01	0.8	1.7E-01	-0.5	6.0E-01
ENSMUST00000184862	mitochondrial ribosome associated GTPase 2 [Source:MGI Symbol;Acc:MGI:106565]	I6L986		-4.0	1.3E-03	2.4	4.4E-02	-0.4	6.8E-01	0.5	5.3E-01
ENSMUST00000184863	dexamethasone-induced transcript [Source:MGI Symbol;Acc:MGI:1926236]		Q9WUQ7	6.7	4.0E-04	-5.3	3.0E-04	0.1	8.8E-01	-0.8	4.5E-01
ENSMUST00000184876	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI	V9GXH9		-4.2	1.3E-03	6.4	1.6E-04	-0.5	6.3E-01	-1.1	8.8E-02
ENSMUST00000184877	SNAP-associated protein [Source:MGI Symbol;Acc:MGI:1333745]	V9GXT7		-5.8	2.6E-04	-5.2	1.1E-03	-1.8	8.3E-03	0.0	9.7E-01
ENSMUST00000184882	CREB regulated transcription coactivator 2 [Source:MGI Symbol;Acc:MGI:1921593]	V9GXK6		-2.6	5.0E-03	4.4	3.3E-04	0.3	6.6E-01	-0.2	7.7E-01
ENSMUST00000184895	TRM2 tRNA methyltransferase 2A [Source:MGI Symbol;Acc:MGI:96270]			-2.6	3.3E-02	-5.8	8.2E-03	-0.2	7.5E-01	1.3	4.7E-01
ENSMUST00000141283	5,10-methylenetetrahydrofolate reductase [Source:MGI Symbol;Acc:MGI:106639]	A2A7F9		1.4	2.7E-01	3.8	4.2E-02	0.8	5.8E-01	-1.5	2.1E-01
ENSMUST00000141285				-0.7	5.0E-01	0.0	9.9E-01	0.6	5.3E-01	-0.1	9.6E-01
ENSMUST00000184931	exostoses (multiple) 2 [Source:MGI Symbol;Acc:MGI:108050]	V9GX32		6.9	4.2E-04	7.7	5.1E-04	-0.7	6.6E-01	0.1	8.7E-01
ENSMUST00000184932	pantothenate kinase 2 [Source:MGI Symbol;Acc:MGI:1921700]	V9GXP9		-2.1	2.1E-02	6.4	1.2E-04	-1.9	1.1E-01	0.8	1.7E-01
ENSMUST00000185001	PNN interacting serine/arginine-rich [Source:MGI Symbol;Acc:MGI:1913875]	A2AJT3		-3.1	1.5E-02	2.5	4.1E-01	-0.3	9.0E-01	2.6	2.8E-01
ENSMUST00000185052	myocyte enhancer factor 2C [Source:MGI Symbol;Acc:MGI:99458]		Q8CFN5	3.2	7.7E-03	3.6	4.7E-03	-2.8	3.6E-02	-0.5	5.5E-01
ENSMUST00000185058	RAN binding protein 1 [Source:MGI Symbol;Acc:MGI:96269]			-2.3	8.9E-03	3.1	1.0E-02	-0.5	5.5E-01	0.2	7.7E-01
ENSMUST00000141305	intraflagellar transport 122 [Source:MGI Symbol;Acc:MGI:1932386]	S4R282		4.7	4.0E-02	5.6	2.4E-02	-1.2	5.9E-01	-2.1	1.7E-01
ENSMUST00000185081				8.2	7.9E-04	4.0	9.1E-03	-3.2	4.7E-02	-1.0	2.6E-01
ENSMUST00000185102	stimulated by retinoic acid gene 8 [Source:MGI Symbol;Acc:MGI:107917]	V9GXG4		4.2	6.2E-03	-4.8	1.0E-01	1.0	3.8E-01	-1.1	7.2E-01
ENSMUST00000185113	vacuolar protein sorting 13 D (yeast) [Source:MGI Symbol;Acc:MGI:2448530]	V9GX23		-6.2	1.9E-05	-3.2	4.9E-02	1.9	2.6E-02	-0.9	5.7E-01
ENSMUST00000185121	thiamine triphosphatase [Source:MGI Symbol;Acc:MGI:2446078]	A0A087WPV5		7.1	3.0E-05	5.4	7.4E-03	1.4	3.7E-01	-0.7	4.5E-01
ENSMUST00000185164	regulator of G-protein signaling like 1 [Source:MGI Symbol;Acc:MGI:2685048]	V9GXV7		7.0	7.8E-05	6.0	1.2E-03	-1.1	4.5E-01	-0.1	8.9E-01
ENSMUST00000141337				-3.7	6.6E-02	-1.6	5.5E-01	1.8	2.9E-01	-0.2	9.3E-01
ENSMUST00000185175	Kruppel-like factor 13 [Source:MGI Symbol;Acc:MGI:1354948]	A0A087WQX4		-2.9	1.0E-02	5.8	2.6E-04	0.2	8.3E-01	0.1	8.1E-01
ENSMUST00000185176	leucine zipper, putative tumor suppressor 1 [Source:MGI Symbol;Acc:MGI:2684762]		P60853	5.2	6.0E-05	4.8	6.8E-03	-0.1	9.7E-01	-1.2	1.6E-01
ENSMUST00000141357				-1.6	1.4E-01	-1.1	4.7E-01	1.0	3.3E-01	0.5	7.1E-01
ENSMUST00000185178	predicted gene 17190 [Source:MGI Symbol;Acc:MGI:4938017]	V9GX38		7.4	1.3E-04	-2.2	1.7E-01	0.7	4.0E-01	0.0	9.8E-01
ENSMUST00000185184	transcription factor 24 [Source:MGI Symbol;Acc:MGI:3780500]	V9GWT9		2.1	1.4E-02	4.0	6.6E-03	-0.9	4.3E-01	-0.6	4.7E-01
ENSMUST00000185187	tachykinin 1 [Source:MGI Symbol;Acc:MGI:98474]	Q149W7	P41539	5.9	2.6E-04	4.5	2.5E-04	0.1	8.5E-01	-0.5	4.0E-01
ENSMUST00000141369				0.7	4.9E-01	1.0	4.3E-01	0.0	1.0E+00	-0.3	8.0E-01
ENSMUST00000141372				-4.6	8.8E-02	-4.5	9.0E-02	-1.8	2.0E-01	-1.9	5.2E-01
ENSMUST00000185188	vav 2 oncogene [Source:MGI Symbol;Acc:MGI:102718]	Q7TSI6		8.7	1.9E-04	6.5	1.1E-04	0.8	4.1E-01	-0.1	8.5E-01
ENSMUST00000141382	artilage intermediate layer protein, nucleotide pyrophosphohydrolase [Source:MGI Symbol;Acc:MGI:2444507	D6RD06		4.6	1.2E-01	7.4	2.3E-02	-1.3	6.9E-01	-4.0	3.1E-02
ENSMUST00000141384				1.8	9.4E-02	4.6	1.9E-02	2.1	1.9E-01	-0.7	4.6E-01
ENSMUST00000185269	dystonin [Source:MGI Symbol;Acc:MGI:104627]	A0A087WSP0		6.8	1.3E-03	5.7	7.5E-04	-0.6	6.3E-01	0.0	9.4E-01
ENSMUST00000185315	high mobility group nucleosomal binding domain 3 [Source:MGI Symbol;Acc:MGI:2138069]		Q9DCB1	4.7	4.3E-04	6.9	1.4E-03	-0.7	6.6E-01	-0.1	8.8E-01
ENSMUST00000185333	potassium voltage-gated channel, shaker-related, subfamily, member 6 [Source:MGI Symbol;Acc:MGI:96663]		Q61923	7.0	1.8E-02	7.2	5.5E-05	-0.7	5.4E-01	0.9	1.3E-01
ENSMUST00000141392				1.5	5.2E-01	2.4	2.8E-01	-2.5	2.4E-01	-3.5	1.1E-01
ENSMUST00000185356	laminin, gamma 2 [Source:MGI Symbol;Acc:MGI:99913]	G5E874		8.2	1.4E-03	3.7	8.0E-02	-1.2	5.1E-01	0.6	6.5E-01
ENSMUST00000185361	RIKEN cDNA 2610001J05 gene [Source:MGI Symbol;Acc:MGI:1913770]	F2Z3Y9		-7.5	1.0E-05	7.3	9.3E-05	-0.6	6.2E-01	-0.8	1.9E-01
ENSMUST00000185362	glutaredoxin 2 (thioltransferase) [Source:MGI Symbol;Acc:MGI:1916617]	A2A5W4	Q923X4	-4.3	2.1E-02	4.3	1.8E-02	-0.8	6.0E-01	1.0	3.9E-01
ENSMUST00000185374	malic enzyme 1, NADP(+)-dependent, cytosolic [Source:MGI Symbol;Acc:MGI:97043]	Q3TQP6		7.1	4.0E-05	-1.2	8.3E-02	-0.4	3.6E-01	-0.6	3.3E-01
ENSMUST00000185384	RIKEN cDNA 1810022K09 gene [Source:MGI Symbol;Acc:MGI:1916376]	G3UW58		-4.2	3.7E-04	4.6	9.7E-03	-0.2	9.1E-01	0.9	3.4E-01
ENSMUST00000185393	transcription elongation factor B (SIII), polypeptide 1 [Source:MGI Symbol;Acc:MGI:1915173]	A0A087WQE6		-6.4	2.0E-04	5.1	2.0E-05	-0.9	1.8E-01	-0.3	5.0E-01
ENSMUST00000185406	mucin 2 [Source:MGI Symbol;Acc:MGI:1339364]	A0A087WSG8		7.7	2.9E-05	5.6	4.7E-04	-2.0	1.1E-01	0.1	9.2E-01
ENSMUST00000185459	cathepsin H [Source:MGI Symbol;Acc:MGI:107285]	A0A087WR20		-7.6	2.6E-05	5.3	8.3E-04	-1.5	2.4E-01	0.0	1.0E+00
ENSMUST00000185462	ucine-rich repeat, immunoglobulin-like and transmembrane domains 3 [Source:MGI Symbol;Acc:MGI:268526	W8DXL4		7.0	3.7E-05	6.0	6.5E-04	-0.6	6.2E-01	-1.3	1.0E-01
ENSMUST00000185470	ankyrin repeat domain 34C [Source:MGI Symbol;Acc:MGI:2685617]	B2RPW9	Q8BLB8	7.2	6.2E-05	-3.1	8.4E-02	0.0	9.9E-01	-0.7	6.8E-01
ENSMUST00000185472	Fas apoptotic inhibitory molecule [Source:MGI Symbol;Acc:MGI:1344387]	A0A087WRH2		-4.0	7.1E-03	-2.8	1.9E-01	0.4	7.3E-01	-0.3	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000185482	autophagy related 4B, cysteine peptidase [Source:MGI Symbol;Acc:MGI:1913865]	A0A087WRT0		-6.5	3.7E-04	-0.3	8.3E-01	1.1	1.9E-01	-1.8	2.2E-01
ENSMUST00000141435				2.3	4.0E-02	2.7	6.1E-02	0.1	9.4E-01	-0.3	7.6E-01
ENSMUST00000141442				2.1	6.9E-02	2.6	1.0E-01	0.2	8.5E-01	-0.2	8.2E-01
ENSMUST00000185488	RIKEN cDNA 1810009A15 gene [Source:MGI Symbol;Acc:MGI:1913526]	A0A087WQJ5		-5.1	1.0E-03	-2.7	2.0E-02	-0.6	3.2E-01	-1.5	1.9E-01
ENSMUST00000141447	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	E0CYX5		0.7	4.9E-01	-1.5	2.8E-01	-1.4	1.2E-01	0.8	5.7E-01
ENSMUST00000185493	ubiquitin carboxyl-terminal esterase L5 [Source:MGI Symbol;Acc:MGI:1914848]	A0A087WP81		-4.2	2.0E-03	6.4	3.1E-04	-0.6	6.1E-01	-0.4	5.2E-01
ENSMUST00000141453	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]	Q52KR6		2.6	3.0E-01	-1.1	6.5E-01	-4.3	9.4E-02	-0.7	7.5E-01
ENSMUST00000185502	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1 [Source:MGI Symbol;Acc:MGI:105371]	Q6DIC9		7.9	1.2E-05	6.5	7.4E-04	0.0	9.8E-01	-0.9	2.6E-01
ENSMUST00000185533	nudix (nucleoside diphosphate linked moiety X)-type motif 16 [Source:MGI Symbol;Acc:MGI:1922936]	A0A087WSB5		8.2	1.7E-04	5.5	1.4E-03	0.8	4.9E-01	1.4	9.8E-02
ENSMUST00000185534	nucleic acid binding protein 1 [Source:MGI Symbol;Acc:MGI:1923258]		Q8BGW5	-6.7	3.4E-04	3.4	6.2E-02	0.1	9.2E-01	1.3	2.3E-01
ENSMUST00000141466				2.4	1.1E-01	5.9	1.9E-02	2.0	3.4E-01	-1.5	2.4E-01
ENSMUST00000185558	RIKEN cDNA 1810043H04 gene [Source:MGI Symbol;Acc:MGI:1913676]	A0A087WQY7		-2.7	6.4E-03	-2.5	1.5E-02	-0.4	4.8E-01	-2.6	4.2E-02
ENSMUST00000141480				2.6	7.7E-02	1.8	2.4E-01	-1.9	1.8E-01	-1.0	4.3E-01
ENSMUST00000185560	transmembrane protein 163 [Source:MGI Symbol;Acc:MGI:1919410]		Q8C996	10.1	3.9E-06	6.1	3.0E-04	-0.5	6.8E-01	-1.6	3.3E-02
ENSMUST00000141486				-2.2	4.3E-02	-2.3	9.8E-02	-0.3	6.9E-01	-0.2	8.9E-01
ENSMUST00000185569	integral membrane protein 2C [Source:MGI Symbol;Acc:MGI:1927594]	A0A087WRM2		-6.1	2.1E-04	-4.5	2.1E-02	0.5	4.4E-01	-0.7	6.8E-01
ENSMUST00000141496				-0.2	7.7E-01	1.6	9.5E-02	1.4	7.5E-02	-0.4	6.2E-01
ENSMUST00000141497	Ral GTPase activating protein, beta subunit (non-catalytic) [Source:MGI Symbol;Acc:MGI:2444531]	A2ACC7		-4.4	4.0E-02	-1.4	5.5E-01	2.5	1.3E-01	-0.5	8.3E-01
ENSMUST00000185641	ɴthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9) [Source:MGI Symbol;Acc:MGI:19		P56383	-4.9	8.0E-03	4.5	9.6E-03	-0.3	8.1E-01	-0.8	4.0E-01
ENSMUST00000185692	RIKEN cDNA 2310035C23 gene [Source:MGI Symbol;Acc:MGI:1922832]	A0A087WPW3		-5.7	7.6E-03	5.8	5.3E-04	-0.5	6.5E-01	-1.7	3.5E-02
ENSMUST00000185698	phosducin [Source:MGI Symbol;Acc:MGI:98090]	A0A087WRK4		5.1	8.8E-03	5.9	7.3E-03	-1.4	4.5E-01	0.9	3.9E-01
ENSMUST00000185715	proteasome (prosome, macropain) 26S subunit, ATPase 3 [Source:MGI Symbol;Acc:MGI:1098754]	A0A087WPH7		-6.5	3.5E-05	0.7	5.2E-01	0.9	2.8E-01	-3.8	1.3E-02
ENSMUST00000185800	BCL2-associated transcription factor 1 [Source:MGI Symbol;Acc:MGI:1917580]		Q8K019	-5.1	4.6E-04	5.4	2.6E-04	-0.9	3.6E-01	-0.3	6.6E-01
ENSMUST00000185863	lymphocyte antigen 6 complex, locus E [Source:MGI Symbol;Acc:MGI:106651]	A0A087WQ65		-3.3	9.2E-03	-3.2	7.9E-02	0.9	3.9E-01	-1.5	4.5E-01
ENSMUST00000185874	poly(rC) binding protein 4 [Source:MGI Symbol;Acc:MGI:1890471]	A0A087WSI1		6.8	8.7E-05	3.6	1.9E-03	0.3	6.6E-01	-0.2	7.1E-01
ENSMUST00000185897	dystonin [Source:MGI Symbol;Acc:MGI:104627]	A0A087WPR7		6.0	3.0E-03	7.6	5.7E-05	-0.5	6.7E-01	-0.5	3.7E-01
ENSMUST00000141525	choline/ethanolaminephosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2139793]	D3Z5Y5		-0.1	9.3E-01	0.1	9.1E-01	-2.1	5.9E-02	-2.3	7.9E-02
ENSMUST00000185909	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]	A0A087WQ02		-1.9	1.9E-02	6.8	2.6E-04	-0.3	8.1E-01	-0.5	4.4E-01
ENSMUST00000185914	predicted gene 5157 [Source:MGI Symbol;Acc:MGI:3648211]	A0A087WRH8		5.5	4.0E-03	-3.7	8.9E-02	0.7	5.0E-01	0.3	8.8E-01
ENSMUST00000185926	predicted gene, 21778 [Source:MGI Symbol;Acc:MGI:5433942]	A0A087WNP8		6.1	4.3E-04	4.5	1.1E-01	-0.7	7.9E-01	0.9	6.1E-01
ENSMUST00000141531				4.3	5.4E-02	-0.2	9.2E-01	-5.1	2.0E-02	-0.6	7.3E-01
ENSMUST00000185985	GRAM domain containing 1A [Source:MGI Symbol;Acc:MGI:105490]			-6.7	1.6E-02	6.9	1.3E-04	0.0	9.7E-01	-0.2	8.0E-01
ENSMUST00000141534				-1.5	2.6E-01	-0.6	7.0E-01	0.5	6.1E-01	-0.4	8.0E-01
ENSMUST00000141536				2.6	1.2E-01	-0.3	8.2E-01	-3.9	1.4E-02	-1.0	4.8E-01
ENSMUST00000141539				-1.3	3.4E-01	0.3	8.7E-01	0.6	6.3E-01	-1.0	5.5E-01
ENSMUST00000186003	nucleic acid binding protein 1 [Source:MGI Symbol;Acc:MGI:1923258]		Q8BGW5	-3.3	3.5E-02	-0.1	9.6E-01	-0.8	3.5E-01	4.1	7.7E-03
ENSMUST00000141557	trafficking protein particle complex 13 [Source:MGI Symbol;Acc:MGI:1914225]		Q3TIR1	0.2	9.2E-01	-2.8	3.0E-01	-1.0	5.5E-01	2.0	4.5E-01
ENSMUST00000186014	RIKEN cDNA D730001G18 gene [Source:MGI Symbol;Acc:MGI:1925975]	A0A087WQU7		5.1	5.3E-03	4.2	9.2E-04	-0.5	5.5E-01	0.0	9.4E-01
ENSMUST00000186023	membrane-spanning 4-domains, subfamily A, member 3 [Source:MGI Symbol;Acc:MGI:2158468]	Q53ZU3	Q920C4	-6.3	3.4E-04	-4.0	5.6E-02	0.0	9.9E-01	0.3	8.6E-01
ENSMUST00000141569				-2.9	5.0E-02	-4.0	6.3E-02	-0.8	3.7E-01	0.3	9.0E-01
ENSMUST00000141572	RIKEN cDNA D130043K22 gene [Source:MGI Symbol;Acc:MGI:3036268]	F2Z497		3.6	1.2E-01	1.6	5.9E-01	-0.4	8.8E-01	1.7	4.7E-01
ENSMUST00000186037	family with sequence similarity 134, member A [Source:MGI Symbol;Acc:MGI:2388278]	A0A087WPR9		-4.7	1.2E-03	6.4	1.0E-03	0.0	9.8E-01	0.2	7.9E-01
ENSMUST00000141579				0.1	8.8E-01	0.6	6.0E-01	0.2	8.6E-01	-0.3	7.7E-01
ENSMUST00000141584				-1.1	3.6E-01	-1.8	2.7E-01	0.2	8.5E-01	0.9	5.3E-01
ENSMUST00000186051	sulfatase 1 [Source:MGI Symbol;Acc:MGI:2138563]			6.4	9.2E-05	6.3	3.3E-03	-0.7	6.8E-01	0.6	5.1E-01
ENSMUST00000141589				-1.2	3.0E-01	-0.3	8.2E-01	0.9	4.7E-01	0.0	9.8E-01
ENSMUST00000141596				0.4	7.4E-01	3.2	6.6E-02	1.5	2.9E-01	-1.3	3.2E-01
ENSMUST00000186057	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	A0A087WSP5		-7.4	3.6E-05	4.7	1.5E-03	0.0	1.0E+00	-0.2	7.5E-01
ENSMUST00000186075	twist basic helix-loop-helix transcription factor 2 [Source:MGI Symbol;Acc:MGI:104685]	A5D6P6		7.5	8.5E-05	6.2	7.4E-04	0.9	4.6E-01	0.0	9.7E-01
ENSMUST00000141602	actin related protein 2/3 complex, subunit 1B [Source:MGI Symbol;Acc:MGI:1343142]	D3Z6S0		-1.3	3.5E-01	0.8	6.5E-01	0.7	6.3E-01	-1.4	3.7E-01
ENSMUST00000186096	LMBR1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1915671]	A0A087WS60		-3.7	1.8E-02	6.9	2.3E-04	0.5	7.0E-01	0.4	5.5E-01
ENSMUST00000186100	BCL2-associated transcription factor 1 [Source:MGI Symbol;Acc:MGI:1917580]	A0A087WQA0		-3.9	2.2E-02	3.4	1.3E-02	0.1	9.2E-01	-0.1	8.8E-01
ENSMUST00000186156	cDNA sequence BC034090 [Source:MGI Symbol;Acc:MGI:2672904]	A0A087WP46		8.7	1.7E-04	-3.3	1.5E-02	0.7	2.5E-01	-0.7	5.4E-01
ENSMUST00000141613				-3.3	1.5E-01	-1.9	5.4E-01	1.1	5.8E-01	-0.3	9.1E-01
ENSMUST00000141615				0.6	7.3E-01	-0.2	9.3E-01	-1.5	3.9E-01	-0.7	6.8E-01
ENSMUST00000141616				-0.8	6.0E-01	-0.6	7.3E-01	-0.4	7.6E-01	-0.6	7.0E-01
ENSMUST00000186164	high density lipoprotein (HDL) binding protein [Source:MGI Symbol;Acc:MGI:99256]	A0A087WP83		-6.7	3.5E-03	3.1	1.9E-03	-0.4	5.1E-01	0.1	9.1E-01
ENSMUST00000141618				1.7	2.4E-01	1.3	4.9E-01	0.1	9.7E-01	0.5	7.8E-01
ENSMUST00000186190	LMBR1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1915671]	A0A087WPS2		-5.0	8.8E-04	-0.5	6.7E-01	0.4	6.3E-01	-1.9	1.8E-01
ENSMUST00000186195	phosphatidylinositol glycan anchor biosynthesis, class N [Source:MGI Symbol;Acc:MGI:1351629]	A0A087WNT9		4.5	8.7E-05	-4.7	3.1E-02	1.3	1.0E-01	0.1	9.5E-01
ENSMUST00000186212	predicted gene 5891 [Source:MGI Symbol;Acc:MGI:3649014]	Q3UT86		6.3	5.5E-04	-4.4	2.5E-02	0.3	6.9E-01	-0.8	6.5E-01
ENSMUST00000186215	predicted gene 10681 [Source:MGI Symbol;Acc:MGI:3711284]	Q3UIU9	Q61767	6.0	2.0E-02	-3.3	1.4E-01	0.3	7.7E-01	-0.9	7.0E-01
ENSMUST00000186245	ankyrin repeat domain 27 (VPS9 domain) [Source:MGI Symbol;Acc:MGI:2444103]			1.7	2.8E-02	6.7	2.2E-03	-1.2	5.1E-01	-1.2	2.3E-01
ENSMUST00000186247	ankyrin 3, epithelial [Source:MGI Symbol;Acc:MGI:88026]	A0A087WNU5		10.2	9.7E-06	7.7	1.2E-02	-0.7	8.1E-01	-2.1	1.5E-01
ENSMUST00000186265	glioblastoma amplified sequence [Source:MGI Symbol;Acc:MGI:1278343]	Q7TMG8		-3.5	1.6E-02	4.9	3.4E-02	0.1	9.4E-01	1.2	3.8E-01
ENSMUST00000186287	serine/threonine kinase 25 (yeast) [Source:MGI Symbol;Acc:MGI:1891699]	A0A087WQY6		6.5	7.3E-05	4.8	2.1E-05	-1.0	1.3E-01	0.4	3.7E-01
ENSMUST00000186298	G protein-coupled receptor 35 [Source:MGI Symbol;Acc:MGI:1929509]	Q3TBY9	Q9ES90	-6.2	1.1E-04	3.8	3.7E-02	-1.3	4.2E-01	-0.1	9.0E-01
ENSMUST00000141662	alpha tubulin acetyltransferase 1 [Source:MGI Symbol;Acc:MGI:1913869]		Q8K341	1.0	4.8E-01	0.4	8.5E-01	0.3	8.3E-01	0.9	5.9E-01
ENSMUST00000186302	ArfGAP with FG repeats 1 [Source:MGI Symbol;Acc:MGI:1333754]		Q8K2K6	-7.2	3.5E-03	3.9	1.9E-02	-0.8	5.8E-01	0.0	9.8E-01
ENSMUST00000186363	tripartite motif-containing 43C [Source:MGI Symbol;Acc:MGI:3647365]	A0A087WPC1		7.9	1.0E-05	-4.3	3.2E-03	-0.8	1.4E-01	-0.8	5.3E-01
ENSMUST00000141670				1.3	1.3E-01	0.6	5.3E-01	-0.5	5.6E-01	0.2	8.3E-01
ENSMUST00000186364	phospholipid scramblase 1 [Source:MGI Symbol;Acc:MGI:893575]		Q9JJ00	-7.4	4.0E-07	-4.1	4.0E-02	0.1	9.0E-01	0.1	9.5E-01
ENSMUST00000141683				3.0	2.0E-01	2.3	4.3E-01	-0.9	7.2E-01	-0.1	9.7E-01
ENSMUST00000141691				4.8	4.7E-02	3.8	1.5E-01	-1.2	6.3E-01	-0.2	9.0E-01
ENSMUST00000186368	nicotinamide nucleotide adenylyltransferase 2 [Source:MGI Symbol;Acc:MGI:2444155]	A0A087WRE3		8.4	1.0E-05	5.0	9.5E-04	-1.9	1.2E-01	-0.2	7.7E-01
ENSMUST00000186373	cholinergic receptor, nicotinic, delta polypeptide [Source:MGI Symbol;Acc:MGI:87893]	A0A087WNX8		9.7	1.8E-02	6.7	1.8E-04	-1.4	2.8E-01	-0.3	6.1E-01
ENSMUST00000186382	neuromedin B receptor [Source:MGI Symbol;Acc:MGI:1100525]	A0A087WP36		5.4	7.4E-03	0.1	9.3E-01	0.3	6.1E-01	-2.2	2.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000186452	paired related homeobox protein-like 1 [Source:MGI Symbol;Acc:MGI:2148204]		Q8BYH0	9.0	6.1E-05	4.5	2.8E-03	-1.6	2.3E-01	0.0	9.7E-01
ENSMUST00000186458	regulator of G-protein signaling 6 [Source:MGI Symbol;Acc:MGI:1354730]		Q9Z2H2	8.2	9.8E-06	7.7	1.3E-04	-1.2	3.8E-01	-0.2	7.4E-01
ENSMUST00000141706				3.1	1.4E-01	5.6	1.7E-02	-0.5	8.1E-01	-3.1	4.7E-02
ENSMUST00000186459	RIKEN cDNA 1700088E04 gene [Source:MGI Symbol;Acc:MGI:1920774]	A0A087WPZ1		3.8	7.3E-04	6.9	2.0E-04	-0.6	6.3E-01	-0.1	8.5E-01
ENSMUST00000186465	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]		G5E870	-4.2	1.9E-02	-0.1	8.7E-01	0.5	3.4E-01	-1.4	8.4E-02
ENSMUST00000186469	ras homolog gene family, member f [Source:MGI Symbol;Acc:MGI:1345629]	Q4VA10	Q8BYP3	3.4	1.9E-03	9.3	8.9E-06	-0.6	6.0E-01	-0.2	6.8E-01
ENSMUST00000141721				-0.3	8.1E-01	6.0	2.3E-02	5.0	3.6E-02	-1.3	3.2E-01
ENSMUST00000186485	phosphatidylinositol glycan anchor biosynthesis, class N [Source:MGI Symbol;Acc:MGI:1351629]	G3X9F1		-6.9	2.0E-05	-2.3	8.4E-02	2.0	1.8E-02	-1.4	3.1E-01
ENSMUST00000186528	(constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	A0A087WRH6		-6.4	4.6E-04	-5.9	1.7E-03	1.1	4.4E-02	-1.3	4.3E-01
ENSMUST00000186538	solute carrier family 35, member A4 [Source:MGI Symbol;Acc:MGI:1915093]		Q9D321	2.3	1.2E-02	7.5	3.0E-04	-0.8	6.0E-01	1.1	1.3E-01
ENSMUST00000186548	tet methylcytosine dioxygenase 3 [Source:MGI Symbol;Acc:MGI:2446229]	L0HN04		3.0	7.4E-03	0.8	6.9E-01	-2.1	2.1E-01	1.9	2.8E-01
ENSMUST00000141754				-5.2	5.1E-02	1.6	6.4E-01	6.5	1.7E-02	-0.3	9.2E-01
ENSMUST00000186568	neutrophil cytosolic factor 2 [Source:MGI Symbol;Acc:MGI:97284]		O70145	4.1	7.9E-04	4.3	1.1E-04	-0.2	7.8E-01	0.1	8.0E-01
ENSMUST00000186574	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	Q99K94		-4.1	4.0E-03	5.4	1.9E-03	-1.5	2.7E-01	1.0	2.4E-01
ENSMUST00000186591	non-catalytic region of tyrosine kinase adaptor protein 1 [Source:MGI Symbol;Acc:MGI:109601]	A0A087WSB1		-4.2	5.3E-03	7.5	6.6E-06	-1.9	6.9E-02	0.8	7.3E-02
ENSMUST00000186617	transformed mouse 3T3 cell double minute 4 [Source:MGI Symbol;Acc:MGI:107934]	A0A087WRX7		5.8	3.7E-05	10.1	2.7E-05	-1.0	4.8E-01	0.4	5.1E-01
ENSMUST00000141779				2.2	6.3E-02	1.6	1.6E-01	-2.5	3.0E-02	-1.9	7.2E-02
ENSMUST00000141781				-1.6	1.8E-01	0.1	9.6E-01	0.3	7.4E-01	-1.3	3.2E-01
ENSMUST00000141793				1.2	1.1E-01	1.9	5.4E-02	0.2	8.1E-01	-0.5	4.9E-01
ENSMUST00000186619	RIKEN cDNA 2610044O15 gene [Source:MGI Symbol;Acc:MGI:1919389]	A0A087WRJ1		2.4	1.2E-03	7.1	5.3E-05	0.1	9.1E-01	-0.8	1.4E-01
ENSMUST00000186634	GRAM domain containing 1A [Source:MGI Symbol;Acc:MGI:105490]		Q8VEF1	-5.1	2.4E-02	-8.8	7.7E-03	-2.6	1.3E-02	0.2	9.4E-01
ENSMUST00000186648	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]	A0A087WNZ7		-8.2	2.6E-05	1.2	3.7E-01	2.4	5.0E-02	-3.4	2.9E-02
ENSMUST00000141820				-0.7	7.1E-01	2.9	2.8E-01	2.8	2.5E-01	-0.8	6.8E-01
ENSMUST00000141821	ceroid-lipofuscinosis, neuronal 6 [Source:MGI Symbol;Acc:MGI:2159324]	D6RE34		2.8	1.6E-01	3.2	1.4E-01	-1.0	6.5E-01	-1.4	3.5E-01
ENSMUST00000186694	transforming growth factor, beta receptor associated protein 1 [Source:MGI Symbol;Acc:MGI:2447427]		Q3UR70	-6.3	4.7E-04	-6.4	4.1E-03	-1.0	2.0E-01	-0.1	9.8E-01
ENSMUST00000186722	RIKEN cDNA 4930474N05 gene [Source:MGI Symbol;Acc:MGI:3586330]	Q3V0P0		8.0	1.7E-05	4.8	4.6E-03	0.7	5.9E-01	-0.8	3.1E-01
ENSMUST00000141839				-0.8	5.1E-01	-3.5	7.8E-02	-1.6	1.6E-01	1.1	5.4E-01
ENSMUST00000186723	GRAM domain containing 1A [Source:MGI Symbol;Acc:MGI:105490]	A0A087WPB6		-1.8	3.0E-02	2.0	1.1E-01	-0.4	6.6E-01	0.7	4.8E-01
ENSMUST00000141851				-1.3	6.3E-01	-0.3	9.3E-01	-0.3	8.8E-01	-1.3	6.6E-01
ENSMUST00000186726	lysine (K)-specific demethylase 5D [Source:MGI Symbol;Acc:MGI:99780]	A0A087WR43		7.6	1.1E-07	2.3	1.1E-02	-4.5	8.6E-04	0.2	7.9E-01
ENSMUST00000186733	PHD finger protein 3 [Source:MGI Symbol;Acc:MGI:2446126]	B2RQG2		-3.2	1.3E-04	4.8	1.4E-03	-1.2	2.7E-01	0.3	6.9E-01
ENSMUST00000186777	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Source:MGI Symbol;Acc:MGI:107815]	A0A087WRW5		4.7	1.6E-03	-0.7	4.9E-01	-4.6	2.3E-03	-0.5	6.6E-01
ENSMUST00000186780	family with sequence similarity 174, member A [Source:MGI Symbol;Acc:MGI:1914948]		Q9D3L0	2.5	1.4E-02	2.9	7.0E-03	-0.5	5.2E-01	-0.3	6.6E-01
ENSMUST00000186796	matrin 3 [Source:MGI Symbol;Acc:MGI:1298379]	A0A087WSP7		-6.3	1.0E-02	3.6	1.1E-02	0.5	6.4E-01	1.0	2.0E-01
ENSMUST00000186807	RIKEN cDNA 2310035C23 gene [Source:MGI Symbol;Acc:MGI:1922832]	A0A087WRM8		-4.3	1.2E-03	6.5	1.0E-03	-0.1	9.7E-01	-0.1	9.1E-01
ENSMUST00000186811	autophagy related 4B, cysteine peptidase [Source:MGI Symbol;Acc:MGI:1913865]	A0A087WNR6		-4.1	5.1E-03	2.4	4.6E-03	-1.1	9.8E-02	0.1	8.5E-01
ENSMUST00000141874				-0.7	2.1E-01	0.7	3.2E-01	0.9	9.9E-02	-0.5	4.5E-01
ENSMUST00000186857	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	Q8C3V4		-9.0	4.1E-05	4.5	8.9E-03	1.5	2.3E-01	0.9	3.3E-01
ENSMUST00000186867	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Source:MGI Symbol;Acc:MGI:107815]	A0A087WRW5		5.2	3.2E-03	3.3	1.1E-02	0.0	9.7E-01	0.0	9.9E-01
ENSMUST00000186882	(constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:19			-3.1	1.1E-02	4.6	2.4E-02	-0.8	6.5E-01	-0.6	6.5E-01
ENSMUST00000141887	phospholipase A2, group XVI [Source:MGI Symbol;Acc:MGI:2179715]	D3YYG1		1.4	5.9E-02	-2.3	1.5E-02	-2.2	3.5E-03	1.4	8.7E-02
ENSMUST00000186889	calcium channel, voltage-dependent, L type, alpha 1C subunit [Source:MGI Symbol;Acc:MGI:103013]	Q0PCR6		10.8	8.0E-06	6.4	2.6E-04	-0.6	5.9E-01	-0.4	5.4E-01
ENSMUST00000186910	predicted gene, 20924 [Source:MGI Symbol;Acc:MGI:5434280]	Q810R8		7.3	1.1E-03	-9.7	2.2E-03	-0.1	8.6E-01	1.4	5.7E-01
ENSMUST00000186928	predicted gene 10662 [Source:MGI Symbol;Acc:MGI:3642760]	Q3UT86		6.3	5.5E-04	-1.8	5.1E-02	0.0	9.4E-01	-0.5	5.2E-01
ENSMUST00000186948	transcription elongation factor B (SIII), polypeptide 1 [Source:MGI Symbol;Acc:MGI:1915173]		P83940	-5.5	3.4E-04	2.7	4.0E-01	-0.9	7.6E-01	3.5	1.8E-01
ENSMUST00000186949	basic leucine zipper and W2 domains 1 [Source:MGI Symbol;Acc:MGI:1914132]	A0A087WQS2		-6.2	1.4E-02	1.6	3.5E-01	-1.1	4.7E-01	1.7	2.1E-01
ENSMUST00000186952	ɲthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9) [Source:MGI Symbol;Acc:MGI:19	A0A087WSE2		5.3	1.1E-02	8.5	2.5E-05	-0.5	6.6E-01	-0.4	4.1E-01
ENSMUST00000141925				-2.0	6.6E-02	-2.7	6.2E-02	-0.7	3.9E-01	0.0	1.0E+00
ENSMUST00000186954	Snf2-related CREBBP activator protein [Source:MGI Symbol;Acc:MGI:2444036]	A0A087WNX7		-4.7	3.2E-02	-1.8	2.5E-01	1.2	1.9E-01	-0.4	7.9E-01
ENSMUST00000186956				-3.1	3.5E-03	2.9	7.0E-02	-1.1	4.5E-01	-0.2	8.5E-01
ENSMUST00000186961	serine/arginine repetitive matrix 2 [Source:MGI Symbol;Acc:MGI:1923206]	A0A087WRX8		5.1	3.0E-03	8.2	5.8E-05	-0.7	5.9E-01	-1.4	4.5E-02
ENSMUST00000141939				1.8	1.3E-01	-0.1	9.6E-01	-1.5	1.9E-01	0.4	7.4E-01
ENSMUST00000186969	selection and upkeep of intraepithelial T cells 2 [Source:MGI Symbol;Acc:MGI:3649629]		A7XUX6	6.0	1.6E-04	4.1	5.7E-03	-2.2	8.7E-02	-1.0	2.6E-01
ENSMUST00000186971	tubulin, alpha 4A [Source:MGI Symbol;Acc:MGI:1095410]	A0A087WQS4		-7.4	8.5E-05	6.1	1.8E-03	7.7	2.1E-04	-0.3	7.2E-01
ENSMUST00000187005	WD repeat and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:1916618]	A0A087WPX9		-6.0	2.1E-05	5.3	2.3E-05	-0.7	3.3E-01	0.6	1.9E-01
ENSMUST00000187028	zinc finger protein 383 [Source:MGI Symbol;Acc:MGI:1920979]	A0A087WSF1		3.2	6.1E-04	-6.2	1.1E-03	-2.2	3.7E-03	-1.6	3.3E-01
ENSMUST00000141966	solute carrier family 4 (anion exchanger), member 2 [Source:MGI Symbol;Acc:MGI:109351]	D3Z5G3		-0.6	6.4E-01	0.8	5.8E-01	0.1	9.5E-01	-1.3	3.5E-01
ENSMUST00000141974	heterogeneous nuclear ribonucleoprotein A3 [Source:MGI Symbol;Acc:MGI:1917171]	A2AL13		1.9	2.1E-01	-5.0	1.2E-01	-1.6	2.5E-01	5.3	9.2E-02
ENSMUST00000187083	human immunodeficiency virus type I enhancer binding protein 2 [Source:MGI Symbol;Acc:MGI:1338076]		Q3UHF7	8.5	1.4E-03	6.5	2.1E-03	-0.2	9.0E-01	0.9	2.8E-01
ENSMUST00000141979				-5.3	3.9E-02	-6.1	7.8E-02	-1.3	3.1E-01	-0.5	8.8E-01
ENSMUST00000187182	kin of IRRE like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1914953]		Q8BR86	5.6	1.3E-02	-1.0	4.0E-01	1.3	6.6E-02	-0.1	9.5E-01
ENSMUST00000141997	fused in sarcoma [Source:MGI Symbol;Acc:MGI:1353633]	G3UZD2		-3.2	6.2E-02	-1.8	3.3E-01	0.2	8.5E-01	-1.2	5.3E-01
ENSMUST00000187183	RIKEN cDNA 2010005H15 gene [Source:MGI Symbol;Acc:MGI:1924020]	Q9D8D6		6.7	1.4E-04	4.6	8.4E-05	-0.9	1.7E-01	-0.8	1.5E-01
ENSMUST00000187194	erythrocyte membrane protein band 4.1 like 5 [Source:MGI Symbol;Acc:MGI:103006]	A0A087WP93		5.4	4.3E-04	4.6	4.2E-03	-0.4	7.3E-01	-0.8	3.2E-01
ENSMUST00000187213	potassium voltage-gated channel, subfamily Q, member 1 [Source:MGI Symbol;Acc:MGI:108083]	A0A087WPA8		6.8	6.0E-05	7.7	3.4E-04	2.3	1.0E-01	0.6	3.9E-01
ENSMUST00000142006				1.4	3.4E-01	1.6	3.4E-01	-0.6	6.5E-01	-0.9	5.7E-01
ENSMUST00000187285	pleckstrin homology domain containing, family A member 6 [Source:MGI Symbol;Acc:MGI:2388662]	A0A087WRB7		8.4	2.7E-05	4.8	5.3E-04	2.1	2.8E-02	0.4	5.1E-01
ENSMUST00000142012	ankyrin repeat domain 9 [Source:MGI Symbol;Acc:MGI:1921501]	D3Z2N1		-2.4	2.8E-01	1.2	7.2E-01	3.9	1.4E-01	0.3	9.1E-01
ENSMUST00000187304	proline rich 30 [Source:MGI Symbol;Acc:MGI:1923877]		Q9D9B7	7.5	4.9E-04	6.8	1.1E-04	0.1	9.3E-01	-0.3	6.5E-01
ENSMUST00000187386	calcium channel, voltage-dependent, L type, alpha 1C subunit [Source:MGI Symbol;Acc:MGI:103013]	A0A087WQT9		6.2	1.1E-03	6.1	9.5E-05	-0.2	8.2E-01	-0.2	7.7E-01
ENSMUST00000142017	cytoplasmic FMR1 interacting protein 2 [Source:MGI Symbol;Acc:MGI:1924134]	F6QD74		2.1	4.0E-01	3.3	3.0E-01	1.4	5.9E-01	0.2	9.5E-01
ENSMUST00000142020				3.2	5.5E-02	2.6	1.5E-01	-0.8	6.1E-01	-0.2	8.9E-01
ENSMUST00000142027				3.9	6.9E-02	5.9	5.6E-02	2.4	3.4E-01	0.4	8.2E-01
ENSMUST00000187407	NIMA (never in mitosis gene a)-related expressed kinase 7 [Source:MGI Symbol;Acc:MGI:1890645]		Q9ES74	-2.1	3.4E-03	-1.3	1.6E-01	0.9	1.3E-01	-0.5	6.1E-01
ENSMUST00000187418	predicted gene, 21118 [Source:MGI Symbol;Acc:MGI:5434473]	J3QPK8		5.9	8.4E-04	-3.1	3.4E-02	2.8	3.1E-03	-1.1	4.2E-01
ENSMUST00000142039				1.3	2.9E-01	2.4	2.0E-01	0.7	6.4E-01	-0.3	8.0E-01
ENSMUST00000187455	predicted gene 28360 [Source:MGI Symbol;Acc:MGI:5579066]	A0A087WR25		7.1	5.4E-05	6.4	8.6E-05	-1.5	1.8E-01	-0.2	7.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000187467	membrane-spanning 4-domains, subfamily A, member 14 [Source:MGI Symbol;Acc:MGI:2686122]	A0A087WSD2		11.3	7.3E-04	5.0	1.6E-04	0.3	7.2E-01	0.6	2.6E-01
ENSMUST00000187485	adhesion G protein-coupled receptor B1 [Source:MGI Symbol;Acc:MGI:1933736]	A0A087WSA1		3.2	8.8E-05	2.7	2.6E-02	-1.2	2.1E-01	0.8	3.4E-01
ENSMUST00000187504	LBH domain containing 1 [Source:MGI Symbol;Acc:MGI:5516029]	A0A087WPA0		1.6	1.2E-02	7.6	3.6E-05	-0.5	6.4E-01	-0.7	2.2E-01
ENSMUST00000187512	keratin associated protein 5-3 [Source:MGI Symbol;Acc:MGI:1924465]	A0A087WSN0		8.5	2.3E-04	5.8	4.3E-03	0.0	9.9E-01	-0.5	6.1E-01
ENSMUST00000187521	inhibitor of Bruton agammaglobulinemia tyrosine kinase [Source:MGI Symbol;Acc:MGI:1918677]	A0A087WNN3		-7.2	9.9E-05	2.5	7.3E-02	-3.0	4.3E-02	-0.7	5.0E-01
ENSMUST00000142061	tumor protein, translationally-controlled 1 [Source:MGI Symbol;Acc:MGI:104890]	D3YU75		-0.4	8.7E-01	-0.5	8.6E-01	-1.0	6.4E-01	-0.9	7.2E-01
ENSMUST00000142062	eukaryotic translation elongation factor 1 beta 2 [Source:MGI Symbol;Acc:MGI:1929520]	M0QWK5		-1.8	6.8E-01	-8.0	9.0E-02	-5.8	3.0E-02	0.4	9.4E-01
ENSMUST00000142063	death effector domain-containing [Source:MGI Symbol;Acc:MGI:1333874]	D3Z0F7		1.5	4.6E-01	2.1	4.1E-01	0.7	7.3E-01	0.1	9.8E-01
ENSMUST00000187530	predicted gene, 21761 [Source:MGI Symbol;Acc:MGI:5433925]	J3QK00		7.8	1.0E-04	-3.8	6.8E-03	-0.6	2.8E-01	-1.6	2.3E-01
ENSMUST00000187541	calcium channel, voltage-dependent, R type, alpha 1E subunit [Source:MGI Symbol;Acc:MGI:106217]	A0A087WS83		4.9	1.9E-03	5.1	4.6E-05	-1.4	7.8E-02	0.5	2.6E-01
ENSMUST00000187549	menage a trois 1 [Source:MGI Symbol;Acc:MGI:106207]	A0A087WSG5		5.1	7.3E-04	6.4	6.2E-04	-0.6	6.8E-01	-0.7	3.8E-01
ENSMUST00000142075				-1.8	1.9E-01	1.4	3.2E-01	1.0	3.5E-01	-2.1	1.5E-01
ENSMUST00000187584	tensin 1 [Source:MGI Symbol;Acc:MGI:104552]	A0A087WQM0		8.8	2.0E-02	5.7	6.6E-03	-0.7	7.1E-01	-0.1	8.9E-01
ENSMUST00000142080	Wolf-Hirschhorn syndrome candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1276574]	F6S6G6		3.3	7.4E-02	1.0	5.8E-01	-2.1	2.3E-01	0.2	9.0E-01
ENSMUST00000142084				0.5	5.0E-01	-0.1	9.0E-01	-0.1	9.0E-01	0.5	5.6E-01
ENSMUST00000142090	diacylglycerol kinase zeta [Source:MGI Symbol;Acc:MGI:1278339]	D6RIP2		0.7	7.5E-01	2.5	3.3E-01	0.7	7.3E-01	-1.1	6.3E-01
ENSMUST00000187603	RIKEN cDNA 1700025G04 gene [Source:MGI Symbol;Acc:MGI:1916649]	Q3TJL3	Q8K207	3.3	6.2E-04	0.6	6.6E-01	-4.6	1.5E-02	-0.6	6.0E-01
ENSMUST00000187625	kin of IRRE like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1914953]	G5E8B6		-4.2	1.2E-02	1.2	2.0E-01	-0.4	5.8E-01	0.1	8.7E-01
ENSMUST00000187627	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]	A0A087WS99		-3.8	2.8E-02	6.4	1.7E-04	-0.6	6.1E-01	-0.9	1.4E-01
ENSMUST00000187810	ADP-ribosylation factor-like 4C [Source:MGI Symbol;Acc:MGI:2445172]		P61208	4.1	3.7E-03	-3.9	1.5E-01	0.6	6.3E-01	-0.1	9.6E-01
ENSMUST00000187824	autophagy related 4B, cysteine peptidase [Source:MGI Symbol;Acc:MGI:1913865]	A0A087WNY2		-4.3	2.8E-03	4.4	1.1E-03	-0.4	6.6E-01	-0.4	5.8E-01
ENSMUST00000187856	predicted gene, 20747 [Source:MGI Symbol;Acc:MGI:5434103]	Q5FWB5		6.9	1.9E-04	6.6	6.6E-05	-0.9	4.1E-01	0.3	6.4E-01
ENSMUST00000187896	galactose-3-O-sulfotransferase 2 [Source:MGI Symbol;Acc:MGI:2685834]	A0A087WRM6		5.5	3.8E-03	7.5	1.0E-04	-0.5	6.9E-01	-1.3	5.4E-02
ENSMUST00000187900	R3H domain containing 1 [Source:MGI Symbol;Acc:MGI:2448514]	Q80ZH9		4.5	3.2E-02	5.3	6.6E-05	-1.4	1.1E-01	-0.2	6.7E-01
ENSMUST00000187944	twinfilin, actin-binding protein, homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1346078]	A0A087WPT3		5.0	3.0E-04	5.7	6.0E-04	0.0	9.9E-01	0.0	9.9E-01
ENSMUST00000187945	mucin 2 [Source:MGI Symbol;Acc:MGI:1339364]	A0A087WSP1		8.4	3.4E-04	6.9	6.8E-06	-0.8	3.2E-01	0.1	8.7E-01
ENSMUST00000187953	leucine rich repeat containing 28 [Source:MGI Symbol;Acc:MGI:1915689]	A0A087WQI4		5.8	1.7E-03	-4.1	2.8E-02	0.0	1.0E+00	1.0	5.4E-01
ENSMUST00000187976	RIKEN cDNA K230010J24 gene [Source:MGI Symbol;Acc:MGI:3588184]	A0A087WQQ1		4.9	3.6E-03	6.7	2.2E-04	0.0	9.9E-01	-0.2	7.9E-01
ENSMUST00000142147				1.6	1.3E-01	0.6	6.3E-01	0.6	5.5E-01	1.6	2.0E-01
ENSMUST00000142148				-1.1	2.8E-01	-0.6	6.1E-01	-0.2	8.3E-01	-0.7	5.5E-01
ENSMUST00000187978	calcium response factor [Source:MGI Symbol;Acc:MGI:2182269]		Q8VHI4	3.1	1.1E-03	-2.2	1.5E-01	1.6	9.2E-02	0.2	8.9E-01
ENSMUST00000187990	olfactory receptor 1252 [Source:MGI Symbol;Acc:MGI:3031086]	Q7TQZ2		6.4	6.4E-04	-1.6	2.8E-01	1.0	3.2E-01	-3.0	1.1E-01
ENSMUST00000188000	atypical chemokine receptor 4 [Source:MGI Symbol;Acc:MGI:2181676]		Q924I3	7.1	3.0E-02	4.1	5.9E-02	-0.7	7.0E-01	0.8	5.5E-01
ENSMUST00000188005	keratin associated protein 28-13 [Source:MGI Symbol;Acc:MGI:1918636]	A0A087WQP5		7.8	4.2E-05	5.9	5.1E-05	-1.9	6.2E-02	0.0	9.3E-01
ENSMUST00000188030	SH3 domain binding glutamic acid-rich protein like 2 [Source:MGI Symbol;Acc:MGI:1915350]	A0A087WQU5		7.2	2.1E-04	5.3	2.9E-04	-1.4	1.7E-01	0.3	6.1E-01
ENSMUST00000188044	predicted gene 28062 [Source:MGI Symbol;Acc:MGI:5578768]	A0A087WPX7		3.1	1.7E-02	5.0	8.5E-03	-0.6	7.1E-01	0.2	8.7E-01
ENSMUST00000188073	protein kinase, AMP-activated, gamma 3 non-catatlytic subunit [Source:MGI Symbol;Acc:MGI:1891343]		Q8BGM7	7.3	6.3E-05	5.5	1.9E-02	-0.7	7.4E-01	0.8	5.2E-01
ENSMUST00000188081	ankyrin repeat and SOCS box-containing 1 [Source:MGI Symbol;Acc:MGI:1929735]	A0A087WQE9		4.1	8.7E-03	3.9	5.6E-03	1.1	2.8E-01	-0.4	6.0E-01
ENSMUST00000188090	transformed mouse 3T3 cell double minute 4 [Source:MGI Symbol;Acc:MGI:107934]		O35618	-3.0	4.7E-03	8.4	1.0E-03	-1.4	5.0E-01	1.0	2.9E-01
ENSMUST00000188096	predicted gene 4767 [Source:MGI Symbol;Acc:MGI:3644409]	A0A087WNP5		6.9	2.2E-02	4.5	1.3E-02	-0.9	5.9E-01	0.1	8.8E-01
ENSMUST00000188154	osphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2 [Source:MGI Symbol;Acc:MGI:19233	A0A087WRD8		7.0	2.4E-06	3.7	6.5E-03	0.2	8.1E-01	0.4	6.0E-01
ENSMUST00000142184	ataxin 7-like 1 [Source:MGI Symbol;Acc:MGI:3584458]	F6RLA6		0.3	7.1E-01	1.0	3.4E-01	0.9	2.5E-01	0.2	7.9E-01
ENSMUST00000188161	predicted gene 996 [Source:MGI Symbol;Acc:MGI:2685842]		A2AJA9	5.1	3.9E-03	-3.9	3.9E-02	0.0	9.9E-01	0.1	9.5E-01
ENSMUST00000188169	LEM domain containing 1 [Source:MGI Symbol;Acc:MGI:1922403]	A0A087WR92		9.5	1.2E-04	-5.5	9.3E-04	-1.3	2.2E-02	-0.4	7.6E-01
ENSMUST00000188204	nucleic acid binding protein 1 [Source:MGI Symbol;Acc:MGI:1923258]		Q8BGW5	-6.8	2.3E-04	4.8	6.7E-03	-1.7	2.6E-01	0.0	9.9E-01
ENSMUST00000142203				-1.7	3.6E-01	-0.9	6.6E-01	-0.4	7.7E-01	-1.2	5.5E-01
ENSMUST00000188211	La ribonucleoprotein domain family, member 4B [Source:MGI Symbol;Acc:MGI:106330]		Q6A0A2	-2.9	4.0E-03	6.5	3.1E-04	-0.5	7.2E-01	-1.4	5.9E-02
ENSMUST00000142215				-1.3	2.7E-01	-2.4	2.4E-01	0.5	5.7E-01	1.6	4.2E-01
ENSMUST00000188214	lymphocyte antigen 6 complex, locus C2 [Source:MGI Symbol;Acc:MGI:3712069]		P0CW03	-7.5	3.3E-06	6.3	1.5E-04	-0.6	6.0E-01	0.0	9.6E-01
ENSMUST00000188223	delta-like 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2146838]	A0A087WSS3		5.9	5.9E-03	5.0	8.0E-04	-1.1	2.9E-01	0.1	8.3E-01
ENSMUST00000142226				1.8	1.9E-01	2.3	2.0E-01	0.1	9.4E-01	-0.4	7.8E-01
ENSMUST00000142227	structural maintenance of chromosomes 2 [Source:MGI Symbol;Acc:MGI:106067]	B1AWH6		2.7	2.1E-01	5.9	4.2E-02	1.3	6.0E-01	-1.8	3.3E-01
ENSMUST00000188241	SH3 domain binding glutamic acid-rich protein like 2 [Source:MGI Symbol;Acc:MGI:1915350]	A0A087WS96		6.6	2.2E-03	-3.7	3.7E-02	0.9	2.6E-01	-2.7	1.9E-01
ENSMUST00000188257	CH domain containing, RNA binding, signal transduction associated 2 [Source:MGI Symbol;Acc:MGI:2159649		Q9WU01	7.8	4.6E-05	-7.7	2.3E-04	-0.8	9.2E-02	-0.7	6.3E-01
ENSMUST00000188274	keratin associated protein 5-1 [Source:MGI Symbol;Acc:MGI:1354732]		Q64507	8.8	2.2E-05	5.1	3.6E-04	-1.6	1.5E-01	-0.6	3.7E-01
ENSMUST00000142241	flap structure specific endonuclease 1 [Source:MGI Symbol;Acc:MGI:102779]	Q91Z50		-2.5	8.1E-02	3.0	3.9E-02	0.1	9.3E-01	-5.4	2.1E-03
ENSMUST00000142247	zinc finger protein 91 [Source:MGI Symbol;Acc:MGI:104854]	E0CY81		0.8	7.5E-01	-3.6	2.5E-01	-3.6	7.9E-02	0.7	8.1E-01
ENSMUST00000188298	serum/glucocorticoid regulated kinase 3 [Source:MGI Symbol;Acc:MGI:2182368]	A0A087WPW2		-3.5	5.4E-03	3.0	1.4E-02	-1.7	1.2E-01	-0.2	7.8E-01
ENSMUST00000188313	tripeptidyl peptidase II [Source:MGI Symbol;Acc:MGI:102724]		Q64514	-5.1	9.4E-03	-3.5	1.4E-01	0.9	4.2E-01	0.5	8.1E-01
ENSMUST00000188317	predicted gene, 20379 [Source:MGI Symbol;Acc:MGI:5012564]	A0A087WR34		4.6	1.7E-04	4.4	1.9E-02	-0.7	6.6E-01	1.7	1.4E-01
ENSMUST00000142259	leucine-zipper-like transcriptional regulator, 1 [Source:MGI Symbol;Acc:MGI:1914113]	F6VJI5		-0.9	4.0E-01	-0.8	5.9E-01	0.8	4.2E-01	0.8	5.7E-01
ENSMUST00000188332	ubiquitin specific peptidase 40 [Source:MGI Symbol;Acc:MGI:2443184]	A0A087WRD2		5.6	1.1E-02	6.6	2.2E-04	-1.1	3.6E-01	0.8	2.2E-01
ENSMUST00000188347	autophagy related 9A [Source:MGI Symbol;Acc:MGI:2138446]	Q3ZAQ4		-5.3	2.8E-03	5.1	7.0E-02	-0.8	7.5E-01	0.1	9.6E-01
ENSMUST00000188366	ST3 beta-galactoside alpha-2,3-sialyltransferase 5 [Source:MGI Symbol;Acc:MGI:1339963]			-4.7	4.1E-03	3.5	1.0E-03	-0.4	6.1E-01	-0.3	5.9E-01
ENSMUST00000188371	telomeric repeat binding factor 1 [Source:MGI Symbol;Acc:MGI:109634]		P70371	4.0	3.0E-04	2.2	2.8E-01	1.4	4.1E-01	2.5	1.2E-01
ENSMUST00000188382	RIKEN cDNA 2410002F23 gene [Source:MGI Symbol;Acc:MGI:1914226]	Q3TE80		9.2	1.6E-05	2.9	2.5E-02	0.2	8.6E-01	-0.1	8.7E-01
ENSMUST00000188454	solute carrier organic anion transporter family, member 5A1 [Source:MGI Symbol;Acc:MGI:2443431]	E9PVD9		9.4	1.8E-05	6.5	2.5E-04	-0.6	6.4E-01	0.0	9.8E-01
ENSMUST00000142276				0.4	7.4E-01	0.3	8.2E-01	-0.7	5.4E-01	-0.6	6.1E-01
ENSMUST00000188468	lipid phosphate phosphatase-related protein type 2 [Source:MGI Symbol;Acc:MGI:2384575]	A0A087WQF0		6.2	4.8E-04	-6.0	4.8E-04	-1.6	5.1E-03	-1.8	1.9E-01
ENSMUST00000188489	zinc finger protein 207 [Source:MGI Symbol;Acc:MGI:1340045]		Q9JMD0	-2.6	3.1E-02	0.4	7.1E-01	-0.4	5.9E-01	-3.6	8.9E-03
ENSMUST00000142283	homeodomain leucine zipper-encoding gene [Source:MGI Symbol;Acc:MGI:2678023]			-1.5	2.1E-01	0.7	6.2E-01	1.1	3.4E-01	-1.2	4.0E-01
ENSMUST00000142284				-1.0	6.8E-01	5.4	1.2E-01	3.9	2.1E-01	-2.4	2.8E-01
ENSMUST00000142288				1.0	3.9E-01	3.1	3.5E-02	0.7	5.4E-01	-1.4	2.2E-01
ENSMUST00000188507	transmembrane protein 194B [Source:MGI Symbol;Acc:MGI:2444113]	A0A087WQD9		-4.8	1.8E-02	6.2	2.9E-04	-0.5	6.7E-01	-0.8	2.5E-01
ENSMUST00000142295	PR domain containing 15 [Source:MGI Symbol;Acc:MGI:1930121]	D6RIL7		3.0	1.1E-01	1.9	4.1E-01	-1.3	5.5E-01	-0.2	9.1E-01
ENSMUST00000142296				0.0	9.8E-01	0.2	8.4E-01	-0.4	6.3E-01	-0.6	5.3E-01
ENSMUST00000142298				-0.3	6.9E-01	0.3	7.9E-01	0.4	6.3E-01	-0.2	8.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000188522	calcium channel, voltage-dependent, L type, alpha 1C subunit [Source:MGI Symbol;Acc:MGI:103013]	A0A087WS67		5.2	3.3E-03	5.6	1.1E-04	-0.1	9.1E-01	-1.1	7.9E-02
ENSMUST00000188524	eukaryotic translation elongation factor 1 beta 2 [Source:MGI Symbol;Acc:MGI:1929520]	A0A087WS46		-8.2	5.0E-06	5.7	7.4E-04	0.1	9.4E-01	0.3	6.3E-01
ENSMUST00000188587	collagen, type VI, alpha 3 [Source:MGI Symbol;Acc:MGI:88461]	A0A087WS16		4.4	2.2E-02	5.3	5.2E-03	-0.1	9.5E-01	1.1	2.9E-01
ENSMUST00000188593	tubulin, alpha 4A [Source:MGI Symbol;Acc:MGI:1095410]	A0A087WS35		-7.8	1.0E-04	2.5	5.1E-02	-0.2	8.4E-01	0.0	9.8E-01
ENSMUST00000188618	abl-interactor 2 [Source:MGI Symbol;Acc:MGI:106913]	Q6AXD2		4.3	5.8E-03	6.2	7.9E-04	-0.5	7.1E-01	-1.7	4.6E-02
ENSMUST00000188630	basic leucine zipper and W2 domains 1 [Source:MGI Symbol;Acc:MGI:1914132]	A0A087WS48		-7.1	6.7E-05	-3.1	6.9E-02	0.8	3.0E-01	-0.6	7.3E-01
ENSMUST00000188633	predicted gene 8369 [Source:MGI Symbol;Acc:MGI:3645380]	E9PZI3		7.0	1.4E-04	-3.9	3.5E-02	1.1	1.4E-01	0.0	1.0E+00
ENSMUST00000188641	transcription elongation factor B (SIII), polypeptide 1 [Source:MGI Symbol;Acc:MGI:1915173]		P83940	-3.9	6.2E-04	4.4	3.9E-05	-0.8	1.9E-01	-0.2	6.8E-01
ENSMUST00000188656	Ral GEF with PH domain and SH3 binding motif 2 [Source:MGI Symbol;Acc:MGI:1925505]	A0A087WQU0		7.5	3.1E-04	6.8	1.8E-04	-1.9	1.7E-01	0.1	9.3E-01
ENSMUST00000188666	neuralized E3 ubiquitin protein ligase 3 [Source:MGI Symbol;Acc:MGI:2429944]	A0A087WP78		-1.6	2.5E-02	3.3	2.5E-03	-0.3	6.4E-01	0.4	5.2E-01
ENSMUST00000188670	non-catalytic region of tyrosine kinase adaptor protein 1 [Source:MGI Symbol;Acc:MGI:109601]	A0A087WQD1		-2.9	1.1E-02	5.1	7.6E-04	0.6	5.4E-01	-0.6	3.1E-01
ENSMUST00000188677	opioid growth factor receptor-like 1 [Source:MGI Symbol;Acc:MGI:1917405]	A0A087WNQ8		-7.2	3.2E-03	4.9	2.9E-03	0.8	5.4E-01	-1.0	2.2E-01
ENSMUST00000142344	eukaryotic translation initiation factor 4, gamma 1 [Source:MGI Symbol;Acc:MGI:2384784]	E9Q770		1.4	4.9E-01	0.6	8.2E-01	-0.2	9.2E-01	0.6	8.2E-01
ENSMUST00000142345				1.1	9.9E-02	1.1	1.8E-01	-0.3	6.2E-01	-0.3	7.0E-01
ENSMUST00000142351	vascular endothelial growth factor A [Source:MGI Symbol;Acc:MGI:103178]	F8WH81		2.3	2.3E-01	1.4	5.5E-01	0.2	9.1E-01	1.2	5.8E-01
ENSMUST00000188691	gasdermin C2 [Source:MGI Symbol;Acc:MGI:2146102]		Q2KHK6	6.3	1.5E-02	11.7	2.9E-03	-0.7	8.4E-01	1.7	1.4E-01
ENSMUST00000142356	septin 1 [Source:MGI Symbol;Acc:MGI:1858916]	D3YVG1		0.5	8.4E-01	-2.9	3.9E-01	-2.2	2.5E-01	1.1	7.4E-01
ENSMUST00000188702	RIKEN cDNA 1700020L24 gene [Source:MGI Symbol;Acc:MGI:1913580]	A0A087WRJ9		-4.3	3.5E-03	1.8	8.1E-02	0.3	7.3E-01	0.8	2.8E-01
ENSMUST00000142363				1.6	4.6E-02	2.2	3.6E-02	0.3	6.9E-01	-0.4	6.4E-01
ENSMUST00000188710	CLIP associating protein 1 [Source:MGI Symbol;Acc:MGI:1923957]	A0A087WRE8		5.0	1.4E-04	3.9	8.3E-04	-2.2	2.2E-02	-0.2	7.4E-01
ENSMUST00000188807	predicted gene, 21655 [Source:MGI Symbol;Acc:MGI:5435010]	A0A0G2JFD5		6.6	6.6E-05	2.8	3.1E-03	-1.1	1.3E-01	-0.9	1.5E-01
ENSMUST00000142376				1.4	2.5E-01	-0.2	8.9E-01	-0.6	6.0E-01	1.0	5.0E-01
ENSMUST00000188815	laminin, alpha 3 [Source:MGI Symbol;Acc:MGI:99909]		Q61789	7.0	4.7E-03	7.3	2.1E-05	0.4	6.8E-01	-0.5	3.1E-01
ENSMUST00000142379				0.9	1.9E-01	1.8	5.7E-02	0.5	4.5E-01	-0.3	6.2E-01
ENSMUST00000142381				0.9	6.9E-02	0.8	1.7E-01	-0.6	1.8E-01	-0.5	3.6E-01
ENSMUST00000188842	synaptotagmin II [Source:MGI Symbol;Acc:MGI:99666]			8.6	8.2E-05	4.4	1.9E-03	-4.4	4.7E-03	-1.0	1.8E-01
ENSMUST00000188873	family with sequence similarity 134, member A [Source:MGI Symbol;Acc:MGI:2388278]	A0A087WNV4		-7.0	4.1E-04	7.1	1.0E-04	-1.9	1.8E-01	-1.3	6.6E-02
ENSMUST00000188894	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]	A0A087WR50		-5.1	8.2E-03	4.4	1.1E-02	0.5	7.1E-01	0.6	5.1E-01
ENSMUST00000188972	protein tyrosine phosphatase, non-receptor type 18 [Source:MGI Symbol;Acc:MGI:108410]	Q3V441		-4.8	7.2E-03	2.8	5.8E-04	-0.2	7.3E-01	-0.4	3.5E-01
ENSMUST00000142395	Wolf-Hirschhorn syndrome candidate 1-like 1 (human) [Source:MGI Symbol;Acc:MGI:2142581]	D3Z357		-1.6	4.1E-01	-3.3	1.9E-01	-1.6	2.8E-01	0.2	9.4E-01
ENSMUST00000188994	zinc finger homeobox 3 [Source:MGI Symbol;Acc:MGI:99948]	A0A087WQ36		6.5	7.8E-05	3.7	7.2E-02	-1.8	3.4E-01	0.4	7.7E-01
ENSMUST00000142398				-3.2	6.1E-02	0.5	8.2E-01	2.8	7.0E-02	-0.8	6.6E-01
ENSMUST00000188995	membrane-spanning 4-domains, subfamily A, member 4A [Source:MGI Symbol;Acc:MGI:3643932]	A0A087WRT7		-4.1	2.9E-03	5.1	1.4E-03	-2.5	7.0E-02	-0.4	5.7E-01
ENSMUST00000188997	Erbb2 interacting protein [Source:MGI Symbol;Acc:MGI:1890169]	B2RUJ2		-5.8	5.8E-05	5.9	3.8E-05	0.6	4.6E-01	0.5	2.7E-01
ENSMUST00000189003	predicted gene 29644 [Source:MGI Symbol;Acc:MGI:5580350]	A0A087WPG2		7.1	3.9E-04	1.5	6.5E-02	0.1	8.5E-01	0.7	3.1E-01
ENSMUST00000189006	predicted gene 29423 [Source:MGI Symbol;Acc:MGI:5580129]	A0A087WRM1		6.0	2.4E-02	-7.8	4.0E-05	0.0	9.8E-01	-2.1	1.4E-01
ENSMUST00000142418				0.9	2.8E-01	1.1	2.9E-01	-0.2	8.5E-01	-0.3	7.0E-01
ENSMUST00000142421				-2.2	5.5E-02	-1.7	3.5E-01	1.7	1.6E-01	1.2	4.8E-01
ENSMUST00000142422				-1.8	5.2E-02	-1.1	4.4E-01	2.3	2.0E-02	1.6	2.4E-01
ENSMUST00000189017	FAT tumor suppressor homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:109168]	A0A087WRT4		7.2	4.4E-04	-5.1	5.6E-04	-0.2	7.0E-01	-0.8	4.8E-01
ENSMUST00000189037	secretin receptor [Source:MGI Symbol;Acc:MGI:2441720]		Q5FWI2	6.5	2.1E-03	4.3	3.7E-02	-0.6	7.6E-01	1.8	1.4E-01
ENSMUST00000142430				-0.1	8.6E-01	0.5	3.8E-01	0.0	9.8E-01	-0.5	2.7E-01
ENSMUST00000189066	transmembrane protein 108 [Source:MGI Symbol;Acc:MGI:1932411]		Q8BHE4	6.1	1.7E-02	3.3	9.6E-03	-0.7	4.5E-01	0.8	3.3E-01
ENSMUST00000189095	predicted gene 15448 [Source:MGI Symbol;Acc:MGI:3705216]	A0A087WSB3		-9.4	1.7E-06	9.0	4.1E-04	-0.1	9.6E-01	1.4	9.4E-02
ENSMUST00000189109	Sycp3 like Y-linked [Source:MGI Symbol;Acc:MGI:2687328]	A0A087WSR0		8.1	7.6E-04	6.2	5.5E-04	-0.4	7.4E-01	-1.4	6.4E-02
ENSMUST00000189137	transient receptor potential cation channel, subfamily C, member 1 [Source:MGI Symbol;Acc:MGI:109528]	B2RPS7		6.7	2.5E-04	4.9	1.2E-02	-1.3	4.5E-01	-0.8	4.8E-01
ENSMUST00000142440				2.7	6.1E-02	3.4	4.2E-02	0.0	9.9E-01	-0.7	5.6E-01
ENSMUST00000142442				0.2	8.3E-01	2.3	1.0E-01	1.0	3.3E-01	-1.0	3.7E-01
ENSMUST00000189181	progesterone receptor [Source:MGI Symbol;Acc:MGI:97567]	A6H6A5		8.1	1.3E-05	5.1	2.1E-02	-1.3	4.9E-01	0.6	6.4E-01
ENSMUST00000142455				-2.2	7.1E-02	-1.6	2.9E-01	0.5	5.5E-01	0.0	9.8E-01
ENSMUST00000189185	predicted gene 29666 [Source:MGI Symbol;Acc:MGI:5580372]	A0A087WQ99		5.8	2.0E-07	5.5	4.7E-02	-0.9	7.4E-01	-0.2	9.2E-01
ENSMUST00000189186	lymphocyte antigen 6 complex, locus E [Source:MGI Symbol;Acc:MGI:106651]	A0A087WNS9		3.9	7.1E-03	5.1	1.5E-04	0.8	3.1E-01	0.2	7.6E-01
ENSMUST00000189201	predicted gene, 21244 [Source:MGI Symbol;Acc:MGI:5434599]	J3QK38		5.5	1.4E-06	-2.7	1.9E-01	2.5	3.5E-02	-0.9	6.6E-01
ENSMUST00000189246	CLOCK interacting protein, circadian [Source:MGI Symbol;Acc:MGI:1919185]	Z4YJJ0		4.2	1.1E-02	-4.1	7.2E-03	-1.4	3.9E-02	-1.8	2.0E-01
ENSMUST00000189248	RIKEN cDNA 1810041L15 gene [Source:MGI Symbol;Acc:MGI:1919551]	A0A087WSN1		9.7	9.0E-04	4.1	1.3E-03	0.2	8.5E-01	0.8	2.1E-01
ENSMUST00000189268	transforming growth factor beta regulated gene 4 [Source:MGI Symbol;Acc:MGI:1100868]		Q91YM4	4.8	1.1E-02	7.1	1.2E-04	-0.5	6.6E-01	-0.5	3.9E-01
ENSMUST00000189300	CD164 antigen [Source:MGI Symbol;Acc:MGI:1859568]	A0A087WP12		-4.6	1.3E-02	7.3	2.7E-04	-0.1	9.2E-01	-0.6	4.2E-01
ENSMUST00000189301	interleukin 17F [Source:MGI Symbol;Acc:MGI:2676631]	A0A087WQB4		9.7	1.6E-05	3.0	7.1E-02	0.0	1.0E+00	1.8	1.3E-01
ENSMUST00000189314	mucin 6, gastric [Source:MGI Symbol;Acc:MGI:2663233]	Q0VAV1		5.9	5.2E-04	7.0	9.4E-05	-0.6	6.3E-01	-0.8	2.1E-01
ENSMUST00000142481				0.1	9.5E-01	0.7	5.2E-01	0.4	6.3E-01	-0.3	8.0E-01
ENSMUST00000189316	Ral GEF with PH domain and SH3 binding motif 2 [Source:MGI Symbol;Acc:MGI:1925505]	Q8C134		7.0	3.8E-05	-5.6	1.5E-03	-0.8	1.5E-01	0.2	8.9E-01
ENSMUST00000142483				2.8	9.4E-02	3.9	8.6E-02	0.1	9.5E-01	-0.9	5.1E-01
ENSMUST00000142491				-1.7	2.1E-01	-0.8	6.6E-01	0.3	8.0E-01	-0.6	7.3E-01
ENSMUST00000142495	jumonji domain containing 6 [Source:MGI Symbol;Acc:MGI:1858910]	G3UVU9		0.5	7.8E-01	-1.2	4.9E-01	-2.9	5.8E-02	-1.2	5.2E-01
ENSMUST00000142496	mitogen-activated protein kinase kinase kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346883]	D6RCZ7		-5.0	4.4E-02	-2.8	3.8E-01	1.8	3.3E-01	-0.4	8.9E-01
ENSMUST00000189341	TRAF3 interacting protein 1 [Source:MGI Symbol;Acc:MGI:1921269]	A0A087WQD8		7.0	3.6E-05	4.2	3.0E-02	-0.5	7.8E-01	0.2	8.2E-01
ENSMUST00000189403	cyclin Pas1/PHO80 domain containing 1 [Source:MGI Symbol;Acc:MGI:1916421]	A0A087WSI6		-3.0	9.2E-04	6.9	4.2E-05	0.6	4.9E-01	-0.2	7.2E-01
ENSMUST00000142508				-1.7	1.2E-01	-2.3	1.0E-01	-1.3	1.3E-01	-0.7	6.0E-01
ENSMUST00000189409	ubiquitin specific peptidase 40 [Source:MGI Symbol;Acc:MGI:2443184]	A0A087WQL1		2.8	1.1E-03	5.3	1.2E-04	-1.4	1.2E-01	-0.7	2.6E-01
ENSMUST00000189450	predicted gene 28062 [Source:MGI Symbol;Acc:MGI:5578768]	A0A087WPF1		-5.8	1.3E-03	5.1	2.2E-04	-2.7	2.6E-02	0.0	9.7E-01
ENSMUST00000142522	pleckstrin and Sec7 domain containing 4 [Source:MGI Symbol;Acc:MGI:2674093]	A0A0A6YXA6		0.5	7.6E-01	2.0	3.7E-01	1.4	4.4E-01	-0.1	9.5E-01
ENSMUST00000189452	zinc finger protein 119b [Source:MGI Symbol;Acc:MGI:2385323]	A0A087WPI5		4.3	2.0E-02	7.0	4.6E-05	-0.5	6.0E-01	0.3	5.9E-01
ENSMUST00000142530	RIKEN cDNA 4933427D14 gene [Source:MGI Symbol;Acc:MGI:1921727]	F2Z3W1		-1.1	4.8E-01	-1.7	5.6E-01	1.8	3.4E-01	2.4	3.6E-01
ENSMUST00000142531				1.2	3.1E-01	2.2	2.0E-01	0.0	1.0E+00	-1.0	4.2E-01
ENSMUST00000142532				0.2	8.5E-01	1.4	3.9E-01	0.5	6.9E-01	-0.6	6.4E-01
ENSMUST00000142539	CREB3 regulatory factor [Source:MGI Symbol;Acc:MGI:1924378]	B8JJI2		-1.1	3.5E-01	-3.7	4.9E-02	-1.1	2.6E-01	1.5	3.8E-01
ENSMUST00000189456	RIKEN cDNA 1700113H08 gene [Source:MGI Symbol;Acc:MGI:1923890]	A0A087WR28		5.6	1.1E-03	5.8	3.6E-02	-0.7	7.9E-01	1.9	2.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000189482	OVO homolog-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2388075]		D3YYM0	6.8	1.3E-04	6.3	4.4E-04	-0.6	6.6E-01	0.0	9.9E-01
ENSMUST00000142555				1.8	6.4E-01	0.8	7.9E-01	-4.4	1.8E-01	-3.4	3.1E-01
ENSMUST00000142558	cyclin-dependent kinase 4 [Source:MGI Symbol;Acc:MGI:88357]	D6RHS5		-1.4	6.1E-01	-3.5	3.2E-01	-2.5	2.2E-01	-0.4	9.1E-01
ENSMUST00000142559				-3.5	7.5E-02	0.2	9.2E-01	1.7	3.9E-01	-2.1	3.3E-01
ENSMUST00000189488	predicted gene 29096 [Source:MGI Symbol;Acc:MGI:5579802]	A0A087WRU3		6.6	6.3E-05	5.3	5.3E-03	-0.6	7.0E-01	-0.9	4.0E-01
ENSMUST00000142562				0.2	8.2E-01	-1.1	5.1E-01	0.5	6.4E-01	1.9	2.5E-01
ENSMUST00000189503	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Source:MGI Symbol;Acc:MGI:1914523]	A0A087WRD4		-7.5	2.8E-06	4.9	3.0E-03	-1.7	2.4E-01	-0.4	6.5E-01
ENSMUST00000142570				-2.2	1.8E-01	-1.5	4.2E-01	0.3	7.9E-01	-0.4	8.4E-01
ENSMUST00000142572	PHD and ring finger domains 1 [Source:MGI Symbol;Acc:MGI:2141847]	F7ANA1		-2.7	4.3E-02	-0.9	5.7E-01	1.2	2.6E-01	-0.5	7.4E-01
ENSMUST00000189528	contactin 2 [Source:MGI Symbol;Acc:MGI:104518]	A0A087WST5		8.8	1.7E-05	8.9	8.0E-04	-1.1	6.1E-01	1.3	1.5E-01
ENSMUST00000142574				3.3	5.6E-02	5.1	7.7E-03	-0.5	7.5E-01	-2.3	7.2E-02
ENSMUST00000189529	phenylalanyl-tRNA synthetase, beta subunit [Source:MGI Symbol;Acc:MGI:1346035]	A0A087WQ15		-5.5	1.0E-02	5.9	6.5E-03	2.2	2.0E-01	-0.1	8.9E-01
ENSMUST00000142577				0.0	1.0E+00	0.5	5.3E-01	0.4	4.8E-01	-0.1	9.0E-01
ENSMUST00000189540	meiosis defective 1 [Source:MGI Symbol;Acc:MGI:3028590]		Q9D4I2	6.9	1.9E-02	-4.6	2.1E-03	-1.9	1.2E-02	-2.2	1.4E-01
ENSMUST00000189542	nucleic acid binding protein 1 [Source:MGI Symbol;Acc:MGI:1923258]		Q8BGW5	-4.0	2.3E-02	6.9	1.5E-04	-0.4	7.1E-01	0.1	8.8E-01
ENSMUST00000142593				0.3	8.3E-01	-4.7	3.9E-03	-5.3	1.7E-04	-0.3	8.1E-01
ENSMUST00000189545	RAS protein-specific guanine nucleotide-releasing factor 1 [Source:MGI Symbol;Acc:MGI:99694]	A0A087WS68		9.4	3.0E-06	2.2	1.2E-01	0.0	9.9E-01	0.5	6.1E-01
ENSMUST00000189556	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4 [Source:MGI Symbol;Acc:MGI:106018]	A0A087WRA0		5.6	4.3E-06	-3.9	1.6E-02	0.9	1.9E-01	0.6	6.5E-01
ENSMUST00000189588	transmembrane protein 108 [Source:MGI Symbol;Acc:MGI:1932411]		Q8BHE4	7.3	1.4E-02	4.1	3.2E-04	-1.9	3.3E-02	-0.2	7.3E-01
ENSMUST00000189592	predicted gene, 21677 [Source:MGI Symbol;Acc:MGI:5435032]		O35698	6.1	2.0E-02	-6.0	1.8E-05	-0.2	6.4E-01	-1.0	2.1E-01
ENSMUST00000189593	protamine 2 [Source:MGI Symbol;Acc:MGI:97766]	Q545M0	P07978	7.2	4.8E-05	7.6	1.2E-05	-1.2	2.5E-01	-0.4	3.6E-01
ENSMUST00000189605	abhydrolase domain containing 17A [Source:MGI Symbol;Acc:MGI:106388]	A0A087WST3		-3.2	8.9E-03	4.8	1.1E-05	-0.9	1.3E-01	0.2	6.3E-01
ENSMUST00000189644	menage a trois 1 [Source:MGI Symbol;Acc:MGI:106207]	A0A087WSQ7		-4.6	1.3E-04	5.1	1.1E-03	-0.6	6.0E-01	1.2	8.4E-02
ENSMUST00000142613	vesicle-associated membrane protein 8 [Source:MGI Symbol;Acc:MGI:1336882]			-0.2	7.3E-01	0.2	8.6E-01	0.3	6.2E-01	-0.1	9.3E-01
ENSMUST00000189655	tRNA methyltransferase 1 like [Source:MGI Symbol;Acc:MGI:1916185]	A0A087WQ23		-7.5	6.2E-04	5.2	5.5E-03	-1.8	2.7E-01	0.0	1.0E+00
ENSMUST00000142616	telomeric repeat binding factor 2 [Source:MGI Symbol;Acc:MGI:1195972]	F6VIR4		-1.1	1.9E-01	2.7	2.0E-02	1.7	5.6E-02	-2.1	3.5E-02
ENSMUST00000189664	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Source:MGI Symbol;Acc:MGI:2443241]	A0A087WRY4		2.3	1.0E-02	7.6	3.2E-05	-0.1	9.4E-01	0.6	2.3E-01
ENSMUST00000189665	autophagy related 9A [Source:MGI Symbol;Acc:MGI:2138446]	A0A087WQ26		-3.9	2.6E-03	5.8	4.2E-04	1.2	2.5E-01	0.5	4.8E-01
ENSMUST00000189670	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]	A0A087WRV6		-8.4	9.0E-05	5.8	3.5E-04	-0.6	6.0E-01	0.6	3.4E-01
ENSMUST00000189688	hemopoietic cell kinase [Source:MGI Symbol;Acc:MGI:96052]		P08103	-6.5	5.6E-06	-5.4	7.3E-02	1.0	3.8E-01	-1.2	7.0E-01
ENSMUST00000142629	Xrcc1 N-terminal domain containing 1 [Source:MGI Symbol;Acc:MGI:5546359]	F6R278		3.3	7.2E-02	2.3	2.5E-01	-1.1	5.5E-01	0.0	1.0E+00
ENSMUST00000142630				2.2	5.8E-02	3.6	8.1E-03	-0.4	6.8E-01	-1.9	6.0E-02
ENSMUST00000189694	protein phosphatase 1, regulatory subunit 26 [Source:MGI Symbol;Acc:MGI:2685193]		Q6A025	8.5	9.4E-04	6.8	1.5E-05	-1.4	1.5E-01	-0.8	1.4E-01
ENSMUST00000189697	G protein-coupled receptor 35 [Source:MGI Symbol;Acc:MGI:1929509]	A0A087WPI1		4.4	3.6E-06	4.9	3.9E-02	-0.6	7.7E-01	1.2	3.7E-01
ENSMUST00000189704	RIKEN cDNA 1700020D05 gene [Source:MGI Symbol;Acc:MGI:1922805]	Q99PB1		2.3	5.4E-03	-2.6	3.1E-02	0.3	6.5E-01	0.4	7.0E-01
ENSMUST00000189707	protein phosphatase 2 (formerly 2A), regulatory subunit B", delta [Source:MGI Symbol;Acc:MGI:1335093]	A0A087WS63		-3.1	3.5E-03	6.0	4.8E-04	-0.5	6.8E-01	0.6	3.8E-01
ENSMUST00000142640	oteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki) [Source:MGI Symbol;Acc:MGI:10963(	A2A4J3		2.6	8.3E-02	4.1	1.0E-02	-1.0	4.6E-01	-2.5	4.9E-02
ENSMUST00000189718	CD22 antigen [Source:MGI Symbol;Acc:MGI:88322]	Q3UP36		7.1	8.9E-04	0.0	9.9E-01	1.9	8.3E-02	-2.1	1.5E-01
ENSMUST00000189735	doublecortin domain containing 2C [Source:MGI Symbol;Acc:MGI:1915761]		Q9D1B8	5.3	5.8E-04	3.9	2.0E-04	-0.9	2.0E-01	-0.1	7.6E-01
ENSMUST00000189749	dynein, axonemal, heavy chain 7C [Source:MGI Symbol;Acc:MGI:3639762]	A0A087WR13		8.3	1.8E-05	5.3	8.2E-03	0.2	9.1E-01	-0.4	7.0E-01
ENSMUST00000189753	SH2 domain containing 1A [Source:MGI Symbol;Acc:MGI:1328352]	Q544F1	O88890	8.8	7.5E-05	3.7	2.4E-02	-0.2	8.5E-01	-0.6	5.0E-01
ENSMUST00000189788	lactate dehydrogenase A-like 6B [Source:MGI Symbol;Acc:MGI:2146830]	Q8BVP2		5.6	9.4E-05	7.0	3.0E-04	-0.2	9.0E-01	-0.3	6.6E-01
ENSMUST00000189837	RIKEN cDNA 2810474O19 gene [Source:MGI Symbol;Acc:MGI:1914496]	A0A087WP74		-4.7	1.4E-03	3.6	6.7E-04	0.6	3.7E-01	0.0	9.4E-01
ENSMUST00000142663	Hermansky-Pudlak syndrome 5 homolog (human) [Source:MGI Symbol;Acc:MGI:2180307]		P59438	-5.3	4.9E-02	1.9	5.9E-01	6.0	3.7E-02	-1.2	7.0E-01
ENSMUST00000189849	cystin 1 [Source:MGI Symbol;Acc:MGI:2177632]			5.7	1.8E-02	-3.6	1.2E-02	-0.3	5.4E-01	-0.3	7.8E-01
ENSMUST00000189851	olfactory receptor 1392 [Source:MGI Symbol;Acc:MGI:3031226]	Q8VFA6		5.3	7.7E-04	3.4	1.6E-03	0.1	9.2E-01	-0.3	6.0E-01
ENSMUST00000142672				0.6	8.1E-01	-3.7	2.8E-01	-4.4	5.3E-02	-0.1	9.8E-01
ENSMUST00000189874	GPI-anchored HDL-binding protein 1 [Source:MGI Symbol;Acc:MGI:1915703]	A0A087WPI6		6.5	9.0E-05	6.2	3.0E-04	-0.6	6.1E-01	0.2	7.0E-01
ENSMUST00000189877	leucine rich repeat and fibronectin type III domain containing 1 [Source:MGI Symbol;Acc:MGI:2136810]		Q2WF71	5.9	2.0E-03	5.5	2.1E-04	0.4	6.6E-01	-0.4	5.1E-01
ENSMUST00000189878	H domain containing, RNA binding, signal transduction associated 2 [Source:MGI Symbol;Acc:MGI:2159649	A0A087WSL3		6.7	2.2E-05	-5.1	3.3E-02	-0.8	3.5E-01	-0.7	7.8E-01
ENSMUST00000189897	myelin regulatory factor [Source:MGI Symbol;Acc:MGI:2684944]		Q3UR85	5.5	9.6E-03	4.6	4.5E-03	0.8	5.5E-01	0.6	4.1E-01
ENSMUST00000189911	olfactory receptor 318 [Source:MGI Symbol;Acc:MGI:3030152]	Q5NCD7		6.4	9.7E-05	2.2	4.6E-01	-0.5	8.4E-01	2.9	2.2E-01
ENSMUST00000189936	ubiquitin carboxyl-terminal esterase L5 [Source:MGI Symbol;Acc:MGI:1914848]		Q9WUP7	-5.3	2.6E-03	-3.5	3.7E-03	0.8	1.0E-01	0.5	6.0E-01
ENSMUST00000142684				0.7	3.3E-01	2.3	2.6E-02	1.1	1.6E-01	-0.5	4.8E-01
ENSMUST00000142685				1.0	1.7E-01	1.8	5.7E-02	0.4	6.0E-01	-0.4	5.8E-01
ENSMUST00000189946	nuclear casein kinase and cyclin-dependent kinase substrate 1 [Source:MGI Symbol;Acc:MGI:1934811]	A0A087WRY3		2.1	1.0E-02	7.0	7.7E-05	-0.5	6.5E-01	-0.7	2.4E-01
ENSMUST00000189980	abl-interactor 2 [Source:MGI Symbol;Acc:MGI:106913]	Q6AXH6		6.1	1.2E-03	5.1	8.2E-05	0.5	4.6E-01	-0.3	6.0E-01
ENSMUST00000142693				1.3	1.5E-01	4.6	3.2E-03	2.2	6.2E-02	-1.1	2.1E-01
ENSMUST00000189991	gamma-glutamyltransferase 5 [Source:MGI Symbol;Acc:MGI:1346063]	A0A087WSM3		-3.4	7.3E-03	5.8	1.3E-03	-0.7	6.2E-01	0.4	6.1E-01
ENSMUST00000142701	BRCA1 associated protein [Source:MGI Symbol;Acc:MGI:1919649]	A0A0G2JF68		1.3	1.1E-01	2.5	2.7E-02	0.3	7.0E-01	-0.8	3.1E-01
ENSMUST00000189999	B cell leukemia/lymphoma 2 [Source:MGI Symbol;Acc:MGI:88138]	Q6NTH7	P10417	5.5	4.7E-05	3.7	2.0E-03	-1.4	1.6E-01	-0.2	7.9E-01
ENSMUST00000142718	myelin basic protein expression factor 2, repressor [Source:MGI Symbol;Acc:MGI:104592]	A2ATP6		4.4	4.1E-02	-3.3	1.1E-01	-6.4	3.7E-03	1.4	4.9E-01
ENSMUST00000142724				0.7	4.9E-01	3.1	1.1E-02	-0.1	9.3E-01	-2.5	2.7E-02
ENSMUST00000142726				1.0	5.8E-01	-1.5	5.5E-01	-2.3	2.0E-01	0.3	9.0E-01
ENSMUST00000190029	matrin 3 [Source:MGI Symbol;Acc:MGI:1298379]	Q5BL18	Q8K310	-7.5	3.6E-04	3.1	5.1E-03	0.0	9.5E-01	-0.4	5.7E-01
ENSMUST00000142733				-0.2	8.1E-01	1.6	1.2E-01	-0.3	7.3E-01	-2.1	4.4E-02
ENSMUST00000190078	centrosomal protein 70 [Source:MGI Symbol;Acc:MGI:1915371]	A0A087WSG9		4.9	3.2E-03	-4.7	7.4E-03	-0.1	8.2E-01	-0.9	5.5E-01
ENSMUST00000190103	nucleic acid binding protein 1 [Source:MGI Symbol;Acc:MGI:1923258]		Q8BGW5	-7.1	2.0E-02	-3.2	1.5E-02	-0.9	2.3E-01	-0.4	7.1E-01
ENSMUST00000142736				-2.8	2.2E-01	0.2	9.3E-01	0.7	7.2E-01	-2.3	3.6E-01
ENSMUST00000190116	THAP domain containing 4 [Source:MGI Symbol;Acc:MGI:1914276]		Q6P3Z3	5.8	4.2E-05	5.8	8.0E-04	-0.5	6.8E-01	0.6	3.9E-01
ENSMUST00000142739	nemo like kinase [Source:MGI Symbol;Acc:MGI:1201387]		O54949	0.9	3.8E-02	0.7	2.2E-01	0.2	5.8E-01	0.5	3.3E-01
ENSMUST00000190155	(constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana) [Source:MGI Symbol;Acc:MGI:13	A0A087WQ60		-6.2	1.3E-04	9.3	2.4E-06	-1.4	2.0E-01	0.3	4.9E-01
ENSMUST00000190157	RIKEN cDNA 2610044O15 gene [Source:MGI Symbol;Acc:MGI:1919389]	Q8BG62		2.1	1.7E-03	3.1	1.9E-02	-1.1	3.0E-01	-0.7	4.5E-01
ENSMUST00000190193	collagen, type VI, alpha 5 [Source:MGI Symbol;Acc:MGI:3648134]		A6H584	8.8	3.0E-06	-6.2	6.4E-03	-0.1	8.8E-01	-0.9	6.5E-01
ENSMUST00000190195	LMBR1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1915671]	A0A087WR85		-5.4	4.3E-04	6.5	2.0E-03	1.7	2.8E-01	-0.5	5.6E-01
ENSMUST00000142763				1.4	1.2E-01	1.4	1.7E-01	-0.2	8.0E-01	-0.2	8.0E-01
ENSMUST00000190196	proline rich basic protein 1 [Source:MGI Symbol;Acc:MGI:2686460]	A0A087WR45		8.5	5.3E-05	5.7	2.1E-03	-0.3	8.1E-01	0.7	3.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000190212	sialidase 4 [Source:MGI Symbol;Acc:MGI:2661364]	C5NTX9	Q8BZL1	6.8	2.3E-04	6.6	9.0E-04	-0.8	5.4E-01	1.0	2.3E-01
ENSMUST00000142768				-1.1	2.6E-01	-1.1	4.0E-01	0.0	9.6E-01	0.0	9.8E-01
ENSMUST00000190213	caspase 8 [Source:MGI Symbol;Acc:MGI:1261423]	A0A087WQT6		-6.6	3.7E-04	6.1	9.2E-06	-0.5	4.4E-01	0.3	5.3E-01
ENSMUST00000190222	C-type lectin domain family 18, member A [Source:MGI Symbol;Acc:MGI:2672935]	A0A087WP55		7.6	3.3E-04	6.1	4.2E-05	-0.3	7.3E-01	-0.4	4.6E-01
ENSMUST00000142771				3.3	4.4E-02	4.3	4.6E-02	0.2	9.1E-01	-0.8	5.5E-01
ENSMUST00000190233	RIKEN cDNA 1700025B11 gene [Source:MGI Symbol;Acc:MGI:1923659]	A0A087WNZ6		7.1	4.9E-05	6.6	2.3E-03	-0.8	6.6E-01	-0.3	7.2E-01
ENSMUST00000190240	family with sequence similarity 134, member A [Source:MGI Symbol;Acc:MGI:2388278]		Q6NS82	-6.3	9.0E-04	-4.6	5.9E-03	-0.8	1.7E-01	1.6	2.3E-01
ENSMUST00000190245	nei endonuclease VIII-like 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1920024]		Q8K4Q6	2.9	2.2E-03	5.5	6.7E-04	-0.9	4.4E-01	0.3	6.7E-01
ENSMUST00000190262	lymphocyte antigen 6 complex, locus G [Source:MGI Symbol;Acc:MGI:109440]	A0A087WQF5		-8.4	3.3E-06	5.9	4.4E-04	-0.5	6.7E-01	-0.5	4.8E-01
ENSMUST00000142778				-0.3	7.8E-01	0.7	5.6E-01	0.2	8.1E-01	-0.8	5.1E-01
ENSMUST00000190268	proline rich 29 [Source:MGI Symbol;Acc:MGI:1922823]	A0A087WPX8		5.1	3.5E-04	5.9	6.4E-04	-0.6	6.6E-01	-0.6	4.1E-01
ENSMUST00000190279	anaphase promoting complex subunit 13 [Source:MGI Symbol;Acc:MGI:1916260]		Q8R034	-4.3	3.7E-03	4.4	3.2E-03	-0.8	4.8E-01	-0.9	2.8E-01
ENSMUST00000190298	neuron navigator 1 [Source:MGI Symbol;Acc:MGI:2183683]		Q8CH77	3.6	4.6E-03	2.9	7.1E-03	-1.1	1.8E-01	-0.3	6.8E-01
ENSMUST00000190315	predicted gene, 21874 [Source:MGI Symbol;Acc:MGI:5434038]	J3QNZ6		9.4	2.8E-06	-4.0	1.7E-03	-0.6	1.7E-01	-1.8	1.1E-01
ENSMUST00000190323	neutrophil cytosolic factor 2 [Source:MGI Symbol;Acc:MGI:97284]	A0A087WPH0		-5.4	6.4E-04	-2.0	1.1E-01	0.8	2.6E-01	-0.6	6.1E-01
ENSMUST00000142797				3.1	4.3E-02	2.5	1.2E-01	-1.0	4.5E-01	-0.4	7.4E-01
ENSMUST00000190339	m large conductance calcium-activated channel, subfamily M, alpha member 1 [Source:MGI Symbol;Acc:MGI	A0A087WSQ4		7.2	9.8E-05	7.7	7.4E-04	1.6	2.8E-01	0.7	4.2E-01
ENSMUST00000190348	cAMP responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:88494]	Q547S9	Q01147	-3.7	4.5E-03	4.9	1.8E-03	-0.9	4.6E-01	0.2	7.5E-01
ENSMUST00000190349	predicted gene, 20806 [Source:MGI Symbol;Acc:MGI:5434162]	Q9D9T3		6.5	1.3E-03	6.2	1.7E-04	-0.5	6.2E-01	-0.6	3.5E-01
ENSMUST00000190368	predicted gene 28465 [Source:MGI Symbol;Acc:MGI:5579171]	A0A087WSK3		5.0	1.8E-04	3.8	9.4E-03	-1.8	1.7E-01	-0.3	7.3E-01
ENSMUST00000190387	lipid phosphate phosphatase-related protein type 2 [Source:MGI Symbol;Acc:MGI:2384575]		Q8VCY8	6.4	1.6E-02	-2.9	4.8E-02	0.1	9.2E-01	0.0	9.7E-01
ENSMUST00000190391	predicted gene, 21854 [Source:MGI Symbol;Acc:MGI:5434018]	A0A087WNM4		5.0	1.5E-03	6.2	4.3E-06	0.0	9.9E-01	0.0	9.2E-01
ENSMUST00000190393	mutS homolog 3 (E. coli) [Source:MGI Symbol;Acc:MGI:109519]	A0A087WSS2		6.8	3.6E-07	4.6	2.2E-02	-0.4	7.8E-01	0.0	9.7E-01
ENSMUST00000142819	DnaJ (Hsp40) homolog, subfamily B, member 12 [Source:MGI Symbol;Acc:MGI:1931881]		Q9QYI4	1.5	8.1E-02	1.0	3.1E-01	-0.4	6.6E-01	0.2	8.1E-01
ENSMUST00000142820	RAB22A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:105072]	D6RFT6		1.3	6.4E-01	1.6	6.6E-01	1.5	6.5E-01	1.1	6.9E-01
ENSMUST00000190404	ribulose-5-phosphate-3-epimerase [Source:MGI Symbol;Acc:MGI:1913896]	A0A087WQM3		-4.3	3.8E-03	6.8	2.6E-04	0.9	4.5E-01	1.2	6.8E-02
ENSMUST00000190433	secreted Ly6/Plaur domain containing 1 [Source:MGI Symbol;Acc:MGI:1930923]		Q9Z0K7	8.5	3.9E-05	6.7	6.3E-04	0.4	7.7E-01	-1.0	2.1E-01
ENSMUST00000190436	cDNA sequence CN725425 [Source:MGI Symbol;Acc:MGI:3613655]	A0A087WRU1		4.8	2.3E-02	4.6	1.6E-02	-0.5	7.8E-01	1.0	3.5E-01
ENSMUST00000142837	DENN/MADD domain containing 4C [Source:MGI Symbol;Acc:MGI:1914769]		A6H8H2	0.1	9.5E-01	-2.4	4.9E-01	-1.3	5.1E-01	1.3	7.1E-01
ENSMUST00000190447	MX dynamin-like GTPase 2 [Source:MGI Symbol;Acc:MGI:97244]			6.9	5.3E-05	5.3	1.9E-02	-0.8	6.9E-01	-0.6	6.1E-01
ENSMUST00000190456	keratin associated protein 5-2 [Source:MGI Symbol;Acc:MGI:1918873]	A0A087WRV2		8.5	6.1E-05	6.6	7.1E-04	-0.5	7.0E-01	1.2	1.4E-01
ENSMUST00000190457	RIKEN cDNA 2210011C24 gene [Source:MGI Symbol;Acc:MGI:1917384]	A0A087WQ89		6.0	1.4E-04	2.3	9.2E-02	-0.2	8.2E-01	0.8	4.1E-01
ENSMUST00000142844				-0.5	5.8E-01	0.9	4.4E-01	0.1	9.1E-01	-1.2	2.5E-01
ENSMUST00000190472	RIKEN cDNA 2410004B18 gene [Source:MGI Symbol;Acc:MGI:1913671]	A0A087WQ28		-6.3	1.7E-05	-3.3	5.0E-02	0.4	6.3E-01	-0.6	7.2E-01
ENSMUST00000190495	omosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1	Q3ULG5		4.3	1.3E-02	4.9	2.4E-04	-1.7	8.9E-02	-0.7	2.9E-01
ENSMUST00000142867	UBX domain protein 2A [Source:MGI Symbol;Acc:MGI:2442310]		Q99KJ0	1.3	5.8E-01	4.6	9.2E-02	0.3	8.9E-01	-3.0	2.1E-01
ENSMUST00000190496	protein phosphatase 1, regulatory subunit 18 [Source:MGI Symbol;Acc:MGI:1923698]	A0A087WRI9		-11.0	6.4E-05	-1.2	3.8E-01	0.5	5.2E-01	-1.6	2.9E-01
ENSMUST00000190522	predicted gene 6976 [Source:MGI Symbol;Acc:MGI:3644617]	A0A087WS10		7.1	6.5E-05	4.5	2.0E-03	0.6	5.7E-01	-0.8	2.8E-01
ENSMUST00000190549	kin of IRRE like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:1914953]	A0A087WPC0		3.1	3.0E-02	6.9	1.8E-04	-0.1	9.4E-01	-0.3	6.4E-01
ENSMUST00000190564	WD repeat domain containing 82 [Source:MGI Symbol;Acc:MGI:1924555]	A0A087WQ38		-3.0	1.7E-02	-1.8	3.3E-02	1.2	2.2E-02	0.2	8.0E-01
ENSMUST00000190565	spermiogenesis specific transcript on the Y 2 [Source:MGI Symbol;Acc:MGI:1917259]	Q149W4		7.0	5.6E-05	5.1	8.3E-02	1.3	6.1E-01	1.8	2.8E-01
ENSMUST00000190574	zinc finger, BED type containing 6 [Source:MGI Symbol;Acc:MGI:3828086]	G0LE24	D2EAC2	-4.4	5.1E-03	-7.1	4.4E-05	-0.5	1.1E-01	-0.1	9.1E-01
ENSMUST00000142902				2.6	1.7E-01	3.5	1.4E-01	-0.2	9.1E-01	-1.2	4.6E-01
ENSMUST00000190618	DIS3 mitotic control homolog (S. cerevisiae)-like 2 [Source:MGI Symbol;Acc:MGI:2442555]	A0A087WP08		5.9	2.1E-04	6.7	2.1E-04	-0.5	6.9E-01	-1.9	1.9E-02
ENSMUST00000142910				1.7	4.8E-01	1.5	6.5E-01	-0.4	8.7E-01	-0.2	9.4E-01
ENSMUST00000190626	neurexin III [Source:MGI Symbol;Acc:MGI:1096389]	A0A087WPQ9		7.3	5.8E-04	7.6	4.2E-04	-0.7	6.6E-01	-0.3	6.9E-01
ENSMUST00000190641	aturin, neural progenitor differentiation regulator homolog (Xenopus) [Source:MGI Symbol;Acc:MGI:191548		Q8CGA4	3.0	7.9E-05	3.2	7.1E-02	-1.2	4.6E-01	1.3	2.9E-01
ENSMUST00000190647	brain-enriched guanylate kinase-associated [Source:MGI Symbol;Acc:MGI:3044626]	F8WIG2		8.1	2.9E-05	4.4	5.4E-04	-1.5	1.3E-01	-1.3	6.3E-02
ENSMUST00000142925				-2.7	1.3E-01	-1.5	5.2E-01	0.8	6.1E-01	-0.4	8.7E-01
ENSMUST00000142926				0.4	4.3E-01	1.3	7.2E-02	-0.4	4.0E-01	-1.3	5.1E-02
ENSMUST00000190648	Ral GEF with PH domain and SH3 binding motif 2 [Source:MGI Symbol;Acc:MGI:1925505]	A0A087WQ61		4.6	2.5E-02	7.6	4.7E-06	0.0	9.7E-01	0.5	2.3E-01
ENSMUST00000190654	alcohol dehydrogenase, iron containing, 1 [Source:MGI Symbol;Acc:MGI:1923437]	A0A087WRE7		4.0	6.5E-03	7.2	6.9E-05	-0.5	6.5E-01	-0.1	9.2E-01
ENSMUST00000142936				-3.6	6.1E-02	-5.5	4.6E-02	-1.9	9.5E-02	-0.1	9.8E-01
ENSMUST00000142938	myotubularin related protein 14 [Source:MGI Symbol;Acc:MGI:1916075]	D6RFN8		2.1	5.2E-02	2.7	7.2E-02	0.5	6.6E-01	0.0	9.7E-01
ENSMUST00000142939				-1.8	1.9E-01	-2.0	1.1E-01	-2.0	4.4E-02	-1.8	2.1E-01
ENSMUST00000142942				-0.3	5.7E-01	-0.3	5.9E-01	-0.2	7.2E-01	-0.1	8.2E-01
ENSMUST00000190679	cyclin Pas1/PHO80 domain containing 1 [Source:MGI Symbol;Acc:MGI:1916421]		Q8K158	-6.5	2.5E-05	3.9	3.3E-04	-0.6	3.6E-01	0.7	1.9E-01
ENSMUST00000190686	serine/arginine repetitive matrix 2 [Source:MGI Symbol;Acc:MGI:1923206]		Q8BTI8	-6.6	8.1E-03	4.5	1.2E-03	0.2	8.3E-01	0.8	2.3E-01
ENSMUST00000142951	nucleoporin 210 [Source:MGI Symbol;Acc:MGI:1859555]	F6XGN0		1.8	3.7E-01	0.4	8.8E-01	-1.2	5.1E-01	0.2	9.2E-01
ENSMUST00000142952	partner and localizer of BRCA2 [Source:MGI Symbol;Acc:MGI:3040695]	D6RDD1		1.5	3.8E-01	7.3	1.5E-03	0.8	6.4E-01	-5.0	3.4E-03
ENSMUST00000190696	TAR DNA binding protein [Source:MGI Symbol;Acc:MGI:2387629]	A0A087WP57		-3.7	1.1E-02	0.7	7.2E-01	2.4	1.2E-01	-2.2	2.3E-01
ENSMUST00000142959				-1.3	4.0E-01	-1.1	6.0E-01	1.0	5.0E-01	0.7	7.3E-01
ENSMUST00000190703	perilipin 4 [Source:MGI Symbol;Acc:MGI:1929709]		O88492	4.1	1.6E-04	7.0	8.5E-05	-0.6	6.0E-01	-0.9	1.4E-01
ENSMUST00000190715	centrosomal protein 70 [Source:MGI Symbol;Acc:MGI:1915371]	A0A087WQX1		6.7	7.9E-05	5.7	2.8E-05	-0.6	4.5E-01	0.4	4.4E-01
ENSMUST00000142975				-3.5	2.8E-01	-4.6	2.6E-01	-1.4	4.7E-01	-0.4	9.3E-01
ENSMUST00000190723	kinesin family member 1A [Source:MGI Symbol;Acc:MGI:108391]	A0A087WQE8		8.1	5.3E-05	-3.2	1.3E-01	0.7	5.5E-01	0.1	9.5E-01
ENSMUST00000142980				-0.2	8.2E-01	-0.2	8.7E-01	-0.2	8.6E-01	-0.2	8.5E-01
ENSMUST00000190729	adenylate kinase 6 [Source:MGI Symbol;Acc:MGI:5510732]	A0A087WRI5		-5.0	5.9E-03	3.8	5.1E-03	-0.3	7.5E-01	-0.3	7.4E-01
ENSMUST00000142989				-0.7	4.4E-01	-1.5	2.2E-01	0.1	9.2E-01	0.9	4.5E-01
ENSMUST00000142993	NFKB inhibitor interacting Ras-like protein 2 [Source:MGI Symbol;Acc:MGI:1919216]	F6XZA4		3.9	4.9E-02	2.7	2.0E-01	-2.3	2.8E-01	-1.1	4.6E-01
ENSMUST00000142994	transmembrane protein 180 [Source:MGI Symbol;Acc:MGI:1922396]	D6RFE3		1.8	4.4E-01	1.2	7.3E-01	0.3	8.9E-01	0.9	7.7E-01
ENSMUST00000142997	methyl-CpG binding domain protein 3 [Source:MGI Symbol;Acc:MGI:1333812]	F6WZH1		-1.8	5.3E-02	-1.1	3.2E-01	0.4	5.6E-01	-0.3	7.7E-01
ENSMUST00000190736	UBX domain protein 4 [Source:MGI Symbol;Acc:MGI:1915062]	A0A087WSK5		-5.0	8.2E-05	0.0	9.9E-01	0.6	5.8E-01	-3.1	5.8E-02
ENSMUST00000190780	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]	B9EHT6		-7.6	1.0E-02	4.0	3.9E-03	1.0	3.0E-01	-0.2	7.4E-01
ENSMUST00000143024				2.3	2.9E-01	2.7	2.8E-01	0.1	9.6E-01	-0.3	8.9E-01
ENSMUST00000143026	cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:1889272]	E0CY16		3.9	1.3E-01	2.8	3.4E-01	-0.3	9.2E-01	0.9	6.5E-01
ENSMUST00000190824	olute carrier family 22 (organic anion/cation transporter), member 15 [Source:MGI Symbol;Acc:MGI:3607704	A0A087WNW1		-6.3	3.6E-05	3.8	1.6E-03	-0.2	8.4E-01	-0.1	8.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000143031	spectrin repeat containing, nuclear envelope 2 [Source:MGI Symbol;Acc:MGI:2449316]	E9QP46		-0.4	4.8E-01	0.9	2.1E-01	0.9	1.3E-01	-0.5	4.8E-01
ENSMUST00000190827	VGF nerve growth factor inducible [Source:MGI Symbol;Acc:MGI:1343180]	Q0VGU4		7.2	6.1E-05	4.3	1.0E-02	0.3	8.0E-01	-0.4	6.2E-01
ENSMUST00000190840	teneurin transmembrane protein 3 [Source:MGI Symbol;Acc:MGI:1345183]	G3X907		8.7	4.4E-06	8.0	6.6E-06	-2.4	3.8E-02	-0.3	5.0E-01
ENSMUST00000190844	olfactory receptor 1411 [Source:MGI Symbol;Acc:MGI:3031245]	Q8VFC4		6.7	6.1E-05	6.9	5.7E-07	-0.7	2.3E-01	-0.3	3.3E-01
ENSMUST00000143039				0.6	5.1E-01	2.3	4.3E-02	0.0	9.6E-01	-1.8	6.7E-02
ENSMUST00000143040	splA/ryanodine receptor domain and SOCS box containing 2 [Source:MGI Symbol;Acc:MGI:1315199]	D3YX10		-3.0	4.9E-02	1.6	3.2E-01	1.8	1.6E-01	-2.7	8.9E-02
ENSMUST00000190876	cAMP responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:88494]	Q61441		-4.0	2.5E-03	5.4	7.6E-04	-0.8	5.0E-01	-0.4	5.6E-01
ENSMUST00000190900	aminoacylase 1 [Source:MGI Symbol;Acc:MGI:87913]	A0A087WRE0		5.4	3.4E-04	4.8	7.6E-04	-1.2	2.6E-01	1.4	4.7E-02
ENSMUST00000143051	tau tubulin kinase 2 [Source:MGI Symbol;Acc:MGI:2155779]	A2AW13		1.7	3.8E-01	1.4	5.5E-01	-0.6	7.2E-01	-0.3	8.7E-01
ENSMUST00000143052	vascular endothelial zinc finger 1 [Source:MGI Symbol;Acc:MGI:1313291]	Q5SXC3		-0.4	8.7E-01	0.3	9.1E-01	0.6	7.9E-01	-0.1	9.6E-01
ENSMUST00000143054	3 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:191		P61216	0.0	9.9E-01	-1.2	1.3E-01	-1.4	2.0E-02	-0.2	7.4E-01
ENSMUST00000190907	mucin 6, gastric [Source:MGI Symbol;Acc:MGI:2663233]	A0A087WR59		9.4	6.6E-04	4.4	9.2E-02	-1.8	4.9E-01	0.4	8.2E-01
ENSMUST00000190940	dishevelled 2, dsh homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:106613]		Q60838	1.6	3.5E-02	5.5	1.5E-03	-0.6	6.7E-01	-1.5	8.6E-02
ENSMUST00000190993	serine/arginine-rich splicing factor 2 [Source:MGI Symbol;Acc:MGI:98284]		Q62093	-5.5	3.7E-03	5.0	2.1E-03	-1.0	4.6E-01	-0.1	9.3E-01
ENSMUST00000143069				1.4	3.4E-01	1.3	4.2E-01	-0.7	6.2E-01	-0.6	6.9E-01
ENSMUST00000143073				2.3	5.9E-02	0.7	5.3E-01	-2.8	2.0E-02	-1.2	2.4E-01
ENSMUST00000190995	angiotensin I converting enzyme (peptidyl-dipeptidase A) 3 [Source:MGI Symbol;Acc:MGI:3644400]	D0G895		6.9	1.2E-04	9.4	3.1E-06	0.2	8.2E-01	1.0	6.9E-02
ENSMUST00000143076				1.7	2.2E-01	2.7	1.7E-01	1.0	5.4E-01	0.0	9.8E-01
ENSMUST00000143078				-2.0	1.2E-01	-0.3	8.4E-01	0.4	6.8E-01	-1.3	3.4E-01
ENSMUST00000190997	retinoblastoma binding protein 5 [Source:MGI Symbol;Acc:MGI:1918367]		Q8BX09	-3.1	1.8E-02	2.9	5.5E-03	0.9	2.1E-01	0.3	6.7E-01
ENSMUST00000191010	ciliogenesis associated TTC17 interacting protein [Source:MGI Symbol;Acc:MGI:2685062]		B9EKE5	3.4	5.2E-03	17.2	6.1E-06	0.9	6.4E-01	0.1	8.6E-01
ENSMUST00000191011	amyloid beta (A4) precursor protein-binding, family B, member 1 [Source:MGI Symbol;Acc:MGI:107765]			6.3	9.4E-04	0.0	9.6E-01	0.7	2.6E-01	-1.9	5.3E-02
ENSMUST00000191030	C-type lectin domain family 18, member A [Source:MGI Symbol;Acc:MGI:2672935]		Q7TSQ1	4.1	1.3E-03	8.0	2.8E-04	1.2	3.9E-01	0.4	5.8E-01
ENSMUST00000191035	leucine rich repeat containing 28 [Source:MGI Symbol;Acc:MGI:1915689]	Q8C1S3		-3.9	3.0E-03	5.2	6.7E-05	-0.1	9.4E-01	-1.4	2.3E-02
ENSMUST00000191046	erythrocyte membrane protein band 4.1 like 5 [Source:MGI Symbol;Acc:MGI:103006]		Q8BGS1	6.7	3.0E-05	6.4	3.1E-03	-0.6	7.2E-01	-2.1	6.3E-02
ENSMUST00000191104	tensin 1 [Source:MGI Symbol;Acc:MGI:104552]	A0A087WQS0		-6.6	4.2E-03	-3.2	2.2E-03	-0.5	3.0E-01	-1.1	2.1E-01
ENSMUST00000143115				1.8	1.3E-01	2.4	6.8E-02	-1.2	2.7E-01	-1.8	1.2E-01
ENSMUST00000143125	aminolevulinic acid synthase 1 [Source:MGI Symbol;Acc:MGI:87989]	F6RYA6		-1.7	5.6E-02	-0.1	8.9E-01	-0.3	6.0E-01	-1.9	4.5E-02
ENSMUST00000191108	serine/threonine kinase 16 [Source:MGI Symbol;Acc:MGI:1313271]	Q05DP1		-6.8	4.3E-04	5.7	2.6E-03	-0.6	6.9E-01	-0.2	8.5E-01
ENSMUST00000143137	ectonucleotide pyrophosphatase/phosphodiesterase 4 [Source:MGI Symbol;Acc:MGI:2682634]		Q8BTJ4	1.4	1.1E-01	-4.3	2.9E-02	-0.4	5.5E-01	5.3	1.0E-02
ENSMUST00000191124	Parkinson disease (autosomal recessive, juvenile) 2, parkin [Source:MGI Symbol;Acc:MGI:1355296]		Q9WVS6	5.8	1.1E-02	8.2	6.1E-05	-0.1	9.1E-01	-1.0	1.1E-01
ENSMUST00000191127	lymphocyte antigen 6 complex, locus E [Source:MGI Symbol;Acc:MGI:106651]	A0A087WPY4		-6.3	1.7E-03	-5.0	1.2E-01	2.8	3.9E-02	-1.3	7.0E-01
ENSMUST00000143146				0.0	9.8E-01	-1.7	1.3E-01	-1.1	1.5E-01	0.6	5.3E-01
ENSMUST00000191142	NOP58 ribonucleoprotein [Source:MGI Symbol;Acc:MGI:1933184]		Q6DFW4	4.9	2.5E-05	3.1	2.0E-02	0.5	6.4E-01	1.6	7.3E-02
ENSMUST00000191151	predicted gene 28079 [Source:MGI Symbol;Acc:MGI:5578785]	A0A087WP82		8.2	3.0E-05	6.0	8.1E-05	-0.3	7.8E-01	0.0	9.3E-01
ENSMUST00000191169	predicted gene 6902 [Source:MGI Symbol;Acc:MGI:3647238]	Q3UTA8		4.9	1.8E-02	7.8	6.0E-05	-0.8	4.7E-01	0.1	8.4E-01
ENSMUST00000191192	nuclear protein transcription regulator 1 [Source:MGI Symbol;Acc:MGI:1891834]	A0A087WNT8		-7.1	2.3E-05	4.4	8.5E-04	0.3	7.3E-01	-0.2	7.6E-01
ENSMUST00000191201	caspase 8 [Source:MGI Symbol;Acc:MGI:1261423]	A0A087WQT6		-5.0	9.8E-04	7.1	3.8E-03	1.1	5.6E-01	1.8	9.3E-02
ENSMUST00000143168				-1.3	1.4E-01	-1.8	2.0E-01	0.3	7.0E-01	0.8	5.4E-01
ENSMUST00000191213	U2 snRNP-associated SURP domain containing [Source:MGI Symbol;Acc:MGI:1915208]	A0A087WRG2		-6.2	2.5E-03	-6.1	1.9E-04	-0.5	1.8E-01	-0.3	8.0E-01
ENSMUST00000191218	family with sequence similarity 181, member A [Source:MGI Symbol;Acc:MGI:3647570]	J3QNB7		5.5	1.4E-02	2.9	2.6E-03	0.5	3.7E-01	-0.5	4.6E-01
ENSMUST00000191234	Na+/K+ transporting ATPase interacting 2 [Source:MGI Symbol;Acc:MGI:1923447]		Q4PNJ2	6.7	7.5E-05	4.0	4.4E-04	-1.2	1.2E-01	-1.4	3.6E-02
ENSMUST00000191237	transmembrane protein 183A [Source:MGI Symbol;Acc:MGI:1914729]	A0A087WPL2		-4.2	4.2E-03	3.8	8.1E-05	1.0	5.9E-02	-0.3	5.3E-01
ENSMUST00000143180	F-box and leucine-rich repeat protein 2 [Source:MGI Symbol;Acc:MGI:1919429]	D6RFC8		-0.4	7.7E-01	4.6	2.5E-02	3.9	2.9E-02	-1.1	4.2E-01
ENSMUST00000191275	Erbb2 interacting protein [Source:MGI Symbol;Acc:MGI:1890169]	B2RUK2	Q80TH2	-4.2	1.6E-03	4.6	1.0E-04	-0.3	6.4E-01	-0.2	7.4E-01
ENSMUST00000143188	cell cycle associated protein 1 [Source:MGI Symbol;Acc:MGI:1858234]	F6YLI0		-0.1	9.5E-01	-0.9	6.7E-01	-2.6	1.3E-01	-1.7	4.9E-01
ENSMUST00000191368	ubiquitin-conjugating enzyme E2F (putative) [Source:MGI Symbol;Acc:MGI:1915171]		Q9CY34	-6.1	1.2E-03	6.3	1.6E-04	-0.5	6.5E-01	-0.3	6.4E-01
ENSMUST00000143199				0.0	9.8E-01	1.6	2.5E-01	1.1	3.5E-01	-0.4	6.6E-01
ENSMUST00000191388	RIKEN cDNA 2510002D24 gene [Source:MGI Symbol;Acc:MGI:1919557]	A0A087WSJ3		5.3	2.6E-03	5.4	1.5E-04	-0.2	8.3E-01	0.5	4.0E-01
ENSMUST00000191407	RIKEN cDNA D730001G18 gene [Source:MGI Symbol;Acc:MGI:1925975]	A0A087WRX0		7.8	9.0E-05	8.5	1.3E-03	-1.0	6.4E-01	-0.2	8.3E-01
ENSMUST00000191428	FAT tumor suppressor homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:109168]	F2Z4A3		11.1	1.2E-03	4.3	2.3E-03	-0.7	5.2E-01	0.3	6.9E-01
ENSMUST00000191431	hemopoietic cell kinase [Source:MGI Symbol;Acc:MGI:96052]	F6UND7		-6.5	5.6E-06	7.6	1.4E-05	-1.7	1.2E-01	-0.1	8.2E-01
ENSMUST00000191436	lymphocyte antigen 6 complex, locus E [Source:MGI Symbol;Acc:MGI:106651]	Q99JA5		-10.2	9.7E-04	-7.3	1.1E-04	0.7	8.0E-02	0.1	9.1E-01
ENSMUST00000191451	lymphocyte antigen 6 complex, locus C2 [Source:MGI Symbol;Acc:MGI:3712069]		P0CW03	-6.4	3.4E-03	-3.7	5.0E-03	0.5	3.4E-01	-0.7	5.2E-01
ENSMUST00000191469	C-type lectin domain family 18, member A [Source:MGI Symbol;Acc:MGI:2672935]		Q7TSQ1	6.9	1.6E-02	4.2	6.2E-03	0.7	5.3E-01	0.3	7.3E-01
ENSMUST00000143228	cyclin-dependent kinase-like 3 [Source:MGI Symbol;Acc:MGI:2388268]	F2Z3Z6		0.5	6.4E-01	1.8	1.8E-01	0.7	5.2E-01	-0.6	5.9E-01
ENSMUST00000191471	LMBR1 domain containing 1 [Source:MGI Symbol;Acc:MGI:1915671]		Q8K0B2	-7.4	1.7E-05	-4.2	3.1E-03	0.9	9.9E-02	-2.4	1.0E-01
ENSMUST00000191485	src homology 2 domain-containing transforming protein C1 [Source:MGI Symbol;Acc:MGI:98296]		P98083	-4.6	6.6E-03	1.8	2.2E-02	0.2	7.1E-01	0.0	1.0E+00
ENSMUST00000191497	ubiquitin specific peptidase 27, X chromosome [Source:MGI Symbol;Acc:MGI:1859645]		Q8CEG8	6.4	2.6E-05	5.8	4.3E-04	-0.5	6.7E-01	0.3	5.9E-01
ENSMUST00000143239				-1.5	3.0E-01	-0.6	7.5E-01	0.3	8.4E-01	-0.7	6.7E-01
ENSMUST00000143241	adaptor-related protein complex AP-4, mu 1 [Source:MGI Symbol;Acc:MGI:1337063]	E9Q416		-2.7	1.1E-01	-1.3	5.4E-01	0.7	6.2E-01	-0.7	7.3E-01
ENSMUST00000143243				1.1	2.6E-01	1.2	3.6E-01	0.7	4.5E-01	0.7	5.4E-01
ENSMUST00000191501	solute carrier family 18 (vesicular monoamine), member 3 [Source:MGI Symbol;Acc:MGI:1101061]	Q3TYJ1		8.0	5.0E-05	-3.6	8.1E-03	0.2	7.1E-01	-0.7	5.3E-01
ENSMUST00000191506	ornithine decarboxylase antizyme 3 [Source:MGI Symbol;Acc:MGI:1858170]	A0A087WNM3		6.4	7.3E-05	6.1	1.1E-03	0.1	9.7E-01	-0.3	6.8E-01
ENSMUST00000191509	mutS homolog 3 (E. coli) [Source:MGI Symbol;Acc:MGI:109519]	A0A087WSR8		5.1	6.1E-05	6.2	3.7E-05	-2.2	3.9E-02	0.1	8.1E-01
ENSMUST00000191544	ARP3 actin-related protein 3 [Source:MGI Symbol;Acc:MGI:1921367]	A0A087WP86		-5.9	9.5E-03	-4.1	4.5E-03	1.1	6.6E-02	-1.7	2.0E-01
ENSMUST00000191578	ARP3 actin-related protein 3 [Source:MGI Symbol;Acc:MGI:1921367]	A0A087WPR6		-10.1	1.3E-02	5.1	4.2E-03	-0.5	7.2E-01	-0.1	9.1E-01
ENSMUST00000143262				2.7	1.1E-01	6.0	9.4E-03	0.5	7.9E-01	-2.8	5.5E-02
ENSMUST00000191642	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C [Source:MGI		Q64151	8.6	4.0E-04	7.8	3.5E-05	-1.1	3.5E-01	0.8	1.8E-01
ENSMUST00000143275	synaptopodin [Source:MGI Symbol;Acc:MGI:1099446]		Q8CC35	4.1	1.0E-01	5.3	3.1E-02	-3.2	2.1E-01	-4.5	1.3E-02
ENSMUST00000191670	inositol (myo)-1(or 4)-monophosphatase 1 [Source:MGI Symbol;Acc:MGI:1933158]	A0A0A6YW07		-5.9	4.9E-05	4.4	9.8E-03	1.6	2.3E-01	-0.2	7.8E-01
ENSMUST00000191677	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C [Source:MGI		Q64151	5.7	3.3E-02	4.6	1.4E-02	-1.5	3.5E-01	-1.6	1.7E-01
ENSMUST00000191689	DDB1 and CUL4 associated factor 8 [Source:MGI Symbol;Acc:MGI:91860]		Q8N7N5	-8.1	2.2E-04	6.0	2.8E-04	0.1	9.3E-01	-0.8	1.9E-01
ENSMUST00000191711	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]			-3.7	8.7E-03	4.4	1.2E-02	1.7	2.2E-01	-0.2	8.6E-01
ENSMUST00000191752	doublecortin-like kinase 2 [Source:MGI Symbol;Acc:MGI:1918012]		Q6PGN3	5.8	1.2E-04	2.9	8.9E-03	-2.3	2.7E-02	-0.4	5.5E-01
ENSMUST00000191758	RIKEN cDNA D930015E06 gene [Source:MGI Symbol;Acc:MGI:2443399]		Q3U3D7	-3.6	1.3E-02	5.8	1.4E-02	0.0	9.9E-01	-1.1	3.5E-01
ENSMUST00000143310	RNA binding motif protein, X chromosome [Source:MGI Symbol;Acc:MGI:1343044]	S4R1F6		0.7	7.4E-01	0.5	7.9E-01	-3.2	1.0E-01	-2.9	1.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000191774	YTH domain family 3 [Source:MGI Symbol;Acc:MGI:1918850]		Q8BYK6	-4.2	7.9E-03	2.0	1.3E-01	0.6	5.6E-01	1.3	2.2E-01
ENSMUST00000191775	complement component (3b/4b) receptor 1-like [Source:MGI Symbol;Acc:MGI:88513]	A0A0A6YVT1		-7.6	3.3E-05	-4.6	2.3E-03	-0.4	4.3E-01	0.2	8.4E-01
ENSMUST00000191783	zinc finger protein 639 [Source:MGI Symbol;Acc:MGI:1915028]		Q99KZ6	-4.1	5.6E-04	4.5	3.1E-03	-1.9	1.6E-01	-0.2	7.7E-01
ENSMUST00000191820	toll-like receptor 5 [Source:MGI Symbol;Acc:MGI:1858171]	Q05AH3		7.1	1.9E-04	-4.8	6.8E-02	-0.4	6.8E-01	-0.3	9.1E-01
ENSMUST00000143337	ring finger protein 38 [Source:MGI Symbol;Acc:MGI:1920719]	B1AWE7		-1.6	2.1E-01	0.6	6.5E-01	0.6	5.3E-01	-1.6	2.6E-01
ENSMUST00000191826	charged multivesicular body protein 4C [Source:MGI Symbol;Acc:MGI:1913621]	A0A0A6YWM4		6.7	3.6E-04	5.7	6.3E-03	0.4	8.1E-01	0.3	8.2E-01
ENSMUST00000191829	dachsous 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685263]	A0A0A6YW72		9.0	7.5E-06	-4.2	3.8E-02	-0.3	6.8E-01	0.3	8.6E-01
ENSMUST00000191837	protocadherin 7 [Source:MGI Symbol;Acc:MGI:1860487]	A0A0A6YY83		7.2	5.9E-05	6.3	4.1E-03	1.6	3.3E-01	0.4	6.8E-01
ENSMUST00000191854	protocadherin 15 [Source:MGI Symbol;Acc:MGI:1891428]		Q99PJ1	7.3	2.1E-05	-4.0	5.6E-03	0.1	8.7E-01	-1.1	4.2E-01
ENSMUST00000191896	zinc finger CCCH type containing 11A [Source:MGI Symbol;Acc:MGI:1917829]	Q3UL31	Q6NZF1	-5.9	1.5E-02	5.7	4.2E-06	-0.5	4.3E-01	0.2	6.0E-01
ENSMUST00000191906	MON1 homolog A (yeast) [Source:MGI Symbol;Acc:MGI:1920075]			1.9	3.5E-03	6.8	1.5E-04	-0.6	6.1E-01	0.1	8.7E-01
ENSMUST00000191936	erine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1 [Source:MGI Symbol;Acc:MGI:8809	A0A0A6YXS8		6.6	2.2E-03	6.4	1.4E-04	1.1	2.9E-01	0.4	4.7E-01
ENSMUST00000191946	major facilitator superfamily domain containing 7B [Source:MGI Symbol;Acc:MGI:2444881]	A0A0A6YWJ7		2.8	8.4E-04	4.0	1.2E-03	-0.8	3.3E-01	-1.1	1.4E-01
ENSMUST00000143373	ATPase type 13A5 [Source:MGI Symbol;Acc:MGI:2444068]	D3YU82		2.1	8.1E-02	7.4	4.5E-05	-0.5	6.3E-01	-5.9	4.4E-05
ENSMUST00000191952	jade family PHD finger 1 [Source:MGI Symbol;Acc:MGI:1925835]		Q6ZPI0	1.7	1.5E-02	5.8	8.8E-05	0.4	6.0E-01	-0.4	5.0E-01
ENSMUST00000191973	lysine (K)-specific methyltransferase 2D [Source:MGI Symbol;Acc:MGI:2682319]	A0A0A6YY77		-4.5	5.1E-03	4.8	1.6E-02	-0.4	8.2E-01	-0.5	6.1E-01
ENSMUST00000191997	glutathione peroxidase 1 [Source:MGI Symbol;Acc:MGI:104887]	A0A0A6YY34		-11.7	1.5E-04	4.2	1.6E-02	-1.2	3.8E-01	0.1	8.9E-01
ENSMUST00000192027	predicted gene, 38119 [Source:MGI Symbol;Acc:MGI:5611347]	A0A0A6YX29		6.3	7.5E-04	-4.5	8.6E-03	1.2	6.2E-02	0.2	8.7E-01
ENSMUST00000143395				-1.4	4.3E-01	-0.4	8.5E-01	-0.1	9.3E-01	-1.1	5.9E-01
ENSMUST00000143400	ankyrin repeat and SOCS box-containing 8 [Source:MGI Symbol;Acc:MGI:1925791]			-1.0	1.7E-01	-0.1	9.4E-01	1.1	1.0E-01	0.2	7.8E-01
ENSMUST00000143402				-0.5	4.3E-01	-1.6	5.9E-02	-1.1	6.7E-02	-0.1	9.3E-01
ENSMUST00000192044	ring finger and WD repeat domain 2 [Source:MGI Symbol;Acc:MGI:1347046]	A0A0A6YWC5		-5.8	8.2E-04	-2.9	6.5E-02	0.4	5.8E-01	-0.3	8.1E-01
ENSMUST00000143414	tripartite motif-containing 34A [Source:MGI Symbol;Acc:MGI:2137359]		Q99PP6	-1.0	3.5E-01	0.3	7.9E-01	0.8	4.5E-01	-0.5	6.5E-01
ENSMUST00000143415	centrosomal protein 128 [Source:MGI Symbol;Acc:MGI:1922466]	F7CIB0		1.4	5.0E-01	6.6	5.2E-02	3.7	2.2E-01	-1.4	4.5E-01
ENSMUST00000192045	predicted pseudogene 8797 [Source:MGI Symbol;Acc:MGI:3643769]	A0A0A6YW67		-6.2	5.7E-07	0.3	8.0E-01	-2.1	6.3E-02	0.9	3.8E-01
ENSMUST00000192047	selectin, lymphocyte [Source:MGI Symbol;Acc:MGI:98279]	Q3TCF3		-6.4	1.6E-05	5.1	7.9E-02	-0.7	8.1E-01	0.2	9.0E-01
ENSMUST00000192069	tenascin R [Source:MGI Symbol;Acc:MGI:99516]		Q8BYI9	8.9	1.1E-06	5.7	2.6E-03	-0.7	6.7E-01	-0.7	3.9E-01
ENSMUST00000192095	RIKEN cDNA D930015E06 gene [Source:MGI Symbol;Acc:MGI:2443399]		Q3U3D7	-7.4	7.8E-04	4.2	1.9E-02	0.0	9.8E-01	-0.2	8.7E-01
ENSMUST00000192099	TBC1 domain family, member 8 [Source:MGI Symbol;Acc:MGI:1927225]	A0A0A6YVT5		-4.2	7.4E-03	5.6	9.4E-04	-2.7	7.7E-02	-1.3	1.2E-01
ENSMUST00000143436	zinc finger and BTB domain containing 49 [Source:MGI Symbol;Acc:MGI:1922329]	D6RGL5		-2.7	4.3E-02	3.0	3.3E-02	2.5	3.4E-02	-3.1	2.4E-02
ENSMUST00000192145	LPS-responsive beige-like anchor [Source:MGI Symbol;Acc:MGI:1933162]	A0A0A6YXX3		7.0	2.1E-04	2.9	6.5E-02	0.4	7.3E-01	0.1	9.4E-01
ENSMUST00000143439				-1.6	2.4E-01	-0.1	9.7E-01	1.2	3.4E-01	-0.3	8.6E-01
ENSMUST00000192150	centromere protein L [Source:MGI Symbol;Acc:MGI:1917704]	M0QWX6		-5.9	7.5E-04	7.3	4.4E-04	1.6	2.6E-01	-0.2	8.2E-01
ENSMUST00000192155	patched homolog 1 [Source:MGI Symbol;Acc:MGI:105373]	A0A0A6YWC4		4.1	4.2E-03	-1.8	1.2E-01	1.6	2.8E-02	0.4	6.9E-01
ENSMUST00000192168	protocadherin alpha 5 [Source:MGI Symbol;Acc:MGI:1298371]	Q91Y15		7.5	1.1E-04	4.6	2.0E-02	-2.8	1.4E-01	-0.5	6.5E-01
ENSMUST00000192188	immunoglobulin heavy constant gamma 2B [Source:MGI Symbol;Acc:MGI:96445]	A0A0A6YVP0		7.1	5.3E-05	4.1	8.2E-03	-0.3	8.2E-01	-1.4	1.6E-01
ENSMUST00000192195	SLAM family member 7 [Source:MGI Symbol;Acc:MGI:1922595]			3.3	2.4E-03	-3.7	6.7E-02	0.3	7.6E-01	-1.3	5.3E-01
ENSMUST00000143463	lymphocyte antigen 9 [Source:MGI Symbol;Acc:MGI:96885]	M0QWN5		-1.7	9.1E-02	-2.1	1.3E-01	-0.5	4.9E-01	-0.2	8.7E-01
ENSMUST00000143465				-1.3	6.4E-01	-1.5	6.9E-01	-0.3	8.8E-01	-0.2	9.5E-01
ENSMUST00000192215	ring finger and WD repeat domain 2 [Source:MGI Symbol;Acc:MGI:1347046]	A0A0A6YVV7		-5.8	7.0E-05	3.9	1.3E-03	0.7	3.9E-01	-1.3	9.4E-02
ENSMUST00000192221	protocadherin 9 [Source:MGI Symbol;Acc:MGI:1306801]	A0A0A6YY37		6.0	3.3E-02	-6.6	5.4E-04	-1.9	4.1E-03	-0.3	8.6E-01
ENSMUST00000143470				1.4	4.9E-01	2.6	3.5E-01	0.9	7.1E-01	-0.3	8.8E-01
ENSMUST00000143472	calpain 7 [Source:MGI Symbol;Acc:MGI:1338030]	F2Z3X0		-3.4	6.3E-02	-4.0	1.0E-01	0.5	7.2E-01	1.1	6.4E-01
ENSMUST00000192237	thioredoxin domain containing 9 [Source:MGI Symbol;Acc:MGI:2138153]	A0A0A6YWP9		-4.8	1.2E-02	3.8	1.9E-02	0.1	9.1E-01	-0.7	4.3E-01
ENSMUST00000192249	mitochondrial ribosomal protein S23 [Source:MGI Symbol;Acc:MGI:1928138]			-4.8	1.3E-04	4.4	4.1E-03	1.0	3.7E-01	-0.1	8.9E-01
ENSMUST00000192345	solute carrier family 9 (sodium/hydrogen exchanger), member 2 [Source:MGI Symbol;Acc:MGI:105075]	Q3TM63		5.1	6.1E-03	5.7	2.3E-02	1.0	6.3E-01	1.2	3.8E-01
ENSMUST00000192409	protocadherin beta 22 [Source:MGI Symbol;Acc:MGI:2136760]	Q91XZ8		6.6	4.7E-07	1.7	4.0E-01	9.6	8.8E-05	-1.0	5.5E-01
ENSMUST00000192436	TIP41, TOR signalling pathway regulator-like (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1915087]	A0A0A6YWU8		-4.6	1.0E-04	3.6	5.9E-02	-1.0	5.5E-01	0.8	4.9E-01
ENSMUST00000143498	family with sequence similarity 63, member A [Source:MGI Symbol;Acc:MGI:1922257]	A0A0G2JDK1		-2.1	8.9E-02	-1.4	4.4E-01	1.4	2.6E-01	0.7	6.6E-01
ENSMUST00000143502				1.9	1.6E-01	3.5	5.2E-02	0.3	8.3E-01	-1.3	3.2E-01
ENSMUST00000192477	SLIT and NTRK-like family, member 3 [Source:MGI Symbol;Acc:MGI:2679447]		Q810B9	9.1	7.8E-05	0.6	7.6E-01	3.3	6.3E-02	-1.6	3.7E-01
ENSMUST00000143509				-4.0	4.5E-02	0.9	6.1E-01	0.5	7.1E-01	-4.3	3.5E-02
ENSMUST00000192503	protocadherin alpha 3 [Source:MGI Symbol;Acc:MGI:2447313]	Q91Y16		7.9	1.2E-05	-3.2	2.8E-02	0.2	8.1E-01	-0.5	7.2E-01
ENSMUST00000192507	solute carrier family 26, member 6 [Source:MGI Symbol;Acc:MGI:2159728]	A0A087WS07		3.1	1.4E-02	-4.8	6.8E-03	-0.7	2.8E-01	-0.4	8.1E-01
ENSMUST00000143517	mitogen-activated protein kinase kinase 2 [Source:MGI Symbol;Acc:MGI:1346867]		Q63932	-1.4	5.9E-02	-0.4	6.4E-01	0.6	3.3E-01	-0.4	6.0E-01
ENSMUST00000192509	mitogen-activated protein kinase kinase kinase kinase 4 [Source:MGI Symbol;Acc:MGI:1349394]	A0A0A6YWR8		-4.2	5.7E-03	5.0	1.1E-03	-1.1	3.2E-01	-3.3	2.3E-03
ENSMUST00000192527	hedgehog interacting protein-like 2 [Source:MGI Symbol;Acc:MGI:1926022]		Q9D2G9	5.0	2.7E-02	-5.4	1.4E-01	0.8	5.3E-01	-0.1	9.9E-01
ENSMUST00000192532	histocompatibility 2, blastocyst [Source:MGI Symbol;Acc:MGI:892004]			-5.0	1.0E-03	5.4	1.2E-02	-0.4	8.5E-01	-1.5	1.9E-01
ENSMUST00000192538	predicted pseudogene 9774 [Source:MGI Symbol;Acc:MGI:3642386]	A0A0A6YVU8		8.7	2.4E-05	7.5	1.3E-04	-1.1	3.9E-01	1.1	9.6E-02
ENSMUST00000143524				-1.3	3.0E-01	-0.8	6.6E-01	0.9	4.6E-01	0.5	7.6E-01
ENSMUST00000143528				-0.4	8.6E-01	-0.9	6.7E-01	-1.3	4.3E-01	-0.8	7.1E-01
ENSMUST00000192539	CUE domain containing 1 [Source:MGI Symbol;Acc:MGI:2144281]			5.5	3.1E-03	5.3	1.2E-02	0.8	6.5E-01	0.9	4.1E-01
ENSMUST00000192557	protocadherin 20 [Source:MGI Symbol;Acc:MGI:2443376]		Q8BIZ0	6.5	7.0E-05	-0.4	6.6E-01	0.7	3.4E-01	-2.0	8.5E-02
ENSMUST00000192591	immunoglobulin heavy variable 8-8 [Source:MGI Symbol;Acc:MGI:3815333]	A0A0A6YXQ0		7.4	2.3E-05	2.2	6.4E-03	-0.9	1.2E-01	0.4	4.0E-01
ENSMUST00000143536				-0.2	8.7E-01	-1.3	5.5E-01	-0.1	9.4E-01	0.9	6.4E-01
ENSMUST00000192615	guanine nucleotide binding protein (G protein), alpha inhibiting 2 [Source:MGI Symbol;Acc:MGI:95772]		P08752	-9.0	3.3E-04	-0.8	6.4E-01	2.2	8.9E-02	-0.2	9.1E-01
ENSMUST00000143539	lymphocyte cytosolic protein 1 [Source:MGI Symbol;Acc:MGI:104808]	D3YZ25		-0.2	7.8E-01	0.0	1.0E+00	0.3	6.8E-01	0.1	9.1E-01
ENSMUST00000192630	surfactant associated protein B [Source:MGI Symbol;Acc:MGI:109516]		P50405	4.9	1.4E-02	3.4	7.6E-03	-0.9	4.0E-01	-0.5	4.7E-01
ENSMUST00000192631	protocadherin alpha 7 [Source:MGI Symbol;Acc:MGI:1298369]	Q91Y13		7.3	2.8E-05	-1.0	2.3E-01	0.6	3.3E-01	-1.4	1.1E-01
ENSMUST00000192639	peroxiredoxin 6 [Source:MGI Symbol;Acc:MGI:894320]	A0A0A6YXQ7		-7.1	2.3E-04	3.9	1.2E-02	-3.1	6.4E-02	0.0	9.9E-01
ENSMUST00000143566				1.0	2.2E-01	1.5	1.3E-01	-0.2	7.9E-01	-0.6	4.4E-01
ENSMUST00000192650	SRY (sex determining region Y)-box 17 [Source:MGI Symbol;Acc:MGI:107543]	A0A0A6YXS3		6.7	2.7E-04	5.1	1.6E-05	0.4	5.0E-01	0.3	4.0E-01
ENSMUST00000143570				-3.8	3.7E-01	-6.6	1.9E-01	-3.3	2.3E-01	-0.6	9.1E-01
ENSMUST00000143573	SEC23 homolog B, COPII coat complex component [Source:MGI Symbol;Acc:MGI:1350925]	A2ANA0		-1.5	1.5E-01	1.4	2.3E-01	1.4	1.8E-01	-1.5	1.6E-01
ENSMUST00000143575				1.8	4.6E-02	1.5	1.6E-01	-0.1	9.0E-01	0.2	8.3E-01
ENSMUST00000143576				2.3	2.6E-01	0.3	9.3E-01	-0.8	7.2E-01	1.2	6.5E-01
ENSMUST00000143579				0.9	1.3E-01	0.4	6.0E-01	0.0	9.5E-01	0.5	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000143580				0.3	8.7E-01	-1.8	3.9E-01	-3.5	4.1E-02	-1.4	5.5E-01
ENSMUST00000143584				0.7	5.6E-01	3.1	3.9E-02	0.7	5.3E-01	-1.7	1.5E-01
ENSMUST00000143587				2.7	1.8E-01	0.3	9.0E-01	-1.6	4.2E-01	0.8	6.7E-01
ENSMUST00000192698	ATPase, H+ transporting, lysosomal V1 subunit H [Source:MGI Symbol;Acc:MGI:1914864]	A0A0A6YX18		-6.4	1.1E-04	6.0	5.7E-05	-2.0	7.1E-02	0.0	9.6E-01
ENSMUST00000143594	RUN and FYVE domain-containing 2 [Source:MGI Symbol;Acc:MGI:1917682]	Q8BR30		1.8	2.1E-01	1.2	4.8E-01	0.0	9.9E-01	0.6	6.6E-01
ENSMUST00000192700	signal-regulatory protein beta 1A [Source:MGI Symbol;Acc:MGI:2444824]	Q6F5F2		-10.8	2.3E-05	3.8	4.1E-03	-0.2	8.0E-01	-0.2	8.4E-01
ENSMUST00000192704	DDB1 and CUL4 associated factor 8 [Source:MGI Symbol;Acc:MGI:91860]		Q8N7N5	-4.6	7.4E-04	-2.2	2.1E-01	2.8	2.3E-02	-2.0	2.8E-01
ENSMUST00000192715	myoneurin [Source:MGI Symbol;Acc:MGI:1931415]		Q99MD8	4.0	1.1E-02	5.5	2.6E-04	0.6	5.4E-01	0.8	1.7E-01
ENSMUST00000192762	ring finger and WD repeat domain 2 [Source:MGI Symbol;Acc:MGI:1347046]	A0A0A6YXK6		-5.5	2.1E-03	4.8	1.7E-03	0.4	7.0E-01	0.4	6.1E-01
ENSMUST00000192773	doublecortin-like kinase 2 [Source:MGI Symbol;Acc:MGI:1918012]	A0A0A6YWI6		6.0	5.7E-06	3.7	3.4E-03	-3.1	1.7E-02	-0.1	9.3E-01
ENSMUST00000192829	BRO1 domain and CAAX motif containing [Source:MGI Symbol;Acc:MGI:1918928]	A0A0A6YWK4		3.7	8.5E-04	4.4	4.2E-02	-0.8	6.5E-01	-0.7	6.1E-01
ENSMUST00000192856	T cell receptor beta, constant region 1 [Source:MGI Symbol;Acc:MGI:4439726]	A0A0A6YWV4		-4.9	3.2E-03	4.0	1.6E-03	-1.0	2.9E-01	0.2	7.1E-01
ENSMUST00000192886	T cell leukemia translocation altered gene [Source:MGI Symbol;Acc:MGI:1918829]	A0A0A6YXI4		-2.5	2.5E-02	6.3	5.5E-04	-0.7	6.1E-01	0.2	7.2E-01
ENSMUST00000192937	tigger transposable element derived 5 [Source:MGI Symbol;Acc:MGI:2145902]		Q499M4	5.3	6.5E-05	7.7	2.0E-03	-0.6	7.6E-01	-1.2	2.4E-01
ENSMUST00000143630	autophagy related 16-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1920933]		Q6KAU8	-2.2	1.9E-01	-2.4	4.2E-01	0.8	6.4E-01	1.0	7.1E-01
ENSMUST00000192949	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:MGI Symbol;Acc:MGI:2181202]	A0A0A6YY64		-4.5	4.2E-03	-3.2	8.8E-03	0.7	1.9E-01	0.1	8.9E-01
ENSMUST00000143632	polyhomeotic-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1860454]	D6REH8		-3.1	1.1E-01	-1.9	5.1E-01	1.2	5.0E-01	0.1	9.8E-01
ENSMUST00000192960	thioredoxin domain containing 9 [Source:MGI Symbol;Acc:MGI:2138153]	A0A0A6YVV3		-6.4	8.1E-05	7.0	1.5E-02	0.5	8.4E-01	-0.9	5.5E-01
ENSMUST00000192980	vesicle-associated membrane protein 8 [Source:EntrezGene;Acc:22320]			-7.9	2.9E-06	9.7	9.5E-06	0.1	9.2E-01	0.2	7.1E-01
ENSMUST00000193018	nocturnin [Source:MGI Symbol;Acc:MGI:109382]	A0A0A6YY01		-5.8	4.4E-03	5.1	1.5E-02	1.3	4.6E-01	-0.3	7.8E-01
ENSMUST00000143662	family with sequence similarity 129, member C [Source:MGI Symbol;Acc:MGI:3686743]	D3YZB0		1.8	3.4E-01	3.1	6.6E-02	-1.2	4.4E-01	-2.6	1.1E-01
ENSMUST00000193053	WD repeat domain 20 [Source:MGI Symbol;Acc:MGI:1916891]	Q9D721		-2.7	1.2E-02	7.3	4.3E-05	0.1	9.1E-01	-0.9	1.1E-01
ENSMUST00000143674	phosphodiesterase 6D, cGMP-specific, rod, delta [Source:MGI Symbol;Acc:MGI:1270843]	M0QWR1		3.4	4.4E-02	1.1	6.4E-01	0.2	9.2E-01	2.5	2.2E-01
ENSMUST00000193075	DNA segment, Chr 3, ERATO Doi 751, expressed [Source:MGI Symbol;Acc:MGI:1289213]	A0A0A6YWY5		5.1	7.8E-04	4.7	6.5E-02	-0.8	7.2E-01	0.9	5.7E-01
ENSMUST00000193143	potassium channel tetramerisation domain containing 3 [Source:MGI Symbol;Acc:MGI:2444629]	A0A0A6YX67		5.1	7.5E-03	6.3	9.3E-03	-0.6	7.6E-01	-1.5	2.2E-01
ENSMUST00000143680				1.3	1.8E-01	1.2	3.7E-01	0.2	8.4E-01	0.3	7.6E-01
ENSMUST00000193168	ribosomal protein L22 like 1 [Source:MGI Symbol;Acc:MGI:1915278]	A0A0A6YW21		-5.0	8.2E-04	7.0	4.7E-02	0.6	8.5E-01	1.1	5.7E-01
ENSMUST00000193190	ariadne homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1344361]	A0A0A6YXB0		-2.8	1.9E-02	-0.6	7.4E-01	1.7	1.7E-01	-1.8	3.0E-01
ENSMUST00000193200	synaptic Ras GTPase activating protein 1 homolog (rat) [Source:MGI Symbol;Acc:MGI:3039785]	A0A0A6YVS6		4.2	2.0E-03	4.6	5.9E-03	-1.2	3.9E-01	-0.2	7.6E-01
ENSMUST00000143692	protein kinase C, beta [Source:MGI Symbol;Acc:MGI:97596]		P68404	-0.9	9.9E-02	-0.4	5.7E-01	0.8	1.1E-01	0.3	6.6E-01
ENSMUST00000193201	purinergic receptor P2Y, G-protein coupled 1 [Source:MGI Symbol;Acc:MGI:105049]	Q544J5	P49650	3.3	4.4E-03	-6.3	5.6E-02	-1.2	3.5E-01	-1.1	7.4E-01
ENSMUST00000143696	Rho GTPase activating protein 4 [Source:MGI Symbol;Acc:MGI:2159577]	F6YWG4		-2.3	1.5E-01	-2.4	3.1E-01	0.4	7.9E-01	0.5	8.3E-01
ENSMUST00000193210	cytochrome c oxidase subunit Vb [Source:MGI Symbol;Acc:MGI:88475]	Q9D881		-3.5	2.6E-04	4.7	1.1E-03	0.1	8.8E-01	-0.2	7.5E-01
ENSMUST00000143699				3.9	2.3E-01	-0.2	9.6E-01	-3.5	2.5E-01	0.6	8.6E-01
ENSMUST00000193229	Fc receptor-like 5 [Source:MGI Symbol;Acc:MGI:3053558]		Q68SN8	7.0	3.9E-05	-3.7	2.1E-03	1.1	2.5E-02	-1.9	8.5E-02
ENSMUST00000143702	zinc finger CCCH type, antiviral 1 [Source:MGI Symbol;Acc:MGI:1926031]		Q3UPF5	-0.1	8.9E-01	1.5	4.5E-02	0.0	9.4E-01	-1.6	3.0E-02
ENSMUST00000143704				3.8	5.1E-02	5.9	1.2E-02	-0.4	8.6E-01	-2.5	6.0E-02
ENSMUST00000193252	protocadherin 10 [Source:MGI Symbol;Acc:MGI:1338042]	Q6P0A6		7.7	9.4E-05	7.0	4.6E-04	-0.6	6.9E-01	-0.8	3.1E-01
ENSMUST00000193254	acylpeptide hydrolase [Source:MGI Symbol;Acc:MGI:88041]		Q8R146	-6.2	1.9E-04	-0.3	8.8E-01	2.9	3.5E-02	-0.6	7.2E-01
ENSMUST00000143713	sialophorin [Source:MGI Symbol;Acc:MGI:98384]	Q544C5	P15702	1.1	1.3E-01	1.5	1.0E-01	1.0	1.7E-01	0.5	5.0E-01
ENSMUST00000193258	glutamine-rich 1 [Source:MGI Symbol;Acc:MGI:1916482]	Q8BUN3		6.2	6.9E-03	4.9	8.6E-05	0.3	7.0E-01	0.5	3.7E-01
ENSMUST00000143720	A kinase (PRKA) anchor protein 1 [Source:MGI Symbol;Acc:MGI:104729]		O08715	0.7	6.2E-01	6.4	2.1E-02	4.1	8.9E-02	-1.5	2.9E-01
ENSMUST00000193266	N(alpha)-acetyltransferase 15, NatA auxiliary subunit [Source:MGI Symbol;Acc:MGI:1922088]	A0A0A6YW80		3.2	3.9E-03	7.9	2.3E-05	0.1	9.3E-01	-0.6	2.1E-01
ENSMUST00000143723				0.7	3.8E-01	-0.3	7.8E-01	-0.1	9.1E-01	1.0	4.1E-01
ENSMUST00000193279	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 [Source:MGI Symbol;Acc:MGI:1913627]		Q9CQY9	-5.5	2.2E-04	5.6	2.8E-02	-0.4	8.6E-01	-1.2	4.2E-01
ENSMUST00000193319	potassium channel, subfamily K, member 2 [Source:MGI Symbol;Acc:MGI:109366]		P97438	6.4	2.7E-04	8.9	4.7E-05	-0.9	5.0E-01	0.8	1.3E-01
ENSMUST00000193334	S-adenosylmethionine synthase isoform type-2 [Source:UniProtKB/Swiss-Prot;Acc:Q3THS6]	Q99J57	Q3THS6	-1.9	4.9E-03	-3.3	1.8E-02	0.2	7.2E-01	-2.1	1.5E-01
ENSMUST00000143736				-2.9	4.9E-02	-2.4	1.4E-01	-0.4	7.1E-01	-0.9	5.6E-01
ENSMUST00000143744				-0.5	6.2E-01	1.2	3.1E-01	0.7	5.2E-01	-1.0	3.1E-01
ENSMUST00000143746	zinc and ring finger 3 [Source:MGI Symbol;Acc:MGI:3039616]	F7D553		3.2	4.0E-02	5.4	3.9E-03	-0.4	7.7E-01	-2.6	2.6E-02
ENSMUST00000193374	RIKEN cDNA 2310009B15 gene [Source:MGI Symbol;Acc:MGI:1916799]	A0A0A6YWI4		2.8	3.7E-03	-4.7	8.6E-03	0.5	4.6E-01	1.2	4.0E-01
ENSMUST00000193382	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C [Source:MGI	A0A0A6YXK9		5.7	6.2E-03	2.6	6.8E-03	0.6	3.9E-01	0.3	6.0E-01
ENSMUST00000193389	protocadherin alpha 6 [Source:MGI Symbol;Acc:MGI:1298367]	B9EKB6		7.1	1.2E-04	8.1	4.5E-05	-0.6	6.0E-01	0.1	7.9E-01
ENSMUST00000193404	protocadherin gamma subfamily A, 10 [Source:MGI Symbol;Acc:MGI:1935227]	Q91XY9		5.9	2.5E-04	5.2	7.3E-05	-0.3	7.1E-01	0.4	4.5E-01
ENSMUST00000143771	patatin-like phospholipase domain containing 8 [Source:MGI Symbol;Acc:MGI:1914702]	E9QAC9		-3.4	1.4E-01	-1.2	7.1E-01	1.6	4.2E-01	-0.7	8.2E-01
ENSMUST00000193414	protocadherin gamma subfamily A, 5 [Source:MGI Symbol;Acc:MGI:1935217]	Q91XY3		5.6	3.5E-04	5.4	1.0E-03	-0.6	6.5E-01	-0.1	8.4E-01
ENSMUST00000193433	solute carrier family 25, member 44 [Source:MGI Symbol;Acc:MGI:2444391]		Q8BGF9	-7.2	9.1E-04	-6.6	1.5E-04	0.4	3.3E-01	-0.6	6.3E-01
ENSMUST00000193441	carbohydrate sulfotransferase 10 [Source:MGI Symbol;Acc:MGI:2138283]	A0A0A6YXK3		8.5	4.7E-05	5.4	3.2E-03	-0.6	6.9E-01	-1.3	1.8E-01
ENSMUST00000143784				1.5	4.7E-01	-3.0	1.4E-01	-5.7	4.1E-03	-1.2	5.7E-01
ENSMUST00000143786	adenosine monophosphate deaminase 3 [Source:MGI Symbol;Acc:MGI:1096344]	F6XQD0		-1.0	2.5E-01	0.1	9.5E-01	0.3	6.3E-01	-0.7	4.8E-01
ENSMUST00000193446	transmembrane and coiled-coil domains 1 [Source:MGI Symbol;Acc:MGI:1921173]	A0A0A6YVS2		-6.8	3.3E-03	4.9	1.2E-03	-1.2	3.0E-01	0.2	8.0E-01
ENSMUST00000193449	ubiquitin specific peptidase 39 [Source:MGI Symbol;Acc:MGI:107622]		Q3TIX9	-3.2	8.4E-05	2.6	7.1E-03	-4.7	1.0E-03	-1.0	1.6E-01
ENSMUST00000193476	protocadherin gamma subfamily A, 7 [Source:MGI Symbol;Acc:MGI:1935219]	A0A0A6YXT1		6.2	3.0E-04	6.1	3.3E-04	-3.6	1.9E-02	0.1	8.7E-01
ENSMUST00000193480	zinc finger and BTB domain containing 18 [Source:MGI Symbol;Acc:MGI:1353609]	A0A0A6YWR6		-5.9	3.7E-04	-4.7	5.2E-04	-0.3	4.3E-01	-2.1	7.8E-02
ENSMUST00000193491	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]		Q6PDM2	-5.0	5.9E-04	2.7	6.1E-02	-1.6	2.1E-01	-0.7	5.4E-01
ENSMUST00000143805				1.3	5.6E-01	-1.0	7.9E-01	-0.2	9.3E-01	2.0	5.2E-01
ENSMUST00000143806				0.9	6.8E-02	0.6	3.2E-01	0.0	9.4E-01	0.3	6.3E-01
ENSMUST00000143807				-2.1	1.2E-01	-2.6	2.2E-01	0.6	6.0E-01	1.1	5.7E-01
ENSMUST00000193509	ring finger protein 181 [Source:MGI Symbol;Acc:MGI:1913760]		Q9CY62	-5.2	5.7E-04	5.2	1.0E-03	-0.4	7.2E-01	1.8	3.5E-02
ENSMUST00000193517	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	A0A0A6YVV8		-7.8	1.7E-04	3.1	1.4E-02	0.0	9.8E-01	0.6	4.3E-01
ENSMUST00000193547	neural cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97281]	A0A0A6YY47		-4.3	1.5E-03	-1.3	2.0E-01	2.1	6.1E-03	-0.3	7.2E-01
ENSMUST00000193560	inositol hexaphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:1923750]	A0A0A6YWM3		-4.8	2.9E-04	7.4	1.9E-04	-0.7	6.1E-01	0.0	9.6E-01
ENSMUST00000143834				0.3	6.9E-01	1.3	1.9E-01	0.7	3.5E-01	-0.2	7.7E-01
ENSMUST00000193565	predicted gene, 37596 [Source:MGI Symbol;Acc:MGI:5610824]	A0A0A6YXL2		6.3	1.4E-04	4.9	2.1E-03	-2.2	1.1E-01	-0.4	6.2E-01
ENSMUST00000143842	G patch domain containing 8 [Source:MGI Symbol;Acc:MGI:1918667]		A2A6A1	-1.4	3.8E-02	-0.5	5.0E-01	0.9	1.3E-01	0.0	9.6E-01
ENSMUST00000143850	Der1-like domain family, member 2 [Source:MGI Symbol;Acc:MGI:2151483]		Q8BNI4	-1.7	1.1E-01	-1.6	3.0E-01	1.0	3.1E-01	0.8	5.6E-01
ENSMUST00000193603	neuroligin 1 [Source:MGI Symbol;Acc:MGI:2179435]		Q99K10	8.8	9.4E-06	6.3	1.5E-03	-0.7	6.4E-01	-0.4	6.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000143854				-0.5	6.0E-01	-1.4	3.6E-01	0.6	5.1E-01	1.5	3.1E-01
ENSMUST00000193621	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum) [Source:MGI Symbol;Acc:MGI:1921693]	A0A0A6YX56		6.5	1.8E-04	5.0	6.2E-04	1.4	1.3E-01	-0.6	3.2E-01
ENSMUST00000193625	axin interactor, dorsalization associated [Source:MGI Symbol;Acc:MGI:1919737]		Q8C4Q6	-4.2	4.8E-04	4.4	1.5E-03	-2.7	3.5E-02	0.0	9.4E-01
ENSMUST00000143867	solute carrier family 35, member F6 [Source:MGI Symbol;Acc:MGI:1922169]	D6RFU7		-1.2	6.7E-01	-2.9	4.2E-01	-2.1	3.2E-01	-0.4	9.2E-01
ENSMUST00000193636	ignal transducing adaptor molecule (SH3 domain and ITAM motif) 1 [Source:MGI Symbol;Acc:MGI:1329014	A0A0A6YVP6		-6.4	1.8E-05	4.0	7.2E-02	-1.4	5.1E-01	-0.4	7.7E-01
ENSMUST00000193638	DDB1 and CUL4 associated factor 8 [Source:MGI Symbol;Acc:MGI:91860]		Q8N7N5	-3.7	1.7E-03	9.0	1.8E-02	0.8	8.1E-01	-2.0	2.8E-01
ENSMUST00000193675	vimentin [Source:MGI Symbol;Acc:MGI:98932]	A0A0A6YWC8		-11.1	5.5E-06	4.0	2.3E-03	0.2	8.6E-01	0.5	5.0E-01
ENSMUST00000143874				2.8	2.1E-01	2.6	2.4E-01	-0.5	8.2E-01	-0.3	8.5E-01
ENSMUST00000143878				1.6	6.4E-02	1.6	1.4E-01	0.2	8.5E-01	0.1	8.7E-01
ENSMUST00000193682	mitogen-activated protein kinase kinase kinase kinase 4 [Source:MGI Symbol;Acc:MGI:1349394]	B2RUE8		-8.5	4.6E-05	6.0	1.0E-03	-0.6	6.7E-01	-0.4	5.9E-01
ENSMUST00000193683	NME/NM23 family member 7 [Source:MGI Symbol;Acc:MGI:2449121]	Q3UMG6		-4.8	1.3E-03	4.6	1.1E-03	-1.3	2.3E-01	0.6	3.9E-01
ENSMUST00000193687	toll-like receptor 5 [Source:MGI Symbol;Acc:MGI:1858171]	A0A0A6YVY4		3.5	3.1E-02	-4.2	1.3E-02	0.2	7.5E-01	-0.3	8.3E-01
ENSMUST00000193703	enabled homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108360]		Q03173	4.7	2.1E-03	6.3	6.7E-03	1.3	4.6E-01	0.3	7.5E-01
ENSMUST00000143908	l RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:133(	S4R1B9		1.1	6.1E-01	1.3	6.0E-01	0.3	8.9E-01	0.0	9.9E-01
ENSMUST00000143909				1.7	7.6E-02	2.6	4.3E-02	0.7	4.7E-01	-0.2	8.4E-01
ENSMUST00000193784	phosphatidylinositol glycan anchor biosynthesis, class C [Source:MGI Symbol;Acc:MGI:1914542]		Q9CXR4	2.1	1.4E-02	4.9	5.4E-03	-1.2	4.2E-01	0.3	6.9E-01
ENSMUST00000193823	TBC1 domain family, member 8 [Source:MGI Symbol;Acc:MGI:1927225]	A0A0A6YWY1		-1.5	2.1E-02	7.8	3.5E-05	-0.5	6.7E-01	-0.7	1.8E-01
ENSMUST00000193828	protocadherin 1 [Source:MGI Symbol;Acc:MGI:104692]	A0A0A6YY88		5.0	8.6E-04	4.6	1.6E-04	-0.2	7.9E-01	0.2	6.4E-01
ENSMUST00000193832	thioredoxin domain containing 9 [Source:MGI Symbol;Acc:MGI:2138153]	A0A0A6YXY0		2.7	8.4E-04	6.6	3.8E-03	-0.7	6.9E-01	-1.8	1.2E-01
ENSMUST00000193839	protocadherin alpha 1 [Source:MGI Symbol;Acc:MGI:2150982]	Q641K6		7.9	2.7E-05	7.3	3.3E-03	-1.1	6.0E-01	1.0	3.6E-01
ENSMUST00000193869	protocadherin gamma subfamily A, 2 [Source:MGI Symbol;Acc:MGI:1935214]	Q91XY6		7.2	3.6E-05	5.1	1.4E-02	-0.2	9.0E-01	1.2	2.6E-01
ENSMUST00000193872	transmembrane protein 79 [Source:MGI Symbol;Acc:MGI:1919163]	A0A0A6YX45		3.4	6.1E-04	6.8	2.5E-04	-0.6	6.3E-01	-0.3	6.7E-01
ENSMUST00000143939	eukaryotic translation initiation factor 4, gamma 1 [Source:MGI Symbol;Acc:MGI:2384784]			-2.8	2.1E-01	-0.2	9.4E-01	2.8	2.4E-01	0.1	9.6E-01
ENSMUST00000193924	guanylate cyclase 1, soluble, alpha 3 [Source:MGI Symbol;Acc:MGI:1926562]		Q9ERL9	6.7	1.5E-02	1.0	5.3E-01	-2.8	8.8E-02	2.4	8.2E-02
ENSMUST00000193943	purinergic receptor P2Y, G-protein coupled 1 [Source:MGI Symbol;Acc:MGI:105049]	Q544J5	P49650	-2.3	5.4E-03	-4.0	2.0E-02	-0.6	4.3E-01	-0.5	7.5E-01
ENSMUST00000143958	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome [Source:MGI Symbol;Acc:MGI:894810]	D6RJL0		4.0	4.7E-02	4.5	5.9E-02	-0.6	7.8E-01	-1.1	4.9E-01
ENSMUST00000193947	zinc finger protein 704 [Source:MGI Symbol;Acc:MGI:2180715]	A0A0A6YWL6		4.2	2.4E-04	6.5	2.2E-06	-2.5	4.3E-03	0.2	6.5E-01
ENSMUST00000143961	t-complex protein 1 [Source:MGI Symbol;Acc:MGI:98535]	F2Z483		-1.0	4.9E-01	-3.6	7.1E-02	-2.5	3.5E-02	0.1	9.8E-01
ENSMUST00000193973	Fc receptor, IgE, high affinity I, gamma polypeptide [Source:MGI Symbol;Acc:MGI:95496]	A0A0A6YVS1		-5.2	2.6E-03	5.6	3.7E-03	-1.1	4.6E-01	0.1	9.0E-01
ENSMUST00000193977	denticleless homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1924093]	A0A0A6YXS0		7.1	7.7E-06	-5.2	5.2E-03	-2.8	4.5E-03	-0.7	6.4E-01
ENSMUST00000193987	glutathione peroxidase 1 [Source:MGI Symbol;Acc:MGI:104887]	A0A0A6YVV2		-9.8	3.4E-04	4.7	4.7E-04	-0.9	3.1E-01	0.4	5.4E-01
ENSMUST00000193989	WD repeat domain 49 [Source:MGI Symbol;Acc:MGI:3645287]			5.7	1.3E-03	5.9	4.8E-04	-0.7	5.9E-01	0.5	4.1E-01
ENSMUST00000194016	peroxisomal biogenesis factor 5-like [Source:MGI Symbol;Acc:MGI:1916672]	F8SLQ1		7.0	1.8E-04	-2.4	9.0E-04	-0.6	6.4E-02	-0.5	3.1E-01
ENSMUST00000194038	protocadherin alpha 8 [Source:MGI Symbol;Acc:MGI:2681879]	Q91Y12		8.1	4.8E-05	6.4	2.0E-06	-0.5	3.8E-01	0.0	8.9E-01
ENSMUST00000194039	in, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F [Source:MGI Symbol;Acc:MG	A0A0A6YY06		4.8	2.9E-02	-2.2	9.4E-02	-0.5	4.8E-01	-1.5	2.9E-01
ENSMUST00000194047	ubiquinol-cytochrome c reductase core protein 1 [Source:MGI Symbol;Acc:MGI:107876]	A0A0A6YW82		-4.9	8.1E-03	3.5	1.0E-02	-0.5	6.2E-01	0.2	8.4E-01
ENSMUST00000194062	complement component (3b/4b) receptor 1-like [Source:MGI Symbol;Acc:MGI:88513]	A0A0A6YXR6		-7.1	1.7E-03	-0.4	7.6E-01	4.1	3.5E-04	-0.9	4.5E-01
ENSMUST00000194073	ariadne homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1344361]	A0A0A6YW24		-4.4	1.3E-02	6.0	1.3E-03	0.7	6.2E-01	0.1	9.2E-01
ENSMUST00000194102	Fc receptor-like 5 [Source:MGI Symbol;Acc:MGI:3053558]		Q68SN8	6.6	5.1E-05	-5.0	2.1E-03	-1.3	5.6E-02	-0.9	4.9E-01
ENSMUST00000194111	complement component (3b/4b) receptor 1-like [Source:MGI Symbol;Acc:MGI:88513]	A0A0A6YXN9		-3.0	1.5E-03	5.0	2.4E-03	-0.6	6.4E-01	-1.6	7.3E-02
ENSMUST00000194134	membrane metallo endopeptidase [Source:MGI Symbol;Acc:MGI:97004]		Q61391	7.4	3.3E-06	3.0	1.2E-02	-0.2	7.8E-01	0.2	7.9E-01
ENSMUST00000194144	signal-regulatory protein beta 1A [Source:MGI Symbol;Acc:MGI:2444824]	A0A0A6YWR3		-8.9	1.8E-05	3.1	1.0E-01	0.7	6.5E-01	1.1	3.6E-01
ENSMUST00000144000				-2.0	1.9E-01	-1.7	4.5E-01	1.1	4.5E-01	0.8	6.9E-01
ENSMUST00000144003				3.8	1.5E-01	4.0	1.9E-01	-0.3	9.3E-01	-0.5	8.1E-01
ENSMUST00000194171	ubiquitin specific peptidase 19 [Source:MGI Symbol;Acc:MGI:1918722]	A0A0A6YWN9		-5.8	2.2E-03	7.2	1.4E-03	-0.6	7.3E-01	0.7	4.2E-01
ENSMUST00000194204	potassium inwardly-rectifying channel, subfamily J, member 9 [Source:MGI Symbol;Acc:MGI:108007]	Q544N3	P48543	4.5	3.4E-03	6.5	1.2E-03	-0.6	6.8E-01	-0.9	2.8E-01
ENSMUST00000194207	Vitamin K-dependent gamma-carboxylase [Source:UniProtKB/Swiss-Prot;Acc:Q9QYC7]	B2RS80	Q9QYC7	3.0	6.7E-04	-1.5	2.8E-01	1.6	8.5E-02	-0.8	5.8E-01
ENSMUST00000144030	lin-54 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2140902]	D6RJL6		1.2	6.3E-01	-0.9	8.0E-01	-1.2	6.2E-01	0.9	7.9E-01
ENSMUST00000144037				-0.7	2.2E-01	-1.2	1.1E-01	-0.7	1.7E-01	-0.3	6.8E-01
ENSMUST00000194220	cDNA sequence BC026585 [Source:MGI Symbol;Acc:MGI:2448516]	A0A0A6YXW5		5.0	5.1E-06	6.1	1.4E-04	-2.5	4.5E-02	0.3	5.6E-01
ENSMUST00000194224	ubiquitin specific peptidase 4 (proto-oncogene) [Source:MGI Symbol;Acc:MGI:98905]	A0A0A6YVY7		3.4	7.4E-05	5.3	3.9E-04	-2.4	6.8E-02	-0.1	8.6E-01
ENSMUST00000144051				-1.0	5.5E-01	-0.5	7.5E-01	-1.4	2.9E-01	-1.9	3.0E-01
ENSMUST00000194237	SET and MYND domain containing 3 [Source:MGI Symbol;Acc:MGI:1916976]	A0A0A6YWP2		6.1	2.9E-04	0.3	7.6E-01	0.8	3.2E-01	-1.6	1.0E-01
ENSMUST00000144060	trafficking protein particle complex 13 [Source:MGI Symbol;Acc:MGI:1914225]		Q3TIR1	-4.7	7.3E-02	0.8	7.9E-01	2.9	2.6E-01	-2.7	3.3E-01
ENSMUST00000144061	sterile alpha motif domain containing 8 [Source:MGI Symbol;Acc:MGI:1914880]	D6REI9		-2.0	3.9E-02	-1.8	1.9E-01	1.6	7.7E-02	1.3	2.9E-01
ENSMUST00000144064	2'-5' oligoadenylate synthetase-like 2 [Source:MGI Symbol;Acc:MGI:1344390]	F6Y3A6		-3.1	1.2E-01	-2.6	2.8E-01	-0.2	8.7E-01	-0.7	7.8E-01
ENSMUST00000194252	neural cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97281]	A0A0A6YY91		9.5	5.7E-05	-0.3	7.2E-01	0.7	2.8E-01	-1.8	1.0E-01
ENSMUST00000194257	immunoglobulin heavy variable V8-5 [Source:MGI Symbol;Acc:MGI:3645478]	A0A0A6YY60		5.5	1.0E-04	-4.0	2.2E-03	0.2	7.2E-01	-0.6	6.0E-01
ENSMUST00000144075				-0.9	3.5E-01	-2.7	6.5E-02	-1.0	2.0E-01	0.8	5.4E-01
ENSMUST00000144080				0.1	8.8E-01	0.0	9.8E-01	-0.5	4.2E-01	-0.4	5.9E-01
ENSMUST00000194279	interleukin 7 [Source:MGI Symbol;Acc:MGI:96561]	Q544C8	P10168	7.7	1.8E-05	7.6	5.0E-04	0.0	9.9E-01	-0.5	5.0E-01
ENSMUST00000194296	interleukin 1 receptor-like 2 [Source:MGI Symbol;Acc:MGI:1913107]	Q149G7	Q9ERS7	1.2	2.3E-02	-2.7	1.5E-01	0.6	5.2E-01	0.1	9.5E-01
ENSMUST00000144087	zinc finger RNA binding protein 2 [Source:MGI Symbol;Acc:MGI:2143792]	D3YXQ2		3.9	3.6E-02	2.8	2.6E-01	1.2	5.7E-01	2.4	1.9E-01
ENSMUST00000194304	immunoglobulin heavy constant gamma 1 (G1m marker) [Source:MGI Symbol;Acc:MGI:96446]	A0A0A6YWR2		5.9	7.4E-05	3.9	8.0E-03	-2.2	1.2E-01	-1.2	1.8E-01
ENSMUST00000194367	predicted gene 5150 [Source:MGI Symbol;Acc:MGI:3779469]	Q1AN92		-7.1	2.6E-05	7.1	7.2E-03	-0.8	7.2E-01	-1.4	2.6E-01
ENSMUST00000144097				-0.7	4.5E-01	1.5	2.6E-01	1.2	2.5E-01	-1.0	3.7E-01
ENSMUST00000194369	astrotactin 1 [Source:MGI Symbol;Acc:MGI:1098567]	A0A0A6YXJ4		4.6	6.1E-03	5.1	4.8E-04	1.0	3.0E-01	0.7	1.9E-01
ENSMUST00000194381	DH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3 [Source:MGI Symbol;Acc:MGI:19139	A0A0A6YVW1		-4.0	4.5E-03	2.3	3.4E-02	0.8	3.5E-01	0.5	5.6E-01
ENSMUST00000144108				0.8	3.9E-01	0.2	8.9E-01	0.6	5.1E-01	1.2	3.1E-01
ENSMUST00000194391	predicted gene, 38100 [Source:MGI Symbol;Acc:MGI:5611328]			7.5	2.1E-05	4.8	1.4E-04	-1.4	9.8E-02	-1.1	9.8E-02
ENSMUST00000194392	mitochondrial ribosomal protein L41 [Source:MGI Symbol;Acc:MGI:1333816]	A0A0A6YXF9		5.8	6.4E-04	-8.8	5.3E-04	-1.3	3.2E-02	-0.2	9.3E-01
ENSMUST00000194404	transmembrane protein 150A [Source:MGI Symbol;Acc:MGI:2385244]			2.9	1.5E-02	-1.8	3.1E-01	1.3	2.3E-01	-3.1	1.5E-01
ENSMUST00000194418	protocadherin gamma subfamily A, 4 [Source:MGI Symbol;Acc:MGI:1935216]		Q91XY4	8.4	3.3E-05	6.7	1.4E-04	-0.5	6.5E-01	-0.5	3.9E-01
ENSMUST00000194434	poly (ADP-ribose) polymerase family, member 1 [Source:MGI Symbol;Acc:MGI:1340806]	A0A0A6YX03		5.9	1.4E-03	9.5	3.5E-04	1.3	4.6E-01	0.5	5.1E-01
ENSMUST00000144129				1.3	3.2E-01	2.0	2.8E-01	0.8	6.1E-01	0.1	9.4E-01
ENSMUST00000194542	kelch-like ECH-associated protein 1 [Source:MGI Symbol;Acc:MGI:1858732]		Q9Z2X8	-3.4	6.6E-05	6.4	2.7E-02	-0.9	7.5E-01	-0.6	6.9E-01
ENSMUST00000144132	regulatory factor X, 5 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:1858421]	D6RDE5		-2.7	2.6E-01	-3.3	2.5E-01	-1.5	3.5E-01	-0.9	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000194552	phosducin-like 3 [Source:MGI Symbol;Acc:MGI:1916083]	A0A0A6YXV1		-4.2	2.0E-04	8.0	8.2E-07	-0.2	8.0E-01	0.1	7.9E-01
ENSMUST00000144141	F-box and leucine-rich repeat protein 3 [Source:MGI Symbol;Acc:MGI:1354702]	D3YWZ0		-1.6	4.0E-01	0.3	8.4E-01	-1.4	3.0E-01	-3.2	1.0E-01
ENSMUST00000144143	ylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria [Source:MGI Symbol;Acc:MGI:192	A2AQT7		-1.8	1.2E-01	-1.2	3.3E-01	0.0	1.0E+00	-0.6	6.6E-01
ENSMUST00000194555	regulator of G protein signaling 7 [Source:MGI Symbol;Acc:MGI:1346089]	Q80XD3		5.5	2.5E-02	7.6	6.1E-05	0.0	9.9E-01	-0.1	8.0E-01
ENSMUST00000194558	karyopherin (importin) alpha 4 [Source:MGI Symbol;Acc:MGI:1100848]	Q4FJX1	O35343	-8.6	1.4E-06	6.4	1.5E-02	-1.6	5.1E-01	-1.4	3.2E-01
ENSMUST00000194592	rine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1 [Source:MGI Symbol;Acc:MGI:8809	A0A0A6YWH7		6.2	2.6E-04	5.5	6.4E-04	-1.5	2.4E-01	-1.5	4.7E-02
ENSMUST00000144160				2.6	1.8E-01	5.3	1.5E-02	-0.6	7.6E-01	-3.3	4.0E-02
ENSMUST00000194595	predicted gene 4858 [Source:MGI Symbol;Acc:MGI:3645677]	Q3UT66		5.8	6.0E-04	4.5	3.8E-04	0.0	9.9E-01	0.4	4.9E-01
ENSMUST00000144162				3.5	5.2E-02	2.6	2.6E-01	-0.3	8.8E-01	0.6	7.2E-01
ENSMUST00000144165				0.9	4.2E-01	0.9	4.7E-01	-0.3	7.6E-01	-0.3	7.9E-01
ENSMUST00000144167	transmembrane protein 38B [Source:MGI Symbol;Acc:MGI:1098718]	X1W117		-1.3	2.7E-01	-0.6	7.4E-01	1.5	2.3E-01	0.8	6.2E-01
ENSMUST00000194598	synaptic Ras GTPase activating protein 1 homolog (rat) [Source:MGI Symbol;Acc:MGI:3039785]		F6SEU4	4.1	9.9E-04	4.5	2.4E-02	-0.7	6.9E-01	1.8	1.3E-01
ENSMUST00000194632	quiescin Q6 sulfhydryl oxidase 1 [Source:MGI Symbol;Acc:MGI:1330818]		Q8BND5	-11.5	2.5E-05	-2.4	8.7E-02	-6.9	1.0E-03	0.9	5.0E-01
ENSMUST00000194649	ribosomal protein L22 like 1 [Source:MGI Symbol;Acc:MGI:1915278]		Q9D7S7	-7.6	1.3E-05	6.8	1.0E-04	-0.6	5.9E-01	-0.6	3.0E-01
ENSMUST00000144189	dachsous 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2685011]	F6TP58		3.0	3.7E-01	4.0	2.4E-01	-0.5	8.9E-01	-1.4	5.9E-01
ENSMUST00000194657	carbohydrate sulfotransferase 10 [Source:MGI Symbol;Acc:MGI:2138283]	A0A0A6YWB7		6.0	2.1E-04	-2.7	3.8E-02	0.3	6.5E-01	0.6	5.9E-01
ENSMUST00000194690	discoidin domain receptor family, member 2 [Source:MGI Symbol;Acc:MGI:1345277]		Q62371	10.8	3.6E-05	5.4	2.2E-02	0.5	8.2E-01	-0.1	9.1E-01
ENSMUST00000194701	ras homolog gene family, member A [Source:MGI Symbol;Acc:MGI:1096342]	A0A0A6YXF6		-7.9	5.9E-05	2.6	4.0E-03	0.4	4.5E-01	0.0	9.5E-01
ENSMUST00000194727	centrosomal protein 170 [Source:MGI Symbol;Acc:MGI:1918348]		Q6A065	5.8	2.1E-02	5.7	9.2E-04	-0.5	6.5E-01	1.5	7.1E-02
ENSMUST00000194738	immunoglobulin heavy constant alpha [Source:MGI Symbol;Acc:MGI:96444]	A0A0A6YXW6		5.6	7.1E-04	7.5	1.1E-04	-0.6	6.1E-01	0.3	6.5E-01
ENSMUST00000194740	RAB3 GTPase activating protein subunit 2 [Source:MGI Symbol;Acc:MGI:1916043]	A0A0A6YWM5		-3.2	9.1E-05	4.5	7.3E-04	-0.6	4.5E-01	-0.6	3.7E-01
ENSMUST00000194746	ribosomal protein L31 [Source:MGI Symbol;Acc:MGI:2149632]	A0A0A6YX26		-4.3	2.7E-03	2.9	1.6E-02	-0.4	6.5E-01	-0.5	5.5E-01
ENSMUST00000194751	protocadherin alpha 6 [Source:MGI Symbol;Acc:MGI:1298367]	A0A0A6YY55		5.8	2.3E-02	5.1	3.1E-03	-0.5	7.2E-01	-0.2	7.8E-01
ENSMUST00000194759	LPS-responsive beige-like anchor [Source:MGI Symbol;Acc:MGI:1933162]	A0A0A6YXL6		9.5	2.2E-06	3.5	8.8E-02	-2.2	3.0E-01	-0.9	5.2E-01
ENSMUST00000144221	CREB3 regulatory factor [Source:MGI Symbol;Acc:MGI:1924378]	B8JJI0		-2.6	3.4E-01	-3.2	2.0E-01	-2.6	1.2E-01	-2.0	5.1E-01
ENSMUST00000144226				1.4	1.0E-01	1.1	3.4E-01	0.4	6.8E-01	0.6	5.1E-01
ENSMUST00000194785	integrator complex subunit 7 [Source:MGI Symbol;Acc:MGI:1924315]	A0A0A6YX34		-4.1	8.1E-03	2.6	9.2E-02	-0.2	8.7E-01	0.7	5.6E-01
ENSMUST00000194810	vesicle-associated membrane protein 4 [Source:MGI Symbol;Acc:MGI:1858730]	A0A0A6YY66		-7.0	2.2E-04	3.2	8.1E-03	-0.2	7.9E-01	0.8	2.9E-01
ENSMUST00000144234	solute carrier family 19 (folate transporter), member 1 [Source:MGI Symbol;Acc:MGI:103182]	Q542F3	P41438	3.8	7.3E-02	-1.6	6.3E-01	-1.9	3.3E-01	3.5	2.7E-01
ENSMUST00000144235				2.1	4.2E-01	-2.6	5.5E-01	-1.6	5.7E-01	3.1	4.4E-01
ENSMUST00000144236	multiple coagulation factor deficiency 2 [Source:MGI Symbol;Acc:MGI:2183439]	D0EW11	Q8K5B2	-0.3	8.4E-01	0.7	7.2E-01	0.3	8.8E-01	-0.8	6.5E-01
ENSMUST00000144238				0.5	6.1E-01	-0.6	6.7E-01	0.3	7.0E-01	1.4	2.9E-01
ENSMUST00000144239				-2.3	5.4E-02	-1.0	4.4E-01	0.2	8.0E-01	-1.0	4.2E-01
ENSMUST00000194857	mitochondrial ribosomal protein L30 [Source:MGI Symbol;Acc:MGI:1333820]	A0A0A6YXW4		-5.9	1.6E-04	7.4	9.3E-05	-0.5	6.7E-01	-0.4	5.0E-01
ENSMUST00000144247	additional sex combs like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1922552]	D6RI62		-1.4	2.2E-01	-1.4	3.6E-01	0.9	3.3E-01	0.9	5.5E-01
ENSMUST00000144248	leukocyte receptor cluster (LRC) member 8 [Source:MGI Symbol;Acc:MGI:2142195]	D3YXV8		-0.2	9.3E-01	1.3	7.0E-01	0.8	7.3E-01	-0.7	8.3E-01
ENSMUST00000194888	protocadherin gamma subfamily A, 1 [Source:MGI Symbol;Acc:MGI:1935212]	A0A0A6YW27		6.8	2.3E-05	4.7	5.4E-04	-0.8	4.0E-01	-0.3	5.8E-01
ENSMUST00000194913	interleukin 1 receptor, type II [Source:MGI Symbol;Acc:MGI:96546]			-6.0	4.4E-05	5.5	3.5E-04	-1.1	3.0E-01	-0.4	5.2E-01
ENSMUST00000144255	scaffold attachment factor B2 [Source:MGI Symbol;Acc:MGI:2146808]	D6RJ78		-3.5	2.7E-01	-3.4	3.7E-01	-0.8	7.1E-01	-0.8	8.4E-01
ENSMUST00000194928	protocadherin gamma subfamily B, 7 [Source:MGI Symbol;Acc:MGI:1935199]	Q91XX3		3.1	1.8E-03	-4.1	1.9E-02	1.2	1.4E-01	-2.1	2.4E-01
ENSMUST00000194951	rine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10 [Source:MGI Symbol;Acc:MGI:213864			-5.6	1.8E-04	6.3	3.4E-05	-0.9	3.2E-01	-0.8	1.6E-01
ENSMUST00000194959	ubiquitin specific peptidase 4 (proto-oncogene) [Source:MGI Symbol;Acc:MGI:98905]	A0A0A6YW28		-7.7	2.3E-04	-5.6	1.4E-02	-1.3	1.8E-01	-0.8	7.0E-01
ENSMUST00000194965	sperm mitochondria-associated cysteine-rich protein [Source:MGI Symbol;Acc:MGI:96945]		P15265	6.5	1.5E-02	-5.6	5.4E-03	1.2	1.5E-01	-0.2	9.1E-01
ENSMUST00000195008	fibronectin type III domain containing 3B [Source:MGI Symbol;Acc:MGI:1919257]			-4.4	2.4E-03	5.5	2.0E-03	-0.9	5.1E-01	-1.2	1.7E-01
ENSMUST00000195014	signal sequence receptor, beta [Source:MGI Symbol;Acc:MGI:1913506]		Q9CPW5	-6.3	4.1E-04	-4.8	2.5E-03	-0.4	4.7E-01	-0.6	6.4E-01
ENSMUST00000195015	transmembrane and coiled-coil domains 1 [Source:MGI Symbol;Acc:MGI:1921173]		Q921L3	-4.2	3.0E-03	3.6	4.0E-02	-1.0	4.9E-01	-1.1	3.0E-01
ENSMUST00000144280				-0.3	6.8E-01	1.7	5.5E-02	1.3	7.4E-02	-0.7	3.2E-01
ENSMUST00000195019	Vesicle-associated membrane protein 5 [Source:UniProtKB/Swiss-Prot;Acc:Q9Z2P8]	Q791P0	Q9Z2P8	3.3	3.4E-03	-3.8	1.5E-02	0.1	8.4E-01	-0.5	7.2E-01
ENSMUST00000195032	thioredoxin domain containing 9 [Source:MGI Symbol;Acc:MGI:2138153]		Q9CQ79	-4.6	5.5E-03	6.4	2.0E-04	-2.9	4.1E-02	0.1	9.3E-01
ENSMUST00000195044	ring finger and WD repeat domain 2 [Source:MGI Symbol;Acc:MGI:1347046]	A0A0A6YVP2		-6.7	6.8E-04	6.9	1.4E-04	1.0	3.4E-01	-0.6	3.4E-01
ENSMUST00000195067	zinc finger CCCH type containing 11A [Source:MGI Symbol;Acc:MGI:1917829]	A0A0A6YX41		-2.9	5.3E-03	1.5	7.6E-02	-1.4	5.6E-02	0.1	8.3E-01
ENSMUST00000144295				0.9	1.6E-01	1.0	2.1E-01	0.3	6.0E-01	0.2	7.3E-01
ENSMUST00000195120	complement receptor 2 [Source:MGI Symbol;Acc:MGI:88489]	A0A0A6YWG3		5.6	8.3E-04	8.3	2.4E-04	-0.5	7.3E-01	-2.5	1.2E-02
ENSMUST00000195123	ribosomal protein L31 [Source:MGI Symbol;Acc:MGI:2149632]	A0A0A6YXL3		-9.1	1.8E-05	7.8	5.6E-05	-0.6	5.9E-01	-0.2	6.6E-01
ENSMUST00000195136	ring finger protein 149 [Source:MGI Symbol;Acc:MGI:2677438]	A0A0A6YWR9		-4.4	9.5E-03	-1.0	3.2E-01	1.2	1.1E-01	0.2	8.5E-01
ENSMUST00000144300				-3.3	7.3E-02	-2.2	3.4E-01	0.2	8.8E-01	-0.9	6.8E-01
ENSMUST00000195151	cytochrome c oxidase subunit Vb [Source:MGI Symbol;Acc:MGI:88475]	A0A0A6YVR0		-6.0	8.8E-05	8.4	8.9E-04	0.0	9.9E-01	1.2	1.3E-01
ENSMUST00000144303	adaptor protein complex AP-1, sigma 1 [Source:MGI Symbol;Acc:MGI:1098244]	D3Z0D6		-2.9	6.3E-02	-3.3	9.6E-02	-0.6	5.2E-01	-0.2	9.2E-01
ENSMUST00000195164	immunoglobulin superfamily, member 3 [Source:MGI Symbol;Acc:MGI:1926158]	A0A0A6YX40		5.1	2.1E-02	-3.3	6.4E-02	0.4	6.3E-01	1.2	4.5E-01
ENSMUST00000195169	catechol-O-methyltransferase [Source:MGI Symbol;Acc:MGI:88470]		O88587	-4.0	8.8E-04	2.9	6.1E-03	0.3	6.9E-01	0.1	9.3E-01
ENSMUST00000144308				2.1	2.2E-01	2.3	2.5E-01	-0.4	8.4E-01	-0.6	7.3E-01
ENSMUST00000144310				-3.5	4.4E-02	-3.6	1.2E-01	0.5	6.7E-01	0.6	8.0E-01
ENSMUST00000144317				-2.8	4.2E-02	-2.3	1.6E-01	-0.3	7.7E-01	-0.8	6.3E-01
ENSMUST00000195233	melanoma inhibitory activity 3 [Source:MGI Symbol;Acc:MGI:2443183]	A0A0A6YX61		-3.8	1.1E-02	5.1	2.9E-03	-0.1	9.3E-01	-0.1	9.3E-01
ENSMUST00000195234	cDNA sequence AF067063 [Source:MGI Symbol;Acc:MGI:2687009]	O70618		6.6	2.8E-04	3.5	1.7E-01	0.8	7.2E-01	2.1	2.0E-01
ENSMUST00000195235	cytochrome b-561 domain containing 2 [Source:MGI Symbol;Acc:MGI:1929280]		Q9WUE3	-2.3	1.5E-02	-2.5	1.1E-02	1.3	1.7E-02	-0.7	4.0E-01
ENSMUST00000144328				3.6	1.0E-01	3.4	1.6E-01	-1.6	4.7E-01	-1.5	3.9E-01
ENSMUST00000195247	thioredoxin domain containing 9 [Source:MGI Symbol;Acc:MGI:2138153]		Q9CQ79	-4.6	1.3E-03	5.7	5.4E-04	0.8	4.5E-01	-0.8	2.4E-01
ENSMUST00000195262	neurotrophic tyrosine kinase, receptor, type 3 [Source:MGI Symbol;Acc:MGI:97385]	A0A0A6YWL7		5.8	3.0E-02	2.1	1.9E-01	7.5	1.2E-04	0.5	6.9E-01
ENSMUST00000144337	thymosin, beta 10 [Source:MGI Symbol;Acc:MGI:109146]			1.5	7.7E-02	0.6	5.1E-01	-0.1	8.6E-01	0.7	4.0E-01
ENSMUST00000195271	bone morphogenic protein/retinoic acid inducible neural-specific 2 [Source:MGI Symbol;Acc:MGI:2443333]	A0A0A6YWU9		8.6	1.8E-04	5.1	7.3E-04	-1.5	2.0E-01	0.3	6.4E-01
ENSMUST00000195278	RIKEN cDNA 2210017I01 gene [Source:MGI Symbol;Acc:MGI:3588251]	A0A0A6YVV1		7.0	3.5E-06	7.5	5.5E-05	-0.4	6.8E-01	0.3	6.0E-01
ENSMUST00000195354	synaptotagmin XIV [Source:MGI Symbol;Acc:MGI:2444490]		Q7TN84	6.5	8.5E-05	6.3	3.4E-04	0.7	5.5E-01	-0.1	8.1E-01
ENSMUST00000144364	intermediate filament family orphan 1 [Source:MGI Symbol;Acc:MGI:2444516]	D6RH90		1.8	2.2E-01	0.6	7.3E-01	-1.5	2.6E-01	-0.4	8.3E-01
ENSMUST00000195355	protocadherin 8 [Source:MGI Symbol;Acc:MGI:1306800]		Q7TSK3	5.4	9.4E-03	7.8	2.3E-04	-0.7	6.3E-01	-0.4	5.7E-01
ENSMUST00000195358	selectin, lymphocyte [Source:MGI Symbol;Acc:MGI:98279]	A0A0A6YW25		-9.0	1.4E-05	-7.6	2.3E-03	1.0	8.5E-02	2.4	2.0E-01
ENSMUST00000195372	dispatched homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1916147]		Q3TDN0	6.3	2.7E-02	5.1	9.2E-03	-0.6	7.0E-01	-0.5	5.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000144377	pyruvate dehydrogenase phosphatase regulatory subunit [Source:MGI Symbol;Acc:MGI:2442188]	D6RD07		1.6	8.4E-02	0.9	4.6E-01	-0.4	6.6E-01	0.4	6.9E-01
ENSMUST00000144378				0.1	8.0E-01	0.3	6.6E-01	0.1	8.4E-01	-0.1	9.1E-01
ENSMUST00000195373	mitochondrial ribosomal protein L30 [Source:MGI Symbol;Acc:MGI:1333820]		Q9D7N6	-5.9	2.4E-04	-3.9	4.3E-02	-0.7	3.9E-01	-0.1	9.6E-01
ENSMUST00000195432	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]	A0A0A6YY68		3.9	2.0E-03	-7.2	8.6E-04	0.7	1.4E-01	-0.1	9.3E-01
ENSMUST00000195465	IQ motif containing GTPase activating protein 3 [Source:MGI Symbol;Acc:MGI:3028642]	A0A0A6YXJ2		6.0	5.8E-05	6.5	4.4E-05	0.3	7.0E-01	0.1	8.5E-01
ENSMUST00000195514	inositol hexaphosphate kinase 2 [Source:MGI Symbol;Acc:MGI:1923750]	A0A0A6YX46		-4.8	1.2E-04	3.0	2.2E-02	-0.9	3.7E-01	-0.5	6.2E-01
ENSMUST00000195533	protein tyrosine phosphatase, receptor type, C [Source:MGI Symbol;Acc:MGI:97810]	A0A0A6YXM4		-5.1	6.7E-03	4.7	8.4E-04	0.5	5.8E-01	0.6	3.5E-01
ENSMUST00000195563	glutamine-rich 1 [Source:MGI Symbol;Acc:MGI:1916482]	A0A0A6YWV5		5.3	5.5E-03	3.3	3.5E-03	1.0	1.9E-01	-0.3	6.8E-01
ENSMUST00000195574	predicted gene, 33815 [Source:MGI Symbol;Acc:MGI:5592974]	A0A087WNV3		9.4	3.2E-05	10.1	1.2E-04	-1.5	4.2E-01	-0.5	4.6E-01
ENSMUST00000144390				-1.6	5.9E-01	-1.1	7.0E-01	-0.9	6.8E-01	-1.4	6.8E-01
ENSMUST00000195576	flavin containing monooxygenase 6 [Source:MGI Symbol;Acc:MGI:2681841]			4.6	1.5E-02	6.5	8.3E-04	-0.6	6.9E-01	-1.1	1.7E-01
ENSMUST00000144397				0.3	7.2E-01	1.6	1.0E-01	-0.1	8.9E-01	-1.4	1.3E-01
ENSMUST00000195589	C-type lectin domain family 7, member a [Source:MGI Symbol;Acc:MGI:1861431]			-6.7	1.9E-04	7.5	2.8E-04	-0.6	6.8E-01	-0.9	2.1E-01
ENSMUST00000195590	protocadherin alpha 2 [Source:MGI Symbol;Acc:MGI:2681880]	B9EJ92		8.0	2.0E-05	4.6	2.8E-03	1.0	3.5E-01	1.4	1.1E-01
ENSMUST00000195612	zinc finger and BTB domain containing 18 [Source:MGI Symbol;Acc:MGI:1353609]		Q9WUK6	-4.0	1.3E-02	7.6	1.9E-04	0.4	7.4E-01	-0.4	5.4E-01
ENSMUST00000195617	macrophage stimulating 1 receptor (c-met-related tyrosine kinase) [Source:MGI Symbol;Acc:MGI:99614]	A0A0A6YXY9		3.6	6.2E-04	5.6	3.8E-03	-0.3	8.6E-01	1.0	2.7E-01
ENSMUST00000195656	SLAM family member 6 [Source:MGI Symbol;Acc:MGI:1353620]	Q18PJ0	Q9ET39	5.1	2.2E-05	4.6	1.1E-04	0.1	8.4E-01	0.4	4.1E-01
ENSMUST00000144408	prostaglandin I receptor (IP) [Source:MGI Symbol;Acc:MGI:99535]		P43252	0.8	5.4E-02	1.5	2.1E-02	1.1	2.6E-02	0.4	3.8E-01
ENSMUST00000144409	splicing factor 1 [Source:MGI Symbol;Acc:MGI:1095403]	D6RDB7		-1.3	1.8E-01	-2.3	6.0E-02	-0.6	4.0E-01	0.5	6.7E-01
ENSMUST00000195657	solute carrier family 25, member 44 [Source:MGI Symbol;Acc:MGI:2444391]		Q8BGF9	-5.4	6.1E-04	4.7	1.6E-03	-2.6	5.8E-02	-0.5	4.5E-01
ENSMUST00000195681	hyaluronoglucosaminidase 2 [Source:MGI Symbol;Acc:MGI:1196334]	A0A0A6YX37		5.1	6.5E-04	-6.7	3.3E-02	0.5	7.0E-01	0.5	8.8E-01
ENSMUST00000144431	RIKEN cDNA 2810408A11 gene [Source:MGI Symbol;Acc:MGI:1917669]	J3QNJ8		3.9	1.2E-01	3.3	1.8E-01	-1.6	5.3E-01	-0.9	5.9E-01
ENSMUST00000195707	immunoglobulin heavy variable 2-5 [Source:MGI Symbol;Acc:MGI:4439517]	A0A0A6YY69		8.2	9.4E-06	-6.4	1.3E-03	0.6	3.4E-01	-1.0	5.3E-01
ENSMUST00000195708	Rap guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:2659071]	A0A0A6YWG7		-1.6	9.7E-03	6.1	4.9E-06	-0.6	3.2E-01	0.3	4.3E-01
ENSMUST00000195717	centrosomal protein 170 [Source:MGI Symbol;Acc:MGI:1918348]	H7BX26		-6.2	2.1E-05	5.4	6.8E-04	-0.9	4.3E-01	0.0	9.4E-01
ENSMUST00000195751	myoneurin [Source:MGI Symbol;Acc:MGI:1931415]		Q99MD8	-6.3	1.1E-03	5.8	1.5E-03	-1.5	3.0E-01	0.2	8.1E-01
ENSMUST00000195752	hyaluronoglucosaminidase 2 [Source:MGI Symbol;Acc:MGI:1196334]	Q3UZE4	O35632	6.3	2.4E-04	-4.4	5.7E-03	1.1	8.6E-02	-2.1	1.8E-01
ENSMUST00000144458	ubiquitin specific peptidase 10 [Source:MGI Symbol;Acc:MGI:894652]		P52479	2.9	1.1E-01	2.7	8.0E-02	-2.8	1.0E-01	-2.6	6.6E-02
ENSMUST00000144459	rier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16 [Source:MGI Symbol;Acc:MGI:	D3YVC9		-0.9	6.8E-01	-3.0	2.7E-01	-2.4	1.3E-01	-0.3	9.1E-01
ENSMUST00000144468	PQ loop repeat containing 1 [Source:MGI Symbol;Acc:MGI:1914193]	D3Z2D5		0.5	5.7E-01	0.9	3.8E-01	-0.8	3.6E-01	-1.1	2.4E-01
ENSMUST00000195764	protocadherin gamma subfamily B, 8 [Source:MGI Symbol;Acc:MGI:1935200]			7.5	4.0E-05	1.6	1.7E-01	1.1	2.5E-01	-3.7	1.6E-02
ENSMUST00000195779	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:MGI Symbol;Acc:MGI:2181202]	A0A0A6YW89		-5.3	8.9E-03	-5.0	8.2E-03	-1.0	1.4E-01	0.5	7.6E-01
ENSMUST00000144476	regulator of G-protein signaling 19 [Source:MGI Symbol;Acc:MGI:1915153]	F6WK59		-6.0	6.2E-02	-4.4	2.8E-01	1.3	4.6E-01	-0.3	9.5E-01
ENSMUST00000195797	DNA segment, Chr 13, ERATO Doi 608, expressed [Source:MGI Symbol;Acc:MGI:1277199]	Q3UPR8		5.3	1.1E-04	8.4	1.2E-04	0.1	9.2E-01	-0.5	4.4E-01
ENSMUST00000144484	centrosomal protein 57 [Source:MGI Symbol;Acc:MGI:1915551]	D6RDE1		1.7	1.2E-01	1.7	1.7E-01	-0.7	5.0E-01	-0.7	4.8E-01
ENSMUST00000195798	ATA box binding protein (Tbp)-associated factor, RNA polymerase I, A [Source:MGI Symbol;Acc:MGI:10957	A0A0A6YW00		3.8	7.2E-04	8.2	3.9E-05	-0.7	5.7E-01	-0.7	2.3E-01
ENSMUST00000195823	protocadherin gamma subfamily A, 6 [Source:MGI Symbol;Acc:MGI:1935218]	Q91XY2		7.1	1.0E-04	-3.8	1.6E-02	-0.9	2.0E-01	-1.6	3.0E-01
ENSMUST00000144498	ribonucleotide reductase M2 B (TP53 inducible) [Source:MGI Symbol;Acc:MGI:2155865]	D6RFP5		-3.0	4.5E-02	-2.6	1.0E-01	-1.3	1.7E-01	-1.6	3.3E-01
ENSMUST00000195855	peroxisomal biogenesis factor 2 [Source:MGI Symbol;Acc:MGI:107486]	Q91YZ5		-6.1	4.1E-05	5.0	3.4E-04	-0.1	8.8E-01	-1.0	1.1E-01
ENSMUST00000142355				14.0	3.5E-04	7.5	6.0E-05	-0.6	6.1E-01	-0.3	5.9E-01
ENSMUST00000125227				12.8	6.3E-06	-2.7	1.9E-01	1.3	2.4E-01	0.9	6.6E-01
ENSMUST00000132120				12.6	9.3E-05	-2.2	2.2E-02	0.0	9.9E-01	-0.3	6.7E-01
ENSMUST00000144521	bromodomain and WD repeat domain containing 3 [Source:MGI Symbol;Acc:MGI:3029414]	G3UXF9		-2.0	2.0E-01	-1.5	5.9E-01	2.1	2.5E-01	1.6	5.0E-01
ENSMUST00000149910				12.6	1.4E-05	6.8	2.2E-04	-0.6	6.6E-01	-0.9	1.7E-01
ENSMUST00000155669				12.3	1.4E-07	0.1	9.7E-01	3.0	5.5E-02	-1.6	3.8E-01
ENSMUST00000144524	tumor necrosis factor receptor superfamily, member 1a [Source:MGI Symbol;Acc:MGI:1314884]	F7A4X5		-2.3	2.1E-01	-2.1	3.9E-01	0.8	6.6E-01	0.5	8.1E-01
ENSMUST00000127782				12.1	3.3E-05	-3.9	1.9E-02	-0.4	5.9E-01	0.0	9.9E-01
ENSMUST00000122435				12.0	3.6E-05	-6.5	3.6E-03	-0.9	1.6E-01	0.6	7.4E-01
ENSMUST00000144534				-0.8	5.7E-01	0.2	9.2E-01	1.5	4.3E-01	0.4	8.3E-01
ENSMUST00000191999				12.0	2.5E-05	6.6	2.2E-04	-0.4	7.0E-01	0.6	3.3E-01
ENSMUST00000129013				11.9	3.1E-05	-2.2	1.8E-01	0.9	3.8E-01	-0.1	9.3E-01
ENSMUST00000146820				11.9	1.9E-06	2.6	8.8E-03	0.4	4.9E-01	-0.1	8.8E-01
ENSMUST00000155637				11.9	8.1E-06	5.3	1.4E-02	-1.4	4.4E-01	-0.8	4.5E-01
ENSMUST00000183608				11.9	5.1E-06	6.1	4.0E-04	-0.6	6.0E-01	0.1	8.4E-01
ENSMUST00000118506				11.8	1.1E-07	-3.2	6.4E-02	0.7	3.7E-01	0.6	7.2E-01
ENSMUST00000144571				-2.4	3.9E-02	-1.0	4.4E-01	0.6	5.0E-01	-0.9	4.8E-01
ENSMUST00000189727				11.8	1.7E-05	4.8	5.8E-04	-3.6	8.1E-03	0.4	4.5E-01
ENSMUST00000138771				11.6	1.2E-06	5.2	2.9E-04	-2.3	5.0E-02	-0.1	8.5E-01
ENSMUST00000127253				11.6	1.0E-05	-6.5	1.6E-03	0.1	8.0E-01	0.3	8.2E-01
ENSMUST00000186941				11.5	9.7E-06	-1.3	3.8E-01	2.2	4.7E-02	0.3	8.6E-01
ENSMUST00000144577	mediator complex subunit 8 [Source:MGI Symbol;Acc:MGI:1915269]	A2A9C6		-2.1	6.6E-02	-3.4	2.4E-02	-0.3	7.3E-01	1.0	4.5E-01
ENSMUST00000188054				11.5	1.7E-04	2.9	4.6E-03	0.3	6.6E-01	-0.2	7.0E-01
ENSMUST00000144583				2.1	1.0E-01	-0.9	6.5E-01	0.0	9.8E-01	3.0	1.2E-01
ENSMUST00000099459				11.5	8.7E-05	-3.2	1.4E-01	1.3	2.5E-01	-0.6	7.7E-01
ENSMUST00000144586				3.5	4.6E-02	0.5	7.6E-01	-1.9	2.4E-01	1.1	4.7E-01
ENSMUST00000117895				11.4	1.4E-03	7.5	3.9E-04	-0.6	6.8E-01	0.6	4.5E-01
ENSMUST00000144588				1.6	5.8E-02	2.2	6.0E-02	0.8	4.3E-01	0.1	8.8E-01
ENSMUST00000195022				11.4	2.9E-05	6.8	4.1E-02	-0.3	9.2E-01	-0.2	8.9E-01
ENSMUST00000081929				11.3	4.6E-05	6.4	1.2E-03	-2.1	2.2E-01	-0.9	2.5E-01
ENSMUST00000144620	patched homolog 2 [Source:MGI Symbol;Acc:MGI:1095405]	D6RG83		0.9	6.5E-01	6.5	1.1E-02	0.2	9.1E-01	-5.4	7.8E-03
ENSMUST00000144622				4.7	6.2E-02	8.1	1.3E-02	1.1	6.8E-01	-2.2	2.0E-01
ENSMUST00000144624				-0.1	9.7E-01	-2.4	6.4E-01	-1.4	6.5E-01	0.8	8.7E-01
ENSMUST00000134808				11.3	1.7E-04	7.4	4.7E-05	-0.5	6.4E-01	-0.9	1.5E-01
ENSMUST00000119799				11.3	1.2E-07	5.0	1.1E-02	-0.6	7.1E-01	-1.0	3.6E-01
ENSMUST00000144630				3.4	1.1E-01	0.4	9.1E-01	0.6	7.9E-01	3.6	2.4E-01
ENSMUST00000144636				-0.7	5.5E-01	-2.1	2.8E-01	-0.6	6.1E-01	0.8	6.5E-01
ENSMUST00000188559				11.3	1.2E-04	-2.4	4.7E-02	0.3	6.3E-01	-0.1	9.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000156753				11.3	2.9E-04	-0.4	7.4E-01	-5.3	2.7E-03	-1.5	1.5E-01
ENSMUST00000142573				11.3	1.1E-04	4.9	9.2E-04	-2.2	8.4E-02	0.2	7.6E-01
ENSMUST00000144662	family with sequence similarity 111, member A [Source:MGI Symbol;Acc:MGI:1915508]		Q9D2L9	-1.3	3.6E-01	6.1	2.9E-03	2.1	1.8E-01	-5.3	1.8E-03
ENSMUST00000122031				11.2	2.8E-04	3.0	2.6E-03	-0.3	6.4E-01	-0.2	7.4E-01
ENSMUST00000132127				11.2	1.3E-05	3.7	1.8E-03	-1.8	6.8E-02	0.3	6.7E-01
ENSMUST00000178408				11.2	5.6E-05	4.7	1.8E-03	0.4	7.0E-01	-0.1	9.0E-01
ENSMUST00000144388				11.0	4.8E-05	-4.3	2.3E-02	0.8	3.6E-01	-2.0	3.2E-01
ENSMUST00000177105				11.0	1.1E-05	-4.0	1.4E-02	1.8	1.8E-02	-1.6	3.3E-01
ENSMUST00000144674				4.0	3.9E-02	2.2	3.0E-01	-0.9	6.1E-01	1.0	5.7E-01
ENSMUST00000179462				10.9	1.7E-05	7.6	1.2E-04	-0.4	7.5E-01	-1.1	1.1E-01
ENSMUST00000163148				10.9	1.2E-04	7.7	5.6E-05	0.0	1.0E+00	0.5	4.2E-01
ENSMUST00000128064				10.9	2.5E-05	4.4	6.5E-03	0.3	7.8E-01	-0.4	6.3E-01
ENSMUST00000120169				10.9	1.7E-08	5.8	1.2E-03	-0.5	7.1E-01	-1.6	5.6E-02
ENSMUST00000144687				2.0	4.1E-02	2.4	6.7E-02	0.5	6.4E-01	0.1	9.3E-01
ENSMUST00000195740				10.9	2.2E-06	-3.7	1.4E-02	0.1	8.9E-01	-2.8	9.6E-02
ENSMUST00000165058				10.8	2.8E-04	3.4	1.2E-03	-0.7	3.5E-01	-0.4	4.4E-01
ENSMUST00000144700	in homology domain containing, family G (with RhoGef domain) member 2 [Source:MGI Symbol;Acc:MGI:2			2.3	3.0E-01	4.3	1.1E-01	-0.1	9.8E-01	-2.1	3.1E-01
ENSMUST00000165520				10.8	1.0E-03	-1.3	3.3E-01	0.5	5.7E-01	-1.6	2.5E-01
ENSMUST00000144716				1.0	1.9E-01	1.2	3.5E-01	2.0	5.1E-02	1.9	7.7E-02
ENSMUST00000142177				10.8	1.6E-04	4.5	1.8E-02	-0.3	8.4E-01	-1.0	3.5E-01
ENSMUST00000150490				10.8	5.6E-05	0.0	9.9E-01	1.3	3.6E-01	-2.4	1.5E-01
ENSMUST00000144729				1.5	8.4E-02	3.2	6.6E-03	0.4	6.4E-01	-1.3	1.2E-01
ENSMUST00000144739	oculocutaneous albinism II [Source:MGI Symbol;Acc:MGI:97454]	D6RIQ8		5.5	3.6E-02	4.3	1.4E-01	-0.5	8.5E-01	0.7	6.9E-01
ENSMUST00000182205				10.8	2.8E-04	7.8	2.6E-04	0.0	1.0E+00	0.6	3.8E-01
ENSMUST00000173612				10.8	2.4E-04	-2.8	5.0E-02	0.9	1.8E-01	-1.4	3.5E-01
ENSMUST00000159482				10.7	4.5E-06	4.5	7.2E-03	0.0	9.7E-01	0.2	8.1E-01
ENSMUST00000144748				1.5	1.8E-01	1.5	1.9E-01	-1.4	1.7E-01	-1.4	1.9E-01
ENSMUST00000144751				0.1	9.5E-01	2.2	1.4E-01	-0.2	8.7E-01	-2.3	9.9E-02
ENSMUST00000144754				4.2	1.5E-01	6.6	4.7E-02	-0.2	9.6E-01	-2.5	1.8E-01
ENSMUST00000120687				10.7	2.0E-06	5.3	8.0E-03	-0.5	7.5E-01	-0.5	6.1E-01
ENSMUST00000128712				10.7	7.4E-05	5.7	1.8E-04	-1.4	1.7E-01	-0.6	3.2E-01
ENSMUST00000154445				10.7	6.2E-06	-6.0	3.0E-02	-0.7	4.7E-01	-1.0	7.2E-01
ENSMUST00000144766				1.2	2.1E-01	0.2	8.5E-01	0.3	7.5E-01	1.2	3.1E-01
ENSMUST00000181439				10.7	1.4E-05	-2.3	1.2E-01	1.2	1.2E-01	-0.3	8.6E-01
ENSMUST00000119155				10.7	4.3E-04	7.5	1.2E-04	-0.6	6.3E-01	-1.1	1.2E-01
ENSMUST00000144777				0.0	9.7E-01	1.1	5.1E-01	1.3	3.8E-01	0.1	9.3E-01
ENSMUST00000144779				0.0	9.6E-01	1.4	1.9E-01	0.5	5.0E-01	-0.8	3.9E-01
ENSMUST00000144782				2.5	4.2E-01	3.8	3.9E-01	2.2	6.1E-01	0.8	7.7E-01
ENSMUST00000124213				10.7	7.6E-06	2.2	9.1E-03	-0.2	7.6E-01	-0.3	5.7E-01
ENSMUST00000144791				-1.5	1.9E-01	-1.2	3.8E-01	-0.6	5.5E-01	-0.9	5.0E-01
ENSMUST00000143729				10.7	2.1E-06	4.5	3.2E-03	-1.1	3.2E-01	0.3	6.4E-01
ENSMUST00000108744				10.6	6.9E-04	7.0	4.5E-04	0.5	7.0E-01	-0.6	4.0E-01
ENSMUST00000156279				10.6	3.7E-06	6.7	5.8E-04	0.5	7.2E-01	-1.1	1.6E-01
ENSMUST00000127303				10.6	1.5E-05	5.4	5.4E-03	-0.9	5.6E-01	0.2	8.4E-01
ENSMUST00000144806	osteopetrosis associated transmembrane protein 1 [Source:MGI Symbol;Acc:MGI:2655574]	D3Z4W7		0.5	8.3E-01	-1.3	6.0E-01	-2.6	1.6E-01	-0.8	7.5E-01
ENSMUST00000108009				10.6	1.3E-05	-1.2	4.0E-01	0.9	3.1E-01	-0.8	6.1E-01
ENSMUST00000144811				0.8	5.8E-01	1.2	3.8E-01	-1.9	1.5E-01	-2.3	1.3E-01
ENSMUST00000144812				0.7	3.4E-01	0.3	7.0E-01	-0.1	8.8E-01	0.2	7.5E-01
ENSMUST00000120782				10.6	2.2E-05	-2.6	1.7E-01	0.5	5.9E-01	-0.1	9.6E-01
ENSMUST00000144819				-0.5	5.6E-01	0.8	4.7E-01	0.1	8.7E-01	-1.1	2.6E-01
ENSMUST00000124524				10.6	2.0E-07	4.5	2.2E-03	0.4	6.8E-01	0.5	5.1E-01
ENSMUST00000176608				10.6	1.6E-06	2.7	2.4E-03	0.4	5.1E-01	-0.3	6.3E-01
ENSMUST00000162537				10.5	3.5E-06	5.5	1.0E-03	-0.5	6.7E-01	-0.3	6.6E-01
ENSMUST00000164110				10.5	1.2E-04	2.7	9.5E-02	-0.1	9.5E-01	1.0	3.8E-01
ENSMUST00000121335				10.5	3.9E-05	-3.8	2.9E-02	0.2	8.3E-01	-1.1	5.2E-01
ENSMUST00000126892				10.5	2.9E-04	6.1	3.8E-04	-0.6	6.2E-01	0.4	5.4E-01
ENSMUST00000121696				10.4	4.6E-04	6.3	8.3E-05	-1.6	1.6E-01	0.3	5.5E-01
ENSMUST00000144843	SLAIN motif family, member 2 [Source:MGI Symbol;Acc:MGI:1923241]		Q8CI08	-5.4	4.2E-02	-5.8	8.5E-02	-0.6	6.1E-01	-0.2	9.5E-01
ENSMUST00000144845	cystatin C [Source:MGI Symbol;Acc:MGI:102519]	A2APX3		-1.3	6.1E-01	-7.1	7.3E-02	-4.9	1.9E-02	1.0	7.9E-01
ENSMUST00000149030				10.4	1.9E-05	4.8	6.8E-03	-0.3	8.1E-01	-0.9	3.8E-01
ENSMUST00000144851	yrdC domain containing (E.coli) [Source:MGI Symbol;Acc:MGI:2387201]	G8JL83		1.5	5.0E-02	1.7	5.5E-02	0.3	6.4E-01	0.1	9.0E-01
ENSMUST00000144857				0.7	4.2E-01	2.3	6.0E-02	0.4	6.4E-01	-1.1	2.4E-01
ENSMUST00000186942				10.4	1.4E-04	-8.6	1.1E-04	-0.4	2.9E-01	0.4	7.5E-01
ENSMUST00000116643				10.4	2.2E-04	6.6	7.2E-05	-0.7	4.9E-01	-0.5	3.5E-01
ENSMUST00000144868				-3.7	1.0E-01	-0.1	9.6E-01	0.6	6.8E-01	-3.0	1.9E-01
ENSMUST00000118203				10.4	3.4E-06	5.7	7.3E-04	-1.4	2.8E-01	-0.1	8.9E-01
ENSMUST00000153801				10.4	1.1E-06	8.5	8.1E-04	1.5	4.0E-01	1.0	2.1E-01
ENSMUST00000151343				10.3	3.5E-04	-3.4	3.0E-02	-0.5	5.1E-01	0.4	7.8E-01
ENSMUST00000188384				10.3	3.1E-06	5.0	3.1E-03	0.5	6.5E-01	0.2	7.6E-01
ENSMUST00000144883	serine/threonine kinase 11 [Source:MGI Symbol;Acc:MGI:1341870]		Q9WTK7	-1.6	6.7E-02	-1.1	3.5E-01	1.0	1.7E-01	0.5	6.3E-01
ENSMUST00000120188				10.3	1.9E-05	5.1	3.5E-04	-1.1	2.4E-01	0.3	5.9E-01
ENSMUST00000131538				10.3	2.8E-05	3.4	1.2E-01	-0.6	7.7E-01	1.4	3.1E-01
ENSMUST00000144890				-1.5	6.6E-01	2.1	5.2E-01	0.1	9.6E-01	-3.4	3.0E-01
ENSMUST00000191847				10.3	6.6E-06	6.0	2.9E-03	1.4	3.4E-01	0.5	5.7E-01
ENSMUST00000144893				0.3	7.8E-01	2.2	8.2E-02	-0.2	8.8E-01	-2.0	8.2E-02
ENSMUST00000126982				10.3	1.3E-03	5.4	9.1E-05	-0.6	4.5E-01	0.6	2.1E-01
ENSMUST00000188428				10.3	4.5E-05	4.9	2.0E-05	0.1	8.4E-01	0.4	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000195094				10.3	3.1E-06	4.6	5.6E-03	-0.8	5.6E-01	-1.7	9.6E-02
ENSMUST00000127826				10.3	4.5E-06	-0.7	3.6E-01	0.8	1.3E-01	-0.2	7.5E-01
ENSMUST00000144917				-10.3	6.0E-02	-2.4	6.7E-01	5.6	9.1E-02	-2.3	7.2E-01
ENSMUST00000144918				0.2	7.8E-01	2.4	4.7E-02	1.1	2.3E-01	-1.0	2.7E-01
ENSMUST00000144920	cytidine monophospho-N-acetylneuraminic acid synthetase [Source:MGI Symbol;Acc:MGI:1337124]			0.5	6.1E-01	1.2	3.4E-01	-0.4	7.0E-01	-1.0	3.6E-01
ENSMUST00000182142				10.3	2.0E-05	7.8	4.4E-05	-0.6	6.2E-01	-2.4	3.4E-03
ENSMUST00000162664				10.3	1.3E-05	4.7	7.9E-03	-0.5	7.4E-01	-0.6	5.2E-01
ENSMUST00000144934				2.0	1.8E-01	2.8	7.5E-02	-0.5	7.1E-01	-1.3	2.9E-01
ENSMUST00000194164				10.3	2.4E-05	-1.8	1.7E-01	1.4	9.6E-02	-1.2	3.9E-01
ENSMUST00000144942	sterol regulatory element binding transcription factor 1 [Source:MGI Symbol;Acc:MGI:107606]	A0A0A0MQK3		0.5	8.6E-01	1.4	7.3E-01	2.4	4.5E-01	1.5	6.7E-01
ENSMUST00000135077				10.3	9.0E-07	6.7	9.9E-04	0.8	5.6E-01	-0.3	7.4E-01
ENSMUST00000144946				-4.4	4.4E-02	-5.2	1.6E-01	0.4	7.6E-01	1.2	7.4E-01
ENSMUST00000144958				-0.6	4.9E-01	-1.1	2.3E-01	-1.7	4.2E-02	-1.2	2.2E-01
ENSMUST00000144962				-0.5	5.8E-01	-1.7	3.8E-01	1.7	1.9E-01	2.9	1.1E-01
ENSMUST00000144964				0.1	8.6E-01	0.7	4.9E-01	0.1	8.9E-01	-0.4	6.2E-01
ENSMUST00000144967	RNA binding motif protein 33 [Source:MGI Symbol;Acc:MGI:1919670]	F6RNF9		1.6	3.6E-01	2.9	1.4E-01	-1.0	5.7E-01	-2.2	1.9E-01
ENSMUST00000117603				10.3	3.8E-05	6.4	3.3E-05	-1.3	1.7E-01	-0.5	3.8E-01
ENSMUST00000161465				10.3	3.6E-04	4.1	2.4E-03	0.6	5.3E-01	-0.7	2.8E-01
ENSMUST00000144973				6.3	7.4E-02	4.8	2.2E-01	-0.4	9.1E-01	1.1	6.8E-01
ENSMUST00000144978				-1.4	5.5E-01	-4.2	1.3E-01	-3.3	6.6E-02	-0.4	8.8E-01
ENSMUST00000140759				10.2	1.0E-03	7.9	8.0E-05	-0.6	6.1E-01	-0.1	8.6E-01
ENSMUST00000117724				10.2	1.0E-04	6.1	1.5E-03	-1.0	5.0E-01	-0.7	3.7E-01
ENSMUST00000162206				10.2	1.1E-04	2.5	2.4E-01	0.1	9.7E-01	1.2	4.3E-01
ENSMUST00000141771				10.2	6.4E-07	-1.4	1.9E-01	1.1	1.0E-01	-0.8	4.8E-01
ENSMUST00000153802				10.2	2.6E-05	6.3	5.2E-04	-1.3	3.3E-01	0.3	6.2E-01
ENSMUST00000165903				10.2	2.4E-04	3.8	1.7E-03	0.3	7.2E-01	0.5	4.1E-01
ENSMUST00000121099				10.2	1.5E-03	5.6	2.0E-06	-0.7	2.2E-01	-0.2	5.1E-01
ENSMUST00000191725				10.2	5.1E-05	-4.0	3.0E-03	0.2	7.2E-01	-0.5	6.1E-01
ENSMUST00000145025				-0.5	5.4E-01	-0.4	7.5E-01	0.9	3.3E-01	0.7	5.0E-01
ENSMUST00000145027	WD repeat domain 62 [Source:MGI Symbol;Acc:MGI:1923696]	E9PUI7		6.0	9.3E-02	6.4	8.5E-02	-0.9	8.1E-01	-1.3	5.6E-01
ENSMUST00000145034	transmembrane channel-like gene family 4 [Source:MGI Symbol;Acc:MGI:2669035]			-1.2	3.3E-01	-1.2	4.7E-01	0.0	9.8E-01	0.0	9.8E-01
ENSMUST00000129030				10.2	2.1E-06	6.1	3.8E-04	-0.5	6.9E-01	-0.5	4.2E-01
ENSMUST00000178472				10.2	1.1E-06	5.3	3.1E-03	-0.6	6.8E-01	0.4	6.1E-01
ENSMUST00000143036				10.2	1.6E-06	6.0	1.4E-04	-2.9	2.5E-02	0.2	6.6E-01
ENSMUST00000146850				10.1	6.7E-06	7.0	2.4E-04	-0.4	7.6E-01	-0.5	4.0E-01
ENSMUST00000136971				10.1	7.6E-06	7.3	7.7E-05	-0.5	6.4E-01	-0.5	3.5E-01
ENSMUST00000137155				10.1	1.3E-04	-2.4	1.0E-01	0.8	3.1E-01	0.0	9.9E-01
ENSMUST00000124730				10.1	3.1E-06	2.5	5.8E-02	-0.6	5.6E-01	-0.8	3.3E-01
ENSMUST00000186554				10.1	1.2E-06	5.2	4.4E-03	-0.4	7.6E-01	-1.0	3.2E-01
ENSMUST00000145065				-6.1	5.9E-02	-1.0	7.9E-01	4.0	1.2E-01	-1.1	7.7E-01
ENSMUST00000145067	mcf.2 transforming sequence-like [Source:MGI Symbol;Acc:MGI:103263]	G3UX72		3.6	5.6E-02	7.4	2.1E-02	3.2	2.4E-01	-0.7	6.6E-01
ENSMUST00000109542				10.1	2.0E-06	5.2	1.2E-03	-0.5	6.9E-01	0.0	9.8E-01
ENSMUST00000139480				10.1	3.1E-05	6.3	2.0E-04	-0.6	6.1E-01	0.1	8.9E-01
ENSMUST00000145073	protein phosphatase 1, regulatory (inhibitor) subunit 16B [Source:MGI Symbol;Acc:MGI:2151841]	A2AC90		0.8	6.6E-01	7.0	9.1E-03	4.6	5.2E-02	-1.6	2.8E-01
ENSMUST00000145074				-0.2	9.2E-01	1.9	4.0E-01	-0.2	9.2E-01	-2.3	2.5E-01
ENSMUST00000145079	gamma-glutamyltransferase 1 [Source:MGI Symbol;Acc:MGI:95706]	D3YYH6		-2.0	5.2E-02	-0.2	8.5E-01	1.6	6.2E-02	-0.2	8.8E-01
ENSMUST00000134324				10.1	1.0E-05	5.6	1.3E-03	-0.5	6.9E-01	-2.9	1.1E-02
ENSMUST00000145083				2.8	6.9E-02	3.6	4.9E-02	-1.3	4.1E-01	-2.1	9.8E-02
ENSMUST00000182441				10.1	1.1E-06	5.3	4.2E-03	-2.6	1.2E-01	1.0	3.1E-01
ENSMUST00000169787				10.0	4.7E-06	-4.2	1.5E-02	0.6	4.2E-01	-0.7	6.2E-01
ENSMUST00000190333				10.0	5.4E-06	7.6	8.8E-05	0.4	7.0E-01	-0.2	6.8E-01
ENSMUST00000121090				10.0	4.9E-05	3.0	1.3E-03	-0.3	5.5E-01	0.2	7.7E-01
ENSMUST00000145098				3.0	1.6E-01	4.9	4.0E-02	-0.3	8.9E-01	-2.1	2.0E-01
ENSMUST00000145104				-0.8	7.3E-01	-2.4	4.3E-01	-1.9	2.7E-01	-0.4	9.0E-01
ENSMUST00000140789				10.0	5.1E-05	7.8	2.6E-05	-0.5	6.3E-01	-0.7	1.8E-01
ENSMUST00000172658				10.0	1.3E-04	4.6	3.4E-03	0.5	6.6E-01	1.2	1.2E-01
ENSMUST00000159575				10.0	1.1E-04	5.8	3.1E-04	-0.3	8.0E-01	-0.3	6.8E-01
ENSMUST00000133465				10.0	9.0E-06	4.1	1.2E-02	-1.0	4.3E-01	-0.4	6.7E-01
ENSMUST00000145125				0.4	7.9E-01	0.3	8.5E-01	-3.1	3.0E-02	-2.9	7.4E-02
ENSMUST00000190388				10.0	3.8E-06	5.4	2.2E-05	-0.5	4.4E-01	-0.6	1.9E-01
ENSMUST00000145128				-1.9	7.5E-02	-0.6	6.6E-01	0.7	3.9E-01	-0.6	6.0E-01
ENSMUST00000118172				10.0	3.5E-06	-2.0	2.4E-01	0.2	8.7E-01	-1.2	4.9E-01
ENSMUST00000138584				10.0	1.0E-06	8.2	8.2E-05	-0.7	5.9E-01	-1.7	3.2E-02
ENSMUST00000145138				-2.8	1.3E-01	-1.2	6.0E-01	1.9	2.4E-01	0.4	8.7E-01
ENSMUST00000117747				10.0	1.0E-05	5.9	3.3E-04	0.5	6.3E-01	0.5	3.8E-01
ENSMUST00000133876				10.0	6.0E-05	7.0	1.4E-05	-0.3	7.1E-01	-0.3	5.0E-01
ENSMUST00000145152	diablo homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1913843]	Q8R1D8		1.7	4.6E-02	1.0	3.1E-01	-0.1	9.4E-01	0.6	4.5E-01
ENSMUST00000123147				10.0	3.9E-04	6.5	3.4E-04	0.4	7.1E-01	-0.6	3.5E-01
ENSMUST00000114579				9.9	6.5E-05	-3.5	2.7E-02	-0.3	6.6E-01	-0.5	7.3E-01
ENSMUST00000145157	nucleolar protein 12 [Source:MGI Symbol;Acc:MGI:2146285]	B7ZBY4		-2.1	5.8E-02	-2.1	1.7E-01	1.0	2.7E-01	1.0	4.7E-01
ENSMUST00000151252				9.9	4.0E-07	5.7	1.6E-03	-0.5	6.9E-01	-0.4	6.0E-01
ENSMUST00000148923				9.9	2.4E-06	-7.2	8.7E-03	1.2	1.1E-01	-0.9	7.3E-01
ENSMUST00000145160				1.3	3.4E-01	-1.2	3.8E-01	-3.9	7.3E-03	-1.4	2.9E-01
ENSMUST00000145164				0.2	8.5E-01	0.6	6.3E-01	-0.1	9.0E-01	-0.5	6.3E-01
ENSMUST00000145165	mitogen-activated protein kinase kinase 7 [Source:MGI Symbol;Acc:MGI:1346871]		Q8CE90	-0.4	7.9E-01	1.9	3.5E-01	1.1	5.1E-01	-1.2	4.8E-01
ENSMUST00000145167	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific) [Source:MGI Symbol;Acc:MGI:107898]		Q80TA1	0.2	7.3E-01	0.4	5.9E-01	0.0	9.3E-01	-0.2	8.2E-01
ENSMUST00000131709				9.9	1.1E-06	5.4	1.7E-03	-0.6	6.5E-01	1.1	1.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000120264				9.9	1.9E-04	5.8	3.6E-04	-0.6	6.1E-01	0.6	3.7E-01
ENSMUST00000143794				9.9	1.1E-05	2.5	2.4E-02	-0.4	6.5E-01	0.3	7.2E-01
ENSMUST00000118780				9.8	2.1E-05	2.3	2.4E-02	-2.2	4.2E-02	-0.2	7.6E-01
ENSMUST00000192283				9.8	5.9E-06	7.7	1.6E-05	0.3	7.4E-01	-0.1	8.0E-01
ENSMUST00000170286				9.8	4.7E-05	6.7	2.3E-04	-0.6	6.0E-01	-0.7	3.0E-01
ENSMUST00000176180				9.8	2.4E-05	7.5	3.9E-05	-0.5	6.5E-01	-0.3	5.4E-01
ENSMUST00000145212	tetraspanin 32 [Source:MGI Symbol;Acc:MGI:1350360]	D6RHS4		0.6	6.2E-01	1.6	2.0E-01	-1.5	1.8E-01	-2.4	7.4E-02
ENSMUST00000192709				9.8	7.9E-06	-2.1	7.1E-02	2.9	7.8E-04	0.4	7.1E-01
ENSMUST00000145849				9.8	4.0E-05	5.1	3.4E-02	-0.8	7.3E-01	0.0	1.0E+00
ENSMUST00000189829				9.8	6.3E-05	4.1	5.9E-03	-1.0	4.1E-01	0.4	6.4E-01
ENSMUST00000145219				3.3	8.1E-02	4.5	3.8E-02	-0.2	9.2E-01	-1.5	3.0E-01
ENSMUST00000190945				9.8	5.8E-09	4.5	7.2E-04	-1.5	1.4E-01	-0.1	8.6E-01
ENSMUST00000125260				9.8	3.2E-05	1.0	6.4E-01	-4.1	7.6E-02	2.8	1.1E-01
ENSMUST00000145491				9.8	3.2E-06	5.4	1.7E-02	-0.6	7.5E-01	1.4	2.3E-01
ENSMUST00000176956				9.8	1.8E-06	-1.8	2.6E-01	0.7	4.6E-01	-1.0	5.4E-01
ENSMUST00000189723				9.8	3.5E-06	3.9	1.9E-02	-0.4	7.9E-01	0.9	3.2E-01
ENSMUST00000131532				9.8	1.8E-07	4.5	1.8E-02	-0.7	6.9E-01	0.4	6.7E-01
ENSMUST00000145259	non-SMC condensin II complex, subunit H2 [Source:MGI Symbol;Acc:MGI:1289164]	D6RGR7		-4.0	4.5E-02	-5.1	4.3E-02	-1.6	1.2E-01	-0.5	8.3E-01
ENSMUST00000163068				9.8	3.3E-06	7.9	7.8E-05	0.4	7.1E-01	-0.7	2.9E-01
ENSMUST00000169113				9.8	1.1E-04	-1.9	4.0E-02	-0.6	3.1E-01	-1.9	6.9E-02
ENSMUST00000145265				-4.5	7.4E-02	-6.4	5.6E-02	-2.0	1.1E-01	-0.1	9.8E-01
ENSMUST00000143640				9.8	1.1E-06	-2.9	5.5E-02	0.3	6.4E-01	1.0	4.6E-01
ENSMUST00000145271				-0.9	1.5E-01	-3.9	3.2E-03	-1.5	1.6E-02	1.5	1.5E-01
ENSMUST00000178263				9.7	6.9E-06	-3.0	1.3E-01	1.3	2.0E-01	-0.2	9.2E-01
ENSMUST00000145275				-1.1	5.7E-01	0.3	9.0E-01	0.8	6.8E-01	-0.6	7.9E-01
ENSMUST00000172395				9.7	1.0E-05	6.3	4.2E-05	-1.9	7.0E-02	-0.3	5.5E-01
ENSMUST00000179014				9.7	4.0E-04	4.3	4.3E-04	-0.4	6.3E-01	0.7	2.0E-01
ENSMUST00000145300				-1.7	8.2E-02	-0.7	5.4E-01	0.2	7.4E-01	-0.8	4.8E-01
ENSMUST00000159310				9.7	2.2E-04	-6.3	1.1E-03	0.3	6.4E-01	-1.0	5.2E-01
ENSMUST00000145304				3.0	3.9E-02	5.6	1.8E-03	-0.9	5.1E-01	-3.4	5.5E-03
ENSMUST00000120893				9.7	9.0E-05	5.0	2.3E-02	-0.7	7.2E-01	0.2	8.7E-01
ENSMUST00000135199				9.7	3.0E-05	2.8	7.1E-03	-0.5	5.3E-01	0.8	2.5E-01
ENSMUST00000152232				9.7	5.0E-05	4.0	1.1E-02	-0.1	9.4E-01	0.6	4.6E-01
ENSMUST00000143523				9.7	6.1E-06	6.1	1.7E-03	-0.4	7.7E-01	2.0	3.9E-02
ENSMUST00000145313				1.3	1.7E-01	2.0	1.0E-01	0.3	7.6E-01	-0.4	6.6E-01
ENSMUST00000145315				0.4	8.1E-01	2.4	1.8E-01	1.5	3.6E-01	-0.6	6.8E-01
ENSMUST00000154262				9.7	9.3E-05	5.4	7.2E-04	-2.0	1.3E-01	-0.5	4.9E-01
ENSMUST00000143267				9.7	5.1E-06	2.2	9.4E-02	6.0	9.9E-05	-0.8	4.5E-01
ENSMUST00000153329				9.7	3.6E-05	6.5	2.0E-04	-0.5	6.7E-01	0.5	4.4E-01
ENSMUST00000165478				9.7	5.0E-06	8.1	6.4E-05	-0.6	6.2E-01	-0.1	8.6E-01
ENSMUST00000123017				9.7	1.7E-05	1.6	1.8E-01	-0.3	7.0E-01	1.4	1.7E-01
ENSMUST00000136176				9.7	1.3E-06	-5.4	5.6E-04	-0.4	3.7E-01	0.3	7.8E-01
ENSMUST00000128208				9.7	1.3E-06	4.2	1.3E-04	-0.4	5.4E-01	-0.7	1.8E-01
ENSMUST00000145335				-2.2	1.6E-01	-4.0	6.9E-02	-1.5	1.9E-01	0.3	8.9E-01
ENSMUST00000187364				9.7	4.1E-06	4.6	4.8E-04	-0.1	8.6E-01	0.3	6.1E-01
ENSMUST00000141187				9.7	6.8E-06	4.8	3.4E-03	0.0	1.0E+00	-0.3	6.4E-01
ENSMUST00000128512				9.7	1.5E-05	-3.3	3.4E-02	0.8	2.6E-01	-0.6	6.8E-01
ENSMUST00000133810				9.7	3.5E-06	4.6	8.0E-02	-0.5	8.4E-01	1.2	4.1E-01
ENSMUST00000145350				-2.7	1.1E-01	-3.1	2.7E-01	1.0	5.3E-01	1.4	5.7E-01
ENSMUST00000156587				9.7	3.1E-04	-0.6	5.7E-01	0.5	4.6E-01	-2.1	8.0E-02
ENSMUST00000193132				9.7	8.1E-05	-2.5	1.8E-02	1.0	6.4E-02	-0.1	8.7E-01
ENSMUST00000078939				9.7	8.6E-05	2.1	9.3E-02	-3.7	2.3E-02	-1.6	1.8E-01
ENSMUST00000183313				9.6	1.1E-06	5.0	8.2E-05	-1.0	1.9E-01	-0.1	8.6E-01
ENSMUST00000144301				9.6	7.7E-05	5.2	8.2E-03	-2.3	2.0E-01	-0.7	4.8E-01
ENSMUST00000079389				9.6	2.6E-08	-7.4	1.4E-02	0.8	3.8E-01	-2.7	3.9E-01
ENSMUST00000145368	capping protein (actin filament) muscle Z-line, beta [Source:MGI Symbol;Acc:MGI:104652]	A0A0A0MQI9		-0.5	8.3E-01	-2.2	3.6E-01	-3.6	4.6E-02	-1.9	4.8E-01
ENSMUST00000132129				9.6	4.9E-06	4.8	6.4E-04	0.2	8.2E-01	-0.1	8.6E-01
ENSMUST00000177263				9.6	2.8E-06	-4.6	4.5E-03	0.4	4.8E-01	-0.6	6.4E-01
ENSMUST00000140144				9.6	9.5E-05	5.9	7.7E-04	0.1	9.1E-01	-1.0	1.8E-01
ENSMUST00000145384				1.8	3.1E-01	3.8	1.5E-01	2.0	3.8E-01	-0.1	9.7E-01
ENSMUST00000134610				9.6	4.4E-06	4.5	6.3E-04	-1.2	2.0E-01	0.0	9.8E-01
ENSMUST00000121294				9.6	1.4E-06	7.3	7.9E-05	-0.6	5.8E-01	0.2	6.9E-01
ENSMUST00000148441				9.6	8.1E-05	8.0	2.2E-06	1.2	1.4E-01	0.0	9.4E-01
ENSMUST00000132567				9.6	3.4E-06	5.3	2.0E-02	-0.5	8.0E-01	1.9	1.3E-01
ENSMUST00000137375				9.6	5.0E-06	7.5	3.6E-03	1.2	5.1E-01	1.2	3.0E-01
ENSMUST00000145394	rho/rac guanine nucleotide exchange factor (GEF) 18 [Source:MGI Symbol;Acc:MGI:2142567]	D3YWI3		0.0	9.6E-01	1.7	2.4E-01	1.3	2.4E-01	-0.3	8.0E-01
ENSMUST00000187431				9.6	3.1E-03	3.6	6.5E-03	1.1	2.5E-01	-0.4	5.9E-01
ENSMUST00000154036				9.6	3.8E-05	6.6	1.2E-03	0.2	8.8E-01	-0.5	5.5E-01
ENSMUST00000167843				9.6	1.6E-05	-3.3	9.4E-03	0.8	1.2E-01	-0.5	6.3E-01
ENSMUST00000145414				1.6	4.2E-02	1.3	1.4E-01	-0.7	2.9E-01	-0.4	5.6E-01
ENSMUST00000184330				9.6	3.5E-05	3.1	1.2E-03	-0.6	3.7E-01	0.6	2.9E-01
ENSMUST00000131753				9.6	9.7E-06	3.1	4.1E-02	0.0	1.0E+00	1.0	3.6E-01
ENSMUST00000145422	senataxin [Source:MGI Symbol;Acc:MGI:2443480]	F6R186		3.0	8.2E-02	0.3	8.8E-01	-2.3	1.4E-01	0.3	8.5E-01
ENSMUST00000161530				9.5	4.6E-05	3.8	9.1E-03	-2.1	1.2E-01	0.7	4.3E-01
ENSMUST00000145432	tetratricopeptide repeat domain 3 [Source:MGI Symbol;Acc:MGI:1276539]	Q05BF2		4.0	1.0E-01	4.3	6.6E-02	-1.8	4.6E-01	-2.0	2.1E-01
ENSMUST00000149997				9.5	3.1E-05	6.4	6.7E-03	0.5	7.8E-01	0.1	9.3E-01
ENSMUST00000172717				9.5	3.8E-08	1.8	3.9E-02	-1.8	2.5E-02	0.4	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000127295				9.5	1.2E-05	5.4	7.8E-03	-0.7	7.0E-01	0.7	4.8E-01
ENSMUST00000132050				9.5	1.1E-04	5.5	1.0E-02	0.0	9.9E-01	-1.0	3.6E-01
ENSMUST00000145447				0.4	6.0E-01	0.7	4.1E-01	0.5	5.0E-01	0.1	9.0E-01
ENSMUST00000145454	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]	E9QAJ4		-0.4	6.7E-01	-0.3	8.0E-01	0.4	6.6E-01	0.3	7.8E-01
ENSMUST00000145455	deoxyguanosine kinase [Source:MGI Symbol;Acc:MGI:1351602]	S4R1F5		2.2	9.3E-02	2.7	1.3E-01	0.3	8.3E-01	-0.1	9.1E-01
ENSMUST00000131243				9.5	1.5E-04	3.2	3.3E-03	-0.1	8.4E-01	0.7	2.3E-01
ENSMUST00000145459	ankyrin repeat and zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1098746]	J3KMQ5		-2.8	1.1E-01	1.3	7.0E-01	5.9	2.8E-02	1.8	5.2E-01
ENSMUST00000159161				9.5	2.2E-06	7.3	7.5E-05	-2.1	1.1E-01	0.7	2.9E-01
ENSMUST00000145463	BCL2-associated agonist of cell death [Source:MGI Symbol;Acc:MGI:1096330]	F6S493		-1.9	5.0E-02	-0.7	4.2E-01	-1.2	7.6E-02	-2.5	2.1E-02
ENSMUST00000145466				2.4	1.4E-01	-1.9	3.5E-01	-3.3	4.3E-02	1.1	5.8E-01
ENSMUST00000145467	cyclin G associated kinase [Source:MGI Symbol;Acc:MGI:2442153]	D6RHK5		-1.5	3.0E-01	-1.8	3.4E-01	0.0	9.8E-01	0.4	8.5E-01
ENSMUST00000145470				-2.1	3.5E-02	-4.0	2.2E-02	-1.1	1.4E-01	0.8	5.8E-01
ENSMUST00000145477	spermine synthase [Source:MGI Symbol;Acc:MGI:109490]	E9PZ58		0.0	1.0E+00	-0.9	5.1E-01	-0.8	4.8E-01	0.2	9.1E-01
ENSMUST00000118130				9.5	3.6E-06	6.4	6.3E-03	0.3	8.8E-01	-1.5	2.1E-01
ENSMUST00000135250				9.5	7.8E-06	-4.8	1.9E-03	-1.0	9.8E-02	-1.3	3.4E-01
ENSMUST00000188239				9.5	1.7E-04	6.0	4.1E-04	-0.5	6.6E-01	0.2	7.4E-01
ENSMUST00000145484				-3.1	5.1E-02	-1.3	6.0E-01	2.7	1.0E-01	0.9	6.9E-01
ENSMUST00000176697				9.5	6.7E-06	6.6	1.6E-02	-0.9	7.2E-01	-1.1	4.3E-01
ENSMUST00000136089				9.5	7.5E-05	6.3	8.7E-05	-2.6	3.3E-02	0.9	1.1E-01
ENSMUST00000152345				9.5	1.5E-06	6.1	5.3E-04	0.1	9.6E-01	0.0	9.7E-01
ENSMUST00000167658				9.5	2.4E-05	6.2	2.8E-03	-0.4	8.3E-01	-1.9	6.6E-02
ENSMUST00000150641				9.5	6.0E-06	5.6	7.4E-04	-2.2	9.6E-02	-0.2	8.1E-01
ENSMUST00000149856				9.5	6.7E-06	4.4	4.1E-03	-1.0	3.7E-01	-1.0	2.8E-01
ENSMUST00000191695				9.4	8.8E-05	5.6	8.5E-05	-0.3	7.1E-01	0.1	8.8E-01
ENSMUST00000037284				9.4	1.4E-04	1.8	9.6E-02	-0.4	6.2E-01	0.0	9.8E-01
ENSMUST00000133882				9.4	4.3E-06	5.1	5.3E-03	-0.3	8.1E-01	1.9	5.0E-02
ENSMUST00000145514				0.7	4.2E-01	1.0	3.4E-01	-0.8	3.9E-01	-1.0	3.0E-01
ENSMUST00000145518	structural maintenance of chromosomes 1A [Source:MGI Symbol;Acc:MGI:1344345]	S4R179		-1.7	3.6E-01	-3.8	1.3E-01	-1.8	2.1E-01	0.2	9.3E-01
ENSMUST00000164211				9.4	2.8E-05	8.2	3.5E-04	-0.2	8.9E-01	0.5	5.0E-01
ENSMUST00000140110				9.4	1.8E-05	5.0	8.8E-03	-0.6	7.0E-01	0.4	6.6E-01
ENSMUST00000134823				9.4	6.2E-06	8.0	1.1E-02	-0.8	7.7E-01	-1.9	2.1E-01
ENSMUST00000173024				9.4	2.3E-05	6.3	1.4E-04	-0.4	7.4E-01	-0.1	8.9E-01
ENSMUST00000127214				9.4	7.9E-06	2.2	3.0E-01	-1.9	3.6E-01	0.8	6.4E-01
ENSMUST00000145539	otassium voltage-gated channel, subfamily H (eag-related), member 6 [Source:MGI Symbol;Acc:MGI:2684139	M0QW64		3.4	1.5E-01	5.3	4.0E-02	-0.5	8.2E-01	-2.5	1.5E-01
ENSMUST00000164020				9.4	6.7E-06	5.9	3.0E-03	-0.5	7.2E-01	-0.6	5.1E-01
ENSMUST00000146249				9.4	1.2E-05	3.6	9.5E-02	0.0	9.9E-01	3.2	3.0E-02
ENSMUST00000153182				9.4	1.9E-05	-3.6	8.0E-02	0.0	9.7E-01	0.3	9.0E-01
ENSMUST00000145566				0.3	8.0E-01	-1.1	6.1E-01	1.3	3.7E-01	2.8	1.7E-01
ENSMUST00000145567	cullin 7 [Source:MGI Symbol;Acc:MGI:1913765]	E9Q6H4		0.9	6.2E-01	-1.6	5.8E-01	-0.3	8.9E-01	2.2	4.0E-01
ENSMUST00000132700				9.4	6.0E-06	5.2	2.7E-02	-0.6	7.5E-01	-1.3	3.0E-01
ENSMUST00000160803				9.4	6.9E-05	-2.4	6.5E-02	0.3	7.1E-01	0.6	6.2E-01
ENSMUST00000093146				9.4	2.1E-05	5.2	4.3E-02	-0.6	8.2E-01	-0.2	8.6E-01
ENSMUST00000123449				9.4	9.5E-05	-2.0	1.3E-01	1.1	1.4E-01	-0.7	6.0E-01
ENSMUST00000138757				9.4	7.1E-05	3.2	7.2E-02	0.4	8.0E-01	0.8	5.0E-01
ENSMUST00000144287				9.4	1.9E-05	5.8	3.4E-03	0.9	5.4E-01	-0.1	9.3E-01
ENSMUST00000145607				0.7	5.7E-01	2.5	1.2E-01	0.9	5.0E-01	-1.0	4.3E-01
ENSMUST00000145855				9.4	1.8E-04	6.8	2.2E-05	-1.4	1.3E-01	0.4	3.4E-01
ENSMUST00000141746				9.4	2.3E-05	-7.9	1.3E-04	0.2	6.1E-01	-1.7	2.8E-01
ENSMUST00000118538				9.4	2.8E-05	2.9	9.9E-05	-0.5	2.6E-01	-0.5	1.6E-01
ENSMUST00000129619				9.4	5.4E-04	6.2	1.8E-04	-0.5	6.4E-01	-0.9	1.6E-01
ENSMUST00000145622	zinc finger protein 715 [Source:MGI Symbol;Acc:MGI:1917180]	S4R1I9		-1.0	2.0E-01	0.9	2.9E-01	0.8	2.1E-01	-1.0	2.2E-01
ENSMUST00000131039				9.4	4.4E-06	5.7	5.9E-03	-0.7	6.8E-01	-0.8	4.2E-01
ENSMUST00000132894				9.4	2.4E-05	1.9	2.3E-02	0.9	1.2E-01	0.7	2.4E-01
ENSMUST00000146332				9.4	3.3E-05	-5.4	6.7E-04	-0.6	1.7E-01	-0.8	5.0E-01
ENSMUST00000117151				9.4	4.4E-06	6.9	5.3E-04	-0.7	6.3E-01	0.5	4.6E-01
ENSMUST00000145640	TAO kinase 3 [Source:MGI Symbol;Acc:MGI:3041177]			0.3	9.0E-01	1.5	6.3E-01	0.9	6.3E-01	-0.2	9.3E-01
ENSMUST00000154061				9.4	4.7E-06	2.6	3.7E-03	-0.2	6.9E-01	-0.1	8.8E-01
ENSMUST00000117124				9.4	1.9E-04	4.5	1.9E-03	-1.8	1.5E-01	-0.4	5.6E-01
ENSMUST00000145651				-2.3	1.8E-01	-3.1	3.6E-01	2.0	2.2E-01	2.8	3.8E-01
ENSMUST00000145657	ubiquitination factor E4A [Source:MGI Symbol;Acc:MGI:2154580]	D6RGN7		0.0	9.9E-01	0.9	6.9E-01	-1.5	4.7E-01	-2.4	3.3E-01
ENSMUST00000184461				9.3	1.4E-06	-2.9	2.8E-02	0.7	2.7E-01	-1.4	2.9E-01
ENSMUST00000125420				9.3	1.3E-05	7.1	1.1E-04	-0.9	4.4E-01	-1.5	4.2E-02
ENSMUST00000129555				9.3	3.0E-05	-1.6	4.2E-01	1.7	2.6E-01	-0.6	7.4E-01
ENSMUST00000152575				9.3	1.2E-02	-5.2	3.8E-02	2.0	3.5E-02	3.3	1.5E-01
ENSMUST00000145668				1.8	3.5E-01	1.2	6.1E-01	-0.9	6.0E-01	-0.3	8.7E-01
ENSMUST00000194624				9.3	1.8E-04	4.2	2.9E-02	-3.0	1.2E-01	1.8	1.4E-01
ENSMUST00000154222				9.3	8.3E-04	5.2	1.1E-03	-1.0	4.0E-01	0.2	8.1E-01
ENSMUST00000145675	histone deacetylase 6 [Source:MGI Symbol;Acc:MGI:1333752]	Q3UG37		2.5	3.3E-01	4.0	2.5E-01	0.8	8.0E-01	-0.8	7.6E-01
ENSMUST00000194575				9.3	1.1E-05	-8.1	1.3E-04	-0.8	6.7E-02	-2.2	1.6E-01
ENSMUST00000145680				0.8	4.3E-01	1.3	3.3E-01	0.6	5.4E-01	0.1	9.3E-01
ENSMUST00000191684				9.3	2.3E-05	-2.8	2.1E-02	1.6	1.0E-02	-0.6	5.9E-01
ENSMUST00000145689				1.8	4.2E-02	1.6	1.3E-01	-0.2	8.2E-01	0.1	9.4E-01
ENSMUST00000145692				4.8	7.2E-02	2.4	3.8E-01	-1.6	5.4E-01	0.8	6.9E-01
ENSMUST00000127700				9.3	3.5E-05	-7.4	2.3E-04	0.9	4.9E-02	-0.1	9.2E-01
ENSMUST00000145696				-1.3	1.1E-01	-1.2	1.2E-01	-2.2	4.4E-03	-2.3	1.3E-02
ENSMUST00000185363				9.3	5.8E-05	4.6	1.1E-03	-2.2	6.2E-02	-0.1	8.7E-01
ENSMUST00000111906				9.3	6.9E-05	5.6	2.8E-02	-0.6	7.9E-01	0.8	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000184462				9.3	7.1E-06	6.5	2.2E-04	0.0	9.8E-01	-0.2	7.3E-01
ENSMUST00000145701	inositol polyphosphate-5-phosphatase E [Source:MGI Symbol;Acc:MGI:1927753]		Q9JII1	-3.2	8.2E-02	-4.2	1.6E-01	0.6	6.4E-01	1.6	5.8E-01
ENSMUST00000145702				3.3	5.4E-02	2.2	2.4E-01	-1.5	3.5E-01	-0.4	8.1E-01
ENSMUST00000130887				9.3	6.6E-05	6.8	1.4E-04	-0.6	5.9E-01	-2.2	8.3E-03
ENSMUST00000194559				9.3	4.2E-05	-3.9	4.7E-03	1.1	8.1E-02	-2.3	1.1E-01
ENSMUST00000145714				3.4	4.9E-02	5.6	4.7E-03	-0.5	7.6E-01	-2.8	2.9E-02
ENSMUST00000145720				0.7	3.1E-01	0.6	5.7E-01	0.6	4.0E-01	0.8	3.8E-01
ENSMUST00000145726	tumor necrosis factor, alpha-induced protein 8 [Source:MGI Symbol;Acc:MGI:2147191]	J3QNA5		0.1	9.5E-01	-3.4	1.3E-01	-5.1	9.6E-03	-1.5	5.4E-01
ENSMUST00000145953				9.3	4.5E-06	5.9	2.8E-03	0.4	7.6E-01	-0.8	4.1E-01
ENSMUST00000182704				9.3	2.0E-02	1.4	2.2E-01	-0.5	6.1E-01	0.7	5.0E-01
ENSMUST00000124269				9.3	5.5E-07	7.6	4.7E-04	-0.4	7.7E-01	-1.0	1.8E-01
ENSMUST00000173160				9.3	2.5E-05	5.7	1.2E-04	-0.2	8.3E-01	0.5	4.2E-01
ENSMUST00000145734				-1.0	2.9E-01	0.6	5.9E-01	0.3	7.3E-01	-1.2	2.3E-01
ENSMUST00000185887				9.3	1.8E-05	-3.7	1.1E-04	0.0	8.9E-01	-0.7	2.4E-01
ENSMUST00000127362				9.3	1.9E-05	4.5	1.2E-02	-1.7	3.2E-01	-1.5	1.6E-01
ENSMUST00000184051				9.3	3.9E-05	1.6	1.9E-01	1.8	7.2E-02	-3.0	2.3E-02
ENSMUST00000145741				-0.7	7.5E-01	-3.0	4.0E-01	-1.0	6.0E-01	1.2	7.3E-01
ENSMUST00000134505				9.2	2.8E-05	-2.8	1.9E-01	0.4	7.6E-01	-4.0	1.6E-01
ENSMUST00000166958				9.2	1.3E-04	3.8	5.4E-02	-0.4	8.1E-01	1.0	4.1E-01
ENSMUST00000145747				-0.6	3.8E-01	-1.2	1.7E-01	-0.6	3.2E-01	0.0	9.7E-01
ENSMUST00000185430				9.2	3.2E-06	-0.2	8.2E-01	0.7	3.4E-01	-1.4	1.9E-01
ENSMUST00000143207				9.2	4.3E-04	4.7	6.8E-04	-0.9	3.9E-01	-1.4	6.3E-02
ENSMUST00000145760	ring finger protein 38 [Source:MGI Symbol;Acc:MGI:1920719]	B1AWE9		-2.5	8.7E-02	-1.1	5.5E-01	0.8	5.2E-01	-0.6	7.4E-01
ENSMUST00000145772	WD repeat and SOCS box-containing 1 [Source:MGI Symbol;Acc:MGI:1926139]	M0QWT9		-0.3	6.5E-01	-2.2	2.3E-02	-1.2	4.3E-02	0.7	4.0E-01
ENSMUST00000166800				9.2	3.4E-06	2.6	5.5E-03	-0.2	7.1E-01	0.4	4.7E-01
ENSMUST00000145778	IscU iron-sulfur cluster scaffold homolog (E. coli) [Source:MGI Symbol;Acc:MGI:1913633]	F6ZBG7		-0.7	5.2E-01	-1.1	4.0E-01	-0.8	4.2E-01	-0.3	7.9E-01
ENSMUST00000145781	leucine rich repeat containing 45 [Source:MGI Symbol;Acc:MGI:2387183]	E9PVE2		1.3	6.2E-01	4.7	2.7E-01	2.9	4.6E-01	-0.5	8.4E-01
ENSMUST00000145783				-2.2	6.9E-02	-1.7	2.6E-01	0.5	5.6E-01	0.1	9.6E-01
ENSMUST00000152774				9.2	4.2E-05	4.4	5.7E-04	-0.2	8.3E-01	-0.5	4.1E-01
ENSMUST00000145791	, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3 [Source:MGI Symbol;Acc:MGI:135	Q9JHF5		-1.1	5.2E-01	0.3	8.7E-01	-0.1	9.6E-01	-1.6	4.1E-01
ENSMUST00000145793				-2.6	6.2E-02	1.4	4.1E-01	1.7	2.4E-01	-2.2	1.3E-01
ENSMUST00000110971				9.2	1.9E-05	3.5	1.3E-02	0.8	4.6E-01	-0.4	5.7E-01
ENSMUST00000057521				9.2	1.2E-05	6.0	5.9E-03	-0.6	7.4E-01	-1.9	1.1E-01
ENSMUST00000145040				9.2	7.8E-06	5.9	4.8E-04	-1.3	3.0E-01	-0.4	6.1E-01
ENSMUST00000139315				9.2	9.7E-07	6.2	3.7E-04	1.6	1.5E-01	-0.7	3.3E-01
ENSMUST00000145805				-0.2	9.1E-01	-0.3	8.8E-01	-1.6	3.4E-01	-1.5	5.3E-01
ENSMUST00000184639				9.2	1.8E-04	-3.3	1.0E-01	0.1	9.5E-01	-0.2	9.1E-01
ENSMUST00000145819				0.9	5.3E-01	-3.0	2.0E-01	-2.7	6.4E-02	1.2	5.8E-01
ENSMUST00000145821	vacuolar protein sorting 29 (S. pombe) [Source:MGI Symbol;Acc:MGI:1928344]	D3YYD5		1.2	4.8E-01	-4.4	3.6E-02	-5.8	1.5E-03	-0.3	8.8E-01
ENSMUST00000117856				9.2	4.5E-06	-1.3	3.2E-01	2.5	8.5E-03	-2.5	7.3E-02
ENSMUST00000128871				9.2	3.2E-06	0.9	5.6E-01	2.5	6.8E-02	-3.8	5.9E-02
ENSMUST00000194447				9.2	9.9E-06	3.3	6.2E-03	0.3	7.2E-01	0.5	5.1E-01
ENSMUST00000056767				9.2	1.1E-05	7.7	1.6E-04	-0.2	9.1E-01	-0.8	2.0E-01
ENSMUST00000109501				9.2	1.2E-05	6.2	1.0E-03	1.3	3.2E-01	-0.8	3.0E-01
ENSMUST00000124858				9.2	1.2E-05	5.0	2.2E-04	-0.6	4.6E-01	0.3	5.6E-01
ENSMUST00000149805				9.2	8.0E-06	-6.2	2.7E-04	-1.0	7.8E-02	-0.2	8.4E-01
ENSMUST00000143959				9.2	1.6E-07	7.9	2.2E-04	-1.3	4.0E-01	0.7	3.5E-01
ENSMUST00000150524				9.2	4.9E-06	-5.9	7.2E-02	1.3	2.6E-01	0.5	8.8E-01
ENSMUST00000188175				9.2	6.7E-06	-3.1	2.6E-02	-0.2	7.7E-01	-0.8	5.1E-01
ENSMUST00000182212				9.2	1.6E-05	6.6	2.4E-03	-1.9	3.0E-01	0.8	3.9E-01
ENSMUST00000152427				9.2	4.2E-06	5.0	8.1E-05	0.0	9.7E-01	0.3	5.2E-01
ENSMUST00000194313				9.2	1.0E-05	2.7	3.5E-03	-0.4	5.3E-01	-0.7	2.0E-01
ENSMUST00000161510				9.2	7.2E-04	6.7	3.8E-04	-0.4	7.4E-01	-0.3	6.3E-01
ENSMUST00000120245				9.2	1.8E-05	7.3	3.7E-05	1.1	2.6E-01	-0.2	7.0E-01
ENSMUST00000177412				9.2	1.5E-05	4.5	4.8E-03	-0.7	5.7E-01	-0.1	9.0E-01
ENSMUST00000145867				2.6	6.5E-02	0.0	1.0E+00	1.5	4.0E-01	4.1	3.2E-02
ENSMUST00000145877				2.0	4.0E-02	1.9	1.1E-01	0.0	1.0E+00	0.1	8.9E-01
ENSMUST00000145881				2.8	5.4E-02	2.7	1.0E-01	-0.8	6.1E-01	-0.7	5.6E-01
ENSMUST00000173988				9.2	1.5E-05	7.4	1.7E-03	-0.7	7.0E-01	-1.5	1.5E-01
ENSMUST00000105503				9.2	1.8E-05	5.2	1.7E-03	1.0	3.7E-01	-0.8	3.3E-01
ENSMUST00000193355				9.1	8.8E-06	4.1	2.2E-03	0.3	7.8E-01	-0.1	8.9E-01
ENSMUST00000147443				9.1	4.2E-05	4.7	1.7E-04	0.1	8.7E-01	-0.7	2.1E-01
ENSMUST00000191870				9.1	1.6E-04	3.0	6.8E-03	0.2	7.6E-01	0.6	4.3E-01
ENSMUST00000134536				9.1	4.3E-05	1.5	8.9E-02	-0.2	8.0E-01	0.5	4.7E-01
ENSMUST00000188942				9.1	7.8E-06	-3.6	4.0E-03	0.3	4.6E-01	-0.7	5.3E-01
ENSMUST00000162142				9.1	2.7E-06	5.4	1.6E-03	-1.0	4.5E-01	-0.1	9.1E-01
ENSMUST00000145910	striatin, calmodulin binding protein [Source:MGI Symbol;Acc:MGI:1333757]		O55106	0.1	8.7E-01	0.8	2.7E-01	1.4	2.3E-02	0.7	2.7E-01
ENSMUST00000145917				-0.6	5.2E-01	1.3	2.9E-01	0.8	4.4E-01	-1.1	2.8E-01
ENSMUST00000145919	HMG box domain containing 4 [Source:MGI Symbol;Acc:MGI:1918073]	G3UX81		0.0	9.3E-01	0.4	4.5E-01	0.0	1.0E+00	-0.5	3.9E-01
ENSMUST00000141201				9.1	8.7E-03	4.9	1.5E-02	-0.6	7.3E-01	-0.9	4.1E-01
ENSMUST00000143216				9.1	2.2E-06	4.6	1.6E-02	-1.1	5.0E-01	0.2	8.8E-01
ENSMUST00000190416				9.1	1.2E-04	5.7	3.0E-04	-1.0	3.6E-01	1.0	1.5E-01
ENSMUST00000145934	ankyrin repeat domain 13b [Source:MGI Symbol;Acc:MGI:2144501]	Q5F260		3.0	1.5E-01	3.3	1.1E-01	-1.4	4.7E-01	-1.8	3.0E-01
ENSMUST00000031523				9.1	5.7E-05	4.4	4.4E-02	-0.8	7.0E-01	0.5	6.8E-01
ENSMUST00000145939				-1.8	7.9E-02	-0.8	5.4E-01	0.6	4.3E-01	-0.4	7.3E-01
ENSMUST00000145952				0.5	7.8E-01	0.8	7.6E-01	0.8	7.0E-01	0.6	7.8E-01
ENSMUST00000177762				9.1	1.7E-05	8.4	3.1E-05	-0.6	6.0E-01	0.3	5.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000145958	glia maturation factor, beta [Source:MGI Symbol;Acc:MGI:1927133]	D3YY93		-2.4	5.2E-02	-3.4	2.0E-02	-2.2	1.5E-02	-1.2	3.8E-01
ENSMUST00000179851				9.1	1.7E-05	2.5	1.6E-01	5.7	1.3E-03	-0.6	6.8E-01
ENSMUST00000152411				9.1	7.9E-06	4.8	1.0E-02	-0.6	7.0E-01	-0.9	4.1E-01
ENSMUST00000189055				9.1	7.3E-04	-0.7	5.4E-01	-0.1	9.0E-01	-2.1	9.7E-02
ENSMUST00000149219				9.1	3.0E-06	6.4	1.8E-04	0.2	8.9E-01	-0.3	6.3E-01
ENSMUST00000145976				0.5	7.1E-01	4.3	4.8E-02	2.5	1.8E-01	-1.3	3.4E-01
ENSMUST00000145980	ring finger protein 11 [Source:MGI Symbol;Acc:MGI:1352759]	Z4YLT8		-2.0	1.3E-01	-3.3	4.0E-02	-1.9	5.6E-02	-0.6	7.1E-01
ENSMUST00000145982				-3.6	4.4E-02	-4.0	9.2E-02	0.1	9.0E-01	0.6	8.0E-01
ENSMUST00000132094				9.1	4.7E-05	2.4	2.9E-02	0.1	9.3E-01	-0.2	7.9E-01
ENSMUST00000164673				9.1	2.0E-05	5.3	1.2E-03	-1.5	2.7E-01	-1.1	1.4E-01
ENSMUST00000150260				9.1	2.9E-06	7.1	1.0E-04	0.3	8.0E-01	-1.1	1.1E-01
ENSMUST00000168116				9.0	3.3E-06	3.7	1.0E-03	-1.1	1.5E-01	0.3	6.6E-01
ENSMUST00000187624				9.0	1.3E-05	5.9	2.6E-03	0.0	9.7E-01	-0.3	7.3E-01
ENSMUST00000119250				9.0	1.0E-04	4.0	1.6E-01	0.3	8.9E-01	1.7	3.2E-01
ENSMUST00000141287				9.0	3.0E-06	2.0	4.5E-02	0.1	8.6E-01	0.0	9.8E-01
ENSMUST00000146013				-3.0	1.8E-01	-1.2	6.3E-01	0.2	9.3E-01	-1.6	5.2E-01
ENSMUST00000177287				9.0	6.2E-05	-6.3	4.9E-03	-0.7	3.6E-01	-1.8	4.3E-01
ENSMUST00000146022				2.3	1.1E-01	-0.3	8.5E-01	-2.0	1.4E-01	0.6	7.2E-01
ENSMUST00000146023				0.5	7.7E-01	2.9	1.5E-01	-0.5	7.5E-01	-2.9	1.1E-01
ENSMUST00000051224				9.0	9.7E-06	-3.2	5.8E-02	2.1	1.8E-02	-0.8	6.3E-01
ENSMUST00000188910				9.0	5.5E-06	5.1	3.6E-03	0.0	9.7E-01	0.2	7.8E-01
ENSMUST00000031488				9.0	7.8E-05	7.0	4.1E-05	-0.4	6.9E-01	0.0	9.4E-01
ENSMUST00000117162				9.0	3.6E-06	0.2	8.7E-01	-2.7	6.1E-02	1.1	4.0E-01
ENSMUST00000186071				9.0	2.1E-04	2.2	1.7E-02	0.0	9.9E-01	0.2	7.5E-01
ENSMUST00000132225				9.0	8.2E-05	6.4	2.6E-05	-0.9	3.1E-01	0.5	3.0E-01
ENSMUST00000124193				9.0	1.8E-04	-2.8	1.7E-01	0.9	4.3E-01	-0.5	7.9E-01
ENSMUST00000146044	G protein-coupled receptor kinase-interactor 2 [Source:MGI Symbol;Acc:MGI:1347053]	F6U8T2		1.5	4.7E-01	6.3	3.4E-02	3.6	1.8E-01	-1.2	4.8E-01
ENSMUST00000146053	RAD51 homolog D [Source:MGI Symbol;Acc:MGI:1261809]	Q9EP65		-3.3	1.3E-01	0.9	6.9E-01	1.3	4.9E-01	-2.9	2.1E-01
ENSMUST00000155653				9.0	4.2E-06	-1.9	2.6E-01	1.6	9.1E-02	-0.1	9.6E-01
ENSMUST00000146061				1.4	6.5E-01	3.9	2.8E-01	1.0	7.5E-01	-1.5	6.2E-01
ENSMUST00000176225				9.0	3.6E-07	5.5	7.1E-05	0.8	3.1E-01	0.7	1.8E-01
ENSMUST00000189930				9.0	5.5E-06	-3.6	1.5E-02	-0.9	1.9E-01	-2.2	1.7E-01
ENSMUST00000188321				9.0	7.4E-06	2.3	1.2E-03	0.5	2.5E-01	-0.1	7.5E-01
ENSMUST00000149852				9.0	8.9E-06	7.7	2.8E-04	-0.7	6.2E-01	0.1	8.8E-01
ENSMUST00000146077				-7.7	5.6E-02	-3.9	2.1E-01	-0.5	7.5E-01	-4.3	3.0E-01
ENSMUST00000149976				9.0	1.7E-05	4.3	4.2E-02	-0.1	9.6E-01	2.1	1.2E-01
ENSMUST00000146079				-5.3	6.0E-02	-0.8	8.0E-01	2.6	2.3E-01	-1.9	5.6E-01
ENSMUST00000125588				9.0	2.6E-05	6.8	3.6E-03	-0.2	9.0E-01	-2.1	7.0E-02
ENSMUST00000125557				9.0	4.8E-04	-4.1	3.3E-02	0.8	3.0E-01	-0.8	6.5E-01
ENSMUST00000146087				0.9	1.0E-01	1.2	7.5E-02	-0.8	1.3E-01	-1.1	8.0E-02
ENSMUST00000187688				8.9	3.1E-05	2.7	5.9E-03	0.4	5.8E-01	0.3	6.1E-01
ENSMUST00000118908				8.9	1.4E-05	3.6	2.2E-02	-0.3	8.1E-01	0.3	8.0E-01
ENSMUST00000173974				8.9	4.4E-05	5.2	2.9E-04	-1.9	8.8E-02	-1.1	8.2E-02
ENSMUST00000169065				8.9	3.2E-06	3.9	4.6E-02	-2.6	2.0E-01	-0.6	6.0E-01
ENSMUST00000146100	FCH domain only 1 [Source:MGI Symbol;Acc:MGI:1921265]		Q8K285	1.2	6.3E-01	2.7	5.6E-01	2.9	4.2E-01	1.4	6.9E-01
ENSMUST00000185417				8.9	3.4E-05	-5.1	8.6E-03	1.8	1.9E-02	-1.2	4.9E-01
ENSMUST00000121011				8.9	9.2E-04	3.8	3.3E-02	-1.3	3.9E-01	0.3	7.7E-01
ENSMUST00000132436				8.9	1.4E-05	5.9	1.3E-04	0.0	9.6E-01	-0.4	4.8E-01
ENSMUST00000149798				8.9	1.8E-05	5.0	3.5E-04	0.0	9.6E-01	1.2	6.3E-02
ENSMUST00000190877				8.9	4.0E-08	-3.9	1.5E-02	0.4	5.2E-01	-0.2	9.0E-01
ENSMUST00000146136				0.8	3.4E-01	1.1	2.6E-01	-0.4	5.8E-01	-0.8	3.8E-01
ENSMUST00000174486				8.9	1.2E-05	4.7	1.5E-02	0.1	9.7E-01	1.3	2.1E-01
ENSMUST00000141048				8.9	1.5E-06	6.8	4.8E-05	-0.6	5.4E-01	0.2	7.2E-01
ENSMUST00000126954				8.9	4.0E-05	-3.4	6.9E-02	0.4	6.4E-01	-1.9	3.4E-01
ENSMUST00000146151				1.3	1.2E-01	0.4	6.6E-01	-1.2	1.4E-01	-0.3	7.4E-01
ENSMUST00000160441				8.9	5.8E-05	4.4	4.9E-03	0.6	5.7E-01	-0.1	8.8E-01
ENSMUST00000135604				8.9	8.6E-06	6.3	9.9E-02	-0.9	8.1E-01	1.1	5.9E-01
ENSMUST00000146158				-2.5	1.0E-01	1.4	4.7E-01	1.9	2.7E-01	-2.1	2.1E-01
ENSMUST00000145521				8.9	6.1E-05	5.9	1.9E-03	-0.5	7.5E-01	-0.2	7.8E-01
ENSMUST00000154760				8.9	6.0E-05	2.7	2.0E-02	-1.1	2.3E-01	-0.8	3.2E-01
ENSMUST00000118055				8.9	1.8E-05	5.5	3.3E-02	-1.4	5.4E-01	-0.7	6.4E-01
ENSMUST00000146561				8.9	1.1E-05	6.5	4.0E-04	-0.6	6.5E-01	0.1	8.7E-01
ENSMUST00000146175	nuclear receptor subfamily 2, group C, member 2 [Source:MGI Symbol;Acc:MGI:1352466]	Q3ZAR9		0.9	7.3E-01	-1.8	5.5E-01	-1.2	5.8E-01	1.5	6.2E-01
ENSMUST00000173012				8.9	1.5E-05	5.9	3.5E-04	-0.1	9.2E-01	0.7	2.9E-01
ENSMUST00000184008				8.9	5.9E-05	2.5	2.1E-02	-0.1	9.5E-01	-0.6	4.0E-01
ENSMUST00000186779				8.9	1.2E-05	6.5	3.3E-04	-1.0	4.0E-01	0.5	4.3E-01
ENSMUST00000188083				8.9	7.7E-06	7.5	5.5E-05	-0.6	5.8E-01	0.0	9.4E-01
ENSMUST00000146193				-1.3	2.1E-01	-2.9	5.4E-02	-1.3	1.1E-01	0.3	8.6E-01
ENSMUST00000146201	F-box protein 22 [Source:MGI Symbol;Acc:MGI:1926014]	Q3V492		2.7	1.9E-01	2.5	3.3E-01	-0.5	8.4E-01	-0.3	8.8E-01
ENSMUST00000190812				8.9	7.7E-06	5.4	7.6E-04	-1.4	2.4E-01	-0.6	3.9E-01
ENSMUST00000187416				8.9	7.4E-06	7.4	4.0E-05	-0.5	6.3E-01	-0.3	5.8E-01
ENSMUST00000146207	transmembrane protein 175 [Source:MGI Symbol;Acc:MGI:1919642]	Q8BHJ8		2.2	4.9E-02	2.1	8.3E-02	-0.7	4.9E-01	-0.6	5.1E-01
ENSMUST00000146212				0.9	1.6E-01	0.8	3.0E-01	0.0	9.8E-01	0.0	1.0E+00
ENSMUST00000145673				8.9	3.7E-04	3.6	2.1E-03	0.1	9.1E-01	0.1	9.2E-01
ENSMUST00000117050				8.9	1.7E-04	4.4	1.4E-02	-2.2	1.9E-01	-0.4	6.5E-01
ENSMUST00000146225				-2.1	7.0E-02	-1.5	1.8E-01	-0.7	3.6E-01	-1.3	2.5E-01
ENSMUST00000187830				8.9	3.1E-06	-2.1	2.1E-01	1.8	6.1E-02	-0.2	9.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000146229				2.0	4.4E-01	-0.1	9.8E-01	-0.4	9.0E-01	1.7	5.8E-01
ENSMUST00000137068				8.9	9.2E-06	0.5	6.3E-01	-3.7	3.8E-03	-0.5	5.6E-01
ENSMUST00000146234				-0.5	8.6E-01	0.1	9.9E-01	0.3	9.0E-01	-0.3	9.3E-01
ENSMUST00000176529				8.9	1.5E-05	3.4	7.8E-03	-2.0	6.5E-02	-0.2	8.3E-01
ENSMUST00000146241				0.0	9.8E-01	-0.2	8.6E-01	-0.4	6.0E-01	-0.2	8.4E-01
ENSMUST00000132910				8.9	4.3E-06	0.0	9.8E-01	0.9	5.5E-02	-0.3	6.1E-01
ENSMUST00000175840				8.8	1.8E-06	7.6	1.0E-04	-0.8	5.6E-01	1.1	1.2E-01
ENSMUST00000186012				8.8	2.3E-04	-2.4	1.7E-02	0.3	6.3E-01	-0.2	8.4E-01
ENSMUST00000127212				8.8	7.6E-06	6.2	1.1E-03	-0.7	6.3E-01	0.9	2.8E-01
ENSMUST00000146259				0.1	9.2E-01	0.6	7.5E-01	0.7	6.4E-01	0.2	8.8E-01
ENSMUST00000185367				8.8	2.6E-05	3.8	8.9E-04	-0.5	4.6E-01	-0.8	2.3E-01
ENSMUST00000146262				-0.8	5.5E-01	0.4	8.1E-01	0.7	6.2E-01	-0.5	7.5E-01
ENSMUST00000144572				8.8	8.0E-06	6.6	9.6E-05	0.5	5.7E-01	0.0	9.3E-01
ENSMUST00000146267	major facilitator superfamily domain containing 4 [Source:MGI Symbol;Acc:MGI:2442786]	H7BXC0		3.3	6.3E-02	4.7	1.6E-02	-0.5	7.5E-01	-2.0	1.4E-01
ENSMUST00000193321				8.8	6.9E-08	5.2	9.9E-03	-0.1	9.7E-01	1.3	2.4E-01
ENSMUST00000156759				8.8	7.3E-04	5.7	6.7E-03	-0.4	8.4E-01	-0.8	4.5E-01
ENSMUST00000194538				8.8	6.8E-06	-3.3	1.3E-02	2.3	1.7E-03	0.0	9.7E-01
ENSMUST00000146281				-2.4	7.4E-02	-0.4	7.4E-01	-0.5	5.8E-01	-2.5	7.1E-02
ENSMUST00000155201				8.8	3.5E-05	6.6	1.3E-03	-0.6	6.9E-01	-1.0	2.4E-01
ENSMUST00000177346				8.8	5.5E-07	-5.8	2.9E-02	0.9	3.0E-01	0.3	9.1E-01
ENSMUST00000191419				8.8	2.1E-05	-1.7	2.2E-01	0.3	7.4E-01	-2.6	1.2E-01
ENSMUST00000146610				8.8	4.3E-05	3.7	8.3E-02	-0.7	7.4E-01	3.1	3.3E-02
ENSMUST00000146293				-1.7	6.6E-02	-1.1	3.3E-01	0.4	5.9E-01	-0.2	8.5E-01
ENSMUST00000146297	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	Q3U313	Q8VH51	-6.6	1.8E-01	-0.6	9.1E-01	4.5	2.9E-01	-1.5	7.9E-01
ENSMUST00000146298				-1.2	2.2E-01	-0.3	7.6E-01	-0.5	5.5E-01	-1.4	2.1E-01
ENSMUST00000187770				8.8	7.0E-05	5.8	3.1E-04	-0.4	7.4E-01	1.1	9.2E-02
ENSMUST00000061046				8.8	1.2E-04	5.2	2.7E-03	-0.5	6.9E-01	-0.6	5.1E-01
ENSMUST00000146303				-1.9	9.2E-02	-0.6	6.7E-01	0.5	5.9E-01	-0.8	5.1E-01
ENSMUST00000165816				8.8	4.1E-05	5.5	8.4E-04	-1.5	2.0E-01	-0.2	7.6E-01
ENSMUST00000128515				8.8	4.9E-05	1.7	3.1E-01	8.2	8.4E-05	-0.6	6.7E-01
ENSMUST00000146317	epsin 1 [Source:MGI Symbol;Acc:MGI:1333763]	D3Z4V3		-3.0	7.1E-02	-0.4	8.4E-01	1.2	4.1E-01	-1.5	4.4E-01
ENSMUST00000162857				8.8	6.8E-07	-5.5	2.9E-02	-0.5	6.0E-01	-2.0	4.6E-01
ENSMUST00000118951				8.8	8.3E-05	3.3	6.4E-03	-0.8	3.7E-01	-0.1	9.4E-01
ENSMUST00000125651				8.8	3.3E-05	-1.4	4.3E-01	1.1	3.4E-01	-2.0	3.1E-01
ENSMUST00000107148				8.8	9.7E-05	6.9	2.4E-04	-0.6	6.7E-01	0.3	6.2E-01
ENSMUST00000184741				8.8	1.0E-06	3.4	3.7E-02	-1.9	1.8E-01	-0.5	6.9E-01
ENSMUST00000118770				8.8	2.8E-05	6.8	3.9E-04	-2.7	8.6E-02	-0.2	8.1E-01
ENSMUST00000139022				8.8	7.6E-05	0.1	8.2E-01	1.0	4.6E-02	-0.7	2.5E-01
ENSMUST00000145088				8.8	1.4E-04	2.9	1.4E-02	0.1	8.8E-01	-0.5	5.5E-01
ENSMUST00000150218				8.8	5.7E-06	4.8	1.2E-04	-1.4	7.2E-02	-0.6	2.6E-01
ENSMUST00000180565				8.8	1.1E-05	2.5	5.3E-03	-0.7	3.0E-01	0.2	7.5E-01
ENSMUST00000190601				8.8	9.7E-05	-3.0	1.1E-02	0.7	2.1E-01	-1.9	1.3E-01
ENSMUST00000146355				-1.6	1.4E-01	-1.5	3.4E-01	0.4	6.5E-01	0.3	8.3E-01
ENSMUST00000187819				8.8	2.2E-03	7.2	1.5E-04	-0.6	6.6E-01	-0.9	1.9E-01
ENSMUST00000189490				8.8	2.2E-03	7.2	6.2E-04	0.8	5.7E-01	1.2	1.3E-01
ENSMUST00000121157				8.8	5.0E-06	4.1	1.4E-02	-1.5	3.0E-01	0.1	9.1E-01
ENSMUST00000162689				8.8	1.6E-05	-3.1	1.9E-01	1.6	1.9E-01	-0.7	7.6E-01
ENSMUST00000121279				8.8	1.6E-06	6.7	1.4E-04	0.4	6.8E-01	0.7	2.0E-01
ENSMUST00000146375	lysine (K)-specific methyltransferase 2E [Source:MGI Symbol;Acc:MGI:1924825]	A0A0G2JDX7		-2.0	8.2E-02	-1.5	4.5E-01	1.8	1.4E-01	1.3	4.7E-01
ENSMUST00000085929				8.8	2.4E-05	5.1	7.0E-04	0.2	8.5E-01	0.9	1.6E-01
ENSMUST00000155890				8.8	4.8E-05	3.4	2.7E-03	-2.5	2.9E-02	-0.8	2.5E-01
ENSMUST00000122908				8.8	3.7E-07	5.7	1.3E-03	-0.9	5.3E-01	-0.2	7.9E-01
ENSMUST00000137491				8.8	3.5E-05	5.9	1.5E-03	-0.6	6.9E-01	0.3	6.8E-01
ENSMUST00000130283				8.8	5.5E-06	2.3	4.1E-03	-0.2	6.8E-01	-0.3	5.9E-01
ENSMUST00000193123				8.8	2.4E-05	7.1	3.4E-05	-1.5	1.7E-01	0.3	5.2E-01
ENSMUST00000120589				8.8	6.1E-06	6.5	2.0E-04	-0.6	6.2E-01	0.0	9.9E-01
ENSMUST00000154349				8.8	2.5E-04	-3.9	1.8E-02	0.8	2.7E-01	-0.3	8.4E-01
ENSMUST00000148911				8.8	3.2E-05	1.5	3.4E-02	0.5	2.9E-01	0.4	4.0E-01
ENSMUST00000152826				8.8	2.3E-04	-1.9	3.2E-01	1.2	2.5E-01	-0.3	8.8E-01
ENSMUST00000142328				8.8	3.0E-05	5.3	3.9E-04	-2.5	4.5E-02	0.2	7.7E-01
ENSMUST00000149573				8.8	3.6E-05	6.0	1.0E-03	-1.0	4.9E-01	-0.1	8.9E-01
ENSMUST00000097943				8.8	6.4E-05	3.1	9.9E-02	-2.3	2.3E-01	0.6	6.0E-01
ENSMUST00000190468				8.8	1.0E-04	6.2	1.6E-04	-0.6	6.0E-01	-0.1	8.6E-01
ENSMUST00000131800				8.8	7.6E-06	3.6	1.3E-03	-0.4	5.7E-01	0.6	3.4E-01
ENSMUST00000143161				8.8	5.3E-06	4.9	2.0E-03	0.3	8.0E-01	0.7	3.9E-01
ENSMUST00000146428				1.2	3.9E-01	2.8	1.1E-01	0.1	9.7E-01	-1.5	2.9E-01
ENSMUST00000134125				8.7	4.5E-06	5.4	1.6E-03	-1.7	1.9E-01	0.0	9.7E-01
ENSMUST00000146430	TBC1 domain family, member 14 [Source:MGI Symbol;Acc:MGI:1098708]	E9Q8K4		-5.1	1.4E-01	-5.9	3.4E-01	0.9	7.7E-01	1.7	7.7E-01
ENSMUST00000141388				8.7	8.2E-06	2.8	6.4E-02	1.0	3.9E-01	1.0	3.4E-01
ENSMUST00000188339				8.7	4.5E-05	5.5	2.6E-03	-0.7	5.8E-01	-0.2	7.5E-01
ENSMUST00000168705				8.7	1.4E-03	1.2	3.4E-01	-4.5	1.5E-02	-1.2	2.9E-01
ENSMUST00000146443	erythrocyte membrane protein band 4.1 [Source:MGI Symbol;Acc:MGI:95401]	F7BUB8		-5.6	5.3E-02	0.8	7.4E-01	2.0	3.3E-01	-4.4	1.1E-01
ENSMUST00000060215				8.7	2.4E-05	-4.4	1.8E-03	0.6	2.3E-01	-0.2	8.3E-01
ENSMUST00000177472				8.7	4.9E-07	6.5	1.1E-04	-1.5	2.0E-01	0.6	3.1E-01
ENSMUST00000133390				8.7	1.1E-05	8.3	2.7E-05	-0.5	6.5E-01	-0.8	1.5E-01
ENSMUST00000193031				8.7	2.9E-06	4.3	6.8E-03	1.3	2.8E-01	0.3	6.9E-01
ENSMUST00000151525				8.7	1.4E-06	6.4	1.0E-04	-1.1	2.7E-01	0.2	7.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000140921				8.7	1.5E-05	7.8	6.6E-03	-0.9	7.3E-01	-2.4	9.8E-02
ENSMUST00000146459				0.8	1.3E-01	2.2	9.5E-03	0.9	1.2E-01	-0.4	4.5E-01
ENSMUST00000146466				2.2	1.6E-01	6.8	7.6E-03	2.5	2.2E-01	-2.1	1.0E-01
ENSMUST00000146468	lectin, galactose binding, soluble 3 [Source:MGI Symbol;Acc:MGI:96778]	Q8C253		1.0	3.8E-01	1.7	2.9E-01	0.9	4.8E-01	0.3	8.3E-01
ENSMUST00000144587				8.7	6.9E-05	5.2	1.0E-03	-0.7	5.6E-01	0.8	2.6E-01
ENSMUST00000152145				8.7	2.4E-04	1.7	4.0E-02	-0.4	5.4E-01	-0.1	9.3E-01
ENSMUST00000149336				8.7	1.1E-05	6.6	3.2E-04	-0.5	7.1E-01	-0.2	7.2E-01
ENSMUST00000162331				8.7	1.4E-06	4.0	1.7E-02	-2.6	1.2E-01	-0.9	3.9E-01
ENSMUST00000072800				8.7	2.8E-05	6.5	1.5E-04	-0.6	6.2E-01	-0.5	4.0E-01
ENSMUST00000135335				8.7	3.4E-03	7.5	5.1E-04	0.0	9.8E-01	0.2	7.9E-01
ENSMUST00000150996				8.7	1.6E-04	3.5	3.6E-03	-1.2	1.7E-01	0.0	9.6E-01
ENSMUST00000124807				8.7	2.2E-05	5.9	4.9E-04	-1.4	2.7E-01	0.6	4.3E-01
ENSMUST00000124408				8.7	3.1E-05	6.0	5.6E-03	-0.9	6.0E-01	0.4	6.2E-01
ENSMUST00000182444				8.7	6.2E-05	6.0	4.8E-04	-0.5	7.0E-01	-0.8	2.3E-01
ENSMUST00000183548				8.7	1.2E-04	-0.4	8.0E-01	1.0	3.7E-01	-2.0	2.2E-01
ENSMUST00000156514				8.7	1.4E-05	5.6	1.6E-03	-1.2	3.7E-01	-0.8	3.2E-01
ENSMUST00000146502	phosphatidic acid phosphatase type 2 domain containing 3 [Source:MGI Symbol;Acc:MGI:2445183]	A0A0A6YX24		4.4	3.8E-02	5.2	2.7E-02	-0.9	6.8E-01	-1.7	2.1E-01
ENSMUST00000187294				8.7	6.1E-06	5.1	5.3E-03	-0.5	7.6E-01	-0.5	5.5E-01
ENSMUST00000141705				8.7	3.8E-05	-1.9	2.6E-01	1.5	1.1E-01	-0.8	6.3E-01
ENSMUST00000112073				8.7	1.5E-05	-1.1	3.9E-01	1.2	1.6E-01	-0.7	6.0E-01
ENSMUST00000172626				8.7	3.9E-06	-2.4	3.4E-02	0.8	1.5E-01	1.6	1.1E-01
ENSMUST00000146516	midnolin [Source:MGI Symbol;Acc:MGI:1890222]	D3Z7H2		2.1	4.7E-02	2.7	5.2E-02	-0.2	8.3E-01	-0.8	3.6E-01
ENSMUST00000146525				-1.5	1.7E-01	-3.1	7.0E-02	-0.7	3.9E-01	0.9	5.5E-01
ENSMUST00000146526				-1.0	4.5E-01	-0.5	8.2E-01	1.7	2.5E-01	1.2	5.4E-01
ENSMUST00000117079				8.7	9.5E-06	3.1	1.0E-01	-1.7	3.5E-01	0.6	6.5E-01
ENSMUST00000188982				8.7	7.6E-05	5.2	5.7E-03	-1.3	4.0E-01	-1.4	1.9E-01
ENSMUST00000189465				8.7	2.3E-05	5.9	3.3E-05	-0.1	9.3E-01	0.8	1.3E-01
ENSMUST00000121765				8.7	1.1E-05	8.1	1.2E-03	1.0	5.6E-01	0.4	6.4E-01
ENSMUST00000146545				-2.2	6.3E-02	-4.3	1.1E-02	-2.1	1.8E-02	0.0	9.8E-01
ENSMUST00000144124				8.7	4.1E-05	7.1	2.5E-02	-1.0	7.4E-01	-0.3	8.5E-01
ENSMUST00000188436				8.7	6.0E-06	7.8	7.0E-05	-0.7	5.8E-01	0.4	4.9E-01
ENSMUST00000183308				8.7	1.1E-05	4.6	3.7E-04	-0.9	2.6E-01	0.0	9.6E-01
ENSMUST00000121582				8.7	1.9E-05	6.7	3.1E-04	-0.6	6.7E-01	-0.1	8.8E-01
ENSMUST00000146569	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:106299]	F6XZI3		1.9	8.2E-02	0.3	8.0E-01	-0.5	6.1E-01	1.1	3.8E-01
ENSMUST00000186086				8.7	4.7E-04	-6.3	4.1E-02	-0.7	5.6E-01	-1.4	6.7E-01
ENSMUST00000146584				0.0	9.7E-01	-1.5	3.1E-01	-0.5	5.8E-01	1.0	4.9E-01
ENSMUST00000146585				0.0	9.9E-01	2.3	4.2E-02	1.1	2.2E-01	-1.3	1.7E-01
ENSMUST00000135206				8.7	7.5E-06	-5.0	1.2E-02	0.6	3.5E-01	1.2	4.9E-01
ENSMUST00000146591				2.7	5.7E-02	2.9	2.8E-02	-2.1	1.1E-01	-2.2	5.2E-02
ENSMUST00000161858				8.7	2.0E-06	4.3	3.1E-03	-2.2	1.0E-01	-1.1	1.8E-01
ENSMUST00000151019				8.7	5.4E-06	4.9	6.7E-05	-1.2	1.2E-01	-0.2	6.5E-01
ENSMUST00000194627				8.7	3.0E-05	1.2	1.3E-01	-2.1	1.2E-02	-0.2	7.5E-01
ENSMUST00000162785				8.7	1.8E-05	-2.1	3.5E-03	-0.3	4.0E-01	-0.6	2.7E-01
ENSMUST00000146600				1.0	2.3E-01	1.6	1.4E-01	0.4	5.9E-01	-0.1	8.9E-01
ENSMUST00000139748				8.7	5.0E-05	-3.7	8.3E-03	-0.4	4.5E-01	-0.2	8.9E-01
ENSMUST00000146603				-1.7	3.8E-01	3.4	1.8E-01	2.2	3.0E-01	-2.8	1.6E-01
ENSMUST00000160619				8.7	9.8E-06	8.1	5.2E-04	0.8	5.9E-01	1.0	2.1E-01
ENSMUST00000151977				8.7	1.5E-05	8.0	2.0E-04	-0.7	6.2E-01	0.2	8.2E-01
ENSMUST00000162408				8.7	1.3E-04	5.0	4.3E-03	-0.9	5.3E-01	1.7	5.5E-02
ENSMUST00000189059				8.7	5.3E-05	5.3	4.8E-02	-0.8	7.4E-01	0.5	7.1E-01
ENSMUST00000134690				8.6	2.9E-05	3.1	1.2E-02	-1.4	1.7E-01	-0.5	5.2E-01
ENSMUST00000141919				8.6	1.2E-05	-2.3	2.0E-03	1.0	9.4E-03	-0.4	5.2E-01
ENSMUST00000146625	inhibitor of growth family, member 2 [Source:MGI Symbol;Acc:MGI:1916510]	B6ZI39		3.9	7.3E-02	4.4	7.3E-02	-0.4	8.6E-01	-0.9	5.3E-01
ENSMUST00000146628	desumoylating isopeptidase 1 [Source:MGI Symbol;Acc:MGI:106313]	D6RDE8		4.7	1.1E-01	3.7	2.3E-01	-3.0	3.4E-01	-2.1	3.3E-01
ENSMUST00000146630	pre B cell leukemia transcription factor interacting protein 1 [Source:MGI Symbol;Acc:MGI:2441670]	D3YY15		-1.1	1.4E-01	-2.7	5.9E-02	0.6	3.2E-01	2.3	9.8E-02
ENSMUST00000178345				8.6	3.0E-05	-3.5	3.6E-03	-1.6	1.9E-02	-2.0	1.1E-01
ENSMUST00000183284				8.6	3.1E-06	0.5	6.9E-01	0.8	3.8E-01	-4.4	1.2E-02
ENSMUST00000146641				-0.2	8.6E-01	2.1	1.5E-01	1.0	3.5E-01	-1.2	3.2E-01
ENSMUST00000117208				8.6	9.6E-04	7.2	2.3E-04	-0.6	6.6E-01	0.1	8.6E-01
ENSMUST00000129276				8.6	2.5E-04	-0.3	8.2E-01	2.4	3.4E-02	-1.3	3.2E-01
ENSMUST00000146666				2.3	8.5E-02	2.0	1.7E-01	-1.3	3.0E-01	-0.9	4.2E-01
ENSMUST00000154544				8.6	6.9E-06	2.6	2.7E-02	-2.0	8.6E-02	-0.1	8.9E-01
ENSMUST00000146677				2.1	3.5E-01	7.8	5.3E-02	4.3	2.3E-01	-1.4	5.2E-01
ENSMUST00000146684				-2.4	3.0E-01	-2.3	3.3E-01	-1.0	5.3E-01	-1.1	6.7E-01
ENSMUST00000151226				8.6	3.6E-05	4.3	3.6E-03	1.3	2.2E-01	0.8	3.1E-01
ENSMUST00000146691				-5.8	6.0E-02	-11.2	6.7E-03	-7.0	7.9E-04	-1.7	6.5E-01
ENSMUST00000146692	tumor necrosis factor receptor superfamily, member 22 [Source:MGI Symbol;Acc:MGI:1930270]		Q9ER62	4.4	1.0E-01	5.5	1.3E-01	1.4	6.8E-01	0.3	8.8E-01
ENSMUST00000159491				8.6	8.9E-05	-3.4	1.2E-02	-1.6	2.6E-02	-1.9	1.5E-01
ENSMUST00000119631				8.6	1.5E-05	-2.3	2.7E-01	0.6	6.0E-01	-0.5	7.8E-01
ENSMUST00000114588				8.6	4.5E-05	6.1	2.5E-04	-0.5	6.6E-01	-2.2	7.5E-03
ENSMUST00000155954				8.6	7.8E-06	3.9	4.9E-03	0.8	3.8E-01	0.2	7.9E-01
ENSMUST00000146711				-1.0	2.0E-01	1.2	2.7E-01	1.4	9.3E-02	-0.7	4.2E-01
ENSMUST00000173151				8.6	7.4E-06	1.5	7.0E-02	-0.3	6.0E-01	0.9	2.1E-01
ENSMUST00000184534				8.6	1.5E-05	6.4	2.7E-04	-2.0	1.4E-01	-0.1	9.0E-01
ENSMUST00000178227				8.6	8.7E-06	-3.2	1.8E-01	2.7	5.7E-02	-0.2	9.5E-01
ENSMUST00000180976				8.6	8.7E-06	2.9	3.4E-02	0.3	8.1E-01	-0.4	6.9E-01
ENSMUST00000193758				8.6	5.8E-06	7.3	4.7E-04	-0.6	6.9E-01	-0.9	2.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000146740	chromatin target of PRMT1 [Source:MGI Symbol;Acc:MGI:1913761]	D3Z7T7		2.6	1.7E-01	0.4	8.3E-01	-2.5	1.6E-01	-0.3	8.7E-01
ENSMUST00000146446				8.6	8.2E-06	0.9	5.1E-01	-1.0	3.9E-01	3.6	1.3E-02
ENSMUST00000146752				0.6	6.9E-01	1.3	4.8E-01	-0.6	7.0E-01	-1.3	3.7E-01
ENSMUST00000133883				8.6	9.2E-06	4.5	3.6E-03	-0.2	8.8E-01	0.4	6.2E-01
ENSMUST00000153836				8.6	2.8E-05	1.8	2.1E-02	-0.2	7.2E-01	0.2	7.5E-01
ENSMUST00000137978				8.6	1.1E-04	4.0	7.1E-03	-0.2	8.7E-01	-0.7	4.8E-01
ENSMUST00000146760	FMS-like tyrosine kinase 3 ligand [Source:MGI Symbol;Acc:MGI:95560]	A9QW46	P49772	-1.5	1.2E-01	4.0	3.4E-02	5.2	3.1E-03	-0.2	8.3E-01
ENSMUST00000146763	solute carrier organic anion transporter family, member 5A1 [Source:MGI Symbol;Acc:MGI:2443431]	A0A087WP15		2.9	1.1E-01	6.2	4.3E-03	-0.5	7.8E-01	-3.8	9.8E-03
ENSMUST00000149522				8.6	3.5E-06	2.8	1.3E-02	0.5	5.6E-01	-0.1	8.4E-01
ENSMUST00000137427				8.6	2.9E-06	2.1	2.4E-02	0.2	8.2E-01	0.2	8.1E-01
ENSMUST00000146776				-0.3	8.7E-01	-3.3	8.4E-02	-3.9	1.1E-02	-0.9	6.5E-01
ENSMUST00000130409				8.6	3.5E-03	4.2	9.3E-03	-0.7	6.1E-01	0.2	8.2E-01
ENSMUST00000132612				8.6	3.1E-05	-5.2	5.7E-03	1.2	6.6E-02	-0.4	8.0E-01
ENSMUST00000136733				8.6	1.0E-04	6.6	2.3E-04	-0.6	6.3E-01	-0.5	4.2E-01
ENSMUST00000142264				8.6	1.7E-05	-1.2	5.3E-01	1.9	9.5E-02	0.1	9.5E-01
ENSMUST00000146794	protease, serine 45 [Source:MGI Symbol;Acc:MGI:3605764]		Q8K4I7	3.3	5.1E-02	5.7	2.8E-03	-1.4	3.8E-01	-3.8	4.9E-03
ENSMUST00000155910				8.6	2.0E-05	5.6	4.0E-04	-0.1	9.2E-01	0.0	9.7E-01
ENSMUST00000153751				8.6	4.3E-05	2.5	1.6E-01	-2.0	2.0E-01	-0.6	6.7E-01
ENSMUST00000151150				8.6	3.8E-05	0.4	7.5E-01	-1.5	2.3E-01	1.5	2.4E-01
ENSMUST00000129798				8.6	6.0E-06	5.3	1.6E-03	-0.2	8.8E-01	0.3	6.8E-01
ENSMUST00000145323				8.6	1.9E-05	-2.9	1.2E-01	1.6	9.7E-02	-1.0	6.0E-01
ENSMUST00000160707				8.6	9.8E-05	4.7	1.2E-03	-1.4	2.1E-01	0.1	8.9E-01
ENSMUST00000141286				8.6	1.2E-04	11.2	3.3E-06	-0.4	7.3E-01	0.2	6.0E-01
ENSMUST00000189597				8.6	2.5E-04	-3.6	1.4E-03	-0.4	3.5E-01	-0.4	6.0E-01
ENSMUST00000146832	SNF related kinase [Source:MGI Symbol;Acc:MGI:108104]	D3YVW4		-2.6	3.6E-02	-2.5	1.2E-01	0.3	6.9E-01	0.2	8.9E-01
ENSMUST00000117587				8.6	2.1E-05	2.8	5.5E-03	-3.0	1.0E-02	0.7	2.7E-01
ENSMUST00000156213				8.6	2.3E-05	6.9	7.4E-06	-0.5	4.9E-01	-0.1	8.3E-01
ENSMUST00000150014				8.6	2.5E-06	8.1	9.2E-05	-0.9	5.0E-01	1.1	1.0E-01
ENSMUST00000146852				0.9	5.7E-01	-0.5	7.7E-01	-0.8	5.8E-01	0.6	7.2E-01
ENSMUST00000191069				8.6	8.6E-06	5.6	3.0E-04	-1.7	1.4E-01	-0.7	2.6E-01
ENSMUST00000146861				3.9	5.5E-02	5.9	3.0E-02	1.8	4.3E-01	-0.2	9.0E-01
ENSMUST00000146864	syntaxin 18 [Source:MGI Symbol;Acc:MGI:1918366]			-1.8	1.3E-01	-0.3	8.5E-01	1.4	2.2E-01	-0.1	9.6E-01
ENSMUST00000139279				8.6	9.0E-05	-2.1	7.8E-02	1.6	2.6E-02	0.8	4.5E-01
ENSMUST00000159167				8.6	9.9E-06	6.3	8.3E-04	-0.7	6.3E-01	-1.3	1.3E-01
ENSMUST00000146869				-5.0	6.6E-02	-4.5	1.2E-01	-1.1	4.0E-01	-1.6	6.0E-01
ENSMUST00000154826				8.6	9.7E-05	4.2	4.2E-04	-0.6	4.4E-01	0.0	9.3E-01
ENSMUST00000191294				8.6	9.0E-06	6.1	9.1E-04	1.2	3.7E-01	-1.4	8.8E-02
ENSMUST00000188254				8.6	8.8E-05	2.9	5.6E-03	-3.6	4.6E-03	-0.6	3.9E-01
ENSMUST00000146886				-2.4	1.6E-01	-0.2	9.2E-01	0.7	6.3E-01	-1.5	4.0E-01
ENSMUST00000177134				8.6	1.4E-04	6.3	3.1E-05	-0.4	6.4E-01	0.3	4.7E-01
ENSMUST00000126845				8.6	3.3E-06	-2.7	7.5E-02	-0.7	4.2E-01	-1.0	4.9E-01
ENSMUST00000189742				8.6	1.8E-05	7.4	5.1E-05	0.5	5.9E-01	-0.1	9.0E-01
ENSMUST00000140417				8.6	1.4E-03	1.9	1.1E-01	-2.9	2.2E-02	-1.9	7.9E-02
ENSMUST00000146903	symplekin [Source:MGI Symbol;Acc:MGI:1915438]	S4R2Q3		0.8	2.6E-01	1.2	2.1E-01	0.1	8.6E-01	-0.3	7.3E-01
ENSMUST00000128845				8.6	5.7E-06	1.3	7.4E-02	-1.0	1.2E-01	-0.2	6.7E-01
ENSMUST00000166771				8.6	9.3E-06	4.5	1.3E-03	-0.9	3.6E-01	-0.1	8.5E-01
ENSMUST00000146911				-0.8	1.8E-01	-0.5	5.3E-01	-0.4	4.4E-01	-0.8	3.1E-01
ENSMUST00000182849				8.6	5.9E-05	-2.4	9.9E-02	0.2	8.0E-01	-1.8	2.7E-01
ENSMUST00000137436				8.6	5.9E-05	-5.9	4.6E-03	1.4	9.4E-02	-0.2	9.2E-01
ENSMUST00000146921				0.9	6.3E-01	0.5	8.6E-01	1.1	6.2E-01	1.5	4.6E-01
ENSMUST00000146923	mitogen-activated protein kinase 8 interacting protein 3 [Source:MGI Symbol;Acc:MGI:1353598]	Q3UHB5	Q9ESN9	1.6	4.9E-02	2.6	1.6E-02	0.5	5.1E-01	-0.5	5.1E-01
ENSMUST00000163064				8.6	6.8E-04	-8.0	4.4E-04	0.6	2.0E-01	0.1	9.6E-01
ENSMUST00000125660				8.6	3.8E-05	2.3	4.0E-01	-0.6	7.8E-01	2.8	1.9E-01
ENSMUST00000152445				8.6	3.7E-04	-4.0	8.1E-02	0.1	9.6E-01	0.3	8.8E-01
ENSMUST00000121458				8.5	2.4E-05	5.6	1.1E-03	-1.6	2.1E-01	1.0	2.1E-01
ENSMUST00000146948	RIKEN cDNA 4932438A13 gene [Source:MGI Symbol;Acc:MGI:2444631]	F6RPM4		-3.2	3.5E-01	-4.9	2.0E-01	-3.2	1.2E-01	-1.5	7.2E-01
ENSMUST00000170449				8.5	8.0E-06	-1.2	5.7E-01	4.4	6.5E-03	-0.3	8.6E-01
ENSMUST00000146955	nucleobindin 1 [Source:MGI Symbol;Acc:MGI:97388]	H3BK79		-3.2	3.6E-02	-1.8	3.4E-01	1.3	3.1E-01	-0.1	9.4E-01
ENSMUST00000146968	WD repeat domain 91 [Source:MGI Symbol;Acc:MGI:2141558]	S4R1X1		-2.4	2.4E-01	-0.3	9.1E-01	2.5	2.0E-01	0.3	9.0E-01
ENSMUST00000189893				8.5	1.8E-05	3.4	2.9E-03	-0.8	3.6E-01	-0.1	9.3E-01
ENSMUST00000146974				0.8	3.5E-01	2.2	3.8E-02	0.2	7.6E-01	-1.2	1.6E-01
ENSMUST00000146977				-1.9	3.5E-02	-1.4	2.7E-01	1.2	1.0E-01	0.7	5.3E-01
ENSMUST00000143252				8.5	3.0E-06	-5.0	8.9E-04	-1.1	4.3E-02	-2.3	9.5E-02
ENSMUST00000187682				8.5	8.2E-05	3.8	6.5E-03	0.1	9.4E-01	-0.5	5.4E-01
ENSMUST00000127553				8.5	2.8E-06	6.0	2.6E-04	-0.9	4.1E-01	-0.4	5.4E-01
ENSMUST00000121847				8.5	7.2E-04	2.1	2.0E-02	-1.6	4.1E-02	0.0	9.4E-01
ENSMUST00000190676				8.5	1.3E-05	6.4	2.2E-03	-0.7	6.6E-01	-0.9	3.3E-01
ENSMUST00000147307				8.5	4.6E-05	5.0	1.5E-01	-0.7	8.4E-01	1.3	5.4E-01
ENSMUST00000147856				8.5	5.4E-07	-0.8	1.8E-01	0.2	5.1E-01	-0.6	2.9E-01
ENSMUST00000149704				8.5	1.5E-05	-4.1	4.8E-03	0.5	2.9E-01	-1.4	2.8E-01
ENSMUST00000128182				8.5	7.1E-06	-1.2	3.9E-01	3.3	4.5E-03	-1.0	4.7E-01
ENSMUST00000149008				8.5	1.0E-05	-6.9	5.8E-03	0.7	3.8E-01	2.2	2.9E-01
ENSMUST00000147009	required for meiotic nuclear division 5 homolog B (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1913339]	F6VIG0		-1.0	5.5E-01	-0.4	8.7E-01	1.9	3.1E-01	1.3	5.6E-01
ENSMUST00000121425				8.5	3.2E-05	1.5	2.4E-01	-3.4	2.7E-02	-0.2	8.6E-01
ENSMUST00000147014				2.5	2.3E-01	5.1	2.7E-02	-1.0	6.4E-01	-3.6	5.0E-02
ENSMUST00000128096				8.5	8.2E-05	3.8	2.3E-02	-0.7	6.2E-01	-0.1	9.1E-01
ENSMUST00000153025				8.5	5.3E-05	6.6	9.5E-05	-1.1	2.9E-01	0.4	5.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000147022				-2.8	7.8E-02	1.0	6.3E-01	4.1	2.1E-02	0.3	8.9E-01
ENSMUST00000132535				8.5	1.0E-06	5.6	6.0E-04	-0.9	4.2E-01	-0.5	4.7E-01
ENSMUST00000107515				8.5	9.9E-05	6.4	3.6E-04	-0.6	6.3E-01	-0.5	5.1E-01
ENSMUST00000147028				-2.1	7.8E-02	-2.4	6.8E-02	-1.6	7.4E-02	-1.3	3.2E-01
ENSMUST00000147030	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	F6XCT0		4.2	7.8E-02	1.2	6.4E-01	-1.0	6.8E-01	2.0	3.3E-01
ENSMUST00000146075				8.5	6.5E-05	5.7	4.8E-03	-0.4	8.1E-01	-0.6	5.4E-01
ENSMUST00000155627				8.5	3.1E-05	5.6	6.5E-04	-0.6	6.3E-01	0.2	7.5E-01
ENSMUST00000147040				1.6	6.3E-01	-1.4	7.5E-01	-3.0	3.7E-01	0.0	1.0E+00
ENSMUST00000189873				8.5	1.3E-04	6.5	2.6E-04	0.2	8.3E-01	-0.6	3.4E-01
ENSMUST00000186253				8.5	1.1E-04	5.8	9.5E-04	-0.6	6.7E-01	-0.3	6.4E-01
ENSMUST00000160328				8.5	8.0E-06	4.5	7.7E-05	-0.9	2.2E-01	0.1	8.8E-01
ENSMUST00000097717				8.5	9.0E-06	7.2	1.1E-04	-0.2	8.8E-01	-0.4	5.5E-01
ENSMUST00000147054				2.6	7.6E-02	1.2	3.8E-01	-2.8	4.6E-02	-1.4	2.4E-01
ENSMUST00000176713				8.5	2.5E-05	-4.5	9.6E-03	2.3	3.5E-03	-1.0	5.0E-01
ENSMUST00000128068				8.5	6.4E-06	-2.8	1.1E-01	0.6	5.0E-01	-0.7	6.9E-01
ENSMUST00000132592				8.5	6.4E-06	6.8	1.7E-03	-0.8	6.6E-01	0.0	1.0E+00
ENSMUST00000147070				0.6	5.8E-01	2.7	1.0E-01	1.1	4.2E-01	-1.0	3.8E-01
ENSMUST00000119088				8.5	1.4E-05	5.8	3.1E-03	-0.1	9.7E-01	0.4	6.8E-01
ENSMUST00000147076				2.8	5.5E-02	1.2	5.3E-01	0.9	5.7E-01	2.4	1.5E-01
ENSMUST00000117465				8.5	3.6E-04	6.8	2.9E-05	0.1	9.4E-01	0.4	4.1E-01
ENSMUST00000118797				8.5	9.7E-06	3.8	2.2E-02	-0.4	7.4E-01	-1.0	3.3E-01
ENSMUST00000161973				8.5	1.5E-05	0.7	4.4E-01	-1.0	2.0E-01	0.4	6.3E-01
ENSMUST00000147091				3.5	1.1E-01	3.3	1.3E-01	-2.3	2.6E-01	-2.1	2.5E-01
ENSMUST00000132629				8.5	8.7E-07	6.1	8.8E-04	-0.6	6.7E-01	-0.1	8.9E-01
ENSMUST00000147096				-0.4	5.1E-01	0.0	9.7E-01	-0.9	1.6E-01	-1.3	1.0E-01
ENSMUST00000150986				8.5	1.3E-04	-5.8	5.2E-04	0.0	9.7E-01	-0.4	7.2E-01
ENSMUST00000162227				8.5	2.6E-05	3.9	7.8E-03	-1.2	3.0E-01	-0.3	7.3E-01
ENSMUST00000147101	Von Willebrand factor homolog [Source:MGI Symbol;Acc:MGI:98941]	S4R195		-2.8	4.7E-02	-0.3	8.1E-01	0.0	9.6E-01	-2.5	8.5E-02
ENSMUST00000147102				1.7	1.6E-01	2.8	6.8E-02	0.9	5.0E-01	-0.3	7.6E-01
ENSMUST00000120593				8.5	1.3E-05	7.7	1.8E-04	-0.8	5.5E-01	0.0	9.6E-01
ENSMUST00000147105	myelin basic protein expression factor 2, repressor [Source:MGI Symbol;Acc:MGI:104592]	A2ATP5		3.1	1.7E-01	5.3	6.4E-02	0.4	8.7E-01	-1.8	3.2E-01
ENSMUST00000184544				8.5	7.9E-06	7.0	5.5E-04	-0.7	6.5E-01	-0.7	3.7E-01
ENSMUST00000118689				8.5	9.3E-06	-3.4	5.8E-02	2.8	8.7E-03	-1.0	5.4E-01
ENSMUST00000147115	centrosomal protein 57 [Source:MGI Symbol;Acc:MGI:1915551]	B8JJE7		-3.1	2.1E-01	-3.4	1.8E-01	-2.6	1.0E-01	-2.3	4.3E-01
ENSMUST00000147116				2.0	1.7E-01	0.4	8.0E-01	-1.4	3.1E-01	0.2	8.9E-01
ENSMUST00000147120				0.6	4.6E-01	1.2	3.1E-01	0.9	3.5E-01	0.3	7.1E-01
ENSMUST00000164420				8.5	1.2E-07	2.0	5.6E-02	-0.5	5.3E-01	0.7	3.6E-01
ENSMUST00000147139	lipoma HMGIC fusion partner [Source:MGI Symbol;Acc:MGI:1920048]		Q8BM86	4.7	4.5E-02	-0.5	8.0E-01	-4.5	4.2E-02	0.7	6.9E-01
ENSMUST00000132688				8.5	2.5E-04	2.5	2.4E-01	7.1	1.5E-03	-0.3	8.6E-01
ENSMUST00000141006				8.5	1.3E-06	4.6	4.9E-03	-0.6	6.3E-01	0.9	2.8E-01
ENSMUST00000184110				8.5	9.9E-05	-6.8	9.0E-05	0.0	9.7E-01	-0.8	4.8E-01
ENSMUST00000147150	furin (paired basic amino acid cleaving enzyme) [Source:MGI Symbol;Acc:MGI:97513]	D3YTP7		2.7	5.0E-02	3.1	5.2E-02	-1.3	3.6E-01	-1.7	1.4E-01
ENSMUST00000173200				8.5	3.7E-05	5.3	2.3E-05	-0.9	2.1E-01	0.1	8.6E-01
ENSMUST00000129090				8.5	8.7E-06	6.2	3.2E-04	0.1	9.6E-01	0.1	8.8E-01
ENSMUST00000132710				8.5	1.9E-05	6.3	2.5E-04	-0.5	6.8E-01	-1.0	1.3E-01
ENSMUST00000147157	AHA1, activator of heat shock protein ATPase 2 [Source:MGI Symbol;Acc:MGI:1916133]	A2AF81		-3.0	5.5E-02	-3.8	3.1E-02	-1.5	9.1E-02	-0.8	6.5E-01
ENSMUST00000147162				1.8	4.5E-02	1.6	1.1E-01	-0.5	5.4E-01	-0.3	7.0E-01
ENSMUST00000147163	jumonji domain containing 4 [Source:MGI Symbol;Acc:MGI:2144404]		Q8BFT6	2.3	4.6E-01	5.8	1.4E-01	0.6	8.7E-01	-3.0	2.6E-01
ENSMUST00000147164				-0.6	4.9E-01	-1.2	3.0E-01	-0.1	8.9E-01	0.5	6.7E-01
ENSMUST00000147165				2.9	1.6E-01	1.2	6.8E-01	1.0	6.9E-01	2.7	2.3E-01
ENSMUST00000147727				8.5	1.4E-05	4.6	1.7E-02	-0.7	6.8E-01	0.8	4.6E-01
ENSMUST00000136198				8.5	1.1E-04	3.7	1.3E-03	-1.3	1.2E-01	-0.5	4.4E-01
ENSMUST00000147182				2.8	1.9E-01	5.0	1.7E-01	3.4	3.0E-01	1.2	5.4E-01
ENSMUST00000127140				8.5	1.0E-02	4.0	4.2E-05	0.0	9.5E-01	-0.2	6.3E-01
ENSMUST00000129374				8.5	4.1E-05	6.2	3.8E-05	0.9	2.7E-01	-0.1	8.8E-01
ENSMUST00000147190				-1.1	1.6E-01	-2.1	6.5E-02	-0.1	9.0E-01	1.0	3.3E-01
ENSMUST00000147193	dynein cytoplasmic 2 heavy chain 1 [Source:MGI Symbol;Acc:MGI:107736]		Q45VK7	-1.7	5.8E-01	2.2	5.5E-01	2.2	5.1E-01	-1.7	5.7E-01
ENSMUST00000147200	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI	D3YUM4		2.4	2.4E-01	4.8	1.9E-01	3.7	1.9E-01	1.3	6.3E-01
ENSMUST00000147203				1.8	7.1E-02	0.1	9.2E-01	-1.2	1.8E-01	0.5	6.2E-01
ENSMUST00000147210				-1.3	5.9E-01	-0.5	8.9E-01	1.5	5.6E-01	0.7	8.3E-01
ENSMUST00000121567				8.5	2.4E-05	5.6	3.6E-04	-1.3	2.4E-01	-0.3	6.3E-01
ENSMUST00000186279				8.5	2.1E-05	6.1	2.3E-04	-0.5	6.4E-01	-0.4	4.9E-01
ENSMUST00000147217	extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:103060]	D3YZV0		-1.0	4.3E-01	-0.7	7.2E-01	1.1	3.5E-01	0.9	6.3E-01
ENSMUST00000186664				8.5	1.2E-05	-2.7	2.2E-02	0.0	9.3E-01	0.5	6.1E-01
ENSMUST00000144987				8.5	2.3E-05	-3.1	1.3E-02	0.2	7.3E-01	-1.6	1.7E-01
ENSMUST00000193730				8.5	8.2E-06	4.1	4.8E-04	-0.6	4.1E-01	0.0	9.5E-01
ENSMUST00000126433				8.4	3.5E-06	4.4	9.8E-03	-1.2	4.1E-01	-1.3	1.9E-01
ENSMUST00000135227				8.4	7.3E-05	7.2	1.5E-02	-1.1	6.8E-01	-0.6	6.1E-01
ENSMUST00000123883				8.4	7.8E-06	7.1	1.9E-04	2.9	2.7E-02	0.7	3.0E-01
ENSMUST00000124862				8.4	1.2E-04	8.8	1.2E-03	1.9	3.1E-01	-0.3	7.9E-01
ENSMUST00000145311				8.4	4.1E-05	5.2	1.0E-03	0.5	6.4E-01	0.5	5.1E-01
ENSMUST00000147232				-1.6	1.8E-01	-1.9	2.8E-01	0.1	8.9E-01	0.4	8.0E-01
ENSMUST00000164606				8.4	2.0E-07	-4.0	1.2E-01	-0.4	7.3E-01	-2.5	3.9E-01
ENSMUST00000136222				8.4	3.7E-05	5.8	6.4E-04	-0.6	6.6E-01	0.1	8.8E-01
ENSMUST00000185775				8.4	3.7E-05	3.8	3.5E-04	-0.6	3.4E-01	-0.6	2.9E-01
ENSMUST00000093229				8.4	4.9E-06	4.5	1.4E-03	0.4	6.4E-01	-0.1	8.6E-01
ENSMUST00000182636				8.4	9.5E-05	5.6	7.3E-04	-1.4	2.9E-01	-0.3	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000144015				8.4	1.2E-04	4.1	4.1E-04	0.3	6.3E-01	-0.5	3.2E-01
ENSMUST00000123319				8.4	4.9E-06	5.5	5.0E-04	-1.7	1.3E-01	0.5	5.1E-01
ENSMUST00000147265				0.3	7.1E-01	0.3	7.5E-01	-0.1	9.0E-01	-0.1	9.0E-01
ENSMUST00000147267				0.8	3.4E-01	2.9	4.6E-02	2.4	5.0E-02	0.4	7.0E-01
ENSMUST00000147272	zinc finger, CCHC domain containing 7 [Source:MGI Symbol;Acc:MGI:2442912]		B1AX39	0.2	6.8E-01	-0.8	2.9E-01	-0.3	5.1E-01	0.7	3.3E-01
ENSMUST00000147273				1.3	1.7E-01	1.9	9.7E-02	0.2	8.6E-01	-0.5	6.0E-01
ENSMUST00000144740				8.4	4.7E-05	-2.9	7.4E-02	1.0	2.0E-01	0.0	9.8E-01
ENSMUST00000147277	inositol polyphosphate multikinase [Source:MGI Symbol;Acc:MGI:1916968]		Q7TT16	-0.6	8.1E-01	-2.7	4.0E-01	-2.2	2.4E-01	-0.1	9.8E-01
ENSMUST00000136018				8.4	7.9E-05	8.0	2.1E-03	0.5	8.1E-01	-1.5	1.5E-01
ENSMUST00000136576				8.4	2.2E-05	2.5	5.3E-02	-2.2	6.1E-02	-0.6	5.2E-01
ENSMUST00000155375				8.4	1.1E-05	5.8	7.0E-04	-0.6	6.4E-01	0.6	3.9E-01
ENSMUST00000161357				8.4	2.1E-05	4.1	1.1E-03	-0.2	7.8E-01	-1.1	1.2E-01
ENSMUST00000191773				8.4	5.3E-06	4.3	1.0E-03	-0.9	3.2E-01	-0.2	7.6E-01
ENSMUST00000137365				8.4	1.0E-05	6.6	7.7E-04	-0.6	6.8E-01	-0.8	3.1E-01
ENSMUST00000126309				8.4	1.3E-04	5.9	2.0E-02	-0.6	8.1E-01	-1.1	3.9E-01
ENSMUST00000147301	growth arrest-specific 2 like 2 [Source:MGI Symbol;Acc:MGI:3652048]	F2Z4A6		4.9	1.4E-01	5.4	1.5E-01	0.1	9.7E-01	-0.4	8.6E-01
ENSMUST00000154508				8.4	1.1E-04	-2.7	1.4E-01	0.1	8.8E-01	-0.1	9.6E-01
ENSMUST00000173950				8.4	2.9E-04	7.7	2.2E-04	-0.7	6.1E-01	0.2	8.2E-01
ENSMUST00000119996				8.4	9.7E-06	3.3	5.3E-04	0.2	7.1E-01	-0.4	4.4E-01
ENSMUST00000133376				8.4	4.6E-06	-6.8	2.0E-05	-0.8	2.7E-02	-0.5	5.5E-01
ENSMUST00000185025				8.4	9.7E-06	4.4	4.1E-03	-1.7	2.0E-01	0.5	5.0E-01
ENSMUST00000171194				8.4	6.7E-06	-2.9	1.9E-02	0.3	5.9E-01	-0.6	5.7E-01
ENSMUST00000185197				8.4	1.6E-05	-5.0	2.2E-02	1.4	8.7E-02	0.4	8.4E-01
ENSMUST00000159154				8.4	2.6E-05	6.4	8.4E-05	-1.3	2.4E-01	-0.8	1.7E-01
ENSMUST00000193847				8.4	7.9E-05	4.8	1.1E-03	-2.0	1.1E-01	-0.5	4.6E-01
ENSMUST00000194554				8.4	1.1E-04	6.4	2.3E-03	-1.0	5.4E-01	-0.5	6.0E-01
ENSMUST00000120161				8.4	5.0E-05	-5.7	2.4E-02	0.0	9.7E-01	1.5	5.0E-01
ENSMUST00000154373				8.4	4.3E-06	5.1	5.8E-04	0.9	3.3E-01	-0.4	5.4E-01
ENSMUST00000147343				1.3	9.0E-02	1.4	1.8E-01	1.1	2.2E-01	0.9	2.5E-01
ENSMUST00000191231				8.4	1.1E-04	-2.8	8.3E-02	1.3	1.2E-01	-0.1	9.6E-01
ENSMUST00000147356	glutamate receptor interacting protein 1 [Source:MGI Symbol;Acc:MGI:1921303]	Q6GQT7		3.4	5.4E-02	5.7	5.7E-03	-0.5	7.7E-01	-2.8	3.3E-02
ENSMUST00000147360				-2.9	2.6E-01	-4.3	2.0E-01	-0.6	7.7E-01	0.8	7.9E-01
ENSMUST00000118684				8.4	5.7E-05	6.1	2.8E-04	1.9	7.4E-02	0.0	9.8E-01
ENSMUST00000132085				8.4	3.3E-04	-0.6	6.5E-01	1.8	6.1E-02	-1.3	2.9E-01
ENSMUST00000190892				8.4	9.2E-07	5.5	2.0E-03	0.2	8.5E-01	0.2	8.3E-01
ENSMUST00000117535				8.4	1.5E-03	-4.1	4.5E-02	-0.3	7.3E-01	0.6	7.5E-01
ENSMUST00000150082				8.4	1.9E-04	3.9	9.2E-03	-2.1	1.1E-01	0.3	7.7E-01
ENSMUST00000147383				3.3	1.2E-01	4.0	1.5E-01	-0.1	9.7E-01	-0.8	6.4E-01
ENSMUST00000172807				8.4	4.4E-06	5.6	5.7E-04	1.0	3.3E-01	-0.1	8.8E-01
ENSMUST00000147393	Holliday junction recognition protein [Source:MGI Symbol;Acc:MGI:2685821]	D6RI36		0.2	9.3E-01	-3.4	4.6E-01	-1.4	6.0E-01	2.2	6.1E-01
ENSMUST00000148925				8.4	1.0E-05	5.2	5.4E-02	2.7	2.4E-01	3.0	7.1E-02
ENSMUST00000192685				8.4	2.1E-04	-7.8	3.4E-02	-0.1	9.3E-01	1.7	6.1E-01
ENSMUST00000132199				8.4	1.5E-05	0.7	6.3E-01	-2.8	4.9E-02	0.6	6.0E-01
ENSMUST00000147404				-0.4	7.0E-01	2.1	1.9E-01	2.6	6.6E-02	0.1	9.5E-01
ENSMUST00000148225				8.4	3.8E-05	-2.7	7.3E-02	-0.6	5.0E-01	-0.5	7.1E-01
ENSMUST00000191942				8.4	6.4E-07	4.7	3.5E-03	-0.2	8.5E-01	-0.5	5.0E-01
ENSMUST00000147416				1.9	7.4E-02	2.7	5.4E-02	0.5	6.7E-01	-0.3	7.6E-01
ENSMUST00000147421				1.2	2.2E-01	2.0	9.3E-02	0.6	5.5E-01	-0.3	7.4E-01
ENSMUST00000147423				-0.4	6.4E-01	0.3	7.8E-01	-0.1	9.1E-01	-0.9	4.3E-01
ENSMUST00000195430				8.4	7.3E-06	7.0	3.0E-04	1.0	4.2E-01	0.4	5.7E-01
ENSMUST00000129907				8.4	3.5E-06	3.3	4.2E-02	0.4	7.5E-01	-0.2	8.3E-01
ENSMUST00000130394				8.4	1.1E-05	-7.8	5.6E-03	-0.2	7.7E-01	4.0	9.7E-02
ENSMUST00000147436				1.5	5.1E-01	3.4	2.7E-01	1.7	5.0E-01	-0.3	9.1E-01
ENSMUST00000147441				0.2	6.7E-01	0.8	2.7E-01	0.4	5.1E-01	-0.2	7.4E-01
ENSMUST00000151869				8.4	3.1E-04	6.9	4.4E-04	-1.4	3.3E-01	0.8	2.8E-01
ENSMUST00000062902				8.4	1.4E-05	6.1	6.4E-04	-0.5	6.7E-01	-0.6	4.0E-01
ENSMUST00000128272				8.4	7.5E-05	-4.9	9.6E-04	-0.2	5.7E-01	1.4	1.9E-01
ENSMUST00000147462				0.1	9.6E-01	-1.7	5.0E-01	-2.2	1.5E-01	-0.4	8.6E-01
ENSMUST00000173298				8.4	3.8E-05	-1.2	5.2E-01	-5.1	1.3E-02	2.2	2.2E-01
ENSMUST00000188803				8.4	2.6E-05	1.4	2.4E-01	-1.9	8.8E-02	-0.7	4.8E-01
ENSMUST00000177572				8.3	1.5E-05	5.3	1.6E-04	-2.0	5.6E-02	0.4	4.7E-01
ENSMUST00000147484	NADH dehydrogenase (ubiquinone) flavoprotein 2 [Source:MGI Symbol;Acc:MGI:1920150]	D6RGN4		-0.9	5.1E-01	-5.9	5.5E-03	-4.4	6.3E-04	0.6	7.3E-01
ENSMUST00000130489				8.3	9.2E-05	-4.8	8.5E-03	0.7	2.8E-01	-1.3	4.2E-01
ENSMUST00000147490	cDNA sequence BC017643 [Source:MGI Symbol;Acc:MGI:2384959]	X1WI15		-2.6	7.0E-02	-0.5	7.6E-01	1.8	9.2E-02	-0.3	8.4E-01
ENSMUST00000173277				8.3	1.7E-05	3.7	9.0E-03	0.4	7.0E-01	-0.2	8.2E-01
ENSMUST00000147818				8.3	2.2E-05	2.6	3.2E-01	-0.8	7.2E-01	2.8	1.7E-01
ENSMUST00000147498				-1.9	1.4E-01	-0.5	6.8E-01	-0.7	4.9E-01	-2.1	1.2E-01
ENSMUST00000147510				-4.0	6.1E-02	-4.7	1.8E-01	0.8	6.4E-01	1.6	6.3E-01
ENSMUST00000183167				8.3	4.4E-04	-4.5	9.5E-03	0.1	8.7E-01	-1.0	5.2E-01
ENSMUST00000097867				8.3	5.5E-04	3.3	4.0E-03	-0.8	3.2E-01	0.2	7.3E-01
ENSMUST00000147515				-0.8	5.4E-01	0.3	8.5E-01	0.2	8.7E-01	-1.0	5.3E-01
ENSMUST00000120337				8.3	1.1E-04	4.0	1.4E-02	-2.0	1.9E-01	-0.1	9.3E-01
ENSMUST00000190398				8.3	1.5E-05	4.4	1.3E-02	-0.6	6.9E-01	1.5	1.6E-01
ENSMUST00000147535	lactate dehydrogenase A [Source:MGI Symbol;Acc:MGI:96759]	D3YZQ9		-0.7	4.2E-01	-1.4	1.9E-01	-0.6	4.0E-01	0.1	9.3E-01
ENSMUST00000133354				8.3	8.0E-05	4.7	4.0E-04	-1.2	1.9E-01	0.1	9.0E-01
ENSMUST00000147540	transformation related protein 53 binding protein 1 [Source:MGI Symbol;Acc:MGI:1351320]	F6QNC8		-1.6	2.0E-01	-0.7	5.8E-01	-0.2	8.5E-01	-1.1	4.4E-01
ENSMUST00000147545	coiled-coil domain containing 6 [Source:MGI Symbol;Acc:MGI:1923801]		D3YZP9	0.7	1.4E-01	1.7	2.0E-02	0.8	1.4E-01	-0.2	6.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000195038				8.3	3.0E-05	-5.0	5.9E-03	0.6	3.2E-01	-0.3	8.3E-01
ENSMUST00000147553				-0.6	8.1E-01	-3.3	3.2E-01	-2.4	2.1E-01	0.4	9.1E-01
ENSMUST00000142542				8.3	3.3E-03	5.2	2.2E-02	-0.6	7.5E-01	0.8	4.9E-01
ENSMUST00000147561				-0.4	6.5E-01	-0.5	7.0E-01	0.5	5.5E-01	0.6	6.0E-01
ENSMUST00000191055				8.3	1.7E-05	-1.3	1.0E-01	1.6	5.3E-03	-0.4	5.8E-01
ENSMUST00000119194				8.3	3.5E-05	2.5	1.4E-02	-0.2	8.1E-01	0.3	6.3E-01
ENSMUST00000147566	lysophosphatidylcholine acyltransferase 1 [Source:MGI Symbol;Acc:MGI:2384812]	D6RFA8		2.5	2.8E-01	5.7	1.2E-01	4.0	1.8E-01	0.8	7.7E-01
ENSMUST00000147567	l-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase [Source:MGI Symbol;Acc:MGI:1351598	D3Z6C9		0.5	8.1E-01	-0.6	7.7E-01	-2.5	1.7E-01	-1.4	5.4E-01
ENSMUST00000147570	small nuclear ribonucleoprotein B [Source:MGI Symbol;Acc:MGI:98342]	A0A0G2JGN4		1.2	4.6E-01	5.0	6.6E-02	3.3	1.8E-01	-0.5	7.1E-01
ENSMUST00000147572	polyhomeotic-like 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1860454]	B1ASA3		1.9	1.4E-01	0.6	7.9E-01	2.0	2.0E-01	3.3	1.0E-01
ENSMUST00000136769				8.3	4.5E-05	-1.7	1.4E-01	1.4	4.5E-02	-1.6	2.0E-01
ENSMUST00000173700				8.3	8.5E-06	7.4	9.8E-07	0.2	7.1E-01	0.1	7.4E-01
ENSMUST00000130693				8.3	5.2E-05	7.4	7.2E-05	-0.5	6.5E-01	0.1	8.6E-01
ENSMUST00000122918				8.3	5.8E-05	6.6	5.4E-04	-0.4	7.6E-01	-1.3	9.7E-02
ENSMUST00000119067				8.3	3.8E-05	2.6	1.1E-02	0.0	9.4E-01	0.7	3.0E-01
ENSMUST00000147588	nuclear factor of activated T cells 5 [Source:MGI Symbol;Acc:MGI:1859333]	Q80TR0		-2.5	8.3E-02	3.1	1.7E-01	5.3	7.7E-03	-0.3	8.5E-01
ENSMUST00000142607				8.3	5.0E-06	-5.5	1.1E-03	0.1	8.5E-01	-0.9	5.2E-01
ENSMUST00000146604				8.3	3.5E-05	6.8	1.8E-04	-0.5	6.8E-01	-1.6	3.5E-02
ENSMUST00000117667				8.3	4.6E-06	5.8	3.9E-05	-0.8	3.2E-01	0.7	1.4E-01
ENSMUST00000147604	absent in melanoma 2 [Source:MGI Symbol;Acc:MGI:2686159]		Q91VJ1	-1.3	1.7E-01	0.5	6.5E-01	0.6	4.4E-01	-1.2	2.7E-01
ENSMUST00000136698				8.3	9.1E-06	-3.2	8.0E-03	0.8	1.0E-01	-1.9	1.1E-01
ENSMUST00000187844				8.3	1.5E-05	5.8	2.1E-04	0.5	5.6E-01	-0.3	5.9E-01
ENSMUST00000050128				8.3	1.1E-04	-3.8	1.5E-02	0.3	6.3E-01	-0.4	7.8E-01
ENSMUST00000147973				8.3	1.1E-06	7.5	5.4E-05	-0.5	6.6E-01	-0.7	2.0E-01
ENSMUST00000147616				2.5	2.6E-01	3.0	1.8E-01	-0.5	8.3E-01	-0.9	5.8E-01
ENSMUST00000132027				8.3	4.0E-05	6.7	1.5E-04	-0.6	6.1E-01	-0.7	2.5E-01
ENSMUST00000147627	copine I [Source:MGI Symbol;Acc:MGI:2386621]	E9Q806		-0.7	6.7E-01	-2.2	3.0E-01	-1.5	2.8E-01	0.0	9.8E-01
ENSMUST00000147630	zinc finger protein 97 [Source:MGI Symbol;Acc:MGI:105921]	E9PZP6		0.7	3.3E-01	0.6	5.7E-01	0.0	9.6E-01	0.2	8.1E-01
ENSMUST00000133627				8.3	8.2E-06	-0.9	2.5E-01	-0.4	5.4E-01	-2.5	2.4E-02
ENSMUST00000121973				8.3	2.9E-04	-3.8	3.1E-02	0.4	6.1E-01	-2.9	1.4E-01
ENSMUST00000147637				1.1	2.5E-01	2.5	5.6E-02	0.8	4.0E-01	-0.5	5.6E-01
ENSMUST00000147643				3.3	1.1E-01	0.8	7.2E-01	-2.1	2.9E-01	0.5	8.0E-01
ENSMUST00000147647				2.8	1.4E-01	2.9	2.3E-01	0.6	8.0E-01	0.5	7.7E-01
ENSMUST00000162767				8.3	8.2E-06	1.9	2.2E-01	-1.1	4.2E-01	1.0	4.5E-01
ENSMUST00000147650				3.5	6.9E-02	5.8	2.9E-02	1.5	4.9E-01	-0.9	5.8E-01
ENSMUST00000179203				8.3	1.5E-02	-3.7	7.7E-03	-0.6	2.7E-01	-0.8	5.2E-01
ENSMUST00000147656	transmembrane protein 161A [Source:MGI Symbol;Acc:MGI:2384577]	M0QWV0		-3.2	6.6E-02	1.6	3.9E-01	1.8	2.5E-01	-3.0	1.0E-01
ENSMUST00000186256				8.3	7.0E-05	5.7	1.5E-04	-0.5	6.3E-01	1.0	1.1E-01
ENSMUST00000127492				8.3	2.6E-05	5.8	4.7E-04	-0.1	9.2E-01	0.7	3.0E-01
ENSMUST00000140461				8.3	1.4E-05	4.1	6.2E-04	0.5	4.8E-01	-0.6	3.5E-01
ENSMUST00000139557				8.3	9.1E-05	6.5	7.4E-04	-0.7	6.3E-01	0.1	8.9E-01
ENSMUST00000147679				-0.8	5.0E-01	-1.1	5.3E-01	0.5	6.2E-01	0.8	6.2E-01
ENSMUST00000154302				8.3	4.6E-05	2.8	8.9E-02	-2.1	1.9E-01	-0.9	4.7E-01
ENSMUST00000147684	S-phase kinase-associated protein 1A [Source:MGI Symbol;Acc:MGI:103575]	E9Q3Q7		-1.4	3.5E-01	-2.9	9.1E-02	-2.1	5.6E-02	-0.6	7.5E-01
ENSMUST00000122964				8.3	1.1E-05	7.1	4.2E-05	-0.7	5.4E-01	-0.2	7.2E-01
ENSMUST00000147696	family with sequence similarity 189, member B [Source:MGI Symbol;Acc:MGI:1915771]	D6RFB2		3.8	1.2E-01	-0.5	8.6E-01	-2.1	4.0E-01	2.2	3.4E-01
ENSMUST00000107507				8.3	1.6E-04	4.6	4.8E-03	-1.3	3.3E-01	-0.5	5.8E-01
ENSMUST00000147703	phosducin-like [Source:MGI Symbol;Acc:MGI:1914716]	A2AVP3		-2.5	2.3E-01	-4.2	6.5E-02	-3.4	1.7E-02	-1.7	4.7E-01
ENSMUST00000129045				8.3	2.4E-05	-6.0	8.3E-04	0.4	3.2E-01	-0.2	8.8E-01
ENSMUST00000147712	Bardet-Biedl syndrome 9 (human) [Source:MGI Symbol;Acc:MGI:2442833]		Q811G0	0.7	7.7E-01	-1.1	6.7E-01	-2.5	2.4E-01	-0.6	8.2E-01
ENSMUST00000132735				8.3	1.4E-06	-3.1	9.3E-03	0.8	1.4E-01	0.5	5.8E-01
ENSMUST00000146720				8.3	5.7E-05	5.9	7.7E-04	-0.5	6.7E-01	0.7	2.9E-01
ENSMUST00000147718	v-crk sarcoma virus CT10 oncogene homolog (avian) [Source:MGI Symbol;Acc:MGI:88508]	F7D232		0.0	9.6E-01	-0.6	4.7E-01	-1.4	6.1E-02	-0.7	4.2E-01
ENSMUST00000125504				8.3	5.9E-05	5.2	4.7E-04	-2.5	4.7E-02	0.8	1.9E-01
ENSMUST00000128746				8.3	1.1E-06	4.1	3.5E-03	-0.9	3.8E-01	-0.7	4.0E-01
ENSMUST00000189097				8.3	1.4E-05	-3.1	5.1E-02	1.0	1.7E-01	-1.6	3.3E-01
ENSMUST00000152400				8.3	9.1E-06	-6.0	4.1E-02	0.8	3.7E-01	3.8	1.7E-01
ENSMUST00000147738				1.4	1.8E-01	2.6	5.3E-02	0.5	6.7E-01	-0.7	4.6E-01
ENSMUST00000147741	WNK lysine deficient protein kinase 4 [Source:MGI Symbol;Acc:MGI:1917097]	E9PZ38		3.6	8.1E-02	4.3	1.8E-01	2.5	3.9E-01	1.8	3.2E-01
ENSMUST00000170486				8.3	2.1E-03	2.1	2.5E-01	-0.7	6.7E-01	1.8	1.5E-01
ENSMUST00000190002				8.3	1.0E-05	3.6	5.6E-04	-0.7	3.3E-01	-0.4	4.0E-01
ENSMUST00000147748				-1.7	1.1E-01	-0.4	7.2E-01	0.0	9.7E-01	-1.3	2.6E-01
ENSMUST00000147755	Rap guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:104580]	E0CXV1		-0.3	9.1E-01	3.8	2.5E-01	1.5	5.8E-01	-2.6	3.7E-01
ENSMUST00000147758	major facilitator superfamily domain containing 6 [Source:MGI Symbol;Acc:MGI:1922925]	F6U3S2		-1.4	1.9E-01	-1.5	2.7E-01	0.5	5.5E-01	0.6	6.4E-01
ENSMUST00000147759	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 [Source:MGI Symbol;Acc:MGI:102676]	E9Q1I5		0.7	8.0E-01	3.6	3.8E-01	3.8	2.3E-01	0.8	8.1E-01
ENSMUST00000155312				8.3	2.1E-05	6.8	9.7E-04	-1.3	4.3E-01	-0.6	4.5E-01
ENSMUST00000183700				8.3	3.8E-05	6.2	8.9E-04	-0.2	9.0E-01	-0.3	6.9E-01
ENSMUST00000144139				8.3	2.0E-07	6.3	7.1E-04	0.0	9.9E-01	-0.1	8.6E-01
ENSMUST00000147781	regulatory associated protein of MTOR, complex 1 [Source:MGI Symbol;Acc:MGI:1921620]	E9PXZ5		-2.7	3.5E-02	-0.7	6.0E-01	0.7	4.2E-01	-1.3	3.4E-01
ENSMUST00000146945				8.3	4.0E-05	2.3	1.5E-02	-0.3	6.7E-01	0.2	8.0E-01
ENSMUST00000120993				8.3	3.5E-05	4.3	2.9E-03	-2.8	4.0E-02	0.5	4.4E-01
ENSMUST00000127280				8.3	1.4E-05	5.4	8.7E-04	-0.4	7.4E-01	0.0	9.8E-01
ENSMUST00000188805				8.3	2.3E-06	5.3	3.3E-02	-0.1	9.7E-01	-0.3	8.0E-01
ENSMUST00000147806				1.4	3.2E-01	5.0	5.2E-02	3.5	1.2E-01	-0.1	9.4E-01
ENSMUST00000193276				8.3	6.8E-05	5.9	2.6E-04	-1.5	2.1E-01	0.2	7.3E-01
ENSMUST00000147815				-0.1	9.5E-01	-0.8	6.1E-01	-0.5	6.4E-01	0.3	8.7E-01
ENSMUST00000162475				8.3	6.9E-06	-2.5	2.4E-01	1.4	2.2E-01	-1.0	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000188679				8.3	1.1E-05	8.3	4.6E-05	-0.6	6.1E-01	-0.6	3.2E-01
ENSMUST00000194407				8.3	1.7E-07	2.0	3.0E-02	0.3	6.7E-01	-0.1	8.3E-01
ENSMUST00000120304				8.2	3.3E-04	6.5	1.4E-05	-1.2	1.5E-01	0.3	4.7E-01
ENSMUST00000147826	RIKEN cDNA A430005L14 gene [Source:MGI Symbol;Acc:MGI:2140680]	D6RH81		-2.8	1.2E-01	-2.0	2.3E-01	-1.1	3.0E-01	-1.9	3.3E-01
ENSMUST00000124939				8.2	2.8E-05	-2.4	2.0E-01	0.2	8.9E-01	-1.4	4.9E-01
ENSMUST00000127704				8.2	2.5E-05	5.1	6.2E-05	-0.1	9.0E-01	0.3	5.5E-01
ENSMUST00000190150				8.2	4.1E-05	3.5	6.5E-03	0.8	3.9E-01	1.2	1.2E-01
ENSMUST00000130490				8.2	8.1E-05	2.7	2.3E-02	-1.6	1.4E-01	-1.2	1.5E-01
ENSMUST00000142617				8.2	1.3E-06	5.3	6.5E-05	-0.3	7.0E-01	0.3	6.1E-01
ENSMUST00000140766				8.2	9.9E-06	-2.9	4.6E-02	0.6	3.2E-01	-0.3	8.4E-01
ENSMUST00000147842	reticulocalbin 2 [Source:MGI Symbol;Acc:MGI:1349765]	D6RHL9		3.1	4.3E-02	4.9	5.1E-02	2.5	2.3E-01	0.8	5.9E-01
ENSMUST00000125341				8.2	2.4E-05	-1.7	2.3E-01	0.5	5.4E-01	-1.6	2.9E-01
ENSMUST00000130441				8.2	1.6E-07	5.6	2.7E-04	-1.5	2.0E-01	0.1	8.0E-01
ENSMUST00000136651				8.2	2.1E-06	3.5	6.4E-03	-2.0	9.8E-02	-0.5	5.2E-01
ENSMUST00000142842				8.2	2.5E-05	7.4	2.3E-05	-0.5	6.1E-01	0.7	1.6E-01
ENSMUST00000191520				8.2	2.2E-05	3.6	2.9E-04	-0.3	6.3E-01	0.2	6.5E-01
ENSMUST00000190884				8.2	6.7E-06	3.6	2.1E-03	0.6	4.1E-01	-0.1	8.4E-01
ENSMUST00000189933				8.2	9.9E-06	4.1	2.2E-04	0.2	7.9E-01	0.0	9.8E-01
ENSMUST00000113954				8.2	7.6E-05	2.9	4.9E-03	0.0	9.9E-01	-0.4	5.5E-01
ENSMUST00000144838				8.2	1.3E-05	-5.6	4.5E-04	0.8	6.3E-02	-0.9	4.6E-01
ENSMUST00000139991				8.2	1.2E-05	2.6	2.9E-02	-0.8	4.1E-01	-1.1	2.1E-01
ENSMUST00000118838				8.2	3.7E-04	4.3	4.1E-05	-0.2	6.9E-01	-0.9	4.0E-02
ENSMUST00000125421				8.2	3.2E-05	1.8	2.5E-01	-1.2	3.5E-01	2.9	3.3E-02
ENSMUST00000147888				1.4	5.8E-02	1.7	5.4E-02	-0.4	4.9E-01	-0.7	2.9E-01
ENSMUST00000132554				8.2	1.7E-04	-3.3	3.4E-02	0.5	5.3E-01	-0.1	9.3E-01
ENSMUST00000147893	mannosidase 2, alpha B2 [Source:MGI Symbol;Acc:MGI:1195262]	F6Z025		3.2	1.3E-01	3.6	1.4E-01	-1.0	6.5E-01	-1.4	4.1E-01
ENSMUST00000147894				0.8	1.5E-01	1.3	8.6E-02	0.1	8.4E-01	-0.4	5.7E-01
ENSMUST00000147897				1.5	1.8E-01	1.1	4.4E-01	-0.5	6.8E-01	-0.1	9.0E-01
ENSMUST00000147898				0.8	4.8E-01	-2.2	1.8E-01	-0.4	7.0E-01	2.6	1.1E-01
ENSMUST00000135637				8.2	8.5E-06	5.9	1.2E-03	-0.6	6.4E-01	-0.8	3.2E-01
ENSMUST00000162442				8.2	3.0E-05	6.2	3.5E-03	-0.5	7.6E-01	-2.0	6.7E-02
ENSMUST00000117417				8.2	2.1E-03	7.0	3.5E-04	-0.6	6.6E-01	-0.5	5.0E-01
ENSMUST00000147914	DnaJ (Hsp40) homolog, subfamily B, member 12 [Source:MGI Symbol;Acc:MGI:1931881]	Q8C4C9		-1.7	4.6E-02	0.7	4.8E-01	1.3	1.0E-01	-1.1	2.4E-01
ENSMUST00000147915				3.9	4.2E-02	3.7	7.0E-02	-1.2	5.3E-01	-1.1	4.3E-01
ENSMUST00000161353				8.2	4.0E-05	2.6	2.1E-02	-2.2	5.4E-02	-0.7	3.8E-01
ENSMUST00000131760				8.2	1.9E-05	5.4	6.2E-03	0.2	8.7E-01	-1.3	2.0E-01
ENSMUST00000147926				1.1	1.6E-01	3.8	1.8E-03	1.6	7.1E-02	-1.2	1.1E-01
ENSMUST00000112216				8.2	9.1E-05	2.9	1.4E-04	-1.2	2.2E-02	-0.7	9.5E-02
ENSMUST00000191757				8.2	8.8E-05	4.3	4.2E-04	0.2	8.3E-01	-0.2	7.9E-01
ENSMUST00000149234				8.2	1.7E-05	-3.8	8.4E-03	-0.5	3.8E-01	-1.1	3.9E-01
ENSMUST00000147938	TGF-beta activated kinase 1/MAP3K7 binding protein 2 [Source:MGI Symbol;Acc:MGI:1915902]	D3Z216		0.8	5.1E-01	3.5	3.3E-02	1.6	2.0E-01	-1.1	3.9E-01
ENSMUST00000147941				-2.6	2.4E-01	-2.2	4.3E-01	0.3	8.7E-01	-0.1	9.6E-01
ENSMUST00000127200				8.2	5.9E-05	5.1	2.7E-02	0.2	8.9E-01	0.6	6.6E-01
ENSMUST00000147950				-1.3	5.6E-01	-3.2	3.6E-01	-1.0	6.2E-01	0.9	7.8E-01
ENSMUST00000147952	vaccinia related kinase 3 [Source:MGI Symbol;Acc:MGI:2182465]	E9Q754		-1.6	1.1E-01	3.6	2.7E-02	3.7	1.1E-02	-1.4	1.9E-01
ENSMUST00000089593				8.2	2.7E-04	-3.8	1.0E-02	0.2	8.0E-01	0.0	9.8E-01
ENSMUST00000147961				0.3	8.2E-01	1.2	4.2E-01	-0.3	7.8E-01	-1.2	3.4E-01
ENSMUST00000149555				8.2	1.3E-04	2.8	5.5E-02	0.1	9.1E-01	-0.2	8.1E-01
ENSMUST00000132390				8.2	4.6E-06	6.8	5.1E-04	-0.7	6.1E-01	-0.1	8.6E-01
ENSMUST00000134680				8.2	1.5E-05	4.4	6.3E-05	-1.3	5.6E-02	-0.8	1.2E-01
ENSMUST00000141506				8.2	6.1E-04	7.9	8.6E-06	-0.1	9.3E-01	0.4	4.0E-01
ENSMUST00000185215				8.2	1.3E-05	3.5	1.7E-03	-0.9	2.5E-01	-0.5	4.1E-01
ENSMUST00000135522				8.2	1.2E-05	-5.5	3.6E-02	1.2	1.7E-01	1.4	5.4E-01
ENSMUST00000139800				8.2	1.4E-04	2.7	1.1E-03	0.3	5.9E-01	0.2	7.4E-01
ENSMUST00000147979	v-raf-leukemia viral oncogene 1 [Source:MGI Symbol;Acc:MGI:97847]	F6TUC4		2.3	3.9E-02	1.9	1.7E-01	0.2	8.5E-01	0.5	6.3E-01
ENSMUST00000156689				8.2	2.1E-05	6.2	3.2E-04	0.2	8.5E-01	-0.1	8.6E-01
ENSMUST00000182315				8.2	6.1E-05	7.1	6.5E-03	-0.8	7.2E-01	-1.6	2.0E-01
ENSMUST00000144678				8.2	1.2E-05	-4.9	8.2E-03	1.4	7.0E-02	-0.2	9.0E-01
ENSMUST00000123200				8.2	2.0E-05	4.9	4.1E-04	-2.8	1.9E-02	0.3	5.8E-01
ENSMUST00000167880				8.2	5.6E-07	6.7	4.5E-06	-0.2	8.2E-01	-0.1	8.4E-01
ENSMUST00000123838				8.2	9.0E-06	6.8	5.4E-03	-0.9	6.8E-01	1.0	3.4E-01
ENSMUST00000145639				8.2	7.5E-05	6.7	2.3E-02	1.3	5.9E-01	1.7	2.2E-01
ENSMUST00000122293				8.2	6.8E-06	5.7	5.4E-04	-1.0	4.3E-01	0.2	7.8E-01
ENSMUST00000148016				-0.8	4.0E-01	2.3	6.2E-02	0.9	3.7E-01	-2.2	4.5E-02
ENSMUST00000191149				8.2	6.7E-05	5.7	1.1E-03	-0.5	6.9E-01	0.1	9.3E-01
ENSMUST00000167499				8.2	8.8E-06	6.3	1.5E-03	0.4	7.7E-01	1.0	2.2E-01
ENSMUST00000123481				8.2	6.1E-06	0.4	6.2E-01	1.0	8.0E-02	-1.4	9.4E-02
ENSMUST00000148037				-0.2	8.7E-01	0.6	6.7E-01	0.6	5.1E-01	-0.1	9.5E-01
ENSMUST00000118512				8.2	1.9E-05	7.1	2.0E-04	-0.4	7.5E-01	0.1	8.4E-01
ENSMUST00000148040				3.5	1.1E-01	7.7	3.0E-02	2.5	4.1E-01	-1.8	3.1E-01
ENSMUST00000144340				8.2	6.7E-06	0.7	2.8E-01	-1.1	7.5E-02	0.4	4.9E-01
ENSMUST00000148045				3.7	6.5E-02	1.0	7.1E-01	0.0	1.0E+00	2.7	2.2E-01
ENSMUST00000190826				8.2	6.2E-07	5.7	2.9E-04	-1.9	1.2E-01	-0.1	8.3E-01
ENSMUST00000146191				8.2	1.3E-05	5.8	7.2E-05	-1.5	1.1E-01	0.3	5.6E-01
ENSMUST00000142932				8.2	5.6E-07	-5.1	1.7E-02	-0.6	4.0E-01	0.0	9.8E-01
ENSMUST00000190127				8.2	3.3E-04	3.6	8.1E-04	-3.8	2.1E-03	0.1	8.9E-01
ENSMUST00000129325				8.2	7.7E-05	4.2	1.3E-02	-0.4	7.4E-01	0.1	9.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000177203				8.2	2.3E-06	-4.4	8.2E-03	-1.6	4.3E-02	-0.7	6.2E-01
ENSMUST00000180843				8.2	2.9E-05	-0.6	7.7E-01	2.3	1.5E-01	-2.0	3.7E-01
ENSMUST00000144491				8.2	2.1E-05	6.0	3.7E-04	-0.5	6.5E-01	-0.3	6.0E-01
ENSMUST00000165542				8.2	1.1E-05	6.2	3.4E-03	-0.7	6.7E-01	-0.5	5.9E-01
ENSMUST00000117576				8.2	7.8E-07	3.9	3.6E-02	-0.8	6.1E-01	1.1	3.2E-01
ENSMUST00000156184				8.2	2.6E-05	-5.6	1.3E-03	0.2	6.3E-01	0.0	9.8E-01
ENSMUST00000148085				-1.9	1.8E-01	-2.6	1.5E-01	-0.5	6.6E-01	0.2	9.0E-01
ENSMUST00000124419				8.2	1.3E-04	5.3	1.0E-04	0.5	5.3E-01	-0.5	4.2E-01
ENSMUST00000148098				-0.7	4.5E-01	-0.1	9.2E-01	0.6	5.3E-01	0.0	9.9E-01
ENSMUST00000131312				8.2	2.1E-07	-0.3	7.6E-01	-1.4	9.4E-02	1.3	1.4E-01
ENSMUST00000148105				-1.5	1.8E-01	-3.1	3.7E-02	-1.3	1.1E-01	0.3	8.1E-01
ENSMUST00000140106				8.2	3.6E-06	0.5	8.6E-01	-3.1	2.3E-01	3.3	1.7E-01
ENSMUST00000148110				-1.6	3.0E-01	-0.1	9.6E-01	0.0	1.0E+00	-1.5	3.5E-01
ENSMUST00000182037				8.2	1.4E-05	7.2	1.1E-04	-0.5	6.6E-01	-0.2	7.9E-01
ENSMUST00000127890				8.2	9.8E-06	3.6	2.3E-04	0.0	1.0E+00	0.3	5.5E-01
ENSMUST00000148119				1.7	1.2E-01	2.6	9.7E-02	0.2	8.5E-01	-0.7	5.4E-01
ENSMUST00000144297				8.2	1.8E-05	0.1	9.6E-01	2.2	4.6E-02	-1.0	4.8E-01
ENSMUST00000124423				8.2	1.2E-03	-2.5	4.2E-02	0.5	5.1E-01	0.3	8.0E-01
ENSMUST00000131569				8.2	7.6E-06	7.8	8.4E-05	-0.6	6.4E-01	-1.5	3.8E-02
ENSMUST00000145386				8.2	1.5E-05	3.1	9.0E-03	-3.0	2.4E-02	-0.6	4.2E-01
ENSMUST00000151444				8.2	1.1E-05	7.4	8.8E-05	-0.6	6.1E-01	0.0	9.3E-01
ENSMUST00000148144	myosin VA [Source:MGI Symbol;Acc:MGI:105976]	F6TDE5		0.8	6.6E-01	0.5	8.4E-01	-0.6	7.2E-01	-0.3	9.0E-01
ENSMUST00000151186				8.2	2.4E-04	5.8	3.1E-04	-0.5	6.5E-01	0.3	6.5E-01
ENSMUST00000148151				-0.2	9.1E-01	0.5	7.7E-01	-0.1	9.5E-01	-0.8	6.5E-01
ENSMUST00000139052				8.2	1.9E-06	2.9	6.2E-03	-0.8	3.0E-01	-0.4	5.9E-01
ENSMUST00000148158				2.9	2.1E-01	4.1	8.2E-02	-1.3	5.8E-01	-2.5	1.5E-01
ENSMUST00000140071				8.2	1.1E-05	-4.0	4.1E-04	1.4	4.9E-03	-1.4	9.5E-02
ENSMUST00000189439				8.2	8.4E-06	7.1	3.0E-03	0.7	7.1E-01	-0.7	5.1E-01
ENSMUST00000148178	heterogeneous nuclear ribonucleoprotein M [Source:MGI Symbol;Acc:MGI:1926465]		Q9D0E1	0.8	2.7E-01	1.8	4.9E-02	-0.1	9.3E-01	-1.1	1.5E-01
ENSMUST00000148189				-2.1	7.3E-02	-1.2	3.5E-01	0.5	6.0E-01	-0.4	7.6E-01
ENSMUST00000131703				8.2	3.7E-05	7.9	3.6E-04	2.2	1.4E-01	0.0	9.7E-01
ENSMUST00000148191				-0.2	5.4E-01	0.2	6.1E-01	0.4	2.5E-01	-0.1	9.0E-01
ENSMUST00000159849				8.2	1.5E-05	-3.5	1.7E-02	0.3	6.1E-01	-0.5	7.1E-01
ENSMUST00000148204	SUZ RNA binding domain containing 1 [Source:MGI Symbol;Acc:MGI:1098672]	A2AA85		-1.3	1.6E-01	-0.8	5.1E-01	1.0	2.1E-01	0.5	6.3E-01
ENSMUST00000118329				8.1	1.6E-05	8.0	1.1E-03	0.7	6.9E-01	-0.9	3.4E-01
ENSMUST00000079568				8.1	2.0E-05	-5.6	6.9E-03	0.5	3.8E-01	-0.5	7.7E-01
ENSMUST00000148220				-1.2	2.6E-01	0.0	9.7E-01	0.7	4.9E-01	-0.5	6.6E-01
ENSMUST00000134523				8.1	1.5E-06	8.2	1.2E-04	-0.2	8.8E-01	0.0	9.5E-01
ENSMUST00000152959				8.1	2.7E-05	2.7	6.1E-03	-0.1	8.6E-01	-0.4	5.0E-01
ENSMUST00000152253				8.1	1.1E-04	5.4	3.1E-03	0.2	8.7E-01	-0.3	7.5E-01
ENSMUST00000188492				8.1	6.6E-05	-5.0	7.4E-04	0.0	9.4E-01	-0.2	8.2E-01
ENSMUST00000117448				8.1	2.5E-05	1.7	4.2E-01	7.1	9.8E-04	0.9	5.8E-01
ENSMUST00000148241				0.4	6.5E-01	-0.7	4.5E-01	-1.2	1.4E-01	-0.1	9.3E-01
ENSMUST00000174115				8.1	1.2E-05	-3.3	6.0E-02	0.6	4.2E-01	-0.6	7.3E-01
ENSMUST00000050900				8.1	4.5E-05	-3.3	2.9E-01	1.6	3.3E-01	0.5	8.5E-01
ENSMUST00000186404				8.1	1.9E-06	8.0	3.1E-05	-0.5	6.7E-01	-0.9	1.0E-01
ENSMUST00000187850				8.1	3.4E-07	-7.7	1.1E-04	0.3	5.2E-01	-1.3	3.6E-01
ENSMUST00000065567				8.1	1.0E-06	7.0	1.9E-04	0.0	9.9E-01	0.0	9.8E-01
ENSMUST00000123061				8.1	2.4E-05	5.3	5.1E-04	0.6	5.6E-01	0.1	8.6E-01
ENSMUST00000128827				8.1	1.1E-04	8.3	7.8E-06	0.2	8.5E-01	0.2	6.8E-01
ENSMUST00000148258	heterogeneous nuclear ribonucleoprotein M [Source:MGI Symbol;Acc:MGI:1926465]	F6W322		-4.6	4.0E-02	-2.0	4.7E-01	1.8	3.0E-01	-0.8	7.7E-01
ENSMUST00000147824				8.1	1.6E-06	5.6	5.7E-05	-0.2	7.4E-01	1.0	5.4E-02
ENSMUST00000124907				8.1	2.9E-05	-6.2	5.4E-03	0.9	2.7E-01	-0.7	7.3E-01
ENSMUST00000148263	DEAH (Asp-Glu-Ala-His) box polypeptide 40 [Source:MGI Symbol;Acc:MGI:1914737]	Q5SXR4		-0.8	7.4E-01	-3.9	2.2E-01	-3.3	7.7E-02	-0.2	9.5E-01
ENSMUST00000148264	RAB guanine nucleotide exchange factor (GEF) 1 [Source:MGI Symbol;Acc:MGI:1929459]	D3Z2L2		-2.3	7.7E-02	-0.7	6.8E-01	1.3	2.6E-01	-0.3	8.6E-01
ENSMUST00000148265	CDC-like kinase 2 [Source:MGI Symbol;Acc:MGI:1098669]	D3Z4P7		0.3	8.7E-01	-1.4	5.6E-01	-2.1	1.7E-01	-0.4	8.7E-01
ENSMUST00000186103				8.1	2.2E-04	6.1	3.2E-04	-0.5	6.9E-01	-0.4	4.9E-01
ENSMUST00000070453				8.1	3.8E-05	5.6	1.1E-03	-0.4	7.4E-01	-0.3	6.8E-01
ENSMUST00000148269	choline/ethanolaminephosphotransferase 1 [Source:MGI Symbol;Acc:MGI:2139793]	D3YX12		0.8	7.8E-01	-6.9	1.0E-01	-5.9	1.5E-02	1.9	6.5E-01
ENSMUST00000125551				8.1	2.0E-04	-2.4	2.0E-01	1.8	6.8E-02	-0.2	9.3E-01
ENSMUST00000147016				8.1	1.2E-05	6.2	2.8E-04	-0.6	6.2E-01	-0.1	9.1E-01
ENSMUST00000148278				-4.3	5.0E-02	-3.5	1.5E-01	0.3	7.8E-01	-0.4	8.8E-01
ENSMUST00000163531				8.1	2.0E-05	-6.8	2.0E-05	-0.8	2.7E-02	-0.5	5.5E-01
ENSMUST00000190556				8.1	2.2E-04	-3.9	3.2E-03	0.8	8.3E-02	-0.6	6.0E-01
ENSMUST00000191984				8.1	6.0E-05	-1.2	2.3E-01	0.7	2.7E-01	-2.6	4.6E-02
ENSMUST00000172893				8.1	2.5E-05	3.1	3.4E-02	0.2	8.9E-01	-0.5	6.0E-01
ENSMUST00000190106				8.1	7.9E-04	3.1	2.0E-02	0.2	8.0E-01	0.6	4.7E-01
ENSMUST00000148315				1.0	4.9E-02	1.3	4.5E-02	-0.3	5.5E-01	-0.6	3.0E-01
ENSMUST00000148319				0.1	9.8E-01	-3.2	4.5E-01	-3.8	1.6E-01	-0.6	8.9E-01
ENSMUST00000138980				8.1	4.3E-04	1.4	6.9E-01	10.5	1.9E-03	-1.6	6.0E-01
ENSMUST00000156608				8.1	7.1E-07	-7.8	9.2E-03	-0.4	5.8E-01	-0.6	8.3E-01
ENSMUST00000121211				8.1	1.1E-06	-3.8	7.8E-03	0.9	1.4E-01	0.2	8.4E-01
ENSMUST00000126347				8.1	5.5E-05	7.6	4.2E-05	-0.6	6.0E-01	-1.0	8.5E-02
ENSMUST00000143830				8.1	4.6E-05	7.2	4.1E-03	-0.7	7.3E-01	-1.4	2.3E-01
ENSMUST00000148344	pleckstrin homology-like domain, family B, member 1 [Source:MGI Symbol;Acc:MGI:2143230]	F6RUK9		4.3	1.3E-01	5.8	9.1E-02	0.5	8.8E-01	-1.0	6.1E-01
ENSMUST00000069773				8.1	1.6E-04	6.3	6.5E-05	0.4	6.6E-01	0.2	7.6E-01
ENSMUST00000135334				8.1	6.1E-04	6.7	4.2E-05	0.0	9.6E-01	0.8	1.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000148351	importin 4 [Source:MGI Symbol;Acc:MGI:1923001]	D6RES6		-2.0	3.3E-01	1.1	7.2E-01	2.4	3.1E-01	-0.7	7.8E-01
ENSMUST00000064383				8.1	8.8E-05	2.7	4.3E-02	0.9	3.8E-01	0.6	5.2E-01
ENSMUST00000137302				8.1	2.3E-03	5.4	3.1E-03	-0.1	9.5E-01	0.7	4.2E-01
ENSMUST00000170512				8.1	1.6E-04	5.0	1.9E-03	-0.8	4.7E-01	0.1	9.0E-01
ENSMUST00000149165				8.1	9.2E-05	-1.0	5.8E-01	1.6	1.8E-01	-0.5	7.6E-01
ENSMUST00000148367				0.9	2.8E-01	1.1	2.5E-01	-0.4	6.5E-01	-0.6	4.8E-01
ENSMUST00000148373				0.6	7.3E-01	0.6	8.2E-01	-0.5	7.8E-01	-0.4	8.5E-01
ENSMUST00000134937				8.1	4.5E-05	-3.3	4.3E-03	-1.3	1.9E-02	-1.7	1.1E-01
ENSMUST00000148489				8.1	9.3E-04	5.6	1.9E-04	0.0	9.8E-01	-0.6	3.3E-01
ENSMUST00000148385	structural maintenance of chromosomes 4 [Source:MGI Symbol;Acc:MGI:1917349]	D6RCX2		-3.0	3.6E-01	-3.4	2.5E-01	-2.1	2.9E-01	-1.7	6.3E-01
ENSMUST00000100464				8.1	1.1E-05	6.3	4.2E-04	-3.6	2.3E-02	-0.9	2.3E-01
ENSMUST00000064930				8.1	2.3E-05	6.0	1.9E-04	1.0	3.2E-01	-0.5	4.4E-01
ENSMUST00000146189				8.1	2.5E-05	4.0	2.8E-02	-1.3	4.3E-01	-0.6	5.7E-01
ENSMUST00000189311				8.1	4.1E-03	6.5	2.8E-04	2.2	6.6E-02	-0.6	3.5E-01
ENSMUST00000150222				8.1	4.6E-05	6.0	5.9E-04	-0.6	6.4E-01	-0.5	5.1E-01
ENSMUST00000186478				8.1	3.7E-05	4.7	4.6E-03	-0.5	7.3E-01	0.9	2.7E-01
ENSMUST00000147578				8.1	1.7E-05	7.0	2.8E-04	0.6	6.4E-01	0.8	2.0E-01
ENSMUST00000101382				8.1	2.7E-05	4.6	7.8E-04	-1.0	2.8E-01	1.0	1.3E-01
ENSMUST00000148410				0.0	9.8E-01	-1.5	3.8E-01	-0.1	9.6E-01	1.5	3.6E-01
ENSMUST00000148418				3.6	4.9E-02	5.3	1.3E-02	-0.4	8.3E-01	-2.1	9.0E-02
ENSMUST00000148430	t-complex-associated testis expressed 2 [Source:MGI Symbol;Acc:MGI:98641]	Q9Z1F3		1.8	2.3E-01	1.6	4.9E-01	1.3	4.8E-01	1.5	4.0E-01
ENSMUST00000154643				8.1	7.7E-03	6.0	1.6E-03	-0.4	7.7E-01	-0.6	5.1E-01
ENSMUST00000154767				8.1	2.5E-04	3.2	1.5E-02	1.0	3.1E-01	0.9	2.9E-01
ENSMUST00000144370				8.1	9.3E-05	4.8	2.3E-03	0.7	4.9E-01	0.6	4.1E-01
ENSMUST00000131046				8.1	2.4E-06	6.3	7.1E-06	0.5	5.1E-01	-0.5	2.3E-01
ENSMUST00000153403				8.1	5.5E-04	5.0	2.5E-03	-3.6	3.8E-02	1.0	2.3E-01
ENSMUST00000167151				8.1	2.4E-05	6.2	5.3E-03	0.2	9.0E-01	-1.4	2.5E-01
ENSMUST00000071101				8.1	2.4E-05	6.6	1.1E-04	2.1	5.7E-02	0.4	5.2E-01
ENSMUST00000138093				8.1	3.5E-05	7.5	1.5E-04	-0.7	6.2E-01	-1.3	7.2E-02
ENSMUST00000100870				8.0	5.2E-04	6.2	2.9E-04	-0.5	6.5E-01	0.3	6.4E-01
ENSMUST00000183285				8.0	2.4E-04	5.3	7.5E-05	-0.4	6.2E-01	0.5	3.4E-01
ENSMUST00000148454				0.3	8.2E-01	3.2	1.1E-01	0.8	6.2E-01	-2.1	1.6E-01
ENSMUST00000118338				8.0	1.8E-04	-3.4	6.7E-02	1.2	2.2E-01	0.6	7.2E-01
ENSMUST00000126864				8.0	3.4E-04	-2.8	2.2E-02	-0.2	6.8E-01	-2.5	7.1E-02
ENSMUST00000148467				-0.8	5.9E-02	-0.7	1.4E-01	-0.6	8.5E-02	-0.7	1.6E-01
ENSMUST00000148138				8.0	2.2E-05	4.1	2.0E-03	-0.6	5.3E-01	-0.1	9.2E-01
ENSMUST00000128146				8.0	1.6E-05	7.2	6.8E-04	-0.8	6.3E-01	-0.1	9.0E-01
ENSMUST00000127661				8.0	8.0E-04	4.7	5.1E-04	-0.4	6.3E-01	1.0	1.4E-01
ENSMUST00000140004				8.0	3.9E-05	5.2	1.8E-02	-0.7	7.2E-01	0.1	9.4E-01
ENSMUST00000146448				8.0	1.7E-05	0.2	8.6E-01	0.5	5.2E-01	-3.2	3.5E-02
ENSMUST00000138717				8.0	1.5E-05	-3.7	1.9E-02	1.5	3.1E-02	-0.7	6.1E-01
ENSMUST00000151277				8.0	1.2E-07	7.6	1.6E-04	-0.5	7.0E-01	-2.1	1.5E-02
ENSMUST00000168795				8.0	3.2E-05	5.5	2.6E-03	-0.5	7.4E-01	-2.4	2.6E-02
ENSMUST00000129385				8.0	6.7E-05	6.7	5.3E-03	-0.8	6.9E-01	0.6	5.8E-01
ENSMUST00000148497	piezo-type mechanosensitive ion channel component 1 [Source:MGI Symbol;Acc:MGI:3603204]	F6PYU5		2.4	1.2E-01	5.1	5.5E-02	3.9	9.5E-02	1.2	4.3E-01
ENSMUST00000128975				8.0	1.1E-02	-1.1	4.2E-01	0.8	3.9E-01	-2.7	1.1E-01
ENSMUST00000148503				1.9	2.6E-01	3.4	1.4E-01	0.7	7.2E-01	-0.8	6.5E-01
ENSMUST00000148510				-1.0	4.1E-01	2.1	1.1E-01	0.2	8.6E-01	-2.9	3.5E-02
ENSMUST00000177789				8.0	1.7E-05	5.2	4.7E-05	0.5	4.9E-01	0.5	3.0E-01
ENSMUST00000127731				8.0	1.2E-05	3.6	5.6E-03	-0.2	8.0E-01	-0.5	5.0E-01
ENSMUST00000117109				8.0	2.5E-04	4.1	1.7E-03	-1.7	1.1E-01	-1.0	1.6E-01
ENSMUST00000127633				8.0	2.4E-05	4.5	4.8E-03	0.0	9.7E-01	-1.2	1.7E-01
ENSMUST00000186225				8.0	1.2E-05	5.4	2.5E-04	-0.3	7.5E-01	0.1	9.0E-01
ENSMUST00000148535				-1.7	1.2E-01	0.2	8.7E-01	0.4	6.5E-01	-1.5	2.0E-01
ENSMUST00000148537				-1.1	2.1E-01	-0.6	5.4E-01	0.5	5.2E-01	0.0	9.8E-01
ENSMUST00000121982				8.0	1.9E-04	5.8	9.2E-04	-1.2	3.5E-01	-0.3	7.2E-01
ENSMUST00000144873				8.0	7.7E-05	-4.0	3.3E-02	0.5	4.6E-01	2.2	1.9E-01
ENSMUST00000063585				8.0	1.8E-04	7.0	3.1E-04	-0.5	7.0E-01	0.4	5.4E-01
ENSMUST00000127431				8.0	8.9E-06	5.2	3.5E-04	0.1	9.0E-01	0.7	2.8E-01
ENSMUST00000134865				8.0	4.4E-05	4.5	4.9E-03	-3.7	2.2E-02	-0.5	5.5E-01
ENSMUST00000133830				8.0	2.3E-03	-4.9	5.6E-04	-0.9	3.8E-02	1.6	1.2E-01
ENSMUST00000188979				8.0	1.5E-04	5.8	8.3E-03	-2.1	3.2E-01	-1.4	2.1E-01
ENSMUST00000148571				0.8	5.1E-01	2.4	2.0E-01	0.7	6.5E-01	-0.9	5.0E-01
ENSMUST00000140923				8.0	1.2E-05	-8.6	4.3E-05	-1.2	8.0E-03	-0.8	5.3E-01
ENSMUST00000148583	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha [Source:MGI Symbol;Acc:MGI:1298206]	A2ASS3		-2.4	5.0E-02	0.0	9.8E-01	1.3	2.3E-01	-1.1	4.1E-01
ENSMUST00000166954				8.0	1.9E-05	5.6	4.0E-04	-1.8	1.4E-01	0.3	6.0E-01
ENSMUST00000148589	NADPH dependent diflavin oxidoreductase 1 [Source:MGI Symbol;Acc:MGI:1926047]	E0CYR1		-2.3	1.4E-01	0.4	8.5E-01	0.8	6.0E-01	-1.9	2.8E-01
ENSMUST00000148590				1.3	8.3E-02	0.2	7.9E-01	-0.4	5.6E-01	0.7	3.7E-01
ENSMUST00000148592				-1.3	2.5E-01	-1.0	4.8E-01	0.8	4.4E-01	0.5	7.2E-01
ENSMUST00000193666				8.0	3.1E-05	4.3	5.9E-04	-2.5	2.5E-02	-0.2	7.4E-01
ENSMUST00000161138				8.0	2.3E-05	-5.8	2.3E-02	0.9	2.6E-01	1.6	4.8E-01
ENSMUST00000148602	cortactin binding protein 2 [Source:MGI Symbol;Acc:MGI:1353467]	R7RU63	B9EJA2	6.8	4.0E-02	4.8	1.7E-01	-0.9	8.0E-01	1.1	6.2E-01
ENSMUST00000168178				8.0	3.2E-04	6.9	4.9E-03	-0.8	7.1E-01	0.3	7.5E-01
ENSMUST00000148609				1.1	4.6E-01	3.0	1.6E-01	2.0	2.6E-01	0.1	9.4E-01
ENSMUST00000148612				3.7	3.9E-02	1.4	4.1E-01	-3.4	4.6E-02	-1.0	4.9E-01
ENSMUST00000148613				-2.4	2.9E-01	-1.9	4.3E-01	-1.0	5.7E-01	-1.5	5.5E-01
ENSMUST00000106074				8.0	5.3E-04	-0.5	7.3E-01	-1.9	1.1E-01	2.9	3.5E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000189416				8.0	1.2E-04	6.7	2.3E-06	0.1	9.2E-01	-0.2	6.3E-01
ENSMUST00000131659				8.0	5.8E-05	4.5	1.8E-03	-1.3	2.3E-01	-0.4	6.0E-01
ENSMUST00000148628				0.2	8.4E-01	1.3	2.3E-01	-0.1	8.7E-01	-1.3	2.0E-01
ENSMUST00000148631	F-box and leucine-rich repeat protein 12 [Source:MGI Symbol;Acc:MGI:1354738]		Q9EPX5	0.1	9.0E-01	-1.7	3.1E-01	1.7	7.8E-02	3.5	4.6E-02
ENSMUST00000161493				8.0	6.2E-06	3.8	2.2E-03	-1.1	2.6E-01	1.2	7.4E-02
ENSMUST00000170927				8.0	4.6E-07	-2.8	4.1E-04	0.9	1.4E-02	-1.1	6.6E-02
ENSMUST00000154378				8.0	5.3E-05	2.8	8.7E-03	-0.5	5.3E-01	-0.9	2.5E-01
ENSMUST00000148643	engulfment and cell motility 2 [Source:MGI Symbol;Acc:MGI:2153045]	F6YXR3		-2.3	4.8E-01	0.4	8.8E-01	-1.4	5.3E-01	-4.0	2.1E-01
ENSMUST00000140025				8.0	9.9E-04	-7.5	6.7E-03	0.4	5.7E-01	0.5	8.3E-01
ENSMUST00000193477				8.0	2.2E-05	4.9	1.3E-02	-0.7	6.9E-01	0.1	9.1E-01
ENSMUST00000132002				8.0	1.5E-05	-0.4	6.8E-01	1.3	5.4E-02	-0.1	9.1E-01
ENSMUST00000148001				8.0	1.3E-05	2.1	4.0E-01	-2.2	2.9E-01	0.5	8.0E-01
ENSMUST00000194756				8.0	7.7E-06	5.1	2.2E-03	-0.4	7.4E-01	0.5	5.3E-01
ENSMUST00000148677	flavin containing monooxygenase 9 [Source:MGI Symbol;Acc:MGI:3606068]	Q14DT3		2.9	2.6E-01	4.0	1.4E-01	-0.4	8.7E-01	-1.6	4.0E-01
ENSMUST00000148679				-0.9	5.7E-01	-1.7	4.2E-01	-0.8	5.9E-01	0.1	9.6E-01
ENSMUST00000148681	heterochromatin protein 1, binding protein 3 [Source:MGI Symbol;Acc:MGI:109369]	A2AM65		0.0	9.9E-01	-2.0	5.3E-01	-2.5	2.3E-01	-0.5	8.8E-01
ENSMUST00000168388				8.0	1.4E-05	5.7	6.6E-04	-3.5	2.6E-02	0.0	1.0E+00
ENSMUST00000137804				8.0	4.8E-04	1.8	5.9E-02	-1.5	8.1E-02	-0.5	5.1E-01
ENSMUST00000125081				8.0	1.7E-04	-2.3	6.7E-02	-0.3	6.7E-01	-3.2	5.9E-02
ENSMUST00000148706				-0.2	9.3E-01	-2.9	3.1E-01	-2.2	2.9E-01	0.5	8.8E-01
ENSMUST00000118480				8.0	1.7E-04	7.2	7.4E-05	2.0	6.9E-02	0.0	9.8E-01
ENSMUST00000148710				-1.2	3.5E-01	-1.8	3.4E-01	-0.6	5.9E-01	0.0	9.9E-01
ENSMUST00000148711				2.6	2.4E-01	2.0	3.9E-01	-2.1	3.7E-01	-1.5	4.3E-01
ENSMUST00000105048				8.0	7.4E-06	6.3	9.0E-04	0.7	5.6E-01	0.4	5.3E-01
ENSMUST00000118819				8.0	2.2E-04	5.3	1.5E-03	0.5	6.5E-01	1.6	5.7E-02
ENSMUST00000138925				8.0	2.7E-05	-1.5	2.8E-01	0.8	3.3E-01	-1.9	2.2E-01
ENSMUST00000183531				8.0	2.8E-05	7.0	3.1E-04	-1.4	3.2E-01	-0.9	2.4E-01
ENSMUST00000148717				1.2	1.1E-01	2.7	9.9E-03	0.9	2.5E-01	-0.7	3.4E-01
ENSMUST00000133230				8.0	4.7E-06	-0.6	7.1E-01	1.5	2.4E-01	-1.9	2.7E-01
ENSMUST00000182708				8.0	6.4E-05	2.7	1.2E-01	1.2	4.0E-01	1.5	2.0E-01
ENSMUST00000148738				-0.3	7.8E-01	1.4	3.3E-01	0.6	5.9E-01	-1.1	3.8E-01
ENSMUST00000125848				8.0	3.7E-04	7.8	5.4E-05	-0.1	9.3E-01	-0.5	3.9E-01
ENSMUST00000189430				8.0	9.6E-07	5.2	6.8E-03	0.1	9.5E-01	-0.3	7.6E-01
ENSMUST00000130378				8.0	7.6E-06	-1.4	5.1E-01	1.7	2.1E-01	-1.9	4.0E-01
ENSMUST00000118151				8.0	1.2E-05	5.6	8.6E-05	-2.1	5.5E-02	0.2	6.8E-01
ENSMUST00000156934				8.0	3.4E-07	4.0	3.1E-04	-0.4	5.6E-01	0.1	8.1E-01
ENSMUST00000129260				8.0	1.1E-06	5.8	1.4E-03	-0.6	6.7E-01	-0.5	4.8E-01
ENSMUST00000188105				8.0	6.2E-06	2.3	1.4E-02	-1.8	2.4E-02	-1.1	1.2E-01
ENSMUST00000148759	SMEK homolog 2, suppressor of mek1 (Dictyostelium) [Source:MGI Symbol;Acc:MGI:2144474]	M0QW93		-3.5	2.6E-01	-5.0	1.7E-01	-2.5	1.8E-01	-1.0	7.9E-01
ENSMUST00000159432				8.0	1.3E-04	5.3	2.4E-03	0.8	5.4E-01	-1.0	2.4E-01
ENSMUST00000190853				8.0	1.1E-06	-8.1	7.3E-04	-1.4	2.0E-02	-1.4	4.7E-01
ENSMUST00000181661				8.0	1.5E-04	6.8	4.9E-04	0.0	9.9E-01	1.0	2.0E-01
ENSMUST00000148771				0.1	9.0E-01	0.9	2.9E-01	0.4	5.7E-01	-0.5	5.5E-01
ENSMUST00000145004				8.0	3.6E-05	2.6	2.4E-02	0.1	9.5E-01	0.1	8.6E-01
ENSMUST00000131456				8.0	1.8E-03	-6.5	3.8E-02	-1.0	3.4E-01	0.0	9.9E-01
ENSMUST00000148780				-0.9	2.9E-01	-2.3	9.7E-02	0.0	9.8E-01	1.4	2.8E-01
ENSMUST00000162214				8.0	1.6E-04	5.2	5.6E-04	-0.3	7.7E-01	-1.0	1.7E-01
ENSMUST00000148787				1.5	9.8E-02	1.6	1.0E-01	-0.9	2.7E-01	-1.1	1.8E-01
ENSMUST00000150998				8.0	3.0E-05	7.6	9.1E-05	-0.6	6.3E-01	-0.8	2.0E-01
ENSMUST00000172672				8.0	9.6E-04	-5.7	1.8E-02	0.1	8.6E-01	-0.7	7.8E-01
ENSMUST00000112332				8.0	2.4E-05	-5.8	5.2E-03	-0.8	2.1E-01	-0.5	7.7E-01
ENSMUST00000179487				8.0	2.4E-05	5.3	1.3E-03	-0.9	4.9E-01	-0.3	7.1E-01
ENSMUST00000152588				8.0	1.2E-04	-5.1	1.7E-02	0.6	4.4E-01	0.6	7.3E-01
ENSMUST00000152811				8.0	5.1E-05	5.6	5.6E-02	-0.8	7.9E-01	-0.6	7.1E-01
ENSMUST00000128546				8.0	3.2E-05	0.1	9.0E-01	-1.4	4.4E-02	0.7	3.2E-01
ENSMUST00000148809				3.0	7.7E-02	5.0	4.5E-02	2.2	3.1E-01	0.2	8.7E-01
ENSMUST00000194922				8.0	5.4E-06	-4.4	1.7E-04	0.9	2.5E-02	0.5	4.7E-01
ENSMUST00000136924				8.0	6.4E-05	6.5	2.2E-05	-0.6	4.4E-01	0.1	8.6E-01
ENSMUST00000129799				8.0	8.4E-05	4.1	4.3E-04	0.1	8.6E-01	-0.4	4.4E-01
ENSMUST00000148822				-0.9	2.7E-01	-0.7	5.2E-01	-0.1	8.5E-01	-0.4	7.1E-01
ENSMUST00000148824				-1.8	2.9E-01	0.3	8.7E-01	0.2	9.1E-01	-1.9	2.8E-01
ENSMUST00000136064				7.9	1.5E-05	5.5	1.9E-03	-0.4	7.7E-01	-0.4	6.3E-01
ENSMUST00000148833	lycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:10489	D6RHS8		-0.8	7.9E-01	-2.9	5.4E-01	-1.2	6.5E-01	0.9	8.5E-01
ENSMUST00000160716				7.9	5.6E-05	4.7	1.7E-03	-2.0	1.2E-01	-0.1	8.4E-01
ENSMUST00000182648				7.9	1.7E-02	2.1	2.2E-01	6.0	6.9E-04	-0.8	5.6E-01
ENSMUST00000153383				7.9	1.0E-04	7.2	9.3E-05	-0.6	6.3E-01	-0.3	6.3E-01
ENSMUST00000161765				7.9	1.2E-03	1.5	1.0E-01	-0.6	4.6E-01	0.9	2.6E-01
ENSMUST00000148846				-1.3	4.4E-01	-1.2	6.1E-01	-0.1	9.7E-01	-0.2	9.3E-01
ENSMUST00000148851	zinc finger protein 105 [Source:MGI Symbol;Acc:MGI:1277119]	D3Z140		4.0	6.3E-02	5.2	3.8E-02	-0.3	8.8E-01	-1.5	2.8E-01
ENSMUST00000126118				7.9	3.0E-05	5.8	1.1E-03	0.2	8.5E-01	0.2	8.3E-01
ENSMUST00000148861				-1.6	3.1E-01	-0.2	9.2E-01	-0.2	8.8E-01	-1.7	3.4E-01
ENSMUST00000189662				7.9	2.7E-04	6.6	3.0E-04	-0.5	7.1E-01	-0.6	3.7E-01
ENSMUST00000155561				7.9	2.8E-05	-2.1	5.5E-02	0.5	3.2E-01	-0.6	5.6E-01
ENSMUST00000184901				7.9	2.8E-05	4.9	6.7E-03	-0.5	7.7E-01	0.5	5.7E-01
ENSMUST00000148874				2.3	7.4E-02	2.9	8.6E-02	0.3	8.2E-01	-0.3	7.6E-01
ENSMUST00000146414				7.9	2.4E-05	3.4	1.1E-02	1.2	2.2E-01	1.1	1.7E-01
ENSMUST00000140480				7.9	1.4E-07	3.5	1.7E-03	-5.0	1.0E-03	0.6	3.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000148894	Luc7 homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:1914228]	D6RGP6		-1.3	1.8E-01	-3.2	9.4E-02	0.7	4.3E-01	2.5	1.5E-01
ENSMUST00000193222				7.9	7.9E-05	-4.0	1.1E-02	0.7	2.4E-01	-0.7	6.0E-01
ENSMUST00000173411				7.9	3.1E-05	7.2	1.8E-04	0.5	7.0E-01	-0.9	2.0E-01
ENSMUST00000170155				7.9	6.0E-06	6.5	1.0E-02	-0.3	9.1E-01	-1.6	2.2E-01
ENSMUST00000155590				7.9	8.3E-06	-5.5	4.5E-03	-0.1	8.6E-01	-1.6	3.6E-01
ENSMUST00000148906				-1.0	5.1E-01	2.2	1.9E-01	0.1	9.4E-01	-3.1	5.3E-02
ENSMUST00000172998				7.9	7.7E-05	6.8	3.4E-04	-1.5	2.8E-01	0.5	4.6E-01
ENSMUST00000148913				2.0	5.0E-02	1.9	9.9E-02	-0.3	7.2E-01	-0.2	8.2E-01
ENSMUST00000120042				7.9	3.6E-05	8.9	1.3E-05	-0.5	6.7E-01	0.5	3.1E-01
ENSMUST00000154313				7.9	2.4E-05	7.7	4.6E-05	-0.6	5.9E-01	0.1	8.6E-01
ENSMUST00000174107				7.9	5.3E-04	5.4	1.4E-03	-1.0	4.7E-01	0.7	3.4E-01
ENSMUST00000148933				2.2	3.2E-01	-1.8	5.5E-01	-1.5	4.6E-01	2.5	4.0E-01
ENSMUST00000148934	pantothenate kinase 4 [Source:MGI Symbol;Acc:MGI:2387466]	F7B6K4		-1.4	6.0E-01	-1.7	5.0E-01	-1.7	3.8E-01	-1.3	6.3E-01
ENSMUST00000124245				7.9	9.4E-06	3.6	3.3E-02	-1.9	2.5E-01	0.6	5.5E-01
ENSMUST00000148939	inositol polyphosphate 5-phosphatase J [Source:MGI Symbol;Acc:MGI:2158663]	V9GXL7		2.1	4.1E-01	1.2	6.8E-01	-1.1	6.8E-01	-0.2	9.2E-01
ENSMUST00000129072				7.9	3.1E-05	3.7	2.4E-03	-0.3	7.6E-01	-0.4	5.6E-01
ENSMUST00000155097				7.9	3.3E-05	-3.3	5.8E-02	0.3	7.5E-01	-1.6	3.8E-01
ENSMUST00000162591				7.9	2.7E-05	2.3	3.2E-01	-0.7	7.4E-01	4.3	3.1E-02
ENSMUST00000182294				7.9	3.6E-04	6.1	4.2E-03	-0.2	9.2E-01	-0.9	3.8E-01
ENSMUST00000122892				7.9	8.5E-06	6.0	7.7E-06	-0.3	6.0E-01	-0.3	4.8E-01
ENSMUST00000195869				7.9	1.3E-05	3.9	1.2E-02	-1.9	1.5E-01	-1.1	3.2E-01
ENSMUST00000151048				7.9	3.7E-05	-5.8	4.2E-04	-0.5	2.5E-01	-0.6	6.2E-01
ENSMUST00000124749				7.9	5.6E-04	-3.7	2.1E-03	-0.1	8.5E-01	-0.9	3.7E-01
ENSMUST00000148961				1.5	3.7E-01	-1.0	5.8E-01	-2.3	1.3E-01	0.2	9.0E-01
ENSMUST00000137809				7.9	3.4E-05	5.9	1.8E-02	-0.8	7.3E-01	-1.3	3.1E-01
ENSMUST00000148971				0.9	5.9E-01	3.3	1.1E-01	0.2	9.0E-01	-2.2	2.3E-01
ENSMUST00000148973				1.8	5.5E-01	1.5	5.9E-01	-2.2	4.2E-01	-2.0	4.7E-01
ENSMUST00000108219				7.9	4.4E-05	-4.8	4.9E-02	1.0	2.8E-01	1.0	6.5E-01
ENSMUST00000116186				7.9	9.1E-05	8.2	6.8E-04	-0.4	8.1E-01	-1.6	6.3E-02
ENSMUST00000156464				7.9	1.7E-04	4.1	5.4E-03	-0.8	4.6E-01	-1.4	1.7E-01
ENSMUST00000186586				7.9	7.2E-05	-7.4	1.6E-02	-1.7	6.9E-02	1.3	6.4E-01
ENSMUST00000117573				7.9	3.6E-05	3.8	4.7E-04	-1.7	3.3E-02	-0.1	7.9E-01
ENSMUST00000125290				7.9	1.1E-03	-4.7	1.8E-01	2.6	1.4E-01	1.9	5.4E-01
ENSMUST00000121830				7.9	2.6E-04	8.0	2.4E-04	0.5	6.9E-01	1.1	1.1E-01
ENSMUST00000149010				-2.1	1.4E-01	-1.3	4.5E-01	0.1	9.2E-01	-0.6	7.2E-01
ENSMUST00000145277				7.9	5.5E-06	6.1	1.5E-05	0.7	3.6E-01	-0.1	7.2E-01
ENSMUST00000149013				-1.9	1.8E-01	3.0	6.7E-02	1.7	2.0E-01	-3.2	4.0E-02
ENSMUST00000149016				4.1	8.6E-02	0.6	7.7E-01	-2.9	2.1E-01	0.6	7.2E-01
ENSMUST00000183974				7.9	8.0E-06	4.5	1.0E-04	-0.5	4.7E-01	-0.9	9.2E-02
ENSMUST00000143588				7.9	1.2E-05	-3.0	1.4E-01	0.9	3.9E-01	-1.4	5.1E-01
ENSMUST00000149022	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	F6RL59		-1.7	3.0E-01	-2.4	2.4E-01	-0.6	6.3E-01	0.1	9.4E-01
ENSMUST00000190870				7.9	2.5E-05	5.5	1.7E-03	-0.7	6.3E-01	-0.2	8.3E-01
ENSMUST00000149024	sorting nexin 10 [Source:MGI Symbol;Acc:MGI:1919232]	S4R1A0		-3.7	2.4E-01	-7.0	7.9E-02	-3.8	4.5E-02	-0.5	9.0E-01
ENSMUST00000117339				7.9	1.9E-04	3.3	8.3E-02	0.1	9.4E-01	0.5	6.5E-01
ENSMUST00000159227				7.9	6.5E-03	3.0	2.3E-03	-0.1	9.3E-01	-0.5	4.1E-01
ENSMUST00000079186				7.9	1.8E-05	8.9	7.4E-05	-0.8	6.0E-01	0.7	2.6E-01
ENSMUST00000149032				1.8	3.3E-01	1.1	6.3E-01	-1.1	5.3E-01	-0.3	8.7E-01
ENSMUST00000152582				7.9	1.3E-05	3.0	1.4E-02	0.5	5.9E-01	-0.3	7.3E-01
ENSMUST00000155979				7.9	1.4E-05	3.6	4.2E-03	0.4	6.8E-01	0.9	2.0E-01
ENSMUST00000143164				7.9	1.4E-04	6.4	1.0E-03	-0.6	6.9E-01	-1.1	1.8E-01
ENSMUST00000173521				7.9	1.9E-04	6.3	2.1E-04	-0.6	6.2E-01	-0.3	5.9E-01
ENSMUST00000097413				7.9	8.3E-06	7.3	1.9E-05	1.6	8.0E-02	0.0	9.5E-01
ENSMUST00000149051				1.3	1.9E-01	2.1	1.1E-01	0.1	9.6E-01	-0.7	5.1E-01
ENSMUST00000123203				7.9	6.6E-06	6.3	2.2E-04	-0.6	6.2E-01	0.1	8.6E-01
ENSMUST00000156312				7.9	1.3E-06	3.6	5.9E-03	0.8	3.7E-01	-0.1	8.9E-01
ENSMUST00000120414				7.9	5.8E-05	1.8	6.4E-03	0.7	1.0E-01	0.2	5.9E-01
ENSMUST00000161692				7.9	1.4E-05	6.1	1.5E-04	-0.9	3.9E-01	-0.9	1.8E-01
ENSMUST00000120242				7.9	1.1E-05	4.5	1.5E-03	-2.8	3.4E-02	-0.2	7.2E-01
ENSMUST00000159896				7.9	4.7E-05	-0.8	4.8E-01	1.2	1.2E-01	-0.3	7.7E-01
ENSMUST00000149079				6.1	8.6E-02	7.8	3.1E-02	-2.0	6.0E-01	-3.7	4.9E-02
ENSMUST00000163114				7.9	9.4E-05	0.2	8.2E-01	0.3	7.0E-01	-3.4	2.2E-02
ENSMUST00000129671				7.9	3.0E-04	2.8	1.1E-02	0.2	7.9E-01	-0.2	7.6E-01
ENSMUST00000149089	neurobeachin-like 2 [Source:MGI Symbol;Acc:MGI:2448554]	D3Z2K6		0.2	8.9E-01	0.9	6.0E-01	1.4	3.4E-01	0.6	6.9E-01
ENSMUST00000149091				-1.0	4.0E-01	0.7	5.7E-01	0.4	6.7E-01	-1.3	3.1E-01
ENSMUST00000148474				7.9	1.8E-04	3.8	6.8E-03	-0.4	6.8E-01	0.0	9.9E-01
ENSMUST00000172746				7.9	1.0E-06	3.7	2.8E-03	0.8	3.0E-01	0.3	6.4E-01
ENSMUST00000149106	sterol carrier protein 2, liver [Source:MGI Symbol;Acc:MGI:98254]	A2APS4		-0.9	6.4E-01	-3.6	2.2E-01	-1.9	2.4E-01	0.8	7.9E-01
ENSMUST00000149111	nuclear factor, erythroid derived 2 [Source:MGI Symbol;Acc:MGI:97308]			-0.2	7.7E-01	-0.3	6.5E-01	-0.7	2.4E-01	-0.5	5.0E-01
ENSMUST00000153660				7.9	2.5E-04	6.1	9.2E-04	-0.5	7.3E-01	-0.6	4.1E-01
ENSMUST00000174381				7.9	3.7E-05	3.7	8.6E-04	-3.1	7.9E-03	0.4	5.2E-01
ENSMUST00000136885				7.9	2.3E-02	3.0	1.2E-02	0.9	3.0E-01	0.5	4.7E-01
ENSMUST00000149122	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 [Source:MGI Symbol;Acc:MGI:1344370]			-0.9	6.4E-01	-6.2	6.1E-02	-3.6	3.1E-02	1.7	5.7E-01
ENSMUST00000185837				7.9	1.1E-07	-0.6	6.5E-01	0.4	6.6E-01	-2.4	9.6E-02
ENSMUST00000149134				-1.9	1.8E-01	-1.8	3.8E-01	0.0	1.0E+00	-0.1	9.6E-01
ENSMUST00000149143				-1.8	3.7E-01	-6.2	2.1E-02	-4.8	3.1E-03	-0.3	9.1E-01
ENSMUST00000177691				7.9	2.8E-05	-5.0	2.1E-03	0.1	8.9E-01	-0.7	6.1E-01
ENSMUST00000191300				7.9	2.4E-05	-4.3	1.1E-01	-0.1	9.2E-01	-1.1	6.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000125019				7.9	2.3E-06	8.6	5.8E-05	-0.2	8.8E-01	-0.2	7.4E-01
ENSMUST00000149147	ring finger protein 157 [Source:MGI Symbol;Acc:MGI:2442484]	F7D0T8		3.2	6.4E-02	3.6	3.9E-02	-2.2	1.7E-01	-2.6	8.3E-02
ENSMUST00000173333				7.9	5.5E-05	7.2	4.8E-05	2.3	3.0E-02	-0.4	4.8E-01
ENSMUST00000149151	Prkr interacting protein 1 (IL11 inducible) [Source:MGI Symbol;Acc:MGI:1914051]	D3YXD3		-2.3	7.5E-02	-3.8	2.6E-02	-1.5	8.7E-02	0.0	9.8E-01
ENSMUST00000145233				7.9	2.3E-03	6.1	2.9E-03	-0.7	6.7E-01	-1.2	2.0E-01
ENSMUST00000150734				7.9	2.5E-05	6.8	1.9E-04	-0.6	6.5E-01	-0.5	4.4E-01
ENSMUST00000149155				-0.9	3.3E-01	-0.5	7.1E-01	0.8	3.4E-01	0.4	7.6E-01
ENSMUST00000126344				7.9	1.1E-05	-2.0	4.8E-02	0.3	5.9E-01	-0.4	6.8E-01
ENSMUST00000149160				-0.2	7.9E-01	-3.5	3.7E-02	-0.9	2.3E-01	2.4	1.2E-01
ENSMUST00000149161				2.1	2.3E-01	6.4	3.9E-03	0.8	6.4E-01	-3.5	2.3E-02
ENSMUST00000190613				7.9	1.5E-05	5.6	1.4E-02	0.3	8.9E-01	-0.6	6.0E-01
ENSMUST00000132989				7.9	2.4E-05	7.2	4.5E-04	-0.7	6.3E-01	0.2	7.7E-01
ENSMUST00000155761				7.9	4.0E-06	6.8	4.2E-03	-1.5	4.7E-01	0.5	6.3E-01
ENSMUST00000149175				1.0	4.7E-01	-3.9	3.2E-02	-4.6	1.0E-03	0.2	8.8E-01
ENSMUST00000149178				0.2	9.1E-01	-0.2	9.4E-01	-2.6	1.6E-01	-2.2	3.5E-01
ENSMUST00000159111				7.9	1.5E-05	2.9	3.1E-01	-1.3	6.0E-01	1.9	3.4E-01
ENSMUST00000193098				7.9	8.5E-08	7.1	5.1E-03	-0.3	9.0E-01	-2.1	9.8E-02
ENSMUST00000190015				7.9	5.4E-05	2.4	9.7E-03	-0.2	8.1E-01	-0.2	7.3E-01
ENSMUST00000149194	Y box protein 2 [Source:MGI Symbol;Acc:MGI:1096372]	J3QNB9		4.6	7.4E-02	3.9	2.2E-01	0.2	9.3E-01	1.0	6.3E-01
ENSMUST00000182530				7.8	2.3E-05	6.7	9.5E-05	-1.5	2.0E-01	-0.5	4.3E-01
ENSMUST00000149204				-0.6	8.3E-01	-4.3	2.3E-01	-3.0	1.3E-01	0.7	8.5E-01
ENSMUST00000149205				-3.7	2.5E-01	1.7	7.3E-01	5.5	1.7E-01	0.0	9.9E-01
ENSMUST00000184027				7.8	2.4E-05	3.1	2.3E-02	-0.9	4.1E-01	-0.4	6.9E-01
ENSMUST00000149210				-0.5	6.9E-01	-0.7	6.8E-01	-0.5	7.0E-01	-0.2	8.8E-01
ENSMUST00000121527				7.8	1.4E-05	0.8	5.8E-01	-0.1	9.2E-01	3.3	2.0E-02
ENSMUST00000181997				7.8	1.7E-05	7.0	3.6E-05	-1.8	1.1E-01	0.3	5.4E-01
ENSMUST00000119333				7.8	1.7E-06	4.9	3.5E-03	0.9	4.5E-01	0.3	7.2E-01
ENSMUST00000149225	DENN/MADD domain containing 2D [Source:MGI Symbol;Acc:MGI:2181193]	A0A0A6YWK8		-0.8	3.5E-01	-0.7	5.1E-01	-0.1	8.6E-01	-0.3	7.8E-01
ENSMUST00000124751				7.8	4.8E-05	7.4	4.5E-05	-1.5	2.1E-01	-0.7	2.5E-01
ENSMUST00000149240				1.6	1.5E-01	-3.0	1.8E-03	-7.4	8.0E-06	-2.8	9.3E-03
ENSMUST00000187003				7.8	1.7E-05	2.1	1.1E-02	-0.3	6.5E-01	-0.6	2.8E-01
ENSMUST00000149244				-0.4	7.2E-01	-0.2	9.0E-01	0.3	8.0E-01	0.1	9.6E-01
ENSMUST00000146038				7.8	2.5E-06	2.3	2.9E-01	-3.5	1.2E-01	1.1	4.9E-01
ENSMUST00000150052				7.8	2.2E-04	3.2	9.3E-04	-1.0	1.6E-01	-0.5	3.6E-01
ENSMUST00000195624				7.8	2.6E-05	3.1	1.6E-03	-1.5	4.2E-02	-0.5	3.7E-01
ENSMUST00000141770				7.8	8.8E-05	4.1	1.4E-02	-1.5	3.3E-01	1.9	5.8E-02
ENSMUST00000149259				0.0	9.9E-01	-2.0	5.4E-01	-2.5	2.4E-01	-0.5	8.9E-01
ENSMUST00000183189				7.8	8.4E-06	-9.9	8.9E-05	0.6	2.1E-01	1.5	3.3E-01
ENSMUST00000149271				4.1	4.2E-02	6.5	1.2E-02	0.5	8.1E-01	-1.9	1.6E-01
ENSMUST00000146488				7.8	4.9E-05	7.6	8.3E-05	-0.6	6.4E-01	-0.5	3.9E-01
ENSMUST00000173356				7.8	2.3E-05	4.5	4.7E-05	-1.1	9.3E-02	-0.5	2.3E-01
ENSMUST00000194870				7.8	2.3E-05	5.6	2.1E-03	-0.1	9.5E-01	-0.4	6.2E-01
ENSMUST00000153864				7.8	3.5E-05	3.8	3.1E-03	-2.5	4.6E-02	-0.8	3.0E-01
ENSMUST00000177398				7.8	3.1E-06	5.9	5.9E-05	-1.4	1.5E-01	-0.3	5.7E-01
ENSMUST00000149293				0.2	8.6E-01	0.0	9.9E-01	-0.1	9.2E-01	0.1	9.4E-01
ENSMUST00000149301	expressed sequence AI314180 [Source:MGI Symbol;Acc:MGI:2140220]	A2ALV7		2.6	2.3E-01	1.9	5.9E-01	2.1	3.7E-01	2.7	3.9E-01
ENSMUST00000149311				1.9	8.3E-02	3.9	2.0E-02	1.0	4.5E-01	-0.9	3.4E-01
ENSMUST00000142518				7.8	3.4E-05	-2.6	1.2E-02	-0.2	7.3E-01	-1.1	2.6E-01
ENSMUST00000129725				7.8	1.4E-04	6.0	1.4E-04	0.9	3.3E-01	0.4	5.1E-01
ENSMUST00000167872				7.8	7.5E-06	3.6	6.3E-03	-4.3	6.9E-03	-2.6	1.8E-02
ENSMUST00000188006				7.8	1.9E-04	-3.1	6.5E-02	0.2	7.9E-01	0.8	5.9E-01
ENSMUST00000150170				7.8	1.5E-04	-2.8	7.6E-02	0.5	5.5E-01	-0.4	8.0E-01
ENSMUST00000142162				7.8	8.6E-06	4.9	9.1E-03	-0.6	7.2E-01	-0.3	7.4E-01
ENSMUST00000195292				7.8	2.9E-05	7.7	2.3E-05	-1.9	1.1E-01	-0.9	1.2E-01
ENSMUST00000097631				7.8	1.8E-05	4.9	1.9E-03	-0.9	4.6E-01	0.8	3.1E-01
ENSMUST00000152646				7.8	7.8E-05	-5.2	5.5E-03	1.6	1.8E-02	-0.5	7.5E-01
ENSMUST00000155416				7.8	6.9E-05	4.0	3.1E-05	0.7	1.5E-01	-0.2	6.7E-01
ENSMUST00000149368	adhesion G protein-coupled receptor E5 [Source:MGI Symbol;Acc:MGI:1347095]	S4R1V8		-1.7	1.6E-01	-0.8	5.8E-01	0.0	9.6E-01	-0.9	5.4E-01
ENSMUST00000120500				7.8	5.9E-05	1.4	3.1E-01	0.4	7.6E-01	1.5	1.8E-01
ENSMUST00000151626				7.8	1.4E-05	5.0	3.1E-04	-1.1	2.4E-01	0.3	6.4E-01
ENSMUST00000149383	mitogen-activated protein kinase associated protein 1 [Source:MGI Symbol;Acc:MGI:2444554]	A0A0A6YW60		-0.4	6.7E-01	-0.5	7.2E-01	0.4	6.8E-01	0.5	7.2E-01
ENSMUST00000130508				7.8	3.8E-05	-5.6	1.3E-03	-1.1	6.9E-02	-0.3	8.4E-01
ENSMUST00000192875				7.8	5.9E-06	6.0	1.6E-03	0.5	7.4E-01	-0.8	3.4E-01
ENSMUST00000142527				7.8	9.6E-06	-5.6	6.7E-02	0.3	8.2E-01	0.9	7.6E-01
ENSMUST00000149393				2.0	1.6E-01	1.9	2.2E-01	-0.9	4.8E-01	-0.9	5.1E-01
ENSMUST00000149394	DOT1-like, histone H3 methyltransferase (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2143886]	F6SJX8		3.1	4.7E-02	4.4	3.7E-02	0.7	7.0E-01	-0.6	6.1E-01
ENSMUST00000159667				7.8	2.0E-04	-5.8	1.4E-04	-0.5	2.2E-01	-0.7	5.1E-01
ENSMUST00000149400				-1.8	2.2E-01	-0.8	6.2E-01	0.0	1.0E+00	-1.0	5.5E-01
ENSMUST00000126161				7.8	6.6E-05	-4.0	2.3E-04	0.0	9.8E-01	-2.6	1.3E-02
ENSMUST00000149407	rhophilin, Rho GTPase binding protein 1 [Source:MGI Symbol;Acc:MGI:1098783]	Q80WU2		4.0	8.7E-02	5.4	6.5E-02	0.6	8.1E-01	-0.8	6.3E-01
ENSMUST00000188190				7.8	3.3E-04	5.6	1.3E-02	1.2	4.9E-01	0.7	6.0E-01
ENSMUST00000186196				7.8	1.7E-04	-3.3	2.2E-02	0.3	6.5E-01	-1.6	2.8E-01
ENSMUST00000133222				7.8	8.0E-05	-4.3	1.5E-02	0.8	3.2E-01	0.3	8.7E-01
ENSMUST00000149417				0.6	6.1E-01	0.2	8.8E-01	-0.1	9.5E-01	0.3	8.4E-01
ENSMUST00000148770				7.8	4.2E-05	-4.0	1.6E-02	0.1	8.8E-01	-0.6	6.9E-01
ENSMUST00000149422				-0.8	5.6E-01	-0.8	7.2E-01	1.7	3.3E-01	1.7	3.7E-01
ENSMUST00000154870				7.8	2.3E-07	2.8	8.4E-02	-0.3	8.2E-01	-0.3	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000178724				7.8	8.8E-08	4.0	4.4E-03	-1.1	2.9E-01	-1.1	1.4E-01
ENSMUST00000149431	ankyrin repeat and SOCS box-containing 2 [Source:MGI Symbol;Acc:MGI:1929743]		Q8K0L0	0.7	6.2E-01	1.4	4.6E-01	-0.1	9.3E-01	-0.8	5.6E-01
ENSMUST00000187982				7.8	1.2E-05	2.9	2.0E-01	0.2	9.1E-01	2.1	2.1E-01
ENSMUST00000186874				7.8	7.6E-05	4.3	1.2E-02	0.3	7.9E-01	0.1	9.1E-01
ENSMUST00000149441	MPN domain containing [Source:MGI Symbol;Acc:MGI:1915297]		Q3TV65	-4.1	8.8E-02	-4.0	2.1E-01	1.0	6.2E-01	0.9	7.6E-01
ENSMUST00000054470				7.8	8.3E-06	2.9	6.4E-03	0.0	9.7E-01	0.7	3.2E-01
ENSMUST00000136032				7.8	1.2E-04	-5.6	1.3E-03	1.0	5.4E-02	0.2	8.9E-01
ENSMUST00000173664				7.8	2.5E-05	6.0	1.3E-04	-0.1	9.5E-01	-0.8	2.0E-01
ENSMUST00000138659				7.8	1.7E-05	6.6	1.3E-02	0.3	9.0E-01	-1.6	2.2E-01
ENSMUST00000118407				7.8	1.2E-03	5.3	5.9E-04	-1.5	2.1E-01	-0.2	7.2E-01
ENSMUST00000185446				7.8	7.0E-05	6.0	3.0E-02	1.0	6.8E-01	2.5	1.0E-01
ENSMUST00000163054				7.8	2.7E-05	4.9	2.4E-03	0.8	5.0E-01	0.1	8.9E-01
ENSMUST00000149470				5.3	3.7E-02	6.3	4.0E-02	0.5	8.6E-01	-0.5	7.7E-01
ENSMUST00000161624				7.8	2.1E-07	-3.1	7.8E-02	1.0	2.8E-01	0.8	6.3E-01
ENSMUST00000184249				7.8	4.9E-05	2.6	3.7E-01	-0.8	7.5E-01	3.1	1.8E-01
ENSMUST00000195033				7.8	4.9E-05	-4.9	5.1E-04	0.1	8.9E-01	-0.8	4.2E-01
ENSMUST00000149486	bromodomain PHD finger transcription factor [Source:MGI Symbol;Acc:MGI:2444008]	A2A653		1.1	2.1E-01	1.7	1.7E-01	0.7	4.7E-01	0.0	9.8E-01
ENSMUST00000183025				7.8	7.4E-05	2.9	1.9E-03	0.4	4.5E-01	0.2	7.1E-01
ENSMUST00000149490				-0.7	4.3E-01	-0.3	7.5E-01	0.1	9.1E-01	-0.2	8.1E-01
ENSMUST00000098518				7.8	2.1E-05	5.9	8.6E-04	-0.6	6.7E-01	-0.1	8.8E-01
ENSMUST00000149499	Ral GTPase activating protein, alpha subunit 2 (catalytic) [Source:MGI Symbol;Acc:MGI:3036245]	F7CGP0		0.7	7.3E-01	1.7	5.2E-01	0.8	6.4E-01	-0.2	9.2E-01
ENSMUST00000149510	serine/arginine-rich splicing factor 9 [Source:MGI Symbol;Acc:MGI:104896]	F6RTE1		-4.2	7.6E-02	-1.3	6.4E-01	1.5	4.4E-01	-1.5	5.8E-01
ENSMUST00000117770				7.8	1.7E-04	5.9	5.0E-06	-0.5	3.7E-01	0.0	9.4E-01
ENSMUST00000100795				7.8	1.1E-05	2.9	2.0E-01	5.5	8.9E-03	-0.7	7.0E-01
ENSMUST00000123627				7.8	3.8E-05	5.1	5.6E-04	-1.3	1.9E-01	-0.1	9.1E-01
ENSMUST00000142118				7.8	1.5E-05	8.6	3.2E-05	0.5	6.7E-01	0.5	3.8E-01
ENSMUST00000149525	inhibitor of kappaB kinase gamma [Source:MGI Symbol;Acc:MGI:1338074]	A3KG38		-1.9	1.5E-01	-3.6	4.8E-02	-1.8	6.6E-02	-0.1	9.4E-01
ENSMUST00000149528				-2.1	5.0E-01	-4.1	3.8E-01	-1.7	4.5E-01	0.3	9.5E-01
ENSMUST00000157002				7.8	1.5E-05	-2.6	1.7E-02	-1.3	6.2E-02	-0.7	4.3E-01
ENSMUST00000149531				-0.9	6.5E-01	-1.8	3.5E-01	-2.4	1.4E-01	-1.5	4.4E-01
ENSMUST00000149537				0.9	6.0E-01	5.9	2.0E-02	2.2	2.9E-01	-2.7	8.0E-02
ENSMUST00000146329				7.8	4.0E-05	2.3	1.8E-02	-1.0	2.0E-01	-1.4	7.1E-02
ENSMUST00000182148				7.8	7.6E-06	5.5	1.0E-02	0.2	8.9E-01	0.9	3.8E-01
ENSMUST00000149553				-1.1	4.0E-01	-0.2	8.6E-01	-0.2	8.6E-01	-1.1	4.8E-01
ENSMUST00000120769				7.8	3.8E-05	6.2	3.2E-03	-0.9	5.5E-01	1.1	2.7E-01
ENSMUST00000129154				7.8	5.8E-04	6.3	2.6E-05	0.1	8.6E-01	-0.1	8.5E-01
ENSMUST00000146256				7.8	1.2E-04	-0.7	6.0E-01	0.8	3.7E-01	-3.3	5.4E-02
ENSMUST00000171467				7.8	1.3E-04	4.0	3.2E-03	0.8	4.3E-01	0.2	7.8E-01
ENSMUST00000064271				7.8	2.9E-06	-12.0	7.8E-05	-0.9	5.0E-02	-0.2	9.3E-01
ENSMUST00000040486				7.8	1.4E-04	6.4	1.9E-03	-0.8	6.4E-01	0.1	8.9E-01
ENSMUST00000124835				7.8	3.0E-04	8.4	2.6E-04	0.4	8.0E-01	0.8	2.7E-01
ENSMUST00000152800				7.8	7.7E-05	4.9	2.0E-02	-0.5	7.9E-01	-0.8	5.1E-01
ENSMUST00000149579	AT rich interactive domain 4B (RBP1-like) [Source:MGI Symbol;Acc:MGI:2137512]	F6R6U0		-1.1	9.4E-02	-0.8	3.2E-01	-0.3	5.8E-01	-0.6	4.1E-01
ENSMUST00000131726				7.8	4.2E-05	-5.5	8.5E-04	-1.7	5.5E-03	-0.3	8.4E-01
ENSMUST00000142140				7.8	6.0E-07	0.8	6.1E-01	1.9	1.6E-01	-2.8	8.6E-02
ENSMUST00000149584				2.5	2.0E-01	5.1	1.8E-02	-1.8	3.7E-01	-4.4	1.2E-02
ENSMUST00000141694				7.8	4.3E-05	1.5	1.7E-01	-0.8	3.9E-01	0.0	9.9E-01
ENSMUST00000149589	transmembrane channel-like gene family 6 [Source:MGI Symbol;Acc:MGI:1098686]	F7D254		0.6	4.9E-01	1.1	2.9E-01	-0.3	7.6E-01	-0.8	4.0E-01
ENSMUST00000140440				7.8	3.8E-05	3.5	3.0E-02	0.0	1.0E+00	0.2	8.0E-01
ENSMUST00000155666				7.8	1.8E-05	-3.0	1.6E-02	-0.4	4.7E-01	-0.7	5.5E-01
ENSMUST00000090166				7.8	8.0E-05	7.4	6.3E-05	0.1	9.0E-01	-0.4	4.4E-01
ENSMUST00000149610	triosephosphate isomerase 1 [Source:MGI Symbol;Acc:MGI:98797]	H7BXC3		-1.0	5.6E-01	-3.8	2.2E-01	-0.5	7.3E-01	2.2	4.6E-01
ENSMUST00000118044				7.8	5.3E-04	5.4	1.8E-04	-0.8	4.0E-01	-0.2	7.5E-01
ENSMUST00000189975				7.8	5.7E-05	5.4	4.3E-03	-0.5	7.5E-01	-2.3	5.0E-02
ENSMUST00000149623	X-box binding protein 1 [Source:MGI Symbol;Acc:MGI:98970]	H3BLF6		-1.2	2.0E-01	0.7	4.8E-01	-0.1	9.0E-01	-2.1	6.4E-02
ENSMUST00000135921				7.8	1.1E-04	4.8	1.0E-04	-2.9	8.5E-03	-0.3	5.3E-01
ENSMUST00000186558				7.8	1.9E-03	-4.9	3.1E-02	-0.9	3.2E-01	-0.1	9.7E-01
ENSMUST00000184944				7.8	2.3E-06	-4.3	5.7E-03	-0.7	2.3E-01	1.0	4.2E-01
ENSMUST00000149645				1.0	2.4E-01	1.8	1.1E-01	0.1	9.1E-01	-0.7	4.6E-01
ENSMUST00000186797				7.8	5.8E-05	6.5	1.7E-04	-0.6	5.9E-01	-1.0	1.3E-01
ENSMUST00000119465				7.8	5.1E-05	3.2	2.6E-03	-1.1	1.5E-01	-0.4	4.8E-01
ENSMUST00000125231				7.8	4.1E-05	5.9	7.1E-04	-0.6	6.2E-01	0.0	9.9E-01
ENSMUST00000195461				7.8	2.3E-07	6.3	3.1E-04	-1.0	4.4E-01	-0.4	5.1E-01
ENSMUST00000056900				7.7	6.7E-06	4.8	5.3E-04	0.0	1.0E+00	0.3	6.6E-01
ENSMUST00000104977				7.7	1.3E-04	5.6	2.1E-04	-0.9	3.6E-01	-0.7	2.5E-01
ENSMUST00000126917				7.7	8.8E-06	-4.4	4.8E-04	0.2	7.0E-01	-0.6	4.9E-01
ENSMUST00000186658				7.7	2.0E-06	3.7	7.0E-02	-4.0	7.1E-02	2.1	1.1E-01
ENSMUST00000144505				7.7	2.2E-05	5.7	7.2E-05	0.2	8.1E-01	0.2	6.4E-01
ENSMUST00000149675				2.4	4.0E-02	0.7	5.4E-01	-1.4	1.8E-01	0.2	8.2E-01
ENSMUST00000134067				7.7	5.2E-05	6.5	1.4E-04	0.3	7.6E-01	-0.4	4.8E-01
ENSMUST00000178056				7.7	1.6E-05	5.1	2.0E-03	-0.1	9.5E-01	0.5	5.2E-01
ENSMUST00000106680				7.7	4.2E-05	-2.3	1.4E-01	-0.1	9.4E-01	-1.8	2.8E-01
ENSMUST00000118665				7.7	6.4E-05	4.3	4.0E-04	0.0	9.6E-01	-1.0	1.3E-01
ENSMUST00000193556				7.7	2.4E-04	6.8	1.4E-04	-0.6	6.2E-01	-0.1	9.0E-01
ENSMUST00000149700	perilipin 2 [Source:MGI Symbol;Acc:MGI:87920]	B1AXR5		-1.8	1.4E-01	-4.6	3.5E-02	-1.8	5.9E-02	1.0	6.2E-01
ENSMUST00000118197				7.7	4.1E-05	7.2	2.9E-04	-0.2	8.5E-01	1.1	1.4E-01
ENSMUST00000147476				7.7	7.4E-06	5.4	7.6E-04	-0.5	6.3E-01	0.7	3.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159255				7.7	3.5E-05	3.2	3.4E-03	-2.5	1.5E-02	-0.5	4.5E-01
ENSMUST00000173446				7.7	2.2E-05	6.3	1.9E-02	-0.7	7.7E-01	-1.3	3.6E-01
ENSMUST00000136118				7.7	3.4E-04	4.3	4.7E-02	-0.4	8.3E-01	0.3	7.9E-01
ENSMUST00000137819				7.7	2.2E-05	6.1	2.6E-04	-0.9	4.3E-01	-0.7	3.0E-01
ENSMUST00000184743				7.7	2.1E-05	-4.1	7.2E-02	-0.2	8.4E-01	0.1	9.7E-01
ENSMUST00000097346				7.7	3.1E-05	2.8	8.3E-03	0.6	4.4E-01	0.2	7.3E-01
ENSMUST00000152497				7.7	1.8E-05	5.1	4.0E-02	-0.8	7.3E-01	1.2	4.0E-01
ENSMUST00000149729				-3.1	2.5E-01	-3.0	2.4E-01	-1.8	2.7E-01	-1.9	5.2E-01
ENSMUST00000159240				7.7	4.8E-04	4.0	4.8E-03	-0.6	5.7E-01	0.1	9.0E-01
ENSMUST00000149734				-0.6	6.3E-01	-1.3	4.4E-01	-0.1	9.3E-01	0.6	6.9E-01
ENSMUST00000178280				7.7	7.9E-07	4.8	2.3E-04	-0.7	4.1E-01	0.5	3.3E-01
ENSMUST00000117685				7.7	3.4E-04	7.3	6.0E-05	-0.5	6.4E-01	-1.3	4.7E-02
ENSMUST00000149745	ras responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:2443664]		Q3UH06	1.7	1.4E-01	1.5	4.0E-01	2.2	9.1E-02	2.4	1.4E-01
ENSMUST00000142040				7.7	1.7E-05	2.3	1.2E-02	-1.4	5.9E-02	0.5	4.6E-01
ENSMUST00000160982				7.7	4.4E-06	5.4	4.0E-02	-0.8	7.5E-01	-0.9	5.4E-01
ENSMUST00000149750				-2.2	7.8E-02	0.7	6.2E-01	1.7	1.1E-01	-1.2	4.0E-01
ENSMUST00000128917				7.7	2.9E-06	-4.4	1.2E-02	-0.3	7.0E-01	1.4	3.3E-01
ENSMUST00000149203				7.7	2.5E-05	4.5	2.4E-05	-0.4	4.7E-01	0.3	3.8E-01
ENSMUST00000148586				7.7	3.6E-05	7.0	6.2E-04	-0.1	9.7E-01	0.5	5.4E-01
ENSMUST00000149764				-0.4	7.4E-01	-0.3	8.5E-01	0.9	4.8E-01	0.8	6.3E-01
ENSMUST00000192281				7.7	1.7E-06	-3.7	4.8E-02	0.6	4.6E-01	-0.8	6.7E-01
ENSMUST00000120917				7.7	5.2E-05	4.5	3.2E-04	-0.2	8.3E-01	-0.2	6.6E-01
ENSMUST00000149778	abhydrolase domain containing 11 [Source:MGI Symbol;Acc:MGI:1916008]			-1.1	3.9E-01	-2.3	1.9E-01	-1.2	2.7E-01	0.0	9.9E-01
ENSMUST00000148557				7.7	1.8E-04	2.2	2.0E-01	-0.7	6.6E-01	0.9	4.6E-01
ENSMUST00000133888				7.7	9.1E-05	2.8	7.4E-03	-0.8	3.0E-01	-0.5	4.6E-01
ENSMUST00000120719				7.7	8.0E-05	6.3	8.6E-04	-0.6	6.6E-01	-0.3	6.6E-01
ENSMUST00000159058				7.7	7.9E-06	4.2	4.4E-04	-0.6	4.3E-01	-0.8	2.1E-01
ENSMUST00000191664				7.7	2.5E-04	6.9	4.0E-04	0.2	8.7E-01	0.4	5.7E-01
ENSMUST00000120160				7.7	9.5E-05	-3.3	1.5E-03	-0.3	4.9E-01	-1.5	8.4E-02
ENSMUST00000146453				7.7	4.0E-06	6.1	4.2E-04	-1.6	2.1E-01	1.2	1.1E-01
ENSMUST00000177223				7.7	1.3E-04	7.6	7.3E-05	-1.4	2.7E-01	1.1	8.2E-02
ENSMUST00000189779				7.7	1.9E-04	3.3	5.3E-04	-0.1	8.3E-01	-0.1	8.0E-01
ENSMUST00000159354				7.7	1.6E-05	7.8	1.7E-04	-0.6	6.6E-01	0.9	2.0E-01
ENSMUST00000190922				7.7	2.7E-04	-4.2	1.0E-02	1.3	8.9E-02	-2.0	2.2E-01
ENSMUST00000149816				-4.2	9.0E-02	-0.6	8.4E-01	3.1	2.3E-01	-0.4	8.8E-01
ENSMUST00000149272				7.7	4.1E-05	5.6	7.0E-04	0.1	9.4E-01	-0.6	3.7E-01
ENSMUST00000149827				1.9	1.1E-01	1.5	2.6E-01	-0.5	6.3E-01	-0.1	9.3E-01
ENSMUST00000152668				7.7	6.0E-06	-2.8	8.0E-02	0.8	3.0E-01	-1.4	4.1E-01
ENSMUST00000156600				7.7	1.0E-04	-5.1	1.5E-03	0.3	5.2E-01	-0.8	5.2E-01
ENSMUST00000187145				7.7	8.1E-05	4.5	6.3E-04	-0.5	5.5E-01	0.1	8.4E-01
ENSMUST00000149847				1.7	8.8E-02	1.8	1.5E-01	0.2	8.4E-01	0.1	9.3E-01
ENSMUST00000149850				-0.1	9.6E-01	6.7	3.0E-02	3.7	1.7E-01	-3.1	1.2E-01
ENSMUST00000191106				7.7	2.8E-05	8.0	5.8E-05	-0.5	7.0E-01	0.5	3.9E-01
ENSMUST00000120451				7.7	8.9E-05	-2.9	2.8E-01	3.5	3.6E-02	1.6	5.3E-01
ENSMUST00000131882				7.7	1.5E-05	7.3	3.2E-05	-2.4	5.9E-02	-0.3	6.2E-01
ENSMUST00000138827				7.7	2.9E-06	-4.6	1.7E-02	1.2	1.2E-01	-0.5	7.8E-01
ENSMUST00000146552				7.7	1.4E-02	3.0	8.8E-02	0.2	8.9E-01	0.2	8.3E-01
ENSMUST00000146613				7.7	1.6E-04	-2.7	7.9E-02	0.2	8.3E-01	-0.1	9.5E-01
ENSMUST00000149871				0.3	8.9E-01	4.0	1.5E-01	0.1	9.6E-01	-3.6	1.8E-01
ENSMUST00000149874				-1.5	1.2E-01	-1.8	1.2E-01	-1.0	1.8E-01	-0.8	5.0E-01
ENSMUST00000123112				7.7	5.5E-04	-2.9	5.1E-02	-2.1	2.9E-02	-2.7	1.2E-01
ENSMUST00000149884	SNAP-associated protein [Source:MGI Symbol;Acc:MGI:1333745]		Q9Z266	-2.5	3.0E-01	-1.7	3.6E-01	-2.4	1.2E-01	-3.3	1.8E-01
ENSMUST00000144206				7.7	3.9E-05	3.0	1.1E-02	0.1	9.1E-01	0.5	5.1E-01
ENSMUST00000190330				7.7	2.0E-05	6.5	1.1E-04	-0.5	6.2E-01	-0.5	4.3E-01
ENSMUST00000172574				7.7	1.0E-03	-5.5	1.5E-03	1.1	4.4E-02	0.1	9.6E-01
ENSMUST00000093603				7.7	5.4E-06	4.7	1.6E-03	-0.2	8.5E-01	0.8	2.8E-01
ENSMUST00000149899				5.2	4.2E-02	1.5	4.4E-01	-4.4	6.5E-02	-0.7	6.9E-01
ENSMUST00000149903	coiled-coil domain containing 180 [Source:MGI Symbol;Acc:MGI:2685871]	F6QNN0		0.6	6.3E-01	1.9	2.1E-01	-0.6	6.4E-01	-1.9	1.6E-01
ENSMUST00000190792				7.7	1.0E-05	3.7	7.5E-03	-1.2	2.9E-01	-0.6	4.6E-01
ENSMUST00000187287				7.7	1.4E-04	2.5	2.5E-03	-0.1	9.2E-01	-0.4	3.8E-01
ENSMUST00000153759				7.7	6.6E-05	13.1	6.9E-05	1.3	5.3E-01	0.8	2.3E-01
ENSMUST00000119110				7.7	1.9E-03	5.1	1.7E-02	0.2	9.1E-01	-0.8	4.8E-01
ENSMUST00000149918	docking protein 1 [Source:MGI Symbol;Acc:MGI:893587]			0.9	6.0E-01	2.3	3.5E-01	0.6	7.7E-01	-0.8	6.6E-01
ENSMUST00000141587				7.7	5.3E-04	5.5	7.5E-04	-0.5	6.6E-01	0.0	9.9E-01
ENSMUST00000151105				7.7	2.9E-04	-9.3	4.4E-05	0.8	2.7E-02	-0.6	6.7E-01
ENSMUST00000155715				7.7	2.3E-05	5.0	3.7E-03	1.5	2.5E-01	-0.4	5.6E-01
ENSMUST00000149936				-0.8	4.0E-01	-0.7	5.6E-01	0.1	8.6E-01	0.0	9.7E-01
ENSMUST00000117255				7.7	6.8E-05	5.9	8.0E-04	-0.6	6.5E-01	-0.1	8.5E-01
ENSMUST00000117739				7.7	5.6E-04	-9.0	8.1E-05	1.5	7.0E-03	1.4	3.1E-01
ENSMUST00000146484				7.7	4.4E-05	6.5	1.8E-04	-1.0	4.1E-01	-0.3	6.3E-01
ENSMUST00000139096				7.7	1.2E-06	8.6	5.1E-05	-0.6	6.6E-01	0.1	8.9E-01
ENSMUST00000149969				2.3	1.6E-01	-1.7	4.9E-01	-1.5	3.1E-01	2.5	3.0E-01
ENSMUST00000149971				0.3	7.8E-01	-0.8	5.5E-01	-0.7	4.8E-01	0.4	7.5E-01
ENSMUST00000194196				7.7	9.7E-07	-5.1	9.6E-02	1.1	3.0E-01	2.0	4.8E-01
ENSMUST00000151700				7.7	3.6E-05	8.4	9.7E-05	0.1	9.4E-01	0.6	3.4E-01
ENSMUST00000139148				7.7	5.1E-04	6.7	1.2E-04	-0.2	8.4E-01	0.1	8.0E-01
ENSMUST00000178809				7.7	2.2E-05	-5.3	9.7E-04	1.9	1.5E-03	0.2	9.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000149985				1.4	9.4E-02	0.8	4.4E-01	0.2	8.4E-01	0.7	4.5E-01
ENSMUST00000094228				7.7	1.3E-05	7.4	1.1E-04	-0.6	6.3E-01	-0.4	5.1E-01
ENSMUST00000149989				-4.7	3.8E-02	0.4	8.9E-01	3.7	8.8E-02	-1.5	5.8E-01
ENSMUST00000156089				7.7	1.7E-05	5.4	3.2E-04	-2.3	6.1E-02	-0.3	6.7E-01
ENSMUST00000149992	CCR4-NOT transcription complex, subunit 7 [Source:MGI Symbol;Acc:MGI:1298230]	Q543X5	Q60809	-0.1	8.9E-01	-0.7	2.6E-01	0.2	7.3E-01	0.8	1.8E-01
ENSMUST00000177272				7.7	1.2E-04	8.2	1.3E-04	-1.0	5.1E-01	0.4	5.6E-01
ENSMUST00000139950				7.7	2.5E-04	-1.0	3.2E-01	0.8	2.5E-01	-2.2	8.3E-02
ENSMUST00000150006	cell division cycle associated 2 [Source:MGI Symbol;Acc:MGI:1919787]		Q14B71	0.3	7.9E-01	-0.5	7.6E-01	0.2	9.0E-01	1.0	5.1E-01
ENSMUST00000141422				7.7	2.3E-05	5.6	1.4E-03	0.0	9.8E-01	-0.6	4.3E-01
ENSMUST00000150010				1.1	4.3E-01	2.4	2.1E-01	0.3	8.3E-01	-0.9	5.1E-01
ENSMUST00000101463				7.7	3.7E-06	8.7	7.4E-06	0.1	9.0E-01	0.0	9.8E-01
ENSMUST00000140623				7.7	3.9E-05	-3.6	2.3E-01	1.7	2.7E-01	-0.6	8.4E-01
ENSMUST00000162835				7.7	2.3E-05	-5.9	1.9E-02	0.7	4.4E-01	-0.4	8.5E-01
ENSMUST00000145930				7.6	1.3E-05	1.4	1.8E-01	-1.5	1.1E-01	0.4	6.0E-01
ENSMUST00000150028				-2.7	4.2E-02	-0.1	9.3E-01	1.6	1.7E-01	-1.1	4.6E-01
ENSMUST00000147256				7.6	1.7E-05	-2.7	3.2E-01	1.7	3.1E-01	-0.8	7.7E-01
ENSMUST00000117287				7.6	3.1E-04	5.4	9.7E-04	-0.9	4.5E-01	0.2	7.8E-01
ENSMUST00000153677				7.6	1.8E-05	5.5	1.2E-03	0.2	8.8E-01	-0.3	6.5E-01
ENSMUST00000191464				7.6	7.6E-05	5.6	3.0E-04	-2.0	1.1E-01	-0.3	6.4E-01
ENSMUST00000189254				7.6	8.7E-05	5.9	4.4E-04	-0.5	6.6E-01	-0.5	4.7E-01
ENSMUST00000184686				7.6	3.4E-05	1.9	6.1E-02	-0.6	4.4E-01	0.4	5.9E-01
ENSMUST00000125048				7.6	4.0E-04	5.8	5.7E-05	-1.0	2.7E-01	0.0	9.5E-01
ENSMUST00000125976				7.6	2.4E-05	-7.6	1.3E-03	-0.7	3.0E-01	-0.8	6.7E-01
ENSMUST00000182474				7.6	3.0E-05	3.9	4.4E-04	0.9	2.0E-01	-0.5	4.2E-01
ENSMUST00000110261				7.6	1.3E-03	0.6	7.6E-01	5.5	1.6E-03	-2.0	3.2E-01
ENSMUST00000191264				7.6	5.3E-04	8.4	1.5E-02	-0.9	7.7E-01	-2.1	2.2E-01
ENSMUST00000107994				7.6	8.8E-05	5.0	3.8E-04	-0.4	6.8E-01	-1.0	1.6E-01
ENSMUST00000145496				7.6	3.8E-05	6.1	5.0E-03	-0.4	8.2E-01	1.4	1.7E-01
ENSMUST00000191390				7.6	2.0E-04	5.2	3.0E-03	-0.5	7.4E-01	0.0	1.0E+00
ENSMUST00000147808				7.6	3.1E-05	4.0	1.8E-02	-1.4	3.7E-01	0.0	9.8E-01
ENSMUST00000183623				7.6	2.1E-05	-1.9	9.0E-02	1.0	1.6E-01	0.4	6.8E-01
ENSMUST00000194050				7.6	1.0E-04	4.3	1.5E-02	-0.9	5.4E-01	0.3	7.5E-01
ENSMUST00000161956				7.6	6.7E-05	-1.1	3.7E-01	0.7	3.2E-01	-0.5	6.6E-01
ENSMUST00000192483				7.6	2.4E-05	7.2	1.7E-03	-0.4	8.2E-01	0.7	3.8E-01
ENSMUST00000144538				7.6	7.1E-06	-0.5	7.3E-01	1.5	1.6E-01	-1.1	4.2E-01
ENSMUST00000154893				7.6	1.0E-05	5.3	2.4E-02	-0.5	8.1E-01	-1.2	3.7E-01
ENSMUST00000150090				2.1	6.2E-02	1.3	3.3E-01	0.2	8.5E-01	1.0	3.8E-01
ENSMUST00000168699				7.6	1.0E-05	3.6	2.1E-02	-2.3	1.2E-01	0.0	9.9E-01
ENSMUST00000149988				7.6	2.1E-05	-1.9	3.1E-01	1.2	3.3E-01	-0.1	9.5E-01
ENSMUST00000150096	protein tyrosine phosphatase, receptor type, F [Source:MGI Symbol;Acc:MGI:102695]	F6Y3V0		3.5	1.8E-01	5.2	6.6E-02	-0.5	8.5E-01	-2.3	2.2E-01
ENSMUST00000150101				0.2	8.5E-01	1.1	4.5E-01	0.9	4.2E-01	0.0	9.8E-01
ENSMUST00000148113				7.6	3.6E-05	2.9	3.8E-03	-0.1	8.6E-01	0.4	4.7E-01
ENSMUST00000177264				7.6	9.4E-06	5.4	2.5E-03	-0.5	7.1E-01	-0.1	8.6E-01
ENSMUST00000182351				7.6	9.6E-05	5.4	6.2E-03	-1.4	3.9E-01	-0.9	3.5E-01
ENSMUST00000130879				7.6	1.7E-04	-3.7	5.1E-02	-0.2	8.4E-01	-1.3	5.2E-01
ENSMUST00000150122				2.1	8.4E-02	3.2	6.3E-02	0.0	9.8E-01	-1.0	3.7E-01
ENSMUST00000130136				7.6	1.0E-04	5.0	9.2E-03	-0.6	6.9E-01	0.5	6.2E-01
ENSMUST00000152330				7.6	4.9E-05	5.5	5.3E-05	-0.1	8.9E-01	-0.3	4.9E-01
ENSMUST00000146359				7.6	2.9E-05	5.2	2.3E-02	-0.5	7.9E-01	1.7	1.8E-01
ENSMUST00000165401				7.6	2.0E-04	5.6	5.4E-03	0.0	1.0E+00	-0.8	4.7E-01
ENSMUST00000153518				7.6	2.1E-04	3.5	8.2E-03	-2.0	1.0E-01	0.6	4.3E-01
ENSMUST00000145107				7.6	1.6E-05	-4.0	1.2E-03	0.9	6.1E-02	-1.1	2.9E-01
ENSMUST00000150137				-2.7	3.5E-01	-7.9	2.8E-02	-6.0	9.3E-03	-0.7	8.4E-01
ENSMUST00000140915				7.6	1.5E-05	6.2	1.7E-04	-0.6	6.0E-01	-1.4	4.5E-02
ENSMUST00000119880				7.6	3.0E-06	4.7	1.0E-04	-0.2	7.5E-01	0.0	9.9E-01
ENSMUST00000148050				7.6	4.4E-06	-5.4	7.9E-03	0.0	9.8E-01	-0.9	6.4E-01
ENSMUST00000185734				7.6	1.0E-07	7.4	1.5E-04	0.1	9.1E-01	0.5	4.1E-01
ENSMUST00000173577				7.6	2.3E-03	-3.6	8.3E-02	2.9	9.1E-03	-1.1	6.1E-01
ENSMUST00000150552				7.6	1.4E-05	4.8	2.0E-04	0.4	6.3E-01	-0.2	7.0E-01
ENSMUST00000151691				7.6	1.7E-03	-3.1	1.9E-02	0.3	6.4E-01	0.7	5.5E-01
ENSMUST00000150165				-0.8	3.1E-01	-4.7	5.2E-03	-1.5	3.6E-02	2.4	8.7E-02
ENSMUST00000182242				7.6	6.0E-06	3.8	1.1E-01	-1.8	4.6E-01	-0.2	9.0E-01
ENSMUST00000193798				7.6	5.5E-05	8.5	2.0E-04	-0.2	9.0E-01	-0.9	2.1E-01
ENSMUST00000185373				7.6	4.4E-05	6.2	5.9E-04	0.5	6.6E-01	0.8	3.2E-01
ENSMUST00000150174				-1.7	5.7E-02	-1.6	1.0E-01	-1.2	9.5E-02	-1.3	1.9E-01
ENSMUST00000150182	paternally expressed 3 [Source:MGI Symbol;Acc:MGI:104748]	D6RGA4		2.6	1.9E-01	2.6	2.0E-01	-0.5	8.0E-01	-0.4	7.8E-01
ENSMUST00000190353				7.6	4.9E-05	6.2	1.5E-03	0.1	9.4E-01	-0.4	6.0E-01
ENSMUST00000160647				7.6	1.9E-05	5.0	2.5E-02	-0.8	6.8E-01	1.1	3.7E-01
ENSMUST00000150188	glutamate-rich WD repeat containing 1 [Source:MGI Symbol;Acc:MGI:2141989]	F7CPC6		3.1	1.8E-01	1.1	5.6E-01	-3.3	1.3E-01	-1.3	4.7E-01
ENSMUST00000141978				7.6	7.3E-05	-2.9	1.9E-02	1.0	6.8E-02	-0.5	6.4E-01
ENSMUST00000147797				7.6	5.7E-05	4.7	9.1E-04	0.4	6.9E-01	0.6	3.3E-01
ENSMUST00000150208				-0.3	8.3E-01	0.2	9.1E-01	0.5	7.4E-01	0.0	9.8E-01
ENSMUST00000150213				-0.6	8.4E-01	-2.2	5.6E-01	-1.8	4.7E-01	-0.3	9.4E-01
ENSMUST00000151530				7.6	1.7E-05	-3.6	5.1E-03	-0.1	8.1E-01	-1.7	1.6E-01
ENSMUST00000161303				7.6	6.5E-05	5.8	3.2E-04	-0.2	8.2E-01	0.2	8.0E-01
ENSMUST00000154816				7.6	1.2E-04	5.6	1.4E-04	-3.0	1.6E-02	0.2	6.8E-01
ENSMUST00000130542				7.6	7.2E-05	7.0	2.8E-04	-0.7	6.0E-01	0.4	6.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000150225				1.4	9.3E-02	2.2	3.5E-02	0.4	5.6E-01	-0.4	5.9E-01
ENSMUST00000152904				7.6	3.0E-05	5.8	1.8E-04	-1.9	8.9E-02	-0.2	7.2E-01
ENSMUST00000118322				7.6	2.2E-05	5.6	1.7E-04	0.5	5.6E-01	-0.1	8.1E-01
ENSMUST00000150232	mitochondrial carrier homolog 2 (C. elegans) [Source:MGI Symbol;Acc:MGI:1929260]	Q9D050		-0.1	9.9E-01	-4.7	6.6E-02	-6.8	4.2E-03	-2.1	4.8E-01
ENSMUST00000150234				3.3	3.6E-02	5.7	2.7E-03	-0.4	7.8E-01	-2.9	1.4E-02
ENSMUST00000125141				7.6	3.6E-04	6.8	1.9E-04	-0.5	7.0E-01	-1.4	5.1E-02
ENSMUST00000185709				7.6	1.3E-07	3.4	8.2E-04	-1.0	1.5E-01	0.1	7.8E-01
ENSMUST00000148247				7.6	2.5E-05	-3.5	4.0E-03	-1.9	8.8E-03	-1.0	3.3E-01
ENSMUST00000191179				7.6	3.9E-05	4.1	1.3E-02	-1.2	3.8E-01	-0.2	8.3E-01
ENSMUST00000150258	sphingosine phosphate lyase 1 [Source:MGI Symbol;Acc:MGI:1261415]	D6REF7		3.4	2.2E-01	1.4	7.0E-01	-1.7	6.0E-01	0.3	9.0E-01
ENSMUST00000194458				7.6	3.0E-08	5.7	8.8E-04	-0.2	8.4E-01	0.8	2.7E-01
ENSMUST00000164783				7.6	5.6E-05	7.0	1.9E-05	-1.9	7.4E-02	0.1	8.3E-01
ENSMUST00000150267	N-ethylmaleimide sensitive fusion protein attachment protein gamma [Source:MGI Symbol;Acc:MGI:104561]	D3Z4B2		-2.0	1.7E-01	-4.1	3.6E-02	-2.3	3.2E-02	-0.1	9.6E-01
ENSMUST00000160058				7.6	1.0E-06	-5.3	6.4E-03	-0.7	3.0E-01	-0.5	7.7E-01
ENSMUST00000160737				7.6	5.3E-05	0.9	2.7E-01	-1.2	8.3E-02	-0.3	6.7E-01
ENSMUST00000175780				7.6	2.4E-05	2.4	1.8E-02	-0.5	4.7E-01	-0.1	8.9E-01
ENSMUST00000125460				7.6	6.5E-05	5.5	8.8E-04	-1.2	3.3E-01	-0.6	4.1E-01
ENSMUST00000126306				7.6	2.3E-04	3.9	1.5E-01	0.2	9.1E-01	1.9	2.7E-01
ENSMUST00000150288				3.7	4.0E-02	3.4	7.6E-02	-0.9	5.7E-01	-0.7	6.2E-01
ENSMUST00000146141				7.6	9.2E-06	-11.7	9.8E-05	0.6	1.2E-01	1.1	5.7E-01
ENSMUST00000154940				7.6	4.0E-05	5.0	8.2E-03	0.2	9.1E-01	0.5	5.8E-01
ENSMUST00000155558				7.6	4.8E-05	7.1	3.0E-04	-0.5	7.0E-01	-0.7	3.1E-01
ENSMUST00000181063				7.6	5.3E-07	7.2	3.7E-04	-0.6	6.7E-01	-1.6	6.0E-02
ENSMUST00000131744				7.6	2.1E-04	5.0	1.6E-02	-1.0	5.5E-01	-0.2	8.8E-01
ENSMUST00000150310				1.0	1.1E-01	1.7	4.1E-02	0.1	8.4E-01	-0.6	3.6E-01
ENSMUST00000131894				7.6	3.2E-05	-2.2	5.9E-02	1.0	1.0E-01	-1.1	3.4E-01
ENSMUST00000150320				0.3	6.7E-01	1.6	9.8E-02	0.4	6.0E-01	-0.9	2.7E-01
ENSMUST00000137513				7.6	1.7E-04	4.2	5.1E-02	0.3	8.6E-01	-0.3	8.4E-01
ENSMUST00000150324	hydroxyacylglutathione hydrolase-like [Source:MGI Symbol;Acc:MGI:1919877]		Q9DB32	0.1	9.5E-01	3.0	3.6E-01	2.5	2.7E-01	-0.3	9.3E-01
ENSMUST00000141521				7.6	2.9E-05	4.2	7.7E-04	0.2	7.8E-01	-0.1	8.4E-01
ENSMUST00000150328				-1.1	3.7E-01	-0.9	6.6E-01	1.2	3.8E-01	1.0	5.9E-01
ENSMUST00000150330				-2.6	2.6E-01	1.4	6.8E-01	3.8	1.6E-01	-0.2	9.4E-01
ENSMUST00000119460				7.6	3.2E-05	6.3	4.2E-05	-0.1	9.4E-01	-0.1	8.0E-01
ENSMUST00000134834				7.6	9.7E-07	3.4	2.9E-02	1.1	3.5E-01	0.4	6.3E-01
ENSMUST00000144605				7.6	4.1E-04	4.5	3.2E-03	-0.6	6.1E-01	1.6	4.7E-02
ENSMUST00000192458				7.6	2.0E-06	-5.1	9.8E-04	0.1	8.3E-01	0.5	6.5E-01
ENSMUST00000150352	ankyrin repeat, family A (RFXANK-like), 2 [Source:MGI Symbol;Acc:MGI:1915808]	Q6AXE4		2.5	1.1E-01	2.0	2.3E-01	-1.6	3.0E-01	-1.1	4.2E-01
ENSMUST00000174730				7.6	6.6E-05	4.2	2.9E-02	-2.8	1.5E-01	0.5	6.5E-01
ENSMUST00000187766				7.6	1.9E-04	6.1	8.4E-04	0.8	5.3E-01	-0.7	4.1E-01
ENSMUST00000186676				7.6	5.6E-05	6.5	6.3E-04	-0.1	9.5E-01	0.0	9.7E-01
ENSMUST00000136569				7.6	4.9E-05	5.1	3.3E-03	-0.1	9.1E-01	-0.7	3.6E-01
ENSMUST00000150368				0.1	9.8E-01	-3.1	2.6E-01	-3.7	5.5E-02	-0.5	8.6E-01
ENSMUST00000150369				-0.1	9.5E-01	1.6	4.5E-01	0.9	6.4E-01	-0.9	6.3E-01
ENSMUST00000149757				7.6	1.3E-04	-2.5	1.9E-02	0.2	7.0E-01	-1.3	2.1E-01
ENSMUST00000150371	apoptotic chromatin condensation inducer 1 [Source:MGI Symbol;Acc:MGI:1891824]	B8JJ91		2.8	2.7E-01	2.7	2.5E-01	-3.9	1.2E-01	-3.8	9.0E-02
ENSMUST00000194405				7.6	1.7E-05	4.6	3.3E-03	-1.5	2.7E-01	-0.2	7.4E-01
ENSMUST00000194729				7.6	1.7E-04	5.8	8.0E-04	-0.6	6.3E-01	-0.1	8.6E-01
ENSMUST00000150387	FK506 binding protein 4 [Source:MGI Symbol;Acc:MGI:95543]	F6S2D5		-1.6	1.9E-01	2.0	1.8E-01	2.1	1.1E-01	-1.6	2.3E-01
ENSMUST00000150390				0.1	9.2E-01	0.3	6.6E-01	-0.2	6.7E-01	-0.5	4.9E-01
ENSMUST00000134123				7.5	7.2E-06	7.2	3.3E-04	0.6	6.5E-01	-0.7	2.8E-01
ENSMUST00000150395	Bardet-Biedl syndrome 9 (human) [Source:MGI Symbol;Acc:MGI:2442833]		Q811G0	-3.8	2.2E-01	2.1	6.4E-01	5.0	1.7E-01	-0.9	8.1E-01
ENSMUST00000150396	intraflagellar transport 52 [Source:MGI Symbol;Acc:MGI:2387217]	F6RBL8		-0.8	4.5E-01	-2.1	1.7E-01	-0.2	8.2E-01	1.0	4.6E-01
ENSMUST00000150399	protein phosphatase 1, regulatory (inhibitor) subunit 16A [Source:MGI Symbol;Acc:MGI:1920312]	Q8CFW6		-1.3	2.7E-01	-2.5	1.7E-01	0.2	8.0E-01	1.5	3.9E-01
ENSMUST00000121478				7.5	1.8E-02	6.3	9.5E-05	0.3	7.6E-01	0.6	2.6E-01
ENSMUST00000133309				7.5	1.4E-05	3.7	8.4E-04	-0.3	6.9E-01	-0.1	8.0E-01
ENSMUST00000150792				7.5	4.2E-05	4.4	1.6E-03	0.1	8.9E-01	0.1	9.4E-01
ENSMUST00000194587				7.5	5.0E-06	4.4	3.7E-03	-4.5	7.9E-03	-2.4	1.4E-02
ENSMUST00000121552				7.5	8.3E-07	6.5	1.0E-02	2.1	2.9E-01	-0.5	6.5E-01
ENSMUST00000126657				7.5	2.1E-05	-5.1	5.6E-03	0.8	1.6E-01	0.3	8.6E-01
ENSMUST00000150419				-2.1	7.4E-02	-2.7	9.2E-02	0.0	9.7E-01	0.6	6.7E-01
ENSMUST00000162926				7.5	2.4E-04	5.5	2.3E-02	-0.6	7.8E-01	1.0	4.2E-01
ENSMUST00000118399				7.5	4.7E-06	-5.0	6.0E-03	0.9	1.4E-01	-0.8	6.1E-01
ENSMUST00000151255				7.5	2.3E-05	7.5	9.7E-05	-0.5	6.7E-01	-0.6	3.0E-01
ENSMUST00000150431				1.4	1.0E-01	1.7	9.2E-02	0.1	9.3E-01	-0.3	7.4E-01
ENSMUST00000147063				7.5	4.7E-04	-0.9	4.2E-01	0.1	9.0E-01	-1.7	1.8E-01
ENSMUST00000171630				7.5	2.3E-06	-1.9	1.0E-01	0.0	9.6E-01	-0.3	7.7E-01
ENSMUST00000150444				-1.0	4.2E-01	0.0	9.8E-01	1.4	3.0E-01	0.4	7.9E-01
ENSMUST00000194840				7.5	2.7E-05	4.5	1.8E-02	-0.7	6.6E-01	1.6	1.5E-01
ENSMUST00000144044				7.5	1.1E-04	5.2	9.1E-03	-1.4	3.8E-01	-0.3	8.0E-01
ENSMUST00000134544				7.5	2.9E-07	3.9	3.2E-04	-0.9	2.0E-01	0.1	8.8E-01
ENSMUST00000150456	myosin, light chain 12A, regulatory, non-sarcomeric [Source:MGI Symbol;Acc:MGI:1914518]	D3YV37		-2.0	2.0E-01	0.8	6.3E-01	0.0	9.7E-01	-2.7	9.6E-02
ENSMUST00000188017				7.5	2.0E-05	5.4	5.1E-04	-0.6	6.2E-01	0.8	2.3E-01
ENSMUST00000140188				7.5	8.8E-04	3.7	1.0E-03	-2.2	3.4E-02	-0.7	2.6E-01
ENSMUST00000160210				7.5	2.6E-05	5.7	1.4E-03	0.4	7.5E-01	-0.3	6.5E-01
ENSMUST00000150479	translocase of inner mitochondrial membrane 10B [Source:MGI Symbol;Acc:MGI:1315196]	D6RJ48		-2.4	7.7E-02	-3.8	5.9E-02	-0.4	6.7E-01	1.0	5.8E-01
ENSMUST00000156274				7.5	6.6E-05	4.6	6.4E-04	-0.8	3.7E-01	-0.1	8.4E-01
ENSMUST00000185133				7.5	6.6E-05	8.6	3.1E-04	-1.4	4.4E-01	0.8	2.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000189884				7.5	9.0E-04	4.0	1.2E-02	-3.3	4.7E-02	-0.7	4.1E-01
ENSMUST00000123192				7.5	1.4E-05	5.8	5.0E-03	-0.7	6.9E-01	0.1	9.1E-01
ENSMUST00000150497				-1.6	1.3E-01	-1.1	2.9E-01	-1.1	2.0E-01	-1.5	1.8E-01
ENSMUST00000148836				7.5	3.4E-05	3.1	1.0E-02	-4.1	8.2E-03	0.2	8.3E-01
ENSMUST00000150499				1.2	5.4E-01	-0.6	8.0E-01	-1.6	3.8E-01	0.1	9.5E-01
ENSMUST00000144245				7.5	4.0E-05	3.2	1.7E-01	-1.0	6.5E-01	1.8	3.1E-01
ENSMUST00000195104				7.5	5.5E-05	5.1	6.4E-03	-0.4	7.8E-01	-0.6	4.7E-01
ENSMUST00000118418				7.5	7.4E-05	4.6	9.1E-03	-0.3	8.1E-01	0.3	7.5E-01
ENSMUST00000150508	CD82 antigen [Source:MGI Symbol;Acc:MGI:104651]	A2AIJ2		-1.7	1.1E-01	-1.0	4.3E-01	-0.1	8.8E-01	-0.9	4.5E-01
ENSMUST00000165217				7.5	4.0E-05	8.5	2.9E-05	-0.2	8.6E-01	0.5	3.7E-01
ENSMUST00000150525	leucine rich repeat containing 40 [Source:MGI Symbol;Acc:MGI:1914394]	D6RHB1		-2.5	4.8E-02	-3.4	5.1E-02	-0.8	3.1E-01	0.0	9.9E-01
ENSMUST00000186891				7.5	3.2E-05	-3.3	4.0E-02	1.2	1.0E-01	-0.8	5.9E-01
ENSMUST00000114665				7.5	7.4E-05	5.5	3.5E-02	-0.7	7.6E-01	-0.9	5.4E-01
ENSMUST00000150355				7.5	1.4E-03	-0.9	2.6E-01	0.0	9.3E-01	-1.0	1.7E-01
ENSMUST00000167898				7.5	2.0E-05	3.1	8.0E-02	-2.2	2.2E-01	0.6	6.0E-01
ENSMUST00000150549				1.0	3.1E-01	4.6	9.6E-03	2.2	1.0E-01	-1.3	2.0E-01
ENSMUST00000134429				7.5	1.4E-04	4.1	2.6E-03	-2.3	4.7E-02	1.2	9.0E-02
ENSMUST00000150553				1.5	1.1E-01	1.7	1.3E-01	0.1	9.1E-01	-0.1	9.3E-01
ENSMUST00000150554	filamin, alpha [Source:MGI Symbol;Acc:MGI:95556]	J3JS91		-6.8	1.7E-01	-6.3	2.9E-01	-0.9	7.2E-01	-1.3	8.4E-01
ENSMUST00000193920				7.5	2.4E-03	3.0	1.6E-01	-4.4	6.1E-02	0.5	7.1E-01
ENSMUST00000150558				1.8	8.3E-02	2.6	6.5E-02	1.0	3.8E-01	0.1	8.8E-01
ENSMUST00000124325				7.5	2.1E-05	5.8	7.5E-04	-0.5	7.0E-01	0.2	8.0E-01
ENSMUST00000143367				7.5	3.4E-05	3.6	3.1E-02	-2.5	1.3E-01	0.1	9.4E-01
ENSMUST00000150565				3.0	1.1E-01	2.0	3.3E-01	-1.6	3.6E-01	-0.6	7.1E-01
ENSMUST00000116110				7.5	2.4E-04	4.8	2.2E-04	0.2	7.9E-01	0.9	1.1E-01
ENSMUST00000176186				7.5	1.5E-04	6.0	1.9E-03	-0.6	6.9E-01	0.3	6.8E-01
ENSMUST00000150575	makorin, ring finger protein, 1 [Source:MGI Symbol;Acc:MGI:1859353]	F6QJX8		-1.3	4.8E-01	-2.7	2.4E-01	-1.7	2.1E-01	-0.3	9.0E-01
ENSMUST00000162933				7.5	2.8E-06	-4.2	2.8E-03	-1.2	6.1E-02	0.7	5.1E-01
ENSMUST00000185855				7.5	3.1E-05	5.6	1.2E-04	-0.5	5.8E-01	0.7	2.1E-01
ENSMUST00000150582				1.0	5.2E-02	0.9	1.4E-01	-0.2	6.7E-01	-0.1	8.5E-01
ENSMUST00000150585	vacuolar protein sorting 33B (yeast) [Source:MGI Symbol;Acc:MGI:2446237]	S4R1H4		1.6	5.6E-01	-1.5	7.5E-01	-0.2	9.5E-01	2.9	5.0E-01
ENSMUST00000122021				7.5	4.2E-05	-2.5	1.1E-01	0.9	2.5E-01	-0.9	5.7E-01
ENSMUST00000148346				7.5	1.0E-06	5.3	4.8E-02	-0.8	7.5E-01	-0.3	8.6E-01
ENSMUST00000150593				-2.1	1.9E-01	-3.7	2.0E-01	0.1	9.3E-01	1.7	5.3E-01
ENSMUST00000150597				-0.1	9.8E-01	-1.2	6.0E-01	-2.5	1.7E-01	-1.4	5.5E-01
ENSMUST00000130147				7.5	6.4E-05	5.1	4.5E-03	-1.1	4.5E-01	-0.4	6.7E-01
ENSMUST00000150605				3.3	6.2E-02	3.9	9.6E-02	0.2	9.3E-01	-0.4	7.8E-01
ENSMUST00000150606				2.4	1.0E-01	4.6	4.3E-02	1.5	4.3E-01	-0.7	6.1E-01
ENSMUST00000152719				7.5	1.4E-04	-8.7	4.8E-03	-2.4	1.1E-02	-0.7	8.0E-01
ENSMUST00000160159				7.5	8.0E-05	7.0	1.3E-04	1.3	2.5E-01	-1.5	4.3E-02
ENSMUST00000152113				7.5	3.0E-04	-4.2	5.7E-02	2.7	1.0E-02	-0.8	7.0E-01
ENSMUST00000180588				7.5	6.5E-05	-3.8	2.7E-02	-0.3	6.6E-01	-1.8	3.2E-01
ENSMUST00000150637				0.0	9.8E-01	1.2	3.7E-01	0.3	7.9E-01	-0.9	4.2E-01
ENSMUST00000117650				7.5	8.6E-05	6.4	1.4E-02	-0.5	8.2E-01	-1.4	2.8E-01
ENSMUST00000150640				2.2	2.4E-01	-0.6	8.4E-01	0.3	8.9E-01	3.0	2.9E-01
ENSMUST00000192021				7.5	4.0E-05	7.1	3.6E-05	-2.6	4.2E-02	-0.3	6.2E-01
ENSMUST00000150227				7.5	2.4E-05	-5.2	2.8E-02	0.9	2.8E-01	-0.2	9.2E-01
ENSMUST00000150655	N(alpha)-acetyltransferase 60, NatF catalytic subunit [Source:MGI Symbol;Acc:MGI:1922013]		Q9DBU2	-1.7	8.4E-02	0.2	8.5E-01	1.2	1.7E-01	-0.7	5.2E-01
ENSMUST00000195403				7.5	9.3E-05	4.0	1.1E-02	-1.5	2.7E-01	-1.0	3.0E-01
ENSMUST00000120236				7.5	3.9E-04	5.3	9.9E-04	-0.8	5.0E-01	-0.4	6.2E-01
ENSMUST00000155298				7.5	6.1E-05	4.3	7.0E-03	-0.2	8.6E-01	0.3	7.5E-01
ENSMUST00000105451				7.5	6.2E-04	2.1	7.8E-03	-0.8	1.5E-01	-0.2	7.3E-01
ENSMUST00000124507				7.5	1.5E-04	4.9	4.1E-03	-1.5	3.3E-01	-0.1	9.0E-01
ENSMUST00000173807				7.5	6.0E-03	7.1	1.4E-02	-0.6	8.3E-01	-1.9	2.0E-01
ENSMUST00000151168				7.5	5.9E-05	-2.6	3.4E-02	0.0	9.8E-01	-0.3	7.5E-01
ENSMUST00000150683				1.3	1.5E-01	0.8	4.8E-01	0.3	7.2E-01	0.8	4.2E-01
ENSMUST00000150684				1.5	1.7E-01	-0.8	6.6E-01	0.3	8.1E-01	2.7	1.3E-01
ENSMUST00000187698				7.5	2.7E-05	5.6	5.5E-03	-0.7	6.9E-01	-0.1	9.5E-01
ENSMUST00000149258				7.5	2.7E-04	5.7	1.6E-05	-0.5	4.5E-01	0.1	7.3E-01
ENSMUST00000195384				7.5	3.9E-05	5.3	1.6E-03	-1.9	1.7E-01	0.0	9.7E-01
ENSMUST00000150709	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase [Source:MGI Symbol;Acc:MGI:1098791]	D6RGM2		-3.1	1.3E-01	1.7	5.1E-01	2.8	1.9E-01	-1.9	3.8E-01
ENSMUST00000153416				7.5	1.0E-05	-2.4	1.0E-01	0.5	5.3E-01	-1.0	4.8E-01
ENSMUST00000189197				7.5	1.4E-04	4.0	3.3E-04	-1.4	7.0E-02	0.1	8.2E-01
ENSMUST00000142048				7.5	2.1E-05	5.0	5.9E-05	-0.5	4.7E-01	-0.7	1.7E-01
ENSMUST00000150728				1.2	1.7E-01	1.0	3.4E-01	-0.2	7.6E-01	-0.1	9.3E-01
ENSMUST00000189370				7.5	2.9E-04	3.8	9.8E-03	-0.5	6.8E-01	-0.2	8.1E-01
ENSMUST00000195878				7.5	2.5E-05	6.7	4.2E-03	-1.0	6.1E-01	-0.4	7.3E-01
ENSMUST00000150731				-1.0	2.6E-01	-0.9	4.7E-01	0.7	3.9E-01	0.6	5.9E-01
ENSMUST00000118740				7.5	1.4E-02	8.2	3.6E-05	-0.6	5.9E-01	-0.9	1.2E-01
ENSMUST00000177515				7.5	1.4E-03	6.1	1.5E-03	-0.5	7.3E-01	-2.5	1.7E-02
ENSMUST00000192318				7.5	1.6E-02	-5.3	4.3E-02	-0.1	9.1E-01	1.1	6.5E-01
ENSMUST00000146539				7.5	1.8E-04	2.3	1.5E-01	-2.4	1.3E-01	-0.5	6.7E-01
ENSMUST00000118042				7.5	4.4E-05	-4.9	1.9E-02	-0.2	7.4E-01	-0.3	8.9E-01
ENSMUST00000150759				4.7	8.4E-02	-1.4	7.5E-01	-1.3	6.6E-01	4.8	2.2E-01
ENSMUST00000137047				7.5	2.2E-04	-4.9	1.8E-02	0.4	5.3E-01	-0.4	8.3E-01
ENSMUST00000155404				7.5	6.8E-05	8.2	2.1E-04	-0.8	6.2E-01	-0.3	7.1E-01
ENSMUST00000182030				7.5	5.5E-05	5.0	1.1E-03	0.5	6.3E-01	-1.6	9.0E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000150766	ankyrin repeat domain 12 [Source:MGI Symbol;Acc:MGI:1914357]	Q3U569		1.1	5.5E-01	1.4	5.8E-01	0.3	8.6E-01	0.0	1.0E+00
ENSMUST00000150767				-2.4	4.1E-02	-1.3	3.0E-01	0.0	9.5E-01	-1.1	4.0E-01
ENSMUST00000150768	potassium channel tetramerisation domain containing 9 [Source:MGI Symbol;Acc:MGI:2145579]	E9PUA6		-0.5	8.2E-01	-0.1	9.7E-01	-0.8	6.8E-01	-1.2	6.6E-01
ENSMUST00000150776				0.1	9.1E-01	0.2	9.0E-01	-0.1	9.1E-01	-0.2	8.9E-01
ENSMUST00000185525				7.5	4.1E-05	5.2	1.9E-03	-0.9	5.1E-01	0.1	8.6E-01
ENSMUST00000150780				-2.4	3.8E-02	0.0	9.9E-01	0.7	4.3E-01	-1.7	1.8E-01
ENSMUST00000136795				7.5	2.1E-04	-3.8	2.4E-01	3.0	5.1E-02	1.1	7.3E-01
ENSMUST00000152614				7.5	6.5E-05	3.6	8.9E-04	-1.2	1.3E-01	-0.5	4.3E-01
ENSMUST00000173410				7.5	3.8E-04	6.4	3.4E-04	1.8	1.2E-01	-1.0	1.7E-01
ENSMUST00000192096				7.5	6.2E-04	3.5	5.2E-02	-0.8	6.2E-01	1.1	3.8E-01
ENSMUST00000119791				7.5	9.7E-03	5.9	4.3E-04	0.2	8.8E-01	1.3	6.2E-02
ENSMUST00000138333				7.5	7.0E-05	7.2	1.2E-04	-0.6	6.0E-01	-0.3	6.1E-01
ENSMUST00000150802				1.5	2.3E-01	-1.3	4.9E-01	-0.5	6.7E-01	2.3	2.0E-01
ENSMUST00000147761				7.5	3.5E-04	7.9	6.9E-05	1.5	2.1E-01	0.2	6.7E-01
ENSMUST00000150806	ring finger protein 44 [Source:MGI Symbol;Acc:MGI:2145310]		Q3UHJ8	-5.3	4.6E-02	-4.9	3.0E-01	2.3	3.1E-01	1.9	6.6E-01
ENSMUST00000150813	TBC1 domain family, member 14 [Source:MGI Symbol;Acc:MGI:1098708]	E9PZY7		1.7	6.5E-02	2.6	4.2E-02	0.3	7.8E-01	-0.6	4.6E-01
ENSMUST00000129111				7.5	2.6E-07	5.8	4.4E-03	-1.4	4.3E-01	-1.4	1.9E-01
ENSMUST00000163297				7.5	1.8E-04	7.8	1.5E-04	1.0	4.1E-01	-0.9	2.1E-01
ENSMUST00000071847				7.5	1.8E-04	6.6	2.6E-04	-0.8	4.8E-01	0.6	3.8E-01
ENSMUST00000128406				7.5	7.3E-03	-6.3	8.1E-02	1.4	2.2E-01	3.4	3.1E-01
ENSMUST00000182483				7.5	6.0E-04	-9.4	4.4E-03	-0.4	5.6E-01	-0.3	9.1E-01
ENSMUST00000190721				7.5	2.7E-04	5.4	1.0E-03	-0.3	7.7E-01	-0.2	8.3E-01
ENSMUST00000137501				7.5	3.4E-05	5.3	2.5E-03	0.8	5.4E-01	-1.1	1.6E-01
ENSMUST00000150837				-1.1	2.5E-01	-2.3	1.1E-01	-0.1	9.3E-01	1.2	3.9E-01
ENSMUST00000145393				7.5	5.2E-04	3.4	1.1E-01	-3.7	1.0E-01	0.9	5.2E-01
ENSMUST00000150840				-1.6	4.6E-01	-3.5	1.8E-01	-2.7	7.8E-02	-0.8	7.6E-01
ENSMUST00000150841				2.7	6.0E-02	3.2	5.4E-02	0.0	9.9E-01	-0.5	6.9E-01
ENSMUST00000182360				7.5	2.9E-04	1.0	6.5E-01	3.2	8.2E-02	-3.1	1.4E-01
ENSMUST00000150848	oid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Source:MGI Symbol;Acc:M		Q9QZQ1	1.8	5.0E-01	1.9	5.8E-01	-0.2	9.4E-01	-0.3	9.3E-01
ENSMUST00000048086				7.5	1.8E-05	6.3	6.5E-05	0.4	6.7E-01	0.5	3.5E-01
ENSMUST00000150853				-1.4	4.5E-02	0.6	4.7E-01	1.7	1.9E-02	-0.3	6.9E-01
ENSMUST00000128470				7.5	1.8E-04	3.1	2.4E-03	-0.4	6.0E-01	0.5	3.7E-01
ENSMUST00000190579				7.4	5.7E-05	-1.3	3.4E-01	6.6	1.3E-05	-2.1	1.7E-01
ENSMUST00000150858				-1.2	2.7E-01	-0.2	8.8E-01	1.6	1.3E-01	0.6	6.7E-01
ENSMUST00000132057				7.4	2.8E-05	8.1	1.0E-04	-0.7	6.2E-01	-2.1	1.5E-02
ENSMUST00000150885				2.1	1.0E-01	3.5	5.5E-02	1.3	3.7E-01	0.0	9.8E-01
ENSMUST00000150891				-3.9	3.3E-01	-1.3	8.0E-01	1.6	5.9E-01	-1.0	8.5E-01
ENSMUST00000144452				7.4	1.6E-04	6.5	1.6E-04	-0.6	6.2E-01	0.5	3.8E-01
ENSMUST00000145321				7.4	3.3E-05	6.3	5.6E-03	0.7	6.6E-01	1.5	1.7E-01
ENSMUST00000150899				1.8	9.0E-02	0.3	8.4E-01	0.0	9.9E-01	1.5	2.3E-01
ENSMUST00000191232				7.4	5.7E-06	1.1	4.5E-01	-2.5	9.2E-02	2.2	8.8E-02
ENSMUST00000150916	ankyrin repeat, family A (RFXANK-like), 2 [Source:MGI Symbol;Acc:MGI:1915808]	D3Z4I1		-1.5	2.0E-01	-0.5	6.7E-01	-1.1	2.1E-01	-2.1	9.3E-02
ENSMUST00000150919				-1.8	9.2E-02	-1.1	3.6E-01	-0.3	7.1E-01	-1.0	3.7E-01
ENSMUST00000125066				7.4	2.0E-05	2.9	2.2E-03	0.0	9.5E-01	0.2	7.6E-01
ENSMUST00000189217				7.4	1.1E-04	-7.3	1.0E-02	1.6	5.3E-02	1.1	6.7E-01
ENSMUST00000182589				7.4	4.7E-05	4.9	4.6E-02	0.9	6.8E-01	0.3	8.5E-01
ENSMUST00000150928	Rap1 GTPase-activating protein [Source:MGI Symbol;Acc:MGI:109338]	A2ALS3		3.6	8.9E-02	5.8	2.8E-02	0.0	9.9E-01	-2.2	1.3E-01
ENSMUST00000189469				7.4	4.3E-05	2.1	1.7E-01	0.2	8.8E-01	1.1	3.4E-01
ENSMUST00000117964				7.4	2.0E-06	5.2	2.2E-04	-0.8	3.5E-01	0.0	9.8E-01
ENSMUST00000150942				1.0	1.8E-01	1.6	9.9E-02	1.0	2.0E-01	0.4	6.3E-01
ENSMUST00000121545				7.4	2.3E-03	6.7	3.6E-05	0.1	8.9E-01	0.8	1.3E-01
ENSMUST00000174428				7.4	2.0E-05	2.0	6.0E-03	-0.7	1.6E-01	-0.2	6.6E-01
ENSMUST00000132683				7.4	2.6E-04	9.4	7.7E-06	-0.6	5.8E-01	-0.5	2.3E-01
ENSMUST00000127217				7.4	1.3E-06	-6.8	8.6E-04	-0.7	1.7E-01	-0.8	6.1E-01
ENSMUST00000180176				7.4	4.9E-05	5.2	2.5E-03	-1.0	4.7E-01	-1.2	1.9E-01
ENSMUST00000142632				7.4	9.1E-06	5.5	3.5E-04	-1.4	2.2E-01	0.0	1.0E+00
ENSMUST00000150960				0.1	9.6E-01	0.9	5.7E-01	-1.3	3.5E-01	-2.1	1.8E-01
ENSMUST00000139352				7.4	6.8E-05	4.7	2.1E-02	-1.9	2.8E-01	0.0	9.8E-01
ENSMUST00000173096				7.4	2.1E-05	-3.7	8.5E-02	0.1	8.9E-01	-0.2	9.4E-01
ENSMUST00000127205				7.4	1.0E-04	-3.9	4.0E-03	0.3	5.3E-01	-0.5	6.5E-01
ENSMUST00000153717				7.4	1.7E-05	-5.8	4.4E-03	0.6	2.8E-01	-0.1	9.5E-01
ENSMUST00000150975	poly(A) binding protein, nuclear 1 [Source:MGI Symbol;Acc:MGI:1859158]	G3UY42		-4.2	1.2E-01	-0.7	8.0E-01	0.3	8.7E-01	-3.1	2.8E-01
ENSMUST00000189866				7.4	9.2E-05	6.6	2.6E-05	1.0	2.3E-01	0.0	9.8E-01
ENSMUST00000137425				7.4	3.1E-06	7.1	1.7E-03	-0.2	9.1E-01	1.2	2.0E-01
ENSMUST00000150991				3.7	8.2E-02	6.4	1.4E-02	-0.3	9.0E-01	-3.0	4.4E-02
ENSMUST00000150127				7.4	1.8E-03	5.7	4.6E-04	-0.6	5.9E-01	0.2	7.0E-01
ENSMUST00000193045				7.4	4.1E-06	7.8	1.5E-03	-0.4	8.1E-01	0.5	5.8E-01
ENSMUST00000150997				-1.5	1.5E-01	-2.0	9.4E-02	-1.5	8.3E-02	-1.0	4.0E-01
ENSMUST00000121290				7.4	1.0E-03	6.0	9.5E-05	-2.0	9.3E-02	0.0	9.7E-01
ENSMUST00000117459				7.4	5.6E-05	7.7	3.7E-04	1.1	4.2E-01	-1.0	2.1E-01
ENSMUST00000151012	OTU domain containing 6B [Source:MGI Symbol;Acc:MGI:1919451]	F6VDQ9		-2.2	9.5E-02	-3.2	4.3E-02	-0.6	5.2E-01	0.5	7.4E-01
ENSMUST00000151016	ribulose-5-phosphate-3-epimerase [Source:MGI Symbol;Acc:MGI:1913896]	M0QWJ2		0.7	4.1E-01	1.5	1.5E-01	-0.2	8.6E-01	-1.0	2.8E-01
ENSMUST00000137894				7.4	3.1E-05	7.1	2.3E-05	-2.0	7.8E-02	-0.4	4.2E-01
ENSMUST00000142589				7.4	4.0E-05	4.9	2.7E-02	-0.5	8.2E-01	0.7	5.7E-01
ENSMUST00000122183				7.4	6.1E-05	3.4	3.2E-02	0.5	6.5E-01	1.3	2.0E-01
ENSMUST00000151030				2.1	7.1E-02	2.3	1.5E-01	0.4	7.4E-01	0.3	8.2E-01
ENSMUST00000151034				-4.4	1.6E-01	-4.3	3.3E-01	-0.1	9.5E-01	-0.3	9.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000151036				1.2	4.8E-01	0.4	8.5E-01	-1.1	5.0E-01	-0.3	8.9E-01
ENSMUST00000151045	glutamate receptor, ionotropic, AMPA1 (alpha 1) [Source:MGI Symbol;Acc:MGI:95808]	F6YNQ1		4.4	9.1E-02	6.8	2.7E-02	-0.2	9.4E-01	-2.6	1.1E-01
ENSMUST00000169968				7.4	2.8E-06	2.2	8.9E-02	-0.1	9.0E-01	1.4	1.6E-01
ENSMUST00000144145				7.4	2.3E-05	7.2	1.6E-04	-0.6	6.2E-01	0.1	8.7E-01
ENSMUST00000148054				7.4	2.0E-05	2.1	3.0E-02	-0.9	2.4E-01	0.7	3.0E-01
ENSMUST00000118377				7.4	4.0E-05	5.7	3.6E-04	1.0	3.0E-01	0.3	6.6E-01
ENSMUST00000151059				-1.2	5.0E-01	-0.6	7.3E-01	-1.4	3.5E-01	-2.1	2.5E-01
ENSMUST00000151061				-1.0	3.3E-01	0.5	7.2E-01	0.7	4.7E-01	-0.8	5.3E-01
ENSMUST00000161877				7.4	8.5E-05	2.9	1.4E-01	0.0	9.9E-01	1.5	2.4E-01
ENSMUST00000137347				7.4	2.7E-05	-2.5	4.7E-02	0.5	4.3E-01	-1.8	1.7E-01
ENSMUST00000110549				7.4	8.5E-06	-2.3	3.7E-02	0.5	3.8E-01	0.1	8.8E-01
ENSMUST00000151073				4.3	5.3E-02	5.0	4.1E-02	-0.9	6.8E-01	-1.6	2.7E-01
ENSMUST00000151078	ubiquinol-cytochrome c reductase complex assembly factor 1 [Source:MGI Symbol;Acc:MGI:1929472]	D6RDC3		4.9	1.2E-01	-1.2	7.7E-01	-3.9	2.4E-01	2.2	5.3E-01
ENSMUST00000151080				3.7	6.3E-02	5.6	1.7E-02	-0.4	8.7E-01	-2.2	9.3E-02
ENSMUST00000130725				7.4	4.3E-05	7.0	2.0E-04	-1.8	2.3E-01	0.5	4.8E-01
ENSMUST00000182717				7.4	4.8E-05	5.0	6.7E-03	-0.2	8.8E-01	-0.2	8.0E-01
ENSMUST00000151092				4.3	7.3E-02	3.3	1.7E-01	-0.6	8.1E-01	0.4	8.0E-01
ENSMUST00000188965				7.4	1.0E-05	3.7	2.5E-02	-1.0	5.0E-01	-1.1	2.9E-01
ENSMUST00000184818				7.4	2.8E-07	5.9	4.1E-03	-0.3	8.5E-01	1.4	1.6E-01
ENSMUST00000151106				-2.2	2.1E-01	-0.3	8.7E-01	0.0	9.9E-01	-1.8	3.3E-01
ENSMUST00000151114	nuclear factor of activated T cells 5 [Source:MGI Symbol;Acc:MGI:1859333]		Q9WV30	2.1	4.0E-01	0.9	7.7E-01	-1.4	5.4E-01	-0.3	9.2E-01
ENSMUST00000119658				7.4	2.3E-04	-11.8	4.6E-05	-1.1	1.7E-02	0.7	7.0E-01
ENSMUST00000127914				7.4	2.7E-05	-7.4	2.3E-03	0.8	2.7E-01	-0.5	7.9E-01
ENSMUST00000151125				-1.2	6.3E-01	-2.4	4.6E-01	-1.5	4.1E-01	-0.3	9.2E-01
ENSMUST00000128197				7.4	3.3E-05	5.8	2.0E-04	-1.5	1.8E-01	0.4	4.5E-01
ENSMUST00000137085				7.4	3.0E-05	3.0	4.4E-02	8.4	2.5E-05	-1.2	2.8E-01
ENSMUST00000151131				1.1	2.8E-01	0.4	7.1E-01	-0.2	8.2E-01	0.4	6.9E-01
ENSMUST00000173877				7.4	2.6E-07	7.1	1.5E-04	0.9	4.3E-01	0.1	9.1E-01
ENSMUST00000150428				7.4	5.4E-05	-4.8	3.3E-02	1.0	2.5E-01	-0.2	9.3E-01
ENSMUST00000151143				-2.5	1.9E-01	-1.9	3.9E-01	-0.3	8.4E-01	-0.8	7.3E-01
ENSMUST00000181246				7.4	1.7E-05	7.7	1.9E-04	-0.7	6.1E-01	0.2	7.8E-01
ENSMUST00000129536				7.4	2.8E-05	-2.4	1.1E-01	-0.4	6.7E-01	-1.5	3.4E-01
ENSMUST00000190450				7.4	1.6E-04	6.9	2.6E-04	-0.7	6.1E-01	-0.4	5.6E-01
ENSMUST00000136147				7.4	2.4E-05	6.5	1.4E-03	-0.3	8.6E-01	-0.5	5.3E-01
ENSMUST00000183350				7.4	2.9E-05	-3.1	2.7E-02	-0.3	6.4E-01	0.4	7.2E-01
ENSMUST00000151163				1.9	4.9E-02	-0.5	6.1E-01	-2.5	9.7E-03	-0.1	9.3E-01
ENSMUST00000151165	cytohesin 1 [Source:MGI Symbol;Acc:MGI:1334257]	B1AQE4		-0.9	2.9E-01	2.5	3.4E-02	1.5	1.2E-01	-1.9	5.2E-02
ENSMUST00000185431				7.4	4.2E-06	8.5	8.2E-05	0.4	7.9E-01	-0.7	2.7E-01
ENSMUST00000186414				7.4	3.6E-05	3.1	9.0E-04	-0.2	7.5E-01	-0.4	4.2E-01
ENSMUST00000151177	cleavage and polyadenylation factor subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919579]	F6UFZ5		-1.7	2.0E-01	-1.8	3.2E-01	0.5	6.2E-01	0.7	7.1E-01
ENSMUST00000148789				7.4	6.1E-05	2.9	1.7E-01	0.3	8.8E-01	3.6	2.5E-02
ENSMUST00000119549				7.4	2.6E-05	-4.4	3.4E-02	1.7	6.8E-02	-1.9	3.8E-01
ENSMUST00000172688				7.4	1.1E-04	9.0	2.0E-03	1.5	4.7E-01	0.7	4.6E-01
ENSMUST00000131308				7.4	9.8E-05	4.7	8.2E-04	0.0	9.7E-01	0.0	9.5E-01
ENSMUST00000132737				7.4	2.4E-05	-6.5	1.0E-04	0.5	1.5E-01	0.1	8.9E-01
ENSMUST00000125522				7.4	1.4E-05	-5.6	1.4E-03	0.7	1.6E-01	-0.9	5.1E-01
ENSMUST00000151195				-0.5	3.2E-01	0.0	9.9E-01	0.2	7.3E-01	-0.4	5.6E-01
ENSMUST00000035939				7.4	1.4E-04	6.1	3.9E-03	0.7	6.7E-01	0.7	4.6E-01
ENSMUST00000151203	MAP kinase-interacting serine/threonine kinase 1 [Source:MGI Symbol;Acc:MGI:894316]	F6YIU3		-0.6	8.4E-01	0.5	8.9E-01	1.2	6.6E-01	0.0	9.9E-01
ENSMUST00000149991				7.4	3.9E-05	-6.6	4.5E-03	0.8	2.9E-01	0.0	9.9E-01
ENSMUST00000151222				-0.7	5.1E-01	0.5	6.4E-01	-0.6	4.8E-01	-1.8	1.1E-01
ENSMUST00000181349				7.4	2.6E-06	7.7	1.6E-04	-0.7	6.3E-01	0.0	9.8E-01
ENSMUST00000195642				7.4	5.7E-05	3.7	2.2E-03	1.1	1.8E-01	-0.5	4.9E-01
ENSMUST00000129508				7.4	4.6E-05	7.7	1.9E-04	-0.8	5.9E-01	0.2	7.3E-01
ENSMUST00000153974				7.4	9.5E-06	7.2	4.9E-04	-0.7	6.2E-01	-1.9	4.1E-02
ENSMUST00000151235				-2.1	1.4E-01	0.9	5.1E-01	0.1	9.2E-01	-2.9	5.8E-02
ENSMUST00000151237	inositol polyphosphate-5-phosphatase F [Source:MGI Symbol;Acc:MGI:2141867]			-5.1	7.1E-02	-3.7	2.5E-01	0.2	8.8E-01	-1.2	7.3E-01
ENSMUST00000125900				7.4	6.7E-05	6.3	6.1E-06	-0.6	3.6E-01	-0.2	6.8E-01
ENSMUST00000129289				7.4	1.2E-03	5.1	1.0E-04	0.2	7.5E-01	-0.2	6.4E-01
ENSMUST00000145508				7.4	4.6E-05	0.6	7.4E-01	2.6	1.3E-01	-1.6	3.4E-01
ENSMUST00000151251				0.8	3.7E-01	2.0	7.3E-02	0.1	9.0E-01	-1.1	2.4E-01
ENSMUST00000174429				7.4	1.1E-05	9.7	8.3E-06	0.8	4.4E-01	1.0	3.7E-02
ENSMUST00000184843				7.4	2.4E-04	4.0	4.1E-04	-3.6	3.4E-03	0.0	1.0E+00
ENSMUST00000151258	alkaline ceramidase 3 [Source:MGI Symbol;Acc:MGI:1913440]	Q8CIG2		4.1	2.1E-01	1.9	5.5E-01	-3.4	2.9E-01	-1.2	6.6E-01
ENSMUST00000151263				-0.7	6.4E-01	-0.8	6.8E-01	0.6	6.3E-01	0.8	7.0E-01
ENSMUST00000151264	SR-related CTD-associated factor 1 [Source:MGI Symbol;Acc:MGI:2141980]	D3YYM8		0.7	3.9E-01	-0.2	8.6E-01	0.5	5.7E-01	1.3	1.8E-01
ENSMUST00000134175				7.4	1.8E-03	-2.8	1.5E-01	1.4	2.0E-01	-0.5	8.0E-01
ENSMUST00000153946				7.4	2.6E-04	7.2	5.1E-05	-0.5	6.1E-01	-1.2	6.1E-02
ENSMUST00000151273	√-acetylglucosamine-1-phosphate transferase, alpha and beta subunits [Source:MGI Symbol;Acc:MGI:3643902	D6RJ30		0.4	8.5E-01	4.3	7.7E-02	1.9	3.7E-01	-1.9	2.8E-01
ENSMUST00000126884				7.4	1.3E-05	7.7	1.2E-06	-0.3	6.3E-01	0.0	9.4E-01
ENSMUST00000149629				7.4	1.4E-05	-4.5	1.5E-03	0.6	2.0E-01	-0.9	4.0E-01
ENSMUST00000129016				7.4	1.2E-04	-0.5	7.4E-01	5.4	1.8E-04	-0.3	8.4E-01
ENSMUST00000121675				7.4	6.9E-05	-2.8	5.5E-03	-0.2	6.7E-01	-0.6	4.9E-01
ENSMUST00000125996				7.4	2.1E-06	3.0	1.3E-03	-0.4	4.9E-01	-0.3	5.9E-01
ENSMUST00000192245				7.4	3.2E-04	-5.7	3.0E-04	0.2	6.8E-01	-0.5	6.5E-01
ENSMUST00000143816				7.4	2.9E-05	2.0	2.0E-01	-1.2	3.6E-01	0.2	9.0E-01
ENSMUST00000151304				0.9	1.5E-01	1.9	2.6E-02	0.2	7.7E-01	-0.8	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000151307	family with sequence similarity 111, member A [Source:MGI Symbol;Acc:MGI:1915508]	D3YYD2		2.7	2.0E-01	-1.9	5.8E-01	-1.2	5.5E-01	3.4	3.0E-01
ENSMUST00000151314	adaptor protein complex AP-1, gamma 2 subunit [Source:MGI Symbol;Acc:MGI:1328307]	D6RFT7		-1.2	8.9E-02	0.6	4.9E-01	0.7	2.7E-01	-1.0	1.9E-01
ENSMUST00000144573				7.4	2.7E-05	-5.7	4.1E-03	-0.6	3.5E-01	-0.8	6.3E-01
ENSMUST00000151323				-1.5	1.1E-01	-3.1	2.1E-02	-1.6	3.4E-02	0.0	9.7E-01
ENSMUST00000146490				7.4	2.2E-04	2.9	4.8E-02	-0.5	6.9E-01	-0.9	3.3E-01
ENSMUST00000151334				3.1	8.8E-02	1.1	6.0E-01	-1.0	5.8E-01	1.1	5.1E-01
ENSMUST00000161580				7.4	2.3E-05	-8.0	4.3E-02	-1.0	4.1E-01	-1.1	7.8E-01
ENSMUST00000125274				7.4	9.5E-03	0.2	8.8E-01	-5.3	1.4E-03	-0.6	5.1E-01
ENSMUST00000124535				7.4	2.1E-05	5.9	4.5E-04	1.2	3.0E-01	0.1	9.2E-01
ENSMUST00000176980				7.4	2.2E-06	9.1	8.3E-03	0.8	7.9E-01	2.0	1.4E-01
ENSMUST00000118363				7.4	7.9E-06	-6.3	2.2E-03	-0.8	1.7E-01	-0.3	8.5E-01
ENSMUST00000163478				7.4	2.0E-05	5.5	9.9E-05	1.4	1.0E-01	1.8	6.1E-03
ENSMUST00000151354				4.4	3.7E-02	0.1	9.8E-01	-2.8	1.5E-01	1.5	4.4E-01
ENSMUST00000151361				0.9	7.1E-01	1.9	5.3E-01	1.6	5.2E-01	0.6	8.3E-01
ENSMUST00000153149				7.4	5.2E-04	4.2	6.4E-04	-0.8	3.5E-01	-0.4	5.3E-01
ENSMUST00000151365	ubiquitin-conjugating enzyme E2 variant 1 [Source:MGI Symbol;Acc:MGI:1913839]	B7ZBY7		-3.3	4.2E-02	-2.6	3.2E-01	1.8	2.7E-01	1.1	6.4E-01
ENSMUST00000151366				-0.9	4.6E-01	-1.8	3.4E-01	-0.2	8.3E-01	0.6	7.1E-01
ENSMUST00000154634				7.4	1.1E-03	-1.3	1.6E-01	0.6	3.4E-01	-0.3	7.2E-01
ENSMUST00000151370				-1.4	2.7E-01	-0.4	7.8E-01	-0.4	7.1E-01	-1.4	3.5E-01
ENSMUST00000151372	isoprenylcysteine carboxyl methyltransferase [Source:MGI Symbol;Acc:MGI:1888594]	Q6PGA6		-1.9	3.1E-01	-1.0	6.9E-01	1.4	4.7E-01	0.6	7.9E-01
ENSMUST00000119030				7.4	1.8E-04	4.5	2.0E-02	0.0	9.8E-01	-0.3	8.0E-01
ENSMUST00000147968				7.4	1.5E-04	13.1	6.4E-08	-1.0	2.6E-01	-0.7	3.9E-02
ENSMUST00000151384				-0.2	8.4E-01	-3.3	9.4E-02	-0.4	7.0E-01	2.6	1.5E-01
ENSMUST00000151385	oteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki) [Source:MGI Symbol;Acc:MGI:10963(	A2A4J1		0.5	8.1E-01	0.4	8.8E-01	-0.2	9.0E-01	-0.1	9.6E-01
ENSMUST00000165388				7.4	1.6E-04	6.8	1.5E-04	-0.6	6.1E-01	0.0	9.4E-01
ENSMUST00000151390	thymine DNA glycosylase [Source:MGI Symbol;Acc:MGI:108247]		P56581	0.9	1.9E-01	2.8	6.5E-03	0.7	3.5E-01	-1.2	9.9E-02
ENSMUST00000151393	WW domain binding protein 1 [Source:MGI Symbol;Acc:MGI:104710]			-0.1	9.8E-01	4.4	1.2E-01	1.8	4.7E-01	-2.7	2.2E-01
ENSMUST00000079261				7.4	3.7E-04	-5.0	1.7E-03	-1.7	1.3E-02	-0.7	6.0E-01
ENSMUST00000117257				7.4	9.3E-05	8.9	2.5E-05	-0.6	6.5E-01	0.0	9.9E-01
ENSMUST00000188039				7.4	3.5E-07	6.5	3.1E-04	-0.7	5.9E-01	-0.6	3.7E-01
ENSMUST00000155755				7.4	5.1E-05	7.1	1.2E-04	-0.5	6.5E-01	-1.4	4.8E-02
ENSMUST00000174162				7.4	7.0E-03	4.9	1.5E-03	-1.4	2.1E-01	-0.3	7.0E-01
ENSMUST00000118892				7.4	1.0E-03	3.2	9.6E-03	0.2	8.2E-01	-0.2	8.4E-01
ENSMUST00000143048				7.4	2.2E-05	8.2	2.1E-05	-0.5	6.5E-01	-0.5	3.2E-01
ENSMUST00000148946				7.4	1.9E-03	-5.1	1.2E-02	-1.9	3.4E-02	-1.5	4.5E-01
ENSMUST00000151431				0.9	6.7E-01	-1.8	5.0E-01	-2.3	1.6E-01	0.4	8.8E-01
ENSMUST00000155918				7.4	7.8E-05	4.9	1.5E-04	-0.8	3.1E-01	0.0	9.9E-01
ENSMUST00000151435				-4.1	6.5E-02	-1.8	4.6E-01	0.7	6.4E-01	-1.6	5.1E-01
ENSMUST00000151439				2.4	9.7E-02	3.1	1.1E-01	0.0	9.8E-01	-0.6	6.1E-01
ENSMUST00000188901				7.4	1.9E-05	2.7	8.7E-02	-0.8	4.9E-01	1.4	2.6E-01
ENSMUST00000189743				7.4	8.8E-05	7.2	3.7E-05	-1.5	1.9E-01	-0.5	3.4E-01
ENSMUST00000123783				7.4	3.1E-05	-0.8	5.1E-01	1.1	1.8E-01	-1.5	2.7E-01
ENSMUST00000193961				7.4	5.8E-05	-2.2	1.7E-01	0.6	4.6E-01	0.5	7.4E-01
ENSMUST00000151455				2.8	3.8E-02	6.8	3.9E-03	2.5	1.7E-01	-1.5	1.5E-01
ENSMUST00000184968				7.4	5.4E-05	4.1	3.0E-03	-2.7	4.3E-02	-0.3	6.9E-01
ENSMUST00000141085				7.4	1.1E-04	6.7	1.2E-03	0.0	1.0E+00	-0.7	4.4E-01
ENSMUST00000160031				7.4	7.0E-07	3.3	3.4E-03	-2.8	1.9E-02	-1.1	1.2E-01
ENSMUST00000193251				7.4	1.2E-04	5.3	1.7E-03	-0.3	8.2E-01	-0.5	5.5E-01
ENSMUST00000151477	trinucleotide repeat containing 18 [Source:MGI Symbol;Acc:MGI:3648294]	D3YV17		-2.1	1.3E-01	-2.5	1.1E-01	-1.0	2.7E-01	-0.6	7.2E-01
ENSMUST00000151481				3.7	1.1E-01	5.8	3.1E-02	-0.3	9.2E-01	-2.3	1.2E-01
ENSMUST00000151482				1.2	2.2E-01	-0.4	8.0E-01	0.7	5.0E-01	2.3	1.2E-01
ENSMUST00000123618				7.4	1.6E-04	6.7	1.0E-04	0.5	6.2E-01	0.2	7.6E-01
ENSMUST00000151484	cereblon [Source:MGI Symbol;Acc:MGI:1913277]			1.0	6.5E-01	-3.5	1.5E-01	-5.7	9.2E-03	-1.1	6.7E-01
ENSMUST00000138453				7.4	4.0E-05	-0.2	8.5E-01	0.2	7.7E-01	-3.1	4.0E-02
ENSMUST00000135011				7.4	3.9E-05	-3.2	2.2E-03	0.4	3.0E-01	-0.9	2.9E-01
ENSMUST00000151489				-2.2	1.5E-01	0.1	9.5E-01	0.0	9.9E-01	-2.3	1.8E-01
ENSMUST00000151496	dehydrogenase/reductase (SDR family) member 11 [Source:MGI Symbol;Acc:MGI:2652816]	F2Z445		1.4	1.7E-01	2.1	1.4E-01	1.1	3.6E-01	0.4	7.2E-01
ENSMUST00000151498	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	Q3UV08		-0.8	2.8E-01	0.5	5.5E-01	0.9	2.1E-01	-0.5	5.9E-01
ENSMUST00000151499				1.1	4.0E-01	6.0	1.4E-02	2.7	1.8E-01	-2.2	1.0E-01
ENSMUST00000194501				7.4	4.1E-05	-0.8	6.0E-01	1.8	9.6E-02	-0.4	8.1E-01
ENSMUST00000125228				7.4	1.4E-03	-4.6	3.4E-02	0.0	9.6E-01	-0.8	7.0E-01
ENSMUST00000161933				7.4	1.5E-04	8.0	7.7E-04	2.9	9.6E-02	-0.9	2.5E-01
ENSMUST00000150730				7.4	8.4E-04	4.4	1.2E-02	-1.5	3.5E-01	0.8	4.3E-01
ENSMUST00000151513	eukaryotic translation initiation factor 1 [Source:MGI Symbol;Acc:MGI:105125]	J3QPZ8		-1.9	1.4E-01	-0.9	4.9E-01	0.2	8.2E-01	-0.7	5.9E-01
ENSMUST00000151517				-1.4	1.3E-01	0.0	9.9E-01	0.7	3.8E-01	-0.7	4.7E-01
ENSMUST00000126434				7.3	3.1E-05	4.8	6.6E-04	0.3	7.3E-01	-0.1	8.2E-01
ENSMUST00000151524	SMC5-SMC6 complex localization factor 1 [Source:MGI Symbol;Acc:MGI:2145448]		Q8R3P9	-0.4	5.7E-01	-1.2	2.8E-01	-0.1	8.9E-01	0.7	5.1E-01
ENSMUST00000129783				7.3	5.2E-05	7.7	8.4E-06	-0.7	4.5E-01	0.4	4.3E-01
ENSMUST00000133142				7.3	2.5E-05	2.9	4.5E-01	-0.9	7.8E-01	4.6	1.4E-01
ENSMUST00000182774				7.3	3.3E-05	6.4	2.4E-04	-1.1	3.4E-01	0.1	9.0E-01
ENSMUST00000133063				7.3	1.4E-04	4.1	1.7E-02	0.2	9.0E-01	1.6	1.4E-01
ENSMUST00000151546				-0.8	3.6E-01	-0.3	8.0E-01	0.2	8.0E-01	-0.3	7.6E-01
ENSMUST00000172205				7.3	1.8E-04	-3.1	4.9E-02	0.7	3.3E-01	-0.3	8.6E-01
ENSMUST00000155324				7.3	1.4E-06	6.8	2.3E-04	-0.1	9.5E-01	-0.5	4.9E-01
ENSMUST00000137428				7.3	5.1E-07	-0.6	5.6E-01	-0.3	6.4E-01	2.9	9.6E-03
ENSMUST00000151388				7.3	4.1E-05	3.1	2.2E-03	-0.4	5.4E-01	-1.0	1.4E-01
ENSMUST00000153004				7.3	7.9E-06	5.8	1.5E-03	-0.7	6.4E-01	0.7	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159919				7.3	5.3E-05	-3.8	2.0E-02	0.1	9.1E-01	-3.6	7.1E-02
ENSMUST00000164509				7.3	5.8E-05	-2.5	2.0E-01	2.4	2.3E-02	1.1	5.6E-01
ENSMUST00000151573	C2 calcium-dependent domain containing 3 [Source:MGI Symbol;Acc:MGI:2142166]	F6WK98		2.9	1.1E-01	1.2	5.2E-01	-0.7	6.6E-01	0.9	5.9E-01
ENSMUST00000151581				1.3	4.6E-01	-2.5	2.6E-01	-4.0	2.8E-02	-0.1	9.5E-01
ENSMUST00000194240				7.3	2.7E-05	4.3	9.3E-05	-0.4	5.7E-01	0.4	3.7E-01
ENSMUST00000117973				7.3	1.8E-03	3.9	7.6E-03	-0.2	8.5E-01	0.4	5.8E-01
ENSMUST00000123721				7.3	6.4E-06	3.4	1.3E-03	-0.4	5.5E-01	-0.3	6.4E-01
ENSMUST00000188752				7.3	5.4E-05	6.4	2.2E-04	-0.6	6.1E-01	-1.4	5.5E-02
ENSMUST00000190894				7.3	5.9E-05	6.1	1.2E-03	-0.6	6.6E-01	-0.5	5.0E-01
ENSMUST00000151600				-2.9	3.8E-01	-4.8	2.1E-01	-3.0	1.6E-01	-1.1	7.9E-01
ENSMUST00000126235				7.3	1.3E-06	-5.0	1.5E-02	-0.2	8.1E-01	2.3	1.8E-01
ENSMUST00000069044				7.3	6.7E-05	-2.7	1.7E-02	-0.2	8.0E-01	-0.8	4.4E-01
ENSMUST00000151612				0.5	6.5E-01	-2.3	3.4E-01	0.4	7.9E-01	3.2	1.5E-01
ENSMUST00000151613				-0.6	4.5E-01	-0.1	9.1E-01	0.7	3.7E-01	0.2	8.5E-01
ENSMUST00000151620				1.7	5.1E-02	2.4	2.2E-02	-0.4	6.5E-01	-1.1	1.7E-01
ENSMUST00000151622	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast) [Source:MGI Symbol;Acc:MGI:2445092]	E9Q9S3		2.7	2.2E-01	1.2	6.7E-01	0.2	9.2E-01	1.8	4.5E-01
ENSMUST00000125691				7.3	2.6E-05	7.2	3.3E-04	0.2	8.6E-01	0.8	2.4E-01
ENSMUST00000151627				1.2	4.7E-01	-0.5	8.1E-01	-0.2	9.2E-01	1.6	4.1E-01
ENSMUST00000151629				0.4	7.2E-01	1.0	4.6E-01	0.7	4.7E-01	0.1	9.5E-01
ENSMUST00000141708				7.3	6.0E-05	5.9	1.6E-03	-0.6	6.9E-01	0.0	9.6E-01
ENSMUST00000192011				7.3	2.0E-04	-4.1	9.3E-02	0.9	3.8E-01	-0.7	7.8E-01
ENSMUST00000173851				7.3	1.0E-03	-0.1	9.2E-01	3.2	8.3E-03	-0.7	6.1E-01
ENSMUST00000147599				7.3	9.5E-07	6.3	1.2E-03	0.4	7.7E-01	0.9	2.8E-01
ENSMUST00000151920				7.3	4.2E-05	7.3	1.5E-03	0.3	8.4E-01	0.0	9.7E-01
ENSMUST00000161139				7.3	8.0E-05	5.9	1.7E-04	0.6	5.5E-01	-0.2	7.8E-01
ENSMUST00000134139				7.3	9.2E-05	5.0	2.4E-02	-0.7	7.4E-01	-0.4	7.5E-01
ENSMUST00000139824				7.3	3.6E-05	5.4	8.6E-04	-1.2	3.5E-01	0.0	9.6E-01
ENSMUST00000076538				7.3	5.7E-04	-3.0	5.1E-03	-0.4	3.6E-01	0.4	6.6E-01
ENSMUST00000154971				7.3	6.3E-05	6.3	9.8E-05	-1.2	2.5E-01	-0.2	7.1E-01
ENSMUST00000150945				7.3	1.1E-06	5.1	2.0E-03	0.3	7.9E-01	-0.5	5.3E-01
ENSMUST00000094493				7.3	4.7E-04	4.9	7.5E-02	-2.7	3.2E-01	-0.8	6.6E-01
ENSMUST00000151681	CREB3 regulatory factor [Source:MGI Symbol;Acc:MGI:1924378]	B8JJI3		-2.6	3.5E-01	-4.1	2.0E-01	-2.8	1.2E-01	-1.3	7.1E-01
ENSMUST00000151689	magnesium transporter 1 [Source:MGI Symbol;Acc:MGI:1914325]	A2ADH1		-1.8	1.4E-01	-4.9	6.0E-02	0.0	9.9E-01	3.2	1.9E-01
ENSMUST00000151690				-2.0	2.8E-01	-1.8	3.2E-01	-0.9	5.3E-01	-1.0	5.9E-01
ENSMUST00000165187				7.3	1.1E-04	3.3	8.0E-02	-3.5	9.7E-02	0.8	5.1E-01
ENSMUST00000172970				7.3	2.7E-05	-5.2	1.2E-03	1.2	4.2E-02	-0.3	8.0E-01
ENSMUST00000136619				7.3	1.6E-04	7.4	1.0E-04	-0.6	6.3E-01	-0.3	6.1E-01
ENSMUST00000151701				-0.2	9.6E-01	0.9	8.1E-01	0.2	9.4E-01	-0.8	8.1E-01
ENSMUST00000117439				7.3	1.0E-04	-8.9	1.8E-03	-0.6	3.6E-01	-0.5	8.3E-01
ENSMUST00000151705				0.2	8.4E-01	0.3	8.5E-01	0.8	4.5E-01	0.7	5.9E-01
ENSMUST00000151711				-2.4	2.9E-01	0.1	9.5E-01	-1.0	5.1E-01	-3.5	1.2E-01
ENSMUST00000135325				7.3	3.6E-03	3.7	1.3E-03	-3.9	3.8E-03	-2.0	1.5E-02
ENSMUST00000151728				0.6	5.1E-01	2.9	3.4E-02	0.8	4.7E-01	-1.5	1.1E-01
ENSMUST00000151732				2.2	3.6E-01	-1.1	7.3E-01	-3.1	1.8E-01	0.2	9.4E-01
ENSMUST00000156053				7.3	1.2E-02	6.0	1.3E-04	-1.1	2.9E-01	-1.2	8.6E-02
ENSMUST00000151734				-1.8	7.1E-02	-2.1	7.4E-02	-0.8	2.6E-01	-0.5	6.8E-01
ENSMUST00000119159				7.3	5.9E-05	5.9	1.9E-03	-0.4	7.8E-01	-0.3	6.6E-01
ENSMUST00000151738	striatin interacting protein 2 [Source:MGI Symbol;Acc:MGI:2444363]	F6RUA3		3.2	1.5E-01	3.6	8.7E-02	-1.4	4.9E-01	-1.8	2.9E-01
ENSMUST00000119302				7.3	2.5E-05	3.5	6.2E-04	0.5	3.7E-01	0.5	3.3E-01
ENSMUST00000151741				0.6	5.2E-01	0.4	7.2E-01	-0.1	9.2E-01	0.1	9.4E-01
ENSMUST00000138874				7.3	2.4E-06	4.0	6.3E-04	-0.1	9.4E-01	0.2	7.1E-01
ENSMUST00000180541				7.3	2.4E-05	4.0	4.6E-03	0.4	7.0E-01	-0.2	7.6E-01
ENSMUST00000151751				0.2	8.7E-01	0.4	8.1E-01	-1.2	4.1E-01	-1.3	3.9E-01
ENSMUST00000151752				4.8	4.4E-02	-1.8	4.9E-01	-2.7	2.1E-01	3.9	1.2E-01
ENSMUST00000182883				7.3	3.5E-04	6.6	2.2E-03	-0.1	9.6E-01	0.3	7.4E-01
ENSMUST00000182747				7.3	5.1E-07	2.1	1.5E-02	-0.4	5.6E-01	-0.2	6.8E-01
ENSMUST00000070021				7.3	9.0E-05	-1.2	4.9E-01	2.5	6.3E-02	0.6	7.1E-01
ENSMUST00000151771				1.7	3.0E-01	1.6	5.0E-01	1.6	4.0E-01	1.7	3.6E-01
ENSMUST00000150035				7.3	4.8E-05	5.5	8.9E-03	-0.5	7.6E-01	0.9	3.9E-01
ENSMUST00000183129				7.3	2.1E-05	2.7	1.1E-03	0.1	8.2E-01	0.1	9.1E-01
ENSMUST00000151793	polymerase (DNA directed), delta 1, catalytic subunit [Source:MGI Symbol;Acc:MGI:97741]	D6RFB8		5.2	9.7E-02	2.9	3.4E-01	-2.7	4.0E-01	-0.4	8.5E-01
ENSMUST00000065530				7.3	4.3E-05	5.3	3.8E-03	2.2	1.1E-01	0.1	8.6E-01
ENSMUST00000151799	reticulon 4 receptor-like 2 [Source:MGI Symbol;Acc:MGI:2669796]	A2ATS6		0.3	8.4E-01	5.9	1.7E-02	3.4	1.0E-01	-2.2	1.2E-01
ENSMUST00000182410				7.3	3.7E-04	5.3	3.0E-03	-0.8	5.9E-01	0.0	9.6E-01
ENSMUST00000151802				3.1	9.7E-02	4.5	4.5E-02	-0.1	9.5E-01	-1.5	2.9E-01
ENSMUST00000151803	mannoside acetylglucosaminyltransferase 4, isoenzyme B [Source:MGI Symbol;Acc:MGI:2143974]	F7BME0		-1.9	3.0E-01	-1.7	5.7E-01	0.8	6.8E-01	0.6	8.2E-01
ENSMUST00000151809	ubiquitin protein ligase E3B [Source:MGI Symbol;Acc:MGI:1891295]	A0A0G2JEX8		1.8	2.6E-01	0.7	7.2E-01	-0.4	8.1E-01	0.7	7.2E-01
ENSMUST00000189426				7.3	7.6E-05	5.1	3.2E-03	-0.3	8.1E-01	-1.1	2.0E-01
ENSMUST00000151813	protein tyrosine phosphatase, non-receptor type 12 [Source:MGI Symbol;Acc:MGI:104673]	D6RGT2		0.4	8.1E-01	2.5	2.4E-01	1.9	2.2E-01	-0.1	9.4E-01
ENSMUST00000193219				7.3	3.2E-05	7.5	3.8E-05	1.6	1.2E-01	-0.2	7.2E-01
ENSMUST00000170572				7.3	3.4E-05	4.9	2.1E-05	0.3	6.1E-01	-0.1	8.7E-01
ENSMUST00000126813				7.3	1.7E-05	3.6	1.4E-03	-0.2	7.6E-01	-0.1	8.8E-01
ENSMUST00000151829				1.8	1.3E-01	2.3	1.6E-01	0.8	5.8E-01	0.3	8.1E-01
ENSMUST00000151832				0.0	1.0E+00	-1.1	7.3E-01	-1.3	5.5E-01	-0.2	9.4E-01
ENSMUST00000155368				7.3	3.7E-06	1.6	2.0E-01	-1.3	2.4E-01	0.8	4.3E-01
ENSMUST00000151839	ArfGAP with FG repeats 2 [Source:MGI Symbol;Acc:MGI:2443267]	Q3TBU7		2.8	8.4E-02	5.9	7.9E-03	0.6	7.6E-01	-2.5	4.4E-02
ENSMUST00000151843				-0.5	4.1E-01	0.6	4.3E-01	0.3	6.2E-01	-0.8	2.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000151849				1.5	2.4E-01	2.7	1.4E-01	1.0	5.2E-01	-0.2	8.7E-01
ENSMUST00000184938				7.3	4.7E-04	6.3	3.4E-04	-0.6	6.4E-01	-1.1	1.5E-01
ENSMUST00000164536				7.3	3.1E-04	2.8	1.3E-02	-3.8	7.1E-03	-0.4	5.8E-01
ENSMUST00000151854				-0.3	7.6E-01	1.5	2.8E-01	1.7	1.6E-01	-0.1	9.4E-01
ENSMUST00000151855	cytosolic thiouridylase subunit 2 homolog (S. pombe) [Source:MGI Symbol;Acc:MGI:1914215]	G3UXB4		1.4	5.4E-01	6.3	9.6E-02	3.2	3.4E-01	-1.7	4.3E-01
ENSMUST00000151856	ash2 (absent, small, or homeotic)-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1344416]	D6RET1		1.3	7.2E-02	1.5	8.5E-02	0.1	8.8E-01	-0.1	8.9E-01
ENSMUST00000159052				7.3	9.4E-05	6.3	4.8E-04	-0.6	6.3E-01	-0.9	2.2E-01
ENSMUST00000182379				7.3	1.8E-03	5.0	3.8E-03	-1.6	2.8E-01	0.4	6.7E-01
ENSMUST00000151863	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 [Source:MGI Symbol;Acc:MGI:1928767]	A0A0A6YXS2		-3.6	5.8E-02	-1.7	5.0E-01	1.4	3.8E-01	-0.6	8.0E-01
ENSMUST00000173275				7.3	3.5E-05	3.8	3.9E-03	-0.1	9.1E-01	0.0	9.9E-01
ENSMUST00000187077				7.3	1.1E-05	4.0	1.5E-02	-1.5	3.0E-01	-0.2	8.6E-01
ENSMUST00000189034				7.3	1.2E-04	3.0	1.5E-01	-0.8	6.3E-01	4.6	1.4E-02
ENSMUST00000151874	eukaryotic translation initiation factor 2D [Source:MGI Symbol;Acc:MGI:109342]		Q61211	-0.5	8.2E-01	-2.1	4.5E-01	-2.0	2.3E-01	-0.4	9.0E-01
ENSMUST00000192199				7.3	2.3E-04	-1.9	1.4E-01	0.0	9.7E-01	-1.0	4.2E-01
ENSMUST00000143141				7.3	6.1E-05	-4.8	6.4E-03	-1.4	8.3E-02	-1.1	4.6E-01
ENSMUST00000151882				-0.2	7.3E-01	1.0	1.7E-01	1.3	2.9E-02	0.2	8.0E-01
ENSMUST00000151886				2.4	2.7E-01	2.1	4.0E-01	-0.2	9.3E-01	0.1	9.5E-01
ENSMUST00000151887				1.6	5.0E-02	2.0	5.1E-02	0.7	3.7E-01	0.3	7.1E-01
ENSMUST00000187980				7.3	3.5E-05	1.9	2.8E-02	-0.3	6.8E-01	0.5	4.2E-01
ENSMUST00000131032				7.3	1.1E-04	4.1	5.6E-02	0.3	8.5E-01	0.5	7.1E-01
ENSMUST00000120164				7.3	5.7E-05	5.3	4.5E-04	-0.3	7.5E-01	0.2	8.0E-01
ENSMUST00000156064				7.3	4.8E-04	8.0	6.1E-04	0.1	9.4E-01	0.4	6.2E-01
ENSMUST00000194591				7.3	2.2E-04	3.0	2.5E-02	-0.1	9.4E-01	0.0	9.7E-01
ENSMUST00000107177				7.3	1.2E-02	6.0	4.5E-04	-0.6	6.4E-01	-0.1	8.9E-01
ENSMUST00000151911	phosphatidylinositol glycan anchor biosynthesis, class A [Source:MGI Symbol;Acc:MGI:99461]	M0QWY7		3.9	4.9E-02	0.3	9.1E-01	-1.2	5.5E-01	2.4	3.3E-01
ENSMUST00000184481				7.3	5.7E-05	6.6	1.1E-04	-0.6	6.1E-01	0.0	9.8E-01
ENSMUST00000117669				7.3	3.8E-05	4.4	3.7E-03	0.2	8.1E-01	0.3	7.5E-01
ENSMUST00000146839				7.3	1.5E-06	9.0	8.5E-05	-0.8	5.9E-01	0.7	2.6E-01
ENSMUST00000164753				7.3	2.3E-06	6.3	9.9E-04	-0.7	6.4E-01	0.2	8.1E-01
ENSMUST00000123567				7.3	6.1E-05	7.1	8.4E-04	1.1	4.4E-01	1.3	8.9E-02
ENSMUST00000151925				-0.2	8.0E-01	0.0	1.0E+00	-0.5	5.4E-01	-0.7	4.9E-01
ENSMUST00000151927	rosbin, round spermatid basic protein 1 [Source:MGI Symbol;Acc:MGI:2444993]	D6RG56		-0.5	6.4E-01	-1.9	2.1E-01	0.0	9.8E-01	1.4	3.3E-01
ENSMUST00000151928	splicing factor 3a, subunit 2 [Source:MGI Symbol;Acc:MGI:104912]	D3YW09		-2.4	1.9E-01	-2.4	3.3E-01	-0.1	9.3E-01	-0.1	9.6E-01
ENSMUST00000151936				0.5	6.3E-01	0.9	4.6E-01	0.0	9.9E-01	-0.4	7.1E-01
ENSMUST00000128108				7.3	7.6E-05	1.9	1.7E-02	0.6	3.1E-01	0.4	4.6E-01
ENSMUST00000151938				0.3	5.9E-01	-0.7	3.3E-01	-1.1	5.6E-02	-0.1	9.1E-01
ENSMUST00000160002				7.3	2.2E-05	-6.0	1.3E-03	0.6	2.5E-01	-0.7	6.1E-01
ENSMUST00000179197				7.3	4.1E-05	4.6	1.2E-02	-1.2	4.4E-01	0.8	4.7E-01
ENSMUST00000151952	mannoside acetylglucosaminyltransferase 4, isoenzyme A [Source:MGI Symbol;Acc:MGI:2662992]		Q812G0	-0.4	7.9E-01	-1.6	4.9E-01	-0.1	9.3E-01	1.0	6.5E-01
ENSMUST00000151957				-1.1	2.4E-01	-0.6	6.3E-01	0.0	9.7E-01	-0.5	6.5E-01
ENSMUST00000151958				-5.4	6.1E-02	-6.7	1.4E-01	-0.5	7.5E-01	0.8	8.6E-01
ENSMUST00000137015				7.3	1.4E-06	-1.7	2.1E-01	0.8	2.7E-01	0.0	9.8E-01
ENSMUST00000163240				7.3	1.8E-04	-0.2	8.5E-01	1.1	8.9E-02	-1.6	1.4E-01
ENSMUST00000151966				-1.6	6.8E-02	-2.3	7.6E-02	0.7	3.4E-01	1.3	2.7E-01
ENSMUST00000120696				7.3	2.2E-04	-2.9	4.9E-02	1.2	9.1E-02	-0.6	6.7E-01
ENSMUST00000153862				7.3	6.8E-05	3.4	6.5E-02	-1.4	4.1E-01	0.6	6.2E-01
ENSMUST00000174655				7.3	1.3E-04	2.1	2.6E-02	0.2	7.5E-01	0.2	7.4E-01
ENSMUST00000183459				7.3	1.3E-03	7.4	1.1E-04	-0.6	6.2E-01	0.7	2.7E-01
ENSMUST00000066794				7.3	1.5E-04	4.3	2.1E-04	0.1	8.2E-01	0.3	6.1E-01
ENSMUST00000151980				1.0	1.5E-01	0.8	3.3E-01	-0.3	6.4E-01	-0.1	8.7E-01
ENSMUST00000151981				-2.9	1.9E-01	-5.3	1.1E-01	-1.3	3.4E-01	1.2	7.1E-01
ENSMUST00000151982	seizure related gene 6 [Source:MGI Symbol;Acc:MGI:104745]	F6XNR8		2.7	9.1E-02	6.7	9.1E-04	-0.4	7.7E-01	-4.5	1.6E-03
ENSMUST00000161108				7.3	4.9E-05	2.9	2.1E-02	1.4	1.5E-01	0.8	3.8E-01
ENSMUST00000160277				7.3	9.4E-04	1.8	3.5E-01	-1.2	4.8E-01	1.4	3.9E-01
ENSMUST00000132697				7.3	2.2E-07	8.1	5.0E-05	-0.7	5.9E-01	-0.4	4.4E-01
ENSMUST00000152000				2.3	7.9E-02	2.4	1.2E-01	-0.4	7.3E-01	-0.5	6.7E-01
ENSMUST00000122150				7.3	3.0E-05	5.8	1.7E-03	-0.5	7.3E-01	-0.5	5.6E-01
ENSMUST00000152005	capping protein (actin filament) muscle Z-line, alpha 2 [Source:MGI Symbol;Acc:MGI:106222]			2.0	7.4E-02	-4.5	9.9E-04	-7.3	9.5E-06	-0.7	4.8E-01
ENSMUST00000152006	Rho guanine nucleotide exchange factor (GEF) 11 [Source:MGI Symbol;Acc:MGI:2441869]	D6RGQ8		-1.7	1.0E-01	-2.7	7.1E-02	0.5	5.4E-01	1.5	2.9E-01
ENSMUST00000152007				-1.6	5.7E-02	-1.4	1.6E-01	-0.3	5.8E-01	-0.5	5.6E-01
ENSMUST00000185389				7.3	1.8E-06	6.2	8.9E-04	-0.9	5.1E-01	-0.7	4.0E-01
ENSMUST00000121772				7.3	5.7E-07	6.0	9.8E-04	-0.4	7.4E-01	-1.5	8.0E-02
ENSMUST00000190935				7.3	1.8E-05	4.9	3.9E-03	-1.1	4.4E-01	-1.4	1.3E-01
ENSMUST00000149690				7.3	4.2E-05	2.6	2.5E-02	0.1	8.7E-01	0.2	7.6E-01
ENSMUST00000152026				1.3	2.0E-01	0.7	5.3E-01	-0.2	8.2E-01	0.3	7.4E-01
ENSMUST00000174565				7.3	2.1E-04	4.2	1.7E-02	1.5	2.6E-01	1.9	7.5E-02
ENSMUST00000179251				7.3	9.9E-04	-5.3	5.2E-03	0.5	4.2E-01	-0.8	6.2E-01
ENSMUST00000152037	ubiquitin-like modifier activating enzyme 2 [Source:MGI Symbol;Acc:MGI:1858313]	H3BJQ2		-0.9	6.5E-01	-2.5	3.0E-01	-2.1	1.8E-01	-0.5	8.5E-01
ENSMUST00000182961				7.3	9.1E-05	4.9	8.3E-04	0.0	9.7E-01	0.5	5.0E-01
ENSMUST00000151675				7.3	1.7E-05	4.1	6.3E-03	-2.9	5.2E-02	-2.0	3.5E-02
ENSMUST00000152059				-3.5	5.4E-02	0.0	9.9E-01	3.1	1.2E-01	-0.4	8.5E-01
ENSMUST00000154261				7.3	1.8E-05	-3.9	3.5E-03	-0.4	4.3E-01	-0.8	4.7E-01
ENSMUST00000133985				7.3	2.4E-05	1.6	8.2E-02	0.0	9.6E-01	0.0	9.8E-01
ENSMUST00000152068				2.6	4.1E-02	2.2	1.8E-01	-0.3	8.1E-01	0.1	9.3E-01
ENSMUST00000152071	myelin basic protein [Source:MGI Symbol;Acc:MGI:96925]	F6TYB7		1.3	6.2E-01	0.6	8.0E-01	-2.2	3.2E-01	-1.6	5.3E-01
ENSMUST00000170135				7.3	1.1E-05	-2.3	1.7E-02	1.5	1.0E-02	0.4	6.3E-01
ENSMUST00000152081				0.2	7.0E-01	1.0	1.6E-01	1.0	8.3E-02	0.2	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000152083				0.2	8.1E-01	0.9	5.8E-01	1.6	1.6E-01	0.9	5.3E-01
ENSMUST00000118815				7.3	2.3E-04	4.3	5.2E-03	-0.7	5.6E-01	-0.4	5.8E-01
ENSMUST00000152091				1.2	1.3E-01	1.1	2.0E-01	-0.6	4.3E-01	-0.5	4.8E-01
ENSMUST00000152095	RIKEN cDNA 9330182L06 gene [Source:MGI Symbol;Acc:MGI:2443264]	D6RHB7		4.2	1.1E-01	3.7	1.4E-01	-1.7	5.2E-01	-1.3	4.4E-01
ENSMUST00000130390				7.3	6.1E-05	-2.5	1.0E-01	0.3	6.9E-01	-1.5	3.7E-01
ENSMUST00000136138				7.3	1.3E-04	5.7	4.2E-05	-0.6	4.2E-01	0.7	1.6E-01
ENSMUST00000179039				7.3	1.2E-05	3.2	6.7E-03	0.0	9.8E-01	0.4	5.5E-01
ENSMUST00000131236				7.3	6.7E-05	3.3	1.3E-01	-2.2	3.6E-01	1.6	3.1E-01
ENSMUST00000152110				-0.2	9.0E-01	0.4	8.4E-01	1.1	4.8E-01	0.5	7.9E-01
ENSMUST00000174816				7.3	2.6E-05	6.9	9.5E-04	-0.7	6.4E-01	-0.2	8.2E-01
ENSMUST00000144654				7.3	8.2E-05	-6.5	1.1E-02	1.0	2.0E-01	0.0	9.9E-01
ENSMUST00000148407				7.3	1.6E-05	5.6	1.4E-04	-2.3	4.4E-02	-1.1	7.2E-02
ENSMUST00000127173				7.3	1.4E-02	3.7	2.5E-03	-0.9	2.8E-01	-0.2	8.1E-01
ENSMUST00000152138				5.0	4.0E-02	7.2	1.3E-02	-0.1	9.7E-01	-2.3	1.2E-01
ENSMUST00000159847				7.3	4.0E-06	7.3	2.0E-03	-0.3	8.6E-01	1.1	2.5E-01
ENSMUST00000152151				-1.7	5.7E-01	-1.2	7.5E-01	-0.2	9.2E-01	-0.7	8.4E-01
ENSMUST00000152156				2.6	3.7E-01	-2.5	4.9E-01	-3.8	1.5E-01	1.3	7.1E-01
ENSMUST00000118271				7.3	3.6E-04	5.7	2.9E-04	-2.1	9.3E-02	-0.2	8.0E-01
ENSMUST00000152167				1.6	3.8E-01	-1.1	6.5E-01	-2.5	1.8E-01	0.3	9.1E-01
ENSMUST00000152171	small integral membrane protein 5 [Source:MGI Symbol;Acc:MGI:1913778]		Q8BT42	1.4	6.9E-02	1.9	5.1E-02	-0.1	8.9E-01	-0.5	4.7E-01
ENSMUST00000152182	calpain 7 [Source:MGI Symbol;Acc:MGI:1338030]	F2Z3X0		-2.1	5.1E-01	2.2	5.2E-01	0.6	8.4E-01	-3.7	2.6E-01
ENSMUST00000152186				2.9	4.7E-02	3.2	1.1E-01	0.4	8.1E-01	0.2	8.9E-01
ENSMUST00000152189	nucleoside-triphosphatase, cancer-related [Source:MGI Symbol;Acc:MGI:1913816]	D3YXL1		-0.1	9.8E-01	-0.8	7.3E-01	-2.7	2.1E-01	-2.0	4.7E-01
ENSMUST00000145193				7.3	5.9E-06	-2.4	1.6E-01	1.0	3.2E-01	-0.1	9.7E-01
ENSMUST00000154090				7.3	3.2E-04	1.4	1.0E-01	-0.2	8.0E-01	-4.9	1.0E-03
ENSMUST00000156962				7.3	3.6E-05	5.3	3.2E-03	-2.0	1.9E-01	-1.9	7.5E-02
ENSMUST00000152213				0.6	4.8E-01	1.0	3.5E-01	1.2	1.6E-01	0.8	4.1E-01
ENSMUST00000119476				7.3	5.1E-04	5.1	7.0E-05	-0.3	6.4E-01	0.1	7.6E-01
ENSMUST00000152223	eva-1 homolog C (C. elegans) [Source:MGI Symbol;Acc:MGI:1918217]	D6RCJ7		2.7	5.0E-02	6.0	5.8E-04	-0.5	6.8E-01	-3.8	1.9E-03
ENSMUST00000134989				7.3	6.9E-05	-4.5	1.2E-02	1.2	6.5E-02	-0.2	9.2E-01
ENSMUST00000147674				7.3	1.8E-04	-4.5	7.7E-02	1.0	3.0E-01	1.8	4.4E-01
ENSMUST00000162640				7.3	3.8E-05	7.9	5.0E-04	-0.8	6.3E-01	1.0	2.1E-01
ENSMUST00000182880				7.3	1.5E-04	-5.5	4.4E-04	0.1	8.4E-01	-1.3	2.9E-01
ENSMUST00000125560				7.3	6.1E-05	4.8	4.5E-04	-0.1	9.4E-01	0.5	3.9E-01
ENSMUST00000152240				-1.4	2.6E-01	-1.0	5.1E-01	-0.1	9.4E-01	-0.4	7.7E-01
ENSMUST00000185918				7.3	5.8E-05	6.2	3.1E-03	-0.7	6.8E-01	-0.2	8.5E-01
ENSMUST00000148812				7.3	2.3E-06	-2.8	1.7E-01	1.0	3.6E-01	0.5	7.8E-01
ENSMUST00000152251				-2.6	6.5E-02	-3.2	6.7E-02	-0.5	5.9E-01	0.1	9.3E-01
ENSMUST00000129058				7.3	5.2E-05	7.9	3.1E-04	-0.3	8.5E-01	0.0	9.7E-01
ENSMUST00000152259				-0.9	5.0E-01	-2.7	1.7E-01	-0.1	9.5E-01	1.7	3.5E-01
ENSMUST00000145052				7.3	4.0E-05	4.5	5.5E-03	-1.2	3.7E-01	0.4	6.6E-01
ENSMUST00000143037				7.3	1.6E-07	3.9	4.6E-03	-0.3	7.7E-01	-0.4	6.2E-01
ENSMUST00000152265	TRAF type zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1923551]	D3YWU1		-1.9	3.8E-02	-2.1	5.7E-02	-0.2	7.0E-01	0.0	9.9E-01
ENSMUST00000152267	septin 1 [Source:MGI Symbol;Acc:MGI:1858916]			-0.9	7.9E-01	-1.7	7.0E-01	-0.9	7.3E-01	-0.1	9.8E-01
ENSMUST00000139760				7.3	8.7E-07	-1.9	3.6E-01	1.8	1.5E-01	-0.4	8.4E-01
ENSMUST00000147575				7.3	2.0E-07	5.3	3.8E-04	-0.8	4.2E-01	0.4	4.8E-01
ENSMUST00000173335				7.3	1.5E-04	-6.1	1.6E-02	-0.7	3.4E-01	0.1	9.5E-01
ENSMUST00000152277				1.6	9.0E-02	1.9	9.4E-02	0.1	9.5E-01	-0.2	7.9E-01
ENSMUST00000152285				-1.0	3.1E-01	1.7	9.7E-02	0.1	8.9E-01	-2.6	2.2E-02
ENSMUST00000152287				-1.2	2.6E-01	-0.2	8.8E-01	0.4	6.6E-01	-0.6	6.5E-01
ENSMUST00000184257				7.3	5.5E-05	-3.6	2.0E-01	1.9	2.1E-01	-0.7	7.9E-01
ENSMUST00000173082				7.3	4.9E-05	5.2	1.1E-03	0.0	1.0E+00	-2.1	2.4E-02
ENSMUST00000152297				-0.8	5.3E-01	-2.1	1.0E-01	-3.4	5.7E-03	-2.1	1.4E-01
ENSMUST00000152298				-1.1	2.7E-01	-0.6	6.5E-01	0.3	7.4E-01	-0.3	8.3E-01
ENSMUST00000146300				7.3	2.3E-05	4.5	7.5E-04	-1.1	2.4E-01	0.4	5.6E-01
ENSMUST00000160411				7.3	6.4E-03	9.2	2.5E-05	-1.7	2.3E-01	0.6	2.9E-01
ENSMUST00000193262				7.3	2.2E-03	4.9	9.1E-04	-0.2	8.2E-01	0.3	6.7E-01
ENSMUST00000138901				7.2	3.5E-05	4.2	5.1E-02	-0.3	8.9E-01	-0.2	8.8E-01
ENSMUST00000144969				7.2	9.4E-06	-3.7	6.4E-03	0.6	2.2E-01	-0.6	5.8E-01
ENSMUST00000169740				7.2	1.7E-04	4.7	5.5E-02	-0.7	7.4E-01	0.0	9.8E-01
ENSMUST00000152323				3.3	1.1E-01	2.4	3.7E-01	-0.6	8.0E-01	0.4	8.3E-01
ENSMUST00000152326				3.0	9.4E-02	5.1	9.6E-03	-1.1	5.2E-01	-3.2	2.5E-02
ENSMUST00000152327	RAD51 homolog [Source:MGI Symbol;Acc:MGI:97890]	D6RCK1		1.8	8.2E-02	0.9	6.1E-01	1.8	1.6E-01	2.8	8.2E-02
ENSMUST00000179800				7.2	5.3E-05	2.4	7.9E-02	-0.9	4.5E-01	0.0	9.7E-01
ENSMUST00000152848				7.2	2.4E-04	6.5	3.3E-04	-0.7	6.0E-01	0.5	4.6E-01
ENSMUST00000190073				7.2	8.9E-07	6.7	4.6E-04	0.4	7.9E-01	-1.5	7.8E-02
ENSMUST00000140228				7.2	7.5E-04	2.8	8.6E-03	-0.3	7.1E-01	-0.5	4.6E-01
ENSMUST00000152334				-0.6	4.7E-01	-0.4	7.8E-01	1.1	2.3E-01	0.9	4.8E-01
ENSMUST00000159561				7.2	1.7E-04	2.0	2.6E-01	-1.0	5.3E-01	1.7	2.0E-01
ENSMUST00000185435				7.2	8.1E-06	-3.3	1.1E-02	-1.5	3.6E-02	-3.0	5.8E-02
ENSMUST00000127888				7.2	4.5E-05	7.4	6.2E-05	-1.0	3.5E-01	1.1	7.2E-02
ENSMUST00000152347	zinc finger protein 106 [Source:MGI Symbol;Acc:MGI:1270153]	F6UL00		0.9	5.6E-01	0.7	7.4E-01	-0.5	7.2E-01	-0.3	8.8E-01
ENSMUST00000152348				-0.9	4.3E-01	-0.8	5.2E-01	-0.7	4.6E-01	-0.8	5.3E-01
ENSMUST00000161226				7.2	8.1E-05	4.7	8.7E-04	-0.5	5.8E-01	0.8	2.8E-01
ENSMUST00000185561				7.2	3.7E-05	7.7	2.5E-05	1.6	1.1E-01	0.1	9.0E-01
ENSMUST00000152357	polyhomeotic-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2181434]	D6REI6		0.5	7.7E-01	0.4	8.7E-01	-0.6	7.4E-01	-0.5	8.5E-01
ENSMUST00000152358				-1.7	1.9E-01	-2.9	1.1E-01	-0.3	7.3E-01	0.8	6.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000064445				7.2	8.6E-05	6.0	2.8E-05	-0.3	7.1E-01	0.0	9.3E-01
ENSMUST00000145133				7.2	1.3E-04	-6.2	1.1E-02	-1.7	4.7E-02	0.0	1.0E+00
ENSMUST00000172766				7.2	1.0E-04	-4.4	4.5E-03	-0.4	5.4E-01	-1.9	2.1E-01
ENSMUST00000180507				7.2	2.1E-06	-2.0	7.9E-02	0.0	9.9E-01	-0.1	9.0E-01
ENSMUST00000124685				7.2	4.7E-05	5.6	6.7E-04	-0.1	9.3E-01	1.0	1.8E-01
ENSMUST00000128161				7.2	6.0E-04	6.1	5.5E-04	-0.6	6.2E-01	-0.8	2.5E-01
ENSMUST00000187704				7.2	5.5E-05	5.8	4.3E-04	-1.3	2.7E-01	-1.1	1.3E-01
ENSMUST00000152387	lin-54 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2140902]	E9Q8B7		1.0	6.5E-01	0.3	8.8E-01	-2.8	1.5E-01	-2.1	3.7E-01
ENSMUST00000159918				7.2	6.9E-04	-5.2	1.3E-03	-0.7	1.8E-01	-0.3	8.4E-01
ENSMUST00000172631				7.2	4.5E-03	-2.1	2.2E-01	0.2	8.2E-01	-1.0	5.7E-01
ENSMUST00000153192				7.2	1.8E-04	-3.7	3.5E-03	-2.0	7.7E-03	-0.4	7.1E-01
ENSMUST00000156348				7.2	2.1E-04	6.8	5.5E-05	-1.5	1.9E-01	0.0	9.3E-01
ENSMUST00000152404	tousled-like kinase 2 (Arabidopsis) [Source:MGI Symbol;Acc:MGI:1346023]	F6XSD0		0.9	6.2E-01	-1.6	5.2E-01	-1.9	2.3E-01	0.7	7.8E-01
ENSMUST00000152408	ubiquitin specific peptidase 46 [Source:MGI Symbol;Acc:MGI:1916977]			2.0	5.2E-02	2.5	4.0E-02	-0.3	7.2E-01	-0.8	4.0E-01
ENSMUST00000159397				7.2	4.3E-05	8.3	2.4E-05	-1.1	3.5E-01	-0.3	5.3E-01
ENSMUST00000152417	complement component 2 (within H-2S) [Source:MGI Symbol;Acc:MGI:88226]	B8JJN2		5.1	9.3E-02	2.7	3.4E-01	-3.8	2.3E-01	-1.3	5.2E-01
ENSMUST00000187617				7.2	6.7E-05	-2.6	8.0E-02	1.5	7.1E-02	-2.3	1.5E-01
ENSMUST00000081193				7.2	1.0E-04	-4.8	2.4E-03	0.2	6.5E-01	-1.9	1.8E-01
ENSMUST00000121434				7.2	9.5E-05	-3.6	2.1E-02	-1.0	1.6E-01	-0.6	6.6E-01
ENSMUST00000121823				7.2	7.2E-04	6.9	3.5E-05	-2.4	4.4E-02	-0.1	8.0E-01
ENSMUST00000119936				7.2	6.9E-05	4.2	1.5E-02	-1.0	4.9E-01	-1.6	1.4E-01
ENSMUST00000140690				7.2	4.9E-06	-2.5	3.8E-02	-0.7	2.8E-01	-0.6	6.2E-01
ENSMUST00000164336				7.2	5.4E-05	6.5	2.1E-04	-1.5	2.4E-01	-0.9	1.7E-01
ENSMUST00000120777				7.2	2.5E-05	-7.2	2.0E-03	-1.4	8.4E-02	-0.9	6.5E-01
ENSMUST00000118303				7.2	1.1E-04	1.2	3.6E-01	-1.4	2.5E-01	1.9	1.2E-01
ENSMUST00000123746				7.2	2.5E-04	5.4	1.3E-02	-0.7	7.2E-01	2.5	4.0E-02
ENSMUST00000182609				7.2	4.1E-05	-2.9	2.0E-02	1.5	1.5E-02	0.1	9.1E-01
ENSMUST00000192789				7.2	1.0E-03	5.3	2.4E-04	-2.0	7.4E-02	-0.3	5.7E-01
ENSMUST00000152454				2.9	4.4E-02	0.8	5.8E-01	-2.3	9.1E-02	-0.1	9.3E-01
ENSMUST00000160327				7.2	3.0E-05	2.3	3.5E-01	-0.7	7.4E-01	2.4	2.3E-01
ENSMUST00000118714				7.2	8.9E-05	-5.6	1.8E-02	0.8	4.3E-01	-2.0	4.5E-01
ENSMUST00000185574				7.2	4.8E-05	6.1	1.9E-02	-0.8	7.2E-01	-0.6	6.2E-01
ENSMUST00000143626				7.2	1.1E-04	5.0	4.5E-04	0.2	8.4E-01	-0.4	5.0E-01
ENSMUST00000152475				-2.3	9.3E-02	-0.5	7.3E-01	0.2	8.8E-01	-1.7	3.0E-01
ENSMUST00000078739				7.2	1.1E-02	6.2	5.4E-04	-0.5	7.2E-01	-0.8	2.9E-01
ENSMUST00000152479				2.7	4.8E-02	2.8	1.2E-01	0.3	8.3E-01	0.2	8.5E-01
ENSMUST00000133011				7.2	5.4E-04	0.2	8.7E-01	-4.1	1.7E-02	0.6	6.3E-01
ENSMUST00000152481				0.4	5.1E-01	-1.0	2.6E-01	-0.9	1.6E-01	0.5	5.4E-01
ENSMUST00000140373				7.2	3.0E-04	5.5	2.9E-02	-0.8	7.3E-01	0.2	8.7E-01
ENSMUST00000152493				1.2	3.2E-01	2.3	1.9E-01	0.4	8.0E-01	-0.7	5.7E-01
ENSMUST00000163410				7.2	4.0E-04	6.8	2.4E-04	-0.8	5.2E-01	0.1	8.7E-01
ENSMUST00000129970				7.2	6.5E-04	4.2	1.0E-02	-0.1	9.1E-01	-0.6	5.4E-01
ENSMUST00000187997				7.2	7.5E-06	5.6	3.4E-05	0.0	9.5E-01	0.0	9.8E-01
ENSMUST00000154755				7.2	4.5E-07	5.9	7.4E-04	2.0	9.6E-02	-0.5	4.9E-01
ENSMUST00000138790				7.2	6.6E-05	1.3	5.0E-01	-1.2	4.5E-01	4.0	2.4E-02
ENSMUST00000150706				7.2	1.7E-04	6.0	1.9E-04	-0.6	6.1E-01	-0.1	9.1E-01
ENSMUST00000162922				7.2	2.5E-04	3.6	1.0E-02	-3.2	3.1E-02	-0.4	5.8E-01
ENSMUST00000194658				7.2	2.3E-04	-4.7	7.7E-04	-1.8	6.0E-03	-2.5	5.9E-02
ENSMUST00000144082				7.2	8.7E-05	5.5	6.4E-06	-0.2	6.9E-01	0.0	9.4E-01
ENSMUST00000152521	eukaryotic translation initiation factor 1 [Source:MGI Symbol;Acc:MGI:105125]	J3QN87		-3.8	7.0E-02	-0.4	8.6E-01	1.5	3.8E-01	-1.9	4.3E-01
ENSMUST00000169178				7.2	1.9E-04	5.2	6.1E-03	5.6	2.1E-03	-3.4	1.3E-02
ENSMUST00000152529				3.2	2.3E-01	5.3	6.9E-02	-0.6	8.4E-01	-2.6	1.8E-01
ENSMUST00000190796				7.2	1.0E-04	6.7	2.3E-03	-0.7	6.5E-01	-0.5	6.0E-01
ENSMUST00000152535				2.1	3.1E-01	-0.9	6.5E-01	-3.9	4.8E-02	-1.0	6.0E-01
ENSMUST00000152537				-1.6	1.1E-01	-0.9	3.2E-01	-0.6	4.1E-01	-1.3	2.3E-01
ENSMUST00000152539				-0.2	8.5E-01	0.0	9.8E-01	0.6	5.2E-01	0.4	7.5E-01
ENSMUST00000152540				-1.0	5.8E-01	0.9	6.9E-01	0.0	9.8E-01	-2.0	3.2E-01
ENSMUST00000153331				7.2	3.3E-05	3.0	2.4E-02	1.1	3.0E-01	0.1	8.5E-01
ENSMUST00000135845				7.2	3.3E-05	6.5	1.6E-03	-0.6	7.0E-01	-0.5	5.7E-01
ENSMUST00000152548				1.1	1.3E-01	1.2	1.8E-01	-0.2	7.8E-01	-0.3	7.0E-01
ENSMUST00000180453				7.2	1.2E-04	-4.0	2.9E-03	-0.8	1.2E-01	1.6	1.3E-01
ENSMUST00000152555	secretory carrier membrane protein 1 [Source:MGI Symbol;Acc:MGI:1349480]	Q3TSA8		-2.4	1.9E-01	2.1	3.4E-01	2.8	1.1E-01	-1.7	4.2E-01
ENSMUST00000152559				0.9	4.7E-01	3.2	9.1E-02	1.5	3.5E-01	-0.7	5.6E-01
ENSMUST00000155042				7.2	3.0E-05	5.0	8.2E-05	-0.1	8.5E-01	0.3	5.0E-01
ENSMUST00000152564	RIKEN cDNA 4932438A13 gene [Source:MGI Symbol;Acc:MGI:2444631]		A2AAE1	-3.6	1.3E-01	-4.4	3.5E-01	1.9	4.0E-01	2.7	5.5E-01
ENSMUST00000075496				7.2	2.8E-04	-3.2	1.0E-01	2.2	2.8E-02	2.2	2.3E-01
ENSMUST00000152566	phospholipid scramblase 3 [Source:MGI Symbol;Acc:MGI:1917560]	Q5F284		-1.8	1.2E-01	-2.8	1.4E-01	1.1	2.1E-01	2.2	2.5E-01
ENSMUST00000193631				7.2	4.6E-05	5.7	1.5E-03	-0.6	6.7E-01	-1.1	1.9E-01
ENSMUST00000117118				7.2	6.4E-04	-0.6	5.4E-01	0.3	6.5E-01	-1.2	2.4E-01
ENSMUST00000120853				7.2	2.0E-06	2.8	3.6E-01	-2.6	4.3E-01	4.0	1.1E-01
ENSMUST00000133994				7.2	8.0E-05	4.8	2.9E-04	0.2	7.8E-01	0.4	4.6E-01
ENSMUST00000168226				7.2	2.1E-05	4.8	1.9E-04	-0.4	6.3E-01	-0.9	1.3E-01
ENSMUST00000152580				2.4	6.9E-02	2.0	2.4E-01	-0.1	9.5E-01	0.3	7.8E-01
ENSMUST00000029124				7.2	3.8E-04	7.0	2.3E-04	-0.3	8.2E-01	0.7	3.2E-01
ENSMUST00000128440				7.2	3.4E-04	6.6	9.1E-04	-0.7	6.2E-01	0.6	4.2E-01
ENSMUST00000127388				7.2	4.3E-05	-2.0	1.4E-01	1.9	2.5E-02	-2.3	1.2E-01
ENSMUST00000152594	zinc finger and BTB domain containing 38 [Source:MGI Symbol;Acc:MGI:2442866]	Q3LR78		-0.2	6.2E-01	0.1	9.4E-01	0.5	2.6E-01	0.2	6.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000153099				7.2	1.8E-05	6.7	4.9E-04	3.3	2.1E-02	-1.0	1.7E-01
ENSMUST00000152605				2.8	7.3E-02	0.6	7.6E-01	0.6	7.5E-01	2.7	1.2E-01
ENSMUST00000174300				7.2	2.5E-05	-5.6	4.2E-04	-0.4	3.7E-01	-0.3	7.7E-01
ENSMUST00000185391				7.2	2.0E-04	1.6	2.8E-01	0.0	9.9E-01	1.4	2.5E-01
ENSMUST00000125559				7.2	4.6E-04	7.3	2.4E-04	0.0	1.0E+00	0.2	8.1E-01
ENSMUST00000152617				1.8	4.4E-01	7.7	3.4E-02	3.8	2.4E-01	-2.1	2.6E-01
ENSMUST00000152618	kinesin family member 1C [Source:MGI Symbol;Acc:MGI:1098260]	Q3V3Y9		0.1	9.4E-01	3.7	2.9E-02	1.7	1.9E-01	-1.9	1.4E-01
ENSMUST00000125381				7.2	6.3E-05	-5.4	6.0E-03	-1.0	2.1E-01	-1.2	4.9E-01
ENSMUST00000185936				7.2	2.7E-06	3.3	3.0E-03	-2.2	3.3E-02	-0.1	8.4E-01
ENSMUST00000132550				7.2	3.0E-05	6.6	2.3E-04	1.0	3.8E-01	0.8	1.8E-01
ENSMUST00000156792				7.2	1.3E-03	4.9	6.4E-03	0.7	5.9E-01	0.1	9.0E-01
ENSMUST00000168949				7.2	7.3E-06	0.7	3.4E-01	-0.5	3.3E-01	0.4	5.6E-01
ENSMUST00000152640				0.9	1.9E-01	1.9	3.6E-02	0.1	8.7E-01	-0.9	2.0E-01
ENSMUST00000121659				7.2	3.3E-06	7.1	3.2E-04	-0.7	6.2E-01	0.0	9.4E-01
ENSMUST00000118433				7.2	1.1E-04	5.1	3.5E-05	0.4	5.5E-01	0.3	5.4E-01
ENSMUST00000152658				0.0	9.9E-01	2.1	2.4E-01	1.6	2.9E-01	-0.5	7.1E-01
ENSMUST00000152659	oxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1 [Source:MGI Symbol;Acc:MGI	F7AIT6		-2.3	1.7E-01	-4.0	5.2E-02	-1.8	9.4E-02	-0.1	9.5E-01
ENSMUST00000152662				1.6	4.4E-01	-2.9	1.9E-01	-4.8	1.6E-02	-0.3	8.8E-01
ENSMUST00000152666				1.3	8.6E-02	1.2	1.8E-01	-0.3	6.5E-01	-0.3	7.4E-01
ENSMUST00000190471				7.2	8.2E-05	5.7	1.2E-04	-1.1	2.4E-01	0.8	1.6E-01
ENSMUST00000171054				7.2	4.7E-05	6.6	7.4E-05	0.0	9.8E-01	0.4	4.3E-01
ENSMUST00000152681	DDB1 and CUL4 associated factor 11 [Source:MGI Symbol;Acc:MGI:90168]	D6REI5		0.7	7.6E-01	0.1	9.7E-01	-1.0	6.5E-01	-0.4	9.0E-01
ENSMUST00000152682				-0.4	8.7E-01	0.7	8.4E-01	0.7	7.6E-01	-0.4	9.0E-01
ENSMUST00000189454				7.2	2.1E-03	-4.9	1.1E-01	0.5	7.0E-01	-0.6	8.5E-01
ENSMUST00000120298				7.2	5.9E-05	6.9	2.3E-02	-0.9	7.4E-01	-0.9	5.8E-01
ENSMUST00000194398				7.2	3.9E-06	5.4	1.9E-02	-0.5	8.2E-01	-0.6	6.1E-01
ENSMUST00000118680				7.2	1.7E-03	-4.6	8.4E-03	-0.8	2.9E-01	-1.1	4.5E-01
ENSMUST00000152701				0.7	7.6E-01	-1.6	5.9E-01	-1.3	4.8E-01	1.0	7.4E-01
ENSMUST00000149945				7.2	6.1E-05	6.1	1.8E-04	0.1	9.4E-01	-0.2	7.9E-01
ENSMUST00000152703	tumor necrosis factor receptor superfamily, member 23 [Source:MGI Symbol;Acc:MGI:1930269]	Q3U3F7	Q9ER63	-0.4	4.3E-01	-1.4	3.7E-02	-0.6	1.6E-01	0.4	4.9E-01
ENSMUST00000147083				7.2	4.6E-06	-9.0	2.3E-04	-0.3	5.0E-01	0.1	9.5E-01
ENSMUST00000142402				7.2	1.1E-04	-6.0	1.5E-04	-1.8	1.5E-03	-0.9	4.1E-01
ENSMUST00000152927				7.2	2.0E-03	-2.5	7.5E-03	0.6	1.9E-01	-1.0	2.4E-01
ENSMUST00000190474				7.2	1.2E-04	3.1	8.8E-02	-2.0	2.4E-01	0.0	9.7E-01
ENSMUST00000117765				7.2	3.5E-05	6.0	7.5E-04	-1.8	2.0E-01	-0.4	6.1E-01
ENSMUST00000128173				7.2	1.4E-04	2.3	8.3E-02	6.2	8.3E-05	-0.7	4.9E-01
ENSMUST00000152729				0.4	7.0E-01	-0.6	6.1E-01	-1.2	1.8E-01	-0.3	7.6E-01
ENSMUST00000128409				7.2	5.9E-06	3.3	9.2E-02	-0.6	7.1E-01	0.1	9.5E-01
ENSMUST00000134684				7.2	1.4E-04	4.8	3.7E-03	-0.2	9.0E-01	0.3	7.4E-01
ENSMUST00000151919				7.2	2.2E-04	-5.4	1.5E-02	-0.6	4.3E-01	0.6	7.5E-01
ENSMUST00000152747				-1.0	4.6E-01	1.5	3.7E-01	0.9	4.8E-01	-1.6	3.1E-01
ENSMUST00000137067				7.2	3.1E-05	6.6	1.5E-05	0.0	9.5E-01	0.3	4.9E-01
ENSMUST00000152753				-0.9	1.6E-01	-0.9	3.2E-01	0.4	5.2E-01	0.3	6.7E-01
ENSMUST00000154273				7.2	2.0E-05	-4.1	7.4E-03	-1.2	6.0E-02	-0.5	7.0E-01
ENSMUST00000140565				7.2	3.5E-05	6.4	4.9E-05	0.5	5.4E-01	0.1	8.6E-01
ENSMUST00000150423				7.2	3.4E-03	3.7	5.6E-02	-1.1	5.3E-01	-0.7	6.0E-01
ENSMUST00000188463				7.2	1.1E-05	3.8	3.7E-04	-1.1	1.3E-01	-0.2	7.4E-01
ENSMUST00000187707				7.2	2.0E-05	8.7	7.6E-04	1.0	5.8E-01	1.5	8.6E-02
ENSMUST00000132781				7.2	4.9E-04	-2.3	4.3E-02	-1.1	1.0E-01	-1.6	2.0E-01
ENSMUST00000189824				7.2	4.3E-05	5.9	1.1E-03	-0.5	7.2E-01	-0.4	6.0E-01
ENSMUST00000123651				7.2	1.0E-03	1.6	5.5E-02	-1.7	2.8E-02	0.9	1.9E-01
ENSMUST00000152783	RIKEN cDNA 2410004B18 gene [Source:MGI Symbol;Acc:MGI:1913671]	F6XV67		2.1	3.0E-01	-3.1	2.5E-01	-3.5	4.6E-02	1.7	5.3E-01
ENSMUST00000186157				7.2	5.5E-04	4.8	7.7E-04	-1.4	1.7E-01	0.4	5.4E-01
ENSMUST00000124143				7.2	4.5E-05	5.5	2.1E-04	-1.1	2.8E-01	0.2	7.3E-01
ENSMUST00000172004				7.2	4.6E-05	3.8	2.8E-02	0.4	7.5E-01	0.9	3.3E-01
ENSMUST00000152796	YTH domain family 2 [Source:MGI Symbol;Acc:MGI:2444233]		Q91YT7	-0.5	4.0E-01	1.5	9.8E-02	1.7	2.5E-02	-0.3	6.6E-01
ENSMUST00000174201				7.2	1.0E-05	6.9	1.5E-03	0.7	6.4E-01	1.6	1.2E-01
ENSMUST00000108257				7.2	3.6E-05	3.0	5.7E-03	-1.0	2.2E-01	-0.4	6.0E-01
ENSMUST00000152805	adducin 1 (alpha) [Source:MGI Symbol;Acc:MGI:87918]	F6RDR0		-4.5	2.1E-01	-0.9	7.9E-01	0.4	8.7E-01	-3.3	3.8E-01
ENSMUST00000155239				7.2	1.5E-04	3.5	3.3E-03	-1.4	1.4E-01	0.0	9.7E-01
ENSMUST00000152807				2.2	6.0E-02	1.9	2.6E-01	0.9	5.3E-01	1.2	3.1E-01
ENSMUST00000167648				7.2	6.4E-04	7.9	1.0E-04	-0.6	6.4E-01	-0.6	3.6E-01
ENSMUST00000183157				7.2	5.7E-07	-2.7	1.9E-01	0.8	4.9E-01	-0.1	9.6E-01
ENSMUST00000154325				7.2	5.0E-05	6.1	8.3E-04	-2.6	1.3E-01	0.1	9.2E-01
ENSMUST00000176181				7.2	1.7E-04	6.0	5.8E-03	0.0	9.8E-01	0.3	7.3E-01
ENSMUST00000185696				7.2	4.9E-05	5.5	6.5E-03	-0.7	7.0E-01	-0.5	6.3E-01
ENSMUST00000152830	special AT-rich sequence binding protein 1 [Source:MGI Symbol;Acc:MGI:105084]		Q60611	1.5	4.4E-02	2.5	1.1E-02	0.6	3.8E-01	-0.4	5.3E-01
ENSMUST00000127510				7.2	2.3E-04	7.1	1.0E-04	-0.5	6.9E-01	0.7	2.2E-01
ENSMUST00000152833				2.2	3.5E-01	-3.1	2.0E-01	-5.4	1.6E-02	-0.1	9.5E-01
ENSMUST00000147657				7.2	1.1E-05	4.4	7.4E-03	-0.3	7.8E-01	0.4	7.2E-01
ENSMUST00000159525				7.1	2.6E-05	2.3	1.1E-01	6.0	2.0E-04	-0.7	5.2E-01
ENSMUST00000134609				7.1	7.5E-06	7.1	5.1E-04	-0.6	6.8E-01	-0.4	5.5E-01
ENSMUST00000152853	nuclear receptor subfamily 3, group C, member 1 [Source:MGI Symbol;Acc:MGI:95824]	E9Q310		-1.1	4.0E-01	-0.1	9.4E-01	0.2	8.5E-01	-0.8	6.0E-01
ENSMUST00000121786				7.1	1.7E-05	-2.2	7.5E-03	0.0	9.8E-01	-0.5	4.3E-01
ENSMUST00000126108				7.1	5.8E-04	6.4	1.4E-04	0.5	6.3E-01	-1.2	5.7E-02
ENSMUST00000126285				7.1	1.1E-05	-3.9	2.0E-03	-0.6	1.7E-01	-1.8	1.1E-01
ENSMUST00000141059				7.1	1.1E-05	-6.6	6.5E-04	-3.6	1.6E-04	0.5	7.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000152878	matrix metallopeptidase 27 [Source:MGI Symbol;Acc:MGI:3039232]	F6QKX8		0.8	6.8E-01	-0.6	7.5E-01	-1.8	3.0E-01	-0.4	8.4E-01
ENSMUST00000152882				1.4	1.1E-01	-0.1	9.1E-01	-0.6	4.6E-01	0.9	3.1E-01
ENSMUST00000143938				7.1	9.4E-05	6.0	2.0E-04	-0.5	6.2E-01	0.3	5.6E-01
ENSMUST00000183234				7.1	2.8E-05	3.2	1.5E-02	-2.2	9.6E-02	0.3	7.4E-01
ENSMUST00000152888				-1.3	2.5E-01	1.6	2.4E-01	1.2	2.6E-01	-1.6	1.9E-01
ENSMUST00000133305				7.1	3.2E-05	5.4	7.6E-04	-0.9	4.1E-01	-0.4	5.9E-01
ENSMUST00000152894				4.1	1.2E-01	7.7	4.3E-02	1.3	7.0E-01	-2.2	2.6E-01
ENSMUST00000146565				7.1	9.8E-05	8.3	3.8E-05	-0.1	9.2E-01	-0.9	1.3E-01
ENSMUST00000117827				7.1	1.4E-05	6.0	1.8E-03	0.7	6.2E-01	-0.6	4.9E-01
ENSMUST00000152912				-1.5	2.7E-01	-2.9	2.2E-01	0.6	6.9E-01	2.0	3.7E-01
ENSMUST00000144398				7.1	2.2E-04	6.8	1.8E-05	0.0	9.7E-01	0.0	9.6E-01
ENSMUST00000152918				-0.3	7.8E-01	0.3	8.0E-01	-0.8	4.8E-01	-1.5	2.8E-01
ENSMUST00000152919	RNA binding motif protein 39 [Source:MGI Symbol;Acc:MGI:2157953]	D6RCZ8		-2.5	4.4E-02	-3.9	8.5E-03	-2.7	3.0E-03	-1.3	3.5E-01
ENSMUST00000182426				7.1	2.4E-06	5.2	1.2E-02	0.0	9.8E-01	-0.8	5.0E-01
ENSMUST00000124242				7.1	9.0E-04	5.7	3.8E-02	-0.6	8.1E-01	0.9	5.2E-01
ENSMUST00000123695				7.1	1.2E-04	5.5	1.8E-03	-1.0	4.8E-01	-0.4	6.2E-01
ENSMUST00000067705				7.1	8.9E-04	6.8	2.2E-04	0.0	9.9E-01	0.1	8.7E-01
ENSMUST00000147909				7.1	1.6E-04	4.9	4.6E-03	0.7	5.9E-01	-1.3	1.6E-01
ENSMUST00000179984				7.1	1.2E-04	1.3	1.5E-01	0.1	8.7E-01	0.8	2.7E-01
ENSMUST00000183161				7.1	4.1E-05	-5.9	1.3E-03	0.6	2.0E-01	0.9	5.3E-01
ENSMUST00000152954	histidyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:1918041]		Q99KK9	-1.2	9.5E-02	-1.3	1.6E-01	0.6	3.5E-01	0.7	4.4E-01
ENSMUST00000138546				7.1	2.3E-04	1.5	1.1E-01	0.0	9.6E-01	0.3	7.2E-01
ENSMUST00000146403				7.1	5.2E-05	6.3	5.9E-04	-1.1	4.0E-01	0.8	2.6E-01
ENSMUST00000122827				7.1	3.8E-05	5.8	5.5E-04	-0.6	6.3E-01	-0.3	6.9E-01
ENSMUST00000140235				7.1	1.0E-03	-1.7	2.7E-01	2.2	2.5E-02	-0.6	7.0E-01
ENSMUST00000152966	transmembrane protein 198b [Source:MGI Symbol;Acc:MGI:1921077]	D6RES3		1.5	1.2E-01	1.5	2.5E-01	0.3	7.2E-01	0.3	7.5E-01
ENSMUST00000152967				-0.5	4.5E-01	-0.5	5.0E-01	-1.8	1.3E-02	-1.8	3.6E-02
ENSMUST00000152970				0.5	4.5E-01	1.1	2.0E-01	-0.4	5.4E-01	-1.0	2.2E-01
ENSMUST00000123037				7.1	2.6E-06	-1.1	3.3E-01	-6.2	1.5E-03	1.8	1.2E-01
ENSMUST00000152981	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha [Source:MGI Symbol;Acc:MGI:1298206]	F6RJE8		1.2	5.3E-01	1.3	6.6E-01	0.2	9.0E-01	0.2	9.5E-01
ENSMUST00000152982				1.9	4.2E-02	2.6	1.5E-02	-0.5	5.4E-01	-1.3	1.2E-01
ENSMUST00000152983	calpain 10 [Source:MGI Symbol;Acc:MGI:1344392]	D6RGR0		0.0	9.8E-01	-0.6	6.6E-01	0.5	6.5E-01	1.0	4.4E-01
ENSMUST00000152985				4.7	5.1E-02	4.3	8.7E-02	-1.9	4.2E-01	-1.4	4.2E-01
ENSMUST00000119097				7.1	5.0E-05	4.3	1.7E-03	-0.2	8.3E-01	0.4	5.7E-01
ENSMUST00000123393				7.1	7.2E-06	5.3	4.6E-05	0.3	6.6E-01	0.7	1.3E-01
ENSMUST00000140593				7.1	3.1E-03	6.5	8.9E-05	-0.5	5.9E-01	0.3	5.1E-01
ENSMUST00000190711				7.1	9.3E-06	5.8	1.9E-03	-0.7	6.5E-01	-0.1	8.5E-01
ENSMUST00000153018				-1.1	1.5E-01	-0.8	4.4E-01	0.6	4.1E-01	0.3	7.9E-01
ENSMUST00000155458				7.1	5.4E-05	8.8	1.6E-04	0.3	8.5E-01	0.0	9.5E-01
ENSMUST00000142824				7.1	1.1E-05	8.2	1.9E-04	0.8	5.4E-01	1.3	6.2E-02
ENSMUST00000119513				7.1	3.2E-03	-2.0	2.2E-01	-0.3	7.7E-01	-3.2	1.4E-01
ENSMUST00000128985				7.1	2.8E-05	5.4	2.6E-04	-1.4	1.8E-01	-0.2	7.0E-01
ENSMUST00000153054				1.3	2.1E-01	1.0	4.1E-01	-0.8	4.5E-01	-0.4	6.8E-01
ENSMUST00000147716				7.1	2.1E-05	-7.9	3.1E-05	-0.7	5.1E-02	-0.6	5.9E-01
ENSMUST00000153065	RIKEN cDNA 4833439L19 gene [Source:MGI Symbol;Acc:MGI:1921162]	D3Z1F7		-3.3	5.2E-02	-1.9	3.7E-01	2.2	1.2E-01	0.7	7.3E-01
ENSMUST00000153067				-1.7	9.3E-02	1.3	2.3E-01	1.0	2.5E-01	-2.0	7.0E-02
ENSMUST00000153070	solute carrier family 25, member 36 [Source:MGI Symbol;Acc:MGI:1924909]	D6RH79		2.8	2.0E-01	0.8	7.7E-01	-0.8	7.0E-01	1.1	6.7E-01
ENSMUST00000188838				7.1	5.0E-05	-2.4	2.1E-01	0.2	8.4E-01	-1.2	5.4E-01
ENSMUST00000195043				7.1	2.9E-06	3.1	1.9E-01	-2.1	3.6E-01	-0.1	9.6E-01
ENSMUST00000153076	sperm associated antigen 9 [Source:MGI Symbol;Acc:MGI:1918084]	Z4YMB8		-3.2	6.8E-02	-5.7	1.1E-01	0.2	8.5E-01	2.7	4.2E-01
ENSMUST00000153077				1.1	4.2E-01	-0.5	7.6E-01	-0.6	6.5E-01	1.0	5.3E-01
ENSMUST00000195307				7.1	8.3E-05	2.1	1.4E-02	-0.1	8.6E-01	-0.4	4.7E-01
ENSMUST00000173442				7.1	1.0E-05	-1.7	1.5E-01	1.7	3.7E-02	-0.1	8.9E-01
ENSMUST00000180296				7.1	1.0E-05	7.1	5.6E-04	0.3	8.5E-01	-0.2	7.9E-01
ENSMUST00000116171				7.1	6.6E-05	2.8	4.6E-04	-0.1	7.9E-01	-0.5	2.2E-01
ENSMUST00000132030				7.1	8.5E-05	5.7	9.7E-04	-0.9	4.9E-01	-0.8	3.4E-01
ENSMUST00000142471				7.1	5.7E-05	5.7	1.1E-03	2.9	3.1E-02	-0.5	4.8E-01
ENSMUST00000194713				7.1	2.5E-06	5.5	2.3E-04	-1.2	2.2E-01	0.4	4.8E-01
ENSMUST00000153101				0.8	7.9E-01	-1.6	5.6E-01	-3.9	1.3E-01	-1.5	6.2E-01
ENSMUST00000117457				7.1	1.0E-04	-4.6	1.2E-03	0.2	6.0E-01	-0.6	5.8E-01
ENSMUST00000153109				1.0	2.7E-01	1.9	1.1E-01	0.2	8.1E-01	-0.6	5.0E-01
ENSMUST00000134240				7.1	4.0E-05	4.9	5.1E-03	-0.5	6.8E-01	-0.8	3.7E-01
ENSMUST00000165409				7.1	1.2E-04	-2.2	6.9E-02	1.9	9.6E-03	0.5	6.6E-01
ENSMUST00000141184				7.1	2.7E-06	-1.4	1.2E-01	0.6	2.8E-01	-0.9	3.0E-01
ENSMUST00000188227				7.1	3.8E-05	6.9	7.3E-04	-0.7	6.4E-01	-0.1	8.6E-01
ENSMUST00000193331				7.1	6.2E-05	5.9	2.9E-03	-0.6	7.1E-01	-0.6	4.9E-01
ENSMUST00000130877				7.1	6.6E-06	2.5	3.7E-02	-0.3	7.3E-01	1.2	1.6E-01
ENSMUST00000131281				7.1	2.6E-05	5.5	2.7E-05	-2.1	2.4E-02	0.2	6.9E-01
ENSMUST00000162889				7.1	4.7E-05	5.8	1.0E-02	-0.7	7.3E-01	-1.3	3.1E-01
ENSMUST00000153128	cyclin M4 [Source:MGI Symbol;Acc:MGI:2151060]		Q69ZF7	-0.3	5.4E-01	0.5	4.9E-01	1.0	9.5E-02	0.2	8.2E-01
ENSMUST00000153136	bromodomain adjacent to zinc finger domain, 2B [Source:MGI Symbol;Acc:MGI:2442782]	A2AUY3		-2.2	8.4E-02	-0.1	9.6E-01	0.5	5.5E-01	-1.6	2.9E-01
ENSMUST00000120800				7.1	9.6E-06	5.8	4.5E-03	-1.1	5.1E-01	-0.3	7.2E-01
ENSMUST00000132250				7.1	5.4E-05	5.1	1.0E-02	-0.7	6.9E-01	1.6	1.3E-01
ENSMUST00000153152				-0.7	8.0E-01	-0.7	8.3E-01	-0.9	7.2E-01	-0.9	7.6E-01
ENSMUST00000153154				1.5	3.1E-01	-1.0	6.1E-01	-0.4	7.8E-01	2.1	2.6E-01
ENSMUST00000143089				7.1	5.1E-05	1.9	1.2E-01	-1.3	2.5E-01	-0.3	7.9E-01
ENSMUST00000153159				0.3	6.6E-01	0.7	3.6E-01	-0.3	6.1E-01	-0.8	3.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000156423				7.1	5.4E-05	5.3	1.0E-03	-0.6	6.5E-01	0.4	5.7E-01
ENSMUST00000133262				7.1	3.2E-05	5.1	1.1E-03	0.5	6.2E-01	0.0	9.8E-01
ENSMUST00000153162				2.4	4.8E-02	2.9	1.0E-01	0.9	5.6E-01	0.4	7.4E-01
ENSMUST00000155148				7.1	4.1E-04	3.6	1.8E-03	0.9	2.2E-01	-0.5	4.4E-01
ENSMUST00000153165	AF4/FMR2 family, member 1 [Source:MGI Symbol;Acc:MGI:1100819]	B1AVP1		3.5	5.3E-02	3.1	1.3E-01	-1.1	5.4E-01	-0.7	6.4E-01
ENSMUST00000134058				7.1	5.1E-05	3.2	2.8E-04	-2.3	3.4E-03	-0.3	4.3E-01
ENSMUST00000135000				7.1	8.4E-04	2.8	1.8E-01	-1.7	3.6E-01	-0.2	8.9E-01
ENSMUST00000153179				0.8	4.8E-01	1.5	2.9E-01	0.3	8.1E-01	-0.5	6.8E-01
ENSMUST00000123946				7.1	7.8E-04	7.4	5.8E-04	-1.1	4.7E-01	1.0	2.1E-01
ENSMUST00000153183	transducin (beta)-like 2 [Source:MGI Symbol;Acc:MGI:1351652]		Q9R099	1.2	5.7E-02	1.7	5.1E-02	0.4	5.5E-01	-0.1	8.8E-01
ENSMUST00000149795				7.1	7.8E-05	6.8	1.4E-02	-0.7	7.7E-01	-2.2	1.5E-01
ENSMUST00000128196				7.1	2.8E-04	4.7	5.2E-03	-1.6	2.7E-01	0.1	8.8E-01
ENSMUST00000153187				-0.2	9.5E-01	-1.6	6.8E-01	-1.3	6.1E-01	0.1	9.7E-01
ENSMUST00000153191	chitinase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915288]		Q922Q9	-4.1	9.9E-02	-3.4	3.4E-01	0.5	8.1E-01	-0.2	9.6E-01
ENSMUST00000156447				7.1	2.3E-03	6.2	1.1E-03	-0.6	7.0E-01	0.5	5.3E-01
ENSMUST00000153193	SEC11 homolog C, signal peptidase complex subunit [Source:MGI Symbol;Acc:MGI:1913536]	D3Z5H3		2.3	7.5E-02	-5.2	1.2E-03	-7.2	2.7E-05	0.3	7.8E-01
ENSMUST00000144625				7.1	3.4E-05	4.4	5.7E-02	0.1	9.5E-01	1.0	4.7E-01
ENSMUST00000153197	MPN domain containing [Source:MGI Symbol;Acc:MGI:1915297]	F7BQ76		-2.7	9.0E-02	0.3	8.9E-01	2.0	2.4E-01	-0.9	5.9E-01
ENSMUST00000173919				7.1	6.7E-05	-3.8	6.9E-03	-1.4	5.5E-02	-1.0	3.9E-01
ENSMUST00000149117				7.1	3.1E-05	-4.4	6.1E-03	-0.7	2.5E-01	0.1	9.7E-01
ENSMUST00000194681				7.1	1.9E-04	4.5	1.6E-03	0.5	6.0E-01	-0.2	7.5E-01
ENSMUST00000142639				7.1	7.0E-05	5.0	1.9E-02	0.6	7.2E-01	0.8	5.2E-01
ENSMUST00000153218	hemoglobin, beta adult s chain [Source:MGI Symbol;Acc:MGI:5474852]	E9Q223		2.1	3.5E-01	-1.6	5.3E-01	-3.9	6.9E-02	-0.2	9.4E-01
ENSMUST00000146429				7.1	6.0E-05	3.6	2.3E-03	-0.5	5.3E-01	-0.5	4.8E-01
ENSMUST00000153222	leucine rich repeat containing 61 [Source:MGI Symbol;Acc:MGI:2652848]	D3Z0E0		-1.3	1.7E-01	-0.8	4.8E-01	0.3	6.4E-01	-0.2	8.7E-01
ENSMUST00000168914				7.1	3.1E-05	3.5	1.5E-02	-1.8	1.7E-01	0.3	7.3E-01
ENSMUST00000153230				-1.7	1.2E-01	-0.6	6.9E-01	1.1	2.7E-01	-0.1	9.6E-01
ENSMUST00000190979				7.1	3.6E-05	-3.7	5.2E-02	0.4	6.4E-01	-0.1	9.6E-01
ENSMUST00000173045				7.1	3.8E-05	5.0	1.1E-04	0.8	2.8E-01	-0.5	3.1E-01
ENSMUST00000120883				7.1	3.5E-05	1.8	2.1E-01	-0.3	8.1E-01	1.6	1.8E-01
ENSMUST00000153244				-0.9	1.9E-01	-2.5	4.6E-02	-0.1	8.2E-01	1.5	1.8E-01
ENSMUST00000156384				7.1	3.4E-04	-2.4	3.0E-02	0.9	1.2E-01	-1.5	1.8E-01
ENSMUST00000153246				-0.3	7.8E-01	-1.7	1.9E-01	-1.6	1.2E-01	-0.2	8.8E-01
ENSMUST00000136957				7.1	1.9E-04	8.0	1.8E-02	-0.6	8.5E-01	-1.8	2.6E-01
ENSMUST00000153255				1.1	2.0E-01	1.2	3.0E-01	0.5	5.6E-01	0.4	6.5E-01
ENSMUST00000153256	PDZ domain containing 1 [Source:MGI Symbol;Acc:MGI:1928901]			5.7	5.6E-02	5.3	9.7E-02	-0.7	8.3E-01	-0.3	8.8E-01
ENSMUST00000135898				7.1	5.2E-05	5.5	1.3E-03	0.8	4.6E-01	-0.8	3.1E-01
ENSMUST00000149725				7.1	4.4E-03	9.6	5.0E-05	-0.8	5.9E-01	0.5	3.6E-01
ENSMUST00000133879				7.1	4.4E-05	3.7	4.5E-03	-0.5	6.2E-01	-0.2	7.8E-01
ENSMUST00000151561				7.1	2.0E-04	4.9	6.0E-03	0.6	6.5E-01	0.6	4.6E-01
ENSMUST00000137178				7.1	1.6E-04	5.9	2.8E-05	0.7	3.7E-01	0.4	4.4E-01
ENSMUST00000133554				7.1	4.4E-05	-4.9	1.2E-02	1.1	1.6E-01	-2.5	2.3E-01
ENSMUST00000145169				7.1	1.4E-04	-2.0	1.1E-01	-5.4	6.0E-04	0.8	4.8E-01
ENSMUST00000176692				7.1	4.0E-07	6.3	1.2E-03	0.2	8.6E-01	-0.6	4.5E-01
ENSMUST00000153309				0.4	6.7E-01	1.5	2.1E-01	1.4	1.5E-01	0.3	7.7E-01
ENSMUST00000153310				0.4	7.9E-01	-1.8	3.2E-01	-2.6	9.2E-02	-0.4	7.9E-01
ENSMUST00000153312				1.3	2.9E-01	4.7	1.0E-03	-0.5	6.0E-01	-4.0	3.0E-03
ENSMUST00000153314	glutathione S-transferase, mu 1 [Source:MGI Symbol;Acc:MGI:95860]	F6WHQ7		2.0	2.0E-01	5.9	1.4E-02	2.2	2.7E-01	-1.8	1.7E-01
ENSMUST00000134568				7.1	6.4E-07	0.0	9.7E-01	3.6	3.0E-03	-0.3	8.3E-01
ENSMUST00000153320	voltage-dependent anion channel 2 [Source:MGI Symbol;Acc:MGI:106915]	D3YZT5		-0.7	7.7E-01	-7.3	5.0E-02	-5.7	6.0E-03	0.9	8.0E-01
ENSMUST00000159650				7.1	1.8E-04	7.9	1.2E-03	-0.1	9.6E-01	1.7	7.8E-02
ENSMUST00000193299				7.1	2.7E-04	7.1	7.5E-05	-0.6	6.2E-01	-0.5	4.3E-01
ENSMUST00000120504				7.1	3.7E-04	5.5	4.6E-03	0.3	8.4E-01	-0.6	5.3E-01
ENSMUST00000118872				7.1	6.5E-05	2.3	3.0E-02	0.3	6.5E-01	0.3	7.2E-01
ENSMUST00000137897				7.1	4.1E-05	-5.0	3.9E-03	-1.0	1.3E-01	0.1	9.6E-01
ENSMUST00000139491				7.1	6.7E-05	6.5	1.1E-04	0.8	4.2E-01	-0.6	3.0E-01
ENSMUST00000144837				7.1	6.7E-05	6.0	2.0E-03	-0.6	7.1E-01	-2.0	5.2E-02
ENSMUST00000153359				0.6	3.9E-01	1.0	2.9E-01	0.5	4.4E-01	0.1	8.9E-01
ENSMUST00000170429				7.1	2.8E-05	-3.8	2.3E-02	-0.1	8.6E-01	-1.5	3.4E-01
ENSMUST00000136655				7.1	1.5E-04	4.4	3.4E-02	-0.6	7.1E-01	-0.5	6.5E-01
ENSMUST00000098551				7.1	7.2E-05	6.5	9.8E-04	-0.1	9.6E-01	-1.7	5.7E-02
ENSMUST00000136812				7.1	6.1E-05	5.5	2.3E-05	0.0	1.0E+00	-0.1	7.8E-01
ENSMUST00000166052				7.1	1.3E-04	-1.5	3.3E-01	0.6	5.6E-01	-0.9	5.6E-01
ENSMUST00000153377	mesoderm development candidate 2 [Source:MGI Symbol;Acc:MGI:1891421]	F6SWV4		1.5	1.0E-01	2.8	3.4E-02	1.0	3.5E-01	-0.3	7.1E-01
ENSMUST00000130572				7.1	1.2E-04	2.7	2.4E-02	-1.5	1.6E-01	-0.9	3.1E-01
ENSMUST00000176734				7.1	5.2E-05	2.4	1.0E-01	0.0	1.0E+00	1.3	2.3E-01
ENSMUST00000165944				7.1	8.3E-04	7.2	3.2E-04	-1.0	4.9E-01	-0.2	7.5E-01
ENSMUST00000153386				5.3	8.0E-02	0.9	7.8E-01	-3.7	2.2E-01	0.6	8.3E-01
ENSMUST00000153394	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) [Source:MGI Symbol;Acc:MGI:2140356]	A2A7A8		-0.6	6.4E-01	0.0	9.8E-01	-0.3	7.8E-01	-0.8	5.7E-01
ENSMUST00000153395				-2.2	1.8E-01	-2.0	3.0E-01	-0.6	6.3E-01	-0.8	6.6E-01
ENSMUST00000166043				7.1	2.4E-04	6.2	1.1E-02	-0.1	9.7E-01	1.8	1.6E-01
ENSMUST00000187490				7.1	1.1E-05	-2.6	5.4E-02	-0.7	3.1E-01	-1.3	3.3E-01
ENSMUST00000179730				7.1	1.6E-04	7.4	2.7E-05	-0.2	8.5E-01	-0.1	8.0E-01
ENSMUST00000182335				7.1	8.5E-05	6.2	1.4E-03	-2.6	1.3E-01	-0.4	5.8E-01
ENSMUST00000153425	Sfi1 homolog, spindle assembly associated (yeast) [Source:MGI Symbol;Acc:MGI:1926137]	E9Q8V3		2.1	3.7E-01	1.8	6.8E-01	2.7	4.3E-01	3.0	3.6E-01
ENSMUST00000190406				7.1	1.8E-04	3.6	1.4E-02	-1.7	2.1E-01	0.5	5.5E-01
ENSMUST00000153428	PHD finger protein 12 [Source:MGI Symbol;Acc:MGI:1924057]	Q5SS87		-3.7	5.3E-02	-0.5	8.0E-01	2.2	1.4E-01	-1.0	6.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000146888				7.1	3.1E-06	4.1	5.5E-03	-1.7	1.5E-01	-0.2	7.5E-01
ENSMUST00000153437				-0.3	8.1E-01	2.3	1.0E-01	0.9	4.5E-01	-1.7	1.3E-01
ENSMUST00000176985				7.1	1.8E-02	4.4	1.5E-04	-0.4	5.1E-01	-0.5	3.4E-01
ENSMUST00000191777				7.1	2.7E-05	7.0	2.9E-04	0.0	9.8E-01	0.0	9.8E-01
ENSMUST00000153440	BRCA1-associated ATM activator 1 [Source:MGI Symbol;Acc:MGI:1891679]	D6RE40		0.7	8.4E-01	-3.6	3.6E-01	-5.1	4.7E-02	-0.8	8.4E-01
ENSMUST00000123496				7.1	2.8E-02	-5.6	1.3E-02	0.4	5.9E-01	0.3	8.6E-01
ENSMUST00000182582				7.1	2.6E-05	3.7	1.3E-04	-0.5	3.4E-01	-0.3	4.9E-01
ENSMUST00000128783				7.1	7.6E-05	7.1	1.4E-03	0.0	9.9E-01	-0.5	5.8E-01
ENSMUST00000153459				0.6	8.0E-01	0.4	8.4E-01	-1.4	4.4E-01	-1.3	5.7E-01
ENSMUST00000153462	potassium channel tetramerisation domain containing 20 [Source:MGI Symbol;Acc:MGI:1914239]	B2KF10		0.6	6.8E-01	0.1	9.5E-01	-0.3	8.2E-01	0.2	9.3E-01
ENSMUST00000153470	lethal, Chr 7, Rinchik 6 [Source:MGI Symbol;Acc:MGI:96738]		Q9DD02	2.0	1.3E-01	2.8	6.0E-02	-0.7	5.5E-01	-1.5	2.1E-01
ENSMUST00000153472				-1.9	9.6E-02	-1.2	3.3E-01	0.0	9.5E-01	-0.7	5.6E-01
ENSMUST00000153476	arylalkylamine N-acetyltransferase [Source:MGI Symbol;Acc:MGI:1328365]	Q14A64	O88816	4.2	4.1E-02	5.1	7.2E-02	1.3	5.9E-01	0.3	8.5E-01
ENSMUST00000153480	TATA box binding protein [Source:MGI Symbol;Acc:MGI:101838]	F6XYI9		-1.7	1.4E-01	-2.2	2.7E-01	1.5	1.9E-01	2.0	2.9E-01
ENSMUST00000153485	xylosyltransferase II [Source:MGI Symbol;Acc:MGI:2444797]	F2Z436		2.7	7.6E-02	6.0	1.8E-03	-0.2	8.8E-01	-3.5	9.1E-03
ENSMUST00000135586				7.1	6.9E-05	0.0	9.9E-01	1.1	2.2E-01	-2.4	6.4E-02
ENSMUST00000153498				-2.1	9.4E-02	1.5	3.3E-01	1.9	8.9E-02	-1.7	2.6E-01
ENSMUST00000153499	seryl-aminoacyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:102809]	A2AFS1		-2.2	4.2E-02	-1.5	2.4E-01	0.5	4.7E-01	-0.2	9.0E-01
ENSMUST00000153500	P450 (cytochrome) oxidoreductase [Source:MGI Symbol;Acc:MGI:97744]	E9Q997		-1.8	2.6E-01	0.7	7.3E-01	1.1	4.7E-01	-1.4	4.6E-01
ENSMUST00000143866				7.1	7.1E-05	-3.8	2.7E-02	-0.3	6.2E-01	0.0	9.7E-01
ENSMUST00000174043				7.1	1.1E-07	4.0	8.5E-03	0.1	9.3E-01	-0.2	8.0E-01
ENSMUST00000153506	coiled-coil domain containing 109B [Source:MGI Symbol;Acc:MGI:1914065]	D6RIL8		-1.4	5.2E-01	-4.9	1.1E-01	-3.0	6.7E-02	0.5	8.6E-01
ENSMUST00000059118				7.1	2.0E-05	5.6	5.3E-03	-0.2	9.0E-01	-1.1	2.9E-01
ENSMUST00000153510	zinc finger protein 692 [Source:MGI Symbol;Acc:MGI:2144276]		Q3U381	-2.5	4.3E-01	-1.5	6.1E-01	-1.2	5.8E-01	-2.1	5.3E-01
ENSMUST00000122296				7.1	6.8E-05	-7.4	9.1E-03	-0.4	5.9E-01	-1.1	6.8E-01
ENSMUST00000189730				7.1	4.2E-07	-2.3	2.5E-01	1.4	2.0E-01	-0.6	7.6E-01
ENSMUST00000189085				7.1	5.0E-05	5.6	3.0E-03	-0.7	6.5E-01	1.3	1.5E-01
ENSMUST00000126975				7.1	3.5E-05	-8.0	8.7E-03	-3.2	1.4E-02	-0.8	7.8E-01
ENSMUST00000153525				0.9	6.2E-01	4.8	4.9E-02	1.0	6.3E-01	-2.9	1.1E-01
ENSMUST00000153526				5.4	5.0E-02	2.8	2.2E-01	-4.7	6.6E-02	-2.1	3.2E-01
ENSMUST00000143969				7.1	6.7E-05	-6.3	8.9E-03	-0.5	4.7E-01	0.3	8.9E-01
ENSMUST00000153531				1.5	2.2E-01	0.7	6.1E-01	-0.4	7.5E-01	0.4	7.7E-01
ENSMUST00000142164				7.1	2.7E-05	5.3	3.6E-04	-1.3	2.5E-01	0.3	6.6E-01
ENSMUST00000160807				7.1	4.7E-05	-5.0	1.0E-03	-0.7	1.3E-01	-0.6	6.1E-01
ENSMUST00000117166				7.1	5.9E-05	-5.0	1.6E-02	0.5	5.3E-01	-1.0	5.8E-01
ENSMUST00000125041				7.1	7.7E-05	-4.3	5.5E-03	-2.0	1.1E-02	-2.3	1.3E-01
ENSMUST00000153558	secretory carrier membrane protein 1 [Source:MGI Symbol;Acc:MGI:1349480]	Q3TSA8		-1.5	6.5E-01	-5.2	2.7E-01	-2.6	2.5E-01	1.1	8.2E-01
ENSMUST00000133611				7.1	2.2E-04	5.8	3.6E-04	-0.6	6.2E-01	0.7	2.4E-01
ENSMUST00000188174				7.1	8.5E-05	2.3	9.4E-03	-0.4	5.2E-01	0.0	9.7E-01
ENSMUST00000138435				7.1	1.7E-05	4.5	9.5E-03	-0.5	7.0E-01	1.4	1.5E-01
ENSMUST00000132720				7.1	6.6E-07	2.5	2.2E-02	-1.8	6.3E-02	0.2	7.5E-01
ENSMUST00000189189				7.1	6.7E-05	-4.7	1.1E-03	0.4	3.0E-01	-0.6	5.6E-01
ENSMUST00000153578				2.3	5.2E-02	3.9	2.0E-02	0.7	5.8E-01	-0.9	3.3E-01
ENSMUST00000089221				7.1	6.5E-04	4.5	5.5E-03	0.4	7.6E-01	1.2	1.5E-01
ENSMUST00000153590	ribosomal protein L5 [Source:MGI Symbol;Acc:MGI:102854]	D3YYV8		2.9	4.1E-02	4.4	2.2E-02	0.4	7.8E-01	-1.0	3.7E-01
ENSMUST00000137576				7.1	1.2E-04	-5.9	6.0E-04	0.9	5.3E-02	-0.7	5.7E-01
ENSMUST00000129203				7.1	4.4E-06	-1.8	2.8E-02	0.8	1.1E-01	-0.5	4.6E-01
ENSMUST00000153604				-0.8	4.7E-01	-1.4	3.0E-01	-1.0	3.2E-01	-0.4	7.7E-01
ENSMUST00000132174				7.1	4.9E-05	-3.8	9.3E-03	-1.1	1.1E-01	0.2	8.4E-01
ENSMUST00000153611				-0.5	8.7E-01	-6.3	1.6E-01	-4.5	5.5E-02	1.3	7.7E-01
ENSMUST00000161979				7.1	1.2E-04	4.2	1.4E-01	-0.7	7.7E-01	1.0	5.7E-01
ENSMUST00000186005				7.1	8.5E-05	5.2	8.4E-03	-0.3	8.3E-01	-0.8	4.5E-01
ENSMUST00000118291				7.0	1.6E-04	3.8	3.9E-03	-0.2	8.3E-01	-0.7	4.2E-01
ENSMUST00000183029				7.0	4.1E-05	1.1	3.5E-01	-1.0	2.8E-01	0.8	4.3E-01
ENSMUST00000146365				7.0	6.5E-06	4.0	3.4E-03	0.4	6.9E-01	-0.7	3.4E-01
ENSMUST00000176409				7.0	8.5E-06	4.7	9.0E-03	-0.5	7.3E-01	1.2	2.1E-01
ENSMUST00000153627	tyrosyl-DNA phosphodiesterase 1 [Source:MGI Symbol;Acc:MGI:1920036]	B8JJC1		-0.8	7.6E-01	-3.6	3.3E-01	-1.9	3.4E-01	0.8	8.2E-01
ENSMUST00000144872				7.0	1.3E-04	-4.2	3.4E-03	0.6	2.1E-01	-1.3	2.8E-01
ENSMUST00000153634	copine I [Source:MGI Symbol;Acc:MGI:2386621]	B7ZCP5		-2.5	3.6E-01	-1.2	7.2E-01	-0.1	9.5E-01	-1.5	6.7E-01
ENSMUST00000155636				7.0	8.7E-04	6.0	1.7E-03	-0.1	9.4E-01	0.6	4.5E-01
ENSMUST00000153638				1.7	4.4E-02	1.9	6.8E-02	-0.1	9.2E-01	-0.3	7.1E-01
ENSMUST00000153641	surfeit gene 4 [Source:MGI Symbol;Acc:MGI:98445]	E0CXD9		-1.1	4.1E-01	-1.3	5.7E-01	1.2	4.0E-01	1.4	5.1E-01
ENSMUST00000189259				7.0	7.6E-06	5.5	1.1E-03	-2.1	1.3E-01	-1.7	5.7E-02
ENSMUST00000153655	zinc finger, MYND-type containing 8 [Source:MGI Symbol;Acc:MGI:1918025]	A2A480		-1.3	4.7E-01	2.7	2.6E-01	1.4	5.3E-01	-2.6	1.5E-01
ENSMUST00000153658	mitochondrial carrier homolog 1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1929261]	D3YXC2		-2.5	1.2E-01	0.8	6.5E-01	1.5	3.2E-01	-1.8	2.7E-01
ENSMUST00000128044				7.0	3.9E-05	6.2	9.7E-03	-0.6	7.4E-01	1.1	3.0E-01
ENSMUST00000119182				7.0	6.6E-04	-4.2	3.6E-03	0.8	1.0E-01	1.3	2.4E-01
ENSMUST00000124608				7.0	3.0E-07	2.9	1.7E-02	1.4	1.3E-01	-4.4	2.0E-03
ENSMUST00000188525				7.0	2.5E-04	-5.1	1.9E-02	-0.8	3.2E-01	1.4	4.6E-01
ENSMUST00000156941				7.0	1.5E-02	-2.1	2.3E-01	1.8	8.8E-02	-4.8	5.1E-02
ENSMUST00000153670				0.1	9.7E-01	1.1	7.3E-01	-0.1	9.8E-01	-1.1	7.0E-01
ENSMUST00000125015				7.0	7.7E-05	-3.4	3.5E-02	0.0	9.7E-01	-2.2	2.1E-01
ENSMUST00000128938				7.0	4.9E-05	5.3	5.6E-05	-2.9	1.2E-02	-0.5	3.7E-01
ENSMUST00000153679				-0.4	7.4E-01	1.0	4.9E-01	0.9	4.0E-01	-0.4	7.5E-01
ENSMUST00000153681				0.1	8.9E-01	-0.2	8.3E-01	-0.4	6.5E-01	0.0	9.7E-01
ENSMUST00000153684	PHD finger protein 23 [Source:MGI Symbol;Acc:MGI:1925496]		Q8BSN5	-7.3	8.1E-02	-5.0	3.3E-01	1.5	4.8E-01	-0.8	8.9E-01
ENSMUST00000193766				7.0	5.2E-05	9.4	6.6E-04	0.3	8.6E-01	0.7	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000153688				-2.1	5.0E-01	3.2	3.1E-01	1.0	7.1E-01	-4.3	1.7E-01
ENSMUST00000153689				-0.5	6.9E-01	2.2	1.6E-01	0.3	8.1E-01	-2.4	7.7E-02
ENSMUST00000096092				7.0	4.4E-05	5.6	4.4E-04	-0.1	9.1E-01	-2.5	7.2E-03
ENSMUST00000142171				7.0	3.1E-03	-3.9	3.3E-02	1.1	1.8E-01	-2.6	2.2E-01
ENSMUST00000153708				1.6	1.3E-01	0.5	6.4E-01	-1.2	2.2E-01	-0.1	8.9E-01
ENSMUST00000170329				7.0	1.3E-04	4.1	2.4E-03	0.0	9.8E-01	-0.2	8.1E-01
ENSMUST00000153710	predicted gene 6483 [Source:MGI Symbol;Acc:MGI:3644574]	D3Z1Y8		-0.1	9.7E-01	-3.9	1.8E-01	-4.5	2.8E-02	-0.7	8.1E-01
ENSMUST00000135889				7.0	2.4E-06	4.9	2.4E-03	-0.8	5.1E-01	-1.4	1.2E-01
ENSMUST00000194814				7.0	3.5E-05	-4.1	1.9E-02	0.2	8.1E-01	-0.5	7.6E-01
ENSMUST00000136029				7.0	1.2E-04	5.3	1.8E-04	-1.8	8.1E-02	0.3	6.3E-01
ENSMUST00000142674				7.0	6.0E-05	0.4	8.0E-01	0.3	8.1E-01	3.2	4.3E-02
ENSMUST00000152678				7.0	7.8E-06	3.7	3.6E-02	-0.6	7.1E-01	0.9	4.0E-01
ENSMUST00000195832				7.0	4.3E-05	3.8	2.7E-02	-0.7	6.1E-01	1.1	3.2E-01
ENSMUST00000144773				7.0	1.1E-04	2.4	1.3E-02	-0.3	6.3E-01	0.1	8.6E-01
ENSMUST00000171712				7.0	2.1E-03	-5.4	2.2E-03	0.8	1.7E-01	-1.6	3.1E-01
ENSMUST00000113014				7.0	2.4E-04	5.7	4.8E-02	-0.1	9.6E-01	1.0	5.2E-01
ENSMUST00000117387				7.0	8.1E-04	0.9	1.6E-01	-0.5	2.8E-01	0.0	9.4E-01
ENSMUST00000121383				7.0	2.8E-05	3.8	7.9E-03	1.3	2.4E-01	0.1	8.7E-01
ENSMUST00000122829				7.0	6.6E-05	6.2	3.9E-04	-2.2	1.1E-01	0.2	8.2E-01
ENSMUST00000136929				7.0	5.6E-06	3.9	2.7E-03	-0.1	8.7E-01	0.4	5.2E-01
ENSMUST00000143629				7.0	2.1E-03	5.8	9.7E-04	-0.7	6.1E-01	1.2	1.1E-01
ENSMUST00000149982				7.0	3.0E-05	5.0	1.3E-03	-0.6	5.8E-01	-1.4	7.0E-02
ENSMUST00000186734				7.0	4.9E-05	-1.9	4.2E-01	1.9	2.2E-01	-1.3	5.8E-01
ENSMUST00000032395				7.0	3.2E-04	-3.5	2.8E-02	0.7	3.0E-01	-0.7	6.5E-01
ENSMUST00000153765	transmembrane protein 260 [Source:MGI Symbol;Acc:MGI:2443219]	D6RHS9		0.4	8.5E-01	-0.3	9.0E-01	-1.0	5.3E-01	-0.3	9.0E-01
ENSMUST00000154536				7.0	1.7E-04	-2.2	5.4E-02	0.2	7.8E-01	-1.4	2.1E-01
ENSMUST00000195598				7.0	6.5E-04	6.0	6.8E-04	-0.5	6.7E-01	-1.4	6.8E-02
ENSMUST00000134555				7.0	5.2E-05	-3.4	2.6E-02	0.2	7.1E-01	0.2	9.0E-01
ENSMUST00000185706				7.0	6.8E-05	5.0	3.2E-02	0.0	9.8E-01	0.1	9.6E-01
ENSMUST00000124025				7.0	4.6E-05	7.3	1.0E-02	2.1	3.7E-01	-0.4	7.3E-01
ENSMUST00000153789	Hermansky-Pudlak syndrome 5 homolog (human) [Source:MGI Symbol;Acc:MGI:2180307]	F6Q7C7		-1.6	2.2E-01	-1.2	5.2E-01	0.7	5.6E-01	0.3	8.6E-01
ENSMUST00000153790				-1.0	3.1E-01	-0.1	9.3E-01	0.1	8.9E-01	-0.7	5.1E-01
ENSMUST00000153793				1.5	1.7E-01	1.8	1.6E-01	-0.4	7.1E-01	-0.7	5.3E-01
ENSMUST00000162856				7.0	3.8E-05	5.9	4.1E-04	0.1	9.2E-01	-0.3	5.9E-01
ENSMUST00000153799	SRY (sex determining region Y)-box 13 [Source:MGI Symbol;Acc:MGI:98361]		Q04891	2.0	2.4E-01	6.3	1.6E-02	1.7	4.5E-01	-2.6	6.9E-02
ENSMUST00000119050				7.0	2.6E-05	9.6	4.7E-06	-0.6	5.8E-01	0.2	6.4E-01
ENSMUST00000184753				7.0	4.6E-05	10.4	7.9E-05	0.2	9.1E-01	0.0	9.7E-01
ENSMUST00000188549				7.0	1.4E-04	4.6	9.3E-03	-1.1	4.8E-01	0.4	7.0E-01
ENSMUST00000153815				1.1	6.9E-02	1.3	8.8E-02	-0.2	7.4E-01	-0.4	5.5E-01
ENSMUST00000153819				-3.8	4.2E-02	-2.0	3.0E-01	0.4	7.1E-01	-1.3	5.2E-01
ENSMUST00000121836				7.0	3.2E-04	3.9	8.7E-04	-0.4	5.9E-01	-0.1	8.3E-01
ENSMUST00000153832	solute carrier family 15, member 4 [Source:MGI Symbol;Acc:MGI:2140796]	D6RDC2		-3.0	1.9E-01	1.4	6.3E-01	4.1	9.7E-02	-0.4	8.8E-01
ENSMUST00000164343				7.0	1.8E-05	10.0	1.3E-04	1.2	4.7E-01	-0.2	7.9E-01
ENSMUST00000148984				7.0	9.0E-04	-2.2	3.0E-03	0.5	1.2E-01	-0.2	7.4E-01
ENSMUST00000155774				7.0	1.3E-05	5.4	6.1E-05	-1.0	2.4E-01	0.5	3.4E-01
ENSMUST00000153842				1.4	3.4E-01	1.4	4.1E-01	-0.4	7.5E-01	-0.5	7.5E-01
ENSMUST00000167053				7.0	6.0E-05	4.9	5.3E-04	-0.1	9.1E-01	-0.3	6.1E-01
ENSMUST00000117756				7.0	1.2E-04	-6.4	8.7E-06	-0.8	3.5E-02	-3.5	5.5E-03
ENSMUST00000153848				-3.5	5.3E-02	-2.2	3.4E-01	0.8	5.3E-01	-0.5	8.1E-01
ENSMUST00000161399				7.0	2.1E-06	6.1	8.2E-03	-0.2	9.1E-01	-1.2	3.0E-01
ENSMUST00000153854				2.2	5.3E-02	0.9	4.4E-01	-1.3	2.2E-01	0.0	9.9E-01
ENSMUST00000121706				7.0	1.5E-04	3.2	9.7E-03	0.3	7.4E-01	0.5	4.6E-01
ENSMUST00000195034				7.0	1.1E-02	-0.7	5.4E-01	1.0	2.2E-01	-1.3	3.0E-01
ENSMUST00000153858				0.0	9.7E-01	0.7	5.8E-01	0.1	9.5E-01	-0.6	6.0E-01
ENSMUST00000153859				1.1	2.2E-01	2.4	3.9E-02	0.5	5.5E-01	-0.8	3.8E-01
ENSMUST00000153860	dysferlin [Source:MGI Symbol;Acc:MGI:1349385]			2.4	5.3E-02	6.4	1.8E-04	-0.5	6.5E-01	-4.5	3.4E-04
ENSMUST00000153861	syndecan binding protein [Source:MGI Symbol;Acc:MGI:1337026]	A2AKJ6		-1.0	7.5E-01	-7.1	4.9E-02	-7.9	2.9E-03	-1.9	6.3E-01
ENSMUST00000138446				7.0	4.3E-05	7.0	1.9E-04	-0.6	6.4E-01	-0.3	6.7E-01
ENSMUST00000107207				7.0	6.5E-04	8.4	3.5E-05	-0.9	5.0E-01	-1.4	2.2E-02
ENSMUST00000153867	minichromosome maintenance deficient 7 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1298398]	D3Z2K9		-1.8	2.4E-01	-1.9	2.6E-01	-0.2	8.4E-01	-0.1	9.6E-01
ENSMUST00000153871	RIKEN cDNA 9930012K11 gene [Source:MGI Symbol;Acc:MGI:2145726]		Q66JV7	-0.2	8.9E-01	1.6	3.2E-01	1.0	4.9E-01	-0.8	4.9E-01
ENSMUST00000125546				7.0	2.9E-04	3.6	2.8E-02	0.3	8.0E-01	-0.5	6.4E-01
ENSMUST00000138065				7.0	2.2E-04	3.0	8.7E-03	-0.3	7.0E-01	-0.3	7.3E-01
ENSMUST00000144447				7.0	3.7E-07	3.4	8.9E-04	0.2	7.5E-01	0.2	6.9E-01
ENSMUST00000153890				0.4	5.8E-01	1.9	5.4E-02	0.5	5.3E-01	-1.0	2.1E-01
ENSMUST00000147052				7.0	5.5E-05	-3.3	6.5E-04	-0.2	5.8E-01	-1.1	1.3E-01
ENSMUST00000153895				-3.6	1.6E-01	0.0	1.0E+00	0.9	6.5E-01	-2.8	2.9E-01
ENSMUST00000153896				2.4	3.9E-02	4.6	9.6E-03	1.1	4.3E-01	-1.1	2.4E-01
ENSMUST00000146727				7.0	3.6E-04	-4.8	1.0E-03	-0.4	4.2E-01	-0.7	5.1E-01
ENSMUST00000153915				1.7	3.3E-01	3.8	5.9E-02	-0.2	9.1E-01	-2.3	1.6E-01
ENSMUST00000153920				1.2	1.7E-01	-0.7	5.6E-01	-0.5	5.4E-01	1.4	2.1E-01
ENSMUST00000142070				7.0	2.2E-06	6.9	1.0E-03	0.3	8.6E-01	-0.4	6.7E-01
ENSMUST00000116315				7.0	1.6E-04	4.7	1.5E-04	1.3	9.2E-02	0.1	8.2E-01
ENSMUST00000153928				-1.3	4.3E-01	-0.4	8.7E-01	1.4	4.6E-01	0.6	7.7E-01
ENSMUST00000148449				7.0	5.9E-05	1.8	1.0E-01	0.2	8.3E-01	0.3	7.1E-01
ENSMUST00000153938	calmodulin binding transcription activator 1 [Source:MGI Symbol;Acc:MGI:2140230]	Q3TYE0		-0.3	8.0E-01	0.6	6.9E-01	-0.2	8.9E-01	-1.0	4.4E-01
ENSMUST00000153939				0.7	3.3E-01	1.7	6.7E-02	-0.3	7.1E-01	-1.3	1.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000134119				7.0	2.8E-04	3.5	3.7E-03	0.7	3.7E-01	-0.3	6.9E-01
ENSMUST00000150789				7.0	7.0E-06	5.1	2.2E-03	-1.1	3.9E-01	-0.2	8.0E-01
ENSMUST00000109282				7.0	1.0E-04	6.3	4.3E-04	-2.0	1.8E-01	-0.9	2.3E-01
ENSMUST00000153957				-0.1	9.2E-01	-2.1	1.6E-01	-0.7	4.6E-01	1.4	3.4E-01
ENSMUST00000123649				7.0	2.7E-04	6.2	1.7E-03	-0.6	7.0E-01	-0.3	7.1E-01
ENSMUST00000153965	angiomotin-like 2 [Source:MGI Symbol;Acc:MGI:1929286]	B8JK87		-0.4	9.1E-01	-1.5	7.5E-01	-1.3	7.1E-01	-0.2	9.6E-01
ENSMUST00000141336				7.0	4.0E-04	3.0	2.6E-02	-2.2	7.7E-02	1.1	2.0E-01
ENSMUST00000117628				7.0	2.4E-04	-6.3	3.8E-03	0.5	3.8E-01	-1.1	5.5E-01
ENSMUST00000121807				7.0	4.2E-05	0.2	9.1E-01	6.3	4.8E-04	0.5	7.8E-01
ENSMUST00000153973				-1.4	2.2E-01	-0.5	6.6E-01	-0.2	8.4E-01	-1.1	3.8E-01
ENSMUST00000134701				7.0	1.5E-04	8.3	2.7E-05	0.7	5.0E-01	-0.2	7.1E-01
ENSMUST00000142273				7.0	6.9E-05	4.8	9.3E-04	0.5	5.6E-01	-0.2	7.4E-01
ENSMUST00000150898				7.0	2.3E-04	5.1	1.9E-02	0.8	6.5E-01	0.4	6.8E-01
ENSMUST00000189720				7.0	2.0E-03	2.4	8.3E-03	-1.2	9.3E-02	-0.2	7.9E-01
ENSMUST00000125449				7.0	2.0E-05	3.1	1.2E-03	-0.4	5.4E-01	-0.5	3.7E-01
ENSMUST00000130968				7.0	6.0E-04	-2.4	4.2E-01	1.9	3.4E-01	-1.6	6.0E-01
ENSMUST00000153996	SEC16 homolog A, endoplasmic reticulum export factor [Source:MGI Symbol;Acc:MGI:2139207]	F6T8X6		-1.1	2.3E-01	-1.6	2.9E-01	0.8	3.5E-01	1.2	4.0E-01
ENSMUST00000174724				7.0	1.1E-04	5.1	1.7E-03	-1.3	3.1E-01	0.0	9.9E-01
ENSMUST00000185616				7.0	2.9E-05	5.2	7.2E-05	0.5	5.1E-01	0.3	5.3E-01
ENSMUST00000128252				7.0	1.2E-04	4.6	1.1E-02	-0.4	7.8E-01	-0.9	3.6E-01
ENSMUST00000160066				7.0	4.1E-05	-3.0	2.2E-02	1.8	1.7E-02	-2.5	9.7E-02
ENSMUST00000183897				7.0	7.0E-04	-3.2	1.7E-02	0.5	3.4E-01	-0.6	6.1E-01
ENSMUST00000145832				7.0	7.6E-05	3.1	4.8E-03	-0.9	2.9E-01	-0.2	7.5E-01
ENSMUST00000154021	inositol 1,4,5-triphosphate receptor interacting protein-like 1 [Source:MGI Symbol;Acc:MGI:1920588]		A2ASA8	2.5	6.3E-02	6.1	5.5E-03	2.4	1.8E-01	-1.2	2.4E-01
ENSMUST00000156824				7.0	6.0E-04	2.6	8.1E-02	-1.1	3.9E-01	0.6	5.1E-01
ENSMUST00000154029				0.2	9.1E-01	2.1	3.3E-01	-0.3	8.8E-01	-2.2	2.7E-01
ENSMUST00000154031				-1.9	5.7E-02	-2.8	8.7E-02	0.6	4.4E-01	1.5	3.2E-01
ENSMUST00000188088				7.0	3.2E-05	-4.7	7.3E-03	1.1	1.1E-01	-2.0	2.6E-01
ENSMUST00000151775				7.0	9.5E-04	6.5	8.9E-04	-1.9	2.3E-01	1.2	1.4E-01
ENSMUST00000154043	numb gene homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:107423]		Q9QZS3	0.1	9.5E-01	3.7	2.4E-01	1.7	5.0E-01	-1.9	4.9E-01
ENSMUST00000122035				7.0	1.2E-04	4.2	1.2E-03	-0.4	6.7E-01	0.8	2.5E-01
ENSMUST00000145526				7.0	1.6E-02	0.8	6.3E-01	-0.6	6.5E-01	5.0	6.8E-03
ENSMUST00000154051	ATPase, class VI, type 11C [Source:MGI Symbol;Acc:MGI:1859661]	F6Q8D3		1.1	7.1E-01	4.9	2.7E-01	1.7	6.6E-01	-2.0	5.0E-01
ENSMUST00000084345				7.0	7.2E-05	5.1	1.1E-03	-1.4	2.6E-01	-1.1	1.8E-01
ENSMUST00000129050				7.0	2.3E-04	4.8	9.4E-02	-0.7	8.2E-01	0.4	8.0E-01
ENSMUST00000130327				7.0	5.9E-05	8.4	2.6E-05	-0.6	6.0E-01	0.4	4.4E-01
ENSMUST00000154075				-1.0	3.7E-01	1.8	1.7E-01	0.5	6.7E-01	-2.3	5.4E-02
ENSMUST00000154077				0.7	5.6E-01	-0.8	6.3E-01	-0.3	8.3E-01	1.3	4.4E-01
ENSMUST00000145140				7.0	5.9E-06	5.0	3.3E-04	0.1	8.6E-01	0.4	4.7E-01
ENSMUST00000189506				7.0	4.0E-05	-4.0	3.9E-02	0.8	3.4E-01	0.4	8.1E-01
ENSMUST00000128962				7.0	2.9E-04	4.2	4.1E-04	0.4	5.3E-01	0.4	5.1E-01
ENSMUST00000173265				7.0	1.3E-04	7.3	2.6E-03	0.0	1.0E+00	-0.1	9.4E-01
ENSMUST00000154091				0.6	8.0E-01	-2.4	3.2E-01	-3.9	3.4E-02	-0.9	7.2E-01
ENSMUST00000189018				7.0	5.6E-07	-2.5	4.3E-02	0.2	7.2E-01	0.2	8.9E-01
ENSMUST00000098624				7.0	2.0E-04	1.6	5.0E-01	-1.1	6.1E-01	1.9	2.9E-01
ENSMUST00000145730				7.0	1.2E-04	3.1	3.8E-03	0.7	3.4E-01	0.0	9.4E-01
ENSMUST00000188890				7.0	1.8E-04	-3.3	3.0E-02	-0.6	3.6E-01	-0.9	5.5E-01
ENSMUST00000154124				-4.4	9.3E-02	-4.2	1.9E-01	-0.3	8.4E-01	-0.5	8.7E-01
ENSMUST00000187459				7.0	1.8E-04	5.9	1.2E-03	-0.5	7.4E-01	-0.5	4.9E-01
ENSMUST00000192231				7.0	1.4E-04	0.6	5.1E-01	2.2	1.7E-02	-2.1	5.5E-02
ENSMUST00000127083				7.0	2.7E-04	-1.2	3.1E-01	0.5	5.4E-01	-1.2	3.0E-01
ENSMUST00000154145				1.5	1.4E-01	2.6	3.9E-02	0.0	9.6E-01	-1.2	2.2E-01
ENSMUST00000129913				7.0	7.1E-05	4.9	5.3E-03	-2.2	1.8E-01	0.6	5.3E-01
ENSMUST00000121518				7.0	2.5E-06	-4.9	3.5E-04	0.2	5.9E-01	1.3	1.9E-01
ENSMUST00000154151				-0.2	8.4E-01	-0.8	4.8E-01	-0.7	4.8E-01	0.0	9.9E-01
ENSMUST00000156772				7.0	1.2E-06	8.8	6.2E-05	-0.7	6.1E-01	-0.4	5.1E-01
ENSMUST00000154162				-0.5	8.4E-01	-4.3	1.6E-01	-4.7	1.9E-02	-0.9	7.8E-01
ENSMUST00000154163	forkhead box P1 [Source:MGI Symbol;Acc:MGI:1914004]	D3Z2T4		-0.4	7.7E-01	0.4	8.2E-01	0.9	4.7E-01	0.2	9.3E-01
ENSMUST00000176984				7.0	1.6E-04	-2.6	4.1E-02	1.1	1.1E-01	-2.9	6.0E-02
ENSMUST00000154184	shisa family member 5 [Source:MGI Symbol;Acc:MGI:1915044]		Q9D7I0	-4.0	1.7E-01	-0.5	9.0E-01	3.0	3.4E-01	-0.4	9.1E-01
ENSMUST00000142620				7.0	4.7E-05	6.4	1.1E-03	0.0	9.9E-01	0.1	8.5E-01
ENSMUST00000154187	olute carrier family 16 (monocarboxylic acid transporters), member 3 [Source:MGI Symbol;Acc:MGI:1933438	B1ATM1		-3.8	1.0E-01	-1.2	6.3E-01	1.6	2.6E-01	-1.0	7.0E-01
ENSMUST00000152101				7.0	3.1E-06	2.5	3.7E-03	-0.5	3.9E-01	-0.4	5.1E-01
ENSMUST00000182177				7.0	1.7E-03	6.9	4.2E-04	1.0	4.1E-01	0.4	6.2E-01
ENSMUST00000118925				7.0	1.6E-04	4.0	5.7E-02	-3.0	1.7E-01	0.4	7.4E-01
ENSMUST00000154207	eukaryotic translation elongation factor 1 alpha 1 [Source:MGI Symbol;Acc:MGI:1096881]	D3YZ68		-1.1	7.7E-01	-7.3	2.0E-01	-3.5	2.4E-01	2.7	6.3E-01
ENSMUST00000154208	dehydrogenase/reductase (SDR family) member 3 [Source:MGI Symbol;Acc:MGI:1315215]		O88876	0.0	1.0E+00	1.9	1.9E-01	0.5	6.8E-01	-1.4	2.6E-01
ENSMUST00000135240				7.0	1.7E-04	5.4	2.2E-03	0.2	8.5E-01	-0.5	5.3E-01
ENSMUST00000148249				7.0	5.7E-05	0.8	5.7E-01	-1.5	2.4E-01	1.3	3.2E-01
ENSMUST00000154218				-1.7	2.3E-01	-0.1	9.4E-01	0.5	7.1E-01	-1.1	4.9E-01
ENSMUST00000182749				7.0	5.5E-05	-3.2	1.1E-02	2.7	8.9E-04	-1.3	2.5E-01
ENSMUST00000179745				7.0	4.4E-03	5.8	2.5E-02	-0.8	7.3E-01	2.8	5.3E-02
ENSMUST00000154231				-0.2	8.8E-01	3.3	3.1E-02	0.7	5.5E-01	-2.7	3.0E-02
ENSMUST00000121889				7.0	2.8E-04	-3.7	1.8E-02	1.0	1.7E-01	-0.6	6.7E-01
ENSMUST00000154235	Luc7 homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:1914228]	D6REI1		2.1	3.8E-02	2.7	4.5E-02	0.2	8.7E-01	-0.4	6.0E-01
ENSMUST00000127458				7.0	3.7E-05	-2.0	2.6E-01	0.5	5.9E-01	-0.7	6.7E-01
ENSMUST00000144169				7.0	9.0E-04	5.9	2.6E-02	0.8	7.5E-01	2.0	1.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000182765				7.0	2.5E-04	4.9	1.2E-02	-0.7	6.9E-01	1.3	2.3E-01
ENSMUST00000154241	MpV17 mitochondrial inner membrane protein [Source:MGI Symbol;Acc:MGI:97138]		P19258	-2.5	1.7E-01	-3.6	1.2E-01	-0.3	8.1E-01	0.8	7.2E-01
ENSMUST00000186422				7.0	5.7E-05	5.1	3.7E-03	0.5	7.1E-01	0.1	9.2E-01
ENSMUST00000117954				7.0	6.7E-05	-3.4	1.5E-02	0.4	5.3E-01	-0.2	8.6E-01
ENSMUST00000154255	tetratricopeptide repeat domain 7 [Source:MGI Symbol;Acc:MGI:1920999]	F6ZVR4		-1.2	5.4E-01	-0.2	9.5E-01	0.7	7.3E-01	-0.3	9.0E-01
ENSMUST00000119061				7.0	2.7E-03	-6.0	1.5E-03	0.9	1.1E-01	0.7	6.6E-01
ENSMUST00000154260				-2.3	1.2E-01	-0.3	8.8E-01	0.6	6.3E-01	-1.4	4.4E-01
ENSMUST00000153439				7.0	1.0E-04	4.8	2.6E-04	-2.1	4.5E-02	0.3	5.6E-01
ENSMUST00000165185				7.0	5.7E-05	7.5	1.3E-03	-0.8	6.4E-01	1.4	1.3E-01
ENSMUST00000171876				7.0	4.3E-05	5.4	3.5E-04	0.9	3.3E-01	-0.1	8.8E-01
ENSMUST00000154266	testis derived transcript [Source:MGI Symbol;Acc:MGI:105081]	D6RH72		1.5	5.0E-01	-4.5	1.1E-01	-4.8	1.7E-02	1.2	6.6E-01
ENSMUST00000147285				7.0	1.0E-04	5.7	5.2E-04	-2.0	1.1E-01	-0.1	8.5E-01
ENSMUST00000194185				7.0	3.3E-03	8.2	1.0E-04	1.0	4.3E-01	-0.1	9.3E-01
ENSMUST00000154274				1.3	1.4E-01	2.0	1.4E-01	1.0	3.5E-01	0.4	6.9E-01
ENSMUST00000193160				7.0	5.2E-04	-4.4	1.1E-01	0.4	7.1E-01	0.6	8.2E-01
ENSMUST00000128808				7.0	1.1E-03	4.8	1.4E-03	-1.7	1.8E-01	0.2	8.3E-01
ENSMUST00000155555				7.0	1.2E-06	5.4	8.6E-04	0.3	7.9E-01	0.3	6.5E-01
ENSMUST00000176088				7.0	6.2E-04	6.2	7.6E-03	-0.6	7.5E-01	-1.8	1.3E-01
ENSMUST00000186351				7.0	7.0E-05	6.0	7.3E-03	-0.7	7.1E-01	-0.7	4.9E-01
ENSMUST00000121199				7.0	5.5E-05	3.1	1.3E-02	-0.2	8.2E-01	-0.1	8.6E-01
ENSMUST00000180786				7.0	4.3E-05	-0.7	6.3E-01	1.1	2.6E-01	-1.3	4.2E-01
ENSMUST00000154289				1.1	3.1E-01	1.0	4.3E-01	-0.2	8.3E-01	-0.1	9.0E-01
ENSMUST00000154292	Usher syndrome 1C [Source:MGI Symbol;Acc:MGI:1919338]	E9PYX1		3.9	1.0E-01	5.1	9.3E-02	0.7	8.0E-01	-0.5	7.9E-01
ENSMUST00000132870				7.0	6.0E-03	8.0	5.6E-04	0.5	7.4E-01	0.8	3.0E-01
ENSMUST00000154303				2.0	9.4E-02	1.5	3.5E-01	-0.1	9.6E-01	0.5	6.8E-01
ENSMUST00000137517				7.0	1.4E-04	-3.3	4.4E-03	0.9	5.1E-02	-1.3	2.1E-01
ENSMUST00000154307				0.3	8.0E-01	2.6	7.9E-02	0.6	6.1E-01	-1.7	1.2E-01
ENSMUST00000189717				7.0	8.0E-05	7.9	4.9E-05	-0.5	7.1E-01	-0.4	4.3E-01
ENSMUST00000190134				7.0	8.0E-05	2.9	8.9E-02	-0.5	7.2E-01	0.8	4.4E-01
ENSMUST00000125096				7.0	2.5E-04	7.1	2.0E-04	0.6	6.3E-01	0.6	4.1E-01
ENSMUST00000145171				7.0	5.0E-05	4.3	3.4E-02	1.1	4.9E-01	1.1	3.3E-01
ENSMUST00000142452				7.0	1.4E-03	-3.4	7.9E-03	-1.4	4.9E-02	-1.4	2.3E-01
ENSMUST00000177231				7.0	4.3E-05	5.3	1.0E-03	-0.5	6.9E-01	-0.2	7.4E-01
ENSMUST00000154336				1.0	4.5E-01	3.7	2.1E-02	-0.1	9.6E-01	-2.8	4.1E-02
ENSMUST00000154340				-1.7	1.4E-01	-0.4	6.7E-01	-1.4	1.2E-01	-2.6	3.8E-02
ENSMUST00000151860				7.0	3.0E-04	8.1	8.1E-04	-0.9	6.3E-01	-0.2	8.3E-01
ENSMUST00000139746				7.0	1.9E-04	-7.4	1.5E-02	-2.6	2.1E-02	-1.0	7.4E-01
ENSMUST00000173130				7.0	4.8E-04	5.3	3.2E-04	1.1	2.3E-01	0.1	8.6E-01
ENSMUST00000143446				7.0	1.6E-03	0.5	7.0E-01	2.1	5.0E-02	-3.5	2.5E-02
ENSMUST00000149291				7.0	1.1E-05	4.5	7.0E-03	-1.6	2.9E-01	-0.8	3.9E-01
ENSMUST00000154371	transmembrane protein 123 [Source:MGI Symbol;Acc:MGI:1919179]	D6RI40		-3.5	4.8E-02	-3.9	4.3E-02	-1.0	3.2E-01	-0.6	7.7E-01
ENSMUST00000166417				7.0	1.2E-05	7.0	5.0E-05	-1.2	2.6E-01	0.2	7.1E-01
ENSMUST00000121278				7.0	1.0E-03	6.7	4.2E-04	1.1	3.7E-01	-1.6	4.7E-02
ENSMUST00000128838				7.0	3.0E-04	6.2	2.1E-03	-0.1	9.7E-01	1.8	7.2E-02
ENSMUST00000191472				7.0	6.5E-05	-5.4	1.6E-03	0.5	2.6E-01	-0.7	6.0E-01
ENSMUST00000139336				7.0	5.6E-05	4.7	3.5E-03	-0.6	6.5E-01	0.7	4.0E-01
ENSMUST00000154383	transmembrane protein 216 [Source:MGI Symbol;Acc:MGI:1920020]		Q9CQC4	-2.3	1.2E-01	-4.0	1.2E-01	-0.2	8.7E-01	1.5	5.1E-01
ENSMUST00000141060				7.0	1.2E-05	6.2	7.5E-04	-0.7	6.3E-01	-1.0	2.0E-01
ENSMUST00000154396	breast carcinoma amplified sequence 3 [Source:MGI Symbol;Acc:MGI:2385848]	F7C0F2		-2.0	2.2E-01	-2.2	3.4E-01	0.5	7.4E-01	0.7	7.7E-01
ENSMUST00000173181				7.0	2.5E-04	4.1	5.6E-03	0.6	5.5E-01	0.0	1.0E+00
ENSMUST00000124290				7.0	3.7E-05	-1.6	2.6E-01	1.0	2.8E-01	-4.2	4.1E-02
ENSMUST00000140739				7.0	9.7E-05	1.5	2.2E-01	-2.4	4.8E-02	0.3	7.2E-01
ENSMUST00000160771				7.0	1.9E-05	5.6	4.2E-04	-0.6	5.4E-01	0.0	9.8E-01
ENSMUST00000139325				7.0	1.2E-04	6.1	7.4E-04	-0.7	6.1E-01	-0.2	7.5E-01
ENSMUST00000144677				7.0	1.2E-04	-6.3	5.9E-03	-1.6	5.7E-02	-0.8	7.0E-01
ENSMUST00000160743				7.0	1.3E-04	3.6	1.9E-02	-0.4	7.5E-01	-0.3	7.7E-01
ENSMUST00000161131				7.0	3.4E-05	2.5	2.4E-01	-0.2	9.2E-01	3.0	8.9E-02
ENSMUST00000195181				7.0	5.7E-05	6.0	1.2E-03	2.8	4.2E-02	-0.8	3.0E-01
ENSMUST00000154428	unc-45 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:2142246]	D6RIN1		2.2	4.2E-01	4.2	2.0E-01	0.3	9.1E-01	-1.7	5.1E-01
ENSMUST00000135771				7.0	2.3E-05	-0.3	7.2E-01	-0.1	8.5E-01	-4.1	4.5E-03
ENSMUST00000126627				7.0	4.3E-05	3.7	3.1E-03	0.4	6.5E-01	0.0	1.0E+00
ENSMUST00000139678				7.0	2.3E-06	2.1	3.4E-01	-2.5	2.5E-01	0.3	8.5E-01
ENSMUST00000053075				7.0	3.4E-05	-2.9	3.9E-02	0.6	3.3E-01	-0.9	5.0E-01
ENSMUST00000122401				7.0	6.8E-05	-4.6	8.9E-04	-0.6	1.8E-01	-1.3	2.6E-01
ENSMUST00000173949				7.0	4.7E-03	5.2	1.1E-03	-1.3	3.2E-01	-1.5	6.4E-02
ENSMUST00000129465				7.0	1.8E-04	8.0	5.7E-05	-1.5	2.8E-01	1.2	6.0E-02
ENSMUST00000141853				7.0	5.4E-05	7.4	1.1E-05	-1.5	1.2E-01	-0.4	3.7E-01
ENSMUST00000155509				7.0	1.6E-04	5.1	1.2E-02	0.0	9.8E-01	-0.3	7.5E-01
ENSMUST00000162766				7.0	5.1E-05	-4.3	7.7E-04	0.1	8.1E-01	-0.2	8.6E-01
ENSMUST00000176112				7.0	2.1E-04	5.3	1.6E-03	-1.0	4.7E-01	-0.9	2.6E-01
ENSMUST00000154465				-0.7	4.0E-01	0.4	6.6E-01	0.0	9.5E-01	-1.1	2.1E-01
ENSMUST00000121066				7.0	1.1E-03	5.5	4.6E-06	0.0	9.5E-01	0.7	8.5E-02
ENSMUST00000156116				7.0	1.4E-02	2.7	8.1E-03	0.8	2.2E-01	0.0	1.0E+00
ENSMUST00000192175				7.0	2.6E-06	-3.0	6.1E-03	0.1	8.2E-01	-1.7	1.4E-01
ENSMUST00000118734				7.0	1.1E-04	-3.7	1.1E-02	0.3	6.1E-01	-1.5	2.8E-01
ENSMUST00000154474	nuclear factor of activated T cells 5 [Source:MGI Symbol;Acc:MGI:1859333]	D6RH40		2.0	3.6E-01	0.9	7.4E-01	-1.4	4.9E-01	-0.3	9.0E-01
ENSMUST00000142612				7.0	6.3E-05	0.3	7.1E-01	-6.2	5.1E-04	-0.5	5.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000154477				-2.7	1.3E-01	-0.1	9.8E-01	0.7	6.8E-01	-2.0	3.0E-01
ENSMUST00000125471				7.0	1.2E-04	2.8	3.1E-03	-4.8	5.1E-04	-1.7	2.0E-02
ENSMUST00000147107				7.0	3.2E-04	-2.3	2.6E-01	1.6	2.4E-01	-0.8	6.9E-01
ENSMUST00000154484				3.9	1.2E-01	6.0	3.9E-02	-0.3	9.3E-01	-2.4	1.5E-01
ENSMUST00000156273				7.0	4.0E-05	2.5	5.1E-02	-3.6	2.3E-02	-2.4	5.1E-02
ENSMUST00000190859				7.0	4.7E-04	3.5	3.6E-02	-1.7	2.5E-01	-0.4	7.0E-01
ENSMUST00000154494				-1.3	3.0E-01	0.3	8.2E-01	0.1	9.2E-01	-1.5	3.0E-01
ENSMUST00000123846				7.0	1.7E-02	6.0	8.4E-04	0.3	7.9E-01	-0.1	9.1E-01
ENSMUST00000129547				7.0	8.0E-08	5.3	1.6E-02	0.1	9.6E-01	-0.9	4.1E-01
ENSMUST00000154501	helicase (DNA) B [Source:MGI Symbol;Acc:MGI:2152895]	D6RGT6		-1.0	7.0E-01	-1.2	7.1E-01	-0.6	7.7E-01	-0.4	9.1E-01
ENSMUST00000173838				7.0	2.1E-04	-3.4	2.5E-02	1.2	7.3E-02	-1.3	3.7E-01
ENSMUST00000118017				7.0	6.0E-05	6.7	5.2E-04	-1.9	2.2E-01	-0.2	8.3E-01
ENSMUST00000135371				7.0	4.2E-07	-1.7	7.2E-02	1.1	8.8E-02	-1.8	9.6E-02
ENSMUST00000150958				7.0	6.1E-05	3.0	3.5E-03	-0.5	4.6E-01	0.2	7.7E-01
ENSMUST00000085290				6.9	8.4E-05	-6.1	1.3E-03	-3.0	6.3E-04	-0.7	6.4E-01
ENSMUST00000154529				-0.4	6.9E-01	-1.1	5.5E-01	0.7	4.7E-01	1.4	4.3E-01
ENSMUST00000121929				6.9	3.2E-04	-9.2	1.1E-03	-2.1	1.1E-02	-0.2	9.4E-01
ENSMUST00000191983				6.9	1.0E-04	6.4	1.0E-03	0.0	9.8E-01	0.7	4.0E-01
ENSMUST00000101258				6.9	2.6E-04	3.2	2.9E-01	-0.2	9.5E-01	2.6	2.1E-01
ENSMUST00000150574				6.9	4.0E-04	5.1	2.3E-05	0.2	7.6E-01	0.4	3.4E-01
ENSMUST00000134874				6.9	1.4E-04	5.5	3.6E-03	-0.5	7.4E-01	0.4	6.5E-01
ENSMUST00000172851				6.9	3.6E-05	8.7	1.3E-05	-0.5	6.4E-01	-0.6	2.2E-01
ENSMUST00000162143				6.9	2.8E-04	6.0	1.7E-04	0.9	3.4E-01	0.4	5.5E-01
ENSMUST00000154546				2.2	2.8E-01	0.4	8.8E-01	-0.7	7.2E-01	1.1	6.2E-01
ENSMUST00000187223				6.9	1.1E-04	-6.3	2.0E-03	-0.6	2.5E-01	0.5	7.4E-01
ENSMUST00000154551	Rho GTPase activating protein 26 [Source:MGI Symbol;Acc:MGI:1918552]	F6XTB7		1.8	3.3E-01	1.6	5.7E-01	0.8	6.7E-01	1.0	6.9E-01
ENSMUST00000134030				6.9	3.7E-05	-7.4	4.7E-04	0.3	4.6E-01	0.3	8.2E-01
ENSMUST00000147329				6.9	3.9E-05	7.1	7.3E-04	-0.1	9.5E-01	-1.2	1.2E-01
ENSMUST00000154573				1.6	5.7E-02	1.6	9.8E-02	-0.5	4.8E-01	-0.5	5.1E-01
ENSMUST00000154574				0.6	6.6E-01	1.1	5.3E-01	-0.6	6.5E-01	-1.0	5.0E-01
ENSMUST00000154575				2.4	6.1E-02	2.5	5.8E-02	-1.7	1.4E-01	-1.9	1.1E-01
ENSMUST00000155651				6.9	1.0E-04	6.7	1.1E-04	-0.5	6.4E-01	-1.7	1.6E-02
ENSMUST00000185759				6.9	3.7E-05	6.1	3.1E-04	0.4	6.8E-01	-0.5	4.7E-01
ENSMUST00000193110				6.9	1.2E-04	-0.3	7.2E-01	0.3	6.0E-01	-1.2	1.7E-01
ENSMUST00000124649				6.9	3.3E-05	-2.9	1.8E-01	0.8	4.8E-01	-1.0	6.4E-01
ENSMUST00000171450				6.9	5.6E-05	4.2	4.0E-02	-1.8	3.5E-01	2.0	1.2E-01
ENSMUST00000077420				6.9	6.3E-04	4.4	6.0E-02	-0.1	9.4E-01	-0.4	7.9E-01
ENSMUST00000154591				-1.3	2.5E-01	-0.1	9.3E-01	0.6	5.4E-01	-0.6	6.8E-01
ENSMUST00000105067				6.9	9.8E-05	-3.2	3.0E-02	0.5	4.6E-01	-0.9	5.5E-01
ENSMUST00000154602	IKAROS family zinc finger 5 [Source:MGI Symbol;Acc:MGI:1914393]	D3YYG0		1.9	1.3E-01	-0.4	6.8E-01	-3.2	1.1E-02	-0.9	4.1E-01
ENSMUST00000138124				6.9	5.4E-05	3.3	3.0E-02	-2.0	1.6E-01	-0.5	6.3E-01
ENSMUST00000140146				6.9	1.7E-04	7.7	6.7E-06	0.7	4.1E-01	-0.1	7.8E-01
ENSMUST00000154607				6.3	3.8E-02	7.3	3.7E-02	-0.2	9.5E-01	-1.2	5.1E-01
ENSMUST00000154609	high mobility group 20B [Source:MGI Symbol;Acc:MGI:1341190]	E9Q2W1		-2.7	3.6E-02	-1.2	4.2E-01	0.9	3.9E-01	-0.6	7.1E-01
ENSMUST00000142769				6.9	1.1E-06	-0.4	5.4E-01	0.4	3.4E-01	-0.6	4.2E-01
ENSMUST00000155457				6.9	9.1E-05	6.0	9.1E-03	-1.3	5.2E-01	-2.6	5.4E-02
ENSMUST00000154620				-2.2	1.1E-01	2.4	1.8E-01	2.5	8.9E-02	-2.1	1.8E-01
ENSMUST00000154623	arrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 [Source:MGI Symbol;Acc:MGI:1	A2A9V3		1.9	2.5E-01	4.3	6.6E-02	1.3	5.2E-01	-1.1	4.5E-01
ENSMUST00000118350				6.9	1.3E-05	6.5	3.3E-04	-0.6	6.5E-01	-0.3	6.2E-01
ENSMUST00000122994				6.9	5.5E-05	7.5	2.2E-05	1.4	1.4E-01	-1.0	5.1E-02
ENSMUST00000154626				0.4	8.5E-01	1.4	6.3E-01	0.7	7.0E-01	-0.3	9.3E-01
ENSMUST00000188101				6.9	2.1E-07	3.7	1.4E-02	0.3	8.2E-01	0.6	5.0E-01
ENSMUST00000182041				6.9	1.4E-03	6.3	1.7E-04	-0.5	6.6E-01	0.2	7.2E-01
ENSMUST00000166404				6.9	2.3E-04	4.0	4.8E-04	0.5	4.9E-01	-0.1	8.7E-01
ENSMUST00000176049				6.9	6.0E-04	6.2	5.6E-03	-0.8	6.8E-01	0.4	6.7E-01
ENSMUST00000192986				6.9	1.6E-04	5.6	9.2E-04	-0.5	7.1E-01	-1.4	6.5E-02
ENSMUST00000057650				6.9	2.6E-03	-5.9	7.8E-03	-0.7	3.5E-01	1.2	5.4E-01
ENSMUST00000138200				6.9	4.2E-06	5.7	6.0E-02	-0.7	8.2E-01	1.7	2.9E-01
ENSMUST00000154645				1.0	6.1E-01	-0.5	8.3E-01	-2.0	3.0E-01	-0.4	8.7E-01
ENSMUST00000145042				6.9	2.2E-05	4.9	9.3E-03	-1.6	3.5E-01	-0.7	4.8E-01
ENSMUST00000172082				6.9	1.9E-06	-5.3	4.3E-02	-0.3	7.7E-01	2.0	3.9E-01
ENSMUST00000182910				6.9	4.8E-05	6.5	1.9E-03	0.2	9.0E-01	-0.7	4.6E-01
ENSMUST00000140430				6.9	1.0E-04	6.4	1.7E-03	-1.5	3.8E-01	-1.4	1.6E-01
ENSMUST00000154660				-1.1	1.2E-01	-0.6	4.4E-01	-0.3	6.1E-01	-0.8	3.3E-01
ENSMUST00000107891				6.9	4.3E-04	6.4	2.2E-04	-0.5	6.6E-01	-0.9	1.7E-01
ENSMUST00000122140				6.9	2.5E-04	7.6	2.8E-04	-0.7	6.5E-01	0.4	6.1E-01
ENSMUST00000129567				6.9	2.2E-04	4.1	8.5E-03	-2.6	6.0E-02	-0.3	7.2E-01
ENSMUST00000194772				6.9	2.0E-06	2.9	1.3E-02	0.2	8.0E-01	0.0	9.8E-01
ENSMUST00000016698				6.9	9.6E-05	4.1	2.7E-02	-1.1	4.7E-01	-0.4	7.3E-01
ENSMUST00000192014				6.9	1.1E-05	-3.2	8.1E-02	0.8	3.4E-01	-0.2	9.0E-01
ENSMUST00000154679	polymerase (RNA) III (DNA directed) polypeptide C [Source:MGI Symbol;Acc:MGI:1921664]	B2RX77	Q9D483	0.4	7.5E-01	-1.1	6.1E-01	2.2	1.8E-01	3.6	5.5E-02
ENSMUST00000122048				6.9	1.2E-04	6.0	8.9E-04	-1.2	3.7E-01	-0.7	3.6E-01
ENSMUST00000194788				6.9	5.5E-05	-6.4	1.7E-03	-1.5	2.6E-02	-0.3	8.6E-01
ENSMUST00000154687				0.2	8.6E-01	0.6	6.5E-01	-0.8	4.7E-01	-1.2	3.6E-01
ENSMUST00000130495				6.9	6.9E-05	2.9	7.0E-03	0.1	9.2E-01	0.8	2.1E-01
ENSMUST00000154691	FAD-dependent oxidoreductase domain containing 1 [Source:MGI Symbol;Acc:MGI:2446262]	D6RCV5		1.4	2.6E-01	2.7	1.3E-01	1.0	5.2E-01	-0.4	7.4E-01
ENSMUST00000159579				6.9	1.1E-04	5.5	2.0E-04	-1.0	3.0E-01	-0.4	5.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000194088				6.9	7.6E-05	2.4	2.4E-03	-0.1	9.2E-01	0.3	5.0E-01
ENSMUST00000127159				6.9	4.6E-05	5.5	1.3E-04	-0.5	5.8E-01	0.0	9.8E-01
ENSMUST00000127357				6.9	4.6E-05	4.8	4.3E-02	-1.4	5.2E-01	0.6	6.8E-01
ENSMUST00000154710				-1.2	2.2E-01	-0.7	5.8E-01	0.4	7.0E-01	-0.2	8.8E-01
ENSMUST00000154721				2.8	1.5E-01	0.7	7.3E-01	-1.3	5.0E-01	0.9	6.1E-01
ENSMUST00000154727	in homology domain containing, family G (with RhoGef domain) member 1 [Source:MGI Symbol;Acc:MGI:2(	F7C583		3.0	1.5E-01	3.7	2.3E-01	2.0	4.4E-01	1.3	5.3E-01
ENSMUST00000157007				6.9	7.7E-05	4.8	4.3E-04	0.5	5.6E-01	-0.9	2.0E-01
ENSMUST00000154742	ataxin 7-like 1 [Source:MGI Symbol;Acc:MGI:3584458]	D3Z7I2		-0.5	5.9E-01	0.6	6.0E-01	0.2	7.7E-01	-0.8	4.4E-01
ENSMUST00000173214				6.9	3.3E-04	5.7	4.9E-05	-0.8	3.1E-01	-0.8	1.2E-01
ENSMUST00000180011				6.9	3.3E-03	5.8	3.8E-04	0.2	8.5E-01	0.2	7.9E-01
ENSMUST00000116006				6.9	6.4E-04	7.2	2.0E-06	0.0	9.4E-01	0.0	9.6E-01
ENSMUST00000154756	inositol polyphosphate 5-phosphatase J [Source:MGI Symbol;Acc:MGI:2158663]	A0A075B6D7		3.7	1.8E-01	1.6	4.9E-01	-3.0	2.6E-01	-0.9	6.8E-01
ENSMUST00000140837				6.9	8.7E-06	5.5	4.7E-03	0.4	7.9E-01	0.7	4.1E-01
ENSMUST00000159504				6.9	3.7E-06	7.2	8.5E-04	-1.1	5.1E-01	0.6	4.4E-01
ENSMUST00000145090				6.9	2.2E-05	4.3	1.9E-02	-1.6	3.3E-01	2.2	7.0E-02
ENSMUST00000184700				6.9	8.3E-05	-6.1	4.8E-05	-1.0	4.2E-02	-0.9	3.3E-01
ENSMUST00000135398				6.9	1.7E-02	6.1	6.3E-05	0.2	8.0E-01	-1.3	4.7E-02
ENSMUST00000142738				6.9	1.2E-04	-4.3	2.6E-03	-0.2	6.7E-01	-0.9	4.3E-01
ENSMUST00000154782	kinase non-catalytic C-lobe domain (KIND) containing 1 [Source:MGI Symbol;Acc:MGI:1923734]	F6SPU5		3.3	1.7E-01	2.2	5.3E-01	0.7	8.1E-01	1.8	5.0E-01
ENSMUST00000139572				6.9	3.8E-03	-4.2	3.3E-03	0.0	9.5E-01	-0.9	4.5E-01
ENSMUST00000189693				6.9	7.7E-05	0.3	7.2E-01	-0.3	5.6E-01	-2.7	9.4E-03
ENSMUST00000119196				6.9	1.9E-04	7.5	1.1E-04	-0.1	9.1E-01	-0.8	2.5E-01
ENSMUST00000119775				6.9	3.7E-05	5.6	5.4E-04	-0.2	8.8E-01	-0.7	3.2E-01
ENSMUST00000189618				6.9	7.8E-05	-2.9	7.8E-02	1.4	1.1E-01	-1.8	3.1E-01
ENSMUST00000117484				6.9	6.2E-05	2.1	1.2E-01	-3.2	3.7E-02	0.2	8.2E-01
ENSMUST00000154815				-0.8	7.3E-01	-2.3	4.4E-01	-1.9	2.8E-01	-0.4	9.1E-01
ENSMUST00000148030				6.9	1.7E-04	5.7	2.9E-03	-0.3	8.1E-01	1.6	1.1E-01
ENSMUST00000154818	adhesion G protein-coupled receptor G4 [Source:MGI Symbol;Acc:MGI:2685213]		B7ZCC9	6.1	4.4E-02	6.0	6.1E-02	-0.9	7.7E-01	-0.8	6.5E-01
ENSMUST00000154824	microtubule-actin crosslinking factor 1 [Source:MGI Symbol;Acc:MGI:108559]	F6YKN8		-4.2	1.4E-01	-1.9	6.5E-01	2.4	3.5E-01	0.1	9.8E-01
ENSMUST00000124190				6.9	1.6E-04	6.0	8.9E-04	-3.4	3.7E-02	-0.8	3.0E-01
ENSMUST00000133716				6.9	2.7E-04	2.1	3.2E-02	0.6	3.7E-01	0.2	7.8E-01
ENSMUST00000140795				6.9	1.7E-04	3.1	7.1E-03	-0.1	8.7E-01	-0.2	7.8E-01
ENSMUST00000122282				6.9	3.6E-05	6.0	4.5E-04	-1.5	2.5E-01	-0.7	3.4E-01
ENSMUST00000123677				6.9	7.0E-04	-4.7	2.7E-01	5.1	3.8E-02	-1.2	7.8E-01
ENSMUST00000151762				6.9	2.8E-04	2.9	7.1E-03	0.6	4.2E-01	-0.4	5.7E-01
ENSMUST00000152933				6.9	1.9E-05	-3.7	7.2E-02	0.7	4.5E-01	1.7	3.8E-01
ENSMUST00000117060				6.9	7.5E-05	-3.0	3.2E-02	0.1	9.1E-01	-0.2	8.6E-01
ENSMUST00000154851	methyl-CpG binding domain protein 6 [Source:MGI Symbol;Acc:MGI:106378]	G3UXV1		-2.2	7.6E-02	-0.1	9.1E-01	-0.2	7.9E-01	-2.3	9.9E-02
ENSMUST00000133408				6.9	2.6E-04	4.2	9.8E-04	-1.1	2.4E-01	0.6	3.6E-01
ENSMUST00000077233				6.9	1.9E-05	-3.6	2.0E-01	1.4	3.0E-01	0.0	9.9E-01
ENSMUST00000154867				3.6	3.9E-02	2.9	5.4E-02	-1.7	2.8E-01	-1.0	3.9E-01
ENSMUST00000130579				6.9	9.6E-06	7.0	1.3E-06	-0.9	1.6E-01	-0.1	8.1E-01
ENSMUST00000154871				-1.9	1.1E-01	-1.5	3.6E-01	0.7	5.1E-01	0.3	8.7E-01
ENSMUST00000185805				6.9	4.5E-04	6.3	1.6E-03	-0.6	7.1E-01	-1.8	5.7E-02
ENSMUST00000119999				6.9	2.2E-04	2.4	2.2E-01	-2.8	2.0E-01	0.1	9.6E-01
ENSMUST00000115074				6.9	1.5E-04	4.1	8.0E-04	0.7	3.7E-01	0.2	7.7E-01
ENSMUST00000154882				-0.9	2.9E-01	0.4	6.6E-01	1.1	1.7E-01	-0.2	8.1E-01
ENSMUST00000154883				2.0	8.9E-02	3.2	4.7E-02	-0.1	9.6E-01	-1.3	2.2E-01
ENSMUST00000154890				2.0	1.5E-01	4.1	3.7E-02	0.7	6.4E-01	-1.4	2.7E-01
ENSMUST00000187239				6.9	3.4E-04	2.1	6.0E-01	7.7	1.8E-02	-1.4	7.0E-01
ENSMUST00000110264				6.9	1.1E-04	5.6	3.6E-05	-2.2	3.0E-02	-0.2	6.3E-01
ENSMUST00000154896				-1.5	9.7E-02	-0.9	3.9E-01	0.3	6.6E-01	-0.2	8.4E-01
ENSMUST00000177031				6.9	2.9E-05	7.0	6.4E-04	-0.7	6.3E-01	-1.0	2.1E-01
ENSMUST00000154899	family with sequence similarity 188, member A [Source:MGI Symbol;Acc:MGI:1914210]	D6RCI2		-2.6	9.9E-02	-1.5	5.0E-01	1.1	4.4E-01	0.0	9.9E-01
ENSMUST00000154902	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 [Source:MGI Symbol;Acc:MGI:1928387]	F2Z3X1		1.8	1.9E-01	-0.1	9.4E-01	-1.3	3.3E-01	0.6	6.6E-01
ENSMUST00000154903				-0.1	8.5E-01	0.5	6.2E-01	-0.2	7.5E-01	-0.8	3.6E-01
ENSMUST00000168370				6.9	7.5E-06	2.4	4.4E-03	-0.8	1.7E-01	-0.1	7.9E-01
ENSMUST00000142653				6.9	1.4E-04	2.2	1.3E-02	-0.5	4.8E-01	-0.1	8.2E-01
ENSMUST00000118796				6.9	1.6E-04	-4.7	9.4E-05	0.1	8.0E-01	-3.2	8.6E-03
ENSMUST00000154917	aminopeptidase puromycin sensitive [Source:MGI Symbol;Acc:MGI:1101358]	F2Z3V5		0.7	5.4E-01	0.3	8.6E-01	0.6	6.2E-01	1.0	5.0E-01
ENSMUST00000154921	lin-54 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2140902]	E9PV28		-1.1	7.4E-01	-3.4	3.0E-01	-2.3	3.0E-01	0.0	9.9E-01
ENSMUST00000120010				6.9	6.4E-04	5.8	1.6E-03	-0.2	9.0E-01	-0.5	5.5E-01
ENSMUST00000120731				6.9	1.1E-04	-2.5	2.6E-02	0.5	3.9E-01	-1.8	1.2E-01
ENSMUST00000154933	sialic acid binding Ig-like lectin H [Source:MGI Symbol;Acc:MGI:2443256]	D6RFU8		3.5	4.9E-02	4.5	3.8E-02	0.6	7.6E-01	-0.4	7.5E-01
ENSMUST00000154606				6.9	1.3E-06	6.7	2.1E-04	-0.9	4.6E-01	0.0	9.4E-01
ENSMUST00000125772				6.9	1.4E-04	3.8	4.1E-04	-0.1	8.8E-01	-0.6	2.9E-01
ENSMUST00000137481				6.9	6.6E-04	-4.6	1.8E-03	-0.1	8.9E-01	-0.8	5.2E-01
ENSMUST00000154955				2.1	3.6E-01	4.7	1.6E-01	2.0	5.2E-01	-0.7	7.5E-01
ENSMUST00000154960				-3.3	7.6E-02	-2.4	3.1E-01	0.7	6.4E-01	-0.1	9.5E-01
ENSMUST00000154961				-1.2	2.6E-01	-1.7	2.5E-01	-0.2	8.4E-01	0.4	8.1E-01
ENSMUST00000150295				6.9	1.9E-04	6.1	8.2E-04	0.8	5.2E-01	-0.1	8.6E-01
ENSMUST00000124644				6.9	1.7E-04	6.5	5.1E-03	-3.1	1.6E-01	-3.0	3.9E-02
ENSMUST00000138036				6.9	3.9E-04	8.8	2.4E-04	1.2	4.5E-01	-0.3	6.1E-01
ENSMUST00000154972				0.1	7.5E-01	0.2	7.9E-01	-0.1	8.2E-01	-0.1	8.5E-01
ENSMUST00000154974				1.4	8.6E-02	1.0	2.8E-01	0.4	6.0E-01	0.7	3.8E-01
ENSMUST00000155253				6.9	9.0E-05	-1.8	2.5E-01	-5.5	3.6E-03	1.4	3.3E-01
ENSMUST00000136119				6.9	1.5E-04	4.6	4.1E-03	0.0	9.9E-01	-0.3	7.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000192302				6.9	2.2E-02	3.1	4.0E-02	-0.5	6.9E-01	-0.4	7.3E-01
ENSMUST00000120962				6.9	7.2E-05	5.2	1.8E-04	-0.4	6.4E-01	-0.1	8.3E-01
ENSMUST00000190746				6.9	5.6E-05	3.9	5.7E-04	-2.9	1.0E-02	-0.8	1.8E-01
ENSMUST00000119058				6.9	7.4E-05	-4.2	3.3E-02	0.0	9.6E-01	-0.7	7.1E-01
ENSMUST00000154991	scaffold attachment factor B2 [Source:MGI Symbol;Acc:MGI:2146808]	F6Z0Y5		-0.1	9.4E-01	0.3	8.9E-01	0.9	5.0E-01	0.5	7.3E-01
ENSMUST00000154995				-1.8	4.1E-02	0.6	4.7E-01	0.0	9.7E-01	-2.4	1.5E-02
ENSMUST00000154998				3.0	6.4E-02	-1.7	5.1E-01	-1.0	5.0E-01	3.7	1.4E-01
ENSMUST00000171163				6.9	9.5E-05	-6.6	3.8E-04	0.7	1.1E-01	0.6	6.7E-01
ENSMUST00000107660				6.9	1.1E-04	0.6	6.2E-01	4.1	9.5E-04	0.8	4.5E-01
ENSMUST00000153841				6.9	4.7E-06	-7.8	1.7E-05	-1.1	1.8E-02	-3.5	1.7E-02
ENSMUST00000174340				6.9	4.3E-05	5.6	1.4E-02	-1.9	3.7E-01	-1.6	2.4E-01
ENSMUST00000151647				6.9	6.5E-04	-4.1	8.2E-02	0.3	7.4E-01	-0.8	7.4E-01
ENSMUST00000141212				6.9	4.6E-05	4.6	6.3E-02	0.3	8.7E-01	1.1	4.5E-01
ENSMUST00000194895				6.9	1.0E-04	8.6	3.1E-05	-0.6	6.4E-01	-0.8	1.5E-01
ENSMUST00000172620				6.9	3.0E-05	3.8	1.9E-03	-0.2	7.6E-01	0.3	6.9E-01
ENSMUST00000185314				6.9	7.2E-05	6.1	4.0E-04	-0.5	7.0E-01	-0.3	6.5E-01
ENSMUST00000185433				6.9	9.7E-06	6.8	9.0E-05	-0.6	5.9E-01	-0.2	7.0E-01
ENSMUST00000118528				6.9	7.6E-04	7.6	4.6E-04	1.6	2.6E-01	-0.8	3.1E-01
ENSMUST00000155050	polynucleotide kinase 3'- phosphatase [Source:MGI Symbol;Acc:MGI:1891698]			1.1	1.2E-01	0.4	6.6E-01	-0.1	8.5E-01	0.6	4.2E-01
ENSMUST00000155061				0.4	7.3E-01	1.6	3.0E-01	0.0	9.8E-01	-1.2	3.7E-01
ENSMUST00000125007				6.9	8.5E-04	-2.8	3.3E-02	-0.7	3.6E-01	-2.2	1.4E-01
ENSMUST00000155068	zinc finger, CCHC domain containing 11 [Source:MGI Symbol;Acc:MGI:2445126]	A0A0A0MQJ6		4.5	5.9E-02	7.6	1.6E-02	1.5	5.7E-01	-1.5	3.6E-01
ENSMUST00000154240				6.9	7.8E-04	4.6	6.8E-03	-1.5	3.1E-01	-0.7	4.7E-01
ENSMUST00000177016				6.9	3.5E-05	6.5	2.4E-03	1.5	3.3E-01	0.7	4.0E-01
ENSMUST00000155083				-1.3	2.1E-01	1.0	4.2E-01	1.3	2.0E-01	-1.0	4.0E-01
ENSMUST00000162465				6.9	1.6E-04	6.6	3.7E-04	-0.5	7.1E-01	-0.1	8.9E-01
ENSMUST00000126331				6.9	4.3E-04	5.0	2.5E-04	-1.4	1.5E-01	-0.1	8.8E-01
ENSMUST00000139607				6.9	8.6E-07	2.5	9.3E-02	-0.5	6.7E-01	3.4	8.2E-03
ENSMUST00000155220				6.9	4.8E-05	2.2	9.5E-02	-3.1	4.6E-02	1.0	2.8E-01
ENSMUST00000155094	nuclear antigen Sp100 [Source:MGI Symbol;Acc:MGI:109561]		O35892	-3.7	1.5E-01	-5.9	8.0E-02	-2.4	9.5E-02	-0.2	9.5E-01
ENSMUST00000152884				6.9	3.7E-05	7.9	6.2E-05	-0.7	6.0E-01	-0.7	2.7E-01
ENSMUST00000155099				-0.9	1.3E-01	0.2	7.8E-01	0.8	1.3E-01	-0.3	6.7E-01
ENSMUST00000153740				6.9	1.0E-02	3.5	5.5E-04	-0.2	7.1E-01	-0.4	5.0E-01
ENSMUST00000155107	polymerase (DNA directed), gamma 2, accessory subunit [Source:MGI Symbol;Acc:MGI:1354947]	D6RFU3		0.9	1.4E-01	1.3	1.1E-01	0.7	2.4E-01	0.3	6.5E-01
ENSMUST00000139021				6.9	8.1E-04	3.4	2.6E-03	-0.1	8.8E-01	0.1	9.0E-01
ENSMUST00000140433				6.9	1.1E-02	-3.6	4.3E-02	1.7	4.1E-02	-1.1	5.4E-01
ENSMUST00000149653				6.9	1.2E-04	2.5	3.2E-04	-0.1	8.5E-01	-0.6	1.3E-01
ENSMUST00000138053				6.9	9.5E-05	3.5	2.7E-02	-0.2	8.5E-01	0.8	4.8E-01
ENSMUST00000155123	PHD and ring finger domains 1 [Source:MGI Symbol;Acc:MGI:2141847]	D6RI35		-1.0	7.3E-01	1.5	6.1E-01	0.3	9.2E-01	-2.2	4.4E-01
ENSMUST00000182442				6.9	3.9E-05	2.5	3.2E-02	-2.0	7.8E-02	-0.8	3.4E-01
ENSMUST00000092138				6.9	2.8E-07	7.4	2.1E-03	-1.4	4.7E-01	0.4	6.7E-01
ENSMUST00000120559				6.9	5.3E-05	-4.3	3.7E-02	-0.9	3.3E-01	0.3	8.6E-01
ENSMUST00000156814				6.9	2.4E-04	3.1	2.6E-02	-1.5	2.6E-01	-0.8	3.8E-01
ENSMUST00000155146				1.5	6.5E-02	1.7	9.1E-02	0.0	9.8E-01	-0.1	8.8E-01
ENSMUST00000170531				6.9	9.5E-06	6.5	5.9E-03	-0.5	7.8E-01	0.2	8.7E-01
ENSMUST00000188760				6.9	7.4E-05	-5.5	5.3E-03	0.3	6.4E-01	-0.9	5.8E-01
ENSMUST00000121884				6.9	9.9E-05	3.8	1.6E-02	-1.0	4.4E-01	0.1	9.3E-01
ENSMUST00000100448				6.9	5.4E-05	3.2	1.1E-01	-1.9	3.5E-01	1.1	4.0E-01
ENSMUST00000155160				-1.5	8.2E-02	0.2	8.4E-01	1.3	1.3E-01	-0.5	6.2E-01
ENSMUST00000155161				1.3	4.5E-01	2.8	1.7E-01	0.0	1.0E+00	-1.5	3.7E-01
ENSMUST00000186789				6.9	2.0E-06	4.4	1.5E-02	-1.4	3.8E-01	0.9	4.0E-01
ENSMUST00000121113				6.9	1.7E-04	3.8	1.5E-02	0.6	6.3E-01	0.5	5.8E-01
ENSMUST00000155169				1.3	7.5E-02	2.7	6.4E-03	0.0	9.5E-01	-1.3	6.6E-02
ENSMUST00000135874				6.9	1.1E-05	4.9	1.6E-04	0.0	9.7E-01	-0.4	5.0E-01
ENSMUST00000104965				6.9	2.4E-05	-4.9	2.3E-02	1.0	1.9E-01	-0.4	8.6E-01
ENSMUST00000126754				6.9	1.0E-04	6.2	3.8E-04	-0.6	6.5E-01	-3.4	2.7E-03
ENSMUST00000128720				6.9	3.9E-05	7.7	4.5E-05	-1.3	3.0E-01	-0.2	7.8E-01
ENSMUST00000148131				6.9	1.2E-04	5.7	3.4E-03	-0.7	6.7E-01	0.5	5.8E-01
ENSMUST00000181643				6.9	1.8E-05	5.2	3.8E-04	-0.4	6.4E-01	0.7	3.1E-01
ENSMUST00000155207	mortality factor 4 like 2 [Source:MGI Symbol;Acc:MGI:1927167]	A2AEB3		-0.4	8.8E-01	-4.6	1.6E-01	-4.9	2.5E-02	-0.7	8.4E-01
ENSMUST00000137994				6.9	5.2E-04	0.9	5.2E-01	0.6	6.3E-01	3.4	1.4E-02
ENSMUST00000155216	adenylate cyclase 10 [Source:MGI Symbol;Acc:MGI:2660854]	M0QWB5		4.1	7.2E-02	6.5	2.0E-02	0.3	9.2E-01	-2.2	1.6E-01
ENSMUST00000152751				6.9	1.7E-06	6.2	2.8E-04	-0.6	6.1E-01	-0.4	5.7E-01
ENSMUST00000148259				6.9	1.3E-06	6.1	2.3E-04	-0.6	6.1E-01	0.2	7.2E-01
ENSMUST00000155226	E26 avian leukemia oncogene 2, 3' domain [Source:MGI Symbol;Acc:MGI:95456]	D3Z4F9		2.3	1.8E-01	-0.3	9.1E-01	-2.3	1.9E-01	0.2	9.2E-01
ENSMUST00000155227	FERM domain containing 8 [Source:MGI Symbol;Acc:MGI:1914707]	D3Z5B2		0.4	8.1E-01	0.6	7.6E-01	0.5	7.2E-01	0.3	8.4E-01
ENSMUST00000155271				6.9	1.8E-05	5.5	9.9E-04	-1.4	2.9E-01	0.2	8.0E-01
ENSMUST00000155242	heat shock protein 90, alpha (cytosolic), class A member 1 [Source:MGI Symbol;Acc:MGI:96250]	B7ZC50		1.6	4.3E-01	-4.8	1.3E-02	-8.2	5.9E-04	-1.8	3.4E-01
ENSMUST00000118247				6.9	1.8E-04	5.8	2.1E-03	-0.6	6.7E-01	0.2	7.9E-01
ENSMUST00000122095				6.9	1.5E-04	5.1	7.9E-04	-0.7	5.1E-01	-0.6	3.7E-01
ENSMUST00000122388				6.9	8.0E-05	5.9	4.6E-04	-2.7	5.5E-02	-0.2	8.1E-01
ENSMUST00000162013				6.9	6.6E-04	6.4	2.8E-04	-0.6	6.0E-01	-0.2	7.7E-01
ENSMUST00000190211				6.9	3.4E-05	5.0	3.6E-04	-0.3	7.6E-01	0.3	5.5E-01
ENSMUST00000142550				6.9	1.3E-04	-4.5	7.7E-04	0.1	8.6E-01	-1.5	1.8E-01
ENSMUST00000144338				6.9	6.4E-05	2.3	5.0E-03	-0.9	1.5E-01	-0.7	2.0E-01
ENSMUST00000145316				6.9	1.3E-04	3.8	6.6E-04	-0.2	8.0E-01	-0.7	2.3E-01
ENSMUST00000164864				6.9	2.4E-04	6.1	2.2E-03	-0.1	9.6E-01	-0.6	4.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000187024				6.9	3.2E-04	8.0	3.1E-05	0.5	6.3E-01	-0.6	2.7E-01
ENSMUST00000135005				6.9	3.8E-04	7.0	3.4E-02	2.8	3.0E-01	1.7	3.6E-01
ENSMUST00000155277				0.9	2.4E-01	1.2	2.1E-01	-0.2	7.7E-01	-0.5	5.3E-01
ENSMUST00000177032				6.9	5.0E-04	-3.5	2.0E-01	2.1	1.0E-01	-0.1	9.8E-01
ENSMUST00000155281	zinc finger, NFX1-type containing 1 [Source:MGI Symbol;Acc:MGI:2138982]	A2A5R5		-2.8	4.7E-02	1.7	4.2E-01	4.4	2.0E-02	-0.2	9.2E-01
ENSMUST00000148446				6.9	1.7E-04	-3.2	9.4E-02	2.3	3.2E-02	-0.5	7.6E-01
ENSMUST00000155284	RalBP1 associated Eps domain containing protein [Source:MGI Symbol;Acc:MGI:1196373]	D6RIN6		0.3	8.8E-01	2.7	4.6E-01	4.3	1.7E-01	1.9	4.6E-01
ENSMUST00000155285	transformed mouse 3T3 cell double minute 2 [Source:MGI Symbol;Acc:MGI:96952]	J3QP04		-1.1	4.3E-01	0.2	9.1E-01	1.2	3.5E-01	-0.1	9.3E-01
ENSMUST00000155287				-0.4	7.2E-01	1.3	3.2E-01	0.4	7.1E-01	-1.3	2.7E-01
ENSMUST00000155288				0.3	8.8E-01	0.2	9.3E-01	-2.0	2.6E-01	-1.9	3.4E-01
ENSMUST00000188425				6.9	1.2E-04	-5.6	2.5E-04	0.5	2.4E-01	-0.5	6.1E-01
ENSMUST00000030951				6.9	2.0E-04	6.0	2.1E-03	-0.6	6.7E-01	0.9	2.6E-01
ENSMUST00000150578				6.9	5.2E-06	4.5	6.5E-03	-0.5	6.7E-01	-0.1	8.8E-01
ENSMUST00000155310				2.0	1.5E-01	4.6	1.2E-02	0.7	6.2E-01	-1.8	1.3E-01
ENSMUST00000159477				6.9	2.1E-04	6.1	2.7E-04	-1.4	2.5E-01	0.8	2.2E-01
ENSMUST00000174378				6.9	8.5E-04	5.2	1.8E-02	-0.5	7.8E-01	0.7	5.5E-01
ENSMUST00000100555				6.8	1.2E-03	6.9	1.9E-05	-0.3	7.1E-01	0.1	7.7E-01
ENSMUST00000129772				6.8	1.5E-04	-1.6	7.4E-02	0.1	8.3E-01	-0.7	4.3E-01
ENSMUST00000155327				0.1	8.8E-01	1.0	3.0E-01	0.3	7.2E-01	-0.6	4.7E-01
ENSMUST00000155329	ankyrin repeat and KH domain containing 1 [Source:MGI Symbol;Acc:MGI:1921733]	E9PUR0		-2.5	2.2E-01	-1.0	6.8E-01	0.3	8.3E-01	-1.2	6.2E-01
ENSMUST00000155331				1.7	6.8E-02	2.5	5.3E-02	0.6	5.1E-01	-0.1	8.9E-01
ENSMUST00000155336				1.6	3.1E-01	3.1	9.2E-02	-0.2	9.0E-01	-1.7	2.5E-01
ENSMUST00000167639				6.8	3.2E-03	-1.2	3.1E-01	0.7	3.4E-01	-1.0	4.0E-01
ENSMUST00000183748				6.8	2.2E-03	2.9	4.0E-02	-0.6	6.2E-01	0.3	7.5E-01
ENSMUST00000155342	tec protein tyrosine kinase [Source:MGI Symbol;Acc:MGI:98662]	F6W1T9		2.6	2.3E-01	-4.8	1.4E-01	-4.1	3.9E-02	3.2	3.0E-01
ENSMUST00000155348	peptidase inhibitor 16 [Source:MGI Symbol;Acc:MGI:1921366]	F6QYZ5		-0.6	4.6E-01	0.6	6.1E-01	1.4	1.1E-01	0.3	7.9E-01
ENSMUST00000155351				0.9	1.2E-01	1.6	3.0E-02	-0.5	3.7E-01	-1.2	6.4E-02
ENSMUST00000119454				6.8	5.4E-05	5.9	3.1E-03	-0.5	7.6E-01	-2.0	5.3E-02
ENSMUST00000124236				6.8	2.7E-04	6.8	7.7E-04	0.3	8.4E-01	-0.6	4.5E-01
ENSMUST00000152917				6.8	1.7E-06	-8.3	3.9E-03	-1.1	1.2E-01	1.2	6.3E-01
ENSMUST00000155367	plasminogen receptor, C-terminal lysine transmembrane protein [Source:MGI Symbol;Acc:MGI:1915009]	D3YY76		-0.8	4.2E-01	-1.1	3.5E-01	-0.6	4.5E-01	-0.4	7.3E-01
ENSMUST00000157073				6.8	3.0E-05	6.7	2.5E-05	0.1	9.3E-01	0.7	1.7E-01
ENSMUST00000155370	ERGIC and golgi 3 [Source:MGI Symbol;Acc:MGI:1913616]	F6RK81		-4.3	8.6E-02	2.2	5.4E-01	6.4	2.7E-02	-0.1	9.7E-01
ENSMUST00000155371				-1.0	4.4E-01	1.0	5.1E-01	0.8	5.3E-01	-1.2	3.8E-01
ENSMUST00000142696				6.8	2.2E-04	7.5	3.4E-05	-1.2	3.1E-01	-0.3	5.6E-01
ENSMUST00000155377				-1.3	3.8E-01	-0.2	9.1E-01	1.7	3.5E-01	0.7	6.9E-01
ENSMUST00000155378	THUMP domain containing 3 [Source:MGI Symbol;Acc:MGI:1277973]	D3YYB2		-2.1	6.0E-02	-4.4	7.7E-03	-1.5	4.6E-02	0.9	5.3E-01
ENSMUST00000155381	RAB11 family interacting protein 4 (class II) [Source:MGI Symbol;Acc:MGI:2442920]	F6YI06		-0.3	7.2E-01	0.6	5.5E-01	-0.3	6.4E-01	-1.2	2.1E-01
ENSMUST00000148013				6.8	1.1E-04	6.5	6.6E-04	-0.7	6.4E-01	-1.3	1.2E-01
ENSMUST00000155523				6.8	1.7E-04	3.6	1.6E-02	0.8	4.9E-01	-0.3	7.6E-01
ENSMUST00000174246				6.8	4.9E-03	3.5	3.0E-02	-1.5	2.6E-01	-0.1	9.5E-01
ENSMUST00000156336				6.8	1.9E-04	6.0	2.4E-04	-0.4	7.4E-01	-1.2	8.1E-02
ENSMUST00000136944				6.8	2.3E-04	6.5	3.7E-04	-0.6	6.2E-01	0.3	6.5E-01
ENSMUST00000124306				6.8	9.7E-04	5.0	4.3E-03	0.6	6.5E-01	-0.4	5.6E-01
ENSMUST00000155408				3.3	5.0E-02	7.3	5.6E-03	1.8	3.8E-01	-2.3	9.3E-02
ENSMUST00000127187				6.8	4.8E-05	-4.2	1.4E-02	-0.7	3.1E-01	-0.6	6.9E-01
ENSMUST00000127393				6.8	5.4E-05	-2.3	2.9E-02	0.8	1.5E-01	-0.3	7.2E-01
ENSMUST00000143707				6.8	3.2E-04	7.6	1.2E-03	0.8	6.3E-01	1.0	2.3E-01
ENSMUST00000155685				6.8	6.1E-05	6.4	6.2E-04	0.7	5.6E-01	0.0	9.6E-01
ENSMUST00000155422				5.5	3.6E-02	4.8	1.0E-01	-0.2	9.5E-01	0.5	7.9E-01
ENSMUST00000155431				-0.6	6.9E-01	-2.1	4.2E-01	0.8	5.9E-01	2.3	3.6E-01
ENSMUST00000135615				6.8	6.9E-04	2.8	2.2E-03	0.6	3.2E-01	1.1	5.5E-02
ENSMUST00000155434				-2.4	1.6E-01	-2.7	2.8E-01	-0.4	7.7E-01	-0.1	9.6E-01
ENSMUST00000155436				2.9	5.6E-02	4.2	2.6E-02	0.3	8.2E-01	-0.9	4.8E-01
ENSMUST00000142218				6.8	3.9E-05	1.4	4.5E-02	-1.6	1.5E-02	-0.2	7.6E-01
ENSMUST00000155452	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit [Source:MGI Symbol;Acc:MGI:106341]	F6XVM5		-3.9	9.7E-02	-5.1	9.9E-02	-1.2	3.9E-01	0.0	1.0E+00
ENSMUST00000192223				6.8	6.0E-05	6.4	3.2E-04	-0.5	7.1E-01	0.0	9.5E-01
ENSMUST00000143963				6.8	1.5E-04	7.5	6.7E-05	-0.6	6.1E-01	-1.0	1.2E-01
ENSMUST00000143972				6.8	3.3E-07	2.2	2.6E-02	0.0	9.5E-01	-0.1	9.3E-01
ENSMUST00000155461				3.7	6.8E-02	3.5	2.1E-01	1.4	5.2E-01	1.6	4.6E-01
ENSMUST00000178167				6.8	2.4E-04	2.2	1.6E-01	-0.8	5.1E-01	2.2	8.0E-02
ENSMUST00000134564				6.8	1.8E-05	7.2	5.4E-05	0.5	6.1E-01	-0.4	4.5E-01
ENSMUST00000155477				-1.1	3.7E-01	2.5	9.7E-02	1.6	1.8E-01	-2.0	1.5E-01
ENSMUST00000120625				6.8	9.4E-04	6.5	3.4E-03	-1.3	4.6E-01	-1.2	2.0E-01
ENSMUST00000121562				6.8	4.9E-05	-6.2	1.0E-03	1.2	3.3E-02	-0.3	8.3E-01
ENSMUST00000137320				6.8	1.4E-05	7.9	4.1E-05	-0.6	6.1E-01	-0.3	5.2E-01
ENSMUST00000190841				6.8	1.8E-06	-2.2	1.6E-01	1.9	3.7E-02	-0.5	7.6E-01
ENSMUST00000193931				6.8	5.3E-04	-4.9	1.0E-02	-1.2	1.4E-01	-2.0	3.1E-01
ENSMUST00000119778				6.8	7.8E-05	2.4	1.1E-01	2.7	4.1E-02	-3.2	4.7E-02
ENSMUST00000128568				6.8	1.5E-04	1.4	4.7E-01	5.1	3.5E-03	-1.0	5.8E-01
ENSMUST00000134164				6.8	1.3E-04	-3.0	1.8E-02	-0.3	6.0E-01	0.2	8.3E-01
ENSMUST00000155507				-1.0	1.6E-01	-0.9	3.0E-01	-0.2	7.2E-01	-0.3	7.6E-01
ENSMUST00000124364				6.8	1.7E-05	5.2	1.9E-03	-1.9	1.6E-01	-0.1	8.4E-01
ENSMUST00000155512				-1.2	1.2E-01	0.1	9.1E-01	0.7	3.4E-01	-0.7	4.6E-01
ENSMUST00000155514				-0.2	8.6E-01	-1.3	5.7E-01	0.4	7.9E-01	1.4	4.8E-01
ENSMUST00000100443				6.8	2.9E-05	-1.1	4.1E-01	2.7	1.3E-02	-0.2	8.9E-01
ENSMUST00000174683				6.8	1.0E-03	7.3	3.6E-04	0.7	6.1E-01	-1.3	1.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000140860				6.8	3.5E-05	7.0	1.5E-04	-0.5	6.5E-01	-1.3	7.0E-02
ENSMUST00000139013				6.8	4.4E-04	-4.5	4.5E-03	0.6	2.6E-01	-0.8	5.3E-01
ENSMUST00000139436				6.8	2.2E-03	5.6	7.2E-04	1.1	3.0E-01	-0.8	2.6E-01
ENSMUST00000195447				6.8	7.5E-05	6.9	1.9E-03	0.9	5.5E-01	0.9	3.0E-01
ENSMUST00000155530	family with sequence similarity 188, member A [Source:MGI Symbol;Acc:MGI:1914210]	D6RGT9		-4.0	1.7E-01	-3.4	3.3E-01	-0.3	8.5E-01	-1.0	8.0E-01
ENSMUST00000116191				6.8	1.4E-03	11.4	1.1E-04	-1.0	6.1E-01	0.4	5.8E-01
ENSMUST00000170839				6.8	5.4E-05	4.6	3.3E-03	0.7	5.5E-01	0.6	4.5E-01
ENSMUST00000145441				6.8	1.2E-03	7.8	2.3E-04	1.1	4.2E-01	-0.3	6.3E-01
ENSMUST00000128226				6.8	2.8E-03	5.3	2.5E-02	-0.8	7.3E-01	-0.2	8.7E-01
ENSMUST00000155551	DDB1 and CUL4 associated factor 10 [Source:MGI Symbol;Acc:MGI:2140179]		A2AKB9	0.5	3.6E-01	1.8	3.2E-02	1.0	9.8E-02	-0.3	6.6E-01
ENSMUST00000155552				-2.3	3.3E-01	-3.9	1.8E-01	-2.4	1.4E-01	-0.8	7.9E-01
ENSMUST00000129151				6.8	2.6E-06	3.6	1.1E-02	0.2	8.8E-01	0.3	7.1E-01
ENSMUST00000154707				6.8	6.2E-03	5.7	3.4E-05	0.0	9.9E-01	1.3	2.0E-02
ENSMUST00000194199				6.8	6.3E-05	5.4	1.3E-03	-1.5	2.7E-01	-0.6	4.5E-01
ENSMUST00000139854				6.8	7.8E-06	6.6	7.1E-04	-0.7	6.0E-01	0.2	7.5E-01
ENSMUST00000140351				6.8	1.3E-04	2.6	2.6E-03	-5.4	1.6E-04	-0.1	8.6E-01
ENSMUST00000177379				6.8	6.2E-05	7.2	1.2E-04	-0.6	6.0E-01	0.0	9.4E-01
ENSMUST00000137504				6.8	8.0E-05	6.7	3.6E-04	-0.4	7.8E-01	-0.5	4.2E-01
ENSMUST00000155566				0.2	8.3E-01	-0.3	7.7E-01	-0.2	7.9E-01	0.3	7.8E-01
ENSMUST00000155569				2.6	1.8E-01	1.8	5.4E-01	1.1	5.9E-01	1.8	5.0E-01
ENSMUST00000155571	family with sequence similarity 222, member B [Source:MGI Symbol;Acc:MGI:2384939]		Q6P539	0.2	8.1E-01	1.5	2.8E-01	1.1	3.4E-01	-0.2	8.5E-01
ENSMUST00000170348				6.8	1.2E-03	7.9	3.3E-04	0.7	6.2E-01	-1.0	2.0E-01
ENSMUST00000141425				6.8	1.2E-04	4.7	1.8E-03	1.5	1.7E-01	-0.3	6.3E-01
ENSMUST00000167426				6.8	1.9E-02	-5.2	2.7E-02	0.8	3.2E-01	-0.8	7.2E-01
ENSMUST00000146391				6.8	3.2E-04	-4.7	5.2E-03	1.0	1.0E-01	2.2	1.1E-01
ENSMUST00000155579	SERTA domain containing 4 [Source:MGI Symbol;Acc:MGI:2443496]		A7DTG3	2.7	6.8E-02	6.4	7.2E-04	-0.5	7.2E-01	-4.2	2.0E-03
ENSMUST00000155582				-0.6	4.8E-01	-1.0	3.7E-01	-0.1	9.0E-01	0.3	7.6E-01
ENSMUST00000183354				6.8	1.5E-04	-5.3	6.4E-03	0.4	4.6E-01	-0.1	9.6E-01
ENSMUST00000161889				6.8	2.2E-03	7.4	1.9E-05	-0.9	3.9E-01	-0.4	4.2E-01
ENSMUST00000155592	TCF3 (E2A) fusion partner [Source:MGI Symbol;Acc:MGI:1916964]		Q3U1J1	-2.6	4.3E-02	-2.0	2.5E-01	1.0	3.1E-01	0.4	8.1E-01
ENSMUST00000155599				0.7	7.1E-01	0.1	9.4E-01	-1.4	4.0E-01	-0.9	6.4E-01
ENSMUST00000183378				6.8	2.0E-06	-4.7	2.9E-02	0.7	3.7E-01	0.5	7.9E-01
ENSMUST00000155604				-2.7	9.0E-02	-1.4	4.6E-01	0.8	5.1E-01	-0.5	8.0E-01
ENSMUST00000119812				6.8	1.7E-04	-4.7	1.2E-02	-2.5	1.2E-02	-2.1	2.7E-01
ENSMUST00000155607				4.3	5.6E-02	3.1	2.1E-01	-2.0	4.0E-01	-0.7	6.8E-01
ENSMUST00000173538				6.8	1.9E-05	4.9	1.5E-03	-0.2	8.8E-01	-0.1	8.4E-01
ENSMUST00000181716				6.8	8.0E-05	5.8	4.4E-04	0.2	8.1E-01	0.0	9.6E-01
ENSMUST00000155616				-1.6	3.2E-01	1.2	5.9E-01	1.4	4.5E-01	-1.4	4.3E-01
ENSMUST00000192551				6.8	6.3E-05	4.5	2.4E-02	-0.9	6.2E-01	-0.3	8.0E-01
ENSMUST00000140085				6.8	3.2E-03	-2.2	4.1E-02	-0.2	7.9E-01	-2.6	4.6E-02
ENSMUST00000119296				6.8	4.2E-07	8.1	8.9E-05	-0.6	6.5E-01	-0.2	7.5E-01
ENSMUST00000161036				6.8	7.4E-04	4.0	1.3E-01	-0.8	7.2E-01	1.4	4.3E-01
ENSMUST00000119217				6.8	7.4E-04	-1.0	5.8E-01	0.9	4.3E-01	-2.5	2.3E-01
ENSMUST00000155634	solute carrier family 2 (facilitated glucose transporter), member 9 [Source:MGI Symbol;Acc:MGI:2152844]	B9EHN5		1.3	3.0E-01	0.9	6.2E-01	0.6	6.8E-01	1.0	4.8E-01
ENSMUST00000155635				0.7	7.0E-01	0.0	9.9E-01	-0.7	6.7E-01	0.0	9.9E-01
ENSMUST00000145544				6.8	1.9E-03	5.9	2.7E-03	-1.4	4.0E-01	-0.3	7.4E-01
ENSMUST00000151645				6.8	1.7E-04	10.3	5.4E-05	-0.8	6.3E-01	0.8	1.7E-01
ENSMUST00000165966				6.8	2.2E-05	-1.2	5.3E-01	2.2	8.7E-02	-0.7	6.9E-01
ENSMUST00000134269				6.8	2.2E-06	5.0	9.5E-04	0.3	8.0E-01	-0.6	4.2E-01
ENSMUST00000194842				6.8	1.8E-04	6.3	4.3E-04	-0.5	7.1E-01	0.2	7.4E-01
ENSMUST00000152788				6.8	3.2E-05	7.2	2.2E-05	-1.9	8.6E-02	-0.1	8.0E-01
ENSMUST00000155655				-3.1	2.6E-01	1.7	6.4E-01	2.2	4.5E-01	-2.6	4.0E-01
ENSMUST00000120581				6.8	2.1E-03	3.1	2.5E-01	-0.7	7.7E-01	1.6	3.9E-01
ENSMUST00000185329				6.8	4.9E-05	4.8	1.4E-05	-0.1	8.6E-01	-0.7	7.7E-02
ENSMUST00000128762				6.8	2.4E-04	6.5	1.8E-04	-1.2	3.1E-01	0.1	8.9E-01
ENSMUST00000134832				6.8	7.8E-05	9.7	1.1E-06	-1.2	2.0E-01	1.3	6.5E-03
ENSMUST00000155671	vacuolar protein sorting 29 (S. pombe) [Source:MGI Symbol;Acc:MGI:1928344]		Q9QZ88	1.0	6.1E-02	0.4	5.3E-01	-0.2	7.1E-01	0.4	4.7E-01
ENSMUST00000163708				6.8	1.4E-05	-1.6	1.4E-01	1.1	1.1E-01	-1.2	2.8E-01
ENSMUST00000117977				6.8	1.3E-04	0.1	9.7E-01	5.0	1.0E-02	-1.1	6.5E-01
ENSMUST00000137844				6.8	9.6E-06	-0.2	8.4E-01	1.5	7.7E-02	-2.5	5.7E-02
ENSMUST00000155679	myotubularin related protein 2 [Source:MGI Symbol;Acc:MGI:1924366]	Q6P572		-2.6	3.5E-01	-2.3	3.6E-01	-2.3	2.3E-01	-2.6	3.8E-01
ENSMUST00000128212				6.8	6.7E-05	6.3	8.4E-04	-0.5	7.3E-01	-0.2	8.0E-01
ENSMUST00000188518				6.8	7.3E-04	6.4	1.9E-04	-0.6	6.1E-01	-0.1	8.1E-01
ENSMUST00000155689	RFT1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:3607791]	D6RFD6		3.7	1.5E-01	6.7	8.1E-02	3.1	3.6E-01	0.1	9.7E-01
ENSMUST00000121081				6.8	1.1E-04	6.0	3.3E-04	-0.6	6.1E-01	0.2	7.3E-01
ENSMUST00000146891				6.8	6.8E-06	-6.5	1.9E-02	1.0	2.3E-01	1.9	4.2E-01
ENSMUST00000155700				3.3	5.6E-02	4.3	4.8E-02	0.2	9.3E-01	-0.9	5.4E-01
ENSMUST00000153534				6.8	4.7E-05	2.6	2.9E-01	-0.8	7.1E-01	2.6	1.8E-01
ENSMUST00000191574				6.8	1.3E-04	3.9	3.8E-02	0.1	9.4E-01	-0.2	8.4E-01
ENSMUST00000098625				6.8	6.7E-05	-3.9	6.8E-03	0.4	4.8E-01	-0.6	6.1E-01
ENSMUST00000144402				6.8	3.5E-05	-2.4	1.1E-01	1.2	1.5E-01	-3.1	8.4E-02
ENSMUST00000146475				6.8	1.3E-04	7.4	6.4E-05	-0.5	6.6E-01	-0.2	7.4E-01
ENSMUST00000152132				6.8	4.3E-05	-1.1	4.7E-01	0.6	5.8E-01	-2.5	1.6E-01
ENSMUST00000155720				1.2	5.1E-01	1.3	6.5E-01	2.5	2.9E-01	2.4	2.6E-01
ENSMUST00000145363				6.8	1.2E-03	7.9	3.4E-04	-0.3	8.3E-01	-0.6	3.8E-01
ENSMUST00000164876				6.8	3.1E-04	4.9	2.5E-03	0.3	8.2E-01	1.7	4.1E-02
ENSMUST00000186139				6.8	4.2E-06	5.6	1.3E-03	-0.2	8.8E-01	0.1	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000187992				6.8	1.3E-04	5.8	1.4E-03	1.2	3.6E-01	-1.3	1.1E-01
ENSMUST00000150045				6.8	1.7E-05	4.3	2.1E-03	0.0	9.7E-01	-1.1	2.1E-01
ENSMUST00000130080				6.8	2.4E-04	2.7	4.5E-03	-0.1	8.4E-01	0.3	5.9E-01
ENSMUST00000155744				-4.9	1.5E-01	-3.8	3.3E-01	-0.7	7.9E-01	-1.8	6.5E-01
ENSMUST00000177892				6.8	2.5E-04	7.7	1.9E-04	0.7	6.1E-01	0.3	5.9E-01
ENSMUST00000120258				6.8	3.4E-06	-3.0	2.1E-02	1.0	1.1E-01	-0.8	5.1E-01
ENSMUST00000155757	Ras-related GTP binding C [Source:MGI Symbol;Acc:MGI:1858751]		Q99K70	-1.6	1.4E-01	1.0	4.0E-01	0.3	7.6E-01	-2.3	6.5E-02
ENSMUST00000155760				3.6	6.6E-02	5.8	9.4E-03	-0.5	8.1E-01	-2.7	5.2E-02
ENSMUST00000123484				6.8	4.2E-04	6.6	1.4E-04	-0.3	8.0E-01	1.0	1.3E-01
ENSMUST00000155764	RIKEN cDNA 9330182L06 gene [Source:MGI Symbol;Acc:MGI:2443264]	E9PUJ3		3.2	1.3E-01	4.7	8.1E-02	0.5	8.6E-01	-1.1	5.0E-01
ENSMUST00000142254				6.8	6.1E-04	6.9	3.0E-04	-0.4	7.5E-01	-1.6	4.6E-02
ENSMUST00000195361				6.8	2.9E-05	2.7	3.0E-01	0.4	8.7E-01	2.6	2.2E-01
ENSMUST00000156078				6.8	7.1E-07	6.5	2.8E-04	-0.1	9.3E-01	0.4	4.7E-01
ENSMUST00000155778	zinc finger, DHHC domain containing 3 [Source:MGI Symbol;Acc:MGI:1926134]	Q05D46		-1.7	3.9E-01	3.2	3.2E-01	4.7	7.1E-02	-0.3	9.2E-01
ENSMUST00000188077				6.8	1.0E-03	-3.5	2.1E-02	0.5	4.7E-01	1.0	4.4E-01
ENSMUST00000186061				6.8	2.4E-04	-1.4	3.1E-02	-0.3	4.9E-01	-0.5	3.2E-01
ENSMUST00000184160				6.8	3.7E-06	13.5	4.0E-07	-1.1	3.6E-01	-0.3	3.1E-01
ENSMUST00000145390				6.8	1.1E-06	6.6	2.2E-04	-0.5	6.8E-01	-1.6	3.5E-02
ENSMUST00000148005				6.8	1.3E-06	4.2	1.3E-02	0.6	6.7E-01	0.6	4.4E-01
ENSMUST00000133332				6.8	8.9E-05	3.3	6.4E-02	-1.6	3.6E-01	0.7	5.7E-01
ENSMUST00000139786				6.8	3.3E-05	4.2	5.8E-05	0.1	9.0E-01	0.0	9.7E-01
ENSMUST00000141693				6.8	1.3E-04	-3.0	7.1E-03	0.2	6.8E-01	-2.8	3.3E-02
ENSMUST00000152246				6.8	1.1E-03	-5.9	3.3E-02	0.6	5.0E-01	-2.2	4.5E-01
ENSMUST00000169967				6.8	8.6E-05	5.4	9.2E-04	-0.6	5.9E-01	-0.8	2.6E-01
ENSMUST00000146309				6.8	3.9E-05	5.3	3.4E-03	-0.8	5.8E-01	-0.3	7.2E-01
ENSMUST00000150259				6.8	9.8E-05	3.6	1.5E-03	-0.6	4.2E-01	0.4	4.8E-01
ENSMUST00000155848				2.1	2.0E-01	6.5	3.3E-03	0.1	9.4E-01	-4.2	5.6E-03
ENSMUST00000155849				0.1	9.2E-01	0.6	4.9E-01	0.3	6.2E-01	-0.2	8.0E-01
ENSMUST00000150445				6.8	6.7E-04	-6.4	6.0E-05	0.5	1.5E-01	-0.9	3.8E-01
ENSMUST00000127009				6.8	3.6E-04	-1.4	1.9E-01	0.9	2.0E-01	-1.0	3.3E-01
ENSMUST00000155868				0.1	9.5E-01	0.8	6.6E-01	0.9	5.5E-01	0.2	8.9E-01
ENSMUST00000164248				6.8	6.5E-05	-0.9	5.6E-01	3.9	2.8E-03	-0.7	6.5E-01
ENSMUST00000118624				6.8	7.1E-04	5.0	3.1E-03	-0.3	8.0E-01	0.2	8.5E-01
ENSMUST00000155871				-0.1	8.7E-01	-0.9	2.9E-01	-0.6	3.3E-01	0.2	8.1E-01
ENSMUST00000189210				6.8	6.6E-05	-10.0	3.3E-03	-2.6	1.6E-02	0.4	9.0E-01
ENSMUST00000155875				0.8	6.8E-01	-1.5	7.1E-01	1.1	6.7E-01	3.5	3.3E-01
ENSMUST00000155887				-1.1	3.0E-01	0.7	5.6E-01	0.2	8.1E-01	-1.6	2.0E-01
ENSMUST00000141603				6.8	5.4E-05	6.7	5.8E-04	-1.8	2.2E-01	0.3	6.8E-01
ENSMUST00000191976				6.8	9.5E-05	-1.9	2.5E-01	0.7	4.3E-01	-0.4	8.1E-01
ENSMUST00000155894				-1.0	4.3E-01	-0.6	6.8E-01	-0.2	8.7E-01	-0.5	7.2E-01
ENSMUST00000155896				4.5	4.1E-02	2.7	2.9E-01	-0.1	9.8E-01	1.8	3.5E-01
ENSMUST00000193162				6.8	4.1E-06	5.5	2.4E-04	-1.2	2.3E-01	-0.2	7.6E-01
ENSMUST00000145483				6.8	9.2E-05	-1.1	2.4E-01	1.1	8.2E-02	-0.5	6.1E-01
ENSMUST00000155905	testis expressed gene 10 [Source:MGI Symbol;Acc:MGI:1344413]	F6ZZ61		-2.8	7.9E-02	-0.7	6.5E-01	-0.1	9.1E-01	-2.3	1.9E-01
ENSMUST00000133597				6.8	1.6E-04	6.8	1.5E-04	-0.5	6.7E-01	-0.1	8.1E-01
ENSMUST00000077309				6.8	2.4E-04	-4.6	3.8E-02	1.6	6.7E-02	-0.7	7.2E-01
ENSMUST00000187311				6.8	1.0E-03	7.4	8.5E-05	-1.0	4.4E-01	0.2	7.1E-01
ENSMUST00000119578				6.8	1.5E-04	1.2	1.1E-01	-0.5	4.1E-01	0.1	8.2E-01
ENSMUST00000129445				6.8	8.8E-05	7.5	1.3E-04	-0.6	6.5E-01	-0.7	2.7E-01
ENSMUST00000139515				6.8	9.7E-05	5.9	2.2E-04	1.5	1.3E-01	0.3	6.1E-01
ENSMUST00000188100				6.8	1.8E-04	5.8	1.8E-03	0.0	9.9E-01	-1.0	2.3E-01
ENSMUST00000132410				6.8	1.8E-05	-4.0	8.3E-02	1.2	2.4E-01	1.3	5.3E-01
ENSMUST00000155941				-4.6	4.8E-02	-2.4	4.2E-01	1.4	4.2E-01	-0.8	7.7E-01
ENSMUST00000155946				-2.7	5.9E-02	-3.5	1.0E-01	0.4	6.9E-01	1.2	5.5E-01
ENSMUST00000155948				-0.3	6.4E-01	-1.1	2.4E-01	-0.5	4.3E-01	0.2	8.0E-01
ENSMUST00000148544				6.8	2.3E-04	1.9	4.1E-01	-2.5	2.5E-01	0.1	9.5E-01
ENSMUST00000155953				-1.6	4.1E-01	-2.2	4.8E-01	1.1	5.3E-01	1.7	5.8E-01
ENSMUST00000120436				6.8	3.6E-03	7.4	3.2E-05	-1.5	1.9E-01	-0.2	6.7E-01
ENSMUST00000133897				6.8	6.2E-04	6.7	8.6E-04	-0.2	9.0E-01	-3.2	8.2E-03
ENSMUST00000120207				6.8	6.6E-04	-3.0	7.9E-02	-0.2	8.6E-01	-0.3	8.4E-01
ENSMUST00000140551				6.8	2.5E-05	-1.9	4.2E-01	3.9	1.7E-02	-1.4	5.7E-01
ENSMUST00000155969				-3.6	8.5E-02	0.6	7.1E-01	0.9	5.1E-01	-3.3	1.2E-01
ENSMUST00000155970				-2.0	1.5E-01	-3.9	5.9E-02	-1.1	2.5E-01	0.8	6.9E-01
ENSMUST00000155973	splicing factor 1 [Source:MGI Symbol;Acc:MGI:1095403]	D3YVH4		-1.9	1.1E-01	-0.6	7.1E-01	0.8	4.9E-01	-0.5	7.0E-01
ENSMUST00000141533				6.8	5.3E-05	6.3	9.4E-05	-1.5	1.8E-01	0.1	9.1E-01
ENSMUST00000162853				6.8	1.2E-04	6.0	3.7E-06	-0.4	5.4E-01	0.1	8.8E-01
ENSMUST00000155986				3.0	1.3E-01	-2.0	2.2E-01	-5.9	4.8E-03	-0.9	6.0E-01
ENSMUST00000194739				6.8	9.2E-06	-1.0	6.3E-01	1.6	2.9E-01	-2.1	3.5E-01
ENSMUST00000123322				6.8	7.0E-05	4.3	7.9E-03	-0.7	5.5E-01	-0.8	4.1E-01
ENSMUST00000155994				-0.6	7.4E-01	-2.7	2.7E-01	-1.9	2.3E-01	0.2	9.3E-01
ENSMUST00000155998	ankyrin repeat and FYVE domain containing 1 [Source:MGI Symbol;Acc:MGI:1337008]		Q810B6	-1.2	9.3E-02	-1.3	1.3E-01	-0.6	2.9E-01	-0.5	5.3E-01
ENSMUST00000155696				6.8	6.9E-05	3.6	1.4E-03	-0.6	4.1E-01	-0.2	8.0E-01
ENSMUST00000156003				-2.6	8.6E-02	-1.3	4.7E-01	0.0	9.7E-01	-1.3	4.6E-01
ENSMUST00000080945				6.8	1.2E-03	2.9	7.4E-04	-0.5	3.7E-01	-0.4	3.8E-01
ENSMUST00000153635				6.8	3.3E-04	4.4	5.3E-03	-1.6	2.2E-01	0.0	9.9E-01
ENSMUST00000099093				6.8	8.4E-04	5.6	3.1E-03	-0.5	7.3E-01	-0.5	5.5E-01
ENSMUST00000156012				-1.9	1.9E-01	0.3	8.5E-01	0.0	9.9E-01	-2.2	1.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000120352				6.8	7.1E-05	-3.4	4.0E-02	0.0	9.6E-01	-0.4	8.2E-01
ENSMUST00000156029				2.4	5.4E-02	2.7	1.2E-01	0.5	7.6E-01	0.1	9.4E-01
ENSMUST00000119013				6.8	9.2E-05	-4.5	5.4E-03	-1.0	1.1E-01	-0.5	7.0E-01
ENSMUST00000120032				6.8	3.4E-04	1.4	3.3E-02	0.1	7.8E-01	-0.1	7.7E-01
ENSMUST00000138730				6.8	9.1E-05	8.3	1.7E-04	-1.4	3.7E-01	0.7	2.8E-01
ENSMUST00000140151				6.8	3.6E-04	3.3	5.4E-02	-3.5	6.2E-02	-0.7	5.3E-01
ENSMUST00000195092				6.8	6.0E-05	6.8	1.6E-04	-0.2	8.6E-01	-0.4	5.6E-01
ENSMUST00000151240				6.7	1.1E-06	5.8	6.8E-04	-0.6	6.0E-01	0.2	8.3E-01
ENSMUST00000110138				6.7	3.5E-03	8.0	1.0E-02	-0.9	7.6E-01	-1.6	2.8E-01
ENSMUST00000119112				6.7	1.2E-04	-3.6	2.4E-03	-0.5	3.3E-01	-0.2	7.9E-01
ENSMUST00000145697				6.7	7.3E-05	4.8	7.5E-03	-2.4	1.5E-01	0.1	8.8E-01
ENSMUST00000148277				6.7	8.1E-05	3.0	1.2E-01	-0.5	7.8E-01	2.7	5.3E-02
ENSMUST00000156073				1.1	2.2E-01	2.0	4.3E-02	-0.5	5.4E-01	-1.4	1.0E-01
ENSMUST00000156077				-0.1	8.6E-01	1.1	2.5E-01	0.3	7.0E-01	-0.9	3.0E-01
ENSMUST00000143837				6.7	3.3E-04	4.7	2.5E-05	-1.9	9.2E-03	0.2	6.0E-01
ENSMUST00000156082	patatin-like phospholipase domain containing 8 [Source:MGI Symbol;Acc:MGI:1914702]	F7B2N8		-4.8	9.6E-02	-3.2	3.4E-01	0.4	8.1E-01	-1.2	7.3E-01
ENSMUST00000187104				6.7	1.1E-04	2.1	5.4E-02	-1.0	2.5E-01	0.0	9.7E-01
ENSMUST00000121159				6.7	1.0E-04	7.0	1.1E-04	-0.1	9.0E-01	0.5	4.1E-01
ENSMUST00000145260				6.7	5.8E-05	-4.3	7.7E-02	0.0	9.9E-01	-0.4	8.6E-01
ENSMUST00000184037				6.7	1.3E-04	3.0	1.3E-02	-0.3	7.8E-01	-0.9	2.3E-01
ENSMUST00000156093	leucine rich repeat containing 4B [Source:MGI Symbol;Acc:MGI:3027390]	D3Z2D1		3.9	7.2E-02	4.7	6.0E-02	-0.4	8.6E-01	-1.2	4.3E-01
ENSMUST00000156094				0.6	6.4E-01	2.5	8.4E-02	0.2	8.8E-01	-1.7	1.8E-01
ENSMUST00000156096	alcium/calmodulin-dependent serine protein kinase (MAGUK family) [Source:MGI Symbol;Acc:MGI:130948	A0A067XG53		0.7	7.4E-01	2.3	4.5E-01	1.4	6.0E-01	-0.2	9.2E-01
ENSMUST00000156097	DNA-damage regulated autophagy modulator 1 [Source:MGI Symbol;Acc:MGI:1918962]	D6RJL8		4.9	6.1E-02	7.2	3.5E-02	1.4	6.3E-01	-0.8	6.7E-01
ENSMUST00000118355				6.7	1.9E-04	6.6	1.5E-03	0.3	8.2E-01	-0.4	6.3E-01
ENSMUST00000156108				-2.5	4.4E-02	-1.6	2.9E-01	0.8	4.3E-01	-0.1	9.4E-01
ENSMUST00000161124				6.7	5.2E-04	-5.7	4.2E-02	0.8	4.1E-01	2.0	4.3E-01
ENSMUST00000177407				6.7	7.1E-05	7.3	1.7E-02	-0.9	7.4E-01	-1.2	4.2E-01
ENSMUST00000156120				-1.8	5.5E-02	-0.8	4.5E-01	0.2	7.8E-01	-0.8	4.4E-01
ENSMUST00000187559				6.7	9.2E-03	2.3	2.6E-02	-1.4	1.0E-01	-1.0	2.3E-01
ENSMUST00000120609				6.7	2.8E-04	5.4	1.1E-03	0.9	4.4E-01	-1.4	1.1E-01
ENSMUST00000156125	acyl-Coenzyme A oxidase 3, pristanoyl [Source:MGI Symbol;Acc:MGI:1933156]	D3Z2N6		-2.4	3.6E-02	-1.6	2.3E-01	0.6	3.7E-01	-0.1	9.3E-01
ENSMUST00000121141				6.7	5.5E-05	4.3	3.3E-04	-0.3	6.7E-01	0.3	5.8E-01
ENSMUST00000137076				6.7	9.9E-06	4.4	1.0E-03	-0.4	6.6E-01	-1.0	1.6E-01
ENSMUST00000156130				-1.5	8.3E-02	-0.4	7.1E-01	0.3	6.9E-01	-0.9	3.8E-01
ENSMUST00000156349				6.7	3.8E-04	2.8	2.6E-02	0.1	9.0E-01	1.2	1.7E-01
ENSMUST00000129612				6.7	2.1E-04	7.9	2.5E-05	-1.3	2.7E-01	-1.0	6.1E-02
ENSMUST00000156140				0.9	3.9E-01	2.3	1.2E-01	1.4	2.7E-01	0.0	9.8E-01
ENSMUST00000156145				-0.1	9.3E-01	1.5	1.5E-01	0.5	5.0E-01	-1.0	2.5E-01
ENSMUST00000156154				1.6	6.8E-02	3.9	8.4E-03	2.0	8.9E-02	-0.4	6.4E-01
ENSMUST00000144130				6.7	1.5E-02	6.7	4.4E-04	-0.1	9.4E-01	-1.2	1.2E-01
ENSMUST00000156158	TRAF type zinc finger domain containing 1 [Source:MGI Symbol;Acc:MGI:1923551]	A0A0G2JG49		0.1	9.4E-01	0.9	5.4E-01	0.1	9.4E-01	-0.7	5.8E-01
ENSMUST00000154624				6.7	1.3E-04	8.2	1.6E-05	-0.9	4.1E-01	-0.7	1.4E-01
ENSMUST00000156160				0.9	6.1E-01	-2.2	2.0E-01	-4.3	1.1E-02	-1.3	4.7E-01
ENSMUST00000184369				6.7	9.6E-05	6.2	8.9E-03	-1.1	5.7E-01	0.9	3.9E-01
ENSMUST00000156173	olgi associated, gamma adaptin ear containing, ARF binding protein 3 [Source:MGI Symbol;Acc:MGI:238415	S4R2D2		-3.2	1.8E-01	1.5	6.3E-01	4.2	9.9E-02	-0.6	8.4E-01
ENSMUST00000194329				6.7	1.1E-04	4.9	2.4E-04	-0.8	3.4E-01	-0.7	3.0E-01
ENSMUST00000176907				6.7	4.2E-04	-5.2	2.2E-03	-0.3	5.6E-01	-0.9	5.1E-01
ENSMUST00000132286				6.7	7.3E-05	5.9	9.7E-04	-1.2	3.8E-01	1.1	1.5E-01
ENSMUST00000130314				6.7	6.5E-04	5.9	1.4E-03	0.8	5.4E-01	-0.5	5.4E-01
ENSMUST00000142775				6.7	1.3E-04	7.6	4.3E-05	-0.5	6.3E-01	-0.5	3.7E-01
ENSMUST00000156192				3.8	1.4E-01	1.9	5.5E-01	-0.2	9.4E-01	1.7	4.9E-01
ENSMUST00000123446				6.7	1.4E-04	3.9	4.8E-02	-0.1	9.7E-01	-0.1	9.1E-01
ENSMUST00000156201	smoothelin [Source:MGI Symbol;Acc:MGI:1354727]	D3YZ10		3.3	8.9E-02	4.7	2.4E-02	-0.5	8.1E-01	-1.9	1.6E-01
ENSMUST00000126164				6.7	3.2E-05	3.7	8.5E-03	0.3	7.5E-01	-1.1	2.0E-01
ENSMUST00000156212				-2.4	2.1E-01	-3.4	2.9E-01	0.6	7.5E-01	1.6	5.8E-01
ENSMUST00000133984				6.7	2.3E-06	7.2	3.9E-04	-0.7	6.2E-01	0.7	3.5E-01
ENSMUST00000190309				6.7	1.6E-04	3.7	9.9E-04	-1.5	7.8E-02	0.1	9.1E-01
ENSMUST00000177499				6.7	6.4E-04	6.5	7.9E-04	-0.7	6.3E-01	0.3	7.1E-01
ENSMUST00000191215				6.7	2.0E-04	-1.5	5.5E-01	5.1	7.3E-03	-0.9	7.1E-01
ENSMUST00000156218	zinc finger protein 938 [Source:MGI Symbol;Acc:MGI:3621440]	D6RJ82		3.9	6.9E-02	-1.4	5.5E-01	-4.0	6.8E-02	1.2	5.4E-01
ENSMUST00000156226	eukaryotic translation initiation factor 4, gamma 1 [Source:MGI Symbol;Acc:MGI:2384784]	D6RCH1		-0.9	6.6E-01	-1.1	6.6E-01	-0.6	7.6E-01	-0.4	8.6E-01
ENSMUST00000120476				6.7	3.9E-04	-2.4	1.7E-01	1.0	2.7E-01	-1.0	5.7E-01
ENSMUST00000156231				-1.9	6.3E-02	-1.9	1.5E-01	0.1	9.1E-01	0.1	9.3E-01
ENSMUST00000142764				6.7	6.5E-05	6.5	4.4E-04	0.7	5.7E-01	-0.2	8.2E-01
ENSMUST00000156250				-0.7	7.7E-01	-2.9	4.2E-01	-1.0	6.4E-01	1.2	7.3E-01
ENSMUST00000143606				6.7	1.4E-04	5.7	5.7E-03	0.6	7.1E-01	1.1	2.5E-01
ENSMUST00000140250				6.7	1.3E-03	5.7	5.3E-03	1.2	4.1E-01	-0.8	4.5E-01
ENSMUST00000188996				6.7	1.4E-03	1.2	6.1E-01	-1.9	3.4E-01	2.4	2.0E-01
ENSMUST00000192425				6.7	6.1E-04	-4.3	6.2E-03	-0.6	3.3E-01	0.2	8.6E-01
ENSMUST00000131750				6.7	2.1E-04	5.7	2.7E-02	-2.3	3.8E-01	-2.3	1.5E-01
ENSMUST00000150457				6.7	5.5E-05	6.4	8.9E-04	0.2	8.6E-01	0.8	3.2E-01
ENSMUST00000186699				6.7	1.2E-03	7.1	2.3E-04	-0.2	8.7E-01	0.2	7.7E-01
ENSMUST00000185578				6.7	2.1E-06	6.2	1.8E-03	-0.6	7.1E-01	-0.8	3.6E-01
ENSMUST00000140435				6.7	1.8E-04	9.3	2.9E-05	-0.7	6.1E-01	0.7	2.3E-01
ENSMUST00000189392				6.7	9.7E-05	6.4	1.6E-04	-0.6	6.0E-01	-2.3	5.5E-03
ENSMUST00000136126				6.7	9.7E-07	4.6	4.4E-03	-1.6	2.6E-01	-0.8	3.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000146537				6.7	3.3E-06	5.8	8.0E-04	-0.1	9.2E-01	-0.5	4.6E-01
ENSMUST00000185256				6.7	5.4E-05	4.0	2.3E-04	-1.3	6.8E-02	1.2	3.3E-02
ENSMUST00000156294	cytochrome b5 domain containing 2 [Source:MGI Symbol;Acc:MGI:2684848]		Q5SSH8	0.0	9.5E-01	0.7	4.4E-01	0.8	2.3E-01	0.2	8.4E-01
ENSMUST00000156299				0.6	4.3E-01	0.6	5.0E-01	-0.3	7.1E-01	-0.3	7.2E-01
ENSMUST00000038090				6.7	2.4E-03	7.0	4.9E-03	0.3	8.8E-01	-2.0	1.1E-01
ENSMUST00000156308				-3.7	8.7E-02	-2.8	2.6E-01	0.0	9.8E-01	-1.0	7.1E-01
ENSMUST00000075809				6.7	5.4E-05	6.3	8.4E-06	-1.6	6.2E-02	0.0	9.6E-01
ENSMUST00000144413				6.7	1.8E-04	4.9	4.5E-02	-1.2	6.0E-01	-0.7	6.2E-01
ENSMUST00000173412				6.7	1.5E-04	2.6	7.1E-02	-2.2	1.1E-01	0.2	8.4E-01
ENSMUST00000118760				6.7	7.7E-05	5.7	4.0E-03	-0.7	6.9E-01	-0.9	3.3E-01
ENSMUST00000156321	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish)) [Source:MGI Symbol;Acc:MGI:1915291	F6XIS3		-1.2	2.9E-01	1.8	2.0E-01	1.4	2.2E-01	-1.7	2.1E-01
ENSMUST00000156325				-0.1	9.3E-01	0.0	9.9E-01	0.3	7.2E-01	0.2	8.4E-01
ENSMUST00000126776				6.7	1.9E-03	-1.7	1.8E-01	0.7	4.0E-01	-0.4	7.5E-01
ENSMUST00000131541				6.7	6.5E-05	4.5	8.7E-05	0.3	6.2E-01	0.1	8.7E-01
ENSMUST00000156333	piezo-type mechanosensitive ion channel component 1 [Source:MGI Symbol;Acc:MGI:3603204]	F7AC58		0.0	1.0E+00	-4.4	2.5E-01	-4.1	6.6E-02	0.3	9.3E-01
ENSMUST00000163185				6.7	9.3E-05	-1.6	8.4E-02	-0.9	1.7E-01	-1.7	1.0E-01
ENSMUST00000185629				6.7	1.5E-04	4.5	2.2E-02	-1.8	3.1E-01	-0.4	7.3E-01
ENSMUST00000122273				6.7	1.8E-04	6.0	6.3E-04	-1.4	3.0E-01	-0.6	4.3E-01
ENSMUST00000156343				-2.4	1.4E-01	-2.4	3.0E-01	0.9	5.2E-01	0.9	7.0E-01
ENSMUST00000133016				6.7	6.7E-03	-6.2	2.3E-03	-0.6	2.6E-01	0.5	7.7E-01
ENSMUST00000156346				3.2	7.0E-02	2.8	1.6E-01	-1.1	5.0E-01	-0.7	6.5E-01
ENSMUST00000159520				6.7	3.1E-04	6.3	1.1E-03	-0.4	8.0E-01	0.6	4.9E-01
ENSMUST00000187949				6.7	1.3E-05	6.3	1.6E-03	0.0	9.8E-01	0.5	5.4E-01
ENSMUST00000124262				6.7	9.0E-05	-2.9	1.2E-01	0.8	4.2E-01	1.0	5.7E-01
ENSMUST00000156353				0.3	8.2E-01	-2.3	4.0E-01	0.6	7.0E-01	3.2	1.9E-01
ENSMUST00000173798				6.7	1.9E-04	4.9	7.3E-04	0.2	8.6E-01	1.2	6.5E-02
ENSMUST00000156357				-1.7	2.5E-01	-0.8	6.5E-01	0.5	6.8E-01	-0.4	8.1E-01
ENSMUST00000180475				6.7	2.7E-04	1.3	7.1E-01	7.9	1.2E-02	-0.5	8.8E-01
ENSMUST00000192091				6.7	1.6E-05	2.2	1.1E-02	0.4	5.1E-01	0.1	9.3E-01
ENSMUST00000142798				6.7	7.1E-05	-3.9	4.8E-02	0.5	5.2E-01	-0.9	6.4E-01
ENSMUST00000131270				6.7	6.9E-05	-10.3	3.3E-04	-0.8	1.1E-01	-0.6	7.7E-01
ENSMUST00000178317				6.7	3.7E-04	-3.4	3.0E-02	0.5	5.5E-01	-1.8	2.6E-01
ENSMUST00000193097				6.7	6.8E-05	-1.3	1.9E-01	0.8	2.5E-01	-0.3	7.9E-01
ENSMUST00000118018				6.7	7.1E-05	4.7	2.3E-02	0.0	9.9E-01	-1.0	3.8E-01
ENSMUST00000187356				6.7	1.3E-04	-6.2	3.7E-05	-0.3	4.9E-01	-0.5	5.7E-01
ENSMUST00000192774				6.7	9.5E-05	5.4	3.5E-03	-0.7	6.5E-01	1.0	2.7E-01
ENSMUST00000183106				6.7	2.9E-06	-1.2	2.6E-01	0.3	6.5E-01	-1.8	1.7E-01
ENSMUST00000118084				6.7	3.0E-05	-5.9	5.6E-04	1.3	1.0E-02	-0.8	5.6E-01
ENSMUST00000156398				0.1	9.0E-01	-2.9	1.4E-02	-5.5	1.1E-04	-2.5	4.9E-02
ENSMUST00000119646				6.7	4.0E-05	3.8	3.9E-03	5.1	2.7E-04	-0.4	5.1E-01
ENSMUST00000125761				6.7	1.1E-04	4.5	1.9E-03	0.2	8.3E-01	-0.4	5.8E-01
ENSMUST00000138577				6.7	1.9E-04	5.2	4.4E-04	-0.6	5.2E-01	0.4	5.7E-01
ENSMUST00000190202				6.7	7.4E-06	5.9	1.5E-04	0.3	7.0E-01	-1.3	5.8E-02
ENSMUST00000156420				1.9	4.0E-01	2.1	5.9E-01	2.3	4.6E-01	2.1	4.9E-01
ENSMUST00000192117				6.7	1.3E-03	4.4	1.4E-03	-2.1	7.8E-02	0.6	3.7E-01
ENSMUST00000056191				6.7	3.9E-04	-2.3	5.6E-02	0.4	5.5E-01	-1.4	2.7E-01
ENSMUST00000169090				6.7	1.5E-04	4.9	1.2E-04	-0.2	7.4E-01	0.4	4.3E-01
ENSMUST00000156436				2.0	5.8E-02	0.1	9.1E-01	-0.7	4.4E-01	1.1	3.1E-01
ENSMUST00000156440	ZPR1 zinc finger [Source:MGI Symbol;Acc:MGI:1330262]		Q62384	0.3	5.8E-01	0.3	6.8E-01	-0.6	2.7E-01	-0.5	4.2E-01
ENSMUST00000138456				6.7	3.3E-07	-5.7	1.4E-02	1.2	1.1E-01	-0.9	6.8E-01
ENSMUST00000170634				6.7	3.9E-06	1.9	2.1E-01	0.2	8.7E-01	2.0	9.8E-02
ENSMUST00000186984				6.7	8.2E-05	4.5	2.2E-02	-3.3	1.0E-01	-0.6	5.7E-01
ENSMUST00000156450				0.4	9.0E-01	-1.3	7.8E-01	0.0	9.9E-01	1.7	6.9E-01
ENSMUST00000156455				-0.3	9.1E-01	-2.6	4.5E-01	-3.2	1.8E-01	-0.9	7.9E-01
ENSMUST00000119589				6.7	9.6E-04	3.7	6.7E-03	-0.3	7.8E-01	-0.1	8.6E-01
ENSMUST00000188646				6.7	1.1E-04	-4.3	1.6E-03	1.5	6.9E-03	-1.1	3.3E-01
ENSMUST00000118189				6.7	7.8E-05	2.3	1.3E-01	-0.8	5.5E-01	0.8	4.4E-01
ENSMUST00000187545				6.7	8.2E-04	5.4	2.8E-03	-1.6	3.0E-01	1.0	2.7E-01
ENSMUST00000087562				6.7	3.3E-05	3.1	6.0E-03	1.1	1.5E-01	-0.1	9.2E-01
ENSMUST00000129818				6.7	8.7E-05	-3.0	3.5E-02	1.6	2.4E-02	-0.7	6.1E-01
ENSMUST00000133708				6.7	1.4E-04	-3.8	1.1E-01	1.0	3.3E-01	-0.8	7.1E-01
ENSMUST00000188150				6.7	1.9E-04	5.5	4.9E-03	1.8	2.5E-01	-0.6	4.9E-01
ENSMUST00000138583				6.7	8.2E-05	6.3	3.7E-03	0.1	9.7E-01	0.0	9.8E-01
ENSMUST00000134501				6.7	8.7E-05	4.8	5.0E-03	0.7	5.5E-01	-0.5	5.4E-01
ENSMUST00000139467				6.7	5.9E-07	-5.7	4.2E-04	-0.2	6.0E-01	0.0	9.9E-01
ENSMUST00000128673				6.7	1.2E-04	2.5	1.0E-02	-0.9	2.4E-01	-0.2	8.1E-01
ENSMUST00000156513				0.4	5.9E-01	1.0	3.6E-01	1.1	2.1E-01	0.6	5.6E-01
ENSMUST00000126082				6.7	5.9E-06	7.9	4.7E-05	-0.8	5.2E-01	0.0	9.5E-01
ENSMUST00000140856				6.7	7.0E-05	3.5	3.9E-03	-0.7	4.3E-01	0.4	5.9E-01
ENSMUST00000191813				6.7	1.1E-04	-1.7	1.8E-01	1.6	4.8E-02	-1.5	2.6E-01
ENSMUST00000156522	Trk-fused gene [Source:MGI Symbol;Acc:MGI:1338041]	B8JJG3		-3.0	4.8E-02	-2.7	1.4E-01	-0.4	6.8E-01	-0.7	6.7E-01
ENSMUST00000132387				6.7	1.7E-06	-4.3	7.5E-03	1.0	1.3E-01	0.9	5.1E-01
ENSMUST00000177915				6.7	1.2E-04	-4.4	1.7E-02	-0.7	3.4E-01	0.0	9.9E-01
ENSMUST00000169120				6.7	2.8E-04	5.9	4.1E-04	-0.6	6.4E-01	-0.4	5.5E-01
ENSMUST00000121977				6.7	2.7E-04	4.9	1.5E-03	1.4	2.1E-01	-0.5	4.8E-01
ENSMUST00000156546	ceramide kinase [Source:MGI Symbol;Acc:MGI:2386052]	D3Z254		0.7	7.6E-01	0.9	7.7E-01	-0.1	9.7E-01	-0.3	9.1E-01
ENSMUST00000156550	synovial apoptosis inhibitor 1, synoviolin [Source:MGI Symbol;Acc:MGI:1921376]	D3Z1Y1		0.9	6.2E-01	-2.1	4.4E-01	-1.0	5.1E-01	1.9	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000156552				-1.1	7.4E-01	-1.9	6.7E-01	-0.3	9.0E-01	0.5	9.1E-01
ENSMUST00000156561				0.6	4.7E-01	1.5	1.1E-01	-0.1	8.6E-01	-1.1	1.8E-01
ENSMUST00000156562				0.3	7.7E-01	-0.8	5.6E-01	-0.6	5.4E-01	0.5	7.0E-01
ENSMUST00000142877				6.7	9.4E-05	3.1	2.1E-03	-0.7	2.8E-01	0.0	9.4E-01
ENSMUST00000190871				6.7	9.0E-05	3.2	4.1E-02	-0.1	9.5E-01	-0.4	6.9E-01
ENSMUST00000194374				6.7	1.1E-04	4.8	1.8E-02	-0.2	9.1E-01	0.2	8.6E-01
ENSMUST00000146618				6.7	1.1E-02	0.3	6.3E-01	-1.2	6.6E-02	1.0	1.2E-01
ENSMUST00000156581				-1.7	2.7E-01	1.0	5.3E-01	0.5	7.1E-01	-2.2	1.8E-01
ENSMUST00000120309				6.7	1.5E-04	-2.7	1.3E-01	0.0	9.6E-01	-1.4	4.6E-01
ENSMUST00000140066				6.7	8.1E-05	8.8	1.3E-03	-0.4	8.4E-01	0.5	6.1E-01
ENSMUST00000156593	integrin alpha M [Source:MGI Symbol;Acc:MGI:96607]	D6RJ73		-0.9	3.2E-01	-2.0	1.7E-01	-0.3	7.0E-01	0.8	5.4E-01
ENSMUST00000142633				6.7	5.4E-03	-2.0	2.3E-01	1.2	2.8E-01	-1.8	3.0E-01
ENSMUST00000166347				6.7	5.6E-05	-6.8	3.6E-03	-1.1	8.6E-02	0.9	6.2E-01
ENSMUST00000180189				6.7	5.7E-05	6.2	1.4E-03	-0.4	7.6E-01	1.1	2.1E-01
ENSMUST00000172709				6.7	6.2E-05	5.0	2.1E-05	-1.2	8.9E-02	0.0	1.0E+00
ENSMUST00000156607				-2.4	6.9E-02	-1.4	5.0E-01	2.0	1.6E-01	1.0	6.0E-01
ENSMUST00000122844				6.7	1.1E-04	8.3	9.3E-06	0.5	5.8E-01	0.4	4.1E-01
ENSMUST00000183633				6.7	1.6E-04	6.9	9.8E-03	-0.8	7.3E-01	-2.4	1.1E-01
ENSMUST00000177441				6.7	6.9E-05	7.9	1.3E-04	4.9	1.9E-03	-0.5	4.2E-01
ENSMUST00000189949				6.7	1.7E-04	-3.4	2.2E-02	-1.4	6.6E-02	-0.5	6.9E-01
ENSMUST00000156622				-1.9	7.8E-02	-4.2	1.6E-02	-1.2	1.1E-01	1.1	4.8E-01
ENSMUST00000156623				-2.7	1.0E-01	-6.4	1.1E-02	-3.8	2.2E-03	-0.1	9.7E-01
ENSMUST00000156626				0.5	7.5E-01	5.6	1.1E-02	1.1	5.2E-01	-3.9	2.0E-02
ENSMUST00000183337				6.7	2.3E-05	6.9	3.2E-04	-0.4	7.6E-01	-0.9	2.2E-01
ENSMUST00000141106				6.7	8.4E-05	7.0	7.0E-05	-0.5	6.4E-01	-1.2	6.4E-02
ENSMUST00000159766				6.7	8.0E-05	6.6	2.4E-02	-0.9	7.4E-01	-0.7	6.4E-01
ENSMUST00000125876				6.7	3.6E-05	-3.3	1.1E-01	0.4	6.5E-01	0.6	7.4E-01
ENSMUST00000186922				6.7	3.2E-06	-3.0	4.7E-03	-0.1	8.0E-01	0.3	7.4E-01
ENSMUST00000141890				6.7	1.0E-04	-5.4	3.7E-02	0.3	7.2E-01	-1.1	6.7E-01
ENSMUST00000178248				6.7	2.0E-04	-3.4	5.0E-02	0.4	6.4E-01	-2.8	1.7E-01
ENSMUST00000156645				-1.1	3.9E-01	2.0	2.1E-01	0.9	5.1E-01	-2.2	1.1E-01
ENSMUST00000187890				6.7	1.3E-04	-2.6	1.0E-01	0.1	9.3E-01	-0.1	9.6E-01
ENSMUST00000156653				0.7	6.1E-01	0.5	8.0E-01	0.2	8.7E-01	0.4	7.9E-01
ENSMUST00000128638				6.7	5.1E-04	5.2	1.7E-04	-1.8	7.3E-02	-0.5	4.1E-01
ENSMUST00000142122				6.7	1.4E-04	2.0	4.8E-03	-1.1	4.7E-02	0.4	3.5E-01
ENSMUST00000156659				3.2	9.9E-02	5.4	2.1E-02	0.0	9.8E-01	-2.3	1.2E-01
ENSMUST00000150803				6.7	1.5E-05	1.9	3.0E-01	-3.1	7.8E-02	-0.2	8.8E-01
ENSMUST00000156662	predicted gene 766 [Source:MGI Symbol;Acc:MGI:2685612]	Q3UN63		-1.6	6.5E-02	-0.2	8.2E-01	0.0	9.8E-01	-1.4	1.4E-01
ENSMUST00000172289				6.7	9.9E-05	-3.9	5.3E-02	0.3	6.9E-01	-0.5	8.0E-01
ENSMUST00000156673				1.2	2.0E-01	3.3	1.4E-02	0.6	5.1E-01	-1.4	1.4E-01
ENSMUST00000038304				6.7	1.4E-03	-5.8	2.5E-03	0.2	7.5E-01	-1.1	4.9E-01
ENSMUST00000156679	ankyrin repeat domain 33B [Source:MGI Symbol;Acc:MGI:1917904]		Q3U0L2	1.5	3.7E-01	1.3	5.7E-01	0.3	8.5E-01	0.5	7.9E-01
ENSMUST00000156680	family with sequence similarity 76, member B [Source:MGI Symbol;Acc:MGI:1920076]	D6RG49		-3.6	2.1E-01	-3.9	2.5E-01	-1.2	4.8E-01	-0.9	7.9E-01
ENSMUST00000154898				6.7	5.0E-04	3.6	9.8E-04	-0.2	8.1E-01	0.3	6.0E-01
ENSMUST00000156685				-0.4	5.8E-01	-1.1	2.1E-01	0.2	7.9E-01	0.9	2.7E-01
ENSMUST00000195464				6.7	5.0E-05	3.9	1.8E-04	0.4	5.1E-01	0.3	4.7E-01
ENSMUST00000161766				6.7	9.3E-05	7.2	1.2E-04	-0.6	6.0E-01	0.3	6.0E-01
ENSMUST00000176801				6.7	2.1E-06	-2.0	1.3E-01	0.8	3.1E-01	-2.6	8.2E-02
ENSMUST00000156694	RAS related protein 2a [Source:MGI Symbol;Acc:MGI:97855]	F6W8Q2		-1.2	4.3E-01	0.3	8.8E-01	1.1	3.9E-01	-0.3	8.6E-01
ENSMUST00000156695	islet cell autoantigen 1 [Source:MGI Symbol;Acc:MGI:96391]	S4R217		-2.7	4.5E-02	-1.9	2.3E-01	0.1	9.2E-01	-0.7	6.7E-01
ENSMUST00000187969				6.7	5.3E-04	5.9	3.4E-05	0.0	9.9E-01	0.0	9.8E-01
ENSMUST00000167734				6.7	2.5E-04	-4.3	1.0E-02	0.6	3.6E-01	0.0	9.8E-01
ENSMUST00000156701				1.2	7.0E-02	1.5	5.2E-02	-0.9	1.6E-01	-1.1	9.9E-02
ENSMUST00000156702	carnitine acetyltransferase [Source:MGI Symbol;Acc:MGI:109501]	D6REV7		1.9	4.5E-01	0.2	9.4E-01	-1.4	5.2E-01	0.2	9.2E-01
ENSMUST00000128468				6.7	8.2E-05	-5.1	2.1E-02	0.8	2.8E-01	-0.9	6.7E-01
ENSMUST00000156713	phosphoribosylglycinamide formyltransferase [Source:MGI Symbol;Acc:MGI:95654]	D6RCG1		-2.1	1.4E-01	-4.3	1.3E-01	0.4	7.2E-01	2.6	3.4E-01
ENSMUST00000151507				6.7	7.4E-04	5.5	3.3E-03	1.1	4.3E-01	-0.5	5.6E-01
ENSMUST00000156716				2.2	6.3E-02	1.0	3.8E-01	-1.9	9.4E-02	-0.8	4.4E-01
ENSMUST00000190624				6.7	2.7E-05	8.6	1.3E-02	-0.9	7.9E-01	-1.3	3.9E-01
ENSMUST00000154277				6.7	1.7E-04	5.1	5.4E-06	0.0	9.5E-01	0.1	8.3E-01
ENSMUST00000118124				6.7	2.0E-04	-4.0	9.0E-02	1.0	4.0E-01	-3.2	2.8E-01
ENSMUST00000156735				1.4	2.6E-01	0.8	6.2E-01	0.7	5.5E-01	1.3	3.6E-01
ENSMUST00000156739				1.1	1.5E-01	3.2	7.8E-03	1.4	9.9E-02	-0.6	4.5E-01
ENSMUST00000156740	nuclear receptor co-repressor 1 [Source:MGI Symbol;Acc:MGI:1349717]	F7C134		-0.8	4.5E-01	-5.0	1.0E-02	-2.4	1.2E-02	1.8	2.8E-01
ENSMUST00000119116				6.7	6.7E-05	-5.6	3.8E-03	-0.4	4.7E-01	-0.8	6.1E-01
ENSMUST00000156742	lysosomal-associated protein transmembrane 5 [Source:MGI Symbol;Acc:MGI:108046]	F6WX18		-3.7	1.1E-01	-1.8	5.7E-01	1.6	3.6E-01	-0.3	9.2E-01
ENSMUST00000123276				6.7	2.4E-04	-5.1	7.8E-03	-0.6	3.9E-01	-0.3	8.5E-01
ENSMUST00000142971				6.7	6.3E-05	9.7	3.7E-03	-0.1	9.8E-01	1.5	1.8E-01
ENSMUST00000161173				6.7	6.7E-05	5.8	6.5E-03	-3.6	1.0E-01	-0.6	5.2E-01
ENSMUST00000187481				6.7	1.2E-04	-7.5	7.2E-03	1.5	5.8E-02	-1.2	6.4E-01
ENSMUST00000135208				6.7	1.9E-06	5.8	1.1E-05	-1.3	7.6E-02	-0.1	8.4E-01
ENSMUST00000119114				6.7	2.6E-04	5.4	2.4E-03	-0.7	6.4E-01	-0.2	8.3E-01
ENSMUST00000156782	GATA binding protein 4 [Source:MGI Symbol;Acc:MGI:95664]	A4K4Z6		4.3	4.3E-02	5.4	2.1E-02	-0.7	7.5E-01	-1.8	2.1E-01
ENSMUST00000155164				6.7	9.6E-04	5.6	2.2E-02	-0.8	7.2E-01	-0.5	6.9E-01
ENSMUST00000173914				6.7	1.7E-04	-5.7	8.0E-04	-0.6	2.3E-01	0.2	8.5E-01
ENSMUST00000147252				6.7	1.7E-04	-3.4	9.7E-02	0.3	7.2E-01	-0.5	7.9E-01
ENSMUST00000111950				6.7	3.8E-04	5.1	1.7E-02	-0.7	6.9E-01	1.3	2.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000153454				6.7	7.6E-04	-2.8	5.4E-02	0.4	5.9E-01	-2.1	1.6E-01
ENSMUST00000163038				6.7	5.5E-05	-2.9	6.6E-02	0.3	7.3E-01	-3.6	7.7E-02
ENSMUST00000150347				6.7	9.9E-05	4.2	5.8E-04	-0.3	6.5E-01	0.0	1.0E+00
ENSMUST00000156800				-0.8	7.1E-01	-4.0	4.7E-02	-5.1	5.3E-03	-1.9	4.0E-01
ENSMUST00000155680				6.7	2.3E-04	4.8	3.1E-03	-2.1	1.3E-01	0.0	1.0E+00
ENSMUST00000136193				6.7	1.4E-04	4.2	1.5E-04	0.1	8.7E-01	-0.1	9.1E-01
ENSMUST00000156820	colony stimulating factor 1 (macrophage) [Source:MGI Symbol;Acc:MGI:1339753]	F6RNW8		-2.6	7.5E-02	-1.7	4.2E-01	1.4	3.1E-01	0.4	8.1E-01
ENSMUST00000119300				6.7	1.1E-04	-5.4	4.3E-03	-0.8	2.0E-01	-0.3	8.4E-01
ENSMUST00000166973				6.7	1.9E-03	6.1	2.6E-03	-0.7	6.8E-01	0.2	7.8E-01
ENSMUST00000189009				6.7	3.9E-04	5.6	1.3E-02	0.0	9.9E-01	-0.6	6.4E-01
ENSMUST00000142427				6.7	1.7E-03	2.9	2.1E-01	-0.6	7.9E-01	1.6	2.9E-01
ENSMUST00000156836	exonuclease 5 [Source:MGI Symbol;Acc:MGI:1920422]	A0A0A0MQI0		3.9	6.2E-02	0.5	8.3E-01	-2.6	1.8E-01	0.8	6.6E-01
ENSMUST00000156838				-1.8	1.7E-01	-2.7	1.5E-01	0.3	7.7E-01	1.2	5.0E-01
ENSMUST00000135396				6.6	6.7E-05	6.2	1.1E-03	1.3	3.5E-01	0.5	5.1E-01
ENSMUST00000156846	TruB pseudouridine (psi) synthase homolog 2 (E. coli) [Source:MGI Symbol;Acc:MGI:2442186]	H3BLS1		0.5	4.7E-01	1.3	1.9E-01	0.2	7.6E-01	-0.5	5.2E-01
ENSMUST00000156847				0.1	8.2E-01	0.4	6.0E-01	0.2	8.1E-01	-0.1	8.7E-01
ENSMUST00000145886				6.6	2.1E-03	5.0	2.1E-04	-0.9	3.2E-01	0.5	3.5E-01
ENSMUST00000118691				6.6	1.6E-03	2.7	3.8E-02	-0.4	6.8E-01	0.2	8.4E-01
ENSMUST00000175873				6.6	6.3E-05	1.4	8.8E-02	-0.9	1.9E-01	0.0	9.5E-01
ENSMUST00000156855	RELT tumor necrosis factor receptor [Source:MGI Symbol;Acc:MGI:2443373]	D3YWL9		-1.0	1.1E-01	-1.6	1.5E-01	1.2	7.3E-02	1.7	1.1E-01
ENSMUST00000146181				6.6	1.1E-05	2.3	2.2E-01	-0.5	7.7E-01	0.6	6.6E-01
ENSMUST00000156859	nase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit [Sou		Q8BMS1	-0.7	9.6E-02	0.2	6.1E-01	0.1	7.7E-01	-0.8	9.4E-02
ENSMUST00000156861	torsin family 3, member A [Source:MGI Symbol;Acc:MGI:1353652]	A0A087WRX4		1.6	4.3E-01	2.6	3.6E-01	1.0	6.9E-01	0.0	9.9E-01
ENSMUST00000181828				6.6	2.6E-05	5.2	7.6E-04	0.4	6.7E-01	0.0	9.7E-01
ENSMUST00000156872				-0.7	6.4E-01	0.2	8.9E-01	0.5	7.2E-01	-0.4	8.0E-01
ENSMUST00000156046				6.6	3.5E-05	2.2	5.8E-01	10.9	6.1E-03	0.3	9.2E-01
ENSMUST00000183578				6.6	4.5E-06	-2.3	1.1E-01	1.1	1.9E-01	-1.7	2.8E-01
ENSMUST00000187302				6.6	8.2E-05	2.4	2.9E-02	0.8	3.0E-01	0.3	6.8E-01
ENSMUST00000188924				6.6	1.8E-04	6.4	3.1E-04	-0.5	6.7E-01	-0.8	2.3E-01
ENSMUST00000190470				6.6	1.7E-04	4.8	5.7E-03	0.4	7.6E-01	-0.7	4.8E-01
ENSMUST00000125722				6.6	3.4E-05	4.2	4.5E-03	1.4	2.1E-01	0.5	5.2E-01
ENSMUST00000156891				-2.8	8.0E-02	-2.3	3.2E-01	0.9	5.0E-01	0.4	8.6E-01
ENSMUST00000156896				-1.7	2.9E-01	-2.4	3.1E-01	-0.1	9.4E-01	0.5	8.2E-01
ENSMUST00000147666				6.6	3.2E-05	-1.7	1.2E-01	0.9	1.4E-01	-4.4	7.8E-03
ENSMUST00000173438				6.6	5.7E-05	5.0	3.0E-04	-0.3	7.1E-01	0.0	9.8E-01
ENSMUST00000185291				6.6	2.1E-04	-3.6	4.2E-03	0.1	9.1E-01	-0.2	8.8E-01
ENSMUST00000128081				6.6	3.9E-04	4.9	1.9E-03	0.6	6.1E-01	-0.9	2.8E-01
ENSMUST00000156907				2.5	4.9E-02	3.8	2.4E-02	0.3	8.2E-01	-1.0	3.3E-01
ENSMUST00000132132				6.6	4.2E-04	-3.0	7.1E-03	0.1	7.9E-01	-0.1	9.1E-01
ENSMUST00000156911				2.9	1.0E-01	0.4	8.6E-01	-0.9	6.3E-01	1.6	4.7E-01
ENSMUST00000156923				3.2	8.4E-02	5.6	5.3E-02	1.9	4.5E-01	-0.5	7.5E-01
ENSMUST00000194860				6.6	2.0E-04	2.2	5.7E-01	8.2	1.2E-02	-1.5	6.8E-01
ENSMUST00000156931				0.7	4.2E-01	1.1	2.8E-01	-0.6	4.6E-01	-1.1	2.6E-01
ENSMUST00000156933	centriolin [Source:MGI Symbol;Acc:MGI:1889576]	R4GML6	A2AL36	-1.6	6.4E-01	-5.5	3.2E-01	-2.1	3.9E-01	1.8	7.5E-01
ENSMUST00000174324				6.6	8.0E-05	7.3	2.3E-06	-0.6	4.0E-01	0.1	7.7E-01
ENSMUST00000156938				2.6	2.1E-01	1.5	4.9E-01	-1.3	5.2E-01	-0.2	9.0E-01
ENSMUST00000118359				6.6	5.3E-04	8.4	7.9E-03	-0.9	7.6E-01	-2.3	1.3E-01
ENSMUST00000128935				6.6	2.6E-05	3.5	5.4E-03	-1.1	2.3E-01	-0.2	8.3E-01
ENSMUST00000132851				6.6	9.1E-05	-1.7	2.2E-01	0.6	4.0E-01	-0.1	9.6E-01
ENSMUST00000139990				6.6	1.7E-03	2.6	1.4E-01	0.6	7.1E-01	0.9	4.5E-01
ENSMUST00000176672				6.6	3.9E-04	5.8	2.4E-03	-0.6	7.0E-01	-0.1	9.3E-01
ENSMUST00000156958				-1.1	5.9E-01	-1.6	5.2E-01	-1.2	4.6E-01	-0.7	7.8E-01
ENSMUST00000181855				6.6	1.2E-04	6.9	1.0E-04	-0.6	6.0E-01	-0.3	6.6E-01
ENSMUST00000156963	zinc finger, HIT domain containing 1 [Source:MGI Symbol;Acc:MGI:1917353]			0.1	8.5E-01	1.2	1.8E-01	-0.2	7.8E-01	-1.2	1.2E-01
ENSMUST00000184141				6.6	3.9E-04	7.4	6.0E-04	0.7	6.1E-01	1.2	1.4E-01
ENSMUST00000123309				6.6	1.2E-03	-1.9	1.4E-01	1.9	2.5E-02	1.4	2.6E-01
ENSMUST00000156970	phenylalanyl-tRNA synthetase, alpha subunit [Source:MGI Symbol;Acc:MGI:1913840]	D6RIJ2		5.1	8.6E-02	-0.1	9.7E-01	-2.7	3.8E-01	2.5	4.7E-01
ENSMUST00000156975				1.5	1.2E-01	1.8	1.5E-01	0.4	7.0E-01	0.1	9.5E-01
ENSMUST00000156988	eukaryotic translation elongation factor 1 alpha 1 [Source:MGI Symbol;Acc:MGI:1096881]	D3Z3I8		-0.9	5.7E-01	0.6	7.8E-01	0.8	6.4E-01	-0.6	7.2E-01
ENSMUST00000156990	transcription factor 3 [Source:MGI Symbol;Acc:MGI:98510]	F6T941		4.0	1.5E-01	5.3	1.4E-01	2.5	4.3E-01	1.3	6.0E-01
ENSMUST00000156992	myosin VIIA [Source:MGI Symbol;Acc:MGI:104510]			1.2	1.5E-01	-2.6	5.8E-02	-0.9	2.3E-01	2.9	3.3E-02
ENSMUST00000132303				6.6	3.5E-04	4.2	8.6E-03	1.7	1.7E-01	-0.1	8.9E-01
ENSMUST00000156999				2.4	4.7E-02	5.1	1.3E-03	0.1	9.3E-01	-2.6	1.3E-02
ENSMUST00000157001				1.2	3.5E-01	-4.4	1.6E-02	-5.0	6.1E-04	0.5	7.4E-01
ENSMUST00000192015				6.6	9.7E-05	7.3	4.9E-05	-0.6	6.1E-01	-0.1	8.8E-01
ENSMUST00000117877				6.6	6.8E-04	8.1	6.5E-05	-0.4	7.4E-01	1.1	8.2E-02
ENSMUST00000124405				6.6	1.8E-04	4.7	9.6E-04	-2.3	6.4E-02	-0.1	9.3E-01
ENSMUST00000159758				6.6	2.4E-05	6.1	2.3E-03	-0.6	7.0E-01	-1.0	2.7E-01
ENSMUST00000172987				6.6	7.2E-05	4.6	2.9E-02	-0.6	7.6E-01	0.7	5.8E-01
ENSMUST00000134124				6.6	8.1E-05	6.7	1.7E-05	0.3	7.1E-01	0.1	8.6E-01
ENSMUST00000140259				6.6	1.4E-02	4.4	1.2E-03	-0.6	5.1E-01	-0.3	7.0E-01
ENSMUST00000117787				6.6	2.2E-04	-4.1	2.8E-02	-0.3	7.3E-01	-0.5	7.7E-01
ENSMUST00000137040				6.6	7.9E-05	5.1	1.7E-03	-0.6	6.2E-01	-0.5	5.7E-01
ENSMUST00000123068				6.6	9.2E-05	7.4	6.6E-05	0.4	6.9E-01	-0.8	1.9E-01
ENSMUST00000161635				6.6	1.9E-04	-2.5	1.0E-01	2.6	1.1E-02	-0.6	6.6E-01
ENSMUST00000174716				6.6	2.2E-06	2.6	2.7E-02	-1.3	1.7E-01	-0.4	6.7E-01
ENSMUST00000120287				6.6	2.8E-03	3.3	2.1E-03	-0.1	9.1E-01	0.0	9.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000157045				-1.0	5.2E-01	-0.1	9.1E-01	-2.7	3.6E-02	-3.6	3.8E-02
ENSMUST00000157050	paxillin [Source:MGI Symbol;Acc:MGI:108295]			-0.9	4.2E-01	0.5	7.4E-01	1.2	2.4E-01	-0.1	9.2E-01
ENSMUST00000121407				6.6	2.2E-04	5.8	2.8E-04	-0.4	7.3E-01	-0.9	1.6E-01
ENSMUST00000191529				6.6	1.1E-05	4.0	8.2E-03	0.2	8.7E-01	-0.6	4.5E-01
ENSMUST00000117642				6.6	2.7E-03	6.5	3.1E-05	-1.3	1.9E-01	-1.0	1.0E-01
ENSMUST00000162048				6.6	1.8E-03	4.7	1.8E-04	0.1	9.0E-01	0.2	7.4E-01
ENSMUST00000185866				6.6	2.3E-03	6.2	1.5E-03	-0.7	6.5E-01	-0.6	4.9E-01
ENSMUST00000159002	nuclear receptor binding factor 2 [Source:MGI Symbol;Acc:MGI:1354950]	E0CZ57		0.7	5.8E-01	0.5	7.0E-01	-1.8	1.6E-01	-1.5	2.5E-01
ENSMUST00000123782				6.6	4.2E-03	-4.8	2.4E-02	0.8	3.4E-01	-0.1	9.4E-01
ENSMUST00000139654				6.6	1.8E-04	7.8	4.9E-03	2.0	3.3E-01	-0.7	5.8E-01
ENSMUST00000159016	polymerase (RNA) mitochondrial (DNA directed) [Source:MGI Symbol;Acc:MGI:1915843]	E9PWD9		-0.3	9.0E-01	-2.8	3.4E-01	-1.5	4.4E-01	1.0	7.1E-01
ENSMUST00000125390				6.6	3.9E-04	-7.8	2.2E-03	-1.9	1.7E-02	0.0	9.9E-01
ENSMUST00000159020	serglycin [Source:MGI Symbol;Acc:MGI:97756]	E0CZH1		-3.1	3.5E-02	-3.8	3.5E-02	-1.5	9.6E-02	-0.8	6.5E-01
ENSMUST00000133710				6.6	4.1E-05	-5.7	1.6E-03	-1.0	9.5E-02	-0.8	5.7E-01
ENSMUST00000159029				-0.7	4.1E-01	1.0	3.7E-01	1.2	1.9E-01	-0.5	5.9E-01
ENSMUST00000173290				6.6	8.7E-05	1.4	5.5E-01	-0.8	6.8E-01	2.8	1.5E-01
ENSMUST00000185851				6.6	3.2E-06	6.2	4.3E-03	-0.4	8.1E-01	-0.4	7.1E-01
ENSMUST00000159048	calcium channel, voltage-dependent, T type, alpha 1H subunit [Source:MGI Symbol;Acc:MGI:1928842]	E0CYZ3		6.9	6.4E-02	5.7	1.2E-01	-0.8	8.3E-01	0.4	8.6E-01
ENSMUST00000159050	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	E0CXS9		0.0	9.9E-01	4.8	2.4E-01	4.7	1.3E-01	-0.1	9.7E-01
ENSMUST00000119801				6.6	1.4E-03	6.4	8.0E-04	0.0	9.9E-01	0.9	2.2E-01
ENSMUST00000172439				6.6	1.0E-04	6.5	4.9E-03	-0.2	9.0E-01	-2.1	9.1E-02
ENSMUST00000185353				6.6	5.8E-04	6.6	5.8E-05	-0.7	4.5E-01	0.4	5.1E-01
ENSMUST00000185401				6.6	6.7E-05	8.0	3.6E-05	-0.6	6.2E-01	-5.6	6.1E-05
ENSMUST00000159063	nuclear transcription factor-Y alpha [Source:MGI Symbol;Acc:MGI:97316]			-0.7	7.7E-01	-0.6	8.3E-01	-0.2	8.9E-01	-0.3	9.3E-01
ENSMUST00000159064	RIKEN cDNA 4933434E20 gene [Source:MGI Symbol;Acc:MGI:1914027]		Q8R092	0.1	9.6E-01	-4.1	1.4E-01	-5.5	1.2E-02	-1.2	6.9E-01
ENSMUST00000159065	transmembrane protein 191C [Source:MGI Symbol;Acc:MGI:107238]		Q9JJB1	5.1	4.7E-02	5.5	4.7E-02	-0.8	7.5E-01	-1.1	5.0E-01
ENSMUST00000187195				6.6	1.1E-05	6.6	1.0E-03	-1.1	4.8E-01	-0.2	8.2E-01
ENSMUST00000129424				6.6	2.9E-05	7.9	1.8E-04	0.2	8.7E-01	-0.2	7.1E-01
ENSMUST00000159069				-0.8	2.8E-01	0.5	5.5E-01	0.9	2.1E-01	-0.5	5.9E-01
ENSMUST00000159073	guanine nucleotide binding protein (G protein), gamma 2 [Source:MGI Symbol;Acc:MGI:102705]		P63213	0.6	7.5E-01	-1.6	4.2E-01	-3.3	8.3E-02	-1.2	5.2E-01
ENSMUST00000133954				6.6	6.7E-06	2.3	2.7E-02	-1.0	2.4E-01	-0.7	3.3E-01
ENSMUST00000138113				6.6	3.5E-03	2.4	1.4E-02	-0.8	2.8E-01	-0.6	3.7E-01
ENSMUST00000159086	zinc finger protein 871 [Source:MGI Symbol;Acc:MGI:1921793]	G5E905		0.1	8.5E-01	0.6	1.9E-01	0.3	3.5E-01	-0.2	5.8E-01
ENSMUST00000159091				-2.7	1.6E-01	-0.2	9.3E-01	0.8	6.2E-01	-1.7	4.2E-01
ENSMUST00000159092				-1.6	1.9E-01	-1.3	2.9E-01	-1.4	1.4E-01	-1.7	2.0E-01
ENSMUST00000147319				6.6	2.5E-04	6.0	1.2E-02	-0.8	7.2E-01	-0.9	4.4E-01
ENSMUST00000182513				6.6	3.2E-02	-2.3	1.0E-01	1.6	4.5E-02	-1.7	2.5E-01
ENSMUST00000159099	f-box protein 9 [Source:MGI Symbol;Acc:MGI:1918788]		Q8BK06	0.1	9.1E-01	0.7	6.7E-01	0.6	6.7E-01	0.0	9.8E-01
ENSMUST00000147095				6.6	2.8E-04	-1.5	1.7E-01	-0.5	4.5E-01	3.4	5.4E-03
ENSMUST00000159104	Wilms tumour 1-associating protein [Source:MGI Symbol;Acc:MGI:1926395]	F7CCI4		-3.4	6.0E-02	-2.8	1.9E-01	-0.1	8.9E-01	-0.7	7.5E-01
ENSMUST00000159109	zinc finger protein 609 [Source:MGI Symbol;Acc:MGI:2674092]		Q8BZ47	0.8	6.2E-02	1.6	1.1E-02	0.6	1.5E-01	-0.2	6.9E-01
ENSMUST00000142974				6.6	3.3E-06	-6.3	2.3E-02	1.9	3.6E-02	0.9	7.3E-01
ENSMUST00000173026				6.6	1.9E-02	6.6	5.7E-05	-1.3	2.4E-01	-0.1	9.2E-01
ENSMUST00000120324				6.6	5.0E-04	5.4	4.5E-04	-1.0	3.6E-01	-1.3	8.9E-02
ENSMUST00000121173				6.6	2.1E-04	8.7	9.3E-04	1.4	4.6E-01	-0.4	6.3E-01
ENSMUST00000159123	cDNA sequence BC037034 [Source:MGI Symbol;Acc:MGI:2385896]	E9Q6X8		-5.6	4.2E-02	-3.5	3.1E-01	1.2	5.3E-01	-0.9	7.9E-01
ENSMUST00000159830				6.6	8.0E-05	3.8	3.9E-02	-5.3	2.2E-02	-3.9	1.1E-02
ENSMUST00000159130	mannosidase, alpha, class 2C, member 1 [Source:MGI Symbol;Acc:MGI:1920994]	E0CZB0		1.1	4.3E-01	1.1	5.7E-01	-0.1	9.4E-01	-0.1	9.4E-01
ENSMUST00000118387				6.6	8.8E-05	6.4	1.0E-02	0.7	7.2E-01	-0.9	5.4E-01
ENSMUST00000127053				6.6	2.3E-04	1.8	6.6E-02	0.0	9.9E-01	-0.1	8.6E-01
ENSMUST00000159145	tetratricopeptide repeat domain 26 [Source:MGI Symbol;Acc:MGI:2444853]	E0CX73		6.8	6.4E-02	5.3	1.7E-01	-0.5	8.9E-01	0.9	7.0E-01
ENSMUST00000159150				-0.3	9.2E-01	-4.1	1.7E-01	-5.1	1.9E-02	-1.3	6.9E-01
ENSMUST00000160151				6.6	3.4E-05	6.3	1.4E-03	0.5	7.0E-01	0.7	4.0E-01
ENSMUST00000164622				6.6	1.2E-04	5.8	3.8E-04	-2.1	1.1E-01	0.5	4.8E-01
ENSMUST00000159159	alcohol dehydrogenase 1 (class I) [Source:MGI Symbol;Acc:MGI:87921]	E0CXV3		4.1	5.4E-02	1.8	2.6E-01	-3.9	5.9E-02	-1.6	2.7E-01
ENSMUST00000138322				6.6	3.0E-04	7.6	3.1E-05	-1.6	1.6E-01	0.3	5.6E-01
ENSMUST00000150400				6.6	4.9E-06	4.7	1.5E-04	0.6	4.0E-01	-0.2	7.1E-01
ENSMUST00000097869				6.6	9.0E-05	7.5	3.6E-05	-0.9	4.5E-01	0.2	6.7E-01
ENSMUST00000159168	UMAP1-MVP12 associated (UMA) domain containing 1 [Source:MGI Symbol;Acc:MGI:3840148]	E0CXP6		-5.2	6.3E-02	3.3	3.6E-01	6.5	3.3E-02	-2.0	5.2E-01
ENSMUST00000138441				6.6	2.3E-05	5.1	1.4E-03	-0.3	8.2E-01	-1.6	5.7E-02
ENSMUST00000159171	Fc receptor-like A [Source:MGI Symbol;Acc:MGI:2138647]		Q920A9	1.7	4.3E-01	-2.3	3.2E-01	-3.3	7.1E-02	0.6	7.9E-01
ENSMUST00000159176				-3.8	6.9E-02	-1.1	7.1E-01	2.6	1.9E-01	-0.1	9.7E-01
ENSMUST00000146791				6.6	1.1E-04	7.0	2.7E-04	-0.4	7.5E-01	-1.1	1.5E-01
ENSMUST00000147211				6.6	6.1E-05	2.9	2.7E-02	-2.6	6.4E-02	0.1	9.5E-01
ENSMUST00000159186	tassium voltage-gated channel, shaker-related subfamily, beta member 2 [Source:MGI Symbol;Acc:MGI:10923	E0CXZ9		1.1	6.0E-01	3.9	1.7E-01	0.4	8.7E-01	-2.4	2.9E-01
ENSMUST00000127745				6.6	4.1E-06	7.7	3.0E-05	-0.6	6.1E-01	-0.7	2.0E-01
ENSMUST00000159197	TATA box binding protein [Source:MGI Symbol;Acc:MGI:101838]	E9Q6D9		5.1	3.8E-02	3.2	3.0E-01	0.6	8.1E-01	2.6	2.9E-01
ENSMUST00000147026				6.6	1.6E-04	-6.0	1.6E-02	-1.0	3.2E-01	-1.4	5.6E-01
ENSMUST00000153086				6.6	3.0E-04	7.1	3.7E-05	0.1	9.1E-01	0.1	7.9E-01
ENSMUST00000160637				6.6	2.0E-03	8.2	2.4E-04	-0.3	8.6E-01	0.2	7.5E-01
ENSMUST00000159203				1.9	1.3E-01	3.3	6.9E-02	0.2	9.0E-01	-1.2	3.2E-01
ENSMUST00000160995				6.6	6.2E-03	-1.1	2.7E-01	0.8	2.3E-01	-0.7	4.7E-01
ENSMUST00000159209	transmembrane BAX inhibitor motif containing 6 [Source:MGI Symbol;Acc:MGI:99682]		Q9D2C7	-2.5	4.6E-02	-1.0	4.6E-01	0.9	3.0E-01	-0.7	6.3E-01
ENSMUST00000096981				6.6	6.9E-05	-0.1	9.6E-01	-0.2	8.8E-01	3.7	2.2E-02
ENSMUST00000114646				6.6	5.1E-04	5.7	3.3E-03	0.4	8.0E-01	-0.6	4.6E-01
ENSMUST00000159216	selenoprotein P, plasma, 1 [Source:MGI Symbol;Acc:MGI:894288]		P70274	4.6	6.4E-02	4.0	2.5E-01	2.0	4.7E-01	2.5	3.6E-01
ENSMUST00000159217				1.6	5.1E-01	-4.3	1.7E-01	-4.6	3.0E-02	1.3	6.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159218	maestro heat-like repeat family member 1 [Source:MGI Symbol;Acc:MGI:2442558]	G3XA21		-6.2	3.9E-02	0.9	8.5E-01	7.2	4.0E-02	0.1	9.8E-01
ENSMUST00000159219				4.0	7.7E-02	4.8	7.3E-02	-1.4	5.7E-01	-2.2	2.1E-01
ENSMUST00000152544				6.6	8.0E-04	1.5	5.0E-01	-4.0	1.2E-01	2.4	1.7E-01
ENSMUST00000159230	solute carrier family 19 (thiamine transporter), member 2 [Source:MGI Symbol;Acc:MGI:1928761]	Q8R4Y1		-1.3	1.9E-01	-1.3	3.4E-01	0.8	3.5E-01	0.8	5.2E-01
ENSMUST00000159234				0.2	7.2E-01	0.5	5.5E-01	-0.2	7.1E-01	-0.5	5.4E-01
ENSMUST00000114101				6.6	3.7E-04	5.5	4.3E-03	-0.6	6.6E-01	-0.5	5.7E-01
ENSMUST00000138074				6.6	1.2E-04	3.1	1.2E-03	-1.4	5.5E-02	-0.2	6.7E-01
ENSMUST00000192435				6.6	4.3E-03	6.4	2.9E-03	-0.7	6.8E-01	0.6	5.4E-01
ENSMUST00000141960				6.6	1.8E-06	-0.2	8.3E-01	-2.5	1.9E-02	1.1	3.1E-01
ENSMUST00000129974				6.6	5.9E-05	5.0	1.2E-04	-3.5	6.9E-03	-0.8	1.9E-01
ENSMUST00000155899				6.6	3.5E-05	3.8	7.2E-04	-1.9	3.3E-02	-0.8	1.9E-01
ENSMUST00000049520				6.6	3.2E-04	0.9	2.7E-01	-1.4	7.4E-02	-0.2	7.3E-01
ENSMUST00000128702				6.6	1.0E-04	7.3	3.4E-04	-0.9	5.5E-01	-0.6	4.1E-01
ENSMUST00000143056				6.6	1.9E-02	-2.5	2.5E-02	0.5	3.4E-01	-0.7	4.7E-01
ENSMUST00000137596				6.6	5.3E-06	5.0	3.0E-02	-1.4	5.0E-01	-0.9	5.4E-01
ENSMUST00000138469				6.6	5.8E-04	2.1	1.3E-02	0.1	8.8E-01	-0.1	8.1E-01
ENSMUST00000141526				6.6	1.2E-04	-5.1	8.0E-04	-0.6	2.2E-01	0.2	8.8E-01
ENSMUST00000149478				6.6	1.3E-02	6.3	5.6E-05	0.1	8.9E-01	0.8	1.3E-01
ENSMUST00000159297				-1.6	4.6E-01	-3.9	1.5E-01	-2.6	9.3E-02	-0.3	9.2E-01
ENSMUST00000195849				6.6	4.2E-04	5.1	2.0E-03	-0.5	7.1E-01	0.4	5.7E-01
ENSMUST00000135705				6.6	1.0E-02	7.0	1.5E-03	-1.5	4.3E-01	1.3	1.8E-01
ENSMUST00000190421				6.6	1.7E-04	-3.0	6.1E-02	0.1	8.8E-01	-3.1	1.2E-01
ENSMUST00000194084				6.6	4.1E-06	6.7	1.9E-04	0.7	5.2E-01	0.2	7.4E-01
ENSMUST00000159321				-0.2	8.4E-01	0.7	5.0E-01	0.4	6.3E-01	-0.5	6.1E-01
ENSMUST00000120254				6.6	9.5E-05	3.7	2.4E-03	-1.5	1.0E-01	0.7	2.9E-01
ENSMUST00000174687				6.6	2.4E-04	8.6	4.6E-05	1.4	2.6E-01	-0.8	1.7E-01
ENSMUST00000194305				6.6	3.1E-04	2.4	2.5E-02	-1.3	1.5E-01	0.2	8.0E-01
ENSMUST00000195069				6.6	7.4E-06	2.6	7.8E-02	-0.6	6.3E-01	3.2	1.0E-02
ENSMUST00000183601				6.6	5.9E-05	5.6	5.5E-04	-0.8	4.8E-01	-0.9	2.3E-01
ENSMUST00000150495				6.6	1.4E-03	5.8	4.0E-03	0.0	1.0E+00	-1.5	1.5E-01
ENSMUST00000177503				6.6	5.3E-04	-3.5	1.8E-02	1.1	9.2E-02	-1.3	3.5E-01
ENSMUST00000143198				6.6	6.2E-05	-7.2	1.1E-04	0.4	3.1E-01	-0.2	9.0E-01
ENSMUST00000122244				6.6	1.8E-04	3.4	2.1E-03	-3.6	3.2E-03	-1.3	8.5E-02
ENSMUST00000159351	RAS guanyl releasing protein 4 [Source:MGI Symbol;Acc:MGI:2386851]		Q8BTM9	-3.7	1.0E-01	-2.2	4.7E-01	1.2	4.8E-01	-0.3	9.1E-01
ENSMUST00000149890				6.6	5.2E-05	7.1	6.7E-05	-0.6	6.1E-01	0.1	9.3E-01
ENSMUST00000184102				6.6	2.8E-04	3.2	1.5E-02	-1.6	1.5E-01	-0.2	7.8E-01
ENSMUST00000159365	adrenergic receptor, alpha 1a [Source:MGI Symbol;Acc:MGI:104773]	Q8BUE5		2.1	9.0E-02	6.6	1.6E-04	-0.5	6.3E-01	-5.0	2.0E-04
ENSMUST00000159367	ribosomal protein S6 kinase polypeptide 1 [Source:MGI Symbol;Acc:MGI:2443419]	E0CYA1		1.5	4.8E-01	5.5	4.2E-02	-0.6	8.1E-01	-4.5	3.8E-02
ENSMUST00000191316				6.6	6.8E-05	6.0	5.2E-04	-0.5	6.9E-01	-0.4	5.5E-01
ENSMUST00000133540				6.6	3.5E-06	-2.3	2.3E-01	1.1	2.9E-01	-1.1	5.5E-01
ENSMUST00000119952				6.6	2.2E-04	3.7	3.3E-02	0.9	5.0E-01	0.0	9.9E-01
ENSMUST00000152786				6.6	4.1E-05	6.2	2.6E-03	0.4	7.8E-01	-0.7	4.5E-01
ENSMUST00000178604				6.6	1.7E-04	-4.9	4.6E-02	1.1	3.4E-01	2.3	3.1E-01
ENSMUST00000186674				6.6	3.2E-04	3.2	2.1E-03	-4.4	1.3E-03	-0.4	5.2E-01
ENSMUST00000145529				6.6	4.8E-05	6.8	2.2E-03	2.4	1.4E-01	-0.8	3.8E-01
ENSMUST00000143931				6.6	1.3E-03	2.3	1.0E-02	-0.8	2.2E-01	-0.2	6.8E-01
ENSMUST00000159394	synaptotagmin-like 3 [Source:MGI Symbol;Acc:MGI:1933367]	E0CYJ1		3.6	6.7E-02	6.3	8.4E-03	-0.3	8.7E-01	-3.1	2.7E-02
ENSMUST00000144895				6.6	1.5E-06	6.9	1.3E-04	-0.5	6.7E-01	-0.1	8.1E-01
ENSMUST00000151269				6.6	5.4E-05	4.4	8.5E-06	-0.7	1.6E-01	-0.4	1.9E-01
ENSMUST00000178846				6.6	1.0E-04	5.2	4.6E-04	1.5	1.2E-01	-0.8	2.2E-01
ENSMUST00000185296				6.6	2.6E-02	-2.5	5.3E-02	1.8	1.3E-02	-0.6	6.0E-01
ENSMUST00000159414	filamin A interacting protein 1-like [Source:MGI Symbol;Acc:MGI:1925999]	E0CYM1		-2.3	1.3E-01	-5.8	4.6E-02	-0.6	5.6E-01	2.9	2.8E-01
ENSMUST00000125999				6.6	4.5E-04	6.2	4.4E-04	0.4	7.1E-01	-0.5	4.7E-01
ENSMUST00000127561				6.6	1.1E-04	6.2	1.1E-05	-0.4	6.1E-01	0.1	7.2E-01
ENSMUST00000000228				6.6	1.2E-02	5.3	1.7E-02	-0.7	7.2E-01	-0.7	5.6E-01
ENSMUST00000141451				6.6	1.4E-04	-3.5	2.6E-02	0.7	2.8E-01	-0.2	9.0E-01
ENSMUST00000179090				6.6	9.0E-05	3.3	2.6E-02	0.1	9.2E-01	0.4	6.2E-01
ENSMUST00000159425				-2.7	8.5E-02	1.3	3.5E-01	0.0	9.8E-01	-3.9	2.2E-02
ENSMUST00000186430				6.6	7.8E-05	6.2	6.8E-05	-0.1	9.3E-01	-0.4	4.6E-01
ENSMUST00000195559				6.6	3.3E-04	-3.2	8.5E-02	0.2	8.3E-01	-0.9	6.1E-01
ENSMUST00000143851				6.6	6.2E-04	-3.9	3.6E-02	0.2	8.2E-01	-0.1	9.5E-01
ENSMUST00000150493				6.6	7.9E-04	6.5	2.1E-03	-0.7	6.6E-01	0.7	4.0E-01
ENSMUST00000159433	UMAP1-MVP12 associated (UMA) domain containing 1 [Source:MGI Symbol;Acc:MGI:3840148]	E0CXP6		-4.1	1.9E-01	-5.1	1.8E-01	-2.0	2.8E-01	-0.9	8.2E-01
ENSMUST00000138636				6.6	2.5E-04	1.5	3.3E-02	-1.1	6.2E-02	-0.7	2.1E-01
ENSMUST00000159447	ubinuclein 2 [Source:MGI Symbol;Acc:MGI:2444236]	F6UTU1		1.8	1.0E-01	4.3	8.8E-03	1.8	1.6E-01	-0.7	4.9E-01
ENSMUST00000156051				6.6	1.1E-04	5.4	3.8E-03	-0.5	7.3E-01	0.0	9.6E-01
ENSMUST00000194157				6.6	4.9E-05	-8.6	2.4E-02	-2.5	4.9E-02	-0.8	8.4E-01
ENSMUST00000132408				6.6	6.5E-05	5.0	8.8E-03	-0.6	7.0E-01	-0.1	9.6E-01
ENSMUST00000159469				0.2	9.3E-01	-4.2	2.3E-01	-3.4	1.1E-01	1.1	7.6E-01
ENSMUST00000121874				6.6	7.8E-05	4.7	5.3E-03	-1.2	3.7E-01	0.9	3.3E-01
ENSMUST00000147624				6.6	8.9E-05	6.0	5.6E-05	-0.3	6.8E-01	-0.3	6.3E-01
ENSMUST00000131251				6.6	5.1E-06	8.8	2.0E-05	-1.1	3.8E-01	0.8	1.3E-01
ENSMUST00000137884				6.6	2.8E-04	7.1	7.5E-04	-0.8	6.2E-01	0.7	3.7E-01
ENSMUST00000190584				6.6	1.8E-04	6.2	3.3E-02	0.0	9.9E-01	-0.3	8.2E-01
ENSMUST00000159497				0.7	3.7E-01	2.6	2.7E-02	0.9	3.2E-01	-1.0	2.6E-01
ENSMUST00000151662				6.6	1.3E-04	7.7	2.6E-04	0.4	7.9E-01	-0.9	2.1E-01
ENSMUST00000159500	retinol dehydrogenase 11 [Source:MGI Symbol;Acc:MGI:102581]	E0CYX0		0.8	6.6E-01	-3.7	1.8E-01	-4.1	2.0E-02	0.4	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000129454				6.6	5.7E-04	7.1	3.8E-05	0.1	8.8E-01	0.0	9.3E-01
ENSMUST00000151399				6.6	1.7E-04	6.5	1.2E-04	-0.5	6.2E-01	-0.8	2.0E-01
ENSMUST00000187610				6.6	3.6E-06	6.1	1.5E-03	0.5	7.3E-01	-0.1	9.1E-01
ENSMUST00000159514	N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source:MGI Symbol;Acc:MGI:1919367]		Q6PGB6	-1.3	5.8E-01	-3.8	2.0E-01	-1.9	2.6E-01	0.5	8.6E-01
ENSMUST00000146838				6.6	8.8E-05	6.0	7.5E-04	-0.4	7.4E-01	-0.5	4.5E-01
ENSMUST00000193232				6.6	3.8E-05	7.8	3.6E-04	0.5	7.6E-01	-0.6	4.0E-01
ENSMUST00000131102				6.6	2.6E-04	7.0	1.7E-04	-0.5	7.1E-01	-0.1	9.3E-01
ENSMUST00000132970				6.6	4.0E-06	6.5	6.7E-05	-1.5	1.7E-01	-0.9	1.4E-01
ENSMUST00000175896				6.6	9.7E-05	5.9	1.1E-02	-0.8	7.2E-01	-0.9	4.6E-01
ENSMUST00000159530	RB1-inducible coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1341850]	F6TLJ4		-0.6	5.9E-01	-1.6	2.1E-01	-1.1	2.3E-01	-0.1	9.6E-01
ENSMUST00000150030				6.6	2.0E-04	1.5	2.4E-02	-1.9	4.8E-03	-0.4	3.9E-01
ENSMUST00000159534				1.6	8.1E-02	1.9	1.3E-01	0.7	4.6E-01	0.4	6.5E-01
ENSMUST00000159538				3.0	8.3E-02	6.4	2.7E-02	2.2	3.5E-01	-1.2	4.3E-01
ENSMUST00000187612				6.6	1.9E-04	-7.4	5.5E-05	1.8	4.1E-04	-0.8	4.9E-01
ENSMUST00000194692				6.6	1.4E-03	4.1	2.2E-03	0.2	8.6E-01	0.6	3.8E-01
ENSMUST00000118988				6.6	6.9E-05	-3.2	2.3E-02	0.1	8.1E-01	-0.6	6.7E-01
ENSMUST00000137124				6.6	4.1E-05	-2.6	1.7E-01	0.5	6.3E-01	-0.5	7.7E-01
ENSMUST00000159553				-2.9	6.6E-02	-2.3	1.4E-01	-0.9	3.5E-01	-1.5	3.7E-01
ENSMUST00000159558	staufen (RNA binding protein) homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1352508]		Q8CJ67	2.6	8.0E-02	6.4	7.7E-04	-0.5	7.4E-01	-4.3	1.6E-03
ENSMUST00000159559	WNK lysine deficient protein kinase 2 [Source:MGI Symbol;Acc:MGI:1922857]	E0CYT1		5.7	1.1E-01	6.5	7.9E-02	-0.9	8.1E-01	-1.7	4.6E-01
ENSMUST00000116162				6.6	1.3E-03	4.8	4.7E-03	-0.6	6.5E-01	1.8	4.8E-02
ENSMUST00000168961				6.6	2.2E-04	6.7	6.3E-05	-0.1	8.8E-01	0.1	8.9E-01
ENSMUST00000120271				6.6	6.3E-05	4.6	3.5E-04	0.5	5.0E-01	-0.8	2.3E-01
ENSMUST00000146856				6.6	1.1E-04	-0.2	8.0E-01	0.6	2.1E-01	-1.0	1.2E-01
ENSMUST00000117656				6.6	7.5E-06	3.6	5.4E-02	-1.3	4.2E-01	-0.6	6.4E-01
ENSMUST00000146483				6.6	7.3E-05	2.6	7.0E-03	-0.3	7.1E-01	0.5	4.4E-01
ENSMUST00000148342				6.6	4.6E-03	8.8	5.4E-04	-0.9	6.4E-01	0.3	6.9E-01
ENSMUST00000176791				6.6	7.3E-06	8.4	9.7E-06	-1.0	3.2E-01	-0.7	9.5E-02
ENSMUST00000159578	expressed sequence C87414 [Source:MGI Symbol;Acc:MGI:2141341]	E0CYF0		2.5	1.7E-01	2.9	1.9E-01	-0.3	8.9E-01	-0.7	7.0E-01
ENSMUST00000185066				6.6	1.2E-05	6.7	2.6E-04	-0.6	6.3E-01	-0.4	5.7E-01
ENSMUST00000186409				6.6	1.1E-04	6.4	5.7E-03	0.1	9.4E-01	-1.8	1.5E-01
ENSMUST00000134249				6.6	3.0E-03	7.1	1.1E-04	-0.6	6.0E-01	-0.9	1.6E-01
ENSMUST00000150962				6.6	9.9E-04	-3.3	3.2E-03	-2.5	1.5E-03	-3.1	1.7E-02
ENSMUST00000159590	F-box and WD-40 domain protein 4 [Source:MGI Symbol;Acc:MGI:1354698]	E0CYL5		3.1	1.8E-01	4.9	1.4E-01	1.7	5.2E-01	-0.1	9.8E-01
ENSMUST00000159592	slingshot homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:2686240]		Q76I79	-0.1	8.6E-01	0.9	2.0E-01	0.9	1.0E-01	-0.1	8.7E-01
ENSMUST00000172937				6.6	1.6E-04	3.0	2.4E-02	-1.2	2.7E-01	-1.0	2.9E-01
ENSMUST00000134546				6.6	1.0E-02	7.0	3.2E-04	1.5	2.2E-01	0.3	6.2E-01
ENSMUST00000159600				4.0	7.8E-02	6.0	2.7E-02	-0.3	9.1E-01	-2.2	1.3E-01
ENSMUST00000117799				6.6	2.8E-04	-3.1	9.0E-02	0.7	4.6E-01	-1.2	5.2E-01
ENSMUST00000159606	WD repeat and FYVE domain containing 4 [Source:MGI Symbol;Acc:MGI:3584510]	E0CXD5		-2.4	4.6E-02	-0.2	8.9E-01	0.4	6.1E-01	-1.9	1.7E-01
ENSMUST00000123804				6.6	1.9E-03	6.2	9.7E-04	-0.7	6.3E-01	0.0	9.6E-01
ENSMUST00000148148				6.5	6.5E-05	6.5	2.2E-02	-0.8	7.7E-01	-0.5	7.1E-01
ENSMUST00000159615				-1.5	3.5E-01	-1.9	4.7E-01	0.6	6.7E-01	1.1	6.6E-01
ENSMUST00000159619	argininosuccinate lyase [Source:MGI Symbol;Acc:MGI:88084]		Q91YI0	-0.6	8.2E-01	0.0	9.9E-01	-1.1	6.7E-01	-1.7	5.8E-01
ENSMUST00000169699				6.5	2.5E-03	6.2	2.0E-04	-0.9	4.2E-01	0.6	3.5E-01
ENSMUST00000182188				6.5	1.2E-05	7.1	4.0E-03	0.9	6.2E-01	-0.8	4.7E-01
ENSMUST00000127035				6.5	1.7E-04	-1.1	4.4E-01	3.3	5.3E-03	1.8	2.1E-01
ENSMUST00000159634	Berardinelli-Seip congenital lipodystrophy 2 homolog (seipin) [Source:MGI Symbol;Acc:MGI:1298392]		Q9Z2E9	-2.2	1.4E-01	-0.6	7.4E-01	1.1	4.0E-01	-0.5	7.9E-01
ENSMUST00000159636				0.7	3.5E-01	1.1	2.3E-01	0.1	9.3E-01	-0.3	6.6E-01
ENSMUST00000159644	hydroxysteroid 11-beta dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:103562]	F2Z3U6		-1.2	5.3E-01	-5.9	1.5E-02	-5.2	1.5E-03	-0.5	8.2E-01
ENSMUST00000144886				6.5	1.2E-05	6.2	1.4E-02	0.6	7.4E-01	1.5	2.6E-01
ENSMUST00000155565				6.5	8.0E-05	-0.9	3.1E-01	0.3	6.0E-01	-2.2	5.8E-02
ENSMUST00000117617				6.5	2.7E-04	-5.8	2.1E-02	1.6	6.5E-02	-0.8	7.4E-01
ENSMUST00000140126				6.5	7.8E-05	6.1	1.1E-03	-0.9	5.2E-01	0.1	8.7E-01
ENSMUST00000159652				-2.3	1.3E-01	-2.8	2.0E-01	0.7	5.5E-01	1.2	5.8E-01
ENSMUST00000156656				6.5	3.2E-05	-1.7	2.9E-01	0.9	3.3E-01	-1.4	4.0E-01
ENSMUST00000180577				6.5	5.1E-04	6.5	1.6E-04	-0.5	6.4E-01	-0.7	3.0E-01
ENSMUST00000191852				6.5	1.3E-04	7.3	7.0E-04	-0.3	8.6E-01	0.3	7.5E-01
ENSMUST00000159672				-2.0	8.2E-02	-1.6	3.1E-01	0.1	9.5E-01	-0.3	8.1E-01
ENSMUST00000153961				6.5	7.1E-04	6.5	6.4E-04	-0.1	9.6E-01	-0.8	2.9E-01
ENSMUST00000159685	H3 histone, family 3A [Source:MGI Symbol;Acc:MGI:1097686]	E0CYN1		-5.5	1.4E-01	-9.0	7.0E-02	-3.9	3.9E-02	-0.4	9.4E-01
ENSMUST00000159687	proteasome (prosome, macropain) activator subunit 2 (PA28 beta) [Source:MGI Symbol;Acc:MGI:1096365]	E0CZ90		-2.3	4.9E-01	-4.3	3.1E-01	-2.3	2.8E-01	-0.4	9.4E-01
ENSMUST00000182564				6.5	2.5E-05	-9.5	1.7E-02	-3.1	1.4E-02	-0.3	9.3E-01
ENSMUST00000185787				6.5	9.5E-05	-3.6	1.6E-02	-0.7	3.0E-01	-3.7	4.9E-02
ENSMUST00000188361				6.5	2.0E-03	3.9	5.6E-04	-0.3	6.4E-01	0.4	5.1E-01
ENSMUST00000121432				6.5	1.4E-04	3.5	1.1E-01	8.0	1.4E-03	0.4	7.7E-01
ENSMUST00000119018				6.5	5.3E-05	4.7	3.0E-02	-2.0	3.4E-01	-1.3	3.0E-01
ENSMUST00000125348				6.5	1.5E-04	4.3	1.6E-03	-1.4	1.9E-01	0.0	9.5E-01
ENSMUST00000149787				6.5	3.5E-04	2.4	7.7E-02	-3.0	4.8E-02	0.6	5.2E-01
ENSMUST00000159698				-0.2	8.2E-01	-0.7	4.0E-01	-0.4	5.6E-01	0.2	8.0E-01
ENSMUST00000188325				6.5	9.1E-05	2.4	1.1E-01	-0.5	7.0E-01	3.5	8.5E-03
ENSMUST00000191135				6.5	1.0E-05	4.2	2.5E-02	1.2	4.0E-01	0.6	5.5E-01
ENSMUST00000159704	KIF1 binding protein [Source:MGI Symbol;Acc:MGI:1919570]	H3BIY2		1.0	5.7E-02	1.5	4.2E-02	0.7	1.8E-01	0.2	6.9E-01
ENSMUST00000118868				6.5	3.1E-05	3.9	2.9E-03	-1.1	2.6E-01	-0.8	2.9E-01
ENSMUST00000119637				6.5	1.0E-03	3.0	1.1E-02	-1.0	3.0E-01	-0.3	6.6E-01
ENSMUST00000143886				6.5	7.3E-05	-6.2	8.2E-03	0.8	3.2E-01	1.3	5.1E-01
ENSMUST00000127839				6.5	1.3E-04	0.5	6.7E-01	-0.8	4.4E-01	1.6	1.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159768				6.5	8.4E-05	3.0	5.7E-03	0.0	9.6E-01	-0.4	5.0E-01
ENSMUST00000189602				6.5	1.1E-04	4.5	1.2E-04	-0.4	5.7E-01	0.8	1.0E-01
ENSMUST00000172676				6.5	2.1E-04	5.9	5.9E-05	-0.5	5.3E-01	-0.7	1.7E-01
ENSMUST00000159727	PHD finger protein 21A [Source:MGI Symbol;Acc:MGI:2384756]	F6U6L3		0.9	6.4E-01	0.7	7.9E-01	-0.3	8.8E-01	-0.1	9.7E-01
ENSMUST00000141574				6.5	3.6E-04	5.0	4.1E-03	-0.7	6.4E-01	0.7	4.3E-01
ENSMUST00000151946				6.5	1.1E-03	4.5	2.8E-02	-1.2	4.7E-01	-0.2	8.7E-01
ENSMUST00000171314				6.5	3.7E-04	7.2	2.2E-04	1.3	3.1E-01	-0.1	8.8E-01
ENSMUST00000177469				6.5	1.8E-04	5.1	9.6E-04	-1.1	3.2E-01	0.2	8.0E-01
ENSMUST00000159742	amylo-1,6-glucosidase, 4-alpha-glucanotransferase [Source:MGI Symbol;Acc:MGI:1924809]	A0A0G2JGI9		-0.7	5.6E-01	0.1	9.6E-01	0.2	8.3E-01	-0.5	6.9E-01
ENSMUST00000159745				-0.9	4.1E-01	0.5	6.8E-01	0.6	5.4E-01	-0.8	5.2E-01
ENSMUST00000190965				6.5	1.5E-04	8.3	2.0E-04	-0.7	6.5E-01	0.3	6.5E-01
ENSMUST00000159753	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	E0CYX7		-3.5	5.9E-02	-5.4	3.0E-02	-2.3	4.0E-02	-0.4	8.6E-01
ENSMUST00000120403				6.5	7.5E-05	6.4	3.7E-04	0.1	9.3E-01	-0.3	6.8E-01
ENSMUST00000181363				6.5	3.2E-04	-4.6	1.9E-03	0.4	4.0E-01	-1.2	3.5E-01
ENSMUST00000194054				6.5	3.2E-06	1.6	1.2E-01	-4.3	5.1E-03	-0.4	6.5E-01
ENSMUST00000119037				6.5	2.1E-04	6.2	5.7E-04	0.4	7.4E-01	0.8	1.9E-01
ENSMUST00000140038				6.5	2.2E-04	-2.6	1.1E-01	1.3	1.4E-01	-1.8	3.0E-01
ENSMUST00000159762				1.2	1.8E-01	0.4	7.4E-01	0.3	7.0E-01	1.1	2.8E-01
ENSMUST00000159764				-3.8	2.8E-01	-2.9	4.3E-01	-1.2	5.6E-01	-2.1	6.1E-01
ENSMUST00000144805				6.5	6.3E-04	5.3	1.4E-03	-1.5	2.5E-01	-0.1	8.7E-01
ENSMUST00000144090				6.5	7.5E-03	6.2	1.2E-04	-1.4	2.2E-01	-1.0	1.3E-01
ENSMUST00000159771	potassium channel tetramerisation domain containing 17 [Source:MGI Symbol;Acc:MGI:1920094]	E0CZ97		1.5	3.5E-01	2.9	2.6E-01	2.1	3.5E-01	0.8	6.4E-01
ENSMUST00000146988				6.5	1.0E-04	-5.9	1.6E-04	0.6	9.1E-02	-0.1	9.2E-01
ENSMUST00000159774	RIKEN cDNA 3110057O12 gene [Source:MGI Symbol;Acc:MGI:1915468]		Q8C1A9	1.5	5.2E-01	0.5	8.6E-01	-0.6	7.8E-01	0.3	8.9E-01
ENSMUST00000151460				6.5	3.0E-04	8.0	7.1E-05	0.5	6.9E-01	-0.6	3.0E-01
ENSMUST00000125150				6.5	1.7E-04	6.6	4.2E-04	-0.6	6.4E-01	-1.0	1.8E-01
ENSMUST00000145430				6.5	3.1E-04	6.5	1.8E-03	-0.6	6.9E-01	-2.0	4.9E-02
ENSMUST00000152491				6.5	7.5E-03	-1.8	4.0E-01	2.1	1.7E-01	-2.4	2.8E-01
ENSMUST00000128689				6.5	1.3E-04	4.4	1.5E-04	-2.9	5.7E-03	-0.4	5.0E-01
ENSMUST00000129490				6.5	2.8E-04	-10.7	2.7E-03	-0.9	1.7E-01	1.6	5.8E-01
ENSMUST00000159794	cell division cycle 73, Paf1/RNA polymerase II complex component [Source:MGI Symbol;Acc:MGI:2384876]	A0A087WPQ2		-0.2	8.5E-01	1.0	3.6E-01	0.8	3.3E-01	-0.4	7.2E-01
ENSMUST00000128058				6.5	7.0E-05	2.8	2.1E-02	-1.2	2.2E-01	-0.6	5.1E-01
ENSMUST00000182363				6.5	1.1E-04	7.0	3.4E-04	0.4	7.4E-01	-0.6	4.1E-01
ENSMUST00000159805				0.4	5.9E-01	3.9	2.5E-03	1.7	7.7E-02	-1.8	3.2E-02
ENSMUST00000159807				2.1	3.1E-01	2.7	1.9E-01	-0.9	6.5E-01	-1.5	4.2E-01
ENSMUST00000159808				-2.0	1.5E-01	0.6	6.7E-01	0.2	8.2E-01	-2.4	1.2E-01
ENSMUST00000159810	SNF2 histone linker PHD RING helicase [Source:MGI Symbol;Acc:MGI:1917581]		Q7TPQ3	1.7	4.3E-01	1.6	5.0E-01	0.4	8.5E-01	0.4	8.5E-01
ENSMUST00000120319				6.5	4.4E-04	-3.4	9.5E-02	1.2	2.0E-01	-1.1	6.1E-01
ENSMUST00000161563				6.5	2.3E-04	-1.4	3.8E-02	0.4	3.2E-01	0.4	5.0E-01
ENSMUST00000159815				0.7	4.4E-01	2.5	4.9E-02	1.2	2.2E-01	-0.6	5.0E-01
ENSMUST00000177340				6.5	3.2E-03	7.2	1.9E-02	-0.9	7.6E-01	-1.0	5.2E-01
ENSMUST00000159819				0.9	6.8E-01	-3.4	1.7E-01	-3.8	3.3E-02	0.4	8.6E-01
ENSMUST00000031089				6.5	5.2E-03	1.7	1.3E-01	0.4	6.4E-01	0.7	4.2E-01
ENSMUST00000159825				3.2	2.1E-01	-1.1	7.3E-01	-3.7	1.2E-01	0.6	8.5E-01
ENSMUST00000121202				6.5	1.5E-04	6.0	3.2E-04	-0.5	6.7E-01	0.1	8.6E-01
ENSMUST00000131413				6.5	1.1E-04	1.8	5.4E-02	-0.6	4.1E-01	-0.5	5.0E-01
ENSMUST00000107527				6.5	9.1E-04	3.3	1.8E-01	-1.2	5.8E-01	0.0	1.0E+00
ENSMUST00000150561				6.5	1.9E-04	4.6	6.6E-03	-1.0	4.7E-01	-0.8	4.4E-01
ENSMUST00000152275				6.5	2.9E-05	3.8	6.4E-03	-0.1	9.3E-01	-1.0	2.5E-01
ENSMUST00000192252				6.5	2.4E-05	-4.0	6.2E-02	1.3	2.0E-01	-0.3	8.7E-01
ENSMUST00000164228				6.5	1.4E-04	5.7	6.4E-05	-1.3	1.5E-01	0.4	5.0E-01
ENSMUST00000118939				6.5	1.6E-04	7.1	9.3E-05	-0.6	6.0E-01	0.5	4.3E-01
ENSMUST00000159855	MYC binding protein 2 [Source:MGI Symbol;Acc:MGI:2179432]	E9PUJ6		3.8	1.4E-01	4.0	2.0E-01	0.3	9.0E-01	0.1	9.6E-01
ENSMUST00000159856				-1.4	2.4E-01	-4.7	1.4E-02	-2.8	6.2E-03	0.6	7.3E-01
ENSMUST00000123524				6.5	4.7E-04	7.2	1.0E-04	-1.1	3.2E-01	0.9	1.6E-01
ENSMUST00000159866	C-type lectin domain family 2, member i [Source:MGI Symbol;Acc:MGI:2136650]	B7ZP15	Q9WVF9	-1.7	4.1E-02	-1.2	3.0E-01	0.7	3.5E-01	0.1	9.2E-01
ENSMUST00000159877	SH2 domain containing 6 [Source:MGI Symbol;Acc:MGI:1918380]	E0CYY5		3.4	8.8E-02	5.4	1.7E-02	-0.5	8.2E-01	-2.4	8.4E-02
ENSMUST00000140647				6.5	1.6E-06	1.4	4.4E-02	0.0	9.9E-01	0.3	5.2E-01
ENSMUST00000173260				6.5	1.2E-04	7.6	5.0E-04	-0.8	6.4E-01	-2.1	3.3E-02
ENSMUST00000185947				6.5	1.5E-04	6.9	7.0E-04	0.8	5.9E-01	-0.6	4.5E-01
ENSMUST00000117711				6.5	6.7E-05	-1.5	1.7E-01	2.9	2.1E-03	-0.2	8.5E-01
ENSMUST00000159888				-1.6	2.2E-01	-0.4	7.7E-01	0.5	6.6E-01	-0.7	6.3E-01
ENSMUST00000121388				6.5	2.8E-04	5.5	4.6E-03	-0.4	7.9E-01	-0.6	5.4E-01
ENSMUST00000127351				6.5	4.7E-04	5.1	1.3E-04	-1.3	1.5E-01	0.6	2.9E-01
ENSMUST00000134510				6.5	7.7E-06	-4.9	3.7E-03	0.2	6.8E-01	-0.9	5.3E-01
ENSMUST00000159895				0.1	8.2E-01	1.2	1.7E-01	0.4	5.8E-01	-0.7	3.7E-01
ENSMUST00000149451				6.5	1.0E-04	7.8	2.8E-04	0.6	6.5E-01	0.8	2.7E-01
ENSMUST00000159898				-2.4	5.0E-02	-1.3	3.8E-01	0.7	4.6E-01	-0.5	7.4E-01
ENSMUST00000159899	phosphatidylinositol glycan anchor biosynthesis, class K [Source:MGI Symbol;Acc:MGI:1913863]		Q9CXY9	-0.1	7.7E-01	-0.6	3.7E-01	-0.7	1.2E-01	-0.3	6.3E-01
ENSMUST00000154186				6.5	3.4E-04	-6.5	1.1E-01	0.9	5.1E-01	1.6	6.8E-01
ENSMUST00000159908				-2.6	5.0E-02	-2.6	2.0E-01	0.8	4.3E-01	0.9	6.5E-01
ENSMUST00000159909				-0.8	5.4E-01	0.9	5.6E-01	0.1	9.2E-01	-1.6	2.9E-01
ENSMUST00000139923				6.5	7.6E-04	-4.6	2.4E-03	-0.5	3.9E-01	-2.3	1.1E-01
ENSMUST00000117876				6.5	1.3E-04	4.7	1.3E-03	-1.3	2.6E-01	-0.5	4.8E-01
ENSMUST00000172377				6.5	1.4E-04	5.5	2.8E-02	-0.2	9.3E-01	-0.6	6.5E-01
ENSMUST00000193914				6.5	1.4E-05	-6.3	9.7E-04	1.0	4.6E-02	-0.1	9.4E-01
ENSMUST00000130873				6.5	6.2E-05	3.2	5.9E-02	-2.6	1.2E-01	1.4	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000192588				6.5	7.8E-05	5.5	5.4E-04	-1.7	1.7E-01	0.2	7.6E-01
ENSMUST00000117613				6.5	7.4E-04	5.9	2.8E-04	-0.2	8.3E-01	-0.3	6.1E-01
ENSMUST00000159929				-0.6	5.5E-01	-0.7	6.5E-01	0.3	7.6E-01	0.4	8.0E-01
ENSMUST00000118067				6.5	8.1E-05	-2.1	1.1E-02	1.1	2.1E-02	-0.2	7.7E-01
ENSMUST00000159936	LUC7-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2183260]	E0CYQ8		-1.0	3.1E-01	-0.6	7.0E-01	1.4	2.0E-01	0.9	5.2E-01
ENSMUST00000124318				6.5	1.3E-04	7.1	1.6E-03	0.6	7.0E-01	0.0	9.7E-01
ENSMUST00000159944	claudin domain containing 1 [Source:MGI Symbol;Acc:MGI:2447860]	E0CY66		0.3	9.2E-01	-1.2	6.3E-01	-3.5	1.2E-01	-2.0	4.8E-01
ENSMUST00000159945	family 9, subfamily C (Na+-transporting carboxylic acid decarboxylase), member 1 [Source:MGI Symbol;Acc:M		Q6UJY2	4.2	9.6E-02	6.1	3.7E-02	-0.2	9.4E-01	-2.1	1.8E-01
ENSMUST00000130726				6.5	9.1E-05	4.4	1.0E-02	-0.6	6.5E-01	0.5	6.0E-01
ENSMUST00000188050				6.5	1.5E-04	8.4	3.3E-04	-0.7	7.0E-01	-4.5	1.2E-03
ENSMUST00000118325				6.5	9.0E-05	-3.8	5.2E-02	-0.6	4.7E-01	-0.4	8.5E-01
ENSMUST00000135524				6.5	1.7E-04	4.7	4.6E-03	-0.8	5.5E-01	-0.6	4.8E-01
ENSMUST00000141868				6.5	4.3E-04	7.4	9.7E-03	-0.7	7.8E-01	-2.1	1.4E-01
ENSMUST00000134496				6.5	7.7E-05	2.7	3.7E-03	-2.1	1.5E-02	0.3	5.3E-01
ENSMUST00000146273				6.5	6.3E-04	-3.3	2.3E-02	-1.2	1.2E-01	-1.5	3.0E-01
ENSMUST00000159969	Fc receptor, IgG, low affinity IIb [Source:MGI Symbol;Acc:MGI:95499]	A0A0B4J1E6		-1.5	6.6E-01	-2.7	4.3E-01	-2.9	2.2E-01	-1.7	6.6E-01
ENSMUST00000159970				0.2	8.9E-01	1.0	5.9E-01	0.5	7.5E-01	-0.3	8.2E-01
ENSMUST00000189934				6.5	6.0E-05	8.4	8.8E-05	-0.4	7.8E-01	-0.7	2.4E-01
ENSMUST00000120958				6.5	8.0E-06	3.0	2.8E-02	1.1	2.6E-01	0.4	6.4E-01
ENSMUST00000159975	RAS guanyl releasing protein 4 [Source:MGI Symbol;Acc:MGI:2386851]		Q8BTM9	-1.8	6.2E-01	-0.3	9.6E-01	1.2	7.1E-01	-0.3	9.5E-01
ENSMUST00000159976	kin of IRRE like (Drosophila) [Source:MGI Symbol;Acc:MGI:1891396]		Q80W68	5.4	1.2E-01	-1.4	5.7E-01	-6.6	5.1E-02	0.2	9.2E-01
ENSMUST00000157024				6.5	4.1E-06	3.7	1.1E-01	-1.3	5.4E-01	2.4	1.3E-01
ENSMUST00000159984	anoctamin 2 [Source:MGI Symbol;Acc:MGI:2387214]	F6UR69		-1.9	1.5E-01	-1.0	5.6E-01	1.4	2.3E-01	0.5	7.5E-01
ENSMUST00000142013				6.5	1.5E-05	7.3	3.6E-05	-1.3	2.7E-01	-1.2	4.0E-02
ENSMUST00000159986	Wilms tumour 1-associating protein [Source:MGI Symbol;Acc:MGI:1926395]		Q9ER69	-1.3	2.7E-01	-1.6	3.8E-01	0.2	8.8E-01	0.4	8.1E-01
ENSMUST00000152513				6.5	5.7E-05	7.3	5.8E-05	-0.5	6.3E-01	-0.7	2.3E-01
ENSMUST00000153044				6.5	3.8E-05	0.1	8.9E-01	0.3	6.5E-01	-2.6	3.0E-02
ENSMUST00000195747				6.5	2.7E-03	6.3	3.8E-06	-1.3	7.2E-02	0.7	6.7E-02
ENSMUST00000112153				6.5	7.1E-05	7.3	5.4E-06	-0.3	6.9E-01	0.0	9.2E-01
ENSMUST00000149042				6.5	8.6E-05	7.0	9.9E-04	-0.2	8.8E-01	0.2	8.0E-01
ENSMUST00000140537				6.5	1.8E-04	-1.7	1.7E-01	1.5	4.8E-02	-1.5	2.4E-01
ENSMUST00000167568				6.5	5.4E-04	4.7	1.8E-04	-3.1	7.8E-03	-0.5	3.6E-01
ENSMUST00000193260				6.5	1.1E-04	3.1	1.0E-02	0.1	9.2E-01	0.2	8.1E-01
ENSMUST00000126439				6.5	1.3E-05	-2.4	7.9E-02	-0.3	7.1E-01	-1.1	4.3E-01
ENSMUST00000160009	myelocytomatosis oncogene [Source:MGI Symbol;Acc:MGI:97250]		P01108	-0.1	9.1E-01	-0.9	5.4E-01	0.4	6.6E-01	1.2	3.7E-01
ENSMUST00000137441				6.5	4.8E-04	3.1	7.3E-03	1.1	2.1E-01	0.0	9.5E-01
ENSMUST00000180225				6.5	6.4E-05	-2.8	2.0E-02	0.7	2.6E-01	-2.5	7.2E-02
ENSMUST00000137271				6.5	1.4E-06	-2.6	3.1E-03	-0.2	5.8E-01	0.5	4.1E-01
ENSMUST00000160019	SH3 and cysteine rich domain 3 [Source:MGI Symbol;Acc:MGI:3606571]		Q8BZ71	0.6	7.6E-01	1.4	4.7E-01	-1.5	4.0E-01	-2.4	2.1E-01
ENSMUST00000124823				6.5	1.5E-06	1.9	4.1E-01	-2.7	2.5E-01	2.8	1.6E-01
ENSMUST00000130457				6.5	1.2E-04	2.2	5.1E-03	-1.1	8.0E-02	-0.3	5.9E-01
ENSMUST00000133209				6.5	1.2E-04	7.5	3.0E-06	0.3	6.9E-01	0.2	6.7E-01
ENSMUST00000140261				6.5	7.0E-04	-1.9	1.8E-01	1.2	1.8E-01	-2.2	1.8E-01
ENSMUST00000160033				-2.4	1.8E-01	1.7	4.6E-01	3.0	1.2E-01	-1.1	5.7E-01
ENSMUST00000194831				6.5	3.7E-05	4.7	1.3E-03	0.7	4.8E-01	-0.2	7.4E-01
ENSMUST00000123523				6.5	2.0E-04	-4.8	9.8E-04	-0.3	4.5E-01	-2.8	4.8E-02
ENSMUST00000173496				6.5	2.4E-04	4.8	7.7E-03	-1.5	3.1E-01	-0.3	7.7E-01
ENSMUST00000121816				6.5	2.1E-02	-8.5	3.1E-05	-0.6	9.3E-02	-0.3	7.8E-01
ENSMUST00000160057				-2.3	1.0E-01	-1.2	5.9E-01	1.9	1.4E-01	0.7	7.4E-01
ENSMUST00000131842				6.5	4.4E-07	6.5	3.1E-05	-0.8	3.3E-01	0.2	6.6E-01
ENSMUST00000117511				6.5	1.6E-04	6.3	1.8E-04	-0.6	6.2E-01	0.1	8.0E-01
ENSMUST00000160069				-0.9	3.7E-01	0.7	5.7E-01	1.1	2.6E-01	-0.5	6.7E-01
ENSMUST00000121342				6.5	7.5E-04	-2.1	8.8E-02	-1.2	1.3E-01	-2.3	8.9E-02
ENSMUST00000160081				6.0	4.3E-02	4.0	1.9E-01	-1.5	6.1E-01	0.5	8.1E-01
ENSMUST00000130525				6.5	1.8E-05	2.8	3.6E-03	-0.7	3.3E-01	-1.0	1.2E-01
ENSMUST00000140981				6.5	1.0E-04	4.0	1.5E-03	-2.0	7.0E-02	-0.1	9.2E-01
ENSMUST00000142143				6.5	9.6E-05	6.9	7.1E-04	-0.6	7.1E-01	-1.1	1.9E-01
ENSMUST00000193824				6.5	1.4E-04	6.1	6.1E-04	-0.6	6.7E-01	0.1	9.2E-01
ENSMUST00000160106				-1.1	9.5E-02	-0.7	3.6E-01	0.0	9.9E-01	-0.4	6.2E-01
ENSMUST00000147243				6.5	1.6E-04	-6.1	2.9E-04	-0.7	9.6E-02	-0.9	4.6E-01
ENSMUST00000164794				6.5	1.4E-04	3.8	2.6E-03	-2.1	7.5E-02	-0.4	5.7E-01
ENSMUST00000152010				6.5	3.4E-04	4.4	3.2E-02	1.4	3.8E-01	1.3	2.4E-01
ENSMUST00000182293				6.5	2.0E-04	7.3	5.7E-04	-0.7	6.5E-01	0.1	9.4E-01
ENSMUST00000160119				0.7	4.5E-01	1.0	4.3E-01	0.4	7.2E-01	0.1	9.5E-01
ENSMUST00000144756				6.5	5.1E-05	5.1	1.9E-03	-0.4	7.2E-01	0.6	4.6E-01
ENSMUST00000174210				6.5	6.1E-04	5.0	5.0E-03	-1.5	3.2E-01	0.5	5.7E-01
ENSMUST00000160130				1.5	6.6E-02	2.4	2.6E-02	0.5	5.4E-01	-0.4	5.8E-01
ENSMUST00000160132	eukaryotic translation initiation factor 4, gamma 2 [Source:MGI Symbol;Acc:MGI:109207]	F6TW20		-0.4	8.9E-01	-4.0	2.9E-01	-2.5	2.4E-01	1.2	7.6E-01
ENSMUST00000181823				6.5	1.5E-05	-2.2	1.8E-01	1.1	2.2E-01	0.2	8.8E-01
ENSMUST00000151909				6.5	1.4E-04	6.3	5.0E-04	-0.5	7.1E-01	-0.6	4.0E-01
ENSMUST00000128574				6.5	1.1E-04	4.5	7.0E-03	-1.5	2.9E-01	-0.1	9.3E-01
ENSMUST00000139758				6.5	7.2E-05	3.6	7.5E-03	-3.0	3.1E-02	1.3	1.0E-01
ENSMUST00000160144	ring finger protein 146 [Source:MGI Symbol;Acc:MGI:1915281]		Q9CZW6	-1.7	1.9E-01	-0.1	9.6E-01	-0.1	8.8E-01	-1.7	1.9E-01
ENSMUST00000142192				6.5	3.0E-04	-2.2	1.9E-01	3.0	5.5E-03	0.1	9.3E-01
ENSMUST00000176094				6.5	1.5E-04	3.1	1.1E-03	-0.5	3.9E-01	-0.2	6.7E-01
ENSMUST00000130503				6.5	1.8E-03	6.4	2.9E-02	2.2	3.7E-01	1.3	4.3E-01
ENSMUST00000133659				6.5	8.1E-05	1.6	1.0E-01	-0.7	3.6E-01	-0.1	8.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000134186				6.5	1.5E-04	4.9	6.7E-04	-1.4	1.8E-01	0.3	6.3E-01
ENSMUST00000160155				-1.2	1.8E-01	0.1	9.0E-01	0.3	7.1E-01	-1.0	3.0E-01
ENSMUST00000188828				6.5	1.8E-04	-2.8	1.6E-03	-0.3	4.4E-01	-0.1	9.3E-01
ENSMUST00000160283				6.5	4.1E-04	7.3	6.3E-04	0.6	6.8E-01	0.8	3.3E-01
ENSMUST00000160160	predicted gene 42669 [Source:MGI Symbol;Acc:MGI:5662806]	A0A0G2JDB2		5.3	5.3E-02	4.5	9.3E-02	-1.5	5.8E-01	-0.7	6.6E-01
ENSMUST00000189234				6.5	8.0E-05	4.7	4.3E-02	0.0	1.0E+00	0.0	9.9E-01
ENSMUST00000130638				6.5	9.9E-04	5.2	2.4E-05	0.6	3.2E-01	0.4	3.3E-01
ENSMUST00000160174				3.1	8.1E-02	1.9	2.6E-01	-1.7	2.9E-01	-0.5	7.3E-01
ENSMUST00000160180	cytochrome b5 type A (microsomal) [Source:MGI Symbol;Acc:MGI:1926952]	Q544Z9	P56395	-0.5	7.3E-01	0.6	7.1E-01	-1.3	3.7E-01	-2.5	1.5E-01
ENSMUST00000155219				6.5	1.1E-04	3.0	5.6E-03	0.8	2.8E-01	-0.5	5.2E-01
ENSMUST00000160194	RAS guanyl releasing protein 4 [Source:MGI Symbol;Acc:MGI:2386851]	E0CX54		-0.2	7.9E-01	-1.0	4.5E-01	-0.1	9.4E-01	0.7	5.7E-01
ENSMUST00000160197	exocyst complex component 6B [Source:MGI Symbol;Acc:MGI:1923164]		A6H5Z3	0.6	2.1E-01	0.9	1.7E-01	0.7	1.6E-01	0.4	5.2E-01
ENSMUST00000160204				-1.0	7.7E-01	0.0	1.0E+00	1.8	6.0E-01	0.8	8.6E-01
ENSMUST00000160207	EGF-like, fibronectin type III and laminin G domains [Source:MGI Symbol;Acc:MGI:2146149]	E0CXM4		2.9	6.3E-02	6.5	7.6E-04	-0.5	7.2E-01	-4.2	2.3E-03
ENSMUST00000175676				6.5	6.8E-05	7.4	7.9E-05	-0.3	7.7E-01	-0.2	8.0E-01
ENSMUST00000120981				6.5	1.1E-04	-8.0	1.4E-02	0.4	6.2E-01	-1.3	6.8E-01
ENSMUST00000128732				6.5	1.4E-04	5.5	1.9E-02	-0.6	7.7E-01	0.6	6.0E-01
ENSMUST00000160217	predicted gene 42641 [Source:MGI Symbol;Acc:MGI:5662778]	I6L9G2		1.8	1.0E-01	2.6	4.9E-02	-0.3	7.9E-01	-1.1	2.8E-01
ENSMUST00000190706				6.5	1.0E-04	6.6	1.8E-04	-0.6	5.9E-01	-0.6	3.2E-01
ENSMUST00000160222				3.4	8.1E-02	4.9	9.5E-02	2.4	3.6E-01	1.0	5.6E-01
ENSMUST00000125273				6.5	9.1E-05	3.1	2.9E-02	-1.1	3.7E-01	-0.3	7.7E-01
ENSMUST00000182916				6.5	7.8E-05	5.6	2.3E-03	-1.4	3.5E-01	-0.9	3.1E-01
ENSMUST00000160248	zinc finger and AT hook domain containing [Source:MGI Symbol;Acc:MGI:2681865]		Q7TS63	1.2	2.5E-01	-1.1	5.8E-01	0.7	5.9E-01	3.0	9.9E-02
ENSMUST00000195367				6.5	7.0E-05	0.0	9.9E-01	5.6	5.6E-04	-0.8	6.6E-01
ENSMUST00000140182				6.5	3.2E-02	0.6	6.1E-01	-1.1	2.7E-01	1.4	1.9E-01
ENSMUST00000160253				1.3	5.5E-01	3.5	2.7E-01	1.0	7.2E-01	-1.2	5.9E-01
ENSMUST00000160260	POU domain, class 2, transcription factor 1 [Source:MGI Symbol;Acc:MGI:101898]			-2.2	1.6E-01	0.3	8.6E-01	0.6	6.3E-01	-1.9	2.9E-01
ENSMUST00000160262	armadillo repeat containing 2 [Source:MGI Symbol;Acc:MGI:1916449]		Q3URY6	5.6	1.4E-01	2.5	4.6E-01	-2.6	5.0E-01	0.5	8.4E-01
ENSMUST00000187575				6.5	3.1E-06	-3.4	1.8E-02	3.6	1.4E-04	-1.0	4.4E-01
ENSMUST00000136459				6.5	1.1E-03	1.7	8.1E-02	-0.4	5.7E-01	-0.1	8.9E-01
ENSMUST00000189620				6.5	1.7E-06	-7.2	5.7E-06	0.3	2.8E-01	-3.3	1.1E-02
ENSMUST00000126158				6.5	9.4E-05	5.3	5.4E-02	-0.8	7.5E-01	-0.5	7.5E-01
ENSMUST00000166792				6.5	3.8E-05	6.2	4.3E-03	-0.7	7.0E-01	0.3	7.3E-01
ENSMUST00000160280				-1.0	4.9E-01	2.4	1.8E-01	0.5	7.7E-01	-3.0	6.0E-02
ENSMUST00000160281	polymerase (DNA-directed), epsilon 4 (p12 subunit) [Source:MGI Symbol;Acc:MGI:1914229]	E0CYA9		-1.5	3.4E-01	-4.1	4.0E-02	-2.2	5.3E-02	0.4	8.1E-01
ENSMUST00000160282				-1.9	4.0E-01	-0.6	8.2E-01	-0.2	9.2E-01	-1.5	5.5E-01
ENSMUST00000162286				6.5	1.1E-04	5.9	1.3E-03	-0.7	6.3E-01	-0.1	8.8E-01
ENSMUST00000160819				6.5	3.7E-04	6.6	3.3E-04	-0.5	7.1E-01	-0.2	8.0E-01
ENSMUST00000177309				6.5	4.6E-05	1.5	1.9E-01	-1.7	9.6E-02	0.2	8.1E-01
ENSMUST00000118460				6.5	1.7E-05	-5.3	1.9E-03	-0.1	7.9E-01	-0.6	6.5E-01
ENSMUST00000160290	cDNA sequence BC035044 [Source:MGI Symbol;Acc:MGI:2448540]	E0CXF8		-1.0	1.8E-01	-0.3	7.4E-01	-0.1	8.6E-01	-0.8	3.3E-01
ENSMUST00000160294				-2.5	6.9E-02	-1.4	3.7E-01	0.5	6.3E-01	-0.5	7.3E-01
ENSMUST00000176382				6.5	5.8E-04	4.2	2.2E-02	-1.1	4.8E-01	-1.2	3.1E-01
ENSMUST00000127908				6.5	2.2E-04	6.6	5.3E-03	0.0	9.9E-01	-2.1	8.8E-02
ENSMUST00000136734				6.5	3.6E-04	4.0	6.8E-04	-0.1	8.6E-01	-0.7	2.8E-01
ENSMUST00000183013				6.5	1.0E-04	-4.4	1.3E-02	-0.1	8.5E-01	0.1	9.6E-01
ENSMUST00000184928				6.5	9.3E-06	-4.7	1.0E-02	1.3	9.3E-02	-3.2	1.4E-01
ENSMUST00000189766				6.5	1.3E-04	6.7	1.1E-04	-0.5	6.5E-01	0.0	9.8E-01
ENSMUST00000176412				6.5	3.1E-04	8.5	6.0E-05	0.1	9.3E-01	0.1	8.3E-01
ENSMUST00000182101				6.5	6.7E-04	5.8	4.6E-02	2.4	3.3E-01	1.5	3.4E-01
ENSMUST00000160335				-2.9	6.0E-02	-1.0	5.6E-01	0.7	5.6E-01	-1.1	5.2E-01
ENSMUST00000160337	ZW10 interactor [Source:MGI Symbol;Acc:MGI:1289227]		Q9CQU5	-1.8	6.5E-02	-3.7	6.0E-03	-2.1	1.1E-02	-0.2	8.5E-01
ENSMUST00000160341				2.8	1.3E-01	2.6	2.7E-01	-0.5	8.2E-01	-0.3	8.4E-01
ENSMUST00000160349				0.8	4.2E-01	2.4	1.4E-01	1.0	4.4E-01	-0.5	6.2E-01
ENSMUST00000142135				6.4	8.8E-06	-3.8	4.3E-02	0.1	8.6E-01	-0.3	8.8E-01
ENSMUST00000120085				6.4	1.0E-04	-5.5	5.7E-04	-0.3	4.3E-01	-0.7	5.4E-01
ENSMUST00000135377				6.4	2.5E-05	6.7	6.5E-03	-0.7	7.3E-01	-1.7	1.6E-01
ENSMUST00000179787				6.4	1.2E-05	6.3	2.5E-04	-0.5	6.8E-01	0.3	5.7E-01
ENSMUST00000134565				6.4	2.7E-04	5.1	2.1E-04	-1.8	6.4E-02	-0.2	7.7E-01
ENSMUST00000174516				6.4	3.4E-04	5.4	6.3E-02	-0.8	7.9E-01	0.4	8.0E-01
ENSMUST00000132088				6.4	4.9E-04	3.4	3.0E-02	-2.4	1.1E-01	1.0	3.5E-01
ENSMUST00000160396	RAS guanyl releasing protein 4 [Source:MGI Symbol;Acc:MGI:2386851]	F7BK25		-0.5	8.2E-01	-3.1	3.4E-01	-1.9	3.0E-01	0.6	8.4E-01
ENSMUST00000160399	enoyl Coenzyme A hydratase domain containing 1 [Source:MGI Symbol;Acc:MGI:1277169]		Q9D9V3	-2.5	7.9E-02	-3.8	4.7E-02	-0.7	5.0E-01	0.7	6.9E-01
ENSMUST00000160403				-2.4	3.6E-02	-1.2	4.2E-01	1.2	2.1E-01	-0.1	9.3E-01
ENSMUST00000193919				6.4	3.2E-03	-4.9	8.0E-03	0.0	9.9E-01	0.8	5.9E-01
ENSMUST00000160406				0.6	6.5E-01	2.3	2.4E-01	1.3	4.3E-01	-0.3	8.1E-01
ENSMUST00000127349				6.4	7.9E-05	-3.7	3.2E-02	-0.1	9.2E-01	0.7	6.6E-01
ENSMUST00000135069				6.4	3.8E-04	5.4	4.6E-02	-0.9	7.2E-01	1.0	5.0E-01
ENSMUST00000160413	potassium channel, subfamily K, member 13 [Source:MGI Symbol;Acc:MGI:2384976]	Q3TYG8	Q8R1P5	-2.0	1.3E-01	-1.4	3.5E-01	-0.7	4.6E-01	-1.4	3.6E-01
ENSMUST00000160418				5.4	9.5E-02	3.8	2.6E-01	-0.4	9.0E-01	1.1	5.9E-01
ENSMUST00000136867				6.4	9.0E-05	-5.5	8.1E-04	1.2	1.9E-02	-0.9	4.8E-01
ENSMUST00000123397				6.4	6.5E-04	5.5	1.4E-04	-1.1	2.4E-01	-0.1	7.9E-01
ENSMUST00000160430				-3.9	4.6E-02	-5.0	9.3E-02	0.2	8.9E-01	1.3	6.4E-01
ENSMUST00000160437				0.4	6.4E-01	0.9	4.7E-01	0.3	7.4E-01	-0.2	8.7E-01
ENSMUST00000151555				6.4	7.4E-05	-3.3	5.2E-03	0.9	1.2E-01	-3.6	1.4E-02
ENSMUST00000156627				6.4	2.8E-04	8.7	3.3E-04	-0.3	8.6E-01	0.0	9.5E-01
ENSMUST00000188327				6.4	4.4E-04	5.0	1.1E-02	-0.7	6.9E-01	0.6	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000120003				6.4	5.8E-05	4.3	2.0E-03	-0.2	8.8E-01	-1.2	1.3E-01
ENSMUST00000160452	RAB6A GEF complex partner 1 [Source:MGI Symbol;Acc:MGI:1924893]	F7CN51		-0.6	5.9E-01	-1.3	3.4E-01	-0.4	7.0E-01	0.4	7.5E-01
ENSMUST00000155318				6.4	3.4E-03	-0.1	8.9E-01	0.2	7.4E-01	-1.7	9.2E-02
ENSMUST00000173047				6.4	3.1E-04	3.9	7.9E-02	-0.7	7.0E-01	0.6	6.8E-01
ENSMUST00000148563				6.4	4.6E-03	2.7	3.4E-02	-2.5	4.7E-02	0.3	7.5E-01
ENSMUST00000160465	sterol O-acyltransferase 2 [Source:MGI Symbol;Acc:MGI:1332226]	F6SMH4		-0.9	4.5E-01	-2.7	1.3E-01	-0.6	5.0E-01	1.3	4.5E-01
ENSMUST00000066658				6.4	6.3E-05	-2.7	3.2E-02	-0.5	4.2E-01	-1.8	1.7E-01
ENSMUST00000177321				6.4	9.2E-05	5.9	5.3E-04	0.9	4.3E-01	-0.1	8.9E-01
ENSMUST00000160471	G patch domain containing 2 [Source:MGI Symbol;Acc:MGI:1915019]		Q7TQC7	2.2	2.9E-01	2.5	3.9E-01	0.2	9.5E-01	-0.1	9.5E-01
ENSMUST00000119695				6.4	1.0E-04	-1.5	1.7E-01	2.9	2.1E-03	-0.2	8.5E-01
ENSMUST00000160092				6.4	7.0E-04	1.7	1.3E-01	-1.4	1.8E-01	0.7	4.4E-01
ENSMUST00000160484	amylo-1,6-glucosidase, 4-alpha-glucanotransferase [Source:MGI Symbol;Acc:MGI:1924809]	F6XXE6		1.5	7.1E-02	2.5	2.2E-02	0.1	9.1E-01	-0.9	2.5E-01
ENSMUST00000130656				6.4	1.6E-07	-2.7	1.3E-01	1.5	1.4E-01	-1.0	5.9E-01
ENSMUST00000137111				6.4	1.7E-04	-3.5	2.3E-03	-1.3	2.3E-02	0.6	4.7E-01
ENSMUST00000160496	anoctamin 2 [Source:MGI Symbol;Acc:MGI:2387214]		Q8CFW1	5.3	3.8E-02	5.8	2.9E-02	-1.4	5.8E-01	-2.0	1.9E-01
ENSMUST00000173715				6.4	5.3E-05	5.6	8.5E-05	0.5	5.2E-01	0.0	9.5E-01
ENSMUST00000135677				6.4	7.3E-07	-3.2	1.0E-01	-0.2	8.6E-01	-0.9	6.7E-01
ENSMUST00000160505	complement component 1, s subcomponent 1 [Source:MGI Symbol;Acc:MGI:1355312]	E9Q6C2		2.6	8.1E-02	-4.6	5.4E-03	-7.3	9.0E-05	-0.1	9.5E-01
ENSMUST00000160506				-0.8	6.7E-01	-0.6	8.1E-01	0.8	7.0E-01	0.7	7.6E-01
ENSMUST00000154684				6.4	1.7E-04	-3.4	2.8E-02	2.0	9.9E-03	1.6	2.4E-01
ENSMUST00000160510				1.6	1.9E-01	2.4	1.8E-01	1.2	4.4E-01	0.4	7.3E-01
ENSMUST00000162955				6.4	8.4E-05	-5.2	9.1E-03	0.4	5.6E-01	-2.2	2.7E-01
ENSMUST00000148864				6.4	1.8E-04	6.7	7.5E-05	0.4	6.9E-01	-0.6	3.1E-01
ENSMUST00000154049				6.4	1.7E-04	4.9	1.1E-04	-0.4	5.7E-01	-0.7	1.9E-01
ENSMUST00000176622				6.4	2.5E-04	-2.4	1.0E-01	0.7	3.7E-01	-1.0	5.1E-01
ENSMUST00000143912				6.4	5.6E-04	8.3	2.0E-04	-0.6	7.1E-01	-1.4	7.5E-02
ENSMUST00000140234				6.4	3.4E-06	4.2	7.9E-03	0.9	4.1E-01	0.3	7.7E-01
ENSMUST00000159498				6.4	3.0E-04	5.0	8.0E-03	-0.6	7.1E-01	0.0	9.7E-01
ENSMUST00000185369				6.4	4.1E-06	6.7	1.8E-04	-0.1	9.1E-01	-0.7	2.9E-01
ENSMUST00000160553				-2.2	4.6E-01	-0.9	7.9E-01	0.3	9.0E-01	-1.0	7.9E-01
ENSMUST00000160554				0.6	3.2E-01	1.7	3.7E-02	0.3	6.8E-01	-0.8	2.0E-01
ENSMUST00000119349				6.4	1.9E-04	3.0	7.2E-02	0.5	7.4E-01	1.1	3.4E-01
ENSMUST00000140889				6.4	3.3E-04	4.4	4.8E-03	-1.2	3.1E-01	0.3	7.0E-01
ENSMUST00000150172				6.4	3.9E-05	4.4	8.9E-03	-3.8	3.3E-02	-1.0	3.1E-01
ENSMUST00000155984				6.4	8.9E-07	5.6	1.0E-03	0.5	6.6E-01	-0.5	4.8E-01
ENSMUST00000160576	BCL2-associated athanogene 5 [Source:MGI Symbol;Acc:MGI:1917619]		Q8CI32	1.8	4.6E-01	-0.4	8.6E-01	-2.8	2.1E-01	-0.6	7.9E-01
ENSMUST00000160583	ubinuclein 2 [Source:MGI Symbol;Acc:MGI:2444236]		Q80WC1	0.0	9.1E-01	0.7	2.2E-01	0.8	9.0E-02	0.0	9.7E-01
ENSMUST00000160586				0.9	2.9E-01	0.5	6.7E-01	0.3	7.4E-01	0.7	4.9E-01
ENSMUST00000121550				6.4	7.6E-04	5.1	5.3E-02	0.7	7.7E-01	1.0	5.2E-01
ENSMUST00000126509				6.4	2.3E-04	-1.0	1.7E-01	0.5	3.0E-01	-1.8	2.4E-02
ENSMUST00000148619				6.4	6.0E-07	-4.6	1.5E-03	-0.1	7.8E-01	-0.8	4.7E-01
ENSMUST00000176139				6.4	1.6E-04	6.5	6.0E-04	0.0	9.8E-01	-0.9	2.6E-01
ENSMUST00000121784				6.4	2.5E-03	7.5	8.3E-04	1.6	3.2E-01	-1.0	2.4E-01
ENSMUST00000160597	optic atrophy 1 [Source:MGI Symbol;Acc:MGI:1921393]		P58281	-0.3	5.4E-01	0.4	5.6E-01	0.1	7.7E-01	-0.5	3.7E-01
ENSMUST00000117575				6.4	5.9E-04	6.5	5.4E-04	0.7	6.0E-01	-1.1	1.6E-01
ENSMUST00000129573				6.4	7.0E-05	8.1	3.5E-05	-0.6	5.9E-01	-0.1	8.7E-01
ENSMUST00000178959				6.4	2.5E-04	5.7	6.7E-06	-0.7	2.8E-01	-0.3	4.6E-01
ENSMUST00000119195				6.4	1.4E-04	-3.2	4.5E-02	0.4	6.0E-01	-1.6	3.8E-01
ENSMUST00000173560				6.4	7.7E-05	-2.5	2.8E-02	0.9	1.5E-01	-3.1	3.7E-02
ENSMUST00000117864				6.4	1.2E-04	-3.5	3.5E-01	2.1	3.0E-01	-0.6	8.7E-01
ENSMUST00000160636				-1.2	4.9E-01	-3.9	1.4E-01	-1.7	2.2E-01	0.9	7.1E-01
ENSMUST00000152637				6.4	1.7E-05	4.5	2.0E-02	-1.5	4.2E-01	0.6	5.8E-01
ENSMUST00000173594				6.4	1.5E-04	-1.0	2.8E-01	0.2	8.0E-01	-1.0	2.7E-01
ENSMUST00000160641	calcium channel, voltage-dependent, L type, alpha 1S subunit [Source:MGI Symbol;Acc:MGI:88294]	E9Q7B5		5.7	1.1E-01	4.7	2.1E-01	-0.7	8.6E-01	0.3	9.0E-01
ENSMUST00000160645	family with sequence similarity 20, member C [Source:MGI Symbol;Acc:MGI:2136853]	E0CY01		-1.0	3.0E-01	-1.2	4.2E-01	1.1	2.4E-01	1.2	3.8E-01
ENSMUST00000132534				6.4	1.2E-03	8.9	1.8E-05	0.2	8.8E-01	-1.1	4.5E-02
ENSMUST00000160648	ribosomal RNA adenine dimethylase domain containing 1 [Source:MGI Symbol;Acc:MGI:2387197]	E9PZV3		-0.7	6.1E-01	-0.1	9.6E-01	2.0	2.0E-01	1.4	4.1E-01
ENSMUST00000177443				6.4	2.1E-03	2.3	3.3E-02	-0.9	3.1E-01	0.4	5.7E-01
ENSMUST00000160653	thioredoxin domain containing 5 [Source:MGI Symbol;Acc:MGI:2145316]	E9PXX7		3.3	2.1E-01	5.2	1.4E-01	1.4	6.4E-01	-0.4	8.5E-01
ENSMUST00000182829				6.4	6.9E-06	6.0	2.6E-04	-0.4	7.1E-01	-0.2	7.4E-01
ENSMUST00000160656	major facilitator superfamily domain containing 4 [Source:MGI Symbol;Acc:MGI:2442786]	F7D4J0		-1.3	6.7E-02	-3.6	1.5E-02	0.3	5.2E-01	2.6	5.4E-02
ENSMUST00000138498				6.4	5.3E-05	7.2	3.2E-05	2.1	4.4E-02	-0.1	8.2E-01
ENSMUST00000161547				6.4	7.4E-04	-5.6	1.2E-02	1.5	5.1E-02	4.1	4.2E-02
ENSMUST00000125668				6.4	3.9E-03	6.0	5.6E-04	-0.7	5.8E-01	-0.4	6.2E-01
ENSMUST00000136765				6.4	2.5E-04	-6.7	1.1E-03	-1.6	1.6E-02	-0.8	6.0E-01
ENSMUST00000160670				0.9	4.2E-01	0.0	9.9E-01	-0.3	8.1E-01	0.6	6.4E-01
ENSMUST00000145490				6.4	1.2E-02	4.1	1.0E-02	-0.9	4.7E-01	0.0	9.7E-01
ENSMUST00000153568				6.4	4.4E-04	-0.8	2.9E-01	0.7	1.9E-01	-0.9	2.5E-01
ENSMUST00000153186				6.4	5.3E-04	-9.4	1.1E-05	0.0	9.9E-01	-0.9	4.8E-01
ENSMUST00000159177				6.4	2.9E-04	-7.5	2.1E-04	-0.6	1.6E-01	-0.9	5.3E-01
ENSMUST00000191566				6.4	8.8E-04	-5.0	9.0E-02	0.8	4.4E-01	2.0	4.5E-01
ENSMUST00000193568				6.4	4.2E-05	3.0	5.9E-02	-2.1	1.5E-01	0.3	8.1E-01
ENSMUST00000122295				6.4	2.8E-04	-8.7	3.1E-04	-1.3	2.4E-02	-0.7	6.8E-01
ENSMUST00000128535				6.4	3.5E-04	3.5	2.7E-02	-3.6	4.4E-02	-0.3	7.6E-01
ENSMUST00000161299				6.4	2.2E-04	7.0	4.5E-04	-0.6	6.6E-01	-1.5	7.6E-02
ENSMUST00000188534				6.4	2.8E-04	-3.5	1.3E-02	-0.5	3.9E-01	-2.0	1.6E-01
ENSMUST00000195768				6.4	1.9E-04	-3.9	4.4E-03	0.9	9.7E-02	-0.6	5.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000172858				6.4	3.7E-04	6.5	8.0E-04	0.4	7.6E-01	-0.2	7.9E-01
ENSMUST00000190854				6.4	2.1E-04	7.9	2.3E-04	-1.7	3.0E-01	-1.0	1.5E-01
ENSMUST00000154543				6.4	7.8E-04	-0.5	4.5E-01	0.8	7.4E-02	-0.1	8.3E-01
ENSMUST00000150850				6.4	7.8E-06	4.2	1.6E-02	0.3	8.5E-01	-0.4	6.4E-01
ENSMUST00000194748				6.4	1.5E-04	8.7	7.0E-05	-0.2	8.8E-01	-1.0	1.3E-01
ENSMUST00000068485				6.4	7.6E-05	6.6	2.7E-04	-1.3	3.3E-01	0.0	1.0E+00
ENSMUST00000147298				6.4	5.5E-04	3.1	3.7E-02	0.9	4.6E-01	0.2	8.5E-01
ENSMUST00000162427				6.4	2.2E-04	3.2	7.0E-04	-0.7	2.5E-01	0.2	6.9E-01
ENSMUST00000177434				6.4	7.5E-05	8.1	3.6E-04	0.0	9.9E-01	-0.2	7.6E-01
ENSMUST00000139858				6.4	7.4E-07	4.2	2.3E-04	0.0	9.9E-01	0.2	6.9E-01
ENSMUST00000140046				6.4	5.3E-06	6.8	1.2E-04	-0.6	6.1E-01	0.6	3.0E-01
ENSMUST00000173218				6.4	8.2E-04	4.6	2.4E-03	-0.4	7.2E-01	-0.4	6.2E-01
ENSMUST00000161983				6.4	7.1E-05	6.2	3.1E-04	-1.3	3.1E-01	-0.2	7.4E-01
ENSMUST00000156852				6.4	1.4E-05	6.6	3.0E-04	-0.5	6.7E-01	0.4	5.0E-01
ENSMUST00000127480				6.4	3.7E-04	-3.6	9.6E-02	-0.7	5.1E-01	-1.4	5.4E-01
ENSMUST00000184471				6.4	1.1E-04	5.9	4.9E-04	-1.4	2.6E-01	-0.4	5.8E-01
ENSMUST00000160757				3.2	9.8E-02	5.6	5.2E-02	1.5	5.4E-01	-0.9	5.4E-01
ENSMUST00000160758	MYC binding protein 2 [Source:MGI Symbol;Acc:MGI:2179432]	F6SMY7		-0.6	4.8E-01	-2.5	9.8E-02	0.4	6.1E-01	2.3	1.1E-01
ENSMUST00000160764	predicted gene 21970 [Source:MGI Symbol;Acc:MGI:5439439]	F6XX07		-0.1	9.6E-01	3.8	3.3E-01	3.7	2.2E-01	-0.2	9.5E-01
ENSMUST00000138839				6.4	4.2E-05	5.6	3.1E-04	-2.0	9.3E-02	-0.9	1.7E-01
ENSMUST00000153626				6.4	2.8E-04	4.5	8.8E-03	-0.2	8.9E-01	1.5	1.3E-01
ENSMUST00000161134				6.4	4.6E-04	3.6	1.0E-03	-4.0	1.2E-03	0.8	1.8E-01
ENSMUST00000128755				6.4	5.9E-05	6.6	1.1E-04	-0.4	6.8E-01	-0.1	9.0E-01
ENSMUST00000133112				6.4	3.2E-05	2.2	6.2E-01	10.4	6.2E-03	-1.6	6.9E-01
ENSMUST00000183202				6.4	7.3E-06	2.8	1.2E-02	0.1	8.8E-01	-0.1	9.0E-01
ENSMUST00000131987				6.4	3.6E-05	-1.1	1.7E-01	1.1	3.4E-02	-0.5	5.2E-01
ENSMUST00000134377				6.4	3.4E-03	-7.7	5.0E-05	-0.3	4.5E-01	-0.8	4.9E-01
ENSMUST00000148077				6.4	1.6E-03	6.0	1.1E-03	-0.6	6.2E-01	0.7	3.8E-01
ENSMUST00000122346				6.4	5.5E-04	6.6	2.0E-04	-0.1	9.0E-01	-0.9	1.5E-01
ENSMUST00000160792	RIKEN cDNA A530032D15Rik gene [Source:MGI Symbol;Acc:MGI:3037746]	E9PV05		0.6	3.7E-01	0.5	5.0E-01	-0.3	6.4E-01	-0.2	7.4E-01
ENSMUST00000160801	WD repeat domain 41 [Source:MGI Symbol;Acc:MGI:2445123]		Q3UDP0	-1.6	7.1E-02	-3.3	3.4E-02	0.7	3.3E-01	2.4	9.8E-02
ENSMUST00000191380				6.4	6.1E-04	5.6	1.8E-04	-0.7	4.4E-01	-0.7	2.6E-01
ENSMUST00000137641				6.4	2.8E-05	7.7	6.5E-04	-0.8	6.3E-01	0.9	2.7E-01
ENSMUST00000160805	SLAIN motif family, member 1 [Source:MGI Symbol;Acc:MGI:2145578]	F7D4S5		1.9	3.1E-01	2.8	1.6E-01	-1.8	3.1E-01	-2.7	1.4E-01
ENSMUST00000160806				1.4	1.1E-01	2.8	1.5E-02	-0.1	9.5E-01	-1.5	1.0E-01
ENSMUST00000183131				6.4	6.2E-05	7.1	9.1E-05	-0.6	5.9E-01	-0.6	3.0E-01
ENSMUST00000160810	endothelin converting enzyme-like 1 [Source:MGI Symbol;Acc:MGI:1343461]		Q9JMI0	2.8	7.4E-02	4.8	8.1E-03	-0.6	7.0E-01	-2.5	4.8E-02
ENSMUST00000020226				6.4	1.3E-04	4.8	2.7E-03	-1.8	1.9E-01	-0.1	8.9E-01
ENSMUST00000120669				6.4	8.5E-06	5.4	8.9E-05	-0.2	8.0E-01	-0.3	6.2E-01
ENSMUST00000190438				6.4	2.7E-04	3.2	6.6E-03	0.2	8.2E-01	0.4	6.1E-01
ENSMUST00000162463				6.4	2.4E-04	-4.4	4.4E-02	1.9	4.3E-02	-1.7	4.5E-01
ENSMUST00000130830				6.4	3.4E-05	5.2	9.4E-04	-0.5	6.6E-01	-0.4	5.5E-01
ENSMUST00000160834	neurobeachin like 1 [Source:MGI Symbol;Acc:MGI:2444343]	E9PYP2		-0.3	4.6E-01	-0.2	6.5E-01	-0.4	3.6E-01	-0.4	4.2E-01
ENSMUST00000160840				-1.9	2.7E-01	-1.5	5.2E-01	0.1	9.6E-01	-0.4	8.7E-01
ENSMUST00000144522				6.4	1.9E-04	8.5	2.1E-04	-0.3	8.7E-01	0.3	6.8E-01
ENSMUST00000160852	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human) [Source:MGI Symbol;Acc:MGI:1913482]	Q545N1	P56873	1.7	7.0E-02	2.3	1.1E-01	2.1	9.6E-02	1.5	1.6E-01
ENSMUST00000139124				6.4	1.6E-04	-6.2	1.6E-03	1.1	4.2E-02	0.5	7.5E-01
ENSMUST00000129271				6.4	1.8E-06	6.0	1.9E-04	-2.1	9.6E-02	-0.3	5.8E-01
ENSMUST00000145674				6.4	2.1E-04	2.6	1.5E-02	0.1	8.7E-01	-0.5	5.2E-01
ENSMUST00000194730				6.4	7.7E-05	5.7	7.4E-05	-2.6	2.3E-02	-0.2	7.0E-01
ENSMUST00000160866				-1.4	2.3E-01	-0.5	7.1E-01	-0.6	5.2E-01	-1.5	2.2E-01
ENSMUST00000160871	RB1-inducible coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1341850]	E0CYY6		-2.5	3.8E-02	-3.3	3.2E-02	-1.1	1.5E-01	-0.2	8.6E-01
ENSMUST00000051826				6.4	2.1E-04	-0.4	8.6E-01	4.1	1.5E-02	-1.4	5.4E-01
ENSMUST00000119218				6.4	1.4E-04	-2.6	3.8E-02	1.9	7.3E-03	-0.3	7.7E-01
ENSMUST00000160881	phosphatidylinositol glycan anchor biosynthesis, class C [Source:MGI Symbol;Acc:MGI:1914542]	E0CXG9		-0.7	4.2E-01	-2.6	7.7E-02	-0.9	2.4E-01	1.0	4.4E-01
ENSMUST00000149511				6.4	8.2E-07	-3.4	1.4E-01	3.7	4.6E-03	-0.6	7.9E-01
ENSMUST00000153967				6.4	1.6E-04	-4.3	4.2E-02	-0.3	7.4E-01	0.7	7.0E-01
ENSMUST00000182876				6.4	8.7E-04	3.9	6.8E-02	-3.8	9.6E-02	-0.5	6.7E-01
ENSMUST00000160885	transcription factor 19 [Source:MGI Symbol;Acc:MGI:103180]	G3XA31		1.1	5.4E-01	5.0	5.4E-02	2.7	2.5E-01	-1.3	4.0E-01
ENSMUST00000187605				6.4	2.8E-06	0.5	6.2E-01	1.2	2.0E-01	-5.3	4.9E-03
ENSMUST00000160893	R3H domain and coiled-coil containing 1 like [Source:MGI Symbol;Acc:MGI:1196316]	E0CZA8		-0.2	9.4E-01	-4.5	1.4E-01	-3.9	3.1E-02	0.4	9.0E-01
ENSMUST00000110954				6.4	1.6E-04	3.6	6.3E-03	-1.1	2.5E-01	0.3	6.9E-01
ENSMUST00000160896	unkempt-like (Drosophila) [Source:MGI Symbol;Acc:MGI:1921404]	E0CYD7		3.0	6.1E-02	7.0	1.1E-02	3.0	1.9E-01	-1.1	3.9E-01
ENSMUST00000160899	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) [Source:MGI Symbol;Acc:MGI:1924148]	Q8R531		2.7	3.5E-01	3.6	2.0E-01	-0.5	8.7E-01	-1.4	5.0E-01
ENSMUST00000160902	hypoxia up-regulated 1 [Source:MGI Symbol;Acc:MGI:108030]		Q9JKR6	-0.4	6.6E-01	1.1	3.7E-01	0.5	5.9E-01	-1.0	3.7E-01
ENSMUST00000128117				6.4	8.3E-05	5.3	1.5E-03	-1.0	4.3E-01	-1.0	1.9E-01
ENSMUST00000174208				6.4	8.3E-04	3.9	3.3E-03	-2.4	5.2E-02	-2.9	7.0E-03
ENSMUST00000118562				6.4	9.6E-04	2.8	1.2E-02	0.3	6.8E-01	0.2	8.3E-01
ENSMUST00000160914	MAF1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916127]	E0CYK4		-2.2	1.4E-01	-0.4	8.4E-01	1.1	4.2E-01	-0.7	7.0E-01
ENSMUST00000160916				1.8	6.1E-02	1.6	2.0E-01	0.3	7.7E-01	0.4	6.1E-01
ENSMUST00000132214				6.4	2.0E-04	6.6	9.1E-04	-2.2	1.9E-01	0.4	5.9E-01
ENSMUST00000160922				-0.8	7.6E-01	-2.9	4.6E-01	-1.2	5.5E-01	0.8	8.3E-01
ENSMUST00000160927				2.0	6.4E-02	2.1	1.5E-01	0.4	7.4E-01	0.3	7.7E-01
ENSMUST00000167089				6.4	6.7E-04	1.4	4.0E-01	-3.0	1.0E-01	-0.1	9.5E-01
ENSMUST00000118379				6.4	2.0E-05	7.5	5.0E-04	-1.7	3.2E-01	0.1	9.0E-01
ENSMUST00000160940	tectorin alpha [Source:MGI Symbol;Acc:MGI:109575]		O08523	4.4	1.7E-01	2.6	4.0E-01	-1.6	6.2E-01	0.2	9.4E-01
ENSMUST00000119516				6.4	1.2E-04	3.9	9.2E-05	-2.1	5.1E-03	-0.6	1.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000149492				6.4	2.9E-04	8.4	2.7E-05	-0.7	5.8E-01	-0.3	5.8E-01
ENSMUST00000160959	COMM domain containing 2 [Source:MGI Symbol;Acc:MGI:1098806]	Q497T6	Q8BXC6	-1.1	4.0E-02	-1.0	1.2E-01	-0.1	8.6E-01	-0.2	7.5E-01
ENSMUST00000160961	chloride channel, voltage-sensitive 7 [Source:MGI Symbol;Acc:MGI:1347048]	E9PYL4		-0.5	6.4E-01	2.0	2.5E-01	2.7	6.9E-02	0.1	9.1E-01
ENSMUST00000121704				6.4	2.0E-04	-5.8	5.9E-03	1.8	1.4E-02	0.0	9.8E-01
ENSMUST00000143363				6.4	6.9E-07	5.2	1.0E-01	-0.6	8.5E-01	2.9	1.0E-01
ENSMUST00000149943				6.4	2.6E-04	-0.4	8.2E-01	1.5	2.7E-01	-1.6	3.8E-01
ENSMUST00000160978				-2.3	1.2E-01	-4.0	1.7E-02	-2.1	4.1E-02	-0.4	7.9E-01
ENSMUST00000141386				6.4	1.9E-04	6.7	8.9E-05	-0.8	4.5E-01	0.3	6.4E-01
ENSMUST00000189133				6.4	8.8E-05	3.7	6.0E-03	0.5	6.3E-01	0.8	3.0E-01
ENSMUST00000160987	serglycin [Source:MGI Symbol;Acc:MGI:97756]		P13609	-1.5	6.3E-02	-1.4	1.6E-01	-0.2	7.2E-01	-0.4	7.0E-01
ENSMUST00000193843				6.4	5.5E-04	5.5	2.4E-03	-0.7	6.2E-01	-0.3	7.5E-01
ENSMUST00000119377				6.4	2.9E-04	2.5	2.4E-01	-1.2	5.1E-01	1.1	4.5E-01
ENSMUST00000160993				0.6	4.0E-01	1.8	5.3E-02	0.3	6.7E-01	-0.9	2.3E-01
ENSMUST00000135611				6.4	1.7E-04	7.8	6.6E-03	0.4	8.6E-01	-0.7	4.9E-01
ENSMUST00000183153				6.4	7.1E-05	7.5	2.0E-02	-0.6	8.5E-01	-1.6	3.1E-01
ENSMUST00000173123				6.4	6.8E-05	-5.0	2.3E-02	0.3	7.4E-01	-0.4	8.4E-01
ENSMUST00000161009				-1.1	9.5E-02	-0.7	4.8E-01	1.4	4.5E-02	1.0	2.8E-01
ENSMUST00000161011	ataxin 3 [Source:MGI Symbol;Acc:MGI:1099442]	E9Q717		-2.7	2.4E-01	-3.4	2.4E-01	-1.3	4.2E-01	-0.6	8.3E-01
ENSMUST00000161012	transcription factor 19 [Source:MGI Symbol;Acc:MGI:103180]	G3XA31		-2.6	4.3E-02	-4.5	4.1E-02	0.3	7.6E-01	2.2	2.8E-01
ENSMUST00000119904				6.4	2.3E-04	3.6	4.8E-04	0.1	8.2E-01	0.0	9.8E-01
ENSMUST00000140408				6.4	3.7E-07	7.0	3.7E-06	0.8	2.8E-01	-0.3	4.4E-01
ENSMUST00000179648				6.4	2.9E-05	-4.3	1.8E-02	2.2	8.1E-03	-0.9	5.8E-01
ENSMUST00000161023	SRA stem-loop interacting RNA binding protein [Source:MGI Symbol;Acc:MGI:1916394]	Q14AR0	Q9D8T7	0.3	7.2E-01	0.1	9.2E-01	-0.7	3.8E-01	-0.5	5.6E-01
ENSMUST00000193495				6.4	7.8E-04	-4.8	4.4E-04	-0.7	1.5E-01	-2.2	7.0E-02
ENSMUST00000194471				6.4	1.3E-04	6.8	2.2E-04	-1.7	2.3E-01	-0.4	5.8E-01
ENSMUST00000161031	PHD finger protein 11D [Source:MGI Symbol;Acc:MGI:1277133]		A6H5X4	2.6	1.0E-01	-3.8	3.9E-02	-5.9	1.1E-03	0.5	7.8E-01
ENSMUST00000161032	importin 9 [Source:MGI Symbol;Acc:MGI:1918944]	E0CXB2		-2.5	5.5E-02	0.4	7.9E-01	1.8	1.5E-01	-1.1	4.6E-01
ENSMUST00000144449				6.4	1.4E-04	4.2	4.6E-03	-1.4	2.7E-01	-1.8	5.9E-02
ENSMUST00000152360				6.4	7.5E-06	6.9	1.2E-03	-0.6	7.1E-01	-0.7	4.3E-01
ENSMUST00000143676				6.4	9.1E-03	6.1	1.1E-04	0.9	3.3E-01	-0.9	1.4E-01
ENSMUST00000161038				0.0	9.5E-01	0.8	4.6E-01	1.4	1.2E-01	0.7	4.6E-01
ENSMUST00000178218				6.4	5.2E-05	3.0	2.4E-03	-1.2	9.8E-02	0.2	7.7E-01
ENSMUST00000161046	ubiquitin specific peptidase 7 [Source:MGI Symbol;Acc:MGI:2182061]	F8VPX1		-1.2	6.7E-01	3.8	2.5E-01	2.3	3.6E-01	-2.7	3.9E-01
ENSMUST00000161047	neurexophilin and PC-esterase domain family, member 5 [Source:MGI Symbol;Acc:MGI:3584036]	E0CX47		-1.7	5.4E-02	-4.3	1.1E-03	-3.0	2.5E-04	-0.4	7.2E-01
ENSMUST00000185777				6.4	4.2E-04	-9.2	1.9E-05	0.9	1.4E-02	0.0	9.7E-01
ENSMUST00000056675				6.4	1.1E-04	4.9	3.7E-02	-0.7	7.6E-01	-0.2	8.6E-01
ENSMUST00000134647				6.4	1.4E-04	7.6	6.1E-05	-0.6	6.2E-01	-0.3	5.4E-01
ENSMUST00000161064	ataxin 2 [Source:MGI Symbol;Acc:MGI:1277223]	F6U2C2		-2.6	8.9E-02	-1.1	5.6E-01	1.3	3.6E-01	-0.3	8.7E-01
ENSMUST00000138064				6.4	1.3E-04	7.7	5.2E-03	-0.5	8.2E-01	-2.7	4.6E-02
ENSMUST00000166666				6.4	7.6E-04	-3.0	3.0E-02	-0.6	3.9E-01	-0.2	8.4E-01
ENSMUST00000125199				6.4	3.8E-04	-0.1	9.4E-01	1.1	1.9E-01	-1.8	1.3E-01
ENSMUST00000161078	F-box protein 41 [Source:MGI Symbol;Acc:MGI:1261912]	Q3UGY7	Q6NS60	2.6	3.1E-01	3.3	1.9E-01	-0.5	8.6E-01	-1.2	5.3E-01
ENSMUST00000161083	liver glycogen phosphorylase [Source:MGI Symbol;Acc:MGI:97829]	Q3UEJ6		3.3	5.7E-02	3.4	1.2E-01	-1.3	5.0E-01	-1.4	3.4E-01
ENSMUST00000161085				-1.8	5.5E-01	-3.5	3.5E-01	-2.1	3.1E-01	-0.3	9.3E-01
ENSMUST00000161089	tetratricopeptide repeat domain 16 [Source:MGI Symbol;Acc:MGI:2443048]	Q3V0B6		7.2	4.6E-02	5.5	1.1E-01	-1.4	6.9E-01	0.2	9.1E-01
ENSMUST00000161094	argininosuccinate lyase [Source:MGI Symbol;Acc:MGI:88084]		Q91YI0	-3.3	3.6E-02	-4.8	3.6E-02	-0.5	5.6E-01	0.9	6.7E-01
ENSMUST00000161099				-1.5	5.4E-02	-0.8	3.8E-01	0.4	5.0E-01	-0.3	7.5E-01
ENSMUST00000167014				6.4	2.0E-04	5.8	4.1E-04	-0.1	8.9E-01	-0.1	9.2E-01
ENSMUST00000182164				6.4	3.6E-04	4.3	2.6E-02	-0.4	8.3E-01	0.6	6.0E-01
ENSMUST00000149372				6.4	1.3E-05	-3.7	7.0E-02	1.3	1.6E-01	2.4	1.9E-01
ENSMUST00000144262				6.4	1.2E-05	5.2	1.3E-03	-1.9	1.7E-01	-1.1	1.8E-01
ENSMUST00000134706				6.4	1.1E-04	7.3	8.8E-05	-0.6	6.1E-01	-0.7	2.8E-01
ENSMUST00000187740				6.4	8.6E-04	5.5	5.4E-03	-0.6	7.1E-01	-0.2	8.2E-01
ENSMUST00000137534				6.4	3.7E-05	-2.9	1.5E-02	0.6	2.3E-01	-0.7	5.1E-01
ENSMUST00000178732				6.4	2.4E-04	5.7	4.2E-05	0.4	5.5E-01	0.6	2.1E-01
ENSMUST00000132774				6.4	4.2E-05	-3.4	6.6E-02	0.5	5.8E-01	-0.1	9.6E-01
ENSMUST00000138143				6.4	3.9E-06	5.9	5.7E-02	-0.3	9.3E-01	1.5	3.7E-01
ENSMUST00000126673				6.4	2.9E-04	4.3	5.1E-03	-1.9	1.6E-01	-0.4	6.1E-01
ENSMUST00000161123	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:97502]	F6TXE3		-1.4	5.7E-01	-4.3	2.7E-01	-1.7	3.8E-01	1.2	7.5E-01
ENSMUST00000185905				6.4	2.2E-04	6.1	4.1E-03	-1.1	5.0E-01	-0.4	6.4E-01
ENSMUST00000161129				-1.0	4.2E-01	-2.0	2.4E-01	-1.1	3.1E-01	0.0	9.8E-01
ENSMUST00000123589				6.4	2.0E-04	8.4	2.4E-04	2.2	1.4E-01	0.7	2.9E-01
ENSMUST00000161132	centrosomal protein 295 [Source:MGI Symbol;Acc:MGI:2442521]		Q8BQ48	0.0	1.0E+00	4.1	2.8E-01	4.0	1.7E-01	-0.2	9.5E-01
ENSMUST00000125201				6.4	3.8E-05	4.2	7.5E-03	-1.8	1.9E-01	0.3	7.1E-01
ENSMUST00000136574				6.4	1.6E-03	-5.7	5.6E-03	0.2	7.8E-01	0.6	7.0E-01
ENSMUST00000163008				6.4	1.9E-04	6.8	1.7E-04	-0.6	5.9E-01	0.6	3.7E-01
ENSMUST00000188621				6.4	9.1E-05	6.6	1.8E-04	-1.3	3.1E-01	-0.5	4.6E-01
ENSMUST00000150447				6.4	9.8E-04	6.8	1.3E-04	-0.5	6.6E-01	-0.3	5.8E-01
ENSMUST00000185411				6.4	2.5E-06	-3.5	2.0E-02	0.7	2.3E-01	0.3	7.9E-01
ENSMUST00000192621				6.4	8.5E-05	-3.0	5.2E-02	0.3	6.2E-01	-0.1	9.7E-01
ENSMUST00000118843				6.4	1.3E-03	6.3	1.3E-03	-0.4	7.9E-01	-0.9	3.0E-01
ENSMUST00000161157	membrane-spanning 4-domains, subfamily A, member 6B [Source:MGI Symbol;Acc:MGI:1917024]	E0CZC1		-0.6	4.3E-01	-2.2	4.1E-02	-1.0	1.2E-01	0.6	5.2E-01
ENSMUST00000151483				6.4	3.3E-05	3.9	5.3E-05	0.4	4.1E-01	-0.4	2.6E-01
ENSMUST00000164694				6.4	1.8E-04	5.0	1.7E-05	-1.4	4.3E-02	0.2	5.9E-01
ENSMUST00000188166				6.4	3.7E-04	1.0	1.3E-01	-3.0	6.0E-04	-0.3	5.6E-01
ENSMUST00000190107				6.4	8.7E-04	6.2	4.9E-04	-0.4	7.2E-01	0.0	9.5E-01
ENSMUST00000192738				6.4	2.0E-04	6.9	3.0E-02	-0.9	7.7E-01	-0.4	8.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000132315				6.4	3.5E-04	6.0	5.1E-04	-0.5	7.0E-01	-0.4	5.7E-01
ENSMUST00000116179				6.3	1.6E-04	-1.9	2.9E-01	1.1	3.6E-01	-1.4	4.8E-01
ENSMUST00000161182	mannosidase, alpha, class 2C, member 1 [Source:MGI Symbol;Acc:MGI:1920994]	E9PZ88		-2.5	2.2E-01	-1.7	3.8E-01	-0.8	5.7E-01	-1.6	4.9E-01
ENSMUST00000189168				6.3	1.4E-04	-1.1	4.2E-01	2.1	2.5E-02	-0.5	7.1E-01
ENSMUST00000161187	ring finger protein 214 [Source:MGI Symbol;Acc:MGI:2444451]		Q8BFU3	-2.4	1.4E-01	-2.0	3.5E-01	-0.2	9.1E-01	-0.6	7.6E-01
ENSMUST00000161189	importin 9 [Source:MGI Symbol;Acc:MGI:1918944]	E0CY46		-3.2	7.2E-02	-0.8	7.2E-01	0.6	6.8E-01	-1.9	3.7E-01
ENSMUST00000191933				6.3	2.1E-05	3.7	2.2E-02	-1.0	4.6E-01	-0.8	4.7E-01
ENSMUST00000117076				6.3	1.4E-03	2.8	7.6E-02	0.2	8.6E-01	0.0	9.9E-01
ENSMUST00000147039				6.3	1.4E-04	5.3	1.8E-04	1.0	2.3E-01	-0.1	8.3E-01
ENSMUST00000155544				6.3	1.6E-04	4.0	1.5E-02	0.0	1.0E+00	0.0	9.9E-01
ENSMUST00000189614				6.3	1.2E-04	3.4	8.6E-02	-1.3	5.0E-01	-0.1	9.1E-01
ENSMUST00000147424				6.3	4.2E-05	-3.6	1.3E-02	1.2	6.2E-02	-0.8	5.4E-01
ENSMUST00000189734				6.3	1.2E-03	-1.6	4.4E-02	-0.2	6.3E-01	-0.4	5.7E-01
ENSMUST00000161207	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	E0CY14		-1.0	7.4E-01	0.9	8.3E-01	2.1	4.3E-01	0.3	9.5E-01
ENSMUST00000130426				6.3	6.1E-05	-5.2	2.7E-03	-2.4	3.4E-03	-0.2	8.8E-01
ENSMUST00000161220	histamine receptor H1 [Source:MGI Symbol;Acc:MGI:107619]	B3Y5T0	P70174	3.7	1.4E-01	1.9	5.4E-01	-0.2	9.4E-01	1.6	5.1E-01
ENSMUST00000161221				-2.1	6.7E-02	-1.1	4.8E-01	1.5	1.1E-01	0.5	7.4E-01
ENSMUST00000194834				6.3	1.0E-03	6.8	7.7E-04	-0.5	7.5E-01	-1.1	1.8E-01
ENSMUST00000128338				6.3	1.2E-04	6.9	5.9E-04	-0.1	9.7E-01	0.3	7.2E-01
ENSMUST00000161227	LUC7-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2183260]	Q05CX5		-0.6	6.3E-01	0.4	7.7E-01	0.3	7.2E-01	-0.6	6.5E-01
ENSMUST00000182032				6.3	7.6E-06	3.2	4.9E-03	0.7	3.6E-01	-0.6	3.8E-01
ENSMUST00000116118				6.3	9.2E-05	-3.4	3.6E-03	-0.1	8.0E-01	-0.9	3.6E-01
ENSMUST00000161240	acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 [Source:MGI Symbol;Acc:MGI		O08832	-0.5	3.6E-01	0.9	2.4E-01	1.2	6.3E-02	-0.3	7.0E-01
ENSMUST00000161241	upstream transcription factor 1 [Source:MGI Symbol;Acc:MGI:99542]	Q3UQH7	Q61069	-1.3	2.7E-01	-1.3	3.8E-01	-0.1	9.5E-01	0.0	9.9E-01
ENSMUST00000141064				6.3	1.2E-04	-0.1	9.6E-01	3.2	2.0E-02	-0.7	6.2E-01
ENSMUST00000148214				6.3	1.6E-03	-2.1	3.4E-02	0.0	9.4E-01	-3.1	1.8E-02
ENSMUST00000117850				6.3	2.5E-04	2.2	4.0E-02	-1.2	1.8E-01	-0.5	5.2E-01
ENSMUST00000161250	transmembrane BAX inhibitor motif containing 6 [Source:MGI Symbol;Acc:MGI:99682]		Q9D2C7	-2.2	9.5E-02	-2.5	2.7E-01	1.3	3.1E-01	1.6	4.1E-01
ENSMUST00000161254	NACHT and WD repeat domain containing 1 [Source:MGI Symbol;Acc:MGI:2442268]	E0CX99		2.4	2.3E-01	6.4	1.1E-02	0.1	9.7E-01	-3.9	3.0E-02
ENSMUST00000161259				-1.3	9.7E-02	-0.6	5.4E-01	-0.4	5.0E-01	-1.2	1.9E-01
ENSMUST00000121961				6.3	1.5E-04	8.4	2.0E-05	-0.6	6.0E-01	-0.5	2.8E-01
ENSMUST00000137599				6.3	2.6E-03	-2.5	1.2E-02	0.2	6.5E-01	0.8	3.2E-01
ENSMUST00000140256				6.3	4.2E-04	-3.2	3.1E-02	0.9	1.9E-01	-1.4	3.5E-01
ENSMUST00000161273	phosphatidylinositol transfer protein, membrane-associated 2 [Source:MGI Symbol;Acc:MGI:1336192]	E9PYJ7		2.6	1.8E-01	5.3	1.4E-02	-0.6	7.6E-01	-3.3	3.8E-02
ENSMUST00000161278	MYC binding protein 2 [Source:MGI Symbol;Acc:MGI:2179432]	F7CZG3		1.0	2.0E-01	0.5	6.2E-01	-0.1	8.8E-01	0.4	6.4E-01
ENSMUST00000127364				6.3	9.5E-07	-3.1	9.6E-02	0.3	7.0E-01	-0.1	9.4E-01
ENSMUST00000152828				6.3	5.0E-04	6.5	2.0E-04	1.8	1.2E-01	-0.1	8.2E-01
ENSMUST00000159336				6.3	1.5E-04	-3.2	8.8E-04	-0.2	6.2E-01	0.1	9.1E-01
ENSMUST00000189483				6.3	3.6E-04	7.5	3.6E-05	-0.6	5.9E-01	-0.4	4.4E-01
ENSMUST00000122332				6.3	4.4E-04	5.6	6.4E-04	-1.5	2.5E-01	-0.7	3.1E-01
ENSMUST00000161695				6.3	2.7E-04	-2.5	6.2E-02	1.4	6.8E-02	-1.0	4.3E-01
ENSMUST00000176492				6.3	2.9E-03	6.4	4.9E-04	-0.2	8.7E-01	0.9	2.0E-01
ENSMUST00000161304				-2.6	6.5E-02	1.4	3.2E-01	1.3	2.5E-01	-2.7	7.4E-02
ENSMUST00000181451				6.3	2.0E-04	4.8	1.0E-03	-2.1	1.0E-01	-0.6	3.8E-01
ENSMUST00000161308	H3 histone, family 3A [Source:MGI Symbol;Acc:MGI:1097686]		P84244	-3.2	5.5E-02	-2.2	2.4E-01	0.1	8.9E-01	-0.8	6.7E-01
ENSMUST00000186455				6.3	2.5E-04	4.3	7.5E-03	0.1	9.2E-01	-0.9	3.3E-01
ENSMUST00000064305				6.3	3.8E-05	5.6	5.8E-04	-0.1	9.6E-01	-0.7	3.8E-01
ENSMUST00000105272				6.3	8.8E-04	5.3	2.3E-03	-1.0	5.0E-01	-0.5	5.2E-01
ENSMUST00000161318	hypoxia up-regulated 1 [Source:MGI Symbol;Acc:MGI:108030]		Q9JKR6	-1.7	5.7E-01	-1.4	5.8E-01	-2.9	1.6E-01	-3.3	3.0E-01
ENSMUST00000128599				6.3	3.9E-04	-6.1	3.3E-04	1.3	7.2E-03	-0.8	5.1E-01
ENSMUST00000135598				6.3	1.4E-04	-0.1	8.9E-01	1.1	1.1E-01	-1.0	2.4E-01
ENSMUST00000161336	amylo-1,6-glucosidase, 4-alpha-glucanotransferase [Source:MGI Symbol;Acc:MGI:1924809]	E0CYU6		0.1	9.5E-01	1.7	6.2E-01	2.0	3.8E-01	0.4	9.0E-01
ENSMUST00000162993				6.3	8.4E-04	4.8	1.8E-04	-0.8	3.1E-01	-0.4	4.8E-01
ENSMUST00000194802				6.3	1.1E-02	7.1	5.4E-04	-0.2	9.2E-01	-1.8	4.8E-02
ENSMUST00000161351	F-box protein 33 [Source:MGI Symbol;Acc:MGI:1917861]	E0CZ63		-1.9	7.4E-02	-0.4	7.1E-01	0.3	7.0E-01	-1.2	2.9E-01
ENSMUST00000118269				6.3	4.7E-03	6.9	3.1E-04	-0.7	6.1E-01	0.6	3.9E-01
ENSMUST00000140536				6.3	6.8E-05	7.9	1.5E-04	0.2	8.5E-01	-0.8	2.6E-01
ENSMUST00000161356	reelin [Source:MGI Symbol;Acc:MGI:103022]		Q60841	6.1	6.5E-02	4.6	1.7E-01	-1.5	6.8E-01	0.0	9.9E-01
ENSMUST00000185953				6.3	7.3E-05	8.2	5.1E-05	-0.6	6.1E-01	-0.4	4.8E-01
ENSMUST00000121103				6.3	3.0E-04	4.2	1.5E-04	-1.2	7.4E-02	0.3	5.2E-01
ENSMUST00000161363	oxysterol binding protein-like 9 [Source:MGI Symbol;Acc:MGI:1923784]	E9Q6C1		0.3	8.8E-01	4.1	1.9E-01	3.7	1.9E-01	-0.2	9.3E-01
ENSMUST00000121873				6.3	5.6E-04	-9.4	5.4E-05	-0.2	6.8E-01	-1.0	4.9E-01
ENSMUST00000175985				6.3	8.3E-04	-1.9	3.9E-01	2.0	1.8E-01	-1.2	6.0E-01
ENSMUST00000129689				6.3	1.8E-04	-3.9	2.6E-02	0.8	2.7E-01	0.1	9.4E-01
ENSMUST00000145732				6.3	1.2E-05	1.6	5.4E-01	-0.9	6.9E-01	2.8	1.7E-01
ENSMUST00000155724				6.3	3.3E-05	-1.5	3.2E-01	1.1	2.6E-01	-1.7	3.2E-01
ENSMUST00000118349				6.3	8.9E-05	6.6	7.1E-04	-0.6	6.9E-01	-1.3	1.0E-01
ENSMUST00000161381	membrane-type frizzled-related protein [Source:MGI Symbol;Acc:MGI:2385957]		Q8K480	3.8	9.5E-02	1.9	4.9E-01	-0.5	8.5E-01	1.5	4.9E-01
ENSMUST00000121445				6.3	3.0E-04	7.2	2.1E-03	-0.7	7.0E-01	0.7	4.7E-01
ENSMUST00000174777				6.3	1.5E-04	-4.1	9.4E-02	1.0	3.6E-01	0.5	8.2E-01
ENSMUST00000124708				6.3	2.3E-04	5.6	1.8E-05	-1.8	2.9E-02	-0.4	3.6E-01
ENSMUST00000190119				6.3	9.2E-05	0.8	1.8E-01	-0.7	1.4E-01	-0.1	8.0E-01
ENSMUST00000133721				6.3	3.6E-06	3.3	5.9E-03	0.1	9.2E-01	0.4	5.3E-01
ENSMUST00000159665				6.3	1.1E-04	7.3	7.7E-05	0.1	9.4E-01	-0.4	5.3E-01
ENSMUST00000161410	tryptophanyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:104630]	Q3U6U7	P32921	1.0	7.2E-01	-3.4	3.2E-01	-3.6	1.2E-01	0.7	8.3E-01
ENSMUST00000161415				-3.5	4.4E-02	-1.4	4.3E-01	0.8	4.9E-01	-1.2	5.1E-01
ENSMUST00000165787				6.3	1.1E-03	6.5	2.7E-03	-0.5	7.4E-01	0.5	5.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000161428	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [Source:MGI Symbol;Acc:MGI:97502]	F6V9F1		-0.6	6.6E-01	-1.1	5.3E-01	-0.4	7.2E-01	0.1	9.7E-01
ENSMUST00000131969				6.3	2.0E-04	4.4	3.1E-02	0.9	5.8E-01	0.8	5.9E-01
ENSMUST00000161434				0.4	8.1E-01	-0.3	8.8E-01	0.0	1.0E+00	0.7	7.1E-01
ENSMUST00000173255				6.3	1.0E-04	6.1	3.7E-04	0.2	8.2E-01	-0.6	3.9E-01
ENSMUST00000161441	arrestin domain containing 3 [Source:MGI Symbol;Acc:MGI:2145242]	E0CZE1		0.5	8.6E-01	-2.7	4.5E-01	-2.6	2.9E-01	0.7	8.5E-01
ENSMUST00000119759				6.3	2.8E-04	6.1	1.4E-04	-0.6	5.5E-01	-1.0	1.2E-01
ENSMUST00000122900				6.3	9.4E-04	-5.2	3.4E-03	0.5	3.9E-01	0.9	5.4E-01
ENSMUST00000140873				6.3	1.6E-05	6.1	1.7E-03	-0.4	8.0E-01	0.1	9.0E-01
ENSMUST00000185708				6.3	4.6E-04	-4.4	1.3E-03	-1.4	1.2E-02	-0.7	4.9E-01
ENSMUST00000161458	zinc finger protein 949 [Source:MGI Symbol;Acc:MGI:1918890]	E9Q732		-2.2	1.7E-01	3.7	3.0E-01	8.0	2.6E-02	2.1	3.2E-01
ENSMUST00000161459	SET domain, bifurcated 2 [Source:MGI Symbol;Acc:MGI:2685139]	B2RXP3		-0.5	4.5E-01	0.2	7.5E-01	-0.1	8.4E-01	-0.9	2.6E-01
ENSMUST00000161460				-0.5	3.5E-01	-0.6	3.0E-01	-0.8	8.1E-02	-0.7	2.8E-01
ENSMUST00000191582				6.3	4.6E-04	5.4	1.5E-02	-3.3	1.3E-01	1.5	2.2E-01
ENSMUST00000192665				6.3	1.1E-03	7.1	4.9E-04	-0.4	8.0E-01	-0.6	4.2E-01
ENSMUST00000161476	PRP3 pre-mRNA processing factor 3 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1918017]		Q922U1	-1.9	4.1E-02	-2.2	5.6E-02	0.0	9.7E-01	0.4	6.9E-01
ENSMUST00000136033				6.3	1.0E-04	-1.6	2.1E-01	1.1	1.3E-01	-0.5	6.8E-01
ENSMUST00000148029				6.3	3.0E-04	3.1	5.3E-03	-0.7	3.5E-01	-0.5	4.5E-01
ENSMUST00000161488				-2.8	9.6E-02	-1.5	5.2E-01	1.4	3.6E-01	0.1	9.6E-01
ENSMUST00000127867				6.3	4.6E-04	1.7	7.6E-02	-5.3	1.2E-03	0.5	5.2E-01
ENSMUST00000155556				6.3	3.8E-04	7.6	1.9E-05	-0.5	6.4E-01	0.0	9.3E-01
ENSMUST00000129961				6.3	2.1E-03	4.0	2.0E-03	0.6	4.9E-01	-1.3	1.1E-01
ENSMUST00000161499				1.4	2.6E-01	0.9	5.6E-01	-0.4	7.7E-01	0.2	8.8E-01
ENSMUST00000133072				6.3	7.7E-06	-4.0	2.8E-03	-0.1	8.3E-01	2.5	2.9E-02
ENSMUST00000161502	fucosyltransferase 10 [Source:MGI Symbol;Acc:MGI:2384748]		Q5F2L2	4.7	3.7E-02	4.8	5.1E-02	-0.5	8.3E-01	-0.6	6.5E-01
ENSMUST00000156952				6.3	2.8E-04	-0.5	4.5E-01	-0.7	2.2E-01	-2.2	1.3E-02
ENSMUST00000130138				6.3	1.7E-04	-2.4	2.7E-01	3.2	3.0E-02	0.3	9.0E-01
ENSMUST00000147330				6.3	1.8E-04	7.2	5.7E-03	-1.0	6.7E-01	1.1	3.7E-01
ENSMUST00000074309				6.3	9.1E-05	6.5	1.2E-02	-0.7	7.7E-01	-1.9	1.7E-01
ENSMUST00000161515	CCR4-NOT transcription complex, subunit 11 [Source:MGI Symbol;Acc:MGI:106580]		Q9CWN7	0.4	8.5E-01	0.1	9.6E-01	-1.8	3.8E-01	-1.5	5.3E-01
ENSMUST00000152464				6.3	1.1E-02	6.9	1.1E-04	-0.5	6.7E-01	-0.5	3.8E-01
ENSMUST00000134295				6.3	4.9E-03	1.8	2.4E-01	7.0	1.3E-04	-1.0	4.4E-01
ENSMUST00000187149				6.3	1.1E-04	5.9	8.4E-04	-0.6	6.1E-01	-0.3	7.0E-01
ENSMUST00000147996				6.3	8.3E-03	-3.8	1.7E-02	1.8	1.9E-02	-1.1	4.8E-01
ENSMUST00000119764				6.3	8.3E-05	7.1	2.7E-04	-0.7	6.2E-01	-1.2	1.3E-01
ENSMUST00000137105				6.3	2.7E-04	-4.7	1.5E-03	1.1	2.8E-02	-1.2	3.3E-01
ENSMUST00000149519				6.3	1.4E-05	8.3	1.7E-04	-1.1	4.8E-01	0.1	8.7E-01
ENSMUST00000136041				6.3	3.5E-05	4.4	5.9E-05	0.1	9.1E-01	-0.1	8.2E-01
ENSMUST00000161538	LUC7-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2183260]		Q7TNC4	-0.1	8.6E-01	-0.1	9.1E-01	-0.1	9.1E-01	-0.1	9.1E-01
ENSMUST00000184200				6.3	7.8E-05	6.9	3.9E-04	0.0	1.0E+00	-0.6	3.9E-01
ENSMUST00000193215				6.3	6.4E-05	2.6	4.5E-03	-0.5	4.1E-01	-0.5	3.8E-01
ENSMUST00000119342				6.3	1.3E-04	0.7	5.9E-01	-2.2	6.6E-02	5.1	1.3E-03
ENSMUST00000119537				6.3	1.6E-04	4.5	1.4E-02	-0.7	6.6E-01	1.2	2.6E-01
ENSMUST00000131504				6.3	7.8E-04	-0.5	4.2E-01	1.3	1.5E-02	-0.4	5.7E-01
ENSMUST00000132677				6.3	9.3E-04	3.8	6.7E-02	-1.7	4.4E-01	1.5	2.8E-01
ENSMUST00000068526				6.3	2.6E-04	3.2	2.3E-03	-0.6	4.2E-01	-0.4	5.3E-01
ENSMUST00000125997				6.3	4.6E-04	6.9	2.8E-04	-0.6	6.7E-01	-0.9	2.1E-01
ENSMUST00000130149				6.3	1.7E-04	-1.2	3.4E-01	1.3	1.1E-01	-0.2	9.0E-01
ENSMUST00000185623				6.3	7.1E-04	-0.5	2.2E-01	0.2	4.3E-01	-0.7	1.2E-01
ENSMUST00000161572				-3.3	2.1E-01	-6.3	6.3E-02	-3.2	5.2E-02	-0.1	9.7E-01
ENSMUST00000161574	ring finger protein (C3H2C3 type) 6 [Source:MGI Symbol;Acc:MGI:1921382]	E0CYZ9		2.2	2.6E-01	-1.3	5.4E-01	-3.0	9.8E-02	0.5	8.1E-01
ENSMUST00000122465				6.3	3.9E-04	-4.5	6.4E-03	0.9	1.4E-01	-1.5	3.4E-01
ENSMUST00000131107				6.3	2.0E-05	5.9	6.8E-04	-0.8	4.9E-01	0.6	3.4E-01
ENSMUST00000161586	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma [Source:MGI Symbol;Acc:MGI:1298224]	F6SMP3		0.1	8.9E-01	0.4	8.0E-01	0.6	5.8E-01	0.4	7.4E-01
ENSMUST00000132868				6.3	7.3E-04	1.5	6.8E-02	0.0	9.6E-01	0.0	9.7E-01
ENSMUST00000147382				6.3	2.8E-04	-0.6	7.1E-01	1.2	2.3E-01	-1.7	3.0E-01
ENSMUST00000187548				6.3	1.7E-06	3.6	1.4E-03	0.3	7.2E-01	0.1	8.8E-01
ENSMUST00000161600	family with sequence similarity 126, member B [Source:MGI Symbol;Acc:MGI:1098784]		Q8C729	1.4	6.5E-02	1.8	5.2E-02	0.2	7.9E-01	-0.3	6.7E-01
ENSMUST00000190365				6.3	5.4E-03	-1.1	4.9E-01	2.0	1.3E-01	-1.2	4.6E-01
ENSMUST00000161608	potassium channel tetramerisation domain containing 18 [Source:MGI Symbol;Acc:MGI:3603813]	E9PYP3		-1.5	5.7E-01	-0.1	9.6E-01	-1.7	3.4E-01	-3.0	2.5E-01
ENSMUST00000192505				6.3	2.3E-04	-1.4	3.9E-02	0.7	9.2E-02	-0.2	7.1E-01
ENSMUST00000151154				6.3	3.3E-04	-1.6	1.4E-01	-11.5	1.8E-04	0.8	4.1E-01
ENSMUST00000152518				6.3	4.8E-04	6.3	3.3E-04	-0.6	6.2E-01	-1.0	1.6E-01
ENSMUST00000182136				6.3	7.5E-06	8.1	8.2E-07	0.6	3.7E-01	0.3	4.9E-01
ENSMUST00000161630	zinc finger protein 263 [Source:MGI Symbol;Acc:MGI:1921370]	E0CZ03		3.0	1.4E-01	0.7	8.2E-01	0.6	7.8E-01	2.9	3.2E-01
ENSMUST00000189364				6.3	3.9E-04	-0.5	7.7E-01	1.6	1.2E-01	-1.0	5.2E-01
ENSMUST00000161633				5.2	4.2E-02	5.3	4.3E-02	-1.5	5.5E-01	-1.6	2.8E-01
ENSMUST00000179291				6.3	4.0E-05	6.5	4.3E-04	-0.7	6.0E-01	-0.5	4.8E-01
ENSMUST00000161639	G elongation factor, mitochondrial 2 [Source:MGI Symbol;Acc:MGI:2444783]		Q8R2Q4	-3.6	2.6E-01	2.3	6.3E-01	5.0	1.8E-01	-0.9	8.3E-01
ENSMUST00000190958				6.3	2.8E-04	-2.4	2.4E-01	2.1	8.8E-02	-0.6	7.5E-01
ENSMUST00000117378				6.3	3.0E-04	-3.4	7.2E-02	1.4	1.3E-01	0.5	7.7E-01
ENSMUST00000119277				6.3	7.8E-05	-4.3	3.0E-02	0.6	4.0E-01	-0.1	9.8E-01
ENSMUST00000121570				6.3	7.8E-05	6.9	2.1E-03	-0.7	7.0E-01	-2.9	2.3E-02
ENSMUST00000177273				6.3	1.4E-02	5.2	2.5E-03	-0.5	7.4E-01	-0.1	8.6E-01
ENSMUST00000138079				6.3	1.2E-03	5.3	2.2E-02	0.1	9.5E-01	-0.3	8.0E-01
ENSMUST00000161663	mannosidase, alpha, class 2C, member 1 [Source:MGI Symbol;Acc:MGI:1920994]	E9PYM7		1.4	5.7E-01	1.4	6.6E-01	-0.3	9.1E-01	-0.3	9.2E-01
ENSMUST00000161667				-1.3	3.6E-01	0.6	7.1E-01	-0.4	7.5E-01	-2.2	1.4E-01
ENSMUST00000161669	transmembrane protein 55b [Source:MGI Symbol;Acc:MGI:2448501]	F7CNA9		-2.7	4.8E-02	-2.6	1.6E-01	0.8	4.1E-01	0.7	7.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000170960				6.3	4.1E-05	6.4	5.6E-04	0.0	9.9E-01	-0.5	4.8E-01
ENSMUST00000161673				2.9	6.0E-02	3.0	1.1E-01	-1.0	5.4E-01	-1.1	3.9E-01
ENSMUST00000161680	RIKEN cDNA 1700019B03 gene [Source:MGI Symbol;Acc:MGI:1923656]	G3XA23		-1.3	4.0E-01	3.2	9.0E-02	1.9	2.4E-01	-2.7	1.2E-01
ENSMUST00000161682				2.5	2.1E-01	2.2	3.6E-01	-0.6	7.7E-01	-0.3	9.0E-01
ENSMUST00000161683				0.2	8.5E-01	0.7	5.2E-01	0.3	7.1E-01	-0.2	8.0E-01
ENSMUST00000188319				6.3	1.3E-04	-3.2	3.0E-03	-0.8	1.3E-01	-1.6	1.1E-01
ENSMUST00000134866				6.3	1.4E-03	2.5	3.9E-02	0.2	7.9E-01	-0.2	8.5E-01
ENSMUST00000187230				6.3	3.5E-04	4.2	1.3E-03	0.0	9.8E-01	-0.6	3.6E-01
ENSMUST00000131672				6.3	3.5E-06	3.7	2.9E-03	-0.5	5.7E-01	0.9	2.1E-01
ENSMUST00000172523				6.3	1.2E-05	6.9	3.3E-05	-1.6	1.5E-01	-0.6	2.6E-01
ENSMUST00000024798				6.3	2.1E-02	-2.6	2.9E-01	1.1	4.1E-01	-1.6	5.2E-01
ENSMUST00000119244				6.3	1.7E-04	5.1	1.5E-03	-1.4	2.9E-01	-0.1	9.0E-01
ENSMUST00000134713				6.3	3.3E-04	5.3	1.1E-04	0.4	6.5E-01	0.4	5.0E-01
ENSMUST00000137791				6.3	9.2E-05	-5.9	6.0E-04	-0.2	7.0E-01	-0.9	5.0E-01
ENSMUST00000157079				6.3	7.4E-04	5.0	5.6E-04	-2.8	3.4E-02	0.4	5.9E-01
ENSMUST00000174098				6.3	5.0E-03	6.4	6.8E-03	-0.7	7.1E-01	-1.4	2.3E-01
ENSMUST00000161705				-1.1	2.6E-01	-1.0	3.8E-01	-0.4	6.5E-01	-0.5	6.5E-01
ENSMUST00000161707				1.4	3.7E-01	6.2	2.7E-02	2.8	2.4E-01	-2.0	1.8E-01
ENSMUST00000161711	optic atrophy 3 [Source:MGI Symbol;Acc:MGI:2686271]			0.8	5.2E-01	1.9	2.3E-01	0.6	6.4E-01	-0.5	6.9E-01
ENSMUST00000161712	alkB, alkylation repair homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:2384034]	E0CX46		2.7	6.0E-02	0.6	7.5E-01	-0.5	7.5E-01	1.6	3.1E-01
ENSMUST00000181783				6.3	1.7E-04	5.0	1.8E-02	-0.6	7.6E-01	0.4	7.4E-01
ENSMUST00000149718				6.3	6.8E-05	6.2	5.9E-04	-0.5	7.2E-01	-0.7	3.5E-01
ENSMUST00000161724	RIKEN cDNA A530032D15Rik gene [Source:MGI Symbol;Acc:MGI:3037746]	E9Q422		-0.8	3.8E-01	-2.4	7.3E-02	-1.2	1.6E-01	0.4	7.7E-01
ENSMUST00000161539				6.3	3.3E-04	5.7	1.1E-04	-0.7	4.3E-01	-0.1	8.6E-01
ENSMUST00000161736				-2.2	1.4E-01	-3.9	5.5E-02	-2.2	4.1E-02	-0.4	8.2E-01
ENSMUST00000189622				6.3	1.1E-04	-5.3	8.2E-06	0.2	4.9E-01	-0.3	6.4E-01
ENSMUST00000118221				6.3	3.3E-04	5.1	2.2E-03	-1.2	3.9E-01	-0.2	8.0E-01
ENSMUST00000120294				6.3	2.6E-03	2.7	1.0E-01	6.2	4.3E-04	-0.5	6.9E-01
ENSMUST00000120986				6.3	9.7E-07	-5.9	9.6E-04	-1.3	5.1E-02	-0.6	6.6E-01
ENSMUST00000161748				-2.4	3.0E-01	-2.3	4.2E-01	-0.7	6.8E-01	-0.8	7.8E-01
ENSMUST00000179385				6.3	4.9E-03	3.4	5.4E-03	-2.0	9.3E-02	-0.3	7.4E-01
ENSMUST00000161758	Vpr (HIV-1) binding protein [Source:MGI Symbol;Acc:MGI:2445220]		Q80TR8	-0.8	6.2E-01	-2.8	2.2E-01	0.2	9.1E-01	2.2	3.1E-01
ENSMUST00000193721				6.3	3.9E-04	4.7	4.9E-03	-0.4	7.3E-01	0.6	5.3E-01
ENSMUST00000126370				6.3	2.2E-02	-4.5	3.1E-02	0.2	8.5E-01	0.6	7.6E-01
ENSMUST00000127395				6.3	9.5E-05	-2.3	1.3E-01	0.3	6.9E-01	-1.9	2.6E-01
ENSMUST00000193379				6.3	3.9E-05	5.7	1.7E-02	-1.2	5.8E-01	1.1	3.8E-01
ENSMUST00000195222				6.3	3.4E-04	5.2	5.9E-04	-1.7	1.4E-01	-0.3	6.7E-01
ENSMUST00000118730				6.3	3.0E-04	-3.4	3.7E-02	0.5	5.1E-01	-1.7	3.1E-01
ENSMUST00000167622				6.3	2.5E-04	-5.2	4.7E-04	0.6	1.8E-01	-2.5	5.7E-02
ENSMUST00000118722				6.3	3.2E-04	5.2	8.5E-04	0.5	6.5E-01	0.3	6.7E-01
ENSMUST00000161778	transmembrane BAX inhibitor motif containing 6 [Source:MGI Symbol;Acc:MGI:99682]	E0CX98		-1.1	3.6E-01	-2.2	2.1E-01	0.1	9.0E-01	1.2	4.9E-01
ENSMUST00000130728				6.3	1.5E-04	2.3	2.6E-03	0.4	3.7E-01	0.2	6.4E-01
ENSMUST00000138348				6.3	7.0E-04	3.4	3.8E-03	-1.5	1.1E-01	-0.3	6.0E-01
ENSMUST00000122909				6.3	2.4E-04	6.1	5.4E-04	-0.4	7.3E-01	-0.4	5.7E-01
ENSMUST00000161785	zinc finger protein 41 [Source:MGI Symbol;Acc:MGI:99186]		Q02526	0.5	7.8E-01	1.9	3.6E-01	0.8	6.3E-01	-0.6	7.3E-01
ENSMUST00000113982				6.3	2.7E-03	7.2	7.1E-05	3.1	1.1E-02	-0.8	1.8E-01
ENSMUST00000161790				2.8	1.0E-01	-1.7	2.7E-01	-4.8	5.8E-03	-0.3	8.4E-01
ENSMUST00000119849				6.3	5.7E-04	4.5	2.3E-04	-1.1	1.9E-01	0.1	8.3E-01
ENSMUST00000146202				6.3	1.7E-04	-4.0	8.7E-03	0.3	6.0E-01	-0.7	6.2E-01
ENSMUST00000110508				6.3	2.0E-04	5.9	1.6E-03	-0.5	7.2E-01	0.0	9.6E-01
ENSMUST00000145700				6.3	1.0E-04	-3.4	6.9E-03	0.5	2.8E-01	-1.5	2.1E-01
ENSMUST00000177474				6.3	7.6E-06	9.0	1.0E-04	-0.1	9.6E-01	-0.3	6.0E-01
ENSMUST00000120023				6.3	6.5E-06	-5.7	9.8E-05	-0.3	4.9E-01	-0.5	6.2E-01
ENSMUST00000133801				6.3	2.8E-04	-7.0	2.1E-04	-1.2	1.9E-02	-1.7	2.5E-01
ENSMUST00000184806				6.3	2.9E-04	3.1	1.9E-02	0.3	7.7E-01	0.0	9.7E-01
ENSMUST00000161809				0.0	9.8E-01	0.7	7.3E-01	0.8	6.2E-01	0.1	9.6E-01
ENSMUST00000161816				-0.6	5.0E-01	-3.3	7.0E-02	0.4	5.9E-01	3.1	7.4E-02
ENSMUST00000116671				6.3	3.6E-04	-3.6	4.3E-03	-0.2	7.4E-01	-1.3	2.4E-01
ENSMUST00000161825	G elongation factor, mitochondrial 2 [Source:MGI Symbol;Acc:MGI:2444783]	E9Q7N5		0.8	2.7E-01	1.1	2.3E-01	-0.1	8.5E-01	-0.4	5.9E-01
ENSMUST00000161840				1.5	1.1E-01	1.4	2.5E-01	0.5	6.0E-01	0.7	4.9E-01
ENSMUST00000161843				0.0	9.4E-01	2.3	2.1E-02	0.6	3.6E-01	-1.6	5.2E-02
ENSMUST00000161846	catenin (cadherin associated protein), alpha 2 [Source:MGI Symbol;Acc:MGI:88275]		Q61301	4.2	8.8E-02	5.4	5.8E-02	-0.3	9.2E-01	-1.4	3.6E-01
ENSMUST00000161849				0.9	3.3E-01	1.3	1.9E-01	-0.7	4.1E-01	-1.2	2.1E-01
ENSMUST00000141182				6.3	2.9E-02	-0.1	9.0E-01	1.0	4.3E-02	-6.1	1.4E-04
ENSMUST00000193115				6.3	1.6E-04	8.0	1.9E-02	-1.3	7.0E-01	-1.5	4.4E-01
ENSMUST00000188445				6.3	1.3E-04	7.2	2.2E-05	-1.3	1.9E-01	0.2	6.9E-01
ENSMUST00000109519				6.3	2.1E-04	-2.1	4.8E-02	1.0	1.0E-01	-2.3	6.8E-02
ENSMUST00000134743				6.3	1.2E-03	6.5	2.1E-03	1.7	2.7E-01	-0.1	9.2E-01
ENSMUST00000141861				6.3	5.2E-05	-2.7	2.9E-04	-0.1	8.2E-01	0.2	6.0E-01
ENSMUST00000153160				6.3	1.8E-04	-0.8	5.7E-01	0.3	7.1E-01	-2.0	2.1E-01
ENSMUST00000178845				6.3	3.2E-05	-3.0	1.0E-01	2.6	1.1E-02	-1.2	5.1E-01
ENSMUST00000144016				6.3	8.8E-04	6.5	4.8E-04	-0.7	6.1E-01	0.3	6.7E-01
ENSMUST00000190399				6.3	1.6E-02	5.0	1.1E-02	-0.6	7.3E-01	-0.5	6.1E-01
ENSMUST00000192067				6.3	1.4E-03	4.6	3.4E-02	-1.4	4.9E-01	-0.1	9.3E-01
ENSMUST00000123299				6.3	2.0E-04	-8.0	1.6E-02	-1.0	2.5E-01	-0.5	8.8E-01
ENSMUST00000131429				6.3	2.9E-04	4.3	2.5E-02	-3.2	1.0E-01	-0.7	5.1E-01
ENSMUST00000159042				6.3	1.4E-03	-2.3	8.7E-02	0.8	2.8E-01	-0.9	5.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000169844				6.3	1.5E-03	4.7	6.1E-05	-2.1	1.5E-02	-0.8	1.2E-01
ENSMUST00000054860				6.3	6.0E-04	5.6	1.1E-03	0.5	6.6E-01	0.1	9.3E-01
ENSMUST00000117567				6.3	1.5E-04	-3.1	7.0E-02	1.3	1.3E-01	-1.6	3.7E-01
ENSMUST00000155154				6.3	6.6E-03	5.6	3.0E-03	-0.5	7.6E-01	-0.8	3.3E-01
ENSMUST00000147074				6.3	2.9E-04	4.5	6.2E-05	0.3	6.3E-01	0.0	9.9E-01
ENSMUST00000161915	zinc finger, DHHC domain containing 4 [Source:MGI Symbol;Acc:MGI:1920131]		Q9D6H5	-0.2	8.9E-01	4.0	6.2E-02	2.9	1.1E-01	-1.2	3.9E-01
ENSMUST00000151134				6.3	4.7E-05	-0.5	7.9E-01	2.9	4.2E-02	-0.8	6.6E-01
ENSMUST00000150674				6.3	8.3E-04	6.9	2.1E-03	0.0	9.9E-01	-1.0	3.0E-01
ENSMUST00000134859				6.3	8.4E-07	5.7	5.2E-04	0.1	9.0E-01	-0.2	7.5E-01
ENSMUST00000187211				6.3	3.7E-06	7.9	1.5E-04	-0.7	6.2E-01	-1.3	9.5E-02
ENSMUST00000190692				6.3	1.1E-04	2.9	3.1E-01	-0.8	7.3E-01	2.2	3.1E-01
ENSMUST00000141634				6.3	2.3E-02	5.6	5.0E-04	-0.5	6.3E-01	0.4	5.8E-01
ENSMUST00000161944				-1.1	1.6E-01	-1.9	5.1E-02	-0.7	3.0E-01	0.1	8.6E-01
ENSMUST00000142072				6.3	3.8E-04	5.4	1.3E-03	-1.3	3.2E-01	-0.7	3.3E-01
ENSMUST00000134535				6.3	3.0E-05	-1.5	8.1E-02	1.3	2.8E-02	0.3	6.5E-01
ENSMUST00000154204				6.3	5.6E-05	6.2	8.9E-02	-0.9	8.1E-01	0.8	7.1E-01
ENSMUST00000181854				6.3	6.3E-04	6.6	1.4E-04	-1.7	1.8E-01	-0.7	2.5E-01
ENSMUST00000182480				6.3	8.0E-06	2.2	2.0E-02	-0.6	4.0E-01	-0.3	6.3E-01
ENSMUST00000161966	nitric oxide synthase 1 (neuronal) adaptor protein [Source:MGI Symbol;Acc:MGI:1917979]	E9PYK5		-1.8	4.5E-02	1.8	8.7E-02	2.5	1.1E-02	-1.2	2.1E-01
ENSMUST00000127901				6.3	2.7E-06	6.1	4.9E-04	-0.8	5.5E-01	-2.1	2.5E-02
ENSMUST00000161972	vomeronasal 2, receptor 7 [Source:MGI Symbol;Acc:MGI:2441693]	E9PYL5		4.5	5.4E-02	1.9	5.0E-01	-0.4	8.8E-01	2.2	3.1E-01
ENSMUST00000186853				6.3	7.9E-05	6.5	2.5E-04	-0.6	6.0E-01	1.3	5.6E-02
ENSMUST00000161976	myelocytomatosis oncogene [Source:MGI Symbol;Acc:MGI:97250]		P01108	-1.0	4.4E-01	2.1	1.8E-01	0.8	5.1E-01	-2.2	1.1E-01
ENSMUST00000126670				6.3	2.6E-04	6.2	4.4E-04	-0.6	6.0E-01	0.5	4.6E-01
ENSMUST00000138297				6.3	3.7E-04	5.7	1.0E-03	-0.8	5.3E-01	0.5	4.7E-01
ENSMUST00000186040				6.3	9.8E-05	7.3	1.3E-04	0.7	5.4E-01	-0.2	7.5E-01
ENSMUST00000161986	glyceronephosphate O-acyltransferase [Source:MGI Symbol;Acc:MGI:1343460]	Q05DV2		1.6	3.6E-01	2.9	1.5E-01	-0.5	7.5E-01	-1.9	2.7E-01
ENSMUST00000189690				6.3	2.9E-04	4.3	7.1E-05	-0.8	2.1E-01	-0.1	8.2E-01
ENSMUST00000161989	protein phosphatase 3, catalytic subunit, beta isoform [Source:MGI Symbol;Acc:MGI:107163]	E9Q6P2		-1.8	6.5E-02	-1.7	3.1E-01	1.7	8.2E-02	1.6	2.9E-01
ENSMUST00000161991	TBC1 domain family, member 4 [Source:MGI Symbol;Acc:MGI:2429660]	E9Q6Q8		4.9	5.3E-02	3.6	2.9E-01	1.3	6.5E-01	2.6	3.3E-01
ENSMUST00000161993	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	E0CY76		0.6	7.6E-01	1.7	5.2E-01	0.9	6.2E-01	-0.2	9.3E-01
ENSMUST00000161995	src homology three (SH3) and cysteine rich domain [Source:MGI Symbol;Acc:MGI:1201400]	F2Z462		3.8	8.5E-02	4.9	9.2E-02	0.8	7.6E-01	-0.2	9.0E-01
ENSMUST00000132162				6.3	4.6E-04	5.9	2.2E-03	-0.8	5.9E-01	-0.2	8.2E-01
ENSMUST00000161729				6.3	1.3E-05	6.2	1.2E-03	-0.2	9.1E-01	-0.3	6.6E-01
ENSMUST00000115977				6.2	2.4E-04	-1.4	3.2E-01	1.2	2.2E-01	-1.9	2.2E-01
ENSMUST00000189286				6.2	1.0E-04	-1.4	3.5E-01	1.3	1.6E-01	-1.1	4.5E-01
ENSMUST00000162006				3.3	1.3E-01	5.5	5.1E-02	0.7	7.8E-01	-1.5	3.2E-01
ENSMUST00000127822				6.2	3.1E-04	6.8	5.4E-03	-0.2	9.3E-01	-0.1	9.4E-01
ENSMUST00000147151				6.2	2.5E-06	4.3	5.8E-05	0.9	1.1E-01	0.0	9.2E-01
ENSMUST00000162023	suppressor of var1, 3-like 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2441711]	M0QWM4		2.2	2.2E-01	2.1	4.2E-01	1.6	4.8E-01	1.7	3.6E-01
ENSMUST00000162030				2.2	6.8E-02	3.3	3.0E-02	0.8	5.4E-01	-0.3	7.3E-01
ENSMUST00000174248				6.2	3.6E-04	-1.3	7.0E-02	-0.3	5.5E-01	-0.6	3.8E-01
ENSMUST00000192882				6.2	3.1E-04	-3.7	7.0E-03	0.0	9.6E-01	0.1	9.6E-01
ENSMUST00000182420				6.2	2.4E-04	6.3	5.8E-04	-0.5	7.3E-01	-0.8	2.6E-01
ENSMUST00000162036	arginine/serine-rich coiled-coil 1 [Source:MGI Symbol;Acc:MGI:1914130]		Q9DBU6	-0.5	7.7E-01	-3.9	1.3E-01	-2.3	1.1E-01	1.2	6.4E-01
ENSMUST00000162037				3.9	1.4E-01	2.9	3.3E-01	-0.2	9.4E-01	0.7	7.1E-01
ENSMUST00000128479				6.2	7.6E-04	-1.4	1.2E-01	0.0	9.6E-01	-2.2	3.8E-02
ENSMUST00000142078				6.2	2.6E-03	3.6	8.1E-03	0.3	7.6E-01	1.7	3.9E-02
ENSMUST00000137300				6.2	3.2E-04	-0.6	6.4E-01	0.6	5.3E-01	-3.4	4.7E-02
ENSMUST00000142225				6.2	4.6E-05	2.0	3.8E-02	-0.5	4.9E-01	-0.1	9.3E-01
ENSMUST00000156496				6.2	1.8E-03	6.7	1.1E-04	-0.5	6.3E-01	-1.0	1.1E-01
ENSMUST00000134923				6.2	9.8E-05	-4.2	5.8E-02	1.5	1.3E-01	-0.8	7.1E-01
ENSMUST00000135594				6.2	1.6E-04	6.0	6.5E-03	-0.7	6.9E-01	-0.1	9.6E-01
ENSMUST00000173563				6.2	2.8E-04	3.8	1.9E-02	-1.8	2.0E-01	-1.1	2.8E-01
ENSMUST00000189546				6.2	1.4E-04	6.9	3.3E-04	-0.5	7.1E-01	-1.5	6.6E-02
ENSMUST00000125889				6.2	4.4E-04	5.9	3.6E-03	-0.4	7.8E-01	0.1	9.4E-01
ENSMUST00000159506				6.2	8.4E-05	1.1	9.4E-02	0.7	1.2E-01	-1.5	2.1E-02
ENSMUST00000162057	claudin domain containing 1 [Source:MGI Symbol;Acc:MGI:2447860]		Q9CQX5	1.1	6.0E-01	4.3	1.1E-01	1.9	3.8E-01	-1.2	5.8E-01
ENSMUST00000162064				1.1	2.2E-01	1.8	1.7E-01	1.0	2.9E-01	0.3	7.6E-01
ENSMUST00000160668				6.2	2.6E-04	-2.8	4.8E-02	0.0	9.4E-01	-2.6	1.1E-01
ENSMUST00000162073	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase) [Source:MGI Symbol;Acc:MGI:1924753]	E0CZF3		-0.6	7.6E-01	2.2	3.3E-01	0.9	6.6E-01	-1.9	3.1E-01
ENSMUST00000137495				6.2	8.5E-05	3.6	5.6E-03	-4.6	3.0E-03	-0.1	9.0E-01
ENSMUST00000122007				6.2	1.7E-03	5.4	1.9E-02	2.7	1.6E-01	0.8	5.2E-01
ENSMUST00000142568				6.2	5.3E-04	4.6	3.6E-02	-0.7	7.4E-01	1.6	2.2E-01
ENSMUST00000162086	ir cross-complementing rodent repair deficiency, complementation group 6 like 2 [Source:MGI Symbol;Acc:M	F7DFI4		1.0	1.9E-01	0.0	9.9E-01	-1.0	1.8E-01	0.1	9.4E-01
ENSMUST00000182194				6.2	6.5E-06	-12.3	2.9E-06	-1.0	6.0E-03	-0.7	5.7E-01
ENSMUST00000162088				2.6	3.7E-01	0.5	9.0E-01	0.3	9.3E-01	2.4	4.5E-01
ENSMUST00000097731				6.2	1.5E-04	6.3	3.5E-04	-0.5	7.0E-01	-0.7	3.0E-01
ENSMUST00000162096	2'-5' oligoadenylate synthetase 1G [Source:MGI Symbol;Acc:MGI:97429]	Q05BJ7		-2.9	1.1E-01	-0.6	7.6E-01	0.4	7.6E-01	-1.9	3.4E-01
ENSMUST00000162099	inosine 5'-phosphate dehydrogenase 1 [Source:MGI Symbol;Acc:MGI:96567]		P50096	-2.5	4.1E-02	-1.2	4.5E-01	0.8	4.1E-01	-0.6	7.0E-01
ENSMUST00000132166				6.2	1.9E-03	5.6	3.2E-03	-0.7	6.6E-01	-0.2	8.5E-01
ENSMUST00000162106	E2F-associated phosphoprotein [Source:MGI Symbol;Acc:MGI:1913516]	E0CYG0		-2.6	1.0E-01	-5.6	1.1E-02	-3.1	5.7E-03	-0.1	9.6E-01
ENSMUST00000162109	protein phosphatase 4, regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1917601]	E0CXK8		-6.3	8.5E-02	4.8	2.2E-01	6.7	6.5E-02	-4.4	2.1E-01
ENSMUST00000139281				6.2	1.2E-04	5.9	9.0E-06	0.5	4.6E-01	-0.8	8.7E-02
ENSMUST00000162112	gene regulated by estrogen in breast cancer protein [Source:MGI Symbol;Acc:MGI:2149712]		Q3UHK3	6.3	1.0E-01	6.8	9.4E-02	-0.9	8.2E-01	-1.4	5.7E-01
ENSMUST00000165907				6.2	7.8E-05	2.4	3.3E-03	-0.1	9.2E-01	0.4	4.0E-01
ENSMUST00000162116	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	Q3TDW1	P97808	-0.2	9.3E-01	-5.6	5.9E-02	-6.2	4.0E-03	-0.8	7.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000162118	H3 histone, family 3A [Source:MGI Symbol;Acc:MGI:1097686]	E0CYR7		-0.4	8.2E-01	-3.3	9.8E-02	-3.1	3.5E-02	-0.2	9.3E-01
ENSMUST00000162127	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	F6TS96		0.8	7.8E-01	-3.4	3.4E-01	-4.5	4.8E-02	-0.4	9.2E-01
ENSMUST00000190130				6.2	5.1E-03	-1.7	4.4E-01	3.1	4.1E-02	-0.7	7.6E-01
ENSMUST00000124866				6.2	1.9E-04	4.4	7.0E-03	-1.5	3.1E-01	0.0	9.5E-01
ENSMUST00000162138	programmed cell death 10 [Source:MGI Symbol;Acc:MGI:1928396]	E0CY82		-1.2	6.0E-01	2.8	5.0E-01	4.9	1.6E-01	0.9	7.7E-01
ENSMUST00000163020				6.2	2.8E-04	6.4	1.1E-03	0.0	9.7E-01	-0.5	5.1E-01
ENSMUST00000182357				6.2	1.8E-05	6.9	3.0E-05	-2.1	5.2E-02	0.1	7.8E-01
ENSMUST00000150215				6.2	3.4E-05	6.9	3.8E-04	-1.0	5.0E-01	-1.0	2.0E-01
ENSMUST00000188126				6.2	1.6E-03	5.0	1.7E-04	0.9	2.5E-01	0.0	9.7E-01
ENSMUST00000162147	protein kinase, cGMP-dependent, type II [Source:MGI Symbol;Acc:MGI:108173]	Q3TMJ2		3.5	4.9E-02	0.4	7.1E-01	-6.4	1.4E-03	-3.3	1.4E-02
ENSMUST00000124688				6.2	2.4E-05	4.9	2.5E-03	-1.4	3.1E-01	0.6	4.5E-01
ENSMUST00000130350				6.2	1.6E-05	-4.6	4.4E-03	-0.9	2.3E-01	0.4	7.7E-01
ENSMUST00000162155	calcium channel, voltage-dependent, alpha 1I subunit [Source:MGI Symbol;Acc:MGI:2178051]	E0CXK2		4.7	5.4E-02	6.2	3.1E-02	-0.3	9.0E-01	-1.8	2.3E-01
ENSMUST00000162156	protein inhibitor of activated STAT 3 [Source:MGI Symbol;Acc:MGI:1913126]	H3BLM4		1.3	2.2E-01	0.9	5.0E-01	0.3	7.5E-01	0.7	5.3E-01
ENSMUST00000153923				6.2	7.4E-04	4.9	6.9E-03	-0.5	6.9E-01	0.3	7.4E-01
ENSMUST00000162159	leucine rich repeat containing 9 [Source:MGI Symbol;Acc:MGI:1925507]		Q8CDN9	3.9	8.6E-02	5.7	3.2E-02	-0.3	9.1E-01	-2.1	1.6E-01
ENSMUST00000119613				6.2	5.8E-05	-13.4	1.3E-02	-2.1	7.8E-02	-0.6	9.0E-01
ENSMUST00000162170	PILR alpha associated neural protein [Source:MGI Symbol;Acc:MGI:2441908]		Q6P1B3	1.2	9.6E-02	2.3	1.7E-02	-0.3	6.9E-01	-1.3	8.0E-02
ENSMUST00000140134				6.2	9.6E-06	5.0	1.1E-03	-0.5	6.5E-01	0.8	2.7E-01
ENSMUST00000118330				6.2	1.1E-03	-3.8	3.0E-02	0.4	5.9E-01	-0.8	6.4E-01
ENSMUST00000122866				6.2	8.5E-05	4.9	1.1E-04	-0.6	4.2E-01	0.3	5.4E-01
ENSMUST00000162183	asparagine-linked glycosylation 12 (alpha-1,6-mannosyltransferase) [Source:MGI Symbol;Acc:MGI:2385025]		Q8VDB2	-2.8	9.2E-02	1.6	4.0E-01	1.2	4.5E-01	-3.1	7.2E-02
ENSMUST00000164469				6.2	2.3E-04	6.1	2.0E-03	-0.4	8.1E-01	0.8	3.6E-01
ENSMUST00000155089				6.2	4.0E-05	4.1	6.4E-03	-1.1	3.9E-01	-0.6	4.6E-01
ENSMUST00000162193				-0.2	7.2E-01	0.7	3.6E-01	0.2	7.1E-01	-0.7	3.3E-01
ENSMUST00000157032				6.2	6.4E-05	5.2	3.2E-04	-0.5	5.9E-01	-0.4	5.2E-01
ENSMUST00000189303				6.2	6.3E-03	4.4	1.1E-02	-1.0	4.8E-01	0.4	6.5E-01
ENSMUST00000190494				6.2	2.7E-04	3.5	1.0E-02	-0.7	5.1E-01	-0.6	4.1E-01
ENSMUST00000144383				6.2	9.9E-06	6.7	1.9E-03	-3.3	1.1E-01	0.3	7.3E-01
ENSMUST00000162207	zinc finger protein 263 [Source:MGI Symbol;Acc:MGI:1921370]	E9PXW0		-1.5	2.6E-01	-0.5	7.6E-01	1.0	3.8E-01	0.0	9.8E-01
ENSMUST00000189249				6.2	3.9E-05	7.0	2.4E-03	-0.1	9.3E-01	0.8	3.5E-01
ENSMUST00000162219	ring finger protein (C3H2C3 type) 6 [Source:MGI Symbol;Acc:MGI:1921382]	F6VG71		0.4	8.5E-01	-1.0	6.4E-01	-2.5	1.5E-01	-1.0	6.6E-01
ENSMUST00000136855				6.2	1.7E-04	4.1	1.3E-01	-0.8	7.5E-01	2.0	2.6E-01
ENSMUST00000155092				6.2	9.0E-04	6.5	5.7E-04	0.2	8.9E-01	-1.1	1.5E-01
ENSMUST00000131881				6.2	1.1E-03	3.9	5.1E-04	0.4	5.5E-01	0.5	3.9E-01
ENSMUST00000136556				6.2	5.8E-06	6.9	5.0E-04	-0.8	5.3E-01	0.7	3.3E-01
ENSMUST00000133357				6.2	4.6E-05	5.6	8.1E-04	0.4	7.0E-01	0.3	6.1E-01
ENSMUST00000135587				6.2	1.2E-04	-1.4	2.1E-01	-1.0	1.7E-01	-3.4	2.3E-02
ENSMUST00000162237	splicing factor 1 [Source:MGI Symbol;Acc:MGI:1095403]	F6SRV1		-1.2	3.6E-01	-2.0	2.6E-01	0.0	9.7E-01	0.8	6.6E-01
ENSMUST00000190205				6.2	3.8E-04	2.7	3.7E-02	-0.4	6.7E-01	0.2	8.6E-01
ENSMUST00000162241				-0.2	8.2E-01	-1.8	3.1E-01	-0.5	6.1E-01	1.0	5.4E-01
ENSMUST00000136416				6.2	4.3E-04	3.8	4.1E-03	0.2	7.9E-01	-1.3	1.4E-01
ENSMUST00000129103				6.2	2.5E-04	-2.0	8.1E-02	-0.4	5.9E-01	-1.8	1.6E-01
ENSMUST00000162245	stromal antigen 3 [Source:MGI Symbol;Acc:MGI:1355311]		O70576	-3.1	2.3E-01	1.7	5.1E-01	2.3	2.8E-01	-2.4	3.6E-01
ENSMUST00000162247	alkB, alkylation repair homolog 1 (E. coli) [Source:MGI Symbol;Acc:MGI:2384034]	E0CYA7		-1.8	4.5E-01	2.3	5.5E-01	4.3	1.8E-01	0.3	9.3E-01
ENSMUST00000162249				1.7	1.7E-01	3.1	3.9E-02	-0.3	8.1E-01	-1.7	1.5E-01
ENSMUST00000134038				6.2	4.5E-06	-8.6	4.9E-04	0.3	5.6E-01	-0.8	6.7E-01
ENSMUST00000080726				6.2	3.6E-04	7.2	1.2E-04	-0.7	5.9E-01	-0.2	7.2E-01
ENSMUST00000162256				1.2	2.6E-01	2.8	4.4E-02	0.6	5.9E-01	-1.0	3.5E-01
ENSMUST00000140874				6.2	2.8E-04	-5.9	1.5E-02	1.2	1.2E-01	1.4	5.1E-01
ENSMUST00000162272	protein phosphatase 4, regulatory subunit 1 [Source:MGI Symbol;Acc:MGI:1917601]	F6TLH3		-0.2	8.4E-01	2.2	8.7E-02	2.5	3.0E-02	0.1	9.2E-01
ENSMUST00000126247				6.2	2.6E-04	8.1	7.4E-05	-0.9	4.9E-01	0.9	1.5E-01
ENSMUST00000186839				6.2	3.2E-03	1.8	4.6E-02	-1.6	4.6E-02	0.2	7.9E-01
ENSMUST00000046121				6.2	2.8E-05	-4.9	7.6E-02	-0.4	7.2E-01	-0.5	8.7E-01
ENSMUST00000143883				6.2	4.6E-04	9.7	3.5E-04	0.9	6.2E-01	0.6	4.0E-01
ENSMUST00000146814				6.2	1.4E-04	6.5	1.9E-04	-0.5	6.5E-01	-0.6	3.5E-01
ENSMUST00000180787				6.2	9.0E-05	-2.6	7.4E-02	0.7	3.2E-01	-0.6	6.6E-01
ENSMUST00000117239				6.2	9.0E-05	5.6	1.5E-05	0.3	6.9E-01	-0.3	5.1E-01
ENSMUST00000149059				6.2	1.1E-04	8.2	3.4E-05	-2.0	1.5E-01	0.4	4.8E-01
ENSMUST00000156407				6.2	5.1E-05	3.3	3.7E-02	0.0	9.9E-01	0.4	6.3E-01
ENSMUST00000177305				6.2	3.5E-06	-1.5	4.4E-02	-0.5	2.6E-01	-0.9	2.0E-01
ENSMUST00000162305				-2.8	5.6E-02	-1.1	4.7E-01	0.7	5.3E-01	-0.9	5.5E-01
ENSMUST00000146990				6.2	1.5E-03	4.3	6.8E-03	0.3	7.9E-01	0.5	5.7E-01
ENSMUST00000147779				6.2	3.0E-04	3.9	3.0E-02	0.7	6.2E-01	2.0	7.6E-02
ENSMUST00000162312				-0.4	8.4E-01	2.4	3.2E-01	2.8	2.2E-01	-0.1	9.7E-01
ENSMUST00000150693				6.2	1.7E-03	4.6	4.8E-04	0.6	4.8E-01	-0.3	6.7E-01
ENSMUST00000191371				6.2	3.3E-05	8.0	1.6E-05	-0.5	5.8E-01	0.2	6.9E-01
ENSMUST00000126606				6.2	4.2E-05	-3.5	2.0E-02	-0.2	7.3E-01	-0.7	6.1E-01
ENSMUST00000154467				6.2	4.7E-07	4.0	2.6E-03	-0.7	4.6E-01	-0.1	9.0E-01
ENSMUST00000174049				6.2	8.3E-06	4.5	1.0E-03	-0.4	6.4E-01	-0.6	4.5E-01
ENSMUST00000151404				6.2	1.7E-04	6.8	3.8E-05	0.6	4.8E-01	0.5	3.6E-01
ENSMUST00000161225				6.2	8.6E-04	-4.1	8.6E-02	0.8	4.5E-01	0.1	9.6E-01
ENSMUST00000162355	ring finger protein 123 [Source:MGI Symbol;Acc:MGI:2148796]		Q5XPI3	-0.7	1.9E-01	0.2	8.3E-01	1.2	2.9E-02	0.4	5.6E-01
ENSMUST00000162359	homeodomain interacting protein kinase 2 [Source:MGI Symbol;Acc:MGI:1314872]	Q5D0E9	Q9QZR5	0.3	8.1E-01	-0.3	8.8E-01	0.5	6.3E-01	1.1	5.1E-01
ENSMUST00000144253				6.2	7.1E-05	-5.0	1.1E-03	-0.5	2.5E-01	-0.5	6.9E-01
ENSMUST00000162364	MOB family member 4, phocein [Source:MGI Symbol;Acc:MGI:104899]		Q6PEB6	-0.3	5.6E-01	-0.5	4.4E-01	0.0	9.3E-01	0.2	6.7E-01
ENSMUST00000148355				6.2	6.3E-04	-2.5	5.9E-02	0.5	4.1E-01	-0.5	7.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000134225				6.2	1.7E-04	3.2	1.6E-03	-0.2	7.5E-01	0.2	7.0E-01
ENSMUST00000162372	solute carrier family 30 (zinc transporter), member 9 [Source:MGI Symbol;Acc:MGI:1923690]		Q5IRJ6	-0.9	6.3E-02	-0.6	2.8E-01	0.1	8.5E-01	-0.2	7.2E-01
ENSMUST00000184507				6.2	3.6E-04	5.3	9.7E-04	-1.3	2.9E-01	0.0	1.0E+00
ENSMUST00000118582				6.2	7.1E-04	-4.1	6.5E-03	-0.9	1.4E-01	-1.7	2.4E-01
ENSMUST00000162384	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 [Source:MGI Symbol;Acc:MGI:1921601]	E0CXN3		2.5	5.1E-02	3.0	2.0E-02	-1.4	2.0E-01	-1.9	7.9E-02
ENSMUST00000164817				6.2	5.2E-06	6.2	8.8E-04	-0.6	6.6E-01	-0.4	6.0E-01
ENSMUST00000162390				-1.0	4.1E-01	2.3	2.2E-01	2.6	1.2E-01	-0.7	5.9E-01
ENSMUST00000162392				-1.9	4.8E-02	-1.3	2.8E-01	0.6	3.9E-01	0.0	9.7E-01
ENSMUST00000162393	predicted gene, 28042 [Source:MGI Symbol;Acc:MGI:5547778]	E0CXG8		-0.1	9.8E-01	5.4	1.7E-01	2.9	4.2E-01	-2.6	3.2E-01
ENSMUST00000170406				6.2	2.3E-04	-2.7	9.1E-02	1.9	3.4E-02	-0.3	8.6E-01
ENSMUST00000051493				6.2	2.1E-04	6.0	1.7E-03	-1.8	2.7E-01	0.9	3.2E-01
ENSMUST00000140658				6.2	1.4E-05	1.2	8.8E-02	-0.4	5.1E-01	0.1	8.2E-01
ENSMUST00000151597				6.2	6.3E-04	6.8	1.2E-04	-0.5	6.7E-01	-2.1	7.9E-03
ENSMUST00000156602				6.2	2.1E-06	-5.1	4.6E-03	-1.0	1.8E-01	-1.6	3.4E-01
ENSMUST00000182903				6.2	9.7E-05	3.4	6.2E-02	-1.3	4.2E-01	-0.2	8.5E-01
ENSMUST00000117522				6.2	2.2E-04	-3.9	1.6E-04	0.6	8.4E-02	-0.1	9.0E-01
ENSMUST00000162418				-0.8	3.4E-01	-0.5	5.6E-01	-0.4	5.1E-01	-0.7	4.7E-01
ENSMUST00000171502				6.2	1.6E-04	7.2	8.1E-04	-2.8	1.5E-01	1.3	1.5E-01
ENSMUST00000118281				6.2	6.4E-04	3.5	3.8E-02	0.1	9.7E-01	-0.1	8.9E-01
ENSMUST00000120431				6.2	3.4E-04	-2.4	6.8E-02	-0.3	5.9E-01	-0.5	6.8E-01
ENSMUST00000141255				6.2	6.7E-04	7.7	3.7E-04	-0.7	6.4E-01	-0.1	8.9E-01
ENSMUST00000123379				6.2	1.6E-05	-7.8	2.6E-04	-0.9	6.0E-02	-0.7	6.3E-01
ENSMUST00000160655				6.2	3.9E-05	6.3	4.6E-04	-0.5	7.0E-01	-0.4	5.3E-01
ENSMUST00000125595				6.2	3.2E-06	7.9	1.1E-04	-0.2	9.0E-01	-0.2	7.8E-01
ENSMUST00000162435	staufen (RNA binding protein) homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1352508]		Q8CJ67	3.9	5.3E-02	3.6	6.2E-02	-2.0	3.2E-01	-1.6	2.3E-01
ENSMUST00000131667				6.2	3.1E-04	3.5	2.6E-03	-0.2	7.8E-01	-0.4	4.9E-01
ENSMUST00000133907				6.2	5.3E-05	8.3	9.9E-05	-0.8	5.6E-01	-0.8	2.0E-01
ENSMUST00000040649				6.2	6.6E-04	2.0	1.1E-01	-3.3	2.0E-02	-0.7	4.5E-01
ENSMUST00000162445				-1.3	2.2E-01	0.5	7.2E-01	1.0	3.0E-01	-0.8	5.5E-01
ENSMUST00000162455				-2.1	7.2E-02	-0.4	7.2E-01	0.7	3.8E-01	-0.9	4.8E-01
ENSMUST00000162456	par-3 family cell polarity regulator [Source:MGI Symbol;Acc:MGI:2135608]			3.0	1.2E-01	7.1	2.7E-03	-0.5	7.9E-01	-4.6	4.1E-03
ENSMUST00000162460	nuclear transcription factor-Y alpha [Source:MGI Symbol;Acc:MGI:97316]	Q3UP82	P23708	-5.0	6.1E-02	-5.0	1.4E-01	0.1	9.7E-01	0.1	9.8E-01
ENSMUST00000186840				6.2	7.0E-04	-5.1	7.4E-04	0.7	1.1E-01	-0.8	4.8E-01
ENSMUST00000123968				6.2	5.4E-04	6.2	5.6E-04	-0.5	7.3E-01	-0.3	6.8E-01
ENSMUST00000126652				6.2	2.1E-03	5.6	1.2E-03	-0.6	6.3E-01	0.6	3.9E-01
ENSMUST00000162466	NEDD8 activating enzyme E1 subunit 1 [Source:MGI Symbol;Acc:MGI:2384561]	E0CZE0		-3.6	1.7E-01	-5.1	1.0E-01	-2.5	1.1E-01	-1.0	7.5E-01
ENSMUST00000134292				6.2	4.3E-03	7.2	2.2E-05	-1.2	2.5E-01	-0.1	8.2E-01
ENSMUST00000162479	GTP-binding protein 8 (putative) [Source:MGI Symbol;Acc:MGI:1913317]	F6SMJ7		2.6	1.2E-01	2.4	8.1E-02	-3.6	2.4E-02	-3.4	1.8E-02
ENSMUST00000162488	DENN/MADD domain containing 3 [Source:MGI Symbol;Acc:MGI:2146009]	F7B6S5		5.2	3.7E-02	2.5	3.9E-01	-0.6	8.3E-01	2.2	3.4E-01
ENSMUST00000132058				6.2	1.3E-04	4.2	3.3E-02	-3.6	7.2E-02	-1.2	3.1E-01
ENSMUST00000162492	RAB6A GEF complex partner 1 [Source:MGI Symbol;Acc:MGI:1924893]	F6S7U1		-1.8	1.3E-01	0.5	7.0E-01	-0.3	7.7E-01	-2.5	6.7E-02
ENSMUST00000118505				6.2	4.1E-04	2.6	2.4E-01	-5.6	3.6E-02	0.6	7.0E-01
ENSMUST00000156251				6.2	1.0E-03	-1.6	4.5E-02	-0.4	3.8E-01	-0.8	3.0E-01
ENSMUST00000194593				6.2	4.8E-04	4.3	7.2E-05	0.0	9.7E-01	-0.3	4.9E-01
ENSMUST00000101214				6.2	2.3E-04	-4.9	7.7E-03	-1.5	4.6E-02	0.8	6.0E-01
ENSMUST00000162512	GTP-binding protein 8 (putative) [Source:MGI Symbol;Acc:MGI:1913317]		Q9CY28	0.0	9.2E-01	0.7	2.9E-01	0.7	1.6E-01	0.0	9.4E-01
ENSMUST00000121086				6.2	2.3E-04	6.2	2.1E-04	-0.5	6.5E-01	-0.7	2.7E-01
ENSMUST00000125630				6.2	2.0E-03	7.4	1.6E-04	-0.7	6.1E-01	0.5	4.4E-01
ENSMUST00000131082				6.2	1.1E-06	5.3	4.4E-04	-0.9	4.0E-01	-0.1	9.0E-01
ENSMUST00000138339				6.2	1.8E-04	4.3	1.3E-02	0.1	9.5E-01	-0.4	6.3E-01
ENSMUST00000142809				6.2	8.1E-07	5.9	2.3E-03	-0.8	6.2E-01	-0.9	3.5E-01
ENSMUST00000143871				6.2	3.1E-02	5.7	9.1E-04	-0.5	6.7E-01	-2.7	1.2E-02
ENSMUST00000162529	SID1 transmembrane family, member 2 [Source:MGI Symbol;Acc:MGI:2446134]	F7DF36		-2.2	1.4E-01	0.3	8.7E-01	1.7	2.0E-01	-0.7	6.8E-01
ENSMUST00000162530				-2.0	5.2E-02	-1.9	2.0E-01	0.0	1.0E+00	-0.1	9.1E-01
ENSMUST00000162534	endoplasmic reticulum metallopeptidase 1 [Source:MGI Symbol;Acc:MGI:106250]	F6TQS9		-2.2	1.2E-01	-1.4	4.3E-01	0.6	5.3E-01	-0.1	9.4E-01
ENSMUST00000146115				6.2	6.4E-06	8.9	4.0E-05	-0.8	5.2E-01	0.8	1.7E-01
ENSMUST00000162538	cytokine induced apoptosis inhibitor 1 [Source:MGI Symbol;Acc:MGI:1922083]		Q8WTY4	0.6	2.5E-01	0.3	6.6E-01	0.3	5.8E-01	0.6	3.8E-01
ENSMUST00000162540	RIKEN cDNA 1700112E06 gene [Source:MGI Symbol;Acc:MGI:1923883]	E0CY73		1.1	1.6E-01	1.0	2.4E-01	-1.5	6.6E-02	-1.3	1.2E-01
ENSMUST00000190893				6.2	5.8E-06	-3.2	1.0E-01	0.6	5.5E-01	0.1	9.4E-01
ENSMUST00000162543	transmembrane protein 33 [Source:MGI Symbol;Acc:MGI:1915128]	Q9CZM3		-3.3	5.8E-02	-5.6	1.5E-02	-2.7	1.3E-02	-0.3	9.0E-01
ENSMUST00000050706				6.2	2.8E-04	6.6	1.9E-04	-0.6	5.9E-01	-1.0	1.3E-01
ENSMUST00000118082				6.2	3.5E-05	5.1	1.9E-02	0.0	9.8E-01	1.0	3.6E-01
ENSMUST00000159319				6.2	5.4E-05	3.1	5.1E-02	6.7	2.6E-04	-0.3	8.1E-01
ENSMUST00000162544				6.2	1.6E-04	3.9	2.0E-02	-0.4	7.8E-01	-0.6	6.1E-01
ENSMUST00000134596				6.2	2.1E-05	-5.3	1.0E-03	-0.5	3.1E-01	-0.1	9.4E-01
ENSMUST00000162564	UMAP1-MVP12 associated (UMA) domain containing 1 [Source:MGI Symbol;Acc:MGI:3840148]	E0CZ38		-1.4	3.5E-01	-2.5	3.6E-01	0.7	5.9E-01	1.8	4.9E-01
ENSMUST00000087486				6.2	2.2E-02	-5.8	1.5E-04	0.6	1.1E-01	-0.9	3.8E-01
ENSMUST00000183184				6.2	8.2E-05	3.7	5.9E-04	-0.9	2.0E-01	-0.1	8.0E-01
ENSMUST00000162573				-0.8	5.1E-01	1.1	3.5E-01	-0.8	4.4E-01	-2.6	4.1E-02
ENSMUST00000183527				6.2	5.4E-04	5.0	6.9E-05	0.3	6.8E-01	0.3	5.8E-01
ENSMUST00000132895				6.2	1.3E-03	7.5	4.1E-05	-0.5	6.3E-01	-1.9	9.8E-03
ENSMUST00000122236				6.2	2.2E-04	2.5	5.9E-01	9.8	9.3E-03	-1.6	7.1E-01
ENSMUST00000126796				6.2	1.6E-05	2.5	9.1E-04	-5.5	5.0E-05	-0.8	1.0E-01
ENSMUST00000133164				6.2	8.3E-04	7.1	1.4E-04	-0.6	6.5E-01	0.3	6.7E-01
ENSMUST00000162592	zinc finger protein 27 [Source:MGI Symbol;Acc:MGI:99174]		P10077	3.7	1.0E-01	2.4	2.6E-01	-2.1	3.6E-01	-0.8	6.4E-01
ENSMUST00000162593	ubinuclein 2 [Source:MGI Symbol;Acc:MGI:2444236]	F6TB64		2.3	1.1E-01	1.3	5.2E-01	0.0	9.8E-01	1.0	5.7E-01
ENSMUST00000190446				6.2	2.1E-03	-7.2	3.7E-04	0.0	9.5E-01	-0.3	8.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000117226				6.2	2.0E-04	5.3	2.3E-03	-0.5	7.2E-01	-0.2	8.5E-01
ENSMUST00000160140				6.2	3.1E-04	-1.0	1.3E-01	-0.4	3.7E-01	-4.4	4.3E-04
ENSMUST00000134204				6.2	6.8E-03	-4.3	6.3E-02	-0.1	9.5E-01	1.2	5.7E-01
ENSMUST00000162617	TBC1 domain family, member 4 [Source:MGI Symbol;Acc:MGI:2429660]	E0CX53		2.6	1.6E-01	0.7	5.2E-01	-5.5	3.3E-03	-3.6	2.3E-02
ENSMUST00000162618	apoptotic peptidase activating factor 1 [Source:MGI Symbol;Acc:MGI:1306796]	G3XA09		3.9	5.1E-02	3.6	1.9E-01	1.9	3.6E-01	2.1	3.5E-01
ENSMUST00000162624	transmembrane BAX inhibitor motif containing 6 [Source:MGI Symbol;Acc:MGI:99682]	E0CXR0		-2.5	4.5E-02	-2.1	2.0E-01	0.4	6.7E-01	-0.1	9.5E-01
ENSMUST00000142238				6.2	1.1E-04	-3.6	2.5E-02	1.2	9.7E-02	-0.8	6.0E-01
ENSMUST00000168753				6.2	4.3E-03	5.7	5.1E-04	-1.5	2.1E-01	0.0	9.9E-01
ENSMUST00000143953				6.2	1.8E-03	5.4	3.6E-04	-0.7	4.9E-01	-0.4	5.6E-01
ENSMUST00000170684				6.2	2.0E-03	-1.1	9.5E-02	1.2	9.8E-03	-0.6	3.3E-01
ENSMUST00000191174				6.2	2.2E-04	6.5	4.8E-04	-0.6	6.7E-01	-0.6	3.8E-01
ENSMUST00000162648	KIF1 binding protein [Source:MGI Symbol;Acc:MGI:1919570]	F7DEX6		-0.3	8.8E-01	-1.0	6.6E-01	-1.2	5.0E-01	-0.6	7.9E-01
ENSMUST00000123897				6.2	3.6E-06	-5.5	8.7E-03	0.1	9.0E-01	-0.9	6.5E-01
ENSMUST00000189595				6.2	9.8E-06	6.3	1.5E-04	-0.3	7.6E-01	-0.4	5.0E-01
ENSMUST00000143323				6.2	3.9E-04	10.0	2.1E-04	0.4	8.2E-01	0.7	3.6E-01
ENSMUST00000162671	FYVE, RhoGEF and PH domain containing 4 [Source:MGI Symbol;Acc:MGI:2183747]		Q91ZT5	-6.0	1.7E-01	-8.0	1.5E-01	-3.1	1.5E-01	-1.2	8.4E-01
ENSMUST00000162680	NADPH dependent diflavin oxidoreductase 1 [Source:MGI Symbol;Acc:MGI:1926047]	E0CX27		1.0	7.3E-01	2.0	5.2E-01	-0.5	8.6E-01	-1.6	5.6E-01
ENSMUST00000152355				6.2	5.2E-06	-4.9	6.8E-03	-0.2	8.0E-01	-0.9	5.8E-01
ENSMUST00000162684				-1.2	2.4E-01	0.5	6.6E-01	0.7	3.9E-01	-1.0	4.0E-01
ENSMUST00000162688				-2.2	4.7E-02	-3.4	6.5E-02	0.3	7.0E-01	1.5	3.6E-01
ENSMUST00000188606				6.2	1.2E-04	7.2	1.4E-04	-1.1	3.7E-01	0.4	5.1E-01
ENSMUST00000118040				6.2	3.1E-04	4.3	1.9E-03	-4.2	6.2E-03	-4.3	8.3E-04
ENSMUST00000119574				6.2	2.8E-04	8.6	3.0E-04	-0.8	6.2E-01	0.9	2.4E-01
ENSMUST00000174515				6.2	1.0E-03	-5.1	2.6E-03	0.7	2.5E-01	-1.8	2.6E-01
ENSMUST00000127884				6.2	1.2E-04	5.5	5.3E-03	1.5	3.3E-01	0.1	8.8E-01
ENSMUST00000162718				0.0	9.9E-01	1.2	5.3E-01	-0.4	7.8E-01	-1.6	3.1E-01
ENSMUST00000130805				6.2	3.3E-05	3.5	1.8E-03	-1.2	1.7E-01	0.4	5.6E-01
ENSMUST00000138899				6.2	3.3E-04	6.0	5.1E-03	-0.6	7.2E-01	-0.7	4.6E-01
ENSMUST00000142803				6.2	8.9E-05	-1.6	9.9E-02	1.0	1.0E-01	-0.3	7.3E-01
ENSMUST00000162731	zinc finger protein 579 [Source:MGI Symbol;Acc:MGI:1915740]		Q80VM4	1.1	3.9E-01	-1.2	5.5E-01	1.0	5.4E-01	3.3	5.8E-02
ENSMUST00000162733	FXYD domain-containing ion transport regulator 5 [Source:MGI Symbol;Acc:MGI:1201785]	E0CXN1		0.0	9.7E-01	-0.7	6.3E-01	-0.1	9.0E-01	0.6	6.4E-01
ENSMUST00000151801				6.2	5.5E-04	5.8	1.6E-03	0.2	8.5E-01	0.6	4.7E-01
ENSMUST00000124257				6.2	1.1E-04	-2.5	2.9E-01	1.3	3.7E-01	-0.9	6.9E-01
ENSMUST00000121549				6.2	8.6E-05	-1.2	1.1E-01	0.2	6.2E-01	-0.5	5.1E-01
ENSMUST00000143134				6.2	9.2E-04	5.6	8.6E-04	-0.9	4.6E-01	0.1	9.3E-01
ENSMUST00000149541				6.2	6.4E-04	3.0	1.5E-03	0.1	8.3E-01	-0.6	3.3E-01
ENSMUST00000162942				6.2	7.7E-05	3.7	1.3E-01	0.0	1.0E+00	2.3	1.5E-01
ENSMUST00000193093				6.2	5.5E-06	3.6	1.1E-02	0.1	9.1E-01	0.5	5.5E-01
ENSMUST00000162760				1.0	3.6E-01	2.8	5.5E-02	0.7	5.3E-01	-1.1	3.2E-01
ENSMUST00000180112				6.2	2.8E-02	6.0	3.5E-03	0.5	7.3E-01	0.1	9.4E-01
ENSMUST00000195195				6.2	7.3E-03	4.6	2.1E-03	-1.3	2.4E-01	-1.1	1.5E-01
ENSMUST00000176837				6.2	2.3E-02	5.2	2.0E-03	-1.0	4.3E-01	-0.1	8.9E-01
ENSMUST00000181698				6.2	2.8E-05	-2.0	1.0E-01	0.4	6.0E-01	-1.4	2.5E-01
ENSMUST00000189537				6.2	3.6E-04	6.0	1.6E-04	-1.3	2.5E-01	-0.4	5.7E-01
ENSMUST00000098650				6.2	1.0E-04	6.3	1.8E-04	-1.2	2.7E-01	0.8	2.3E-01
ENSMUST00000142457				6.2	1.8E-02	7.1	6.6E-05	-0.6	6.1E-01	-0.9	1.6E-01
ENSMUST00000122355				6.2	1.0E-03	4.9	4.8E-03	-0.6	6.3E-01	0.5	5.6E-01
ENSMUST00000146169				6.2	1.3E-02	7.1	1.1E-04	-1.6	1.9E-01	0.0	9.5E-01
ENSMUST00000160628				6.2	1.4E-06	-11.0	2.0E-03	-2.0	1.3E-02	0.1	9.7E-01
ENSMUST00000168806				6.2	1.5E-05	-6.7	1.5E-02	-0.4	6.5E-01	-0.2	9.4E-01
ENSMUST00000182678				6.2	2.2E-04	-6.3	2.1E-03	1.0	7.0E-02	-0.8	6.4E-01
ENSMUST00000189952				6.2	9.3E-03	-4.1	3.8E-03	0.7	1.7E-01	-0.5	6.5E-01
ENSMUST00000154411				6.1	2.0E-05	2.2	8.4E-02	-0.7	5.2E-01	0.9	3.5E-01
ENSMUST00000167363				6.1	8.6E-05	5.0	9.4E-05	0.7	3.4E-01	-0.6	2.9E-01
ENSMUST00000135283				6.1	2.7E-04	2.9	2.5E-02	-1.1	3.0E-01	0.0	9.8E-01
ENSMUST00000139128				6.1	6.9E-06	-3.0	5.8E-02	0.0	9.9E-01	-1.4	3.8E-01
ENSMUST00000119471				6.1	3.0E-04	3.1	1.9E-02	-0.7	4.9E-01	0.2	8.6E-01
ENSMUST00000162814	H3 histone, family 3A [Source:MGI Symbol;Acc:MGI:1097686]		P84244	-9.9	2.4E-01	-13.3	2.3E-01	-5.0	1.1E-01	-1.5	9.0E-01
ENSMUST00000136708				6.1	2.5E-05	6.5	6.4E-04	1.5	2.3E-01	-0.1	8.8E-01
ENSMUST00000154699				6.1	4.5E-05	-4.3	4.9E-02	1.2	1.9E-01	1.2	5.5E-01
ENSMUST00000161782				6.1	2.8E-04	-2.3	2.0E-01	-0.1	9.1E-01	-3.6	1.3E-01
ENSMUST00000162827	zinc finger protein 949 [Source:MGI Symbol;Acc:MGI:1918890]	E9Q732		-1.7	3.8E-01	-2.4	2.7E-01	-1.5	3.1E-01	-0.8	7.3E-01
ENSMUST00000121543				6.1	1.6E-04	7.3	7.5E-05	-0.5	6.5E-01	-0.9	1.3E-01
ENSMUST00000162656				6.1	4.5E-05	-3.2	5.5E-02	0.4	5.7E-01	-0.3	8.6E-01
ENSMUST00000162834	cytochrome b5 reductase 3 [Source:MGI Symbol;Acc:MGI:94893]	A0A0A0MQM3		0.8	6.9E-01	3.4	1.8E-01	0.6	7.8E-01	-1.9	3.6E-01
ENSMUST00000168137				6.1	4.9E-06	7.0	6.9E-04	0.6	6.5E-01	1.3	1.1E-01
ENSMUST00000173792				6.1	5.7E-04	4.7	5.6E-03	-1.5	3.3E-01	-0.1	9.2E-01
ENSMUST00000193742				6.1	3.3E-04	6.6	4.9E-03	-0.5	7.8E-01	-1.2	2.8E-01
ENSMUST00000162845	kinesin family member 2A [Source:MGI Symbol;Acc:MGI:108390]	F6SUU5		-1.3	5.0E-01	-4.8	5.4E-02	-4.3	6.3E-03	-0.8	7.6E-01
ENSMUST00000141802				6.1	5.1E-05	5.1	3.7E-05	-0.2	7.4E-01	0.1	7.3E-01
ENSMUST00000195055				6.1	7.4E-06	5.6	7.0E-03	0.2	9.1E-01	0.1	9.4E-01
ENSMUST00000193619				6.1	3.4E-06	5.4	1.5E-03	-0.6	6.2E-01	0.8	3.6E-01
ENSMUST00000162854	kinesin family member 6 [Source:MGI Symbol;Acc:MGI:1098238]	E9PX57		6.2	3.8E-02	4.1	1.9E-01	-0.8	8.0E-01	1.3	5.1E-01
ENSMUST00000122074				6.1	4.4E-04	6.9	8.8E-05	-0.5	6.2E-01	-0.4	4.7E-01
ENSMUST00000141645				6.1	1.5E-06	7.6	4.7E-06	-0.9	2.8E-01	0.4	4.0E-01
ENSMUST00000171277				6.1	2.0E-04	6.0	1.6E-03	-0.1	9.3E-01	-0.8	3.2E-01
ENSMUST00000138594				6.1	1.8E-04	8.7	2.2E-02	0.0	1.0E+00	-1.3	4.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000162864	tRNA methyltransferase 10A [Source:MGI Symbol;Acc:MGI:1920421]			6.8	4.2E-02	9.5	9.2E-03	-0.8	8.2E-01	-3.6	4.8E-02
ENSMUST00000162865				-2.5	5.5E-02	-2.7	1.4E-01	0.3	7.7E-01	0.4	8.0E-01
ENSMUST00000148267				6.1	1.7E-04	-3.7	7.2E-03	0.3	5.4E-01	-0.9	4.3E-01
ENSMUST00000148632				6.1	3.6E-05	5.5	4.9E-04	-0.7	5.2E-01	-0.3	6.7E-01
ENSMUST00000192240				6.1	1.9E-04	7.8	2.3E-05	-1.9	1.3E-01	-0.5	3.4E-01
ENSMUST00000162883	MPN domain containing [Source:MGI Symbol;Acc:MGI:1915297]	E0CYJ7		-5.8	6.1E-02	-2.1	6.0E-01	2.6	2.8E-01	-1.2	7.6E-01
ENSMUST00000031305				6.1	4.1E-04	7.5	2.0E-04	-0.2	8.9E-01	-0.5	4.0E-01
ENSMUST00000189811				6.1	2.8E-04	6.8	2.2E-04	2.3	6.0E-02	-1.0	1.4E-01
ENSMUST00000132345				6.1	1.9E-04	4.3	1.0E-04	-0.1	8.5E-01	-0.2	6.5E-01
ENSMUST00000162904				-1.9	5.3E-01	-4.5	1.4E-01	-4.8	2.2E-02	-2.2	5.2E-01
ENSMUST00000022493				6.1	9.9E-04	4.3	2.6E-02	0.2	8.8E-01	-0.7	5.3E-01
ENSMUST00000162920				1.2	1.7E-01	1.4	1.5E-01	-0.5	4.9E-01	-0.8	3.5E-01
ENSMUST00000160767				6.1	4.4E-04	4.6	5.5E-03	-2.3	1.3E-01	0.3	7.3E-01
ENSMUST00000162104				6.1	1.1E-03	-2.3	1.9E-01	1.9	8.1E-02	-0.9	5.9E-01
ENSMUST00000182039				6.1	4.7E-03	-3.3	4.2E-02	-1.5	1.1E-01	-1.1	4.8E-01
ENSMUST00000162925	Sp140 nuclear body protein [Source:MGI Symbol;Acc:MGI:3702467]	F6V9G0		-1.4	5.2E-01	-3.7	2.7E-01	-1.3	4.7E-01	1.0	7.5E-01
ENSMUST00000193443				6.1	5.7E-05	6.5	1.2E-03	-0.7	6.4E-01	0.3	7.1E-01
ENSMUST00000118857				6.1	1.5E-04	5.1	5.9E-03	1.3	3.7E-01	0.6	5.2E-01
ENSMUST00000162929				0.9	3.7E-01	0.0	1.0E+00	0.3	8.1E-01	1.2	3.7E-01
ENSMUST00000162930				0.8	5.6E-01	1.1	4.5E-01	-0.8	5.3E-01	-1.2	3.8E-01
ENSMUST00000148937				6.1	1.7E-03	5.0	1.0E-04	-1.6	7.0E-02	0.9	9.7E-02
ENSMUST00000162934	protein inhibitor of activated STAT 3 [Source:MGI Symbol;Acc:MGI:1913126]	E0CZ31		-2.0	1.7E-01	-0.1	9.3E-01	-0.7	5.3E-01	-2.6	1.1E-01
ENSMUST00000162939				-0.1	8.8E-01	0.9	3.5E-01	0.7	3.2E-01	-0.3	7.3E-01
ENSMUST00000118220				6.1	2.7E-03	7.9	6.7E-04	-0.1	9.3E-01	0.7	3.7E-01
ENSMUST00000188808				6.1	1.3E-04	7.2	6.9E-05	0.1	9.6E-01	-1.0	1.0E-01
ENSMUST00000190689				6.1	2.8E-05	5.6	1.6E-03	1.0	3.9E-01	0.5	5.7E-01
ENSMUST00000128881				6.1	2.2E-06	-4.1	1.1E-03	0.8	6.6E-02	-0.7	4.3E-01
ENSMUST00000162946				0.3	8.8E-01	2.2	4.5E-01	1.7	3.8E-01	-0.2	9.4E-01
ENSMUST00000140848				6.1	7.7E-04	5.6	7.5E-02	-0.9	7.7E-01	0.5	7.6E-01
ENSMUST00000162954				1.0	2.2E-01	2.0	9.2E-02	0.9	3.4E-01	-0.1	8.8E-01
ENSMUST00000146164				6.1	8.3E-04	5.3	6.7E-04	-0.5	6.4E-01	0.6	3.2E-01
ENSMUST00000156881				6.1	2.3E-04	-2.8	2.9E-01	1.8	2.5E-01	-0.8	7.6E-01
ENSMUST00000148398				6.1	2.8E-04	4.6	4.1E-04	0.5	4.9E-01	0.2	7.6E-01
ENSMUST00000162962				1.8	4.9E-01	-1.2	7.5E-01	-1.7	5.3E-01	1.3	7.1E-01
ENSMUST00000162963	WD repeat domain 26 [Source:MGI Symbol;Acc:MGI:1923825]	E0CYH4		-1.5	7.1E-02	-0.7	4.8E-01	1.1	1.4E-01	0.3	7.3E-01
ENSMUST00000174735				6.1	2.1E-02	6.5	1.2E-04	-0.5	6.2E-01	-0.2	7.7E-01
ENSMUST00000162965				1.4	5.2E-01	-0.6	7.8E-01	-2.9	1.5E-01	-0.9	6.6E-01
ENSMUST00000162972				-1.3	2.7E-01	-3.0	3.9E-02	-2.3	1.9E-02	-0.6	6.7E-01
ENSMUST00000188844				6.1	1.5E-04	-7.4	2.2E-02	1.3	1.7E-01	-0.9	7.7E-01
ENSMUST00000162974				-3.3	4.7E-02	-1.8	4.0E-01	1.2	4.0E-01	-0.3	8.7E-01
ENSMUST00000162977				4.2	1.6E-01	5.9	4.3E-02	-0.8	7.7E-01	-2.6	1.9E-01
ENSMUST00000162985				-0.2	7.9E-01	1.4	1.1E-01	0.9	1.8E-01	-0.7	3.8E-01
ENSMUST00000160126				6.1	1.1E-04	6.8	7.2E-04	1.9	1.8E-01	-0.3	6.6E-01
ENSMUST00000065411				6.1	1.2E-05	6.5	1.2E-03	-0.6	6.9E-01	-0.8	3.3E-01
ENSMUST00000162997	giant axonal neuropathy [Source:MGI Symbol;Acc:MGI:1890619]	F6TZU3		0.6	6.0E-01	3.4	6.3E-02	2.2	1.5E-01	-0.6	5.9E-01
ENSMUST00000187328				6.1	1.2E-03	7.4	2.1E-04	-0.4	7.7E-01	-0.7	2.7E-01
ENSMUST00000163003				-0.3	7.1E-01	0.6	5.3E-01	1.0	2.0E-01	0.1	9.2E-01
ENSMUST00000119625				6.1	1.0E-04	6.4	3.5E-04	-0.5	7.0E-01	-0.6	4.1E-01
ENSMUST00000179577				6.1	2.3E-05	4.1	1.9E-03	0.1	8.9E-01	0.3	6.7E-01
ENSMUST00000188423				6.1	1.6E-04	7.9	9.8E-04	1.3	4.4E-01	-0.7	4.7E-01
ENSMUST00000163016				-1.1	7.6E-02	-1.6	8.9E-02	0.3	5.6E-01	0.8	3.2E-01
ENSMUST00000176469				6.1	1.8E-04	6.8	1.6E-03	-0.8	6.3E-01	1.5	1.1E-01
ENSMUST00000188291				6.1	1.9E-03	5.2	1.7E-03	-0.5	6.7E-01	0.4	5.4E-01
ENSMUST00000087431				6.1	2.5E-04	5.3	1.6E-03	-1.1	3.9E-01	-0.7	3.6E-01
ENSMUST00000163030	SET domain containing 1B [Source:MGI Symbol;Acc:MGI:2652820]		Q8CFT2	-1.5	1.8E-01	-1.8	2.5E-01	0.9	3.7E-01	1.2	4.3E-01
ENSMUST00000142016				6.1	1.7E-05	-3.0	8.4E-04	-0.8	6.3E-02	-0.3	6.5E-01
ENSMUST00000163034	signal-regulatory protein alpha [Source:MGI Symbol;Acc:MGI:108563]	E0CX65		0.0	9.8E-01	1.7	5.7E-01	1.0	6.2E-01	-0.7	8.1E-01
ENSMUST00000192567				6.1	4.6E-04	7.6	3.5E-05	-0.5	6.2E-01	-0.2	6.9E-01
ENSMUST00000119765				6.1	1.8E-03	6.6	1.8E-04	-0.3	8.1E-01	-0.3	7.0E-01
ENSMUST00000120168				6.1	3.6E-04	5.8	9.0E-04	0.8	5.3E-01	-0.9	2.1E-01
ENSMUST00000148475				6.1	2.5E-05	3.7	1.3E-01	-0.7	7.4E-01	1.1	5.0E-01
ENSMUST00000163046				3.1	1.2E-01	5.8	3.3E-02	1.4	5.4E-01	-1.4	4.1E-01
ENSMUST00000163047	LUC7-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2183260]	E9Q715		-3.3	2.6E-01	-2.1	6.0E-01	1.2	6.3E-01	-0.1	9.8E-01
ENSMUST00000163048	KRR1, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1289274]		Q8BGA5	0.2	7.2E-01	0.7	4.6E-01	0.2	7.7E-01	-0.2	8.0E-01
ENSMUST00000071184				6.1	3.5E-04	8.1	5.2E-05	-0.1	9.1E-01	-0.4	4.3E-01
ENSMUST00000126749				6.1	7.6E-04	-1.0	4.0E-01	0.7	3.3E-01	-1.3	3.1E-01
ENSMUST00000163058	amyotrophic lateral sclerosis 2 (juvenile) [Source:MGI Symbol;Acc:MGI:1921268]		Q920R0	4.6	9.5E-02	4.5	1.5E-01	-0.4	9.1E-01	-0.3	8.8E-01
ENSMUST00000152930				6.1	5.1E-04	6.9	7.1E-04	-0.3	8.2E-01	-0.4	5.7E-01
ENSMUST00000163061	potassium channel tetramerisation domain containing 18 [Source:MGI Symbol;Acc:MGI:3603813]	E9PYP3		4.8	6.5E-02	4.0	1.6E-01	-0.6	8.2E-01	0.2	9.1E-01
ENSMUST00000134460				6.1	1.6E-04	3.8	1.1E-01	-0.1	9.8E-01	1.0	5.1E-01
ENSMUST00000037640				6.1	3.8E-04	5.4	2.0E-02	-0.8	7.1E-01	2.4	6.7E-02
ENSMUST00000043553				6.1	1.0E-04	8.8	1.6E-05	-0.9	4.4E-01	0.1	7.8E-01
ENSMUST00000114370				6.1	1.7E-04	-3.2	6.3E-02	1.1	2.5E-01	-3.2	1.3E-01
ENSMUST00000118766				6.1	2.1E-04	-8.5	1.6E-03	1.0	9.7E-02	0.6	7.6E-01
ENSMUST00000119539				6.1	1.2E-04	-3.8	2.0E-02	0.9	2.1E-01	-0.8	6.0E-01
ENSMUST00000135333				6.1	2.4E-06	8.3	1.8E-05	-1.4	2.3E-01	0.1	9.0E-01
ENSMUST00000163082	disabled 2, mitogen-responsive phosphoprotein [Source:MGI Symbol;Acc:MGI:109175]	F6TQN9		3.6	5.8E-02	-2.9	1.2E-01	-5.7	3.9E-03	0.7	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000135276				6.1	1.8E-04	-3.3	1.7E-03	-0.6	1.8E-01	-2.4	2.0E-02
ENSMUST00000135899				6.1	4.9E-05	-6.7	1.7E-03	-0.5	3.6E-01	-0.1	9.6E-01
ENSMUST00000149650				6.1	1.5E-04	-4.2	4.5E-02	-0.2	8.6E-01	-1.6	4.6E-01
ENSMUST00000163088				-2.7	4.8E-02	-0.3	8.4E-01	1.0	3.8E-01	-1.4	3.4E-01
ENSMUST00000163092	WD repeat domain 66 [Source:MGI Symbol;Acc:MGI:1918495]	E9PVE7		2.8	3.3E-01	4.4	1.4E-01	-0.4	8.9E-01	-2.1	3.2E-01
ENSMUST00000124538				6.1	1.8E-04	-2.6	4.2E-02	0.4	5.3E-01	-3.9	2.9E-02
ENSMUST00000163100	cell division cycle associated 2 [Source:MGI Symbol;Acc:MGI:1919787]		Q14B71	-0.2	9.0E-01	1.1	5.4E-01	0.5	7.1E-01	-0.8	6.4E-01
ENSMUST00000163107	widely-interspaced zinc finger motifs [Source:MGI Symbol;Acc:MGI:1332638]	E9PZC6		-1.0	5.6E-01	-2.1	4.1E-01	-0.2	9.1E-01	0.9	7.0E-01
ENSMUST00000130049				6.1	5.7E-04	6.9	5.2E-04	-0.7	6.2E-01	0.3	6.7E-01
ENSMUST00000165609				6.1	1.1E-02	8.4	1.2E-05	0.2	8.2E-01	0.6	2.2E-01
ENSMUST00000122466				6.1	1.3E-03	4.1	9.6E-03	0.4	7.2E-01	-0.7	4.2E-01
ENSMUST00000150123				6.1	1.4E-03	-3.2	4.0E-02	1.0	1.7E-01	0.4	7.8E-01
ENSMUST00000150129				6.1	2.5E-04	2.8	9.1E-03	0.3	7.3E-01	-0.5	4.7E-01
ENSMUST00000118142				6.1	9.8E-04	5.0	1.1E-04	0.1	8.7E-01	0.2	6.6E-01
ENSMUST00000134556				6.1	3.9E-04	5.3	1.6E-02	-1.4	4.8E-01	-2.2	9.2E-02
ENSMUST00000162763				6.1	2.0E-04	6.1	2.6E-03	1.7	2.4E-01	-1.2	1.9E-01
ENSMUST00000118922				6.1	3.1E-04	5.9	1.6E-04	-1.6	1.6E-01	-0.1	9.3E-01
ENSMUST00000123902				6.1	3.4E-03	3.9	7.3E-04	-3.1	5.3E-03	-0.9	1.5E-01
ENSMUST00000163140				0.4	8.4E-01	0.7	7.0E-01	-0.9	5.7E-01	-1.3	4.7E-01
ENSMUST00000161180				6.1	2.4E-04	8.8	5.4E-04	-1.5	4.4E-01	0.6	4.7E-01
ENSMUST00000176499				6.1	9.0E-03	-1.6	5.6E-02	0.5	2.7E-01	-1.0	2.3E-01
ENSMUST00000163159	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3 [Source:MGI Symbol;Acc:M	E9Q287		3.5	7.6E-02	5.8	3.0E-02	0.0	1.0E+00	-2.3	1.3E-01
ENSMUST00000135737				6.1	1.2E-03	-4.9	2.2E-03	0.0	9.5E-01	-0.2	8.9E-01
ENSMUST00000163180				1.6	4.6E-01	-0.4	9.0E-01	0.4	8.4E-01	2.5	4.4E-01
ENSMUST00000163284				6.1	1.5E-05	-4.3	1.4E-02	0.5	4.6E-01	0.7	6.2E-01
ENSMUST00000129650				6.1	9.7E-04	6.6	3.0E-04	0.1	9.3E-01	0.2	7.6E-01
ENSMUST00000163188				0.1	9.3E-01	4.9	1.1E-02	4.1	1.5E-02	-0.7	5.1E-01
ENSMUST00000163189	latent transforming growth factor beta binding protein 2 [Source:MGI Symbol;Acc:MGI:99502]	E9Q1D6		6.1	8.5E-02	6.3	8.6E-02	-0.9	8.1E-01	-1.1	6.1E-01
ENSMUST00000051179				6.1	1.1E-05	6.8	7.1E-05	-1.1	3.0E-01	-0.1	8.7E-01
ENSMUST00000163192	etoposide induced 2.4 mRNA [Source:MGI Symbol;Acc:MGI:108090]			1.5	4.4E-01	-3.1	1.4E-01	-3.9	2.0E-02	0.6	7.6E-01
ENSMUST00000163193	e synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase) [Source:MGI Symbol;Ac	Q3TZ03	Q920N2	-2.1	2.0E-01	2.7	9.6E-02	0.3	8.4E-01	-4.5	1.2E-02
ENSMUST00000163205	casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]	E9Q4G7		0.1	9.0E-01	0.1	9.1E-01	0.3	6.6E-01	0.2	7.3E-01
ENSMUST00000054711				6.1	4.4E-03	4.3	6.6E-04	-3.1	1.4E-02	-0.8	2.5E-01
ENSMUST00000163210	kinesin family member 5B [Source:MGI Symbol;Acc:MGI:1098268]	E9QAK5		-0.1	9.7E-01	5.8	2.2E-01	5.9	9.6E-02	0.0	1.0E+00
ENSMUST00000163222				3.0	1.9E-01	7.0	6.0E-02	1.9	5.6E-01	-2.1	2.9E-01
ENSMUST00000163226	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]	Q8CCM0		1.3	1.2E-01	1.8	6.9E-02	-0.4	5.9E-01	-0.9	2.6E-01
ENSMUST00000107202				6.1	3.0E-05	3.8	4.5E-02	-2.9	1.3E-01	1.1	3.5E-01
ENSMUST00000118871				6.1	1.1E-03	1.9	2.4E-01	4.2	6.9E-03	-0.8	4.9E-01
ENSMUST00000162836				6.1	9.0E-04	-5.3	1.4E-03	0.1	7.5E-01	-0.7	6.1E-01
ENSMUST00000180626				6.1	3.6E-04	7.0	4.7E-04	-0.7	6.2E-01	-0.4	6.1E-01
ENSMUST00000142507				6.1	9.5E-06	-5.6	3.8E-05	1.2	5.1E-03	-0.2	8.2E-01
ENSMUST00000148404				6.1	4.5E-04	1.3	5.5E-01	8.4	6.0E-04	-1.2	5.2E-01
ENSMUST00000193422				6.1	4.7E-04	7.2	4.1E-04	1.8	1.9E-01	-0.5	5.2E-01
ENSMUST00000163257	family with sequence similarity 172, member A [Source:MGI Symbol;Acc:MGI:1915925]		Q3TNH5	-1.7	5.1E-01	-2.6	3.7E-01	-1.9	3.0E-01	-0.9	7.6E-01
ENSMUST00000135997				6.1	6.8E-04	4.4	4.2E-02	-0.7	7.2E-01	1.9	1.5E-01
ENSMUST00000163265	Rho GTPase activating protein 19 [Source:MGI Symbol;Acc:MGI:1918335]	E9Q4T1		6.1	5.4E-02	7.1	3.3E-02	-1.4	6.8E-01	-2.4	1.9E-01
ENSMUST00000149557				6.1	6.2E-06	-1.1	4.9E-01	2.0	1.3E-01	-1.2	4.6E-01
ENSMUST00000162549				6.1	9.3E-04	7.6	9.0E-03	2.7	2.5E-01	-0.5	6.6E-01
ENSMUST00000163272	suppressor of zeste 12 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1261758]	E9PW15		-0.1	9.6E-01	-5.7	2.6E-01	-1.5	5.4E-01	4.1	4.1E-01
ENSMUST00000119286				6.1	4.1E-06	-5.6	6.2E-05	0.5	1.6E-01	-0.7	4.4E-01
ENSMUST00000132372				6.1	1.6E-04	5.8	2.0E-04	-0.2	8.2E-01	0.1	8.0E-01
ENSMUST00000185649				6.1	1.2E-03	-2.4	1.5E-01	3.9	1.0E-03	-1.2	4.7E-01
ENSMUST00000136865				6.1	7.9E-04	5.5	2.1E-03	-1.4	3.3E-01	0.6	4.7E-01
ENSMUST00000123134				6.1	1.5E-03	-0.2	8.1E-01	0.0	9.7E-01	-3.4	1.5E-02
ENSMUST00000133767				6.1	7.6E-04	1.7	3.8E-01	-2.2	2.6E-01	2.7	7.6E-02
ENSMUST00000135852				6.1	3.4E-04	-5.3	1.1E-02	1.3	1.4E-01	-0.1	9.7E-01
ENSMUST00000163324	F-box protein 34 [Source:MGI Symbol;Acc:MGI:1926188]		Q80XI1	-2.8	9.0E-02	-1.8	4.8E-01	1.2	4.4E-01	0.2	9.4E-01
ENSMUST00000163326	ATPase, Ca++ transporting, ubiquitous [Source:MGI Symbol;Acc:MGI:1194503]	E9Q559		-2.2	5.4E-01	0.3	9.2E-01	-2.2	3.3E-01	-4.7	2.0E-01
ENSMUST00000182572				6.1	1.0E-05	-3.3	6.3E-03	1.0	6.6E-02	0.1	9.6E-01
ENSMUST00000183550				6.1	3.1E-04	-2.8	2.0E-02	-0.2	7.6E-01	-0.6	6.0E-01
ENSMUST00000163336	nuclear receptor coactivator 4 [Source:MGI Symbol;Acc:MGI:1350932]	Q5U4H9		-2.1	1.2E-01	0.5	6.9E-01	0.2	8.7E-01	-2.4	1.0E-01
ENSMUST00000163348	zinc finger protein 426 [Source:MGI Symbol;Acc:MGI:1920248]	G5E8Y1		-2.5	2.7E-01	-4.7	9.0E-02	-3.1	4.5E-02	-0.9	7.6E-01
ENSMUST00000163350	poly (ADP-ribose) glycohydrolase [Source:MGI Symbol;Acc:MGI:1347094]		O88622	-0.1	9.6E-01	-0.5	8.1E-01	-2.7	1.8E-01	-2.3	3.4E-01
ENSMUST00000163354				2.7	1.9E-01	1.2	5.0E-01	-2.5	1.8E-01	-1.1	5.4E-01
ENSMUST00000137027				6.1	5.8E-03	6.1	1.1E-03	-0.6	6.6E-01	-0.3	6.5E-01
ENSMUST00000163370	T cell lymphoma invasion and metastasis 1 [Source:MGI Symbol;Acc:MGI:103306]	G3UWG2		-0.8	8.0E-01	-1.4	7.8E-01	0.0	9.9E-01	0.6	9.1E-01
ENSMUST00000189910				6.1	1.3E-04	-3.4	1.2E-02	0.1	8.0E-01	1.0	3.9E-01
ENSMUST00000141173				6.1	1.3E-02	1.5	3.0E-01	9.7	7.0E-06	-0.2	8.9E-01
ENSMUST00000163392	RIKEN cDNA 3830406C13 gene [Source:MGI Symbol;Acc:MGI:1917937]		Q8BGD0	-1.4	8.4E-02	-2.6	4.0E-02	0.0	9.6E-01	1.1	3.2E-01
ENSMUST00000147772				6.1	6.7E-04	3.8	3.2E-04	-3.7	1.8E-03	-1.5	2.1E-02
ENSMUST00000148345				6.1	1.6E-05	6.0	4.8E-04	0.3	8.0E-01	-0.3	6.6E-01
ENSMUST00000114486				6.1	1.8E-04	1.4	1.0E-01	-0.1	8.5E-01	0.4	5.3E-01
ENSMUST00000126757				6.1	1.1E-04	-2.4	2.6E-01	2.3	8.5E-02	-1.2	5.5E-01
ENSMUST00000163401	regulatory factor X, 7 [Source:MGI Symbol;Acc:MGI:2442675]	F8VPJ6		0.1	7.4E-01	0.8	1.4E-01	0.7	9.0E-02	0.0	9.3E-01
ENSMUST00000163402	synaptojanin 2 binding protein [Source:MGI Symbol;Acc:MGI:1344347]		Q9D6K5	2.5	3.8E-02	0.4	7.4E-01	-0.6	6.0E-01	1.5	2.2E-01
ENSMUST00000163406				2.9	1.9E-01	4.6	5.9E-02	-0.4	8.5E-01	-2.2	2.0E-01
ENSMUST00000180378				6.1	8.0E-05	5.3	3.1E-03	-0.5	7.3E-01	-1.2	1.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000163409	kelch-like 7 [Source:MGI Symbol;Acc:MGI:1196453]	G3UW75		3.9	7.8E-02	6.6	1.1E-02	-0.5	8.4E-01	-3.2	3.9E-02
ENSMUST00000192242				6.1	3.6E-04	4.4	1.7E-02	-0.7	6.5E-01	2.1	5.9E-02
ENSMUST00000163418				0.6	5.6E-01	1.2	3.4E-01	-0.1	9.1E-01	-0.7	5.0E-01
ENSMUST00000168843				6.1	2.5E-05	-0.5	7.2E-01	0.8	4.1E-01	-2.2	1.4E-01
ENSMUST00000120916				6.1	1.1E-02	-2.9	1.7E-01	2.9	1.3E-02	1.8	3.7E-01
ENSMUST00000153812				6.1	1.7E-03	-4.4	2.1E-05	0.5	7.6E-02	0.0	9.3E-01
ENSMUST00000178911				6.1	1.2E-02	-7.8	4.8E-02	-0.9	4.2E-01	1.8	6.2E-01
ENSMUST00000188289				6.1	9.9E-05	7.1	1.2E-04	0.0	9.7E-01	-0.9	1.7E-01
ENSMUST00000163441	testis expressed gene 264 [Source:MGI Symbol;Acc:MGI:1096570]	E9Q137		-0.1	9.7E-01	1.3	3.2E-01	-2.6	5.7E-02	-4.0	2.6E-02
ENSMUST00000128747				6.1	1.6E-03	1.8	5.3E-01	-4.5	1.5E-01	1.8	3.8E-01
ENSMUST00000129105				6.1	3.6E-04	-1.8	2.6E-02	-7.4	2.4E-05	-1.0	1.8E-01
ENSMUST00000163452	replication initiator 1 [Source:MGI Symbol;Acc:MGI:1889817]		Q5U4E2	1.5	3.5E-01	0.1	9.8E-01	2.3	2.3E-01	3.8	1.4E-01
ENSMUST00000163455	matrilin 2 [Source:MGI Symbol;Acc:MGI:109613]	A0A0A0MQM7		4.0	1.2E-01	5.3	6.7E-02	-0.5	8.5E-01	-1.8	3.3E-01
ENSMUST00000137720				6.1	4.4E-04	-2.9	6.4E-02	0.3	7.1E-01	-0.7	6.7E-01
ENSMUST00000145523				6.1	1.4E-03	1.6	6.2E-02	0.1	9.1E-01	0.5	4.8E-01
ENSMUST00000163476	sphingomyelin phosphodiesterase 4 [Source:MGI Symbol;Acc:MGI:1924876]		Q6ZPR5	-3.7	2.0E-01	2.0	6.3E-01	4.7	1.6E-01	-1.0	7.8E-01
ENSMUST00000164955				6.1	7.5E-04	4.8	1.4E-04	-3.0	9.1E-03	-0.4	4.7E-01
ENSMUST00000163483	RAB1A, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:97842]	Q0PD67	P62821	-8.9	4.0E-02	2.4	6.7E-01	9.8	2.6E-02	-1.4	7.9E-01
ENSMUST00000124275				6.1	8.1E-03	-7.5	2.5E-04	0.6	1.8E-01	-1.3	4.1E-01
ENSMUST00000130299				6.1	7.9E-04	5.8	1.8E-02	-0.7	7.5E-01	-1.3	3.1E-01
ENSMUST00000163495	thyroglobulin [Source:MGI Symbol;Acc:MGI:98733]	F6Y2X8		0.8	6.0E-01	2.4	2.8E-01	1.0	5.8E-01	-0.5	7.6E-01
ENSMUST00000191645				6.1	2.2E-05	0.4	7.0E-01	-0.2	7.7E-01	-3.8	7.7E-03
ENSMUST00000122395				6.1	1.7E-04	-2.8	2.1E-01	1.5	2.1E-01	-0.2	9.3E-01
ENSMUST00000134490				6.1	3.4E-03	-1.2	5.5E-01	3.8	8.7E-03	0.3	8.9E-01
ENSMUST00000163507	phosphofructokinase, muscle [Source:MGI Symbol;Acc:MGI:97548]		P47857	0.3	8.7E-01	-0.5	8.9E-01	1.3	5.8E-01	2.1	4.9E-01
ENSMUST00000163511	interferon regulatory factor 5 [Source:MGI Symbol;Acc:MGI:1350924]	Q3U169	P56477	-0.2	7.8E-01	0.6	5.1E-01	0.0	9.6E-01	-0.7	3.8E-01
ENSMUST00000163516	ral precursor cell expressed, developmentally down-regulated gene 4-like [Source:MGI Symbol;Acc:MGI:1933	E9PXB7		-1.6	2.0E-01	0.8	5.6E-01	1.2	3.0E-01	-1.3	3.5E-01
ENSMUST00000163524	teneurin transmembrane protein 2 [Source:MGI Symbol;Acc:MGI:1345184]	A0A0A0MQB7		5.8	3.8E-02	5.8	5.2E-02	-0.8	7.8E-01	-0.7	6.9E-01
ENSMUST00000163528	BRO1 domain and CAAX motif containing [Source:MGI Symbol;Acc:MGI:1918928]		Q8K2Q7	1.4	4.7E-01	1.1	5.2E-01	-3.4	5.3E-02	-3.1	1.1E-01
ENSMUST00000163530	threonyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:1919057]	E9Q7H6		1.3	5.6E-01	6.0	8.4E-02	2.9	3.5E-01	-1.8	3.4E-01
ENSMUST00000167012				6.1	7.4E-04	8.4	7.7E-05	0.1	9.2E-01	-0.1	8.3E-01
ENSMUST00000133816				6.1	3.4E-03	-0.7	6.7E-01	2.1	6.2E-02	-1.1	5.3E-01
ENSMUST00000163558	DH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2 [Source:MGI Symbol;Acc:MGI:19228		Q59J78	-0.3	7.6E-01	-2.9	1.5E-02	-2.6	6.1E-03	0.1	9.3E-01
ENSMUST00000150280				6.1	4.1E-04	4.7	9.7E-03	-0.6	6.7E-01	1.5	1.4E-01
ENSMUST00000185742				6.1	4.6E-05	4.8	4.1E-04	0.4	6.7E-01	0.4	4.9E-01
ENSMUST00000134003				6.1	8.0E-05	10.9	1.7E-05	0.7	6.0E-01	-0.8	1.2E-01
ENSMUST00000163569	pumilio RNA-binding family member 2 [Source:MGI Symbol;Acc:MGI:1931751]		Q80U58	-2.6	4.5E-01	-4.1	3.6E-01	-1.8	4.2E-01	-0.2	9.6E-01
ENSMUST00000163574	family with sequence similarity 71, member E2 [Source:MGI Symbol;Acc:MGI:3045311]	M0QW72		3.1	3.1E-01	5.4	9.9E-02	-0.5	8.9E-01	-2.7	2.1E-01
ENSMUST00000164106				6.1	3.7E-05	7.6	2.7E-03	1.9	3.2E-01	0.2	8.5E-01
ENSMUST00000121855				6.1	6.1E-04	4.3	9.0E-04	-1.1	2.5E-01	-1.1	1.3E-01
ENSMUST00000141460				6.1	1.4E-04	3.2	1.8E-03	-4.3	1.2E-03	0.5	4.6E-01
ENSMUST00000162091				6.1	2.4E-04	5.8	3.9E-05	-0.8	3.2E-01	0.3	5.9E-01
ENSMUST00000183567				6.1	1.6E-04	-4.4	3.5E-03	0.2	6.9E-01	0.2	8.6E-01
ENSMUST00000189501				6.1	1.3E-03	-3.2	1.7E-02	-0.4	5.0E-01	-1.7	2.0E-01
ENSMUST00000163602				2.9	1.1E-01	-3.4	1.8E-01	-4.3	2.0E-02	2.1	3.9E-01
ENSMUST00000190834				6.1	5.3E-04	3.7	1.4E-04	-0.2	7.3E-01	0.2	5.8E-01
ENSMUST00000142836				6.1	1.7E-03	0.1	9.8E-01	3.8	1.4E-02	0.2	9.0E-01
ENSMUST00000163619	RIKEN cDNA 4931406B18 gene [Source:MGI Symbol;Acc:MGI:1921304]	A0A0B4J1M4		1.6	5.9E-02	1.6	1.2E-01	-0.1	8.5E-01	-0.1	8.8E-01
ENSMUST00000163623	eural precursor cell expressed, developmentally down-regulated gene 9 [Source:MGI Symbol;Acc:MGI:97302			0.7	6.0E-01	1.8	2.7E-01	-0.4	7.9E-01	-1.4	3.3E-01
ENSMUST00000163624	IQ motif containing H [Source:MGI Symbol;Acc:MGI:1925500]	B7ZNG8		2.1	1.1E-01	6.9	2.0E-04	-0.6	6.6E-01	-5.3	2.2E-04
ENSMUST00000145036				6.1	2.2E-04	7.1	1.6E-04	-0.5	6.8E-01	-0.6	3.7E-01
ENSMUST00000119313				6.1	3.8E-04	-1.0	1.1E-01	0.6	1.3E-01	-0.5	3.8E-01
ENSMUST00000131089				6.1	4.9E-03	5.2	1.2E-03	-1.4	2.9E-01	0.2	7.3E-01
ENSMUST00000169552				6.1	3.6E-05	5.8	4.8E-04	1.4	1.8E-01	0.6	4.0E-01
ENSMUST00000191713				6.1	9.4E-05	-2.7	5.9E-02	-0.6	4.4E-01	-1.8	2.1E-01
ENSMUST00000161107				6.1	6.0E-04	-10.5	4.1E-06	-0.5	6.5E-02	-0.6	6.1E-01
ENSMUST00000163667	parvin, gamma [Source:MGI Symbol;Acc:MGI:2158329]	E9PYG5		4.1	4.6E-02	7.2	7.4E-03	1.2	5.6E-01	-2.0	2.4E-01
ENSMUST00000163677	sorting nexin 13 [Source:MGI Symbol;Acc:MGI:2661416]	E9Q7T4		1.7	1.5E-01	2.6	6.1E-02	-0.2	8.6E-01	-1.1	3.1E-01
ENSMUST00000163691	maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian) [Source:MGI Symbol;Acc:MGI:9691	Q3U0G5	O54791	0.8	1.7E-01	1.0	2.1E-01	0.6	3.1E-01	0.4	4.9E-01
ENSMUST00000128222				6.1	1.4E-04	-4.7	2.3E-02	0.3	7.0E-01	-0.7	7.3E-01
ENSMUST00000163695	ubiquitin fusion degradation 1 like [Source:MGI Symbol;Acc:MGI:109353]	E9Q0Y6		-0.4	8.0E-01	-3.6	9.1E-02	-3.7	1.1E-02	-0.5	8.1E-01
ENSMUST00000140742				6.1	3.2E-03	5.2	2.5E-04	-0.4	6.4E-01	0.4	4.7E-01
ENSMUST00000148712				6.1	8.1E-05	7.1	1.7E-04	0.4	7.4E-01	-1.0	1.4E-01
ENSMUST00000169605				6.1	1.3E-04	6.7	5.5E-04	-0.6	6.5E-01	0.4	5.9E-01
ENSMUST00000186252				6.1	7.9E-05	5.5	1.1E-04	-1.2	1.9E-01	0.0	9.3E-01
ENSMUST00000151468				6.1	1.4E-03	-4.1	8.8E-03	-0.5	4.5E-01	-0.9	5.4E-01
ENSMUST00000156539				6.1	1.8E-04	6.1	3.9E-04	-1.1	4.0E-01	-1.8	3.2E-02
ENSMUST00000163717	ribonucleic acid binding protein S1 [Source:MGI Symbol;Acc:MGI:97960]		Q99M28	-1.6	1.4E-01	-3.2	1.3E-01	1.1	2.8E-01	2.7	1.9E-01
ENSMUST00000173120				6.1	8.3E-03	4.8	1.3E-02	-0.6	7.2E-01	-1.1	3.1E-01
ENSMUST00000163727	suppression of tumorigenicity 18 [Source:MGI Symbol;Acc:MGI:2446700]	Q148A0	Q80TY4	6.7	6.0E-02	6.2	1.0E-01	-0.8	8.2E-01	-0.3	8.8E-01
ENSMUST00000163739	adaptor-related protein complex 3, mu 2 subunit [Source:MGI Symbol;Acc:MGI:1929214]		Q8R2R9	-0.2	6.8E-01	0.6	3.2E-01	0.5	2.7E-01	-0.3	5.9E-01
ENSMUST00000172786				6.1	1.2E-04	1.8	2.9E-01	-1.9	2.0E-01	4.6	6.3E-03
ENSMUST00000177972				6.1	2.8E-04	-2.6	1.3E-01	1.6	9.3E-02	-0.5	7.4E-01
ENSMUST00000183006				6.1	1.4E-04	3.8	3.9E-02	-0.4	7.7E-01	1.8	1.5E-01
ENSMUST00000163750	eural precursor cell expressed, developmentally down-regulated gene 8 [Source:MGI Symbol;Acc:MGI:97301	Q3UI46	P29595	-0.5	7.6E-01	-4.4	3.1E-02	-4.4	4.1E-03	-0.4	8.4E-01
ENSMUST00000128949				6.1	4.1E-04	-3.1	4.5E-02	0.9	2.3E-01	-1.1	4.8E-01
ENSMUST00000159754				6.1	9.5E-05	2.7	8.6E-03	0.5	4.8E-01	0.6	3.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000163755				1.1	2.8E-01	2.2	8.6E-02	0.2	8.4E-01	-0.9	3.6E-01
ENSMUST00000163762	proline rich 5 like [Source:MGI Symbol;Acc:MGI:1919696]		A2AVJ5	-1.4	6.2E-01	3.5	4.6E-01	6.6	8.1E-02	1.7	6.5E-01
ENSMUST00000163764	jade family PHD finger 1 [Source:MGI Symbol;Acc:MGI:1925835]		Q6ZPI0	1.3	6.2E-01	5.2	1.3E-01	0.8	7.8E-01	-3.1	2.5E-01
ENSMUST00000163765	nucleoporin 155 [Source:MGI Symbol;Acc:MGI:2181182]		Q99P88	0.0	9.0E-01	-0.3	6.2E-01	0.0	9.4E-01	0.2	7.1E-01
ENSMUST00000163766	zinc finger SCAN domains 29 [Source:MGI Symbol;Acc:MGI:2139317]	E9Q5B4		2.0	3.6E-01	2.6	3.2E-01	1.0	6.3E-01	0.4	8.5E-01
ENSMUST00000174827				6.1	8.7E-06	7.7	5.3E-05	-0.6	5.9E-01	0.1	8.7E-01
ENSMUST00000187705				6.1	2.0E-06	6.8	5.5E-05	-1.0	3.3E-01	-0.2	7.0E-01
ENSMUST00000190462				6.1	7.2E-04	7.0	6.2E-03	-0.4	8.4E-01	-1.3	2.5E-01
ENSMUST00000163798				0.1	9.0E-01	1.0	3.6E-01	0.6	4.7E-01	-0.2	7.8E-01
ENSMUST00000129274				6.1	6.6E-04	4.4	5.7E-02	-1.7	4.5E-01	0.0	9.9E-01
ENSMUST00000163800	predicted gene 5458 [Source:MGI Symbol;Acc:MGI:3646663]	E9Q6Y1		4.1	1.4E-01	4.7	1.2E-01	-0.2	9.5E-01	-0.8	6.4E-01
ENSMUST00000147048				6.1	4.1E-04	5.9	1.6E-03	-0.5	7.5E-01	-0.7	3.6E-01
ENSMUST00000163812	protein regulator of cytokinesis 1 [Source:MGI Symbol;Acc:MGI:1858961]	G3UW86		-1.2	6.1E-01	-2.3	3.7E-01	-1.6	3.7E-01	-0.5	8.6E-01
ENSMUST00000186624				6.1	1.8E-04	7.3	4.2E-02	0.5	8.8E-01	0.0	9.8E-01
ENSMUST00000188281				6.1	2.6E-04	4.5	4.7E-03	-0.4	7.1E-01	-0.2	8.4E-01
ENSMUST00000151023				6.1	5.4E-03	-5.7	3.3E-04	0.2	6.1E-01	0.4	7.5E-01
ENSMUST00000163837	trans-2,3-enoyl-CoA reductase [Source:MGI Symbol;Acc:MGI:1915408]	Q52L67		-3.0	1.0E-01	0.1	9.4E-01	0.7	6.5E-01	-2.5	2.2E-01
ENSMUST00000159369				6.1	2.5E-04	3.0	1.0E-02	0.2	8.4E-01	0.0	9.7E-01
ENSMUST00000163844	catenin (cadherin associated protein), beta 1 [Source:MGI Symbol;Acc:MGI:88276]	E9PW26		-0.5	8.9E-01	-6.3	1.4E-01	-6.4	1.6E-02	-0.5	9.1E-01
ENSMUST00000140617				6.0	4.9E-04	-7.6	1.2E-04	1.2	6.0E-03	0.3	8.4E-01
ENSMUST00000163846				-2.5	4.8E-02	-1.5	2.8E-01	-0.1	8.7E-01	-1.1	4.5E-01
ENSMUST00000186275				6.0	1.6E-03	5.1	1.4E-03	-0.6	6.2E-01	1.5	4.7E-02
ENSMUST00000163854	mitogen-activated protein kinase kinase kinase kinase 4 [Source:MGI Symbol;Acc:MGI:1349394]	E9PVG7		-3.9	2.9E-01	-2.1	5.1E-01	-1.3	5.5E-01	-3.1	4.3E-01
ENSMUST00000163855	activating transcription factor 1 [Source:MGI Symbol;Acc:MGI:1298366]	E9PYW2		0.4	8.8E-01	-3.0	3.6E-01	-3.1	1.4E-01	0.3	9.3E-01
ENSMUST00000163858	ankyrin repeat domain 13 family, member D [Source:MGI Symbol;Acc:MGI:1915673]	E9Q821		0.6	6.9E-01	2.1	3.4E-01	2.1	2.8E-01	0.5	7.7E-01
ENSMUST00000094840				6.0	2.0E-05	1.7	6.4E-02	-0.5	5.1E-01	-0.2	7.4E-01
ENSMUST00000193788				6.0	1.6E-04	8.4	3.8E-05	1.3	2.7E-01	-0.4	4.4E-01
ENSMUST00000072381				6.0	2.1E-03	6.6	2.5E-04	-0.6	6.2E-01	-0.8	2.5E-01
ENSMUST00000163879	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]	Q8BMS7		-2.8	3.8E-02	-3.7	8.2E-02	-0.2	8.6E-01	0.8	6.8E-01
ENSMUST00000135024				6.0	7.6E-04	-4.4	3.5E-03	0.7	1.8E-01	-0.8	5.4E-01
ENSMUST00000136332				6.0	1.3E-03	5.8	3.0E-04	-0.6	6.1E-01	0.2	7.2E-01
ENSMUST00000163887	proline rich 18 [Source:MGI Symbol;Acc:MGI:2443403]		Q6PAN7	0.6	7.6E-01	3.6	1.5E-01	0.0	9.9E-01	-3.0	1.3E-01
ENSMUST00000163888	myocyte enhancer factor 2C [Source:MGI Symbol;Acc:MGI:99458]	A0A0H2UH28		-2.0	1.9E-01	-0.1	9.4E-01	0.5	6.7E-01	-1.4	4.1E-01
ENSMUST00000142799				6.0	3.1E-04	-5.0	3.8E-03	1.1	5.9E-02	0.3	8.3E-01
ENSMUST00000163892				-1.1	7.8E-02	-0.3	7.0E-01	0.2	6.2E-01	-0.6	4.1E-01
ENSMUST00000159478				6.0	9.3E-06	1.2	4.7E-01	-3.0	7.9E-02	0.2	9.0E-01
ENSMUST00000163898	insulin-like growth factor binding protein 7 [Source:MGI Symbol;Acc:MGI:1352480]	E9Q5D9		3.0	4.2E-02	2.9	6.1E-02	-1.4	3.1E-01	-1.3	2.7E-01
ENSMUST00000117116				6.0	3.4E-04	-6.2	2.5E-02	0.3	7.4E-01	0.1	9.8E-01
ENSMUST00000133000				6.0	2.6E-04	5.7	2.2E-03	-0.6	6.8E-01	-2.0	5.6E-02
ENSMUST00000163914				2.5	3.0E-01	5.6	2.9E-02	-0.6	8.0E-01	-3.7	5.4E-02
ENSMUST00000173402				6.0	2.7E-04	5.4	3.1E-03	-0.3	8.0E-01	-0.7	4.5E-01
ENSMUST00000146266				6.0	1.4E-05	-2.9	1.9E-02	0.6	2.9E-01	-1.2	3.1E-01
ENSMUST00000171395				6.0	1.4E-03	-2.5	3.3E-02	1.6	1.2E-02	-0.8	4.6E-01
ENSMUST00000172641				6.0	4.4E-06	6.1	5.3E-04	-0.8	5.2E-01	0.1	9.2E-01
ENSMUST00000122207				6.0	1.2E-04	-3.5	1.9E-01	1.6	1.9E-01	-0.7	8.1E-01
ENSMUST00000163972	polymerase (RNA) II (DNA directed) polypeptide M [Source:MGI Symbol;Acc:MGI:107282]		Q6P6I6	3.2	1.2E-01	-1.1	6.5E-01	-2.1	2.9E-01	2.3	3.3E-01
ENSMUST00000124127				6.0	7.8E-05	4.4	2.6E-03	-1.2	2.7E-01	0.3	7.5E-01
ENSMUST00000125966				6.0	1.2E-06	2.3	4.4E-01	1.3	5.5E-01	4.1	1.3E-01
ENSMUST00000163991	sphingomyelin phosphodiesterase 5 [Source:MGI Symbol;Acc:MGI:3709877]	D6MZJ6		-1.3	2.0E-01	0.4	7.1E-01	1.3	1.8E-01	-0.4	7.0E-01
ENSMUST00000151857				6.0	3.5E-04	4.6	6.5E-04	-1.6	1.2E-01	-0.2	7.5E-01
ENSMUST00000163995				-1.2	2.9E-01	3.1	1.3E-01	5.1	5.3E-03	0.9	5.7E-01
ENSMUST00000164016	patatin-like phospholipase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914103]		Q8BJ56	1.3	1.5E-01	3.0	5.7E-02	1.6	2.2E-01	0.0	9.7E-01
ENSMUST00000163697				6.0	3.2E-05	7.4	4.5E-05	-1.9	1.3E-01	0.2	7.2E-01
ENSMUST00000149923				6.0	2.2E-04	-5.3	4.8E-02	0.9	4.2E-01	-1.0	6.9E-01
ENSMUST00000164027				-1.8	6.3E-02	-0.9	4.9E-01	1.4	1.1E-01	0.4	7.1E-01
ENSMUST00000164035	AT rich interactive domain 3B (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1930768]		Q9Z1N7	1.6	4.5E-02	1.2	2.1E-01	0.0	9.4E-01	0.4	6.1E-01
ENSMUST00000176657				6.0	1.4E-05	8.2	2.3E-03	-0.8	7.4E-01	-3.5	1.6E-02
ENSMUST00000162775				6.0	2.1E-04	7.2	1.2E-04	0.5	6.4E-01	-0.8	2.3E-01
ENSMUST00000152779				6.0	5.2E-04	10.4	1.3E-05	0.3	8.0E-01	1.2	3.9E-02
ENSMUST00000182841				6.0	1.1E-05	-12.9	2.2E-06	-0.9	1.0E-02	-0.8	5.4E-01
ENSMUST00000150503				6.0	1.6E-02	-1.0	5.9E-01	3.8	4.3E-03	-0.9	6.3E-01
ENSMUST00000182521				6.0	2.8E-04	-5.4	3.7E-03	1.2	4.9E-02	-1.1	4.9E-01
ENSMUST00000187747				6.0	1.5E-04	2.7	2.8E-03	0.2	7.5E-01	0.1	8.3E-01
ENSMUST00000193543				6.0	1.6E-04	2.2	3.7E-02	-0.6	4.4E-01	-0.8	3.5E-01
ENSMUST00000164056	zinc finger protein 710 [Source:MGI Symbol;Acc:MGI:1921747]		Q3U288	-2.4	8.5E-02	-3.6	9.5E-02	1.0	3.4E-01	2.2	2.8E-01
ENSMUST00000164066	acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI	F6PYE1		-0.8	7.5E-01	-1.3	6.0E-01	-3.0	1.2E-01	-2.6	3.7E-01
ENSMUST00000164076	brain expressed, associated with Nedd4, 1 [Source:MGI Symbol;Acc:MGI:1929597]	E9Q314		2.3	4.1E-01	4.1	2.0E-01	0.2	9.5E-01	-1.6	4.5E-01
ENSMUST00000134878				6.0	3.2E-05	0.1	9.4E-01	-0.6	2.9E-01	-5.2	7.1E-04
ENSMUST00000086508				6.0	2.3E-02	-0.8	2.6E-01	0.1	7.7E-01	-0.6	4.2E-01
ENSMUST00000149614				6.0	4.8E-05	-2.1	8.6E-02	-0.2	7.5E-01	-2.8	6.3E-02
ENSMUST00000164083	activating signal cointegrator 1 complex subunit 1 [Source:MGI Symbol;Acc:MGI:1916340]		Q9D8Z1	1.2	5.4E-01	-0.9	6.2E-01	-3.3	6.5E-02	-1.2	5.2E-01
ENSMUST00000164088	CCR4-NOT transcription complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1919318]	E9Q027		-5.8	5.2E-02	0.4	8.7E-01	3.0	1.7E-01	-3.3	2.7E-01
ENSMUST00000164093	cytochrome P450, family 2, subfamily t, polypeptide 4 [Source:MGI Symbol;Acc:MGI:2686296]	E9PWV0		2.8	2.1E-01	2.8	3.9E-01	0.1	9.7E-01	0.1	9.6E-01
ENSMUST00000164095	the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 [Source:MGI Symb		Q4U2R1	-1.7	3.4E-01	-2.1	4.1E-01	0.6	6.9E-01	1.0	6.9E-01
ENSMUST00000124934				6.0	4.4E-04	5.9	2.5E-04	0.4	6.4E-01	0.1	8.3E-01
ENSMUST00000164099	sorting nexin 19 [Source:MGI Symbol;Acc:MGI:1921581]	Q6P4T1		0.2	7.2E-01	1.1	1.1E-01	0.7	1.8E-01	-0.2	6.7E-01
ENSMUST00000164101	inhibitor of kappaB kinase gamma [Source:MGI Symbol;Acc:MGI:1338074]		O88522	1.3	6.5E-01	2.4	5.9E-01	1.4	6.9E-01	0.2	9.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000136559				6.0	4.6E-05	4.7	5.9E-04	-1.4	1.3E-01	0.0	9.9E-01
ENSMUST00000164107	breakpoint cluster region [Source:MGI Symbol;Acc:MGI:88141]		Q6PAJ1	0.0	9.8E-01	0.8	1.3E-01	0.8	7.8E-02	-0.1	8.9E-01
ENSMUST00000148952				6.0	2.2E-06	-4.5	1.3E-02	1.3	6.7E-02	-0.4	7.8E-01
ENSMUST00000195402				6.0	9.8E-04	6.4	4.1E-03	-2.7	1.7E-01	1.4	1.7E-01
ENSMUST00000154568				6.0	2.7E-04	6.5	2.4E-04	0.0	9.8E-01	-0.4	6.0E-01
ENSMUST00000164119	epithelial membrane protein 3 [Source:MGI Symbol;Acc:MGI:1098729]		O35912	-0.5	4.8E-01	0.3	7.2E-01	0.2	7.3E-01	-0.5	4.7E-01
ENSMUST00000164120	TPX2, microtubule-associated protein homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1919369]		A2APB8	3.2	8.8E-02	-1.7	6.1E-01	-0.1	9.5E-01	4.8	1.2E-01
ENSMUST00000164134				1.6	1.4E-01	1.5	1.7E-01	-1.3	1.9E-01	-1.3	2.1E-01
ENSMUST00000164137				1.2	4.6E-01	3.8	1.1E-01	1.6	4.5E-01	-1.0	5.3E-01
ENSMUST00000192510				6.0	4.8E-04	6.5	9.7E-03	-0.4	8.4E-01	-2.2	9.2E-02
ENSMUST00000122337				6.0	3.7E-03	6.5	4.5E-03	-0.7	7.0E-01	-1.5	1.8E-01
ENSMUST00000189982				6.0	2.1E-04	-0.3	8.7E-01	1.1	4.8E-01	-3.3	1.1E-01
ENSMUST00000118943				6.0	5.4E-03	6.0	1.2E-03	-0.7	6.5E-01	0.0	9.5E-01
ENSMUST00000134379				6.0	2.2E-04	0.0	9.6E-01	0.9	1.4E-01	-0.7	3.9E-01
ENSMUST00000192578				6.0	1.7E-04	-4.5	2.5E-05	-0.1	7.2E-01	-0.5	4.5E-01
ENSMUST00000193579				6.0	1.2E-03	5.0	8.4E-04	-0.9	4.3E-01	-0.1	9.1E-01
ENSMUST00000081029				6.0	2.4E-03	7.4	1.0E-05	-2.5	2.5E-02	0.0	9.2E-01
ENSMUST00000096222				6.0	7.3E-04	3.1	7.3E-03	-1.0	2.7E-01	-0.8	2.8E-01
ENSMUST00000149735				6.0	1.6E-05	-7.8	4.1E-06	-0.6	6.9E-02	-0.6	4.3E-01
ENSMUST00000164182	carboxylesterase 2A [Source:MGI Symbol;Acc:MGI:2142491]		Q8QZR3	3.9	4.2E-02	4.2	8.0E-03	-3.1	7.4E-02	-3.5	1.1E-02
ENSMUST00000164183	WD repeat domain 37 [Source:MGI Symbol;Acc:MGI:1920393]	Q05BF4		4.1	4.1E-02	-0.2	9.2E-01	-2.7	1.4E-01	1.6	3.9E-01
ENSMUST00000162002				6.0	5.4E-04	-3.8	3.7E-03	0.4	3.9E-01	0.5	6.5E-01
ENSMUST00000164189	5-oxoprolinase (ATP-hydrolysing) [Source:MGI Symbol;Acc:MGI:1922725]	E9Q484		3.9	9.7E-02	4.7	1.7E-01	0.9	7.8E-01	0.1	9.5E-01
ENSMUST00000182543				6.0	1.9E-04	4.4	3.7E-03	-2.0	1.5E-01	-0.6	5.1E-01
ENSMUST00000172659				6.0	7.0E-04	4.9	6.7E-02	-0.8	7.4E-01	0.4	7.9E-01
ENSMUST00000164199	nucleic acid binding protein 2 [Source:MGI Symbol;Acc:MGI:1917167]		Q8R2Y9	0.2	6.7E-01	1.1	1.5E-01	0.3	6.1E-01	-0.6	3.8E-01
ENSMUST00000164202	RNA binding motif protein 20 [Source:MGI Symbol;Acc:MGI:1920963]		Q3UQS8	4.5	2.1E-01	3.7	3.5E-01	-0.1	9.7E-01	0.6	8.0E-01
ENSMUST00000164208	:etyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15 [Source:MGI Symbol;Acc:MGI	G3UWF7		2.3	2.3E-01	5.2	4.0E-02	-0.1	9.5E-01	-3.1	7.5E-02
ENSMUST00000137177				6.0	2.8E-02	-3.4	1.0E-02	0.6	2.4E-01	-0.3	8.0E-01
ENSMUST00000145842				6.0	2.5E-05	7.4	2.2E-04	-1.6	2.6E-01	0.4	5.4E-01
ENSMUST00000164215	ATP/GTP binding protein 1 [Source:MGI Symbol;Acc:MGI:2159437]		Q641K1	1.1	1.8E-01	-0.1	8.9E-01	-1.3	9.6E-02	-0.1	9.3E-01
ENSMUST00000162758				6.0	1.0E-02	2.9	1.5E-01	-2.7	2.2E-01	1.4	3.3E-01
ENSMUST00000185249				6.0	3.3E-02	9.0	4.1E-05	-0.6	6.4E-01	-1.2	7.6E-02
ENSMUST00000142770				6.0	6.6E-06	6.6	2.4E-04	-0.5	6.6E-01	-0.6	3.4E-01
ENSMUST00000190838				6.0	1.3E-03	3.3	3.2E-03	0.1	9.4E-01	-0.6	3.4E-01
ENSMUST00000164235	mitogen-activated protein kinase 1 interacting protein 1-like [Source:MGI Symbol;Acc:MGI:2444022]		Q8BH93	0.9	7.7E-01	5.7	8.6E-02	0.1	9.7E-01	-4.7	9.4E-02
ENSMUST00000164242	coiled-coil alpha-helical rod protein 1 [Source:MGI Symbol;Acc:MGI:2385321]		Q8K2I2	1.6	4.0E-01	1.9	3.2E-01	-1.1	5.4E-01	-1.4	4.3E-01
ENSMUST00000133937				6.0	5.5E-06	-4.4	1.4E-03	0.4	3.7E-01	-1.3	2.6E-01
ENSMUST00000154664				6.0	1.9E-04	6.9	1.1E-04	-0.6	6.0E-01	-0.7	2.5E-01
ENSMUST00000130270				6.0	2.4E-04	-5.3	3.0E-03	0.5	4.0E-01	0.8	5.8E-01
ENSMUST00000145493				6.0	2.1E-04	4.1	4.2E-02	-0.7	7.0E-01	2.0	1.3E-01
ENSMUST00000148477				6.0	5.2E-03	8.4	6.1E-05	-0.7	6.1E-01	-0.7	2.8E-01
ENSMUST00000164273	pannexin 1 [Source:MGI Symbol;Acc:MGI:1860055]		Q9JIP4	3.0	4.8E-02	7.0	9.5E-03	2.9	1.8E-01	-1.1	3.9E-01
ENSMUST00000127447				6.0	6.1E-04	6.6	2.0E-04	-0.6	6.2E-01	-1.2	8.0E-02
ENSMUST00000121068				6.0	6.9E-04	7.6	5.6E-05	-0.6	6.1E-01	-0.3	5.6E-01
ENSMUST00000121448				6.0	1.2E-03	-3.4	1.9E-02	1.7	1.5E-02	-0.6	6.6E-01
ENSMUST00000117343				6.0	2.2E-04	-1.8	3.1E-01	0.3	7.9E-01	-3.2	1.5E-01
ENSMUST00000145861				6.0	9.0E-06	-5.3	3.6E-03	1.3	6.3E-02	-1.5	3.7E-01
ENSMUST00000164309	chromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:103	Q52KC3		-0.3	6.0E-01	0.2	8.0E-01	0.7	2.1E-01	0.2	7.6E-01
ENSMUST00000154382				6.0	2.7E-04	4.9	1.5E-04	-1.0	2.1E-01	-0.3	5.7E-01
ENSMUST00000164326	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:109301]	E9Q5Z1		0.8	7.3E-01	-2.6	2.3E-01	-4.1	3.5E-02	-0.7	7.6E-01
ENSMUST00000147444				6.0	1.8E-04	-3.6	6.1E-03	-0.3	5.8E-01	-0.9	4.5E-01
ENSMUST00000062127				6.0	2.1E-04	6.6	1.8E-04	-0.4	7.6E-01	0.3	6.8E-01
ENSMUST00000164337	ATH1, acid trehalase-like 1 (yeast) [Source:MGI Symbol;Acc:MGI:2444047]	E9Q4H7		0.7	5.7E-01	3.0	1.1E-01	0.7	6.6E-01	-1.6	2.5E-01
ENSMUST00000164342	tight junction associated protein 1 [Source:MGI Symbol;Acc:MGI:1921344]		Q9DCD5	-3.1	8.5E-02	-1.1	6.3E-01	2.0	2.6E-01	-0.1	9.6E-01
ENSMUST00000120649				6.0	1.1E-04	6.9	2.3E-04	0.1	9.2E-01	0.2	7.4E-01
ENSMUST00000145974				6.0	9.4E-05	-3.5	1.2E-02	0.4	4.3E-01	0.3	7.9E-01
ENSMUST00000146416				6.0	5.3E-03	-5.5	1.1E-02	1.6	3.6E-02	0.7	7.2E-01
ENSMUST00000119360				6.0	4.0E-04	3.8	2.2E-02	-1.7	2.5E-01	-0.6	6.0E-01
ENSMUST00000164372	predicted gene 2244 [Source:MGI Symbol;Acc:MGI:3780414]	L7N2A3		5.0	9.2E-02	3.7	2.9E-01	-0.2	9.4E-01	1.1	6.1E-01
ENSMUST00000161723				6.0	4.1E-04	2.8	2.9E-01	-0.8	7.5E-01	2.8	1.6E-01
ENSMUST00000164374				1.6	5.0E-02	2.3	3.0E-02	0.4	6.4E-01	-0.3	7.3E-01
ENSMUST00000120088				6.0	5.7E-04	-1.8	8.9E-02	1.1	8.0E-02	-0.6	5.8E-01
ENSMUST00000140202				6.0	2.9E-04	5.6	3.9E-02	7.7	5.1E-03	-1.4	3.2E-01
ENSMUST00000142110				6.0	1.4E-04	-2.5	8.9E-02	-0.1	9.4E-01	-1.6	3.2E-01
ENSMUST00000137369				6.0	7.4E-03	-3.5	2.7E-02	-0.3	6.9E-01	-1.7	2.7E-01
ENSMUST00000148676				6.0	4.2E-04	4.7	2.8E-04	-2.8	1.5E-02	0.3	6.4E-01
ENSMUST00000154706				6.0	1.8E-05	-0.2	8.9E-01	1.2	2.1E-01	-2.4	9.7E-02
ENSMUST00000156354				6.0	1.0E-05	8.4	4.4E-07	0.5	4.4E-01	0.5	2.3E-01
ENSMUST00000119629				6.0	1.8E-03	-3.7	1.1E-02	0.2	7.2E-01	-0.9	4.7E-01
ENSMUST00000129620				6.0	3.7E-04	8.8	5.3E-04	-0.9	6.5E-01	0.5	5.1E-01
ENSMUST00000137971				6.0	1.0E-03	8.1	3.5E-05	-0.6	6.0E-01	0.2	7.1E-01
ENSMUST00000164427				-2.0	7.2E-02	-1.4	3.0E-01	0.2	7.9E-01	-0.4	7.7E-01
ENSMUST00000164428	predicted gene, 17455 [Source:MGI Symbol;Acc:MGI:4937089]	G3UW87		-1.0	2.6E-01	-1.6	2.2E-01	0.2	7.9E-01	0.8	4.9E-01
ENSMUST00000022851				6.0	3.6E-03	-5.3	1.0E-02	1.2	1.0E-01	0.6	7.2E-01
ENSMUST00000130883				6.0	6.9E-05	-1.0	2.1E-01	0.1	7.7E-01	-1.4	1.0E-01
ENSMUST00000142308				6.0	8.9E-05	1.9	4.3E-01	6.1	6.8E-03	0.5	7.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000161894				6.0	1.1E-05	7.9	5.2E-05	-0.6	6.0E-01	-0.5	3.6E-01
ENSMUST00000164458	peptidylprolyl isomerase (cyclophilin)-like 2 [Source:MGI Symbol;Acc:MGI:2447857]		Q9D787	-4.7	4.0E-02	-6.8	1.8E-02	-3.2	1.7E-02	-1.1	6.8E-01
ENSMUST00000144929				6.0	2.0E-04	4.7	5.0E-02	-0.6	7.9E-01	0.4	7.6E-01
ENSMUST00000164460				-1.4	1.1E-01	0.0	1.0E+00	0.2	8.2E-01	-1.3	2.1E-01
ENSMUST00000164465	oligodendrocyte myelin glycoprotein [Source:MGI Symbol;Acc:MGI:106586]	G3XA53		1.9	5.9E-02	0.8	4.7E-01	-0.8	3.7E-01	0.3	7.3E-01
ENSMUST00000137934				6.0	1.0E-05	-6.4	2.0E-03	-0.9	1.4E-01	0.4	7.9E-01
ENSMUST00000182922				6.0	1.7E-03	3.2	2.6E-02	-2.0	1.4E-01	1.0	2.5E-01
ENSMUST00000152260				6.0	4.2E-04	-2.4	4.4E-02	0.4	5.3E-01	-2.1	1.2E-01
ENSMUST00000164474	in homology domain containing, family H (with MyTH4 domain) member 3 [Source:MGI Symbol;Acc:MGI:2		Q8VCE9	2.7	2.9E-01	0.4	8.5E-01	-3.9	1.0E-01	-1.6	4.2E-01
ENSMUST00000164476				-2.4	1.1E-01	-2.7	1.6E-01	-0.7	5.3E-01	-0.4	8.2E-01
ENSMUST00000154281				6.0	4.7E-03	5.4	1.8E-03	-0.6	6.6E-01	0.0	9.6E-01
ENSMUST00000160046				6.0	6.5E-04	5.4	4.5E-04	-0.5	6.6E-01	-0.3	7.1E-01
ENSMUST00000175650				6.0	1.6E-03	6.3	3.9E-03	-0.6	7.2E-01	-1.0	3.2E-01
ENSMUST00000139448				6.0	1.3E-04	8.9	1.9E-04	-0.8	6.1E-01	0.5	4.5E-01
ENSMUST00000142265				6.0	2.2E-02	-2.9	9.3E-02	1.4	1.4E-01	0.7	6.7E-01
ENSMUST00000142514				6.0	2.9E-05	-3.0	9.9E-03	0.5	3.4E-01	-1.8	1.2E-01
ENSMUST00000164506	coiled-coil domain containing 43 [Source:MGI Symbol;Acc:MGI:1289318]	E9Q2S9		4.3	5.6E-02	0.2	9.5E-01	-2.2	3.0E-01	1.9	4.4E-01
ENSMUST00000138543				6.0	2.1E-04	6.9	1.9E-04	-0.6	6.5E-01	-0.1	9.0E-01
ENSMUST00000164512	predicted gene 2974 [Source:MGI Symbol;Acc:MGI:3781152]	L7N2C2		3.3	4.0E-02	5.4	3.3E-03	-0.5	7.3E-01	-2.7	2.4E-02
ENSMUST00000164513	C-type lectin domain family 9, member a [Source:MGI Symbol;Acc:MGI:2444608]		Q8BRU4	2.7	8.8E-02	5.8	2.5E-02	2.7	2.3E-01	-0.4	7.5E-01
ENSMUST00000144792				6.0	9.5E-05	6.3	2.3E-04	0.1	9.5E-01	-0.3	6.0E-01
ENSMUST00000130197				6.0	8.2E-03	7.8	1.6E-03	-0.2	9.2E-01	0.3	7.6E-01
ENSMUST00000154475				6.0	9.7E-04	4.4	1.2E-02	-1.5	3.7E-01	-0.4	6.7E-01
ENSMUST00000164529	leukemia inhibitory factor receptor [Source:MGI Symbol;Acc:MGI:96788]		P42703	1.2	4.5E-02	1.2	6.8E-02	-0.7	2.2E-01	-0.7	2.4E-01
ENSMUST00000160141				6.0	9.3E-04	-7.8	8.7E-04	0.9	1.3E-01	-2.0	3.1E-01
ENSMUST00000126650				6.0	8.7E-06	6.8	1.1E-03	-0.3	8.7E-01	0.3	7.2E-01
ENSMUST00000174106				6.0	2.3E-04	9.9	2.8E-05	-1.7	2.8E-01	0.6	3.0E-01
ENSMUST00000174575				6.0	1.8E-03	7.5	6.3E-05	-0.5	6.5E-01	0.0	9.9E-01
ENSMUST00000182694				6.0	1.1E-04	-6.6	4.6E-04	-2.0	3.0E-03	-1.0	4.8E-01
ENSMUST00000189290				6.0	4.8E-06	3.2	7.8E-02	-0.7	6.7E-01	2.5	6.2E-02
ENSMUST00000128735				6.0	1.2E-04	-4.5	3.4E-03	0.9	7.5E-02	-0.4	7.6E-01
ENSMUST00000120712				6.0	1.9E-04	-7.3	2.8E-04	0.0	9.9E-01	0.2	9.0E-01
ENSMUST00000164558	YLP motif containing 1 [Source:MGI Symbol;Acc:MGI:1926195]	F6YTL8		-3.8	1.3E-01	-3.0	3.1E-01	-0.3	8.7E-01	-1.1	7.4E-01
ENSMUST00000137377				6.0	7.5E-06	7.4	8.3E-06	1.6	8.4E-02	0.1	7.4E-01
ENSMUST00000141296				6.0	6.3E-04	-2.6	2.7E-01	3.2	4.2E-02	-0.2	9.1E-01
ENSMUST00000147537				6.0	3.1E-05	-2.6	3.6E-02	1.3	5.7E-02	-0.2	8.5E-01
ENSMUST00000152354				6.0	4.6E-05	5.7	2.9E-04	-3.2	2.0E-02	-0.2	7.2E-01
ENSMUST00000133760				6.0	2.6E-05	-9.2	1.6E-04	-0.8	1.8E-01	-2.6	2.0E-01
ENSMUST00000164591	interferon gamma receptor 1 [Source:MGI Symbol;Acc:MGI:107655]	E9PX11		-2.1	4.7E-02	0.9	5.1E-01	3.6	4.4E-03	0.6	6.5E-01
ENSMUST00000064349				6.0	5.3E-04	1.3	1.2E-01	0.5	4.3E-01	1.0	1.6E-01
ENSMUST00000121036				6.0	4.6E-04	5.8	1.2E-04	1.6	8.7E-02	-0.7	2.3E-01
ENSMUST00000128177				6.0	2.5E-04	8.0	7.8E-07	-0.6	4.2E-01	-0.1	7.9E-01
ENSMUST00000164614	alpha 1,4-galactosyltransferase [Source:MGI Symbol;Acc:MGI:3512453]	Q3UF00	Q67BJ4	4.0	1.4E-01	5.3	7.5E-02	-0.5	8.5E-01	-1.8	3.3E-01
ENSMUST00000126445				6.0	1.7E-03	2.8	2.5E-02	-0.3	7.6E-01	-0.4	6.3E-01
ENSMUST00000147278				6.0	2.5E-03	5.3	6.0E-04	-1.4	2.5E-01	-0.1	9.0E-01
ENSMUST00000072570				6.0	4.1E-04	4.5	7.7E-02	-1.4	5.8E-01	0.1	9.3E-01
ENSMUST00000126605				6.0	6.0E-03	-1.0	3.6E-01	1.2	1.6E-01	-2.7	6.2E-02
ENSMUST00000164639	5-hydroxytryptamine (serotonin) receptor 7 [Source:MGI Symbol;Acc:MGI:99841]		P32304	-0.2	8.9E-01	2.5	2.6E-01	1.7	3.6E-01	-1.0	5.5E-01
ENSMUST00000135254				6.0	2.3E-04	5.7	3.4E-02	-0.8	7.4E-01	2.1	1.5E-01
ENSMUST00000159803				6.0	1.7E-04	8.5	9.8E-03	-0.9	7.6E-01	-1.8	2.4E-01
ENSMUST00000195415				6.0	1.3E-05	4.6	2.1E-03	-0.6	5.7E-01	-0.3	7.2E-01
ENSMUST00000073347				6.0	4.0E-04	9.3	3.2E-03	-0.8	7.7E-01	-3.5	1.9E-02
ENSMUST00000164665	ankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 [Source:MGI Symbol;Acc:MGI:1921743	F6V619		-2.9	5.8E-02	-0.8	6.5E-01	1.4	1.9E-01	-0.7	6.9E-01
ENSMUST00000152300				6.0	2.1E-05	5.7	7.2E-04	0.4	7.1E-01	0.5	4.2E-01
ENSMUST00000127507				6.0	6.6E-04	5.8	5.4E-03	0.5	7.4E-01	-1.4	1.5E-01
ENSMUST00000129406				6.0	8.3E-05	6.6	3.5E-04	-1.7	2.1E-01	0.7	3.2E-01
ENSMUST00000164680				-1.4	1.3E-01	1.2	3.5E-01	1.9	8.9E-02	-0.7	4.9E-01
ENSMUST00000123133				6.0	4.5E-03	-6.5	2.6E-02	2.0	4.9E-02	0.7	8.0E-01
ENSMUST00000130623				6.0	9.7E-06	5.2	3.3E-04	-2.3	5.8E-02	-1.2	1.0E-01
ENSMUST00000190030				6.0	5.2E-03	5.8	1.6E-03	-0.6	7.0E-01	-0.5	5.5E-01
ENSMUST00000164713	stonin 2 [Source:MGI Symbol;Acc:MGI:1918272]	E9PXP7		5.4	8.4E-02	1.8	5.5E-01	-3.7	2.7E-01	-0.1	9.6E-01
ENSMUST00000164717				0.1	9.6E-01	1.7	4.7E-01	-0.8	6.9E-01	-2.4	2.7E-01
ENSMUST00000164721	neuregulin 4 [Source:MGI Symbol;Acc:MGI:1933833]		Q9WTX4	5.9	4.7E-02	6.7	5.8E-02	1.6	6.2E-01	0.8	7.3E-01
ENSMUST00000164727	coagulation factor XIII, A1 subunit [Source:MGI Symbol;Acc:MGI:1921395]		Q8BH61	-0.9	7.8E-01	0.6	8.8E-01	0.1	9.6E-01	-1.3	6.8E-01
ENSMUST00000164728	activated leukocyte cell adhesion molecule [Source:MGI Symbol;Acc:MGI:1313266]	E9Q4G8		-2.3	1.5E-01	1.0	6.0E-01	1.2	4.5E-01	-2.1	2.1E-01
ENSMUST00000085826				6.0	1.5E-05	-1.3	5.0E-01	5.9	4.3E-04	-0.6	7.5E-01
ENSMUST00000164733	transmembrane protein 176B [Source:MGI Symbol;Acc:MGI:1916348]		Q9R1Q6	0.0	9.8E-01	1.1	5.1E-01	-0.2	8.7E-01	-1.4	3.8E-01
ENSMUST00000164744	ubiquitin-like modifier activating enzyme 3 [Source:MGI Symbol;Acc:MGI:1341217]	Q3TL72		-4.5	1.1E-01	-2.8	4.1E-01	0.5	8.1E-01	-1.1	7.4E-01
ENSMUST00000140994				6.0	3.5E-05	-7.5	6.5E-05	-0.3	3.8E-01	-0.7	5.6E-01
ENSMUST00000164748	retinoic acid receptor, alpha [Source:MGI Symbol;Acc:MGI:97856]	Q3U3R3	P11416	-1.6	5.0E-01	-3.9	4.5E-01	2.4	3.1E-01	4.8	3.4E-01
ENSMUST00000159301				6.0	3.8E-04	1.5	8.0E-02	-2.0	1.9E-02	0.1	8.8E-01
ENSMUST00000130535				6.0	4.0E-04	6.7	7.7E-06	-1.2	1.6E-01	-0.6	1.8E-01
ENSMUST00000136295				6.0	7.3E-06	-5.2	1.1E-04	0.9	3.3E-02	0.1	9.1E-01
ENSMUST00000147518				6.0	2.0E-03	-1.6	1.3E-01	-1.0	1.7E-01	-3.2	2.8E-02
ENSMUST00000164759	SET binding factor 2 [Source:MGI Symbol;Acc:MGI:1921831]	E9Q305		0.1	9.1E-01	-1.9	1.5E-01	-0.2	7.6E-01	1.7	1.7E-01
ENSMUST00000154479				6.0	1.6E-04	6.2	8.8E-02	-0.9	8.0E-01	0.4	8.2E-01
ENSMUST00000161946				6.0	5.4E-04	-2.6	1.9E-01	0.8	4.8E-01	-1.4	5.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000164765				-3.4	6.7E-02	-2.7	2.3E-01	0.4	7.2E-01	-0.2	9.2E-01
ENSMUST00000178818				6.0	1.1E-02	0.6	5.6E-01	-1.9	5.0E-02	1.2	2.3E-01
ENSMUST00000117318				6.0	1.8E-04	6.2	2.3E-02	-0.6	8.0E-01	-1.4	3.3E-01
ENSMUST00000164773	pleckstrin homology-like domain, family A, member 1 [Source:MGI Symbol;Acc:MGI:1096880]		Q62392	1.0	7.1E-02	0.8	2.5E-01	0.4	4.8E-01	0.5	3.5E-01
ENSMUST00000149114				6.0	6.0E-04	-1.8	3.1E-01	2.1	6.2E-02	-0.6	7.1E-01
ENSMUST00000164776	MMS19 (MET18 S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919449]	E9PUY8		-3.3	1.0E-01	-5.6	4.3E-02	-1.8	1.0E-01	0.5	8.5E-01
ENSMUST00000164782	coagulation factor C homolog (Limulus polyphemus) [Source:MGI Symbol;Acc:MGI:1278313]		Q62507	3.8	5.2E-02	6.4	5.5E-03	-0.5	8.0E-01	-3.1	2.6E-02
ENSMUST00000180618				6.0	1.9E-04	6.0	3.1E-04	-2.0	1.2E-01	-0.4	5.3E-01
ENSMUST00000127386				6.0	4.4E-04	7.0	1.7E-04	-0.5	6.6E-01	-0.5	4.3E-01
ENSMUST00000153944				6.0	5.6E-04	6.0	2.3E-02	-0.8	7.5E-01	-1.3	3.9E-01
ENSMUST00000164275				6.0	2.3E-04	6.8	8.5E-05	-0.6	6.1E-01	-1.0	1.2E-01
ENSMUST00000126304				6.0	1.7E-04	-8.9	1.5E-02	-0.5	5.8E-01	1.9	5.5E-01
ENSMUST00000137083				6.0	7.9E-05	5.1	3.1E-04	-2.6	3.6E-02	-1.2	8.3E-02
ENSMUST00000138634				6.0	6.4E-04	-6.7	5.7E-04	-1.2	3.3E-02	-0.4	7.9E-01
ENSMUST00000145505				6.0	8.5E-06	4.5	4.2E-02	0.0	9.9E-01	-0.5	7.2E-01
ENSMUST00000163013				6.0	6.0E-04	1.9	1.7E-02	0.2	6.6E-01	0.5	4.1E-01
ENSMUST00000119105				6.0	2.8E-04	6.2	2.3E-05	-0.7	4.0E-01	-0.6	2.0E-01
ENSMUST00000164821				2.9	8.7E-02	3.4	1.2E-01	-0.5	7.8E-01	-1.0	4.9E-01
ENSMUST00000146436				6.0	1.9E-04	-1.6	1.2E-01	1.0	1.1E-01	-1.0	3.3E-01
ENSMUST00000152890				6.0	1.3E-04	-5.4	9.2E-03	-0.5	4.8E-01	0.0	9.9E-01
ENSMUST00000164831	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]	E9Q9D6		1.8	4.1E-01	1.3	6.5E-01	-0.9	6.7E-01	-0.3	9.0E-01
ENSMUST00000155728				6.0	4.8E-04	-5.4	6.1E-03	-0.3	6.1E-01	-0.8	6.3E-01
ENSMUST00000174258				6.0	3.0E-04	4.8	2.5E-03	-1.4	2.9E-01	-0.8	3.3E-01
ENSMUST00000186997				6.0	3.7E-04	-1.4	2.7E-01	0.6	4.3E-01	-1.5	2.5E-01
ENSMUST00000188944				6.0	5.9E-05	6.2	2.2E-04	-1.5	2.2E-01	-0.2	7.7E-01
ENSMUST00000118978				6.0	6.2E-03	-5.0	3.8E-03	1.6	1.8E-02	-3.1	1.1E-01
ENSMUST00000124181				6.0	3.8E-03	8.0	6.4E-05	-0.7	6.0E-01	-0.2	7.2E-01
ENSMUST00000146499				6.0	6.0E-04	5.8	1.5E-04	-1.9	8.8E-02	0.0	9.7E-01
ENSMUST00000184922				6.0	4.8E-04	7.4	5.7E-05	0.5	6.7E-01	-0.4	4.7E-01
ENSMUST00000127718				6.0	1.6E-05	6.6	4.2E-04	-0.4	7.5E-01	-0.9	2.3E-01
ENSMUST00000161922				6.0	2.2E-03	-2.2	8.6E-02	-0.7	3.5E-01	-3.1	5.7E-02
ENSMUST00000136260				6.0	2.2E-03	5.1	1.6E-03	-2.1	1.3E-01	-0.3	6.6E-01
ENSMUST00000145439				6.0	2.0E-03	5.7	1.7E-03	-0.6	6.5E-01	0.4	5.9E-01
ENSMUST00000156278				6.0	1.3E-03	4.8	7.5E-02	0.0	9.9E-01	0.3	8.3E-01
ENSMUST00000164884	family with sequence similarity 96, member B [Source:MGI Symbol;Acc:MGI:1915773]		Q9D187	3.7	6.1E-02	0.6	7.9E-01	-1.8	3.1E-01	1.3	5.1E-01
ENSMUST00000172539				6.0	7.6E-05	-5.0	3.9E-06	-0.5	6.7E-02	-1.0	7.5E-02
ENSMUST00000164890	lysophosphatidic acid receptor 2 [Source:MGI Symbol;Acc:MGI:1858422]	Q6P290		2.3	5.0E-01	-2.8	6.7E-01	-0.6	8.6E-01	4.5	4.5E-01
ENSMUST00000164900				-2.4	5.9E-02	-3.5	4.0E-02	-1.2	1.5E-01	-0.1	9.5E-01
ENSMUST00000162050				6.0	5.2E-04	-4.8	1.3E-03	-0.7	2.0E-01	-0.7	5.3E-01
ENSMUST00000164907	vimentin-type intermediate filament associated coiled-coil protein [Source:MGI Symbol;Acc:MGI:2146912]	G3XA49		0.3	7.8E-01	0.3	8.2E-01	1.4	2.1E-01	1.4	2.9E-01
ENSMUST00000165917				6.0	3.7E-04	6.9	3.7E-04	0.2	8.8E-01	0.0	1.0E+00
ENSMUST00000164916	coiled-coil domain containing 58 [Source:MGI Symbol;Acc:MGI:2146423]		Q8R3Q6	-1.8	4.3E-01	0.1	9.3E-01	-2.2	1.8E-01	-4.2	7.7E-02
ENSMUST00000164927	calcium activated nucleotidase 1 [Source:MGI Symbol;Acc:MGI:1923275]		Q8VCF1	2.6	1.9E-01	2.8	2.6E-01	-0.6	7.7E-01	-0.8	6.7E-01
ENSMUST00000119840				6.0	4.8E-04	6.7	1.4E-04	-0.6	6.0E-01	-0.3	6.4E-01
ENSMUST00000129902				6.0	6.7E-06	2.5	1.2E-02	0.6	4.1E-01	-0.1	8.6E-01
ENSMUST00000117847				6.0	6.7E-04	7.8	6.7E-05	-0.2	8.9E-01	0.3	6.2E-01
ENSMUST00000121213				6.0	9.7E-03	7.6	2.0E-04	1.7	1.9E-01	-0.4	5.2E-01
ENSMUST00000164939				0.9	6.2E-02	0.5	4.3E-01	-0.2	6.2E-01	0.2	6.9E-01
ENSMUST00000123226				6.0	4.2E-04	-7.7	9.0E-04	-1.3	4.1E-02	-0.9	6.3E-01
ENSMUST00000185273				6.0	1.3E-05	7.3	1.1E-04	-0.6	6.0E-01	0.2	6.8E-01
ENSMUST00000164950	transmembrane protein 191C [Source:MGI Symbol;Acc:MGI:107238]		Q9JJB1	2.9	8.1E-02	6.0	2.4E-03	-0.5	7.4E-01	-3.6	9.4E-03
ENSMUST00000150094				6.0	1.6E-03	6.9	5.9E-05	-0.9	4.0E-01	-0.8	1.8E-01
ENSMUST00000134380				6.0	9.2E-05	4.7	1.0E-02	0.0	9.9E-01	1.4	1.7E-01
ENSMUST00000144391				6.0	8.5E-04	-10.1	6.4E-04	1.3	2.9E-02	-0.3	9.1E-01
ENSMUST00000141515				6.0	5.1E-05	6.7	3.4E-04	-0.3	7.8E-01	-0.7	3.2E-01
ENSMUST00000145306				6.0	5.8E-03	-0.1	8.9E-01	0.2	7.5E-01	-3.5	1.7E-02
ENSMUST00000195160				6.0	5.7E-04	3.8	2.1E-03	0.1	9.4E-01	0.0	9.9E-01
ENSMUST00000164980	coronin, actin binding protein 1C [Source:MGI Symbol;Acc:MGI:1345964]	E9PX03		-1.7	4.4E-01	-0.5	8.3E-01	-0.4	7.9E-01	-1.6	4.9E-01
ENSMUST00000164989	nischarin [Source:MGI Symbol;Acc:MGI:1928323]		Q80TM9	0.3	8.9E-01	-0.6	8.5E-01	-1.2	6.2E-01	-0.2	9.3E-01
ENSMUST00000109390				5.9	1.1E-03	-3.3	1.7E-02	0.3	6.0E-01	-1.1	4.2E-01
ENSMUST00000119651				5.9	6.1E-04	6.1	5.4E-04	-0.5	7.0E-01	-0.3	6.4E-01
ENSMUST00000146093				5.9	1.2E-04	0.3	8.4E-01	1.9	1.4E-01	-2.4	1.8E-01
ENSMUST00000165015	tripartite motif-containing 13 [Source:MGI Symbol;Acc:MGI:1913847]		Q9CYB0	3.8	1.1E-01	5.0	1.5E-01	0.7	8.1E-01	-0.4	8.4E-01
ENSMUST00000165017	nucleolar and coiled-body phosphoprotein 1 [Source:MGI Symbol;Acc:MGI:1918019]	E9Q5C9		0.1	8.0E-01	-1.1	7.9E-02	-1.2	1.3E-02	0.0	9.7E-01
ENSMUST00000186356				5.9	3.3E-03	8.0	1.3E-03	0.0	9.9E-01	0.4	5.8E-01
ENSMUST00000121061				5.9	5.9E-04	0.2	9.0E-01	-1.8	1.8E-01	1.8	2.1E-01
ENSMUST00000163992				5.9	5.4E-05	-1.6	1.1E-01	0.3	6.6E-01	-0.5	5.9E-01
ENSMUST00000165033	early growth response 1 [Source:MGI Symbol;Acc:MGI:95295]	Q544D6	P08046	-3.1	3.1E-01	-0.7	8.5E-01	1.1	6.8E-01	-1.4	6.9E-01
ENSMUST00000117959				5.9	2.4E-04	4.5	3.8E-04	-0.8	3.1E-01	-0.5	4.4E-01
ENSMUST00000165052	inositol polyphosphate phosphatase-like 1 [Source:MGI Symbol;Acc:MGI:1333787]		Q6P549	-4.2	4.7E-02	-3.4	1.6E-01	0.7	5.9E-01	0.0	1.0E+00
ENSMUST00000121587				5.9	1.2E-02	9.2	1.7E-03	-1.0	6.7E-01	0.7	4.9E-01
ENSMUST00000126861				5.9	6.1E-04	6.7	2.8E-04	-0.5	6.7E-01	0.1	8.8E-01
ENSMUST00000165066	INO80 complex subunit D [Source:MGI Symbol;Acc:MGI:3027003]	E9Q9Q0		1.9	4.6E-01	1.4	7.0E-01	-0.8	7.7E-01	-0.2	9.5E-01
ENSMUST00000165079	BTB (POZ) domain containing 6 [Source:MGI Symbol;Acc:MGI:3026623]		Q8K2J9	0.3	7.6E-01	-2.0	2.0E-01	0.2	8.1E-01	2.6	9.5E-02
ENSMUST00000165087	male germ cell-associated kinase [Source:MGI Symbol;Acc:MGI:96913]		Q04859	7.1	3.6E-02	2.0	5.0E-01	-2.9	3.9E-01	2.2	3.1E-01
ENSMUST00000119363				5.9	2.5E-06	7.1	1.3E-04	-0.6	6.1E-01	-0.6	3.2E-01
ENSMUST00000165095	protein kinase C and casein kinase substrate in neurons 2 [Source:MGI Symbol;Acc:MGI:1345153]	Q3TDA7	Q9WVE8	4.4	1.9E-01	8.0	8.8E-02	1.4	7.5E-01	-2.2	3.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000119048				5.9	5.7E-05	-4.0	4.4E-04	1.0	2.5E-02	-0.3	7.3E-01
ENSMUST00000189126				5.9	4.4E-05	3.3	1.6E-03	0.4	5.4E-01	-0.2	7.4E-01
ENSMUST00000156698				5.9	1.2E-05	-3.9	9.3E-02	0.2	8.7E-01	-0.8	7.3E-01
ENSMUST00000176526				5.9	1.4E-05	5.0	2.0E-03	-2.0	1.6E-01	-0.5	5.1E-01
ENSMUST00000191276				5.9	8.0E-04	-7.4	9.0E-04	1.2	3.0E-02	-0.7	6.7E-01
ENSMUST00000165114	zinc finger protein 36, C3H type-like 1 [Source:MGI Symbol;Acc:MGI:107946]	Q543H2	P23950	3.6	2.7E-01	-0.7	8.2E-01	-4.1	1.7E-01	0.2	9.5E-01
ENSMUST00000135387				5.9	4.8E-05	2.9	6.7E-04	0.1	9.1E-01	0.3	5.5E-01
ENSMUST00000186367				5.9	9.4E-04	-2.8	1.9E-02	1.5	2.4E-02	-0.7	5.2E-01
ENSMUST00000151737				5.9	9.8E-04	6.4	7.1E-04	-0.6	6.9E-01	-0.5	5.0E-01
ENSMUST00000142861				5.9	9.8E-05	-9.2	1.8E-04	-0.6	1.8E-01	-0.3	8.5E-01
ENSMUST00000165969				5.9	3.2E-03	8.6	1.4E-04	-0.8	6.1E-01	0.0	9.5E-01
ENSMUST00000090704				5.9	2.7E-04	-4.7	2.7E-03	-1.4	5.5E-02	-2.6	1.1E-01
ENSMUST00000119163				5.9	1.1E-03	2.8	1.4E-02	0.1	9.1E-01	-0.4	5.5E-01
ENSMUST00000150939				5.9	1.4E-05	8.6	5.9E-06	0.1	9.4E-01	0.2	6.2E-01
ENSMUST00000140404				5.9	7.2E-05	5.9	5.9E-04	-1.0	4.3E-01	-0.3	7.1E-01
ENSMUST00000165149	olute carrier family 37 (glycerol-3-phosphate transporter), member 1 [Source:MGI Symbol;Acc:MGI:2446181	Q8R070		1.0	3.9E-02	1.5	2.7E-02	0.7	1.5E-01	0.2	6.6E-01
ENSMUST00000165153				-3.9	1.5E-01	-4.2	2.5E-01	-0.3	8.3E-01	0.0	1.0E+00
ENSMUST00000165163	tonsoku-like, DNA repair protein [Source:MGI Symbol;Acc:MGI:1919999]	F7A0T4		0.6	3.3E-01	-0.4	5.9E-01	-0.8	1.6E-01	0.1	8.4E-01
ENSMUST00000165164	polycomb group ring finger 1 [Source:MGI Symbol;Acc:MGI:1917087]		Q8R023	-0.7	7.4E-01	-4.0	1.6E-01	-2.2	1.7E-01	1.2	6.8E-01
ENSMUST00000165165	collagen, type VI, alpha 5 [Source:MGI Symbol;Acc:MGI:3648134]			6.0	5.2E-02	4.6	9.0E-02	-3.6	2.5E-01	-2.3	1.9E-01
ENSMUST00000189260				5.9	9.5E-04	6.8	1.6E-04	-0.6	6.2E-01	0.0	9.7E-01
ENSMUST00000172555				5.9	3.8E-05	6.4	2.0E-03	-0.6	7.4E-01	-2.9	2.0E-02
ENSMUST00000165179				-1.4	5.8E-01	0.3	9.1E-01	0.0	9.9E-01	-1.7	5.3E-01
ENSMUST00000126308				5.9	7.4E-03	6.0	2.9E-03	-0.5	7.8E-01	-0.3	7.7E-01
ENSMUST00000165183	somatostatin receptor 5 [Source:MGI Symbol;Acc:MGI:894282]		O08858	5.2	6.7E-02	4.5	1.4E-01	-0.8	7.9E-01	-0.1	9.8E-01
ENSMUST00000120906				5.9	3.2E-04	6.7	1.6E-04	-0.6	6.0E-01	-0.3	6.0E-01
ENSMUST00000056103				5.9	1.5E-03	5.3	1.5E-03	-1.9	1.5E-01	0.1	9.1E-01
ENSMUST00000150817				5.9	1.1E-04	2.5	1.1E-01	-0.6	6.2E-01	3.7	7.1E-03
ENSMUST00000185736				5.9	1.3E-04	6.6	6.5E-04	-0.7	6.2E-01	-0.7	3.7E-01
ENSMUST00000165199	arylsulfatase A [Source:MGI Symbol;Acc:MGI:88077]		P50428	-0.1	8.4E-01	1.1	1.8E-01	1.0	1.3E-01	-0.3	6.9E-01
ENSMUST00000165201	trichorhinophalangeal syndrome I (human) [Source:MGI Symbol;Acc:MGI:1927616]	G3UW90		-1.6	7.1E-02	-0.6	5.8E-01	0.7	3.0E-01	-0.3	7.9E-01
ENSMUST00000133539				5.9	4.4E-03	5.7	3.1E-05	-1.5	6.2E-02	0.3	5.4E-01
ENSMUST00000135133				5.9	9.9E-03	7.0	2.6E-05	-1.2	2.3E-01	-0.6	2.4E-01
ENSMUST00000165210	plectin [Source:MGI Symbol;Acc:MGI:1277961]	F6R059		3.3	1.2E-01	0.8	8.1E-01	0.1	9.7E-01	2.6	3.9E-01
ENSMUST00000165212	sorbin and SH3 domain containing 1 [Source:MGI Symbol;Acc:MGI:700014]	E9PYX6		-3.0	5.0E-02	-0.7	7.3E-01	1.8	1.7E-01	-0.6	7.6E-01
ENSMUST00000165216	aminopeptidase puromycin sensitive [Source:MGI Symbol;Acc:MGI:1101358]	F6QYF8		-2.6	1.3E-01	3.6	1.9E-01	6.0	1.1E-02	-0.2	9.3E-01
ENSMUST00000156783				5.9	1.1E-02	6.5	2.3E-04	-0.6	6.0E-01	0.4	5.7E-01
ENSMUST00000169128				5.9	1.0E-05	4.2	2.2E-02	0.4	7.7E-01	0.0	9.8E-01
ENSMUST00000139968				5.9	4.0E-03	9.2	6.4E-04	-0.2	9.1E-01	1.3	1.6E-01
ENSMUST00000165221	myosin, heavy polypeptide 3, skeletal muscle, embryonic [Source:MGI Symbol;Acc:MGI:1339709]		P13541	6.0	4.9E-02	8.4	1.5E-02	-0.3	9.2E-01	-2.7	1.3E-01
ENSMUST00000195095				5.9	1.2E-03	-4.8	1.3E-01	2.0	1.8E-01	0.3	9.0E-01
ENSMUST00000126030				5.9	9.8E-05	6.0	6.0E-03	-0.6	7.6E-01	-1.5	1.6E-01
ENSMUST00000165239	capicua homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1918972]	E9Q6T8		0.3	9.3E-01	1.1	8.1E-01	1.7	5.6E-01	0.9	8.3E-01
ENSMUST00000163393				5.9	9.6E-05	1.5	2.6E-02	-0.1	8.5E-01	0.4	4.1E-01
ENSMUST00000165252	predicted gene 5616 [Source:MGI Symbol;Acc:MGI:3646416]		Q9D0T1	0.6	8.0E-01	-1.5	5.0E-01	-4.0	5.9E-02	-1.9	4.1E-01
ENSMUST00000155363				5.9	5.4E-04	5.9	3.6E-04	-0.6	6.2E-01	-0.1	9.0E-01
ENSMUST00000190288				5.9	8.6E-05	6.4	3.1E-04	0.0	9.8E-01	-0.9	2.1E-01
ENSMUST00000145217				5.9	1.0E-02	7.9	1.2E-03	0.2	9.0E-01	0.8	3.4E-01
ENSMUST00000120231				5.9	1.1E-04	-2.6	5.1E-02	0.2	7.8E-01	-1.8	2.1E-01
ENSMUST00000140013				5.9	1.0E-04	9.7	1.9E-05	-0.8	5.6E-01	-0.8	1.5E-01
ENSMUST00000165293	pumilio RNA-binding family member 2 [Source:MGI Symbol;Acc:MGI:1931751]	E9Q0P1		5.5	4.8E-02	-0.8	8.1E-01	-4.1	1.6E-01	2.2	4.6E-01
ENSMUST00000165306	G patch domain and ankyrin repeats 1 [Source:MGI Symbol;Acc:MGI:2148975]	Q6PES3		-2.0	6.6E-02	1.1	4.0E-01	1.9	7.6E-02	-1.2	3.1E-01
ENSMUST00000184180				5.9	1.0E-03	-2.8	1.1E-01	0.5	5.6E-01	0.3	8.7E-01
ENSMUST00000165308	RIKEN cDNA 1600014C10 gene [Source:MGI Symbol;Acc:MGI:1919494]		Q8WUR0	-0.2	8.0E-01	0.4	6.4E-01	0.1	8.3E-01	-0.5	5.9E-01
ENSMUST00000165310	membrane-spanning 4-domains, subfamily A, member 6C [Source:MGI Symbol;Acc:MGI:2385644]		Q99N08	0.4	5.3E-01	-0.2	7.9E-01	-0.7	2.1E-01	-0.2	7.9E-01
ENSMUST00000187010				5.9	3.1E-04	7.5	2.4E-05	-1.5	2.0E-01	-0.1	8.4E-01
ENSMUST00000132006				5.9	1.4E-04	-6.1	1.8E-02	1.3	1.2E-01	0.1	9.7E-01
ENSMUST00000123448				5.9	2.5E-04	-5.0	1.2E-02	2.2	6.1E-03	-0.8	6.4E-01
ENSMUST00000165316	isoleucine-tRNA synthetase [Source:MGI Symbol;Acc:MGI:2145219]		Q8BU30	4.2	1.7E-01	5.4	1.1E-01	-0.5	8.8E-01	-1.7	4.1E-01
ENSMUST00000152756				5.9	6.3E-06	4.9	5.1E-02	2.0	3.7E-01	1.4	3.2E-01
ENSMUST00000165320	Flt3 interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1344336]	Q3TRV0	Q9WTJ4	0.6	4.8E-01	0.1	9.3E-01	0.4	6.3E-01	0.9	4.0E-01
ENSMUST00000146140				5.9	4.3E-04	-4.9	3.6E-03	1.5	1.4E-02	0.4	7.8E-01
ENSMUST00000175715				5.9	4.3E-05	-4.8	8.9E-02	0.1	9.1E-01	1.3	6.2E-01
ENSMUST00000130129				5.9	2.5E-05	-2.9	4.5E-02	1.1	1.4E-01	0.8	5.2E-01
ENSMUST00000165335	guanine nucleotide binding protein (G protein), beta 1 [Source:MGI Symbol;Acc:MGI:95781]	Q3TQ70	P62874	-2.6	4.8E-01	-5.5	2.7E-01	-1.9	3.7E-01	1.0	8.5E-01
ENSMUST00000150114				5.9	1.5E-03	7.7	9.1E-05	-0.4	7.3E-01	-0.7	2.6E-01
ENSMUST00000150392				5.9	1.2E-04	6.6	6.2E-03	1.9	3.2E-01	-1.1	3.1E-01
ENSMUST00000160702				5.9	4.6E-04	6.9	8.6E-05	-0.5	6.2E-01	0.0	9.9E-01
ENSMUST00000165363	sphingomyelin phosphodiesterase 4 [Source:MGI Symbol;Acc:MGI:1924876]		Q6ZPR5	-2.4	6.9E-02	-3.1	5.5E-02	-1.3	1.3E-01	-0.6	7.2E-01
ENSMUST00000165365	CD276 antigen [Source:MGI Symbol;Acc:MGI:2183926]	A6MDC5	Q8VE98	2.7	1.8E-01	5.4	1.6E-02	-0.6	7.7E-01	-3.3	4.6E-02
ENSMUST00000162035				5.9	4.8E-04	6.6	1.1E-03	2.0	1.6E-01	-2.2	2.4E-02
ENSMUST00000184602				5.9	3.7E-05	7.6	1.4E-03	-0.8	6.7E-01	0.4	6.8E-01
ENSMUST00000165381				3.2	5.9E-02	4.4	2.8E-02	-0.3	8.5E-01	-1.5	2.9E-01
ENSMUST00000165387	microtubule-associated protein, RP/EB family, member 2 [Source:MGI Symbol;Acc:MGI:106271]	E9Q1B7		2.0	3.4E-01	1.7	5.2E-01	-0.4	8.2E-01	-0.2	9.5E-01
ENSMUST00000121728				5.9	1.5E-03	6.2	1.7E-03	-0.1	9.4E-01	1.1	2.2E-01
ENSMUST00000154986				5.9	1.2E-04	-5.0	5.5E-04	1.2	9.3E-03	-0.7	5.2E-01
ENSMUST00000127675				5.9	5.4E-04	5.2	2.6E-04	0.1	9.5E-01	-0.3	6.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159325				5.9	3.8E-05	2.6	1.7E-01	6.2	2.0E-03	1.0	4.7E-01
ENSMUST00000154863				5.9	4.4E-05	-3.7	8.8E-02	1.0	4.0E-01	-0.2	9.3E-01
ENSMUST00000165400	expressed sequence AW554918 [Source:MGI Symbol;Acc:MGI:2147376]	E9QAK8		1.4	1.5E-01	-0.9	6.3E-01	1.6	2.2E-01	3.9	3.2E-02
ENSMUST00000176032				5.9	1.3E-03	6.7	7.9E-04	-1.3	3.8E-01	-0.4	6.0E-01
ENSMUST00000119411				5.9	9.3E-04	7.0	4.5E-04	-0.7	6.3E-01	-0.5	5.4E-01
ENSMUST00000167064				5.9	2.1E-04	6.5	4.8E-04	-0.6	6.5E-01	0.0	9.8E-01
ENSMUST00000135655				5.9	7.8E-05	4.7	4.3E-02	-0.5	8.0E-01	-0.4	8.0E-01
ENSMUST00000165413	serine/threonine kinase 35 [Source:MGI Symbol;Acc:MGI:1914583]		Q80ZW0	0.6	3.0E-01	0.9	2.8E-01	0.9	1.7E-01	0.6	3.9E-01
ENSMUST00000161672				5.9	4.0E-04	-4.0	4.6E-04	1.4	5.3E-03	-0.5	5.4E-01
ENSMUST00000165418	zinc finger protein 148 [Source:MGI Symbol;Acc:MGI:1332234]	Q548L0	Q61624	-0.4	3.6E-01	-0.3	5.9E-01	0.2	6.0E-01	0.1	8.5E-01
ENSMUST00000162874				5.9	1.5E-04	-4.4	9.7E-03	1.0	1.1E-01	-0.7	6.5E-01
ENSMUST00000150548				5.9	4.5E-03	0.7	3.2E-01	-1.2	6.2E-02	-0.1	8.6E-01
ENSMUST00000173765				5.9	6.4E-04	-0.1	8.4E-01	1.1	2.1E-02	-0.5	3.8E-01
ENSMUST00000189968				5.9	8.4E-04	5.8	2.5E-03	-0.6	6.8E-01	-0.5	5.5E-01
ENSMUST00000165457	C-terminal binding protein 2 [Source:MGI Symbol;Acc:MGI:1201686]	E9Q123		1.2	3.7E-01	6.0	4.3E-03	1.3	4.2E-01	-3.6	1.2E-02
ENSMUST00000165460	protein homolog associated with actin, golgi membranes and microtubules [Source:MGI Symbol;Acc:MGI:214		Q571B6	-1.5	3.5E-02	-0.9	2.8E-01	0.5	3.2E-01	-0.1	9.4E-01
ENSMUST00000129442				5.9	2.7E-04	5.1	7.3E-04	-2.0	1.1E-01	-0.2	7.2E-01
ENSMUST00000134843				5.9	2.8E-04	-0.7	6.7E-01	2.3	4.3E-02	-0.2	9.0E-01
ENSMUST00000143966				5.9	2.1E-05	4.3	1.6E-02	0.0	9.9E-01	0.6	5.6E-01
ENSMUST00000173966				5.9	2.0E-04	8.1	1.2E-04	-1.0	4.5E-01	0.6	3.3E-01
ENSMUST00000193710				5.9	8.2E-05	-1.6	1.4E-01	0.1	8.3E-01	-2.4	7.2E-02
ENSMUST00000179460				5.9	9.3E-05	-2.8	5.2E-02	1.6	2.0E-02	-0.3	8.1E-01
ENSMUST00000121722				5.9	8.9E-04	3.2	4.4E-03	0.6	4.0E-01	-0.4	5.3E-01
ENSMUST00000192768				5.9	5.4E-05	8.3	9.1E-05	-0.2	8.7E-01	0.2	7.1E-01
ENSMUST00000139457				5.9	6.1E-04	5.9	2.8E-04	-0.2	8.2E-01	0.6	3.1E-01
ENSMUST00000148360				5.9	1.5E-04	-1.4	1.4E-01	1.6	2.3E-02	-0.1	8.7E-01
ENSMUST00000176733				5.9	1.4E-04	7.4	1.1E-04	-0.7	5.9E-01	-1.3	6.6E-02
ENSMUST00000165515	cytochrome P450, family 4, subfamily f, polypeptide 16 [Source:MGI Symbol;Acc:MGI:1917351]	E9PW68		0.7	7.0E-01	4.8	3.8E-02	2.5	2.1E-01	-1.6	3.1E-01
ENSMUST00000192854				5.9	3.1E-04	3.3	7.7E-04	0.0	9.7E-01	0.2	6.4E-01
ENSMUST00000137816				5.9	4.8E-04	8.4	1.0E-02	-0.6	8.5E-01	1.9	1.8E-01
ENSMUST00000151733				5.9	7.6E-05	5.4	2.9E-04	-1.6	1.5E-01	0.5	4.5E-01
ENSMUST00000161613				5.9	3.0E-04	-6.2	2.8E-05	-1.0	1.4E-02	-0.8	3.8E-01
ENSMUST00000192977				5.9	3.6E-04	-3.1	8.2E-04	0.5	1.3E-01	-0.1	8.5E-01
ENSMUST00000050139				5.9	2.0E-04	8.0	2.3E-05	-0.6	5.9E-01	-0.6	2.3E-01
ENSMUST00000084824				5.9	3.1E-04	-1.6	1.5E-01	0.3	6.6E-01	-3.3	3.4E-02
ENSMUST00000121348				5.9	9.5E-05	8.0	2.6E-05	-0.6	6.1E-01	-0.5	3.8E-01
ENSMUST00000128278				5.9	2.9E-04	-2.9	3.9E-02	-1.1	1.4E-01	-0.8	5.5E-01
ENSMUST00000132222				5.9	2.7E-04	-4.2	8.1E-03	0.0	9.7E-01	-0.5	7.5E-01
ENSMUST00000142294				5.9	2.2E-04	5.1	7.2E-04	-0.6	5.3E-01	1.2	1.0E-01
ENSMUST00000165561	small integral membrane protein 13 [Source:MGI Symbol;Acc:MGI:2652854]		E9Q942	-0.6	2.3E-01	1.2	7.7E-02	1.5	1.2E-02	-0.3	5.6E-01
ENSMUST00000172364				5.9	1.4E-03	-4.4	3.5E-02	0.7	4.4E-01	0.6	7.5E-01
ENSMUST00000195472				5.9	3.4E-03	1.6	3.8E-02	0.1	8.1E-01	-0.1	9.3E-01
ENSMUST00000165572				1.3	5.9E-01	0.3	8.9E-01	-3.2	1.1E-01	-2.2	3.3E-01
ENSMUST00000165576	family with sequence similarity 3, member C [Source:MGI Symbol;Acc:MGI:107892]		Q91VU0	-0.1	8.4E-01	0.2	8.3E-01	-0.2	7.7E-01	-0.5	5.4E-01
ENSMUST00000165582	suppression of tumorigenicity 13 [Source:MGI Symbol;Acc:MGI:1917606]	E9Q1V0		-1.1	1.3E-01	-2.5	3.1E-02	-0.7	2.3E-01	0.7	5.0E-01
ENSMUST00000165593	ankyrin repeat domain 55 [Source:MGI Symbol;Acc:MGI:1924568]	E9Q0E9		7.1	4.2E-02	6.1	9.0E-02	-1.0	7.8E-01	0.0	9.9E-01
ENSMUST00000146884				5.9	2.2E-04	-7.8	9.4E-05	-0.1	7.4E-01	-0.2	8.4E-01
ENSMUST00000165596	DEAH (Asp-Glu-Ala-His) box polypeptide 30 [Source:MGI Symbol;Acc:MGI:1920081]		Q99PU8	-2.4	6.9E-02	-0.2	9.0E-01	0.3	7.4E-01	-1.9	2.0E-01
ENSMUST00000165599	cytoplasmic FMR1 interacting protein 2 [Source:MGI Symbol;Acc:MGI:1924134]		Q5SQX6	-0.7	4.6E-01	-1.3	4.3E-01	1.9	6.6E-02	2.5	1.0E-01
ENSMUST00000161103				5.9	1.3E-04	5.6	4.0E-04	-0.4	7.4E-01	-0.5	4.2E-01
ENSMUST00000135836				5.9	8.8E-03	-3.8	2.4E-01	2.9	8.9E-02	-0.2	9.5E-01
ENSMUST00000170456				5.9	2.3E-04	-5.6	2.6E-02	1.1	1.8E-01	-0.4	8.8E-01
ENSMUST00000187694				5.9	1.2E-04	6.6	1.2E-02	-0.8	7.4E-01	-1.3	3.4E-01
ENSMUST00000165617	programmed cell death 4 [Source:MGI Symbol;Acc:MGI:107490]		Q61823	-0.5	8.4E-01	-3.1	3.5E-01	-2.0	2.9E-01	0.6	8.7E-01
ENSMUST00000165619	predicted gene 3252 [Source:MGI Symbol;Acc:MGI:3781430]	E9PUT9		3.3	9.1E-02	4.9	2.1E-02	-0.5	7.8E-01	-2.2	1.3E-01
ENSMUST00000165623				1.1	3.1E-01	1.5	3.2E-01	0.6	6.2E-01	0.2	8.7E-01
ENSMUST00000165628	ke RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor [Source:MGI Symbol;Acc:MGI:1		Q91WQ5	-1.5	1.1E-01	-3.7	2.2E-02	0.6	4.5E-01	2.7	6.8E-02
ENSMUST00000097270				5.9	8.6E-03	-3.1	2.0E-01	1.6	2.4E-01	0.3	8.9E-01
ENSMUST00000165630	target of myb1 homolog (chicken) [Source:MGI Symbol;Acc:MGI:1338026]	Q561M4	O88746	1.3	6.3E-01	7.1	3.5E-02	2.3	4.3E-01	-3.5	1.7E-01
ENSMUST00000156775				5.9	7.6E-04	6.1	2.4E-02	0.1	9.5E-01	-0.4	7.4E-01
ENSMUST00000165648	zinc finger, DHHC domain containing 23 [Source:MGI Symbol;Acc:MGI:2685625]		Q5Y5T3	2.6	1.5E-01	1.3	6.4E-01	-0.2	9.4E-01	1.2	5.7E-01
ENSMUST00000166147				5.9	4.3E-04	-5.2	3.8E-03	0.0	9.7E-01	-1.0	5.1E-01
ENSMUST00000165654				2.3	5.4E-02	1.3	3.2E-01	-0.4	7.4E-01	0.6	5.6E-01
ENSMUST00000177522				5.9	4.3E-06	3.8	1.6E-03	0.9	2.4E-01	0.7	3.2E-01
ENSMUST00000188343				5.9	1.3E-05	6.5	7.8E-03	-4.8	7.1E-02	-2.8	3.9E-02
ENSMUST00000165677				2.8	1.2E-01	3.1	1.8E-01	1.6	4.1E-01	1.2	4.8E-01
ENSMUST00000139242				5.9	4.0E-04	4.9	1.2E-04	0.1	9.0E-01	-0.3	5.8E-01
ENSMUST00000182382				5.9	2.3E-04	6.7	3.1E-05	-0.6	5.2E-01	0.7	1.7E-01
ENSMUST00000165684	mediator complex subunit 16 [Source:MGI Symbol;Acc:MGI:2158394]	G3UW74		0.5	8.5E-01	4.1	2.6E-01	2.1	4.7E-01	-1.5	6.3E-01
ENSMUST00000165686				-0.3	7.1E-01	-0.3	7.3E-01	-0.2	7.4E-01	-0.2	8.4E-01
ENSMUST00000132634				5.9	1.4E-03	7.2	1.1E-04	0.0	9.7E-01	-0.5	4.3E-01
ENSMUST00000165690	TraB domain containing [Source:MGI Symbol;Acc:MGI:1915226]		Q99JY4	-1.0	3.0E-01	0.0	9.8E-01	0.4	6.7E-01	-0.6	5.9E-01
ENSMUST00000165704	polypyrimidine tract binding protein 1 [Source:MGI Symbol;Acc:MGI:97791]	Q8BGJ5		1.6	2.6E-01	7.1	8.6E-03	3.9	8.2E-02	-1.5	2.3E-01
ENSMUST00000142776				5.9	1.6E-04	-4.0	4.6E-03	-1.3	4.4E-02	0.1	9.1E-01
ENSMUST00000165709	ubiquitin specific peptidase 24 [Source:MGI Symbol;Acc:MGI:1919936]	E9PV45		2.8	2.2E-01	2.8	2.7E-01	0.1	9.7E-01	0.0	9.9E-01
ENSMUST00000165711	unc-93 homolog B1 (C. elegans) [Source:MGI Symbol;Acc:MGI:1859307]	E9Q8P6		0.0	1.0E+00	-1.0	8.0E-01	0.4	8.9E-01	1.4	6.8E-01
ENSMUST00000165713	predicted gene 8279 [Source:MGI Symbol;Acc:MGI:3779794]	L7N2C6		3.5	9.5E-02	5.4	2.9E-02	-0.3	8.9E-01	-2.2	1.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000165714	F-box protein 34 [Source:MGI Symbol;Acc:MGI:1926188]		Q80XI1	2.1	4.2E-01	0.8	8.0E-01	-2.1	4.5E-01	-0.8	7.6E-01
ENSMUST00000145922				5.9	2.8E-03	-9.4	6.7E-06	-0.7	3.0E-02	-0.5	6.7E-01
ENSMUST00000120909				5.9	2.8E-04	4.9	7.7E-04	-2.5	5.0E-02	0.3	6.0E-01
ENSMUST00000142367				5.9	3.6E-05	-6.7	3.0E-04	0.6	1.7E-01	-0.1	9.1E-01
ENSMUST00000130018				5.9	3.2E-04	6.0	2.8E-05	0.4	5.9E-01	-0.6	2.4E-01
ENSMUST00000165738	poly (ADP-ribose) polymerase family, member 10 [Source:MGI Symbol;Acc:MGI:3712326]	Q8CIE4		-0.9	9.9E-02	-5.8	6.3E-04	-0.6	1.9E-01	4.4	3.6E-03
ENSMUST00000135528				5.9	2.8E-05	-7.2	5.0E-04	1.3	1.5E-02	1.0	4.7E-01
ENSMUST00000165743	RIKEN cDNA 5031439G07 gene [Source:MGI Symbol;Acc:MGI:2444899]	B1APX2		1.7	6.3E-01	0.1	9.9E-01	2.4	4.9E-01	4.0	4.6E-01
ENSMUST00000141102				5.9	2.0E-04	5.8	7.2E-04	-0.1	9.3E-01	-0.3	6.4E-01
ENSMUST00000165754				1.0	2.2E-01	1.8	7.3E-02	0.1	9.1E-01	-0.8	3.6E-01
ENSMUST00000165762	histamine receptor H3 [Source:MGI Symbol;Acc:MGI:2139279]	E9Q292		3.0	1.3E-01	2.7	1.9E-01	-0.5	8.1E-01	-0.2	9.1E-01
ENSMUST00000165764	cytochrome P450, family 27, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1098274]		O35084	6.0	4.0E-02	4.4	1.3E-01	-0.8	7.7E-01	0.8	6.9E-01
ENSMUST00000165766	dynamin 2 [Source:MGI Symbol;Acc:MGI:109547]	Q3T9X3		2.1	2.7E-01	1.8	3.0E-01	-2.9	1.1E-01	-2.6	1.3E-01
ENSMUST00000165770	zinc finger protein 423 [Source:MGI Symbol;Acc:MGI:1891217]	G3UW89		6.8	5.0E-02	6.0	1.1E-01	-0.9	8.1E-01	0.0	9.9E-01
ENSMUST00000161155				5.9	1.2E-03	-5.4	1.1E-03	-1.6	1.6E-02	-0.9	5.0E-01
ENSMUST00000121361				5.9	7.0E-05	6.3	1.6E-04	-0.5	6.4E-01	0.2	7.1E-01
ENSMUST00000165783				0.8	2.8E-01	0.1	8.9E-01	0.4	5.8E-01	1.0	2.4E-01
ENSMUST00000152477				5.9	4.1E-04	7.2	2.1E-03	0.2	8.9E-01	-0.7	5.3E-01
ENSMUST00000168016				5.9	3.0E-04	4.2	1.5E-02	-0.2	8.8E-01	0.0	9.7E-01
ENSMUST00000152702				5.9	7.2E-05	-3.4	1.1E-03	0.4	3.0E-01	-0.6	4.3E-01
ENSMUST00000071458				5.9	6.0E-05	8.0	3.9E-05	-0.6	6.1E-01	-0.7	2.4E-01
ENSMUST00000134211				5.9	5.3E-05	8.9	1.6E-04	0.1	9.6E-01	0.0	9.6E-01
ENSMUST00000165819	ceramide synthase 1 [Source:MGI Symbol;Acc:MGI:2136690]		P20863	2.9	1.8E-01	2.3	2.9E-01	-0.5	8.1E-01	0.1	9.4E-01
ENSMUST00000144793				5.9	3.5E-04	8.0	9.4E-05	-0.6	6.3E-01	-0.1	8.8E-01
ENSMUST00000147982				5.9	3.6E-05	6.2	3.8E-03	-1.6	4.0E-01	0.3	7.5E-01
ENSMUST00000154059				5.9	3.3E-02	3.0	9.6E-02	-1.1	4.8E-01	0.3	8.3E-01
ENSMUST00000194828				5.9	4.8E-05	5.4	9.6E-03	-0.4	8.4E-01	-0.8	4.6E-01
ENSMUST00000165838	meteorin, glial cell differentiation regulator [Source:MGI Symbol;Acc:MGI:1917333]	A2RSN4	Q8C1Q4	1.0	2.0E-01	1.4	1.6E-01	1.0	2.4E-01	0.6	4.8E-01
ENSMUST00000123833				5.9	3.2E-06	-0.5	5.1E-01	1.1	4.7E-02	-0.5	5.0E-01
ENSMUST00000185619				5.9	6.6E-05	-3.6	3.6E-03	0.4	4.6E-01	-1.0	3.1E-01
ENSMUST00000125543				5.9	2.2E-04	3.9	6.8E-02	-2.6	2.6E-01	-1.2	4.0E-01
ENSMUST00000165856	cetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 [Source:MGI Symbol;Acc:MGI:	Q3TB05		-2.0	1.2E-01	0.8	5.9E-01	1.1	3.5E-01	-1.8	2.2E-01
ENSMUST00000142608				5.9	9.6E-07	-1.7	4.8E-01	3.3	8.1E-02	0.2	9.2E-01
ENSMUST00000150306				5.9	1.5E-03	-3.7	3.1E-01	2.4	2.1E-01	1.7	6.0E-01
ENSMUST00000123066				5.9	1.8E-02	-2.1	3.9E-01	2.3	1.3E-01	-0.2	9.2E-01
ENSMUST00000145224				5.9	7.0E-05	6.5	5.1E-04	-0.7	6.2E-01	0.2	7.3E-01
ENSMUST00000143768				5.9	4.6E-06	3.6	3.4E-02	-4.3	3.0E-02	-0.6	5.4E-01
ENSMUST00000124544				5.9	4.2E-04	3.8	1.1E-01	-0.5	8.1E-01	1.1	4.5E-01
ENSMUST00000112503				5.9	5.5E-04	-2.0	1.1E-01	1.1	1.5E-01	-1.6	2.2E-01
ENSMUST00000165874	family with sequence similarity 78, member B [Source:MGI Symbol;Acc:MGI:2443050]		Q8BQN5	3.8	1.2E-01	7.3	1.9E-02	0.8	7.8E-01	-2.7	1.0E-01
ENSMUST00000165876	microtubule-associated protein 4 [Source:MGI Symbol;Acc:MGI:97178]	A0A0B4J1M9	P27546	-0.6	8.6E-01	-1.5	6.7E-01	-1.0	7.3E-01	0.0	9.9E-01
ENSMUST00000117514				5.9	4.2E-05	-5.6	3.4E-03	0.5	4.8E-01	-2.3	2.0E-01
ENSMUST00000165887	dermokine [Source:MGI Symbol;Acc:MGI:1920962]	E9Q2P1		5.4	5.3E-02	3.4	2.3E-01	-0.7	8.0E-01	1.2	5.1E-01
ENSMUST00000165901	tsukushi, small leucine rich proteoglycan [Source:MGI Symbol;Acc:MGI:2443855]	Q08EE6	Q8CBR6	4.1	1.4E-01	1.9	5.8E-01	-0.2	9.5E-01	2.0	4.6E-01
ENSMUST00000137051				5.9	5.4E-05	8.4	1.8E-03	-0.9	6.7E-01	0.9	3.9E-01
ENSMUST00000195488				5.9	1.0E-04	4.5	5.1E-04	-0.7	4.1E-01	0.3	5.8E-01
ENSMUST00000121420				5.9	4.1E-04	6.3	1.4E-04	-0.6	6.0E-01	-0.6	3.0E-01
ENSMUST00000123573				5.9	3.7E-05	6.9	9.8E-04	-0.8	6.3E-01	0.8	3.5E-01
ENSMUST00000165913	F-box protein 46 [Source:MGI Symbol;Acc:MGI:2444918]		Q8BG80	0.7	8.2E-01	3.2	3.5E-01	0.7	8.2E-01	-1.8	5.7E-01
ENSMUST00000161113				5.9	2.4E-06	5.5	1.1E-03	-0.5	7.0E-01	-0.1	9.2E-01
ENSMUST00000117181				5.9	6.1E-03	0.5	7.1E-01	-4.1	9.4E-03	-1.1	3.9E-01
ENSMUST00000140137				5.9	5.7E-04	2.7	2.5E-01	0.7	6.4E-01	2.1	3.1E-01
ENSMUST00000143493				5.9	5.9E-03	5.6	6.7E-04	-2.9	4.7E-02	-0.8	2.5E-01
ENSMUST00000159426				5.9	3.9E-05	6.6	1.8E-02	-0.5	8.4E-01	-1.2	4.2E-01
ENSMUST00000160988				5.9	4.9E-04	6.3	1.1E-04	-1.9	1.1E-01	-0.3	5.7E-01
ENSMUST00000153120				5.9	1.8E-03	7.0	1.5E-03	-0.8	6.5E-01	-0.7	4.4E-01
ENSMUST00000113222				5.9	2.0E-02	4.2	6.3E-05	-5.4	1.6E-04	-1.1	3.0E-02
ENSMUST00000165952	large tumor suppressor [Source:MGI Symbol;Acc:MGI:1333883]		Q8BYR2	-1.1	5.5E-02	-0.2	7.4E-01	1.0	6.4E-02	0.1	8.6E-01
ENSMUST00000186517				5.9	2.1E-04	-2.8	4.3E-02	0.7	2.6E-01	0.2	9.0E-01
ENSMUST00000122167				5.9	2.7E-05	-3.0	1.2E-01	1.1	2.7E-01	0.3	8.7E-01
ENSMUST00000171234				5.9	4.8E-03	3.4	1.5E-04	-0.5	3.1E-01	-0.4	3.8E-01
ENSMUST00000165957	vaccinia related kinase 3 [Source:MGI Symbol;Acc:MGI:2182465]	E9PW85		0.5	6.4E-01	-0.1	9.3E-01	1.8	1.9E-01	2.5	1.3E-01
ENSMUST00000120448				5.9	2.4E-04	4.7	9.6E-02	-0.2	9.3E-01	2.0	2.4E-01
ENSMUST00000165964	ligase I, DNA, ATP-dependent [Source:MGI Symbol;Acc:MGI:101789]	Q3U4X8		2.8	2.8E-01	3.8	1.5E-01	-1.8	4.9E-01	-2.8	1.8E-01
ENSMUST00000143067				5.9	3.4E-04	7.8	3.2E-05	-0.2	8.6E-01	-1.1	5.2E-02
ENSMUST00000124938				5.9	4.6E-04	5.2	2.8E-03	-1.4	3.4E-01	-0.8	3.4E-01
ENSMUST00000142406				5.9	5.0E-06	5.2	1.1E-02	-0.6	7.2E-01	0.1	8.9E-01
ENSMUST00000150589				5.9	2.0E-02	-1.9	8.3E-03	-0.5	2.1E-01	-0.2	7.0E-01
ENSMUST00000165978	tectonin beta-propeller repeat containing 2 [Source:MGI Symbol;Acc:MGI:2144865]	Q3UH45		1.0	3.1E-01	-1.3	4.0E-01	0.7	5.2E-01	3.0	6.2E-02
ENSMUST00000146595				5.9	8.2E-06	-7.0	2.4E-05	-1.1	1.7E-02	-1.8	9.8E-02
ENSMUST00000165981	nischarin [Source:MGI Symbol;Acc:MGI:1928323]		Q80TM9	-2.0	5.2E-02	-2.1	1.5E-01	0.6	4.6E-01	0.7	6.0E-01
ENSMUST00000136967				5.9	9.8E-04	-7.1	1.2E-04	0.1	7.3E-01	-0.3	8.2E-01
ENSMUST00000119443				5.9	5.2E-04	-8.7	1.8E-03	0.4	4.7E-01	-1.2	6.0E-01
ENSMUST00000121358				5.9	2.0E-06	5.6	2.1E-03	-0.5	7.5E-01	-0.4	6.2E-01
ENSMUST00000165999	cytochrome P450, family 4, subfamily f, polypeptide 17 [Source:MGI Symbol;Acc:MGI:3646233]	G3UW78		-0.2	5.7E-01	0.3	5.5E-01	0.3	5.0E-01	-0.3	5.6E-01
ENSMUST00000166004	microtubule associated serine/threonine kinase 3 [Source:MGI Symbol;Acc:MGI:2683541]	E9Q8S5		-1.0	1.3E-01	-0.7	4.2E-01	0.9	1.5E-01	0.6	4.7E-01
ENSMUST00000166019	ribosomal RNA processing 7 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1922028]	E9PYF0		-1.0	5.0E-01	2.4	2.9E-01	2.5	1.8E-01	-0.9	6.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000166020	SET binding factor 2 [Source:MGI Symbol;Acc:MGI:1921831]	E9Q0D4		1.8	4.9E-01	4.5	2.0E-01	1.7	5.8E-01	-1.0	6.8E-01
ENSMUST00000166021	G patch domain containing 4 [Source:MGI Symbol;Acc:MGI:1913864]		Q3TFK5	4.5	5.9E-02	1.1	4.9E-01	-4.4	4.7E-02	-1.0	5.2E-01
ENSMUST00000133208				5.9	6.2E-04	3.7	1.5E-02	-0.6	6.1E-01	2.6	1.8E-02
ENSMUST00000166025	predicted gene 3269 [Source:MGI Symbol;Acc:MGI:3781447]	K7N735		4.2	8.3E-02	5.8	3.9E-02	-0.3	9.2E-01	-1.9	2.2E-01
ENSMUST00000139205				5.9	2.2E-04	4.9	8.8E-04	0.8	3.9E-01	1.2	8.5E-02
ENSMUST00000147838				5.9	1.0E-05	3.7	8.8E-02	-0.1	9.6E-01	0.0	1.0E+00
ENSMUST00000189517				5.9	5.3E-04	-3.5	3.4E-03	0.4	4.5E-01	-0.8	4.2E-01
ENSMUST00000155546				5.9	9.6E-03	6.5	5.0E-03	-0.7	7.3E-01	-2.2	7.9E-02
ENSMUST00000166040	palmitoyl-protein thioesterase 2 [Source:MGI Symbol;Acc:MGI:1860075]		O35448	-1.4	2.7E-01	4.9	2.0E-02	5.0	1.1E-02	-1.3	3.2E-01
ENSMUST00000120698				5.9	1.5E-05	4.5	3.4E-03	-1.9	1.7E-01	0.7	4.1E-01
ENSMUST00000166044	kinesin family member 20A [Source:MGI Symbol;Acc:MGI:1201682]		P97329	-0.1	9.0E-01	-1.4	1.7E-01	-0.9	1.7E-01	0.4	6.9E-01
ENSMUST00000123981				5.9	6.6E-04	4.3	9.6E-03	-0.6	6.4E-01	2.1	3.9E-02
ENSMUST00000124661				5.9	2.0E-02	6.1	2.3E-04	-0.6	6.0E-01	0.7	2.6E-01
ENSMUST00000166057				3.9	7.3E-02	1.8	4.8E-01	-0.5	8.3E-01	1.6	4.3E-01
ENSMUST00000168894				5.9	1.8E-02	-6.8	3.7E-04	0.3	4.5E-01	0.1	9.6E-01
ENSMUST00000131055				5.9	4.8E-04	-3.9	4.5E-03	1.6	8.9E-03	-0.8	4.7E-01
ENSMUST00000166082	chitinase domain containing 1 [Source:MGI Symbol;Acc:MGI:1915288]			-4.1	2.6E-01	0.2	9.4E-01	0.5	8.6E-01	-3.8	2.9E-01
ENSMUST00000154125				5.9	7.4E-04	2.7	3.4E-01	-0.8	7.4E-01	2.6	2.2E-01
ENSMUST00000183067				5.9	2.6E-04	-3.8	7.4E-02	0.4	7.0E-01	-3.3	2.0E-01
ENSMUST00000123209				5.9	2.3E-02	6.5	1.4E-05	-0.9	2.9E-01	0.1	7.7E-01
ENSMUST00000166103	ubiquitin specific peptidase 19 [Source:MGI Symbol;Acc:MGI:1918722]	E9Q9M5		-1.1	2.4E-01	2.3	1.1E-01	1.8	1.4E-01	-1.6	1.4E-01
ENSMUST00000148432				5.8	1.1E-03	-5.7	3.2E-04	-2.1	1.0E-03	-0.8	5.0E-01
ENSMUST00000125475				5.8	8.9E-04	9.4	8.1E-05	-0.3	8.2E-01	0.7	3.3E-01
ENSMUST00000166109				0.4	5.9E-01	-2.0	1.1E-01	-0.9	1.9E-01	1.5	2.0E-01
ENSMUST00000174611				5.8	2.1E-04	-1.7	4.4E-01	2.9	3.0E-02	1.7	4.1E-01
ENSMUST00000171355				5.8	1.8E-04	2.2	1.5E-02	0.6	3.8E-01	0.3	6.7E-01
ENSMUST00000166121	PHD finger protein 11B [Source:MGI Symbol;Acc:MGI:3645789]	B4XVQ1		0.1	9.2E-01	-3.3	1.1E-02	-3.6	1.7E-03	-0.2	8.3E-01
ENSMUST00000123350				5.8	1.4E-04	-2.1	2.7E-02	1.2	3.0E-02	-0.7	4.5E-01
ENSMUST00000136045				5.8	5.2E-05	7.4	4.7E-05	0.3	7.6E-01	0.4	4.6E-01
ENSMUST00000166135	solute carrier family 2 (facilitated glucose transporter), member 3 [Source:MGI Symbol;Acc:MGI:95757]	E9PZF2		-0.7	7.7E-01	1.0	7.9E-01	1.4	5.3E-01	-0.3	9.4E-01
ENSMUST00000166137	absent in melanoma 2 [Source:MGI Symbol;Acc:MGI:2686159]		Q91VJ1	1.6	4.4E-02	2.3	2.0E-02	0.3	6.7E-01	-0.4	5.4E-01
ENSMUST00000166139	vasohibin 2 [Source:MGI Symbol;Acc:MGI:2444826]		Q8C5G2	4.3	4.9E-02	1.3	5.4E-01	-2.3	2.5E-01	0.7	7.0E-01
ENSMUST00000145115				5.8	1.5E-04	3.6	4.4E-03	1.2	1.9E-01	0.7	3.1E-01
ENSMUST00000184851				5.8	1.6E-06	4.7	2.4E-03	-1.4	2.6E-01	-0.2	7.5E-01
ENSMUST00000166151				-1.3	2.9E-01	2.9	8.9E-02	1.5	2.9E-01	-2.7	5.1E-02
ENSMUST00000166156	polycystic kidney disease 2-like 2 [Source:MGI Symbol;Acc:MGI:1858231]		Q9JLG4	-1.7	2.2E-01	-1.2	4.6E-01	-0.5	6.3E-01	-1.0	5.3E-01
ENSMUST00000166168	leucine rich repeat containing 49 [Source:MGI Symbol;Acc:MGI:2442689]	E9Q8C9		-0.2	8.9E-01	-3.9	9.6E-02	-3.4	2.6E-02	0.3	9.0E-01
ENSMUST00000166169	zinc finger protein 219 [Source:MGI Symbol;Acc:MGI:1917140]	Q6IQX8		2.7	1.6E-01	2.8	3.2E-01	2.6	3.2E-01	2.5	1.9E-01
ENSMUST00000150238				5.8	3.0E-04	4.9	8.6E-03	-0.6	7.2E-01	2.3	2.8E-02
ENSMUST00000134111				5.8	5.5E-03	-5.7	7.1E-02	1.1	3.2E-01	1.7	5.6E-01
ENSMUST00000175695				5.8	9.5E-04	2.2	7.5E-04	-0.2	6.1E-01	-0.1	7.0E-01
ENSMUST00000175882				5.8	1.5E-04	2.9	7.6E-03	-0.1	8.7E-01	-0.8	2.6E-01
ENSMUST00000137859				5.8	7.0E-03	9.7	3.9E-06	-0.6	5.8E-01	-0.7	1.1E-01
ENSMUST00000126357				5.8	1.6E-04	5.0	1.5E-02	-3.3	1.2E-01	-2.1	1.2E-01
ENSMUST00000166214	WD repeat domain 36 [Source:MGI Symbol;Acc:MGI:1917819]	Q3TA68		-0.5	6.7E-01	-5.1	7.1E-02	-1.1	3.3E-01	3.4	1.9E-01
ENSMUST00000129882				5.8	5.5E-04	-4.0	4.6E-02	-0.1	9.1E-01	-2.3	3.1E-01
ENSMUST00000144555				5.8	2.6E-03	2.6	3.4E-02	-0.5	6.2E-01	-0.4	6.7E-01
ENSMUST00000166223	solute carrier family 38, member 4 [Source:MGI Symbol;Acc:MGI:1916604]		Q8R1S9	3.8	8.5E-02	3.2	8.9E-02	-2.6	2.1E-01	-2.1	1.6E-01
ENSMUST00000169476				5.8	1.8E-05	5.4	3.0E-02	-0.7	7.4E-01	-1.1	4.5E-01
ENSMUST00000195159				5.8	2.9E-03	2.8	6.8E-03	-6.3	4.4E-04	0.4	5.7E-01
ENSMUST00000145615				5.8	1.5E-04	-2.4	1.9E-02	0.0	9.5E-01	0.6	4.9E-01
ENSMUST00000166234				-0.9	6.0E-01	-0.3	9.3E-01	2.5	3.0E-01	1.9	4.2E-01
ENSMUST00000173796				5.8	1.1E-03	-9.2	2.4E-03	1.5	3.4E-02	0.3	9.0E-01
ENSMUST00000143777				5.8	3.2E-04	0.8	7.4E-01	-4.4	6.0E-02	1.7	4.1E-01
ENSMUST00000146807				5.8	3.7E-04	6.5	3.0E-04	-0.7	6.0E-01	0.2	7.3E-01
ENSMUST00000165968				5.8	1.2E-03	6.2	2.9E-04	0.4	7.1E-01	-0.1	9.0E-01
ENSMUST00000166247	transmembrane protein 176B [Source:MGI Symbol;Acc:MGI:1916348]		Q9R1Q6	2.3	1.9E-01	-1.0	5.3E-01	-3.5	3.0E-02	-0.2	8.9E-01
ENSMUST00000166250	zinc finger protein 710 [Source:MGI Symbol;Acc:MGI:1921747]		Q3U288	-2.1	1.7E-01	-1.4	4.5E-01	0.2	8.4E-01	-0.5	7.7E-01
ENSMUST00000166259	neuraminidase 2 [Source:MGI Symbol;Acc:MGI:1344417]	Q0VGI4	Q9JMH3	5.3	3.7E-02	3.3	2.1E-01	-0.6	8.2E-01	1.3	4.4E-01
ENSMUST00000166278	G protein-coupled receptor 160 [Source:MGI Symbol;Acc:MGI:1919112]		Q3U3F9	-3.3	1.1E-01	-0.9	7.2E-01	1.8	2.6E-01	-0.6	8.0E-01
ENSMUST00000166282	serine/threonine kinase 35 [Source:MGI Symbol;Acc:MGI:1914583]	E9PXA2		-0.4	4.4E-01	0.4	5.5E-01	0.8	1.5E-01	-0.1	9.2E-01
ENSMUST00000188408				5.8	6.7E-04	1.1	2.7E-01	-0.5	5.4E-01	1.4	1.1E-01
ENSMUST00000166294	interleukin 1 receptor accessory protein [Source:MGI Symbol;Acc:MGI:104975]	E9Q6I2		-1.5	3.2E-01	-0.6	6.5E-01	-1.9	1.0E-01	-2.8	7.6E-02
ENSMUST00000159094				5.8	9.5E-03	6.0	1.6E-02	0.4	8.4E-01	0.6	6.8E-01
ENSMUST00000166312	LUC7-like 3 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914934]		Q5SUF2	1.5	4.9E-02	1.2	1.9E-01	0.0	9.7E-01	0.3	7.2E-01
ENSMUST00000162139				5.8	9.2E-04	-1.7	3.1E-01	0.5	6.3E-01	-2.6	2.0E-01
ENSMUST00000188923				5.8	2.2E-06	6.3	8.7E-04	0.4	7.4E-01	-0.4	5.7E-01
ENSMUST00000166323				0.8	7.0E-01	1.4	5.1E-01	-1.1	5.6E-01	-1.8	3.6E-01
ENSMUST00000118266				5.8	2.9E-05	6.4	2.8E-04	-0.5	6.9E-01	-0.6	3.2E-01
ENSMUST00000166329	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:109301]	E9PVN7		1.6	5.2E-01	2.2	5.0E-01	0.3	9.1E-01	-0.3	9.2E-01
ENSMUST00000135736				5.8	8.7E-06	6.2	2.3E-03	1.6	2.7E-01	-1.0	3.2E-01
ENSMUST00000139877				5.8	5.6E-05	6.6	6.7E-03	0.7	6.8E-01	0.6	6.6E-01
ENSMUST00000149037				5.8	1.0E-03	0.4	7.5E-01	-2.9	1.6E-02	3.3	1.2E-02
ENSMUST00000166352				-0.3	7.8E-01	-0.6	6.3E-01	-0.1	8.8E-01	0.2	8.7E-01
ENSMUST00000159732				5.8	2.1E-04	7.8	3.3E-05	-1.5	2.1E-01	-0.4	4.8E-01
ENSMUST00000126299				5.8	2.1E-03	-1.0	1.2E-01	-1.5	6.4E-03	-5.0	1.7E-04
ENSMUST00000150380				5.8	6.1E-04	6.5	2.5E-04	0.6	6.3E-01	-1.4	5.2E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000135957				5.8	6.0E-04	5.8	4.9E-03	0.4	7.9E-01	0.8	4.2E-01
ENSMUST00000166382				1.5	2.5E-01	2.5	2.8E-01	3.6	8.7E-02	2.5	1.3E-01
ENSMUST00000145158				5.8	7.5E-04	-7.5	1.3E-03	0.1	8.4E-01	-0.7	6.9E-01
ENSMUST00000178932				5.8	3.2E-03	-5.2	1.4E-02	0.8	2.5E-01	-0.6	7.5E-01
ENSMUST00000084451				5.8	1.0E-04	2.6	1.2E-02	-0.5	4.9E-01	-0.3	7.0E-01
ENSMUST00000166396				-0.2	7.7E-01	1.8	9.9E-02	0.5	5.4E-01	-1.6	1.1E-01
ENSMUST00000146381				5.8	2.3E-05	-3.7	2.6E-01	2.1	2.4E-01	0.8	8.0E-01
ENSMUST00000153091				5.8	6.3E-04	6.5	6.4E-04	-0.7	6.3E-01	-0.3	7.2E-01
ENSMUST00000177157				5.8	2.6E-04	-3.9	1.9E-04	0.7	5.5E-02	-0.8	2.9E-01
ENSMUST00000122825				5.8	3.7E-05	3.2	1.8E-02	-0.4	7.3E-01	0.3	7.6E-01
ENSMUST00000154389				5.8	6.2E-04	5.0	5.2E-02	8.5	2.0E-03	-0.9	5.2E-01
ENSMUST00000166411	Sjogren syndrome antigen B [Source:MGI Symbol;Acc:MGI:98423]	Q564E6	P32067	-0.3	9.0E-01	-3.9	2.2E-01	-3.1	9.3E-02	0.5	8.9E-01
ENSMUST00000138586				5.8	8.5E-04	-5.8	9.0E-04	0.4	3.8E-01	-0.8	5.3E-01
ENSMUST00000141272				5.8	1.8E-04	2.0	7.6E-02	-0.1	8.7E-01	0.2	8.0E-01
ENSMUST00000156269				5.8	3.5E-02	6.5	1.0E-04	0.0	1.0E+00	0.5	3.8E-01
ENSMUST00000107406				5.8	1.6E-02	4.4	6.2E-02	-1.2	5.7E-01	-1.3	4.1E-01
ENSMUST00000166426	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]	Q3UF95		2.4	1.8E-01	4.0	3.1E-02	-1.4	4.2E-01	-3.1	4.2E-02
ENSMUST00000120503				5.8	3.0E-04	4.3	1.2E-03	0.8	3.3E-01	-0.3	5.8E-01
ENSMUST00000166429	signal-induced proliferation-associated 1 like 1 [Source:MGI Symbol;Acc:MGI:2443679]		Q8C0T5	0.1	7.2E-01	-0.1	8.9E-01	0.6	1.6E-01	0.9	1.4E-01
ENSMUST00000128893				5.8	9.9E-04	-4.7	2.8E-03	1.1	4.3E-02	-0.7	5.8E-01
ENSMUST00000156103				5.8	8.2E-04	-4.8	5.1E-03	-1.2	7.0E-02	-0.6	6.8E-01
ENSMUST00000145541				5.8	7.0E-04	6.0	4.7E-03	-0.6	7.3E-01	-1.5	1.5E-01
ENSMUST00000147798				5.8	1.5E-04	4.3	1.3E-02	-0.7	6.1E-01	-0.4	6.7E-01
ENSMUST00000166462	family with sequence similarity 71, member F1 [Source:MGI Symbol;Acc:MGI:3032524]	B7XG46		1.4	1.9E-01	6.2	1.5E-04	0.1	9.2E-01	-4.8	1.9E-04
ENSMUST00000182560				5.8	2.0E-05	-3.6	1.2E-02	2.6	1.0E-03	-1.0	4.5E-01
ENSMUST00000166467	solute carrier family 17 (sodium phosphate), member 3 [Source:MGI Symbol;Acc:MGI:2389216]	G3UWD9		4.9	7.3E-02	4.5	1.2E-01	-0.7	7.9E-01	-0.3	8.8E-01
ENSMUST00000128631				5.8	1.4E-04	1.5	4.8E-02	-3.7	4.2E-04	-0.1	8.1E-01
ENSMUST00000166471	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:109301]	F6VTN8		1.7	4.8E-01	-1.9	5.3E-01	-2.9	1.6E-01	0.7	8.2E-01
ENSMUST00000166472	cDNA sequence BC052040 [Source:MGI Symbol;Acc:MGI:3026886]	E9PWV4		5.9	4.8E-02	2.6	3.9E-01	-2.8	3.5E-01	0.5	8.3E-01
ENSMUST00000166478	mortality factor 4 like 2 [Source:MGI Symbol;Acc:MGI:1927167]		Q9R0Q4	2.8	3.5E-01	0.6	8.9E-01	-2.0	5.5E-01	0.3	9.3E-01
ENSMUST00000146097				5.8	7.5E-03	5.0	1.1E-04	0.7	3.3E-01	0.0	9.3E-01
ENSMUST00000166489	ubiquitin-conjugating enzyme E2J 2 [Source:MGI Symbol;Acc:MGI:2153608]		Q6P073	4.8	1.0E-01	7.3	3.3E-02	-0.2	9.6E-01	-2.7	1.3E-01
ENSMUST00000148756				5.8	7.2E-04	6.7	7.8E-03	-0.3	9.0E-01	-0.3	7.6E-01
ENSMUST00000166495	DnaJ (Hsp40) homolog, subfamily C, member 1 [Source:MGI Symbol;Acc:MGI:103268]		Q61712	0.1	8.1E-01	1.2	1.1E-01	0.4	4.4E-01	-0.6	3.2E-01
ENSMUST00000187871				5.8	3.7E-03	1.7	2.9E-01	-1.9	1.9E-01	1.4	2.9E-01
ENSMUST00000176495				5.8	3.4E-04	6.5	1.6E-04	-0.5	6.4E-01	0.1	9.1E-01
ENSMUST00000155839				5.8	7.0E-04	7.2	5.5E-03	-0.8	7.0E-01	-2.3	8.4E-02
ENSMUST00000183069				5.8	2.2E-04	4.2	2.6E-03	-0.3	7.9E-01	0.8	2.7E-01
ENSMUST00000194320				5.8	1.0E-03	-8.2	1.6E-03	-0.9	1.6E-01	0.2	9.2E-01
ENSMUST00000121523				5.8	1.9E-04	-4.4	1.2E-02	0.3	6.1E-01	1.7	2.4E-01
ENSMUST00000166537	S-phase kinase-associated protein 1A [Source:MGI Symbol;Acc:MGI:103575]	E9PUV4		-3.3	5.3E-02	-5.4	1.4E-02	-2.9	9.2E-03	-0.7	7.3E-01
ENSMUST00000166539				-1.3	5.6E-02	1.6	5.0E-02	0.5	4.3E-01	-2.4	5.1E-03
ENSMUST00000139183				5.8	4.6E-03	-1.8	3.8E-01	3.5	1.8E-02	-0.8	7.0E-01
ENSMUST00000135606				5.8	9.7E-06	9.4	2.7E-03	1.6	5.0E-01	0.7	5.2E-01
ENSMUST00000152004				5.8	9.3E-04	2.5	2.6E-03	-0.6	3.2E-01	-0.6	2.3E-01
ENSMUST00000163973				5.8	1.7E-04	6.3	1.3E-04	-1.3	2.7E-01	-1.2	6.7E-02
ENSMUST00000142600				5.8	4.5E-05	6.9	9.4E-05	-0.6	6.2E-01	-0.5	3.6E-01
ENSMUST00000166554	G protein-coupled receptor associated sorting protein 1 [Source:MGI Symbol;Acc:MGI:1917418]		Q5U4C1	-1.7	3.9E-01	1.6	6.6E-01	5.2	6.8E-02	2.0	5.1E-01
ENSMUST00000185247				5.8	1.1E-03	3.1	3.5E-03	0.1	9.4E-01	0.4	5.3E-01
ENSMUST00000194660				5.8	5.8E-05	4.6	8.7E-04	-2.9	2.6E-02	-1.7	2.8E-02
ENSMUST00000107009				5.8	6.5E-04	4.5	9.1E-03	-1.7	2.7E-01	-0.7	4.5E-01
ENSMUST00000148268				5.8	5.1E-04	-2.6	7.7E-02	1.5	5.6E-02	2.1	1.1E-01
ENSMUST00000125331				5.8	2.9E-03	5.8	3.1E-02	-0.1	9.8E-01	-0.3	8.4E-01
ENSMUST00000134385				5.8	3.0E-05	7.3	1.9E-05	-0.5	5.9E-01	-1.2	3.7E-02
ENSMUST00000140360				5.8	7.7E-05	-3.1	1.6E-02	1.4	3.9E-02	-0.9	4.6E-01
ENSMUST00000166608	nucleic acid binding protein 2 [Source:MGI Symbol;Acc:MGI:1917167]	E9Q199		-4.3	5.5E-02	-3.7	2.9E-01	1.8	2.7E-01	1.2	7.2E-01
ENSMUST00000173038				5.8	5.0E-04	-3.5	1.4E-02	-1.1	1.1E-01	0.3	7.9E-01
ENSMUST00000166610	RNA binding protein, fox-1 homolog (C. elegans) 2 [Source:MGI Symbol;Acc:MGI:1933973]		Q8BP71	2.9	1.3E-01	3.0	2.2E-01	0.2	9.0E-01	0.2	9.3E-01
ENSMUST00000183496				5.8	3.0E-05	-2.1	9.7E-03	0.9	3.7E-02	-0.2	7.4E-01
ENSMUST00000137294				5.8	1.7E-02	-2.3	1.7E-01	0.1	9.1E-01	-2.6	1.9E-01
ENSMUST00000143370				5.8	2.3E-05	-4.8	2.1E-02	0.8	2.7E-01	-0.5	7.9E-01
ENSMUST00000166646	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 [Source:MGI Symbol;Acc:MGI:2443111]	E9Q467		-0.2	9.0E-01	-0.4	8.4E-01	1.3	3.9E-01	1.5	4.1E-01
ENSMUST00000149678				5.8	5.5E-05	7.6	4.0E-05	-0.5	6.5E-01	0.0	9.9E-01
ENSMUST00000166652	phosphodiesterase 2A, cGMP-stimulated [Source:MGI Symbol;Acc:MGI:2446107]	Q5PR72		0.6	8.3E-01	3.1	3.2E-01	2.3	3.7E-01	-0.2	9.4E-01
ENSMUST00000119729				5.8	2.8E-04	5.3	2.0E-03	3.0	2.8E-02	-0.4	6.3E-01
ENSMUST00000166658	prefoldin 5 [Source:MGI Symbol;Acc:MGI:1928753]		Q9WU28	0.0	9.9E-01	0.2	8.7E-01	-0.6	5.0E-01	-0.8	4.5E-01
ENSMUST00000121498				5.8	1.2E-03	3.4	3.7E-02	-1.5	3.4E-01	1.5	1.4E-01
ENSMUST00000125088				5.8	4.7E-05	8.5	3.6E-04	-0.9	6.2E-01	0.8	3.0E-01
ENSMUST00000127641				5.8	1.1E-05	3.6	6.7E-04	-0.8	2.3E-01	0.6	3.0E-01
ENSMUST00000166682	ataxin 2-like [Source:MGI Symbol;Acc:MGI:2446242]	E9Q5Q0		-0.5	7.3E-01	-0.2	9.4E-01	1.4	3.9E-01	1.1	5.5E-01
ENSMUST00000166684				3.7	1.1E-01	1.9	5.7E-01	0.6	8.1E-01	2.4	3.2E-01
ENSMUST00000170983				5.8	2.0E-03	-6.2	2.5E-02	1.5	9.8E-02	2.1	3.8E-01
ENSMUST00000166691				1.4	1.9E-01	1.7	2.4E-01	-0.3	8.4E-01	-0.5	6.2E-01
ENSMUST00000166701	GTP binding protein 2 [Source:MGI Symbol;Acc:MGI:1860138]	F7A4M1		-1.2	2.4E-01	0.6	5.9E-01	0.6	4.5E-01	-1.1	3.0E-01
ENSMUST00000166711	adenylosuccinate lyase [Source:MGI Symbol;Acc:MGI:103202]	E9Q0A0		1.3	4.0E-02	1.5	5.2E-02	-0.3	5.4E-01	-0.5	4.1E-01
ENSMUST00000166712	CDK2 associated, cullin domain 1 [Source:MGI Symbol;Acc:MGI:1926082]	E9PV69		3.6	2.0E-01	-3.1	2.3E-01	-6.1	2.6E-02	0.7	7.8E-01
ENSMUST00000166716	parathyroid hormone 1 receptor [Source:MGI Symbol;Acc:MGI:97801]		P41593	3.5	9.2E-02	4.7	3.8E-02	-0.6	7.6E-01	-1.9	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000166719	exportin 6 [Source:MGI Symbol;Acc:MGI:2429950]	F6ZUE3		0.1	9.5E-01	-0.5	8.1E-01	0.5	7.0E-01	1.2	5.6E-01
ENSMUST00000121901				5.8	3.2E-04	7.0	3.7E-06	0.8	2.9E-01	-0.7	7.0E-02
ENSMUST00000193029				5.8	2.1E-04	-0.3	7.6E-01	1.0	1.4E-01	-0.5	5.0E-01
ENSMUST00000044101				5.8	4.5E-06	-1.0	6.1E-01	3.3	1.7E-02	-1.2	5.3E-01
ENSMUST00000067277				5.8	1.2E-05	7.8	5.6E-06	-0.2	8.1E-01	0.1	8.6E-01
ENSMUST00000166743	mitogen-activated protein kinase 1 interacting protein 1-like [Source:MGI Symbol;Acc:MGI:2444022]		Q8BH93	-2.9	9.1E-02	-3.3	1.7E-01	1.1	3.5E-01	1.6	4.8E-01
ENSMUST00000166748	period circadian clock 1 [Source:MGI Symbol;Acc:MGI:1098283]		O35973	0.5	8.7E-01	-1.8	6.9E-01	-1.2	6.7E-01	1.1	8.1E-01
ENSMUST00000182471				5.8	6.0E-04	-3.7	2.1E-04	0.7	4.4E-02	0.5	4.4E-01
ENSMUST00000123587				5.8	2.2E-04	-3.3	2.0E-02	0.9	1.4E-01	2.5	5.2E-02
ENSMUST00000161314				5.8	1.0E-03	4.7	1.1E-03	2.0	5.2E-02	0.2	7.7E-01
ENSMUST00000166769	eukaryotic translation initiation factor 2B, subunit 4 delta [Source:MGI Symbol;Acc:MGI:95300]		Q61749	-2.9	3.6E-01	-1.6	6.8E-01	0.4	8.7E-01	-0.9	8.3E-01
ENSMUST00000118839				5.8	8.7E-05	9.2	4.6E-05	0.8	5.3E-01	0.2	6.5E-01
ENSMUST00000129859				5.8	7.3E-06	5.5	1.6E-02	-0.7	7.4E-01	1.4	2.3E-01
ENSMUST00000147899				5.8	7.5E-04	6.8	5.1E-04	-0.9	5.2E-01	-1.3	1.2E-01
ENSMUST00000166775	retinoid X receptor alpha [Source:MGI Symbol;Acc:MGI:98214]	A2AJP1	P28700	3.5	1.1E-01	3.8	1.1E-01	-0.8	7.1E-01	-1.1	5.5E-01
ENSMUST00000155765				5.8	6.0E-04	3.1	5.0E-02	-2.5	1.4E-01	1.5	1.7E-01
ENSMUST00000195622				5.8	3.8E-05	4.2	1.2E-03	-1.4	1.4E-01	0.1	9.0E-01
ENSMUST00000124441				5.8	3.0E-04	-0.9	3.3E-01	1.2	6.1E-02	-0.1	9.3E-01
ENSMUST00000127691				5.8	7.2E-04	7.9	1.7E-04	1.4	2.9E-01	0.0	9.5E-01
ENSMUST00000130241				5.8	2.2E-02	1.5	1.2E-02	-0.7	9.9E-02	-0.6	1.5E-01
ENSMUST00000120117				5.8	2.2E-04	7.7	1.2E-05	-2.0	8.2E-02	-0.5	3.1E-01
ENSMUST00000142170				5.8	1.9E-03	0.5	7.4E-01	0.0	1.0E+00	-4.7	2.3E-02
ENSMUST00000121854				5.8	8.7E-04	2.0	3.2E-01	5.5	4.6E-03	0.5	7.7E-01
ENSMUST00000166821	mutL homolog 3 (E coli) [Source:MGI Symbol;Acc:MGI:1353455]	Q68FG1		-1.6	3.3E-01	3.1	8.3E-02	0.6	6.9E-01	-4.1	2.2E-02
ENSMUST00000166823	OCIA domain containing 1 [Source:MGI Symbol;Acc:MGI:1915345]		Q9CRD0	-0.4	5.2E-01	0.5	5.1E-01	0.4	4.0E-01	-0.4	5.7E-01
ENSMUST00000166836	predicted gene 20425 [Source:MGI Symbol;Acc:MGI:5141890]	E9Q035		-3.1	5.0E-02	-3.0	1.5E-01	1.3	2.3E-01	1.3	5.3E-01
ENSMUST00000161116				5.8	7.2E-04	6.6	1.8E-04	-0.9	4.7E-01	-0.8	2.3E-01
ENSMUST00000128542				5.8	1.4E-04	3.4	4.5E-04	-0.1	8.3E-01	-0.2	7.3E-01
ENSMUST00000128685				5.8	2.2E-04	5.0	8.3E-04	-0.9	3.7E-01	0.4	5.4E-01
ENSMUST00000129623				5.8	1.3E-03	1.8	8.5E-02	-2.3	2.8E-02	-1.1	2.1E-01
ENSMUST00000166853				0.0	9.8E-01	1.8	3.2E-01	-0.3	8.3E-01	-2.1	2.1E-01
ENSMUST00000117188				5.8	1.7E-04	6.5	5.8E-05	-1.4	1.8E-01	0.2	7.7E-01
ENSMUST00000134408				5.8	7.1E-03	-6.1	8.5E-04	1.0	4.9E-02	-0.9	5.1E-01
ENSMUST00000121316				5.8	1.9E-04	5.2	3.9E-02	1.3	5.5E-01	1.8	2.0E-01
ENSMUST00000118023				5.8	1.5E-03	5.4	4.8E-02	-0.6	8.1E-01	-0.3	8.3E-01
ENSMUST00000118380				5.8	3.2E-04	-6.6	2.8E-04	0.7	1.0E-01	-0.8	5.5E-01
ENSMUST00000160790				5.8	1.1E-04	-2.6	2.7E-03	0.6	1.2E-01	0.0	9.6E-01
ENSMUST00000192414				5.8	3.7E-05	9.8	1.7E-06	0.7	4.4E-01	0.9	5.7E-02
ENSMUST00000166905	dystroglycan 1 [Source:MGI Symbol;Acc:MGI:101864]	Q544G5	Q62165	4.6	4.0E-02	8.8	1.5E-02	3.7	2.0E-01	-0.5	7.8E-01
ENSMUST00000193661				5.8	1.2E-04	3.3	1.4E-03	-0.2	7.9E-01	0.8	1.6E-01
ENSMUST00000106465				5.8	7.4E-04	-7.4	1.4E-04	0.0	9.6E-01	2.3	6.8E-02
ENSMUST00000148079				5.8	1.3E-03	-3.5	3.0E-02	0.0	9.9E-01	-0.4	8.1E-01
ENSMUST00000122830				5.8	9.9E-03	7.8	2.2E-04	-0.7	6.2E-01	-0.2	7.2E-01
ENSMUST00000131367				5.8	1.2E-05	6.5	4.4E-04	-0.5	7.0E-01	-0.4	5.3E-01
ENSMUST00000162137				5.8	1.0E-03	-4.8	4.9E-02	-0.4	6.5E-01	0.5	8.4E-01
ENSMUST00000166931	enhancer of rudimentary homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108089]	G3UW85		-2.3	9.8E-02	-4.4	2.6E-02	-2.6	1.7E-02	-0.5	7.7E-01
ENSMUST00000166933				1.3	2.0E-01	2.8	2.5E-02	-0.4	6.7E-01	-1.9	6.4E-02
ENSMUST00000187579				5.8	6.5E-05	-3.6	1.5E-01	0.8	4.7E-01	-0.7	7.8E-01
ENSMUST00000166939	adhesion G protein-coupled receptor E5 [Source:MGI Symbol;Acc:MGI:1347095]	Q9DC42		2.8	6.4E-02	6.5	6.1E-04	-0.5	7.1E-01	-4.2	1.7E-03
ENSMUST00000134150				5.8	2.6E-02	3.9	1.6E-02	1.5	2.4E-01	0.2	8.2E-01
ENSMUST00000166943				0.7	4.1E-01	-0.5	6.5E-01	-0.3	6.8E-01	0.8	4.1E-01
ENSMUST00000189049				5.8	3.2E-03	-1.3	1.9E-01	-1.6	4.1E-02	-2.7	2.2E-02
ENSMUST00000130337				5.8	8.9E-03	8.0	4.0E-05	-0.6	6.2E-01	-0.6	3.2E-01
ENSMUST00000131154				5.8	2.0E-02	7.3	8.1E-05	-0.5	6.5E-01	-0.6	3.4E-01
ENSMUST00000138828				5.8	1.9E-04	4.1	1.7E-02	-4.1	4.4E-02	-2.3	7.9E-02
ENSMUST00000146866				5.8	8.7E-04	7.9	9.7E-04	-0.4	8.3E-01	1.0	2.7E-01
ENSMUST00000149893				5.8	7.1E-05	4.9	2.3E-03	1.0	3.8E-01	0.2	7.7E-01
ENSMUST00000100944				5.8	9.1E-05	7.8	7.6E-04	-1.2	4.9E-01	0.6	4.6E-01
ENSMUST00000151433				5.8	2.0E-05	5.1	7.3E-03	-2.7	1.3E-01	-1.1	2.9E-01
ENSMUST00000166975	inner membrane protein, mitochondrial [Source:MGI Symbol;Acc:MGI:1923864]	E9QAY6		2.6	3.5E-01	0.6	8.5E-01	-1.1	6.7E-01	0.8	7.9E-01
ENSMUST00000166976	kelch-like 26 [Source:MGI Symbol;Acc:MGI:2443079]	E9Q4C1		0.1	9.8E-01	-4.0	3.6E-01	-0.8	7.3E-01	3.3	4.3E-01
ENSMUST00000166977	phospholipase A2, group VI [Source:MGI Symbol;Acc:MGI:1859152]	Q3UN31	P97819	2.4	5.3E-02	0.5	7.4E-01	0.0	1.0E+00	1.9	1.7E-01
ENSMUST00000134806				5.8	2.0E-04	-1.7	2.5E-01	0.9	3.4E-01	-2.5	1.5E-01
ENSMUST00000137581				5.8	1.4E-05	1.6	5.8E-02	-0.3	6.0E-01	-0.1	8.8E-01
ENSMUST00000162157				5.8	4.8E-04	6.1	1.1E-02	-0.7	7.3E-01	-1.2	3.3E-01
ENSMUST00000166990	casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]	E9PWB2		-1.8	4.4E-01	-2.6	3.2E-01	-1.7	3.1E-01	-0.9	7.4E-01
ENSMUST00000148803				5.8	3.5E-02	3.4	6.4E-03	-1.3	1.9E-01	-0.1	9.2E-01
ENSMUST00000161760				5.8	6.5E-04	2.8	9.5E-04	-0.3	5.3E-01	0.1	7.9E-01
ENSMUST00000150814				5.8	4.8E-03	5.3	1.1E-04	-0.2	8.3E-01	0.1	7.9E-01
ENSMUST00000184266				5.8	8.3E-04	-4.2	6.9E-03	-0.2	7.3E-01	1.1	3.6E-01
ENSMUST00000117397				5.8	3.0E-04	-0.3	5.6E-01	0.6	1.3E-01	-0.6	2.5E-01
ENSMUST00000124880				5.8	1.4E-03	-1.3	2.8E-01	1.5	6.2E-02	0.4	7.5E-01
ENSMUST00000131778				5.8	2.8E-02	5.7	2.4E-03	-0.1	9.6E-01	0.3	6.9E-01
ENSMUST00000140730				5.8	2.8E-02	6.1	4.9E-04	-0.5	6.9E-01	-0.2	7.2E-01
ENSMUST00000190735				5.8	3.1E-05	-4.3	5.2E-03	1.0	7.4E-02	-0.7	5.8E-01
ENSMUST00000154751				5.8	8.7E-05	-2.5	1.0E-01	0.6	4.6E-01	-1.3	4.0E-01
ENSMUST00000147156				5.8	2.6E-04	-4.6	9.0E-03	-0.2	7.1E-01	-0.9	5.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000167042	U2 small nuclear RNA auxiliary factor 1-like 4 [Source:MGI Symbol;Acc:MGI:2678374]		Q8BGJ9	0.1	9.7E-01	1.4	6.1E-01	-0.3	9.1E-01	-1.5	4.6E-01
ENSMUST00000192645				5.8	6.5E-06	5.6	5.6E-04	-0.6	6.3E-01	0.8	2.2E-01
ENSMUST00000167055	carnosine synthase 1 [Source:MGI Symbol;Acc:MGI:2147595]	E9PX09		-0.7	3.8E-01	-0.8	4.6E-01	-0.2	8.0E-01	-0.1	9.1E-01
ENSMUST00000151850				5.8	4.5E-04	4.5	9.7E-04	0.3	7.5E-01	1.2	8.7E-02
ENSMUST00000195575				5.8	1.4E-03	6.9	1.2E-04	-0.6	6.0E-01	-0.6	3.3E-01
ENSMUST00000124313				5.8	1.5E-05	4.9	2.6E-03	-0.6	6.3E-01	0.4	5.9E-01
ENSMUST00000136802				5.8	1.2E-04	2.0	1.1E-01	-1.1	2.9E-01	0.8	4.4E-01
ENSMUST00000141342				5.8	2.5E-05	4.6	5.8E-03	0.4	7.2E-01	0.6	4.6E-01
ENSMUST00000123622				5.8	3.3E-06	-6.0	1.1E-03	0.6	2.4E-01	-0.7	6.1E-01
ENSMUST00000167080	protein tyrosine phosphatase, non-receptor type 7 [Source:MGI Symbol;Acc:MGI:2156893]		Q8BUM3	-0.5	8.0E-01	-0.6	7.9E-01	0.2	9.1E-01	0.3	8.9E-01
ENSMUST00000167086	CD101 antigen [Source:MGI Symbol;Acc:MGI:2685862]	A0A0B4J1L8		2.5	4.0E-01	3.6	3.0E-01	-1.2	7.0E-01	-2.3	3.9E-01
ENSMUST00000174240				5.8	2.1E-03	6.2	1.5E-03	-0.6	7.1E-01	-0.3	6.8E-01
ENSMUST00000167091	poly (ADP-ribose) polymerase family, member 6 [Source:MGI Symbol;Acc:MGI:1914537]	Q05BZ2		-3.6	3.5E-02	-0.4	7.9E-01	1.0	3.7E-01	-2.2	2.1E-01
ENSMUST00000167097	palmitoyl-protein thioesterase 2 [Source:MGI Symbol;Acc:MGI:1860075]	G5E8W7		-1.8	6.1E-02	-0.5	7.0E-01	1.2	1.7E-01	-0.1	9.0E-01
ENSMUST00000167103	neurexin III [Source:MGI Symbol;Acc:MGI:1096389]	E9Q2X2		4.5	1.7E-01	7.6	4.0E-02	-0.3	9.4E-01	-3.4	1.0E-01
ENSMUST00000167106	toll-like receptor 3 [Source:MGI Symbol;Acc:MGI:2156367]		Q99MB1	2.0	2.6E-01	1.4	4.4E-01	-2.2	2.1E-01	-1.6	3.3E-01
ENSMUST00000167107	zinc finger protein 101 [Source:MGI Symbol;Acc:MGI:107547]	Q8BP18		-0.8	2.3E-01	0.8	3.4E-01	1.1	1.3E-01	-0.6	4.5E-01
ENSMUST00000167110	nuclear factor, erythroid derived 2,-like 1 [Source:MGI Symbol;Acc:MGI:99421]		Q61985	1.8	9.8E-02	7.0	5.8E-05	0.1	9.2E-01	-5.1	8.0E-05
ENSMUST00000191504				5.8	4.4E-06	5.8	1.2E-03	1.3	3.0E-01	-0.6	4.0E-01
ENSMUST00000140680				5.7	4.8E-04	6.3	5.2E-03	-1.0	5.6E-01	-2.9	3.8E-02
ENSMUST00000149674				5.7	1.0E-05	-2.1	1.1E-01	1.6	5.5E-02	-0.8	5.5E-01
ENSMUST00000174209				5.7	4.3E-04	-5.5	9.6E-04	-3.0	5.1E-04	-2.3	1.4E-01
ENSMUST00000167845				5.7	3.1E-04	-0.7	7.2E-01	2.7	6.5E-02	-3.0	1.5E-01
ENSMUST00000187825				5.7	2.2E-03	7.5	8.0E-05	-0.6	6.1E-01	-0.1	8.5E-01
ENSMUST00000141419				5.7	3.8E-06	9.0	1.3E-05	2.4	3.7E-02	-0.7	1.4E-01
ENSMUST00000167156	ALX homeobox 1 [Source:MGI Symbol;Acc:MGI:104621]		Q8C8B0	4.2	7.0E-02	6.6	1.7E-02	-0.3	9.0E-01	-2.7	6.6E-02
ENSMUST00000117498				5.7	9.4E-04	-2.2	3.8E-02	-0.1	8.8E-01	0.3	7.2E-01
ENSMUST00000117071				5.7	8.4E-05	-2.1	2.0E-01	1.9	7.8E-02	-2.0	2.6E-01
ENSMUST00000167162				-2.2	8.7E-02	-2.2	2.6E-01	0.8	5.2E-01	0.7	6.7E-01
ENSMUST00000167164	glutamate receptor, metabotropic 5 [Source:MGI Symbol;Acc:MGI:1351342]	B2BH30	Q3UVX5	4.3	8.5E-02	5.7	5.0E-02	-0.2	9.3E-01	-1.6	3.2E-01
ENSMUST00000167172				-1.7	1.1E-01	-0.6	6.5E-01	0.6	5.1E-01	-0.5	6.6E-01
ENSMUST00000117105				5.7	7.9E-06	5.4	4.2E-03	-0.4	7.9E-01	-1.2	1.9E-01
ENSMUST00000167174				-1.4	2.1E-01	0.6	7.1E-01	1.9	1.8E-01	-0.2	8.9E-01
ENSMUST00000167178	tubulin, delta 1 [Source:MGI Symbol;Acc:MGI:1891826]	Q5SWF8	Q9R1K7	-0.4	7.3E-01	3.9	8.0E-03	0.0	9.8E-01	-4.3	3.1E-03
ENSMUST00000118901				5.7	3.2E-04	-3.5	4.5E-02	-0.7	4.0E-01	0.0	9.9E-01
ENSMUST00000120811				5.7	3.6E-03	-3.6	6.1E-02	0.4	6.9E-01	-0.1	9.4E-01
ENSMUST00000167187	casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]	E9Q2U6		-1.3	6.3E-01	-2.8	4.6E-01	-1.5	4.5E-01	-0.1	9.8E-01
ENSMUST00000136917				5.7	3.3E-04	5.6	1.0E-03	-1.2	3.7E-01	-1.8	3.0E-02
ENSMUST00000167199	mitochondrial ribosomal protein L16 [Source:MGI Symbol;Acc:MGI:2137219]		Q99N93	-1.1	3.7E-02	-1.0	1.0E-01	-0.4	3.6E-01	-0.5	3.7E-01
ENSMUST00000167200	Fc receptor-like 1 [Source:MGI Symbol;Acc:MGI:2442862]	E9Q5S9		-4.7	4.5E-02	-3.8	1.6E-01	-0.1	9.3E-01	-1.0	7.2E-01
ENSMUST00000133190				5.7	2.8E-04	6.4	5.4E-05	-0.7	4.5E-01	0.6	2.4E-01
ENSMUST00000184424				5.7	9.8E-06	4.6	5.3E-04	-3.1	1.6E-02	-0.5	4.8E-01
ENSMUST00000167220	lysine (K)-specific demethylase 3A [Source:MGI Symbol;Acc:MGI:98847]		Q6PCM1	2.0	4.3E-01	4.7	1.2E-01	-0.3	9.2E-01	-2.9	2.2E-01
ENSMUST00000157016				5.7	2.0E-03	-1.1	2.9E-01	0.5	4.6E-01	-1.9	1.3E-01
ENSMUST00000192205				5.7	2.0E-04	-4.8	3.4E-03	1.6	2.5E-02	-2.3	1.8E-01
ENSMUST00000193645				5.7	7.2E-05	3.6	1.0E-01	-0.5	7.9E-01	2.3	1.1E-01
ENSMUST00000159925				5.7	4.7E-05	2.8	1.2E-01	-2.8	1.8E-01	-0.4	7.5E-01
ENSMUST00000161360				5.7	5.2E-06	2.4	4.4E-01	0.1	9.8E-01	2.8	2.5E-01
ENSMUST00000171235				5.7	1.9E-03	-5.5	1.6E-01	1.9	2.2E-01	-0.7	8.5E-01
ENSMUST00000122877				5.7	2.0E-03	6.4	1.8E-04	-4.4	9.2E-03	-0.4	4.6E-01
ENSMUST00000167243	glutamate decarboxylase 1, pseudogene [Source:MGI Symbol;Acc:MGI:95633]			-1.2	2.7E-01	-1.2	4.0E-01	0.2	8.6E-01	0.2	9.1E-01
ENSMUST00000125510				5.7	2.0E-05	4.2	6.5E-04	-0.1	9.0E-01	0.6	3.0E-01
ENSMUST00000130797				5.7	1.2E-03	-4.0	5.2E-03	-0.5	3.6E-01	-0.6	6.0E-01
ENSMUST00000148857				5.7	2.8E-04	6.7	1.4E-02	-0.6	8.0E-01	-1.8	2.0E-01
ENSMUST00000167250	lipid phosphate phosphatase-related protein type 3 [Source:MGI Symbol;Acc:MGI:2388640]	E9QAX3		1.9	4.3E-02	2.4	4.5E-02	0.3	7.4E-01	-0.2	8.4E-01
ENSMUST00000167252	interferon regulatory factor 5 [Source:MGI Symbol;Acc:MGI:1350924]	F6Z6C6		-1.0	6.8E-01	-1.2	6.1E-01	-1.8	3.2E-01	-1.6	5.4E-01
ENSMUST00000114774				5.7	9.5E-05	7.5	7.9E-05	-0.6	6.4E-01	-0.2	7.2E-01
ENSMUST00000121443				5.7	7.8E-04	7.3	1.1E-04	-0.5	7.0E-01	-1.6	2.8E-02
ENSMUST00000148166				5.7	3.1E-03	9.0	8.0E-04	-0.9	6.6E-01	0.1	9.0E-01
ENSMUST00000160520				5.7	2.3E-05	-5.8	3.8E-04	0.5	2.0E-01	0.6	5.8E-01
ENSMUST00000167268				2.4	4.5E-02	3.3	3.8E-02	-0.1	9.5E-01	-1.0	3.0E-01
ENSMUST00000179326				5.7	1.2E-04	7.0	1.8E-04	-0.6	6.1E-01	-1.3	9.2E-02
ENSMUST00000167273	protein phosphatase 1, regulatory (inhibitor) subunit 15A [Source:MGI Symbol;Acc:MGI:1927072]	B2RRL7	P17564	4.8	4.7E-02	3.8	1.5E-01	-1.2	6.3E-01	-0.2	9.0E-01
ENSMUST00000127088				5.7	4.8E-03	-1.3	1.9E-01	0.9	1.4E-01	-0.2	8.3E-01
ENSMUST00000159696				5.7	2.2E-04	-2.3	7.4E-03	0.5	2.0E-01	0.4	5.4E-01
ENSMUST00000125226				5.7	7.1E-06	0.0	9.9E-01	2.8	1.2E-02	-0.7	6.4E-01
ENSMUST00000151899				5.7	6.4E-05	8.1	2.2E-02	-0.3	9.2E-01	-1.2	4.8E-01
ENSMUST00000167299	solute carrier family 5 (sodium/glucose cotransporter), member 11 [Source:MGI Symbol;Acc:MGI:1919316]		Q8K0E3	3.9	7.5E-02	3.9	1.3E-01	-0.4	8.5E-01	-0.5	8.0E-01
ENSMUST00000121385				5.7	1.8E-04	4.6	8.9E-04	-2.4	4.8E-02	-3.4	2.2E-03
ENSMUST00000123195				5.7	2.3E-04	-5.3	1.4E-03	0.3	4.7E-01	-0.6	6.2E-01
ENSMUST00000167315				0.5	6.1E-01	1.2	3.9E-01	0.6	6.0E-01	-0.1	9.5E-01
ENSMUST00000152885				5.7	9.3E-04	-2.3	7.4E-03	1.0	3.4E-02	0.0	9.5E-01
ENSMUST00000167320	neurobeachin-like 2 [Source:MGI Symbol;Acc:MGI:2448554]	E9Q9L6		-3.0	6.5E-02	-3.5	1.8E-01	1.9	2.0E-01	2.4	3.1E-01
ENSMUST00000167322	RIKEN cDNA 9030617O03 gene [Source:MGI Symbol;Acc:MGI:2444813]		Q8BH86	3.3	7.0E-02	2.5	4.5E-01	3.2	2.2E-01	4.0	1.3E-01
ENSMUST00000164140				5.7	5.8E-03	8.7	5.3E-05	1.7	1.8E-01	0.5	3.7E-01
ENSMUST00000177599				5.7	1.1E-03	-1.8	1.4E-02	0.7	6.8E-02	-1.8	2.4E-02
ENSMUST00000125486				5.7	7.4E-04	5.9	9.3E-04	-1.5	3.0E-01	-2.6	1.1E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000145996				5.7	1.1E-04	-4.0	1.4E-02	0.5	4.5E-01	-0.3	8.1E-01
ENSMUST00000188486				5.7	9.8E-05	10.5	3.6E-04	3.4	9.6E-02	0.4	5.4E-01
ENSMUST00000121305				5.7	1.5E-03	2.7	1.4E-02	-0.3	6.8E-01	0.2	8.2E-01
ENSMUST00000124292				5.7	2.2E-06	1.3	4.6E-01	-3.3	5.5E-02	2.1	1.7E-01
ENSMUST00000140048				5.7	2.7E-03	-4.6	8.0E-04	-0.6	2.3E-01	-3.4	2.6E-02
ENSMUST00000151823				5.7	1.3E-05	7.8	1.7E-04	-0.7	6.2E-01	-0.5	4.3E-01
ENSMUST00000167360	ATP-binding cassette, sub-family C (CFTR/MRP), member 10 [Source:MGI Symbol;Acc:MGI:2386976]		Q8R4P9	-2.4	4.4E-02	-1.7	3.2E-01	1.8	1.2E-01	1.0	5.2E-01
ENSMUST00000136694				5.7	4.9E-05	-1.9	3.3E-01	2.2	6.9E-02	-1.3	5.0E-01
ENSMUST00000144664				5.7	8.9E-05	6.4	2.4E-04	-0.1	9.4E-01	-0.3	6.6E-01
ENSMUST00000148521				5.7	3.4E-05	6.9	4.4E-05	-0.5	5.9E-01	-0.5	3.2E-01
ENSMUST00000172770				5.7	3.6E-04	6.0	8.9E-04	-0.8	5.4E-01	-0.7	3.7E-01
ENSMUST00000159682				5.7	8.7E-04	-1.9	7.8E-02	0.9	1.3E-01	-0.2	8.7E-01
ENSMUST00000161791				5.7	2.3E-05	-5.0	2.2E-06	0.7	1.2E-02	-0.7	1.5E-01
ENSMUST00000176122				5.7	1.0E-03	-4.9	4.0E-02	1.1	2.7E-01	-1.0	6.7E-01
ENSMUST00000167386				-1.5	2.6E-01	-0.7	7.2E-01	0.6	6.1E-01	-0.3	8.8E-01
ENSMUST00000167388	glycoprotein Ib, beta polypeptide [Source:MGI Symbol;Acc:MGI:107852]		P56400	1.3	1.0E-01	-1.8	6.8E-02	-1.4	5.4E-02	1.6	7.6E-02
ENSMUST00000148664				5.7	3.4E-03	4.0	3.2E-02	-2.5	2.0E-01	-2.0	1.3E-01
ENSMUST00000181294				5.7	1.1E-03	4.0	1.4E-02	-3.2	4.9E-02	1.6	1.4E-01
ENSMUST00000167399	fetuin beta [Source:MGI Symbol;Acc:MGI:1890221]		Q9QXC1	3.4	1.2E-01	2.7	2.4E-01	-0.5	8.4E-01	0.2	9.0E-01
ENSMUST00000167400	mannoside acetylglucosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI:96973]	Q544F0	P27808	-2.9	1.5E-01	-3.8	2.5E-01	0.8	5.8E-01	1.6	6.1E-01
ENSMUST00000167404				-0.3	8.6E-01	-0.5	8.1E-01	0.4	7.8E-01	0.6	7.4E-01
ENSMUST00000183118				5.7	1.5E-04	6.4	1.6E-04	-0.6	6.0E-01	0.0	9.6E-01
ENSMUST00000143045				5.7	2.0E-04	5.4	7.7E-02	-0.9	7.7E-01	0.5	7.6E-01
ENSMUST00000166883				5.7	2.6E-02	5.9	4.2E-03	-0.7	6.8E-01	-0.5	5.7E-01
ENSMUST00000167429				1.1	2.0E-01	2.6	2.4E-02	1.1	2.2E-01	-0.4	5.9E-01
ENSMUST00000098228				5.7	9.8E-04	5.6	1.0E-02	-0.4	8.5E-01	-0.5	6.4E-01
ENSMUST00000113164				5.7	1.4E-05	-6.3	8.1E-03	0.7	2.6E-01	0.6	7.7E-01
ENSMUST00000167439	junctophilin 3 [Source:MGI Symbol;Acc:MGI:1891497]		Q9ET77	2.9	4.8E-02	2.9	1.1E-01	1.0	5.0E-01	1.0	4.6E-01
ENSMUST00000167446	Fanconi anemia, complementation group B [Source:MGI Symbol;Acc:MGI:2448558]	Q3TEX6		0.5	5.6E-01	-1.4	3.0E-01	0.1	9.0E-01	2.0	1.1E-01
ENSMUST00000167447				-0.9	3.3E-01	-0.2	8.2E-01	-0.1	8.9E-01	-0.8	4.9E-01
ENSMUST00000134858				5.7	1.6E-04	-1.8	2.4E-01	2.3	3.3E-02	-0.5	7.2E-01
ENSMUST00000126037				5.7	5.3E-04	2.6	2.5E-01	-0.8	7.0E-01	0.6	6.8E-01
ENSMUST00000126595				5.7	2.0E-02	4.2	1.9E-03	1.2	1.9E-01	-0.3	6.5E-01
ENSMUST00000167458	high mobility group box transcription factor 1 [Source:MGI Symbol;Acc:MGI:894659]	E9Q469		0.2	7.4E-01	0.7	3.2E-01	0.1	8.8E-01	-0.4	5.0E-01
ENSMUST00000148551				5.7	1.9E-05	-1.9	9.1E-02	0.7	2.7E-01	-2.2	7.9E-02
ENSMUST00000182832				5.7	6.1E-04	2.1	2.9E-01	-0.2	9.0E-01	2.3	1.2E-01
ENSMUST00000167466	sel-1 suppressor of lin-12-like (C. elegans) [Source:MGI Symbol;Acc:MGI:1329016]	Q6GTY4	Q9Z2G6	-3.7	4.3E-02	-3.4	8.0E-02	0.1	9.2E-01	-0.2	9.4E-01
ENSMUST00000167483	ribosomal RNA processing 7 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1922028]	E9QAX0		0.5	7.1E-01	2.4	2.1E-01	1.3	4.3E-01	-0.6	6.5E-01
ENSMUST00000118225				5.7	8.0E-04	5.0	3.1E-03	-0.5	7.1E-01	-1.1	2.0E-01
ENSMUST00000169224				5.7	2.9E-03	5.7	1.4E-03	1.8	1.5E-01	0.2	7.6E-01
ENSMUST00000167488	BEN domain containing 3 [Source:MGI Symbol;Acc:MGI:2677212]		Q6PAL0	3.0	1.6E-01	2.4	5.4E-01	2.7	3.8E-01	3.4	2.8E-01
ENSMUST00000167491	calcium release activated channel regulator 2B [Source:MGI Symbol;Acc:MGI:2446129]	E9PZB6		3.3	1.2E-01	0.3	8.8E-01	-2.7	1.9E-01	0.4	8.2E-01
ENSMUST00000161443				5.7	1.0E-04	-3.6	2.1E-02	1.2	1.1E-01	-1.8	2.3E-01
ENSMUST00000167495				-0.9	2.4E-01	0.0	9.9E-01	-0.1	9.1E-01	-1.0	2.9E-01
ENSMUST00000167496	ring finger protein 20 [Source:MGI Symbol;Acc:MGI:1925927]		Q5DTM8	-2.5	8.0E-02	0.6	7.3E-01	1.2	3.2E-01	-1.8	2.5E-01
ENSMUST00000167498				1.4	9.9E-02	1.2	2.1E-01	-0.8	2.9E-01	-0.6	4.5E-01
ENSMUST00000175659				5.7	1.4E-05	6.2	6.3E-05	-2.2	4.6E-02	-0.2	6.8E-01
ENSMUST00000160593				5.7	6.1E-04	-2.4	4.7E-03	-0.4	3.8E-01	-0.7	3.3E-01
ENSMUST00000188406				5.7	2.6E-04	5.6	2.1E-02	-0.7	7.5E-01	1.4	2.5E-01
ENSMUST00000124029				5.7	7.7E-04	-3.7	1.2E-03	-0.4	3.9E-01	-2.1	5.7E-02
ENSMUST00000167518	family with sequence similarity 168, member B [Source:MGI Symbol;Acc:MGI:2448487]	G3UWF0		-1.3	4.7E-01	-2.4	5.1E-01	2.7	1.9E-01	3.9	2.7E-01
ENSMUST00000167525	short coiled-coil protein [Source:MGI Symbol;Acc:MGI:1927654]		Q78YZ6	-3.4	1.6E-01	-2.6	2.2E-01	-1.9	2.1E-01	-2.7	3.0E-01
ENSMUST00000167528	tudor domain containing 5 [Source:MGI Symbol;Acc:MGI:2684949]	J3QPB7		2.5	2.3E-01	3.2	2.6E-01	0.9	7.1E-01	0.2	9.2E-01
ENSMUST00000182740				5.7	2.1E-04	-2.7	6.7E-02	0.9	2.8E-01	-3.8	5.2E-02
ENSMUST00000193613				5.7	6.8E-04	-5.5	2.6E-02	0.2	8.2E-01	2.5	2.7E-01
ENSMUST00000194528				5.7	4.6E-04	2.3	1.3E-02	0.4	5.5E-01	-0.3	6.3E-01
ENSMUST00000122963				5.7	2.6E-03	1.1	1.0E-01	-0.5	3.6E-01	0.1	9.0E-01
ENSMUST00000168010				5.7	1.4E-02	5.4	1.9E-03	-2.5	1.0E-01	0.1	8.6E-01
ENSMUST00000167556	polo-like kinase 4 [Source:MGI Symbol;Acc:MGI:101783]	E9PVH4	Q64702	0.5	5.1E-01	1.7	6.8E-02	0.6	4.0E-01	-0.7	4.0E-01
ENSMUST00000167565	zinc finger protein 712 [Source:MGI Symbol;Acc:MGI:1925501]	E9PXJ4		0.6	2.6E-01	1.2	9.5E-02	0.7	2.2E-01	0.1	8.3E-01
ENSMUST00000188141				5.7	4.1E-04	5.6	2.5E-03	-0.7	6.6E-01	0.2	7.7E-01
ENSMUST00000188949				5.7	1.3E-04	-1.2	4.4E-01	3.3	5.2E-03	-1.8	3.1E-01
ENSMUST00000167571	G1 to S phase transition 1 [Source:MGI Symbol;Acc:MGI:1316728]		Q8R050	0.1	8.0E-01	0.7	3.8E-01	0.9	1.6E-01	0.4	6.1E-01
ENSMUST00000128407				5.7	9.7E-03	3.7	3.0E-02	0.8	5.6E-01	0.1	8.9E-01
ENSMUST00000137149				5.7	2.6E-04	1.8	3.6E-01	-0.6	7.0E-01	4.3	2.2E-02
ENSMUST00000167577				4.3	1.7E-01	5.3	1.2E-01	-0.2	9.5E-01	-1.3	5.2E-01
ENSMUST00000177406				5.7	1.2E-03	6.0	3.3E-05	-2.3	4.2E-02	0.0	9.6E-01
ENSMUST00000192832				5.7	6.2E-04	7.8	5.1E-05	0.6	6.0E-01	-0.4	5.0E-01
ENSMUST00000167594				1.6	3.3E-01	1.4	5.7E-01	0.4	8.0E-01	0.6	7.8E-01
ENSMUST00000120163				5.7	9.2E-05	-2.1	1.1E-01	0.7	3.3E-01	-3.4	5.2E-02
ENSMUST00000141229				5.7	2.0E-04	-7.1	1.3E-03	-0.1	9.0E-01	1.6	3.1E-01
ENSMUST00000167619	diaphanous homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1858500]	E9Q4U7		-1.3	6.6E-01	-0.5	8.4E-01	-1.9	3.9E-01	-2.6	3.6E-01
ENSMUST00000129098				5.7	7.0E-05	5.9	6.7E-04	-0.6	6.3E-01	-0.3	7.1E-01
ENSMUST00000167624	glyoxalase 1 [Source:MGI Symbol;Acc:MGI:95742]	A5GZX3	Q9CPU0	-2.9	8.7E-02	-2.5	1.4E-01	-1.0	3.7E-01	-1.4	4.4E-01
ENSMUST00000130079				5.7	5.9E-03	4.4	6.7E-02	-0.7	7.5E-01	0.7	6.1E-01
ENSMUST00000135973				5.7	5.9E-06	6.9	3.9E-04	-0.6	6.4E-01	-0.1	8.4E-01
ENSMUST00000162604				5.7	8.8E-04	-6.0	1.3E-03	1.4	2.1E-02	-1.7	3.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000121885				5.7	7.3E-06	5.5	1.9E-02	-0.6	7.7E-01	0.8	5.2E-01
ENSMUST00000167642				-1.2	6.6E-01	-0.5	8.5E-01	-1.9	3.4E-01	-2.6	3.8E-01
ENSMUST00000127773				5.7	9.1E-03	-9.6	1.6E-04	-1.7	3.8E-03	-0.7	7.1E-01
ENSMUST00000142136				5.7	2.6E-04	6.2	2.8E-03	-0.7	6.7E-01	0.2	8.2E-01
ENSMUST00000167655				-0.2	8.6E-01	0.3	8.1E-01	0.7	5.0E-01	0.2	8.8E-01
ENSMUST00000145385				5.7	5.6E-05	4.6	1.5E-03	0.6	5.3E-01	0.1	8.8E-01
ENSMUST00000117381				5.7	4.6E-04	6.5	3.0E-04	-2.7	6.9E-02	0.3	6.7E-01
ENSMUST00000133571				5.7	5.9E-03	-4.5	1.8E-03	0.2	6.2E-01	-0.9	4.4E-01
ENSMUST00000167662	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 [Source:MGI Symbol;Acc:MGI:1914708]	Q4FK22	Q9DC16	-1.4	7.7E-02	-0.7	4.5E-01	0.2	7.2E-01	-0.5	5.8E-01
ENSMUST00000167667	beclin 1, autophagy related [Source:MGI Symbol;Acc:MGI:1891828]	E9PX06		-2.4	4.1E-01	-0.6	8.8E-01	1.1	6.9E-01	-0.8	8.4E-01
ENSMUST00000187751				5.7	3.3E-04	5.6	2.2E-02	-0.8	7.3E-01	1.9	1.6E-01
ENSMUST00000159724				5.7	3.3E-06	4.6	5.9E-04	-1.2	1.9E-01	-0.1	8.5E-01
ENSMUST00000167671	cytoskeleton-associated protein 4 [Source:MGI Symbol;Acc:MGI:2444926]		Q8BMK4	1.6	6.2E-01	-0.6	9.0E-01	0.4	9.0E-01	2.6	5.8E-01
ENSMUST00000167673	RIKEN cDNA A630033H20 gene [Source:MGI Symbol;Acc:MGI:2441814]	Q8BY68		-1.3	6.3E-01	-3.9	2.3E-01	-3.1	1.0E-01	-0.5	8.8E-01
ENSMUST00000167678	alveolar soft part sarcoma chromosome region, candidate 1 (human) [Source:MGI Symbol;Acc:MGI:1916188]	F7B7K7		1.7	1.1E-01	3.6	2.1E-02	1.1	3.6E-01	-0.8	4.0E-01
ENSMUST00000183741				5.7	2.2E-04	0.9	5.8E-01	-0.7	5.9E-01	2.5	7.7E-02
ENSMUST00000195419				5.7	5.9E-05	3.2	3.0E-02	-1.2	3.4E-01	-0.5	6.2E-01
ENSMUST00000167708	ataxin 1 [Source:MGI Symbol;Acc:MGI:104783]		P54254	6.7	9.7E-02	-0.4	9.2E-01	-4.2	2.9E-01	3.0	4.3E-01
ENSMUST00000152520				5.7	1.1E-06	-0.4	8.4E-01	2.0	2.3E-01	-2.9	2.0E-01
ENSMUST00000167717				2.5	3.6E-01	2.7	5.4E-01	1.0	7.8E-01	0.8	8.0E-01
ENSMUST00000167721	actin, beta [Source:MGI Symbol;Acc:MGI:87904]	E9Q1F2		-2.9	5.7E-01	0.4	9.5E-01	2.7	5.4E-01	-0.6	9.1E-01
ENSMUST00000167724	ankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 [Source:MGI Symbol;Acc:MGI:1921743	F6YVU7		0.8	7.0E-01	-0.8	7.6E-01	-2.0	2.8E-01	-0.4	8.8E-01
ENSMUST00000187555				5.7	7.0E-04	1.8	2.1E-01	0.9	4.3E-01	1.7	1.3E-01
ENSMUST00000167732				-0.3	8.7E-01	-1.4	5.8E-01	-1.3	4.0E-01	-0.3	9.0E-01
ENSMUST00000114941				5.7	2.6E-04	6.8	4.3E-04	-0.5	7.2E-01	-0.6	4.3E-01
ENSMUST00000167746	cytidine monophospho-N-acetylneuraminic acid hydroxylase [Source:MGI Symbol;Acc:MGI:103227]		Q61419	-2.6	8.8E-02	2.1	2.4E-01	2.8	7.6E-02	-1.8	2.4E-01
ENSMUST00000131852				5.7	8.5E-04	-6.4	3.9E-04	-0.3	5.9E-01	-1.1	4.2E-01
ENSMUST00000167753	predicted gene 4450 [Source:MGI Symbol;Acc:MGI:3782634]	E9Q007		3.7	2.5E-01	4.2	2.3E-01	-0.1	9.7E-01	-0.6	7.8E-01
ENSMUST00000146797				5.7	3.4E-05	6.9	1.5E-05	-2.5	3.3E-02	0.0	9.7E-01
ENSMUST00000128215				5.7	7.5E-04	-2.7	9.1E-02	1.0	2.5E-01	0.0	9.8E-01
ENSMUST00000143603				5.7	1.2E-05	4.0	1.9E-02	-0.7	6.2E-01	-0.3	7.8E-01
ENSMUST00000167761				5.2	4.3E-02	4.8	9.0E-02	-0.5	8.4E-01	-0.1	9.5E-01
ENSMUST00000167767	MAP/microtubule affinity regulating kinase 2 [Source:MGI Symbol;Acc:MGI:99638]	F6UY70		-2.4	6.7E-02	2.8	1.5E-01	4.7	6.6E-03	-0.5	7.6E-01
ENSMUST00000186220				5.7	1.0E-04	12.1	5.3E-04	0.9	7.3E-01	2.2	3.8E-02
ENSMUST00000167772				4.5	6.5E-02	5.5	4.7E-02	-0.5	8.4E-01	-1.4	3.6E-01
ENSMUST00000167773	dipeptidylpeptidase 8 [Source:MGI Symbol;Acc:MGI:1921638]		Q80YA7	-0.7	3.5E-01	1.3	2.1E-01	1.7	4.9E-02	-0.3	7.3E-01
ENSMUST00000167776	transducin-like enhancer of split 4, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104633]	F6ZBY9		0.1	8.7E-01	-2.1	7.5E-02	-0.8	2.3E-01	1.4	2.1E-01
ENSMUST00000123222				5.7	3.1E-04	-1.5	2.1E-01	0.5	5.2E-01	-0.9	4.5E-01
ENSMUST00000149660				5.7	7.6E-05	-2.6	1.2E-01	0.8	3.6E-01	-1.0	5.7E-01
ENSMUST00000153000				5.7	5.1E-06	-5.8	2.5E-04	0.0	9.3E-01	-0.6	5.7E-01
ENSMUST00000136805				5.7	7.6E-04	1.4	1.6E-01	-1.1	2.1E-01	0.9	2.7E-01
ENSMUST00000167804	Flt3 interacting zinc finger protein 1 [Source:MGI Symbol;Acc:MGI:1344336]	Q3TRV0	Q9WTJ4	-0.4	8.8E-01	-2.7	5.1E-01	-1.4	5.5E-01	0.9	8.2E-01
ENSMUST00000140231				5.7	7.1E-04	3.5	9.0E-03	0.7	4.8E-01	0.2	8.0E-01
ENSMUST00000137739				5.7	2.5E-04	-5.7	2.9E-04	-0.2	6.5E-01	-0.6	6.1E-01
ENSMUST00000166987				5.7	1.0E-02	8.1	4.8E-04	0.0	9.9E-01	0.9	2.7E-01
ENSMUST00000124692				5.7	2.5E-03	-5.8	2.1E-02	1.6	6.5E-02	-0.8	7.4E-01
ENSMUST00000167841	endoglin [Source:MGI Symbol;Acc:MGI:95392]	Q3UAM9		-1.0	4.9E-01	-4.2	2.9E-02	-3.3	1.0E-02	-0.2	9.3E-01
ENSMUST00000163023				5.7	7.8E-04	8.2	6.0E-05	-1.8	2.2E-01	-0.3	5.0E-01
ENSMUST00000156010				5.7	1.7E-03	6.5	2.5E-04	-0.5	6.7E-01	-1.2	8.5E-02
ENSMUST00000146001				5.7	4.3E-04	0.2	8.8E-01	-4.5	1.4E-03	-0.6	5.7E-01
ENSMUST00000124219				5.7	9.4E-06	7.3	2.2E-02	-0.8	7.8E-01	-1.8	2.8E-01
ENSMUST00000167860	vascular endothelial growth factor A [Source:MGI Symbol;Acc:MGI:103178]	F6ZE01		0.4	7.6E-01	-1.8	3.4E-01	-0.2	8.7E-01	1.9	2.7E-01
ENSMUST00000137448				5.7	2.9E-03	-2.3	2.1E-02	0.8	1.1E-01	-0.4	6.5E-01
ENSMUST00000160547				5.7	2.3E-03	5.4	6.3E-04	-0.5	6.4E-01	0.5	3.8E-01
ENSMUST00000120029				5.7	5.8E-04	-1.1	1.2E-01	0.1	8.7E-01	-0.5	4.7E-01
ENSMUST00000131704				5.7	1.3E-03	7.1	1.1E-04	-0.5	6.7E-01	-1.0	1.4E-01
ENSMUST00000120764				5.7	1.5E-03	7.2	4.7E-05	-0.7	5.0E-01	-0.1	8.5E-01
ENSMUST00000118105				5.7	3.1E-02	-5.0	2.3E-03	-0.6	2.4E-01	-1.4	3.1E-01
ENSMUST00000139054				5.7	5.5E-06	8.6	2.3E-06	0.2	7.9E-01	-0.2	6.4E-01
ENSMUST00000167893	deafness, autosomal dominant 5 (human) [Source:MGI Symbol;Acc:MGI:1889850]	E9Q308		-0.6	2.5E-01	-1.3	9.6E-02	0.1	8.6E-01	0.7	2.8E-01
ENSMUST00000122338				5.7	6.8E-05	7.2	5.9E-05	-0.6	6.0E-01	-0.2	6.5E-01
ENSMUST00000125677				5.7	3.3E-04	4.2	5.5E-03	-0.6	5.6E-01	-0.4	6.3E-01
ENSMUST00000149682				5.7	2.5E-04	6.0	7.4E-03	-0.3	8.7E-01	-0.3	7.6E-01
ENSMUST00000160802				5.7	9.1E-05	12.5	1.9E-03	-0.7	8.2E-01	3.0	1.3E-02
ENSMUST00000191026				5.7	2.9E-03	6.8	1.4E-03	-0.6	7.3E-01	-0.5	5.4E-01
ENSMUST00000181042				5.7	7.1E-05	-4.9	5.7E-04	0.6	1.7E-01	-1.6	1.8E-01
ENSMUST00000167913	predicted gene 3476 [Source:MGI Symbol;Acc:MGI:3781652]	K7N6V0		4.4	1.3E-01	4.4	1.8E-01	-0.2	9.4E-01	-0.2	9.1E-01
ENSMUST00000167918	GTPase activating protein (SH3 domain) binding protein 2 [Source:MGI Symbol;Acc:MGI:2442040]	Q542W3	P97379	3.1	1.4E-01	-0.3	8.6E-01	-2.8	1.5E-01	0.6	7.4E-01
ENSMUST00000119680				5.7	7.4E-03	4.1	7.8E-04	-2.8	1.8E-02	-0.6	3.5E-01
ENSMUST00000167924	tumor necrosis factor [Source:MGI Symbol;Acc:MGI:104798]			3.5	9.7E-02	4.8	1.7E-01	3.6	1.7E-01	2.2	4.3E-01
ENSMUST00000134073				5.7	3.9E-04	3.6	1.3E-03	-3.3	7.2E-03	0.2	7.4E-01
ENSMUST00000137762				5.7	2.8E-02	3.9	3.2E-02	-2.6	1.5E-01	-0.4	6.9E-01
ENSMUST00000109776				5.7	1.0E-03	2.9	2.7E-02	0.6	5.2E-01	0.5	5.8E-01
ENSMUST00000167930	adaptor-related protein complex 2, alpha 1 subunit [Source:MGI Symbol;Acc:MGI:101921]		P17426	-3.5	2.6E-01	-5.9	1.3E-01	-2.3	2.0E-01	0.1	9.8E-01
ENSMUST00000167935	acyl-CoA synthetase medium-chain family member 2 [Source:MGI Symbol;Acc:MGI:2385289]		Q8K0L3	7.8	3.7E-02	9.5	1.9E-02	-0.6	8.7E-01	-2.3	1.9E-01
ENSMUST00000167950	RNA binding motif protein 47 [Source:MGI Symbol;Acc:MGI:2384294]		Q91WT8	-3.7	5.4E-02	-3.1	1.8E-01	0.5	6.9E-01	-0.1	9.7E-01
ENSMUST00000135418				5.7	8.3E-05	5.9	2.6E-04	-1.4	2.3E-01	-0.5	4.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000146932				5.7	1.6E-02	-4.7	2.2E-02	0.5	5.0E-01	2.2	2.2E-01
ENSMUST00000148190				5.7	1.2E-04	5.0	3.7E-04	-0.6	4.9E-01	-0.4	4.8E-01
ENSMUST00000192306				5.7	1.4E-02	7.1	2.5E-04	-0.6	6.8E-01	-0.3	6.3E-01
ENSMUST00000167972	nuclear respiratory factor 1 [Source:MGI Symbol;Acc:MGI:1332235]		Q9WU00	-0.1	9.8E-01	0.9	7.6E-01	0.7	7.2E-01	-0.3	9.3E-01
ENSMUST00000175636				5.7	1.2E-05	6.5	8.2E-03	-0.6	7.7E-01	-1.9	1.3E-01
ENSMUST00000188304				5.7	1.0E-02	-3.7	5.8E-02	0.9	3.5E-01	-0.1	9.6E-01
ENSMUST00000128067				5.7	6.4E-05	2.5	5.2E-02	-1.6	1.7E-01	-0.4	6.9E-01
ENSMUST00000120860				5.7	1.7E-04	2.5	1.5E-02	-1.2	1.3E-01	-0.2	8.0E-01
ENSMUST00000124411				5.7	5.5E-04	-5.8	2.6E-03	0.1	7.7E-01	-0.5	7.4E-01
ENSMUST00000112141				5.7	7.7E-03	2.9	8.8E-04	-0.6	2.6E-01	0.1	8.3E-01
ENSMUST00000150667				5.7	1.8E-04	-3.6	1.6E-03	-1.5	8.5E-03	0.6	4.6E-01
ENSMUST00000189935				5.7	2.3E-04	3.2	6.7E-03	0.1	9.2E-01	0.0	1.0E+00
ENSMUST00000167670				5.7	5.7E-05	5.8	2.1E-03	-0.7	6.6E-01	0.2	7.7E-01
ENSMUST00000167998	glucosidase, beta, acid [Source:MGI Symbol;Acc:MGI:95665]		P17439	-2.3	6.0E-02	0.1	9.2E-01	0.3	7.8E-01	-2.1	1.2E-01
ENSMUST00000130978				5.6	5.7E-05	2.3	1.9E-01	-3.8	8.1E-02	2.2	1.3E-01
ENSMUST00000133886				5.6	5.8E-03	5.2	7.3E-02	-0.7	8.0E-01	0.0	9.8E-01
ENSMUST00000120050				5.6	1.7E-05	5.9	1.7E-02	-0.8	7.3E-01	-1.0	4.6E-01
ENSMUST00000168012				0.8	6.9E-01	-3.5	3.5E-01	-0.8	7.0E-01	3.5	3.2E-01
ENSMUST00000155255				5.6	3.9E-05	-0.6	6.5E-01	0.6	5.4E-01	-4.8	1.6E-02
ENSMUST00000107643				5.6	1.2E-04	-6.6	1.4E-02	0.9	2.4E-01	-1.7	5.1E-01
ENSMUST00000189552				5.6	9.3E-05	6.2	3.7E-04	-0.5	7.1E-01	-0.8	2.5E-01
ENSMUST00000146361				5.6	8.6E-04	-5.9	8.6E-03	0.4	5.8E-01	-0.7	7.4E-01
ENSMUST00000128356				5.6	4.5E-04	-7.4	6.6E-03	-1.4	1.1E-01	0.1	9.8E-01
ENSMUST00000144945				5.6	2.3E-04	-5.4	2.9E-04	-0.8	6.2E-02	-0.8	4.7E-01
ENSMUST00000168031				-1.6	4.2E-01	-3.4	1.7E-01	-2.0	2.1E-01	-0.2	9.4E-01
ENSMUST00000191013				5.6	4.5E-04	6.0	3.9E-03	-0.4	8.3E-01	-1.1	2.6E-01
ENSMUST00000168036	CCR4-NOT transcription complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1919318]	E9Q027		-0.1	9.7E-01	-3.3	3.3E-01	-3.7	9.2E-02	-0.5	8.9E-01
ENSMUST00000077435				5.6	9.6E-04	5.2	1.5E-03	-0.6	6.6E-01	-0.2	8.2E-01
ENSMUST00000168047	ATPase type 13A2 [Source:MGI Symbol;Acc:MGI:1922022]	E9PYX5		1.5	1.6E-01	2.8	8.2E-02	0.5	6.8E-01	-0.7	5.1E-01
ENSMUST00000127960				5.6	2.8E-05	8.3	1.9E-03	-0.9	6.8E-01	1.0	3.1E-01
ENSMUST00000168055	glyoxalase domain containing 4 [Source:MGI Symbol;Acc:MGI:1914451]	F7BB55		-0.8	7.5E-01	-3.9	1.3E-01	-4.6	1.3E-02	-1.4	6.1E-01
ENSMUST00000168058	ankyrin repeat domain 17 [Source:MGI Symbol;Acc:MGI:1932101]	E9Q804		1.3	5.5E-01	1.1	7.2E-01	1.0	6.1E-01	1.3	6.4E-01
ENSMUST00000141414				5.6	9.1E-04	6.7	5.6E-04	-0.6	6.5E-01	-0.3	7.3E-01
ENSMUST00000156246				5.6	2.8E-04	6.1	1.1E-02	-0.7	7.4E-01	-1.8	1.8E-01
ENSMUST00000168070				0.3	6.2E-01	1.5	6.2E-02	0.2	6.8E-01	-1.0	1.6E-01
ENSMUST00000120369				5.6	4.8E-04	5.9	7.4E-03	-0.7	7.1E-01	-0.9	3.9E-01
ENSMUST00000138524				5.6	1.1E-03	7.1	1.5E-03	-0.5	7.7E-01	-0.2	8.5E-01
ENSMUST00000140318				5.6	1.9E-05	-1.4	4.5E-01	1.6	2.0E-01	-1.2	5.3E-01
ENSMUST00000168076	solute carrier family 39 (zinc transporter), member 3 [Source:MGI Symbol;Acc:MGI:2147269]		Q99K24	-1.1	7.2E-01	3.7	2.3E-01	0.2	9.3E-01	-4.6	1.4E-01
ENSMUST00000140428				5.6	1.1E-03	4.0	1.7E-02	-1.4	3.1E-01	-0.1	9.5E-01
ENSMUST00000168081	eyes absent 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109344]	F6YST4		3.5	7.9E-02	2.0	3.9E-01	-0.5	8.1E-01	1.0	5.8E-01
ENSMUST00000168086	jade family PHD finger 1 [Source:MGI Symbol;Acc:MGI:1925835]		Q6ZPI0	-1.2	6.7E-01	-0.7	7.5E-01	-2.1	2.9E-01	-2.6	3.6E-01
ENSMUST00000168088	predicted gene 6337 [Source:MGI Symbol;Acc:MGI:3646283]	K7N6X9		4.2	1.1E-01	5.8	5.1E-02	-0.2	9.5E-01	-1.9	2.6E-01
ENSMUST00000168092	RasGEF domain family, member 1B [Source:MGI Symbol;Acc:MGI:2443755]		Q8JZL7	-1.8	1.1E-01	1.1	1.9E-01	-1.0	1.9E-01	-3.9	3.2E-03
ENSMUST00000137238				5.6	5.8E-04	-5.7	1.8E-03	1.2	5.4E-02	3.2	3.8E-02
ENSMUST00000127271				5.6	2.0E-04	-1.7	4.5E-01	1.4	3.4E-01	-1.5	5.2E-01
ENSMUST00000168098	nuclear receptor subfamily 6, group A, member 1 [Source:MGI Symbol;Acc:MGI:1352459]		Q64249	3.4	2.2E-01	2.2	4.9E-01	-1.6	5.9E-01	-0.3	8.9E-01
ENSMUST00000127659				5.6	1.3E-03	-6.4	2.0E-03	-0.7	2.9E-01	-1.9	3.2E-01
ENSMUST00000142157				5.6	7.0E-03	3.0	1.9E-01	-2.3	2.9E-01	0.6	6.9E-01
ENSMUST00000168037				5.6	4.9E-04	-6.1	1.0E-04	-0.1	6.8E-01	-0.8	4.6E-01
ENSMUST00000168106	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Source:MGI Symbol;Acc:MGI:1913721]	E9Q0X5		3.9	1.2E-01	3.3	1.6E-01	-4.2	1.1E-01	-3.7	6.1E-02
ENSMUST00000136065				5.6	6.3E-04	3.6	4.5E-02	1.0	5.0E-01	0.3	7.6E-01
ENSMUST00000146343				5.6	1.7E-05	-3.8	3.1E-02	0.3	7.1E-01	1.1	4.9E-01
ENSMUST00000168112	calcium binding and coiled coil domain 1 [Source:MGI Symbol;Acc:MGI:1914738]	F6Q5V4		-1.4	5.7E-01	-2.5	5.1E-01	-0.2	9.3E-01	0.9	8.0E-01
ENSMUST00000190208				5.6	2.3E-04	-5.8	2.5E-04	-0.3	3.7E-01	-0.2	8.7E-01
ENSMUST00000191249				5.6	4.1E-03	7.3	1.5E-05	-1.9	7.7E-02	-0.2	6.5E-01
ENSMUST00000125488				5.6	3.2E-04	6.1	3.0E-04	0.4	7.2E-01	0.0	9.9E-01
ENSMUST00000168120	acyl-CoA thioesterase 1 [Source:MGI Symbol;Acc:MGI:1349396]		O55137	-1.0	3.2E-01	0.7	6.2E-01	2.2	8.0E-02	0.4	7.4E-01
ENSMUST00000129920				5.6	1.3E-03	-3.8	1.4E-02	0.5	4.5E-01	-0.8	5.8E-01
ENSMUST00000136784				5.6	2.2E-02	4.9	2.9E-03	-1.2	3.9E-01	-0.6	4.6E-01
ENSMUST00000076585				5.6	1.3E-03	4.7	9.7E-03	-0.6	6.9E-01	2.1	4.5E-02
ENSMUST00000191486				5.6	1.1E-03	-5.0	6.7E-02	0.7	5.0E-01	1.5	5.5E-01
ENSMUST00000168134	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Source:MGI Symbol;Ac	B2RXW8		2.7	3.1E-01	1.8	6.5E-01	0.4	9.1E-01	1.3	6.4E-01
ENSMUST00000100308				5.6	5.6E-03	5.8	5.2E-05	0.3	7.0E-01	0.6	2.0E-01
ENSMUST00000183377				5.6	8.0E-05	-1.9	5.7E-01	3.2	1.4E-01	-1.8	6.1E-01
ENSMUST00000176895				5.6	8.5E-05	5.7	1.7E-03	-0.9	5.5E-01	-0.7	3.8E-01
ENSMUST00000168157	ciliary rootlet coiled-coil, rootletin [Source:MGI Symbol;Acc:MGI:3529431]		Q8CJ40	0.8	7.9E-01	0.5	8.5E-01	-2.7	2.9E-01	-2.5	3.7E-01
ENSMUST00000191005				5.6	1.1E-03	8.5	3.2E-05	-0.6	6.2E-01	-0.2	7.3E-01
ENSMUST00000061201				5.6	1.9E-04	0.7	7.1E-01	-4.4	3.1E-02	2.1	1.9E-01
ENSMUST00000131572				5.6	1.6E-03	5.7	7.9E-04	-0.6	6.1E-01	1.1	1.3E-01
ENSMUST00000168166	cAMP-regulated phosphoprotein 19 [Source:MGI Symbol;Acc:MGI:1891691]		P56212	0.1	9.3E-01	-0.4	6.6E-01	-0.9	2.1E-01	-0.4	6.4E-01
ENSMUST00000186855				5.6	1.9E-04	-4.8	1.6E-03	0.8	1.2E-01	2.3	5.8E-02
ENSMUST00000122287				5.6	7.0E-04	6.5	1.3E-04	-0.5	6.5E-01	-0.5	4.3E-01
ENSMUST00000143341				5.6	1.5E-03	3.2	4.3E-01	-1.0	7.8E-01	3.6	2.5E-01
ENSMUST00000168177	transcriptional regulator, SIN3A (yeast) [Source:MGI Symbol;Acc:MGI:107157]		Q60520	1.4	5.8E-01	-2.8	4.7E-01	-1.2	5.8E-01	3.0	4.4E-01
ENSMUST00000155421				5.6	1.3E-04	2.7	1.4E-01	-2.5	1.6E-01	2.8	4.2E-02
ENSMUST00000192547				5.6	1.5E-04	6.5	2.7E-04	-0.1	9.2E-01	-1.2	9.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000194236				5.6	9.0E-05	3.6	2.3E-03	0.6	4.1E-01	-0.3	6.9E-01
ENSMUST00000130890				5.6	9.9E-05	-5.5	1.2E-03	0.9	1.0E-01	-2.0	2.1E-01
ENSMUST00000146750				5.6	6.6E-04	6.8	6.0E-04	-0.7	6.2E-01	0.7	3.6E-01
ENSMUST00000187060				5.6	4.8E-04	-0.8	2.7E-01	0.7	1.7E-01	-0.9	1.9E-01
ENSMUST00000168195	runt related transcription factor 1 [Source:MGI Symbol;Acc:MGI:99852]	G3UWD2		-2.9	5.7E-02	-0.5	7.5E-01	0.9	4.6E-01	-1.5	3.1E-01
ENSMUST00000188395				5.6	1.4E-04	-2.5	2.8E-02	0.9	1.2E-01	0.3	7.6E-01
ENSMUST00000168218	transmembrane protein 11 [Source:MGI Symbol;Acc:MGI:2144726]	E9Q933		-0.8	7.9E-01	0.0	1.0E+00	0.1	9.8E-01	-0.7	8.3E-01
ENSMUST00000155614				5.6	5.0E-05	-5.3	1.9E-02	0.5	5.9E-01	0.0	9.8E-01
ENSMUST00000139821				5.6	8.5E-05	6.8	1.2E-04	0.0	9.7E-01	0.5	4.0E-01
ENSMUST00000168236				1.1	5.6E-01	-1.0	6.6E-01	-1.6	3.8E-01	0.5	8.1E-01
ENSMUST00000168237	DIS3 mitotic control homolog (S. cerevisiae)-like 2 [Source:MGI Symbol;Acc:MGI:2442555]		Q8CI75	0.4	8.6E-01	3.1	3.8E-01	3.1	3.2E-01	0.4	8.7E-01
ENSMUST00000124857				5.6	2.4E-03	-6.0	6.1E-04	-0.7	1.6E-01	-1.8	2.3E-01
ENSMUST00000168254	interferon induced protein with tetratricpeptide repeats 1B like 1 [Source:MGI Symbol;Acc:MGI:3650685]	E9PXF7		3.7	5.2E-02	1.8	2.4E-01	-4.0	4.0E-02	-2.2	1.0E-01
ENSMUST00000168260	cytokine inducible SH2-containing protein [Source:MGI Symbol;Acc:MGI:103159]	E9Q273		0.1	9.2E-01	6.2	1.4E-02	4.0	6.7E-02	-2.0	1.3E-01
ENSMUST00000168264	armadillo repeat containing, X-linked 2 [Source:MGI Symbol;Acc:MGI:1914666]		Q6A058	3.2	2.3E-01	5.2	1.4E-01	1.3	6.8E-01	-0.6	7.5E-01
ENSMUST00000168266	structure specific recognition protein 1 [Source:MGI Symbol;Acc:MGI:107912]		Q08943	-2.3	1.2E-01	2.2	3.1E-01	5.2	1.2E-02	0.7	6.8E-01
ENSMUST00000168271				1.0	3.7E-01	-0.1	9.5E-01	0.0	9.8E-01	1.1	3.8E-01
ENSMUST00000168275	tudor domain containing 3 [Source:MGI Symbol;Acc:MGI:2444023]		Q91W18	4.2	4.3E-02	-0.5	7.8E-01	-3.8	5.4E-02	1.0	5.8E-01
ENSMUST00000168280	interferon gamma induced GTPase [Source:MGI Symbol;Acc:MGI:107729]	E9Q9N8		-4.5	1.5E-01	-6.3	9.4E-02	-2.8	1.0E-01	-1.0	8.0E-01
ENSMUST00000124663				5.6	4.3E-06	8.2	1.4E-02	-0.8	8.0E-01	-2.3	1.7E-01
ENSMUST00000128386				5.6	1.7E-02	-3.7	6.5E-02	1.6	1.0E-01	-1.4	4.8E-01
ENSMUST00000140748				5.6	1.2E-03	5.5	2.9E-03	-0.2	8.8E-01	0.2	7.9E-01
ENSMUST00000191117				5.6	2.9E-04	6.6	4.3E-04	-0.7	6.2E-01	0.6	3.8E-01
ENSMUST00000122018				5.6	1.1E-03	-3.4	1.0E-02	-0.3	5.9E-01	0.2	8.8E-01
ENSMUST00000168309	anterior pharynx defective 1b homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:3522097]	Q3TRQ2	Q8C7N7	-1.2	5.7E-01	-3.7	2.3E-01	-2.0	2.2E-01	0.4	9.0E-01
ENSMUST00000138284				5.6	1.7E-05	5.5	1.5E-03	-0.6	6.5E-01	0.5	5.1E-01
ENSMUST00000128367				5.6	7.5E-04	6.4	3.9E-04	0.5	6.9E-01	0.2	8.1E-01
ENSMUST00000168334	nuclear receptor coactivator 4 [Source:MGI Symbol;Acc:MGI:1350932]	E9Q8Q4		3.0	2.0E-01	0.6	8.1E-01	-1.8	4.2E-01	0.6	8.1E-01
ENSMUST00000168341	olfactory receptor 1344 [Source:MGI Symbol;Acc:MGI:3031178]	Q7TQV3		3.1	1.3E-01	2.5	2.2E-01	-0.5	8.2E-01	0.1	9.7E-01
ENSMUST00000143422				5.6	1.7E-03	-5.2	1.4E-04	-0.3	5.0E-01	1.0	2.5E-01
ENSMUST00000137459				5.6	4.2E-05	4.4	3.6E-03	-4.3	8.7E-03	-0.4	5.9E-01
ENSMUST00000168350	serine (or cysteine) peptidase inhibitor, clade B, member 6a [Source:MGI Symbol;Acc:MGI:103123]	E9Q6X2		-2.0	4.9E-01	-6.2	8.4E-02	-4.9	1.7E-02	-0.7	8.6E-01
ENSMUST00000168351				-3.6	4.9E-02	-1.5	3.9E-01	-0.1	9.0E-01	-2.3	2.3E-01
ENSMUST00000179930				5.6	9.5E-04	-4.7	1.0E-02	0.1	8.7E-01	-1.4	4.1E-01
ENSMUST00000168361	pumilio RNA-binding family member 2 [Source:MGI Symbol;Acc:MGI:1931751]		Q80U58	-2.1	3.4E-01	0.7	7.9E-01	2.9	2.2E-01	0.0	9.9E-01
ENSMUST00000142921				5.6	2.3E-03	4.2	1.1E-03	-0.3	7.0E-01	-0.5	4.5E-01
ENSMUST00000153286				5.6	7.6E-06	2.2	1.5E-02	-0.4	5.7E-01	-0.8	2.6E-01
ENSMUST00000126838				5.6	9.9E-03	-3.3	3.7E-02	1.4	6.5E-02	-0.6	6.7E-01
ENSMUST00000153225				5.6	5.0E-04	7.1	1.3E-05	-0.4	6.8E-01	-0.5	2.6E-01
ENSMUST00000168378	TBC1 domain family, member 24 [Source:MGI Symbol;Acc:MGI:2443456]		Q3UUG6	0.3	8.6E-01	3.1	1.7E-01	1.2	5.1E-01	-1.6	4.0E-01
ENSMUST00000159881				5.6	4.9E-04	-6.6	3.0E-04	-0.9	4.7E-02	-0.9	5.0E-01
ENSMUST00000128283				5.6	1.4E-04	7.8	1.1E-04	-0.7	6.1E-01	0.1	8.8E-01
ENSMUST00000166788				5.6	6.0E-05	8.0	1.1E-05	1.1	2.3E-01	-0.1	7.7E-01
ENSMUST00000124796				5.6	1.1E-03	2.6	6.9E-02	-0.6	6.0E-01	3.4	7.2E-03
ENSMUST00000131598				5.6	5.4E-05	8.0	3.1E-05	-0.5	6.3E-01	-0.5	3.3E-01
ENSMUST00000168396	heterogeneous nuclear ribonucleoprotein D [Source:MGI Symbol;Acc:MGI:101947]	E9Q4W5		-2.7	5.2E-02	0.6	6.7E-01	1.0	4.1E-01	-2.4	1.0E-01
ENSMUST00000168410	TBC1 domain family, member 24 [Source:MGI Symbol;Acc:MGI:2443456]		Q3UUG6	1.5	5.8E-01	-1.3	7.8E-01	-0.2	9.5E-01	2.6	5.3E-01
ENSMUST00000176606				5.6	3.0E-05	2.9	1.4E-01	-3.6	9.8E-02	-1.6	2.5E-01
ENSMUST00000191337				5.6	2.9E-04	-2.1	1.7E-02	-0.2	6.5E-01	-5.5	6.9E-04
ENSMUST00000118284				5.6	1.3E-04	-0.9	4.8E-01	0.7	3.8E-01	-1.4	2.5E-01
ENSMUST00000181429				5.6	2.3E-04	-3.6	1.1E-02	0.8	1.8E-01	-0.1	9.6E-01
ENSMUST00000168434	gametogenetin binding protein 2 [Source:MGI Symbol;Acc:MGI:2387356]		Q5SV77	2.6	1.0E-01	4.8	7.8E-03	-0.6	7.1E-01	-2.8	3.4E-02
ENSMUST00000128754				5.6	3.7E-04	5.2	4.2E-02	-2.8	3.3E-01	-1.1	5.2E-01
ENSMUST00000194536				5.6	1.6E-04	6.1	8.3E-04	-0.5	7.0E-01	-0.7	3.6E-01
ENSMUST00000149152				5.6	1.8E-03	-1.4	1.1E-01	1.3	2.6E-02	0.2	8.2E-01
ENSMUST00000177067				5.6	9.5E-03	6.0	7.9E-04	-0.9	5.2E-01	0.4	5.7E-01
ENSMUST00000154495				5.6	1.3E-04	-5.8	1.9E-03	-1.2	5.1E-02	-0.2	8.8E-01
ENSMUST00000168463	cytochrome c oxidase assembly protein 16 [Source:MGI Symbol;Acc:MGI:1913522]	E9Q3U7		-3.7	5.0E-02	-5.6	1.6E-02	-1.9	6.8E-02	0.1	9.8E-01
ENSMUST00000160273				5.6	3.0E-02	4.2	1.7E-02	-0.4	7.6E-01	0.0	9.7E-01
ENSMUST00000168479	NYN domain and retroviral integrase containing [Source:MGI Symbol;Acc:MGI:2652872]		Q5DTZ0	3.2	5.6E-02	8.7	3.5E-03	3.5	1.5E-01	-2.1	9.5E-02
ENSMUST00000125216				5.6	1.2E-03	2.2	1.8E-01	-0.4	7.5E-01	3.9	7.6E-03
ENSMUST00000131037				5.6	2.6E-02	8.0	2.2E-02	-0.9	7.8E-01	-0.8	6.4E-01
ENSMUST00000177386				5.6	8.7E-04	6.5	2.7E-04	-0.5	6.7E-01	-1.8	2.1E-02
ENSMUST00000168495				1.1	3.0E-01	0.2	8.5E-01	-0.5	6.0E-01	0.3	7.9E-01
ENSMUST00000180714				5.6	2.2E-03	-3.1	2.9E-02	1.3	6.5E-02	-4.1	3.4E-02
ENSMUST00000168500	DBF4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1351328]	E9PW04		-1.2	5.8E-02	-0.9	1.8E-01	-0.9	8.1E-02	-1.2	9.3E-02
ENSMUST00000168501	PHD finger protein 8 [Source:MGI Symbol;Acc:MGI:2444341]		Q80TJ7	0.6	6.1E-01	-0.2	9.2E-01	1.0	4.5E-01	1.8	3.1E-01
ENSMUST00000098368				5.6	1.8E-04	3.4	1.2E-01	3.2	9.7E-02	-5.6	1.6E-02
ENSMUST00000168507	potassium channel tetramerisation domain containing 20 [Source:MGI Symbol;Acc:MGI:1914239]		Q8CDD8	1.7	4.6E-01	3.7	1.7E-01	0.3	8.8E-01	-1.7	4.6E-01
ENSMUST00000134167				5.6	2.3E-02	6.6	1.8E-04	-0.6	5.9E-01	-0.8	2.5E-01
ENSMUST00000134642				5.6	2.1E-03	6.0	3.6E-02	-0.8	7.6E-01	3.2	4.4E-02
ENSMUST00000190599				5.6	9.1E-04	-5.8	1.3E-03	0.1	9.1E-01	-0.6	6.6E-01
ENSMUST00000133929				5.6	5.0E-04	-6.6	2.7E-04	0.2	6.2E-01	0.2	8.9E-01
ENSMUST00000168531	camello-like 3 [Source:MGI Symbol;Acc:MGI:2136449]			0.7	6.7E-01	4.3	2.8E-02	0.2	8.8E-01	-3.4	4.2E-02
ENSMUST00000153730				5.6	1.1E-03	5.8	1.4E-02	-3.9	1.2E-01	-1.9	1.4E-01
ENSMUST00000120110				5.6	2.7E-03	-7.3	5.6E-05	0.7	5.6E-02	0.0	9.8E-01
ENSMUST00000168545	adenylate cyclase 7 [Source:MGI Symbol;Acc:MGI:102891]		P51829	-3.2	4.2E-01	-2.2	6.4E-01	-0.1	9.8E-01	-1.0	8.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000168546	inositol polyphosphate-4-phosphatase, type I [Source:MGI Symbol;Acc:MGI:1931123]	F6R4N2		-1.0	5.5E-01	-1.5	5.7E-01	1.0	5.4E-01	1.5	5.5E-01
ENSMUST00000168552	dishevelled, dsh homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:94941]		P51141	0.0	1.0E+00	1.0	7.5E-01	0.8	7.2E-01	-0.3	9.3E-01
ENSMUST00000133679				5.6	9.2E-05	2.6	9.4E-03	-0.8	3.1E-01	0.5	4.7E-01
ENSMUST00000150983				5.6	1.0E-05	6.5	1.3E-03	-0.7	6.5E-01	-1.3	1.7E-01
ENSMUST00000145253				5.6	3.1E-03	7.2	2.7E-05	-0.9	3.8E-01	-0.4	4.3E-01
ENSMUST00000167000				5.6	1.8E-05	-1.8	2.1E-01	0.9	2.7E-01	-1.7	2.7E-01
ENSMUST00000168565	oxysterol binding protein-like 7 [Source:MGI Symbol;Acc:MGI:1918490]	F8VQM4		-3.7	5.6E-02	-2.3	1.8E-01	-1.4	2.1E-01	-2.9	1.6E-01
ENSMUST00000168568				-1.9	8.2E-02	-0.4	7.8E-01	1.4	1.6E-01	0.0	9.8E-01
ENSMUST00000168574	phosphotyrosine interaction domain containing 1 [Source:MGI Symbol;Acc:MGI:2138391]		Q3UBG2	1.7	6.1E-02	-0.2	8.2E-01	-0.5	5.4E-01	1.4	1.7E-01
ENSMUST00000168575	paraspeckle protein 1 [Source:MGI Symbol;Acc:MGI:1913895]	F7D909		-3.5	4.2E-02	-1.9	2.2E-01	-0.3	7.6E-01	-1.9	2.8E-01
ENSMUST00000176008				5.6	1.1E-04	1.2	1.6E-01	-2.8	5.2E-03	0.0	9.9E-01
ENSMUST00000191763				5.6	1.3E-03	-1.6	2.3E-01	0.9	2.8E-01	-0.4	7.5E-01
ENSMUST00000168584	glycosyltransferase 8 domain containing 1 [Source:MGI Symbol;Acc:MGI:1923735]		Q6NSU3	0.3	7.4E-01	1.2	2.5E-01	0.4	6.1E-01	-0.5	5.9E-01
ENSMUST00000123674				5.6	2.6E-04	-5.0	7.9E-03	1.0	1.3E-01	0.6	7.0E-01
ENSMUST00000168589	src-like adaptor [Source:MGI Symbol;Acc:MGI:104295]	Q4FJX0	Q60898	-1.2	5.6E-01	0.5	8.7E-01	1.4	4.4E-01	-0.3	9.2E-01
ENSMUST00000189222				5.6	1.1E-05	6.5	9.6E-05	-0.9	3.7E-01	0.1	8.8E-01
ENSMUST00000120104				5.6	7.3E-04	3.4	1.1E-01	-0.9	6.5E-01	0.3	8.5E-01
ENSMUST00000168615	rearranged L-myc fusion sequence [Source:MGI Symbol;Acc:MGI:1924705]	E9Q532		3.2	1.3E-01	4.7	1.2E-01	2.8	3.1E-01	1.2	5.0E-01
ENSMUST00000168621	protein tyrosine phosphatase, receptor type, J [Source:MGI Symbol;Acc:MGI:104574]	E9Q4S7		-2.2	6.0E-02	-1.4	2.6E-01	0.3	7.0E-01	-0.4	7.5E-01
ENSMUST00000187376				5.6	4.5E-03	8.0	4.3E-04	-0.2	8.8E-01	0.4	5.4E-01
ENSMUST00000192198				5.6	3.2E-05	5.0	1.3E-04	0.0	9.8E-01	-0.4	4.5E-01
ENSMUST00000168645	polyhomeotic-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2181434]		Q8CHP6	-0.3	5.2E-01	0.1	9.4E-01	0.3	5.1E-01	-0.1	9.2E-01
ENSMUST00000077990				5.6	1.3E-03	2.9	1.8E-03	-0.6	3.4E-01	-0.2	7.5E-01
ENSMUST00000164487				5.6	2.9E-04	-1.1	2.6E-01	1.0	1.2E-01	-1.1	2.8E-01
ENSMUST00000145990				5.6	7.0E-04	2.2	1.8E-01	-2.0	2.0E-01	0.1	9.3E-01
ENSMUST00000175862				5.6	7.4E-04	-0.7	5.8E-01	1.1	2.3E-01	-1.2	3.5E-01
ENSMUST00000170463				5.6	3.1E-04	-3.0	1.1E-01	1.2	2.6E-01	0.2	9.0E-01
ENSMUST00000182889				5.6	3.2E-04	8.2	1.8E-05	0.1	9.1E-01	-0.6	2.0E-01
ENSMUST00000120626				5.6	8.1E-04	3.4	1.7E-02	-2.0	1.3E-01	-0.3	7.4E-01
ENSMUST00000139393				5.6	1.3E-04	6.2	2.2E-04	-0.5	6.4E-01	-0.2	7.6E-01
ENSMUST00000141459				5.6	7.9E-04	1.4	5.3E-01	8.7	2.1E-04	1.1	5.8E-01
ENSMUST00000168698	coactosin-like 1 (Dictyostelium) [Source:MGI Symbol;Acc:MGI:1919292]	Q544F6	Q9CQI6	-3.0	2.0E-01	2.3	6.0E-01	6.4	5.6E-02	1.1	7.6E-01
ENSMUST00000151724				5.6	5.2E-04	5.6	1.6E-04	-1.5	1.4E-01	0.5	4.3E-01
ENSMUST00000187574				5.6	1.9E-04	-5.6	3.5E-03	0.6	2.6E-01	0.7	6.5E-01
ENSMUST00000116491				5.6	1.4E-03	4.7	5.4E-04	-1.1	2.7E-01	-0.2	7.3E-01
ENSMUST00000168704				0.3	4.0E-01	-0.1	9.2E-01	-0.2	5.3E-01	0.2	7.6E-01
ENSMUST00000128828				5.6	3.6E-04	3.3	1.4E-01	-1.5	5.2E-01	3.9	1.6E-02
ENSMUST00000168716	receptor-interacting serine-threonine kinase 3 [Source:MGI Symbol;Acc:MGI:2154952]	E9PZP3		2.5	6.0E-02	3.0	1.1E-01	0.5	7.7E-01	0.0	9.7E-01
ENSMUST00000168720	cyclin Pas1/PHO80 domain containing 1 [Source:MGI Symbol;Acc:MGI:1916421]		Q8K158	0.1	9.0E-01	0.7	4.7E-01	0.7	3.4E-01	0.1	9.3E-01
ENSMUST00000150829				5.6	2.6E-04	2.3	1.8E-02	0.0	9.7E-01	0.0	9.7E-01
ENSMUST00000168725				2.5	2.1E-01	3.7	1.5E-01	2.0	3.8E-01	0.8	6.4E-01
ENSMUST00000188376				5.6	8.5E-05	7.5	4.3E-05	-0.5	6.3E-01	-0.3	5.7E-01
ENSMUST00000168729	transglutaminase 1, K polypeptide [Source:MGI Symbol;Acc:MGI:98730]			-3.0	9.0E-02	0.6	7.4E-01	1.4	3.9E-01	-2.2	2.1E-01
ENSMUST00000168733	predicted gene 3468 [Source:MGI Symbol;Acc:MGI:3781644]	A6NAS8		4.8	4.3E-02	1.5	5.8E-01	-0.9	7.0E-01	2.4	2.8E-01
ENSMUST00000168740	olute carrier family 16 (monocarboxylic acid transporters), member 6 [Source:MGI Symbol;Acc:MGI:2144585	H9KV19		1.0	2.3E-01	0.8	4.4E-01	-0.3	6.8E-01	-0.1	9.3E-01
ENSMUST00000168741	golgi apparatus protein 1 [Source:MGI Symbol;Acc:MGI:104967]	F6RSH1		-2.7	7.5E-02	-1.4	3.6E-01	-0.3	7.4E-01	-1.6	3.5E-01
ENSMUST00000184633				5.6	1.6E-02	-4.9	5.5E-02	2.6	1.7E-02	1.1	6.3E-01
ENSMUST00000121915				5.6	7.0E-03	2.6	4.0E-03	0.1	8.6E-01	0.0	9.5E-01
ENSMUST00000143442				5.6	2.1E-04	3.8	6.9E-02	-0.6	7.7E-01	1.8	1.8E-01
ENSMUST00000154656				5.6	2.1E-03	2.6	1.7E-01	4.3	1.5E-02	-3.0	6.0E-02
ENSMUST00000084199				5.6	3.3E-04	-7.3	9.1E-03	-0.2	8.1E-01	0.3	9.0E-01
ENSMUST00000153433				5.6	2.2E-04	5.1	5.7E-03	-1.1	5.0E-01	-0.8	4.2E-01
ENSMUST00000117205				5.6	4.3E-04	8.0	3.8E-05	-0.7	5.8E-01	-0.3	5.9E-01
ENSMUST00000168772	MARVEL (membrane-associating) domain containing 2 [Source:MGI Symbol;Acc:MGI:2446166]	A1BQX3	Q3UZP0	4.4	6.8E-02	3.6	2.1E-01	0.5	8.6E-01	1.3	4.9E-01
ENSMUST00000168774	ets variant 5 [Source:MGI Symbol;Acc:MGI:1096867]	Q8BJR1		4.1	8.0E-02	4.3	1.2E-01	-1.5	5.6E-01	-1.6	3.8E-01
ENSMUST00000168776	septin 2 [Source:MGI Symbol;Acc:MGI:97298]		P42208	-3.3	2.4E-01	-6.2	7.9E-02	-3.7	3.9E-02	-0.8	8.2E-01
ENSMUST00000127573				5.6	1.7E-05	3.4	4.1E-03	-0.3	7.4E-01	-0.4	5.7E-01
ENSMUST00000168782	inter alpha-trypsin inhibitor, heavy chain 4 [Source:MGI Symbol;Acc:MGI:109536]	E9Q5L2		2.2	3.8E-01	2.7	3.6E-01	-0.8	7.8E-01	-1.3	5.5E-01
ENSMUST00000168783	inositol polyphosphate-5-phosphatase D [Source:MGI Symbol;Acc:MGI:107357]		Q9ES52	2.3	4.1E-01	0.5	9.3E-01	2.1	4.9E-01	4.0	4.0E-01
ENSMUST00000168785				3.2	1.0E-01	2.6	1.7E-01	-2.0	2.5E-01	-1.4	4.2E-01
ENSMUST00000168786	IQ motif and Sec7 domain 2 [Source:MGI Symbol;Acc:MGI:3528396]	A4GZ26		4.0	6.3E-02	1.7	4.9E-01	-0.5	8.2E-01	1.8	3.7E-01
ENSMUST00000168787	BTB (POZ) domain containing 9 [Source:MGI Symbol;Acc:MGI:1916625]		Q8C726	0.3	5.7E-01	2.0	7.9E-03	1.0	6.3E-02	-0.7	1.8E-01
ENSMUST00000137483				5.6	7.3E-05	0.5	7.2E-01	-3.4	1.4E-02	4.1	3.7E-03
ENSMUST00000165643				5.6	9.1E-03	-2.2	3.5E-02	1.6	9.0E-03	1.5	1.0E-01
ENSMUST00000124925				5.6	1.8E-06	-2.6	5.5E-02	-0.5	4.5E-01	-0.3	7.9E-01
ENSMUST00000176758				5.6	5.3E-03	4.4	5.3E-04	-1.3	1.4E-01	0.4	4.8E-01
ENSMUST00000140162				5.6	2.7E-06	8.0	6.7E-05	-0.7	6.1E-01	0.2	7.1E-01
ENSMUST00000168817				-2.5	9.0E-02	-3.9	7.1E-02	0.6	5.8E-01	2.0	3.2E-01
ENSMUST00000141374				5.6	2.3E-05	-0.9	4.8E-01	-0.3	7.3E-01	-2.9	5.9E-02
ENSMUST00000159507				5.6	3.7E-04	7.0	1.9E-04	-0.7	6.1E-01	-0.4	5.9E-01
ENSMUST00000136631				5.6	1.9E-05	-0.6	5.3E-01	1.4	5.3E-02	0.0	9.8E-01
ENSMUST00000168833	F-box protein 34 [Source:MGI Symbol;Acc:MGI:1926188]		Q80XI1	-2.2	1.4E-01	-0.1	9.4E-01	0.1	9.2E-01	-2.0	2.5E-01
ENSMUST00000155268				5.6	7.6E-04	5.1	7.0E-04	-0.2	8.6E-01	-0.4	5.4E-01
ENSMUST00000143384				5.6	1.3E-03	5.9	4.3E-03	-0.5	7.6E-01	-1.2	2.2E-01
ENSMUST00000168839	myosin IXb [Source:MGI Symbol;Acc:MGI:106624]	E9PWZ6		-2.2	4.7E-01	-0.8	8.5E-01	1.1	6.8E-01	-0.3	9.4E-01
ENSMUST00000168841	chemokine (C-C motif) receptor 2 [Source:MGI Symbol;Acc:MGI:106185]	Q543S8	P51683	-0.1	8.5E-01	0.6	2.9E-01	0.0	9.4E-01	-0.7	1.8E-01
ENSMUST00000159181				5.6	1.2E-03	5.8	4.1E-04	-0.1	9.5E-01	0.2	7.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000168844	DIS3 mitotic control homolog (S. cerevisiae)-like [Source:MGI Symbol;Acc:MGI:2143272]		Q8C0S1	0.8	4.6E-01	-1.2	4.5E-01	-0.1	9.5E-01	1.9	1.9E-01
ENSMUST00000182295				5.6	3.8E-04	-3.5	9.4E-04	1.0	2.7E-02	-0.9	2.7E-01
ENSMUST00000168852				0.4	5.7E-01	-0.2	8.5E-01	0.6	4.4E-01	1.3	2.7E-01
ENSMUST00000168855	3-hydroxy-3-methylglutaryl-Coenzyme A reductase [Source:MGI Symbol;Acc:MGI:96159]	E9Q149		2.2	1.5E-01	-3.8	7.7E-02	-4.0	9.7E-03	2.0	3.1E-01
ENSMUST00000168863	TraB domain containing [Source:MGI Symbol;Acc:MGI:1915226]	E9Q7A5		-2.9	8.6E-02	-2.8	1.9E-01	0.1	9.4E-01	0.0	9.9E-01
ENSMUST00000086502				5.6	8.2E-04	6.5	8.1E-03	0.0	9.9E-01	-1.4	2.8E-01
ENSMUST00000118248				5.6	1.3E-02	4.7	3.7E-02	-0.7	7.2E-01	-0.5	7.4E-01
ENSMUST00000138038				5.6	3.0E-04	7.4	1.0E-04	0.5	6.8E-01	-0.5	4.2E-01
ENSMUST00000168872	MAP/microtubule affinity regulating kinase 2 [Source:MGI Symbol;Acc:MGI:99638]	E9Q9N6		-0.6	8.4E-01	1.2	7.6E-01	1.5	5.6E-01	-0.3	9.4E-01
ENSMUST00000152216				5.6	7.6E-06	6.6	2.1E-03	-0.4	8.0E-01	-1.1	2.3E-01
ENSMUST00000050132				5.6	2.4E-04	4.6	6.6E-02	-1.5	5.5E-01	-0.1	9.7E-01
ENSMUST00000168887	protein kinase D3 [Source:MGI Symbol;Acc:MGI:1922542]		Q8K1Y2	1.9	4.4E-01	0.7	7.7E-01	-1.5	5.3E-01	-0.4	8.7E-01
ENSMUST00000159912				5.6	4.4E-04	6.4	1.7E-02	-0.7	7.7E-01	-1.2	3.9E-01
ENSMUST00000170401				5.6	3.8E-03	-4.0	4.9E-03	-0.3	6.0E-01	0.0	1.0E+00
ENSMUST00000142179				5.6	2.6E-03	-5.5	4.4E-04	0.3	4.5E-01	-0.9	4.5E-01
ENSMUST00000175964				5.6	5.1E-04	6.4	3.3E-04	-0.4	7.4E-01	0.3	6.2E-01
ENSMUST00000168918	SMAD family member 7 [Source:MGI Symbol;Acc:MGI:1100518]	B2RPW6	O35253	0.2	9.4E-01	1.7	5.3E-01	-0.6	8.1E-01	-2.1	3.5E-01
ENSMUST00000189582				5.6	7.2E-04	-3.9	6.5E-03	-0.1	9.2E-01	-0.5	6.8E-01
ENSMUST00000168922	valyl-tRNA synthetase 2, mitochondrial (putative) [Source:MGI Symbol;Acc:MGI:1916165]	F6YJY2		4.7	4.1E-02	3.5	1.3E-01	-2.1	3.3E-01	-1.0	5.8E-01
ENSMUST00000135503				5.6	1.1E-02	2.2	3.9E-02	-1.3	1.6E-01	0.6	4.6E-01
ENSMUST00000142891				5.6	1.7E-02	3.1	1.5E-01	-0.4	8.0E-01	2.3	1.7E-01
ENSMUST00000168933				-4.0	1.3E-01	1.3	6.1E-01	2.1	3.6E-01	-3.2	2.2E-01
ENSMUST00000168937	mitogen-activated protein kinase 6 [Source:MGI Symbol;Acc:MGI:1354946]		Q61532	-2.5	2.2E-01	1.3	6.1E-01	1.7	4.3E-01	-2.1	3.4E-01
ENSMUST00000168938	PHD finger protein 10 [Source:MGI Symbol;Acc:MGI:1919307]	E9Q5L7		-0.2	7.4E-01	0.6	4.3E-01	0.2	7.5E-01	-0.6	3.9E-01
ENSMUST00000145624				5.6	4.2E-03	6.5	3.5E-05	-1.0	2.9E-01	-0.2	6.5E-01
ENSMUST00000168953				5.0	1.1E-01	7.2	4.3E-02	-0.1	9.7E-01	-2.4	1.8E-01
ENSMUST00000161655				5.6	9.9E-04	4.4	8.6E-03	0.0	9.7E-01	-1.3	1.5E-01
ENSMUST00000168956				0.7	5.2E-01	1.4	4.0E-01	0.9	5.4E-01	0.2	8.8E-01
ENSMUST00000121511				5.6	9.0E-04	5.0	2.3E-02	-1.1	5.8E-01	-0.8	5.4E-01
ENSMUST00000125755				5.6	1.5E-03	6.0	9.9E-04	0.0	9.7E-01	0.6	4.2E-01
ENSMUST00000168967	PDZ and LIM domain 5 [Source:MGI Symbol;Acc:MGI:1927489]	D9J303		3.3	1.5E-01	1.8	5.0E-01	-1.1	6.0E-01	0.4	8.6E-01
ENSMUST00000137368				5.6	1.3E-03	-3.4	2.2E-02	1.7	2.9E-02	-2.4	1.2E-01
ENSMUST00000168977	YLP motif containing 1 [Source:MGI Symbol;Acc:MGI:1926195]	E9Q803		-2.3	2.8E-01	0.3	8.8E-01	0.6	7.3E-01	-2.0	3.7E-01
ENSMUST00000118646				5.6	1.9E-03	4.8	4.9E-05	0.9	1.5E-01	-0.1	8.0E-01
ENSMUST00000168991	metadherin [Source:MGI Symbol;Acc:MGI:1914404]	E9PUX0		0.9	6.3E-01	-3.2	1.6E-01	-3.8	2.5E-02	0.3	9.0E-01
ENSMUST00000164325				5.6	1.2E-05	7.8	6.6E-05	-0.6	6.3E-01	-0.5	4.3E-01
ENSMUST00000169003	RNA binding protein with multiple splicing 2 [Source:MGI Symbol;Acc:MGI:1919223]	Q9CWY6		1.1	4.4E-01	2.9	8.9E-02	0.0	9.7E-01	-1.9	1.9E-01
ENSMUST00000169009	transforming growth factor, beta 1 [Source:MGI Symbol;Acc:MGI:98725]	E9Q6I6		1.0	6.7E-01	2.3	3.1E-01	-1.0	5.9E-01	-2.3	3.2E-01
ENSMUST00000125120				5.6	1.4E-03	6.5	5.8E-03	-0.5	7.9E-01	-2.4	5.9E-02
ENSMUST00000124295				5.6	9.5E-06	2.4	1.9E-01	-5.5	1.9E-02	-0.5	7.0E-01
ENSMUST00000125344				5.6	6.5E-05	-8.2	2.5E-04	-0.3	6.3E-01	-1.9	2.8E-01
ENSMUST00000131732				5.6	7.0E-05	-1.0	1.1E-01	0.9	4.1E-02	0.0	9.7E-01
ENSMUST00000190383				5.6	7.5E-05	6.4	3.5E-04	-0.5	7.2E-01	-1.1	1.4E-01
ENSMUST00000110797				5.6	1.1E-03	-7.0	1.5E-02	-1.2	1.8E-01	-0.8	7.6E-01
ENSMUST00000169035	cytoplasmic polyadenylation element binding protein 2 [Source:MGI Symbol;Acc:MGI:2442640]	E9Q5X2		1.4	6.5E-02	0.9	3.3E-01	-0.2	7.5E-01	0.3	6.8E-01
ENSMUST00000169037	adenylate cyclase 7 [Source:MGI Symbol;Acc:MGI:102891]		P51829	4.0	8.4E-02	7.4	7.2E-03	-0.5	8.5E-01	-3.9	1.6E-02
ENSMUST00000169040	peroxisome proliferator activator receptor delta [Source:MGI Symbol;Acc:MGI:101884]	E9PV57		2.9	1.7E-01	-0.4	8.6E-01	-3.1	1.6E-01	0.2	9.4E-01
ENSMUST00000169051				-2.1	1.1E-01	-3.9	3.3E-02	-0.6	4.4E-01	1.1	5.0E-01
ENSMUST00000141396				5.6	4.6E-03	7.6	7.5E-04	-0.7	6.8E-01	-4.0	3.9E-03
ENSMUST00000191381				5.6	1.1E-04	6.3	7.4E-04	-0.5	7.2E-01	-0.7	3.5E-01
ENSMUST00000118450				5.6	1.9E-03	-5.8	2.2E-03	1.7	7.5E-03	-0.9	5.7E-01
ENSMUST00000119716				5.6	2.9E-02	4.0	1.3E-01	-0.4	8.7E-01	2.7	9.8E-02
ENSMUST00000169062	predicted gene 8267 [Source:MGI Symbol;Acc:MGI:3648993]	E9PW76		3.7	9.4E-02	3.1	2.1E-01	-0.4	8.7E-01	0.2	8.9E-01
ENSMUST00000162230				5.6	7.6E-05	7.0	3.0E-05	-1.7	1.1E-01	0.3	5.6E-01
ENSMUST00000174273				5.6	1.6E-04	3.0	8.7E-02	-2.0	2.6E-01	0.2	8.5E-01
ENSMUST00000169068	testis expressed gene 264 [Source:MGI Symbol;Acc:MGI:1096570]	E9Q137		-3.4	1.5E-01	-3.5	3.5E-01	1.0	5.6E-01	1.1	7.7E-01
ENSMUST00000174523				5.6	5.3E-05	6.7	2.9E-04	0.7	5.4E-01	-0.9	2.1E-01
ENSMUST00000169074	ninein [Source:MGI Symbol;Acc:MGI:105108]		Q61043	-3.4	3.4E-01	2.5	6.7E-01	5.7	2.0E-01	-0.2	9.7E-01
ENSMUST00000179820				5.6	3.5E-04	4.2	4.1E-04	-0.4	5.8E-01	-0.2	7.1E-01
ENSMUST00000126566				5.6	3.2E-03	2.1	2.1E-02	-1.0	1.7E-01	-0.8	2.4E-01
ENSMUST00000169083	Erbb2 interacting protein [Source:MGI Symbol;Acc:MGI:1890169]	B7ZNX6		-1.5	3.6E-01	6.3	7.7E-03	3.8	6.0E-02	-4.1	2.0E-02
ENSMUST00000136011				5.6	4.3E-05	3.1	1.3E-01	-5.7	2.7E-02	-0.3	8.0E-01
ENSMUST00000169089	pumilio RNA-binding family member 2 [Source:MGI Symbol;Acc:MGI:1931751]		Q80U58	0.0	9.9E-01	-2.9	5.6E-01	-3.0	3.0E-01	-0.1	9.8E-01
ENSMUST00000176431				5.6	2.2E-04	5.6	9.7E-04	-0.5	7.1E-01	0.6	4.0E-01
ENSMUST00000169094	GTPase activating protein (SH3 domain) binding protein 2 [Source:MGI Symbol;Acc:MGI:2442040]	Q3U541	P97379	-2.6	3.8E-01	-3.3	2.3E-01	-3.1	1.3E-01	-2.4	4.6E-01
ENSMUST00000169104	lipid droplet associated hydrolase [Source:MGI Symbol;Acc:MGI:1916082]	A0A0F6AIX6		-0.1	8.8E-01	-0.1	8.9E-01	-1.0	3.8E-02	-1.0	9.5E-02
ENSMUST00000119367				5.5	1.3E-04	9.0	6.5E-04	0.1	9.7E-01	0.8	3.6E-01
ENSMUST00000134113				5.5	2.2E-05	-2.5	6.2E-03	-0.9	5.3E-02	-1.0	2.3E-01
ENSMUST00000169116	inositol polyphosphate-4-phosphatase, type II [Source:MGI Symbol;Acc:MGI:2158925]	Q3URI3		3.5	9.2E-02	4.5	5.4E-02	-0.5	8.1E-01	-1.4	3.4E-01
ENSMUST00000148133				5.5	9.0E-04	6.6	5.8E-04	-0.5	7.0E-01	-0.5	5.4E-01
ENSMUST00000149288				5.5	6.8E-04	9.4	1.5E-05	-0.6	6.5E-01	-2.0	3.9E-03
ENSMUST00000122447				5.5	3.4E-03	6.4	1.4E-03	-0.1	9.4E-01	0.0	9.7E-01
ENSMUST00000127051				5.5	2.4E-04	5.0	1.3E-04	-0.9	2.4E-01	0.0	9.5E-01
ENSMUST00000188831				5.5	8.9E-05	6.8	2.5E-04	-0.5	6.8E-01	-1.3	8.9E-02
ENSMUST00000131729				5.5	2.0E-05	6.1	5.9E-04	-0.5	7.0E-01	-0.8	2.7E-01
ENSMUST00000169133	mercaptopyruvate sulfurtransferase [Source:MGI Symbol;Acc:MGI:2179733]	Q3UW66		1.2	6.0E-01	1.1	7.3E-01	0.9	7.3E-01	0.9	7.2E-01
ENSMUST00000173427				5.5	1.4E-02	-2.8	1.4E-01	0.9	3.4E-01	-0.1	9.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000169139				-0.6	8.1E-01	-3.6	3.7E-01	-0.3	8.6E-01	2.7	4.9E-01
ENSMUST00000192179				5.5	8.5E-05	7.4	6.8E-05	-0.5	6.9E-01	0.0	9.3E-01
ENSMUST00000169142	zinc finger protein 595 [Source:MGI Symbol;Acc:MGI:3040707]	Q8BIN6		-2.5	3.4E-01	2.1	5.9E-01	4.2	1.7E-01	-0.3	9.2E-01
ENSMUST00000169159	membrane-spanning 4-domains, subfamily A, member 1 [Source:MGI Symbol;Acc:MGI:88321]	Q542S5	P19437	-1.0	3.2E-01	-3.0	2.0E-02	-2.7	5.5E-03	-0.7	5.5E-01
ENSMUST00000155820				5.5	4.3E-04	5.0	4.5E-04	1.0	2.6E-01	-0.9	2.2E-01
ENSMUST00000169172	TBC1 domain containing kinase [Source:MGI Symbol;Acc:MGI:2445052]	E9Q1W7		-0.4	5.3E-01	-0.8	4.3E-01	1.1	1.1E-01	1.5	1.3E-01
ENSMUST00000179703				5.5	5.6E-03	7.3	3.1E-04	-0.7	6.3E-01	-0.8	3.1E-01
ENSMUST00000169179	naked cuticle 1 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:2135954]	E9Q5K6		4.6	4.1E-02	6.0	2.7E-02	-0.6	8.0E-01	-1.9	2.4E-01
ENSMUST00000156157				5.5	7.4E-04	-9.2	7.1E-05	0.0	9.6E-01	-0.5	7.2E-01
ENSMUST00000169190	BEN domain containing 4 [Source:MGI Symbol;Acc:MGI:3648414]		P86174	-0.7	2.0E-01	-0.5	5.1E-01	1.0	8.1E-02	0.7	2.7E-01
ENSMUST00000143691				5.5	1.3E-03	-1.8	8.0E-02	0.8	1.8E-01	0.5	5.9E-01
ENSMUST00000169198	G protein-coupled receptor 35 [Source:MGI Symbol;Acc:MGI:1929509]	Q3TBY9	Q9ES90	1.8	1.2E-01	2.0	1.8E-01	-0.1	9.5E-01	-0.2	8.7E-01
ENSMUST00000169200	hydroxyacyl glutathione hydrolase [Source:MGI Symbol;Acc:MGI:95745]	E9PYA3		-2.2	8.4E-02	-2.2	2.0E-01	0.0	9.6E-01	-0.1	9.7E-01
ENSMUST00000169212	fibroblast growth factor receptor 3 [Source:MGI Symbol;Acc:MGI:95524]	Q7TSI8		4.4	5.7E-02	7.0	1.1E-02	-0.3	8.9E-01	-3.0	3.7E-02
ENSMUST00000169214				1.3	4.2E-01	-3.1	1.5E-01	-4.6	5.1E-03	-0.1	9.5E-01
ENSMUST00000154333				5.5	3.7E-04	-8.3	7.7E-04	1.0	6.9E-02	-0.9	6.4E-01
ENSMUST00000169222	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI		Q62178	1.6	6.5E-01	-3.3	5.1E-01	-3.8	2.2E-01	1.1	8.2E-01
ENSMUST00000191505				5.5	1.3E-03	6.3	4.6E-03	0.1	9.6E-01	-0.5	5.9E-01
ENSMUST00000191883				5.5	2.1E-02	6.4	6.9E-04	-0.6	6.9E-01	-1.2	1.3E-01
ENSMUST00000169232	LY6/PLAUR domain containing 6 [Source:MGI Symbol;Acc:MGI:2443848]		Q8BPP5	4.1	1.4E-01	5.2	8.9E-02	-0.2	9.4E-01	-1.4	4.4E-01
ENSMUST00000129911				5.5	2.9E-05	3.4	2.6E-03	-0.3	6.7E-01	-0.7	3.3E-01
ENSMUST00000155870				5.5	8.9E-04	5.3	4.1E-03	1.0	4.8E-01	-0.3	6.8E-01
ENSMUST00000169237	Rab geranylgeranyl transferase, a subunit [Source:MGI Symbol;Acc:MGI:1860443]		Q9JHK4	1.1	5.6E-01	1.7	5.2E-01	0.5	8.2E-01	-0.1	9.6E-01
ENSMUST00000134900				5.5	8.3E-04	-6.4	2.3E-02	1.5	8.5E-02	0.0	1.0E+00
ENSMUST00000169255				-1.4	5.9E-01	-2.5	4.5E-01	-0.7	7.1E-01	0.4	9.0E-01
ENSMUST00000121771				5.5	2.7E-02	7.3	3.7E-05	-2.7	3.9E-02	-0.9	8.4E-02
ENSMUST00000169266	capicua homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1918972]		Q924A2	-0.6	4.3E-01	0.2	8.4E-01	1.2	1.5E-01	0.3	7.1E-01
ENSMUST00000140457				5.5	1.3E-05	-2.3	5.4E-03	1.0	2.9E-02	-0.2	8.1E-01
ENSMUST00000169282	anterior pharynx defective 1c homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1915568]		Q9DCZ9	-0.5	3.1E-01	0.0	1.0E+00	0.6	2.4E-01	0.1	9.2E-01
ENSMUST00000128761				5.5	1.1E-06	6.0	4.2E-03	-0.7	6.8E-01	-0.3	7.3E-01
ENSMUST00000129085				5.5	6.0E-06	-0.8	4.4E-01	-0.6	4.5E-01	-3.9	1.3E-02
ENSMUST00000129836				5.5	9.7E-05	1.6	6.1E-02	-1.5	5.7E-02	-0.4	5.1E-01
ENSMUST00000141031				5.5	4.0E-06	6.7	1.1E-04	-1.5	2.1E-01	0.3	5.8E-01
ENSMUST00000192420				5.5	2.2E-06	6.3	1.4E-04	-1.5	2.0E-01	-0.4	4.7E-01
ENSMUST00000169308	RIKEN cDNA 0610011F06 gene [Source:MGI Symbol;Acc:MGI:1915597]	G5E8X1		2.2	2.8E-01	-2.9	3.9E-01	-1.3	4.8E-01	3.8	2.5E-01
ENSMUST00000169309	nucleoporin 37 [Source:MGI Symbol;Acc:MGI:1919964]		Q9CWU9	4.5	8.6E-02	-0.2	9.2E-01	-3.6	1.7E-01	1.1	5.8E-01
ENSMUST00000169310	autophagy related 7 [Source:MGI Symbol;Acc:MGI:1921494]	A0A0A0MQN4		4.3	1.7E-01	4.2	2.4E-01	-0.2	9.6E-01	0.0	9.9E-01
ENSMUST00000105697				5.5	1.3E-03	-5.7	3.6E-03	1.8	7.1E-03	4.3	1.6E-02
ENSMUST00000169314	isopentenyl-diphosphate delta isomerase [Source:MGI Symbol;Acc:MGI:2442264]	G3XA48		-0.1	8.6E-01	-0.5	3.7E-01	-0.7	1.3E-01	-0.3	6.3E-01
ENSMUST00000151002				5.5	4.7E-04	4.4	7.7E-03	-0.5	7.0E-01	-1.9	6.5E-02
ENSMUST00000169343	lymphocyte antigen 6 complex, locus E [Source:MGI Symbol;Acc:MGI:106651]	Q99JA5		1.6	4.3E-01	1.8	5.3E-01	0.3	9.1E-01	0.1	9.7E-01
ENSMUST00000159757				5.5	1.5E-03	7.9	9.2E-05	-0.7	6.0E-01	-0.1	8.1E-01
ENSMUST00000169347	myosin 1H [Source:MGI Symbol;Acc:MGI:1914674]	E9PWM9		2.0	3.4E-01	2.9	2.5E-01	0.6	8.0E-01	-0.3	8.8E-01
ENSMUST00000173081				5.5	8.2E-04	9.7	6.3E-05	-0.7	6.6E-01	-0.4	5.3E-01
ENSMUST00000169353	kinesin family member C3 [Source:MGI Symbol;Acc:MGI:109202]			-1.6	3.3E-01	-1.1	5.7E-01	-0.2	8.8E-01	-0.7	7.1E-01
ENSMUST00000105820				5.5	2.3E-04	1.9	5.9E-02	0.1	9.5E-01	0.3	7.2E-01
ENSMUST00000138733				5.5	1.3E-05	5.7	5.5E-03	-0.6	7.2E-01	-1.1	2.7E-01
ENSMUST00000169371	centlein, centrosomal protein [Source:MGI Symbol;Acc:MGI:2443104]		A2AM05	-0.7	7.1E-01	-0.6	8.2E-01	0.7	7.0E-01	0.6	8.1E-01
ENSMUST00000169377	mitogen-activated protein kinase kinase kinase 12 [Source:MGI Symbol;Acc:MGI:1346881]		Q60700	4.0	6.0E-02	1.4	5.2E-01	-1.9	3.3E-01	0.7	7.3E-01
ENSMUST00000139789				5.5	2.0E-03	4.1	5.7E-03	0.6	5.9E-01	-0.9	2.8E-01
ENSMUST00000100731				5.5	1.9E-04	5.2	5.0E-03	-0.8	6.1E-01	1.6	1.0E-01
ENSMUST00000169382	predicted gene, 21704 [Source:MGI Symbol;Acc:MGI:5435059]		O35698	3.0	2.1E-01	5.5	4.3E-02	-0.3	9.0E-01	-2.8	1.0E-01
ENSMUST00000169383	GTP binding protein 2 [Source:MGI Symbol;Acc:MGI:1860138]	E9PVQ4		-0.8	7.2E-01	7.2	3.8E-02	3.5	2.5E-01	-4.5	5.6E-02
ENSMUST00000169385	retinoic acid induced 14 [Source:MGI Symbol;Acc:MGI:1922896]		Q9EP71	-2.1	4.0E-02	-1.4	2.9E-02	-3.9	3.7E-05	-4.5	4.7E-04
ENSMUST00000124085				5.5	9.1E-03	6.1	6.8E-04	-0.7	6.1E-01	0.6	3.6E-01
ENSMUST00000169390	enolase-phosphatase 1 [Source:MGI Symbol;Acc:MGI:1915120]		Q8BGB7	-0.8	6.8E-01	2.3	3.5E-01	1.2	5.9E-01	-2.0	3.3E-01
ENSMUST00000169392	capicua homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1918972]	E9PWB7		1.1	5.9E-01	2.2	2.9E-01	-0.5	7.7E-01	-1.7	4.2E-01
ENSMUST00000172945				5.5	2.2E-03	-4.0	3.5E-02	0.3	6.6E-01	-1.7	4.0E-01
ENSMUST00000137044				5.5	1.4E-02	6.8	6.4E-05	-0.9	4.1E-01	-0.3	5.9E-01
ENSMUST00000169399	ribosomal L24 domain containing 1 [Source:MGI Symbol;Acc:MGI:2681840]	G3UW80		-2.7	6.4E-02	-0.1	9.8E-01	3.3	3.0E-02	0.6	7.4E-01
ENSMUST00000169401	tetratricopeptide repeat domain 39C [Source:MGI Symbol;Acc:MGI:1919997]	E9PV21		-0.4	4.5E-01	-0.4	5.4E-01	-0.6	2.9E-01	-0.6	4.0E-01
ENSMUST00000131521				5.5	2.0E-03	7.0	1.0E-03	-0.5	7.3E-01	-2.3	2.7E-02
ENSMUST00000135950				5.5	4.9E-04	4.9	2.2E-03	0.5	6.7E-01	0.2	8.5E-01
ENSMUST00000169407	ring finger protein (C3H2C3 type) 6 [Source:MGI Symbol;Acc:MGI:1921382]		Q9DBU5	-3.2	1.3E-01	-2.4	5.4E-01	3.1	2.1E-01	2.4	5.0E-01
ENSMUST00000169408	activating transcription factor 1 [Source:MGI Symbol;Acc:MGI:1298366]	E9Q356		1.2	4.9E-01	1.7	4.7E-01	0.2	9.2E-01	-0.3	8.9E-01
ENSMUST00000143919				5.5	7.1E-03	5.1	1.1E-02	-0.6	7.5E-01	-1.5	2.3E-01
ENSMUST00000152503				5.5	6.5E-06	-7.1	1.3E-02	-0.3	7.1E-01	2.0	4.0E-01
ENSMUST00000120824				5.5	6.5E-04	9.2	9.9E-05	-0.8	6.1E-01	0.4	5.5E-01
ENSMUST00000173375				5.5	1.8E-04	5.6	7.8E-04	-0.5	6.6E-01	-0.8	2.4E-01
ENSMUST00000133330				5.5	9.0E-04	4.6	3.7E-03	-3.4	3.2E-02	0.6	4.4E-01
ENSMUST00000169438	plectin [Source:MGI Symbol;Acc:MGI:1277961]	E9Q3W4		-1.2	6.5E-01	-1.1	7.6E-01	-0.5	8.6E-01	-0.5	8.6E-01
ENSMUST00000169447				3.0	1.3E-01	5.9	1.1E-02	-0.5	8.0E-01	-3.4	2.8E-02
ENSMUST00000154927				5.5	1.0E-03	3.9	5.1E-02	-0.2	9.1E-01	0.7	5.7E-01
ENSMUST00000124311				5.5	6.7E-06	9.6	9.5E-04	0.0	1.0E+00	-1.3	1.7E-01
ENSMUST00000169453	nuclear factor of activated T cells 5 [Source:MGI Symbol;Acc:MGI:1859333]		Q9WV30	1.8	5.3E-01	1.8	6.7E-01	1.1	7.5E-01	1.1	7.5E-01
ENSMUST00000169454				-0.3	8.0E-01	0.8	6.0E-01	-0.1	9.3E-01	-1.2	3.9E-01
ENSMUST00000176133				5.5	4.1E-04	3.4	8.9E-04	0.2	7.2E-01	0.6	2.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000119806				5.5	1.1E-03	7.1	6.6E-03	-0.7	7.5E-01	-2.5	7.4E-02
ENSMUST00000169461				-2.0	1.3E-01	1.0	5.3E-01	1.7	2.1E-01	-1.3	3.6E-01
ENSMUST00000150722				5.5	1.4E-05	5.2	6.3E-02	-0.4	8.8E-01	0.8	5.8E-01
ENSMUST00000127581				5.5	3.1E-04	5.6	1.2E-04	-0.2	8.0E-01	0.0	9.5E-01
ENSMUST00000169480	special AT-rich sequence binding protein 1 [Source:MGI Symbol;Acc:MGI:105084]		Q60611	2.5	3.4E-01	0.0	9.9E-01	-2.1	3.6E-01	0.3	9.0E-01
ENSMUST00000146564				5.5	3.8E-05	3.2	1.6E-03	0.8	2.2E-01	-0.3	5.3E-01
ENSMUST00000169486	early B cell factor 3 [Source:MGI Symbol;Acc:MGI:894289]	Q6NXL3		7.1	6.3E-02	5.8	1.5E-01	-0.6	8.8E-01	0.7	7.6E-01
ENSMUST00000169488	widely-interspaced zinc finger motifs [Source:MGI Symbol;Acc:MGI:1332638]	F6ZBR8		0.1	9.3E-01	2.3	1.1E-01	1.0	3.5E-01	-1.2	3.4E-01
ENSMUST00000182668				5.5	2.5E-04	-4.2	2.0E-02	1.4	6.3E-02	-1.9	3.0E-01
ENSMUST00000136477				5.5	9.3E-04	6.1	1.8E-04	-0.6	6.0E-01	0.3	6.2E-01
ENSMUST00000118999				5.5	8.5E-04	-1.0	4.4E-01	1.4	1.2E-01	-1.3	3.4E-01
ENSMUST00000152560				5.5	1.0E-05	4.2	1.2E-02	1.8	1.7E-01	0.5	5.5E-01
ENSMUST00000169507	CCR4-NOT transcription complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1919318]	E9Q8R6		-2.4	6.1E-02	-3.5	2.7E-02	-1.7	4.2E-02	-0.6	6.9E-01
ENSMUST00000169529				1.2	2.6E-01	2.4	7.2E-02	0.4	7.0E-01	-0.7	4.9E-01
ENSMUST00000135271				5.5	5.4E-04	7.3	1.2E-03	-0.9	5.9E-01	1.0	2.6E-01
ENSMUST00000159730				5.5	2.8E-03	7.0	7.0E-05	-0.5	6.4E-01	-0.9	1.5E-01
ENSMUST00000169536	zinc finger, FYVE domain containing 27 [Source:MGI Symbol;Acc:MGI:1919602]		Q3TXX3	-1.1	1.5E-01	-0.3	7.1E-01	0.8	2.6E-01	0.0	9.8E-01
ENSMUST00000169541	MAP/microtubule affinity regulating kinase 2 [Source:MGI Symbol;Acc:MGI:99638]	E9Q8H5		3.0	1.5E-01	2.6	2.3E-01	-0.5	8.2E-01	0.0	1.0E+00
ENSMUST00000151532				5.5	6.4E-04	2.3	2.7E-01	-1.8	4.1E-01	2.1	1.7E-01
ENSMUST00000169547	solute carrier family 43, member 2 [Source:MGI Symbol;Acc:MGI:2442746]		Q8CGA3	-3.6	8.2E-02	0.9	6.4E-01	0.8	5.5E-01	-3.7	1.0E-01
ENSMUST00000169550	RIKEN cDNA 9430015G10 gene [Source:MGI Symbol;Acc:MGI:2444364]	A2ASP7		5.0	4.4E-02	-0.2	9.4E-01	-4.8	4.3E-02	0.3	8.7E-01
ENSMUST00000155827				5.5	4.1E-03	5.2	1.0E-03	-0.5	6.2E-01	0.3	5.8E-01
ENSMUST00000132605				5.5	1.9E-05	8.5	3.8E-04	0.9	5.9E-01	0.5	4.2E-01
ENSMUST00000133132				5.5	2.7E-04	6.2	1.9E-04	-0.6	6.0E-01	-0.1	8.9E-01
ENSMUST00000169557				1.6	5.0E-02	3.7	2.1E-03	0.9	2.5E-01	-1.2	1.3E-01
ENSMUST00000149314				5.5	1.7E-05	-5.4	1.8E-02	0.4	6.3E-01	-1.2	5.8E-01
ENSMUST00000124178				5.5	1.2E-05	7.5	1.5E-04	-0.7	6.1E-01	-0.1	9.4E-01
ENSMUST00000137679				5.5	1.5E-02	-1.2	1.3E-01	-0.2	6.8E-01	-3.2	8.3E-03
ENSMUST00000169572	guanylate binding protein 2 [Source:MGI Symbol;Acc:MGI:102772]	E9Q2N7		-1.2	6.7E-01	-3.3	1.8E-01	-4.5	2.5E-02	-2.4	4.3E-01
ENSMUST00000169576	CCR4-NOT transcription complex, subunit 2 [Source:MGI Symbol;Acc:MGI:1919318]	E9Q7M5		-2.5	9.8E-02	-1.8	3.0E-01	0.0	9.9E-01	-0.6	7.2E-01
ENSMUST00000169580				1.1	3.1E-01	-1.2	4.0E-01	-0.2	8.0E-01	2.1	1.5E-01
ENSMUST00000169582	predicted gene 608 [Source:MGI Symbol;Acc:MGI:2685454]	B2RUQ2		-0.3	7.6E-01	-1.5	3.6E-01	0.9	3.7E-01	2.1	2.0E-01
ENSMUST00000147397				5.5	4.0E-03	7.3	4.1E-05	-0.9	3.9E-01	0.7	2.1E-01
ENSMUST00000166322				5.5	2.1E-04	6.0	3.9E-03	-0.7	6.9E-01	0.9	3.4E-01
ENSMUST00000162848				5.5	5.1E-06	-4.5	3.8E-02	0.1	9.1E-01	0.3	8.7E-01
ENSMUST00000186661				5.5	2.0E-04	-3.2	1.4E-01	1.7	1.3E-01	0.7	7.2E-01
ENSMUST00000169594	ubiquitin specific peptidase 9, X chromosome [Source:MGI Symbol;Acc:MGI:894681]	E9PWA9		0.7	5.1E-01	1.7	2.5E-01	1.8	1.4E-01	0.8	5.3E-01
ENSMUST00000117195				5.5	1.6E-03	6.9	1.4E-04	0.0	9.9E-01	-0.8	2.2E-01
ENSMUST00000130831				5.5	1.8E-03	-4.6	9.7E-03	0.3	6.7E-01	-1.1	5.4E-01
ENSMUST00000118508				5.5	1.3E-02	-1.7	2.3E-02	-0.2	6.4E-01	-0.1	9.1E-01
ENSMUST00000169612	InaF motif containing 1 [Source:MGI Symbol;Acc:MGI:1913550]	E9PV59		-0.1	8.8E-01	1.0	2.2E-01	0.8	2.2E-01	-0.3	6.6E-01
ENSMUST00000173435				5.5	1.0E-02	-3.0	2.2E-02	-0.3	6.9E-01	0.4	7.0E-01
ENSMUST00000185677				5.5	2.3E-03	-2.9	9.4E-02	-1.0	3.1E-01	-1.7	3.5E-01
ENSMUST00000169627	tensin 2 [Source:MGI Symbol;Acc:MGI:2387586]		Q8CGB6	-1.6	3.2E-01	2.1	2.2E-01	0.6	6.6E-01	-3.1	8.0E-02
ENSMUST00000143257				5.5	1.4E-03	-1.9	3.4E-01	1.3	2.7E-01	-2.9	2.2E-01
ENSMUST00000144346				5.5	5.8E-05	-1.4	2.0E-01	0.8	2.4E-01	-2.9	5.3E-02
ENSMUST00000185267				5.5	1.7E-04	-1.3	2.1E-01	0.8	2.3E-01	0.3	7.3E-01
ENSMUST00000142208				5.5	5.2E-04	5.6	1.8E-04	-0.6	5.4E-01	-0.6	3.3E-01
ENSMUST00000185932				5.5	3.1E-02	8.1	5.6E-06	1.0	2.8E-01	-0.1	7.2E-01
ENSMUST00000095015				5.5	1.7E-02	4.6	4.2E-02	-0.5	8.0E-01	0.9	4.6E-01
ENSMUST00000188756				5.5	2.5E-04	2.3	6.1E-03	0.4	4.6E-01	1.1	5.0E-02
ENSMUST00000169665	patatin-like phospholipase domain containing 2 [Source:MGI Symbol;Acc:MGI:1914103]	E9PZA4		-3.3	1.6E-01	-1.3	5.2E-01	0.1	9.4E-01	-1.9	4.5E-01
ENSMUST00000121474				5.5	2.6E-03	3.1	1.2E-02	-3.2	1.6E-02	-1.2	1.3E-01
ENSMUST00000169668	mannosidase 2, alpha 1 [Source:MGI Symbol;Acc:MGI:104669]	F6QMB7		-0.9	7.1E-01	-3.0	3.9E-01	-2.1	3.0E-01	0.0	9.9E-01
ENSMUST00000152320				5.5	2.0E-02	8.4	2.3E-04	-0.8	6.4E-01	-0.1	8.4E-01
ENSMUST00000169673	centrosomal protein 55 [Source:MGI Symbol;Acc:MGI:1921357]		Q8BT07	0.2	7.5E-01	-0.3	6.9E-01	-0.2	7.8E-01	0.4	6.4E-01
ENSMUST00000159695				5.5	1.4E-02	4.5	1.3E-02	-1.2	4.4E-01	0.0	9.9E-01
ENSMUST00000038366				5.5	7.4E-04	-3.0	1.3E-04	0.6	3.7E-02	-0.5	3.1E-01
ENSMUST00000169684	protease, serine 57 [Source:MGI Symbol;Acc:MGI:1920356]		Q14B24	1.8	3.8E-01	-0.5	8.3E-01	-0.7	7.2E-01	1.6	4.8E-01
ENSMUST00000139674				5.5	4.7E-05	5.0	2.0E-02	-0.7	7.1E-01	0.8	5.3E-01
ENSMUST00000126935				5.5	1.6E-02	-5.1	2.1E-03	-0.5	3.3E-01	-0.2	8.5E-01
ENSMUST00000131618				5.5	6.7E-04	-1.5	2.1E-01	1.0	1.9E-01	-1.0	4.3E-01
ENSMUST00000169698	peptidoglycan recognition protein 4 [Source:MGI Symbol;Acc:MGI:2686324]	B7ZMZ4		-1.1	1.1E-01	1.2	1.6E-01	1.4	5.3E-02	-0.9	2.4E-01
ENSMUST00000117794				5.5	2.7E-04	5.2	1.6E-02	-0.6	7.7E-01	0.8	4.8E-01
ENSMUST00000134231				5.5	9.9E-03	-3.9	5.4E-03	-0.5	3.8E-01	-0.7	5.8E-01
ENSMUST00000176264				5.5	2.2E-02	-1.2	5.7E-02	0.8	4.9E-02	0.0	9.8E-01
ENSMUST00000169712	mitochondrial fission regulator 2 [Source:MGI Symbol;Acc:MGI:1919054]		Q8VED8	0.9	9.3E-02	1.6	3.2E-02	0.4	4.2E-01	-0.2	6.5E-01
ENSMUST00000134708				5.5	4.1E-05	4.8	2.8E-03	-3.3	3.5E-02	0.6	4.5E-01
ENSMUST00000169714	plectin [Source:MGI Symbol;Acc:MGI:1277961]		Q9QXS1	0.3	8.9E-01	0.1	9.8E-01	-0.6	8.0E-01	-0.3	9.3E-01
ENSMUST00000124820				5.5	7.4E-03	8.6	5.4E-04	0.2	8.9E-01	-0.4	6.6E-01
ENSMUST00000132842				5.5	6.7E-04	-7.1	1.6E-02	-2.4	2.3E-02	-0.2	9.4E-01
ENSMUST00000059190				5.5	1.9E-04	0.5	5.6E-01	1.1	1.2E-01	-1.2	1.7E-01
ENSMUST00000169728	ribonuclease H2, subunit B [Source:MGI Symbol;Acc:MGI:1914403]	F6WF94		-2.0	3.8E-02	-4.6	9.0E-03	-1.3	7.7E-02	1.3	3.6E-01
ENSMUST00000169734	vacuolar protein sorting 53 (yeast) [Source:MGI Symbol;Acc:MGI:1915549]	E9Q648		1.2	4.2E-01	1.6	4.2E-01	0.0	9.8E-01	-0.3	8.6E-01
ENSMUST00000169736				-0.4	7.9E-01	0.2	9.2E-01	0.0	9.9E-01	-0.6	7.3E-01
ENSMUST00000060997				5.5	4.1E-03	5.9	6.0E-04	-2.4	9.6E-02	-1.0	1.8E-01
ENSMUST00000159949				5.5	6.0E-04	-5.7	1.2E-02	1.2	8.2E-02	3.1	1.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000169748	kinesin family member C3 [Source:MGI Symbol;Acc:MGI:109202]	E9PWU7		0.5	5.8E-01	0.6	6.8E-01	1.8	9.7E-02	1.7	1.9E-01
ENSMUST00000192286				5.5	1.5E-05	-3.9	1.3E-02	0.6	3.8E-01	-2.0	2.2E-01
ENSMUST00000135974				5.5	2.4E-04	3.5	2.5E-03	-0.6	4.7E-01	0.8	2.4E-01
ENSMUST00000145218				5.5	2.9E-04	-4.1	1.3E-01	-7.4	6.2E-03	2.8	2.7E-01
ENSMUST00000169778				-1.4	1.6E-01	-1.7	2.3E-01	0.3	7.4E-01	0.5	7.0E-01
ENSMUST00000169779				-2.0	2.2E-01	-1.6	2.8E-01	-1.3	2.4E-01	-1.7	3.1E-01
ENSMUST00000127277				5.5	5.4E-04	1.8	3.2E-02	-0.2	8.0E-01	0.7	2.6E-01
ENSMUST00000169786	tensin 1 [Source:MGI Symbol;Acc:MGI:104552]	E9Q0S6		6.0	3.9E-02	2.6	4.4E-01	-0.6	8.4E-01	2.8	3.0E-01
ENSMUST00000130302				5.5	9.8E-04	9.4	1.8E-05	-0.7	5.7E-01	0.0	9.4E-01
ENSMUST00000169800	olfactory receptor 772 [Source:MGI Symbol;Acc:MGI:3030606]	Q8VGC5		3.6	1.7E-01	4.5	1.3E-01	-0.3	9.1E-01	-1.2	5.1E-01
ENSMUST00000147828				5.5	1.1E-05	9.0	3.4E-05	-0.7	6.1E-01	0.2	7.4E-01
ENSMUST00000169807	polycomb group ring finger 2 [Source:MGI Symbol;Acc:MGI:99161]		P23798	4.0	8.4E-02	2.7	2.3E-01	-1.7	4.2E-01	-0.5	8.0E-01
ENSMUST00000169817	transformed mouse 3T3 cell double minute 1 [Source:MGI Symbol;Acc:MGI:96951]	E9Q0B1		-3.0	3.8E-02	-3.8	6.7E-02	-0.4	6.5E-01	0.3	8.6E-01
ENSMUST00000148828				5.5	7.0E-04	-6.6	6.4E-06	-0.9	1.7E-02	-0.9	2.6E-01
ENSMUST00000169828	nuclear factor, erythroid derived 2,-like 1 [Source:MGI Symbol;Acc:MGI:99421]	Q3V3M1		0.3	9.1E-01	-4.0	4.3E-01	-0.7	7.9E-01	3.7	4.7E-01
ENSMUST00000169833	heat shock protein, alpha-crystallin-related, B9 [Source:MGI Symbol;Acc:MGI:1922732]	G3UWB9		2.8	5.7E-02	4.5	3.4E-02	1.6	3.6E-01	-0.1	9.5E-01
ENSMUST00000152202				5.5	2.7E-03	7.4	4.3E-05	-0.5	6.2E-01	-1.2	5.1E-02
ENSMUST00000169838	T cell lymphoma invasion and metastasis 2 [Source:MGI Symbol;Acc:MGI:1344338]		Q6ZPF3	0.7	5.3E-01	1.6	3.2E-01	1.0	4.4E-01	0.2	9.0E-01
ENSMUST00000169841	ADP-ribosylation factor 5 [Source:MGI Symbol;Acc:MGI:99434]		P84084	-2.6	5.1E-01	-4.9	3.7E-01	-2.3	3.7E-01	0.0	1.0E+00
ENSMUST00000123199				5.5	2.1E-03	4.8	1.3E-02	-0.5	7.5E-01	0.9	3.7E-01
ENSMUST00000169845				-2.5	6.2E-02	-2.2	1.2E-01	-1.4	1.5E-01	-1.6	2.7E-01
ENSMUST00000169850	glial cell line derived neurotrophic factor family receptor alpha 1 [Source:MGI Symbol;Acc:MGI:1100842]		P97785	2.6	1.6E-01	6.8	6.0E-03	0.2	9.2E-01	-4.0	9.5E-03
ENSMUST00000156320				5.5	3.4E-03	4.6	3.7E-04	-1.0	2.4E-01	-0.2	7.1E-01
ENSMUST00000115580				5.5	1.8E-05	-5.6	1.1E-03	1.1	7.0E-02	-0.5	6.8E-01
ENSMUST00000169854	signal-induced proliferation associated gene 1 [Source:MGI Symbol;Acc:MGI:107576]	E9Q0Y4		-2.1	7.0E-02	-0.5	7.4E-01	1.6	2.2E-01	0.0	9.9E-01
ENSMUST00000142840				5.5	1.5E-02	-8.9	1.8E-04	1.1	1.6E-02	-0.4	8.1E-01
ENSMUST00000123436				5.5	6.4E-03	-0.8	6.3E-01	4.3	4.4E-03	1.0	4.9E-01
ENSMUST00000126863				5.5	1.9E-02	2.5	3.9E-03	0.1	9.0E-01	-0.3	5.7E-01
ENSMUST00000169863	family with sequence similarity 169, member A [Source:MGI Symbol;Acc:MGI:2444268]		Q5XG69	0.1	9.3E-01	4.1	2.4E-02	0.7	6.3E-01	-3.3	3.1E-02
ENSMUST00000131393				5.5	4.0E-05	-3.2	2.3E-01	2.2	2.0E-01	0.5	8.3E-01
ENSMUST00000139026				5.5	1.7E-02	-9.2	1.5E-04	0.2	6.8E-01	-0.9	5.7E-01
ENSMUST00000147942				5.5	5.1E-03	4.7	3.4E-03	-2.0	1.6E-01	-0.2	8.3E-01
ENSMUST00000169888	R3H domain containing 2 [Source:MGI Symbol;Acc:MGI:1919000]	F6Z9T5		-3.2	8.7E-02	2.0	2.0E-01	0.5	7.4E-01	-4.7	1.3E-02
ENSMUST00000169891	TraB domain containing [Source:MGI Symbol;Acc:MGI:1915226]	E9Q8R5		-1.5	2.6E-01	-0.7	7.0E-01	0.4	7.4E-01	-0.5	7.7E-01
ENSMUST00000190401				5.5	1.2E-05	2.6	3.1E-01	-0.8	7.2E-01	2.7	1.7E-01
ENSMUST00000169895	ribonuclease, RNase A family 4 [Source:MGI Symbol;Acc:MGI:1926217]	Q8C7E4		1.0	5.4E-01	2.0	3.8E-01	0.6	7.7E-01	-0.4	8.2E-01
ENSMUST00000140358				5.5	3.3E-02	-3.1	5.2E-02	1.0	1.9E-01	0.1	9.5E-01
ENSMUST00000182787				5.5	1.6E-03	-1.8	7.4E-02	-0.6	3.9E-01	-2.3	6.2E-02
ENSMUST00000169906	nischarin [Source:MGI Symbol;Acc:MGI:1928323]	E9PZT1		-1.9	5.3E-02	0.1	9.1E-01	0.3	6.9E-01	-1.7	1.1E-01
ENSMUST00000136379				5.5	5.6E-06	-7.1	1.7E-03	-0.9	1.4E-01	-0.2	9.2E-01
ENSMUST00000169910	WAPL cohesin release factor [Source:MGI Symbol;Acc:MGI:2675859]		Q65Z40	1.7	5.5E-01	2.2	5.7E-01	0.2	9.4E-01	-0.2	9.4E-01
ENSMUST00000169918				-0.1	8.7E-01	1.1	2.9E-01	0.0	1.0E+00	-1.2	2.1E-01
ENSMUST00000188684				5.5	2.5E-05	-4.2	1.8E-03	-0.1	9.1E-01	-1.7	1.6E-01
ENSMUST00000119193				5.5	3.7E-04	-1.5	6.1E-02	0.2	7.3E-01	0.0	9.9E-01
ENSMUST00000126550				5.5	1.7E-03	-4.5	3.2E-03	0.1	7.9E-01	1.1	3.4E-01
ENSMUST00000169928	integrin beta 4 [Source:MGI Symbol;Acc:MGI:96613]	A2A864		3.3	2.8E-01	5.4	1.1E-01	-0.4	9.0E-01	-2.5	2.4E-01
ENSMUST00000169935	RIKEN cDNA A330050F15 gene [Source:MGI Symbol;Acc:MGI:2444600]		G3UWD5	1.4	1.4E-01	4.6	3.5E-03	2.6	3.8E-02	-0.7	4.3E-01
ENSMUST00000169938	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:1093301]	E9QAY4		-2.7	1.6E-01	-3.5	3.3E-01	1.5	4.5E-01	2.2	4.8E-01
ENSMUST00000169941	tolloid-like 2 [Source:MGI Symbol;Acc:MGI:1346044]	E9Q5B9		3.7	1.5E-01	5.4	5.6E-02	-0.5	8.4E-01	-2.2	2.2E-01
ENSMUST00000140740				5.5	6.4E-05	6.4	6.7E-04	-0.5	7.4E-01	-0.6	4.5E-01
ENSMUST00000188469				5.5	1.1E-03	0.5	4.3E-01	1.5	6.5E-03	-0.8	1.4E-01
ENSMUST00000169960	DIP2 disco-interacting protein 2 homolog C (Drosophila) [Source:MGI Symbol;Acc:MGI:1920179]	B7ZMZ7		3.5	3.6E-02	1.7	3.4E-01	-1.7	2.5E-01	0.1	9.5E-01
ENSMUST00000156843				5.5	2.8E-04	-2.4	1.0E-01	-1.2	1.6E-01	-2.7	1.1E-01
ENSMUST00000187379				5.5	5.7E-05	7.1	1.2E-04	-0.6	6.1E-01	-0.9	1.7E-01
ENSMUST00000187885				5.5	3.0E-05	6.3	4.6E-05	-0.9	3.1E-01	0.2	7.2E-01
ENSMUST00000169972	predicted gene 9611 [Source:MGI Symbol;Acc:MGI:3780019]	L7N476		2.5	7.4E-02	6.2	6.1E-04	-0.5	7.1E-01	-4.2	1.4E-03
ENSMUST00000169979				-2.5	4.2E-02	-0.5	6.6E-01	0.1	8.6E-01	-1.9	1.7E-01
ENSMUST00000169982	DnaJ (Hsp40) homolog, subfamily C, member 28 [Source:MGI Symbol;Acc:MGI:2181053]	E9Q1L7		0.0	9.5E-01	-0.3	6.9E-01	-0.5	2.6E-01	-0.2	7.0E-01
ENSMUST00000114403				5.5	6.7E-06	-5.0	3.2E-05	-0.9	1.9E-02	-0.3	6.5E-01
ENSMUST00000170002	poly (A) polymerase alpha [Source:MGI Symbol;Acc:MGI:109301]	E9PZR3		-1.9	1.6E-01	0.8	6.6E-01	2.6	6.1E-02	-0.1	9.7E-01
ENSMUST00000170007	transmembrane 9 superfamily member 2 [Source:MGI Symbol;Acc:MGI:1915309]	E9Q850		1.5	5.4E-01	1.6	4.5E-01	-2.0	3.3E-01	-2.1	3.7E-01
ENSMUST00000135967				5.5	2.2E-05	-1.0	6.9E-01	3.5	4.5E-02	-1.7	4.8E-01
ENSMUST00000170033	ligase IV, DNA, ATP-dependent [Source:MGI Symbol;Acc:MGI:1335098]		Q8BTF7	3.7	6.8E-02	2.6	1.5E-01	-2.8	1.3E-01	-1.7	2.8E-01
ENSMUST00000177506				5.5	1.5E-05	-4.6	2.2E-02	0.1	8.6E-01	-0.8	6.9E-01
ENSMUST00000166583				5.5	2.4E-03	-3.2	6.4E-02	0.6	4.9E-01	-0.5	7.4E-01
ENSMUST00000193838				5.4	5.9E-04	5.3	2.0E-03	-0.3	8.3E-01	0.5	5.4E-01
ENSMUST00000152312				5.4	1.6E-04	4.9	2.3E-04	-2.6	3.0E-02	0.4	4.8E-01
ENSMUST00000143986				5.4	6.2E-04	0.3	9.1E-01	4.4	2.9E-02	-0.7	7.9E-01
ENSMUST00000175971				5.4	3.2E-03	-1.0	1.4E-01	-5.4	7.6E-05	-0.8	2.6E-01
ENSMUST00000136435				5.4	2.8E-04	-1.4	4.4E-01	0.5	6.7E-01	-2.8	2.0E-01
ENSMUST00000170055	tubulin tyrosine ligase-like family, member 7 [Source:MGI Symbol;Acc:MGI:1918142]	E9PWB8		3.2	8.4E-02	4.4	2.2E-02	-1.7	3.1E-01	-2.9	5.5E-02
ENSMUST00000177327				5.4	1.8E-04	3.0	1.3E-03	0.6	3.3E-01	0.5	3.0E-01
ENSMUST00000170065	cilia and flagella associated protein 54 [Source:MGI Symbol;Acc:MGI:1922208]	F6V4L0		1.0	5.3E-01	2.6	2.2E-01	-0.2	9.2E-01	-1.8	2.5E-01
ENSMUST00000181009				5.4	2.6E-04	1.8	6.0E-01	8.2	1.0E-02	1.8	5.1E-01
ENSMUST00000170069	transmembrane protease, serine 4 [Source:MGI Symbol;Acc:MGI:2384877]	E9Q4A7		4.8	4.1E-02	2.4	4.0E-01	-0.1	9.6E-01	2.3	3.1E-01
ENSMUST00000170075	Fas death domain-associated protein [Source:MGI Symbol;Acc:MGI:1197015]	Q3UKR0		1.9	3.0E-01	0.7	7.0E-01	-1.8	3.1E-01	-0.6	7.4E-01
ENSMUST00000170083				5.5	1.0E-01	7.7	1.5E-01	2.1	6.6E-01	0.0	1.0E+00

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000182228				5.4	5.7E-03	-5.1	1.1E-02	0.4	5.6E-01	0.1	9.7E-01
ENSMUST00000170089	GATA binding protein 2 [Source:MGI Symbol;Acc:MGI:95662]	Q3U320	O09100	0.3	7.6E-01	-1.8	3.2E-01	1.4	2.6E-01	3.5	4.7E-02
ENSMUST00000136606				5.4	1.3E-03	-5.3	2.3E-04	-3.0	3.1E-04	0.4	6.8E-01
ENSMUST00000170092	family with sequence similarity 168, member B [Source:MGI Symbol;Acc:MGI:2448487]	E9Q917		-2.5	4.3E-02	-0.5	6.8E-01	1.1	1.7E-01	-0.8	5.6E-01
ENSMUST00000190553				5.4	3.7E-04	2.9	1.4E-02	0.7	4.3E-01	0.4	6.4E-01
ENSMUST00000170102	leucine zipper protein 1 [Source:MGI Symbol;Acc:MGI:107629]		Q8R4U7	2.1	3.9E-01	8.9	1.2E-02	1.2	6.9E-01	-5.6	1.0E-02
ENSMUST00000142438				5.4	4.3E-03	7.9	8.7E-05	-0.4	7.5E-01	-0.7	2.2E-01
ENSMUST00000125616				5.4	1.2E-02	-4.6	2.2E-02	0.1	8.9E-01	0.6	7.3E-01
ENSMUST00000143529				5.4	1.7E-03	3.3	3.7E-03	0.3	7.2E-01	0.5	4.6E-01
ENSMUST00000170116	upregulator of cell proliferation [Source:MGI Symbol;Acc:MGI:1919296]		Q5NCI0	2.0	3.0E-01	5.1	3.1E-02	0.1	9.8E-01	-3.1	8.5E-02
ENSMUST00000189384				5.4	6.6E-04	5.6	1.0E-02	-0.4	8.5E-01	-0.5	6.4E-01
ENSMUST00000160112				5.4	6.9E-04	5.1	4.2E-03	-0.3	8.2E-01	0.5	6.1E-01
ENSMUST00000170125	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Source:MGI Symbol;Acc:MGI:1913721]	E9Q2G1		-2.1	7.8E-02	-2.3	6.8E-02	-1.8	3.5E-02	-1.6	2.3E-01
ENSMUST00000122169				5.4	2.5E-04	-6.6	3.7E-03	-0.7	2.7E-01	1.4	4.6E-01
ENSMUST00000170134	RAN GTPase activating protein 1 [Source:MGI Symbol;Acc:MGI:103071]		P46061	6.2	5.5E-02	7.6	7.2E-02	2.4	5.2E-01	1.1	6.6E-01
ENSMUST00000191503				5.4	7.1E-04	7.3	6.2E-05	0.5	6.1E-01	0.5	3.5E-01
ENSMUST00000192239				5.4	2.8E-05	-7.8	1.8E-04	0.5	2.6E-01	-1.4	3.6E-01
ENSMUST00000147049				5.4	7.8E-06	8.3	2.0E-05	0.7	5.2E-01	-0.1	8.3E-01
ENSMUST00000170153	family with sequence similarity 83, member H [Source:MGI Symbol;Acc:MGI:2145900]		Q148V8	4.8	4.7E-02	4.9	2.3E-02	-4.1	9.6E-02	-4.2	1.0E-02
ENSMUST00000134323				5.4	8.6E-05	8.0	2.0E-05	0.1	9.5E-01	0.0	9.7E-01
ENSMUST00000188303				5.4	9.1E-05	8.0	1.7E-02	-0.7	8.2E-01	-1.8	2.6E-01
ENSMUST00000170157	rrier family 3 (activators of dibasic and neutral amino acid transport), member 2 [Source:MGI Symbol;Acc:MC		P10852	0.4	7.8E-01	2.5	1.7E-01	-0.3	8.4E-01	-2.4	1.3E-01
ENSMUST00000137216				5.4	2.4E-04	-4.2	8.7E-02	0.6	5.5E-01	0.9	6.8E-01
ENSMUST00000170167	prefoldin 4 [Source:MGI Symbol;Acc:MGI:1923512]	E9Q4Q8		3.1	8.3E-02	3.2	3.2E-02	-2.6	1.0E-01	-2.7	4.7E-02
ENSMUST00000170176	WD repeat domain 4 [Source:MGI Symbol;Acc:MGI:1889002]	F6VLT8		2.6	2.9E-01	3.1	1.9E-01	-0.5	8.4E-01	-1.0	5.6E-01
ENSMUST00000170186	arachidonate 5-lipoxygenase [Source:MGI Symbol;Acc:MGI:87999]	E9Q6H6		-1.6	6.1E-01	0.5	9.1E-01	1.9	5.1E-01	-0.3	9.5E-01
ENSMUST00000170188	protein tyrosine phosphatase, non-receptor type 21 [Source:MGI Symbol;Acc:MGI:1344406]	G5E8J4		2.9	2.5E-01	0.3	9.2E-01	-2.4	3.0E-01	0.2	9.4E-01
ENSMUST00000146006				5.4	1.8E-02	-1.9	1.6E-02	0.3	5.2E-01	-1.1	1.3E-01
ENSMUST00000154981				5.4	3.4E-05	6.6	3.2E-04	-0.5	7.1E-01	-1.0	1.6E-01
ENSMUST00000126970				5.4	1.2E-05	1.8	2.8E-01	-1.8	2.4E-01	0.4	7.9E-01
ENSMUST00000170217	phenylalanyl-tRNA synthetase, beta subunit [Source:MGI Symbol;Acc:MGI:1346035]		Q9WUA2	0.4	8.4E-01	-5.7	1.1E-02	-6.7	4.3E-04	-0.7	7.3E-01
ENSMUST00000170219	ım channel, voltage-dependent, beta subunit associated regulatory protein [Source:MGI Symbol;Acc:MGI:135	E9QP85		2.5	3.2E-01	1.8	5.1E-01	-0.9	7.0E-01	-0.3	9.1E-01
ENSMUST00000170223	adenylate cyclase 4 [Source:MGI Symbol;Acc:MGI:99674]		Q91WF3	3.3	1.8E-01	4.4	1.4E-01	-1.0	7.3E-01	-2.1	2.8E-01
ENSMUST00000147035				5.4	2.4E-03	-3.1	2.7E-02	1.0	1.1E-01	0.8	5.1E-01
ENSMUST00000170226	poly (ADP-ribose) polymerase family, member 10 [Source:MGI Symbol;Acc:MGI:3712326]	F6Z9X8		-0.1	9.3E-01	1.1	6.1E-01	1.0	6.1E-01	-0.3	8.6E-01
ENSMUST00000156288				5.4	1.7E-03	7.1	1.3E-04	0.0	9.7E-01	-0.9	1.8E-01
ENSMUST00000182107				5.4	4.0E-05	5.6	3.8E-02	-0.8	7.6E-01	0.0	9.9E-01
ENSMUST00000184801				5.4	1.0E-05	-8.9	6.9E-06	0.6	5.3E-02	0.2	8.4E-01
ENSMUST00000170242	myosin IXb [Source:MGI Symbol;Acc:MGI:106624]	E9PZW8		-1.6	1.2E-01	-3.2	6.7E-02	1.1	2.2E-01	2.7	9.7E-02
ENSMUST00000170248	Fras1 related extracellular matrix protein 1 [Source:MGI Symbol;Acc:MGI:2670972]	E9Q5Z7		4.1	1.5E-01	1.9	5.9E-01	-0.2	9.6E-01	2.0	4.5E-01
ENSMUST00000120048				5.4	3.8E-03	8.0	2.8E-06	-1.7	8.9E-02	-0.4	3.7E-01
ENSMUST00000170263	dCMP deaminase [Source:MGI Symbol;Acc:MGI:2444529]	G3X908		2.7	1.5E-01	5.2	1.3E-02	-0.6	7.5E-01	-3.1	4.3E-02
ENSMUST00000170265	phosphodiesterase 7B [Source:MGI Symbol;Acc:MGI:1352752]	E9PZN2		0.9	6.2E-01	-2.4	3.1E-01	-1.7	2.7E-01	1.7	4.9E-01
ENSMUST00000138025				5.4	9.3E-05	7.0	1.0E-02	-0.8	7.3E-01	-1.6	2.4E-01
ENSMUST00000170269	Ngfi-A binding protein 1 [Source:MGI Symbol;Acc:MGI:107564]	E9PZ64		-1.9	5.2E-01	-2.0	5.3E-01	-1.8	3.8E-01	-1.7	6.4E-01
ENSMUST00000136279				5.4	5.6E-04	6.8	3.0E-04	-0.6	6.5E-01	0.0	9.8E-01
ENSMUST00000133732				5.4	7.3E-05	3.3	2.1E-02	-1.6	1.9E-01	-0.8	4.3E-01
ENSMUST00000151970				5.4	4.2E-03	5.7	8.4E-04	-0.5	7.1E-01	-0.3	6.4E-01
ENSMUST00000170281				0.8	2.5E-01	-0.1	9.5E-01	-0.4	5.5E-01	0.4	5.5E-01
ENSMUST00000127024				5.4	4.5E-04	0.3	9.2E-01	5.9	1.3E-02	-1.0	6.8E-01
ENSMUST00000146069				5.4	8.4E-06	8.0	7.9E-04	-0.6	7.0E-01	1.2	1.9E-01
ENSMUST00000170287	3-hydroxy-3-methylglutaryl-Coenzyme A reductase [Source:MGI Symbol;Acc:MGI:96159]	F2Z470		0.5	6.7E-01	0.3	8.2E-01	0.1	8.9E-01	0.3	8.3E-01
ENSMUST00000149002				5.4	1.7E-05	-6.0	4.3E-02	2.1	4.3E-02	-0.4	8.8E-01
ENSMUST00000170295	family with sequence similarity 178, member B [Source:MGI Symbol;Acc:MGI:3026913]	E9PXB2		4.1	1.6E-01	4.9	1.3E-01	-0.3	9.3E-01	-1.2	5.3E-01
ENSMUST00000170300	inositol polyphosphate-5-phosphatase D [Source:MGI Symbol;Acc:MGI:107357]		Q9ES52	-4.6	1.2E-01	4.6	3.1E-01	8.5	3.9E-02	-0.7	8.3E-01
ENSMUST00000183980				5.4	1.2E-05	-8.7	1.5E-03	-1.2	6.8E-02	0.8	7.1E-01
ENSMUST00000121284				5.4	4.7E-04	3.0	2.5E-01	-0.7	7.7E-01	1.7	3.7E-01
ENSMUST00000127624				5.4	6.0E-04	-5.6	6.3E-05	-0.6	1.4E-01	-2.2	4.7E-02
ENSMUST00000155072				5.4	1.9E-03	7.5	7.6E-05	-0.5	6.8E-01	-0.3	5.8E-01
ENSMUST00000143677				5.4	1.3E-02	5.3	7.6E-05	-0.3	7.0E-01	-0.4	4.1E-01
ENSMUST00000154578				5.4	2.7E-04	7.3	1.9E-04	0.0	1.0E+00	-0.5	4.7E-01
ENSMUST00000179572				5.4	2.4E-04	5.4	4.1E-04	-0.4	6.5E-01	-0.8	2.4E-01
ENSMUST00000130748				5.4	1.4E-05	2.6	1.0E-01	-0.6	6.6E-01	3.9	6.3E-03
ENSMUST00000140232				5.4	1.3E-03	-3.2	1.3E-01	-5.4	3.5E-03	2.5	2.2E-01
ENSMUST00000150169				5.4	3.3E-02	-1.7	4.1E-02	0.4	4.3E-01	-0.9	2.5E-01
ENSMUST00000170347	coiled-coil domain containing 125 [Source:MGI Symbol;Acc:MGI:1923291]	G3UWA1		2.1	3.6E-01	0.4	8.9E-01	-1.1	6.8E-01	0.7	7.6E-01
ENSMUST00000152038				5.4	7.4E-05	6.2	1.2E-02	0.5	8.1E-01	1.1	3.6E-01
ENSMUST00000189484				5.4	2.9E-04	6.2	1.9E-03	-0.6	6.9E-01	-0.9	2.8E-01
ENSMUST00000170350	transportin 3 [Source:MGI Symbol;Acc:MGI:1196412]	E9Q0H8		0.1	9.4E-01	-1.1	5.2E-01	-0.9	4.3E-01	0.3	8.7E-01
ENSMUST00000139410				5.4	2.6E-03	-1.3	4.3E-01	2.1	6.5E-02	0.4	8.1E-01
ENSMUST00000170361	PDZ and LIM domain 5 [Source:MGI Symbol;Acc:MGI:1927489]	E9Q8P5		0.8	8.0E-01	3.9	4.5E-01	2.9	5.4E-01	-0.2	9.6E-01
ENSMUST00000144154				5.4	5.9E-04	5.9	9.0E-04	-0.1	9.1E-01	-0.9	2.3E-01
ENSMUST00000170371	ATPase, H+/K+ exchanging, gastric, alpha polypeptide [Source:MGI Symbol;Acc:MGI:88113]	Q91WH7		3.1	3.1E-01	4.1	2.0E-01	-0.4	9.0E-01	-1.5	4.9E-01
ENSMUST00000170373	atlastin GTPase 3 [Source:MGI Symbol;Acc:MGI:1924270]	E9PYT3		1.1	4.5E-01	4.3	5.2E-02	1.9	3.0E-01	-1.3	3.7E-01
ENSMUST00000159889				5.4	3.1E-03	-2.0	3.1E-02	-0.2	6.1E-01	0.0	9.5E-01
ENSMUST00000170375				3.7	5.9E-02	2.5	3.0E-01	-1.1	6.2E-01	0.2	9.2E-01
ENSMUST00000188740				5.4	3.2E-04	-2.8	8.3E-02	0.7	3.7E-01	-2.2	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000134244				5.4	2.6E-03	-4.7	4.6E-03	-0.2	6.9E-01	0.4	7.6E-01
ENSMUST00000159291				5.4	1.8E-02	4.7	7.0E-04	-1.1	2.8E-01	0.3	6.7E-01
ENSMUST00000144889				5.4	1.2E-02	-6.7	6.5E-04	-0.6	3.0E-01	-0.8	6.3E-01
ENSMUST00000146108				5.4	7.1E-05	2.9	3.1E-02	-0.5	6.6E-01	-0.2	8.1E-01
ENSMUST00000153307				5.4	1.1E-03	7.0	1.9E-03	-0.3	8.5E-01	1.1	2.0E-01
ENSMUST00000154054				5.4	7.0E-04	7.3	3.0E-04	-0.7	6.4E-01	-1.0	2.0E-01
ENSMUST00000170400	solute carrier family 22 (organic cation transporter), member 14 [Source:MGI Symbol;Acc:MGI:2685974]	Q497L9		3.1	1.8E-01	4.9	5.4E-02	-0.5	8.2E-01	-2.3	1.7E-01
ENSMUST00000119461				5.4	1.7E-03	5.1	2.6E-02	-1.1	5.7E-01	-0.6	5.8E-01
ENSMUST00000174594				5.4	1.2E-02	6.1	2.4E-03	-0.4	7.9E-01	-1.7	8.1E-02
ENSMUST00000147372				5.4	8.5E-04	6.7	6.4E-04	0.4	7.7E-01	-0.1	8.6E-01
ENSMUST00000118772				5.4	2.4E-03	6.9	1.4E-04	-0.6	6.2E-01	-0.8	2.2E-01
ENSMUST00000170416	sorting nexin 25 [Source:MGI Symbol;Acc:MGI:2142610]		Q3ZT31	-2.5	4.5E-02	-4.5	5.1E-02	0.0	9.5E-01	2.1	3.2E-01
ENSMUST00000170419	vomeronasal 2, receptor 9 [Source:MGI Symbol;Acc:MGI:3643093]	K7N6Z8		3.5	1.2E-01	5.7	3.3E-02	-0.2	9.3E-01	-2.4	1.2E-01
ENSMUST00000152236				5.4	5.7E-05	5.8	1.3E-03	-0.4	7.5E-01	-0.7	3.9E-01
ENSMUST00000121519				5.4	2.0E-03	5.2	4.0E-02	-0.7	7.5E-01	-0.3	8.3E-01
ENSMUST00000155656				5.4	3.3E-02	7.2	5.0E-05	-0.5	6.2E-01	-0.6	2.7E-01
ENSMUST00000117893				5.4	3.3E-04	-1.2	2.9E-02	-0.1	6.6E-01	-0.3	5.5E-01
ENSMUST00000170436	nischarin [Source:MGI Symbol;Acc:MGI:1928323]	F6ZL22		-1.6	1.8E-01	-0.6	7.3E-01	0.9	4.2E-01	-0.1	9.4E-01
ENSMUST00000170438	CUGBP, Elav-like family member 2 [Source:MGI Symbol;Acc:MGI:1338822]	E9QA47		-1.5	1.2E-01	-0.9	4.7E-01	0.5	5.4E-01	-0.2	8.9E-01
ENSMUST00000137806				5.4	8.0E-06	-7.2	8.3E-04	1.3	2.2E-02	-0.9	6.0E-01
ENSMUST00000154278				5.4	7.3E-05	5.7	6.9E-02	-1.0	7.5E-01	-0.3	8.9E-01
ENSMUST00000194670				5.4	2.2E-05	8.7	1.3E-05	-0.6	6.2E-01	-0.8	1.3E-01
ENSMUST00000126755				5.4	4.3E-06	5.8	4.5E-04	-0.5	6.8E-01	-0.4	5.0E-01
ENSMUST00000142041				5.4	2.2E-05	5.0	5.1E-04	-0.5	6.0E-01	-0.5	5.0E-01
ENSMUST00000145298				5.4	1.7E-05	8.1	6.5E-05	-0.4	7.5E-01	-0.4	4.5E-01
ENSMUST00000148627				5.4	5.1E-04	5.4	6.3E-04	-0.9	4.4E-01	-0.7	3.0E-01
ENSMUST00000160587				5.4	1.9E-02	1.3	4.2E-01	4.1	7.1E-03	-2.7	9.9E-02
ENSMUST00000170468	pseudouridine synthase 1 [Source:MGI Symbol;Acc:MGI:1929237]		Q9WU56	-3.4	7.6E-02	-3.0	2.0E-01	-0.3	8.0E-01	-0.8	7.3E-01
ENSMUST00000182171				5.4	1.6E-03	-2.9	7.6E-02	1.5	8.3E-02	1.6	2.9E-01
ENSMUST00000130784				5.4	1.5E-04	4.1	4.3E-03	0.8	4.6E-01	0.2	7.9E-01
ENSMUST00000170476	ubiquitin specific peptidase 20 [Source:MGI Symbol;Acc:MGI:1921520]		Q8C6M1	0.2	9.2E-01	0.2	9.3E-01	-0.3	8.5E-01	-0.3	8.7E-01
ENSMUST00000170479				1.6	8.1E-02	1.9	1.3E-01	0.7	4.6E-01	0.4	6.5E-01
ENSMUST00000170480	predicted gene 3002 [Source:MGI Symbol;Acc:MGI:3781180]	E9PW72		3.7	8.0E-02	1.9	4.3E-01	-0.5	8.3E-01	1.2	5.2E-01
ENSMUST00000170481	methyl CpG binding protein 2 [Source:MGI Symbol;Acc:MGI:99918]		Q9Z2D6	-1.6	3.6E-02	0.2	8.3E-01	0.5	3.4E-01	-1.3	1.3E-01
ENSMUST00000170482				-1.6	8.8E-02	0.2	8.3E-01	0.7	4.3E-01	-1.2	2.6E-01
ENSMUST00000100407				5.4	2.3E-04	5.7	2.6E-02	-0.7	7.6E-01	1.8	1.9E-01
ENSMUST00000182253				5.4	8.0E-04	-4.0	2.8E-05	0.4	1.2E-01	-0.6	2.8E-01
ENSMUST00000121575				5.4	4.2E-04	-1.3	1.5E-01	0.5	3.4E-01	-0.2	7.7E-01
ENSMUST00000170500				-1.2	2.7E-01	1.8	1.3E-01	0.9	3.3E-01	-2.0	8.3E-02
ENSMUST00000120221				5.4	1.5E-03	4.1	3.8E-03	-2.7	5.0E-02	0.5	5.3E-01
ENSMUST00000138138				5.4	9.3E-04	6.9	2.2E-04	-0.7	6.1E-01	-1.9	2.0E-02
ENSMUST00000170506				-2.0	1.1E-01	0.1	9.2E-01	0.4	6.4E-01	-1.7	2.0E-01
ENSMUST00000170507	RIKEN cDNA 4632428N05 gene [Source:MGI Symbol;Acc:MGI:1921298]	E9Q251		-2.3	2.0E-01	2.9	1.4E-01	1.9	2.5E-01	-3.3	8.2E-02
ENSMUST00000176091				5.4	3.4E-03	8.8	2.8E-02	-0.9	8.1E-01	-0.3	8.7E-01
ENSMUST00000121657				5.4	9.0E-04	7.6	4.8E-04	-0.6	7.0E-01	-0.1	8.5E-01
ENSMUST00000126504				5.4	3.8E-05	6.5	1.7E-02	-0.6	7.9E-01	-1.8	2.1E-01
ENSMUST00000145153				5.4	3.4E-04	-1.3	1.7E-01	1.2	5.3E-02	0.3	7.4E-01
ENSMUST00000185549				5.4	2.6E-04	-5.6	4.3E-03	0.2	7.7E-01	1.3	3.9E-01
ENSMUST00000077868				5.4	1.1E-03	4.5	1.7E-04	-0.5	4.6E-01	0.1	8.5E-01
ENSMUST00000119636				5.4	5.4E-03	7.7	9.7E-05	1.5	2.2E-01	0.6	2.9E-01
ENSMUST00000120326				5.4	3.3E-04	3.4	9.1E-02	-0.9	5.8E-01	3.1	2.8E-02
ENSMUST00000182838				5.4	3.1E-05	-3.9	8.2E-04	0.1	7.3E-01	0.4	6.3E-01
ENSMUST00000088263				5.4	3.3E-02	5.3	1.3E-04	-0.8	3.5E-01	0.2	6.9E-01
ENSMUST00000174670				5.4	1.2E-02	6.6	1.5E-04	-0.6	6.0E-01	0.1	8.4E-01
ENSMUST00000120359				5.4	5.5E-04	7.5	1.0E-04	-0.6	6.2E-01	0.0	9.6E-01
ENSMUST00000140062				5.4	1.8E-03	7.4	3.5E-03	2.3	2.3E-01	-0.6	5.5E-01
ENSMUST00000191417				5.4	4.1E-05	5.3	1.6E-03	0.1	9.2E-01	-0.4	6.5E-01
ENSMUST00000141427				5.4	7.9E-04	2.6	2.7E-03	0.1	8.6E-01	0.0	9.4E-01
ENSMUST00000159628				5.4	3.6E-03	6.1	5.8E-04	-0.7	6.1E-01	-0.8	2.5E-01
ENSMUST00000170984				5.4	1.6E-05	8.6	1.3E-05	0.9	4.1E-01	-0.2	5.9E-01
ENSMUST00000170584	caspase recruitment domain family, member 10 [Source:MGI Symbol;Acc:MGI:2146012]		P58660	4.6	6.2E-02	-0.6	8.6E-01	-1.6	5.4E-01	3.5	2.0E-01
ENSMUST00000191456				5.4	4.0E-05	6.2	2.2E-04	-0.5	6.3E-01	-0.2	8.0E-01
ENSMUST00000127966				5.4	2.6E-06	6.4	6.3E-04	-0.5	7.1E-01	-0.4	6.1E-01
ENSMUST00000170617	widely-interspaced zinc finger motifs [Source:MGI Symbol;Acc:MGI:1332638]	E9Q5W4		-1.0	3.3E-01	3.2	2.4E-02	2.0	7.2E-02	-2.2	6.4E-02
ENSMUST00000133858				5.4	5.3E-03	9.1	4.4E-05	-0.1	9.6E-01	0.1	8.3E-01
ENSMUST00000170625	transmembrane protein 40 [Source:MGI Symbol;Acc:MGI:2137870]	E9Q6I9		-2.7	4.2E-02	-2.5	2.4E-01	1.1	3.2E-01	0.9	6.6E-01
ENSMUST00000156289				5.4	5.2E-04	5.0	4.3E-03	-0.4	7.6E-01	-1.5	1.1E-01
ENSMUST00000160832				5.4	3.5E-04	3.6	1.0E-03	1.5	4.3E-02	-0.1	8.9E-01
ENSMUST00000161928				5.4	2.6E-04	3.4	3.8E-03	-1.1	2.0E-01	-0.5	5.3E-01
ENSMUST00000138473				5.4	3.6E-05	6.6	4.6E-05	0.6	4.7E-01	0.7	1.8E-01
ENSMUST00000170644				2.0	3.1E-01	-0.2	9.3E-01	-2.2	2.7E-01	0.1	9.8E-01
ENSMUST00000170647	transportin 3 [Source:MGI Symbol;Acc:MGI:1196412]	F6TDZ2		-4.5	2.1E-01	-6.6	1.4E-01	-2.5	1.9E-01	-0.5	9.2E-01
ENSMUST00000170651	dynein, axonemal, heavy chain 8 [Source:MGI Symbol;Acc:MGI:107714]		Q91XQ0	-0.2	6.1E-01	1.1	1.0E-01	1.1	4.2E-02	-0.2	6.8E-01
ENSMUST00000189812				5.4	3.5E-04	-4.0	8.2E-02	2.4	2.8E-02	-0.7	7.5E-01
ENSMUST00000120203				5.4	6.6E-04	7.2	2.5E-04	-0.6	6.4E-01	0.4	5.0E-01
ENSMUST00000170665	transmembrane epididymal family member 3 [Source:MGI Symbol;Acc:MGI:1913811]	Q9CQH1		-0.6	3.9E-01	0.5	5.8E-01	0.6	3.8E-01	-0.5	5.3E-01
ENSMUST00000123062				5.4	4.1E-03	7.1	1.9E-03	-0.7	6.9E-01	0.6	4.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000170675				-1.0	2.7E-01	-0.1	9.1E-01	0.2	8.2E-01	-0.7	5.3E-01
ENSMUST00000118855				5.4	9.8E-03	5.1	1.1E-02	-0.6	7.3E-01	0.5	6.4E-01
ENSMUST00000135470				5.4	2.7E-03	-7.6	9.7E-03	1.6	4.3E-02	2.4	3.3E-01
ENSMUST00000170699	upstream transcription factor 2 [Source:MGI Symbol;Acc:MGI:99961]	E9PZY3		-1.6	5.9E-01	-2.3	5.7E-01	-0.8	7.1E-01	-0.1	9.8E-01
ENSMUST00000144172				5.4	7.8E-03	-6.2	3.1E-03	-0.9	1.6E-01	-0.7	6.8E-01
ENSMUST00000146593				5.4	1.1E-03	4.2	5.1E-02	-1.3	4.9E-01	-0.5	7.0E-01
ENSMUST00000170716	enolase 3, beta muscle [Source:MGI Symbol;Acc:MGI:95395]		P21550	-0.1	9.7E-01	-1.2	7.5E-01	-1.8	4.6E-01	-0.8	8.3E-01
ENSMUST00000176812				5.4	2.7E-03	5.7	1.7E-03	-0.4	7.8E-01	-0.5	5.6E-01
ENSMUST00000183176				5.4	3.1E-06	-4.7	2.5E-03	0.0	9.3E-01	-1.0	4.2E-01
ENSMUST00000187633				5.4	1.3E-02	3.3	5.6E-03	-1.2	1.9E-01	0.0	9.8E-01
ENSMUST00000072123				5.4	5.4E-04	-4.8	8.5E-04	0.1	8.9E-01	-0.6	5.8E-01
ENSMUST00000190687				5.4	6.3E-04	6.7	4.1E-02	-2.9	3.8E-01	-2.0	3.0E-01
ENSMUST00000140072				5.4	1.4E-03	4.7	1.6E-03	2.1	6.0E-02	0.5	4.4E-01
ENSMUST00000124272				5.4	9.8E-05	3.8	2.7E-03	0.0	9.8E-01	-0.2	8.0E-01
ENSMUST00000191339				5.4	5.2E-05	3.7	4.9E-05	-0.2	7.0E-01	0.2	6.5E-01
ENSMUST00000192230				5.4	1.5E-04	-2.6	1.6E-03	-1.0	2.0E-02	-0.8	2.1E-01
ENSMUST00000136845				5.4	2.6E-02	1.3	5.4E-01	-3.1	2.0E-01	2.5	1.1E-01
ENSMUST00000114170				5.4	3.9E-04	4.2	2.8E-02	-1.3	4.2E-01	0.0	9.8E-01
ENSMUST00000146029				5.4	3.0E-04	5.6	5.4E-03	-0.6	7.2E-01	-1.1	2.9E-01
ENSMUST00000194915				5.4	2.8E-03	8.0	1.3E-04	-0.2	9.0E-01	0.5	4.4E-01
ENSMUST00000170794	protein kinase domain containing, cytoplasmic [Source:MGI Symbol;Acc:MGI:2147077]		Q5RJI4	2.3	6.6E-02	1.5	2.6E-01	-1.8	1.5E-01	-0.9	4.0E-01
ENSMUST00000152632				5.4	1.6E-04	-0.5	3.3E-01	0.9	3.0E-02	-0.4	4.4E-01
ENSMUST00000125459				5.4	3.5E-04	2.8	2.2E-02	-0.1	9.2E-01	-0.2	8.4E-01
ENSMUST00000168080				5.4	1.8E-03	-2.1	5.7E-02	-0.1	8.3E-01	-0.8	4.6E-01
ENSMUST00000170800	discoidin domain receptor family, member 2 [Source:MGI Symbol;Acc:MGI:1345277]		Q62371	0.6	5.4E-01	-3.9	3.4E-03	-4.3	1.5E-04	0.2	8.6E-01
ENSMUST00000170801	ER lipid raft associated 1 [Source:MGI Symbol;Acc:MGI:2387613]			1.9	5.0E-01	9.0	2.5E-02	2.8	4.0E-01	-4.3	1.1E-01
ENSMUST00000170802	microtubule-associated protein, RP/EB family, member 2 [Source:MGI Symbol;Acc:MGI:106271]	E9Q6X0		3.8	2.1E-01	3.9	2.5E-01	-0.1	9.7E-01	-0.3	9.0E-01
ENSMUST00000173421				5.4	1.0E-03	5.6	3.1E-04	-0.6	5.7E-01	0.4	4.9E-01
ENSMUST00000156899				5.4	4.6E-05	-5.4	5.7E-02	0.9	3.6E-01	0.0	9.9E-01
ENSMUST00000192428				5.4	1.8E-05	-6.1	1.8E-03	0.1	7.8E-01	1.1	4.9E-01
ENSMUST00000061947				5.3	5.2E-04	-3.1	1.4E-01	1.9	1.0E-01	-0.6	7.6E-01
ENSMUST00000123988				5.3	1.5E-03	6.0	4.7E-03	-0.7	6.9E-01	2.3	2.8E-02
ENSMUST00000136214				5.3	9.4E-04	6.9	4.8E-03	0.0	9.9E-01	0.1	9.6E-01
ENSMUST00000118352				5.3	1.4E-02	-6.7	1.0E-05	-0.7	6.3E-02	-0.9	2.7E-01
ENSMUST00000132439				5.3	2.9E-03	5.5	2.6E-04	-1.4	2.2E-01	0.0	9.3E-01
ENSMUST00000170840	poly (ADP-ribose) glycohydrolase [Source:MGI Symbol;Acc:MGI:1347094]	E9Q088		-3.5	3.5E-02	-3.7	1.0E-01	0.2	8.7E-01	0.3	8.7E-01
ENSMUST00000170841	lamin tail domain containing 2 [Source:MGI Symbol;Acc:MGI:1919250]	B7ZMW1		4.1	1.3E-01	2.1	6.0E-01	0.8	8.1E-01	2.8	3.7E-01
ENSMUST00000170846	family with sequence similarity 214, member A [Source:MGI Symbol;Acc:MGI:2387648]		Q69ZK7	-2.3	6.1E-02	-0.4	7.8E-01	0.4	6.4E-01	-1.5	2.8E-01
ENSMUST00000170850				1.2	4.7E-01	4.9	9.8E-02	3.3	2.0E-01	-0.4	8.2E-01
ENSMUST00000170853	synaptojanin 1 [Source:MGI Symbol;Acc:MGI:1354961]	E9Q7S0		1.6	5.8E-01	5.5	1.8E-01	2.5	4.8E-01	-1.3	6.6E-01
ENSMUST00000154875				5.3	2.5E-02	5.7	4.2E-04	-0.2	8.4E-01	-0.9	2.0E-01
ENSMUST00000170857	BTG3 associated nuclear protein [Source:MGI Symbol;Acc:MGI:1889023]		Q8VBU8	1.2	1.0E-01	2.5	1.6E-02	0.4	6.3E-01	-0.9	2.2E-01
ENSMUST00000170862	casein kinase 1, alpha 1 [Source:MGI Symbol;Acc:MGI:1934950]	E9Q3W1		-4.6	2.0E-01	1.8	7.4E-01	5.8	1.7E-01	-0.6	8.9E-01
ENSMUST00000170863				0.9	7.2E-01	4.7	2.6E-01	4.2	2.0E-01	0.4	9.2E-01
ENSMUST00000170870				2.5	2.3E-01	4.9	6.2E-02	0.5	8.4E-01	-1.9	2.3E-01
ENSMUST00000123329				5.3	1.4E-04	3.6	2.8E-04	-5.6	1.7E-04	-0.3	4.9E-01
ENSMUST00000146527				5.3	8.6E-03	-1.0	1.6E-01	-0.1	8.8E-01	-0.7	3.0E-01
ENSMUST00000151656				5.3	1.3E-02	4.4	7.6E-04	1.7	5.1E-02	0.1	8.4E-01
ENSMUST00000153368				5.3	7.5E-06	-4.8	5.3E-03	0.2	7.1E-01	0.0	9.8E-01
ENSMUST00000119745				5.3	2.3E-02	3.0	5.6E-03	-1.0	2.0E-01	-0.2	7.3E-01
ENSMUST00000142905				5.3	5.7E-04	-5.2	8.4E-02	-0.3	7.8E-01	-2.5	4.5E-01
ENSMUST00000170905	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 1 [Source:MGI Symbol;Acc:MGI:102469	B5B2N2		3.8	8.4E-02	4.2	8.8E-02	-0.5	8.3E-01	-0.9	5.7E-01
ENSMUST00000191430				5.3	8.8E-04	-3.5	6.8E-05	0.4	1.4E-01	0.0	9.3E-01
ENSMUST00000145126				5.3	7.9E-06	6.2	2.5E-04	-0.5	6.4E-01	0.1	9.2E-01
ENSMUST00000151866				5.3	9.9E-04	-2.8	1.1E-01	1.3	1.2E-01	1.2	4.4E-01
ENSMUST00000123756				5.3	1.1E-02	8.1	2.0E-06	0.7	3.7E-01	0.6	1.2E-01
ENSMUST00000170935	MON2 homolog (yeast) [Source:MGI Symbol;Acc:MGI:1914324]	B9EKJ3		1.8	6.3E-01	1.4	7.6E-01	-1.7	6.5E-01	-1.3	7.3E-01
ENSMUST00000139016				5.3	1.8E-04	6.2	3.9E-03	0.2	9.0E-01	-1.8	1.3E-01
ENSMUST00000145857				5.3	1.6E-05	-3.0	1.1E-03	1.1	1.5E-02	0.2	7.6E-01
ENSMUST00000131628				5.3	9.1E-06	-6.0	6.3E-04	-0.5	3.6E-01	-1.3	3.3E-01
ENSMUST00000171823				5.3	2.0E-03	3.4	1.2E-01	-0.5	8.2E-01	1.6	2.4E-01
ENSMUST00000170957	geranylgeranyl diphosphate synthase 1 [Source:MGI Symbol;Acc:MGI:1341724]	Q3V0T8	Q9WTN0	-0.8	9.1E-02	-0.3	5.0E-01	-0.1	8.3E-01	-0.5	3.3E-01
ENSMUST00000182804				5.3	1.2E-04	7.6	1.6E-04	1.1	3.8E-01	-0.2	7.7E-01
ENSMUST00000154048				5.3	6.2E-05	8.9	1.3E-02	-0.7	8.4E-01	-0.8	5.9E-01
ENSMUST00000170971	integrin alpha L [Source:MGI Symbol;Acc:MGI:96606]		P24063	-3.9	4.6E-01	-5.0	4.9E-01	-1.2	6.8E-01	0.0	1.0E+00
ENSMUST00000183269				5.3	2.8E-04	6.2	2.4E-03	-0.4	8.2E-01	-0.7	4.0E-01
ENSMUST00000192106				5.3	1.5E-04	4.0	3.6E-04	-1.2	1.2E-01	0.2	7.3E-01
ENSMUST00000170988	cytochrome P450, family 39, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1927096]	Q544S6	Q9JKJ9	0.6	2.7E-01	1.4	4.9E-02	0.0	9.3E-01	-0.8	2.0E-01
ENSMUST00000170989	enoyl-Coenzyme A delta isomerase 2 [Source:MGI Symbol;Acc:MGI:1346064]	E9PUY9		-2.1	4.0E-02	-0.9	2.6E-01	-0.8	2.2E-01	-1.9	6.1E-02
ENSMUST00000170992	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	E9PY90		1.8	5.4E-01	-1.1	7.5E-01	-3.4	2.2E-01	-0.5	8.8E-01
ENSMUST00000127261				5.3	7.1E-03	5.2	4.2E-04	-1.5	1.7E-01	-0.2	7.6E-01
ENSMUST00000144755				5.3	4.5E-03	7.0	1.6E-05	1.5	8.2E-02	-0.2	6.8E-01
ENSMUST00000183440				5.3	4.6E-05	-5.9	6.7E-03	0.2	7.7E-01	-0.9	6.6E-01
ENSMUST00000171018	brain expressed, associated with Nedd4, 1 [Source:MGI Symbol;Acc:MGI:1929597]	E9PVP2		3.6	1.5E-01	4.8	8.6E-02	-0.4	8.7E-01	-1.6	3.6E-01
ENSMUST00000171023	KRIT1, ankyrin repeat containing [Source:MGI Symbol;Acc:MGI:1930618]		Q6S5J6	1.8	1.3E-01	-2.8	9.0E-02	-1.3	2.5E-01	3.3	3.9E-02
ENSMUST00000120086				5.3	1.5E-04	4.6	3.5E-05	0.8	1.9E-01	-0.4	3.4E-01
ENSMUST00000104985				5.3	4.8E-04	-5.0	2.1E-02	-1.0	2.2E-01	-0.4	8.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000171031	cyclin D3 [Source:MGI Symbol;Acc:MGI:88315]	Q3TSW4	P30282	-1.0	1.3E-01	-0.2	7.9E-01	-0.1	8.6E-01	-0.9	2.5E-01
ENSMUST00000123031				5.3	2.8E-05	4.9	2.2E-03	-0.6	6.6E-01	1.1	1.4E-01
ENSMUST00000171040	F1 small subunit (SSU) processome component homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:19209	E9Q186		-0.6	7.0E-01	-2.1	3.9E-01	-0.5	7.4E-01	0.9	6.7E-01
ENSMUST00000131054				5.3	9.8E-05	-3.9	6.1E-03	0.2	7.2E-01	-0.8	5.1E-01
ENSMUST00000146908				5.3	2.3E-04	2.5	1.4E-01	-3.9	4.7E-02	-1.9	1.5E-01
ENSMUST00000171045	thyroglobulin [Source:MGI Symbol;Acc:MGI:98733]	F6XYF6		-0.5	8.0E-01	-2.7	2.8E-01	-2.7	8.1E-02	-0.6	8.3E-01
ENSMUST00000154369				5.3	2.4E-03	7.3	8.2E-05	-0.5	7.0E-01	-0.6	3.4E-01
ENSMUST00000171058	actin related protein 2/3 complex, subunit 4 [Source:MGI Symbol;Acc:MGI:1915339]	E9PWA7		2.9	1.5E-01	3.2	3.3E-01	2.8	3.4E-01	2.4	2.7E-01
ENSMUST00000172730				5.3	3.4E-04	5.5	8.0E-04	0.1	9.3E-01	0.5	4.3E-01
ENSMUST00000188478				5.3	4.0E-05	5.9	6.7E-04	-0.4	7.3E-01	0.2	7.3E-01
ENSMUST00000132188				5.3	1.3E-02	3.2	6.9E-02	0.0	9.8E-01	0.7	5.8E-01
ENSMUST00000171071	zinc finger protein 236 [Source:MGI Symbol;Acc:MGI:1926950]	B2RR24		-0.5	4.3E-01	0.7	3.2E-01	0.3	6.3E-01	-0.9	1.9E-01
ENSMUST00000171077	sialic acid binding Ig-like lectin H [Source:MGI Symbol;Acc:MGI:2443256]	Q4QQK7		2.3	5.9E-02	6.1	1.2E-04	-1.3	2.2E-01	-5.1	1.6E-04
ENSMUST00000171080	fidgetin-like 1 [Source:MGI Symbol;Acc:MGI:1890648]		Q8BPY9	-0.9	6.8E-01	4.5	1.0E-01	2.9	2.5E-01	-2.5	2.2E-01
ENSMUST00000171088	proline rich 5 like [Source:MGI Symbol;Acc:MGI:1919696]		A2AVJ5	-2.7	1.1E-01	0.0	9.8E-01	0.5	6.9E-01	-2.2	2.3E-01
ENSMUST00000171095	dedicator of cyto-kinesis 3 [Source:MGI Symbol;Acc:MGI:2429763]	F6VMI1		2.5	1.4E-01	4.2	5.4E-02	0.1	9.7E-01	-1.7	2.5E-01
ENSMUST00000150292				5.3	2.3E-03	-1.8	2.0E-01	4.6	1.4E-04	-0.1	9.4E-01
ENSMUST00000171108	retinoic acid induced 1 [Source:MGI Symbol;Acc:MGI:103291]		Q61818	1.6	6.1E-01	1.9	6.6E-01	1.2	7.2E-01	0.9	8.1E-01
ENSMUST00000153582				5.3	1.5E-04	3.1	1.3E-01	-1.7	4.0E-01	2.0	1.5E-01
ENSMUST00000193940				5.3	8.2E-06	8.3	1.3E-03	1.4	4.6E-01	-0.3	7.3E-01
ENSMUST00000171120	predicted gene 5428 [Source:MGI Symbol;Acc:MGI:3647789]	E9PUX4		-0.1	9.5E-01	-0.4	7.9E-01	-1.4	2.8E-01	-1.1	4.8E-01
ENSMUST00000145113				5.3	1.7E-04	-2.9	9.4E-02	1.8	7.1E-02	-0.3	8.6E-01
ENSMUST00000171127	histone cluster 1, H2ac [Source:MGI Symbol;Acc:MGI:2448287]	B2RVF0	P22752	0.1	9.0E-01	2.5	2.3E-02	0.3	7.4E-01	-2.1	4.1E-02
ENSMUST00000182082				5.3	1.3E-03	-4.7	2.8E-02	0.2	7.9E-01	-0.1	9.6E-01
ENSMUST00000183672				5.3	3.1E-05	7.5	4.4E-05	-0.6	5.9E-01	-0.5	3.6E-01
ENSMUST00000171137	receptor (TNFRSF)-interacting serine-threonine kinase 1 [Source:MGI Symbol;Acc:MGI:108212]	F7D1J2		0.1	9.6E-01	1.1	7.3E-01	0.9	6.9E-01	-0.2	9.6E-01
ENSMUST00000126802				5.3	4.4E-04	-5.0	5.0E-02	0.9	3.7E-01	-1.0	6.9E-01
ENSMUST00000171143	family with sequence similarity 102, member B [Source:MGI Symbol;Acc:MGI:3036259]	E9Q4R1		-1.4	2.3E-01	3.1	3.6E-02	1.7	1.4E-01	-2.7	3.9E-02
ENSMUST00000126808				5.3	3.9E-04	-3.1	3.3E-02	0.7	2.5E-01	-0.6	6.8E-01
ENSMUST00000133278				5.3	2.4E-03	7.2	4.2E-04	-0.5	7.1E-01	-1.2	1.3E-01
ENSMUST00000142054				5.3	3.5E-03	6.2	3.1E-04	-0.6	6.3E-01	-1.1	1.1E-01
ENSMUST00000171155	kelch-like 25 [Source:MGI Symbol;Acc:MGI:2668031]		Q8R2P1	-0.7	7.1E-01	1.4	6.1E-01	2.9	2.2E-01	0.8	7.1E-01
ENSMUST00000153185				5.3	3.3E-02	0.4	6.3E-01	-4.6	4.9E-04	0.0	9.7E-01
ENSMUST00000174415				5.3	2.4E-02	5.5	5.9E-04	-1.4	2.4E-01	0.0	9.6E-01
ENSMUST00000171165	ubiquitin-conjugating enzyme E2F (putative) [Source:MGI Symbol;Acc:MGI:1915171]		Q9CY34	0.5	3.2E-01	0.6	3.9E-01	-0.1	8.7E-01	-0.1	8.2E-01
ENSMUST00000119395				5.3	2.9E-03	3.8	5.7E-04	-0.2	8.0E-01	-0.8	2.1E-01
ENSMUST00000171171	WD repeat domain 4 [Source:MGI Symbol;Acc:MGI:1889002]	E9Q156		2.2	1.9E-01	0.8	7.5E-01	0.1	9.6E-01	1.6	4.1E-01
ENSMUST00000134676				5.3	1.1E-03	-0.4	5.8E-01	0.6	2.2E-01	-1.1	1.8E-01
ENSMUST00000171176	transient receptor potential cation channel, subfamily M, member 8 [Source:MGI Symbol;Acc:MGI:2181435]		Q8R4D5	3.6	9.6E-02	2.0	4.5E-01	-0.5	8.4E-01	1.2	5.6E-01
ENSMUST00000171182	zinc and ring finger 1 [Source:MGI Symbol;Acc:MGI:2177308]	E9PZB7		-2.2	2.2E-01	0.2	9.0E-01	0.0	9.9E-01	-2.4	2.4E-01
ENSMUST00000171189	TBC1 domain family, member 24 [Source:MGI Symbol;Acc:MGI:2443456]		Q3UUG6	0.2	9.6E-01	5.0	2.1E-01	3.6	3.4E-01	-1.2	6.5E-01
ENSMUST00000171192	sphingomyelin phosphodiesterase 5 [Source:MGI Symbol;Acc:MGI:3709877]	G3UXH6		-2.7	5.0E-02	-1.1	5.4E-01	1.1	3.5E-01	-0.6	7.1E-01
ENSMUST00000138067				5.3	1.5E-02	8.0	1.1E-05	-0.9	4.0E-01	-0.5	3.0E-01
ENSMUST00000171203				-1.2	3.5E-01	-0.5	7.8E-01	0.5	6.8E-01	-0.3	8.5E-01
ENSMUST00000171205	sperm associated antigen 1 [Source:MGI Symbol;Acc:MGI:1349387]		Q80ZX8	0.3	6.2E-01	0.8	3.0E-01	0.2	7.2E-01	-0.3	6.8E-01
ENSMUST00000171211	mitogen-activated protein kinase kinase kinase kinase 5 [Source:MGI Symbol;Acc:MGI:1925503]	E9Q1T3		1.3	4.2E-01	-0.3	8.4E-01	-4.3	1.0E-02	-2.8	7.7E-02
ENSMUST00000145704				5.3	4.8E-04	4.9	6.5E-03	-0.4	7.9E-01	0.0	9.9E-01
ENSMUST00000171215	zinc finger protein 106 [Source:MGI Symbol;Acc:MGI:1270153]	E9Q7S1		1.9	1.1E-01	4.7	9.7E-03	2.5	7.4E-02	-0.4	7.5E-01
ENSMUST00000148438				5.3	9.7E-06	-4.2	2.3E-02	-0.2	8.0E-01	-0.4	8.0E-01
ENSMUST00000075147				5.3	1.4E-02	-4.1	5.5E-04	-0.8	1.3E-01	-3.8	6.6E-03
ENSMUST00000171231	histocompatibility 2, class II, locus Mb2 [Source:MGI Symbol;Acc:MGI:95923]	F7AD18		-1.8	1.5E-01	0.6	5.7E-01	-1.8	5.6E-02	-4.2	5.7E-03
ENSMUST00000171233	olute carrier family 37 (glycerol-3-phosphate transporter), member 1 [Source:MGI Symbol;Acc:MGI:2446181	Q8R070		-0.9	3.0E-01	0.1	9.5E-01	0.6	4.3E-01	-0.3	7.4E-01
ENSMUST00000140285				5.3	6.9E-04	5.5	8.6E-03	-1.5	4.2E-01	-1.1	3.1E-01
ENSMUST00000144219				5.3	5.5E-04	2.9	2.8E-02	-2.3	1.0E-01	0.5	6.1E-01
ENSMUST00000130248				5.3	2.6E-03	-4.7	8.1E-04	-0.2	5.6E-01	-0.9	3.9E-01
ENSMUST00000194232				5.3	2.0E-03	0.1	9.0E-01	0.3	3.9E-01	-3.5	2.2E-04
ENSMUST00000078012				5.3	1.3E-02	-3.7	2.9E-02	0.8	2.8E-01	-0.1	9.6E-01
ENSMUST00000150124				5.3	1.5E-05	-3.6	9.0E-02	1.0	3.5E-01	0.2	9.1E-01
ENSMUST00000171249	nudix (nucleoside diphosphate linked moiety X)-type motif 17 [Source:MGI Symbol;Acc:MGI:1925623]		Q9CWD3	3.4	1.1E-01	-1.6	6.0E-01	-2.5	2.4E-01	2.6	3.8E-01
ENSMUST00000162197				5.3	7.1E-05	6.9	1.3E-03	-0.1	9.7E-01	-0.4	6.3E-01
ENSMUST00000140918				5.3	4.3E-04	-3.2	1.3E-01	1.0	3.8E-01	-0.9	6.6E-01
ENSMUST00000147299				5.3	2.1E-02	-3.8	1.1E-02	-0.4	4.8E-01	-0.9	5.2E-01
ENSMUST00000171260	cyclin D-type binding-protein 1 [Source:MGI Symbol;Acc:MGI:109595]		Q3TVC7	-0.5	7.3E-01	0.2	9.3E-01	-0.2	8.8E-01	-0.9	6.1E-01
ENSMUST00000171263	guanylate binding protein 7 [Source:MGI Symbol;Acc:MGI:2444421]	Q91Z40		-1.1	1.4E-01	-2.3	2.4E-02	-1.4	3.0E-02	-0.1	8.7E-01
ENSMUST00000144292				5.3	4.9E-05	6.5	5.7E-04	0.5	7.1E-01	0.2	8.2E-01
ENSMUST00000171279	poly (ADP-ribose) glycohydrolase [Source:MGI Symbol;Acc:MGI:1347094]	E9Q954		1.7	3.0E-01	-1.2	5.5E-01	-2.4	9.7E-02	0.5	8.1E-01
ENSMUST00000171284	methyltransferase like 4 [Source:MGI Symbol;Acc:MGI:1924031]		Q3U034	0.3	6.3E-01	2.6	1.7E-02	1.2	1.4E-01	-1.0	2.0E-01
ENSMUST00000171289	calcium/calmodulin-dependent protein kinase II, delta [Source:MGI Symbol;Acc:MGI:1341265]	E9Q1T1		0.0	1.0E+00	0.2	9.6E-01	-0.3	8.9E-01	-0.4	8.8E-01
ENSMUST00000143496				5.3	2.4E-03	9.0	4.4E-05	-0.9	4.9E-01	0.4	4.9E-01
ENSMUST00000171300	sulfatase modifying factor 2 [Source:MGI Symbol;Acc:MGI:1915152]		Q8BPG6	2.7	1.7E-01	2.0	3.1E-01	-2.6	1.8E-01	-1.9	2.9E-01
ENSMUST00000119390				5.3	2.6E-04	5.3	5.3E-04	-0.7	4.9E-01	-0.3	6.2E-01
ENSMUST00000126125				5.3	2.9E-06	6.4	6.5E-04	-0.7	6.2E-01	-0.3	6.4E-01
ENSMUST00000189509				5.3	4.8E-03	6.0	1.2E-03	-0.7	6.3E-01	-0.1	8.5E-01
ENSMUST00000046816				5.3	1.7E-04	-6.1	2.2E-02	0.2	8.3E-01	2.7	2.6E-01
ENSMUST00000171320				0.5	7.0E-01	-0.3	8.6E-01	-0.7	5.7E-01	0.1	9.4E-01
ENSMUST00000142806				5.3	1.2E-03	-4.9	2.0E-02	1.4	8.3E-02	0.4	8.2E-01
ENSMUST00000161696				5.3	2.4E-05	8.5	2.6E-04	0.1	9.6E-01	0.7	3.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000127057				5.3	1.4E-03	7.0	1.6E-04	1.6	1.5E-01	0.9	1.5E-01
ENSMUST00000171330	SLAM family member 6 [Source:MGI Symbol;Acc:MGI:1353620]	Q18PG5	Q9ET39	-0.6	3.2E-01	-2.0	2.0E-02	-1.3	3.1E-02	0.1	8.8E-01
ENSMUST00000148964				5.3	2.1E-02	3.8	5.0E-05	-7.4	5.4E-06	-0.6	1.2E-01
ENSMUST00000171338				-0.5	7.3E-01	-4.2	3.7E-02	-3.7	5.4E-03	0.0	9.8E-01
ENSMUST00000171340	5-oxoprolinase (ATP-hydrolysing) [Source:MGI Symbol;Acc:MGI:1922725]		Q8K010	4.6	1.0E-01	7.2	2.8E-02	-0.2	9.4E-01	-2.8	1.0E-01
ENSMUST00000187217				5.3	1.8E-02	0.3	7.1E-01	-6.8	1.5E-04	-0.5	5.2E-01
ENSMUST00000135235				5.3	1.9E-04	0.5	6.2E-01	1.2	1.1E-01	-1.7	1.3E-01
ENSMUST00000171347	cytotoxic T lymphocyte-associated protein 2 beta [Source:MGI Symbol;Acc:MGI:88555]			-0.5	6.8E-01	-1.8	1.3E-01	-3.3	6.4E-03	-2.1	1.1E-01
ENSMUST00000171348	predicted gene 11239 [Source:MGI Symbol;Acc:MGI:3702319]	E9Q5Z9		5.3	4.5E-02	2.5	4.3E-01	-0.5	8.5E-01	2.3	3.4E-01
ENSMUST00000171349	C2 calcium-dependent domain containing 5 [Source:MGI Symbol;Acc:MGI:1921991]	E9Q026		-2.4	1.9E-01	-2.1	3.5E-01	0.3	8.1E-01	0.0	1.0E+00
ENSMUST00000171352	MAP/microtubule affinity regulating kinase 2 [Source:MGI Symbol;Acc:MGI:99638]	F7A3Q3		1.3	7.3E-02	1.7	8.2E-02	0.4	5.4E-01	0.0	9.8E-01
ENSMUST00000142825				5.3	8.2E-04	6.0	2.8E-04	-0.8	4.9E-01	-0.9	2.1E-01
ENSMUST00000171366	dispatched homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1916147]		Q3TDN0	6.1	4.7E-02	-0.8	7.3E-01	-6.0	3.7E-02	0.8	6.9E-01
ENSMUST00000150480				5.3	1.4E-04	-6.1	9.2E-03	-1.5	6.8E-02	1.5	4.5E-01
ENSMUST00000171376	palmitoyl-protein thioesterase 2 [Source:MGI Symbol;Acc:MGI:1860075]		O35448	4.1	9.2E-02	2.0	4.8E-01	-1.7	5.0E-01	0.4	8.5E-01
ENSMUST00000149445				5.3	1.3E-04	0.6	4.2E-01	-4.4	2.5E-04	-0.3	6.0E-01
ENSMUST00000153127				5.3	1.4E-02	-9.2	1.7E-03	0.8	1.9E-01	-1.1	6.6E-01
ENSMUST00000171393	MAP/microtubule affinity regulating kinase 2 [Source:MGI Symbol;Acc:MGI:99638]	E9Q2J6		-0.8	3.9E-01	0.1	9.6E-01	1.9	8.5E-02	1.0	4.9E-01
ENSMUST00000143902				5.3	2.9E-03	8.0	5.2E-05	-0.6	6.1E-01	-0.5	4.2E-01
ENSMUST00000149282				5.3	1.3E-03	3.7	1.6E-02	-2.1	1.7E-01	0.2	8.1E-01
ENSMUST00000194187				5.3	4.2E-03	8.4	7.4E-04	-0.1	9.4E-01	0.9	3.1E-01
ENSMUST00000124212				5.3	4.7E-05	7.7	1.9E-04	-0.7	6.2E-01	0.2	7.7E-01
ENSMUST00000141942				5.3	1.2E-03	5.7	3.3E-02	0.0	9.9E-01	-1.0	4.8E-01
ENSMUST00000171404	general transcription factor IIIC, polypeptide 4 [Source:MGI Symbol;Acc:MGI:2138937]	E9Q2B0		0.2	9.1E-01	-0.7	8.4E-01	0.0	9.9E-01	0.9	7.5E-01
ENSMUST00000171405	mannoside acetylglucosaminyltransferase 5 [Source:MGI Symbol;Acc:MGI:894701]	Q059T5	Q8R4G6	1.0	5.1E-01	1.6	4.5E-01	0.3	8.5E-01	-0.3	8.8E-01
ENSMUST00000171409	mitochondrial calcium uptake 1 [Source:MGI Symbol;Acc:MGI:2384909]	E9Q9E0		-3.9	7.4E-02	-1.6	5.6E-01	1.5	3.9E-01	-0.8	7.7E-01
ENSMUST00000159418				5.3	1.1E-02	-6.7	2.8E-04	0.3	5.1E-01	-1.0	4.8E-01
ENSMUST00000171412	dystroglycan 1 [Source:MGI Symbol;Acc:MGI:101864]	Q544G5	Q62165	1.1	6.4E-01	4.5	9.7E-02	0.6	7.9E-01	-2.8	2.4E-01
ENSMUST00000171415	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 [Source:MGI Symbol;Acc:MGI:1914514]	Q3V406		-0.8	3.2E-01	0.6	5.9E-01	1.1	1.9E-01	-0.3	7.4E-01
ENSMUST00000075898				5.3	2.9E-04	10.7	9.7E-04	2.2	3.6E-01	0.8	4.6E-01
ENSMUST00000171419	actin, beta [Source:MGI Symbol;Acc:MGI:87904]	E9Q5F4		-4.2	3.8E-02	-5.4	1.1E-01	0.0	9.7E-01	1.3	6.9E-01
ENSMUST00000171425	complement component 5a receptor 2 [Source:MGI Symbol;Acc:MGI:2442013]	E9PVQ2		1.3	1.5E-01	0.4	6.7E-01	-1.0	2.5E-01	-0.1	8.9E-01
ENSMUST00000141153				5.3	2.6E-03	11.1	9.8E-04	-0.8	7.6E-01	1.4	2.4E-01
ENSMUST00000186403				5.3	1.1E-04	-3.7	1.3E-01	0.5	6.4E-01	-0.2	9.2E-01
ENSMUST00000191297				5.3	1.6E-04	1.3	6.3E-01	-1.5	4.8E-01	2.4	2.9E-01
ENSMUST00000171444	AT rich interactive domain 3B (BRIGHT-like) [Source:MGI Symbol;Acc:MGI:1930768]		Q9Z1N7	3.5	8.7E-02	5.0	8.6E-02	1.0	6.9E-01	-0.4	8.0E-01
ENSMUST00000171445	EPS8-like 1 [Source:MGI Symbol;Acc:MGI:1914675]	E9Q4X5		3.8	4.0E-02	5.0	7.5E-03	-2.0	2.6E-01	-3.2	1.7E-02
ENSMUST00000146235				5.3	3.4E-04	6.4	8.0E-04	-0.2	8.6E-01	0.3	6.3E-01
ENSMUST00000171456	adenylate cyclase 7 [Source:MGI Symbol;Acc:MGI:102891]		P51829	2.7	4.6E-01	0.0	1.0E+00	-2.4	5.4E-01	0.3	9.3E-01
ENSMUST00000120166				5.3	2.3E-04	4.7	3.0E-02	-1.9	3.0E-01	0.8	5.9E-01
ENSMUST00000171461	ring finger protein 14 [Source:MGI Symbol;Acc:MGI:1929668]		Q9JI90	-0.8	1.8E-01	-0.2	7.5E-01	0.5	3.7E-01	-0.1	8.8E-01
ENSMUST00000157031				5.3	7.2E-04	7.5	4.4E-04	-0.2	9.0E-01	0.1	9.2E-01
ENSMUST00000126983				5.3	2.7E-04	2.7	2.2E-02	0.0	9.7E-01	0.8	3.0E-01
ENSMUST00000171474	ring finger protein 168 [Source:MGI Symbol;Acc:MGI:1917488]	E9PYW4		3.3	1.5E-01	6.1	7.7E-02	2.6	3.5E-01	-0.1	9.6E-01
ENSMUST00000174852				5.3	1.1E-05	4.5	2.6E-03	1.2	2.5E-01	0.3	6.6E-01
ENSMUST00000149188				5.3	1.4E-02	8.1	5.6E-05	-0.9	4.8E-01	-0.2	7.4E-01
ENSMUST00000155518				5.3	6.4E-04	6.9	1.4E-04	-0.5	6.6E-01	-1.2	8.2E-02
ENSMUST00000138801				5.3	2.8E-05	5.0	4.0E-03	0.2	8.7E-01	-0.1	9.4E-01
ENSMUST00000172476				5.3	1.6E-02	-4.7	7.1E-03	-1.0	1.6E-01	-1.1	4.8E-01
ENSMUST00000130544				5.3	1.7E-02	-6.0	3.2E-03	1.0	1.1E-01	-0.9	6.0E-01
ENSMUST00000140125				5.3	9.2E-06	8.1	2.5E-04	-0.8	6.2E-01	-0.3	6.9E-01
ENSMUST00000171535				1.4	1.2E-01	2.8	1.9E-02	0.5	5.7E-01	-0.9	3.1E-01
ENSMUST00000120384				5.3	8.4E-03	6.4	7.3E-04	-0.7	6.3E-01	-0.1	8.9E-01
ENSMUST00000152735				5.3	7.9E-04	2.8	3.6E-02	-3.5	2.2E-02	-1.7	8.0E-02
ENSMUST00000124593				5.3	8.0E-04	6.1	7.7E-03	0.6	7.5E-01	0.3	7.5E-01
ENSMUST00000171549	protein tyrosine phosphatase, non-receptor type 6 [Source:MGI Symbol;Acc:MGI:96055]	Q3UCJ0	P29351	-1.7	3.4E-01	2.6	3.0E-01	2.1	3.4E-01	-2.2	2.5E-01
ENSMUST00000171557				-5.6	4.2E-02	-3.5	3.1E-01	1.2	5.3E-01	-0.9	7.9E-01
ENSMUST00000128620				5.3	1.3E-03	5.4	2.6E-02	-5.4	4.6E-02	-0.8	5.8E-01
ENSMUST00000171564	methionine-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1345633]	E9QB02		2.4	4.2E-02	-4.4	1.2E-03	-7.4	8.3E-06	-0.7	5.3E-01
ENSMUST00000130116				5.3	8.9E-04	4.8	4.0E-03	-1.4	2.9E-01	-0.9	2.8E-01
ENSMUST00000171572	dishevelled 3, dsh homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108100]	E9Q967		-0.9	1.6E-01	1.0	2.5E-01	1.3	5.8E-02	-0.6	4.3E-01
ENSMUST00000161910				5.3	2.7E-03	4.8	4.6E-02	0.1	9.6E-01	0.2	8.7E-01
ENSMUST00000171583	acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 [Source:MGI Symbol;Acc:MGI	E9PVK6		-1.3	3.7E-01	0.3	8.5E-01	1.2	3.4E-01	-0.4	8.0E-01
ENSMUST00000162310				5.3	8.5E-04	6.3	5.4E-04	1.0	4.3E-01	-1.6	4.7E-02
ENSMUST00000171587	guanylate binding protein 11 [Source:MGI Symbol;Acc:MGI:3646307]	A9YVJ5		2.5	1.5E-01	4.6	1.9E-02	-1.4	4.3E-01	-3.4	2.4E-02
ENSMUST00000171588	leukemia inhibitory factor receptor [Source:MGI Symbol;Acc:MGI:96788]		P42703	1.3	4.6E-02	1.4	7.4E-02	-0.6	3.3E-01	-0.6	3.2E-01
ENSMUST00000171569				5.3	4.0E-04	-3.7	6.3E-02	-0.4	6.4E-01	-0.5	8.0E-01
ENSMUST00000117570				5.3	3.4E-04	1.1	5.9E-01	-1.0	5.7E-01	2.2	2.3E-01
ENSMUST00000154542				5.3	3.9E-06	3.7	6.1E-03	-0.7	4.8E-01	-0.2	7.7E-01
ENSMUST00000171621	TRAF-interacting protein with forkhead-associated domain [Source:MGI Symbol;Acc:MGI:2182965]	I3PQW8	Q793I8	-0.4	8.3E-01	-2.3	3.3E-01	-0.5	7.4E-01	1.4	5.4E-01
ENSMUST00000171629	Rho guanine nucleotide exchange factor (GEF) 37 [Source:MGI Symbol;Acc:MGI:3045339]	E9Q5R6		0.6	3.2E-01	0.4	5.6E-01	-0.2	7.4E-01	0.0	9.6E-01
ENSMUST00000172432				5.2	9.8E-04	7.4	1.7E-05	-0.6	5.3E-01	-0.4	4.2E-01
ENSMUST00000121636				5.2	3.8E-03	6.7	2.2E-04	-0.6	6.3E-01	0.0	9.6E-01
ENSMUST00000145743				5.2	6.2E-03	-0.1	9.3E-01	1.6	1.5E-01	-2.8	1.1E-01
ENSMUST00000153216				5.2	3.8E-03	-4.3	2.7E-02	2.3	9.8E-03	-0.9	6.3E-01
ENSMUST00000160909				5.2	9.6E-04	5.6	3.8E-02	-0.8	7.5E-01	-0.1	9.5E-01
ENSMUST00000173076				5.2	1.7E-02	3.1	7.6E-02	0.0	9.9E-01	0.1	9.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000171645	Ras-like without CAAX 1 [Source:MGI Symbol;Acc:MGI:108053]	E9Q3Z0		-2.0	9.4E-02	-4.3	1.2E-02	-1.7	4.0E-02	0.7	6.4E-01
ENSMUST00000171654	thrombospondin, type I, domain containing 4 [Source:MGI Symbol;Acc:MGI:2672033]		Q3UTY6	6.6	4.0E-02	4.9	1.5E-01	-1.6	6.2E-01	0.1	9.7E-01
ENSMUST00000053319				5.2	4.3E-05	3.4	1.7E-02	0.8	4.4E-01	0.1	9.0E-01
ENSMUST00000126989				5.2	4.5E-04	7.8	7.1E-05	-0.7	5.9E-01	0.1	8.2E-01
ENSMUST00000148513				5.2	8.3E-06	-3.9	1.5E-01	2.1	1.1E-01	-1.0	7.1E-01
ENSMUST00000162222				5.2	9.2E-04	5.5	3.3E-03	-0.4	8.0E-01	0.0	9.6E-01
ENSMUST00000171683	cytidine and dCMP deaminase domain containing 1 [Source:MGI Symbol;Acc:MGI:1919141]		Q8BMD5	-1.6	5.9E-02	-0.3	7.0E-01	-0.1	8.8E-01	-1.3	1.5E-01
ENSMUST00000161341				5.2	5.9E-05	6.1	1.8E-04	-0.3	7.5E-01	-0.2	7.0E-01
ENSMUST00000174062				5.2	1.6E-04	6.7	2.2E-03	-0.5	7.5E-01	-0.5	6.5E-01
ENSMUST00000171688	angiogenin, ribonuclease, RNase A family, 5 [Source:MGI Symbol;Acc:MGI:88022]	Q3TBG7	P21570	0.1	9.4E-01	-2.5	1.1E-01	-0.7	4.3E-01	1.8	2.0E-01
ENSMUST00000171689	uclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 [Source:MGI Symbol;Acc:MGI:102463	Q8C443		2.5	1.7E-01	5.2	1.2E-02	-0.6	7.5E-01	-3.3	3.3E-02
ENSMUST00000133747				5.2	9.2E-04	4.3	1.6E-01	0.6	8.3E-01	2.2	2.9E-01
ENSMUST00000132533				5.2	5.8E-05	7.6	9.8E-03	-0.6	8.2E-01	-1.5	3.2E-01
ENSMUST00000188625				5.2	5.0E-06	-5.3	1.5E-02	1.0	1.6E-01	1.1	5.6E-01
ENSMUST00000157054				5.2	2.5E-04	4.5	1.3E-03	0.8	3.9E-01	-0.1	8.6E-01
ENSMUST00000171702	Rac GTPase-activating protein 1 [Source:MGI Symbol;Acc:MGI:1349423]		Q9WVM1	1.3	3.4E-01	2.3	2.4E-01	1.9	2.4E-01	0.9	5.3E-01
ENSMUST00000194441				5.2	3.0E-03	6.1	8.1E-04	-0.5	7.2E-01	-0.8	2.8E-01
ENSMUST00000128895				5.2	3.3E-04	-2.4	9.1E-02	0.7	3.5E-01	0.0	9.8E-01
ENSMUST00000134952				5.2	2.5E-02	5.4	1.6E-02	-0.7	7.2E-01	0.9	4.3E-01
ENSMUST00000184625				5.2	1.5E-05	6.6	2.4E-04	-0.5	6.9E-01	-0.7	3.1E-01
ENSMUST00000187909				5.2	9.0E-04	-3.9	1.4E-02	0.4	5.9E-01	-0.5	7.2E-01
ENSMUST00000194619				5.2	1.1E-04	4.0	2.2E-03	-0.4	6.5E-01	0.0	9.9E-01
ENSMUST00000171737	ornithine decarboxylase, structural 1 [Source:MGI Symbol;Acc:MGI:97402]		P00860	-0.6	1.7E-01	-1.2	5.0E-02	-0.9	3.5E-02	-0.4	5.1E-01
ENSMUST00000195812				5.2	4.8E-04	5.9	3.5E-05	-0.8	3.2E-01	-0.5	3.7E-01
ENSMUST00000171751	RNA binding protein, fox-1 homolog (C. elegans) 2 [Source:MGI Symbol;Acc:MGI:1933973]		Q8BP71	3.5	3.0E-01	5.6	1.2E-01	-0.6	8.8E-01	-2.6	2.6E-01
ENSMUST00000127308				5.2	2.2E-02	-2.6	2.7E-02	1.0	1.0E-01	0.0	9.9E-01
ENSMUST00000171755				-0.3	9.0E-01	-1.2	6.6E-01	-1.3	4.4E-01	-0.4	9.0E-01
ENSMUST00000147229				5.2	1.4E-04	3.7	7.8E-03	-3.3	2.9E-02	-0.7	4.0E-01
ENSMUST00000127866				5.2	4.1E-04	-1.4	2.4E-01	0.1	8.5E-01	-1.9	1.4E-01
ENSMUST00000182518				5.2	1.9E-05	-3.7	9.5E-03	0.4	4.7E-01	0.6	6.4E-01
ENSMUST00000171774	dishevelled 3, dsh homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108100]	E9Q150		-0.1	9.7E-01	-3.3	2.1E-01	-3.0	7.9E-02	0.2	9.3E-01
ENSMUST00000134904				5.2	1.4E-05	-4.4	2.2E-02	1.9	2.4E-02	-0.8	6.7E-01
ENSMUST00000174618				5.2	1.6E-04	3.6	1.7E-01	-2.5	3.5E-01	1.5	3.6E-01
ENSMUST00000131887				5.2	1.4E-04	-6.4	2.5E-04	-1.4	8.7E-03	-0.9	4.8E-01
ENSMUST00000125424				5.2	3.6E-06	2.9	1.7E-01	-4.8	4.4E-02	-0.4	7.8E-01
ENSMUST00000171795	prolyl endopeptidase-like [Source:MGI Symbol;Acc:MGI:2441932]		Q8C167	-2.5	9.8E-02	-2.0	2.9E-01	0.3	8.0E-01	-0.2	9.2E-01
ENSMUST00000181560				5.2	4.3E-04	7.7	6.3E-04	-1.6	3.7E-01	0.3	6.8E-01
ENSMUST00000182327				5.2	4.9E-04	3.0	9.7E-04	-0.1	9.1E-01	-0.1	8.4E-01
ENSMUST00000188705				5.2	1.5E-03	7.5	1.5E-04	0.0	9.8E-01	-0.1	8.2E-01
ENSMUST00000171799	cDNA sequence BC049352 [Source:MGI Symbol;Acc:MGI:3040681]	E9Q2Z6		2.8	6.5E-02	1.5	3.8E-01	-0.7	6.1E-01	0.6	6.7E-01
ENSMUST00000121713				5.2	4.2E-03	3.5	7.3E-02	-0.5	7.6E-01	2.1	1.1E-01
ENSMUST00000171808	DBF4 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1351328]	B2RS44	Q9QZ41	-3.9	4.4E-02	1.8	5.2E-01	5.4	2.5E-02	-0.3	9.0E-01
ENSMUST00000166517				5.2	8.2E-05	2.7	5.6E-02	-2.4	8.6E-02	0.2	8.5E-01
ENSMUST00000149711				5.2	1.2E-04	-2.9	1.6E-01	0.5	6.3E-01	-1.8	4.0E-01
ENSMUST00000125140				5.2	3.5E-03	6.4	6.0E-03	-0.7	7.0E-01	0.5	6.1E-01
ENSMUST00000171838	calcium binding and coiled coil domain 1 [Source:MGI Symbol;Acc:MGI:1914738]	E9Q7U2		0.0	9.8E-01	1.2	1.3E-01	-0.1	8.2E-01	-1.4	8.0E-02
ENSMUST00000145247				5.2	1.2E-03	7.4	5.0E-05	-0.6	6.1E-01	0.0	9.5E-01
ENSMUST00000195579				5.2	7.4E-05	5.5	4.8E-02	-0.8	7.5E-01	-0.6	6.9E-01
ENSMUST00000144274				5.2	1.9E-03	6.2	5.1E-04	-1.9	1.8E-01	0.4	6.2E-01
ENSMUST00000171861	exportin 6 [Source:MGI Symbol;Acc:MGI:2429950]	F6YJ47		-7.1	6.7E-02	-4.1	3.0E-01	0.8	6.8E-01	-2.2	6.2E-01
ENSMUST00000195398				5.2	7.8E-04	5.4	2.6E-04	-2.0	7.7E-02	-0.5	4.4E-01
ENSMUST00000155463				5.2	6.6E-04	4.5	2.9E-03	-2.0	1.4E-01	-1.2	1.6E-01
ENSMUST00000181673				5.2	6.6E-04	0.6	5.0E-01	-1.3	9.7E-02	0.2	7.9E-01
ENSMUST00000113402				5.2	4.8E-06	6.8	4.5E-03	-0.6	7.7E-01	-2.0	9.4E-02
ENSMUST00000171912	U2 small nuclear RNA auxiliary factor 1-like 4 [Source:MGI Symbol;Acc:MGI:2678374]		Q8BGJ9	-1.6	5.4E-01	-1.5	5.3E-01	-2.5	1.9E-01	-2.5	3.6E-01
ENSMUST00000114853				5.2	2.0E-06	6.8	2.0E-04	-0.5	6.8E-01	-1.4	5.4E-02
ENSMUST00000171920				-1.2	2.0E-01	-2.9	9.3E-02	0.1	8.8E-01	1.8	2.6E-01
ENSMUST00000171922				2.3	4.9E-02	4.1	1.6E-02	0.9	4.9E-01	-0.9	3.5E-01
ENSMUST00000178244				5.2	2.9E-05	4.5	7.6E-02	-0.7	7.7E-01	0.5	7.4E-01
ENSMUST00000156725				5.2	9.2E-07	5.3	3.0E-04	0.0	9.6E-01	-0.3	6.7E-01
ENSMUST00000171929	centromere protein F [Source:MGI Symbol;Acc:MGI:1313302]	E9Q3P4		0.9	9.6E-02	0.5	3.7E-01	-0.6	2.5E-01	-0.2	6.8E-01
ENSMUST00000142435				5.2	9.9E-04	5.6	2.1E-02	-0.6	7.9E-01	-1.4	2.9E-01
ENSMUST00000171942	vomeronasal 2, receptor 40 [Source:MGI Symbol;Acc:MGI:3757872]	F6W043		4.1	8.1E-02	3.0	2.7E-01	-0.3	9.1E-01	0.7	7.0E-01
ENSMUST00000133842				5.2	6.4E-05	10.4	1.5E-05	-0.4	7.9E-01	-0.8	1.0E-01
ENSMUST00000124145				5.2	1.2E-04	-3.8	2.4E-01	2.0	2.7E-01	0.1	9.7E-01
ENSMUST00000125824				5.2	9.4E-03	5.4	2.6E-03	-1.6	2.9E-01	0.8	3.6E-01
ENSMUST00000156215				5.2	4.6E-05	7.0	2.5E-04	-0.2	9.0E-01	-0.1	8.2E-01
ENSMUST00000124701				5.2	1.5E-04	-2.6	2.1E-02	1.3	2.9E-02	-0.1	9.1E-01
ENSMUST00000131797				5.2	1.5E-02	1.1	4.6E-01	-1.2	3.7E-01	2.0	1.0E-01
ENSMUST00000119875				5.2	6.0E-04	4.4	7.1E-03	0.2	8.9E-01	0.1	9.4E-01
ENSMUST00000171986	RAB11 family interacting protein 2 (class I) [Source:MGI Symbol;Acc:MGI:1922248]	G3UW57		0.1	8.9E-01	1.1	2.8E-01	0.1	9.0E-01	-0.9	3.4E-01
ENSMUST00000188598				5.2	1.9E-05	8.2	5.0E-05	-0.5	6.8E-01	-0.3	5.8E-01
ENSMUST00000128188				5.2	1.1E-02	6.5	1.7E-03	-0.4	8.0E-01	-0.8	3.9E-01
ENSMUST00000142946				5.2	9.6E-06	-1.8	4.0E-01	-3.4	5.2E-02	2.9	1.6E-01
ENSMUST00000017077				5.2	1.0E-02	6.6	1.8E-03	-0.6	7.1E-01	-0.6	5.1E-01
ENSMUST00000132790				5.2	2.3E-04	6.4	3.3E-04	0.0	9.9E-01	0.8	2.5E-01
ENSMUST00000172013	ubiquitin fusion degradation 1 like [Source:MGI Symbol;Acc:MGI:109353]	E9Q646		-2.2	3.3E-01	-4.3	1.1E-01	-2.7	7.9E-02	-0.7	8.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000172015	potassium inwardly-rectifying channel, subfamily J, member 1 [Source:MGI Symbol;Acc:MGI:1927248]	G3UWE7		3.4	1.1E-01	6.8	8.2E-03	0.4	8.5E-01	-3.0	5.0E-02
ENSMUST00000185261				5.2	2.9E-03	4.1	1.3E-03	0.3	6.9E-01	-0.6	3.6E-01
ENSMUST00000172018	WW domain containing adaptor with coiled-coil [Source:MGI Symbol;Acc:MGI:2387357]	E9Q5D5		-0.8	7.7E-01	-1.3	7.3E-01	-0.9	7.2E-01	-0.5	9.0E-01
ENSMUST00000129659				5.2	2.5E-02	-1.6	3.7E-01	1.2	2.5E-01	-2.0	3.0E-01
ENSMUST00000172031	inositol polyphosphate-4-phosphatase, type II [Source:MGI Symbol;Acc:MGI:2158925]	E9PVM1		1.0	2.0E-01	0.5	5.7E-01	-0.6	4.5E-01	-0.1	9.4E-01
ENSMUST00000148707				5.2	3.0E-05	7.1	1.9E-04	-0.6	6.1E-01	-0.7	3.1E-01
ENSMUST00000172035	gem (nuclear organelle) associated protein 5 [Source:MGI Symbol;Acc:MGI:2449311]	E9PUU4		0.9	1.8E-01	2.4	8.0E-03	0.2	7.1E-01	-1.3	6.0E-02
ENSMUST00000182234				5.2	1.0E-03	2.5	3.0E-02	-3.0	1.1E-02	-0.4	6.0E-01
ENSMUST00000172069	cytochrome P450, family 27, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1098274]	E9Q3C2		3.5	1.6E-01	5.0	7.3E-02	-0.5	8.6E-01	-2.0	2.7E-01
ENSMUST00000132060				5.2	3.2E-04	5.0	6.1E-03	1.3	3.9E-01	0.6	4.7E-01
ENSMUST00000135354				5.2	3.3E-03	4.9	5.8E-05	-1.5	6.5E-02	0.6	1.8E-01
ENSMUST00000172088	zinc finger protein 239 [Source:MGI Symbol;Acc:MGI:1306812]		P24399	3.0	9.9E-02	0.9	6.1E-01	-2.4	1.8E-01	-0.3	8.5E-01
ENSMUST00000152694				5.2	9.4E-03	7.7	2.9E-05	-0.5	6.3E-01	-1.1	6.4E-02
ENSMUST00000118893				5.2	2.2E-04	4.3	3.1E-02	1.1	5.0E-01	1.0	3.7E-01
ENSMUST00000132265				5.2	3.1E-04	-3.6	6.1E-04	-0.2	6.3E-01	0.0	9.7E-01
ENSMUST00000172122	RNA binding motif protein 26 [Source:MGI Symbol;Acc:MGI:1921463]			-2.1	8.0E-02	-1.2	3.5E-01	0.1	8.8E-01	-0.7	5.7E-01
ENSMUST00000137973				5.2	3.1E-04	-4.4	4.6E-04	0.1	7.5E-01	-0.6	5.2E-01
ENSMUST00000172136	PWWP domain containing 2B [Source:MGI Symbol;Acc:MGI:2142008]	E9Q9M8		1.9	4.1E-01	5.0	9.8E-02	0.2	9.3E-01	-2.8	1.8E-01
ENSMUST00000155403				5.2	2.9E-04	5.5	4.2E-03	-0.4	8.0E-01	-0.5	5.4E-01
ENSMUST00000100641				5.2	2.7E-04	-3.4	5.5E-03	0.7	1.8E-01	0.0	1.0E+00
ENSMUST00000172153	thyroglobulin [Source:MGI Symbol;Acc:MGI:98733]	F7AYJ4		-3.7	5.6E-02	-1.5	5.4E-01	1.6	3.0E-01	-0.6	7.9E-01
ENSMUST00000172154	activating transcription factor 1 [Source:MGI Symbol;Acc:MGI:1298366]	E9PWM8		-0.7	6.2E-01	-1.1	4.7E-01	-1.5	1.8E-01	-1.1	4.6E-01
ENSMUST00000161105				5.2	5.5E-03	5.4	5.1E-05	0.0	9.6E-01	0.1	7.7E-01
ENSMUST00000119909				5.2	1.3E-03	4.1	5.3E-03	-0.8	4.9E-01	-0.2	8.5E-01
ENSMUST00000133579				5.2	4.4E-03	5.7	2.6E-04	-2.0	1.0E-01	0.1	8.6E-01
ENSMUST00000122873				5.2	9.0E-04	-3.2	8.2E-02	1.5	1.5E-01	-1.6	3.8E-01
ENSMUST00000172170	GTP binding protein 2 [Source:MGI Symbol;Acc:MGI:1860138]	E9QA45		-3.2	2.2E-01	1.6	5.4E-01	2.8	2.3E-01	-2.0	4.4E-01
ENSMUST00000194065				5.2	4.3E-04	3.5	4.3E-03	0.3	6.9E-01	-0.9	2.4E-01
ENSMUST00000124124				5.2	6.2E-03	5.8	5.5E-04	-0.6	6.5E-01	-0.3	6.6E-01
ENSMUST00000029664				5.2	8.9E-03	5.9	2.0E-03	-0.5	7.5E-01	-1.3	1.5E-01
ENSMUST00000154964				5.2	2.4E-04	7.2	5.8E-05	-0.6	6.1E-01	-1.7	1.9E-02
ENSMUST00000182445				5.2	3.8E-06	7.0	4.8E-04	-0.6	6.7E-01	-0.2	7.5E-01
ENSMUST00000137217				5.2	3.9E-04	-0.9	4.3E-01	1.0	2.4E-01	-4.9	8.4E-03
ENSMUST00000154581				5.2	2.0E-04	6.5	4.3E-04	-0.6	6.2E-01	-0.7	3.2E-01
ENSMUST00000172235	ring finger protein 213 [Source:MGI Symbol;Acc:MGI:1289196]	Q3U0U2		-3.9	3.7E-02	-4.6	1.1E-01	-0.1	9.5E-01	0.6	8.2E-01
ENSMUST00000172237	endothelin receptor type B [Source:MGI Symbol;Acc:MGI:102720]		P48302	6.1	4.9E-02	-4.6	2.9E-02	-10.3	2.0E-03	0.3	8.8E-01
ENSMUST00000170369				5.2	2.9E-04	-8.0	1.7E-02	0.7	4.0E-01	2.8	3.4E-01
ENSMUST00000183928				5.2	1.3E-04	2.4	6.1E-03	-0.3	6.3E-01	-0.5	4.3E-01
ENSMUST00000191966				5.2	2.9E-05	-5.8	5.7E-03	0.6	3.7E-01	-1.1	5.5E-01
ENSMUST00000192049				5.2	3.7E-05	7.3	1.2E-02	-0.6	8.4E-01	-1.3	4.1E-01
ENSMUST00000194566				5.2	5.9E-03	5.9	1.7E-02	-1.0	6.6E-01	-0.6	6.5E-01
ENSMUST00000153075				5.2	3.0E-02	8.6	3.2E-05	-0.1	9.2E-01	0.3	6.2E-01
ENSMUST00000153729				5.2	2.2E-03	-7.0	1.7E-03	0.0	9.3E-01	2.5	1.6E-01
ENSMUST00000161754				5.2	9.0E-04	5.1	4.8E-02	-0.5	8.4E-01	-0.6	6.9E-01
ENSMUST00000117789				5.2	7.6E-04	7.6	3.4E-05	-0.5	6.3E-01	-0.3	5.7E-01
ENSMUST00000132029				5.2	4.9E-04	-3.0	1.5E-01	0.5	6.7E-01	-2.1	3.7E-01
ENSMUST00000149843				5.2	8.7E-05	-3.1	2.0E-02	1.6	2.0E-02	-2.0	1.7E-01
ENSMUST00000172284	WD repeat domain 4 [Source:MGI Symbol;Acc:MGI:1889002]	F6YNC4		1.4	5.9E-01	1.1	8.0E-01	1.3	6.7E-01	1.6	6.7E-01
ENSMUST00000177704				5.2	1.5E-03	6.9	1.5E-04	-0.5	6.7E-01	-0.7	2.7E-01
ENSMUST00000182622				5.2	1.6E-03	-2.8	6.8E-02	1.3	1.2E-01	0.8	5.5E-01
ENSMUST00000187136				5.2	6.9E-05	5.6	9.6E-03	-1.1	5.3E-01	0.3	7.9E-01
ENSMUST00000123165				5.2	3.2E-04	6.0	1.4E-02	-0.6	7.8E-01	-1.6	2.3E-01
ENSMUST00000172302	very low density lipoprotein receptor [Source:MGI Symbol;Acc:MGI:98935]	Q91YY0		2.7	7.0E-02	4.6	7.2E-03	-0.6	6.9E-01	-2.4	4.3E-02
ENSMUST00000172303	myosin XVIIIA [Source:MGI Symbol;Acc:MGI:2667185]		Q9JMH9	-3.2	9.4E-02	-1.6	5.6E-01	1.9	3.4E-01	0.2	9.2E-01
ENSMUST00000172306	dual specificity phosphatase 7 [Source:MGI Symbol;Acc:MGI:2387100]		Q91Z46	-0.4	3.8E-01	0.3	6.3E-01	0.7	1.0E-01	0.1	9.0E-01
ENSMUST00000060415				5.2	8.8E-04	2.4	3.3E-01	-0.7	7.3E-01	2.2	2.6E-01
ENSMUST00000184282				5.2	1.3E-04	-5.8	1.1E-05	0.2	5.3E-01	-0.9	2.4E-01
ENSMUST00000172321	CD8 antigen, alpha chain [Source:MGI Symbol;Acc:MGI:88346]	Q8CAX3		2.8	4.6E-01	2.3	6.5E-01	0.1	9.9E-01	0.6	8.7E-01
ENSMUST00000116168				5.2	1.6E-03	-0.8	2.4E-01	1.4	1.1E-02	-0.6	3.8E-01
ENSMUST00000120439				5.2	3.4E-02	-6.3	1.1E-03	-0.2	6.8E-01	-0.6	6.7E-01
ENSMUST00000172336				-0.4	5.6E-01	0.0	9.8E-01	0.4	5.6E-01	0.0	9.6E-01
ENSMUST00000167964				5.2	3.3E-05	6.2	1.9E-04	-0.5	6.4E-01	-2.1	7.4E-03
ENSMUST00000172352	T-box 6 [Source:MGI Symbol;Acc:MGI:102539]		P70327	-1.2	3.8E-01	-0.8	7.1E-01	1.3	3.9E-01	0.9	5.9E-01
ENSMUST00000173338				5.2	1.1E-03	6.2	3.4E-04	0.2	8.5E-01	0.2	7.8E-01
ENSMUST00000140111				5.2	3.7E-07	6.5	1.1E-03	-0.6	7.0E-01	-2.0	4.1E-02
ENSMUST00000176562				5.2	2.6E-04	2.4	6.1E-03	-0.7	2.4E-01	-0.8	1.8E-01
ENSMUST00000172362	protein phosphatase 6, regulatory subunit 3 [Source:MGI Symbol;Acc:MGI:1921807]		Q922D4	-3.4	5.9E-02	-2.1	2.9E-01	0.5	6.8E-01	-0.8	6.9E-01
ENSMUST00000146530				5.2	5.5E-03	5.2	2.1E-03	-2.0	1.7E-01	-1.3	1.8E-01
ENSMUST00000119441				5.2	1.6E-03	4.1	8.3E-03	0.1	9.0E-01	-0.9	3.3E-01
ENSMUST00000124892				5.2	5.1E-04	3.0	5.1E-04	0.1	9.0E-01	0.2	7.1E-01
ENSMUST00000112197				5.2	1.8E-05	7.9	5.8E-05	-0.5	6.9E-01	-1.9	1.1E-02
ENSMUST00000172387	mitochondrial ribosomal protein L13 [Source:MGI Symbol;Acc:MGI:2137218]		Q9D1P0	-1.3	4.9E-02	-2.2	9.6E-03	-1.6	6.9E-03	-0.7	3.6E-01
ENSMUST00000150257				5.2	1.2E-03	6.3	2.9E-04	-0.5	6.5E-01	-0.3	5.9E-01
ENSMUST00000150507				5.2	6.0E-04	8.8	4.6E-05	-0.7	6.0E-01	0.2	7.0E-01
ENSMUST00000123479				5.2	5.4E-04	4.8	8.3E-04	-0.5	6.2E-01	-0.2	7.2E-01
ENSMUST00000137925				5.2	2.4E-05	3.4	5.1E-01	11.3	5.8E-03	0.9	8.4E-01
ENSMUST00000172409	Ena-vasodilator stimulated phosphoprotein [Source:MGI Symbol;Acc:MGI:1194884]	E9PVP4		-1.2	1.6E-01	-0.7	5.0E-01	-0.1	9.3E-01	-0.6	5.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000172416	INO80 complex subunit D [Source:MGI Symbol;Acc:MGI:3027003]	B1AT32		-3.5	7.2E-02	-5.3	1.3E-01	0.6	6.6E-01	2.4	4.7E-01
ENSMUST00000155049				5.2	4.9E-04	-3.9	1.7E-02	0.6	3.5E-01	0.4	7.9E-01
ENSMUST00000172429	proline-rich polypeptide 3 [Source:MGI Symbol;Acc:MGI:1922460]	Q3V0R7		0.6	2.3E-01	1.0	1.2E-01	0.7	1.9E-01	0.2	7.5E-01
ENSMUST00000176080				5.2	1.6E-04	7.0	2.0E-04	-0.6	6.3E-01	-4.2	8.4E-04
ENSMUST00000137975				5.2	1.9E-02	6.2	5.6E-04	-0.5	7.1E-01	-1.4	7.8E-02
ENSMUST00000161687				5.2	9.2E-05	5.5	2.6E-03	1.1	3.9E-01	-1.6	9.7E-02
ENSMUST00000133966				5.1	1.9E-03	5.6	6.3E-04	-0.5	6.5E-01	0.5	4.8E-01
ENSMUST00000172442				0.3	7.4E-01	0.2	8.6E-01	0.3	7.3E-01	0.4	7.2E-01
ENSMUST00000172444				2.1	2.9E-01	-3.0	1.8E-01	-5.9	4.1E-03	-0.7	7.5E-01
ENSMUST00000151649				5.1	5.6E-05	-1.7	1.3E-02	0.4	2.8E-01	-0.1	9.2E-01
ENSMUST00000172452	uridine phosphorylase 1 [Source:MGI Symbol;Acc:MGI:1097668]	E9Q391		-2.0	8.2E-02	0.2	8.5E-01	1.4	1.4E-01	-0.9	4.9E-01
ENSMUST00000166450				5.1	7.8E-03	-1.6	4.5E-01	1.6	2.6E-01	-0.7	7.3E-01
ENSMUST00000173681				5.1	1.4E-02	-1.7	1.4E-01	-0.2	8.0E-01	-1.2	3.1E-01
ENSMUST00000177007				5.1	2.0E-02	4.9	2.7E-04	-0.3	7.2E-01	-0.2	6.8E-01
ENSMUST00000172466	neurexin I [Source:MGI Symbol;Acc:MGI:1096391]	A0A0H2UH29		5.1	5.8E-02	4.5	1.2E-01	-0.7	8.0E-01	-0.1	9.8E-01
ENSMUST00000172467	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b [Source:MGI Symbol;Acc:MGI:1330302]		Q9Z188	4.3	9.0E-02	0.1	9.6E-01	-4.5	8.0E-02	-0.3	8.6E-01
ENSMUST00000156568				5.1	2.4E-03	3.2	1.6E-01	-1.0	6.3E-01	1.0	5.3E-01
ENSMUST00000172482	dynamin 2 [Source:MGI Symbol;Acc:MGI:109547]		P39054	-1.5	6.5E-01	2.9	4.8E-01	3.6	2.4E-01	-0.8	8.4E-01
ENSMUST00000172484				3.9	9.8E-02	6.0	3.1E-02	-0.2	9.3E-01	-2.3	1.3E-01
ENSMUST00000172489				2.0	2.9E-01	-1.1	6.9E-01	-1.5	3.7E-01	1.6	5.5E-01
ENSMUST00000183311				5.1	8.1E-05	5.1	8.9E-05	-2.6	1.1E-02	-0.2	7.1E-01
ENSMUST00000118446				5.1	1.0E-03	7.1	5.2E-05	-1.3	2.6E-01	-0.4	4.9E-01
ENSMUST00000128824				5.1	1.2E-03	-5.2	1.7E-02	0.8	2.7E-01	0.8	6.8E-01
ENSMUST00000155625				5.1	1.0E-02	0.5	8.0E-01	3.2	2.9E-02	-0.8	6.4E-01
ENSMUST00000144249				5.1	9.3E-05	-6.4	9.9E-03	-0.8	2.9E-01	0.9	6.6E-01
ENSMUST00000159385				5.1	1.4E-03	-6.8	8.9E-04	-0.5	3.2E-01	-0.3	8.4E-01
ENSMUST00000131043				5.1	1.2E-04	6.5	1.2E-04	0.4	6.9E-01	0.2	7.0E-01
ENSMUST00000144116				5.1	1.2E-04	-7.3	5.6E-04	0.8	1.1E-01	-0.6	7.2E-01
ENSMUST00000133285				5.1	1.1E-03	5.1	3.3E-02	1.8	3.7E-01	1.2	3.5E-01
ENSMUST00000172533	ucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase [Source:MGI Symbol;Acc:MGI:135495	G3UYD5		-3.2	5.8E-02	-1.3	5.3E-01	1.2	3.8E-01	-0.6	7.5E-01
ENSMUST00000125160				5.1	9.9E-06	-2.1	4.7E-02	0.1	8.2E-01	-0.8	4.3E-01
ENSMUST00000130133				5.1	5.8E-05	3.6	2.3E-03	-1.5	1.2E-01	0.9	2.1E-01
ENSMUST00000130737				5.1	1.0E-03	7.3	5.4E-05	0.9	3.8E-01	-0.5	3.9E-01
ENSMUST00000140392				5.1	1.1E-03	-0.6	5.6E-01	-0.1	8.9E-01	-2.8	3.7E-02
ENSMUST00000126638				5.1	1.6E-03	-3.0	8.5E-02	2.1	2.1E-02	-0.6	7.2E-01
ENSMUST00000172559	MAS-related GPR, member A2B [Source:MGI Symbol;Acc:MGI:3033098]	K4DID7		3.8	1.3E-01	2.8	3.3E-01	-0.2	9.4E-01	0.8	6.9E-01
ENSMUST00000155247				5.1	1.8E-04	8.6	4.6E-04	-0.8	6.6E-01	-0.6	4.4E-01
ENSMUST00000141029				5.1	1.3E-03	3.8	2.0E-01	-0.8	7.8E-01	1.6	3.9E-01
ENSMUST00000130056				5.1	1.0E-03	-3.4	2.9E-04	-0.5	2.2E-01	-1.6	3.5E-02
ENSMUST00000143714				5.1	1.2E-05	1.3	6.3E-01	-0.8	6.9E-01	5.5	3.1E-02
ENSMUST00000172578	KH domain containing 3, subcortical maternal complex member [Source:MGI Symbol;Acc:MGI:1914241]	G3UXW5		0.4	6.3E-01	0.1	9.6E-01	0.6	5.3E-01	0.9	3.9E-01
ENSMUST00000123503				5.1	1.1E-04	8.4	3.1E-05	-0.9	4.7E-01	0.0	9.9E-01
ENSMUST00000193937				5.1	5.2E-03	5.9	1.3E-03	0.8	5.3E-01	-1.0	2.0E-01
ENSMUST00000144318				5.1	8.2E-04	-1.9	6.1E-02	-0.1	9.1E-01	-3.6	1.1E-02
ENSMUST00000153173				5.1	9.0E-06	-1.1	2.6E-01	0.3	6.6E-01	-2.4	4.3E-02
ENSMUST00000172599				-0.3	5.2E-01	-1.1	1.0E-01	-0.6	1.5E-01	0.2	7.9E-01
ENSMUST00000172602	family with sequence similarity 161, member A [Source:MGI Symbol;Acc:MGI:1921123]	B1AVK0		4.7	5.7E-02	3.1	1.7E-01	-2.9	2.5E-01	-1.4	3.7E-01
ENSMUST00000191744				5.1	4.7E-05	2.8	8.8E-02	-1.3	3.6E-01	-0.6	6.2E-01
ENSMUST00000132178				5.1	1.3E-03	-1.1	1.8E-01	1.6	1.1E-02	0.0	9.9E-01
ENSMUST00000121510				5.1	3.4E-03	3.1	1.5E-03	-1.4	4.3E-02	0.8	1.6E-01
ENSMUST00000156175				5.1	1.2E-04	6.7	1.3E-04	-1.1	3.3E-01	-0.9	1.6E-01
ENSMUST00000146000				5.1	3.9E-05	5.2	1.9E-04	-3.2	8.9E-03	0.3	5.7E-01
ENSMUST00000152715				5.1	4.4E-03	6.7	7.9E-03	0.6	7.9E-01	-1.2	3.1E-01
ENSMUST00000127355				5.1	1.8E-02	2.8	2.2E-01	-2.8	2.3E-01	1.7	2.9E-01
ENSMUST00000172633				-0.7	1.5E-01	-0.9	1.3E-01	-0.8	5.0E-02	-0.7	2.2E-01
ENSMUST00000172637				-0.1	9.5E-01	1.7	3.6E-01	0.5	7.6E-01	-1.3	3.7E-01
ENSMUST00000186198				5.1	1.5E-03	4.9	5.7E-05	-0.8	2.4E-01	0.3	5.4E-01
ENSMUST00000126850				5.1	3.1E-05	3.5	9.6E-02	-0.6	7.6E-01	2.1	1.3E-01
ENSMUST00000132594				5.1	5.6E-03	-0.7	4.0E-01	0.5	4.5E-01	-2.4	3.0E-02
ENSMUST00000131517				5.1	6.2E-05	9.8	3.0E-04	-0.9	6.6E-01	-0.7	4.2E-01
ENSMUST00000152836				5.1	1.0E-03	5.0	3.1E-03	-1.2	4.1E-01	-0.2	8.1E-01
ENSMUST00000172660				-0.4	7.7E-01	1.5	4.5E-01	2.2	1.2E-01	0.3	8.9E-01
ENSMUST00000172667	double homeobox B-like 1 [Source:MGI Symbol;Acc:MGI:1916048]	Q3UY88		2.9	2.0E-01	3.6	1.5E-01	-0.5	8.5E-01	-1.1	5.2E-01
ENSMUST00000153776				5.1	1.1E-03	4.8	2.1E-03	-0.6	6.2E-01	-0.8	3.5E-01
ENSMUST00000186281				5.1	6.2E-04	6.1	1.1E-02	-0.4	8.4E-01	1.5	2.1E-01
ENSMUST00000180673				5.1	2.1E-04	7.0	4.8E-04	-0.2	8.9E-01	-0.6	4.0E-01
ENSMUST00000173911				5.1	2.0E-02	5.2	1.3E-04	0.0	9.5E-01	0.0	9.4E-01
ENSMUST00000125118				5.1	7.2E-03	7.5	1.9E-04	-0.4	7.6E-01	-0.6	4.0E-01
ENSMUST00000144376				5.1	1.9E-03	4.3	1.6E-02	1.1	4.4E-01	1.8	8.8E-02
ENSMUST00000172693	allograft inflammatory factor 1 [Source:MGI Symbol;Acc:MGI:1343098]	Q4FJL9	O70200	-3.4	1.3E-01	-6.0	5.3E-02	-2.6	8.1E-02	0.0	9.9E-01
ENSMUST00000172695	poly(A) binding protein, nuclear 1 [Source:MGI Symbol;Acc:MGI:1859158]	G3UX74		-0.9	7.0E-01	-3.1	3.1E-01	-2.6	1.6E-01	-0.4	9.0E-01
ENSMUST00000154805				5.1	1.1E-04	3.2	1.0E-01	-0.5	7.9E-01	2.7	4.7E-02
ENSMUST00000133738				5.1	5.3E-04	4.2	6.2E-04	-2.1	3.1E-02	0.7	2.3E-01
ENSMUST00000172702	checkpoint kinase 1 [Source:MGI Symbol;Acc:MGI:1202065]		O35280	5.4	3.6E-02	3.1	1.2E-01	-3.3	1.6E-01	-1.0	5.2E-01
ENSMUST00000173787				5.1	5.2E-03	6.3	5.8E-04	-0.3	7.9E-01	0.1	9.3E-01
ENSMUST00000172711	tripartite motif-containing 40 [Source:MGI Symbol;Acc:MGI:2684881]	B7ZWG4		5.6	3.8E-02	3.8	1.9E-01	-0.7	8.1E-01	1.1	5.3E-01
ENSMUST00000179479				5.1	5.0E-04	9.4	3.6E-07	0.6	3.9E-01	0.7	7.0E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000149334				5.1	3.4E-03	4.4	6.4E-03	0.4	7.3E-01	1.3	1.4E-01
ENSMUST00000172732	replication factor C (activator 1) 1 [Source:MGI Symbol;Acc:MGI:97891]	G3UZD0		-2.5	1.8E-01	-3.7	1.3E-01	-0.2	8.6E-01	1.0	6.7E-01
ENSMUST00000149658				5.1	8.7E-05	-5.4	4.3E-04	0.6	1.5E-01	-0.8	4.8E-01
ENSMUST00000172734	aldehyde dehydrogenase family 7, member A1 [Source:MGI Symbol;Acc:MGI:108186]	G3UYR8		2.6	5.1E-02	6.0	5.2E-04	-0.5	6.8E-01	-3.9	1.7E-03
ENSMUST00000061823				5.1	2.1E-05	-6.8	4.4E-05	-0.1	8.3E-01	-0.8	4.6E-01
ENSMUST00000172739				3.2	3.7E-02	4.4	1.5E-02	0.1	9.4E-01	-1.1	3.3E-01
ENSMUST00000172740				0.2	9.0E-01	0.4	8.1E-01	-0.7	5.7E-01	-0.9	5.6E-01
ENSMUST00000124069				5.1	1.5E-02	7.7	1.9E-02	-0.7	8.1E-01	-1.8	2.7E-01
ENSMUST00000130408				5.1	6.2E-04	10.0	9.0E-06	2.2	6.6E-02	0.1	8.6E-01
ENSMUST00000135482				5.1	1.3E-02	6.3	3.4E-04	-0.5	7.0E-01	-1.9	1.9E-02
ENSMUST00000185750				5.1	2.3E-04	2.1	5.4E-03	-0.4	5.0E-01	-0.2	7.1E-01
ENSMUST00000127616				5.1	1.4E-03	6.5	3.4E-04	-0.6	6.6E-01	-0.3	6.9E-01
ENSMUST00000172755				-0.2	8.8E-01	-1.8	4.7E-01	0.8	6.3E-01	2.3	2.9E-01
ENSMUST00000172757				-2.0	2.6E-01	0.0	9.9E-01	1.0	5.7E-01	-1.0	6.3E-01
ENSMUST00000172761	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b [Source:MGI Symbol;Acc:MGI:1330302]		Q9Z188	-1.3	4.0E-01	2.0	3.1E-01	1.6	3.4E-01	-1.7	3.1E-01
ENSMUST00000160498				5.1	3.7E-05	-6.4	2.3E-02	0.7	4.1E-01	-0.9	7.4E-01
ENSMUST00000119086				5.1	1.1E-02	6.9	3.1E-04	-0.7	6.1E-01	-0.3	6.8E-01
ENSMUST00000120729				5.1	1.8E-03	-3.7	2.3E-03	0.4	3.8E-01	-0.8	4.2E-01
ENSMUST00000126941				5.1	1.5E-02	6.2	2.8E-04	-0.7	5.6E-01	-1.1	1.4E-01
ENSMUST00000127475				5.1	6.4E-04	3.2	5.3E-03	0.0	9.7E-01	0.0	9.7E-01
ENSMUST00000134016				5.1	2.0E-04	1.7	3.9E-01	5.5	4.8E-03	-1.0	5.7E-01
ENSMUST00000172780				-2.9	2.1E-01	1.8	6.0E-01	4.6	9.6E-02	-0.1	9.7E-01
ENSMUST00000172782				0.0	9.6E-01	0.8	2.8E-01	0.1	9.2E-01	-0.8	2.9E-01
ENSMUST00000172783	tumor necrosis factor, alpha-induced protein 2 [Source:MGI Symbol;Acc:MGI:104960]	G3UXC6		-3.0	1.5E-01	-0.3	9.0E-01	1.9	2.7E-01	-0.8	7.7E-01
ENSMUST00000134820				5.1	5.7E-05	-6.5	2.4E-04	1.0	6.3E-02	0.2	8.5E-01
ENSMUST00000118518				5.1	4.6E-04	6.9	8.7E-05	-0.5	6.3E-01	-1.4	4.0E-02
ENSMUST00000172789	gamma-aminobutyric acid (GABA) B receptor, 1 [Source:MGI Symbol;Acc:MGI:1860139]	Q3TWR2		2.0	5.7E-02	2.9	5.1E-02	0.8	5.2E-01	-0.1	8.9E-01
ENSMUST00000136355				5.1	1.8E-04	3.2	4.2E-02	1.0	4.2E-01	1.2	2.4E-01
ENSMUST00000172794	GRB10 interacting GYF protein 2 [Source:MGI Symbol;Acc:MGI:2138584]	G3UYG6		-0.1	9.7E-01	3.3	3.3E-01	3.2	1.7E-01	-0.2	9.5E-01
ENSMUST00000172795	cytochrome b5 reductase 1 [Source:MGI Symbol;Acc:MGI:1919267]	G3UXV8		-2.1	1.2E-01	-1.1	4.3E-01	0.0	9.7E-01	-1.0	5.2E-01
ENSMUST00000155838				5.1	3.1E-04	3.7	4.9E-04	-0.3	6.2E-01	0.6	2.2E-01
ENSMUST00000124851				5.1	4.2E-04	-5.7	1.1E-02	-0.9	2.4E-01	1.6	3.8E-01
ENSMUST00000144804				5.1	1.0E-03	7.6	2.2E-05	-0.4	7.2E-01	0.4	4.0E-01
ENSMUST00000172809	G protein pathway suppressor 1 [Source:MGI Symbol;Acc:MGI:2384801]	G3UXW9		-2.0	1.5E-01	1.0	4.2E-01	-0.1	9.1E-01	-3.1	2.8E-02
ENSMUST00000172815	predicted gene, 19345 [Source:MGI Symbol;Acc:MGI:5011530]	G3UYD9		1.6	7.6E-02	2.0	5.1E-02	-0.5	5.2E-01	-1.0	2.4E-01
ENSMUST00000172818	praja 2, RING-H2 motif containing [Source:MGI Symbol;Acc:MGI:2159342]		Q80U04	-2.3	1.4E-01	-5.4	2.3E-02	-1.2	2.7E-01	1.9	3.7E-01
ENSMUST00000151475				5.1	7.6E-04	5.5	1.4E-03	-0.5	6.9E-01	-0.1	9.3E-01
ENSMUST00000178186				5.1	1.5E-03	5.9	7.9E-02	-0.9	7.9E-01	0.4	8.1E-01
ENSMUST00000159114				5.1	4.9E-04	-5.7	6.5E-04	0.1	8.1E-01	0.0	9.8E-01
ENSMUST00000172831	regulator of G-protein signalling 22 [Source:MGI Symbol;Acc:MGI:3613651]		G3UYX5	4.7	9.1E-02	6.6	4.0E-02	-0.2	9.4E-01	-2.1	2.1E-01
ENSMUST00000172832				0.8	2.4E-01	2.0	5.1E-02	0.9	2.3E-01	-0.2	7.5E-01
ENSMUST00000132031				5.1	7.0E-04	-5.0	3.0E-04	-0.6	2.1E-01	-1.8	1.3E-01
ENSMUST00000172836	ubiquitination factor E4B [Source:MGI Symbol;Acc:MGI:1927086]	G3UZD6		3.3	2.1E-01	1.1	8.0E-01	0.3	9.2E-01	2.5	5.1E-01
ENSMUST00000172846	flotillin 1 [Source:MGI Symbol;Acc:MGI:1100500]	G3UZZ5		-0.9	2.3E-01	1.4	1.4E-01	1.7	4.4E-02	-0.6	4.4E-01
ENSMUST00000135376				5.1	2.1E-04	6.3	1.5E-04	-0.6	6.1E-01	0.1	8.4E-01
ENSMUST00000172854	lymphocyte antigen 6 complex, locus G5B [Source:MGI Symbol;Acc:MGI:2385809]		Q8K1T4	3.2	7.4E-02	1.3	5.3E-01	-0.8	6.1E-01	1.1	5.4E-01
ENSMUST00000176386				5.1	1.7E-05	0.2	8.5E-01	0.8	3.7E-01	-2.5	7.4E-02
ENSMUST00000090043				5.1	1.9E-04	5.8	1.3E-03	-0.6	6.7E-01	0.0	9.7E-01
ENSMUST00000124574				5.1	1.4E-03	0.9	7.2E-01	-3.4	1.3E-01	0.7	7.3E-01
ENSMUST00000172868	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]	Q8CFZ0		-0.4	5.5E-01	-0.7	4.1E-01	-0.2	7.3E-01	0.1	8.6E-01
ENSMUST00000172869				1.3	4.9E-02	2.8	2.3E-03	-0.5	4.6E-01	-1.9	8.1E-03
ENSMUST00000114185				5.1	8.0E-05	7.3	6.6E-05	-1.4	2.4E-01	-0.2	7.4E-01
ENSMUST00000134749				5.1	2.3E-02	7.1	1.8E-04	-0.5	6.8E-01	0.5	4.8E-01
ENSMUST00000172894	RAB11B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:99425]	G3UZL4		-3.0	4.0E-02	-4.3	2.9E-02	-1.9	5.2E-02	-0.6	7.6E-01
ENSMUST00000172904				-2.6	2.0E-01	-3.2	1.9E-01	0.0	9.8E-01	0.6	7.9E-01
ENSMUST00000172906	ankyrin repeat domain 11 [Source:MGI Symbol;Acc:MGI:1924337]	G3UY79		-0.7	6.2E-01	-2.2	3.3E-01	0.5	7.0E-01	2.0	3.8E-01
ENSMUST00000135098				5.1	2.6E-04	4.7	7.4E-03	0.3	8.0E-01	-0.6	4.9E-01
ENSMUST00000146753				5.1	5.6E-04	-4.6	6.0E-03	2.0	4.0E-03	-0.6	6.6E-01
ENSMUST00000081361				5.1	8.6E-04	-4.0	1.2E-02	0.3	5.8E-01	1.3	3.2E-01
ENSMUST00000175768				5.1	3.2E-02	7.6	1.3E-03	2.4	1.7E-01	-1.2	1.9E-01
ENSMUST00000159783				5.1	5.1E-03	4.4	2.6E-02	-0.6	7.1E-01	0.0	9.8E-01
ENSMUST00000193719				5.1	3.3E-04	2.9	2.7E-01	-0.7	7.8E-01	3.3	8.8E-02
ENSMUST00000136537				5.1	1.1E-05	6.6	2.8E-04	-0.6	6.5E-01	-0.6	3.7E-01
ENSMUST00000134509				5.1	1.9E-03	6.7	7.0E-04	-0.4	7.6E-01	-0.6	4.5E-01
ENSMUST00000136448				5.1	6.1E-06	5.6	2.8E-03	-0.6	7.1E-01	-1.7	9.5E-02
ENSMUST00000172941				-0.1	9.8E-01	-0.7	7.8E-01	-0.5	8.0E-01	0.2	9.3E-01
ENSMUST00000146301				5.1	9.5E-04	5.9	3.7E-03	0.0	9.8E-01	-0.4	6.9E-01
ENSMUST00000134645				5.1	2.8E-03	2.4	7.6E-03	0.8	2.0E-01	1.0	1.0E-01
ENSMUST00000172947	DNA segment, Chr 7, ERATO Doi 443, expressed [Source:MGI Symbol;Acc:MGI:1196431]	G3UZF7		4.5	9.4E-02	4.5	1.1E-01	-0.7	8.1E-01	-0.7	7.1E-01
ENSMUST00000136142				5.1	1.8E-03	5.7	5.2E-03	-0.4	8.1E-01	-0.5	6.2E-01
ENSMUST00000172960				-0.1	9.5E-01	0.5	6.9E-01	0.2	8.1E-01	-0.3	7.6E-01
ENSMUST00000172969				3.6	1.1E-01	5.0	5.2E-02	-0.3	9.1E-01	-1.7	2.5E-01
ENSMUST00000137781				5.1	6.8E-03	6.4	9.2E-05	-1.5	1.8E-01	-0.6	3.2E-01
ENSMUST00000191483				5.1	5.5E-03	-0.6	5.5E-01	0.1	9.4E-01	-1.5	1.7E-01
ENSMUST00000172983	apolipoprotein E [Source:MGI Symbol;Acc:MGI:88057]	G3UWN5		0.4	7.4E-01	-1.3	5.2E-01	0.3	8.3E-01	2.0	2.5E-01
ENSMUST00000126961				5.1	4.4E-05	5.6	1.0E-03	-0.9	4.5E-01	0.1	9.3E-01
ENSMUST00000134912				5.1	1.1E-03	4.1	1.6E-02	-1.2	4.3E-01	-0.4	6.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000118361				5.1	2.4E-03	4.0	4.0E-02	-0.5	7.6E-01	0.6	6.1E-01
ENSMUST00000126183				5.1	4.6E-03	4.3	2.3E-02	0.0	1.0E+00	0.1	9.3E-01
ENSMUST00000172996	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 [Source:MGI Symbol;Ac	G3UX35		-0.4	5.9E-01	3.1	9.4E-03	2.0	3.4E-02	-1.5	8.3E-02
ENSMUST00000172997	UNC homeobox [Source:MGI Symbol;Acc:MGI:108013]	G3UYF8	O08934	3.6	7.2E-02	5.7	1.4E-02	-0.5	8.3E-01	-2.6	7.0E-02
ENSMUST00000135089				5.1	1.3E-03	7.1	4.4E-04	-0.2	8.8E-01	0.6	4.0E-01
ENSMUST00000153341				5.1	6.2E-05	4.1	3.7E-02	-0.8	6.5E-01	1.1	3.3E-01
ENSMUST00000173010	activating transcription factor 2 [Source:MGI Symbol;Acc:MGI:109349]	G3UXC3		-4.1	2.3E-01	-5.7	1.8E-01	-2.4	2.1E-01	-0.9	8.5E-01
ENSMUST00000195741				5.1	2.5E-04	9.9	2.5E-05	0.4	7.6E-01	-0.6	3.0E-01
ENSMUST00000173013	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10 [Source:MGI Symbol;Acc:M	G3UZ08		4.1	7.5E-02	5.0	8.5E-02	0.9	7.1E-01	0.0	9.9E-01
ENSMUST00000142949				5.1	8.9E-05	5.1	6.9E-03	-0.4	7.9E-01	0.7	4.5E-01
ENSMUST00000146777				5.1	1.4E-03	-5.6	8.2E-03	-0.8	2.7E-01	-0.6	7.6E-01
ENSMUST00000172300				5.1	2.3E-02	-4.7	2.0E-03	-0.5	3.4E-01	-0.4	7.6E-01
ENSMUST00000122076				5.1	5.6E-04	8.2	7.0E-05	-0.8	5.8E-01	0.4	5.0E-01
ENSMUST00000154002				5.1	1.7E-05	6.9	2.3E-02	-0.8	7.8E-01	-1.1	4.8E-01
ENSMUST00000173027				3.6	2.0E-01	3.7	2.4E-01	-0.2	9.4E-01	-0.3	8.7E-01
ENSMUST00000173031	transmembrane and coiled coil domains 1 [Source:MGI Symbol;Acc:MGI:2442368]	Q3TQU9		-0.5	3.2E-01	-0.6	3.7E-01	-0.4	4.0E-01	-0.3	5.7E-01
ENSMUST00000173033	molybdenum cofactor synthesis 1 [Source:MGI Symbol;Acc:MGI:1928904]		Q5RKZ7	-1.1	1.6E-01	0.0	1.0E+00	1.4	7.4E-02	0.3	7.3E-01
ENSMUST00000173037				2.0	2.7E-01	0.1	9.6E-01	1.4	5.3E-01	3.3	2.5E-01
ENSMUST00000186537				5.1	2.0E-03	6.3	5.0E-04	-0.5	6.9E-01	-1.0	1.7E-01
ENSMUST00000173039	sorting nexin 14 [Source:MGI Symbol;Acc:MGI:2155664]	G3UXB6		3.5	3.9E-02	-3.1	1.0E-02	-8.0	8.0E-05	-1.4	2.4E-01
ENSMUST00000173040	chromodomain helicase DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:88393]	G3UWS6		0.0	1.0E+00	-0.5	8.8E-01	-0.3	8.7E-01	0.1	9.7E-01
ENSMUST00000078431				5.1	5.4E-03	-2.7	7.3E-02	0.2	8.3E-01	-0.4	7.9E-01
ENSMUST00000130294				5.1	6.4E-05	6.6	1.2E-04	-0.6	6.0E-01	-0.1	8.1E-01
ENSMUST00000140441				5.1	4.7E-06	6.4	7.6E-04	-0.2	8.9E-01	-0.2	8.4E-01
ENSMUST00000173065	negative elongation factor complex member E, Rdbp [Source:MGI Symbol;Acc:MGI:102744]	G3UY39		3.8	6.0E-02	1.1	6.8E-01	-0.5	8.1E-01	2.2	3.2E-01
ENSMUST00000173075	histocompatibility 2, K1, K region [Source:MGI Symbol;Acc:MGI:95904]	G3UXW2		-0.2	9.5E-01	3.8	2.8E-01	2.3	4.3E-01	-1.8	5.7E-01
ENSMUST00000151582				5.1	6.5E-06	5.2	1.7E-02	-2.0	3.3E-01	-2.0	1.2E-01
ENSMUST00000173078	OTU domain containing 4 [Source:MGI Symbol;Acc:MGI:1098801]		B2RRE7	1.6	5.4E-01	-4.1	3.3E-01	-2.4	3.0E-01	3.3	4.3E-01
ENSMUST00000153849				5.1	1.3E-02	2.9	5.7E-02	-0.8	5.6E-01	1.8	1.0E-01
ENSMUST00000163125				5.1	2.5E-05	4.8	8.6E-04	-2.3	5.7E-02	0.2	8.0E-01
ENSMUST00000159014				5.1	5.8E-03	-3.2	2.7E-02	0.1	9.0E-01	-1.1	4.3E-01
ENSMUST00000130957				5.1	1.1E-03	-5.8	6.3E-04	-1.4	1.7E-02	-0.8	5.2E-01
ENSMUST00000162040				5.1	1.4E-04	-11.4	3.7E-04	0.3	5.2E-01	1.5	4.8E-01
ENSMUST00000138398				5.1	1.1E-04	6.1	1.2E-04	-1.5	1.8E-01	-0.1	8.7E-01
ENSMUST00000120244				5.1	3.5E-04	-6.2	1.0E-02	-2.2	1.8E-02	0.0	9.8E-01
ENSMUST00000166034				5.1	1.4E-02	7.3	7.5E-05	-0.5	6.5E-01	-0.7	2.7E-01
ENSMUST00000134917				5.1	7.9E-04	4.1	1.7E-01	-0.8	7.6E-01	1.1	5.9E-01
ENSMUST00000182305				5.1	1.7E-03	-4.0	6.4E-02	2.3	4.2E-02	-3.0	2.7E-01
ENSMUST00000149276				5.1	9.4E-06	-7.1	3.5E-03	-1.7	2.5E-02	-0.4	8.3E-01
ENSMUST00000108670				5.1	1.1E-05	6.5	2.5E-04	-0.5	6.8E-01	-0.7	2.9E-01
ENSMUST00000127197				5.1	1.7E-02	5.8	1.5E-02	-0.8	7.1E-01	-0.6	6.3E-01
ENSMUST00000160671				5.1	1.5E-03	6.0	9.4E-04	-1.0	4.2E-01	-0.6	3.6E-01
ENSMUST00000173125				3.7	4.0E-02	4.6	3.8E-02	-0.1	9.5E-01	-1.0	4.4E-01
ENSMUST00000124837				5.1	6.2E-06	4.2	5.8E-03	-0.1	9.2E-01	0.6	4.7E-01
ENSMUST00000153778				5.1	1.7E-02	6.4	5.7E-04	-0.7	6.3E-01	0.4	5.9E-01
ENSMUST00000125573				5.1	2.3E-02	6.5	1.5E-03	-0.7	6.7E-01	-0.2	8.3E-01
ENSMUST00000125393				5.1	9.7E-04	-4.0	4.1E-02	0.0	9.7E-01	-0.9	6.2E-01
ENSMUST00000134980				5.1	5.7E-03	-2.7	1.9E-02	0.0	1.0E+00	-0.2	8.4E-01
ENSMUST00000122256				5.1	1.9E-02	-3.0	1.6E-01	1.2	2.4E-01	-0.4	8.6E-01
ENSMUST00000124048				5.1	1.4E-04	7.3	4.5E-05	-1.3	2.3E-01	0.0	9.7E-01
ENSMUST00000173156	ubiquitin specific peptidase 32 [Source:MGI Symbol;Acc:MGI:2144475]	G3UX31		-2.4	3.5E-01	-4.2	1.6E-01	-2.9	8.5E-02	-1.1	7.2E-01
ENSMUST00000173159				2.3	2.0E-01	2.6	1.7E-01	-1.1	4.9E-01	-1.4	3.8E-01
ENSMUST00000118477				5.0	4.2E-03	8.4	1.1E-04	-0.7	6.3E-01	0.2	7.7E-01
ENSMUST00000172276				5.0	3.5E-02	4.2	2.5E-03	0.4	6.9E-01	0.4	5.2E-01
ENSMUST00000143294				5.0	2.9E-04	-4.4	4.2E-02	1.3	2.0E-01	-1.8	4.1E-01
ENSMUST00000165733				5.0	2.7E-05	3.0	6.0E-02	-2.7	9.2E-02	0.2	8.6E-01
ENSMUST00000174585				5.0	9.6E-04	5.9	1.3E-03	-0.7	6.2E-01	0.3	6.6E-01
ENSMUST00000173183				2.9	1.5E-01	1.8	3.0E-01	-2.9	1.4E-01	-1.8	2.6E-01
ENSMUST00000148384				5.0	1.2E-04	2.2	4.5E-02	0.5	5.4E-01	0.3	7.4E-01
ENSMUST00000173189				-0.8	5.5E-01	-0.5	7.4E-01	-0.6	6.0E-01	-0.8	5.9E-01
ENSMUST00000160168				5.0	5.5E-06	-8.5	1.7E-04	-0.5	2.7E-01	-0.6	6.9E-01
ENSMUST00000173194	Rho GTPase activating protein 21 [Source:MGI Symbol;Acc:MGI:1918685]	B7ZCJ0		-2.5	6.6E-02	-3.3	6.0E-02	-0.5	5.7E-01	0.3	8.5E-01
ENSMUST00000136173				5.0	2.4E-05	-4.5	4.4E-03	0.8	1.5E-01	-1.3	3.7E-01
ENSMUST00000145864				5.0	8.5E-04	6.2	6.3E-04	-1.6	2.4E-01	0.7	3.5E-01
ENSMUST00000173204	bromodomain containing 2 [Source:MGI Symbol;Acc:MGI:99495]	S4R1Z1		-1.6	1.2E-01	-1.4	4.3E-01	1.6	1.2E-01	1.4	4.0E-01
ENSMUST00000173206	DENN/MADD domain containing 2C [Source:MGI Symbol;Acc:MGI:3036254]	G3UYA7		0.6	6.5E-01	4.9	6.7E-03	1.1	4.5E-01	-3.2	2.0E-02
ENSMUST00000150031				5.0	2.3E-04	6.7	7.6E-04	-0.7	6.5E-01	-0.4	5.8E-01
ENSMUST00000189677				5.0	6.1E-04	5.7	2.9E-03	-0.6	6.8E-01	0.0	9.7E-01
ENSMUST00000119448				5.0	1.3E-04	3.3	1.3E-03	0.3	6.4E-01	-0.2	7.2E-01
ENSMUST00000173229				-2.3	6.8E-02	-1.5	2.7E-01	-0.2	7.7E-01	-1.0	4.7E-01
ENSMUST00000173231	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]	G3UWL6		2.7	6.4E-02	3.2	9.8E-02	0.5	7.6E-01	-0.1	9.5E-01
ENSMUST00000123334				5.0	1.1E-03	3.9	1.9E-02	-2.9	6.9E-02	0.8	4.2E-01
ENSMUST00000173236				-0.5	4.8E-01	0.0	9.7E-01	-0.1	9.0E-01	-0.6	4.6E-01
ENSMUST00000173238				0.7	3.6E-01	1.4	1.2E-01	-0.1	9.1E-01	-0.8	2.7E-01
ENSMUST00000135445				5.0	7.8E-06	-2.1	2.8E-02	0.9	1.0E-01	0.6	4.7E-01
ENSMUST00000173247				0.7	5.2E-01	2.6	1.1E-01	1.2	3.7E-01	-0.7	5.6E-01
ENSMUST00000150008				5.0	3.3E-04	2.8	3.9E-03	-0.4	5.9E-01	-0.4	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000173253				-0.3	6.7E-01	-0.2	8.2E-01	-0.2	7.6E-01	-0.3	7.2E-01
ENSMUST00000173254	BTG3 associated nuclear protein [Source:MGI Symbol;Acc:MGI:1889023]		Q8VBU8	0.7	7.0E-01	2.9	2.4E-01	0.5	7.9E-01	-1.6	4.6E-01
ENSMUST00000162723				5.0	1.3E-04	6.2	2.2E-04	-0.5	6.4E-01	-0.4	4.8E-01
ENSMUST00000173258				-1.2	2.6E-01	-1.0	4.8E-01	0.5	6.3E-01	0.3	8.4E-01
ENSMUST00000166677				5.0	2.0E-05	6.2	3.3E-04	-0.6	6.2E-01	-0.3	6.7E-01
ENSMUST00000194061				5.0	3.2E-02	5.6	1.2E-03	-0.5	7.0E-01	0.9	2.1E-01
ENSMUST00000172925				5.0	3.8E-03	3.1	2.6E-03	-0.1	8.7E-01	0.2	8.0E-01
ENSMUST00000170327				5.0	1.1E-04	-2.2	8.7E-02	-0.7	3.9E-01	-3.0	6.6E-02
ENSMUST00000173269				-1.8	8.7E-02	-1.0	4.2E-01	0.4	5.9E-01	-0.4	7.6E-01
ENSMUST00000173273				-2.4	1.2E-01	-2.5	3.1E-01	1.1	4.6E-01	1.1	6.0E-01
ENSMUST00000170457				5.0	2.1E-04	6.6	2.0E-04	-0.1	9.4E-01	0.6	3.7E-01
ENSMUST00000119247				5.0	4.0E-04	7.2	4.6E-05	-2.0	1.1E-01	-0.8	1.7E-01
ENSMUST00000123670				5.0	4.2E-04	-6.1	2.2E-04	0.1	8.6E-01	-0.7	5.3E-01
ENSMUST00000125480				5.0	1.2E-03	6.0	3.2E-03	0.0	9.9E-01	-0.7	4.5E-01
ENSMUST00000135722				5.0	1.3E-04	-3.9	7.9E-02	1.5	1.5E-01	-1.5	5.1E-01
ENSMUST00000173286	OTU domain containing 4 [Source:MGI Symbol;Acc:MGI:1098801]			-3.7	5.1E-02	1.2	5.3E-01	1.9	1.8E-01	-3.0	1.4E-01
ENSMUST00000145339				5.0	7.7E-05	6.6	5.7E-05	-2.6	3.6E-02	-0.1	8.6E-01
ENSMUST00000146382				5.0	7.0E-04	5.4	7.0E-04	-0.6	6.3E-01	0.7	3.1E-01
ENSMUST00000173292	DENN/MADD domain containing 3 [Source:MGI Symbol;Acc:MGI:2146009]	G3UYA1		-1.6	1.1E-01	-0.6	5.6E-01	-0.4	6.1E-01	-1.3	2.4E-01
ENSMUST00000127499				5.0	2.5E-02	6.1	2.6E-04	-0.6	6.1E-01	0.4	4.7E-01
ENSMUST00000094227				5.0	6.8E-04	7.4	8.7E-05	-1.8	1.9E-01	-0.8	1.7E-01
ENSMUST00000173299				-1.2	1.7E-01	-0.4	7.4E-01	0.2	7.6E-01	-0.6	5.6E-01
ENSMUST00000143350				5.0	1.5E-03	1.5	2.8E-01	-0.7	5.4E-01	0.5	6.2E-01
ENSMUST00000173307				3.4	1.6E-01	2.9	3.7E-01	0.5	8.5E-01	1.0	6.9E-01
ENSMUST00000173311	chromodomain helicase DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:88393]	Q8C7Q2		3.7	1.0E-01	2.3	4.6E-01	0.7	7.4E-01	2.1	4.1E-01
ENSMUST00000173318				-2.2	8.0E-02	-1.6	3.1E-01	-0.1	9.5E-01	-0.7	6.7E-01
ENSMUST00000173320	WD repeat domain 81 [Source:MGI Symbol;Acc:MGI:2681828]		Q5ND34	-0.6	6.4E-01	2.1	2.4E-01	0.8	6.1E-01	-1.9	1.8E-01
ENSMUST00000173327				4.4	3.6E-02	6.7	1.4E-02	0.9	6.8E-01	-1.3	3.5E-01
ENSMUST00000127373				5.0	1.1E-04	-6.4	2.5E-03	1.2	4.6E-02	0.7	6.6E-01
ENSMUST00000192923				5.0	2.3E-02	3.2	2.9E-03	0.6	4.2E-01	-0.5	4.3E-01
ENSMUST00000127594				5.0	5.3E-05	7.2	2.1E-04	-0.7	6.0E-01	-0.1	9.2E-01
ENSMUST00000131766				5.0	3.2E-06	5.5	1.1E-03	-2.5	7.6E-02	-0.8	3.2E-01
ENSMUST00000176422				5.0	3.3E-03	5.9	7.8E-04	-0.6	6.7E-01	-1.3	1.0E-01
ENSMUST00000173341	general transcription factor II I [Source:MGI Symbol;Acc:MGI:1202722]	Q3UHU8		-2.8	9.6E-02	-2.2	3.7E-01	0.6	7.1E-01	0.0	1.0E+00
ENSMUST00000173345	unc-13 homolog D (C. elegans) [Source:MGI Symbol;Acc:MGI:1917700]			1.9	4.6E-01	3.9	2.3E-01	-0.7	8.3E-01	-2.6	2.6E-01
ENSMUST00000154625				5.0	3.7E-05	7.0	8.5E-05	-1.4	2.3E-01	-0.3	6.4E-01
ENSMUST00000173353	predicted gene 8909 [Source:MGI Symbol;Acc:MGI:3704134]	G3UXE9		5.0	6.0E-02	5.7	4.2E-02	-0.8	7.6E-01	-1.5	3.8E-01
ENSMUST00000173354	retinoid X receptor beta [Source:MGI Symbol;Acc:MGI:98215]	Q8VCR0		-2.4	1.5E-01	-1.0	6.2E-01	1.3	3.9E-01	-0.1	9.6E-01
ENSMUST00000147293				5.0	1.3E-04	6.8	9.4E-05	-1.3	2.6E-01	-0.3	5.8E-01
ENSMUST00000187062				5.0	4.6E-04	-3.0	6.7E-02	0.1	9.5E-01	-0.5	7.4E-01
ENSMUST00000173362	molybdenum cofactor synthesis 1 [Source:MGI Symbol;Acc:MGI:1928904]	G3UYX9		-2.4	2.5E-01	2.1	4.1E-01	2.3	2.5E-01	-2.2	3.6E-01
ENSMUST00000173369	tripartite motif-containing 39 [Source:MGI Symbol;Acc:MGI:1890659]	G3UWI0		-2.7	1.1E-01	-3.4	1.1E-01	-1.0	4.1E-01	-0.3	9.0E-01
ENSMUST00000123986				5.0	7.7E-03	-5.3	2.4E-03	-1.4	2.3E-02	-0.5	7.3E-01
ENSMUST00000129257				5.0	5.2E-06	6.1	1.0E-03	0.9	4.8E-01	0.3	7.0E-01
ENSMUST00000173379				-2.9	4.6E-02	0.8	6.0E-01	2.4	7.6E-02	-1.3	3.7E-01
ENSMUST00000122190				5.0	4.0E-03	-5.3	8.8E-03	0.8	2.1E-01	0.1	9.4E-01
ENSMUST00000173385				-0.9	5.1E-01	1.9	2.8E-01	1.4	3.4E-01	-1.4	3.5E-01
ENSMUST00000173389	notch 4 [Source:MGI Symbol;Acc:MGI:107471]	G3UX69		7.5	3.6E-02	3.7	3.1E-01	-0.8	8.3E-01	3.0	2.0E-01
ENSMUST00000173393	RNA binding motif protein 38 [Source:MGI Symbol;Acc:MGI:1889294]		Q62176	0.6	5.6E-01	6.3	3.3E-03	3.9	2.7E-02	-1.8	8.1E-02
ENSMUST00000122951				5.0	3.2E-05	6.5	1.6E-02	-0.8	7.5E-01	-1.1	4.2E-01
ENSMUST00000183629				5.0	2.5E-02	-7.0	3.3E-04	0.8	9.5E-02	0.5	7.4E-01
ENSMUST00000144401				5.0	2.9E-04	6.4	2.2E-04	-1.0	4.2E-01	-1.4	6.2E-02
ENSMUST00000026048				5.0	3.3E-03	3.7	4.3E-03	0.5	6.0E-01	-0.4	5.4E-01
ENSMUST00000171928				5.0	1.5E-04	6.2	1.6E-03	-0.8	6.1E-01	0.5	5.9E-01
ENSMUST00000168069				5.0	2.2E-02	8.5	1.1E-04	0.3	8.5E-01	-0.3	6.2E-01
ENSMUST00000150952				5.0	3.1E-03	6.9	2.4E-04	-0.6	6.1E-01	-0.8	2.5E-01
ENSMUST00000124097				5.0	2.0E-03	3.3	9.7E-03	-1.8	1.1E-01	-0.7	4.1E-01
ENSMUST00000140616				5.0	1.5E-05	3.8	2.1E-03	-2.3	4.7E-02	-0.3	6.4E-01
ENSMUST00000120676				5.0	1.3E-03	5.7	1.1E-03	-0.6	6.8E-01	-0.9	2.2E-01
ENSMUST00000173426				-0.9	3.1E-01	-0.7	5.3E-01	-0.1	9.4E-01	-0.2	8.2E-01
ENSMUST00000124410				5.0	1.1E-04	3.2	1.5E-01	-1.5	4.7E-01	0.9	5.6E-01
ENSMUST00000146509				5.0	3.2E-03	7.4	3.5E-04	0.1	9.6E-01	0.1	9.3E-01
ENSMUST00000162580				5.0	1.6E-05	-8.6	6.4E-04	0.5	2.9E-01	-0.2	9.3E-01
ENSMUST00000173434				-1.3	2.2E-01	-0.3	7.8E-01	0.1	9.5E-01	-0.9	4.7E-01
ENSMUST00000183159				5.0	4.5E-03	6.8	5.2E-03	-0.7	7.2E-01	-2.0	1.0E-01
ENSMUST00000183380				5.0	2.4E-03	6.8	9.8E-05	-0.5	6.4E-01	-0.6	2.8E-01
ENSMUST00000126921				5.0	3.0E-04	-4.9	1.0E-04	0.0	9.6E-01	-2.4	3.1E-02
ENSMUST00000161772				5.0	8.5E-05	7.1	1.2E-04	-0.1	9.1E-01	-0.1	8.1E-01
ENSMUST00000126352				5.0	3.6E-03	6.5	1.8E-04	-0.6	6.0E-01	0.6	2.9E-01
ENSMUST00000140522				5.0	6.1E-04	6.5	1.6E-04	-0.5	6.3E-01	-1.7	2.4E-02
ENSMUST00000173454	membrane-associated ring finger (C3HC4) 2 [Source:MGI Symbol;Acc:MGI:1925915]	G3UY44		0.0	9.8E-01	-3.5	1.4E-01	-4.1	1.3E-02	-0.6	8.2E-01
ENSMUST00000179398				5.0	1.4E-03	6.2	5.1E-04	-0.5	7.2E-01	-0.6	3.9E-01
ENSMUST00000110898				5.0	1.3E-02	-8.2	1.1E-05	0.6	4.9E-02	-0.8	4.2E-01
ENSMUST00000130923				5.0	1.6E-03	6.5	3.0E-04	-0.5	6.7E-01	0.5	4.0E-01
ENSMUST00000191572				5.0	2.1E-04	-5.6	5.8E-04	-0.8	1.1E-01	-0.4	7.3E-01
ENSMUST00000131970				5.0	6.0E-04	6.9	1.3E-04	-0.6	6.1E-01	-0.5	4.0E-01
ENSMUST00000142561				5.0	2.9E-03	2.5	2.6E-01	-1.0	5.9E-01	1.0	5.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000124139				5.0	1.7E-05	8.1	4.5E-04	-0.9	5.9E-01	1.3	1.2E-01
ENSMUST00000152577				5.0	4.7E-05	-7.7	1.3E-05	0.0	9.1E-01	-0.9	3.8E-01
ENSMUST00000155772				5.0	2.5E-02	-2.7	3.4E-02	-0.3	6.8E-01	-1.2	3.3E-01
ENSMUST00000173491	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]	G3UYZ0		2.3	2.8E-01	1.2	7.3E-01	1.2	5.9E-01	2.4	4.3E-01
ENSMUST00000173492	kinesin family member C1 [Source:MGI Symbol;Acc:MGI:109596]		Q9QWT9	0.3	8.2E-01	0.7	6.7E-01	0.3	7.9E-01	-0.1	9.6E-01
ENSMUST00000173493	flotillin 1 [Source:MGI Symbol;Acc:MGI:1100500]	G3UZZ5		-1.0	5.7E-01	5.3	5.2E-02	4.2	8.1E-02	-2.1	2.6E-01
ENSMUST00000188896				5.0	1.7E-05	6.0	4.0E-05	0.2	8.0E-01	0.3	5.4E-01
ENSMUST00000119515				5.0	1.9E-04	4.7	4.2E-03	-0.6	6.3E-01	1.2	1.5E-01
ENSMUST00000151090				5.0	1.4E-03	2.7	4.6E-03	0.0	9.8E-01	-0.5	4.4E-01
ENSMUST00000173502				-0.6	5.5E-01	-0.1	9.5E-01	0.5	6.0E-01	0.0	9.9E-01
ENSMUST00000176462				5.0	5.4E-04	-4.9	6.4E-04	0.9	4.6E-02	-0.8	5.0E-01
ENSMUST00000142327				5.0	5.7E-06	-0.9	2.6E-01	-0.1	7.8E-01	-1.0	2.2E-01
ENSMUST00000150230				5.0	3.4E-05	3.8	7.4E-03	-0.8	4.7E-01	0.3	7.5E-01
ENSMUST00000173516	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Source:MGI Symbol;Acc:MGI:1321390]	G3UXY9		3.7	7.6E-02	-3.2	1.3E-01	-5.8	6.1E-03	1.1	5.9E-01
ENSMUST00000186596				5.0	9.0E-04	6.5	5.3E-04	-0.6	6.8E-01	-1.3	1.1E-01
ENSMUST00000174264				5.0	1.5E-03	6.8	7.3E-04	-1.8	2.5E-01	-0.7	4.1E-01
ENSMUST00000173522	short chain dehydrogenase/reductase family 42E, member 1 [Source:MGI Symbol;Acc:MGI:1921282]		Q9D665	0.3	5.0E-01	2.8	9.1E-04	0.5	2.9E-01	-1.9	3.8E-03
ENSMUST00000173525				3.4	5.2E-02	3.4	1.0E-01	-1.1	5.5E-01	-1.0	4.7E-01
ENSMUST00000117365				5.0	5.0E-04	5.3	2.1E-02	-0.7	7.3E-01	-0.5	6.9E-01
ENSMUST00000173533	prostaglandin E receptor 3 (subtype EP3) [Source:MGI Symbol;Acc:MGI:97795]	G3UYL9		-0.8	5.2E-01	-0.3	8.8E-01	2.6	7.8E-02	2.2	2.4E-01
ENSMUST00000173535	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]	G3UXT8		-0.7	5.0E-01	1.1	4.8E-01	2.0	1.1E-01	0.2	9.1E-01
ENSMUST00000151052				5.0	8.1E-05	6.6	7.6E-05	-0.3	7.8E-01	-0.1	8.4E-01
ENSMUST00000160895				5.0	1.8E-04	3.9	3.5E-02	-0.1	9.6E-01	1.8	1.4E-01
ENSMUST00000173543				-3.0	7.2E-02	-2.3	2.2E-01	-0.3	8.1E-01	-0.9	6.2E-01
ENSMUST00000173544				1.2	9.2E-02	1.5	6.8E-02	-0.7	3.0E-01	-1.0	1.6E-01
ENSMUST00000173548	transmembrane and coiled coil domains 1 [Source:MGI Symbol;Acc:MGI:2442368]			0.2	9.4E-01	0.0	9.9E-01	-2.8	1.8E-01	-2.6	3.3E-01
ENSMUST00000195474				5.0	2.8E-04	-5.3	5.8E-03	1.0	1.6E-01	-1.9	3.3E-01
ENSMUST00000173551				5.3	4.8E-02	4.4	1.3E-01	-0.7	7.9E-01	0.1	9.3E-01
ENSMUST00000141481				5.0	6.4E-04	-4.1	2.1E-03	-0.9	1.0E-01	-1.3	2.5E-01
ENSMUST00000119850				5.0	2.7E-03	-4.2	8.0E-02	1.7	1.1E-01	-0.3	9.1E-01
ENSMUST00000143918				5.0	2.1E-05	6.7	1.0E-04	-0.6	6.0E-01	-0.9	1.6E-01
ENSMUST00000179847				5.0	1.9E-05	6.5	4.4E-04	-0.1	9.1E-01	-0.4	5.4E-01
ENSMUST00000125441				5.0	2.2E-02	4.2	3.4E-03	-0.2	8.8E-01	-1.3	1.4E-01
ENSMUST00000161313				5.0	6.2E-04	5.6	2.6E-03	-0.4	7.9E-01	-0.2	7.7E-01
ENSMUST00000120433				5.0	5.8E-04	5.5	2.3E-02	-0.6	7.8E-01	1.5	2.4E-01
ENSMUST00000173578				-0.7	4.4E-01	-0.5	6.5E-01	0.3	7.6E-01	0.1	9.2E-01
ENSMUST00000140193				5.0	4.4E-05	-3.2	1.6E-02	-1.2	7.2E-02	-0.5	7.0E-01
ENSMUST00000133652				5.0	3.4E-04	9.6	1.6E-04	-0.9	6.1E-01	0.5	4.9E-01
ENSMUST00000173584	valyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:90675]	G3UY93		2.4	2.9E-01	1.2	7.5E-01	1.5	5.3E-01	2.8	4.0E-01
ENSMUST00000172859				5.0	3.0E-02	6.2	3.6E-04	-0.6	6.3E-01	-0.3	6.0E-01
ENSMUST00000121581				5.0	3.1E-02	7.3	1.1E-04	-0.5	6.9E-01	-0.7	3.1E-01
ENSMUST00000126807				5.0	1.1E-03	-6.4	2.3E-04	2.8	3.4E-05	0.6	6.2E-01
ENSMUST00000173602				0.4	8.2E-01	1.3	5.2E-01	-0.4	8.2E-01	-1.3	4.9E-01
ENSMUST00000136656				5.0	1.2E-03	9.5	1.2E-03	-0.5	8.3E-01	0.7	4.3E-01
ENSMUST00000154441				5.0	1.1E-03	2.6	2.2E-01	-0.5	8.0E-01	1.3	3.6E-01
ENSMUST00000147853				5.0	1.6E-03	5.1	1.1E-03	-1.3	2.9E-01	-0.7	3.0E-01
ENSMUST00000150147				5.0	2.3E-05	5.1	1.8E-02	-0.7	7.2E-01	-0.2	8.9E-01
ENSMUST00000132719				5.0	7.8E-03	-4.5	6.0E-03	0.2	8.0E-01	-1.0	5.2E-01
ENSMUST00000173627	polyadenylate binding protein-interacting protein 1 [Source:MGI Symbol;Acc:MGI:2384993]	G3UYE5		-1.8	2.9E-01	0.1	9.7E-01	3.4	1.0E-01	1.5	5.9E-01
ENSMUST00000188850				5.0	3.7E-05	-3.2	5.7E-02	1.3	1.4E-01	-0.6	7.0E-01
ENSMUST00000173631	thioredoxin 2 [Source:MGI Symbol;Acc:MGI:1929468]	G3UZY2		-2.6	2.4E-01	-1.1	7.1E-01	1.0	5.8E-01	-0.5	8.5E-01
ENSMUST00000173642	transcription elongation regulator 1 (CA150) [Source:MGI Symbol;Acc:MGI:1926421]		Q8CGF7	1.9	3.3E-01	3.1	2.1E-01	-0.2	9.2E-01	-1.4	4.5E-01
ENSMUST00000189241				5.0	4.4E-05	0.5	5.8E-01	0.9	2.4E-01	-2.3	3.8E-02
ENSMUST00000127309				5.0	1.7E-02	5.6	4.3E-03	-0.1	9.6E-01	-0.9	3.5E-01
ENSMUST00000190135				5.0	4.7E-04	4.1	2.6E-02	0.6	7.0E-01	1.1	3.1E-01
ENSMUST00000117362				5.0	1.2E-03	5.6	1.0E-03	-1.0	4.3E-01	0.1	9.2E-01
ENSMUST00000133965				5.0	5.9E-03	-3.5	3.5E-02	-0.1	8.9E-01	0.1	9.5E-01
ENSMUST00000150463				5.0	1.0E-03	7.7	5.1E-05	-0.6	6.2E-01	-0.5	3.4E-01
ENSMUST00000156316				5.0	1.1E-03	4.2	2.0E-02	-2.0	2.3E-01	0.6	6.2E-01
ENSMUST00000173666				-1.7	6.4E-01	-8.2	7.7E-02	-6.0	1.6E-02	0.5	9.2E-01
ENSMUST00000173669				2.3	5.9E-02	-1.9	1.1E-01	-3.7	3.9E-03	0.5	6.2E-01
ENSMUST00000173679	elongation factor Tu GTP binding domain containing 2 [Source:MGI Symbol;Acc:MGI:1336880]	G3UZ34		4.6	4.3E-02	2.4	2.1E-01	-5.1	2.9E-02	-2.9	8.4E-02
ENSMUST00000156128				5.0	3.8E-05	2.9	8.0E-02	-3.1	1.0E-01	-0.9	4.8E-01
ENSMUST00000173684				-0.5	4.6E-01	-1.0	3.6E-01	-0.3	6.3E-01	0.1	9.1E-01
ENSMUST00000098007				5.0	1.7E-04	-6.0	2.4E-04	-0.2	6.5E-01	-1.0	4.0E-01
ENSMUST00000173689	jumonji domain containing 1C [Source:MGI Symbol;Acc:MGI:1918614]		Q69ZK6	-1.3	4.5E-01	-3.2	1.6E-01	-0.8	5.4E-01	1.0	6.4E-01
ENSMUST00000173696	karyopherin (importin) alpha 1 [Source:MGI Symbol;Acc:MGI:103560]	G3UZK5		-0.7	7.6E-01	-4.5	1.7E-01	-3.2	7.7E-02	0.6	8.4E-01
ENSMUST00000175682				5.0	1.4E-04	7.0	2.4E-05	-1.6	1.5E-01	-0.2	6.4E-01
ENSMUST00000173704	jumonji, AT rich interactive domain 2 [Source:MGI Symbol;Acc:MGI:104813]		Q62315	-0.6	6.2E-01	2.6	9.2E-02	1.3	2.7E-01	-2.0	1.8E-01
ENSMUST00000173708				-0.1	9.3E-01	0.1	9.0E-01	0.1	9.0E-01	-0.1	9.2E-01
ENSMUST00000147610				5.0	5.4E-05	-4.8	1.1E-03	0.0	9.7E-01	-1.5	2.2E-01
ENSMUST00000140165				5.0	4.8E-03	6.4	1.3E-04	-0.4	7.2E-01	-0.4	5.3E-01
ENSMUST00000173718				-0.6	7.0E-01	-2.0	3.9E-01	0.1	9.4E-01	1.5	4.3E-01
ENSMUST00000173722	ligase III, DNA, ATP-dependent [Source:MGI Symbol;Acc:MGI:109152]	Q80ZH7		-3.7	4.1E-02	-3.7	1.9E-01	1.5	3.1E-01	1.6	5.4E-01
ENSMUST00000142812				5.0	7.2E-03	-0.1	9.4E-01	0.6	3.5E-01	-3.2	1.2E-02
ENSMUST00000173729	integrin beta 1 binding protein 1 [Source:MGI Symbol;Acc:MGI:1306802]		O35671	-0.3	5.2E-01	0.2	8.1E-01	0.1	8.9E-01	-0.4	4.8E-01
ENSMUST00000173731	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B [Source:MGI Symbol;Acc:MGI:99240]		Q9Z1N5	1.9	1.3E-01	2.0	3.1E-01	1.7	3.1E-01	1.6	2.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000173734	KH domain containing 3, subcortical maternal complex member [Source:MGI Symbol;Acc:MGI:1914241]		Q9CWU5	0.0	9.9E-01	4.4	5.6E-02	2.6	1.8E-01	-1.7	2.7E-01
ENSMUST00000173739	apolipoprotein E [Source:MGI Symbol;Acc:MGI:88057]	Q3TXU4	P08226	-1.2	1.9E-01	0.6	6.0E-01	1.1	2.4E-01	-0.7	4.9E-01
ENSMUST00000173750				-0.4	5.6E-01	-0.4	6.6E-01	0.0	9.4E-01	0.1	9.5E-01
ENSMUST00000191493				5.0	3.0E-05	5.7	3.0E-04	0.1	9.5E-01	0.4	5.5E-01
ENSMUST00000173760	modulator of apoptosis 1 [Source:MGI Symbol;Acc:MGI:1915555]		Q9ERH6	-1.5	2.3E-01	1.6	3.4E-01	1.8	2.1E-01	-1.3	3.5E-01
ENSMUST00000173761				5.3	3.7E-02	5.3	6.5E-02	-0.2	9.3E-01	-0.2	9.1E-01
ENSMUST00000194674				5.0	9.8E-05	-3.4	3.5E-02	-1.0	2.6E-01	-0.6	6.9E-01
ENSMUST00000186700				5.0	6.1E-03	5.6	1.7E-03	-0.5	7.1E-01	-0.2	8.1E-01
ENSMUST00000118497				5.0	3.2E-05	-7.8	7.2E-03	1.5	5.3E-02	-0.2	9.4E-01
ENSMUST00000140304				5.0	2.3E-03	-3.0	2.8E-02	1.2	1.1E-01	-3.0	6.1E-02
ENSMUST00000187872				5.0	2.3E-03	-5.0	4.1E-03	-1.3	5.4E-02	-1.2	4.4E-01
ENSMUST00000160470				4.9	1.9E-04	6.1	3.2E-03	-0.4	8.1E-01	-1.4	1.6E-01
ENSMUST00000132617				4.9	5.2E-06	3.2	4.4E-03	-1.3	1.2E-01	-0.1	8.5E-01
ENSMUST00000173790	H2A histone family, member Z [Source:MGI Symbol;Acc:MGI:1888388]	G3UWL7		-2.0	4.6E-01	-5.2	6.4E-02	-4.6	2.7E-02	-1.4	6.3E-01
ENSMUST00000121031				4.9	5.0E-03	5.7	1.1E-03	-1.0	4.8E-01	-0.6	4.7E-01
ENSMUST00000138969				4.9	1.2E-02	5.3	2.3E-03	-0.8	5.8E-01	-0.2	7.9E-01
ENSMUST00000097855				4.9	6.8E-05	6.4	5.2E-04	-0.4	7.4E-01	-0.1	8.4E-01
ENSMUST00000173801	synaptotagmin binding, cytoplasmic RNA interacting protein [Source:MGI Symbol;Acc:MGI:1891690]		Q7TMK9	-0.4	4.5E-01	-0.7	3.5E-01	-0.3	5.6E-01	-0.1	9.4E-01
ENSMUST00000173804	G protein-coupled receptor associated sorting protein 2 [Source:MGI Symbol;Acc:MGI:2442071]		Q8BUY8	4.0	4.5E-02	5.3	1.5E-02	-0.6	7.3E-01	-1.9	1.7E-01
ENSMUST00000141208				4.9	1.7E-04	4.2	6.6E-02	-4.0	1.1E-01	-0.7	6.0E-01
ENSMUST00000184598				4.9	9.9E-03	-4.3	1.7E-01	1.5	3.5E-01	-0.8	7.8E-01
ENSMUST00000173823	gamma-aminobutyric acid (GABA) B receptor, 1 [Source:MGI Symbol;Acc:MGI:1860139]	G3UXR6		-1.1	5.5E-01	-3.6	2.3E-01	-1.0	5.2E-01	1.5	6.1E-01
ENSMUST00000132340				4.9	1.1E-05	-1.0	6.8E-01	3.9	2.2E-02	-0.7	7.6E-01
ENSMUST00000142702				4.9	4.1E-04	5.7	2.9E-03	-1.5	3.8E-01	-1.7	1.1E-01
ENSMUST00000189790				4.9	6.7E-04	-2.5	1.3E-01	0.7	3.7E-01	-0.2	9.2E-01
ENSMUST00000125800				4.9	2.1E-04	5.7	2.1E-03	-0.2	9.2E-01	-1.2	2.0E-01
ENSMUST00000132939				4.9	5.7E-04	6.9	4.2E-04	-0.7	6.3E-01	-0.6	4.2E-01
ENSMUST00000131391				4.9	1.1E-02	-7.7	2.4E-03	-1.3	1.0E-01	-0.2	9.2E-01
ENSMUST00000149821				4.9	5.4E-04	-1.1	3.1E-01	-0.7	3.2E-01	-3.7	1.6E-02
ENSMUST00000152651				4.9	5.9E-06	4.6	1.8E-03	0.6	5.3E-01	-0.3	7.0E-01
ENSMUST00000139930				4.9	2.9E-04	5.6	8.5E-03	-0.8	6.7E-01	0.9	3.8E-01
ENSMUST00000173853	chaperonin containing Tcp1, subunit 4 (delta) [Source:MGI Symbol;Acc:MGI:104689]	G3UXG2		3.2	6.5E-02	-1.8	1.3E-01	-6.5	6.4E-04	-1.5	2.4E-01
ENSMUST00000173858	EFR3 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1923990]		Q8BG67	1.8	3.9E-01	0.9	7.5E-01	-0.7	7.5E-01	0.2	9.3E-01
ENSMUST00000194639				4.9	1.4E-04	-1.4	3.2E-01	1.3	1.7E-01	-1.7	2.7E-01
ENSMUST00000129549				4.9	1.6E-04	-2.3	2.8E-02	0.4	5.0E-01	-2.7	2.8E-02
ENSMUST00000122992				4.9	2.8E-03	1.0	3.5E-01	-1.3	1.9E-01	0.0	9.8E-01
ENSMUST00000173870	upstream binding transcription factor, RNA polymerase I [Source:MGI Symbol;Acc:MGI:98512]	A2AWT5		3.5	4.2E-02	3.3	1.4E-01	0.2	9.3E-01	0.4	8.0E-01
ENSMUST00000155608				4.9	4.5E-04	-0.4	8.4E-01	-4.3	3.9E-02	2.6	1.9E-01
ENSMUST00000173875	steroid receptor RNA activator 1 [Source:MGI Symbol;Acc:MGI:1344414]		Q80VJ2	1.7	3.5E-02	2.5	1.8E-02	0.2	7.5E-01	-0.5	4.4E-01
ENSMUST00000127747				4.9	4.1E-05	6.8	1.4E-06	-0.6	3.3E-01	0.0	9.8E-01
ENSMUST00000193502				4.9	7.7E-05	-0.2	9.0E-01	2.9	5.7E-03	0.8	4.9E-01
ENSMUST00000173888	general transcription factor II I [Source:MGI Symbol;Acc:MGI:1202722]		Q9ESZ8	3.2	2.0E-01	4.8	2.0E-01	1.7	5.9E-01	0.1	9.6E-01
ENSMUST00000069778				4.9	9.9E-04	7.7	6.2E-05	-0.6	6.2E-01	-0.3	6.2E-01
ENSMUST00000173907				-1.0	5.2E-01	-1.3	6.0E-01	0.1	9.6E-01	0.3	8.7E-01
ENSMUST00000124389				4.9	1.9E-04	1.1	6.0E-01	1.1	5.5E-01	3.3	4.8E-02
ENSMUST00000167244				4.9	4.5E-05	3.2	1.1E-01	-2.5	2.4E-01	-0.7	6.3E-01
ENSMUST00000121386				4.9	6.0E-04	6.4	2.3E-04	-0.5	6.4E-01	-0.4	4.9E-01
ENSMUST00000173913	protein kinase N2 [Source:MGI Symbol;Acc:MGI:109211]	G3UYE1		-3.6	2.5E-01	-1.8	4.4E-01	-2.1	2.6E-01	-3.9	2.2E-01
ENSMUST00000151469				4.9	7.4E-04	5.6	5.2E-03	-0.3	8.2E-01	0.7	4.2E-01
ENSMUST00000126222				4.9	3.2E-02	6.6	5.9E-03	-0.8	7.1E-01	0.6	6.1E-01
ENSMUST00000136896				4.9	1.9E-05	6.0	3.2E-04	-0.5	6.8E-01	0.6	3.6E-01
ENSMUST00000190139				4.9	4.9E-04	-3.8	1.8E-02	1.1	9.1E-02	0.3	8.2E-01
ENSMUST00000173928				-0.4	7.2E-01	-0.2	9.1E-01	1.0	4.9E-01	0.8	6.2E-01
ENSMUST00000173929	bl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene) [Source:MGI Symbol;Acc:MGI:878(	G3UWQ2		2.7	1.0E-01	4.6	1.0E-02	-0.8	5.9E-01	-2.7	4.4E-02
ENSMUST00000131468				4.9	1.1E-02	-1.4	5.2E-01	3.6	2.6E-02	-0.3	8.8E-01
ENSMUST00000182605				4.9	3.9E-04	-3.2	1.4E-01	0.6	6.1E-01	0.3	8.8E-01
ENSMUST00000021701				4.9	3.0E-05	6.6	1.4E-04	-0.6	6.2E-01	-0.4	5.4E-01
ENSMUST00000120106				4.9	1.8E-05	-6.0	2.1E-03	-0.6	3.1E-01	0.6	6.8E-01
ENSMUST00000173945				0.9	2.0E-01	1.7	6.3E-02	0.3	6.1E-01	-0.5	4.9E-01
ENSMUST00000141647				4.9	5.9E-03	3.0	1.5E-01	-2.5	2.5E-01	1.4	3.2E-01
ENSMUST00000154436				4.9	2.9E-02	6.5	2.2E-03	-1.6	3.6E-01	0.3	7.4E-01
ENSMUST00000173952	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]	G3V013		0.1	9.2E-01	-1.4	4.8E-01	0.3	8.3E-01	1.8	2.9E-01
ENSMUST00000138313				4.9	5.4E-05	-6.8	1.8E-04	0.5	2.0E-01	0.0	9.7E-01
ENSMUST00000173955				2.4	1.5E-01	1.0	5.3E-01	-2.4	1.2E-01	-1.0	5.0E-01
ENSMUST00000173960				2.5	5.2E-02	6.2	3.1E-04	-0.5	6.7E-01	-4.2	7.9E-04
ENSMUST00000173964	large tumor suppressor 2 [Source:MGI Symbol;Acc:MGI:1354386]	G3UYM3		3.4	4.5E-02	-0.8	5.4E-01	-4.0	1.2E-02	0.2	9.0E-01
ENSMUST00000189044				4.9	6.9E-05	3.9	3.7E-03	-2.2	5.4E-02	-0.3	7.0E-01
ENSMUST00000173969	cDNA sequence AK010878 [Source:MGI Symbol;Acc:MGI:4845848]		P0C8B4	0.6	2.6E-01	0.9	1.7E-01	0.3	4.8E-01	0.0	9.7E-01
ENSMUST00000183259				4.9	3.4E-03	2.9	5.7E-02	0.6	6.1E-01	0.6	6.0E-01
ENSMUST00000185053				4.9	1.5E-02	7.3	8.0E-04	-0.6	6.8E-01	1.0	2.2E-01
ENSMUST00000173975				0.5	5.1E-01	-0.1	9.5E-01	-0.2	7.4E-01	0.3	7.1E-01
ENSMUST00000122260				4.9	3.8E-03	-1.1	4.5E-01	2.1	4.1E-02	-1.8	2.8E-01
ENSMUST00000173984	activating transcription factor 6 beta [Source:MGI Symbol;Acc:MGI:105121]	G3UX19		0.1	9.6E-01	2.4	2.5E-01	0.6	7.2E-01	-1.8	3.2E-01
ENSMUST00000189981				4.9	6.7E-06	4.9	1.1E-02	-0.6	7.1E-01	0.9	3.7E-01
ENSMUST00000173987	RAB11B, member RAS oncogene family [Source:MGI Symbol;Acc:MGI:99425]	G3UY29		0.6	2.9E-01	0.6	3.8E-01	0.6	2.8E-01	0.5	4.4E-01
ENSMUST00000119653				4.9	1.0E-02	8.3	1.6E-04	0.1	9.4E-01	0.9	1.6E-01
ENSMUST00000173989				-1.4	1.4E-01	-0.3	7.7E-01	0.1	8.8E-01	-0.9	3.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000094051				4.9	5.6E-03	2.1	2.1E-02	-1.3	9.0E-02	0.2	7.2E-01
ENSMUST00000173995	decapping exoribonuclease [Source:MGI Symbol;Acc:MGI:1890444]	G3UZP8		1.6	1.6E-01	-0.5	7.8E-01	1.2	4.0E-01	3.3	5.5E-02
ENSMUST00000173996	transmembrane protein 29 [Source:MGI Symbol;Acc:MGI:1923420]	A2ANF5		2.6	3.6E-02	5.5	3.1E-04	-1.5	1.9E-01	-4.4	4.3E-04
ENSMUST00000173999				-0.1	9.7E-01	-0.7	6.4E-01	-1.0	3.9E-01	-0.4	8.0E-01
ENSMUST00000150206				4.9	5.2E-05	-2.5	9.2E-02	-0.9	3.0E-01	-1.8	2.7E-01
ENSMUST00000174001	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]		P63280	3.3	7.8E-02	2.3	3.6E-01	0.6	7.5E-01	1.6	4.4E-01
ENSMUST00000186975				4.9	1.1E-04	-6.1	5.1E-03	-0.8	2.1E-01	-0.1	9.6E-01
ENSMUST00000120176				4.9	1.1E-03	-6.2	3.5E-04	0.8	7.6E-02	-0.6	6.4E-01
ENSMUST00000133386				4.9	1.5E-04	3.8	4.6E-04	0.2	8.1E-01	-0.5	3.5E-01
ENSMUST00000136068				4.9	3.6E-03	5.0	2.0E-02	-0.5	7.9E-01	0.7	5.3E-01
ENSMUST00000174024	casein kinase 2, beta polypeptide [Source:MGI Symbol;Acc:MGI:88548]	G3UZX4		-1.5	5.4E-01	0.3	8.9E-01	-0.4	8.4E-01	-2.2	3.8E-01
ENSMUST00000174026	mutS homolog 5 (E. coli) [Source:MGI Symbol;Acc:MGI:1329021]	G3UZ06		1.9	7.5E-02	2.8	6.0E-02	0.3	7.8E-01	-0.6	5.5E-01
ENSMUST00000146330				4.9	4.5E-03	-3.9	4.0E-03	0.7	1.4E-01	-1.0	3.9E-01
ENSMUST00000128698				4.9	1.2E-03	-3.4	3.0E-03	0.4	3.6E-01	-2.6	3.7E-02
ENSMUST00000174284				4.9	4.0E-03	-5.7	6.1E-04	-0.7	1.3E-01	-0.8	5.4E-01
ENSMUST00000194620				4.9	1.0E-03	-0.4	7.2E-01	0.1	9.4E-01	-2.4	5.2E-02
ENSMUST00000147226				4.9	6.8E-05	5.3	4.6E-03	1.1	4.2E-01	-0.5	5.3E-01
ENSMUST00000171581				4.9	9.0E-03	6.6	3.7E-04	-2.1	1.5E-01	-0.9	2.3E-01
ENSMUST00000127532				4.9	6.2E-05	7.6	4.3E-07	0.6	2.9E-01	0.1	7.2E-01
ENSMUST00000124148				4.9	2.3E-04	2.6	6.0E-02	-0.9	4.4E-01	0.9	3.7E-01
ENSMUST00000126648				4.9	7.2E-05	-4.6	2.2E-03	0.2	7.1E-01	-0.9	4.7E-01
ENSMUST00000184695				4.9	6.4E-04	7.5	3.9E-05	1.4	1.7E-01	0.1	8.4E-01
ENSMUST00000174050	dynamin 2 [Source:MGI Symbol;Acc:MGI:109547]	G3UZZ3		-0.5	9.0E-01	5.5	4.1E-01	6.3	1.9E-01	0.4	9.5E-01
ENSMUST00000132347				4.9	2.2E-02	0.8	6.2E-01	-3.4	6.8E-02	0.2	9.0E-01
ENSMUST00000174054				1.3	1.5E-01	2.8	2.4E-02	0.9	3.2E-01	-0.6	5.0E-01
ENSMUST00000150451				4.9	2.4E-05	12.4	4.9E-05	-1.0	6.1E-01	0.0	9.6E-01
ENSMUST00000129244				4.9	5.1E-06	4.8	8.1E-04	-2.2	7.0E-02	-3.7	1.6E-03
ENSMUST00000144404				4.9	1.5E-05	6.9	4.7E-04	1.9	1.6E-01	0.2	7.6E-01
ENSMUST00000181162				4.9	2.4E-05	4.9	1.8E-03	-2.7	5.5E-02	-0.6	4.1E-01
ENSMUST00000139714				4.9	3.8E-03	-6.6	2.1E-03	-1.0	1.2E-01	2.0	2.2E-01
ENSMUST00000174070	sorting nexin family member 21 [Source:MGI Symbol;Acc:MGI:1917729]	G3UWM2		1.3	3.5E-01	5.5	6.7E-03	1.5	3.4E-01	-2.7	3.6E-02
ENSMUST00000138097				4.9	7.9E-05	-5.4	6.3E-02	0.6	5.4E-01	1.4	6.0E-01
ENSMUST00000131604				4.9	7.7E-03	3.9	7.3E-03	0.3	8.1E-01	-1.0	2.2E-01
ENSMUST00000174080	flotillin 1 [Source:MGI Symbol;Acc:MGI:1100500]	G3UYU4		-2.0	5.8E-01	-1.0	7.8E-01	-0.3	8.9E-01	-1.3	7.4E-01
ENSMUST00000146870				4.9	5.8E-05	2.2	1.2E-01	-1.7	1.8E-01	0.6	5.7E-01
ENSMUST00000174088	actin-like 9 [Source:MGI Symbol;Acc:MGI:1916731]		Q8CG27	4.5	6.9E-02	5.4	4.8E-02	-0.5	8.4E-01	-1.5	3.4E-01
ENSMUST00000152480				4.9	9.1E-03	-0.8	6.3E-01	2.3	7.7E-02	-0.2	8.9E-01
ENSMUST00000174096	calumenin [Source:MGI Symbol;Acc:MGI:1097158]	G3UY49		-1.3	6.3E-01	-4.1	2.2E-01	-3.3	8.6E-02	-0.5	8.9E-01
ENSMUST00000152806				4.9	2.5E-04	3.7	1.0E-01	0.0	9.9E-01	2.6	7.3E-02
ENSMUST00000174104				3.4	1.3E-01	7.0	2.8E-02	2.8	2.8E-01	-0.9	6.5E-01
ENSMUST00000173127				4.9	4.0E-04	5.7	5.8E-04	-0.5	6.8E-01	-0.2	7.1E-01
ENSMUST00000148251				4.9	1.7E-04	5.5	9.3E-03	-0.8	6.6E-01	1.7	1.3E-01
ENSMUST00000174108				6.5	6.4E-02	4.1	2.3E-01	-2.0	5.7E-01	0.4	8.6E-01
ENSMUST00000139028				4.9	1.1E-04	6.1	1.4E-04	-1.4	2.0E-01	0.6	2.9E-01
ENSMUST00000174120	trafficking protein, kinesin binding 2 [Source:MGI Symbol;Acc:MGI:1918077]	G3UYW9		-1.5	4.3E-01	2.8	2.3E-01	1.8	3.3E-01	-2.6	2.4E-01
ENSMUST00000174135				3.6	4.5E-02	6.0	1.1E-02	0.9	6.5E-01	-1.6	1.9E-01
ENSMUST00000139405				4.9	6.7E-04	4.2	5.7E-05	-0.5	4.0E-01	0.0	9.2E-01
ENSMUST00000172991				4.9	5.7E-03	8.2	1.4E-05	-2.1	9.0E-02	-0.2	7.0E-01
ENSMUST00000174144	apolipoprotein E [Source:MGI Symbol;Acc:MGI:88057]	G3UWN5		-3.2	7.4E-02	0.7	7.3E-01	1.6	3.3E-01	-2.3	2.1E-01
ENSMUST00000192890				4.9	2.7E-04	-4.3	1.2E-01	1.8	1.9E-01	-0.7	7.9E-01
ENSMUST00000138559				4.9	6.1E-05	-4.1	5.7E-02	0.1	8.7E-01	0.2	9.1E-01
ENSMUST00000174160	myotubularin related protein 12 [Source:MGI Symbol;Acc:MGI:2443034]	G3UZ04		-4.1	1.5E-01	-4.9	1.7E-01	-1.5	3.4E-01	-0.7	8.5E-01
ENSMUST00000174161				1.5	1.5E-01	1.3	3.1E-01	0.1	9.5E-01	0.2	8.3E-01
ENSMUST00000137744				4.9	5.3E-03	5.4	4.6E-02	-0.9	7.2E-01	1.0	4.9E-01
ENSMUST00000174164				-1.4	7.5E-02	-1.3	2.0E-01	0.3	6.8E-01	0.2	8.6E-01
ENSMUST00000174170				1.9	1.6E-01	2.0	1.1E-01	-1.6	1.8E-01	-1.7	1.8E-01
ENSMUST00000174171	interleukin 1 receptor accessory protein [Source:MGI Symbol;Acc:MGI:104975]	G3UY13		-2.3	5.0E-01	-5.5	2.5E-01	-3.2	1.7E-01	0.0	9.9E-01
ENSMUST00000174172	protein regulator of cytokinesis 1 [Source:MGI Symbol;Acc:MGI:1858961]	G3UWQ7		0.7	7.3E-01	1.0	7.1E-01	0.1	9.8E-01	-0.3	9.2E-01
ENSMUST00000172752				4.9	1.1E-03	9.6	1.3E-04	-0.7	6.8E-01	-0.1	8.3E-01
ENSMUST00000150505				4.9	4.5E-03	-3.2	5.7E-02	1.4	7.3E-02	-0.1	9.3E-01
ENSMUST00000120647				4.9	1.0E-03	7.1	2.6E-04	-0.5	7.1E-01	-0.9	2.3E-01
ENSMUST00000132479				4.9	1.9E-05	-3.2	2.2E-02	-0.1	8.9E-01	-0.2	9.0E-01
ENSMUST00000174199	protein regulator of cytokinesis 1 [Source:MGI Symbol;Acc:MGI:1858961]	G3XA79		2.0	3.5E-01	0.4	8.6E-01	-2.2	2.8E-01	-0.6	7.9E-01
ENSMUST00000137243				4.9	2.2E-03	6.1	9.4E-05	-0.7	4.7E-01	0.4	4.7E-01
ENSMUST00000151442				4.9	1.3E-03	-2.3	1.1E-02	-0.3	4.8E-01	-1.4	8.5E-02
ENSMUST00000130051				4.9	1.8E-03	4.8	2.1E-03	-0.6	5.6E-01	0.6	4.1E-01
ENSMUST00000147970				4.9	1.7E-05	5.8	2.6E-03	-0.6	6.9E-01	-0.1	9.5E-01
ENSMUST00000182455				4.9	1.2E-03	5.5	8.7E-04	-1.2	3.5E-01	-1.0	2.2E-01
ENSMUST00000193237				4.9	2.1E-04	4.2	1.2E-02	-2.3	1.2E-01	0.0	9.9E-01
ENSMUST00000075152				4.9	3.6E-03	6.6	4.9E-03	1.2	4.9E-01	0.6	6.3E-01
ENSMUST00000174216	ubiquitin-conjugating enzyme E2I [Source:MGI Symbol;Acc:MGI:107365]	G3UZL6		-1.8	1.1E-01	-2.3	1.8E-01	0.4	6.9E-01	0.9	5.6E-01
ENSMUST00000194153				4.9	3.9E-04	-0.8	4.5E-01	0.6	3.9E-01	-1.7	1.5E-01
ENSMUST00000174226				-2.2	2.8E-01	0.5	8.5E-01	0.8	7.2E-01	-1.9	4.0E-01
ENSMUST00000174228	ol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) [Source:MGI Symbol;Acc:M	G3UXY8		1.7	4.2E-01	3.9	9.1E-02	-0.5	8.1E-01	-2.6	1.9E-01
ENSMUST00000124817				4.9	2.1E-05	-3.2	4.8E-02	-1.4	1.4E-01	-2.1	2.3E-01
ENSMUST00000132143				4.9	1.1E-05	-8.2	2.3E-03	-0.8	2.1E-01	-0.6	7.8E-01
ENSMUST00000189746				4.9	7.7E-04	5.1	1.6E-02	0.5	7.8E-01	1.1	3.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000123890				4.9	8.6E-03	3.8	9.8E-02	-0.6	7.9E-01	2.4	1.0E-01
ENSMUST00000146083				4.9	1.3E-02	4.6	3.4E-03	-1.4	3.1E-01	0.3	6.8E-01
ENSMUST00000152999				4.9	1.6E-04	-3.4	7.8E-03	0.8	1.6E-01	0.0	1.0E+00
ENSMUST00000148742				4.8	3.4E-03	6.2	5.1E-04	-0.6	6.3E-01	-0.6	4.3E-01
ENSMUST00000174252	SCY1-like 2 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1289172]		Q8CFE4	-0.5	3.2E-01	1.0	1.5E-01	1.5	1.1E-02	0.1	9.3E-01
ENSMUST00000122349				4.8	2.8E-03	2.1	4.7E-01	5.4	2.9E-02	-2.3	3.9E-01
ENSMUST00000140340				4.8	5.2E-04	5.6	7.9E-04	-0.6	6.4E-01	-0.3	7.0E-01
ENSMUST00000159136				4.8	1.5E-02	-5.7	2.3E-04	-0.1	7.3E-01	-1.9	1.3E-01
ENSMUST00000165410				4.8	2.2E-02	3.1	3.7E-02	-0.1	9.2E-01	-0.6	5.3E-01
ENSMUST00000152332				4.8	1.6E-03	3.4	1.6E-02	-1.9	1.2E-01	-0.3	7.3E-01
ENSMUST00000130921				4.8	7.0E-05	-7.2	1.5E-04	1.0	1.8E-02	-0.8	5.6E-01
ENSMUST00000134883				4.8	2.8E-05	-6.8	2.3E-04	0.8	5.4E-02	-0.6	6.2E-01
ENSMUST00000129520				4.8	5.8E-05	4.2	2.9E-02	-1.5	3.8E-01	-0.5	6.5E-01
ENSMUST00000144161				4.8	4.5E-05	5.1	1.8E-03	0.3	7.9E-01	0.8	3.0E-01
ENSMUST00000134605				4.8	6.3E-04	2.3	2.7E-01	0.4	8.2E-01	2.7	1.1E-01
ENSMUST00000174281	BCL2-associated athanogene 6 [Source:MGI Symbol;Acc:MGI:1919439]	Q3TDL4		3.8	1.2E-01	1.3	7.4E-01	1.4	6.0E-01	3.8	3.0E-01
ENSMUST00000136385				4.8	4.9E-06	-5.2	3.7E-04	-0.3	4.1E-01	-0.8	4.6E-01
ENSMUST00000151339				4.8	3.9E-03	4.1	1.3E-02	-1.2	4.3E-01	-0.4	6.2E-01
ENSMUST00000174288	transmembrane protein 127 [Source:MGI Symbol;Acc:MGI:1916720]	G3UZT7		2.9	1.8E-01	-0.7	8.0E-01	-2.9	1.8E-01	0.7	7.9E-01
ENSMUST00000192332				4.8	5.2E-03	0.0	9.8E-01	5.9	5.6E-05	-1.0	3.9E-01
ENSMUST00000142433				4.8	3.6E-04	5.1	3.9E-03	0.0	9.7E-01	-0.6	5.0E-01
ENSMUST00000174297				-1.1	2.9E-01	0.3	7.8E-01	0.4	6.9E-01	-1.0	3.8E-01
ENSMUST00000174298	tumor necrosis factor, alpha-induced protein 2 [Source:MGI Symbol;Acc:MGI:104960]	G3UWJ7		-1.2	3.8E-01	-2.2	3.0E-01	-0.1	9.4E-01	1.0	6.1E-01
ENSMUST00000174299	retinoid X receptor beta [Source:MGI Symbol;Acc:MGI:98215]	G3UXP8		-0.4	8.9E-01	5.8	2.0E-01	4.7	1.9E-01	-1.5	7.0E-01
ENSMUST00000136442				4.8	3.7E-03	6.0	2.5E-04	-0.3	7.4E-01	0.9	1.9E-01
ENSMUST00000174302	upstream binding transcription factor, RNA polymerase I [Source:MGI Symbol;Acc:MGI:98512]	A2AWT5		4.4	2.0E-01	4.8	3.8E-01	2.4	6.4E-01	2.0	5.1E-01
ENSMUST00000190239				4.8	3.0E-04	4.1	4.9E-03	-0.8	4.7E-01	-2.1	3.8E-02
ENSMUST00000180647				4.8	9.5E-04	3.0	1.1E-02	-1.5	1.4E-01	0.2	7.8E-01
ENSMUST00000114684				4.8	1.4E-04	-3.1	4.2E-02	1.5	5.4E-02	0.5	7.3E-01
ENSMUST00000174311				0.5	6.3E-01	0.6	6.4E-01	0.9	4.0E-01	0.7	5.3E-01
ENSMUST00000125179				4.8	6.2E-05	3.2	6.3E-02	-0.5	7.4E-01	2.1	1.0E-01
ENSMUST00000174317	jumonji domain containing 1C [Source:MGI Symbol;Acc:MGI:1918614]	G3UYW3		2.5	9.3E-02	4.3	3.3E-02	1.1	5.0E-01	-0.7	6.1E-01
ENSMUST00000138565				4.8	4.3E-03	6.8	7.0E-05	0.2	8.6E-01	-0.6	2.7E-01
ENSMUST00000147099				4.8	1.3E-03	5.0	6.2E-04	-2.0	9.4E-02	-0.3	6.5E-01
ENSMUST00000162762				4.8	5.9E-04	-2.1	2.4E-01	1.7	1.6E-01	-0.8	6.4E-01
ENSMUST00000174337	neurexin I [Source:MGI Symbol;Acc:MGI:1096391]	G3UXK2	P0DI97	3.6	1.2E-01	4.9	6.1E-02	-0.5	8.4E-01	-1.8	2.9E-01
ENSMUST00000133699				4.8	3.5E-04	7.1	6.7E-05	-0.5	6.2E-01	-0.7	2.1E-01
ENSMUST00000174343	ubiquitination factor E4B [Source:MGI Symbol;Acc:MGI:1927086]	G3UZM6		-0.6	8.3E-01	2.0	5.4E-01	1.5	5.6E-01	-1.1	7.3E-01
ENSMUST00000119584				4.8	7.5E-04	5.3	4.8E-04	0.5	5.7E-01	-0.4	4.7E-01
ENSMUST00000174348	-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10 [Source:MGI Symbol;Acc:M	G3UXX0		0.8	5.0E-01	0.9	5.9E-01	0.5	7.4E-01	0.3	8.1E-01
ENSMUST00000174350				1.5	6.1E-02	1.4	1.0E-01	-0.8	2.8E-01	-0.7	3.2E-01
ENSMUST00000139717				4.8	1.0E-05	-2.8	1.7E-01	0.9	3.9E-01	-0.5	7.8E-01
ENSMUST00000185610				4.8	1.0E-04	-11.1	6.0E-06	-2.0	7.1E-05	-0.1	9.6E-01
ENSMUST00000174363				-1.2	3.8E-01	-2.1	3.1E-01	-0.1	9.1E-01	0.7	7.2E-01
ENSMUST00000174366	DEAH (Asp-Glu-Ala-His) box polypeptide 16 [Source:MGI Symbol;Acc:MGI:1916442]	Q05BH3		-4.9	1.3E-01	3.1	2.7E-01	1.6	5.2E-01	-6.4	5.1E-02
ENSMUST00000192138				4.8	2.7E-03	8.4	8.8E-05	-0.4	7.9E-01	-0.3	5.9E-01
ENSMUST00000134927				4.8	6.0E-05	6.3	2.2E-02	-0.5	8.4E-01	-1.4	3.2E-01
ENSMUST00000174372	solute carrier family 2 (facilitated glucose transporter), member 1 [Source:MGI Symbol;Acc:MGI:95755]	G3V010		-1.3	5.5E-01	-3.0	2.6E-01	-1.1	5.2E-01	0.6	8.1E-01
ENSMUST00000138604				4.8	5.5E-04	4.9	1.3E-02	-0.6	7.3E-01	1.4	1.9E-01
ENSMUST00000140602				4.8	1.4E-02	7.2	6.8E-05	-1.4	2.5E-01	-0.7	2.4E-01
ENSMUST00000153366				4.8	2.7E-03	-3.0	2.9E-02	-0.3	6.2E-01	-2.2	1.4E-01
ENSMUST00000193006				4.8	6.4E-05	-4.4	9.2E-02	2.4	8.1E-02	0.2	9.5E-01
ENSMUST00000120982				4.8	2.9E-03	7.4	2.6E-04	-0.4	7.5E-01	-0.5	4.4E-01
ENSMUST00000154492				4.8	5.3E-03	8.0	5.0E-05	0.5	7.0E-01	0.1	8.9E-01
ENSMUST00000174396				-0.1	9.3E-01	2.6	9.8E-02	0.5	6.9E-01	-2.2	8.0E-02
ENSMUST00000188840				4.8	1.4E-04	7.9	1.2E-05	0.1	8.8E-01	-0.9	7.5E-02
ENSMUST00000174399				-2.7	1.3E-01	-1.9	4.0E-01	0.1	9.3E-01	-0.7	7.7E-01
ENSMUST00000120530				4.8	1.3E-03	2.6	1.0E-01	-0.3	8.2E-01	0.5	6.1E-01
ENSMUST00000132491				4.8	8.9E-04	3.0	2.4E-03	0.7	2.8E-01	0.3	6.4E-01
ENSMUST00000174407	zinc finger protein 141 [Source:MGI Symbol;Acc:MGI:3584269]	G3UY09		0.1	8.7E-01	0.2	6.9E-01	0.3	5.6E-01	0.1	8.7E-01
ENSMUST00000191512				4.8	6.0E-04	-5.3	1.1E-02	0.4	6.6E-01	-2.6	2.3E-01
ENSMUST00000145605				4.8	1.5E-03	5.0	5.2E-03	-0.2	8.9E-01	-1.6	1.6E-01
ENSMUST00000127761				4.8	4.5E-05	5.4	6.6E-02	-0.6	8.3E-01	-0.7	6.7E-01
ENSMUST00000174418	myotubularin related protein 12 [Source:MGI Symbol;Acc:MGI:2443034]	G3XA69		-1.4	5.0E-02	0.3	6.8E-01	0.5	3.7E-01	-1.3	1.2E-01
ENSMUST00000174422	protein kinase N2 [Source:MGI Symbol;Acc:MGI:109211]	G3UZM9		-0.2	9.3E-01	4.4	3.0E-01	4.5	1.7E-01	-0.1	9.7E-01
ENSMUST00000155153				4.8	1.1E-03	6.9	7.5E-05	-0.6	6.2E-01	0.0	9.7E-01
ENSMUST00000123806				4.8	1.0E-03	5.6	5.7E-04	-0.3	7.8E-01	1.5	5.1E-02
ENSMUST00000144385				4.8	6.1E-05	8.0	3.5E-04	-0.8	6.2E-01	0.6	4.5E-01
ENSMUST00000180726				4.8	1.1E-03	6.0	6.2E-04	0.4	7.1E-01	-0.5	4.6E-01
ENSMUST00000174442				-1.5	2.0E-01	-0.2	8.7E-01	0.8	4.3E-01	-0.5	7.2E-01
ENSMUST00000159261				4.8	1.4E-04	6.4	3.7E-02	-0.8	7.9E-01	0.2	8.9E-01
ENSMUST00000150725				4.8	3.5E-05	5.6	1.1E-03	-0.9	4.9E-01	0.4	5.6E-01
ENSMUST00000174459	glycophorin C [Source:MGI Symbol;Acc:MGI:1098566]		Q78HU7	2.4	2.6E-01	5.4	1.4E-01	3.8	2.5E-01	0.9	6.8E-01
ENSMUST00000174461	chromodomain helicase DNA binding protein 1 [Source:MGI Symbol;Acc:MGI:88393]	G3V014		-3.0	4.9E-02	1.4	2.9E-01	1.2	2.5E-01	-3.2	4.9E-02
ENSMUST00000174462	zinc finger protein 266 [Source:MGI Symbol;Acc:MGI:1924769]	E9Q2S7		0.7	2.0E-01	0.5	4.0E-01	0.0	9.2E-01	0.1	9.0E-01
ENSMUST00000121462				4.8	2.4E-03	-2.7	9.2E-03	-0.5	3.1E-01	-0.3	7.7E-01
ENSMUST00000194493				4.8	7.4E-04	-2.5	6.3E-02	0.7	3.3E-01	-1.6	2.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000141548				4.8	2.5E-04	-3.1	4.9E-03	-0.2	6.8E-01	-0.3	6.9E-01
ENSMUST00000142000				4.8	3.4E-05	7.4	1.6E-06	-0.2	7.2E-01	0.1	7.6E-01
ENSMUST00000174485	OTU domain containing 4 [Source:MGI Symbol;Acc:MGI:1098801]	G3UXM1		2.5	2.0E-01	1.2	5.2E-01	-2.1	2.1E-01	-0.8	6.7E-01
ENSMUST00000144320				4.8	2.3E-02	6.0	5.1E-05	-3.1	1.5E-02	-0.2	7.3E-01
ENSMUST00000139650				4.8	2.8E-05	7.3	4.7E-05	0.5	6.3E-01	-0.2	7.5E-01
ENSMUST00000153781				4.8	1.3E-02	8.2	1.5E-04	-0.8	6.1E-01	0.9	1.7E-01
ENSMUST00000175820				4.8	6.4E-04	4.9	5.0E-04	0.7	4.3E-01	-0.2	7.3E-01
ENSMUST00000182251				4.8	2.7E-03	-2.1	2.9E-02	0.6	1.9E-01	-0.1	8.7E-01
ENSMUST00000149162				4.8	1.1E-02	5.3	3.7E-06	-0.3	5.9E-01	-0.4	2.9E-01
ENSMUST00000174514	CDK2-associated protein 2 [Source:MGI Symbol;Acc:MGI:1098779]	G3UYI1		-2.3	3.7E-02	-0.6	6.1E-01	0.2	8.0E-01	-1.5	1.9E-01
ENSMUST00000170577				4.8	7.1E-04	3.3	6.7E-02	-0.1	9.7E-01	2.8	3.3E-02
ENSMUST00000127743				4.8	4.8E-05	6.3	7.2E-04	-0.6	6.4E-01	-0.5	5.1E-01
ENSMUST00000145382				4.8	1.2E-03	6.1	1.3E-04	-1.8	1.1E-01	-0.4	5.3E-01
ENSMUST00000123246				4.8	9.3E-03	8.8	5.9E-05	-0.7	6.3E-01	-0.5	4.1E-01
ENSMUST00000138597				4.8	2.1E-05	6.1	6.9E-05	-0.1	9.2E-01	-0.6	2.3E-01
ENSMUST00000143724				4.8	2.0E-02	2.0	3.5E-01	-1.4	5.0E-01	1.9	2.0E-01
ENSMUST00000174533	polyadenylate binding protein-interacting protein 1 [Source:MGI Symbol;Acc:MGI:2384993]	G3UZ67		-2.7	3.8E-01	-0.7	8.7E-01	1.3	6.5E-01	-0.8	8.4E-01
ENSMUST00000174534				4.1	1.5E-01	6.2	5.5E-02	-0.2	9.6E-01	-2.2	2.3E-01
ENSMUST00000174536				0.5	4.8E-01	-1.1	2.7E-01	-0.4	6.1E-01	1.3	1.9E-01
ENSMUST00000144198				4.8	1.9E-02	1.2	8.0E-02	0.3	5.5E-01	0.3	6.5E-01
ENSMUST00000174551				0.0	9.7E-01	-0.6	6.5E-01	0.2	8.2E-01	0.8	4.9E-01
ENSMUST00000122013				4.8	1.6E-03	1.6	4.6E-02	-0.7	2.6E-01	0.3	6.2E-01
ENSMUST00000174554				1.3	3.9E-01	2.7	1.8E-01	0.3	8.6E-01	-1.1	4.4E-01
ENSMUST00000174556	mutS homolog 5 (E. coli) [Source:MGI Symbol;Acc:MGI:1329021]	G3UYF3		0.8	3.5E-01	1.1	3.0E-01	-0.1	9.3E-01	-0.4	6.8E-01
ENSMUST00000163567				4.8	3.4E-05	6.9	3.6E-04	0.8	5.4E-01	-0.7	3.0E-01
ENSMUST00000174559	WAPL cohesin release factor [Source:MGI Symbol;Acc:MGI:2675859]	G3UXQ2		-0.4	8.2E-01	-2.5	1.3E-01	-4.2	8.8E-03	-2.2	2.6E-01
ENSMUST00000191526				4.8	9.8E-03	-9.2	4.6E-04	0.5	2.6E-01	3.6	6.1E-02
ENSMUST00000150668				4.8	5.1E-04	-6.9	1.6E-04	0.0	9.4E-01	-0.9	4.8E-01
ENSMUST00000167340				4.8	3.6E-03	7.2	1.7E-04	-1.9	2.0E-01	-1.8	2.4E-02
ENSMUST00000180545				4.8	1.0E-04	4.1	7.2E-02	-0.7	7.4E-01	-0.4	8.0E-01
ENSMUST00000120575				4.8	1.6E-03	-4.5	9.7E-04	0.1	7.6E-01	-0.8	4.4E-01
ENSMUST00000153509				4.8	7.2E-03	4.2	1.4E-02	-1.4	3.7E-01	0.3	7.1E-01
ENSMUST00000157025				4.8	1.9E-04	-5.6	5.8E-05	-0.1	7.6E-01	-0.7	4.0E-01
ENSMUST00000174579				-0.8	6.9E-01	-2.0	5.3E-01	0.0	9.9E-01	1.1	6.9E-01
ENSMUST00000174580				5.5	4.2E-02	8.5	6.8E-03	-0.7	7.9E-01	-3.7	2.7E-02
ENSMUST00000174583				2.0	4.6E-02	2.9	2.0E-02	0.4	7.0E-01	-0.5	5.4E-01
ENSMUST00000135463				4.8	1.6E-03	4.7	9.2E-03	-0.4	7.9E-01	0.0	9.7E-01
ENSMUST00000142473				4.8	1.3E-03	-6.4	6.2E-04	1.1	5.7E-02	1.5	2.7E-01
ENSMUST00000143308				4.8	4.9E-04	-1.4	1.9E-01	0.7	3.2E-01	-0.1	9.0E-01
ENSMUST00000174589				1.9	4.1E-02	1.5	1.9E-01	0.0	9.9E-01	0.4	6.5E-01
ENSMUST00000137327				4.8	4.0E-03	7.1	4.0E-03	-0.7	7.2E-01	-2.4	5.5E-02
ENSMUST00000163830				4.8	5.5E-04	-4.6	7.8E-02	2.0	6.6E-02	2.2	3.6E-01
ENSMUST00000174598	WD repeat and FYVE domain containing 3 [Source:MGI Symbol;Acc:MGI:1096875]	G3UYW1		4.9	6.0E-02	3.5	2.8E-01	0.8	7.8E-01	2.1	4.0E-01
ENSMUST00000174602	ubiquitin specific peptidase 32 [Source:MGI Symbol;Acc:MGI:2144475]	G3UZF4		-1.2	3.1E-01	-0.6	7.2E-01	0.7	5.4E-01	0.1	9.4E-01
ENSMUST00000128722				4.8	1.8E-02	-9.5	1.6E-03	-0.6	3.3E-01	1.0	6.6E-01
ENSMUST00000169448				4.8	6.2E-03	7.0	1.0E-04	-0.5	6.5E-01	-1.7	2.0E-02
ENSMUST00000144220				4.8	2.4E-02	5.6	2.1E-04	-0.4	7.0E-01	-0.7	2.8E-01
ENSMUST00000174620				1.0	2.9E-01	0.2	8.4E-01	-1.5	9.6E-02	-0.7	4.6E-01
ENSMUST00000174625				1.4	3.9E-02	3.0	3.3E-03	1.0	1.5E-01	-0.6	3.3E-01
ENSMUST00000174628	protein phosphatase 2, regulatory subunit A, beta [Source:MGI Symbol;Acc:MGI:1920949]	G3UWS4		4.5	6.7E-02	4.0	2.6E-01	2.6	3.5E-01	3.1	2.8E-01
ENSMUST00000174629	janus kinase and microtubule interacting protein 1 [Source:MGI Symbol;Acc:MGI:1923321]	G3UYZ9		1.6	2.6E-01	6.9	6.6E-04	0.4	7.9E-01	-4.9	1.3E-03
ENSMUST00000174632	fused in sarcoma [Source:MGI Symbol;Acc:MGI:1353633]	G3UXT7		-4.2	1.9E-01	-1.6	6.8E-01	1.6	4.9E-01	-1.0	8.0E-01
ENSMUST00000185614				4.8	5.3E-04	7.4	8.9E-05	-1.2	3.6E-01	0.2	7.7E-01
ENSMUST00000174647	molybdenum cofactor synthesis 1 [Source:MGI Symbol;Acc:MGI:1928904]	G3UXJ3		-2.3	1.8E-01	0.0	9.9E-01	0.5	7.2E-01	-1.8	3.7E-01
ENSMUST00000174651	predicted gene 20604 [Source:MGI Symbol;Acc:MGI:5305180]	F8WIA3		-1.4	5.2E-02	0.9	2.9E-01	1.3	6.1E-02	-1.0	2.1E-01
ENSMUST00000174653	KRR1, small subunit (SSU) processome component, homolog (yeast) [Source:MGI Symbol;Acc:MGI:1289274]	G3UZA0		-1.9	5.2E-01	-5.4	1.4E-01	-4.1	4.7E-02	-0.6	8.8E-01
ENSMUST00000121299				4.8	2.5E-05	6.9	4.0E-04	-0.7	6.2E-01	-0.2	7.4E-01
ENSMUST00000139970				4.8	2.1E-04	3.9	2.4E-03	-0.1	8.7E-01	-1.2	1.1E-01
ENSMUST00000174661	paired-like homeodomain transcription factor 2 [Source:MGI Symbol;Acc:MGI:109340]		P97474	3.4	8.9E-02	5.2	2.1E-02	-0.4	8.3E-01	-2.2	1.1E-01
ENSMUST00000174666				-0.1	9.5E-01	-1.2	6.5E-01	-1.6	4.1E-01	-0.5	8.3E-01
ENSMUST00000124330				4.8	2.4E-03	3.8	1.4E-02	-4.2	3.0E-02	-2.7	3.6E-02
ENSMUST00000118339				4.8	1.3E-03	-0.7	4.6E-01	0.5	4.0E-01	-0.7	4.8E-01
ENSMUST00000120534				4.8	2.8E-03	5.9	6.4E-03	-0.7	7.1E-01	-1.7	1.5E-01
ENSMUST00000153619				4.8	6.0E-03	5.2	2.5E-02	-1.2	5.4E-01	0.4	7.2E-01
ENSMUST00000183163				4.8	3.1E-05	6.5	4.8E-04	-0.7	6.0E-01	-0.6	4.2E-01
ENSMUST00000174689				0.0	9.9E-01	-3.7	1.3E-01	-3.3	2.9E-02	0.3	8.9E-01
ENSMUST00000174691	polyadenylate binding protein-interacting protein 1 [Source:MGI Symbol;Acc:MGI:2384993]	G3UZH8		-0.2	9.4E-01	-3.4	2.9E-01	-3.7	8.1E-02	-0.5	8.7E-01
ENSMUST00000174692	tumor necrosis factor, alpha-induced protein 2 [Source:MGI Symbol;Acc:MGI:104960]	G3UX17		-1.2	6.9E-01	1.4	7.5E-01	2.4	3.9E-01	-0.2	9.6E-01
ENSMUST00000174694	large tumor suppressor 2 [Source:MGI Symbol;Acc:MGI:1354386]	G3UXG3		2.3	2.5E-01	0.9	7.1E-01	-0.6	7.4E-01	0.8	7.1E-01
ENSMUST00000130433				4.8	7.5E-03	7.4	1.1E-04	-0.7	5.9E-01	0.9	1.4E-01
ENSMUST00000174698	WD repeat and FYVE domain containing 3 [Source:MGI Symbol;Acc:MGI:1096875]		Q6VNB8	1.9	1.5E-01	4.6	1.6E-02	1.9	1.9E-01	-0.8	5.1E-01
ENSMUST00000142470				4.8	9.5E-05	2.8	2.8E-03	-0.6	3.3E-01	-0.9	1.5E-01
ENSMUST00000144744				4.8	1.1E-03	3.0	3.4E-03	-0.5	5.0E-01	-0.7	2.8E-01
ENSMUST00000174709				2.8	5.7E-02	5.2	1.7E-02	1.0	5.6E-01	-1.3	2.9E-01
ENSMUST00000093856				4.8	1.7E-02	-6.9	6.5E-04	-0.5	3.0E-01	0.3	8.3E-01
ENSMUST00000174713	platelet endothelial aggregation receptor 1 [Source:MGI Symbol;Acc:MGI:1920432]	G3UYT5		0.7	6.3E-01	5.4	1.7E-02	1.8	3.5E-01	-2.9	5.2E-02
ENSMUST00000156661				4.8	1.6E-02	6.6	3.8E-05	0.6	4.6E-01	0.6	2.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000174717	kelch domain containing 4 [Source:MGI Symbol;Acc:MGI:2384569]	G3UZ63		-1.1	3.5E-01	-0.2	9.0E-01	2.0	1.4E-01	1.1	4.8E-01
ENSMUST00000156869				4.8	2.4E-04	3.7	5.7E-03	-3.5	1.3E-02	-0.2	7.5E-01
ENSMUST00000119832				4.8	1.4E-03	7.7	2.7E-04	-0.1	9.5E-01	-0.2	7.4E-01
ENSMUST00000160989				4.8	8.7E-03	-3.5	8.5E-04	-0.2	6.4E-01	-3.5	5.3E-03
ENSMUST00000137698				4.8	2.5E-05	-6.1	7.9E-03	0.5	3.9E-01	4.8	2.4E-02
ENSMUST00000161967				4.8	2.2E-03	6.7	2.0E-02	-0.8	7.8E-01	-1.4	3.5E-01
ENSMUST00000174740				-0.1	9.1E-01	-0.5	8.1E-01	0.7	6.2E-01	1.1	5.4E-01
ENSMUST00000174741				-1.9	5.2E-01	-1.7	6.1E-01	-1.0	6.5E-01	-1.1	7.5E-01
ENSMUST00000174743	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 [Source:MGI Symbol;Acc:MGI:1916327]	G3UWV7		-0.6	7.8E-01	-5.0	7.6E-02	-4.9	5.9E-03	-0.6	8.4E-01
ENSMUST00000174751	histocompatibility 2, class II antigen A, alpha [Source:MGI Symbol;Acc:MGI:95895]	G3UWR9		-0.7	4.7E-01	-5.8	3.1E-03	-3.9	4.6E-04	1.2	4.4E-01
ENSMUST00000179040				4.8	6.6E-05	-1.8	1.0E-01	-0.2	6.9E-01	-0.5	6.2E-01
ENSMUST00000174766	l(3)mbt-like 3 (Drosophila) [Source:MGI Symbol;Acc:MGI:2143628]		Q8BLB7	-1.4	1.1E-01	0.1	9.6E-01	1.2	1.4E-01	-0.3	7.6E-01
ENSMUST00000185352				4.8	5.6E-04	4.9	1.7E-03	-0.6	6.1E-01	0.8	2.9E-01
ENSMUST00000109105				4.8	4.3E-04	0.6	2.8E-01	-0.3	4.1E-01	0.3	5.2E-01
ENSMUST00000174779	casein kinase 2, beta polypeptide [Source:MGI Symbol;Acc:MGI:88548]	G3UXG7		-4.8	3.9E-02	-1.8	4.7E-01	1.8	2.7E-01	-1.1	6.7E-01
ENSMUST00000136685				4.8	8.5E-05	-1.6	3.6E-01	1.0	3.4E-01	-1.9	3.1E-01
ENSMUST00000145121				4.8	9.7E-04	-0.4	6.7E-01	1.2	9.9E-02	-1.3	1.9E-01
ENSMUST00000120894				4.8	1.1E-03	3.2	1.0E-02	0.3	7.4E-01	-0.1	9.1E-01
ENSMUST00000119008				4.8	2.6E-03	6.2	2.4E-03	-0.7	6.8E-01	-0.4	6.9E-01
ENSMUST00000182049				4.8	8.9E-06	-4.4	3.8E-03	0.6	3.5E-01	-3.1	7.9E-02
ENSMUST00000174805	proline-rich coiled-coil 2A [Source:MGI Symbol;Acc:MGI:1915467]	G3UX48		-1.8	4.5E-02	-0.9	4.0E-01	1.0	1.9E-01	0.1	9.4E-01
ENSMUST00000174806	sorting nexin 14 [Source:MGI Symbol;Acc:MGI:2155664]	G3UX33		-2.1	3.8E-01	-3.3	3.2E-01	-1.0	5.6E-01	0.2	9.5E-01
ENSMUST00000152770				4.8	4.2E-05	7.3	1.3E-04	-0.2	8.4E-01	-0.2	6.7E-01
ENSMUST00000174817	DNA methyltransferase 3A [Source:MGI Symbol;Acc:MGI:1261827]		O88508	1.9	3.2E-01	1.5	5.0E-01	-0.4	8.4E-01	0.0	1.0E+00
ENSMUST00000136180				4.8	9.2E-04	4.6	1.3E-03	-2.2	8.5E-02	-1.3	1.6E-01
ENSMUST00000174822	unc-13 homolog D (C. elegans) [Source:MGI Symbol;Acc:MGI:1917700]		B2RUP2	0.7	8.0E-01	3.7	4.1E-01	4.2	1.9E-01	1.2	7.6E-01
ENSMUST00000160161				4.8	1.9E-02	-1.9	5.0E-02	-0.9	1.7E-01	-2.1	4.9E-02
ENSMUST00000187166				4.8	1.1E-03	5.8	6.5E-05	0.2	8.2E-01	0.4	4.5E-01
ENSMUST00000191021				4.8	7.9E-04	7.8	5.2E-03	-0.3	9.1E-01	1.3	2.2E-01
ENSMUST00000174833				-0.3	6.1E-01	-0.4	5.3E-01	-0.1	9.0E-01	0.1	8.6E-01
ENSMUST00000174835				-1.0	3.0E-01	0.6	5.7E-01	-0.2	8.2E-01	-1.9	9.4E-02
ENSMUST00000174836	SET domain containing 1B [Source:MGI Symbol;Acc:MGI:2652820]		Q8CFT2	2.2	3.8E-01	2.6	4.4E-01	0.6	8.2E-01	0.3	9.1E-01
ENSMUST00000174839				-3.7	1.1E-01	-2.8	2.8E-01	0.3	8.6E-01	-0.6	8.2E-01
ENSMUST00000133107				4.7	1.8E-06	3.4	8.8E-03	-2.5	6.8E-02	0.7	4.1E-01
ENSMUST00000174850	regulatory factor X, 3 (influences HLA class II expression) [Source:MGI Symbol;Acc:MGI:106582]		P48381	-1.5	2.2E-01	1.2	4.3E-01	2.0	1.4E-01	-0.8	5.8E-01
ENSMUST00000171504				4.7	1.2E-03	4.7	6.6E-05	-0.6	3.9E-01	0.0	9.7E-01
ENSMUST00000174854				1.2	1.1E-01	0.6	5.3E-01	-0.4	6.0E-01	0.3	7.4E-01
ENSMUST00000176005				4.7	4.4E-05	6.8	5.7E-07	0.0	9.7E-01	-0.3	2.6E-01
ENSMUST00000131831				4.7	9.3E-05	4.7	7.1E-02	-0.6	8.2E-01	3.2	4.0E-02
ENSMUST00000174878				-0.9	4.0E-01	-0.1	9.5E-01	0.6	5.7E-01	-0.2	8.5E-01
ENSMUST00000157074				4.7	2.3E-05	-5.5	1.5E-02	1.9	2.4E-02	-0.9	6.6E-01
ENSMUST00000174887				-0.1	9.6E-01	-3.0	2.9E-01	-3.4	7.5E-02	-0.6	8.5E-01
ENSMUST00000174888				-2.3	6.3E-02	-1.3	3.1E-01	-0.2	8.2E-01	-1.3	3.3E-01
ENSMUST00000126014				4.7	4.5E-03	-8.1	2.8E-04	-1.0	4.2E-02	-0.3	8.7E-01
ENSMUST00000135422				4.7	2.0E-03	4.9	1.5E-04	-0.5	5.4E-01	0.3	5.8E-01
ENSMUST00000141666				4.7	3.7E-03	-1.5	1.6E-01	0.6	3.5E-01	-1.6	1.7E-01
ENSMUST00000121539				4.7	2.9E-03	3.3	2.5E-02	-3.2	4.4E-02	-0.5	5.9E-01
ENSMUST00000175654				5.2	1.1E-01	7.5	4.4E-02	-0.2	9.6E-01	-2.5	1.9E-01
ENSMUST00000175656	N-acylethanolamine acid amidase [Source:MGI Symbol;Acc:MGI:1914361]	H3BL13		-2.3	3.9E-02	-1.3	3.6E-01	0.6	5.1E-01	-0.5	7.3E-01
ENSMUST00000175658	popeye domain containing 3 [Source:MGI Symbol;Acc:MGI:1930153]	H3BKF9		6.4	4.0E-02	6.3	5.9E-02	-0.8	8.1E-01	-0.6	7.1E-01
ENSMUST00000174137				4.7	7.4E-06	4.7	2.7E-04	-0.1	8.9E-01	0.9	1.3E-01
ENSMUST00000123849				4.7	3.4E-04	7.1	9.6E-04	-0.4	8.2E-01	-0.7	3.6E-01
ENSMUST00000123888				4.7	5.7E-05	6.1	3.1E-03	-0.8	6.4E-01	1.1	2.5E-01
ENSMUST00000139953				4.7	1.7E-03	4.8	1.0E-02	-0.1	9.7E-01	0.9	3.9E-01
ENSMUST00000143182				4.7	2.8E-05	5.5	5.4E-04	-0.5	6.3E-01	0.5	5.2E-01
ENSMUST00000142056				4.7	5.5E-03	5.7	1.0E-02	1.6	3.7E-01	0.7	5.3E-01
ENSMUST00000133775				4.7	1.1E-04	6.2	8.5E-03	-0.8	6.8E-01	0.7	5.4E-01
ENSMUST00000143604				4.7	1.9E-04	4.2	8.9E-04	-1.1	2.2E-01	-0.3	6.3E-01
ENSMUST00000175684				1.3	4.4E-01	3.7	6.0E-02	-0.4	8.3E-01	-2.8	8.9E-02
ENSMUST00000175689	geminin [Source:MGI Symbol;Acc:MGI:1927344]	H3BLK4		-0.8	6.5E-01	-0.2	9.2E-01	-0.3	8.8E-01	-0.9	6.5E-01
ENSMUST00000175692	RWD domain containing 4A [Source:MGI Symbol;Acc:MGI:2681000]	H3BJI4		-2.4	4.6E-02	-4.1	1.5E-02	-0.6	4.6E-01	1.2	4.3E-01
ENSMUST00000154249				4.7	6.1E-04	6.0	6.3E-06	-1.7	3.2E-02	0.0	9.2E-01
ENSMUST00000118634				4.7	3.7E-04	6.9	8.2E-04	0.1	9.7E-01	-1.0	2.4E-01
ENSMUST00000137947				4.7	5.3E-03	-7.7	3.0E-04	-1.6	6.4E-03	-0.8	5.8E-01
ENSMUST00000161860				4.7	1.1E-03	-4.4	4.2E-03	0.9	1.1E-01	-0.7	5.7E-01
ENSMUST00000155932				4.7	2.5E-03	5.7	3.3E-04	0.0	9.9E-01	0.2	7.1E-01
ENSMUST00000175726	RIKEN cDNA 9930021J03 gene [Source:MGI Symbol;Acc:MGI:2444398]	H3BL88		-0.5	5.2E-01	0.3	7.8E-01	0.7	3.3E-01	0.0	9.6E-01
ENSMUST00000124519				4.7	2.1E-03	-4.9	2.1E-04	-0.2	6.2E-01	-2.1	6.0E-02
ENSMUST00000130854				4.7	5.1E-04	5.1	2.0E-02	-0.6	7.4E-01	0.5	6.5E-01
ENSMUST00000175734	pleckstrin and Sec7 domain containing 2 [Source:MGI Symbol;Acc:MGI:1921252]		Q6P1I6	4.6	1.1E-01	5.2	5.6E-02	-3.8	2.0E-01	-4.5	3.0E-02
ENSMUST00000175741	peroxisomal biogenesis factor 12 [Source:MGI Symbol;Acc:MGI:2144177]	Q5SWQ8	Q8VC48	-0.9	8.0E-01	-1.2	7.8E-01	-1.2	6.6E-01	-0.9	8.4E-01
ENSMUST00000175743	acetyl-Coenzyme A acyltransferase 1A [Source:MGI Symbol;Acc:MGI:2148491]	H3BKL5		-1.3	6.2E-01	-2.6	4.5E-01	-1.6	4.1E-01	-0.4	9.2E-01
ENSMUST00000153982				4.7	4.6E-03	4.9	3.2E-02	-0.5	7.6E-01	-0.5	7.0E-01
ENSMUST00000175752	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 [Source:MGI Symbol;Acc:MGI:1933111]	H3BKE5		-5.3	3.8E-02	1.9	5.6E-01	5.9	2.8E-02	-1.3	6.6E-01
ENSMUST00000154458				4.7	7.4E-03	-5.9	3.1E-02	0.1	9.4E-01	-0.5	8.6E-01
ENSMUST00000175764	RIKEN cDNA 9930021J03 gene [Source:MGI Symbol;Acc:MGI:2444398]	H3BJL2		-2.8	9.4E-02	-3.0	3.1E-01	1.9	2.2E-01	2.1	4.6E-01
ENSMUST00000142648				4.7	6.7E-03	-1.2	9.2E-02	1.0	4.6E-02	-0.2	7.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000176741				4.7	6.0E-05	5.1	4.0E-02	-0.2	9.4E-01	-0.2	8.7E-01
ENSMUST00000149390				4.7	2.1E-03	-8.5	6.4E-03	-2.5	1.9E-02	-1.1	7.1E-01
ENSMUST00000175774	POU domain, class 2, transcription factor 2 [Source:MGI Symbol;Acc:MGI:101897]		Q00196	-2.2	1.8E-01	-3.6	1.9E-01	0.0	9.8E-01	1.4	5.8E-01
ENSMUST00000195026				4.7	2.1E-05	-7.2	1.4E-02	-1.1	2.0E-01	0.0	9.9E-01
ENSMUST00000147907				4.7	1.0E-02	1.3	3.5E-01	3.9	5.0E-03	-4.2	1.6E-02
ENSMUST00000175779	rho/rac guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:103264]	H3BJ40		1.0	6.9E-01	4.7	2.5E-01	3.9	2.5E-01	0.2	9.4E-01
ENSMUST00000152337				4.7	6.3E-03	7.8	3.5E-05	-0.6	6.1E-01	-0.8	1.4E-01
ENSMUST00000124415				4.7	1.1E-02	1.6	2.9E-02	-0.9	9.4E-02	-0.2	7.3E-01
ENSMUST00000175791	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	H3BKJ3		-2.7	1.7E-01	-2.8	2.4E-01	-0.8	5.4E-01	-0.7	7.8E-01
ENSMUST00000145063				4.7	5.9E-03	-1.1	6.0E-01	2.9	8.0E-02	-2.5	2.9E-01
ENSMUST00000185700				4.7	1.5E-02	2.6	7.6E-02	-5.3	1.6E-02	-1.0	3.8E-01
ENSMUST00000168474				4.7	5.1E-03	2.0	3.1E-01	8.6	1.9E-04	-0.9	5.7E-01
ENSMUST00000175805	zinc fingers and homeoboxes 1 [Source:MGI Symbol;Acc:MGI:109271]		P70121	2.1	3.2E-01	5.9	2.3E-02	1.2	5.6E-01	-2.6	1.7E-01
ENSMUST00000175806	Pbx/knotted 1 homeobox [Source:MGI Symbol;Acc:MGI:1201409]		O70477	2.0	5.4E-02	2.0	1.4E-01	0.7	5.1E-01	0.7	5.0E-01
ENSMUST00000133958				4.7	4.9E-03	-4.0	1.2E-01	2.1	7.7E-02	1.0	6.8E-01
ENSMUST00000143381				4.7	1.1E-02	2.7	3.0E-02	-0.4	6.4E-01	-0.4	6.7E-01
ENSMUST00000188973				4.7	9.9E-04	4.6	4.7E-03	-0.7	5.9E-01	-0.5	5.5E-01
ENSMUST00000178890				4.7	9.2E-04	3.8	1.8E-02	-1.3	3.4E-01	-1.4	1.5E-01
ENSMUST00000175823				3.7	4.2E-02	4.6	1.2E-02	-1.9	2.7E-01	-2.8	2.9E-02
ENSMUST00000175835	predicted gene 7120 [Source:MGI Symbol;Acc:MGI:3648543]	H3BJ86		2.4	2.6E-01	1.4	5.6E-01	-1.2	5.7E-01	-0.2	9.2E-01
ENSMUST00000117213				4.7	1.5E-03	5.6	1.8E-02	-0.7	7.3E-01	2.0	1.1E-01
ENSMUST00000182346				4.7	3.4E-03	-4.5	1.8E-02	0.0	9.6E-01	-0.8	6.7E-01
ENSMUST00000172162				4.7	1.2E-03	9.4	9.2E-06	0.7	5.1E-01	0.2	7.0E-01
ENSMUST00000140936				4.7	3.1E-03	-3.3	8.3E-02	-0.7	4.6E-01	-2.3	3.1E-01
ENSMUST00000175848	RAS-like, family 10, member B [Source:MGI Symbol;Acc:MGI:2685575]	H3BLI7		2.8	9.2E-02	5.2	5.2E-03	-0.5	7.4E-01	-3.0	2.4E-02
ENSMUST00000175849				0.9	5.3E-02	1.4	1.4E-02	-0.3	5.2E-01	-0.8	8.7E-02
ENSMUST00000142677				4.7	2.0E-04	5.4	1.3E-04	-1.1	2.6E-01	-0.8	1.8E-01
ENSMUST00000184548				4.7	2.0E-04	4.1	5.5E-05	-4.4	2.0E-04	-0.5	2.7E-01
ENSMUST00000150087				4.7	3.1E-02	-3.3	3.5E-02	0.5	4.3E-01	-0.8	5.7E-01
ENSMUST00000107383				4.7	1.1E-04	5.9	9.6E-04	-0.4	7.5E-01	-0.7	3.4E-01
ENSMUST00000129157				4.7	4.0E-04	9.0	4.2E-04	-0.9	6.4E-01	0.3	7.3E-01
ENSMUST00000192637				4.7	4.9E-03	-4.6	8.3E-03	1.4	4.6E-02	-1.0	5.1E-01
ENSMUST00000148395				4.7	8.5E-03	6.5	1.4E-04	-0.5	6.2E-01	-0.4	4.7E-01
ENSMUST00000077493				4.7	4.8E-03	3.3	3.1E-02	-2.4	1.3E-01	0.8	3.7E-01
ENSMUST00000175876	ceramide synthase 5 [Source:MGI Symbol;Acc:MGI:1919199]	H3BJ49		0.2	8.1E-01	-0.1	8.9E-01	0.2	7.8E-01	0.5	5.7E-01
ENSMUST00000145495				4.7	8.1E-03	-2.0	3.9E-01	1.3	3.5E-01	-0.7	7.5E-01
ENSMUST00000175881	forkhead box O3 [Source:MGI Symbol;Acc:MGI:1890081]		Q9WVH4	0.2	9.3E-01	-1.6	6.3E-01	-0.5	8.2E-01	1.3	6.8E-01
ENSMUST00000148434				4.7	2.9E-04	6.3	1.6E-04	-0.5	6.3E-01	-1.0	1.2E-01
ENSMUST00000175883	receptor-like tyrosine kinase [Source:MGI Symbol;Acc:MGI:101766]		Q01887	0.5	5.9E-01	-1.2	4.4E-01	0.0	9.6E-01	1.6	2.6E-01
ENSMUST00000175885	non-SMC condensin I complex, subunit H [Source:MGI Symbol;Acc:MGI:2444777]	H3BL21		-3.0	5.4E-02	0.6	6.8E-01	0.7	5.2E-01	-2.8	7.7E-02
ENSMUST00000139994				4.7	2.2E-02	-8.3	2.0E-04	0.0	9.7E-01	-1.0	5.1E-01
ENSMUST00000133729				4.7	1.5E-04	5.6	5.3E-04	-0.6	6.2E-01	0.3	5.9E-01
ENSMUST00000175898	sine oculis-related homeobox 3 [Source:MGI Symbol;Acc:MGI:102764]		Q62233	3.7	6.8E-02	6.5	3.2E-02	1.5	5.5E-01	-1.3	4.1E-01
ENSMUST00000175900	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Source:MGI Symbol;Acc:MGI:1920591]	H3BKQ0		-2.0	6.6E-02	-2.8	5.3E-02	-0.9	2.2E-01	-0.1	9.2E-01
ENSMUST00000147223				4.7	6.4E-05	5.7	3.0E-03	-0.7	6.6E-01	0.6	4.5E-01
ENSMUST00000175911	rho/rac guanine nucleotide exchange factor (GEF) 2 [Source:MGI Symbol;Acc:MGI:103264]		Q60875	0.3	7.4E-01	2.3	8.7E-02	0.2	8.3E-01	-1.7	1.1E-01
ENSMUST00000149433				4.7	1.1E-02	5.2	5.9E-04	-1.5	2.0E-01	0.8	2.4E-01
ENSMUST00000175915	WD repeat domain 17 [Source:MGI Symbol;Acc:MGI:1924662]	H3BLI8		3.0	7.8E-02	4.7	1.4E-02	-0.5	7.4E-01	-2.2	9.3E-02
ENSMUST00000124483				4.7	6.9E-05	7.3	8.5E-05	-1.5	2.5E-01	-1.3	5.4E-02
ENSMUST00000159400				4.7	2.4E-06	2.1	8.5E-02	-1.0	3.2E-01	0.7	4.4E-01
ENSMUST00000175919	apolipoprotein L 7a [Source:MGI Symbol;Acc:MGI:1923011]	B2RT54		5.0	6.8E-02	3.7	1.2E-01	-2.4	3.7E-01	-1.2	4.9E-01
ENSMUST00000175934	Treacher Collins Franceschetti syndrome 1, homolog [Source:MGI Symbol;Acc:MGI:892003]	H3BL37		-1.8	1.3E-01	1.1	3.9E-01	0.3	7.5E-01	-2.6	6.5E-02
ENSMUST00000148060				4.7	1.3E-03	-2.6	7.9E-02	0.0	9.6E-01	-0.9	5.2E-01
ENSMUST00000152907				4.7	1.3E-03	6.2	1.6E-02	-0.8	7.4E-01	-1.5	2.6E-01
ENSMUST00000107833				4.7	1.6E-02	-1.8	1.5E-01	0.3	7.1E-01	-4.7	2.9E-02
ENSMUST00000118148				4.7	5.0E-04	7.8	4.5E-04	-0.8	6.4E-01	-0.4	6.2E-01
ENSMUST00000175952				-2.9	2.3E-01	-2.0	4.3E-01	-1.1	4.9E-01	-2.0	4.7E-01
ENSMUST00000175954				-1.0	5.0E-01	-3.8	4.7E-02	-3.7	5.9E-03	-0.9	6.3E-01
ENSMUST00000130479				4.7	7.8E-03	4.8	8.3E-04	-1.6	1.7E-01	-0.3	6.0E-01
ENSMUST00000142042				4.7	4.3E-04	6.9	1.7E-04	-1.0	4.4E-01	0.8	2.0E-01
ENSMUST00000150356				4.7	9.4E-04	4.3	1.7E-02	-0.5	7.2E-01	0.8	4.0E-01
ENSMUST00000159215				4.7	2.9E-03	8.7	9.1E-04	0.7	7.1E-01	1.0	2.2E-01
ENSMUST00000175966	sodium channel, nonvoltage-gated 1 alpha [Source:MGI Symbol;Acc:MGI:101782]	H3BKW1		2.6	2.1E-01	-0.5	8.2E-01	-2.2	2.4E-01	1.0	6.9E-01
ENSMUST00000163408				4.7	4.1E-03	5.9	3.3E-03	-0.4	8.0E-01	-0.9	3.4E-01
ENSMUST00000186879				4.7	1.3E-04	-1.6	3.5E-01	2.9	1.7E-02	0.7	6.9E-01
ENSMUST00000124659				4.7	1.7E-04	4.1	1.4E-03	0.2	7.9E-01	-0.6	3.7E-01
ENSMUST00000175975	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	H3BK24		1.7	5.0E-01	7.2	8.3E-02	5.0	1.5E-01	-0.4	8.7E-01
ENSMUST00000133019				4.7	1.0E-03	-7.6	2.3E-04	-1.1	3.1E-02	-0.9	5.4E-01
ENSMUST00000175981	ring finger protein 141 [Source:MGI Symbol;Acc:MGI:1914400]	H3BJU0		0.9	2.2E-01	1.0	2.1E-01	-0.5	4.5E-01	-0.7	3.9E-01
ENSMUST00000190856				4.7	4.7E-03	5.9	2.1E-03	-0.7	6.7E-01	-0.3	7.5E-01
ENSMUST00000133902				4.7	2.9E-02	3.3	3.3E-03	-0.5	5.4E-01	-0.2	8.1E-01
ENSMUST00000141749				4.7	1.4E-02	7.0	1.3E-02	-0.2	9.4E-01	-2.0	1.6E-01
ENSMUST00000175991	ubiquitin-like modifier activating enzyme 2 [Source:MGI Symbol;Acc:MGI:1858313]	H3BLR3		0.9	6.9E-01	-2.3	4.0E-01	-2.9	1.2E-01	0.3	9.1E-01
ENSMUST00000188596				4.7	3.6E-04	-10.2	1.9E-04	0.5	2.4E-01	-0.9	6.3E-01
ENSMUST00000176004				3.8	5.5E-02	4.4	8.1E-02	0.8	7.1E-01	0.2	8.9E-01
ENSMUST00000149730				4.7	2.8E-04	4.8	1.0E-04	-0.6	4.3E-01	-0.6	2.3E-01
ENSMUST00000166992				4.7	5.7E-04	6.5	2.2E-04	0.3	7.8E-01	-0.6	3.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000195283				4.7	6.1E-04	-9.2	4.2E-04	-0.6	3.7E-01	-1.4	5.0E-01
ENSMUST00000153111				4.7	1.2E-03	5.2	1.2E-02	0.0	1.0E+00	-0.9	4.3E-01
ENSMUST00000184852				4.7	1.1E-02	-4.1	1.3E-02	-0.3	6.1E-01	-1.0	5.3E-01
ENSMUST00000176014	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]	H3BJY2		3.6	1.8E-01	5.2	2.2E-01	3.4	2.8E-01	1.8	6.0E-01
ENSMUST00000126634				4.7	1.8E-02	5.7	1.6E-02	-0.1	9.6E-01	-1.5	2.4E-01
ENSMUST00000176018	ceramide synthase 6 [Source:MGI Symbol;Acc:MGI:2442564]	H3BL08		-1.9	1.9E-01	-1.8	2.9E-01	-0.4	6.8E-01	-0.4	8.2E-01
ENSMUST00000176029	early B cell factor 2 [Source:MGI Symbol;Acc:MGI:894332]		O08792	3.8	1.2E-01	2.8	3.2E-01	-0.3	9.2E-01	0.7	6.9E-01
ENSMUST00000130036				4.7	5.3E-05	-5.6	4.0E-03	0.7	1.9E-01	4.1	1.9E-02
ENSMUST00000134468				4.7	1.8E-02	6.2	1.7E-03	-0.5	7.3E-01	-0.8	3.6E-01
ENSMUST00000176033				0.4	8.7E-01	2.8	3.5E-01	2.2	2.7E-01	-0.2	9.4E-01
ENSMUST00000176035	archaelysin family metallopeptidase 1 [Source:MGI Symbol;Acc:MGI:2442258]	H3BKS3		2.8	1.3E-01	0.7	7.1E-01	-1.5	4.0E-01	0.6	7.2E-01
ENSMUST00000176041	chaperonin containing Tcp1, subunit 8 (theta) [Source:MGI Symbol;Acc:MGI:107183]	H3BKG2		-3.1	6.1E-02	-6.3	7.7E-03	-2.8	7.1E-03	0.3	8.8E-01
ENSMUST00000144881				4.7	4.9E-04	6.4	1.9E-03	-0.5	7.7E-01	0.0	9.9E-01
ENSMUST00000176054	metastasis associated 3 [Source:MGI Symbol;Acc:MGI:2151172]	H3BIY7		-4.3	8.9E-02	-1.9	5.3E-01	1.5	3.9E-01	-0.9	7.6E-01
ENSMUST00000176059	histone cluster 2, H3c1 [Source:MGI Symbol;Acc:MGI:2448355]	B9EI85	P84228	-0.9	2.0E-01	0.7	4.3E-01	1.0	1.6E-01	-0.6	4.5E-01
ENSMUST00000176060	Rho GTPase activating protein 18 [Source:MGI Symbol;Acc:MGI:1921160]	H3BJL1		-2.1	1.1E-01	-5.1	2.1E-02	-2.2	2.8E-02	0.7	7.2E-01
ENSMUST00000119237				4.7	5.7E-03	3.8	3.2E-02	-1.5	3.8E-01	-1.2	2.8E-01
ENSMUST00000139686				4.7	1.7E-04	5.2	5.4E-04	-0.9	3.6E-01	-0.9	1.7E-01
ENSMUST00000160523				4.7	5.4E-05	7.0	4.4E-04	-0.7	6.3E-01	-0.5	4.4E-01
ENSMUST00000064809				4.7	1.1E-03	-4.9	3.2E-02	0.0	1.0E+00	-0.6	7.9E-01
ENSMUST00000145309				4.7	1.2E-03	4.6	5.0E-03	-1.9	2.1E-01	0.4	6.2E-01
ENSMUST00000190712				4.7	1.8E-04	3.3	4.4E-02	-2.0	2.2E-01	0.1	9.2E-01
ENSMUST00000184234				4.7	1.3E-04	3.6	1.9E-03	0.1	9.0E-01	0.5	3.8E-01
ENSMUST00000184506				4.7	1.3E-04	7.0	1.5E-04	-0.6	6.4E-01	-1.1	1.0E-01
ENSMUST00000176096	C-type lectin domain family 4, member e [Source:MGI Symbol;Acc:MGI:1861232]	H3BL75		-2.1	2.5E-01	-5.0	1.8E-02	-5.2	8.4E-04	-2.3	2.8E-01
ENSMUST00000184619				4.7	6.1E-04	4.8	3.1E-03	0.7	5.5E-01	0.0	9.9E-01
ENSMUST00000182911				4.7	4.3E-05	-3.8	1.1E-02	-0.6	3.4E-01	-0.1	9.1E-01
ENSMUST00000176110	sodium channel, nonvoltage-gated 1 alpha [Source:MGI Symbol;Acc:MGI:101782]	H3BJC3		-2.5	7.7E-02	-1.9	3.1E-01	1.5	2.0E-01	0.9	6.3E-01
ENSMUST00000128558				4.7	1.5E-03	4.2	6.4E-03	-1.5	2.8E-01	1.2	1.4E-01
ENSMUST00000176113	lin-28 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:1890546]	H3BK51		-1.2	7.9E-02	-0.6	5.3E-01	1.4	3.3E-02	0.9	3.8E-01
ENSMUST00000127302				4.7	6.2E-04	4.9	2.5E-02	-0.6	7.7E-01	-1.1	3.9E-01
ENSMUST00000117700				4.7	6.6E-05	-2.1	1.2E-01	1.7	3.4E-02	0.8	5.2E-01
ENSMUST00000121073				4.7	3.2E-03	5.9	1.4E-03	-0.4	7.6E-01	-0.7	4.0E-01
ENSMUST00000176128	homeobox containing 1 [Source:MGI Symbol;Acc:MGI:2445066]	H3BKM3		3.6	1.0E-01	1.6	6.5E-01	1.2	6.1E-01	3.2	3.2E-01
ENSMUST00000139809				4.7	5.9E-03	7.2	1.1E-04	-0.6	6.5E-01	0.1	8.1E-01
ENSMUST00000128127				4.7	2.2E-02	6.3	3.1E-04	-0.5	6.7E-01	-1.3	8.0E-02
ENSMUST00000142924				4.7	5.9E-04	6.4	2.9E-04	-0.6	6.5E-01	-0.6	3.9E-01
ENSMUST00000176144	hyaluronan synthase 3 [Source:MGI Symbol;Acc:MGI:109599]		O08650	2.3	3.2E-01	1.0	7.4E-01	-0.7	8.0E-01	0.6	7.7E-01
ENSMUST00000176150				2.6	2.0E-01	2.6	2.0E-01	-0.5	8.0E-01	-0.5	7.4E-01
ENSMUST00000132902				4.7	1.3E-03	3.9	2.8E-02	-0.9	5.5E-01	1.0	3.4E-01
ENSMUST00000180888				4.7	1.0E-03	-4.5	7.7E-03	0.0	9.3E-01	-0.8	5.8E-01
ENSMUST00000155930				4.7	7.2E-05	6.7	6.9E-05	-1.5	1.9E-01	0.1	8.7E-01
ENSMUST00000144684				4.7	2.8E-03	4.7	7.4E-04	0.6	5.4E-01	-1.6	4.7E-02
ENSMUST00000176172	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	H3BJQ9		2.5	2.5E-01	-2.3	5.0E-01	-1.9	3.4E-01	3.0	3.8E-01
ENSMUST00000176665				4.7	1.1E-02	6.0	5.8E-03	0.0	9.8E-01	0.3	7.9E-01
ENSMUST00000119397				4.7	6.7E-03	10.4	1.8E-04	1.0	5.7E-01	0.5	4.6E-01
ENSMUST00000149450				4.7	3.1E-02	5.4	1.9E-03	-0.7	6.0E-01	1.1	2.1E-01
ENSMUST00000176182				-3.8	6.5E-02	-1.6	5.2E-01	1.4	4.0E-01	-0.7	7.6E-01
ENSMUST00000182658				4.7	5.2E-04	4.0	1.2E-02	-1.8	2.0E-01	1.7	9.2E-02
ENSMUST00000182716				4.7	4.6E-04	3.3	2.3E-02	-2.1	1.1E-01	0.1	8.9E-01
ENSMUST00000129240				4.7	4.2E-04	6.6	1.2E-03	-0.2	8.9E-01	0.1	9.3E-01
ENSMUST00000160730				4.7	9.1E-04	7.2	1.5E-03	-0.6	7.3E-01	-0.5	5.8E-01
ENSMUST00000135305				4.7	1.6E-03	7.0	1.6E-02	-0.6	8.1E-01	-2.1	1.7E-01
ENSMUST00000145796				4.7	1.9E-02	2.4	1.9E-01	0.1	9.5E-01	5.5	1.8E-03
ENSMUST00000176205	zinc finger protein 536 [Source:MGI Symbol;Acc:MGI:1926102]		Q8K083	2.7	6.8E-02	6.3	7.5E-04	-0.5	7.1E-01	-4.1	2.2E-03
ENSMUST00000176207	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]		P61979	0.8	7.5E-01	-3.4	3.3E-01	-2.3	2.5E-01	1.9	5.9E-01
ENSMUST00000176209	proprotein convertase subtilisin/kexin type 6 [Source:MGI Symbol;Acc:MGI:102897]	H3BJL4		4.3	1.7E-01	5.1	1.4E-01	0.0	1.0E+00	-0.8	7.0E-01
ENSMUST00000176212				2.5	2.3E-01	5.9	2.9E-02	0.1	9.8E-01	-3.4	7.2E-02
ENSMUST00000174304				4.7	6.7E-04	-3.0	6.5E-02	4.2	4.9E-04	-0.9	5.4E-01
ENSMUST00000176222	interleukin 10 receptor, alpha [Source:MGI Symbol;Acc:MGI:96538]	H3BKN6		-1.4	5.0E-01	1.2	6.3E-01	-0.1	9.6E-01	-2.6	2.3E-01
ENSMUST00000152020				4.7	3.4E-03	8.8	1.5E-06	-0.1	9.1E-01	0.0	9.3E-01
ENSMUST00000176242	ect2 oncogene [Source:MGI Symbol;Acc:MGI:95281]		Q07139	-1.6	5.8E-01	-2.8	4.5E-01	-1.6	4.5E-01	-0.4	9.2E-01
ENSMUST00000176250	neuroplastin [Source:MGI Symbol;Acc:MGI:108077]		P97300	0.8	2.1E-01	1.1	1.3E-01	-0.6	3.4E-01	-0.9	1.6E-01
ENSMUST00000151364				4.7	1.6E-04	-6.8	3.6E-04	0.2	6.1E-01	-0.7	5.9E-01
ENSMUST00000185528				4.7	1.6E-04	1.3	2.0E-01	3.1	3.5E-03	-3.4	7.3E-03
ENSMUST00000127776				4.6	2.5E-03	-4.9	2.9E-03	0.5	3.5E-01	-0.3	8.4E-01
ENSMUST00000133359				4.6	2.5E-04	6.7	1.3E-02	-0.6	8.1E-01	-1.8	1.9E-01
ENSMUST00000129125				4.6	2.6E-03	2.6	8.1E-03	-0.2	8.2E-01	0.1	8.2E-01
ENSMUST00000135576				4.6	4.4E-04	-1.3	1.4E-01	0.6	2.6E-01	-0.6	4.7E-01
ENSMUST00000152857				4.6	3.1E-04	6.8	1.1E-04	-0.5	6.3E-01	0.0	9.3E-01
ENSMUST00000176282	carboxylesterase 1E [Source:MGI Symbol;Acc:MGI:95432]	H3BL34		3.3	9.5E-02	1.8	4.3E-01	-0.4	8.4E-01	1.0	5.8E-01
ENSMUST00000141565				4.6	1.5E-04	-2.0	6.6E-02	0.1	9.0E-01	-1.6	1.6E-01
ENSMUST00000154211				4.6	6.9E-04	4.0	4.1E-03	-0.3	7.3E-01	-0.7	3.5E-01
ENSMUST00000176295	dynactin 5 [Source:MGI Symbol;Acc:MGI:1891689]	H3BKU6		0.3	8.6E-01	3.6	7.1E-02	0.5	7.5E-01	-2.8	1.0E-01
ENSMUST00000127593				4.6	2.4E-04	8.8	3.0E-03	1.2	5.8E-01	-0.9	4.0E-01
ENSMUST00000137323				4.6	2.2E-02	-5.3	6.1E-03	1.3	7.5E-02	1.0	5.2E-01
ENSMUST00000152028				4.6	7.7E-04	-7.6	3.2E-05	0.7	3.5E-02	-0.1	9.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000176321	CD200 receptor 4 [Source:MGI Symbol;Acc:MGI:3036289]	H3BJX3		2.1	3.2E-01	0.0	9.9E-01	-2.2	2.5E-01	-0.1	9.4E-01
ENSMUST00000152087				4.6	1.4E-03	-5.2	2.3E-02	1.3	1.3E-01	-0.7	7.4E-01
ENSMUST00000131158				4.6	1.5E-03	8.0	3.3E-04	-0.9	5.8E-01	0.8	2.8E-01
ENSMUST00000139295				4.6	2.3E-04	-5.1	8.4E-03	2.6	1.8E-03	-0.9	6.0E-01
ENSMUST00000176343	sulfide quinone reductase-like (yeast) [Source:MGI Symbol;Acc:MGI:1929899]	H3BLH2		-5.4	2.0E-01	1.5	8.4E-01	6.9	2.1E-01	0.0	1.0E+00
ENSMUST00000176347	ras homolog gene family, member C [Source:MGI Symbol;Acc:MGI:106028]	H3BL56		-0.1	9.7E-01	-0.7	8.2E-01	-1.8	3.9E-01	-1.2	6.8E-01
ENSMUST00000146487				4.6	2.4E-04	-5.5	9.5E-04	0.9	5.0E-02	-0.6	6.2E-01
ENSMUST00000162111				4.6	2.1E-05	-4.7	1.4E-02	-0.3	6.6E-01	-1.6	3.7E-01
ENSMUST00000131069				4.6	1.3E-04	-2.1	3.5E-01	5.0	3.7E-03	-0.9	6.9E-01
ENSMUST00000131258				4.6	1.4E-04	5.0	5.8E-04	-1.2	2.6E-01	-0.2	7.7E-01
ENSMUST00000147013				4.6	6.3E-03	6.6	3.4E-04	-0.7	6.1E-01	-0.8	2.6E-01
ENSMUST00000161285				4.6	9.4E-05	2.3	4.5E-02	-1.3	1.9E-01	-0.2	8.6E-01
ENSMUST00000176381	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]		Q8K1E0	1.7	6.6E-02	0.2	8.7E-01	-0.4	6.3E-01	1.1	2.4E-01
ENSMUST00000143309				4.6	1.8E-02	4.5	5.7E-03	-2.2	1.4E-01	-0.3	7.6E-01
ENSMUST00000127168				4.6	3.2E-03	7.8	2.2E-04	-0.1	9.7E-01	-2.0	2.5E-02
ENSMUST00000137983				4.6	2.0E-04	4.3	4.3E-04	0.4	5.4E-01	1.2	5.2E-02
ENSMUST00000132185				4.6	2.1E-04	4.7	7.9E-05	-2.4	1.0E-02	-1.2	2.9E-02
ENSMUST00000176401				-1.2	3.9E-01	0.9	5.6E-01	-0.2	8.7E-01	-2.2	1.2E-01
ENSMUST00000176404				-2.3	3.7E-01	-2.6	3.7E-01	-1.7	3.4E-01	-1.4	6.5E-01
ENSMUST00000136999				4.6	3.0E-05	8.7	2.5E-05	1.3	2.4E-01	-0.3	5.6E-01
ENSMUST00000176411	guanine nucleotide binding protein (G protein), beta 1 [Source:MGI Symbol;Acc:MGI:95781]	H3BLF7		0.1	9.7E-01	1.0	7.2E-01	-0.5	8.2E-01	-1.4	5.5E-01
ENSMUST00000177261				4.6	7.6E-04	5.9	1.1E-03	-0.6	6.5E-01	0.0	9.5E-01
ENSMUST00000176416	ubiquitin specific peptidase 2 [Source:MGI Symbol;Acc:MGI:1858178]		O88623	-2.0	9.9E-02	1.2	2.9E-01	1.2	1.7E-01	-1.9	1.3E-01
ENSMUST00000155841				4.6	8.4E-05	4.0	6.3E-02	-0.1	9.7E-01	-0.6	6.6E-01
ENSMUST00000176419	tubulin polymerization-promoting protein family member 3 [Source:MGI Symbol;Acc:MGI:1915221]		Q9CRB6	-2.1	2.3E-01	-2.4	2.1E-01	-1.0	4.1E-01	-0.7	7.2E-01
ENSMUST00000120165				4.6	6.8E-04	3.4	4.5E-02	-1.7	2.5E-01	-0.1	9.5E-01
ENSMUST00000176423	cut-like homeobox 1 [Source:MGI Symbol;Acc:MGI:88568]	H3BJL7		-2.6	3.9E-02	-0.8	5.9E-01	1.3	2.1E-01	-0.5	7.5E-01
ENSMUST00000154099				4.6	2.2E-02	-5.1	1.0E-01	-0.2	8.9E-01	-1.0	7.7E-01
ENSMUST00000168601				4.6	2.4E-02	2.8	2.6E-02	0.8	3.9E-01	1.2	1.2E-01
ENSMUST00000186418				4.6	1.9E-04	5.6	5.2E-04	-0.7	5.5E-01	-0.8	3.0E-01
ENSMUST00000176438	zinc finger E-box binding homeobox 2 [Source:MGI Symbol;Acc:MGI:1344407]		Q9R0G7	0.9	7.2E-01	7.0	1.1E-01	3.7	3.6E-01	-2.4	3.1E-01
ENSMUST00000124696				4.6	8.8E-05	4.0	1.9E-04	-0.4	5.8E-01	-0.2	6.1E-01
ENSMUST00000153333				4.6	3.5E-03	5.9	5.6E-04	0.1	9.2E-01	-0.8	2.8E-01
ENSMUST00000181890				4.6	2.1E-04	4.2	3.6E-05	-0.6	2.6E-01	0.1	8.4E-01
ENSMUST00000193664				4.6	9.6E-05	-0.8	5.8E-01	1.3	1.8E-01	-0.5	7.0E-01
ENSMUST00000176467	predicted gene 4070 [Source:MGI Symbol;Acc:MGI:3782245]		Q80SU7	-3.7	4.3E-02	-5.5	3.8E-02	-0.1	9.6E-01	1.8	4.7E-01
ENSMUST00000154636				4.6	1.8E-03	6.4	2.4E-04	-0.6	6.3E-01	-0.8	2.1E-01
ENSMUST00000176472	pleckstrin and Sec7 domain containing 2 [Source:MGI Symbol;Acc:MGI:1921252]	H3BK80		2.7	2.2E-01	1.6	6.8E-01	2.1	4.6E-01	3.2	3.1E-01
ENSMUST00000176477				4.0	5.5E-02	2.5	4.3E-01	1.4	5.1E-01	2.8	3.1E-01
ENSMUST00000176478				3.2	4.5E-02	2.0	3.1E-01	-1.2	5.0E-01	0.1	9.5E-01
ENSMUST00000176480	cleavage and polyadenylation specific factor 6 [Source:MGI Symbol;Acc:MGI:1913948]	H3BKW0		-3.2	1.4E-01	-1.4	5.3E-01	-0.2	8.6E-01	-2.1	3.8E-01
ENSMUST00000144931				4.6	5.3E-03	3.7	2.8E-02	-1.2	3.9E-01	-0.3	7.7E-01
ENSMUST00000176485	NOL1/NOP2/Sun domain family member 2 [Source:MGI Symbol;Acc:MGI:107252]	H3BKN0		0.4	8.5E-01	-1.2	6.6E-01	-2.2	2.7E-01	-0.5	8.5E-01
ENSMUST00000176491	salt inducible kinase 2 [Source:MGI Symbol;Acc:MGI:2445031]	H3BKG1		-1.0	7.2E-01	-1.4	6.9E-01	-1.0	6.9E-01	-0.5	8.9E-01
ENSMUST00000145736				4.6	1.2E-02	4.6	3.1E-02	-0.7	7.0E-01	1.0	4.1E-01
ENSMUST00000156518				4.6	2.5E-04	4.4	6.2E-03	-1.1	3.6E-01	0.3	7.7E-01
ENSMUST00000136900				4.6	1.8E-05	-4.7	2.4E-02	0.6	4.4E-01	1.1	5.6E-01
ENSMUST00000055220				4.6	4.5E-03	2.5	1.2E-01	-4.4	3.4E-02	-0.8	5.3E-01
ENSMUST00000172799				4.6	2.2E-05	1.7	6.0E-02	-5.4	5.7E-04	-0.6	4.1E-01
ENSMUST00000119497				4.6	2.6E-04	4.4	6.2E-04	0.9	2.9E-01	-0.6	4.0E-01
ENSMUST00000176503				3.5	4.5E-02	3.0	1.9E-01	0.9	6.5E-01	1.5	3.3E-01
ENSMUST00000176505				-1.0	4.6E-01	-0.8	6.5E-01	0.4	7.1E-01	0.2	8.9E-01
ENSMUST00000127473				4.6	8.5E-05	4.7	8.1E-04	-3.5	9.5E-03	-0.9	1.5E-01
ENSMUST00000127072				4.6	1.0E-03	4.2	2.9E-03	-3.5	2.3E-02	0.2	8.1E-01
ENSMUST00000176520	high mobility group box transcription factor 1 [Source:MGI Symbol;Acc:MGI:894659]	H3BJW8		-2.9	4.4E-01	-7.0	1.3E-01	-4.5	5.1E-02	-0.5	9.3E-01
ENSMUST00000156186				4.6	1.8E-03	5.4	1.1E-04	-0.8	3.3E-01	-0.3	5.5E-01
ENSMUST00000130867				4.6	1.5E-02	8.1	2.9E-05	-1.2	3.2E-01	-0.5	3.1E-01
ENSMUST00000176531	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein [Source:MGI Symbol;Acc:MGI:2152213]	H3BKL1		-1.7	8.5E-02	-2.6	6.0E-02	0.0	1.0E+00	0.9	4.7E-01
ENSMUST00000176538	phosphatase, orphan 1 [Source:MGI Symbol;Acc:MGI:2447348]	H3BLB1		-3.6	6.9E-02	-4.3	5.6E-02	-0.7	5.5E-01	0.1	9.7E-01
ENSMUST00000176540	pre B cell leukemia homeobox 1 [Source:MGI Symbol;Acc:MGI:97495]		P41778	-1.6	5.2E-02	-1.6	1.5E-01	0.8	2.5E-01	0.8	4.4E-01
ENSMUST00000137004				4.6	5.0E-04	5.9	1.0E-03	-0.6	6.4E-01	-0.1	8.5E-01
ENSMUST00000153161				4.6	2.1E-04	7.3	6.5E-04	-1.7	3.0E-01	-3.7	6.0E-03
ENSMUST00000176557	neuroplastin [Source:MGI Symbol;Acc:MGI:108077]		P97300	-6.1	5.6E-02	3.2	5.7E-01	9.4	3.6E-02	0.1	9.8E-01
ENSMUST00000176558	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	Q8BT23		-0.7	5.0E-01	1.0	4.5E-01	0.4	7.4E-01	-1.4	2.6E-01
ENSMUST00000148472				4.6	5.4E-04	5.9	4.6E-04	-2.5	6.7E-02	-0.2	7.0E-01
ENSMUST00000193618				4.6	2.2E-03	6.6	4.3E-04	1.2	3.3E-01	-0.2	7.7E-01
ENSMUST00000176563				-1.6	1.4E-01	-1.8	2.5E-01	0.2	8.6E-01	0.4	7.8E-01
ENSMUST00000144824				4.6	2.2E-04	3.4	5.4E-02	0.3	8.5E-01	0.8	4.5E-01
ENSMUST00000150242				4.6	4.2E-05	6.5	3.8E-03	-0.7	7.1E-01	-0.5	6.3E-01
ENSMUST00000176585				-3.0	4.1E-02	-0.6	6.5E-01	-0.2	8.6E-01	-2.6	9.6E-02
ENSMUST00000161781				4.6	3.0E-04	7.0	1.5E-04	-0.9	4.6E-01	-1.2	9.8E-02
ENSMUST00000188013				4.6	2.7E-03	-4.8	1.4E-01	1.1	4.8E-01	-0.7	8.2E-01
ENSMUST00000142645				4.6	2.6E-05	-0.4	6.2E-01	0.8	1.7E-01	-0.5	5.6E-01
ENSMUST00000176604				0.3	8.0E-01	1.7	3.5E-01	1.5	3.0E-01	0.1	9.3E-01
ENSMUST00000194226				4.6	1.1E-03	6.3	2.1E-04	0.9	3.7E-01	0.2	6.6E-01
ENSMUST00000136082				4.6	2.0E-03	10.2	1.4E-05	0.1	9.1E-01	0.5	3.4E-01
ENSMUST00000176610	ke RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor [Source:MGI Symbol;Acc:MGI:2	H3BK01		0.1	9.4E-01	2.1	3.3E-01	1.4	4.1E-01	-0.5	7.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000188572				4.6	2.7E-04	-7.2	3.9E-02	-0.7	4.9E-01	-1.1	7.5E-01
ENSMUST00000176620				2.8	3.5E-02	6.1	4.0E-04	-0.6	6.4E-01	-3.8	1.5E-03
ENSMUST00000121757				4.6	2.7E-03	5.9	5.8E-04	-0.9	4.7E-01	-0.4	6.2E-01
ENSMUST00000146418				4.6	7.6E-05	5.4	3.0E-04	-2.8	4.7E-02	-0.7	2.9E-01
ENSMUST00000176625	N(alpha)-acetyltransferase 60, NatF catalytic subunit [Source:MGI Symbol;Acc:MGI:1922013]	H3BIY0		-0.5	5.5E-01	0.0	9.8E-01	2.0	3.9E-02	1.5	2.0E-01
ENSMUST00000176629	zinc finger CCCH-type containing 18 [Source:MGI Symbol;Acc:MGI:1923264]	H3BIW0		-1.6	3.4E-01	-2.6	3.8E-01	0.9	6.3E-01	1.9	4.8E-01
ENSMUST00000176630	Treacher Collins Franceschetti syndrome 1, homolog [Source:MGI Symbol;Acc:MGI:892003]		O08784	-0.7	7.6E-01	-4.8	2.4E-01	-1.1	6.5E-01	3.0	4.1E-01
ENSMUST00000190610				4.6	1.5E-03	-1.4	4.0E-01	2.0	6.6E-02	-2.4	2.0E-01
ENSMUST00000118720				4.6	5.0E-04	-4.3	1.6E-02	-2.7	9.3E-03	-2.4	2.0E-01
ENSMUST00000140390				4.6	2.1E-03	2.0	9.7E-02	-0.1	8.9E-01	0.1	9.3E-01
ENSMUST00000176640	SUMO/sentrin specific peptidase 6 [Source:MGI Symbol;Acc:MGI:1922075]	H3BKR4		0.2	8.7E-01	-0.8	6.3E-01	0.1	9.2E-01	1.2	4.8E-01
ENSMUST00000176643	high mobility group box transcription factor 1 [Source:MGI Symbol;Acc:MGI:894659]	H3BKV0		-3.8	1.6E-01	-2.5	4.2E-01	0.3	8.9E-01	-1.0	7.6E-01
ENSMUST00000176644				3.2	1.1E-01	3.0	2.4E-01	-0.4	8.6E-01	-0.2	9.0E-01
ENSMUST00000159362				4.6	1.2E-03	5.2	3.2E-02	-0.2	9.4E-01	-0.1	9.6E-01
ENSMUST00000176655	sodium channel, nonvoltage-gated 1 alpha [Source:MGI Symbol;Acc:MGI:101782]	H3BLI2		4.8	5.2E-02	-4.5	3.7E-02	-7.6	3.1E-03	1.7	3.9E-01
ENSMUST00000194408				4.6	1.8E-02	5.4	1.3E-04	-0.8	3.3E-01	-0.1	8.2E-01
ENSMUST00000123965				4.6	4.9E-04	-2.2	2.1E-01	1.6	1.2E-01	0.0	9.8E-01
ENSMUST00000136144				4.6	2.7E-04	4.1	4.3E-02	-0.3	8.7E-01	0.3	8.4E-01
ENSMUST00000147743				4.6	4.7E-03	-4.6	9.8E-04	1.0	7.2E-02	-4.9	7.5E-03
ENSMUST00000166453				4.6	3.1E-03	-1.2	4.3E-01	3.7	2.4E-03	-0.5	7.1E-01
ENSMUST00000145478				4.6	2.0E-02	-5.1	1.6E-03	1.0	5.6E-02	-0.7	5.7E-01
ENSMUST00000151587				4.6	4.3E-04	6.4	1.6E-03	0.3	8.3E-01	0.5	5.1E-01
ENSMUST00000176673				0.4	7.2E-01	0.8	5.9E-01	-0.4	7.1E-01	-0.8	5.5E-01
ENSMUST00000176674	golgi phosphoprotein 3-like [Source:MGI Symbol;Acc:MGI:1917129]	H3BJ82		-1.2	6.7E-01	-1.4	5.3E-01	-3.6	8.2E-02	-3.4	2.3E-01
ENSMUST00000121188				4.6	4.0E-04	-7.8	8.6E-04	-0.9	2.1E-01	0.6	7.3E-01
ENSMUST00000176684	Iroquois related homeobox 4 (Drosophila) [Source:MGI Symbol;Acc:MGI:1355275]		Q9QY61	4.7	6.8E-02	6.4	3.1E-02	-0.3	9.2E-01	-2.0	1.9E-01
ENSMUST00000172670				4.6	1.4E-03	-0.8	5.3E-01	1.2	1.4E-01	-1.2	3.4E-01
ENSMUST00000112256				4.6	3.4E-05	6.8	1.6E-06	-0.5	4.7E-01	-0.2	6.0E-01
ENSMUST00000123641				4.6	4.6E-05	6.7	2.4E-05	-2.4	4.6E-02	0.3	5.1E-01
ENSMUST00000176701	Pbx/knotted 1 homeobox [Source:MGI Symbol;Acc:MGI:1201409]		O70477	4.5	1.3E-01	5.0	1.3E-01	-0.3	9.2E-01	-0.8	6.6E-01
ENSMUST00000183399				4.6	7.4E-04	6.9	5.2E-04	-0.1	9.2E-01	1.4	8.3E-02
ENSMUST00000191844				4.6	1.7E-02	5.0	8.0E-03	-0.3	8.6E-01	-0.8	4.5E-01
ENSMUST00000176727	CTAGE family, member 5 [Source:MGI Symbol;Acc:MGI:1346056]	H3BL86		0.0	9.9E-01	3.9	3.0E-01	3.7	2.0E-01	-0.2	9.4E-01
ENSMUST00000136242				4.6	1.4E-04	-5.2	4.2E-02	0.8	3.8E-01	-0.6	8.3E-01
ENSMUST00000118050				4.6	5.3E-04	4.1	2.4E-03	-1.0	3.3E-01	0.7	3.1E-01
ENSMUST00000153365				4.6	8.0E-03	5.8	2.5E-04	-1.3	2.4E-01	0.0	9.6E-01
ENSMUST00000176740	fumarate hydratase 1 [Source:MGI Symbol;Acc:MGI:95530]	H3BKG7		-2.6	2.5E-01	-3.6	1.7E-01	-2.1	1.6E-01	-1.1	6.9E-01
ENSMUST00000156796				4.6	1.1E-04	4.5	1.7E-04	-1.3	9.5E-02	-1.0	8.8E-02
ENSMUST00000125957				4.6	5.6E-05	-6.2	1.5E-03	1.2	2.8E-02	-0.7	6.6E-01
ENSMUST00000176751	predicted gene 20683 [Source:MGI Symbol;Acc:MGI:5313130]	H3BKJ1		4.3	8.2E-02	1.7	5.5E-01	-2.2	3.9E-01	0.5	8.3E-01
ENSMUST00000176753	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1919837]	H3BJH6		0.9	6.3E-01	1.7	5.0E-01	0.6	7.3E-01	-0.2	9.2E-01
ENSMUST00000141461				4.6	3.5E-03	-0.9	5.8E-01	2.7	3.3E-02	-2.2	2.2E-01
ENSMUST00000176756	dynein, axonemal, heavy chain 11 [Source:MGI Symbol;Acc:MGI:1100864]	H3BLD7		6.1	4.6E-02	4.4	1.8E-01	-0.8	8.1E-01	0.9	6.7E-01
ENSMUST00000148394				4.6	1.3E-04	6.9	6.7E-03	1.3	5.1E-01	0.0	9.9E-01
ENSMUST00000120413				4.6	8.5E-04	-0.7	7.9E-01	3.4	7.6E-02	-1.2	6.4E-01
ENSMUST00000176768	ucine-rich repeats and calponin homology (CH) domain containing 4 [Source:MGI Symbol;Acc:MGI:1917193	H3BK42		0.0	9.6E-01	-0.7	5.2E-01	-0.1	8.9E-01	0.6	5.9E-01
ENSMUST00000176769	ed, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:MGI Symbol;Ac	H3BJK2		0.4	9.0E-01	-2.6	3.1E-01	-4.7	5.5E-02	-1.7	5.7E-01
ENSMUST00000155537				4.6	4.1E-04	-4.0	2.7E-02	2.2	8.9E-03	-0.3	8.8E-01
ENSMUST00000162336				4.5	4.0E-04	2.8	4.7E-03	0.8	2.0E-01	0.9	1.5E-01
ENSMUST00000129672				4.5	3.9E-05	-4.4	2.8E-02	0.7	3.7E-01	0.1	9.5E-01
ENSMUST00000186691				4.5	1.9E-02	-4.8	1.8E-02	-0.8	2.9E-01	-0.4	8.4E-01
ENSMUST00000160572				4.5	6.0E-04	5.5	1.7E-04	-0.3	7.0E-01	0.8	1.9E-01
ENSMUST00000176792				3.9	1.4E-01	6.1	4.8E-02	-0.2	9.4E-01	-2.4	1.8E-01
ENSMUST00000148784				4.5	4.1E-04	4.8	1.4E-05	-0.1	9.1E-01	-0.5	2.3E-01
ENSMUST00000176796				0.9	8.4E-02	1.3	7.7E-02	0.2	7.6E-01	-0.2	7.7E-01
ENSMUST00000159547				4.5	2.0E-04	-6.2	2.0E-04	-0.2	6.6E-01	-1.1	3.7E-01
ENSMUST00000154770				4.5	2.7E-04	-4.3	1.4E-02	0.6	3.6E-01	1.0	4.9E-01
ENSMUST00000187859				4.5	6.6E-05	7.8	9.1E-06	0.6	4.5E-01	-0.4	3.2E-01
ENSMUST00000176808	interleukin 10 receptor, alpha [Source:MGI Symbol;Acc:MGI:96538]	H3BKE8		2.0	3.8E-01	-2.4	3.0E-01	-3.5	9.0E-02	0.8	7.1E-01
ENSMUST00000176810	glycosyltransferase-like 1B [Source:MGI Symbol;Acc:MGI:2443769]	A2AHG6		2.7	2.2E-01	2.6	2.3E-01	-0.5	8.2E-01	-0.4	8.0E-01
ENSMUST00000153569				4.5	4.0E-04	6.7	1.0E-03	-0.7	6.5E-01	-2.1	3.7E-02
ENSMUST00000176819	CD200 receptor 4 [Source:MGI Symbol;Acc:MGI:3036289]		Q6XJV4	0.7	7.5E-01	-4.1	1.4E-01	-5.1	1.1E-02	-0.3	9.2E-01
ENSMUST00000187038				4.5	3.9E-04	6.2	2.6E-04	-0.6	6.1E-01	-0.6	3.3E-01
ENSMUST00000176824	salt inducible kinase 2 [Source:MGI Symbol;Acc:MGI:2445031]	H3BJC9		1.1	5.6E-02	2.5	6.9E-03	1.1	9.2E-02	-0.3	6.5E-01
ENSMUST00000095050				4.5	8.6E-03	-3.6	6.6E-02	0.4	6.2E-01	-0.7	7.1E-01
ENSMUST00000121457				4.5	2.8E-02	4.6	2.9E-02	-2.7	2.2E-01	-0.6	6.3E-01
ENSMUST00000127842				4.5	1.6E-03	0.5	7.9E-01	-2.7	7.8E-02	2.6	1.2E-01
ENSMUST00000123078				4.5	1.4E-03	-2.9	1.6E-02	-0.2	6.9E-01	0.3	7.7E-01
ENSMUST00000176834	serine/arginine-rich splicing factor 2 [Source:MGI Symbol;Acc:MGI:98284]	H3BJA4		-4.9	1.3E-01	-3.9	3.0E-01	-0.2	9.3E-01	-1.1	7.8E-01
ENSMUST00000187353				4.5	2.8E-06	0.4	8.7E-01	-3.1	2.0E-01	2.6	2.9E-01
ENSMUST00000143615				4.5	1.4E-02	5.3	2.2E-02	-1.3	5.4E-01	-1.8	1.8E-01
ENSMUST00000145920				4.5	1.4E-02	-5.5	3.2E-04	0.8	5.1E-02	-0.6	5.8E-01
ENSMUST00000127131				4.5	7.6E-06	1.7	4.0E-02	0.2	7.7E-01	0.7	3.0E-01
ENSMUST00000126715				4.5	2.8E-04	5.6	3.6E-03	-2.7	1.3E-01	-1.4	1.5E-01
ENSMUST00000131355				4.5	9.2E-04	-0.2	7.7E-01	0.7	2.2E-01	-1.0	2.6E-01
ENSMUST00000176858				-3.3	1.3E-01	-5.2	8.4E-02	-1.8	1.5E-01	0.1	9.8E-01
ENSMUST00000138623				4.5	9.7E-04	6.8	3.0E-04	0.4	7.3E-01	-1.0	1.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000124225				4.5	1.0E-03	0.4	7.1E-01	1.7	5.0E-02	-0.7	4.5E-01
ENSMUST00000174084				4.5	4.0E-03	11.7	4.2E-06	-0.7	6.1E-01	-0.3	4.0E-01
ENSMUST00000142461				4.5	8.7E-05	6.0	8.8E-04	0.0	9.9E-01	-1.1	2.3E-01
ENSMUST00000185474				4.5	1.0E-03	-4.2	5.5E-03	-0.2	6.8E-01	0.3	8.1E-01
ENSMUST00000132503				4.5	8.0E-03	-4.2	2.6E-02	2.3	7.8E-03	-0.7	6.8E-01
ENSMUST00000142391				4.5	1.4E-03	1.6	1.4E-01	-0.7	4.1E-01	0.1	9.0E-01
ENSMUST00000155951				4.5	3.3E-02	5.5	3.0E-04	-0.4	7.0E-01	-0.2	7.2E-01
ENSMUST00000122378				4.5	2.1E-03	-6.5	6.2E-04	0.1	8.8E-01	-0.9	5.3E-01
ENSMUST00000176900				-1.2	4.0E-01	-0.7	7.2E-01	0.5	7.5E-01	-0.1	9.7E-01
ENSMUST00000176906	ribosomal protein L41 [Source:MGI Symbol;Acc:MGI:1915195]	H3BK91		-5.0	1.3E-01	-5.2	1.9E-01	-1.3	4.9E-01	-1.1	8.0E-01
ENSMUST00000129061				4.5	5.6E-05	6.7	7.7E-04	-0.6	7.0E-01	-0.6	4.6E-01
ENSMUST00000172940				4.5	7.5E-03	4.3	9.4E-03	-0.6	6.8E-01	1.6	9.7E-02
ENSMUST00000176922	WD repeat domain 37 [Source:MGI Symbol;Acc:MGI:1920393]	Q05BF4		0.7	3.9E-01	1.3	2.6E-01	1.2	2.1E-01	0.6	5.6E-01
ENSMUST00000176923	WD repeat domain 90 [Source:MGI Symbol;Acc:MGI:1921267]		Q6ZPG2	5.2	6.8E-02	5.5	1.4E-01	0.3	9.2E-01	0.0	1.0E+00
ENSMUST00000176932				4.6	4.6E-02	7.5	1.3E-02	0.8	7.5E-01	-2.1	1.5E-01
ENSMUST00000162414				4.5	1.1E-02	2.8	1.9E-02	-0.5	6.0E-01	0.5	5.6E-01
ENSMUST00000176939	aldehyde dehydrogenase 18 family, member A1 [Source:MGI Symbol;Acc:MGI:1888908]		Q9Z110	-0.4	6.5E-01	-2.3	1.6E-01	0.2	8.6E-01	2.0	2.0E-01
ENSMUST00000176953				-0.4	7.0E-01	-1.4	4.6E-01	1.0	4.5E-01	2.0	2.6E-01
ENSMUST00000142117				4.5	4.5E-04	8.3	8.6E-06	-1.5	1.7E-01	0.0	9.3E-01
ENSMUST00000191845				4.5	1.1E-02	-6.9	8.3E-05	0.4	3.3E-01	-0.5	6.7E-01
ENSMUST00000176960				-2.3	7.5E-02	-1.7	4.1E-01	2.0	1.4E-01	1.5	4.4E-01
ENSMUST00000145445				4.5	1.1E-02	6.2	2.9E-04	-2.0	1.3E-01	-0.7	2.8E-01
ENSMUST00000176966				-2.0	1.6E-01	-1.9	1.7E-01	-1.0	3.3E-01	-1.0	5.0E-01
ENSMUST00000176968	syntaxin 5A [Source:MGI Symbol;Acc:MGI:1928483]	H3BKP3		-2.9	3.6E-02	-2.9	1.0E-01	-0.1	9.1E-01	-0.1	9.4E-01
ENSMUST00000127536				4.5	4.5E-05	6.3	9.0E-03	-1.4	5.3E-01	-1.5	2.5E-01
ENSMUST00000140913				4.5	2.5E-02	6.9	8.0E-06	-0.8	3.5E-01	-0.3	5.1E-01
ENSMUST00000141597				4.5	4.5E-04	3.1	2.5E-01	-0.8	7.5E-01	2.2	2.5E-01
ENSMUST00000122149				4.5	1.4E-04	4.4	3.7E-03	-1.9	1.6E-01	0.8	3.3E-01
ENSMUST00000133744				4.5	6.1E-03	6.6	3.5E-02	-0.9	7.7E-01	-0.4	7.9E-01
ENSMUST00000176988				2.5	4.7E-02	2.5	1.2E-01	0.3	8.0E-01	0.3	7.7E-01
ENSMUST00000181923				4.5	1.4E-04	-0.7	5.5E-01	1.3	1.1E-01	-0.2	8.6E-01
ENSMUST00000176994	predicted gene 4070 [Source:MGI Symbol;Acc:MGI:3782245]	H3BL64		0.6	6.6E-01	-1.8	2.5E-01	-2.9	3.3E-02	-0.5	7.2E-01
ENSMUST00000138868				4.5	3.6E-05	2.4	2.0E-02	0.0	9.5E-01	0.0	9.5E-01
ENSMUST00000177005	glycosylated lysosomal membrane protein [Source:MGI Symbol;Acc:MGI:1913318]		Q9JHJ3	0.5	3.4E-01	1.9	2.5E-02	0.8	2.0E-01	-0.6	3.7E-01
ENSMUST00000177006	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 [Source:MGI Symbol;Acc:MGI:1933111]	H3BKS5		-2.6	2.7E-01	0.3	9.2E-01	0.7	7.3E-01	-2.2	4.2E-01
ENSMUST00000189160				4.5	2.4E-03	1.8	3.3E-01	-2.5	2.1E-01	0.9	5.6E-01
ENSMUST00000144214				4.5	2.0E-04	4.5	1.4E-04	0.2	7.9E-01	-0.2	6.8E-01
ENSMUST00000177014	aftiphilin [Source:MGI Symbol;Acc:MGI:1923012]	H3BKM5		-2.3	2.3E-01	-0.5	8.4E-01	1.3	5.1E-01	-0.5	8.3E-01
ENSMUST00000160296				4.5	1.7E-02	7.3	5.1E-05	-0.6	5.7E-01	-1.1	6.9E-02
ENSMUST00000128655				4.5	1.4E-03	3.1	5.5E-02	0.4	7.7E-01	0.0	9.9E-01
ENSMUST00000118143				4.5	1.8E-04	4.9	6.9E-04	-0.2	8.2E-01	-0.4	5.6E-01
ENSMUST00000118874				4.5	2.8E-05	3.1	6.3E-03	-1.3	1.6E-01	-0.4	5.8E-01
ENSMUST00000123510				4.5	7.5E-04	7.2	2.8E-04	0.8	5.3E-01	0.5	5.2E-01
ENSMUST00000119136				4.5	1.4E-02	6.8	9.2E-04	-0.7	6.4E-01	-0.7	4.2E-01
ENSMUST00000135523				4.5	2.9E-02	3.3	5.1E-03	-5.3	1.5E-03	-1.2	1.6E-01
ENSMUST00000177035	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Source:MGI Symbol;Acc:MGI:1342335]	H3BKD4		-0.4	8.8E-01	0.6	8.5E-01	0.8	7.3E-01	-0.3	9.4E-01
ENSMUST00000137473				4.5	1.2E-05	-2.8	3.0E-02	-0.1	8.3E-01	-1.5	2.5E-01
ENSMUST00000147175				4.5	1.8E-04	7.4	7.1E-04	-0.7	6.5E-01	-0.8	3.7E-01
ENSMUST00000156946				4.5	5.8E-04	-6.3	2.9E-02	1.2	1.9E-01	-0.3	9.0E-01
ENSMUST00000177053	ecotropic viral integration site 5 like [Source:MGI Symbol;Acc:MGI:2442167]	H3BJX1		0.7	5.6E-01	-0.9	6.5E-01	1.0	4.2E-01	2.5	1.9E-01
ENSMUST00000187359				4.5	1.1E-04	6.2	1.1E-03	-0.4	7.6E-01	-0.7	3.6E-01
ENSMUST00000126643				4.5	3.9E-05	-4.2	5.3E-02	0.9	3.7E-01	-1.0	6.2E-01
ENSMUST00000128008				4.5	2.2E-03	3.5	2.4E-02	-1.5	3.0E-01	-1.1	3.4E-01
ENSMUST00000120372				4.5	1.5E-03	3.7	7.0E-02	-2.1	2.9E-01	-0.2	8.8E-01
ENSMUST00000124726				4.5	9.1E-04	-5.6	3.5E-04	1.1	1.6E-02	-0.6	5.9E-01
ENSMUST00000177069	metastasis associated 3 [Source:MGI Symbol;Acc:MGI:2151172]	H3BJP3		1.0	1.1E-01	1.1	1.8E-01	0.2	7.9E-01	0.1	9.4E-01
ENSMUST00000139757				4.5	1.3E-03	-5.6	3.1E-04	1.3	5.9E-03	-0.7	5.5E-01
ENSMUST00000174295				4.5	1.2E-03	-6.4	1.6E-02	1.1	1.6E-01	0.2	9.2E-01
ENSMUST00000177086	V-set and immunoglobulin domain containing 8 [Source:MGI Symbol;Acc:MGI:3642995]		Q6P3A4	3.0	1.0E-01	5.3	5.6E-02	0.9	7.1E-01	-1.4	3.4E-01
ENSMUST00000176714				4.5	4.7E-03	6.4	1.5E-04	-0.5	6.3E-01	-2.0	8.5E-03
ENSMUST00000125859				4.5	3.8E-04	3.3	3.1E-03	-0.6	4.7E-01	-0.4	5.0E-01
ENSMUST00000185668				4.5	3.0E-02	-5.1	9.4E-03	-0.3	6.9E-01	0.2	9.0E-01
ENSMUST00000177098	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 [Source:MGI Symbol;Acc:MGI:1933111]	H3BJQ3		-0.4	5.8E-01	-0.1	9.4E-01	-0.5	3.9E-01	-0.9	2.9E-01
ENSMUST00000177099				0.7	4.8E-01	1.1	3.7E-01	0.1	8.9E-01	-0.3	7.5E-01
ENSMUST00000193729				4.5	3.6E-05	6.7	1.1E-03	-1.8	2.6E-01	0.2	7.7E-01
ENSMUST00000192950				4.5	1.0E-02	4.7	9.3E-03	-0.7	6.6E-01	2.3	3.2E-02
ENSMUST00000134107				4.5	1.6E-05	9.5	7.0E-05	-0.3	8.2E-01	1.2	8.8E-02
ENSMUST00000128711				4.5	8.4E-05	2.2	4.3E-01	-0.7	7.7E-01	3.1	1.9E-01
ENSMUST00000183113				4.5	2.1E-05	5.9	3.7E-02	-0.4	8.8E-01	0.4	7.9E-01
ENSMUST00000177117	heterogeneous nuclear ribonucleoprotein K [Source:MGI Symbol;Acc:MGI:99894]	H3BJS9		2.0	3.3E-01	-1.0	6.4E-01	-3.5	6.4E-02	-0.6	7.9E-01
ENSMUST00000177122				2.9	1.2E-01	0.1	9.7E-01	-2.7	1.2E-01	0.1	9.3E-01
ENSMUST00000192530				4.5	3.0E-02	2.8	2.7E-03	-0.7	2.8E-01	-0.3	6.5E-01
ENSMUST00000177125	family with sequence similarity 107, member B [Source:MGI Symbol;Acc:MGI:1913790]	H3BLE6		-1.0	7.5E-01	-3.9	2.5E-01	-2.6	2.4E-01	0.3	9.3E-01
ENSMUST00000145583				4.5	1.4E-02	2.5	2.5E-02	-0.2	8.1E-01	0.0	9.7E-01
ENSMUST00000177129	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein [Source:MGI Symbol;Acc:MGI:2152213]	H3BKL1		1.7	3.3E-01	3.3	1.2E-01	0.5	7.7E-01	-1.1	5.4E-01
ENSMUST00000152922				4.5	9.2E-03	8.3	3.0E-04	-0.7	6.6E-01	-0.5	5.0E-01
ENSMUST00000177138	neuralized E3 ubiquitin protein ligase 4 [Source:MGI Symbol;Acc:MGI:1921092]	H3BK72		0.8	7.5E-01	0.2	9.2E-01	-2.5	2.1E-01	-1.9	4.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000155181				4.5	5.5E-05	8.2	1.4E-02	-0.9	7.6E-01	-1.6	3.3E-01
ENSMUST00000177145	cleavage and polyadenylation specific factor 6 [Source:MGI Symbol;Acc:MGI:1913948]		Q6NVF9	0.1	9.7E-01	2.2	2.9E-01	-0.3	8.5E-01	-2.5	1.6E-01
ENSMUST00000162570				4.5	6.3E-05	2.0	3.1E-02	-0.4	5.3E-01	-0.7	3.1E-01
ENSMUST00000177155	RIKEN cDNA 9930021J03 gene [Source:MGI Symbol;Acc:MGI:2444398]	H3BKP8		-1.0	6.4E-02	0.8	2.0E-01	0.6	2.2E-01	-1.2	5.2E-02
ENSMUST00000046516				4.5	1.2E-02	6.1	3.4E-04	-0.5	6.9E-01	-0.7	2.6E-01
ENSMUST00000177158	inositol hexaphosphate kinase 1 [Source:MGI Symbol;Acc:MGI:1351633]	H3BIW9		-3.4	7.1E-02	-0.8	7.3E-01	1.4	3.6E-01	-1.3	5.7E-01
ENSMUST00000191907				4.5	2.1E-03	4.2	2.1E-03	0.1	9.4E-01	-0.5	4.8E-01
ENSMUST00000147385				4.5	2.4E-04	-4.4	2.9E-02	-1.1	2.6E-01	-2.1	3.0E-01
ENSMUST00000148751				4.5	3.6E-05	3.2	1.3E-01	-0.5	8.2E-01	1.9	1.7E-01
ENSMUST00000177165				2.4	5.4E-02	3.9	1.1E-02	0.0	9.8E-01	-1.5	1.5E-01
ENSMUST00000177170				1.1	6.7E-01	3.1	2.4E-01	-1.1	6.4E-01	-3.1	2.3E-01
ENSMUST00000177172	Treacher Collins Franceschetti syndrome 1, homolog [Source:MGI Symbol;Acc:MGI:892003]	H3BIX0		0.6	8.5E-01	5.3	1.7E-01	3.4	3.3E-01	-1.3	6.5E-01
ENSMUST00000145340				4.5	7.1E-04	4.8	6.0E-03	-1.6	3.0E-01	-0.2	7.8E-01
ENSMUST00000177177	polycomb group ring finger 1 [Source:MGI Symbol;Acc:MGI:1917087]	H3BK85		-3.8	1.2E-01	-3.6	2.4E-01	-0.1	9.3E-01	-0.3	9.3E-01
ENSMUST00000177178	C-type lectin domain family 5, member a [Source:MGI Symbol;Acc:MGI:1345151]			-3.3	2.5E-01	-2.7	3.8E-01	-1.1	5.7E-01	-1.7	6.3E-01
ENSMUST00000145371				4.5	3.8E-04	6.0	9.4E-03	-0.5	8.0E-01	-1.8	1.4E-01
ENSMUST00000177183	thyroid hormone receptor interactor 11 [Source:MGI Symbol;Acc:MGI:1924393]	H3BJG4		1.4	4.6E-01	1.4	6.3E-01	0.9	6.4E-01	0.9	7.4E-01
ENSMUST00000177184	vomeronasal 2, receptor 5 [Source:MGI Symbol;Acc:MGI:3649074]	K7N788		4.3	9.4E-02	2.5	4.2E-01	-0.2	9.4E-01	1.6	5.0E-01
ENSMUST00000162307				4.5	3.1E-03	-2.4	1.9E-01	1.1	2.9E-01	-1.6	4.1E-01
ENSMUST00000152444				4.5	2.3E-03	7.4	4.4E-04	-0.1	9.4E-01	0.7	3.7E-01
ENSMUST00000177202	POU domain, class 6, transcription factor 1 [Source:MGI Symbol;Acc:MGI:102935]	H3BKJ6		0.5	8.3E-01	2.3	3.6E-01	-0.6	7.8E-01	-2.4	3.1E-01
ENSMUST00000129730				4.5	5.5E-03	7.1	2.2E-05	-0.5	5.8E-01	0.6	2.2E-01
ENSMUST00000174566				4.5	1.8E-02	6.7	1.4E-03	0.8	5.9E-01	-1.5	1.2E-01
ENSMUST00000133909				4.5	9.7E-04	-5.6	1.7E-03	-0.6	2.4E-01	-0.8	5.9E-01
ENSMUST00000177218	Pbx/knotted 1 homeobox 2 [Source:MGI Symbol;Acc:MGI:2445415]		Q8BG99	5.0	3.5E-02	4.3	6.3E-02	-1.8	4.1E-01	-1.1	5.1E-01
ENSMUST00000155121				4.5	2.7E-03	6.1	1.3E-03	-0.7	6.3E-01	0.9	2.4E-01
ENSMUST00000187641				4.5	1.1E-03	2.0	1.3E-01	-3.1	3.5E-02	2.0	6.0E-02
ENSMUST00000177229	forkhead box P1 [Source:MGI Symbol;Acc:MGI:1914004]	H3BJ24		-0.3	9.2E-01	3.1	3.4E-01	2.6	2.5E-01	-0.7	8.2E-01
ENSMUST00000121117				4.5	2.4E-03	7.3	5.5E-05	-0.6	6.2E-01	-0.9	1.3E-01
ENSMUST00000150656				4.4	4.0E-03	5.4	8.0E-04	0.8	4.4E-01	0.2	8.0E-01
ENSMUST00000180027				4.4	3.6E-03	-3.4	9.9E-04	0.4	2.7E-01	0.7	3.8E-01
ENSMUST00000177254	tubulin tyrosine ligase-like family, member 8 [Source:MGI Symbol;Acc:MGI:1922902]	H3BJ58		5.8	5.2E-02	6.1	5.2E-02	-0.9	7.7E-01	-1.2	5.1E-01
ENSMUST00000138920				4.4	3.7E-05	4.6	4.2E-03	-0.5	6.7E-01	-0.5	5.0E-01
ENSMUST00000135018				4.4	1.9E-04	7.5	1.8E-05	-2.0	8.6E-02	0.1	7.5E-01
ENSMUST00000128335				4.4	1.1E-04	7.0	7.5E-05	-0.7	5.3E-01	0.0	9.3E-01
ENSMUST00000142250				4.4	1.4E-03	5.7	1.3E-03	-1.5	2.9E-01	0.5	4.9E-01
ENSMUST00000117499				4.4	4.3E-03	6.7	1.6E-02	-0.8	7.4E-01	-1.2	3.8E-01
ENSMUST00000177276	zinc fingers and homeoboxes 1 [Source:MGI Symbol;Acc:MGI:109271]	H3BK31		2.3	2.1E-01	5.3	3.0E-02	1.8	3.3E-01	-1.1	5.1E-01
ENSMUST00000136267				4.4	1.0E-03	-5.1	1.1E-03	0.2	6.0E-01	0.5	6.7E-01
ENSMUST00000027895				4.4	3.3E-03	-6.0	2.3E-05	-0.6	1.2E-01	-3.4	9.5E-03
ENSMUST00000120913				4.4	6.8E-04	7.5	1.5E-03	-0.2	9.0E-01	1.3	1.5E-01
ENSMUST00000123785				4.4	4.2E-05	6.1	4.8E-04	-0.6	6.2E-01	0.7	2.8E-01
ENSMUST00000133304				4.4	8.4E-03	3.7	5.3E-04	0.1	8.8E-01	0.1	9.0E-01
ENSMUST00000107381				4.4	9.4E-03	-5.1	4.8E-02	0.4	6.8E-01	-0.9	7.1E-01
ENSMUST00000177302	zinc finger E-box binding homeobox 2 [Source:MGI Symbol;Acc:MGI:1344407]		Q9R0G7	-3.8	4.2E-02	-2.6	1.0E-01	-1.6	1.0E-01	-2.8	1.5E-01
ENSMUST00000134315				4.4	6.2E-04	4.5	9.6E-05	-1.5	4.5E-02	0.2	6.9E-01
ENSMUST00000195498				4.4	7.4E-04	-3.2	2.5E-02	-0.1	8.3E-01	-0.5	7.1E-01
ENSMUST00000131895				4.4	4.0E-04	6.0	1.3E-04	-1.2	2.4E-01	-0.8	1.9E-01
ENSMUST00000131721				4.4	2.8E-04	5.5	5.1E-04	-0.9	4.5E-01	0.0	9.6E-01
ENSMUST00000187251				4.4	3.1E-03	-1.5	3.8E-02	0.9	4.9E-02	-4.3	8.3E-04
ENSMUST00000118911				4.4	1.0E-03	5.2	2.6E-03	0.6	6.4E-01	0.8	3.5E-01
ENSMUST00000177329	sodium channel, nonvoltage-gated 1 alpha [Source:MGI Symbol;Acc:MGI:101782]	H3BJC3		-1.4	7.4E-01	-0.9	8.7E-01	0.2	9.5E-01	-0.3	9.6E-01
ENSMUST00000126160				4.4	1.0E-03	7.2	7.2E-04	0.9	5.1E-01	1.0	1.7E-01
ENSMUST00000177334	ATPase, Ca++-sequestering [Source:MGI Symbol;Acc:MGI:1889008]	H3BJ99		-1.0	3.2E-01	2.5	1.0E-01	2.4	6.8E-02	-1.1	3.3E-01
ENSMUST00000177335				1.1	5.1E-01	3.2	9.4E-02	0.3	8.6E-01	-1.9	2.4E-01
ENSMUST00000162341				4.4	6.7E-04	5.5	1.1E-02	-1.1	5.5E-01	-0.1	9.3E-01
ENSMUST00000192194				4.4	1.9E-04	8.5	3.9E-06	-0.1	9.0E-01	0.2	5.3E-01
ENSMUST00000129080				4.4	1.3E-03	7.2	4.9E-03	2.2	2.6E-01	1.6	1.5E-01
ENSMUST00000177354				0.5	7.2E-01	1.2	5.0E-01	0.2	8.9E-01	-0.5	7.1E-01
ENSMUST00000177359	cysteine and histidine rich 1 [Source:MGI Symbol;Acc:MGI:1859320]		Q9QXA1	1.1	5.9E-01	2.0	3.3E-01	-0.6	7.5E-01	-1.5	4.3E-01
ENSMUST00000130598				4.4	5.8E-03	7.6	2.6E-04	-1.5	3.0E-01	-0.2	7.8E-01
ENSMUST00000138935				4.4	1.8E-03	-9.9	9.1E-04	-1.0	1.0E-01	-1.0	6.8E-01
ENSMUST00000086958				4.4	5.2E-04	-2.1	1.4E-01	1.4	9.1E-02	1.3	3.1E-01
ENSMUST00000169078				4.4	8.6E-05	2.1	1.4E-01	6.5	9.3E-05	-0.8	4.6E-01
ENSMUST00000140700				4.4	1.7E-04	7.2	2.3E-03	-0.8	6.8E-01	0.5	6.1E-01
ENSMUST00000159581				4.4	2.7E-02	-6.9	4.3E-04	0.6	2.0E-01	-0.2	9.1E-01
ENSMUST00000177378	Ros1 proto-oncogene [Source:MGI Symbol;Acc:MGI:97999]	H3BJA2		4.3	1.0E-01	6.5	3.5E-02	-0.2	9.4E-01	-2.4	1.5E-01
ENSMUST00000147015				4.4	3.4E-03	7.3	7.0E-05	-0.6	6.3E-01	-1.0	1.0E-01
ENSMUST00000177380	neuroplastin [Source:MGI Symbol;Acc:MGI:108077]	A0A0A0MQN8		0.3	9.1E-01	-5.4	6.3E-02	-6.2	5.2E-03	-0.5	8.6E-01
ENSMUST00000162927				4.4	1.8E-03	3.7	2.7E-02	-1.1	4.5E-01	0.9	3.7E-01
ENSMUST00000172074				4.4	2.9E-03	-7.5	4.5E-05	-0.7	7.2E-02	-0.8	5.0E-01
ENSMUST00000161041				4.4	7.4E-05	-1.8	1.3E-01	0.0	9.4E-01	-0.4	7.1E-01
ENSMUST00000141152				4.4	6.5E-04	6.7	8.6E-06	-1.3	1.3E-01	-0.2	7.0E-01
ENSMUST00000184726				4.4	2.1E-05	5.8	2.8E-03	-1.1	4.4E-01	-1.2	2.1E-01
ENSMUST00000138588				4.4	1.8E-03	6.1	1.8E-04	-1.2	3.1E-01	-0.5	3.8E-01
ENSMUST00000136923				4.4	2.1E-03	7.0	1.8E-04	-1.3	3.2E-01	0.8	2.0E-01
ENSMUST00000177418				1.3	4.1E-01	0.8	6.9E-01	-0.9	5.4E-01	-0.4	8.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000176793				4.4	5.4E-06	3.0	3.3E-02	0.8	4.7E-01	0.5	6.1E-01
ENSMUST00000186826				4.4	4.1E-05	6.5	1.3E-04	-0.6	6.1E-01	-0.7	2.7E-01
ENSMUST00000184247				4.4	2.4E-03	-5.5	2.0E-03	0.1	8.1E-01	1.5	2.7E-01
ENSMUST00000183715				4.4	3.0E-03	5.9	3.1E-04	-0.6	6.1E-01	0.2	7.9E-01
ENSMUST00000177442	bolA-like 1 (E. coli) [Source:MGI Symbol;Acc:MGI:1916418]		Q9D8S9	-1.7	1.9E-01	0.1	9.0E-01	-1.3	1.6E-01	-3.2	3.0E-02
ENSMUST00000195526				4.4	6.7E-03	4.2	1.7E-02	-2.3	1.9E-01	0.0	9.8E-01
ENSMUST00000177445				-0.2	9.2E-01	-2.2	2.4E-01	-4.2	1.8E-02	-2.2	3.4E-01
ENSMUST00000177451	forkhead box N3 [Source:MGI Symbol;Acc:MGI:1918625]		Q499D0	2.5	1.3E-01	3.2	5.6E-02	-1.5	3.2E-01	-2.2	1.3E-01
ENSMUST00000186492				4.4	2.2E-05	8.0	1.7E-03	-2.3	3.1E-01	1.9	7.9E-02
ENSMUST00000143698				4.4	2.4E-04	-4.3	2.2E-03	-0.7	1.5E-01	-0.7	5.2E-01
ENSMUST00000177466	sin3 associated polypeptide [Source:MGI Symbol;Acc:MGI:3802945]	H3BLC5		-0.3	8.5E-01	-1.0	5.9E-01	-0.2	8.8E-01	0.6	7.5E-01
ENSMUST00000168654				4.4	1.5E-02	6.7	2.7E-04	-0.6	6.5E-01	-0.7	2.8E-01
ENSMUST00000177470				0.0	9.4E-01	0.6	4.9E-01	0.6	4.0E-01	0.0	9.8E-01
ENSMUST00000124440				4.4	3.1E-02	8.7	6.1E-06	0.0	9.9E-01	0.0	9.8E-01
ENSMUST00000173418				4.4	1.9E-03	6.7	5.4E-05	0.3	7.6E-01	-0.1	8.4E-01
ENSMUST00000177476	neuralized E3 ubiquitin protein ligase 4 [Source:MGI Symbol;Acc:MGI:1921092]	H3BJZ3		-0.4	8.9E-01	4.2	3.9E-01	4.5	2.2E-01	-0.1	9.8E-01
ENSMUST00000177494				-1.3	5.4E-01	-0.7	8.0E-01	0.1	9.7E-01	-0.5	8.4E-01
ENSMUST00000177495	Rho GTPase activating protein 19 [Source:MGI Symbol;Acc:MGI:1918335]		Q8BRH3	2.1	3.4E-01	4.7	6.4E-02	0.2	9.3E-01	-2.3	2.3E-01
ENSMUST00000182523				4.4	4.3E-04	-4.8	7.3E-02	0.7	4.6E-01	2.1	4.0E-01
ENSMUST00000187674				4.4	2.5E-03	5.3	2.7E-03	-1.9	2.3E-01	-0.4	6.3E-01
ENSMUST00000177501	transmembrane protein 70 [Source:MGI Symbol;Acc:MGI:1915068]			0.0	1.0E+00	6.6	8.3E-03	6.6	5.3E-03	0.0	9.8E-01
ENSMUST00000126683				4.4	4.7E-05	5.5	3.0E-03	-0.6	7.1E-01	0.5	5.2E-01
ENSMUST00000185944				4.4	1.1E-04	6.9	5.4E-06	0.0	9.5E-01	-1.4	1.0E-02
ENSMUST00000141363				4.4	1.5E-03	-2.8	6.6E-02	0.0	9.7E-01	-1.1	4.3E-01
ENSMUST00000139730				4.4	1.4E-05	6.2	7.0E-03	-0.8	6.8E-01	0.5	6.5E-01
ENSMUST00000177517	unc-13 homolog A (C. elegans) [Source:MGI Symbol;Acc:MGI:3051532]	H3BJZ7		4.2	6.8E-02	5.6	3.6E-02	-0.3	9.0E-01	-1.7	2.3E-01
ENSMUST00000177520	ring finger protein 141 [Source:MGI Symbol;Acc:MGI:1914400]	H3BJE9		2.4	6.7E-02	2.3	1.0E-01	-0.2	8.6E-01	-0.2	8.7E-01
ENSMUST00000147224				4.4	7.3E-03	6.4	1.4E-05	0.3	6.8E-01	-0.3	5.6E-01
ENSMUST00000123518				4.4	7.8E-04	2.5	3.8E-01	-0.8	7.5E-01	2.4	2.7E-01
ENSMUST00000132606				4.4	2.1E-04	-3.3	5.6E-02	1.0	2.3E-01	0.9	5.7E-01
ENSMUST00000177530	zinc finger protein 169 [Source:MGI Symbol;Acc:MGI:1915161]	E9Q3R6		0.8	2.0E-01	0.8	3.4E-01	0.1	8.3E-01	0.2	8.3E-01
ENSMUST00000120460				4.4	8.4E-03	6.7	6.9E-04	-0.6	6.6E-01	-0.5	5.6E-01
ENSMUST00000121000				4.4	7.7E-04	5.5	3.1E-04	0.7	4.1E-01	-0.8	2.2E-01
ENSMUST00000177543	aftiphilin [Source:MGI Symbol;Acc:MGI:1923012]	H3BJH7		-1.5	6.4E-01	-3.9	4.2E-01	-1.2	6.0E-01	1.2	8.1E-01
ENSMUST00000129896				4.4	2.6E-02	-3.6	3.0E-02	0.4	6.3E-01	-0.1	9.3E-01
ENSMUST00000177549	potassium channel, subfamily K, member 13 [Source:MGI Symbol;Acc:MGI:2384976]	Q3TYG8	Q8R1P5	4.6	7.1E-02	-0.5	8.6E-01	-4.6	8.1E-02	0.5	8.5E-01
ENSMUST00000179635				4.4	4.2E-04	5.4	2.3E-03	-2.1	1.4E-01	-1.0	1.9E-01
ENSMUST00000161037				4.4	1.9E-04	7.5	3.5E-04	0.1	9.5E-01	0.2	8.0E-01
ENSMUST00000190700				4.4	1.1E-04	-5.0	1.8E-03	-0.3	5.8E-01	-0.8	5.4E-01
ENSMUST00000125787				4.4	8.6E-04	7.7	6.3E-05	-0.7	5.9E-01	0.0	9.5E-01
ENSMUST00000177585	UL16 binding protein 1 [Source:MGI Symbol;Acc:MGI:1925027]	Q8HWA3		-0.9	1.0E-01	-0.6	3.4E-01	0.3	5.6E-01	0.0	9.8E-01
ENSMUST00000177592	DNA-damage inducible protein 2 [Source:MGI Symbol;Acc:MGI:1917244]		Q9ER99	-0.9	8.0E-01	-3.4	6.2E-01	-0.1	9.8E-01	2.4	7.3E-01
ENSMUST00000166419				4.4	3.5E-02	4.4	6.7E-02	-0.6	7.7E-01	-0.5	7.6E-01
ENSMUST00000180089				4.4	2.9E-05	3.8	1.1E-02	-1.8	1.8E-01	0.1	9.2E-01
ENSMUST00000132468				4.4	1.8E-04	15.2	4.5E-07	-0.3	8.0E-01	-0.8	1.9E-02
ENSMUST00000177604	spindle and kinetochore associated complex subunit 1 [Source:MGI Symbol;Acc:MGI:1913718]			3.3	2.3E-01	1.6	5.3E-01	-2.6	3.6E-01	-0.8	6.9E-01
ENSMUST00000177608	sulfatase 1 [Source:MGI Symbol;Acc:MGI:2138563]		Q8K007	4.4	4.0E-02	4.4	2.8E-02	-2.9	1.6E-01	-2.8	4.8E-02
ENSMUST00000151065				4.4	6.9E-03	10.2	3.2E-03	-1.2	7.0E-01	1.0	3.6E-01
ENSMUST00000151915				4.4	7.8E-04	-1.7	3.7E-01	3.3	4.0E-02	-0.3	8.8E-01
ENSMUST00000167760				4.4	2.6E-03	0.1	9.5E-01	-2.0	1.0E-01	1.8	1.6E-01
ENSMUST00000123830				4.4	4.5E-05	5.0	1.6E-02	-0.7	7.1E-01	-0.5	6.5E-01
ENSMUST00000174045				4.4	3.1E-03	-7.3	8.6E-02	2.0	1.9E-01	-0.9	8.4E-01
ENSMUST00000123671				4.4	9.2E-03	11.8	8.7E-05	1.4	4.5E-01	1.4	4.6E-02
ENSMUST00000189219				4.4	6.8E-03	-2.9	1.1E-02	0.5	3.6E-01	-1.7	1.3E-01
ENSMUST00000177680				4.1	8.5E-02	5.5	4.5E-02	-0.3	9.1E-01	-1.7	2.6E-01
ENSMUST00000121596				4.4	1.8E-04	7.3	9.6E-05	-0.6	6.2E-01	0.0	9.6E-01
ENSMUST00000165802				4.4	2.2E-03	6.9	5.3E-04	-0.1	9.3E-01	-0.6	4.4E-01
ENSMUST00000122275				4.4	3.8E-03	5.2	7.9E-03	0.2	9.1E-01	0.1	9.2E-01
ENSMUST00000123090				4.4	1.8E-04	-4.0	6.8E-02	0.3	7.1E-01	0.0	9.9E-01
ENSMUST00000173788				4.4	2.5E-04	2.5	1.2E-02	0.6	4.0E-01	0.4	5.7E-01
ENSMUST00000145497				4.4	3.1E-03	-4.1	6.3E-03	-2.1	9.3E-03	-1.5	2.7E-01
ENSMUST00000154265				4.4	4.7E-04	9.5	4.2E-04	-0.2	9.2E-01	-1.6	5.1E-02
ENSMUST00000177736	lethal giant larvae homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1918843]	J3QJU5		1.3	4.8E-01	5.8	1.1E-01	5.0	1.3E-01	0.5	8.2E-01
ENSMUST00000177738	RNA binding motif protein 10 [Source:MGI Symbol;Acc:MGI:2384310]		Q99KG3	-1.6	5.4E-01	-1.9	5.4E-01	-1.0	5.9E-01	-0.7	8.3E-01
ENSMUST00000177750				4.1	8.5E-02	5.5	4.5E-02	-0.3	9.1E-01	-1.7	2.6E-01
ENSMUST00000127211				4.4	5.4E-06	-3.2	2.9E-03	-1.4	1.8E-02	-0.1	9.4E-01
ENSMUST00000177754	DNA methyltransferase (cytosine-5) 1 [Source:MGI Symbol;Acc:MGI:94912]	J3QNW0		-1.6	2.3E-01	0.9	6.3E-01	1.1	4.8E-01	-1.4	3.5E-01
ENSMUST00000177761	WNK lysine deficient protein kinase 1 [Source:MGI Symbol;Acc:MGI:2442092]		P83741	5.0	6.6E-02	4.5	5.9E-02	-3.3	2.1E-01	-2.9	9.6E-02
ENSMUST00000129057				4.4	1.4E-04	8.2	8.0E-05	-0.7	5.9E-01	0.1	8.2E-01
ENSMUST00000160723				4.4	4.5E-05	7.5	1.1E-02	-0.9	7.4E-01	-1.8	2.3E-01
ENSMUST00000172994				4.3	4.3E-03	-0.3	9.3E-01	4.4	1.1E-01	-3.5	2.5E-01
ENSMUST00000177768	family with sequence similarity 177, member A [Source:MGI Symbol;Acc:MGI:1920635]		Q8BR63	0.0	9.4E-01	0.8	2.6E-01	0.6	2.9E-01	-0.2	7.4E-01
ENSMUST00000177778	RIKEN cDNA 5730507C01 gene [Source:MGI Symbol;Acc:MGI:1917882]	J3QPX0		2.8	5.0E-02	6.6	3.4E-04	-0.5	6.9E-01	-4.3	9.1E-04
ENSMUST00000177779	prosaposin [Source:MGI Symbol;Acc:MGI:97783]	J3QPG5		1.2	4.9E-01	0.6	8.2E-01	0.4	8.4E-01	1.0	6.4E-01
ENSMUST00000177780				2.7	2.2E-01	3.1	1.5E-01	-2.5	2.3E-01	-3.0	1.3E-01
ENSMUST00000126315				4.3	1.7E-03	8.0	5.4E-05	-1.0	4.2E-01	-1.0	9.7E-02
ENSMUST00000177806	predicted gene 13290 [Source:MGI Symbol;Acc:MGI:3701990]		Q8CD73	3.5	4.7E-02	6.3	2.5E-03	-0.5	7.7E-01	-3.4	1.2E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000177808	cDNA sequence BC022687 [Source:MGI Symbol;Acc:MGI:2443738]		Q8BHN9	3.5	8.3E-02	4.2	9.2E-02	0.0	9.9E-01	-0.7	6.9E-01
ENSMUST00000148093				4.3	1.2E-04	4.1	2.8E-02	-0.7	6.6E-01	2.3	5.9E-02
ENSMUST00000150409				4.3	3.0E-04	16.6	7.0E-07	1.4	3.2E-01	-0.6	9.2E-02
ENSMUST00000194978				4.3	5.5E-04	4.2	2.0E-04	0.0	9.6E-01	0.5	2.7E-01
ENSMUST00000177825	cytokine receptor-like factor 3 [Source:MGI Symbol;Acc:MGI:1860086]	J3QMV5		0.7	7.8E-01	-4.3	1.8E-01	-4.7	2.9E-02	0.3	9.2E-01
ENSMUST00000147413				4.3	1.4E-03	-6.5	5.6E-04	-0.5	3.0E-01	-0.7	6.1E-01
ENSMUST00000125224				4.3	9.7E-04	-2.4	1.2E-01	0.7	4.4E-01	-0.7	6.4E-01
ENSMUST00000177846	LIM homeobox protein 8 [Source:MGI Symbol;Acc:MGI:1096343]		O35652	3.8	8.5E-02	6.0	2.1E-02	-0.3	9.0E-01	-2.5	8.7E-02
ENSMUST00000133227				4.3	5.1E-04	-3.8	3.7E-02	0.8	3.5E-01	-0.9	6.2E-01
ENSMUST00000119789				4.3	2.2E-02	-4.2	2.6E-03	-0.1	8.2E-01	-0.8	5.0E-01
ENSMUST00000177851	GATA zinc finger domain containing 2A [Source:MGI Symbol;Acc:MGI:2384585]		Q8CHY6	-0.1	9.4E-01	-0.4	8.4E-01	0.6	6.2E-01	0.9	6.2E-01
ENSMUST00000150051				4.3	4.6E-04	13.4	1.0E-07	-1.5	1.6E-01	-0.6	4.3E-02
ENSMUST00000119381				4.3	1.6E-03	7.3	4.1E-04	-0.4	7.9E-01	-0.9	2.4E-01
ENSMUST00000133552				4.3	3.2E-03	10.4	1.2E-03	-1.1	6.7E-01	1.0	2.8E-01
ENSMUST00000176015				4.3	3.0E-02	8.3	1.5E-05	-2.6	5.2E-02	0.0	9.3E-01
ENSMUST00000138117				4.3	7.8E-05	6.3	7.6E-04	-0.6	6.8E-01	-0.1	8.9E-01
ENSMUST00000151677				4.3	7.6E-04	5.6	5.3E-04	-1.5	2.3E-01	-0.4	5.0E-01
ENSMUST00000154362				4.3	1.1E-04	6.5	2.7E-04	-0.6	6.3E-01	-0.4	5.4E-01
ENSMUST00000171985				4.3	1.6E-03	-4.2	2.2E-03	0.3	4.6E-01	-0.8	4.9E-01
ENSMUST00000153176				4.3	2.2E-02	8.9	1.1E-04	0.5	6.9E-01	1.4	8.6E-02
ENSMUST00000177927	forkhead box J2 [Source:MGI Symbol;Acc:MGI:1926805]		Q9ES18	-1.4	3.3E-01	-2.3	2.7E-01	1.1	3.6E-01	2.0	3.2E-01
ENSMUST00000152792				4.3	2.1E-03	6.3	3.7E-04	-0.5	7.0E-01	-0.6	3.5E-01
ENSMUST00000177939	FK506 binding protein 5 [Source:MGI Symbol;Acc:MGI:104670]	Q4FJN2	Q64378	3.3	6.3E-02	2.6	4.3E-01	3.1	2.3E-01	3.8	1.4E-01
ENSMUST00000177943	solute carrier family 45, member 3 [Source:MGI Symbol;Acc:MGI:1922082]		Q8K0H7	0.3	8.5E-01	2.9	4.9E-02	-0.8	5.4E-01	-3.4	3.8E-02
ENSMUST00000186569				4.3	1.3E-04	-2.6	5.7E-02	0.2	8.2E-01	-1.7	2.3E-01
ENSMUST00000177947				4.1	8.5E-02	5.5	4.5E-02	-0.3	9.1E-01	-1.7	2.6E-01
ENSMUST00000177950	ring finger protein 44 [Source:MGI Symbol;Acc:MGI:2145310]		Q3UHJ8	-3.2	1.1E-01	-5.5	6.1E-02	-1.6	1.7E-01	0.8	7.9E-01
ENSMUST00000141917				4.3	8.7E-03	-4.1	1.6E-03	0.7	1.2E-01	-1.2	2.7E-01
ENSMUST00000151518				4.3	2.7E-04	-4.0	5.2E-03	-0.2	7.3E-01	-0.2	8.4E-01
ENSMUST00000069553				4.3	8.9E-04	6.6	3.4E-04	-0.7	5.9E-01	-0.1	8.3E-01
ENSMUST00000125881				4.3	1.3E-03	4.4	9.4E-03	-0.8	5.6E-01	-0.7	4.9E-01
ENSMUST00000139416				4.3	7.7E-04	12.0	1.6E-06	-0.5	7.0E-01	-0.6	9.4E-02
ENSMUST00000153438				4.3	7.6E-05	5.2	1.4E-03	-0.5	7.1E-01	0.4	5.7E-01
ENSMUST00000177974	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Source:MGI Symbol;Acc:MGI:88110]		O55143	-1.0	3.1E-01	0.4	7.4E-01	0.7	4.2E-01	-0.6	5.7E-01
ENSMUST00000142784				4.3	1.6E-03	-4.2	2.5E-03	0.7	1.7E-01	0.4	7.1E-01
ENSMUST00000177983	RIKEN cDNA 1600014C10 gene [Source:MGI Symbol;Acc:MGI:1919494]	J3QPY0		-1.4	3.1E-01	-1.0	5.2E-01	0.0	9.8E-01	-0.3	8.5E-01
ENSMUST00000147512				4.3	2.4E-04	6.1	3.0E-04	-0.5	6.6E-01	-1.5	3.6E-02
ENSMUST00000186163				4.3	2.2E-03	4.8	4.2E-03	-0.5	6.9E-01	0.8	3.0E-01
ENSMUST00000178011	synuclein, alpha interacting protein (synphilin) [Source:MGI Symbol;Acc:MGI:1915097]	E9Q4E2		5.1	6.1E-02	3.6	2.1E-01	-0.6	8.5E-01	1.0	5.7E-01
ENSMUST00000195565				4.3	4.5E-05	-7.5	5.7E-02	1.0	4.0E-01	0.1	9.8E-01
ENSMUST00000123790				4.3	5.5E-03	6.8	2.5E-03	-0.9	5.8E-01	0.7	4.3E-01
ENSMUST00000154023				4.3	2.1E-03	14.2	3.4E-05	-1.0	6.3E-01	0.7	2.0E-01
ENSMUST00000178028				0.3	9.1E-01	3.0	4.3E-01	2.8	3.6E-01	0.1	9.8E-01
ENSMUST00000139399				4.3	7.5E-03	-7.6	1.1E-02	1.8	2.8E-02	2.3	3.7E-01
ENSMUST00000178036	axonemal dynein light chain domain containing 1 [Source:MGI Symbol;Acc:MGI:1924602]	J3QPL7		2.8	1.8E-01	4.1	6.7E-02	-1.3	5.5E-01	-2.6	1.2E-01
ENSMUST00000138214				4.3	4.9E-03	4.5	5.1E-03	0.7	5.4E-01	-0.1	9.0E-01
ENSMUST00000178048	kinesin family member 7 [Source:MGI Symbol;Acc:MGI:1098239]	J3QNW9		4.5	4.1E-02	1.2	6.6E-01	-0.9	6.9E-01	2.4	3.1E-01
ENSMUST00000154976				4.3	7.8E-04	-1.1	1.6E-02	-0.8	2.4E-02	-0.9	4.1E-02
ENSMUST00000178052				0.1	9.0E-01	6.1	6.7E-03	5.0	1.3E-02	-1.0	3.3E-01
ENSMUST00000130070				4.3	1.3E-04	5.5	1.1E-04	-3.0	1.3E-02	-0.7	2.1E-01
ENSMUST00000155824				4.3	1.2E-03	7.7	6.7E-05	-0.9	4.6E-01	0.5	4.3E-01
ENSMUST00000178070	germ cell-less homolog 1 (Drosophila)-like [Source:MGI Symbol;Acc:MGI:1919097]	J3KMQ0		4.8	1.6E-01	4.8	2.0E-01	-0.2	9.6E-01	-0.2	9.1E-01
ENSMUST00000140418				4.3	2.0E-04	-6.3	3.5E-03	1.0	1.2E-01	-1.4	4.8E-01
ENSMUST00000150785				4.3	1.7E-04	12.7	1.8E-06	-0.4	7.6E-01	-0.6	1.2E-01
ENSMUST00000178079	ribosomal protein L31 [Source:MGI Symbol;Acc:MGI:2149632]	Q5M9K9	P62900	-5.6	5.5E-02	-2.6	2.7E-01	-0.6	7.1E-01	-3.6	2.2E-01
ENSMUST00000178087	leucine zipper, putative tumor suppressor 2 [Source:MGI Symbol;Acc:MGI:2385095]		Q91YU6	2.2	1.9E-01	-3.7	2.0E-01	-2.0	2.2E-01	3.9	1.6E-01
ENSMUST00000192611				4.3	7.4E-05	-7.2	7.2E-05	-0.6	1.1E-01	1.2	2.6E-01
ENSMUST00000143873				4.3	3.2E-04	7.1	9.1E-04	-0.7	6.5E-01	-0.6	4.5E-01
ENSMUST00000178098	٩1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2150		Q3UT23	-2.3	7.8E-02	-1.1	4.5E-01	0.2	8.3E-01	-1.0	4.8E-01
ENSMUST00000156330				4.3	1.9E-05	3.1	6.5E-03	-0.7	3.9E-01	0.2	7.5E-01
ENSMUST00000178105	dynein light chain LC8-type 2 [Source:MGI Symbol;Acc:MGI:1915347]		Q9D0M5	-2.0	4.7E-02	-4.0	4.5E-02	0.9	2.4E-01	2.9	1.2E-01
ENSMUST00000178107				-2.6	6.6E-02	-3.3	1.2E-01	-0.1	9.0E-01	0.6	7.8E-01
ENSMUST00000174345				4.3	2.5E-04	6.0	1.9E-04	-3.2	2.4E-02	0.5	3.8E-01
ENSMUST00000178113	transducin-like enhancer of split 3, homolog of Drosophila E(spl) [Source:MGI Symbol;Acc:MGI:104634]	J3KMT7		-2.1	1.6E-01	-2.1	3.2E-01	0.7	5.5E-01	0.7	7.3E-01
ENSMUST00000178114	lysosomal acid lipase A [Source:MGI Symbol;Acc:MGI:96789]		Q9Z0M5	-0.4	9.1E-01	-2.8	2.8E-01	-4.4	6.0E-02	-1.9	5.4E-01
ENSMUST00000178116	arginyl aminopeptidase (aminopeptidase B)-like 1 [Source:MGI Symbol;Acc:MGI:1914170]	J3QJW7		0.1	9.8E-01	3.9	2.9E-01	2.6	4.2E-01	-1.3	7.1E-01
ENSMUST00000152638				4.3	2.3E-03	5.1	3.0E-04	-2.0	7.3E-02	-0.4	5.0E-01
ENSMUST00000178134	midasin homolog (yeast) [Source:MGI Symbol;Acc:MGI:1926159]	J3QMC5		4.4	1.8E-01	-0.1	9.9E-01	-2.4	4.8E-01	2.0	5.3E-01
ENSMUST00000178136	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 [Source:MGI Symbol;Acc:MGI:1923658]	J3QML2		1.3	3.5E-01	0.6	7.2E-01	-0.1	9.5E-01	0.6	7.1E-01
ENSMUST00000190921				4.3	8.4E-05	-0.5	4.1E-01	1.5	2.7E-03	-0.1	8.3E-01
ENSMUST00000041218				4.3	4.9E-04	3.2	6.7E-04	-0.4	5.2E-01	-0.2	7.1E-01
ENSMUST00000178147				6.3	3.5E-02	5.6	7.8E-02	-0.6	8.6E-01	0.2	9.2E-01
ENSMUST00000133057				4.3	6.9E-04	2.2	3.1E-01	-0.3	8.5E-01	3.2	6.9E-02
ENSMUST00000155025				4.3	1.7E-04	-3.7	1.5E-02	0.6	3.7E-01	2.6	6.0E-02
ENSMUST00000159239				4.3	8.3E-05	6.9	1.2E-05	0.8	3.2E-01	-0.6	1.8E-01
ENSMUST00000178162	zinc finger protein 790 [Source:MGI Symbol;Acc:MGI:1923431]	Q80ZX2		-4.0	7.1E-02	0.2	9.1E-01	1.2	4.7E-01	-3.1	1.5E-01
ENSMUST00000178164	Sin3A associated protein [Source:MGI Symbol;Acc:MGI:1919782]	J3QNK5		-1.4	3.7E-01	-1.6	5.7E-01	1.3	4.5E-01	1.5	5.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000191719				4.3	2.9E-04	5.7	1.4E-03	-0.7	6.3E-01	0.4	5.6E-01
ENSMUST00000178171				-1.4	7.5E-02	-1.3	1.3E-01	-1.3	4.5E-02	-1.3	1.3E-01
ENSMUST00000137291				4.3	2.6E-03	8.0	1.7E-04	-0.8	5.5E-01	0.7	3.1E-01
ENSMUST00000178178	RIKEN cDNA 1700001F09 gene [Source:MGI Symbol;Acc:MGI:1919076]	Q9DAR5		4.9	3.8E-02	3.1	2.0E-01	-0.7	7.7E-01	1.1	5.1E-01
ENSMUST00000137943				4.3	2.7E-04	5.5	3.1E-03	0.0	1.0E+00	-0.4	6.7E-01
ENSMUST00000178195	polycystic kidney disease 1 like 1 [Source:MGI Symbol;Acc:MGI:2156538]	A0A0A0MQP1		1.3	4.7E-01	6.3	1.8E-02	1.6	4.8E-01	-3.5	3.6E-02
ENSMUST00000178202	epsin 2 [Source:MGI Symbol;Acc:MGI:1333766]		Q8CHU3	4.3	1.8E-01	4.6	2.0E-01	-0.2	9.5E-01	-0.5	8.2E-01
ENSMUST00000123032				4.3	1.5E-05	5.4	4.4E-04	-0.6	5.8E-01	0.3	5.7E-01
ENSMUST00000178219	predicted gene, 21681 [Source:MGI Symbol;Acc:MGI:5435036]	A2BFZ7		3.0	2.5E-01	5.1	7.3E-02	-0.4	8.7E-01	-2.6	1.8E-01
ENSMUST00000171976				4.3	3.4E-03	7.0	3.1E-05	-1.6	1.2E-01	-0.1	8.9E-01
ENSMUST00000195051				4.3	3.4E-03	-2.7	6.8E-02	-0.6	4.2E-01	-1.8	2.6E-01
ENSMUST00000077991				4.3	2.7E-04	8.4	2.2E-05	-0.5	7.0E-01	-0.3	5.6E-01
ENSMUST00000117963				4.3	6.6E-03	9.7	1.5E-04	-0.1	9.7E-01	0.4	5.6E-01
ENSMUST00000137683				4.3	5.4E-06	5.1	1.6E-03	0.6	5.8E-01	0.3	7.1E-01
ENSMUST00000127855				4.3	6.6E-03	-2.5	8.9E-02	1.2	1.7E-01	-1.0	4.8E-01
ENSMUST00000129590				4.3	2.2E-03	4.7	8.3E-05	-0.6	3.7E-01	-0.8	1.7E-01
ENSMUST00000145418				4.3	4.7E-05	4.3	3.9E-04	-0.3	7.0E-01	0.6	2.8E-01
ENSMUST00000160928				4.3	2.5E-02	6.8	3.3E-04	-0.5	7.3E-01	-0.6	3.8E-01
ENSMUST00000140969				4.3	3.2E-04	4.6	1.3E-03	0.7	4.6E-01	-0.5	4.5E-01
ENSMUST00000192422				4.3	4.3E-04	-3.5	2.9E-01	1.7	3.4E-01	-3.6	3.9E-01
ENSMUST00000178257	perilipin 1 [Source:MGI Symbol;Acc:MGI:1890505]		Q8CGN5	3.1	2.3E-01	2.3	3.3E-01	-1.4	5.8E-01	-0.6	7.5E-01
ENSMUST00000079761				4.3	4.2E-03	7.1	8.3E-05	-1.9	1.4E-01	0.8	1.7E-01
ENSMUST00000117933				4.3	2.2E-02	-3.1	7.9E-03	-0.1	8.6E-01	-0.6	5.5E-01
ENSMUST00000149464				4.3	7.9E-04	7.1	3.8E-06	-0.7	3.5E-01	0.0	9.1E-01
ENSMUST00000178282	immunoglobulin heavy constant alpha [Source:MGI Symbol;Acc:MGI:96444]	A0A075B6A3		-0.7	5.9E-01	-4.1	1.0E-02	-4.7	4.4E-04	-1.2	4.0E-01
ENSMUST00000120192				4.3	3.2E-03	5.6	5.0E-04	-0.4	6.8E-01	0.3	6.3E-01
ENSMUST00000147729				4.3	8.9E-04	-8.5	7.5E-03	-0.5	4.8E-01	2.2	4.1E-01
ENSMUST00000124680				4.3	6.9E-03	11.8	7.2E-05	0.4	8.1E-01	1.4	9.0E-02
ENSMUST00000161432				4.3	1.4E-02	6.1	1.2E-03	-0.6	6.6E-01	-0.1	9.2E-01
ENSMUST00000178324	NIMA (never in mitosis gene a)-related expressed kinase 3 [Source:MGI Symbol;Acc:MGI:1344371]		Q9R0A5	0.4	7.4E-01	2.2	1.5E-01	-0.2	9.0E-01	-1.9	1.6E-01
ENSMUST00000161537				4.3	1.8E-05	6.5	1.9E-03	-0.6	7.1E-01	-0.6	5.1E-01
ENSMUST00000182336				4.3	1.9E-03	-9.6	6.8E-03	1.2	1.3E-01	2.3	4.2E-01
ENSMUST00000132022				4.3	4.7E-05	8.6	3.2E-05	-0.5	6.9E-01	-0.1	8.0E-01
ENSMUST00000178340	purinergic receptor P2Y, G-protein coupled 2 [Source:MGI Symbol;Acc:MGI:105107]			-1.8	1.8E-01	-0.1	9.7E-01	1.4	2.4E-01	-0.3	8.5E-01
ENSMUST00000178341				3.2	3.2E-01	5.2	1.3E-01	-0.4	9.1E-01	-2.4	2.8E-01
ENSMUST00000135750				4.3	3.1E-03	4.6	8.9E-04	0.4	6.7E-01	-0.1	8.7E-01
ENSMUST00000178344	inositol 1,4,5-triphosphate receptor interacting protein-like 2 [Source:MGI Symbol;Acc:MGI:2442416]		Q3UV16	-0.4	4.0E-01	-0.2	7.2E-01	1.0	5.5E-02	0.8	1.9E-01
ENSMUST00000183098				4.3	1.4E-05	7.5	1.9E-04	-0.7	6.0E-01	0.4	5.4E-01
ENSMUST00000190355				4.3	2.4E-02	15.9	2.1E-07	1.0	4.1E-01	-0.5	6.6E-02
ENSMUST00000178352				3.3	1.7E-01	2.7	3.2E-01	-0.4	8.9E-01	0.3	8.8E-01
ENSMUST00000142761				4.3	3.6E-03	3.8	3.2E-03	1.2	2.0E-01	0.9	2.2E-01
ENSMUST00000173161				4.3	5.7E-04	5.4	7.4E-05	-0.4	5.8E-01	-0.3	5.5E-01
ENSMUST00000182732				4.3	2.6E-03	2.7	1.0E-02	-0.8	3.1E-01	-0.8	2.9E-01
ENSMUST00000131725				4.3	7.7E-03	4.5	6.6E-02	-1.9	4.4E-01	2.1	1.6E-01
ENSMUST00000178384	modulator of apoptosis 1 [Source:MGI Symbol;Acc:MGI:1915555]		Q9ERH6	-2.2	2.5E-01	-1.7	5.0E-01	0.5	7.6E-01	0.0	9.9E-01
ENSMUST00000134485				4.3	4.8E-03	-6.8	3.9E-04	0.7	1.4E-01	0.3	8.1E-01
ENSMUST00000184123				4.3	4.2E-05	3.5	1.4E-03	-0.9	2.8E-01	-0.4	5.1E-01
ENSMUST00000151811				4.3	3.7E-03	7.7	6.9E-04	-2.2	2.3E-01	1.2	1.5E-01
ENSMUST00000117903				4.3	9.9E-04	5.6	4.0E-02	-0.6	8.0E-01	1.3	3.7E-01
ENSMUST00000123023				4.3	5.1E-03	6.7	5.0E-04	-0.4	7.7E-01	-1.4	9.2E-02
ENSMUST00000129384				4.3	3.3E-04	-5.0	7.7E-03	1.4	4.1E-02	-0.3	8.6E-01
ENSMUST00000178429	predicted gene 3187 [Source:MGI Symbol;Acc:MGI:3781366]	J3QJZ7		4.2	9.3E-02	1.7	6.0E-01	-0.2	9.3E-01	2.3	3.4E-01
ENSMUST00000178433				3.1	1.8E-01	6.4	2.5E-02	0.1	9.6E-01	-3.2	5.8E-02
ENSMUST00000150925				4.3	2.1E-02	4.6	2.8E-02	-0.5	7.7E-01	1.7	1.7E-01
ENSMUST00000178451	predicted gene, 21092 [Source:MGI Symbol;Acc:MGI:5434447]	J3QPW4		-0.3	8.0E-01	-2.7	1.2E-01	-0.9	4.0E-01	1.6	3.5E-01
ENSMUST00000178462	sel-1 suppressor of lin-12-like (C. elegans) [Source:MGI Symbol;Acc:MGI:1329016]	J3QJX3		-2.0	5.0E-01	5.7	1.9E-01	6.6	1.0E-01	-1.1	7.1E-01
ENSMUST00000153711				4.3	3.5E-03	8.1	4.6E-06	-2.3	3.8E-02	-0.2	5.9E-01
ENSMUST00000160114				4.3	3.5E-03	-4.6	1.5E-02	0.7	2.7E-01	-0.2	9.0E-01
ENSMUST00000152316				4.3	1.3E-02	-7.2	4.7E-06	1.0	6.6E-03	-3.8	5.0E-03
ENSMUST00000183727				4.3	2.6E-03	6.9	1.1E-04	-1.0	3.8E-01	0.1	8.7E-01
ENSMUST00000178486	lysine (K)-specific methyltransferase 2D [Source:MGI Symbol;Acc:MGI:2682319]		Q6PDK2	-1.0	3.8E-01	-5.3	1.3E-01	2.2	8.8E-02	6.4	6.9E-02
ENSMUST00000136426				4.3	2.5E-04	-7.7	2.6E-03	-0.9	1.5E-01	1.5	4.5E-01
ENSMUST00000027054				4.2	2.7E-03	5.2	1.3E-03	-0.9	4.7E-01	-0.1	8.8E-01
ENSMUST00000178514	adhesion G protein-coupled receptor A2 [Source:MGI Symbol;Acc:MGI:1925810]	J3QMG7		3.6	1.6E-01	2.9	1.8E-01	-2.6	2.4E-01	-2.0	3.4E-01
ENSMUST00000178515	serine/threonine/tyrosine interacting-like 1 [Source:MGI Symbol;Acc:MGI:1923821]	Q9DAG7		2.0	1.9E-01	4.0	4.8E-02	0.7	6.7E-01	-1.3	3.5E-01
ENSMUST00000193204				4.2	5.1E-03	0.4	8.1E-01	3.5	7.7E-03	-0.2	8.9E-01
ENSMUST00000151742				4.2	8.6E-05	8.2	8.5E-03	-1.6	6.0E-01	-1.3	3.9E-01
ENSMUST00000162902				4.2	4.2E-05	6.1	1.9E-04	-0.6	5.9E-01	-0.2	7.2E-01
ENSMUST00000178534	arginyltransferase 1 [Source:MGI Symbol;Acc:MGI:1333870]	J3QNU1		1.5	4.1E-01	-0.6	7.6E-01	-1.7	2.8E-01	0.4	8.5E-01
ENSMUST00000183879				4.2	2.6E-02	6.1	2.6E-04	-0.6	6.1E-01	-0.1	9.1E-01
ENSMUST00000178543	mitogen-activated protein kinase 9 [Source:MGI Symbol;Acc:MGI:1346862]		Q9WTU6	5.0	4.3E-02	3.1	2.2E-01	-0.7	7.9E-01	1.2	4.8E-01
ENSMUST00000122886				4.2	1.7E-05	7.2	8.7E-05	-0.6	6.2E-01	0.1	8.7E-01
ENSMUST00000178547				6.2	5.6E-02	5.7	9.1E-02	-0.9	7.8E-01	-0.5	8.1E-01
ENSMUST00000144231				4.2	3.8E-04	6.3	2.4E-03	-0.5	7.7E-01	-0.9	3.2E-01
ENSMUST00000121487				4.2	2.0E-02	7.1	2.2E-03	-0.8	6.7E-01	1.2	2.2E-01
ENSMUST00000117842				4.2	1.7E-02	-6.3	7.9E-04	-1.2	6.4E-02	0.3	8.0E-01
ENSMUST00000136843				4.2	2.0E-03	5.5	1.7E-02	-0.7	7.3E-01	2.4	5.3E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000178562	butyrophilin-like 2 [Source:MGI Symbol;Acc:MGI:1859549]	J3QP12		4.0	1.2E-01	0.9	7.8E-01	-1.2	6.6E-01	1.9	4.5E-01
ENSMUST00000163012				4.2	3.0E-04	1.6	1.5E-01	-4.7	4.4E-03	-2.7	2.7E-02
ENSMUST00000178564	small nuclear ribonucleoprotein 48 (U11/U12) [Source:MGI Symbol;Acc:MGI:1915047]	J3QMA8		-2.0	5.8E-02	-3.0	1.4E-02	-1.4	6.2E-02	-0.4	6.8E-01
ENSMUST00000194094				4.2	5.8E-04	8.4	1.9E-05	-0.5	6.7E-01	-0.4	4.0E-01
ENSMUST00000125343				4.2	1.9E-04	-5.9	7.4E-03	-0.8	2.4E-01	2.0	2.6E-01
ENSMUST00000143148				4.2	4.8E-04	7.7	1.7E-04	-0.7	6.2E-01	-0.2	7.5E-01
ENSMUST00000178590	pleckstrin homology domain containing, family S member 1 [Source:MGI Symbol;Acc:MGI:2443041]		Q8BW88	3.8	4.1E-02	3.5	9.5E-02	-0.7	6.8E-01	-0.4	8.0E-01
ENSMUST00000120954				4.2	2.7E-02	6.3	1.9E-04	-0.5	6.3E-01	-0.3	6.4E-01
ENSMUST00000192433				4.2	3.2E-04	-0.9	1.9E-01	0.7	1.5E-01	0.1	9.3E-01
ENSMUST00000190108				4.2	1.2E-04	6.1	5.2E-04	-0.6	6.3E-01	-0.1	8.4E-01
ENSMUST00000136954				4.2	5.7E-03	-5.6	2.2E-02	-0.1	9.3E-01	0.0	9.9E-01
ENSMUST00000145360				4.2	1.9E-02	9.1	3.8E-04	-0.2	9.1E-01	-1.2	1.2E-01
ENSMUST00000138165				4.2	6.4E-04	-2.4	2.8E-02	0.1	8.5E-01	-1.2	2.6E-01
ENSMUST00000178622	SLU7 splicing factor homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2385598]		Q8BHJ9	0.0	1.0E+00	6.5	1.1E-01	5.7	1.3E-01	-0.7	7.7E-01
ENSMUST00000189615				4.2	7.8E-04	-6.3	8.0E-04	0.3	5.4E-01	0.2	8.6E-01
ENSMUST00000192411				4.2	6.3E-04	6.2	1.8E-04	-0.6	6.1E-01	0.1	9.1E-01
ENSMUST00000178636	La ribonucleoprotein domain family, member 1 [Source:MGI Symbol;Acc:MGI:1890165]		Q6ZQ58	-0.7	4.4E-01	-4.6	1.5E-02	0.3	6.8E-01	4.2	1.9E-02
ENSMUST00000162960				4.2	1.1E-04	1.9	5.4E-02	0.3	7.3E-01	0.7	3.6E-01
ENSMUST00000149220				4.2	8.3E-04	14.8	9.6E-06	1.0	5.6E-01	-0.7	1.2E-01
ENSMUST00000152579				4.2	1.5E-04	5.7	3.6E-03	0.1	9.5E-01	1.2	1.7E-01
ENSMUST00000171614				4.2	1.3E-03	6.4	7.8E-03	-0.5	8.1E-01	-2.3	7.4E-02
ENSMUST00000018343				4.2	1.3E-03	1.4	1.9E-01	-1.8	8.5E-02	-0.6	5.3E-01
ENSMUST00000188847				4.2	8.2E-05	2.0	4.5E-02	0.2	7.7E-01	0.3	7.2E-01
ENSMUST00000125004				4.2	4.7E-04	-3.1	6.6E-02	0.7	4.3E-01	1.1	4.5E-01
ENSMUST00000123158				4.2	2.9E-04	-3.8	2.4E-04	1.4	3.2E-03	-0.7	3.2E-01
ENSMUST00000155991				4.2	5.0E-03	6.4	1.3E-03	-0.4	8.1E-01	0.3	7.3E-01
ENSMUST00000178684	phenazine biosynthesis-like protein domain containing 2 [Source:MGI Symbol;Acc:MGI:1914557]		Q9DCG6	2.2	3.2E-01	1.4	5.5E-01	-1.2	5.7E-01	-0.5	8.2E-01
ENSMUST00000150745				4.2	1.8E-02	4.5	5.3E-04	1.2	1.7E-01	-0.2	7.3E-01
ENSMUST00000178686	myeloid cell leukemia sequence 1 [Source:MGI Symbol;Acc:MGI:101769]		P97287	-0.7	8.8E-01	-1.5	7.6E-01	-1.3	7.0E-01	-0.4	9.3E-01
ENSMUST00000155647				4.2	4.2E-04	6.3	4.1E-04	0.5	6.8E-01	0.4	5.4E-01
ENSMUST00000121251				4.2	6.9E-03	-3.6	4.8E-02	0.4	6.2E-01	1.2	4.9E-01
ENSMUST00000178695	filaggrin [Source:MGI Symbol;Acc:MGI:95553]	A0A0A6YW46		8.0	4.2E-02	6.0	1.4E-01	-0.8	8.5E-01	1.1	6.2E-01
ENSMUST00000140478				4.2	9.7E-04	5.6	3.7E-04	-0.6	5.5E-01	-0.8	2.6E-01
ENSMUST00000178707				2.5	1.3E-01	4.9	8.9E-03	-0.6	7.3E-01	-3.0	3.1E-02
ENSMUST00000178710	CLIP associating protein 1 [Source:MGI Symbol;Acc:MGI:1923957]	J3QP81		-3.8	1.7E-01	-0.3	9.1E-01	1.4	5.5E-01	-2.1	4.9E-01
ENSMUST00000178723				5.6	5.8E-02	3.6	2.4E-01	-0.7	8.1E-01	1.2	5.3E-01
ENSMUST00000144666				4.2	3.5E-04	7.0	3.5E-07	-1.3	3.7E-02	-0.5	7.8E-02
ENSMUST00000187362				4.2	3.2E-05	-7.0	1.4E-02	1.1	1.9E-01	-0.8	7.7E-01
ENSMUST00000149905				4.2	2.6E-03	6.2	5.3E-04	-0.7	6.1E-01	-0.5	5.1E-01
ENSMUST00000178737				4.6	1.1E-01	5.6	8.6E-02	-0.2	9.5E-01	-1.2	5.1E-01
ENSMUST00000178744	RIKEN cDNA A130010J15 gene [Source:MGI Symbol;Acc:MGI:2441776]		Q9DAE8	2.5	1.3E-01	3.8	4.5E-02	-0.3	8.4E-01	-1.6	2.4E-01
ENSMUST00000133167				4.2	2.9E-04	2.3	1.7E-01	-0.4	7.6E-01	2.8	4.5E-02
ENSMUST00000151897				4.2	1.4E-02	8.7	6.3E-04	1.0	5.6E-01	0.3	6.6E-01
ENSMUST00000161912				4.2	3.0E-05	5.6	2.2E-02	-0.7	7.6E-01	1.4	2.8E-01
ENSMUST00000188660				4.2	2.3E-03	4.6	1.1E-04	0.6	3.8E-01	-0.3	5.8E-01
ENSMUST00000160295				4.2	1.5E-02	6.6	1.0E-03	-0.4	8.0E-01	-0.8	3.5E-01
ENSMUST00000178765	chemokine (C-C motif) ligand 21C (leucine) [Source:MGI Symbol;Acc:MGI:1891386]		P86792	2.8	1.2E-01	6.4	4.0E-03	-0.4	8.2E-01	-4.0	8.1E-03
ENSMUST00000154406				4.2	1.2E-03	6.9	1.6E-04	-0.6	6.2E-01	-0.4	5.1E-01
ENSMUST00000178772	ankyrin repeat domain 66 [Source:MGI Symbol;Acc:MGI:1925106]	J3QNN4		0.8	3.1E-01	0.1	8.9E-01	-0.5	4.7E-01	0.1	8.6E-01
ENSMUST00000154322				4.2	3.8E-03	-10.1	3.6E-03	-1.5	7.1E-02	-0.1	9.8E-01
ENSMUST00000115574				4.2	7.1E-04	6.6	3.7E-04	-0.5	7.1E-01	-1.3	8.4E-02
ENSMUST00000178797	beta galactoside alpha 2,6 sialyltransferase 1 [Source:MGI Symbol;Acc:MGI:108470]		Q64685	-0.8	7.1E-01	-2.1	4.0E-01	-1.6	3.6E-01	-0.3	9.0E-01
ENSMUST00000178798	potassium inwardly-rectifying channel, subfamily J, member 16 [Source:MGI Symbol;Acc:MGI:1314842]		Q9Z307	3.6	1.6E-01	5.0	8.3E-02	-0.5	8.7E-01	-1.9	3.1E-01
ENSMUST00000126185				4.2	1.3E-04	-2.6	2.5E-02	1.6	1.3E-02	-0.8	4.6E-01
ENSMUST00000139437				4.2	4.4E-04	7.8	3.7E-05	-0.6	6.0E-01	-0.7	1.9E-01
ENSMUST00000159571				4.2	1.8E-02	-5.1	8.1E-04	0.5	3.2E-01	-1.0	3.8E-01
ENSMUST00000193267				4.2	9.9E-05	-5.0	1.2E-02	1.1	1.1E-01	-0.3	8.7E-01
ENSMUST00000150160				4.2	8.7E-05	4.3	9.3E-03	0.2	8.4E-01	0.7	4.3E-01
ENSMUST00000168923				4.2	1.0E-03	4.7	5.3E-02	-0.8	7.4E-01	0.6	6.8E-01
ENSMUST00000131791				4.2	1.5E-04	5.6	2.9E-03	-0.7	6.5E-01	0.8	3.5E-01
ENSMUST00000130167				4.2	1.9E-05	-6.7	6.7E-05	1.4	1.2E-03	-0.1	9.6E-01
ENSMUST00000178839	upstream binding transcription factor, RNA polymerase I [Source:MGI Symbol;Acc:MGI:98512]	A2AWT6		1.2	3.5E-01	1.4	4.3E-01	0.3	8.0E-01	0.2	9.0E-01
ENSMUST00000178840				-1.8	1.5E-01	-1.9	2.3E-01	0.4	7.0E-01	0.5	7.2E-01
ENSMUST00000100716				4.2	5.9E-04	7.7	3.3E-05	-0.5	6.5E-01	-0.7	2.1E-01
ENSMUST00000140612				4.2	7.4E-05	7.3	5.0E-05	0.5	6.1E-01	-0.5	4.0E-01
ENSMUST00000130742				4.2	2.7E-03	6.3	2.7E-04	-0.6	6.2E-01	-0.3	6.6E-01
ENSMUST00000133854				4.2	1.5E-04	5.2	1.2E-02	-1.8	3.2E-01	-0.5	6.5E-01
ENSMUST00000135697				4.2	1.2E-02	-3.0	8.4E-02	0.3	7.3E-01	0.6	7.0E-01
ENSMUST00000126888				4.2	5.7E-03	6.5	5.6E-04	0.1	9.7E-01	-1.3	9.9E-02
ENSMUST00000038450				4.2	6.7E-05	1.6	5.4E-01	6.8	5.4E-03	1.4	4.8E-01
ENSMUST00000122315				4.2	8.5E-03	2.7	7.3E-02	1.1	3.6E-01	0.7	4.9E-01
ENSMUST00000178884	RAS guanyl releasing protein 1 [Source:MGI Symbol;Acc:MGI:1314635]		Q9Z1S3	-1.1	4.3E-01	-4.3	1.2E-01	-0.9	4.5E-01	2.3	3.7E-01
ENSMUST00000135382				4.2	8.9E-03	4.4	2.3E-03	-1.3	2.5E-01	-1.0	1.7E-01
ENSMUST00000151505				4.2	3.2E-03	-2.6	3.6E-01	2.2	1.8E-01	0.5	8.6E-01
ENSMUST00000136817				4.2	4.7E-05	4.2	4.4E-04	0.7	3.4E-01	0.5	3.6E-01
ENSMUST00000178899				1.9	2.4E-01	6.2	2.3E-03	-0.2	9.1E-01	-4.5	3.8E-03
ENSMUST00000117614				4.2	1.6E-03	4.7	1.0E-03	-1.1	3.1E-01	-0.2	7.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000178905				2.0	3.1E-01	1.4	5.3E-01	-1.3	5.0E-01	-0.7	7.3E-01
ENSMUST00000178908	abl-interactor 1 [Source:MGI Symbol;Acc:MGI:104913]	J3QNK8		1.2	6.4E-01	-3.1	2.3E-01	-3.8	7.4E-02	0.4	8.8E-01
ENSMUST00000169413				4.2	2.7E-02	7.2	7.6E-03	-0.8	7.4E-01	-1.9	1.5E-01
ENSMUST00000155660				4.2	8.8E-06	6.5	1.9E-03	-0.7	6.6E-01	-0.7	4.3E-01
ENSMUST00000149093				4.2	1.7E-03	-4.8	3.8E-02	-0.1	9.0E-01	1.0	6.5E-01
ENSMUST00000132062				4.2	3.2E-03	3.3	2.7E-02	-2.3	1.4E-01	0.2	8.4E-01
ENSMUST00000154590				4.2	2.1E-02	4.9	1.2E-04	0.3	6.8E-01	0.4	5.1E-01
ENSMUST00000135002				4.2	1.1E-03	2.7	1.4E-01	-2.1	2.4E-01	1.1	3.9E-01
ENSMUST00000135944				4.2	1.3E-04	4.0	6.3E-03	0.0	1.0E+00	-1.1	2.2E-01
ENSMUST00000145757				4.2	1.3E-03	2.6	2.9E-01	-0.8	7.0E-01	4.5	3.4E-02
ENSMUST00000146090				4.2	4.7E-03	7.0	2.6E-04	-0.6	6.5E-01	-1.1	1.3E-01
ENSMUST00000121190				4.2	1.5E-02	6.1	1.9E-04	-0.6	5.9E-01	-0.2	7.2E-01
ENSMUST00000193696				4.2	3.7E-04	5.5	1.0E-03	-0.6	6.4E-01	0.9	2.0E-01
ENSMUST00000127031				4.2	7.1E-04	10.9	5.2E-06	-0.8	5.5E-01	0.6	2.0E-01
ENSMUST00000178969	mitogen-activated protein kinase 8 interacting protein 3 [Source:MGI Symbol;Acc:MGI:1353598]	J3QNR6		0.4	9.0E-01	1.9	4.9E-01	-2.2	3.8E-01	-3.7	1.9E-01
ENSMUST00000149211				4.2	7.7E-04	6.1	6.6E-04	-1.0	4.3E-01	-0.8	2.5E-01
ENSMUST00000159708				4.2	1.2E-03	-1.9	4.6E-02	0.0	9.3E-01	-3.0	1.9E-02
ENSMUST00000162709				4.2	2.9E-03	2.1	1.1E-02	-0.1	9.0E-01	-0.3	5.4E-01
ENSMUST00000135506				4.2	1.6E-04	-2.9	1.4E-01	0.4	6.9E-01	-0.9	6.3E-01
ENSMUST00000186976				4.2	1.8E-04	6.1	2.9E-03	-0.6	7.1E-01	1.0	2.5E-01
ENSMUST00000178993				-5.6	1.6E-01	-7.8	1.2E-01	-2.7	1.7E-01	-0.4	9.4E-01
ENSMUST00000178995	predicted gene, 21092 [Source:MGI Symbol;Acc:MGI:5434447]	J3QMZ6		0.2	8.0E-01	0.3	7.2E-01	0.5	4.1E-01	0.4	6.2E-01
ENSMUST00000178997	TPX2, microtubule-associated protein homolog (Xenopus laevis) [Source:MGI Symbol;Acc:MGI:1919369]		A2APB8	0.6	5.0E-01	4.8	5.7E-03	2.5	7.1E-02	-1.7	8.9E-02
ENSMUST00000123659				4.2	2.0E-04	3.5	6.3E-02	-1.9	2.7E-01	0.6	6.4E-01
ENSMUST00000179000	glycolipid transfer protein domain containing 2 [Source:MGI Symbol;Acc:MGI:2444527]	Q8K1B3		3.5	4.4E-02	4.6	1.8E-02	-0.5	7.6E-01	-1.6	2.0E-01
ENSMUST00000154087				4.2	8.4E-05	-3.5	1.6E-02	0.3	6.3E-01	-4.1	2.1E-02
ENSMUST00000179002	unc-79 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:2684729]	E5CYJ9		3.1	1.8E-01	4.6	8.1E-02	-0.4	8.7E-01	-1.8	2.9E-01
ENSMUST00000128578				4.2	1.0E-02	6.1	1.3E-03	-3.9	6.1E-02	-0.3	6.9E-01
ENSMUST00000131266				4.2	9.6E-03	-1.4	2.8E-01	0.5	5.0E-01	-2.4	1.3E-01
ENSMUST00000149746				4.2	1.2E-04	5.7	5.0E-04	-0.5	6.8E-01	-0.6	3.6E-01
ENSMUST00000170278				4.2	6.8E-03	-6.8	2.0E-04	0.9	6.5E-02	-0.1	9.3E-01
ENSMUST00000182881				4.2	3.9E-05	7.5	1.8E-04	-0.5	7.2E-01	0.0	9.7E-01
ENSMUST00000122856				4.1	4.3E-04	3.9	1.3E-01	-0.6	8.2E-01	1.5	3.4E-01
ENSMUST00000133466				4.1	5.4E-05	5.9	2.2E-04	-0.6	5.6E-01	0.8	2.3E-01
ENSMUST00000191799				4.1	1.4E-04	7.0	8.4E-05	1.7	1.1E-01	-0.6	3.3E-01
ENSMUST00000182170				4.1	2.3E-03	4.2	3.4E-02	-2.3	2.2E-01	-1.5	3.0E-01
ENSMUST00000179054	RIKEN cDNA E030030I06 gene [Source:MGI Symbol;Acc:MGI:2442914]	J3QML9		6.7	6.6E-02	7.9	3.9E-02	-1.3	7.4E-01	-2.5	2.0E-01
ENSMUST00000146971				4.1	3.9E-04	7.8	4.1E-05	-0.5	7.0E-01	-0.3	5.9E-01
ENSMUST00000128834				4.1	5.7E-03	1.7	8.2E-02	-1.3	1.4E-01	-0.3	6.9E-01
ENSMUST00000179078	Rieske (Fe-S) domain containing [Source:MGI Symbol;Acc:MGI:2145198]		Q8K2P6	-1.0	1.5E-01	-1.6	7.8E-02	-0.2	7.2E-01	0.4	6.1E-01
ENSMUST00000161196				4.1	2.3E-04	5.1	1.1E-03	-0.6	6.1E-01	0.9	1.8E-01
ENSMUST00000132942				4.1	3.5E-03	-8.0	2.5E-03	1.0	9.3E-02	2.2	2.8E-01
ENSMUST00000179097	m large conductance calcium-activated channel, subfamily M, alpha member 1 [Source:MGI Symbol;Acc:MGI	J3QN27		3.2	3.6E-01	5.3	1.6E-01	-0.3	9.3E-01	-2.4	3.1E-01
ENSMUST00000150738				4.1	9.9E-03	7.6	1.4E-02	0.9	7.2E-01	-1.3	4.3E-01
ENSMUST00000179114	rabaptin, RAB GTPase binding effector protein 1 [Source:MGI Symbol;Acc:MGI:1860236]	Q3U983		-0.2	7.7E-01	3.1	6.4E-03	1.8	3.9E-02	-1.5	6.9E-02
ENSMUST00000153762				4.1	1.0E-03	5.4	9.0E-04	-1.5	2.5E-01	-0.4	5.3E-01
ENSMUST00000141867				4.1	6.2E-04	-4.8	6.8E-04	0.2	7.0E-01	-0.8	4.5E-01
ENSMUST00000117585				4.1	5.6E-03	2.6	1.9E-02	-0.3	7.1E-01	0.6	4.4E-01
ENSMUST00000155829				4.1	1.1E-05	-6.2	1.4E-03	1.3	2.0E-02	0.2	8.8E-01
ENSMUST00000179139	peptidyl-tRNA hydrolase domain containing 1 [Source:MGI Symbol;Acc:MGI:1916959]		D3Z4S3	-0.3	5.6E-01	-0.1	8.9E-01	-0.5	2.6E-01	-0.7	2.3E-01
ENSMUST00000176456				4.1	4.8E-05	-1.5	1.6E-01	0.3	6.2E-01	-1.8	1.1E-01
ENSMUST00000139373				4.1	1.9E-03	6.1	3.1E-04	0.0	9.8E-01	-0.5	3.6E-01
ENSMUST00000153290				4.1	5.8E-03	-2.0	1.8E-01	-3.1	2.3E-02	3.7	1.8E-02
ENSMUST00000179172	ornithine decarboxylase antizyme 1 [Source:MGI Symbol;Acc:MGI:109433]	J3QM96		-3.3	3.3E-01	-6.7	1.2E-01	-3.5	8.1E-02	0.0	1.0E+00
ENSMUST00000179175	predicted gene 13247 [Source:MGI Symbol;Acc:MGI:3700965]	A2A8V7		4.0	8.7E-02	4.0	1.2E-01	-0.7	7.9E-01	-0.7	6.7E-01
ENSMUST00000179189	RNA binding motif protein 4 [Source:MGI Symbol;Acc:MGI:1100865]	J3QPA9		-1.9	2.1E-01	-1.2	5.0E-01	0.2	8.9E-01	-0.5	7.9E-01
ENSMUST00000179191	limb region 1 [Source:MGI Symbol;Acc:MGI:1861746]	J3QM78		1.8	4.9E-01	2.9	2.8E-01	-1.6	5.3E-01	-2.7	2.3E-01
ENSMUST00000132152				4.1	1.2E-03	6.1	1.9E-04	-0.6	5.9E-01	-0.2	7.2E-01
ENSMUST00000124906				4.1	2.9E-03	5.9	4.0E-04	-0.6	6.0E-01	0.8	2.1E-01
ENSMUST00000144330				4.1	5.2E-04	6.2	7.9E-02	-0.6	8.6E-01	1.5	4.0E-01
ENSMUST00000145421				4.1	3.1E-03	-1.1	3.7E-01	0.5	5.5E-01	-1.0	3.9E-01
ENSMUST00000149912				4.1	1.3E-02	-5.6	2.8E-03	-0.6	3.0E-01	0.3	8.3E-01
ENSMUST00000179224	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]	J3QNH2		0.9	6.6E-01	2.3	4.3E-01	1.9	3.7E-01	0.5	8.6E-01
ENSMUST00000179226	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein [Source:MGI Symbol;Acc:MGI:1915268]		Q9EQG9	1.9	3.9E-01	5.3	7.9E-02	2.9	2.1E-01	-0.4	8.5E-01
ENSMUST00000154003				4.1	4.6E-03	6.5	1.1E-03	0.1	9.2E-01	-0.2	8.3E-01
ENSMUST00000095717				4.1	1.5E-02	-3.8	1.6E-01	1.7	2.2E-01	-0.3	9.1E-01
ENSMUST00000179243	retinaldehyde binding protein 1 [Source:MGI Symbol;Acc:MGI:97930]	Q544Y3	Q9Z275	2.5	5.2E-02	6.6	1.1E-04	-1.5	2.1E-01	-5.5	1.0E-04
ENSMUST00000135746				4.1	1.6E-03	8.3	2.1E-04	-0.5	7.5E-01	-1.4	6.9E-02
ENSMUST00000124114				4.1	3.5E-03	8.5	6.1E-04	-0.3	8.8E-01	-1.5	8.0E-02
ENSMUST00000143980				4.1	1.2E-03	12.7	5.0E-06	0.1	9.3E-01	-0.8	8.4E-02
ENSMUST00000179265	HECT domain containing 1 [Source:MGI Symbol;Acc:MGI:2384768]		Q69ZR2	3.0	2.5E-01	3.0	3.4E-01	-1.3	6.4E-01	-1.4	5.5E-01
ENSMUST00000163040				4.1	2.2E-03	5.0	7.1E-04	-0.8	4.3E-01	-1.1	1.2E-01
ENSMUST00000146032				4.1	1.1E-02	16.2	1.5E-07	1.6	1.6E-01	-0.6	3.2E-02
ENSMUST00000192180				4.1	8.6E-03	-5.8	9.0E-04	1.2	2.3E-02	-0.3	8.2E-01
ENSMUST00000132960				4.1	3.6E-04	5.9	2.9E-06	-0.8	1.6E-01	0.5	1.8E-01
ENSMUST00000179290	zinc finger protein 691 [Source:MGI Symbol;Acc:MGI:3041163]	A2A7P4		-2.9	2.0E-01	4.9	7.3E-02	3.0	2.2E-01	-4.9	3.8E-02
ENSMUST00000135943				4.1	2.5E-05	5.6	1.2E-03	0.3	8.2E-01	1.0	1.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000147403				4.1	9.5E-03	2.6	1.9E-02	-0.3	7.1E-01	0.6	4.4E-01
ENSMUST00000192284				4.1	2.5E-03	6.3	6.2E-04	-0.6	6.5E-01	-1.0	1.9E-01
ENSMUST00000195125				4.1	9.8E-04	4.1	9.9E-05	-0.4	4.9E-01	0.1	7.4E-01
ENSMUST00000145836				4.1	2.0E-03	-4.8	1.9E-02	-0.6	4.0E-01	0.8	6.5E-01
ENSMUST00000179305	alin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G [Source:MGI		Q9WUH7	3.6	5.5E-02	3.2	1.0E-01	-1.5	3.9E-01	-1.1	4.9E-01
ENSMUST00000160720				4.1	4.5E-05	5.2	4.0E-05	-0.3	7.2E-01	-0.1	8.3E-01
ENSMUST00000185766				4.1	4.8E-03	9.5	1.1E-05	-0.6	6.4E-01	-0.3	4.9E-01
ENSMUST00000182767				4.1	1.8E-03	5.8	9.1E-02	-0.9	8.0E-01	1.0	6.1E-01
ENSMUST00000188843				4.1	3.3E-04	5.4	3.5E-03	-0.4	8.0E-01	-0.7	3.9E-01
ENSMUST00000138336				4.1	4.4E-04	7.2	7.5E-06	-0.3	7.1E-01	0.1	8.0E-01
ENSMUST00000117512				4.1	9.9E-04	-8.1	9.2E-05	0.1	9.0E-01	0.7	6.0E-01
ENSMUST00000192641				4.1	3.7E-03	-4.1	1.3E-02	1.4	4.6E-02	-1.0	5.2E-01
ENSMUST00000145008				4.1	2.1E-04	5.5	4.3E-04	0.1	9.1E-01	0.3	5.9E-01
ENSMUST00000179331	fG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans) [Source:MGI Symbol;Acc:MGI:19197	J3QQ22		1.8	5.6E-01	1.5	7.1E-01	-0.6	8.5E-01	-0.2	9.5E-01
ENSMUST00000185377				4.1	1.7E-03	3.6	2.3E-01	-1.7	5.6E-01	3.1	1.5E-01
ENSMUST00000146327				4.1	7.7E-04	-0.1	9.5E-01	1.9	4.0E-02	-2.2	1.2E-01
ENSMUST00000150729				4.1	1.1E-03	-1.8	2.0E-02	1.2	1.3E-02	0.1	8.6E-01
ENSMUST00000147862				4.1	2.6E-05	9.6	1.9E-06	-1.0	3.1E-01	0.3	4.0E-01
ENSMUST00000128339				4.1	6.4E-04	5.8	2.1E-04	-1.5	1.9E-01	-0.6	3.4E-01
ENSMUST00000110805				4.1	3.2E-03	2.7	2.5E-01	-0.6	7.8E-01	2.0	2.2E-01
ENSMUST00000131396				4.1	4.5E-04	-7.8	7.4E-03	-1.7	5.0E-02	-0.1	9.7E-01
ENSMUST00000182329				4.1	1.5E-02	8.3	1.3E-03	-0.2	9.0E-01	-1.7	8.5E-02
ENSMUST00000108332				4.1	4.9E-03	2.3	2.2E-01	-0.7	6.8E-01	2.7	6.7E-02
ENSMUST00000126156				4.1	6.6E-03	-3.7	1.0E-04	0.0	9.2E-01	-1.6	2.6E-02
ENSMUST00000167656				4.1	5.4E-04	7.5	1.7E-04	-0.7	6.2E-01	0.0	9.5E-01
ENSMUST00000179379	B interacting protein, apical-basolateral polarity regulator, spe-39 homolog [Source:MGI Symbol;Acc:MGI:21		Q8BGQ1	-0.5	8.6E-01	6.5	1.3E-01	4.7	2.3E-01	-2.2	3.9E-01
ENSMUST00000117943				4.1	6.0E-04	5.2	2.1E-02	-0.5	7.9E-01	0.5	6.7E-01
ENSMUST00000123546				4.1	1.6E-03	5.3	2.5E-04	1.4	1.2E-01	-0.9	1.8E-01
ENSMUST00000138749				4.1	6.2E-05	2.5	5.4E-03	0.5	3.7E-01	0.2	7.4E-01
ENSMUST00000177011				4.1	7.5E-05	6.5	6.3E-04	-0.1	9.5E-01	-1.6	6.0E-02
ENSMUST00000179402				4.1	8.5E-02	5.5	4.5E-02	-0.3	9.1E-01	-1.7	2.6E-01
ENSMUST00000179404	predicted gene 10256 [Source:MGI Symbol;Acc:MGI:3710530]	B2RWR6		4.6	9.8E-02	4.6	1.1E-01	-0.7	8.1E-01	-0.7	7.0E-01
ENSMUST00000078094				4.1	5.8E-04	3.0	5.7E-03	0.4	6.3E-01	0.3	6.5E-01
ENSMUST00000144500				4.1	2.6E-04	5.8	4.2E-04	-0.5	6.5E-01	-0.2	7.0E-01
ENSMUST00000120793				4.1	1.6E-04	7.1	5.8E-04	0.6	6.6E-01	0.1	8.7E-01
ENSMUST00000140370				4.1	6.6E-04	4.6	1.6E-02	-2.5	1.9E-01	-1.7	2.0E-01
ENSMUST00000127660				4.1	4.2E-04	0.5	6.7E-01	-0.2	8.0E-01	1.8	1.2E-01
ENSMUST00000149017				4.1	9.5E-05	-7.0	5.4E-03	-0.9	1.9E-01	-0.1	9.5E-01
ENSMUST00000162145				4.1	1.0E-04	8.3	4.1E-03	-0.9	7.1E-01	0.5	6.8E-01
ENSMUST00000128516				4.1	2.6E-03	-4.8	2.3E-02	1.5	1.1E-01	-0.2	9.3E-01
ENSMUST00000138495				4.1	1.1E-04	6.0	2.3E-04	-0.3	8.0E-01	-0.4	5.4E-01
ENSMUST00000132339				4.1	6.3E-04	9.5	1.4E-04	0.0	9.9E-01	1.5	5.2E-02
ENSMUST00000179466	predicted gene 2964 [Source:MGI Symbol;Acc:MGI:3781142]	J3QMW9		2.8	3.4E-01	4.5	1.5E-01	-0.4	9.0E-01	-2.1	3.2E-01
ENSMUST00000194362				4.1	1.5E-03	8.0	1.1E-04	1.7	2.0E-01	-0.4	4.5E-01
ENSMUST00000179474	family with sequence similarity 160, member A2 [Source:MGI Symbol;Acc:MGI:1921599]	J3QP99		0.2	7.7E-01	1.3	1.7E-01	1.1	1.5E-01	0.0	9.6E-01
ENSMUST00000135849				4.1	2.0E-04	-5.1	8.4E-03	0.5	4.7E-01	2.1	1.9E-01
ENSMUST00000135880				4.1	1.8E-04	5.6	7.8E-04	-0.3	7.8E-01	-0.8	3.0E-01
ENSMUST00000179483	erythroid differentiation regulator 1 [Source:MGI Symbol;Acc:MGI:2384747]	J3QMM0		1.6	2.3E-01	1.9	2.0E-01	-0.1	9.2E-01	-0.5	6.9E-01
ENSMUST00000167456				4.1	3.0E-02	7.9	5.4E-05	-0.5	6.5E-01	-0.5	4.2E-01
ENSMUST00000181354				4.1	2.5E-04	3.2	1.2E-01	-1.5	4.6E-01	1.8	2.0E-01
ENSMUST00000179489	elongation factor Tu GTP binding domain containing 1 [Source:MGI Symbol;Acc:MGI:2141969]		Q8C0D5	-2.2	3.1E-01	2.5	3.5E-01	2.2	3.4E-01	-2.5	2.7E-01
ENSMUST00000179503	RIKEN cDNA 1600014C10 gene [Source:MGI Symbol;Acc:MGI:1919494]			-2.1	2.1E-01	-1.5	5.8E-01	0.8	6.0E-01	0.1	9.5E-01
ENSMUST00000179505	phosphatidylserine decarboxylase [Source:HGNC Symbol;Acc:HGNC:8999]			-0.2	8.1E-01	1.2	2.8E-01	0.1	8.7E-01	-1.3	2.1E-01
ENSMUST00000179506	spermatogenesis associated glutamate (E)-rich protein 4C [Source:MGI Symbol;Acc:MGI:1914023]	J3QMF9		6.3	3.9E-02	3.5	2.9E-01	-0.6	8.4E-01	2.2	3.3E-01
ENSMUST00000186522				4.1	1.8E-02	-0.7	4.2E-01	0.4	4.4E-01	-1.8	6.3E-02
ENSMUST00000101051				4.1	3.5E-02	7.9	3.7E-05	-0.6	5.7E-01	-1.2	5.9E-02
ENSMUST00000153124				4.1	6.3E-04	-7.6	1.7E-03	1.2	6.3E-02	0.1	9.8E-01
ENSMUST00000179531	arginyl aminopeptidase (aminopeptidase B)-like 1 [Source:MGI Symbol;Acc:MGI:1914170]	J3QNU3		1.4	7.5E-02	3.1	7.8E-03	0.9	2.5E-01	-0.7	3.4E-01
ENSMUST00000179543	nucleolar complex associated 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1931051]	J3QK52		-2.7	7.4E-02	-4.6	3.9E-02	-0.2	8.4E-01	1.7	4.1E-01
ENSMUST00000179549	coiled-coil domain containing 85B [Source:MGI Symbol;Acc:MGI:2147607]		Q6PDY0	-0.7	3.2E-01	-0.1	8.7E-01	-0.7	3.2E-01	-1.3	1.2E-01
ENSMUST00000134890				4.1	2.2E-04	-5.3	8.7E-03	-1.8	3.0E-02	0.6	7.2E-01
ENSMUST00000149437				4.1	2.2E-03	-10.4	1.8E-04	-0.4	3.8E-01	1.7	3.5E-01
ENSMUST00000179556	zinc finger protein 574 [Source:MGI Symbol;Acc:MGI:2442951]		Q8BY46	-0.6	6.5E-01	-1.8	4.5E-01	1.9	3.0E-01	3.1	1.4E-01
ENSMUST00000179563	FCH domain only 2 [Source:MGI Symbol;Acc:MGI:3505790]	J3QPQ1		1.7	4.0E-01	2.9	3.2E-01	1.9	3.5E-01	0.7	7.7E-01
ENSMUST00000168363				4.1	5.8E-04	-8.2	3.0E-06	-0.6	6.2E-02	-2.1	6.7E-02
ENSMUST00000145457				4.1	1.1E-04	6.5	9.0E-04	0.4	7.5E-01	-0.6	3.8E-01
ENSMUST00000176078				4.1	2.3E-02	5.9	1.0E-04	-0.2	8.6E-01	0.1	8.5E-01
ENSMUST00000117871				4.0	7.0E-03	-6.0	5.8E-03	2.1	5.9E-03	-0.8	6.7E-01
ENSMUST00000179592	fibroblast growth factor receptor 1 [Source:MGI Symbol;Acc:MGI:95522]	J3QN85		6.1	5.1E-02	3.3	3.1E-01	-0.8	8.1E-01	2.0	3.6E-01
ENSMUST00000179593				-1.3	2.8E-01	-1.5	3.6E-01	0.0	9.7E-01	0.2	9.0E-01
ENSMUST00000179598	predicted gene, 38394 [Source:MGI Symbol;Acc:MGI:5614057]	G0LE24	D2EAC2	0.0	9.4E-01	0.2	8.1E-01	0.9	1.0E-01	0.8	2.6E-01
ENSMUST00000172583				4.0	2.5E-03	-3.4	9.8E-03	0.2	7.4E-01	0.7	5.2E-01
ENSMUST00000145307				4.0	2.0E-04	7.9	3.6E-03	-0.9	6.8E-01	0.8	4.7E-01
ENSMUST00000122826				4.0	1.1E-04	5.4	8.1E-04	-0.5	6.5E-01	0.8	2.1E-01
ENSMUST00000130164				4.0	2.0E-02	3.3	2.2E-01	0.3	8.8E-01	1.6	4.0E-01
ENSMUST00000128752				4.0	2.0E-03	-4.3	1.1E-02	1.7	3.7E-02	-2.4	1.7E-01
ENSMUST00000154628				4.0	2.3E-03	5.3	1.0E-03	0.2	8.2E-01	-0.7	3.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000141248				4.0	2.2E-02	4.9	1.1E-01	-1.4	6.5E-01	0.8	6.8E-01
ENSMUST00000185449				4.0	2.9E-04	6.4	5.2E-05	-0.7	4.6E-01	-0.7	2.0E-01
ENSMUST00000134247				4.0	2.3E-04	4.0	5.6E-03	-2.2	1.0E-01	0.5	5.0E-01
ENSMUST00000145787				4.0	4.2E-04	2.1	1.9E-01	0.3	7.9E-01	0.9	4.6E-01
ENSMUST00000160986				4.0	4.9E-04	3.3	4.7E-02	-0.6	6.5E-01	1.7	1.5E-01
ENSMUST00000192159				4.0	1.1E-02	4.3	5.8E-04	-0.4	6.0E-01	0.8	1.7E-01
ENSMUST00000129600				4.0	2.1E-02	5.0	2.7E-02	0.7	7.1E-01	1.2	3.1E-01
ENSMUST00000156684				4.0	1.4E-04	-3.3	6.5E-02	1.6	7.5E-02	-1.2	5.2E-01
ENSMUST00000179718				0.0	9.7E-01	1.8	2.9E-01	0.2	8.9E-01	-1.5	3.4E-01
ENSMUST00000170626				4.0	9.8E-03	3.2	1.2E-03	-1.2	1.0E-01	-0.8	1.6E-01
ENSMUST00000123717				4.0	6.1E-05	3.5	5.3E-04	-0.2	7.1E-01	-0.3	5.6E-01
ENSMUST00000143996				4.0	3.1E-03	11.2	1.4E-06	1.1	2.8E-01	-0.2	5.1E-01
ENSMUST00000177030				4.0	7.9E-04	3.5	6.0E-04	0.0	9.6E-01	-0.1	9.1E-01
ENSMUST00000188913				4.0	4.3E-04	7.2	6.6E-04	0.7	6.5E-01	0.5	4.9E-01
ENSMUST00000179734	predicted gene 2163 [Source:MGI Symbol;Acc:MGI:3780332]	Q6PCY5		1.6	4.3E-01	7.7	2.8E-02	2.9	3.4E-01	-3.2	7.7E-02
ENSMUST00000194832				4.0	7.1E-04	8.8	1.2E-05	-0.6	5.9E-01	-0.9	8.2E-02
ENSMUST00000134594				4.0	5.3E-05	3.7	1.1E-01	-0.6	7.9E-01	2.7	7.5E-02
ENSMUST00000133481				4.0	1.1E-04	-5.5	2.0E-04	-1.3	7.1E-03	-0.9	4.1E-01
ENSMUST00000179755	arrestin, beta 1 [Source:MGI Symbol;Acc:MGI:99473]	J3QNU6		-0.6	4.7E-01	2.2	1.0E-01	2.7	2.9E-02	-0.1	8.8E-01
ENSMUST00000150854				4.0	1.4E-04	-5.2	2.0E-03	-0.6	2.8E-01	-1.0	4.9E-01
ENSMUST00000137328				4.0	2.3E-04	5.4	1.9E-03	0.9	4.8E-01	-0.4	6.5E-01
ENSMUST00000131943				4.0	2.5E-04	-5.0	8.2E-04	0.1	8.1E-01	-1.9	1.2E-01
ENSMUST00000176093				4.0	1.4E-04	4.7	1.4E-01	-0.6	8.4E-01	1.3	5.1E-01
ENSMUST00000161191				4.0	1.3E-02	7.4	2.5E-04	-0.7	6.3E-01	0.2	7.3E-01
ENSMUST00000152732				4.0	1.5E-02	7.7	2.3E-04	-0.7	6.1E-01	-1.3	1.2E-01
ENSMUST00000179770	eukaryotic translation initiation factor 4E nuclear import factor 1 [Source:MGI Symbol;Acc:MGI:1921453]		Q9EST3	2.1	3.5E-01	3.8	1.7E-01	0.7	7.6E-01	-1.1	6.4E-01
ENSMUST00000174507				4.0	2.3E-04	5.4	2.0E-03	-2.9	5.7E-02	-3.7	4.4E-03
ENSMUST00000119494				4.0	5.2E-04	-8.1	1.3E-03	0.1	7.8E-01	1.4	4.5E-01
ENSMUST00000156463				4.0	9.3E-03	-3.5	1.1E-02	-7.8	1.9E-05	4.3	2.9E-03
ENSMUST00000153980				4.0	4.5E-04	6.1	1.3E-04	-0.2	8.5E-01	0.2	7.4E-01
ENSMUST00000125031				4.0	6.2E-05	-0.7	2.3E-01	-0.4	4.5E-01	-1.2	6.7E-02
ENSMUST00000118061				4.0	2.5E-04	5.7	5.9E-04	-0.6	6.4E-01	1.0	1.6E-01
ENSMUST00000179801	predicted gene 7694 [Source:MGI Symbol;Acc:MGI:3649135]	J3QNH8		-1.3	5.1E-02	0.6	4.7E-01	1.8	1.5E-02	-0.1	8.7E-01
ENSMUST00000118584				4.0	2.5E-04	3.0	1.2E-03	-0.7	2.5E-01	0.1	8.4E-01
ENSMUST00000179803	predicted gene 3015 [Source:MGI Symbol;Acc:MGI:3781193]	J3QN18		4.4	1.1E-01	5.3	8.4E-02	-0.2	9.4E-01	-1.2	4.9E-01
ENSMUST00000128856				4.0	1.2E-02	4.2	6.2E-03	-0.5	6.8E-01	0.9	3.1E-01
ENSMUST00000149257				4.0	1.4E-04	6.5	1.5E-04	-0.5	6.4E-01	0.1	8.7E-01
ENSMUST00000183411				4.0	1.2E-02	-0.2	9.0E-01	-4.7	2.3E-02	2.1	1.7E-01
ENSMUST00000132008				4.0	3.3E-03	6.8	1.7E-04	-0.5	6.9E-01	-0.7	2.9E-01
ENSMUST00000179837	arginyl aminopeptidase (aminopeptidase B)-like 1 [Source:MGI Symbol;Acc:MGI:1914170]	J3QNA8		-0.7	4.5E-01	0.5	7.1E-01	1.6	1.1E-01	0.5	7.0E-01
ENSMUST00000128582				4.0	5.3E-05	12.4	1.2E-05	0.1	9.7E-01	-1.0	5.7E-02
ENSMUST00000149788				4.0	2.8E-04	4.6	7.8E-05	-1.1	1.2E-01	-0.6	2.1E-01
ENSMUST00000186192				4.0	5.2E-04	8.2	8.0E-05	-0.7	5.9E-01	0.1	8.2E-01
ENSMUST00000179852	TBC1 domain family, member 7 [Source:MGI Symbol;Acc:MGI:1914296]		Q9D0K0	-0.3	8.6E-01	0.6	7.3E-01	-0.4	7.6E-01	-1.3	4.4E-01
ENSMUST00000179854				0.1	8.8E-01	0.3	7.2E-01	0.3	7.1E-01	0.0	9.8E-01
ENSMUST00000162799				4.0	3.1E-03	-0.8	1.4E-01	0.0	9.8E-01	-0.3	6.4E-01
ENSMUST00000192467				4.0	5.7E-04	-1.4	1.4E-01	1.1	1.0E-01	-0.4	6.2E-01
ENSMUST00000179865	calnexin [Source:MGI Symbol;Acc:MGI:88261]	Q5SUC3	P35564	0.3	7.1E-01	0.9	4.0E-01	0.2	8.0E-01	-0.4	7.0E-01
ENSMUST00000129123				4.0	8.4E-05	-2.1	3.7E-03	0.3	3.2E-01	0.3	6.2E-01
ENSMUST00000131382				4.0	2.7E-02	8.4	1.9E-05	-0.5	6.7E-01	-0.4	4.0E-01
ENSMUST00000134854				4.0	1.4E-02	14.5	2.3E-07	-0.5	6.5E-01	-0.7	4.7E-02
ENSMUST00000179886	nucleolar complex associated 2 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1931051]	Q8BHX6		-2.7	2.9E-01	4.8	1.8E-01	4.9	1.4E-01	-2.5	3.2E-01
ENSMUST00000149430				4.0	1.4E-03	2.0	2.3E-01	-0.4	7.8E-01	3.2	2.5E-02
ENSMUST00000170209				4.0	2.1E-02	-6.0	1.4E-03	-1.0	9.6E-02	-0.8	5.9E-01
ENSMUST00000172915				4.0	8.0E-03	4.8	5.8E-04	0.3	7.2E-01	0.1	9.0E-01
ENSMUST00000179894				1.2	3.0E-01	0.6	7.2E-01	-0.2	8.8E-01	0.5	7.1E-01
ENSMUST00000184196				4.0	5.6E-04	10.6	4.4E-05	-0.3	8.5E-01	-0.6	2.9E-01
ENSMUST00000138345				4.0	5.7E-05	6.5	1.6E-04	-0.5	6.6E-01	-0.8	2.1E-01
ENSMUST00000125490				4.0	3.1E-03	5.1	8.1E-06	-0.8	1.7E-01	-0.5	1.8E-01
ENSMUST00000136968				4.0	9.0E-04	1.0	2.3E-01	1.4	4.8E-02	-2.3	1.7E-02
ENSMUST00000147648				4.0	1.2E-02	7.1	2.2E-03	-0.8	6.7E-01	1.2	2.2E-01
ENSMUST00000195203				4.0	7.2E-04	4.0	5.8E-04	0.5	4.5E-01	0.2	7.5E-01
ENSMUST00000179926	MON1 homolog b (yeast) [Source:MGI Symbol;Acc:MGI:1923231]		Q8BMQ8	0.9	1.6E-01	1.8	8.9E-02	2.2	1.7E-02	1.4	1.0E-01
ENSMUST00000193070				4.0	5.2E-03	-5.9	2.4E-03	0.2	7.6E-01	-0.7	6.8E-01
ENSMUST00000137231				4.0	4.0E-04	5.0	2.0E-03	-1.9	1.7E-01	-1.3	1.4E-01
ENSMUST00000179936	epsin 2 [Source:MGI Symbol;Acc:MGI:1333766]	J3QNT7		2.5	5.6E-02	6.8	1.8E-04	-0.5	6.5E-01	-4.8	3.2E-04
ENSMUST00000179937	tumor necrosis factor, alpha-induced protein 8 [Source:MGI Symbol;Acc:MGI:2147191]		Q921Z5	-0.6	3.3E-01	0.5	5.5E-01	0.6	3.1E-01	-0.5	5.3E-01
ENSMUST00000147931				4.0	1.4E-04	1.5	6.3E-01	-0.4	8.6E-01	4.1	1.4E-01
ENSMUST00000153446				4.0	2.4E-05	7.5	1.1E-02	-0.9	7.4E-01	-2.8	9.4E-02
ENSMUST00000179943	SH3-domain binding protein 2 [Source:MGI Symbol;Acc:MGI:1346349]	Q5U3L0		2.7	3.5E-01	2.8	3.5E-01	-2.1	4.6E-01	-2.2	3.9E-01
ENSMUST00000186897				4.0	1.1E-04	6.5	1.8E-04	-0.6	6.1E-01	-0.2	7.3E-01
ENSMUST00000187475				4.0	1.0E-03	6.7	4.6E-03	-0.4	8.2E-01	-0.7	5.1E-01
ENSMUST00000132778				4.0	3.1E-05	2.9	3.5E-01	-0.8	7.6E-01	2.4	3.1E-01
ENSMUST00000179954	ribosomal protein L31 [Source:MGI Symbol;Acc:MGI:2149632]	Q5M9K9	P62900	0.6	3.3E-01	-1.5	9.7E-02	-1.4	3.6E-02	0.7	3.7E-01
ENSMUST00000161199				4.0	3.5E-03	7.2	6.0E-04	-0.4	8.1E-01	-1.3	1.3E-01
ENSMUST00000179976	SH2 domain containing 1B1 [Source:MGI Symbol;Acc:MGI:1349420]	Q149T1		-0.6	3.4E-01	-0.3	7.0E-01	-0.1	8.2E-01	-0.4	5.6E-01
ENSMUST00000182925				4.0	1.3E-02	1.9	2.9E-02	0.6	3.2E-01	0.5	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000097152				4.0	2.5E-03	15.2	2.0E-07	0.1	9.6E-01	-0.3	3.9E-01
ENSMUST00000193991				3.9	4.0E-04	8.0	8.5E-05	-0.6	6.4E-01	-1.5	4.7E-02
ENSMUST00000179989	neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4 [Source:MGI Symbc	Q8C3J2		-0.3	8.7E-01	2.1	4.1E-01	2.7	2.1E-01	0.3	8.6E-01
ENSMUST00000136077				3.9	2.6E-02	-7.1	1.6E-03	-1.9	1.1E-02	0.1	9.7E-01
ENSMUST00000179992	RIKEN cDNA 1600014C10 gene [Source:MGI Symbol;Acc:MGI:1919494]			0.3	7.1E-01	0.8	4.6E-01	-0.2	7.8E-01	-0.7	4.7E-01
ENSMUST00000179993	arginyl aminopeptidase (aminopeptidase B)-like 1 [Source:MGI Symbol;Acc:MGI:1914170]	J3QQ46		-0.1	9.0E-01	1.1	3.3E-01	0.7	4.2E-01	-0.5	6.2E-01
ENSMUST00000182989				3.9	3.1E-02	4.1	1.3E-04	-0.1	9.0E-01	-0.5	3.0E-01
ENSMUST00000151864				3.9	7.9E-04	2.0	2.0E-01	-3.3	8.8E-02	1.6	2.1E-01
ENSMUST00000180015	adenylosuccinate synthetase like 1 [Source:MGI Symbol;Acc:MGI:87947]	J3QN31		-1.4	3.1E-01	-2.7	7.3E-02	-2.4	2.9E-02	-1.1	4.9E-01
ENSMUST00000180020	heterogeneous nuclear ribonucleoprotein F [Source:MGI Symbol;Acc:MGI:2138741]		Q9Z2X1	-1.8	4.7E-01	3.0	2.9E-01	3.1	2.4E-01	-1.6	4.7E-01
ENSMUST00000180022				4.8	8.9E-02	4.3	1.6E-01	-0.5	8.8E-01	0.0	9.9E-01
ENSMUST00000137039				3.9	7.0E-03	2.8	7.7E-02	-0.6	6.1E-01	5.0	1.1E-03
ENSMUST00000180025	basic helix-loop-helix domain containing, class B9 [Source:MGI Symbol;Acc:MGI:1917487]		Q6PB60	1.3	1.1E-01	-0.2	8.7E-01	0.2	7.8E-01	1.7	1.3E-01
ENSMUST00000071237				3.9	2.8E-02	3.7	2.3E-02	-0.3	8.3E-01	0.5	6.4E-01
ENSMUST00000130617				3.9	1.7E-02	4.8	3.9E-04	0.8	3.4E-01	-0.3	5.4E-01
ENSMUST00000135101				3.9	1.2E-03	-7.5	1.3E-03	1.4	4.7E-02	-2.0	3.6E-01
ENSMUST00000180037	baculoviral IAP repeat-containing 6 [Source:MGI Symbol;Acc:MGI:1276108]		O88738	3.9	9.5E-02	4.7	1.1E-01	-0.5	8.5E-01	-1.3	4.9E-01
ENSMUST00000180041	START domain containing 9 [Source:MGI Symbol;Acc:MGI:3045258]		Q80TF6	-1.7	2.5E-01	10.2	1.7E-03	6.8	1.2E-02	-5.1	3.9E-03
ENSMUST00000180043	decapping exoribonuclease [Source:MGI Symbol;Acc:MGI:1890444]			0.0	9.9E-01	1.5	5.8E-01	-1.8	4.6E-01	-3.4	2.2E-01
ENSMUST00000180046	ubiquitin specific peptidase 34 [Source:MGI Symbol;Acc:MGI:109473]		Q6ZQ93	4.4	7.4E-02	3.5	2.8E-01	1.8	4.9E-01	2.7	2.7E-01
ENSMUST00000122896				3.9	6.9E-03	3.6	1.7E-01	0.2	9.5E-01	3.1	5.9E-02
ENSMUST00000127662				3.9	2.8E-03	-8.3	1.8E-05	-0.4	1.9E-01	-0.8	4.6E-01
ENSMUST00000135049				3.9	1.3E-04	-4.5	9.1E-03	-1.1	1.3E-01	-0.3	8.3E-01
ENSMUST00000138620				3.9	1.6E-02	6.7	1.7E-04	-0.6	6.1E-01	-0.1	8.6E-01
ENSMUST00000180084				4.4	1.7E-01	4.1	2.3E-01	-0.4	9.0E-01	-0.2	9.4E-01
ENSMUST00000180086	H1 histone family, member 0 [Source:MGI Symbol;Acc:MGI:95893]		P10922	-0.5	5.2E-01	-2.0	7.1E-02	-1.5	4.4E-02	0.0	9.8E-01
ENSMUST00000180088	TBC1 domain family, member 10a [Source:MGI Symbol;Acc:MGI:2144164]		P58802	-1.8	8.1E-02	0.2	8.7E-01	0.5	5.2E-01	-1.5	2.1E-01
ENSMUST00000145329				3.9	8.4E-05	8.0	2.3E-05	3.9	2.3E-03	0.3	4.6E-01
ENSMUST00000147830				3.9	5.6E-04	5.7	5.6E-02	-0.9	7.6E-01	0.0	9.8E-01
ENSMUST00000149651				3.9	3.3E-04	6.6	2.1E-04	-3.1	3.9E-02	-0.2	6.8E-01
ENSMUST00000169235				3.9	6.0E-03	-3.0	5.1E-02	1.0	1.8E-01	-1.5	3.3E-01
ENSMUST00000147682				3.9	2.8E-02	5.3	4.1E-04	-0.5	6.2E-01	-0.1	8.5E-01
ENSMUST00000132434				3.9	5.4E-05	8.1	4.7E-04	0.8	6.1E-01	1.5	6.7E-02
ENSMUST00000180110	ataxin 1 [Source:MGI Symbol;Acc:MGI:104783]	J3QPR1		0.4	8.9E-01	3.9	2.9E-01	1.4	6.8E-01	-2.1	4.7E-01
ENSMUST00000141278				3.9	1.9E-04	6.9	2.5E-02	-0.6	8.3E-01	-1.3	3.9E-01
ENSMUST00000118010				3.9	1.6E-02	2.6	1.9E-02	-0.3	7.1E-01	0.6	4.4E-01
ENSMUST00000191387				3.9	9.1E-05	6.3	1.3E-04	-0.8	4.5E-01	-0.1	8.6E-01
ENSMUST00000180140	host cell factor C1 regulator 1 (XPO1-dependent) [Source:MGI Symbol;Acc:MGI:2663619]		Q9CYQ5	-4.4	5.0E-02	-3.1	2.8E-01	1.1	4.9E-01	-0.3	9.3E-01
ENSMUST00000180142	ATP-binding cassette, sub-family B (MDR/TAP), member 11 [Source:MGI Symbol;Acc:MGI:1351619]	J3QNY6		2.5	1.1E-01	4.8	8.0E-03	-0.6	7.1E-01	-2.9	3.1E-02
ENSMUST00000146800				3.9	2.0E-02	6.7	5.0E-04	-0.4	7.7E-01	-1.4	9.2E-02
ENSMUST00000177066				3.9	2.1E-02	7.1	2.0E-04	-0.5	6.8E-01	-0.3	6.3E-01
ENSMUST00000191338				3.9	5.4E-05	-4.0	2.2E-03	-0.5	3.7E-01	-1.1	3.0E-01
ENSMUST00000147247				3.9	6.8E-04	3.2	1.1E-01	-0.6	7.4E-01	4.3	7.0E-03
ENSMUST00000177541				3.9	3.8E-04	4.9	6.6E-05	-0.7	3.1E-01	-0.7	2.0E-01
ENSMUST00000167073				3.9	3.1E-03	7.1	1.3E-04	-0.5	6.8E-01	-1.1	9.2E-02
ENSMUST00000137992				3.9	1.3E-04	5.9	6.0E-04	0.9	4.5E-01	-0.5	4.9E-01
ENSMUST00000139555				3.9	2.9E-04	7.0	5.1E-04	0.4	7.6E-01	0.9	2.4E-01
ENSMUST00000180180	ECSIT homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1349469]			-1.8	2.1E-01	2.2	3.3E-01	4.2	3.9E-02	0.2	9.0E-01
ENSMUST00000180182	RIKEN cDNA A630033H20 gene [Source:MGI Symbol;Acc:MGI:2441814]	Q8BY68		2.7	1.2E-01	0.3	8.8E-01	0.0	9.8E-01	2.3	1.8E-01
ENSMUST00000159166				3.9	1.3E-04	6.6	6.5E-04	-0.2	8.9E-01	-0.1	8.5E-01
ENSMUST00000132993				3.9	5.9E-04	0.9	3.6E-01	-0.8	3.6E-01	0.9	3.1E-01
ENSMUST00000180200	NLR family, CARD domain containing 3 [Source:MGI Symbol;Acc:MGI:2444070]		Q5DU56	-0.1	9.6E-01	-0.6	7.6E-01	-0.8	6.3E-01	-0.2	9.1E-01
ENSMUST00000180214	zinc finger protein 518B [Source:MGI Symbol;Acc:MGI:2140750]	J3QNT5		4.0	4.3E-02	1.1	6.0E-01	-1.8	3.6E-01	1.1	5.1E-01
ENSMUST00000153709				3.9	9.0E-04	6.5	5.2E-03	-2.8	2.1E-01	-2.5	6.3E-02
ENSMUST00000121179				3.9	9.9E-03	6.2	1.4E-04	-1.1	3.0E-01	-0.9	1.8E-01
ENSMUST00000183228				3.9	1.6E-03	4.8	1.6E-02	-0.7	6.9E-01	2.2	5.8E-02
ENSMUST00000145802				3.9	5.8E-04	-1.5	1.7E-01	0.4	5.1E-01	-0.6	5.6E-01
ENSMUST00000137287				3.9	2.8E-05	5.0	6.6E-03	-1.7	2.9E-01	-0.4	6.6E-01
ENSMUST00000180250	eyes absent 3 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:109339]		P97480	3.6	2.5E-01	5.0	1.4E-01	-0.3	9.4E-01	-1.8	4.0E-01
ENSMUST00000189651				3.9	1.7E-04	10.1	5.4E-04	1.2	5.3E-01	0.7	3.5E-01
ENSMUST00000137256				3.9	8.4E-04	-3.2	2.8E-02	2.1	6.6E-03	-0.9	4.9E-01
ENSMUST00000180283	tight junction associated protein 1 [Source:MGI Symbol;Acc:MGI:1921344]		Q9DCD5	0.7	3.9E-01	1.8	7.5E-02	0.2	8.4E-01	-1.0	2.4E-01
ENSMUST00000189544				3.9	1.5E-02	-2.2	1.5E-01	0.0	9.8E-01	-3.0	1.2E-01
ENSMUST00000120191				3.9	2.2E-02	3.9	7.6E-04	0.4	5.4E-01	0.2	7.3E-01
ENSMUST00000176567				3.9	6.0E-03	8.9	1.1E-04	-0.7	6.5E-01	0.4	4.9E-01
ENSMUST00000148114				3.9	2.6E-05	7.1	1.2E-04	-0.1	9.1E-01	-0.1	8.1E-01
ENSMUST00000140683				3.9	2.5E-02	8.1	6.8E-05	-0.7	6.0E-01	-0.3	5.8E-01
ENSMUST00000180300	proline-rich nuclear receptor coactivator 2 [Source:MGI Symbol;Acc:MGI:106512]	J3QJZ8		-2.8	1.4E-01	-4.7	3.5E-02	-3.5	8.3E-03	-1.6	4.8E-01
ENSMUST00000150326				3.9	3.8E-04	6.6	3.9E-03	-0.9	6.2E-01	0.7	4.9E-01
ENSMUST00000142183				3.9	1.3E-03	2.4	3.0E-03	0.7	1.7E-01	0.0	9.7E-01
ENSMUST00000145898				3.9	2.6E-04	4.8	1.8E-02	-0.7	6.9E-01	1.4	2.3E-01
ENSMUST00000180321	predicted gene 9726 [Source:MGI Symbol;Acc:MGI:3648149]	A6H624	Q9D0E3	-2.3	5.2E-02	-3.6	1.2E-01	1.2	2.4E-01	2.5	2.4E-01
ENSMUST00000120376				3.9	2.1E-03	2.7	7.0E-02	-2.0	1.6E-01	-0.9	4.2E-01
ENSMUST00000143163				3.9	6.0E-04	7.1	2.8E-04	0.0	9.9E-01	-0.5	4.9E-01
ENSMUST00000180339	RIKEN cDNA 4931406C07 gene [Source:MGI Symbol;Acc:MGI:1918234]		Q91V76	3.1	4.5E-02	0.9	3.3E-01	-5.4	8.5E-04	-3.2	1.0E-02
ENSMUST00000147975				3.9	4.3E-04	-3.8	4.5E-04	0.9	4.4E-02	-4.4	1.6E-03
ENSMUST00000118158				3.9	3.2E-04	6.1	1.9E-04	-0.6	5.9E-01	-0.2	7.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000187175				3.9	1.1E-03	8.0	1.9E-04	0.8	5.6E-01	0.8	2.2E-01
ENSMUST00000130539				3.9	6.2E-05	4.4	5.6E-03	0.6	5.8E-01	0.1	9.2E-01
ENSMUST00000180358	polymerase (RNA) III (DNA directed) polypeptide D [Source:MGI Symbol;Acc:MGI:1914315]		Q91WD1	-0.1	9.4E-01	3.4	8.6E-02	1.5	3.9E-01	-2.1	1.6E-01
ENSMUST00000180359	abhydrolase domain containing 4 [Source:MGI Symbol;Acc:MGI:1915938]	Q8C0M2		2.4	5.5E-02	2.4	1.7E-01	1.0	4.8E-01	1.0	4.1E-01
ENSMUST00000180360	EH domain binding protein 1 [Source:MGI Symbol;Acc:MGI:2667252]		Q69ZW3	1.9	1.6E-01	3.9	3.4E-03	-3.0	2.5E-02	-5.0	6.5E-04
ENSMUST00000180362	AS (guanine nucleotide binding protein, alpha stimulating) complex locus [Source:MGI Symbol;Acc:MGI:957		Q9Z0F1	3.5	1.1E-01	2.2	3.1E-01	-0.5	8.1E-01	0.7	6.6E-01
ENSMUST00000136455				3.9	2.4E-03	-3.3	3.1E-02	-0.1	8.7E-01	0.9	5.1E-01
ENSMUST00000180375	methionine aminopeptidase 2 [Source:MGI Symbol;Acc:MGI:1929701]	M0QWM9		-0.1	9.7E-01	-3.1	2.1E-01	-5.4	1.5E-02	-2.5	3.9E-01
ENSMUST00000123386				3.9	2.3E-03	-0.4	4.3E-01	0.7	7.7E-02	-0.1	8.3E-01
ENSMUST00000127468				3.9	1.3E-02	5.4	4.7E-04	-1.1	3.0E-01	-0.4	5.2E-01
ENSMUST00000129177				3.9	2.4E-03	-3.0	2.3E-02	-5.9	1.7E-04	4.0	4.0E-03
ENSMUST00000180392	methionine aminopeptidase 2 [Source:MGI Symbol;Acc:MGI:1929701]	M0QW69		-1.8	1.3E-01	0.2	9.0E-01	0.9	3.9E-01	-1.1	4.4E-01
ENSMUST00000146621				3.9	2.1E-03	6.4	2.5E-03	-0.4	8.1E-01	-2.6	2.2E-02
ENSMUST00000159211				3.9	1.1E-02	3.0	2.2E-02	-0.2	8.6E-01	0.2	7.8E-01
ENSMUST00000121277				3.9	2.5E-03	-2.1	1.1E-01	0.5	4.8E-01	0.1	9.4E-01
ENSMUST00000147183				3.9	1.1E-05	2.6	3.0E-02	-1.7	9.3E-02	-0.6	5.3E-01
ENSMUST00000180417	ER membrane protein complex subunit 8 [Source:MGI Symbol;Acc:MGI:1343095]	M0QWC9		-1.0	2.3E-01	0.3	7.4E-01	-0.2	7.2E-01	-1.5	1.0E-01
ENSMUST00000142981				3.9	3.2E-03	-6.0	3.4E-05	0.2	6.0E-01	0.8	3.7E-01
ENSMUST00000156406				3.9	1.2E-03	7.2	1.4E-05	-0.5	6.0E-01	0.2	6.4E-01
ENSMUST00000072982				3.9	1.0E-02	-6.1	2.1E-05	-0.1	6.3E-01	-1.6	9.9E-02
ENSMUST00000181970				3.9	1.2E-02	6.5	3.5E-04	-0.6	6.5E-01	-1.0	1.7E-01
ENSMUST00000125592				3.9	6.8E-05	6.5	5.2E-04	-0.5	7.1E-01	0.2	7.5E-01
ENSMUST00000156563				3.9	1.9E-04	4.5	1.0E-03	0.7	4.6E-01	-0.2	7.2E-01
ENSMUST00000180463	retinal degeneration 3 [Source:MGI Symbol;Acc:MGI:1921273]		Q8BRE0	2.2	4.9E-02	5.1	6.8E-03	1.7	2.5E-01	-1.2	1.9E-01
ENSMUST00000130820				3.9	1.1E-03	6.4	7.1E-04	-0.7	6.2E-01	-0.3	6.5E-01
ENSMUST00000150414				3.9	1.5E-02	-3.0	2.2E-02	-0.3	6.9E-01	0.4	7.0E-01
ENSMUST00000182743				3.9	8.0E-04	7.1	7.6E-04	-0.6	7.1E-01	0.3	6.6E-01
ENSMUST00000191475				3.9	5.3E-04	5.3	3.1E-02	-0.6	7.8E-01	0.3	8.4E-01
ENSMUST00000188002				3.9	2.7E-03	1.6	3.2E-02	-0.1	8.6E-01	0.0	9.4E-01
ENSMUST00000181993				3.9	1.7E-03	4.8	4.9E-05	-2.2	1.0E-02	0.2	7.0E-01
ENSMUST00000180521	RIKEN cDNA 1810049J17 gene [Source:MGI Symbol;Acc:MGI:3704453]	Q3V2G9		-1.9	4.2E-01	-4.6	7.5E-02	-2.7	9.2E-02	0.0	9.9E-01
ENSMUST00000140147				3.9	5.3E-03	3.7	5.9E-05	0.3	5.4E-01	-0.6	1.2E-01
ENSMUST00000120199				3.9	1.7E-03	-8.5	3.7E-03	-1.3	8.4E-02	-1.4	5.9E-01
ENSMUST00000180539				0.9	2.1E-01	0.9	3.2E-01	0.6	4.0E-01	0.6	4.4E-01
ENSMUST00000180355				3.9	1.7E-03	7.1	8.0E-05	-0.5	6.6E-01	-0.3	6.0E-01
ENSMUST00000143094				3.9	2.8E-04	6.3	3.2E-04	0.5	6.6E-01	-0.2	7.9E-01
ENSMUST00000118661				3.9	4.0E-03	5.1	3.7E-04	0.2	8.4E-01	-0.1	8.7E-01
ENSMUST00000180548				-0.9	2.8E-01	0.1	9.3E-01	0.5	5.3E-01	-0.5	6.0E-01
ENSMUST00000127101				3.9	2.9E-02	3.1	1.9E-03	0.0	9.6E-01	-0.1	7.9E-01
ENSMUST00000139908				3.9	3.9E-03	5.1	1.0E-02	-0.8	6.5E-01	-1.9	9.5E-02
ENSMUST00000183755				3.9	1.8E-03	-2.5	9.8E-02	0.0	9.8E-01	-0.3	8.5E-01
ENSMUST00000194953				3.9	3.3E-05	8.3	4.0E-05	-0.6	6.4E-01	-0.1	9.1E-01
ENSMUST00000180572	agrin [Source:MGI Symbol;Acc:MGI:87961]	M0QWP1		1.3	2.0E-01	-1.2	4.3E-01	-0.3	7.6E-01	2.1	1.3E-01
ENSMUST00000127340				3.9	1.2E-03	-4.9	1.2E-03	1.5	1.2E-02	-0.8	5.1E-01
ENSMUST00000122138				3.9	3.6E-03	4.8	3.4E-03	-1.4	3.1E-01	0.3	7.1E-01
ENSMUST00000180587	mor necrosis factor (ligand) superfamily, membrane-bound member 13 [Source:MGI Symbol;Acc:MGI:384507	Q8BXS2		0.0	1.0E+00	0.1	9.3E-01	-0.9	4.4E-01	-1.1	4.4E-01
ENSMUST00000127725				3.9	2.7E-04	8.1	6.9E-05	-0.5	7.2E-01	-1.1	9.1E-02
ENSMUST00000180600				-3.0	7.6E-02	-0.3	8.6E-01	1.0	4.2E-01	-1.7	3.5E-01
ENSMUST00000182266				3.9	3.3E-04	-0.5	6.6E-01	0.6	4.8E-01	-1.4	2.7E-01
ENSMUST00000147922				3.9	8.9E-03	-2.4	9.7E-02	1.3	9.9E-02	-1.6	3.0E-01
ENSMUST00000182058				3.8	9.3E-03	4.6	2.6E-03	-1.0	3.9E-01	0.4	5.7E-01
ENSMUST00000180619				1.1	1.4E-01	0.3	6.9E-01	-1.1	1.2E-01	-0.3	7.0E-01
ENSMUST00000156459				3.8	8.8E-04	-2.7	6.0E-03	0.7	1.2E-01	0.0	9.5E-01
ENSMUST00000125944				3.8	6.9E-03	4.8	2.5E-03	-1.2	3.4E-01	0.1	9.3E-01
ENSMUST00000180636	solute carrier family 35, member A5 [Source:MGI Symbol;Acc:MGI:1921352]	M0QWG7		-3.8	8.0E-02	-5.9	6.4E-02	-1.8	1.3E-01	0.2	9.4E-01
ENSMUST00000126511				3.8	2.5E-03	7.9	3.2E-05	-0.5	6.4E-01	-0.8	1.7E-01
ENSMUST00000182882				3.8	1.7E-02	3.4	1.3E-02	-1.8	1.1E-01	-0.4	6.7E-01
ENSMUST00000143029				3.8	4.6E-04	5.8	1.7E-04	-2.5	3.9E-02	-0.7	2.4E-01
ENSMUST00000118752				3.8	1.7E-03	4.9	3.0E-04	-0.5	5.7E-01	-0.3	6.4E-01
ENSMUST00000180654				3.1	1.1E-01	3.3	7.2E-02	-2.4	1.8E-01	-2.6	1.1E-01
ENSMUST00000150407				3.8	2.0E-04	-0.3	6.8E-01	-0.2	7.5E-01	-3.2	1.3E-02
ENSMUST00000136323				3.8	2.5E-04	-2.3	1.3E-01	0.8	3.0E-01	0.8	5.7E-01
ENSMUST00000156196				3.8	1.4E-02	-5.7	7.5E-03	1.4	6.1E-02	0.4	8.3E-01
ENSMUST00000146686				3.8	1.0E-03	3.8	3.7E-03	0.1	9.0E-01	1.4	5.9E-02
ENSMUST00000141876				3.8	1.8E-03	-6.4	6.0E-04	-2.0	3.9E-03	-0.4	8.1E-01
ENSMUST00000180710	protein tyrosine phosphatase, receptor type, C polypeptide-associated protein [Source:EntrezGene;Acc:19265]	Q542J3	Q64697	-1.4	5.7E-02	-1.2	1.7E-01	-0.2	6.8E-01	-0.4	5.7E-01
ENSMUST00000183478				3.8	1.7E-02	5.2	5.6E-03	-0.5	7.6E-01	-0.1	8.9E-01
ENSMUST00000180716	SUMO1/sentrin specific peptidase 1 [Source:MGI Symbol;Acc:MGI:2445054]	M0QWV7		-0.9	4.3E-01	0.9	6.0E-01	1.8	2.0E-01	-0.1	9.6E-01
ENSMUST00000180720				0.2	5.5E-01	1.1	6.1E-02	0.8	7.7E-02	-0.1	8.4E-01
ENSMUST00000134987				3.8	1.9E-03	5.8	9.4E-04	0.0	9.9E-01	-1.0	2.2E-01
ENSMUST00000180746	predicted gene 9125 [Source:MGI Symbol;Acc:MGI:3702970]		P0DMR6	4.4	1.0E-01	5.7	6.3E-02	-0.2	9.5E-01	-1.5	3.6E-01
ENSMUST00000153269				3.8	1.7E-03	-3.6	1.1E-02	0.8	2.5E-01	-2.7	8.8E-02
ENSMUST00000180765	nudix (nucleoside diphosphate linked moiety X)-type motif 22 [Source:MGI Symbol;Acc:MGI:1915573]		Q9DD16	-0.4	6.8E-01	-2.7	2.1E-01	0.5	6.5E-01	2.7	1.7E-01
ENSMUST00000143597				3.8	1.3E-03	3.2	3.0E-03	0.4	6.0E-01	0.1	8.2E-01
ENSMUST00000132305				3.8	2.9E-03	7.3	1.3E-04	0.1	9.5E-01	-1.0	1.5E-01
ENSMUST00000180402				3.8	2.9E-03	6.4	2.2E-04	1.1	3.1E-01	-1.7	2.1E-02
ENSMUST00000182529				3.8	6.5E-03	3.9	2.6E-03	-0.2	8.1E-01	-0.4	5.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000098457				3.8	7.0E-05	7.3	1.4E-04	0.4	7.3E-01	0.1	8.3E-01
ENSMUST00000123130				3.8	2.6E-03	6.6	1.0E-04	-0.6	6.1E-01	-1.0	1.2E-01
ENSMUST00000180792	sorting nexin 29 [Source:MGI Symbol;Acc:MGI:1921728]		Q9D3S3	-0.3	7.7E-01	-0.8	5.8E-01	0.0	9.8E-01	0.5	7.5E-01
ENSMUST00000187244				3.8	3.8E-03	6.1	2.9E-03	0.9	5.8E-01	0.4	6.0E-01
ENSMUST00000166408				3.8	2.4E-03	6.9	1.8E-04	-0.8	5.2E-01	0.5	4.8E-01
ENSMUST00000180845	myosin, heavy polypeptide 13, skeletal muscle [Source:MGI Symbol;Acc:MGI:1339967]	B1AR69		3.5	1.6E-01	1.6	6.1E-01	-0.3	9.0E-01	1.6	5.3E-01
ENSMUST00000186203				3.8	1.5E-02	4.5	1.5E-04	0.5	4.9E-01	-0.6	3.0E-01
ENSMUST00000068663				3.8	6.1E-04	4.9	1.3E-02	-0.6	7.1E-01	-0.6	6.0E-01
ENSMUST00000195267				3.8	1.3E-02	5.7	8.3E-04	0.5	6.9E-01	-0.6	4.0E-01
ENSMUST00000180925	cardiotrophin-like cytokine factor 1 [Source:MGI Symbol;Acc:MGI:1930088]		Q9QZM3	-0.2	8.1E-01	-2.5	8.7E-02	-1.7	5.9E-02	0.6	6.8E-01
ENSMUST00000142332				3.8	5.6E-04	5.3	4.8E-04	-0.6	5.7E-01	-0.7	2.9E-01
ENSMUST00000180956	CDK2-associated protein 2 [Source:MGI Symbol;Acc:MGI:1098779]			-2.3	3.7E-02	-0.6	6.1E-01	0.2	8.0E-01	-1.5	1.9E-01
ENSMUST00000180327				3.8	1.7E-02	5.0	4.2E-04	0.7	4.1E-01	0.3	6.5E-01
ENSMUST00000191058				3.8	5.3E-04	8.4	2.2E-05	-0.5	7.0E-01	-0.3	5.6E-01
ENSMUST00000180979				0.3	6.3E-01	1.1	2.5E-01	0.8	2.6E-01	0.1	9.2E-01
ENSMUST00000122400				3.8	1.2E-02	-0.7	2.7E-01	0.6	2.0E-01	0.1	8.8E-01
ENSMUST00000153211				3.8	5.2E-04	4.9	1.7E-03	-0.6	5.6E-01	-0.1	8.8E-01
ENSMUST00000147245				3.8	1.4E-04	-6.9	1.3E-03	-0.5	3.8E-01	0.6	7.3E-01
ENSMUST00000183179				3.8	3.3E-03	3.0	6.7E-03	0.0	9.7E-01	-0.6	4.0E-01
ENSMUST00000183906				3.8	2.2E-04	-4.0	1.2E-02	0.3	5.8E-01	1.3	3.2E-01
ENSMUST00000184165				3.8	2.2E-04	5.0	4.3E-04	-0.5	5.6E-01	0.1	8.7E-01
ENSMUST00000141150				3.8	7.7E-04	-6.0	2.8E-03	0.1	9.2E-01	0.4	8.2E-01
ENSMUST00000194301				3.8	6.2E-04	-2.4	1.7E-01	0.7	4.5E-01	-0.5	7.7E-01
ENSMUST00000152502				3.8	3.3E-03	2.3	6.7E-02	-1.1	3.0E-01	0.1	9.4E-01
ENSMUST00000136854				3.8	2.0E-03	7.6	1.4E-06	-0.6	3.9E-01	-0.6	1.3E-01
ENSMUST00000181069				-2.9	1.0E-01	-1.6	5.0E-01	1.0	5.2E-01	-0.4	8.7E-01
ENSMUST00000147338				3.8	4.9E-04	5.4	9.2E-04	-0.1	9.0E-01	-0.5	5.2E-01
ENSMUST00000135608				3.8	2.6E-03	-3.7	2.0E-01	1.1	5.2E-01	-1.7	5.5E-01
ENSMUST00000181108				-3.4	2.4E-01	-5.2	1.3E-01	-2.7	1.2E-01	-0.9	8.1E-01
ENSMUST00000143224				3.8	1.3E-03	5.7	1.2E-03	0.4	7.3E-01	-0.3	6.9E-01
ENSMUST00000181150				1.0	6.4E-01	4.0	1.4E-01	1.3	6.0E-01	-1.7	3.7E-01
ENSMUST00000132656				3.8	1.3E-02	6.3	5.6E-05	1.5	9.7E-02	0.1	8.5E-01
ENSMUST00000152261				3.8	2.1E-03	6.5	4.1E-04	0.2	8.6E-01	0.4	5.4E-01
ENSMUST00000135272				3.8	9.0E-04	-2.3	9.2E-02	0.7	3.6E-01	-0.5	6.8E-01
ENSMUST00000137029				3.8	3.3E-03	7.0	2.2E-05	0.1	9.4E-01	0.6	2.4E-01
ENSMUST00000170898				3.8	5.6E-04	3.8	1.6E-04	0.1	8.2E-01	0.2	7.0E-01
ENSMUST00000149590				3.8	4.4E-03	-8.0	3.3E-04	-0.9	8.5E-02	-0.8	6.3E-01
ENSMUST00000181181				1.6	7.3E-02	3.1	1.5E-02	0.8	3.9E-01	-0.7	4.1E-01
ENSMUST00000137621				3.8	5.7E-04	7.3	2.3E-04	-0.6	6.7E-01	-0.9	1.9E-01
ENSMUST00000181907				3.8	1.5E-04	-3.6	6.9E-02	2.1	3.0E-02	-1.4	4.9E-01
ENSMUST00000181219				-2.1	7.3E-02	-1.2	3.5E-01	0.5	6.0E-01	-0.4	7.6E-01
ENSMUST00000141932				3.8	9.4E-03	3.9	4.9E-04	0.3	6.6E-01	-0.1	8.2E-01
ENSMUST00000126727				3.8	3.6E-04	-4.2	2.8E-04	0.2	5.7E-01	0.1	8.7E-01
ENSMUST00000181233				3.7	9.9E-02	4.5	4.1E-02	-1.8	4.1E-01	-2.6	9.7E-02
ENSMUST00000181236				2.4	1.9E-01	-1.5	3.9E-01	-4.0	2.2E-02	0.0	1.0E+00
ENSMUST00000169457				3.8	1.0E-04	-0.7	5.4E-01	1.5	8.5E-02	-1.1	3.7E-01
ENSMUST00000181245	ribosomal protein S6 kinase, polypeptide 2 [Source:MGI Symbol;Acc:MGI:1927343]		Q9Z1M4	-0.8	6.0E-01	-2.0	4.7E-01	0.5	7.5E-01	1.7	4.7E-01
ENSMUST00000144723				3.8	1.2E-02	6.8	4.2E-04	0.6	6.2E-01	1.2	1.3E-01
ENSMUST00000149254				3.8	1.7E-04	2.4	1.1E-02	0.5	4.8E-01	0.3	6.5E-01
ENSMUST00000181283	slingshot homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:2679255]			-2.3	3.1E-01	-0.8	8.1E-01	1.3	5.1E-01	-0.3	9.3E-01
ENSMUST00000159170				3.8	3.4E-03	7.0	1.1E-03	0.7	6.5E-01	-0.6	4.9E-01
ENSMUST00000123744				3.8	3.5E-04	6.6	9.0E-04	-0.5	7.5E-01	-1.7	6.1E-02
ENSMUST00000054664				3.8	9.1E-03	6.4	2.0E-03	0.8	6.3E-01	-1.2	1.8E-01
ENSMUST00000149780				3.8	1.2E-02	-3.9	2.6E-03	0.1	8.1E-01	-0.4	7.1E-01
ENSMUST00000181321	predicted gene, 26602 [Source:MGI Symbol;Acc:MGI:5477096]	M0QWA4		-3.3	2.9E-01	-1.5	6.7E-01	0.5	8.3E-01	-1.3	7.4E-01
ENSMUST00000162302				3.8	4.0E-03	7.5	1.1E-04	-0.6	6.2E-01	-0.8	2.3E-01
ENSMUST00000143372				3.8	7.4E-04	6.0	1.5E-03	-0.5	7.5E-01	0.0	9.6E-01
ENSMUST00000155554				3.8	1.5E-03	-0.9	4.1E-01	1.2	1.0E-01	-0.6	5.5E-01
ENSMUST00000181339	cholecystokinin B receptor [Source:MGI Symbol;Acc:MGI:99479]	Q8BYG7		3.6	4.5E-02	4.6	2.4E-02	-0.5	7.9E-01	-1.4	2.5E-01
ENSMUST00000160036				3.8	1.3E-03	6.0	3.5E-05	-0.9	2.7E-01	0.5	3.4E-01
ENSMUST00000191977				3.7	7.1E-04	2.5	1.1E-02	-0.9	2.4E-01	0.6	3.5E-01
ENSMUST00000156888				3.7	4.3E-03	5.4	1.4E-03	-1.4	3.0E-01	-0.3	6.6E-01
ENSMUST00000151047				3.7	2.3E-03	5.8	5.3E-03	0.0	1.0E+00	0.5	6.2E-01
ENSMUST00000181372				0.5	7.1E-01	-0.4	8.0E-01	-0.7	5.5E-01	0.1	9.3E-01
ENSMUST00000162522				3.7	6.7E-03	-2.4	2.8E-02	1.2	3.7E-02	-0.2	8.0E-01
ENSMUST00000135119				3.7	1.9E-03	1.9	1.6E-02	-0.9	1.2E-01	0.1	8.6E-01
ENSMUST00000182237				3.7	5.3E-03	3.5	6.6E-04	0.0	9.6E-01	0.0	9.4E-01
ENSMUST00000181402				0.6	5.5E-01	0.8	5.3E-01	0.3	7.4E-01	0.1	9.1E-01
ENSMUST00000125954				3.7	3.8E-04	-1.1	5.6E-01	3.2	1.5E-02	-0.4	8.1E-01
ENSMUST00000142786				3.7	7.1E-04	3.8	3.7E-03	-1.5	1.5E-01	0.3	7.3E-01
ENSMUST00000071573				3.7	2.3E-02	8.5	6.9E-05	-1.8	2.4E-01	0.4	4.7E-01
ENSMUST00000155213				3.7	3.1E-03	5.3	8.4E-04	-1.5	2.4E-01	-0.5	4.8E-01
ENSMUST00000173850				3.7	1.1E-03	2.2	4.3E-02	0.0	1.0E+00	0.5	5.0E-01
ENSMUST00000152801				3.7	8.7E-04	3.4	7.2E-02	-0.5	7.8E-01	1.6	2.1E-01
ENSMUST00000181468				0.4	8.3E-01	-1.6	5.6E-01	-1.8	3.2E-01	0.2	9.4E-01
ENSMUST00000181470	methionine aminopeptidase 2 [Source:MGI Symbol;Acc:MGI:1929701]	M0QWX0		-2.2	3.5E-01	-4.6	1.1E-01	-2.9	7.0E-02	-0.4	8.8E-01
ENSMUST00000130227				3.7	2.2E-03	-5.1	6.5E-04	0.8	1.1E-01	-1.0	3.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000154018				3.7	6.9E-04	5.1	4.3E-03	-1.8	2.2E-01	0.3	7.3E-01
ENSMUST00000181512	retinal degeneration 3 [Source:MGI Symbol;Acc:MGI:1921273]	Q05D96		-2.0	6.6E-02	-2.1	2.5E-01	1.8	1.0E-01	1.8	2.9E-01
ENSMUST00000181521	microtubule-associated protein 1 light chain 3 beta [Source:MGI Symbol;Acc:MGI:1914693]	M0QWT8		-4.5	1.6E-01	-6.8	8.5E-02	-2.7	1.2E-01	-0.3	9.4E-01
ENSMUST00000181541	TD and POZ domain containing 1 [Source:MGI Symbol;Acc:MGI:2449436]		P0DMR5	4.0	1.0E-01	1.8	5.7E-01	-0.2	9.4E-01	2.0	3.9E-01
ENSMUST00000127365				3.7	8.8E-04	4.5	9.2E-04	-1.9	1.0E-01	-0.1	9.3E-01
ENSMUST00000155167				3.7	3.3E-03	7.1	6.3E-05	-0.6	6.0E-01	-0.3	6.2E-01
ENSMUST00000162797				3.7	3.6E-03	8.3	1.6E-05	-0.5	6.4E-01	-0.5	2.6E-01
ENSMUST00000162798				3.7	2.0E-04	2.8	2.2E-02	-1.5	1.6E-01	0.9	2.7E-01
ENSMUST00000192934				3.7	2.4E-03	6.3	3.1E-04	-0.5	6.7E-01	-0.7	2.8E-01
ENSMUST00000155341				3.7	2.4E-03	-4.5	1.7E-02	-1.7	4.3E-02	-0.9	6.1E-01
ENSMUST00000181586	cytochrome c oxidase subunit IV isoform 1 [Source:MGI Symbol;Acc:MGI:88473]	A2RSV8	P19783	-3.3	7.9E-02	-1.1	6.3E-01	1.6	3.0E-01	-0.6	8.0E-01
ENSMUST00000181601	predicted gene, 26566 [Source:MGI Symbol;Acc:MGI:5477060]	Q8CAC1		1.9	1.9E-01	3.0	6.3E-02	-1.4	3.3E-01	-2.4	8.4E-02
ENSMUST00000151827				3.7	3.7E-04	0.8	4.4E-01	0.9	2.4E-01	-3.3	1.6E-02
ENSMUST00000126790				3.7	3.6E-03	-3.8	3.8E-02	1.1	1.4E-01	-0.9	6.0E-01
ENSMUST00000140024				3.7	6.5E-04	8.0	2.7E-05	-0.2	8.3E-01	0.1	8.4E-01
ENSMUST00000181614				0.6	3.3E-01	2.3	9.4E-03	0.6	3.6E-01	-1.2	8.5E-02
ENSMUST00000129453				3.7	2.0E-04	7.3	1.3E-04	-0.5	6.7E-01	0.3	6.5E-01
ENSMUST00000130352				3.7	7.4E-04	5.7	1.5E-04	-0.7	5.0E-01	0.5	3.6E-01
ENSMUST00000156444				3.7	2.9E-03	6.2	8.5E-03	2.4	1.9E-01	0.1	9.1E-01
ENSMUST00000181650				3.0	1.4E-01	6.3	8.4E-03	-0.5	8.2E-01	-3.8	1.7E-02
ENSMUST00000192597				3.7	4.8E-04	5.6	2.0E-03	-1.3	3.8E-01	1.1	2.4E-01
ENSMUST00000181662				-3.0	3.4E-01	1.4	7.5E-01	3.6	2.5E-01	-0.7	8.5E-01
ENSMUST00000181663	F-box protein 31 [Source:MGI Symbol;Acc:MGI:1354708]	M0QWM6		1.2	7.8E-02	2.7	7.4E-03	0.9	2.1E-01	-0.6	4.0E-01
ENSMUST00000140354				3.7	3.3E-03	5.9	3.5E-05	-0.8	3.2E-01	-0.5	3.7E-01
ENSMUST00000156129				3.7	1.0E-03	4.2	6.8E-03	-0.2	8.6E-01	0.8	3.2E-01
ENSMUST00000181677				0.4	3.8E-01	1.3	5.5E-02	0.2	6.7E-01	-0.7	2.4E-01
ENSMUST00000129852				3.7	6.9E-05	-4.4	3.8E-03	0.6	3.5E-01	-3.1	7.9E-02
ENSMUST00000138316				3.7	1.4E-03	6.3	2.4E-04	-0.6	6.3E-01	-0.8	2.0E-01
ENSMUST00000154523				3.7	3.0E-04	7.5	9.1E-05	1.4	2.3E-01	0.0	9.8E-01
ENSMUST00000164971				3.7	3.8E-04	6.1	6.9E-04	-0.5	6.9E-01	0.2	8.0E-01
ENSMUST00000181715	phosphatidylinositol transfer protein, membrane-associated 1 [Source:MGI Symbol;Acc:MGI:1197524]		O35954	-0.3	7.9E-01	-1.2	3.8E-01	-0.1	8.7E-01	0.8	5.3E-01
ENSMUST00000172911				3.7	5.4E-03	6.1	3.2E-04	-0.6	6.0E-01	0.0	9.4E-01
ENSMUST00000181736	retinitis pigmentosa GTPase regulator interacting protein 1 [Source:MGI Symbol;Acc:MGI:1932134]	M0QWL3		3.6	7.1E-02	2.3	3.7E-01	0.9	7.0E-01	2.1	2.7E-01
ENSMUST00000181744				-1.1	2.4E-01	-0.6	6.3E-01	0.0	9.7E-01	-0.5	6.5E-01
ENSMUST00000181745	predicted gene, 26657 [Source:MGI Symbol;Acc:MGI:5477151]	Q9CVR1		4.9	4.7E-02	2.0	4.6E-01	-0.8	7.6E-01	2.2	2.9E-01
ENSMUST00000181753				0.3	8.0E-01	2.6	7.9E-02	0.6	6.1E-01	-1.7	1.2E-01
ENSMUST00000180781				3.7	1.3E-03	-3.0	3.6E-03	0.1	8.7E-01	-0.9	3.0E-01
ENSMUST00000117921				3.7	4.5E-03	7.6	1.3E-05	-0.6	5.1E-01	0.3	5.2E-01
ENSMUST00000146989				3.7	3.4E-04	6.4	2.7E-04	-0.6	6.3E-01	-0.7	2.7E-01
ENSMUST00000155133				3.7	1.3E-02	6.6	5.5E-04	-0.4	8.0E-01	-0.2	8.1E-01
ENSMUST00000193044				3.7	1.8E-02	-4.4	5.4E-02	1.4	1.5E-01	-0.8	7.1E-01
ENSMUST00000181798	phosphatidylinositol transfer protein, membrane-associated 1 [Source:MGI Symbol;Acc:MGI:1197524]			-0.2	8.8E-01	1.1	5.3E-01	-0.4	8.1E-01	-1.7	2.6E-01
ENSMUST00000181810	tumor necrosis factor (ligand) superfamily, member 12 [Source:MGI Symbol;Acc:MGI:1196259]	Q5F2A0	O54907	0.3	7.2E-01	-0.6	6.0E-01	-0.7	4.6E-01	0.3	8.0E-01
ENSMUST00000136764				3.7	8.0E-03	6.8	1.4E-04	0.2	8.9E-01	-0.2	7.6E-01
ENSMUST00000181826				0.9	1.7E-01	0.5	5.0E-01	-0.1	8.4E-01	0.2	7.5E-01
ENSMUST00000137908				3.7	1.8E-03	6.0	1.5E-04	-0.5	5.9E-01	0.1	8.3E-01
ENSMUST00000194303				3.7	2.6E-02	6.4	4.2E-04	-0.1	9.2E-01	-0.3	6.9E-01
ENSMUST00000194565				3.7	3.5E-04	-3.1	1.0E-02	0.6	2.8E-01	-0.7	5.0E-01
ENSMUST00000139071				3.7	2.8E-05	6.5	1.6E-03	-0.8	6.4E-01	-1.6	9.8E-02
ENSMUST00000181850	RIKEN cDNA 9330151L19 gene [Source:MGI Symbol;Acc:MGI:3041168]	M0QWC1		-0.2	8.1E-01	0.6	4.9E-01	0.5	4.4E-01	-0.3	7.5E-01
ENSMUST00000186865				3.7	5.3E-04	5.5	2.3E-03	-1.4	3.4E-01	-0.6	4.2E-01
ENSMUST00000131330				3.7	9.5E-03	8.0	4.9E-04	2.5	1.1E-01	1.1	1.8E-01
ENSMUST00000181869				-0.7	3.8E-01	-0.8	4.6E-01	-0.2	8.0E-01	-0.1	9.1E-01
ENSMUST00000139098				3.7	4.2E-04	3.3	5.0E-03	-0.3	6.7E-01	-0.6	4.2E-01
ENSMUST00000121691				3.7	1.6E-03	5.5	3.0E-03	-0.6	7.1E-01	-0.4	6.1E-01
ENSMUST00000128105				3.7	1.7E-03	5.3	9.1E-04	0.4	6.7E-01	-0.2	7.4E-01
ENSMUST00000076633				3.7	4.5E-03	-2.4	3.2E-03	0.1	8.1E-01	0.1	8.5E-01
ENSMUST00000181894				1.7	4.3E-01	0.8	7.4E-01	-1.2	5.6E-01	-0.3	9.0E-01
ENSMUST00000143826				3.7	1.6E-03	6.2	7.3E-04	-0.1	9.3E-01	0.6	3.8E-01
ENSMUST00000144696				3.7	3.1E-04	4.0	4.5E-04	0.2	7.9E-01	0.0	9.8E-01
ENSMUST00000153243				3.7	7.3E-03	5.3	3.2E-04	0.3	7.3E-01	-0.5	4.6E-01
ENSMUST00000125672				3.7	1.4E-03	-9.8	4.4E-05	-1.2	2.6E-02	-1.9	2.5E-01
ENSMUST00000181945	junctional sarcoplasmic reticulum protein 1 [Source:MGI Symbol;Acc:MGI:1916700]	M0QWR3		3.3	5.8E-02	6.0	3.8E-03	-0.5	7.7E-01	-3.2	1.7E-02
ENSMUST00000151049				3.7	5.4E-04	-10.9	1.9E-05	-0.6	1.2E-01	-0.7	6.3E-01
ENSMUST00000136358				3.7	9.4E-03	-2.5	3.4E-02	1.4	2.8E-02	-0.9	4.3E-01
ENSMUST00000159714				3.7	2.0E-03	5.5	2.3E-03	-0.5	7.5E-01	-0.5	4.8E-01
ENSMUST00000175822				3.7	7.3E-03	-2.8	2.3E-02	0.7	2.3E-01	0.0	9.7E-01
ENSMUST00000155521				3.7	1.2E-03	6.2	7.1E-04	-0.6	6.6E-01	-2.9	8.5E-03
ENSMUST00000150786				3.7	8.8E-04	3.7	1.6E-02	0.3	7.7E-01	0.3	7.4E-01
ENSMUST00000177160				3.7	8.1E-04	7.4	8.3E-05	-0.5	6.5E-01	-0.6	3.0E-01
ENSMUST00000181983	RNA binding motif protein 25 [Source:MGI Symbol;Acc:MGI:1914289]	S4R2B0		1.5	1.1E-01	0.0	1.0E+00	-1.1	2.2E-01	0.5	6.6E-01
ENSMUST00000153381				3.7	5.8E-03	-5.9	3.6E-02	-0.3	7.5E-01	2.1	4.1E-01
ENSMUST00000193372				3.7	2.4E-05	5.3	6.0E-04	-0.9	3.8E-01	0.0	9.8E-01
ENSMUST00000181991				-0.1	9.8E-01	-3.6	1.7E-01	-4.1	2.9E-02	-0.6	8.3E-01
ENSMUST00000129320				3.7	1.4E-04	4.2	6.5E-03	0.1	9.6E-01	-0.3	7.2E-01
ENSMUST00000133592				3.7	1.7E-02	6.0	2.7E-04	-1.4	2.2E-01	0.4	5.2E-01
ENSMUST00000180035				3.7	3.0E-04	1.1	6.2E-01	-2.2	3.4E-01	2.8	1.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000182009				1.3	4.2E-01	0.4	8.6E-01	-0.8	5.9E-01	0.1	9.6E-01
ENSMUST00000098564				3.7	2.2E-03	4.5	1.7E-03	1.3	2.0E-01	0.3	6.8E-01
ENSMUST00000182015	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	S4R1G6		-2.7	3.3E-01	-6.3	6.9E-02	-4.4	2.0E-02	-0.8	8.1E-01
ENSMUST00000153236				3.7	1.8E-04	-8.6	4.6E-05	-0.2	6.6E-01	-0.9	5.1E-01
ENSMUST00000154490				3.7	3.5E-02	0.8	4.2E-01	-4.8	1.6E-03	0.5	6.1E-01
ENSMUST00000182022	RNA binding motif protein 5 [Source:MGI Symbol;Acc:MGI:1933204]	S4R1V5		-2.2	4.3E-02	-1.4	3.2E-01	0.9	3.2E-01	0.1	9.5E-01
ENSMUST00000153503				3.7	2.4E-03	-3.8	4.4E-03	0.0	9.7E-01	0.8	4.3E-01
ENSMUST00000182026	RNA binding motif protein 5 [Source:MGI Symbol;Acc:MGI:1933204]	S4R273		-1.6	5.0E-02	-0.5	5.3E-01	-0.7	2.9E-01	-1.7	4.6E-02
ENSMUST00000090237				3.7	8.9E-03	7.5	1.7E-04	0.0	9.9E-01	0.0	9.5E-01
ENSMUST00000182031				0.8	2.8E-01	-0.2	7.8E-01	-0.4	5.5E-01	0.6	4.5E-01
ENSMUST00000138652				3.6	7.9E-03	6.1	2.5E-05	-0.3	7.0E-01	-0.1	8.3E-01
ENSMUST00000144683				3.6	3.8E-03	7.8	3.4E-05	-0.9	4.5E-01	-0.6	2.6E-01
ENSMUST00000149442				3.6	6.2E-04	6.2	7.4E-03	-0.4	8.5E-01	-0.4	6.8E-01
ENSMUST00000182040				0.4	4.1E-01	1.6	5.4E-02	1.4	2.8E-02	0.3	6.1E-01
ENSMUST00000119864				3.6	3.2E-04	6.2	4.6E-03	-0.7	7.0E-01	0.1	9.4E-01
ENSMUST00000159423				3.6	3.3E-03	2.9	1.6E-02	-4.5	3.5E-03	-3.1	6.5E-03
ENSMUST00000160651				3.6	1.6E-03	4.5	3.3E-05	-0.7	2.4E-01	-0.4	3.7E-01
ENSMUST00000182056	BAI1-associated protein 3 [Source:MGI Symbol;Acc:MGI:2685783]	S4R1E7		4.1	1.4E-01	4.8	1.6E-01	0.3	9.4E-01	-0.4	8.2E-01
ENSMUST00000137590				3.6	3.5E-02	3.7	2.0E-02	-1.0	4.5E-01	-0.8	4.9E-01
ENSMUST00000069786				3.6	3.1E-02	-3.3	1.5E-03	-0.5	2.8E-01	-0.7	3.8E-01
ENSMUST00000191040				3.6	5.6E-03	3.2	2.2E-03	-0.1	8.6E-01	0.2	7.1E-01
ENSMUST00000181979				3.6	3.1E-03	2.4	2.3E-02	-0.2	8.3E-01	-0.1	8.6E-01
ENSMUST00000182076				-2.4	5.3E-02	-1.6	2.8E-01	-0.2	7.8E-01	-1.0	4.9E-01
ENSMUST00000161403				3.6	5.9E-04	-1.8	3.9E-01	-3.4	7.8E-02	3.5	8.1E-02
ENSMUST00000154421				3.6	9.1E-03	6.0	1.1E-03	-0.5	7.1E-01	-1.2	1.5E-01
ENSMUST00000137060				3.6	3.9E-03	4.5	8.1E-03	-1.7	2.7E-01	0.3	7.5E-01
ENSMUST00000098239				3.6	1.1E-02	6.1	6.2E-05	0.1	8.7E-01	-0.5	3.6E-01
ENSMUST00000182115				-4.0	3.8E-01	-4.4	4.8E-01	-0.4	8.9E-01	0.1	9.9E-01
ENSMUST00000182122	zinc finger protein 236 [Source:MGI Symbol;Acc:MGI:1926950]	S4R299		-1.5	2.7E-01	-1.9	3.1E-01	0.9	4.3E-01	1.3	4.8E-01
ENSMUST00000182123				2.1	2.8E-01	-1.3	4.9E-01	-3.5	5.3E-02	0.0	9.9E-01
ENSMUST00000129789				3.6	7.7E-03	6.8	2.0E-04	-0.6	6.3E-01	-0.6	3.6E-01
ENSMUST00000141061				3.6	1.3E-03	-0.9	4.1E-01	1.2	1.2E-01	-0.8	4.8E-01
ENSMUST00000182131				-0.5	5.3E-01	-0.3	7.2E-01	0.0	1.0E+00	-0.1	9.0E-01
ENSMUST00000156378				3.6	2.9E-02	6.5	9.3E-05	0.5	5.9E-01	0.4	4.7E-01
ENSMUST00000182138				-1.4	2.1E-01	-0.1	9.3E-01	1.1	2.9E-01	-0.2	8.9E-01
ENSMUST00000149621				3.6	2.9E-02	7.7	2.0E-04	-1.4	3.7E-01	1.2	1.0E-01
ENSMUST00000182147				3.2	8.3E-02	3.8	5.6E-02	-1.2	5.0E-01	-1.7	2.3E-01
ENSMUST00000153219				3.6	8.4E-04	7.4	7.8E-05	-0.5	6.7E-01	-0.1	8.0E-01
ENSMUST00000182149	proline-rich coiled-coil 2C [Source:MGI Symbol;Acc:MGI:1913754]	S4R294		-0.5	6.1E-01	-1.0	5.6E-01	1.6	2.0E-01	2.0	2.1E-01
ENSMUST00000160561				3.6	1.4E-02	7.6	3.3E-04	-0.5	7.6E-01	-0.8	2.8E-01
ENSMUST00000182157				1.5	4.3E-01	-3.3	2.6E-01	-3.2	7.3E-02	1.5	5.9E-01
ENSMUST00000180457				3.6	4.7E-04	1.6	1.3E-01	0.0	9.8E-01	0.5	6.0E-01
ENSMUST00000182161	sosondowah ankyrin repeat domain family member C [Source:MGI Symbol;Acc:MGI:3606051]		Q8C0J6	0.6	5.1E-01	2.3	7.6E-02	1.8	1.0E-01	0.0	1.0E+00
ENSMUST00000144904				3.6	1.1E-02	2.9	2.2E-02	-3.6	1.1E-02	-0.2	8.3E-01
ENSMUST00000146156				3.6	2.2E-03	3.9	7.8E-03	-0.6	5.6E-01	-0.4	6.4E-01
ENSMUST00000155115				3.6	4.3E-04	6.5	8.3E-04	-0.5	7.2E-01	-1.6	7.2E-02
ENSMUST00000123273				3.6	4.2E-03	2.4	2.1E-02	-0.1	8.5E-01	-0.2	8.1E-01
ENSMUST00000131176				3.6	1.9E-04	5.9	6.5E-03	-1.5	4.4E-01	-0.3	7.3E-01
ENSMUST00000135356				3.6	1.3E-03	-6.7	1.4E-04	-0.4	3.5E-01	-1.0	4.1E-01
ENSMUST00000143803				3.6	1.5E-02	6.0	6.3E-05	-0.4	6.5E-01	0.2	7.7E-01
ENSMUST00000182189				3.6	1.5E-01	4.8	7.2E-02	-1.2	6.5E-01	-2.5	1.7E-01
ENSMUST00000139916				3.6	6.3E-04	6.1	2.6E-05	-0.6	4.8E-01	-0.4	3.7E-01
ENSMUST00000144995				3.6	3.0E-02	-4.6	2.4E-03	-0.8	1.4E-01	-0.4	7.4E-01
ENSMUST00000182199	oxysterol binding protein-like 10 [Source:MGI Symbol;Acc:MGI:1921736]	S4R1G3		3.1	6.2E-02	6.9	1.0E-03	-0.5	7.6E-01	-4.3	2.3E-03
ENSMUST00000151833				3.6	5.2E-03	8.5	5.3E-03	-0.4	8.7E-01	1.9	1.5E-01
ENSMUST00000074205				3.6	1.9E-03	-9.5	5.3E-04	1.9	2.4E-03	0.8	7.0E-01
ENSMUST00000152102				3.6	7.9E-04	8.0	1.5E-04	-0.4	7.5E-01	0.7	2.9E-01
ENSMUST00000114514				3.6	2.5E-03	-3.9	7.3E-02	0.1	8.9E-01	-0.1	9.7E-01
ENSMUST00000193273				3.6	1.1E-04	7.3	2.5E-04	-0.7	6.3E-01	0.0	9.5E-01
ENSMUST00000194613				3.6	1.1E-04	5.9	6.0E-04	-0.5	7.0E-01	-1.6	4.6E-02
ENSMUST00000182223				-2.9	2.1E-01	2.1	4.4E-01	3.7	1.3E-01	-1.3	5.8E-01
ENSMUST00000182225	natural killer tumor recognition sequence [Source:MGI Symbol;Acc:MGI:97346]	Q8CBP6		2.0	8.0E-02	3.6	1.8E-02	0.6	5.6E-01	-0.9	3.9E-01
ENSMUST00000182226	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Source:MGI Symbol;Ac	B2RXQ2		-1.9	2.0E-01	-2.7	1.4E-01	-0.1	9.5E-01	0.7	6.9E-01
ENSMUST00000129027				3.6	5.9E-03	4.5	2.8E-02	-0.6	7.4E-01	0.3	7.9E-01
ENSMUST00000125299				3.6	3.0E-03	4.6	8.9E-03	-0.6	6.7E-01	1.6	9.9E-02
ENSMUST00000131719				3.6	6.9E-05	3.9	5.4E-03	-1.5	2.4E-01	-0.1	8.9E-01
ENSMUST00000145604				3.6	1.1E-02	4.4	3.4E-03	-0.7	5.6E-01	-1.4	1.3E-01
ENSMUST00000182241	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	S4R1G6		-4.8	4.8E-02	1.8	5.6E-01	5.4	3.6E-02	-1.2	6.6E-01
ENSMUST00000149207				3.6	6.1E-03	7.1	1.5E-04	0.6	5.7E-01	1.1	9.0E-02
ENSMUST00000182243				0.4	6.8E-01	2.3	6.3E-02	1.0	3.2E-01	-1.0	3.2E-01
ENSMUST00000143660				3.6	1.5E-02	-1.8	1.5E-01	1.1	1.2E-01	0.0	9.8E-01
ENSMUST00000175986				3.6	6.4E-04	6.8	5.3E-03	2.3	2.2E-01	0.2	8.3E-01
ENSMUST00000100834				3.6	9.2E-03	6.0	7.2E-04	-0.4	7.4E-01	-1.0	1.7E-01
ENSMUST00000134383				3.6	2.9E-03	-2.2	3.8E-02	0.3	5.7E-01	-0.7	4.4E-01
ENSMUST00000191147				3.6	2.6E-04	-4.5	1.0E-01	-0.2	8.8E-01	-0.8	7.7E-01
ENSMUST00000167979				3.6	7.0E-04	5.1	3.2E-04	0.5	5.6E-01	-0.7	2.6E-01
ENSMUST00000126115				3.6	6.0E-03	5.9	4.8E-04	-3.2	5.2E-02	-1.8	4.8E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000142576				3.6	1.0E-02	-4.3	1.3E-02	-0.3	6.3E-01	1.1	4.5E-01
ENSMUST00000182281				-0.3	6.5E-01	0.9	3.2E-01	0.9	1.8E-01	-0.2	7.6E-01
ENSMUST00000159703				3.6	7.9E-03	-12.8	1.7E-05	-0.7	7.7E-02	-0.8	6.5E-01
ENSMUST00000194083				3.6	3.6E-04	6.8	1.9E-04	-0.3	8.2E-01	-0.6	3.7E-01
ENSMUST00000146215				3.6	7.7E-04	5.7	5.7E-03	-0.8	6.6E-01	1.5	1.4E-01
ENSMUST00000127089				3.6	1.7E-03	6.4	3.0E-04	-0.1	9.3E-01	-1.0	1.7E-01
ENSMUST00000182301				0.1	8.6E-01	2.3	4.2E-02	1.1	2.0E-01	-1.0	2.3E-01
ENSMUST00000162369				3.6	2.0E-04	3.0	2.2E-02	-2.3	7.2E-02	-0.2	8.2E-01
ENSMUST00000150322				3.6	2.8E-02	-8.8	4.3E-03	-1.8	3.3E-02	-0.9	7.3E-01
ENSMUST00000182314	dystonin [Source:MGI Symbol;Acc:MGI:104627]	A0A0A6YXR1		5.7	1.2E-01	5.7	9.1E-02	-3.0	4.3E-01	-3.0	1.7E-01
ENSMUST00000152432				3.6	1.5E-02	8.1	1.3E-04	-0.3	8.4E-01	-0.2	7.9E-01
ENSMUST00000183152				3.6	2.8E-04	6.2	2.8E-04	-0.5	6.5E-01	-1.5	4.0E-02
ENSMUST00000185275				3.6	4.1E-04	-7.2	1.2E-04	0.3	3.8E-01	1.8	1.5E-01
ENSMUST00000148763				3.6	3.3E-03	3.4	5.1E-02	-0.5	7.3E-01	0.2	8.7E-01
ENSMUST00000183872				3.6	4.5E-04	5.9	3.8E-04	-1.5	2.3E-01	-0.3	6.0E-01
ENSMUST00000121399				3.6	1.3E-02	2.4	3.1E-02	-1.7	1.2E-01	0.2	8.4E-01
ENSMUST00000170754				3.6	1.1E-03	4.6	6.0E-03	-1.3	3.2E-01	-1.2	2.3E-01
ENSMUST00000143534				3.6	9.4E-05	5.1	8.2E-04	-2.5	5.2E-02	0.3	6.7E-01
ENSMUST00000191293				3.6	2.6E-05	6.8	7.5E-04	0.2	8.8E-01	1.0	2.2E-01
ENSMUST00000182355				-0.7	7.5E-01	-0.6	7.7E-01	-1.5	4.3E-01	-1.5	4.8E-01
ENSMUST00000140458				3.6	7.0E-03	7.6	1.8E-05	-1.9	1.0E-01	0.2	6.6E-01
ENSMUST00000151103				3.6	1.7E-02	6.4	2.0E-04	0.7	5.1E-01	0.5	3.9E-01
ENSMUST00000167990				3.6	5.5E-05	6.3	2.2E-03	-0.4	7.8E-01	0.7	4.6E-01
ENSMUST00000141351				3.6	9.2E-03	6.7	1.6E-04	-0.5	6.6E-01	-0.8	2.4E-01
ENSMUST00000133061				3.6	1.3E-03	-8.2	3.8E-03	0.0	9.9E-01	-1.0	6.8E-01
ENSMUST00000182378				-0.6	3.8E-01	-0.2	7.7E-01	-0.2	6.7E-01	-0.6	4.5E-01
ENSMUST00000141873				3.6	1.3E-04	5.2	2.2E-02	-0.8	7.0E-01	1.3	3.0E-01
ENSMUST00000180769				3.6	1.2E-03	5.6	5.8E-04	-0.5	6.7E-01	-0.2	7.1E-01
ENSMUST00000182011				3.6	9.8E-04	6.7	2.5E-02	-0.3	9.1E-01	-1.2	4.2E-01
ENSMUST00000141617				3.6	2.5E-04	6.7	7.9E-04	-0.1	9.4E-01	-0.3	7.3E-01
ENSMUST00000120708				3.6	1.0E-03	-3.5	1.6E-01	0.9	4.1E-01	1.0	6.7E-01
ENSMUST00000182394				0.0	9.9E-01	0.0	9.7E-01	-0.3	7.1E-01	-0.3	8.0E-01
ENSMUST00000154881				3.6	3.3E-04	-5.0	4.8E-02	0.8	3.9E-01	-0.8	7.6E-01
ENSMUST00000182405	K(lysine) acetyltransferase 6B [Source:MGI Symbol;Acc:MGI:1858746]		Q8BRB7	6.4	5.1E-02	2.9	3.2E-01	-4.6	1.6E-01	-1.2	6.1E-01
ENSMUST00000161686				3.6	9.9E-04	8.4	9.9E-03	-1.1	7.1E-01	1.9	1.7E-01
ENSMUST00000182409				4.4	1.0E-01	6.2	6.6E-02	1.4	6.5E-01	-0.4	8.3E-01
ENSMUST00000127249				3.6	2.6E-02	7.4	1.2E-03	0.3	8.6E-01	0.2	8.0E-01
ENSMUST00000171700				3.6	1.0E-03	-3.3	7.9E-02	-0.5	6.1E-01	-0.2	9.0E-01
ENSMUST00000099974				3.6	3.1E-02	6.0	5.6E-04	-0.6	6.6E-01	-0.3	6.3E-01
ENSMUST00000162276				3.6	6.5E-04	8.9	1.3E-05	1.8	1.0E-01	0.1	8.7E-01
ENSMUST00000182428	autophagy related 7 [Source:MGI Symbol;Acc:MGI:1921494]	S4R2T5		-4.6	7.0E-02	-1.4	4.6E-01	-0.4	7.5E-01	-3.6	1.6E-01
ENSMUST00000182432	PDZ and LIM domain 1 (elfin) [Source:MGI Symbol;Acc:MGI:1860611]	S4R1V0		-0.1	9.4E-01	-3.3	5.1E-02	-0.9	3.1E-01	2.3	1.4E-01
ENSMUST00000136582				3.6	7.1E-04	2.8	7.6E-02	1.1	4.2E-01	1.1	2.8E-01
ENSMUST00000153924				3.6	1.0E-04	9.3	5.0E-06	-0.4	7.1E-01	0.4	4.2E-01
ENSMUST00000107842				3.6	4.7E-05	6.6	1.7E-04	0.1	9.6E-01	0.3	6.0E-01
ENSMUST00000141054				3.5	1.1E-03	8.5	8.5E-06	1.1	2.5E-01	-0.1	8.5E-01
ENSMUST00000157036				3.5	2.8E-03	7.5	4.0E-04	-0.7	6.2E-01	0.5	5.3E-01
ENSMUST00000111283				3.5	1.1E-03	4.8	2.4E-05	0.1	8.9E-01	0.4	3.1E-01
ENSMUST00000117384				3.5	2.0E-02	-7.1	3.2E-02	-0.5	6.5E-01	-0.2	9.4E-01
ENSMUST00000182454				2.0	1.6E-01	1.8	2.4E-01	-0.9	4.8E-01	-0.8	5.4E-01
ENSMUST00000134528				3.5	5.5E-04	5.9	6.0E-04	-0.5	7.0E-01	-1.6	4.6E-02
ENSMUST00000137797				3.5	5.0E-03	2.6	3.8E-01	-0.8	7.6E-01	2.9	2.0E-01
ENSMUST00000182463				1.7	4.4E-02	1.5	1.1E-01	-0.2	7.4E-01	0.0	9.5E-01
ENSMUST00000172609				3.5	2.6E-02	5.4	2.2E-04	2.7	1.0E-02	-0.5	3.7E-01
ENSMUST00000140809				3.5	6.4E-05	6.1	1.1E-03	-0.1	9.5E-01	-0.4	6.3E-01
ENSMUST00000130187				3.5	3.5E-03	6.8	1.8E-04	-0.7	5.5E-01	0.1	8.2E-01
ENSMUST00000182479	mast cell immunoglobulin like receptor 1 [Source:MGI Symbol;Acc:MGI:2685731]	S4R1V2		1.4	2.0E-01	-5.9	2.0E-04	-8.2	3.8E-06	-0.9	4.3E-01
ENSMUST00000148819				3.5	2.6E-04	4.1	1.4E-04	-2.2	1.2E-02	0.0	9.9E-01
ENSMUST00000182481	phospholipase C, epsilon 1 [Source:MGI Symbol;Acc:MGI:1921305]		Q8K4S1	3.5	6.8E-02	1.9	3.9E-01	-0.5	8.1E-01	1.1	5.3E-01
ENSMUST00000162204				3.5	2.0E-03	7.1	1.5E-03	-0.7	6.9E-01	-0.4	6.8E-01
ENSMUST00000182484	signal-induced proliferation-associated 1 like 3 [Source:MGI Symbol;Acc:MGI:1921456]	S4R2N4		1.2	5.7E-01	1.9	5.5E-01	1.6	4.8E-01	0.9	7.4E-01
ENSMUST00000182485	cullin 9 [Source:MGI Symbol;Acc:MGI:1925559]	S4R1Y1		0.7	7.9E-01	1.3	6.1E-01	-1.6	4.9E-01	-2.2	3.9E-01
ENSMUST00000100847				3.5	1.2E-04	7.4	7.2E-04	1.5	3.0E-01	0.4	6.1E-01
ENSMUST00000182494				-3.6	4.5E-02	-1.6	4.7E-01	1.3	3.7E-01	-0.7	7.4E-01
ENSMUST00000124467				3.5	2.4E-03	7.6	4.4E-07	0.3	6.0E-01	0.3	3.9E-01
ENSMUST00000182065				3.5	2.5E-04	-8.0	2.7E-05	-0.4	2.9E-01	-1.7	1.7E-01
ENSMUST00000138716				3.5	4.3E-03	-1.6	1.5E-01	0.5	4.3E-01	-0.4	7.3E-01
ENSMUST00000194302				3.5	5.0E-04	3.9	9.0E-02	-2.2	3.5E-01	0.0	9.8E-01
ENSMUST00000122925				3.5	1.3E-03	0.5	8.9E-01	-2.4	4.3E-01	3.8	2.0E-01
ENSMUST00000182515	myeloid zinc finger 1 [Source:MGI Symbol;Acc:MGI:107457]	A1L358		2.2	1.9E-01	6.8	4.8E-03	1.1	5.7E-01	-3.6	1.9E-02
ENSMUST00000148487				3.5	2.2E-02	4.6	1.6E-04	-0.9	2.3E-01	-0.2	6.9E-01
ENSMUST00000170473				3.5	1.3E-03	4.5	3.0E-03	-1.4	2.8E-01	0.2	7.6E-01
ENSMUST00000181223				3.5	2.1E-04	4.1	2.3E-03	-0.1	9.0E-01	0.1	8.4E-01
ENSMUST00000124472				3.5	4.5E-03	3.5	2.1E-02	-0.8	5.1E-01	-0.5	6.4E-01
ENSMUST00000135480				3.5	1.3E-03	5.7	3.7E-04	-1.5	2.1E-01	0.7	2.7E-01
ENSMUST00000179719				3.5	3.8E-04	-6.3	8.4E-04	0.9	7.8E-02	0.1	9.2E-01
ENSMUST00000182538	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent) [Source:MGI Symbol;Acc:MGI:1098272]	Q3T9T6		-0.8	2.9E-01	-1.2	2.5E-01	0.4	5.7E-01	0.8	4.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000129311				3.5	1.4E-04	-3.7	4.6E-02	0.6	4.3E-01	-2.1	2.9E-01
ENSMUST00000182540				-1.3	9.1E-02	-0.8	3.5E-01	-0.5	4.8E-01	-1.0	2.5E-01
ENSMUST00000148941				3.5	1.2E-03	6.2	2.8E-04	-0.5	6.7E-01	-0.7	2.8E-01
ENSMUST00000182559	Rho GTPase activating protein 12 [Source:MGI Symbol;Acc:MGI:1922665]		Q8C0D4	0.4	8.4E-01	-0.9	7.1E-01	-1.3	5.0E-01	0.0	9.9E-01
ENSMUST00000159392				3.5	7.5E-03	6.0	2.2E-04	0.5	6.1E-01	0.3	6.3E-01
ENSMUST00000133056				3.5	2.6E-03	6.3	4.3E-05	-1.1	2.7E-01	-0.8	1.6E-01
ENSMUST00000182565				1.8	6.6E-02	4.7	2.0E-03	0.9	3.8E-01	-2.0	3.5E-02
ENSMUST00000156501				3.5	5.0E-03	7.2	4.9E-05	1.3	2.1E-01	0.2	7.7E-01
ENSMUST00000182573	ATPase type 13A4 [Source:MGI Symbol;Acc:MGI:1924456]	S4R2M1		-2.4	1.0E-01	0.7	5.6E-01	-0.7	5.0E-01	-3.8	1.9E-02
ENSMUST00000182574	bridging integrator 2 [Source:MGI Symbol;Acc:MGI:3611448]	S4R171		1.7	3.5E-01	1.4	5.1E-01	-0.6	7.1E-01	-0.4	8.6E-01
ENSMUST00000162080				3.5	1.4E-02	4.6	2.4E-04	-1.3	1.1E-01	-0.3	5.8E-01
ENSMUST00000182581				0.5	4.2E-01	1.4	9.0E-02	-0.3	6.2E-01	-1.2	1.1E-01
ENSMUST00000139925				3.5	1.0E-03	5.1	6.9E-04	-1.1	3.1E-01	0.9	1.7E-01
ENSMUST00000142269				3.5	2.9E-04	-6.1	1.6E-03	-0.8	1.4E-01	-0.9	5.7E-01
ENSMUST00000182588				2.6	3.1E-01	4.9	1.1E-01	0.1	9.7E-01	-2.1	2.8E-01
ENSMUST00000140933				3.5	1.3E-03	7.5	8.9E-05	-0.5	6.8E-01	-0.6	3.4E-01
ENSMUST00000182593	proline-rich coiled-coil 2C [Source:MGI Symbol;Acc:MGI:1913754]	S4R2J9		-2.3	1.1E-01	0.3	8.3E-01	0.1	9.2E-01	-2.5	1.3E-01
ENSMUST00000156658				3.5	3.5E-05	-2.6	3.4E-01	1.9	1.9E-01	-0.5	8.5E-01
ENSMUST00000182603	zinc finger protein 229 [Source:MGI Symbol;Acc:MGI:2679295]	E9PWT2		2.4	3.1E-01	5.7	6.5E-02	0.0	9.9E-01	-3.2	1.3E-01
ENSMUST00000028406				3.5	6.2E-04	2.5	1.7E-02	-0.4	6.1E-01	-0.5	5.3E-01
ENSMUST00000142743				3.5	7.2E-03	8.2	2.5E-04	2.1	1.5E-01	-1.1	1.2E-01
ENSMUST00000129310				3.5	3.3E-04	5.6	2.1E-04	-2.3	5.5E-02	-0.7	2.7E-01
ENSMUST00000165664				3.5	3.6E-04	5.1	1.9E-03	-1.3	3.3E-01	-1.2	1.5E-01
ENSMUST00000180856				3.5	2.9E-04	5.0	1.8E-04	0.5	5.1E-01	-0.1	9.0E-01
ENSMUST00000193412				3.5	1.1E-03	3.0	2.5E-03	-0.8	2.7E-01	-0.4	4.8E-01
ENSMUST00000182634	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Source:MGI Symbol;Acc:MGI:95653]	S4R2G5		2.1	2.3E-01	1.7	5.3E-01	0.8	7.3E-01	1.1	5.8E-01
ENSMUST00000134325				3.5	2.7E-04	6.1	1.3E-03	-1.7	2.7E-01	0.6	4.2E-01
ENSMUST00000182646				-0.5	6.5E-01	-0.1	9.2E-01	0.4	7.3E-01	0.0	1.0E+00
ENSMUST00000147930				3.5	2.7E-05	6.0	7.4E-02	-0.8	8.1E-01	1.1	5.3E-01
ENSMUST00000156906				3.5	3.4E-03	5.2	8.8E-04	0.0	9.7E-01	-0.6	4.3E-01
ENSMUST00000182659	RNA binding motif protein 5 [Source:MGI Symbol;Acc:MGI:1933204]		Q91YE7	0.5	8.3E-01	2.6	5.3E-01	4.1	2.1E-01	1.9	5.5E-01
ENSMUST00000182660	proline-rich coiled-coil 2C [Source:MGI Symbol;Acc:MGI:1913754]		Q3TLH4	0.9	7.5E-01	4.6	3.0E-01	3.6	3.7E-01	-0.1	9.7E-01
ENSMUST00000133840				3.5	1.1E-02	2.9	3.0E-03	-0.1	8.8E-01	-1.4	4.7E-02
ENSMUST00000182662				3.2	2.3E-01	3.1	2.9E-01	-0.3	9.1E-01	-0.2	9.2E-01
ENSMUST00000134790				3.5	2.2E-02	-5.9	8.6E-05	0.0	9.8E-01	-1.0	3.6E-01
ENSMUST00000148985				3.5	8.7E-03	6.6	1.1E-04	-4.3	5.6E-03	-0.3	5.8E-01
ENSMUST00000143998				3.5	1.5E-02	7.2	4.0E-04	1.0	4.6E-01	-0.7	3.2E-01
ENSMUST00000182675	in-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 [Source:MGI Symbol;Acc:MGI:2441	S4R1A9		-1.1	3.7E-01	-1.7	3.2E-01	-0.6	5.1E-01	-0.1	9.5E-01
ENSMUST00000138224				3.5	2.4E-02	5.5	8.6E-04	-0.6	6.4E-01	0.1	9.1E-01
ENSMUST00000182682				2.0	5.9E-02	3.3	2.8E-02	0.3	8.0E-01	-1.0	2.7E-01
ENSMUST00000182685	protein kinase, cGMP-dependent, type I [Source:MGI Symbol;Acc:MGI:108174]	Q8BQ38		4.4	6.8E-02	5.7	4.1E-02	-0.3	9.0E-01	-1.6	2.9E-01
ENSMUST00000190926				3.5	2.1E-02	6.6	9.9E-05	-0.5	6.2E-01	-1.1	7.5E-02
ENSMUST00000182697	dystonin [Source:MGI Symbol;Acc:MGI:104627]	A0A0A6YX28		8.4	3.8E-02	7.3	8.4E-02	-0.8	8.5E-01	0.2	9.2E-01
ENSMUST00000150105				3.5	2.8E-04	10.1	1.6E-02	-0.9	8.2E-01	-1.7	3.3E-01
ENSMUST00000129945				3.5	3.5E-03	6.4	1.0E-03	-1.0	4.8E-01	0.6	4.4E-01
ENSMUST00000177091				3.5	8.0E-04	-7.2	2.6E-04	0.1	7.8E-01	0.0	9.9E-01
ENSMUST00000182715	transmembrane protein 161A [Source:MGI Symbol;Acc:MGI:2384577]	S4R1Z2		1.5	4.1E-01	3.2	1.4E-01	0.2	9.2E-01	-1.5	3.9E-01
ENSMUST00000025040				3.5	1.4E-03	5.8	5.3E-04	0.9	4.4E-01	-0.3	6.7E-01
ENSMUST00000144384				3.5	6.8E-03	7.1	1.5E-04	-0.6	6.3E-01	-0.2	7.3E-01
ENSMUST00000183251				3.5	7.9E-04	2.7	3.2E-01	-0.6	8.2E-01	2.3	2.2E-01
ENSMUST00000182720				1.9	5.7E-02	2.6	2.5E-02	-0.2	8.1E-01	-1.0	2.7E-01
ENSMUST00000144228				3.5	1.8E-02	-7.2	2.9E-04	0.2	7.0E-01	-0.8	5.9E-01
ENSMUST00000182726				7.8	3.7E-02	5.1	1.5E-01	-1.9	6.1E-01	0.8	7.2E-01
ENSMUST00000184377				3.5	4.9E-04	4.6	1.0E-02	-0.2	8.9E-01	-0.5	5.6E-01
ENSMUST00000151588				3.5	3.9E-04	5.8	3.6E-04	-0.5	6.5E-01	-0.6	3.5E-01
ENSMUST00000139971				3.5	1.2E-03	2.5	2.4E-02	-3.5	5.9E-03	-1.5	9.1E-02
ENSMUST00000126584				3.5	4.7E-03	2.5	2.1E-02	-0.8	3.2E-01	0.5	4.9E-01
ENSMUST00000135715				3.5	1.8E-03	6.6	9.4E-06	-0.2	7.8E-01	0.6	1.9E-01
ENSMUST00000151739				3.5	1.1E-04	6.7	1.5E-04	-0.5	6.5E-01	-0.2	6.8E-01
ENSMUST00000181062				3.5	4.5E-03	6.7	2.2E-03	-0.8	6.7E-01	-0.4	7.0E-01
ENSMUST00000146758				3.5	7.7E-03	-3.9	3.5E-03	-0.4	4.5E-01	1.7	1.1E-01
ENSMUST00000145091				3.5	1.3E-04	2.7	1.3E-02	-1.3	1.4E-01	-1.7	4.9E-02
ENSMUST00000187446				3.5	6.3E-03	-8.1	1.5E-02	0.9	4.1E-01	0.8	7.7E-01
ENSMUST00000023469				3.5	2.1E-03	6.5	1.6E-03	-0.3	8.4E-01	0.2	8.2E-01
ENSMUST00000119442				3.5	1.2E-03	2.2	2.7E-02	-2.7	1.6E-02	-0.9	2.6E-01
ENSMUST00000124847				3.5	2.4E-02	5.7	1.2E-03	-0.6	6.4E-01	-0.3	6.9E-01
ENSMUST00000183265				3.5	8.4E-05	7.2	7.1E-05	-0.6	6.1E-01	-0.5	4.1E-01
ENSMUST00000182775	bridging integrator 2 [Source:MGI Symbol;Acc:MGI:3611448]	S4R2J8		5.5	6.6E-02	0.6	9.1E-01	1.2	7.5E-01	6.1	2.0E-01
ENSMUST00000180394				3.5	4.1E-03	5.9	1.1E-02	-0.8	7.2E-01	-0.9	4.5E-01
ENSMUST00000185697				3.5	3.1E-03	5.6	1.9E-03	-0.6	6.6E-01	-0.7	3.9E-01
ENSMUST00000182790	anoctamin 4 [Source:MGI Symbol;Acc:MGI:2443344]	S4R1L3		3.3	1.8E-01	4.9	7.3E-02	-0.4	8.7E-01	-2.0	2.5E-01
ENSMUST00000145825				3.5	1.0E-03	1.3	2.0E-01	-0.2	7.7E-01	0.4	6.1E-01
ENSMUST00000191345				3.5	1.4E-03	-4.2	9.5E-02	2.0	6.7E-02	-0.6	8.1E-01
ENSMUST00000125527				3.5	8.4E-03	5.6	3.3E-04	2.3	2.9E-02	-0.8	2.4E-01
ENSMUST00000138879				3.5	1.1E-02	4.7	4.3E-04	-1.0	2.8E-01	-0.4	5.3E-01
ENSMUST00000182808	oligonucleotide/oligosaccharide-binding fold containing 1 [Source:MGI Symbol;Acc:MGI:1915581]	Q3UXU8		1.2	2.1E-01	1.1	2.9E-01	-0.4	6.6E-01	-0.3	7.3E-01
ENSMUST00000182813				-1.9	1.0E-01	-0.5	6.7E-01	-0.7	4.6E-01	-2.1	9.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000137872				3.4	1.7E-03	2.1	1.5E-01	-3.6	3.8E-02	-0.5	7.1E-01
ENSMUST00000160287				3.4	5.1E-03	7.4	1.2E-04	-0.6	6.3E-01	-0.5	4.2E-01
ENSMUST00000148313				3.4	2.1E-03	6.3	2.5E-05	-0.4	6.3E-01	0.6	2.1E-01
ENSMUST00000125734				3.4	1.8E-03	5.6	1.1E-04	0.0	9.6E-01	0.8	1.6E-01
ENSMUST00000141862				3.4	2.7E-02	4.9	1.3E-02	-0.6	7.4E-01	0.6	5.5E-01
ENSMUST00000161014				3.4	1.4E-04	5.3	2.1E-03	-0.9	4.8E-01	-0.5	5.1E-01
ENSMUST00000182834	pleckstrin homology domain containing, family A member 7 [Source:MGI Symbol;Acc:MGI:2445094]		Q3UIL6	2.6	1.4E-01	5.1	1.1E-02	-0.6	7.4E-01	-3.1	3.7E-02
ENSMUST00000137465				3.4	5.3E-03	6.2	5.3E-05	0.3	7.5E-01	-0.6	2.4E-01
ENSMUST00000162896				3.4	1.6E-03	5.3	1.2E-04	-0.1	8.8E-01	0.6	2.9E-01
ENSMUST00000182629				3.4	6.4E-04	6.9	5.7E-04	-0.9	5.3E-01	0.7	3.4E-01
ENSMUST00000154633				3.4	3.1E-04	-2.2	3.0E-01	1.4	2.8E-01	-0.5	7.9E-01
ENSMUST00000182855	K(lysine) acetyltransferase 6B [Source:MGI Symbol;Acc:MGI:1858746]		Q8BRB7	0.7	5.3E-01	-1.8	3.3E-01	0.1	9.1E-01	2.7	1.4E-01
ENSMUST00000134221				3.4	1.8E-04	7.5	1.9E-04	-0.7	6.3E-01	-0.2	7.1E-01
ENSMUST00000174400				3.4	8.0E-03	-3.3	4.2E-01	2.8	2.3E-01	-1.6	7.0E-01
ENSMUST00000182869	sterile alpha motif domain containing 15 [Source:MGI Symbol;Acc:MGI:2685109]		F6XZJ7	1.6	5.7E-02	3.8	2.7E-03	1.1	2.0E-01	-1.0	1.8E-01
ENSMUST00000161595				3.4	4.1E-04	-3.5	1.1E-02	-0.2	7.8E-01	-0.1	9.6E-01
ENSMUST00000194253				3.4	1.0E-03	5.4	4.1E-03	-0.6	7.1E-01	0.4	6.8E-01
ENSMUST00000151746				3.4	2.1E-03	-4.1	7.0E-03	-0.1	8.8E-01	0.6	6.5E-01
ENSMUST00000141009				3.4	1.7E-02	3.6	1.2E-02	-2.5	6.4E-02	1.1	2.2E-01
ENSMUST00000137409				3.4	2.2E-02	3.8	3.4E-04	-0.3	6.8E-01	0.1	8.6E-01
ENSMUST00000149886				3.4	1.3E-03	4.9	7.5E-03	-0.4	8.1E-01	-1.4	1.8E-01
ENSMUST00000160911				3.4	1.5E-02	5.7	2.9E-03	-1.9	2.2E-01	-0.3	7.2E-01
ENSMUST00000149686				3.4	5.3E-04	7.2	2.9E-05	-2.0	8.9E-02	-0.8	1.3E-01
ENSMUST00000182886	Sec31 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916412]		Q3UPL0	2.3	2.2E-01	1.9	5.0E-01	1.1	5.5E-01	1.5	5.6E-01
ENSMUST00000160824				3.4	1.6E-03	5.8	4.3E-04	-0.5	6.4E-01	-0.8	2.2E-01
ENSMUST00000182892				-2.2	1.7E-01	0.4	8.2E-01	1.1	4.7E-01	-1.6	4.0E-01
ENSMUST00000182898	anaphase promoting complex subunit 16 [Source:MGI Symbol;Acc:MGI:1289325]		Q9CPV2	-0.4	5.2E-01	-0.7	3.6E-01	-0.3	5.3E-01	0.0	9.9E-01
ENSMUST00000160146				3.4	1.7E-04	-2.8	2.3E-01	1.8	1.7E-01	-0.6	8.0E-01
ENSMUST00000161562				3.4	6.3E-04	6.5	1.2E-04	-0.5	6.2E-01	-0.9	1.6E-01
ENSMUST00000137434				3.4	1.4E-02	2.3	2.4E-02	-0.1	8.9E-01	-0.2	7.6E-01
ENSMUST00000153881				3.4	1.4E-04	6.5	4.9E-04	-0.6	6.4E-01	-0.2	7.8E-01
ENSMUST00000137553				3.4	2.0E-03	3.9	3.5E-03	-0.6	5.0E-01	-1.7	7.4E-02
ENSMUST00000182907	ankyrin repeat and sterile alpha motif domain containing 1B [Source:MGI Symbol;Acc:MGI:1924781]	S4R2E7		5.0	6.7E-02	4.4	1.3E-01	-0.8	7.9E-01	-0.2	9.3E-01
ENSMUST00000185332				3.4	7.6E-04	-6.5	1.3E-03	-0.8	1.4E-01	-1.0	5.4E-01
ENSMUST00000153855				3.4	9.5E-04	7.5	4.9E-05	-0.5	6.4E-01	-1.1	7.2E-02
ENSMUST00000133733				3.4	2.6E-02	5.1	1.3E-04	0.5	4.9E-01	0.1	9.2E-01
ENSMUST00000188708				3.4	1.5E-03	-3.8	5.6E-03	-1.2	5.2E-02	-0.9	4.3E-01
ENSMUST00000152510				3.4	1.6E-03	5.2	1.9E-02	-1.6	4.3E-01	-1.4	2.8E-01
ENSMUST00000157037				3.4	3.6E-04	7.1	4.2E-04	0.3	8.4E-01	-0.3	6.2E-01
ENSMUST00000182917				0.7	4.0E-01	-0.7	4.6E-01	-1.3	1.2E-01	0.1	8.9E-01
ENSMUST00000173267				3.4	4.1E-04	5.6	4.3E-03	-0.7	6.7E-01	-0.3	7.5E-01
ENSMUST00000091090				3.4	1.6E-03	4.4	1.0E-02	-1.1	4.5E-01	-1.5	1.9E-01
ENSMUST00000141051				3.4	2.1E-03	5.7	6.8E-04	-0.6	6.4E-01	-3.0	5.8E-03
ENSMUST00000182944	baculoviral IAP repeat-containing 6 [Source:MGI Symbol;Acc:MGI:1276108]	S4R2P8		-3.2	1.6E-01	-2.7	3.1E-01	-0.6	6.5E-01	-1.1	7.1E-01
ENSMUST00000146352				3.4	2.7E-04	6.0	8.5E-04	-0.6	6.5E-01	0.2	7.7E-01
ENSMUST00000182948				-3.1	2.4E-01	-3.8	2.2E-01	-1.6	3.3E-01	-0.9	7.9E-01
ENSMUST00000182951	scaffold attachment factor B [Source:MGI Symbol;Acc:MGI:2146974]	S4R1W0		-1.2	6.4E-01	2.5	3.5E-01	0.3	9.0E-01	-3.5	1.8E-01
ENSMUST00000146802				3.4	1.4E-02	3.4	1.1E-03	-0.2	7.4E-01	-1.3	5.8E-02
ENSMUST00000193024				3.4	3.7E-03	-3.7	1.1E-02	3.1	6.5E-04	-1.2	3.6E-01
ENSMUST00000131496				3.4	1.1E-03	-1.3	3.6E-01	0.4	6.8E-01	-1.7	3.0E-01
ENSMUST00000155193				3.4	1.6E-02	6.1	6.6E-04	-0.8	5.3E-01	0.4	6.4E-01
ENSMUST00000138450				3.4	1.0E-02	2.4	2.5E-02	-0.3	6.9E-01	0.3	7.0E-01
ENSMUST00000182964	K(lysine) acetyltransferase 6B [Source:MGI Symbol;Acc:MGI:1858746]		Q8BRB7	-0.8	5.3E-01	3.5	1.6E-01	5.5	1.1E-02	1.1	5.6E-01
ENSMUST00000145901				3.4	9.8E-04	1.2	2.1E-01	-0.9	2.2E-01	0.5	5.6E-01
ENSMUST00000059704				3.4	3.1E-04	2.1	1.6E-02	-0.1	8.8E-01	-0.6	3.6E-01
ENSMUST00000162909				3.4	1.8E-02	-4.7	1.0E-02	0.2	7.5E-01	0.3	8.5E-01
ENSMUST00000182982				1.8	2.7E-01	6.4	1.8E-02	3.2	1.7E-01	-1.5	3.1E-01
ENSMUST00000182985				-0.6	5.3E-01	-0.3	7.8E-01	-0.6	4.2E-01	-1.0	4.0E-01
ENSMUST00000182988	Sec31 homolog A (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916412]	S4R2A9		0.5	4.0E-01	-2.3	6.4E-02	0.1	8.6E-01	2.9	2.0E-02
ENSMUST00000156890				3.4	2.2E-03	0.4	8.1E-01	-2.8	8.9E-02	0.8	5.8E-01
ENSMUST00000194914				3.4	2.5E-04	4.2	8.3E-04	-2.9	1.4E-02	-0.3	6.6E-01
ENSMUST00000182996	K(lysine) acetyltransferase 6B [Source:MGI Symbol;Acc:MGI:1858746]	S4R2Q8		3.0	2.2E-01	3.6	1.9E-01	-0.5	8.7E-01	-1.0	6.0E-01
ENSMUST00000135910				3.4	1.2E-03	5.9	2.0E-04	-1.3	2.6E-01	-1.1	8.6E-02
ENSMUST00000183008				1.5	4.3E-01	1.8	3.4E-01	-1.7	3.3E-01	-2.1	2.4E-01
ENSMUST00000159802				3.4	4.3E-03	6.2	2.6E-04	-0.5	6.6E-01	-0.3	6.2E-01
ENSMUST00000071115				3.4	6.6E-03	-3.8	3.5E-03	-0.9	7.6E-02	-1.2	2.8E-01
ENSMUST00000130932				3.4	1.3E-03	7.4	9.6E-04	0.3	8.4E-01	0.7	3.9E-01
ENSMUST00000141881				3.4	4.1E-03	8.4	5.4E-05	0.5	6.8E-01	-0.9	1.5E-01
ENSMUST00000046188				3.4	1.7E-03	-6.8	2.3E-03	0.2	7.1E-01	-0.8	6.6E-01
ENSMUST00000183034	dystonin [Source:MGI Symbol;Acc:MGI:104627]	S4R1P5		7.1	1.2E-01	4.4	2.2E-01	-5.4	2.4E-01	-2.7	2.7E-01
ENSMUST00000134711				3.4	3.9E-03	-5.9	9.6E-04	-0.2	7.2E-01	-1.5	2.8E-01
ENSMUST00000183038	coiled-coil serine rich 2 [Source:MGI Symbol;Acc:MGI:101859]			0.0	9.8E-01	-2.9	3.3E-01	-1.7	3.0E-01	1.1	7.1E-01
ENSMUST00000138549				3.4	5.0E-04	-2.7	1.8E-02	0.3	5.7E-01	-1.1	3.1E-01
ENSMUST00000130287				3.4	5.0E-04	-7.4	7.8E-04	0.2	6.4E-01	-0.6	7.3E-01
ENSMUST00000138116				3.4	2.8E-03	-0.9	6.6E-01	-4.8	2.7E-02	0.8	6.8E-01
ENSMUST00000138635				3.4	2.8E-03	7.0	1.9E-05	-0.2	8.5E-01	0.3	5.6E-01
ENSMUST00000155105				3.4	2.8E-04	2.6	4.3E-03	-1.0	1.3E-01	-0.5	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000186731				3.3	2.7E-04	5.2	9.4E-04	-1.2	3.3E-01	-0.5	4.8E-01
ENSMUST00000150835				3.3	8.9E-03	6.7	1.4E-04	-0.5	6.7E-01	-1.4	4.3E-02
ENSMUST00000135399				3.3	9.2E-04	2.4	7.4E-03	0.3	6.7E-01	-0.1	8.2E-01
ENSMUST00000183073	REX1, RNA exonuclease 1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1914182]	S4R1Q7		0.1	9.2E-01	0.5	7.0E-01	0.3	7.8E-01	-0.1	9.2E-01
ENSMUST00000183090				-2.3	5.2E-01	-1.8	6.9E-01	-0.6	8.6E-01	-1.1	7.9E-01
ENSMUST00000183091	CUGBP, Elav-like family member 2 [Source:MGI Symbol;Acc:MGI:1338822]	S4R2U7		-0.3	9.0E-01	-3.5	2.7E-01	-3.4	7.2E-02	-0.2	9.5E-01
ENSMUST00000183096	signal-induced proliferation-associated 1 like 3 [Source:MGI Symbol;Acc:MGI:1921456]	G3X9J0		-1.3	8.8E-02	0.2	8.6E-01	1.1	1.1E-01	-0.3	7.0E-01
ENSMUST00000189121				3.3	2.5E-02	3.1	4.7E-04	-0.8	1.6E-01	0.4	4.2E-01
ENSMUST00000139548				3.3	6.7E-03	4.6	5.5E-03	-2.4	1.3E-01	-1.0	3.0E-01
ENSMUST00000150027				3.3	3.5E-03	7.2	2.9E-05	0.8	3.8E-01	0.3	4.4E-01
ENSMUST00000136275				3.3	3.5E-04	4.0	6.6E-04	0.9	2.3E-01	-0.4	4.9E-01
ENSMUST00000126485				3.3	5.4E-03	6.1	3.3E-04	-0.6	6.2E-01	0.1	8.2E-01
ENSMUST00000142650				3.3	1.0E-02	4.6	1.1E-04	0.4	5.6E-01	0.2	6.2E-01
ENSMUST00000126345				3.3	1.9E-03	4.2	2.2E-03	-1.2	2.3E-01	0.2	7.5E-01
ENSMUST00000183125	zinc finger protein 386 (Kruppel-like) [Source:MGI Symbol;Acc:MGI:1930708]	Q1WWJ5		0.7	2.7E-01	0.3	7.1E-01	-0.3	5.6E-01	0.1	9.3E-01
ENSMUST00000127155				3.3	5.0E-03	3.1	2.3E-03	-0.7	3.0E-01	-1.7	2.5E-02
ENSMUST00000195870				3.3	5.6E-04	6.5	1.1E-04	-0.5	6.3E-01	0.3	6.1E-01
ENSMUST00000195839				3.3	1.2E-03	7.4	6.0E-04	1.8	2.2E-01	0.7	3.3E-01
ENSMUST00000124349				3.3	5.2E-03	5.5	3.5E-04	1.3	1.8E-01	0.1	9.2E-01
ENSMUST00000148516				3.3	3.2E-03	-4.2	1.3E-03	-0.3	5.4E-01	-0.1	8.9E-01
ENSMUST00000183147	arginine/serine-rich coiled-coil 2 [Source:MGI Symbol;Acc:MGI:1913489]	S4R254		-0.6	8.2E-01	-6.0	7.7E-02	-6.0	7.4E-03	-0.7	8.5E-01
ENSMUST00000166839				3.3	1.1E-04	3.3	1.5E-03	-0.3	7.1E-01	0.0	9.9E-01
ENSMUST00000159247				3.3	5.8E-03	4.6	2.7E-03	-1.0	3.4E-01	0.8	3.4E-01
ENSMUST00000183154	RNA binding motif protein 25 [Source:MGI Symbol;Acc:MGI:1914289]	S4R2J4		-0.8	4.7E-01	-2.2	1.3E-01	-0.9	2.6E-01	0.5	7.5E-01
ENSMUST00000194779				3.3	2.2E-03	6.7	2.9E-06	0.2	7.7E-01	0.7	9.2E-02
ENSMUST00000132962				3.3	4.6E-03	4.9	1.3E-02	0.3	8.6E-01	0.4	7.0E-01
ENSMUST00000087699				3.3	3.8E-04	6.8	9.2E-05	-0.9	4.4E-01	-0.5	3.9E-01
ENSMUST00000161309				3.3	1.2E-02	5.1	1.1E-04	0.1	9.0E-01	-0.2	6.7E-01
ENSMUST00000183164				1.9	8.3E-02	2.9	6.4E-02	0.7	6.1E-01	-0.3	7.8E-01
ENSMUST00000123964				3.3	1.8E-02	5.7	7.7E-03	-1.5	4.1E-01	1.2	3.0E-01
ENSMUST00000139580				3.3	3.0E-03	5.6	8.7E-06	0.4	5.0E-01	0.1	7.2E-01
ENSMUST00000130666				3.3	1.9E-03	-4.0	8.6E-02	1.1	2.6E-01	0.6	7.8E-01
ENSMUST00000144639				3.3	2.9E-02	7.0	1.2E-04	-0.1	9.1E-01	0.4	4.8E-01
ENSMUST00000174061				3.3	1.8E-02	5.1	3.3E-03	0.2	8.7E-01	-1.1	2.0E-01
ENSMUST00000139700				3.3	1.9E-03	4.3	5.1E-03	-1.0	3.9E-01	0.9	2.5E-01
ENSMUST00000138662				3.3	2.8E-03	7.1	1.6E-04	-0.5	7.0E-01	-0.8	2.4E-01
ENSMUST00000143487				3.3	2.8E-03	6.1	1.1E-04	-1.2	2.2E-01	0.5	3.7E-01
ENSMUST00000183193				-2.8	5.4E-02	-1.2	4.5E-01	0.5	6.8E-01	-1.1	4.8E-01
ENSMUST00000149802				3.3	1.2E-04	5.7	6.2E-04	-0.6	6.0E-01	1.0	1.5E-01
ENSMUST00000183201				5.7	3.8E-02	5.4	6.9E-02	-0.7	8.2E-01	-0.4	8.3E-01
ENSMUST00000156858				3.3	2.9E-02	4.8	8.9E-05	-2.2	1.5E-02	-0.6	2.7E-01
ENSMUST00000183204				-2.3	3.7E-01	-1.1	6.2E-01	-1.3	4.6E-01	-2.5	3.4E-01
ENSMUST00000151292				3.3	2.6E-02	-5.1	6.0E-03	1.3	8.2E-02	-4.2	6.7E-02
ENSMUST00000141266				3.3	3.5E-03	5.8	2.9E-02	-0.8	7.3E-01	1.9	1.7E-01
ENSMUST00000154951				3.3	3.4E-04	2.3	1.6E-01	5.3	1.8E-03	-2.7	6.6E-02
ENSMUST00000183224	baculoviral IAP repeat-containing 6 [Source:MGI Symbol;Acc:MGI:1276108]	S4R1L5		-2.6	1.4E-01	-0.4	8.4E-01	0.9	5.1E-01	-1.2	5.7E-01
ENSMUST00000188037				3.3	1.2E-03	4.8	1.0E-03	0.3	7.8E-01	-0.6	3.9E-01
ENSMUST00000183233				-0.1	9.7E-01	1.8	5.8E-01	1.7	4.5E-01	-0.2	9.4E-01
ENSMUST00000134518				3.3	7.4E-04	7.3	4.8E-05	-0.5	6.2E-01	-0.7	2.3E-01
ENSMUST00000139485				3.3	3.4E-03	-7.4	3.5E-04	-0.4	4.0E-01	-0.7	6.2E-01
ENSMUST00000143418				3.3	1.0E-02	-4.0	2.4E-02	0.1	9.1E-01	0.2	9.0E-01
ENSMUST00000183250				1.2	1.7E-01	1.8	8.6E-02	-0.1	8.8E-01	-0.8	3.7E-01
ENSMUST00000135487				3.3	2.9E-04	3.6	1.6E-03	-0.3	7.0E-01	-0.4	5.5E-01
ENSMUST00000166997				3.3	8.1E-05	1.4	6.6E-02	-1.5	3.7E-02	-0.6	3.4E-01
ENSMUST00000183255	olute carrier family 22 (organic anion/cation transporter), member 15 [Source:MGI Symbol;Acc:MGI:3607704	S4R1S9		0.2	8.5E-01	1.2	2.7E-01	0.8	3.7E-01	-0.3	7.8E-01
ENSMUST00000183256	cyclin D3 [Source:MGI Symbol;Acc:MGI:88315]	S4R275		-1.2	4.8E-01	0.7	7.2E-01	0.8	6.0E-01	-1.1	5.8E-01
ENSMUST00000190857				3.3	1.7E-03	4.9	5.8E-03	-0.9	5.6E-01	-0.8	3.7E-01
ENSMUST00000160447				3.3	3.8E-03	4.0	2.1E-04	0.9	1.8E-01	0.3	5.4E-01
ENSMUST00000183267	synaptotagmin XI [Source:MGI Symbol;Acc:MGI:1859547]	S4R1M8		1.2	5.2E-01	-2.2	4.3E-01	-2.0	2.3E-01	1.4	6.1E-01
ENSMUST00000141328				3.3	1.3E-02	4.0	4.5E-03	-1.0	3.2E-01	0.3	7.4E-01
ENSMUST00000147085				3.3	1.1E-02	-3.5	1.9E-03	0.3	4.5E-01	-1.0	2.9E-01
ENSMUST00000148884				3.3	1.3E-03	3.8	1.6E-02	-0.2	8.8E-01	2.5	2.3E-02
ENSMUST00000153380				3.3	9.9E-03	-2.7	8.9E-02	-0.2	8.4E-01	0.1	9.4E-01
ENSMUST00000183277	son of sevenless homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:98355]		Q02384	-1.1	4.9E-02	-0.9	2.1E-01	0.6	2.0E-01	0.4	5.9E-01
ENSMUST00000145325				3.3	2.6E-03	6.2	6.4E-05	-1.7	1.0E-01	0.7	1.9E-01
ENSMUST00000195316				3.3	2.5E-03	6.6	1.9E-03	-0.7	6.8E-01	0.8	3.7E-01
ENSMUST00000183291	2'-5' oligoadenylate synthetase 1B [Source:MGI Symbol;Acc:MGI:97430]			2.2	2.0E-01	-1.0	6.7E-01	-0.3	8.3E-01	2.9	2.2E-01
ENSMUST00000140350				3.3	3.5E-04	-5.8	2.0E-04	-1.2	1.9E-02	-3.2	3.3E-02
ENSMUST00000124944				3.3	3.5E-03	8.2	7.1E-05	-0.4	7.5E-01	-0.9	1.5E-01
ENSMUST00000183305				0.3	7.8E-01	2.8	4.8E-02	-0.6	6.0E-01	-3.1	2.4E-02
ENSMUST00000154432				3.3	1.4E-03	-1.5	1.7E-01	0.7	2.8E-01	0.0	1.0E+00
ENSMUST00000124390				3.3	1.9E-02	6.5	9.0E-05	-1.9	1.2E-01	0.3	6.2E-01
ENSMUST00000152329				3.3	1.4E-02	-1.5	1.4E-01	-0.3	6.2E-01	-1.7	1.4E-01
ENSMUST00000120200				3.3	9.0E-03	4.7	5.7E-04	-0.3	7.1E-01	0.1	8.4E-01
ENSMUST00000128015				3.3	7.8E-03	7.8	9.7E-06	-1.7	1.0E-01	0.2	6.4E-01
ENSMUST00000132956				3.3	1.2E-02	-4.4	8.2E-03	1.0	1.2E-01	1.2	3.8E-01
ENSMUST00000183330	signal-induced proliferation-associated 1 like 3 [Source:MGI Symbol;Acc:MGI:1921456]	S4R1S0		-0.8	4.6E-01	1.5	2.7E-01	1.0	3.7E-01	-1.3	2.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000173909				3.3	3.3E-02	2.3	9.3E-03	0.2	7.7E-01	-0.4	5.1E-01
ENSMUST00000148156				3.3	1.3E-03	5.9	1.4E-04	-0.7	4.8E-01	0.1	8.9E-01
ENSMUST00000153621				3.3	4.2E-03	6.6	1.4E-04	-0.5	6.3E-01	0.2	7.0E-01
ENSMUST00000183352	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]		Q6PDM2	-1.9	5.3E-02	-2.0	1.4E-01	0.7	4.0E-01	0.8	5.1E-01
ENSMUST00000137289				3.3	5.1E-03	5.4	1.3E-03	-1.2	3.7E-01	0.3	7.0E-01
ENSMUST00000183355				1.3	1.8E-01	2.7	4.1E-02	0.7	4.8E-01	-0.7	5.1E-01
ENSMUST00000129185				3.3	5.1E-03	7.1	1.0E-02	-0.8	7.4E-01	-1.5	2.6E-01
ENSMUST00000132675				3.3	5.0E-03	5.5	6.1E-04	-0.6	6.3E-01	0.7	2.5E-01
ENSMUST00000162238				3.3	7.6E-03	4.1	3.0E-03	0.0	9.6E-01	1.5	6.5E-02
ENSMUST00000156853				3.3	7.9E-03	7.9	7.9E-06	0.4	6.2E-01	-0.6	1.5E-01
ENSMUST00000147123				3.3	1.9E-03	3.2	3.2E-02	-1.5	2.9E-01	0.3	7.4E-01
ENSMUST00000135319				3.3	2.4E-02	-4.6	1.3E-02	-0.2	7.7E-01	1.2	4.4E-01
ENSMUST00000135758				3.3	1.6E-02	6.3	6.0E-04	-0.6	6.3E-01	-0.7	3.3E-01
ENSMUST00000132215				3.3	1.2E-03	4.5	1.4E-03	-1.1	2.9E-01	-1.0	2.1E-01
ENSMUST00000146699				3.3	3.6E-03	-3.6	5.5E-02	0.5	5.0E-01	0.1	9.5E-01
ENSMUST00000187494				3.3	7.7E-03	3.8	9.5E-04	-0.3	7.0E-01	0.1	8.1E-01
ENSMUST00000177123				3.3	3.9E-04	7.9	1.9E-02	-0.7	8.4E-01	-1.8	2.7E-01
ENSMUST00000155734				3.2	9.7E-03	2.2	1.2E-01	-1.7	2.0E-01	0.0	1.0E+00
ENSMUST00000087655				3.2	8.6E-04	-1.7	4.2E-02	0.0	9.5E-01	-0.1	8.7E-01
ENSMUST00000148520				3.2	5.7E-03	6.0	2.1E-02	-0.5	8.2E-01	-0.9	5.3E-01
ENSMUST00000187522				3.2	7.2E-03	4.9	4.0E-03	-0.8	5.5E-01	0.6	5.3E-01
ENSMUST00000171169				3.2	7.1E-04	4.9	1.0E-02	-0.4	8.2E-01	0.0	9.9E-01
ENSMUST00000182931				3.2	2.0E-02	5.5	5.4E-05	-1.2	1.6E-01	-0.2	7.4E-01
ENSMUST00000183437	family with sequence similarity 83, member B [Source:MGI Symbol;Acc:MGI:2685362]		Q0VBM2	2.6	1.0E-01	5.7	3.0E-03	-0.5	7.5E-01	-3.5	1.0E-02
ENSMUST00000147287				3.2	1.6E-03	5.9	2.6E-04	0.5	6.5E-01	-0.2	7.8E-01
ENSMUST00000183448	cyclin D binding myb-like transcription factor 1 [Source:MGI Symbol;Acc:MGI:1344415]		Q8CE22	1.0	6.5E-01	-2.6	3.6E-01	-3.4	8.4E-02	0.1	9.6E-01
ENSMUST00000162437				3.2	1.3E-03	-1.9	8.5E-02	0.9	1.2E-01	-1.9	1.1E-01
ENSMUST00000139504				3.2	3.3E-02	7.2	3.5E-03	-0.1	9.7E-01	0.0	9.8E-01
ENSMUST00000121815				3.2	4.5E-03	-5.7	2.4E-02	0.7	3.9E-01	1.3	5.5E-01
ENSMUST00000149096				3.2	1.1E-03	4.2	1.8E-02	0.7	6.3E-01	-0.5	6.7E-01
ENSMUST00000084599				3.2	1.6E-03	3.3	3.5E-03	-0.8	3.0E-01	0.2	7.3E-01
ENSMUST00000134839				3.2	3.3E-03	-1.0	3.9E-01	-5.9	1.3E-03	-1.0	3.2E-01
ENSMUST00000186670				3.2	3.6E-03	6.1	2.2E-04	0.8	4.5E-01	0.6	3.4E-01
ENSMUST00000183489	predicted gene, 28040 [Source:MGI Symbol;Acc:MGI:5547776]		Q9DCQ3	2.0	8.9E-02	5.1	5.6E-04	-1.3	2.5E-01	-4.4	4.7E-04
ENSMUST00000137009				3.2	2.8E-04	4.7	3.8E-04	-1.2	1.8E-01	-0.1	9.2E-01
ENSMUST00000145776				3.2	2.4E-04	-6.2	4.6E-04	0.1	8.9E-01	-0.8	5.3E-01
ENSMUST00000183516				-1.3	1.1E-01	-2.7	6.3E-02	-0.1	8.4E-01	1.2	3.3E-01
ENSMUST00000130772				3.2	3.6E-03	-2.7	2.4E-02	1.0	7.9E-02	-2.2	8.4E-02
ENSMUST00000137953				3.2	5.3E-03	6.3	8.6E-04	-0.7	6.5E-01	-0.8	3.3E-01
ENSMUST00000138752				3.2	1.1E-02	-4.2	2.4E-03	-2.7	3.0E-03	-2.4	9.2E-02
ENSMUST00000147582				3.2	5.3E-04	6.6	1.6E-04	-1.4	2.7E-01	0.0	9.4E-01
ENSMUST00000172776				3.2	1.9E-03	6.5	3.7E-03	-1.5	4.1E-01	0.7	4.5E-01
ENSMUST00000136545				3.2	5.7E-03	6.6	3.4E-04	-0.4	7.3E-01	-0.9	1.9E-01
ENSMUST00000138721				3.2	4.1E-03	4.9	9.4E-04	-1.3	2.5E-01	-0.1	8.5E-01
ENSMUST00000110828				3.2	4.9E-04	9.1	1.7E-05	2.2	6.6E-02	-0.3	5.1E-01
ENSMUST00000051080				3.2	2.8E-02	-1.1	3.7E-01	1.0	2.7E-01	-1.4	2.9E-01
ENSMUST00000120260				3.2	4.4E-03	5.1	8.3E-04	-1.4	2.0E-01	0.1	8.5E-01
ENSMUST00000183607				-1.7	1.7E-01	-0.2	8.4E-01	-0.9	2.8E-01	-2.4	7.2E-02
ENSMUST00000136982				3.2	2.1E-04	7.3	2.4E-05	-3.4	2.2E-02	1.1	4.6E-02
ENSMUST00000183610	platelet/endothelial cell adhesion molecule 1 [Source:MGI Symbol;Acc:MGI:97537]		Q08481	0.2	9.5E-01	-4.2	2.1E-01	-3.3	9.9E-02	1.0	7.5E-01
ENSMUST00000125797				3.2	3.3E-04	6.9	3.4E-05	-1.5	1.9E-01	-0.7	2.0E-01
ENSMUST00000130335				3.2	2.3E-03	0.7	3.2E-01	-1.2	6.2E-02	-0.1	8.6E-01
ENSMUST00000147255				3.2	6.1E-04	6.2	1.1E-02	-0.7	7.5E-01	-1.9	1.6E-01
ENSMUST00000153699				3.2	6.4E-03	-4.7	1.2E-03	-0.1	7.5E-01	-0.3	7.9E-01
ENSMUST00000129298				3.2	4.8E-04	6.0	6.3E-04	-0.5	7.2E-01	0.2	7.6E-01
ENSMUST00000170750				3.2	1.8E-03	7.1	2.5E-04	-0.6	6.5E-01	-0.1	8.8E-01
ENSMUST00000183663	interleukin 6 signal transducer [Source:MGI Symbol;Acc:MGI:96560]		Q00560	0.5	3.0E-01	1.5	3.2E-02	0.9	9.9E-02	-0.1	7.8E-01
ENSMUST00000160005				3.2	2.7E-03	4.7	3.8E-04	-0.6	4.6E-01	0.0	9.4E-01
ENSMUST00000156512				3.2	9.6E-04	5.1	2.1E-03	0.4	7.6E-01	-0.4	6.3E-01
ENSMUST00000138895				3.2	2.7E-02	8.4	6.0E-03	2.5	2.8E-01	0.5	6.4E-01
ENSMUST00000126026				3.2	7.9E-03	5.4	8.0E-04	-2.0	1.2E-01	0.8	2.7E-01
ENSMUST00000183703	ELKS/RAB6-interacting/CAST family member 1 [Source:MGI Symbol;Acc:MGI:2151013]	F8VPM7		2.9	3.4E-01	3.0	3.8E-01	-1.3	6.8E-01	-1.4	6.1E-01
ENSMUST00000146984				3.2	7.5E-03	7.0	1.6E-04	-0.6	6.0E-01	-0.2	7.7E-01
ENSMUST00000129632				3.2	2.4E-04	5.4	5.7E-03	0.3	8.5E-01	-0.7	4.5E-01
ENSMUST00000132080				3.2	6.7E-04	5.3	4.4E-03	0.2	8.7E-01	-0.8	3.5E-01
ENSMUST00000136816				3.2	5.8E-04	3.2	5.2E-02	-2.4	1.4E-01	0.7	4.7E-01
ENSMUST00000183733	copine I [Source:MGI Symbol;Acc:MGI:2386621]	V9GXM6		-3.1	1.3E-01	-3.6	1.6E-01	-0.9	4.5E-01	-0.3	9.0E-01
ENSMUST00000098929				3.2	1.4E-03	5.9	6.4E-03	0.3	8.6E-01	-0.6	5.7E-01
ENSMUST00000125453				3.2	2.0E-03	4.5	6.3E-03	-0.9	4.8E-01	0.4	6.5E-01
ENSMUST00000141226				3.2	3.3E-04	-3.1	1.6E-02	0.7	2.3E-01	-1.2	3.3E-01
ENSMUST00000183746	phosphatidylinositol glycan anchor biosynthesis, class B [Source:MGI Symbol;Acc:MGI:1891825]		Q9JJQ0	0.5	3.3E-01	-0.3	6.2E-01	-0.9	6.9E-02	-0.1	8.4E-01
ENSMUST00000155740				3.2	5.6E-04	4.8	1.8E-02	-1.4	4.5E-01	0.6	6.0E-01
ENSMUST00000188576				3.2	2.5E-02	5.4	1.5E-03	0.6	6.3E-01	-1.0	2.0E-01
ENSMUST00000183767	Friend leukemia integration 1 [Source:MGI Symbol;Acc:MGI:95554]	V9GX50		2.7	1.7E-01	-1.0	6.2E-01	-3.5	6.5E-02	0.3	8.9E-01
ENSMUST00000163135				3.2	1.0E-02	-2.8	5.4E-02	0.3	6.7E-01	-0.7	6.2E-01
ENSMUST00000125432				3.2	1.3E-03	5.3	2.7E-02	-0.8	7.2E-01	0.6	6.4E-01
ENSMUST00000183792				-0.2	8.2E-01	-0.8	5.8E-01	-0.1	9.1E-01	0.4	7.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000183827	pre B cell leukemia homeobox 2 [Source:MGI Symbol;Acc:MGI:1341793]	V9GXB8		0.8	6.8E-01	0.7	7.8E-01	-0.4	8.4E-01	-0.3	9.1E-01
ENSMUST00000183830	zinc finger protein 335 [Source:MGI Symbol;Acc:MGI:2682313]	Q6P5F4		3.9	1.0E-01	0.9	6.7E-01	-4.7	6.3E-02	-1.6	3.6E-01
ENSMUST00000136624				3.2	1.9E-03	1.1	5.6E-01	5.5	2.5E-03	-1.4	4.1E-01
ENSMUST00000172017				3.1	1.4E-03	4.1	5.2E-03	-1.7	2.0E-01	0.1	9.3E-01
ENSMUST00000156123				3.1	9.6E-03	7.4	1.6E-04	-1.6	2.7E-01	0.2	7.5E-01
ENSMUST00000183846	kinesin family member 7 [Source:MGI Symbol;Acc:MGI:1098239]	J3QNW9		4.3	1.2E-01	5.2	9.0E-02	-0.5	8.6E-01	-1.5	4.4E-01
ENSMUST00000183850	termediate/small conductance calcium-activated channel, subfamily N, member 2 [Source:MGI Symbol;Acc:M		P58390	4.2	3.6E-02	5.1	2.6E-02	-0.4	8.5E-01	-1.3	2.9E-01
ENSMUST00000174011				3.1	4.9E-04	6.9	1.1E-04	-0.6	6.1E-01	-0.3	6.5E-01
ENSMUST00000183061				3.1	5.6E-04	-2.9	8.6E-02	0.2	8.0E-01	-0.4	8.1E-01
ENSMUST00000147493				3.1	4.2E-03	4.1	7.6E-04	0.4	5.7E-01	-0.1	8.4E-01
ENSMUST00000159594				3.1	1.5E-02	3.0	1.1E-01	-2.2	2.5E-01	-0.9	4.7E-01
ENSMUST00000131594				3.1	5.6E-04	5.6	1.5E-04	-1.6	1.1E-01	0.1	8.2E-01
ENSMUST00000183889				1.3	1.6E-01	1.9	1.2E-01	0.5	5.9E-01	0.0	9.9E-01
ENSMUST00000156085				3.1	4.6E-03	5.0	1.1E-02	-0.6	7.3E-01	1.4	1.8E-01
ENSMUST00000156489				3.1	1.7E-02	4.3	2.3E-04	-0.2	7.9E-01	-0.7	2.3E-01
ENSMUST00000154286				3.1	5.5E-03	1.8	5.2E-02	0.4	5.6E-01	0.6	4.1E-01
ENSMUST00000183912				0.2	8.2E-01	0.3	7.6E-01	0.1	9.4E-01	-0.1	9.4E-01
ENSMUST00000100526				3.1	3.0E-02	3.2	2.0E-03	1.6	2.7E-02	0.7	2.4E-01
ENSMUST00000141233				3.1	7.5E-04	6.8	2.2E-04	-0.6	6.5E-01	-0.6	3.9E-01
ENSMUST00000141849				3.1	9.0E-03	6.7	1.8E-04	1.2	3.0E-01	-0.3	5.8E-01
ENSMUST00000151908				3.1	5.5E-03	6.7	4.9E-04	0.6	6.4E-01	0.4	5.5E-01
ENSMUST00000183939	nuclear RNA export factor 1 [Source:MGI Symbol;Acc:MGI:1858330]	V9GXW3		0.9	6.0E-01	-0.2	9.3E-01	-1.2	4.9E-01	0.0	9.9E-01
ENSMUST00000178685				3.1	1.5E-03	7.5	1.9E-03	0.9	6.0E-01	0.4	6.9E-01
ENSMUST00000130165				3.1	5.4E-03	-7.0	4.9E-04	-0.3	5.4E-01	-1.4	3.7E-01
ENSMUST00000186513				3.1	2.5E-04	-1.1	1.8E-01	1.3	3.0E-02	-0.1	9.2E-01
ENSMUST00000130651				3.1	1.8E-04	6.8	1.4E-04	-0.6	5.8E-01	-1.2	8.3E-02
ENSMUST00000139367				3.1	1.6E-02	-1.6	4.7E-02	0.8	1.0E-01	-0.2	8.1E-01
ENSMUST00000145174				3.1	3.4E-03	-1.8	2.5E-01	0.6	4.8E-01	-0.5	7.3E-01
ENSMUST00000183973	cyclin D binding myb-like transcription factor 1 [Source:MGI Symbol;Acc:MGI:1344415]	V9GXX1		3.0	1.2E-01	4.3	5.6E-02	-0.1	9.6E-01	-1.4	4.3E-01
ENSMUST00000141605				3.1	8.7E-03	9.1	5.3E-05	1.5	2.6E-01	0.3	5.9E-01
ENSMUST00000149929				3.1	5.4E-03	5.5	5.7E-05	0.3	6.6E-01	0.3	5.9E-01
ENSMUST00000183984	CUGBP, Elav-like family member 2 [Source:MGI Symbol;Acc:MGI:1338822]	V9GX43		2.6	2.0E-01	0.7	7.8E-01	-2.0	3.1E-01	-0.1	9.5E-01
ENSMUST00000190620				3.1	2.6E-04	-3.5	2.3E-02	-0.1	8.5E-01	0.2	8.8E-01
ENSMUST00000128772				3.1	1.1E-02	7.2	6.1E-04	-0.8	6.2E-01	0.9	2.5E-01
ENSMUST00000144663				3.1	6.4E-04	7.4	7.3E-05	-0.6	6.1E-01	-0.2	7.3E-01
ENSMUST00000184032				1.7	4.1E-01	0.3	9.0E-01	-1.3	5.5E-01	0.0	1.0E+00
ENSMUST00000184035	phosphatidylinositol glycan anchor biosynthesis, class B [Source:MGI Symbol;Acc:MGI:1891825]		Q9JJQ0	2.1	2.6E-01	1.2	6.6E-01	0.4	8.1E-01	1.3	6.1E-01
ENSMUST00000121238				3.1	9.9E-03	6.6	3.5E-04	-0.1	9.2E-01	0.0	1.0E+00
ENSMUST00000136680				3.1	1.7E-03	8.2	4.0E-04	-0.3	8.3E-01	0.8	3.2E-01
ENSMUST00000152293				3.1	1.2E-02	8.8	4.6E-06	-0.6	5.5E-01	-0.6	1.8E-01
ENSMUST00000125762				3.1	5.4E-03	5.6	8.0E-04	-2.1	1.2E-01	-0.6	4.2E-01
ENSMUST00000184076				1.3	1.7E-01	1.9	9.7E-02	0.2	8.6E-01	-0.5	6.0E-01
ENSMUST00000184988				3.1	2.1E-03	6.7	1.5E-03	0.1	9.3E-01	0.0	9.8E-01
ENSMUST00000193301				3.1	1.6E-02	-4.0	1.1E-02	0.3	6.5E-01	0.1	9.3E-01
ENSMUST00000130450				3.1	2.1E-02	8.7	1.1E-03	1.3	5.0E-01	1.0	2.5E-01
ENSMUST00000160250				3.1	8.7E-03	5.8	9.8E-04	-1.1	3.9E-01	-1.2	1.4E-01
ENSMUST00000146596				3.1	1.5E-03	5.5	9.2E-04	-0.5	6.6E-01	0.8	2.5E-01
ENSMUST00000167572				3.1	1.7E-02	2.5	1.2E-02	0.6	4.0E-01	0.4	5.7E-01
ENSMUST00000195387				3.1	1.5E-02	4.9	5.8E-05	-0.1	9.2E-01	-0.7	1.7E-01
ENSMUST00000149781				3.1	1.9E-03	8.0	1.3E-04	-0.3	8.2E-01	0.1	8.1E-01
ENSMUST00000154832				3.1	2.2E-03	3.9	3.5E-02	-0.1	9.6E-01	1.8	1.4E-01
ENSMUST00000173567				3.1	8.2E-03	8.9	3.3E-03	-0.9	7.2E-01	-3.6	2.0E-02
ENSMUST00000141866				3.1	2.3E-03	5.2	2.4E-03	-1.9	1.9E-01	-0.4	6.3E-01
ENSMUST00000141517				3.1	1.7E-03	6.2	3.9E-03	-0.7	7.0E-01	-1.2	2.5E-01
ENSMUST00000154909				3.1	3.5E-04	-7.1	1.5E-03	0.5	2.9E-01	2.2	2.1E-01
ENSMUST00000184149				-0.4	5.2E-01	-1.3	1.1E-01	-0.8	1.4E-01	0.1	9.0E-01
ENSMUST00000190377				3.1	3.7E-04	2.9	1.6E-01	-3.5	9.3E-02	1.3	3.5E-01
ENSMUST00000186835				3.0	3.9E-03	-1.6	6.0E-01	2.8	1.7E-01	-1.7	6.0E-01
ENSMUST00000125614				3.0	4.1E-03	6.9	3.1E-05	0.1	9.3E-01	0.0	9.9E-01
ENSMUST00000181879				3.0	2.0E-03	4.3	2.3E-04	-0.2	7.9E-01	-0.7	2.3E-01
ENSMUST00000140528				3.0	5.4E-03	-6.8	1.4E-04	0.8	4.5E-02	-0.8	5.3E-01
ENSMUST00000184179	ATP synthase mitochondrial F1 complex assembly factor 1 [Source:MGI Symbol;Acc:MGI:2180560]	V9GX21		1.2	1.9E-01	2.4	4.6E-02	0.5	6.0E-01	-0.7	4.2E-01
ENSMUST00000148433				3.0	3.6E-03	5.2	3.1E-03	-1.9	2.0E-01	-1.1	2.3E-01
ENSMUST00000184186	MARVEL (membrane-associating) domain containing 1 [Source:MGI Symbol;Acc:MGI:2147570]	V9GXP6		1.1	1.7E-01	2.9	2.3E-02	1.4	1.5E-01	-0.4	6.5E-01
ENSMUST00000142375				3.0	1.3E-03	5.1	4.1E-04	0.6	5.4E-01	-0.6	3.9E-01
ENSMUST00000161169				3.0	5.2E-05	6.4	1.3E-04	-0.5	6.3E-01	-0.6	3.0E-01
ENSMUST00000182962				3.0	3.9E-03	-2.4	8.4E-02	-0.3	6.7E-01	-0.1	9.6E-01
ENSMUST00000148758				3.0	1.7E-03	-6.0	1.8E-03	-0.2	7.1E-01	-0.8	6.0E-01
ENSMUST00000153989				3.0	5.3E-04	4.6	5.9E-04	0.1	8.9E-01	0.2	7.1E-01
ENSMUST00000127090				3.0	1.5E-03	6.4	3.9E-04	-0.2	8.6E-01	0.9	2.0E-01
ENSMUST00000147672				3.0	1.0E-03	5.5	2.8E-03	1.2	4.0E-01	0.1	9.0E-01
ENSMUST00000148735				3.0	1.8E-02	7.6	1.1E-04	-0.6	6.5E-01	-0.4	5.0E-01
ENSMUST00000142665				3.0	1.1E-03	6.7	1.9E-04	-0.6	6.0E-01	-0.1	8.6E-01
ENSMUST00000172370				3.0	1.3E-02	5.2	2.4E-04	-2.2	4.8E-02	0.2	6.7E-01
ENSMUST00000125375				3.0	2.1E-03	4.8	8.1E-03	-0.9	5.4E-01	0.1	9.5E-01
ENSMUST00000184280	striatin, calmodulin binding protein 4 [Source:MGI Symbol;Acc:MGI:2142346]	V9GXT1		2.7	1.2E-01	5.2	1.4E-02	0.0	1.0E+00	-2.5	8.5E-02
ENSMUST00000111727				3.0	8.2E-03	4.4	1.1E-03	-0.4	6.6E-01	0.3	6.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000131636				3.0	6.1E-03	2.4	1.0E-01	-0.6	6.0E-01	0.5	6.2E-01
ENSMUST00000156007				3.0	2.1E-04	-5.8	8.8E-03	1.2	9.2E-02	0.2	9.3E-01
ENSMUST00000166287				3.0	3.1E-03	-1.5	1.7E-01	0.4	5.1E-01	-0.6	5.6E-01
ENSMUST00000184306				3.9	1.0E-01	5.7	3.8E-02	-0.2	9.3E-01	-2.1	1.7E-01
ENSMUST00000126676				3.0	5.8E-03	7.7	5.6E-04	1.3	3.9E-01	0.8	3.3E-01
ENSMUST00000144293				3.0	1.3E-03	2.3	3.1E-01	-0.7	7.5E-01	2.3	2.0E-01
ENSMUST00000184326	KRI1 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:2384899]	V9GXJ9		1.2	5.5E-01	-2.2	3.7E-01	-2.3	2.0E-01	1.1	6.5E-01
ENSMUST00000118511				3.0	1.4E-02	7.4	2.7E-04	-1.4	3.6E-01	0.8	2.8E-01
ENSMUST00000123528				3.0	5.3E-03	4.6	3.7E-03	0.5	6.3E-01	0.4	5.8E-01
ENSMUST00000184339				2.3	4.0E-02	2.0	8.7E-02	-1.1	2.9E-01	-0.7	4.4E-01
ENSMUST00000139698				3.0	2.1E-03	5.5	2.0E-02	-0.7	7.4E-01	0.5	7.0E-01
ENSMUST00000184350	trin homology domain containing, family M (with RUN domain) member 1 [Source:MGI Symbol;Acc:MGI:24	V9GWX7		-2.6	5.5E-02	-0.6	7.3E-01	1.7	1.4E-01	-0.4	8.3E-01
ENSMUST00000192220				3.0	5.7E-03	5.3	6.4E-04	-0.8	4.8E-01	0.7	3.2E-01
ENSMUST00000195264				3.0	1.5E-03	4.6	1.8E-03	-1.4	2.6E-01	0.7	2.8E-01
ENSMUST00000125064				3.0	1.2E-03	3.1	2.2E-03	-0.6	3.5E-01	-0.3	6.5E-01
ENSMUST00000184390	staufen (RNA binding protein) homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1338864]	V9GX87		-1.2	2.6E-01	0.2	8.8E-01	1.0	3.2E-01	-0.4	7.6E-01
ENSMUST00000184410				-2.8	4.9E-02	-3.5	7.7E-02	-0.9	3.4E-01	-0.1	9.4E-01
ENSMUST00000186105				3.0	1.2E-02	7.3	1.9E-05	1.6	8.0E-02	0.0	9.5E-01
ENSMUST00000138873				3.0	2.6E-02	5.5	6.5E-05	0.4	6.2E-01	0.6	2.2E-01
ENSMUST00000150921				3.0	2.9E-04	6.5	1.5E-03	-0.6	7.0E-01	-1.4	1.3E-01
ENSMUST00000184454	inositol polyphosphate-5-phosphatase B [Source:MGI Symbol;Acc:MGI:103257]		Q8K337	0.6	6.9E-01	0.3	8.8E-01	0.4	8.2E-01	0.7	7.1E-01
ENSMUST00000189420				3.0	1.3E-02	8.9	3.1E-05	0.2	8.9E-01	0.6	2.3E-01
ENSMUST00000176501				3.0	2.0E-03	8.8	1.6E-04	0.9	5.2E-01	1.4	5.0E-02
ENSMUST00000147564				3.0	1.7E-03	5.8	2.7E-04	-1.5	2.1E-01	-0.9	1.6E-01
ENSMUST00000186064				3.0	1.3E-02	6.7	2.1E-04	-0.6	6.0E-01	-0.1	9.2E-01
ENSMUST00000190473				3.0	2.3E-03	-0.9	3.3E-01	1.3	6.6E-02	-2.0	8.3E-02
ENSMUST00000141070				3.0	9.4E-03	-1.3	2.0E-01	0.6	3.2E-01	-0.5	6.3E-01
ENSMUST00000189726				3.0	2.2E-02	4.6	5.9E-04	0.1	8.9E-01	0.2	7.1E-01
ENSMUST00000129874				3.0	1.0E-02	6.3	5.7E-04	-0.7	6.2E-01	-0.7	3.3E-01
ENSMUST00000184515	phosphomevalonate kinase [Source:MGI Symbol;Acc:MGI:1915853]		Q9D1G2	1.6	4.5E-01	3.0	2.7E-01	-0.5	8.5E-01	-1.9	3.5E-01
ENSMUST00000153625				3.0	3.2E-03	2.2	2.8E-01	-1.4	4.7E-01	1.1	4.5E-01
ENSMUST00000128803				3.0	3.1E-03	8.0	5.6E-05	-0.7	5.9E-01	0.0	9.4E-01
ENSMUST00000184535	RIKEN cDNA 1700037H04 gene [Source:MGI Symbol;Acc:MGI:1914576]	Q6IR22		-0.8	6.2E-01	2.4	2.8E-01	1.8	3.6E-01	-1.4	4.0E-01
ENSMUST00000184539				0.6	7.8E-01	0.7	8.4E-01	0.2	9.2E-01	0.2	9.6E-01
ENSMUST00000150764				3.0	1.4E-02	-2.9	2.8E-03	0.1	8.4E-01	1.0	1.9E-01
ENSMUST00000152612				3.0	1.4E-02	7.1	4.2E-05	-1.5	1.9E-01	-0.1	9.0E-01
ENSMUST00000180767				3.0	1.0E-03	5.5	2.1E-04	0.4	6.6E-01	-0.4	5.1E-01
ENSMUST00000159532				2.9	3.9E-04	-4.9	6.9E-02	1.7	1.1E-01	1.4	5.7E-01
ENSMUST00000140990				2.9	5.4E-03	6.7	8.3E-05	0.1	9.2E-01	-1.0	1.0E-01
ENSMUST00000184565	reproductive homeobox 3A2 [Source:MGI Symbol;Acc:MGI:5434440]	Q4TU90		3.4	1.7E-01	4.6	8.7E-02	-0.4	8.7E-01	-1.6	3.6E-01
ENSMUST00000135638				2.9	1.9E-02	-4.7	4.1E-03	-0.3	5.6E-01	-0.8	5.6E-01
ENSMUST00000132804				2.9	2.4E-03	1.3	2.2E-01	0.4	5.9E-01	1.2	1.8E-01
ENSMUST00000156565				2.9	1.7E-02	-8.1	5.9E-04	-1.5	1.5E-02	-0.8	6.6E-01
ENSMUST00000136387				2.9	2.7E-04	-6.8	8.1E-04	-1.0	7.3E-02	0.7	6.7E-01
ENSMUST00000153157				2.9	2.2E-02	5.9	1.9E-02	-0.9	6.8E-01	-1.8	1.9E-01
ENSMUST00000187623				2.9	5.0E-03	4.1	2.5E-02	-1.7	3.3E-01	-0.8	4.4E-01
ENSMUST00000159836				2.9	9.6E-03	7.2	1.2E-04	0.6	5.7E-01	-0.6	2.7E-01
ENSMUST00000187358				2.9	2.8E-02	1.8	4.1E-02	0.8	2.1E-01	0.7	3.2E-01
ENSMUST00000184618				-1.3	1.0E-01	-1.3	1.6E-01	-0.4	5.0E-01	-0.4	6.3E-01
ENSMUST00000194743				2.9	5.7E-03	5.9	6.9E-04	0.9	4.5E-01	-0.3	6.9E-01
ENSMUST00000184620	cyclin D binding myb-like transcription factor 1 [Source:MGI Symbol;Acc:MGI:1344415]	V9GWT2		-4.3	4.7E-02	-2.1	4.3E-01	1.4	4.0E-01	-0.8	7.6E-01
ENSMUST00000138052				2.9	4.3E-03	5.2	6.8E-05	-0.6	4.3E-01	-0.5	2.9E-01
ENSMUST00000192874				2.9	1.7E-04	7.5	1.2E-02	0.9	7.1E-01	-1.0	5.0E-01
ENSMUST00000184635	heterogeneous nuclear ribonucleoprotein L-like [Source:MGI Symbol;Acc:MGI:1919942]		Q921F4	-3.5	5.5E-02	-1.7	4.9E-01	1.9	2.0E-01	0.1	9.6E-01
ENSMUST00000117317				2.9	1.5E-02	6.6	1.4E-03	-2.0	2.5E-01	0.6	4.8E-01
ENSMUST00000184642				-0.2	8.6E-01	0.1	8.8E-01	-0.9	2.3E-01	-1.3	2.4E-01
ENSMUST00000143456				2.9	2.7E-02	2.7	3.1E-02	-2.9	3.6E-02	-0.4	6.3E-01
ENSMUST00000184651	a disintegrin and metallopeptidase domain 15 (metargidin) [Source:MGI Symbol;Acc:MGI:1333882]		O88839	-1.5	1.8E-01	1.6	2.7E-01	2.0	9.3E-02	-1.1	4.0E-01
ENSMUST00000184659				0.8	4.3E-01	-1.5	2.8E-01	-0.2	8.6E-01	2.1	1.2E-01
ENSMUST00000161248				2.9	6.4E-03	5.7	3.3E-04	-0.6	5.9E-01	0.4	5.1E-01
ENSMUST00000195762				2.9	6.4E-03	8.5	3.2E-05	-0.2	9.0E-01	-0.4	4.7E-01
ENSMUST00000184677	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]	V9GXK9		-1.5	2.0E-01	-2.0	1.6E-01	-1.0	2.0E-01	-0.6	7.0E-01
ENSMUST00000146166				2.9	7.3E-03	7.0	1.3E-04	-0.6	6.3E-01	0.0	9.9E-01
ENSMUST00000129959				2.9	6.2E-03	5.8	1.8E-03	0.6	6.3E-01	-0.3	6.8E-01
ENSMUST00000143478				2.9	1.5E-02	6.4	2.8E-04	-0.6	6.1E-01	-0.1	8.8E-01
ENSMUST00000140226				2.9	1.3E-02	3.3	3.9E-04	-1.1	7.4E-02	0.0	9.8E-01
ENSMUST00000159401				2.9	2.3E-03	7.8	3.1E-05	0.0	9.8E-01	1.1	5.2E-02
ENSMUST00000124297				2.9	5.9E-03	7.3	6.0E-05	-0.9	4.4E-01	-0.4	4.3E-01
ENSMUST00000180554				2.9	7.1E-04	-2.8	4.1E-03	1.0	5.1E-02	-1.0	2.4E-01
ENSMUST00000182436				2.9	1.8E-02	7.7	1.8E-04	0.8	5.1E-01	0.2	8.0E-01
ENSMUST00000173972				2.9	2.4E-02	5.0	2.4E-02	-0.7	7.4E-01	0.3	7.7E-01
ENSMUST00000138598				2.9	1.5E-04	5.9	3.2E-06	-0.5	3.6E-01	-0.4	3.1E-01
ENSMUST00000184850				2.9	1.0E-02	2.5	6.3E-03	-0.6	3.3E-01	-0.3	6.1E-01
ENSMUST00000191568				2.9	1.1E-03	2.3	8.1E-03	-0.4	4.9E-01	-0.7	2.7E-01
ENSMUST00000129557				2.9	2.9E-04	5.0	5.9E-05	-0.2	7.2E-01	0.2	7.0E-01
ENSMUST00000139961				2.9	3.5E-02	5.3	1.3E-03	-1.2	3.7E-01	-0.2	7.4E-01
ENSMUST00000117591				2.9	1.0E-02	6.9	1.8E-04	-0.6	6.1E-01	-0.7	2.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000159718				2.9	1.5E-02	6.6	1.9E-06	-0.8	2.4E-01	0.1	8.8E-01
ENSMUST00000184826	nuclear RNA export factor 1 [Source:MGI Symbol;Acc:MGI:1858330]	V9GXM5		-3.1	3.4E-01	-5.0	1.9E-01	-3.1	1.4E-01	-1.1	7.8E-01
ENSMUST00000182906				2.9	1.2E-02	-4.9	1.5E-04	-0.4	3.0E-01	-0.6	5.0E-01
ENSMUST00000124006				2.9	1.1E-02	2.1	5.1E-02	-5.1	2.3E-03	0.2	7.8E-01
ENSMUST00000151174				2.9	3.5E-04	-2.8	2.6E-02	-0.8	2.3E-01	-2.1	1.2E-01
ENSMUST00000143856				2.9	2.1E-03	3.3	2.5E-02	0.4	7.6E-01	-0.1	9.4E-01
ENSMUST00000131645				2.9	9.8E-04	5.8	7.0E-06	0.0	9.9E-01	0.1	8.9E-01
ENSMUST00000133062				2.9	3.6E-03	5.3	9.9E-03	-0.5	7.8E-01	-1.1	3.0E-01
ENSMUST00000135353				2.9	5.7E-03	5.1	1.2E-04	1.0	2.2E-01	-0.5	3.3E-01
ENSMUST00000184861				0.6	6.8E-01	-6.9	1.7E-03	-8.1	4.0E-05	-0.6	7.2E-01
ENSMUST00000141115				2.9	3.8E-04	-1.9	1.2E-01	1.5	2.8E-02	-0.5	6.6E-01
ENSMUST00000141077				2.9	1.0E-03	5.3	2.0E-03	-2.4	1.1E-01	-0.9	2.7E-01
ENSMUST00000181377				2.9	4.3E-04	-2.2	9.7E-02	1.5	3.7E-02	-0.5	6.8E-01
ENSMUST00000135724				2.8	3.4E-03	-4.6	5.1E-03	0.3	5.3E-01	-0.8	5.5E-01
ENSMUST00000192377				2.8	3.4E-02	-0.8	4.0E-01	0.5	4.3E-01	-1.4	1.5E-01
ENSMUST00000184885	trichorhinophalangeal syndrome I (human) [Source:MGI Symbol;Acc:MGI:1927616]	Q80V18		1.8	3.6E-01	1.2	6.2E-01	-0.9	6.1E-01	-0.3	8.8E-01
ENSMUST00000184889				1.1	9.2E-02	1.4	8.9E-02	-0.2	7.9E-01	-0.5	5.0E-01
ENSMUST00000128277				2.8	1.4E-03	-0.6	6.8E-01	1.4	1.7E-01	-0.6	6.7E-01
ENSMUST00000146901				2.8	2.7E-02	8.0	8.6E-05	0.1	9.4E-01	0.1	9.2E-01
ENSMUST00000184914	solute carrier family 25, member 37 [Source:MGI Symbol;Acc:MGI:1914962]		Q920G8	-1.4	2.4E-01	-1.6	2.8E-01	-1.1	2.0E-01	-0.9	5.2E-01
ENSMUST00000126517				2.8	1.3E-03	-3.4	1.4E-02	0.0	9.3E-01	-0.7	5.9E-01
ENSMUST00000149426				2.8	3.3E-02	5.6	1.2E-03	-0.4	7.4E-01	-0.1	8.8E-01
ENSMUST00000098778				2.8	1.3E-03	5.2	1.0E-04	-1.2	1.5E-01	0.0	9.6E-01
ENSMUST00000184776				2.8	8.8E-04	5.6	2.8E-03	-0.6	7.1E-01	0.7	4.2E-01
ENSMUST00000148698				2.8	5.4E-03	-2.5	3.0E-02	-0.2	7.7E-01	0.2	8.3E-01
ENSMUST00000174303				2.8	2.5E-02	6.8	1.4E-03	-0.6	7.1E-01	-0.2	8.6E-01
ENSMUST00000190632				2.8	1.2E-03	8.3	2.2E-05	1.0	3.2E-01	0.5	3.0E-01
ENSMUST00000184945	neuron navigator 2 [Source:MGI Symbol;Acc:MGI:2183691]	V9GX91		2.3	4.6E-02	3.2	2.9E-02	0.5	6.3E-01	-0.4	7.3E-01
ENSMUST00000174660				2.8	7.1E-03	1.8	3.1E-02	-0.9	1.7E-01	-0.6	3.9E-01
ENSMUST00000184965				-3.8	3.0E-01	-4.3	3.8E-01	-0.8	7.0E-01	-0.3	9.5E-01
ENSMUST00000155446				2.8	6.9E-04	7.0	7.3E-04	-0.2	9.0E-01	0.2	8.2E-01
ENSMUST00000184970	nuclear RNA export factor 1 [Source:MGI Symbol;Acc:MGI:1858330]	V9GXF3		-1.6	5.7E-02	-1.5	1.3E-01	-0.1	8.8E-01	-0.2	8.5E-01
ENSMUST00000184973	ectonucleoside triphosphate diphosphohydrolase 4 [Source:MGI Symbol;Acc:MGI:1914714]		Q9DBT4	-0.6	2.5E-01	-0.3	6.4E-01	0.0	9.6E-01	-0.3	5.7E-01
ENSMUST00000151410				2.8	6.3E-03	2.6	1.8E-02	-0.2	8.4E-01	0.3	6.5E-01
ENSMUST00000184996	golgi autoantigen, golgin subfamily a, 1 [Source:MGI Symbol;Acc:MGI:1924149]		Q9CW79	-2.9	2.6E-01	-2.7	4.3E-01	-0.4	8.4E-01	-0.6	8.5E-01
ENSMUST00000161808				2.8	1.3E-02	-3.2	3.9E-02	-0.5	4.5E-01	-0.5	7.6E-01
ENSMUST00000185005	SNAP-associated protein [Source:MGI Symbol;Acc:MGI:1333745]	V9GXI0		0.8	7.0E-01	-4.6	1.7E-01	-2.4	1.7E-01	2.9	3.6E-01
ENSMUST00000147864				2.8	2.1E-03	8.3	2.2E-05	-0.6	5.9E-01	-0.5	3.2E-01
ENSMUST00000185027				1.0	2.3E-01	0.9	3.9E-01	0.2	7.8E-01	0.3	7.3E-01
ENSMUST00000185029	F-box and leucine-rich repeat protein 4 [Source:MGI Symbol;Acc:MGI:2140367]	V9GWT8		2.0	3.1E-01	3.1	1.8E-01	-0.7	7.5E-01	-1.7	3.7E-01
ENSMUST00000185030	catechol-O-methyltransferase [Source:MGI Symbol;Acc:MGI:88470]		O88587	1.5	3.4E-01	3.0	1.3E-01	-0.2	9.0E-01	-1.7	2.5E-01
ENSMUST00000159393				2.8	1.0E-03	3.8	6.5E-03	-0.8	3.9E-01	-1.4	1.5E-01
ENSMUST00000143519				2.8	1.4E-02	7.2	8.8E-03	2.0	3.6E-01	-0.3	8.5E-01
ENSMUST00000185056				-3.6	2.5E-01	-0.7	8.0E-01	-0.1	9.5E-01	-3.0	3.4E-01
ENSMUST00000139155				2.8	9.5E-03	-4.1	1.2E-02	0.0	9.5E-01	1.8	1.8E-01
ENSMUST00000192566				2.8	1.5E-04	6.0	1.1E-04	-0.1	8.8E-01	0.4	4.7E-01
ENSMUST00000185072	predicted gene, 21685 [Source:MGI Symbol;Acc:MGI:5435040]		Q9DBT4	-0.6	2.5E-01	-0.3	6.4E-01	0.0	9.6E-01	-0.3	5.7E-01
ENSMUST00000186246				2.8	2.7E-03	9.4	5.7E-04	-0.2	9.3E-01	-1.4	8.8E-02
ENSMUST00000135776				2.8	8.6E-05	1.8	2.6E-01	-0.1	9.4E-01	2.3	7.7E-02
ENSMUST00000122846				2.8	4.8E-03	-5.0	6.1E-04	0.6	1.3E-01	-0.5	6.2E-01
ENSMUST00000185117	transcription factor 12 [Source:MGI Symbol;Acc:MGI:101877]		Q61286	-3.2	2.9E-01	-4.7	2.0E-01	-2.3	2.1E-01	-0.8	8.4E-01
ENSMUST00000129686				2.8	2.4E-02	7.5	3.9E-05	-0.6	6.0E-01	-0.9	1.1E-01
ENSMUST00000153872				2.8	2.5E-02	7.1	2.3E-04	-0.2	8.7E-01	0.2	7.7E-01
ENSMUST00000185137	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:MGI	V9GWW2		-0.5	5.1E-01	0.2	8.7E-01	0.4	5.8E-01	-0.3	7.8E-01
ENSMUST00000153733				2.8	2.0E-03	2.4	1.0E-01	-0.6	6.1E-01	4.0	3.8E-03
ENSMUST00000185168	RIKEN cDNA 1190007I07 gene [Source:MGI Symbol;Acc:MGI:3698433]		Q8BTC1	2.8	1.8E-01	0.3	9.3E-01	-0.3	8.9E-01	2.2	3.8E-01
ENSMUST00000174706				2.8	2.8E-03	-1.7	1.2E-01	0.7	2.5E-01	-0.5	6.7E-01
ENSMUST00000123059				2.8	1.1E-02	6.5	1.5E-04	1.2	2.5E-01	-0.1	8.5E-01
ENSMUST00000134892				2.8	7.1E-03	6.8	4.5E-04	-0.7	6.2E-01	-0.1	8.7E-01
ENSMUST00000173406				2.8	3.5E-03	4.6	1.9E-03	2.2	4.6E-02	-0.2	7.6E-01
ENSMUST00000123184				2.8	1.0E-02	5.7	6.6E-04	-0.5	7.1E-01	-0.2	7.9E-01
ENSMUST00000174788				2.8	8.8E-03	6.7	2.3E-03	-0.7	6.8E-01	1.3	1.8E-01
ENSMUST00000173221				2.8	9.6E-04	8.4	3.2E-05	-0.5	6.6E-01	-0.5	3.4E-01
ENSMUST00000150672				2.8	6.6E-04	6.1	1.2E-04	-2.0	9.1E-02	0.1	8.6E-01
ENSMUST00000185230				-1.2	4.8E-01	1.5	3.8E-01	1.6	3.0E-01	-1.1	5.1E-01
ENSMUST00000185233	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Source:MGI Symbol;Acc:MGI:107815]	Q6GTL7		-0.1	8.8E-01	-0.4	6.6E-01	0.4	5.4E-01	0.7	4.0E-01
ENSMUST00000138407				2.8	8.4E-03	4.5	4.3E-03	-1.6	2.5E-01	-0.3	7.3E-01
ENSMUST00000173250				2.8	1.4E-03	7.6	1.5E-02	-0.7	8.1E-01	-2.3	1.7E-01
ENSMUST00000180531				2.8	1.1E-04	6.7	1.1E-04	-0.6	5.9E-01	-0.5	3.7E-01
ENSMUST00000144970				2.8	3.8E-03	5.5	3.4E-03	-0.4	8.0E-01	-0.7	4.2E-01
ENSMUST00000194128				2.8	4.4E-03	4.3	2.9E-03	-0.9	4.1E-01	0.4	6.1E-01
ENSMUST00000132704				2.8	1.9E-02	2.1	1.4E-01	-4.5	9.4E-03	0.2	9.0E-01
ENSMUST00000135762				2.8	5.4E-03	5.8	8.6E-05	-0.3	7.5E-01	-0.1	8.4E-01
ENSMUST00000186050				2.8	2.4E-02	2.3	1.0E-02	-1.6	3.0E-02	-0.4	5.7E-01
ENSMUST00000136102				2.8	2.0E-02	4.8	1.6E-03	-1.5	2.4E-01	0.3	6.9E-01
ENSMUST00000159376				2.8	2.8E-02	8.0	1.4E-02	-0.9	7.7E-01	-2.4	1.6E-01
ENSMUST00000126739				2.8	9.0E-05	6.7	1.7E-04	-0.5	6.8E-01	-0.3	6.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000156122				2.8	7.1E-03	2.3	1.3E-02	-3.2	4.1E-03	-0.8	2.6E-01
ENSMUST00000187963				2.8	5.5E-03	6.3	1.8E-04	-0.5	6.3E-01	0.0	9.7E-01
ENSMUST00000175812				2.7	1.1E-02	2.2	1.7E-02	-1.5	6.3E-02	-0.3	6.8E-01
ENSMUST00000143019				2.7	4.0E-03	2.9	3.2E-01	-0.8	7.9E-01	3.2	1.3E-01
ENSMUST00000178364				2.7	4.6E-03	2.5	2.5E-02	-2.2	4.2E-02	0.1	8.8E-01
ENSMUST00000145643				2.7	1.0E-03	7.6	8.4E-04	0.8	6.2E-01	-0.2	8.4E-01
ENSMUST00000148777				2.7	7.4E-03	0.6	6.8E-01	-5.6	1.0E-02	2.0	1.3E-01
ENSMUST00000185357				3.5	1.8E-01	5.3	6.2E-02	-0.5	8.5E-01	-2.4	2.0E-01
ENSMUST00000124624				2.7	1.7E-03	-6.6	1.2E-04	0.1	7.9E-01	-0.8	4.9E-01
ENSMUST00000179673				2.7	3.0E-02	0.2	8.9E-01	1.0	3.2E-01	-3.4	6.5E-02
ENSMUST00000115772				2.7	2.3E-03	7.9	3.8E-04	-0.4	8.1E-01	1.0	2.1E-01
ENSMUST00000137391				2.7	2.3E-03	7.6	2.0E-04	-0.6	6.7E-01	0.6	3.8E-01
ENSMUST00000147309				2.7	4.8E-04	5.5	2.3E-05	-1.5	5.8E-02	-0.6	1.7E-01
ENSMUST00000147790				2.7	2.6E-03	6.6	2.5E-04	-0.7	5.9E-01	0.3	6.1E-01
ENSMUST00000125108				2.7	7.0E-03	7.3	6.7E-05	-0.6	6.3E-01	-0.8	2.1E-01
ENSMUST00000185375				0.6	3.1E-01	1.4	7.0E-02	0.6	2.8E-01	-0.2	7.4E-01
ENSMUST00000129608				2.7	4.5E-03	5.4	8.8E-04	0.1	9.0E-01	-1.2	1.5E-01
ENSMUST00000146718				2.7	1.8E-03	-5.0	1.7E-03	-0.2	7.2E-01	0.6	6.3E-01
ENSMUST00000154667				2.7	5.5E-03	6.3	1.5E-05	-0.4	6.0E-01	0.6	1.7E-01
ENSMUST00000139045				2.7	5.6E-03	6.2	4.6E-04	-2.4	1.0E-01	-1.4	8.1E-02
ENSMUST00000136832				2.7	7.9E-03	-5.8	2.9E-03	0.5	3.9E-01	-0.1	9.3E-01
ENSMUST00000121359				2.7	1.0E-03	6.3	1.0E-03	0.3	8.4E-01	0.6	3.8E-01
ENSMUST00000129171				2.7	6.9E-03	7.6	6.4E-05	-0.5	6.6E-01	-0.4	4.4E-01
ENSMUST00000185408				-3.3	8.5E-02	-5.5	3.9E-02	-1.1	3.8E-01	1.1	6.6E-01
ENSMUST00000153750				2.7	8.5E-03	7.3	6.2E-06	0.8	3.1E-01	-0.1	7.3E-01
ENSMUST00000173305				2.7	2.2E-02	8.1	1.4E-04	-0.7	6.2E-01	0.1	9.1E-01
ENSMUST00000185419	aspartyl aminopeptidase [Source:MGI Symbol;Acc:MGI:1278328]	Q8BPW9		0.9	2.1E-01	2.1	2.8E-02	0.2	7.8E-01	-1.0	1.7E-01
ENSMUST00000185429				1.0	1.1E-01	1.5	5.2E-02	-0.2	7.7E-01	-0.7	2.9E-01
ENSMUST00000177024				2.7	2.1E-02	8.5	7.1E-06	-0.9	4.1E-01	-0.1	7.6E-01
ENSMUST00000128010				2.7	8.4E-03	7.6	4.1E-05	0.2	8.3E-01	0.0	9.7E-01
ENSMUST00000117319				2.7	1.4E-02	6.0	1.2E-04	-1.0	3.0E-01	-0.1	8.3E-01
ENSMUST00000185434	CLOCK interacting protein, circadian [Source:MGI Symbol;Acc:MGI:1919185]	A0A087WRF0		3.8	8.8E-02	0.9	7.7E-01	-0.5	8.4E-01	2.5	3.7E-01
ENSMUST00000118776				2.7	2.2E-02	4.8	2.1E-04	-2.2	2.9E-02	0.3	5.8E-01
ENSMUST00000170796				2.7	1.2E-02	7.1	4.1E-04	0.0	9.7E-01	0.6	4.0E-01
ENSMUST00000185447				1.5	4.2E-02	1.8	4.2E-02	0.3	6.0E-01	0.0	9.6E-01
ENSMUST00000151894				2.7	1.1E-03	4.2	6.3E-04	0.3	6.9E-01	0.1	8.4E-01
ENSMUST00000149055				2.7	4.5E-03	-4.9	1.2E-03	0.3	5.0E-01	-2.3	8.7E-02
ENSMUST00000092878				2.7	1.1E-02	6.2	1.1E-04	-1.5	1.8E-01	-0.7	2.4E-01
ENSMUST00000150342				2.7	1.8E-02	-4.8	1.2E-03	-0.7	1.4E-01	0.0	9.9E-01
ENSMUST00000151556				2.7	3.1E-03	7.5	9.0E-05	-0.7	5.9E-01	-0.9	1.5E-01
ENSMUST00000131747				2.7	1.1E-02	-2.8	6.2E-02	0.0	1.0E+00	-1.3	4.0E-01
ENSMUST00000160913				2.7	6.6E-03	4.6	1.0E-03	-0.9	3.7E-01	-1.1	1.4E-01
ENSMUST00000152022				2.7	5.1E-03	-4.9	9.8E-03	1.0	1.2E-01	-0.6	7.1E-01
ENSMUST00000147977				2.6	2.7E-04	-6.0	1.6E-03	-1.3	3.8E-02	-0.3	8.2E-01
ENSMUST00000139778				2.6	3.0E-02	-4.8	4.3E-03	-0.8	1.7E-01	-0.2	9.0E-01
ENSMUST00000134071				2.6	8.1E-03	7.8	2.6E-05	-0.6	6.0E-01	-0.5	3.1E-01
ENSMUST00000131059				2.6	3.1E-02	1.5	3.1E-01	0.9	5.0E-01	1.9	9.1E-02
ENSMUST00000144307				2.6	4.0E-03	4.4	1.3E-03	-2.7	3.2E-02	0.3	6.1E-01
ENSMUST00000185526	gasdermin C3 [Source:MGI Symbol;Acc:MGI:3580656]		Q8CB12	4.5	9.0E-02	5.6	4.4E-02	-1.5	5.9E-01	-2.6	1.3E-01
ENSMUST00000139535				2.6	3.0E-02	5.3	1.4E-04	-0.4	6.8E-01	-1.0	1.0E-01
ENSMUST00000119183				2.6	3.5E-03	8.5	1.1E-03	1.7	3.7E-01	1.4	1.5E-01
ENSMUST00000195631				2.6	1.2E-02	-7.0	1.3E-03	-1.1	7.3E-02	-0.8	6.4E-01
ENSMUST00000138263				2.6	9.2E-03	6.4	1.4E-04	-0.6	6.1E-01	-1.6	2.6E-02
ENSMUST00000164617				2.6	1.6E-02	-4.7	9.8E-04	-2.1	2.6E-03	-0.2	8.7E-01
ENSMUST00000161544				2.6	1.6E-03	7.7	2.6E-05	-2.5	5.2E-02	-0.1	8.3E-01
ENSMUST00000178657				2.6	2.1E-02	6.9	1.9E-04	0.0	9.8E-01	0.4	5.0E-01
ENSMUST00000125531				2.6	3.7E-03	-5.7	1.6E-03	-0.3	5.0E-01	-0.7	6.4E-01
ENSMUST00000059474				2.6	1.4E-02	5.0	5.2E-04	-3.0	2.1E-02	-0.7	2.6E-01
ENSMUST00000191247				2.6	2.7E-03	6.9	5.1E-06	0.1	9.0E-01	0.0	9.4E-01
ENSMUST00000185589				-0.2	8.0E-01	0.7	5.1E-01	-0.3	7.4E-01	-1.2	2.4E-01
ENSMUST00000185591				-1.7	2.4E-01	0.8	7.2E-01	1.3	4.1E-01	-1.1	5.2E-01
ENSMUST00000185594	cAMP responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:88494]	Q543W0	Q01147	-0.9	6.4E-01	-3.3	2.2E-01	-1.6	2.9E-01	0.7	7.9E-01
ENSMUST00000185596	SLIT-ROBO Rho GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:109605]	A0A087WSQ1		-0.3	7.7E-01	1.4	4.1E-01	1.0	5.1E-01	-0.8	5.4E-01
ENSMUST00000149489				2.6	7.6E-04	4.5	1.8E-03	0.1	8.9E-01	0.5	4.5E-01
ENSMUST00000132354				2.6	9.7E-03	3.8	7.2E-03	-0.6	5.3E-01	0.4	6.5E-01
ENSMUST00000135099				2.6	2.8E-02	7.2	6.6E-05	-0.1	9.2E-01	-0.3	5.8E-01
ENSMUST00000138468				2.6	7.6E-04	5.0	3.6E-04	-0.8	4.0E-01	0.0	9.6E-01
ENSMUST00000190318				2.6	2.1E-03	6.4	1.2E-03	-0.5	7.4E-01	-0.6	5.0E-01
ENSMUST00000139699				2.6	1.7E-02	6.1	7.5E-04	-0.1	9.3E-01	0.5	4.7E-01
ENSMUST00000185633	5'-3' exoribonuclease 1 [Source:MGI Symbol;Acc:MGI:891964]	A0A087WQN7		0.1	7.8E-01	0.2	7.8E-01	0.4	3.4E-01	0.3	5.1E-01
ENSMUST00000126275				2.6	1.4E-03	-5.1	2.4E-02	-0.9	3.6E-01	-0.6	7.7E-01
ENSMUST00000185642				4.2	1.1E-01	5.4	7.1E-02	-0.2	9.4E-01	-1.4	4.1E-01
ENSMUST00000149371				2.6	2.7E-02	5.6	3.4E-03	-0.7	6.6E-01	-0.2	7.8E-01
ENSMUST00000185656	zinc finger protein 287 [Source:MGI Symbol;Acc:MGI:2176561]		Q9EQB9	5.2	4.7E-02	4.8	8.0E-02	-1.3	6.3E-01	-0.9	5.8E-01
ENSMUST00000147471				2.6	3.4E-02	2.1	1.2E-02	0.0	9.7E-01	-0.4	5.2E-01
ENSMUST00000172946				2.6	7.7E-04	6.1	1.5E-02	-0.5	7.9E-01	-2.2	1.5E-01
ENSMUST00000185675	glucuronyl C5-epimerase [Source:MGI Symbol;Acc:MGI:2136405]		Q9EPS3	-1.0	6.8E-01	0.0	1.0E+00	0.1	9.7E-01	-0.9	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000160779				2.6	7.9E-03	-9.0	3.2E-04	-1.3	2.8E-02	-1.0	5.7E-01
ENSMUST00000133756				2.6	1.8E-03	5.4	4.0E-03	-0.4	7.8E-01	-0.4	6.5E-01
ENSMUST00000186009				2.6	4.1E-03	2.8	1.8E-01	5.4	8.7E-03	-3.1	1.2E-01
ENSMUST00000189075				2.6	5.0E-03	5.1	6.8E-04	-1.5	2.1E-01	0.5	4.1E-01
ENSMUST00000140369				2.6	1.7E-03	4.1	4.5E-03	0.3	7.6E-01	-0.3	7.0E-01
ENSMUST00000137093				2.6	1.9E-02	5.8	7.1E-03	-0.4	8.3E-01	-1.1	3.1E-01
ENSMUST00000141049				2.6	6.7E-03	3.2	1.6E-01	-1.3	5.2E-01	0.3	8.6E-01
ENSMUST00000142272				2.6	1.7E-02	5.7	4.6E-04	-1.0	3.9E-01	0.4	5.9E-01
ENSMUST00000185707	RNA binding motif protein 15B [Source:MGI Symbol;Acc:MGI:1923598]	A0A087WPD2		0.8	6.5E-01	-1.4	6.1E-01	-0.1	9.6E-01	2.1	4.4E-01
ENSMUST00000176166				2.6	1.3E-02	5.1	4.0E-03	-0.7	6.1E-01	0.6	5.2E-01
ENSMUST00000131648				2.6	6.3E-03	7.6	7.5E-07	0.0	9.9E-01	0.0	9.6E-01
ENSMUST00000128820				2.6	8.7E-03	-6.6	1.7E-04	-1.0	3.4E-02	-0.8	5.2E-01
ENSMUST00000185721	topoisomerase (DNA) II binding protein 1 [Source:MGI Symbol;Acc:MGI:1920018]	A0A087WS55		-0.5	8.1E-01	-2.6	3.0E-01	-2.4	1.2E-01	-0.3	9.1E-01
ENSMUST00000185724	activating transcription factor 7 interacting protein [Source:MGI Symbol;Acc:MGI:1858965]	A0A087WR39		2.6	1.3E-01	4.7	2.6E-02	0.0	9.9E-01	-2.2	1.6E-01
ENSMUST00000185731	rosbin, round spermatid basic protein 1 [Source:MGI Symbol;Acc:MGI:2444993]	A0A0H2UH30		3.9	5.0E-02	6.7	1.4E-02	1.3	5.5E-01	-1.5	3.1E-01
ENSMUST00000182968				2.6	5.7E-03	8.2	2.6E-07	0.8	1.9E-01	0.2	4.8E-01
ENSMUST00000133520				2.6	2.5E-02	5.5	1.9E-03	-0.6	6.6E-01	-0.1	8.5E-01
ENSMUST00000145728				2.6	2.1E-02	4.2	2.9E-04	-2.5	1.3E-02	-0.6	3.0E-01
ENSMUST00000140268				2.6	1.2E-02	4.8	2.0E-03	-0.4	7.0E-01	-0.1	9.0E-01
ENSMUST00000143276				2.6	1.9E-02	6.0	3.3E-04	-0.5	6.4E-01	0.4	5.7E-01
ENSMUST00000125743				2.6	1.4E-02	5.4	1.4E-03	-0.5	7.1E-01	-1.8	4.0E-02
ENSMUST00000117937				2.6	2.6E-03	5.3	8.1E-04	-2.4	7.6E-02	0.7	3.3E-01
ENSMUST00000142393				2.6	3.2E-04	5.9	1.3E-03	-0.5	7.1E-01	0.0	9.6E-01
ENSMUST00000127162				2.6	5.5E-03	7.0	1.1E-04	-0.5	6.6E-01	-1.0	1.3E-01
ENSMUST00000185790	transmembrane protein 194B [Source:MGI Symbol;Acc:MGI:2444113]	A0A087WQU8		0.0	9.8E-01	-0.8	7.3E-01	-2.0	2.6E-01	-1.1	6.6E-01
ENSMUST00000150048				2.6	1.9E-03	-7.5	9.7E-04	-1.2	5.9E-02	1.2	4.6E-01
ENSMUST00000129808				2.6	3.2E-02	6.0	2.0E-03	-0.7	6.6E-01	0.2	7.8E-01
ENSMUST00000185821				-1.1	7.1E-01	-2.2	6.1E-01	-0.6	8.3E-01	0.5	9.0E-01
ENSMUST00000149027				2.6	1.3E-03	-4.4	3.7E-03	-0.1	8.6E-01	1.1	3.5E-01
ENSMUST00000117941				2.5	3.4E-03	7.1	7.1E-07	0.0	9.5E-01	0.7	4.1E-02
ENSMUST00000139901				2.5	3.7E-03	6.5	3.2E-05	0.6	4.5E-01	0.8	1.2E-01
ENSMUST00000147878				2.5	4.6E-03	5.7	2.9E-04	-1.5	2.0E-01	0.3	6.0E-01
ENSMUST00000159719				2.5	4.3E-03	-2.5	7.2E-02	0.1	9.1E-01	-0.7	6.2E-01
ENSMUST00000122404				2.5	5.0E-03	5.2	1.6E-02	-0.8	6.8E-01	0.7	5.4E-01
ENSMUST00000046349				2.5	5.3E-04	5.0	5.9E-04	-2.4	5.4E-02	-0.6	3.7E-01
ENSMUST00000185886				1.3	1.4E-01	0.1	8.8E-01	-0.4	6.5E-01	0.8	3.8E-01
ENSMUST00000185523				2.5	2.5E-02	8.0	2.6E-04	-0.4	7.5E-01	0.8	2.3E-01
ENSMUST00000132966				2.5	7.8E-03	6.2	1.2E-03	-3.4	5.0E-02	-3.7	4.9E-03
ENSMUST00000129163				2.5	1.9E-03	6.8	2.3E-04	-0.4	7.3E-01	-0.9	1.8E-01
ENSMUST00000152333				2.5	5.6E-03	-3.4	1.4E-02	0.3	6.4E-01	1.8	1.4E-01
ENSMUST00000185912	KAT8 regulatory NSL complex subunit 3 [Source:MGI Symbol;Acc:MGI:1918055]		A2RSY1	1.1	6.7E-01	2.6	3.4E-01	0.2	9.3E-01	-1.3	5.9E-01
ENSMUST00000154914				2.5	2.5E-03	4.3	2.8E-02	-0.6	7.3E-01	0.6	5.8E-01
ENSMUST00000174403				2.5	1.1E-03	6.5	2.5E-04	-0.4	7.3E-01	0.3	6.5E-01
ENSMUST00000185919	dopey family member 1 [Source:MGI Symbol;Acc:MGI:1289294]	A0A087WQ48		0.5	4.8E-01	7.2	1.8E-04	5.6	5.2E-04	-1.1	1.4E-01
ENSMUST00000185920	serine/threonine kinase 17b (apoptosis-inducing) [Source:MGI Symbol;Acc:MGI:2138162]	A0A087WPR0		-1.6	4.3E-01	-2.4	4.5E-01	-0.1	9.5E-01	0.7	8.2E-01
ENSMUST00000151560				2.5	2.9E-03	5.1	9.7E-03	0.0	9.9E-01	1.0	3.1E-01
ENSMUST00000185929	inositol polyphosphate phosphatase-like 1 [Source:MGI Symbol;Acc:MGI:1333787]	A0A087WPT7		2.7	1.2E-01	4.3	7.1E-02	0.9	6.3E-01	-0.6	6.9E-01
ENSMUST00000143438				2.5	2.7E-02	7.3	1.1E-02	-0.8	7.4E-01	-2.6	1.0E-01
ENSMUST00000189330				2.5	5.2E-04	6.1	2.5E-05	-0.3	7.1E-01	0.8	1.4E-01
ENSMUST00000188655				2.5	1.2E-02	4.9	2.5E-04	0.3	7.0E-01	-0.2	7.3E-01
ENSMUST00000143178				2.5	2.6E-04	-2.8	3.9E-02	-1.5	8.2E-02	-2.7	1.0E-01
ENSMUST00000150946				2.5	6.6E-04	6.3	6.7E-04	0.1	9.2E-01	0.3	6.7E-01
ENSMUST00000131284				2.5	2.4E-03	7.0	6.4E-05	-0.5	6.2E-01	-1.2	5.8E-02
ENSMUST00000185975				4.5	9.7E-02	6.6	3.7E-02	-0.2	9.4E-01	-2.3	1.8E-01
ENSMUST00000194126				2.5	6.8E-03	-5.7	4.6E-02	0.6	6.2E-01	-0.3	9.1E-01
ENSMUST00000131653				2.5	7.8E-03	-0.2	8.9E-01	0.3	8.0E-01	-2.9	9.8E-02
ENSMUST00000136981				2.5	8.1E-03	5.2	1.4E-03	-0.6	6.4E-01	1.2	9.7E-02
ENSMUST00000155260				2.5	1.7E-03	-5.7	3.5E-02	2.8	9.6E-03	0.2	9.2E-01
ENSMUST00000123020				2.5	2.2E-03	3.5	1.6E-03	0.2	7.3E-01	-0.7	3.0E-01
ENSMUST00000193482				2.5	7.0E-03	8.3	9.6E-04	-0.2	9.2E-01	0.4	6.3E-01
ENSMUST00000140014				2.5	2.6E-03	6.1	2.9E-03	-0.7	6.9E-01	-1.6	1.1E-01
ENSMUST00000186017	NIMA (never in mitosis gene a)-related expressed kinase 7 [Source:MGI Symbol;Acc:MGI:1890645]		Q9ES74	4.3	6.9E-02	0.1	9.7E-01	-3.2	1.4E-01	1.0	6.4E-01
ENSMUST00000182604				2.5	1.1E-02	-4.1	1.0E-02	0.7	2.9E-01	-1.5	3.1E-01
ENSMUST00000159080				2.5	9.9E-03	-1.8	1.6E-01	1.5	6.0E-02	-1.4	3.1E-01
ENSMUST00000140181				2.5	2.3E-02	6.3	1.8E-04	-0.5	6.4E-01	-0.5	3.9E-01
ENSMUST00000186045	serine/arginine repetitive matrix 2 [Source:MGI Symbol;Acc:MGI:1923206]	A0A087WPU0		-0.8	2.9E-01	-0.1	8.8E-01	-0.1	8.6E-01	-0.8	3.5E-01
ENSMUST00000130969				2.5	8.5E-03	3.3	1.4E-02	-0.7	4.9E-01	-1.3	1.9E-01
ENSMUST00000192899				2.5	1.2E-02	6.7	1.2E-04	-0.6	6.1E-01	-0.9	1.6E-01
ENSMUST00000162045				2.5	6.5E-03	0.3	7.9E-01	5.8	5.9E-05	-2.0	1.2E-01
ENSMUST00000182798				2.5	5.8E-03	5.9	8.3E-04	-1.6	2.5E-01	-0.7	3.5E-01
ENSMUST00000146035				2.5	4.0E-03	0.9	4.1E-01	-1.9	7.5E-02	0.2	8.4E-01
ENSMUST00000186322				2.4	1.8E-02	9.4	3.1E-04	-0.3	8.9E-01	-0.7	3.5E-01
ENSMUST00000151333				2.4	3.1E-02	6.9	3.0E-04	-0.7	6.2E-01	0.0	9.8E-01
ENSMUST00000131773				2.4	8.6E-04	7.2	3.0E-03	-0.8	6.7E-01	0.6	5.5E-01
ENSMUST00000186089	pleckstrin homology domain interacting protein [Source:MGI Symbol;Acc:MGI:1932404]	A0A087WP89		1.5	3.5E-01	1.4	4.9E-01	-0.5	7.6E-01	-0.3	8.5E-01
ENSMUST00000148227				2.4	3.1E-03	-2.5	7.7E-02	0.1	8.9E-01	-1.1	4.7E-01
ENSMUST00000149720				2.4	3.3E-03	-2.8	3.9E-02	-1.6	6.0E-02	-2.7	1.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000135229				2.4	1.7E-02	7.0	1.4E-03	-0.3	8.7E-01	0.8	3.3E-01
ENSMUST00000148298				2.4	2.7E-02	2.4	9.6E-02	0.0	9.7E-01	0.5	5.9E-01
ENSMUST00000186116	F-box and leucine-rich repeat protein 19 [Source:MGI Symbol;Acc:MGI:3039600]	A0A087WQ84		-1.7	1.6E-01	0.4	8.0E-01	1.3	2.7E-01	-0.8	5.6E-01
ENSMUST00000186129	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]	A0A087WSN6		-2.9	1.6E-01	-3.9	1.8E-01	-0.5	7.8E-01	0.4	8.7E-01
ENSMUST00000148636				2.4	9.3E-03	6.0	7.4E-05	-0.1	8.7E-01	0.6	2.5E-01
ENSMUST00000153088				2.4	4.7E-04	8.1	6.5E-04	-0.3	8.7E-01	0.3	6.8E-01
ENSMUST00000161962				2.4	4.7E-03	6.3	2.3E-03	-0.8	6.5E-01	0.1	9.0E-01
ENSMUST00000165371				2.4	2.8E-02	4.5	5.0E-03	-0.3	8.2E-01	-0.4	6.0E-01
ENSMUST00000129785				2.4	3.1E-02	-0.9	6.1E-01	2.6	4.2E-02	-3.2	1.3E-01
ENSMUST00000176894				2.4	2.0E-02	-4.2	4.2E-03	-1.3	3.3E-02	-2.1	1.4E-01
ENSMUST00000182073				2.4	1.0E-02	5.3	9.0E-04	1.1	3.2E-01	-0.3	7.0E-01
ENSMUST00000127999				2.4	6.6E-03	6.5	9.5E-05	1.7	9.2E-02	-0.3	6.4E-01
ENSMUST00000140279				2.4	2.1E-03	7.7	8.1E-04	0.1	9.7E-01	0.2	8.1E-01
ENSMUST00000159102				2.4	2.6E-03	3.9	4.2E-03	-2.1	9.9E-02	-0.9	3.1E-01
ENSMUST00000152603				2.4	1.3E-02	-3.9	3.5E-02	-1.1	2.1E-01	-0.2	9.0E-01
ENSMUST00000135937				2.4	2.8E-02	6.3	1.3E-03	-0.1	9.2E-01	-2.7	1.6E-02
ENSMUST00000186207	F-box and leucine-rich repeat protein 19 [Source:MGI Symbol;Acc:MGI:3039600]		Q6PB97	4.1	4.1E-02	3.4	1.0E-01	-1.5	3.9E-01	-0.8	6.4E-01
ENSMUST00000154425				2.4	1.6E-02	6.6	1.0E-03	-0.1	9.3E-01	-0.5	5.9E-01
ENSMUST00000186213	tubulin, alpha 4A [Source:MGI Symbol;Acc:MGI:1095410]		P68368	-0.2	7.9E-01	1.1	2.0E-01	0.8	2.3E-01	-0.5	5.3E-01
ENSMUST00000156997				2.4	1.7E-02	5.0	4.6E-02	-1.3	5.8E-01	-0.3	8.4E-01
ENSMUST00000186219	zinc finger protein 951 [Source:MGI Symbol;Acc:MGI:2441896]	A0A087WRH0		0.7	5.1E-01	3.0	9.4E-02	1.9	2.1E-01	-0.3	7.6E-01
ENSMUST00000148104				2.4	1.1E-02	4.8	2.2E-04	-1.6	1.0E-01	-0.7	2.7E-01
ENSMUST00000134821				2.4	3.0E-02	9.0	5.7E-05	0.1	9.5E-01	-0.8	1.3E-01
ENSMUST00000030743				2.4	1.5E-02	4.0	4.4E-04	1.2	9.7E-02	-0.5	4.0E-01
ENSMUST00000156854				2.4	5.1E-03	2.5	6.6E-03	-0.5	4.4E-01	-1.4	5.5E-02
ENSMUST00000133777				2.4	2.0E-03	3.8	2.2E-03	0.8	3.4E-01	-0.2	7.6E-01
ENSMUST00000142173				2.4	2.2E-02	8.8	3.2E-05	-1.4	2.9E-01	-0.1	8.3E-01
ENSMUST00000130213				2.4	1.9E-02	5.7	6.8E-04	0.5	6.6E-01	0.9	2.4E-01
ENSMUST00000124534				2.4	1.9E-02	6.8	1.1E-03	-0.8	6.3E-01	1.0	2.5E-01
ENSMUST00000186255	prothymosin alpha [Source:MGI Symbol;Acc:MGI:97803]	A0A087WP98		-4.9	2.7E-01	-10.0	1.0E-01	-4.4	8.4E-02	0.7	9.2E-01
ENSMUST00000138699				2.4	2.0E-03	6.8	5.9E-04	-0.7	6.2E-01	0.7	3.3E-01
ENSMUST00000186259	serine/arginine repetitive matrix 2 [Source:MGI Symbol;Acc:MGI:1923206]	A0A087WR98		1.6	4.8E-01	1.2	6.1E-01	-1.1	6.0E-01	-0.8	7.0E-01
ENSMUST00000149087				2.4	8.1E-03	-3.7	3.5E-02	-0.6	4.6E-01	-0.4	8.3E-01
ENSMUST00000178637				2.4	6.5E-03	6.8	1.3E-03	-0.7	6.8E-01	-1.4	1.3E-01
ENSMUST00000125786				2.4	3.0E-03	7.7	1.0E-04	-0.7	5.9E-01	0.1	8.4E-01
ENSMUST00000139151				2.4	2.6E-02	5.7	8.4E-04	-0.3	8.0E-01	-0.8	2.4E-01
ENSMUST00000142362				2.4	5.5E-03	6.4	1.5E-04	-0.6	5.9E-01	-0.5	3.8E-01
ENSMUST00000186294	centrosome and spindle pole associated protein 1 [Source:MGI Symbol;Acc:MGI:2681832]		B2RX88	0.7	7.5E-01	1.3	4.7E-01	-2.4	1.6E-01	-3.0	1.5E-01
ENSMUST00000149191				2.4	4.1E-03	-6.0	7.6E-04	-0.5	3.0E-01	-0.6	6.4E-01
ENSMUST00000154104				2.4	6.7E-03	-3.7	2.4E-01	3.3	5.8E-02	-0.2	9.5E-01
ENSMUST00000186303	predicted gene 28557 [Source:MGI Symbol;Acc:MGI:5579263]	A0A087WQQ0		0.3	8.3E-01	1.9	2.7E-01	0.7	6.2E-01	-0.9	5.1E-01
ENSMUST00000186316				-3.1	8.8E-02	-2.2	4.5E-01	1.7	2.8E-01	0.8	7.7E-01
ENSMUST00000186319				7.2	3.7E-02	6.4	7.6E-02	-0.9	8.1E-01	-0.2	9.4E-01
ENSMUST00000148354				2.3	3.0E-02	4.6	4.7E-03	2.0	1.1E-01	-0.2	8.2E-01
ENSMUST00000186350				-1.5	3.9E-01	2.0	2.9E-01	0.2	8.8E-01	-3.2	7.4E-02
ENSMUST00000166415				2.3	2.0E-02	5.2	7.4E-04	-1.5	2.1E-01	0.3	6.2E-01
ENSMUST00000153096				2.3	1.3E-02	5.3	1.0E-02	-0.7	7.1E-01	0.0	9.6E-01
ENSMUST00000143749				2.3	3.2E-03	7.6	1.3E-05	-1.5	1.6E-01	-1.1	4.1E-02
ENSMUST00000120098				2.3	1.2E-02	-7.5	1.5E-05	0.5	1.3E-01	0.6	5.1E-01
ENSMUST00000181037				2.3	1.2E-02	6.3	1.1E-03	-0.4	7.7E-01	-0.8	3.1E-01
ENSMUST00000159974				2.3	1.9E-02	8.6	4.3E-05	0.4	7.4E-01	0.2	7.3E-01
ENSMUST00000182954				2.3	5.2E-03	9.4	2.7E-02	-1.0	8.1E-01	-0.7	7.1E-01
ENSMUST00000186375	N(alpha)-acetyltransferase 60, NatF catalytic subunit [Source:MGI Symbol;Acc:MGI:1922013]		Q9DBU2	-1.0	7.4E-01	1.8	6.0E-01	0.1	9.7E-01	-2.7	4.2E-01
ENSMUST00000186380	DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Source:MGI Symbol;Acc:MGI:108177]	A0A087WPL5		-3.2	4.0E-01	-3.2	4.4E-01	-0.5	8.5E-01	-0.5	9.1E-01
ENSMUST00000146724				2.3	3.1E-02	3.2	1.3E-01	-0.4	8.4E-01	1.8	1.9E-01
ENSMUST00000071842				2.3	1.3E-02	3.2	1.2E-03	0.6	3.4E-01	-0.3	5.8E-01
ENSMUST00000186242				2.3	4.2E-03	5.5	1.2E-04	-0.6	4.9E-01	-0.8	1.8E-01
ENSMUST00000147882				2.3	3.5E-02	7.0	1.8E-05	-0.7	4.0E-01	0.4	3.9E-01
ENSMUST00000140001				2.3	1.3E-02	6.9	1.5E-04	-0.5	6.6E-01	-0.9	1.7E-01
ENSMUST00000195260				2.3	6.0E-03	4.6	8.3E-04	-2.9	2.2E-02	-0.1	8.7E-01
ENSMUST00000145859				2.3	3.7E-03	4.3	1.6E-03	0.2	8.5E-01	0.5	4.5E-01
ENSMUST00000123079				2.3	3.5E-02	5.2	6.0E-04	-0.9	4.0E-01	0.9	1.9E-01
ENSMUST00000186425	death-associated protein [Source:MGI Symbol;Acc:MGI:1918190]	A0A087WR57		2.5	1.4E-01	-0.2	9.1E-01	-2.5	9.3E-02	0.2	9.1E-01
ENSMUST00000176999				2.3	1.2E-02	6.7	1.3E-04	-0.5	6.6E-01	-0.7	2.8E-01
ENSMUST00000186445	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B [Source:MGI Symbol;Acc:MGI:2442593]		Q8BND4	-0.2	9.5E-01	-1.8	5.5E-01	-3.2	1.8E-01	-1.5	6.2E-01
ENSMUST00000186446				3.2	2.3E-01	3.1	2.9E-01	-1.5	5.9E-01	-1.3	5.4E-01
ENSMUST00000186398				2.3	2.4E-03	7.8	3.6E-04	-0.7	6.4E-01	0.5	5.3E-01
ENSMUST00000156092				2.3	2.3E-02	5.8	1.0E-03	-0.1	9.3E-01	0.4	5.7E-01
ENSMUST00000124217				2.3	1.5E-03	8.8	3.3E-05	0.7	5.7E-01	0.1	9.2E-01
ENSMUST00000189298				2.3	7.9E-03	5.4	6.8E-04	1.1	2.8E-01	-0.5	5.1E-01
ENSMUST00000175783				2.3	1.8E-03	-0.9	5.8E-01	0.9	4.1E-01	-2.5	1.9E-01
ENSMUST00000130473				2.3	1.5E-02	5.1	8.9E-04	0.5	6.3E-01	-1.2	1.1E-01
ENSMUST00000186470	KAT8 regulatory NSL complex subunit 3 [Source:MGI Symbol;Acc:MGI:1918055]		A2RSY1	0.6	6.8E-01	-1.7	4.5E-01	-0.5	7.1E-01	1.8	4.0E-01
ENSMUST00000186476	predicted gene, 38394 [Source:MGI Symbol;Acc:MGI:5614057]	G0LE24	D2EAC2	0.0	9.4E-01	0.2	8.1E-01	0.9	1.0E-01	0.8	2.6E-01
ENSMUST00000145795				2.3	2.0E-02	7.9	8.0E-05	-0.6	6.7E-01	-0.4	4.6E-01
ENSMUST00000139847				2.3	3.0E-03	-6.1	3.2E-04	0.2	6.2E-01	-0.6	6.0E-01
ENSMUST00000186489				1.1	3.8E-01	3.1	9.1E-02	0.9	5.4E-01	-1.0	3.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000162754				2.3	2.6E-03	4.5	9.6E-05	0.3	6.0E-01	0.2	6.1E-01
ENSMUST00000183253				2.3	5.4E-03	3.5	3.2E-04	0.0	1.0E+00	-0.4	4.2E-01
ENSMUST00000182754				2.3	1.8E-02	4.2	3.0E-03	-1.3	2.3E-01	0.4	6.3E-01
ENSMUST00000140841				2.3	1.7E-02	6.3	2.5E-03	-0.4	8.2E-01	-2.6	2.1E-02
ENSMUST00000137717				2.3	4.8E-03	-6.8	1.4E-03	-1.3	4.1E-02	-0.9	6.2E-01
ENSMUST00000186534	free fatty acid receptor 2 [Source:MGI Symbol;Acc:MGI:2441731]	A0A087WQJ1		-0.8	2.5E-01	1.7	8.0E-02	1.9	2.7E-02	-0.7	4.0E-01
ENSMUST00000146392				2.3	1.7E-03	4.1	2.0E-02	-1.0	4.7E-01	-0.1	9.2E-01
ENSMUST00000173497				2.3	4.1E-03	4.0	5.3E-03	1.7	1.1E-01	0.1	9.1E-01
ENSMUST00000186543	SLIT-ROBO Rho GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:109605]	A0A087WNM1		1.2	2.8E-01	-1.2	5.6E-01	1.5	2.1E-01	3.9	5.9E-02
ENSMUST00000192394				2.3	1.8E-03	4.0	4.4E-03	0.7	4.6E-01	-0.3	6.9E-01
ENSMUST00000176639				2.3	2.5E-02	-6.7	1.4E-02	-1.7	8.0E-02	-0.9	7.1E-01
ENSMUST00000146339				2.2	1.6E-02	9.9	3.0E-06	-0.6	6.0E-01	-0.4	3.4E-01
ENSMUST00000194051				2.2	1.4E-03	8.9	1.3E-03	-0.4	8.5E-01	-1.6	1.1E-01
ENSMUST00000148805				2.2	7.3E-03	4.7	6.3E-04	-0.2	7.9E-01	-0.9	2.1E-01
ENSMUST00000145060				2.2	3.1E-02	4.8	3.0E-04	0.4	6.6E-01	-0.2	7.8E-01
ENSMUST00000149033				2.2	2.0E-02	-6.5	3.6E-03	-0.3	7.0E-01	2.1	2.4E-01
ENSMUST00000186575				1.6	2.1E-01	-2.4	1.1E-01	-4.0	3.5E-03	-0.1	9.6E-01
ENSMUST00000186583	ash1 (absent, small, or homeotic)-like (Drosophila) [Source:MGI Symbol;Acc:MGI:2183158]		Q99MY8	2.1	8.8E-02	-1.6	3.4E-01	-1.1	3.5E-01	2.7	1.1E-01
ENSMUST00000162243				2.2	2.9E-02	9.0	8.0E-05	0.2	9.1E-01	-0.9	1.4E-01
ENSMUST00000130621				2.2	4.6E-03	-4.0	3.1E-02	0.0	9.5E-01	-0.2	9.1E-01
ENSMUST00000133790				2.2	1.6E-02	5.2	3.2E-03	0.0	9.8E-01	-0.2	8.1E-01
ENSMUST00000123021				2.2	1.3E-02	-1.7	3.8E-02	0.6	2.3E-01	0.6	3.6E-01
ENSMUST00000149586				2.2	2.9E-02	6.5	2.0E-04	0.7	5.1E-01	0.0	9.5E-01
ENSMUST00000182467				2.2	4.5E-03	1.9	1.5E-02	-0.4	5.0E-01	0.2	7.7E-01
ENSMUST00000186622	calcium channel, voltage-dependent, alpha 2/delta subunit 4 [Source:MGI Symbol;Acc:MGI:2442632]	A0A087WQH4		4.6	5.8E-02	4.1	1.1E-01	-0.7	7.7E-01	-0.3	8.8E-01
ENSMUST00000127440				2.2	2.2E-02	6.4	2.3E-04	-0.6	6.2E-01	-0.9	1.8E-01
ENSMUST00000186627	kinectin 1 [Source:MGI Symbol;Acc:MGI:109153]	A0A087WS29		-3.5	5.7E-02	-1.3	6.1E-01	2.1	2.2E-01	-0.1	9.6E-01
ENSMUST00000151763				2.2	3.6E-03	-3.8	2.4E-01	1.2	4.8E-01	-0.1	9.8E-01
ENSMUST00000186641	anoctamin 7 [Source:MGI Symbol;Acc:MGI:3052714]		Q14AT5	3.3	1.1E-01	6.8	3.5E-02	1.4	6.2E-01	-2.1	2.0E-01
ENSMUST00000186647				3.3	2.5E-01	0.9	7.5E-01	-2.7	3.3E-01	-0.3	9.0E-01
ENSMUST00000153334				2.2	9.9E-03	-4.7	1.1E-03	1.0	5.5E-02	-2.5	7.3E-02
ENSMUST00000184947				2.2	7.9E-03	8.5	1.6E-05	0.8	4.5E-01	0.0	9.4E-01
ENSMUST00000192884				2.2	2.1E-02	4.9	1.7E-03	-0.4	6.8E-01	0.2	8.4E-01
ENSMUST00000125106				2.2	2.7E-02	9.3	1.2E-05	-0.5	7.0E-01	-1.3	2.2E-02
ENSMUST00000181276				2.2	6.8E-03	2.6	2.3E-02	-0.3	7.4E-01	0.3	6.9E-01
ENSMUST00000160148				2.2	1.8E-02	4.8	2.3E-03	-2.1	1.3E-01	-0.3	6.4E-01
ENSMUST00000189042				2.2	8.0E-03	6.7	3.1E-04	-0.5	7.1E-01	0.4	5.3E-01
ENSMUST00000186684	nucleic acid binding protein 1 [Source:MGI Symbol;Acc:MGI:1923258]		Q8BGW5	-2.2	4.3E-01	-3.5	3.6E-01	-1.0	6.3E-01	0.3	9.5E-01
ENSMUST00000155460				2.2	9.1E-03	5.7	1.0E-02	-0.3	8.6E-01	-1.5	1.9E-01
ENSMUST00000126381				2.2	1.6E-02	-2.4	4.3E-02	0.9	1.5E-01	-3.0	4.9E-02
ENSMUST00000182904				2.2	1.3E-02	8.5	3.8E-04	-0.4	8.2E-01	-2.2	2.3E-02
ENSMUST00000153164				2.2	9.8E-03	4.9	1.1E-02	-0.7	6.7E-01	-0.7	5.1E-01
ENSMUST00000186711	TAR DNA binding protein [Source:MGI Symbol;Acc:MGI:2387629]	A0A087WQ63		-1.9	1.1E-01	-1.8	1.9E-01	0.0	9.7E-01	-0.1	9.5E-01
ENSMUST00000071745				2.2	2.0E-02	8.2	3.5E-05	-0.1	9.3E-01	-0.3	5.5E-01
ENSMUST00000190095				2.2	3.5E-02	-1.1	2.5E-01	0.7	3.3E-01	0.0	9.9E-01
ENSMUST00000133993				2.2	1.6E-02	6.5	4.9E-07	-1.4	3.1E-02	-0.3	3.0E-01
ENSMUST00000119836				2.2	1.6E-02	4.0	3.2E-04	0.0	9.5E-01	-0.7	2.0E-01
ENSMUST00000128847				2.2	1.7E-02	-1.9	1.3E-02	0.8	5.9E-02	-0.5	4.7E-01
ENSMUST00000145506				2.2	2.7E-02	5.7	5.0E-04	-1.2	3.0E-01	0.1	8.4E-01
ENSMUST00000186740				4.0	5.4E-02	2.2	3.7E-01	-1.4	5.5E-01	0.4	8.4E-01
ENSMUST00000186745	influenza virus NS1A binding protein [Source:MGI Symbol;Acc:MGI:2152389]		Q920Q8	-2.0	4.6E-02	-4.5	6.1E-03	-1.2	7.9E-02	1.4	3.0E-01
ENSMUST00000128523				2.2	9.7E-03	1.6	5.1E-02	-0.3	6.0E-01	-0.3	6.3E-01
ENSMUST00000186764	Ngfi-A binding protein 1 [Source:MGI Symbol;Acc:MGI:107564]	A0A087WSU4		-0.1	9.5E-01	1.0	4.7E-01	1.3	2.1E-01	0.3	8.2E-01
ENSMUST00000151971				2.1	6.5E-03	4.7	5.8E-03	-0.2	8.7E-01	-0.3	7.8E-01
ENSMUST00000138436				2.1	2.2E-02	7.0	3.6E-04	-0.9	5.1E-01	1.0	1.7E-01
ENSMUST00000125119				2.1	3.7E-03	1.8	1.0E-01	-0.4	6.3E-01	0.4	6.7E-01
ENSMUST00000186788	DnaJ (Hsp40) homolog, subfamily C, member 13 [Source:MGI Symbol;Acc:MGI:2676368]	D4AFX7		1.7	4.5E-01	1.7	6.2E-01	2.0	3.6E-01	2.0	5.4E-01
ENSMUST00000193923				2.1	1.1E-02	7.2	2.6E-06	-0.5	4.7E-01	-0.8	5.8E-02
ENSMUST00000124448				2.1	4.9E-03	-6.3	3.4E-02	-0.5	5.9E-01	-0.5	8.6E-01
ENSMUST00000126312				2.1	9.4E-03	6.6	4.0E-04	-0.7	6.0E-01	0.5	4.7E-01
ENSMUST00000151225				2.1	1.3E-02	-3.6	1.5E-02	0.2	7.2E-01	-0.6	6.7E-01
ENSMUST00000128157				2.1	7.3E-03	-2.3	1.0E-01	1.3	1.1E-01	-0.5	7.5E-01
ENSMUST00000146771				2.1	5.6E-03	-0.3	7.5E-01	-0.1	8.6E-01	-2.4	6.5E-02
ENSMUST00000165492				2.1	1.5E-02	3.6	4.5E-04	-0.6	4.0E-01	0.2	6.9E-01
ENSMUST00000186833				1.5	1.5E-01	1.9	1.6E-01	0.3	7.6E-01	-0.1	9.4E-01
ENSMUST00000147087				2.1	2.2E-02	2.1	3.8E-02	-1.4	1.1E-01	-0.5	5.4E-01
ENSMUST00000149907				2.1	1.9E-03	5.3	1.3E-02	-0.7	7.3E-01	0.2	8.4E-01
ENSMUST00000189977				2.1	2.6E-02	5.8	1.9E-03	-0.6	6.7E-01	-0.2	7.7E-01
ENSMUST00000124949				2.1	8.7E-03	5.8	3.7E-04	-0.1	9.4E-01	0.4	5.6E-01
ENSMUST00000145396				2.1	2.3E-02	5.8	4.0E-04	0.0	9.7E-01	-0.1	8.2E-01
ENSMUST00000160010				2.1	1.7E-02	-7.8	7.0E-04	0.4	4.2E-01	-0.8	6.4E-01
ENSMUST00000186864	receptor accessory protein 6 [Source:MGI Symbol;Acc:MGI:1917585]		Q9JM62	3.5	6.9E-02	-0.3	9.0E-01	-0.9	6.3E-01	2.9	2.4E-01
ENSMUST00000124101				2.1	2.8E-02	4.1	7.3E-04	0.0	9.8E-01	-0.4	5.2E-01
ENSMUST00000144199				2.1	2.7E-03	4.0	3.7E-02	-0.9	5.6E-01	0.2	8.6E-01
ENSMUST00000126822				2.1	7.6E-03	7.9	1.2E-04	-0.6	6.4E-01	-0.8	2.4E-01
ENSMUST00000184578				2.1	1.8E-02	3.2	4.5E-03	-0.9	2.6E-01	0.6	4.0E-01
ENSMUST00000159823				2.1	2.5E-02	-0.1	9.5E-01	2.3	2.5E-02	-0.7	6.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000164055				2.1	2.8E-02	10.1	1.5E-05	-0.4	7.6E-01	0.2	7.0E-01
ENSMUST00000193539				2.1	1.5E-02	6.6	1.1E-04	-1.2	2.9E-01	-0.4	5.4E-01
ENSMUST00000186894	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]	A0A0B4J1N9		0.4	8.8E-01	2.6	4.8E-01	1.9	4.9E-01	-0.3	9.2E-01
ENSMUST00000189089				2.1	2.1E-02	4.6	2.4E-04	0.4	5.8E-01	-0.2	7.1E-01
ENSMUST00000186903				-0.6	5.5E-01	-1.2	4.1E-01	0.5	6.3E-01	1.1	4.5E-01
ENSMUST00000192090				2.1	1.1E-02	4.9	2.1E-02	-0.6	7.5E-01	1.8	1.3E-01
ENSMUST00000117472				2.1	3.5E-02	-3.5	8.1E-03	-1.4	3.7E-02	-0.3	7.9E-01
ENSMUST00000183907				2.1	9.3E-03	-1.7	2.0E-01	-0.2	7.6E-01	-1.7	2.2E-01
ENSMUST00000186915	insulin induced gene 2 [Source:MGI Symbol;Acc:MGI:1920249]	A0A087WQP7		1.6	3.5E-01	0.0	1.0E+00	0.3	9.0E-01	1.9	4.2E-01
ENSMUST00000182159				2.1	2.6E-02	6.4	1.6E-05	0.0	9.7E-01	0.3	4.7E-01
ENSMUST00000186927				2.9	1.2E-01	3.9	9.7E-02	-0.9	6.7E-01	-1.9	2.6E-01
ENSMUST00000152942				2.1	1.1E-02	6.6	1.0E-03	-0.1	9.3E-01	-0.5	5.9E-01
ENSMUST00000186932				-2.7	1.5E-01	-6.0	1.9E-02	-3.3	1.1E-02	0.0	9.9E-01
ENSMUST00000186933				0.8	3.7E-01	0.0	9.9E-01	0.7	4.8E-01	1.5	2.2E-01
ENSMUST00000106686				2.1	3.2E-02	10.2	5.2E-05	-0.9	6.0E-01	0.4	4.6E-01
ENSMUST00000152541				2.0	2.5E-02	8.8	8.6E-04	-0.9	6.5E-01	0.6	4.7E-01
ENSMUST00000186947	TAR DNA binding protein [Source:MGI Symbol;Acc:MGI:2387629]	A0A087WR97		1.9	2.1E-01	-4.3	1.4E-02	-6.4	2.2E-04	-0.2	9.0E-01
ENSMUST00000144784				2.0	3.8E-03	-2.0	6.9E-02	1.0	1.1E-01	-2.5	5.5E-02
ENSMUST00000124084				2.0	7.9E-03	-8.8	9.8E-03	-2.2	3.0E-02	0.5	8.8E-01
ENSMUST00000191728				2.0	1.7E-02	5.6	1.3E-02	-0.6	7.7E-01	-0.9	4.2E-01
ENSMUST00000132951				2.0	1.2E-02	-2.0	4.2E-01	3.7	2.4E-02	0.9	7.2E-01
ENSMUST00000118424				2.0	8.8E-03	-1.8	7.0E-02	0.3	6.6E-01	-1.1	2.7E-01
ENSMUST00000146471				2.0	9.2E-03	4.2	1.5E-02	-1.4	3.5E-01	-0.6	5.7E-01
ENSMUST00000186964				-3.0	2.7E-01	-1.9	5.0E-01	-0.1	9.5E-01	-1.2	7.1E-01
ENSMUST00000163395				2.0	1.6E-02	6.1	1.8E-04	-1.2	2.8E-01	-1.3	6.2E-02
ENSMUST00000160270				2.0	2.4E-02	-6.3	1.8E-03	0.9	1.0E-01	-0.2	8.9E-01
ENSMUST00000184782				2.0	6.1E-03	4.2	1.9E-03	0.1	9.5E-01	0.8	2.6E-01
ENSMUST00000133096				2.0	3.2E-02	4.1	5.2E-04	-0.4	5.8E-01	-0.4	4.6E-01
ENSMUST00000186978	membrane-spanning 4-domains, subfamily A, member 2 [Source:MGI Symbol;Acc:MGI:95495]	A0A0B4J1P0		0.6	4.0E-01	1.0	3.3E-01	0.9	2.4E-01	0.5	5.3E-01
ENSMUST00000186983	zinc finger, CCHC domain containing 2 [Source:MGI Symbol;Acc:MGI:2444114]	A0A087WSQ9		2.1	2.2E-01	2.2	2.5E-01	-0.4	8.2E-01	-0.5	7.6E-01
ENSMUST00000139311				2.0	2.3E-03	6.9	2.1E-04	-0.3	8.1E-01	-0.5	4.1E-01
ENSMUST00000186987				1.2	4.6E-01	3.5	1.1E-01	1.1	5.4E-01	-1.1	4.8E-01
ENSMUST00000144106				2.0	2.8E-02	5.4	1.9E-03	-0.4	7.6E-01	0.1	8.8E-01
ENSMUST00000155120				2.0	5.0E-04	7.1	7.7E-05	-0.7	5.1E-01	0.0	9.8E-01
ENSMUST00000126819				2.0	4.9E-03	-5.2	4.1E-04	0.3	5.0E-01	-0.6	5.5E-01
ENSMUST00000178661				2.0	1.6E-02	5.8	8.4E-04	-0.1	9.2E-01	0.0	9.6E-01
ENSMUST00000133893				2.0	1.7E-02	5.9	2.4E-03	0.0	9.9E-01	1.0	2.6E-01
ENSMUST00000159831				2.0	2.4E-02	6.0	2.1E-04	3.2	7.5E-03	0.3	5.9E-01
ENSMUST00000135162				2.0	1.6E-02	-3.7	9.4E-03	0.2	7.6E-01	-0.5	6.7E-01
ENSMUST00000187037				-0.3	7.5E-01	2.8	4.0E-02	1.4	1.9E-01	-1.6	1.0E-01
ENSMUST00000190128				2.0	1.6E-02	3.6	2.7E-03	-1.3	1.7E-01	-0.3	6.0E-01
ENSMUST00000187040	Snf2-related CREBBP activator protein [Source:MGI Symbol;Acc:MGI:2444036]	A0A087WQ44		-1.7	2.0E-01	1.4	2.7E-01	0.3	7.5E-01	-2.7	5.6E-02
ENSMUST00000187048	ring finger protein 2 [Source:MGI Symbol;Acc:MGI:1101759]		Q9CQJ4	1.2	1.5E-01	1.6	1.9E-01	1.0	3.0E-01	0.7	4.5E-01
ENSMUST00000187049	integrin-linked kinase-associated serine/threonine phosphatase 2C [Source:MGI Symbol;Acc:MGI:1914694]	A0A087WRS5		1.0	1.6E-01	2.2	2.6E-02	0.6	4.2E-01	-0.6	3.9E-01
ENSMUST00000187058	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:MGI Symbol;Acc:MGI:1928739]		Q9QYI5	-1.3	4.9E-01	-0.7	8.1E-01	1.3	5.2E-01	0.6	8.2E-01
ENSMUST00000120430				2.0	1.0E-02	5.1	2.7E-03	-0.2	8.6E-01	0.3	7.0E-01
ENSMUST00000124012				2.0	8.2E-03	6.0	8.9E-04	0.5	6.8E-01	-0.5	4.9E-01
ENSMUST00000187066				0.8	3.2E-01	-0.4	6.9E-01	-0.8	3.1E-01	0.4	6.5E-01
ENSMUST00000131905				2.0	3.3E-02	6.6	2.0E-04	-0.4	7.4E-01	0.3	6.0E-01
ENSMUST00000141231				2.0	1.6E-02	5.9	9.0E-03	-2.9	1.9E-01	-0.4	7.4E-01
ENSMUST00000143466				1.9	2.5E-02	-5.4	5.7E-03	0.8	1.8E-01	0.7	6.3E-01
ENSMUST00000131562				1.9	1.6E-02	6.5	2.8E-04	-0.6	6.3E-01	-0.3	6.2E-01
ENSMUST00000187105				0.4	6.2E-01	0.0	9.9E-01	0.4	6.9E-01	0.8	4.5E-01
ENSMUST00000187113				-0.4	6.5E-01	0.3	7.5E-01	0.1	9.4E-01	-0.7	5.1E-01
ENSMUST00000143174				1.9	8.1E-03	-4.0	4.8E-02	4.6	3.5E-03	-2.9	1.4E-01
ENSMUST00000166654				1.9	3.1E-02	4.8	1.5E-04	-1.3	1.2E-01	-1.0	1.0E-01
ENSMUST00000153936				1.9	2.8E-02	7.2	2.6E-04	-0.6	6.7E-01	-0.1	9.2E-01
ENSMUST00000192057				1.9	3.7E-03	5.7	8.1E-04	-0.9	4.5E-01	-0.3	6.5E-01
ENSMUST00000159441				1.9	7.1E-03	7.1	1.3E-03	1.9	2.2E-01	-0.4	6.4E-01
ENSMUST00000187168	eukaryotic translation initiation factor 4A2 [Source:MGI Symbol;Acc:MGI:106906]	Q8BTU6		0.2	9.6E-01	-6.7	8.6E-02	-6.4	8.9E-03	0.4	9.1E-01
ENSMUST00000190059				1.9	6.6E-03	4.1	5.1E-03	-0.3	7.9E-01	-0.5	4.9E-01
ENSMUST00000163864				1.9	2.0E-02	1.7	4.2E-01	-3.3	1.5E-01	0.6	7.0E-01
ENSMUST00000137499				1.9	1.2E-02	4.4	9.2E-04	-2.6	3.9E-02	-0.2	7.1E-01
ENSMUST00000187188				-2.5	4.4E-02	-0.2	9.0E-01	1.4	1.4E-01	-0.9	5.5E-01
ENSMUST00000127304				1.9	8.9E-03	5.7	5.7E-04	-0.5	6.6E-01	-0.8	2.3E-01
ENSMUST00000121035				1.9	4.8E-03	6.3	1.9E-04	0.1	9.4E-01	0.4	4.9E-01
ENSMUST00000161230				1.9	1.8E-02	5.2	9.4E-05	-0.3	7.2E-01	0.8	1.1E-01
ENSMUST00000182792				1.9	2.8E-02	7.0	8.8E-05	-0.6	6.1E-01	-0.8	2.0E-01
ENSMUST00000146008				1.9	2.1E-02	2.4	3.3E-01	-0.7	7.3E-01	2.2	2.7E-01
ENSMUST00000146182				1.9	3.0E-02	6.3	4.5E-04	-0.5	6.9E-01	0.2	8.1E-01
ENSMUST00000189008				1.9	2.7E-02	5.9	9.6E-04	-0.6	6.3E-01	-0.3	7.2E-01
ENSMUST00000187231	integrin-linked kinase-associated serine/threonine phosphatase 2C [Source:MGI Symbol;Acc:MGI:1914694]	A0A087WPY0		-0.3	7.6E-01	0.2	8.0E-01	-0.9	3.0E-01	-1.4	1.7E-01
ENSMUST00000124598				1.9	1.9E-02	5.4	3.0E-03	-0.5	7.2E-01	0.9	2.7E-01
ENSMUST00000124229				1.9	9.4E-03	5.4	2.4E-03	1.4	2.7E-01	-0.2	8.4E-01
ENSMUST00000187250				0.5	4.5E-01	0.8	3.0E-01	-0.2	7.1E-01	-0.5	4.4E-01
ENSMUST00000154839				1.9	2.6E-02	7.1	2.9E-03	2.5	1.6E-01	-0.2	8.3E-01
ENSMUST00000187264				3.9	1.1E-01	4.6	9.8E-02	-0.3	9.0E-01	-1.1	5.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000189858				1.9	4.0E-03	-0.8	2.9E-01	-1.1	6.6E-02	1.1	1.3E-01
ENSMUST00000125920				1.8	1.7E-02	7.1	1.9E-04	-0.6	6.2E-01	0.6	3.7E-01
ENSMUST00000138265				1.8	3.4E-02	6.2	4.4E-03	0.1	9.3E-01	1.6	1.3E-01
ENSMUST00000155911				1.8	9.7E-03	7.9	3.1E-05	-0.5	6.4E-01	0.3	5.7E-01
ENSMUST00000149539				1.8	2.8E-02	6.3	2.4E-04	-0.6	6.0E-01	-0.2	7.0E-01
ENSMUST00000156878				1.8	2.0E-02	4.1	1.7E-02	-2.2	1.8E-01	1.1	2.7E-01
ENSMUST00000187308	histone deacetylase 4 [Source:MGI Symbol;Acc:MGI:3036234]	A0A087WQ92		-2.1	6.1E-02	-0.8	5.1E-01	0.4	6.2E-01	-1.0	4.4E-01
ENSMUST00000123178				1.8	2.2E-02	5.8	6.2E-03	-0.7	6.7E-01	0.2	8.1E-01
ENSMUST00000187323				-1.7	1.7E-01	-2.1	1.6E-01	-0.9	3.1E-01	-0.5	7.1E-01
ENSMUST00000131408				1.8	3.1E-02	2.4	1.9E-01	-0.5	7.7E-01	3.3	3.4E-02
ENSMUST00000187347	lymphocyte antigen 6 complex, locus C1 [Source:MGI Symbol;Acc:MGI:96882]		P0CW02	-2.7	4.9E-01	-5.9	1.7E-01	-4.4	6.6E-02	-1.2	8.0E-01
ENSMUST00000139314				1.8	1.7E-02	4.5	1.0E-05	-0.3	6.0E-01	-0.2	5.0E-01
ENSMUST00000168364				1.8	1.8E-02	6.6	2.9E-04	-0.4	7.3E-01	-0.3	6.2E-01
ENSMUST00000178987				1.8	9.2E-03	3.3	2.9E-02	0.0	1.0E+00	-0.4	7.2E-01
ENSMUST00000164592				1.8	8.8E-03	4.4	3.7E-04	-0.4	6.3E-01	-0.3	6.5E-01
ENSMUST00000154468				1.8	1.2E-02	3.4	2.1E-04	-1.3	4.1E-02	-0.5	2.5E-01
ENSMUST00000135635				1.8	2.5E-02	8.1	7.9E-05	-1.1	3.9E-01	0.5	4.2E-01
ENSMUST00000127167				1.8	5.6E-03	6.5	3.2E-03	-0.4	8.3E-01	-1.2	2.1E-01
ENSMUST00000127121				1.8	3.2E-02	4.1	6.7E-04	-2.1	2.6E-02	-0.7	2.5E-01
ENSMUST00000188270				1.8	1.2E-02	6.5	1.6E-03	-0.6	7.0E-01	-0.9	3.3E-01
ENSMUST00000139147				1.8	1.0E-02	-0.9	2.5E-01	1.2	3.1E-02	-0.1	9.2E-01
ENSMUST00000150272				1.8	2.4E-02	8.4	2.5E-05	-0.5	7.0E-01	0.0	9.6E-01
ENSMUST00000187417				-2.2	6.0E-02	-3.1	9.2E-02	0.3	7.6E-01	1.1	5.0E-01
ENSMUST00000153079				1.8	1.2E-02	6.4	8.0E-04	-0.5	7.4E-01	-1.1	1.9E-01
ENSMUST00000187420	solute carrier family 40 (iron-regulated transporter), member 1 [Source:MGI Symbol;Acc:MGI:1315204]	C5H8V4		-0.1	9.6E-01	-5.0	1.1E-01	-5.4	1.1E-02	-0.5	8.7E-01
ENSMUST00000187427				1.1	2.2E-01	1.2	2.6E-01	0.2	8.6E-01	0.0	9.8E-01
ENSMUST00000187429	activating transcription factor 7 interacting protein [Source:MGI Symbol;Acc:MGI:1858965]	A0A087WR75		-1.6	5.8E-01	3.1	2.5E-01	0.3	8.7E-01	-4.3	1.5E-01
ENSMUST00000128725				1.8	1.7E-02	10.1	9.5E-03	1.0	7.7E-01	0.5	7.3E-01
ENSMUST00000187434	predicted gene, 20777 [Source:MGI Symbol;Acc:MGI:5434133]	Q3TTD8		2.1	1.2E-01	6.8	2.0E-04	-0.5	6.8E-01	-5.3	2.4E-04
ENSMUST00000160189				1.8	2.1E-02	5.5	7.3E-03	2.5	1.2E-01	0.5	5.7E-01
ENSMUST00000128633				1.7	3.1E-02	6.8	1.5E-04	-0.6	6.3E-01	-0.3	6.8E-01
ENSMUST00000183332				1.7	1.1E-02	5.9	1.1E-03	-0.7	6.2E-01	0.4	5.9E-01
ENSMUST00000180306				1.7	4.8E-03	-6.8	2.0E-04	-1.8	2.4E-03	0.1	9.6E-01
ENSMUST00000152955				1.7	2.4E-02	8.4	5.5E-03	-1.2	6.4E-01	1.6	2.2E-01
ENSMUST00000152063				1.7	2.7E-02	4.1	2.7E-03	-0.2	8.3E-01	-0.4	6.4E-01
ENSMUST00000140187				1.7	3.0E-02	6.8	2.0E-04	-0.5	7.1E-01	-0.6	3.4E-01
ENSMUST00000145629				1.7	8.4E-03	3.5	2.6E-04	0.3	5.9E-01	0.0	9.2E-01
ENSMUST00000141217				1.7	2.6E-02	6.4	7.3E-05	-0.6	5.4E-01	0.1	9.1E-01
ENSMUST00000142101				1.7	3.5E-02	5.3	1.0E-03	-0.2	8.4E-01	-2.2	1.2E-02
ENSMUST00000182661				1.7	2.6E-02	-6.7	5.5E-04	-0.5	2.8E-01	1.9	1.7E-01
ENSMUST00000159140				1.7	2.9E-02	2.0	1.4E-02	0.4	4.6E-01	0.0	9.9E-01
ENSMUST00000187507	sterol O-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:104665]	A0A087WNN8		2.3	3.6E-01	1.4	6.1E-01	-0.4	8.8E-01	0.5	8.3E-01
ENSMUST00000187510	cholinergic receptor, muscarinic 3, cardiac [Source:MGI Symbol;Acc:MGI:88398]	Q542R4	Q9ERZ3	-1.3	9.0E-02	-0.6	5.0E-01	0.4	4.8E-01	-0.2	7.8E-01
ENSMUST00000185661				1.7	1.3E-02	7.2	1.5E-03	-0.8	6.5E-01	0.6	5.3E-01
ENSMUST00000187516	arrier family 11 (proton-coupled divalent metal ion transporters), member 1 [Source:MGI Symbol;Acc:MGI:13	A0A087WNR0		-2.0	2.3E-01	1.1	5.3E-01	0.1	9.7E-01	-3.0	8.5E-02
ENSMUST00000139082				1.7	2.5E-02	-6.9	2.2E-04	0.2	6.3E-01	-0.1	9.2E-01
ENSMUST00000137143				1.6	2.0E-02	1.4	3.0E-01	-0.2	8.8E-01	1.7	1.3E-01
ENSMUST00000177148				1.6	2.7E-02	8.3	1.3E-04	-0.4	8.0E-01	-0.8	2.0E-01
ENSMUST00000167547				1.6	1.7E-02	5.5	7.9E-03	0.5	7.6E-01	-0.1	9.2E-01
ENSMUST00000154829				1.6	3.0E-02	6.4	2.2E-03	-0.4	8.1E-01	-0.1	9.4E-01
ENSMUST00000143233				1.6	1.2E-02	7.3	2.8E-06	0.8	2.5E-01	-0.1	7.3E-01
ENSMUST00000136593				1.6	1.7E-02	3.6	8.2E-03	-1.6	1.6E-01	-0.1	8.9E-01
ENSMUST00000187550	RIKEN cDNA 1700088E04 gene [Source:MGI Symbol;Acc:MGI:1920774]	Q4V9V4		2.9	9.2E-02	2.1	1.5E-01	-2.5	1.1E-01	-1.7	2.0E-01
ENSMUST00000147822				1.6	2.6E-02	6.0	9.2E-04	-0.5	6.9E-01	-0.8	2.8E-01
ENSMUST00000186755				1.6	2.3E-02	3.7	1.5E-01	-0.7	7.9E-01	2.4	1.5E-01
ENSMUST00000187562				-3.2	3.7E-02	-0.3	8.5E-01	1.3	2.3E-01	-1.6	3.0E-01
ENSMUST00000187573				1.6	1.8E-01	2.0	1.5E-01	-0.5	6.8E-01	-0.8	5.0E-01
ENSMUST00000136901				1.6	3.3E-02	6.0	3.1E-04	0.1	9.2E-01	-0.3	6.0E-01
ENSMUST00000098119				1.6	8.4E-03	6.0	1.6E-05	-0.2	7.7E-01	0.3	5.5E-01
ENSMUST00000187578				1.0	2.4E-01	0.0	9.7E-01	-0.4	6.5E-01	0.6	5.4E-01
ENSMUST00000134909				1.6	1.0E-02	5.6	2.3E-04	-0.3	7.4E-01	-0.1	8.8E-01
ENSMUST00000129761				1.6	2.3E-02	2.6	4.0E-01	-3.7	3.1E-01	2.5	2.5E-01
ENSMUST00000187586				-0.9	1.4E-01	-1.0	2.7E-01	0.5	3.8E-01	0.5	5.4E-01
ENSMUST00000136412				1.6	3.3E-02	6.5	1.9E-04	3.0	1.3E-02	-0.1	8.2E-01
ENSMUST00000182970				1.6	2.2E-02	5.2	3.3E-05	-0.8	2.5E-01	0.3	4.5E-01
ENSMUST00000187609	nuclear protein transcription regulator 1 [Source:MGI Symbol;Acc:MGI:1891834]			-2.9	2.4E-01	-4.2	1.6E-01	-2.1	1.9E-01	-0.7	8.1E-01
ENSMUST00000129977				1.6	3.4E-02	5.8	2.7E-05	-0.7	3.8E-01	0.1	7.5E-01
ENSMUST00000152639				1.5	1.8E-02	6.2	1.4E-03	-0.1	9.7E-01	0.3	7.2E-01
ENSMUST00000117281				1.5	1.8E-02	7.1	2.2E-04	-0.2	9.0E-01	0.0	9.6E-01
ENSMUST00000133715				1.5	2.0E-02	2.8	1.4E-02	-0.5	5.2E-01	-0.4	6.4E-01
ENSMUST00000137261				1.5	3.4E-02	7.4	6.9E-05	-1.4	2.5E-01	0.2	7.9E-01
ENSMUST00000153748				1.4	1.5E-02	-0.4	7.4E-01	0.4	6.7E-01	-3.4	4.6E-02
ENSMUST00000187279				1.4	3.1E-02	-4.9	3.3E-02	-1.5	1.2E-01	-0.5	8.2E-01
ENSMUST00000119892				1.4	5.3E-03	5.1	3.9E-02	0.5	8.1E-01	0.8	5.7E-01
ENSMUST00000129591				1.4	1.4E-02	4.0	7.0E-03	-0.2	8.9E-01	0.3	7.2E-01
ENSMUST00000187656	predicted gene 3604 [Source:MGI Symbol;Acc:MGI:3781781]	A0A087WPN2		1.1	8.8E-02	1.4	6.4E-02	0.1	8.9E-01	-0.3	6.7E-01
ENSMUST00000187672				0.5	3.9E-01	0.4	5.1E-01	-1.2	5.3E-02	-1.1	1.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000149057				1.3	6.3E-03	2.7	5.1E-02	-0.9	4.3E-01	0.8	4.4E-01
ENSMUST00000174778				1.2	1.5E-02	7.5	4.5E-04	-0.7	6.3E-01	0.3	6.7E-01
ENSMUST00000121042				1.2	2.3E-02	8.5	5.4E-05	-1.0	4.7E-01	-0.5	3.3E-01
ENSMUST00000187690	protein phosphatase 1, regulatory subunit 18 [Source:MGI Symbol;Acc:MGI:1923698]		Q8BQ30	-2.1	1.5E-01	-4.0	2.3E-01	2.2	1.9E-01	4.1	1.9E-01
ENSMUST00000187691	tensin 1 [Source:MGI Symbol;Acc:MGI:104552]	Q9DBT6		2.9	1.5E-01	1.6	5.5E-01	0.1	9.7E-01	1.4	5.2E-01
ENSMUST00000113628				-1.0	1.6E-02	6.1	7.9E-04	0.5	6.9E-01	0.3	6.3E-01
ENSMUST00000178049				-1.3	3.8E-03	6.0	2.0E-04	-1.5	2.0E-01	0.0	9.5E-01
ENSMUST00000187699	adiponectin receptor 2 [Source:MGI Symbol;Acc:MGI:93830]	A0A087WPB1		2.4	3.3E-01	1.1	7.6E-01	0.3	9.0E-01	1.6	6.4E-01
ENSMUST00000140322				-1.3	1.9E-02	7.8	9.2E-05	0.0	9.9E-01	-0.5	3.9E-01
ENSMUST00000136408				-1.4	2.6E-02	5.1	1.7E-05	-0.7	2.9E-01	0.2	5.4E-01
ENSMUST00000146514				-1.5	2.1E-02	5.1	9.6E-05	-2.3	3.0E-02	-0.2	7.3E-01
ENSMUST00000187711	family with sequence similarity 46, member A [Source:MGI Symbol;Acc:MGI:2670964]	A0A087WS27		4.5	7.0E-02	3.0	3.3E-01	-0.6	8.1E-01	0.9	7.1E-01
ENSMUST00000187729				3.3	2.6E-01	5.4	9.2E-02	-0.6	8.6E-01	-2.6	2.1E-01
ENSMUST00000187733	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]	A0A087WRK9		-4.9	6.4E-02	-1.5	7.5E-01	4.7	1.2E-01	1.3	7.6E-01
ENSMUST00000178598				-1.5	1.3E-02	4.9	8.7E-03	-0.6	6.8E-01	0.8	3.8E-01
ENSMUST00000152551				-1.6	2.7E-02	5.7	2.4E-03	0.0	9.8E-01	0.4	5.7E-01
ENSMUST00000187750				3.0	2.3E-01	5.3	5.1E-02	-0.6	8.3E-01	-2.8	1.3E-01
ENSMUST00000186608				-1.6	1.4E-02	5.8	5.3E-04	-0.6	6.4E-01	-0.7	3.1E-01
ENSMUST00000187758	ubiquitin specific peptidase 40 [Source:MGI Symbol;Acc:MGI:2443184]		Q8BWR4	-1.7	2.7E-01	-0.8	7.2E-01	0.9	5.6E-01	0.1	9.8E-01
ENSMUST00000194747				-1.6	2.5E-02	6.5	1.0E-03	-0.7	6.3E-01	0.3	7.1E-01
ENSMUST00000146999				-1.6	4.9E-03	5.8	1.3E-03	-2.2	1.5E-01	0.8	2.9E-01
ENSMUST00000144909				-1.7	1.6E-02	-6.4	4.6E-04	-1.2	6.4E-02	-3.3	6.3E-02
ENSMUST00000187774	dedicator of cytokinesis 10 [Source:MGI Symbol;Acc:MGI:2146320]	A0A087WQ86		-3.4	2.7E-01	-3.1	3.4E-01	-1.9	3.5E-01	-2.2	5.4E-01
ENSMUST00000187776				-0.2	7.9E-01	1.8	1.2E-01	1.2	1.8E-01	-0.8	4.1E-01
ENSMUST00000187792	9 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:1888	A0A087WQ57		3.4	6.7E-02	-2.8	1.4E-01	-4.5	1.4E-02	1.7	3.5E-01
ENSMUST00000192776				-1.7	3.3E-02	5.3	1.8E-03	-0.1	9.3E-01	-1.4	1.5E-01
ENSMUST00000187811	cAMP responsive element binding protein 1 [Source:MGI Symbol;Acc:MGI:88494]	A0A087WRI6		2.8	8.8E-02	-1.2	4.9E-01	-3.5	2.8E-02	0.5	7.8E-01
ENSMUST00000187814	CLOCK interacting protein, circadian [Source:MGI Symbol;Acc:MGI:1919185]		Q8R0W1	-0.6	2.8E-01	0.0	9.5E-01	0.3	4.9E-01	-0.3	6.5E-01
ENSMUST00000192548				-1.7	6.2E-03	8.4	5.0E-03	-0.8	7.6E-01	-0.4	7.6E-01
ENSMUST00000156404				-1.7	1.2E-02	-2.1	1.5E-01	1.5	6.9E-02	-0.6	6.6E-01
ENSMUST00000173510				-1.7	2.4E-02	4.9	8.6E-03	-1.2	4.6E-01	-0.3	7.3E-01
ENSMUST00000032918				-1.8	1.3E-02	8.4	7.2E-06	-0.8	4.2E-01	-0.4	3.3E-01
ENSMUST00000187834				-0.4	8.3E-01	0.8	7.1E-01	0.5	7.7E-01	-0.7	7.5E-01
ENSMUST00000187836	aspartyl aminopeptidase [Source:MGI Symbol;Acc:MGI:1278328]		Q9Z2W0	-0.9	3.9E-01	-0.7	5.7E-01	0.2	8.3E-01	0.1	9.5E-01
ENSMUST00000129577				-1.8	1.3E-03	6.7	9.5E-05	-1.5	2.1E-01	0.1	8.8E-01
ENSMUST00000127712				-1.8	2.3E-02	8.1	1.5E-06	0.1	9.4E-01	0.1	8.8E-01
ENSMUST00000187852	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1 [Source:MGI Symbol;Acc:MGI:105371]	Q8BM07		3.7	1.0E-01	4.9	4.5E-02	-0.5	8.2E-01	-1.8	2.6E-01
ENSMUST00000182751				-1.8	1.4E-02	7.3	2.3E-04	-0.6	6.7E-01	-0.9	1.9E-01
ENSMUST00000167159				-1.8	2.8E-02	2.0	2.3E-02	-1.7	2.4E-02	0.8	2.2E-01
ENSMUST00000187864				1.6	4.2E-02	1.1	2.4E-01	-0.5	5.0E-01	0.1	9.0E-01
ENSMUST00000138674				-1.8	2.5E-02	3.9	2.8E-02	-2.0	2.5E-01	-0.2	8.7E-01
ENSMUST00000125137				-1.8	2.3E-02	3.5	8.6E-03	-2.5	5.4E-02	-1.1	2.3E-01
ENSMUST00000135550				-1.8	6.7E-03	4.2	3.8E-04	-1.4	9.5E-02	-0.1	8.1E-01
ENSMUST00000187886				2.5	4.7E-02	6.4	1.9E-04	-0.5	6.5E-01	-4.4	4.2E-04
ENSMUST00000130415				-1.8	2.5E-02	6.3	3.6E-04	-0.6	6.4E-01	-0.2	7.4E-01
ENSMUST00000150547				-1.8	1.3E-02	5.2	8.2E-03	-0.6	7.2E-01	-0.3	7.2E-01
ENSMUST00000187899	ArfGAP with FG repeats 1 [Source:MGI Symbol;Acc:MGI:1333754]	A0A087WNV1		3.0	1.3E-01	-3.2	2.4E-02	-8.7	2.6E-04	-2.4	1.2E-01
ENSMUST00000183414				-1.9	8.5E-03	6.9	1.1E-02	0.1	9.5E-01	-2.2	1.1E-01
ENSMUST00000187901	family with sequence similarity 134, member A [Source:MGI Symbol;Acc:MGI:2388278]	A0A087WRH7		2.7	8.1E-02	2.3	2.4E-01	0.0	9.9E-01	0.4	8.0E-01
ENSMUST00000117207				-1.9	1.1E-02	5.7	2.3E-03	-0.2	8.8E-01	-0.7	4.3E-01
ENSMUST00000187910	transcription elongation factor B (SIII), polypeptide 1 [Source:MGI Symbol;Acc:MGI:1915173]	A0A087WNT1		-3.6	1.8E-01	-3.9	2.1E-01	-1.4	4.0E-01	-1.1	7.4E-01
ENSMUST00000187938	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]	Q3UHL6		-2.3	4.7E-01	-1.3	6.7E-01	-1.3	6.1E-01	-2.3	4.9E-01
ENSMUST00000187943	predicted gene, 20809 [Source:MGI Symbol;Acc:MGI:5434165]	Q62458		3.5	1.5E-01	2.8	2.9E-01	-0.4	8.7E-01	0.3	8.9E-01
ENSMUST00000162504				-1.9	8.0E-03	4.2	2.2E-03	-1.5	1.7E-01	-0.7	2.9E-01
ENSMUST00000174671				-1.9	2.9E-02	8.5	8.5E-04	-0.2	9.3E-01	-0.3	7.5E-01
ENSMUST00000176856				-2.0	1.9E-02	6.9	8.3E-05	0.2	8.4E-01	0.0	9.7E-01
ENSMUST00000187951	ER degradation enhancer, mannosidase alpha-like 3 [Source:MGI Symbol;Acc:MGI:1914217]	B7ZNP0		1.6	5.2E-01	-0.7	8.3E-01	-2.7	2.3E-01	-0.4	8.9E-01
ENSMUST00000191395				-2.0	2.0E-02	-3.4	3.1E-01	1.5	3.7E-01	-1.3	7.2E-01
ENSMUST00000131534				-2.0	6.1E-03	6.6	1.2E-03	-0.6	6.8E-01	-1.4	1.2E-01
ENSMUST00000184540				-2.0	3.2E-03	4.2	1.6E-03	1.1	2.3E-01	-0.4	6.3E-01
ENSMUST00000133280				-2.0	2.7E-02	7.2	6.0E-04	-0.4	7.8E-01	-0.9	2.4E-01
ENSMUST00000161503				-2.0	1.2E-02	-11.8	6.5E-04	-0.9	1.3E-01	1.9	4.5E-01
ENSMUST00000170491				-2.0	1.2E-02	6.2	1.3E-03	-0.6	6.8E-01	-1.8	5.2E-02
ENSMUST00000144299				-2.0	1.9E-02	2.3	1.6E-02	-0.3	6.6E-01	0.4	5.4E-01
ENSMUST00000133033				-2.0	2.2E-02	5.0	4.4E-04	-2.7	2.6E-02	-0.4	5.6E-01
ENSMUST00000121229				-2.0	1.5E-03	6.9	5.7E-05	-0.9	4.2E-01	0.0	1.0E+00
ENSMUST00000187985	protein tyrosine phosphatase, non-receptor type 7 [Source:MGI Symbol;Acc:MGI:2156893]		Q8BUM3	-0.6	6.7E-01	0.2	9.2E-01	1.4	3.7E-01	0.6	7.8E-01
ENSMUST00000152398				-2.0	2.3E-02	-1.6	1.2E-01	0.0	9.9E-01	-2.1	9.0E-02
ENSMUST00000118786				-2.1	1.7E-03	6.1	1.5E-03	-0.7	6.6E-01	-0.4	6.6E-01
ENSMUST00000043161				-2.1	8.4E-03	6.2	4.9E-04	-0.6	6.2E-01	0.0	9.9E-01
ENSMUST00000138258				-2.1	1.9E-02	6.8	5.8E-05	-0.6	5.1E-01	-0.2	7.1E-01
ENSMUST00000154796				-2.1	2.5E-02	7.1	5.4E-02	1.1	7.5E-01	1.1	6.1E-01
ENSMUST00000144058				-2.1	2.7E-02	1.5	1.5E-01	-2.4	3.2E-02	0.0	1.0E+00
ENSMUST00000148036				-2.1	9.4E-03	6.0	3.3E-04	-1.3	2.9E-01	0.5	4.2E-01
ENSMUST00000138401				-2.1	9.1E-03	7.8	2.2E-03	1.2	5.3E-01	1.2	2.4E-01
ENSMUST00000152371				-2.1	2.6E-02	6.3	1.3E-03	0.7	6.1E-01	-1.0	2.5E-01
ENSMUST00000142773				-2.1	2.0E-02	6.3	8.7E-05	-1.4	1.9E-01	-0.2	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000188025				0.3	8.8E-01	-0.2	9.0E-01	-0.6	6.9E-01	-0.1	9.4E-01
ENSMUST00000188027	sterol O-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:104665]	A0A087WSJ5		-0.4	8.7E-01	-2.3	4.6E-01	-1.6	3.7E-01	0.3	9.2E-01
ENSMUST00000145588				-2.1	3.1E-02	6.5	8.2E-04	-0.6	6.7E-01	0.1	9.2E-01
ENSMUST00000188032				6.1	5.3E-02	2.2	4.3E-01	-4.6	1.5E-01	-0.7	7.3E-01
ENSMUST00000166609				-2.1	3.3E-02	3.0	7.8E-03	-0.1	9.0E-01	0.2	8.2E-01
ENSMUST00000169194				-2.1	1.0E-02	7.0	1.5E-06	-0.4	5.2E-01	0.0	9.6E-01
ENSMUST00000188042	lymphocyte antigen 6 complex, locus E [Source:MGI Symbol;Acc:MGI:106651]	Q99JA5		0.0	1.0E+00	-0.3	7.7E-01	0.1	8.8E-01	0.5	6.7E-01
ENSMUST00000118761				-2.1	4.8E-03	-5.1	8.5E-04	-7.8	1.2E-05	0.4	7.2E-01
ENSMUST00000137430				-2.1	3.2E-02	7.2	1.2E-04	-0.6	6.4E-01	-1.3	6.7E-02
ENSMUST00000188053				1.2	2.3E-01	1.2	3.4E-01	0.1	8.9E-01	0.2	8.6E-01
ENSMUST00000122928				-2.2	2.4E-02	9.9	9.6E-04	-1.0	6.7E-01	0.6	4.8E-01
ENSMUST00000183307				-2.2	1.7E-02	6.2	3.1E-04	-1.3	3.1E-01	-0.2	7.4E-01
ENSMUST00000131108				-2.2	1.7E-03	7.7	7.6E-04	-0.5	7.8E-01	-1.4	1.3E-01
ENSMUST00000174588				-2.2	1.9E-02	6.1	4.9E-03	1.0	5.3E-01	-0.9	3.6E-01
ENSMUST00000132929				-2.2	3.3E-02	8.0	4.3E-05	-0.4	7.1E-01	0.5	3.6E-01
ENSMUST00000134138				-2.2	1.4E-02	6.1	3.4E-04	-0.2	8.6E-01	0.7	3.0E-01
ENSMUST00000137691				-2.2	1.1E-02	-2.3	5.5E-02	0.6	3.3E-01	-0.1	9.5E-01
ENSMUST00000188094				-0.1	9.5E-01	-0.7	7.9E-01	-0.9	6.2E-01	-0.4	8.6E-01
ENSMUST00000139762				-2.2	1.2E-02	9.5	1.2E-02	0.0	9.9E-01	-2.6	1.3E-01
ENSMUST00000151368				-2.2	1.2E-02	5.6	8.1E-04	-2.0	1.4E-01	-0.8	2.8E-01
ENSMUST00000127085				-2.2	3.1E-02	7.3	7.1E-07	0.4	5.5E-01	0.0	9.7E-01
ENSMUST00000129860				-2.3	2.3E-02	6.5	1.6E-04	-0.6	5.5E-01	0.9	1.7E-01
ENSMUST00000188109	isocitrate dehydrogenase 1 (NADP+), soluble [Source:MGI Symbol;Acc:MGI:96413]	A0A087WRS9		0.2	9.2E-01	-4.4	6.0E-02	-5.2	4.4E-03	-0.7	7.8E-01
ENSMUST00000188111	RIKEN cDNA 2410002F23 gene [Source:MGI Symbol;Acc:MGI:1914226]	Q3TE80		1.2	5.4E-01	8.3	2.8E-03	1.7	4.3E-01	-5.4	9.4E-03
ENSMUST00000188124	Snf2-related CREBBP activator protein [Source:MGI Symbol;Acc:MGI:2444036]	A0A087WS36		-1.6	1.3E-01	-0.6	6.8E-01	0.9	3.2E-01	-0.1	9.4E-01
ENSMUST00000129540				-2.3	3.3E-02	3.4	6.0E-02	-1.9	2.3E-01	0.9	4.5E-01
ENSMUST00000168798				-2.3	1.9E-03	6.2	4.2E-04	-0.5	6.9E-01	-1.0	1.8E-01
ENSMUST00000188142	pseudopodium-enriched atypical kinase 1 [Source:MGI Symbol;Acc:MGI:2442366]	A0A087WQ01		0.8	9.6E-02	0.5	3.4E-01	-0.8	1.0E-01	-0.5	3.6E-01
ENSMUST00000191143				-2.3	1.5E-02	7.1	3.5E-04	0.3	8.5E-01	-0.2	8.1E-01
ENSMUST00000188151	ribosomal protein L22 [Source:MGI Symbol;Acc:MGI:99262]	Q4VAG4	P67984	-1.7	1.4E-01	-0.6	6.2E-01	-0.7	4.2E-01	-1.8	1.7E-01
ENSMUST00000148547				-2.3	2.0E-02	7.2	1.0E-05	-0.2	7.8E-01	-0.4	3.7E-01
ENSMUST00000180658				-2.3	3.5E-02	5.5	1.6E-03	-1.3	3.5E-01	-1.7	8.6E-02
ENSMUST00000141908				-2.3	6.1E-03	5.9	1.1E-03	-0.4	7.5E-01	0.0	9.9E-01
ENSMUST00000123046				-2.3	3.5E-02	7.9	8.8E-04	-1.2	5.1E-01	0.4	6.1E-01
ENSMUST00000195408				-2.3	2.7E-02	4.7	3.3E-03	-1.3	3.2E-01	1.1	1.9E-01
ENSMUST00000124112				-2.3	2.4E-02	8.2	3.6E-05	-0.6	6.0E-01	0.3	5.6E-01
ENSMUST00000167285				-2.3	7.5E-03	6.2	2.9E-03	-0.7	6.6E-01	0.9	3.1E-01
ENSMUST00000149076				-2.3	2.0E-02	-4.8	6.7E-03	0.5	4.5E-01	-1.6	3.2E-01
ENSMUST00000188205				0.2	8.7E-01	-2.4	1.8E-01	-0.2	8.1E-01	2.3	1.6E-01
ENSMUST00000129003				-2.3	2.1E-02	-1.0	2.9E-01	0.5	3.9E-01	-1.5	1.5E-01
ENSMUST00000130219				-2.3	2.6E-02	-6.9	4.4E-05	-0.2	5.4E-01	-0.8	4.3E-01
ENSMUST00000145749				-2.4	1.8E-02	4.5	4.0E-02	-0.8	7.0E-01	0.6	6.2E-01
ENSMUST00000186913				-2.4	2.9E-02	6.6	1.3E-04	-0.6	5.9E-01	-0.1	8.5E-01
ENSMUST00000141996				-2.4	1.9E-02	-6.9	4.3E-05	-1.6	9.1E-03	-6.1	5.5E-03
ENSMUST00000188237				2.0	3.6E-02	1.7	1.4E-01	-0.1	9.5E-01	0.2	8.1E-01
ENSMUST00000129428				-2.4	1.3E-02	7.5	1.3E-03	-0.8	6.6E-01	1.1	2.4E-01
ENSMUST00000168805				-2.4	2.5E-02	4.9	2.2E-02	-0.5	7.8E-01	1.2	2.9E-01
ENSMUST00000188252				2.5	3.6E-02	-4.9	5.8E-04	-8.0	4.4E-06	-0.6	5.4E-01
ENSMUST00000148561				-2.4	1.5E-03	8.1	4.8E-04	-0.5	7.5E-01	0.0	9.9E-01
ENSMUST00000138650				-2.4	1.7E-02	6.6	3.5E-04	-1.0	4.4E-01	0.3	6.7E-01
ENSMUST00000156948				-2.4	2.6E-02	1.6	2.4E-02	-1.4	3.0E-02	-1.2	4.6E-02
ENSMUST00000156377				-2.4	1.3E-02	7.5	1.7E-04	-0.7	6.0E-01	0.6	3.8E-01
ENSMUST00000188275	matrin 3 [Source:MGI Symbol;Acc:MGI:1298379]	A0A087WQZ1		0.7	7.4E-01	2.7	1.7E-01	-0.8	6.7E-01	-2.8	1.3E-01
ENSMUST00000023292				-2.4	5.5E-03	6.2	4.3E-04	-0.6	6.4E-01	-0.7	3.2E-01
ENSMUST00000137139				-2.4	1.4E-02	-1.2	2.6E-01	0.9	2.2E-01	-0.4	7.0E-01
ENSMUST00000155325				-2.4	5.4E-03	5.6	7.8E-04	-0.1	9.0E-01	0.4	6.2E-01
ENSMUST00000184497				-2.4	1.0E-02	5.6	5.5E-03	-0.3	8.5E-01	0.2	8.6E-01
ENSMUST00000176831				-2.4	8.5E-03	-2.9	4.9E-03	-2.2	2.6E-03	-2.9	1.9E-02
ENSMUST00000135249				-2.4	1.1E-02	-4.5	3.9E-03	0.1	8.3E-01	-1.7	2.4E-01
ENSMUST00000188302	tripeptidyl peptidase II [Source:MGI Symbol;Acc:MGI:102724]	Q05DJ9		-0.2	9.4E-01	4.3	3.0E-01	4.4	1.7E-01	-0.2	9.6E-01
ENSMUST00000188288				-2.4	1.1E-02	5.0	6.6E-04	-0.5	5.8E-01	-0.1	8.7E-01
ENSMUST00000142637				-2.4	8.7E-03	6.4	8.3E-03	-0.8	7.2E-01	-1.5	2.2E-01
ENSMUST00000149329				-2.4	3.2E-02	-3.1	1.0E-01	0.5	6.2E-01	-1.5	4.6E-01
ENSMUST00000121413				-2.4	2.0E-03	5.4	5.2E-04	0.4	6.5E-01	-0.4	5.7E-01
ENSMUST00000155497				-2.4	1.2E-02	6.9	1.3E-04	-0.5	6.5E-01	-1.1	9.9E-02
ENSMUST00000152437				-2.4	1.9E-02	8.2	1.1E-04	0.5	6.7E-01	1.3	5.6E-02
ENSMUST00000144304				-2.5	2.5E-02	6.7	1.5E-04	-0.5	6.6E-01	-0.7	2.8E-01
ENSMUST00000156334				-2.5	2.0E-02	6.3	8.8E-04	-0.6	6.7E-01	-0.5	5.3E-01
ENSMUST00000174472				-2.5	5.4E-03	7.0	4.8E-03	-0.7	7.3E-01	-2.1	8.5E-02
ENSMUST00000188333				0.9	8.7E-02	1.6	2.6E-02	-0.5	3.6E-01	-1.1	6.9E-02
ENSMUST00000137896				-2.5	2.3E-02	7.0	5.2E-04	-0.7	6.1E-01	1.0	1.8E-01
ENSMUST00000151608				-2.5	1.6E-02	5.2	1.4E-04	-0.9	2.7E-01	-0.2	7.2E-01
ENSMUST00000188346	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:MGI Symbol;Acc:MGI:1928739]		Q9QYI5	-0.4	8.8E-01	-1.3	7.3E-01	-1.4	5.8E-01	-0.6	8.7E-01
ENSMUST00000126272				-2.5	7.6E-03	-6.3	1.8E-02	1.2	1.2E-01	2.2	3.5E-01
ENSMUST00000128374				-2.5	2.4E-02	5.1	1.4E-02	-0.7	6.8E-01	0.7	5.1E-01
ENSMUST00000188362				-1.6	1.5E-01	-1.6	2.8E-01	0.2	8.2E-01	0.2	8.9E-01
ENSMUST00000127505				-2.5	1.0E-03	-1.3	3.1E-01	0.7	3.8E-01	-2.7	7.7E-02

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000144516				-2.5	3.5E-03	4.2	1.4E-03	0.9	3.2E-01	0.6	3.4E-01
ENSMUST00000180398				-2.5	1.0E-02	4.9	9.5E-04	-0.6	5.4E-01	0.0	9.6E-01
ENSMUST00000188377	translocating chain-associating membrane protein 1 [Source:MGI Symbol;Acc:MGI:1919515]	A0A087WR72		-0.7	5.6E-01	-0.9	4.5E-01	-0.8	3.7E-01	-0.5	6.9E-01
ENSMUST00000189173				-2.5	2.8E-03	5.1	1.1E-03	-2.9	3.7E-02	1.2	1.1E-01
ENSMUST00000154092				-2.5	9.5E-03	9.5	1.3E-05	-0.7	5.8E-01	0.1	7.9E-01
ENSMUST00000188389	dual serine/threonine and tyrosine protein kinase [Source:MGI Symbol;Acc:MGI:1925064]	A0A087WP69		3.0	1.3E-01	4.0	1.1E-01	-0.1	9.7E-01	-1.0	5.8E-01
ENSMUST00000123511				-2.5	5.4E-03	4.6	2.7E-04	-1.8	7.6E-02	-0.8	2.0E-01
ENSMUST00000188402	inhibitor of growth family, member 5 [Source:MGI Symbol;Acc:MGI:1922816]	A0A087WRR4		1.2	4.4E-01	6.8	2.2E-02	5.5	4.0E-02	-0.2	9.1E-01
ENSMUST00000144877				-2.5	2.0E-02	5.6	9.1E-04	0.1	9.3E-01	0.2	7.8E-01
ENSMUST00000138484				-2.5	3.2E-02	6.2	8.2E-04	-0.4	7.5E-01	-0.8	3.0E-01
ENSMUST00000188414	ır family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13 [Source:MGI Symbol;Acc:MG		Q9QXX4	2.7	4.5E-02	6.6	2.5E-04	-0.5	6.7E-01	-4.4	6.4E-04
ENSMUST00000156620				-2.5	3.0E-02	6.3	2.5E-04	-0.5	6.6E-01	-0.7	2.9E-01
ENSMUST00000140439				-2.5	3.2E-02	5.7	7.1E-04	-0.9	4.7E-01	0.2	7.6E-01
ENSMUST00000126493				-2.5	1.2E-02	8.8	3.2E-04	-0.7	7.0E-01	0.9	2.4E-01
ENSMUST00000131358				-2.5	4.8E-04	7.3	3.7E-05	-1.2	2.7E-01	0.2	7.2E-01
ENSMUST00000161106				-2.6	2.0E-02	-0.4	7.6E-01	1.0	3.0E-01	-1.3	3.0E-01
ENSMUST00000131255				-2.6	7.8E-03	0.7	3.5E-01	-6.1	1.1E-04	-0.5	4.7E-01
ENSMUST00000137835				-2.6	4.0E-03	6.8	1.3E-04	-1.6	2.1E-01	1.0	1.2E-01
ENSMUST00000188458				5.8	3.9E-02	5.7	5.3E-02	-0.8	7.7E-01	-0.7	6.7E-01
ENSMUST00000188459	MAP kinase-activated protein kinase 2 [Source:MGI Symbol;Acc:MGI:109298]	A0A087WSN7		2.0	3.8E-02	2.4	6.0E-02	1.1	2.7E-01	0.7	4.7E-01
ENSMUST00000160157				-2.6	6.8E-04	6.4	1.4E-04	-0.1	8.9E-01	0.6	2.9E-01
ENSMUST00000156641				-2.6	2.8E-03	6.7	6.7E-04	-0.2	8.7E-01	-0.7	3.9E-01
ENSMUST00000133121				-2.6	1.2E-02	6.6	6.7E-04	0.0	9.8E-01	-1.2	1.4E-01
ENSMUST00000134084				-2.6	1.3E-02	5.9	2.5E-04	0.7	4.9E-01	0.1	8.2E-01
ENSMUST00000188484	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked [Source:MGI Symbol;Acc:MGI:1349406]	A0A087WQV7		-2.5	5.1E-01	-6.9	1.6E-01	-4.2	7.4E-02	0.2	9.7E-01
ENSMUST00000186822				-2.6	3.3E-02	5.3	6.6E-04	-0.2	8.7E-01	0.2	7.4E-01
ENSMUST00000136269				-2.6	3.3E-02	-3.1	6.6E-02	0.7	4.3E-01	1.1	4.5E-01
ENSMUST00000133697				-2.6	1.2E-02	7.3	3.2E-04	-0.7	6.4E-01	0.2	7.9E-01
ENSMUST00000188495	myeloblastosis oncogene [Source:MGI Symbol;Acc:MGI:97249]	A0A087WPA7		-0.2	7.6E-01	0.0	9.8E-01	0.9	1.2E-01	0.7	3.1E-01
ENSMUST00000188496				4.3	1.1E-01	4.6	1.3E-01	-0.3	9.2E-01	-0.6	7.5E-01
ENSMUST00000188497	ARP3 actin-related protein 3 [Source:MGI Symbol;Acc:MGI:1921367]	A0A087WRA1		0.5	8.5E-01	-7.0	2.6E-02	-6.9	1.8E-03	0.6	8.5E-01
ENSMUST00000139545				-2.6	1.1E-02	-3.5	5.6E-02	-0.7	4.5E-01	-2.0	3.3E-01
ENSMUST00000172455				-2.7	2.1E-02	-4.5	5.3E-04	-0.1	7.7E-01	-1.6	1.2E-01
ENSMUST00000188513				4.2	1.1E-01	6.1	4.5E-02	-0.2	9.4E-01	-2.1	2.1E-01
ENSMUST00000150243				-2.7	1.0E-02	5.9	2.9E-03	-0.7	6.6E-01	0.1	8.9E-01
ENSMUST00000165706				-2.7	6.0E-03	6.4	1.6E-03	-0.5	7.7E-01	-1.7	7.2E-02
ENSMUST00000150161				-2.7	7.9E-03	-5.0	8.6E-05	0.7	8.3E-02	-2.6	2.2E-02
ENSMUST00000143085				-2.7	6.3E-03	7.4	3.0E-03	1.9	3.3E-01	1.5	1.2E-01
ENSMUST00000188533	prothymosin alpha [Source:MGI Symbol;Acc:MGI:97803]	A0A087WPN6		-5.8	2.9E-01	-8.0	1.4E-01	-4.3	1.1E-01	-2.1	7.5E-01
ENSMUST00000136346				-2.7	1.5E-03	7.8	2.8E-04	0.7	6.3E-01	-0.7	3.2E-01
ENSMUST00000126507				-2.7	3.0E-02	-2.8	6.5E-02	0.9	2.3E-01	-2.4	1.5E-01
ENSMUST00000151068				-2.7	5.2E-03	5.5	9.6E-04	-1.5	2.6E-01	0.0	9.9E-01
ENSMUST00000173644				-2.7	1.6E-02	9.7	7.0E-04	-1.0	6.6E-01	0.6	4.6E-01
ENSMUST00000188570				-2.4	5.6E-02	-2.2	2.0E-01	0.4	6.7E-01	0.2	8.9E-01
ENSMUST00000135209				-2.7	1.4E-02	7.0	2.7E-04	1.8	1.4E-01	-0.6	3.8E-01
ENSMUST00000053271				-2.7	5.1E-03	1.6	4.2E-01	0.7	6.6E-01	2.2	1.7E-01
ENSMUST00000188580	F-box and leucine-rich repeat protein 19 [Source:MGI Symbol;Acc:MGI:3039600]		Q6PB97	-1.5	2.3E-01	3.7	3.7E-02	2.3	1.4E-01	-3.0	3.3E-02
ENSMUST00000188583				0.5	7.0E-01	0.6	6.8E-01	-0.3	8.3E-01	-0.4	7.7E-01
ENSMUST00000131354				-2.7	2.4E-02	2.7	9.9E-02	-4.1	3.1E-02	-2.3	9.3E-02
ENSMUST00000148128				-2.7	8.3E-03	-5.0	3.0E-03	0.8	2.2E-01	-2.0	1.8E-01
ENSMUST00000021322				-2.7	1.6E-02	2.6	2.2E-02	-1.6	9.3E-02	0.5	5.5E-01
ENSMUST00000156351				-2.7	3.2E-02	5.6	1.4E-04	0.4	6.1E-01	0.0	9.8E-01
ENSMUST00000156647				-2.7	3.1E-02	6.3	2.0E-04	-0.5	6.4E-01	-0.6	3.0E-01
ENSMUST00000172613				-2.7	1.0E-03	6.0	4.7E-03	1.6	3.4E-01	0.0	9.8E-01
ENSMUST00000097690				-2.8	1.3E-02	4.6	1.1E-03	-1.1	2.9E-01	0.7	3.2E-01
ENSMUST00000149755				-2.8	8.3E-03	4.0	8.7E-05	-1.1	8.0E-02	0.1	7.6E-01
ENSMUST00000113725				-2.8	2.2E-02	-6.6	1.5E-03	0.7	1.8E-01	0.2	9.0E-01
ENSMUST00000141620				-2.8	3.1E-02	4.4	3.7E-03	-1.7	1.6E-01	0.8	3.4E-01
ENSMUST00000126908				-2.8	6.3E-03	-3.6	3.5E-03	-0.4	4.5E-01	-0.6	5.1E-01
ENSMUST00000140419				-2.8	2.9E-02	5.4	9.1E-04	-0.9	4.6E-01	0.4	5.5E-01
ENSMUST00000188650	twinfilin, actin-binding protein, homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1346078]		Q9Z0P5	-0.3	8.2E-01	1.8	4.0E-01	1.9	2.9E-01	-0.2	9.2E-01
ENSMUST00000180560				-2.8	2.9E-02	4.0	3.7E-03	1.0	2.9E-01	-0.5	5.6E-01
ENSMUST00000152778				-2.8	1.7E-02	3.2	4.2E-02	-3.0	6.2E-02	1.3	2.2E-01
ENSMUST00000188444				-2.8	2.5E-02	6.2	2.2E-03	1.7	2.6E-01	-0.3	7.0E-01
ENSMUST00000142735				-2.8	1.1E-02	-1.4	9.9E-02	0.0	9.8E-01	-0.2	7.9E-01
ENSMUST00000137447				-2.8	2.3E-02	0.5	5.9E-01	1.0	1.6E-01	-2.4	3.5E-02
ENSMUST00000188674	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]	A0A087WS56		-3.6	1.1E-01	-4.8	4.8E-02	-3.1	2.9E-02	-1.9	4.5E-01
ENSMUST00000188675	dopey family member 1 [Source:MGI Symbol;Acc:MGI:1289294]	A0A0B4J1N8		0.0	9.9E-01	-1.0	7.2E-01	-1.3	4.2E-01	-0.4	8.9E-01
ENSMUST00000137249				-2.8	6.4E-03	-1.9	3.8E-01	3.5	3.6E-02	-1.7	4.4E-01
ENSMUST00000146254				-2.8	1.9E-03	6.9	4.8E-04	-0.2	8.6E-01	1.1	1.1E-01
ENSMUST00000188681	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	A0A087WSQ5		1.3	5.4E-01	2.1	4.7E-01	1.6	4.3E-01	0.8	7.6E-01
ENSMUST00000144638				-2.8	3.6E-03	5.2	1.4E-04	-0.9	2.9E-01	-0.6	2.9E-01
ENSMUST00000188685	zinc finger protein 709 [Source:MGI Symbol;Acc:MGI:2384299]	Q8VC29		1.4	9.7E-02	2.5	2.8E-02	0.4	6.4E-01	-0.7	4.1E-01
ENSMUST00000129633				-2.8	1.7E-02	5.5	4.2E-02	-0.6	8.0E-01	0.1	9.3E-01
ENSMUST00000135207				-2.8	2.1E-02	-1.7	1.4E-01	0.7	3.3E-01	-1.9	1.6E-01
ENSMUST00000151879				-2.8	1.8E-02	4.3	9.9E-03	-0.6	6.7E-01	0.3	7.0E-01
ENSMUST00000188706	predicted gene, 20917 [Source:MGI Symbol;Acc:MGI:5434273]	Q62457		2.9	2.0E-01	3.6	1.4E-01	-0.5	8.4E-01	-1.2	4.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000142281				-2.9	2.3E-02	3.0	6.4E-03	-0.9	2.7E-01	-0.6	3.9E-01
ENSMUST00000121735				-2.9	3.7E-03	6.3	3.7E-04	1.8	1.3E-01	0.5	4.7E-01
ENSMUST00000188731	retrotransposon gag domain containing 4 [Source:MGI Symbol;Acc:MGI:3045324]	Q8C065	Q5DTT4	2.8	8.6E-02	2.6	1.4E-01	-1.3	3.8E-01	-1.1	4.3E-01
ENSMUST00000188738	serum/glucocorticoid regulated kinase 3 [Source:MGI Symbol;Acc:MGI:2182368]	A0A087WR70		-3.8	7.6E-02	-5.1	7.8E-02	-1.0	3.8E-01	0.3	9.3E-01
ENSMUST00000189563				-2.9	2.4E-02	5.7	7.0E-04	0.1	9.7E-01	-0.2	7.6E-01
ENSMUST00000188746				-0.8	6.8E-01	0.7	7.5E-01	-0.4	8.2E-01	-1.8	3.9E-01
ENSMUST00000153663				-2.9	1.7E-02	6.4	1.8E-04	-1.5	2.2E-01	-0.6	3.6E-01
ENSMUST00000129503				-2.9	9.8E-03	4.8	9.3E-04	-0.8	4.7E-01	0.0	9.6E-01
ENSMUST00000140714				-2.9	2.4E-02	7.1	1.1E-04	-0.5	6.7E-01	-0.7	2.5E-01
ENSMUST00000188770	SLIT-ROBO Rho GTPase activating protein 2 [Source:MGI Symbol;Acc:MGI:109605]	A0A087WS59		-0.8	3.9E-01	1.3	2.9E-01	0.7	4.4E-01	-1.4	2.2E-01
ENSMUST00000188775	histone cluster 1, H3h [Source:MGI Symbol;Acc:MGI:2448349]		P68433	2.6	1.7E-01	2.1	2.2E-01	-2.4	1.7E-01	-1.9	2.4E-01
ENSMUST00000188780	PHD finger protein 3 [Source:MGI Symbol;Acc:MGI:2446126]	A0A087WS81		1.2	5.7E-01	0.0	9.9E-01	-0.9	6.2E-01	0.3	9.1E-01
ENSMUST00000188789	transmembrane protein 81 [Source:MGI Symbol;Acc:MGI:1921876]		Q9D5K1	-1.8	3.5E-01	3.2	1.8E-01	1.6	4.4E-01	-3.3	9.3E-02
ENSMUST00000155340				-2.9	1.2E-02	7.5	1.2E-04	-0.7	6.0E-01	0.2	8.0E-01
ENSMUST00000188804	myeloid nuclear differentiation antigen like [Source:MGI Symbol;Acc:MGI:3780953]		D0QMC3	0.3	8.9E-01	-0.8	6.7E-01	-4.0	4.5E-02	-2.9	2.0E-01
ENSMUST00000137537				-2.9	3.1E-02	8.6	2.9E-05	1.2	2.7E-01	0.9	1.0E-01
ENSMUST00000179515				-2.9	3.9E-03	5.4	4.9E-04	-0.9	4.2E-01	0.3	6.4E-01
ENSMUST00000132124				-2.9	3.2E-02	4.5	2.4E-03	-0.9	3.9E-01	0.6	4.1E-01
ENSMUST00000147303				-2.9	3.2E-02	2.6	2.0E-01	-2.4	2.8E-01	1.9	1.7E-01
ENSMUST00000133906				-2.9	2.6E-02	6.3	3.9E-04	-0.6	6.2E-01	-0.5	4.6E-01
ENSMUST00000120980				-2.9	1.6E-03	6.2	1.3E-04	-0.4	6.9E-01	-1.1	1.0E-01
ENSMUST00000127094				-2.9	2.0E-02	5.8	3.2E-04	-0.9	4.2E-01	0.4	5.6E-01
ENSMUST00000194118				-2.9	2.6E-02	4.1	2.4E-03	0.1	9.5E-01	0.8	2.7E-01
ENSMUST00000109805				-2.9	3.4E-02	6.9	7.0E-04	-1.2	4.5E-01	0.5	4.9E-01
ENSMUST00000182130				-2.9	9.4E-03	3.4	3.3E-03	-0.6	4.3E-01	0.1	9.3E-01
ENSMUST00000124553				-2.9	9.2E-03	6.8	4.7E-04	0.8	5.2E-01	0.1	8.7E-01
ENSMUST00000168657				-2.9	1.9E-02	3.8	5.5E-04	-0.4	5.2E-01	0.0	9.6E-01
ENSMUST00000030346				-2.9	2.2E-02	5.9	7.7E-05	0.6	4.6E-01	-0.4	5.2E-01
ENSMUST00000188851				-0.1	8.3E-01	0.0	1.0E+00	-0.1	9.2E-01	-0.2	7.9E-01
ENSMUST00000188859				-3.1	4.8E-02	-3.3	8.4E-02	-0.9	3.6E-01	-0.7	7.0E-01
ENSMUST00000188868				1.0	3.0E-01	-1.1	3.7E-01	-1.0	2.9E-01	1.2	3.2E-01
ENSMUST00000182246				-2.9	4.7E-03	-4.8	1.9E-02	1.5	5.3E-02	-0.7	6.9E-01
ENSMUST00000137685				-2.9	2.0E-02	-4.1	7.7E-03	-0.7	2.3E-01	-0.7	6.3E-01
ENSMUST00000151500				-2.9	2.6E-02	5.8	2.0E-03	-0.4	7.8E-01	0.8	3.9E-01
ENSMUST00000138962				-3.0	3.0E-02	-7.6	1.4E-02	-2.1	3.2E-02	0.4	9.0E-01
ENSMUST00000160407				-3.0	1.6E-02	5.8	3.3E-05	0.3	6.8E-01	-0.5	3.0E-01
ENSMUST00000188898	basic leucine zipper and W2 domains 1 [Source:MGI Symbol;Acc:MGI:1914132]	A0A087WPF9		-1.3	6.7E-01	-5.9	1.4E-01	-4.6	4.1E-02	0.1	9.8E-01
ENSMUST00000155891				-3.0	2.4E-02	6.9	8.4E-05	-0.3	7.7E-01	0.1	8.1E-01
ENSMUST00000099676				-3.0	1.1E-03	8.1	5.1E-05	-0.6	6.1E-01	0.3	6.1E-01
ENSMUST00000188912	pre B cell leukemia homeobox 1 [Source:MGI Symbol;Acc:MGI:97495]	Q71VB4	P41778	-0.7	3.4E-01	1.0	3.3E-01	1.3	1.2E-01	-0.4	6.3E-01
ENSMUST00000170335				-3.0	1.0E-03	4.6	6.3E-04	0.0	9.7E-01	-0.6	3.6E-01
ENSMUST00000186200				-3.0	2.9E-02	5.4	1.5E-05	0.0	9.9E-01	0.4	3.4E-01
ENSMUST00000132886				-3.0	1.1E-02	5.8	1.7E-03	-0.1	9.6E-01	0.7	3.8E-01
ENSMUST00000188931	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:MGI Symbol;Acc:MGI:1928739]	Q3TB24		0.7	2.1E-01	1.4	7.9E-02	0.5	4.2E-01	-0.2	7.6E-01
ENSMUST00000133020				-3.0	2.3E-02	7.9	2.4E-05	-1.0	3.9E-01	0.2	6.2E-01
ENSMUST00000139308				-3.0	1.2E-03	4.9	2.1E-03	-0.6	6.0E-01	0.4	5.1E-01
ENSMUST00000154649				-3.0	3.4E-02	7.2	5.6E-04	1.5	2.6E-01	0.1	9.3E-01
ENSMUST00000188952	Eph receptor A4 [Source:MGI Symbol;Acc:MGI:98277]		Q03137	6.3	3.6E-02	5.3	6.7E-02	-1.7	5.6E-01	-0.7	7.0E-01
ENSMUST00000188964	torsin family 3, member A [Source:MGI Symbol;Acc:MGI:1353652]		Q9ER38	-0.1	9.6E-01	-2.3	1.8E-01	-1.1	2.7E-01	1.2	4.8E-01
ENSMUST00000153370				-3.0	3.3E-02	7.7	1.3E-04	1.0	3.9E-01	0.7	2.4E-01
ENSMUST00000143445				-3.0	2.2E-03	-3.7	1.2E-02	-1.2	1.3E-01	-2.2	1.8E-01
ENSMUST00000146792				-3.0	3.0E-02	5.3	1.7E-03	-0.3	8.3E-01	-0.8	3.2E-01
ENSMUST00000139857				-3.0	2.9E-02	5.9	2.7E-03	-0.7	6.6E-01	1.4	1.2E-01
ENSMUST00000146889				-3.0	2.7E-02	6.2	1.2E-03	-1.5	3.3E-01	1.0	2.5E-01
ENSMUST00000174218				-3.0	8.2E-03	6.2	1.6E-03	1.3	3.4E-01	1.5	9.0E-02
ENSMUST00000172538				-3.0	4.9E-03	-3.9	9.8E-03	-0.3	6.7E-01	-0.6	6.6E-01
ENSMUST00000162924				-3.0	3.3E-02	3.5	8.3E-02	-0.2	9.3E-01	3.0	3.7E-02
ENSMUST00000172914				-3.0	3.6E-03	-3.2	1.4E-02	2.0	3.5E-03	-0.7	5.7E-01
ENSMUST00000181040				-3.0	3.6E-03	7.6	4.5E-04	-0.6	7.3E-01	-1.1	1.9E-01
ENSMUST00000136509				-3.0	2.5E-03	8.0	6.9E-03	-0.8	7.6E-01	-2.8	7.0E-02
ENSMUST00000153857				-3.0	1.2E-02	3.3	3.6E-03	0.5	5.1E-01	-0.9	1.9E-01
ENSMUST00000128649				-3.0	1.5E-02	7.0	4.7E-04	-0.6	6.7E-01	-1.0	2.1E-01
ENSMUST00000123358				-3.0	3.2E-03	2.4	7.9E-02	-4.0	1.4E-02	0.9	3.8E-01
ENSMUST00000134135				-3.0	9.1E-03	5.8	7.6E-06	-0.8	2.4E-01	0.4	2.9E-01
ENSMUST00000189027	RIKEN cDNA 1700101E01 gene [Source:MGI Symbol;Acc:MGI:2685669]	A0A087WQ85		6.3	7.3E-02	5.8	1.2E-01	-0.7	8.4E-01	-0.2	9.3E-01
ENSMUST00000182415				-3.0	2.5E-02	6.3	7.3E-04	-0.4	7.6E-01	0.6	4.4E-01
ENSMUST00000127810				-3.0	2.1E-02	5.3	1.3E-02	-0.7	7.1E-01	0.6	6.1E-01
ENSMUST00000138743				-3.0	2.6E-02	2.6	7.1E-03	0.0	9.9E-01	-0.4	5.0E-01
ENSMUST00000189043				2.1	1.4E-01	2.2	2.9E-01	1.2	5.0E-01	1.1	4.3E-01
ENSMUST00000139643				-3.0	2.6E-03	5.8	2.2E-04	0.6	5.5E-01	-0.3	6.1E-01
ENSMUST00000168111				-3.0	9.2E-03	5.6	4.7E-03	-1.0	5.6E-01	-0.8	4.1E-01
ENSMUST00000139149				-3.0	9.4E-03	7.2	5.7E-03	-0.9	6.9E-01	1.0	4.0E-01
ENSMUST00000163057				-3.0	1.3E-02	6.8	3.0E-04	-1.8	2.2E-01	0.1	8.7E-01
ENSMUST00000162613				-3.1	2.8E-02	4.9	2.9E-02	-2.1	3.6E-01	-0.9	5.1E-01
ENSMUST00000105240				-3.1	1.6E-02	1.0	2.3E-01	-1.5	5.7E-02	0.1	8.8E-01
ENSMUST00000127993				-3.1	4.4E-03	6.1	2.9E-04	-0.6	6.1E-01	0.4	5.4E-01
ENSMUST00000171711				-3.1	5.9E-03	3.0	7.2E-03	0.4	6.0E-01	-0.6	4.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000125369				-3.1	9.5E-03	-8.3	3.5E-05	0.4	2.5E-01	-0.8	5.4E-01
ENSMUST00000119064				-3.1	8.1E-04	5.1	4.1E-04	-2.4	4.2E-02	0.7	2.4E-01
ENSMUST00000100115				-3.1	1.7E-02	6.1	7.2E-03	-0.8	6.7E-01	1.1	3.0E-01
ENSMUST00000069169				-3.1	2.6E-02	2.2	1.8E-01	-0.1	9.4E-01	1.0	4.5E-01
ENSMUST00000189124	aldehyde dehydrogenase 3 family, member B3 [Source:MGI Symbol;Acc:MGI:1920708]	A0A087WS45		5.0	5.5E-02	6.2	7.4E-02	0.5	8.7E-01	-0.7	7.4E-01
ENSMUST00000102570				-3.1	6.9E-04	4.7	1.6E-04	-1.9	4.5E-02	-0.6	3.3E-01
ENSMUST00000195042				-3.1	1.3E-02	6.4	1.0E-03	0.6	6.5E-01	0.5	4.7E-01
ENSMUST00000144506				-3.1	2.6E-02	-5.8	3.2E-03	0.8	1.7E-01	-0.5	7.7E-01
ENSMUST00000186914				-3.1	1.4E-02	4.7	8.6E-03	-1.7	2.6E-01	0.3	7.7E-01
ENSMUST00000150086				-3.1	2.1E-02	4.0	1.9E-02	-1.1	4.4E-01	-0.6	4.8E-01
ENSMUST00000136866				-3.1	6.4E-03	5.0	1.1E-03	-1.3	2.7E-01	0.0	9.5E-01
ENSMUST00000151768				-3.1	3.4E-02	0.6	4.3E-01	0.8	1.8E-01	-2.4	9.8E-03
ENSMUST00000129025				-3.1	2.8E-03	7.8	3.4E-05	-0.6	6.1E-01	-0.3	5.8E-01
ENSMUST00000128410				-3.1	5.8E-03	5.7	7.4E-07	-0.4	4.0E-01	-0.3	3.8E-01
ENSMUST00000143965				-3.1	1.8E-02	3.7	3.4E-03	-3.0	2.0E-02	-2.9	6.2E-03
ENSMUST00000124653				-3.1	1.5E-02	5.9	7.4E-04	-1.3	3.2E-01	-0.1	8.6E-01
ENSMUST00000142142				-3.1	1.2E-02	7.0	4.6E-04	-0.7	6.2E-01	-0.2	8.1E-01
ENSMUST00000155131				-3.1	3.0E-02	5.6	4.2E-06	-0.1	8.7E-01	-0.2	6.8E-01
ENSMUST00000174824				-3.1	5.2E-03	7.0	9.7E-05	-0.6	6.2E-01	-0.8	1.9E-01
ENSMUST00000121217				-3.1	1.3E-02	6.6	5.3E-04	-0.7	6.1E-01	0.2	7.9E-01
ENSMUST00000139166				-3.1	1.4E-02	6.2	1.0E-03	-0.6	6.9E-01	-2.5	1.7E-02
ENSMUST00000189220	ArfGAP with FG repeats 1 [Source:MGI Symbol;Acc:MGI:1333754]		Q8K2K6	-1.3	7.8E-02	-0.9	3.1E-01	0.1	7.9E-01	-0.2	7.8E-01
ENSMUST00000130530				-3.1	3.2E-02	4.7	1.0E-04	-0.8	2.8E-01	0.1	8.0E-01
ENSMUST00000148126				-3.1	1.9E-02	5.6	1.0E-03	-0.5	6.9E-01	0.4	5.2E-01
ENSMUST00000126215				-3.1	1.5E-02	2.5	1.1E-02	-1.7	3.9E-02	0.8	2.1E-01
ENSMUST00000189244	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	Q8CFQ1		3.3	9.3E-02	6.1	1.8E-02	2.0	3.5E-01	-0.7	6.3E-01
ENSMUST00000119128				-3.1	3.5E-02	2.1	9.8E-02	-4.3	8.2E-03	-2.2	6.0E-02
ENSMUST00000141434				-3.2	1.8E-02	4.9	4.4E-02	-1.6	5.1E-01	3.2	3.3E-02
ENSMUST00000172800				-3.2	1.1E-02	7.3	1.4E-04	0.5	7.0E-01	-0.7	2.6E-01
ENSMUST00000131688				-3.2	7.1E-04	6.9	3.7E-04	-0.7	6.2E-01	0.1	9.2E-01
ENSMUST00000183386				-3.2	1.0E-02	6.1	1.6E-04	0.1	9.1E-01	1.1	8.2E-02
ENSMUST00000165329				-3.2	3.7E-03	5.1	4.4E-03	-0.9	5.3E-01	-0.1	8.8E-01
ENSMUST00000189262	CLIP associating protein 1 [Source:MGI Symbol;Acc:MGI:1923957]	A0A087WS18		0.8	6.6E-01	1.9	4.8E-01	0.8	6.4E-01	-0.2	9.3E-01
ENSMUST00000153411				-3.2	1.4E-02	1.8	2.1E-01	-5.6	3.9E-03	-2.6	5.9E-02
ENSMUST00000145058				-3.2	1.5E-02	6.7	1.2E-04	-0.5	6.2E-01	-1.0	1.3E-01
ENSMUST00000185827				-3.2	1.2E-03	5.1	5.6E-05	-1.0	1.7E-01	-0.2	7.1E-01
ENSMUST00000129303				-3.2	2.2E-02	2.5	1.0E-02	-0.4	5.3E-01	-0.6	3.6E-01
ENSMUST00000153596				-3.2	3.4E-04	-6.1	1.3E-02	-1.1	1.7E-01	0.4	8.7E-01
ENSMUST00000195165				-3.2	2.6E-02	7.1	1.6E-04	-1.9	1.8E-01	0.7	2.3E-01
ENSMUST00000144816				-3.2	2.9E-02	0.7	7.9E-01	-1.9	3.4E-01	3.6	1.3E-01
ENSMUST00000189309				-1.1	5.5E-01	3.1	1.7E-01	0.9	6.7E-01	-3.4	8.3E-02
ENSMUST00000144471				-3.2	2.8E-02	7.1	1.3E-02	-1.0	7.0E-01	0.0	9.9E-01
ENSMUST00000126193				-3.2	1.3E-02	6.9	7.2E-04	0.5	7.5E-01	-0.5	4.9E-01
ENSMUST00000136786				-3.2	1.9E-02	5.8	3.8E-04	-0.8	4.8E-01	0.4	5.6E-01
ENSMUST00000139931				-3.2	1.6E-02	1.6	2.4E-02	-0.4	4.1E-01	0.5	3.7E-01
ENSMUST00000189336	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	A0A087WRI1		-4.4	3.6E-02	-1.7	4.0E-01	1.0	4.7E-01	-1.7	4.5E-01
ENSMUST00000110339				-3.2	1.7E-02	3.0	1.7E-03	-4.5	7.0E-04	-0.5	4.1E-01
ENSMUST00000189347	signal transducer and activator of transcription 1 [Source:MGI Symbol;Acc:MGI:103063]	Q99K94		-3.8	3.7E-01	-4.0	4.5E-01	-0.9	7.4E-01	-0.7	9.0E-01
ENSMUST00000189361	hosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4 [Source:MGI Symbol;Ac	A0A087WPM2		1.1	4.3E-01	6.8	3.2E-04	-0.9	4.9E-01	-6.6	1.8E-04
ENSMUST00000137297				-3.2	7.3E-03	6.4	6.3E-04	-0.5	7.0E-01	-0.7	3.7E-01
ENSMUST00000135264				-3.2	5.5E-03	4.4	6.4E-03	-3.0	6.6E-02	0.1	9.1E-01
ENSMUST00000189374				3.7	1.4E-01	5.8	4.3E-02	-0.2	9.4E-01	-2.3	1.6E-01
ENSMUST00000189378	amyloid beta (A4) precursor protein-binding, family B, member 1 [Source:MGI Symbol;Acc:MGI:107765]			5.4	5.4E-02	2.6	3.0E-01	-3.9	1.7E-01	-1.2	5.2E-01
ENSMUST00000155961				-3.2	3.0E-02	4.5	7.5E-03	-0.8	5.6E-01	0.2	8.0E-01
ENSMUST00000189388	tripeptidyl peptidase II [Source:MGI Symbol;Acc:MGI:102724]	A0A087WRC0		0.0	1.0E+00	4.7	1.9E-01	3.4	2.4E-01	-1.2	6.6E-01
ENSMUST00000138118				-3.2	3.3E-02	6.9	1.5E-04	-0.6	6.3E-01	-0.7	2.6E-01
ENSMUST00000189400	progestin and adipoQ receptor family member VIII [Source:MGI Symbol;Acc:MGI:1921479]		Q80ZE5	2.1	3.3E-01	1.7	6.0E-01	0.4	8.8E-01	0.8	7.3E-01
ENSMUST00000150095				-3.2	3.3E-02	-1.0	1.8E-01	1.0	6.3E-02	-1.0	2.1E-01
ENSMUST00000130142				-3.2	1.5E-02	2.6	5.6E-03	-0.3	6.7E-01	-0.1	8.3E-01
ENSMUST00000189413	kinesin family member 14 [Source:MGI Symbol;Acc:MGI:1098226]		L0N7N1	1.4	3.0E-01	6.0	1.8E-02	3.3	1.2E-01	-1.3	3.3E-01
ENSMUST00000149595				-3.2	3.2E-03	6.4	8.5E-04	-1.5	3.2E-01	0.1	8.8E-01
ENSMUST00000138979				-3.2	2.9E-03	2.3	7.0E-02	-0.7	4.8E-01	0.0	1.0E+00
ENSMUST00000117262				-3.2	3.1E-02	7.5	2.5E-04	0.4	7.3E-01	0.3	7.2E-01
ENSMUST00000127189				-3.2	1.4E-02	7.9	5.0E-06	0.1	9.3E-01	0.1	7.8E-01
ENSMUST00000160006				-3.2	1.6E-02	-1.8	1.2E-01	1.7	2.4E-02	-3.1	3.4E-02
ENSMUST00000132561				-3.2	1.0E-02	6.6	2.0E-04	-1.3	2.6E-01	0.2	7.6E-01
ENSMUST00000152397				-3.2	3.0E-02	-2.2	1.2E-01	0.9	2.4E-01	-2.7	1.0E-01
ENSMUST00000147452				-3.2	3.3E-04	3.4	1.4E-01	-0.1	9.7E-01	0.8	5.8E-01
ENSMUST00000156908				-3.2	1.1E-03	5.4	1.8E-02	-0.7	7.1E-01	1.0	4.0E-01
ENSMUST00000191958				-3.2	7.6E-03	3.8	2.5E-02	-0.5	7.4E-01	1.3	2.0E-01
ENSMUST00000189463	predicted gene, 21394 [Source:MGI Symbol;Acc:MGI:5434749]	Q497R7		3.5	1.9E-01	5.0	9.2E-02	-0.4	8.8E-01	-1.9	3.0E-01
ENSMUST00000145740				-3.3	1.1E-02	7.4	5.3E-04	0.4	7.9E-01	1.6	5.2E-02
ENSMUST00000149513				-3.3	2.8E-02	6.2	3.3E-04	-0.6	6.3E-01	0.7	2.9E-01
ENSMUST00000189472	THAP domain containing 4 [Source:MGI Symbol;Acc:MGI:1914276]	A0A087WPE8		-1.0	2.5E-01	0.8	4.1E-01	0.5	5.7E-01	-1.4	1.6E-01
ENSMUST00000189474				3.6	6.1E-02	2.8	1.3E-01	-1.9	2.9E-01	-1.1	4.7E-01
ENSMUST00000138800				-3.3	1.8E-02	6.6	3.1E-04	-0.6	6.2E-01	-0.4	5.8E-01
ENSMUST00000144540				-3.3	3.0E-02	6.9	3.5E-04	-0.6	6.6E-01	-1.2	1.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000182255				-3.3	1.6E-03	7.6	1.5E-04	1.2	3.6E-01	-1.0	1.4E-01
ENSMUST00000189486	dedicator of cytokinesis 10 [Source:MGI Symbol;Acc:MGI:2146320]	A0A087WS26		-1.1	3.4E-01	-1.2	4.0E-01	-0.3	7.3E-01	-0.2	8.9E-01
ENSMUST00000129700				-3.3	2.8E-02	5.1	2.3E-04	-2.1	5.6E-02	-0.7	2.5E-01
ENSMUST00000132240				-3.3	6.0E-03	8.4	5.0E-03	-0.8	7.6E-01	-0.4	7.6E-01
ENSMUST00000145264				-3.3	4.8E-03	7.1	1.1E-03	0.0	1.0E+00	-1.1	2.3E-01
ENSMUST00000136374				-3.3	2.5E-02	-6.8	3.9E-05	-0.1	6.7E-01	-0.8	4.4E-01
ENSMUST00000120584				-3.3	2.2E-03	6.2	1.2E-04	-1.5	1.9E-01	-0.6	2.8E-01
ENSMUST00000174196				-3.3	1.4E-02	4.3	1.7E-02	-1.6	3.3E-01	-0.6	5.4E-01
ENSMUST00000144380				-3.3	1.8E-02	5.4	1.3E-03	-1.0	4.5E-01	-0.5	5.1E-01
ENSMUST00000148869				-3.3	2.0E-03	8.2	9.7E-05	0.0	9.9E-01	0.6	3.1E-01
ENSMUST00000129457				-3.3	2.4E-03	0.2	9.0E-01	2.4	9.5E-02	-3.3	9.3E-02
ENSMUST00000195209				-3.3	2.4E-02	4.8	2.3E-03	-1.3	3.1E-01	0.1	9.4E-01
ENSMUST00000133712				-3.3	3.5E-02	8.4	9.1E-03	-0.8	7.8E-01	-2.4	1.2E-01
ENSMUST00000121323				-3.3	1.5E-03	-3.9	1.4E-01	2.0	1.4E-01	1.8	4.6E-01
ENSMUST00000135194				-3.3	1.7E-02	4.6	1.9E-02	0.0	9.9E-01	-0.8	4.9E-01
ENSMUST00000152196				-3.3	8.8E-03	8.1	8.5E-06	-1.4	1.9E-01	-0.1	8.6E-01
ENSMUST00000154843				-3.3	5.7E-03	5.2	1.9E-03	-0.7	5.5E-01	0.4	6.3E-01
ENSMUST00000162154				-3.3	1.5E-02	4.7	6.5E-04	-1.2	2.1E-01	-0.2	7.4E-01
ENSMUST00000174094				-3.3	1.8E-02	4.5	7.8E-05	-0.6	3.5E-01	0.5	3.1E-01
ENSMUST00000123976				-3.3	5.0E-04	-2.2	1.5E-01	0.9	3.3E-01	0.2	8.8E-01
ENSMUST00000189564				-4.8	3.8E-02	-1.4	5.7E-01	1.9	2.5E-01	-1.5	5.6E-01
ENSMUST00000189895				-3.3	2.9E-02	4.8	3.8E-03	-0.5	6.9E-01	0.2	7.8E-01
ENSMUST00000139538				-3.3	4.5E-03	5.4	7.7E-02	-0.9	7.7E-01	1.0	5.6E-01
ENSMUST00000156060				-3.3	9.1E-04	3.7	2.0E-01	-0.7	7.9E-01	1.7	3.8E-01
ENSMUST00000130908				-3.3	2.9E-02	6.0	2.4E-04	-1.5	2.0E-01	-0.3	5.8E-01
ENSMUST00000144569				-3.3	8.8E-03	5.4	7.4E-05	-0.4	6.2E-01	0.4	4.7E-01
ENSMUST00000189596				-0.8	2.0E-01	-1.3	1.9E-01	0.5	4.1E-01	1.0	2.9E-01
ENSMUST00000138741				-3.3	2.1E-03	10.0	1.7E-03	1.1	6.5E-01	-0.3	6.9E-01
ENSMUST00000149475				-3.3	1.4E-02	6.7	2.5E-04	-0.3	7.8E-01	-0.5	4.9E-01
ENSMUST00000131339				-3.3	4.1E-03	-2.4	1.8E-01	1.4	1.2E-01	0.6	7.0E-01
ENSMUST00000133266				-3.4	1.2E-03	6.2	2.5E-04	-0.6	6.3E-01	-0.5	4.7E-01
ENSMUST00000133971				-3.4	1.2E-03	5.0	3.3E-03	0.8	4.9E-01	0.0	9.5E-01
ENSMUST00000189616	male-specific lethal 2 homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1925103]	A0A087WNL5		-2.7	8.0E-02	-1.6	3.4E-01	0.0	9.7E-01	-1.1	5.3E-01
ENSMUST00000123580				-3.4	4.2E-03	7.4	1.4E-04	0.0	9.7E-01	-0.5	4.7E-01
ENSMUST00000152755				-3.4	5.7E-03	6.2	8.8E-06	-0.3	6.4E-01	-0.1	8.9E-01
ENSMUST00000145547				-3.4	3.2E-02	7.1	9.8E-05	-0.1	9.2E-01	-0.9	1.5E-01
ENSMUST00000189629	predicted gene 42715 [Source:MGI Symbol;Acc:MGI:5662852]	A0A087WP63		1.6	1.7E-01	3.7	6.7E-02	1.6	3.5E-01	-0.4	6.9E-01
ENSMUST00000129399				-3.4	2.5E-02	-5.7	1.5E-04	-1.7	2.1E-03	-0.6	5.7E-01
ENSMUST00000126276				-3.4	1.8E-02	4.5	2.1E-04	0.1	9.2E-01	-0.5	3.5E-01
ENSMUST00000131203				-3.4	1.1E-02	-1.9	1.0E-01	0.6	4.2E-01	-5.0	1.0E-02
ENSMUST00000189661	sterol O-acyltransferase 1 [Source:MGI Symbol;Acc:MGI:104665]		Q61263	-1.6	4.5E-02	-0.2	8.4E-01	1.1	1.1E-01	-0.3	7.4E-01
ENSMUST00000154332				-3.4	5.2E-03	7.0	1.4E-03	-0.3	8.7E-01	0.6	4.7E-01
ENSMUST00000028055				-3.4	7.9E-03	-0.3	7.4E-01	-1.6	4.2E-02	1.0	2.3E-01
ENSMUST00000131627				-3.4	3.3E-02	-2.3	8.8E-02	1.2	1.4E-01	-0.4	7.5E-01
ENSMUST00000142874				-3.4	1.7E-02	-7.0	2.1E-03	0.9	1.0E-01	-0.4	8.4E-01
ENSMUST00000189672	predicted gene 10778 [Source:MGI Symbol;Acc:MGI:3809656]	A0A087WNP5		-0.6	7.0E-01	-4.0	2.2E-01	0.0	9.8E-01	3.3	2.9E-01
ENSMUST00000125703				-3.4	1.3E-02	3.6	1.1E-02	-0.9	4.4E-01	0.5	5.3E-01
ENSMUST00000189679	runt related transcription factor 1 [Source:MGI Symbol;Acc:MGI:99852]	A0A087WR69		0.8	2.7E-01	1.4	1.1E-01	0.1	9.3E-01	-0.6	4.2E-01
ENSMUST00000159935				-3.4	1.4E-04	-5.3	1.6E-04	0.9	4.2E-02	-0.3	7.6E-01
ENSMUST00000142791				-3.4	5.6E-03	7.5	1.2E-04	-0.6	6.5E-01	-1.9	2.1E-02
ENSMUST00000145132				-3.4	2.6E-02	6.8	4.7E-04	-0.2	8.9E-01	0.0	9.5E-01
ENSMUST00000138639				-3.4	6.9E-03	3.6	9.7E-02	-1.9	3.6E-01	3.0	4.7E-02
ENSMUST00000181606				-3.4	9.2E-03	3.7	2.4E-05	-1.2	2.0E-02	-0.5	1.5E-01
ENSMUST00000189698	serine/threonine kinase 16 [Source:MGI Symbol;Acc:MGI:1313271]	A0A087WQT0		-0.1	9.7E-01	0.6	7.7E-01	0.6	6.3E-01	0.0	9.8E-01
ENSMUST00000189702	autophagy related 9A [Source:MGI Symbol;Acc:MGI:2138446]	Q3ZAQ4		-0.3	7.8E-01	-2.0	3.2E-01	0.2	9.0E-01	1.8	3.1E-01
ENSMUST00000131375				-3.4	7.1E-03	3.4	2.4E-03	1.2	1.4E-01	0.1	9.3E-01
ENSMUST00000133035				-3.4	2.2E-02	-1.8	7.0E-02	0.3	6.6E-01	-1.1	2.7E-01
ENSMUST00000146696				-3.4	2.9E-02	-1.2	2.9E-01	0.0	9.6E-01	-3.4	3.4E-02
ENSMUST00000189711	RIKEN cDNA 1700101E01 gene [Source:MGI Symbol;Acc:MGI:2685669]	A0A087WRI3		-1.0	5.8E-01	0.0	9.9E-01	1.4	5.2E-01	0.3	8.7E-01
ENSMUST00000153199				-3.4	5.2E-03	7.2	1.3E-04	-0.5	7.1E-01	-0.6	3.0E-01
ENSMUST00000182873				-3.4	2.5E-03	6.1	1.7E-02	0.3	8.9E-01	1.3	3.2E-01
ENSMUST00000141274				-3.4	4.3E-03	5.6	1.7E-02	0.1	9.8E-01	1.5	2.3E-01
ENSMUST00000139391				-3.4	8.4E-03	9.2	1.3E-05	-0.7	5.8E-01	-0.1	9.1E-01
ENSMUST00000129618				-3.4	1.2E-04	2.1	2.1E-01	-0.3	8.1E-01	0.6	6.6E-01
ENSMUST00000140944				-3.4	2.0E-02	8.7	1.3E-04	-1.7	3.2E-01	1.3	7.6E-02
ENSMUST00000189728	THAP domain containing 4 [Source:MGI Symbol;Acc:MGI:1914276]			-3.5	6.9E-02	-2.6	2.6E-01	0.2	9.0E-01	-0.8	7.3E-01
ENSMUST00000152191				-3.4	1.5E-02	5.4	7.1E-06	-1.2	6.7E-02	0.5	1.9E-01
ENSMUST00000130528				-3.4	2.8E-02	3.5	3.4E-02	-1.8	2.5E-01	1.0	3.5E-01
ENSMUST00000141431				-3.4	3.3E-02	6.2	1.0E-03	0.8	5.3E-01	0.0	9.8E-01
ENSMUST00000189738	CLIP associating protein 1 [Source:MGI Symbol;Acc:MGI:1923957]	A0A087WRK0		-0.3	9.1E-01	4.6	3.2E-01	4.8	1.6E-01	-0.1	9.8E-01
ENSMUST00000129229				-3.4	1.3E-02	8.4	4.8E-05	-0.4	7.3E-01	-0.2	6.8E-01
ENSMUST00000134184				-3.4	1.7E-02	6.1	3.0E-04	-1.9	1.4E-01	-0.7	3.4E-01
ENSMUST00000139886				-3.4	2.3E-02	6.5	1.7E-04	-0.5	6.5E-01	-2.2	7.7E-03
ENSMUST00000127832				-3.4	1.9E-02	8.2	4.1E-05	-0.5	6.7E-01	-0.5	4.1E-01
ENSMUST00000151450				-3.4	7.6E-03	7.1	2.8E-04	-2.5	1.2E-01	-0.8	2.2E-01
ENSMUST00000125266				-3.4	1.1E-02	5.3	1.0E-03	-0.6	6.1E-01	0.6	3.8E-01
ENSMUST00000124718				-3.4	3.0E-03	5.0	1.7E-03	-2.4	9.8E-02	0.3	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000127223				-3.4	1.1E-02	5.7	2.5E-04	-0.1	9.6E-01	-0.1	8.5E-01
ENSMUST00000146497				-3.5	3.0E-02	5.0	1.6E-03	-0.8	5.1E-01	-0.8	2.9E-01
ENSMUST00000189799	DPH5 homolog (S. cerevisiae) [Source:MGI Symbol;Acc:MGI:1916990]		Q9CWQ0	-1.6	4.0E-02	-2.9	8.3E-03	-0.9	1.3E-01	0.4	6.7E-01
ENSMUST00000141927				-3.5	1.5E-02	6.8	2.5E-04	-0.6	6.1E-01	-1.3	8.3E-02
ENSMUST00000161593				-3.5	2.2E-02	5.2	1.0E-03	-0.9	4.4E-01	-0.7	3.1E-01
ENSMUST00000189817	dopey family member 1 [Source:MGI Symbol;Acc:MGI:1289294]	A0A087WP61		-2.7	3.6E-02	-3.5	5.2E-02	-0.4	6.1E-01	0.3	8.5E-01
ENSMUST00000189820	autophagy related 9A [Source:MGI Symbol;Acc:MGI:2138446]	A0A087WP33		0.5	7.2E-01	1.3	5.1E-01	0.8	6.3E-01	0.0	9.9E-01
ENSMUST00000189821	fibronectin 1 [Source:MGI Symbol;Acc:MGI:95566]	B7ZNJ1		-6.2	5.0E-02	-6.6	1.2E-01	-1.0	5.5E-01	-0.6	8.8E-01
ENSMUST00000137109				-3.5	1.7E-02	4.1	2.0E-03	-2.5	4.2E-02	0.5	4.2E-01
ENSMUST00000124950				-3.5	1.1E-02	6.3	2.0E-03	-2.0	2.3E-01	1.6	1.0E-01
ENSMUST00000144525				-3.5	8.5E-03	-3.6	2.4E-02	1.6	4.8E-02	0.5	7.2E-01
ENSMUST00000189841	thyroid hormone receptor interactor 12 [Source:MGI Symbol;Acc:MGI:1309481]	A0A087WS33		1.6	3.3E-01	1.0	6.4E-01	-0.7	6.3E-01	-0.2	9.2E-01
ENSMUST00000182877				-3.5	1.4E-03	7.0	9.8E-03	-0.8	7.3E-01	-2.1	1.5E-01
ENSMUST00000149878				-3.5	3.2E-02	5.2	1.1E-03	-1.3	3.0E-01	-1.2	1.1E-01
ENSMUST00000118448				-3.5	3.2E-03	2.0	1.2E-02	0.5	4.0E-01	0.3	5.7E-01
ENSMUST00000189862				-2.4	2.1E-01	2.4	2.5E-01	0.7	7.1E-01	-4.2	4.6E-02
ENSMUST00000144714				-3.5	1.3E-02	6.7	3.9E-04	-0.7	6.1E-01	0.1	9.0E-01
ENSMUST00000123885				-3.5	1.2E-03	7.6	6.2E-04	-0.8	6.3E-01	0.2	8.4E-01
ENSMUST00000031402				-3.5	4.5E-04	6.6	1.6E-04	-0.5	6.4E-01	-0.6	3.2E-01
ENSMUST00000122807				-3.5	2.5E-03	3.5	5.7E-02	-2.1	2.3E-01	0.4	7.5E-01
ENSMUST00000156263				-3.5	3.4E-03	5.3	2.7E-04	-0.9	3.3E-01	0.5	4.2E-01
ENSMUST00000189881				1.6	4.9E-01	0.8	8.2E-01	1.6	5.1E-01	2.4	4.7E-01
ENSMUST00000153085				-3.5	2.2E-03	5.3	1.3E-02	-0.7	7.2E-01	1.5	1.8E-01
ENSMUST00000138509				-3.5	5.0E-03	6.7	5.9E-04	0.1	9.2E-01	1.9	3.0E-02
ENSMUST00000181172				-3.5	4.9E-03	-1.4	4.4E-01	1.3	2.3E-01	-0.6	7.5E-01
ENSMUST00000149313				-3.5	7.3E-04	4.7	2.0E-02	-2.6	1.9E-01	-1.8	1.5E-01
ENSMUST00000148479				-3.5	1.6E-02	6.3	1.9E-04	-0.5	6.4E-01	-0.7	2.3E-01
ENSMUST00000149085				-3.5	1.7E-02	5.6	7.4E-04	0.0	9.7E-01	0.9	1.9E-01
ENSMUST00000145806				-3.5	1.5E-02	7.2	2.6E-05	-2.0	8.5E-02	-0.3	5.6E-01
ENSMUST00000189932	RIKEN cDNA 2810474O19 gene [Source:MGI Symbol;Acc:MGI:1914496]	B2KFD2	Q5DTW7	-0.1	9.8E-01	1.5	6.8E-01	1.3	6.1E-01	-0.3	9.3E-01
ENSMUST00000118681				-3.5	1.2E-02	5.8	1.5E-04	-1.9	8.7E-02	0.5	3.7E-01
ENSMUST00000148061				-3.5	8.0E-03	9.0	7.0E-05	1.4	3.1E-01	-1.1	7.8E-02
ENSMUST00000182060				-3.5	2.8E-04	3.0	2.4E-02	-1.5	1.8E-01	1.2	1.9E-01
ENSMUST00000143344				-3.5	1.6E-02	-3.1	4.4E-02	1.3	1.2E-01	-0.8	5.9E-01
ENSMUST00000153501				-3.5	5.5E-03	-5.2	2.5E-05	0.5	1.3E-01	-1.9	2.4E-02
ENSMUST00000151151				-3.6	2.0E-02	1.1	2.5E-01	0.0	9.5E-01	1.1	2.0E-01
ENSMUST00000192334				-3.6	1.0E-02	6.9	2.6E-04	-0.4	7.4E-01	-0.7	3.2E-01
ENSMUST00000189951				1.8	9.0E-02	2.2	6.7E-02	-0.5	6.2E-01	-0.9	3.9E-01
ENSMUST00000138357				-3.6	2.9E-03	5.7	1.1E-02	-2.2	3.0E-01	-1.8	1.6E-01
ENSMUST00000189955				3.2	5.0E-02	4.5	2.6E-02	0.0	9.8E-01	-1.3	2.7E-01
ENSMUST00000151250				-3.6	3.1E-02	4.5	4.1E-03	-2.2	1.2E-01	-0.8	3.5E-01
ENSMUST00000189972	gamma-glutamyltransferase 5 [Source:MGI Symbol;Acc:MGI:1346063]	A0A087WNR3		-0.2	8.6E-01	0.7	6.0E-01	0.9	3.8E-01	0.0	1.0E+00
ENSMUST00000161281				-3.6	1.7E-02	7.7	1.2E-04	-0.5	6.9E-01	-0.5	4.3E-01
ENSMUST00000167223				-3.6	7.0E-03	1.3	2.8E-01	0.2	8.0E-01	1.0	2.8E-01
ENSMUST00000152812				-3.6	2.6E-02	4.1	7.3E-03	-2.4	9.2E-02	-0.4	6.9E-01
ENSMUST00000148379				-3.6	1.1E-03	4.2	1.2E-04	-0.2	7.1E-01	0.5	3.2E-01
ENSMUST00000121106				-3.6	4.1E-03	5.8	6.7E-04	-0.6	6.1E-01	-0.4	5.5E-01
ENSMUST00000172507				-3.6	2.1E-02	-0.1	9.4E-01	1.7	8.6E-02	-1.6	1.9E-01
ENSMUST00000135351				-3.6	9.7E-03	3.7	2.2E-03	-1.3	1.4E-01	0.6	3.9E-01
ENSMUST00000175935				-3.6	7.0E-03	7.0	4.6E-05	-1.5	1.9E-01	-0.1	7.8E-01
ENSMUST00000153203				-3.6	3.8E-03	8.0	9.3E-05	-0.6	6.5E-01	-0.7	2.6E-01
ENSMUST00000146057				-3.6	1.1E-02	-8.6	1.0E-03	-1.0	1.0E-01	0.2	9.3E-01
ENSMUST00000143008				-3.6	2.5E-02	3.7	8.3E-02	-0.6	7.6E-01	1.7	2.2E-01
ENSMUST00000190037	solute carrier family 35, member F5 [Source:MGI Symbol;Acc:MGI:1921400]	A0A087WP59		1.8	1.9E-01	0.3	8.5E-01	-2.1	1.1E-01	-0.6	6.6E-01
ENSMUST00000190046	ArfGAP with FG repeats 1 [Source:MGI Symbol;Acc:MGI:1333754]	A0A087WR52		-1.6	4.9E-01	-3.5	2.6E-01	-1.5	3.4E-01	0.3	9.3E-01
ENSMUST00000172653				-3.6	1.9E-03	-7.4	9.2E-04	0.6	2.3E-01	-0.4	8.0E-01
ENSMUST00000143408				-3.6	7.0E-03	2.6	5.3E-03	0.2	8.0E-01	-0.5	3.8E-01
ENSMUST00000190061	diacylglycerol kinase, delta [Source:MGI Symbol;Acc:MGI:2138334]	A0A087WP73		-1.9	1.2E-01	-1.2	4.0E-01	0.4	6.3E-01	-0.2	8.8E-01
ENSMUST00000190068	p53 induced death domain protein 1 [Source:MGI Symbol;Acc:MGI:1889507]	A0A087WPX5		0.7	7.1E-01	0.8	7.6E-01	-0.3	8.9E-01	-0.4	8.9E-01
ENSMUST00000190071	myeloid nuclear differentiation antigen like [Source:MGI Symbol;Acc:MGI:3780953]	A0A087WSH9		2.8	6.1E-02	-3.9	1.6E-02	-6.2	3.2E-04	0.5	7.2E-01
ENSMUST00000146824				-3.6	2.1E-04	7.9	2.9E-06	0.1	8.5E-01	-0.5	1.8E-01
ENSMUST00000187987				-3.6	4.8E-03	5.6	2.6E-03	-0.5	7.2E-01	-1.1	1.9E-01
ENSMUST00000147369				-3.7	4.2E-03	2.3	4.5E-02	0.3	7.5E-01	0.1	8.9E-01
ENSMUST00000190096	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:MGI Symbol;Acc:MGI:2653690]	A0A087WRF2		-2.1	3.6E-02	-4.4	4.4E-02	1.2	1.6E-01	3.5	8.9E-02
ENSMUST00000192442				-3.7	4.0E-03	1.8	6.8E-01	7.8	3.2E-02	-1.1	7.6E-01
ENSMUST00000154126				-3.7	2.9E-03	9.5	5.0E-04	-0.2	9.2E-01	-1.6	6.0E-02
ENSMUST00000134042				-3.7	3.4E-04	4.8	1.0E-02	-0.7	6.7E-01	0.9	3.6E-01
ENSMUST00000159966				-3.7	1.0E-02	3.6	1.1E-03	-0.5	4.7E-01	0.2	8.0E-01
ENSMUST00000147430				-3.7	3.8E-03	4.9	3.1E-04	-0.8	3.9E-01	0.1	8.1E-01
ENSMUST00000136199				-3.7	1.3E-02	6.4	1.6E-04	-0.6	6.1E-01	-0.7	2.9E-01
ENSMUST00000190121	matrin 3 [Source:MGI Symbol;Acc:MGI:1298379]	A0A087WSP7		-2.1	5.5E-01	-5.5	2.0E-01	-4.0	8.4E-02	-0.6	9.0E-01
ENSMUST00000122862				-3.7	2.8E-02	5.3	1.5E-02	-1.1	5.6E-01	1.8	1.3E-01
ENSMUST00000169625				-3.7	2.8E-02	2.7	5.2E-03	-0.5	4.8E-01	-1.3	8.1E-02
ENSMUST00000162764				-3.7	3.0E-03	6.3	6.7E-03	-0.5	7.9E-01	-0.5	6.5E-01
ENSMUST00000173486				-3.7	4.8E-03	7.2	1.3E-04	-0.5	7.1E-01	-0.6	3.0E-01
ENSMUST00000141568				-3.7	2.0E-02	3.6	3.3E-03	-1.7	1.1E-01	-0.3	7.0E-01
ENSMUST00000149332				-3.7	8.6E-03	4.7	4.1E-03	1.0	3.8E-01	1.2	1.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000161453				-3.7	1.1E-03	7.0	2.2E-04	-1.2	3.9E-01	0.1	8.5E-01
ENSMUST00000138235				-3.7	8.9E-03	-4.9	2.2E-03	0.0	9.6E-01	-1.3	3.4E-01
ENSMUST00000181584				-3.7	1.9E-02	2.4	2.0E-03	-0.3	5.0E-01	-0.6	2.0E-01
ENSMUST00000190165	9 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Source:MGI Symbol;Acc:MGI:1888	A0A087WNM2		-3.2	1.6E-01	-3.2	1.0E-01	-2.9	4.1E-02	-2.9	2.2E-01
ENSMUST00000125741				-3.7	2.6E-02	4.6	4.3E-05	-4.1	7.3E-04	0.0	9.5E-01
ENSMUST00000146695				-3.7	5.1E-03	-2.7	7.1E-02	2.1	1.3E-02	-0.6	6.6E-01
ENSMUST00000164758				-3.7	1.1E-02	6.6	6.3E-04	-1.9	2.0E-01	-0.1	9.3E-01
ENSMUST00000118956				-3.7	1.5E-03	6.7	1.5E-05	-0.5	5.5E-01	-0.5	2.6E-01
ENSMUST00000140660				-3.7	1.3E-02	5.8	1.2E-03	-0.6	6.5E-01	-0.1	8.4E-01
ENSMUST00000107813				-3.8	7.1E-03	6.1	3.7E-04	-0.3	7.9E-01	-0.8	2.8E-01
ENSMUST00000143631				-3.8	3.1E-04	7.0	4.0E-04	0.5	7.2E-01	0.4	5.6E-01
ENSMUST00000128857				-3.8	9.6E-04	6.3	7.4E-04	-0.7	6.2E-01	-0.1	8.5E-01
ENSMUST00000132456				-3.8	1.8E-02	-6.8	2.7E-03	-0.1	9.1E-01	0.1	9.7E-01
ENSMUST00000152528				-3.8	5.9E-03	5.5	2.9E-03	-2.0	2.1E-01	0.1	9.4E-01
ENSMUST00000190226	carnitine deficiency-associated gene expressed in ventricle 3 [Source:MGI Symbol;Acc:MGI:2448759]	A0A087WS49		-2.8	2.5E-01	2.3	4.9E-01	3.6	2.2E-01	-1.6	5.7E-01
ENSMUST00000117772				-3.8	2.0E-02	6.6	1.6E-04	-0.6	5.9E-01	-0.2	7.9E-01
ENSMUST00000178868				-3.8	9.1E-03	3.8	2.4E-03	-1.6	1.1E-01	-0.6	4.4E-01
ENSMUST00000128189				-3.8	6.5E-03	-2.4	2.3E-01	3.3	1.2E-02	-0.6	7.4E-01
ENSMUST00000147839				-3.8	3.0E-03	2.9	8.9E-03	0.2	7.8E-01	0.2	8.1E-01
ENSMUST00000190247	protein tyrosine phosphatase, receptor type, N polypeptide 2 [Source:MGI Symbol;Acc:MGI:107418]	Q3UU93		5.4	6.0E-02	5.8	5.4E-02	-0.9	7.7E-01	-1.3	4.8E-01
ENSMUST00000164184				-3.8	2.0E-04	-7.2	7.0E-05	0.7	9.9E-02	-0.4	7.1E-01
ENSMUST00000142187				-3.8	1.1E-02	6.6	1.1E-04	-0.6	5.8E-01	-2.0	8.1E-03
ENSMUST00000141002				-3.8	2.2E-02	-5.7	4.3E-02	-1.0	4.5E-01	-4.8	1.9E-01
ENSMUST00000153766				-3.8	1.7E-03	-4.8	1.2E-02	-1.0	1.9E-01	-0.5	7.7E-01
ENSMUST00000174233				-3.8	2.5E-02	4.0	1.4E-03	-2.4	2.9E-02	-0.5	4.6E-01
ENSMUST00000126165				-3.8	1.5E-02	2.0	1.5E-01	-1.3	3.0E-01	0.4	6.9E-01
ENSMUST00000117987				-3.8	3.6E-03	5.1	1.8E-03	-0.6	6.3E-01	1.0	2.1E-01
ENSMUST00000190313	chemokine (C-X-C motif) receptor 1 [Source:MGI Symbol;Acc:MGI:2448715]		Q810W6	-1.4	4.4E-02	-0.5	5.3E-01	0.3	6.1E-01	-0.6	4.1E-01
ENSMUST00000147325				-3.8	1.1E-03	9.4	5.8E-06	-0.6	6.0E-01	-0.6	1.6E-01
ENSMUST00000136532				-3.8	4.4E-04	2.5	8.3E-03	-0.3	6.6E-01	-0.2	7.6E-01
ENSMUST00000121950				-3.8	2.3E-02	-3.5	8.8E-03	-0.1	8.2E-01	-2.0	1.2E-01
ENSMUST00000127011				-3.8	1.2E-03	5.1	3.0E-04	-2.1	6.2E-02	0.5	3.8E-01
ENSMUST00000162832				-3.8	4.8E-03	8.6	4.4E-05	-0.7	5.8E-01	0.7	1.9E-01
ENSMUST00000169134				-3.9	1.4E-02	6.8	2.8E-04	-0.6	6.6E-01	-0.1	8.3E-01
ENSMUST00000190341	baculoviral IAP repeat-containing 2 [Source:MGI Symbol;Acc:MGI:1197009]		Q62210	-5.0	5.0E-02	-1.8	4.4E-01	0.6	7.1E-01	-2.6	3.2E-01
ENSMUST00000032884				-3.9	2.0E-03	-4.8	4.7E-03	-1.3	5.0E-02	-0.3	8.5E-01
ENSMUST00000123701				-3.9	4.5E-03	8.0	5.4E-04	-0.3	8.4E-01	-1.8	4.6E-02
ENSMUST00000176799				-3.9	1.4E-03	7.8	8.0E-05	-0.4	7.5E-01	-0.6	2.8E-01
ENSMUST00000136858				-3.9	1.6E-03	4.9	2.1E-02	-0.5	7.7E-01	-1.1	3.4E-01
ENSMUST00000143510				-3.9	2.6E-03	6.7	4.0E-03	-1.0	6.0E-01	-1.4	2.4E-01
ENSMUST00000170163				-3.9	1.4E-02	5.0	1.1E-03	0.8	4.0E-01	0.9	2.5E-01
ENSMUST00000135914				-3.9	1.3E-02	3.3	1.1E-03	0.0	9.9E-01	-0.2	6.9E-01
ENSMUST00000190378	protein arginine N-methyltransferase 6 [Source:MGI Symbol;Acc:MGI:2139971]		Q6NZB1	-0.3	8.9E-01	2.4	3.7E-01	2.7	2.6E-01	0.0	9.9E-01
ENSMUST00000132189				-3.9	2.5E-02	5.2	3.7E-04	-1.0	3.1E-01	-0.6	3.7E-01
ENSMUST00000154150				-3.9	9.5E-05	4.7	6.7E-02	-1.4	5.9E-01	0.3	8.3E-01
ENSMUST00000134870				-3.9	2.9E-02	8.5	2.8E-05	-0.4	7.6E-01	1.1	6.6E-02
ENSMUST00000190390	Snf2-related CREBBP activator protein [Source:MGI Symbol;Acc:MGI:2444036]	A0A087WNL7		-0.9	7.5E-01	-2.7	6.3E-01	0.7	8.2E-01	2.5	6.4E-01
ENSMUST00000133252				-3.9	2.3E-02	4.5	2.0E-03	-1.8	1.3E-01	-1.3	1.5E-01
ENSMUST00000147274				-3.9	4.4E-03	6.3	3.7E-06	-0.1	8.1E-01	0.3	3.5E-01
ENSMUST00000164961				-3.9	6.4E-03	7.5	1.1E-04	-0.5	6.8E-01	0.3	5.7E-01
ENSMUST00000143747				-3.9	1.6E-03	2.5	4.0E-01	-0.8	7.7E-01	3.0	1.9E-01
ENSMUST00000146631				-3.9	3.8E-03	5.4	6.4E-05	-0.6	4.3E-01	-0.5	3.7E-01
ENSMUST00000194798				-3.9	6.3E-03	-3.6	1.3E-02	-0.8	2.7E-01	-1.5	2.7E-01
ENSMUST00000122361				-3.9	1.2E-04	6.7	5.2E-04	-0.7	6.3E-01	-0.3	7.2E-01
ENSMUST00000159587				-3.9	2.9E-03	8.8	3.0E-04	-0.8	6.5E-01	-0.5	5.4E-01
ENSMUST00000159550				-3.9	2.1E-03	5.8	7.6E-04	-0.6	6.5E-01	0.2	7.4E-01
ENSMUST00000105586				-3.9	5.7E-03	8.1	1.1E-04	-0.7	6.1E-01	-0.3	6.2E-01
ENSMUST00000140774				-3.9	1.9E-03	4.1	8.7E-02	-0.9	6.7E-01	-0.2	8.8E-01
ENSMUST00000137476				-3.9	2.9E-03	5.6	9.1E-04	-1.4	3.0E-01	-0.5	4.5E-01
ENSMUST00000162287				-3.9	3.7E-03	5.7	7.6E-03	0.0	9.9E-01	0.4	6.7E-01
ENSMUST00000131960				-3.9	2.2E-02	7.3	7.1E-05	-0.6	6.3E-01	-0.9	1.5E-01
ENSMUST00000190448	proviral integration site 2 [Source:MGI Symbol;Acc:MGI:97587]	A0A087WRF4		-0.2	7.5E-01	1.0	3.4E-01	0.8	2.8E-01	-0.4	6.8E-01
ENSMUST00000150719				-3.9	4.2E-03	2.7	1.2E-01	-0.6	6.7E-01	4.1	7.0E-03
ENSMUST00000137445				-3.9	5.1E-05	7.1	5.2E-04	-0.7	6.3E-01	0.8	3.1E-01
ENSMUST00000142252				-3.9	1.8E-02	5.4	6.1E-04	-0.5	6.3E-01	0.1	8.9E-01
ENSMUST00000190459				1.3	2.2E-01	0.8	6.2E-01	0.6	6.3E-01	1.1	4.1E-01
ENSMUST00000129093				-3.9	2.7E-03	6.4	1.6E-03	0.4	8.0E-01	0.0	9.7E-01
ENSMUST00000185945				-3.9	1.7E-02	7.3	5.5E-04	-1.0	5.4E-01	0.5	5.5E-01
ENSMUST00000155517				-3.9	3.3E-03	7.8	1.8E-04	0.4	7.7E-01	-0.8	2.6E-01
ENSMUST00000147827				-4.0	3.0E-02	6.6	2.7E-04	-0.6	6.4E-01	0.0	9.5E-01
ENSMUST00000177513				-4.0	5.1E-03	-0.9	3.8E-01	4.3	9.7E-05	-1.0	3.3E-01
ENSMUST00000138323				-4.0	2.2E-03	2.5	1.1E-02	-1.0	1.9E-01	-0.5	4.4E-01
ENSMUST00000150965				-4.0	2.1E-02	5.6	1.1E-03	-1.0	4.6E-01	0.6	4.6E-01
ENSMUST00000190476	inhibitor of growth family, member 5 [Source:MGI Symbol;Acc:MGI:1922816]		Q9D8Y8	1.8	3.5E-01	1.4	4.5E-01	-2.8	1.5E-01	-2.5	1.4E-01
ENSMUST00000190481				4.3	9.8E-02	5.7	5.2E-02	-0.2	9.4E-01	-1.7	2.9E-01
ENSMUST00000154254				-4.0	1.4E-03	7.1	4.5E-04	0.7	6.3E-01	-0.2	7.5E-01
ENSMUST00000142643				-4.0	9.2E-03	2.2	1.5E-01	-2.5	1.1E-01	-0.3	8.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000125919				-4.0	1.4E-02	-9.1	1.4E-03	1.2	5.5E-02	-0.7	7.5E-01
ENSMUST00000190503	ankyrin repeat domain 27 (VPS9 domain) [Source:MGI Symbol;Acc:MGI:2444103]		Q3UMR0	2.4	1.9E-01	3.7	3.1E-02	-3.1	9.6E-02	-4.4	8.4E-03
ENSMUST00000190511				-2.4	3.3E-01	-4.2	2.5E-01	-1.0	5.7E-01	0.8	8.3E-01
ENSMUST00000147954				-4.0	1.7E-03	6.7	1.9E-04	-0.5	6.7E-01	-0.2	7.8E-01
ENSMUST00000120641				-4.0	6.1E-05	-5.5	2.2E-03	-0.5	4.0E-01	-1.0	5.1E-01
ENSMUST00000190535	kinectin 1 [Source:MGI Symbol;Acc:MGI:109153]	A0A087WPX0		-1.8	4.4E-01	-5.3	6.4E-02	-4.4	1.5E-02	-1.0	7.4E-01
ENSMUST00000143954				-4.0	5.0E-03	6.8	2.6E-04	-0.6	6.5E-01	-4.3	8.4E-04
ENSMUST00000172453				-4.0	2.8E-02	7.1	9.4E-05	-0.5	6.9E-01	-2.2	5.5E-03
ENSMUST00000080598				-4.0	4.5E-05	6.9	1.3E-03	-0.8	6.5E-01	0.4	6.2E-01
ENSMUST00000139992				-4.0	8.1E-04	2.7	1.3E-01	5.2	2.3E-03	-0.5	7.1E-01
ENSMUST00000150370				-4.0	5.7E-04	2.2	1.3E-01	-0.5	6.8E-01	4.3	1.7E-03
ENSMUST00000190568				-3.3	3.7E-02	-2.4	1.8E-01	0.1	9.1E-01	-0.8	6.7E-01
ENSMUST00000143316				-4.0	3.4E-04	1.0	3.5E-01	1.0	2.3E-01	-4.4	6.6E-03
ENSMUST00000119599				-4.0	1.9E-03	3.3	2.5E-03	-4.2	2.4E-03	0.0	9.8E-01
ENSMUST00000129297				-4.0	6.3E-03	5.5	1.1E-03	-0.6	6.4E-01	0.4	5.4E-01
ENSMUST00000190595	dedicator of cytokinesis 10 [Source:MGI Symbol;Acc:MGI:2146320]			-0.1	9.7E-01	3.6	2.3E-01	2.3	4.0E-01	-1.4	5.1E-01
ENSMUST00000126912				-4.0	4.5E-03	6.0	1.0E-03	-0.6	6.4E-01	-1.0	1.9E-01
ENSMUST00000149684				-4.0	1.4E-02	8.1	3.7E-04	-0.5	7.6E-01	0.2	8.1E-01
ENSMUST00000160468				-4.0	4.8E-03	5.1	6.3E-03	0.3	8.1E-01	-0.2	7.9E-01
ENSMUST00000156429				-4.0	1.7E-03	8.5	1.5E-05	-0.6	6.1E-01	-1.2	3.1E-02
ENSMUST00000147062				-4.0	9.6E-03	5.4	2.4E-04	-1.9	9.3E-02	-1.4	4.5E-02
ENSMUST00000138837				-4.0	9.6E-03	3.8	3.0E-04	0.8	2.1E-01	0.1	7.9E-01
ENSMUST00000159661				-4.0	1.0E-02	6.7	8.9E-05	-0.7	5.1E-01	-0.7	2.6E-01
ENSMUST00000124083				-4.0	6.5E-04	2.7	2.1E-01	0.0	9.9E-01	4.7	1.2E-02
ENSMUST00000151644				-4.0	3.1E-03	2.2	2.6E-02	0.4	6.0E-01	0.9	1.8E-01
ENSMUST00000129665				-4.0	4.5E-04	2.8	5.1E-04	-0.3	5.6E-01	-0.1	8.3E-01
ENSMUST00000190642				1.5	3.7E-02	2.8	5.0E-03	0.3	6.5E-01	-0.9	1.7E-01
ENSMUST00000141528				-4.0	1.0E-02	6.6	9.8E-05	-2.3	7.7E-02	-0.8	2.1E-01
ENSMUST00000174148				-4.0	1.7E-02	4.7	2.7E-02	-1.7	4.0E-01	-1.8	1.7E-01
ENSMUST00000107608				-4.0	9.4E-03	5.2	7.7E-03	0.8	5.9E-01	-0.4	6.9E-01
ENSMUST00000161242				-4.0	4.1E-03	8.8	2.0E-05	-0.4	7.2E-01	-0.7	1.6E-01
ENSMUST00000154642				-4.0	8.8E-03	-4.2	2.1E-03	1.2	3.3E-02	-1.1	3.1E-01
ENSMUST00000184916				-4.0	1.5E-03	-3.6	5.5E-02	0.4	6.4E-01	-2.6	2.6E-01
ENSMUST00000148460				-4.0	8.2E-03	4.8	8.7E-03	-0.6	6.4E-01	-0.1	9.3E-01
ENSMUST00000106806				-4.0	2.9E-02	6.6	2.3E-04	0.8	4.7E-01	0.3	6.0E-01
ENSMUST00000150001				-4.0	2.8E-03	5.8	4.0E-04	-0.6	5.9E-01	-0.2	8.1E-01
ENSMUST00000151394				-4.1	3.7E-03	-5.1	9.1E-03	-1.0	2.3E-01	0.4	8.2E-01
ENSMUST00000146226				-4.1	6.4E-03	1.8	3.7E-02	-1.7	3.3E-02	0.9	2.0E-01
ENSMUST00000114724				-4.1	2.4E-02	4.1	7.6E-04	0.2	8.2E-01	0.1	8.4E-01
ENSMUST00000125838				-4.1	2.6E-03	6.6	1.6E-04	-0.5	6.7E-01	-0.7	3.0E-01
ENSMUST00000160529				-4.1	7.2E-03	7.5	8.3E-05	0.0	9.7E-01	-0.4	4.0E-01
ENSMUST00000183014				-4.1	9.1E-04	4.1	1.7E-03	-0.2	7.8E-01	0.4	5.6E-01
ENSMUST00000170110				-4.1	3.7E-03	6.4	2.1E-04	-0.6	5.8E-01	-0.4	5.7E-01
ENSMUST00000190717	tubulin, alpha 4A [Source:MGI Symbol;Acc:MGI:1095410]	A0A087WSL5		-1.3	1.5E-01	-3.1	3.5E-02	-0.4	5.2E-01	1.3	3.2E-01
ENSMUST00000122810				-4.1	1.0E-03	6.1	1.8E-03	-0.8	6.3E-01	0.6	5.0E-01
ENSMUST00000130354				-4.1	3.4E-02	8.1	9.5E-05	-0.5	7.0E-01	-0.6	3.3E-01
ENSMUST00000141672				-4.1	8.1E-03	-3.4	1.1E-01	1.7	1.3E-01	0.2	9.2E-01
ENSMUST00000156036				-4.1	2.5E-03	5.5	1.3E-04	-0.3	7.6E-01	0.0	9.9E-01
ENSMUST00000172422				-4.1	2.3E-03	3.1	2.5E-02	6.8	4.0E-05	-1.2	2.3E-01
ENSMUST00000143685				-4.1	1.2E-02	5.8	2.4E-04	-1.5	1.9E-01	-0.4	5.0E-01
ENSMUST00000190774				-1.1	3.2E-01	-0.5	7.1E-01	-0.3	7.3E-01	-1.0	4.8E-01
ENSMUST00000190776				1.0	6.8E-01	2.8	1.5E-01	-2.2	2.4E-01	-4.0	8.8E-02
ENSMUST00000188882				-4.1	2.4E-03	-7.3	6.4E-02	-0.3	8.6E-01	-0.6	8.8E-01
ENSMUST00000190788				2.6	5.4E-02	2.7	1.3E-01	-0.2	8.8E-01	-0.3	8.0E-01
ENSMUST00000123381				-4.1	1.4E-02	7.1	4.9E-05	-0.4	7.2E-01	0.2	7.4E-01
ENSMUST00000185466				-4.1	3.8E-04	7.0	2.8E-04	-0.4	7.5E-01	-0.2	8.0E-01
ENSMUST00000190801	importin 11 [Source:MGI Symbol;Acc:MGI:2442377]	A0A087WS00		-0.6	6.2E-01	-2.8	5.9E-02	-2.7	1.9E-02	-0.4	7.5E-01
ENSMUST00000190811	phosphatidylinositol glycan anchor biosynthesis, class N [Source:MGI Symbol;Acc:MGI:1351629]	A0A087WS03		-0.5	6.4E-01	0.5	7.1E-01	0.6	5.0E-01	-0.3	7.9E-01
ENSMUST00000119733				-4.1	2.4E-03	8.0	4.3E-05	-0.4	7.1E-01	0.5	3.6E-01
ENSMUST00000139254				-4.1	1.6E-03	-6.0	3.7E-04	0.1	8.8E-01	-0.2	8.9E-01
ENSMUST00000190825	retinoblastoma binding protein 5 [Source:MGI Symbol;Acc:MGI:1918367]			-1.2	5.3E-01	3.2	2.1E-01	1.4	5.3E-01	-3.1	1.4E-01
ENSMUST00000151554				-4.1	3.0E-03	7.4	5.2E-06	-0.5	5.5E-01	0.3	4.8E-01
ENSMUST00000152710				-4.1	8.8E-05	7.3	1.1E-04	-0.6	6.5E-01	-0.6	3.3E-01
ENSMUST00000138006				-4.1	2.7E-02	5.5	1.7E-03	-1.1	4.3E-01	-0.5	5.7E-01
ENSMUST00000123661				-4.1	3.2E-03	3.5	3.6E-02	-0.9	5.7E-01	1.7	1.3E-01
ENSMUST00000155410				-4.1	4.8E-03	8.5	1.1E-05	-0.5	6.2E-01	-0.3	4.5E-01
ENSMUST00000156586				-4.1	2.4E-02	4.8	5.9E-05	-1.7	3.4E-02	0.3	4.7E-01
ENSMUST00000124596				-4.1	1.7E-02	6.7	1.2E-04	-0.6	6.0E-01	-0.6	3.3E-01
ENSMUST00000131402				-4.1	1.2E-04	8.4	3.8E-06	-0.4	6.6E-01	-0.8	7.7E-02
ENSMUST00000195231				-4.1	2.4E-02	6.3	4.3E-04	-0.6	6.1E-01	-0.6	4.3E-01
ENSMUST00000136013				-4.1	5.0E-03	2.8	3.1E-02	-1.8	1.7E-01	0.1	9.4E-01
ENSMUST00000149639				-4.1	1.9E-02	5.1	5.5E-04	1.7	9.2E-02	-0.1	8.4E-01
ENSMUST00000147345				-4.1	3.2E-03	7.1	1.6E-03	0.1	9.7E-01	0.0	9.7E-01
ENSMUST00000130675				-4.1	2.1E-03	7.1	1.1E-04	-0.8	4.9E-01	0.0	9.7E-01
ENSMUST00000150739				-4.1	1.2E-02	6.1	3.2E-04	-0.6	6.2E-01	0.0	9.5E-01
ENSMUST00000190874				-3.1	4.3E-02	-4.4	3.2E-02	-1.4	1.3E-01	0.0	1.0E+00
ENSMUST00000169571				-4.1	1.4E-03	-2.3	5.7E-02	-0.3	5.9E-01	-2.0	1.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000155639				-4.1	1.1E-02	9.0	1.5E-07	0.5	3.5E-01	0.4	2.2E-01
ENSMUST00000183041				-4.2	6.3E-04	7.2	2.5E-05	-1.5	1.6E-01	-0.4	4.1E-01
ENSMUST00000134977				-4.2	1.5E-02	8.0	6.1E-06	-0.5	6.0E-01	-0.1	8.5E-01
ENSMUST00000130412				-4.2	9.5E-04	5.6	2.5E-05	-1.0	2.1E-01	-0.4	3.9E-01
ENSMUST00000140896				-4.2	3.4E-03	5.4	7.0E-04	-1.0	4.0E-01	0.9	2.1E-01
ENSMUST00000140011				-4.2	1.8E-03	5.8	3.8E-04	-0.5	6.7E-01	-0.9	1.7E-01
ENSMUST00000174250				-4.2	4.6E-04	10.2	5.8E-03	2.2	4.6E-01	1.4	2.2E-01
ENSMUST00000190915				-0.8	5.5E-01	-1.4	2.6E-01	-1.5	1.3E-01	-0.8	5.3E-01
ENSMUST00000122919				-4.2	2.4E-02	4.1	5.6E-04	-0.4	5.4E-01	-0.2	7.1E-01
ENSMUST00000164332				-4.2	8.4E-04	7.1	1.9E-03	0.1	9.8E-01	0.6	4.8E-01
ENSMUST00000176498				-4.2	4.2E-03	-0.3	8.3E-01	-2.9	4.0E-02	0.9	4.9E-01
ENSMUST00000190932				5.2	1.7E-01	6.0	1.4E-01	-0.7	8.7E-01	-1.5	5.5E-01
ENSMUST00000123355				-4.2	2.8E-03	7.7	3.9E-04	1.3	3.5E-01	0.9	1.7E-01
ENSMUST00000129487				-4.2	1.6E-02	3.0	4.2E-03	0.2	7.8E-01	-1.1	1.1E-01
ENSMUST00000153233				-4.2	9.0E-03	8.6	5.6E-08	-0.5	3.1E-01	0.6	3.7E-02
ENSMUST00000135312				-4.2	9.9E-03	6.1	1.3E-03	-0.4	7.6E-01	-0.2	8.5E-01
ENSMUST00000152274				-4.2	2.5E-02	6.4	3.1E-04	-0.5	6.7E-01	-0.4	5.1E-01
ENSMUST00000190968				5.1	1.1E-01	8.2	2.6E-02	-0.2	9.6E-01	-3.2	7.6E-02
ENSMUST00000127084				-4.2	1.1E-02	6.7	1.2E-04	-1.2	2.9E-01	-0.8	2.3E-01
ENSMUST00000190983	dedicator of cytokinesis 10 [Source:MGI Symbol;Acc:MGI:2146320]	A0A087WRP5		0.8	7.4E-01	-3.1	4.5E-01	-1.8	4.5E-01	2.2	5.8E-01
ENSMUST00000118431				-4.2	3.5E-03	-4.5	8.5E-03	-0.8	2.6E-01	-1.8	3.1E-01
ENSMUST00000135851				-4.2	1.8E-02	6.4	4.2E-04	-0.5	6.9E-01	0.0	9.6E-01
ENSMUST00000141668				-4.2	9.0E-04	-4.6	4.6E-02	0.5	5.5E-01	2.0	3.4E-01
ENSMUST00000191004	ARP3 actin-related protein 3 [Source:MGI Symbol;Acc:MGI:1921367]	A0A087WS98		-2.1	1.3E-01	-3.6	5.3E-02	-1.0	2.6E-01	0.4	8.1E-01
ENSMUST00000142849				-4.2	4.7E-03	6.0	1.4E-03	-0.5	7.5E-01	-0.8	3.3E-01
ENSMUST00000134462				-4.2	1.7E-02	5.1	4.3E-03	1.6	2.4E-01	-0.1	8.7E-01
ENSMUST00000056292				-4.2	1.5E-04	4.1	2.3E-02	-0.4	7.8E-01	1.7	1.2E-01
ENSMUST00000126934				-4.2	3.1E-03	6.3	3.7E-04	-0.6	6.6E-01	-1.3	9.0E-02
ENSMUST00000161111				-4.2	3.8E-04	6.3	5.0E-04	0.8	5.2E-01	-0.7	2.9E-01
ENSMUST00000129575				-4.2	8.0E-04	6.0	3.6E-03	-0.4	8.1E-01	-0.8	3.9E-01
ENSMUST00000161373				-4.2	9.3E-03	0.7	6.5E-01	0.7	5.7E-01	4.1	1.1E-02
ENSMUST00000168074				-4.3	2.2E-02	-3.4	2.0E-02	-0.2	7.8E-01	-0.6	6.5E-01
ENSMUST00000125720				-4.3	2.2E-05	3.3	1.6E-02	-1.2	2.9E-01	-0.9	3.0E-01
ENSMUST00000137082				-4.3	2.9E-02	6.7	7.2E-05	-0.4	7.3E-01	-0.4	4.6E-01
ENSMUST00000137516				-4.3	2.9E-03	7.6	5.6E-05	-0.9	4.4E-01	-0.2	7.3E-01
ENSMUST00000124637				-4.3	6.3E-03	4.4	1.1E-03	0.6	4.6E-01	0.1	9.1E-01
ENSMUST00000143503				-4.3	1.7E-02	8.6	1.7E-05	-0.6	6.2E-01	-0.6	2.3E-01
ENSMUST00000191073	predicted gene 10668 [Source:MGI Symbol;Acc:MGI:3642587]	Q3UTA8		5.2	5.4E-02	3.5	2.0E-01	-0.7	8.0E-01	1.0	6.0E-01
ENSMUST00000191076				1.8	2.6E-01	3.2	1.4E-01	1.1	5.2E-01	-0.3	8.7E-01
ENSMUST00000187500				-4.3	2.2E-04	-5.2	2.8E-04	-0.7	1.1E-01	-0.8	4.3E-01
ENSMUST00000155062				-4.3	6.2E-03	-2.2	1.5E-01	0.5	5.8E-01	-4.0	6.6E-02
ENSMUST00000161641				-4.3	4.2E-03	6.7	1.7E-04	-0.6	6.1E-01	0.4	5.0E-01
ENSMUST00000153516				-4.3	1.2E-02	-5.9	1.1E-02	1.0	1.5E-01	0.2	9.3E-01
ENSMUST00000191116				4.3	6.1E-02	5.2	2.9E-02	-1.4	5.3E-01	-2.3	1.4E-01
ENSMUST00000131227				-4.3	3.2E-03	4.8	4.0E-03	-0.4	7.8E-01	0.5	5.2E-01
ENSMUST00000154429				-4.3	2.2E-03	5.4	2.4E-02	-0.8	7.2E-01	-0.3	7.9E-01
ENSMUST00000154014				-4.3	7.3E-04	-5.2	1.9E-02	0.4	5.9E-01	-0.6	7.6E-01
ENSMUST00000131443				-4.3	1.8E-02	7.7	4.5E-05	0.8	4.4E-01	-0.4	4.5E-01
ENSMUST00000161604				-4.3	1.1E-02	4.1	1.8E-04	-0.8	2.4E-01	-0.1	9.0E-01
ENSMUST00000163268				-4.3	1.1E-02	-1.4	1.3E-01	-0.6	3.5E-01	-1.5	1.1E-01
ENSMUST00000138089				-4.3	3.0E-03	4.9	1.6E-04	1.0	2.0E-01	-0.4	5.1E-01
ENSMUST00000105400				-4.3	1.5E-02	6.4	1.0E-03	-0.3	8.5E-01	1.6	6.1E-02
ENSMUST00000191150				1.2	9.7E-02	0.5	5.1E-01	-1.2	9.1E-02	-0.5	4.6E-01
ENSMUST00000122336				-4.3	4.4E-04	8.8	3.5E-05	-0.4	7.7E-01	-1.0	8.4E-02
ENSMUST00000191160				-0.4	6.3E-01	0.5	6.2E-01	-0.1	9.4E-01	-0.9	3.0E-01
ENSMUST00000141043				-4.3	2.4E-02	3.1	6.8E-02	-1.9	2.9E-01	-0.1	9.6E-01
ENSMUST00000132679				-4.3	2.6E-03	6.3	3.6E-04	-0.5	6.7E-01	-0.6	3.5E-01
ENSMUST00000152062				-4.3	4.6E-04	6.5	1.4E-04	-1.6	2.0E-01	-0.5	3.7E-01
ENSMUST00000191183				-2.1	7.0E-02	-1.5	2.1E-01	-1.1	2.1E-01	-1.6	1.9E-01
ENSMUST00000191189	mortality factor 4 like 1 [Source:MGI Symbol;Acc:MGI:1096551]	A0A087WQB0		-5.6	9.2E-02	-9.6	3.7E-02	-3.6	1.8E-02	0.4	9.3E-01
ENSMUST00000155605				-4.3	2.1E-02	-5.3	1.0E-03	0.8	1.1E-01	-0.9	4.5E-01
ENSMUST00000156788				-4.3	1.4E-02	-5.1	1.4E-03	-1.5	1.9E-02	-1.3	3.3E-01
ENSMUST00000191203	predicted gene, 21698 [Source:MGI Symbol;Acc:MGI:5435053]	A0A087WQP8		6.0	9.3E-02	5.5	1.4E-01	-0.6	8.8E-01	-0.1	9.6E-01
ENSMUST00000146913				-4.3	9.1E-03	-5.0	9.5E-03	-0.9	2.4E-01	-2.0	2.9E-01
ENSMUST00000136069				-4.3	2.0E-03	6.1	7.3E-04	-0.6	6.7E-01	0.1	9.2E-01
ENSMUST00000191216	lymphocyte antigen 6 complex, locus C1 [Source:MGI Symbol;Acc:MGI:96882]	A0A087WRP7		-1.3	4.3E-01	-5.0	2.3E-02	-4.5	1.8E-03	-0.8	7.0E-01
ENSMUST00000127478				-4.3	8.8E-04	7.1	5.3E-03	-0.8	7.1E-01	-2.4	7.4E-02
ENSMUST00000125675				-4.4	3.1E-03	6.8	1.0E-03	-0.8	6.3E-01	0.8	3.1E-01
ENSMUST00000187031				-4.4	7.9E-04	6.3	7.0E-05	-0.8	4.0E-01	0.4	4.8E-01
ENSMUST00000159427				-4.4	1.1E-02	7.2	8.1E-05	-0.5	6.4E-01	-1.0	1.1E-01
ENSMUST00000159420				-4.4	1.6E-03	-2.2	1.4E-01	0.5	5.2E-01	-1.4	3.5E-01
ENSMUST00000191242				-2.9	7.5E-02	1.4	4.3E-01	2.4	1.1E-01	-1.8	2.6E-01
ENSMUST00000148270				-4.4	6.5E-03	1.5	1.0E-01	-0.2	7.8E-01	0.9	2.5E-01
ENSMUST00000134299				-4.4	4.7E-03	5.4	8.5E-03	-0.4	8.0E-01	-0.2	8.4E-01
ENSMUST00000154080				-4.4	4.4E-03	5.8	2.6E-03	-2.5	1.4E-01	-0.6	5.0E-01
ENSMUST00000191267				2.6	1.5E-01	3.6	1.9E-01	2.2	3.8E-01	1.2	4.5E-01
ENSMUST00000191268	ohosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150 [Source:MGI Symbol;Acc:MGI:1922919		Q8VD65	-0.5	7.6E-01	-1.3	6.2E-01	0.3	8.9E-01	1.0	6.5E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000020824				-4.4	3.6E-03	-4.0	2.0E-02	1.2	9.0E-02	1.0	5.3E-01
ENSMUST00000165629				-4.4	2.0E-02	6.1	1.3E-03	-0.5	7.5E-01	-0.6	4.7E-01
ENSMUST00000157029				-4.4	6.5E-03	3.5	2.0E-04	0.4	4.0E-01	0.5	3.1E-01
ENSMUST00000128229				-4.4	3.1E-03	7.2	8.0E-05	-0.6	5.8E-01	0.7	2.3E-01
ENSMUST00000167794				-4.4	8.2E-03	6.1	3.1E-04	0.8	4.7E-01	0.0	9.8E-01
ENSMUST00000126451				-4.4	2.1E-03	7.1	1.9E-04	-0.4	7.6E-01	0.4	5.0E-01
ENSMUST00000191303	splicing factor 3b, subunit 1 [Source:MGI Symbol;Acc:MGI:1932339]	A0A087WNS2		-2.5	1.4E-01	-4.7	4.9E-02	-1.6	1.4E-01	0.7	7.7E-01
ENSMUST00000162803				-4.4	5.0E-03	6.1	2.3E-04	-0.6	6.0E-01	-0.1	9.0E-01
ENSMUST00000191324				2.3	1.8E-01	5.8	4.4E-02	3.0	2.4E-01	-0.6	6.8E-01
ENSMUST00000191329	PHD finger protein 3 [Source:MGI Symbol;Acc:MGI:2446126]	A0A087WP76		-1.3	2.3E-01	-1.8	2.0E-01	-0.5	5.5E-01	0.0	1.0E+00
ENSMUST00000137544				-4.4	1.4E-02	3.9	7.3E-03	-0.9	4.3E-01	0.9	3.0E-01
ENSMUST00000139952				-4.4	1.5E-03	3.2	6.8E-04	-0.7	2.7E-01	0.1	9.1E-01
ENSMUST00000131214				-4.4	1.1E-02	6.1	1.1E-04	0.4	6.8E-01	-0.3	5.7E-01
ENSMUST00000159293				-4.4	3.8E-04	5.1	1.2E-03	0.9	3.9E-01	-0.7	3.0E-01
ENSMUST00000191353	mortality factor 4 like 1 [Source:MGI Symbol;Acc:MGI:1096551]	A0A087WQ34		1.6	5.5E-01	-4.7	1.6E-01	-5.9	1.8E-02	0.4	9.1E-01
ENSMUST00000118066				-4.4	3.2E-05	-4.0	2.2E-02	0.8	3.1E-01	-1.3	4.5E-01
ENSMUST00000126743				-4.4	4.3E-04	5.1	3.5E-04	-1.0	2.7E-01	0.1	8.7E-01
ENSMUST00000146117				-4.4	1.3E-03	6.1	2.6E-03	-0.4	8.0E-01	-0.1	8.8E-01
ENSMUST00000142469				-4.4	2.1E-03	2.8	1.7E-02	-1.9	5.4E-02	0.8	3.3E-01
ENSMUST00000135833				-4.4	9.3E-04	3.3	8.0E-04	-0.7	3.0E-01	-0.1	8.6E-01
ENSMUST00000152843				-4.4	4.6E-04	6.7	1.9E-03	0.9	5.9E-01	-0.5	5.9E-01
ENSMUST00000133736				-4.4	1.0E-03	7.1	6.6E-04	-0.7	6.5E-01	-0.1	8.9E-01
ENSMUST00000150201				-4.4	3.3E-04	-1.8	8.5E-02	0.6	3.9E-01	0.4	7.0E-01
ENSMUST00000141138				-4.5	6.2E-04	7.0	3.9E-04	-0.7	6.1E-01	0.1	9.3E-01
ENSMUST00000086725				-4.5	2.6E-02	6.0	9.5E-05	0.3	7.0E-01	-0.3	5.8E-01
ENSMUST00000138179				-4.5	6.9E-03	9.3	2.8E-05	-0.6	6.7E-01	-1.0	8.4E-02
ENSMUST00000154437				-4.5	1.5E-03	2.4	3.4E-01	-5.7	6.2E-02	3.0	7.8E-02
ENSMUST00000145273				-4.5	6.6E-03	7.0	5.0E-04	0.7	6.3E-01	-1.0	2.0E-01
ENSMUST00000121594				-4.5	4.1E-05	-5.3	1.6E-04	0.9	4.2E-02	-0.3	7.6E-01
ENSMUST00000173557				-4.5	4.1E-04	-8.5	1.2E-02	0.8	3.6E-01	-1.0	7.6E-01
ENSMUST00000191438	BCL2-associated transcription factor 1 [Source:MGI Symbol;Acc:MGI:1917580]	A0A087WRN1		-2.4	9.4E-02	-3.9	7.4E-02	-0.7	5.3E-01	0.8	6.8E-01
ENSMUST00000191439				0.5	4.3E-01	1.0	2.2E-01	0.1	8.3E-01	-0.4	6.1E-01
ENSMUST00000148338				-4.5	7.8E-04	-6.3	5.0E-03	-1.5	6.8E-02	-1.6	4.5E-01
ENSMUST00000136667				-4.5	2.3E-02	5.0	1.8E-04	-0.4	5.9E-01	-0.1	9.2E-01
ENSMUST00000123762				-4.5	2.0E-04	6.5	4.9E-04	-0.7	6.1E-01	0.5	5.2E-01
ENSMUST00000132288				-4.5	1.1E-03	8.7	6.4E-03	-0.8	7.8E-01	-2.6	7.9E-02
ENSMUST00000142318				-4.5	2.3E-03	-7.4	1.6E-04	0.2	5.1E-01	0.2	8.5E-01
ENSMUST00000156230				-4.5	6.1E-03	6.2	3.4E-04	-1.6	1.9E-01	-0.8	2.3E-01
ENSMUST00000144523				-4.5	1.1E-02	4.2	6.2E-04	-0.6	4.8E-01	-0.9	2.0E-01
ENSMUST00000151488				-4.5	4.6E-05	4.4	2.0E-02	-0.4	8.2E-01	0.3	7.8E-01
ENSMUST00000127543				-4.5	2.7E-04	-2.5	1.7E-01	0.7	4.7E-01	-1.5	4.2E-01
ENSMUST00000144493				-4.5	3.2E-03	5.6	3.3E-03	-0.4	7.9E-01	-0.4	6.5E-01
ENSMUST00000149796				-4.5	7.1E-05	3.9	3.9E-04	-0.9	2.0E-01	0.1	8.3E-01
ENSMUST00000189708				-4.5	6.4E-03	5.6	5.0E-04	-0.4	6.8E-01	0.3	6.3E-01
ENSMUST00000143248				-4.5	4.7E-04	7.3	1.8E-04	-0.6	6.3E-01	0.0	9.7E-01
ENSMUST00000133229				-4.5	1.9E-05	4.3	6.1E-03	-1.3	2.9E-01	-0.2	8.1E-01
ENSMUST00000126328				-4.5	8.4E-04	6.2	9.8E-06	-0.2	7.5E-01	-0.6	1.4E-01
ENSMUST00000173268				-4.5	6.4E-03	4.3	1.0E-02	-1.3	3.7E-01	0.0	9.9E-01
ENSMUST00000120770				-4.5	2.4E-03	6.7	1.0E-04	-0.5	6.4E-01	-0.8	1.9E-01
ENSMUST00000161391				-4.5	1.5E-02	5.7	3.1E-04	0.2	8.7E-01	-0.4	5.1E-01
ENSMUST00000191510				1.4	5.8E-02	1.1	1.9E-01	-0.2	7.9E-01	0.1	8.9E-01
ENSMUST00000128376				-4.5	2.2E-04	3.4	4.5E-03	-1.6	1.2E-01	-0.2	7.7E-01
ENSMUST00000140286				-4.5	2.1E-03	6.7	4.4E-04	-0.8	5.1E-01	0.7	3.1E-01
ENSMUST00000136970				-4.5	6.5E-03	5.0	1.4E-02	-0.5	7.9E-01	-0.7	5.4E-01
ENSMUST00000117155				-4.5	6.3E-04	6.1	6.8E-05	-0.3	7.6E-01	0.3	6.3E-01
ENSMUST00000140701				-4.5	1.1E-02	-3.5	2.1E-01	2.3	7.5E-02	-0.1	9.8E-01
ENSMUST00000191550	mutS homolog 3 (E. coli) [Source:MGI Symbol;Acc:MGI:109519]	A0A087WRJ5		0.4	8.3E-01	-0.6	8.0E-01	-1.5	3.7E-01	-0.5	8.5E-01
ENSMUST00000146290				-4.5	8.2E-03	6.4	1.6E-03	-0.4	8.0E-01	-0.4	6.2E-01
ENSMUST00000193868				-4.5	3.2E-05	3.2	1.4E-03	-0.4	5.4E-01	-0.7	2.1E-01
ENSMUST00000152965				-4.5	3.0E-03	4.5	2.1E-03	-0.2	8.7E-01	0.3	6.7E-01
ENSMUST00000142191				-4.6	7.0E-04	6.3	4.2E-04	-0.6	6.4E-01	-0.1	8.7E-01
ENSMUST00000191577	myosin binding protein H [Source:MGI Symbol;Acc:MGI:1858196]		P70402	-1.9	2.9E-01	0.1	9.6E-01	0.9	5.7E-01	-1.1	5.4E-01
ENSMUST00000145320				-4.6	2.0E-04	-6.3	3.9E-02	0.5	7.1E-01	-3.2	4.0E-01
ENSMUST00000119877				-4.6	1.2E-04	5.1	4.0E-03	-0.7	6.1E-01	0.6	5.2E-01
ENSMUST00000191598	NADH dehydrogenase (ubiquinone) flavoprotein 3 [Source:MGI Symbol;Acc:MGI:1890894]	A0A087WQ40		-2.0	7.0E-02	0.0	9.9E-01	0.6	5.0E-01	-1.3	2.4E-01
ENSMUST00000191602	predicted gene 996 [Source:MGI Symbol;Acc:MGI:2685842]		A2AJA9	4.5	8.9E-02	-0.5	8.5E-01	-3.1	2.1E-01	1.9	4.5E-01
ENSMUST00000191606				4.4	2.7E-01	1.5	7.7E-01	0.2	9.7E-01	3.0	4.5E-01
ENSMUST00000191615				-1.5	1.9E-01	-1.7	2.5E-01	0.0	9.8E-01	0.1	9.2E-01
ENSMUST00000159371				-4.6	8.7E-03	5.0	2.2E-02	-0.8	6.8E-01	2.7	3.9E-02
ENSMUST00000126529				-4.6	3.3E-03	6.0	6.8E-05	-0.1	8.8E-01	-0.1	9.0E-01
ENSMUST00000118481				-4.6	6.4E-04	5.5	2.6E-03	-1.4	3.5E-01	0.7	3.9E-01
ENSMUST00000191666	Fc receptor-like 1 [Source:MGI Symbol;Acc:MGI:2442862]	A0A0A6YXB2		0.4	8.7E-01	-0.9	6.7E-01	-2.7	1.5E-01	-1.4	5.6E-01
ENSMUST00000148239				-4.6	1.0E-03	-6.4	1.5E-04	-1.3	7.2E-03	-0.8	4.8E-01
ENSMUST00000191671	interleukin 1 receptor, type II [Source:MGI Symbol;Acc:MGI:96546]	A0A0A6YX83		1.1	1.8E-01	1.2	1.9E-01	-0.8	2.9E-01	-1.0	2.3E-01
ENSMUST00000141815				-4.6	4.8E-03	6.7	1.7E-02	-1.5	5.7E-01	-2.6	1.1E-01
ENSMUST00000001162				-4.6	8.3E-04	6.9	2.6E-04	-1.7	2.4E-01	0.7	2.7E-01
ENSMUST00000002490				-4.6	2.8E-04	-6.4	4.7E-03	0.8	2.3E-01	-0.9	6.6E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000131683				-4.6	4.7E-03	7.9	6.4E-04	-0.8	6.5E-01	0.7	3.5E-01
ENSMUST00000154596				-4.6	3.4E-03	-5.9	3.4E-04	-0.7	1.4E-01	-0.9	4.4E-01
ENSMUST00000191706				-0.6	6.9E-01	-1.4	5.6E-01	0.4	7.9E-01	1.2	5.5E-01
ENSMUST00000140385				-4.6	1.6E-03	-3.1	6.9E-02	0.4	6.0E-01	-0.3	8.6E-01
ENSMUST00000159887				-4.6	2.6E-04	5.9	1.2E-03	-0.1	9.3E-01	0.1	8.8E-01
ENSMUST00000160474				-4.6	2.6E-04	5.1	3.5E-04	0.1	8.8E-01	-0.7	2.8E-01
ENSMUST00000081241				-4.6	3.0E-04	8.4	3.2E-04	-1.4	4.2E-01	0.4	5.7E-01
ENSMUST00000142482				-4.6	6.5E-04	1.9	5.6E-02	0.1	9.0E-01	0.2	7.5E-01
ENSMUST00000140213				-4.6	4.4E-03	5.9	2.7E-04	1.7	1.0E-01	0.9	1.7E-01
ENSMUST00000191747	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	Q3U570		-4.0	1.8E-01	-1.7	5.7E-01	-0.2	9.0E-01	-2.5	4.5E-01
ENSMUST00000167455				-4.6	3.3E-03	5.5	1.3E-03	-0.8	5.3E-01	-0.5	4.6E-01
ENSMUST00000107798				-4.6	2.6E-04	7.7	4.2E-04	-0.4	7.9E-01	0.1	8.4E-01
ENSMUST00000174325				-4.6	6.6E-03	-2.6	1.7E-01	1.5	1.5E-01	0.5	7.9E-01
ENSMUST00000148498				-4.6	1.0E-02	6.3	1.8E-03	0.2	9.2E-01	-0.6	5.2E-01
ENSMUST00000098689				-4.6	5.2E-05	6.6	4.8E-05	-1.5	1.5E-01	0.3	5.8E-01
ENSMUST00000142111				-4.6	2.8E-02	-2.6	9.3E-02	0.7	4.5E-01	-1.0	5.2E-01
ENSMUST00000133223				-4.6	5.9E-03	-5.1	1.4E-03	0.5	2.8E-01	-2.0	1.5E-01
ENSMUST00000112182				-4.6	1.4E-02	7.4	6.3E-05	0.0	9.9E-01	-0.4	5.6E-01
ENSMUST00000131400				-4.6	9.2E-05	-3.7	5.3E-03	0.2	6.5E-01	-0.1	8.9E-01
ENSMUST00000191790				-1.4	1.1E-01	-0.5	6.4E-01	0.5	5.3E-01	-0.4	6.6E-01
ENSMUST00000191794	protocadherin 18 [Source:MGI Symbol;Acc:MGI:1920423]	A0A0A6YXH7		5.1	8.4E-02	6.4	4.2E-02	-1.2	7.0E-01	-2.6	1.3E-01
ENSMUST00000151268				-4.6	1.2E-02	4.0	4.5E-04	-0.2	7.3E-01	-0.1	8.1E-01
ENSMUST00000191804				3.3	2.8E-01	0.6	8.7E-01	-1.2	6.9E-01	1.4	6.7E-01
ENSMUST00000162737				-4.7	1.9E-02	5.3	9.2E-04	-0.9	4.6E-01	0.5	4.9E-01
ENSMUST00000175860				-4.7	1.7E-03	7.3	2.8E-04	-0.4	7.7E-01	-0.7	3.2E-01
ENSMUST00000145327				-4.7	2.5E-04	7.9	3.5E-04	0.1	9.5E-01	-1.1	1.7E-01
ENSMUST00000191828				1.2	5.4E-01	-0.7	7.3E-01	-2.8	1.0E-01	-0.8	7.0E-01
ENSMUST00000107053				-4.7	7.3E-05	8.7	2.0E-05	-0.5	7.0E-01	-0.2	7.0E-01
ENSMUST00000143331				-4.7	2.9E-02	5.3	2.1E-04	-2.5	3.8E-02	-0.6	3.1E-01
ENSMUST00000145216				-4.7	5.6E-05	5.6	1.4E-02	0.4	8.5E-01	-0.7	5.4E-01
ENSMUST00000155626				-4.7	1.2E-03	6.0	3.7E-03	-0.4	8.3E-01	-1.9	7.2E-02
ENSMUST00000145409				-4.7	2.3E-04	8.7	1.0E-04	-0.7	6.2E-01	0.9	1.6E-01
ENSMUST00000191849	ankyrin repeat domain 23 [Source:MGI Symbol;Acc:MGI:1925571]	Q8K1D0		0.9	4.2E-01	5.1	2.8E-02	4.3	3.8E-02	0.1	9.3E-01
ENSMUST00000191851				0.2	8.6E-01	7.8	1.8E-02	5.9	5.2E-02	-1.7	1.8E-01
ENSMUST00000145015				-4.7	1.9E-04	6.8	1.9E-04	-0.5	7.1E-01	-0.7	2.7E-01
ENSMUST00000160000				-4.7	9.0E-04	7.4	3.7E-05	-0.6	6.1E-01	-0.7	2.1E-01
ENSMUST00000191860				1.2	1.4E-01	1.9	9.1E-02	0.6	5.2E-01	-0.1	8.9E-01
ENSMUST00000094307				-4.7	3.8E-03	8.4	1.1E-03	0.0	9.9E-01	0.7	4.2E-01
ENSMUST00000191872	La ribonucleoprotein domain family, member 1B [Source:MGI Symbol;Acc:MGI:1914604]	Q3TQS1		2.6	9.1E-02	1.7	2.8E-01	-1.4	3.2E-01	-0.6	6.8E-01
ENSMUST00000191878	lamin B receptor [Source:MGI Symbol;Acc:MGI:2138281]	A0A0A6YXT6		-1.3	3.8E-01	-0.7	7.6E-01	0.5	7.2E-01	-0.1	9.5E-01
ENSMUST00000191882				1.9	1.8E-01	3.5	9.8E-02	1.9	2.9E-01	0.3	8.5E-01
ENSMUST00000136107				-4.7	5.5E-04	4.4	7.5E-02	-0.8	7.4E-01	0.4	8.1E-01
ENSMUST00000130308				-4.7	7.2E-03	-0.9	7.6E-01	4.7	2.9E-02	-0.3	9.1E-01
ENSMUST00000191897				-3.1	8.6E-02	-1.2	5.0E-01	0.9	5.0E-01	-1.0	6.1E-01
ENSMUST00000191899	dystroglycan 1 [Source:MGI Symbol;Acc:MGI:101864]	Q544G5	Q62165	0.0	9.6E-01	0.2	8.1E-01	0.5	2.9E-01	0.4	5.4E-01
ENSMUST00000146638				-4.7	5.1E-03	2.5	2.9E-03	0.2	7.2E-01	-0.4	4.7E-01
ENSMUST00000172777				-4.7	4.7E-03	5.8	1.3E-03	0.5	6.9E-01	-0.8	3.0E-01
ENSMUST00000191925	protein phosphatase 2, regulatory subunit B', alpha [Source:MGI Symbol;Acc:MGI:2388479]	A0A0A6YVV9		-4.0	5.2E-02	-1.2	5.9E-01	0.9	5.6E-01	-1.9	3.8E-01
ENSMUST00000192841				-4.7	3.0E-03	4.7	7.9E-04	-1.5	1.2E-01	0.1	8.1E-01
ENSMUST00000132633				-4.7	3.2E-03	4.2	3.5E-02	-1.5	4.2E-01	1.0	4.1E-01
ENSMUST00000118829				-4.7	1.0E-03	7.5	5.3E-06	-0.7	4.2E-01	0.2	6.8E-01
ENSMUST00000178557				-4.7	1.0E-03	2.6	4.0E-03	-0.1	8.5E-01	0.1	8.5E-01
ENSMUST00000153716				-4.7	2.3E-03	2.9	3.8E-03	1.1	1.3E-01	-0.2	7.6E-01
ENSMUST00000191955	rine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10 [Source:MGI Symbol;Acc:MGI:213864	G3UYR4		-5.1	1.0E-01	-6.1	1.0E-01	-2.2	2.0E-01	-1.2	7.6E-01
ENSMUST00000149420				-4.7	1.9E-03	-3.0	5.0E-02	0.6	4.5E-01	0.3	8.2E-01
ENSMUST00000191960	TD and POZ domain containing 2 [Source:MGI Symbol;Acc:MGI:3027902]	A0A0A6YVW8		3.7	1.1E-01	5.1	4.7E-02	-0.3	9.1E-01	-1.8	2.3E-01
ENSMUST00000125448				-4.7	1.3E-02	5.9	1.5E-04	1.1	2.5E-01	0.4	5.4E-01
ENSMUST00000192659				-4.7	4.4E-03	-2.6	1.0E-01	0.5	5.4E-01	-1.4	4.1E-01
ENSMUST00000141608				-4.8	4.4E-04	6.1	3.7E-04	-0.6	6.3E-01	0.1	9.3E-01
ENSMUST00000148976				-4.8	3.2E-03	4.0	3.6E-03	0.7	4.9E-01	0.4	5.8E-01
ENSMUST00000130130				-4.8	2.9E-03	5.6	4.2E-04	-1.3	2.7E-01	0.0	9.5E-01
ENSMUST00000156091				-4.8	1.7E-02	6.0	6.8E-04	-1.5	2.8E-01	0.7	3.7E-01
ENSMUST00000155756				-4.8	3.4E-04	-8.8	4.8E-04	-0.3	5.8E-01	-3.3	1.6E-01
ENSMUST00000129054				-4.8	5.9E-03	10.6	1.3E-04	-0.9	6.3E-01	0.5	4.8E-01
ENSMUST00000192001	calmodulin regulated spectrin-associated protein family, member 2 [Source:MGI Symbol;Acc:MGI:1922434]		Q8C1B1	-0.1	8.9E-01	-1.4	5.0E-01	1.9	1.5E-01	3.1	9.9E-02
ENSMUST00000135277				-4.8	6.9E-03	5.8	1.7E-03	-0.7	6.3E-01	0.8	3.2E-01
ENSMUST00000124067				-4.8	5.2E-04	6.3	3.1E-04	-0.2	8.3E-01	0.4	4.7E-01
ENSMUST00000128733				-4.8	3.5E-03	6.4	2.8E-04	-0.2	8.9E-01	0.1	8.8E-01
ENSMUST00000141470				-4.8	1.4E-03	6.9	1.5E-04	-0.6	6.3E-01	0.0	9.6E-01
ENSMUST00000049675				-4.8	5.4E-04	4.5	1.3E-02	-0.7	6.6E-01	1.1	2.7E-01
ENSMUST00000192031				0.9	2.7E-01	0.1	9.5E-01	0.3	7.5E-01	1.1	2.9E-01
ENSMUST00000118047				-4.8	8.6E-03	-2.5	1.4E-01	2.5	1.1E-02	-0.8	6.4E-01
ENSMUST00000165489				-4.8	7.2E-04	-5.6	8.5E-06	0.1	5.9E-01	-0.5	4.6E-01
ENSMUST00000143899				-4.8	5.7E-03	-5.8	2.5E-04	0.3	5.4E-01	-0.4	7.3E-01
ENSMUST00000174475				-4.8	1.5E-03	5.6	6.5E-05	0.2	7.6E-01	-0.2	7.4E-01
ENSMUST00000153245				-4.8	3.0E-04	2.5	4.3E-03	0.5	3.7E-01	-0.1	9.2E-01
ENSMUST00000147816				-4.8	1.3E-02	5.2	4.8E-03	-1.4	3.7E-01	-0.4	6.7E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000162397				-4.8	1.4E-03	7.5	1.4E-05	-0.5	5.6E-01	0.8	9.8E-02
ENSMUST00000123972				-4.8	8.2E-04	-2.6	2.5E-01	0.8	5.4E-01	-1.7	4.7E-01
ENSMUST00000147145				-4.8	2.4E-03	2.4	1.1E-02	0.3	6.1E-01	0.0	9.5E-01
ENSMUST00000151067				-4.8	6.7E-04	6.4	3.0E-04	0.4	7.2E-01	0.7	2.7E-01
ENSMUST00000131940				-4.9	3.1E-04	-4.7	5.8E-03	0.7	3.2E-01	-2.0	2.7E-01
ENSMUST00000153537				-4.9	3.5E-04	6.4	3.3E-03	-0.3	8.7E-01	0.8	4.0E-01
ENSMUST00000040980				-4.9	2.2E-04	-3.4	1.1E-01	1.6	1.2E-01	0.8	6.9E-01
ENSMUST00000153764				-4.9	1.2E-03	4.7	6.5E-04	-1.1	2.6E-01	-0.5	4.7E-01
ENSMUST00000130500				-4.9	8.4E-03	5.9	4.8E-03	-0.7	6.8E-01	0.1	9.1E-01
ENSMUST00000164421				-4.9	5.9E-04	6.4	1.1E-03	0.0	9.8E-01	-1.6	7.2E-02
ENSMUST00000192144	RIKEN cDNA 0610030E20 gene [Source:MGI Symbol;Acc:MGI:1915614]		Q149G0	-0.9	5.9E-02	0.3	5.7E-01	1.3	1.2E-02	0.1	8.8E-01
ENSMUST00000085387				-4.9	5.2E-04	7.5	2.3E-04	-0.5	7.4E-01	-1.0	1.6E-01
ENSMUST00000136721				-4.9	4.6E-03	-2.0	1.8E-01	1.7	5.7E-02	-2.3	1.6E-01
ENSMUST00000159406				-4.9	3.2E-04	3.0	1.3E-01	2.0	2.2E-01	3.1	3.7E-02
ENSMUST00000192158	REST corepressor 3 [Source:MGI Symbol;Acc:MGI:2441920]	A0A0A6YX54		1.0	6.9E-01	1.2	6.7E-01	-0.5	8.3E-01	-0.7	7.7E-01
ENSMUST00000129565				-4.9	1.1E-03	1.9	2.0E-01	-1.8	1.8E-01	0.3	8.1E-01
ENSMUST00000132521				-4.9	2.7E-03	6.5	6.4E-04	-0.6	6.7E-01	0.5	5.2E-01
ENSMUST00000192174				-2.7	3.7E-02	-2.7	1.2E-01	1.0	2.5E-01	1.0	5.5E-01
ENSMUST00000156821				-4.9	8.5E-04	7.3	2.9E-05	0.5	6.0E-01	0.2	6.7E-01
ENSMUST00000187462				-4.9	1.8E-04	4.6	1.1E-03	-0.5	6.3E-01	0.5	4.4E-01
ENSMUST00000131820				-4.9	6.4E-03	4.4	1.1E-02	-0.5	6.7E-01	-0.8	4.8E-01
ENSMUST00000192181				5.0	5.5E-02	4.2	1.3E-01	-0.6	8.3E-01	0.2	9.2E-01
ENSMUST00000192185	SFT2 domain containing 2 [Source:MGI Symbol;Acc:MGI:1917362]	A0A0A6YX21		-1.4	3.5E-01	0.0	9.9E-01	0.8	5.4E-01	-0.6	7.3E-01
ENSMUST00000147219				-4.9	3.5E-04	3.5	2.3E-03	-3.1	9.9E-03	0.4	5.1E-01
ENSMUST00000192193	DNA segment, Chr 3, ERATO Doi 751, expressed [Source:MGI Symbol;Acc:MGI:1289213]		Q8BGN2	3.9	3.6E-02	6.2	1.1E-02	0.4	8.2E-01	-1.9	1.5E-01
ENSMUST00000124177				-4.9	4.4E-03	4.6	5.9E-04	0.1	9.2E-01	-0.1	8.2E-01
ENSMUST00000148068				-4.9	2.8E-02	2.3	2.6E-02	-1.3	1.3E-01	-0.4	6.3E-01
ENSMUST00000140606				-4.9	2.4E-03	5.5	9.2E-05	-0.7	3.8E-01	-0.6	2.9E-01
ENSMUST00000118998				-4.9	8.7E-04	6.6	1.4E-03	0.2	8.8E-01	1.0	2.8E-01
ENSMUST00000192204	predicted gene, 21454 [Source:MGI Symbol;Acc:MGI:5434809]	J3QPX2		4.0	1.7E-01	3.3	3.2E-01	-0.2	9.5E-01	0.5	8.0E-01
ENSMUST00000162557				-4.9	2.7E-04	5.3	8.1E-04	-0.5	6.4E-01	-0.1	8.7E-01
ENSMUST00000153038				-4.9	2.5E-02	-3.2	1.5E-02	1.9	4.7E-03	-0.7	5.7E-01
ENSMUST00000164636				-4.9	2.4E-03	3.8	7.1E-03	-0.4	7.1E-01	-1.2	1.4E-01
ENSMUST00000129284				-4.9	4.7E-04	3.6	2.2E-01	-0.7	8.1E-01	1.7	3.6E-01
ENSMUST00000192222	REST corepressor 3 [Source:MGI Symbol;Acc:MGI:2441920]	A0A0A6YVU5		2.1	4.3E-02	1.5	1.7E-01	-0.8	4.2E-01	-0.2	8.6E-01
ENSMUST00000150757				-4.9	4.3E-03	6.1	1.6E-04	-1.5	1.9E-01	-0.8	2.3E-01
ENSMUST00000162866				-4.9	2.9E-04	4.9	1.6E-03	-0.4	7.0E-01	0.0	9.8E-01
ENSMUST00000149391				-4.9	3.2E-02	6.4	3.7E-04	-1.0	4.5E-01	-0.3	6.1E-01
ENSMUST00000192235	n, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) [Source:MGI Symbol;Acc:MGI:18	A0A0A6YW76		1.9	2.0E-01	0.2	9.3E-01	-0.8	5.6E-01	1.0	5.8E-01
ENSMUST00000015948				-5.0	1.9E-04	-6.7	7.1E-03	-2.5	9.6E-03	-0.7	7.5E-01
ENSMUST00000194801				-5.0	2.5E-03	5.3	9.7E-05	0.0	9.7E-01	0.1	8.1E-01
ENSMUST00000138010				-5.0	1.6E-02	4.6	8.5E-04	-1.9	9.5E-02	-0.4	5.9E-01
ENSMUST00000192241	lipocalin 2 [Source:MGI Symbol;Acc:MGI:96757]	A0A0A6YW77		-1.1	1.3E-01	0.2	8.3E-01	0.0	9.6E-01	-1.3	1.4E-01
ENSMUST00000140199				-5.0	1.4E-03	3.8	1.3E-02	-1.2	3.6E-01	1.1	2.1E-01
ENSMUST00000148800				-5.0	2.1E-03	5.8	4.8E-03	-1.2	4.4E-01	0.4	7.0E-01
ENSMUST00000195045				-5.0	2.0E-03	-4.0	2.2E-03	0.2	7.2E-01	-0.6	6.0E-01
ENSMUST00000132611				-5.0	1.3E-02	4.9	1.4E-04	-1.9	4.7E-02	-0.3	5.6E-01
ENSMUST00000192274				2.7	8.5E-02	6.8	8.5E-04	-0.5	7.4E-01	-4.6	1.5E-03
ENSMUST00000173786				-5.0	2.1E-03	6.9	1.1E-05	-0.5	5.2E-01	0.3	5.7E-01
ENSMUST00000138646				-5.0	1.7E-02	8.2	2.9E-05	-1.1	3.9E-01	0.5	3.3E-01
ENSMUST00000118246				-5.0	6.3E-03	1.9	9.8E-02	-2.6	2.9E-02	-0.4	6.8E-01
ENSMUST00000132800				-5.0	1.7E-02	5.8	6.4E-05	0.4	5.8E-01	0.2	7.4E-01
ENSMUST00000195605				-5.0	7.8E-03	6.9	3.2E-02	-1.0	7.5E-01	-1.0	5.7E-01
ENSMUST00000192075				-5.0	1.8E-02	4.9	4.2E-02	-0.7	7.6E-01	0.1	9.7E-01
ENSMUST00000192314	calmodulin regulated spectrin-associated protein family, member 2 [Source:MGI Symbol;Acc:MGI:1922434]	A0A0A6YY67		0.5	8.2E-01	2.6	2.0E-01	-2.4	2.2E-01	-4.4	5.3E-02
ENSMUST00000135258				-5.0	2.0E-05	5.1	1.1E-01	-0.9	7.8E-01	1.5	4.4E-01
ENSMUST00000192328	transducin (beta)-like 1X-linked receptor 1 [Source:MGI Symbol;Acc:MGI:2441730]		Q8BHJ5	-0.1	9.0E-01	0.4	7.0E-01	0.5	5.0E-01	0.0	9.9E-01
ENSMUST00000159604				-5.0	7.3E-03	4.6	1.2E-02	-0.4	8.0E-01	-0.2	8.2E-01
ENSMUST00000154774				-5.0	4.3E-04	-1.7	1.8E-01	0.0	1.0E+00	-1.9	1.8E-01
ENSMUST00000166619				-5.0	1.2E-02	6.1	4.4E-03	0.0	9.9E-01	-1.0	3.0E-01
ENSMUST00000192365				-0.8	5.0E-01	-0.1	9.0E-01	-0.8	4.1E-01	-1.4	2.4E-01
ENSMUST00000192369	dual specificity phosphatase 27 (putative) [Source:MGI Symbol;Acc:MGI:2685055]		Q148W8	3.4	2.5E-01	5.4	1.0E-01	-0.5	8.9E-01	-2.4	2.5E-01
ENSMUST00000137709				-5.0	7.1E-04	1.6	3.3E-01	-0.6	6.7E-01	0.6	5.9E-01
ENSMUST00000149834				-5.0	2.5E-03	1.7	2.4E-02	-0.5	4.0E-01	0.1	8.8E-01
ENSMUST00000192401				-0.8	3.5E-01	-0.8	5.0E-01	0.8	3.1E-01	0.8	4.3E-01
ENSMUST00000135597				-5.0	1.2E-02	6.0	2.1E-06	-0.7	2.1E-01	-0.1	7.0E-01
ENSMUST00000031839				-5.0	4.9E-05	3.8	2.3E-03	-1.1	2.0E-01	-0.7	3.5E-01
ENSMUST00000136161				-5.0	2.5E-04	5.1	2.5E-04	-0.4	6.7E-01	0.3	5.8E-01
ENSMUST00000126475				-5.1	3.3E-05	4.7	2.1E-05	-0.5	3.5E-01	0.3	4.9E-01
ENSMUST00000145659				-5.1	7.2E-04	4.5	6.7E-04	-0.5	5.5E-01	-0.7	2.5E-01
ENSMUST00000144835				-5.1	2.7E-03	7.4	5.8E-04	-0.4	8.0E-01	-1.1	1.9E-01
ENSMUST00000130121				-5.1	3.0E-04	4.7	2.9E-04	-0.1	9.4E-01	0.6	2.8E-01
ENSMUST00000109183				-5.1	1.4E-02	4.5	1.8E-03	0.4	6.7E-01	0.2	8.0E-01
ENSMUST00000192489				-5.1	5.9E-03	5.2	2.3E-02	-0.8	7.1E-01	0.6	6.5E-01
ENSMUST00000152706				-5.1	1.1E-04	-3.7	1.0E-02	2.2	2.3E-03	1.4	2.6E-01
ENSMUST00000184842				-5.1	2.2E-05	-4.3	2.4E-03	-1.4	3.7E-02	-0.8	5.2E-01
ENSMUST00000177669				-5.1	1.5E-04	5.8	4.0E-05	-1.3	1.3E-01	0.5	2.9E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000192462	crystallin, zeta [Source:MGI Symbol;Acc:MGI:88527]		P47199	0.9	1.4E-01	1.2	1.2E-01	-0.1	8.6E-01	-0.4	5.7E-01
ENSMUST00000145684				-5.1	1.3E-04	4.5	4.6E-04	-0.5	5.3E-01	-1.1	1.3E-01
ENSMUST00000078246				-5.1	9.5E-04	8.0	4.1E-04	-0.7	6.6E-01	0.4	6.3E-01
ENSMUST00000144265				-5.1	1.3E-02	6.4	2.5E-04	-0.9	4.6E-01	0.3	5.9E-01
ENSMUST00000192488	cytotoxic T-lymphocyte-associated protein 4 [Source:EntrezGene;Acc:12477]			1.4	2.8E-01	-0.3	8.0E-01	-3.1	2.0E-02	-1.3	2.9E-01
ENSMUST00000149771				-5.1	3.2E-03	-2.6	9.8E-02	1.1	2.5E-01	-1.4	4.2E-01
ENSMUST00000160697				-5.1	9.4E-04	6.7	9.0E-05	-0.5	6.3E-01	0.6	2.6E-01
ENSMUST00000160145				-5.1	1.2E-03	5.4	1.2E-03	-0.6	6.6E-01	0.3	6.5E-01
ENSMUST00000192506				-0.3	6.2E-01	0.2	7.8E-01	0.4	4.5E-01	-0.1	9.0E-01
ENSMUST00000136289				-5.1	1.9E-02	3.3	4.3E-02	-0.1	9.5E-01	-0.3	7.6E-01
ENSMUST00000156344				-5.1	6.9E-04	-2.2	2.1E-01	1.5	1.3E-01	-0.4	7.9E-01
ENSMUST00000125098				-5.1	3.9E-03	5.8	1.1E-03	-0.6	6.7E-01	-0.3	6.6E-01
ENSMUST00000093430				-5.1	1.5E-03	5.1	5.8E-02	0.7	7.9E-01	0.5	7.2E-01
ENSMUST00000121368				-5.1	1.0E-04	6.5	3.1E-02	1.7	4.8E-01	-0.3	8.6E-01
ENSMUST00000192531	TBC1 domain family, member 8 [Source:MGI Symbol;Acc:MGI:1927225]	A0A0A6YXU3		2.1	4.1E-01	4.2	2.1E-01	2.2	4.1E-01	0.1	9.7E-01
ENSMUST00000134803				-5.1	7.8E-03	-4.8	6.9E-03	-0.1	8.9E-01	-0.3	8.6E-01
ENSMUST00000097723				-5.1	8.7E-05	5.3	6.9E-04	-3.0	3.3E-02	0.5	4.9E-01
ENSMUST00000127252				-5.1	7.4E-05	2.1	1.2E-01	-3.2	3.7E-02	0.2	8.2E-01
ENSMUST00000192544	F-box protein 28 [Source:MGI Symbol;Acc:MGI:1261890]	A0A0A6YX52		-2.5	3.7E-02	-3.0	9.8E-02	0.4	6.4E-01	0.8	6.3E-01
ENSMUST00000036976				-5.1	2.9E-03	7.4	1.1E-04	1.0	4.1E-01	-0.8	1.8E-01
ENSMUST00000162923				-5.2	2.1E-03	-3.1	1.4E-03	-0.7	8.6E-02	0.7	3.4E-01
ENSMUST00000140682				-5.2	5.1E-04	6.7	3.6E-04	-0.2	8.6E-01	-0.1	8.7E-01
ENSMUST00000154550				-5.2	5.6E-04	7.0	7.0E-05	-0.5	6.4E-01	-1.1	8.7E-02
ENSMUST00000130225				-5.2	1.4E-04	2.1	3.6E-03	-0.6	2.2E-01	0.1	8.5E-01
ENSMUST00000129001				-5.2	3.6E-03	5.9	1.9E-03	-0.7	6.4E-01	-0.5	5.6E-01
ENSMUST00000130809				-5.2	1.1E-02	5.6	9.1E-04	-0.9	4.6E-01	-0.4	6.0E-01
ENSMUST00000153763				-5.2	1.7E-02	5.9	5.0E-04	0.1	9.5E-01	0.7	3.2E-01
ENSMUST00000131814				-5.2	2.8E-04	5.0	1.3E-04	-3.4	5.3E-03	-1.0	1.0E-01
ENSMUST00000008284				-5.2	3.9E-03	3.6	1.9E-03	0.0	9.7E-01	0.1	8.5E-01
ENSMUST00000154784				-5.2	2.1E-04	5.5	7.8E-05	0.9	2.3E-01	-0.3	6.2E-01
ENSMUST00000111895				-5.2	7.4E-03	-7.3	1.1E-02	1.8	3.3E-02	0.0	9.9E-01
ENSMUST00000115538				-5.2	7.4E-05	6.0	2.5E-04	-0.5	6.3E-01	-0.2	7.8E-01
ENSMUST00000121585				-5.2	2.1E-03	5.2	4.2E-02	1.3	5.5E-01	1.1	4.2E-01
ENSMUST00000131713				-5.2	2.4E-04	7.5	4.1E-05	-0.6	6.2E-01	-0.8	1.8E-01
ENSMUST00000135703				-5.2	7.3E-04	5.4	1.7E-03	-1.6	2.5E-01	-2.3	2.2E-02
ENSMUST00000117356				-5.2	4.4E-05	-2.7	3.2E-02	1.6	2.7E-02	-2.8	6.2E-02
ENSMUST00000137254				-5.2	5.5E-05	4.3	6.2E-03	0.3	8.0E-01	0.1	8.8E-01
ENSMUST00000149411				-5.2	9.1E-04	4.7	9.4E-05	-0.7	2.9E-01	0.3	4.9E-01
ENSMUST00000184573				-5.2	5.1E-04	7.3	2.5E-04	-0.5	7.2E-01	-1.1	1.4E-01
ENSMUST00000191097				-5.2	8.8E-05	3.9	5.6E-02	6.4	3.0E-03	-2.2	1.3E-01
ENSMUST00000152276				-5.2	3.7E-03	5.9	2.9E-03	-0.7	6.8E-01	-0.3	7.6E-01
ENSMUST00000192666	major facilitator superfamily domain containing 7B [Source:MGI Symbol;Acc:MGI:2444881]	A0A0A6YXG8		-0.9	4.5E-01	1.5	2.6E-01	0.2	8.4E-01	-2.2	1.1E-01
ENSMUST00000192671	calpain 8 [Source:MGI Symbol;Acc:MGI:2181366]	A0A0A6YVU9		2.6	9.7E-02	4.9	9.9E-03	0.0	9.8E-01	-2.2	8.5E-02
ENSMUST00000176257				-5.2	3.9E-04	8.2	8.5E-04	0.3	8.6E-01	0.5	5.8E-01
ENSMUST00000139511				-5.2	4.1E-04	-4.7	4.4E-03	0.9	1.0E-01	-0.8	5.7E-01
ENSMUST00000128910				-5.2	2.9E-03	-8.8	2.4E-04	-0.4	3.9E-01	-2.4	1.9E-01
ENSMUST00000150214				-5.3	2.4E-04	-4.8	1.5E-03	-0.7	1.6E-01	-0.5	7.0E-01
ENSMUST00000193359				-5.3	1.7E-03	7.7	7.0E-05	-1.4	2.7E-01	0.7	2.2E-01
ENSMUST00000046149				-5.3	3.2E-04	2.7	7.1E-02	-1.8	1.9E-01	-0.5	6.4E-01
ENSMUST00000160591				-5.3	1.2E-04	6.2	4.1E-04	-0.6	6.1E-01	-0.5	4.4E-01
ENSMUST00000192757	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	A0A0A6YXL7		-1.6	3.8E-01	-3.1	1.6E-01	-2.2	1.0E-01	-0.7	7.7E-01
ENSMUST00000192758				0.4	6.8E-01	1.9	1.9E-01	1.4	2.4E-01	-0.1	9.0E-01
ENSMUST00000135052				-5.3	2.3E-03	-3.6	9.1E-02	2.4	2.2E-02	0.5	8.1E-01
ENSMUST00000138282				-5.3	1.1E-02	6.0	2.0E-04	-0.7	5.0E-01	-0.8	2.4E-01
ENSMUST00000148285				-5.3	7.0E-05	6.2	4.6E-05	-0.1	9.1E-01	-0.3	5.8E-01
ENSMUST00000124386				-5.3	3.7E-03	7.0	1.2E-04	-0.6	6.3E-01	-0.9	1.7E-01
ENSMUST00000192775				-1.6	4.4E-02	-2.6	4.6E-02	-0.1	8.7E-01	0.8	4.6E-01
ENSMUST00000176761				-5.3	1.7E-02	-1.1	3.1E-01	1.4	5.6E-02	0.8	4.6E-01
ENSMUST00000154954				-5.3	1.4E-04	5.2	1.9E-02	-0.5	7.9E-01	1.5	2.6E-01
ENSMUST00000192793	poly(A) binding protein, cytoplasmic 4-like [Source:MGI Symbol;Acc:MGI:3643087]	G5E8X2		3.4	1.1E-01	1.8	4.8E-01	-0.4	8.6E-01	1.2	5.5E-01
ENSMUST00000192807	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	Q3U581		-1.6	6.3E-01	-3.8	4.5E-01	-1.5	5.5E-01	0.7	8.9E-01
ENSMUST00000192811				2.0	3.5E-02	2.2	5.7E-02	0.5	5.9E-01	0.3	7.3E-01
ENSMUST00000125841				-5.3	1.4E-04	3.2	4.6E-03	-0.8	3.2E-01	-0.3	7.0E-01
ENSMUST00000173086				-5.3	2.7E-04	4.5	4.0E-03	-1.3	3.1E-01	-0.2	8.3E-01
ENSMUST00000125959				-5.3	4.4E-03	-2.0	2.8E-01	2.3	4.1E-02	-0.4	8.1E-01
ENSMUST00000192844				1.3	1.6E-01	1.0	3.8E-01	0.6	4.7E-01	0.9	4.2E-01
ENSMUST00000192847	ATPase, H+ transporting, lysosomal V1 subunit H [Source:MGI Symbol;Acc:MGI:1914864]	A0A0A6YWP6		-2.8	5.9E-02	-1.1	5.5E-01	1.1	3.9E-01	-0.6	7.2E-01
ENSMUST00000192852	transmembrane protein 89 [Source:MGI Symbol;Acc:MGI:1916634]		Q9DA04	2.4	9.7E-02	6.2	4.2E-03	1.2	4.9E-01	-2.7	2.7E-02
ENSMUST00000160032				-5.3	3.1E-03	3.4	2.1E-02	-1.2	3.1E-01	1.3	2.0E-01
ENSMUST00000140236				-5.3	6.5E-04	-2.1	5.2E-02	-0.9	2.2E-01	-3.7	1.6E-02
ENSMUST00000192869	Vesicle-associated membrane protein 5 [Source:UniProtKB/Swiss-Prot;Acc:Q9Z2P8]	Q791P0	Q9Z2P8	-3.0	4.0E-02	-4.5	4.1E-02	0.2	8.6E-01	1.7	4.1E-01
ENSMUST00000147005				-5.3	1.7E-03	3.0	6.1E-04	-0.2	6.5E-01	-0.4	4.2E-01
ENSMUST00000149145				-5.3	2.5E-02	8.7	8.8E-06	0.1	9.3E-01	-0.8	1.1E-01
ENSMUST00000137633				-5.3	3.8E-03	6.8	5.3E-04	-0.4	8.0E-01	-0.9	2.4E-01
ENSMUST00000128679				-5.3	2.8E-03	1.5	1.4E-01	-0.3	7.6E-01	0.4	5.9E-01
ENSMUST00000195230				-5.3	2.0E-03	-2.9	6.1E-02	1.0	1.7E-01	1.4	3.3E-01
ENSMUST00000156793				-5.3	1.3E-03	5.2	1.8E-03	0.5	6.6E-01	0.1	8.4E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000152519				-5.3	5.8E-04	4.0	2.9E-03	0.9	3.2E-01	-0.6	4.3E-01
ENSMUST00000143457				-5.4	1.0E-02	5.6	2.0E-02	-0.5	8.1E-01	-1.1	3.8E-01
ENSMUST00000192927	centrosomal protein 170 [Source:MGI Symbol;Acc:MGI:1918348]	A0A0A6YXK7		1.2	6.5E-01	-2.0	6.0E-01	-2.1	3.9E-01	1.1	7.6E-01
ENSMUST00000128596				-5.4	1.5E-02	4.9	4.0E-03	0.8	5.0E-01	-0.3	6.5E-01
ENSMUST00000149003				-5.4	8.3E-03	6.0	2.9E-04	0.7	5.2E-01	-0.1	8.7E-01
ENSMUST00000150541				-5.4	1.1E-03	0.2	8.9E-01	2.2	5.1E-02	-2.5	9.0E-02
ENSMUST00000168020				-5.4	5.9E-05	5.5	4.0E-03	-0.6	7.2E-01	-1.6	1.3E-01
ENSMUST00000192956	protoporphyrinogen oxidase [Source:MGI Symbol;Acc:MGI:104968]	A0A0A6YX50		-0.7	7.8E-01	-3.4	3.6E-01	-1.5	4.7E-01	1.2	7.3E-01
ENSMUST00000134641				-5.4	5.6E-05	-5.3	1.6E-03	0.1	8.3E-01	-1.0	4.6E-01
ENSMUST00000192961	centrosomal protein 170 [Source:MGI Symbol;Acc:MGI:1918348]		Q6A065	2.6	4.2E-02	5.9	7.3E-03	2.1	2.2E-01	-1.1	2.8E-01
ENSMUST00000171237				-5.4	6.5E-05	5.7	1.1E-03	-0.1	9.4E-01	0.1	8.6E-01
ENSMUST00000133286				-5.4	3.3E-03	-6.9	2.4E-05	-0.4	3.1E-01	-1.4	1.6E-01
ENSMUST00000031092				-5.4	3.9E-03	6.0	8.1E-04	-0.6	6.4E-01	0.3	6.9E-01
ENSMUST00000167361				-5.4	4.5E-03	5.8	9.0E-05	0.1	8.7E-01	-0.8	1.8E-01
ENSMUST00000145846				-5.4	1.9E-04	0.3	7.8E-01	-0.3	7.1E-01	-6.5	2.3E-03
ENSMUST00000131286				-5.4	2.2E-04	2.6	3.3E-02	-0.2	8.2E-01	0.5	5.2E-01
ENSMUST00000187103				-5.4	2.3E-04	5.8	1.5E-03	0.1	9.2E-01	0.1	8.9E-01
ENSMUST00000193030	lamin B receptor [Source:MGI Symbol;Acc:MGI:2138281]	A0A0A6YW01		-2.0	7.5E-02	-2.1	1.3E-01	0.3	6.9E-01	0.5	7.4E-01
ENSMUST00000146362				-5.4	1.2E-02	7.8	1.1E-05	-0.9	3.6E-01	0.1	8.7E-01
ENSMUST00000193042	astrotactin 1 [Source:MGI Symbol;Acc:MGI:1098567]		Q61137	4.9	1.8E-01	3.3	4.2E-01	-0.1	9.8E-01	1.5	5.5E-01
ENSMUST00000132618				-5.4	8.0E-03	3.8	2.5E-02	-1.2	4.0E-01	-1.3	2.5E-01
ENSMUST00000151503				-5.4	4.5E-03	7.5	6.2E-05	0.9	3.8E-01	0.8	1.5E-01
ENSMUST00000193051				1.0	4.7E-01	1.1	4.6E-01	-1.5	3.0E-01	-1.6	2.7E-01
ENSMUST00000139378				-5.5	1.3E-02	-5.5	7.7E-03	-0.7	3.2E-01	2.1	2.1E-01
ENSMUST00000193063				0.9	7.9E-01	-2.1	6.1E-01	-3.5	2.4E-01	-0.5	9.1E-01
ENSMUST00000140960				-5.5	1.5E-03	3.0	2.4E-02	-1.3	2.7E-01	-0.3	7.7E-01
ENSMUST00000180422				-5.5	6.9E-06	-4.9	3.8E-04	-0.6	2.3E-01	-1.4	1.7E-01
ENSMUST00000125775				-5.5	6.8E-04	6.1	5.0E-04	-0.1	9.4E-01	-1.2	1.1E-01
ENSMUST00000193083	ankyrin repeat domain 23 [Source:MGI Symbol;Acc:MGI:1925571]	A0A0A6YW48		0.0	9.9E-01	-1.9	5.5E-01	-1.6	4.0E-01	0.3	9.4E-01
ENSMUST00000148779				-5.5	1.9E-02	6.4	3.3E-05	0.6	5.0E-01	0.4	4.6E-01
ENSMUST00000193094	complement component (3b/4b) receptor 1-like [Source:MGI Symbol;Acc:MGI:88513]	A0A0A6YY75		1.4	4.0E-02	2.6	7.3E-03	0.7	2.9E-01	-0.5	4.5E-01
ENSMUST00000133762				-5.5	4.0E-03	5.6	1.1E-03	-0.1	9.4E-01	1.1	1.7E-01
ENSMUST00000054148				-5.5	1.6E-04	7.3	4.3E-07	-0.7	2.1E-01	-0.1	6.2E-01
ENSMUST00000193105				0.2	8.2E-01	0.7	4.7E-01	0.8	2.6E-01	0.3	7.4E-01
ENSMUST00000139264				-5.5	2.0E-03	7.5	1.4E-04	-0.1	9.5E-01	-0.7	3.0E-01
ENSMUST00000145089				-5.5	8.5E-04	6.2	3.0E-04	-0.9	4.4E-01	-0.8	2.2E-01
ENSMUST00000129346				-5.5	4.4E-03	6.4	3.5E-04	-1.5	2.7E-01	0.9	1.9E-01
ENSMUST00000107835				-5.5	4.7E-04	6.7	1.3E-03	-1.3	4.4E-01	1.7	6.9E-02
ENSMUST00000161271				-5.5	6.2E-04	2.6	6.3E-02	-3.9	2.2E-02	-1.4	2.2E-01
ENSMUST00000138094				-5.5	2.0E-04	5.4	3.6E-03	-1.5	3.4E-01	0.1	9.3E-01
ENSMUST00000162638				-5.5	5.0E-04	5.8	1.4E-04	-0.3	7.1E-01	0.7	2.2E-01
ENSMUST00000125074				-5.5	1.4E-03	-3.5	2.2E-02	0.5	4.1E-01	-1.0	4.8E-01
ENSMUST00000193170	coiled-coil domain containing 71 [Source:MGI Symbol;Acc:MGI:1919704]		Q8VEG0	-0.9	6.4E-01	1.2	6.6E-01	1.2	6.1E-01	-0.9	6.8E-01
ENSMUST00000138150				-5.5	7.5E-04	-0.9	4.4E-01	0.6	4.2E-01	-1.2	3.3E-01
ENSMUST00000021101				-5.5	2.0E-03	6.0	1.2E-03	1.3	3.2E-01	-0.5	5.3E-01
ENSMUST00000142153				-5.5	5.7E-03	1.7	1.4E-01	-1.0	2.7E-01	0.6	5.2E-01
ENSMUST00000156503				-5.5	1.3E-04	5.9	1.1E-02	1.8	3.3E-01	0.1	9.1E-01
ENSMUST00000162134				-5.5	5.6E-03	-4.8	1.6E-04	-0.7	1.0E-01	0.7	4.2E-01
ENSMUST00000130759				-5.5	6.4E-03	5.8	1.6E-04	-1.5	1.6E-01	-0.9	1.2E-01
ENSMUST00000133625				-5.5	1.5E-03	7.3	6.7E-05	-0.5	6.6E-01	-0.5	4.1E-01
ENSMUST00000152622				-5.5	2.2E-03	7.7	1.9E-04	-0.7	6.2E-01	-0.5	4.9E-01
ENSMUST00000148795				-5.6	1.6E-03	6.4	1.5E-04	-0.6	6.0E-01	0.0	9.8E-01
ENSMUST00000111057				-5.6	1.4E-03	7.1	6.5E-05	0.1	9.5E-01	-0.4	4.2E-01
ENSMUST00000141961				-5.6	1.2E-03	-7.0	1.5E-04	-0.3	5.1E-01	-1.7	2.2E-01
ENSMUST00000131025				-5.6	1.8E-04	3.2	2.0E-03	-2.2	2.3E-02	-0.5	4.1E-01
ENSMUST00000193242				-2.1	3.6E-02	-1.2	2.0E-01	-0.9	2.2E-01	-1.8	8.8E-02
ENSMUST00000099371				-5.6	2.8E-04	6.4	6.1E-04	-0.7	6.2E-01	0.2	7.4E-01
ENSMUST00000143733				-5.6	8.1E-04	6.4	7.0E-04	-0.7	6.4E-01	0.7	3.6E-01
ENSMUST00000145378				-5.6	2.3E-04	-2.7	1.3E-02	1.1	5.4E-02	-2.5	5.3E-02
ENSMUST00000131327				-5.6	3.5E-03	2.3	1.6E-01	-3.3	8.9E-02	0.6	6.7E-01
ENSMUST00000161767				-5.6	1.2E-03	6.6	1.8E-04	-0.6	5.9E-01	-0.8	2.5E-01
ENSMUST00000110798				-5.6	5.7E-03	5.4	1.9E-02	-0.6	7.6E-01	1.2	3.2E-01
ENSMUST00000146280				-5.6	5.7E-05	6.5	5.7E-04	2.9	3.6E-02	-0.4	5.4E-01
ENSMUST00000133628				-5.6	1.7E-06	3.6	9.9E-04	-0.2	7.3E-01	0.3	5.7E-01
ENSMUST00000152608				-5.6	6.6E-05	3.5	2.4E-04	-0.7	2.7E-01	-0.6	2.4E-01
ENSMUST00000136804				-5.6	3.8E-04	6.5	4.4E-04	-1.2	3.7E-01	0.5	4.9E-01
ENSMUST00000139322				-5.6	8.6E-04	-5.4	1.3E-03	-0.7	2.0E-01	-0.8	5.3E-01
ENSMUST00000193288	ubiquitin specific peptidase 4 (proto-oncogene) [Source:MGI Symbol;Acc:MGI:98905]	A0A0A6YWM7		-3.9	1.5E-01	-3.1	4.1E-01	0.8	7.2E-01	0.0	1.0E+00
ENSMUST00000193291	solute carrier family 26, member 6 [Source:MGI Symbol;Acc:MGI:2159728]	A0A087WS07		-1.2	2.6E-01	-1.0	4.4E-01	0.5	5.2E-01	0.4	7.7E-01
ENSMUST00000163086				-5.6	5.5E-03	6.5	1.0E-03	-0.2	8.7E-01	0.3	6.6E-01
ENSMUST00000154306				-5.6	4.7E-05	6.0	2.2E-03	1.2	4.0E-01	-1.7	8.7E-02
ENSMUST00000074245				-5.6	9.3E-07	5.1	2.3E-03	-0.5	6.9E-01	0.8	2.9E-01
ENSMUST00000124421				-5.6	3.4E-06	8.8	3.7E-07	0.5	4.3E-01	0.5	1.8E-01
ENSMUST00000132082				-5.6	1.1E-03	6.0	4.0E-04	-0.6	6.1E-01	0.5	4.6E-01
ENSMUST00000193332				2.4	4.6E-02	2.9	5.5E-02	0.8	5.1E-01	0.2	8.4E-01
ENSMUST00000137630				-5.6	7.9E-03	-1.4	6.0E-02	0.2	6.6E-01	-0.4	6.0E-01
ENSMUST00000193353				-1.3	1.4E-01	-3.0	5.0E-02	-0.1	9.1E-01	1.7	2.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000147511				-5.6	7.6E-04	8.4	8.6E-05	0.3	8.2E-01	1.0	1.3E-01
ENSMUST00000156487				-5.6	4.2E-03	-0.6	6.8E-01	2.9	2.9E-02	-1.7	2.6E-01
ENSMUST00000150416				-5.7	2.8E-04	3.2	3.8E-04	0.0	9.2E-01	0.4	3.1E-01
ENSMUST00000119949				-5.7	2.9E-05	2.1	2.8E-02	-0.9	2.4E-01	-0.2	7.6E-01
ENSMUST00000151642				-5.7	8.1E-03	6.3	9.2E-05	-0.4	7.0E-01	-0.4	5.1E-01
ENSMUST00000173625				-5.7	8.4E-04	1.5	4.3E-01	-1.8	3.2E-01	2.4	1.6E-01
ENSMUST00000153671				-5.7	2.1E-03	2.1	1.8E-01	-0.4	7.4E-01	4.6	2.6E-03
ENSMUST00000193391	interleukin 18 receptor 1 [Source:MGI Symbol;Acc:MGI:105383]	Q8C257		-0.9	3.6E-01	-0.4	7.3E-01	0.0	9.7E-01	-0.5	6.8E-01
ENSMUST00000193394	guanine nucleotide binding protein (G protein), alpha inhibiting 2 [Source:MGI Symbol;Acc:MGI:95772]	A0A0A6YWA9		2.6	1.7E-01	3.6	1.0E-01	-0.5	7.7E-01	-1.5	3.9E-01
ENSMUST00000156374				-5.7	1.8E-03	5.7	2.7E-03	0.0	9.8E-01	0.2	8.4E-01
ENSMUST00000193411				-0.9	7.2E-01	-1.6	6.0E-01	-1.1	5.3E-01	-0.4	9.0E-01
ENSMUST00000128555				-5.7	6.2E-04	3.9	2.0E-03	0.4	6.5E-01	0.0	1.0E+00
ENSMUST00000171960				-5.7	1.8E-02	7.3	2.7E-04	0.9	4.8E-01	-0.7	3.0E-01
ENSMUST00000153524				-5.7	2.9E-02	6.8	3.9E-04	-0.6	6.4E-01	-1.3	9.3E-02
ENSMUST00000193432	component of oligomeric golgi complex 6 [Source:MGI Symbol;Acc:MGI:1914792]	Q8BRB0		-2.1	1.2E-01	-1.5	3.0E-01	-0.8	4.2E-01	-1.4	3.4E-01
ENSMUST00000193073				-5.7	6.2E-05	-4.0	6.5E-02	2.2	2.9E-02	-1.0	6.5E-01
ENSMUST00000141013				-5.7	2.0E-04	7.1	2.4E-04	-1.6	2.6E-01	-0.2	8.0E-01
ENSMUST00000125548				-5.7	1.3E-04	6.7	8.3E-05	0.1	9.4E-01	-0.5	3.5E-01
ENSMUST00000122119				-5.7	1.7E-04	-1.0	6.9E-01	4.8	1.5E-02	-1.0	6.7E-01
ENSMUST00000181051				-5.7	7.5E-04	-2.2	4.7E-03	0.7	8.6E-02	-0.3	5.7E-01
ENSMUST00000193463				4.0	8.6E-02	6.8	3.2E-02	1.3	6.4E-01	-1.5	3.5E-01
ENSMUST00000138999				-5.7	1.1E-03	7.4	3.0E-04	0.4	7.8E-01	-0.8	2.9E-01
ENSMUST00000150784				-5.7	7.5E-03	6.3	2.8E-04	-1.1	3.5E-01	0.6	3.4E-01
ENSMUST00000150760				-5.7	1.6E-03	-4.3	1.0E-02	0.7	2.6E-01	-0.8	5.9E-01
ENSMUST00000052145				-5.8	1.7E-04	1.6	1.2E-01	-0.2	8.2E-01	0.7	4.0E-01
ENSMUST00000194917				-5.8	1.6E-04	-3.9	2.6E-02	1.2	8.9E-02	0.2	9.0E-01
ENSMUST00000124993				-5.8	1.4E-03	6.3	1.4E-03	-0.6	7.0E-01	-0.5	5.1E-01
ENSMUST00000137589				-5.8	3.6E-05	4.8	3.9E-04	0.1	8.9E-01	0.3	6.7E-01
ENSMUST00000146147				-5.8	5.7E-03	-6.3	2.3E-03	0.2	7.7E-01	1.3	4.3E-01
ENSMUST00000140039				-5.8	8.3E-03	-4.5	7.6E-03	1.3	5.8E-02	-2.0	2.2E-01
ENSMUST00000193518	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	A0A0A6YXQ4		-0.2	9.6E-01	-3.8	3.3E-01	-4.2	8.6E-02	-0.5	9.1E-01
ENSMUST00000159903				-5.8	1.6E-02	-4.9	6.5E-02	0.5	6.4E-01	-0.6	8.2E-01
ENSMUST00000148083				-5.8	1.3E-04	2.7	8.5E-03	0.5	4.9E-01	-0.2	8.1E-01
ENSMUST00000135740				-5.8	8.9E-03	6.5	1.6E-04	-0.6	6.2E-01	-1.0	1.2E-01
ENSMUST00000170720				-5.8	2.2E-04	-0.7	4.6E-01	1.4	6.4E-02	-2.2	7.6E-02
ENSMUST00000193552	ariadne homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1344361]	A0A0A6YXR5		-1.6	1.9E-01	-2.2	2.1E-01	0.0	1.0E+00	0.6	7.1E-01
ENSMUST00000127760				-5.8	2.9E-05	6.7	1.2E-03	-0.7	6.6E-01	0.3	7.2E-01
ENSMUST00000140291				-5.8	1.1E-03	-1.8	4.4E-02	0.4	4.5E-01	-2.7	1.9E-02
ENSMUST00000122915				-5.8	1.9E-04	6.7	1.8E-04	-0.5	6.7E-01	-0.9	1.8E-01
ENSMUST00000105294				-5.9	7.7E-03	6.0	2.5E-04	0.2	8.4E-01	0.6	3.2E-01
ENSMUST00000138860				-5.9	7.3E-04	6.1	2.0E-03	-0.7	6.6E-01	-0.7	3.9E-01
ENSMUST00000178676				-5.9	1.6E-06	7.0	7.4E-05	-1.5	2.2E-01	0.3	5.5E-01
ENSMUST00000193611				-2.3	3.9E-02	-1.2	3.0E-01	0.3	7.2E-01	-0.7	5.4E-01
ENSMUST00000131837				-5.9	2.1E-03	6.4	6.6E-04	-0.1	9.4E-01	-0.8	3.0E-01
ENSMUST00000146953				-5.9	1.8E-03	5.3	3.4E-03	0.4	7.5E-01	-0.3	7.4E-01
ENSMUST00000148958				-5.9	7.2E-05	6.8	9.5E-06	0.5	5.4E-01	-0.2	6.6E-01
ENSMUST00000152226				-5.9	3.8E-04	6.1	5.4E-04	-0.5	6.9E-01	-0.1	8.8E-01
ENSMUST00000127778				-5.9	9.3E-03	-3.9	3.3E-03	-0.3	5.2E-01	-0.6	5.9E-01
ENSMUST00000193628				0.6	5.2E-01	1.7	2.6E-01	1.3	3.0E-01	0.3	7.9E-01
ENSMUST00000135498				-5.9	1.3E-03	6.9	1.3E-04	-0.5	6.9E-01	-0.2	7.6E-01
ENSMUST00000193634				1.7	1.6E-01	2.4	1.7E-01	0.2	9.1E-01	-0.5	6.9E-01
ENSMUST00000181608				-5.9	1.3E-03	-5.2	4.8E-04	0.4	3.1E-01	-0.8	4.8E-01
ENSMUST00000135754				-5.9	1.2E-03	-1.3	1.3E-01	0.2	7.4E-01	-2.1	4.8E-02
ENSMUST00000193643	ariadne homolog 2 (Drosophila) [Source:MGI Symbol;Acc:MGI:1344361]	A0A0A6YW29		-1.3	4.5E-01	1.2	4.3E-01	-0.1	9.5E-01	-2.6	1.5E-01
ENSMUST00000168019				-5.9	3.6E-03	4.6	5.1E-04	-1.6	1.2E-01	-0.4	5.1E-01
ENSMUST00000193646				0.8	3.9E-01	3.9	1.8E-02	2.0	1.3E-01	-1.1	2.6E-01
ENSMUST00000193647	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	A0A0A6YWG1		1.0	7.1E-01	-3.0	3.0E-01	-4.8	3.5E-02	-0.9	7.6E-01
ENSMUST00000152689				-5.9	1.6E-02	5.8	3.8E-04	0.1	8.9E-01	0.1	8.9E-01
ENSMUST00000160012				-5.9	3.6E-04	4.5	8.5E-04	0.5	5.6E-01	0.6	3.2E-01
ENSMUST00000141318				-5.9	4.2E-04	6.7	1.4E-04	-1.5	2.3E-01	-0.2	7.8E-01
ENSMUST00000193538				-5.9	7.7E-03	-11.0	1.4E-04	0.3	4.6E-01	0.2	9.1E-01
ENSMUST00000186552				-5.9	7.7E-03	-6.6	1.9E-03	1.3	3.1E-02	-0.7	6.9E-01
ENSMUST00000133609				-5.9	3.3E-03	-4.2	1.1E-02	-0.3	6.5E-01	-0.9	5.2E-01
ENSMUST00000160669				-5.9	4.9E-04	1.3	5.4E-01	0.1	9.3E-01	2.3	2.4E-01
ENSMUST00000128417				-5.9	7.9E-03	4.1	1.2E-03	-0.2	8.3E-01	-0.2	8.2E-01
ENSMUST00000193700				-2.7	8.5E-02	-0.5	8.1E-01	2.2	2.0E-01	0.1	9.7E-01
ENSMUST00000152364				-5.9	8.1E-04	5.2	8.7E-03	1.3	3.9E-01	0.8	4.3E-01
ENSMUST00000125710				-6.0	6.4E-05	5.8	1.4E-04	-0.9	3.8E-01	-0.8	2.2E-01
ENSMUST00000193714	RCSD domain containing 1 [Source:MGI Symbol;Acc:MGI:2676394]	A0A0A6YXA9		-2.5	8.3E-02	-3.0	1.0E-01	-0.1	8.9E-01	0.3	8.5E-01
ENSMUST00000121239				-6.0	7.5E-05	5.8	6.9E-04	0.3	8.1E-01	-0.4	5.8E-01
ENSMUST00000124613				-6.0	1.4E-03	6.1	8.5E-04	-0.6	6.6E-01	-0.4	5.7E-01
ENSMUST00000193726				-1.4	2.5E-01	1.4	3.7E-01	1.5	2.3E-01	-1.4	3.5E-01
ENSMUST00000193727	pyrin and HIN domain family, member 1 [Source:MGI Symbol;Acc:MGI:2138243]	A0A0A6YXV9		-3.6	5.5E-02	-3.3	9.7E-02	-1.2	2.9E-01	-1.5	4.7E-01
ENSMUST00000154502				-6.0	5.0E-04	3.7	4.2E-04	-0.5	4.9E-01	0.3	5.6E-01
ENSMUST00000173381				-6.0	4.7E-04	7.3	2.5E-05	-1.4	2.0E-01	-0.3	5.2E-01
ENSMUST00000193734	transducin (beta)-like 1X-linked receptor 1 [Source:MGI Symbol;Acc:MGI:2441730]		Q8BHJ5	-0.9	5.9E-01	-5.5	1.6E-01	0.5	7.0E-01	5.2	1.8E-01
ENSMUST00000147001				-6.0	1.2E-04	6.9	1.9E-03	1.5	3.7E-01	0.7	4.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000193754				-1.7	1.3E-01	-1.4	3.6E-01	0.5	5.5E-01	0.1	9.5E-01
ENSMUST00000141807				-6.0	9.2E-03	6.8	6.1E-05	-1.3	2.2E-01	0.5	4.2E-01
ENSMUST00000155675				-6.0	7.4E-03	6.7	1.7E-04	-0.6	6.4E-01	-0.2	7.9E-01
ENSMUST00000193767				2.0	6.9E-02	1.2	3.8E-01	0.3	7.9E-01	1.1	3.6E-01
ENSMUST00000193779	fibronectin type III domain containing 3B [Source:MGI Symbol;Acc:MGI:1919257]	A0A0A6YX88		-0.4	7.0E-01	-1.0	5.0E-01	-0.3	8.0E-01	0.3	8.1E-01
ENSMUST00000128203				-6.0	1.5E-05	3.1	6.1E-03	1.4	8.9E-02	0.5	5.2E-01
ENSMUST00000154768				-6.0	1.9E-05	6.3	2.8E-04	-0.3	7.9E-01	-0.6	3.9E-01
ENSMUST00000094549				-6.0	5.8E-04	7.7	7.0E-04	1.0	5.0E-01	1.0	2.6E-01
ENSMUST00000176354				-6.0	1.3E-03	-1.2	1.3E-01	0.0	9.3E-01	-0.3	6.5E-01
ENSMUST00000139797				-6.0	1.2E-02	6.2	3.4E-04	-0.6	6.1E-01	-0.4	5.9E-01
ENSMUST00000128519				-6.0	1.8E-03	5.5	8.0E-04	-0.5	6.8E-01	-1.0	1.5E-01
ENSMUST00000117148				-6.0	1.1E-05	2.8	1.5E-03	-0.4	5.0E-01	-0.6	2.9E-01
ENSMUST00000140527				-6.0	4.2E-05	4.7	8.3E-03	0.5	7.4E-01	1.2	2.3E-01
ENSMUST00000190530				-6.0	2.8E-04	6.3	2.9E-04	-0.6	6.1E-01	0.9	1.6E-01
ENSMUST00000133384				-6.0	1.2E-03	6.7	7.1E-04	-0.6	6.9E-01	-0.9	2.7E-01
ENSMUST00000188512				-6.0	1.9E-05	8.5	1.3E-04	-0.7	6.7E-01	-0.8	2.6E-01
ENSMUST00000107840				-6.0	5.4E-05	-1.8	1.4E-02	0.5	2.1E-01	-2.2	1.0E-02
ENSMUST00000155830				-6.0	2.6E-04	6.8	1.1E-04	-0.5	6.5E-01	-0.1	8.2E-01
ENSMUST00000124894				-6.1	1.6E-03	2.9	5.1E-03	-0.7	3.7E-01	-0.1	8.9E-01
ENSMUST00000193897				0.0	9.7E-01	1.1	3.3E-01	0.0	9.7E-01	-1.1	2.9E-01
ENSMUST00000193901	protocadherin 9 [Source:MGI Symbol;Acc:MGI:1306801]	A0A0A6YWY8		4.0	1.7E-01	4.3	1.8E-01	-0.2	9.4E-01	-0.6	7.8E-01
ENSMUST00000188546				-6.1	7.2E-04	8.7	7.3E-06	0.9	3.6E-01	-1.3	1.7E-02
ENSMUST00000147233				-6.1	3.0E-02	-7.2	6.8E-03	1.3	8.3E-02	2.0	3.7E-01
ENSMUST00000135570				-6.1	7.0E-04	4.4	3.1E-02	-1.3	5.0E-01	0.7	5.4E-01
ENSMUST00000122000				-6.1	2.3E-04	6.1	1.2E-02	-0.8	7.2E-01	0.6	6.0E-01
ENSMUST00000139066				-6.1	5.2E-03	2.3	2.8E-02	0.4	6.2E-01	0.2	8.0E-01
ENSMUST00000154806				-6.1	1.7E-03	7.5	1.2E-02	-0.8	7.7E-01	-1.6	2.7E-01
ENSMUST00000193925				-0.7	2.6E-01	-1.3	1.2E-01	-0.3	6.3E-01	0.3	6.6E-01
ENSMUST00000153633				-6.1	8.0E-05	4.3	7.9E-03	-2.3	1.4E-01	0.2	7.7E-01
ENSMUST00000146979				-6.1	2.3E-04	4.2	1.7E-02	-1.5	3.8E-01	-0.6	5.4E-01
ENSMUST00000138944				-6.1	3.4E-03	4.4	7.2E-05	-1.5	3.2E-02	-0.6	2.1E-01
ENSMUST00000187952				-6.1	3.2E-02	-0.4	5.8E-01	0.9	1.2E-01	-1.0	2.1E-01
ENSMUST00000138722				-6.1	9.0E-05	5.0	4.5E-04	0.4	6.1E-01	-0.3	6.4E-01
ENSMUST00000144119				-6.1	6.1E-03	5.8	8.7E-05	-1.9	1.0E-01	-0.3	5.7E-01
ENSMUST00000125208				-6.1	2.2E-03	-6.1	1.0E-02	-0.3	6.2E-01	0.5	8.0E-01
ENSMUST00000193975				-0.6	5.4E-01	-0.8	5.5E-01	0.4	6.5E-01	0.6	6.3E-01
ENSMUST00000173558				-6.2	3.7E-03	6.8	3.1E-05	-0.5	6.2E-01	-0.1	7.8E-01
ENSMUST00000193979	unc-50 homolog (C. elegans) [Source:MGI Symbol;Acc:MGI:1914637]	A0A0A6YX35		0.4	8.8E-01	-2.2	3.1E-01	-5.1	2.2E-02	-2.5	3.7E-01
ENSMUST00000193982	kelch-like ECH-associated protein 1 [Source:MGI Symbol;Acc:MGI:1858732]		Q9Z2X8	3.0	2.2E-01	-1.2	6.8E-01	-3.5	1.4E-01	0.6	8.1E-01
ENSMUST00000071083				-6.2	5.0E-05	-6.7	6.4E-03	1.0	2.7E-01	-2.1	3.6E-01
ENSMUST00000144375				-6.2	5.1E-05	5.8	2.1E-03	-0.4	7.8E-01	-0.5	5.4E-01
ENSMUST00000191699				-6.2	4.6E-05	4.4	6.9E-04	0.6	5.0E-01	0.1	8.7E-01
ENSMUST00000096370				-6.2	6.2E-04	7.7	1.6E-04	-0.6	6.6E-01	-1.3	8.5E-02
ENSMUST00000194029				0.2	8.7E-01	1.6	2.9E-01	0.6	6.3E-01	-0.8	5.3E-01
ENSMUST00000194033	dispatched homolog 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1916147]	A0A0A6YWR7		5.3	3.7E-02	4.4	1.2E-01	0.9	7.3E-01	1.7	3.6E-01
ENSMUST00000123925				-6.2	1.6E-04	7.2	2.5E-04	-0.6	6.4E-01	0.3	7.0E-01
ENSMUST00000166215				-6.2	5.5E-03	2.4	2.2E-01	-3.5	1.1E-01	-1.1	4.6E-01
ENSMUST00000194045	glutaminyl-tRNA synthetase [Source:MGI Symbol;Acc:MGI:1915851]	A0A0A6YY08		-1.9	5.3E-01	-4.4	2.2E-01	-3.0	1.4E-01	-0.5	9.0E-01
ENSMUST00000123795				-6.2	8.8E-05	1.7	2.7E-01	2.4	8.7E-02	-4.2	2.0E-02
ENSMUST00000195084				-6.2	1.4E-03	6.6	5.6E-04	-0.6	6.9E-01	0.5	5.2E-01
ENSMUST00000118533				-6.2	1.4E-05	1.2	5.6E-02	-1.1	4.4E-02	-0.1	8.6E-01
ENSMUST00000168697				-6.2	2.6E-04	7.1	2.3E-05	0.5	5.8E-01	-0.1	7.7E-01
ENSMUST00000194056	protocadherin 9 [Source:MGI Symbol;Acc:MGI:1306801]	A0A0A6YWM0		2.9	1.1E-01	5.0	1.3E-02	-0.6	7.5E-01	-2.7	6.3E-02
ENSMUST00000133472				-6.2	6.2E-04	4.6	2.5E-02	-2.6	2.3E-01	-2.1	1.4E-01
ENSMUST00000159784				-6.2	5.1E-03	-4.5	5.0E-02	1.3	2.0E-01	-1.3	5.8E-01
ENSMUST00000150153				-6.2	8.1E-04	4.9	1.3E-03	-0.4	7.3E-01	-0.1	8.8E-01
ENSMUST00000194069	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	A0A0A6YWB0		-2.7	8.8E-02	0.5	8.0E-01	1.9	2.0E-01	-1.3	4.4E-01
ENSMUST00000114605				-6.2	1.7E-04	-4.2	4.6E-02	-0.7	4.1E-01	-0.9	6.5E-01
ENSMUST00000194079	n, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) [Source:MGI Symbol;Acc:MGI:18	A0A0A6YX12		-1.7	2.7E-01	0.0	1.0E+00	0.0	9.7E-01	-1.6	3.4E-01
ENSMUST00000149859				-6.2	6.5E-04	4.0	8.7E-04	0.5	5.4E-01	0.1	9.3E-01
ENSMUST00000149841				-6.3	7.1E-05	6.1	2.1E-05	-0.2	8.2E-01	0.4	4.4E-01
ENSMUST00000161027				-6.3	1.2E-04	6.1	6.5E-04	-0.4	7.2E-01	0.4	6.2E-01
ENSMUST00000159198				-6.3	7.1E-03	7.0	1.3E-04	1.1	3.1E-01	-1.7	3.6E-02
ENSMUST00000125284				-6.3	3.5E-04	3.6	2.2E-03	-3.4	6.0E-03	-0.4	5.7E-01
ENSMUST00000145822				-6.3	1.5E-04	-2.3	1.8E-02	-0.2	7.2E-01	-0.8	3.4E-01
ENSMUST00000188299				-6.3	2.6E-04	-1.6	2.1E-01	-0.2	8.0E-01	-1.5	2.7E-01
ENSMUST00000150644				-6.3	1.8E-03	2.4	1.8E-02	-0.2	8.1E-01	-0.1	8.7E-01
ENSMUST00000194127				3.9	6.0E-02	3.4	8.3E-02	-2.3	2.6E-01	-1.7	2.2E-01
ENSMUST00000057740				-6.3	3.9E-06	3.6	2.4E-03	0.3	7.5E-01	-0.6	4.4E-01
ENSMUST00000131873				-6.4	1.2E-05	8.6	8.8E-06	0.8	4.2E-01	-0.4	3.8E-01
ENSMUST00000194139				-0.5	8.1E-01	-0.8	7.4E-01	-0.8	6.6E-01	-0.5	8.3E-01
ENSMUST00000178816				-6.4	4.1E-04	-9.5	7.8E-05	-1.1	2.0E-02	-0.5	7.5E-01
ENSMUST00000091130				-6.4	3.1E-03	4.3	1.5E-03	-1.0	3.0E-01	-0.5	5.1E-01
ENSMUST00000146285				-6.4	2.3E-03	6.5	1.0E-04	-0.6	6.0E-01	-0.5	3.6E-01
ENSMUST00000194162	immunoglobulin heavy constant delta [Source:MGI Symbol;Acc:MGI:96447]	A0A0A6YW14		0.3	6.2E-01	-1.5	4.1E-02	-1.8	2.5E-03	0.0	9.8E-01
ENSMUST00000126343				-6.4	1.5E-06	8.5	2.4E-04	-0.8	6.0E-01	1.0	1.7E-01
ENSMUST00000194170				-1.4	7.7E-02	-3.9	2.1E-03	-1.7	9.4E-03	0.8	4.1E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000017922				-6.4	1.2E-03	-5.4	2.5E-02	0.6	4.5E-01	0.2	9.4E-01
ENSMUST00000123625				-6.4	2.1E-03	5.4	2.0E-02	-0.8	7.2E-01	0.8	5.2E-01
ENSMUST00000122170				-6.4	2.3E-04	5.3	6.7E-03	-0.5	7.7E-01	-0.5	5.7E-01
ENSMUST00000163902				-6.5	3.4E-03	7.8	4.3E-06	0.2	7.7E-01	0.1	8.3E-01
ENSMUST00000175758				-6.5	5.6E-03	6.2	2.5E-04	-0.5	6.7E-01	0.1	8.4E-01
ENSMUST00000119272				-6.5	2.2E-04	6.3	2.3E-03	1.0	5.0E-01	-0.8	3.9E-01
ENSMUST00000194206	CaM kinase-like vesicle-associated [Source:MGI Symbol;Acc:MGI:2384296]	A0A0A6YW88		5.3	4.4E-02	2.4	4.7E-01	0.0	1.0E+00	2.9	2.5E-01
ENSMUST00000121320				-6.5	1.3E-03	3.2	1.7E-03	0.3	5.8E-01	0.1	8.1E-01
ENSMUST00000194213	F-box protein 28 [Source:MGI Symbol;Acc:MGI:1261890]	A0A0A6YVQ6		-1.9	1.1E-01	0.4	7.9E-01	2.4	5.9E-02	0.1	9.6E-01
ENSMUST00000147590				-6.5	6.6E-05	5.4	6.9E-06	-0.3	5.9E-01	-0.7	7.8E-02
ENSMUST00000162047				-6.5	1.9E-03	2.5	2.8E-03	-0.3	5.6E-01	0.5	3.3E-01
ENSMUST00000117444				-6.5	2.8E-06	4.6	2.4E-03	-0.9	4.1E-01	-1.0	2.4E-01
ENSMUST00000117571				-6.5	2.8E-06	4.9	2.5E-03	-1.6	2.5E-01	-1.3	1.5E-01
ENSMUST00000194235				3.7	1.5E-01	5.1	7.4E-02	-0.5	8.6E-01	-1.9	2.9E-01
ENSMUST00000121779				-6.5	2.8E-06	6.4	7.6E-05	-0.1	9.2E-01	-0.9	1.6E-01
ENSMUST00000147311				-6.5	2.8E-06	4.6	3.2E-03	-1.0	4.2E-01	0.5	5.0E-01
ENSMUST00000148282				-6.5	2.8E-06	6.7	6.4E-05	-0.9	4.1E-01	-0.2	7.1E-01
ENSMUST00000118490				-6.5	1.4E-04	9.1	4.2E-04	0.0	9.9E-01	0.5	5.4E-01
ENSMUST00000114311				-6.5	7.3E-03	3.7	2.0E-03	0.1	9.4E-01	-0.2	7.4E-01
ENSMUST00000167796				-6.5	1.6E-05	6.7	2.2E-04	0.2	8.2E-01	-0.9	1.7E-01
ENSMUST00000194278	TRAF3 interacting protein 3 [Source:MGI Symbol;Acc:MGI:2441706]	A0A0A6YWR4		0.8	7.7E-01	0.2	9.6E-01	0.0	1.0E+00	0.6	8.6E-01
ENSMUST00000143799				-6.5	3.3E-05	7.8	3.2E-05	-0.5	6.4E-01	-0.6	2.3E-01
ENSMUST00000189437				-6.5	2.0E-04	1.2	5.8E-02	0.1	8.3E-01	0.1	8.8E-01
ENSMUST00000193916				-6.5	2.6E-04	5.4	5.2E-04	0.9	3.7E-01	-0.7	2.9E-01
ENSMUST00000031105				-6.5	8.0E-05	1.1	1.6E-01	-1.8	2.3E-02	0.6	3.4E-01
ENSMUST00000138679				-6.6	2.4E-03	2.2	1.2E-01	-2.2	1.3E-01	-0.7	5.2E-01
ENSMUST00000155296				-6.6	9.2E-06	4.4	1.6E-03	-1.3	1.8E-01	0.2	7.4E-01
ENSMUST00000144693				-6.6	5.3E-04	6.1	9.3E-04	-0.6	6.6E-01	-0.1	8.5E-01
ENSMUST00000128586				-6.6	2.7E-02	8.0	5.7E-05	-0.5	6.6E-01	0.7	3.5E-01
ENSMUST00000140056				-6.6	5.9E-05	5.5	2.6E-03	-0.6	6.9E-01	-0.3	7.4E-01
ENSMUST00000194327	BRO1 domain and CAAX motif containing [Source:MGI Symbol;Acc:MGI:1918928]	A0A0A6YVS9		-1.3	1.5E-01	0.4	7.5E-01	2.6	1.4E-02	0.9	4.9E-01
ENSMUST00000125166				-6.6	2.4E-04	6.8	1.9E-04	-0.6	6.2E-01	-0.7	3.0E-01
ENSMUST00000169025				-6.6	7.2E-03	5.7	1.7E-03	1.0	4.5E-01	-0.7	3.7E-01
ENSMUST00000161698				-6.6	4.7E-05	-7.5	3.4E-04	0.0	9.5E-01	0.4	7.5E-01
ENSMUST00000139623				-6.6	2.5E-06	3.0	8.5E-02	-0.4	8.0E-01	1.2	3.5E-01
ENSMUST00000126751				-6.6	2.2E-02	6.8	1.8E-04	-0.6	6.3E-01	-0.7	2.8E-01
ENSMUST00000122373				-6.7	1.5E-04	-4.2	1.1E-02	-1.0	1.6E-01	-0.8	6.1E-01
ENSMUST00000123190				-6.7	7.5E-05	6.9	9.3E-05	-0.6	6.0E-01	0.1	8.8E-01
ENSMUST00000150424				-6.7	1.9E-04	4.3	5.2E-03	-1.6	2.2E-01	-0.2	8.5E-01
ENSMUST00000184222				-6.7	1.8E-04	7.6	1.7E-05	0.4	6.3E-01	0.0	1.0E+00
ENSMUST00000147705				-6.7	4.7E-05	3.0	1.8E-02	-0.9	3.8E-01	-0.9	3.0E-01
ENSMUST00000091117				-6.7	1.3E-03	7.6	3.3E-05	-0.6	6.0E-01	-0.6	2.6E-01
ENSMUST00000129033				-6.7	6.3E-05	8.7	9.1E-07	0.4	6.3E-01	-0.1	8.6E-01
ENSMUST00000131300				-6.7	9.8E-03	0.9	6.2E-01	-1.8	2.9E-01	1.9	2.6E-01
ENSMUST00000194410				-0.4	8.7E-01	0.3	9.1E-01	0.6	7.9E-01	-0.1	9.6E-01
ENSMUST00000194415	lamin B receptor [Source:MGI Symbol;Acc:MGI:2138281]	A0A0A6YY12		0.0	1.0E+00	-2.2	3.8E-01	-5.4	3.5E-02	-3.1	3.2E-01
ENSMUST00000173809				-6.7	1.0E-02	4.9	1.2E-03	-2.7	5.1E-02	0.8	2.7E-01
ENSMUST00000194432				2.0	4.0E-02	2.5	5.6E-02	0.4	7.1E-01	-0.1	9.2E-01
ENSMUST00000168103				-6.7	7.7E-06	3.9	2.6E-02	-0.5	7.5E-01	1.5	1.3E-01
ENSMUST00000194440	IQ motif containing GTPase activating protein 3 [Source:MGI Symbol;Acc:MGI:3028642]	Q3UQP1		3.2	5.3E-02	4.8	1.8E-02	0.8	6.2E-01	-0.8	5.1E-01
ENSMUST00000063040				-6.7	1.0E-04	1.7	1.9E-01	-3.5	2.3E-02	0.1	9.2E-01
ENSMUST00000194446	microtubule associated serine/threonine kinase family member 4 [Source:MGI Symbol;Acc:MGI:1918885]	A0A0A6YXG1		5.0	7.5E-02	6.8	5.1E-02	1.8	5.5E-01	0.0	9.9E-01
ENSMUST00000137318				-6.7	5.3E-04	7.7	8.9E-05	-0.7	6.0E-01	0.8	1.6E-01
ENSMUST00000145850				-6.7	5.2E-03	7.0	1.7E-07	-0.7	1.6E-01	-0.1	5.8E-01
ENSMUST00000031975				-6.8	4.6E-05	6.3	2.6E-04	-0.6	6.0E-01	-0.5	4.2E-01
ENSMUST00000152441				-6.8	1.7E-03	4.8	2.5E-03	0.0	9.7E-01	0.1	9.1E-01
ENSMUST00000075924				-6.8	8.0E-04	7.1	1.1E-04	-0.6	6.4E-01	-0.3	6.4E-01
ENSMUST00000125814				-6.8	1.8E-04	6.5	3.4E-04	-0.5	7.2E-01	-1.2	9.2E-02
ENSMUST00000119024				-6.8	3.7E-04	5.6	1.4E-03	0.6	6.4E-01	0.5	4.8E-01
ENSMUST00000057216				-6.8	3.3E-05	6.3	6.9E-05	-2.7	2.7E-02	-0.2	7.6E-01
ENSMUST00000194540				5.0	4.8E-02	-2.2	2.3E-01	-6.4	9.7E-03	0.8	6.6E-01
ENSMUST00000123292				-6.8	1.9E-04	-1.1	6.5E-02	0.6	1.0E-01	-1.6	2.1E-02
ENSMUST00000194543	melanoma inhibitory activity 3 [Source:MGI Symbol;Acc:MGI:2443183]			-0.4	5.6E-01	1.2	1.6E-01	0.9	1.5E-01	-0.6	4.0E-01
ENSMUST00000194546	immunoglobulin superfamily, member 10 [Source:MGI Symbol;Acc:MGI:1923481]		Q3V1M1	7.1	4.7E-02	7.2	6.0E-02	-0.7	8.6E-01	-0.7	7.1E-01
ENSMUST00000154999				-6.8	1.3E-05	-5.2	3.0E-04	-1.0	4.6E-02	0.0	9.9E-01
ENSMUST00000154403				-6.8	3.0E-03	7.4	2.3E-03	0.0	1.0E+00	1.0	2.8E-01
ENSMUST00000156794				-6.8	2.4E-03	4.9	6.4E-02	-0.6	8.1E-01	0.0	1.0E+00
ENSMUST00000139177				-6.8	8.6E-05	-7.9	2.8E-05	1.0	7.5E-03	0.3	8.1E-01
ENSMUST00000129992				-6.8	3.0E-05	8.3	2.1E-04	-0.7	6.3E-01	0.3	6.8E-01
ENSMUST00000194563	transmembrane protein 131 [Source:MGI Symbol;Acc:MGI:1927110]		O70472	-2.2	2.9E-01	-1.2	6.5E-01	0.9	6.7E-01	-0.1	9.7E-01
ENSMUST00000142604				-6.8	1.1E-06	3.0	3.6E-03	-0.5	4.9E-01	0.2	7.2E-01
ENSMUST00000136618				-6.8	3.9E-05	4.9	1.6E-02	0.0	9.8E-01	0.3	7.8E-01
ENSMUST00000175727				-6.8	2.2E-05	10.1	1.5E-05	-0.1	9.2E-01	-0.9	8.0E-02
ENSMUST00000123642				-6.8	3.5E-04	6.3	1.0E-04	-0.8	4.4E-01	0.5	3.5E-01
ENSMUST00000132010				-6.8	3.2E-04	5.9	1.8E-03	-0.7	6.4E-01	0.7	3.6E-01
ENSMUST00000130460				-6.8	1.4E-05	7.0	1.9E-04	-0.7	6.0E-01	-1.4	6.6E-02
ENSMUST00000156642				-6.9	3.7E-03	6.5	6.4E-04	-0.7	6.2E-01	-1.0	2.2E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000141308				-6.9	8.5E-03	5.3	1.3E-03	-1.2	3.8E-01	-0.6	4.0E-01
ENSMUST00000139846				-6.9	5.0E-04	4.5	2.0E-03	0.2	8.1E-01	-0.3	7.4E-01
ENSMUST00000141045				-6.9	1.3E-05	3.6	5.0E-04	0.6	3.7E-01	0.5	3.1E-01
ENSMUST00000194617				0.4	7.2E-01	-0.4	8.1E-01	0.7	5.8E-01	1.5	3.5E-01
ENSMUST00000150949				-6.9	1.5E-04	4.1	6.9E-04	-1.6	8.3E-02	-0.5	4.1E-01
ENSMUST00000112557				-6.9	1.4E-03	3.6	5.7E-03	-1.7	1.3E-01	-0.4	6.0E-01
ENSMUST00000171140				-6.9	3.5E-03	6.1	1.7E-03	-2.5	1.6E-01	0.7	4.4E-01
ENSMUST00000150049				-6.9	1.0E-03	8.4	1.3E-04	0.0	9.8E-01	0.3	6.6E-01
ENSMUST00000182663				-6.9	2.3E-05	-9.3	7.2E-04	1.5	1.3E-02	-0.6	7.6E-01
ENSMUST00000148900				-6.9	4.9E-04	4.5	8.7E-04	-1.1	2.5E-01	-0.6	3.6E-01
ENSMUST00000194641	E74-like factor 2 [Source:MGI Symbol;Acc:MGI:1916507]		Q9JHC9	-0.4	6.0E-01	1.4	1.5E-01	0.9	2.3E-01	-0.9	3.0E-01
ENSMUST00000146318				-6.9	8.5E-03	-5.6	2.7E-04	-0.2	5.6E-01	-2.2	8.2E-02
ENSMUST00000194650				0.5	7.8E-01	0.5	7.8E-01	-1.5	3.4E-01	-1.6	3.8E-01
ENSMUST00000167379				-7.0	2.2E-03	6.7	2.5E-04	-0.1	9.3E-01	-0.8	2.5E-01
ENSMUST00000142033				-7.0	4.4E-05	7.1	7.3E-04	0.0	9.7E-01	0.1	8.9E-01
ENSMUST00000071641				-7.0	1.2E-04	6.5	1.1E-04	0.1	9.4E-01	-0.6	3.0E-01
ENSMUST00000194663	patched homolog 1 [Source:MGI Symbol;Acc:MGI:105373]	A0A0A6YWZ4		4.6	7.8E-02	4.9	3.0E-02	-2.8	2.6E-01	-3.2	6.1E-02
ENSMUST00000194666				-0.7	3.5E-01	-1.6	1.2E-01	-0.5	4.6E-01	0.4	6.8E-01
ENSMUST00000146577				-7.0	1.6E-02	4.7	2.4E-04	-0.4	5.7E-01	0.2	6.5E-01
ENSMUST00000126458				-7.0	5.8E-05	5.2	5.8E-04	0.3	7.8E-01	0.0	9.6E-01
ENSMUST00000194675				1.2	2.3E-01	2.9	3.8E-02	1.4	2.1E-01	-0.3	7.9E-01
ENSMUST00000194677	laminin, beta 3 [Source:MGI Symbol;Acc:MGI:99915]		Q61087	1.5	9.2E-02	-0.5	7.0E-01	-0.1	9.5E-01	1.9	9.9E-02
ENSMUST00000146310				-7.0	5.1E-05	8.4	1.9E-04	0.4	7.7E-01	-0.9	2.1E-01
ENSMUST00000194687	predicted gene, 20807 [Source:MGI Symbol;Acc:MGI:5434163]	A0A0A6YXX7		3.4	1.3E-01	6.0	2.1E-02	-0.3	9.1E-01	-2.9	5.9E-02
ENSMUST00000101192				-7.0	1.3E-05	5.0	3.2E-03	-6.3	3.0E-03	-0.5	4.8E-01
ENSMUST00000194691				4.4	8.7E-02	6.3	3.5E-02	-0.2	9.3E-01	-2.2	1.8E-01
ENSMUST00000133547				-7.0	1.0E-03	5.8	5.5E-03	-0.2	9.2E-01	0.6	5.6E-01
ENSMUST00000189135				-7.1	1.6E-04	-8.7	2.5E-04	-0.5	2.3E-01	0.3	8.6E-01
ENSMUST00000142757				-7.1	6.9E-04	6.2	2.0E-05	-0.5	5.3E-01	0.4	3.8E-01
ENSMUST00000123488				-7.1	3.1E-05	2.8	3.2E-01	-0.8	7.4E-01	2.2	3.2E-01
ENSMUST00000183511				-7.1	3.0E-05	7.0	6.4E-04	-0.5	7.4E-01	0.0	9.8E-01
ENSMUST00000150022				-7.1	1.3E-03	5.5	4.3E-04	-0.5	6.3E-01	0.3	6.0E-01
ENSMUST00000194732				0.0	9.7E-01	0.9	3.3E-01	0.3	6.1E-01	-0.6	4.9E-01
ENSMUST00000128408				-7.1	3.9E-04	2.8	1.5E-02	-3.4	1.2E-02	-0.6	4.7E-01
ENSMUST00000144667				-7.1	1.8E-03	6.6	1.9E-04	0.6	5.8E-01	0.8	2.2E-01
ENSMUST00000156678				-7.1	2.1E-04	-1.6	2.1E-02	1.0	2.0E-02	-0.6	3.7E-01
ENSMUST00000147635				-7.1	1.2E-03	3.4	2.2E-02	0.9	4.2E-01	0.5	5.6E-01
ENSMUST00000167911				-7.1	2.7E-05	-6.5	9.9E-04	-2.0	1.3E-02	0.2	9.2E-01
ENSMUST00000020770				-7.1	1.8E-05	-1.7	5.0E-02	0.2	7.3E-01	0.3	7.2E-01
ENSMUST00000092620				-7.2	1.9E-04	6.3	3.2E-04	-0.5	6.5E-01	-0.4	5.0E-01
ENSMUST00000145742				-7.2	1.4E-02	6.7	1.5E-02	-0.8	7.5E-01	-1.7	2.5E-01
ENSMUST00000080152				-7.2	2.0E-04	7.0	2.8E-05	-1.2	2.4E-01	-0.2	6.9E-01
ENSMUST00000133412				-7.2	1.5E-04	5.4	1.3E-04	-4.1	2.1E-03	-0.1	8.6E-01
ENSMUST00000120938				-7.2	5.8E-04	5.9	1.1E-05	-1.4	6.8E-02	-0.4	3.3E-01
ENSMUST00000194774	nephronophthisis 3 (adolescent) [Source:MGI Symbol;Acc:MGI:1921275]	H9KV07		6.5	4.3E-02	2.0	5.2E-01	-3.7	2.6E-01	0.8	7.1E-01
ENSMUST00000136604				-7.2	8.7E-04	3.9	2.3E-03	0.0	9.7E-01	-0.6	4.1E-01
ENSMUST00000117469				-7.2	2.4E-05	-3.8	5.3E-02	0.3	7.2E-01	0.0	9.8E-01
ENSMUST00000194786	Fc receptor-like 1 [Source:MGI Symbol;Acc:MGI:2442862]	A0A0A6YY56		2.3	2.1E-01	-0.9	6.3E-01	-3.0	8.0E-02	0.1	9.4E-01
ENSMUST00000151193				-7.2	4.1E-05	6.8	1.3E-04	-0.6	6.0E-01	-0.4	4.8E-01
ENSMUST00000194797	CD244 natural killer cell receptor 2B4 [Source:MGI Symbol;Acc:MGI:109294]	Q3TAZ6		-1.1	3.5E-01	-0.3	8.2E-01	0.1	9.2E-01	-0.7	6.2E-01
ENSMUST00000121317				-7.2	3.0E-05	-5.1	2.9E-02	0.2	8.2E-01	1.4	5.0E-01
ENSMUST00000139959				-7.2	1.1E-03	-3.6	5.0E-02	1.0	2.6E-01	-0.3	8.4E-01
ENSMUST00000134219				-7.2	2.0E-02	2.6	3.4E-01	-0.8	7.2E-01	2.8	1.9E-01
ENSMUST00000194808	calmodulin regulated spectrin-associated protein family, member 2 [Source:MGI Symbol;Acc:MGI:1922434]	A0A0A6YXV8		-0.8	3.4E-01	0.4	7.1E-01	0.6	5.0E-01	-0.7	5.0E-01
ENSMUST00000124099				-7.3	3.1E-04	-5.4	5.5E-03	0.7	2.6E-01	-0.9	5.9E-01
ENSMUST00000194813				-0.6	4.1E-01	0.8	4.7E-01	2.2	1.5E-02	0.8	4.3E-01
ENSMUST00000122817				-7.3	6.5E-05	6.6	1.1E-04	-0.6	6.0E-01	-0.2	7.4E-01
ENSMUST00000151943				-7.3	5.5E-05	4.7	4.0E-04	-1.5	1.1E-01	-0.3	6.4E-01
ENSMUST00000145709				-7.3	1.1E-04	6.6	5.2E-04	0.5	6.6E-01	0.4	5.4E-01
ENSMUST00000166466				-7.3	2.5E-05	5.7	7.8E-04	1.3	2.6E-01	-0.4	5.5E-01
ENSMUST00000137456				-7.3	3.8E-06	6.4	2.2E-03	-0.2	8.9E-01	-0.3	7.5E-01
ENSMUST00000147881				-7.3	1.0E-05	7.2	4.1E-05	-1.5	2.0E-01	-1.2	5.2E-02
ENSMUST00000151221				-7.3	2.7E-04	7.4	2.6E-04	0.0	9.8E-01	-0.6	3.8E-01
ENSMUST00000154533				-7.3	2.8E-04	-4.9	8.6E-04	-0.9	8.1E-02	-1.8	1.5E-01
ENSMUST00000146021				-7.3	3.5E-03	5.3	1.1E-03	-1.4	2.7E-01	-0.1	9.4E-01
ENSMUST00000149358				-7.3	1.0E-04	7.7	5.0E-05	-0.6	6.0E-01	-0.5	3.5E-01
ENSMUST00000194877	integrator complex subunit 7 [Source:MGI Symbol;Acc:MGI:1924315]	A0A0A6YWX4		0.7	7.1E-01	1.7	5.1E-01	0.7	6.8E-01	-0.3	9.1E-01
ENSMUST00000148646				-7.3	6.7E-04	7.7	2.6E-05	0.1	9.3E-01	-0.8	1.2E-01
ENSMUST00000118048				-7.4	3.4E-05	7.2	1.4E-04	-0.6	6.4E-01	-0.9	1.9E-01
ENSMUST00000194904	inosine 5'-phosphate dehydrogenase 2 [Source:MGI Symbol;Acc:MGI:109367]	A0A0A6YY72		-2.4	3.5E-01	-1.7	4.5E-01	-2.1	2.2E-01	-2.9	2.9E-01
ENSMUST00000136131				-7.4	9.9E-06	-4.9	2.2E-04	-0.8	8.8E-02	-1.9	7.7E-02
ENSMUST00000053298				-7.4	1.1E-04	3.3	9.9E-04	-0.4	5.5E-01	-0.3	5.3E-01
ENSMUST00000161020				-7.4	1.7E-04	4.6	8.3E-03	-2.1	1.7E-01	-1.4	1.9E-01
ENSMUST00000136915				-7.4	8.8E-03	-0.3	8.0E-01	5.3	2.0E-04	-0.2	9.1E-01
ENSMUST00000169496				-7.4	3.6E-04	7.1	3.4E-05	-0.5	6.0E-01	0.3	5.5E-01
ENSMUST00000117405				-7.5	1.6E-06	4.2	3.5E-03	1.7	1.1E-01	0.6	4.1E-01
ENSMUST00000194932				-1.9	4.0E-01	3.7	2.6E-01	4.0	1.7E-01	-1.6	5.0E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000194939				-2.3	4.3E-02	-0.4	7.1E-01	0.6	5.0E-01	-1.3	2.9E-01
ENSMUST00000194948				0.9	5.3E-01	-0.1	9.7E-01	-1.7	1.9E-01	-0.8	5.9E-01
ENSMUST00000149808				-7.5	3.1E-04	-5.3	6.6E-04	-1.2	2.6E-02	-1.5	2.5E-01
ENSMUST00000138160				-7.5	3.1E-05	4.0	9.3E-05	0.3	6.2E-01	0.1	8.6E-01
ENSMUST00000135041				-7.5	4.7E-04	-6.7	6.0E-03	1.0	1.3E-01	0.0	1.0E+00
ENSMUST00000165982				-7.5	9.1E-06	5.0	7.4E-02	-0.8	7.5E-01	0.6	7.0E-01
ENSMUST00000143232				-7.5	1.3E-04	4.2	1.5E-03	-0.6	5.0E-01	-0.4	5.7E-01
ENSMUST00000194984				-1.3	3.0E-01	-3.9	6.6E-02	-1.8	9.0E-02	0.7	7.1E-01
ENSMUST00000194993				-0.6	3.7E-01	-0.8	3.7E-01	-0.6	3.4E-01	-0.5	5.7E-01
ENSMUST00000156217				-7.5	1.4E-03	3.3	7.6E-02	6.3	1.4E-03	-1.4	3.1E-01
ENSMUST00000130610				-7.6	1.6E-05	-4.9	1.4E-03	-0.3	5.6E-01	-1.7	2.3E-01
ENSMUST00000144454				-7.6	1.2E-04	-3.6	8.9E-03	-1.0	1.3E-01	-1.7	2.0E-01
ENSMUST00000150157				-7.6	5.7E-04	3.9	2.7E-03	-0.1	9.2E-01	-0.7	3.8E-01
ENSMUST00000153592				-7.6	1.6E-05	8.5	2.8E-04	-2.1	2.3E-01	0.8	3.1E-01
ENSMUST00000119438				-7.6	1.9E-03	3.9	4.1E-04	0.1	8.5E-01	1.0	8.7E-02
ENSMUST00000127300				-7.6	1.8E-05	-3.7	2.2E-02	-0.5	5.0E-01	-1.4	3.8E-01
ENSMUST00000123590				-7.6	9.8E-04	7.0	2.1E-04	-0.7	6.1E-01	0.1	9.0E-01
ENSMUST00000189941				-7.6	6.3E-07	7.1	1.5E-02	-0.8	7.6E-01	-0.9	5.3E-01
ENSMUST00000134230				-7.7	6.4E-04	6.9	2.9E-04	-0.7	6.1E-01	0.8	2.4E-01
ENSMUST00000122878				-7.7	1.8E-04	-2.6	1.1E-01	0.3	7.1E-01	-0.2	9.0E-01
ENSMUST00000096232				-7.7	1.9E-07	7.1	4.0E-05	0.1	9.4E-01	0.0	9.2E-01
ENSMUST00000132786				-7.7	9.0E-04	-2.5	1.4E-01	2.7	1.2E-02	-1.6	3.7E-01
ENSMUST00000026843				-7.7	2.4E-04	-2.1	1.1E-01	0.3	6.8E-01	-2.6	9.0E-02
ENSMUST00000144117				-7.7	1.5E-04	1.1	4.6E-01	-1.2	3.7E-01	2.0	1.0E-01
ENSMUST00000120557				-7.7	2.1E-04	6.3	2.9E-05	-0.1	9.1E-01	-0.2	6.6E-01
ENSMUST00000195059	enabled homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:108360]	A0A0A6YW06		2.8	1.4E-01	2.1	3.1E-01	-1.1	5.0E-01	-0.4	8.1E-01
ENSMUST00000144859				-7.7	8.2E-06	-1.7	1.6E-01	1.4	4.0E-02	0.3	8.3E-01
ENSMUST00000150046				-7.7	4.9E-04	5.9	4.4E-05	-0.5	5.2E-01	0.2	7.0E-01
ENSMUST00000195077	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	A0A0A6YXP3		-0.1	9.6E-01	-1.1	6.3E-01	-0.5	7.2E-01	0.5	8.3E-01
ENSMUST00000117288				-7.8	5.2E-04	-4.1	3.9E-02	1.0	2.0E-01	-1.2	5.5E-01
ENSMUST00000160683				-7.8	2.6E-05	6.2	2.1E-04	-0.5	6.4E-01	0.0	9.7E-01
ENSMUST00000148262				-7.8	1.8E-03	8.0	7.1E-05	-1.3	3.1E-01	1.0	1.2E-01
ENSMUST00000177051				-7.8	1.8E-03	6.3	1.4E-03	-0.6	6.8E-01	-1.0	2.4E-01
ENSMUST00000147059				-7.8	4.7E-05	8.2	8.8E-05	0.4	7.8E-01	-0.3	5.9E-01
ENSMUST00000195117	activating transcription factor 3 [Source:MGI Symbol;Acc:MGI:109384]	Q4FJW1	Q60765	-0.6	6.9E-01	1.7	3.8E-01	1.7	3.2E-01	-0.6	7.0E-01
ENSMUST00000120234				-7.8	5.9E-05	4.9	2.7E-03	-1.4	2.9E-01	-0.7	4.5E-01
ENSMUST00000153056				-7.8	4.6E-06	-9.0	1.3E-04	-0.7	1.1E-01	-0.8	6.3E-01
ENSMUST00000052882				-7.9	2.8E-05	3.6	1.2E-02	-0.5	6.3E-01	0.0	9.9E-01
ENSMUST00000136788				-7.9	7.4E-03	-4.4	6.0E-02	0.4	7.0E-01	0.4	8.6E-01
ENSMUST00000171411				-7.9	1.8E-05	-5.1	4.7E-04	-1.1	3.1E-02	-2.1	9.5E-02
ENSMUST00000153968				-8.0	1.7E-04	4.6	1.7E-02	-1.1	5.4E-01	0.2	8.8E-01
ENSMUST00000172763				-8.0	1.7E-03	6.1	2.0E-03	0.3	8.2E-01	0.2	8.0E-01
ENSMUST00000176359				-8.0	4.6E-04	5.5	2.2E-02	-0.6	7.9E-01	-0.9	4.6E-01
ENSMUST00000139982				-8.0	4.6E-04	2.5	2.4E-01	5.7	4.8E-03	0.0	9.9E-01
ENSMUST00000144443				-8.0	5.7E-05	-3.6	4.0E-03	-1.0	7.4E-02	-1.3	2.4E-01
ENSMUST00000118459				-8.0	1.1E-05	5.8	1.2E-03	-0.2	8.7E-01	1.0	2.2E-01
ENSMUST00000129493				-8.0	1.3E-05	1.8	3.3E-01	-2.7	1.8E-01	1.6	2.8E-01
ENSMUST00000125936				-8.1	5.3E-05	5.4	8.8E-04	0.8	4.5E-01	-0.6	3.8E-01
ENSMUST00000148764				-8.1	2.3E-04	-2.2	1.7E-01	-0.1	9.2E-01	-1.2	4.5E-01
ENSMUST00000134855				-8.1	1.0E-02	6.5	5.2E-04	-0.6	6.5E-01	-0.8	3.0E-01
ENSMUST00000146103				-8.1	1.4E-04	2.8	1.7E-01	6.4	1.9E-03	-1.8	2.9E-01
ENSMUST00000166857				-8.1	1.9E-05	-2.3	2.4E-01	0.7	5.7E-01	-1.1	5.7E-01
ENSMUST00000177767				-8.1	1.4E-02	-2.4	2.0E-01	1.8	7.1E-02	0.3	8.5E-01
ENSMUST00000167840				-8.2	6.7E-04	6.4	6.8E-04	-0.6	6.6E-01	-0.3	6.5E-01
ENSMUST00000160052				-8.2	4.4E-06	-3.3	2.1E-02	0.2	7.1E-01	1.3	3.0E-01
ENSMUST00000134812				-8.2	2.4E-02	-3.3	4.8E-02	1.1	1.6E-01	-0.2	8.8E-01
ENSMUST00000075082				-8.3	6.8E-06	4.8	5.2E-04	1.4	1.1E-01	-1.0	1.2E-01
ENSMUST00000186008				-8.3	3.1E-04	5.6	5.4E-02	-0.8	7.7E-01	-0.5	7.4E-01
ENSMUST00000117045				-8.3	1.3E-05	3.3	3.4E-03	0.4	5.9E-01	0.1	9.1E-01
ENSMUST00000134053				-8.3	4.5E-06	4.1	4.9E-02	1.3	4.3E-01	1.0	4.0E-01
ENSMUST00000156732				-8.3	9.3E-03	7.7	4.9E-04	-0.7	6.7E-01	0.2	8.3E-01
ENSMUST00000195275	LIM homeobox protein 4 [Source:MGI Symbol;Acc:MGI:101776]	A0A0A6YWR5		3.2	6.1E-02	6.4	1.9E-03	-0.5	7.7E-01	-3.7	6.1E-03
ENSMUST00000193235				-8.4	1.5E-05	7.6	2.7E-05	0.8	3.8E-01	0.3	5.6E-01
ENSMUST00000103009				-8.4	9.3E-05	4.3	6.0E-03	-0.6	5.9E-01	-0.2	7.8E-01
ENSMUST00000195291	digestive organ expansion factor homolog (zebrafish) [Source:MGI Symbol;Acc:MGI:2138080]	A0A0A6YWS6		-3.6	2.8E-01	2.5	4.4E-01	2.1	4.6E-01	-3.9	2.3E-01
ENSMUST00000098980				-8.4	2.6E-04	7.4	9.9E-05	-0.6	6.3E-01	-0.1	8.2E-01
ENSMUST00000195302	syntaxin 6 [Source:MGI Symbol;Acc:MGI:1926235]		Q9JKK1	-1.9	1.0E-01	-0.8	5.1E-01	0.9	3.0E-01	-0.3	8.1E-01
ENSMUST00000195305				-0.1	8.9E-01	-0.2	8.1E-01	-0.4	5.6E-01	-0.3	7.6E-01
ENSMUST00000176308				-8.4	1.4E-06	6.5	3.1E-04	-0.6	6.1E-01	0.0	9.9E-01
ENSMUST00000140155				-8.4	3.7E-05	3.4	1.3E-02	0.8	4.4E-01	0.7	4.2E-01
ENSMUST00000187771				-8.4	2.1E-04	7.5	1.2E-04	0.5	6.7E-01	-0.5	4.1E-01
ENSMUST00000190051				-8.5	5.1E-05	6.0	4.1E-03	-1.2	5.1E-01	-1.9	1.1E-01
ENSMUST00000173192				-8.6	1.5E-05	-7.1	4.9E-04	0.8	1.0E-01	-1.0	5.0E-01
ENSMUST00000121497				-8.6	2.1E-05	7.4	7.7E-05	0.5	6.6E-01	-0.2	7.8E-01
ENSMUST00000180532				-8.6	1.1E-03	5.5	4.0E-04	-0.6	6.1E-01	0.4	5.5E-01
ENSMUST00000120360				-8.6	7.0E-05	8.2	8.7E-03	-0.8	7.8E-01	-2.7	9.1E-02
ENSMUST00000036712				-8.7	3.5E-05	-6.4	9.9E-04	-1.1	6.1E-02	-0.5	7.3E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102708				-8.7	5.3E-05	7.2	9.9E-05	-0.6	6.0E-01	-0.4	5.3E-01
ENSMUST00000140974				-8.7	3.7E-04	3.5	3.7E-02	0.8	5.5E-01	0.4	7.1E-01
ENSMUST00000195394				-0.1	8.4E-01	0.2	7.9E-01	0.2	7.4E-01	-0.2	8.4E-01
ENSMUST00000088063				-8.7	8.5E-05	6.4	5.4E-04	0.2	9.0E-01	-1.0	1.8E-01
ENSMUST00000075723				-8.8	8.1E-05	4.9	4.3E-03	-1.5	3.3E-01	-0.3	7.1E-01
ENSMUST00000185676				-8.8	5.1E-05	7.0	8.8E-04	0.0	9.8E-01	0.6	4.9E-01
ENSMUST00000167225				-8.8	1.6E-04	-4.0	4.6E-03	-2.1	6.0E-03	-0.4	7.6E-01
ENSMUST00000118909				-8.8	8.0E-06	5.4	5.2E-05	-0.9	2.5E-01	-0.4	4.2E-01
ENSMUST00000077389				-8.8	6.4E-07	5.4	7.6E-04	-0.2	8.1E-01	0.1	9.1E-01
ENSMUST00000130172				-8.9	1.8E-02	6.5	7.4E-05	-1.6	1.5E-01	0.2	7.2E-01
ENSMUST00000129533				-8.9	8.2E-05	3.7	7.0E-03	-0.4	6.8E-01	-0.3	7.6E-01
ENSMUST00000195433	centrosomal protein 170 [Source:MGI Symbol;Acc:MGI:1918348]	A0A0A6YXR9		-1.3	4.1E-01	-0.1	9.6E-01	-0.8	5.3E-01	-2.0	2.8E-01
ENSMUST00000195443	uridine-cytidine kinase 2 [Source:MGI Symbol;Acc:MGI:1931744]	A0A0A6YXG9		-2.5	5.2E-02	-3.4	5.0E-02	-0.5	5.4E-01	0.4	7.9E-01
ENSMUST00000122151				-8.9	7.1E-05	6.7	1.6E-04	-0.5	6.6E-01	-0.4	4.8E-01
ENSMUST00000090749				-8.9	5.3E-05	7.8	6.1E-07	-0.3	6.4E-01	-0.3	3.1E-01
ENSMUST00000127652				-9.0	1.6E-04	6.3	1.5E-04	-0.6	6.1E-01	-0.2	7.5E-01
ENSMUST00000121046				-9.0	2.3E-06	4.8	3.0E-04	-1.8	6.4E-02	-0.7	3.0E-01
ENSMUST00000102669				-9.0	2.4E-05	2.8	7.3E-02	-3.1	7.3E-02	0.0	9.7E-01
ENSMUST00000153847				-9.1	3.0E-06	5.3	1.9E-03	0.4	7.1E-01	0.1	8.9E-01
ENSMUST00000187973				-9.1	7.4E-05	5.9	2.9E-04	0.1	9.5E-01	0.1	9.3E-01
ENSMUST00000149944				-9.1	2.4E-06	3.6	1.3E-02	-0.6	5.8E-01	0.2	7.5E-01
ENSMUST00000140687				-9.1	2.6E-02	-2.7	2.0E-02	1.4	1.6E-02	-0.7	5.0E-01
ENSMUST00000195515	cornulin [Source:MGI Symbol;Acc:MGI:2685861]	D3YUU6		2.5	1.6E-01	5.1	1.1E-02	-0.6	7.4E-01	-3.2	3.1E-02
ENSMUST00000195524	LPS-responsive beige-like anchor [Source:MGI Symbol;Acc:MGI:1933162]	Q8BSM6		0.6	6.3E-01	3.0	5.7E-02	1.1	4.2E-01	-1.4	2.7E-01
ENSMUST00000122956				-9.2	5.7E-04	4.4	5.3E-03	-2.0	1.6E-01	-2.1	4.5E-02
ENSMUST00000145159				-9.3	3.7E-04	-5.6	1.8E-02	-0.6	4.3E-01	-0.1	9.6E-01
ENSMUST00000148248				-9.3	1.2E-05	4.4	9.6E-03	-0.5	7.2E-01	1.7	8.9E-02
ENSMUST00000121658				-9.3	3.1E-06	5.1	1.2E-02	0.2	9.1E-01	0.4	7.5E-01
ENSMUST00000122226				-9.3	1.7E-05	5.1	6.9E-05	0.4	6.0E-01	-0.4	3.8E-01
ENSMUST00000195571	centromere protein L [Source:MGI Symbol;Acc:MGI:1917704]	Q05CX4		0.9	6.7E-01	3.1	1.9E-01	0.2	9.4E-01	-2.1	3.1E-01
ENSMUST00000182017				-9.3	3.5E-06	8.9	1.1E-04	-0.4	8.1E-01	0.2	7.5E-01
ENSMUST00000163489				-9.4	1.8E-05	5.1	2.7E-03	-1.5	3.0E-01	-0.9	3.3E-01
ENSMUST00000190277				-9.5	1.2E-02	6.6	2.2E-03	-0.7	7.0E-01	-2.7	3.0E-02
ENSMUST00000138226				-9.5	1.5E-04	4.7	3.6E-04	-0.9	2.9E-01	-0.4	5.6E-01
ENSMUST00000071523				-9.5	7.2E-05	-6.5	1.6E-03	0.3	6.6E-01	0.1	9.7E-01
ENSMUST00000145679				-9.5	1.4E-05	7.4	7.0E-05	-0.6	6.0E-01	0.0	9.5E-01
ENSMUST00000118307				-9.6	1.7E-06	4.8	1.2E-02	-1.1	5.1E-01	1.1	2.6E-01
ENSMUST00000138939				-9.6	1.8E-05	-1.3	5.5E-01	3.3	2.0E-02	-0.4	8.6E-01
ENSMUST00000160213				-9.6	1.3E-03	-2.4	1.2E-01	0.2	7.8E-01	-1.4	3.9E-01
ENSMUST00000076842				-9.7	1.4E-04	6.3	1.4E-04	1.8	8.2E-02	-0.9	1.6E-01
ENSMUST00000195620	ulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C [Source:MGI		Q64151	2.8	8.3E-02	-0.2	8.9E-01	-2.6	9.9E-02	0.5	7.7E-01
ENSMUST00000140626				-9.7	1.0E-04	5.7	3.7E-04	1.0	3.3E-01	1.1	1.2E-01
ENSMUST00000102482				-9.7	4.9E-05	7.3	8.4E-05	-0.6	6.1E-01	-0.1	8.4E-01
ENSMUST00000195628				-1.1	2.6E-01	-0.5	6.5E-01	-0.8	3.5E-01	-1.4	1.9E-01
ENSMUST00000124641				-9.8	6.8E-05	3.4	8.0E-03	-0.1	9.6E-01	-0.8	3.1E-01
ENSMUST00000195636	mitogen-activated protein kinase kinase kinase kinase 4 [Source:MGI Symbol;Acc:MGI:1349394]	A0A0A6YWM8		-0.1	9.0E-01	-0.3	8.1E-01	-1.2	2.0E-01	-1.1	4.1E-01
ENSMUST00000195640	microtubule-associated protein 9 [Source:MGI Symbol;Acc:MGI:2442208]		Q3TRR0	0.6	7.0E-01	3.5	4.3E-02	-0.6	7.1E-01	-3.4	3.7E-02
ENSMUST00000142408				-9.8	1.3E-05	6.5	2.8E-04	-0.6	6.1E-01	0.2	7.2E-01
ENSMUST00000195650	denticleless homolog (Drosophila) [Source:MGI Symbol;Acc:MGI:1924093]	A0A0A6YVQ5		7.8	4.1E-02	7.7	5.4E-02	-1.0	7.9E-01	-1.0	6.6E-01
ENSMUST00000195654	calcyclin binding protein [Source:MGI Symbol;Acc:MGI:1270839]	A0A0A6YY29		-3.4	4.9E-02	-5.2	2.2E-02	-1.9	7.1E-02	-0.1	9.8E-01
ENSMUST00000145610				-9.8	2.5E-05	3.6	4.1E-04	-1.6	4.1E-02	-0.1	9.0E-01
ENSMUST00000136353				-9.9	1.0E-03	-1.3	3.9E-01	3.4	4.4E-03	-0.6	6.9E-01
ENSMUST00000195669	zinc finger CCCH type containing 11A [Source:MGI Symbol;Acc:MGI:1917829]	A0A0A6YXI9		0.4	7.4E-01	0.5	7.7E-01	0.0	1.0E+00	-0.1	9.5E-01
ENSMUST00000151118				-10.0	8.9E-06	7.2	2.9E-04	1.1	3.9E-01	-1.0	1.7E-01
ENSMUST00000195686				1.1	3.7E-01	1.2	4.4E-01	-0.3	8.2E-01	-0.5	7.1E-01
ENSMUST00000084614				-10.1	2.4E-06	7.9	2.7E-05	-0.6	5.9E-01	-0.3	5.9E-01
ENSMUST00000119780				-10.1	2.8E-05	-5.8	9.1E-04	0.7	9.7E-02	5.0	2.2E-03
ENSMUST00000195715				-1.5	2.5E-01	0.6	6.0E-01	-0.2	8.7E-01	-2.3	1.1E-01
ENSMUST00000088480				-10.1	4.6E-05	-6.3	1.5E-04	0.3	4.0E-01	0.4	7.0E-01
ENSMUST00000195728				0.8	4.7E-01	-0.4	7.6E-01	-0.4	6.9E-01	0.8	5.4E-01
ENSMUST00000138145				-10.1	9.4E-07	9.9	2.0E-05	0.3	8.0E-01	1.3	4.7E-02
ENSMUST00000088299				-10.1	3.0E-07	5.2	7.2E-04	-0.7	5.1E-01	-0.8	2.6E-01
ENSMUST00000156766				-10.1	2.2E-04	4.2	3.6E-02	-1.4	4.7E-01	1.0	3.9E-01
ENSMUST00000195749	NOL1/NOP2/Sun domain family member 6 [Source:MGI Symbol;Acc:MGI:1921705]		Q7TS68	4.3	5.9E-02	2.4	2.8E-01	-2.2	3.2E-01	-0.3	8.5E-01
ENSMUST00000155008				-10.2	7.3E-06	-3.2	1.1E-01	2.0	6.8E-02	-1.1	5.6E-01
ENSMUST00000111388				-10.2	9.7E-06	6.4	3.7E-04	-0.6	6.4E-01	-0.7	3.0E-01
ENSMUST00000120421				-10.3	2.2E-05	3.2	1.0E-02	0.0	9.9E-01	-0.3	6.8E-01
ENSMUST00000118499				-10.3	3.8E-06	5.4	6.8E-04	-1.4	2.3E-01	0.7	2.8E-01
ENSMUST00000140426				-10.4	1.3E-04	6.0	5.6E-04	-0.5	7.0E-01	-0.1	8.9E-01
ENSMUST00000195770	interleukin 1 receptor, type II [Source:MGI Symbol;Acc:MGI:96546]	A0A0A6YX23		-5.4	1.7E-01	-4.9	3.3E-01	0.1	9.8E-01	-0.5	9.2E-01
ENSMUST00000134040				-10.4	3.8E-05	2.8	2.0E-01	6.8	2.5E-03	-1.3	5.0E-01
ENSMUST00000138900				-10.5	8.5E-07	4.0	3.3E-04	-2.0	3.0E-02	-0.7	2.3E-01
ENSMUST00000116115				-10.6	4.2E-06	2.6	1.7E-02	-0.7	4.0E-01	0.5	5.0E-01
ENSMUST00000195800	ring finger and WD repeat domain 2 [Source:MGI Symbol;Acc:MGI:1347046]	A0A0A6YXD2		-1.2	5.8E-01	-2.3	3.9E-01	-0.8	6.3E-01	0.3	9.0E-01
ENSMUST00000195802	serine/arginine-rich splicing factor 1 [Source:MGI Symbol;Acc:MGI:98283]			-4.5	2.3E-01	-4.9	2.9E-01	-1.3	5.4E-01	-0.9	8.5E-01
ENSMUST00000195804				-3.2	8.3E-02	-0.4	8.2E-01	-0.2	8.9E-01	-3.0	1.3E-01
ENSMUST00000181935				-10.6	2.2E-05	3.4	3.6E-03	-2.4	3.2E-02	-0.5	4.8E-01

				Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Description	Uniprot_Trembl	Uniprot_Swissprot	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000195817	muscleblind-like 1 (Drosophila) [Source:MGI Symbol;Acc:MGI:1928482]	A0A0A6YWJ5		-1.2	6.0E-01	-2.7	3.3E-01	-2.1	2.0E-01	-0.6	8.3E-01
ENSMUST00000145364				-10.8	1.1E-03	5.0	1.0E-03	-2.7	4.7E-02	-0.6	3.9E-01
ENSMUST00000136238				-10.9	7.5E-06	6.0	6.1E-05	-1.9	8.3E-02	-0.8	1.5E-01
ENSMUST00000164587				-10.9	9.4E-05	4.6	1.7E-03	1.1	2.5E-01	-0.1	9.0E-01
ENSMUST00000154837				-11.0	3.8E-03	5.1	3.9E-03	-0.7	6.4E-01	0.8	3.6E-01
ENSMUST00000003245				-11.2	1.2E-07	-6.3	1.9E-04	-0.9	3.6E-02	-0.8	5.1E-01
ENSMUST00000188231				-11.4	8.3E-05	7.9	2.7E-05	-0.6	5.9E-01	-0.6	2.7E-01
ENSMUST00000187117				-11.4	3.7E-05	4.7	5.0E-04	1.1	2.1E-01	-0.3	6.0E-01
ENSMUST00000195876	vesicle-associated membrane protein 8 [Source:EntrezGene;Acc:22320]			-0.2	7.3E-01	0.2	8.6E-01	0.3	6.2E-01	-0.1	9.3E-01
ENSMUST00000175995				-11.6	7.6E-06	6.9	9.4E-05	-0.6	6.0E-01	0.0	9.4E-01

Raw Reads miRNA

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpql0673	hpql0674	hpql0675	hpql0676	hpql0677	hpql0678	hpql0679	hpql0680	hpql0523	hpql0524	hpql0525	hpql0555	hpql0556	hpql0557	hpql0558	hpql0559	hpql0560	mirBase_accession	mirBase name
ENSMUST00000083460	ENSMUSG00000065394	5	39337	60788	25776	116224	52633	43627	29245	36487	1600	3167	518	2	19603	3086	1105	2770	433	MI0000689	Mir25
ENSMUST00000083461	ENSMUSG00000065395	11	2	27	9	88	72	836	42	302	1	5	0	0	4	1	0	0	0	MI0000235	Mir193a
ENSMUST00000083462	ENSMUSG00000065396	17	130	2739	64	12143	141	4299	149	1682	5	13	11	2	288	83	28	352	34	MI0000147	Mir99b
ENSMUST00000083463	ENSMUSG00000065397	16	159	154	92	889	385	448	493	682	42	50	1	0	967	110	158	461	40	MI0000177	Mir155
ENSMUST00000083464	ENSMUSG00000065398	X	36	15	41	83	492	794	206	469	6	7	0	0	51	9	2	1	2	MI0000230	Mir188
ENSMUST00000083465	ENSMUSG00000065399	18	0	12	0	22	3	175	2	34	0	0	0	0	1	0	1	0	1	MI0000159	Mir133a-1
ENSMUST00000083466	ENSMUSG00000065400	4	9	14	5	54	23	75	12	70	0	1	2	0	19	5	1	0	1	MI0000554	Mir200a
ENSMUST00000083467	ENSMUSG00000065401	11	2150	1373	402	10083	1938	8084	505	3408	460	862	94	2	1043	424	107	260	421	MI0000168	Mir144
ENSMUST00000083468	ENSMUSG00000065402	18	0	1376	0	17	0	127	0	0	0	0	0	0	0	0	0	0	0	MI0000256	Mir122
ENSMUST00000083469	ENSMUSG00000065403	14	74	78	127	341	3622	4034	2556	3076	342	97	17	0	8137	547	146	328	20	MI0000567	Mir18
ENSMUST00000083470	ENSMUSG00000065404	X	0	1	0	2	1	2	0	2	0	0	0	0	0	0	0	0	0	MI0000244	Mir201
ENSMUST00000083471	ENSMUSG00000065405	1	3499	25016	1441	25157	6807	16191	2996	7723	1712	724	80	10	2601	414	114	214	134	MI0000144	Mir30a
ENSMUST00000083472	ENSMUSG00000065406	10	33992	33387	26930	98674	66849	27393	36519	31116	8900	4834	706	15	48869	4417	1230	2428	616	MI0000138	Mirlet7i
ENSMUST00000083473	ENSMUSG00000065407	9	4	2	2	6	4	6	6	21	0	1	0	0	17	0	1	0	0	MI0000161	Mir135a-1
ENSMUST00000083474	ENSMUSG00000065408	4	17	235	13	886	380	16202	220	4614	4	15	1	0	80	31	18	15	3	MI0000579	Mir31
ENSMUST00000083475	ENSMUSG00000065409	4	38246	21314	34078	125247	177560	164233	87307	119400	7160	3638	342	127	46283	5697	2404	3360	1238	MI0000259	Mir30c
ENSMUST00000083476	ENSMUSG00000065410	2	135	80	96	702	1755	2866	1222	1424	9	38	15	1	265	126	35	52	37	MI0000398	Mir298
ENSMUST00000083477	ENSMUSG00000065411	11	3	27	1	34	16	65	14	29	0	2	0	0	29	4	2	2	0	MI0000237	Mir195a
ENSMUST00000083478	ENSMUSG00000065412	1	64	42	125	198	1297	1618	691	1256	128	49	0	2	1254	82	24	39	1	MI0000712	Mir29b-2
ENSMUST00000083479	ENSMUSG00000065413	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0003531	Mir367
ENSMUST00000083480	ENSMUSG00000065414	9	1	0	3	29	274	348	113	148	0	3	0	0	24	10	3	0	0	MI0000722	Mir138-1
ENSMUST00000083481	ENSMUSG00000065415	11	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	MI0000731	Mir217
ENSMUST00000083482	ENSMUSG00000065416	14	256	331	464	1080	3986	5087	2277	4723	1727	209	1	2	1024	73	65	114	50	MI0000688	Mir19a
ENSMUST00000083483	ENSMUSG00000065417	11	26230	19054	28013	82465	69025	64453	50008	85955	2688	2400	121	12	17729	1430	1188	1086	1914	MI0000623	Mir340
ENSMUST00000083484	ENSMUSG00000065418	X	3242	782	2593	11224	17015	16472	9293	19504	53	118	65	1	1688	233	159	246	109	MI0000590	Mir322
ENSMUST00000083485	ENSMUSG00000098807	12	14	55	12	46	38	76	25	20	0	2	0	0	2	0	0	0	0	MI0000400	Mir300
ENSMUST00000083486	ENSMUSG00000065420	11	84076	34941	63385	246644	597234	1063460	518977	1037260	10254	12081	26020	140	207748	33890	21843	39823	15798	MI0026028	Mir142b
ENSMUST00000083487	ENSMUSG00000065421	13	4245	2687	2374	16899	31638	9801	20320	18368	544	897	44	0	25246	2821	1946	3951	267	MI0000556	Mirlet7a-1
ENSMUST00000083488	ENSMUSG00000065422	X	7554	4661	6119	20295	17376	13072	9430	9624	1309	1756	286	11	10151	1516	590	1197	270	MI0000709	Mir221
ENSMUST00000083489	ENSMUSG00000065423	2	14740	11759	10560	67206	83814	78942	51377	74946	814	5121	1225	38	9088	3898	2618	3692	1737	MI0000223	Mir181a-2
ENSMUST00000083490	ENSMUSG00000065424	13	3	22	0	259	0	354	1	168	0	0	0	0	5	0	0	0	0	MI0000157	Mir9-2
ENSMUST00000083491	ENSMUSG00000065425	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000597	Mir325
ENSMUST00000083492	ENSMUSG00000065426	12	5	14	1	3	14	26	7	1	3	1	0	0	7	1	0	2	0	MI0000160	Mir134
ENSMUST00000083493	ENSMUSG00000065427	4	4	11	6	64	29	76	31	78	0	3	0	0	22	6	2	0	0	MI0001642	Mir429
ENSMUST00000083494	ENSMUSG00000065428	12	0	1	0	0	3	1	9	1	1	0	0	0	3	0	0	0	0	MI0000799	Mir382
ENSMUST00000083495	ENSMUSG00000065429	12	234	182	128	581	1844	899	645	606	126	138	51	1	779	110	49	106	25	MI0000632	Mir345
ENSMUST00000083496	ENSMUSG00000065430	10	55283	29340	45499	270524	592832	380833	228397	443536	5383	5586	1443	116	96212	20216	12808	37915	9232	MI0000706	Mir26a-2
ENSMUST00000083497	ENSMUSG00000065431	3	6638	4058	3778	19038	36960	30256	19600	17042	859	1275	183	60	4549	736	401	1024	442	MI0000228	Mir186
ENSMUST00000083498	ENSMUSG00000065432	14	0	0	0	0	2	243	87	94	0	0	0	0	0	0	0	0	0	MI0000555	Mir208a
ENSMUST00000083499	ENSMUSG00000065433	12	0	0	0	1	0	4	0	1	0	0	0	0	0	0	0	2	0	MI0001165	Mir370
ENSMUST00000083500	ENSMUSG00000065434	13	23	13	27	83	288	197	394	284	860	79	4	0	560	17	20	196	7	MI0000728	Mir7-1
ENSMUST00000083501	ENSMUSG00000065435	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000646	Mir135b
ENSMUST00000083502	ENSMUSG00000065436	12	70	134	49	554	1887	2059	994	1602	120	169	117	1	1144	214	328	1531	137	MI0000627	Mir342
ENSMUST00000083503	ENSMUSG00000065437	15	28800	27119	26884	123889	245646	214976	231097	172284	6183	3400	840	206	68279	17854	6713	10520	3312	MI0000549	Mir30d
ENSMUST00000083504	ENSMUSG00000065438	12	1	0	0	2	3	7	2	0	0	0	0	0	0	0	0	0	0	MI0000794	Mir377
ENSMUST00000083505	ENSMUSG00000065439	8	11451	15152	12189	33205	69301	45382	38766	47937	3518	3430	1561	51	23919	5139	1236	1465	976	MI0000165	Mir140
ENSMUST00000083506	ENSMUSG00000065440	9	2198	6069	4778	12961	35637	15122	20520	24274	737	660	55	14	15623	1500	771	1575	162	MI0000137	Mirlet7g
ENSMUST00000083507	ENSMUSG00000065441	9	18	19	0	75	52	97	31	47	0	2	1	0	9	3	4	0	0	MI0000726	Mir128-2
ENSMUST00000083508	ENSMUSG00000065442	14	384	251	526	1134	5955	5522	7779	5544	548	195	5	0	7179	425	214	439	38	MI0000568	Mir20a
ENSMUST00000083509	ENSMUSG00000065443	6	155	28	113	727	430	283	247	151	67	45	3	0	158	23	21	35	0	MI0001151	Mir196b
ENSMUST00000083510	ENSMUSG00000065444	8	5066	3571	4280	22881	31222	32585	14868	31327	446	881	270	8	4415	799	287	970	260	MI0000578	Mir27a
ENSMUST00000083511	ENSMUSG00000065445	18	30	5721	33	2634	49	2326	27	606	10	4	0	11	164	14	1	2	5	MI0000257	Mir143
ENSMUST00000083512	ENSMUSG00000065446	7	551	350	445	2178	7882	4699	6699	7467	400	700	72	2	5989	1269	856	2168	157	MI0000693	Mir139
ENSMUST00000083513	ENSMUSG00000065447	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0003718	Mir302d
ENSMUST00000083514	ENSMUSG00000065448	12	1	6	0	3	2	4	0	1	0	0	0	0	4	0	0	0	0	MI0000176	Mir154
ENSMUST00000083515	ENSMUSG00000065449	16	2	3	2	10	27	0	66	50	2	0	0	0	24	2	0	6	0	MI0000768	Mir365-1
ENSMUST00000083516	ENSMUSG00000065450	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0001638	Mir448
ENSMUST00000083517	ENSMUSG00000065451	4	4074	6691	3360	15562	7605	10756	3494	12904	622	641	20	4	1563	143	105	56	212	MI0000148	Mir101a
ENSMUST00000083518	ENSMUSG00000065452	4	0	0	0	1	0	1	0	0	0	0	1	2	0	0	0	1	1	MI0000250	Mir207
ENSMUST00000083519	ENSMUSG00000065453	13	1161	1201	713	7025	14000	10535	9939	10664	165	243	77	5	6466	2177	820	1672	255	MI0000405	Mirlet7d
ENSMUST00000083520	ENSMUSG00000065454	2	0	1	0	0	6	3	0	3	0	0	0	0	1	0	0	0	0	MI0000150	Mir124a-3
ENSMUST00000083521	ENSMUSG00000065455	11	191224	111749	154639	430184	938891	952031	426172	691612	103884	68223	1603	87	271807	19441	13665	32535	4683	MI0000569	Mir21a
ENSMUST00000083522	ENSMUSG00000065456	X	5	12	14	12	193	139	129	104	8	5	0	0	134	14	7	22	1	MI0000406	Mir106a
ENSMUST00000083523	ENSMUSG00000065457	8	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	MI0000800	Mir383
ENSMUST00000083524	ENSMUSG00000065458	1	1250	657	798	3009	4723	3634	3848	2566	24	154	0	0	50	39	42	10	58	MI0000723	Mir181b-1
ENSMUST00000083526	ENSMUSG00000065460	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000820	Mir133a-2
ENSMUST00000083528	ENSMUSG00000065462	6	14	7	6	16	217	377	661	246	16	10	0	0	618	92	32	99	5	MI0000694	Mir200c
ENSMUST00000083530	ENSMUSG00000065464	16	37	46	34	86	255	232	500	290	68	47	10	0	222	39	18	74	3	MI0000227	Mir185
ENSMUST00000083531	ENSMUSG00000065465	15	38	17	35	140	865	1482	497	1170	17	16	0	0	104	11	11	2	6	MI0000707	Mir33
ENSMUST00000083534	ENSMUSG00000065468	1	29836	14792	27499	91062	111315	55068	58740	90815	1241	2531	238	8	46478	4293	1939	3855	1607	MI0000575	Mir26b
ENSMUST00000083535	ENSMUSG00000065469	6	7	0	0	14	8	15	8	6	0	186	28	0	3	0	0	0	0	MI0000222	Mir129-1
ENSMUST00000083536	ENSMUSG00000065470	1	48	228	90	553	11894	21406	7663	15868	81	206	84	1	885	524	158	438	44	MI0000171	Mir149
ENSMUST00000083537	ENSMUSG00000065471	X	1233	1098	759	5410	12484	19821	10263	7912	286	323	51	0	2900	760	248	508	94	MI0000710	Mir222
ENSMUST00000083538	ENSMUSG00000065472	16	7	88	3	264	53	394	7	168	0	0	3	1	16	1	3	2	0	MI0000152	Mir125b-2
ENSMUST00000083539	ENSMUSG00000065473	X	623	1113	1194	3120	9275	11764	5246	12080	6199	1360	14	2	6794	291	201	261	63	MI0000546	Mir19b-2
ENSMUST00000083540	ENSMUSG00000065474	6	243	163	190	836	1227	947	502	800	30	36	5	0	325	41	21	93	8	MI0000166	Mir141
ENSMUST00000083541	ENSMUSG00000065475	13	38479	31533	24407	129195	188710	132716	74202	85441	884	4078	1277	31	15157	2051	1022	2208	948	MI0000142	Mir27b
ENSMUST00000083542	ENSMUSG00000065476	15	105	445	339	1288	26635	43696	18290	45392	303	170	51	2	9023	1153	566	955	159	MI0000145	Mir30b
ENSMUST00000083543	ENSMUSG00000065477	12	10	98	9	155	135	341	100	85	0	0	0	0	25	3	0	0	0	MI0001163	Mir411
ENSMUST00000083545	ENSMUSG00000065479	17	46	803	26	5337	314	7585	295	3673	0	16	11	5	143	281	54	196	75	MI0000151	Mir125a
ENSMUST00000083546	ENSMUSG00000065480	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000821	Mir133b
ENSMUST00000083547	ENSMUSG00000065481	14	0	0	0	0	2	0	0	0	0	1	0	0	0	0	2	2	0	MI0000634	Mir346
ENSMUST00000083548	ENSMUSG00000065482	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0003717	Mir302c
ENSMUST00000083549	ENSMUSG00000065483	8	2197	1665	1281	11653	8847	9984	4051	8658	129	506	43	0	1504	257	131	121	161	MI0000724	Mir181c
ENSMUST00000083550	ENSMUSG00000065484	2	124	1567	123	4721	473	4150	456	2472	15	11	3	4	927	341	27	41	122	MI0000156	Mir130a
ENSMUST00000083551	ENSMUSG00000065485	2	0	0	2	2	3	11	7	6	2	1	0	0	6	0	0	0	4	MI0000741	Mir219a-2
ENSMUST00000083552	ENSMUSG00000065486	X	0	2	0	2	12	19	9	17	12	0	0	0	14	0	0	0	0	MI0001653	Mir450-1
ENSMUST00000083554	ENSMUSG00000065488	15	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000553	Mir196a-2
ENSMUST00000083555	ENSMUSG00000065489	11	0	3	0	32	35	142	26	35	0	0	0	0	0	0	0	0	0	MI0001645	Mir365-2
ENSMUST00000083556	ENSMUSG00000065490	4	178	87	102	520	7196	7632	3766	4030	100	152	0	0	840	230	89	80	40	MI0000547	Mir30c-1
ENSMUST00000083557	ENSMUSG00000065491	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000730	Mir7b
ENSMUST00000083558	ENSMUSG00000065492	9	1	1	0	7	0	5	1	0	0	0	0	0	4	0	0	0	0	MI0000404	Mir34b
ENSMUST00000083559	ENSMUSG00000065493	4	17	14	22	131	32	97	28	64	18	19	2	0	56	3	5	8	1	MI0000584	Mir34a
ENSMUST00000083560	ENSMUSG00000065494	16	1150	701	743	2693	3497	4793	2626	2800	125	151	49	5	1393	263	93	455	57	MI0000690	Mir28a
ENSMUST00000083561	ENSMUSG00000065495	7	234	1680	240	5954	58720	103092	32731	112773	140	396	127	1	8170	3681	1387	6170	461	MI0000172	Mir150
ENSMUST00000083563	ENSMUSG00000065497	12	17	71	18	77	46	44	44	24	3	1	0	0	8	1	2	0	0	MI0001161	Mir410

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000083564	ENSMUSG00000065498	12	0	0	0	1	2	10	6	1	0	0	0	0	2	0	0	0	0	MI0000796	Mir379
ENSMUST00000083565	ENSMUSG00000065499	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0001146	Mir384
ENSMUST00000083566	ENSMUSG00000065500	2	32	765	10	1217	78	1845	51	590	11	44	5	0	77	1	3	66	4	MI0000221	Mir10b
ENSMUST00000083567	ENSMUSG00000065501	6	6	25	5	88	8	120	20	52	1	2	0	0	45	6	0	5	0	MI0000817	Mir335
ENSMUST00000083568	ENSMUSG00000065502	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000245	Mir202
ENSMUST00000083569	ENSMUSG00000065503	X	447	354	233	1778	31060	23640	26105	11019	254	344	236	11	1795	1334	379	1097	104	MI0000643	Mir351
ENSMUST00000083571	ENSMUSG00000065505	6	40070	60171	28037	125545	256378	135587	116607	142303	2385	5828	788	104	17485	2839	1837	4250	2635	MI0000550	Mir148a
ENSMUST00000083573	ENSMUSG00000065507	19	0	0	0	1	4	3	2	7	0	1	0	0	0	0	0	0	0	MI0000247	Mir204
ENSMUST00000083574	ENSMUSG00000065508	14	480	324	836	1533	8114	10015	7077	9369	329	174	11	0	4888	553	301	409	35	MI0000687	Mir17
ENSMUST00000083575	ENSMUSG00000065509	X	867	666	612	2980	4381	4178	4377	2813	23	46	5	0	319	140	86	184	158	MI0005496	Mir421
ENSMUST00000083576	ENSMUSG00000065510	X	1305	559	819	3237	7255	5220	6469	3765	192	212	86	1	3806	817	414	1743	237	MI0000761	Mir361
ENSMUST00000083577	ENSMUSG00000065511	2	182	91	90	301	483	263	413	245	61	69	66	3	496	142	80	166	14	MI0000585	Mir129-2
ENSMUST00000083578	ENSMUSG00000065512	8	0	2	0	5	17	12	6	5	0	0	0	0	3	0	2	4	0	MI0000164	Mir138-2
ENSMUST00000083579	ENSMUSG00000065513	9	942	162	680	4724	13471	9053	5860	10827	74	8	34	0	543	272	161	136	162	MI0000573	Mir26a-1
ENSMUST00000083580	ENSMUSG00000065514	5	1414	1696	1147	5101	11499	13915	6862	12511	217	362	144	3	3115	452	184	326	73	MI0000407	Mir106b
ENSMUST00000083581	ENSMUSG00000065515	11	5	71	12	131	57	246	42	109	3	0	0	0	51	11	7	11	1	MI0000174	Mir152
ENSMUST00000083582	ENSMUSG00000065516	1	0	5	1	13	1	19	1	1	0	0	0	0	0	0	0	0	0	MI0000698	Mir214
ENSMUST00000083584	ENSMUSG00000065518	11	5150	2431	2440	21280	91049	165998	80458	87775	402	739	642	167	6544	7144	2285	2901	2839	MI0004637	Mir423
ENSMUST00000083585	ENSMUSG00000065519	11	44543	17630	22608	98183	280326	78841	105514	86498	9936	12441	4880	116	41531	3957	3237	36374	2470	MI0000685	Mir10a
ENSMUST00000083586	ENSMUSG00000065520	1	481	771	311	5916	2187	6433	2979	6074	24	58	56	0	732	294	36	79	123	MI0000155	Mir128-1
ENSMUST00000083587	ENSMUSG00000065521	2	28	14	15	87	157	297	83	238	9	14	7	0	128	50	7	13	10	MI0000394	Mir296
ENSMUST00000083589	ENSMUSG00000065523	19	1219	29269	1568	5158	32746	21305	18058	18330	235	592	215	8	2748	389	249	999	137	MI0000551	Mir192
ENSMUST00000083590	ENSMUSG00000065524	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000715	Mir135a-2
ENSMUST00000083592	ENSMUSG00000065526	12	1	2	1	11	12	9	13	5	0	0	0	0	3	0	0	0	0	MI0000615	Mir337
ENSMUST00000083593	ENSMUSG00000065527	5	2281	4245	3109	11184	42718	38314	31471	35997	886	641	66	2	8559	1522	552	676	93	MI0000581	Mir93
ENSMUST00000083594	ENSMUSG00000065528	14	939	1324	411	5543	1855	4291	2864	1692	84	150	141	98	793	630	126	119	216	MI0000704	Mir320
ENSMUST00000083595	ENSMUSG00000065529	11	292200	188895	236133	883543	993419	1043010	623615	658021	8723	30572	37907	2902	127055	32830	14902	19203	30273	MI0000570	Mir22
ENSMUST00000083596	ENSMUSG00000065530	16	20	143	5	353	98	333	43	187	0	6	3	0	39	14	3	39	3	MI0000146	Mir99a
ENSMUST00000083598	ENSMUSG00000065532	18	0	7	0	7	3	18	1	5	0	0	0	0	8	0	0	0	0	MI0000229	Mir187
ENSMUST00000083599	ENSMUSG00000065533	1	0	23	0	43	0	282	0	35	0	2	0	2	1	4	0	0	2	MI0000248	Mir205
ENSMUST00000083600	ENSMUSG00000065534	11	70	64	60	264	618	636	268	343	13	48	16	0	338	100	38	38	12	MI0000595	Mir324
ENSMUST00000083602	ENSMUSG00000065536	X	1675	609	1126	3011	7710	1356	6692	2471	1534	758	10	0	6618	309	307	404	64	MI0000586	Mir98
ENSMUST00000083603	ENSMUSG00000065537	11	32	143	26	842	152	2340	76	644	0	8	8	0	45	14	16	36	17	MI0000158	Mir132
ENSMUST00000083604	ENSMUSG00000065538	12	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	MI0000175	Mir153
ENSMUST00000083605	ENSMUSG00000065539	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000699	Mir216a
ENSMUST00000083606	ENSMUSG00000065540	2	396	2689	353	1702	1652	2873	812	1136	18	21	3	0	269	35	7	57	12	MI0000153	Mir126a
ENSMUST00000083607	ENSMUSG00000065541	8	1688	821	1310	3583	21516	21754	10573	8402	195	227	262	5	4883	694	277	1872	79	MI0000572	Mir24-2
ENSMUST00000083608	ENSMUSG00000065542	X	0	9	0	45	3	25	0	10	0	0	0	0	2	0	1	0	0	MI0000711	Mir224
ENSMUST00000083609	ENSMUSG00000065543	7	132	55	98	282	5437	4922	2672	3050	85	141	32	2	426	212	65	87	16	MI0000607	Mir330
ENSMUST00000083610	ENSMUSG00000065544	4	125	65	53	454	151	333	134	384	28	13	0	0	138	16	4	6	8	MI0000691	Mir32
ENSMUST00000083612	ENSMUSG00000065546	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000552	Mir196a-1
ENSMUST00000083613	ENSMUSG00000065547	9	17	340	16	731	57	497	38	328	2	3	0	0	4	0	1	0	0	MI0000241	Mir199a-1
ENSMUST00000083614	ENSMUSG00000065548	1	637	348	732	3016	4115	6426	2908	6446	56	68	7	2	880	84	39	81	57	MI0000577	Mir29c
ENSMUST00000083615	ENSMUSG00000065549	4	41	19	21	131	108	365	171	302	0	5	0	1	53	13	5	25	1	MI0000243	Mir200b
ENSMUST00000083617	ENSMUSG00000065551	7	1131	605	491	1576	5148	5911	1402	1988	268	142	101	0	1126	186	25	32	23	MI0000695	Mir210
ENSMUST00000083618	ENSMUSG00000065552	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000402	Mir302a
ENSMUST00000083619	ENSMUSG00000065553	11	1972	3268	92	2507	6732	4038	3305	1255	355	95	0	1	1307	334	176	0	65	MI0000587	Mir103-1
ENSMUST00000083621	ENSMUSG00000065555	17	23	20	16	69	169	169	110	153	95	21	1	0	130	7	2	3	6	MI0000702	Mir219a-1
ENSMUST00000083622	ENSMUSG00000065556	19	1810	5563	1454	6899	4271	6050	1964	5549	233	227	1	0	1180	124	53	33	70	MI0000649	Mir101b
ENSMUST00000083623	ENSMUSG00000065557	16	8	22	7	93	92	167	69	190	0	0	0	0	89	7	12	4	0	MI0000559	Mirlet7c-1
ENSMUST00000083625	ENSMUSG00000065559	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000249	Mir206
ENSMUST00000083626	ENSMUSG00000065560	15	4023	2032	3386	12071	39789	28447	18508	23529	693	769	125	13	7124	1002	660	7926	320	MI0000617	Mir148b
ENSMUST00000083627	ENSMUSG00000065561	12	2	2	0	10	5	8	3	7	0	0	0	0	0	0	0	0	0	MI0003535	Mir369
ENSMUST00000083628	ENSMUSG00000065562	1	0	7	2	12	25	41	19	22	0	0	0	0	5	0	0	0	0	MI0000974	Mir215
ENSMUST00000083629	ENSMUSG00000065563	2	5917	3268	7568	15043	33264	33682	23138	29488	780	665	108	1	10720	1838	440	916	65	MI0000588	Mir103-2
ENSMUST00000083630	ENSMUSG00000065564	15	867	1064	405	4097	1451	2218	1498	1319	165	195	79	0	3479	974	283	699	71	MI0000558	Mirlet7b
ENSMUST00000083631	ENSMUSG00000065565	1	99	174	117	812	2737	3968	1512	2910	37	69	4	0	164	64	56	50	4	MI0000697	Mir181a-1
ENSMUST00000083632	ENSMUSG00000098838	12	12	48	7	49	33	42	11	10	0	1	0	0	0	0	1	0	0	MI0000798	Mir381
ENSMUST00000083633	ENSMUSG00000065567	1	22	606	148	1963	33192	65291	31018	66400	674	181	72	2	15482	3091	1028	2890	222	MI0000548	Mir30c-2
ENSMUST00000083634	ENSMUSG00000065568	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000630	Mir344
ENSMUST00000083635	ENSMUSG00000065569	3	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	MI0000163	Mir137
ENSMUST00000083636	ENSMUSG00000065570	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0001164	Mir412
ENSMUST00000083637	ENSMUSG00000065571	7	30	32	27	164	825	821	412	833	26	81	25	1	391	125	41	44	24	MI0000598	Mir326
ENSMUST00000083638	ENSMUSG00000065572	16	1144	733	902	3442	10342	9091	9425	7190	60	112	28	3	1742	464	187	331	98	MI0000408	Mir130b
ENSMUST00000083639	ENSMUSG00000065573	1	191	160	163	824	1551	1152	1035	948	25	76	8	2	410	101	68	83	32	MI0000640	Mir350
ENSMUST00000083640	ENSMUSG00000065574	12	10	76	10	110	148	320	91	417	3	7	0	0	107	12	9	20	4	MI0000246	Mir203
ENSMUST00000083641	ENSMUSG00000065575	13	7	9	7	67	19	36	5	16	0	7	0	0	6	0	0	0	0	MI0001649	Mir449a
ENSMUST00000083643	ENSMUSG00000065577	12	0	1	0	3	4	3	0	4	0	2	0	0	0	0	0	0	0	MI0000605	Mir329
ENSMUST00000083644	ENSMUSG00000065578	2	701	435	428	2749	6768	5755	4389	2903	239	283	97	0	1983	598	186	406	133	MI0000823	Mir181b-2
ENSMUST00000083645	ENSMUSG00000065579	9	1683	684	1210	6053	18198	14939	18758	11638	224	265	167	16	5887	1521	485	759	242	MI0001447	Mir425
ENSMUST00000083646	ENSMUSG00000065580	3	1059	737	901	5749	20625	12996	14742	14454	69	100	28	0	4764	770	387	1297	138	MI0000140	Mir15b
ENSMUST00000083647	ENSMUSG00000065581	1	172	784	80	620	963	1310	600	1210	0	0	0	0	0	16	16	84	6	MI0000236	Mir194-1
ENSMUST00000083648	ENSMUSG00000065582	19	68	173	102	230	1051	1033	533	831	35	23	4	0	781	71	20	80	15	MI0000733	Mir194-2
ENSMUST00000083649	ENSMUSG00000065583	11	1	3	0	0	3	23	0	6	1	0	0	0	2	0	0	0	0	MI0000701	Mir218-2
ENSMUST00000083651	ENSMUSG00000065585	7	1	6	2	10	31	34	8	29	0	0	0	0	20	8	1	12	3	MI0000708	Mir211
ENSMUST00000083652	ENSMUSG00000065586	6	2	4	2	27	7	46	6	19	5	0	0	0	0	0	0	0	0	MI0000583	Mir96
ENSMUST00000083653	ENSMUSG00000065587	9	1	18	2	79	6	38	0	17	0	0	0	0	7	0	0	0	0	MI0000403	Mir34c
ENSMUST00000083655	ENSMUSG00000065589	11	71	223	130	634	22325	22701	10135	18422	149	126	3	0	2779	367	190	273	16	MI0000401	Mir301
ENSMUST00000083656	ENSMUSG00000065590	11	3	21	0	130	29	960	24	304	2	1	2	0	11	1	4	39	0	MI0000696	Mir212
ENSMUST00000083658	ENSMUSG00000065592	18	0	51	1	8	2	58	0	6	0	0	0	0	1	0	0	0	0	MI0000169	Mir145a
ENSMUST00000083659	ENSMUSG00000065593	5	1309	946	1470	3523	6230	9731	4139	6407	80	196	402	5	762	301	99	155	85	MI0000621	Mir339
ENSMUST00000083660	ENSMUSG00000065594	19	84	75	87	295	983	898	555	775	12	25	9	0	246	53	25	24	6	MI0000684	Mir107
ENSMUST00000083662	ENSMUSG00000065596	9	1	4	3	45	4	12	3	8	0	0	0	4	5	8	0	0	0	MI0000226	Mir184
ENSMUST00000083663	ENSMUSG00000065597	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000716	Mir124a-1
ENSMUST00000083665	ENSMUSG00000065599	13	182	121	207	550	9739	3066	4534	2381	45	86	67	2	1547	426	218	660	73	MI0000141	Mir23b
ENSMUST00000083666	ENSMUSG00000065600	11	1007	283	734	3420	5501	6075	3105	5183	116	241	232	4	1147	119	57	135	117	MI0000619	Mir338
ENSMUST00000083667	ENSMUSG00000065601	11	4398	2888	5277	13950	358	1548	438	1097	572	5617	4578	116	2728	247	531	8975	397	MI0000170	Mir146
ENSMUST00000083668	ENSMUSG00000065602	X	12805	6560	6874	43848	73748	35883	50080	61154	3834	2068	81	2	30763	2635	1545	3238	823	MI0000563	Mirlet7f-2
ENSMUST00000083669	ENSMUSG00000065603	5	1	3	0	25	3	30	0	11	1	0	0	0	2	0	0	0	0	MI0000700	Mir218-1
ENSMUST00000083670	ENSMUSG00000065604	6	1	3	2	6	34	79	56	40	2	0	2	0	14	3	0	0	1	MI0000143	Mir29b-1
ENSMUST00000083672	ENSMUSG00000065606	3	3817	1763	2458	11490	18166	14855	12521	11761	245	387	169	0	5035	870	481	637	252	MI0000566	Mir16-2
ENSMUST00000083673	ENSMUSG00000065607	10	10	9	8	54	254	342	295	213	2	23	10	1	179	84	36	31	5	MI0000609	Mir331
ENSMUST00000083674	ENSMUSG00000065608	15	5416	8391	3240	37210	10229	8053	8115	5223	266	520	142	2	11610	1997	711	1524	340	MI0000560	Mirlet7c-2
ENSMUST00000083675	ENSMUSG00000065609	7	1	1	0	0	1	0	10	0	1	0	0	0	0	0	0	0	0	MI0000729	Mir7-2
ENSMUST00000083676	ENSMUSG00000065610	6	8378	4557	7366	37756	37571	48513	29325	48870	626	1404	192	3	15202	2034	744	1534	882	MI0000576	Mir29a
ENSMUST00000083677	ENSMUSG00000065611	8	1970	915	1789	6321	20919	11640	9736	10729	161	360	263	2	4854	998	495	1656	367	MI0000571	Mir23a
ENSMUST00000083678	ENSMUSG00000065612	15	603	2314	243	10865	5211	17494	2900	8300	113	160	175	18	2229	930	212	841	174	MI0000173	Mir151

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000083679	ENSMUSG00000065613	X	4066	3595	1097	14522	40303	26264	29488	20010	62	253	474	2	3061	2742	1179	3443	810	MI0000580	Mir92-2
ENSMUST00000083682	ENSMUSG00000065616	1	1	5	1	63	18	37	12	90	0	0	0	0	1	1	1	0	0	MI0000792	Mir375
ENSMUST00000083683	ENSMUSG00000065617	12	0	2	0	0	0	8	0	3	0	0	0	0	0	0	0	0	0	MI0000592	Mir323
ENSMUST00000083685	ENSMUSG00000065619	6	10	292	18	389	563	1963	247	657	16	12	1	0	53	4	9	189	1	MI0000225	Mir183
ENSMUST00000084675	ENSMUSG00000076118	2	8	9	7	61	13	23	12	23	9	1	1	0	93	17	7	19	0	MI0004673	Mir669c
ENSMUST00000093557	ENSMUSG00000070065	11	9507	16065	3169	41671	11340	21155	3401	7722	5527	11242	1058	8	33972	7195	1359	2841	1417	MI0001730	Mir451a
ENSMUST00000093560	ENSMUSG00000095782	X	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005500	Mir465c-1
ENSMUST00000093563	ENSMUSG00000070071	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0002400	Mir465
ENSMUST00000093564	ENSMUSG00000070072	12	1	2	1	2	3	13	4	5	0	0	0	0	0	0	0	0	0	MI0001525	Mir433
ENSMUST00000093565	ENSMUSG00000070073	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0002405	Mir470
ENSMUST00000093566	ENSMUSG00000070074	16	1313	1033	824	4521	24530	20690	15324	12232	44	173	192	33	2933	1713	673	2489	796	MI0003491	Mir484
ENSMUST00000093567	ENSMUSG00000070075	6	0	1	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	MI0005002	Mir490
ENSMUST00000093568	ENSMUSG00000070076	12	120	406	85	874	1429	1705	660	385	22	102	74	0	149	52	20	81	2	MI0000154	Mir127
ENSMUST00000093569	ENSMUSG00000070077	4	0	0	0	3	1	6	3	6	1	0	0	0	4	0	0	1	0	MI0004680	Mir491
ENSMUST00000093570	ENSMUSG00000070078	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0002398	Mir463
ENSMUST00000093572	ENSMUSG00000070080	12	4	1	0	3	19	37	15	10	0	0	0	0	0	0	0	0	0	MI0001524	Mir431
ENSMUST00000093573	ENSMUSG00000070081	X	9	12	4	34	49	81	37	31	4	1	0	0	32	8	1	5	0	MI0004706	Mir505
ENSMUST00000093576	ENSMUSG00000070084	8	106685	634154	23128	469419	64523	166477	32083	40157	43874	45171	52288	2180	21057	22198	3443	34670	17372	MI0003493	Mir486
ENSMUST00000093591	ENSMUSG00000070099	2	0	0	0	4	60	93	100	195	0	1	0	0	6	23	8	14	3	MI0002401	Mir466
ENSMUST00000093592	ENSMUSG00000070100	X	255	79	221	342	361	403	192	438	49	27	12	0	242	20	12	39	1	MI0000763	Mir362
ENSMUST00000093593	ENSMUSG00000070101	12	3	10	2	9	13	21	5	3	0	0	2	0	0	0	0	0	0	MI0000625	Mir341
ENSMUST00000093594	ENSMUSG00000070102	4	0	10	0	1	5	52	30	47	0	0	0	0	7	3	1	3	0	MI0004679	Mir455
ENSMUST00000093595	ENSMUSG00000070103	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004633	Mir488
ENSMUST00000093596	ENSMUSG00000070104	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0002406	Mir471
ENSMUST00000093597	ENSMUSG00000070105	12	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	MI0004639	Mir495
ENSMUST00000093598	ENSMUSG00000070106	X	200	71	98	374	1032	711	647	543	5	14	3	0	194	33	18	55	19	MI0000765	Mir363
ENSMUST00000093599	ENSMUSG00000070107	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0003476	Mir489
ENSMUST00000093600	ENSMUSG00000070108	X	49	5	27	104	242	243	178	179	33	22	1	0	109	27	5	7	2	MI0004702	Mir500
ENSMUST00000093601	ENSMUSG00000070109	11	2	23	2	88	1	147	0	59	0	0	0	0	1	2	0	0	0	MI0026030	Mir497b
ENSMUST00000093602	ENSMUSG00000070110	X	0	0	0	0	0	4	1	8	0	0	0	0	4	0	0	1	0	MI0005515	Mir504
ENSMUST00000093618	ENSMUSG00000070126	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	MI0000713	Mir199a-2
ENSMUST00000093619	ENSMUSG00000070127	19	48573	19857	58365	56236	485163	153510	197518	66258	89437	42341	18703	445	165764	19336	6776	101706	3731	MI0004665	Mir146b
ENSMUST00000093620	ENSMUSG00000070128	12	0	4	0	3	4	4	5	2	0	0	0	0	0	0	0	0	0	MI0003492	Mir485
ENSMUST00000093621	ENSMUSG00000070129	12	9	12	7	72	34	78	17	34	0	1	0	0	3	2	0	0	0	MI0014034	Mir136
ENSMUST00000093622	ENSMUSG00000070130	8	302	481	189	2702	6939	13632	3734	5422	181	336	451	12	837	838	143	221	732	MI0000603	Mir328
ENSMUST00000093625	ENSMUSG00000070133	12	26	85	23	186	97	231	78	59	2	4	0	0	4	0	2	2	0	MI0001526	Mir434
ENSMUST00000093626	ENSMUSG00000096500	7	0	0	0	0	3	5	0	0	0	0	0	0	0	1	0	1	5		Gm23087
ENSMUST00000093627	ENSMUSG00000070136	12	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004589	Mir496a
ENSMUST00000093629	ENSMUSG00000070138	X	0	0	0	2	0	1	0	2	0	0	0	0	0	0	0	0	0	MI0001734	Mir452
ENSMUST00000093630	ENSMUSG00000070139	X	1306	1736	1349	4227	8283	7287	5789	4612	126	159	28	0	1576	298	140	248	51	MI0003206	Mir532
ENSMUST00000093631	ENSMUSG00000070140	7	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	MI0003484	Mir483
ENSMUST00000093632	ENSMUSG00000070141	12	0	1	0	0	7	2	3	1	0	0	0	0	1	0	0	0	0	MI0003532	Mir494
ENSMUST00000093635	ENSMUSG00000070144	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000139	Mir1a-1
ENSMUST00000101027	ENSMUSG00000077844	16	17	0	5	24	11	5	4	5	27	12	26	2	6	11	7	6	2		Gm22231
ENSMUST00000102051	ENSMUSG00000076005	X	0	2	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	MI0003523	Mir547
ENSMUST00000102052	ENSMUSG00000076006	12	1	1	1	2	1	7	0	3	0	0	0	0	0	0	0	0	0	MI0003533	Mir376b
ENSMUST00000102055	ENSMUSG00000076009	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004653	Mir688
ENSMUST00000102056	ENSMUSG00000076010	15	0	3	0	0	7	16	0	3	0	0	0	0	1	0	0	1	1	MI0005004	Mir615
ENSMUST00000102057	ENSMUSG00000076011	X	3279	1822	2270	6139	18761	6287	14942	4024	648	475	185	9	5580	1702	504	787	269	MI0004965	Mir652
ENSMUST00000102058	ENSMUSG00000076012	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	MI0004689	Mir705
ENSMUST00000102060	ENSMUSG00000076014	2	0	2	0	3	12	11	13	20	0	1	0	0	28	7	2	1	0	MI0004667	Mir669a-2
ENSMUST00000102074	ENSMUSG00000076028	2	0	0	0	5	5	0	0	6	0	0	0	0	4	0	0	2	0	MI0004668	Mir669a-3
ENSMUST00000102075	ENSMUSG00000096567	15	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24098
ENSMUST00000102076	ENSMUSG00000076030	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22750
ENSMUST00000102077	ENSMUSG00000076031	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22751
ENSMUST00000102078	ENSMUSG00000095297	15	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25381
ENSMUST00000102079	ENSMUSG00000076033	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004661	Mir692-3
ENSMUST00000102081	ENSMUSG00000094403	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004661	Mir692-2
ENSMUST00000102082	ENSMUSG00000076036	7	11	7	10	37	20	14	12	2	42	155	4	0	10	5	96	138	27		Gm22133
ENSMUST00000102083	ENSMUSG00000076037	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22752
ENSMUST00000102084	ENSMUSG00000076038	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22774
ENSMUST00000102085	ENSMUSG00000076039	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22137
ENSMUST00000102087	ENSMUSG00000076041	X	20	7	10	56	217	201	187	190	16	13	0	0	205	33	9	20	1	MI0003536	Mir20b
ENSMUST00000102088	ENSMUSG00000076042	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004694	Mir710
ENSMUST00000102089	ENSMUSG00000095509	2	0	6	6	38	0	0	0	0	0	2	0	0	0	0	0	0	4	MI0004671	Mir467b
ENSMUST00000102094	ENSMUSG00000076049	14	0	2	0	2	0	1	0	1	0	0	0	0	1	0	0	0	0	MI0005556	Mir598
ENSMUST00000102095	ENSMUSG00000076050	X	819	276	667	2410	6639	3950	2684	4274	102	122	8	2	1189	102	66	73	30	MI0004705	Mir450b
ENSMUST00000102096	ENSMUSG00000076051	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004691	Mir707
ENSMUST00000102097	ENSMUSG00000076052	12	5	31	1	22	281	331	178	58	14	1	1	0	27	15	0	9	0	MI0003521	Mir541
ENSMUST00000102099	ENSMUSG00000094933	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004646	Mir683-2
ENSMUST00000102105	ENSMUSG00000072837	10	0	0	0	0	0	0	1	1	1	0	0	0	0	0	1	0	4	MI0003517	Mir546
ENSMUST00000102106	ENSMUSG00000076060	6	6	0	2	6	10	12	17	13	0	0	0	0	3	3	2	1	0	MI0004688	Mir704
ENSMUST00000102108	ENSMUSG00000076062	14	38874	43042	21655	157863	717782	480684	496640	379241	4261	7759	5354	72	77975	49594	18057	37270	6048	MI0000719	Mir92-1
ENSMUST00000102109	ENSMUSG00000076063	12	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	MI0003520	Mir539
ENSMUST00000102110	ENSMUSG00000076064	16	3	0	0	10	2	0	0	0	0	0	0	0	0	0	3	7	0	MI0004658	Mir690
ENSMUST00000102111	ENSMUSG00000076065	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004643	Mir681
ENSMUST00000102112	ENSMUSG00000076066	X	44694	17871	38468	160306	402460	332977	239979	410696	5462	6532	1026	75	57874	10864	9092	17860	4387	MI0000703	Mir223
ENSMUST00000102113	ENSMUSG00000076067	6	3	56	2	29	0	2	1	9	0	0	0	0	0	4	0	0	0	MI0004127	Mir592
ENSMUST00000102114	ENSMUSG00000076068	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004635	Mir678
ENSMUST00000102163	ENSMUSG00000076117	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004641	Mir680-2
ENSMUST00000102164	ENSMUSG00000076119	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004682	Mir698
ENSMUST00000102165	ENSMUSG00000076120	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004131	Mir551b
ENSMUST00000102166	ENSMUSG00000076121	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	MI0004652	Mir687
ENSMUST00000102167	ENSMUSG00000072900	12	6	7	2	9	14	29	9	2	0	0	5	0	2	0	2	0	0	MI0003518	Mir540
ENSMUST00000102168	ENSMUSG00000076122	X	14	9	16	65	349	263	225	223	13	16	1	0	162	14	11	39	5	MI0003538	Mir503
ENSMUST00000102169	ENSMUSG00000076123	4	13	5	2	22	127	97	180	98	2	4	4	0	57	19	9	31	0	MI0004684	Mir700
ENSMUST00000102172	ENSMUSG00000076126	2	0	2	0	0	5	33	0	19	0	0	0	0	30	3	0	4	0	MI0004666	Mir669b
ENSMUST00000102173	ENSMUSG00000076127	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004707	Mir718
ENSMUST00000102174	ENSMUSG00000076128	14	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	1	0	MI0004650	Mir686
ENSMUST00000102175	ENSMUSG00000076129	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22920
ENSMUST00000102181	ENSMUSG00000076135	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24276
ENSMUST00000102182	ENSMUSG00000076136	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24951
ENSMUST00000102183	ENSMUSG00000076137	17	0	0	0	0	3	0	0	0	0	0	0	0	0	0	4	0	0		Gm26384
ENSMUST00000102184	ENSMUSG00000076138	9	3	0	2	5	21	4	39	12	36	8	1	0	17	7	23	18	29		Gm26377
ENSMUST00000102186	ENSMUSG00000076140	X	496	186	437	1254	1366	1067	760	1127	131	66	9	4	874	58	28	38	27	MI0003522	Mir542
ENSMUST00000102187	ENSMUSG00000076141	17	3	1	1	6	13	8	6	6	1	0	2	0	1	0	0	0	0	MI0004662	Mir693
ENSMUST00000102188	ENSMUSG00000076142	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004695	Mir711

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ENSMUST00000102189	ENSMUSG00000076143	7	1	3	0	2	1	10	0	3	0	0	0	0	0	0	0	0	1	MI0004692	Mir708
ENSMUST00000102190	ENSMUSG00000076144	8	312	221	91	801	177	298	278	262	10946	1890	1040	78	3882	5502	2594	3928	937	MI0004693	Mir709
ENSMUST00000102191	ENSMUSG00000076145	12	1	1	0	1	3	0	2	0	0	0	0	0	0	0	1	0	0	MI0004638	Mir679
ENSMUST00000102192	ENSMUSG00000076146	13	1	0	0	9	9	24	1	6	0	0	0	0	0	0	0	0	0	MI0004645	Mir449c
ENSMUST00000102193	ENSMUSG00000076147	18	0	0	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0	MI0004664	Mir694
ENSMUST00000102205	ENSMUSG00000093907	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014053	Gm25022
ENSMUST00000102207	ENSMUSG00000096624	2	15	6	6	38	185	449	229	343	4	2	0	0	165	24	14	51	0	MI0002402	Mir467a-1
ENSMUST00000102208	ENSMUSG00000076163	5	1	0	0	4	2	3	0	4	0	0	0	0	3	0	0	0	0	MI0004685	Mir701
ENSMUST00000102225	ENSMUSG00000076180	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24938
ENSMUST00000102235	ENSMUSG00000076190	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23256
ENSMUST00000102244	ENSMUSG00000076199	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23255
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ENSMUST00000102257	ENSMUSG00000076212	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004640	Mir680-1
ENSMUST00000102259	ENSMUSG00000076214	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004704	Mir717
ENSMUST00000102261	ENSMUSG00000076216	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004675	Mir695
ENSMUST00000102262	ENSMUSG00000076217	6	10	4	4	7	1	3	11	2	61	29	17	0	11	23	35	114	21	MI0004690	Mir706
ENSMUST00000102263	ENSMUSG00000076218	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004660	Mir692-1
ENSMUST00000102265	ENSMUSG00000076219	12	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	MI0003534	Mir487b
ENSMUST00000102268	ENSMUSG00000076222	2	0	2	1	0	15	13	5	33	0	0	0	0	7	3	0	0	0	MI0004674	Mir297b
ENSMUST00000102272	ENSMUSG00000076227	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25593
ENSMUST00000102273	ENSMUSG00000076228	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25595
ENSMUST00000102274	ENSMUSG00000076229	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25594
ENSMUST00000102275	ENSMUSG00000076230	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22758
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ENSMUST00000102278	ENSMUSG00000076233	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22761
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ENSMUST00000102281	ENSMUSG00000076236	13	8	2	0	2	3	3	8	4	34	19	8	0	3	1	45	41	8	MI0004644	Mir682
ENSMUST00000102282	ENSMUSG00000076237	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26300
ENSMUST00000102283	ENSMUSG00000076238	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22582
ENSMUST00000102285	ENSMUSG00000076240	5	10	5	5	19	323	169	273	289	24	7	5	0	86	54	10	34	12	MI0004686	Mir702
ENSMUST00000102286	ENSMUSG00000076241	12	0	6	0	0	1	6	3	0	0	0	0	0	0	0	0	0	0	MI0003519	Mir543
ENSMUST00000102291	ENSMUSG00000076246	13	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		Gm22256
ENSMUST00000102295	ENSMUSG00000096212	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23739
ENSMUST00000102296	ENSMUSG00000076251	X	1544	728	455	2045	658	555	477	226	86	43	41	4	585	82	81	544	60	MI0004703	Mir501
ENSMUST00000102297	ENSMUSG00000076252	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0003716	Mir302b
ENSMUST00000102298	ENSMUSG00000076253	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004642	Mir680-3
ENSMUST00000102300	ENSMUSG00000076255	3	162	138	83	511	3252	3250	3154	1860	11	26	21	0	203	153	54	124	35	MI0005521	Mir92b
ENSMUST00000102301	ENSMUSG00000076256	14	0	0	2	0	47	34	23	15	8	6	0	0	12	0	2	0	0	MI0000718	Mir19b-1
ENSMUST00000102303	ENSMUSG00000076258	16	1048	1123	798	4411	128	285	186	244	1328	14781	19391	20158	316	800	22346	1491	258374		Gm23935
ENSMUST00000102314	ENSMUSG00000076269	X	955	165	684	844	645	562	846	705	86	129	20	0	2506	272	141	351	36	MI0004125	Mir374b
ENSMUST00000102315	ENSMUSG00000076270	14	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	3	1	MI0004651	Mir719
ENSMUST00000102316	ENSMUSG00000076271	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	MI0004681	Mir697
ENSMUST00000102317	ENSMUSG00000076272	12	0	3	0	6	0	19	1	0	0	0	0	0	0	0	0	0	0	MI0004553	Mir666
ENSMUST00000102319	ENSMUSG00000076274	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25083
ENSMUST00000102320	ENSMUSG00000076275	7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	MI0004123	Mir675
ENSMUST00000102326	ENSMUSG00000076281	9	1048	1123	798	4411	128	285	186	244	1328	14781	19391	20158	316	800	22346	1491	258374		Gm24270
ENSMUST00000102327	ENSMUSG00000076282	10	26	14	22	72	17	17	23	13	10	6	14	0	3	5	7	6	10		Gm24271
ENSMUST00000102329	ENSMUSG00000076284	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24272
ENSMUST00000102331	ENSMUSG00000076286	X	2	1	3	10	1	4	7	6	2	0	0	0	2	0	0	0	0	MI0004258	Mir672
ENSMUST00000102332	ENSMUSG00000076287	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24273
ENSMUST00000102333	ENSMUSG00000076288	16	2	19	11	27	1530	1329	797	919	7	19	1	0	169	14	9	23	0	MI0004122	Mir301b
ENSMUST00000102339	ENSMUSG00000076294	4	34	9	30	115	7	9	7	7	45	27	14	0	4	7	34	21	13		Gm26154
ENSMUST00000102345	ENSMUSG00000076300	19	5	8	27	27	6	19	12	6	0	7	0	0	2	2	34	27	2		Gm23060
ENSMUST00000102348	ENSMUSG00000076303	19	0	0	1	2	0	0	0	0	0	1	5	0	0	2	1	4	0		Gm23061
ENSMUST00000102349	ENSMUSG00000076304	16	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0		Gm23062
ENSMUST00000102350	ENSMUSG00000076305	19	4	2	0	5	3	0	2	0	3	1	5	0	0	0	1	0	0		Gm23063
ENSMUST00000102354	ENSMUSG00000076309	2	1901	724	2027	3670	17422	14934	7995	9657	441	529	35	3	3158	325	162	232	70	MI0005482	Mir147
ENSMUST00000102357	ENSMUSG00000076312	2	1	0	1	9	1	3	0	1	0	0	0	0	0	0	0	0	0	MI0004676	Mir499
ENSMUST00000102358	ENSMUSG00000076313	12	0	1	0	0	4	6	1	1	0	0	0	0	0	0	0	0	0	MI0004171	Mir665
ENSMUST00000102360	ENSMUSG00000076315	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005494	Mir343
ENSMUST00000102361	ENSMUSG00000076316	12	1	4	0	6	8	12	10	12	0	0	0	0	0	0	0	0	0	MI0004601	Mir673
ENSMUST00000102363	ENSMUSG00000076318	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004126	Mir216b
ENSMUST00000102365	ENSMUSG00000076320	5	0	0	0	0	37	4	47	16	26	129	0	18	110	20	144	250	34		Gm26340
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ENSMUST00000102380	ENSMUSG00000076335	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	MI0004295	Mir670
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ENSMUST00000102383	ENSMUSG00000076338	8	550	586	242	3844	1826	2333	1313	1713	102	151	17	0	732	136	57	112	58	MI0005450	Mir181d
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ENSMUST00000102400	ENSMUSG00000076355	9	397	269	431	1483	496	701	439	257	0	154	40	7	286	577	3574	3732	821		Gm27509
ENSMUST00000102402	ENSMUSG00000076357	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005557	Mir653
ENSMUST00000102405	ENSMUSG00000076360	16	9	10	0	12	19	45	26	11	63	14	21	1	10	11	4	6	9		Gm24047
ENSMUST00000102406	ENSMUSG00000076361	6	28	188	24	935	2786	9985	1708	3851	29	19	3	2	109	30	24	63	8	MI0000224	Mir182
ENSMUST00000102409	ENSMUSG00000076364	2	0	6	0	4	7	12	10	5	4	2	9	0	3	0	11	10	11		Gm24049
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ENSMUST00000102415	ENSMUSG00000076370	19	45	23	55	154	17	76	3	0	60	33	0	0	21	117	113	49	8		Gm22369
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ENSMUST00000102417	ENSMUSG00000076372	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005517	Mir568
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ENSMUST00000102422	ENSMUSG00000076377	10	16	10	3	12	0	6	3	2	6	2	2	0	1	2	6	0	0		Gm22370
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ENSMUST00000102427	ENSMUSG00000076382	8	7	4	16	19	0	8	2	2	8	7	6	0	3	0	5	3	0		Gm23193
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ENSMUST00000102432	ENSMUSG00000076387	5	53	74	29	142	1134	1263	757	807	32	11	16	1	106	54	7	28	19	MI0004133	Mir671
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ENSMUST00000102437	ENSMUSG00000076392	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0		Gm25992
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ENSMUST00000102441	ENSMUSG00000076396	12	0	1	0	0	4	12	5	6	0	0	0	0	0	0	0	0	1	MI0004196	Mir667
ENSMUST00000102443	ENSMUSG00000076398	X	105	134	37	413	168	287	157	149	8	23	10	2	56	25	2	7	5	MI0005003	Mir676
ENSMUST00000102444	ENSMUSG00000076399	X	312	49	127	748	2087	1253	1044	1589	15	31	5	0	843	87	56	89	16	MI0003537	Mir450-2
ENSMUST00000102452	ENSMUSG00000076407	13	1	0	1	0	1	2	0	0	1	0	0	0	0	0	0	0	0		Gm22689
ENSMUST00000102469	ENSMUSG00000076424	16	1	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0		Gm25986
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ENSMUST00000103246	ENSMUSG00000076445	7	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0		Gm24865
ENSMUST00000103249	ENSMUSG00000076448	10	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004516	Mir763
ENSMUST00000103251	ENSMUSG00000076450	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005203	Mir804
ENSMUST00000103252	ENSMUSG00000076451	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004203	Mir770
ENSMUST00000103254	ENSMUSG00000076453	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004554	Mir759
ENSMUST00000103255	ENSMUSG00000076454	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	MI0004215	Mir762
ENSMUST00000103256	ENSMUSG00000076455	X	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	MI0012530	Mir767
ENSMUST00000103257	ENSMUSG00000076456	3	0	0	0	3	3	2	1	3	0	0	0	0	1	0	2	0	0	MI0004605	Mir760
ENSMUST00000103258	ENSMUSG00000076457	16	0	70	0	0	0	26	0	1	0	0	0	0	0	0	0	0	0	MI0004249	Mir802
ENSMUST00000103259	ENSMUSG00000076458	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	MI0004310	Mir764
ENSMUST00000103260	ENSMUSG00000076459	12	0	0	0	0	1	1	5	0	0	0	0	0	0	0	0	0	0	MI0004129	Mir758
ENSMUST00000103261	ENSMUSG00000076460	11	195	507	335	1806	18455	56390	38486	42571	67	91	47	2	1506	1717	512	547	108	MI0004124	Mir744
ENSMUST00000103753	ENSMUSG00000076941	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22065
ENSMUST00000103756	ENSMUSG00000076944	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22064
ENSMUST00000103758	ENSMUSG00000076946	13	1581	1159	1445	3565	5024	2837	4599	3653	235	221	68	28	1254	192	129	203	183	MI0006127	Mir582
ENSMUST00000103760	ENSMUSG00000076948	2	4	3	2	24	30	98	22	125	2	1	0	0	32	2	0	15	8	MI0006128	Mir467e
ENSMUST00000103761	ENSMUSG00000076949	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22066
ENSMUST00000103762	ENSMUSG00000076950	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24933
ENSMUST00000103763	ENSMUSG00000076951	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24932
ENSMUST00000103764	ENSMUSG00000076952	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24934
ENSMUST00000103768	ENSMUSG00000076956	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005488	Mir297a-3
ENSMUST00000103770	ENSMUSG00000076958	13	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		Gm24935
ENSMUST00000103771	ENSMUSG00000076959	2	2	0	2	5	7	25	5	20	0	0	0	0	15	1	0	0	1	MI0009942	Mir669l
ENSMUST00000103773	ENSMUSG00000076961	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23251
ENSMUST00000103776	ENSMUSG00000076964	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23252
ENSMUST00000103778	ENSMUSG00000076966	2	0	0	0	0	21	96	33	83	0	0	0	0	0	0	0	0	0	MI0005503	Mir466b-2
ENSMUST00000103784	ENSMUSG00000076972	16	1	14	2	116	20	23	4	24	0	2	3	0	5	4	1	3	4	MI0005484	Mir193b
ENSMUST00000103788	ENSMUSG00000076976	2	0	0	0	0	5	18	0	13	0	0	1	0	4	0	1	0	3	MI0005492	Mir297c
ENSMUST00000103789	ENSMUSG00000076977	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26067
ENSMUST00000103791	ENSMUSG00000096053	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005502	Gm25943
ENSMUST00000103795	ENSMUSG00000076983	2	2	0	0	5	0	9	4	3	0	0	0	0	0	0	0	0	0	MI0000397	Mir297a-2
ENSMUST00000103799	ENSMUSG00000076987	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24115
ENSMUST00000103800	ENSMUSG00000094316	7	0	0	0	0	3	5	0	0	0	0	0	0	0	1	0	0	0	MI0000395	Mir297-1
ENSMUST00000103804	ENSMUSG00000096360	2	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	MI0005502	Mir466b-7
ENSMUST00000103806	ENSMUSG00000076994	2	0	0	0	3	20	59	0	9	0	0	0	0	13	0	0	8	0	MI0005504	Mir466b-3
ENSMUST00000103807	ENSMUSG00000096441	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26140
ENSMUST00000103811	ENSMUSG00000076999	1	2	1	2	3	18	7	1	0	7	13	2	0	0	0	3	1	3		Gm22426
ENSMUST00000103813	ENSMUSG00000077001	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005555	Mir544
ENSMUST00000103816	ENSMUSG00000077004	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23876
ENSMUST00000103822	ENSMUSG00000077010	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22189
ENSMUST00000103823	ENSMUSG00000095529	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23612
ENSMUST00000103827	ENSMUSG00000077015	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22190
ENSMUST00000103831	ENSMUSG00000077019	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22191
ENSMUST00000103832	ENSMUSG00000094077	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22323
ENSMUST00000103833	ENSMUSG00000077021	2	11	4	6	94	134	441	118	348	0	2	1	0	23	11	10	10	1	MI0005513	Mir467d
ENSMUST00000103834	ENSMUSG00000077022	7	4	0	0	2	0	0	0	0	0	1	5	0	1	2	1	4	0		Gm22707
ENSMUST00000103837	ENSMUSG00000077025	12	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	MI0005514	Mir493
ENSMUST00000103842	ENSMUSG00000096298	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23931
ENSMUST00000103846	ENSMUSG00000095539	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25287
ENSMUST00000103849	ENSMUSG00000096411	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24721
ENSMUST00000103850	ENSMUSG00000077038	2	0	2	0	0	5	17	5	14	1	0	2	0	18	1	1	9	0	MI0006287	Mir669f
ENSMUST00000103851	ENSMUSG00000077039	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25537
ENSMUST00000103852	ENSMUSG00000077040	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26209
ENSMUST00000103854	ENSMUSG00000077042	5	254	145	249	548	1428	1055	1737	1322	151	127	29	0	548	147	58	91	18	MI0005518	Mir574
ENSMUST00000103855	ENSMUSG00000096586	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22918
ENSMUST00000103861	ENSMUSG00000077049	2	19	6	6	39	103	193	85	151	0	2	0	0	37	8	7	5	3	MI0005512	Mir467c
ENSMUST00000103862	ENSMUSG00000077050	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24544
ENSMUST00000103867	ENSMUSG00000077055	19	0	0	0	3	0	0	0	0	0	0	0	0	0	2	2	0	0		Gm24543
ENSMUST00000103868	ENSMUSG00000093900	2	0	0	2	0	15	9	0	2	8	0	0	0	0	2	0	0	0	MI0014064	Mir669p-2
ENSMUST00000103869	ENSMUSG00000099228	Y	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm28018
ENSMUST00000103870	ENSMUSG00000077058	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24542
ENSMUST00000103871	ENSMUSG00000077059	7	2	5	1	8	9	4	10	6	17	12	20	0	2	9	13	11	2		Gm24541
ENSMUST00000103877	ENSMUSG00000077065	11	0	2	0	0	0	0	3	0	0	2	1	0	12	0	0	0	0		Gm25040
ENSMUST00000103883	ENSMUSG00000095269	2	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	MI0005506	Mir466b-8
ENSMUST00000103884	ENSMUSG00000096134	2	0	0	2	0	15	9	0	2	8	0	0	0	0	2	0	0	0	MI0014064	Mir669p-1
ENSMUST00000103887	ENSMUSG00000093970	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23358
ENSMUST00000103889	ENSMUSG00000095604	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23424
ENSMUST00000103893	ENSMUSG00000077081	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23701
ENSMUST00000103894	ENSMUSG00000077082	10	0	36	0	0	0	0	88	72	16	0	21	0	0	0	122	0	0		Gm23766
ENSMUST00000103895	ENSMUSG00000094381	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25068
ENSMUST00000103897	ENSMUSG00000077085	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23697
ENSMUST00000103898	ENSMUSG00000077086	2	6	0	0	22	8	10	15	14	0	4	0	0	35	6	5	0	5	MI0009945	Mir669o
ENSMUST00000103900	ENSMUSG00000096113	2	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	MI0005502	Mir466b-5
ENSMUST00000103902	ENSMUSG00000077090	10	0	0	0	0	1	0	0	0	0	2	2	0	1	0	0	0	0		Gm22117
ENSMUST00000103904	ENSMUSG00000077092	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005206	Mir742
ENSMUST00000103905	ENSMUSG00000096560	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24096
ENSMUST00000103907	ENSMUSG00000077095	2	0	1	0	4	0	0	1	1	4	4	0	0	0	0	1	0	2		Gm24342
ENSMUST00000103908	ENSMUSG00000077096	12	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	2		Gm22015
ENSMUST00000103916	ENSMUSG00000077104	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25263
ENSMUST00000103919	ENSMUSG00000077107	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014096	Mir344c
ENSMUST00000103922	ENSMUSG00000077110	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22427
ENSMUST00000103923	ENSMUSG00000077111	X	5	4	7	15	129	81	100	47	3	3	0	0	69	5	10	11	1	MI0005483	Mir18b
ENSMUST00000103925	ENSMUSG00000077113	2	0	0	0	0	0	13	12	8	0	0	0	0	0	0	0	0	0	MI0014078	Mir466p
ENSMUST00000103931	ENSMUSG00000077119	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005205	Mir741
ENSMUST00000103937	ENSMUSG00000077125	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26399
ENSMUST00000103939	ENSMUSG00000077127	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005207	Mir743
ENSMUST00000103940	ENSMUSG00000094894	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005498	Mir465b-1
ENSMUST00000103943	ENSMUSG00000077131	2	0	0	3	0	0	0	0	0	0	0	0	0	9	0	0	0	1		Gm23578
ENSMUST00000103950	ENSMUSG00000077138	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23577
ENSMUST00000104232	ENSMUSG00000077420	3	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0		Gm24282
ENSMUST00000104625	ENSMUSG00000095146	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24387
ENSMUST00000104627	ENSMUSG00000077815	7	2	0	3	8	29	30	28	22	0	0	0	0	10	0	2	5	0	MI0000388	Mir290a
ENSMUST00000104632	ENSMUSG00000077821	9	1	0	0	0	0	0	0	0	1	0	0	0	6	2	0	2	0		Gm27450
ENSMUST00000104639	ENSMUSG00000077829	3	27	6	8	23	0	1	8	3	79	18	55	0	20	14	12	18	4		Gm23237
ENSMUST00000104640	ENSMUSG00000077830	12	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0		Gm26050
ENSMUST00000104642	ENSMUSG00000077832	5	1	0	0	1	0	0	0	0	5	4	4	0	0	0	2	0	0		Gm26051

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpgl0673	hpgl0674	hpgl0675	hpgl0676	hpgl0677	hpgl0678	hpgl0679	hpgl0680	hpgl0523	hpgl0524	hpgl0525	hpgl0555	hpgl0556	hpgl0557	hpgl0558	hpgl0559	hpgl0560	mirBase_accession	mirBase name
ENSMUST00000104644	ENSMUSG00000077834	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0006281	Mir669d
ENSMUST00000104646	ENSMUSG00000077836	11	2	1	0	0	2	0	1	0	1	1	1	0	6	2	8	0	0		Gm26052
ENSMUST00000104654	ENSMUSG00000077846	1	0	0	0	2	0	0	0	0	1	0	0	0	1	0	0	0	0		Gm22232
ENSMUST00000104655	ENSMUSG00000077847	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005481	Mir105
ENSMUST00000104659	ENSMUSG00000077851	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005480	Mir876
ENSMUST00000104662	ENSMUSG00000096504	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005498	Mir465b-2
ENSMUST00000104666	ENSMUSG00000077858	X	8	4	3	17	3	1	0	1	19	4	26	0	8	13	4	2	5		Gm25063
ENSMUST00000104677	ENSMUSG00000077869	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014094	Mir344e
ENSMUST00000104680	ENSMUSG00000077872	X	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005548	Mir878
ENSMUST00000104685	ENSMUSG00000096079	6	6	0	1	1	1	0	1	0	13	0	6	0	1	0	1	2	0		Gm23961
ENSMUST00000104687	ENSMUSG00000077879	12	0	0	0	0	1	3	0	0	2	0	0	0	0	1	0	0	0		Gm23912
ENSMUST00000104689	ENSMUSG00000077881	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005475	Mir882
ENSMUST00000104692	ENSMUSG00000077884	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0		Gm24557
ENSMUST00000104694	ENSMUSG00000077886	7	2	0	1	5	6	18	3	10	0	1	0	0	8	0	0	0	1	MI0000393	Mir295
ENSMUST00000104698	ENSMUSG00000077890	15	0	0	0	1	0	3	0	3	0	0	0	0	0	0	0	0	0	MI0005551	Mir875
ENSMUST00000104700	ENSMUSG00000077892	3	1	0	0	0	0	0	0	0	0	0	0	3	0	0	1	0	1		Gm22901
ENSMUST00000104703	ENSMUSG00000077896	5	11	10	5	75	37	128	17	105	0	3	0	1	7	1	0	0	0	MI0005472	Mir879
ENSMUST00000104704	ENSMUSG00000077897	2	0	9	1	16	17	670	12	182	0	0	0	0	6	0	0	0	0	MI0005554	Mir511
ENSMUST00000104709	ENSMUSG00000077902	7	2	0	0	0	0	0	0	1	12	0	19	0	4	5	9	3	0		Gm25787
ENSMUST00000104710	ENSMUSG00000077903	7	0	0	0	2	0	0	0	1	0	0	0	0	0	1	0	0	0	MI0000392	Mir294
ENSMUST00000104728	ENSMUSG00000077921	4	121	215	213	781	2857	2603	2094	1933	21	19	3	0	500	61	33	56	11	MI0005549	Mir872
ENSMUST00000104732	ENSMUSG00000077925	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005497	Mir453
ENSMUST00000104735	ENSMUSG00000077928	14	0	0	0	2	1	3	3	4	0	0	0	0	0	0	0	0	0	MI0005552	Mir208b
ENSMUST00000104738	ENSMUSG00000077931	17	13	15	11	66	492	964	527	363	6	6	15	0	104	116	40	52	27	MI0005553	Mir877
ENSMUST00000104745	ENSMUSG00000077938	8	0	0	0	0	0	0	0	0	0	3	3	0	0	1	0	0	0		Gm24132
ENSMUST00000104746	ENSMUSG00000077939	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24133
ENSMUST00000104748	ENSMUSG00000077941	2	1	0	0	0	13	10	16	8	2	2	0	0	22	5	1	0	0	MI0005511	Mir466h
ENSMUST00000104751	ENSMUSG00000094184	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005470	Mir743b
ENSMUST00000104755	ENSMUSG00000077948	14	0	0	2	1	0	0	0	1	3	0	0	0	3	1	0	0	0		Gm23438
ENSMUST00000104757	ENSMUSG00000095006	X	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005500	Mir465c-2
ENSMUST00000104761	ENSMUSG00000077954	2	0	0	0	0	7	22	0	35	0	0	0	0	25	7	1	0	3	MI0005489	Mir297a-4
ENSMUST00000104763	ENSMUSG00000096628	X	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	MI0005471	Mir871
ENSMUST00000104769	ENSMUSG00000077962	13	5	1	0	6	48	40	10	21	0	3	0	0	9	4	1	4	0	MI0005479	Mir874
ENSMUST00000104772	ENSMUSG00000077965	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24605
ENSMUST00000104778	ENSMUSG00000077971	13	3	0	2	5	4	0	0	0	9	0	4	0	0	5	9	9	4		Gm26259
ENSMUST00000104779	ENSMUSG00000077972	2	3	0	0	2	1	0	0	0	0	4	8	0	0	0	0	4	0	MI0005507	Mir466f-1
ENSMUST00000104784	ENSMUSG00000095188	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26376
ENSMUST00000104787	ENSMUSG00000077980	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005520	Mir654
ENSMUST00000104788	ENSMUSG00000077981	2	1	0	0	2	20	11	13	26	0	4	3	0	25	17	6	2	0	MI0005509	Mir466f-3
ENSMUST00000104797	ENSMUSG00000077990	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23134
ENSMUST00000104798	ENSMUSG00000077991	2	0	0	1	0	8	8	10	10	3	0	0	0	0	0	0	0	0	MI0014079	Mir466n
ENSMUST00000104803	ENSMUSG00000077996	3	64	36	51	77	30	14	54	21	10	5	2	0	79	5	1	5	0	MI0005478	Mir190b
ENSMUST00000104805	ENSMUSG00000077998	2	0	0	0	0	26	46	13	39	0	1	2	0	30	27	9	5	4	MI0005508	Mir466f-2
ENSMUST00000104809	ENSMUSG00000078002	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005473	Mir880
ENSMUST00000104810	ENSMUSG00000094677	9	0	0	0	5	0	0	0	0	0	0	1	0	2	0	0	0	1		Gm22008
ENSMUST00000104813	ENSMUSG00000078006	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0		Gm26301
ENSMUST00000104815	ENSMUSG00000078008	7	30	6	12	39	177	104	74	89	5	2	1	0	21	9	4	3	0	MI0000389	Mir291a
ENSMUST00000104824	ENSMUSG00000078017	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005476	Mir883a
ENSMUST00000104829	ENSMUSG00000095880	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26429
ENSMUST00000104830	ENSMUSG00000078024	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005477	Mir883b
ENSMUST00000104831	ENSMUSG00000078025	2	0	1	0	0	23	71	41	78	2	0	0	1	19	4	3	1	6	MI0005510	Mir466g
ENSMUST00000104832	ENSMUSG00000078026	2	0	0	0	0	2	0	0	3	0	0	0	0	4	0	1	0	0	MI0014052	Mir466o
ENSMUST00000104833	ENSMUSG00000078027	13	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	MI0005547	Mir449b
ENSMUST00000104837	ENSMUSG00000078031	2	0	0	0	10	20	50	16	50	0	0	0	0	37	5	6	9	0	MI0005546	Mir466d
ENSMUST00000104838	ENSMUSG00000078032	7	1	0	0	2	2	0	0	0	2	0	0	0	0	0	0	0	0	MI0003539	Mir291b
ENSMUST00000104840	ENSMUSG00000078034	X	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		Gm24683
ENSMUST00000104841	ENSMUSG00000078035	7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	MI0000391	Mir293
ENSMUST00000104844	ENSMUSG00000078038	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005474	Mir881
ENSMUST00000104847	ENSMUSG00000078041	7	4	2	1	2	103	80	171	107	0	1	0	0	10	5	4	6	1	MI0000390	Mir292
ENSMUST00000104848	ENSMUSG00000078042	6	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0		Gm24855
ENSMUST00000104850	ENSMUSG00000093935	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25529
ENSMUST00000104863	ENSMUSG00000078057	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005550	Mir873a
ENSMUST00000104866	ENSMUSG00000078060	2	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	MI0006278	Mir466l
ENSMUST00000104867	ENSMUSG00000078061	2	2	0	3	2	0	0	0	1	1	4	3	0	2	0	0	1	0		Gm22824
ENSMUST00000116680	ENSMUSG00000080330	3	0	0	0	0	6	0	0	1	0	0	0	0	0	0	0	0	0		Gm22468
ENSMUST00000116681	ENSMUSG00000080331	X	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	MI0004300	Mir1298
ENSMUST00000116684	ENSMUSG00000080334	8	4	2	0	0	0	0	2	0	0	0	8	0	3	0	1	0	0		Gm25110
ENSMUST00000116686	ENSMUSG00000080336	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25111
ENSMUST00000116692	ENSMUSG00000080342	17	3	2	1	7	0	3	1	4	0	0	1	0	0	0	0	1	1		Gm24589
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ENSMUST00000116696	ENSMUSG00000080346	13	2	0	1	5	0	0	0	0	4	0	2	0	0	0	1	0	4		Gm24588
ENSMUST00000116697	ENSMUSG00000080347	10	2	0	1	3	0	0	0	1	2	0	3	0	0	0	0	0	0		Gm24587
ENSMUST00000116698	ENSMUSG00000080348	8	0	0	0	0	0	0	0	0	5	2	0	0	0	0	4	1	11		Gm24591
ENSMUST00000116699	ENSMUSG00000080349	12	0	0	0	0	0	2	0	0	0	2	0	0	0	0	4	6	0		Gm24590
ENSMUST00000116700	ENSMUSG00000080350	7	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm26248
ENSMUST00000116701	ENSMUSG00000096196	3	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm26137
ENSMUST00000116704	ENSMUSG00000095069	9	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm26190
ENSMUST00000116705	ENSMUSG00000095541	18	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm24617
ENSMUST00000116706	ENSMUSG00000080356	12	0	1	0	4	0	8	1	5	0	0	0	0	0	2	0	0	0	MI0004120	Mir1247
ENSMUST00000116709	ENSMUSG00000080359	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26250
ENSMUST00000116710	ENSMUSG00000080360	4	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0		Gm25779
ENSMUST00000116713	ENSMUSG00000080363	7	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm25778
ENSMUST00000116716	ENSMUSG00000080366	8	4	2	0	0	0	0	2	0	0	0	8	0	3	0	1	0	0		Gm25775
ENSMUST00000116717	ENSMUSG00000080367	7	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm25774
ENSMUST00000116718	ENSMUSG00000080368	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25773
ENSMUST00000116724	ENSMUSG00000080374	2	0	0	0	2	1	0	3	1	15	1	1	0	0	1	20	39	2		Gm22953
ENSMUST00000116730	ENSMUSG00000080380	X	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm22102
ENSMUST00000116733	ENSMUSG00000080383	X	3	0	0	1	6	0	2	0	0	3	2	0	0	0	0	3	1	MI0006299	Mir22103
ENSMUST00000116737	ENSMUSG00000095894	16	4	2	0	0	0	0	2	0	0	0	8	0	3	0	1	0	0		Gm24795
ENSMUST00000116741	ENSMUSG00000080391	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23785
ENSMUST00000116751	ENSMUSG00000080401	9	1	0	0	0	0	0	1	0	0	0	0	0	4	2	0	0	0		Gm23653
ENSMUST00000116752	ENSMUSG00000080402	14	0	0	2	4	0	1	0	0	5	4	0	0	0	2	3	0	2		Gm23652
ENSMUST00000116755	ENSMUSG00000080405	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23651
ENSMUST00000116756	ENSMUSG00000080406	12	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0006290	Mir1188
ENSMUST00000116758	ENSMUSG00000080408	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23654
ENSMUST00000116759	ENSMUSG00000080409	9	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	MI0006302	Mir467h
ENSMUST00000116760	ENSMUSG00000080410	1	2	2	0	0	1	0	0	0	4	3	1	0	5	4	5	1	0		Gm26472

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpgl0673	hpgl0674	hpgl0675	hpgl0676	hpgl0677	hpgl0678	hpgl0679	hpgl0680	hpgl0523	hpgl0524	hpgl0525	hpgl0555	hpgl0556	hpgl0557	hpgl0558	hpgl0559	hpgl0560	mirBase_accession	mirBase name
ENSMUST00000116761	ENSMUSG00000080411	12	1	0	0	0	0	1	1	3	0	0	1	0	0	0	0	0	MI0006298	Mir1193
ENSMUST00000116762	ENSMUSG00000080412	5	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0	0	0		Gm26474
ENSMUST00000116765	ENSMUSG00000080415	2	10	2	0	18	2	0	4	2	3	0	30	0	1	4	7	7	0		Gm26469
ENSMUST00000116769	ENSMUSG00000080419	X	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26475
ENSMUST00000116774	ENSMUSG00000080424	3	2	0	0	0	2	1	0	0	1	1	3	0	5	1	0	0	0	MI0006292	Mir466k
ENSMUST00000116777	ENSMUSG00000080427	X	4	0	0	0	0	0	0	0	14	4	0	0	4	0	0	0	0		Gm24835
ENSMUST00000116780	ENSMUSG00000080430	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24275
ENSMUST00000116782	ENSMUSG00000080432	14	6	0	0	0	0	0	0	0	0	0	3	0	3	0	8	15	3		Gm23178
ENSMUST00000116784	ENSMUSG00000080434	8	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm23177
ENSMUST00000116791	ENSMUSG00000080441	15	8	2	6	19	451	573	303	990	6	8	7	0	78	114	25	18	11	MI0004132	Mir1249
ENSMUST00000116792	ENSMUSG00000094943	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25753
ENSMUST00000116793	ENSMUSG00000080443	12	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		Gm25847
ENSMUST00000116801	ENSMUSG00000080451	13	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm24193
ENSMUST00000116802	ENSMUSG00000080452	16	9	10	12	56	182	279	218	353	4	0	0	0	32	24	7	5	6	MI0009935	Mir1306
ENSMUST00000116804	ENSMUSG00000080454	13	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0		Gm24195
ENSMUST00000116805	ENSMUSG00000080455	17	2	0	0	2	0	0	0	0	7	0	3	0	2	5	0	0	0		Gm24194
ENSMUST00000116809	ENSMUSG00000080459	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	MI0006280	Mir669g
ENSMUST00000116812	ENSMUSG00000093807	14	3	0	0	1	6	0	2	0	0	3	2	0	0	0	0	3	1	MI0006299	Gm23620
ENSMUST00000116818	ENSMUSG00000080468	17	8	2	1	14	1	5	0	6	8	10	10	0	1	2	5	3	1	MI0006303	Mir1195
ENSMUST00000116823	ENSMUSG00000080473	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25315
ENSMUST00000116824	ENSMUSG00000080474	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25317
ENSMUST00000116826	ENSMUSG00000080476	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25316
ENSMUST00000116833	ENSMUSG00000094593	3	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm24744
ENSMUST00000116835	ENSMUSG00000080485	16	1	0	0	3	1	0	3	0	10	0	2	0	3	0	4	1	3		Gm23493
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ENSMUST00000116852	ENSMUSG00000094571	6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0		Gm23551
ENSMUST00000116854	ENSMUSG00000080504	2	3	0	0	3	8	31	10	27	0	0	0	0	12	6	0	0	0	MI0014051	Mir669d-2
ENSMUST00000116856	ENSMUSG00000080506	3	1	0	0	0	0	0	1	0	2	0	0	0	0	2	0	0	0		Gm25042
ENSMUST00000116857	ENSMUSG00000080507	2	0	0	0	1	0	0	0	0	5	0	1	0	0	0	1	0	1		Gm22071
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ENSMUST00000116865	ENSMUSG00000080515	5	2	0	0	0	2	0	1	0	0	0	6	0	3	1	2	0	0		Gm22196
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ENSMUST00000116869	ENSMUSG00000080519	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22194
ENSMUST00000116872	ENSMUSG00000080522	14	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0		Gm23881
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ENSMUST00000116877	ENSMUSG00000080527	15	0	1	0	0	0	0	0	0	0	2	2	0	0	0	0	1	1		Gm23880
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ENSMUST00000116893	ENSMUSG00000080543	18	1	0	0	0	0	0	0	1	3	0	0	0	3	0	5	12	16		Gm22709
ENSMUST00000116896	ENSMUSG00000094175	17	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm24427
ENSMUST00000116899	ENSMUSG00000080549	8	1	0	0	3	1	0	1	1	0	3	4	0	8	3	2	1	0		Gm22715
ENSMUST00000116906	ENSMUSG00000080556	5	0	0	0	2	0	0	0	0	1	0	0	4	0	0	0	0	0	MI0006301	Mir467g
ENSMUST00000116908	ENSMUSG00000080558	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22091
ENSMUST00000116911	ENSMUSG00000080561	1	2	0	0	0	0	0	0	0	1	1	2	0	5	0	5	0	0		Gm26042
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ENSMUST00000116918	ENSMUSG00000095035	17	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm22346
ENSMUST00000116923	ENSMUSG00000080573	11	1	1	0	0	0	0	1	1	1	0	0	0	0	0	0	2	0	MI0006293	Mir467f
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ENSMUST00000116925	ENSMUSG00000080575	12	2	1	3	2	13	17	6	7	2	0	0	0	8	0	0	0	0	MI0006294	Mir1190
ENSMUST00000116926	ENSMUSG00000095000	7	4	2	0	0	0	0	2	0	0	0	8	0	3	0	1	0	0		Gm25171
ENSMUST00000116930	ENSMUSG00000080580	13	0	0	0	0	0	0	0	0	0	4	1	0	0	4	0	0	0	MI0006291	Mir466f-4
ENSMUST00000116935	ENSMUSG00000095255	13	0	0	0	0	0	2	0	0	4	1	0	0	0	0	0	0	0		Gm23086
ENSMUST00000116936	ENSMUSG00000080586	5	0	0	0	0	0	0	4	0	0	0	0	0	2	0	0	0	0	MI0006285	Mir1187
ENSMUST00000116938	ENSMUSG00000095437	18	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm23606
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ENSMUST00000116940	ENSMUSG00000080590	3	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm22029
ENSMUST00000116942	ENSMUSG00000080592	8	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0		Gm22030
ENSMUST00000116944	ENSMUSG00000080594	2	12	2	0	3	1	2	3	2	6	2	2	0	8	1	4	5	1	MI0006289	Mir669h
ENSMUST00000116946	ENSMUSG00000080596	15	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	4		Gm22032
ENSMUST00000116947	ENSMUSG00000080597	4	3	0	0	3	0	0	0	0	13	2	10	0	0	2	0	1	0		Gm22033
ENSMUST00000116948	ENSMUSG00000095786	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24673
ENSMUST00000116949	ENSMUSG00000096782	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24640
ENSMUST00000116950	ENSMUSG00000080600	11	29	5	13	131	51	0	37	16	409	112	33	13	24	94	83	120	81		Gm23840
ENSMUST00000116951	ENSMUSG00000080601	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23841
ENSMUST00000116956	ENSMUSG00000095798	9	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm26298
ENSMUST00000116959	ENSMUSG00000080609	7	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm23844
ENSMUST00000116962	ENSMUSG00000096748	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22635
ENSMUST00000116963	ENSMUSG00000080613	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22151
ENSMUST00000116974	ENSMUSG00000080624	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22678
ENSMUST00000116975	ENSMUSG00000080625	1	0	0	0	2	0	1	0	0	0	1	1	0	2	1	0	0	0		Gm22679
ENSMUST00000116976	ENSMUSG00000080626	19	22	3	7	15	1	2	8	3	58	20	23	2	24	19	56	42	12	MI0006297	Mir1192
ENSMUST00000116977	ENSMUSG00000080627	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1		Gm22677
ENSMUST00000116981	ENSMUSG00000080631	11	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25507
ENSMUST00000116985	ENSMUSG00000080635	18	1	0	0	0	0	2	1	1	0	0	1	0	3	1	3	0	0		Gm25509
ENSMUST00000116986	ENSMUSG00000080636	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25510
ENSMUST00000116990	ENSMUSG00000094457	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22626
ENSMUST00000116995	ENSMUSG00000080645	X	1095	878	601	2397	4441	2931	5100	2590	274	390	50	7	4490	1471	431	844	62	MI0006306	Mir1198
ENSMUST00000116999	ENSMUSG00000080649	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26156
ENSMUST00000117002	ENSMUSG00000094330	2	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0		Gm22051
ENSMUST00000117003	ENSMUSG00000080653	2	0	0	0	1	0	9	2	2	0	0	0	0	2	0	0	0	0	MI0006300	Mir669e
ENSMUST00000117005	ENSMUSG00000080655	10	1	0	0	0	0	0	1	0	4	0	0	0	8	3	0	7	0		Gm24482
ENSMUST00000117007	ENSMUSG00000080657	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0006288	Mir669i
ENSMUST00000117009	ENSMUSG00000080659	19	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm24484
ENSMUST00000117012	ENSMUSG00000080662	18	0	0	1	4	2	5	7	2	0	0	0	0	6	1	0	0	0	MI0006283	Mir1b
ENSMUST00000117013	ENSMUSG00000080663	4	1	0	0	6	0	0	2	0	3	0	0	0	2	0	0	6	4		Gm25002
ENSMUST00000117015	ENSMUSG00000080665	8	0	3	0	2	0	6	0	2	0	2	0	0	1	0	0	0	0	MI0006307	Mir1199
ENSMUST00000117016	ENSMUSG00000080666	13	9	0	1	4	0	1	0	1	1	1	11	0	12	5	0	7	3		Gm25000
ENSMUST00000117018	ENSMUSG00000080668	13	2	0	0	0	4	1	0	3	0	0	0	0	0	1	0	1	2		Gm24999
ENSMUST00000117019	ENSMUSG00000080669	16	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	MI0004118	Mir1224
ENSMUST00000117021	ENSMUSG00000080671	18	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0		Gm23335
ENSMUST00000117026	ENSMUSG00000080676	3	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm25347
ENSMUST00000117028	ENSMUSG00000080678	19	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	19	7		Gm23334

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ENSMUST00000117030	ENSMUSG00000080680	12	1	0	0	2	0	0	0	1	1	0	2	0	4	2	0	0	0		Gm23989
ENSMUST00000117031	ENSMUSG00000080681	11	0	0	0	0	3	3	3	0	0	0	0	0	0	2	0	6	1		Gm23990
ENSMUST00000117032	ENSMUSG00000096779	1	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm22112
ENSMUST00000117034	ENSMUSG00000080684	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23988
ENSMUST00000117036	ENSMUSG00000080686	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24806
ENSMUST00000117037	ENSMUSG00000080687	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0006305	Mir1197
ENSMUST00000122474	ENSMUSG00000084423	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25109
ENSMUST00000122509	ENSMUSG00000084458	15	0	2	0	0	2	2	0	0	3	0	0	0	1	0	0	0	0	MI0008325	Mir1907
ENSMUST00000122519	ENSMUSG00000084468	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22955
ENSMUST00000122559	ENSMUSG00000084508	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25325
ENSMUST00000122565	ENSMUSG00000084514	18	0	0	0	0	8	19	5	0	3	3	1	0	1	1	4	3	1	MI0008327	Mir1893
ENSMUST00000122567	ENSMUSG00000084516	2	0	2	0	0	2	2	0	0	0	1	0	0	1	5	1	0	1	MI0008313	Mir1902
ENSMUST00000122574	ENSMUSG00000084523	8	0	1	0	0	0	1	1	0	2	0	2	0	0	0	3	4	1	MI0008317	Mir1903
ENSMUST00000122586	ENSMUSG00000084535	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0008321	Mir1906-1
ENSMUST00000122610	ENSMUSG00000084559	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0008321	Mir1906-2
ENSMUST00000122615	ENSMUSG00000084564	3	2	1	1	3	1	1	0	1	2	18	2	2	1	0	14	16	2	MI0008316	Mir1895
ENSMUST00000122616	ENSMUSG00000084565	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	MI0008328	Mir1901
ENSMUST00000122641	ENSMUSG00000084590	13	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	MI0008322	Mir1896
ENSMUST00000122643	ENSMUSG00000084592	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	MI0008324	Mir1898
ENSMUST00000122651	ENSMUSG00000084600	17	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0		Gm22201
ENSMUST00000122702	ENSMUSG00000084651	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0008323	Mir1904
ENSMUST00000122709	ENSMUSG00000084658	10	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	1	0		Gm22721
ENSMUST00000122714	ENSMUSG00000084663	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0008319	Mir1900
ENSMUST00000122764	ENSMUSG00000084713	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24627
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ENSMUST00000122798	ENSMUSG00000084747	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0008318	Mir1899
ENSMUST00000122802	ENSMUSG00000084751	17	0	0	0	0	2	1	0	2	0	0	0	0	0	0	0	3	0	MI0008326	Mir1894
ENSMUST00000157119	ENSMUSG00000087744	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25149
ENSMUST00000157182	ENSMUSG00000087807	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25559
ENSMUST00000157195	ENSMUSG00000087820	1	6644	1644	6111	20138	717	676	530	498	19111	4391	11989	214	2473	2101	2012	1192	10686	MI0009917	Mir1928
ENSMUST00000157219	ENSMUSG00000087844	4	2	1	2	2	9	0	1	4	0	0	0	0	7	0	0	0	1	MI0009955	Mir1958
ENSMUST00000157230	ENSMUSG00000087855	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0012528	Mir432
ENSMUST00000157270	ENSMUSG00000087895	10	0	1	0	2	0	0	0	0	6	0	0	0	2	0	0	0	1		Gm25281
ENSMUST00000157274	ENSMUSG00000087899	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0009931	Mir1942
ENSMUST00000157307	ENSMUSG00000087932	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0009970	Mir1971
ENSMUST00000157318	ENSMUSG00000087943	4	1048	1123	798	4411	128	285	186	244	1328	14781	19391	20158	316	800	22346	1491	258374		Gm24245
ENSMUST00000157325	ENSMUSG00000087950	18	18	60	8	74	255	122	161	97	0	0	0	0	9	3	3	9	6	MI0009939	Mir1948
ENSMUST00000157368	ENSMUSG00000087993	10	0	1	0	0	42	22	34	14	0	0	1	0	8	9	1	8	0	MI0009993	Mir1982
ENSMUST00000157390	ENSMUSG00000088015	11	2	0	2	4	10	6	8	4	2	0	0	0	1	0	0	0	0	MI0009921	Mir1932
ENSMUST00000157411	ENSMUSG00000088036	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24993
ENSMUST00000157429	ENSMUSG00000088054	8	0	19	2	41	2	19	1	14	2	1	0	0	7	10	0	0	0	MI0009965	Mir1968
ENSMUST00000157488	ENSMUSG00000088113	5	7	4	4	14	15	11	3	6	1	2	0	0	3	2	1	1	0	MI0009957	Mir1960
ENSMUST00000157491	ENSMUSG00000088116	7	0	1	1	0	2	0	3	0	0	0	3	0	2	0	0	2	0		Gm24063
ENSMUST00000157516	ENSMUSG00000088141	7	2	2	1	9	10	6	10	3	2	0	0	0	2	1	0	0	0	MI0009959	Mir1962
ENSMUST00000157523	ENSMUSG00000088148	13	481	147	301	825	2002	1391	1370	765	3484	3765	1369	17	1018	610	777	761	1941	MI0009990	Mir1983
ENSMUST00000157579	ENSMUSG00000088204	9	0	0	0	0	0	0	0	0	1	2	0	0	0	0	1	1	1		Gm23391
ENSMUST00000157621	ENSMUSG00000088246	1	1	1	2	0	0	1	0	0	0	7	30	5	0	0	8	0	92		Gm25911
ENSMUST00000157623	ENSMUSG00000088248	8	0	0	0	1	0	1	4	1	0	0	0	0	0	0	0	0	0	MI0009966	Mir1969
ENSMUST00000157729	ENSMUSG00000088354	7	116	5	16	17	9	14	11	2	88	90	334	0	13	9	33	38	5		Gm27592
ENSMUST00000157748	ENSMUSG00000088373	3	2	1	0	3	25	30	10	11	0	1	0	0	1	1	1	5	0	MI0009952	Mir1956
ENSMUST00000157768	ENSMUSG00000088393	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26308
ENSMUST00000157789	ENSMUSG00000088414	8	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	MI0009964	Mir1967
ENSMUST00000157821	ENSMUSG00000088446	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23556
ENSMUST00000157834	ENSMUSG00000088459	15	0	0	1	3	10	13	6	13	0	0	0	0	1	3	0	2	0	MI0009930	Mir1941
ENSMUST00000157839	ENSMUSG00000088464	X	0	0	1	3	2	0	0	3	1	2	0	0	0	0	1	0	0	MI0009968	Mir1970
ENSMUST00000157853	ENSMUSG00000088478	9	2	0	0	10	1	0	1	0	5	4	7	0	4	4	3	3	6	MI0009967	Mir1946b
ENSMUST00000157866	ENSMUSG00000088491	2	0	0	1	0	4	8	2	2	0	2	1	0	2	0	0	2	0	MI0009948	Mir1953
ENSMUST00000157919	ENSMUSG00000088544	16	0	2	3	5	7	8	6	4	0	0	0	0	3	0	0	1	0	MI0009934	Mir1945
ENSMUST00000157927	ENSMUSG00000088552	4	2899	9578	5653	7975	3735	2340	2487	3393	347585	53168	68854	1919	21506	19026	15477	6279	90284	MI0009954	Mir1957a
ENSMUST00000157934	ENSMUSG00000088559	1	27	27	15	115	392	623	430	297	5	1	0	0	69	54	6	31	22	MI0009992	Mir1981
ENSMUST00000157981	ENSMUSG00000088606	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	MI0009946	Mir1951
ENSMUST00000157984	ENSMUSG00000088609	13	1	1	0	7	0	0	0	0	22	19	15	45	1	1	128	2	832		Gm24187
ENSMUST00000158014	ENSMUSG00000088639	2	10	5	11	14	184	111	107	69	0	0	2	0	12	9	3	3	0	MI0009950	Mir1955
ENSMUST00000158016	ENSMUSG00000088641	8	37	10	7	33	3	2	2	0	7	21	154	0	3	7	9	5	0		Gm26483
ENSMUST00000158074	ENSMUSG00000088699	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22328
ENSMUST00000158117	ENSMUSG00000088742	5	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0		Gm23222
ENSMUST00000158127	ENSMUSG00000088752	11	67	44	30	139	327	701	343	289	891	170	53	0	206	240	134	142	40	MI0009923	Mir1934
ENSMUST00000158158	ENSMUSG00000088783	5	1	3	1	2	0	0	0	2	1	0	4	0	0	0	0	0	3		Gm25374
ENSMUST00000158184	ENSMUSG00000088809	4	0	0	1	1	1	5	1	0	0	3	0	0	0	0	0	3	0		Gm24078
ENSMUST00000158208	ENSMUSG00000088833	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23542
ENSMUST00000158235	ENSMUSG00000088860	16	46	21	26	128	275	222	185	104	3	10	11	0	20	15	1	9	4	MI0009937	Mir1947
ENSMUST00000158247	ENSMUSG00000088872	12	4	0	4	15	0	0	0	2	7	0	32	0	3	0	5	0	0		Gm25865
ENSMUST00000158267	ENSMUSG00000088892	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22518
ENSMUST00000158276	ENSMUSG00000088901	15	127	79	52	216	359	204	336	139	3	2	92	3	33	16	4	29	18	MI0009932	Mir1943
ENSMUST00000158348	ENSMUSG00000088973	1	3	0	2	4	0	1	0	1	1	0	11	0	0	0	0	1	0		Gm23762
ENSMUST00000158355	ENSMUSG00000088980	2	0	0	0	5	2	0	1	0	0	1	0	0	1	0	0	0	0	MI0009944	Mir669m-2
ENSMUST00000158358	ENSMUSG00000088983	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0009947	Mir1952
ENSMUST00000158360	ENSMUSG00000088985	16	0	0	0	2	0	4	1	1	8	4	6	0	1	1	2	2	0	MI0009936	Mir1946a
ENSMUST00000158361	ENSMUSG00000088986	9	0	2	0	1	3	8	5	2	2	3	3	0	0	1	4	0	1		Gm25603
ENSMUST00000158463	ENSMUSG00000089088	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3		Gm24001
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ENSMUST00000158526	ENSMUSG00000089151	19	1	1	1	1	3	4	7	5	0	2	0	0	2	1	0	0	0	MI0009941	Mir1950
ENSMUST00000158562	ENSMUSG00000089187	14	1	2	4	2	0	0	0	2	5	4	11	0	0	0	0	0	0		Gm22949
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ENSMUST00000158588	ENSMUSG00000089213	8	1	3	0	27	9	22	15	22	10	131	24	2	3	6	5	2	6		Gm23388
ENSMUST00000158589	ENSMUSG00000089214	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	MI0009920	Mir1931
ENSMUST00000158594	ENSMUSG00000089219	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	MI0009960	Mir1963
ENSMUST00000158619	ENSMUSG00000089244	5	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0		Gm24054
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ENSMUST00000158635	ENSMUSG00000089260	10	1	1	0	1	20	12	10	12	1	0	0	0	10	0	0	0	0	MI0009918	Mir1929
ENSMUST00000158636	ENSMUSG00000089261	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0009951	Mir669n
ENSMUST00000158638	ENSMUSG00000089263	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22892
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ENSMUST00000158669	ENSMUSG00000089294	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0010752	Mir2139
ENSMUST00000158698	ENSMUSG00000089323	4	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0		Gm25978
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
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ENSMUST00000158746	ENSMUSG00000089371	12	1	1	1	8	9	6	2	0	3	17	2	0	2	3	7	6	1	MI0009927	Mir1938
ENSMUST00000158781	ENSMUSG00000089406	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0010749	Mir2136
ENSMUST00000158799	ENSMUSG00000089424	10	1	3	5	15	16	12	21	14	0	2	0	0	7	3	0	3	0	MI0009919	Mir1930
ENSMUST00000158807	ENSMUSG00000089432	8	0	0	0	0	1	7	1	3	2	0	0	1	2	0	0	0	0	MI0009963	Mir1966
ENSMUST00000158842	ENSMUSG00000089467	7	3	0	1	3	0	1	0	0	5	2	22	0	0	0	0	0	0		Gm23700
ENSMUST00000158919	ENSMUSG00000089544	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25837
ENSMUST00000158930	ENSMUSG00000089555	11	25	20	22	69	219	183	53	93	1	5	2	0	12	1	1	1	2	MI0009922	Mir1933
ENSMUST00000158945	ENSMUSG00000089570	2	0	0	0	5	2	0	1	0	0	1	0	0	1	0	0	0	0	MI0009943	Mir669m-1
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ENSMUST00000174892	ENSMUSG00000092633	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	MI0016967	Mir3962
ENSMUST00000174896	ENSMUSG00000094253	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014701	Mir3471-2
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ENSMUST00000174922	ENSMUSG00000094173	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0019196	Mir344h-1
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ENSMUST00000175000	ENSMUSG00000092741	13	19	9	9	22	420	366	246	110	5	14	0	0	182	42	27	155	0	MI0014037	Mir3074-1
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ENSMUST00000175047	ENSMUSG00000094247	2	40	58	42	149	74	78	47	25	62	163	176	0	9	13	90	166	36		Gm23968
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ENSMUST00000175138	ENSMUSG00000092879	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	MI0030344	Gm22650
ENSMUST00000175139	ENSMUSG00000092880	4	1	1	3	1	0	0	0	0	2	9	1	0	2	2	1	0	0	MI0014699	Mir3471-1
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ENSMUST00000175148	ENSMUSG00000092889	11	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2		Gm22121
ENSMUST00000175150	ENSMUSG00000092891	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		Gm23810
ENSMUST00000175153	ENSMUSG00000092894	11	46	35	22	109	15	18	9	16	43	43	66	5	2	5	19	37	22		Gm23813
ENSMUST00000175155	ENSMUSG00000092896	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23811
ENSMUST00000175156	ENSMUSG00000092897	8	0	0	0	0	1	0	0	2	0	0	0	0	1	0	0	0	0		Gm23812
ENSMUST00000175160	ENSMUSG00000092901	14	0	0	0	1	26	40	19	26	0	1	2	0	6	3	6	1	2	MI0018042	Mir5130
ENSMUST00000175165	ENSMUSG00000092906	1	0	0	35	0	0	0	0	0	0	0	117	0	0	0	0	0	0		Gm25736
ENSMUST00000175166	ENSMUSG00000092907	X	0	2	1	0	8	19	7	7	0	0	0	0	8	3	4	2	0	MI0018044	Mir5132
ENSMUST00000175167	ENSMUSG00000092908	17	0	0	0	0	0	0	0	0	0	0	0	23	0	0	0	0	0		Gm25731
ENSMUST00000175168	ENSMUSG00000092909	4	135	255	269	564	453	453	296	287	696	7410	929	49	431	635	5322	1324	706		Gm25732
ENSMUST00000175169	ENSMUSG00000095747	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22475
ENSMUST00000175172	ENSMUSG00000092913	17	0	0	0	3	0	0	0	6	8	0	0	0	0	0	0	0	0		Gm24085
ENSMUST00000175173	ENSMUSG00000092914	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24084
ENSMUST00000175174	ENSMUSG00000092915	9	4449	17182	9842	27546	672331	212671	644430	201696	1546	4167	2995	207	50188	20088	13325	69559	3875		Gm24083
ENSMUST00000175175	ENSMUSG00000092916	5	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0		Gm24082
ENSMUST00000175176	ENSMUSG00000092917	X	2	0	5	11	0	1	3	3	1	3	18	0	2	5	4	9	2	MI0014704	Mir3472
ENSMUST00000175177	ENSMUSG00000092918	2	12	20	20	129	0	0	11	17	0	26	75	0	0	5	17	68	0		Gm24081
ENSMUST00000175178	ENSMUSG00000092919	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0		Gm24080
ENSMUST00000175190	ENSMUSG00000092921	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014095	Mir344b
ENSMUST00000175181	ENSMUSG00000092922	12	2	0	0	1	6	9	7	8	3	0	1	0	0	0	0	0	0	MI0018009	Mir5101
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ENSMUST00000175187	ENSMUSG00000092928	6	0	0	0	0	1	0	2	0	0	0	0	0	0	0	2	2	1		Gm24563
ENSMUST00000175190	ENSMUSG00000092931	12	6	1	12	40	9	34	16	22	42	23	26	9	34	17	20	22	7		Gm22904
ENSMUST00000175193	ENSMUSG00000092934	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22903
ENSMUST00000175194	ENSMUSG00000092935	18	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1		Gm22697
ENSMUST00000175195	ENSMUSG00000094528	6	16	7	10	46	0	1	7	4	7	15	60	0	5	4	6	11	8		Gm22914
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ENSMUST00000175205	ENSMUSG00000094952	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014033	Mir3070b
ENSMUST00000175207	ENSMUSG00000092948	1	7	8	5	16	2	1	3	3	28	15	0	0	4	11	11	4	1		Gm23393
ENSMUST00000175208	ENSMUSG00000092949	12	2	0	0	4	4	0	3	4	0	0	0	0	2	1	1	1	0		Gm23394
ENSMUST00000175211	ENSMUSG00000092952	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004412	Mir3059
ENSMUST00000175212	ENSMUSG00000092953	7	1	3	2	1	2	0	1	1	70	81	11	0	3	1	10	65	0		Gm26217
ENSMUST00000175215	ENSMUSG00000092956	6	0	0	1	3	2	7	5	1	0	0	2	0	0	1	7	7	2		Gm26220
ENSMUST00000175216	ENSMUSG00000092957	16	5	4	5	14	59	15	4	12	0	0	1	0	0	0	0	0	3		Gm26219
ENSMUST00000175217	ENSMUSG00000092958	2	7	2	5	23	35	92	71	25	18	5	0	0	6	4	2	5	6	MI0018040	Mir5128
ENSMUST00000175218	ENSMUSG00000096830	9	0	0	0	0	0	0	0	0	0	29	0	0	0	0	0	0	0		Gm26231
ENSMUST00000175220	ENSMUSG00000092961	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22239
ENSMUST00000175222	ENSMUSG00000092963	9	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0		Gm22238
ENSMUST00000175223	ENSMUSG00000095323	6	55	44	32	307	11	3	6	4	10	20	216	0	1	8	8	11	5	MI0014696	Mir3470a
ENSMUST00000175225	ENSMUSG00000092966	19	0	0	0	0	3	16	11	4	0	0	0	0	2	1	1	0	1		Gm22240
ENSMUST00000175230	ENSMUSG00000095871	4	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0		Gm25931
ENSMUST00000175231	ENSMUSG00000092972	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014041	Mir3078
ENSMUST00000175232	ENSMUSG00000092973	18	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0		Gm25071
ENSMUST00000175235	ENSMUSG00000096080	10	5	2	3	21	1	0	0	0	0	3	22	0	0	0	0	3	0		Gm24710
ENSMUST00000175237	ENSMUSG00000092978	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25070
ENSMUST00000175238	ENSMUSG00000092979	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0		Gm25069
ENSMUST00000175240	ENSMUSG00000092981	17	0	0	1	4	3	0	2	2	0	2	0	0	0	0	3	2	0	MI0018036	Mir5125

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000175244	ENSMUSG00000092985	11	1	0	2	5	5	6	5	11	0	0	0	0	0	0	1	0	0	MI0016973	Mir378b
ENSMUST00000175247	ENSMUSG00000092988	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014086	Mir3093
ENSMUST00000175249	ENSMUSG00000092990	3	0	0	0	0	1	8	1	0	0	0	0	0	1	0	0	1	0	MI0018032	Mir466q
ENSMUST00000175254	ENSMUSG00000092995	14	141460	66089	104553	479259	597522	472783	496275	410192	2081	3786	1099	38	145295	24599	9242	16547	9009	MI0000565	Mir16-1
ENSMUST00000175256	ENSMUSG00000092997	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23917
ENSMUST00000175257	ENSMUSG00000092998	12	330	549	98	1076	14516	65105	17055	17097	7997	5760	98	18	29646	48206	29752	40187	528	MI0018007	Mir5099
ENSMUST00000175259	ENSMUSG00000093000	3	0	0	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0		Gm24155
ENSMUST00000175262	ENSMUSG00000093003	1	4	0	8	40	5	5	0	5	2	10	5	0	0	5	4	1	0	MI0018015	Mir3473c
ENSMUST00000175263	ENSMUSG00000093004	11	1	0	0	1	2	2	0	0	0	0	0	0	0	0	0	0	0		Gm24158
ENSMUST00000175264	ENSMUSG00000093005	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24159
ENSMUST00000175265	ENSMUSG00000093006	11	1	1	0	2	12	6	4	6	0	6	2	0	1	5	14	11	2		Gm24157
ENSMUST00000175266	ENSMUSG00000093007	14	5980	2536	4555	22948	23111	26043	13220	25715	303	397	87	6	6831	813	291	410	381	MI0000564	Mir15a
ENSMUST00000175269	ENSMUSG00000093010	13	23	0	0	0	0	0	0	0	0	0	11	0	0	0	15	0	0		Gm22460
ENSMUST00000175270	ENSMUSG00000093011	9	184	491	57	3694	91	1081	86	318	0	3	0	0	23	1	1	14	4	MI0000692	Mir100
ENSMUST00000175272	ENSMUSG00000093013	11	1	1	3	3	3	1	0	0	3	0	6	0	0	3	10	3	1		Gm22461
ENSMUST00000175273	ENSMUSG00000093014	X	70	27	10	207	16	13	6	11	221	75	202	1	6	8	7	7	1		Gm22464
ENSMUST00000175274	ENSMUSG00000093015	1	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm22463
ENSMUST00000175276	ENSMUSG00000093017	10	2	3	1	7	0	0	0	2	0	0	0	2	0	1	0	0	0	MI0018017	Mir5108
ENSMUST00000175278	ENSMUSG00000093019	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22466
ENSMUST00000175280	ENSMUSG00000093021	15	23	14	12	24	2	4	12	0	26	47	236	1	2	7	14	16	0		Gm25303
ENSMUST00000175281	ENSMUSG00000095289	3	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm22547
ENSMUST00000175283	ENSMUSG00000093024	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25299
ENSMUST00000175285	ENSMUSG00000093026	18	3870	8364	4622	12990	43247	40163	27313	25741	1834	1776	1372	64	10566	2006	860	1037	410		Gm25301
ENSMUST00000175288	ENSMUSG00000093029	5	1	5	4	21	1	3	0	0	11	10	10	3	1	2	4	0	12		Gm25306
ENSMUST00000175289	ENSMUSG00000093030	10	461	405	202	1202	238	301	253	179	283	424	973	46	36	74	303	509	373		Gm23632
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ENSMUST00000175292	ENSMUSG00000093033	2	0	0	0	0	0	0	0	0	1	0	0	0	1	0	4	0	0		Gm23630
ENSMUST00000175293	ENSMUSG00000093034	14	8	0	0	1	0	0	0	1	0	0	4	0	0	0	0	0	1		Gm23633
ENSMUST00000175295	ENSMUSG00000093036	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0018039	Mir5127
ENSMUST00000175296	ENSMUSG00000093037	12	1	2	3	14	19	17	42	20	4	1	0	0	14	0	2	0	0	MI0014028	Mir3066
ENSMUST00000175297	ENSMUSG00000094523	10	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm22913
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ENSMUST00000175299	ENSMUSG00000093040	2	18	22	13	52	14	11	11	4	115	52	55	0	7	11	22	25	15		Gm26141
ENSMUST00000175300	ENSMUSG00000093041	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		Gm26455
ENSMUST00000175301	ENSMUSG00000093042	9	1	1	2	1	96	57	57	40	4	3	0	0	4	4	0	0	2	MI0014106	Mir3109
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ENSMUST00000175306	ENSMUSG00000095684	13	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm23282
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ENSMUST00000175311	ENSMUSG00000093052	6	0	1	0	0	0	0	0	2	0	0	0	0	0	6	1	0	0		Gm24816
ENSMUST00000175313	ENSMUSG00000093054	3	6	0	1	0	4	2	0	0	27	7	1	0	27	3	19	5	27		Gm24811
ENSMUST00000175316	ENSMUSG00000096432	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22132
ENSMUST00000175317	ENSMUSG00000093058	15	0	2	0	0	3	2	0	0	31	0	0	0	0	0	14	0	3		Gm24810
ENSMUST00000175319	ENSMUSG00000093060	10	9	2	7	12	49	42	36	34	2	3	0	0	43	3	0	3	1	MI0018012	Mir5104
ENSMUST00000175320	ENSMUSG00000093061	5	75	8	15	31	7	4	26	7	267	93	65	0	60	31	65	124	23	MI0018006	Mir5098
ENSMUST00000175324	ENSMUSG00000093065	4	2	1	0	9	19	60	34	28	0	0	0	2	6	10	29	30	20		Gm23154
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ENSMUST00000175328	ENSMUSG00000094290	1	457	283	202	1068	143	82	106	70	511	450	557	16	51	85	221	278	141		Gm27512
ENSMUST00000175329	ENSMUSG00000093070	5	14	12	5	25	3	1	3	6	11	10	14	0	2	0	5	9	1		Gm25952
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ENSMUST00000175332	ENSMUSG00000093073	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000717	Mir124a-2
ENSMUST00000175334	ENSMUSG00000093075	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25948
ENSMUST00000175335	ENSMUSG00000093076	17	5	17	8	36	157	67	66	49	0	2	0	0	7	3	3	10	1	MI0014045	Mir3082
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ENSMUST00000175341	ENSMUSG00000093082	5	0	0	1	2	1	0	0	0	0	0	1	0	0	1	0	0	0		Gm24322
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ENSMUST00000175348	ENSMUSG00000093089	12	13	68	9	35	35	39	52	13	3	1	0	0	8	1	0	1	1	MI0001160	Gm24321
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ENSMUST00000175351	ENSMUSG00000093092	9	13	3	3	10	2	1	6	2	45	29	9	0	6	12	16	18	16		Gm22643
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ENSMUST00000175356	ENSMUSG00000093097	5	1	0	0	3	0	0	0	3	0	0	0	0	0	0	0	0	0	MI0014090	Mir3097
ENSMUST00000175359	ENSMUSG00000093100	11	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	MI0016981	Mir3971
ENSMUST00000175360	ENSMUSG00000093101	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25533
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ENSMUST00000175364	ENSMUSG00000093105	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0		Gm25535
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ENSMUST00000175367	ENSMUSG00000093108	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014098	Mir344f
ENSMUST00000175372	ENSMUSG00000093113	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22702
ENSMUST00000175373	ENSMUSG00000093114	12	6	1	0	3	1	0	1	1	2	0	0	0	0	0	2	0	0		Gm22696
ENSMUST00000175374	ENSMUSG00000093115	2	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm25972
ENSMUST00000175375	ENSMUSG00000093116	13	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		Gm22698
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ENSMUST00000175378	ENSMUSG00000093119	9	49	32	24	62	15	7	13	10	42	29	96	2	9	8	25	25	23		Gm25640
ENSMUST00000175379	ENSMUSG00000093120	2	1	0	1	3	1	3	1	2	0	0	2	0	0	0	0	1	0	MI0014707	Mir3474
ENSMUST00000175381	ENSMUSG00000093122	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004130	Mir1264
ENSMUST00000175382	ENSMUSG00000094456	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22625
ENSMUST00000175383	ENSMUSG00000093124	8	2	0	0	0	0	0	0	0	4	0	0	0	2	0	1	1	3		Gm24366
ENSMUST00000175384	ENSMUSG00000093125	7	42	25	6	113	12	8	16	7	55	84	93	0	0	0	12	37	22		Gm24365
ENSMUST00000175387	ENSMUSG00000093128	14	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0		Gm24369
ENSMUST00000175388	ENSMUSG00000093129	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24368
ENSMUST00000175391	ENSMUSG00000093132	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25993
ENSMUST00000175392	ENSMUSG00000093133	11	0	0	0	0	1	1	0	0	3	6	0	0	0	1	0	0	0		Gm25994
ENSMUST00000175393	ENSMUSG00000093134	16	1	0	3	4	0	0	1	2	2	1	3	0	2	4	4	1	3		Gm25996
ENSMUST00000175397	ENSMUSG00000093138	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25998
ENSMUST00000175399	ENSMUSG00000093140	8	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	MI0016979	Mir28b
ENSMUST00000175401	ENSMUSG00000093142	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004486	Mir3106
ENSMUST00000175407	ENSMUSG00000093148	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23375
ENSMUST00000175408	ENSMUSG00000093149	16	0	0	0	0	1	0	0	2	0	0	0	0	1	0	0	0	0		Gm23374
ENSMUST00000175410	ENSMUSG00000094435	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0		Gm23617
ENSMUST00000175411	ENSMUSG00000093152	9	0	0	0	0	1	0	0	2	0	0	0	0	1	0	0	0	0		Gm25032
ENSMUST00000175412	ENSMUSG00000093153	7	4	1	2	6	1	1	2	3	5	3	2	0	1	0	4	0	0		Gm25033
ENSMUST00000175414	ENSMUSG00000093155	1	30	17	13	58	22	5	17	7	33	26	63	0	12	5	23	47	12		Gm25035

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000175415	ENSMUSG00000093156	14	4	1	2	9	302	499	277	185	2	1	2	0	18	16	6	10	0	MI0014039	Mir3076
ENSMUST00000175416	ENSMUSG00000093157	6	3	0	6	9	66	92	51	36	3	4	0	0	10	6	2	0	0	MI0014091	Mir3098
ENSMUST00000175417	ENSMUSG00000093158	18	4	2	8	11	46	115	35	57	0	10	3	10	9	11	78	59	91		Gm25036
ENSMUST00000175418	ENSMUSG00000093159	5	2	0	0	0	0	0	0	0	18	0	7	0	0	7	0	6	1		Gm25037
ENSMUST00000175419	ENSMUSG00000093160	2	324	267	190	2524	9	10	11	10	46	47	1380	0	4	14	22	19	10		Gm22773
ENSMUST00000175420	ENSMUSG00000093161	10	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	1	0		Gm22183
ENSMUST00000175421	ENSMUSG00000093162	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22184
ENSMUST00000175422	ENSMUSG00000093163	4	1	2	0	3	3	0	5	0	1	0	0	0	0	6	5	3	0		Gm22994
ENSMUST00000175426	ENSMUSG00000093167	14	0	1	0	0	13	22	13	11	0	0	0	0	0	0	2	0	1	MI0018043	Mir5131
ENSMUST00000175427	ENSMUSG00000093168	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22990
ENSMUST00000175428	ENSMUSG00000093169	15	2	3	2	6	9	27	10	8	12	5	0	0	15	8	3	0	0	MI0014042	Mir3079
ENSMUST00000175429	ENSMUSG00000093170	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23873
ENSMUST00000175431	ENSMUSG00000093172	X	2	0	3	9	9	9	10	9	0	1	1	0	1	0	1	0	0	MI0014109	Mir3112
ENSMUST00000175432	ENSMUSG00000093173	12	42	16	7	51	2627	6550	18543	27447	14	11	65	0	0	473	84	92	7		Gm23872
ENSMUST00000175435	ENSMUSG00000093176	11	0	0	0	15	1	5	1	4	1	1	0	0	4	9	4	6	14	MI0018028	Mir5119
ENSMUST00000175439	ENSMUSG00000093180	4	18	5	14	28	2	1	1	2	9	11	48	0	0	4	11	5	5		Gm25690
ENSMUST00000175443	ENSMUSG00000093184	11	0	0	0	0	0	0	0	0	0	0	4	0	6	0	0	0	0		Gm25693
ENSMUST00000175444	ENSMUSG00000093185	4	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25692
ENSMUST00000175446	ENSMUSG00000093187	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005495	Mir344-2
ENSMUST00000175449	ENSMUSG00000093190	2	102	88	47	319	8	0	13	9	13	74	561	0	0	0	8	17	7		Gm22875
ENSMUST00000175451	ENSMUSG00000093192	14	1	1	0	1	1	0	0	0	0	0	1	0	2	0	1	0	0		Gm22877
ENSMUST00000175454	ENSMUSG00000094834	1	157	84	54	440	932	1406	1367	828	35	124	253	0	20	686	701	671	87		Gm25472
ENSMUST00000175458	ENSMUSG00000095292	7	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	MI0004227	Mir344d-3
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ENSMUST00000175462	ENSMUSG00000093203	2	0	1	0	0	0	0	0	5	0	0	0	9	14	0	0	0	0		Gm22411
ENSMUST00000175465	ENSMUSG00000093206	X	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		Gm22413
ENSMUST00000175466	ENSMUSG00000093207	7	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm22414
ENSMUST00000175467	ENSMUSG00000093208	18	0	4	0	12	22	44	20	22	0	0	0	4	5	12	48	44	35		Gm27325
ENSMUST00000175468	ENSMUSG00000095147	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014032	Mir3070a
ENSMUST00000175470	ENSMUSG00000093211	9	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25250
ENSMUST00000175471	ENSMUSG00000093212	7	2	0	1	0	0	0	0	0	2	0	0	0	0	0	1	0	1		Gm25249
ENSMUST00000175473	ENSMUSG00000093214	12	0	0	0	0	0	0	0	0	0	0	3	0	6	0	0	0	0		Gm25248
ENSMUST00000175474	ENSMUSG00000093215	7	0	1	1	9	24	18	18	16	0	0	2	0	0	3	1	0	0	MI0014100	Mir3103
ENSMUST00000175475	ENSMUSG00000093216	7	7	1	8	15	15	6	7	2	3	7	7	3	1	0	41	35	18		Gm25247
ENSMUST00000175476	ENSMUSG00000093217	X	23	6	6	37	0	0	1	0	4	4	40	0	0	0	0	0	0		Gm25246
ENSMUST00000175477	ENSMUSG00000093218	12	1	1	1	1	2	9	1	1	0	0	0	0	0	0	0	0	0		Gm25252
ENSMUST00000175478	ENSMUSG00000093219	X	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	MI0014111	Mir3113
ENSMUST00000175480	ENSMUSG00000093221	7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014102	Mir3105
ENSMUST00000175482	ENSMUSG00000093223	15	28	26	8	65	4	0	0	0	58	71	115	0	8	9	6	8	0		Gm27903
ENSMUST00000175483	ENSMUSG00000093224	12	0	0	0	0	1	9	6	2	0	0	0	0	1	0	0	0	0		Gm25750
ENSMUST00000175485	ENSMUSG00000093226	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25749
ENSMUST00000175486	ENSMUSG00000093227	10	0	0	0	4	0	2	0	0	0	0	0	0	0	0	0	0	0	MI0014021	Mir1251
ENSMUST00000175487	ENSMUSG00000093228	1	2	0	0	1	0	0	0	0	0	1	3	0	0	0	1	0	0		Gm25748
ENSMUST00000175488	ENSMUSG00000095154	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0019317	Mir344i
ENSMUST00000175489	ENSMUSG00000093230	3	0	1	0	0	1	0	2	1	0	0	0	0	0	0	0	0	0		Gm24109
ENSMUST00000175490	ENSMUSG00000093231	12	0	0	4	17	0	2	5	0	21	0	4	0	3	0	3	0	0		Gm25297
ENSMUST00000175491	ENSMUSG00000093232	13	119	93	72	399	330	204	273	237	48	17	4	0	191	31	9	42	8	MI0000562	Gm24111
ENSMUST00000175493	ENSMUSG00000093234	19	4	1	4	22	13	43	8	49	0	2	0	0	5	0	2	0	2	MI0014048	Mir3085
ENSMUST00000175494	ENSMUSG00000094486	5	128	69	56	348	90	80	90	71	184	182	64	1	37	28	102	152	45		Gm23268
ENSMUST00000175495	ENSMUSG00000093236	19	4	8	3	25	7	6	5	0	19	27	18	0	2	0	4	11	1		Gm24108
ENSMUST00000175497	ENSMUSG00000093238	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0000721	Mir9-3
ENSMUST00000175498	ENSMUSG00000093239	9	2	1	0	2	0	4	0	0	4	3	3	0	0	0	1	0	0		Gm24106
ENSMUST00000175500	ENSMUSG00000093241	8	0	0	0	4	7	11	5	12	1	0	0	0	2	0	0	0	0	MI0014105	Mir3108
ENSMUST00000175501	ENSMUSG00000093242	2	0	0	1	0	4	10	12	5	5	2	2	0	2	0	2	1	0		Gm24574
ENSMUST00000175502	ENSMUSG00000093243	15	67	46	38	107	5	3	4	0	23	32	174	0	2	0	7	16	4		Gm24575
ENSMUST00000175505	ENSMUSG00000093246	16	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	MI0030345	Gm24572
ENSMUST00000175509	ENSMUSG00000095435	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22745
ENSMUST00000175510	ENSMUSG00000093251	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22932
ENSMUST00000175513	ENSMUSG00000093254	1	0	0	1	0	1	3	0	0	0	0	0	0	0	0	2	0	3	MI0018038	Mir5126
ENSMUST00000175515	ENSMUSG00000093256	16	23	7	3	23	3	0	4	1	39	9	20	0	2	4	3	2	3		Gm22933
ENSMUST00000175516	ENSMUSG00000095943	13	410	387	164	1421	78	75	83	43	87	183	873	0	0	29	110	184	132		Gm25197
ENSMUST00000175519	ENSMUSG00000093260	13	3	2	0	4	0	0	0	0	4	0	0	0	0	0	0	0	0		Gm23415
ENSMUST00000175520	ENSMUSG00000093261	15	4	0	0	0	0	0	0	0	1	0	4	0	0	0	0	0	0		Gm23416
ENSMUST00000175521	ENSMUSG00000093262	16	3	6	8	18	8	15	5	8	11	6	18	0	5	0	3	13	6		Gm23413
ENSMUST00000175523	ENSMUSG00000093264	11	0	0	0	2	1	0	0	2	53	13	0	0	1	7	21	19	3		Gm23419
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ENSMUST00000175528	ENSMUSG00000093269	13	3	0	0	2	1	0	1	0	10	7	3	0	0	0	2	2	0	MI0018035	Mir5124a
ENSMUST00000175529	ENSMUSG00000093270	17	2	0	1	1	13	28	9	24	0	2	2	0	2	2	1	1	0	MI0018046	Mir5134
ENSMUST00000175530	ENSMUSG00000093271	6	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	1		Gm26233
ENSMUST00000175531	ENSMUSG00000093476	2	15	5	6	23	17	10	6	0	44	17	11	0	23	6	16	4	11		Gm22355
ENSMUST00000175532	ENSMUSG00000093273	11	5	4	1	9	12	13	12	7	8	3	0	0	3	7	5	3	0	MI0014026	Mir3064
ENSMUST00000175533	ENSMUSG00000093274	18	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm26235
ENSMUST00000175535	ENSMUSG00000093276	8	83	47	43	137	18	33	28	40	64	83	241	4	9	6	33	31	24		Gm26237
ENSMUST00000175537	ENSMUSG00000093278	11	0	1	0	1	0	2	0	0	0	1	2	0	0	0	0	0	2	MI0018019	Mir5110
ENSMUST00000175538	ENSMUSG00000093279	5	0	1	1	1	1	2	5	3	19	0	0	0	5	5	7	6	2		Gm26238
ENSMUST00000175539	ENSMUSG00000093280	2	0	0	0	3	3	8	3	0	0	0	0	0	2	1	3	0	1	MI0013007	Mir2861
ENSMUST00000175540	ENSMUSG00000093281	8	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22565
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ENSMUST00000175545	ENSMUSG00000093286	1	0	0	4	0	5	7	4	3	2	10	0	4	0	2	10	0	16		Gm22569
ENSMUST00000175549	ENSMUSG00000093290	7	0	0	0	2	2	8	1	3	1	1	2	0	4	3	0	0	0	MI0018037	Mir3572
ENSMUST00000175550	ENSMUSG00000093291	12	2	9	3	4	6	10	3	5	1	0	0	0	0	0	0	0	0	MI0019180	Mir299b
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ENSMUST00000175552	ENSMUSG00000093293	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014088	Mir3095
ENSMUST00000175553	ENSMUSG00000093294	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25399
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ENSMUST00000175561	ENSMUSG00000093302	5	0	0	2	1	2	5	2	2	0	2	2	0	3	1	3	5	1		Gm23801
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ENSMUST00000175563	ENSMUSG00000093912	16	14	18	12	47	3	3	7	9	13	36	67	1	3	3	20	28	1	MI0014697	Mir3470b
ENSMUST00000175565	ENSMUSG00000093306	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23802
ENSMUST00000175570	ENSMUSG00000093311	5	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	MI0016972	Mir3965
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ENSMUST00000175574	ENSMUSG00000093315	19	5	7	13	20	244	156	265	63	7	2	0	0	25	19	11	18	2	MI0018023	Mir5114
ENSMUST00000175576	ENSMUSG00000093317	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25470
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ENSMUST00000175586	ENSMUSG00000093327	18	2	3	1	9	6	38	3	57	0	0	0	0	8	7	5	5	2	MI0018016	Mir5107
ENSMUST00000175588	ENSMUSG00000093329	X	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm24973
ENSMUST00000175590	ENSMUSG00000093331	12	0	0	0	1	0	0	0	4	0	0	0	0	0	0	0	0	0		Gm22120
ENSMUST00000175591	ENSMUSG00000094842	4	4	0	0	17	10	28	0	0	16	0	7	14	0	0	30	23	18		Gm22639
ENSMUST00000175593	ENSMUSG00000093334	13	41	13	16	135	37	27	78	57	74	105	69	2	41	32	134	85	71		Gm22118
ENSMUST00000175594	ENSMUSG00000093335	Y	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	5	0		Gm22119
ENSMUST00000175595	ENSMUSG00000093336	2	166	23	20	112	15	25	19	16	333	75	110	7	55	54	112	192	42	MI0009949	Mir1954
ENSMUST00000175597	ENSMUSG00000093338	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	MI0014083	Mir3090
ENSMUST00000175599	ENSMUSG00000093340	15	0	0	0	0	2	5	1	4	0	0	0	0	0	2	6	3	4		Gm26117
ENSMUST00000175600	ENSMUSG00000093341	11	7	6	3	21	0	1	3	0	11	9	19	0	1	4	7	2	1		Gm26116
ENSMUST00000175601	ENSMUSG00000093342	18	11	2	1	12	1	1	0	1	5	0	20	0	1	0	4	0	0		Gm26119
ENSMUST00000175603	ENSMUSG00000093344	5	0	0	0	4	0	1	2	2	14	6	1	0	0	1	2	4	2		Gm26113
ENSMUST00000175605	ENSMUSG00000093346	19	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1		Gm26115
ENSMUST00000175607	ENSMUSG00000093348	7	1	2	1	3	5	14	8	10	2	0	1	0	0	2	1	4	0	MI0014093	Mir3101
ENSMUST00000175610	ENSMUSG00000093351	12	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	MI0014035	Mir3072
ENSMUST00000175611	ENSMUSG00000093352	12	3	3	5	21	0	0	0	1	11	9	18	0	3	3	4	5	1		Gm23291
ENSMUST00000175612	ENSMUSG00000096189	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0019196	Mir344h-2
ENSMUST00000175613	ENSMUSG00000093354	9	38	1577	12	15370	107	17193	95	4656	4	2	4	0	26	23	8	39	12	MI0000725	Mir125b-1
ENSMUST00000175617	ENSMUSG00000093358	11	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	MI0014025	Mir3063
ENSMUST00000175618	ENSMUSG00000093359	7	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm23292
ENSMUST00000175621	ENSMUSG00000093362	14	4	0	0	0	0	0	0	0	24	3	0	0	0	10	7	16	2		Gm22802
ENSMUST00000175622	ENSMUSG00000093363	2	306	115	208	149	6	3	6	5	25	138	148	0	0	0	4	32	29		Gm22002
ENSMUST00000175627	ENSMUSG00000093368	2	0	0	0	0	0	0	0	0	0	1	1	0	15	0	0	0	0		Gm22800
ENSMUST00000175632	ENSMUSG00000093373	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23075
ENSMUST00000175639	ENSMUSG00000093515	1	0	1	0	1	2	8	0	2	0	0	0	0	2	0	0	0	0	MI0019183	Mir1231
ENSMUST00000175907	ENSMUSG00000093615	9	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	MI0019186	Mir5618
ENSMUST00000175928	ENSMUSG00000093746	2	1	0	1	0	3	0	13	2	1	0	0	0	5	1	1	4	0	MI0019190	Mir5622
ENSMUST00000175989	ENSMUSG00000093539	11	0	1	0	1	3	8	3	1	1	2	0	0	2	0	0	0	0	MI0019189	Mir5621
ENSMUST00000176002	ENSMUSG00000093763	9	1	0	0	3	6	4	1	5	0	0	0	0	1	0	0	0	0	MI0019195	Mir5626
ENSMUST00000176065	ENSMUSG00000093690	5	0	0	1	2	1	4	3	2	0	0	1	0	0	0	0	0	0	MI0019187	Mir5619
ENSMUST00000176507	ENSMUSG00000093428	X	135	126	87	727	382	374	369	220	91	163	66	3	98	142	219	238	104		Gm26318
ENSMUST00000176537	ENSMUSG00000093498	10	1	1	1	6	18	12	7	11	0	1	0	0	1	0	0	0	0	MI0019182	Mir5615-2
ENSMUST00000176598	ENSMUSG00000093710	5	0	0	0	0	11	9	4	6	1	0	0	0	1	2	2	0	0	MI0019194	Mir5625
ENSMUST00000176615	ENSMUSG00000093409	6	52	44	23	168	84	39	98	63	70	68	37	0	15	32	68	158	33		Gm25193
ENSMUST00000176631	ENSMUSG00000093757	19	0	0	0	2	2	2	2	2	0	0	0	0	0	0	0	0	0	MI0019191	Mir5623
ENSMUST00000176635	ENSMUSG00000093480	13	1	0	0	7	48	21	29	22	1	1	0	0	17	2	1	0	0	MI0019193	Mir5624
ENSMUST00000176664	ENSMUSG00000093404	10	270	146	127	865	803	798	707	664	1704	799	258	7	387	576	1213	1287	527		Gm25190
ENSMUST00000176783	ENSMUSG00000093508	17	0	0	0	0	1	3	1	0	0	0	0	0	0	0	0	0	0	MI0019318	Mir5709
ENSMUST00000176786	ENSMUSG00000093408	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0019185	Mir5617
ENSMUST00000176884	ENSMUSG00000093441	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0019319	Mir5710
ENSMUST00000176903	ENSMUSG00000093599	7	22	4	5	30	28	28	27	12	17	18	38	2	4	9	8	3	1	MI0019188	Mir5620
ENSMUST00000176930	ENSMUSG00000093684	14	170	148	67	199	0	41	21	57	0	71	369	0	6	0	18	31	61		Gm27857
ENSMUST00000176951	ENSMUSG00000093529	15	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		Gm25397
ENSMUST00000177002	ENSMUSG00000093572	11	41	15	16	40	6	42	15	34	24	31	72	3	11	13	33	36	16		Gm24756
ENSMUST00000177110	ENSMUSG00000093782	1	0	0	0	0	2	1	0	0	2	0	0	0	1	0	0	0	0		Gm22396
ENSMUST00000177217	ENSMUSG00000093403	4	0	0	1	0	4	12	5	5	0	0	0	0	0	0	0	0	0	MI0019184	Mir5616
ENSMUST00000177238	ENSMUSG00000093618	12	1	0	5	2	32	72	13	16	0	0	0	0	4	1	0	0	0	MI0019198	Mir5627
ENSMUST00000177270	ENSMUSG00000093499	3	47	22	24	75	74	48	79	36	29	46	25	10	19	41	61	90	26		Gm25442
ENSMUST00000177317	ENSMUSG00000093762	10	35	5	7	27	14	9	6	3	185	82	34	2	27	38	48	37	13		Gm25591
ENSMUST00000177427	ENSMUSG00000093780	5	49	20	33	187	54	19	54	42	56	71	38	2	27	26	134	186	64		Gm22395
ENSMUST00000177557	ENSMUSG00000093816	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26445
ENSMUST00000177620	ENSMUSG00000094691	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22908
ENSMUST00000177630	ENSMUSG00000094101	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22775
ENSMUST00000177640	ENSMUSG00000096133	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25145
ENSMUST00000177656	ENSMUSG00000095947	17	4	3	2	38	19	35	22	24	82	34	10	26	5	18	37	31	4		Gm25195
ENSMUST00000177681	ENSMUSG00000094067	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25158
ENSMUST00000177685	ENSMUSG00000093897	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26268
ENSMUST00000177687	ENSMUSG00000096352	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25708
ENSMUST00000177693	ENSMUSG00000095933	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25700
ENSMUST00000177728	ENSMUSG00000096075	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25349
ENSMUST00000177733	ENSMUSG00000094009	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24167
ENSMUST00000177742	ENSMUSG00000094297	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0006279	Mir669k
ENSMUST00000177758	ENSMUSG00000096142	7	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0		Gm25817
ENSMUST00000177773	ENSMUSG00000094466	6	1	0	0	1	1	0	0	1	0	3	2	0	0	1	1	0	2		Gm24308
ENSMUST00000177784	ENSMUSG00000094603	17	0	8	0	65	0	0	0	0	0	70	817	0	0	0	2	0	0		Gm25872
ENSMUST00000177790	ENSMUSG00000096587	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014056	Mir467a-6
ENSMUST00000177794	ENSMUSG00000096377	4	22	13	35	54	145	168	96	110	2	2	0	0	47	12	0	1	0	MI0018034	Mir5123
ENSMUST00000177797	ENSMUSG00000094432	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23616
ENSMUST00000177809	ENSMUSG00000095849	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24300
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ENSMUST00000177832	ENSMUSG00000094190	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25451
ENSMUST00000177835	ENSMUSG00000095336	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24315
ENSMUST00000177845	ENSMUSG00000096314	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23521
ENSMUST00000177866	ENSMUSG00000093995	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		Gm26426
ENSMUST00000177899	ENSMUSG00000095047	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22852
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ENSMUST00000178068	ENSMUSG00000095989	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23049
ENSMUST00000178082	ENSMUSG00000095198	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014056	Mir467a-3
ENSMUST00000178119	ENSMUSG00000095727	8	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm23646
ENSMUST00000178126	ENSMUSG00000096174	4	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm22991
ENSMUST00000178138	ENSMUSG00000094041	8	219	152	83	620	2	4	5	4	34	108	968	0	3	2	8	21	6		Gm28019
ENSMUST00000178153	ENSMUSG00000095122	16	0	5	0	11	0	0	0	0	0	0	0	0	0	1	0	0	2		Gm23215
ENSMUST00000178201	ENSMUSG00000094304	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24923
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ENSMUST00000178240	ENSMUSG00000095246	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24752
ENSMUST00000178283	ENSMUSG00000094702	10	0	0	2	1	2	5	2	2	0	2	2	0	3	1	3	5	1		Gm24485
ENSMUST00000178285	ENSMUSG00000094210	7	3	1	4	3	13	11	8	1	0	0	0	0	2	0	2	1	0	MI0030346	Mir23450
ENSMUST00000178287	ENSMUSG00000093959	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24496
ENSMUST00000178295	ENSMUSG00000096264	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23108
ENSMUST00000178305	ENSMUSG00000096784	15	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm24643
ENSMUST00000178322	ENSMUSG00000094359	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25571
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ENSMUST00000178456	ENSMUSG00000096388	4	0	0	0	0	0	0	0	0	0	14	1	0	0	2	0	0	0		Gm25355
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000178484	ENSMUSG00000096193	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26134
ENSMUST00000178512	ENSMUSG00000094467	6	57	0	0	109	0	0	0	0	0	22	0	0	0	0	0	6	0		Gm24307
ENSMUST00000178574	ENSMUSG00000095942	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25198
ENSMUST00000178593	ENSMUSG00000096667	16	17	2	0	98	0	0	2	2	41	19	0	0	3	0	0	0	0		Gm22862
ENSMUST00000178626	ENSMUSG00000096425	17	2	0	16	0	0	11	3	0	122	113	190	0	6	14	29	7	14		Gm24979
ENSMUST00000178635	ENSMUSG00000094688	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014053	Mir467a-7
ENSMUST00000178651	ENSMUSG00000096098	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004698	Mir713
ENSMUST00000178653	ENSMUSG00000094946	1	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm25754
ENSMUST00000178681	ENSMUSG00000095160	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25548
ENSMUST00000178702	ENSMUSG00000096829	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23771
ENSMUST00000178726	ENSMUSG00000095027	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24017
ENSMUST00000178754	ENSMUSG00000095467	9	3	0	0	3	2	2	0	0	0	0	10	0	6	1	3	0	0		Gm22243
ENSMUST00000178780	ENSMUSG00000094968	1	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm22419
ENSMUST00000178795	ENSMUSG00000094969	17	38	107	102	110	47	10	153	55	22	90	196	0	0	7	36	36	5		Gm22420
ENSMUST00000178801	ENSMUSG00000096239	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0005502	Mir466b-4
ENSMUST00000178821	ENSMUSG00000096061	11	170	148	67	199	0	41	21	57	0	71	369	0	6	0	18	31	61		Gm23681
ENSMUST00000178841	ENSMUSG00000093835	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23147
ENSMUST00000178897	ENSMUSG00000093823	1	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm24802
ENSMUST00000178937	ENSMUSG00000094983	3	1	1	2	5	0	0	0	0	0	2	3	0	0	0	5	0	2		Gm23726
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ENSMUST00000178951	ENSMUSG00000095536	2	0	0	0	2	25	34	15	26	0	1	0	0	31	3	0	0	0	MI0005505	Mir466b-5
ENSMUST00000178954	ENSMUSG00000096031	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23189
ENSMUST00000178964	ENSMUSG00000096309	14	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm25208
ENSMUST00000178981	ENSMUSG00000093878	6	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm25458
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ENSMUST00000179003	ENSMUSG00000094572	7	3	0	0	1	6	0	2	0	0	3	0	0	0	0	0	3	0		Gm23550
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ENSMUST00000179154	ENSMUSG00000094267	4	3	0	0	1	6	0	2	0	0	3	2	0	0	0	3	1	1	MI0006299	Gm25123
ENSMUST00000179159	ENSMUSG00000094959	4	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0		Gm24112
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ENSMUST00000179182	ENSMUSG00000096274	7	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0		Gm24766
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ENSMUST00000179268	ENSMUSG00000095843	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26491
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ENSMUST00000179283	ENSMUSG00000096631	7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22171
ENSMUST00000179294	ENSMUSG00000094515	4	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm24567
ENSMUST00000179320	ENSMUSG00000096894	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014056	Mir467a-10
ENSMUST00000179335	ENSMUSG00000094641	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23694
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ENSMUST00000179358	ENSMUSG00000094650	10	1	0	1	0	0	1	0	0	0	1	2	0	0	5	0	0	0		Gm25361
ENSMUST00000179362	ENSMUSG00000095685	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23283
ENSMUST00000179366	ENSMUSG00000096383	14	3	0	0	1	6	0	2	0	0	3	2	0	0	0	0	3	1	MI0006299	Gm25353
ENSMUST00000179371	ENSMUSG00000095697	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0004646	Mir683-1
ENSMUST00000179380	ENSMUSG00000095380	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23952
ENSMUST00000179444	ENSMUSG00000094718	8	2	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm22825
ENSMUST00000179447	ENSMUSG00000096027	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014053	Mir467a-2
ENSMUST00000179485	ENSMUSG00000095555	9	78	148	29	199	0	41	1	57	0	7	216	0	1	0	1	4	6		Gm28010
ENSMUST00000179496	ENSMUSG00000096172	1	3	0	0	1	6	0	2	0	0	3	2	0	0	0	0	3	1	MI0006299	Gm22992
ENSMUST00000179510	ENSMUSG00000096673	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24520
ENSMUST00000179516	ENSMUSG00000095856	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm22619
ENSMUST00000179561	ENSMUSG00000096130	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25144
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ENSMUST00000179603	ENSMUSG00000095951	2	27	4	9	30	10	2	10	13	22	28	38	0	4	6	4	7	7		Gm23963
ENSMUST00000179609	ENSMUSG00000094123	X	1	1	3	9	3	47	3	17	1	3	2	0	1	0	4	1	3		Gm23945
ENSMUST00000179610	ENSMUSG00000094428	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26443
ENSMUST00000179691	ENSMUSG00000096535	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24755
ENSMUST00000179692	ENSMUSG00000096906	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26506
ENSMUST00000179699	ENSMUSG00000094506	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26229
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ENSMUST00000179732	ENSMUSG00000094750	6	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25019
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ENSMUST00000179752	ENSMUSG00000095222	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014053	Mir467a-9
ENSMUST00000179783	ENSMUSG00000095853	1	0	0	0	0	0	0	0	0	0	0	508	0	0	0	0	0	0		Gm22616
ENSMUST00000179798	ENSMUSG00000095699	2	0	2	0	3	12	11	13	20	0	1	0	0	28	7	2	1	0	MI0004523	Mir26092
ENSMUST00000179815	ENSMUSG00000096384	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm25352
ENSMUST00000179866	ENSMUSG00000094477	4	0	0	0	0	0	0	0	0	0	14	1	0	0	2	0	0	0		Gm23064
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ENSMUST00000179906	ENSMUSG00000094165	2	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0		Gm26073
ENSMUST00000179918	ENSMUSG00000094901	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23576
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ENSMUST00000180070	ENSMUSG00000096512	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0014053	Mir467a-8
ENSMUST00000180073	ENSMUSG00000096889	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm23571
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ENSMUST00000180080	ENSMUSG00000096721	6	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0		Gm25942
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000180144	ENSMUSG00000096112	16	9	18	8	58	3	13	8	9	28	44	9	0	7	2	26	33	23		Gm26269
ENSMUST00000180156	ENSMUSG00000095020	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24020
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ENSMUST00000180199	ENSMUSG00000095884	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm26431
ENSMUST00000180209	ENSMUSG00000096184	4	1	1	2	2	2	3	2	2	0	0	1	0	0	0	1	1	0		Gm23304
ENSMUST00000180211	ENSMUSG00000094659	2	0	0	0	2	25	34	15	26	0	1	0	0	31	3	0	0	0	MI0005505	Mir466c-2
ENSMUST00000180212	ENSMUSG00000094780	7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24659
ENSMUST00000180238	ENSMUSG00000096583	2	0	2	0	3	12	11	13	20	0	1	0	0	28	7	2	1	0	MI0004523	Mir669a-1
ENSMUST00000180244	ENSMUSG00000094007	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm24169
ENSMUST00000180257	ENSMUSG00000093791	1	3	0	0	1	6	0	2	0	0	3	2	0	0	0	0	3	1	MI0006299	Gm24092
ENSMUST00000180307	ENSMUSG00000096694	12	1	0	1	0	0	0	0	0	0	0	3	0	0	0	0	0	0		Gm23190
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ENSMUST00000183340	ENSMUSG00000098898	10	64	48	0	194	57	98	77	88	280	326	271	21	35	98	143	94	44		Gm27754
ENSMUST00000183342	ENSMUSG00000098844	19	0	0	0	1	1	1	4	1	0	0	0	0	0	0	0	1	0	MI0022840	Mir6992
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ENSMUST00000183364	ENSMUSG00000098951	5	1	0	0	2	1	0	2	2	0	0	0	0	0	0	0	0	0	MI0024985	Mir7647
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ENSMUST00000183379	ENSMUSG00000098840	11	2	1	2	5	4	12	5	0	0	3	0	0	0	0	0	0	0	MI0025024	Mir7679
ENSMUST00000183384	ENSMUSG00000099331	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023734	Mir7239
ENSMUST00000183385	ENSMUSG00000099308	16	15	3	5	22	0	0	0	0	2	2	22	0	0	0	0	0	0	MI0021896	Mir6367
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ENSMUST00000183406	ENSMUSG00000098563	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021938	Mir6402
ENSMUST00000183408	ENSMUSG00000098731	5	0	0	0	0	2	6	2	3	3	0	0	0	0	0	0	0	0	MI0022876	Mir7027
ENSMUST00000183412	ENSMUSG00000099260	15	0	3	0	0	3	19	3	11	0	0	0	0	1	0	0	0	0	MI0022801	Mir6954
ENSMUST00000183415	ENSMUSG00000098622	3	11	8	7	27	3	17	14	1	22	32	12	0	7	10	8	3	6		Gm27974
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ENSMUST00000183439	ENSMUSG00000099079	8	6	13	2	26	133	75	54	51	0	1	1	0	9	15	5	15	1	MI0022918	Mir7068
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ENSMUST00000183491	ENSMUSG00000098996	15	9	10	10	20	33	78	45	47	9	12	1	0	8	10	6	4	2	MI0025017	Mir7676-1
ENSMUST00000183494	ENSMUSG00000098896	2	3	1	1	7	8	13	10	13	5	7	3	0	2	8	1	1	0	MI0026054	Mir3473g
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ENSMUST00000183498	ENSMUSG00000098651	2	0	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	MI0022847	Mir6999
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ENSMUST00000183555	ENSMUSG00000098765	2	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	MI0025036	Mir7685
ENSMUST00000183556	ENSMUSG00000099264	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021948	Mir6411
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ENSMUST00000183566	ENSMUSG00000099254	5	0	2	1	12	10	12	5	14	0	6	0	0	3	0	0	0	0	MI0022879	Mir7030
ENSMUST00000183568	ENSMUSG00000098931	12	0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	MI0026027	Mir8099-1
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ENSMUST00000183570	ENSMUSG00000099097	X	28	0	19	71	0	0	0	0	0	14	108	0	0	0	0	0	2		Gm27341
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ENSMUST00000183577	ENSMUSG00000098803	19	1446	217	478	1203	1392	2993	7993	8103	13958	11074	4252	313	18608	11388	5310	3395	655		Gm27468
ENSMUST00000183581	ENSMUSG00000098660	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021864	Mir6336
ENSMUST00000183582	ENSMUSG00000099227	1	9	4	3	24	143	370	149	278	11	6	13	0	27	24	18	21	12	MI0026046	Mir8114
ENSMUST00000183584	ENSMUSG00000098611	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021871	Mir6343
ENSMUST00000183592	ENSMUSG00000099174	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021943	Mir6406
ENSMUST00000183596	ENSMUSG00000098851	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021881	Mir6353
ENSMUST00000183597	ENSMUSG00000098606	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022750	Mir6903
ENSMUST00000183598	ENSMUSG00000099180	15	2	3	1	26	103	142	59	110	0	2	2	0	2	0	0	8	1	MI0022803	Mir6956
ENSMUST00000183599	ENSMUSG00000098452	13	77	39	25	95	5	1	1	7	36	36	120	0	2	0	7	2	0		Gm27501
ENSMUST00000183602	ENSMUSG00000098286	19	0	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	MI0026018	Mir8091
ENSMUST00000183603	ENSMUSG00000098500	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021931	Mir6396
ENSMUST00000183606	ENSMUSG00000098839	7	0	2	0	0	6	13	7	3	0	0	0	0	3	0	0	1	0	MI0022903	Mir7054
ENSMUST00000183613	ENSMUSG00000098965	1	1	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0		Gm27844
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpgl0673	hpgl0674	hpgl0675	hpgl0676	hpgl0677	hpgl0678	hpgl0679	hpgl0680	hpgl0523	hpgl0524	hpgl0525	hpgl0555	hpgl0556	hpgl0557	hpgl0558	hpgl0559	hpgl0560	mirBase_accession	mirBase name
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ENSMUST00000183624	ENSMUSG00000098824	2	1	0	0	1	8	7	1	1	0	0	0	0	0	0	0	1	0	MI0022855	Mir7006
ENSMUST00000183639	ENSMUSG00000098876	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021878	Mir6350
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ENSMUST00000183646	ENSMUSG00000098291	17	1	1	0	3	2	4	6	3	0	0	0	0	0	1	1	0	0	MI0022821	Mir6973a
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ENSMUST00000183650	ENSMUSG00000099319	15	1	0	0	1	8	12	15	4	0	0	0	0	1	2	2	2	0	MI0024986	Mir7648
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ENSMUST00000183660	ENSMUSG00000099193	11	0	0	0	0	0	0	0	0	2	0	0	1	1	5	0	1	0		Gm27374
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ENSMUST00000183710	ENSMUSG00000098446	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023737	Mir7242
ENSMUST00000183711	ENSMUSG00000098345	9	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		Gm27847
ENSMUST00000183713	ENSMUSG00000098771	12	100	94	151	545	14	47	17	69	0	73	17	132	3	15	1712	1892	1604	MI0022354	Mir6538
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ENSMUST00000183720	ENSMUSG00000098403	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27415
ENSMUST00000183724	ENSMUSG00000098413	19	3	0	0	1	25	19	9	5	0	1	0	0	4	3	0	0	0	MI0022838	Mir6990
ENSMUST00000183726	ENSMUSG00000098542	14	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		Gm27532
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ENSMUST00000183732	ENSMUSG00000098866	14	0	0	2	0	105	154	86	49	0	4	9	0	14	4	0	0	0	MI0022355	Mir6539
ENSMUST00000183735	ENSMUSG00000099118	19	0	0	0	0	2	0	3	1	0	0	0	0	1	0	3	0	0	MI0026019	Mir8092
ENSMUST00000183739	ENSMUSG00000098652	16	0	0	0	0	0	1	0	0	4	0	0	0	0	0	0	0	0		Gm27671
ENSMUST00000183740	ENSMUSG00000098406	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023717	Mir7222
ENSMUST00000183743	ENSMUSG00000098344	1	204	89	97	434	187	350	240	185	693	223	118	6	112	96	159	148	86	MI0026016	Mir3473f
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ENSMUST00000183751	ENSMUSG00000098653	10	12	4	1	44	2	5	13	0	0	13	16	3	0	1	28	17	15		Gm27672
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ENSMUST00000183771	ENSMUSG00000099078	8	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0026042	Mir8110
ENSMUST00000183772	ENSMUSG00000098258	13	37	9	9	15	5	4	0	3	4	22	152	1	2	7	3	9	4	MI0021898	Mir6369
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ENSMUST00000183777	ENSMUSG00000099152	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022817	Mir6969
ENSMUST00000183778	ENSMUSG00000099211	7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27684
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ENSMUST00000183796	ENSMUSG00000099286	11	0	6	2	3	20	12	9	11	0	1	2	0	10	0	0	2	0	MI0023730	Mir7235
ENSMUST00000183797	ENSMUSG00000099060	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022874	Mir7025
ENSMUST00000183799	ENSMUSG00000099191	14	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		Gm27375
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ENSMUST00000183823	ENSMUSG00000099304	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27420
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ENSMUST00000183847	ENSMUSG00000099222	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023708	Mir7213
ENSMUST00000183849	ENSMUSG00000098431	8	2	0	1	4	3	5	3	2	0	0	0	0	1	2	2	0	0	MI0025006	Mir7666
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ENSMUST00000183852	ENSMUSG00000098822	5	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	MI0022888	Mir7039
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ENSMUST00000183859	ENSMUSG00000098774	11	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	MI0022777	Mir6930
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ENSMUST00000183927	ENSMUSG00000098706	18	4	3	1	3	40	27	28	12	3	2	2	0	17	2	0	4	0	MI0022827	Mir6979
ENSMUST00000183930	ENSMUSG00000099215	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27682
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ENSMUST00000183945	ENSMUSG00000098769	11	49	24	14	72	159	100	190	52	1	13	15	0	24	14	4	15	4	MI0026033	Mir8103
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ENSMUST00000183953	ENSMUSG00000099088	10	3	1	4	6	27	50	20	10	0	3	4	1	4	6	13	10	14		Gm27920
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ENSMUST00000183965	ENSMUSG00000098704	11	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	MI0022781	Mir6934
ENSMUST00000183968	ENSMUSG00000099089	7	9	4	1	31	3	5	1	2	2	6	8	0	2	0	3	1	4		Gm27921
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ENSMUST00000183986	ENSMUSG00000098863	11	1	1	3	1	15	22	15	8	0	4	0	0	2	1	16	7	7	MI0026031	Mir8101
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ENSMUST00000184003	ENSMUSG00000099045	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021903	Mir6374
ENSMUST00000184007	ENSMUSG00000099125	11	0	0	0	4	15	42	27	17	0	0	0	2	1	7	6	8	8		Gm27322
ENSMUST00000184009	ENSMUSG00000099223	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023716	Mir7221
ENSMUST00000184011	ENSMUSG00000099245	14	0	1	0	3	10	31	20	7	0	7	0	0	1	3	6	2	0	MI0026026	Mir8098
ENSMUST00000184024	ENSMUSG00000099275	9	3	0	0	0	3	0	2	1	0	0	0	0	0	0	3	0	0	MI0026038	Mir8107
ENSMUST00000184042	ENSMUSG00000098480	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021919	Mir6387
ENSMUST00000184043	ENSMUSG00000098954	4	0	0	0	2	7	4	10	9	0	1	0	0	0	2	0	1	0	MI0024998	Mir7658
ENSMUST00000184044	ENSMUSG00000099330	7	0	0	0	2	8	7	3	7	0	0	0	0	0	0	0	0	0	MI0022902	Mir7053
ENSMUST00000184048	ENSMUSG00000098521	9	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	MI0025043	Mir7243
ENSMUST00000184049	ENSMUSG00000098887	10	0	2	1	1	0	0	0	0	0	0	1	0	0	4	0	1	0	MI0021950	Mir6413
ENSMUST00000184050	ENSMUSG00000098513	4	0	0	1	0	0	1	3	1	0	0	0	0	0	0	0	0	0	MI0021935	Mir6399
ENSMUST00000184055	ENSMUSG00000099128	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021913	Mir6382
ENSMUST00000184056	ENSMUSG00000098279	10	0	0	0	0	0	4	3	1	0	0	0	0	0	0	0	0	0	MI0022755	Mir6908
ENSMUST00000184059	ENSMUSG00000098833	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021877	Mir6349
ENSMUST00000184064	ENSMUSG00000099160	5	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	MI0021953	Mir6415
ENSMUST00000184068	ENSMUSG00000098539	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021863	Mir133c
ENSMUST00000184071	ENSMUSG00000098544	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023706	Mir7211
ENSMUST00000184074	ENSMUSG00000099031	8	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023735	Mir7240
ENSMUST00000184075	ENSMUSG00000099226	X	1	0	0	1	30	32	21	19	2	0	0	0	8	3	0	0	1	MI0022941	Mir7091
ENSMUST00000184078	ENSMUSG00000099247	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27541
ENSMUST00000184079	ENSMUSG00000098885	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0024999	Mir7659
ENSMUST00000184081	ENSMUSG00000098734	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021862	Mir6335
ENSMUST00000184087	ENSMUSG00000099268	16	486	366	255	1226	199	271	186	124	591	703	977	21	93	117	250	221	119		Gm27773
ENSMUST00000184090	ENSMUSG00000098562	10	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	MI0022757	Mir6910
ENSMUST00000184096	ENSMUSG00000098560	8	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		Gm27530
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ENSMUST00000184108	ENSMUSG00000098271	X	4	0	1	5	3	3	3	0	11	1	3	0	2	2	5	1	0		Gm27828
ENSMUST00000184111	ENSMUSG00000098592	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022764	Mir6917
ENSMUST00000184114	ENSMUSG00000098465	8	1	0	0	2	58	69	58	40	0	0	0	0	5	2	2	2	1	MI0026040	Mir1668
ENSMUST00000184115	ENSMUSG00000098687	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022352	Mir7k
ENSMUST00000184128	ENSMUSG00000098432	11	74	62	33	187	45	44	36	22	179	210	99	3	16	26	38	27	32		Gm27493
ENSMUST00000184134	ENSMUSG00000099145	5	0	0	0	0	1	8	2	2	0	0	0	0	1	2	0	0	0	MI0026048	Mir8116
ENSMUST00000184136	ENSMUSG00000099158	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021897	Mir6368
ENSMUST00000184140	ENSMUSG00000099176	7	1	1	2	2	0	1	0	1	0	4	0	0	2	8	2	0	0	MI0021585	Mir6238
ENSMUST00000184148	ENSMUSG00000098919	11	0	0	0	0	2	3	0	3	0	0	0	0	0	0	0	0	1	MI0026032	Mir8102
ENSMUST00000184150	ENSMUSG00000098441	7	0	0	1	0	1	8	1	6	0	0	0	0	1	0	0	0	0	MI0022353	Mir6537
ENSMUST00000184153	ENSMUSG00000099014	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27359
ENSMUST00000184154	ENSMUSG00000098516	11	4	0	0	3	2	3	3	0	0	0	0	0	1	0	0	0	0	MI0024989	Mir7651
ENSMUST00000184156	ENSMUSG00000099311	9	0	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	MI0021591	Mir6244
ENSMUST00000184158	ENSMUSG00000098759	7	0	1	1	4	16	27	20	20	0	2	0	0	1	0	0	0	0	MI0022912	Mir7063
ENSMUST00000184167	ENSMUSG00000099210	7	2	0	0	3	2	7	4	1	0	0	1	0	3	0	0	0	0	MI0022900	Mir7051
ENSMUST00000184168	ENSMUSG00000098903	5	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0		Gm28022
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ENSMUST00000184178	ENSMUSG00000098381	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023720	Mir7225
ENSMUST00000184185	ENSMUSG00000098686	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022851	Mir6973b
ENSMUST00000184187	ENSMUSG00000098671	8	1	2	0	1	19	13	15	8	0	0	0	0	4	0	0	0	0	MI0022925	Mir7075
ENSMUST00000184191	ENSMUSG00000099022	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27924
ENSMUST00000184194	ENSMUSG00000099184	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021865	Mir6337
ENSMUST00000184195	ENSMUSG00000099272	X	0	0	1	6	7	3	6	3	0	0	0	0	2	2	0	0	0	MI0022943	Mir7093
ENSMUST00000184197	ENSMUSG00000098624	5	0	0	0	0	0	1	1	2	0	0	0	0	0	0	0	0	0	MI0022885	Mir7036
ENSMUST00000184201	ENSMUSG00000099114	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27405
ENSMUST00000184202	ENSMUSG00000098299	2	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	MI0023719	Mir7224
ENSMUST00000184204	ENSMUSG00000098932	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021947	Mir6410
ENSMUST00000184207	ENSMUSG00000098663	15	0	0	0	0	3	5	3	1	0	0	0	0	1	0	0	0	0	MI0022805	Mir6958
ENSMUST00000184212	ENSMUSG00000098414	10	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	MI0022756	Mir6909
ENSMUST00000184213	ENSMUSG00000098307	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27460
ENSMUST00000184215	ENSMUSG00000098798	8	1	0	0	1	1	1	0	1	4	5	1	0	0	0	14	13	2		Gm27288
ENSMUST00000184218	ENSMUSG00000098467	2	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0		Gm27591
ENSMUST00000184219	ENSMUSG00000098334	6	1	2	1	3	38	68	32	66	0	0	0	0	2	1	0	0	0	MI0022892	Mir7043
ENSMUST00000184224	ENSMUSG00000098716	17	16	6	7	23	84	87	35	36	4	4	4	0	14	7	8	7	6		Gm28033
ENSMUST00000184225	ENSMUSG00000098612	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021588	Mir6241
ENSMUST00000184226	ENSMUSG00000098826	17	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	1	0	MI0025022	Mir7677
ENSMUST00000184227	ENSMUSG00000098787	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022938	Mir7088
ENSMUST00000184228	ENSMUSG00000099181	10	1	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	MI0022752	Mir6905
ENSMUST00000184230	ENSMUSG00000098942	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0026029	Mir8100
ENSMUST00000184232	ENSMUSG00000098756	10	0	0	0	0	2	3	1	3	0	2	2	0	2	0	0	0	0	MI0021951	Mir378d
ENSMUST00000184237	ENSMUSG00000098266	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27516
ENSMUST00000184238	ENSMUSG00000098498	3	0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	MI0026027	Mir8099-2
ENSMUST00000184241	ENSMUSG00000098672	10	2	1	0	2	26	34	13	33	0	0	0	0	4	1	0	2	0	MI0022758	Mir6911
ENSMUST00000184242	ENSMUSG00000098899	X	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		Gm27839
ENSMUST00000184244	ENSMUSG00000098811	10	0	1	1	3	6	2	2	2	0	0	0	0	0	0	0	0	0	MI0022760	Mir6913
ENSMUST00000184246	ENSMUSG00000098721	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021885	Mir6357
ENSMUST00000184250	ENSMUSG00000098827	11	2322	711	1177	5605	104	94	95	74	1451	1476	17719	7	35	67	101	121	62		Gm27399
ENSMUST00000184251	ENSMUSG00000099218	14	4	0	1	0	0	1	0	0	2	3	0	0	0	0	0	2	0	MI0021921	Mir5124b
ENSMUST00000184258	ENSMUSG00000098350	5	4	1	0	2	3	0	0	1	27	3	6	3	3	10	0	3	0		Gm27551
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ENSMUST00000184262	ENSMUSG00000098879	12	0	3	3	13	7	4	9	4	0	0	0	0	0	0	0	0	0	MI0025016	Mir7675
ENSMUST00000184268	ENSMUSG00000098815	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27785
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Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000184275	ENSMUSG00000099109	11	1	0	0	2	25	14	7	12	1	4	0	2	3	3	0	1	0	MI0022966	Mir7115
ENSMUST00000184278	ENSMUSG00000098607	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021888	Mir6360
ENSMUST00000184281	ENSMUSG00000098343	5	984	505	476	3341	560	476	524	758	30525	121685	5693	195	2965	4322	13528	7236	2351	MI0021587	Mir6240
ENSMUST00000184284	ENSMUSG00000099134	4	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	MI0022867	Mir7018
ENSMUST00000184285	ENSMUSG00000098733	16	0	0	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0		Gm27833
ENSMUST00000184286	ENSMUSG00000098689	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021873	Mir6345
ENSMUST00000184289	ENSMUSG00000098455	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27428
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ENSMUST00000184295	ENSMUSG00000098886	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021916	Mir6385
ENSMUST00000184300	ENSMUSG00000099096	13	0	0	0	2	23	24	22	14	0	0	0	0	6	3	0	1	0	MI0022792	Mir6945
ENSMUST00000184308	ENSMUSG00000098422	4	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	MI0022865	Mir7016
ENSMUST00000184313	ENSMUSG00000098453	2	0	0	0	1	1	4	4	6	1	0	0	0	2	0	0	0	0	MI0022845	Mir6997
ENSMUST00000184317	ENSMUSG00000098315	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021906	Mir21b
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ENSMUST00000184349	ENSMUSG00000098751	14	0	1	0	0	9	11	3	2	0	4	0	0	1	4	0	1	0	MI0025012	Mir7672
ENSMUST00000184353	ENSMUSG00000099309	9	0	0	0	0	7	3	1	0	0	0	0	0	0	2	0	0	0	MI0022935	Mir7085
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ENSMUST00000184357	ENSMUSG00000099820	12	120	100	75	286	38	45	47	23	94	90	144	13	14	19	31	28	24		Gm27284
ENSMUST00000184358	ENSMUSG00000099101	11	0	0	0	1	2	6	2	3	1	0	1	0	0	0	0	0	0	MI0024993	Mir7653
ENSMUST00000184365	ENSMUSG00000098992	11	1	0	0	1	1	1	0	1	4	5	1	0	0	0	14	13	2		Gm27597
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ENSMUST00000184382	ENSMUSG00000098623	6	2	4	6	12	185	230	265	252	9	9	8	0	23	19	12	27	10	MI0026044	Mir8112
ENSMUST00000184384	ENSMUSG00000099284	5	0	2	2	4	1	2	4	0	0	0	0	0	0	1	1	0	0	MI0022875	Mir7026
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ENSMUST00000184398	ENSMUSG00000098890	3	0	0	0	0	1	1	2	0	0	0	0	0	0	0	0	0	0	MI0022857	Mir7008
ENSMUST00000184405	ENSMUSG00000098780	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021924	Mir6390
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ENSMUST00000184417	ENSMUSG00000098336	12	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021920	Mir6388
ENSMUST00000184426	ENSMUSG00000098416	15	1	0	0	2	1	5	1	4	0	0	0	0	0	0	0	0	0	MI0022968	Mir7117
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ENSMUST00000184433	ENSMUSG00000098359	6	0	1	1	2	10	5	11	8	2	1	1	0	2	0	0	0	0	MI0024987	Mir7649
ENSMUST00000184434	ENSMUSG00000098366	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021890	Mir145b
ENSMUST00000184435	ENSMUSG00000098981	11	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	MI0023731	Mir7236
ENSMUST00000184437	ENSMUSG00000098973	9	1399	607	387	1933	723	475	707	713	2330	34509	22582	1627	1382	2193	8690	5202	6254	MI0021583	Mir6236
ENSMUST00000184438	ENSMUSG00000098666	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022797	Mir6950
ENSMUST00000184453	ENSMUSG00000099066	17	3	3	4	4	60	122	58	64	0	0	5	0	1	4	1	0	0	MI0022826	Mir6978
ENSMUST00000184456	ENSMUSG00000099283	10	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	2	0	MI0022759	Mir6912
ENSMUST00000184460	ENSMUSG00000099119	1	1	0	2	6	78	43	66	16	6	3	0	0	13	3	1	0	0	MI0024983	Mir6546
ENSMUST00000184463	ENSMUSG00000098823	8	1	3	2	9	7	13	4	7	68	22	24	1	13	6	12	15	3	MI0026043	Mir8111
ENSMUST00000184464	ENSMUSG00000098790	13	0	0	0	0	2	4	3	3	2	3	0	0	0	0	0	2	0	MI0022789	Mir6942
ENSMUST00000184465	ENSMUSG00000098700	15	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27525
ENSMUST00000184470	ENSMUSG00000099221	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021900	Mir6371
ENSMUST00000184472	ENSMUSG00000099293	16	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021895	Mir6366
ENSMUST00000184474	ENSMUSG00000098460	17	0	1	0	2	9	10	12	3	0	0	0	0	0	2	1	4	3	MI0022818	Mir6970
ENSMUST00000184477	ENSMUSG00000098522	10	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	MI0021949	Mir6412
ENSMUST00000184478	ENSMUSG00000099036	14	1	2	1	1	41	12	14	7	1	4	0	0	2	0	0	0	1	MI0021923	Mir378c
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ENSMUST00000184484	ENSMUSG00000098577	4	539	132	297	1542	5	17	13	20	42	40	67	6	8	9	29	37	53		Gm27445
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ENSMUST00000184990	ENSMUSG00000098289	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0025026	Mir6715
ENSMUST00000184992	ENSMUSG00000099324	5	8	2	1	29	24	54	19	20	8	5	6	0	5	8	13	5	4	MI0026047	Mir8115
ENSMUST00000184997	ENSMUSG00000098821	15	2	0	0	1	0	0	1	0	0	2	2	0	2	0	0	0	0		Gm27397
ENSMUST00000184998	ENSMUSG00000099142	8	0	1	0	2	6	7	9	5	1	3	0	0	2	2	0	2	0	MI0026039	Mir8108
ENSMUST00000184999	ENSMUSG00000098701	10	0	1	1	7	23	47	30	27	0	0	0	0	2	1	1	0	0	MI0022761	Mir6914
ENSMUST00000185000	ENSMUSG00000098772	14	1	3	1	9	1	2	0	0	0	9	12	0	2	0	3	5	0		Gm27441
ENSMUST00000185003	ENSMUSG00000098964	17	1	1	0	1	0	0	0	0	3	2	0	0	0	1	1	0	0		Gm27700
ENSMUST00000185004	ENSMUSG00000098585	X	2	0	4	0	0	0	0	0	0	0	7	0	0	0	0	2	0		Gm27910
ENSMUST00000185007	ENSMUSG00000099289	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021939	Mir6403
ENSMUST00000185016	ENSMUSG00000098656	5	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	MI0022877	Mir7028
ENSMUST00000185017	ENSMUSG00000098849	X	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0		Gm27892

Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	hpel0673	hpel0674	hpel0675	hpel0676	hpel0677	hpel0678	hpel0679	hpel0680	hpel0523	hpel0524	hpel0525	hpel0555	hpel0556	hpel0557	hpel0558	hpel0559	hpel0560	mirBase_accession	mirBase name
ENSMUST00000185032	ENSMUSG00000098984	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021958	Mir6420
ENSMUST00000185035	ENSMUSG00000098944	3	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	2	0	MI0026052	Mir8120
ENSMUST00000185038	ENSMUSG00000099092	7	2	0	2	1	27	43	26	20	1	0	0	0	8	10	6	5	2	MI0022911	Mir7062
ENSMUST00000185041	ENSMUSG00000098852	10	23	15	9	48	42	44	45	28	71	44	19	0	14	22	36	24	20		Gm27392
ENSMUST00000185043	ENSMUSG00000098972	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	MI0026020	Mir8093
ENSMUST00000185044	ENSMUSG00000098497	11	3	0	0	7	6	8	0	3	3	2	0	0	6	0	0	1	0	MI0022779	Mir6932
ENSMUST00000185048	ENSMUSG00000098565	15	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0		Gm27760
ENSMUST00000185054	ENSMUSG00000098831	4	1	0	0	0	0	2	4	2	0	1	0	0	5	0	0	2	2	MI0022970	Mir7119
ENSMUST00000185055	ENSMUSG00000099004	13	16	7	6	31	10	3	6	3	28	24	34	0	14	3	2	2	19		Gm27656
ENSMUST00000185062	ENSMUSG00000098997	1	1	1	1	7	4	4	0	9	0	0	0	0	0	0	0	0	0	MI0022748	Mir6901
ENSMUST00000185063	ENSMUSG00000098297	18	0	1	0	4	34	60	25	52	0	0	0	0	2	11	0	0	2	MI0022828	Mir6980
ENSMUST00000185074	ENSMUSG00000099037	X	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27554
ENSMUST00000185075	ENSMUSG00000098597	5	0	5	1	15	58	57	208	65	8	0	0	0	11	8	2	2	0	MI0021956	Mir6418
ENSMUST00000185076	ENSMUSG00000098489	2	0	1	2	6	4	30	7	22	2	0	0	0	0	0	0	0	0	MI0025023	Mir7678
ENSMUST00000185077	ENSMUSG00000098600	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0022776	Mir6929
ENSMUST00000185078	ENSMUSG00000099069	19	0	0	0	0	3	4	0	0	0	0	0	0	0	0	0	0	0	MI0026017	Mir8090
ENSMUST00000185079	ENSMUSG00000098252	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021889	Mir6361
ENSMUST00000185080	ENSMUSG00000098553	7	1	0	1	2	9	10	5	2	0	0	0	0	1	0	0	0	0	MI0025014	Mir3569
ENSMUST00000185082	ENSMUSG00000098917	8	0	0	0	0	4	14	4	5	0	0	0	0	5	4	1	3	0	MI0024994	Mir7654
ENSMUST00000185089	ENSMUSG00000098735	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	MI0022854	Mir7005
ENSMUST00000185092	ENSMUSG00000098451	15	0	3	2	5	20	54	22	32	0	0	0	0	2	3	1	0	0	MI0022799	Mir6952
ENSMUST00000185093	ENSMUSG00000098580	4	0	1	1	2	17	20	10	8	2	0	0	0	8	5	0	3	0	MI0022872	Mir7023
ENSMUST00000185094	ENSMUSG00000098860	13	7	2	2	0	0	1	0	0	1	0	10	0	0	2	4	2	0		Gm27704
ENSMUST00000185099	ENSMUSG00000099259	11	0	0	0	1	7	11	3	0	0	0	2	0	0	0	0	2	0	MI0022769	Mir6922
ENSMUST00000185101	ENSMUSG00000098842	1	1	0	0	1	1	1	0	1	4	5	1	0	0	0	14	13	2		Gm27907
ENSMUST00000185103	ENSMUSG00000099071	16	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	1	0	MI0026022	Mir8095
ENSMUST00000185105	ENSMUSG00000099261	19	0	0	1	3	2	1	4	3	1	1	0	0	0	0	2	0	1	MI0022832	Mir6984
ENSMUST00000185107	ENSMUSG00000099237	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0023711	Mir7216
ENSMUST00000185108	ENSMUSG00000099303	1	3	0	2	3	1	0	0	0	4	2	4	0	0	1	2	1	9		Gm27458
ENSMUST00000185110	ENSMUSG00000098532	8	0	0	0	0	2	0	0	1	0	0	0	0	1	0	0	0	0	MI0022914	Mir7065
ENSMUST00000185114	ENSMUSG00000099015	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021901	Mir6372
ENSMUST00000185120	ENSMUSG00000098347	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MI0021867	Mir6339
ENSMUST00000185123	ENSMUSG00000099213	9	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	1	0		Gm27686
ENSMUST00000185129	ENSMUSG00000098621	17	2	0	2	5	16	10	16	15	0	0	0	0	7	3	0	1	0	MI0022815	Gm27740
ENSMUST00000185136	ENSMUSG00000098638	4	116	5	16	17	9	14	11	2	88	90	334	0	13	9	33	38	5		Gm27743
ENSMUST00000185146	ENSMUSG00000098474	11	0	0	0	0	1	4	3	0	0	0	0	0	1	0	0	0	0	MI0022766	Mir6919
ENSMUST00000185149	ENSMUSG00000099095	6	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	MI0021905	Mir6376
ENSMUST00000185150	ENSMUSG00000098457	15	16	16	17	60	59	59	87	58	9	3	3	0	22	7	3	7	0	MI0026025	Mir8097
ENSMUST00000185154	ENSMUSG00000098454	5	1	0	0	0	0	1	0	0	0	0	1	0	0	1	0	0	0	MI0022881	Mir7032
ENSMUST00000185156	ENSMUSG00000098906	11	1	2	3	1	5	3	2	2	1	0	1	0	2	0	1	0	0	MI0024992	Mir7652
ENSMUST00000185158	ENSMUSG00000098995	11	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		Gm27598
ENSMUST00000185165	ENSMUSG00000099225	10	0	0	0	0	2	1	2	0	4	12	1	0	1	1	0	0	1	MI0026034	Mir8104
ENSMUST00000185166	ENSMUSG00000098415	11	1	1	0	1	0	11	2	6	0	0	0	0	1	0	0	0	0	MI0022775	Mir6928
ENSMUST00000185186	ENSMUSG00000099058	13	0	0	1	5	27	41	32	39	0	0	1	0	8	2	4	2	0	MI0022790	Mir6943
ENSMUST00000185190	ENSMUSG00000098728	6	0	0	1	0	0	0	0	0	0	1	0	0	2	0	0	0	0		Gm27336
ENSMUST00000185192	ENSMUSG00000098993	10	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0		Gm27731
ENSMUST00000185196	ENSMUSG00000099074	16	1	0	0	1	0	1	2	2	0	0	0	0	0	0	0	0	0		Gm27564

Differential Expression of miRNA

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000083460	ENSMUSG00000065394	5	microRNA 25	MI0000689	Mir25	2.1	4.5E-05	3.0	2.3E-06	0.1	8.3E-01	-0.8	8.0E-02
ENSMUST00000083461	ENSMUSG00000065395	11	microRNA 193a	MI0000235	Mir193a	-1.0	2.8E-01	-2.1	3.5E-02	-3.3	3.0E-04	-2.2	4.2E-02
ENSMUST00000083462	ENSMUSG00000065396	17	microRNA 99b	MI0000147	Mir99b	2.8	7.8E-03	3.7	7.6E-04	-3.8	2.3E-04	-4.8	5.7E-05
ENSMUST00000083463	ENSMUSG00000065397	16	microRNA 155	MI0000177	Mir155	1.8	1.9E-02	1.8	3.2E-02	-0.2	8.0E-01	-0.2	7.7E-01
ENSMUST00000083464	ENSMUSG00000065398	X	microRNA 188	MI0000230	Mir188	-0.1	8.7E-01	-2.3	1.1E-02	-0.9	1.5E-01	1.3	1.4E-01
ENSMUST00000083465	ENSMUSG00000065399	18	microRNA 133a-1	MI0000159	Mir133a-1	0.1	8.6E-01	-0.8	4.2E-01	-4.8	2.8E-06	-3.8	6.8E-04
ENSMUST00000083466	ENSMUSG00000065400	4	microRNA 200a	MI0000554	Mir200a	1.2	1.7E-01	0.3	7.7E-01	-2.0	1.6E-02	-1.0	3.0E-01
ENSMUST00000083467	ENSMUSG00000065401	11	microRNA 144	MI0000168	Mir144	1.4	7.1E-02	0.2	8.2E-01	-2.3	3.2E-03	-1.0	2.3E-01
ENSMUST00000083468	ENSMUSG00000065402	18	microRNA 122	MI0000256	Mir122	1.7	5.3E-01	5.9	8.9E-02	-4.0	1.8E-01	-8.2	1.8E-02
ENSMUST00000083469	ENSMUSG00000065403	14	microRNA 18	MI0000567	Mir18	-2.3	5.1E-03	-2.7	6.2E-03	0.0	9.5E-01	0.4	6.3E-01
ENSMUST00000083470	ENSMUSG00000065404	X	microRNA 201	MI0000244	Mir201	1.2	9.8E-02	0.7	4.9E-01	-1.5	6.5E-02	-1.0	2.9E-01
ENSMUST00000083471	ENSMUSG00000065405	1	microRNA 30a	MI0000144	Mir30a	0.4	5.1E-01	2.1	2.0E-03	-1.3	1.8E-02	-3.0	5.9E-05
ENSMUST00000083472	ENSMUSG00000065406	10	microRNA let7i	MI0000138	Mirlet7i	1.1	1.6E-02	2.2	2.0E-04	0.8	4.4E-02	-0.3	5.6E-01
ENSMUST00000083473	ENSMUSG00000065407	9	microRNA 135a-1	MI0000161	Mir135a-1	1.7	1.2E-01	-0.1	9.5E-01	-1.2	2.3E-01	0.6	6.3E-01
ENSMUST00000083474	ENSMUSG00000065408	4	microRNA 31	MI0000579	Mir31	-1.0	2.1E-01	-2.1	1.4E-02	-4.8	2.9E-07	-3.8	2.0E-04
ENSMUST00000083475	ENSMUSG00000065409	4	microRNA 30e	MI0000259	Mir30e	0.9	3.9E-02	0.3	5.3E-01	-0.1	7.7E-01	0.5	3.2E-01
ENSMUST00000083476	ENSMUSG00000065410	2	microRNA 298	MI0000398	Mir298	-0.1	8.6E-01	-0.8	2.6E-01	-0.4	4.7E-01	0.3	6.6E-01
ENSMUST00000083477	ENSMUSG00000065411	11	microRNA 195a	MI0000237	Mir195a	0.1	9.5E-01	1.6	1.0E-01	-1.3	9.1E-02	-2.9	7.7E-03
ENSMUST00000083478	ENSMUSG00000065412	1	microRNA 29b-2	MI0000712	Mir29b-2	-0.9	1.8E-01	-2.3	6.7E-03	-0.4	4.3E-01	1.0	2.2E-01
ENSMUST00000083480	ENSMUSG00000065414	9	microRNA 138-1	MI0000722	Mir138-1	-2.6	4.4E-02	-4.2	1.3E-02	-0.3	7.6E-01	1.3	4.3E-01
ENSMUST00000083481	ENSMUSG00000065415	11	microRNA 217	MI0000731	Mir217	2.0	5.1E-03	2.2	3.9E-02	-0.8	2.6E-01	-1.0	2.8E-01
ENSMUST00000083482	ENSMUSG00000065416	14	microRNA 19a	MI0000688	Mir19a	-0.8	2.1E-01	-2.0	1.1E-02	-0.8	1.8E-01	0.4	5.5E-01
ENSMUST00000083483	ENSMUSG00000065417	11	microRNA 340	MI0000623	Mir340	2.0	4.2E-04	0.9	1.2E-01	-0.4	3.9E-01	0.7	2.0E-01
ENSMUST00000083484	ENSMUSG00000065418	X	microRNA 322	MI0000590	Mir322	1.5	1.5E-02	-0.2	7.8E-01	-0.4	4.1E-01	1.3	7.0E-02
ENSMUST00000083485	ENSMUSG00000098807	12	microRNA 300	MI0000400	Mir300	1.3	1.1E-01	2.2	2.6E-02	-0.4	5.4E-01	-1.3	1.7E-01
ENSMUST00000083486	ENSMUSG00000065420	11	microRNA 142b	MI0026028	Mir142b	0.1	7.6E-01	-1.5	3.4E-03	-0.8	2.7E-02	0.8	9.2E-02
ENSMUST00000083487	ENSMUSG00000065421	13	microRNA let7a-1	MI0000556	Mirlet7a-1	0.5	3.3E-01	1.5	2.2E-02	1.1	3.1E-02	0.1	8.7E-01
ENSMUST00000083488	ENSMUSG00000065422	X	microRNA 221	MI0000709	Mir221	1.2	7.8E-03	1.2	2.2E-02	0.3	4.6E-01	0.3	5.5E-01
ENSMUST00000083489	ENSMUSG00000065423	2	microRNA 181a-2	MI0000223	Mir181a-2	0.6	2.0E-01	0.4	4.3E-01	-0.2	5.8E-01	0.0	9.4E-01
ENSMUST00000083490	ENSMUSG00000065424	13	microRNA 9-2	MI0000157	Mir9-2	2.3	3.0E-02	-0.8	4.4E-01	-8.2	2.1E-09	-5.1	8.2E-05
ENSMUST00000083492	ENSMUSG00000065426	12	microRNA 134	MI0000160	Mir134	-0.4	7.5E-01	1.4	3.3E-01	0.8	4.7E-01	-1.0	5.0E-01
ENSMUST00000083493	ENSMUSG00000065427	4	microRNA 429	MI0001642	Mir429	0.6	5.3E-01	0.4	7.1E-01	-1.4	9.9E-02	-1.2	2.7E-01
ENSMUST00000083494	ENSMUSG00000065428	12	microRNA 382	MI0000799	Mir382	-1.2	1.4E-01	0.9	4.6E-01	1.7	7.3E-02	-0.4	7.1E-01
ENSMUST00000083495	ENSMUSG00000065429	12	microRNA 345	MI0000632	Mir345	-0.9	1.3E-01	0.0	1.0E+00	0.7	1.6E-01	-0.1	8.3E-01
ENSMUST00000083496	ENSMUSG00000065430	10	microRNA 26a-2	MI0000706	Mir26a-2	0.8	7.8E-02	0.3	6.3E-01	0.0	9.5E-01	0.6	2.7E-01
ENSMUST00000083497	ENSMUSG00000065431	3	microRNA 186	MI0000228	Mir186	0.2	6.8E-01	0.2	6.5E-01	0.3	5.3E-01	0.2	7.0E-01
ENSMUST00000083498	ENSMUSG00000065432	14	microRNA 208a	MI0000555	Mir208a	-1.4	3.7E-01	-6.3	5.9E-03	-4.3	1.0E-02	0.7	7.1E-01
ENSMUST00000083499	ENSMUSG00000065433	12	microRNA 370	MI0001165	Mir370	2.1	6.6E-03	-0.4	6.9E-01	-2.4	7.6E-03	0.1	8.7E-01
ENSMUST00000083500	ENSMUSG00000065434	13	microRNA 7-1	MI0000728	Mir7-1	-2.4	5.1E-02	-2.5	9.8E-02	0.5	6.3E-01	0.5	7.1E-01
ENSMUST00000083502	ENSMUSG00000065436	12	microRNA 342	MI0000627	Mir342	-1.8	1.1E-02	-1.1	1.8E-01	-0.1	8.0E-01	-0.9	2.5E-01
ENSMUST00000083503	ENSMUSG00000065437	15	microRNA 30d	MI0000549	Mir30d	0.4	3.6E-01	0.6	2.1E-01	0.3	3.7E-01	0.1	8.2E-01
ENSMUST00000083504	ENSMUSG00000065438	12	microRNA 377	MI0000794	Mir377	0.3	7.2E-01	0.3	8.1E-01	0.4	6.3E-01	0.5	6.2E-01
ENSMUST00000083505	ENSMUSG00000065439	8	microRNA 140	MI0000165	Mir140	0.0	9.1E-01	0.4	4.6E-01	0.2	5.9E-01	-0.1	8.1E-01
ENSMUST00000083506	ENSMUSG00000065440	9	microRNA let7g	MI0000137	Mirlet7g	0.2	6.7E-01	1.2	6.1E-02	0.7	1.8E-01	-0.3	6.1E-01
ENSMUST00000083507	ENSMUSG00000065441	9	microRNA 128-2	MI0000726	Mir128-2	-1.6	2.2E-01	0.9	4.9E-01	-0.8	4.3E-01	-3.3	2.3E-02
ENSMUST00000083508	ENSMUSG00000065442	14	microRNA 20a	MI0000568	Mir20a	-0.7	2.4E-01	-1.4	7.5E-02	0.3	5.4E-01	1.0	2.0E-01
ENSMUST00000083509	ENSMUSG00000065443	6	microRNA 196b	MI0001151	Mir196b	0.3	7.0E-01	0.5	6.0E-01	0.6	3.9E-01	0.4	6.4E-01
ENSMUST00000083510	ENSMUSG00000065444	8	microRNA 27a	MI0000578	Mir27a	0.5	2.9E-01	-0.1	8.6E-01	-0.5	2.3E-01	0.1	8.7E-01
ENSMUST00000083511	ENSMUSG00000065445	18	microRNA 143	MI0000257	Mir143	2.1	7.5E-02	3.5	3.8E-03	-4.7	1.2E-04	-6.1	4.1E-05
ENSMUST00000083512	ENSMUSG00000065446	7	microRNA 139	MI0000693	Mir139	-0.9	1.1E-01	-0.9	1.9E-01	0.4	3.8E-01	0.4	5.3E-01
ENSMUST00000083514	ENSMUSG00000065448	12	microRNA 154	MI0000176	Mir154	1.0	2.7E-01	2.1	1.0E-01	-0.8	3.9E-01	-1.9	1.1E-01
ENSMUST00000083515	ENSMUSG00000065449	16	microRNA 365-1	MI0000768	Mir365-1	-1.1	5.9E-01	2.3	3.6E-01	3.1	1.2E-01	-0.2	9.2E-01
ENSMUST00000083517	ENSMUSG00000065451	4	microRNA 101a	MI0000148	Mir101a	1.7	5.5E-03	0.9	1.4E-01	-1.2	2.1E-02	-0.5	4.3E-01
ENSMUST00000083518	ENSMUSG00000065452	4	microRNA 207	MI0000250	Mir207	2.1	7.5E-03	1.1	2.7E-01	-0.7	3.4E-01	0.3	7.2E-01
ENSMUST00000083519	ENSMUSG00000065453	13	microRNA let7d	MI0000405	Mirlet7d	0.0	9.5E-01	0.8	1.7E-01	0.3	4.3E-01	-0.4	4.5E-01
ENSMUST00000083520	ENSMUSG00000065454	2	microRNA 124a-3	MI0000150	Mir124a-3	0.0	9.6E-01	-0.2	8.6E-01	-0.6	5.6E-01	-0.4	7.5E-01
ENSMUST00000083521	ENSMUSG00000065455	11	microRNA 21a	MI0000569	Mir21a	0.1	7.5E-01	-0.7	1.8E-01	-0.3	4.0E-01	0.5	3.3E-01
ENSMUST00000083522	ENSMUSG00000065456	X	microRNA 106a	MI0000406	Mir106a	-1.0	2.3E-01	-1.1	2.6E-01	0.6	3.7E-01	0.7	4.7E-01
ENSMUST00000083523	ENSMUSG00000065457	8	microRNA 383	MI0000800	Mir383	0.9	2.8E-01	1.1	2.5E-01	0.6	4.2E-01	0.4	6.7E-01
ENSMUST00000083524	ENSMUSG00000065458	1	microRNA 181b-1	MI0000723	Mir181b-1	1.8	2.2E-01	1.0	5.4E-01	0.1	9.1E-01	0.9	5.5E-01
ENSMUST00000083528	ENSMUSG00000065462	6	microRNA 200c	MI0000694	Mir200c	-1.5	1.2E-01	-2.2	6.3E-02	0.4	6.1E-01	1.1	3.6E-01
ENSMUST00000083530	ENSMUSG00000065464	16	microRNA 185	MI0000227	Mir185	-1.3	9.0E-02	-0.8	3.8E-01	0.4	5.7E-01	-0.2	8.5E-01
ENSMUST00000083531	ENSMUSG00000065465	15	microRNA 33	MI0000707	Mir33	-1.1	1.6E-01	-3.2	2.1E-03	-1.1	1.0E-01	1.0	3.0E-01
ENSMUST00000083534	ENSMUSG00000065468	1	microRNA 26b	MI0000575	Mir26b	1.9	3.1E-04	1.4	1.6E-02	0.4	3.8E-01	0.9	8.9E-02
ENSMUST00000083535	ENSMUSG00000065469	6	microRNA 129-1	MI0000222	Mir129-1	-2.2	2.0E-01	-3.3	1.4E-01	-0.5	7.3E-01	0.6	7.9E-01
ENSMUST00000083536	ENSMUSG00000065470	1	microRNA 149	MI0000171	Mir149	-3.9	1.4E-06	-3.6	1.9E-05	-0.9	7.1E-02	-1.2	1.1E-01
ENSMUST00000083537	ENSMUSG00000065471	X	microRNA 222	MI0000710	Mir222	-0.6	2.8E-01	-0.4	5.2E-01	-0.1	7.6E-01	-0.3	5.9E-01
ENSMUST00000083538	ENSMUSG00000065472	16	microRNA 125b-2	MI0000152	Mir125b-2	0.3	7.3E-01	1.3	1.6E-01	-3.3	2.4E-04	-4.3	3.7E-04
ENSMUST00000083539	ENSMUSG00000065473	X	microRNA 19b-2	MI0000546	Mir19b-2	-1.5	1.8E-02	-2.1	5.0E-03	-0.8	1.3E-01	-0.1	8.4E-01
ENSMUST00000083540	ENSMUSG00000065474	6	microRNA 141	MI0000166	Mir141	0.9	1.5E-01	0.7	3.0E-01	0.0	9.5E-01	0.2	7.8E-01
ENSMUST00000083541	ENSMUSG00000065475	13	microRNA 27b	MI0000142	Mir27b	0.8	9.4E-02	1.2	2.9E-02	0.2	5.5E-01	-0.2	7.5E-01
ENSMUST00000083542	ENSMUSG00000065476	15	microRNA 30b	MI0000145	Mir30b	-3.0	4.1E-05	-3.4	4.7E-05	-0.8	8.9E-02	-0.4	5.6E-01
ENSMUST00000083543	ENSMUSG00000065477	12	microRNA 411	MI0001163	Mir411	-0.1	9.2E-01	2.2	1.5E-02	-0.5	4.8E-01	-2.7	4.4E-03

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000083545	ENSMUSG00000065479	17	microRNA 125a	MI0000151	Mir125a	1.7	7.8E-02	2.1	3.6E-02	-3.8	1.5E-04	-4.2	2.5E-04
ENSMUST00000083547	ENSMUSG00000065481	14	microRNA 346	MI0000634	Mir346	0.9	2.5E-01	1.6	7.4E-02	1.3	7.1E-02	0.5	5.6E-01
ENSMUST00000083549	ENSMUSG00000065483	8	microRNA 181c	MI0000724	Mir181c	0.9	1.3E-01	0.5	4.4E-01	-0.6	2.4E-01	-0.2	7.2E-01
ENSMUST00000083550	ENSMUSG00000065484	2	microRNA 130a	MI0000156	Mir130a	2.2	2.8E-03	2.6	1.3E-03	-2.5	3.5E-04	-2.9	4.7E-04
ENSMUST00000083551	ENSMUSG00000065485	2	microRNA 219a-2	MI0000741	Mir219a-2	0.4	7.0E-01	-2.5	3.3E-02	-0.9	3.2E-01	2.0	8.4E-02
ENSMUST00000083552	ENSMUSG00000065486	X	microRNA 450-1	MI0001653	Mir450-1	-3.0	1.0E-03	-2.2	5.6E-02	-0.8	3.0E-01	-1.5	1.7E-01
ENSMUST00000083554	ENSMUSG00000065488	15	microRNA 196a-2	MI0000553	Mir196a-2	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01
ENSMUST00000083555	ENSMUSG00000065489	11	microRNA 365-2	MI0001645	Mir365-2	-2.9	1.2E-03	-1.2	2.7E-01	-1.4	6.2E-02	-3.1	1.0E-02
ENSMUST00000083556	ENSMUSG00000065490	4	microRNA 30c-1	MI0000547	Mir30c-1	-1.6	2.0E-02	-2.5	3.0E-03	-0.1	8.7E-01	0.9	2.7E-01
ENSMUST00000083558	ENSMUSG00000065492	9	microRNA 34b	MI0000404	Mir34b	1.8	8.8E-02	2.0	1.5E-01	-0.9	4.0E-01	-1.1	3.7E-01
ENSMUST00000083559	ENSMUSG00000065493	4	microRNA 34a	MI0000584	Mir34a	0.9	2.6E-01	-0.2	7.8E-01	-1.4	5.2E-02	-0.3	7.6E-01
ENSMUST00000083560	ENSMUSG00000065494	16	microRNA 28a	MI0000690	Mir28a	1.0	5.5E-02	0.6	3.6E-01	-0.2	7.2E-01	0.3	6.0E-01
ENSMUST00000083561	ENSMUSG00000065495	7	microRNA 150	MI0000172	Mir150	-3.2	8.6E-06	-2.1	1.6E-03	-1.0	2.5E-02	-2.1	2.8E-03
ENSMUST00000083563	ENSMUSG00000065497	12	microRNA 410	MI0001161	Mir410	1.3	2.1E-01	3.0	1.1E-02	0.2	8.0E-01	-1.5	1.6E-01
ENSMUST00000083564	ENSMUSG00000065498	12	microRNA 379	MI0000796	Mir379	-0.4	6.0E-01	-0.9	3.8E-01	-0.2	8.6E-01	0.3	7.1E-01
ENSMUST00000083566	ENSMUSG00000065500	2	microRNA 10b	MI0000221	Mir10b	-0.3	8.0E-01	0.9	3.5E-01	-3.8	2.1E-04	-5.0	9.7E-05
ENSMUST00000083567	ENSMUSG00000065501	6	microRNA 335	MI0000817	Mir335	1.4	1.8E-01	0.9	3.7E-01	-2.5	9.4E-03	-2.1	6.7E-02
ENSMUST00000083569	ENSMUSG00000065503	X	microRNA 351	MI0000643	Mir351	-3.4	1.1E-05	-2.3	3.0E-03	0.8	1.3E-01	-0.3	7.0E-01
ENSMUST00000083571	ENSMUSG00000065505	6	microRNA 148a	MI0000550	Mir148a	0.6	1.9E-01	1.3	1.4E-02	0.3	3.8E-01	-0.4	4.4E-01
ENSMUST00000083573	ENSMUSG00000065507	19	microRNA 204	MI0000247	Mir204	-0.5	4.6E-01	-1.6	1.0E-01	-0.7	3.7E-01	0.3	7.0E-01
ENSMUST00000083574	ENSMUSG00000065508	14	microRNA 17	MI0000687	Mir17	-0.3	5.7E-01	-1.6	2.3E-02	-0.3	5.7E-01	1.0	1.4E-01
ENSMUST00000083575	ENSMUSG00000065509	X	microRNA 421	MI0005496	Mir421	1.8	5.4E-03	1.6	2.5E-02	0.3	5.7E-01	0.5	4.4E-01
ENSMUST00000083576	ENSMUSG00000065510	X	microRNA 361	MI0000761	Mir361	0.7	2.1E-01	0.6	3.3E-01	0.8	1.1E-01	0.8	1.9E-01
ENSMUST00000083577	ENSMUSG00000065511	2	microRNA 129-2	MI0000585	Mir129-2	0.2	6.8E-01	0.9	1.9E-01	0.9	8.9E-02	0.2	7.2E-01
ENSMUST00000083578	ENSMUSG00000065512	8	microRNA 138-2	MI0000164	Mir138-2	-1.6	3.0E-02	0.7	4.8E-01	0.5	4.5E-01	-1.8	8.5E-02
ENSMUST00000083579	ENSMUSG00000065513	9	microRNA 26a-1	MI0000573	Mir26a-1	0.7	4.4E-01	-0.9	4.0E-01	-0.1	8.7E-01	1.4	1.8E-01
ENSMUST00000083580	ENSMUSG00000065514	5	microRNA 106b	MI0000407	Mir106b	-0.3	5.6E-01	-0.4	4.6E-01	-0.5	2.3E-01	-0.4	4.8E-01
ENSMUST00000083581	ENSMUSG00000065515	11	microRNA 152	MI0000174	Mir152	1.0	2.3E-01	2.0	3.2E-02	-1.5	4.7E-02	-2.5	1.2E-02
ENSMUST00000083582	ENSMUSG00000065516	1	microRNA 214	MI0000698	Mir214	1.6	1.1E-01	1.8	1.4E-01	-2.0	4.3E-02	-2.2	7.3E-02
ENSMUST00000083584	ENSMUSG00000065518	11	microRNA 423	MI0004637	Mir423	-0.5	4.1E-01	-1.4	5.0E-02	-0.5	3.2E-01	0.4	5.5E-01
ENSMUST00000083585	ENSMUSG00000065519	11	microRNA 10a	MI0000685	Mir10a	-0.4	5.4E-01	0.4	5.6E-01	1.2	3.2E-02	0.5	5.0E-01
ENSMUST00000083586	ENSMUSG00000065520	1	microRNA 128-1	MI0000155	Mir128-1	0.8	2.1E-01	0.6	3.7E-01	-1.3	2.5E-02	-1.1	1.1E-01
ENSMUST00000083587	ENSMUSG00000065521	2	microRNA 296	MI0000394	Mir296	0.0	9.7E-01	-1.4	1.1E-01	-1.0	9.7E-02	0.3	6.8E-01
ENSMUST00000083589	ENSMUSG00000065523	19	microRNA 192	MI0000551	Mir192	-1.3	9.8E-02	1.7	4.0E-02	0.4	5.1E-01	-2.6	4.5E-03
ENSMUST00000083592	ENSMUSG00000065526	12	microRNA 337	MI0000615	Mir337	-0.3	6.8E-01	1.1	2.5E-01	0.7	3.1E-01	-0.7	4.5E-01
ENSMUST00000083593	ENSMUSG00000065527	5	microRNA 93	MI0000581	Mir93	-0.8	1.2E-01	-0.4	5.3E-01	0.0	9.8E-01	-0.4	4.5E-01
ENSMUST00000083594	ENSMUSG00000065528	14	microRNA 320	MI0000704	Mir320	1.1	1.0E-01	1.9	1.7E-02	-0.3	5.5E-01	-1.1	1.2E-01
ENSMUST00000083595	ENSMUSG00000065529	11	microRNA 22	MI0000570	Mir22	1.3	3.5E-03	0.8	1.2E-01	-0.1	8.5E-01	0.4	3.5E-01
ENSMUST00000083596	ENSMUSG00000065530	16	microRNA 99a	MI0000146	Mir99a	0.5	5.7E-01	2.4	1.5E-02	-1.6	5.0E-02	-3.4	1.4E-03
ENSMUST00000083598	ENSMUSG00000065532	18	microRNA 187	MI0000229	Mir187	-0.2	8.3E-01	0.8	4.7E-01	-1.8	4.4E-02	-2.8	1.3E-02
ENSMUST00000083599	ENSMUSG00000065533	1	microRNA 205	MI0000248	Mir205	1.8	1.9E-01	-1.2	4.4E-01	-7.7	1.6E-05	-4.7	6.4E-03
ENSMUST00000083600	ENSMUSG00000065534	11	microRNA 324	MI0000595	Mir324	0.0	9.7E-01	0.0	9.5E-01	0.0	9.8E-01	0.0	9.9E-01
ENSMUST00000083602	ENSMUSG00000065536	X	microRNA 98	MI0000586	Mir98	-0.1	8.6E-01	0.9	2.5E-01	1.9	2.0E-03	1.0	1.7E-01
ENSMUST00000083603	ENSMUSG00000065537	11	microRNA 132	MI0000158	Mir132	1.9	2.1E-02	0.8	3.2E-01	-3.3	9.9E-05	-2.1	1.6E-02
ENSMUST00000083604	ENSMUSG00000065538	12	microRNA 153	MI0000175	Mir153	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000083606	ENSMUSG00000065540	2	microRNA 126a	MI0000153	Mir126a	1.5	4.1E-02	2.8	1.2E-03	-0.4	5.0E-01	-1.7	2.7E-02
ENSMUST00000083607	ENSMUSG00000065541	8	microRNA 24-2	MI0000572	Mir24-2	-0.4	5.1E-01	-0.7	3.3E-01	0.4	4.4E-01	0.7	3.2E-01
ENSMUST00000083608	ENSMUSG00000065542	X	microRNA 224	MI0000711	Mir224	0.7	4.4E-01	1.5	1.6E-01	-3.4	4.3E-04	-4.2	3.0E-04
ENSMUST00000083609	ENSMUSG00000065543	7	microRNA 330	MI0000607	Mir330	-2.6	3.0E-04	-3.4	1.1E-04	0.0	9.4E-01	0.8	2.7E-01
ENSMUST00000083610	ENSMUSG00000065544	4	microRNA 32	MI0000691	Mir32	1.7	9.9E-03	0.3	6.4E-01	-1.4	1.9E-02	0.0	9.7E-01
ENSMUST00000083613	ENSMUSG00000065547	9	microRNA 199a-1	MI0000241	Mir199a-1	0.9	3.6E-01	1.7	6.6E-02	-3.3	4.2E-04	-4.2	1.7E-04
ENSMUST00000083614	ENSMUSG00000065548	1	microRNA 29c	MI0000577	Mir29c	1.1	5.0E-02	-0.6	3.4E-01	-0.8	8.8E-02	0.8	1.8E-01
ENSMUST00000083615	ENSMUSG00000065549	4	microRNA 200b	MI0000243	Mir200b	1.9	1.2E-02	0.3	7.1E-01	-1.2	5.2E-02	0.4	6.3E-01
ENSMUST00000083617	ENSMUSG00000065551	7	microRNA 210	MI0000695	Mir210	-0.5	4.0E-01	-0.8	2.6E-01	-0.2	6.5E-01	0.1	9.3E-01
ENSMUST00000083619	ENSMUSG00000065553	11	microRNA 103-1	MI0000587	Mir103-1	-0.9	6.9E-01	2.1	4.0E-01	0.9	6.6E-01	-2.2	4.0E-01
ENSMUST00000083621	ENSMUSG00000065555	17	microRNA 219a-1	MI0000702	Mir219a-1	-1.3	4.8E-02	-1.7	3.5E-02	-0.3	6.3E-01	0.1	9.2E-01
ENSMUST00000083622	ENSMUSG00000065556	19	microRNA 101b	MI0000649	Mir101b	1.9	3.7E-03	1.9	8.7E-03	-1.0	8.5E-02	-0.9	1.6E-01
ENSMUST00000083623	ENSMUSG00000065557	16	microRNA let7c-1	MI0000559	Mirlet7c-1	0.6	4.3E-01	1.2	1.8E-01	-0.9	1.5E-01	-1.5	1.1E-01
ENSMUST00000083626	ENSMUSG00000065560	15	microRNA 148b	MI0000617	Mir148b	0.3	5.8E-01	-0.1	8.7E-01	0.3	5.9E-01	0.7	3.0E-01
ENSMUST00000083627	ENSMUSG00000065561	12	microRNA 369	MI0003535	Mir369	0.1	8.8E-01	0.6	5.5E-01	-1.1	1.4E-01	-1.6	1.2E-01
ENSMUST00000083628	ENSMUSG00000065562	1	microRNA 215	MI0000974	Mir215	-1.2	1.7E-01	0.2	8.8E-01	-0.5	5.1E-01	-1.8	9.2E-02
ENSMUST00000083629	ENSMUSG00000065563	2	microRNA 103-2	MI0000588	Mir103-2	0.7	1.2E-01	-0.1	8.3E-01	-0.1	7.8E-01	0.7	1.8E-01
ENSMUST00000083630	ENSMUSG00000065564	15	microRNA let7b	MI0000558	Mirlet7b	1.2	4.1E-02	2.2	2.9E-03	0.0	9.5E-01	-1.0	1.3E-01
ENSMUST00000083631	ENSMUSG00000065565	1	microRNA 181a-1	MI0000697	Mir181a-1	-1.3	7.0E-02	-1.3	1.0E-01	-0.8	1.9E-01	-0.8	3.0E-01
ENSMUST00000083632	ENSMUSG00000098838	12	microRNA 381	MI0000798	Mir381	1.5	1.7E-01	3.1	1.7E-02	-0.3	7.6E-01	-1.9	1.3E-01
ENSMUST00000083633	ENSMUSG00000065567	1	microRNA 30c-2	MI0000548	Mir30c-2	-5.0	1.3E-06	-3.5	2.8E-04	-0.9	1.4E-01	-2.3	1.1E-02
ENSMUST00000083635	ENSMUSG00000065569	3	microRNA 137	MI0000163	Mir137	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000083637	ENSMUSG00000065571	7	microRNA 326	MI0000598	Mir326	-1.8	1.8E-02	-2.1	1.9E-02	-0.4	5.3E-01	-0.1	9.4E-01
ENSMUST00000083638	ENSMUSG00000065572	16	microRNA 130b	MI0000408	Mir130b	0.6	2.5E-01	0.3	5.7E-01	0.3	4.7E-01	0.6	3.3E-01
ENSMUST00000083639	ENSMUSG00000065573	1	microRNA 350	MI0000640	Mir350	0.4	4.6E-01	0.5	4.0E-01	0.3	5.1E-01	0.2	7.5E-01
ENSMUST00000083640	ENSMUSG00000065574	12	microRNA 203	MI0000246	Mir203	-0.1	9.2E-01	0.4	6.3E-01	-1.4	3.0E-02	-1.9	2.8E-02
ENSMUST00000083641	ENSMUSG00000065575	13	microRNA 449a	MI0001649	Mir449a	1.4	8.9E-02	1.0	2.9E-01	-1.1	1.5E-01	-0.7	4.6E-01
ENSMUST00000083643	ENSMUSG00000065577	12	microRNA 329	MI0000605	Mir329	0.0	9.6E-01	-0.1	9.5E-01	-1.3	1.9E-01	-1.2	3.2E-01
ENSMUST00000083644	ENSMUSG00000065578	2	microRNA 181b-2	MI0000823	Mir181b-2	-0.6	2.1E-01	-0.3	6.7E-01	0.5	2.9E-01	0.1	8.6E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000083645	ENSMUSG00000065579	9	microRNA 425	MI0001447	Mir425	-0.2	6.3E-01	-0.4	4.6E-01	0.5	2.3E-01	0.7	2.2E-01
ENSMUST00000083646	ENSMUSG00000065580	3	microRNA 15b	MI0000140	Mir15b	0.2	7.5E-01	0.3	5.7E-01	0.5	2.3E-01	0.4	5.2E-01
ENSMUST00000083647	ENSMUSG00000065581	1	microRNA 194-1	MI0000236	Mir194-1	2.6	2.8E-01	3.4	1.8E-01	-0.9	6.5E-01	-1.7	5.0E-01
ENSMUST00000083648	ENSMUSG00000065582	19	microRNA 194-2	MI0000733	Mir194-2	-0.1	8.6E-01	0.0	9.9E-01	0.0	9.6E-01	-0.1	8.6E-01
ENSMUST00000083649	ENSMUSG00000065583	11	microRNA 218-2	MI0000701	Mir218-2	0.4	6.7E-01	-1.9	1.7E-01	-2.9	6.0E-03	-0.6	6.2E-01
ENSMUST00000083651	ENSMUSG00000065585	7	microRNA 211	MI0000708	Mir211	0.7	4.5E-01	0.8	4.8E-01	-0.5	5.6E-01	-0.5	6.7E-01
ENSMUST00000083652	ENSMUSG00000065586	6	microRNA 96	MI0000583	Mir96	0.3	7.5E-01	-0.7	5.1E-01	-2.5	6.8E-03	-1.5	2.1E-01
ENSMUST00000083653	ENSMUSG00000065587	9	microRNA 34c	MI0000403	Mir34c	1.9	7.8E-02	1.8	1.0E-01	-3.3	1.2E-03	-3.2	9.0E-03
ENSMUST00000083655	ENSMUSG00000065589	11	microRNA 301	MI0000401	Mir301	-3.6	2.6E-06	-3.3	3.6E-05	-0.3	5.2E-01	-0.6	3.7E-01
ENSMUST00000083656	ENSMUSG00000065590	11	microRNA 212	MI0000696	Mir212	-2.3	4.1E-02	-1.7	1.2E-01	-4.2	7.8E-05	-4.8	3.7E-04
ENSMUST00000083658	ENSMUSG00000065592	18	microRNA 145a	MI0000169	Mir145a	1.5	2.5E-01	1.6	2.6E-01	-3.8	3.7E-03	-3.8	1.3E-02
ENSMUST00000083659	ENSMUSG00000065593	5	microRNA 339	MI0000621	Mir339	0.7	1.6E-01	-0.4	5.4E-01	-0.6	1.8E-01	0.5	4.5E-01
ENSMUST00000083660	ENSMUSG00000065594	19	microRNA 107	MI0000684	Mir107	-0.2	7.2E-01	-0.5	4.8E-01	-0.1	8.6E-01	0.2	7.9E-01
ENSMUST00000083662	ENSMUSG00000065596	9	microRNA 184	MI0000226	Mir184	1.9	5.1E-02	2.0	6.3E-02	-1.3	1.4E-01	-1.4	1.9E-01
ENSMUST00000083665	ENSMUSG00000065599	13	microRNA 23b	MI0000141	Mir23b	-1.5	9.5E-03	-0.8	1.9E-01	1.5	3.0E-03	0.9	1.6E-01
ENSMUST00000083666	ENSMUSG00000065600	11	microRNA 338	MI0000619	Mir338	0.0	9.7E-01	-1.3	4.2E-02	-0.4	4.0E-01	1.0	1.4E-01
ENSMUST00000083667	ENSMUSG00000065601	11	microRNA 146	MI0000170	Mir146	4.2	5.0E-03	2.7	8.5E-02	-1.3	2.8E-01	0.2	8.9E-01
ENSMUST00000083668	ENSMUSG00000065602	X	microRNA let7f-2	MI0000563	Mirlet7f-2	0.2	6.2E-01	0.4	5.4E-01	0.4	3.6E-01	0.3	6.0E-01
ENSMUST00000083669	ENSMUSG00000065603	5	microRNA 218-1	MI0000700	Mir218-1	0.5	5.4E-01	-0.3	7.7E-01	-3.6	2.6E-04	-2.8	1.5E-02
ENSMUST00000083670	ENSMUSG00000065604	6	microRNA 29b-1	MI0000143	Mir29b-1	-1.8	5.0E-02	-2.1	4.9E-02	-0.5	4.9E-01	-0.2	8.6E-01
ENSMUST00000083672	ENSMUSG00000065606	3	microRNA 16-2	MI0000566	Mir16-2	0.8	8.0E-02	0.6	3.0E-01	0.2	5.5E-01	0.5	3.4E-01
ENSMUST00000083673	ENSMUSG00000065607	10	microRNA 331	MI0000609	Mir331	-1.6	6.6E-02	-1.4	1.5E-01	0.1	9.0E-01	-0.1	9.5E-01
ENSMUST00000083674	ENSMUSG00000065608	15	microRNA let7c-2	MI0000560	Mirlet7c-2	2.0	2.8E-04	3.8	6.7E-07	0.7	1.4E-01	-1.1	5.2E-02
ENSMUST00000083675	ENSMUSG00000065609	7	microRNA 7-2	MI0000729	Mir7-2	-0.1	9.0E-01	2.4	6.0E-02	2.4	1.3E-02	-0.1	9.2E-01
ENSMUST00000083676	ENSMUSG00000065610	6	microRNA 29a	MI0000576	Mir29a	1.2	1.3E-02	0.1	8.1E-01	-0.5	2.4E-01	0.6	2.6E-01
ENSMUST00000083677	ENSMUSG00000065611	8	microRNA 23a	MI0000571	Mir23a	0.4	3.6E-01	0.1	8.9E-01	0.6	1.9E-01	0.9	1.1E-01
ENSMUST00000083678	ENSMUSG00000065612	15	microRNA 151	MI0000173	Mir151	-0.4	4.8E-01	0.8	2.1E-01	-1.4	9.2E-03	-2.7	4.5E-04
ENSMUST00000083679	ENSMUSG00000065613	X	microRNA 92-2	MI0000580	Mir92-2	0.2	7.4E-01	1.5	2.3E-02	0.7	1.7E-01	-0.6	3.1E-01
ENSMUST00000083682	ENSMUSG00000065616	1	microRNA 375	MI0000792	Mir375	-0.2	7.9E-01	0.1	8.9E-01	-2.1	9.6E-03	-2.5	3.2E-02
ENSMUST00000083683	ENSMUSG00000065617	12	microRNA 323	MI0000592	Mir323	1.9	1.2E-02	-0.8	4.8E-01	-3.5	2.1E-04	-0.7	4.9E-01
ENSMUST00000083685	ENSMUSG00000065619	6	microRNA 183	MI0000225	Mir183	-1.7	1.2E-01	0.6	5.9E-01	-1.4	1.3E-01	-3.6	3.4E-03
ENSMUST00000084675	ENSMUSG00000076118	2	microRNA 669c	MI0004673	Mir669c	1.2	1.8E-01	1.7	1.3E-01	-0.6	5.0E-01	-1.0	3.6E-01
ENSMUST00000093557	ENSMUSG00000070065	11	microRNA 451a	MI0001730	Mir451a	0.9	3.4E-01	1.7	1.3E-01	-0.7	4.1E-01	-1.5	1.7E-01
ENSMUST00000093560	ENSMUSG00000095782	X	microRNA 465c-1	MI0005500	Mir465c-1	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000093564	ENSMUSG00000070072	12	microRNA 433	MI0001525	Mir433	1.1	2.1E-01	-0.3	7.9E-01	-1.4	7.2E-02	-0.1	9.6E-01
ENSMUST00000093566	ENSMUSG00000070074	16	microRNA 484	MI0003491	Mir484	0.2	6.7E-01	0.3	6.3E-01	0.5	2.8E-01	0.4	4.8E-01
ENSMUST00000093567	ENSMUSG00000070075	6	microRNA 490	MI0005002	Mir490	1.9	2.9E-02	0.5	6.7E-01	-1.9	5.7E-02	-0.5	6.5E-01
ENSMUST00000093568	ENSMUSG00000070076	12	microRNA 127	MI0000154	Mir127	-1.5	3.9E-02	1.0	2.0E-01	0.3	5.8E-01	-2.2	9.3E-03
ENSMUST00000093569	ENSMUSG00000070077	4	microRNA 491	MI0004680	Mir491	-0.1	9.1E-01	-1.5	1.6E-01	-1.5	1.0E-01	0.0	9.7E-01
ENSMUST00000093572	ENSMUSG00000070080	12	microRNA 431	MI0001524	Mir431	-1.1	2.3E-01	-1.5	2.4E-01	-0.5	5.6E-01	-0.1	9.1E-01
ENSMUST00000093573	ENSMUSG00000070081	X	microRNA 505	MI0004706	Mir505	-0.3	7.2E-01	0.5	5.4E-01	-0.1	8.3E-01	-1.0	2.8E-01
ENSMUST00000093576	ENSMUSG00000070084	8	microRNA 486	MI0003493	Mir486	0.9	4.1E-01	3.4	1.7E-02	-0.8	4.1E-01	-3.3	1.7E-02
ENSMUST00000093591	ENSMUSG00000070099	2	microRNA 466	MI0002401	Mir466	-2.7	3.8E-03	-4.0	2.0E-03	-0.8	2.8E-01	0.4	7.1E-01
ENSMUST00000093592	ENSMUSG00000070100	X	microRNA 362	MI0000763	Mir362	1.5	3.9E-02	-0.1	9.4E-01	-0.6	3.7E-01	1.0	2.3E-01
ENSMUST00000093593	ENSMUSG00000070101	12	microRNA 341	MI0000625	Mir341	0.4	6.4E-01	1.6	1.5E-01	-0.1	8.7E-01	-1.3	2.3E-01
ENSMUST00000093594	ENSMUSG00000070102	4	microRNA 455	MI0004679	Mir455	-1.2	2.2E-01	-1.2	3.5E-01	-2.1	2.9E-02	-2.0	1.3E-01
ENSMUST00000093597	ENSMUSG00000070105	12	microRNA 495	MI0004639	Mir495	0.4	5.6E-01	1.6	6.3E-02	1.8	1.2E-02	0.6	4.9E-01
ENSMUST00000093598	ENSMUSG00000070106	X	microRNA 363	MI0000765	Mir363	1.2	5.3E-02	0.7	3.2E-01	0.5	3.4E-01	1.0	1.3E-01
ENSMUST00000093600	ENSMUSG00000070108	X	microRNA 500	MI0004702	Mir500	-0.5	4.7E-01	-2.1	1.7E-02	-0.1	9.0E-01	1.6	6.8E-02
ENSMUST00000093601	ENSMUSG00000070109	11	microRNA 497b	MI0026030	Mir497b	3.5	8.1E-04	0.2	7.9E-01	-6.6	1.2E-08	-3.3	1.6E-03
ENSMUST00000093602	ENSMUSG00000070110	X	microRNA 504	MI0005515	Mir504	1.4	1.4E-01	-1.8	1.1E-01	-2.6	9.1E-03	0.6	5.8E-01
ENSMUST00000093618	ENSMUSG00000070126	1	microRNA 199a-2	MI0000713	Mir199a-2	2.0	1.1E-02	0.2	8.0E-01	-1.2	1.3E-01	0.5	5.9E-01
ENSMUST00000093619	ENSMUSG00000070127	19	microRNA 146b	MI0004665	Mir146b	-1.2	1.9E-01	-0.7	5.3E-01	1.8	3.9E-02	1.3	2.2E-01
ENSMUST00000093620	ENSMUSG00000070128	12	microRNA 485	MI0003492	Mir485	-0.7	3.1E-01	1.7	1.2E-01	0.3	6.8E-01	-2.1	4.2E-02
ENSMUST00000093621	ENSMUSG00000070129	12	microRNA 136	MI0014034	Mir136	1.2	1.3E-01	1.0	2.7E-01	-1.1	1.2E-01	-0.9	3.4E-01
ENSMUST00000093622	ENSMUSG00000070130	8	microRNA 328	MI0000603	Mir328	-1.6	2.4E-02	-1.6	6.1E-02	-0.7	2.1E-01	-0.8	3.1E-01
ENSMUST00000093625	ENSMUSG00000070133	12	microRNA 434	MI0001526	Mir434	0.8	3.8E-01	1.9	7.8E-02	-0.6	4.8E-01	-1.6	1.2E-01
ENSMUST00000093626	ENSMUSG00000096500	7	predicted gene, 23087		Gm23087	1.2	2.6E-01	0.2	8.8E-01	0.0	9.8E-01	1.0	3.9E-01
ENSMUST00000093627	ENSMUSG00000070136	12	microRNA 496a	MI0004589	Mir496a	2.9	1.9E-03	2.5	2.0E-02	0.0	9.7E-01	0.3	7.6E-01
ENSMUST00000093629	ENSMUSG00000070138	X	microRNA 452	MI0001734	Mir452	2.0	3.6E-03	0.0	9.6E-01	-2.0	9.3E-03	0.0	9.7E-01
ENSMUST00000093630	ENSMUSG00000070139	X	microRNA 532	MI0003206	Mir532	0.8	1.3E-01	1.2	5.2E-02	0.3	5.1E-01	-0.1	8.7E-01
ENSMUST00000093631	ENSMUSG00000070140	7	microRNA 483	MI0003484	Mir483	2.0	1.0E-02	0.1	9.4E-01	-1.4	8.9E-02	0.5	6.0E-01
ENSMUST00000093632	ENSMUSG00000070141	12	microRNA 494	MI0003532	Mir494	-1.0	1.6E-01	0.8	4.6E-01	1.5	7.3E-02	-0.3	7.5E-01
ENSMUST00000093635	ENSMUSG00000070144	2	microRNA 1a-1	MI0000139	Mir1a-1	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000101027	ENSMUSG00000077844	16	predicted gene, 22231		Gm22231	0.9	2.8E-01	-1.1	3.3E-01	0.3	7.2E-01	2.2	4.4E-02
ENSMUST00000102051	ENSMUSG00000076005	X	microRNA 547	MI0003523	Mir547	2.0	6.2E-03	1.5	1.6E-01	-1.6	3.9E-02	-1.2	2.2E-01
ENSMUST00000102052	ENSMUSG00000076006	12	microRNA 376b	MI0003533	Mir376b	2.6	2.9E-03	-0.2	8.5E-01	-2.5	2.6E-03	0.3	7.7E-01
ENSMUST00000102056	ENSMUSG00000076010	15	microRNA 615	MI0005004	Mir615	0.1	9.3E-01	-0.6	6.8E-01	-1.4	1.9E-01	-0.7	6.2E-01
ENSMUST00000102057	ENSMUSG00000076011	X	microRNA 652	MI0004965	Mir652	0.3	5.6E-01	1.4	1.5E-02	1.7	2.7E-04	0.6	2.3E-01
ENSMUST00000102058	ENSMUSG00000076012	6	microRNA 705	MI0004689	Mir705	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000102060	ENSMUSG00000076014	2	microRNA 669a-2	MI0004667	Mir669a-2	-1.7	5.5E-02	-0.5	7.0E-01	-0.1	9.2E-01	-1.4	2.5E-01
ENSMUST00000102074	ENSMUSG00000076028	2	microRNA 669a-3	MI0004668	Mir669a-3	0.2	8.9E-01	0.8	6.2E-01	0.5	7.1E-01	-0.2	9.1E-01
ENSMUST00000102075	ENSMUSG00000096567	15	predicted gene, 24098		Gm24098	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01
ENSMUST00000102078	ENSMUSG00000095297	15	predicted gene, 25381		Gm25381	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102082	ENSMUSG00000076036	7	predicted gene, 22133		Gm22133	1.1	1.7E-01	1.9	6.4E-02	1.4	9.1E-02	0.5	5.7E-01
ENSMUST00000102087	ENSMUSG00000076041	X	microRNA 20b	MI0003536	Mir20b	-1.1	1.1E-01	-1.5	7.0E-02	0.1	8.2E-01	0.5	5.1E-01
ENSMUST00000102089	ENSMUSG00000095509	2	microRNA 467b	MI0004671	Mir467b	4.3	5.3E-04	5.6	1.0E-04	0.0	9.6E-01	-1.3	2.8E-01
ENSMUST00000102094	ENSMUSG00000076049	14	microRNA 598	MI0005556	Mir598	1.9	1.2E-02	1.8	1.2E-01	-1.5	7.3E-02	-1.4	1.9E-01
ENSMUST00000102095	ENSMUSG00000076050	X	microRNA 450b	MI0004705	Mir450b	0.3	5.6E-01	-0.6	4.0E-01	0.1	8.1E-01	1.0	1.4E-01
ENSMUST00000102097	ENSMUSG00000076052	12	microRNA 541	MI0003521	Mir541	-4.4	6.2E-04	-0.8	5.1E-01	0.7	4.1E-01	-2.9	2.3E-02
ENSMUST00000102105	ENSMUSG00000072837	10	microRNA 546	MI0003517	Mir546	1.6	5.3E-02	0.4	6.7E-01	-0.3	7.1E-01	0.9	3.5E-01
ENSMUST00000102106	ENSMUSG00000076060	6	microRNA 704	MI0004688	Mir704	1.5	7.7E-02	-0.9	3.4E-01	-0.1	8.6E-01	2.3	3.1E-02
ENSMUST00000102108	ENSMUSG00000076062	14	microRNA 92-1	MI0000719	Mir92-1	-0.8	5.9E-02	0.2	6.6E-01	0.5	1.6E-01	-0.5	3.2E-01
ENSMUST00000102109	ENSMUSG00000076063	12	microRNA 539	MI0003520	Mir539	2.1	8.0E-03	1.6	8.7E-02	-0.1	9.2E-01	0.5	6.0E-01
ENSMUST00000102110	ENSMUSG00000076064	16	microRNA 690	MI0004658	Mir690	2.0	4.9E-02	3.2	1.3E-02	1.2	1.4E-01	0.0	9.7E-01
ENSMUST00000102112	ENSMUSG00000076066	X	microRNA 223	MI0000703	Mir223	0.5	2.3E-01	-0.6	2.5E-01	-0.2	6.0E-01	0.9	8.2E-02
ENSMUST00000102113	ENSMUSG00000076067	6	microRNA 592	MI0004127	Mir592	4.0	2.0E-03	4.6	1.1E-03	-2.7	1.9E-02	-3.3	9.4E-03
ENSMUST00000102166	ENSMUSG00000076121	14	microRNA 687	MI0004652	Mir687	2.1	5.7E-03	1.6	7.0E-02	0.0	9.9E-01	0.5	5.9E-01
ENSMUST00000102167	ENSMUSG00000072900	12	microRNA 540	MI0003518	Mir540	0.6	6.1E-01	1.6	2.4E-01	0.3	8.0E-01	-0.8	5.6E-01
ENSMUST00000102168	ENSMUSG00000076122	X	microRNA 503	MI0003538	Mir503	-1.2	8.8E-02	-1.5	6.9E-02	0.4	5.5E-01	0.7	4.1E-01
ENSMUST00000102169	ENSMUSG00000076123	4	microRNA 700	MI0004684	Mir700	-2.0	2.1E-02	-0.9	3.2E-01	0.7	3.4E-01	-0.4	7.0E-01
ENSMUST00000102172	ENSMUSG00000076126	2	microRNA 669b	MI0004666	Mir669b	0.2	8.6E-01	-2.2	2.7E-01	-3.0	4.5E-02	-0.5	7.8E-01
ENSMUST00000102174	ENSMUSG00000076128	14	microRNA 686	MI0004650	Mir686	1.9	7.8E-03	1.5	6.9E-02	-0.1	9.1E-01	0.3	7.2E-01
ENSMUST00000102183	ENSMUSG00000076137	17	predicted gene, 26384		Gm26384	0.9	3.2E-01	1.8	9.0E-02	1.4	9.0E-02	0.5	6.5E-01
ENSMUST00000102184	ENSMUSG00000076138	9	predicted gene, 26377		Gm26377	-0.7	3.9E-01	-1.6	1.5E-01	1.7	3.1E-02	2.6	2.2E-02
ENSMUST00000102186	ENSMUSG00000076140	X	microRNA 542	MI0003522	Mir542	1.2	4.8E-02	0.1	8.4E-01	0.0	9.5E-01	1.0	1.4E-01
ENSMUST00000102187	ENSMUSG00000076141	17	microRNA 693	MI0004662	Mir693	-0.4	6.2E-01	-0.3	7.6E-01	0.2	7.9E-01	0.1	9.2E-01
ENSMUST00000102189	ENSMUSG00000076143	7	microRNA 708	MI0004692	Mir708	1.8	3.4E-02	0.1	9.0E-01	-2.8	2.0E-03	-1.1	2.9E-01
ENSMUST00000102190	ENSMUSG00000076144	8	microRNA 709	MI0004693	Mir709	0.1	9.3E-01	0.5	6.5E-01	-0.1	9.0E-01	-0.6	6.3E-01
ENSMUST00000102191	ENSMUSG00000076145	12	microRNA 679	MI0004638	Mir679	0.4	5.5E-01	3.2	5.1E-03	2.3	2.5E-03	-0.4	6.7E-01
ENSMUST00000102192	ENSMUSG00000076146	13	microRNA 449c	MI0004645	Mir449c	-0.2	8.4E-01	-1.7	1.6E-01	-1.7	4.4E-02	-0.2	8.7E-01
ENSMUST00000102193	ENSMUSG00000076147	18	microRNA 694	MI0004664	Mir694	2.0	1.0E-02	0.3	7.4E-01	-1.5	7.8E-02	0.2	8.5E-01
ENSMUST00000102207	ENSMUSG00000096624	2	microRNA 467a-1	MI0002402	Mir467a-1	-0.9	2.6E-01	-1.9	5.1E-02	-0.8	2.4E-01	0.2	8.3E-01
ENSMUST00000102208	ENSMUSG00000076163	5	microRNA 701	MI0004685	Mir701	1.1	1.8E-01	-0.7	5.3E-01	-1.5	8.8E-02	0.3	7.7E-01
ENSMUST00000102261	ENSMUSG00000076216	2	microRNA 695	MI0004675	Mir695	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01
ENSMUST00000102262	ENSMUSG00000076217	6	microRNA 706	MI0004690	Mir706	1.8	1.3E-01	1.3	3.9E-01	0.5	6.7E-01	1.0	5.0E-01
ENSMUST00000102265	ENSMUSG00000076219	12	microRNA 487b	MI0003534	Mir487b	0.6	3.5E-01	0.0	9.9E-01	-0.1	8.9E-01	0.5	4.9E-01
ENSMUST00000102268	ENSMUSG00000076222	2	microRNA 297b	MI0004674	Mir297b	-0.7	5.3E-01	-2.0	1.3E-01	-0.9	3.0E-01	0.4	7.6E-01
ENSMUST00000102276	ENSMUSG00000076231	2	predicted gene, 22759		Gm22759	2.1	5.5E-03	2.0	2.5E-02	-0.1	9.0E-01	0.0	9.9E-01
ENSMUST00000102279	ENSMUSG00000076234	2	predicted gene, 22757		Gm22757	1.6	7.6E-02	1.4	1.8E-01	-0.1	8.7E-01	0.0	9.8E-01
ENSMUST00000102281	ENSMUSG00000076236	13	microRNA 682	MI0004644	Mir682	-0.7	5.0E-01	-0.3	7.9E-01	0.1	9.2E-01	-0.2	8.5E-01
ENSMUST00000102285	ENSMUSG00000076240	5	microRNA 702	MI0004686	Mir702	-2.4	2.8E-03	-2.7	5.9E-03	0.5	4.4E-01	0.7	4.3E-01
ENSMUST00000102286	ENSMUSG00000076241	12	microRNA 543	MI0003519	Mir543	0.2	8.5E-01	1.7	2.7E-01	0.2	8.8E-01	-1.3	3.4E-01
ENSMUST00000102291	ENSMUSG00000076246	13	predicted gene, 22256		Gm22256	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000102296	ENSMUSG00000076251	X	microRNA 501	MI0004703	Mir501	3.1	7.2E-04	3.8	4.9E-04	0.8	2.7E-01	0.1	9.1E-01
ENSMUST00000102300	ENSMUSG00000076255	3	microRNA 92b	MI0005521	Mir92b	-0.9	1.7E-01	-0.5	5.1E-01	0.4	5.2E-01	0.0	9.5E-01
ENSMUST00000102301	ENSMUSG00000076256	14	microRNA 19b-1	MI0000718	Mir19b-1	-3.1	1.0E-02	-4.5	8.7E-04	0.4	6.5E-01	1.9	1.3E-01
ENSMUST00000102303	ENSMUSG00000076258	16	predicted gene, 23935		Gm23935	4.3	3.8E-03	2.9	7.8E-02	-1.1	3.8E-01	0.4	7.7E-01
ENSMUST00000102314	ENSMUSG00000076269	X	microRNA 374b	MI0004125	Mir374b	2.8	1.8E-04	1.2	1.3E-01	0.4	5.0E-01	2.0	1.4E-02
ENSMUST00000102315	ENSMUSG00000076270	14	microRNA 719	MI0004651	Mir719	1.7	2.7E-02	1.9	3.4E-02	0.9	1.7E-01	0.7	4.1E-01
ENSMUST00000102316	ENSMUSG00000076271	4	microRNA 697	MI0004681	Mir697	2.1	5.7E-03	1.6	7.0E-02	0.0	9.9E-01	0.5	5.9E-01
ENSMUST00000102317	ENSMUSG00000076272	12	microRNA 666	MI0004553	Mir666	1.4	1.8E-01	1.6	2.8E-01	-2.0	8.9E-02	-2.2	1.2E-01
ENSMUST00000102320	ENSMUSG00000076275	7	microRNA 675	MI0004123	Mir675	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000102326	ENSMUSG00000076281	9	predicted gene, 24270		Gm24270	4.3	3.8E-03	2.9	7.8E-02	-1.1	3.8E-01	0.4	7.7E-01
ENSMUST00000102327	ENSMUSG00000076282	10	predicted gene, 24271		Gm24271	2.3	5.4E-03	2.0	3.8E-02	0.1	8.8E-01	0.4	6.3E-01
ENSMUST00000102331	ENSMUSG00000076286	X	microRNA 672	MI0004258	Mir672	1.9	6.7E-02	0.4	7.2E-01	-1.0	2.8E-01	0.4	7.1E-01
ENSMUST00000102333	ENSMUSG00000076288	16	microRNA 301b	MI0004122	Mir301b	-4.6	4.5E-06	-3.5	3.7E-04	0.1	8.2E-01	-1.0	2.7E-01
ENSMUST00000102339	ENSMUSG00000076294	4	predicted gene, 26154		Gm26154	3.3	1.4E-04	2.2	2.6E-02	-0.5	5.3E-01	0.7	4.2E-01
ENSMUST00000102345	ENSMUSG00000076300	19	predicted gene, 23060		Gm23060	4.3	8.7E-05	2.8	1.7E-02	-0.4	5.9E-01	1.0	3.4E-01
ENSMUST00000102348	ENSMUSG00000076303	19	predicted gene, 23061		Gm23061	2.7	6.0E-03	2.1	5.0E-02	0.0	1.0E+00	0.7	5.2E-01
ENSMUST00000102349	ENSMUSG00000076304	16	predicted gene, 23062		Gm23062	1.2	9.1E-02	0.8	3.3E-01	-0.1	8.5E-01	0.3	7.5E-01
ENSMUST00000102350	ENSMUSG00000076305	19	predicted gene, 23063		Gm23063	-0.5	5.8E-01	3.0	1.1E-02	2.1	1.3E-02	-1.4	2.1E-01
ENSMUST00000102354	ENSMUSG00000076309	2	microRNA 147	MI0005482	Mir147	-0.1	9.1E-01	-1.3	3.5E-02	0.0	9.5E-01	1.3	3.9E-02
ENSMUST00000102357	ENSMUSG00000076312	2	microRNA 499	MI0004676	Mir499	2.7	2.8E-03	0.6	5.9E-01	-1.4	8.9E-02	0.7	4.7E-01
ENSMUST00000102358	ENSMUSG00000076313	12	microRNA 665	MI0004171	Mir665	-0.2	8.1E-01	0.0	9.8E-01	-0.2	7.8E-01	-0.4	7.1E-01
ENSMUST00000102361	ENSMUSG00000076316	12	microRNA 673	MI0004601	Mir673	-1.0	2.0E-01	0.3	7.7E-01	-0.7	3.1E-01	-2.0	5.6E-02
ENSMUST00000102365	ENSMUSG00000076320	5	predicted gene, 26340		Gm26340	-3.4	1.2E-03	-2.5	4.5E-02	2.5	1.6E-02	1.6	1.7E-01
ENSMUST00000102368	ENSMUSG00000076323	19	predicted gene, 26339		Gm26339	0.8	4.1E-01	1.0	3.7E-01	1.1	2.2E-01	0.9	4.4E-01
ENSMUST00000102372	ENSMUSG00000076327	6	predicted gene, 26338		Gm26338	3.0	9.1E-04	1.5	1.5E-01	-0.8	2.9E-01	0.7	4.9E-01
ENSMUST00000102377	ENSMUSG00000076332	7	predicted gene, 24715		Gm24715	4.7	9.9E-04	4.8	5.5E-03	0.8	5.0E-01	0.7	5.8E-01
ENSMUST00000102378	ENSMUSG00000076333	15	microRNA 599	MI0012529	Mir599	2.0	8.0E-03	0.6	5.6E-01	-1.3	1.2E-01	0.2	8.4E-01
ENSMUST00000102380	ENSMUSG00000076335	2	microRNA 670	MI0004295	Mir670	2.1	9.7E-03	1.7	8.2E-02	0.0	9.4E-01	0.4	6.3E-01
ENSMUST00000102382	ENSMUSG00000076337	11	predicted gene, 24714		Gm24714	0.2	8.3E-01	0.6	6.6E-01	1.4	2.4E-01	1.0	3.9E-01
ENSMUST00000102383	ENSMUSG00000076338	8	microRNA 181d	MI0005450	Mir181d	0.5	3.8E-01	1.1	8.0E-02	-0.4	4.5E-01	-1.0	1.1E-01
ENSMUST00000102388	ENSMUSG00000076343	13	predicted gene, 25213		Gm25213	5.5	2.2E-06	2.9	8.9E-03	-2.1	2.8E-02	0.6	5.3E-01
ENSMUST00000102400	ENSMUSG00000076355	9	predicted gene, 27509		Gm27509	5.2	9.5E-07	4.4	7.1E-05	0.4	5.8E-01	1.2	1.5E-01
ENSMUST00000102402	ENSMUSG00000076357	6	microRNA 653	MI0005557	Mir653	2.3	2.4E-03	2.5	1.4E-02	-0.1	9.1E-01	-0.2	8.1E-01
ENSMUST00000102405	ENSMUSG00000076360	16	predicted gene, 24047		Gm24047	-2.9	5.7E-03	-1.1	3.3E-01	-0.3	7.1E-01	-2.1	7.0E-02

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000102406	ENSMUSG00000076361	6	microRNA 182	MI0000224	Mir182	-3.1	3.9E-04	-1.9	2.1E-02	-1.5	1.7E-02	-2.8	2.4E-03
ENSMUST00000102409	ENSMUSG00000076364	2	predicted gene, 24049		Gm24049	-1.9	2.5E-02	0.4	7.3E-01	0.0	9.5E-01	-2.3	3.1E-02
ENSMUST00000102411	ENSMUSG00000076366	3	predicted gene, 24048		Gm24048	0.7	6.1E-01	2.5	2.1E-01	-0.3	8.1E-01	-2.1	2.9E-01
ENSMUST00000102415	ENSMUSG00000076370	19	predicted gene, 22369		Gm22369	4.7	1.4E-02	4.5	5.5E-02	0.4	8.3E-01	0.6	7.4E-01
ENSMUST00000102421	ENSMUSG00000076376	2	microRNA 674	MI0004611	Mir674	-0.4	5.9E-01	-1.0	2.7E-01	-0.6	4.1E-01	0.0	9.9E-01
ENSMUST00000102422	ENSMUSG00000076377	10	predicted gene, 22370		Gm22370	3.5	3.7E-03	1.8	1.6E-01	-2.3	4.6E-02	-0.6	6.3E-01
ENSMUST00000102424	ENSMUSG00000076379	9	microRNA 190a	MI0000232	Mir190a	-2.0	1.9E-02	-1.2	2.9E-01	-0.4	6.4E-01	-1.1	3.0E-01
ENSMUST00000102427	ENSMUSG00000076382	8	predicted gene, 23193		Gm23193	3.9	1.9E-03	1.0	4.5E-01	-2.3	4.9E-02	0.5	6.9E-01
ENSMUST00000102432	ENSMUSG00000076387	5	microRNA 671	MI0004133	Mir671	-1.8	6.1E-03	-1.5	3.9E-02	-0.1	8.1E-01	-0.4	5.3E-01
ENSMUST00000102437	ENSMUSG00000076392	8	predicted gene, 25992		Gm25992	2.1	5.7E-03	1.6	7.0E-02	0.0	9.9E-01	0.5	5.9E-01
ENSMUST00000102439	ENSMUSG00000076394	11	predicted gene, 25991		Gm25991	1.0	4.2E-01	0.4	8.0E-01	1.0	4.1E-01	1.6	2.7E-01
ENSMUST00000102441	ENSMUSG00000076396	12	microRNA 667	MI0004196	Mir667	-0.5	5.0E-01	-1.5	1.7E-01	-1.1	1.7E-01	-0.1	9.4E-01
ENSMUST00000102443	ENSMUSG00000076398	X	microRNA 676	MI0005003	Mir676	0.6	3.6E-01	1.5	6.0E-02	-0.4	5.2E-01	-1.3	1.1E-01
ENSMUST00000102444	ENSMUSG00000076399	X	microRNA 450-2	MI0003537	Mir450-2	0.5	4.4E-01	-0.5	4.9E-01	0.2	6.8E-01	1.3	1.1E-01
ENSMUST00000102452	ENSMUSG00000076407	13	predicted gene, 22689		Gm22689	2.2	2.2E-02	0.2	8.5E-01	-0.3	7.1E-01	1.7	9.1E-02
ENSMUST00000102469	ENSMUSG00000076424	16	predicted gene, 25986		Gm25986	1.6	2.7E-02	2.0	2.0E-02	0.8	2.1E-01	0.4	6.1E-01
ENSMUST00000103246	ENSMUSG00000076445	7	predicted gene, 24865		Gm24865	2.1	5.5E-03	2.0	2.5E-02	-0.1	9.0E-01	0.0	9.9E-01
ENSMUST00000103249	ENSMUSG00000076448	10	microRNA 763	MI0004516	Mir763	2.0	3.2E-03	1.9	2.1E-02	-0.1	9.0E-01	0.0	9.7E-01
ENSMUST00000103255	ENSMUSG00000076454	7	microRNA 762	MI0004215	Mir762	2.2	3.5E-03	1.8	4.7E-02	0.0	9.9E-01	0.4	6.3E-01
ENSMUST00000103256	ENSMUSG00000076455	X	microRNA 767	MI0012530	Mir767	1.7	1.4E-02	1.3	1.2E-01	0.0	9.4E-01	0.4	6.2E-01
ENSMUST00000103257	ENSMUSG00000076456	3	microRNA 760	MI0004605	Mir760	0.3	7.1E-01	-0.1	9.3E-01	-0.4	6.3E-01	0.0	9.7E-01
ENSMUST00000103258	ENSMUSG00000076457	16	microRNA 802	MI0004249	Mir802	1.8	2.8E-01	1.3	5.6E-01	-3.6	5.9E-02	-3.2	1.5E-01
ENSMUST00000103259	ENSMUSG00000076458	X	microRNA 764	MI0004310	Mir764	2.2	2.9E-03	1.6	5.7E-02	-0.1	8.4E-01	0.4	6.2E-01
ENSMUST00000103260	ENSMUSG00000076459	12	microRNA 758	MI0004129	Mir758	0.1	9.3E-01	0.9	3.6E-01	1.4	1.0E-01	0.6	5.3E-01
ENSMUST00000103261	ENSMUSG00000076460	11	microRNA 744	MI0004124	Mir744	-2.0	1.6E-02	-2.6	8.9E-03	-1.0	1.3E-01	-0.5	6.0E-01
ENSMUST00000103758	ENSMUSG00000076946	13	microRNA 582	MI0006127	Mir582	1.1	3.3E-02	1.0	9.1E-02	0.5	2.6E-01	0.6	3.0E-01
ENSMUST00000103760	ENSMUSG00000076948	2	microRNA 467e	MI0006128	Mir467e	0.1	8.9E-01	-1.9	1.3E-01	-1.8	4.1E-02	0.2	8.9E-01
ENSMUST00000103762	ENSMUSG00000076950	2	predicted gene, 24933		Gm24933	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000103770	ENSMUSG00000076958	13	predicted gene, 24935		Gm24935	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000103771	ENSMUSG00000076959	2	microRNA 669l	MI0009942	Mir669l	1.4	1.2E-01	-2.5	2.1E-02	-1.7	3.7E-02	2.3	4.0E-02
ENSMUST00000103778	ENSMUSG00000076966	2	microRNA 466b-2	MI0005503	Mir466b-2	-2.6	1.8E-03	-5.5	8.7E-06	-2.1	6.3E-03	0.8	3.9E-01
ENSMUST00000103784	ENSMUSG00000076972	16	microRNA 193b	MI0005484	Mir193b	0.4	6.7E-01	2.3	3.8E-02	-1.0	2.5E-01	-2.8	1.4E-02
ENSMUST00000103788	ENSMUSG00000076976	2	microRNA 297c	MI0005492	Mir297c	0.3	7.6E-01	-3.4	6.6E-03	-2.8	8.4E-03	0.9	3.9E-01
ENSMUST00000103795	ENSMUSG00000076983	2	microRNA 297a-2	MI0000397	Mir297a-2	1.7	9.1E-02	-1.1	3.9E-01	-2.4	1.7E-02	0.3	7.8E-01
ENSMUST00000103800	ENSMUSG00000094316	7	microRNA 297-1	MI0000395	Mir297-1	0.6	5.2E-01	0.0	9.9E-01	-0.1	9.3E-01	0.5	6.3E-01
ENSMUST00000103804	ENSMUSG00000096360	2	microRNA 466b-7	MI0005502	Mir466b-7	1.8	7.3E-02	1.5	2.0E-01	0.3	7.6E-01	0.6	6.1E-01
ENSMUST00000103806	ENSMUSG00000076994	2	microRNA 466b-3	MI0005504	Mir466b-3	-0.9	5.7E-01	-2.9	1.9E-01	-1.9	2.4E-01	0.1	9.6E-01
ENSMUST00000103811	ENSMUSG00000076999	1	predicted gene, 22426		Gm22426	-0.3	8.1E-01	0.2	8.8E-01	1.5	2.2E-01	1.0	5.3E-01
ENSMUST00000103833	ENSMUSG00000077021	2	microRNA 467d	MI0005513	Mir467d	0.1	9.3E-01	-1.5	9.6E-02	-1.6	1.6E-02	0.0	1.0E+00
ENSMUST00000103834	ENSMUSG00000077022	7	predicted gene, 22707		Gm22707	2.7	4.7E-03	2.1	3.6E-02	0.0	9.8E-01	0.7	4.9E-01
ENSMUST00000103837	ENSMUSG00000077025	12	microRNA 493	MI0005514	Mir493	1.4	4.3E-02	1.0	2.5E-01	-0.1	8.5E-01	0.3	6.8E-01
ENSMUST00000103850	ENSMUSG00000077038	2	microRNA 669f	MI0006287	Mir669f	-1.3	2.1E-01	-1.7	2.2E-01	-1.2	2.2E-01	-0.8	5.6E-01
ENSMUST00000103854	ENSMUSG00000077042	5	microRNA 574	MI0005518	Mir574	-0.4	5.3E-01	-0.7	3.0E-01	0.3	5.4E-01	0.7	3.3E-01
ENSMUST00000103861	ENSMUSG00000077049	2	microRNA 467c	MI0005512	Mir467c	0.9	2.4E-01	-0.6	4.9E-01	-0.8	2.4E-01	0.8	4.1E-01
ENSMUST00000103867	ENSMUSG00000077055	19	predicted gene, 24543		Gm24543	2.4	2.7E-03	2.4	1.0E-02	-0.1	8.4E-01	-0.2	8.6E-01
ENSMUST00000103868	ENSMUSG00000093900	2	microRNA 669p-2	MI0014064	Mir669p-2	-0.1	9.7E-01	-2.2	2.4E-01	-0.5	7.3E-01	1.6	3.8E-01
ENSMUST00000103871	ENSMUSG00000077059	7	predicted gene, 24541		Gm24541	-1.3	1.3E-01	0.7	5.0E-01	0.6	4.1E-01	-1.3	1.9E-01
ENSMUST00000103877	ENSMUSG00000077065	11	predicted gene, 25040		Gm25040	0.2	9.0E-01	2.3	2.0E-01	1.5	2.4E-01	-0.7	6.9E-01
ENSMUST00000103883	ENSMUSG00000095269	2	microRNA 466b-8	MI0005506	Mir466b-8	1.8	3.1E-02	1.5	1.4E-01	0.2	8.1E-01	0.5	5.7E-01
ENSMUST00000103884	ENSMUSG00000096134	2	microRNA 669p-1	MI0014064	Mir669p-1	-0.1	9.7E-01	-2.2	2.4E-01	-0.5	7.3E-01	1.6	3.8E-01
ENSMUST00000103894	ENSMUSG00000077082	10	predicted gene, 23766		Gm23766	-1.4	7.2E-01	0.5	9.3E-01	-1.2	7.7E-01	-3.1	5.2E-01
ENSMUST00000103898	ENSMUSG00000077086	2	microRNA 669o	MI0009945	Mir669o	0.3	8.7E-01	-0.8	7.0E-01	-0.2	8.8E-01	0.8	6.8E-01
ENSMUST00000103900	ENSMUSG00000096113	2	microRNA 466b-5	MI0005502	Mir466b-5	1.8	7.3E-02	1.5	2.0E-01	0.3	7.6E-01	0.6	6.1E-01
ENSMUST00000103902	ENSMUSG00000077090	10	predicted gene, 22117		Gm22117	0.3	7.1E-01	0.9	3.7E-01	1.0	1.9E-01	0.5	6.1E-01
ENSMUST00000103907	ENSMUSG00000077095	2	predicted gene, 24342		Gm24342	0.6	4.4E-01	1.5	2.3E-01	-0.3	6.9E-01	-1.2	3.1E-01
ENSMUST00000103908	ENSMUSG00000077096	12	predicted gene, 22015		Gm22015	2.5	1.2E-02	1.5	1.6E-01	0.2	8.3E-01	1.3	2.3E-01
ENSMUST00000103923	ENSMUSG00000077111	X	microRNA 18b	MI0005483	Mir18b	-0.8	3.0E-01	-0.7	4.6E-01	1.0	1.4E-01	0.9	3.7E-01
ENSMUST00000103925	ENSMUSG00000077113	2	microRNA 466p	MI0014078	Mir466p	0.5	6.7E-01	-2.8	5.0E-02	-2.7	2.3E-02	0.6	6.5E-01
ENSMUST00000103943	ENSMUSG00000077131	2	predicted gene, 23578		Gm23578	3.7	6.7E-03	1.7	1.9E-01	0.3	7.5E-01	2.3	8.8E-02
ENSMUST00000104232	ENSMUSG00000077420	3	predicted gene, 24282		Gm24282	0.6	3.7E-01	0.7	4.4E-01	0.6	4.3E-01	0.5	5.2E-01
ENSMUST00000104627	ENSMUSG00000077815	7	microRNA 290a	MI0000388	Mir290a	0.0	1.0E+00	-1.8	1.1E-01	0.2	7.8E-01	2.0	9.6E-02
ENSMUST00000104632	ENSMUSG00000077821	9	predicted gene, 27450		Gm27450	2.2	2.9E-02	1.7	1.3E-01	0.2	8.0E-01	0.7	5.0E-01
ENSMUST00000104639	ENSMUSG00000077829	3	predicted gene, 23237		Gm23237	2.8	1.8E-02	2.0	1.8E-01	-0.4	7.3E-01	0.4	7.4E-01
ENSMUST00000104640	ENSMUSG00000077830	12	predicted gene, 26050		Gm26050	2.6	6.4E-03	0.4	7.0E-01	-0.9	2.9E-01	1.3	2.0E-01
ENSMUST00000104642	ENSMUSG00000077832	5	predicted gene, 26051		Gm26051	0.7	2.7E-01	0.3	6.9E-01	-0.3	6.0E-01	0.1	9.0E-01
ENSMUST00000104646	ENSMUSG00000077836	11	predicted gene, 26052		Gm26052	0.5	6.2E-01	2.6	3.7E-02	1.9	4.8E-02	-0.2	8.8E-01
ENSMUST00000104654	ENSMUSG00000077846	1	predicted gene, 22232		Gm22232	1.6	2.8E-02	1.6	6.3E-02	0.0	9.9E-01	0.0	9.7E-01
ENSMUST00000104666	ENSMUSG00000077858	X	predicted gene, 25063		Gm25063	2.2	2.7E-02	2.5	3.9E-02	0.1	9.2E-01	-0.2	8.3E-01
ENSMUST00000104680	ENSMUSG00000077872	X	microRNA 878	MI0005548	Mir878	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000104685	ENSMUSG00000096079	6	predicted gene, 23961		Gm23961	1.4	2.1E-01	1.1	3.1E-01	1.4	1.2E-01	1.7	1.4E-01
ENSMUST00000104687	ENSMUSG00000077879	12	predicted gene, 23912		Gm23912	0.7	4.2E-01	-0.2	8.6E-01	-0.5	5.8E-01	0.4	7.1E-01
ENSMUST00000104692	ENSMUSG00000077884	1	predicted gene, 24557		Gm24557	1.9	1.3E-02	1.5	1.0E-01	0.1	8.9E-01	0.5	5.4E-01
ENSMUST00000104694	ENSMUSG00000077886	7	microRNA 295	MI0000393	Mir295	1.0	2.9E-01	-2.3	4.2E-02	-1.4	8.4E-02	1.8	1.0E-01
ENSMUST00000104698	ENSMUSG00000077890	15	microRNA 875	MI0005551	Mir875	2.0	3.4E-03	-1.0	2.3E-01	-2.9	4.3E-04	0.2	8.3E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000104700	ENSMUSG00000077892	3	predicted gene, 22901		Gm22901	2.7	5.2E-04	1.6	5.4E-02	-0.1	8.3E-01	1.0	2.2E-01
ENSMUST00000104703	ENSMUSG00000077896	5	microRNA 879	MI0005472	Mir879	0.7	3.6E-01	-0.6	5.1E-01	-2.2	4.2E-03	-0.8	3.5E-01
ENSMUST00000104704	ENSMUSG00000077897	2	microRNA 511	MI0005554	Mir511	-1.2	2.0E-01	-3.1	4.1E-03	-4.5	1.3E-06	-2.6	2.2E-02
ENSMUST00000104709	ENSMUSG00000077902	7	predicted gene, 25787		Gm25787	1.3	1.2E-01	0.1	9.0E-01	-0.9	3.0E-01	0.3	7.9E-01
ENSMUST00000104710	ENSMUSG00000077903	7	microRNA 294	MI0000392	Mir294	2.1	8.4E-03	1.2	2.4E-01	-0.9	2.5E-01	0.0	9.9E-01
ENSMUST00000104728	ENSMUSG00000077921	4	microRNA 872	MI0005549	Mir872	-0.1	8.0E-01	0.1	8.5E-01	0.2	6.8E-01	-0.1	9.3E-01
ENSMUST00000104735	ENSMUSG00000077928	14	microRNA 208b	MI0005552	Mir208b	0.3	6.6E-01	-0.9	3.6E-01	-1.1	1.8E-01	0.1	9.0E-01
ENSMUST00000104738	ENSMUSG00000077931	17	microRNA 877	MI0005553	Mir877	-1.4	4.7E-02	-1.6	5.2E-02	-0.2	7.5E-01	0.0	9.9E-01
ENSMUST00000104745	ENSMUSG00000077938	8	predicted gene, 24132		Gm24132	1.3	1.4E-01	0.9	4.0E-01	-0.1	8.9E-01	0.3	7.6E-01
ENSMUST00000104748	ENSMUSG00000077941	2	microRNA 466h	MI0005511	Mir466h	-2.1	2.2E-02	-2.6	1.8E-02	0.6	4.7E-01	1.1	2.9E-01
ENSMUST00000104755	ENSMUSG00000077948	14	predicted gene, 23438		Gm23438	2.7	1.2E-02	0.7	5.3E-01	-0.8	4.1E-01	1.2	2.7E-01
ENSMUST00000104757	ENSMUSG00000095006	X	microRNA 465c-2	MI0005500	Mir465c-2	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000104761	ENSMUSG00000077954	2	microRNA 297a-4	MI0005489	Mir297a-4	0.4	8.0E-01	-3.8	3.2E-02	-3.2	2.9E-02	1.0	5.4E-01
ENSMUST00000104763	ENSMUSG00000096628	X	microRNA 871	MI0005471	Mir871	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000104769	ENSMUSG00000077962	13	microRNA 874	MI0005479	Mir874	-1.5	1.5E-01	-1.4	2.5E-01	-0.1	8.9E-01	-0.1	9.3E-01
ENSMUST00000104778	ENSMUSG00000077971	13	predicted gene, 26259		Gm26259	2.6	4.7E-02	2.5	7.7E-02	1.6	1.2E-01	1.8	2.1E-01
ENSMUST00000104779	ENSMUSG00000077972	2	microRNA 466f-1	MI0005507	Mir466f-1	1.2	2.0E-01	1.4	1.6E-01	0.9	2.5E-01	0.7	5.1E-01
ENSMUST00000104788	ENSMUSG00000077981	2	microRNA 466f-3	MI0005509	Mir466f-3	-1.9	6.4E-02	-2.4	4.1E-02	0.1	9.4E-01	0.6	6.1E-01
ENSMUST00000104798	ENSMUSG00000077991	2	microRNA 466n	MI0014079	Mir466n	-1.1	2.7E-01	-2.9	1.2E-02	-0.4	6.8E-01	1.5	1.7E-01
ENSMUST00000104803	ENSMUSG00000077996	3	microRNA 190b	MI0005478	Mir190b	2.1	1.2E-02	2.9	6.7E-03	1.2	1.4E-01	0.5	6.0E-01
ENSMUST00000104805	ENSMUSG00000077998	2	microRNA 466f-2	MI0005508	Mir466f-2	-1.9	4.9E-02	-3.8	1.7E-03	-0.9	2.9E-01	1.0	3.3E-01
ENSMUST00000104810	ENSMUSG00000094677	9	predicted gene, 22008		Gm22008	1.8	4.0E-02	2.1	6.8E-02	0.2	8.4E-01	-0.1	9.2E-01
ENSMUST00000104813	ENSMUSG00000078006	8	predicted gene, 26301		Gm26301	2.2	2.9E-03	1.6	5.7E-02	-0.1	8.4E-01	0.4	6.2E-01
ENSMUST00000104815	ENSMUSG00000078008	7	microRNA 291a	MI0000389	Mir291a	-0.3	7.2E-01	-0.9	3.7E-01	0.2	7.2E-01	0.8	3.8E-01
ENSMUST00000104831	ENSMUSG00000078025	2	microRNA 466g	MI0005510	Mir466g	-2.4	5.2E-03	-4.0	1.3E-03	-1.3	8.0E-02	0.2	8.2E-01
ENSMUST00000104832	ENSMUSG00000078026	2	microRNA 466o	MI0014052	Mir466o	0.8	4.2E-01	0.3	8.2E-01	0.0	9.7E-01	0.6	6.1E-01
ENSMUST00000104833	ENSMUSG00000078027	13	microRNA 449b	MI0005547	Mir449b	2.0	6.0E-03	0.6	4.9E-01	-1.2	1.2E-01	0.2	8.4E-01
ENSMUST00000104837	ENSMUSG00000078031	2	microRNA 466d	MI0005546	Mir466d	-1.5	5.0E-02	-2.2	4.4E-02	-1.2	8.7E-02	-0.4	6.8E-01
ENSMUST00000104838	ENSMUSG00000078032	7	microRNA 291b	MI0003539	Mir291b	0.7	3.7E-01	1.5	9.6E-02	1.1	1.3E-01	0.3	7.5E-01
ENSMUST00000104840	ENSMUSG00000078034	X	predicted gene, 24683		Gm24683	2.5	6.8E-04	1.6	5.2E-02	-0.1	8.1E-01	0.7	3.5E-01
ENSMUST00000104841	ENSMUSG00000078035	7	microRNA 293	MI0000391	Mir293	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000104847	ENSMUSG00000078041	7	microRNA 292	MI0000390	Mir292	-1.6	7.8E-02	-2.2	5.5E-02	0.4	5.2E-01	1.0	3.9E-01
ENSMUST00000104848	ENSMUSG00000078042	6	predicted gene, 24855		Gm24855	1.9	1.3E-02	1.5	1.0E-01	0.1	8.9E-01	0.5	5.4E-01
ENSMUST00000104866	ENSMUSG00000078060	2	microRNA 466l	MI0006278	Mir466l	1.0	1.8E-01	1.4	1.2E-01	0.9	1.8E-01	0.5	5.3E-01
ENSMUST00000104867	ENSMUSG00000078061	2	predicted gene, 22824		Gm22824	3.1	2.3E-03	0.3	7.9E-01	-0.8	3.9E-01	2.1	4.9E-02
ENSMUST00000116680	ENSMUSG00000080330	3	predicted gene, 22468		Gm22468	0.1	9.3E-01	0.7	5.2E-01	1.2	2.0E-01	0.6	5.7E-01
ENSMUST00000116681	ENSMUSG00000080331	X	microRNA 1298	MI0004300	Mir1298	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000116684	ENSMUSG00000080334	8	predicted gene, 25110		Gm25110	1.6	1.6E-01	2.6	6.4E-02	1.0	3.1E-01	-0.1	9.6E-01
ENSMUST00000116692	ENSMUSG00000080342	17	predicted gene, 24589		Gm24589	3.4	7.5E-04	1.3	2.5E-01	-2.3	1.0E-02	-0.2	8.7E-01
ENSMUST00000116696	ENSMUSG00000080346	13	predicted gene, 24588		Gm24588	3.2	4.8E-04	1.6	7.8E-02	-0.2	7.1E-01	1.3	1.6E-01
ENSMUST00000116697	ENSMUSG00000080347	10	predicted gene, 24587		Gm24587	2.7	3.4E-03	0.6	5.5E-01	-1.0	2.2E-01	1.1	2.4E-01
ENSMUST00000116698	ENSMUSG00000080348	8	predicted gene, 24591		Gm24591	1.8	9.6E-03	0.7	4.0E-01	-0.2	7.3E-01	0.9	2.3E-01
ENSMUST00000116699	ENSMUSG00000080349	12	predicted gene, 24590		Gm24590	2.1	5.8E-03	0.5	6.0E-01	-1.2	1.5E-01	0.4	6.2E-01
ENSMUST00000116700	ENSMUSG00000080350	7	predicted gene, 26248		Gm26248	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116701	ENSMUSG00000096196	3	predicted gene, 26137		Gm26137	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116704	ENSMUSG00000095069	9	predicted gene, 26190		Gm26190	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116705	ENSMUSG00000095541	18	predicted gene, 24617		Gm24617	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116706	ENSMUSG00000080356	12	microRNA 1247	MI0004120	Mir1247	1.6	6.5E-02	-0.3	7.9E-01	-3.2	1.1E-03	-1.3	2.5E-01
ENSMUST00000116710	ENSMUSG00000080360	4	predicted gene, 25779		Gm25779	1.4	5.0E-02	1.0	2.1E-01	0.0	9.5E-01	0.3	7.4E-01
ENSMUST00000116713	ENSMUSG00000080363	7	predicted gene, 25778		Gm25778	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116716	ENSMUSG00000080366	8	predicted gene, 25775		Gm25775	1.6	1.6E-01	2.6	6.4E-02	1.0	3.1E-01	-0.1	9.6E-01
ENSMUST00000116717	ENSMUSG00000080367	7	predicted gene, 25774		Gm25774	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116724	ENSMUSG00000080374	2	predicted gene, 22953		Gm22953	0.0	9.7E-01	1.1	4.3E-01	1.1	3.4E-01	0.1	9.5E-01
ENSMUST00000116730	ENSMUSG00000080380	X	predicted gene, 22102		Gm22102	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116733	ENSMUSG00000080383	X	predicted gene, 22103	MI0006299	Gm22103	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000116737	ENSMUSG00000095894	16	predicted gene, 24795		Gm24795	1.6	1.6E-01	2.6	6.4E-02	1.0	3.1E-01	-0.1	9.6E-01
ENSMUST00000116741	ENSMUSG00000080391	1	predicted gene, 23785		Gm23785	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000116751	ENSMUSG00000080401	9	predicted gene, 23653		Gm23653	1.8	5.7E-02	1.7	9.2E-02	0.8	3.4E-01	0.9	3.9E-01
ENSMUST00000116752	ENSMUSG00000080402	14	predicted gene, 23652		Gm23652	2.8	9.3E-03	0.7	5.7E-01	-1.0	2.9E-01	1.2	3.3E-01
ENSMUST00000116756	ENSMUSG00000080406	12	microRNA 1188	MI0006290	Mir1188	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000116759	ENSMUSG00000080409	9	microRNA 467h	MI0006302	Mir467h	1.8	1.4E-02	1.5	1.0E-01	0.0	9.9E-01	0.4	6.6E-01
ENSMUST00000116760	ENSMUSG00000080410	1	predicted gene, 26472		Gm26472	0.8	3.8E-01	2.2	8.4E-02	0.9	2.8E-01	-0.4	7.5E-01
ENSMUST00000116761	ENSMUSG00000080411	12	microRNA 1193	MI0006298	Mir1193	1.5	6.0E-02	-0.8	4.4E-01	-1.6	7.7E-02	0.7	4.1E-01
ENSMUST00000116762	ENSMUSG00000080412	5	predicted gene, 26474		Gm26474	2.1	1.8E-02	0.1	9.2E-01	-1.5	1.1E-01	0.5	6.5E-01
ENSMUST00000116765	ENSMUSG00000080415	2	predicted gene, 26469		Gm26469	0.5	6.7E-01	3.6	1.3E-02	1.2	2.5E-01	-1.9	1.5E-01
ENSMUST00000116769	ENSMUSG00000080419	X	predicted gene, 26475		Gm26475	2.9	1.1E-03	1.5	8.6E-02	0.0	9.5E-01	1.3	1.5E-01
ENSMUST00000116774	ENSMUSG00000080424	3	microRNA 466k	MI0006292	Mir466k	0.3	7.5E-01	0.1	9.2E-01	0.7	4.7E-01	0.9	3.9E-01
ENSMUST00000116777	ENSMUSG00000080427	X	predicted gene, 24835		Gm24835	1.2	1.8E-01	-0.1	9.4E-01	-0.1	8.6E-01	1.1	2.5E-01
ENSMUST00000116782	ENSMUSG00000080432	14	predicted gene, 23178		Gm23178	3.7	3.1E-03	2.1	7.5E-02	0.2	8.0E-01	1.8	1.7E-01
ENSMUST00000116784	ENSMUSG00000080434	8	predicted gene, 23177		Gm23177	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116791	ENSMUSG00000080441	15	microRNA 1249	MI0004132	Mir1249	-2.1	1.4E-02	-4.6	2.2E-04	-1.0	1.3E-01	1.4	1.9E-01
ENSMUST00000116793	ENSMUSG00000080443	12	predicted gene, 25847		Gm25847	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000116801	ENSMUSG00000080451	13	predicted gene, 24193		Gm24193	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116802	ENSMUSG00000080452	16	microRNA 1306	MI0009935	Mir1306	0.2	8.2E-01	-0.8	3.4E-01	-0.7	2.7E-01	0.3	7.4E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000116804	ENSMUSG00000080454	13	predicted gene, 24195		Gm24195	1.1	1.1E-01	-0.1	9.2E-01	-0.7	3.6E-01	0.5	5.3E-01
ENSMUST00000116805	ENSMUSG00000080455	17	predicted gene, 24194		Gm24194	1.5	5.5E-02	1.3	1.3E-01	-0.1	8.9E-01	0.1	9.2E-01
ENSMUST00000116809	ENSMUSG00000080459	2	microRNA 669g	MI0006280	Mir669g	2.1	9.1E-03	0.9	3.7E-01	-0.7	3.8E-01	0.4	6.2E-01
ENSMUST00000116812	ENSMUSG00000093807	14	predicted gene, 23620	MI0006299	Gm23620	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000116818	ENSMUSG00000080468	17	microRNA 1195	MI0006303	Mir1195	2.1	2.1E-02	-0.3	7.9E-01	-2.9	1.3E-03	-0.5	6.1E-01
ENSMUST00000116833	ENSMUSG00000094593	3	predicted gene, 24744		Gm24744	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116835	ENSMUSG00000080485	16	predicted gene, 23493		Gm23493	0.1	9.3E-01	1.6	1.4E-01	1.9	2.8E-02	0.4	7.2E-01
ENSMUST00000116837	ENSMUSG00000080487	11	predicted gene, 23492		Gm23492	1.0	3.7E-01	2.4	8.5E-02	1.0	3.0E-01	-0.4	7.6E-01
ENSMUST00000116845	ENSMUSG00000080495	9	predicted gene, 26303		Gm26303	1.4	8.9E-02	-0.4	7.1E-01	-1.5	1.0E-01	0.3	7.5E-01
ENSMUST00000116848	ENSMUSG00000080498	X	predicted gene, 26302		Gm26302	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000116850	ENSMUSG00000080500	2	predicted gene, 22072		Gm22072	1.6	2.3E-02	1.1	1.8E-01	-0.1	8.7E-01	0.4	6.4E-01
ENSMUST00000116852	ENSMUSG00000094571	6	predicted gene, 23551		Gm23551	1.4	6.9E-02	1.7	6.8E-02	0.7	2.9E-01	0.4	6.1E-01
ENSMUST00000116854	ENSMUSG00000080504	2	microRNA 669d-2	MI0014051	Mir669d-2	-0.4	6.8E-01	-3.1	5.5E-03	-1.6	4.8E-02	1.1	3.0E-01
ENSMUST00000116856	ENSMUSG00000080506	3	predicted gene, 25042		Gm25042	1.5	8.7E-02	1.3	1.8E-01	0.5	5.2E-01	0.6	4.9E-01
ENSMUST00000116857	ENSMUSG00000080507	2	predicted gene, 22071		Gm22071	1.3	6.6E-02	1.0	2.3E-01	-0.2	7.3E-01	0.1	8.9E-01
ENSMUST00000116858	ENSMUSG00000080508	16	predicted gene, 25041		Gm25041	2.1	5.7E-03	1.6	7.0E-02	0.0	9.9E-01	0.5	5.9E-01
ENSMUST00000116861	ENSMUSG00000080511	9	predicted gene, 22195		Gm22195	1.8	3.3E-02	0.6	5.4E-01	0.0	9.7E-01	1.2	2.0E-01
ENSMUST00000116865	ENSMUSG00000080515	5	predicted gene, 22196		Gm22196	0.6	4.8E-01	1.7	7.6E-02	2.0	1.6E-02	0.9	3.5E-01
ENSMUST00000116866	ENSMUSG00000080516	8	predicted gene, 22197		Gm22197	2.7	1.2E-02	0.1	8.9E-01	-0.5	6.1E-01	2.0	6.3E-02
ENSMUST00000116872	ENSMUSG00000080522	14	predicted gene, 23881		Gm23881	0.7	3.5E-01	2.8	2.1E-02	1.3	9.0E-02	-0.7	5.1E-01
ENSMUST00000116876	ENSMUSG00000080526	10	microRNA 466j	MI0006295	Mir466j	2.3	1.7E-02	0.2	8.4E-01	-1.1	1.9E-01	0.9	3.5E-01
ENSMUST00000116877	ENSMUSG00000080527	15	predicted gene, 23880		Gm23880	1.6	7.1E-02	2.0	8.5E-02	0.0	9.7E-01	-0.4	7.3E-01
ENSMUST00000116879	ENSMUSG00000080529	18	predicted gene, 23882		Gm23882	2.0	3.3E-02	1.9	7.5E-02	-0.1	9.3E-01	0.0	9.9E-01
ENSMUST00000116880	ENSMUSG00000080530	11	predicted gene, 25540	MI0006299	Gm25540	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000116883	ENSMUSG00000080533	7	microRNA 1191	MI0006296	Mir1191	-0.9	1.5E-01	-0.9	2.3E-01	0.2	7.2E-01	0.2	8.0E-01
ENSMUST00000116893	ENSMUSG00000080543	18	predicted gene, 22709		Gm22709	2.9	9.1E-03	0.8	5.2E-01	-0.7	5.3E-01	1.4	2.2E-01
ENSMUST00000116896	ENSMUSG00000094175	17	predicted gene, 24427		Gm24427	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116899	ENSMUSG00000080549	8	predicted gene, 22715		Gm22715	0.6	5.4E-01	1.2	2.8E-01	0.9	3.8E-01	0.2	8.3E-01
ENSMUST00000116906	ENSMUSG00000080556	5	microRNA 467g	MI0006301	Mir467g	1.6	1.6E-02	1.6	5.2E-02	-0.1	8.4E-01	-0.1	9.2E-01
ENSMUST00000116911	ENSMUSG00000080561	1	predicted gene, 26042		Gm26042	1.8	6.1E-02	1.0	3.5E-01	-0.1	9.0E-01	0.7	4.9E-01
ENSMUST00000116918	ENSMUSG00000095035	17	predicted gene, 22346		Gm22346	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116923	ENSMUSG00000080573	11	microRNA 467f	MI0006293	Mir467f	1.5	1.2E-01	1.6	2.3E-01	-0.2	8.7E-01	-0.3	8.3E-01
ENSMUST00000116924	ENSMUSG00000080574	13	microRNA 466i	MI0006282	Mir466i	1.2	1.6E-01	0.0	9.7E-01	-0.9	3.2E-01	0.2	8.3E-01
ENSMUST00000116925	ENSMUSG00000080575	12	microRNA 1190	MI0006294	Mir1190	0.3	7.4E-01	-1.3	2.6E-01	-0.2	7.6E-01	1.3	2.4E-01
ENSMUST00000116926	ENSMUSG00000095000	7	predicted gene, 25171		Gm25171	1.6	1.6E-01	2.6	6.4E-02	1.0	3.1E-01	-0.1	9.6E-01
ENSMUST00000116930	ENSMUSG00000080580	13	microRNA 466f-4	MI0006291	Mir466f-4	1.4	1.5E-01	1.0	4.1E-01	-0.1	9.1E-01	0.4	7.4E-01
ENSMUST00000116935	ENSMUSG00000095255	13	predicted gene, 23086		Gm23086	0.9	2.0E-01	-0.7	5.0E-01	-1.3	1.2E-01	0.3	7.2E-01
ENSMUST00000116936	ENSMUSG00000080586	5	microRNA 1187	MI0006285	Mir1187	0.8	3.9E-01	1.6	1.4E-01	1.4	1.1E-01	0.6	5.7E-01
ENSMUST00000116938	ENSMUSG00000095437	18	predicted gene, 23606		Gm23606	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116939	ENSMUSG00000093495	7	predicted gene, 23368		Gm23368	0.7	5.8E-01	0.5	7.3E-01	-0.6	5.7E-01	-0.5	7.5E-01
ENSMUST00000116940	ENSMUSG00000080590	3	predicted gene, 22029		Gm22029	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116942	ENSMUSG00000080592	8	predicted gene, 22030		Gm22030	1.3	5.9E-02	0.8	3.4E-01	-0.1	8.4E-01	0.4	6.2E-01
ENSMUST00000116944	ENSMUSG00000080594	2	microRNA 669h	MI0006289	Mir669h	1.0	3.8E-01	0.9	4.9E-01	-0.2	8.1E-01	-0.2	8.7E-01
ENSMUST00000116946	ENSMUSG00000080596	15	predicted gene, 22032		Gm22032	1.9	1.3E-02	0.2	8.4E-01	-0.9	2.7E-01	0.8	3.3E-01
ENSMUST00000116947	ENSMUSG00000080597	4	predicted gene, 22033		Gm22033	0.8	3.4E-01	0.6	5.5E-01	-0.2	7.5E-01	0.0	9.9E-01
ENSMUST00000116950	ENSMUSG00000080600	11	predicted gene, 23840		Gm23840	0.0	9.9E-01	3.1	5.2E-02	3.7	5.7E-03	0.6	6.5E-01
ENSMUST00000116956	ENSMUSG00000095798	9	predicted gene, 26298		Gm26298	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116959	ENSMUSG00000080609	7	predicted gene, 23844		Gm23844	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000116975	ENSMUSG00000080625	1	predicted gene, 22679		Gm22679	1.5	9.9E-02	0.8	4.8E-01	-0.7	4.5E-01	0.0	9.9E-01
ENSMUST00000116976	ENSMUSG00000080626	19	microRNA 1192	MI0006297	Mir1192	2.7	4.0E-03	1.6	1.9E-01	0.2	8.6E-01	1.3	2.3E-01
ENSMUST00000116977	ENSMUSG00000080627	2	predicted gene, 22677		Gm22677	2.2	9.7E-03	1.5	1.2E-01	-0.1	9.2E-01	0.6	4.9E-01
ENSMUST00000116981	ENSMUSG00000080631	11	predicted gene, 25507		Gm25507	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000116985	ENSMUSG00000080635	18	predicted gene, 25509		Gm25509	1.9	3.6E-02	-0.1	9.4E-01	-1.3	1.7E-01	0.7	4.8E-01
ENSMUST00000116995	ENSMUSG00000080645	X	microRNA 1198	MI0006306	Mir1198	0.3	6.0E-01	1.2	5.7E-02	0.9	6.8E-02	-0.1	9.3E-01
ENSMUST00000117002	ENSMUSG00000094330	2	predicted gene, 22051		Gm22051	2.9	1.7E-03	0.7	4.9E-01	-0.9	2.8E-01	1.3	1.7E-01
ENSMUST00000117003	ENSMUSG00000080653	2	microRNA 669e	MI0006300	Mir669e	1.1	2.1E-01	-1.4	2.1E-01	-2.2	2.4E-02	0.3	7.9E-01
ENSMUST00000117005	ENSMUSG00000080655	10	predicted gene, 24482		Gm24482	1.3	2.6E-01	1.6	2.2E-01	1.0	3.5E-01	0.7	6.0E-01
ENSMUST00000117009	ENSMUSG00000080659	19	predicted gene, 24484		Gm24484	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000117012	ENSMUSG00000080662	18	microRNA 1b	MI0006283	Mir1b	0.6	5.5E-01	-0.2	8.7E-01	0.2	8.7E-01	0.9	4.1E-01
ENSMUST00000117013	ENSMUSG00000080663	4	predicted gene, 25002		Gm25002	1.6	1.9E-01	2.3	1.1E-01	1.1	2.8E-01	0.4	8.1E-01
ENSMUST00000117015	ENSMUSG00000080665	8	microRNA 1199	MI0006307	Mir1199	1.5	7.2E-02	0.2	8.8E-01	-2.9	3.7E-03	-1.6	1.7E-01
ENSMUST00000117016	ENSMUSG00000080666	13	predicted gene, 25000		Gm25000	3.9	1.1E-02	0.4	7.8E-01	-1.2	3.6E-01	2.2	1.6E-01
ENSMUST00000117018	ENSMUSG00000080668	13	predicted gene, 24999		Gm24999	1.6	1.3E-01	-0.2	8.4E-01	-0.4	7.3E-01	1.5	2.0E-01
ENSMUST00000117019	ENSMUSG00000080669	16	microRNA 1224	MI0004118	Mir1224	1.2	1.7E-01	2.5	3.0E-02	0.9	2.5E-01	-0.5	6.6E-01
ENSMUST00000117021	ENSMUSG00000080671	18	predicted gene, 23335		Gm23335	1.9	2.2E-02	1.5	1.3E-01	0.1	8.4E-01	0.5	5.6E-01
ENSMUST00000117026	ENSMUSG00000080676	3	predicted gene, 25347		Gm25347	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000117028	ENSMUSG00000080678	19	predicted gene, 23334		Gm23334	2.7	1.6E-02	1.1	4.5E-01	-0.6	5.9E-01	1.1	4.0E-01
ENSMUST00000117030	ENSMUSG00000080680	12	predicted gene, 23989		Gm23989	1.7	4.6E-02	0.8	4.5E-01	-0.8	3.5E-01	0.1	8.9E-01
ENSMUST00000117031	ENSMUSG00000080681	11	predicted gene, 23990		Gm23990	0.2	8.4E-01	0.9	4.7E-01	1.5	1.5E-01	0.8	4.6E-01
ENSMUST00000117032	ENSMUSG00000096779	1	predicted gene, 22112		Gm22112	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000122509	ENSMUSG00000084458	15	microRNA 1907	MI0008325	Mir1907	0.0	9.9E-01	1.1	4.2E-01	0.2	8.1E-01	-0.8	4.9E-01
ENSMUST00000122565	ENSMUSG00000084514	18	microRNA 1893	MI0008327	Mir1893	-1.8	1.0E-01	-1.4	2.9E-01	1.0	3.6E-01	0.7	5.7E-01
ENSMUST00000122567	ENSMUSG00000084516	2	microRNA 1902	MI0008313	Mir1902	0.8	4.8E-01	1.6	3.3E-01	0.3	8.4E-01	-0.5	7.4E-01
ENSMUST00000122574	ENSMUSG00000084523	8	microRNA 1903	MI0008317	Mir1903	1.2	2.0E-01	1.6	2.1E-01	-0.1	8.9E-01	-0.5	6.6E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000122615	ENSMUSG00000084564	3	microRNA 1895	MI0008316	Mir1895	2.2	1.4E-02	1.1	3.2E-01	-0.7	4.2E-01	0.5	6.2E-01
ENSMUST00000122616	ENSMUSG00000084565	18	microRNA 1901	MI0008328	Mir1901	2.3	1.8E-03	1.6	6.3E-02	-0.1	8.7E-01	0.7	4.1E-01
ENSMUST00000122643	ENSMUSG00000084592	15	microRNA 1898	MI0008324	Mir1898	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000122651	ENSMUSG00000084600	17	predicted gene, 22201		Gm22201	0.8	2.7E-01	1.3	1.4E-01	0.9	2.0E-01	0.4	6.3E-01
ENSMUST00000122709	ENSMUSG00000084658	10	predicted gene, 22721		Gm22721	1.9	3.5E-02	1.4	1.8E-01	0.0	9.7E-01	0.5	6.5E-01
ENSMUST00000122779	ENSMUSG00000084728	3	microRNA 1905	MI0008315	Mir1905	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01
ENSMUST00000122802	ENSMUSG00000084751	17	microRNA 1894	MI0008326	Mir1894	0.8	3.3E-01	-0.2	8.4E-01	-0.5	5.7E-01	0.5	6.0E-01
ENSMUST00000157195	ENSMUSG00000087820	1	microRNA 1928	MI0009917	Mir1928	3.7	4.4E-07	2.7	5.3E-04	0.0	9.6E-01	1.0	1.1E-01
ENSMUST00000157219	ENSMUSG00000087844	4	microRNA 1958	MI0009955	Mir1958	1.7	1.3E-01	1.9	1.7E-01	1.7	1.2E-01	1.4	2.9E-01
ENSMUST00000157270	ENSMUSG00000087895	10	predicted gene, 25281		Gm25281	1.3	1.1E-01	2.2	4.5E-02	0.0	9.8E-01	-1.0	3.7E-01
ENSMUST00000157318	ENSMUSG00000087943	4	predicted gene, 24245		Gm24245	4.3	3.8E-03	2.9	7.8E-02	-1.1	3.8E-01	0.4	7.7E-01
ENSMUST00000157325	ENSMUSG00000087950	18	microRNA 1948	MI0009939	Mir1948	0.4	5.5E-01	2.7	2.8E-03	1.0	1.1E-01	-1.2	1.5E-01
ENSMUST00000157368	ENSMUSG00000087993	10	microRNA 1982	MI0009993	Mir1982	-2.8	7.5E-04	-1.3	2.2E-01	1.3	8.5E-02	-0.3	7.9E-01
ENSMUST00000157390	ENSMUSG00000088015	11	microRNA 1932	MI0009921	Mir1932	0.2	8.3E-01	-1.1	3.0E-01	0.6	4.9E-01	1.8	8.1E-02
ENSMUST00000157429	ENSMUSG00000088054	8	microRNA 1968	MI0009965	Mir1968	1.0	3.5E-01	1.6	1.7E-01	-2.9	5.3E-03	-3.4	5.4E-03
ENSMUST00000157488	ENSMUSG00000088113	5	microRNA 1960	MI0009957	Mir1960	1.5	7.8E-02	1.2	2.5E-01	-0.1	9.0E-01	0.2	8.1E-01
ENSMUST00000157491	ENSMUSG00000088116	7	predicted gene, 24063		Gm24063	0.3	7.1E-01	2.7	2.6E-02	2.7	2.4E-03	0.4	7.5E-01
ENSMUST00000157516	ENSMUSG00000088141	7	microRNA 1962	MI0009959	Mir1962	-0.3	7.2E-01	1.2	2.2E-01	0.9	2.2E-01	-0.6	5.5E-01
ENSMUST00000157523	ENSMUSG00000088148	13	microRNA 1983	MI0009990	Mir1983	-1.0	6.1E-02	-1.7	1.6E-02	0.6	2.5E-01	1.3	6.5E-02
ENSMUST00000157579	ENSMUSG00000088204	9	predicted gene, 23391		Gm23391	1.7	2.1E-02	1.0	2.5E-01	-0.1	8.6E-01	0.6	4.5E-01
ENSMUST00000157621	ENSMUSG00000088246	1	predicted gene, 25911		Gm25911	4.0	2.4E-03	1.0	5.2E-01	-0.9	4.2E-01	2.1	1.5E-01
ENSMUST00000157623	ENSMUSG00000088248	8	microRNA 1969	MI0009966	Mir1969	1.0	2.7E-01	0.3	7.7E-01	-0.4	6.7E-01	0.2	8.2E-01
ENSMUST00000157729	ENSMUSG00000088354	7	predicted gene, 27592		Gm27592	1.7	3.5E-02	0.2	8.5E-01	0.5	5.1E-01	2.0	5.3E-02
ENSMUST00000157748	ENSMUSG00000088373	3	microRNA 1956	MI0009952	Mir1956	-1.4	1.0E-01	-1.1	3.0E-01	-0.1	8.5E-01	-0.4	7.4E-01
ENSMUST00000157789	ENSMUSG00000088414	8	microRNA 1967	MI0009964	Mir1967	1.7	2.8E-02	2.2	4.2E-02	-0.1	9.3E-01	-0.5	6.1E-01
ENSMUST00000157834	ENSMUSG00000088459	15	microRNA 1941	MI0009930	Mir1941	-0.1	8.7E-01	-1.7	9.8E-02	-0.6	4.3E-01	1.0	3.4E-01
ENSMUST00000157839	ENSMUSG00000088464	X	microRNA 1970	MI0009968	Mir1970	1.2	2.5E-01	0.1	9.1E-01	-0.3	7.5E-01	0.7	5.3E-01
ENSMUST00000157853	ENSMUSG00000088478	9	microRNA 1946b	MI0009967	Mir1946b	0.6	5.0E-01	2.1	6.7E-02	1.6	4.7E-02	0.1	9.1E-01
ENSMUST00000157866	ENSMUSG00000088491	2	microRNA 1953	MI0009948	Mir1953	0.1	9.5E-01	-1.7	1.1E-01	-0.2	8.1E-01	1.5	1.3E-01
ENSMUST00000157919	ENSMUSG00000088544	16	microRNA 1945	MI0009934	Mir1945	0.5	5.8E-01	0.9	4.2E-01	0.3	7.3E-01	-0.2	8.9E-01
ENSMUST00000157927	ENSMUSG00000088552	4	microRNA 1957a	MI0009954	Mir1957a	0.3	7.6E-01	0.7	5.6E-01	0.2	8.6E-01	-0.2	8.3E-01
ENSMUST00000157934	ENSMUSG00000088559	1	microRNA 1981	MI0009992	Mir1981	0.3	7.1E-01	0.1	8.5E-01	0.0	1.0E+00	0.1	8.9E-01
ENSMUST00000157981	ENSMUSG00000088606	2	microRNA 1951	MI0009946	Mir1951	2.0	7.8E-03	0.6	5.2E-01	-0.9	2.4E-01	0.5	5.7E-01
ENSMUST00000157984	ENSMUSG00000088609	13	predicted gene, 24187		Gm24187	2.4	2.0E-02	2.3	8.7E-02	-0.3	6.9E-01	-0.3	8.2E-01
ENSMUST00000158014	ENSMUSG00000088639	2	microRNA 1955	MI0009950	Mir1955	-0.1	8.7E-01	-0.4	6.5E-01	0.8	2.3E-01	1.1	2.7E-01
ENSMUST00000158016	ENSMUSG00000088641	8	predicted gene, 26483		Gm26483	2.2	7.6E-03	4.0	4.4E-04	1.3	1.3E-01	-0.5	5.8E-01
ENSMUST00000158117	ENSMUSG00000088742	5	predicted gene, 23222		Gm23222	1.2	1.3E-01	1.6	9.0E-02	0.9	2.3E-01	0.5	5.8E-01
ENSMUST00000158127	ENSMUSG00000088752	11	microRNA 1934	MI0009923	Mir1934	-1.7	8.2E-03	-2.1	6.5E-03	-0.6	2.3E-01	-0.2	8.1E-01
ENSMUST00000158158	ENSMUSG00000088783	5	predicted gene, 25374		Gm25374	3.0	2.8E-03	1.9	1.1E-01	-1.3	1.5E-01	-0.2	8.3E-01
ENSMUST00000158184	ENSMUSG00000088809	4	predicted gene, 24078		Gm24078	1.4	1.8E-01	0.1	9.1E-01	-0.1	9.5E-01	1.2	3.0E-01
ENSMUST00000158208	ENSMUSG00000088833	2	predicted gene, 23542		Gm23542	2.6	9.8E-04	1.5	7.2E-02	-0.1	8.7E-01	1.0	2.3E-01
ENSMUST00000158235	ENSMUSG00000088860	16	microRNA 1947	MI0009937	Mir1947	-0.2	8.1E-01	0.0	9.8E-01	0.6	4.1E-01	0.4	6.8E-01
ENSMUST00000158247	ENSMUSG00000088872	12	predicted gene, 25865		Gm25865	3.2	1.0E-02	0.8	5.9E-01	-1.4	2.3E-01	1.0	4.8E-01
ENSMUST00000158276	ENSMUSG00000088901	15	microRNA 1943	MI0009932	Mir1943	1.0	1.4E-01	2.0	1.8E-02	1.1	1.0E-01	0.1	8.8E-01
ENSMUST00000158348	ENSMUSG00000088973	1	predicted gene, 23762		Gm23762	3.3	8.2E-04	0.1	9.0E-01	-1.7	6.0E-02	1.5	1.5E-01
ENSMUST00000158355	ENSMUSG00000088980	2	microRNA 669m-2	MI0009944	Mir669m-2	0.0	9.8E-01	2.2	3.0E-02	2.0	8.4E-03	-0.2	8.4E-01
ENSMUST00000158360	ENSMUSG00000088985	16	microRNA 1946a	MI0009936	Mir1946a	-0.1	8.6E-01	-1.6	1.4E-01	-1.8	5.2E-02	-0.4	7.0E-01
ENSMUST00000158361	ENSMUSG00000088986	9	predicted gene, 25603		Gm25603	-1.2	2.2E-01	-0.6	6.8E-01	-0.6	5.9E-01	-1.2	3.4E-01
ENSMUST00000158463	ENSMUSG00000089088	1	predicted gene, 24001		Gm24001	2.3	3.1E-03	1.4	1.1E-01	0.0	9.5E-01	0.9	3.0E-01
ENSMUST00000158509	ENSMUSG00000089134	6	predicted gene, 24767		Gm24767	1.5	4.7E-02	1.0	3.0E-01	-0.1	9.0E-01	0.5	5.7E-01
ENSMUST00000158514	ENSMUSG00000089139	7	microRNA 1964	MI0009961	Mir1964	-1.5	5.3E-02	-1.0	2.4E-01	-0.3	6.1E-01	-0.8	3.2E-01
ENSMUST00000158526	ENSMUSG00000089151	19	microRNA 1950	MI0009941	Mir1950	0.6	5.2E-01	-0.3	7.8E-01	-0.1	8.8E-01	0.8	4.9E-01
ENSMUST00000158562	ENSMUSG00000089187	14	predicted gene, 22949		Gm22949	2.2	3.1E-02	0.6	6.6E-01	-1.4	1.6E-01	0.2	8.5E-01
ENSMUST00000158579	ENSMUSG00000089204	1	microRNA 1927	MI0009914	Mir1927	0.5	5.8E-01	-0.9	3.7E-01	0.7	3.2E-01	2.1	5.2E-02
ENSMUST00000158588	ENSMUSG00000089213	8	predicted gene, 23388		Gm23388	-3.1	1.4E-02	-1.9	1.8E-01	-1.3	2.0E-01	-2.5	9.2E-02
ENSMUST00000158589	ENSMUSG00000089214	10	microRNA 1931	MI0009920	Mir1931	2.2	2.9E-03	1.6	5.7E-02	-0.1	8.4E-01	0.4	6.2E-01
ENSMUST00000158594	ENSMUSG00000089219	7	microRNA 1963	MI0009960	Mir1963	2.2	2.2E-03	1.7	4.2E-02	-0.1	9.3E-01	0.4	6.0E-01
ENSMUST00000158619	ENSMUSG00000089244	5	predicted gene, 24054		Gm24054	2.3	2.3E-03	1.8	3.5E-02	0.0	9.7E-01	0.6	5.0E-01
ENSMUST00000158620	ENSMUSG00000089245	1	predicted gene, 24053		Gm24053	2.4	3.5E-03	2.5	1.9E-02	-0.1	8.6E-01	-0.2	8.5E-01
ENSMUST00000158635	ENSMUSG00000089260	10	microRNA 1929	MI0009918	Mir1929	-2.1	1.3E-02	-1.6	1.5E-01	0.3	7.1E-01	-0.3	7.9E-01
ENSMUST00000158669	ENSMUSG00000089294	4	microRNA 2139	MI0010752	Mir2139	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000158698	ENSMUSG00000089323	4	predicted gene, 25978		Gm25978	2.7	5.2E-04	1.9	2.7E-02	-0.1	9.1E-01	0.7	3.9E-01
ENSMUST00000158699	ENSMUSG00000089324	12	microRNA 1936	MI0009925	Mir1936	-0.1	8.8E-01	-1.7	1.4E-01	0.0	9.9E-01	1.6	1.8E-01
ENSMUST00000158732	ENSMUSG00000089357	X	microRNA 2137	MI0010750	Mir2137	6.3	1.4E-07	4.5	3.2E-04	-0.2	8.1E-01	1.6	1.4E-01
ENSMUST00000158746	ENSMUSG00000089371	12	microRNA 1938	MI0009927	Mir1938	-0.3	7.7E-01	1.5	2.7E-01	1.5	1.4E-01	-0.2	8.5E-01
ENSMUST00000158799	ENSMUSG00000089424	10	microRNA 1930	MI0009919	Mir1930	0.5	6.0E-01	1.0	3.7E-01	0.6	4.9E-01	0.0	9.9E-01
ENSMUST00000158807	ENSMUSG00000089432	8	microRNA 1966	MI0009963	Mir1966	0.0	1.0E+00	-2.2	2.8E-02	-1.7	4.2E-02	0.5	5.9E-01
ENSMUST00000158842	ENSMUSG00000089467	7	predicted gene, 23700		Gm23700	1.8	2.7E-02	-0.3	7.5E-01	-1.0	1.9E-01	1.1	2.3E-01
ENSMUST00000158930	ENSMUSG00000089555	11	microRNA 1933	MI0009922	Mir1933	0.3	7.2E-01	-0.2	7.8E-01	-0.1	8.3E-01	0.4	6.7E-01
ENSMUST00000158945	ENSMUSG00000089570	2	microRNA 669m-1	MI0009943	Mir669m-1	0.0	9.8E-01	2.2	3.0E-02	2.0	8.4E-03	-0.2	8.4E-01
ENSMUST00000174892	ENSMUSG00000092633	1	microRNA 3962	MI0016967	Mir3962	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000174897	ENSMUSG00000092638	18	microRNA 5112	MI0018021	Mir5112	1.4	5.8E-02	2.4	1.6E-02	0.7	2.7E-01	-0.3	7.3E-01
ENSMUST00000174898	ENSMUSG00000092639	15	microRNA 3964	MI0016970	Mir3964	0.0	9.8E-01	-2.3	4.0E-02	-0.6	3.8E-01	1.7	1.3E-01
ENSMUST00000174899	ENSMUSG00000095282	1	predicted gene, 22548		Gm22548	0.5	4.6E-01	0.9	2.5E-01	-0.2	7.5E-01	-0.6	4.2E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000174906	ENSMUSG00000092647	12	predicted gene, 22234		Gm22234	4.9	1.9E-04	2.3	1.1E-01	-3.0	1.3E-02	-0.3	8.3E-01
ENSMUST00000174907	ENSMUSG00000092648	13	predicted gene, 23566		Gm23566	0.1	9.6E-01	1.8	1.5E-01	1.9	6.3E-02	0.1	9.1E-01
ENSMUST00000174909	ENSMUSG00000092650	13	predicted gene, 25241		Gm25241	2.0	3.2E-03	1.9	2.1E-02	-0.1	9.0E-01	0.0	9.7E-01
ENSMUST00000174912	ENSMUSG00000092653	12	predicted gene, 25243		Gm25243	2.1	1.6E-02	1.7	1.1E-01	-0.4	6.2E-01	0.0	9.7E-01
ENSMUST00000174914	ENSMUSG00000092655	19	predicted gene, 25238		Gm25238	2.2	1.7E-02	-0.8	4.3E-01	-0.9	2.5E-01	2.0	4.6E-02
ENSMUST00000174915	ENSMUSG00000092656	8	predicted gene, 25239		Gm25239	1.5	4.1E-02	0.5	6.1E-01	-0.6	4.2E-01	0.4	6.7E-01
ENSMUST00000174916	ENSMUSG00000092657	1	predicted gene, 25240		Gm25240	-1.2	3.7E-01	0.4	8.1E-01	1.3	2.7E-01	-0.2	8.8E-01
ENSMUST00000174919	ENSMUSG00000092660	2	predicted gene, 22403		Gm22403	2.4	2.4E-03	1.6	7.3E-02	-0.1	8.9E-01	0.8	3.7E-01
ENSMUST00000174920	ENSMUSG00000092661	4	predicted gene, 22402		Gm22402	3.0	7.4E-04	1.5	8.7E-02	-0.1	9.0E-01	1.4	1.1E-01
ENSMUST00000174923	ENSMUSG00000092664	14	predicted gene, 22406		Gm22406	2.1	4.2E-02	0.6	6.0E-01	-0.6	5.5E-01	0.9	4.2E-01
ENSMUST00000174927	ENSMUSG00000092668	14	predicted gene, 22401		Gm22401	-1.3	1.1E-01	-0.2	8.9E-01	0.2	8.3E-01	-1.0	3.6E-01
ENSMUST00000174930	ENSMUSG00000092671	8	predicted gene, 24103		Gm24103	1.2	1.6E-01	2.0	5.6E-02	0.5	5.6E-01	-0.4	7.1E-01
ENSMUST00000174934	ENSMUSG00000092675	4	predicted gene, 25262		Gm25262	1.9	1.0E-02	3.0	7.4E-03	0.1	9.0E-01	-1.0	3.4E-01
ENSMUST00000174936	ENSMUSG00000092677	4	microRNA 5106	MI0018014	Mir5106	3.2	1.0E-02	1.4	3.1E-01	-0.8	4.8E-01	1.0	4.8E-01
ENSMUST00000174938	ENSMUSG00000092679	2	microRNA 5129	MI0018041	Mir5129	0.2	8.3E-01	-1.6	1.4E-01	-1.4	5.4E-02	0.4	7.0E-01
ENSMUST00000174942	ENSMUSG00000092683	12	predicted gene, 25747		Gm25747	2.0	3.2E-03	3.5	9.5E-04	-0.1	9.1E-01	-1.5	1.0E-01
ENSMUST00000174944	ENSMUSG00000092685	8	predicted gene, 26241		Gm26241	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000174945	ENSMUSG00000092686	10	predicted gene, 25745		Gm25745	0.3	7.9E-01	-0.9	5.0E-01	0.3	7.7E-01	1.5	2.6E-01
ENSMUST00000174949	ENSMUSG00000093388	7	predicted gene, 22655		Gm22655	0.8	2.6E-01	0.8	3.5E-01	-0.4	4.9E-01	-0.4	6.1E-01
ENSMUST00000174952	ENSMUSG00000092693	16	predicted gene, 22923		Gm22923	3.1	2.8E-03	1.6	1.3E-01	0.0	9.5E-01	1.6	1.4E-01
ENSMUST00000174954	ENSMUSG00000092695	3	microRNA 3092	MI0014085	Mir3092	-0.8	3.5E-01	-2.7	1.3E-02	-0.9	2.1E-01	1.0	3.2E-01
ENSMUST00000174955	ENSMUSG00000092696	9	microRNA 5133	MI0018045	Mir5133	-0.6	4.8E-01	-2.3	6.6E-02	-1.4	1.3E-01	0.3	8.2E-01
ENSMUST00000174956	ENSMUSG00000092697	2	predicted gene, 22925		Gm22925	2.8	1.9E-03	1.1	1.9E-01	-0.1	8.6E-01	1.5	8.7E-02
ENSMUST00000174964	ENSMUSG00000092705	1	predicted gene, 24513		Gm24513	1.2	2.3E-01	-1.1	3.6E-01	-1.8	9.5E-02	0.5	6.5E-01
ENSMUST00000174965	ENSMUSG00000092706	17	predicted gene, 24510		Gm24510	2.9	1.1E-03	1.5	8.6E-02	0.0	9.5E-01	1.3	1.5E-01
ENSMUST00000174977	ENSMUSG00000092718	3	predicted gene, 22860		Gm22860	6.1	1.1E-05	4.9	4.7E-04	-3.4	5.1E-03	-2.1	4.8E-02
ENSMUST00000174978	ENSMUSG00000092719	2	predicted gene, 22859		Gm22859	3.1	1.3E-04	3.1	1.1E-03	0.2	7.3E-01	0.2	7.9E-01
ENSMUST00000174981	ENSMUSG00000094086	9	predicted gene, 23992		Gm23992	1.7	3.1E-01	1.5	4.9E-01	0.1	9.4E-01	0.4	8.6E-01
ENSMUST00000174982	ENSMUSG00000092723	4	predicted gene, 24804		Gm24804	-0.1	8.8E-01	-1.8	7.1E-02	-1.1	1.8E-01	0.7	4.8E-01
ENSMUST00000174983	ENSMUSG00000092724	4	predicted gene, 25677		Gm25677	1.2	9.1E-02	1.8	3.4E-02	0.8	1.9E-01	0.2	8.0E-01
ENSMUST00000174984	ENSMUSG00000092725	11	predicted gene, 25678		Gm25678	0.8	3.6E-01	0.6	5.8E-01	0.2	8.6E-01	0.3	7.2E-01
ENSMUST00000174986	ENSMUSG00000092727	11	microRNA 3062	MI0014024	Mir3062	1.9	1.3E-01	0.6	6.8E-01	-1.6	1.8E-01	-0.3	8.2E-01
ENSMUST00000174990	ENSMUSG00000092731	17	predicted gene, 24026		Gm24026	1.9	1.2E-01	0.7	6.2E-01	0.0	9.9E-01	1.2	3.4E-01
ENSMUST00000174993	ENSMUSG00000092734	11	microRNA 5100	MI0018008	Mir5100	3.4	6.2E-06	1.5	5.1E-02	0.1	9.2E-01	2.0	9.3E-03
ENSMUST00000174996	ENSMUSG00000092737	12	predicted gene, 24022		Gm24022	2.0	1.4E-02	1.3	2.4E-01	-0.8	3.0E-01	-0.2	8.7E-01
ENSMUST00000174997	ENSMUSG00000092738	12	microRNA 5135	MI0018047	Mir5135	-0.2	8.0E-01	0.2	8.2E-01	0.0	9.6E-01	-0.4	6.8E-01
ENSMUST00000175000	ENSMUSG00000092741	13	microRNA 3074-1	MI0014037	Mir3074-1	-1.3	1.0E-01	-1.0	2.8E-01	0.9	1.7E-01	0.7	4.7E-01
ENSMUST00000175001	ENSMUSG00000096480	3	predicted gene, 23976		Gm23976	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175004	ENSMUSG00000092745	4	microRNA 5122	MI0018031	Mir5122	-2.7	1.5E-02	-3.9	1.4E-03	0.2	8.0E-01	1.5	2.0E-01
ENSMUST00000175006	ENSMUSG00000092747	4	predicted gene, 22180		Gm22180	1.8	3.1E-02	1.5	1.4E-01	0.2	8.1E-01	0.5	5.7E-01
ENSMUST00000175007	ENSMUSG00000092748	12	predicted gene, 22175		Gm22175	2.1	8.8E-03	1.0	3.1E-01	-0.8	3.4E-01	0.3	7.3E-01
ENSMUST00000175011	ENSMUSG00000092752	X	microRNA 3473a	MI0014706	Mir3473a	0.0	9.7E-01	0.0	9.7E-01	1.0	2.2E-01	1.0	3.5E-01
ENSMUST00000175017	ENSMUSG00000092758	2	predicted gene, 25026		Gm25026	1.7	2.2E-01	0.6	7.3E-01	-0.9	5.0E-01	0.2	9.2E-01
ENSMUST00000175018	ENSMUSG00000092759	16	predicted gene, 25025		Gm25025	1.3	2.5E-01	-0.4	7.6E-01	-1.3	3.0E-01	0.4	7.5E-01
ENSMUST00000175019	ENSMUSG00000092760	6	predicted gene, 23365		Gm23365	0.3	6.9E-01	0.7	5.3E-01	-0.2	7.5E-01	-0.6	6.0E-01
ENSMUST00000175020	ENSMUSG00000092761	4	microRNA 5120	MI0018029	Mir5120	-0.5	5.3E-01	-2.4	3.5E-02	-1.4	1.5E-01	0.5	6.1E-01
ENSMUST00000175021	ENSMUSG00000092762	11	predicted gene, 27626		Gm27626	2.9	2.7E-02	0.0	1.0E+00	-1.2	2.8E-01	1.7	2.6E-01
ENSMUST00000175024	ENSMUSG00000092765	2	predicted gene, 23363	MI0030343	Gm23363	1.7	1.4E-02	1.3	1.2E-01	0.0	9.4E-01	0.4	6.2E-01
ENSMUST00000175029	ENSMUSG00000092770	9	microRNA let7a-2	MI0000557	Mirlet7a-2	-4.5	6.5E-07	-4.1	3.7E-05	0.6	2.8E-01	0.2	8.5E-01
ENSMUST00000175035	ENSMUSG00000092776	9	predicted gene, 26195		Gm26195	1.5	5.9E-02	2.3	1.6E-02	2.0	7.6E-03	1.3	1.6E-01
ENSMUST00000175036	ENSMUSG00000092777	X	predicted gene, 26194		Gm26194	2.1	8.4E-02	0.9	5.1E-01	0.0	9.7E-01	1.2	3.7E-01
ENSMUST00000175040	ENSMUSG00000092781	10	microRNA 3057	MI0014020	Mir3057	0.3	7.2E-01	1.1	2.5E-01	0.9	2.0E-01	0.1	8.8E-01
ENSMUST00000175041	ENSMUSG00000095878	4	predicted gene, 23045		Gm23045	0.9	2.8E-01	2.2	4.4E-02	1.1	2.0E-01	-0.2	8.2E-01
ENSMUST00000175043	ENSMUSG00000092784	14	microRNA 3077	MI0014040	Mir3077	-1.5	3.2E-02	-2.3	1.3E-02	-0.1	9.2E-01	0.7	3.6E-01
ENSMUST00000175046	ENSMUSG00000092787	X	microRNA 5116	MI0018025	Mir5116	-0.5	5.9E-01	-0.7	5.4E-01	0.0	9.9E-01	0.2	8.8E-01
ENSMUST00000175047	ENSMUSG00000094247	2	predicted gene, 23968		Gm23968	0.7	3.6E-01	1.4	9.8E-02	0.3	6.9E-01	-0.5	5.3E-01
ENSMUST00000175049	ENSMUSG00000092790	1	predicted gene, 22693		Gm22693	2.0	1.4E-02	2.0	4.2E-02	0.7	3.0E-01	0.8	3.7E-01
ENSMUST00000175050	ENSMUSG00000096635	2	predicted gene, 22174		Gm22174	-0.6	4.9E-01	-0.9	4.4E-01	-0.3	7.0E-01	0.0	9.7E-01
ENSMUST00000175051	ENSMUSG00000092792	18	predicted gene, 22694		Gm22694	3.5	8.6E-03	4.0	1.3E-02	1.1	2.8E-01	0.7	6.5E-01
ENSMUST00000175052	ENSMUSG00000092793	2	microRNA 466m	MI0014050	Mir466m	0.3	6.9E-01	0.4	7.1E-01	-0.4	6.4E-01	-0.5	6.2E-01
ENSMUST00000175053	ENSMUSG00000092794	X	microRNA 3110	MI0014107	Mir3110	1.2	2.8E-01	0.8	5.5E-01	-0.4	6.4E-01	0.0	1.0E+00
ENSMUST00000175054	ENSMUSG00000092795	4	predicted gene, 22690		Gm22690	0.8	4.5E-01	-1.6	2.0E-01	-1.1	2.9E-01	1.3	2.8E-01
ENSMUST00000175055	ENSMUSG00000092796	2	predicted gene, 22692		Gm22692	5.6	4.7E-02	1.5	6.7E-01	0.0	9.9E-01	4.1	2.2E-01
ENSMUST00000175058	ENSMUSG00000092799	17	predicted gene, 25927		Gm25927	0.2	8.4E-01	-0.2	8.2E-01	-4.1	3.4E-06	-3.7	2.3E-04
ENSMUST00000175060	ENSMUSG00000095278	2	predicted gene, 27634		Gm27634	-0.8	6.6E-01	2.7	2.8E-01	1.8	2.9E-01	-1.6	5.0E-01
ENSMUST00000175061	ENSMUSG00000092802	19	predicted gene, 26460		Gm26460	1.4	6.7E-02	2.8	6.0E-03	1.0	2.0E-01	-0.4	6.4E-01
ENSMUST00000175062	ENSMUSG00000094244	5	predicted gene, 23967		Gm23967	2.1	4.8E-02	1.8	1.5E-01	-0.2	8.2E-01	0.1	9.5E-01
ENSMUST00000175065	ENSMUSG00000092806	5	predicted gene, 26463		Gm26463	4.4	4.7E-06	5.2	6.5E-06	-0.6	4.9E-01	-1.4	8.1E-02
ENSMUST00000175066	ENSMUSG00000092807	2	microRNA 199b	MI0000714	Mir199b	1.1	2.5E-01	-1.8	1.4E-01	-5.3	4.9E-06	-2.4	5.2E-02
ENSMUST00000175070	ENSMUSG00000092811	2	predicted gene, 23636		Gm23636	0.4	6.4E-01	0.5	6.0E-01	0.5	5.1E-01	0.4	6.6E-01
ENSMUST00000175071	ENSMUSG00000092812	4	predicted gene, 23634		Gm23634	-1.0	1.7E-01	-1.5	9.1E-02	0.1	9.4E-01	0.6	4.5E-01
ENSMUST00000175072	ENSMUSG00000092813	19	microRNA 3086	MI0014049	Mir3086	-0.4	5.8E-01	-0.4	6.7E-01	0.2	8.2E-01	0.2	8.2E-01
ENSMUST00000175073	ENSMUSG00000092814	2	predicted gene, 23638		Gm23638	6.7	8.2E-04	2.6	1.4E-01	-4.3	1.3E-02	-0.1	9.3E-01
ENSMUST00000175074	ENSMUSG00000092815	7	microRNA 3099	MI0004485	Mir3099	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000175075	ENSMUSG00000092816	18	predicted gene, 23637		Gm23637	1.6	1.9E-01	2.1	1.4E-01	0.5	6.2E-01	0.0	9.9E-01
ENSMUST00000175076	ENSMUSG00000093886	4	predicted gene, 23158		Gm23158	1.2	4.5E-01	4.2	6.2E-02	2.7	1.3E-01	-0.3	8.8E-01
ENSMUST00000175077	ENSMUSG00000092818	8	predicted gene, 27361		Gm27361	1.8	1.3E-02	1.6	6.1E-02	-0.2	7.8E-01	0.0	9.7E-01
ENSMUST00000175080	ENSMUSG00000092821	8	predicted gene, 23163		Gm23163	2.2	2.4E-02	1.8	1.1E-01	0.1	9.2E-01	0.5	6.6E-01
ENSMUST00000175081	ENSMUSG00000092822	4	predicted gene, 23162		Gm23162	3.0	3.8E-03	2.8	1.4E-02	0.6	4.5E-01	0.7	5.3E-01
ENSMUST00000175084	ENSMUSG00000092825	2	predicted gene, 23164		Gm23164	2.5	9.6E-03	0.7	5.3E-01	-1.8	5.5E-02	0.0	9.8E-01
ENSMUST00000175086	ENSMUSG00000092827	2	microRNA 3091	MI0014084	Mir3091	-0.5	5.2E-01	-2.1	7.5E-02	-1.7	4.3E-02	-0.2	8.8E-01
ENSMUST00000175088	ENSMUSG00000092829	4	predicted gene, 23159		Gm23159	1.9	1.5E-02	1.9	3.2E-02	-0.3	6.3E-01	-0.4	6.4E-01
ENSMUST00000175089	ENSMUSG00000092830	3	microRNA 3963	MI0016968	Mir3963	-0.3	8.4E-01	-1.3	5.1E-01	-2.1	1.4E-01	-1.1	5.3E-01
ENSMUST00000175091	ENSMUSG00000092832	2	microRNA 3088	MI0014081	Mir3088	-0.7	3.7E-01	-1.8	7.5E-02	-0.6	4.8E-01	0.5	5.7E-01
ENSMUST00000175093	ENSMUSG00000092834	14	predicted gene, 24818		Gm24818	1.0	1.4E-01	0.5	5.4E-01	-0.2	8.0E-01	0.4	6.5E-01
ENSMUST00000175097	ENSMUSG00000092838	X	predicted gene, 24824		Gm24824	1.2	1.2E-01	0.2	8.5E-01	0.2	7.5E-01	1.3	2.1E-01
ENSMUST00000175099	ENSMUSG00000092840	13	predicted gene, 24331		Gm24331	1.5	1.3E-01	-0.6	5.9E-01	-0.4	6.8E-01	1.7	1.1E-01
ENSMUST00000175100	ENSMUSG00000092841	10	predicted gene, 24330		Gm24330	1.4	9.8E-02	1.6	1.3E-01	-0.1	9.5E-01	-0.2	8.4E-01
ENSMUST00000175104	ENSMUSG00000092845	2	predicted gene, 24328		Gm24328	2.3	5.7E-03	1.2	2.3E-01	-0.8	2.9E-01	0.2	8.1E-01
ENSMUST00000175106	ENSMUSG00000092847	7	microRNA 344d-1	MI0004524	Mir344d-1	2.2	4.7E-03	2.6	1.9E-02	-2.4	6.3E-03	-2.8	7.2E-03
ENSMUST00000175108	ENSMUSG00000092849	2	predicted gene, 24327		Gm24327	0.1	9.5E-01	0.3	7.7E-01	-1.1	2.2E-01	-1.3	2.3E-01
ENSMUST00000175110	ENSMUSG00000092851	2	predicted gene, 25960		Gm25960	1.3	3.2E-02	1.4	6.6E-02	0.3	5.8E-01	0.2	7.3E-01
ENSMUST00000175111	ENSMUSG00000092852	1	microRNA 5103	MI0018011	Mir5103	0.2	8.2E-01	0.2	8.6E-01	1.7	2.8E-02	1.7	1.2E-01
ENSMUST00000175114	ENSMUSG00000092855	15	predicted gene, 25958		Gm25958	1.8	1.4E-02	1.5	8.1E-02	-0.1	8.9E-01	0.2	8.2E-01
ENSMUST00000175115	ENSMUSG00000092856	7	predicted gene, 25956		Gm25956	-0.8	4.4E-01	0.1	9.1E-01	0.2	7.9E-01	-0.7	5.7E-01
ENSMUST00000175120	ENSMUSG00000096350	4	predicted gene, 25707		Gm25707	-0.8	4.5E-01	-2.7	6.5E-02	-0.8	4.0E-01	1.1	4.5E-01
ENSMUST00000175121	ENSMUSG00000092862	4	microRNA 3094	MI0014087	Mir3094	-0.5	6.3E-01	0.9	5.5E-01	0.3	7.8E-01	-1.0	4.3E-01
ENSMUST00000175126	ENSMUSG00000092867	10	microRNA 3058	MI0004418	Mir3058	-0.1	8.8E-01	0.0	9.9E-01	0.4	5.6E-01	0.3	7.8E-01
ENSMUST00000175127	ENSMUSG00000092868	15	microRNA 5113	MI0018022	Mir5113	-0.9	1.6E-01	-1.8	3.9E-02	0.4	5.1E-01	1.2	1.6E-01
ENSMUST00000175129	ENSMUSG00000092870	11	microRNA 3061	MI0014023	Mir3061	0.0	1.0E+00	-0.4	6.9E-01	0.3	6.6E-01	0.7	4.6E-01
ENSMUST00000175136	ENSMUSG00000095986	6	predicted gene, 23053		Gm23053	1.8	3.1E-02	1.5	1.4E-01	0.2	8.1E-01	0.5	5.7E-01
ENSMUST00000175138	ENSMUSG00000092879	X	predicted gene, 22650	MI0030344	Gm22650	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000175139	ENSMUSG00000092880	4	microRNA 3471-1	MI0014699	Mir3471-1	2.9	6.0E-03	1.8	1.4E-01	-0.1	9.0E-01	1.0	4.1E-01
ENSMUST00000175144	ENSMUSG00000092885	11	predicted gene, 22123		Gm22123	0.6	5.0E-01	0.4	7.4E-01	0.9	3.1E-01	1.2	2.4E-01
ENSMUST00000175148	ENSMUSG00000092889	11	predicted gene, 22121		Gm22121	2.2	5.4E-03	0.6	5.6E-01	-0.9	2.7E-01	0.8	3.6E-01
ENSMUST00000175150	ENSMUSG00000092891	3	predicted gene, 23810		Gm23810	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000175153	ENSMUSG00000092894	11	predicted gene, 23813		Gm23813	2.2	6.8E-03	1.9	3.7E-02	-0.7	3.1E-01	-0.4	5.9E-01
ENSMUST00000175156	ENSMUSG00000092897	8	predicted gene, 23812		Gm23812	1.0	2.1E-01	0.3	7.6E-01	-0.2	8.6E-01	0.6	5.5E-01
ENSMUST00000175160	ENSMUSG00000092901	14	microRNA 5130	MI0018042	Mir5130	-2.4	8.2E-03	-3.5	1.3E-03	-0.5	4.8E-01	0.6	5.0E-01
ENSMUST00000175165	ENSMUSG00000092906	1	predicted gene, 25736		Gm25736	3.7	4.8E-02	1.0	6.2E-01	0.1	9.7E-01	2.8	1.8E-01
ENSMUST00000175166	ENSMUSG00000092907	X	microRNA 5132	MI0018044	Mir5132	0.2	8.6E-01	-0.6	6.3E-01	-0.5	5.8E-01	0.3	8.1E-01
ENSMUST00000175168	ENSMUSG00000092909	4	predicted gene, 25732		Gm25732	0.5	5.5E-01	0.3	7.2E-01	-0.1	9.2E-01	0.1	9.5E-01
ENSMUST00000175172	ENSMUSG00000092913	17	predicted gene, 24085		Gm24085	1.0	2.5E-01	-0.8	5.3E-01	-2.1	4.5E-02	-0.3	7.8E-01
ENSMUST00000175174	ENSMUSG00000092915	9	predicted gene, 24083		Gm24083	-2.3	1.4E-04	-0.1	8.1E-01	1.8	4.2E-04	-0.3	5.7E-01
ENSMUST00000175175	ENSMUSG00000092916	5	predicted gene, 24082		Gm24082	1.4	6.1E-02	1.9	2.8E-02	0.7	2.5E-01	0.2	8.5E-01
ENSMUST00000175176	ENSMUSG00000092917	X	microRNA 3472	MI0014704	Mir3472	3.2	1.2E-02	0.6	7.0E-01	-0.9	4.4E-01	1.8	2.2E-01
ENSMUST00000175177	ENSMUSG00000092918	2	predicted gene, 24081		Gm24081	4.3	3.8E-02	5.2	4.3E-02	-0.6	7.5E-01	-1.5	4.8E-01
ENSMUST00000175178	ENSMUSG00000092919	15	predicted gene, 24080		Gm24080	2.2	2.9E-03	1.6	5.7E-02	-0.1	8.4E-01	0.4	6.2E-01
ENSMUST00000175181	ENSMUSG00000092922	12	microRNA 5101	MI0018009	Mir5101	-1.3	1.4E-01	-2.7	1.1E-02	-0.8	3.4E-01	0.6	5.0E-01
ENSMUST00000175182	ENSMUSG00000092923	2	predicted gene, 24561		Gm24561	2.2	1.5E-02	-1.2	2.9E-01	-2.9	4.7E-03	0.5	6.0E-01
ENSMUST00000175187	ENSMUSG00000092928	6	predicted gene, 24563		Gm24563	1.0	1.7E-01	2.0	2.2E-02	1.8	1.0E-02	0.8	3.5E-01
ENSMUST00000175190	ENSMUSG00000092931	12	predicted gene, 22904		Gm22904	0.7	4.3E-01	-1.7	1.4E-01	-1.2	1.2E-01	1.1	3.1E-01
ENSMUST00000175194	ENSMUSG00000092935	18	predicted gene, 22697		Gm22697	1.3	8.7E-02	0.7	4.4E-01	0.1	8.6E-01	0.7	3.9E-01
ENSMUST00000175195	ENSMUSG00000094528	6	predicted gene, 22914		Gm22914	3.7	3.9E-03	2.9	4.9E-02	-0.7	5.5E-01	0.1	9.7E-01
ENSMUST00000175207	ENSMUSG00000092948	1	predicted gene, 23393		Gm23393	2.3	8.4E-03	2.7	1.1E-02	0.1	9.2E-01	-0.3	7.4E-01
ENSMUST00000175208	ENSMUSG00000092949	12	predicted gene, 23394		Gm23394	0.6	5.3E-01	1.4	2.4E-01	1.3	1.5E-01	0.5	6.2E-01
ENSMUST00000175212	ENSMUSG00000092953	7	predicted gene, 26217		Gm26217	-0.8	5.3E-01	0.8	6.2E-01	1.3	2.9E-01	-0.3	8.5E-01
ENSMUST00000175215	ENSMUSG00000092956	6	predicted gene, 26220		Gm26220	1.4	1.5E-01	0.3	7.8E-01	-0.1	9.4E-01	1.0	3.6E-01
ENSMUST00000175216	ENSMUSG00000092957	16	predicted gene, 26219		Gm26219	1.0	3.5E-01	0.9	5.0E-01	0.5	6.2E-01	0.6	6.5E-01
ENSMUST00000175217	ENSMUSG00000092958	2	microRNA 5128	MI0018040	Mir5128	-0.4	6.7E-01	-1.7	1.5E-01	-0.3	7.1E-01	1.0	4.0E-01
ENSMUST00000175218	ENSMUSG00000096830	9	predicted gene, 26231		Gm26231	1.0	3.0E-01	0.3	7.8E-01	-0.1	9.0E-01	0.5	6.2E-01
ENSMUST00000175222	ENSMUSG00000092963	9	predicted gene, 22238		Gm22238	1.7	1.9E-02	1.2	1.8E-01	-0.1	9.1E-01	0.5	5.6E-01
ENSMUST00000175223	ENSMUSG00000095323	6	microRNA 3470a	MI0014696	Mir3470a	2.9	9.6E-04	5.0	2.8E-05	0.9	2.8E-01	-1.2	1.7E-01
ENSMUST00000175225	ENSMUSG00000092966	19	predicted gene, 22240		Gm22240	-0.5	5.9E-01	-2.1	6.7E-02	-0.7	4.3E-01	0.9	4.0E-01
ENSMUST00000175230	ENSMUSG00000095871	4	predicted gene, 25931		Gm25931	1.3	5.9E-02	0.8	3.4E-01	-0.1	8.4E-01	0.4	6.2E-01
ENSMUST00000175232	ENSMUSG00000092973	18	predicted gene, 25071		Gm25071	0.3	6.8E-01	1.6	5.6E-02	1.9	6.2E-03	0.6	4.8E-01
ENSMUST00000175235	ENSMUSG00000096080	10	predicted gene, 24710		Gm24710	3.0	1.7E-03	4.2	4.4E-04	0.9	2.1E-01	-0.3	7.5E-01
ENSMUST00000175238	ENSMUSG00000092979	17	predicted gene, 25069		Gm25069	2.1	9.7E-03	1.7	8.2E-02	0.0	9.4E-01	0.4	6.3E-01
ENSMUST00000175240	ENSMUSG00000092981	17	microRNA 5125	MI0018036	Mir5125	0.9	3.5E-01	1.3	2.6E-01	1.2	1.9E-01	0.7	5.0E-01
ENSMUST00000175244	ENSMUSG00000092985	11	microRNA 378b	MI0016973	Mir378b	1.4	1.6E-01	-1.2	3.2E-01	-1.0	2.3E-01	1.5	2.1E-01
ENSMUST00000175249	ENSMUSG00000092990	3	microRNA 466q	MI0018032	Mir466q	0.6	4.9E-01	-0.2	8.3E-01	-0.3	7.7E-01	0.6	5.7E-01
ENSMUST00000175254	ENSMUSG00000092995	14	microRNA 16-1	MI0000565	Mir16-1	2.1	1.7E-05	1.7	1.4E-03	0.4	2.7E-01	0.9	6.1E-02
ENSMUST00000175257	ENSMUSG00000092998	12	microRNA 5099	MI0018007	Mir5099	-3.6	1.2E-04	-3.6	6.7E-04	-1.0	1.1E-01	-1.0	2.6E-01
ENSMUST00000175259	ENSMUSG00000093000	3	predicted gene, 24155		Gm24155	1.7	1.4E-02	1.8	3.8E-02	-0.1	9.1E-01	-0.2	8.0E-01
ENSMUST00000175262	ENSMUSG00000093003	1	microRNA 3473c	MI0018015	Mir3473c	2.6	5.0E-02	-0.4	7.8E-01	-1.8	1.7E-01	1.3	4.0E-01
ENSMUST00000175263	ENSMUSG00000093004	11	predicted gene, 24158		Gm24158	1.2	1.3E-01	0.8	4.5E-01	0.1	9.2E-01	0.6	5.3E-01
ENSMUST00000175265	ENSMUSG00000093006	11	predicted gene, 24157		Gm24157	-0.6	4.8E-01	0.0	9.9E-01	0.3	7.5E-01	-0.4	7.4E-01
ENSMUST00000175266	ENSMUSG00000093007	14	microRNA 15a	MI0000564	Mir15a	1.5	4.7E-03	0.3	6.0E-01	-0.5	2.8E-01	0.7	2.0E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000175269	ENSMUSG00000093010	13	predicted gene, 22460		Gm22460	3.5	5.5E-03	1.6	1.9E-01	-0.3	7.7E-01	1.6	2.2E-01
ENSMUST00000175270	ENSMUSG00000093011	9	microRNA 100	MI0000692	Mir100	3.9	6.8E-05	3.8	1.3E-04	-2.6	6.4E-04	-2.5	6.6E-03
ENSMUST00000175272	ENSMUSG00000093013	11	predicted gene, 22461		Gm22461	2.5	4.6E-02	2.7	7.8E-02	0.7	5.3E-01	0.6	7.0E-01
ENSMUST00000175273	ENSMUSG00000093014	X	predicted gene, 22464		Gm22464	0.1	9.2E-01	1.3	1.5E-01	-0.6	4.2E-01	-1.8	4.3E-02
ENSMUST00000175274	ENSMUSG00000093015	1	predicted gene, 22463		Gm22463	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175276	ENSMUSG00000093017	10	microRNA 5108	MI0018017	Mir5108	3.8	1.7E-04	3.3	7.1E-03	-1.3	1.3E-01	-0.7	5.2E-01
ENSMUST00000175280	ENSMUSG00000093021	15	predicted gene, 25303		Gm25303	1.3	2.0E-01	3.3	1.6E-02	1.4	1.9E-01	-0.6	6.1E-01
ENSMUST00000175281	ENSMUSG00000095289	3	predicted gene, 22547		Gm22547	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175285	ENSMUSG00000093026	18	predicted gene, 25301		Gm25301	-0.9	7.2E-02	-0.2	7.5E-01	0.1	7.8E-01	-0.6	2.9E-01
ENSMUST00000175288	ENSMUSG00000093029	5	predicted gene, 25306		Gm25306	2.3	5.2E-02	2.6	6.4E-02	-0.7	5.3E-01	-1.0	4.4E-01
ENSMUST00000175289	ENSMUSG00000093030	10	predicted gene, 23632		Gm23632	1.6	1.2E-02	2.0	1.0E-02	-0.2	7.5E-01	-0.6	4.2E-01
ENSMUST00000175291	ENSMUSG00000093032	7	predicted gene, 23631		Gm23631	0.4	6.5E-01	1.6	1.1E-01	1.8	2.5E-02	0.5	5.5E-01
ENSMUST00000175292	ENSMUSG00000093033	2	predicted gene, 23630		Gm23630	1.9	2.5E-02	1.4	1.3E-01	-0.1	8.9E-01	0.3	7.2E-01
ENSMUST00000175293	ENSMUSG00000093034	14	predicted gene, 23633		Gm23633	3.1	1.8E-03	0.7	4.8E-01	-1.0	2.5E-01	1.4	1.6E-01
ENSMUST00000175296	ENSMUSG00000093037	12	microRNA 3066	MI0014028	Mir3066	-1.1	3.4E-01	-0.5	7.1E-01	0.3	7.9E-01	-0.3	8.1E-01
ENSMUST00000175297	ENSMUSG00000094523	10	predicted gene, 22913		Gm22913	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175299	ENSMUSG00000093040	2	predicted gene, 26141		Gm26141	0.7	3.4E-01	2.0	3.1E-02	0.6	3.7E-01	-0.7	4.1E-01
ENSMUST00000175300	ENSMUSG00000093041	5	predicted gene, 26455		Gm26455	1.6	2.3E-02	1.1	1.8E-01	-0.1	8.7E-01	0.4	6.4E-01
ENSMUST00000175301	ENSMUSG00000093042	9	microRNA 3109	MI0014106	Mir3109	-2.7	8.2E-03	-3.7	3.4E-03	0.5	5.0E-01	1.5	2.0E-01
ENSMUST00000175305	ENSMUSG00000093046	16	microRNA 3081	MI0014044	Mir3081	1.1	1.1E-01	1.5	8.4E-02	0.9	1.9E-01	0.5	5.3E-01
ENSMUST00000175306	ENSMUSG00000095684	13	predicted gene, 23282		Gm23282	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175311	ENSMUSG00000093052	6	predicted gene, 24816		Gm24816	1.8	4.0E-02	2.5	2.7E-02	-0.1	8.5E-01	-0.8	4.3E-01
ENSMUST00000175313	ENSMUSG00000093054	3	predicted gene, 24811		Gm24811	2.0	1.1E-01	-0.2	8.6E-01	0.8	4.7E-01	3.1	2.6E-02
ENSMUST00000175317	ENSMUSG00000093058	15	predicted gene, 24810		Gm24810	-0.1	9.4E-01	0.7	7.3E-01	0.0	9.9E-01	-0.7	6.8E-01
ENSMUST00000175319	ENSMUSG00000093060	10	microRNA 5104	MI0018012	Mir5104	0.2	8.1E-01	-1.3	2.1E-01	0.3	6.6E-01	1.8	8.9E-02
ENSMUST00000175320	ENSMUSG00000093061	5	microRNA 5098	MI0018006	Mir5098	1.6	6.3E-02	1.4	2.6E-01	1.1	2.1E-01	1.4	2.0E-01
ENSMUST00000175324	ENSMUSG00000093065	4	predicted gene, 23154		Gm23154	0.2	7.6E-01	-0.3	7.4E-01	-0.7	3.0E-01	-0.1	9.2E-01
ENSMUST00000175326	ENSMUSG00000093067	9	predicted gene, 23156		Gm23156	1.1	1.1E-01	1.5	8.4E-02	0.9	1.9E-01	0.5	5.3E-01
ENSMUST00000175328	ENSMUSG00000094290	1	predicted gene, 27512		Gm27512	2.0	1.9E-03	2.9	4.1E-04	0.5	3.9E-01	-0.4	5.2E-01
ENSMUST00000175329	ENSMUSG00000093070	5	predicted gene, 25952		Gm25952	1.9	6.0E-02	2.6	2.5E-02	0.0	9.9E-01	-0.8	4.5E-01
ENSMUST00000175330	ENSMUSG00000093071	4	predicted gene, 25951		Gm25951	2.3	4.0E-03	1.7	7.0E-02	0.1	9.4E-01	0.7	4.3E-01
ENSMUST00000175331	ENSMUSG00000093072	13	predicted gene, 25950		Gm25950	0.5	6.5E-01	0.0	9.7E-01	0.0	1.0E+00	0.4	7.4E-01
ENSMUST00000175335	ENSMUSG00000093076	17	microRNA 3082	MI0014045	Mir3082	-0.1	8.9E-01	1.5	7.9E-02	1.0	1.0E-01	-0.6	4.9E-01
ENSMUST00000175339	ENSMUSG00000093080	11	microRNA 3060	MI0014022	Mir3060	-1.5	9.9E-02	-1.4	2.3E-01	0.5	4.5E-01	0.4	7.2E-01
ENSMUST00000175340	ENSMUSG00000093081	14	microRNA 3075	MI0014038	Mir3075	1.8	3.9E-02	-1.7	6.8E-02	-1.3	1.1E-01	2.3	1.7E-02
ENSMUST00000175341	ENSMUSG00000093082	5	predicted gene, 24322		Gm24322	2.0	3.6E-02	2.0	4.2E-02	0.9	2.5E-01	0.9	3.9E-01
ENSMUST00000175342	ENSMUSG00000093083	11	predicted gene, 24323		Gm24323	2.4	4.8E-03	4.9	1.1E-05	2.1	4.7E-03	-0.4	6.7E-01
ENSMUST00000175346	ENSMUSG00000093087	8	microRNA 3473d	MI0018033	Mir3473d	-2.1	7.3E-03	-2.8	3.5E-03	-0.2	6.9E-01	0.4	6.3E-01
ENSMUST00000175348	ENSMUSG00000093089	12	predicted gene, 24321	MI0001160	Gm24321	0.6	4.8E-01	2.8	7.2E-03	0.8	3.5E-01	-1.4	1.4E-01
ENSMUST00000175349	ENSMUSG00000093090	12	microRNA 3073a	MI0014036	Mir3073a	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000175350	ENSMUSG00000093091	2	microRNA 3089	MI0014082	Mir3089	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000175351	ENSMUSG00000093092	9	predicted gene, 22643		Gm22643	1.7	4.7E-02	1.6	1.4E-01	0.8	3.2E-01	0.9	3.7E-01
ENSMUST00000175355	ENSMUSG00000093096	11	microRNA 3968	MI0016977	Mir3968	0.0	1.0E+00	-0.6	5.4E-01	-0.1	9.4E-01	0.6	5.2E-01
ENSMUST00000175356	ENSMUSG00000093097	5	microRNA 3097	MI0014090	Mir3097	2.4	3.1E-03	0.6	5.4E-01	-1.5	6.6E-02	0.3	7.9E-01
ENSMUST00000175359	ENSMUSG00000093100	11	microRNA 3971	MI0016981	Mir3971	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000175361	ENSMUSG00000093102	X	microRNA 3475	MI0004220	Mir3475	0.6	4.6E-01	0.0	9.9E-01	-0.2	7.4E-01	0.3	7.1E-01
ENSMUST00000175364	ENSMUSG00000093105	6	predicted gene, 25535		Gm25535	2.3	3.8E-03	1.7	5.9E-02	-0.1	8.2E-01	0.4	6.7E-01
ENSMUST00000175373	ENSMUSG00000093114	12	predicted gene, 22696		Gm22696	1.6	1.5E-01	2.2	1.0E-01	0.3	7.6E-01	-0.4	7.8E-01
ENSMUST00000175374	ENSMUSG00000093115	2	predicted gene, 25972		Gm25972	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175375	ENSMUSG00000093116	13	predicted gene, 22698		Gm22698	1.6	2.3E-02	1.1	1.8E-01	-0.1	8.7E-01	0.4	6.4E-01
ENSMUST00000175378	ENSMUSG00000093119	9	predicted gene, 25640		Gm25640	2.1	3.1E-03	2.6	3.5E-03	0.6	4.1E-01	0.1	9.4E-01
ENSMUST00000175379	ENSMUSG00000093120	2	microRNA 3474	MI0014707	Mir3474	1.8	3.2E-02	-0.4	7.1E-01	-1.0	1.9E-01	1.1	2.2E-01
ENSMUST00000175383	ENSMUSG00000093124	8	predicted gene, 24366		Gm24366	2.5	9.5E-03	1.1	2.4E-01	0.0	9.5E-01	1.3	2.1E-01
ENSMUST00000175384	ENSMUSG00000093125	7	predicted gene, 24365		Gm24365	0.5	6.3E-01	2.1	7.7E-02	0.3	7.6E-01	-1.3	2.2E-01
ENSMUST00000175387	ENSMUSG00000093128	14	predicted gene, 24369		Gm24369	1.8	6.1E-02	1.5	1.8E-01	0.2	7.7E-01	0.6	6.0E-01
ENSMUST00000175392	ENSMUSG00000093133	11	predicted gene, 25994		Gm25994	0.1	9.1E-01	-0.3	7.8E-01	0.0	9.9E-01	0.4	6.9E-01
ENSMUST00000175393	ENSMUSG00000093134	16	predicted gene, 25996		Gm25996	3.4	3.3E-03	1.0	4.2E-01	-0.6	5.4E-01	1.9	1.1E-01
ENSMUST00000175397	ENSMUSG00000093138	2	predicted gene, 25998		Gm25998	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01
ENSMUST00000175399	ENSMUSG00000093140	8	microRNA 28b	MI0016979	Mir28b	2.0	7.8E-03	0.6	5.2E-01	-0.9	2.4E-01	0.5	5.7E-01
ENSMUST00000175407	ENSMUSG00000093148	6	predicted gene, 23375		Gm23375	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000175408	ENSMUSG00000093149	16	predicted gene, 23374		Gm23374	1.0	2.1E-01	0.3	7.6E-01	-0.2	8.6E-01	0.6	5.5E-01
ENSMUST00000175410	ENSMUSG00000094435	5	predicted gene, 23617		Gm23617	2.2	2.9E-03	1.6	5.7E-02	-0.1	8.4E-01	0.4	6.2E-01
ENSMUST00000175411	ENSMUSG00000093152	9	predicted gene, 25032		Gm25032	1.0	2.1E-01	0.3	7.6E-01	-0.2	8.6E-01	0.6	5.5E-01
ENSMUST00000175412	ENSMUSG00000093153	7	predicted gene, 25033		Gm25033	1.6	1.1E-01	0.5	7.0E-01	-0.7	4.7E-01	0.4	7.2E-01
ENSMUST00000175414	ENSMUSG00000093155	1	predicted gene, 25035		Gm25035	1.0	1.5E-01	2.7	5.1E-03	1.6	3.9E-02	-0.1	8.7E-01
ENSMUST00000175415	ENSMUSG00000093156	14	microRNA 3076	MI0014039	Mir3076	-3.3	1.1E-03	-4.0	1.2E-03	-0.1	8.6E-01	0.6	5.8E-01
ENSMUST00000175416	ENSMUSG00000093157	6	microRNA 3098	MI0014091	Mir3098	-1.1	2.6E-01	-3.8	5.3E-03	-0.2	8.4E-01	2.5	5.6E-02
ENSMUST00000175417	ENSMUSG00000093158	18	predicted gene, 25036		Gm25036	1.9	2.9E-02	-1.3	2.3E-01	-0.9	2.0E-01	2.2	4.3E-02
ENSMUST00000175418	ENSMUSG00000093159	5	predicted gene, 25037		Gm25037	1.4	2.3E-01	0.7	6.1E-01	-0.1	9.2E-01	0.6	6.5E-01
ENSMUST00000175419	ENSMUSG00000093160	2	predicted gene, 22773		Gm22773	4.6	1.2E-06	6.0	3.8E-07	-0.4	6.2E-01	-1.7	2.5E-02
ENSMUST00000175420	ENSMUSG00000093161	10	predicted gene, 22183		Gm22183	1.9	1.4E-02	0.8	3.9E-01	-0.9	2.8E-01	0.2	8.2E-01
ENSMUST00000175422	ENSMUSG00000093163	4	predicted gene, 22994		Gm22994	0.4	6.5E-01	4.5	5.7E-04	2.8	1.9E-03	-1.3	2.4E-01
ENSMUST00000175426	ENSMUSG00000093167	14	microRNA 5131	MI0018043	Mir5131	-1.4	9.7E-02	-1.9	1.2E-01	-0.5	5.0E-01	0.0	1.0E+00
ENSMUST00000175428	ENSMUSG00000093169	15	microRNA 3079	MI0014042	Mir3079	-0.5	6.1E-01	-1.0	3.4E-01	-0.8	3.1E-01	-0.2	8.5E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000175431	ENSMUSG00000093172	X	microRNA 3112	MI0014109	Mir3112	0.8	4.0E-01	-1.2	3.2E-01	-0.2	7.8E-01	1.7	1.5E-01
ENSMUST00000175432	ENSMUSG00000093173	12	predicted gene, 23872		Gm23872	-4.6	3.0E-01	-6.0	2.4E-01	-1.8	5.8E-01	-0.5	9.3E-01
ENSMUST00000175435	ENSMUSG00000093176	11	microRNA 5119	MI0018028	Mir5119	1.4	1.5E-01	0.1	9.3E-01	-1.5	1.3E-01	-0.2	8.4E-01
ENSMUST00000175439	ENSMUSG00000093180	4	predicted gene, 25690		Gm25690	3.8	1.9E-04	2.7	1.9E-02	-0.3	7.3E-01	0.8	4.5E-01
ENSMUST00000175443	ENSMUSG00000093184	11	predicted gene, 25693		Gm25693	1.3	1.9E-01	1.2	3.1E-01	0.3	7.4E-01	0.4	7.2E-01
ENSMUST00000175444	ENSMUSG00000093185	4	predicted gene, 25692		Gm25692	3.1	6.1E-04	1.5	8.0E-02	-0.1	8.6E-01	1.4	1.2E-01
ENSMUST00000175449	ENSMUSG00000093190	2	predicted gene, 22875		Gm22875	3.0	8.4E-03	5.8	2.6E-04	1.7	1.5E-01	-1.1	3.1E-01
ENSMUST00000175451	ENSMUSG00000093192	14	predicted gene, 22877		Gm22877	1.4	9.9E-02	2.8	1.4E-02	0.9	2.0E-01	-0.5	6.3E-01
ENSMUST00000175454	ENSMUSG00000094834	1	predicted gene, 25472		Gm25472	-0.4	7.5E-01	-0.4	7.7E-01	-0.3	7.9E-01	-0.3	8.6E-01
ENSMUST00000175458	ENSMUSG00000095292	7	microRNA 344d-3	MI0004227	Mir344d-3	2.0	1.2E-02	-0.1	9.2E-01	-1.6	6.5E-02	0.5	6.1E-01
ENSMUST00000175461	ENSMUSG00000093202	17	microRNA 3547	MI0022813	Mir3547	2.0	7.0E-03	0.9	3.7E-01	-0.7	3.4E-01	0.5	6.0E-01
ENSMUST00000175462	ENSMUSG00000093203	2	predicted gene, 22411		Gm22411	1.7	2.0E-01	0.7	6.9E-01	-1.4	3.3E-01	-0.5	7.8E-01
ENSMUST00000175465	ENSMUSG00000093206	X	predicted gene, 22413		Gm22413	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000175466	ENSMUSG00000093207	7	predicted gene, 22414		Gm22414	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175467	ENSMUSG00000093208	18	predicted gene, 27325		Gm27325	-0.3	6.8E-01	1.2	1.7E-01	-0.4	4.8E-01	-1.9	3.6E-02
ENSMUST00000175470	ENSMUSG00000093211	9	predicted gene, 25250		Gm25250	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000175471	ENSMUSG00000093212	7	predicted gene, 25249		Gm25249	3.5	2.7E-04	1.2	1.5E-01	-0.2	7.7E-01	2.1	2.9E-02
ENSMUST00000175473	ENSMUSG00000093214	12	predicted gene, 25248		Gm25248	1.4	1.7E-01	1.2	2.9E-01	0.3	7.5E-01	0.4	7.0E-01
ENSMUST00000175474	ENSMUSG00000093215	7	microRNA 3103	MI0014100	Mir3103	-1.5	1.5E-01	-0.6	6.7E-01	0.1	9.4E-01	-0.9	5.2E-01
ENSMUST00000175475	ENSMUSG00000093216	7	predicted gene, 25247		Gm25247	2.2	2.2E-02	1.5	2.2E-01	1.3	1.5E-01	2.0	8.6E-02
ENSMUST00000175476	ENSMUSG00000093217	X	predicted gene, 25246		Gm25246	3.3	4.2E-04	4.3	1.7E-04	0.5	4.6E-01	-0.5	6.3E-01
ENSMUST00000175477	ENSMUSG00000093218	12	predicted gene, 25252		Gm25252	1.8	5.0E-02	0.1	9.0E-01	-1.1	2.1E-01	0.6	6.1E-01
ENSMUST00000175478	ENSMUSG00000093219	X	microRNA 3113	MI0014111	Mir3113	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000175480	ENSMUSG00000093221	7	microRNA 3105	MI0014102	Mir3105	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000175482	ENSMUSG00000093223	15	predicted gene, 27903		Gm27903	1.6	8.2E-02	5.3	1.8E-05	1.8	2.7E-02	-1.9	6.1E-02
ENSMUST00000175483	ENSMUSG00000093224	12	predicted gene, 25750		Gm25750	-0.1	9.3E-01	-1.6	1.4E-01	-0.9	3.1E-01	0.6	5.1E-01
ENSMUST00000175486	ENSMUSG00000093227	10	microRNA 1251	MI0014021	Mir1251	2.0	5.8E-03	1.0	3.1E-01	-1.2	1.2E-01	-0.2	8.3E-01
ENSMUST00000175487	ENSMUSG00000093228	1	predicted gene, 25748		Gm25748	2.1	6.3E-03	1.4	9.1E-02	-0.2	7.8E-01	0.5	5.3E-01
ENSMUST00000175489	ENSMUSG00000093230	3	predicted gene, 24109		Gm24109	0.4	6.2E-01	1.7	1.3E-01	0.9	2.8E-01	-0.4	6.8E-01
ENSMUST00000175490	ENSMUSG00000093231	12	predicted gene, 25297		Gm25297	1.1	5.7E-01	0.9	6.9E-01	0.0	9.8E-01	0.2	9.4E-01
ENSMUST00000175491	ENSMUSG00000093232	13	predicted gene, 24111	MI0000562	Gm24111	0.7	3.0E-01	1.3	8.0E-02	0.5	4.0E-01	-0.2	8.1E-01
ENSMUST00000175493	ENSMUSG00000093234	19	microRNA 3085	MI0014048	Mir3085	1.7	9.5E-02	-1.7	1.6E-01	-2.2	1.2E-02	1.1	3.5E-01
ENSMUST00000175494	ENSMUSG00000094486	5	predicted gene, 23268		Gm23268	1.1	7.4E-02	1.3	7.2E-02	0.0	9.4E-01	-0.2	7.7E-01
ENSMUST00000175495	ENSMUSG00000093236	19	predicted gene, 24108		Gm24108	-0.5	6.0E-01	2.7	2.9E-02	1.7	8.6E-02	-1.5	1.8E-01
ENSMUST00000175498	ENSMUSG00000093239	9	predicted gene, 24106		Gm24106	1.0	2.0E-01	0.1	9.5E-01	-1.8	4.3E-02	-0.9	4.1E-01
ENSMUST00000175500	ENSMUSG00000093241	8	microRNA 3108	MI0014105	Mir3108	-1.5	4.0E-02	-2.3	2.0E-02	-1.0	1.7E-01	-0.1	8.7E-01
ENSMUST00000175501	ENSMUSG00000093242	2	predicted gene, 24574		Gm24574	-1.3	2.0E-01	-3.0	1.3E-02	-0.4	6.7E-01	1.3	2.4E-01
ENSMUST00000175502	ENSMUSG00000093243	15	predicted gene, 24575		Gm24575	3.3	9.9E-04	5.5	4.8E-05	1.8	7.8E-02	-0.4	6.7E-01
ENSMUST00000175505	ENSMUSG00000093246	16	predicted gene, 24572	MI0030345	Gm24572	0.8	3.0E-01	0.4	6.5E-01	0.1	9.3E-01	0.4	6.3E-01
ENSMUST00000175513	ENSMUSG00000093254	1	microRNA 5126	MI0018038	Mir5126	2.8	9.0E-03	0.4	7.0E-01	-0.6	5.5E-01	1.8	1.1E-01
ENSMUST00000175515	ENSMUSG00000093256	16	predicted gene, 22933		Gm22933	1.4	1.2E-01	3.5	2.3E-03	1.7	4.0E-02	-0.4	7.1E-01
ENSMUST00000175516	ENSMUSG00000095943	13	predicted gene, 25197		Gm25197	3.0	6.1E-02	4.0	3.7E-02	-0.1	9.4E-01	-1.1	4.8E-01
ENSMUST00000175519	ENSMUSG00000093260	13	predicted gene, 23415		Gm23415	1.9	1.8E-02	3.0	6.1E-03	-0.2	7.8E-01	-1.3	2.2E-01
ENSMUST00000175520	ENSMUSG00000093261	15	predicted gene, 23416		Gm23416	2.0	1.7E-02	0.9	3.0E-01	-0.2	8.2E-01	0.9	2.9E-01
ENSMUST00000175521	ENSMUSG00000093262	16	predicted gene, 23413		Gm23413	0.8	3.8E-01	0.2	8.2E-01	-0.7	4.2E-01	-0.1	9.1E-01
ENSMUST00000175523	ENSMUSG00000093264	11	predicted gene, 23419		Gm23419	0.3	7.8E-01	-0.2	8.5E-01	-0.4	7.0E-01	0.1	9.2E-01
ENSMUST00000175528	ENSMUSG00000093269	13	microRNA 5124a	MI0018035	Mir5124a	-0.3	7.0E-01	0.6	5.3E-01	1.2	1.1E-01	0.3	7.1E-01
ENSMUST00000175529	ENSMUSG00000093270	17	microRNA 5134	MI0018046	Mir5134	-0.3	7.4E-01	-3.4	5.8E-04	-1.3	7.8E-02	1.9	3.9E-02
ENSMUST00000175530	ENSMUSG00000093271	6	predicted gene, 26233		Gm26233	1.8	3.2E-02	0.5	6.0E-01	-0.6	4.7E-01	0.7	4.9E-01
ENSMUST00000175531	ENSMUSG00000093476	2	predicted gene, 22355		Gm22355	0.7	4.3E-01	2.4	6.6E-02	2.2	3.4E-02	0.5	6.4E-01
ENSMUST00000175532	ENSMUSG00000093273	11	microRNA 3064	MI0014026	Mir3064	-0.4	6.6E-01	0.5	6.4E-01	0.0	9.5E-01	-0.8	4.4E-01
ENSMUST00000175533	ENSMUSG00000093274	18	predicted gene, 26235		Gm26235	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175535	ENSMUSG00000093276	8	predicted gene, 26237		Gm26237	2.0	5.4E-03	1.0	1.9E-01	-1.0	1.1E-01	-0.1	9.3E-01
ENSMUST00000175537	ENSMUSG00000093278	11	microRNA 5110	MI0018019	Mir5110	1.6	6.0E-02	1.1	3.9E-01	-1.2	2.0E-01	-0.6	5.7E-01
ENSMUST00000175538	ENSMUSG00000093279	5	predicted gene, 26238		Gm26238	0.9	3.9E-01	0.4	7.7E-01	-0.2	8.6E-01	0.3	8.1E-01
ENSMUST00000175539	ENSMUSG00000093280	2	microRNA 2861	MI0013007	Mir2861	0.2	8.1E-01	0.7	5.8E-01	0.7	5.2E-01	0.2	8.6E-01
ENSMUST00000175540	ENSMUSG00000093281	8	predicted gene, 22565		Gm22565	2.9	1.1E-03	1.5	8.6E-02	0.0	9.5E-01	1.3	1.5E-01
ENSMUST00000175545	ENSMUSG00000093286	1	predicted gene, 22569		Gm22569	1.4	3.4E-01	-2.1	1.9E-01	-0.4	7.5E-01	3.0	5.9E-02
ENSMUST00000175549	ENSMUSG00000093290	7	microRNA 3572	MI0018037	Mir3572	-0.7	4.4E-01	-2.0	6.3E-02	-1.4	1.3E-01	0.0	9.7E-01
ENSMUST00000175550	ENSMUSG00000093291	12	microRNA 299b	MI0019180	Mir299b	1.3	1.7E-01	1.1	3.5E-01	-0.9	3.3E-01	-0.6	6.0E-01
ENSMUST00000175551	ENSMUSG00000093292	16	microRNA 5118	MI0018027	Mir5118	2.1	3.7E-03	2.5	2.2E-02	-0.9	2.0E-01	-1.3	1.9E-01
ENSMUST00000175555	ENSMUSG00000093296	7	microRNA 3102	MI0014099	Mir3102	2.6	1.7E-02	-0.3	8.1E-01	-3.4	1.1E-03	-0.5	7.0E-01
ENSMUST00000175556	ENSMUSG00000096817	13	predicted gene, 25084		Gm25084	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175557	ENSMUSG00000093298	10	microRNA 3473b	MI0016997	Mir3473b	-2.5	3.1E-03	-3.1	3.2E-03	-0.6	4.5E-01	0.0	9.7E-01
ENSMUST00000175561	ENSMUSG00000093302	5	predicted gene, 23801		Gm23801	1.5	1.3E-01	-0.6	5.9E-01	-0.4	6.8E-01	1.7	1.1E-01
ENSMUST00000175563	ENSMUSG00000093912	16	microRNA 3470b	MI0014697	Mir3470b	1.9	3.6E-02	2.5	1.9E-02	-0.4	6.5E-01	-1.0	2.9E-01
ENSMUST00000175570	ENSMUSG00000093311	5	microRNA 3965	MI0016972	Mir3965	1.1	1.1E-01	1.5	8.4E-02	0.9	1.9E-01	0.5	5.3E-01
ENSMUST00000175573	ENSMUSG00000093314	19	microRNA 5136	MI0018048	Mir5136	-2.3	4.8E-03	-2.0	5.2E-02	0.8	3.6E-01	0.4	6.0E-01
ENSMUST00000175574	ENSMUSG00000093315	19	microRNA 5114	MI0018023	Mir5114	-1.0	2.4E-01	-0.5	6.4E-01	1.3	8.1E-02	0.8	4.6E-01
ENSMUST00000175582	ENSMUSG00000093323	17	predicted gene, 24970		Gm24970	0.0	9.8E-01	1.0	4.6E-01	1.0	3.6E-01	-0.1	9.4E-01
ENSMUST00000175586	ENSMUSG00000093327	18	microRNA 5107	MI0018016	Mir5107	2.1	1.8E-02	-0.6	5.4E-01	-3.0	1.6E-04	-0.4	7.2E-01
ENSMUST00000175588	ENSMUSG00000093329	X	predicted gene, 24973		Gm24973	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175590	ENSMUSG00000093331	12	predicted gene, 22120		Gm22120	2.0	1.2E-02	0.1	8.9E-01	-1.7	5.7E-02	0.2	8.5E-01
ENSMUST00000175591	ENSMUSG00000094842	4	predicted gene, 22639		Gm22639	0.6	7.9E-01	-0.1	9.9E-01	-0.7	7.7E-01	0.0	9.9E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000175593	ENSMUSG00000093334	13	predicted gene, 22118		Gm22118	0.7	3.5E-01	0.5	5.5E-01	0.2	7.8E-01	0.3	7.2E-01
ENSMUST00000175594	ENSMUSG00000093335	Y	predicted gene, 22119		Gm22119	2.3	1.2E-02	1.5	1.4E-01	0.0	9.8E-01	0.8	4.2E-01
ENSMUST00000175595	ENSMUSG00000093336	2	microRNA 1954	MI0009949	Mir1954	2.1	1.0E-02	1.4	1.7E-01	-0.3	6.9E-01	0.5	6.2E-01
ENSMUST00000175597	ENSMUSG00000093338	2	microRNA 3090	MI0014083	Mir3090	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000175599	ENSMUSG00000093340	15	predicted gene, 26117		Gm26117	1.5	5.9E-02	-0.9	3.5E-01	-1.4	8.3E-02	1.0	2.7E-01
ENSMUST00000175600	ENSMUSG00000093341	11	predicted gene, 26116		Gm26116	2.5	1.6E-02	3.6	3.8E-03	0.1	8.9E-01	-1.0	3.6E-01
ENSMUST00000175601	ENSMUSG00000093342	18	predicted gene, 26119		Gm26119	2.3	3.4E-02	2.0	1.4E-01	-1.0	3.3E-01	-0.6	6.1E-01
ENSMUST00000175603	ENSMUSG00000093344	5	predicted gene, 26113		Gm26113	0.1	8.8E-01	-0.9	4.4E-01	-1.2	2.1E-01	-0.2	8.9E-01
ENSMUST00000175605	ENSMUSG00000093346	19	predicted gene, 26115		Gm26115	2.2	6.2E-03	0.6	5.5E-01	-0.9	2.6E-01	0.7	4.2E-01
ENSMUST00000175607	ENSMUSG00000093348	7	microRNA 3101	MI0014093	Mir3101	0.1	9.1E-01	-0.5	6.7E-01	-1.1	2.3E-01	-0.5	7.2E-01
ENSMUST00000175610	ENSMUSG00000093351	12	microRNA 3072	MI0014035	Mir3072	1.9	1.8E-02	0.3	7.4E-01	-1.0	2.3E-01	0.5	5.7E-01
ENSMUST00000175611	ENSMUSG00000093352	12	predicted gene, 23291		Gm23291	3.1	2.4E-03	2.9	2.0E-02	-0.9	3.1E-01	-0.6	5.7E-01
ENSMUST00000175613	ENSMUSG00000093354	9	microRNA 125b-1	MI0000725	Mir125b-1	1.2	2.0E-01	1.4	1.0E-01	-6.4	3.4E-08	-6.6	1.9E-07
ENSMUST00000175617	ENSMUSG00000093358	11	microRNA 3063	MI0014025	Mir3063	2.0	5.0E-03	-0.1	8.8E-01	-1.6	3.4E-02	0.5	5.5E-01
ENSMUST00000175618	ENSMUSG00000093359	7	predicted gene, 23292		Gm23292	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000175621	ENSMUSG00000093362	14	predicted gene, 22802		Gm22802	2.2	3.6E-02	0.9	4.0E-01	-0.2	8.5E-01	1.1	3.4E-01
ENSMUST00000175622	ENSMUSG00000093363	2	predicted gene, 22002		Gm22002	5.5	8.6E-07	4.6	2.6E-04	0.3	7.9E-01	1.2	1.8E-01
ENSMUST00000175627	ENSMUSG00000093368	2	predicted gene, 22800		Gm22800	1.2	2.9E-01	1.0	4.3E-01	0.3	7.5E-01	0.5	6.9E-01
ENSMUST00000175639	ENSMUSG00000093515	1	microRNA 1231	MI0019183	Mir1231	0.6	4.2E-01	-0.3	7.8E-01	-1.7	6.1E-02	-0.7	5.1E-01
ENSMUST00000175907	ENSMUSG00000093615	9	microRNA 5618	MI0019186	Mir5618	2.0	4.2E-03	1.2	1.9E-01	-0.8	2.5E-01	0.0	9.7E-01
ENSMUST00000175928	ENSMUSG00000093746	2	microRNA 5622	MI0019190	Mir5622	0.6	6.1E-01	1.1	3.6E-01	2.5	2.7E-02	1.9	1.1E-01
ENSMUST00000175989	ENSMUSG00000093539	11	microRNA 5621	MI0019189	Mir5621	-1.2	1.4E-01	-0.5	6.4E-01	-0.1	9.0E-01	-0.8	4.7E-01
ENSMUST00000176002	ENSMUSG00000093763	9	microRNA 5626	MI0019195	Mir5626	0.0	9.6E-01	-1.0	3.2E-01	-0.6	4.5E-01	0.4	6.3E-01
ENSMUST00000176065	ENSMUSG00000093690	5	microRNA 5619	MI0019187	Mir5619	1.0	2.4E-01	-0.7	5.0E-01	-0.8	3.5E-01	0.9	3.5E-01
ENSMUST00000176507	ENSMUSG00000093428	X	predicted gene, 26318		Gm26318	0.6	2.8E-01	1.3	6.7E-02	0.2	6.4E-01	-0.4	5.2E-01
ENSMUST00000176537	ENSMUSG00000093498	10	microRNA 5615-2	MI0019182	Mir5615-2	-0.5	4.8E-01	-0.7	5.1E-01	0.0	9.6E-01	0.1	9.4E-01
ENSMUST00000176598	ENSMUSG00000093710	5	microRNA 5625	MI0019194	Mir5625	-1.4	1.0E-01	-2.1	4.8E-02	-0.2	8.2E-01	0.5	5.7E-01
ENSMUST00000176615	ENSMUSG00000093409	6	predicted gene, 25193		Gm25193	0.4	5.5E-01	1.6	6.9E-02	0.6	3.4E-01	-0.5	5.2E-01
ENSMUST00000176631	ENSMUSG00000093757	19	microRNA 5623	MI0019191	Mir5623	0.1	8.8E-01	-0.2	8.2E-01	-0.2	8.1E-01	0.1	8.9E-01
ENSMUST00000176635	ENSMUSG00000093480	13	microRNA 5624	MI0019193	Mir5624	-3.1	1.7E-03	-2.5	3.7E-02	0.8	3.3E-01	0.2	8.9E-01
ENSMUST00000176664	ENSMUSG00000093404	10	predicted gene, 25190		Gm25190	-0.4	4.6E-01	-0.5	4.2E-01	-0.1	8.2E-01	0.0	9.7E-01
ENSMUST00000176783	ENSMUSG00000093508	17	microRNA 5709	MI0019318	Mir5709	0.6	4.0E-01	0.2	8.3E-01	0.1	9.0E-01	0.5	5.4E-01
ENSMUST00000176903	ENSMUSG00000093599	7	microRNA 5620	MI0019188	Mir5620	-0.6	4.9E-01	-0.5	6.0E-01	0.2	7.9E-01	0.2	8.8E-01
ENSMUST00000176930	ENSMUSG00000093684	14	predicted gene, 27857		Gm27857	6.7	8.2E-04	2.6	1.4E-01	-4.3	1.3E-02	-0.1	9.3E-01
ENSMUST00000176951	ENSMUSG00000093529	15	predicted gene, 25397		Gm25397	2.1	8.0E-03	1.6	8.7E-02	-0.1	9.2E-01	0.5	6.0E-01
ENSMUST00000177002	ENSMUSG00000093572	11	predicted gene, 24756		Gm24756	2.5	1.5E-03	-0.1	8.6E-01	-2.1	3.1E-03	0.5	5.2E-01
ENSMUST00000177110	ENSMUSG00000093782	1	predicted gene, 22396		Gm22396	0.1	8.5E-01	0.3	7.5E-01	0.6	4.9E-01	0.4	6.3E-01
ENSMUST00000177217	ENSMUSG00000093403	4	microRNA 5616	MI0019184	Mir5616	0.3	7.7E-01	-2.2	3.0E-02	-1.0	2.2E-01	1.5	1.3E-01
ENSMUST00000177238	ENSMUSG00000093618	12	microRNA 5627	MI0019198	Mir5627	0.2	8.2E-01	-3.2	3.8E-03	-0.6	3.9E-01	2.8	1.4E-02
ENSMUST00000177270	ENSMUSG00000093499	3	predicted gene, 25442		Gm25442	1.0	1.3E-01	1.2	1.5E-01	0.7	2.4E-01	0.5	4.8E-01
ENSMUST00000177317	ENSMUSG00000093762	10	predicted gene, 25591		Gm25591	0.9	2.2E-01	0.8	4.2E-01	0.7	3.2E-01	0.8	3.7E-01
ENSMUST00000177427	ENSMUSG00000093780	5	predicted gene, 22395		Gm22395	1.6	2.4E-02	1.9	2.7E-02	0.8	2.1E-01	0.5	5.6E-01
ENSMUST00000177656	ENSMUSG00000095947	17	predicted gene, 25195		Gm25195	-1.6	6.2E-02	-1.3	1.9E-01	-0.8	2.2E-01	-1.2	2.5E-01
ENSMUST00000177758	ENSMUSG00000096142	7	predicted gene, 25817		Gm25817	1.2	1.4E-01	1.6	1.1E-01	0.9	2.3E-01	0.5	5.8E-01
ENSMUST00000177773	ENSMUSG00000094466	6	predicted gene, 24308		Gm24308	1.5	1.5E-01	0.6	6.0E-01	-0.2	8.8E-01	0.7	5.1E-01
ENSMUST00000177784	ENSMUSG00000094603	17	predicted gene, 25872		Gm25872	-0.7	5.2E-01	4.1	4.9E-03	-0.2	8.2E-01	-4.9	8.7E-04
ENSMUST00000177794	ENSMUSG00000096377	4	microRNA 5123	MI0018034	Mir5123	0.7	2.6E-01	-0.4	6.3E-01	-0.1	8.7E-01	1.0	2.0E-01
ENSMUST00000177816	ENSMUSG00000094608	8	predicted gene, 25871		Gm25871	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000177866	ENSMUSG00000093995	2	predicted gene, 26426		Gm26426	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000177928	ENSMUSG00000095776	12	predicted gene, 23018		Gm23018	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000178119	ENSMUSG00000095727	8	predicted gene, 23646		Gm23646	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000178126	ENSMUSG00000096174	4	predicted gene, 22991		Gm22991	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000178138	ENSMUSG00000094041	8	predicted gene, 28019		Gm28019	4.4	4.7E-06	5.2	6.5E-06	-0.6	4.9E-01	-1.4	8.1E-02
ENSMUST00000178153	ENSMUSG00000095122	16	predicted gene, 23215		Gm23215	2.3	4.9E-03	4.9	5.5E-05	-0.1	9.1E-01	-2.7	1.2E-02
ENSMUST00000178237	ENSMUSG00000095596	6	predicted gene, 24303		Gm24303	5.3	2.9E-02	4.4	1.2E-01	-0.8	7.2E-01	0.1	9.7E-01
ENSMUST00000178283	ENSMUSG00000094702	10	predicted gene, 24485		Gm24485	1.5	1.3E-01	-0.6	5.9E-01	-0.4	6.8E-01	1.7	1.1E-01
ENSMUST00000178285	ENSMUSG00000094210	7	predicted gene, 23450	MI0030346	Gm23450	1.4	1.5E-01	1.1	3.7E-01	1.3	1.4E-01	1.6	2.0E-01
ENSMUST00000178305	ENSMUSG00000096784	15	predicted gene, 24643		Gm24643	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000178350	ENSMUSG00000095842	15	predicted gene, 24302		Gm24302	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000178407	ENSMUSG00000096522	6	predicted gene, 26386		Gm26386	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000178456	ENSMUSG00000096388	4	predicted gene, 25355		Gm25355	1.2	2.5E-01	0.7	5.7E-01	-0.1	9.0E-01	0.4	7.6E-01
ENSMUST00000178484	ENSMUSG00000096193	1	predicted gene, 26134		Gm26134	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000178512	ENSMUSG00000094467	6	predicted gene, 24307		Gm24307	4.2	2.8E-02	3.8	9.7E-02	-0.2	9.1E-01	0.2	9.1E-01
ENSMUST00000178593	ENSMUSG00000096667	16	predicted gene, 22862		Gm22862	0.7	5.9E-01	2.4	1.3E-01	-0.5	6.7E-01	-2.2	1.4E-01
ENSMUST00000178626	ENSMUSG00000096425	17	predicted gene, 24979		Gm24979	1.7	3.2E-01	-2.9	1.8E-01	-1.1	5.2E-01	3.4	9.0E-02
ENSMUST00000178653	ENSMUSG00000094946	1	predicted gene, 25754		Gm25754	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000178754	ENSMUSG00000095467	9	predicted gene, 22243		Gm22243	1.3	2.4E-01	1.1	3.8E-01	0.2	8.1E-01	0.4	7.2E-01
ENSMUST00000178780	ENSMUSG00000094968	1	predicted gene, 22419		Gm22419	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000178795	ENSMUSG00000094969	17	predicted gene, 22420		Gm22420	1.2	5.2E-01	2.8	2.2E-01	1.1	5.4E-01	-0.5	8.2E-01
ENSMUST00000178821	ENSMUSG00000096061	11	predicted gene, 23681		Gm23681	6.7	8.2E-04	2.6	1.4E-01	-4.3	1.3E-02	-0.1	9.3E-01
ENSMUST00000178897	ENSMUSG00000093823	1	predicted gene, 24802		Gm24802	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000178937	ENSMUSG00000094983	3	predicted gene, 23726		Gm23726	3.8	3.1E-04	3.2	7.3E-03	-0.2	8.1E-01	0.4	7.1E-01
ENSMUST00000178951	ENSMUSG00000095536	2	predicted gene, 25285	MI0005505	Gm25285	-2.8	3.9E-03	-3.7	2.6E-03	-0.4	6.1E-01	0.4	7.0E-01
ENSMUST00000178964	ENSMUSG00000096309	14	predicted gene, 25208		Gm25208	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000178981	ENSMUSG00000093878	6	predicted gene, 25458		Gm25458	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000179003	ENSMUSG00000094572	7	predicted gene, 23550		Gm23550	0.1	8.8E-01	1.9	4.9E-02	3.0	3.6E-04	1.2	2.1E-01
ENSMUST00000179085	ENSMUSG00000095516	15	predicted gene, 24135		Gm24135	3.0	1.7E-03	4.2	4.4E-04	0.9	2.1E-01	-0.3	7.5E-01
ENSMUST00000179092	ENSMUSG00000096893	7	microRNA 344d-2	MI0004619	Mir344d-2	2.0	1.2E-02	-0.1	9.2E-01	-1.6	6.5E-02	0.5	6.1E-01
ENSMUST00000179099	ENSMUSG00000094357	6	predicted gene, 25570		Gm25570	2.6	1.5E-02	1.2	2.5E-01	0.0	9.9E-01	1.4	2.1E-01
ENSMUST00000179154	ENSMUSG00000094267	4	predicted gene, 25123	MI0006299	Gm25123	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000179159	ENSMUSG00000094959	4	predicted gene, 24112		Gm24112	2.0	1.4E-02	1.6	9.6E-02	0.0	9.7E-01	0.5	5.9E-01
ENSMUST00000179169	ENSMUSG00000095447	6	predicted gene, 23403		Gm23403	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000179182	ENSMUSG00000096274	7	predicted gene, 24766		Gm24766	1.2	1.4E-01	1.6	1.1E-01	0.9	2.3E-01	0.5	5.8E-01
ENSMUST00000179216	ENSMUSG00000096245	9	predicted gene, 24269		Gm24269	2.9	8.0E-04	2.3	2.0E-02	-0.7	3.5E-01	-0.1	9.2E-01
ENSMUST00000179283	ENSMUSG00000096631	7	predicted gene, 22171		Gm22171	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000179294	ENSMUSG00000094515	4	predicted gene, 24567		Gm24567	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000179358	ENSMUSG00000094650	10	predicted gene, 25361		Gm25361	2.9	8.6E-03	0.5	6.9E-01	-0.8	4.0E-01	1.6	1.6E-01
ENSMUST00000179366	ENSMUSG00000096383	14	predicted gene, 25353	MI0006299	Gm25353	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000179444	ENSMUSG00000094718	8	predicted gene, 22825		Gm22825	4.1	3.2E-05	1.3	1.4E-01	-0.1	8.9E-01	2.7	5.8E-03
ENSMUST00000179485	ENSMUSG00000095555	9	predicted gene, 28010		Gm28010	6.5	9.2E-08	2.4	1.2E-02	-5.8	1.9E-07	-1.7	5.6E-02
ENSMUST00000179496	ENSMUSG00000096172	1	predicted gene, 22992	MI0006299	Gm22992	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000179603	ENSMUSG00000095951	2	predicted gene, 23963		Gm23963	1.3	1.3E-01	0.9	4.2E-01	0.6	4.4E-01	1.0	3.3E-01
ENSMUST00000179609	ENSMUSG00000094123	X	predicted gene, 23945		Gm23945	1.6	1.0E-01	-2.3	4.9E-02	-3.2	5.2E-04	0.6	6.0E-01
ENSMUST00000179712	ENSMUSG00000094128	1	predicted gene, 23943		Gm23943	1.9	2.0E-02	0.8	5.3E-01	-1.7	6.5E-02	-0.5	6.2E-01
ENSMUST00000179732	ENSMUSG00000094750	6	predicted gene, 25019		Gm25019	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000179750	ENSMUSG00000095674	7	predicted gene, 25100		Gm25100	4.4	4.7E-06	5.2	6.5E-06	-0.6	4.9E-01	-1.4	8.1E-02
ENSMUST00000179783	ENSMUSG00000095853	1	predicted gene, 22616		Gm22616	0.4	5.2E-01	0.5	5.9E-01	0.0	9.7E-01	-0.1	9.5E-01
ENSMUST00000179798	ENSMUSG00000095699	2	predicted gene, 26092	MI0004523	Gm26092	-1.7	5.5E-02	-0.5	7.0E-01	-0.1	9.2E-01	-1.4	2.5E-01
ENSMUST00000179866	ENSMUSG00000094477	4	predicted gene, 23064		Gm23064	1.2	2.5E-01	0.7	5.7E-01	-0.1	9.0E-01	0.4	7.6E-01
ENSMUST00000179867	ENSMUSG00000096510	14	predicted gene, 25892	MI0006299	Gm25892	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000179906	ENSMUSG00000094165	2	predicted gene, 26073		Gm26073	2.1	1.6E-02	1.6	1.1E-01	-0.1	9.4E-01	0.4	6.6E-01
ENSMUST00000179974	ENSMUSG00000095010	7	predicted gene, 23490		Gm23490	2.0	1.2E-02	-0.1	9.2E-01	-1.6	6.5E-02	0.5	6.1E-01
ENSMUST00000180080	ENSMUSG00000096721	6	predicted gene, 25942		Gm25942	1.4	4.3E-02	1.0	2.5E-01	-0.1	8.5E-01	0.3	6.8E-01
ENSMUST00000180094	ENSMUSG00000094363	2	predicted gene, 26060		Gm26060	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000180121	ENSMUSG00000094563	14	predicted gene, 25228		Gm25228	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000180144	ENSMUSG00000096112	16	predicted gene, 26269		Gm26269	2.0	1.7E-02	1.7	6.8E-02	-1.2	1.0E-01	-0.9	2.9E-01
ENSMUST00000180209	ENSMUSG00000096184	4	predicted gene, 23304		Gm23304	1.9	3.6E-02	0.9	4.3E-01	-0.4	6.2E-01	0.6	5.7E-01
ENSMUST00000180211	ENSMUSG00000094659	2	microRNA 466c-2	MI0005505	Mir466c-2	-2.8	3.9E-03	-3.7	2.6E-03	-0.4	6.1E-01	0.4	7.0E-01
ENSMUST00000180212	ENSMUSG00000094780	7	predicted gene, 24659		Gm24659	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000180238	ENSMUSG00000096583	2	microRNA 669a-1	MI0004523	Mir669a-1	-1.7	5.5E-02	-0.5	7.0E-01	-0.1	9.2E-01	-1.4	2.5E-01
ENSMUST00000180257	ENSMUSG00000093791	1	predicted gene, 24092	MI0006299	Gm24092	0.0	9.9E-01	1.7	8.3E-02	3.0	5.7E-04	1.3	1.9E-01
ENSMUST00000180307	ENSMUSG00000096694	12	predicted gene, 23190		Gm23190	3.0	5.8E-04	1.3	1.1E-01	-0.1	9.1E-01	1.6	7.1E-02
ENSMUST00000183340	ENSMUSG00000098898	10	predicted gene, 27754		Gm27754	-3.2	9.9E-03	-0.4	7.5E-01	-0.8	3.6E-01	-3.7	8.2E-03
ENSMUST00000183342	ENSMUSG00000098844	19	microRNA 6992	MI0022840	Mir6992	0.2	7.6E-01	0.5	5.8E-01	0.6	4.9E-01	0.3	7.7E-01
ENSMUST00000183343	ENSMUSG00000098904	2	microRNA 6998	MI0022846	Mir6998	0.6	4.5E-01	-1.0	3.1E-01	-1.4	1.1E-01	0.2	8.0E-01
ENSMUST00000183346	ENSMUSG00000098762	6	microRNA 7045	MI0022894	Mir7045	0.0	9.5E-01	-1.0	2.6E-01	-0.5	5.1E-01	0.6	4.9E-01
ENSMUST00000183351	ENSMUSG00000098356	1	predicted gene, 27552		Gm27552	2.4	4.5E-03	-0.2	8.4E-01	-1.8	4.4E-02	0.8	4.0E-01
ENSMUST00000183361	ENSMUSG00000098269	17	microRNA 8094	MI0026021	Mir8094	-2.1	2.2E-02	-1.5	2.1E-01	0.3	7.6E-01	-0.3	7.7E-01
ENSMUST00000183364	ENSMUSG00000098951	5	microRNA 7647	MI0024985	Mir7647	0.9	2.6E-01	0.9	3.6E-01	0.5	5.7E-01	0.5	6.1E-01
ENSMUST00000183370	ENSMUSG00000099267	15	microRNA 6955	MI0022802	Mir6955	-1.2	1.4E-01	-2.0	5.6E-02	-0.6	4.6E-01	0.2	8.2E-01
ENSMUST00000183371	ENSMUSG00000099070	4	microRNA 8119	MI0026051	Mir8119	1.2	1.7E-01	0.8	4.4E-01	0.0	9.8E-01	0.4	7.1E-01
ENSMUST00000183376	ENSMUSG00000099050	2	microRNA 7655	MI0024995	Mir7655	-0.9	3.4E-01	-1.4	2.1E-01	0.2	8.4E-01	0.7	5.3E-01
ENSMUST00000183379	ENSMUSG00000098840	11	microRNA 7679	MI0025024	Mir7679	1.3	2.5E-01	1.2	4.0E-01	0.7	5.2E-01	0.8	5.9E-01
ENSMUST00000183385	ENSMUSG00000099308	16	microRNA 6367	MI0021896	Mir6367	4.0	6.4E-06	3.8	2.3E-04	-0.2	7.2E-01	0.1	9.4E-01
ENSMUST00000183396	ENSMUSG00000098675	16	microRNA 6364	MI0021893	Mir6364	1.8	5.3E-02	0.6	6.2E-01	-1.4	1.5E-01	-0.3	8.1E-01
ENSMUST00000183408	ENSMUSG00000098731	5	microRNA 7027	MI0022876	Mir7027	-0.6	4.5E-01	-2.2	3.0E-02	-1.2	1.6E-01	0.4	6.1E-01
ENSMUST00000183412	ENSMUSG00000099260	15	microRNA 6954	MI0022801	Mir6954	-0.4	5.5E-01	-1.7	1.4E-01	-2.1	9.4E-03	-0.9	4.0E-01
ENSMUST00000183415	ENSMUSG00000098622	3	predicted gene, 27974		Gm27974	1.4	1.6E-01	1.6	2.2E-01	0.0	9.6E-01	-0.1	9.5E-01
ENSMUST00000183420	ENSMUSG00000098740	17	predicted gene, 27475		Gm27475	0.7	3.9E-01	0.7	4.9E-01	0.6	4.9E-01	0.6	5.3E-01
ENSMUST00000183426	ENSMUSG00000098871	3	microRNA 6381	MI0021912	Mir6381	1.5	5.4E-02	1.1	2.3E-01	-0.1	9.4E-01	0.3	7.0E-01
ENSMUST00000183429	ENSMUSG00000098777	7	predicted gene, 27437		Gm27437	1.4	9.3E-02	1.5	1.5E-01	0.0	9.9E-01	-0.1	9.0E-01
ENSMUST00000183434	ENSMUSG00000099322	4	predicted gene, 28017		Gm28017	1.6	4.8E-03	2.3	1.0E-03	0.1	8.9E-01	-0.7	2.7E-01
ENSMUST00000183435	ENSMUSG00000098802	7	microRNA 7046	MI0022895	Mir7046	-2.7	2.7E-02	-3.7	1.4E-02	-0.8	4.0E-01	0.3	8.4E-01
ENSMUST00000183439	ENSMUSG00000099079	8	microRNA 7068	MI0022918	Mir7068	-0.8	3.5E-01	1.2	2.0E-01	0.6	3.3E-01	-1.3	1.8E-01
ENSMUST00000183442	ENSMUSG00000098397	3	microRNA 7669	MI0025009	Mir7669	0.0	9.8E-01	0.5	6.8E-01	1.9	7.7E-02	1.4	2.3E-01
ENSMUST00000183443	ENSMUSG00000098926	1	microRNA 6904	MI0022751	Mir6904	0.0	9.6E-01	-0.8	4.4E-01	-0.1	8.7E-01	0.6	5.0E-01
ENSMUST00000183449	ENSMUSG00000098698	15	microRNA 6960	MI0022807	Mir6960	0.7	4.0E-01	2.1	2.7E-02	0.9	2.0E-01	-0.5	5.4E-01
ENSMUST00000183458	ENSMUSG00000098389	18	microRNA 6983	MI0022831	Mir6983	1.1	1.1E-01	0.8	4.5E-01	-2.4	4.2E-03	-2.0	4.2E-02
ENSMUST00000183464	ENSMUSG00000098712	3	microRNA 7010	MI0022859	Mir7010	1.6	4.3E-02	-0.3	7.4E-01	-2.2	1.7E-02	-0.2	8.0E-01
ENSMUST00000183479	ENSMUSG00000098296	11	microRNA 6918	MI0022765	Mir6918	0.8	2.5E-01	1.7	5.1E-02	1.4	4.2E-02	0.5	5.5E-01
ENSMUST00000183483	ENSMUSG00000098288	1	microRNA 6900	MI0022747	Mir6900	2.2	1.2E-02	2.2	1.3E-02	1.7	1.9E-02	1.6	6.7E-02
ENSMUST00000183486	ENSMUSG00000098267	7	microRNA 7060	MI0022909	Mir7060	0.8	4.3E-01	-1.3	2.7E-01	-1.0	3.3E-01	1.1	3.1E-01
ENSMUST00000183487	ENSMUSG00000099018	X	predicted gene, 27360		Gm27360	1.2	1.1E-01	1.6	7.2E-02	0.9	1.7E-01	0.5	5.7E-01
ENSMUST00000183491	ENSMUSG00000098996	15	microRNA 7676-1	MI0025017	Mir7676-1	0.3	7.2E-01	-0.9	3.3E-01	-0.9	2.0E-01	0.3	7.5E-01
ENSMUST00000183494	ENSMUSG00000098896	2	microRNA 3473g	MI0026054	Mir3473g	-0.8	3.4E-01	-1.6	1.4E-01	-0.8	3.0E-01	0.0	9.9E-01
ENSMUST00000183497	ENSMUSG00000098458	17	microRNA 6971	MI0022819	Mir6971	1.0	2.1E-01	0.3	7.6E-01	-0.2	8.6E-01	0.6	5.5E-01
ENSMUST00000183498	ENSMUSG00000098651	2	microRNA 6999	MI0022847	Mir6999	0.7	3.4E-01	1.0	2.6E-01	0.6	4.3E-01	0.2	7.7E-01
ENSMUST00000183506	ENSMUSG00000099093	2	microRNA 7000	MI0022848	Mir7000	2.0	3.2E-03	2.0	1.9E-02	-0.1	9.0E-01	-0.1	9.2E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000183515	ENSMUSG00000098602	14	microRNA 6946	MI0022793	Mir6946	-0.7	3.5E-01	-0.9	3.7E-01	0.4	6.0E-01	0.6	5.0E-01
ENSMUST00000183523	ENSMUSG00000099059	15	microRNA 7676-2	MI0025017	Mir7676-2	0.3	7.2E-01	-0.9	3.3E-01	-0.9	2.0E-01	0.3	7.5E-01
ENSMUST00000183526	ENSMUSG00000098907	9	microRNA 7082	MI0022932	Mir7082	-1.2	1.6E-01	-2.1	4.4E-02	-0.7	3.7E-01	0.2	8.0E-01
ENSMUST00000183535	ENSMUSG00000098419	15	microRNA 6963	MI0022810	Mir6963	-1.4	1.2E-01	-1.7	1.2E-01	0.1	9.4E-01	0.4	6.4E-01
ENSMUST00000183540	ENSMUSG00000099033	3	microRNA 7013	MI0022862	Mir7013	0.7	4.0E-01	1.0	4.1E-01	-0.1	8.9E-01	-0.4	7.5E-01
ENSMUST00000183547	ENSMUSG00000098282	11	microRNA 6936	MI0022783	Mir6936	-2.7	4.8E-04	-1.3	2.2E-01	0.5	4.6E-01	-1.0	3.2E-01
ENSMUST00000183555	ENSMUSG00000098765	2	microRNA 7685	MI0025036	Mir7685	1.1	1.2E-01	0.8	4.2E-01	0.1	8.7E-01	0.5	5.5E-01
ENSMUST00000183558	ENSMUSG00000098766	9	microRNA 6386	MI0021918	Mir6386	1.8	8.1E-02	0.8	4.7E-01	0.0	1.0E+00	1.0	3.6E-01
ENSMUST00000183564	ENSMUSG00000098648	14	microRNA 6239	MI0021586	Mir6239	1.7	9.0E-02	4.3	5.2E-04	0.1	9.4E-01	-2.6	2.8E-02
ENSMUST00000183565	ENSMUSG00000098679	10	microRNA 7688	MI0025041	Mir7688	1.4	5.6E-02	2.1	2.8E-02	0.6	3.4E-01	-0.1	9.5E-01
ENSMUST00000183566	ENSMUSG00000099254	5	microRNA 7030	MI0022879	Mir7030	-0.9	3.2E-01	-0.5	6.6E-01	-0.8	3.4E-01	-1.2	2.9E-01
ENSMUST00000183568	ENSMUSG00000098931	12	microRNA 8099-1	MI0026027	Mir8099-1	1.0	2.3E-01	0.0	9.8E-01	-0.6	5.4E-01	0.4	6.7E-01
ENSMUST00000183570	ENSMUSG00000099097	X	predicted gene, 27341		Gm27341	5.6	3.6E-06	2.7	4.0E-02	-0.2	8.2E-01	2.7	3.7E-02
ENSMUST00000183577	ENSMUSG00000098803	19	predicted gene, 27468		Gm27468	-1.1	3.1E-01	-3.2	4.4E-02	-0.8	4.4E-01	1.3	3.7E-01
ENSMUST00000183582	ENSMUSG00000099227	1	microRNA 8114	MI0026046	Mir8114	-1.9	1.2E-02	-3.4	6.3E-04	-1.2	3.7E-02	0.2	8.3E-01
ENSMUST00000183598	ENSMUSG00000099180	15	microRNA 6956	MI0022803	Mir6956	-2.5	4.8E-03	-2.1	3.0E-02	-0.6	3.1E-01	-1.0	3.3E-01
ENSMUST00000183599	ENSMUSG00000098452	13	predicted gene, 27501		Gm27501	2.7	8.3E-03	3.2	9.8E-03	-0.5	6.5E-01	-1.0	3.4E-01
ENSMUST00000183602	ENSMUSG00000098286	19	microRNA 8091	MI0026018	Mir8091	0.6	4.1E-01	1.6	1.0E-01	1.5	4.9E-02	0.6	5.1E-01
ENSMUST00000183606	ENSMUSG00000098839	7	microRNA 7054	MI0022903	Mir7054	-1.2	1.2E-01	-0.5	6.5E-01	0.1	9.3E-01	-0.6	5.8E-01
ENSMUST00000183613	ENSMUSG00000098965	1	predicted gene, 27844		Gm27844	2.4	4.5E-03	-0.2	8.4E-01	-1.8	4.4E-02	0.8	4.0E-01
ENSMUST00000183615	ENSMUSG00000098955	11	microRNA 6935	MI0022782	Mir6935	-0.4	6.5E-01	-1.3	2.2E-01	0.5	5.6E-01	1.4	1.9E-01
ENSMUST00000183620	ENSMUSG00000099236	12	microRNA 668	MI0004134	Mir668	1.4	7.2E-02	0.9	3.9E-01	-0.5	5.6E-01	0.1	9.5E-01
ENSMUST00000183624	ENSMUSG00000098824	2	microRNA 7006	MI0022855	Mir7006	-0.2	8.5E-01	-0.6	5.7E-01	0.2	7.9E-01	0.7	4.8E-01
ENSMUST00000183643	ENSMUSG00000099279	10	microRNA 6408	MI0021945	Mir6408	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000183646	ENSMUSG00000098291	17	microRNA 6973a	MI0022821	Mir6973a	0.4	6.3E-01	0.8	5.1E-01	-0.4	6.2E-01	-0.8	4.7E-01
ENSMUST00000183649	ENSMUSG00000098858	14	microRNA 6541	MI0022358	Mir6541	1.2	1.4E-01	2.5	3.9E-02	0.7	3.7E-01	-0.6	6.1E-01
ENSMUST00000183650	ENSMUSG00000099319	15	microRNA 7648	MI0024986	Mir7648	-0.7	3.7E-01	-1.0	3.0E-01	0.4	6.0E-01	0.7	4.4E-01
ENSMUST00000183653	ENSMUSG00000098341	13	microRNA 6944	MI0022791	Mir6944	0.1	9.1E-01	-2.8	1.8E-02	-3.3	2.2E-04	-0.4	7.0E-01
ENSMUST00000183657	ENSMUSG00000099076	8	microRNA 7070	MI0022920	Mir7070	-1.1	1.8E-01	-1.4	2.3E-01	-1.0	2.0E-01	-0.7	5.2E-01
ENSMUST00000183660	ENSMUSG00000099193	11	predicted gene, 27374		Gm27374	1.8	4.6E-02	1.5	1.4E-01	0.1	9.4E-01	0.3	7.5E-01
ENSMUST00000183668	ENSMUSG00000098676	18	microRNA 6359	MI0021887	Mir6359	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000183671	ENSMUSG00000098695	15	predicted gene, 27618		Gm27618	1.6	2.3E-02	1.1	1.8E-01	-0.1	8.7E-01	0.4	6.4E-01
ENSMUST00000183676	ENSMUSG00000098830	5	microRNA 7024	MI0022873	Mir7024	-0.3	6.9E-01	-0.9	3.2E-01	0.0	9.8E-01	0.6	4.2E-01
ENSMUST00000183679	ENSMUSG00000098873	7	microRNA 7668	MI0025008	Mir7668	1.4	7.9E-02	0.8	4.3E-01	-0.1	9.3E-01	0.5	5.7E-01
ENSMUST00000183683	ENSMUSG00000098361	9	microRNA 7086	MI0022936	Mir7086	-0.1	9.5E-01	-1.3	2.2E-01	-0.5	6.0E-01	0.8	4.3E-01
ENSMUST00000183689	ENSMUSG00000098285	6	microRNA 7670	MI0025010	Mir7670	-0.9	2.6E-01	-1.4	1.8E-01	-0.1	8.4E-01	0.3	7.8E-01
ENSMUST00000183692	ENSMUSG00000098268	6	predicted gene, 27514		Gm27514	1.3	1.3E-01	0.9	4.0E-01	0.1	8.7E-01	0.6	5.8E-01
ENSMUST00000183701	ENSMUSG00000099314	16	predicted gene, 27734		Gm27734	2.7	1.3E-03	1.6	8.5E-02	0.1	9.4E-01	1.1	2.0E-01
ENSMUST00000183704	ENSMUSG00000098378	8	predicted gene, 27864		Gm27864	2.6	2.3E-03	2.6	1.3E-02	0.1	9.0E-01	0.1	9.0E-01
ENSMUST00000183708	ENSMUSG00000098631	15	microRNA 6957	MI0022804	Mir6957	-1.0	2.0E-01	-1.8	8.9E-02	0.0	9.6E-01	0.7	4.3E-01
ENSMUST00000183711	ENSMUSG00000098345	9	predicted gene, 27847		Gm27847	2.1	8.0E-03	1.6	8.7E-02	-0.1	9.2E-01	0.5	6.0E-01
ENSMUST00000183713	ENSMUSG00000098771	12	microRNA 6538	MI0022354	Mir6538	7.9	1.7E-10	5.0	3.3E-06	-1.8	1.5E-02	1.2	1.3E-01
ENSMUST00000183719	ENSMUSG00000098547	11	microRNA 6921	MI0022768	Mir6921	0.2	8.5E-01	-0.2	8.4E-01	0.4	6.2E-01	0.8	3.8E-01
ENSMUST00000183724	ENSMUSG00000098413	19	microRNA 6990	MI0022838	Mir6990	-1.4	1.5E-01	-2.2	5.3E-02	0.6	4.7E-01	1.4	2.0E-01
ENSMUST00000183732	ENSMUSG00000098866	14	microRNA 6539	MI0022355	Mir6539	-3.7	2.9E-03	-5.7	8.1E-05	0.1	8.8E-01	2.1	9.2E-02
ENSMUST00000183735	ENSMUSG00000099118	19	microRNA 8092	MI0026019	Mir8092	0.2	8.5E-01	1.1	3.0E-01	1.5	9.9E-02	0.6	5.7E-01
ENSMUST00000183739	ENSMUSG00000098652	16	predicted gene, 27671		Gm27671	1.2	1.0E-01	0.0	9.7E-01	-0.9	2.7E-01	0.3	7.3E-01
ENSMUST00000183743	ENSMUSG00000098344	1	microRNA 3473f	MI0026016	Mir3473f	0.5	3.8E-01	-0.2	7.9E-01	-0.5	3.1E-01	0.1	8.3E-01
ENSMUST00000183749	ENSMUSG00000099043	4	microRNA 7022	MI0022871	Mir7022	2.8	3.2E-02	0.7	6.4E-01	0.3	8.0E-01	2.5	7.6E-02
ENSMUST00000183751	ENSMUSG00000098653	10	predicted gene, 27672		Gm27672	2.4	6.7E-02	4.4	7.8E-03	1.3	3.1E-01	-0.7	6.1E-01
ENSMUST00000183760	ENSMUSG00000098401	3	microRNA 6377	MI0021907	Mir6377	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000183764	ENSMUSG00000098376	10	microRNA 6907	MI0022754	Mir6907	1.0	2.2E-01	0.7	5.1E-01	0.3	7.7E-01	0.6	5.3E-01
ENSMUST00000183768	ENSMUSG00000098655	3	microRNA 7011	MI0022860	Mir7011	-0.6	4.0E-01	-2.7	5.0E-03	-0.7	3.3E-01	1.4	1.2E-01
ENSMUST00000183771	ENSMUSG00000099078	8	microRNA 8110	MI0026042	Mir8110	1.9	8.7E-03	2.4	1.7E-02	0.0	9.5E-01	-0.5	5.7E-01
ENSMUST00000183772	ENSMUSG00000098258	13	microRNA 6369	MI0021898	Mir6369	3.2	4.7E-03	1.5	2.3E-01	-0.9	4.0E-01	0.8	5.2E-01
ENSMUST00000183778	ENSMUSG00000099211	7	predicted gene, 27684		Gm27684	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000183779	ENSMUSG00000099086	15	predicted gene, 27622		Gm27622	1.9	1.7E-02	3.0	1.3E-02	0.0	9.7E-01	-1.1	3.2E-01
ENSMUST00000183787	ENSMUSG00000098569	4	microRNA 7020	MI0022869	Mir7020	1.9	1.3E-02	1.5	1.0E-01	0.1	8.9E-01	0.5	5.4E-01
ENSMUST00000183794	ENSMUSG00000098483	8	microRNA 7078	MI0022928	Mir7078	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000183796	ENSMUSG00000099286	11	microRNA 7235	MI0023730	Mir7235	-1.2	1.7E-01	0.2	8.6E-01	0.5	5.3E-01	-0.9	4.1E-01
ENSMUST00000183799	ENSMUSG00000099191	14	predicted gene, 27375		Gm27375	2.1	8.0E-03	1.6	8.7E-02	-0.1	9.2E-01	0.5	6.0E-01
ENSMUST00000183802	ENSMUSG00000098349	11	predicted gene, 27711		Gm27711	2.6	6.2E-03	1.2	2.3E-01	-0.1	9.3E-01	1.4	1.7E-01
ENSMUST00000183804	ENSMUSG00000098407	1	microRNA 6348	MI0021876	Mir6348	1.7	1.4E-02	1.3	1.2E-01	0.0	9.4E-01	0.4	6.2E-01
ENSMUST00000183805	ENSMUSG00000099183	1	predicted gene, 27881		Gm27881	0.6	4.2E-01	-0.5	6.5E-01	0.5	4.8E-01	1.6	1.3E-01
ENSMUST00000183808	ENSMUSG00000098408	9	microRNA 6237	MI0021584	Mir6237	1.6	2.0E-02	1.2	1.4E-01	0.0	9.4E-01	0.4	6.5E-01
ENSMUST00000183825	ENSMUSG00000099163	6	microRNA 7660	MI0025000	Mir7660	1.4	6.3E-02	1.4	1.8E-01	-0.1	8.9E-01	-0.1	9.5E-01
ENSMUST00000183826	ENSMUSG00000098504	1	microRNA 6351	MI0021879	Mir6351	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000183842	ENSMUSG00000098316	1	microRNA 7683	MI0025031	Mir7683	1.6	2.3E-02	1.1	1.8E-01	-0.1	8.7E-01	0.4	6.4E-01
ENSMUST00000183849	ENSMUSG00000098431	8	microRNA 7666	MI0025006	Mir7666	1.9	3.5E-02	0.1	8.9E-01	-0.3	7.2E-01	1.5	1.4E-01
ENSMUST00000183852	ENSMUSG00000098822	5	microRNA 7039	MI0022888	Mir7039	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000183853	ENSMUSG00000098737	3	microRNA 7014	MI0022863	Mir7014	0.8	2.9E-01	-1.4	1.6E-01	-1.7	4.3E-02	0.4	6.2E-01
ENSMUST00000183857	ENSMUSG00000098588	2	microRNA 6340	MI0021868	Mir6340	2.1	5.8E-03	1.9	3.6E-02	-0.1	9.0E-01	0.1	8.6E-01
ENSMUST00000183859	ENSMUSG00000098774	11	microRNA 6930	MI0022777	Mir6930	1.4	8.6E-02	0.7	5.1E-01	-0.2	8.3E-01	0.5	5.8E-01
ENSMUST00000183860	ENSMUSG00000099063	5	microRNA 7031	MI0022880	Mir7031	-1.1	1.7E-01	-1.9	5.8E-02	-0.6	4.6E-01	0.3	7.8E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000183864	ENSMUSG00000098251	9	microRNA 7656	MI0024996	Mir7656	1.6	3.7E-02	1.5	7.5E-02	0.8	2.1E-01	0.9	3.1E-01
ENSMUST00000183866	ENSMUSG00000098764	17	microRNA 7667	MI0025007	Mir7667	-1.5	9.4E-02	0.7	5.1E-01	1.3	1.0E-01	-0.9	3.9E-01
ENSMUST00000183874	ENSMUSG00000098527	15	microRNA 6961	MI0022808	Mir6961	-0.4	7.1E-01	-0.6	6.7E-01	-1.1	2.8E-01	-0.9	5.1E-01
ENSMUST00000183876	ENSMUSG00000098646	9	microRNA 7084	MI0022934	Mir7084	0.3	7.6E-01	1.7	1.4E-01	0.7	4.2E-01	-0.7	5.0E-01
ENSMUST00000183884	ENSMUSG00000099131	8	microRNA 7074	MI0022924	Mir7074	1.6	2.7E-02	0.4	6.7E-01	-0.8	2.7E-01	0.4	6.5E-01
ENSMUST00000183891	ENSMUSG00000098531	6	microRNA 7041	MI0022890	Mir7041	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000183892	ENSMUSG00000099196	18	microRNA 1258	MI0025040	Mir1258	-0.5	5.3E-01	-0.7	5.0E-01	0.4	6.2E-01	0.6	4.7E-01
ENSMUST00000183900	ENSMUSG00000099199	3	microRNA 7012	MI0022861	Mir7012	-0.1	9.5E-01	-2.8	2.0E-02	-1.2	1.6E-01	1.5	2.1E-01
ENSMUST00000183903	ENSMUSG00000098703	5	predicted gene, 27527		Gm27527	3.1	9.2E-05	2.0	2.2E-02	-0.4	5.8E-01	0.7	3.6E-01
ENSMUST00000183910	ENSMUSG00000099110	15	microRNA 6951	MI0022798	Mir6951	1.2	2.8E-01	-0.4	7.8E-01	-1.2	3.2E-01	0.4	7.4E-01
ENSMUST00000183919	ENSMUSG00000098980	4	microRNA 6397	MI0021933	Mir6397	1.4	5.0E-02	0.2	8.0E-01	-0.9	2.7E-01	0.3	6.9E-01
ENSMUST00000183922	ENSMUSG00000098548	2	microRNA 6996	MI0022844	Mir6996	-1.0	3.2E-01	-1.9	1.2E-01	0.0	9.8E-01	0.9	4.7E-01
ENSMUST00000183927	ENSMUSG00000098706	18	microRNA 6979	MI0022827	Mir6979	-2.1	2.4E-02	-1.2	2.6E-01	1.0	2.2E-01	0.1	9.4E-01
ENSMUST00000183932	ENSMUSG00000099301	5	microRNA 3473e	MI0022357	Mir3473e	3.1	2.0E-03	3.9	8.0E-04	0.7	3.3E-01	-0.1	9.6E-01
ENSMUST00000183945	ENSMUSG00000098769	11	microRNA 8103	MI0026033	Mir8103	0.0	9.9E-01	1.1	2.2E-01	1.2	9.9E-02	0.1	9.1E-01
ENSMUST00000183950	ENSMUSG00000098714	10	microRNA 7663	MI0025003	Mir7663	1.1	1.8E-01	0.7	5.0E-01	-0.2	8.0E-01	0.2	8.6E-01
ENSMUST00000183953	ENSMUSG00000099088	10	predicted gene, 27920		Gm27920	1.1	2.1E-01	-0.7	5.4E-01	0.1	9.4E-01	1.9	1.1E-01
ENSMUST00000183962	ENSMUSG00000098310	4	microRNA 8118	MI0026050	Mir8118	0.7	3.7E-01	0.3	7.6E-01	-1.1	1.4E-01	-0.7	4.7E-01
ENSMUST00000183965	ENSMUSG00000098704	11	microRNA 6934	MI0022781	Mir6934	1.6	2.7E-02	0.4	6.7E-01	-0.8	2.7E-01	0.4	6.5E-01
ENSMUST00000183968	ENSMUSG00000099089	7	predicted gene, 27921		Gm27921	1.6	8.4E-02	1.8	9.8E-02	-0.8	3.7E-01	-1.0	3.4E-01
ENSMUST00000183970	ENSMUSG00000099154	2	predicted gene, 27306		Gm27306	0.5	5.7E-01	0.2	8.2E-01	0.0	9.9E-01	0.2	8.1E-01
ENSMUST00000183975	ENSMUSG00000098329	17	microRNA 6966	MI0022814	Mir6966	2.7	6.5E-03	-1.1	2.9E-01	-2.2	1.8E-02	1.6	1.1E-01
ENSMUST00000183983	ENSMUSG00000098558	7	microRNA 7049	MI0022898	Mir7049	-0.4	6.4E-01	1.8	1.2E-01	1.8	3.5E-02	-0.3	7.7E-01
ENSMUST00000183986	ENSMUSG00000098863	11	microRNA 8101	MI0026031	Mir8101	1.2	1.9E-01	-0.8	4.7E-01	0.1	9.3E-01	2.1	8.4E-02
ENSMUST00000183989	ENSMUSG00000098364	4	predicted gene, 27646		Gm27646	3.0	9.8E-03	-0.3	8.1E-01	-1.7	1.2E-01	1.7	1.8E-01
ENSMUST00000183991	ENSMUSG00000099062	8	microRNA 7077	MI0022927	Mir7077	0.1	9.3E-01	-0.4	7.0E-01	0.1	9.5E-01	0.5	5.7E-01
ENSMUST00000184000	ENSMUSG00000099186	4	predicted gene, 27878		Gm27878	0.8	2.6E-01	0.9	3.4E-01	-0.2	7.3E-01	-0.2	7.8E-01
ENSMUST00000184007	ENSMUSG00000099125	11	predicted gene, 27322		Gm27322	-0.9	2.6E-01	-1.9	8.2E-02	-0.5	4.7E-01	0.5	6.2E-01
ENSMUST00000184011	ENSMUSG00000099245	14	microRNA 8098	MI0026026	Mir8098	-1.8	6.3E-02	-1.1	3.9E-01	-0.4	6.8E-01	-1.1	4.1E-01
ENSMUST00000184024	ENSMUSG00000099275	9	microRNA 8107	MI0026038	Mir8107	1.0	3.2E-01	1.1	3.3E-01	1.4	1.6E-01	1.2	2.7E-01
ENSMUST00000184043	ENSMUSG00000098954	4	microRNA 7658	MI0024998	Mir7658	-1.3	1.4E-01	-1.3	2.6E-01	0.2	7.8E-01	0.2	8.3E-01
ENSMUST00000184044	ENSMUSG00000099330	7	microRNA 7053	MI0022902	Mir7053	-1.0	1.6E-01	-1.7	7.9E-02	-0.5	4.5E-01	0.2	8.5E-01
ENSMUST00000184048	ENSMUSG00000098521	9	microRNA 7243	MI0025043	Mir7243	1.7	1.9E-02	1.2	1.8E-01	-0.1	9.1E-01	0.5	5.6E-01
ENSMUST00000184049	ENSMUSG00000098887	10	microRNA 6413	MI0021950	Mir6413	3.0	6.5E-03	3.4	1.4E-02	0.0	9.7E-01	-0.3	8.0E-01
ENSMUST00000184050	ENSMUSG00000098513	4	microRNA 6399	MI0021935	Mir6399	2.0	5.4E-02	0.1	9.4E-01	-0.5	6.1E-01	1.4	2.1E-01
ENSMUST00000184056	ENSMUSG00000098279	10	microRNA 6908	MI0022755	Mir6908	1.0	2.3E-01	-0.8	4.8E-01	-1.3	1.8E-01	0.5	6.0E-01
ENSMUST00000184064	ENSMUSG00000099160	5	microRNA 6415	MI0021953	Mir6415	1.9	1.3E-02	1.5	1.0E-01	0.1	8.9E-01	0.5	5.4E-01
ENSMUST00000184074	ENSMUSG00000099031	8	microRNA 7240	MI0023735	Mir7240	2.0	4.0E-03	3.0	4.1E-03	-0.1	9.2E-01	-1.0	2.7E-01
ENSMUST00000184075	ENSMUSG00000099226	X	microRNA 7091	MI0022941	Mir7091	-2.5	2.5E-03	-3.5	3.0E-04	0.0	9.7E-01	1.0	2.3E-01
ENSMUST00000184087	ENSMUSG00000099268	16	predicted gene, 27773		Gm27773	1.4	1.5E-02	1.8	1.1E-02	-0.2	7.3E-01	-0.6	3.8E-01
ENSMUST00000184090	ENSMUSG00000098562	10	microRNA 6910	MI0022757	Mir6910	0.6	3.7E-01	0.7	4.4E-01	0.6	4.3E-01	0.5	5.2E-01
ENSMUST00000184096	ENSMUSG00000098560	8	predicted gene, 27530		Gm27530	1.1	1.1E-01	1.5	8.4E-02	0.9	1.9E-01	0.5	5.3E-01
ENSMUST00000184098	ENSMUSG00000098719	15	microRNA 7212	MI0023707	Mir7212	0.5	6.1E-01	0.5	7.4E-01	0.2	8.5E-01	0.3	8.0E-01
ENSMUST00000184108	ENSMUSG00000098271	X	predicted gene, 27828		Gm27828	0.5	6.3E-01	0.4	6.9E-01	1.1	2.4E-01	1.1	3.1E-01
ENSMUST00000184114	ENSMUSG00000098465	8	microRNA 1668	MI0026040	Mir1668	-2.4	3.6E-03	-3.3	1.0E-03	0.1	8.8E-01	1.0	2.7E-01
ENSMUST00000184128	ENSMUSG00000098432	11	predicted gene, 27493		Gm27493	0.7	2.4E-01	1.4	6.5E-02	0.1	9.0E-01	-0.6	3.8E-01
ENSMUST00000184134	ENSMUSG00000099145	5	microRNA 8116	MI0026048	Mir8116	0.4	6.0E-01	-1.4	1.7E-01	-1.3	1.5E-01	0.6	5.4E-01
ENSMUST00000184140	ENSMUSG00000099176	7	microRNA 6238	MI0021585	Mir6238	3.9	1.2E-03	1.5	2.8E-01	-1.6	1.3E-01	0.8	5.5E-01
ENSMUST00000184148	ENSMUSG00000098919	11	microRNA 8102	MI0026032	Mir8102	1.0	2.1E-01	-1.3	1.9E-01	-1.5	8.0E-02	0.8	3.8E-01
ENSMUST00000184150	ENSMUSG00000098441	7	microRNA 6537	MI0022353	Mir6537	1.5	7.5E-02	-2.2	2.5E-02	-2.3	6.9E-03	1.5	1.2E-01
ENSMUST00000184154	ENSMUSG00000098516	11	microRNA 7651	MI0024989	Mir7651	1.0	2.7E-01	1.0	3.5E-01	1.0	2.8E-01	1.0	3.5E-01
ENSMUST00000184156	ENSMUSG00000099311	9	microRNA 6244	MI0021591	Mir6244	1.5	4.3E-02	1.1	2.3E-01	-0.1	8.5E-01	0.3	7.1E-01
ENSMUST00000184158	ENSMUSG00000098759	7	microRNA 7063	MI0022912	Mir7063	-1.5	8.8E-02	-1.9	9.7E-02	-0.6	4.4E-01	-0.2	8.7E-01
ENSMUST00000184167	ENSMUSG00000099210	7	microRNA 7051	MI0022900	Mir7051	0.3	7.7E-01	-0.5	6.5E-01	-0.1	8.8E-01	0.6	5.4E-01
ENSMUST00000184168	ENSMUSG00000098903	5	predicted gene, 28022		Gm28022	1.6	3.4E-02	1.0	2.5E-01	-0.1	9.1E-01	0.5	5.6E-01
ENSMUST00000184173	ENSMUSG00000098263	12	microRNA 6938	MI0022785	Mir6938	0.7	3.2E-01	-0.5	5.5E-01	-0.4	6.5E-01	0.9	2.7E-01
ENSMUST00000184187	ENSMUSG00000098671	8	microRNA 7075	MI0022925	Mir7075	-1.8	2.1E-02	-0.6	5.8E-01	0.6	3.6E-01	-0.6	5.5E-01
ENSMUST00000184195	ENSMUSG00000099272	X	microRNA 7093	MI0022943	Mir7093	0.0	9.6E-01	0.2	8.5E-01	1.0	2.6E-01	0.7	5.0E-01
ENSMUST00000184197	ENSMUSG00000098624	5	microRNA 7036	MI0022885	Mir7036	1.4	7.5E-02	-0.4	6.7E-01	-1.3	1.3E-01	0.5	5.7E-01
ENSMUST00000184202	ENSMUSG00000098299	2	microRNA 7224	MI0023719	Mir7224	1.3	1.0E-01	2.7	2.4E-02	0.7	3.5E-01	-0.7	5.2E-01
ENSMUST00000184207	ENSMUSG00000098663	15	microRNA 6958	MI0022805	Mir6958	-0.4	5.6E-01	-0.8	3.9E-01	0.2	7.6E-01	0.6	4.3E-01
ENSMUST00000184212	ENSMUSG00000098414	10	microRNA 6909	MI0022756	Mir6909	2.0	1.0E-02	0.1	9.4E-01	-1.4	8.9E-02	0.5	6.0E-01
ENSMUST00000184213	ENSMUSG00000098307	3	predicted gene, 27460		Gm27460	2.9	1.1E-03	1.5	8.6E-02	0.0	9.5E-01	1.3	1.5E-01
ENSMUST00000184215	ENSMUSG00000098798	8	predicted gene, 27288		Gm27288	1.2	1.3E-01	-0.3	7.6E-01	-0.9	3.1E-01	0.6	4.7E-01
ENSMUST00000184218	ENSMUSG00000098467	2	predicted gene, 27591		Gm27591	1.4	5.6E-02	2.0	2.9E-02	0.6	3.3E-01	0.1	9.4E-01
ENSMUST00000184219	ENSMUSG00000098334	6	microRNA 7043	MI0022892	Mir7043	-1.4	8.0E-02	-2.5	2.1E-02	-1.0	1.1E-01	0.0	9.9E-01
ENSMUST00000184224	ENSMUSG00000098716	17	predicted gene, 28033		Gm28033	0.2	7.8E-01	-0.6	5.0E-01	0.0	9.9E-01	0.8	3.8E-01
ENSMUST00000184226	ENSMUSG00000098826	17	microRNA 7677	MI0025022	Mir7677	2.3	1.1E-02	0.7	5.3E-01	-1.1	2.2E-01	0.4	6.6E-01
ENSMUST00000184228	ENSMUSG00000099181	10	microRNA 6905	MI0022752	Mir6905	0.5	5.0E-01	1.7	5.3E-02	2.1	3.3E-03	0.9	2.6E-01
ENSMUST00000184230	ENSMUSG00000098942	11	microRNA 8100	MI0026029	Mir8100	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01
ENSMUST00000184232	ENSMUSG00000098756	10	microRNA 378d	MI0021951	Mir378d	-0.6	4.9E-01	-1.8	8.2E-02	-0.7	4.2E-01	0.5	5.4E-01
ENSMUST00000184238	ENSMUSG00000098498	3	microRNA 8099-2	MI0026027	Mir8099-2	1.0	2.3E-01	0.0	9.8E-01	-0.6	5.4E-01	0.4	6.7E-01
ENSMUST00000184241	ENSMUSG00000098672	10	microRNA 6911	MI0022758	Mir6911	-1.5	6.4E-02	-2.1	4.9E-02	-0.7	2.7E-01	-0.1	9.1E-01
ENSMUST00000184242	ENSMUSG00000098899	X	predicted gene, 27839		Gm27839	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000184244	ENSMUSG00000098811	10	microRNA 6913	MI0022760	Mir6913	0.3	6.8E-01	1.2	2.7E-01	0.6	4.4E-01	-0.3	8.1E-01
ENSMUST00000184250	ENSMUSG00000098827	11	predicted gene, 27399		Gm27399	2.9	7.0E-05	3.2	2.4E-04	-0.2	7.8E-01	-0.5	4.8E-01
ENSMUST00000184251	ENSMUSG00000099218	14	microRNA 5124b	MI0021921	Mir5124b	3.1	1.7E-03	0.1	9.2E-01	-0.9	3.2E-01	2.2	3.4E-02
ENSMUST00000184258	ENSMUSG00000098350	5	predicted gene, 27551		Gm27551	-0.6	6.1E-01	0.8	5.8E-01	0.8	4.7E-01	-0.6	6.7E-01
ENSMUST00000184259	ENSMUSG00000099212	5	microRNA 7033	MI0022882	Mir7033	1.0	1.8E-01	0.8	4.2E-01	0.3	7.1E-01	0.6	5.2E-01
ENSMUST00000184262	ENSMUSG00000098879	12	microRNA 7675	MI0025016	Mir7675	0.4	6.6E-01	2.1	8.7E-02	0.6	4.8E-01	-1.1	3.7E-01
ENSMUST00000184275	ENSMUSG00000099109	11	microRNA 7115	MI0022966	Mir7115	-2.3	1.3E-02	-2.8	9.1E-03	0.1	8.5E-01	0.7	4.9E-01
ENSMUST00000184281	ENSMUSG00000098343	5	microRNA 6240	MI0021587	Mir6240	0.0	9.7E-01	-0.1	9.0E-01	-0.2	7.4E-01	-0.1	8.8E-01
ENSMUST00000184284	ENSMUSG00000099134	4	microRNA 7018	MI0022867	Mir7018	2.0	4.2E-03	1.3	1.6E-01	-0.8	2.5E-01	-0.1	9.2E-01
ENSMUST00000184285	ENSMUSG00000098733	16	predicted gene, 27833		Gm27833	1.7	3.3E-02	1.4	1.5E-01	-0.1	9.2E-01	0.3	7.3E-01
ENSMUST00000184293	ENSMUSG00000098608	18	microRNA 6981	MI0022829	Mir6981	-0.3	7.2E-01	-0.1	9.3E-01	0.3	7.3E-01	0.1	9.3E-01
ENSMUST00000184300	ENSMUSG00000099096	13	microRNA 6945	MI0022792	Mir6945	-2.4	2.1E-03	-2.3	1.3E-02	0.3	6.0E-01	0.3	6.9E-01
ENSMUST00000184308	ENSMUSG00000098422	4	microRNA 7016	MI0022865	Mir7016	1.1	1.1E-01	1.5	8.4E-02	0.9	1.9E-01	0.5	5.3E-01
ENSMUST00000184313	ENSMUSG00000098453	2	microRNA 6997	MI0022845	Mir6997	-0.3	7.3E-01	-1.7	8.5E-02	-1.2	1.5E-01	0.2	8.0E-01
ENSMUST00000184329	ENSMUSG00000098448	16	microRNA 6362	MI0021891	Mir6362	2.1	8.0E-03	1.6	8.7E-02	-0.1	9.2E-01	0.5	6.0E-01
ENSMUST00000184334	ENSMUSG00000099011	3	microRNA 6380	MI0021911	Mir6380	0.4	6.5E-01	-1.0	3.4E-01	-1.2	2.2E-01	0.2	8.1E-01
ENSMUST00000184338	ENSMUSG00000098928	19	microRNA 6988	MI0022836	Mir6988	-2.0	3.0E-02	-1.4	2.0E-01	0.2	8.0E-01	-0.4	6.9E-01
ENSMUST00000184349	ENSMUSG00000098751	14	microRNA 7672	MI0025012	Mir7672	-1.4	1.9E-01	-0.8	5.6E-01	0.3	8.0E-01	-0.3	8.3E-01
ENSMUST00000184353	ENSMUSG00000099309	9	microRNA 7085	MI0022935	Mir7085	-0.4	6.4E-01	0.4	7.0E-01	1.5	1.5E-01	0.6	5.7E-01
ENSMUST00000184357	ENSMUSG00000098820	12	predicted gene, 27284		Gm27284	2.0	4.8E-03	2.5	3.6E-03	0.1	9.0E-01	-0.4	5.5E-01
ENSMUST00000184358	ENSMUSG00000099101	11	microRNA 7653	MI0024993	Mir7653	-0.5	4.8E-01	-1.7	6.0E-02	-1.2	1.5E-01	0.1	9.1E-01
ENSMUST00000184365	ENSMUSG00000098992	11	predicted gene, 27597		Gm27597	1.2	1.3E-01	-0.3	7.6E-01	-0.9	3.1E-01	0.6	4.7E-01
ENSMUST00000184367	ENSMUSG00000098472	16	predicted gene, 27887		Gm27887	1.9	2.8E-02	1.8	9.6E-02	0.5	5.6E-01	0.6	5.5E-01
ENSMUST00000184374	ENSMUSG00000098473	9	microRNA 7083	MI0022933	Mir7083	2.0	5.6E-03	-0.7	4.2E-01	-2.2	6.2E-03	0.5	5.6E-01
ENSMUST00000184381	ENSMUSG00000099006	17	microRNA 6974	MI0022822	Mir6974	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000184382	ENSMUSG00000098623	6	microRNA 8112	MI0026044	Mir8112	-2.6	4.6E-03	-3.3	2.9E-03	-0.2	7.1E-01	0.5	6.3E-01
ENSMUST00000184384	ENSMUSG00000099284	5	microRNA 7026	MI0022875	Mir7026	1.8	9.6E-02	3.2	2.7E-02	0.9	3.8E-01	-0.4	7.4E-01
ENSMUST00000184398	ENSMUSG00000098890	3	microRNA 7008	MI0022857	Mir7008	0.4	5.7E-01	0.9	3.5E-01	1.0	2.0E-01	0.6	5.1E-01
ENSMUST00000184412	ENSMUSG00000098710	8	microRNA 7067	MI0022916	Mir7067	-0.5	5.0E-01	-1.3	2.4E-01	-0.1	8.9E-01	0.6	5.2E-01
ENSMUST00000184414	ENSMUSG00000098574	5	microRNA 7037	MI0022886	Mir7037	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000184417	ENSMUSG00000098336	12	microRNA 6388	MI0021920	Mir6388	2.4	1.2E-03	1.5	7.0E-02	-0.1	8.9E-01	0.8	3.2E-01
ENSMUST00000184426	ENSMUSG00000098416	15	microRNA 7117	MI0022968	Mir7117	1.1	1.1E-01	-1.2	1.5E-01	-1.9	1.2E-02	0.4	5.7E-01
ENSMUST00000184427	ENSMUSG00000099169	3	microRNA 7j	MI0021908	Mir7j	-0.1	9.5E-01	0.1	9.2E-01	0.4	6.2E-01	0.2	8.1E-01
ENSMUST00000184433	ENSMUSG00000098359	6	microRNA 7649	MI0024987	Mir7649	-1.8	4.8E-02	-1.1	3.2E-01	0.5	5.6E-01	-0.2	8.6E-01
ENSMUST00000184435	ENSMUSG00000098981	11	microRNA 7236	MI0023731	Mir7236	0.3	6.8E-01	1.6	5.6E-02	1.9	6.2E-03	0.6	4.8E-01
ENSMUST00000184437	ENSMUSG00000098973	9	microRNA 6236	MI0021583	Mir6236	0.7	4.5E-01	0.6	6.0E-01	0.2	7.8E-01	0.3	7.6E-01
ENSMUST00000184453	ENSMUSG00000099066	17	microRNA 6978	MI0022826	Mir6978	-0.9	3.7E-01	-2.3	8.2E-02	-0.8	3.3E-01	0.6	6.8E-01
ENSMUST00000184456	ENSMUSG00000099283	10	microRNA 6912	MI0022759	Mir6912	1.5	7.7E-02	1.0	3.5E-01	0.0	1.0E+00	0.5	6.2E-01
ENSMUST00000184460	ENSMUSG00000099119	1	microRNA 6546	MI0024983	Mir6546	-2.9	4.8E-03	-3.2	1.1E-02	1.2	1.2E-01	1.5	2.1E-01
ENSMUST00000184463	ENSMUSG00000098823	8	microRNA 8111	MI0026043	Mir8111	-1.3	1.3E-01	-1.2	2.6E-01	-0.7	3.2E-01	-0.9	4.1E-01
ENSMUST00000184464	ENSMUSG00000098790	13	microRNA 6942	MI0022789	Mir6942	-1.0	2.1E-01	-2.1	4.4E-02	-0.6	4.9E-01	0.5	5.6E-01
ENSMUST00000184465	ENSMUSG00000098700	15	predicted gene, 27525		Gm27525	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000184472	ENSMUSG00000099293	16	microRNA 6366	MI0021895	Mir6366	2.0	3.2E-03	1.9	2.1E-02	-0.1	9.0E-01	0.0	9.7E-01
ENSMUST00000184474	ENSMUSG00000098460	17	microRNA 6970	MI0022818	Mir6970	-0.7	3.5E-01	0.5	6.4E-01	0.7	3.8E-01	-0.5	6.2E-01
ENSMUST00000184477	ENSMUSG00000098522	10	microRNA 6412	MI0021949	Mir6412	1.7	2.2E-02	0.4	6.5E-01	-0.8	3.1E-01	0.5	5.7E-01
ENSMUST00000184478	ENSMUSG00000099036	14	microRNA 378c	MI0021923	Mir378c	-1.9	3.4E-02	-1.2	2.8E-01	1.3	9.6E-02	0.6	5.9E-01
ENSMUST00000184483	ENSMUSG00000098346	19	microRNA 6986	MI0022834	Mir6986	1.1	3.0E-01	1.5	2.7E-01	1.5	1.3E-01	1.1	3.9E-01
ENSMUST00000184484	ENSMUSG00000098577	4	predicted gene, 27445		Gm27445	6.8	2.7E-09	4.9	6.4E-06	-1.5	5.5E-02	0.4	5.5E-01
ENSMUST00000184490	ENSMUSG00000099147	9	microRNA 7081	MI0022931	Mir7081	-1.7	2.2E-02	-0.7	4.8E-01	1.8	2.5E-02	0.7	4.1E-01
ENSMUST00000184494	ENSMUSG00000098881	11	microRNA 6927	MI0022774	Mir6927	1.7	2.0E-02	0.2	8.6E-01	-1.2	1.5E-01	0.4	6.5E-01
ENSMUST00000184495	ENSMUSG00000099141	1	microRNA 6352	MI0021880	Mir6352	2.9	1.1E-03	1.5	8.6E-02	0.0	9.5E-01	1.3	1.5E-01
ENSMUST00000184508	ENSMUSG00000098253	18	microRNA 7219	MI0023714	Mir7219	-1.1	1.7E-01	-1.8	8.6E-02	-0.1	8.5E-01	0.5	5.8E-01
ENSMUST00000184513	ENSMUSG00000099155	2	predicted gene, 27805		Gm27805	2.1	1.5E-02	4.9	1.7E-05	3.5	3.3E-05	0.6	4.9E-01
ENSMUST00000184514	ENSMUSG00000099292	10	microRNA 6916	MI0022763	Mir6916	-0.8	2.6E-01	-1.1	2.6E-01	-0.3	6.5E-01	-0.1	9.5E-01
ENSMUST00000184519	ENSMUSG00000098808	3	microRNA 7009	MI0022858	Mir7009	0.9	3.0E-01	1.1	4.0E-01	-0.3	7.3E-01	-0.5	6.6E-01
ENSMUST00000184520	ENSMUSG00000098922	9	microRNA 8106	MI0026037	Mir8106	-1.1	2.5E-01	-0.8	5.3E-01	-0.3	7.4E-01	-0.6	6.4E-01
ENSMUST00000184522	ENSMUSG00000098490	9	microRNA 7089	MI0022939	Mir7089	-0.3	7.1E-01	-2.3	2.6E-02	-0.4	5.6E-01	1.6	1.3E-01
ENSMUST00000184524	ENSMUSG00000098464	2	microRNA 7002	MI0022850	Mir7002	0.5	5.4E-01	-0.7	4.5E-01	-0.7	4.3E-01	0.5	5.3E-01
ENSMUST00000184526	ENSMUSG00000098634	1	microRNA 8096	MI0026024	Mir8096	-0.8	3.0E-01	1.8	9.5E-02	0.9	2.8E-01	-1.7	9.1E-02
ENSMUST00000184529	ENSMUSG00000098983	16	predicted gene, 28003		Gm28003	2.3	8.2E-03	1.1	2.5E-01	-1.2	1.2E-01	-0.1	9.1E-01
ENSMUST00000184541	ENSMUSG00000099005	4	microRNA 6398	MI0021934	Mir6398	1.3	1.2E-01	0.3	7.8E-01	-0.6	5.0E-01	0.4	6.9E-01
ENSMUST00000184542	ENSMUSG00000098511	8	microRNA 7072	MI0022922	Mir7072	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000184547	ENSMUSG00000098259	1	predicted gene, 27616		Gm27616	0.1	9.1E-01	0.5	6.2E-01	1.0	2.4E-01	0.6	4.9E-01
ENSMUST00000184549	ENSMUSG00000098276	18	microRNA 6358	MI0021886	Mir6358	1.7	8.1E-02	-0.8	4.9E-01	-1.8	7.0E-02	0.8	5.0E-01
ENSMUST00000184553	ENSMUSG00000098593	7	microRNA 7064	MI0022913	Mir7064	0.4	6.8E-01	2.4	7.3E-02	1.5	1.2E-01	-0.5	7.0E-01
ENSMUST00000184558	ENSMUSG00000098694	14	predicted gene, 27506		Gm27506	2.1	1.3E-02	0.8	4.4E-01	-0.8	3.5E-01	0.5	6.4E-01
ENSMUST00000184562	ENSMUSG00000098317	11	microRNA 6926	MI0022773	Mir6926	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000184567	ENSMUSG00000099072	X	microRNA 7673	MI0025013	Mir7673	1.0	2.9E-01	1.0	3.3E-01	0.7	4.7E-01	0.6	5.3E-01
ENSMUST00000184583	ENSMUSG00000098481	13	predicted gene, 27387		Gm27387	-0.4	5.9E-01	-0.5	6.2E-01	0.5	5.2E-01	0.5	6.0E-01
ENSMUST00000184584	ENSMUSG00000098952	19	microRNA 6405	MI0021941	Mir6405	1.6	2.0E-02	1.2	1.4E-01	0.0	9.4E-01	0.4	6.5E-01
ENSMUST00000184585	ENSMUSG00000098883	1	predicted gene, 27430		Gm27430	1.3	7.6E-02	1.8	7.1E-02	-0.2	7.9E-01	-0.7	4.6E-01
ENSMUST00000184593	ENSMUSG00000098618	12	predicted gene, 27299		Gm27299	1.8	2.1E-02	2.3	1.4E-02	0.2	7.6E-01	-0.3	6.8E-01
ENSMUST00000184595	ENSMUSG00000099258	7	microRNA 7047	MI0022896	Mir7047	1.3	1.5E-01	1.3	2.6E-01	-0.5	5.6E-01	-0.5	6.6E-01
ENSMUST00000184596	ENSMUSG00000098494	6	predicted gene, 27690		Gm27690	2.3	2.5E-03	2.5	6.3E-03	-0.2	7.3E-01	-0.4	6.2E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000184599	ENSMUSG00000099153	11	microRNA 7671	MI0025011	Mir7671	-1.3	1.0E-01	-1.0	3.6E-01	-0.5	4.7E-01	-0.9	4.0E-01
ENSMUST00000184606	ENSMUSG00000099105	3	microRNA 7007	MI0022856	Mir7007	-1.1	1.5E-01	0.5	6.3E-01	2.0	3.2E-02	0.4	6.8E-01
ENSMUST00000184607	ENSMUSG00000099091	2	microRNA 7003	MI0022852	Mir7003	1.6	5.0E-02	1.5	1.0E-01	0.7	3.4E-01	0.7	4.1E-01
ENSMUST00000184608	ENSMUSG00000098410	8	microRNA 1957b	MI0021929	Mir1957b	2.0	6.0E-03	1.2	1.6E-01	-0.1	8.3E-01	0.7	3.8E-01
ENSMUST00000184614	ENSMUSG00000098476	8	predicted gene, 27852		Gm27852	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000184617	ENSMUSG00000098918	3	microRNA 6481	MI0022051	Mir6481	0.8	5.0E-01	-0.9	4.9E-01	1.1	3.0E-01	2.8	3.9E-02
ENSMUST00000184622	ENSMUSG00000098357	12	microRNA 7094-2	MI0022945	Mir7094-2	2.1	2.9E-03	1.6	6.0E-02	-0.1	8.5E-01	0.4	5.9E-01
ENSMUST00000184632	ENSMUSG00000098325	7	microRNA 7048	MI0022897	Mir7048	-0.2	8.6E-01	-1.5	1.8E-01	0.4	6.3E-01	1.7	1.4E-01
ENSMUST00000184636	ENSMUSG00000098783	7	microRNA 7050	MI0022899	Mir7050	0.3	6.8E-01	0.0	9.7E-01	0.3	7.4E-01	0.6	5.3E-01
ENSMUST00000184637	ENSMUSG00000099017	7	microRNA 7058	MI0022907	Mir7058	2.0	7.8E-03	0.6	5.2E-01	-0.9	2.4E-01	0.5	5.7E-01
ENSMUST00000184641	ENSMUSG00000099290	19	microRNA 6985	MI0022833	Mir6985	-0.9	3.2E-01	-2.4	2.6E-02	0.1	8.8E-01	1.6	1.2E-01
ENSMUST00000184667	ENSMUSG00000098636	15	predicted gene, 27742		Gm27742	1.6	2.3E-02	1.1	1.8E-01	-0.1	8.7E-01	0.4	6.4E-01
ENSMUST00000184681	ENSMUSG00000099320	2	microRNA 7664	MI0025004	Mir7664	1.2	1.4E-01	0.4	7.2E-01	-0.6	5.0E-01	0.2	8.2E-01
ENSMUST00000184682	ENSMUSG00000099197	5	microRNA 7034	MI0022883	Mir7034	1.3	1.4E-01	-1.0	3.5E-01	-1.8	6.0E-02	0.5	6.1E-01
ENSMUST00000184685	ENSMUSG00000098353	7	microRNA 7057	MI0022906	Mir7057	-1.2	7.9E-02	-0.5	6.1E-01	0.9	2.4E-01	0.2	8.4E-01
ENSMUST00000184696	ENSMUSG00000099042	8	microRNA 7066	MI0022915	Mir7066	1.4	7.2E-02	1.0	2.7E-01	-0.1	8.5E-01	0.3	7.5E-01
ENSMUST00000184697	ENSMUSG00000098550	8	microRNA 7079	MI0022929	Mir7079	0.6	3.5E-01	1.6	6.1E-02	1.5	2.7E-02	0.5	4.9E-01
ENSMUST00000184699	ENSMUSG00000099140	8	microRNA 7237	MI0023732	Mir7237	-0.4	6.0E-01	-0.1	9.4E-01	0.5	5.8E-01	0.1	8.7E-01
ENSMUST00000184709	ENSMUSG00000098365	14	predicted gene, 27647		Gm27647	1.4	5.7E-02	1.7	5.5E-02	-0.1	9.2E-01	-0.4	6.2E-01
ENSMUST00000184711	ENSMUSG00000098338	12	microRNA 6941	MI0022788	Mir6941	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000184712	ENSMUSG00000098589	9	predicted gene, 27353		Gm27353	0.8	3.0E-01	1.1	2.4E-01	0.8	2.7E-01	0.5	5.4E-01
ENSMUST00000184713	ENSMUSG00000099003	5	microRNA 7035	MI0022884	Mir7035	-0.7	3.6E-01	-0.3	7.8E-01	-0.1	8.6E-01	-0.5	6.2E-01
ENSMUST00000184718	ENSMUSG00000098957	10	microRNA 8105	MI0026035	Mir8105	0.5	4.7E-01	-0.6	5.0E-01	-0.1	9.0E-01	1.1	2.7E-01
ENSMUST00000184721	ENSMUSG00000099285	3	predicted gene, 27989		Gm27989	1.6	4.0E-02	0.4	6.8E-01	-0.9	2.6E-01	0.3	7.5E-01
ENSMUST00000184722	ENSMUSG00000098280	8	microRNA 7687	MI0025039	Mir7687	-1.6	2.5E-02	-0.7	5.0E-01	-0.2	7.7E-01	-1.2	2.4E-01
ENSMUST00000184727	ENSMUSG00000098402	8	predicted gene, 27409		Gm27409	1.4	9.3E-02	1.0	3.3E-01	0.3	7.5E-01	0.6	5.2E-01
ENSMUST00000184733	ENSMUSG00000099123	17	microRNA 6965	MI0022812	Mir6965	-0.5	5.4E-01	-1.7	1.0E-01	-1.1	2.2E-01	0.1	8.9E-01
ENSMUST00000184739	ENSMUSG00000098510	17	microRNA 6968	MI0022816	Mir6968	-1.4	7.5E-02	-2.3	2.6E-02	-0.2	7.7E-01	0.7	4.6E-01
ENSMUST00000184745	ENSMUSG00000098625	15	microRNA 6953	MI0022800	Mir6953	-3.1	9.7E-04	-4.4	2.4E-04	-0.4	6.0E-01	0.9	3.8E-01
ENSMUST00000184761	ENSMUSG00000099185	10	microRNA 7662	MI0025002	Mir7662	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000184765	ENSMUSG00000098331	8	microRNA 7069	MI0022919	Mir7069	-0.4	5.7E-01	-1.5	1.1E-01	-0.9	2.5E-01	0.2	8.3E-01
ENSMUST00000184769	ENSMUSG00000099238	2	microRNA 7001	MI0022849	Mir7001	1.6	2.7E-02	0.4	6.7E-01	-0.8	2.7E-01	0.4	6.5E-01
ENSMUST00000184773	ENSMUSG00000099124	5	microRNA 8117	MI0026049	Mir8117	2.5	7.1E-03	0.0	1.0E+00	-1.9	4.7E-02	0.6	5.6E-01
ENSMUST00000184774	ENSMUSG00000098445	17	microRNA 6972	MI0022820	Mir6972	2.0	7.8E-03	0.6	5.2E-01	-0.9	2.4E-01	0.5	5.7E-01
ENSMUST00000184777	ENSMUSG00000099047	5	microRNA 7029	MI0022878	Mir7029	0.2	8.0E-01	0.4	7.4E-01	0.7	4.2E-01	0.6	5.2E-01
ENSMUST00000184784	ENSMUSG00000099161	2	microRNA 6419	MI0021957	Mir6419	1.4	7.1E-02	1.5	9.5E-02	0.7	3.3E-01	0.5	5.6E-01
ENSMUST00000184785	ENSMUSG00000098770	19	predicted gene, 27440		Gm27440	0.6	4.6E-01	1.1	2.8E-01	1.1	2.0E-01	0.6	5.3E-01
ENSMUST00000184789	ENSMUSG00000098568	19	microRNA 6987	MI0022835	Mir6987	0.8	3.8E-01	0.5	7.0E-01	0.2	8.6E-01	0.5	6.3E-01
ENSMUST00000184790	ENSMUSG00000098752	1	microRNA 6897	MI0022744	Mir6897	1.3	1.5E-01	2.2	8.4E-02	0.1	8.7E-01	-0.8	5.0E-01
ENSMUST00000184791	ENSMUSG00000099082	5	microRNA 7036b	MI0024991	Mir7036b	0.0	9.7E-01	-1.1	3.0E-01	0.4	5.4E-01	1.6	1.5E-01
ENSMUST00000184793	ENSMUSG00000098976	8	microRNA 6769b	MI0022917	Mir6769b	0.6	3.7E-01	0.7	4.4E-01	0.6	4.3E-01	0.5	5.2E-01
ENSMUST00000184798	ENSMUSG00000098487	1	microRNA 6899	MI0022746	Mir6899	-1.3	9.8E-02	-1.5	1.3E-01	0.6	3.0E-01	0.8	4.2E-01
ENSMUST00000184812	ENSMUSG00000099230	19	microRNA 6989	MI0022837	Mir6989	-1.0	2.0E-01	-1.8	9.8E-02	0.5	3.8E-01	1.3	2.5E-01
ENSMUST00000184821	ENSMUSG00000098661	7	microRNA 7052	MI0022901	Mir7052	-0.9	1.7E-01	-1.5	1.3E-01	-1.8	1.2E-02	-1.2	2.1E-01
ENSMUST00000184825	ENSMUSG00000098540	7	microRNA 7059	MI0022908	Mir7059	-1.8	6.3E-02	-1.5	1.9E-01	0.3	6.9E-01	0.0	9.8E-01
ENSMUST00000184827	ENSMUSG00000098442	15	microRNA 6959	MI0022806	Mir6959	2.2	2.1E-02	1.0	4.5E-01	-1.4	1.8E-01	-0.1	9.3E-01
ENSMUST00000184832	ENSMUSG00000098982	3	predicted gene, 28002		Gm28002	1.3	7.0E-02	0.7	3.7E-01	-0.3	6.6E-01	0.2	7.6E-01
ENSMUST00000184833	ENSMUSG00000098319	5	microRNA 7038	MI0022887	Mir7038	0.3	6.9E-01	-0.4	6.6E-01	-0.4	5.8E-01	0.3	7.6E-01
ENSMUST00000184834	ENSMUSG00000098443	1	microRNA 7681	MI0025029	Mir7681	-0.7	3.9E-01	0.8	5.1E-01	0.8	3.4E-01	-0.6	5.8E-01
ENSMUST00000184836	ENSMUSG00000098864	6	predicted gene, 27703		Gm27703	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000184840	ENSMUSG00000098327	9	microRNA 7087	MI0022937	Mir7087	0.2	8.4E-01	0.1	9.6E-01	1.3	2.0E-01	1.5	2.0E-01
ENSMUST00000184841	ENSMUSG00000098613	11	microRNA 6931	MI0022778	Mir6931	0.1	8.9E-01	0.1	9.2E-01	0.6	5.7E-01	0.6	5.7E-01
ENSMUST00000184844	ENSMUSG00000099204	1	predicted gene, 27943		Gm27943	1.0	2.0E-01	1.5	1.0E-01	1.1	1.3E-01	0.6	5.1E-01
ENSMUST00000184847	ENSMUSG00000099080	8	microRNA 7071	MI0022921	Mir7071	0.2	8.5E-01	-0.6	5.8E-01	-0.2	8.5E-01	0.6	5.4E-01
ENSMUST00000184860	ENSMUSG00000098303	7	predicted gene, 27459		Gm27459	1.4	7.2E-02	0.8	3.8E-01	-0.1	9.0E-01	0.5	5.8E-01
ENSMUST00000184880	ENSMUSG00000098482	16	microRNA 6363	MI0021892	Mir6363	2.7	5.9E-04	2.1	1.5E-02	-0.1	8.4E-01	0.5	5.7E-01
ENSMUST00000184893	ENSMUSG00000098723	14	predicted gene, 27332		Gm27332	2.9	1.1E-02	1.0	4.3E-01	-0.8	4.2E-01	1.1	3.7E-01
ENSMUST00000184894	ENSMUSG00000099202	4	microRNA 7017	MI0022866	Mir7017	1.1	3.6E-01	-1.2	3.8E-01	-0.8	4.5E-01	1.4	2.7E-01
ENSMUST00000184898	ENSMUSG00000098680	1	microRNA 6898	MI0022745	Mir6898	0.8	3.5E-01	1.7	7.5E-02	1.5	5.4E-02	0.5	5.6E-01
ENSMUST00000184911	ENSMUSG00000098594	8	predicted gene, 27628		Gm27628	2.0	3.4E-03	1.8	3.1E-02	-0.1	9.1E-01	0.2	8.3E-01
ENSMUST00000184912	ENSMUSG00000098363	19	microRNA 6993	MI0022841	Mir6993	1.4	1.2E-01	0.6	6.1E-01	-0.3	7.3E-01	0.5	6.4E-01
ENSMUST00000184919	ENSMUSG00000098586	17	predicted gene, 27775	MI0022815	Gm27775	0.4	5.9E-01	-1.2	2.0E-01	0.4	5.1E-01	2.1	4.0E-02
ENSMUST00000184923	ENSMUSG00000099144	5	predicted gene, 27486		Gm27486	1.8	4.1E-02	-1.0	3.4E-01	-0.7	3.4E-01	2.2	5.7E-02
ENSMUST00000184943	ENSMUSG00000098884	5	microRNA 7689	MI0025042	Mir7689	2.4	1.0E-03	1.3	1.4E-01	-0.8	2.2E-01	0.2	7.7E-01
ENSMUST00000184953	ENSMUSG00000098596	4	microRNA 7226	MI0023721	Mir7226	1.9	1.1E-02	-0.1	9.3E-01	-2.8	2.2E-03	-0.7	4.8E-01
ENSMUST00000184956	ENSMUSG00000098856	6	microRNA 8113	MI0026045	Mir8113	2.0	1.1E-02	0.2	8.0E-01	-1.2	1.3E-01	0.5	5.9E-01
ENSMUST00000184960	ENSMUSG00000098339	17	microRNA 6977	MI0022825	Mir6977	1.7	2.4E-02	-0.1	9.4E-01	-1.4	9.7E-02	0.4	6.6E-01
ENSMUST00000184964	ENSMUSG00000099075	2	microRNA 7674	MI0025015	Mir7674	-0.8	2.8E-01	-1.1	3.0E-01	0.1	8.7E-01	0.4	6.9E-01
ENSMUST00000184974	ENSMUSG00000098579	12	microRNA 6937	MI0022784	Mir6937	1.5	7.4E-02	1.6	9.6E-02	0.6	4.1E-01	0.5	6.0E-01
ENSMUST00000184975	ENSMUSG00000098281	15	predicted gene, 27529		Gm27529	1.2	1.3E-01	-0.3	7.6E-01	-0.9	3.1E-01	0.6	4.7E-01
ENSMUST00000184981	ENSMUSG00000098380	12	microRNA 6939	MI0022786	Mir6939	-1.7	2.9E-02	-1.7	1.3E-01	-0.3	6.5E-01	-0.4	7.0E-01
ENSMUST00000184982	ENSMUSG00000098958	11	microRNA 6933	MI0022780	Mir6933	-0.4	6.2E-01	0.6	5.3E-01	0.4	6.0E-01	-0.7	5.1E-01
ENSMUST00000184992	ENSMUSG00000099324	5	microRNA 8115	MI0026047	Mir8115	-0.7	4.0E-01	-1.1	3.0E-01	-0.8	2.5E-01	-0.5	6.3E-01
ENSMUST00000184997	ENSMUSG00000098821	15	predicted gene, 27397		Gm27397	1.3	1.7E-01	1.3	2.1E-01	0.8	3.7E-01	0.8	4.4E-01

						Exo vs. Cell (Infl)		Exo vs. Cell (Conv)		Cell Infl vs. Conv		Exo Infl vs. Conv	
Ensembl_Transcript_ID	Ensembl_Gene_ID	Chromosome	Description	mirBase_accession	mirBase name	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value	limma log2(FC)	limma p-value
ENSMUST00000184998	ENSMUSG00000099142	8	microRNA 8108	MI0026039	Mir8108	-1.8	3.4E-02	-0.7	5.6E-01	0.2	8.1E-01	-0.9	3.9E-01
ENSMUST00000184999	ENSMUSG00000098701	10	microRNA 6914	MI0022761	Mir6914	-1.4	1.3E-01	-1.5	2.1E-01	-0.6	4.0E-01	-0.6	6.4E-01
ENSMUST00000185000	ENSMUSG00000098772	14	predicted gene, 27441		Gm27441	1.6	8.6E-02	2.9	2.1E-02	0.0	9.8E-01	-1.3	2.7E-01
ENSMUST00000185003	ENSMUSG00000098964	17	predicted gene, 27700		Gm27700	1.6	3.8E-02	2.0	5.7E-02	-0.2	7.1E-01	-0.6	5.2E-01
ENSMUST00000185004	ENSMUSG00000098585	X	predicted gene, 27910		Gm27910	4.0	1.8E-04	1.4	1.5E-01	0.0	9.9E-01	2.5	2.0E-02
ENSMUST00000185016	ENSMUSG00000098656	5	microRNA 7028	MI0022877	Mir7028	2.0	8.3E-03	0.3	7.4E-01	-1.2	1.4E-01	0.5	5.8E-01
ENSMUST00000185017	ENSMUSG00000098849	X	predicted gene, 27892		Gm27892	0.6	3.5E-01	1.6	6.1E-02	1.5	2.7E-02	0.5	4.9E-01
ENSMUST00000185035	ENSMUSG00000098944	3	microRNA 8120	MI0026052	Mir8120	1.2	1.6E-01	0.3	7.7E-01	-0.4	6.8E-01	0.5	6.2E-01
ENSMUST00000185038	ENSMUSG00000099092	7	microRNA 7062	MI0022911	Mir7062	0.3	6.7E-01	-2.5	5.7E-03	-0.1	8.3E-01	2.7	4.4E-03
ENSMUST00000185041	ENSMUSG00000098852	10	predicted gene, 27392		Gm27392	-0.1	8.3E-01	0.0	9.6E-01	0.0	9.6E-01	-0.2	8.4E-01
ENSMUST00000185043	ENSMUSG00000098972	2	microRNA 8093	MI0026020	Mir8093	1.5	6.5E-02	1.7	7.7E-02	0.7	3.1E-01	0.5	5.9E-01
ENSMUST00000185044	ENSMUSG00000098497	11	microRNA 6932	MI0022779	Mir6932	-0.1	9.3E-01	-1.7	2.4E-01	-1.2	2.8E-01	0.4	7.8E-01
ENSMUST00000185048	ENSMUSG00000098565	15	predicted gene, 27760		Gm27760	1.2	8.8E-02	0.7	4.3E-01	-0.1	8.3E-01	0.4	6.2E-01
ENSMUST00000185054	ENSMUSG00000098831	4	microRNA 7119	MI0022970	Mir7119	1.5	2.4E-01	-0.7	6.4E-01	-0.7	5.6E-01	1.4	2.9E-01
ENSMUST00000185055	ENSMUSG00000099004	13	predicted gene, 27656		Gm27656	0.8	2.9E-01	1.7	8.2E-02	1.2	1.3E-01	0.3	7.7E-01
ENSMUST00000185062	ENSMUSG00000098997	1	microRNA 6901	MI0022748	Mir6901	1.9	4.8E-02	0.1	9.0E-01	-2.0	2.6E-02	-0.2	8.4E-01
ENSMUST00000185063	ENSMUSG00000098297	18	microRNA 6980	MI0022828	Mir6980	-2.5	8.1E-03	-2.6	4.0E-02	-1.0	2.4E-01	-0.9	4.8E-01
ENSMUST00000185075	ENSMUSG00000098597	5	microRNA 6418	MI0021956	Mir6418	-3.6	2.7E-03	-0.8	5.1E-01	0.5	5.4E-01	-2.2	9.8E-02
ENSMUST00000185076	ENSMUSG00000098489	2	microRNA 7678	MI0025023	Mir7678	0.1	9.4E-01	-2.2	8.1E-02	-2.6	6.3E-03	-0.3	8.0E-01
ENSMUST00000185078	ENSMUSG00000099069	19	microRNA 8090	MI0026017	Mir8090	0.5	5.3E-01	0.0	1.0E+00	0.0	1.0E+00	0.5	5.9E-01
ENSMUST00000185080	ENSMUSG00000098553	7	microRNA 3569	MI0025014	Mir3569	0.2	7.5E-01	-0.9	3.3E-01	0.4	5.8E-01	1.6	9.0E-02
ENSMUST00000185082	ENSMUSG00000098917	8	microRNA 7654	MI0024994	Mir7654	-0.2	8.0E-01	-1.6	9.4E-02	-0.8	3.0E-01	0.6	4.7E-01
ENSMUST00000185089	ENSMUSG00000098735	2	microRNA 7005	MI0022854	Mir7005	2.0	6.4E-03	0.7	4.4E-01	-0.8	2.8E-01	0.5	5.7E-01
ENSMUST00000185092	ENSMUSG00000098451	15	microRNA 6952	MI0022799	Mir6952	-0.7	4.6E-01	-1.1	3.3E-01	-1.1	1.7E-01	-0.7	5.8E-01
ENSMUST00000185093	ENSMUSG00000098580	4	microRNA 7023	MI0022872	Mir7023	-1.3	1.8E-01	-1.0	4.0E-01	0.2	7.9E-01	0.0	9.7E-01
ENSMUST00000185094	ENSMUSG00000098860	13	predicted gene, 27704		Gm27704	4.1	3.3E-04	2.0	1.2E-01	-0.9	3.6E-01	1.3	3.0E-01
ENSMUST00000185099	ENSMUSG00000099259	11	microRNA 6922	MI0022769	Mir6922	-1.2	1.8E-01	-0.2	8.4E-01	1.2	2.5E-01	0.2	8.6E-01
ENSMUST00000185101	ENSMUSG00000098842	1	predicted gene, 27907		Gm27907	1.2	1.3E-01	-0.3	7.6E-01	-0.9	3.1E-01	0.6	4.7E-01
ENSMUST00000185103	ENSMUSG00000099071	16	microRNA 8095	MI0026022	Mir8095	1.8	1.7E-02	1.6	8.1E-02	0.0	9.8E-01	0.2	8.1E-01
ENSMUST00000185105	ENSMUSG00000099261	19	microRNA 6984	MI0022832	Mir6984	0.7	4.8E-01	-0.2	8.5E-01	0.1	9.2E-01	1.0	3.7E-01
ENSMUST00000185108	ENSMUSG00000099303	1	predicted gene, 27458		Gm27458	3.0	2.1E-03	1.4	1.4E-01	0.7	3.5E-01	2.3	2.3E-02
ENSMUST00000185110	ENSMUSG00000098532	8	microRNA 7065	MI0022914	Mir7065	0.7	3.9E-01	0.7	4.9E-01	0.6	4.9E-01	0.6	5.3E-01
ENSMUST00000185123	ENSMUSG00000099213	9	predicted gene, 27686		Gm27686	0.9	2.3E-01	1.3	1.6E-01	0.9	2.0E-01	0.6	5.3E-01
ENSMUST00000185129	ENSMUSG00000098621	17	predicted gene, 27740	MI0022815	Gm27740	0.4	5.9E-01	-1.2	2.0E-01	0.4	5.1E-01	2.1	4.0E-02
ENSMUST00000185136	ENSMUSG00000098638	4	predicted gene, 27743		Gm27743	1.7	3.5E-02	0.2	8.5E-01	0.5	5.1E-01	2.0	5.3E-02
ENSMUST00000185146	ENSMUSG00000098474	11	microRNA 6919	MI0022766	Mir6919	0.2	8.2E-01	0.1	9.2E-01	0.5	5.6E-01	0.6	5.2E-01
ENSMUST00000185149	ENSMUSG00000099095	6	microRNA 6376	MI0021905	Mir6376	1.5	3.2E-02	1.1	1.7E-01	0.0	9.4E-01	0.3	7.0E-01
ENSMUST00000185150	ENSMUSG00000098457	15	microRNA 8097	MI0026025	Mir8097	0.0	9.9E-01	0.5	5.5E-01	0.2	8.2E-01	-0.4	6.7E-01
ENSMUST00000185154	ENSMUSG00000098454	5	microRNA 7032	MI0022881	Mir7032	2.2	6.7E-03	0.7	4.7E-01	-0.8	3.0E-01	0.7	4.5E-01
ENSMUST00000185156	ENSMUSG00000098906	11	microRNA 7652	MI0024992	Mir7652	1.2	2.4E-01	0.8	5.3E-01	0.3	7.8E-01	0.7	5.7E-01
ENSMUST00000185158	ENSMUSG00000098995	11	predicted gene, 27598		Gm27598	2.6	1.9E-03	2.5	1.4E-02	-0.1	8.9E-01	0.0	9.9E-01
ENSMUST00000185165	ENSMUSG00000099225	10	microRNA 8104	MI0026034	Mir8104	-1.3	1.5E-01	-0.5	6.5E-01	1.4	1.4E-01	0.6	5.3E-01
ENSMUST00000185166	ENSMUSG00000098415	11	microRNA 6928	MI0022775	Mir6928	1.5	7.7E-02	-1.2	3.0E-01	-3.1	9.9E-04	-0.4	7.4E-01
ENSMUST00000185186	ENSMUSG00000099058	13	microRNA 6943	MI0022790	Mir6943	-1.5	7.8E-02	-2.7	1.4E-02	-0.4	5.1E-01	0.7	5.0E-01
ENSMUST00000185190	ENSMUSG00000098728	6	predicted gene, 27336		Gm27336	2.6	1.0E-02	1.3	2.1E-01	0.1	8.7E-01	1.5	1.7E-01
ENSMUST00000185192	ENSMUSG00000098993	10	predicted gene, 27731		Gm27731	3.2	3.0E-04	1.4	8.5E-02	-0.1	9.1E-01	1.7	5.9E-02
ENSMUST00000185196	ENSMUSG00000099074	16	predicted gene, 27564		Gm27564	1.6	5.2E-02	0.0	9.6E-01	-1.1	2.0E-01	0.6	5.5E-01

Protein identifications for the comparison Exosome Infl. vs. Exosome Conv.

Protein FDR ≤ 0.86%

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
A0A075B5R8	27	3	3	35.9	0	0	0		27	3	3	0.21	35.9	Protein Ighv11-2 (Fragment)	A0A075B5R8	Ighv11-2	Mus musculus
A0A075B5U4	2	2	2	39.22	1	1	1	18.63	3	2	2	0.86	39.22	Protein Ighv1-18	A0A075B5U4	Ighv1-18	Mus musculus
A0A087WR50	962	64	64	45.39	2302	106	106	60.85	3264	108	108	0	60.94	Fibronectin	A0A087WR50	Fn1	Mus musculus
A0A087WSP5	5	3	3	7.95	14	3	3	7.95	19	3	3	0.21	7.95	Signal transducer and activator of transcription	A0A087WSP5	Stat1	Mus musculus
A0A0B4J1J5	0	0	0		13	2	2	27.35	13	2	2	0.86	27.35	Protein Ighv9-3 (Fragment)	A0A0B4J1J5	Ighv9-3	Mus musculus
A0A0D9SEG8	24	5	5	12.98	40	5	5	11.46	64	7	7	0	16.02	Protein Adgre5	A0A0D9SEG8	Adgre5	Mus musculus
A2AFG7	15	3	3	6.08	7	2	2	3.84	22	3	3	0.21	6.08	Neural cell adhesion molecule L1	A2AFG7	L1cam	Mus musculus
A2AIV8	2	1	1	3.54	6	2	2	5.41	8	2	2	0.86	5.41	Caspase recruitment domain-containing protein 9	A2AIV8	Card9	Mus musculus
A2AN08	1	1	1	0.54	22	7	7	3.11	23	7	7	0	3.11	E3 ubiquitin-protein ligase UBR4	A2AN08	Ubr4	Mus musculus
A2AQ07	51	5	5	20.84	35	4	4	16.19	86	5	5	0	20.84	Tubulin beta-1 chain	A2AQ07	Tubb1	Mus musculus
A2ASS6	2	2	2	0.08	1	1	1	0.04	3	2	2	0.86	0.08	Titin	A2ASS6	Ttn	Mus musculus
A2AUR7	43	5	5	45.77	37	5	5	45.77	80	5	5	0	45.77	Ras suppressor protein 1	A2AUR7	Rsu1	Mus musculus
A6H630	2	1	1	6.38	18	3	3	15.95	20	3	3	0.21	15.95	Protein-glutamate O-methyltransferase	A6H630	Armt1	Mus musculus
A6X935	62	7	7	12	10	3	3	6.58	72	7	7	0	12	Inter alpha-trypsin inhibitor, heavy chain 4	A6X935	Itih4	Mus musculus
A6ZI44	1268	25	14	65.07	1590	28	15	55.5	2858	32	17	0	65.07	Fructose-bisphosphate aldolase	A6ZI44	Aldoa	Mus musculus
A6ZI46	471	13	2	34.61	460	14	1	27.45	931	17	2	0.86	34.61	Fructose-bisphosphate aldolase	A6ZI46	Aldoart1	Mus musculus
A8E0Y8	3	2	2	4.84	0	0	0		3	2	2	0.86	4.84	Immunoglobulin superfamily member 2	A8E0Y8	Cd101	Mus musculus
B1AZI6	0	0	0		4	2	2	2.01	4	2	2	0.86	2.01	THO complex subunit 2	B1AZI6	Thoc2	Mus musculus
B2RPV6	8	2	2	2.48	5	2	2	2.48	13	2	2	0.86	2.48	Multimerin-1	B2RPV6	Mmrn1	Mus musculus
B2RQC6	0	0	0		18	7	7	5.75	18	7	7	0	5.75	CAD protein	B2RQC6	Cad	Mus musculus
B2RV77	17	2	2	26.8	53	3	3	44.33	70	3	3	0.21	44.33	MCG130182, isoform CRA_a	B2RV77	Gm5483	Mus musculus
B2RXR6	6	2	2	3.63	15	3	3	5.54	21	4	4	0.14	7.15	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B	B2RXR6	Ankrd44	Mus musculus
B2RY50	1	1	1	1.74	2	2	2	4.15	3	2	2	0.86	4.15	Armadillo repeat-containing protein 4	B2RY50	Armc4	Mus musculus
B5THE2	45	10	10	9.96	73	9	9	8.65	118	11	11	0	10.51	Maltase-glucoamylase	B5THE2	Mgam	Mus musculus
B9EJ54	0	0	0		2	2	2	2.44	2	2	2	0.86	2.44	MCG21756, isoform CRA_b	B9EJ54	Nup205	Mus musculus
D3YVV0	0	0	0		2	2	2	5.25	2	2	2	0.86	5.25	Protein Ttc13	D3YVV0	Ttc13	Mus musculus
D3Z6Q9	89	8	8	24.74	65	7	7	20.65	154	8	8	0	24.74	Bridging integrator 2	D3Z6Q9	Bin2	Mus musculus
D4AFX7	0	0	0		5	2	2	1.2	5	2	2	0.86	1.2	Protein Dnajc13	D4AFX7	Dnajc13	Mus musculus
E9PUM5	5	2	2	4.7	0	0	0		5	2	2	0.86	4.7	Protein Gm4788	E9PUM5	Gm4788	Mus musculus
E9PV24	168	12	12	24.33	241	18	18	31.94	409	19	19	0	31.94	Fibrinogen alpha chain	E9PV24	Fga	Mus musculus
E9PVA8	0	0	0		3	3	3	1.91	3	3	3	0.21	1.91	Protein Gcn1l1	E9PVA8	Gcn1l1	Mus musculus
E9PX59	0	0	0		3	3	3	3.74	3	3	3	0.21	3.74	Sterile alpha motif domain-containing protein 9-like	E9PX59	Samd9l	Mus musculus
E9PYK3	3	2	2	2.79	2	2	2	1.63	5	4	4	0.14	4.42	Protein Parp4	E9PYK3	Parp4	Mus musculus
E9PZF0	12	3	2	15.36	26	5	2	25.09	38	5	2	0.86	25.09	Nucleoside diphosphate kinase	E9PZF0	Gm20390	Mus musculus
E9Q070	40	6	6	38.17	75	8	8	47.95	115	8	8	0	47.95	Uncharacterized protein	E9Q070	Gm8730	Mus musculus
E9Q0F0	13	2	2	1.31	0	0	0		13	2	2	0.86	1.31	Protein Krt78	E9Q0F0	Krt78	Mus musculus
E9Q0K6	155	16	16	41.47	166	17	17	40.25	321	19	19	0	44.09	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	E9Q0K6	Samhd1	Mus musculus
E9Q0Y4	0	0	0		8	3	3	5.88	8	3	3	0.21	5.88	Signal-induced proliferation-associated protein 1	E9Q0Y4	Sipa1	Mus musculus
E9Q397	869	70	69	42.35	151	26	26	20.12	1020	70	69	0	42.35	Spectrin beta chain, erythrocytic	E9Q397	Sptb	Mus musculus
E9Q586	5	3	3	4.92	18	4	4	6.3	23	5	5	0	8.39	Dynactin subunit 1	E9Q586	Dctn1	Mus musculus
E9Q604	613	31	31	44.8	442	27	27	37.09	1055	32	32	0	44.8	Integrin alpha-M	E9Q604	Itgam	Mus musculus
E9Q6Q4	0	0	0		4	3	3	9.5	4	3	3	0.21	9.5	Protein Rap1gds1	E9Q6Q4	Rap1gds1	Mus musculus
E9Q6U4	13	2	2	20.77	30	2	2	20.77	43	2	2	0.86	20.77	Prefoldin subunit 4	E9Q6U4	Pfdn4	Mus musculus
E9QL65	0	0	0		5	2	2	5.68	5	2	2	0.86	5.68	Conserved oligomeric Golgi complex subunit 3	E9QL65	Cog3	Mus musculus
E9QNN1	38	5	5	5.64	89	11	11	12.28	127	11	11	0	12.28	ATP-dependent RNA helicase A	E9QNN1	Dhx9	Mus musculus
E9QPU1	499	44	44	27.34	440	47	47	29.97	939	52	52	0	32.32	von Willebrand factor	E9QPU1	Vwf	Mus musculus
F6RPJ9	12	4	4	4.86	5	3	3	4.26	17	5	5	0	6.08	Insulin-degrading enzyme (Fragment)	F6RPJ9	Ide	Mus musculus
F6ZDS4	4	2	2	1.48	1	1	1	0.74	5	3	3	0.21	2.22	Nucleoprotein TPR	F6ZDS4	Tpr	Mus musculus
F8VPN4	3	2	2	1.89	10	3	3	3.26	13	3	3	0.21	3.26	Protein Agl	F8VPN4	Agl	Mus musculus
F8WI35	558	17	5	31.11	485	14	3	31.11	1043	18	6	0	31.11	Histone H3	F8WI35	H3f3a	Mus musculus
G3UWD6	146	10	2	15.79	209	12	2	17.54	355	13	2	0.86	17.54	Glucose-6-phosphate 1-dehydrogenase	G3UWD6	G6pd2	Mus musculus
G3X8U3	3	2	2	10.65	30	4	4	22.49	33	4	4	0.14	22.49	MCG6895	G3X8U3	2210016F16Ri	Mus musculus
G3X972	2	2	2	4.74	10	3	3	6.2	12	3	3	0.21	6.2	Protein Sec24c	G3X972	Sec24c	Mus musculus
G5E870	0	0	0		5	2	2	1.93	5	2	2	0.86	1.93	E3 ubiquitin-protein ligase TRIP12	G5E870	Trip12	Mus musculus
G5E8K5	3	2	2	1.43	1	1	1	0.87	4	2	2	0.86	1.43	Ankyrin-3	G5E8K5	Ank3	Mus musculus
O08528	0	0	0		14	4	3	7.31	14	4	3	0.21	7.31	Hexokinase-2	O08528	Hk2	Mus musculus
O08553	3	2	2	7.34	15	3	3	10.14	18	3	3	0.21	10.14	Dihydropyrimidinase-related protein 2	O08553	Dpysl2	Mus musculus
O08582	6	2	2	5.54	23	2	2	5.54	29	2	2	0.86	5.54	GTP-binding protein 1	O08582	Gtpbp1	Mus musculus
O08583	24	3	3	21.96	35	4	4	21.96	59	4	4	0.14	21.96	THO complex subunit 4	O08583	Alyref	Mus musculus
O08585	17	1	1	8.94	19	2	2	13.62	36	2	2	0.86	13.62	Clathrin light chain A	O08585	Clta	Mus musculus
O08663	17	2	2	7.53	43	6	6	25.94	60	6	6	0	25.94	Methionine aminopeptidase 2	O08663	Metap2	Mus musculus
O08691	1	1	1	6.78	8	3	3	14.97	9	3	3	0.21	14.97	Arginase-2, mitochondrial	O08691	Arg2	Mus musculus
O08692	807	17	17	56.89	1193	17	17	49.7	2000	20	20	0	57.49	Neutrophilic granule protein	O08692	Ngp	Mus musculus
O08709	104	7	7	48.66	109	8	8	49.55	213	8	8	0	49.55	Peroxiredoxin-6	O08709	Prdx6	Mus musculus
O08738	1	1	1	3.99	26	5	5	19.57	27	5	5	0	19.57	Caspase-6	O08738	Casp6	Mus musculus
O08749	56	8	8	25.74	88	8	8	26.13	144	9	9	0	28.68	Dihydrolipoyl dehydrogenase, mitochondrial	O08749	Dld	Mus musculus
O08795	9	2	2	12.48	11	1	1	4.99	20	2	2	0.86	12.48	Glucosidase 2 subunit beta	O08795	Prkcsh	Mus musculus
O08808	59	8	8	10.84	56	7	7	10.84	115	10	10	0	12.83	Protein diaphanous homolog 1	O08808	Diaph1	Mus musculus
O08810	43	8	8	13.9	119	13	13	22.66	162	14	14	0	24	116 kDa U5 small nuclear ribonucleoprotein component	O08810	Eftud2	Mus musculus
O08917	0	0	0		4	2	2	7.24	4	2	2	0.86	7.24	Flotillin-1	O08917	Flot1	Mus musculus
O08992	86	6	6	37.79	165	9	9	48.49	251	10	10	0	49.5	Syntenin-1	O08992	Sdcbp	Mus musculus
O09043	27	3	3	15.51	52	5	5	22.2	79	5	5	0	22.2	Napsin-A	O09043	Napsa	Mus musculus
O09061	140	11	11	49.17	95	9	9	34.17	235	11	11	0	49.17	Proteasome subunit beta type-1	O09061	Psmb1	Mus musculus
O09106	4	1	1	6.22	16	4	4	15.77	20	4	4	0.14	15.77	Histone deacetylase 1	O09106	Hdac1	Mus musculus
O09110	0	0	0		7	2	2	12.39	7	2	2	0.86	12.39	Dual specificity mitogen-activated protein kinase kinase 3	O09110	Map2k3	Mus musculus
O09126	10	2	2	4.99	5	2	2	4.99	15	2	2	0.86	4.99	Semaphorin-4D	O09126	Sema4d	Mus musculus
O09131	0	0	0		17	4	4	26.67	17	4	4	0.14	26.67	Glutathione S-transferase omega-1	O09131	Gsto1	Mus musculus
O09159	116	12	12	17.28	102	8	8	14.22	218	12	12	0	17.28	Lysosomal alpha-mannosidase	O09159	Man2b1	Mus musculus
O09172	24	2	2	11.31	32	4	4	28.1	56	4	4	0.14	28.1	Glutamate--cysteine ligase regulatory subunit	O09172	Gclm	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
O35218	0	0	0		2	2	2	3.32	2	2	2	0.86	3.32	Cleavage and polyadenylation specificity factor subunit 2	O35218	Cpsf2	Mus musculus
O35286	5	1	1	2.39	37	7	7	12.08	42	7	7	0	12.08	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	O35286	Dhx15	Mus musculus
O35343	43	4	2	17.66	49	3	1	11.32	92	4	2	0.86	17.66	Importin subunit alpha-3	O35343	Kpna4	Mus musculus
O35344	5	2	0	8.06	19	4	2	16.89	24	4	2	0.86	16.89	Importin subunit alpha-4	O35344	Kpna3	Mus musculus
O35350	136	15	15	34.78	148	17	17	39.13	284	18	18	0	39.13	Calpain-1 catalytic subunit	O35350	Capn1	Mus musculus
O35381	10	2	2	18.22	16	2	2	20.24	26	3	3	0.21	20.24	Acidic leucine-rich nuclear phosphoprotein 32 family member A	O35381	Anp32a	Mus musculus
O35459	10	1	1	4.89	19	2	2	11.31	29	2	2	0.86	11.31	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	O35459	Ech1	Mus musculus
O35598	30	5	5	12.42	24	4	4	10.15	54	6	6	0	14.42	Disintegrin and metalloproteinase domain-containing protein 10	O35598	Adam10	Mus musculus
O35638	6	2	2	3.57	22	5	5	6.74	28	5	5	0	6.74	Cohesin subunit SA-2	O35638	Stag2	Mus musculus
O35639	128	10	10	34.06	195	14	14	44.89	323	14	14	0	44.89	Annexin A3	O35639	Anxa3	Mus musculus
O35643	146	11	8	22.69	139	16	11	29.8	285	16	11	0	29.8	AP-1 complex subunit beta-1	O35643	Ap1b1	Mus musculus
O35737	42	2	1	7.57	78	5	4	15.14	120	5	4	0.14	15.14	Heterogeneous nuclear ribonucleoprotein H	O35737	Hnrnph1	Mus musculus
O35744	175	15	15	57.54	288	21	21	61.31	463	23	23	0	65.33	Chitinase-like protein 3	O35744	Chil3	Mus musculus
O35841	26	4	4	20.04	46	7	7	26.59	72	7	7	0	26.59	Apoptosis inhibitor 5	O35841	Api5	Mus musculus
O35855	4	2	2	9.67	21	4	4	17.81	25	4	4	0.14	17.81	Branched-chain-amino-acid aminotransferase, mitochondrial	O35855	Bcat2	Mus musculus
O35900	17	2	2	40	24	2	2	40	41	2	2	0.86	40	U6 snRNA-associated Sm-like protein LSm2	O35900	Lsm2	Mus musculus
O35904	0	0	0		3	3	3	5.56	3	3	3	0.21	5.56	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform	O35904	Pik3cd	Mus musculus
O35930	174	9	9	17.57	66	4	4	10.76	240	9	9	0	17.57	Platelet glycoprotein Ib alpha chain	O35930	Gp1ba	Mus musculus
O35955	21	3	3	17.95	28	2	2	14.65	49	3	3	0.21	17.95	Proteasome subunit beta type-10	O35955	Psmb10	Mus musculus
O54774	0	0	0		11	3	3	5.17	11	3	3	0.21	5.17	AP-3 complex subunit delta-1	O54774	Ap3d1	Mus musculus
O54824	2	2	2	3.48	0	0	0		2	2	2	0.86	3.48	Pro-interleukin-16	O54824	Il16	Mus musculus
O54879	9	2	2	14	1	1	1	6	10	2	2	0.86	14	High mobility group protein B3	O54879	Hmgb3	Mus musculus
O54890	55	8	8	17.53	53	8	8	17.53	108	8	8	0	17.53	Integrin beta-3	O54890	Itgb3	Mus musculus
O54990	0	0	0		3	2	2	3.92	3	2	2	0.86	3.92	Prominin-1	O54990	Prom1	Mus musculus
O55029	4	3	3	7.18	33	5	5	13.15	37	5	5	0	13.15	Coatomer subunit beta'	O55029	Copb2	Mus musculus
O55106	9	3	3	8.33	46	4	4	9.87	55	5	5	0	12.69	Striatin	O55106	Strn	Mus musculus
O55131	15	2	2	9.17	9	2	2	9.17	24	2	2	0.86	9.17	Septin-7	O55131	Sept7	Mus musculus
O55135	11	2	2	20	57	5	5	46.94	68	5	5	0	46.94	Eukaryotic translation initiation factor 6	O55135	Eif6	Mus musculus
O55201	0	0	0		2	2	2	4.44	2	2	2	0.86	4.44	Transcription elongation factor SPT5	O55201	Supt5h	Mus musculus
O55222	8	2	2	10.18	19	3	3	15.04	27	3	3	0.21	15.04	Integrin-linked protein kinase	O55222	Ilk	Mus musculus
O70138	114	9	9	41.72	131	9	9	35.7	245	10	10	0	41.72	Neutrophil collagenase	O70138	Mmp8	Mus musculus
O70145	113	7	7	22.1	226	11	11	35.81	339	11	11	0	35.81	Neutrophil cytosol factor 2	O70145	Ncf2	Mus musculus
O70165	0	0	0		12	2	2	13.47	12	2	2	0.86	13.47	Ficolin-1	O70165	Fcn1	Mus musculus
O70194	1	1	1	5.29	28	3	3	13.32	29	3	3	0.21	13.32	Eukaryotic translation initiation factor 3 subunit D	O70194	Eif3d	Mus musculus
O70251	32	3	3	37.78	37	3	3	37.78	69	3	3	0.21	37.78	Elongation factor 1-beta	O70251	Eef1b	Mus musculus
O70310	20	2	2	7.06	29	4	4	16.33	49	4	4	0.14	16.33	Glycylpeptide N-tetradecanoyltransferase 1	O70310	Nmt1	Mus musculus
O70435	50	5	5	24.31	47	6	6	28.63	97	6	6	0	28.63	Proteasome subunit alpha type-3	O70435	Psma3	Mus musculus
O70497	31	2	2	15.61	30	2	2	15.61	61	2	2	0.86	15.61	Ficolin-2	O70497	Fcn2	Mus musculus
O88307	222	29	29	22.84	355	35	35	25.28	577	36	36	0	25.82	Sortilin-related receptor	O88307	Sorl1	Mus musculus
O88342	446	18	18	58.91	525	19	19	58.91	971	20	20	0	60.89	WD repeat-containing protein 1	O88342	Wdr1	Mus musculus
O88456	2	2	2	14.87	5	2	2	14.5	7	4	4	0.14	29.37	Calpain small subunit 1	O88456	Capns1	Mus musculus
O88487	7	2	2	8.33	6	3	3	11.44	13	3	3	0.21	11.44	Cytoplasmic dynein 1 intermediate chain 2	O88487	Dync1i2	Mus musculus
O88520	1	1	1	5.67	13	3	3	14.95	14	3	3	0.21	14.95	Leucine-rich repeat protein SHOC-2	O88520	Shoc2	Mus musculus
O88544	29	4	4	16.01	48	6	6	23.89	77	7	7	0	26.85	COP9 signalosome complex subunit 4	O88544	Cops4	Mus musculus
O88569	129	11	11	41.64	176	12	12	44.48	305	13	13	0	46.74	Heterogeneous nuclear ribonucleoproteins A2/B1	O88569	Hnrnpa2b1	Mus musculus
O88593	301	7	7	50	296	9	9	50	597	9	9	0	50	Peptidoglycan recognition protein 1	O88593	Pglyrp1	Mus musculus
O88622	0	0	0		2	2	2	5.16	2	2	2	0.86	5.16	Poly(ADP-ribose) glycohydrolase	O88622	Parg	Mus musculus
O88685	55	5	5	21.04	66	6	6	24.89	121	6	6	0	24.89	26S protease regulatory subunit 6A	O88685	Psmc3	Mus musculus
O88712	3	2	2	11.79	16	2	2	11.79	19	2	2	0.86	11.79	C-terminal-binding protein 1	O88712	Ctbp1	Mus musculus
O88783	104	10	10	8.25	37	5	5	3.99	141	10	10	0	8.25	Coagulation factor V	O88783	F5	Mus musculus
O88842	0	0	0		6	2	2	7.09	6	2	2	0.86	7.09	FYVE, RhoGEF and PH domain-containing protein 3	O88842	Fgd3	Mus musculus
O88844	26	4	4	16.67	49	7	7	26.09	75	7	7	0	26.09	Isocitrate dehydrogenase [NADP] cytoplasmic	O88844	Idh1	Mus musculus
O88879	2	2	2	2.24	22	6	6	9.21	24	6	6	0	9.21	Apoptotic protease-activating factor 1	O88879	Apaf1	Mus musculus
O88947	24	3	3	8.94	13	2	2	8.94	37	3	3	0.21	8.94	Coagulation factor X	O88947	F10	Mus musculus
O88958	13	2	2	21.11	11	2	2	17.3	24	3	3	0.21	27.34	Glucosamine-6-phosphate isomerase 1	O88958	Gnpda1	Mus musculus
O88968	96	7	7	34.65	63	6	6	27.67	159	7	7	0	34.65	Transcobalamin-2	O88968	Tcn2	Mus musculus
O89023	12	1	1	6.58	14	3	3	16.9	26	3	3	0.21	16.9	Tripeptidyl-peptidase 1	O89023	Tpp1	Mus musculus
O89051	7	1	1	3.76	17	3	3	20.68	24	3	3	0.21	20.68	Integral membrane protein 2B	O89051	Itm2b	Mus musculus
O89053	231	18	18	41.65	520	27	27	40.78	751	30	30	0	47.07	Coronin-1A	O89053	Coro1a	Mus musculus
O89079	12	2	2	10.06	41	3	3	17.21	53	3	3	0.21	17.21	Coatomer subunit epsilon	O89079	Cope	Mus musculus
O89086	22	2	2	22.22	34	2	2	22.22	56	2	2	0.86	22.22	RNA-binding protein 3	O89086	Rbm3	Mus musculus
P00375	0	0	0		6	2	2	18.18	6	2	2	0.86	18.18	Dihydrofolate reductase	P00375	Dhfr	Mus musculus
P00493	38	5	5	36.7	55	6	6	44.04	93	7	7	0	44.04	Hypoxanthine-guanine phosphoribosyltransferase	P00493	Hprt1	Mus musculus
P01027	893	61	61	48.89	585	51	51	43.96	1478	64	64	0	51.23	Complement C3	P01027	C3	Mus musculus
P01029	21	7	7	9.38	169	16	16	21.23	190	16	16	0	21.23	Complement C4-B	P01029	C4b	Mus musculus
P01326	91	9	9	35.45	94	10	10	35.45	185	11	11	0	35.45	Insulin-2	P01326	Ins2	Mus musculus
P01639	1	1	1	16.92	15	3	3	27.69	16	3	3	0.21	27.69	Ig kappa chain V-V region MOPC 41	P01639	Gm5571	Mus musculus
P01723	1	1	1	19.66	3	2	2	47.86	4	2	2	0.86	47.86	Ig lambda-1 chain V region	P01723		Mus musculus
P01786	14	2	2	21.37	0	0	0		14	2	2	0.86	21.37	Ig heavy chain V region MOPC 47A	P01786		Mus musculus
P01812	1	1	1	18.8	8	2	2	20.51	9	2	2	0.86	20.51	Ig heavy chain V region MOPC 173	P01812		Mus musculus
P01837	33	2	2	45.28	37	2	2	45.28	70	2	2	0.86	45.28	Ig kappa chain C region	P01837		Mus musculus
P01868	16	3	3	21.3	21	3	3	17.28	37	4	4	0.14	25	Ig gamma-1 chain C region secreted form	P01868	Ighg1	Mus musculus
P01872	240	18	18	53.08	168	13	13	31.72	408	22	22	0	53.3	Ig mu chain C region	P01872	Ighm	Mus musculus
P01878	15	2	2	11.05	0	0	0		15	2	2	0.86	11.05	Ig alpha chain C region	P01878		Mus musculus
P01887	11	2	2	19.33	10	2	2	19.33	21	3	3	0.21	19.33	Beta-2-microglobulin	P01887	B2m	Mus musculus
P01900	6	1	1	4.11	5	2	2	7.4	11	2	2	0.86	7.4	H-2 class I histocompatibility antigen, D-D alpha chain	P01900	H2-D1	Mus musculus
P01921	0	0	0		4	2	2	14.34	4	2	2	0.86	14.34	H-2 class II histocompatibility antigen, A-D beta chain	P01921	H2-Ab1	Mus musculus
P01942	899	37	37	80.28	305	14	14	72.54	1204	37	37	0	80.28	Hemoglobin subunit alpha	P01942	Hba	Mus musculus
P02088	1242	31	16	95.24	465	17	9	87.76	1707	31	16	0	95.24	Hemoglobin subunit beta-1	P02088	Hbb-b1	Mus musculus
P02089	1014	24	9	85.71	424	15	7	84.35	1438	25	10	0	85.71	Hemoglobin subunit beta-2	P02089	Hbb-b2	Mus musculus
P02535	9	3	3	6.49	1	1	1	2.11	10	3	3	0.21	6.49	Keratin, type I cytoskeletal 10	P02535	Krt10	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P04104	22	3	3	3.77	21	2	2	3.77	43	3	3	0.21	3.77	Keratin, type II cytoskeletal 1	P04104	Krt1	Mus musculus
P04202	64	6	6	31.54	51	4	4	22.05	115	6	6	0	31.54	Transforming growth factor beta-1	P04202	Tgfb1	Mus musculus
P04228	0	0	0		11	4	4	26.17	11	4	4	0.14	26.17	H-2 class II histocompatibility antigen, A-D alpha chain	P04228	H2-Aa	Mus musculus
P04919	523	27	27	29.17	90	10	10	17.01	613	27	27	0	29.17	Band 3 anion transport protein	P04919	Slc4a1	Mus musculus
P05201	66	7	7	25.18	58	5	5	21.31	124	7	7	0	25.18	Aspartate aminotransferase, cytoplasmic	P05201	Got1	Mus musculus
P05202	71	6	6	22.33	93	6	6	27.91	164	8	8	0	33.95	Aspartate aminotransferase, mitochondrial	P05202	Got2	Mus musculus
P06151	405	16	15	55.42	437	14	14	52.41	842	18	17	0	56.02	L-lactate dehydrogenase A chain	P06151	Ldha	Mus musculus
P06336	12	2	2	10.93	5	2	2	10.93	17	2	2	0.86	10.93	Ig epsilon chain C region	P06336		Mus musculus
P06745	698	23	23	58.06	650	22	22	51.79	1348	27	27	0	60.75	Glucose-6-phosphate isomerase	P06745	Gpi	Mus musculus
P06800	46	6	6	10.84	73	9	9	13.01	119	9	9	0	13.01	Receptor-type tyrosine-protein phosphatase C	P06800	Ptprc	Mus musculus
P06909	45	9	9	14.99	11	4	4	6.32	56	9	9	0	14.99	Complement factor H	P06909	Cfh	Mus musculus
P07356	283	15	15	49.56	365	18	18	51.03	648	19	19	0	51.03	Annexin A2	P07356	Anxa2	Mus musculus
P07607	0	0	0		6	2	2	9.12	6	2	2	0.86	9.12	Thymidylate synthase	P07607	Tyms	Mus musculus
P07724	900	29	29	58.88	466	21	21	50.82	1366	30	30	0	58.88	Serum albumin	P07724	Alb	Mus musculus
P07742	17	2	2	5.93	71	8	8	18.69	88	8	8	0	18.69	Ribonucleoside-diphosphate reductase large subunit	P07742	Rrm1	Mus musculus
P07759	54	6	6	23.92	19	4	4	20.33	73	6	6	0	23.92	Serine protease inhibitor A3K	P07759	Serpina3k	Mus musculus
P07901	71	13	9	23.33	69	10	7	22.37	140	15	11	0	28.65	Heat shock protein HSP 90-alpha	P07901	Hsp90aa1	Mus musculus
P08003	56	7	7	21	48	8	8	21.63	104	8	8	0	21.63	Protein disulfide-isomerase A4	P08003	Pdia4	Mus musculus
P08030	93	8	8	62.78	255	15	15	83.33	348	15	15	0	83.33	Adenine phosphoribosyltransferase	P08030	Aprt	Mus musculus
P08032	1717	119	118	57.47	300	43	43	28.53	2017	119	118	0	57.47	Spectrin alpha chain, erythrocytic 1	P08032	Spta1	Mus musculus
P08071	7031	83	83	72.98	4885	61	61	66.05	11916	86	86	0	72.98	Lactotransferrin	P08071	Ltf	Mus musculus
P08103	0	0	0		15	5	5	16.03	15	5	5	0	16.03	Tyrosine-protein kinase HCK	P08103	Hck	Mus musculus
P08113	50	8	7	18.33	42	9	8	22.07	92	11	10	0	25.69	Endoplasmin	P08113	Hsp90b1	Mus musculus
P08226	32	4	4	22.51	44	3	3	18.33	76	4	4	0.14	22.51	Apolipoprotein E	P08226	Apoe	Mus musculus
P08228	32	5	5	36.36	15	3	3	27.92	47	5	5	0	36.36	Superoxide dismutase [Cu-Zn]	P08228	Sod1	Mus musculus
P08249	122	10	10	38.76	134	11	11	39.05	256	11	11	0	39.05	Malate dehydrogenase, mitochondrial	P08249	Mdh2	Mus musculus
P08556	0	0	0		6	3	3	21.69	6	3	3	0.21	21.69	GTPase NRas	P08556	Nras	Mus musculus
P08607	8	5	5	15.78	207	9	9	24.31	215	9	9	0	24.31	C4b-binding protein	P08607	C4bpa	Mus musculus
P08752	18	6	4	25.35	59	10	8	40.28	77	10	8	0	40.28	Guanine nucleotide-binding protein G(i) subunit alpha-2	P08752	Gnai2	Mus musculus
P08775	0	0	0		4	3	3	2.99	4	3	3	0.21	2.99	DNA-directed RNA polymerase II subunit RPB1	P08775	Polr2a	Mus musculus
P08905	249	10	10	50.68	237	8	8	50.68	486	12	12	0	50.68	Lysozyme C-2	P08905	Lyz2	Mus musculus
P09055	31	5	5	12.53	15	3	3	8.4	46	5	5	0	12.53	Integrin beta-1	P09055	Itgb1	Mus musculus
P09103	216	15	15	41.85	248	15	15	41.26	464	16	16	0	44.2	Protein disulfide-isomerase	P09103	P4hb	Mus musculus
P09405	70	10	10	20.65	90	11	11	21.5	160	13	13	0	24.75	Nucleolin	P09405	Ncl	Mus musculus
P09411	308	13	13	43.41	460	16	16	49.64	768	16	16	0	49.64	Phosphoglycerate kinase 1	P09411	Pgk1	Mus musculus
P09528	32	4	4	35.16	17	2	2	20.33	49	4	4	0.14	35.16	Ferritin heavy chain	P09528	Fth1	Mus musculus
P09581	24	2	2	5.63	14	2	2	2.35	38	3	3	0.21	5.73	Macrophage colony-stimulating factor 1 receptor	P09581	Csf1r	Mus musculus
P0C0S6	1142	15	14	53.91	1572	13	12	53.91	2714	15	14	0	53.91	Histone H2A.Z	P0C0S6	H2afz	Mus musculus
P0CW02	3	2	2	29.77	8	3	3	29.77	11	3	3	0.21	29.77	Lymphocyte antigen 6C1	P0CW02	Ly6c1	Mus musculus
P10107	542	24	24	57.8	831	28	28	62.72	1373	29	29	0	62.72	Annexin A1	P10107	Anxa1	Mus musculus
P10126	174	12	12	35.5	464	24	24	54.11	638	24	24	0	54.11	Elongation factor 1-alpha 1	P10126	Eef1a1	Mus musculus
P10518	109	7	7	37.58	62	5	5	26.06	171	7	7	0	37.58	Delta-aminolevulinic acid dehydratase	P10518	Alad	Mus musculus
P10605	24	4	4	18.29	71	8	8	34.81	95	9	9	0	38.05	Cathepsin B	P10605	Ctsb	Mus musculus
P10639	42	4	4	42.86	17	4	4	37.14	59	5	5	0	53.33	Thioredoxin	P10639	Txn	Mus musculus
P10649	63	4	4	20.18	85	6	6	20.18	148	6	6	0	20.18	Glutathione S-transferase Mu 1	P10649	Gstm1	Mus musculus
P10810	23	4	4	25.68	29	5	5	28.42	52	5	5	0	28.42	Monocyte differentiation antigen CD14	P10810	Cd14	Mus musculus
P10852	0	0	0		12	5	5	21.67	12	5	5	0	21.67	4F2 cell-surface antigen heavy chain	P10852	Slc3a2	Mus musculus
P10853	136	7	7	19.84	81	7	7	26.19	217	8	8	0	26.19	Histone H2B type 1-F/J/L	P10853	Hist1h2bf	Mus musculus
P11031	22	2	2	18.9	32	3	3	25.98	54	3	3	0.21	25.98	Activated RNA polymerase II transcriptional coactivator p15	P11031	Sub1	Mus musculus
P11152	13	3	3	10.55	1	1	1	4.01	14	3	3	0.21	10.55	Lipoprotein lipase	P11152	Lpl	Mus musculus
P11247	516	29	29	38.3	635	32	32	39.42	1151	36	36	0	41.78	Myeloperoxidase	P11247	Mpo	Mus musculus
P11352	67	5	5	51.74	108	9	9	65.17	175	9	9	0	65.17	Glutathione peroxidase 1	P11352	Gpx1	Mus musculus
P11499	55	9	4	22.65	75	13	9	25.97	130	14	9	0	28.73	Heat shock protein HSP 90-beta	P11499	Hsp90ab1	Mus musculus
P11672	92	4	4	28.5	176	6	6	38	268	6	6	0	38	Neutrophil gelatinase-associated lipocalin	P11672	Lcn2	Mus musculus
P11680	31	3	3	11.42	43	2	2	8.41	74	3	3	0.21	11.42	Properdin	P11680	Cfp	Mus musculus
P11835	480	22	22	41.37	342	24	24	42.67	822	24	24	0	42.67	Integrin beta-2	P11835	Itgb2	Mus musculus
P11983	30	2	2	9.35	47	6	6	21.4	77	6	6	0	21.4	T-complex protein 1 subunit alpha	P11983	Tcp1	Mus musculus
P12023	16	3	3	6.62	30	3	3	6.62	46	3	3	0.21	6.62	Amyloid beta A4 protein	P12023	App	Mus musculus
P12246	43	2	2	20.98	17	1	1	8.93	60	2	2	0.86	20.98	Serum amyloid P-component	P12246	Apcs	Mus musculus
P12265	32	6	6	14.81	29	7	7	16.51	61	8	8	0	18.21	Beta-glucuronidase	P12265	Gusb	Mus musculus
P12382	0	0	0		13	2	2	5.51	13	2	2	0.86	5.51	ATP-dependent 6-phosphofructokinase, liver type	P12382	Pfkl	Mus musculus
P12815	26	5	5	47.64	65	5	5	47.64	91	5	5	0	47.64	Programmed cell death protein 6	P12815	Pdcd6	Mus musculus
P12970	0	0	0		12	2	2	16.54	12	2	2	0.86	16.54	60S ribosomal protein L7a	P12970	Rpl7a	Mus musculus
P13020	415	19	19	43.72	293	17	17	38.72	708	19	19	0	43.72	Gelsolin	P13020	Gsn	Mus musculus
P13439	3	1	1	7.07	19	2	2	9.98	22	2	2	0.86	9.98	Uridine 5'-monophosphate synthase	P13439	Umps	Mus musculus
P13609	2	2	2	18.42	0	0	0		2	2	2	0.86	18.42	Serglycin	P13609	Srgn	Mus musculus
P13634	5	2	2	17.62	0	0	0		5	2	2	0.86	17.62	Carbonic anhydrase 1	P13634	Ca1	Mus musculus
P13864	0	0	0		2	2	2	1.98	2	2	2	0.86	1.98	DNA (cytosine-5)-methyltransferase 1	P13864	Dnmt1	Mus musculus
P14069	136	8	8	48.31	179	12	12	65.17	315	12	12	0	65.17	Protein S100-A6	P14069	S100a6	Mus musculus
P14131	0	0	0		10	2	2	14.38	10	2	2	0.86	14.38	40S ribosomal protein S16	P14131	Rps16	Mus musculus
P14152	69	7	7	38.92	47	7	7	34.73	116	8	8	0	41.92	Malate dehydrogenase, cytoplasmic	P14152	Mdh1	Mus musculus
P14206	43	5	5	30.85	79	7	7	29.49	122	8	8	0	34.58	40S ribosomal protein SA	P14206	Rpsa	Mus musculus
P14211	206	14	14	49.28	214	12	12	47.6	420	14	14	0	49.28	Calreticulin	P14211	Calr	Mus musculus
P14234	2	1	1	4.45	55	7	7	23.21	57	7	7	0	23.21	Tyrosine-protein kinase Fgr	P14234	Fgr	Mus musculus
P14685	32	5	5	19.25	38	6	6	22.08	70	7	7	0	24.34	26S proteasome non-ATPase regulatory subunit 3	P14685	Psmd3	Mus musculus
P14733	75	6	6	18.71	67	6	6	14.8	142	8	8	0	21.09	Lamin-B1	P14733	Lmnb1	Mus musculus
P14824	132	11	11	27.04	90	11	11	27.04	222	11	11	0	27.04	Annexin A6	P14824	Anxa6	Mus musculus
P15532	58	3	2	20.39	64	5	2	37.5	122	5	2	0.86	37.5	Nucleoside diphosphate kinase A	P15532	Nme1	Mus musculus
P15864	178	9	2	27.36	272	8	1	25	450	10	2	0.86	27.36	Histone H1.2	P15864	Hist1h1c	Mus musculus
P16110	122	4	4	18.94	116	7	7	27.27	238	7	7	0	27.27	Galectin-3	P16110	Lgals3	Mus musculus
P16125	7	3	2	14.97	1	1	1	4.79	8	4	3	0.21	19.76	L-lactate dehydrogenase B chain	P16125	Ldhb	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P16546	356	41	40	26.98	249	31	31	21.2	605	43	42	0	27.43	Spectrin alpha chain, non-erythrocytic 1	P16546	Sptan1	Mus musculus
P16675	17	2	2	8.23	18	3	3	11.39	35	3	3	0.21	11.39	Lysosomal protective protein	P16675	Ctsa	Mus musculus
P16858	406	15	15	59.46	1608	30	30	64.26	2014	30	30	0	64.26	Glyceraldehyde-3-phosphate dehydrogenase	P16858	Gapdh	Mus musculus
P16879	0	0	0		3	2	2	4.99	3	2	2	0.86	4.99	Tyrosine-protein kinase Fes/Fps	P16879	Fes	Mus musculus
P17182	539	23	23	53.92	2439	41	41	58.29	2978	43	43	0	58.29	Alpha-enolase	P17182	Eno1	Mus musculus
P17426-2	26	4	2	8.69	89	10	8	20.31	115	10	8	0	20.31	Isoform B of AP-2 complex subunit alpha-1	P17426	Ap2a1	Mus musculus
P17427	43	5	3	11.09	86	11	9	19.94	129	11	9	0	19.94	AP-2 complex subunit alpha-2	P17427	Ap2a2	Mus musculus
P17563	0	0	0		3	2	2	8.47	3	2	2	0.86	8.47	Selenium-binding protein 1	P17563	Selenbp1	Mus musculus
P17710	31	6	6	10.06	42	8	7	12.42	73	8	7	0	12.42	Hexokinase-1	P17710	Hk1	Mus musculus
P17742	171	9	9	50	232	10	10	50	403	12	12	0	50	Peptidyl-prolyl cis-trans isomerase A	P17742	Ppia	Mus musculus
P17751	126	8	8	41.47	194	10	10	41.47	320	10	10	0	41.47	Triosephosphate isomerase	P17751	Tpi1	Mus musculus
P17918	0	0	0		9	2	2	12.26	9	2	2	0.86	12.26	Proliferating cell nuclear antigen	P17918	Pcna	Mus musculus
P18242	25	4	4	13.66	43	4	4	17.32	68	5	5	0	20.24	Cathepsin D	P18242	Ctsd	Mus musculus
P18337	5	2	2	7.26	7	1	1	4.57	12	2	2	0.86	7.26	L-selectin	P18337	Sell	Mus musculus
P18572-2	15	3	3	14.29	5	2	2	11.36	20	3	3	0.21	14.29	Isoform 2 of Basigin	P18572	Bsg	Mus musculus
P18653	0	0	0		6	3	3	6.49	6	3	3	0.21	6.49	Ribosomal protein S6 kinase alpha-1	P18653	Rps6ka1	Mus musculus
P18760	194	10	10	57.23	274	12	12	48.8	468	13	13	0	57.23	Cofilin-1	P18760	Cfl1	Mus musculus
P19096	56	12	12	10.42	158	24	24	18.85	214	25	25	0	19.81	Fatty acid synthase	P19096	Fasn	Mus musculus
P19157	8	1	1	7.62	23	4	4	32.86	31	4	4	0.14	32.86	Glutathione S-transferase P 1	P19157	Gstp1	Mus musculus
P19221	2	2	2	7.77	0	0	0		2	2	2	0.86	7.77	Prothrombin	P19221	F2	Mus musculus
P19973	39	6	6	38.18	28	5	5	27.27	67	7	7	0	38.18	Lymphocyte-specific protein 1	P19973	Lsp1	Mus musculus
P20029	423	25	24	47.02	311	21	19	36.18	734	27	25	0	47.02	78 kDa glucose-regulated protein	P20029	Hspa5	Mus musculus
P20060	61	7	7	25.75	54	6	6	22.76	115	7	7	0	25.75	Beta-hexosaminidase subunit beta	P20060	Hexb	Mus musculus
P20108	15	4	4	31.91	15	3	3	22.18	30	4	4	0.14	31.91	Thioredoxin-dependent peroxide reductase, mitochondrial	P20108	Prdx3	Mus musculus
P20152	147	12	12	33.91	157	16	16	45.49	304	18	18	0	47.64	Vimentin	P20152	Vim	Mus musculus
P20918	46	10	10	22.41	1	1	1	2.46	47	10	10	0	22.41	Plasminogen	P20918	Plg	Mus musculus
P21107	53	5	2	22.46	37	4	1	13.33	90	6	2	0.86	22.46	Tropomyosin alpha-3 chain	P21107	Tpm3	Mus musculus
P21107-2	107	11	8	37.5	102	9	6	27.42	209	12	8	0	37.5	Isoform 2 of Tropomyosin alpha-3 chain	P21107	Tpm3	Mus musculus
P21614	38	4	4	15.76	14	2	2	10.29	52	4	4	0.14	15.76	Vitamin D-binding protein	P21614	Gc	Mus musculus
P22366	1	1	1	5.07	3	2	2	13.18	4	2	2	0.86	13.18	Myeloid differentiation primary response protein MyD88	P22366	Myd88	Mus musculus
P22599	6	3	2	14.04	0	0	0		6	3	2	0.86	14.04	Alpha-1-antitrypsin 1-2	P22599	Serpina1b	Mus musculus
P22892	13	3	3	6.81	17	1	1	3.28	30	3	3	0.21	6.81	AP-1 complex subunit gamma-1	P22892	Ap1g1	Mus musculus
P23116	25	5	5	5.95	48	5	5	5.8	73	6	6	0	6.92	Eukaryotic translation initiation factor 3 subunit A	P23116	Eif3a	Mus musculus
P23249	4	3	3	5.18	10	3	3	5.28	14	4	4	0.14	6.87	Putative helicase MOV-10	P23249	Mov10	Mus musculus
P23492	106	8	8	44.98	105	7	7	37.37	211	8	8	0	44.98	Purine nucleoside phosphorylase	P23492	Pnp	Mus musculus
P23591	5	1	1	5.92	17	3	3	19.31	22	3	3	0.21	19.31	GDP-L-fucose synthase	P23591	Tsta3	Mus musculus
P23953	15	2	2	8.3	7	2	2	8.3	22	2	2	0.86	8.3	Carboxylesterase 1C	P23953	Ces1c	Mus musculus
P24063	14	5	5	7.65	32	7	7	11.35	46	8	8	0	11.35	Integrin alpha-L	P24063	Itgal	Mus musculus
P24270	223	17	17	45.35	144	16	16	36.05	367	20	20	0	45.35	Catalase	P24270	Cat	Mus musculus
P24369	21	4	4	24.54	5	3	3	18.52	26	4	4	0.14	24.54	Peptidyl-prolyl cis-trans isomerase B	P24369	Ppib	Mus musculus
P24527	259	20	20	42.06	281	21	21	43.21	540	22	22	0	45.66	Leukotriene A-4 hydrolase	P24527	Lta4h	Mus musculus
P24549	5	3	3	10.18	1	1	1	2	6	3	3	0.21	10.18	Retinal dehydrogenase 1	P24549	Aldh1a1	Mus musculus
P25206	0	0	0		5	2	2	6.16	5	2	2	0.86	6.16	DNA replication licensing factor MCM3	P25206	Mcm3	Mus musculus
P25444	1	1	1	6.48	5	2	2	10.24	6	2	2	0.86	10.24	40S ribosomal protein S2	P25444	Rps2	Mus musculus
P25911	28	6	6	20.51	97	12	12	25.59	125	12	12	0	25.59	Tyrosine-protein kinase Lyn	P25911	Lyn	Mus musculus
P26039	959	65	65	44.71	942	69	69	44.16	1901	76	76	0	48.48	Talin-1	P26039	Tln1	Mus musculus
P26040	174	9	6	21.16	190	9	6	21.16	364	9	6	0	21.16	Ezrin	P26040	Ezr	Mus musculus
P26041	378	16	13	35.88	446	20	17	36.74	824	21	18	0	38.99	Moesin	P26041	Msn	Mus musculus
P26043	144	9	6	22.13	182	10	7	25.56	326	11	8	0	28.64	Radixin	P26043	Rdx	Mus musculus
P26369	18	3	3	14.32	33	5	5	18.11	51	5	5	0	18.11	Splicing factor U2AF 65 kDa subunit	P26369	U2af2	Mus musculus
P26443	88	8	8	25.27	102	9	9	27.24	190	9	9	0	27.24	Glutamate dehydrogenase 1, mitochondrial	P26443	Glud1	Mus musculus
P26450	8	3	3	11.46	22	4	4	13.12	30	4	4	0.14	13.12	Phosphatidylinositol 3-kinase regulatory subunit alpha	P26450	Pik3r1	Mus musculus
P26516	32	6	6	37.07	33	5	5	32.4	65	6	6	0	37.07	26S proteasome non-ATPase regulatory subunit 7	P26516	Psmd7	Mus musculus
P26638	3	1	1	5.47	26	5	5	14.45	29	5	5	0	14.45	Serine--tRNA ligase, cytoplasmic	P26638	Sars	Mus musculus
P26645	0	0	0		2	2	2	20.71	2	2	2	0.86	20.71	Myristoylated alanine-rich C-kinase substrate	P26645	Marcks	Mus musculus
P27005	385	12	12	80.9	412	8	8	74.16	797	12	12	0	80.9	Protein S100-A8	P27005	S100a8	Mus musculus
P27601	0	0	0		5	2	2	10.61	5	2	2	0.86	10.61	Guanine nucleotide-binding protein subunit alpha-13	P27601	Gna13	Mus musculus
P27612	14	4	4	10.33	70	11	11	24.94	84	12	12	0	27.71	Phospholipase A-2-activating protein	P27612	Plaa	Mus musculus
P27661	6229	59	38	55.24	9643	58	32	54.55	15872	65	39	0	55.24	Histone H2AX	P27661	H2afx	Mus musculus
P27773	304	21	21	50.69	283	20	20	48.12	587	23	23	0	53.07	Protein disulfide-isomerase A3	P27773	Pdia3	Mus musculus
P27784	0	0	0		3	2	2	39.66	3	2	2	0.86	39.66	C-C motif chemokine 6	P27784	Ccl6	Mus musculus
P27870	9	4	4	9.11	46	9	9	17.04	55	9	9	0	17.04	Proto-oncogene vav	P27870	Vav1	Mus musculus
P27931	9	3	3	11.71	61	5	5	26.34	70	5	5	0	26.34	Interleukin-1 receptor type 2	P27931	Il1r2	Mus musculus
P28063	19	4	4	15.58	28	4	4	18.48	47	5	5	0	20.65	Proteasome subunit beta type-8	P28063	Psmb8	Mus musculus
P28076	20	2	2	17.35	22	1	1	7.76	42	2	2	0.86	17.35	Proteasome subunit beta type-9	P28076	Psmb9	Mus musculus
P28271	0	0	0		6	2	2	5.4	6	2	2	0.86	5.4	Cytoplasmic aconitate hydratase	P28271	Aco1	Mus musculus
P28293	47	6	6	32.57	123	11	11	42.15	170	11	11	0	42.15	Cathepsin G	P28293	Ctsg	Mus musculus
P28352	48	5	5	28.39	69	6	6	29.34	117	6	6	0	29.34	DNA-(apurinic or apyrimidinic site) lyase	P28352	Apex1	Mus musculus
P28474	9	2	2	9.89	74	6	6	22.73	83	6	6	0	22.73	Alcohol dehydrogenase class-3	P28474	Adh5	Mus musculus
P28650	99	7	7	26.26	137	9	8	31.73	236	10	9	0	35.01	Adenylosuccinate synthetase isozyme 1	P28650	Adssl1	Mus musculus
P28656	24	3	3	15.35	58	3	3	15.35	82	3	3	0.21	15.35	Nucleosome assembly protein 1-like 1	P28656	Nap1l1	Mus musculus
P28658	0	0	0		14	3	3	8.63	14	3	3	0.21	8.63	Ataxin-10	P28658	Atxn10	Mus musculus
P28665	93	14	14	18.09	50	11	11	13.08	143	16	16	0	18.97	Murinoglobulin-1	P28665	Mug1	Mus musculus
P28798	84	10	10	30.56	203	10	10	30.56	287	10	10	0	30.56	Granulins	P28798	Grn	Mus musculus
P28867	16	4	4	10.53	66	10	10	22.85	82	10	10	0	22.85	Protein kinase C delta type	P28867	Prkcd	Mus musculus
P29341	61	6	6	13.05	58	7	7	15.09	119	7	7	0	15.09	Polyadenylate-binding protein 1	P29341	Pabpc1	Mus musculus
P29351	185	17	17	40.5	368	22	22	45.88	553	22	22	0	45.88	Tyrosine-protein phosphatase non-receptor type 6	P29351	Ptpn6	Mus musculus
P29391	88	7	7	51.91	33	4	4	37.16	121	7	7	0	51.91	Ferritin light chain 1	P29391	Ftl1	Mus musculus
P29416	34	11	11	27.84	21	4	4	11.74	55	11	11	0	27.84	Beta-hexosaminidase subunit alpha	P29416	Hexa	Mus musculus
P29452	0	0	0		8	2	2	7.96	8	2	2	0.86	7.96	Caspase-1	P29452	Casp1	Mus musculus
P29621	20	2	2	6.95	8	1	1	6	28	2	2	0.86	6.95	Serine protease inhibitor A3C	P29621	Serpina3c	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P29699	64	4	4	26.38	42	3	3	20.29	106	4	4	0.14	26.38	Alpha-2-HS-glycoprotein	P29699	Ahsg	Mus musculus
P29758	9	3	3	12.07	25	4	4	16.4	34	5	5	0	20.27	Ornithine aminotransferase, mitochondrial	P29758	Oat	Mus musculus
P30416	1	1	1	5.02	11	3	3	13.32	12	3	3	0.21	13.32	Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	Fkbp4	Mus musculus
P30681	118	7	6	40	155	9	8	40.48	273	9	8	0	40.48	High mobility group protein B2	P30681	Hmgb2	Mus musculus
P31725	317	7	7	26.55	622	6	6	13.27	939	8	8	0	26.55	Protein S100-A9	P31725	S100a9	Mus musculus
P31750	7	1	1	4.38	18	2	2	7.08	25	2	2	0.86	7.08	RAC-alpha serine/threonine-protein kinase	P31750	Akt1	Mus musculus
P31938	2	1	1	4.07	24	2	2	12.21	26	2	2	0.86	12.21	Dual specificity mitogen-activated protein kinase kinase 1	P31938	Map2k1	Mus musculus
P32067	5	1	1	3.37	14	2	2	6.75	19	2	2	0.86	6.75	Lupus La protein homolog	P32067	Ssb	Mus musculus
P32921	10	2	2	7.07	72	9	9	25.16	82	9	9	0	25.16	Tryptophan--tRNA ligase, cytoplasmic	P32921	Wars	Mus musculus
P34022	5	3	3	28.08	15	2	2	22.66	20	3	3	0.21	28.08	Ran-specific GTPase-activating protein	P34022	Ranbp1	Mus musculus
P34152	0	0	0		2	2	2	3.03	2	2	2	0.86	3.03	Focal adhesion kinase 1	P34152	Ptk2	Mus musculus
P34884	8	1	1	18.26	31	4	4	44.35	39	4	4	0.14	44.35	Macrophage migration inhibitory factor	P34884	Mif	Mus musculus
P35123	0	0	0		5	3	3	7.8	5	3	3	0.21	7.8	Ubiquitin carboxyl-terminal hydrolase 4	P35123	Usp4	Mus musculus
P35174-2	28	4	4	61.17	77	7	7	64.08	105	7	7	0	64.08	Isoform 2 of Stefin-2	P35174	Stfa2	Mus musculus
P35235	0	0	0		6	3	3	8.71	6	3	3	0.21	8.71	Tyrosine-protein phosphatase non-receptor type 11	P35235	Ptpn11	Mus musculus
P35276	0	0	0		7	3	2	21.46	7	3	2	0.86	21.46	Ras-related protein Rab-3D	P35276	Rab3d	Mus musculus
P35343	3	2	2	10.03	7	2	2	10.03	10	2	2	0.86	10.03	C-X-C chemokine receptor type 2	P35343	Cxcr2	Mus musculus
P35441	1711	52	52	49.49	841	36	36	42.31	2552	53	53	0	49.49	Thrombospondin-1	P35441	Thbs1	Mus musculus
P35461	38	1	1	22.52	39	2	2	24.32	77	2	2	0.86	24.32	Lymphocyte antigen 6G (Fragment)	P35461	Ly6g	Mus musculus
P35486	0	0	0		10	2	2	16.67	10	2	2	0.86	16.67	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	P35486	Pdha1	Mus musculus
P35505	51	4	4	17.42	65	5	5	20.53	116	5	5	0	20.53	Fumarylacetoacetase	P35505	Fah	Mus musculus
P35564	4	3	3	7.78	20	5	5	13.87	24	5	5	0	13.87	Calnexin	P35564	Canx	Mus musculus
P35585	13	2	2	7.33	11	2	2	7.33	24	2	2	0.86	7.33	AP-1 complex subunit mu-1	P35585	Ap1m1	Mus musculus
P35700	55	7	7	47.74	39	5	5	41.71	94	7	7	0	47.74	Peroxiredoxin-1	P35700	Prdx1	Mus musculus
P35821	0	0	0		10	2	2	7.64	10	2	2	0.86	7.64	Tyrosine-protein phosphatase non-receptor type 1	P35821	Ptpn1	Mus musculus
P35979	21	4	4	37.58	52	6	6	49.09	73	6	6	0	49.09	60S ribosomal protein L12	P35979	Rpl12	Mus musculus
P35991	0	0	0		6	3	3	6.22	6	3	3	0.21	6.22	Tyrosine-protein kinase BTK	P35991	Btk	Mus musculus
P36993	0	0	0		4	3	3	10.51	4	3	3	0.21	10.51	Protein phosphatase 1B	P36993	Ppm1b	Mus musculus
P37913	0	0	0		2	2	2	5.9	2	2	2	0.86	5.9	DNA ligase 1	P37913	Lig1	Mus musculus
P38060	1	1	1	4.31	19	4	4	13.23	20	4	4	0.14	13.23	Hydroxymethylglutaryl-CoA lyase, mitochondrial	P38060	Hmgcl	Mus musculus
P38647	2	2	2	1.91	18	4	4	9.13	20	5	5	0	9.13	Stress-70 protein, mitochondrial	P38647	Hspa9	Mus musculus
P39039	16	3	3	31.8	0	0	0		16	3	3	0.21	31.8	Mannose-binding protein A	P39039	Mbl1	Mus musculus
P39054	31	8	8	18.28	71	12	12	24.94	102	12	12	0	24.94	Dynamin-2	P39054	Dnm2	Mus musculus
P39654	71	11	11	32.88	86	13	13	36.95	157	13	13	0	36.95	Arachidonate 15-lipoxygenase	P39654	Alox15	Mus musculus
P39655	127	12	12	32.13	41	7	7	20.97	168	12	12	0	32.13	Arachidonate 12-lipoxygenase, 12S-type	P39655	Alox12	Mus musculus
P40124	565	29	29	61.39	532	24	24	53.38	1097	31	31	0	62.24	Adenylyl cyclase-associated protein 1	P40124	Cap1	Mus musculus
P40142	1175	41	41	51.36	1723	43	43	53.93	2898	51	51	0	54.41	Transketolase	P40142	Tkt	Mus musculus
P40240	51	3	3	16.81	59	4	4	16.81	110	4	4	0.14	16.81	CD9 antigen	P40240	Cd9	Mus musculus
P41241	14	2	2	6.22	38	6	6	17.78	52	6	6	0	17.78	Tyrosine-protein kinase CSK	P41241	Csk	Mus musculus
P41245	1098	26	26	40.41	727	24	24	42.05	1825	28	28	0	42.05	Matrix metalloproteinase-9	P41245	Mmp9	Mus musculus
P42208	11	3	3	13.57	11	3	3	13.57	22	3	3	0.21	13.57	Septin-2	P42208	Sept2	Mus musculus
P42227	23	2	2	7.53	34	5	5	12.6	57	6	6	0	16.75	Signal transducer and activator of transcription 3	P42227	Stat3	Mus musculus
P42232	0	0	0		5	3	3	6.62	5	3	3	0.21	6.62	Signal transducer and activator of transcription 5B	P42232	Stat5b	Mus musculus
P42567	5	2	2	3.9	0	0	0		5	2	2	0.86	3.9	Epidermal growth factor receptor substrate 15	P42567	Eps15	Mus musculus
P42669	27	3	3	24.3	23	2	2	15.26	50	3	3	0.21	24.3	Transcriptional activator protein Pur-alpha	P42669	Pura	Mus musculus
P42932	20	3	3	8.58	45	6	6	13.87	65	6	6	0	13.87	T-complex protein 1 subunit theta	P42932	Cct8	Mus musculus
P43274	156	8	3	24.66	247	9	4	26.03	403	10	4	0.14	26.48	Histone H1.4	P43274	Hist1h1e	Mus musculus
P43275	30	4	3	27.7	73	5	4	20.66	103	6	5	0	29.58	Histone H1.1	P43275	Hist1h1a	Mus musculus
P43276	40	4	4	17.94	93	5	4	17.94	133	5	4	0.14	17.94	Histone H1.5	P43276	Hist1h1b	Mus musculus
P43277	185	10	3	24.43	318	9	2	23.98	503	11	3	0.21	24.43	Histone H1.3	P43277	Hist1h1d	Mus musculus
P45376	10	3	3	19.62	51	4	4	26.27	61	4	4	0.14	26.27	Aldose reductase	P45376	Akr1b1	Mus musculus
P46467	9	2	2	7.88	27	8	8	27.93	36	8	8	0	27.93	Vacuolar protein sorting-associated protein 4B	P46467	Vps4b	Mus musculus
P46471	23	3	3	13.39	23	5	5	21.02	46	5	5	0	21.02	26S protease regulatory subunit 7	P46471	Psmc2	Mus musculus
P46638	31	3	3	19.27	31	3	3	19.27	62	3	3	0.21	19.27	Ras-related protein Rab-11B	P46638	Rab11b	Mus musculus
P46664	12	3	3	10.75	34	5	4	17.54	46	5	4	0.14	17.54	Adenylosuccinate synthetase isozyme 2	P46664	Adss	Mus musculus
P47738	271	19	19	54.34	349	22	22	54.34	620	25	25	0	56.07	Aldehyde dehydrogenase, mitochondrial	P47738	Aldh2	Mus musculus
P47754	55	6	4	33.57	53	8	6	53.15	108	8	6	0	53.15	F-actin-capping protein subunit alpha-2	P47754	Capza2	Mus musculus
P47757	106	8	8	33.21	107	9	9	35.38	213	9	9	0	35.38	F-actin-capping protein subunit beta	P47757	Capzb	Mus musculus
P47791	302	16	16	48.2	280	16	16	48.2	582	16	16	0	48.2	Glutathione reductase, mitochondrial	P47791	Gsr	Mus musculus
P47809	3	2	2	8.31	10	4	4	16.62	13	4	4	0.14	16.62	Dual specificity mitogen-activated protein kinase kinase 4	P47809	Map2k4	Mus musculus
P47811	36	6	6	33.89	65	6	6	33.89	101	6	6	0	33.89	Mitogen-activated protein kinase 14	P47811	Mapk14	Mus musculus
P47911	9	2	2	10.81	34	2	2	10.81	43	2	2	0.86	10.81	60S ribosomal protein L6	P47911	Rpl6	Mus musculus
P47941	0	0	0		3	2	2	9.24	3	2	2	0.86	9.24	Crk-like protein	P47941	Crkl	Mus musculus
P47955	14	2	2	28.95	28	3	3	48.25	42	3	3	0.21	48.25	60S acidic ribosomal protein P1	P47955	Rplp1	Mus musculus
P47962	3	1	1	6.06	28	5	5	28.28	31	5	5	0	28.28	60S ribosomal protein L5	P47962	Rpl5	Mus musculus
P47968	8	2	2	11.22	6	2	2	11.22	14	2	2	0.86	11.22	Ribose-5-phosphate isomerase	P47968	Rpia	Mus musculus
P48024	0	0	0		4	2	2	37.17	4	2	2	0.86	37.17	Eukaryotic translation initiation factor 1	P48024	Eif1	Mus musculus
P48025	15	2	2	6.68	26	3	3	8.59	41	3	3	0.21	8.59	Tyrosine-protein kinase SYK	P48025	Syk	Mus musculus
P48036	95	9	9	38.87	96	8	8	35.74	191	9	9	0	38.87	Annexin A5	P48036	Anxa5	Mus musculus
P48193	61	10	10	17.95	6	1	1	1.75	67	10	10	0	17.95	Protein 4.1	P48193	Epb41	Mus musculus
P48758	0	0	0		11	2	2	16.97	11	2	2	0.86	16.97	Carbonyl reductase [NADPH] 1	P48758	Cbr1	Mus musculus
P48999	0	0	0		4	2	2	4.75	4	2	2	0.86	4.75	Arachidonate 5-lipoxygenase	P48999	Alox5	Mus musculus
P49138	1	1	1	6.99	8	2	2	11.92	9	2	2	0.86	11.92	MAP kinase-activated protein kinase 2	P49138	Mapkapk2	Mus musculus
P49222	17	4	4	12.16	1	1	1	3.04	18	4	4	0.14	12.16	Erythrocyte membrane protein band 4.2	P49222	Epb42	Mus musculus
P49290	6	2	2	4.89	21	3	3	6.7	27	3	3	0.21	6.7	Eosinophil peroxidase	P49290	Epx	Mus musculus
P49312	54	4	4	16.56	76	4	4	16.56	130	4	4	0.14	16.56	Heterogeneous nuclear ribonucleoprotein A1	P49312	Hnrnpa1	Mus musculus
P49710	2	1	1	6.38	7	2	2	7	9	2	2	0.86	7	Hematopoietic lineage cell-specific protein	P49710	Hcls1	Mus musculus
P49718	0	0	0		3	2	2	3.27	3	2	2	0.86	3.27	DNA replication licensing factor MCM5	P49718	Mcm5	Mus musculus
P49722	168	7	7	32.91	150	8	8	32.91	318	8	8	0	32.91	Proteasome subunit alpha type-2	P49722	Psma2	Mus musculus
P49813	10	3	3	9.75	0	0	0		10	3	3	0.21	9.75	Tropomodulin-1	P49813	Tmod1	Mus musculus
P50247	17	3	3	10.65	56	6	6	20.37	73	6	6	0	20.37	Adenosylhomocysteinase	P50247	Ahcy	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P50396	172	14	8	35.79	165	13	7	35.79	337	14	8	0	35.79	Rab GDP dissociation inhibitor alpha	P50396	Gdi1	Mus musculus
P50429	11	3	3	11.42	6	2	2	8.8	17	3	3	0.21	11.42	Arylsulfatase B	P50429	Arsb	Mus musculus
P50431	1	1	1	7.95	12	3	3	10.04	13	4	4	0.14	17.99	Serine hydroxymethyltransferase, cytosolic	P50431	Shmt1	Mus musculus
P50446	19	2	2	4.16	14	1	1	2.17	33	2	2	0.86	4.16	Keratin, type II cytoskeletal 6A	P50446	Krt6a	Mus musculus
P50516	103	10	10	27.07	148	13	13	36.79	251	14	14	0	39.22	V-type proton ATPase catalytic subunit A	P50516	Atp6v1a	Mus musculus
P50518	21	3	3	27.43	35	3	3	15.04	56	4	4	0.14	27.43	V-type proton ATPase subunit E 1	P50518	Atp6v1e1	Mus musculus
P50543	78	4	4	64.29	102	5	5	64.29	180	5	5	0	64.29	Protein S100-A11	P50543	S100a11	Mus musculus
P50544	0	0	0		11	3	3	10.21	11	3	3	0.21	10.21	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	P50544	Acadvl	Mus musculus
P50580	36	5	5	19.8	63	7	7	24.62	99	7	7	0	24.62	Proliferation-associated protein 2G4	P50580	Pa2g4	Mus musculus
P51125	15	4	4	12.69	23	3	3	10.53	38	4	4	0.14	12.69	Calpastatin	P51125	Cast	Mus musculus
P51150	22	4	4	28.02	48	6	6	43	70	7	7	0	47.83	Ras-related protein Rab-7a	P51150	Rab7a	Mus musculus
P51174	13	3	3	8.37	39	8	8	23.95	52	8	8	0	23.95	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	P51174	Acadl	Mus musculus
P51410	6	1	1	9.9	19	4	4	42.71	25	4	4	0.14	42.71	60S ribosomal protein L9	P51410	Rpl9	Mus musculus
P51437	120	7	7	44.51	141	7	7	44.51	261	8	8	0	44.51	Cathelin-related antimicrobial peptide	P51437	Camp	Mus musculus
P51807	0	0	0		13	2	2	30.09	13	2	2	0.86	30.09	Dynein light chain Tctex-type 1	P51807	Dynlt1	Mus musculus
P51859	16	3	3	25.32	5	2	2	18.14	21	3	3	0.21	25.32	Hepatoma-derived growth factor	P51859	Hdgf	Mus musculus
P51863	0	0	0		14	2	2	9.69	14	2	2	0.86	9.69	V-type proton ATPase subunit d 1	P51863	Atp6v0d1	Mus musculus
P51881	0	0	0		7	2	2	13.42	7	2	2	0.86	13.42	ADP/ATP translocase 2	P51881	Slc25a5	Mus musculus
P52480	603	34	34	59.7	1018	45	45	64.03	1621	45	45	0	64.03	Pyruvate kinase PKM	P52480	Pkm	Mus musculus
P52624	22	2	2	18.65	74	6	6	34.41	96	6	6	0	34.41	Uridine phosphorylase 1	P52624	Upp1	Mus musculus
P53994	0	0	0		9	2	2	12.74	9	2	2	0.86	12.74	Ras-related protein Rab-2A	P53994	Rab2a	Mus musculus
P54071	23	3	3	11.73	83	9	9	24.12	106	9	9	0	24.12	Isocitrate dehydrogenase [NADP], mitochondrial	P54071	Idh2	Mus musculus
P54310	0	0	0		4	3	3	8.17	4	3	3	0.21	8.17	Hormone-sensitive lipase	P54310	Lipe	Mus musculus
P54775	71	6	6	27.51	66	7	7	28.47	137	8	8	0	31.1	26S protease regulatory subunit 6B	P54775	Psmc4	Mus musculus
P54822	24	4	4	17.77	12	3	3	11.78	36	5	5	0	21.69	Adenylosuccinate lyase	P54822	Adsl	Mus musculus
P54823	14	2	2	7.25	17	4	4	13.46	31	4	4	0.14	13.46	Probable ATP-dependent RNA helicase DDX6	P54823	Ddx6	Mus musculus
P54923	1	1	1	4.97	3	2	2	9.12	4	2	2	0.86	9.12	[Protein ADP-ribosylarginine] hydrolase	P54923	Adprh	Mus musculus
P55264	12	3	3	22.99	37	7	7	34.9	49	7	7	0	34.9	Adenosine kinase	P55264	Adk	Mus musculus
P56391	2	2	2	29.07	3	1	1	16.28	5	2	2	0.86	29.07	Cytochrome c oxidase subunit 6B1	P56391	Cox6b1	Mus musculus
P56399	59	11	11	25.52	111	15	15	28.9	170	17	17	0	32.05	Ubiquitin carboxyl-terminal hydrolase 5	P56399	Usp5	Mus musculus
P56480	84	8	8	24.76	109	12	12	37.62	193	12	12	0	37.62	ATP synthase subunit beta, mitochondrial	P56480	Atp5b	Mus musculus
P56565	0	0	0		15	2	2	26.6	15	2	2	0.86	26.6	Protein S100-A1	P56565	S100a1	Mus musculus
P56959	28	3	3	12.55	37	4	4	13.51	65	4	4	0.14	13.51	RNA-binding protein FUS	P56959	Fus	Mus musculus
P57716	2	1	1	4.1	2	2	2	7.34	4	2	2	0.86	7.34	Nicastrin	P57716	Ncstn	Mus musculus
P57780	474	33	20	48.46	363	31	18	43.53	837	36	22	0	50.88	Alpha-actinin-4	P57780	Actn4	Mus musculus
P57784	10	2	2	20.39	27	5	5	35.69	37	5	5	0	35.69	U2 small nuclear ribonucleoprotein A'	P57784	Snrpa1	Mus musculus
P58058	20	4	4	16.4	11	2	2	7.97	31	5	5	0	20.5	NAD kinase	P58058	Nadk	Mus musculus
P58252	473	20	20	41.14	744	31	31	47.32	1217	32	32	0	47.32	Elongation factor 2	P58252	Eef2	Mus musculus
P58389	19	1	1	8.98	25	5	5	28.17	44	5	5	0	28.17	Serine/threonine-protein phosphatase 2A activator	P58389	Ppp2r4	Mus musculus
P59108	16	2	1	4.38	23	3	2	8.94	39	3	2	0.86	8.94	Copine-2	P59108	Cpne2	Mus musculus
P59999	95	2	2	17.86	76	2	2	17.86	171	2	2	0.86	17.86	Actin-related protein 2/3 complex subunit 4	P59999	Arpc4	Mus musculus
P60122	15	4	4	14.47	41	6	6	21.71	56	6	6	0	21.71	RuvB-like 1	P60122	Ruvbl1	Mus musculus
P60229	3	2	2	7.19	9	2	2	7.19	12	2	2	0.86	7.19	Eukaryotic translation initiation factor 3 subunit E	P60229	Eif3e	Mus musculus
P60335	9	4	3	19.66	49	5	4	27.81	58	5	4	0.14	27.81	Poly(rC)-binding protein 1	P60335	Pcbp1	Mus musculus
P60670	5	1	1	2.96	18	4	4	16.94	23	4	4	0.14	16.94	Nuclear protein localization protein 4 homolog	P60670	Nploc4	Mus musculus
P60710	2835	53	26	77.07	6375	72	34	81.87	9210	78	37	0	81.87	Actin, cytoplasmic 1	P60710	Actb	Mus musculus
P60766	76	7	7	58.12	186	11	10	58.12	262	11	10	0	58.12	Cell division control protein 42 homolog	P60766	Cdc42	Mus musculus
P60843	48	5	4	19.21	124	16	14	47.78	172	16	14	0	47.78	Eukaryotic initiation factor 4A-I	P60843	Eif4a1	Mus musculus
P61022	1	1	1	10.26	4	2	2	18.46	5	2	2	0.86	18.46	Calcineurin B homologous protein 1	P61022	Chp1	Mus musculus
P61079	12	2	2	28.57	25	2	2	28.57	37	2	2	0.86	28.57	Ubiquitin-conjugating enzyme E2 D3	P61079	Ube2d3	Mus musculus
P61089	12	2	2	31.58	28	2	2	31.58	40	2	2	0.86	31.58	Ubiquitin-conjugating enzyme E2 N	P61089	Ube2n	Mus musculus
P61161	418	17	17	44.92	392	15	15	37.31	810	19	19	0	44.92	Actin-related protein 2	P61161	Actr2	Mus musculus
P61164	57	6	6	24.47	63	5	5	27.13	120	7	7	0	31.91	Alpha-centractin	P61164	Actr1a	Mus musculus
P61202	2	2	2	10.38	3	1	1	5.64	5	2	2	0.86	10.38	COP9 signalosome complex subunit 2	P61202	Cops2	Mus musculus
P61222	0	0	0		23	6	6	17.86	23	6	6	0	17.86	ATP-binding cassette sub-family E member 1	P61222	Abce1	Mus musculus
P61327	4	2	2	21.92	5	3	3	25.34	9	4	4	0.14	39.04	Protein mago nashi homolog	P61327	Magoh	Mus musculus
P61750	52	4	0	31.67	153	10	3	57.78	205	10	3	0.21	57.78	ADP-ribosylation factor 4	P61750	Arf4	Mus musculus
P61965	2	2	2	11.08	5	3	3	14.37	7	3	3	0.21	14.37	WD repeat-containing protein 5	P61965	Wdr5	Mus musculus
P61979	72	8	8	25.92	137	11	11	33.48	209	11	11	0	33.48	Heterogeneous nuclear ribonucleoprotein K	P61979	Hnrnpk	Mus musculus
P61982	111	7	7	44.94	99	7	7	44.94	210	7	7	0	44.94	14-3-3 protein gamma	P61982	Ywhag	Mus musculus
P62082	4	1	1	6.19	38	4	4	33.51	42	4	4	0.14	33.51	40S ribosomal protein S7	P62082	Rps7	Mus musculus
P62137	93	8	3	33.64	176	12	4	37.27	269	12	4	0.14	37.27	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	P62137	Ppp1ca	Mus musculus
P62141	98	7	2	29.66	164	12	4	38.23	262	12	4	0.14	38.23	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	P62141	Ppp1cb	Mus musculus
P62192	0	0	0		3	2	2	6.36	3	2	2	0.86	6.36	26S protease regulatory subunit 4	P62192	Psmc1	Mus musculus
P62196	24	4	4	15.27	19	3	3	15.27	43	4	4	0.14	15.27	26S protease regulatory subunit 8	P62196	Psmc5	Mus musculus
P62204	174	4	4	45.64	172	4	4	45.64	346	4	4	0.14	45.64	Calmodulin	P62204	Calm1	Mus musculus
P62242	0	0	0		9	2	2	13.46	9	2	2	0.86	13.46	40S ribosomal protein S8	P62242	Rps8	Mus musculus
P62259	108	7	6	43.14	99	8	8	43.53	207	9	8	0	47.45	14-3-3 protein epsilon	P62259	Ywhae	Mus musculus
P62267	0	0	0		11	2	2	19.58	11	2	2	0.86	19.58	40S ribosomal protein S23	P62267	Rps23	Mus musculus
P62281	0	0	0		7	2	2	17.72	7	2	2	0.86	17.72	40S ribosomal protein S11	P62281	Rps11	Mus musculus
P62315	29	3	3	27.73	55	5	5	36.97	84	6	6	0	36.97	Small nuclear ribonucleoprotein Sm D1	P62315	Snrpd1	Mus musculus
P62317	28	2	2	16.1	40	2	2	16.1	68	2	2	0.86	16.1	Small nuclear ribonucleoprotein Sm D2	P62317	Snrpd2	Mus musculus
P62320	71	2	2	24.6	80	2	2	24.6	151	2	2	0.86	24.6	Small nuclear ribonucleoprotein Sm D3	P62320	Snrpd3	Mus musculus
P62331	4	1	1	5.71	28	5	5	45.14	32	5	5	0	45.14	ADP-ribosylation factor 6	P62331	Arf6	Mus musculus
P62334	13	2	2	7.46	22	3	3	7.46	35	3	3	0.21	7.46	26S protease regulatory subunit 10B	P62334	Psmc6	Mus musculus
P62482	4	1	1	4.09	9	3	3	17.44	13	3	3	0.21	17.44	Voltage-gated potassium channel subunit beta-2	P62482	Kcnab2	Mus musculus
P62702	2	1	1	4.56	7	3	3	11.79	9	3	3	0.21	11.79	40S ribosomal protein S4, X isoform	P62702	Rps4x	Mus musculus
P62715	22	5	5	32.69	41	6	6	33.66	63	7	7	0	37.22	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	P62715	Ppp2cb	Mus musculus
P62774	7	2	2	32.2	8	2	2	32.2	15	2	2	0.86	32.2	Myotrophin	P62774	Mtpn	Mus musculus
P62806	1905	22	22	60.19	2113	18	18	58.25	4018	23	23	0	60.19	Histone H4	P62806	Hist1h4a	Mus musculus
P62814	86	9	9	25.44	147	10	10	28.38	233	10	10	0	28.38	V-type proton ATPase subunit B, brain isoform	P62814	Atp6v1b2	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P62827	101	10	10	57.41	307	16	16	57.87	408	16	16	0	57.87	GTP-binding nuclear protein Ran	P62827	Ran	Mus musculus
P62830	0	0	0		10	2	2	15	10	2	2	0.86	15	60S ribosomal protein L23	P62830	Rpl23	Mus musculus
P62835	63	5	5	31.52	59	8	8	37.5	122	8	8	0	37.5	Ras-related protein Rap-1A	P62835	Rap1a	Mus musculus
P62874	40	4	3	22.35	67	7	5	31.47	107	7	5	0	31.47	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	P62874	Gnb1	Mus musculus
P62880	18	3	2	21.76	72	10	8	48.53	90	10	8	0	48.53	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	P62880	Gnb2	Mus musculus
P62889	8	1	1	13.91	26	2	2	24.35	34	2	2	0.86	24.35	60S ribosomal protein L30	P62889	Rpl30	Mus musculus
P62908	1	1	1	4.94	38	7	7	39.09	39	7	7	0	39.09	40S ribosomal protein S3	P62908	Rps3	Mus musculus
P62960	23	5	5	29.5	36	4	4	20.5	59	5	5	0	29.5	Nuclease-sensitive element-binding protein 1	P62960	Ybx1	Mus musculus
P62962	53	5	5	41.43	91	5	5	41.43	144	5	5	0	41.43	Profilin-1	P62962	Pfn1	Mus musculus
P62996	17	2	2	10.42	31	4	4	18.75	48	4	4	0.14	18.75	Transformer-2 protein homolog beta	P62996	Tra2b	Mus musculus
P63001	32	9	0	35.42	103	10	2	48.44	135	12	2	0.86	48.44	Ras-related C3 botulinum toxin substrate 1	P63001	Rac1	Mus musculus
P63005	20	2	2	6.34	49	6	6	25.12	69	6	6	0	25.12	Platelet-activating factor acetylhydrolase IB subunit alpha	P63005	Pafah1b1	Mus musculus
P63017	440	31	30	52.79	525	34	32	58.67	965	40	38	0	59.44	Heat shock cognate 71 kDa protein	P63017	Hspa8	Mus musculus
P63028	14	1	1	8.14	19	2	2	8.72	33	2	2	0.86	8.72	Translationally-controlled tumor protein	P63028	Tpt1	Mus musculus
P63073	2	2	2	15.67	16	2	2	20.74	18	3	3	0.21	20.74	Eukaryotic translation initiation factor 4E	P63073	Eif4e	Mus musculus
P63085	5	3	3	15.36	37	6	5	30.45	42	6	5	0	30.45	Mitogen-activated protein kinase 1	P63085	Mapk1	Mus musculus
P63094	0	0	0		17	2	2	9.39	17	2	2	0.86	9.39	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	P63094	Gnas	Mus musculus
P63101	291	11	9	50.61	265	13	12	55.51	556	14	12	0	55.51	14-3-3 protein zeta/delta	P63101	Ywhaz	Mus musculus
P63158	40	5	4	34.88	76	5	4	27.44	116	6	5	0	34.88	High mobility group protein B1	P63158	Hmgb1	Mus musculus
P63242	75	5	5	37.66	110	5	5	37.66	185	5	5	0	37.66	Eukaryotic translation initiation factor 5A-1	P63242	Eif5a	Mus musculus
P63325	6	1	1	5.45	15	3	3	23.64	21	3	3	0.21	23.64	40S ribosomal protein S10	P63325	Rps10	Mus musculus
P63328	7	2	2	9.6	11	3	3	9.79	18	3	3	0.21	9.79	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	P63328	Ppp3ca	Mus musculus
P67778	6	1	1	7.35	23	2	2	13.6	29	2	2	0.86	13.6	Prohibitin	P67778	Phb	Mus musculus
P68033	1139	26	8	57.56	3002	42	13	61.01	4141	43	13	0	61.01	Actin, alpha cardiac muscle 1	P68033	Actc1	Mus musculus
P68037	17	4	4	48.7	17	4	4	42.86	34	5	5	0	48.7	Ubiquitin-conjugating enzyme E2 L3	P68037	Ube2l3	Mus musculus
P68040	95	8	8	46.69	241	16	16	61.83	336	16	16	0	61.83	Guanine nucleotide-binding protein subunit beta-2-like 1	P68040	Gnb2l1	Mus musculus
P68254	81	9	8	45.71	78	8	8	40	159	10	9	0	45.71	14-3-3 protein theta	P68254	Ywhaq	Mus musculus
P68368	178	14	6	48.21	297	16	6	52.01	475	16	6	0	52.01	Tubulin alpha-4A chain	P68368	Tuba4a	Mus musculus
P68369	140	13	5	45.68	243	17	7	53.22	383	17	7	0	53.22	Tubulin alpha-1A chain	P68369	Tuba1a	Mus musculus
P68433	1146	27	17	32.35	1260	24	15	32.35	2406	29	19	0	32.35	Histone H3.1	P68433	Hist1h3a	Mus musculus
P68510	123	9	8	47.97	99	12	12	55.69	222	13	12	0	55.69	14-3-3 protein eta	P68510	Ywhah	Mus musculus
P70168	142	14	14	27.17	179	15	15	28.54	321	18	18	0	30.37	Importin subunit beta-1	P70168	Kpnb1	Mus musculus
P70195	91	7	7	49.46	64	6	6	46.93	155	8	8	0	53.79	Proteasome subunit beta type-7	P70195	Psmb7	Mus musculus
P70268	1	1	1	3.17	27	6	6	11.42	28	6	6	0	11.42	Serine/threonine-protein kinase N1	P70268	Pkn1	Mus musculus
P70290	60	5	5	16.31	32	5	5	13.09	92	7	7	0	16.31	55 kDa erythrocyte membrane protein	P70290	Mpp1	Mus musculus
P70296	27	2	2	19.25	41	3	3	33.16	68	3	3	0.21	33.16	Phosphatidylethanolamine-binding protein 1	P70296	Pebp1	Mus musculus
P70315	1	1	1	4.42	4	2	2	5.96	5	3	3	0.21	10.38	Wiskott-Aldrich syndrome protein homolog	P70315	Was	Mus musculus
P70335	5	3	3	5.39	8	2	2	4.58	13	3	3	0.21	5.39	Rho-associated protein kinase 1	P70335	Rock1	Mus musculus
P70441	12	2	2	13.52	25	4	4	24.23	37	4	4	0.14	24.23	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	P70441	Slc9a3r1	Mus musculus
P70460	20	3	3	9.87	54	2	2	7.2	74	4	4	0.14	10.4	Vasodilator-stimulated phosphoprotein	P70460	Vasp	Mus musculus
P70670	14	1	1	0.69	26	4	4	2.88	40	4	4	0.14	2.88	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	P70670	Naca	Mus musculus
P70677	13	2	2	13	22	2	2	17.33	35	3	3	0.21	22.74	Caspase-3	P70677	Casp3	Mus musculus
P70697	0	0	0		24	3	3	15.8	24	3	3	0.21	15.8	Uroporphyrinogen decarboxylase	P70697	Urod	Mus musculus
P70698	1	1	1	2.71	15	2	2	5.08	16	2	2	0.86	5.08	CTP synthase 1	P70698	Ctps1	Mus musculus
P80313	46	5	5	15.99	87	8	8	27.02	133	8	8	0	27.02	T-complex protein 1 subunit eta	P80313	Cct7	Mus musculus
P80314	64	5	5	16.45	115	10	10	31.78	179	10	10	0	31.78	T-complex protein 1 subunit beta	P80314	Cct2	Mus musculus
P80315	23	4	4	11.13	50	6	6	18.37	73	6	6	0	18.37	T-complex protein 1 subunit delta	P80315	Cct4	Mus musculus
P80316	42	6	6	22.74	79	9	9	31.05	121	9	9	0	31.05	T-complex protein 1 subunit epsilon	P80316	Cct5	Mus musculus
P80317	50	7	7	22.22	71	8	8	22.22	121	8	8	0	22.22	T-complex protein 1 subunit zeta	P80317	Cct6a	Mus musculus
P80318	2	2	2	4.59	18	6	6	16.51	20	6	6	0	16.51	T-complex protein 1 subunit gamma	P80318	Cct3	Mus musculus
P82198	311	17	17	36.75	254	16	16	36.75	565	17	17	0	36.75	Transforming growth factor-beta-induced protein ig-h3	P82198	Tgfbi	Mus musculus
P83917	2	1	1	15.68	11	2	2	16.76	13	2	2	0.86	16.76	Chromobox protein homolog 1	P83917	Cbx1	Mus musculus
P84078	85	7	4	56.35	222	15	8	69.61	307	15	8	0	69.61	ADP-ribosylation factor 1	P84078	Arf1	Mus musculus
P84084	73	7	3	57.78	181	11	3	57.78	254	11	3	0.21	57.78	ADP-ribosylation factor 5	P84084	Arf5	Mus musculus
P84091	1	1	1	6.44	10	2	2	7.13	11	3	3	0.21	13.56	AP-2 complex subunit mu	P84091	Ap2m1	Mus musculus
P84096	92	9	9	61.78	180	10	10	61.78	272	10	10	0	61.78	Rho-related GTP-binding protein RhoG	P84096	Rhog	Mus musculus
P84104	8	1	1	12.8	28	3	3	28.66	36	3	3	0.21	28.66	Serine/arginine-rich splicing factor 3	P84104	Srsf3	Mus musculus
P84228	1899	33	17	32.35	1690	28	14	32.35	3589	34	18	0	32.35	Histone H3.2	P84228	Hist1h3b	Mus musculus
P84244	1017	26	10	32.35	975	26	12	32.35	1992	29	13	0	32.35	Histone H3.3	P84244	H3f3a	Mus musculus
P85094	2	1	1	16.02	12	2	2	29.13	14	2	2	0.86	29.13	Isochorismatase domain-containing protein 2A, mitochondrial	P85094	Isoc2a	Mus musculus
P97310	0	0	0		13	4	4	6.64	13	4	4	0.14	6.64	DNA replication licensing factor MCM2	P97310	Mcm2	Mus musculus
P97311	0	0	0		3	2	2	5.36	3	2	2	0.86	5.36	DNA replication licensing factor MCM6	P97311	Mcm6	Mus musculus
P97315	3	1	1	8.81	5	2	2	17.62	8	2	2	0.86	17.62	Cysteine and glycine-rich protein 1	P97315	Csrp1	Mus musculus
P97351	0	0	0		17	4	4	12.12	17	4	4	0.14	12.12	40S ribosomal protein S3a	P97351	Rps3a	Mus musculus
P97355	0	0	0		14	3	3	19.13	14	3	3	0.21	19.13	Spermine synthase	P97355	Sms	Mus musculus
P97364	1	1	1	4.42	2	2	2	7.74	3	2	2	0.86	7.74	Selenide, water dikinase 2	P97364	Sephs2	Mus musculus
P97369	82	9	9	38.35	172	16	16	43.36	254	16	16	0	43.36	Neutrophil cytosol factor 4	P97369	Ncf4	Mus musculus
P97371	44	4	4	20.88	50	5	5	26.51	94	5	5	0	26.51	Proteasome activator complex subunit 1	P97371	Psme1	Mus musculus
P97372	48	7	7	41.84	57	6	6	35.98	105	7	7	0	41.84	Proteasome activator complex subunit 2	P97372	Psme2	Mus musculus
P97384	130	11	11	22.86	205	14	14	28.23	335	14	14	0	28.23	Annexin A11	P97384	Anxa11	Mus musculus
P97425	70	3	2	39.1	17	3	3	26.92	87	4	3	0.21	39.1	Eosinophil cationic protein 2	P97425	Ear2	Mus musculus
P97426	103	5	4	45.16	22	2	2	25.81	125	5	4	0.14	45.16	Eosinophil cationic protein 1	P97426	Ear1	Mus musculus
P97429	3	1	1	5.02	15	4	4	19.75	18	4	4	0.14	19.75	Annexin A4	P97429	Anxa4	Mus musculus
P97484	0	0	0		6	3	3	8.92	6	3	3	0.21	8.92	Leukocyte immunoglobulin-like receptor subfamily B member 3	P97484	Lilrb3	Mus musculus
P97807	62	3	3	10.45	49	3	3	10.45	111	3	3	0.21	10.45	Fumarate hydratase, mitochondrial	P97807	Fh	Mus musculus
P97821	32	4	4	14.94	29	4	4	13.2	61	5	5	0	17.53	Dipeptidyl peptidase 1	P97821	Ctsc	Mus musculus
P97822	0	0	0		3	3	3	11.54	3	3	3	0.21	11.54	Acidic leucine-rich nuclear phosphoprotein 32 family member E	P97822	Anp32e	Mus musculus
P97823	11	2	2	16.09	77	9	9	49.57	88	9	9	0	49.57	Acyl-protein thioesterase 1	P97823	Lypla1	Mus musculus
P97855	4	1	1	3.66	10	2	2	8.6	14	2	2	0.86	8.6	Ras GTPase-activating protein-binding protein 1	P97855	G3bp1	Mus musculus
P97864	2	1	1	5.61	7	2	2	15.18	9	2	2	0.86	15.18	Caspase-7	P97864	Casp7	Mus musculus
P99024	111	12	3	50.9	290	16	4	51.35	401	16	4	0.14	51.35	Tubulin beta-5 chain	P99024	Tubb5	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P99026	32	6	6	38.64	6	4	4	32.95	38	6	6	0	38.64	Proteasome subunit beta type-4	P99026	Psmb4	Mus musculus
P99027	79	4	4	69.57	99	6	6	91.3	178	6	6	0	91.3	60S acidic ribosomal protein P2	P99027	Rplp2	Mus musculus
P99029	52	7	7	47.62	97	8	8	48.1	149	8	8	0	48.1	Peroxiredoxin-5, mitochondrial	P99029	Prdx5	Mus musculus
Q00519	437	25	25	33.56	383	23	23	28.61	820	27	27	0	34.91	Xanthine dehydrogenase/oxidase	Q00519	Xdh	Mus musculus
Q00612	229	18	10	33.59	373	23	13	43.3	602	28	17	0	43.3	Glucose-6-phosphate 1-dehydrogenase X	Q00612	G6pdx	Mus musculus
Q00623	7	1	1	13.64	8	2	2	18.94	15	2	2	0.86	18.94	Apolipoprotein A-I	Q00623	Apoa1	Mus musculus
Q00896	7	3	2	14.08	0	0	0		7	3	2	0.86	14.08	Alpha-1-antitrypsin 1-3	Q00896	Serpina1c	Mus musculus
Q01102	22	3	3	8.98	7	1	1	4.3	29	3	3	0.21	8.98	P-selectin	Q01102	Selp	Mus musculus
Q01339	23	6	6	29.86	1	1	1	4.93	24	6	6	0	29.86	Beta-2-glycoprotein 1	Q01339	Apoh	Mus musculus
Q01514	8	1	1	4.41	16	2	2	7.64	24	2	2	0.86	7.64	Interferon-induced guanylate-binding protein 1	Q01514	Gbp1	Mus musculus
Q01853	881	47	47	62.16	754	46	46	63.28	1635	52	52	0	67.87	Transitional endoplasmic reticulum ATPase	Q01853	Vcp	Mus musculus
Q02053	324	26	26	38.09	549	36	36	47.73	873	36	36	0	47.73	Ubiquitin-like modifier-activating enzyme 1	Q02053	Uba1	Mus musculus
Q02357	195	22	22	19.76	25	4	4	4.4	220	22	22	0	19.76	Ankyrin-1	Q02357	Ank1	Mus musculus
Q02819	2	1	1	2.4	10	4	4	14.16	12	4	4	0.14	14.16	Nucleobindin-1	Q02819	Nucb1	Mus musculus
Q03265	15	3	3	10.67	36	8	8	15.37	51	8	8	0	15.37	ATP synthase subunit alpha, mitochondrial	Q03265	Atp5a1	Mus musculus
Q04750	89	7	7	13.69	93	8	8	15.25	182	8	8	0	15.25	DNA topoisomerase 1	Q04750	Top1	Mus musculus
Q05144	71	14	5	58.33	244	18	10	60.94	315	20	10	0	60.94	Ras-related C3 botulinum toxin substrate 2	Q05144	Rac2	Mus musculus
Q06890	49	5	5	19.2	16	3	3	11.16	65	5	5	0	19.2	Clusterin	Q06890	Clu	Mus musculus
Q07076	32	5	5	14.04	47	6	6	13.17	79	7	7	0	16.41	Annexin A7	Q07076	Anxa7	Mus musculus
Q07797	111	10	10	31.02	66	6	6	18.2	177	10	10	0	31.02	Galectin-3-binding protein	Q07797	Lgals3bp	Mus musculus
Q08761	16	3	3	9.93	2	2	2	4.89	18	3	3	0.21	9.93	Vitamin K-dependent protein S	Q08761	Pros1	Mus musculus
Q08943	8	3	3	7.91	12	4	4	11.3	20	4	4	0.14	11.3	FACT complex subunit SSRP1	Q08943	Ssrp1	Mus musculus
Q09014	58	5	5	15.9	136	10	10	25.64	194	10	10	0	25.64	Neutrophil cytosol factor 1	Q09014	Ncf1	Mus musculus
Q09200	1	1	1	5.25	9	2	2	7.32	10	2	2	0.86	7.32	Beta-1,4 N-acetylgalactosaminyltransferase 1	Q09200	B4galnt1	Mus musculus
Q09PK2	201	12	12	59	313	13	13	59	514	14	14	0	59	Retroviral-like aspartic protease 1	Q09PK2	Asprv1	Mus musculus
Q11011	160	18	18	30.54	152	16	16	29.24	312	19	19	0	30.65	Puromycin-sensitive aminopeptidase	Q11011	Npepps	Mus musculus
Q11136	11	2	2	5.88	12	2	2	9.53	23	3	3	0.21	11.56	Xaa-Pro dipeptidase	Q11136	Pepd	Mus musculus
Q20BD0	29	3	3	10.54	40	4	4	10.54	69	4	4	0.14	10.54	Heterogeneous nuclear ribonucleoprotein A/B	Q20BD0	Hnrnpab	Mus musculus
Q2NL51	0	0	0		17	3	3	10.41	17	3	3	0.21	10.41	Glycogen synthase kinase-3 alpha	Q2NL51	Gsk3a	Mus musculus
Q2VLH6	0	0	0		10	5	5	7.31	10	5	5	0	7.31	Scavenger receptor cysteine-rich type 1 protein M130	Q2VLH6	Cd163	Mus musculus
Q3TBD2	16	4	4	7.08	34	5	5	7.17	50	5	5	0	7.17	Minor histocompatibility protein HA-1	Q3TBD2	Hmha1	Mus musculus
Q3THK7	15	4	4	13.13	56	7	7	21.21	71	7	7	0	21.21	GMP synthase [glutamine-hydrolyzing]	Q3THK7	Gmps	Mus musculus
Q3TIU4	1	1	1	2.96	3	2	2	6.41	4	2	2	0.86	6.41	2',5'-phosphodiesterase 12	Q3TIU4	Pde12	Mus musculus
Q3TIX9	0	0	0		7	3	3	10.46	7	3	3	0.21	10.46	U4/U6.U5 tri-snRNP-associated protein 2	Q3TIX9	Usp39	Mus musculus
Q3TRM8	408	29	29	46.96	477	31	30	45.99	885	32	31	0	47.18	Hexokinase-3	Q3TRM8	Hk3	Mus musculus
Q3TW96	36	2	2	7.1	58	5	5	18.34	94	5	5	0	18.34	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	Q3TW96	Uap1l1	Mus musculus
Q3TXS7	13	5	5	14.59	37	9	9	21.3	50	9	9	0	21.3	26S proteasome non-ATPase regulatory subunit 1	Q3TXS7	Psmd1	Mus musculus
Q3U0V1	2	2	2	3.74	26	5	5	11.23	28	5	5	0	11.23	Far upstream element-binding protein 2	Q3U0V1	Khsrp	Mus musculus
Q3U0V2	0	0	0		6	2	2	10.32	6	2	2	0.86	10.32	Tumor necrosis factor receptor type 1-associated DEATH domain protein	Q3U0V2	Tradd	Mus musculus
Q3U1J4	71	8	8	13.33	58	6	6	11.4	129	9	9	0	14.82	DNA damage-binding protein 1	Q3U1J4	Ddb1	Mus musculus
Q3U2G2	110	14	14	31.24	125	12	12	24.7	235	16	16	0	34.8	Heat shock 70 kDa protein 4	Q3U2G2	Hspa4	Mus musculus
Q3U5Q7	6	1	1	6.94	21	4	4	15.44	27	4	4	0.14	15.44	UMP-CMP kinase 2, mitochondrial	Q3U5Q7	Cmpk2	Mus musculus
Q3U7R1	29	6	6	10.71	61	7	7	12.18	90	7	7	0	12.18	Extended synaptotagmin-1	Q3U7R1	Esyt1	Mus musculus
Q3UDE2	1	1	1	3.44	16	2	2	5.95	17	2	2	0.86	5.95	Tubulin--tyrosine ligase-like protein 12	Q3UDE2	Ttll12	Mus musculus
Q3UHD6	0	0	0		15	3	3	11.32	15	3	3	0.21	11.32	Sorting nexin-27	Q3UHD6	Snx27	Mus musculus
Q3UJB9	0	0	0		3	2	2	3.63	3	2	2	0.86	3.63	Enhancer of mRNA-decapping protein 4	Q3UJB9	Edc4	Mus musculus
Q3UKJ7	0	0	0		6	2	2	5.46	6	2	2	0.86	5.46	WD40 repeat-containing protein SMU1	Q3UKJ7	Smu1	Mus musculus
Q3ULJ0	0	0	0		29	4	4	23.65	29	4	4	0.14	23.65	Glycerol-3-phosphate dehydrogenase 1-like protein	Q3ULJ0	Gpd1l	Mus musculus
Q3UM45	20	3	3	15.79	29	5	5	22.16	49	5	5	0	22.16	Protein phosphatase 1 regulatory subunit 7	Q3UM45	Ppp1r7	Mus musculus
Q3UND0	17	6	6	41.62	79	9	9	47.49	96	9	9	0	47.49	Src kinase-associated phosphoprotein 2	Q3UND0	Skap2	Mus musculus
Q3UP87	208	11	11	33.58	182	11	11	33.21	390	14	14	0	38.11	Neutrophil elastase	Q3UP87	Elane	Mus musculus
Q3UPH1	0	0	0		2	2	2	14	2	2	2	0.86	14	Protein PRRC1	Q3UPH1	Prrc1	Mus musculus
Q3UPL0	0	0	0		5	3	3	5.28	5	3	3	0.21	5.28	Protein transport protein Sec31A	Q3UPL0	Sec31a	Mus musculus
Q3UQ44	1	1	1	1.78	5	2	2	3.17	6	3	3	0.21	4.95	Ras GTPase-activating-like protein IQGAP2	Q3UQ44	Iqgap2	Mus musculus
Q3UW53	23	7	7	13.5	58	9	9	15.33	81	11	11	0	18.9	Protein Niban	Q3UW53	Fam129a	Mus musculus
Q3UYV9	2	1	1	3.04	20	6	6	14.94	22	6	6	0	14.94	Nuclear cap-binding protein subunit 1	Q3UYV9	Ncbp1	Mus musculus
Q3UZ39	18	3	3	12.07	10	2	2	8.5	28	3	3	0.21	12.07	Leucine-rich repeat flightless-interacting protein 1	Q3UZ39	Lrrfip1	Mus musculus
Q3UZA1	7	2	2	15.53	1	1	1	6.55	8	3	3	0.21	22.09	CapZ-interacting protein	Q3UZA1	Rcsd1	Mus musculus
Q3UZZ4	170	11	11	34.85	211	13	13	37.43	381	13	13	0	37.43	Olfactomedin-4	Q3UZZ4	Olfm4	Mus musculus
Q3V0K9	27	3	1	6.67	19	3	2	10.48	46	4	2	0.86	11.9	Plastin-1	Q3V0K9	Pls1	Mus musculus
Q3V1G4	53	6	6	14.61	35	5	5	12.2	88	6	6	0	14.61	Olfactomedin-like protein 2B	Q3V1G4	Olfml2b	Mus musculus
Q3V1L4	66	10	10	36.61	91	11	11	36.61	157	12	12	0	40.54	Cytosolic purine 5'-nucleotidase	Q3V1L4	Nt5c2	Mus musculus
Q3V3R1	1	1	1	1.54	11	5	5	8.39	12	5	5	0	8.39	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	Q3V3R1	Mthfd1l	Mus musculus
Q4LDD4	0	0	0		3	2	2	2.55	3	2	2	0.86	2.55	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	Q4LDD4	Arap1	Mus musculus
Q501J6	0	0	0		23	3	2	6.92	23	3	2	0.86	6.92	Probable ATP-dependent RNA helicase DDX17	Q501J6	Ddx17	Mus musculus
Q571E4	29	4	4	16.15	21	3	3	12.31	50	4	4	0.14	16.15	N-acetylgalactosamine-6-sulfatase	Q571E4	Galns	Mus musculus
Q571I9	73	7	7	17.71	88	6	6	14.71	161	7	7	0	17.71	Aldehyde dehydrogenase family 16 member A1	Q571I9	Aldh16a1	Mus musculus
Q5FWK3	7	1	1	5.92	11	2	2	10.02	18	2	2	0.86	10.02	Rho GTPase-activating protein 1	Q5FWK3	Arhgap1	Mus musculus
Q5RKN9	106	9	7	44.76	131	10	8	51.75	237	10	8	0	51.75	Capping protein (Actin filament) muscle Z-line, alpha 1	Q5RKN9	Capza1	Mus musculus
Q5SQX6	5	1	1	0.88	4	3	3	3.03	9	3	3	0.21	3.03	Cytoplasmic FMR1-interacting protein 2	Q5SQX6	Cyfip2	Mus musculus
Q5SSL4	0	0	0		3	2	2	3.96	3	2	2	0.86	3.96	Active breakpoint cluster region-related protein	Q5SSL4	Abr	Mus musculus
Q5SUA5	0	0	0		4	2	2	3.71	4	2	2	0.86	3.71	Unconventional myosin-Ig	Q5SUA5	Myo1g	Mus musculus
Q5SUR0	127	19	19	29.84	172	19	19	31.79	299	22	22	0	33.88	Phosphoribosylformylglycinamidine synthase	Q5SUR0	Pfas	Mus musculus
Q5SVD0	1	1	1	8.33	5	2	2	24.07	6	2	2	0.86	24.07	Filamin-interacting protein FAM101B	Q5SVD0	Fam101b	Mus musculus
Q5XJF6	19	2	2	13.36	37	2	2	13.36	56	2	2	0.86	13.36	Ribosomal protein	Q5XJF6	Rpl10a	Mus musculus
Q5XJY5	1	1	1	2.15	3	2	2	4.5	4	2	2	0.86	4.5	Coatomer subunit delta	Q5XJY5	Arcn1	Mus musculus
Q60605-2	107	6	6	62.91	135	8	8	70.2	242	8	8	0	70.2	Isoform Smooth muscle of Myosin light polypeptide 6	Q60605	Myl6	Mus musculus
Q60631	14	4	4	25.35	21	2	2	11.98	35	4	4	0.14	25.35	Growth factor receptor-bound protein 2	Q60631	Grb2	Mus musculus
Q60668	2	1	1	4.79	12	3	3	19.72	14	3	3	0.21	19.72	Heterogeneous nuclear ribonucleoprotein D0	Q60668	Hnrnpd	Mus musculus
Q60675	2	2	2	0.93	0	0	0		2	2	2	0.86	0.93	Laminin subunit alpha-2	Q60675	Lama2	Mus musculus
Q60676	6	2	2	6.41	10	2	2	6.41	16	2	2	0.86	6.41	Serine/threonine-protein phosphatase 5	Q60676	Ppp5c	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q60692	73	4	4	31.93	65	5	5	31.93	138	5	5	0	31.93	Proteasome subunit beta type-6	Q60692	Psmb6	Mus musculus
Q60737	4	1	1	5.37	15	2	2	11	19	2	2	0.86	11	Casein kinase II subunit alpha	Q60737	Csnk2a1	Mus musculus
Q60767	25	4	4	4.24	36	5	5	6.04	61	6	6	0	7.14	Lymphocyte antigen 75	Q60767	Ly75	Mus musculus
Q60864	37	5	5	14	41	4	4	11.79	78	5	5	0	14	Stress-induced-phosphoprotein 1	Q60864	Stip1	Mus musculus
Q60865	11	2	2	5.8	6	3	3	7.5	17	3	3	0.21	7.5	Caprin-1	Q60865	Caprin1	Mus musculus
Q60960	0	0	0		3	2	2	9.48	3	2	2	0.86	9.48	Importin subunit alpha-5	Q60960	Kpna1	Mus musculus
Q60963	10	2	2	6.82	16	4	4	12.95	26	4	4	0.14	12.95	Platelet-activating factor acetylhydrolase	Q60963	Pla2g7	Mus musculus
Q60972	38	5	4	32.47	50	6	4	32.47	88	6	4	0.14	32.47	Histone-binding protein RBBP4	Q60972	Rbbp4	Mus musculus
Q60973	6	4	3	23.76	53	8	6	46.35	59	8	6	0	46.35	Histone-binding protein RBBP7	Q60973	Rbbp7	Mus musculus
Q61024	2	1	1	3.57	11	2	2	6.77	13	2	2	0.86	6.77	Asparagine synthetase [glutamine-hydrolyzing]	Q61024	Asns	Mus musculus
Q61033	29	6	6	16.02	49	9	9	25.54	78	9	9	0	25.54	Lamina-associated polypeptide 2, isoforms alpha/zeta	Q61033	Tmpo	Mus musculus
Q61035	84	8	8	26.13	88	8	8	26.33	172	9	9	0	28.88	Histidine--tRNA ligase, cytoplasmic	Q61035	Hars	Mus musculus
Q61081	6	1	1	5.54	21	3	3	15.3	27	3	3	0.21	15.3	Hsp90 co-chaperone Cdc37	Q61081	Cdc37	Mus musculus
Q61093	4	1	1	4.74	42	8	8	20.88	46	8	8	0	20.88	Cytochrome b-245 heavy chain	Q61093	Cybb	Mus musculus
Q61096	155	9	9	45.28	148	10	10	51.97	303	11	11	0	55.91	Myeloblastin	Q61096	Prtn3	Mus musculus
Q61147	64	9	9	15.08	34	9	9	13.67	98	11	11	0	17.25	Ceruloplasmin	Q61147	Cp	Mus musculus
Q61166	10	2	2	12.31	19	3	3	12.31	29	3	3	0.21	12.31	Microtubule-associated protein RP/EB family member 1	Q61166	Mapre1	Mus musculus
Q61171	326	22	22	81.82	63	10	10	71.72	389	22	22	0	81.82	Peroxiredoxin-2	Q61171	Prdx2	Mus musculus
Q61176	0	0	0		19	5	5	27.24	19	5	5	0	27.24	Arginase-1	Q61176	Arg1	Mus musculus
Q61191	8	1	1	1.32	16	3	3	3.42	24	3	3	0.21	3.42	Host cell factor 1	Q61191	Hcfc1	Mus musculus
Q61207	16	3	3	9.87	31	5	5	15.8	47	5	5	0	15.8	Prosaposin	Q61207	Psap	Mus musculus
Q61210-5	0	0	0		23	9	9	16.24	23	9	9	0	16.24	Isoform 5 of Rho guanine nucleotide exchange factor 1	Q61210	Arhgef1	Mus musculus
Q61233	1097	47	45	69.22	1303	44	43	70.97	2400	52	50	0	73.21	Plastin-2	Q61233	Lcp1	Mus musculus
Q61362	93	7	7	23.14	60	6	6	20.31	153	7	7	0	23.14	Chitinase-3-like protein 1	Q61362	Chi3l1	Mus musculus
Q61508	14	1	1	5.01	46	6	6	19.86	60	6	6	0	19.86	Extracellular matrix protein 1	Q61508	Ecm1	Mus musculus
Q61543	9	4	4	5.53	28	6	6	9.87	37	6	6	0	9.87	Golgi apparatus protein 1	Q61543	Glg1	Mus musculus
Q61545	0	0	0		7	3	3	7.94	7	3	3	0.21	7.94	RNA-binding protein EWS	Q61545	Ewsr1	Mus musculus
Q61550	7	2	2	5.51	4	2	2	5.51	11	2	2	0.86	5.51	Double-strand-break repair protein rad21 homolog	Q61550	Rad21	Mus musculus
Q61578	0	0	0		5	2	2	8.91	5	2	2	0.86	8.91	NADPH:adrenodoxin oxidoreductase, mitochondrial	Q61578	Fdxr	Mus musculus
Q61598	277	21	15	51.69	281	21	15	51.69	558	21	15	0	51.69	Rab GDP dissociation inhibitor beta	Q61598	Gdi2	Mus musculus
Q61599	126	9	9	60.5	138	8	8	59	264	9	9	0	60.5	Rho GDP-dissociation inhibitor 2	Q61599	Arhgdib	Mus musculus
Q61635	26	4	4	13.81	38	10	10	31.19	64	10	10	0	31.19	GTP-binding protein	Q61635	Ifi47	Mus musculus
Q61646	918	15	15	58.79	634	14	14	51.87	1552	16	16	0	58.79	Haptoglobin	Q61646	Hp	Mus musculus
Q61655	0	0	0		21	2	2	9.21	21	2	2	0.86	9.21	ATP-dependent RNA helicase DDX19A	Q61655	Ddx19a	Mus musculus
Q61656	1	1	1	2.44	24	8	7	16.78	25	8	7	0	16.78	Probable ATP-dependent RNA helicase DDX5	Q61656	Ddx5	Mus musculus
Q61704	5	2	2	5.74	0	0	0		5	2	2	0.86	5.74	Inter-alpha-trypsin inhibitor heavy chain H3	Q61704	Itih3	Mus musculus
Q61739	10	3	3	4.67	4	2	2	3.94	14	4	4	0.14	6.87	Integrin alpha-6	Q61739	Itga6	Mus musculus
Q61749	1	1	1	4.2	5	2	2	8.02	6	2	2	0.86	8.02	Translation initiation factor eIF-2B subunit delta	Q61749	Eif2b4	Mus musculus
Q61753	5	1	1	3	42	7	7	22.33	47	7	7	0	22.33	D-3-phosphoglycerate dehydrogenase	Q61753	Phgdh	Mus musculus
Q61768	3	1	1	1.77	20	5	5	8.52	23	5	5	0	8.52	Kinesin-1 heavy chain	Q61768	Kif5b	Mus musculus
Q61838	108	21	21	28.23	40	12	12	17.32	148	21	21	0	28.23	Alpha-2-macroglobulin	Q61838	A2m	Mus musculus
Q61878	11	2	2	19.28	17	2	2	15.7	28	3	3	0.21	24.66	Bone marrow proteoglycan	Q61878	Prg2	Mus musculus
Q61881	0	0	0		9	6	6	15.72	9	6	6	0	15.72	DNA replication licensing factor MCM7	Q61881	Mcm7	Mus musculus
Q61937	45	3	3	21.58	49	3	3	21.58	94	3	3	0.21	21.58	Nucleophosmin	Q61937	Npm1	Mus musculus
Q61990	5	3	2	13.54	30	6	5	31.49	35	6	5	0	31.49	Poly(rC)-binding protein 2	Q61990	Pcbp2	Mus musculus
Q62059	1	1	1	0.45	12	3	3	2.06	13	4	4	0.14	2.5	Versican core protein	Q62059	Vcan	Mus musculus
Q62167	5	3	3	6.65	48	8	8	15.86	53	8	8	0	15.86	ATP-dependent RNA helicase DDX3X	Q62167	Ddx3x	Mus musculus
Q62178	33	6	6	15	58	6	6	15	91	6	6	0	15	Semaphorin-4A	Q62178	Sema4a	Mus musculus
Q62193	1	1	1	8.52	13	2	2	16.67	14	2	2	0.86	16.67	Replication protein A 32 kDa subunit	Q62193	Rpa2	Mus musculus
Q62261	180	23	22	15.91	159	23	23	17.14	339	26	25	0	18.71	Spectrin beta chain, non-erythrocytic 1	Q62261	Sptbn1	Mus musculus
Q62318	0	0	0		7	2	2	6.35	7	2	2	0.86	6.35	Transcription intermediary factor 1-beta	Q62318	Trim28	Mus musculus
Q62348	33	4	4	28.07	15	4	4	24.56	48	5	5	0	33.33	Translin	Q62348	Tsn	Mus musculus
Q62376	1	1	1	2.46	3	2	2	5.58	4	2	2	0.86	5.58	U1 small nuclear ribonucleoprotein 70 kDa	Q62376	Snrnp70	Mus musculus
Q62393	7	1	1	8.48	19	2	2	22.32	26	2	2	0.86	22.32	Tumor protein D52	Q62393	Tpd52	Mus musculus
Q62418	27	4	4	16.74	32	5	5	16.97	59	5	5	0	16.97	Drebrin-like protein	Q62418	Dbnl	Mus musculus
Q62419	0	0	0		7	2	2	8.15	7	2	2	0.86	8.15	Endophilin-A2	Q62419	Sh3gl1	Mus musculus
Q62422	44	4	4	32.09	74	6	6	32.09	118	6	6	0	32.09	Osteoclast-stimulating factor 1	Q62422	Ostf1	Mus musculus
Q62465	18	5	5	19.95	42	6	6	23.65	60	6	6	0	23.65	Synaptic vesicle membrane protein VAT-1 homolog	Q62465	Vat1	Mus musculus
Q62469	3	3	3	4.75	3	1	1	1.19	6	3	3	0.21	4.75	Integrin alpha-2	Q62469	Itga2	Mus musculus
Q62523	12	3	3	14.72	18	3	3	14.54	30	4	4	0.14	17.91	Zyxin	Q62523	Zyx	Mus musculus
Q63810	30	3	3	27.06	36	2	2	27.06	66	3	3	0.21	27.06	Calcineurin subunit B type 1	Q63810	Ppp3r1	Mus musculus
Q63844	3	3	3	11.84	49	9	8	33.95	52	9	8	0	33.95	Mitogen-activated protein kinase 3	Q63844	Mapk3	Mus musculus
Q640N3	0	0	0		4	2	2	2.63	4	2	2	0.86	2.63	Rho GTPase-activating protein 30	Q640N3	Arhgap30	Mus musculus
Q64324	19	6	6	18.38	63	10	10	31.2	82	10	10	0	31.2	Syntaxin-binding protein 2	Q64324	Stxbp2	Mus musculus
Q64442	26	2	2	10.64	9	2	2	12.61	35	3	3	0.21	17.37	Sorbitol dehydrogenase	Q64442	Sord	Mus musculus
Q64455	23	3	3	6.54	11	2	2	4.52	34	3	3	0.21	6.54	Receptor-type tyrosine-protein phosphatase eta	Q64455	Ptprj	Mus musculus
Q64511	0	0	0		11	4	4	3.85	11	4	4	0.14	3.85	DNA topoisomerase 2-beta	Q64511	Top2b	Mus musculus
Q64514	56	9	9	16.4	51	8	8	14.82	107	10	10	0	17.99	Tripeptidyl-peptidase 2	Q64514	Tpp2	Mus musculus
Q64516	0	0	0		5	2	2	8.59	5	2	2	0.86	8.59	Glycerol kinase	Q64516	Gk	Mus musculus
Q64523	5238	30	7	62.79	8206	31	4	58.14	13444	35	7	0	62.79	Histone H2A type 2-C	Q64523	Hist2h2ac	Mus musculus
Q64674	1	1	1	7.28	34	5	5	27.15	35	5	5	0	27.15	Spermidine synthase	Q64674	Srm	Mus musculus
Q64727	307	22	22	33.21	220	19	19	26.17	527	23	23	0	33.21	Vinculin	Q64727	Vcl	Mus musculus
Q64737	3	1	1	2.28	17	4	4	8.71	20	4	4	0.14	8.71	Trifunctional purine biosynthetic protein adenosine-3	Q64737	Gart	Mus musculus
Q68FD5	236	31	31	31.52	372	37	37	32.54	608	42	42	0	35.64	Clathrin heavy chain 1	Q68FD5	Cltc	Mus musculus
Q68FL6	0	0	0		8	4	4	9.53	8	4	4	0.14	9.53	Methionine--tRNA ligase, cytoplasmic	Q68FL6	Mars	Mus musculus
Q69ZK0	0	0	0		7	3	3	3.64	7	3	3	0.21	3.64	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	Q69ZK0	Prex1	Mus musculus
Q6A026	0	0	0		3	2	2	2.03	3	2	2	0.86	2.03	Sister chromatid cohesion protein PDS5 homolog A	Q6A026	Pds5a	Mus musculus
Q6A4J8	22	4	4	7.43	42	7	7	14.23	64	7	7	0	14.23	Ubiquitin carboxyl-terminal hydrolase 7	Q6A4J8	Usp7	Mus musculus
Q6DTY7	0	0	0		5	3	3	10.45	5	3	3	0.21	10.45	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	Q6DTY7	Pfkfb4	Mus musculus
Q6IRU2	115	9	9	38.71	66	6	6	36.29	181	9	9	0	38.71	Tropomyosin alpha-4 chain	Q6IRU2	Tpm4	Mus musculus
Q6NSR8	5	4	4	16.41	0	0	0		5	4	4	0.14	16.41	Probable aminopeptidase NPEPL1	Q6NSR8	Npepl1	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q6NZJ6	6	1	1	0.88	7	3	3	3.44	13	3	3	0.21	3.44	Eukaryotic translation initiation factor 4 gamma 1	Q6NZJ6	Eif4g1	Mus musculus
Q6P069-2	75	7	7	55.74	131	14	14	69.4	206	14	14	0	69.4	Isoform 2 of Sorcin	Q6P069	Sri	Mus musculus
Q6P1B1	38	7	7	21.51	62	10	10	32.42	100	10	10	0	32.42	Xaa-Pro aminopeptidase 1	Q6P1B1	Xpnpep1	Mus musculus
Q6P1F6	1	1	1	3.13	7	2	2	7.61	8	2	2	0.86	7.61	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	Q6P1F6	Ppp2r2a	Mus musculus
Q6P2B1	2	1	1	2.17	6	3	3	6.5	8	3	3	0.21	6.5	Transportin-3	Q6P2B1	Tnpo3	Mus musculus
Q6P4S8	0	0	0		3	2	2	2.64	3	2	2	0.86	2.64	Integrator complex subunit 1	Q6P4S8	Ints1	Mus musculus
Q6P4T2	37	9	9	8.71	65	14	14	13.76	102	14	14	0	13.76	U5 small nuclear ribonucleoprotein 200 kDa helicase	Q6P4T2	Snrnp200	Mus musculus
Q6P542	0	0	0		2	2	2	5.97	2	2	2	0.86	5.97	ATP-binding cassette sub-family F member 1	Q6P542	Abcf1	Mus musculus
Q6P5E4	169	23	23	26.05	163	18	18	22.24	332	24	24	0	27.08	UDP-glucose:glycoprotein glucosyltransferase 1	Q6P5E4	Uggt1	Mus musculus
Q6P5F9	80	7	7	11.76	104	8	8	12.79	184	8	8	0	12.79	Exportin-1	Q6P5F9	Xpo1	Mus musculus
Q6P8X1	2	1	1	2.71	26	4	4	16.5	28	4	4	0.14	16.5	Sorting nexin-6	Q6P8X1	Snx6	Mus musculus
Q6P9Q4	8	1	1	1.59	5	2	2	2.92	13	2	2	0.86	2.92	FH1/FH2 domain-containing protein 1	Q6P9Q4	Fhod1	Mus musculus
Q6PAV2	1	1	1	2.55	8	3	3	5.77	9	4	4	0.14	8.33	Probable E3 ubiquitin-protein ligase HERC4	Q6PAV2	Herc4	Mus musculus
Q6PD03	0	0	0		12	4	4	12.76	12	4	4	0.14	12.76	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	Q6PD03	Ppp2r5a	Mus musculus
Q6PDG5	9	3	3	5.11	19	4	4	7.17	28	4	4	0.14	7.17	SWI/SNF complex subunit SMARCC2	Q6PDG5	Smarcc2	Mus musculus
Q6PDI5	0	0	0		19	6	6	6.52	19	6	6	0	6.52	Proteasome-associated protein ECM29 homolog	Q6PDI5	Ecm29	Mus musculus
Q6PDM2	17	2	2	13.31	18	1	1	9.27	35	2	2	0.86	13.31	Serine/arginine-rich splicing factor 1	Q6PDM2	Srsf1	Mus musculus
Q6PE01	0	0	0		10	4	4	19.55	10	4	4	0.14	19.55	U5 small nuclear ribonucleoprotein 40 kDa protein	Q6PE01	Snrnp40	Mus musculus
Q6PEB6	6	1	1	9.78	18	3	3	24.89	24	3	3	0.21	24.89	MOB-like protein phocein	Q6PEB6	Mob4	Mus musculus
Q6PHU5	17	3	3	6.79	24	3	3	8.48	41	4	4	0.14	10.3	Sortilin	Q6PHU5	Sort1	Mus musculus
Q6PHZ2	0	0	0		11	2	2	7.62	11	2	2	0.86	7.62	Calcium/calmodulin-dependent protein kinase type II subunit delta	Q6PHZ2	Camk2d	Mus musculus
Q6URW6	51	5	2	3.6	54	4	1	2.5	105	6	2	0.86	4.2	Myosin-14	Q6URW6	Myh14	Mus musculus
Q6WVG3	31	6	6	33.64	26	4	4	17.43	57	6	6	0	33.64	BTB/POZ domain-containing protein KCTD12	Q6WVG3	Kctd12	Mus musculus
Q6ZPJ3	4	2	2	4.11	3	1	1	2.48	7	2	2	0.86	4.11	E2/E3 hybrid ubiquitin-protein ligase UBE2O	Q6ZPJ3	Ube2o	Mus musculus
Q6ZQ38	45	8	8	11.22	53	8	8	11.22	98	8	8	0	11.22	Cullin-associated NEDD8-dissociated protein 1	Q6ZQ38	Cand1	Mus musculus
Q6ZQA0	0	0	0		6	2	2	1.79	6	2	2	0.86	1.79	Neurobeachin-like protein 2	Q6ZQA0	Nbeal2	Mus musculus
Q6ZWM4	14	2	2	36.46	15	3	3	61.46	29	3	3	0.21	61.46	U6 snRNA-associated Sm-like protein LSm8	Q6ZWM4	Lsm8	Mus musculus
Q6ZWQ0	2	2	2	0.83	1	1	1	0.25	3	3	3	0.21	1.08	Nesprin-2	Q6ZWQ0	Syne2	Mus musculus
Q6ZWQ9	104	8	8	45.93	119	10	10	45.93	223	10	10	0	45.93	MCG5400	Q6ZWQ9	Myl12a	Mus musculus
Q6ZWR6	35	8	8	1.81	74	17	17	4.03	109	20	20	0	4.42	Nesprin-1	Q6ZWR6	Syne1	Mus musculus
Q6ZWV3	0	0	0		7	2	2	13.55	7	2	2	0.86	13.55	60S ribosomal protein L10	Q6ZWV3	Rpl10	Mus musculus
Q6ZWX6	1	1	1	5.4	20	2	2	14.29	21	2	2	0.86	14.29	Eukaryotic translation initiation factor 2 subunit 1	Q6ZWX6	Eif2s1	Mus musculus
Q76MZ3	98	8	8	24.28	148	12	12	28.86	246	13	13	0	34.97	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	Q76MZ3	Ppp2r1a	Mus musculus
Q78PY7	26	5	5	10	122	16	16	27.47	148	16	16	0	27.47	Staphylococcal nuclease domain-containing protein 1	Q78PY7	Snd1	Mus musculus
Q78ZA7	8	3	3	14.13	16	3	3	14.13	24	3	3	0.21	14.13	Nucleosome assembly protein 1-like 4	Q78ZA7	Nap1l4	Mus musculus
Q7M6Y3	4	2	2	5.45	12	2	2	8.48	16	3	3	0.21	8.48	Phosphatidylinositol-binding clathrin assembly protein	Q7M6Y3	Picalm	Mus musculus
Q7TMB8	0	0	0		2	2	2	2	2	2	2	0.86	2	Cytoplasmic FMR1-interacting protein 1	Q7TMB8	Cyfip1	Mus musculus
Q7TMK9	6	1	1	2.09	27	3	3	7.54	33	3	3	0.21	7.54	Heterogeneous nuclear ribonucleoprotein Q	Q7TMK9	Syncrip	Mus musculus
Q7TNG5	28	5	5	14.64	43	4	4	12.79	71	5	5	0	14.64	Echinoderm microtubule-associated protein-like 2	Q7TNG5	Eml2	Mus musculus
Q7TPR4	702	42	29	57.06	489	39	26	54.04	1191	44	30	0	61.21	Alpha-actinin-1	Q7TPR4	Actn1	Mus musculus
Q7TPV4	0	0	0		22	9	9	12.05	22	9	9	0	12.05	Myb-binding protein 1A	Q7TPV4	Mybbp1a	Mus musculus
Q7TQI3	19	2	2	12.55	46	4	4	21.77	65	4	4	0.14	21.77	Ubiquitin thioesterase OTUB1	Q7TQI3	Otub1	Mus musculus
Q7TSI3	8	2	2	6.07	17	2	2	6.07	25	2	2	0.86	6.07	Serine/threonine-protein phosphatase 6 regulatory subunit 1	Q7TSI3	Ppp6r1	Mus musculus
Q7TSV4	44	4	4	13.23	44	5	5	15.32	88	5	5	0	15.32	Phosphoglucomutase-2	Q7TSV4	Pgm2	Mus musculus
Q80T06	23	3	3	17.08	29	4	4	18.51	52	4	4	0.14	18.51	Elongation factor 1-delta	Q80T06	Eef1d	Mus musculus
Q80UM3	1	1	1	3.24	10	3	3	7.63	11	3	3	0.21	7.63	N-alpha-acetyltransferase 15, NatA auxiliary subunit	Q80UM3	Naa15	Mus musculus
Q80UP5	1	1	1	2.04	3	2	2	4.93	4	2	2	0.86	4.93	Ankyrin repeat domain-containing protein 13A	Q80UP5	Ankrd13a	Mus musculus
Q80UR4	1	1	1	5.66	7	3	3	17.61	8	3	3	0.21	17.61	Mast cell protease-11	Q80UR4	Prss34	Mus musculus
Q80VD1	0	0	0		6	2	2	8.16	6	2	2	0.86	8.16	Protein FAM98B	Q80VD1	Fam98b	Mus musculus
Q80WQ2	0	0	0		2	2	2	4.22	2	2	2	0.86	4.22	Protein VAC14 homolog	Q80WQ2	Vac14	Mus musculus
Q80X41	11	1	1	7.5	32	7	7	23.86	43	7	7	0	23.86	Serine/threonine-protein kinase VRK1	Q80X41	Vrk1	Mus musculus
Q80X90	20	2	1	1.19	24	3	2	1.96	44	4	3	0.21	2.73	Filamin-B	Q80X90	Flnb	Mus musculus
Q80ZJ2	22	3	3	19.2	21	4	4	25	43	4	4	0.14	25	Impa1 protein	Q80ZJ2	Impa1	Mus musculus
Q80ZX0	0	0	0		8	2	2	3.36	8	2	2	0.86	3.36	Protein Sec24b	Q80ZX0	Sec24b	Mus musculus
Q810B6	5	1	1	2.48	20	2	2	4.11	25	2	2	0.86	4.11	Rabankyrin-5	Q810B6	Ankfy1	Mus musculus
Q8BFR5	0	0	0		7	2	2	7.3	7	2	2	0.86	7.3	Elongation factor Tu, mitochondrial	Q8BFR5	Tufm	Mus musculus
Q8BFY6	10	2	2	8.73	10	2	2	8.73	20	2	2	0.86	8.73	Peflin	Q8BFY6	Pef1	Mus musculus
Q8BFY9	30	5	5	11.92	50	6	6	11.69	80	8	8	0	16.04	Transportin-1	Q8BFY9	Tnpo1	Mus musculus
Q8BFZ3	838	22	3	35.11	2674	35	6	42.02	3512	38	6	0	42.02	Beta-actin-like protein 2	Q8BFZ3	Actbl2	Mus musculus
Q8BG05	30	4	4	10.82	87	7	7	21.11	117	7	7	0	21.11	Heterogeneous nuclear ribonucleoprotein A3	Q8BG05	Hnrnpa3	Mus musculus
Q8BG32	9	2	2	6.4	11	4	4	14.22	20	4	4	0.14	14.22	26S proteasome non-ATPase regulatory subunit 11	Q8BG32	Psmd11	Mus musculus
Q8BGD9	22	2	2	8.67	29	2	2	8.67	51	2	2	0.86	8.67	Eukaryotic translation initiation factor 4B	Q8BGD9	Eif4b	Mus musculus
Q8BGE6	0	0	0		15	2	2	8.65	15	2	2	0.86	8.65	Cysteine protease ATG4B	Q8BGE6	Atg4b	Mus musculus
Q8BGJ5	41	6	6	22.31	112	8	8	27.41	153	8	8	0	27.41	MCG13402, isoform CRA_a	Q8BGJ5	Ptbp1	Mus musculus
Q8BGQ7	27	3	3	5.37	66	10	10	18.39	93	10	10	0	18.39	Alanine--tRNA ligase, cytoplasmic	Q8BGQ7	Aars	Mus musculus
Q8BH04	1	1	1	2.5	27	8	8	21.56	28	8	8	0	21.56	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	Q8BH04	Pck2	Mus musculus
Q8BH43	1	1	1	3.82	26	3	3	10.26	27	3	3	0.21	10.26	Wiskott-Aldrich syndrome protein family member 2	Q8BH43	Wasf2	Mus musculus
Q8BH61	75	12	12	21.86	53	7	7	11.48	128	13	13	0	21.86	Coagulation factor XIII A chain	Q8BH61	F13a1	Mus musculus
Q8BH69	2	1	1	5.36	14	2	2	9.18	16	2	2	0.86	9.18	Selenide, water dikinase 1	Q8BH69	Sephs1	Mus musculus
Q8BH95	0	0	0		8	2	2	16.9	8	2	2	0.86	16.9	Enoyl-CoA hydratase, mitochondrial	Q8BH95	Echs1	Mus musculus
Q8BHD7	3	2	2	10.13	29	4	4	21.61	32	4	4	0.14	21.61	Polypyrimidine tract-binding protein 3	Q8BHD7	Ptbp3	Mus musculus
Q8BHG1	77	9	9	15.5	59	11	11	18.26	136	11	11	0	18.26	Nardilysin	Q8BHG1	Nrd1	Mus musculus
Q8BHJ5	5	2	2	8.95	14	2	2	8.95	19	2	2	0.86	8.95	F-box-like/WD repeat-containing protein TBL1XR1	Q8BHJ5	Tbl1xr1	Mus musculus
Q8BHN3	57	9	9	19.17	31	7	7	14.94	88	10	10	0	21.4	Neutral alpha-glucosidase AB	Q8BHN3	Ganab	Mus musculus
Q8BIJ6	0	0	0		13	2	2	3.36	13	2	2	0.86	3.36	Isoleucine--tRNA ligase, mitochondrial	Q8BIJ6	Iars2	Mus musculus
Q8BJ71	1	1	1	3.17	5	2	2	7.08	6	2	2	0.86	7.08	Nuclear pore complex protein Nup93	Q8BJ71	Nup93	Mus musculus
Q8BJS4	3	1	1	3.42	15	4	4	10.4	18	4	4	0.14	10.4	SUN domain-containing protein 2	Q8BJS4	Sun2	Mus musculus
Q8BJW6	0	0	0		2	2	2	7.06	2	2	2	0.86	7.06	Eukaryotic translation initiation factor 2A	Q8BJW6	Eif2a	Mus musculus
Q8BJY1	20	2	2	10.52	26	4	4	17.86	46	4	4	0.14	17.86	26S proteasome non-ATPase regulatory subunit 5	Q8BJY1	Psmd5	Mus musculus
Q8BK67	26	3	3	8.27	104	10	10	31.15	130	10	10	0	31.15	Protein RCC2	Q8BK67	Rcc2	Mus musculus
Q8BKC5	86	9	9	16.77	150	13	13	23.15	236	13	13	0	23.15	Importin-5	Q8BKC5	Ipo5	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q8BL97	19	2	2	14.23	28	2	2	14.23	47	2	2	0.86	14.23	Serine/arginine-rich splicing factor 7	Q8BL97	Srsf7	Mus musculus
Q8BMA6	0	0	0		3	2	2	5.92	3	2	2	0.86	5.92	Signal recognition particle subunit SRP68	Q8BMA6	Srp68	Mus musculus
Q8BMJ2	2	1	1	2.63	14	2	2	4.07	16	2	2	0.86	4.07	Leucine--tRNA ligase, cytoplasmic	Q8BMJ2	Lars	Mus musculus
Q8BMS1	0	0	0		13	2	2	7.47	13	2	2	0.86	7.47	Trifunctional enzyme subunit alpha, mitochondrial	Q8BMS1	Hadha	Mus musculus
Q8BND5	59	8	8	17.51	54	8	8	16.31	113	10	10	0	21.39	Sulfhydryl oxidase 1	Q8BND5	Qsox1	Mus musculus
Q8BP47	7	2	2	6.8	31	5	5	15.92	38	5	5	0	15.92	Asparagine--tRNA ligase, cytoplasmic	Q8BP47	Nars	Mus musculus
Q8BP56	6	1	1	3.77	6	2	2	6.67	12	2	2	0.86	6.67	Acid trehalase-like protein 1	Q8BP56	Athl1	Mus musculus
Q8BPU7	6	2	2	7.29	13	2	2	6.6	19	3	3	0.21	11.42	Engulfment and cell motility protein 1	Q8BPU7	Elmo1	Mus musculus
Q8BRF7	1	1	1	4.07	18	4	4	12.52	19	4	4	0.14	12.52	Sec1 family domain-containing protein 1	Q8BRF7	Scfd1	Mus musculus
Q8BT60	107	9	8	31.14	161	12	11	33.4	268	12	11	0	33.4	Copine-3	Q8BT60	Cpne3	Mus musculus
Q8BTE6	7	1	1	36.51	27	4	4	52.38	34	4	4	0.14	52.38	Protein Wfdc21	Q8BTE6	Wfdc21	Mus musculus
Q8BTM8	1273	79	78	44.5	1227	75	74	41.25	2500	86	85	0	45.56	Filamin-A	Q8BTM8	Flna	Mus musculus
Q8BTZ7	4	1	1	3.61	17	5	5	20	21	5	5	0	20	Mannose-1-phosphate guanyltransferase beta	Q8BTZ7	Gmppb	Mus musculus
Q8BU30	0	0	0		5	2	2	2.14	5	2	2	0.86	2.14	Isoleucine--tRNA ligase, cytoplasmic	Q8BU30	Iars	Mus musculus
Q8BUM3	1	1	1	7.52	10	3	3	17.83	11	3	3	0.21	17.83	Tyrosine-protein phosphatase non-receptor type 7	Q8BUM3	Ptpn7	Mus musculus
Q8BV13	2	1	1	6.82	3	2	2	15.15	5	2	2	0.86	15.15	COP9 signalosome complex subunit 7b	Q8BV13	Cops7b	Mus musculus
Q8BVE3	21	2	2	8.7	22	2	2	8.7	43	2	2	0.86	8.7	V-type proton ATPase subunit H	Q8BVE3	Atp6v1h	Mus musculus
Q8BVG4	9	2	2	5.68	33	2	2	5.68	42	2	2	0.86	5.68	Dipeptidyl peptidase 9	Q8BVG4	Dpp9	Mus musculus
Q8BWT1	5	2	2	12.09	39	8	8	32.49	44	8	8	0	32.49	3-ketoacyl-CoA thiolase, mitochondrial	Q8BWT1	Acaa2	Mus musculus
Q8BWY3	3	2	2	10.98	23	3	3	15.56	26	3	3	0.21	15.56	Eukaryotic peptide chain release factor subunit 1	Q8BWY3	Etf1	Mus musculus
Q8BX94	0	0	0		3	3	3	11.98	3	3	3	0.21	11.98	Oxysterol-binding protein-related protein 2	Q8BX94	Osbpl2	Mus musculus
Q8BXK9	1	1	1	6.77	3	2	2	7.17	4	2	2	0.86	7.17	Chloride intracellular channel protein 5	Q8BXK9	Clic5	Mus musculus
Q8BY71	0	0	0		7	2	2	8.17	7	2	2	0.86	8.17	Histone acetyltransferase type B catalytic subunit	Q8BY71	Hat1	Mus musculus
Q8BYA0	0	0	0		3	3	3	5.02	3	3	3	0.21	5.02	Tubulin-specific chaperone D	Q8BYA0	Tbcd	Mus musculus
Q8BZA9	0	0	0		10	3	3	18.59	10	3	3	0.21	18.59	Fructose-2,6-bisphosphatase TIGAR	Q8BZA9	Tigar	Mus musculus
Q8C0D5	0	0	0		2	2	2	4.7	2	2	2	0.86	4.7	Elongation factor Tu GTP-binding domain-containing protein 1	Q8C0D5	Eftud1	Mus musculus
Q8C0E2	2	1	1	3.87	5	2	2	13.99	7	2	2	0.86	13.99	Vacuolar protein sorting-associated protein 26B	Q8C0E2	Vps26b	Mus musculus
Q8C0I1	0	0	0		5	2	2	6.05	5	2	2	0.86	6.05	Alkyldihydroxyacetonephosphate synthase, peroxisomal	Q8C0I1	Agps	Mus musculus
Q8C147	1	1	1	1.52	8	3	3	3.14	9	4	4	0.14	4.67	Dedicator of cytokinesis protein 8	Q8C147	Dock8	Mus musculus
Q8C166	15	1	1	3.73	27	5	5	19.78	42	5	5	0	19.78	Copine-1	Q8C166	Cpne1	Mus musculus
Q8C1A5	0	0	0		15	5	5	10.77	15	5	5	0	10.77	Thimet oligopeptidase	Q8C1A5	Thop1	Mus musculus
Q8C1B7	13	3	3	13.69	19	3	3	13.69	32	3	3	0.21	13.69	Septin-11	Q8C1B7	Sept11	Mus musculus
Q8C3J5	0	0	0		10	4	4	3.45	10	4	4	0.14	3.45	Dedicator of cytokinesis protein 2	Q8C3J5	Dock2	Mus musculus
Q8C4Y3	0	0	0		2	2	2	6.03	2	2	2	0.86	6.03	Negative elongation factor B	Q8C4Y3	Nelfb	Mus musculus
Q8C570	0	0	0		15	3	3	21.47	15	3	3	0.21	21.47	mRNA export factor	Q8C570	Rae1	Mus musculus
Q8C5P5	0	0	0		20	4	4	12.42	20	4	4	0.14	12.42	5'-nucleotidase domain-containing protein 1	Q8C5P5	Nt5dc1	Mus musculus
Q8C6G8	0	0	0		2	2	2	5.93	2	2	2	0.86	5.93	WD repeat-containing protein 26	Q8C6G8	Wdr26	Mus musculus
Q8C708	9	2	2	14.22	11	2	2	14.22	20	2	2	0.86	14.22	Transmembrane protein C16orf54 homolog	Q8C708		Mus musculus
Q8CBW3	1	1	1	6.86	4	2	2	9.98	5	2	2	0.86	9.98	Abl interactor 1	Q8CBW3	Abi1	Mus musculus
Q8CC86	8	2	2	8.55	48	6	6	18.77	56	6	6	0	18.77	Nicotinate phosphoribosyltransferase	Q8CC86	Naprt	Mus musculus
Q8CCK0	125	6	2	12.37	138	7	3	12.37	263	7	3	0.21	12.37	Core histone macro-H2A.2	Q8CCK0	H2afy2	Mus musculus
Q8CDN6	16	5	5	35.29	45	7	7	35.64	61	8	8	0	35.99	Thioredoxin-like protein 1	Q8CDN6	Txnl1	Mus musculus
Q8CFI7	0	0	0		2	2	2	5.2	2	2	2	0.86	5.2	DNA-directed RNA polymerase II subunit RPB2	Q8CFI7	Polr2b	Mus musculus
Q8CFQ3	0	0	0		2	2	2	3.92	2	2	2	0.86	3.92	Intron-binding protein aquarius	Q8CFQ3	Aqr	Mus musculus
Q8CFV9	0	0	0		4	2	2	38.71	4	2	2	0.86	38.71	Riboflavin kinase	Q8CFV9	Rfk	Mus musculus
Q8CFX1	1	1	1	3.3	2	2	2	5.32	3	3	3	0.21	8.62	GDH/6PGL endoplasmic bifunctional protein	Q8CFX1	H6pd	Mus musculus
Q8CG03	77	9	9	18.73	13	4	4	8.55	90	9	9	0	18.73	cGMP-specific 3',5'-cyclic phosphodiesterase	Q8CG03	Pde5a	Mus musculus
Q8CG19	39	5	5	7.13	8	3	3	5.02	47	5	5	0	7.13	Latent-transforming growth factor beta-binding protein 1	Q8CG19	Ltbp1	Mus musculus
Q8CG29	17	2	2	2.82	35	4	4	5.65	52	4	4	0.14	5.65	Myosin IF	Q8CG29	Myo1f	Mus musculus
Q8CGC7	10	3	3	3.37	46	9	9	10.78	56	9	9	0	10.78	Bifunctional glutamate/proline--tRNA ligase	Q8CGC7	Eprs	Mus musculus
Q8CGP4	3098	15	5	58.14	3726	19	4	58.14	6824	20	5	0	58.14	Histone H2A	Q8CGP4	Hist1h2aa	Mus musculus
Q8CHP8	23	3	3	18.07	33	4	4	23.99	56	4	4	0.14	23.99	Phosphoglycolate phosphatase	Q8CHP8	Pgp	Mus musculus
Q8CI94	52	5	3	9.96	45	6	3	10.91	97	8	5	0	15.18	Glycogen phosphorylase, brain form	Q8CI94	Pygb	Mus musculus
Q8CIE6	5	2	2	3.92	31	11	11	12.5	36	11	11	0	12.5	Coatomer subunit alpha	Q8CIE6	Copa	Mus musculus
Q8CIH5	114	16	16	25.38	150	17	17	25.77	264	22	22	0	33.12	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	Q8CIH5	Plcg2	Mus musculus
Q8CIM3	0	0	0		11	3	3	10.84	11	3	3	0.21	10.84	D-2-hydroxyglutarate dehydrogenase, mitochondrial	Q8CIM3	D2hgdh	Mus musculus
Q8CIN4	17	3	3	13.93	68	6	6	20.42	85	6	6	0	20.42	Serine/threonine-protein kinase PAK 2	Q8CIN4	Pak2	Mus musculus
Q8CJG0	4	3	3	6.28	17	4	4	8.14	21	4	4	0.14	8.14	Protein argonaute-2	Q8CJG0	Ago2	Mus musculus
Q8JZQ9	20	7	7	18.93	45	10	10	22.42	65	11	11	0	24.91	Eukaryotic translation initiation factor 3 subunit B	Q8JZQ9	Eif3b	Mus musculus
Q8JZV7	0	0	0		4	2	2	10.51	4	2	2	0.86	10.51	Putative N-acetylglucosamine-6-phosphate deacetylase	Q8JZV7	Amdhd2	Mus musculus
Q8K0C9	0	0	0		16	4	4	19.35	16	4	4	0.14	19.35	GDP-mannose 4,6 dehydratase	Q8K0C9	Gmds	Mus musculus
Q8K0E8	114	11	11	34.3	279	21	21	43.04	393	21	21	0	43.04	Fibrinogen beta chain	Q8K0E8	Fgb	Mus musculus
Q8K183	3	1	1	6.73	2	2	2	7.37	5	2	2	0.86	7.37	Pyridoxal kinase	Q8K183	Pdxk	Mus musculus
Q8K1B8	185	17	17	40.75	299	20	20	44.36	484	21	21	0	46.62	Fermitin family homolog 3	Q8K1B8	Fermt3	Mus musculus
Q8K1M6	11	3	3	9.03	30	4	4	10.92	41	4	4	0.14	10.92	Dynamin-1-like protein	Q8K1M6	Dnm1l	Mus musculus
Q8K1X4	0	0	0		7	3	3	5.91	7	3	3	0.21	5.91	NCK associated protein 1 like	Q8K1X4	Nckap1l	Mus musculus
Q8K274	0	0	0		2	2	2	13.59	2	2	2	0.86	13.59	Ketosamine-3-kinase	Q8K274	Fn3krp	Mus musculus
Q8K296	1	1	1	1.09	4	2	2	4.26	5	3	3	0.21	5.35	Myotubularin-related protein 3	Q8K296	Mtmr3	Mus musculus
Q8K2B3	5	2	2	6.63	23	5	5	16.57	28	5	5	0	16.57	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Q8K2B3	Sdha	Mus musculus
Q8K2H4	0	0	0		3	2	2	6.89	3	2	2	0.86	6.89	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1	Q8K2H4	Acap1	Mus musculus
Q8K2T1	0	0	0		10	2	2	11	10	2	2	0.86	11	NmrA-like family domain-containing protein 1	Q8K2T1	Nmral1	Mus musculus
Q8K352	3	2	2	6.58	6	3	3	10.79	9	3	3	0.21	10.79	SAM and SH3 domain-containing protein 3	Q8K352	Sash3	Mus musculus
Q8K354	0	0	0		17	4	4	25.27	17	4	4	0.14	25.27	Carbonyl reductase [NADPH] 3	Q8K354	Cbr3	Mus musculus
Q8K411	7	2	2	4.73	22	5	5	11	29	5	5	0	11	Presequence protease, mitochondrial	Q8K411	Pitrm1	Mus musculus
Q8K426	18	3	3	32.48	75	4	4	47.86	93	4	4	0.14	47.86	Myeloid cysteine-rich protein	Q8K426	Retnlg	Mus musculus
Q8K482	60	6	6	12.76	112	10	10	16.39	172	11	11	0	18.72	EMILIN-2	Q8K482	Emilin2	Mus musculus
Q8K4L3	6	1	1	1.47	20	3	3	3.64	26	3	3	0.21	3.64	Supervillin	Q8K4L3	Svil	Mus musculus
Q8K4Z3	4	3	3	23.05	7	4	4	28.72	11	4	4	0.14	28.72	NAD(P)H-hydrate epimerase	Q8K4Z3	Apoa1bp	Mus musculus
Q8K558	13	3	3	17.35	16	4	4	23.34	29	4	4	0.14	23.34	Trem-like transcript 1 protein	Q8K558	Treml1	Mus musculus
Q8QZT1	0	0	0		21	4	4	18.4	21	4	4	0.14	18.4	Acetyl-CoA acetyltransferase, mitochondrial	Q8QZT1	Acat1	Mus musculus
Q8QZY1	59	6	6	18.97	80	8	8	23.94	139	8	8	0	23.94	Eukaryotic translation initiation factor 3 subunit L	Q8QZY1	Eif3l	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q8QZY6	26	2	2	11.85	27	2	2	11.85	53	2	2	0.86	11.85	Tetraspanin-14	Q8QZY6	Tspan14	Mus musculus
Q8QZY9	6	1	1	3.3	13	2	2	8.96	19	2	2	0.86	8.96	Splicing factor 3B subunit 4	Q8QZY9	Sf3b4	Mus musculus
Q8R010	3	1	1	11.25	10	3	3	30.31	13	3	3	0.21	30.31	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	Q8R010	Aimp2	Mus musculus
Q8R016	121	11	11	32.31	76	7	7	20.66	197	11	11	0	32.31	Bleomycin hydrolase	Q8R016	Blmh	Mus musculus
Q8R050	4	2	2	7.86	11	3	3	7.86	15	3	3	0.21	7.86	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	Q8R050	Gspt1	Mus musculus
Q8R081	28	5	5	24.23	87	9	9	26.96	115	9	9	0	26.96	Heterogeneous nuclear ribonucleoprotein L	Q8R081	Hnrnpl	Mus musculus
Q8R0J7	5	2	2	12.28	6	2	2	12.28	11	2	2	0.86	12.28	Vacuolar protein sorting-associated protein 37B	Q8R0J7	Vps37b	Mus musculus
Q8R146	141	13	13	30.33	77	9	9	27.05	218	13	13	0	30.33	Acylamino-acid-releasing enzyme	Q8R146	Apeh	Mus musculus
Q8R180	35	6	6	26.29	40	7	7	27.16	75	8	8	0	32.33	ERO1-like protein alpha	Q8R180	Ero1l	Mus musculus
Q8R1B4	5	2	2	3.07	19	4	4	6.26	24	4	4	0.14	6.26	Eukaryotic translation initiation factor 3 subunit C	Q8R1B4	Eif3c	Mus musculus
Q8R1Q8	0	0	0		7	3	3	17.4	7	3	3	0.21	17.4	Cytoplasmic dynein 1 light intermediate chain 1	Q8R1Q8	Dync1li1	Mus musculus
Q8R2S8	257	17	17	38.92	307	20	20	40.27	564	20	20	0	40.27	CD177 antigen	Q8R2S8	Cd177	Mus musculus
Q8R3G1	0	0	0		9	2	2	6.27	9	2	2	0.86	6.27	Nuclear inhibitor of protein phosphatase 1	Q8R3G1	Ppp1r8	Mus musculus
Q8R550	1	1	1	2.68	8	2	2	5.22	9	2	2	0.86	5.22	SH3 domain-containing kinase-binding protein 1	Q8R550	Sh3kbp1	Mus musculus
Q8R5A3	23	3	3	7.16	31	3	3	7.16	54	3	3	0.21	7.16	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	Q8R5A3	Apbb1ip	Mus musculus
Q8R5H1	3	2	2	4.49	6	3	3	4.59	9	3	3	0.21	4.59	Ubiquitin carboxyl-terminal hydrolase 15	Q8R5H1	Usp15	Mus musculus
Q8R5L1	72	4	4	32.62	82	7	7	37.28	154	7	7	0	37.28	Complement component 1 Q subcomponent-binding protein, mitochondrial	Q8R5L1	C1qbp	Mus musculus
Q8VBT9	1	1	1	2.91	7	2	2	8	8	2	2	0.86	8	Tether containing UBX domain for GLUT4	Q8VBT9	Aspscr1	Mus musculus
Q8VBV7	16	4	4	38.28	28	4	4	31.1	44	5	5	0	38.28	COP9 signalosome complex subunit 8	Q8VBV7	Cops8	Mus musculus
Q8VBW6	1	1	1	5.81	14	3	3	11.61	15	3	3	0.21	11.61	NEDD8-activating enzyme E1 regulatory subunit	Q8VBW6	Nae1	Mus musculus
Q8VC03	0	0	0		9	2	2	4.57	9	2	2	0.86	4.57	Echinoderm microtubule-associated protein-like 3	Q8VC03	Eml3	Mus musculus
Q8VC30	4	2	2	7.96	5	2	2	7.09	9	3	3	0.21	12.11	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	Q8VC30	Dak	Mus musculus
Q8VC88	31	5	5	29.55	57	6	6	30.45	88	7	7	0	30.45	Grancalcin	Q8VC88	Gca	Mus musculus
Q8VCI0	108	11	11	24.18	52	9	9	20	160	11	11	0	24.18	Phospholipase B-like 1	Q8VCI0	Plbd1	Mus musculus
Q8VCM7	135	12	12	44.27	382	20	20	54.59	517	21	21	0	56.42	Fibrinogen gamma chain	Q8VCM7	Fgg	Mus musculus
Q8VCN9	0	0	0		8	2	2	17.6	8	2	2	0.86	17.6	Tubulin-specific chaperone C	Q8VCN9	Tbcc	Mus musculus
Q8VCT3	60	12	12	31.38	126	15	15	39.23	186	16	16	0	39.23	Aminopeptidase B	Q8VCT3	Rnpep	Mus musculus
Q8VDD5	808	54	51	32.76	812	61	58	35.61	1620	64	60	0	36.38	Myosin-9	Q8VDD5	Myh9	Mus musculus
Q8VDK1	13	4	4	26.93	16	4	4	26.93	29	4	4	0.14	26.93	Nitrilase homolog 1	Q8VDK1	Nit1	Mus musculus
Q8VDL4	14	3	3	14.52	28	3	3	14.52	42	3	3	0.21	14.52	ADP-dependent glucokinase	Q8VDL4	Adpgk	Mus musculus
Q8VDM4	93	9	9	17.07	110	9	9	16.41	203	10	10	0	18.5	26S proteasome non-ATPase regulatory subunit 2	Q8VDM4	Psmd2	Mus musculus
Q8VDM6	7	3	3	7.33	80	11	11	20.14	87	12	12	0	20.49	Heterogeneous nuclear ribonucleoprotein U-like protein 1	Q8VDM6	Hnrnpul1	Mus musculus
Q8VDN2	3	2	2	4.2	13	3	3	5.96	16	3	3	0.21	5.96	Sodium/potassium-transporting ATPase subunit alpha-1	Q8VDN2	Atp1a1	Mus musculus
Q8VDP3	19	2	2	3.63	36	3	3	6.11	55	3	3	0.21	6.11	Protein-methionine sulfoxide oxidase MICAL1	Q8VDP3	Mical1	Mus musculus
Q8VDP4	13	4	4	11.39	30	4	4	12.58	43	5	5	0	14.1	Cell cycle and apoptosis regulator protein 2	Q8VDP4	Ccar2	Mus musculus
Q8VDQ8	1	1	1	6.17	9	2	2	11.83	10	2	2	0.86	11.83	NAD-dependent protein deacetylase sirtuin-2	Q8VDQ8	Sirt2	Mus musculus
Q8VDW0	2	1	0	2.34	21	5	3	17.8	23	5	3	0.21	17.8	ATP-dependent RNA helicase DDX39A	Q8VDW0	Ddx39a	Mus musculus
Q8VE11	2	2	2	5.02	9	2	2	5.02	11	2	2	0.86	5.02	Myotubularin-related protein 6	Q8VE11	Mtmr6	Mus musculus
Q8VE37	2	1	1	6.89	19	4	4	19.24	21	4	4	0.14	19.24	Regulator of chromosome condensation	Q8VE37	Rcc1	Mus musculus
Q8VEE0	15	2	2	17.54	17	2	2	17.54	32	2	2	0.86	17.54	Ribulose-phosphate 3-epimerase	Q8VEE0	Rpe	Mus musculus
Q8VEE4	0	0	0		4	2	2	6.74	4	2	2	0.86	6.74	Replication protein A 70 kDa DNA-binding subunit	Q8VEE4	Rpa1	Mus musculus
Q8VEH3	2	1	1	9.14	7	2	2	22.04	9	2	2	0.86	22.04	ADP-ribosylation factor-like protein 8A	Q8VEH3	Arl8a	Mus musculus
Q8VEK3	38	5	5	16.12	91	11	11	27.62	129	11	11	0	27.62	Heterogeneous nuclear ribonucleoprotein U	Q8VEK3	Hnrnpu	Mus musculus
Q8VHM5	1	1	1	2.06	9	2	2	5.38	10	2	2	0.86	5.38	Heterogeneous nuclear ribonucleoprotein R	Q8VHM5	Hnrnpr	Mus musculus
Q8VHX6	23	3	2	1.61	22	2	1	1.61	45	3	2	0.86	1.61	Filamin-C	Q8VHX6	Flnc	Mus musculus
Q8VI36	13	2	2	6.94	23	3	3	9.98	36	3	3	0.21	9.98	Paxillin	Q8VI36	Pxn	Mus musculus
Q8VI93	0	0	0		16	6	6	10.28	16	6	6	0	10.28	2'-5'-oligoadenylate synthase 3	Q8VI93	Oas3	Mus musculus
Q8VIJ6	9	2	2	6.01	40	4	4	10.3	49	5	5	0	10.3	Splicing factor, proline- and glutamine-rich	Q8VIJ6	Sfpq	Mus musculus
Q91UZ5	1	1	1	7.93	8	2	2	15.86	9	2	2	0.86	15.86	Inositol monophosphatase 2	Q91UZ5	Impa2	Mus musculus
Q91V12	5	2	2	5.77	8	2	2	5.77	13	2	2	0.86	5.77	Cytosolic acyl coenzyme A thioester hydrolase	Q91V12	Acot7	Mus musculus
Q91V41	16	5	5	35.35	42	6	5	41.4	58	6	5	0	41.4	Ras-related protein Rab-14	Q91V41	Rab14	Mus musculus
Q91V55	0	0	0		24	3	3	23.53	24	3	3	0.21	23.53	40S ribosomal protein S5	Q91V55	Rps5	Mus musculus
Q91V92	135	16	16	25.48	161	17	17	28.32	296	19	19	0	31.9	ATP-citrate synthase	Q91V92	Acly	Mus musculus
Q91VC3	24	2	1	8.52	67	6	4	17.76	91	6	4	0.14	17.76	Eukaryotic initiation factor 4A-III	Q91VC3	Eif4a3	Mus musculus
Q91VD9	0	0	0		4	3	3	7.15	4	3	3	0.21	7.15	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Q91VD9	Ndufs1	Mus musculus
Q91VH2	0	0	0		7	2	2	7.23	7	2	2	0.86	7.23	Sorting nexin-9	Q91VH2	Snx9	Mus musculus
Q91VH6	0	0	0		35	4	4	26.94	35	4	4	0.14	26.94	Protein MEMO1	Q91VH6	Memo1	Mus musculus
Q91VI7	108	13	13	49.56	250	18	18	70.61	358	18	18	0	70.61	Ribonuclease inhibitor	Q91VI7	Rnh1	Mus musculus
Q91VJ4	0	0	0		19	3	3	14.19	19	3	3	0.21	14.19	Serine/threonine-protein kinase 38	Q91VJ4	Stk38	Mus musculus
Q91VR5	3	1	1	2.84	20	2	2	5	23	2	2	0.86	5	ATP-dependent RNA helicase DDX1	Q91VR5	Ddx1	Mus musculus
Q91W89	5	3	3	5.97	0	0	0		5	3	3	0.21	5.97	Alpha-mannosidase 2C1	Q91W89	Man2c1	Mus musculus
Q91WQ3	6	1	1	4.55	26	4	4	15.34	32	4	4	0.14	15.34	Tyrosine--tRNA ligase, cytoplasmic	Q91WQ3	Yars	Mus musculus
Q91WV0	7	2	2	27.27	22	3	3	34.66	29	3	3	0.21	34.66	Protein Dr1	Q91WV0	Dr1	Mus musculus
Q91X72	93	8	8	31.3	127	11	11	32.83	220	12	12	0	34.78	Hemopexin	Q91X72	Hpx	Mus musculus
Q91XL1	30	4	4	18.42	30	3	3	12.87	60	5	5	0	18.71	Leucine-rich HEV glycoprotein	Q91XL1	Lrg1	Mus musculus
Q91YI4	10	3	3	15.37	46	7	7	27.8	56	7	7	0	27.8	Beta-arrestin-2	Q91YI4	Arrb2	Mus musculus
Q91YP3	14	5	5	26.42	18	6	6	31.45	32	6	6	0	31.45	Deoxyribose-phosphate aldolase	Q91YP3	Dera	Mus musculus
Q91YR9	74	7	7	31.61	72	5	5	23.71	146	7	7	0	31.61	Prostaglandin reductase 1	Q91YR9	Ptgr1	Mus musculus
Q91YT0	0	0	0		6	2	2	10.13	6	2	2	0.86	10.13	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	Q91YT0	Ndufv1	Mus musculus
Q91YX0	0	0	0		5	2	2	9.8	5	2	2	0.86	9.8	Protein THEMIS2	Q91YX0	Themis2	Mus musculus
Q91Z50	21	2	2	8.16	37	4	4	19.74	58	4	4	0.14	19.74	Flap endonuclease 1	Q91Z50	Fen1	Mus musculus
Q91ZJ5	61	6	6	18.11	50	4	4	13.19	111	6	6	0	18.11	UTP--glucose-1-phosphate uridylyltransferase	Q91ZJ5	Ugp2	Mus musculus
Q91ZR1	0	0	0		5	3	3	20.19	5	3	3	0.21	20.19	Ras-related protein Rab-4B	Q91ZR1	Rab4b	Mus musculus
Q91ZW3	0	0	0		11	2	2	2.57	11	2	2	0.86	2.57	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	Q91ZW3	Smarca5	Mus musculus
Q91ZX7	4	2	2	0.62	16	7	7	3.85	20	7	7	0	3.85	Prolow-density lipoprotein receptor-related protein 1	Q91ZX7	Lrp1	Mus musculus
Q920B9	0	0	0		11	2	2	2.2	11	2	2	0.86	2.2	FACT complex subunit SPT16	Q920B9	Supt16h	Mus musculus
Q920E5	73	7	7	30.03	130	9	9	37.68	203	9	9	0	37.68	Farnesyl pyrophosphate synthase	Q920E5	Fdps	Mus musculus
Q921F2	41	4	4	23.19	60	8	8	37.92	101	8	8	0	37.92	TAR DNA-binding protein 43	Q921F2	Tardbp	Mus musculus
Q921F4	4	1	1	2.88	32	6	6	18.1	36	6	6	0	18.1	Heterogeneous nuclear ribonucleoprotein L-like	Q921F4	Hnrnpll	Mus musculus
Q921G6	5	2	2	6.91	8	1	1	2.94	13	2	2	0.86	6.91	Leucine-rich repeat and calponin homology domain-containing protein 4	Q921G6	Lrch4	Mus musculus
Q921H8	8	2	2	9.2	27	5	5	18.4	35	5	5	0	18.4	3-ketoacyl-CoA thiolase A, peroxisomal	Q921H8	Acaa1a	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q921I1	1195	25	25	46.92	688	24	24	45.34	1883	27	27	0	47.2	Serotransferrin	Q921I1	Tf	Mus musculus
Q921M3	121	14	14	20.05	125	12	12	18.98	246	15	15	0	21.36	Splicing factor 3B subunit 3	Q921M3	Sf3b3	Mus musculus
Q921M7	70	8	8	39.81	74	5	5	30.56	144	8	8	0	39.81	Protein FAM49B	Q921M7	Fam49b	Mus musculus
Q921W4	2	1	1	8.33	14	3	3	20.11	16	3	3	0.21	20.11	Quinone oxidoreductase-like protein 1	Q921W4	Cryzl1	Mus musculus
Q921Z5	9	1	1	10.1	21	2	2	21.72	30	2	2	0.86	21.72	Tumor necrosis factor alpha-induced protein 8	Q921Z5	Tnfaip8	Mus musculus
Q922B2	5	2	2	6.79	17	5	5	15.17	22	5	5	0	15.17	Aspartate--tRNA ligase, cytoplasmic	Q922B2	Dars	Mus musculus
Q922D4	9	2	2	4.15	8	2	2	2.96	17	3	3	0.21	5.45	Serine/threonine-protein phosphatase 6 regulatory subunit 3	Q922D4	Ppp6r3	Mus musculus
Q922D8	0	0	0		10	5	5	8.13	10	5	5	0	8.13	C-1-tetrahydrofolate synthase, cytoplasmic	Q922D8	Mthfd1	Mus musculus
Q922F4	62	4	0	14.09	113	7	2	21.48	175	7	2	0.86	21.48	Tubulin beta-6 chain	Q922F4	Tubb6	Mus musculus
Q922R8	105	9	9	28.64	98	11	11	34.55	203	11	11	0	34.55	Protein disulfide-isomerase A6	Q922R8	Pdia6	Mus musculus
Q922S4	19	5	5	13.76	23	6	6	15.39	42	6	6	0	15.39	cGMP-dependent 3',5'-cyclic phosphodiesterase	Q922S4	Pde2a	Mus musculus
Q923B6	0	0	0		6	2	2	7.02	6	2	2	0.86	7.02	Metalloreductase STEAP4	Q923B6	Steap4	Mus musculus
Q923L7	56	2	2	20.65	28	2	2	20.65	84	2	2	0.86	20.65	Ear6 protein	Q923L7	Ear6	Mus musculus
Q93092	51	4	4	11.87	45	4	4	11.87	96	4	4	0.14	11.87	Transaldolase	Q93092	Taldo1	Mus musculus
Q99J09	2	2	2	17.25	27	3	3	22.22	29	3	3	0.21	22.22	Methylosome protein 50	Q99J09	Wdr77	Mus musculus
Q99J45	4	1	1	2.8	8	2	2	7.1	12	2	2	0.86	7.1	Nuclear receptor-binding protein	Q99J45	Nrbp1	Mus musculus
Q99J77	21	2	2	16.71	80	8	8	39.28	101	8	8	0	39.28	N-acetylneuraminic acid synthase (Sialic acid synthase)	Q99J77	Nans	Mus musculus
Q99J99	16	3	3	17.85	74	9	9	35.69	90	9	9	0	35.69	3-mercaptopyruvate sulfurtransferase	Q99J99	Mpst	Mus musculus
Q99JI4	7	3	3	12.34	25	4	4	16.97	32	4	4	0.14	16.97	26S proteasome non-ATPase regulatory subunit 6	Q99JI4	Psmd6	Mus musculus
Q99JT2	0	0	0		23	3	2	14.66	23	3	2	0.86	14.66	Serine/threonine-protein kinase 26	Q99JT2	Stk26	Mus musculus
Q99JW2	12	2	2	10.54	7	2	2	10.54	19	2	2	0.86	10.54	Aminoacylase-1	Q99JW2	Acy1	Mus musculus
Q99JW4	20	1	1	4.62	20	3	3	19.69	40	3	3	0.21	19.69	LIM and senescent cell antigen-like-containing domain protein 1	Q99JW4	Lims1	Mus musculus
Q99JX4	8	3	3	13.9	14	5	5	23.8	22	5	5	0	23.8	Eukaryotic translation initiation factor 3 subunit M	Q99JX4	Eif3m	Mus musculus
Q99JX7	2	1	1	1.94	7	2	2	5.5	9	2	2	0.86	5.5	Nuclear RNA export factor 1	Q99JX7	Nxf1	Mus musculus
Q99JY9	666	24	24	69.86	566	23	23	68.18	1232	26	26	0	73.92	Actin-related protein 3	Q99JY9	Actr3	Mus musculus
Q99K41	37	7	7	12.98	22	3	3	5.7	59	7	7	0	12.98	EMILIN-1	Q99K41	Emilin1	Mus musculus
Q99K48	25	1	1	4.86	38	2	2	11.63	63	2	2	0.86	11.63	Non-POU domain-containing octamer-binding protein	Q99K48	Nono	Mus musculus
Q99K85	9	2	2	10	31	3	3	13.51	40	3	3	0.21	13.51	Phosphoserine aminotransferase	Q99K85	Psat1	Mus musculus
Q99KE1	57	8	8	27.33	164	15	15	43.8	221	15	15	0	43.8	NAD-dependent malic enzyme, mitochondrial	Q99KE1	Me2	Mus musculus
Q99KH8	5	1	1	7.19	30	4	3	18.56	35	4	3	0.21	18.56	Serine/threonine-protein kinase 24	Q99KH8	Stk24	Mus musculus
Q99KI0	10	4	4	9.49	98	12	12	22.31	108	12	12	0	22.31	Aconitate hydratase, mitochondrial	Q99KI0	Aco2	Mus musculus
Q99KJ8	12	4	4	15.92	13	3	3	11.94	25	4	4	0.14	15.92	Dynactin subunit 2	Q99KJ8	Dctn2	Mus musculus
Q99KK2	1	1	1	5.79	6	3	3	12.5	7	3	3	0.21	12.5	N-acylneuraminate cytidylyltransferase	Q99KK2	Cmas	Mus musculus
Q99KK7	170	15	15	38.75	146	13	13	32.25	316	15	15	0	38.75	Dipeptidyl peptidase 3	Q99KK7	Dpp3	Mus musculus
Q99KN1	1	1	1	6.91	23	5	5	29.03	24	5	5	0	29.03	Arrestin domain-containing protein 1	Q99KN1	Arrdc1	Mus musculus
Q99KP6	12	1	1	4.76	51	7	7	30.36	63	7	7	0	30.36	Pre-mRNA-processing factor 19	Q99KP6	Prpf19	Mus musculus
Q99KQ4	9	2	2	10.18	22	4	4	15.89	31	4	4	0.14	15.89	Nicotinamide phosphoribosyltransferase	Q99KQ4	Nampt	Mus musculus
Q99KV1	3	1	1	4.47	5	2	2	8.94	8	2	2	0.86	8.94	DnaJ homolog subfamily B member 11	Q99KV1	Dnajb11	Mus musculus
Q99L04	1	1	1	6.07	10	3	3	18.21	11	3	3	0.21	18.21	Dehydrogenase/reductase SDR family member 1	Q99L04	Dhrs1	Mus musculus
Q99L13	0	0	0		5	2	2	9.25	5	2	2	0.86	9.25	3-hydroxyisobutyrate dehydrogenase, mitochondrial	Q99L13	Hibadh	Mus musculus
Q99LB4	48	6	6	36.96	110	10	10	41.55	158	10	10	0	41.55	Capping protein (Actin filament), gelsolin-like	Q99LB4	Capg	Mus musculus
Q99LC5	17	3	3	18.02	89	10	10	42.34	106	10	10	0	42.34	Electron transfer flavoprotein subunit alpha, mitochondrial	Q99LC5	Etfa	Mus musculus
Q99LD4	9	2	2	13.38	6	1	1	5.94	15	2	2	0.86	13.38	COP9 signalosome complex subunit 1	Q99LD4	Gps1	Mus musculus
Q99LF4	1	1	1	2.77	12	3	3	13.27	13	3	3	0.21	13.27	tRNA-splicing ligase RtcB homolog	Q99LF4	Rtcb	Mus musculus
Q99LL3	12	2	2	8.35	20	4	4	19.57	32	4	4	0.14	19.57	Carbohydrate sulfotransferase 12	Q99LL3	Chst12	Mus musculus
Q99LT0	26	2	2	36.36	31	2	2	36.36	57	2	2	0.86	36.36	Protein dpy-30 homolog	Q99LT0	Dpy30	Mus musculus
Q99LX0	43	4	4	39.15	46	3	3	31.22	89	4	4	0.14	39.15	Protein deglycase DJ-1	Q99LX0	Park7	Mus musculus
Q99M15	0	0	0		7	2	2	8.98	7	2	2	0.86	8.98	Proline-serine-threonine phosphatase-interacting protein 2	Q99M15	Pstpip2	Mus musculus
Q99MK8	1	1	1	1.31	24	5	5	12.92	25	5	5	0	12.92	Beta-adrenergic receptor kinase 1	Q99MK8	Adrbk1	Mus musculus
Q99MN1	13	2	2	7.06	26	3	3	9.41	39	3	3	0.21	9.41	Lysine--tRNA ligase	Q99MN1	Kars	Mus musculus
Q99N15	17	3	3	26.44	78	7	7	49.04	95	7	7	0	49.04	17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase	Q99N15	Hsd17b10	Mus musculus
Q99NB9	20	5	5	7.59	75	11	11	13.73	95	11	11	0	13.73	Splicing factor 3B subunit 1	Q99NB9	Sf3b1	Mus musculus
Q99PT1	46	3	3	27.94	61	4	4	27.94	107	4	4	0.14	27.94	Rho GDP-dissociation inhibitor 1	Q99PT1	Arhgdia	Mus musculus
Q99PV0	12	3	3	2.53	29	8	8	6.42	41	8	8	0	6.42	Pre-mRNA-processing-splicing factor 8	Q99PV0	Prpf8	Mus musculus
Q9CPW4	133	9	9	43.05	158	7	7	43.05	291	10	10	0	43.05	Actin-related protein 2/3 complex subunit 5	Q9CPW4	Arpc5	Mus musculus
Q9CPX6	5	1	1	4.78	14	2	2	8.92	19	2	2	0.86	8.92	Ubiquitin-like-conjugating enzyme ATG3	Q9CPX6	Atg3	Mus musculus
Q9CPY7	0	0	0		15	2	2	7.32	15	2	2	0.86	7.32	Cytosol aminopeptidase	Q9CPY7	Lap3	Mus musculus
Q9CQ60	22	3	3	29.96	38	4	4	38.91	60	4	4	0.14	38.91	6-phosphogluconolactonase	Q9CQ60	Pgls	Mus musculus
Q9CQ80	3	1	1	19.32	13	2	2	27.84	16	2	2	0.86	27.84	Vacuolar protein-sorting-associated protein 25	Q9CQ80	Vps25	Mus musculus
Q9CQC6	10	1	1	6.21	24	3	3	6.68	34	3	3	0.21	6.68	Basic leucine zipper and W2 domain-containing protein 1	Q9CQC6	Bzw1	Mus musculus
Q9CQE1	30	3	3	29.55	39	4	4	33.2	69	4	4	0.14	33.2	Protein NipSnap homolog 3B	Q9CQE1	Nipsnap3b	Mus musculus
Q9CQE8	9	1	1	8.2	26	4	4	21.72	35	4	4	0.14	21.72	UPF0568 protein C14orf166 homolog	Q9CQE8		Mus musculus
Q9CQI6	59	4	4	40.14	58	4	4	40.14	117	4	4	0.14	40.14	Coactosin-like protein	Q9CQI6	Cotl1	Mus musculus
Q9CQR6	26	3	3	15.74	31	5	5	28.85	57	5	5	0	28.85	Serine/threonine-protein phosphatase 6 catalytic subunit	Q9CQR6	Ppp6c	Mus musculus
Q9CQV8	152	12	10	54.47	159	13	12	54.47	311	14	12	0	54.47	14-3-3 protein beta/alpha	Q9CQV8	Ywhab	Mus musculus
Q9CRA5	8	1	1	5.37	36	3	3	17.79	44	3	3	0.21	17.79	Golgi phosphoprotein 3	Q9CRA5	Golph3	Mus musculus
Q9CRA8	0	0	0		6	3	3	25.53	6	3	3	0.21	25.53	Exosome complex component RRP46	Q9CRA8	Exosc5	Mus musculus
Q9CRC8	0	0	0		5	2	2	6.15	5	2	2	0.86	6.15	Leucine-rich repeat-containing protein 40	Q9CRC8	Lrrc40	Mus musculus
Q9CSU0	0	0	0		10	2	2	14.42	10	2	2	0.86	14.42	Regulation of nuclear pre-mRNA domain-containing protein 1B	Q9CSU0	Rprd1b	Mus musculus
Q9CU62	19	3	3	5.52	22	4	4	6.89	41	4	4	0.14	6.89	Structural maintenance of chromosomes protein 1A	Q9CU62	Smc1a	Mus musculus
Q9CVB6	635	20	20	60.33	572	18	18	57.67	1207	22	22	0	60.33	Actin-related protein 2/3 complex subunit 2	Q9CVB6	Arpc2	Mus musculus
Q9CWF2	90	9	2	39.55	228	14	4	47.19	318	14	4	0.14	47.19	Tubulin beta-2B chain	Q9CWF2	Tubb2b	Mus musculus
Q9CWJ9	34	8	8	28.38	95	13	13	39.36	129	14	14	0	39.36	Bifunctional purine biosynthesis protein PURH	Q9CWJ9	Atic	Mus musculus
Q9CX34	5	2	2	11.31	8	2	2	11.31	13	2	2	0.86	11.31	Protein SGT1 homolog	Q9CX34	Sugt1	Mus musculus
Q9CX86	0	0	0		3	2	2	11.8	3	2	2	0.86	11.8	Heterogeneous nuclear ribonucleoprotein A0	Q9CX86	Hnrnpa0	Mus musculus
Q9CXF4	0	0	0		6	2	2	4.02	6	2	2	0.86	4.02	TBC1 domain family member 15	Q9CXF4	Tbc1d15	Mus musculus
Q9CXI5	13	4	4	26.82	25	3	3	17.32	38	4	4	0.14	26.82	Mesencephalic astrocyte-derived neurotrophic factor	Q9CXI5	Manf	Mus musculus
Q9CXT8	0	0	0		4	2	2	9.82	4	2	2	0.86	9.82	Mitochondrial-processing peptidase subunit beta	Q9CXT8	Pmpcb	Mus musculus
Q9CXY6	17	3	3	14.62	32	5	5	28.72	49	5	5	0	28.72	Interleukin enhancer-binding factor 2	Q9CXY6	Ilf2	Mus musculus
Q9CY50	0	0	0		16	2	2	18.53	16	2	2	0.86	18.53	Translocon-associated protein subunit alpha	Q9CY50	Ssr1	Mus musculus
Q9CY58	4	1	1	3.93	7	2	2	3.93	11	2	2	0.86	3.93	Plasminogen activator inhibitor 1 RNA-binding protein	Q9CY58	Serbp1	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9CY64	0	0	0		16	3	3	16.61	16	3	3	0.21	16.61	Biliverdin reductase A	Q9CY64	Blvra	Mus musculus
Q9CYL5	2	1	1	14.29	30	5	5	45.45	32	5	5	0	45.45	Golgi-associated plant pathogenesis-related protein 1	Q9CYL5	Glipr2	Mus musculus
Q9CZ04	28	3	3	23.27	19	3	3	21.82	47	4	4	0.14	28.36	COP9 signalosome complex subunit 7a	Q9CZ04	Cops7a	Mus musculus
Q9CZ13	4	1	1	4.79	14	5	5	21.46	18	5	5	0	21.46	Cytochrome b-c1 complex subunit 1, mitochondrial	Q9CZ13	Uqcrc1	Mus musculus
Q9CZ30	36	4	4	19.19	48	5	5	20.96	84	5	5	0	20.96	Obg-like ATPase 1	Q9CZ30	Ola1	Mus musculus
Q9CZ42	0	0	0		28	6	6	37.32	28	6	6	0	37.32	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	Q9CZ42	Carkd	Mus musculus
Q9CZ44	44	6	6	25.95	60	6	6	25.95	104	6	6	0	25.95	NSFL1 cofactor p47	Q9CZ44	Nsfl1c	Mus musculus
Q9CZD3	8	3	3	7.41	45	4	4	9.33	53	4	4	0.14	9.33	Glycine--tRNA ligase	Q9CZD3	Gars	Mus musculus
Q9CZE3	1	1	1	8.52	9	2	2	16.14	10	2	2	0.86	16.14	Ras-related protein Rab-32	Q9CZE3	Rab32	Mus musculus
Q9CZM2	0	0	0		23	3	3	12.75	23	3	3	0.21	12.75	60S ribosomal protein L15	Q9CZM2	Rpl15	Mus musculus
Q9CZN7	34	3	3	14.48	88	9	9	22.02	122	9	9	0	22.02	Serine hydroxymethyltransferase	Q9CZN7	Shmt2	Mus musculus
Q9CZU3	0	0	0		2	2	2	3.17	2	2	2	0.86	3.17	Superkiller viralicidic activity 2-like 2	Q9CZU3	Skiv2l2	Mus musculus
Q9CZU6	32	2	2	6.03	75	8	8	21.34	107	8	8	0	21.34	Citrate synthase, mitochondrial	Q9CZU6	Cs	Mus musculus
Q9D020	13	4	4	24.17	47	9	9	34.14	60	9	9	0	34.14	Cytosolic 5'-nucleotidase 3A	Q9D020	Nt5c3a	Mus musculus
Q9D071	0	0	0		4	2	2	4.07	4	2	2	0.86	4.07	MMS19 nucleotide excision repair protein homolog	Q9D071	Mms19	Mus musculus
Q9D0F9	27	5	5	17.79	28	4	4	14.77	55	5	5	0	17.79	Phosphoglucomutase-1	Q9D0F9	Pgm1	Mus musculus
Q9D0I9	13	3	3	7.12	23	5	5	13.48	36	6	6	0	15.3	Arginine--tRNA ligase, cytoplasmic	Q9D0I9	Rars	Mus musculus
Q9D0K2	14	3	3	13.08	42	5	5	19.23	56	5	5	0	19.23	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	Q9D0K2	Oxct1	Mus musculus
Q9D0R2	16	3	3	9.42	45	7	7	16.07	61	7	7	0	16.07	Threonine--tRNA ligase, cytoplasmic	Q9D0R2	Tars	Mus musculus
Q9D154	116	10	10	29.02	114	10	10	29.02	230	10	10	0	29.02	Leukocyte elastase inhibitor A	Q9D154	Serpinb1a	Mus musculus
Q9D1A2	9	3	3	13.05	41	8	8	26.11	50	8	8	0	26.11	Cytosolic non-specific dipeptidase	Q9D1A2	Cndp2	Mus musculus
Q9D1G1	15	2	2	17.41	23	5	4	37.31	38	5	4	0.14	37.31	Ras-related protein Rab-1B	Q9D1G1	Rab1b	Mus musculus
Q9D1K2	25	2	2	30.25	19	1	1	20.17	44	2	2	0.86	30.25	V-type proton ATPase subunit F	Q9D1K2	Atp6v1f	Mus musculus
Q9D1M0	11	2	2	12.42	13	2	2	12.42	24	2	2	0.86	12.42	Protein SEC13 homolog	Q9D1M0	Sec13	Mus musculus
Q9D1Q6	37	4	4	20.94	35	4	4	20.94	72	4	4	0.14	20.94	Endoplasmic reticulum resident protein 44	Q9D1Q6	Erp44	Mus musculus
Q9D2V7	94	15	15	34.06	247	25	25	53.04	341	27	27	0	53.04	Coronin-7	Q9D2V7	Coro7	Mus musculus
Q9D4D4	10	2	2	4.78	10	1	1	4.15	20	2	2	0.86	4.78	Transketolase-like protein 2	Q9D4D4	Tktl2	Mus musculus
Q9D554	2	2	2	7.78	7	3	3	10.58	9	4	4	0.14	11.78	Splicing factor 3A subunit 3	Q9D554	Sf3a3	Mus musculus
Q9D662	1	1	1	2.35	3	2	2	4.56	4	2	2	0.86	4.56	Protein transport protein Sec23B	Q9D662	Sec23b	Mus musculus
Q9D6F9	84	9	3	44.37	223	16	8	51.8	307	16	8	0	51.8	Tubulin beta-4A chain	Q9D6F9	Tubb4a	Mus musculus
Q9D6R2	0	0	0		20	4	4	14.75	20	4	4	0.14	14.75	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Q9D6R2	Idh3a	Mus musculus
Q9D6Y9	3	1	1	2.42	17	2	2	4.27	20	2	2	0.86	4.27	1,4-alpha-glucan-branching enzyme	Q9D6Y9	Gbe1	Mus musculus
Q9D6Z1	0	0	0		12	2	2	9.31	12	2	2	0.86	9.31	Nucleolar protein 56	Q9D6Z1	Nop56	Mus musculus
Q9D7G0	1	1	1	5.35	9	3	3	16.04	10	3	3	0.21	16.04	Ribose-phosphate pyrophosphokinase 1	Q9D7G0	Prps1	Mus musculus
Q9D819	0	0	0		12	4	4	23.88	12	4	4	0.14	23.88	Inorganic pyrophosphatase	Q9D819	Ppa1	Mus musculus
Q9D892	7	1	1	11.62	31	2	2	25.25	38	2	2	0.86	25.25	Inosine triphosphate pyrophosphatase	Q9D892	Itpa	Mus musculus
Q9D8B3	1	1	1	7.14	27	2	2	13.39	28	2	2	0.86	13.39	Charged multivesicular body protein 4b	Q9D8B3	Chmp4b	Mus musculus
Q9D8E6	0	0	0		9	3	3	11.22	9	3	3	0.21	11.22	60S ribosomal protein L4	Q9D8E6	Rpl4	Mus musculus
Q9D8N0	69	7	7	29.75	136	12	12	42.11	205	12	12	0	42.11	Elongation factor 1-gamma	Q9D8N0	Eef1g	Mus musculus
Q9D8N2	0	0	0		8	2	2	13.17	8	2	2	0.86	13.17	Protein FAM45A	Q9D8N2	Fam45a	Mus musculus
Q9D8W5	20	3	3	11.84	16	2	2	7.46	36	3	3	0.21	11.84	26S proteasome non-ATPase regulatory subunit 12	Q9D8W5	Psmd12	Mus musculus
Q9D8Y7	2	2	2	18.48	18	3	3	32.61	20	3	3	0.21	32.61	Tumor necrosis factor alpha-induced protein 8-like protein 2	Q9D8Y7	Tnfaip8l2	Mus musculus
Q9D906	6	3	3	8.6	28	6	6	15.47	34	6	6	0	15.47	Ubiquitin-like modifier-activating enzyme ATG7	Q9D906	Atg7	Mus musculus
Q9D964	3	1	1	4.73	10	3	3	12.77	13	3	3	0.21	12.77	Glycine amidinotransferase, mitochondrial	Q9D964	Gatm	Mus musculus
Q9DAR7	13	4	4	19.23	8	4	4	19.23	21	4	4	0.14	19.23	m7GpppX diphosphatase	Q9DAR7	Dcps	Mus musculus
Q9DB05	3	2	2	12.88	25	5	5	30.85	28	5	5	0	30.85	Alpha-soluble NSF attachment protein	Q9DB05	Napa	Mus musculus
Q9DBC7	4	1	1	6.3	5	2	2	10.76	9	2	2	0.86	10.76	cAMP-dependent protein kinase type I-alpha regulatory subunit	Q9DBC7	Prkar1a	Mus musculus
Q9DBG3	124	11	8	20.17	165	16	11	27.11	289	17	12	0	27.43	AP-2 complex subunit beta	Q9DBG3	Ap2b1	Mus musculus
Q9DBG6	5	4	4	12.84	12	5	5	16.64	17	7	7	0	20.92	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	Q9DBG6	Rpn2	Mus musculus
Q9DBJ1	94	9	9	34.65	136	9	9	40.55	230	10	10	0	40.94	Phosphoglycerate mutase 1	Q9DBJ1	Pgam1	Mus musculus
Q9DBK7	17	3	3	7.68	17	3	3	7.68	34	4	4	0.14	9.21	MCG18845, isoform CRA_d	Q9DBK7	Uba7	Mus musculus
Q9DBL1	2	1	1	5.09	16	3	3	14.12	18	3	3	0.21	14.12	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Q9DBL1	Acadsb	Mus musculus
Q9DBR1	5	1	1	2.52	13	2	2	4.1	18	2	2	0.86	4.1	5'-3' exoribonuclease 2	Q9DBR1	Xrn2	Mus musculus
Q9DBR7	6	3	3	4.28	6	3	3	4.28	12	3	3	0.21	4.28	Protein phosphatase 1 regulatory subunit 12A	Q9DBR7	Ppp1r12a	Mus musculus
Q9DBZ5	1	1	1	9.17	7	4	4	31.19	8	4	4	0.14	31.19	Eukaryotic translation initiation factor 3 subunit K	Q9DBZ5	Eif3k	Mus musculus
Q9DC23	2	1	1	2.77	3	2	2	4.29	5	3	3	0.21	7.06	DnaJ homolog subfamily C member 10	Q9DC23	Dnajc10	Mus musculus
Q9DC50	13	2	2	6.05	19	3	3	9.64	32	3	3	0.21	9.64	Peroxisomal carnitine O-octanoyltransferase	Q9DC50	Crot	Mus musculus
Q9DC51	6	2	0	8.19	15	4	2	17.23	21	4	2	0.86	17.23	Guanine nucleotide-binding protein G(k) subunit alpha	Q9DC51	Gnai3	Mus musculus
Q9DC61	6	1	1	3.24	18	3	3	10.88	24	3	3	0.21	10.88	Mitochondrial-processing peptidase subunit alpha	Q9DC61	Pmpca	Mus musculus
Q9DCC5	62	5	5	38.25	60	5	5	38.25	122	5	5	0	38.25	Cbx3 protein	Q9DCC5	Cbx3	Mus musculus
Q9DCD0	471	20	20	44.72	622	24	24	47.41	1093	25	25	0	47.41	6-phosphogluconate dehydrogenase, decarboxylating	Q9DCD0	Pgd	Mus musculus
Q9DCH4	37	3	3	14.13	39	3	3	14.13	76	3	3	0.21	14.13	Eukaryotic translation initiation factor 3 subunit F	Q9DCH4	Eif3f	Mus musculus
Q9DCL9	24	3	3	14.82	28	3	3	14.82	52	3	3	0.21	14.82	Multifunctional protein ADE2	Q9DCL9	Paics	Mus musculus
Q9DCM0	0	0	0		5	2	2	19.29	5	2	2	0.86	19.29	Persulfide dioxygenase ETHE1, mitochondrial	Q9DCM0	Ethe1	Mus musculus
Q9DCS2	0	0	0		12	3	3	31.37	12	3	3	0.21	31.37	UPF0585 protein C16orf13 homolog	Q9DCS2		Mus musculus
Q9DCS3	0	0	0		8	3	3	20.91	8	3	3	0.21	20.91	Trans-2-enoyl-CoA reductase, mitochondrial	Q9DCS3	Mecr	Mus musculus
Q9DCW4	8	1	1	6.67	24	3	3	19.61	32	3	3	0.21	19.61	Electron transfer flavoprotein subunit beta	Q9DCW4	Etfb	Mus musculus
Q9DCZ1	1	1	1	6.38	3	2	2	6.38	4	2	2	0.86	6.38	GMP reductase 1	Q9DCZ1	Gmpr	Mus musculus
Q9EPB4	13	2	2	21.76	12	2	2	21.76	25	2	2	0.86	21.76	Apoptosis-associated speck-like protein containing a CARD	Q9EPB4	Pycard	Mus musculus
Q9EPK2	8	2	2	7.49	3	2	2	7.49	11	2	2	0.86	7.49	Protein XRP2	Q9EPK2	Rp2	Mus musculus
Q9EPK7	3	2	2	4.6	5	2	2	4.6	8	2	2	0.86	4.6	Exportin-7	Q9EPK7	Xpo7	Mus musculus
Q9EPL8	18	3	3	5.3	24	6	6	10.98	42	6	6	0	10.98	Importin-7	Q9EPL8	Ipo7	Mus musculus
Q9EPU0	2	1	1	0.98	15	4	4	5.78	17	4	4	0.14	5.78	Regulator of nonsense transcripts 1	Q9EPU0	Upf1	Mus musculus
Q9EQG9	0	0	0		24	5	5	13.78	24	5	5	0	13.78	Collagen type IV alpha-3-binding protein	Q9EQG9	Col4a3bp	Mus musculus
Q9EQH2	8	2	2	3.01	16	2	2	3.01	24	2	2	0.86	3.01	Endoplasmic reticulum aminopeptidase 1	Q9EQH2	Erap1	Mus musculus
Q9EQH3	63	8	8	16.21	109	15	15	26.51	172	15	15	0	26.51	Vacuolar protein sorting-associated protein 35	Q9EQH3	Vps35	Mus musculus
Q9EQI5	27	3	3	40.71	12	2	2	30.97	39	3	3	0.21	40.71	Chemokine (C-X-C motif) ligand 7, isoform CRA_b	Q9EQI5	Ppbp	Mus musculus
Q9EQK5	258	26	26	47.27	236	23	23	45.06	494	28	28	0	49.71	Major vault protein	Q9EQK5	Mvp	Mus musculus
Q9EQP2	2	1	1	2.59	7	2	2	4.62	9	2	2	0.86	4.62	EH domain-containing protein 4	Q9EQP2	Ehd4	Mus musculus
Q9EQU5	46	4	4	17.3	52	4	4	25.95	98	6	6	0	27.34	Protein SET	Q9EQU5	Set	Mus musculus
Q9ER72	31	3	3	6.5	27	4	4	8.18	58	4	4	0.14	8.18	Cysteine--tRNA ligase, cytoplasmic	Q9ER72	Cars	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9ERF3	9	2	2	13.44	41	4	4	24.26	50	4	4	0.14	24.26	WD repeat-containing protein 61	Q9ERF3	Wdr61	Mus musculus
Q9ERK4	31	6	6	10.92	118	13	13	21.32	149	13	13	0	21.32	Exportin-2	Q9ERK4	Cse1l	Mus musculus
Q9ERL7	4	1	1	16.9	9	3	3	26.06	13	3	3	0.21	26.06	Glia maturation factor gamma	Q9ERL7	Gmfg	Mus musculus
Q9ERR7	20	3	3	37.65	35	3	3	37.65	55	3	3	0.21	37.65	15 kDa selenoprotein	Q9ERR7	Sep15	Mus musculus
Q9ES46	15	2	2	7.67	13	2	2	8.77	28	3	3	0.21	12.6	Beta-parvin	Q9ES46	Parvb	Mus musculus
Q9ES52	22	3	3	4.11	40	5	5	5.63	62	5	5	0	5.63	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	Q9ES52	Inpp5d	Mus musculus
Q9ESP1	15	3	3	36.65	22	2	2	20.81	37	3	3	0.21	36.65	Stromal cell-derived factor 2-like protein 1	Q9ESP1	Sdf2l1	Mus musculus
Q9EST5	11	2	2	11.4	40	2	2	11.4	51	2	2	0.86	11.4	Acidic leucine-rich nuclear phosphoprotein 32 family member B	Q9EST5	Anp32b	Mus musculus
Q9ESU7	0	0	0		4	2	2	6.49	4	2	2	0.86	6.49	Amino acid transporter	Q9ESU7	Slc1a5	Mus musculus
Q9ESX5	0	0	0		12	2	2	5.89	12	2	2	0.86	5.89	H/ACA ribonucleoprotein complex subunit 4	Q9ESX5	Dkc1	Mus musculus
Q9ET01	832	42	40	51.06	825	41	38	45.41	1657	48	45	0	52.71	Glycogen phosphorylase, liver form	Q9ET01	Pygl	Mus musculus
Q9ET66	5	2	2	8.79	4	2	2	8.79	9	2	2	0.86	8.79	Peptidase inhibitor 16	Q9ET66	Pi16	Mus musculus
Q9JHI5	0	0	0		6	2	2	9.91	6	2	2	0.86	9.91	Isovaleryl-CoA dehydrogenase, mitochondrial	Q9JHI5	Ivd	Mus musculus
Q9JHK4	0	0	0		10	3	3	12.17	10	3	3	0.21	12.17	Geranylgeranyl transferase type-2 subunit alpha	Q9JHK4	Rabggta	Mus musculus
Q9JHK5	87	5	5	23.71	101	5	5	23.71	188	5	5	0	23.71	Pleckstrin	Q9JHK5	Plek	Mus musculus
Q9JHU4	20	6	6	2.52	70	18	18	7.84	90	20	20	0	8.35	Cytoplasmic dynein 1 heavy chain 1	Q9JHU4	Dync1h1	Mus musculus
Q9JHU9	28	3	3	9.87	12	2	2	7	40	3	3	0.21	9.87	Inositol-3-phosphate synthase 1	Q9JHU9	Isyna1	Mus musculus
Q9JHW4	0	0	0		4	2	2	8.92	4	2	2	0.86	8.92	Selenocysteine-specific elongation factor	Q9JHW4	Eefsec	Mus musculus
Q9JIF0	4	2	2	7.55	15	3	3	11.32	19	3	3	0.21	11.32	Protein arginine N-methyltransferase 1	Q9JIF0	Prmt1	Mus musculus
Q9JIF7	1	1	1	2.2	13	4	4	7.14	14	4	4	0.14	7.14	Coatomer subunit beta	Q9JIF7	Copb1	Mus musculus
Q9JIZ9	8	2	2	13.18	28	3	3	19.59	36	3	3	0.21	19.59	Phospholipid scramblase 3	Q9JIZ9	Plscr3	Mus musculus
Q9JJ00	2	1	1	6.1	11	2	2	17.07	13	2	2	0.86	17.07	Phospholipid scramblase 1	Q9JJ00	Plscr1	Mus musculus
Q9JJ28	23	6	6	9.36	29	7	7	10.62	52	10	10	0	13.14	Protein flightless-1 homolog	Q9JJ28	Flii	Mus musculus
Q9JJK2	0	0	0		10	3	3	14.44	10	3	3	0.21	14.44	LanC-like protein 2	Q9JJK2	Lancl2	Mus musculus
Q9JKC8	2	1	1	4.07	9	2	2	7.18	11	2	2	0.86	7.18	AP-3 complex subunit mu-1	Q9JKC8	Ap3m1	Mus musculus
Q9JKF1	420	39	39	35.67	541	43	43	38.56	961	48	48	0	40.13	Ras GTPase-activating-like protein IQGAP1	Q9JKF1	Iqgap1	Mus musculus
Q9JKR6	34	5	5	9.31	47	6	6	11.01	81	6	6	0	11.01	Hypoxia up-regulated protein 1	Q9JKR6	Hyou1	Mus musculus
Q9JL26	1	1	1	1.28	28	8	8	12.52	29	8	8	0	12.52	Formin-like protein 1	Q9JL26	Fmnl1	Mus musculus
Q9JLJ2	13	4	4	17.81	45	9	9	29.96	58	9	9	0	29.96	4-trimethylaminobutyraldehyde dehydrogenase	Q9JLJ2	Aldh9a1	Mus musculus
Q9JLQ2	9	1	1	2.54	40	6	6	18.79	49	6	6	0	18.79	ARF GTPase-activating protein GIT2	Q9JLQ2	Git2	Mus musculus
Q9JLT4-2	6	3	2	15.48	3	3	3	14.87	9	4	3	0.21	17.92	Isoform 2 of Thioredoxin reductase 2, mitochondrial	Q9JLT4	Txnrd2	Mus musculus
Q9JLV6	69	10	10	28.54	155	15	15	34.87	224	17	17	0	36.97	Bifunctional polynucleotide phosphatase/kinase	Q9JLV6	Pnkp	Mus musculus
Q9JM14	1	1	1	12.5	33	3	3	28	34	3	3	0.21	28	5'(3')-deoxyribonucleotidase, cytosolic type	Q9JM14	Nt5c	Mus musculus
Q9JM76	82	6	6	42.7	83	5	5	28.65	165	8	8	0	44.94	Actin-related protein 2/3 complex subunit 3	Q9JM76	Arpc3	Mus musculus
Q9JMA1	44	4	4	17.65	59	8	8	23.94	103	8	8	0	23.94	Ubiquitin carboxyl-terminal hydrolase 14	Q9JMA1	Usp14	Mus musculus
Q9JMH6	189	13	12	35.24	204	14	14	35.56	393	15	14	0	38.01	Thioredoxin reductase 1, cytoplasmic	Q9JMH6	Txnrd1	Mus musculus
Q9JMH9	0	0	0		7	4	4	4.2	7	4	4	0.14	4.2	Unconventional myosin-XVIIIa	Q9JMH9	Myo18a	Mus musculus
Q9QUH0	22	1	1	27.1	34	3	3	38.32	56	3	3	0.21	38.32	Glutaredoxin-1	Q9QUH0	Glrx	Mus musculus
Q9QUI0	52	4	4	33.68	123	10	10	58.03	175	10	10	0	58.03	Transforming protein RhoA	Q9QUI0	Rhoa	Mus musculus
Q9QUM0	275	18	18	33.3	219	17	17	30.4	494	20	20	0	33.59	Integrin alpha-IIb	Q9QUM0	Itga2b	Mus musculus
Q9QUM9	83	6	6	29.67	60	6	6	29.67	143	6	6	0	29.67	Proteasome subunit alpha type-6	Q9QUM9	Psma6	Mus musculus
Q9QUR6	95	14	14	31.41	137	16	16	36.2	232	17	17	0	38.03	Prolyl endopeptidase	Q9QUR6	Prep	Mus musculus
Q9QWK4	21	4	4	18.75	5	2	2	9.38	26	4	4	0.14	18.75	CD5 antigen-like	Q9QWK4	Cd5l	Mus musculus
Q9QWR8	10	2	2	7.23	5	1	1	2.65	15	2	2	0.86	7.23	Alpha-N-acetylgalactosaminidase	Q9QWR8	Naga	Mus musculus
Q9QXD6	7	1	1	6.51	2	2	2	14.79	9	2	2	0.86	14.79	Fructose-1,6-bisphosphatase 1	Q9QXD6	Fbp1	Mus musculus
Q9QXG4	0	0	0		4	2	2	5.14	4	2	2	0.86	5.14	Acetyl-coenzyme A synthetase, cytoplasmic	Q9QXG4	Acss2	Mus musculus
Q9QXK3	18	4	2	7.35	46	7	4	12.63	64	7	4	0.14	12.63	Coatomer subunit gamma-2	Q9QXK3	Copg2	Mus musculus
Q9QXS1	63	11	11	4.9	125	21	21	9.21	188	21	21	0	9.21	Plectin	Q9QXS1	Plec	Mus musculus
Q9QYB5	13	2	2	7.65	12	3	3	9.92	25	3	3	0.21	9.92	Gamma-adducin	Q9QYB5	Add3	Mus musculus
Q9QYC0	45	5	5	16.6	30	5	5	16.6	75	5	5	0	16.6	Alpha-adducin	Q9QYC0	Add1	Mus musculus
Q9QYJ0	2	1	1	3.64	9	2	2	11.41	11	2	2	0.86	11.41	DnaJ homolog subfamily A member 2	Q9QYJ0	Dnaja2	Mus musculus
Q9QZ88	0	0	0		12	2	2	14.84	12	2	2	0.86	14.84	Vacuolar protein sorting-associated protein 29	Q9QZ88	Vps29	Mus musculus
Q9QZD9	19	4	4	24.31	36	3	3	19.69	55	4	4	0.14	24.31	Eukaryotic translation initiation factor 3 subunit I	Q9QZD9	Eif3i	Mus musculus
Q9QZE5	23	5	3	12.13	50	9	6	18.31	73	9	6	0	18.31	Coatomer subunit gamma-1	Q9QZE5	Copg1	Mus musculus
Q9QZF2	9	1	1	3.05	4	2	2	5.92	13	2	2	0.86	5.92	Glypican-1	Q9QZF2	Gpc1	Mus musculus
Q9QZK7	12	3	3	14.41	54	8	8	33.78	66	8	8	0	33.78	Docking protein 3	Q9QZK7	Dok3	Mus musculus
Q9QZQ8	2747	30	16	59.14	5422	27	14	56.18	8169	31	17	0	59.14	Core histone macro-H2A.1	Q9QZQ8	H2afy	Mus musculus
Q9QZU3	78	8	8	24.51	20	3	3	12.17	98	8	8	0	24.51	Platelet glycoprotein V (Fragment)	Q9QZU3	Gp5	Mus musculus
Q9R062	84	11	11	48.95	61	9	9	48.95	145	11	11	0	48.95	Glycogenin-1	Q9R062	Gyg1	Mus musculus
Q9R0C8	0	0	0		21	4	4	8.85	21	4	4	0.14	8.85	Guanine nucleotide exchange factor VAV3	Q9R0C8	Vav3	Mus musculus
Q9R0E1	4	2	2	5.4	4	3	3	6.75	8	4	4	0.14	9.99	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	Q9R0E1	Plod3	Mus musculus
Q9R0N0	3	2	2	11.99	38	7	7	26.53	41	7	7	0	26.53	Galactokinase	Q9R0N0	Galk1	Mus musculus
Q9R0P3	97	8	8	60.28	260	14	14	64.89	357	14	14	0	64.89	S-formylglutathione hydrolase	Q9R0P3	Esd	Mus musculus
Q9R0P5	94	5	5	40	364	7	7	57.58	458	7	7	0	57.58	Destrin	Q9R0P5	Dstn	Mus musculus
Q9R0Q7	4	2	2	18.75	36	4	4	27.5	40	4	4	0.14	27.5	Prostaglandin E synthase 3	Q9R0Q7	Ptges3	Mus musculus
Q9R0X4	2	1	1	3.87	4	2	2	7.06	6	2	2	0.86	7.06	Acyl-coenzyme A thioesterase 9, mitochondrial	Q9R0X4	Acot9	Mus musculus
Q9R111	349	15	15	50.22	337	16	16	52.2	686	17	17	0	52.2	Guanine deaminase	Q9R111	Gda	Mus musculus
Q9R1P0	88	8	8	57.47	82	7	7	45.21	170	8	8	0	57.47	Proteasome subunit alpha type-4	Q9R1P0	Psma4	Mus musculus
Q9R1P1	52	2	2	16.59	55	2	2	16.59	107	2	2	0.86	16.59	Proteasome subunit beta type-3	Q9R1P1	Psmb3	Mus musculus
Q9R1P3	103	8	8	41.29	69	6	6	41.29	172	8	8	0	41.29	Proteasome subunit beta type-2	Q9R1P3	Psmb2	Mus musculus
Q9R1P4	86	7	7	44.11	63	6	6	39.54	149	7	7	0	44.11	Proteasome subunit alpha type-1	Q9R1P4	Psma1	Mus musculus
Q9R1T2	28	3	3	16.29	37	4	4	16.29	65	4	4	0.14	16.29	SUMO-activating enzyme subunit 1	Q9R1T2	Sae1	Mus musculus
Q9R1T4	2	2	2	11.52	11	2	2	11.52	13	2	2	0.86	11.52	Septin-6	Q9R1T4	Sept6	Mus musculus
Q9R257	4	1	1	14.74	20	3	3	23.16	24	3	3	0.21	23.16	Heme-binding protein 1	Q9R257	Hebp1	Mus musculus
Q9WTL7	5	1	1	11.26	10	2	2	21.21	15	2	2	0.86	21.21	Acyl-protein thioesterase 2	Q9WTL7	Lypla2	Mus musculus
Q9WTM5	0	0	0		3	2	2	6.7	3	2	2	0.86	6.7	RuvB-like 2	Q9WTM5	Ruvbl2	Mus musculus
Q9WTP6	10	1	1	10.46	20	2	2	17.15	30	2	2	0.86	17.15	Adenylate kinase 2, mitochondrial	Q9WTP6	Ak2	Mus musculus
Q9WTX6	0	0	0		2	2	2	4.51	2	2	2	0.86	4.51	Cullin-1	Q9WTX6	Cul1	Mus musculus
Q9WU28	19	2	2	24.03	28	1	1	11.69	47	2	2	0.86	24.03	Prefoldin subunit 5	Q9WU28	Pfdn5	Mus musculus
Q9WU78	137	11	11	22.9	204	15	15	33.14	341	16	16	0	33.14	Programmed cell death 6-interacting protein	Q9WU78	Pdcd6ip	Mus musculus
Q9WUA2	6	1	1	2.21	18	3	3	6.79	24	3	3	0.21	6.79	Phenylalanine--tRNA ligase beta subunit	Q9WUA2	Farsb	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9WUA3	2	1	1	2.81	21	5	5	13.52	23	5	5	0	13.52	ATP-dependent 6-phosphofructokinase, platelet type	Q9WUA3	Pfkp	Mus musculus
Q9WUM3	41	6	6	21.9	90	9	8	32.44	131	9	8	0	32.44	Coronin-1B	Q9WUM3	Coro1b	Mus musculus
Q9WUM4	55	5	5	18.57	78	6	5	18.57	133	6	5	0	18.57	Coronin-1C	Q9WUM4	Coro1c	Mus musculus
Q9WUP7	0	0	0		11	2	2	10.03	11	2	2	0.86	10.03	Ubiquitin carboxyl-terminal hydrolase isozyme L5	Q9WUP7	Uchl5	Mus musculus
Q9WV02	0	0	0		15	3	3	11	15	3	3	0.21	11	RNA-binding motif protein, X chromosome	Q9WV02	Rbmx	Mus musculus
Q9WV32	239	14	14	44.35	262	12	12	43.01	501	15	15	0	48.12	Actin-related protein 2/3 complex subunit 1B	Q9WV32	Arpc1b	Mus musculus
Q9WV60	1	1	1	6.9	9	2	2	12.62	10	2	2	0.86	12.62	Glycogen synthase kinase-3 beta	Q9WV60	Gsk3b	Mus musculus
Q9WVA3	2	1	1	5.83	21	3	3	18.71	23	3	3	0.21	18.71	Mitotic checkpoint protein BUB3	Q9WVA3	Bub3	Mus musculus
Q9WVA4	60	6	6	38.69	83	6	6	38.69	143	6	6	0	38.69	Transgelin-2	Q9WVA4	Tagln2	Mus musculus
Q9WVG5	28	5	5	20.2	77	8	8	23.6	105	8	8	0	23.6	Endothelial lipase	Q9WVG5	Lipg	Mus musculus
Q9WVJ2	5	4	4	16.49	17	3	3	11.97	22	4	4	0.14	16.49	26S proteasome non-ATPase regulatory subunit 13	Q9WVJ2	Psmd13	Mus musculus
Q9WVK4	42	5	5	17.04	77	11	11	28.84	119	11	11	0	28.84	EH domain-containing protein 1	Q9WVK4	Ehd1	Mus musculus
Q9Z0H3	1	1	1	4.42	2	2	2	11.17	3	3	3	0.21	15.58	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	Q9Z0H3	Smarcb1	Mus musculus
Q9Z0H4	0	0	0		13	3	3	5.71	13	3	3	0.21	5.71	CUGBP Elav-like family member 2	Q9Z0H4	Celf2	Mus musculus
Q9Z0I7	5	1	1	5.93	23	4	4	20.77	28	4	4	0.14	20.77	Protein Slfn1	Q9Z0I7	Slfn1	Mus musculus
Q9Z0N1	25	2	2	11.23	46	6	6	23.09	71	6	6	0	23.09	Eukaryotic translation initiation factor 2 subunit 3, X-linked	Q9Z0N1	Eif2s3x	Mus musculus
Q9Z0P5	61	7	7	37.82	77	8	8	37.82	138	8	8	0	37.82	Twinfilin-2	Q9Z0P5	Twf2	Mus musculus
Q9Z126	308	5	5	38.1	161	5	5	38.1	469	5	5	0	38.1	Platelet factor 4	Q9Z126	Pf4	Mus musculus
Q9Z183	62	9	9	19.97	72	12	12	30.63	134	12	12	0	30.63	Protein-arginine deiminase type-4	Q9Z183	Padi4	Mus musculus
Q9Z1B7	1	1	1	3.55	17	3	3	7.92	18	3	3	0.21	7.92	Mitogen-activated protein kinase 13	Q9Z1B7	Mapk13	Mus musculus
Q9Z1D1	3	1	1	5	12	2	2	15.31	15	2	2	0.86	15.31	Eukaryotic translation initiation factor 3 subunit G	Q9Z1D1	Eif3g	Mus musculus
Q9Z1E4	21	5	5	15.18	42	4	4	12.47	63	6	6	0	18.56	Glycogen [starch] synthase, muscle	Q9Z1E4	Gys1	Mus musculus
Q9Z1F9	8	2	2	10.19	29	7	7	22.41	37	7	7	0	22.41	SUMO-activating enzyme subunit 2	Q9Z1F9	Uba2	Mus musculus
Q9Z1N5	51	5	4	19.86	90	7	5	27.1	141	7	5	0	27.1	Spliceosome RNA helicase Ddx39b	Q9Z1N5	Ddx39b	Mus musculus
Q9Z1Q5	96	7	7	40.25	226	16	16	56.43	322	16	16	0	56.43	Chloride intracellular channel protein 1	Q9Z1Q5	Clic1	Mus musculus
Q9Z1Q9	21	4	4	7.36	83	13	13	22.33	104	13	13	0	22.33	Valine--tRNA ligase	Q9Z1Q9	Vars	Mus musculus
Q9Z1Z0	2	2	2	4.9	1	1	1	1.25	3	3	3	0.21	6.15	General vesicular transport factor p115	Q9Z1Z0	Uso1	Mus musculus
Q9Z1Z2	19	3	3	14.57	57	4	4	18.29	76	4	4	0.14	18.29	Serine-threonine kinase receptor-associated protein	Q9Z1Z2	Strap	Mus musculus
Q9Z2G9	0	0	0		3	2	2	9.5	3	2	2	0.86	9.5	Oxidoreductase HTATIP2	Q9Z2G9	Htatip2	Mus musculus
Q9Z2I8	0	0	0		2	2	2	12.7	2	2	2	0.86	12.7	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Q9Z2I8	Suclg2	Mus musculus
Q9Z2L7	51	4	4	23.76	46	5	5	31.22	97	5	5	0	31.22	Cytokine receptor-like factor 3	Q9Z2L7	Crlf3	Mus musculus
Q9Z2R6	0	0	0		7	3	3	17.92	7	3	3	0.21	17.92	Protein unc-119 homolog A	Q9Z2R6	Unc119	Mus musculus
Q9Z2U0	153	10	10	51.21	98	8	8	46.77	251	10	10	0	51.21	Proteasome subunit alpha type-7	Q9Z2U0	Psma7	Mus musculus
Q9Z2U1	75	5	5	31.12	59	5	5	31.12	134	5	5	0	31.12	Proteasome subunit alpha type-5	Q9Z2U1	Psma5	Mus musculus
Q9Z2W0	101	9	9	39.96	88	8	8	37.21	189	10	10	0	39.96	Aspartyl aminopeptidase	Q9Z2W0	Dnpep	Mus musculus
Q9Z2X1	88	6	5	28.19	128	9	8	35.42	216	9	8	0	35.42	Heterogeneous nuclear ribonucleoprotein F	Q9Z2X1	Hnrnpf	Mus musculus

Protein identifications for the comparison MDSC Infl. vs. MDSC Conv.

Protein FDR ≤ 0.41%

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
A0A087WR50	52	11	11	10.39	309	37	37	29.92	361	38	38	0	29.97	Fibronectin	A0A087WR50	Fn1	Mus musculus
A0A087WSP5	14	2	2	5.83	21	3	3	7.95	35	3	3	0	7.95	Signal transducer and activator of transcription	A0A087WSP5	Stat1	Mus musculus
A0A0D9SEG8	83	7	7	15.19	41	5	5	12.15	124	7	7	0	15.19	Protein Adgre5	A0A0D9SEG8	Adgre5	Mus musculus
A2A8Z1	5	2	2	5.84	8	3	3	8.56	13	3	3	0	8.56	Oxysterol-binding protein-related protein 9	A2A8Z1	Osbpl9	Mus musculus
A2ADY9	8	2	2	8.52	23	4	4	18.8	31	5	5	0	22.56	Protein DDI1 homolog 2	A2ADY9	Ddi2	Mus musculus
A2AFG7	35	6	6	11.84	0	0	0		35	6	6	0	11.84	Neural cell adhesion molecule L1	A2AFG7	L1cam	Mus musculus
A2AIV8	15	3	3	9.14	36	5	5	15.67	51	5	5	0	15.67	Caspase recruitment domain-containing protein 9	A2AIV8	Card9	Mus musculus
A2AJW4	0	0	0		5	2	2	17.2	5	2	2	0.41	17.2	Protein phosphatase 1 regulatory subunit	A2AJW4	Ppp1r3d	Mus musculus
A2AL36	2	1	1	0.6	3	2	2	1.33	5	2	2	0.41	1.33	Centriolin	A2AL36	Cntrl	Mus musculus
A2AN08	12	5	5	2.49	32	9	9	4.5	44	10	10	0	4.88	E3 ubiquitin-protein ligase UBR4	A2AN08	Ubr4	Mus musculus
A2AQ07	57	5	4	19.07	53	12	10	41.91	110	12	10	0	41.91	Tubulin beta-1 chain	A2AQ07	Tubb1	Mus musculus
A2AUR7	33	4	4	38.85	83	10	10	62.69	116	10	10	0	62.69	Ras suppressor protein 1	A2AUR7	Rsu1	Mus musculus
A3KGV1	8	2	2	3.01	2	1	1	1.57	10	2	2	0.41	3.01	Outer dense fiber protein 2	A3KGV1	Odf2	Mus musculus
A6X935	3	2	2	4.46	0	0	0		3	2	2	0.41	4.46	Inter alpha-trypsin inhibitor, heavy chain 4	A6X935	Itih4	Mus musculus
A6ZI44	251	14	14	48.09	632	20	20	49.76	883	21	21	0	51.44	Fructose-bisphosphate aldolase	A6ZI44	Aldoa	Mus musculus
A8E0Y8	2	2	2	3.29	0	0	0		2	2	2	0.41	3.29	Immunoglobulin superfamily member 2	A8E0Y8	Cd101	Mus musculus
B1AUY2	2	2	2	4.45	9	4	4	9.75	11	5	5	0	11.44	Protein Arhgap4	B1AUY2	Arhgap4	Mus musculus
B1AVH7	0	0	0		5	3	3	6.4	5	3	3	0	6.4	TBC1 domain family member 2A	B1AVH7	Tbc1d2	Mus musculus
B2RPV6	9	2	2	2.48	12	2	2	2.48	21	2	2	0.41	2.48	Multimerin-1	B2RPV6	Mmrn1	Mus musculus
B2RQC6	5	4	4	5.17	27	8	8	7.37	32	8	8	0	7.37	CAD protein	B2RQC6	Cad	Mus musculus
B2RUP2	8	2	2	4.42	9	3	3	6.27	17	3	3	0	6.27	Protein unc-13 homolog D	B2RUP2	Unc13d	Mus musculus
B2RV77	30	4	4	44.33	215	10	10	60.82	245	10	10	0	60.82	MCG130182, isoform CRA_a	B2RV77	Gm5483	Mus musculus
B2RXR6	27	5	5	9.97	32	5	5	10.67	59	8	8	0	15.91	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B	B2RXR6	Ankrd44	Mus musculus
B2RY56	5	2	2	4.06	1	1	1	1.79	6	2	2	0.41	4.06	RNA-binding protein 25	B2RY56	Rbm25	Mus musculus
B5THE2	69	13	13	10.51	25	8	8	7.39	94	14	14	0	11.49	Maltase-glucoamylase	B5THE2	Mgam	Mus musculus
B9EJ54	0	0	0		4	2	2	2.79	4	2	2	0.41	2.79	MCG21756, isoform CRA_b	B9EJ54	Nup205	Mus musculus
D3YTQ8	1	1	1	25.97	3	2	2	53.25	4	2	2	0.41	53.25	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 5, isoform CRA_a	D3YTQ8	Ndufa5	Mus musculus
D3YXK2	72	8	8	11.53	46	4	4	6.4	118	8	8	0	11.53	Scaffold attachment factor B1	D3YXK2	Safb	Mus musculus
D3YZZ5	3	2	2	11.16	1	1	1	5.8	4	2	2	0.41	11.16	Protein Tmed7	D3YZZ5	Tmed7	Mus musculus
D3Z6Q9	66	9	9	22.09	84	5	5	14.93	150	9	9	0	22.09	Bridging integrator 2	D3Z6Q9	Bin2	Mus musculus
D4AFX7	14	8	8	5.96	22	5	5	3.96	36	8	8	0	5.96	Protein Dnajc13	D4AFX7	Dnajc13	Mus musculus
E9PV24	83	8	8	22.05	68	10	10	20.79	151	13	13	0	30.04	Fibrinogen alpha chain	E9PV24	Fga	Mus musculus
E9PVA8	2	1	1	0.6	15	3	3	1.61	17	3	3	0	1.61	Protein Gcn1l1	E9PVA8	Gcn1l1	Mus musculus
E9PVX6	70	20	20	10.92	41	8	8	5.7	111	20	20	0	10.92	Protein Mki67	E9PVX6	Mki67	Mus musculus
E9PWG6	4	3	3	5.68	10	3	3	4.68	14	4	4	0	7.37	Protein Ncapg	E9PWG6	Ncapg	Mus musculus
E9PX59	0	0	0		5	4	4	6.84	5	4	4	0	6.84	Sterile alpha motif domain-containing protein 9-like	E9PX59	Samd9l	Mus musculus
E9PZF0	3	1	0	4.49	16	4	3	14.23	19	5	3	0	18.73	Nucleoside diphosphate kinase	E9PZF0	Gm20390	Mus musculus
E9Q070	112	13	13	57.41	173	13	13	54.26	285	16	16	0	58.99	Uncharacterized protein	E9Q070	Gm8730	Mus musculus
E9Q0K6	59	8	8	19.05	104	11	11	24.73	163	12	12	0	26.73	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	E9Q0K6	Samhd1	Mus musculus
E9Q0Y4	11	5	5	11.75	14	5	5	9.54	25	7	7	0	14.93	Signal-induced proliferation-associated protein 1	E9Q0Y4	Sipa1	Mus musculus
E9Q394	18	5	5	3.17	7	3	3	2.09	25	5	5	0	3.17	Protein Akap13	E9Q394	Akap13	Mus musculus
E9Q397	215	34	34	24.01	1	1	1	1.26	216	34	34	0	24.01	Spectrin beta chain, erythrocytic	E9Q397	Sptb	Mus musculus
E9Q555	2	2	2	0.8	0	0	0		2	2	2	0.41	0.8	E3 ubiquitin-protein ligase RNF213	E9Q555	Rnf213	Mus musculus
E9Q586	15	5	5	9.52	17	6	6	11.7	32	7	7	0	12.99	Dynactin subunit 1	E9Q586	Dctn1	Mus musculus
E9Q604	774	46	46	46.36	403	26	26	33.28	1177	48	48	0	46.36	Integrin alpha-M	E9Q604	Itgam	Mus musculus
E9Q616	0	0	0		4	2	2	0.53	4	2	2	0.41	0.53	Protein Ahnak	E9Q616	Ahnak	Mus musculus
E9Q6E5	9	2	2	7.44	0	0	0		9	2	2	0.41	7.44	Protein Srsf11	E9Q6E5	Srsf11	Mus musculus
E9Q6Q4	1	1	1	5.2	12	2	2	8.6	13	2	2	0.41	8.6	Protein Rap1gds1	E9Q6Q4	Rap1gds1	Mus musculus
E9Q6U4	6	1	1	11.54	9	2	2	20.77	15	2	2	0.41	20.77	Prefoldin subunit 4	E9Q6U4	Pfdn4	Mus musculus
E9Q7G0	77	16	16	13.04	50	10	10	9.26	127	17	17	0	14.23	Protein Numa1	E9Q7G0	Numa1	Mus musculus
E9Q8K8	13	3	3	5.82	16	1	1	1.27	29	3	3	0	5.82	Zinc finger CCCH domain-containing protein 4	E9Q8K8	Zc3h4	Mus musculus
E9Q8L9	16	3	3	5.57	5	1	1	2.57	21	3	3	0	5.57	Rab11 family-interacting protein 1	E9Q8L9	Rab11fip1	Mus musculus
E9QNN1	74	9	9	13.08	107	10	10	12.14	181	13	13	0	16.11	ATP-dependent RNA helicase A	E9QNN1	Dhx9	Mus musculus
E9QPU1	73	12	12	9.77	120	22	22	16.26	193	23	23	0	16.58	von Willebrand factor	E9QPU1	Vwf	Mus musculus
F6ZDS4	74	15	15	11.15	58	8	8	5.88	132	15	15	0	11.15	Nucleoprotein TPR	F6ZDS4	Tpr	Mus musculus
F7BJB9	2	2	2	5.1	0	0	0		2	2	2	0.41	5.1	Protein Morc3	F7BJB9	Morc3	Mus musculus
F8VQC1	4	2	2	8.05	13	2	2	8.05	17	2	2	0.41	8.05	Signal recognition particle subunit SRP72	F8VQC1	Srp72	Mus musculus
F8WI35	514	11	3	31.85	235	10	2	31.85	749	12	3	0	31.85	Histone H3	F8WI35	H3f3a	Mus musculus
G5E870	6	2	2	2.57	9	1	1	1.38	15	2	2	0.41	2.57	E3 ubiquitin-protein ligase TRIP12	G5E870	Trip12	Mus musculus
O08528	9	4	3	7.2	12	3	2	5.13	21	5	4	0	9.6	Hexokinase-2	O08528	Hk2	Mus musculus
O08553	1	1	1	2.8	7	2	2	5.59	8	2	2	0.41	5.59	Dihydropyrimidinase-related protein 2	O08553	Dpysl2	Mus musculus
O08582	20	4	4	12.57	16	3	3	9.58	36	4	4	0	12.57	GTP-binding protein 1	O08582	Gtpbp1	Mus musculus
O08583	86	12	12	38.43	67	8	8	37.25	153	12	12	0	38.43	THO complex subunit 4	O08583	Alyref	Mus musculus
O08585	50	3	3	21.28	32	2	2	13.62	82	3	3	0	21.28	Clathrin light chain A	O08585	Clta	Mus musculus
O08663	22	6	6	21.13	27	6	6	28.45	49	8	8	0	33.89	Methionine aminopeptidase 2	O08663	Metap2	Mus musculus
O08677	14	3	3	8.77	2	1	1	3.63	16	3	3	0	8.77	Kininogen-1	O08677	Kng1	Mus musculus
O08692	3227	23	23	68.26	2172	19	19	66.47	5399	26	26	0	75.45	Neutrophilic granule protein	O08692	Ngp	Mus musculus
O08709	126	9	9	53.57	122	9	9	50.45	248	10	10	0	53.57	Peroxiredoxin-6	O08709	Prdx6	Mus musculus
O08734	18	2	2	11	9	2	2	22.97	27	3	3	0	22.97	Bcl-2 homologous antagonist/killer	O08734	Bak1	Mus musculus
O08738	0	0	0		7	2	2	10.14	7	2	2	0.41	10.14	Caspase-6	O08738	Casp6	Mus musculus
O08749	54	5	5	18.27	37	5	5	18.27	91	5	5	0	18.27	Dihydrolipoyl dehydrogenase, mitochondrial	O08749	Dld	Mus musculus
O08759	1	1	1	3.1	6	2	2	6.32	7	2	2	0.41	6.32	Ubiquitin-protein ligase E3A	O08759	Ube3a	Mus musculus
O08795	53	7	7	14.4	29	2	2	5.37	82	7	7	0	14.4	Glucosidase 2 subunit beta	O08795	Prkcsh	Mus musculus
O08807	4	2	2	13.14	0	0	0		4	2	2	0.41	13.14	Peroxiredoxin-4	O08807	Prdx4	Mus musculus
O08808	51	9	9	9.08	72	9	9	9.08	123	10	10	0	10.2	Protein diaphanous homolog 1	O08808	Diaph1	Mus musculus
O08810	102	10	10	19.77	96	9	9	18.13	198	11	11	0	21.63	116 kDa U5 small nuclear ribonucleoprotein component	O08810	Eftud2	Mus musculus
O08917	40	6	6	17.76	44	4	4	15.42	84	7	7	0	21.73	Flotillin-1	O08917	Flot1	Mus musculus
O08992	19	2	2	14.38	14	2	2	14.38	33	2	2	0.41	14.38	Syntenin-1	O08992	Sdcbp	Mus musculus
O08997	9	2	2	47.06	31	3	3	51.47	40	3	3	0	51.47	Copper transport protein ATOX1	O08997	Atox1	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
O09043	31	4	4	22.43	49	3	3	19.33	80	4	4	0	22.43	Napsin-A	O09043	Napsa	Mus musculus
O09061	12	4	4	33.75	41	6	6	33.75	53	6	6	0	33.75	Proteasome subunit beta type-1	O09061	Psmb1	Mus musculus
O09106	27	3	3	11.2	18	3	3	11.2	45	3	3	0	11.2	Histone deacetylase 1	O09106	Hdac1	Mus musculus
O09110	3	1	1	8.07	24	2	2	12.39	27	2	2	0.41	12.39	Dual specificity mitogen-activated protein kinase kinase 3	O09110	Map2k3	Mus musculus
O09130	2	2	2	11.17	4	1	1	6.31	6	2	2	0.41	11.17	NFATC2-interacting protein	O09130	Nfatc2ip	Mus musculus
O09131	0	0	0		5	2	2	12.08	5	2	2	0.41	12.08	Glutathione S-transferase omega-1	O09131	Gsto1	Mus musculus
O09159	73	9	9	17.18	25	7	7	14.51	98	10	10	0	17.18	Lysosomal alpha-mannosidase	O09159	Man2b1	Mus musculus
O09172	19	2	2	16.79	23	4	4	22.63	42	4	4	0	22.63	Glutamate--cysteine ligase regulatory subunit	O09172	Gclm	Mus musculus
O35129	32	3	3	11.71	14	4	4	17.06	46	4	4	0	17.06	Prohibitin-2	O35129	Phb2	Mus musculus
O35218	5	4	4	7.67	0	0	0		5	4	4	0	7.67	Cleavage and polyadenylation specificity factor subunit 2	O35218	Cpsf2	Mus musculus
O35226	14	4	4	21.54	23	6	6	25.8	37	6	6	0	25.8	26S proteasome non-ATPase regulatory subunit 4	O35226	Psmd4	Mus musculus
O35286	6	4	4	7.55	18	4	4	8.68	24	5	5	0	10.31	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	O35286	Dhx15	Mus musculus
O35326	4	2	2	7.43	0	0	0		4	2	2	0.41	7.43	Serine/arginine-rich splicing factor 5	O35326	Srsf5	Mus musculus
O35343	51	5	3	23.22	40	3	2	14.2	91	5	3	0	23.22	Importin subunit alpha-3	O35343	Kpna4	Mus musculus
O35344	13	5	3	21.11	12	3	2	13.44	25	5	3	0	21.11	Importin subunit alpha-4	O35344	Kpna3	Mus musculus
O35350	82	12	12	29.73	99	15	15	34.92	181	16	16	0	36.04	Calpain-1 catalytic subunit	O35350	Capn1	Mus musculus
O35381	95	9	9	44.94	173	7	7	41.3	268	10	10	0	46.96	Acidic leucine-rich nuclear phosphoprotein 32 family member A	O35381	Anp32a	Mus musculus
O35639	110	11	11	42.11	202	17	17	48.92	312	17	17	0	48.92	Annexin A3	O35639	Anxa3	Mus musculus
O35643	76	8	5	20.47	94	8	5	19.62	170	9	6	0	22.69	AP-1 complex subunit beta-1	O35643	Ap1b1	Mus musculus
O35704	3	2	2	6.77	0	0	0		3	2	2	0.41	6.77	Serine palmitoyltransferase 1	O35704	Sptlc1	Mus musculus
O35737	130	12	7	35.41	169	10	6	28.95	299	13	8	0	35.41	Heterogeneous nuclear ribonucleoprotein H	O35737	Hnrnph1	Mus musculus
O35744	389	20	20	55.28	408	26	26	61.81	797	30	30	0	65.33	Chitinase-like protein 3	O35744	Chil3	Mus musculus
O35841	41	7	7	25.6	62	7	7	26.98	103	8	8	0	28.17	Apoptosis inhibitor 5	O35841	Api5	Mus musculus
O35887	10	2	2	12.38	0	0	0		10	2	2	0.41	12.38	Calumenin	O35887	Calu	Mus musculus
O35892	10	2	2	8.3	4	2	2	8.3	14	2	2	0.41	8.3	Nuclear autoantigen Sp-100	O35892	Sp100	Mus musculus
O35900	13	2	2	40	26	2	2	40	39	2	2	0.41	40	U6 snRNA-associated Sm-like protein LSm2	O35900	Lsm2	Mus musculus
O35930	10	3	3	9.13	28	5	5	13.35	38	5	5	0	13.35	Platelet glycoprotein Ib alpha chain	O35930	Gp1ba	Mus musculus
O54734	15	3	3	13.83	1	1	1	6.58	16	3	3	0	13.83	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	O54734	Ddost	Mus musculus
O54774	10	2	2	3.42	4	3	3	5.17	14	3	3	0	5.17	AP-3 complex subunit delta-1	O54774	Ap3d1	Mus musculus
O54824	29	3	3	6.2	19	3	3	6.2	48	3	3	0	6.2	Pro-interleukin-16	O54824	Il16	Mus musculus
O54890	6	3	3	7.75	5	2	2	6.48	11	4	4	0	10.55	Integrin beta-3	O54890	Itgb3	Mus musculus
O54941	11	2	2	6.81	0	0	0		11	2	2	0.41	6.81	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	O54941	Smarce1	Mus musculus
O54950	0	0	0		14	2	2	14.55	14	2	2	0.41	14.55	5'-AMP-activated protein kinase subunit gamma-1	O54950	Prkag1	Mus musculus
O54988	13	1	1	1.7	30	5	5	10.54	43	5	5	0	10.54	STE20-like serine/threonine-protein kinase	O54988	Slk	Mus musculus
O55029	61	11	11	23.65	63	11	11	24.31	124	12	12	0	25.86	Coatomer subunit beta'	O55029	Copb2	Mus musculus
O55098	17	2	2	4.76	24	2	2	4.76	41	2	2	0.41	4.76	Serine/threonine-protein kinase 10	O55098	Stk10	Mus musculus
O55106	34	5	5	13.59	26	5	5	14.49	60	6	6	0	16.28	Striatin	O55106	Strn	Mus musculus
O55131	10	2	2	9.17	32	4	4	21.33	42	4	4	0	21.33	Septin-7	O55131	Sept7	Mus musculus
O55135	61	5	5	46.94	76	5	5	55.51	137	6	6	0	62.86	Eukaryotic translation initiation factor 6	O55135	Eif6	Mus musculus
O55201	10	4	4	8.04	18	4	4	9.8	28	6	6	0	11.83	Transcription elongation factor SPT5	O55201	Supt5h	Mus musculus
O55222	14	1	1	5.75	38	3	3	14.16	52	3	3	0	14.16	Integrin-linked protein kinase	O55222	Ilk	Mus musculus
O70138	69	6	6	26.45	62	6	6	26.02	131	7	7	0	32.47	Neutrophil collagenase	O70138	Mmp8	Mus musculus
O70145	111	7	7	28.57	187	10	10	34.86	298	10	10	0	34.86	Neutrophil cytosol factor 2	O70145	Ncf2	Mus musculus
O70194	8	3	3	12.77	25	2	2	8.58	33	3	3	0	12.77	Eukaryotic translation initiation factor 3 subunit D	O70194	Eif3d	Mus musculus
O70251	40	3	3	23.56	62	5	5	34.22	102	5	5	0	34.22	Elongation factor 1-beta	O70251	Eef1b	Mus musculus
O70252	2	1	1	3.81	2	2	2	9.52	4	2	2	0.41	9.52	Heme oxygenase 2	O70252	Hmox2	Mus musculus
O70310	1	1	1	3.83	5	3	3	11.09	6	3	3	0	11.09	Glycylpeptide N-tetradecanoyltransferase 1	O70310	Nmt1	Mus musculus
O70400	0	0	0		11	3	3	22.32	11	3	3	0	22.32	PDZ and LIM domain protein 1	O70400	Pdlim1	Mus musculus
O70435	0	0	0		5	2	2	9.41	5	2	2	0.41	9.41	Proteasome subunit alpha type-3	O70435	Psma3	Mus musculus
O70492	6	1	1	20.37	17	2	2	29.63	23	2	2	0.41	29.63	Sorting nexin-3	O70492	Snx3	Mus musculus
O70497	14	2	2	15.61	8	1	1	8.92	22	2	2	0.41	15.61	Ficolin-2	O70497	Fcn2	Mus musculus
O70566	0	0	0		2	2	2	3.92	2	2	2	0.41	3.92	Protein diaphanous homolog 2	O70566	Diaph2	Mus musculus
O88307	112	23	23	18.28	32	9	9	6.68	144	24	24	0	18.74	Sortilin-related receptor	O88307	Sorl1	Mus musculus
O88342	212	16	16	47.36	384	22	22	54.46	596	22	22	0	54.46	WD repeat-containing protein 1	O88342	Wdr1	Mus musculus
O88379	6	3	3	2.89	3	2	2	3.09	9	4	4	0	5.27	Bromodomain adjacent to zinc finger domain protein 1A	O88379	Baz1a	Mus musculus
O88520	2	2	2	10.31	9	1	1	5.67	11	2	2	0.41	10.31	Leucine-rich repeat protein SHOC-2	O88520	Shoc2	Mus musculus
O88536	21	3	3	11.11	2	2	2	7.98	23	3	3	0	11.11	Formyl peptide receptor 2	O88536	Fpr2	Mus musculus
O88544	17	2	2	10.59	19	3	3	9.85	36	4	4	0	15.52	COP9 signalosome complex subunit 4	O88544	Cops4	Mus musculus
O88569	311	16	16	44.48	323	13	13	41.64	634	17	17	0	44.48	Heterogeneous nuclear ribonucleoproteins A2/B1	O88569	Hnrnpa2b1	Mus musculus
O88593	1494	18	18	53.3	890	15	15	62.64	2384	19	19	0	62.64	Peptidoglycan recognition protein 1	O88593	Pglyrp1	Mus musculus
O88668	6	2	2	13.18	2	1	1	5	8	2	2	0.41	13.18	Protein CREG1	O88668	Creg1	Mus musculus
O88685	38	6	6	24.89	56	7	7	24.89	94	7	7	0	24.89	26S protease regulatory subunit 6A	O88685	Psmc3	Mus musculus
O88712	14	2	2	11.79	15	2	2	11.79	29	2	2	0.41	11.79	C-terminal-binding protein 1	O88712	Ctbp1	Mus musculus
O88746	33	4	4	15.65	26	2	2	8.94	59	4	4	0	15.65	Target of Myb protein 1	O88746	Tom1	Mus musculus
O88783	129	10	10	8.61	55	5	5	4.76	184	10	10	0	8.61	Coagulation factor V	O88783	F5	Mus musculus
O88842	9	4	4	12.14	17	3	3	9.82	26	4	4	0	12.14	FYVE, RhoGEF and PH domain-containing protein 3	O88842	Fgd3	Mus musculus
O88844	1	1	1	4.83	19	3	3	13.53	20	3	3	0	13.53	Isocitrate dehydrogenase [NADP] cytoplasmic	O88844	Idh1	Mus musculus
O88879	3	1	1	1.2	28	4	4	6.73	31	4	4	0	6.73	Apoptotic protease-activating factor 1	O88879	Apaf1	Mus musculus
O88968	93	8	8	37.44	40	4	4	21.16	133	8	8	0	37.44	Transcobalamin-2	O88968	Tcn2	Mus musculus
O89053	166	16	16	39.48	374	22	22	37.74	540	24	24	0	39.48	Coronin-1A	O89053	Coro1a	Mus musculus
O89079	45	6	6	33.12	34	3	3	17.21	79	6	6	0	33.12	Coatomer subunit epsilon	O89079	Cope	Mus musculus
O89086	51	3	3	22.22	103	3	3	22.22	154	4	4	0	22.22	RNA-binding protein 3	O89086	Rbm3	Mus musculus
P00405	15	2	2	8.81	19	1	1	8.81	34	2	2	0.41	8.81	Cytochrome c oxidase subunit 2	P00405	Mtco2	Mus musculus
P00493	16	4	4	26.15	35	7	7	35.32	51	7	7	0	35.32	Hypoxanthine-guanine phosphoribosyltransferase	P00493	Hprt1	Mus musculus
P01027	437	45	45	38.6	231	25	25	22.61	668	46	46	0	38.67	Complement C3	P01027	C3	Mus musculus
P01029	7	1	1	0.69	10	2	2	2.13	17	2	2	0.41	2.13	Complement C4-B	P01029	C4b	Mus musculus
P01326	21	5	5	33.64	0	0	0		21	5	5	0	33.64	Insulin-2	P01326	Ins2	Mus musculus
P01887	43	2	2	19.33	30	2	2	19.33	73	2	2	0.41	19.33	Beta-2-microglobulin	P01887	B2m	Mus musculus
P01942	261	11	11	78.87	59	3	3	42.25	320	11	11	0	78.87	Hemoglobin subunit alpha	P01942	Hba	Mus musculus
P02088	254	16	10	95.24	23	5	2	46.26	277	16	10	0	95.24	Hemoglobin subunit beta-1	P02088	Hbb-b1	Mus musculus
P02089	186	11	5	85.03	21	4	1	32.65	207	11	5	0	85.03	Hemoglobin subunit beta-2	P02089	Hbb-b2	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P03958	0	0	0		7	3	3	18.75	7	3	3	0	18.75	Adenosine deaminase	P03958	Ada	Mus musculus
P04202	12	2	2	10	14	2	2	10	26	2	2	0.41	10	Transforming growth factor beta-1	P04202	Tgfb1	Mus musculus
P04919	148	13	13	23.47	13	4	4	9.47	161	13	13	0	23.47	Band 3 anion transport protein	P04919	Slc4a1	Mus musculus
P05201	7	2	2	9.69	44	4	4	17.68	51	4	4	0	17.68	Aspartate aminotransferase, cytoplasmic	P05201	Got1	Mus musculus
P05202	82	6	6	25.81	65	5	5	19.53	147	6	6	0	25.81	Aspartate aminotransferase, mitochondrial	P05202	Got2	Mus musculus
P06151	105	7	7	36.75	270	13	13	55.42	375	13	13	0	55.42	L-lactate dehydrogenase A chain	P06151	Ldha	Mus musculus
P06745	118	14	14	39.96	363	19	19	43.01	481	20	20	0	43.01	Glucose-6-phosphate isomerase	P06745	Gpi	Mus musculus
P06800	387	28	28	27.89	177	20	20	23.86	564	29	29	0	27.89	Receptor-type tyrosine-protein phosphatase C	P06800	Ptprc	Mus musculus
P07356	453	26	26	61.06	499	21	21	57.82	952	29	29	0	63.42	Annexin A2	P07356	Anxa2	Mus musculus
P07724	945	35	35	54.93	935	26	26	46.05	1880	38	38	0	54.93	Serum albumin	P07724	Alb	Mus musculus
P07742	11	3	3	9.09	33	5	5	10.98	44	5	5	0	10.98	Ribonucleoside-diphosphate reductase large subunit	P07742	Rrm1	Mus musculus
P07759	61	8	8	30.86	16	4	4	16.99	77	8	8	0	30.86	Serine protease inhibitor A3K	P07759	Serpina3k	Mus musculus
P07901	151	20	14	32.74	201	18	13	31.79	352	22	15	0	36.56	Heat shock protein HSP 90-alpha	P07901	Hsp90aa1	Mus musculus
P08003	37	8	8	18.65	17	5	5	17.4	54	10	10	0	24.61	Protein disulfide-isomerase A4	P08003	Pdia4	Mus musculus
P08030	15	2	2	18.33	46	6	6	42.78	61	6	6	0	42.78	Adenine phosphoribosyltransferase	P08030	Aprt	Mus musculus
P08032	365	49	48	30.93	7	4	4	4.06	372	49	48	0	30.93	Spectrin alpha chain, erythrocytic 1	P08032	Spta1	Mus musculus
P08071	5207	82	82	72.7	2294	60	60	70.44	7501	84	84	0	73.27	Lactotransferrin	P08071	Ltf	Mus musculus
P08103	27	4	4	13.74	21	2	2	8.59	48	4	4	0	13.74	Tyrosine-protein kinase HCK	P08103	Hck	Mus musculus
P08113	313	19	18	32.04	215	16	15	31.17	528	21	20	0	34.91	Endoplasmin	P08113	Hsp90b1	Mus musculus
P08226	7	3	3	18.33	3	2	2	12.22	10	3	3	0	18.33	Apolipoprotein E	P08226	Apoe	Mus musculus
P08228	16	4	4	36.36	40	5	5	36.36	56	5	5	0	36.36	Superoxide dismutase [Cu-Zn]	P08228	Sod1	Mus musculus
P08249	132	11	11	36.39	157	11	11	42.01	289	13	13	0	42.31	Malate dehydrogenase, mitochondrial	P08249	Mdh2	Mus musculus
P08556	22	2	2	21.69	18	2	2	13.76	40	3	3	0	21.69	GTPase NRas	P08556	Nras	Mus musculus
P08607	0	0	0		4	2	2	7.89	4	2	2	0.41	7.89	C4b-binding protein	P08607	C4bpa	Mus musculus
P08752	625	19	13	53.52	402	15	10	44.23	1027	21	15	0	54.37	Guanine nucleotide-binding protein G(i) subunit alpha-2	P08752	Gnai2	Mus musculus
P08775	8	2	2	2.08	6	2	2	1.98	14	3	3	0	3.05	DNA-directed RNA polymerase II subunit RPB1	P08775	Polr2a	Mus musculus
P08905	1018	17	17	50.68	217	8	8	50.68	1235	17	17	0	50.68	Lysozyme C-2	P08905	Lyz2	Mus musculus
P09103	416	25	25	51.67	332	21	21	46.17	748	26	26	0	51.67	Protein disulfide-isomerase	P09103	P4hb	Mus musculus
P09405	90	13	13	21.78	96	14	14	20.23	186	17	17	0	21.78	Nucleolin	P09405	Ncl	Mus musculus
P09411	148	12	12	38.13	356	17	17	45.08	504	17	17	0	45.08	Phosphoglycerate kinase 1	P09411	Pgk1	Mus musculus
P0C0S6	594	12	11	56.25	456	10	9	50	1050	15	14	0	56.25	Histone H2A.Z	P0C0S6	H2afz	Mus musculus
P0CW02	56	5	5	45.8	0	0	0		56	5	5	0	45.8	Lymphocyte antigen 6C1	P0CW02	Ly6c1	Mus musculus
P10107	2824	45	45	67.63	3057	41	41	67.92	5881	49	49	0	68.79	Annexin A1	P10107	Anxa1	Mus musculus
P10126	195	12	12	27.71	670	24	24	42.86	865	24	24	0	42.86	Elongation factor 1-alpha 1	P10126	Eef1a1	Mus musculus
P10518	8	2	2	17.27	4	1	1	11.52	12	2	2	0.41	17.27	Delta-aminolevulinic acid dehydratase	P10518	Alad	Mus musculus
P10605	152	10	10	44.54	106	10	10	43.95	258	11	11	0	48.67	Cathepsin B	P10605	Ctsb	Mus musculus
P10639	77	6	6	60	545	7	7	60	622	9	9	0	60	Thioredoxin	P10639	Txn	Mus musculus
P10649	14	4	4	16.06	88	5	5	21.1	102	6	6	0	22.48	Glutathione S-transferase Mu 1	P10649	Gstm1	Mus musculus
P10711	5	1	1	9.3	8	2	2	9.3	13	2	2	0.41	9.3	Transcription elongation factor A protein 1	P10711	Tcea1	Mus musculus
P10810	32	5	5	30.05	23	3	3	21.31	55	5	5	0	30.05	Monocyte differentiation antigen CD14	P10810	Cd14	Mus musculus
P10852	14	2	2	9.51	16	7	7	31.37	30	7	7	0	31.37	4F2 cell-surface antigen heavy chain	P10852	Slc3a2	Mus musculus
P10853	8	4	4	24.6	21	4	4	24.6	29	5	5	0	24.6	Histone H2B type 1-F/J/L	P10853	Hist1h2bf	Mus musculus
P11247	513	32	32	35.93	709	34	34	35.38	1222	38	38	0	39.69	Myeloperoxidase	P11247	Mpo	Mus musculus
P11352	55	5	5	47.26	77	7	7	47.26	132	7	7	0	47.26	Glutathione peroxidase 1	P11352	Gpx1	Mus musculus
P11499	248	23	16	40.33	270	23	17	41.3	518	28	20	0	45.3	Heat shock protein HSP 90-beta	P11499	Hsp90ab1	Mus musculus
P11672	1869	19	19	43.5	763	15	15	45	2632	20	20	0	49	Neutrophil gelatinase-associated lipocalin	P11672	Lcn2	Mus musculus
P11680	31	2	2	5.82	6	1	1	5.17	37	2	2	0.41	5.82	Properdin	P11680	Cfp	Mus musculus
P11835	328	27	27	37.09	126	13	13	25.94	454	27	27	0	37.09	Integrin beta-2	P11835	Itgb2	Mus musculus
P11983	33	4	4	14.75	53	5	5	18.88	86	5	5	0	18.88	T-complex protein 1 subunit alpha	P11983	Tcp1	Mus musculus
P12023	37	7	7	9.48	20	4	4	6.88	57	8	8	0	11.95	Amyloid beta A4 protein	P12023	App	Mus musculus
P12382	0	0	0		10	2	2	5.51	10	2	2	0.41	5.51	ATP-dependent 6-phosphofructokinase, liver type	P12382	Pfkl	Mus musculus
P12787	58	6	6	42.47	44	4	4	32.19	102	7	7	0	42.47	Cytochrome c oxidase subunit 5A, mitochondrial	P12787	Cox5a	Mus musculus
P12815	10	2	2	29.84	23	3	3	36.65	33	3	3	0	36.65	Programmed cell death protein 6	P12815	Pdcd6	Mus musculus
P12970	3	2	2	9.4	14	3	3	13.53	17	3	3	0	13.53	60S ribosomal protein L7a	P12970	Rpl7a	Mus musculus
P13020	446	27	27	45.9	342	23	23	41.92	788	29	29	0	45.9	Gelsolin	P13020	Gsn	Mus musculus
P13439	1	1	1	7.07	17	2	2	9.98	18	2	2	0.41	9.98	Uridine 5'-monophosphate synthase	P13439	Umps	Mus musculus
P13595	3	2	2	4.39	0	0	0		3	2	2	0.41	4.39	Neural cell adhesion molecule 1	P13595	Ncam1	Mus musculus
P13864	17	3	3	5.49	19	3	3	5.49	36	3	3	0	5.49	DNA (cytosine-5)-methyltransferase 1	P13864	Dnmt1	Mus musculus
P14069	125	8	8	61.8	228	15	15	75.28	353	15	15	0	75.28	Protein S100-A6	P14069	S100a6	Mus musculus
P14115	9	2	2	23.65	6	1	1	14.86	15	2	2	0.41	23.65	60S ribosomal protein L27a	P14115	Rpl27a	Mus musculus
P14148	10	2	2	11.85	2	2	2	11.85	12	2	2	0.41	11.85	60S ribosomal protein L7	P14148	Rpl7	Mus musculus
P14152	13	2	2	9.88	28	4	4	18.56	41	5	5	0	23.35	Malate dehydrogenase, cytoplasmic	P14152	Mdh1	Mus musculus
P14206	36	8	8	37.97	63	5	5	23.73	99	8	8	0	37.97	40S ribosomal protein SA	P14206	Rpsa	Mus musculus
P14211	777	30	30	56.49	564	25	25	55.53	1341	32	32	0	59.62	Calreticulin	P14211	Calr	Mus musculus
P14234	136	10	10	29.98	93	9	9	27.85	229	10	10	0	29.98	Tyrosine-protein kinase Fgr	P14234	Fgr	Mus musculus
P14685	2	2	2	6.79	17	5	5	12.26	19	6	6	0	16.42	26S proteasome non-ATPase regulatory subunit 3	P14685	Psmd3	Mus musculus
P14733	319	24	24	41.84	223	14	14	27.89	542	24	24	0	41.84	Lamin-B1	P14733	Lmnb1	Mus musculus
P14824	61	8	8	20.8	18	6	6	15.45	79	10	10	0	25.41	Annexin A6	P14824	Anxa6	Mus musculus
P15532	10	3	2	20.39	35	4	3	18.42	45	5	3	0	26.32	Nucleoside diphosphate kinase A	P15532	Nme1	Mus musculus
P15864	204	8	2	26.89	171	7	2	25.47	375	8	2	0.41	26.89	Histone H1.2	P15864	Hist1h1c	Mus musculus
P16045	40	4	4	52.59	41	4	4	52.59	81	4	4	0	52.59	Galectin-1	P16045	Lgals1	Mus musculus
P16110	101	6	6	18.94	63	6	6	18.94	164	7	7	0	18.94	Galectin-3	P16110	Lgals3	Mus musculus
P16546	473	59	58	34.99	348	40	40	25.04	821	63	62	0	35.84	Spectrin alpha chain, non-erythrocytic 1	P16546	Sptan1	Mus musculus
P16675	27	4	4	14.35	10	2	2	7.17	37	4	4	0	14.35	Lysosomal protective protein	P16675	Ctsa	Mus musculus
P16858	309	14	14	51.65	1675	28	28	66.97	1984	30	30	0	67.57	Glyceraldehyde-3-phosphate dehydrogenase	P16858	Gapdh	Mus musculus
P16879	0	0	0		10	3	3	7.79	10	3	3	0	7.79	Tyrosine-protein kinase Fes/Fps	P16879	Fes	Mus musculus
P17047	12	4	4	13.01	5	3	3	9.64	17	4	4	0	13.01	Lysosome-associated membrane glycoprotein 2	P17047	Lamp2	Mus musculus
P17182	343	26	26	63.36	1899	37	37	68.89	2242	39	39	0	68.89	Alpha-enolase	P17182	Eno1	Mus musculus
P17426-2	2	2	1	5.13	24	6	5	17.28	26	7	5	0	18.32	Isoform B of AP-2 complex subunit alpha-1	P17426	Ap2a1	Mus musculus
P17427	25	5	4	9.7	32	5	4	12.69	57	8	6	0	16.95	AP-2 complex subunit alpha-2	P17427	Ap2a2	Mus musculus
P17439	15	2	2	12.23	12	2	2	12.23	27	2	2	0.41	12.23	Glucosylceramidase	P17439	Gba	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P17710	30	6	5	9.86	34	7	6	8.21	64	9	8	0	11.81	Hexokinase-1	P17710	Hk1	Mus musculus
P17742	155	12	12	57.93	242	12	12	65.24	397	13	13	0	65.24	Peptidyl-prolyl cis-trans isomerase A	P17742	Ppia	Mus musculus
P17751	94	10	10	42.81	176	11	11	42.81	270	12	12	0	42.81	Triosephosphate isomerase	P17751	Tpi1	Mus musculus
P17918	20	3	3	17.24	40	4	4	26.05	60	5	5	0	30.27	Proliferating cell nuclear antigen	P17918	Pcna	Mus musculus
P18242	70	8	8	36.59	76	8	8	34.15	146	10	10	0	36.59	Cathepsin D	P18242	Ctsd	Mus musculus
P18572-2	15	4	4	19.05	0	0	0		15	4	4	0	19.05	Isoform 2 of Basigin	P18572	Bsg	Mus musculus
P18653	0	0	0		17	3	3	6.49	17	3	3	0	6.49	Ribosomal protein S6 kinase alpha-1	P18653	Rps6ka1	Mus musculus
P18760	523	11	11	57.23	883	12	12	50.6	1406	14	14	0	57.23	Cofilin-1	P18760	Cfl1	Mus musculus
P19096	20	5	5	4.23	134	16	16	14.94	154	16	16	0	14.94	Fatty acid synthase	P19096	Fasn	Mus musculus
P19157	1	1	1	7.62	4	3	3	32.38	5	3	3	0	32.38	Glutathione S-transferase P 1	P19157	Gstp1	Mus musculus
P19221	72	5	5	8.74	10	2	2	2.59	82	5	5	0	8.74	Prothrombin	P19221	F2	Mus musculus
P19536	51	3	3	33.59	31	3	3	30.47	82	4	4	0	34.38	Cytochrome c oxidase subunit 5B, mitochondrial	P19536	Cox5b	Mus musculus
P19973	367	11	11	50	264	7	7	39.09	631	11	11	0	50	Lymphocyte-specific protein 1	P19973	Lsp1	Mus musculus
P20029	791	30	29	49.77	615	25	23	40.61	1406	32	30	0	49.92	78 kDa glucose-regulated protein	P20029	Hspa5	Mus musculus
P20060	34	7	7	25.75	30	5	5	20.9	64	7	7	0	25.75	Beta-hexosaminidase subunit beta	P20060	Hexb	Mus musculus
P20108	30	4	4	27.24	21	3	3	19.46	51	4	4	0	27.24	Thioredoxin-dependent peroxide reductase, mitochondrial	P20108	Prdx3	Mus musculus
P20152	1330	39	39	67.81	1439	31	31	61.37	2769	39	39	0	67.81	Vimentin	P20152	Vim	Mus musculus
P20491	5	2	2	33.72	5	2	2	33.72	10	2	2	0.41	33.72	High affinity immunoglobulin epsilon receptor subunit gamma	P20491	Fcer1g	Mus musculus
P21107	123	9	3	25.96	90	8	3	22.81	213	10	3	0	25.96	Tropomyosin alpha-3 chain	P21107	Tpm3	Mus musculus
P21107-2	280	13	7	36.29	201	12	7	32.66	481	14	7	0	36.29	Isoform 2 of Tropomyosin alpha-3 chain	P21107	Tpm3	Mus musculus
P21614	23	5	5	19.96	22	2	2	10.08	45	5	5	0	19.96	Vitamin D-binding protein	P21614	Gc	Mus musculus
P21619	20	5	5	15.6	15	3	3	11.74	35	5	5	0	15.6	Lamin-B2	P21619	Lmnb2	Mus musculus
P22599	63	7	7	35.84	4	2	2	12.11	67	7	7	0	35.84	Alpha-1-antitrypsin 1-2	P22599	Serpina1b	Mus musculus
P22682	3	1	1	3.29	17	5	5	8.76	20	5	5	0	8.76	E3 ubiquitin-protein ligase CBL	P22682	Cbl	Mus musculus
P23116	9	2	2	2.75	25	3	3	3.65	34	3	3	0	3.65	Eukaryotic translation initiation factor 3 subunit A	P23116	Eif3a	Mus musculus
P23492	17	2	2	11.76	35	5	5	31.83	52	5	5	0	31.83	Purine nucleoside phosphorylase	P23492	Pnp	Mus musculus
P23591	0	0	0		9	2	2	10.9	9	2	2	0.41	10.9	GDP-L-fucose synthase	P23591	Tsta3	Mus musculus
P23953	8	2	2	7.04	2	2	2	5.23	10	3	3	0	10.29	Carboxylesterase 1C	P23953	Ces1c	Mus musculus
P24063	123	14	14	20.29	46	6	6	9.63	169	14	14	0	20.29	Integrin alpha-L	P24063	Itgal	Mus musculus
P24270	10	3	3	9.49	4	1	1	3.98	14	3	3	0	9.49	Catalase	P24270	Cat	Mus musculus
P24369	0	0	0		5	4	4	19.91	5	4	4	0	19.91	Peptidyl-prolyl cis-trans isomerase B	P24369	Ppib	Mus musculus
P24527	40	5	5	14.89	210	22	22	43.7	250	22	22	0	43.7	Leukotriene A-4 hydrolase	P24527	Lta4h	Mus musculus
P24547	0	0	0		20	3	3	10.51	20	3	3	0	10.51	Inosine-5'-monophosphate dehydrogenase 2	P24547	Impdh2	Mus musculus
P25206	45	7	7	17.61	61	6	6	12.93	106	8	8	0	17.73	DNA replication licensing factor MCM3	P25206	Mcm3	Mus musculus
P25444	8	1	1	4.1	5	2	2	8.53	13	2	2	0.41	8.53	40S ribosomal protein S2	P25444	Rps2	Mus musculus
P25911	23	5	5	14.26	17	2	2	6.05	40	5	5	0	14.26	Tyrosine-protein kinase Lyn	P25911	Lyn	Mus musculus
P26039	1005	66	66	42.38	1264	83	83	48.45	2269	85	85	0	49.08	Talin-1	P26039	Tln1	Mus musculus
P26040	69	9	6	17.06	139	10	6	19.62	208	10	6	0	19.62	Ezrin	P26040	Ezr	Mus musculus
P26041	121	10	7	20.1	247	14	10	27.04	368	14	10	0	27.04	Moesin	P26041	Msn	Mus musculus
P26043	21	4	1	7.89	53	7	3	17.67	74	7	3	0	17.67	Radixin	P26043	Rdx	Mus musculus
P26350	98	9	9	62.16	376	13	13	62.16	474	13	13	0	62.16	Prothymosin alpha	P26350	Ptma	Mus musculus
P26369	58	5	5	18.11	46	5	5	18.11	104	5	5	0	18.11	Splicing factor U2AF 65 kDa subunit	P26369	U2af2	Mus musculus
P26443	53	5	5	17.38	46	5	5	16.67	99	6	6	0	20.25	Glutamate dehydrogenase 1, mitochondrial	P26443	Glud1	Mus musculus
P26450	15	2	2	8.7	20	2	2	8.7	35	2	2	0.41	8.7	Phosphatidylinositol 3-kinase regulatory subunit alpha	P26450	Pik3r1	Mus musculus
P26516	21	4	4	28.97	34	5	5	28.97	55	5	5	0	28.97	26S proteasome non-ATPase regulatory subunit 7	P26516	Psmd7	Mus musculus
P27005	806	20	20	78.65	3762	38	38	85.39	4568	39	39	0	85.39	Protein S100-A8	P27005	S100a8	Mus musculus
P27601	5	3	3	14.32	2	2	2	10.34	7	3	3	0	14.32	Guanine nucleotide-binding protein subunit alpha-13	P27601	Gna13	Mus musculus
P27659	8	2	2	5.71	6	1	1	5.71	14	2	2	0.41	5.71	60S ribosomal protein L3	P27659	Rpl3	Mus musculus
P27661	7695	45	21	55.24	5554	37	16	53.15	13249	48	23	0	55.24	Histone H2AX	P27661	H2afx	Mus musculus
P27773	394	24	24	50.69	310	21	21	46.14	704	27	27	0	53.47	Protein disulfide-isomerase A3	P27773	Pdia3	Mus musculus
P27870	31	6	6	11.12	54	7	7	13.02	85	8	8	0	13.14	Proto-oncogene vav	P27870	Vav1	Mus musculus
P27931	0	0	0		13	2	2	11.71	13	2	2	0.41	11.71	Interleukin-1 receptor type 2	P27931	Il1r2	Mus musculus
P28293	166	17	17	46.74	146	16	16	41.76	312	19	19	0	46.74	Cathepsin G	P28293	Ctsg	Mus musculus
P28352	2	2	2	11.36	17	2	2	11.36	19	2	2	0.41	11.36	DNA-(apurinic or apyrimidinic site) lyase	P28352	Apex1	Mus musculus
P28474	0	0	0		6	2	2	9.89	6	2	2	0.41	9.89	Alcohol dehydrogenase class-3	P28474	Adh5	Mus musculus
P28650	6	3	3	13.13	11	3	3	10.72	17	4	4	0	16.19	Adenylosuccinate synthetase isozyme 1	P28650	Adssl1	Mus musculus
P28656	44	3	3	15.35	55	4	4	20.2	99	4	4	0	20.2	Nucleosome assembly protein 1-like 1	P28656	Nap1l1	Mus musculus
P28658	3	2	2	6.53	18	3	3	9.68	21	3	3	0	9.68	Ataxin-10	P28658	Atxn10	Mus musculus
P28665	17	4	4	6.03	1	1	1	1.49	18	4	4	0	6.03	Murinoglobulin-1	P28665	Mug1	Mus musculus
P28667	13	2	2	37	24	3	3	37	37	3	3	0	37	MARCKS-related protein	P28667	Marcksl1	Mus musculus
P28798	566	21	21	41.6	382	18	18	39.22	948	21	21	0	41.6	Granulins	P28798	Grn	Mus musculus
P28867	9	4	4	9.64	20	6	6	13.35	29	7	7	0	15.13	Protein kinase C delta type	P28867	Prkcd	Mus musculus
P29341	51	7	7	15.72	30	6	6	13.52	81	8	8	0	18.24	Polyadenylate-binding protein 1	P29341	Pabpc1	Mus musculus
P29351	118	16	16	36.47	211	19	19	43.87	329	20	20	0	43.87	Tyrosine-protein phosphatase non-receptor type 6	P29351	Ptpn6	Mus musculus
P29416	11	4	4	16.67	5	3	3	10.8	16	5	5	0	16.67	Beta-hexosaminidase subunit alpha	P29416	Hexa	Mus musculus
P29621	22	2	2	6.95	17	2	2	6.95	39	2	2	0.41	6.95	Serine protease inhibitor A3C	P29621	Serpina3c	Mus musculus
P29699	46	5	5	28.41	50	3	3	21.45	96	5	5	0	28.41	Alpha-2-HS-glycoprotein	P29699	Ahsg	Mus musculus
P29758	13	2	2	8.2	13	1	1	4.56	26	2	2	0.41	8.2	Ornithine aminotransferase, mitochondrial	P29758	Oat	Mus musculus
P29788	40	3	3	3.77	4	1	1	3.14	44	3	3	0	3.77	Vitronectin	P29788	Vtn	Mus musculus
P30355	0	0	0		7	3	3	27.33	7	3	3	0	27.33	Arachidonate 5-lipoxygenase-activating protein	P30355	Alox5ap	Mus musculus
P30416	2	1	1	5.24	15	3	3	13.32	17	3	3	0	13.32	Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	Fkbp4	Mus musculus
P30681	115	4	4	27.62	143	3	3	20	258	4	4	0	27.62	High mobility group protein B2	P30681	Hmgb2	Mus musculus
P31230	2	2	2	12.9	2	2	2	17.1	4	3	3	0	23.87	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	P31230	Aimp1	Mus musculus
P31725	1138	9	9	24.78	2321	18	18	62.83	3459	18	18	0	62.83	Protein S100-A9	P31725	S100a9	Mus musculus
P31750	4	1	1	4.38	14	2	2	7.08	18	2	2	0.41	7.08	RAC-alpha serine/threonine-protein kinase	P31750	Akt1	Mus musculus
P31786	13	2	2	22.99	48	2	2	22.99	61	2	2	0.41	22.99	Acyl-CoA-binding protein	P31786	Dbi	Mus musculus
P31809	9	2	2	9.4	0	0	0		9	2	2	0.41	9.4	Carcinoembryonic antigen-related cell adhesion molecule 1	P31809	Ceacam1	Mus musculus
P31938	0	0	0		4	2	2	12.21	4	2	2	0.41	12.21	Dual specificity mitogen-activated protein kinase kinase 1	P31938	Map2k1	Mus musculus
P32020	57	5	5	14.08	45	3	3	12.43	102	5	5	0	14.08	Non-specific lipid-transfer protein	P32020	Scp2	Mus musculus
P32067	9	3	3	13.25	6	1	1	3.37	15	3	3	0	13.25	Lupus La protein homolog	P32067	Ssb	Mus musculus
P34022	27	2	2	28.08	50	5	5	39.9	77	5	5	0	39.9	Ran-specific GTPase-activating protein	P34022	Ranbp1	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P34884	0	0	0		17	2	2	21.74	17	2	2	0.41	21.74	Macrophage migration inhibitory factor	P34884	Mif	Mus musculus
P35123	6	3	3	4.78	29	5	5	10.19	35	5	5	0	10.19	Ubiquitin carboxyl-terminal hydrolase 4	P35123	Usp4	Mus musculus
P35173	0	0	0		58	3	3	37.86	58	3	3	0	37.86	Stefin-3	P35173	Stfa3	Mus musculus
P35174-2	116	5	5	63.11	1725	12	12	78.64	1841	12	12	0	78.64	Isoform 2 of Stefin-2	P35174	Stfa2	Mus musculus
P35276	10	2	2	15.53	11	2	1	13.7	21	3	2	0.41	20.55	Ras-related protein Rab-3D	P35276	Rab3d	Mus musculus
P35278	26	2	2	15.28	17	1	1	8.8	43	2	2	0.41	15.28	Ras-related protein Rab-5C	P35278	Rab5c	Mus musculus
P35282	15	2	2	13.96	12	2	2	13.96	27	2	2	0.41	13.96	Ras-related protein Rab-21	P35282	Rab21	Mus musculus
P35441	112	18	18	24.36	108	18	18	24.96	220	22	22	0	29.49	Thrombospondin-1	P35441	Thbs1	Mus musculus
P35461	55	3	3	24.32	17	1	1	22.52	72	3	3	0	24.32	Lymphocyte antigen 6G (Fragment)	P35461	Ly6g	Mus musculus
P35486	20	2	2	12.05	14	1	1	8.72	34	2	2	0.41	12.05	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	P35486	Pdha1	Mus musculus
P35505	2	2	2	7.64	27	4	4	15.75	29	4	4	0	15.75	Fumarylacetoacetase	P35505	Fah	Mus musculus
P35550	9	3	3	14.07	17	4	4	23.85	26	5	5	0	27.83	rRNA 2'-O-methyltransferase fibrillarin	P35550	Fbl	Mus musculus
P35564	142	13	13	26.9	86	9	9	28.76	228	14	14	0	32.99	Calnexin	P35564	Canx	Mus musculus
P35700	21	4	4	32.16	51	6	6	49.75	72	6	6	0	49.75	Peroxiredoxin-1	P35700	Prdx1	Mus musculus
P35831	4	1	1	2.84	6	3	3	9.03	10	3	3	0	9.03	Tyrosine-protein phosphatase non-receptor type 12	P35831	Ptpn12	Mus musculus
P35979	64	6	6	44.24	74	6	6	44.24	138	6	6	0	44.24	60S ribosomal protein L12	P35979	Rpl12	Mus musculus
P36371	34	1	1	3.28	26	2	2	8.26	60	2	2	0.41	8.26	Antigen peptide transporter 2	P36371	Tap2	Mus musculus
P37040	49	5	5	13.13	33	3	3	8.7	82	5	5	0	13.13	NADPH--cytochrome P450 reductase	P37040	Por	Mus musculus
P37913	4	1	1	2.18	18	4	4	9.72	22	4	4	0	9.72	DNA ligase 1	P37913	Lig1	Mus musculus
P38647	38	5	5	11.49	56	6	6	13.25	94	7	7	0	15.46	Stress-70 protein, mitochondrial	P38647	Hspa9	Mus musculus
P39054	32	6	6	12.3	81	9	9	20.8	113	10	10	0	20.8	Dynamin-2	P39054	Dnm2	Mus musculus
P39654	48	10	10	31.37	60	12	12	35.44	108	12	12	0	35.44	Arachidonate 15-lipoxygenase	P39654	Alox15	Mus musculus
P39655	6	2	2	6.18	39	6	6	15.84	45	6	6	0	15.84	Arachidonate 12-lipoxygenase, 12S-type	P39655	Alox12	Mus musculus
P40124	376	26	26	44.94	747	36	36	60.13	1123	36	36	0	60.13	Adenylyl cyclase-associated protein 1	P40124	Cap1	Mus musculus
P40142	317	20	20	35.79	702	30	30	46.39	1019	30	30	0	46.39	Transketolase	P40142	Tkt	Mus musculus
P40223	3	2	2	4.78	0	0	0		3	2	2	0.41	4.78	Granulocyte colony-stimulating factor receptor	P40223	Csf3r	Mus musculus
P41216	4	1	1	3	2	2	2	5.29	6	2	2	0.41	5.29	Long-chain-fatty-acid--CoA ligase 1	P41216	Acsl1	Mus musculus
P41245	1121	30	30	46.16	419	20	20	42.33	1540	31	31	0	48.08	Matrix metalloproteinase-9	P41245	Mmp9	Mus musculus
P42208	1	1	1	4.71	7	2	2	11.63	8	3	3	0	16.34	Septin-2	P42208	Sept2	Mus musculus
P42227	12	3	3	10.39	35	9	9	26.49	47	9	9	0	26.49	Signal transducer and activator of transcription 3	P42227	Stat3	Mus musculus
P42567	22	5	5	12.6	29	8	8	16.5	51	9	9	0	19.06	Epidermal growth factor receptor substrate 15	P42567	Eps15	Mus musculus
P42669	10	2	2	18.38	10	2	2	18.38	20	2	2	0.41	18.38	Transcriptional activator protein Pur-alpha	P42669	Pura	Mus musculus
P42932	36	6	6	13.87	72	7	7	16.42	108	7	7	0	16.42	T-complex protein 1 subunit theta	P42932	Cct8	Mus musculus
P43024	7	2	2	26.13	16	2	2	26.13	23	2	2	0.41	26.13	Cytochrome c oxidase subunit 6A1, mitochondrial	P43024	Cox6a1	Mus musculus
P43274	192	9	5	26.03	148	6	3	24.2	340	9	5	0	26.03	Histone H1.4	P43274	Hist1h1e	Mus musculus
P43275	71	6	5	29.11	62	5	4	27.7	133	7	6	0	29.11	Histone H1.1	P43275	Hist1h1a	Mus musculus
P43276	102	5	5	17.94	100	4	4	17.94	202	5	5	0	17.94	Histone H1.5	P43276	Hist1h1b	Mus musculus
P43277	236	8	2	25.79	201	7	2	24.43	437	8	2	0.41	25.79	Histone H1.3	P43277	Hist1h1d	Mus musculus
P43430	0	0	0		7	2	2	13.36	7	2	2	0.41	13.36	Mast cell protease 8	P43430	Mcpt8	Mus musculus
P45878	15	4	4	34.29	4	3	3	36.43	19	5	5	0	36.43	Peptidyl-prolyl cis-trans isomerase FKBP2	P45878	Fkbp2	Mus musculus
P46061	21	2	2	9.51	30	4	4	16.13	51	4	4	0	16.13	Ran GTPase-activating protein 1	P46061	Rangap1	Mus musculus
P46414	3	2	2	11.68	12	2	2	11.68	15	2	2	0.41	11.68	Cyclin-dependent kinase inhibitor 1B	P46414	Cdkn1b	Mus musculus
P46460	4	2	2	4.7	6	2	2	3.49	10	3	3	0	6.32	Vesicle-fusing ATPase	P46460	Nsf	Mus musculus
P46471	12	3	3	13.39	17	3	3	14.78	29	4	4	0	18.48	26S protease regulatory subunit 7	P46471	Psmc2	Mus musculus
P46638	61	4	2	24.31	39	5	3	24.31	100	5	3	0	24.31	Ras-related protein Rab-11B	P46638	Rab11b	Mus musculus
P46664	0	0	0		22	2	2	8.55	22	2	2	0.41	8.55	Adenylosuccinate synthetase isozyme 2	P46664	Adss	Mus musculus
P46935	2	2	2	4.17	7	1	1	2.25	9	2	2	0.41	4.17	E3 ubiquitin-protein ligase NEDD4	P46935	Nedd4	Mus musculus
P47738	283	22	22	55.11	247	18	18	55.49	530	24	24	0	60.5	Aldehyde dehydrogenase, mitochondrial	P47738	Aldh2	Mus musculus
P47740	20	2	2	9.09	16	2	2	9.09	36	2	2	0.41	9.09	Fatty aldehyde dehydrogenase	P47740	Aldh3a2	Mus musculus
P47754	60	8	6	53.5	78	8	6	47.2	138	9	7	0	53.5	F-actin-capping protein subunit alpha-2	P47754	Capza2	Mus musculus
P47757	100	9	9	40.79	157	11	11	37.55	257	12	12	0	44.77	F-actin-capping protein subunit beta	P47757	Capzb	Mus musculus
P47791	118	10	10	32.8	129	10	10	34.4	247	11	11	0	35.2	Glutathione reductase, mitochondrial	P47791	Gsr	Mus musculus
P47811	12	1	1	4.17	47	5	5	23.61	59	5	5	0	23.61	Mitogen-activated protein kinase 14	P47811	Mapk14	Mus musculus
P47911	3	2	2	8.78	0	0	0		3	2	2	0.41	8.78	60S ribosomal protein L6	P47911	Rpl6	Mus musculus
P47941	4	3	3	19.8	8	2	2	14.19	12	3	3	0	19.8	Crk-like protein	P47941	Crkl	Mus musculus
P47955	60	5	5	68.42	59	3	3	33.33	119	6	6	0	68.42	60S acidic ribosomal protein P1	P47955	Rplp1	Mus musculus
P47962	6	2	2	15.49	11	2	2	15.49	17	2	2	0.41	15.49	60S ribosomal protein L5	P47962	Rpl5	Mus musculus
P47968	0	0	0		6	2	2	11.22	6	2	2	0.41	11.22	Ribose-5-phosphate isomerase	P47968	Rpia	Mus musculus
P48024	12	2	2	37.17	13	2	2	22.12	25	3	3	0	38.05	Eukaryotic translation initiation factor 1	P48024	Eif1	Mus musculus
P48036	83	9	9	37.93	67	8	8	35.11	150	9	9	0	37.93	Annexin A5	P48036	Anxa5	Mus musculus
P48193	6	2	2	4.66	0	0	0		6	2	2	0.41	4.66	Protein 4.1	P48193	Epb41	Mus musculus
P48999	60	11	11	21.07	61	8	8	16.02	121	12	12	0	23	Arachidonate 5-lipoxygenase	P48999	Alox5	Mus musculus
P49290	19	2	2	4.75	2	2	2	4.75	21	2	2	0.41	4.75	Eosinophil peroxidase	P49290	Epx	Mus musculus
P49312	99	5	5	21.56	67	5	5	21.56	166	5	5	0	21.56	Heterogeneous nuclear ribonucleoprotein A1	P49312	Hnrnpa1	Mus musculus
P49710	144	8	8	26.95	167	11	11	36.01	311	11	11	0	36.01	Hematopoietic lineage cell-specific protein	P49710	Hcls1	Mus musculus
P49717	0	0	0		6	2	2	3.6	6	2	2	0.41	3.6	DNA replication licensing factor MCM4	P49717	Mcm4	Mus musculus
P49722	33	2	2	17.09	49	6	6	36.75	82	6	6	0	36.75	Proteasome subunit alpha type-2	P49722	Psma2	Mus musculus
P50247	1	1	1	3.47	9	3	3	12.04	10	3	3	0	12.04	Adenosylhomocysteinase	P50247	Ahcy	Mus musculus
P50396	42	5	2	20.58	90	7	3	25.06	132	7	3	0	25.06	Rab GDP dissociation inhibitor alpha	P50396	Gdi1	Mus musculus
P50429	51	4	4	12.17	16	2	2	7.87	67	4	4	0	12.17	Arylsulfatase B	P50429	Arsb	Mus musculus
P50516	51	8	8	21.56	185	11	11	31.77	236	11	11	0	31.77	V-type proton ATPase catalytic subunit A	P50516	Atp6v1a	Mus musculus
P50518	11	4	4	27.43	48	4	4	26.99	59	5	5	0	27.43	V-type proton ATPase subunit E 1	P50518	Atp6v1e1	Mus musculus
P50543	1277	15	15	80.61	1012	14	14	80.61	2289	17	17	0	80.61	Protein S100-A11	P50543	S100a11	Mus musculus
P50580	10	5	5	19.54	29	6	6	26.9	39	8	8	0	32.23	Proliferation-associated protein 2G4	P50580	Pa2g4	Mus musculus
P50637	0	0	0		2	2	2	15.38	2	2	2	0.41	15.38	Translocator protein	P50637	Tspo	Mus musculus
P51125	59	8	8	20.81	62	10	10	20.81	121	10	10	0	20.81	Calpastatin	P51125	Cast	Mus musculus
P51150	38	5	5	32.37	46	6	6	32.85	84	6	6	0	32.85	Ras-related protein Rab-7a	P51150	Rab7a	Mus musculus
P51174	2	2	2	6.28	13	5	5	13.49	15	5	5	0	13.49	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	P51174	Acadl	Mus musculus
P51410	15	6	6	57.81	55	7	7	48.96	70	9	9	0	57.81	60S ribosomal protein L9	P51410	Rpl9	Mus musculus
P51437	798	17	17	46.24	357	11	11	46.24	1155	17	17	0	46.24	Cathelin-related antimicrobial peptide	P51437	Camp	Mus musculus
P51859	33	4	4	42.19	33	3	3	32.91	66	4	4	0	42.19	Hepatoma-derived growth factor	P51859	Hdgf	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P51863	61	8	8	33.33	43	6	6	27.64	104	10	10	0	35.9	V-type proton ATPase subunit d 1	P51863	Atp6v0d1	Mus musculus
P51881	31	3	3	17.45	35	3	3	17.45	66	4	4	0	21.48	ADP/ATP translocase 2	P51881	Slc25a5	Mus musculus
P52480	344	28	28	53.3	772	34	34	55.74	1116	38	38	0	58.76	Pyruvate kinase PKM	P52480	Pkm	Mus musculus
P52503	26	2	2	20.69	0	0	0		26	2	2	0.41	20.69	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	P52503	Ndufs6	Mus musculus
P52624	8	2	2	11.9	30	3	3	18.97	38	3	3	0	18.97	Uridine phosphorylase 1	P52624	Upp1	Mus musculus
P52633	5	1	1	4.42	17	3	3	9.56	22	3	3	0	9.56	Signal transducer and transcription activator 6	P52633	Stat6	Mus musculus
P53994	14	4	4	20.28	14	3	3	17.92	28	4	4	0	20.28	Ras-related protein Rab-2A	P53994	Rab2a	Mus musculus
P53996-2	3	2	2	22.35	22	3	3	22.35	25	3	3	0	22.35	Isoform 2 of Cellular nucleic acid-binding protein	P53996	Cnbp	Mus musculus
P54071	29	4	4	13.05	18	4	4	15.49	47	5	5	0	15.49	Isocitrate dehydrogenase [NADP], mitochondrial	P54071	Idh2	Mus musculus
P54103	4	1	1	2.09	7	3	3	7.89	11	3	3	0	7.89	DnaJ homolog subfamily C member 2	P54103	Dnajc2	Mus musculus
P54728	12	1	1	4.57	23	2	2	8.65	35	2	2	0.41	8.65	UV excision repair protein RAD23 homolog B	P54728	Rad23b	Mus musculus
P54775	67	5	5	25.6	81	5	5	25.6	148	5	5	0	25.6	26S protease regulatory subunit 6B	P54775	Psmc4	Mus musculus
P54818	2	2	2	6.43	0	0	0		2	2	2	0.41	6.43	Galactocerebrosidase	P54818	Galc	Mus musculus
P54822	1	1	1	5.99	12	3	3	11.78	13	3	3	0	11.78	Adenylosuccinate lyase	P54822	Adsl	Mus musculus
P54823	10	2	2	8.07	40	3	3	11.59	50	3	3	0	11.59	Probable ATP-dependent RNA helicase DDX6	P54823	Ddx6	Mus musculus
P55772	13	3	3	11.37	0	0	0		13	3	3	0	11.37	Ectonucleoside triphosphate diphosphohydrolase 1	P55772	Entpd1	Mus musculus
P55937	4	2	2	2.49	1	1	1	1.14	5	2	2	0.41	2.49	Golgin subfamily A member 3	P55937	Golga3	Mus musculus
P56391	39	6	6	70.93	18	3	3	40.7	57	6	6	0	70.93	Cytochrome c oxidase subunit 6B1	P56391	Cox6b1	Mus musculus
P56395	2	2	2	25.37	0	0	0		2	2	2	0.41	25.37	Cytochrome b5	P56395	Cyb5a	Mus musculus
P56399	76	6	6	14.34	129	14	14	26.22	205	14	14	0	26.22	Ubiquitin carboxyl-terminal hydrolase 5	P56399	Usp5	Mus musculus
P56480	405	20	20	57.28	474	21	21	58.41	879	22	22	0	58.41	ATP synthase subunit beta, mitochondrial	P56480	Atp5b	Mus musculus
P56546	2	1	1	7.42	13	2	2	13.48	15	2	2	0.41	13.48	C-terminal-binding protein 2	P56546	Ctbp2	Mus musculus
P56565	8	3	3	26.6	24	3	3	26.6	32	3	3	0	26.6	Protein S100-A1	P56565	S100a1	Mus musculus
P56812	10	2	2	19.84	10	1	1	10.32	20	2	2	0.41	19.84	Programmed cell death protein 5	P56812	Pdcd5	Mus musculus
P56959	72	7	5	13.51	56	5	4	12.36	128	7	5	0	13.51	RNA-binding protein FUS	P56959	Fus	Mus musculus
P57716	7	3	3	7.63	1	1	1	5.37	8	3	3	0	7.63	Nicastrin	P57716	Ncstn	Mus musculus
P57746	1	1	1	11.34	10	2	2	17.81	11	2	2	0.41	17.81	V-type proton ATPase subunit D	P57746	Atp6v1d	Mus musculus
P57759	21	2	2	7.25	17	2	2	7.25	38	3	3	0	11.07	Endoplasmic reticulum resident protein 29	P57759	Erp29	Mus musculus
P57780	348	30	17	42	269	29	16	43.31	617	32	19	0	45.18	Alpha-actinin-4	P57780	Actn4	Mus musculus
P57784	22	6	6	41.57	41	6	6	40.39	63	9	9	0	50.59	U2 small nuclear ribonucleoprotein A'	P57784	Snrpa1	Mus musculus
P58058	12	2	2	12.76	8	2	2	12.76	20	2	2	0.41	12.76	NAD kinase	P58058	Nadk	Mus musculus
P58252	304	19	19	35.78	721	29	29	39.28	1025	30	30	0	40.33	Elongation factor 2	P58252	Eef2	Mus musculus
P58389	10	3	3	21.98	30	4	4	16.1	40	5	5	0	21.98	Serine/threonine-protein phosphatase 2A activator	P58389	Ppp2r4	Mus musculus
P58742	9	3	3	12.45	5	1	1	5.86	14	3	3	0	12.45	Aladin	P58742	Aaas	Mus musculus
P59108	27	5	4	17.7	3	1	1	2.74	30	5	4	0	17.7	Copine-2	P59108	Cpne2	Mus musculus
P59325	3	2	2	6.53	6	2	2	6.53	9	2	2	0.41	6.53	Eukaryotic translation initiation factor 5	P59325	Eif5	Mus musculus
P59708	3	2	2	22.4	3	2	2	22.4	6	2	2	0.41	22.4	Splicing factor 3B subunit 6	P59708	Sf3b6	Mus musculus
P59999	10	2	2	17.86	32	2	2	17.86	42	2	2	0.41	17.86	Actin-related protein 2/3 complex subunit 4	P59999	Arpc4	Mus musculus
P60122	34	5	5	17.98	29	4	4	14.91	63	5	5	0	17.98	RuvB-like 1	P60122	Ruvbl1	Mus musculus
P60229	2	1	1	4.27	24	5	5	17.53	26	5	5	0	17.53	Eukaryotic translation initiation factor 3 subunit E	P60229	Eif3e	Mus musculus
P60335	79	5	5	32.58	110	6	6	36.52	189	6	6	0	36.52	Poly(rC)-binding protein 1	P60335	Pcbp1	Mus musculus
P60670	5	2	2	8.72	7	3	3	14.97	12	4	4	0	17.93	Nuclear protein localization protein 4 homolog	P60670	Nploc4	Mus musculus
P60710	1591	34	18	79.47	3938	46	23	80.53	5529	46	23	0	80.53	Actin, cytoplasmic 1	P60710	Actb	Mus musculus
P60766	75	8	7	37.17	106	11	10	48.17	181	11	10	0	48.17	Cell division control protein 42 homolog	P60766	Cdc42	Mus musculus
P60843	48	7	6	26.35	97	9	8	26.35	145	9	8	0	26.35	Eukaryotic initiation factor 4A-I	P60843	Eif4a1	Mus musculus
P60867	0	0	0		3	2	2	19.33	3	2	2	0.41	19.33	40S ribosomal protein S20	P60867	Rps20	Mus musculus
P60898	31	2	2	32	4	2	2	32	35	2	2	0.41	32	DNA-directed RNA polymerase II subunit RPB9	P60898	Polr2i	Mus musculus
P61022	20	2	2	18.46	2	1	1	10.26	22	2	2	0.41	18.46	Calcineurin B homologous protein 1	P61022	Chp1	Mus musculus
P61079	18	1	1	16.33	47	2	2	28.57	65	2	2	0.41	28.57	Ubiquitin-conjugating enzyme E2 D3	P61079	Ube2d3	Mus musculus
P61087	0	0	0		6	2	2	23.5	6	2	2	0.41	23.5	Ubiquitin-conjugating enzyme E2 K	P61087	Ube2k	Mus musculus
P61089	23	4	4	51.32	45	5	5	51.32	68	5	5	0	51.32	Ubiquitin-conjugating enzyme E2 N	P61089	Ube2n	Mus musculus
P61161	118	9	9	30.71	195	15	15	40.86	313	15	15	0	40.86	Actin-related protein 2	P61161	Actr2	Mus musculus
P61164	29	5	5	27.66	28	4	4	14.63	57	6	6	0	27.66	Alpha-centractin	P61164	Actr1a	Mus musculus
P61205	46	7	1	55.25	97	9	2	56.35	143	9	2	0.41	56.35	ADP-ribosylation factor 3	P61205	Arf3	Mus musculus
P61219	0	0	0		5	2	2	19.69	5	2	2	0.41	19.69	DNA-directed RNA polymerases I, II, and III subunit RPABC2	P61219	Polr2f	Mus musculus
P61222	0	0	0		6	3	3	7.51	6	3	3	0	7.51	ATP-binding cassette sub-family E member 1	P61222	Abce1	Mus musculus
P61290	0	0	0		2	2	2	19.69	2	2	2	0.41	19.69	Proteasome activator complex subunit 3	P61290	Psme3	Mus musculus
P61750	39	4	1	38.89	69	8	3	56.67	108	8	3	0	56.67	ADP-ribosylation factor 4	P61750	Arf4	Mus musculus
P61924	5	4	4	40.11	8	3	3	31.64	13	4	4	0	40.11	Coatomer subunit zeta-1	P61924	Copz1	Mus musculus
P61961	10	1	1	41.18	21	3	3	41.18	31	3	3	0	41.18	Ubiquitin-fold modifier 1	P61961	Ufm1	Mus musculus
P61979	222	18	18	49.89	331	18	18	49.89	553	19	19	0	49.89	Heterogeneous nuclear ribonucleoprotein K	P61979	Hnrnpk	Mus musculus
P61982	118	7	7	46.96	169	11	11	48.99	287	12	12	0	52.23	14-3-3 protein gamma	P61982	Ywhag	Mus musculus
P62082	58	9	9	41.24	81	9	9	25.77	139	10	10	0	41.24	40S ribosomal protein S7	P62082	Rps7	Mus musculus
P62137	42	9	3	33.94	90	12	5	40.61	132	12	5	0	40.61	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	P62137	Ppp1ca	Mus musculus
P62141	33	7	1	26.61	71	9	2	29.97	104	9	2	0.41	29.97	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	P62141	Ppp1cb	Mus musculus
P62192	9	1	1	4.55	14	2	2	7.5	23	2	2	0.41	7.5	26S protease regulatory subunit 4	P62192	Psmc1	Mus musculus
P62196	2	1	1	5.17	6	2	2	7.88	8	2	2	0.41	7.88	26S protease regulatory subunit 8	P62196	Psmc5	Mus musculus
P62204	168	3	3	30.87	146	4	4	30.87	314	4	4	0	30.87	Calmodulin	P62204	Calm1	Mus musculus
P62242	18	4	4	27.88	14	3	3	20.67	32	4	4	0	27.88	40S ribosomal protein S8	P62242	Rps8	Mus musculus
P62259	78	5	5	25.49	118	10	9	37.65	196	10	9	0	37.65	14-3-3 protein epsilon	P62259	Ywhae	Mus musculus
P62264	27	5	5	30.46	37	6	6	39.07	64	7	7	0	39.07	40S ribosomal protein S14	P62264	Rps14	Mus musculus
P62267	15	2	2	18.88	27	3	3	19.58	42	3	3	0	19.58	40S ribosomal protein S23	P62267	Rps23	Mus musculus
P62281	21	2	2	12.03	13	2	2	12.03	34	2	2	0.41	12.03	40S ribosomal protein S11	P62281	Rps11	Mus musculus
P62315	5	4	4	31.93	4	1	1	11.76	9	4	4	0	31.93	Small nuclear ribonucleoprotein Sm D1	P62315	Snrpd1	Mus musculus
P62317	15	2	2	16.1	19	2	2	16.1	34	2	2	0.41	16.1	Small nuclear ribonucleoprotein Sm D2	P62317	Snrpd2	Mus musculus
P62320	70	4	4	18.25	91	3	3	18.25	161	4	4	0	18.25	Small nuclear ribonucleoprotein Sm D3	P62320	Snrpd3	Mus musculus
P62331	4	2	2	16	16	2	2	16	20	2	2	0.41	16	ADP-ribosylation factor 6	P62331	Arf6	Mus musculus
P62334	4	2	2	7.46	14	3	3	11.57	18	3	3	0	11.57	26S protease regulatory subunit 10B	P62334	Psmc6	Mus musculus
P62492	42	4	2	26.85	32	4	2	26.85	74	4	2	0.41	26.85	Ras-related protein Rab-11A	P62492	Rab11a	Mus musculus
P62715	22	4	4	28.16	23	6	6	36.25	45	7	7	0	36.89	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	P62715	Ppp2cb	Mus musculus
P62746	36	5	2	25.51	51	5	2	25.51	87	5	2	0.41	25.51	Rho-related GTP-binding protein RhoB	P62746	Rhob	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P62751	16	3	3	11.54	14	2	2	10.9	30	3	3	0	11.54	60S ribosomal protein L23a	P62751	Rpl23a	Mus musculus
P62754	10	4	4	12.85	20	4	4	17.27	30	6	6	0	18.47	40S ribosomal protein S6	P62754	Rps6	Mus musculus
P62774	53	4	4	61.02	45	3	3	55.93	98	4	4	0	61.02	Myotrophin	P62774	Mtpn	Mus musculus
P62806	619	13	13	56.31	579	6	6	43.69	1198	13	13	0	56.31	Histone H4	P62806	Hist1h4a	Mus musculus
P62814	40	7	7	18	46	11	11	28.77	86	12	12	0	28.77	V-type proton ATPase subunit B, brain isoform	P62814	Atp6v1b2	Mus musculus
P62827	17	2	2	13.43	36	4	4	21.76	53	4	4	0	21.76	GTP-binding nuclear protein Ran	P62827	Ran	Mus musculus
P62830	18	3	3	23.57	34	3	3	23.57	52	3	3	0	23.57	60S ribosomal protein L23	P62830	Rpl23	Mus musculus
P62835	55	8	8	44.57	59	8	8	36.96	114	10	10	0	50	Ras-related protein Rap-1A	P62835	Rap1a	Mus musculus
P62858	6	2	2	23.19	12	2	2	21.74	18	3	3	0	27.54	40S ribosomal protein S28	P62858	Rps28	Mus musculus
P62869	0	0	0		8	2	2	53.39	8	2	2	0.41	53.39	Transcription elongation factor B polypeptide 2	P62869	Tceb2	Mus musculus
P62874	74	7	5	31.47	38	6	4	31.47	112	7	5	0	31.47	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	P62874	Gnb1	Mus musculus
P62880	147	11	9	52.06	108	11	9	56.47	255	14	12	0	56.47	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	P62880	Gnb2	Mus musculus
P62889	24	3	3	40.87	16	2	2	30.43	40	3	3	0	40.87	60S ribosomal protein L30	P62889	Rpl30	Mus musculus
P62908	32	5	5	27.98	40	5	5	25.51	72	7	7	0	32.51	40S ribosomal protein S3	P62908	Rps3	Mus musculus
P62960	43	7	7	29.81	42	6	6	29.81	85	7	7	0	29.81	Nuclease-sensitive element-binding protein 1	P62960	Ybx1	Mus musculus
P62962	53	4	4	36.43	199	11	11	58.57	252	11	11	0	58.57	Profilin-1	P62962	Pfn1	Mus musculus
P62983	72	5	5	36.54	74	5	5	36.54	146	5	5	0	36.54	Ubiquitin-40S ribosomal protein S27a	P62983	Rps27a	Mus musculus
P62996	61	4	4	18.06	44	3	3	17.71	105	4	4	0	18.06	Transformer-2 protein homolog beta	P62996	Tra2b	Mus musculus
P63005	4	3	3	9.02	20	2	2	6.34	24	3	3	0	9.02	Platelet-activating factor acetylhydrolase IB subunit alpha	P63005	Pafah1b1	Mus musculus
P63017	521	31	30	51.7	704	33	31	52.63	1225	38	36	0	53.41	Heat shock cognate 71 kDa protein	P63017	Hspa8	Mus musculus
P63024	4	2	2	23.3	0	0	0		4	2	2	0.41	23.3	Vesicle-associated membrane protein 3	P63024	Vamp3	Mus musculus
P63028	16	2	2	16.86	23	4	4	25	39	4	4	0	25	Translationally-controlled tumor protein	P63028	Tpt1	Mus musculus
P63038	117	15	15	36.47	78	10	10	28.97	195	18	18	0	36.65	60 kDa heat shock protein, mitochondrial	P63038	Hspd1	Mus musculus
P63085	0	0	0		5	2	2	10.34	5	2	2	0.41	10.34	Mitogen-activated protein kinase 1	P63085	Mapk1	Mus musculus
P63094	10	3	2	12.18	9	2	2	9.39	19	3	2	0.41	12.18	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	P63094	Gnas	Mus musculus
P63101	296	14	13	58.78	366	18	16	61.22	662	19	16	0	61.22	14-3-3 protein zeta/delta	P63101	Ywhaz	Mus musculus
P63139	18	2	2	11.59	11	1	1	10.14	29	2	2	0.41	11.59	Nuclear transcription factor Y subunit beta	P63139	Nfyb	Mus musculus
P63147	4	1	1	26.32	12	2	2	26.32	16	2	2	0.41	26.32	Ubiquitin-conjugating enzyme E2 B	P63147	Ube2b	Mus musculus
P63242	97	5	5	31.17	135	5	5	41.56	232	6	6	0	46.75	Eukaryotic translation initiation factor 5A-1	P63242	Eif5a	Mus musculus
P63276	39	5	5	42.22	40	4	4	36.3	79	6	6	0	45.19	40S ribosomal protein S17	P63276	Rps17	Mus musculus
P63280	3	1	1	19.62	40	3	3	19.62	43	3	3	0	19.62	SUMO-conjugating enzyme UBC9	P63280	Ube2i	Mus musculus
P63321	6	2	2	22.33	1	1	1	14.56	7	2	2	0.41	22.33	Ras-related protein Ral-A	P63321	Rala	Mus musculus
P67778	124	14	14	68.75	165	14	14	70.59	289	16	16	0	72.06	Prohibitin	P67778	Phb	Mus musculus
P67871	3	1	1	13.95	6	2	2	13.95	9	2	2	0.41	13.95	Casein kinase II subunit beta	P67871	Csnk2b	Mus musculus
P67984	6	3	3	22.66	13	4	4	42.19	19	4	4	0	42.19	60S ribosomal protein L22	P67984	Rpl22	Mus musculus
P68033	1089	22	9	51.46	2880	28	11	55.44	3969	28	11	0	55.44	Actin, alpha cardiac muscle 1	P68033	Actc1	Mus musculus
P68037	18	3	3	36.36	44	4	4	38.96	62	4	4	0	38.96	Ubiquitin-conjugating enzyme E2 L3	P68037	Ube2l3	Mus musculus
P68040	58	8	8	46.69	117	10	10	50.16	175	10	10	0	50.16	Guanine nucleotide-binding protein subunit beta-2-like 1	P68040	Gnb2l1	Mus musculus
P68254	86	9	9	55.1	88	9	8	49.39	174	12	11	0	55.1	14-3-3 protein theta	P68254	Ywhaq	Mus musculus
P68368	455	25	13	62.05	563	24	14	61.16	1018	27	15	0	66.52	Tubulin alpha-4A chain	P68368	Tuba4a	Mus musculus
P68369	444	23	11	66.08	501	24	14	61.64	945	26	14	0	66.96	Tubulin alpha-1A chain	P68369	Tuba1a	Mus musculus
P68372	455	22	2	59.78	668	25	3	65.17	1123	27	3	0	65.17	Tubulin beta-4B chain	P68372	Tubb4b	Mus musculus
P68404-2	10	3	3	10.4	10	2	2	6.54	20	3	3	0	10.4	Isoform Beta-II of Protein kinase C beta type	P68404	Prkcb	Mus musculus
P68433	691	14	6	32.35	342	13	5	32.35	1033	16	7	0	32.35	Histone H3.1	P68433	Hist1h3a	Mus musculus
P68510	82	12	12	55.69	110	11	10	55.69	192	13	12	0	55.69	14-3-3 protein eta	P68510	Ywhah	Mus musculus
P70158	15	2	2	8.31	0	0	0		15	2	2	0.41	8.31	Acid sphingomyelinase-like phosphodiesterase 3a	P70158	Smpdl3a	Mus musculus
P70168	103	14	14	29.91	153	14	14	29.79	256	17	17	0	36.3	Importin subunit beta-1	P70168	Kpnb1	Mus musculus
P70268	8	3	3	6.24	42	7	7	14.59	50	7	7	0	14.59	Serine/threonine-protein kinase N1	P70268	Pkn1	Mus musculus
P70290	27	3	3	9.87	26	6	6	20.6	53	7	7	0	23.18	55 kDa erythrocyte membrane protein	P70290	Mpp1	Mus musculus
P70296	23	3	3	41.71	62	4	4	32.62	85	5	5	0	48.66	Phosphatidylethanolamine-binding protein 1	P70296	Pebp1	Mus musculus
P70315	3	3	3	15.77	15	5	5	19.23	18	5	5	0	19.23	Wiskott-Aldrich syndrome protein homolog	P70315	Was	Mus musculus
P70333	27	5	2	16.7	49	3	0	10.24	76	5	2	0.41	16.7	Heterogeneous nuclear ribonucleoprotein H2	P70333	Hnrnph2	Mus musculus
P70335	13	2	2	4.58	17	2	2	4.58	30	2	2	0.41	4.58	Rho-associated protein kinase 1	P70335	Rock1	Mus musculus
P70349	4	1	1	11.11	31	3	3	32.54	35	3	3	0	32.54	Histidine triad nucleotide-binding protein 1	P70349	Hint1	Mus musculus
P70372	5	2	2	11.66	9	2	2	11.66	14	2	2	0.41	11.66	ELAV-like protein 1	P70372	Elavl1	Mus musculus
P70388	0	0	0		2	2	2	2.74	2	2	2	0.41	2.74	DNA repair protein RAD50	P70388	Rad50	Mus musculus
P70398	0	0	0		21	6	6	4.53	21	6	6	0	4.53	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	P70398	Usp9x	Mus musculus
P70441	26	6	6	28.73	32	5	5	27.61	58	7	7	0	35.21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	P70441	Slc9a3r1	Mus musculus
P70444	2	1	1	9.74	24	3	3	31.79	26	3	3	0	31.79	BH3-interacting domain death agonist	P70444	Bid	Mus musculus
P70460	63	3	3	13.33	90	3	3	10.4	153	4	4	0	13.87	Vasodilator-stimulated phosphoprotein	P70460	Vasp	Mus musculus
P70670	43	3	3	1.33	53	4	4	1.46	96	6	6	0	1.92	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	P70670	Naca	Mus musculus
P70698	0	0	0		4	2	2	5.92	4	2	2	0.41	5.92	CTP synthase 1	P70698	Ctps1	Mus musculus
P70699	3	2	2	3.67	0	0	0		3	2	2	0.41	3.67	Lysosomal alpha-glucosidase	P70699	Gaa	Mus musculus
P80313	51	5	5	20.96	128	6	6	20.96	179	6	6	0	20.96	T-complex protein 1 subunit eta	P80313	Cct7	Mus musculus
P80314	51	5	5	17.38	95	9	9	26.54	146	9	9	0	26.54	T-complex protein 1 subunit beta	P80314	Cct2	Mus musculus
P80315	26	5	5	15.96	68	7	7	19.11	94	7	7	0	19.11	T-complex protein 1 subunit delta	P80315	Cct4	Mus musculus
P80316	64	7	7	25.14	89	9	9	26.8	153	9	9	0	26.8	T-complex protein 1 subunit epsilon	P80316	Cct5	Mus musculus
P80317	73	8	8	22.41	100	6	6	19.21	173	8	8	0	22.41	T-complex protein 1 subunit zeta	P80317	Cct6a	Mus musculus
P80318	2	1	1	2.02	13	3	3	8.99	15	4	4	0	11.01	T-complex protein 1 subunit gamma	P80318	Cct3	Mus musculus
P81117	31	7	7	20.48	21	3	3	13.1	52	7	7	0	20.48	Nucleobindin-2	P81117	Nucb2	Mus musculus
P82198	96	8	8	21.23	85	7	7	19.18	181	9	9	0	23.87	Transforming growth factor-beta-induced protein ig-h3	P82198	Tgfbi	Mus musculus
P83870	22	3	3	32.73	14	2	2	26.36	36	3	3	0	32.73	PHD finger-like domain-containing protein 5A	P83870	Phf5a	Mus musculus
P83917	57	4	4	32.43	33	3	3	25.95	90	4	4	0	32.43	Chromobox protein homolog 1	P83917	Cbx1	Mus musculus
P84078	60	8	2	56.35	120	9	2	56.35	180	9	2	0.41	56.35	ADP-ribosylation factor 1	P84078	Arf1	Mus musculus
P84084	48	6	2	44.44	97	8	2	52.22	145	8	2	0.41	52.22	ADP-ribosylation factor 5	P84084	Arf5	Mus musculus
P84089	16	2	2	44.23	13	3	3	44.23	29	3	3	0	44.23	Enhancer of rudimentary homolog	P84089	Erh	Mus musculus
P84091	1	1	1	3.45	5	2	2	6.44	6	3	3	0	9.89	AP-2 complex subunit mu	P84091	Ap2m1	Mus musculus
P84096	61	8	8	48.17	73	8	8	48.17	134	8	8	0	48.17	Rho-related GTP-binding protein RhoG	P84096	Rhog	Mus musculus
P84099	7	2	2	8.67	15	1	1	8.67	22	2	2	0.41	8.67	60S ribosomal protein L19	P84099	Rpl19	Mus musculus
P84104	59	4	3	28.66	43	3	3	28.66	102	4	3	0	28.66	Serine/arginine-rich splicing factor 3	P84104	Srsf3	Mus musculus
P84228	782	16	5	32.35	406	13	3	32.35	1188	17	5	0	32.35	Histone H3.2	P84228	Hist1h3b	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P84244	716	17	6	32.35	385	13	3	32.35	1101	18	6	0	32.35	Histone H3.3	P84244	H3f3a	Mus musculus
P85094	3	2	2	29.13	12	2	2	29.13	15	2	2	0.41	29.13	Isochorismatase domain-containing protein 2A, mitochondrial	P85094	Isoc2a	Mus musculus
P97302	2	2	2	3.92	1	1	1	2.57	3	3	3	0	6.5	Transcription regulator protein BACH1	P97302	Bach1	Mus musculus
P97310	6	1	1	3.43	13	2	2	5.64	19	2	2	0.41	5.64	DNA replication licensing factor MCM2	P97310	Mcm2	Mus musculus
P97311	21	3	3	9.01	40	7	7	14.25	61	7	7	0	14.25	DNA replication licensing factor MCM6	P97311	Mcm6	Mus musculus
P97315	26	3	3	29.02	37	5	5	44.56	63	6	6	0	45.6	Cysteine and glycine-rich protein 1	P97315	Csrp1	Mus musculus
P97351	20	3	3	6.82	10	3	3	6.82	30	3	3	0	6.82	40S ribosomal protein S3a	P97351	Rps3a	Mus musculus
P97363	3	2	2	6.96	12	1	1	3.57	15	2	2	0.41	6.96	Serine palmitoyltransferase 2	P97363	Sptlc2	Mus musculus
P97369	148	13	13	43.36	209	14	14	42.48	357	15	15	0	43.66	Neutrophil cytosol factor 4	P97369	Ncf4	Mus musculus
P97370	3	2	2	11.15	1	1	1	6.12	4	2	2	0.41	11.15	Sodium/potassium-transporting ATPase subunit beta-3	P97370	Atp1b3	Mus musculus
P97371	56	5	5	25.3	77	5	5	25.3	133	5	5	0	25.3	Proteasome activator complex subunit 1	P97371	Psme1	Mus musculus
P97372	24	6	6	35.98	89	8	8	36.4	113	8	8	0	36.4	Proteasome activator complex subunit 2	P97372	Psme2	Mus musculus
P97376	5	2	2	6.59	4	2	2	6.59	9	2	2	0.41	6.59	Protein FRG1	P97376	Frg1	Mus musculus
P97384	131	12	12	29.03	55	8	8	19.68	186	12	12	0	29.03	Annexin A11	P97384	Anxa11	Mus musculus
P97425	15	4	3	39.1	5	2	2	26.92	20	4	3	0	39.1	Eosinophil cationic protein 2	P97425	Ear2	Mus musculus
P97426	32	5	4	38.06	9	2	2	25.81	41	5	4	0	38.06	Eosinophil cationic protein 1	P97426	Ear1	Mus musculus
P97450	84	3	3	34.26	50	3	3	34.26	134	4	4	0	34.26	ATP synthase-coupling factor 6, mitochondrial	P97450	Atp5j	Mus musculus
P97492	7	4	4	14.81	10	3	3	11.7	17	4	4	0	14.81	Regulator of G-protein signaling 14	P97492	Rgs14	Mus musculus
P97493	5	2	2	21.08	1	1	1	8.43	6	2	2	0.41	21.08	Thioredoxin, mitochondrial	P97493	Txn2	Mus musculus
P97496	0	0	0		6	2	2	3.71	6	2	2	0.41	3.71	SWI/SNF complex subunit SMARCC1	P97496	Smarcc1	Mus musculus
P97797	11	5	5	12.87	0	0	0		11	5	5	0	12.87	Tyrosine-protein phosphatase non-receptor type substrate 1	P97797	Sirpa	Mus musculus
P97807	42	4	4	11.64	30	5	5	14.4	72	5	5	0	14.4	Fumarate hydratase, mitochondrial	P97807	Fh	Mus musculus
P97814	16	2	2	9.16	33	3	3	13.98	49	3	3	0	13.98	Proline-serine-threonine phosphatase-interacting protein 1	P97814	Pstpip1	Mus musculus
P97821	42	5	5	15.15	33	5	5	17.75	75	6	6	0	17.75	Dipeptidyl peptidase 1	P97821	Ctsc	Mus musculus
P97822	17	4	4	18.85	49	7	7	28.46	66	7	7	0	28.46	Acidic leucine-rich nuclear phosphoprotein 32 family member E	P97822	Anp32e	Mus musculus
P97823	3	1	1	6.09	13	3	3	20.87	16	3	3	0	20.87	Acyl-protein thioesterase 1	P97823	Lypla1	Mus musculus
P97855	17	4	4	10.11	26	5	5	16.34	43	6	6	0	16.56	Ras GTPase-activating protein-binding protein 1	P97855	G3bp1	Mus musculus
P97864	1	1	1	7.59	6	2	2	15.18	7	2	2	0.41	15.18	Caspase-7	P97864	Casp7	Mus musculus
P97872	5	3	3	8.26	4	2	2	5.44	9	3	3	0	8.26	Dimethylaniline monooxygenase [N-oxide-forming] 5	P97872	Fmo5	Mus musculus
P98083	13	2	2	7.25	23	3	3	7.25	36	3	3	0	7.25	SHC-transforming protein 1	P98083	Shc1	Mus musculus
P99024	504	27	8	66.67	699	25	7	62.61	1203	31	9	0	66.89	Tubulin beta-5 chain	P99024	Tubb5	Mus musculus
P99027	158	9	9	79.13	182	6	6	77.39	340	10	10	0	80	60S acidic ribosomal protein P2	P99027	Rplp2	Mus musculus
P99028	38	2	2	41.57	40	2	2	41.57	78	2	2	0.41	41.57	Cytochrome b-c1 complex subunit 6, mitochondrial	P99028	Uqcrh	Mus musculus
P99029	172	13	13	60.95	269	15	15	64.76	441	15	15	0	64.76	Peroxiredoxin-5, mitochondrial	P99029	Prdx5	Mus musculus
Q00519	26	3	3	5.32	103	12	12	20.6	129	12	12	0	20.6	Xanthine dehydrogenase/oxidase	Q00519	Xdh	Mus musculus
Q00612	161	17	17	32.62	267	22	22	31.65	428	24	24	0	34.56	Glucose-6-phosphate 1-dehydrogenase X	Q00612	G6pdx	Mus musculus
Q00623	25	4	4	24.24	3	1	1	13.64	28	4	4	0	24.24	Apolipoprotein A-I	Q00623	Apoa1	Mus musculus
Q00PI9	53	9	9	17.58	43	6	6	15.03	96	9	9	0	17.58	Heterogeneous nuclear ribonucleoprotein U-like protein 2	Q00PI9	Hnrnpul2	Mus musculus
Q01102	10	1	1	4.3	7	2	2	6.9	17	2	2	0.41	6.9	P-selectin	Q01102	Selp	Mus musculus
Q01320	29	4	3	3.34	24	5	4	4.45	53	5	4	0	4.45	DNA topoisomerase 2-alpha	Q01320	Top2a	Mus musculus
Q01853	355	28	28	50.5	336	26	26	43.05	691	32	32	0	52.61	Transitional endoplasmic reticulum ATPase	Q01853	Vcp	Mus musculus
Q02053	141	15	15	25.33	333	24	24	32.89	474	24	24	0	32.89	Ubiquitin-like modifier-activating enzyme 1	Q02053	Uba1	Mus musculus
Q02357	25	7	7	6.98	0	0	0		25	7	7	0	6.98	Ankyrin-1	Q02357	Ank1	Mus musculus
Q02819	75	9	9	22.66	42	7	7	22	117	9	9	0	22.66	Nucleobindin-1	Q02819	Nucb1	Mus musculus
Q03265	189	18	18	30.74	181	16	16	36.71	370	20	20	0	37.97	ATP synthase subunit alpha, mitochondrial	Q03265	Atp5a1	Mus musculus
Q04750	51	5	5	10.04	42	4	4	9.91	93	6	6	0	11.6	DNA topoisomerase 1	Q04750	Top1	Mus musculus
Q04998	14	2	2	10.14	1	1	1	5.9	15	2	2	0.41	10.14	Inhibin beta A chain	Q04998	Inhba	Mus musculus
Q05144	48	10	9	53.65	83	10	9	47.4	131	13	12	0	56.25	Ras-related C3 botulinum toxin substrate 2	Q05144	Rac2	Mus musculus
Q06890	13	2	2	8.48	1	1	1	4.02	14	2	2	0.41	8.48	Clusterin	Q06890	Clu	Mus musculus
Q07076	13	3	3	7.78	13	3	3	7.78	26	3	3	0	7.78	Annexin A7	Q07076	Anxa7	Mus musculus
Q07797	9	2	2	7.28	8	2	2	7.28	17	2	2	0.41	7.28	Galectin-3-binding protein	Q07797	Lgals3bp	Mus musculus
Q08093	37	2	2	16.39	33	2	2	16.39	70	2	2	0.41	16.39	Calponin-2	Q08093	Cnn2	Mus musculus
Q08943	31	5	5	12.15	26	3	3	7.91	57	5	5	0	12.15	FACT complex subunit SSRP1	Q08943	Ssrp1	Mus musculus
Q09014	79	9	9	27.44	110	10	10	20.26	189	12	12	0	27.44	Neutrophil cytosol factor 1	Q09014	Ncf1	Mus musculus
Q09PK2	150	11	11	59.29	1203	15	15	59.59	1353	15	15	0	59.59	Retroviral-like aspartic protease 1	Q09PK2	Asprv1	Mus musculus
Q11011	12	4	4	9.78	43	8	8	18.48	55	8	8	0	18.48	Puromycin-sensitive aminopeptidase	Q11011	Npepps	Mus musculus
Q1HFZ0	3	3	3	9.11	7	2	2	5.15	10	5	5	0	11.49	tRNA (cytosine(34)-C(5))-methyltransferase	Q1HFZ0	Nsun2	Mus musculus
Q20BD0	102	7	6	19.58	110	7	6	19.58	212	7	6	0	19.58	Heterogeneous nuclear ribonucleoprotein A/B	Q20BD0	Hnrnpab	Mus musculus
Q2YFS3	2	2	2	9.93	1	1	1	10.93	3	3	3	0	20.86	Paired immunoglobulin-like type 2 receptor alpha	Q2YFS3	Pilra	Mus musculus
Q3TBD2	45	8	8	8.6	70	9	9	11.2	115	10	10	0	11.47	Minor histocompatibility protein HA-1	Q3TBD2	Hmha1	Mus musculus
Q3TDN2	3	2	2	11.46	0	0	0		3	2	2	0.41	11.46	FAS-associated factor 2	Q3TDN2	Faf2	Mus musculus
Q3TGF2	13	2	2	11.45	16	2	2	11.45	29	2	2	0.41	11.45	Protein FAM107B	Q3TGF2	Fam107b	Mus musculus
Q3THE2	694	8	3	45.93	333	7	1	37.21	1027	10	3	0	47.67	Myosin regulatory light chain 12B	Q3THE2	Myl12b	Mus musculus
Q3THK3	0	0	0		8	2	2	5.31	8	2	2	0.41	5.31	General transcription factor IIF subunit 1	Q3THK3	Gtf2f1	Mus musculus
Q3THK7	17	4	4	13.13	15	4	4	13.85	32	5	5	0	18.18	GMP synthase [glutamine-hydrolyzing]	Q3THK7	Gmps	Mus musculus
Q3TIX9	1	1	1	3.37	6	3	3	11.52	7	3	3	0	11.52	U4/U6.U5 tri-snRNP-associated protein 2	Q3TIX9	Usp39	Mus musculus
Q3TJD7	2	2	2	15.1	2	1	1	6.78	4	2	2	0.41	15.1	PDZ and LIM domain protein 7	Q3TJD7	Pdlim7	Mus musculus
Q3TKT4	4	2	2	2.6	0	0	0		4	2	2	0.41	2.6	Transcription activator BRG1	Q3TKT4	Smarca4	Mus musculus
Q3TLH4	1	1	1	0.74	2	2	2	1.41	3	2	2	0.41	1.41	Protein PRRC2C	Q3TLH4	Prrc2c	Mus musculus
Q3TRM8	235	23	22	41.54	386	24	23	39.91	621	25	24	0	43.06	Hexokinase-3	Q3TRM8	Hk3	Mus musculus
Q3TVI8	3	2	2	4.54	1	1	1	2.75	4	3	3	0	7.29	Pre-B-cell leukemia transcription factor-interacting protein 1	Q3TVI8	Pbxip1	Mus musculus
Q3TW96	4	1	1	3.16	24	4	4	10.26	28	4	4	0	10.26	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	Q3TW96	Uap1l1	Mus musculus
Q3TXS7	22	5	5	13.12	42	7	7	17.1	64	7	7	0	17.1	26S proteasome non-ATPase regulatory subunit 1	Q3TXS7	Psmd1	Mus musculus
Q3TZZ7	6	2	2	4.62	0	0	0		6	2	2	0.41	4.62	Extended synaptotagmin-2	Q3TZZ7	Esyt2	Mus musculus
Q3U0V1	106	16	16	26.47	120	14	14	29.41	226	17	17	0	31.82	Far upstream element-binding protein 2	Q3U0V1	Khsrp	Mus musculus
Q3U0V2	3	1	1	9.03	24	3	3	21.94	27	3	3	0	21.94	Tumor necrosis factor receptor type 1-associated DEATH domain protein	Q3U0V2	Tradd	Mus musculus
Q3U141	1	1	1	8.14	3	2	2	11.76	4	2	2	0.41	11.76	Inhibitor of nuclear factor kappa-B kinase subunit beta	Q3U141	Ikbkb	Mus musculus
Q3U1F9	16	1	1	6.76	15	2	2	10.02	31	2	2	0.41	10.02	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1	Q3U1F9	Pag1	Mus musculus
Q3U1J4	38	4	4	7.72	40	6	6	10.61	78	7	7	0	12.19	DNA damage-binding protein 1	Q3U1J4	Ddb1	Mus musculus
Q3U1Z5	69	5	5	37.74	36	4	4	48.43	105	6	6	0	51.57	G-protein-signaling modulator 3	Q3U1Z5	Gpsm3	Mus musculus
Q3U2G2	91	12	12	22.09	104	13	13	24.35	195	15	15	0	26.13	Heat shock 70 kDa protein 4	Q3U2G2	Hspa4	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q3U5V8	3	3	3	20.21	0	0	0		3	3	3	0	20.21	MCG49559	Q3U5V8	Stx11	Mus musculus
Q3U7R1	103	16	16	24.36	102	13	13	20.7	205	17	17	0	24.36	Extended synaptotagmin-1	Q3U7R1	Esyt1	Mus musculus
Q3U9G9	58	9	9	18.05	64	7	7	15.97	122	10	10	0	19.97	Lamin-B receptor	Q3U9G9	Lbr	Mus musculus
Q3UEB3	6	2	2	7.09	9	4	4	13.83	15	4	4	0	13.83	Poly(U)-binding-splicing factor PUF60	Q3UEB3	Puf60	Mus musculus
Q3UI43	29	2	2	19.82	24	2	2	19.82	53	2	2	0.41	19.82	BRISC and BRCA1-A complex member 1	Q3UI43	Babam1	Mus musculus
Q3UJB0	25	6	6	10.71	3	3	3	5.69	28	7	7	0	10.71	Protein Sf3b2	Q3UJB0	Sf3b2	Mus musculus
Q3UJB9	18	6	6	9.25	8	3	3	4.05	26	6	6	0	9.25	Enhancer of mRNA-decapping protein 4	Q3UJB9	Edc4	Mus musculus
Q3ULJ0	2	1	1	9.12	31	6	6	25.93	33	6	6	0	25.93	Glycerol-3-phosphate dehydrogenase 1-like protein	Q3ULJ0	Gpd1l	Mus musculus
Q3UM45	9	1	1	4.99	38	3	3	15.79	47	3	3	0	15.79	Protein phosphatase 1 regulatory subunit 7	Q3UM45	Ppp1r7	Mus musculus
Q3UND0	173	16	16	67.32	183	17	17	69.83	356	18	18	0	70.11	Src kinase-associated phosphoprotein 2	Q3UND0	Skap2	Mus musculus
Q3UP87	476	22	22	44.91	387	17	17	50.94	863	23	23	0	50.94	Neutrophil elastase	Q3UP87	Elane	Mus musculus
Q3UPH1	14	2	2	14	40	4	4	24.83	54	4	4	0	24.83	Protein PRRC1	Q3UPH1	Prrc1	Mus musculus
Q3UQ44	26	5	5	6.92	52	8	8	10.98	78	9	9	0	11.68	Ras GTPase-activating-like protein IQGAP2	Q3UQ44	Iqgap2	Mus musculus
Q3UW53	65	7	7	12.96	83	9	9	17.06	148	10	10	0	18.9	Protein Niban	Q3UW53	Fam129a	Mus musculus
Q3UYV9	11	2	2	4.81	18	2	2	4.81	29	2	2	0.41	4.81	Nuclear cap-binding protein subunit 1	Q3UYV9	Ncbp1	Mus musculus
Q3UZ39	73	10	10	27.3	96	10	10	27.3	169	11	11	0	27.3	Leucine-rich repeat flightless-interacting protein 1	Q3UZ39	Lrrfip1	Mus musculus
Q3UZA1	102	5	5	32.04	103	5	5	32.04	205	5	5	0	32.04	CapZ-interacting protein	Q3UZA1	Rcsd1	Mus musculus
Q3UZZ4	189	13	13	38.02	106	11	11	32.28	295	14	14	0	39.6	Olfactomedin-4	Q3UZZ4	Olfm4	Mus musculus
Q3V1G4	131	11	11	21.98	81	7	7	14.08	212	11	11	0	21.98	Olfactomedin-like protein 2B	Q3V1G4	Olfml2b	Mus musculus
Q3V1L4	0	0	0		26	5	5	16.07	26	5	5	0	16.07	Cytosolic purine 5'-nucleotidase	Q3V1L4	Nt5c2	Mus musculus
Q3V3R1	8	3	3	8.09	4	2	2	2.76	12	4	4	0	8.09	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	Q3V3R1	Mthfd1l	Mus musculus
Q497J0	1	1	1	12.37	81	4	4	34.02	82	4	4	0	34.02	MCG130175, isoform CRA_b	Q497J0	BC100530	Mus musculus
Q4KML4	20	2	2	27.16	35	2	2	40.74	55	3	3	0	51.85	Costars family protein ABRACL	Q4KML4	Abracl	Mus musculus
Q4QRL3	15	4	4	5.87	13	6	6	8.24	28	7	7	0	9.52	Coiled-coil domain-containing protein 88B	Q4QRL3	Ccdc88b	Mus musculus
Q52KI8	30	2	2	5.39	25	1	1	3.59	55	2	2	0.41	5.39	Serine/arginine repetitive matrix protein 1	Q52KI8	Srrm1	Mus musculus
Q569Z6	30	2	2	5.99	32	2	2	5.99	62	2	2	0.41	5.99	Thyroid hormone receptor-associated protein 3	Q569Z6	Thrap3	Mus musculus
Q571E4	39	5	5	17.69	28	5	5	17.69	67	5	5	0	17.69	N-acetylgalactosamine-6-sulfatase	Q571E4	Galns	Mus musculus
Q571I9	31	3	3	7.23	55	4	4	8.98	86	4	4	0	8.98	Aldehyde dehydrogenase family 16 member A1	Q571I9	Aldh16a1	Mus musculus
Q5EG47	9	1	1	3.76	18	2	2	6.44	27	2	2	0.41	6.44	5'-AMP-activated protein kinase catalytic subunit alpha-1	Q5EG47	Prkaa1	Mus musculus
Q5FWK3	16	2	2	10.02	32	4	4	18.45	48	4	4	0	18.45	Rho GTPase-activating protein 1	Q5FWK3	Arhgap1	Mus musculus
Q5RKN9	99	11	9	52.8	100	11	9	52.8	199	11	9	0	52.8	Capping protein (Actin filament) muscle Z-line, alpha 1	Q5RKN9	Capza1	Mus musculus
Q5SFM8	5	2	2	5.75	13	3	3	5.85	18	3	3	0	5.85	RNA-binding protein 27	Q5SFM8	Rbm27	Mus musculus
Q5SUA5	16	7	7	11.52	20	3	3	6.05	36	7	7	0	11.52	Unconventional myosin-Ig	Q5SUA5	Myo1g	Mus musculus
Q5SUH6	8	4	4	14.98	10	3	3	10.92	18	4	4	0	14.98	Clathrin interactor 1	Q5SUH6	Clint1	Mus musculus
Q5SUR0	21	3	3	6.66	52	11	11	20.04	73	12	12	0	21.77	Phosphoribosylformylglycinamidine synthase	Q5SUR0	Pfas	Mus musculus
Q5SVD0	37	3	3	30.09	27	3	3	30.09	64	3	3	0	30.09	Filamin-interacting protein FAM101B	Q5SVD0	Fam101b	Mus musculus
Q5XJY5	16	2	2	5.28	18	2	2	7.24	34	3	3	0	10.18	Coatomer subunit delta	Q5XJY5	Arcn1	Mus musculus
Q60597	1	1	1	1.76	9	3	3	4.99	10	3	3	0	4.99	2-oxoglutarate dehydrogenase, mitochondrial	Q60597	Ogdh	Mus musculus
Q60605-2	212	7	7	58.28	141	7	7	64.9	353	8	8	0	65.56	Isoform Smooth muscle of Myosin light polypeptide 6	Q60605	Myl6	Mus musculus
Q60631	24	4	4	30.88	14	2	2	18.89	38	4	4	0	30.88	Growth factor receptor-bound protein 2	Q60631	Grb2	Mus musculus
Q60634	25	6	6	18.69	13	2	2	5.61	38	6	6	0	18.69	Flotillin-2	Q60634	Flot2	Mus musculus
Q60648	24	3	3	21.24	22	1	1	11.4	46	3	3	0	21.24	Ganglioside GM2 activator	Q60648	Gm2a	Mus musculus
Q60664	18	2	2	7.79	11	1	1	3.71	29	2	2	0.41	7.79	Lymphoid-restricted membrane protein	Q60664	Lrmp	Mus musculus
Q60668	37	5	5	14.37	64	4	4	13.8	101	5	5	0	14.37	Heterogeneous nuclear ribonucleoprotein D0	Q60668	Hnrnpd	Mus musculus
Q60692	11	2	2	23.11	15	4	4	27.31	26	4	4	0	27.31	Proteasome subunit beta type-6	Q60692	Psmb6	Mus musculus
Q60737	13	3	3	14.83	14	3	3	14.83	27	3	3	0	14.83	Casein kinase II subunit alpha	Q60737	Csnk2a1	Mus musculus
Q60739	4	2	2	14.65	13	2	2	14.65	17	2	2	0.41	14.65	BAG family molecular chaperone regulator 1	Q60739	Bag1	Mus musculus
Q60767	13	3	3	3.13	10	2	2	2.79	23	4	4	0	4.76	Lymphocyte antigen 75	Q60767	Ly75	Mus musculus
Q60790	12	2	2	6.71	7	2	2	4.56	19	3	3	0	8.39	Ras GTPase-activating protein 3	Q60790	Rasa3	Mus musculus
Q60864	32	6	6	18.42	44	10	10	23.02	76	10	10	0	23.02	Stress-induced-phosphoprotein 1	Q60864	Stip1	Mus musculus
Q60865	28	3	3	9.05	54	5	5	13.72	82	6	6	0	15.28	Caprin-1	Q60865	Caprin1	Mus musculus
Q60875	13	2	2	4.87	20	4	4	6.6	33	4	4	0	6.6	Rho guanine nucleotide exchange factor 2	Q60875	Arhgef2	Mus musculus
Q60902	20	4	4	9.04	12	1	1	3.53	32	4	4	0	9.04	Epidermal growth factor receptor substrate 15-like 1	Q60902	Eps15l1	Mus musculus
Q60930	20	5	5	30.51	17	5	5	30.51	37	5	5	0	30.51	Voltage-dependent anion-selective channel protein 2	Q60930	Vdac2	Mus musculus
Q60931	2	1	1	3.53	5	2	2	11.31	7	2	2	0.41	11.31	Voltage-dependent anion-selective channel protein 3	Q60931	Vdac3	Mus musculus
Q60932	35	5	5	27.03	25	3	3	16.55	60	5	5	0	27.03	Voltage-dependent anion-selective channel protein 1	Q60932	Vdac1	Mus musculus
Q60953	38	7	7	13.45	1	1	1	2.03	39	7	7	0	13.45	Protein PML	Q60953	Pml	Mus musculus
Q60960	8	3	3	12.08	17	2	2	8.74	25	3	3	0	12.08	Importin subunit alpha-5	Q60960	Kpna1	Mus musculus
Q60972	68	5	4	28.47	74	4	4	28.47	142	5	4	0	28.47	Histone-binding protein RBBP4	Q60972	Rbbp4	Mus musculus
Q60973	26	6	5	33.41	17	5	5	34.12	43	7	6	0	41.41	Histone-binding protein RBBP7	Q60973	Rbbp7	Mus musculus
Q61029	231	15	6	38.5	159	12	4	35.18	390	15	6	0	38.5	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	Q61029	Tmpo	Mus musculus
Q61033	238	15	6	31.31	167	14	6	30.01	405	16	7	0	34.34	Lamina-associated polypeptide 2, isoforms alpha/zeta	Q61033	Tmpo	Mus musculus
Q61035	7	1	1	5.89	23	2	2	10.22	30	2	2	0.41	10.22	Histidine--tRNA ligase, cytoplasmic	Q61035	Hars	Mus musculus
Q61074	29	2	2	13.84	42	3	3	13.84	71	3	3	0	13.84	Protein phosphatase 1G	Q61074	Ppm1g	Mus musculus
Q61081	38	4	4	15.83	62	3	3	15.3	100	4	4	0	15.83	Hsp90 co-chaperone Cdc37	Q61081	Cdc37	Mus musculus
Q61093	192	17	17	30.88	118	10	10	26.32	310	18	18	0	32.81	Cytochrome b-245 heavy chain	Q61093	Cybb	Mus musculus
Q61096	657	26	26	60.24	485	20	20	62.2	1142	28	28	0	64.17	Myeloblastin	Q61096	Prtn3	Mus musculus
Q61103	15	3	3	13.3	13	2	2	9.46	28	3	3	0	13.3	Zinc finger protein ubi-d4	Q61103	Dpf2	Mus musculus
Q61152	25	2	2	10.38	24	2	2	10.38	49	2	2	0.41	10.38	Tyrosine-protein phosphatase non-receptor type 18	Q61152	Ptpn18	Mus musculus
Q61166	23	2	2	11.57	39	4	4	30.97	62	5	5	0	35.45	Microtubule-associated protein RP/EB family member 1	Q61166	Mapre1	Mus musculus
Q61171	50	10	10	80.3	35	7	7	63.64	85	10	10	0	80.3	Peroxiredoxin-2	Q61171	Prdx2	Mus musculus
Q61176	0	0	0		10	5	5	30.96	10	5	5	0	30.96	Arginase-1	Q61176	Arg1	Mus musculus
Q61191	12	2	2	2.89	14	2	2	2.64	26	3	3	0	4.21	Host cell factor 1	Q61191	Hcfc1	Mus musculus
Q61206	3	2	2	22.27	6	1	1	8.3	9	2	2	0.41	22.27	Platelet-activating factor acetylhydrolase IB subunit beta	Q61206	Pafah1b2	Mus musculus
Q61207	69	8	8	16.7	32	6	6	14.72	101	8	8	0	16.7	Prosaposin	Q61207	Psap	Mus musculus
Q61210-5	66	9	9	15.73	92	12	12	20.53	158	13	13	0	22.78	Isoform 5 of Rho guanine nucleotide exchange factor 1	Q61210	Arhgef1	Mus musculus
Q61233	623	37	37	63.8	1437	50	50	68.9	2060	52	52	0	70.49	Plastin-2	Q61233	Lcp1	Mus musculus
Q61362	70	9	9	26.22	40	4	4	16.2	110	9	9	0	26.22	Chitinase-3-like protein 1	Q61362	Chi3l1	Mus musculus
Q61508	1	1	1	5.01	2	2	2	5.72	3	3	3	0	7.69	Extracellular matrix protein 1	Q61508	Ecm1	Mus musculus
Q61543	17	4	4	6.98	2	2	2	4.26	19	4	4	0	6.98	Golgi apparatus protein 1	Q61543	Glg1	Mus musculus
Q61545	29	4	4	10.08	36	3	3	7.79	65	4	4	0	10.08	RNA-binding protein EWS	Q61545	Ewsr1	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q61550	18	4	4	15.12	6	3	3	11.65	24	4	4	0	15.12	Double-strand-break repair protein rad21 homolog	Q61550	Rad21	Mus musculus
Q61598	102	10	7	24.49	174	13	9	28.09	276	13	9	0	28.09	Rab GDP dissociation inhibitor beta	Q61598	Gdi2	Mus musculus
Q61599	187	12	12	65.5	492	14	14	67	679	16	16	0	67	Rho GDP-dissociation inhibitor 2	Q61599	Arhgdib	Mus musculus
Q61635	0	0	0		8	4	4	17.62	8	4	4	0	17.62	GTP-binding protein	Q61635	Ifi47	Mus musculus
Q61646	678	15	15	54.18	389	10	10	46.97	1067	15	15	0	54.18	Haptoglobin	Q61646	Hp	Mus musculus
Q61655	4	2	2	10.46	12	3	3	9.21	16	4	4	0	14.44	ATP-dependent RNA helicase DDX19A	Q61655	Ddx19a	Mus musculus
Q61656	36	5	5	10.59	70	8	8	19.22	106	8	8	0	19.22	Probable ATP-dependent RNA helicase DDX5	Q61656	Ddx5	Mus musculus
Q61687	0	0	0		7	2	2	1.25	7	2	2	0.41	1.25	Transcriptional regulator ATRX	Q61687	Atrx	Mus musculus
Q61704	9	2	2	5.74	0	0	0		9	2	2	0.41	5.74	Inter-alpha-trypsin inhibitor heavy chain H3	Q61704	Itih3	Mus musculus
Q61753	7	3	3	10.69	64	8	8	30.58	71	9	9	0	32.65	D-3-phosphoglycerate dehydrogenase	Q61753	Phgdh	Mus musculus
Q61768	30	5	5	8	42	5	5	6.13	72	6	6	0	8	Kinesin-1 heavy chain	Q61768	Kif5b	Mus musculus
Q61792	12	3	3	11.03	19	3	3	11.79	31	4	4	0	17.11	LIM and SH3 domain protein 1	Q61792	Lasp1	Mus musculus
Q61805	25	3	3	10.81	30	3	3	10.81	55	3	3	0	10.81	Lipopolysaccharide-binding protein	Q61805	Lbp	Mus musculus
Q61878	68	6	6	26.01	33	4	4	20.63	101	6	6	0	26.01	Bone marrow proteoglycan	Q61878	Prg2	Mus musculus
Q61881	8	4	4	11.68	35	7	7	16.13	43	7	7	0	16.13	DNA replication licensing factor MCM7	Q61881	Mcm7	Mus musculus
Q61937	52	4	4	12.33	51	4	4	23.97	103	6	6	0	24.32	Nucleophosmin	Q61937	Npm1	Mus musculus
Q61990	27	4	4	21.55	49	4	4	21.55	76	4	4	0	21.55	Poly(rC)-binding protein 2	Q61990	Pcbp2	Mus musculus
Q62086	13	1	1	8.47	6	2	2	13.28	19	2	2	0.41	13.28	Serum paraoxonase/arylesterase 2	Q62086	Pon2	Mus musculus
Q62167	42	7	7	13.44	47	8	8	14.35	89	9	9	0	16.47	ATP-dependent RNA helicase DDX3X	Q62167	Ddx3x	Mus musculus
Q62178	19	5	5	13.16	9	1	1	2.76	28	5	5	0	13.16	Semaphorin-4A	Q62178	Sema4a	Mus musculus
Q62186	15	3	3	34.3	5	1	1	16.86	20	3	3	0	34.3	Translocon-associated protein subunit delta	Q62186	Ssr4	Mus musculus
Q62193	9	2	2	16.67	4	1	1	8.52	13	2	2	0.41	16.67	Replication protein A 32 kDa subunit	Q62193	Rpa2	Mus musculus
Q62219	0	0	0		7	2	2	8.03	7	2	2	0.41	8.03	Transforming growth factor beta-1-induced transcript 1 protein	Q62219	Tgfb1i1	Mus musculus
Q62261	297	30	30	19.81	241	25	25	18.71	538	32	32	0	21.88	Spectrin beta chain, non-erythrocytic 1	Q62261	Sptbn1	Mus musculus
Q62318	46	10	10	26.14	51	7	7	18.94	97	10	10	0	26.14	Transcription intermediary factor 1-beta	Q62318	Trim28	Mus musculus
Q62376	19	2	2	6.7	6	1	1	4.24	25	2	2	0.41	6.7	U1 small nuclear ribonucleoprotein 70 kDa	Q62376	Snrnp70	Mus musculus
Q62383	2	2	2	2.03	0	0	0		2	2	2	0.41	2.03	Transcription elongation factor SPT6	Q62383	Supt6h	Mus musculus
Q62393	29	2	2	14.73	39	2	2	14.73	68	2	2	0.41	14.73	Tumor protein D52	Q62393	Tpd52	Mus musculus
Q62418	81	6	6	26.83	107	8	8	32.11	188	9	9	0	32.34	Drebrin-like protein	Q62418	Dbnl	Mus musculus
Q62419	11	2	2	8.15	7	1	1	3.8	18	2	2	0.41	8.15	Endophilin-A2	Q62419	Sh3gl1	Mus musculus
Q62422	50	7	7	39.07	96	7	7	39.07	146	8	8	0	39.07	Osteoclast-stimulating factor 1	Q62422	Ostf1	Mus musculus
Q62431	5	1	1	3.66	8	2	2	9.98	13	2	2	0.41	9.98	AT-rich interactive domain-containing protein 3A	Q62431	Arid3a	Mus musculus
Q62448	0	0	0		10	2	2	5.96	10	2	2	0.41	5.96	Eukaryotic translation initiation factor 4 gamma 2	Q62448	Eif4g2	Mus musculus
Q62465	14	6	6	24.14	23	7	7	24.14	37	7	7	0	24.14	Synaptic vesicle membrane protein VAT-1 homolog	Q62465	Vat1	Mus musculus
Q62523	78	8	8	21.45	85	9	9	27.3	163	10	10	0	27.48	Zyxin	Q62523	Zyx	Mus musculus
Q63810	16	2	2	27.06	22	2	2	27.06	38	2	2	0.41	27.06	Calcineurin subunit B type 1	Q63810	Ppp3r1	Mus musculus
Q64012	11	2	2	12.82	17	1	1	7.05	28	2	2	0.41	12.82	RNA-binding protein Raly	Q64012	Raly	Mus musculus
Q64152	17	2	2	23.53	44	2	2	23.53	61	2	2	0.41	23.53	Transcription factor BTF3	Q64152	Btf3	Mus musculus
Q64277	15	3	3	15.11	0	0	0		15	3	3	0	15.11	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2	Q64277	Bst1	Mus musculus
Q64324	58	9	9	29.01	62	10	10	28.33	120	12	12	0	31.7	Syntaxin-binding protein 2	Q64324	Stxbp2	Mus musculus
Q64433	34	3	3	25.49	23	3	3	25.49	57	4	4	0	25.49	10 kDa heat shock protein, mitochondrial	Q64433	Hspe1	Mus musculus
Q64455	27	3	3	6.38	16	2	2	4.52	43	3	3	0	6.38	Receptor-type tyrosine-protein phosphatase eta	Q64455	Ptprj	Mus musculus
Q64511	6	4	3	4.16	10	2	1	1.61	16	4	3	0	4.16	DNA topoisomerase 2-beta	Q64511	Top2b	Mus musculus
Q64514	10	2	2	2.54	34	6	6	10.62	44	6	6	0	10.62	Tripeptidyl-peptidase 2	Q64514	Tpp2	Mus musculus
Q64521	55	8	8	19.39	25	5	5	11.97	80	8	8	0	19.39	Glycerol-3-phosphate dehydrogenase, mitochondrial	Q64521	Gpd2	Mus musculus
Q64523	6435	27	2	58.91	4465	24	2	58.91	10900	28	2	0.41	58.91	Histone H2A type 2-C	Q64523	Hist2h2ac	Mus musculus
Q64727	39	8	8	14.82	88	13	13	23.08	127	14	14	0	24.58	Vinculin	Q64727	Vcl	Mus musculus
Q64737	7	1	1	2.28	13	4	4	6.44	20	4	4	0	6.44	Trifunctional purine biosynthetic protein adenosine-3	Q64737	Gart	Mus musculus
Q65Z40	10	2	2	4.33	5	3	3	5	15	4	4	0	7.17	Wings apart-like protein homolog	Q65Z40	Wapal	Mus musculus
Q66JX5	0	0	0		4	2	2	6.77	4	2	2	0.41	6.77	FGFR1 oncogene partner	Q66JX5	Fgfr1op	Mus musculus
Q68FD5	425	38	38	34.75	503	47	47	38.81	928	47	47	0	38.81	Clathrin heavy chain 1	Q68FD5	Cltc	Mus musculus
Q68FL6	3	2	2	4.88	12	4	4	9.09	15	5	5	0	11.2	Methionine--tRNA ligase, cytoplasmic	Q68FL6	Mars	Mus musculus
Q69ZK0	2	2	2	2.36	13	6	6	8.73	15	6	6	0	8.73	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	Q69ZK0	Prex1	Mus musculus
Q6A026	6	3	3	3.75	16	5	5	6.38	22	5	5	0	6.38	Sister chromatid cohesion protein PDS5 homolog A	Q6A026	Pds5a	Mus musculus
Q6A068	20	6	6	14.84	8	2	2	5.74	28	6	6	0	14.84	Cell division cycle 5-like protein	Q6A068	Cdc5l	Mus musculus
Q6A4J8	15	4	4	8.52	21	5	5	10.06	36	5	5	0	10.06	Ubiquitin carboxyl-terminal hydrolase 7	Q6A4J8	Usp7	Mus musculus
Q6BCL1	21	7	7	21.48	32	8	8	22.22	53	9	9	0	25.78	PML-RARA-regulated adapter molecule 1	Q6BCL1	Pram1	Mus musculus
Q6DFW4	14	1	1	2.8	14	2	2	5.04	28	2	2	0.41	5.04	Nucleolar protein 58	Q6DFW4	Nop58	Mus musculus
Q6DFZ1	2	2	2	2.79	4	1	1	1.4	6	3	3	0	4.19	Golgi-specific brefeldin A-resistance factor 1	Q6DFZ1	Gbf1	Mus musculus
Q6DTY7	3	2	2	7.25	10	4	4	16.84	13	4	4	0	16.84	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	Q6DTY7	Pfkfb4	Mus musculus
Q6GQT9	15	5	5	8.07	7	3	3	5.19	22	5	5	0	8.07	Nodal modulator 1	Q6GQT9	Nomo1	Mus musculus
Q6IRU2	111	9	9	38.71	70	7	7	38.31	181	9	9	0	38.71	Tropomyosin alpha-4 chain	Q6IRU2	Tpm4	Mus musculus
Q6NVF9	25	1	1	4.54	42	2	2	9.8	67	2	2	0.41	9.8	Cleavage and polyadenylation specificity factor subunit 6	Q6NVF9	Cpsf6	Mus musculus
Q6NZB0	19	2	2	17.79	19	2	2	18.18	38	3	3	0	24.51	DnaJ homolog subfamily C member 8	Q6NZB0	Dnajc8	Mus musculus
Q6NZC7	6	2	2	4.61	9	1	1	2.51	15	2	2	0.41	4.61	SEC23-interacting protein	Q6NZC7	Sec23ip	Mus musculus
Q6NZJ6	8	1	1	0.88	35	5	5	6.75	43	5	5	0	6.75	Eukaryotic translation initiation factor 4 gamma 1	Q6NZJ6	Eif4g1	Mus musculus
Q6P069-2	81	7	7	50.82	74	5	5	43.17	155	7	7	0	50.82	Isoform 2 of Sorcin	Q6P069	Sri	Mus musculus
Q6P1B1	4	2	2	10.27	46	6	6	24.4	50	6	6	0	24.4	Xaa-Pro aminopeptidase 1	Q6P1B1	Xpnpep1	Mus musculus
Q6P1F6	0	0	0		6	3	3	12.3	6	3	3	0	12.3	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	Q6P1F6	Ppp2r2a	Mus musculus
Q6P4T2	50	11	11	9.88	68	10	10	9.36	118	12	12	0	11	U5 small nuclear ribonucleoprotein 200 kDa helicase	Q6P4T2	Snrnp200	Mus musculus
Q6P542	14	4	4	12.78	16	2	2	6.93	30	4	4	0	12.78	ATP-binding cassette sub-family F member 1	Q6P542	Abcf1	Mus musculus
Q6P5E4	115	12	12	14.96	59	10	10	12.7	174	13	13	0	16.38	UDP-glucose:glycoprotein glucosyltransferase 1	Q6P5E4	Uggt1	Mus musculus
Q6P5F9	24	5	5	7.56	59	6	6	9.62	83	7	7	0	11.11	Exportin-1	Q6P5F9	Xpo1	Mus musculus
Q6P8X1	7	2	2	7.88	27	3	3	12.56	34	3	3	0	12.56	Sorting nexin-6	Q6P8X1	Snx6	Mus musculus
Q6P9Q6	11	4	4	7.89	10	2	2	4.93	21	4	4	0	7.89	FK506-binding protein 15	Q6P9Q6	Fkbp15	Mus musculus
Q6PCP5	3	2	2	20.27	1	1	1	11	4	2	2	0.41	20.27	Mitochondrial fission factor	Q6PCP5	Mff	Mus musculus
Q6PDG5	29	5	5	10.31	22	3	3	5.36	51	5	5	0	10.31	SWI/SNF complex subunit SMARCC2	Q6PDG5	Smarcc2	Mus musculus
Q6PDI5	7	3	3	4.18	29	7	7	7.01	36	8	8	0	8.32	Proteasome-associated protein ECM29 homolog	Q6PDI5	Ecm29	Mus musculus
Q6PDM2	87	7	7	26.61	28	3	3	15.32	115	7	7	0	26.61	Serine/arginine-rich splicing factor 1	Q6PDM2	Srsf1	Mus musculus
Q6PDQ2	12	4	4	3.39	21	6	6	5.95	33	6	6	0	5.95	Chromodomain-helicase-DNA-binding protein 4	Q6PDQ2	Chd4	Mus musculus
Q6PFD9	13	4	4	3.8	7	3	3	3.25	20	5	5	0	5.07	Nuclear pore complex protein Nup98-Nup96	Q6PFD9	Nup98	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q6PFR5	20	2	2	12.46	4	2	2	12.46	24	2	2	0.41	12.46	Transformer-2 protein homolog alpha	Q6PFR5	Tra2a	Mus musculus
Q6PGG2	5	3	3	5.87	6	3	3	7.31	11	4	4	0	8.96	GEM-interacting protein	Q6PGG2	Gmip	Mus musculus
Q6PHU5	24	3	3	8.36	24	3	3	9.33	48	4	4	0	10.55	Sortilin	Q6PHU5	Sort1	Mus musculus
Q6PHZ2	16	1	1	3.81	26	2	2	7.62	42	2	2	0.41	7.62	Calcium/calmodulin-dependent protein kinase type II subunit delta	Q6PHZ2	Camk2d	Mus musculus
Q6SJQ7	15	3	3	13.35	14	2	2	13.35	29	3	3	0	13.35	CMRF35-like molecule 1	Q6SJQ7	Cd300lf	Mus musculus
Q6URW6	94	8	2	3.7	87	8	2	3.7	181	8	2	0.41	3.7	Myosin-14	Q6URW6	Myh14	Mus musculus
Q6WVG3	18	4	4	21.1	23	5	5	18.96	41	6	6	0	25.08	BTB/POZ domain-containing protein KCTD12	Q6WVG3	Kctd12	Mus musculus
Q6ZQ38	3	3	3	5.2	26	6	6	9.59	29	7	7	0	11.14	Cullin-associated NEDD8-dissociated protein 1	Q6ZQ38	Cand1	Mus musculus
Q6ZQA0	8	5	5	4.6	32	8	8	6.24	40	9	9	0	7	Neurobeachin-like protein 2	Q6ZQA0	Nbeal2	Mus musculus
Q6ZQI3	33	2	2	12.37	12	2	2	12.37	45	2	2	0.41	12.37	Malectin	Q6ZQI3	Mlec	Mus musculus
Q6ZQK5	2	1	1	4.03	9	3	3	8.96	11	3	3	0	8.96	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	Q6ZQK5	Acap2	Mus musculus
Q6ZWM4	10	3	3	70.83	22	3	3	61.46	32	4	4	0	70.83	U6 snRNA-associated Sm-like protein LSm8	Q6ZWM4	Lsm8	Mus musculus
Q6ZWQ0	16	7	7	2.17	10	3	3	1.15	26	7	7	0	2.17	Nesprin-2	Q6ZWQ0	Syne2	Mus musculus
Q6ZWQ9	255	7	3	35.47	215	7	1	37.21	470	9	3	0	37.21	MCG5400	Q6ZWQ9	Myl12a	Mus musculus
Q6ZWR6	327	54	54	11.73	237	41	41	9.04	564	63	63	0	13.32	Nesprin-1	Q6ZWR6	Syne1	Mus musculus
Q6ZWX6	19	3	3	20.63	25	3	3	20.63	44	3	3	0	20.63	Eukaryotic translation initiation factor 2 subunit 1	Q6ZWX6	Eif2s1	Mus musculus
Q6ZWZ6	9	3	3	36.36	25	4	4	41.67	34	5	5	0	56.82	40S ribosomal protein S12	Q6ZWZ6	Rps12	Mus musculus
Q76MZ3	100	8	5	19.19	143	12	8	32.6	243	12	8	0	32.6	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	Q76MZ3	Ppp2r1a	Mus musculus
Q78PY7	58	8	8	18.57	103	15	15	30.44	161	16	16	0	32.75	Staphylococcal nuclease domain-containing protein 1	Q78PY7	Snd1	Mus musculus
Q7M6Y3	8	4	4	17.27	38	5	5	20.3	46	5	5	0	20.3	Phosphatidylinositol-binding clathrin assembly protein	Q7M6Y3	Picalm	Mus musculus
Q7TMK9	30	4	3	9.47	54	7	7	15.09	84	8	7	0	17.01	Heterogeneous nuclear ribonucleoprotein Q	Q7TMK9	Syncrip	Mus musculus
Q7TMY8	0	0	0		9	3	3	1.96	9	3	3	0	1.96	E3 ubiquitin-protein ligase HUWE1	Q7TMY8	Huwe1	Mus musculus
Q7TNC4	13	3	3	11.73	13	4	4	15.31	26	4	4	0	15.31	Putative RNA-binding protein Luc7-like 2	Q7TNC4	Luc7l2	Mus musculus
Q7TNG5	0	0	0		14	6	6	21.73	14	6	6	0	21.73	Echinoderm microtubule-associated protein-like 2	Q7TNG5	Eml2	Mus musculus
Q7TNP2	51	5	2	13.31	73	7	3	16.47	124	7	3	0	16.47	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	Q7TNP2	Ppp2r1b	Mus musculus
Q7TNV0	43	3	3	9.47	18	2	2	6.32	61	3	3	0	9.47	Protein DEK	Q7TNV0	Dek	Mus musculus
Q7TPD0	12	2	2	4.13	15	3	3	6.34	27	3	3	0	6.34	Integrator complex subunit 3	Q7TPD0	Ints3	Mus musculus
Q7TPR4	406	35	22	44.62	341	31	18	43.16	747	38	25	0	46.52	Alpha-actinin-1	Q7TPR4	Actn1	Mus musculus
Q7TPV4	9	4	4	5.65	32	5	5	7.14	41	6	6	0	7.96	Myb-binding protein 1A	Q7TPV4	Mybbp1a	Mus musculus
Q7TSI3	19	5	5	15.3	18	3	3	8.88	37	5	5	0	15.3	Serine/threonine-protein phosphatase 6 regulatory subunit 1	Q7TSI3	Ppp6r1	Mus musculus
Q7TSS2	4	2	2	15.4	15	2	2	15.4	19	2	2	0.41	15.4	Ubiquitin-conjugating enzyme E2 Q1	Q7TSS2	Ube2q1	Mus musculus
Q7TSV4	5	1	1	2.9	22	4	4	11.13	27	4	4	0	11.13	Phosphoglucomutase-2	Q7TSV4	Pgm2	Mus musculus
Q80T06	55	5	5	23.13	67	6	6	28.47	122	6	6	0	28.47	Elongation factor 1-delta	Q80T06	Eef1d	Mus musculus
Q80TH2	8	2	2	3.14	11	2	2	3.14	19	2	2	0.41	3.14	Protein LAP2	Q80TH2	Erbb2ip	Mus musculus
Q80TP3	0	0	0		3	3	3	2.18	3	3	3	0	2.18	E3 ubiquitin-protein ligase UBR5	Q80TP3	Ubr5	Mus musculus
Q80TY0	13	2	2	9.25	24	2	2	9.25	37	2	2	0.41	9.25	Formin-binding protein 1	Q80TY0	Fnbp1	Mus musculus
Q80U16-5	40	4	4	12.64	56	5	5	15.96	96	5	5	0	15.96	Isoform 5 of Protein FAM65B	Q80U16	Fam65b	Mus musculus
Q80U93	4	2	2	1.68	11	2	2	2.88	15	3	3	0	3.5	Nuclear pore complex protein Nup214	Q80U93	Nup214	Mus musculus
Q80UR4	2	2	2	11.95	1	1	1	5.66	3	3	3	0	17.61	Mast cell protease-11	Q80UR4	Prss34	Mus musculus
Q80VD1	27	2	2	12.12	29	3	3	16.55	56	3	3	0	16.55	Protein FAM98B	Q80VD1	Fam98b	Mus musculus
Q80VP1	2	1	1	4	11	2	2	10.09	13	2	2	0.41	10.09	Epsin-1	Q80VP1	Epn1	Mus musculus
Q80VQ0	9	4	4	12.18	9	2	2	5.98	18	4	4	0	12.18	Aldehyde dehydrogenase family 3 member B1	Q80VQ0	Aldh3b1	Mus musculus
Q80WJ7	2	1	1	4.66	4	2	2	11.57	6	2	2	0.41	11.57	Protein LYRIC	Q80WJ7	Mtdh	Mus musculus
Q80WQ2	0	0	0		2	2	2	5.75	2	2	2	0.41	5.75	Protein VAC14 homolog	Q80WQ2	Vac14	Mus musculus
Q80X41	15	4	4	12.95	18	2	2	7.5	33	4	4	0	12.95	Serine/threonine-protein kinase VRK1	Q80X41	Vrk1	Mus musculus
Q80X50	1	1	1	1.72	9	3	3	4.34	10	3	3	0	4.34	Ubiquitin-associated protein 2-like	Q80X50	Ubap2l	Mus musculus
Q80X90	47	9	8	7.15	35	8	7	7.72	82	12	11	0	10.45	Filamin-B	Q80X90	Flnb	Mus musculus
Q80XU3	2	2	2	11.54	0	0	0		2	2	2	0.41	11.54	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	Q80XU3	Nucks1	Mus musculus
Q80Y14	24	2	2	21.71	19	2	2	21.71	43	2	2	0.41	21.71	Glutaredoxin-related protein 5, mitochondrial	Q80Y14	Glrx5	Mus musculus
Q80ZJ2	5	1	1	8.33	11	3	3	21.01	16	3	3	0	21.01	Impa1 protein	Q80ZJ2	Impa1	Mus musculus
Q810A7	6	2	2	4.63	1	1	1	2.26	7	2	2	0.41	4.63	ATP-dependent RNA helicase DDX42	Q810A7	Ddx42	Mus musculus
Q810B6	11	3	3	5.47	16	3	3	6.33	27	5	5	0	9.32	Rabankyrin-5	Q810B6	Ankfy1	Mus musculus
Q8BFQ8	0	0	0		6	2	2	22.27	6	2	2	0.41	22.27	Parkinson disease 7 domain-containing protein 1	Q8BFQ8	Pddc1	Mus musculus
Q8BFR5	17	3	3	13.27	14	3	3	13.27	31	3	3	0	13.27	Elongation factor Tu, mitochondrial	Q8BFR5	Tufm	Mus musculus
Q8BFY6	11	2	2	8.73	1	1	1	4	12	2	2	0.41	8.73	Peflin	Q8BFY6	Pef1	Mus musculus
Q8BFY9	41	8	8	16.82	67	10	10	22.61	108	11	11	0	23.16	Transportin-1	Q8BFY9	Tnpo1	Mus musculus
Q8BFZ3	961	13	3	30.59	2764	20	4	39.36	3725	20	4	0	39.36	Beta-actin-like protein 2	Q8BFZ3	Actbl2	Mus musculus
Q8BG05	110	8	8	21.11	96	7	7	20.32	206	8	8	0	21.11	Heterogeneous nuclear ribonucleoprotein A3	Q8BG05	Hnrnpa3	Mus musculus
Q8BG32	1	1	1	4.74	13	3	3	11.14	14	4	4	0	15.88	26S proteasome non-ATPase regulatory subunit 11	Q8BG32	Psmd11	Mus musculus
Q8BGD9	21	2	2	8.67	39	5	5	11.95	60	5	5	0	11.95	Eukaryotic translation initiation factor 4B	Q8BGD9	Eif4b	Mus musculus
Q8BGG7	0	0	0		6	2	2	7.37	6	2	2	0.41	7.37	Ubiquitin-associated and SH3 domain-containing protein B	Q8BGG7	Ubash3b	Mus musculus
Q8BGJ5	74	8	8	27.98	107	8	8	30.06	181	9	9	0	31	MCG13402, isoform CRA_a	Q8BGJ5	Ptbp1	Mus musculus
Q8BGQ7	12	3	3	6.1	79	11	11	22.93	91	11	11	0	22.93	Alanine--tRNA ligase, cytoplasmic	Q8BGQ7	Aars	Mus musculus
Q8BGT7	19	3	3	24.37	6	3	3	24.37	25	3	3	0	24.37	Survival of motor neuron-related-splicing factor 30	Q8BGT7	Smndc1	Mus musculus
Q8BH04	6	2	2	8.59	6	3	3	8.59	12	3	3	0	8.59	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	Q8BH04	Pck2	Mus musculus
Q8BH43	13	3	3	9.05	9	2	2	6.44	22	3	3	0	9.05	Wiskott-Aldrich syndrome protein family member 2	Q8BH43	Wasf2	Mus musculus
Q8BH59	12	2	2	6.06	2	2	2	5.76	14	3	3	0	8.27	Calcium-binding mitochondrial carrier protein Aralar1	Q8BH59	Slc25a12	Mus musculus
Q8BH61	4	2	2	4.1	3	1	1	1.5	7	3	3	0	5.6	Coagulation factor XIII A chain	Q8BH61	F13a1	Mus musculus
Q8BH74	8	3	3	6.59	5	3	3	5.29	13	4	4	0	8.42	Nuclear pore complex protein Nup107	Q8BH74	Nup107	Mus musculus
Q8BH78	20	2	2	17.98	3	1	1	9.27	23	2	2	0.41	17.98	Reticulon	Q8BH78	Rtn4	Mus musculus
Q8BH95	15	2	2	19.66	20	2	2	19.66	35	2	2	0.41	19.66	Enoyl-CoA hydratase, mitochondrial	Q8BH95	Echs1	Mus musculus
Q8BHD7	34	3	3	18.55	55	6	6	29.45	89	6	6	0	29.45	Polypyrimidine tract-binding protein 3	Q8BHD7	Ptbp3	Mus musculus
Q8BHG1	3	1	1	2.5	33	4	4	7.58	36	4	4	0	7.58	Nardilysin	Q8BHG1	Nrd1	Mus musculus
Q8BHJ5	27	2	2	8.95	19	2	2	8.95	46	2	2	0.41	8.95	F-box-like/WD repeat-containing protein TBL1XR1	Q8BHJ5	Tbl1xr1	Mus musculus
Q8BHN3	46	8	8	17.8	52	7	7	16	98	9	9	0	19.39	Neutral alpha-glucosidase AB	Q8BHN3	Ganab	Mus musculus
Q8BIQ5	21	4	4	12.59	8	2	2	5.17	29	4	4	0	12.59	Cleavage stimulation factor subunit 2	Q8BIQ5	Cstf2	Mus musculus
Q8BIW1	1	1	1	3.74	2	2	2	7.05	3	2	2	0.41	7.05	Protein prune homolog	Q8BIW1	Prune	Mus musculus
Q8BJ71	44	3	3	9.16	37	3	3	9.16	81	3	3	0	9.16	Nuclear pore complex protein Nup93	Q8BJ71	Nup93	Mus musculus
Q8BJS4	61	7	7	18.19	52	8	8	19.97	113	10	10	0	22.71	SUN domain-containing protein 2	Q8BJS4	Sun2	Mus musculus
Q8BJU0	4	2	2	9.21	0	0	0		4	2	2	0.41	9.21	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	Q8BJU0	Sgta	Mus musculus
Q8BJY1	9	2	2	10.52	37	3	3	14.88	46	3	3	0	14.88	26S proteasome non-ATPase regulatory subunit 5	Q8BJY1	Psmd5	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q8BK64	5	2	2	11.24	6	1	1	6.51	11	2	2	0.41	11.24	Activator of 90 kDa heat shock protein ATPase homolog 1	Q8BK64	Ahsa1	Mus musculus
Q8BK67	1	1	1	3.65	6	3	3	10.96	7	3	3	0	10.96	Protein RCC2	Q8BK67	Rcc2	Mus musculus
Q8BKC5	4	1	1	2.83	24	5	5	10.67	28	5	5	0	10.67	Importin-5	Q8BKC5	Ipo5	Mus musculus
Q8BL97	51	4	3	17.6	26	3	3	17.6	77	4	3	0	17.6	Serine/arginine-rich splicing factor 7	Q8BL97	Srsf7	Mus musculus
Q8BMA6	13	3	3	8.8	9	2	2	7.04	22	4	4	0	12	Signal recognition particle subunit SRP68	Q8BMA6	Srp68	Mus musculus
Q8BMD8	8	2	2	9.47	5	1	1	6.11	13	2	2	0.41	9.47	Calcium-binding mitochondrial carrier protein SCaMC-1	Q8BMD8	Slc25a24	Mus musculus
Q8BMJ2	15	1	1	2.63	28	3	3	5.77	43	3	3	0	5.77	Leucine--tRNA ligase, cytoplasmic	Q8BMJ2	Lars	Mus musculus
Q8BMJ3	3	1	1	20.83	10	2	2	30.56	13	2	2	0.41	30.56	Eukaryotic translation initiation factor 1A, X-chromosomal	Q8BMJ3	Eif1ax	Mus musculus
Q8BMK4	52	8	8	21.22	38	5	5	16.35	90	8	8	0	21.22	Cytoskeleton-associated protein 4	Q8BMK4	Ckap4	Mus musculus
Q8BML9	1	1	1	2.45	2	2	2	5.29	3	2	2	0.41	5.29	Glutaminyl-tRNA synthetase	Q8BML9	Qars	Mus musculus
Q8BMS1	75	9	9	21.49	70	5	5	10.75	145	10	10	0	21.49	Trifunctional enzyme subunit alpha, mitochondrial	Q8BMS1	Hadha	Mus musculus
Q8BND5	53	7	7	16.31	39	6	6	14.04	92	7	7	0	16.31	Sulfhydryl oxidase 1	Q8BND5	Qsox1	Mus musculus
Q8BP47	4	3	3	9.84	46	10	10	27.37	50	10	10	0	27.37	Asparagine--tRNA ligase, cytoplasmic	Q8BP47	Nars	Mus musculus
Q8BPU7	26	4	4	12.1	18	4	4	13.07	44	5	5	0	13.76	Engulfment and cell motility protein 1	Q8BPU7	Elmo1	Mus musculus
Q8BQ30	4	2	2	10.44	3	2	2	10.44	7	2	2	0.41	10.44	Phostensin	Q8BQ30	Ppp1r18	Mus musculus
Q8BQ46	26	4	2	12.57	25	2	1	8.98	51	4	2	0.41	12.57	Protein Taf15	Q8BQ46	Taf15	Mus musculus
Q8BQ47	10	1	1	8.57	2	2	2	17.14	12	2	2	0.41	17.14	Protein canopy homolog 4	Q8BQ47	Cnpy4	Mus musculus
Q8BRF7	3	3	3	8.14	7	2	2	6.73	10	4	4	0	12.21	Sec1 family domain-containing protein 1	Q8BRF7	Scfd1	Mus musculus
Q8BRN9	3	2	2	5.66	1	1	1	2.95	4	2	2	0.41	5.66	Coiled-coil and C2 domain-containing protein 1B	Q8BRN9	Cc2d1b	Mus musculus
Q8BT60	212	18	16	41.46	183	13	12	33.21	395	20	18	0	41.84	Copine-3	Q8BT60	Cpne3	Mus musculus
Q8BTE6	234	13	13	61.9	160	9	9	61.9	394	13	13	0	61.9	Protein Wfdc21	Q8BTE6	Wfdc21	Mus musculus
Q8BTI8	7	3	3	2.77	0	0	0		7	3	3	0	2.77	Serine/arginine repetitive matrix protein 2	Q8BTI8	Srrm2	Mus musculus
Q8BTM8	2689	114	113	52.06	2358	109	108	50.36	5047	129	128	0	54.02	Filamin-A	Q8BTM8	Flna	Mus musculus
Q8BTS4	3	2	2	7.06	1	1	1	3.33	4	2	2	0.41	7.06	Nuclear pore complex protein Nup54	Q8BTS4	Nup54	Mus musculus
Q8BTZ7	0	0	0		4	2	2	12.5	4	2	2	0.41	12.5	Mannose-1-phosphate guanyltransferase beta	Q8BTZ7	Gmppb	Mus musculus
Q8BU30	0	0	0		6	3	3	5.63	6	3	3	0	5.63	Isoleucine--tRNA ligase, cytoplasmic	Q8BU30	Iars	Mus musculus
Q8BUK6	10	4	4	11.7	14	4	4	11.7	24	4	4	0	11.7	Protein Hook homolog 3	Q8BUK6	Hook3	Mus musculus
Q8BVE3	18	2	2	8.7	23	2	2	8.7	41	2	2	0.41	8.7	V-type proton ATPase subunit H	Q8BVE3	Atp6v1h	Mus musculus
Q8BVG4	1	1	1	3.25	4	2	2	5.68	5	2	2	0.41	5.68	Dipeptidyl peptidase 9	Q8BVG4	Dpp9	Mus musculus
Q8BWT1	17	4	4	22.42	22	3	3	18.89	39	4	4	0	22.42	3-ketoacyl-CoA thiolase, mitochondrial	Q8BWT1	Acaa2	Mus musculus
Q8BWY3	1	1	1	6.18	11	2	2	10.98	12	2	2	0.41	10.98	Eukaryotic peptide chain release factor subunit 1	Q8BWY3	Etf1	Mus musculus
Q8BXK9	1	1	1	6.77	2	2	2	7.17	3	2	2	0.41	7.17	Chloride intracellular channel protein 5	Q8BXK9	Clic5	Mus musculus
Q8BY71	0	0	0		11	3	3	15.62	11	3	3	0	15.62	Histone acetyltransferase type B catalytic subunit	Q8BY71	Hat1	Mus musculus
Q8BYC6	0	0	0		3	3	3	6.46	3	3	3	0	6.46	Serine/threonine-protein kinase TAO3	Q8BYC6	Taok3	Mus musculus
Q8BYI6	5	1	1	3.86	3	2	2	10.29	8	2	2	0.41	10.29	Lysophosphatidylcholine acyltransferase 2	Q8BYI6	Lpcat2	Mus musculus
Q8BYW1	10	4	4	13.27	5	3	3	7.87	15	6	6	0	17.13	Rho GTPase-activating protein 25	Q8BYW1	Arhgap25	Mus musculus
Q8C079	2	2	2	6.69	6	3	3	8.96	8	3	3	0	8.96	Striatin-interacting protein 1	Q8C079	Strip1	Mus musculus
Q8C0C7	3	1	1	2.76	21	2	2	8.66	24	2	2	0.41	8.66	Phenylalanine--tRNA ligase alpha subunit	Q8C0C7	Farsa	Mus musculus
Q8C0G2	13	2	2	9.75	5	1	1	4.68	18	2	2	0.41	9.75	TRAF3-interacting JNK-activating modulator	Q8C0G2	Traf3ip3	Mus musculus
Q8C0I1	36	8	8	21.4	31	8	8	21.55	67	9	9	0	25.27	Alkyldihydroxyacetonephosphate synthase, peroxisomal	Q8C0I1	Agps	Mus musculus
Q8C0L0	9	4	4	15.52	11	2	2	7.46	20	4	4	0	15.52	Thioredoxin-related transmembrane protein 4	Q8C0L0	Tmx4	Mus musculus
Q8C147	19	4	4	4.38	41	7	7	8.52	60	8	8	0	9.24	Dedicator of cytokinesis protein 8	Q8C147	Dock8	Mus musculus
Q8C166	54	7	6	23.13	53	8	7	25.93	107	9	8	0	26.87	Copine-1	Q8C166	Cpne1	Mus musculus
Q8C1B7	12	2	2	9.05	20	3	3	13.69	32	3	3	0	13.69	Septin-11	Q8C1B7	Sept11	Mus musculus
Q8C2Q3	14	3	3	9.27	22	4	4	11.51	36	4	4	0	11.51	RNA-binding protein 14	Q8C2Q3	Rbm14	Mus musculus
Q8C3J5	7	4	4	4.21	20	4	4	4.54	27	6	6	0	6.07	Dedicator of cytokinesis protein 2	Q8C3J5	Dock2	Mus musculus
Q8C6G8	15	2	2	5.93	9	2	2	5.93	24	2	2	0.41	5.93	WD repeat-containing protein 26	Q8C6G8	Wdr26	Mus musculus
Q8CAQ8	21	5	5	8.98	12	5	5	12.02	33	6	6	0	12.02	MICOS complex subunit Mic60	Q8CAQ8	Immt	Mus musculus
Q8CB87	1	1	1	3.03	18	6	6	16.14	19	6	6	0	16.14	Ras-related protein Rab-44	Q8CB87	Rab44	Mus musculus
Q8CBW3	2	2	2	9.98	4	4	4	13.1	6	4	4	0	13.1	Abl interactor 1	Q8CBW3	Abi1	Mus musculus
Q8CBY8	6	2	2	14.13	10	2	2	14.13	16	2	2	0.41	14.13	Dynactin subunit 4	Q8CBY8	Dctn4	Mus musculus
Q8CC86	2	1	1	5.2	9	3	3	8.74	11	3	3	0	8.74	Nicotinate phosphoribosyltransferase	Q8CC86	Naprt	Mus musculus
Q8CCF0	6	2	2	9.42	2	2	2	9.42	8	2	2	0.41	9.42	U4/U6 small nuclear ribonucleoprotein Prp31	Q8CCF0	Prpf31	Mus musculus
Q8CCJ3	0	0	0		4	2	2	4.92	4	2	2	0.41	4.92	E3 UFM1-protein ligase 1	Q8CCJ3	Ufl1	Mus musculus
Q8CCS6	5	1	1	9.27	5	2	2	20.86	10	2	2	0.41	20.86	Polyadenylate-binding protein 2	Q8CCS6	Pabpn1	Mus musculus
Q8CD10	0	0	0		2	2	2	9.95	2	2	2	0.41	9.95	Calcium uptake protein 2, mitochondrial	Q8CD10	Micu2	Mus musculus
Q8CDN6	26	5	5	29.07	39	7	7	35.99	65	7	7	0	35.99	Thioredoxin-like protein 1	Q8CDN6	Txnl1	Mus musculus
Q8CEC0	8	2	2	5.44	6	2	2	6.91	14	3	3	0	9.96	Nuclear pore complex protein Nup88	Q8CEC0	Nup88	Mus musculus
Q8CEC6	0	0	0		2	2	2	7.89	2	2	2	0.41	7.89	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	Q8CEC6	Ppwd1	Mus musculus
Q8CG03	4	1	1	2.43	6	2	2	4.97	10	2	2	0.41	4.97	cGMP-specific 3',5'-cyclic phosphodiesterase	Q8CG03	Pde5a	Mus musculus
Q8CG19	0	0	0		7	2	2	4.09	7	2	2	0.41	4.09	Latent-transforming growth factor beta-binding protein 1	Q8CG19	Ltbp1	Mus musculus
Q8CG29	94	9	9	10.38	63	8	8	12.48	157	12	12	0	17.03	Myosin IF	Q8CG29	Myo1f	Mus musculus
Q8CGC7	26	3	3	5.22	50	11	11	12.24	76	12	12	0	14.55	Bifunctional glutamate/proline--tRNA ligase	Q8CGC7	Eprs	Mus musculus
Q8CGP4	2916	18	5	58.91	2174	16	4	58.91	5090	19	5	0	58.91	Histone H2A	Q8CGP4	Hist1h2aa	Mus musculus
Q8CH18	3	2	2	2.53	7	2	2	2.53	10	2	2	0.41	2.53	Cell division cycle and apoptosis regulator protein 1	Q8CH18	Ccar1	Mus musculus
Q8CHC4	0	0	0		4	2	2	1.84	4	2	2	0.41	1.84	Synaptojanin-1	Q8CHC4	Synj1	Mus musculus
Q8CHG3	3	2	2	2.32	4	1	1	1.49	7	2	2	0.41	2.32	GRIP and coiled-coil domain-containing protein 2	Q8CHG3	Gcc2	Mus musculus
Q8CHK3	2	1	1	4.65	6	2	2	10.78	8	2	2	0.41	10.78	Lysophospholipid acyltransferase 7	Q8CHK3	Mboat7	Mus musculus
Q8CHP8	3	2	2	10.9	20	4	4	22.12	23	4	4	0	22.12	Phosphoglycolate phosphatase	Q8CHP8	Pgp	Mus musculus
Q8CI94	0	0	0		8	4	2	5.34	8	4	2	0.41	5.34	Glycogen phosphorylase, brain form	Q8CI94	Pygb	Mus musculus
Q8CI95	3	1	1	2.66	3	2	2	9.19	6	3	3	0	11.85	Oxysterol-binding protein-related protein 11	Q8CI95	Osbpl11	Mus musculus
Q8CIE6	18	5	5	7.19	33	9	9	13.07	51	9	9	0	13.07	Coatomer subunit alpha	Q8CIE6	Copa	Mus musculus
Q8CIH5	69	9	9	12.81	79	10	10	15.02	148	11	11	0	16.05	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	Q8CIH5	Plcg2	Mus musculus
Q8CIN4	47	3	3	13.17	113	7	7	26.53	160	7	7	0	26.53	Serine/threonine-protein kinase PAK 2	Q8CIN4	Pak2	Mus musculus
Q8CIS0	2	2	2	2.33	1	1	1	1.29	3	2	2	0.41	2.33	Caspase recruitment domain-containing protein 11	Q8CIS0	Card11	Mus musculus
Q8JZQ9	49	8	8	22.17	80	8	8	20.67	129	11	11	0	26.53	Eukaryotic translation initiation factor 3 subunit B	Q8JZQ9	Eif3b	Mus musculus
Q8K0E8	72	6	6	17.26	105	14	14	46.36	177	14	14	0	46.36	Fibrinogen beta chain	Q8K0E8	Fgb	Mus musculus
Q8K124	40	5	5	26.46	65	6	6	26.87	105	6	6	0	26.87	Pleckstrin homology domain-containing family O member 2	Q8K124	Plekho2	Mus musculus
Q8K1B8	35	6	6	20.9	100	14	14	33.68	135	15	15	0	33.83	Fermitin family homolog 3	Q8K1B8	Fermt3	Mus musculus
Q8K1M6	8	2	2	7.14	15	3	3	8.49	23	4	4	0	12.8	Dynamin-1-like protein	Q8K1M6	Dnm1l	Mus musculus
Q8K1T1	30	3	3	15.82	1	1	1	6.06	31	3	3	0	15.82	Leucine-rich repeat-containing protein 25	Q8K1T1	Lrrc25	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q8K1X4	1	1	1	1.41	15	4	4	7.14	16	5	5	0	8.55	NCK associated protein 1 like	Q8K1X4	Nckap1l	Mus musculus
Q8K296	13	2	2	4.01	12	3	3	5.77	25	3	3	0	5.77	Myotubularin-related protein 3	Q8K296	Mtmr3	Mus musculus
Q8K2B3	18	3	3	9.64	11	2	2	6.63	29	3	3	0	9.64	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Q8K2B3	Sdha	Mus musculus
Q8K2K6	3	2	2	10.52	12	2	2	10.52	15	2	2	0.41	10.52	Arf-GAP domain and FG repeat-containing protein 1	Q8K2K6	Agfg1	Mus musculus
Q8K2Z4	3	1	1	1.29	12	2	2	2.59	15	2	2	0.41	2.59	Condensin complex subunit 1	Q8K2Z4	Ncapd2	Mus musculus
Q8K310	22	4	4	8.27	16	3	3	6.74	38	4	4	0	8.27	Matrin-3	Q8K310	Matr3	Mus musculus
Q8K352	27	5	5	30.53	41	6	6	35.79	68	8	8	0	46.84	SAM and SH3 domain-containing protein 3	Q8K352	Sash3	Mus musculus
Q8K3K8	3	1	1	2.23	4	2	2	5.65	7	2	2	0.41	5.65	Optineurin	Q8K3K8	Optn	Mus musculus
Q8K426	195	6	6	58.12	88	4	4	32.48	283	6	6	0	58.12	Myeloid cysteine-rich protein	Q8K426	Retnlg	Mus musculus
Q8K482	40	4	4	8.1	37	4	4	7.82	77	5	5	0	9.4	EMILIN-2	Q8K482	Emilin2	Mus musculus
Q8K4I3	25	5	5	14.14	25	2	2	5.58	50	5	5	0	14.14	Rho guanine nucleotide exchange factor 6	Q8K4I3	Arhgef6	Mus musculus
Q8K4L3	64	8	8	7.42	47	6	6	5.76	111	8	8	0	7.42	Supervillin	Q8K4L3	Svil	Mus musculus
Q8K4Z5	14	5	5	9.48	11	6	6	9.1	25	7	7	0	11.63	Splicing factor 3A subunit 1	Q8K4Z5	Sf3a1	Mus musculus
Q8K558	4	2	2	11.04	16	4	4	23.34	20	4	4	0	23.34	Trem-like transcript 1 protein	Q8K558	Treml1	Mus musculus
Q8QZT1	20	5	5	13.21	11	3	3	10.14	31	5	5	0	13.21	Acetyl-CoA acetyltransferase, mitochondrial	Q8QZT1	Acat1	Mus musculus
Q8QZW8	5	3	3	10.36	29	5	5	16.28	34	5	5	0	16.28	Protein Arhgap9	Q8QZW8	Arhgap9	Mus musculus
Q8QZY1	18	4	4	12.94	57	6	6	18.97	75	7	7	0	21.63	Eukaryotic translation initiation factor 3 subunit L	Q8QZY1	Eif3l	Mus musculus
Q8QZY9	21	3	3	12.97	16	3	3	13.68	37	4	4	0	17.69	Splicing factor 3B subunit 4	Q8QZY9	Sf3b4	Mus musculus
Q8R016	3	1	1	5.49	12	2	2	10.99	15	2	2	0.41	10.99	Bleomycin hydrolase	Q8R016	Blmh	Mus musculus
Q8R050	12	4	4	11.95	20	5	5	11.95	32	5	5	0	11.95	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	Q8R050	Gspt1	Mus musculus
Q8R081	126	10	10	32.59	162	10	10	32.42	288	11	11	0	32.59	Heterogeneous nuclear ribonucleoprotein L	Q8R081	Hnrnpl	Mus musculus
Q8R0G9	6	3	3	5.45	17	6	6	10.56	23	7	7	0	11.95	Nuclear pore complex protein Nup133	Q8R0G9	Nup133	Mus musculus
Q8R0H9	20	2	2	8.82	26	2	2	4.88	46	3	3	0	8.98	ADP-ribosylation factor-binding protein GGA1	Q8R0H9	Gga1	Mus musculus
Q8R0T6	26	3	3	6.27	15	2	2	5.72	41	3	3	0	6.27	Probable G-protein coupled receptor 97	Q8R0T6	Gpr97	Mus musculus
Q8R146	0	0	0		9	2	2	6.56	9	2	2	0.41	6.56	Acylamino-acid-releasing enzyme	Q8R146	Apeh	Mus musculus
Q8R180	51	5	5	22.2	42	5	5	20.91	93	6	6	0	24.57	ERO1-like protein alpha	Q8R180	Ero1l	Mus musculus
Q8R1B4	6	3	3	4.94	20	6	6	9.33	26	6	6	0	9.33	Eukaryotic translation initiation factor 3 subunit C	Q8R1B4	Eif3c	Mus musculus
Q8R1G6	19	5	5	26.93	3	2	2	15.19	22	5	5	0	26.93	PDZ and LIM domain protein 2	Q8R1G6	Pdlim2	Mus musculus
Q8R1Q8	7	3	3	12.62	9	4	4	18.36	16	7	7	0	30.98	Cytoplasmic dynein 1 light intermediate chain 1	Q8R1Q8	Dync1li1	Mus musculus
Q8R2S8	717	31	31	51.53	332	20	20	39.05	1049	31	31	0	51.53	CD177 antigen	Q8R2S8	Cd177	Mus musculus
Q8R2Y8	1	1	1	11.6	6	2	2	19.89	7	2	2	0.41	19.89	Peptidyl-tRNA hydrolase 2, mitochondrial	Q8R2Y8	Ptrh2	Mus musculus
Q8R307	0	0	0		2	2	2	4.32	2	2	2	0.41	4.32	Vacuolar protein sorting-associated protein 18 homolog	Q8R307	Vps18	Mus musculus
Q8R326	1	1	1	4.4	7	2	2	11.47	8	2	2	0.41	11.47	Paraspeckle component 1	Q8R326	Pspc1	Mus musculus
Q8R460	5	2	2	24.39	19	2	2	24.39	24	2	2	0.41	24.39	Interleukin-36 gamma	Q8R460	Il36g	Mus musculus
Q8R4R6	6	1	1	5.85	11	2	2	12	17	2	2	0.41	12	Nucleoporin NUP53	Q8R4R6	Nup35	Mus musculus
Q8R550	28	4	4	10.72	31	3	3	8.46	59	4	4	0	10.72	SH3 domain-containing kinase-binding protein 1	Q8R550	Sh3kbp1	Mus musculus
Q8R574	2	1	1	6.78	3	2	2	6.78	5	2	2	0.41	6.78	Phosphoribosyl pyrophosphate synthase-associated protein 2	Q8R574	Prpsap2	Mus musculus
Q8R5A3	37	3	3	7.16	38	2	2	5.82	75	3	3	0	7.16	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	Q8R5A3	Apbb1ip	Mus musculus
Q8R5H1	17	3	3	4.69	27	3	3	4.59	44	4	4	0	4.79	Ubiquitin carboxyl-terminal hydrolase 15	Q8R5H1	Usp15	Mus musculus
Q8R5L1	100	8	8	38.71	69	5	5	27.6	169	8	8	0	38.71	Complement component 1 Q subcomponent-binding protein, mitochondrial	Q8R5L1	C1qbp	Mus musculus
Q8VBT6	97	13	13	26.65	130	14	14	27.28	227	15	15	0	31.21	Apolipoprotein B receptor	Q8VBT6	Apobr	Mus musculus
Q8VBV7	0	0	0		21	3	3	24.4	21	3	3	0	24.4	COP9 signalosome complex subunit 8	Q8VBV7	Cops8	Mus musculus
Q8VC88	13	4	4	21.82	28	5	5	27.27	41	5	5	0	27.27	Grancalcin	Q8VC88	Gca	Mus musculus
Q8VCI0	98	8	8	22	50	4	4	13.27	148	8	8	0	22	Phospholipase B-like 1	Q8VCI0	Plbd1	Mus musculus
Q8VCI5	9	2	2	12.71	4	2	2	12.71	13	2	2	0.41	12.71	Peroxisomal biogenesis factor 19	Q8VCI5	Pex19	Mus musculus
Q8VCM7	71	7	7	27.29	75	11	11	41.06	146	12	12	0	43.12	Fibrinogen gamma chain	Q8VCM7	Fgg	Mus musculus
Q8VCT3	4	3	3	11.54	55	7	7	20.62	59	7	7	0	20.62	Aminopeptidase B	Q8VCT3	Rnpep	Mus musculus
Q8VD04	11	3	3	8.56	3	1	1	2.36	14	3	3	0	8.56	GRIP1-associated protein 1	Q8VD04	Gripap1	Mus musculus
Q8VD58	10	2	2	5.86	4	1	1	3.38	14	2	2	0.41	5.86	Protein EVI2B	Q8VD58	Evi2b	Mus musculus
Q8VDD5	1669	69	63	36.33	1713	72	66	40.31	3382	83	77	0	43.57	Myosin-9	Q8VDD5	Myh9	Mus musculus
Q8VDJ3	12	1	1	1.34	20	3	3	4.26	32	3	3	0	4.26	Vigilin	Q8VDJ3	Hdlbp	Mus musculus
Q8VDL4	175	16	16	52.42	104	10	10	39.31	279	17	17	0	55.44	ADP-dependent glucokinase	Q8VDL4	Adpgk	Mus musculus
Q8VDM4	67	9	9	15.86	86	10	10	16.19	153	11	11	0	18.06	26S proteasome non-ATPase regulatory subunit 2	Q8VDM4	Psmd2	Mus musculus
Q8VDM6	55	13	13	28.99	46	10	10	23.52	101	13	13	0	28.99	Heterogeneous nuclear ribonucleoprotein U-like protein 1	Q8VDM6	Hnrnpul1	Mus musculus
Q8VDN2	27	5	5	10.65	12	2	2	4.2	39	5	5	0	10.65	Sodium/potassium-transporting ATPase subunit alpha-1	Q8VDN2	Atp1a1	Mus musculus
Q8VDP3	8	1	1	2.19	12	3	3	6.68	20	3	3	0	6.68	Protein-methionine sulfoxide oxidase MICAL1	Q8VDP3	Mical1	Mus musculus
Q8VDP4	68	7	7	17.46	86	9	9	21.69	154	9	9	0	21.69	Cell cycle and apoptosis regulator protein 2	Q8VDP4	Ccar2	Mus musculus
Q8VDQ8	1	1	1	5.66	13	3	3	13.37	14	3	3	0	13.37	NAD-dependent protein deacetylase sirtuin-2	Q8VDQ8	Sirt2	Mus musculus
Q8VDW0	12	6	2	22.25	13	5	3	18.97	25	8	4	0	24.82	ATP-dependent RNA helicase DDX39A	Q8VDW0	Ddx39a	Mus musculus
Q8VE37	35	3	3	11.4	27	2	2	9.03	62	3	3	0	11.4	Regulator of chromosome condensation	Q8VE37	Rcc1	Mus musculus
Q8VE47	0	0	0		5	2	2	15.63	5	2	2	0.41	15.63	Ubiquitin-like modifier-activating enzyme 5	Q8VE47	Uba5	Mus musculus
Q8VEE0	5	2	2	17.54	22	2	2	17.54	27	2	2	0.41	17.54	Ribulose-phosphate 3-epimerase	Q8VEE0	Rpe	Mus musculus
Q8VEE4	0	0	0		3	2	2	7.87	3	2	2	0.41	7.87	Replication protein A 70 kDa DNA-binding subunit	Q8VEE4	Rpa1	Mus musculus
Q8VEK3	184	14	14	30.88	246	18	18	29.5	430	19	19	0	33.25	Heterogeneous nuclear ribonucleoprotein U	Q8VEK3	Hnrnpu	Mus musculus
Q8VEM8	20	2	2	12.04	9	1	1	7.56	29	2	2	0.41	12.04	Phosphate carrier protein, mitochondrial	Q8VEM8	Slc25a3	Mus musculus
Q8VH51	47	5	5	13.96	38	4	4	11.89	85	5	5	0	13.96	RNA-binding protein 39	Q8VH51	Rbm39	Mus musculus
Q8VHM5	2	1	0	1.9	11	2	2	4.11	13	3	2	0.41	6.01	Heterogeneous nuclear ribonucleoprotein R	Q8VHM5	Hnrnpr	Mus musculus
Q8VI36	44	6	6	17.6	63	10	10	30.12	107	10	10	0	30.12	Paxillin	Q8VI36	Pxn	Mus musculus
Q8VIJ6	119	10	10	11.02	96	8	8	10.87	215	10	10	0	11.02	Splicing factor, proline- and glutamine-rich	Q8VIJ6	Sfpq	Mus musculus
Q91UZ5	0	0	0		7	2	2	15.86	7	2	2	0.41	15.86	Inositol monophosphatase 2	Q91UZ5	Impa2	Mus musculus
Q91V41	15	4	4	27.91	21	4	3	33.02	36	5	4	0	33.02	Ras-related protein Rab-14	Q91V41	Rab14	Mus musculus
Q91V55	50	3	3	26.47	80	5	5	28.92	130	5	5	0	28.92	40S ribosomal protein S5	Q91V55	Rps5	Mus musculus
Q91V92	28	6	6	10.63	132	10	10	18.52	160	10	10	0	18.52	ATP-citrate synthase	Q91V92	Acly	Mus musculus
Q91VC3	30	3	2	14.11	61	4	3	14.84	91	4	3	0	14.84	Eukaryotic initiation factor 4A-III	Q91VC3	Eif4a3	Mus musculus
Q91VD9	24	2	2	5.23	21	3	3	7.7	45	3	3	0	7.7	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Q91VD9	Ndufs1	Mus musculus
Q91VE0	4	3	3	7.62	1	1	1	2.49	5	3	3	0	7.62	Long-chain fatty acid transport protein 4	Q91VE0	Slc27a4	Mus musculus
Q91VI7	143	18	18	64.91	306	21	21	67.98	449	21	21	0	67.98	Ribonuclease inhibitor	Q91VI7	Rnh1	Mus musculus
Q91VJ5	18	3	3	26.24	17	5	5	35.74	35	5	5	0	35.74	Polyglutamine-binding protein 1	Q91VJ5	Pqbp1	Mus musculus
Q91VR2	28	2	2	17.45	14	1	1	11.07	42	2	2	0.41	17.45	ATP synthase subunit gamma, mitochondrial	Q91VR2	Atp5c1	Mus musculus
Q91VR5	9	1	1	2.84	22	2	2	5.41	31	2	2	0.41	5.41	ATP-dependent RNA helicase DDX1	Q91VR5	Ddx1	Mus musculus
Q91VW3	46	5	5	58.06	61	7	7	58.06	107	7	7	0	58.06	SH3 domain-binding glutamic acid-rich-like protein 3	Q91VW3	Sh3bgrl3	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q91W50	2	1	1	2.26	8	2	2	3.88	10	2	2	0.41	3.88	Cold shock domain-containing protein E1	Q91W50	Csde1	Mus musculus
Q91W90	11	4	4	13.91	1	1	1	3.84	12	4	4	0	13.91	Thioredoxin domain-containing protein 5	Q91W90	Txndc5	Mus musculus
Q91WJ8	2	1	1	3.07	12	2	2	4.92	14	2	2	0.41	4.92	Far upstream element-binding protein 1	Q91WJ8	Fubp1	Mus musculus
Q91WK0	8	3	3	8.19	0	0	0		8	3	3	0	8.19	Leucine-rich repeat flightless-interacting protein 2	Q91WK0	Lrrfip2	Mus musculus
Q91WK2	2	1	1	5.68	12	3	3	22.16	14	3	3	0	22.16	Eukaryotic translation initiation factor 3 subunit H	Q91WK2	Eif3h	Mus musculus
Q91WN1	24	4	4	23.55	11	3	3	23.17	35	4	4	0	23.55	DnaJ homolog subfamily C member 9	Q91WN1	Dnajc9	Mus musculus
Q91WQ3	0	0	0		5	2	2	6.63	5	2	2	0.41	6.63	Tyrosine--tRNA ligase, cytoplasmic	Q91WQ3	Yars	Mus musculus
Q91WU5	9	1	1	5.32	14	2	2	11.17	23	2	2	0.41	11.17	Arsenite methyltransferase	Q91WU5	As3mt	Mus musculus
Q91WV0	11	1	1	13.64	9	2	2	31.25	20	2	2	0.41	31.25	Protein Dr1	Q91WV0	Dr1	Mus musculus
Q91X72	94	9	9	30.22	98	10	10	33.91	192	11	11	0	33.91	Hemopexin	Q91X72	Hpx	Mus musculus
Q91XL1	94	9	9	28.07	44	2	2	7.89	138	9	9	0	28.07	Leucine-rich HEV glycoprotein	Q91XL1	Lrg1	Mus musculus
Q91YI4	46	6	6	22.93	99	8	8	31.95	145	9	9	0	31.95	Beta-arrestin-2	Q91YI4	Arrb2	Mus musculus
Q91YQ5	55	8	8	19.74	50	6	6	14.64	105	9	9	0	22.2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Q91YQ5	Rpn1	Mus musculus
Q91YR9	13	3	3	16.41	58	5	5	24.92	71	6	6	0	28.57	Prostaglandin reductase 1	Q91YR9	Ptgr1	Mus musculus
Q91YT0	7	2	2	10.13	11	4	4	20.26	18	4	4	0	20.26	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	Q91YT0	Ndufv1	Mus musculus
Q91YW3	16	3	3	9.33	23	1	1	5.95	39	3	3	0	9.33	DnaJ homolog subfamily C member 3	Q91YW3	Dnajc3	Mus musculus
Q91YX0	5	2	2	9.5	16	5	5	14.78	21	5	5	0	14.78	Protein THEMIS2	Q91YX0	Themis2	Mus musculus
Q91Z50	30	5	5	23.95	34	4	4	21.05	64	5	5	0	23.95	Flap endonuclease 1	Q91Z50	Fen1	Mus musculus
Q91ZJ5	4	2	2	7.48	13	3	3	9.84	17	3	3	0	9.84	UTP--glucose-1-phosphate uridylyltransferase	Q91ZJ5	Ugp2	Mus musculus
Q91ZU6	4	2	2	0.43	0	0	0		4	2	2	0.41	0.43	Dystonin	Q91ZU6	Dst	Mus musculus
Q91ZW3	9	3	3	3.43	7	2	2	2.57	16	4	4	0	4.85	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	Q91ZW3	Smarca5	Mus musculus
Q920B9	11	3	3	7.16	24	4	4	8.6	35	4	4	0	8.6	FACT complex subunit SPT16	Q920B9	Supt16h	Mus musculus
Q920E5	7	3	3	17.85	104	10	10	37.39	111	10	10	0	37.39	Farnesyl pyrophosphate synthase	Q920E5	Fdps	Mus musculus
Q921F2	96	6	6	34.78	101	10	10	38.65	197	10	10	0	38.65	TAR DNA-binding protein 43	Q921F2	Tardbp	Mus musculus
Q921F4	16	1	1	2.88	32	4	4	14.04	48	4	4	0	14.04	Heterogeneous nuclear ribonucleoprotein L-like	Q921F4	Hnrnpll	Mus musculus
Q921G6	37	5	5	16.47	26	6	6	19.71	63	6	6	0	19.71	Leucine-rich repeat and calponin homology domain-containing protein 4	Q921G6	Lrch4	Mus musculus
Q921G7	2	1	1	3.08	2	2	2	6.49	4	2	2	0.41	6.49	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	Q921G7	Etfdh	Mus musculus
Q921H8	26	6	6	22.88	40	5	5	19.34	66	6	6	0	22.88	3-ketoacyl-CoA thiolase A, peroxisomal	Q921H8	Acaa1a	Mus musculus
Q921I1	253	21	21	43.62	178	16	16	34.15	431	22	22	0	43.62	Serotransferrin	Q921I1	Tf	Mus musculus
Q921M3	87	11	11	17.58	63	10	10	13.31	150	13	13	0	17.58	Splicing factor 3B subunit 3	Q921M3	Sf3b3	Mus musculus
Q921M7	30	4	4	27.16	111	7	7	36.42	141	7	7	0	36.42	Protein FAM49B	Q921M7	Fam49b	Mus musculus
Q921Z5	9	1	1	10.1	19	2	2	21.72	28	2	2	0.41	21.72	Tumor necrosis factor alpha-induced protein 8	Q921Z5	Tnfaip8	Mus musculus
Q922B2	2	1	1	2.99	7	2	2	5.59	9	2	2	0.41	5.59	Aspartate--tRNA ligase, cytoplasmic	Q922B2	Dars	Mus musculus
Q922D4	9	2	2	4.27	13	5	5	9.24	22	5	5	0	9.24	Serine/threonine-protein phosphatase 6 regulatory subunit 3	Q922D4	Ppp6r3	Mus musculus
Q922F4	154	10	2	22.6	289	9	2	22.6	443	11	2	0.41	22.82	Tubulin beta-6 chain	Q922F4	Tubb6	Mus musculus
Q922P9	23	3	3	9.16	10	2	2	6.59	33	4	4	0	12.09	Putative oxidoreductase GLYR1	Q922P9	Glyr1	Mus musculus
Q922Q8	17	4	4	15.96	22	4	4	19.87	39	5	5	0	19.87	Leucine-rich repeat-containing protein 59	Q922Q8	Lrrc59	Mus musculus
Q922R8	258	17	17	55.45	178	12	12	35.68	436	18	18	0	55.45	Protein disulfide-isomerase A6	Q922R8	Pdia6	Mus musculus
Q922S4	28	5	5	11.68	53	9	9	21.4	81	11	11	0	25.98	cGMP-dependent 3',5'-cyclic phosphodiesterase	Q922S4	Pde2a	Mus musculus
Q923B6	37	7	7	22.55	13	3	3	13.19	50	7	7	0	22.55	Metalloreductase STEAP4	Q923B6	Steap4	Mus musculus
Q923L7	21	2	2	20.65	4	1	1	8.39	25	2	2	0.41	20.65	Ear6 protein	Q923L7	Ear6	Mus musculus
Q93092	14	2	2	4.75	29	3	3	8.01	43	3	3	0	8.01	Transaldolase	Q93092	Taldo1	Mus musculus
Q99J09	9	1	1	9.36	12	2	2	17.25	21	2	2	0.41	17.25	Methylosome protein 50	Q99J09	Wdr77	Mus musculus
Q99J62	0	0	0		2	2	2	16.21	2	2	2	0.41	16.21	Replication factor C subunit 4	Q99J62	Rfc4	Mus musculus
Q99J77	1	1	1	8.91	21	2	2	16.71	22	2	2	0.41	16.71	N-acetylneuraminic acid synthase (Sialic acid synthase)	Q99J77	Nans	Mus musculus
Q99JB2	12	4	4	23.8	11	2	2	14.16	23	4	4	0	23.8	Stomatin-like protein 2, mitochondrial	Q99JB2	Stoml2	Mus musculus
Q99JI4	3	2	2	8.48	19	3	3	12.34	22	3	3	0	12.34	26S proteasome non-ATPase regulatory subunit 6	Q99JI4	Psmd6	Mus musculus
Q99JR1	26	6	6	29.19	26	3	3	14.91	52	6	6	0	29.19	Sideroflexin-1	Q99JR1	Sfxn1	Mus musculus
Q99JT2	36	4	2	18.75	57	4	2	18.75	93	4	2	0.41	18.75	Serine/threonine-protein kinase 26	Q99JT2	Stk26	Mus musculus
Q99JW4	40	2	2	15.08	57	5	5	32.92	97	5	5	0	32.92	LIM and senescent cell antigen-like-containing domain protein 1	Q99JW4	Lims1	Mus musculus
Q99JX3	30	6	6	24.39	17	5	5	21.73	47	7	7	0	27.05	Golgi reassembly-stacking protein 2	Q99JX3	Gorasp2	Mus musculus
Q99JX4	2	1	1	5.08	11	4	4	15.51	13	4	4	0	15.51	Eukaryotic translation initiation factor 3 subunit M	Q99JX4	Eif3m	Mus musculus
Q99JX7	3	1	1	3.56	12	2	2	7.93	15	2	2	0.41	7.93	Nuclear RNA export factor 1	Q99JX7	Nxf1	Mus musculus
Q99JY0	8	2	2	4.42	6	3	3	9.26	14	3	3	0	9.26	Trifunctional enzyme subunit beta, mitochondrial	Q99JY0	Hadhb	Mus musculus
Q99JY9	284	17	17	55.98	434	19	19	58.13	718	21	21	0	59.33	Actin-related protein 3	Q99JY9	Actr3	Mus musculus
Q99K01	0	0	0		4	3	3	8.13	4	3	3	0	8.13	Pyridoxal-dependent decarboxylase domain-containing protein 1	Q99K01	Pdxdc1	Mus musculus
Q99K41	7	2	2	4.72	19	4	4	8.75	26	4	4	0	8.75	EMILIN-1	Q99K41	Emilin1	Mus musculus
Q99K48	35	1	1	4.86	37	2	2	4.86	72	2	2	0.41	4.86	Non-POU domain-containing octamer-binding protein	Q99K48	Nono	Mus musculus
Q99K85	0	0	0		2	2	2	13.51	2	2	2	0.41	13.51	Phosphoserine aminotransferase	Q99K85	Psat1	Mus musculus
Q99KE1	55	7	7	26.49	56	7	7	27.16	111	8	8	0	29.54	NAD-dependent malic enzyme, mitochondrial	Q99KE1	Me2	Mus musculus
Q99KH8	35	5	3	22.51	57	6	4	22.74	92	6	4	0	22.74	Serine/threonine-protein kinase 24	Q99KH8	Stk24	Mus musculus
Q99KI0	29	5	5	12.05	25	7	7	15.64	54	7	7	0	15.64	Aconitate hydratase, mitochondrial	Q99KI0	Aco2	Mus musculus
Q99KJ8	45	6	6	19.65	34	4	4	14.68	79	6	6	0	19.65	Dynactin subunit 2	Q99KJ8	Dctn2	Mus musculus
Q99KK7	7	2	2	5.96	102	14	14	31.17	109	14	14	0	31.17	Dipeptidyl peptidase 3	Q99KK7	Dpp3	Mus musculus
Q99KP6	30	3	3	17.26	49	3	3	13.69	79	4	4	0	17.26	Pre-mRNA-processing factor 19	Q99KP6	Prpf19	Mus musculus
Q99KY4	3	2	2	5.36	18	2	2	5.36	21	2	2	0.41	5.36	Cyclin-G-associated kinase	Q99KY4	Gak	Mus musculus
Q99L04	3	1	1	6.07	31	4	4	23.64	34	4	4	0	23.64	Dehydrogenase/reductase SDR family member 1	Q99L04	Dhrs1	Mus musculus
Q99L45	10	2	2	9.06	4	2	2	10.57	14	3	3	0	15.11	Eukaryotic translation initiation factor 2 subunit 2	Q99L45	Eif2s2	Mus musculus
Q99LB4	72	7	7	29.8	88	9	9	34.1	160	10	10	0	37.82	Capping protein (Actin filament), gelsolin-like	Q99LB4	Capg	Mus musculus
Q99LC3	8	2	2	9.3	21	2	2	9.3	29	2	2	0.41	9.3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	Q99LC3	Ndufa10	Mus musculus
Q99LC5	45	8	8	43.24	60	7	7	36.34	105	9	9	0	43.24	Electron transfer flavoprotein subunit alpha, mitochondrial	Q99LC5	Etfa	Mus musculus
Q99LF4	2	1	1	5.94	18	3	3	12.48	20	3	3	0	12.48	tRNA-splicing ligase RtcB homolog	Q99LF4	Rtcb	Mus musculus
Q99LL3	26	4	4	19.09	12	3	3	14.8	38	4	4	0	19.09	Carbohydrate sulfotransferase 12	Q99LL3	Chst12	Mus musculus
Q99LP6	10	2	2	9.22	11	2	2	9.22	21	2	2	0.41	9.22	GrpE protein homolog 1, mitochondrial	Q99LP6	Grpel1	Mus musculus
Q99LT0	47	2	2	36.36	51	3	3	36.36	98	3	3	0	36.36	Protein dpy-30 homolog	Q99LT0	Dpy30	Mus musculus
Q99LX0	52	4	4	31.22	88	5	5	31.22	140	5	5	0	31.22	Protein deglycase DJ-1	Q99LX0	Park7	Mus musculus
Q99M15	1	1	1	5.39	14	2	2	8.98	15	2	2	0.41	8.98	Proline-serine-threonine phosphatase-interacting protein 2	Q99M15	Pstpip2	Mus musculus
Q99M31	9	1	1	5.7	9	2	2	11.2	18	2	2	0.41	11.2	Heat shock 70 kDa protein 14	Q99M31	Hspa14	Mus musculus
Q99M46	14	2	2	15.64	3	2	2	15.64	17	2	2	0.41	15.64	DNA-directed RNA polymerase II subunit RPB3	Q99M46	Polr2c	Mus musculus
Q99MD9	20	2	2	6.6	26	3	3	10.22	46	3	3	0	10.22	Nuclear autoantigenic sperm protein	Q99MD9	Nasp	Mus musculus
Q99MK8	2	1	1	3.34	14	3	3	8.56	16	3	3	0	8.56	Beta-adrenergic receptor kinase 1	Q99MK8	Adrbk1	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q99MN1	14	2	2	7.56	37	2	2	7.56	51	2	2	0.41	7.56	Lysine--tRNA ligase	Q99MN1	Kars	Mus musculus
Q99MR6	2	2	2	3.66	0	0	0		2	2	2	0.41	3.66	Serrate RNA effector molecule homolog	Q99MR6	Srrt	Mus musculus
Q99N15	23	3	3	28.35	22	3	3	28.35	45	3	3	0	28.35	17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase	Q99N15	Hsd17b10	Mus musculus
Q99N16	0	0	0		3	2	2	3.24	3	2	2	0.41	3.24	Leukotriene-B(4) omega-hydroxylase 2	Q99N16	Cyp4f3	Mus musculus
Q99N80	9	2	2	6	3	2	2	6	12	2	2	0.41	6	Synaptotagmin-like protein 1	Q99N80	Sytl1	Mus musculus
Q99NB9	63	10	10	15.95	84	11	11	16.87	147	12	12	0	18.25	Splicing factor 3B subunit 1	Q99NB9	Sf3b1	Mus musculus
Q99P88	21	6	6	8.41	29	6	6	8.34	50	7	7	0	9.49	Nuclear pore complex protein Nup155	Q99P88	Nup155	Mus musculus
Q99PL5	61	7	7	6.6	42	6	6	5.42	103	7	7	0	6.6	Ribosome-binding protein 1	Q99PL5	Rrbp1	Mus musculus
Q99PT1	51	3	3	27.94	137	4	4	27.94	188	4	4	0	27.94	Rho GDP-dissociation inhibitor 1	Q99PT1	Arhgdia	Mus musculus
Q99PV0	10	4	4	3.55	31	8	8	6.55	41	9	9	0	7.45	Pre-mRNA-processing-splicing factor 8	Q99PV0	Prpf8	Mus musculus
Q9CPR4	15	5	5	20.11	14	3	3	19.57	29	5	5	0	20.11	60S ribosomal protein L17	Q9CPR4	Rpl17	Mus musculus
Q9CPV4	1	1	1	9.73	11	3	3	16.78	12	3	3	0	16.78	Glyoxalase domain-containing protein 4	Q9CPV4	Glod4	Mus musculus
Q9CPW4	68	4	4	45.7	81	4	4	45.7	149	4	4	0	45.7	Actin-related protein 2/3 complex subunit 5	Q9CPW4	Arpc5	Mus musculus
Q9CPX6	4	2	2	8.92	2	2	2	8.92	6	3	3	0	13.06	Ubiquitin-like-conjugating enzyme ATG3	Q9CPX6	Atg3	Mus musculus
Q9CQ19	60	4	2	34.3	47	4	2	25.58	107	5	2	0.41	36.05	Myosin regulatory light polypeptide 9	Q9CQ19	Myl9	Mus musculus
Q9CQ60	52	6	6	55.64	163	8	8	64.2	215	8	8	0	64.2	6-phosphogluconolactonase	Q9CQ60	Pgls	Mus musculus
Q9CQ92	6	2	2	15.79	4	1	1	7.24	10	2	2	0.41	15.79	Mitochondrial fission 1 protein	Q9CQ92	Fis1	Mus musculus
Q9CQC6	17	5	5	10.5	11	3	3	11.46	28	6	6	0	15.75	Basic leucine zipper and W2 domain-containing protein 1	Q9CQC6	Bzw1	Mus musculus
Q9CQE8	48	5	5	28.28	35	2	2	14.75	83	5	5	0	28.28	UPF0568 protein C14orf166 homolog	Q9CQE8		Mus musculus
Q9CQF3	11	2	2	20.7	12	2	2	12.78	23	3	3	0	20.7	Cleavage and polyadenylation specificity factor subunit 5	Q9CQF3	Nudt21	Mus musculus
Q9CQF9	13	2	2	8.32	9	2	2	8.32	22	2	2	0.41	8.32	Prenylcysteine oxidase	Q9CQF9	Pcyox1	Mus musculus
Q9CQI6	58	5	5	44.37	120	8	8	52.82	178	8	8	0	52.82	Coactosin-like protein	Q9CQI6	Cotl1	Mus musculus
Q9CQI7	2	2	2	10.22	1	1	1	10.22	3	2	2	0.41	10.22	U2 small nuclear ribonucleoprotein B"	Q9CQI7	Snrpb2	Mus musculus
Q9CQK7	0	0	0		10	2	2	19.75	10	2	2	0.41	19.75	RWD domain-containing protein 1	Q9CQK7	Rwdd1	Mus musculus
Q9CQM9	9	4	4	27.6	40	5	5	28.49	49	7	7	0	35.91	Glutaredoxin-3	Q9CQM9	Glrx3	Mus musculus
Q9CQR6	10	2	2	20.33	28	3	3	24.59	38	3	3	0	24.59	Serine/threonine-protein phosphatase 6 catalytic subunit	Q9CQR6	Ppp6c	Mus musculus
Q9CQV8	158	13	12	63.41	192	16	14	65.45	350	18	15	0	65.85	14-3-3 protein beta/alpha	Q9CQV8	Ywhab	Mus musculus
Q9CR16	10	2	2	8.92	11	1	1	5.68	21	2	2	0.41	8.92	Peptidyl-prolyl cis-trans isomerase D	Q9CR16	Ppid	Mus musculus
Q9CR68	7	2	2	17.52	1	1	1	8.03	8	2	2	0.41	17.52	Cytochrome b-c1 complex subunit Rieske, mitochondrial	Q9CR68	Uqcrfs1	Mus musculus
Q9CR86	1	1	1	25.68	5	3	3	25.68	6	3	3	0	25.68	Calcium-regulated heat stable protein 1	Q9CR86	Carhsp1	Mus musculus
Q9CRA5	12	3	3	17.79	12	2	2	13.42	24	3	3	0	17.79	Golgi phosphoprotein 3	Q9CRA5	Golph3	Mus musculus
Q9CRB2	13	2	2	25.49	3	1	1	12.42	16	2	2	0.41	25.49	H/ACA ribonucleoprotein complex subunit 2	Q9CRB2	Nhp2	Mus musculus
Q9CSU0	38	4	4	23.93	30	3	3	19.33	68	4	4	0	23.93	Regulation of nuclear pre-mRNA domain-containing protein 1B	Q9CSU0	Rprd1b	Mus musculus
Q9CU62	41	5	5	8.52	24	3	3	5.52	65	5	5	0	8.52	Structural maintenance of chromosomes protein 1A	Q9CU62	Smc1a	Mus musculus
Q9CVB6	150	11	11	46.33	221	12	12	47.33	371	14	14	0	50.33	Actin-related protein 2/3 complex subunit 2	Q9CVB6	Arpc2	Mus musculus
Q9CW03	6	2	2	3.04	4	2	2	3.37	10	3	3	0	4.68	Structural maintenance of chromosomes protein 3	Q9CW03	Smc3	Mus musculus
Q9CWF2	354	20	3	54.83	574	19	3	51.69	928	23	3	0	55.06	Tubulin beta-2B chain	Q9CWF2	Tubb2b	Mus musculus
Q9CWJ9	12	4	4	17.06	47	7	7	26.69	59	8	8	0	30.07	Bifunctional purine biosynthesis protein PURH	Q9CWJ9	Atic	Mus musculus
Q9CWK3	4	2	2	8.77	3	2	2	8.77	7	2	2	0.41	8.77	CD2 antigen cytoplasmic tail-binding protein 2	Q9CWK3	Cd2bp2	Mus musculus
Q9CWK8	2	1	1	4.62	2	2	2	6.74	4	2	2	0.41	6.74	Sorting nexin-2	Q9CWK8	Snx2	Mus musculus
Q9CWZ3	1	1	1	10.92	6	2	2	24.71	7	2	2	0.41	24.71	RNA-binding protein 8A	Q9CWZ3	Rbm8a	Mus musculus
Q9CWZ7	9	2	2	8.33	2	2	2	8.33	11	2	2	0.41	8.33	Gamma-soluble NSF attachment protein	Q9CWZ7	Napg	Mus musculus
Q9CX34	26	3	3	11.31	33	3	3	11.31	59	3	3	0	11.31	Protein SGT1 homolog	Q9CX34	Sugt1	Mus musculus
Q9CX56	7	1	1	8.78	27	3	3	17	34	3	3	0	17	26S proteasome non-ATPase regulatory subunit 8	Q9CX56	Psmd8	Mus musculus
Q9CX86	39	3	3	14.1	30	3	3	14.1	69	3	3	0	14.1	Heterogeneous nuclear ribonucleoprotein A0	Q9CX86	Hnrnpa0	Mus musculus
Q9CXF4	2	2	2	5.07	9	2	2	5.07	11	2	2	0.41	5.07	TBC1 domain family member 15	Q9CXF4	Tbc1d15	Mus musculus
Q9CXI5	30	5	5	35.2	16	4	4	34.08	46	5	5	0	35.2	Mesencephalic astrocyte-derived neurotrophic factor	Q9CXI5	Manf	Mus musculus
Q9CXR1	4	2	2	12.43	1	1	1	9.47	5	2	2	0.41	12.43	Dehydrogenase/reductase SDR family member 7	Q9CXR1	Dhrs7	Mus musculus
Q9CXW4	15	3	3	15.73	16	1	1	7.87	31	3	3	0	15.73	60S ribosomal protein L11	Q9CXW4	Rpl11	Mus musculus
Q9CXY6	8	3	3	18.21	22	2	2	11.03	30	3	3	0	18.21	Interleukin enhancer-binding factor 2	Q9CXY6	Ilf2	Mus musculus
Q9CY50	33	3	3	22.38	30	2	2	18.53	63	3	3	0	22.38	Translocon-associated protein subunit alpha	Q9CY50	Ssr1	Mus musculus
Q9CY58	7	3	3	12.78	10	4	4	12.78	17	4	4	0	12.78	Plasminogen activator inhibitor 1 RNA-binding protein	Q9CY58	Serbp1	Mus musculus
Q9CYA0	70	5	5	28.86	45	3	3	19.14	115	5	5	0	28.86	Cysteine-rich with EGF-like domain protein 2	Q9CYA0	Creld2	Mus musculus
Q9CYA6	12	3	3	9.17	5	1	1	2.82	17	3	3	0	9.17	Zinc finger CCHC domain-containing protein 8	Q9CYA6	Zcchc8	Mus musculus
Q9CYG7	1	1	1	4.85	17	2	2	10.68	18	2	2	0.41	10.68	Mitochondrial import receptor subunit TOM34	Q9CYG7	Tomm34	Mus musculus
Q9CYL5	24	4	4	40.26	21	2	2	25.32	45	4	4	0	40.26	Golgi-associated plant pathogenesis-related protein 1	Q9CYL5	Glipr2	Mus musculus
Q9CZ04	6	2	2	16.73	13	1	1	10.91	19	2	2	0.41	16.73	COP9 signalosome complex subunit 7a	Q9CZ04	Cops7a	Mus musculus
Q9CZ13	112	8	8	26.46	93	8	8	23.96	205	9	9	0	26.88	Cytochrome b-c1 complex subunit 1, mitochondrial	Q9CZ13	Uqcrc1	Mus musculus
Q9CZ30	1	1	1	3.79	13	2	2	9.85	14	2	2	0.41	9.85	Obg-like ATPase 1	Q9CZ30	Ola1	Mus musculus
Q9CZ44	48	3	3	15.68	60	5	5	24.59	108	5	5	0	24.59	NSFL1 cofactor p47	Q9CZ44	Nsfl1c	Mus musculus
Q9CZD3	2	2	2	4.66	23	4	4	9.33	25	4	4	0	9.33	Glycine--tRNA ligase	Q9CZD3	Gars	Mus musculus
Q9CZN7	33	6	6	17.26	59	7	7	18.25	92	9	9	0	20.83	Serine hydroxymethyltransferase	Q9CZN7	Shmt2	Mus musculus
Q9CZU6	22	4	4	12.93	4	2	2	6.03	26	4	4	0	12.93	Citrate synthase, mitochondrial	Q9CZU6	Cs	Mus musculus
Q9CZX8	5	2	2	17.93	13	2	2	17.93	18	2	2	0.41	17.93	40S ribosomal protein S19	Q9CZX8	Rps19	Mus musculus
Q9D020	0	0	0		25	4	4	26.89	25	4	4	0	26.89	Cytosolic 5'-nucleotidase 3A	Q9D020	Nt5c3a	Mus musculus
Q9D0E1	27	4	4	8.09	11	2	2	5.21	38	4	4	0	8.09	Heterogeneous nuclear ribonucleoprotein M	Q9D0E1	Hnrnpm	Mus musculus
Q9D0F3	15	1	1	6.19	8	2	2	10.06	23	2	2	0.41	10.06	Protein ERGIC-53	Q9D0F3	Lman1	Mus musculus
Q9D0F9	3	2	2	8.36	19	6	6	18.51	22	6	6	0	18.51	Phosphoglucomutase-1	Q9D0F9	Pgm1	Mus musculus
Q9D0I9	10	3	3	9.09	39	3	3	9.09	49	3	3	0	9.09	Arginine--tRNA ligase, cytoplasmic	Q9D0I9	Rars	Mus musculus
Q9D0K2	14	3	3	10	18	5	5	16.92	32	5	5	0	16.92	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	Q9D0K2	Oxct1	Mus musculus
Q9D0L8	1	1	1	4.09	17	4	4	16.56	18	4	4	0	16.56	mRNA cap guanine-N7 methyltransferase	Q9D0L8	Rnmt	Mus musculus
Q9D0M1	0	0	0		2	2	2	7.02	2	2	2	0.41	7.02	Phosphoribosyl pyrophosphate synthase-associated protein 1	Q9D0M1	Prpsap1	Mus musculus
Q9D0M3	47	5	5	18.46	39	2	2	12.31	86	5	5	0	18.46	Cytochrome c1, heme protein, mitochondrial	Q9D0M3	Cyc1	Mus musculus
Q9D0T1	0	0	0		6	2	2	18.75	6	2	2	0.41	18.75	NHP2-like protein 1	Q9D0T1	Nhp2l1	Mus musculus
Q9D154	50	9	9	28.76	266	17	17	54.88	316	17	17	0	54.88	Leukocyte elastase inhibitor A	Q9D154	Serpinb1a	Mus musculus
Q9D1A2	9	2	2	9.89	20	2	2	9.89	29	2	2	0.41	9.89	Cytosolic non-specific dipeptidase	Q9D1A2	Cndp2	Mus musculus
Q9D1G1	20	3	3	21.39	15	3	2	22.89	35	4	3	0	26.87	Ras-related protein Rab-1B	Q9D1G1	Rab1b	Mus musculus
Q9D1K2	14	2	2	21.85	23	1	1	20.17	37	2	2	0.41	21.85	V-type proton ATPase subunit F	Q9D1K2	Atp6v1f	Mus musculus
Q9D1L9	17	2	2	43.96	5	1	1	21.98	22	2	2	0.41	43.96	Ragulator complex protein LAMTOR5	Q9D1L9	Lamtor5	Mus musculus
Q9D1M0	3	2	2	11.8	6	2	2	11.8	9	2	2	0.41	11.8	Protein SEC13 homolog	Q9D1M0	Sec13	Mus musculus
Q9D1P4	2	1	1	4.53	14	2	2	9.06	16	2	2	0.41	9.06	Cysteine and histidine-rich domain-containing protein 1	Q9D1P4	Chordc1	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9D1Q6	50	6	6	32.76	26	3	3	18.47	76	6	6	0	32.76	Endoplasmic reticulum resident protein 44	Q9D1Q6	Erp44	Mus musculus
Q9D2C2	2	1	1	3.59	17	3	3	12.03	19	3	3	0	12.03	Protein SAAL1	Q9D2C2	Saal1	Mus musculus
Q9D2G2	2	2	2	9.69	0	0	0		2	2	2	0.41	9.69	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	Q9D2G2	Dlst	Mus musculus
Q9D2V7	111	11	11	25.27	148	15	15	31.89	259	17	17	0	36.33	Coronin-7	Q9D2V7	Coro7	Mus musculus
Q9D3D9	5	2	2	35.71	7	1	1	23.81	12	2	2	0.41	35.71	ATP synthase subunit delta, mitochondrial	Q9D3D9	Atp5d	Mus musculus
Q9D554	29	8	8	29.34	24	4	4	14.17	53	8	8	0	29.34	Splicing factor 3A subunit 3	Q9D554	Sf3a3	Mus musculus
Q9D5T0	2	2	2	11.63	0	0	0		2	2	2	0.41	11.63	ATPase family AAA domain-containing protein 1	Q9D5T0	Atad1	Mus musculus
Q9D5V6	4	3	3	25.21	15	3	3	25.21	19	3	3	0	25.21	Synapse-associated protein 1	Q9D5V6	Syap1	Mus musculus
Q9D6F9	343	17	1	52.03	513	20	2	52.48	856	21	2	0.41	52.48	Tubulin beta-4A chain	Q9D6F9	Tubb4a	Mus musculus
Q9D6J6	15	4	4	30.65	12	4	4	31.05	27	5	5	0	31.05	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	Q9D6J6	Ndufv2	Mus musculus
Q9D6R2	11	4	4	12.3	5	2	2	9.56	16	4	4	0	12.3	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Q9D6R2	Idh3a	Mus musculus
Q9D6Y7	3	2	2	11.16	14	3	3	22.75	17	4	4	0	27.47	Mitochondrial peptide methionine sulfoxide reductase	Q9D6Y7	Msra	Mus musculus
Q9D6Y9	1	1	1	2.42	11	2	2	5.41	12	2	2	0.41	5.41	1,4-alpha-glucan-branching enzyme	Q9D6Y9	Gbe1	Mus musculus
Q9D6Z1	15	1	1	5.17	15	3	3	9.83	30	3	3	0	9.83	Nucleolar protein 56	Q9D6Z1	Nop56	Mus musculus
Q9D7M8	3	2	2	21.83	0	0	0		3	2	2	0.41	21.83	DNA-directed RNA polymerase II subunit RPB4	Q9D7M8	Polr2d	Mus musculus
Q9D7S9	2	2	2	15.53	3	1	1	8.22	5	2	2	0.41	15.53	Charged multivesicular body protein 5	Q9D7S9	Chmp5	Mus musculus
Q9D824	15	3	3	16.7	8	2	2	11.19	23	3	3	0	16.7	Pre-mRNA 3'-end-processing factor FIP1	Q9D824	Fip1l1	Mus musculus
Q9D855	11	2	2	25.23	1	1	1	13.51	12	2	2	0.41	25.23	Cytochrome b-c1 complex subunit 7	Q9D855	Uqcrb	Mus musculus
Q9D883	17	3	3	15.06	7	2	2	14.64	24	3	3	0	15.06	Splicing factor U2AF 35 kDa subunit	Q9D883	U2af1	Mus musculus
Q9D892	2	2	2	25.25	20	2	2	25.25	22	2	2	0.41	25.25	Inosine triphosphate pyrophosphatase	Q9D892	Itpa	Mus musculus
Q9D8B3	12	2	2	13.39	9	2	2	13.39	21	2	2	0.41	13.39	Charged multivesicular body protein 4b	Q9D8B3	Chmp4b	Mus musculus
Q9D8E6	30	4	4	10.26	21	5	5	12.65	51	5	5	0	12.65	60S ribosomal protein L4	Q9D8E6	Rpl4	Mus musculus
Q9D8N0	50	8	8	29.75	99	10	10	36.84	149	10	10	0	36.84	Elongation factor 1-gamma	Q9D8N0	Eef1g	Mus musculus
Q9D8T2	1	1	1	5.75	6	3	3	11.5	7	3	3	0	11.5	Gasdermin-D	Q9D8T2	Gsdmdc1	Mus musculus
Q9D8W5	8	1	1	2.85	11	2	2	7.46	19	2	2	0.41	7.46	26S proteasome non-ATPase regulatory subunit 12	Q9D8W5	Psmd12	Mus musculus
Q9D8Y0	5	1	1	6.25	15	2	2	6.67	20	2	2	0.41	6.67	EF-hand domain-containing protein D2	Q9D8Y0	Efhd2	Mus musculus
Q9D8Y7	0	0	0		7	2	2	21.74	7	2	2	0.41	21.74	Tumor necrosis factor alpha-induced protein 8-like protein 2	Q9D8Y7	Tnfaip8l2	Mus musculus
Q9D906	5	1	1	4.3	15	5	5	14.47	20	5	5	0	14.47	Ubiquitin-like modifier-activating enzyme ATG7	Q9D906	Atg7	Mus musculus
Q9D964	9	1	1	4.73	7	2	2	8.75	16	2	2	0.41	8.75	Glycine amidinotransferase, mitochondrial	Q9D964	Gatm	Mus musculus
Q9DAR7	0	0	0		24	4	4	19.53	24	4	4	0	19.53	m7GpppX diphosphatase	Q9DAR7	Dcps	Mus musculus
Q9DAU1	11	2	2	13.41	4	1	1	6.88	15	2	2	0.41	13.41	Protein canopy homolog 3	Q9DAU1	Cnpy3	Mus musculus
Q9DB05	39	4	4	25.42	15	3	3	16.95	54	4	4	0	25.42	Alpha-soluble NSF attachment protein	Q9DB05	Napa	Mus musculus
Q9DB15	7	2	2	12.44	17	2	2	12.44	24	2	2	0.41	12.44	39S ribosomal protein L12, mitochondrial	Q9DB15	Mrpl12	Mus musculus
Q9DB20	20	2	2	12.21	30	2	2	12.21	50	2	2	0.41	12.21	ATP synthase subunit O, mitochondrial	Q9DB20	Atp5o	Mus musculus
Q9DB77	25	4	4	22.08	43	4	4	18.98	68	5	5	0	22.08	Cytochrome b-c1 complex subunit 2, mitochondrial	Q9DB77	Uqcrc2	Mus musculus
Q9DBC7	1	1	1	6.3	10	3	3	13.91	11	3	3	0	13.91	cAMP-dependent protein kinase type I-alpha regulatory subunit	Q9DBC7	Prkar1a	Mus musculus
Q9DBG3	64	9	6	18.89	91	12	9	23.91	155	13	10	0	26.15	AP-2 complex subunit beta	Q9DBG3	Ap2b1	Mus musculus
Q9DBG5	24	5	5	23.57	46	8	8	34.78	70	8	8	0	34.78	Perilipin-3	Q9DBG5	Plin3	Mus musculus
Q9DBG6	124	12	12	33.91	106	12	12	33.44	230	14	14	0	39.78	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	Q9DBG6	Rpn2	Mus musculus
Q9DBJ1	33	8	8	40.94	126	10	10	40.94	159	10	10	0	40.94	Phosphoglycerate mutase 1	Q9DBJ1	Pgam1	Mus musculus
Q9DBL1	3	2	2	9.26	6	2	2	9.03	9	3	3	0	14.12	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Q9DBL1	Acadsb	Mus musculus
Q9DBL9	0	0	0		10	2	2	10.54	10	2	2	0.41	10.54	1-acylglycerol-3-phosphate O-acyltransferase ABHD5	Q9DBL9	Abhd5	Mus musculus
Q9DBR0	10	2	2	7.28	5	2	2	7.28	15	2	2	0.41	7.28	A-kinase anchor protein 8	Q9DBR0	Akap8	Mus musculus
Q9DBR1	0	0	0		10	2	2	4.1	10	2	2	0.41	4.1	5'-3' exoribonuclease 2	Q9DBR1	Xrn2	Mus musculus
Q9DBR7	12	2	2	2.24	13	4	4	6.03	25	4	4	0	6.03	Protein phosphatase 1 regulatory subunit 12A	Q9DBR7	Ppp1r12a	Mus musculus
Q9DBS1	6	2	2	10.25	13	2	2	10.25	19	2	2	0.41	10.25	Transmembrane protein 43	Q9DBS1	Tmem43	Mus musculus
Q9DBT5	7	1	1	2.26	13	2	2	5.64	20	2	2	0.41	5.64	AMP deaminase 2	Q9DBT5	Ampd2	Mus musculus
Q9DBZ5	1	1	1	5.05	6	3	3	26.61	7	4	4	0	26.61	Eukaryotic translation initiation factor 3 subunit K	Q9DBZ5	Eif3k	Mus musculus
Q9DC51	437	10	4	35.31	267	7	2	27.68	704	10	4	0	35.31	Guanine nucleotide-binding protein G(k) subunit alpha	Q9DC51	Gnai3	Mus musculus
Q9DCC5	212	8	8	44.81	122	7	7	38.25	334	8	8	0	44.81	Cbx3 protein	Q9DCC5	Cbx3	Mus musculus
Q9DCD0	149	14	14	36.44	372	20	20	39.75	521	20	20	0	39.75	6-phosphogluconate dehydrogenase, decarboxylating	Q9DCD0	Pgd	Mus musculus
Q9DCH4	32	3	3	12.47	42	3	3	12.47	74	3	3	0	12.47	Eukaryotic translation initiation factor 3 subunit F	Q9DCH4	Eif3f	Mus musculus
Q9DCJ5	6	1	1	10.47	3	2	2	22.67	9	2	2	0.41	22.67	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	Q9DCJ5	Ndufa8	Mus musculus
Q9DCL9	1	1	1	8	25	4	4	18.12	26	4	4	0	18.12	Multifunctional protein ADE2	Q9DCL9	Paics	Mus musculus
Q9DCM0	29	4	4	31.5	16	2	2	19.29	45	4	4	0	31.5	Persulfide dioxygenase ETHE1, mitochondrial	Q9DCM0	Ethe1	Mus musculus
Q9DCR2	11	1	1	7.77	9	2	2	17.1	20	2	2	0.41	17.1	AP-3 complex subunit sigma-1	Q9DCR2	Ap3s1	Mus musculus
Q9DCS9	4	1	1	7.95	6	2	2	15.34	10	3	3	0	16.48	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Q9DCS9	Ndufb10	Mus musculus
Q9DCW4	23	3	3	19.61	27	4	4	24.31	50	4	4	0	24.31	Electron transfer flavoprotein subunit beta	Q9DCW4	Etfb	Mus musculus
Q9EPB4	5	1	1	8.81	30	4	4	31.61	35	4	4	0	31.61	Apoptosis-associated speck-like protein containing a CARD	Q9EPB4	Pycard	Mus musculus
Q9EPJ9	9	2	2	12.56	14	2	2	12.56	23	2	2	0.41	12.56	ADP-ribosylation factor GTPase-activating protein 1	Q9EPJ9	Arfgap1	Mus musculus
Q9EPK2	9	2	2	7.49	0	0	0		9	2	2	0.41	7.49	Protein XRP2	Q9EPK2	Rp2	Mus musculus
Q9EPL4	2	1	1	10.69	5	2	2	13.84	7	2	2	0.41	13.84	Methyltransferase-like protein 9	Q9EPL4	Mettl9	Mus musculus
Q9EPL8	0	0	0		15	3	3	4.72	15	3	3	0	4.72	Importin-7	Q9EPL8	Ipo7	Mus musculus
Q9EPU0	5	2	2	1.87	13	4	4	5.25	18	4	4	0	5.25	Regulator of nonsense transcripts 1	Q9EPU0	Upf1	Mus musculus
Q9EQ06	22	3	3	13.09	16	2	2	8.39	38	3	3	0	13.09	Estradiol 17-beta-dehydrogenase 11	Q9EQ06	Hsd17b11	Mus musculus
Q9EQ32	16	2	2	4.56	14	3	3	7.89	30	3	3	0	7.89	Phosphoinositide 3-kinase adapter protein 1	Q9EQ32	Pik3ap1	Mus musculus
Q9EQG9	8	2	2	7.05	31	7	7	19.39	39	7	7	0	19.39	Collagen type IV alpha-3-binding protein	Q9EQG9	Col4a3bp	Mus musculus
Q9EQH2	6	2	2	3.01	0	0	0		6	2	2	0.41	3.01	Endoplasmic reticulum aminopeptidase 1	Q9EQH2	Erap1	Mus musculus
Q9EQH3	58	9	9	17.21	58	10	10	19.97	116	11	11	0	20.23	Vacuolar protein sorting-associated protein 35	Q9EQH3	Vps35	Mus musculus
Q9EQI5	3	1	1	30.97	11	2	2	30.97	14	2	2	0.41	30.97	Chemokine (C-X-C motif) ligand 7, isoform CRA_b	Q9EQI5	Ppbp	Mus musculus
Q9EQK5	86	11	11	26.83	139	18	18	39.14	225	19	19	0	39.14	Major vault protein	Q9EQK5	Mvp	Mus musculus
Q9EQU5	74	6	6	20.76	46	6	6	27.34	120	8	8	0	32.18	Protein SET	Q9EQU5	Set	Mus musculus
Q9ER72	2	1	1	3.85	18	2	2	3.85	20	2	2	0.41	3.85	Cysteine--tRNA ligase, cytoplasmic	Q9ER72	Cars	Mus musculus
Q9ERB0	44	4	4	26.92	17	4	4	27.69	61	5	5	0	27.69	Synaptosomal-associated protein 29	Q9ERB0	Snap29	Mus musculus
Q9ERD8	0	0	0		10	4	4	17.22	10	4	4	0	17.22	Gamma-parvin	Q9ERD8	Parvg	Mus musculus
Q9ERF3	9	1	1	6.89	15	2	2	13.44	24	2	2	0.41	13.44	WD repeat-containing protein 61	Q9ERF3	Wdr61	Mus musculus
Q9ERI2	5	2	2	13.12	8	1	1	7.24	13	2	2	0.41	13.12	Ras-related protein Rab-27A	Q9ERI2	Rab27a	Mus musculus
Q9ERK4	12	1	1	2.16	37	4	4	8.65	49	4	4	0	8.65	Exportin-2	Q9ERK4	Cse1l	Mus musculus
Q9ERL7	12	2	2	9.15	9	2	2	9.15	21	2	2	0.41	9.15	Glia maturation factor gamma	Q9ERL7	Gmfg	Mus musculus
Q9ERR7	30	3	3	37.65	20	4	4	37.65	50	4	4	0	37.65	15 kDa selenoprotein	Q9ERR7	Sep15	Mus musculus
Q9ERU9	8	4	4	2.98	4	3	3	2	12	4	4	0	2.98	E3 SUMO-protein ligase RanBP2	Q9ERU9	Ranbp2	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9ES52	23	3	3	4.28	31	5	5	7.39	54	5	5	0	7.39	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	Q9ES52	Inpp5d	Mus musculus
Q9ESP1	26	3	3	36.65	26	2	2	26.7	52	3	3	0	36.65	Stromal cell-derived factor 2-like protein 1	Q9ESP1	Sdf2l1	Mus musculus
Q9EST5	67	4	4	25.74	130	6	6	36.4	197	6	6	0	36.4	Acidic leucine-rich nuclear phosphoprotein 32 family member B	Q9EST5	Anp32b	Mus musculus
Q9ET01	98	14	14	17.53	247	25	23	31.29	345	25	23	0	31.29	Glycogen phosphorylase, liver form	Q9ET01	Pygl	Mus musculus
Q9ET66	32	3	3	14.11	14	2	2	8.79	46	3	3	0	14.11	Peptidase inhibitor 16	Q9ET66	Pi16	Mus musculus
Q9JHF5	19	7	7	12.11	16	2	2	7.31	35	7	7	0	12.11	V-type proton ATPase subunit a	Q9JHF5	Tcirg1	Mus musculus
Q9JHJ0	74	6	6	21.02	61	6	6	21.02	135	6	6	0	21.02	Tropomodulin-3	Q9JHJ0	Tmod3	Mus musculus
Q9JHK5	61	4	4	16.86	88	7	7	29.71	149	7	7	0	29.71	Pleckstrin	Q9JHK5	Plek	Mus musculus
Q9JHS3	19	2	2	45.6	13	1	1	30.4	32	2	2	0.41	45.6	Ragulator complex protein LAMTOR2	Q9JHS3	Lamtor2	Mus musculus
Q9JHU4	73	14	14	6.18	133	20	20	7.97	206	21	21	0	8.48	Cytoplasmic dynein 1 heavy chain 1	Q9JHU4	Dync1h1	Mus musculus
Q9JIF0	1	1	1	3.77	2	2	2	7.55	3	3	3	0	11.32	Protein arginine N-methyltransferase 1	Q9JIF0	Prmt1	Mus musculus
Q9JIF7	31	7	7	15.95	45	6	6	14.8	76	7	7	0	15.95	Coatomer subunit beta	Q9JIF7	Copb1	Mus musculus
Q9JIX8	46	6	6	6.73	21	3	3	4.63	67	6	6	0	6.73	Apoptotic chromatin condensation inducer in the nucleus	Q9JIX8	Acin1	Mus musculus
Q9JIY5	3	2	2	5.46	1	1	1	2.84	4	2	2	0.41	5.46	Serine protease HTRA2, mitochondrial	Q9JIY5	Htra2	Mus musculus
Q9JJ00	16	3	3	21.04	9	1	1	6.1	25	3	3	0	21.04	Phospholipid scramblase 1	Q9JJ00	Plscr1	Mus musculus
Q9JJ28	55	12	12	18.96	59	10	10	15.42	114	13	13	0	18.96	Protein flightless-1 homolog	Q9JJ28	Flii	Mus musculus
Q9JJU8	5	1	1	22.81	22	3	3	47.37	27	3	3	0	47.37	SH3 domain-binding glutamic acid-rich-like protein	Q9JJU8	Sh3bgrl	Mus musculus
Q9JKC8	1	1	1	4.07	18	5	5	15.55	19	5	5	0	15.55	AP-3 complex subunit mu-1	Q9JKC8	Ap3m1	Mus musculus
Q9JKF1	646	50	50	37.48	669	48	48	34.76	1315	53	53	0	37.48	Ras GTPase-activating-like protein IQGAP1	Q9JKF1	Iqgap1	Mus musculus
Q9JKR6	100	9	9	15.72	65	7	7	11.01	165	10	10	0	15.72	Hypoxia up-regulated protein 1	Q9JKR6	Hyou1	Mus musculus
Q9JKV1	8	2	2	4.91	12	2	2	4.91	20	2	2	0.41	4.91	Proteasomal ubiquitin receptor ADRM1	Q9JKV1	Adrm1	Mus musculus
Q9JKY5	4	2	2	5.43	10	2	2	5.43	14	2	2	0.41	5.43	Huntingtin-interacting protein 1-related protein	Q9JKY5	Hip1r	Mus musculus
Q9JL26	79	9	9	11.88	97	9	9	11.24	176	10	10	0	11.88	Formin-like protein 1	Q9JL26	Fmnl1	Mus musculus
Q9JL62	0	0	0		13	2	2	18.66	13	2	2	0.41	18.66	Glycolipid transfer protein	Q9JL62	Gltp	Mus musculus
Q9JLF6	15	3	3	11.66	11	3	3	11.66	26	3	3	0	11.66	Protein-glutamine gamma-glutamyltransferase K	Q9JLF6	Tgm1	Mus musculus
Q9JLJ2	3	1	1	4.66	9	3	3	8.91	12	3	3	0	8.91	4-trimethylaminobutyraldehyde dehydrogenase	Q9JLJ2	Aldh9a1	Mus musculus
Q9JLQ2	39	3	3	9.32	48	5	5	14.41	87	5	5	0	14.41	ARF GTPase-activating protein GIT2	Q9JLQ2	Git2	Mus musculus
Q9JLV6	62	9	9	31.8	99	11	11	27.97	161	13	13	0	31.99	Bifunctional polynucleotide phosphatase/kinase	Q9JLV6	Pnkp	Mus musculus
Q9JM14	0	0	0		19	2	2	23	19	2	2	0.41	23	5'(3')-deoxyribonucleotidase, cytosolic type	Q9JM14	Nt5c	Mus musculus
Q9JM76	42	4	4	25.28	71	5	5	34.27	113	6	6	0	40.45	Actin-related protein 2/3 complex subunit 3	Q9JM76	Arpc3	Mus musculus
Q9JMA1	23	3	3	14.4	43	2	2	10.75	66	3	3	0	14.4	Ubiquitin carboxyl-terminal hydrolase 14	Q9JMA1	Usp14	Mus musculus
Q9JMH6	3	2	2	7.5	43	6	6	23.98	46	6	6	0	23.98	Thioredoxin reductase 1, cytoplasmic	Q9JMH6	Txnrd1	Mus musculus
Q9JMH9	72	8	8	6.44	18	4	4	3.76	90	8	8	0	6.44	Unconventional myosin-XVIIIa	Q9JMH9	Myo18a	Mus musculus
Q9QUG9	0	0	0		5	2	2	3.95	5	2	2	0.41	3.95	RAS guanyl-releasing protein 2	Q9QUG9	Rasgrp2	Mus musculus
Q9QUH0	20	1	1	27.1	114	7	7	48.6	134	7	7	0	48.6	Glutaredoxin-1	Q9QUH0	Glrx	Mus musculus
Q9QUI0	81	9	6	45.08	95	9	6	45.08	176	10	7	0	45.08	Transforming protein RhoA	Q9QUI0	Rhoa	Mus musculus
Q9QUM0	232	19	19	34.56	118	17	17	30.01	350	22	22	0	34.56	Integrin alpha-IIb	Q9QUM0	Itga2b	Mus musculus
Q9QUM9	1	1	1	4.88	6	2	2	12.2	7	2	2	0.41	12.2	Proteasome subunit alpha type-6	Q9QUM9	Psma6	Mus musculus
Q9QUN7	3	3	3	7.27	0	0	0		3	3	3	0	7.27	Toll-like receptor 2	Q9QUN7	Tlr2	Mus musculus
Q9QUR6	0	0	0		34	5	5	12.54	34	5	5	0	12.54	Prolyl endopeptidase	Q9QUR6	Prep	Mus musculus
Q9QWR8	7	3	3	11.81	4	2	2	7.23	11	4	4	0	14.46	Alpha-N-acetylgalactosaminidase	Q9QWR8	Naga	Mus musculus
Q9QX47	18	5	5	4.79	11	3	3	3.52	29	5	5	0	4.79	Protein SON	Q9QX47	Son	Mus musculus
Q9QXK3	81	7	5	16.42	76	9	7	18.94	157	9	7	0	18.94	Coatomer subunit gamma-2	Q9QXK3	Copg2	Mus musculus
Q9QXS1	332	48	48	16.84	243	38	38	13.88	575	54	54	0	18.61	Plectin	Q9QXS1	Plec	Mus musculus
Q9QXT0	12	3	3	26.37	0	0	0		12	3	3	0	26.37	Protein canopy homolog 2	Q9QXT0	Cnpy2	Mus musculus
Q9QXZ0	12	3	3	1.12	13	5	5	1.89	25	6	6	0	2.16	Microtubule-actin cross-linking factor 1	Q9QXZ0	Macf1	Mus musculus
Q9QY06	5	2	2	2.37	6	1	1	1.37	11	2	2	0.41	2.37	Unconventional myosin-IXb	Q9QY06	Myo9b	Mus musculus
Q9QYB5	4	3	3	11.47	6	3	3	11.61	10	4	4	0	15.44	Gamma-adducin	Q9QYB5	Add3	Mus musculus
Q9QYC0	39	5	5	16.87	31	7	7	21.77	70	7	7	0	21.77	Alpha-adducin	Q9QYC0	Add1	Mus musculus
Q9QYJ0	5	2	2	11.41	5	3	3	11.41	10	3	3	0	11.41	DnaJ homolog subfamily A member 2	Q9QYJ0	Dnaja2	Mus musculus
Q9QZ06	5	4	4	28.83	6	2	2	9.85	11	4	4	0	28.83	Toll-interacting protein	Q9QZ06	Tollip	Mus musculus
Q9QZD9	41	4	4	24.31	18	4	4	24.31	59	4	4	0	24.31	Eukaryotic translation initiation factor 3 subunit I	Q9QZD9	Eif3i	Mus musculus
Q9QZE5	122	14	12	28.6	118	13	11	26.2	240	16	14	0	31.81	Coatomer subunit gamma-1	Q9QZE5	Copg1	Mus musculus
Q9QZK7	30	7	7	27.25	47	6	6	27.03	77	8	8	0	34.68	Docking protein 3	Q9QZK7	Dok3	Mus musculus
Q9QZQ8	3829	28	16	51.61	2650	20	10	47.85	6479	29	17	0	51.61	Core histone macro-H2A.1	Q9QZQ8	H2afy	Mus musculus
Q9QZS3	2	2	2	5.97	0	0	0		2	2	2	0.41	5.97	Protein numb homolog	Q9QZS3	Numb	Mus musculus
Q9QZU3	0	0	0		11	4	4	11.99	11	4	4	0	11.99	Platelet glycoprotein V (Fragment)	Q9QZU3	Gp5	Mus musculus
Q9R059	26	2	2	17.65	21	4	4	30.45	47	4	4	0	30.45	Four and a half LIM domains protein 3	Q9R059	Fhl3	Mus musculus
Q9R062	3	2	2	15.02	20	3	3	25.53	23	3	3	0	25.53	Glycogenin-1	Q9R062	Gyg1	Mus musculus
Q9R078	17	2	2	18.15	16	2	2	18.15	33	2	2	0.41	18.15	5'-AMP-activated protein kinase subunit beta-1	Q9R078	Prkab1	Mus musculus
Q9R0P3	14	4	4	34.75	116	9	9	54.61	130	9	9	0	54.61	S-formylglutathione hydrolase	Q9R0P3	Esd	Mus musculus
Q9R0P5	55	4	4	36.36	329	5	5	40.61	384	6	6	0	47.27	Destrin	Q9R0P5	Dstn	Mus musculus
Q9R0Q7	6	3	3	20	45	5	5	27.5	51	5	5	0	27.5	Prostaglandin E synthase 3	Q9R0Q7	Ptges3	Mus musculus
Q9R0U0	17	2	2	10.31	8	1	1	6.11	25	2	2	0.41	10.31	Serine/arginine-rich splicing factor 10	Q9R0U0	Srsf10	Mus musculus
Q9R111	108	12	12	41.41	210	11	11	43.39	318	14	14	0	45.37	Guanine deaminase	Q9R111	Gda	Mus musculus
Q9R112	29	6	6	15.11	28	6	6	18.44	57	7	7	0	18.44	Sulfide:quinone oxidoreductase, mitochondrial	Q9R112	Sqrdl	Mus musculus
Q9R190	30	4	4	12.72	18	3	3	9.58	48	4	4	0	12.72	Metastasis-associated protein MTA2	Q9R190	Mta2	Mus musculus
Q9R1C7	32	5	5	9.76	8	3	3	5.67	40	5	5	0	9.76	Pre-mRNA-processing factor 40 homolog A	Q9R1C7	Prpf40a	Mus musculus
Q9R1P0	18	2	2	12.26	47	6	6	28.74	65	6	6	0	28.74	Proteasome subunit alpha type-4	Q9R1P0	Psma4	Mus musculus
Q9R1P1	5	1	1	7.8	21	3	3	16.59	26	3	3	0	16.59	Proteasome subunit beta type-3	Q9R1P1	Psmb3	Mus musculus
Q9R1P3	3	2	2	17.91	13	2	2	15.42	16	4	4	0	25.87	Proteasome subunit beta type-2	Q9R1P3	Psmb2	Mus musculus
Q9R1P4	19	2	2	15.59	16	1	1	5.7	35	2	2	0.41	15.59	Proteasome subunit alpha type-1	Q9R1P4	Psma1	Mus musculus
Q9R1T2	20	2	2	9.43	23	5	5	23.71	43	5	5	0	23.71	SUMO-activating enzyme subunit 1	Q9R1T2	Sae1	Mus musculus
Q9R1T4	7	2	2	11.52	11	2	2	11.52	18	2	2	0.41	11.52	Septin-6	Q9R1T4	Sept6	Mus musculus
Q9WTI7	0	0	0		3	2	2	3.57	3	2	2	0.41	3.57	Unconventional myosin-Ic	Q9WTI7	Myo1c	Mus musculus
Q9WTP6	34	5	5	23.85	31	3	3	22.59	65	5	5	0	23.85	Adenylate kinase 2, mitochondrial	Q9WTP6	Ak2	Mus musculus
Q9WTX5	27	1	1	11.66	27	2	2	19.63	54	2	2	0.41	19.63	S-phase kinase-associated protein 1	Q9WTX5	Skp1	Mus musculus
Q9WU78	84	11	11	21.29	130	12	12	21.52	214	13	13	0	22.78	Programmed cell death 6-interacting protein	Q9WU78	Pdcd6ip	Mus musculus
Q9WUA2	0	0	0		13	2	2	3.74	13	2	2	0.41	3.74	Phenylalanine--tRNA ligase beta subunit	Q9WUA2	Farsb	Mus musculus
Q9WUA3	0	0	0		25	7	7	16.71	25	7	7	0	16.71	ATP-dependent 6-phosphofructokinase, platelet type	Q9WUA3	Pfkp	Mus musculus
Q9WUK2	43	7	7	35.08	48	6	6	24.19	91	7	7	0	35.08	Eukaryotic translation initiation factor 4H	Q9WUK2	Eif4h	Mus musculus

Protein	Conv Spectral Counts	Conv Distinct Peptides	Conv Unshared Peptides	Conv Protein Coverage %	Infl Spectral Counts	Infl Distinct Peptides	Infl Unshared Peptides	Infl Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9WUM3	26	6	6	25.21	45	7	7	21.07	71	8	8	0	25.21	Coronin-1B	Q9WUM3	Coro1b	Mus musculus
Q9WUM4	10	4	4	14.35	24	6	6	14.35	34	6	6	0	14.35	Coronin-1C	Q9WUM4	Coro1c	Mus musculus
Q9WUP7	13	2	2	10.03	20	4	4	28.88	33	5	5	0	33.74	Ubiquitin carboxyl-terminal hydrolase isozyme L5	Q9WUP7	Uchl5	Mus musculus
Q9WUU7	54	5	5	24.84	50	6	6	24.84	104	6	6	0	24.84	Cathepsin Z	Q9WUU7	Ctsz	Mus musculus
Q9WV02	12	3	3	9.46	5	2	2	5.37	17	3	3	0	9.46	RNA-binding motif protein, X chromosome	Q9WV02	Rbmx	Mus musculus
Q9WV32	108	11	11	34.95	211	16	16	48.12	319	16	16	0	48.12	Actin-related protein 2/3 complex subunit 1B	Q9WV32	Arpc1b	Mus musculus
Q9WV60	2	2	2	12.62	7	2	2	15.71	9	3	3	0	21.43	Glycogen synthase kinase-3 beta	Q9WV60	Gsk3b	Mus musculus
Q9WV98	11	2	2	35.96	0	0	0		11	2	2	0.41	35.96	Mitochondrial import inner membrane translocase subunit Tim9	Q9WV98	Timm9	Mus musculus
Q9WVA4	67	8	8	40.2	157	9	9	46.23	224	9	9	0	46.23	Transgelin-2	Q9WVA4	Tagln2	Mus musculus
Q9WVE8	2	1	1	3.7	5	2	2	7.41	7	2	2	0.41	7.41	Protein kinase C and casein kinase substrate in neurons protein 2	Q9WVE8	Pacsin2	Mus musculus
Q9WVG5	31	3	3	11.8	19	4	4	15.2	50	4	4	0	15.2	Endothelial lipase	Q9WVG5	Lipg	Mus musculus
Q9WVJ2	1	1	1	4.79	5	4	4	21.28	6	4	4	0	21.28	26S proteasome non-ATPase regulatory subunit 13	Q9WVJ2	Psmd13	Mus musculus
Q9WVK4	29	4	4	10.86	45	5	5	14.23	74	5	5	0	14.23	EH domain-containing protein 1	Q9WVK4	Ehd1	Mus musculus
Q9Z0H3	5	3	3	15.58	31	2	2	11.17	36	3	3	0	15.58	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	Q9Z0H3	Smarcb1	Mus musculus
Q9Z0I7	1	1	1	5.93	4	3	3	13.06	5	3	3	0	13.06	Protein Slfn1	Q9Z0I7	Slfn1	Mus musculus
Q9Z0J0	25	4	4	31.54	18	3	3	22.15	43	4	4	0	31.54	Epididymal secretory protein E1	Q9Z0J0	Npc2	Mus musculus
Q9Z0N1	24	2	2	11.23	44	4	4	16.1	68	4	4	0	16.1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	Q9Z0N1	Eif2s3x	Mus musculus
Q9Z0P4	5	2	2	8.36	3	2	2	8.36	8	2	2	0.41	8.36	Paralemmin-1	Q9Z0P4	Palm	Mus musculus
Q9Z0P5	77	8	8	36.68	123	12	12	46.13	200	13	13	0	46.13	Twinfilin-2	Q9Z0P5	Twf2	Mus musculus
Q9Z0W3	2	2	2	2.5	4	1	1	0.78	6	3	3	0	3.28	Nuclear pore complex protein Nup160	Q9Z0W3	Nup160	Mus musculus
Q9Z0X1	2	2	2	5.72	7	2	2	7.84	9	3	3	0	10.29	Apoptosis-inducing factor 1, mitochondrial	Q9Z0X1	Aifm1	Mus musculus
Q9Z126	43	2	2	29.52	54	3	3	29.52	97	3	3	0	29.52	Platelet factor 4	Q9Z126	Pf4	Mus musculus
Q9Z130	11	2	1	9.3	19	3	2	11.63	30	3	2	0.41	11.63	Heterogeneous nuclear ribonucleoprotein D-like	Q9Z130	Hnrnpdl	Mus musculus
Q9Z183	113	13	13	30.48	83	13	13	26.88	196	18	18	0	33.78	Protein-arginine deiminase type-4	Q9Z183	Padi4	Mus musculus
Q9Z1D1	13	2	2	15.31	8	2	2	7.81	21	3	3	0	18.12	Eukaryotic translation initiation factor 3 subunit G	Q9Z1D1	Eif3g	Mus musculus
Q9Z1E4	21	3	3	9.08	54	5	5	15.58	75	5	5	0	15.58	Glycogen [starch] synthase, muscle	Q9Z1E4	Gys1	Mus musculus
Q9Z1F9	7	2	2	11.29	30	6	6	19.91	37	6	6	0	19.91	SUMO-activating enzyme subunit 2	Q9Z1F9	Uba2	Mus musculus
Q9Z1G3	0	0	0		10	2	2	6.81	10	2	2	0.41	6.81	V-type proton ATPase subunit C 1	Q9Z1G3	Atp6v1c1	Mus musculus
Q9Z1N5	64	7	3	26.87	64	6	4	28.04	128	9	5	0	33.88	Spliceosome RNA helicase Ddx39b	Q9Z1N5	Ddx39b	Mus musculus
Q9Z1Q5	64	5	5	35.27	138	8	8	40.66	202	8	8	0	40.66	Chloride intracellular channel protein 1	Q9Z1Q5	Clic1	Mus musculus
Q9Z1Q9	20	4	4	8.08	77	12	12	22.41	97	12	12	0	22.41	Valine--tRNA ligase	Q9Z1Q9	Vars	Mus musculus
Q9Z1R2	9	1	1	2.69	22	3	3	7.28	31	3	3	0	7.28	Large proline-rich protein BAG6	Q9Z1R2	Bag6	Mus musculus
Q9Z1T1	5	1	1	1.81	17	2	2	3.53	22	2	2	0.41	3.53	AP-3 complex subunit beta-1	Q9Z1T1	Ap3b1	Mus musculus
Q9Z1X4	17	2	2	7.35	11	2	2	6.46	28	3	3	0	9.91	Interleukin enhancer-binding factor 3	Q9Z1X4	Ilf3	Mus musculus
Q9Z1Z0	9	5	5	12.62	19	5	5	11.47	28	7	7	0	13.87	General vesicular transport factor p115	Q9Z1Z0	Uso1	Mus musculus
Q9Z1Z2	17	4	4	22	13	4	4	22.86	30	5	5	0	27.14	Serine-threonine kinase receptor-associated protein	Q9Z1Z2	Strap	Mus musculus
Q9Z204-2	7	3	3	13.33	2	1	1	4	9	3	3	0	13.33	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	Q9Z204	Hnrnpc	Mus musculus
Q9Z277	8	2	2	3.31	1	1	1	1.56	9	2	2	0.41	3.31	Tyrosine-protein kinase BAZ1B	Q9Z277	Baz1b	Mus musculus
Q9Z2D3	8	2	2	11.13	17	3	3	15.23	25	3	3	0	15.23	Non-syndromic hearing impairment protein 5 homolog	Q9Z2D3	Dfna5	Mus musculus
Q9Z2E1	13	2	2	11.84	7	1	1	9.42	20	2	2	0.41	11.84	Methyl-CpG-binding domain protein 2	Q9Z2E1	Mbd2	Mus musculus
Q9Z2I8	7	4	4	23.09	8	3	3	19.17	15	5	5	0	23.09	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Q9Z2I8	Suclg2	Mus musculus
Q9Z2L7	38	6	6	34.39	45	8	8	41.63	83	8	8	0	41.63	Cytokine receptor-like factor 3	Q9Z2L7	Crlf3	Mus musculus
Q9Z2M7	1	1	1	12.4	9	2	2	11.16	10	3	3	0	12.4	Phosphomannomutase 2	Q9Z2M7	Pmm2	Mus musculus
Q9Z2U0	1	1	1	9.27	10	3	3	22.58	11	3	3	0	22.58	Proteasome subunit alpha type-7	Q9Z2U0	Psma7	Mus musculus
Q9Z2U1	30	2	2	12.86	31	2	2	12.86	61	2	2	0.41	12.86	Proteasome subunit alpha type-5	Q9Z2U1	Psma5	Mus musculus
Q9Z2W0	4	1	1	5.92	14	2	2	11.42	18	2	2	0.41	11.42	Aspartyl aminopeptidase	Q9Z2W0	Dnpep	Mus musculus
Q9Z2X1	218	17	14	46.27	292	16	14	39.04	510	20	17	0	46.27	Heterogeneous nuclear ribonucleoprotein F	Q9Z2X1	Hnrnpf	Mus musculus
Q9Z315	6	2	2	5.33	0	0	0		6	2	2	0.41	5.33	U4/U6.U5 tri-snRNP-associated protein 1	Q9Z315	Sart1	Mus musculus

Protein identifications for the comparison Exosomes vs. MDSC irrespective of their inflammation condition (Global comparison)

Protein FDR ≤ 0.95%

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
A0A075B5R8	27	3	3	35.9	0	0	0		27	3	3	0.29	35.9	Protein Ighv11-2 (Fragment)	A0A075B5R8	Ighv11-2	Mus musculus
A0A075B5U4	3	2	2	39.22	0	0	0		3	2	2	0.95	39.22	Protein Ighv1-18	A0A075B5U4	Ighv1-18	Mus musculus
A0A087WR50	3264	108	108	60.94	361	38	38	29.97	3625	112	112	0	62.45	Fibronectin	A0A087WR50	Fn1	Mus musculus
A0A087WSP5	19	3	3	7.95	35	3	3	7.95	54	3	3	0.29	7.95	Signal transducer and activator of transcription	A0A087WSP5	Stat1	Mus musculus
A0A0B4J1J5	13	2	2	27.35	1	1	1	16.24	14	3	3	0.29	33.33	Protein Ighv9-3 (Fragment)	A0A0B4J1J5	Ighv9-3	Mus musculus
A0A0D9SEG8	64	7	7	16.02	124	7	7	15.19	188	9	9	0	19.75	Protein Adgre5	A0A0D9SEG8	Adgre5	Mus musculus
A2A8Z1	1	1	1	2.17	13	3	3	8.56	14	3	3	0.29	8.56	Oxysterol-binding protein-related protein 9	A2A8Z1	Osbpl9	Mus musculus
A2ADY9	4	1	1	6.27	31	5	5	22.56	35	5	5	0	22.56	Protein DDI1 homolog 2	A2ADY9	Ddi2	Mus musculus
A2AFG7	22	3	3	6.08	35	6	6	11.84	57	6	6	0	11.84	Neural cell adhesion molecule L1	A2AFG7	L1cam	Mus musculus
A2AIV8	8	2	2	5.41	51	5	5	15.67	59	5	5	0	15.67	Caspase recruitment domain-containing protein 9	A2AIV8	Card9	Mus musculus
A2AJW4	2	1	1	7.89	5	2	2	17.2	7	3	3	0.29	25.09	Protein phosphatase 1 regulatory subunit	A2AJW4	Ppp1r3d	Mus musculus
A2AL36	0	0	0		5	2	2	1.33	5	2	2	0.95	1.33	Centriolin	A2AL36	Cntrl	Mus musculus
A2AN08	23	7	7	3.11	44	10	10	4.88	67	13	13	0	6.12	E3 ubiquitin-protein ligase UBR4	A2AN08	Ubr4	Mus musculus
A2AQ07	86	5	5	20.84	110	12	10	41.91	196	13	11	0	43.9	Tubulin beta-1 chain	A2AQ07	Tubb1	Mus musculus
A2ASS6	3	2	2	0.08	1	1	1	0.06	4	3	3	0.29	0.14	Titin	A2ASS6	Ttn	Mus musculus
A2AUR7	80	5	5	45.77	116	10	10	62.69	196	11	11	0	62.69	Ras suppressor protein 1	A2AUR7	Rsu1	Mus musculus
A3KGV1	0	0	0		10	2	2	3.01	10	2	2	0.95	3.01	Outer dense fiber protein 2	A3KGV1	Odf2	Mus musculus
A6H630	20	3	3	15.95	0	0	0		20	3	3	0.29	15.95	Protein-glutamate O-methyltransferase	A6H630	Armt1	Mus musculus
A6X935	72	7	7	12	3	2	2	4.46	75	7	7	0	12	Inter alpha-trypsin inhibitor, heavy chain 4	A6X935	Itih4	Mus musculus
A6ZI44	2858	32	17	65.07	883	21	10	51.44	3741	35	18	0	69.86	Fructose-bisphosphate aldolase	A6ZI44	Aldoa	Mus musculus
A6ZI46	931	17	2	34.61	386	12	1	26.97	1317	19	2	0.95	37.95	Fructose-bisphosphate aldolase	A6ZI46	Aldoart1	Mus musculus
A8E0Y8	3	2	2	4.84	2	2	2	3.29	5	3	3	0.29	6.1	Immunoglobulin superfamily member 2	A8E0Y8	Cd101	Mus musculus
B1AUY2	2	1	1	1.91	11	5	5	11.44	13	5	5	0	11.44	Protein Arhgap4	B1AUY2	Arhgap4	Mus musculus
B1AVH7	0	0	0		5	3	3	6.4	5	3	3	0.29	6.4	TBC1 domain family member 2A	B1AVH7	Tbc1d2	Mus musculus
B1AZI6	4	2	2	2.01	1	1	1	1.57	5	3	3	0.29	3.58	THO complex subunit 2	B1AZI6	Thoc2	Mus musculus
B2RPV6	13	2	2	2.48	21	2	2	2.48	34	2	2	0.95	2.48	Multimerin-1	B2RPV6	Mmrn1	Mus musculus
B2RQC6	18	7	7	5.75	32	8	8	7.37	50	9	9	0	7.96	CAD protein	B2RQC6	Cad	Mus musculus
B2RUP2	0	0	0		17	3	3	6.27	17	3	3	0.29	6.27	Protein unc-13 homolog D	B2RUP2	Unc13d	Mus musculus
B2RV77	70	3	3	44.33	245	10	10	60.82	315	10	10	0	60.82	MCG130182, isoform CRA_a	B2RV77	Gm5483	Mus musculus
B2RXR6	21	4	4	7.15	59	8	8	15.91	80	10	10	0	19.34	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B	B2RXR6	Ankrd44	Mus musculus
B2RY50	3	2	2	4.15	0	0	0		3	2	2	0.95	4.15	Armadillo repeat-containing protein 4	B2RY50	Armc4	Mus musculus
B2RY56	0	0	0		6	2	2	4.06	6	2	2	0.95	4.06	RNA-binding protein 25	B2RY56	Rbm25	Mus musculus
B5THE2	118	11	11	10.51	94	14	14	11.49	212	16	16	0	13.36	Maltase-glucoamylase	B5THE2	Mgam	Mus musculus
B9EJ54	2	2	2	2.44	4	2	2	2.79	6	3	3	0.29	4.18	MCG21756, isoform CRA_b	B9EJ54	Nup205	Mus musculus
D3YTQ8	0	0	0		4	2	2	53.25	4	2	2	0.95	53.25	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 5, isoform CRA_a	D3YTQ8	Ndufa5	Mus musculus
D3YVV0	2	2	2	5.25	0	0	0		2	2	2	0.95	5.25	Protein Ttc13	D3YVV0	Ttc13	Mus musculus
D3YXK2	0	0	0		118	8	8	11.53	118	8	8	0	11.53	Scaffold attachment factor B1	D3YXK2	Safb	Mus musculus
D3YZZ5	0	0	0		4	2	2	11.16	4	2	2	0.95	11.16	Protein Tmed7	D3YZZ5	Tmed7	Mus musculus
D3Z6Q9	154	8	8	24.74	150	9	9	22.09	304	10	10	0	26.18	Bridging integrator 2	D3Z6Q9	Bin2	Mus musculus
D4AFX7	5	2	2	1.2	36	8	8	5.96	41	8	8	0	5.96	Protein Dnajc13	D4AFX7	Dnajc13	Mus musculus
E9PUM5	5	2	2	4.7	0	0	0		5	2	2	0.95	4.7	Protein Gm4788	E9PUM5	Gm4788	Mus musculus
E9PV24	409	19	19	31.94	151	13	13	30.04	560	21	21	0	33.08	Fibrinogen alpha chain	E9PV24	Fga	Mus musculus
E9PVA8	3	3	3	1.91	17	3	3	1.61	20	5	5	0	2.92	Protein Gcn1l1	E9PVA8	Gcn1l1	Mus musculus
E9PVX6	1	1	1	0.47	111	20	20	10.92	112	21	21	0	11.39	Protein Mki67	E9PVX6	Mki67	Mus musculus
E9PWG6	0	0	0		14	4	4	7.37	14	4	4	0.19	7.37	Protein Ncapg	E9PWG6	Ncapg	Mus musculus
E9PX59	3	3	3	3.74	5	4	4	6.84	8	6	6	0	9.5	Sterile alpha motif domain-containing protein 9-like	E9PX59	Samd9l	Mus musculus
E9PYK3	5	4	4	4.42	1	1	1	0.81	6	4	4	0.19	4.42	Protein Parp4	E9PYK3	Parp4	Mus musculus
E9PZF0	38	5	2	25.09	19	5	3	18.73	57	6	3	0.29	25.09	Nucleoside diphosphate kinase	E9PZF0	Gm20390	Mus musculus
E9Q070	115	8	8	47.95	285	16	16	58.99	400	17	17	0	58.99	Uncharacterized protein	E9Q070	Gm8730	Mus musculus
E9Q0F0	13	2	2	1.31	0	0	0		13	2	2	0.95	1.31	Protein Krt78	E9Q0F0	Krt78	Mus musculus
E9Q0K6	321	19	19	44.09	163	12	12	26.73	484	21	21	0	44.7	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	E9Q0K6	Samhd1	Mus musculus
E9Q0Y4	8	3	3	5.88	25	7	7	14.93	33	9	9	0	18.69	Signal-induced proliferation-associated protein 1	E9Q0Y4	Sipa1	Mus musculus
E9Q394	0	0	0		25	5	5	3.17	25	5	5	0	3.17	Protein Akap13	E9Q394	Akap13	Mus musculus
E9Q397	1020	70	69	42.35	216	34	34	24.01	1236	72	71	0	43.38	Spectrin beta chain, erythrocytic	E9Q397	Sptb	Mus musculus
E9Q555	2	2	2	0.72	2	2	2	0.8	4	4	4	0.19	1.51	E3 ubiquitin-protein ligase RNF213	E9Q555	Rnf213	Mus musculus
E9Q586	23	5	5	8.39	32	7	7	12.99	55	8	8	0	14.45	Dynactin subunit 1	E9Q586	Dctn1	Mus musculus
E9Q604	1055	32	32	44.8	1177	48	48	46.36	2232	55	55	0	54.51	Integrin alpha-M	E9Q604	Itgam	Mus musculus
E9Q616	1	1	1	0.42	4	2	2	0.53	5	3	3	0.29	0.95	Protein Ahnak	E9Q616	Ahnak	Mus musculus
E9Q6E5	0	0	0		9	2	2	7.44	9	2	2	0.95	7.44	Protein Srsf11	E9Q6E5	Srsf11	Mus musculus
E9Q6Q4	4	3	3	9.5	13	2	2	8.6	17	5	5	0	18.1	Protein Rap1gds1	E9Q6Q4	Rap1gds1	Mus musculus
E9Q6U4	43	2	2	20.77	15	2	2	20.77	58	2	2	0.95	20.77	Prefoldin subunit 4	E9Q6U4	Pfdn4	Mus musculus
E9Q7G0	1	1	1	0.81	127	17	17	14.23	128	17	17	0	14.23	Protein Numa1	E9Q7G0	Numa1	Mus musculus
E9Q8K8	0	0	0		29	3	3	5.82	29	3	3	0.29	5.82	Zinc finger CCCH domain-containing protein 4	E9Q8K8	Zc3h4	Mus musculus
E9Q8L9	0	0	0		21	3	3	5.57	21	3	3	0.29	5.57	Rab11 family-interacting protein 1	E9Q8L9	Rab11fip1	Mus musculus
E9QL65	5	2	2	5.68	9	1	1	3.5	14	2	2	0.95	5.68	Conserved oligomeric Golgi complex subunit 3	E9QL65	Cog3	Mus musculus
E9QNN1	127	11	11	12.28	181	13	13	16.11	308	16	16	0	19	ATP-dependent RNA helicase A	E9QNN1	Dhx9	Mus musculus
E9QPU1	939	52	52	32.32	193	23	23	16.58	1132	54	54	0	34.06	von Willebrand factor	E9QPU1	Vwf	Mus musculus
F6RPJ9	17	5	5	6.08	1	1	1	1.62	18	5	5	0	6.08	Insulin-degrading enzyme (Fragment)	F6RPJ9	Ide	Mus musculus
F6ZDS4	5	3	3	2.22	132	15	15	11.15	137	16	16	0	11.15	Nucleoprotein TPR	F6ZDS4	Tpr	Mus musculus
F7BJB9	0	0	0		2	2	2	5.1	2	2	2	0.95	5.1	Protein Morc3	F7BJB9	Morc3	Mus musculus
F8VPN4	13	3	3	3.26	3	1	1	0.98	16	4	4	0.19	4.24	Protein Agl	F8VPN4	Agl	Mus musculus
F8VQC1	0	0	0		17	2	2	8.05	17	2	2	0.95	8.05	Signal recognition particle subunit SRP72	F8VQC1	Srp72	Mus musculus
F8WI35	1043	18	6	31.11	749	12	3	31.85	1792	19	6	0	31.85	Histone H3	F8WI35	H3f3a	Mus musculus
G3UWD6	355	13	2	17.54	196	13	1	15.79	551	15	2	0.95	17.54	Glucose-6-phosphate 1-dehydrogenase	G3UWD6	G6pd2	Mus musculus
G3X8U3	33	4	4	22.49	0	0	0		33	4	4	0.19	22.49	MCG6895	G3X8U3	2210016F16Ri	Mus musculus
G3X972	12	3	3	6.2	2	1	1	3.38	14	3	3	0.29	6.2	Protein Sec24c	G3X972	Sec24c	Mus musculus
G5E870	5	2	2	1.93	15	2	2	2.57	20	3	3	0.29	3.11	E3 ubiquitin-protein ligase TRIP12	G5E870	Trip12	Mus musculus
G5E8K5	4	2	2	1.43	0	0	0		4	2	2	0.95	1.43	Ankyrin-3	G5E8K5	Ank3	Mus musculus
O08528	14	4	3	7.31	21	5	4	9.6	35	7	6	0	14.18	Hexokinase-2	O08528	Hk2	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
O08553	18	3	3	10.14	8	2	2	5.59	26	4	4	0.19	12.94	Dihydropyrimidinase-related protein 2	O08553	Dpysl2	Mus musculus
O08582	29	2	2	5.54	36	4	4	12.57	65	5	5	0	12.72	GTP-binding protein 1	O08582	Gtpbp1	Mus musculus
O08583	59	4	4	21.96	153	12	12	38.43	212	12	12	0	38.43	THO complex subunit 4	O08583	Alyref	Mus musculus
O08585	36	2	2	13.62	82	3	3	21.28	118	3	3	0.29	21.28	Clathrin light chain A	O08585	Clta	Mus musculus
O08663	60	6	6	25.94	49	8	8	33.89	109	9	9	0	35.77	Methionine aminopeptidase 2	O08663	Metap2	Mus musculus
O08677	9	1	1	3.33	16	3	3	8.77	25	3	3	0.29	8.77	Kininogen-1	O08677	Kng1	Mus musculus
O08691	9	3	3	14.97	0	0	0		9	3	3	0.29	14.97	Arginase-2, mitochondrial	O08691	Arg2	Mus musculus
O08692	2000	20	20	57.49	5399	26	26	75.45	7399	29	29	0	76.05	Neutrophilic granule protein	O08692	Ngp	Mus musculus
O08709	213	8	8	49.55	248	10	10	53.57	461	10	10	0	53.57	Peroxiredoxin-6	O08709	Prdx6	Mus musculus
O08734	0	0	0		27	3	3	22.97	27	3	3	0.29	22.97	Bcl-2 homologous antagonist/killer	O08734	Bak1	Mus musculus
O08738	27	5	5	19.57	7	2	2	10.14	34	5	5	0	19.57	Caspase-6	O08738	Casp6	Mus musculus
O08749	144	9	9	28.68	91	5	5	18.27	235	9	9	0	28.68	Dihydrolipoyl dehydrogenase, mitochondrial	O08749	Dld	Mus musculus
O08759	3	1	1	2.18	7	2	2	6.32	10	3	3	0.29	8.51	Ubiquitin-protein ligase E3A	O08759	Ube3a	Mus musculus
O08795	20	2	2	12.48	82	7	7	14.4	102	8	8	0	21.88	Glucosidase 2 subunit beta	O08795	Prkcsh	Mus musculus
O08807	3	1	1	9.12	4	2	2	13.14	7	2	2	0.95	13.14	Peroxiredoxin-4	O08807	Prdx4	Mus musculus
O08808	115	10	10	12.83	123	10	10	10.2	238	13	13	0	14.26	Protein diaphanous homolog 1	O08808	Diaph1	Mus musculus
O08810	162	14	14	24	198	11	11	21.63	360	16	16	0	29.35	116 kDa U5 small nuclear ribonucleoprotein component	O08810	Eftud2	Mus musculus
O08917	4	2	2	7.24	84	7	7	21.73	88	7	7	0	21.73	Flotillin-1	O08917	Flot1	Mus musculus
O08992	251	10	10	49.5	33	2	2	14.38	284	10	10	0	49.5	Syntenin-1	O08992	Sdcbp	Mus musculus
O08997	2	2	2	47.06	40	3	3	51.47	42	3	3	0.29	51.47	Copper transport protein ATOX1	O08997	Atox1	Mus musculus
O09043	79	5	5	22.2	80	4	4	22.43	159	6	6	0	29.83	Napsin-A	O09043	Napsa	Mus musculus
O09061	235	11	11	49.17	53	6	6	33.75	288	12	12	0	49.17	Proteasome subunit beta type-1	O09061	Psmb1	Mus musculus
O09106	20	4	4	15.77	45	3	3	11.2	65	4	4	0.19	15.77	Histone deacetylase 1	O09106	Hdac1	Mus musculus
O09110	7	2	2	12.39	27	2	2	12.39	34	2	2	0.95	12.39	Dual specificity mitogen-activated protein kinase kinase 3	O09110	Map2k3	Mus musculus
O09126	15	2	2	4.99	0	0	0		15	2	2	0.95	4.99	Semaphorin-4D	O09126	Sema4d	Mus musculus
O09130	0	0	0		6	2	2	11.17	6	2	2	0.95	11.17	NFATC2-interacting protein	O09130	Nfatc2ip	Mus musculus
O09131	17	4	4	26.67	5	2	2	12.08	22	4	4	0.19	26.67	Glutathione S-transferase omega-1	O09131	Gsto1	Mus musculus
O09159	218	12	12	17.28	98	10	10	17.18	316	16	16	0	23.2	Lysosomal alpha-mannosidase	O09159	Man2b1	Mus musculus
O09172	56	4	4	28.1	42	4	4	22.63	98	5	5	0	28.1	Glutamate--cysteine ligase regulatory subunit	O09172	Gclm	Mus musculus
O35129	0	0	0		46	4	4	17.06	46	4	4	0.19	17.06	Prohibitin-2	O35129	Phb2	Mus musculus
O35218	2	2	2	3.32	5	4	4	7.67	7	4	4	0.19	7.67	Cleavage and polyadenylation specificity factor subunit 2	O35218	Cpsf2	Mus musculus
O35226	1	1	1	4.52	37	6	6	25.8	38	6	6	0	25.8	26S proteasome non-ATPase regulatory subunit 4	O35226	Psmd4	Mus musculus
O35286	42	7	7	12.08	24	5	5	10.31	66	8	8	0	14.84	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	O35286	Dhx15	Mus musculus
O35326	0	0	0		4	2	2	7.43	4	2	2	0.95	7.43	Serine/arginine-rich splicing factor 5	O35326	Srsf5	Mus musculus
O35343	92	4	2	17.66	91	5	3	23.22	183	5	3	0.29	23.22	Importin subunit alpha-3	O35343	Kpna4	Mus musculus
O35344	24	4	2	16.89	25	5	3	21.11	49	6	4	0.19	27.45	Importin subunit alpha-4	O35344	Kpna3	Mus musculus
O35350	284	18	18	39.13	181	16	16	36.04	465	20	20	0	43.9	Calpain-1 catalytic subunit	O35350	Capn1	Mus musculus
O35381	26	3	3	20.24	268	10	10	46.96	294	10	10	0	46.96	Acidic leucine-rich nuclear phosphoprotein 32 family member A	O35381	Anp32a	Mus musculus
O35459	29	2	2	11.31	0	0	0		29	2	2	0.95	11.31	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	O35459	Ech1	Mus musculus
O35598	54	6	6	14.42	0	0	0		54	6	6	0	14.42	Disintegrin and metalloproteinase domain-containing protein 10	O35598	Adam10	Mus musculus
O35638	28	5	5	6.74	1	1	1	2.11	29	5	5	0	6.74	Cohesin subunit SA-2	O35638	Stag2	Mus musculus
O35639	323	14	14	44.89	312	17	17	48.92	635	17	17	0	48.92	Annexin A3	O35639	Anxa3	Mus musculus
O35643	285	16	11	29.8	170	9	6	22.69	455	17	12	0	30.12	AP-1 complex subunit beta-1	O35643	Ap1b1	Mus musculus
O35704	0	0	0		3	2	2	6.77	3	2	2	0.95	6.77	Serine palmitoyltransferase 1	O35704	Sptlc1	Mus musculus
O35737	120	5	3	15.14	299	13	8	35.41	419	13	8	0	35.41	Heterogeneous nuclear ribonucleoprotein H	O35737	Hnrnph1	Mus musculus
O35744	463	23	23	65.33	797	30	30	65.33	1260	35	35	0	71.61	Chitinase-like protein 3	O35744	Chil3	Mus musculus
O35841	72	7	7	26.59	103	8	8	28.17	175	9	9	0	28.17	Apoptosis inhibitor 5	O35841	Api5	Mus musculus
O35855	25	4	4	17.81	2	1	1	5.6	27	4	4	0.19	17.81	Branched-chain-amino-acid aminotransferase, mitochondrial	O35855	Bcat2	Mus musculus
O35887	0	0	0		10	2	2	12.38	10	2	2	0.95	12.38	Calumenin	O35887	Calu	Mus musculus
O35892	0	0	0		14	2	2	8.3	14	2	2	0.95	8.3	Nuclear autoantigen Sp-100	O35892	Sp100	Mus musculus
O35900	41	2	2	40	39	2	2	40	80	2	2	0.95	40	U6 snRNA-associated Sm-like protein LSm2	O35900	Lsm2	Mus musculus
O35904	3	3	3	5.56	0	0	0		3	3	3	0.29	5.56	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform	O35904	Pik3cd	Mus musculus
O35930	240	9	9	17.57	38	5	5	13.35	278	9	9	0	17.57	Platelet glycoprotein Ib alpha chain	O35930	Gp1ba	Mus musculus
O35955	49	3	3	17.95	1	1	1	7.33	50	3	3	0.29	17.95	Proteasome subunit beta type-10	O35955	Psmb10	Mus musculus
O54734	0	0	0		16	3	3	13.83	16	3	3	0.29	13.83	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	O54734	Ddost	Mus musculus
O54774	11	3	3	5.17	14	3	3	5.17	25	4	4	0.19	6.92	AP-3 complex subunit delta-1	O54774	Ap3d1	Mus musculus
O54824	2	2	2	3.48	48	3	3	6.2	50	5	5	0	9.68	Pro-interleukin-16	O54824	Il16	Mus musculus
O54879	10	2	2	14	0	0	0		10	2	2	0.95	14	High mobility group protein B3	O54879	Hmgb3	Mus musculus
O54890	108	8	8	17.53	11	4	4	10.55	119	8	8	0	17.53	Integrin beta-3	O54890	Itgb3	Mus musculus
O54941	2	1	1	3.65	11	2	2	6.81	13	2	2	0.95	6.81	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	O54941	Smarce1	Mus musculus
O54950	5	1	1	5.76	14	2	2	14.55	19	2	2	0.95	14.55	5'-AMP-activated protein kinase subunit gamma-1	O54950	Prkag1	Mus musculus
O54988	2	1	1	1.7	43	5	5	10.54	45	5	5	0	10.54	STE20-like serine/threonine-protein kinase	O54988	Slk	Mus musculus
O54990	3	2	2	3.92	0	0	0		3	2	2	0.95	3.92	Prominin-1	O54990	Prom1	Mus musculus
O55029	37	5	5	13.15	124	12	12	25.86	161	12	12	0	25.86	Coatomer subunit beta'	O55029	Copb2	Mus musculus
O55098	9	1	1	2.17	41	2	2	4.76	50	2	2	0.95	4.76	Serine/threonine-protein kinase 10	O55098	Stk10	Mus musculus
O55106	55	5	5	12.69	60	6	6	16.28	115	8	8	0	20.77	Striatin	O55106	Strn	Mus musculus
O55131	24	2	2	9.17	42	4	4	21.33	66	4	4	0.19	21.33	Septin-7	O55131	Sept7	Mus musculus
O55135	68	5	5	46.94	137	6	6	62.86	205	6	6	0	62.86	Eukaryotic translation initiation factor 6	O55135	Eif6	Mus musculus
O55201	2	2	2	4.44	28	6	6	11.83	30	7	7	0	13.59	Transcription elongation factor SPT5	O55201	Supt5h	Mus musculus
O55222	27	3	3	15.04	52	3	3	14.16	79	4	4	0.19	15.04	Integrin-linked protein kinase	O55222	Ilk	Mus musculus
O70138	245	10	10	41.72	131	7	7	32.47	376	10	10	0	41.72	Neutrophil collagenase	O70138	Mmp8	Mus musculus
O70145	339	11	11	35.81	298	10	10	34.86	637	14	14	0	42.67	Neutrophil cytosol factor 2	O70145	Ncf2	Mus musculus
O70165	12	2	2	13.47	0	0	0		12	2	2	0.95	13.47	Ficolin-1	O70165	Fcn1	Mus musculus
O70194	29	3	3	13.32	33	3	3	12.77	62	4	4	0.19	13.32	Eukaryotic translation initiation factor 3 subunit D	O70194	Eif3d	Mus musculus
O70251	69	3	3	37.78	102	5	5	34.22	171	6	6	0	51.11	Elongation factor 1-beta	O70251	Eef1b	Mus musculus
O70252	0	0	0		4	2	2	9.52	4	2	2	0.95	9.52	Heme oxygenase 2	O70252	Hmox2	Mus musculus
O70310	49	4	4	16.33	6	3	3	11.09	55	4	4	0.19	16.33	Glycylpeptide N-tetradecanoyltransferase 1	O70310	Nmt1	Mus musculus
O70400	0	0	0		11	3	3	22.32	11	3	3	0.29	22.32	PDZ and LIM domain protein 1	O70400	Pdlim1	Mus musculus
O70435	97	6	6	28.63	5	2	2	9.41	102	6	6	0	28.63	Proteasome subunit alpha type-3	O70435	Psma3	Mus musculus
O70492	0	0	0		23	2	2	29.63	23	2	2	0.95	29.63	Sorting nexin-3	O70492	Snx3	Mus musculus
O70497	61	2	2	15.61	22	2	2	15.61	83	2	2	0.95	15.61	Ficolin-2	O70497	Fcn2	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
O70566	0	0	0		2	2	2	3.92	2	2	2	0.95	3.92	Protein diaphanous homolog 2	O70566	Diaph2	Mus musculus
O88307	577	36	36	25.82	144	24	24	18.74	721	38	38	0	26.14	Sortilin-related receptor	O88307	Sorl1	Mus musculus
O88342	971	20	20	60.89	596	22	22	54.46	1567	26	26	0	65.84	WD repeat-containing protein 1	O88342	Wdr1	Mus musculus
O88379	0	0	0		9	4	4	5.27	9	4	4	0.19	5.27	Bromodomain adjacent to zinc finger domain protein 1A	O88379	Baz1a	Mus musculus
O88456	7	4	4	29.37	15	1	1	8.92	22	4	4	0.19	29.37	Calpain small subunit 1	O88456	Capns1	Mus musculus
O88487	13	3	3	11.44	9	1	1	3.92	22	3	3	0.29	11.44	Cytoplasmic dynein 1 intermediate chain 2	O88487	Dync1i2	Mus musculus
O88520	14	3	3	14.95	11	2	2	10.31	25	3	3	0.29	14.95	Leucine-rich repeat protein SHOC-2	O88520	Shoc2	Mus musculus
O88536	0	0	0		23	3	3	11.11	23	3	3	0.29	11.11	Formyl peptide receptor 2	O88536	Fpr2	Mus musculus
O88544	77	7	7	26.85	36	4	4	15.52	113	9	9	0	29.56	COP9 signalosome complex subunit 4	O88544	Cops4	Mus musculus
O88569	305	13	13	46.74	634	17	17	44.48	939	19	19	0	49.58	Heterogeneous nuclear ribonucleoproteins A2/B1	O88569	Hnrnpa2b1	Mus musculus
O88593	597	9	9	50	2384	19	19	62.64	2981	19	19	0	62.64	Peptidoglycan recognition protein 1	O88593	Pglyrp1	Mus musculus
O88622	2	2	2	5.16	0	0	0		2	2	2	0.95	5.16	Poly(ADP-ribose) glycohydrolase	O88622	Parg	Mus musculus
O88668	3	1	1	5	8	2	2	13.18	11	2	2	0.95	13.18	Protein CREG1	O88668	Creg1	Mus musculus
O88685	121	6	6	24.89	94	7	7	24.89	215	7	7	0	24.89	26S protease regulatory subunit 6A	O88685	Psmc3	Mus musculus
O88712	19	2	2	11.79	29	2	2	11.79	48	2	2	0.95	11.79	C-terminal-binding protein 1	O88712	Ctbp1	Mus musculus
O88746	0	0	0		59	4	4	15.65	59	4	4	0.19	15.65	Target of Myb protein 1	O88746	Tom1	Mus musculus
O88783	141	10	10	8.25	184	10	10	8.61	325	13	13	0	10.72	Coagulation factor V	O88783	F5	Mus musculus
O88842	6	2	2	7.09	26	4	4	12.14	32	4	4	0.19	12.14	FYVE, RhoGEF and PH domain-containing protein 3	O88842	Fgd3	Mus musculus
O88844	75	7	7	26.09	20	3	3	13.53	95	7	7	0	26.09	Isocitrate dehydrogenase [NADP] cytoplasmic	O88844	Idh1	Mus musculus
O88879	24	6	6	9.21	31	4	4	6.73	55	6	6	0	9.21	Apoptotic protease-activating factor 1	O88879	Apaf1	Mus musculus
O88947	37	3	3	8.94	0	0	0		37	3	3	0.29	8.94	Coagulation factor X	O88947	F10	Mus musculus
O88958	24	3	3	27.34	0	0	0		24	3	3	0.29	27.34	Glucosamine-6-phosphate isomerase 1	O88958	Gnpda1	Mus musculus
O88968	159	7	7	34.65	133	8	8	37.44	292	8	8	0	37.44	Transcobalamin-2	O88968	Tcn2	Mus musculus
O89023	26	3	3	16.9	57	1	1	6.58	83	3	3	0.29	16.9	Tripeptidyl-peptidase 1	O89023	Tpp1	Mus musculus
O89051	24	3	3	20.68	4	1	1	3.76	28	3	3	0.29	20.68	Integral membrane protein 2B	O89051	Itm2b	Mus musculus
O89053	751	30	30	47.07	540	24	24	39.48	1291	37	37	0	49.89	Coronin-1A	O89053	Coro1a	Mus musculus
O89079	53	3	3	17.21	79	6	6	33.12	132	6	6	0	33.12	Coatomer subunit epsilon	O89079	Cope	Mus musculus
O89086	56	2	2	22.22	154	4	4	22.22	210	4	4	0.19	22.22	RNA-binding protein 3	O89086	Rbm3	Mus musculus
P00375	6	2	2	18.18	0	0	0		6	2	2	0.95	18.18	Dihydrofolate reductase	P00375	Dhfr	Mus musculus
P00405	0	0	0		34	2	2	8.81	34	2	2	0.95	8.81	Cytochrome c oxidase subunit 2	P00405	Mtco2	Mus musculus
P00493	93	7	7	44.04	51	7	7	35.32	144	11	11	0	47.25	Hypoxanthine-guanine phosphoribosyltransferase	P00493	Hprt1	Mus musculus
P01027	1478	64	64	51.23	668	46	46	38.67	2146	69	69	0	54.12	Complement C3	P01027	C3	Mus musculus
P01029	190	16	16	21.23	17	2	2	2.13	207	16	16	0	21.23	Complement C4-B	P01029	C4b	Mus musculus
P01326	185	11	11	35.45	21	5	5	33.64	206	11	11	0	35.45	Insulin-2	P01326	Ins2	Mus musculus
P01639	16	3	3	27.69	0	0	0		16	3	3	0.29	27.69	Ig kappa chain V-V region MOPC 41	P01639	Gm5571	Mus musculus
P01723	4	2	2	47.86	0	0	0		4	2	2	0.95	47.86	Ig lambda-1 chain V region	P01723		Mus musculus
P01786	14	2	2	21.37	0	0	0		14	2	2	0.95	21.37	Ig heavy chain V region MOPC 47A	P01786		Mus musculus
P01812	9	2	2	20.51	0	0	0		9	2	2	0.95	20.51	Ig heavy chain V region MOPC 173	P01812		Mus musculus
P01837	70	2	2	45.28	8	1	1	32.08	78	2	2	0.95	45.28	Ig kappa chain C region	P01837		Mus musculus
P01868	37	4	4	25	1	1	1	3.09	38	4	4	0.19	25	Ig gamma-1 chain C region secreted form	P01868	Ighg1	Mus musculus
P01872	408	22	22	53.3	5	2	2	7.71	413	22	22	0	53.3	Ig mu chain C region	P01872	Ighm	Mus musculus
P01878	15	2	2	11.05	0	0	0		15	2	2	0.95	11.05	Ig alpha chain C region	P01878		Mus musculus
P01887	21	3	3	19.33	73	2	2	19.33	94	3	3	0.29	19.33	Beta-2-microglobulin	P01887	B2m	Mus musculus
P01900	11	2	2	7.4	2	2	2	6.85	13	3	3	0.29	10.14	H-2 class I histocompatibility antigen, D-D alpha chain	P01900	H2-D1	Mus musculus
P01921	4	2	2	14.34	0	0	0		4	2	2	0.95	14.34	H-2 class II histocompatibility antigen, A-D beta chain	P01921	H2-Ab1	Mus musculus
P01942	1204	37	37	80.28	320	11	11	78.87	1524	37	37	0	80.28	Hemoglobin subunit alpha	P01942	Hba	Mus musculus
P02088	1707	31	16	95.24	277	16	10	95.24	1984	31	16	0	95.24	Hemoglobin subunit beta-1	P02088	Hbb-b1	Mus musculus
P02089	1438	25	10	85.71	207	11	5	85.03	1645	25	10	0	85.71	Hemoglobin subunit beta-2	P02089	Hbb-b2	Mus musculus
P02535	10	3	3	6.49	0	0	0		10	3	3	0.29	6.49	Keratin, type I cytoskeletal 10	P02535	Krt10	Mus musculus
P03958	0	0	0		7	3	3	18.75	7	3	3	0.29	18.75	Adenosine deaminase	P03958	Ada	Mus musculus
P04104	43	3	3	3.77	12	1	1	1.88	55	3	3	0.29	3.77	Keratin, type II cytoskeletal 1	P04104	Krt1	Mus musculus
P04202	115	6	6	31.54	26	2	2	10	141	6	6	0	31.54	Transforming growth factor beta-1	P04202	Tgfb1	Mus musculus
P04228	11	4	4	26.17	1	1	1	8.98	12	4	4	0.19	26.17	H-2 class II histocompatibility antigen, A-D alpha chain	P04228	H2-Aa	Mus musculus
P04919	613	27	27	29.17	161	13	13	23.47	774	27	27	0	29.17	Band 3 anion transport protein	P04919	Slc4a1	Mus musculus
P05201	124	7	7	25.18	51	4	4	17.68	175	7	7	0	25.18	Aspartate aminotransferase, cytoplasmic	P05201	Got1	Mus musculus
P05202	164	8	8	33.95	147	6	6	25.81	311	9	9	0	40.23	Aspartate aminotransferase, mitochondrial	P05202	Got2	Mus musculus
P06151	842	18	17	56.02	375	13	13	55.42	1217	21	20	0	64.16	L-lactate dehydrogenase A chain	P06151	Ldha	Mus musculus
P06336	17	2	2	10.93	0	0	0		17	2	2	0.95	10.93	Ig epsilon chain C region	P06336		Mus musculus
P06745	1348	27	27	60.75	481	20	20	43.01	1829	31	31	0	61.47	Glucose-6-phosphate isomerase	P06745	Gpi	Mus musculus
P06800	119	9	9	13.01	564	29	29	27.89	683	29	29	0	27.89	Receptor-type tyrosine-protein phosphatase C	P06800	Ptprc	Mus musculus
P06909	56	9	9	14.99	0	0	0		56	9	9	0	14.99	Complement factor H	P06909	Cfh	Mus musculus
P07356	648	19	19	51.03	952	29	29	63.42	1600	31	31	0	63.42	Annexin A2	P07356	Anxa2	Mus musculus
P07607	6	2	2	9.12	1	1	1	3.58	7	3	3	0.29	12.7	Thymidylate synthase	P07607	Tyms	Mus musculus
P07724	1366	30	30	58.88	1880	38	38	54.93	3246	43	43	0	64.64	Serum albumin	P07724	Alb	Mus musculus
P07742	88	8	8	18.69	44	5	5	10.98	132	8	8	0	18.69	Ribonucleoside-diphosphate reductase large subunit	P07742	Rrm1	Mus musculus
P07759	73	6	6	23.92	77	8	8	30.86	150	8	8	0	30.86	Serine protease inhibitor A3K	P07759	Serpina3k	Mus musculus
P07901	140	15	11	28.65	352	22	15	36.56	492	24	17	0	41.88	Heat shock protein HSP 90-alpha	P07901	Hsp90aa1	Mus musculus
P08003	104	8	8	21.63	54	10	10	24.61	158	11	11	0	27.12	Protein disulfide-isomerase A4	P08003	Pdia4	Mus musculus
P08030	348	15	15	83.33	61	6	6	42.78	409	15	15	0	83.33	Adenine phosphoribosyltransferase	P08030	Aprt	Mus musculus
P08032	2017	119	118	57.47	372	49	48	30.93	2389	121	120	0	57.85	Spectrin alpha chain, erythrocytic 1	P08032	Spta1	Mus musculus
P08071	11916	86	86	72.98	7501	84	84	73.27	19417	106	106	0	76.38	Lactotransferrin	P08071	Ltf	Mus musculus
P08103	15	5	5	16.03	48	4	4	13.74	63	5	5	0	16.03	Tyrosine-protein kinase HCK	P08103	Hck	Mus musculus
P08113	92	11	10	25.69	528	21	20	34.91	620	22	21	0	37.91	Endoplasmin	P08113	Hsp90b1	Mus musculus
P08226	76	4	4	22.51	10	3	3	18.33	86	4	4	0.19	22.51	Apolipoprotein E	P08226	Apoe	Mus musculus
P08228	47	5	5	36.36	56	5	5	36.36	103	5	5	0	36.36	Superoxide dismutase [Cu-Zn]	P08228	Sod1	Mus musculus
P08249	256	11	11	39.05	289	13	13	42.31	545	14	14	0	42.31	Malate dehydrogenase, mitochondrial	P08249	Mdh2	Mus musculus
P08556	6	3	3	21.69	40	3	3	21.69	46	3	3	0.29	21.69	GTPase NRas	P08556	Nras	Mus musculus
P08607	215	9	9	24.31	4	2	2	7.89	219	9	9	0	24.31	C4b-binding protein	P08607	C4bpa	Mus musculus
P08752	77	10	8	40.28	1027	21	15	54.37	1104	21	15	0	54.37	Guanine nucleotide-binding protein G(i) subunit alpha-2	P08752	Gnai2	Mus musculus
P08775	4	3	3	2.99	14	3	3	3.05	18	4	4	0.19	3.96	DNA-directed RNA polymerase II subunit RPB1	P08775	Polr2a	Mus musculus
P08905	486	12	12	50.68	1235	17	17	50.68	1721	17	17	0	50.68	Lysozyme C-2	P08905	Lyz2	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P09055	46	5	5	12.53	3	1	1	2.63	49	5	5	0	12.53	Integrin beta-1	P09055	Itgb1	Mus musculus
P09103	464	16	16	44.2	748	26	26	51.67	1212	27	27	0	55.6	Protein disulfide-isomerase	P09103	P4hb	Mus musculus
P09405	160	13	13	24.75	186	17	17	21.78	346	20	20	0	28.01	Nucleolin	P09405	Ncl	Mus musculus
P09411	768	16	16	49.64	504	17	17	45.08	1272	19	19	0	51.32	Phosphoglycerate kinase 1	P09411	Pgk1	Mus musculus
P09528	49	4	4	35.16	0	0	0		49	4	4	0.19	35.16	Ferritin heavy chain	P09528	Fth1	Mus musculus
P09581	38	3	3	5.73	0	0	0		38	3	3	0.29	5.73	Macrophage colony-stimulating factor 1 receptor	P09581	Csf1r	Mus musculus
P0C0S6	2714	15	14	53.91	1050	15	14	56.25	3764	21	20	0	56.25	Histone H2A.Z	P0C0S6	H2afz	Mus musculus
P0CW02	11	3	3	29.77	56	5	5	45.8	67	6	6	0	45.8	Lymphocyte antigen 6C1	P0CW02	Ly6c1	Mus musculus
P10107	1373	29	29	62.72	5881	49	49	68.79	7254	49	49	0	68.79	Annexin A1	P10107	Anxa1	Mus musculus
P10126	638	24	24	54.11	865	24	24	42.86	1503	30	30	0	56.28	Elongation factor 1-alpha 1	P10126	Eef1a1	Mus musculus
P10518	171	7	7	37.58	12	2	2	17.27	183	7	7	0	37.58	Delta-aminolevulinic acid dehydratase	P10518	Alad	Mus musculus
P10605	95	9	9	38.05	258	11	11	48.67	353	13	13	0	51.92	Cathepsin B	P10605	Ctsb	Mus musculus
P10639	59	5	5	53.33	622	9	9	60	681	10	10	0	60	Thioredoxin	P10639	Txn	Mus musculus
P10649	148	6	6	20.18	102	6	6	22.48	250	7	7	0	22.48	Glutathione S-transferase Mu 1	P10649	Gstm1	Mus musculus
P10711	10	1	1	9.3	13	2	2	9.3	23	2	2	0.95	9.3	Transcription elongation factor A protein 1	P10711	Tcea1	Mus musculus
P10810	52	5	5	28.42	55	5	5	30.05	107	6	6	0	32.79	Monocyte differentiation antigen CD14	P10810	Cd14	Mus musculus
P10852	12	5	5	21.67	30	7	7	31.37	42	7	7	0	31.37	4F2 cell-surface antigen heavy chain	P10852	Slc3a2	Mus musculus
P10853	217	8	8	26.19	29	5	5	24.6	246	10	10	0	38.89	Histone H2B type 1-F/J/L	P10853	Hist1h2bf	Mus musculus
P11031	54	3	3	25.98	5	1	1	8.66	59	3	3	0.29	25.98	Activated RNA polymerase II transcriptional coactivator p15	P11031	Sub1	Mus musculus
P11152	14	3	3	10.55	0	0	0		14	3	3	0.29	10.55	Lipoprotein lipase	P11152	Lpl	Mus musculus
P11247	1151	36	36	41.78	1222	38	38	39.69	2373	43	43	0	44.99	Myeloperoxidase	P11247	Mpo	Mus musculus
P11352	175	9	9	65.17	132	7	7	47.26	307	11	11	0	66.17	Glutathione peroxidase 1	P11352	Gpx1	Mus musculus
P11499	130	14	9	28.73	518	28	20	45.3	648	29	21	0	45.3	Heat shock protein HSP 90-beta	P11499	Hsp90ab1	Mus musculus
P11672	268	6	6	38	2632	20	20	49	2900	20	20	0	49	Neutrophil gelatinase-associated lipocalin	P11672	Lcn2	Mus musculus
P11680	74	3	3	11.42	37	2	2	5.82	111	4	4	0.19	12.07	Properdin	P11680	Cfp	Mus musculus
P11835	822	24	24	42.67	454	27	27	37.09	1276	33	33	0	44.75	Integrin beta-2	P11835	Itgb2	Mus musculus
P11983	77	6	6	21.4	86	5	5	18.88	163	8	8	0	24.64	T-complex protein 1 subunit alpha	P11983	Tcp1	Mus musculus
P12023	46	3	3	6.62	57	8	8	11.95	103	8	8	0	11.95	Amyloid beta A4 protein	P12023	App	Mus musculus
P12246	60	2	2	20.98	0	0	0		60	2	2	0.95	20.98	Serum amyloid P-component	P12246	Apcs	Mus musculus
P12265	61	8	8	18.21	0	0	0		61	8	8	0	18.21	Beta-glucuronidase	P12265	Gusb	Mus musculus
P12382	13	2	2	5.51	10	2	2	5.51	23	2	2	0.95	5.51	ATP-dependent 6-phosphofructokinase, liver type	P12382	Pfkl	Mus musculus
P12787	13	1	1	20.55	102	7	7	42.47	115	7	7	0	42.47	Cytochrome c oxidase subunit 5A, mitochondrial	P12787	Cox5a	Mus musculus
P12815	91	5	5	47.64	33	3	3	36.65	124	5	5	0	47.64	Programmed cell death protein 6	P12815	Pdcd6	Mus musculus
P12970	12	2	2	16.54	17	3	3	13.53	29	4	4	0.19	21.05	60S ribosomal protein L7a	P12970	Rpl7a	Mus musculus
P13020	708	19	19	43.72	788	29	29	45.9	1496	31	31	0	50.9	Gelsolin	P13020	Gsn	Mus musculus
P13439	22	2	2	9.98	18	2	2	9.98	40	2	2	0.95	9.98	Uridine 5'-monophosphate synthase	P13439	Umps	Mus musculus
P13595	3	1	1	1.61	3	2	2	4.39	6	2	2	0.95	4.39	Neural cell adhesion molecule 1	P13595	Ncam1	Mus musculus
P13609	2	2	2	18.42	9	1	1	10.53	11	3	3	0.29	28.95	Serglycin	P13609	Srgn	Mus musculus
P13634	5	2	2	17.62	0	0	0		5	2	2	0.95	17.62	Carbonic anhydrase 1	P13634	Ca1	Mus musculus
P13864	2	2	2	1.98	36	3	3	5.49	38	4	4	0.19	6.36	DNA (cytosine-5)-methyltransferase 1	P13864	Dnmt1	Mus musculus
P14069	315	12	12	65.17	353	15	15	75.28	668	17	17	0	75.28	Protein S100-A6	P14069	S100a6	Mus musculus
P14115	4	1	1	14.86	15	2	2	23.65	19	2	2	0.95	23.65	60S ribosomal protein L27a	P14115	Rpl27a	Mus musculus
P14131	10	2	2	14.38	23	1	1	7.53	33	2	2	0.95	14.38	40S ribosomal protein S16	P14131	Rps16	Mus musculus
P14148	1	1	1	7.04	12	2	2	11.85	13	2	2	0.95	11.85	60S ribosomal protein L7	P14148	Rpl7	Mus musculus
P14152	116	8	8	41.92	41	5	5	23.35	157	8	8	0	41.92	Malate dehydrogenase, cytoplasmic	P14152	Mdh1	Mus musculus
P14206	122	8	8	34.58	99	8	8	37.97	221	9	9	0	37.97	40S ribosomal protein SA	P14206	Rpsa	Mus musculus
P14211	420	14	14	49.28	1341	32	32	59.62	1761	32	32	0	59.62	Calreticulin	P14211	Calr	Mus musculus
P14234	57	7	7	23.21	229	10	10	29.98	286	10	10	0	29.98	Tyrosine-protein kinase Fgr	P14234	Fgr	Mus musculus
P14685	70	7	7	24.34	19	6	6	16.42	89	8	8	0	26.04	26S proteasome non-ATPase regulatory subunit 3	P14685	Psmd3	Mus musculus
P14733	142	8	8	21.09	542	24	24	41.84	684	24	24	0	41.84	Lamin-B1	P14733	Lmnb1	Mus musculus
P14824	222	11	11	27.04	79	10	10	25.41	301	11	11	0	27.04	Annexin A6	P14824	Anxa6	Mus musculus
P15532	122	5	2	37.5	45	5	3	26.32	167	6	3	0.29	37.5	Nucleoside diphosphate kinase A	P15532	Nme1	Mus musculus
P15864	450	10	2	27.36	375	8	2	26.89	825	10	2	0.95	27.36	Histone H1.2	P15864	Hist1h1c	Mus musculus
P16045	1	1	1	8.89	81	4	4	52.59	82	4	4	0.19	52.59	Galectin-1	P16045	Lgals1	Mus musculus
P16110	238	7	7	27.27	164	7	7	18.94	402	8	8	0	27.27	Galectin-3	P16110	Lgals3	Mus musculus
P16125	8	4	3	19.76	0	0	0		8	4	3	0.29	19.76	L-lactate dehydrogenase B chain	P16125	Ldhb	Mus musculus
P16546	605	43	42	27.43	821	63	62	35.84	1426	68	67	0	37.86	Spectrin alpha chain, non-erythrocytic 1	P16546	Sptan1	Mus musculus
P16675	35	3	3	11.39	37	4	4	14.35	72	5	5	0	18.35	Lysosomal protective protein	P16675	Ctsa	Mus musculus
P16858	2014	30	30	64.26	1984	30	30	67.57	3998	39	39	0	75.08	Glyceraldehyde-3-phosphate dehydrogenase	P16858	Gapdh	Mus musculus
P16879	3	2	2	4.99	10	3	3	7.79	13	3	3	0.29	7.79	Tyrosine-protein kinase Fes/Fps	P16879	Fes	Mus musculus
P17047	4	1	1	2.17	17	4	4	13.01	21	4	4	0.19	13.01	Lysosome-associated membrane glycoprotein 2	P17047	Lamp2	Mus musculus
P17182	2978	43	43	58.29	2242	39	39	68.89	5220	52	52	0	69.35	Alpha-enolase	P17182	Eno1	Mus musculus
P17426-2	115	10	8	20.31	26	7	5	18.32	141	12	10	0	26.07	Isoform B of AP-2 complex subunit alpha-1	P17426	Ap2a1	Mus musculus
P17427	129	11	9	19.94	57	8	6	16.95	186	13	11	0	24.52	AP-2 complex subunit alpha-2	P17427	Ap2a2	Mus musculus
P17439	6	2	2	12.23	27	2	2	12.23	33	2	2	0.95	12.23	Glucosylceramidase	P17439	Gba	Mus musculus
P17563	3	2	2	8.47	0	0	0		3	2	2	0.95	8.47	Selenium-binding protein 1	P17563	Selenbp1	Mus musculus
P17710	73	8	7	12.42	64	9	8	11.81	137	12	11	0	15.61	Hexokinase-1	P17710	Hk1	Mus musculus
P17742	403	12	12	50	397	13	13	65.24	800	15	15	0	65.24	Peptidyl-prolyl cis-trans isomerase A	P17742	Ppia	Mus musculus
P17751	320	10	10	41.47	270	12	12	42.81	590	13	13	0	42.81	Triosephosphate isomerase	P17751	Tpi1	Mus musculus
P17918	9	2	2	12.26	60	5	5	30.27	69	5	5	0	30.27	Proliferating cell nuclear antigen	P17918	Pcna	Mus musculus
P18242	68	5	5	20.24	146	10	10	36.59	214	10	10	0	36.59	Cathepsin D	P18242	Ctsd	Mus musculus
P18337	12	2	2	7.26	0	0	0		12	2	2	0.95	7.26	L-selectin	P18337	Sell	Mus musculus
P18572-2	20	3	3	14.29	15	4	4	19.05	35	4	4	0.19	19.05	Isoform 2 of Basigin	P18572	Bsg	Mus musculus
P18653	6	3	3	6.49	17	3	3	6.49	23	3	3	0.29	6.49	Ribosomal protein S6 kinase alpha-1	P18653	Rps6ka1	Mus musculus
P18760	468	13	13	57.23	1406	14	14	57.23	1874	16	16	0	57.23	Cofilin-1	P18760	Cfl1	Mus musculus
P19096	214	25	25	19.81	154	16	16	14.94	368	26	26	0	20.17	Fatty acid synthase	P19096	Fasn	Mus musculus
P19157	31	4	4	32.86	5	3	3	32.38	36	5	5	0	42.38	Glutathione S-transferase P 1	P19157	Gstp1	Mus musculus
P19221	2	2	2	7.77	82	5	5	8.74	84	7	7	0	14.56	Prothrombin	P19221	F2	Mus musculus
P19536	13	1	1	14.06	82	4	4	34.38	95	4	4	0.19	34.38	Cytochrome c oxidase subunit 5B, mitochondrial	P19536	Cox5b	Mus musculus
P19973	67	7	7	38.18	631	11	11	50	698	11	11	0	50	Lymphocyte-specific protein 1	P19973	Lsp1	Mus musculus
P20029	734	27	25	47.02	1406	32	30	49.92	2140	35	33	0	51.76	78 kDa glucose-regulated protein	P20029	Hspa5	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P20060	115	7	7	25.75	64	7	7	25.75	179	7	7	0	25.75	Beta-hexosaminidase subunit beta	P20060	Hexb	Mus musculus
P20108	30	4	4	31.91	51	4	4	27.24	81	6	6	0	33.85	Thioredoxin-dependent peroxide reductase, mitochondrial	P20108	Prdx3	Mus musculus
P20152	304	18	18	47.64	2769	39	39	67.81	3073	44	44	0	67.81	Vimentin	P20152	Vim	Mus musculus
P20491	3	1	1	31.4	10	2	2	33.72	13	2	2	0.95	33.72	High affinity immunoglobulin epsilon receptor subunit gamma	P20491	Fcer1g	Mus musculus
P20918	47	10	10	22.41	0	0	0		47	10	10	0	22.41	Plasminogen	P20918	Plg	Mus musculus
P21107	90	6	2	22.46	213	10	3	25.96	303	10	3	0.29	25.96	Tropomyosin alpha-3 chain	P21107	Tpm3	Mus musculus
P21107-2	209	12	8	37.5	481	14	7	36.29	690	15	8	0	41.13	Isoform 2 of Tropomyosin alpha-3 chain	P21107	Tpm3	Mus musculus
P21614	52	4	4	15.76	45	5	5	19.96	97	6	6	0	24.58	Vitamin D-binding protein	P21614	Gc	Mus musculus
P21619	3	1	1	3.86	35	5	5	15.6	38	5	5	0	15.6	Lamin-B2	P21619	Lmnb2	Mus musculus
P22366	4	2	2	13.18	1	1	1	5.07	5	2	2	0.95	13.18	Myeloid differentiation primary response protein MyD88	P22366	Myd88	Mus musculus
P22599	6	3	2	14.04	67	7	3	35.84	73	7	3	0.29	35.84	Alpha-1-antitrypsin 1-2	P22599	Serpina1b	Mus musculus
P22682	0	0	0		20	5	5	8.76	20	5	5	0	8.76	E3 ubiquitin-protein ligase CBL	P22682	Cbl	Mus musculus
P22892	30	3	3	6.81	11	1	1	3.28	41	3	3	0.29	6.81	AP-1 complex subunit gamma-1	P22892	Ap1g1	Mus musculus
P23116	73	6	6	6.92	34	3	3	3.65	107	6	6	0	6.92	Eukaryotic translation initiation factor 3 subunit A	P23116	Eif3a	Mus musculus
P23249	14	4	4	6.87	0	0	0		14	4	4	0.19	6.87	Putative helicase MOV-10	P23249	Mov10	Mus musculus
P23492	211	8	8	44.98	52	5	5	31.83	263	8	8	0	44.98	Purine nucleoside phosphorylase	P23492	Pnp	Mus musculus
P23591	22	3	3	19.31	9	2	2	10.9	31	4	4	0.19	24.3	GDP-L-fucose synthase	P23591	Tsta3	Mus musculus
P23953	22	2	2	8.3	10	3	3	10.29	32	3	3	0.29	10.29	Carboxylesterase 1C	P23953	Ces1c	Mus musculus
P24063	46	8	8	11.35	169	14	14	20.29	215	16	16	0	22.01	Integrin alpha-L	P24063	Itgal	Mus musculus
P24270	367	20	20	45.35	14	3	3	9.49	381	20	20	0	45.35	Catalase	P24270	Cat	Mus musculus
P24369	26	4	4	24.54	5	4	4	19.91	31	6	6	0	26.85	Peptidyl-prolyl cis-trans isomerase B	P24369	Ppib	Mus musculus
P24527	540	22	22	45.66	250	22	22	43.7	790	25	25	0	48.77	Leukotriene A-4 hydrolase	P24527	Lta4h	Mus musculus
P24547	7	1	1	3.5	20	3	3	10.51	27	3	3	0.29	10.51	Inosine-5'-monophosphate dehydrogenase 2	P24547	Impdh2	Mus musculus
P24549	6	3	3	10.18	4	1	1	2	10	3	3	0.29	10.18	Retinal dehydrogenase 1	P24549	Aldh1a1	Mus musculus
P25206	5	2	2	6.16	106	8	8	17.73	111	9	9	0	19.58	DNA replication licensing factor MCM3	P25206	Mcm3	Mus musculus
P25444	6	2	2	10.24	13	2	2	8.53	19	4	4	0.19	14.33	40S ribosomal protein S2	P25444	Rps2	Mus musculus
P25911	125	12	12	25.59	40	5	5	14.26	165	12	12	0	25.59	Tyrosine-protein kinase Lyn	P25911	Lyn	Mus musculus
P26039	1901	76	76	48.48	2269	85	85	49.08	4170	98	98	0	54.43	Talin-1	P26039	Tln1	Mus musculus
P26040	364	9	6	21.16	208	10	6	19.62	572	12	7	0	22.53	Ezrin	P26040	Ezr	Mus musculus
P26041	824	21	18	38.99	368	14	10	27.04	1192	23	18	0	39.17	Moesin	P26041	Msn	Mus musculus
P26043	326	11	8	28.64	74	7	3	17.67	400	13	8	0	28.82	Radixin	P26043	Rdx	Mus musculus
P26350	2	2	2	27.93	474	13	13	62.16	476	13	13	0	62.16	Prothymosin alpha	P26350	Ptma	Mus musculus
P26369	51	5	5	18.11	104	5	5	18.11	155	5	5	0	18.11	Splicing factor U2AF 65 kDa subunit	P26369	U2af2	Mus musculus
P26443	190	9	9	27.24	99	6	6	20.25	289	10	10	0	27.42	Glutamate dehydrogenase 1, mitochondrial	P26443	Glud1	Mus musculus
P26450	30	4	4	13.12	35	2	2	8.7	65	4	4	0.19	13.12	Phosphatidylinositol 3-kinase regulatory subunit alpha	P26450	Pik3r1	Mus musculus
P26516	65	6	6	37.07	55	5	5	28.97	120	7	7	0	37.07	26S proteasome non-ATPase regulatory subunit 7	P26516	Psmd7	Mus musculus
P26638	29	5	5	14.45	14	1	1	5.47	43	5	5	0	14.45	Serine--tRNA ligase, cytoplasmic	P26638	Sars	Mus musculus
P26645	2	2	2	20.71	0	0	0		2	2	2	0.95	20.71	Myristoylated alanine-rich C-kinase substrate	P26645	Marcks	Mus musculus
P27005	797	12	12	80.9	4568	39	39	85.39	5365	40	40	0	85.39	Protein S100-A8	P27005	S100a8	Mus musculus
P27601	5	2	2	10.61	7	3	3	14.32	12	3	3	0.29	14.32	Guanine nucleotide-binding protein subunit alpha-13	P27601	Gna13	Mus musculus
P27612	84	12	12	27.71	1	1	1	2.14	85	12	12	0	27.71	Phospholipase A-2-activating protein	P27612	Plaa	Mus musculus
P27659	1	1	1	6.45	14	2	2	5.71	15	3	3	0.29	12.16	60S ribosomal protein L3	P27659	Rpl3	Mus musculus
P27661	15872	65	39	55.24	13249	48	23	55.24	29121	68	41	0	55.94	Histone H2AX	P27661	H2afx	Mus musculus
P27773	587	23	23	53.07	704	27	27	53.47	1291	29	29	0	55.64	Protein disulfide-isomerase A3	P27773	Pdia3	Mus musculus
P27784	3	2	2	39.66	3	1	1	15.52	6	2	2	0.95	39.66	C-C motif chemokine 6	P27784	Ccl6	Mus musculus
P27870	55	9	9	17.04	85	8	8	13.14	140	10	10	0	17.16	Proto-oncogene vav	P27870	Vav1	Mus musculus
P27931	70	5	5	26.34	13	2	2	11.71	83	5	5	0	26.34	Interleukin-1 receptor type 2	P27931	Il1r2	Mus musculus
P28063	47	5	5	20.65	0	0	0		47	5	5	0	20.65	Proteasome subunit beta type-8	P28063	Psmb8	Mus musculus
P28076	42	2	2	17.35	3	1	1	9.59	45	2	2	0.95	17.35	Proteasome subunit beta type-9	P28076	Psmb9	Mus musculus
P28271	6	2	2	5.4	0	0	0		6	2	2	0.95	5.4	Cytoplasmic aconitate hydratase	P28271	Aco1	Mus musculus
P28293	170	11	11	42.15	312	19	19	46.74	482	21	21	0	50.19	Cathepsin G	P28293	Ctsg	Mus musculus
P28352	117	6	6	29.34	19	2	2	11.36	136	6	6	0	29.34	DNA-(apurinic or apyrimidinic site) lyase	P28352	Apex1	Mus musculus
P28474	83	6	6	22.73	6	2	2	9.89	89	6	6	0	22.73	Alcohol dehydrogenase class-3	P28474	Adh5	Mus musculus
P28650	236	10	9	35.01	17	4	4	16.19	253	10	9	0	35.01	Adenylosuccinate synthetase isozyme 1	P28650	Adssl1	Mus musculus
P28656	82	3	3	15.35	99	4	4	20.2	181	4	4	0.19	20.2	Nucleosome assembly protein 1-like 1	P28656	Nap1l1	Mus musculus
P28658	14	3	3	8.63	21	3	3	9.68	35	4	4	0.19	11.79	Ataxin-10	P28658	Atxn10	Mus musculus
P28665	143	16	16	18.97	18	4	4	6.03	161	16	16	0	18.97	Murinoglobulin-1	P28665	Mug1	Mus musculus
P28667	1	1	1	17	37	3	3	37	38	4	4	0.19	54	MARCKS-related protein	P28667	Marcksl1	Mus musculus
P28798	287	10	10	30.56	948	21	21	41.6	1235	21	21	0	41.6	Granulins	P28798	Grn	Mus musculus
P28867	82	10	10	22.85	29	7	7	15.13	111	12	12	0	25.67	Protein kinase C delta type	P28867	Prkcd	Mus musculus
P29341	119	7	7	15.09	81	8	8	18.24	200	9	9	0	20.6	Polyadenylate-binding protein 1	P29341	Pabpc1	Mus musculus
P29351	553	22	22	45.88	329	20	20	43.87	882	22	22	0	45.88	Tyrosine-protein phosphatase non-receptor type 6	P29351	Ptpn6	Mus musculus
P29391	121	7	7	51.91	0	0	0		121	7	7	0	51.91	Ferritin light chain 1	P29391	Ftl1	Mus musculus
P29416	55	11	11	27.84	16	5	5	16.67	71	13	13	0	32.77	Beta-hexosaminidase subunit alpha	P29416	Hexa	Mus musculus
P29452	8	2	2	7.96	6	1	1	5.47	14	2	2	0.95	7.96	Caspase-1	P29452	Casp1	Mus musculus
P29621	28	2	2	6.95	39	2	2	6.95	67	2	2	0.95	6.95	Serine protease inhibitor A3C	P29621	Serpina3c	Mus musculus
P29699	106	4	4	26.38	96	5	5	28.41	202	5	5	0	28.41	Alpha-2-HS-glycoprotein	P29699	Ahsg	Mus musculus
P29758	34	5	5	20.27	26	2	2	8.2	60	5	5	0	20.27	Ornithine aminotransferase, mitochondrial	P29758	Oat	Mus musculus
P29788	39	1	1	3.77	44	3	3	3.77	83	3	3	0.29	3.77	Vitronectin	P29788	Vtn	Mus musculus
P30355	0	0	0		7	3	3	27.33	7	3	3	0.29	27.33	Arachidonate 5-lipoxygenase-activating protein	P30355	Alox5ap	Mus musculus
P30416	12	3	3	13.32	17	3	3	13.32	29	3	3	0.29	13.32	Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	Fkbp4	Mus musculus
P30681	273	9	8	40.48	258	4	4	27.62	531	9	8	0	40.48	High mobility group protein B2	P30681	Hmgb2	Mus musculus
P31230	0	0	0		4	3	3	23.87	4	3	3	0.29	23.87	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	P31230	Aimp1	Mus musculus
P31725	939	8	8	26.55	3459	18	18	62.83	4398	18	18	0	62.83	Protein S100-A9	P31725	S100a9	Mus musculus
P31750	25	2	2	7.08	18	2	2	7.08	43	2	2	0.95	7.08	RAC-alpha serine/threonine-protein kinase	P31750	Akt1	Mus musculus
P31786	7	1	1	20.69	61	2	2	22.99	68	2	2	0.95	22.99	Acyl-CoA-binding protein	P31786	Dbi	Mus musculus
P31809	2	1	1	6.14	9	2	2	9.4	11	2	2	0.95	9.4	Carcinoembryonic antigen-related cell adhesion molecule 1	P31809	Ceacam1	Mus musculus
P31938	26	2	2	12.21	4	2	2	12.21	30	2	2	0.95	12.21	Dual specificity mitogen-activated protein kinase kinase 1	P31938	Map2k1	Mus musculus
P32020	2	1	1	7.13	102	5	5	14.08	104	5	5	0	14.08	Non-specific lipid-transfer protein	P32020	Scp2	Mus musculus
P32067	19	2	2	6.75	15	3	3	13.25	34	4	4	0.19	16.63	Lupus La protein homolog	P32067	Ssb	Mus musculus
P32921	82	9	9	25.16	7	1	1	3.33	89	9	9	0	25.16	Tryptophan--tRNA ligase, cytoplasmic	P32921	Wars	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P34022	20	3	3	28.08	77	5	5	39.9	97	6	6	0	39.9	Ran-specific GTPase-activating protein	P34022	Ranbp1	Mus musculus
P34152	2	2	2	3.03	0	0	0		2	2	2	0.95	3.03	Focal adhesion kinase 1	P34152	Ptk2	Mus musculus
P34884	39	4	4	44.35	17	2	2	21.74	56	4	4	0.19	44.35	Macrophage migration inhibitory factor	P34884	Mif	Mus musculus
P35123	5	3	3	7.8	35	5	5	10.19	40	6	6	0	11.85	Ubiquitin carboxyl-terminal hydrolase 4	P35123	Usp4	Mus musculus
P35173	0	0	0		58	3	3	37.86	58	3	3	0.29	37.86	Stefin-3	P35173	Stfa3	Mus musculus
P35174-2	105	7	7	64.08	1841	12	12	78.64	1946	13	13	0	78.64	Isoform 2 of Stefin-2	P35174	Stfa2	Mus musculus
P35235	6	3	3	8.71	0	0	0		6	3	3	0.29	8.71	Tyrosine-protein phosphatase non-receptor type 11	P35235	Ptpn11	Mus musculus
P35276	7	3	2	21.46	21	3	2	20.55	28	4	2	0.95	21.46	Ras-related protein Rab-3D	P35276	Rab3d	Mus musculus
P35278	28	1	1	8.8	43	2	2	15.28	71	2	2	0.95	15.28	Ras-related protein Rab-5C	P35278	Rab5c	Mus musculus
P35282	13	1	1	5.41	27	2	2	13.96	40	2	2	0.95	13.96	Ras-related protein Rab-21	P35282	Rab21	Mus musculus
P35343	10	2	2	10.03	2	1	1	5.01	12	2	2	0.95	10.03	C-X-C chemokine receptor type 2	P35343	Cxcr2	Mus musculus
P35441	2552	53	53	49.49	220	22	22	29.49	2772	53	53	0	49.49	Thrombospondin-1	P35441	Thbs1	Mus musculus
P35461	77	2	2	24.32	72	3	3	24.32	149	3	3	0.29	24.32	Lymphocyte antigen 6G (Fragment)	P35461	Ly6g	Mus musculus
P35486	10	2	2	16.67	34	2	2	12.05	44	3	3	0.29	20	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	P35486	Pdha1	Mus musculus
P35505	116	5	5	20.53	29	4	4	15.75	145	5	5	0	20.53	Fumarylacetoacetase	P35505	Fah	Mus musculus
P35550	0	0	0		26	5	5	27.83	26	5	5	0	27.83	rRNA 2'-O-methyltransferase fibrillarin	P35550	Fbl	Mus musculus
P35564	24	5	5	13.87	228	14	14	32.99	252	14	14	0	32.99	Calnexin	P35564	Canx	Mus musculus
P35585	24	2	2	7.33	0	0	0		24	2	2	0.95	7.33	AP-1 complex subunit mu-1	P35585	Ap1m1	Mus musculus
P35700	94	7	7	47.74	72	6	6	49.75	166	8	8	0	52.76	Peroxiredoxin-1	P35700	Prdx1	Mus musculus
P35821	10	2	2	7.64	2	1	1	5.09	12	2	2	0.95	7.64	Tyrosine-protein phosphatase non-receptor type 1	P35821	Ptpn1	Mus musculus
P35831	6	1	1	2.06	10	3	3	9.03	16	3	3	0.29	9.03	Tyrosine-protein phosphatase non-receptor type 12	P35831	Ptpn12	Mus musculus
P35979	73	6	6	49.09	138	6	6	44.24	211	7	7	0	53.33	60S ribosomal protein L12	P35979	Rpl12	Mus musculus
P35991	6	3	3	6.22	0	0	0		6	3	3	0.29	6.22	Tyrosine-protein kinase BTK	P35991	Btk	Mus musculus
P36371	0	0	0		60	2	2	8.26	60	2	2	0.95	8.26	Antigen peptide transporter 2	P36371	Tap2	Mus musculus
P36993	4	3	3	10.51	0	0	0		4	3	3	0.29	10.51	Protein phosphatase 1B	P36993	Ppm1b	Mus musculus
P37040	0	0	0		82	5	5	13.13	82	5	5	0	13.13	NADPH--cytochrome P450 reductase	P37040	Por	Mus musculus
P37913	2	2	2	5.9	22	4	4	9.72	24	4	4	0.19	9.72	DNA ligase 1	P37913	Lig1	Mus musculus
P38060	20	4	4	13.23	11	1	1	4.31	31	4	4	0.19	13.23	Hydroxymethylglutaryl-CoA lyase, mitochondrial	P38060	Hmgcl	Mus musculus
P38647	20	5	5	9.13	94	7	7	15.46	114	8	8	0	15.46	Stress-70 protein, mitochondrial	P38647	Hspa9	Mus musculus
P39039	16	3	3	31.8	0	0	0		16	3	3	0.29	31.8	Mannose-binding protein A	P39039	Mbl1	Mus musculus
P39054	102	12	12	24.94	113	10	10	20.8	215	13	13	0	25.52	Dynamin-2	P39054	Dnm2	Mus musculus
P39654	157	13	13	36.95	108	12	12	35.44	265	13	13	0	36.95	Arachidonate 15-lipoxygenase	P39654	Alox15	Mus musculus
P39655	168	12	12	32.13	45	6	6	15.84	213	12	12	0	32.13	Arachidonate 12-lipoxygenase, 12S-type	P39655	Alox12	Mus musculus
P40124	1097	31	31	62.24	1123	36	36	60.13	2220	43	43	0	66.67	Adenylyl cyclase-associated protein 1	P40124	Cap1	Mus musculus
P40142	2898	51	51	54.41	1019	30	30	46.39	3917	56	56	0	54.74	Transketolase	P40142	Tkt	Mus musculus
P40223	0	0	0		3	2	2	4.78	3	2	2	0.95	4.78	Granulocyte colony-stimulating factor receptor	P40223	Csf3r	Mus musculus
P40240	110	4	4	16.81	0	0	0		110	4	4	0.19	16.81	CD9 antigen	P40240	Cd9	Mus musculus
P41216	0	0	0		6	2	2	5.29	6	2	2	0.95	5.29	Long-chain-fatty-acid--CoA ligase 1	P41216	Acsl1	Mus musculus
P41241	52	6	6	17.78	3	1	1	4	55	6	6	0	17.78	Tyrosine-protein kinase CSK	P41241	Csk	Mus musculus
P41245	1825	28	28	42.05	1540	31	31	48.08	3365	36	36	0	48.08	Matrix metalloproteinase-9	P41245	Mmp9	Mus musculus
P42208	22	3	3	13.57	8	3	3	16.34	30	4	4	0.19	20.78	Septin-2	P42208	Sept2	Mus musculus
P42227	57	6	6	16.75	47	9	9	26.49	104	9	9	0	26.49	Signal transducer and activator of transcription 3	P42227	Stat3	Mus musculus
P42232	5	3	3	6.62	1	1	1	2.8	6	3	3	0.29	6.62	Signal transducer and activator of transcription 5B	P42232	Stat5b	Mus musculus
P42567	5	2	2	3.9	51	9	9	19.06	56	9	9	0	19.06	Epidermal growth factor receptor substrate 15	P42567	Eps15	Mus musculus
P42669	50	3	3	24.3	20	2	2	18.38	70	4	4	0.19	34.58	Transcriptional activator protein Pur-alpha	P42669	Pura	Mus musculus
P42932	65	6	6	13.87	108	7	7	16.42	173	7	7	0	16.42	T-complex protein 1 subunit theta	P42932	Cct8	Mus musculus
P43024	1	1	1	12.61	23	2	2	26.13	24	2	2	0.95	26.13	Cytochrome c oxidase subunit 6A1, mitochondrial	P43024	Cox6a1	Mus musculus
P43274	403	10	4	26.48	340	9	5	26.03	743	11	5	0	26.48	Histone H1.4	P43274	Hist1h1e	Mus musculus
P43275	103	6	5	29.58	133	7	6	29.11	236	9	8	0	30.05	Histone H1.1	P43275	Hist1h1a	Mus musculus
P43276	133	5	4	17.94	202	5	5	17.94	335	6	5	0	17.94	Histone H1.5	P43276	Hist1h1b	Mus musculus
P43277	503	11	3	24.43	437	8	2	25.79	940	12	4	0.19	26.24	Histone H1.3	P43277	Hist1h1d	Mus musculus
P43430	12	1	1	6.07	7	2	2	13.36	19	2	2	0.95	13.36	Mast cell protease 8	P43430	Mcpt8	Mus musculus
P45376	61	4	4	26.27	1	1	1	5.7	62	5	5	0	26.27	Aldose reductase	P45376	Akr1b1	Mus musculus
P45878	0	0	0		19	5	5	36.43	19	5	5	0	36.43	Peptidyl-prolyl cis-trans isomerase FKBP2	P45878	Fkbp2	Mus musculus
P46061	2	1	1	4.07	51	4	4	16.13	53	4	4	0.19	16.13	Ran GTPase-activating protein 1	P46061	Rangap1	Mus musculus
P46414	0	0	0		15	2	2	11.68	15	2	2	0.95	11.68	Cyclin-dependent kinase inhibitor 1B	P46414	Cdkn1b	Mus musculus
P46460	2	1	1	1.88	10	3	3	6.32	12	3	3	0.29	6.32	Vesicle-fusing ATPase	P46460	Nsf	Mus musculus
P46467	36	8	8	27.93	1	1	1	3.83	37	8	8	0	27.93	Vacuolar protein sorting-associated protein 4B	P46467	Vps4b	Mus musculus
P46471	46	5	5	21.02	29	4	4	18.48	75	5	5	0	21.02	26S protease regulatory subunit 7	P46471	Psmc2	Mus musculus
P46638	62	3	2	19.27	100	5	3	24.31	162	5	3	0.29	24.31	Ras-related protein Rab-11B	P46638	Rab11b	Mus musculus
P46664	46	5	4	17.54	22	2	2	8.55	68	5	4	0.19	17.54	Adenylosuccinate synthetase isozyme 2	P46664	Adss	Mus musculus
P46935	0	0	0		9	2	2	4.17	9	2	2	0.95	4.17	E3 ubiquitin-protein ligase NEDD4	P46935	Nedd4	Mus musculus
P47738	620	25	25	56.07	530	24	24	60.5	1150	32	32	0	63.97	Aldehyde dehydrogenase, mitochondrial	P47738	Aldh2	Mus musculus
P47740	0	0	0		36	2	2	9.09	36	2	2	0.95	9.09	Fatty aldehyde dehydrogenase	P47740	Aldh3a2	Mus musculus
P47754	108	8	6	53.15	138	9	7	53.5	246	10	8	0	59.44	F-actin-capping protein subunit alpha-2	P47754	Capza2	Mus musculus
P47757	213	9	9	35.38	257	12	12	44.77	470	13	13	0	46.93	F-actin-capping protein subunit beta	P47757	Capzb	Mus musculus
P47791	582	16	16	48.2	247	11	11	35.2	829	18	18	0	50.8	Glutathione reductase, mitochondrial	P47791	Gsr	Mus musculus
P47809	13	4	4	16.62	2	1	1	4.03	15	4	4	0.19	16.62	Dual specificity mitogen-activated protein kinase kinase 4	P47809	Map2k4	Mus musculus
P47811	101	6	6	33.89	59	5	5	23.61	160	7	7	0	33.89	Mitogen-activated protein kinase 14	P47811	Mapk14	Mus musculus
P47911	43	2	2	10.81	3	2	2	8.78	46	3	3	0.29	13.85	60S ribosomal protein L6	P47911	Rpl6	Mus musculus
P47941	3	2	2	9.24	12	3	3	19.8	15	5	5	0	29.04	Crk-like protein	P47941	Crkl	Mus musculus
P47955	42	3	3	48.25	119	6	6	68.42	161	7	7	0	83.33	60S acidic ribosomal protein P1	P47955	Rplp1	Mus musculus
P47962	31	5	5	28.28	17	2	2	15.49	48	6	6	0	28.28	60S ribosomal protein L5	P47962	Rpl5	Mus musculus
P47968	14	2	2	11.22	6	2	2	11.22	20	2	2	0.95	11.22	Ribose-5-phosphate isomerase	P47968	Rpia	Mus musculus
P48024	4	2	2	37.17	25	3	3	38.05	29	3	3	0.29	38.05	Eukaryotic translation initiation factor 1	P48024	Eif1	Mus musculus
P48025	41	3	3	8.59	12	1	1	3.02	53	3	3	0.29	8.59	Tyrosine-protein kinase SYK	P48025	Syk	Mus musculus
P48036	191	9	9	38.87	150	9	9	37.93	341	10	10	0	41.07	Annexin A5	P48036	Anxa5	Mus musculus
P48193	67	10	10	17.95	6	2	2	4.66	73	10	10	0	17.95	Protein 4.1	P48193	Epb41	Mus musculus
P48758	11	2	2	16.97	0	0	0		11	2	2	0.95	16.97	Carbonyl reductase [NADPH] 1	P48758	Cbr1	Mus musculus
P48999	4	2	2	4.75	121	12	12	23	125	12	12	0	23	Arachidonate 5-lipoxygenase	P48999	Alox5	Mus musculus
P49138	9	2	2	11.92	0	0	0		9	2	2	0.95	11.92	MAP kinase-activated protein kinase 2	P49138	Mapkapk2	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P49222	18	4	4	12.16	4	1	1	3.62	22	4	4	0.19	12.16	Erythrocyte membrane protein band 4.2	P49222	Epb42	Mus musculus
P49290	27	3	3	6.7	21	2	2	4.75	48	3	3	0.29	6.7	Eosinophil peroxidase	P49290	Epx	Mus musculus
P49312	130	4	4	16.56	166	5	5	21.56	296	5	5	0	21.56	Heterogeneous nuclear ribonucleoprotein A1	P49312	Hnrnpa1	Mus musculus
P49710	9	2	2	7	311	11	11	36.01	320	11	11	0	36.01	Hematopoietic lineage cell-specific protein	P49710	Hcls1	Mus musculus
P49717	0	0	0		6	2	2	3.6	6	2	2	0.95	3.6	DNA replication licensing factor MCM4	P49717	Mcm4	Mus musculus
P49718	3	2	2	3.27	2	1	1	1.77	5	3	3	0.29	5.05	DNA replication licensing factor MCM5	P49718	Mcm5	Mus musculus
P49722	318	8	8	32.91	82	6	6	36.75	400	9	9	0	45.3	Proteasome subunit alpha type-2	P49722	Psma2	Mus musculus
P49813	10	3	3	9.75	0	0	0		10	3	3	0.29	9.75	Tropomodulin-1	P49813	Tmod1	Mus musculus
P50247	73	6	6	20.37	10	3	3	12.04	83	6	6	0	20.37	Adenosylhomocysteinase	P50247	Ahcy	Mus musculus
P50396	337	14	8	35.79	132	7	3	25.06	469	15	8	0	36.47	Rab GDP dissociation inhibitor alpha	P50396	Gdi1	Mus musculus
P50429	17	3	3	11.42	67	4	4	12.17	84	5	5	0	15.73	Arylsulfatase B	P50429	Arsb	Mus musculus
P50431	13	4	4	17.99	1	1	1	2.72	14	4	4	0.19	17.99	Serine hydroxymethyltransferase, cytosolic	P50431	Shmt1	Mus musculus
P50446	33	2	2	4.16	1	1	1	2.17	34	2	2	0.95	4.16	Keratin, type II cytoskeletal 6A	P50446	Krt6a	Mus musculus
P50516	251	14	14	39.22	236	11	11	31.77	487	14	14	0	39.22	V-type proton ATPase catalytic subunit A	P50516	Atp6v1a	Mus musculus
P50518	56	4	4	27.43	59	5	5	27.43	115	6	6	0	27.43	V-type proton ATPase subunit E 1	P50518	Atp6v1e1	Mus musculus
P50543	180	5	5	64.29	2289	17	17	80.61	2469	17	17	0	80.61	Protein S100-A11	P50543	S100a11	Mus musculus
P50544	11	3	3	10.21	3	2	2	6.86	14	4	4	0.19	13.26	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	P50544	Acadvl	Mus musculus
P50580	99	7	7	24.62	39	8	8	32.23	138	9	9	0	32.49	Proliferation-associated protein 2G4	P50580	Pa2g4	Mus musculus
P50637	0	0	0		2	2	2	15.38	2	2	2	0.95	15.38	Translocator protein	P50637	Tspo	Mus musculus
P51125	38	4	4	12.69	121	10	10	20.81	159	10	10	0	20.81	Calpastatin	P51125	Cast	Mus musculus
P51150	70	7	7	47.83	84	6	6	32.85	154	9	9	0	50.72	Ras-related protein Rab-7a	P51150	Rab7a	Mus musculus
P51174	52	8	8	23.95	15	5	5	13.49	67	8	8	0	23.95	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	P51174	Acadl	Mus musculus
P51410	25	4	4	42.71	70	9	9	57.81	95	9	9	0	57.81	60S ribosomal protein L9	P51410	Rpl9	Mus musculus
P51437	261	8	8	44.51	1155	17	17	46.24	1416	17	17	0	46.24	Cathelin-related antimicrobial peptide	P51437	Camp	Mus musculus
P51807	13	2	2	30.09	13	1	1	15.93	26	2	2	0.95	30.09	Dynein light chain Tctex-type 1	P51807	Dynlt1	Mus musculus
P51859	21	3	3	25.32	66	4	4	42.19	87	5	5	0	42.19	Hepatoma-derived growth factor	P51859	Hdgf	Mus musculus
P51863	14	2	2	9.69	104	10	10	35.9	118	10	10	0	35.9	V-type proton ATPase subunit d 1	P51863	Atp6v0d1	Mus musculus
P51881	7	2	2	13.42	66	4	4	21.48	73	4	4	0.19	21.48	ADP/ATP translocase 2	P51881	Slc25a5	Mus musculus
P52480	1621	45	45	64.03	1116	38	38	58.76	2737	53	53	0	65.54	Pyruvate kinase PKM	P52480	Pkm	Mus musculus
P52503	0	0	0		26	2	2	20.69	26	2	2	0.95	20.69	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	P52503	Ndufs6	Mus musculus
P52624	96	6	6	34.41	38	3	3	18.97	134	6	6	0	34.41	Uridine phosphorylase 1	P52624	Upp1	Mus musculus
P52633	4	1	1	2.99	22	3	3	9.56	26	3	3	0.29	9.56	Signal transducer and transcription activator 6	P52633	Stat6	Mus musculus
P53994	9	2	2	12.74	28	4	4	20.28	37	5	5	0	26.89	Ras-related protein Rab-2A	P53994	Rab2a	Mus musculus
P53996-2	0	0	0		25	3	3	22.35	25	3	3	0.29	22.35	Isoform 2 of Cellular nucleic acid-binding protein	P53996	Cnbp	Mus musculus
P54071	106	9	9	24.12	47	5	5	15.49	153	9	9	0	24.12	Isocitrate dehydrogenase [NADP], mitochondrial	P54071	Idh2	Mus musculus
P54103	0	0	0		11	3	3	7.89	11	3	3	0.29	7.89	DnaJ homolog subfamily C member 2	P54103	Dnajc2	Mus musculus
P54310	4	3	3	8.17	0	0	0		4	3	3	0.29	8.17	Hormone-sensitive lipase	P54310	Lipe	Mus musculus
P54728	6	1	1	4.57	35	2	2	8.65	41	2	2	0.95	8.65	UV excision repair protein RAD23 homolog B	P54728	Rad23b	Mus musculus
P54775	137	8	8	31.1	148	5	5	25.6	285	9	9	0	31.82	26S protease regulatory subunit 6B	P54775	Psmc4	Mus musculus
P54818	10	1	1	3.36	2	2	2	6.43	12	2	2	0.95	6.43	Galactocerebrosidase	P54818	Galc	Mus musculus
P54822	36	5	5	21.69	13	3	3	11.78	49	5	5	0	21.69	Adenylosuccinate lyase	P54822	Adsl	Mus musculus
P54823	31	4	4	13.46	50	3	3	11.59	81	5	5	0	16.98	Probable ATP-dependent RNA helicase DDX6	P54823	Ddx6	Mus musculus
P54923	4	2	2	9.12	0	0	0		4	2	2	0.95	9.12	[Protein ADP-ribosylarginine] hydrolase	P54923	Adprh	Mus musculus
P55264	49	7	7	34.9	0	0	0		49	7	7	0	34.9	Adenosine kinase	P55264	Adk	Mus musculus
P55772	0	0	0		13	3	3	11.37	13	3	3	0.29	11.37	Ectonucleoside triphosphate diphosphohydrolase 1	P55772	Entpd1	Mus musculus
P55937	0	0	0		5	2	2	2.49	5	2	2	0.95	2.49	Golgin subfamily A member 3	P55937	Golga3	Mus musculus
P56391	5	2	2	29.07	57	6	6	70.93	62	6	6	0	70.93	Cytochrome c oxidase subunit 6B1	P56391	Cox6b1	Mus musculus
P56395	0	0	0		2	2	2	25.37	2	2	2	0.95	25.37	Cytochrome b5	P56395	Cyb5a	Mus musculus
P56399	170	17	17	32.05	205	14	14	26.22	375	19	19	0	33.22	Ubiquitin carboxyl-terminal hydrolase 5	P56399	Usp5	Mus musculus
P56480	193	12	12	37.62	879	22	22	58.41	1072	22	22	0	58.41	ATP synthase subunit beta, mitochondrial	P56480	Atp5b	Mus musculus
P56546	0	0	0		15	2	2	13.48	15	2	2	0.95	13.48	C-terminal-binding protein 2	P56546	Ctbp2	Mus musculus
P56565	15	2	2	26.6	32	3	3	26.6	47	3	3	0.29	26.6	Protein S100-A1	P56565	S100a1	Mus musculus
P56812	0	0	0		20	2	2	19.84	20	2	2	0.95	19.84	Programmed cell death protein 5	P56812	Pdcd5	Mus musculus
P56959	65	4	4	13.51	128	7	5	13.51	193	7	5	0	13.51	RNA-binding protein FUS	P56959	Fus	Mus musculus
P57716	4	2	2	7.34	8	3	3	7.63	12	4	4	0.19	10.88	Nicastrin	P57716	Ncstn	Mus musculus
P57746	4	1	1	11.34	11	2	2	17.81	15	2	2	0.95	17.81	V-type proton ATPase subunit D	P57746	Atp6v1d	Mus musculus
P57759	21	1	1	3.44	38	3	3	11.07	59	3	3	0.29	11.07	Endoplasmic reticulum resident protein 29	P57759	Erp29	Mus musculus
P57780	837	36	22	50.88	617	32	19	45.18	1454	39	24	0	53.84	Alpha-actinin-4	P57780	Actn4	Mus musculus
P57784	37	5	5	35.69	63	9	9	50.59	100	10	10	0	54.12	U2 small nuclear ribonucleoprotein A'	P57784	Snrpa1	Mus musculus
P58058	31	5	5	20.5	20	2	2	12.76	51	5	5	0	20.5	NAD kinase	P58058	Nadk	Mus musculus
P58252	1217	32	32	47.32	1025	30	30	40.33	2242	39	39	0	49.42	Elongation factor 2	P58252	Eef2	Mus musculus
P58389	44	5	5	28.17	40	5	5	21.98	84	6	6	0	28.17	Serine/threonine-protein phosphatase 2A activator	P58389	Ppp2r4	Mus musculus
P58742	0	0	0		14	3	3	12.45	14	3	3	0.29	12.45	Aladin	P58742	Aaas	Mus musculus
P59108	39	3	2	8.94	30	5	4	17.7	69	5	4	0.19	17.7	Copine-2	P59108	Cpne2	Mus musculus
P59325	10	1	1	2.1	9	2	2	6.53	19	2	2	0.95	6.53	Eukaryotic translation initiation factor 5	P59325	Eif5	Mus musculus
P59708	1	1	1	11.2	6	2	2	22.4	7	2	2	0.95	22.4	Splicing factor 3B subunit 6	P59708	Sf3b6	Mus musculus
P59999	171	2	2	17.86	42	2	2	17.86	213	2	2	0.95	17.86	Actin-related protein 2/3 complex subunit 4	P59999	Arpc4	Mus musculus
P60122	56	6	6	21.71	63	5	5	17.98	119	7	7	0	26.1	RuvB-like 1	P60122	Ruvbl1	Mus musculus
P60229	12	2	2	7.19	26	5	5	17.53	38	5	5	0	17.53	Eukaryotic translation initiation factor 3 subunit E	P60229	Eif3e	Mus musculus
P60335	58	5	4	27.81	189	6	6	36.52	247	7	6	0	42.13	Poly(rC)-binding protein 1	P60335	Pcbp1	Mus musculus
P60670	23	4	4	16.94	12	4	4	17.93	35	5	5	0	20.89	Nuclear protein localization protein 4 homolog	P60670	Nploc4	Mus musculus
P60710	9210	78	37	81.87	5529	46	23	80.53	14739	83	40	0	84.8	Actin, cytoplasmic 1	P60710	Actb	Mus musculus
P60766	262	11	10	58.12	181	11	10	48.17	443	13	12	0	59.16	Cell division control protein 42 homolog	P60766	Cdc42	Mus musculus
P60843	172	16	14	47.78	145	9	8	26.35	317	18	16	0	49.26	Eukaryotic initiation factor 4A-I	P60843	Eif4a1	Mus musculus
P60867	2	1	1	10.08	3	2	2	19.33	5	2	2	0.95	19.33	40S ribosomal protein S20	P60867	Rps20	Mus musculus
P60898	0	0	0		35	2	2	32	35	2	2	0.95	32	DNA-directed RNA polymerase II subunit RPB9	P60898	Polr2i	Mus musculus
P61022	5	2	2	18.46	22	2	2	18.46	27	2	2	0.95	18.46	Calcineurin B homologous protein 1	P61022	Chp1	Mus musculus
P61079	37	2	2	28.57	65	2	2	28.57	102	2	2	0.95	28.57	Ubiquitin-conjugating enzyme E2 D3	P61079	Ube2d3	Mus musculus
P61087	3	1	1	14	6	2	2	23.5	9	2	2	0.95	23.5	Ubiquitin-conjugating enzyme E2 K	P61087	Ube2k	Mus musculus
P61089	40	2	2	31.58	68	5	5	51.32	108	5	5	0	51.32	Ubiquitin-conjugating enzyme E2 N	P61089	Ube2n	Mus musculus
P61161	810	19	19	44.92	313	15	15	40.86	1123	23	23	0	53.3	Actin-related protein 2	P61161	Actr2	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P61164	120	7	7	31.91	57	6	6	27.66	177	9	9	0	32.45	Alpha-centractin	P61164	Actr1a	Mus musculus
P61202	5	2	2	10.38	14	1	1	5.64	19	2	2	0.95	10.38	COP9 signalosome complex subunit 2	P61202	Cops2	Mus musculus
P61205	249	12	1	68.51	143	9	2	56.35	392	13	2	0.95	69.61	ADP-ribosylation factor 3	P61205	Arf3	Mus musculus
P61219	0	0	0		5	2	2	19.69	5	2	2	0.95	19.69	DNA-directed RNA polymerases I, II, and III subunit RPABC2	P61219	Polr2f	Mus musculus
P61222	23	6	6	17.86	6	3	3	7.51	29	7	7	0	17.86	ATP-binding cassette sub-family E member 1	P61222	Abce1	Mus musculus
P61290	3	1	1	5.91	2	2	2	19.69	5	3	3	0.29	19.69	Proteasome activator complex subunit 3	P61290	Psme3	Mus musculus
P61327	9	4	4	39.04	2	1	1	13.7	11	4	4	0.19	39.04	Protein mago nashi homolog	P61327	Magoh	Mus musculus
P61750	205	10	3	57.78	108	8	3	56.67	313	10	3	0.29	57.78	ADP-ribosylation factor 4	P61750	Arf4	Mus musculus
P61924	0	0	0		13	4	4	40.11	13	4	4	0.19	40.11	Coatomer subunit zeta-1	P61924	Copz1	Mus musculus
P61961	6	1	1	41.18	31	3	3	41.18	37	3	3	0.29	41.18	Ubiquitin-fold modifier 1	P61961	Ufm1	Mus musculus
P61965	7	3	3	14.37	5	1	1	5.69	12	4	4	0.19	20.06	WD repeat-containing protein 5	P61965	Wdr5	Mus musculus
P61979	209	11	11	33.48	553	19	19	49.89	762	20	20	0	49.89	Heterogeneous nuclear ribonucleoprotein K	P61979	Hnrnpk	Mus musculus
P61982	210	7	7	44.94	287	12	12	52.23	497	12	12	0	52.23	14-3-3 protein gamma	P61982	Ywhag	Mus musculus
P62082	42	4	4	33.51	139	10	10	41.24	181	10	10	0	41.24	40S ribosomal protein S7	P62082	Rps7	Mus musculus
P62137	269	12	4	37.27	132	12	5	40.61	401	14	5	0	41.21	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	P62137	Ppp1ca	Mus musculus
P62141	262	12	4	38.23	104	9	2	29.97	366	13	4	0.19	38.53	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	P62141	Ppp1cb	Mus musculus
P62192	3	2	2	6.36	23	2	2	7.5	26	3	3	0.29	10.91	26S protease regulatory subunit 4	P62192	Psmc1	Mus musculus
P62196	43	4	4	15.27	8	2	2	7.88	51	5	5	0	17.98	26S protease regulatory subunit 8	P62196	Psmc5	Mus musculus
P62204	346	4	4	45.64	314	4	4	30.87	660	5	5	0	45.64	Calmodulin	P62204	Calm1	Mus musculus
P62242	9	2	2	13.46	32	4	4	27.88	41	4	4	0.19	27.88	40S ribosomal protein S8	P62242	Rps8	Mus musculus
P62259	207	9	8	47.45	196	10	9	37.65	403	13	11	0	56.08	14-3-3 protein epsilon	P62259	Ywhae	Mus musculus
P62264	1	1	1	18.54	64	7	7	39.07	65	7	7	0	39.07	40S ribosomal protein S14	P62264	Rps14	Mus musculus
P62267	11	2	2	19.58	42	3	3	19.58	53	3	3	0.29	19.58	40S ribosomal protein S23	P62267	Rps23	Mus musculus
P62281	7	2	2	17.72	34	2	2	12.03	41	3	3	0.29	18.35	40S ribosomal protein S11	P62281	Rps11	Mus musculus
P62315	84	6	6	36.97	9	4	4	31.93	93	8	8	0	36.97	Small nuclear ribonucleoprotein Sm D1	P62315	Snrpd1	Mus musculus
P62317	68	2	2	16.1	34	2	2	16.1	102	2	2	0.95	16.1	Small nuclear ribonucleoprotein Sm D2	P62317	Snrpd2	Mus musculus
P62320	151	2	2	24.6	161	4	4	18.25	312	5	5	0	26.19	Small nuclear ribonucleoprotein Sm D3	P62320	Snrpd3	Mus musculus
P62331	32	5	5	45.14	20	2	2	16	52	5	5	0	45.14	ADP-ribosylation factor 6	P62331	Arf6	Mus musculus
P62334	35	3	3	7.46	18	3	3	11.57	53	4	4	0.19	11.57	26S protease regulatory subunit 10B	P62334	Psmc6	Mus musculus
P62482	13	3	3	17.44	0	0	0		13	3	3	0.29	17.44	Voltage-gated potassium channel subunit beta-2	P62482	Kcnab2	Mus musculus
P62492	39	2	1	19.44	74	4	2	26.85	113	4	2	0.95	26.85	Ras-related protein Rab-11A	P62492	Rab11a	Mus musculus
P62702	9	3	3	11.79	5	1	1	4.94	14	4	4	0.19	11.79	40S ribosomal protein S4, X isoform	P62702	Rps4x	Mus musculus
P62715	63	7	7	37.22	45	7	7	36.89	108	8	8	0	37.22	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	P62715	Ppp2cb	Mus musculus
P62746	87	3	1	25.51	87	5	2	25.51	174	5	2	0.95	25.51	Rho-related GTP-binding protein RhoB	P62746	Rhob	Mus musculus
P62751	0	0	0		30	3	3	11.54	30	3	3	0.29	11.54	60S ribosomal protein L23a	P62751	Rpl23a	Mus musculus
P62754	2	1	1	6.83	30	6	6	18.47	32	6	6	0	18.47	40S ribosomal protein S6	P62754	Rps6	Mus musculus
P62774	15	2	2	32.2	98	4	4	61.02	113	4	4	0.19	61.02	Myotrophin	P62774	Mtpn	Mus musculus
P62806	4018	23	23	60.19	1198	13	13	56.31	5216	23	23	0	60.19	Histone H4	P62806	Hist1h4a	Mus musculus
P62814	233	10	10	28.38	86	12	12	28.77	319	13	13	0	31.12	V-type proton ATPase subunit B, brain isoform	P62814	Atp6v1b2	Mus musculus
P62827	408	16	16	57.87	53	4	4	21.76	461	16	16	0	57.87	GTP-binding nuclear protein Ran	P62827	Ran	Mus musculus
P62830	10	2	2	15	52	3	3	23.57	62	3	3	0.29	23.57	60S ribosomal protein L23	P62830	Rpl23	Mus musculus
P62835	122	8	8	37.5	114	10	10	50	236	10	10	0	50	Ras-related protein Rap-1A	P62835	Rap1a	Mus musculus
P62858	2	1	1	17.39	18	3	3	27.54	20	3	3	0.29	27.54	40S ribosomal protein S28	P62858	Rps28	Mus musculus
P62869	0	0	0		8	2	2	53.39	8	2	2	0.95	53.39	Transcription elongation factor B polypeptide 2	P62869	Tceb2	Mus musculus
P62874	107	7	5	31.47	112	7	5	31.47	219	7	5	0	31.47	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	P62874	Gnb1	Mus musculus
P62880	90	10	8	48.53	255	14	12	56.47	345	16	14	0	65.29	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	P62880	Gnb2	Mus musculus
P62889	34	2	2	24.35	40	3	3	40.87	74	3	3	0.29	40.87	60S ribosomal protein L30	P62889	Rpl30	Mus musculus
P62908	39	7	7	39.09	72	7	7	32.51	111	8	8	0	39.09	40S ribosomal protein S3	P62908	Rps3	Mus musculus
P62960	59	5	5	29.5	85	7	7	29.81	144	7	7	0	29.81	Nuclease-sensitive element-binding protein 1	P62960	Ybx1	Mus musculus
P62962	144	5	5	41.43	252	11	11	58.57	396	11	11	0	58.57	Profilin-1	P62962	Pfn1	Mus musculus
P62983	30	1	1	10.26	146	5	5	36.54	176	5	5	0	36.54	Ubiquitin-40S ribosomal protein S27a	P62983	Rps27a	Mus musculus
P62996	48	4	4	18.75	105	4	4	18.06	153	5	5	0	19.1	Transformer-2 protein homolog beta	P62996	Tra2b	Mus musculus
P63001	135	12	2	48.44	67	9	1	41.15	202	13	3	0.29	48.44	Ras-related C3 botulinum toxin substrate 1	P63001	Rac1	Mus musculus
P63005	69	6	6	25.12	24	3	3	9.02	93	6	6	0	25.12	Platelet-activating factor acetylhydrolase IB subunit alpha	P63005	Pafah1b1	Mus musculus
P63017	965	40	38	59.44	1225	38	36	53.41	2190	48	46	0	61.76	Heat shock cognate 71 kDa protein	P63017	Hspa8	Mus musculus
P63024	0	0	0		4	2	2	23.3	4	2	2	0.95	23.3	Vesicle-associated membrane protein 3	P63024	Vamp3	Mus musculus
P63028	33	2	2	8.72	39	4	4	25	72	4	4	0.19	25	Translationally-controlled tumor protein	P63028	Tpt1	Mus musculus
P63038	0	0	0		195	18	18	36.65	195	18	18	0	36.65	60 kDa heat shock protein, mitochondrial	P63038	Hspd1	Mus musculus
P63073	18	3	3	20.74	2	1	1	15.67	20	3	3	0.29	20.74	Eukaryotic translation initiation factor 4E	P63073	Eif4e	Mus musculus
P63085	42	6	5	30.45	5	2	2	10.34	47	7	6	0	30.45	Mitogen-activated protein kinase 1	P63085	Mapk1	Mus musculus
P63094	17	2	2	9.39	19	3	2	12.18	36	3	2	0.95	12.18	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	P63094	Gnas	Mus musculus
P63101	556	14	12	55.51	662	19	16	61.22	1218	20	16	0	61.22	14-3-3 protein zeta/delta	P63101	Ywhaz	Mus musculus
P63139	0	0	0		29	2	2	11.59	29	2	2	0.95	11.59	Nuclear transcription factor Y subunit beta	P63139	Nfyb	Mus musculus
P63147	1	1	1	26.32	16	2	2	26.32	17	2	2	0.95	26.32	Ubiquitin-conjugating enzyme E2 B	P63147	Ube2b	Mus musculus
P63158	116	6	5	34.88	61	1	1	6.98	177	6	5	0	34.88	High mobility group protein B1	P63158	Hmgb1	Mus musculus
P63242	185	5	5	37.66	232	6	6	46.75	417	7	7	0	58.44	Eukaryotic translation initiation factor 5A-1	P63242	Eif5a	Mus musculus
P63276	2	1	1	16.3	79	6	6	45.19	81	6	6	0	45.19	40S ribosomal protein S17	P63276	Rps17	Mus musculus
P63280	25	1	1	19.62	43	3	3	19.62	68	3	3	0.29	19.62	SUMO-conjugating enzyme UBC9	P63280	Ube2i	Mus musculus
P63321	0	0	0		7	2	2	22.33	7	2	2	0.95	22.33	Ras-related protein Ral-A	P63321	Rala	Mus musculus
P63325	21	3	3	23.64	1	1	1	9.09	22	3	3	0.29	23.64	40S ribosomal protein S10	P63325	Rps10	Mus musculus
P63328	18	3	3	9.79	1	1	1	4.8	19	3	3	0.29	9.79	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	P63328	Ppp3ca	Mus musculus
P67778	29	2	2	13.6	289	16	16	72.06	318	16	16	0	72.06	Prohibitin	P67778	Phb	Mus musculus
P67871	1	1	1	13.95	9	2	2	13.95	10	2	2	0.95	13.95	Casein kinase II subunit beta	P67871	Csnk2b	Mus musculus
P67984	0	0	0		19	4	4	42.19	19	4	4	0.19	42.19	60S ribosomal protein L22	P67984	Rpl22	Mus musculus
P68033	4141	43	13	61.01	3969	28	11	55.44	8110	47	15	0	64.46	Actin, alpha cardiac muscle 1	P68033	Actc1	Mus musculus
P68037	34	5	5	48.7	62	4	4	38.96	96	5	5	0	48.7	Ubiquitin-conjugating enzyme E2 L3	P68037	Ube2l3	Mus musculus
P68040	336	16	16	61.83	175	10	10	50.16	511	16	16	0	61.83	Guanine nucleotide-binding protein subunit beta-2-like 1	P68040	Gnb2l1	Mus musculus
P68254	159	10	9	45.71	174	12	11	55.1	333	14	12	0	55.1	14-3-3 protein theta	P68254	Ywhaq	Mus musculus
P68368	475	16	6	52.01	1018	27	15	66.52	1493	27	15	0	66.52	Tubulin alpha-4A chain	P68368	Tuba4a	Mus musculus
P68369	383	17	7	53.22	945	26	14	66.96	1328	26	14	0	66.96	Tubulin alpha-1A chain	P68369	Tuba1a	Mus musculus
P68372	428	19	1	58.65	1123	27	3	65.17	1551	30	3	0.29	71.91	Tubulin beta-4B chain	P68372	Tubb4b	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
P68404-2	0	0	0		20	3	3	10.4	20	3	3	0.29	10.4	Isoform Beta-II of Protein kinase C beta type	P68404	Prkcb	Mus musculus
P68433	2406	29	19	32.35	1033	16	7	32.35	3439	30	19	0	32.35	Histone H3.1	P68433	Hist1h3a	Mus musculus
P68510	222	13	12	55.69	192	13	12	55.69	414	15	13	0	55.69	14-3-3 protein eta	P68510	Ywhah	Mus musculus
P70158	1	1	1	2.7	15	2	2	8.31	16	2	2	0.95	8.31	Acid sphingomyelinase-like phosphodiesterase 3a	P70158	Smpdl3a	Mus musculus
P70168	321	18	18	30.37	256	17	17	36.3	577	22	22	0	39.61	Importin subunit beta-1	P70168	Kpnb1	Mus musculus
P70195	155	8	8	53.79	0	0	0		155	8	8	0	53.79	Proteasome subunit beta type-7	P70195	Psmb7	Mus musculus
P70268	28	6	6	11.42	50	7	7	14.59	78	8	8	0	17.02	Serine/threonine-protein kinase N1	P70268	Pkn1	Mus musculus
P70290	92	7	7	16.31	53	7	7	23.18	145	10	10	0	26.39	55 kDa erythrocyte membrane protein	P70290	Mpp1	Mus musculus
P70296	68	3	3	33.16	85	5	5	48.66	153	6	6	0	56.15	Phosphatidylethanolamine-binding protein 1	P70296	Pebp1	Mus musculus
P70315	5	3	3	10.38	18	5	5	19.23	23	7	7	0	23.65	Wiskott-Aldrich syndrome protein homolog	P70315	Was	Mus musculus
P70333	34	1	0	3.79	76	5	2	16.7	110	5	2	0.95	16.7	Heterogeneous nuclear ribonucleoprotein H2	P70333	Hnrnph2	Mus musculus
P70335	13	3	3	5.39	30	2	2	4.58	43	3	3	0.29	5.39	Rho-associated protein kinase 1	P70335	Rock1	Mus musculus
P70349	7	1	1	15.87	35	3	3	32.54	42	3	3	0.29	32.54	Histidine triad nucleotide-binding protein 1	P70349	Hint1	Mus musculus
P70372	4	1	1	7.67	14	2	2	11.66	18	2	2	0.95	11.66	ELAV-like protein 1	P70372	Elavl1	Mus musculus
P70388	0	0	0		2	2	2	2.74	2	2	2	0.95	2.74	DNA repair protein RAD50	P70388	Rad50	Mus musculus
P70398	1	1	1	0.7	21	6	6	4.53	22	6	6	0	4.53	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	P70398	Usp9x	Mus musculus
P70441	37	4	4	24.23	58	7	7	35.21	95	7	7	0	35.21	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	P70441	Slc9a3r1	Mus musculus
P70444	2	1	1	9.74	26	3	3	31.79	28	3	3	0.29	31.79	BH3-interacting domain death agonist	P70444	Bid	Mus musculus
P70460	74	4	4	10.4	153	4	4	13.87	227	5	5	0	13.87	Vasodilator-stimulated phosphoprotein	P70460	Vasp	Mus musculus
P70670	40	4	4	2.88	96	6	6	1.92	136	8	8	0	3.48	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	P70670	Naca	Mus musculus
P70677	35	3	3	22.74	15	1	1	7.58	50	3	3	0.29	22.74	Caspase-3	P70677	Casp3	Mus musculus
P70697	24	3	3	15.8	0	0	0		24	3	3	0.29	15.8	Uroporphyrinogen decarboxylase	P70697	Urod	Mus musculus
P70698	16	2	2	5.08	4	2	2	5.92	20	3	3	0.29	8.29	CTP synthase 1	P70698	Ctps1	Mus musculus
P70699	3	1	1	2.41	3	2	2	3.67	6	3	3	0.29	6.09	Lysosomal alpha-glucosidase	P70699	Gaa	Mus musculus
P80313	133	8	8	27.02	179	6	6	20.96	312	8	8	0	27.02	T-complex protein 1 subunit eta	P80313	Cct7	Mus musculus
P80314	179	10	10	31.78	146	9	9	26.54	325	12	12	0	36.07	T-complex protein 1 subunit beta	P80314	Cct2	Mus musculus
P80315	73	6	6	18.37	94	7	7	19.11	167	8	8	0	21.52	T-complex protein 1 subunit delta	P80315	Cct4	Mus musculus
P80316	121	9	9	31.05	153	9	9	26.8	274	11	11	0	32.72	T-complex protein 1 subunit epsilon	P80316	Cct5	Mus musculus
P80317	121	8	8	22.22	173	8	8	22.41	294	9	9	0	24.67	T-complex protein 1 subunit zeta	P80317	Cct6a	Mus musculus
P80318	20	6	6	16.51	15	4	4	11.01	35	8	8	0	22.75	T-complex protein 1 subunit gamma	P80318	Cct3	Mus musculus
P81117	16	1	1	5	52	7	7	20.48	68	7	7	0	20.48	Nucleobindin-2	P81117	Nucb2	Mus musculus
P82198	565	17	17	36.75	181	9	9	23.87	746	17	17	0	36.75	Transforming growth factor-beta-induced protein ig-h3	P82198	Tgfbi	Mus musculus
P83870	14	1	1	14.55	36	3	3	32.73	50	3	3	0.29	32.73	PHD finger-like domain-containing protein 5A	P83870	Phf5a	Mus musculus
P83917	13	2	2	16.76	90	4	4	32.43	103	4	4	0.19	32.43	Chromobox protein homolog 1	P83917	Cbx1	Mus musculus
P84078	307	15	4	69.61	180	9	2	56.35	487	15	4	0.19	69.61	ADP-ribosylation factor 1	P84078	Arf1	Mus musculus
P84084	254	11	3	57.78	145	8	2	52.22	399	11	3	0.29	57.78	ADP-ribosylation factor 5	P84084	Arf5	Mus musculus
P84089	3	2	2	44.23	29	3	3	44.23	32	3	3	0.29	44.23	Enhancer of rudimentary homolog	P84089	Erh	Mus musculus
P84091	11	3	3	13.56	6	3	3	9.89	17	4	4	0.19	13.56	AP-2 complex subunit mu	P84091	Ap2m1	Mus musculus
P84096	272	10	10	61.78	134	8	8	48.17	406	11	11	0	61.78	Rho-related GTP-binding protein RhoG	P84096	Rhog	Mus musculus
P84099	11	1	1	8.67	22	2	2	8.67	33	2	2	0.95	8.67	60S ribosomal protein L19	P84099	Rpl19	Mus musculus
P84104	36	3	3	28.66	102	4	3	28.66	138	4	3	0.29	28.66	Serine/arginine-rich splicing factor 3	P84104	Srsf3	Mus musculus
P84228	3589	34	18	32.35	1188	17	5	32.35	4777	36	18	0	32.35	Histone H3.2	P84228	Hist1h3b	Mus musculus
P84244	1992	29	13	32.35	1101	18	6	32.35	3093	33	15	0	32.35	Histone H3.3	P84244	H3f3a	Mus musculus
P85094	14	2	2	29.13	15	2	2	29.13	29	2	2	0.95	29.13	Isochorismatase domain-containing protein 2A, mitochondrial	P85094	Isoc2a	Mus musculus
P97302	0	0	0		3	3	3	6.5	3	3	3	0.29	6.5	Transcription regulator protein BACH1	P97302	Bach1	Mus musculus
P97310	13	4	4	6.64	19	2	2	5.64	32	5	5	0	10.07	DNA replication licensing factor MCM2	P97310	Mcm2	Mus musculus
P97311	3	2	2	5.36	61	7	7	14.25	64	7	7	0	14.25	DNA replication licensing factor MCM6	P97311	Mcm6	Mus musculus
P97315	8	2	2	17.62	63	6	6	45.6	71	6	6	0	45.6	Cysteine and glycine-rich protein 1	P97315	Csrp1	Mus musculus
P97351	17	4	4	12.12	30	3	3	6.82	47	4	4	0.19	12.12	40S ribosomal protein S3a	P97351	Rps3a	Mus musculus
P97355	14	3	3	19.13	2	1	1	7.1	16	3	3	0.29	19.13	Spermine synthase	P97355	Sms	Mus musculus
P97363	0	0	0		15	2	2	6.96	15	2	2	0.95	6.96	Serine palmitoyltransferase 2	P97363	Sptlc2	Mus musculus
P97364	3	2	2	7.74	0	0	0		3	2	2	0.95	7.74	Selenide, water dikinase 2	P97364	Sephs2	Mus musculus
P97369	254	16	16	43.36	357	15	15	43.66	611	19	19	0	45.43	Neutrophil cytosol factor 4	P97369	Ncf4	Mus musculus
P97370	1	1	1	6.12	4	2	2	11.15	5	2	2	0.95	11.15	Sodium/potassium-transporting ATPase subunit beta-3	P97370	Atp1b3	Mus musculus
P97371	94	5	5	26.51	133	5	5	25.3	227	6	6	0	30.92	Proteasome activator complex subunit 1	P97371	Psme1	Mus musculus
P97372	105	7	7	41.84	113	8	8	36.4	218	9	9	0	42.26	Proteasome activator complex subunit 2	P97372	Psme2	Mus musculus
P97376	0	0	0		9	2	2	6.59	9	2	2	0.95	6.59	Protein FRG1	P97376	Frg1	Mus musculus
P97384	335	14	14	28.23	186	12	12	29.03	521	15	15	0	31.41	Annexin A11	P97384	Anxa11	Mus musculus
P97425	87	4	3	39.1	20	4	3	39.1	107	4	3	0.29	39.1	Eosinophil cationic protein 2	P97425	Ear2	Mus musculus
P97426	125	5	4	45.16	41	5	4	38.06	166	6	5	0	45.16	Eosinophil cationic protein 1	P97426	Ear1	Mus musculus
P97429	18	4	4	19.75	1	1	1	4.7	19	4	4	0.19	19.75	Annexin A4	P97429	Anxa4	Mus musculus
P97450	11	1	1	21.3	134	4	4	34.26	145	4	4	0.19	34.26	ATP synthase-coupling factor 6, mitochondrial	P97450	Atp5j	Mus musculus
P97484	6	3	3	8.92	10	1	1	4.04	16	3	3	0.29	8.92	Leukocyte immunoglobulin-like receptor subfamily B member 3	P97484	Lilrb3	Mus musculus
P97492	0	0	0		17	4	4	14.81	17	4	4	0.19	14.81	Regulator of G-protein signaling 14	P97492	Rgs14	Mus musculus
P97493	0	0	0		6	2	2	21.08	6	2	2	0.95	21.08	Thioredoxin, mitochondrial	P97493	Txn2	Mus musculus
P97496	1	1	1	1.99	6	2	2	3.71	7	2	2	0.95	3.71	SWI/SNF complex subunit SMARCC1	P97496	Smarcc1	Mus musculus
P97797	3	1	1	2.53	11	5	5	12.87	14	5	5	0	12.87	Tyrosine-protein phosphatase non-receptor type substrate 1	P97797	Sirpa	Mus musculus
P97807	111	3	3	10.45	72	5	5	14.4	183	5	5	0	14.4	Fumarate hydratase, mitochondrial	P97807	Fh	Mus musculus
P97814	0	0	0		49	3	3	13.98	49	3	3	0.29	13.98	Proline-serine-threonine phosphatase-interacting protein 1	P97814	Pstpip1	Mus musculus
P97821	61	5	5	17.53	75	6	6	17.75	136	6	6	0	17.75	Dipeptidyl peptidase 1	P97821	Ctsc	Mus musculus
P97822	3	3	3	11.54	66	7	7	28.46	69	7	7	0	28.46	Acidic leucine-rich nuclear phosphoprotein 32 family member E	P97822	Anp32e	Mus musculus
P97823	88	9	9	49.57	16	3	3	20.87	104	9	9	0	49.57	Acyl-protein thioesterase 1	P97823	Lypla1	Mus musculus
P97855	14	2	2	8.6	43	6	6	16.56	57	6	6	0	16.56	Ras GTPase-activating protein-binding protein 1	P97855	G3bp1	Mus musculus
P97864	9	2	2	15.18	7	2	2	15.18	16	4	4	0.19	30.36	Caspase-7	P97864	Casp7	Mus musculus
P97872	0	0	0		9	3	3	8.26	9	3	3	0.29	8.26	Dimethylaniline monooxygenase [N-oxide-forming] 5	P97872	Fmo5	Mus musculus
P98083	7	1	1	4.49	36	3	3	7.25	43	3	3	0.29	7.25	SHC-transforming protein 1	P98083	Shc1	Mus musculus
P99024	401	16	4	51.35	1203	31	9	66.89	1604	31	9	0	66.89	Tubulin beta-5 chain	P99024	Tubb5	Mus musculus
P99026	38	6	6	38.64	6	1	1	5.68	44	6	6	0	38.64	Proteasome subunit beta type-4	P99026	Psmb4	Mus musculus
P99027	178	6	6	91.3	340	10	10	80	518	11	11	0	94.78	60S acidic ribosomal protein P2	P99027	Rplp2	Mus musculus
P99028	2	1	1	20.22	78	2	2	41.57	80	2	2	0.95	41.57	Cytochrome b-c1 complex subunit 6, mitochondrial	P99028	Uqcrh	Mus musculus
P99029	149	8	8	48.1	441	15	15	64.76	590	15	15	0	64.76	Peroxiredoxin-5, mitochondrial	P99029	Prdx5	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q00519	820	27	27	34.91	129	12	12	20.6	949	28	28	0	35.66	Xanthine dehydrogenase/oxidase	Q00519	Xdh	Mus musculus
Q00612	602	28	17	43.3	428	24	12	34.56	1030	33	20	0	46.99	Glucose-6-phosphate 1-dehydrogenase X	Q00612	G6pdx	Mus musculus
Q00623	15	2	2	18.94	28	4	4	24.24	43	4	4	0.19	24.24	Apolipoprotein A-I	Q00623	Apoa1	Mus musculus
Q00896	7	3	2	14.08	52	5	1	29.13	59	6	2	0.95	34.47	Alpha-1-antitrypsin 1-3	Q00896	Serpina1c	Mus musculus
Q00PI9	13	1	1	4.43	96	9	9	17.58	109	9	9	0	17.58	Heterogeneous nuclear ribonucleoprotein U-like protein 2	Q00PI9	Hnrnpul2	Mus musculus
Q01102	29	3	3	8.98	17	2	2	6.9	46	4	4	0.19	11.59	P-selectin	Q01102	Selp	Mus musculus
Q01320	5	3	1	2.62	53	5	4	4.45	58	7	5	0	5.17	DNA topoisomerase 2-alpha	Q01320	Top2a	Mus musculus
Q01339	24	6	6	29.86	0	0	0		24	6	6	0	29.86	Beta-2-glycoprotein 1	Q01339	Apoh	Mus musculus
Q01514	24	2	2	7.64	4	1	1	4.41	28	2	2	0.95	7.64	Interferon-induced guanylate-binding protein 1	Q01514	Gbp1	Mus musculus
Q01853	1635	52	52	67.87	691	32	32	52.61	2326	55	55	0	68.73	Transitional endoplasmic reticulum ATPase	Q01853	Vcp	Mus musculus
Q02053	873	36	36	47.73	474	24	24	32.89	1347	39	39	0	49.81	Ubiquitin-like modifier-activating enzyme 1	Q02053	Uba1	Mus musculus
Q02357	220	22	22	19.76	25	7	7	6.98	245	22	22	0	19.76	Ankyrin-1	Q02357	Ank1	Mus musculus
Q02819	12	4	4	14.16	117	9	9	22.66	129	9	9	0	22.66	Nucleobindin-1	Q02819	Nucb1	Mus musculus
Q03265	51	8	8	15.37	370	20	20	37.97	421	21	21	0	37.97	ATP synthase subunit alpha, mitochondrial	Q03265	Atp5a1	Mus musculus
Q04750	182	8	8	15.25	93	6	6	11.6	275	9	9	0	16.95	DNA topoisomerase 1	Q04750	Top1	Mus musculus
Q04998	0	0	0		15	2	2	10.14	15	2	2	0.95	10.14	Inhibin beta A chain	Q04998	Inhba	Mus musculus
Q05144	315	20	10	60.94	131	13	5	56.25	446	20	10	0	60.94	Ras-related C3 botulinum toxin substrate 2	Q05144	Rac2	Mus musculus
Q06890	65	5	5	19.2	14	2	2	8.48	79	5	5	0	19.2	Clusterin	Q06890	Clu	Mus musculus
Q07076	79	7	7	16.41	26	3	3	7.78	105	7	7	0	16.41	Annexin A7	Q07076	Anxa7	Mus musculus
Q07797	177	10	10	31.02	17	2	2	7.28	194	10	10	0	31.02	Galectin-3-binding protein	Q07797	Lgals3bp	Mus musculus
Q08093	23	1	1	5.57	70	2	2	16.39	93	2	2	0.95	16.39	Calponin-2	Q08093	Cnn2	Mus musculus
Q08761	18	3	3	9.93	0	0	0		18	3	3	0.29	9.93	Vitamin K-dependent protein S	Q08761	Pros1	Mus musculus
Q08943	20	4	4	11.3	57	5	5	12.15	77	6	6	0	15.54	FACT complex subunit SSRP1	Q08943	Ssrp1	Mus musculus
Q09014	194	10	10	25.64	189	12	12	27.44	383	13	13	0	32.31	Neutrophil cytosol factor 1	Q09014	Ncf1	Mus musculus
Q09200	10	2	2	7.32	2	1	1	5.25	12	2	2	0.95	7.32	Beta-1,4 N-acetylgalactosaminyltransferase 1	Q09200	B4galnt1	Mus musculus
Q09PK2	514	14	14	59	1353	15	15	59.59	1867	17	17	0	59.59	Retroviral-like aspartic protease 1	Q09PK2	Asprv1	Mus musculus
Q11011	312	19	19	30.65	55	8	8	18.48	367	20	20	0	33.04	Puromycin-sensitive aminopeptidase	Q11011	Npepps	Mus musculus
Q11136	23	3	3	11.56	5	1	1	3.85	28	3	3	0.29	11.56	Xaa-Pro dipeptidase	Q11136	Pepd	Mus musculus
Q1HFZ0	1	1	1	2.38	10	5	5	11.49	11	5	5	0	11.49	tRNA (cytosine(34)-C(5))-methyltransferase	Q1HFZ0	Nsun2	Mus musculus
Q20BD0	69	4	4	10.54	212	7	6	19.58	281	7	6	0	19.58	Heterogeneous nuclear ribonucleoprotein A/B	Q20BD0	Hnrnpab	Mus musculus
Q2NL51	17	3	3	10.41	6	1	1	7.76	23	4	4	0.19	18.16	Glycogen synthase kinase-3 alpha	Q2NL51	Gsk3a	Mus musculus
Q2VLH6	10	5	5	7.31	0	0	0		10	5	5	0	7.31	Scavenger receptor cysteine-rich type 1 protein M130	Q2VLH6	Cd163	Mus musculus
Q2YFS3	0	0	0		3	3	3	20.86	3	3	3	0.29	20.86	Paired immunoglobulin-like type 2 receptor alpha	Q2YFS3	Pilra	Mus musculus
Q3TBD2	50	5	5	7.17	115	10	10	11.47	165	11	11	0	11.56	Minor histocompatibility protein HA-1	Q3TBD2	Hmha1	Mus musculus
Q3TDN2	0	0	0		3	2	2	11.46	3	2	2	0.95	11.46	FAS-associated factor 2	Q3TDN2	Faf2	Mus musculus
Q3TGF2	0	0	0		29	2	2	11.45	29	2	2	0.95	11.45	Protein FAM107B	Q3TGF2	Fam107b	Mus musculus
Q3THE2	254	9	1	56.4	1027	10	3	47.67	1281	13	3	0.29	58.14	Myosin regulatory light chain 12B	Q3THE2	Myl12b	Mus musculus
Q3THK3	0	0	0		8	2	2	5.31	8	2	2	0.95	5.31	General transcription factor IIF subunit 1	Q3THK3	Gtf2f1	Mus musculus
Q3THK7	71	7	7	21.21	32	5	5	18.18	103	7	7	0	21.21	GMP synthase [glutamine-hydrolyzing]	Q3THK7	Gmps	Mus musculus
Q3TIU4	4	2	2	6.41	1	1	1	3.45	5	2	2	0.95	6.41	2',5'-phosphodiesterase 12	Q3TIU4	Pde12	Mus musculus
Q3TIX9	7	3	3	10.46	7	3	3	11.52	14	4	4	0.19	15.43	U4/U6.U5 tri-snRNP-associated protein 2	Q3TIX9	Usp39	Mus musculus
Q3TJD7	0	0	0		4	2	2	15.1	4	2	2	0.95	15.1	PDZ and LIM domain protein 7	Q3TJD7	Pdlim7	Mus musculus
Q3TKT4	1	1	1	1.24	4	2	2	2.6	5	3	3	0.29	3.84	Transcription activator BRG1	Q3TKT4	Smarca4	Mus musculus
Q3TLH4	0	0	0		3	2	2	1.41	3	2	2	0.95	1.41	Protein PRRC2C	Q3TLH4	Prrc2c	Mus musculus
Q3TRM8	885	32	31	47.18	621	25	24	43.06	1506	33	32	0	48.26	Hexokinase-3	Q3TRM8	Hk3	Mus musculus
Q3TVI8	1	1	1	2.48	4	3	3	7.29	5	3	3	0.29	7.29	Pre-B-cell leukemia transcription factor-interacting protein 1	Q3TVI8	Pbxip1	Mus musculus
Q3TW96	94	5	5	18.34	28	4	4	10.26	122	7	7	0	23.47	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	Q3TW96	Uap1l1	Mus musculus
Q3TXS7	50	9	9	21.3	64	7	7	17.1	114	11	11	0	24.13	26S proteasome non-ATPase regulatory subunit 1	Q3TXS7	Psmd1	Mus musculus
Q3TZZ7	0	0	0		6	2	2	4.62	6	2	2	0.95	4.62	Extended synaptotagmin-2	Q3TZZ7	Esyt2	Mus musculus
Q3U0V1	28	5	5	11.23	226	17	17	31.82	254	17	17	0	31.82	Far upstream element-binding protein 2	Q3U0V1	Khsrp	Mus musculus
Q3U0V2	6	2	2	10.32	27	3	3	21.94	33	4	4	0.19	25.81	Tumor necrosis factor receptor type 1-associated DEATH domain protein	Q3U0V2	Tradd	Mus musculus
Q3U141	0	0	0		4	2	2	11.76	4	2	2	0.95	11.76	Inhibitor of nuclear factor kappa-B kinase subunit beta	Q3U141	Ikbkb	Mus musculus
Q3U1F9	0	0	0		31	2	2	10.02	31	2	2	0.95	10.02	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1	Q3U1F9	Pag1	Mus musculus
Q3U1J4	129	9	9	14.82	78	7	7	12.19	207	11	11	0	17.46	DNA damage-binding protein 1	Q3U1J4	Ddb1	Mus musculus
Q3U1Z5	0	0	0		105	6	6	51.57	105	6	6	0	51.57	G-protein-signaling modulator 3	Q3U1Z5	Gpsm3	Mus musculus
Q3U2G2	235	16	16	34.8	195	15	15	26.13	430	21	21	0	40.14	Heat shock 70 kDa protein 4	Q3U2G2	Hspa4	Mus musculus
Q3U5Q7	27	4	4	15.44	0	0	0		27	4	4	0.19	15.44	UMP-CMP kinase 2, mitochondrial	Q3U5Q7	Cmpk2	Mus musculus
Q3U5V8	0	0	0		3	3	3	20.21	3	3	3	0.29	20.21	MCG49559	Q3U5V8	Stx11	Mus musculus
Q3U7R1	90	7	7	12.18	205	17	17	24.36	295	17	17	0	24.36	Extended synaptotagmin-1	Q3U7R1	Esyt1	Mus musculus
Q3U9G9	1	1	1	3.04	122	10	10	19.97	123	10	10	0	19.97	Lamin-B receptor	Q3U9G9	Lbr	Mus musculus
Q3UDE2	17	2	2	5.95	1	1	1	4.69	18	3	3	0.29	7.2	Tubulin--tyrosine ligase-like protein 12	Q3UDE2	Ttll12	Mus musculus
Q3UEB3	0	0	0		15	4	4	13.83	15	4	4	0.19	13.83	Poly(U)-binding-splicing factor PUF60	Q3UEB3	Puf60	Mus musculus
Q3UHD6	15	3	3	11.32	14	1	1	6.31	29	3	3	0.29	11.32	Sorting nexin-27	Q3UHD6	Snx27	Mus musculus
Q3UI43	0	0	0		53	2	2	19.82	53	2	2	0.95	19.82	BRISC and BRCA1-A complex member 1	Q3UI43	Babam1	Mus musculus
Q3UJB0	2	1	1	1.59	28	7	7	10.71	30	7	7	0	10.71	Protein Sf3b2	Q3UJB0	Sf3b2	Mus musculus
Q3UJB9	3	2	2	3.63	26	6	6	9.25	29	8	8	0	12.87	Enhancer of mRNA-decapping protein 4	Q3UJB9	Edc4	Mus musculus
Q3UKJ7	6	2	2	5.46	1	1	1	5.07	7	3	3	0.29	10.53	WD40 repeat-containing protein SMU1	Q3UKJ7	Smu1	Mus musculus
Q3ULJ0	29	4	4	23.65	33	6	6	25.93	62	8	8	0	33.33	Glycerol-3-phosphate dehydrogenase 1-like protein	Q3ULJ0	Gpd1l	Mus musculus
Q3UM45	49	5	5	22.16	47	3	3	15.79	96	5	5	0	22.16	Protein phosphatase 1 regulatory subunit 7	Q3UM45	Ppp1r7	Mus musculus
Q3UND0	96	9	9	47.49	356	18	18	70.11	452	18	18	0	70.11	Src kinase-associated phosphoprotein 2	Q3UND0	Skap2	Mus musculus
Q3UP87	390	14	14	38.11	863	23	23	50.94	1253	24	24	0	51.32	Neutrophil elastase	Q3UP87	Elane	Mus musculus
Q3UPH1	2	2	2	14	54	4	4	24.83	56	4	4	0.19	24.83	Protein PRRC1	Q3UPH1	Prrc1	Mus musculus
Q3UPL0	5	3	3	5.28	2	2	2	4.47	7	4	4	0.19	7.32	Protein transport protein Sec31A	Q3UPL0	Sec31a	Mus musculus
Q3UQ44	6	3	3	4.95	78	9	9	11.68	84	10	10	0	13.46	Ras GTPase-activating-like protein IQGAP2	Q3UQ44	Iqgap2	Mus musculus
Q3UW53	81	11	11	18.9	148	10	10	18.9	229	13	13	0	24.3	Protein Niban	Q3UW53	Fam129a	Mus musculus
Q3UYV9	22	6	6	14.94	29	2	2	4.81	51	6	6	0	14.94	Nuclear cap-binding protein subunit 1	Q3UYV9	Ncbp1	Mus musculus
Q3UZ39	28	3	3	12.07	169	11	11	27.3	197	11	11	0	27.3	Leucine-rich repeat flightless-interacting protein 1	Q3UZ39	Lrrfip1	Mus musculus
Q3UZA1	8	3	3	22.09	205	5	5	32.04	213	5	5	0	32.04	CapZ-interacting protein	Q3UZA1	Rcsd1	Mus musculus
Q3UZZ4	381	13	13	37.43	295	14	14	39.6	676	15	15	0	39.6	Olfactomedin-4	Q3UZZ4	Olfm4	Mus musculus
Q3V0K9	46	4	2	11.9	11	3	1	6.67	57	4	2	0.95	11.9	Plastin-1	Q3V0K9	Pls1	Mus musculus
Q3V1G4	88	6	6	14.61	212	11	11	21.98	300	11	11	0	21.98	Olfactomedin-like protein 2B	Q3V1G4	Olfml2b	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q3V1L4	157	12	12	40.54	26	5	5	16.07	183	13	13	0	40.54	Cytosolic purine 5'-nucleotidase	Q3V1L4	Nt5c2	Mus musculus
Q3V3R1	12	5	5	8.39	12	4	4	8.09	24	7	7	0	11.05	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	Q3V3R1	Mthfd1l	Mus musculus
Q497J0	0	0	0		82	4	4	34.02	82	4	4	0.19	34.02	MCG130175, isoform CRA_b	Q497J0	BC100530	Mus musculus
Q4KML4	11	1	1	16.05	55	3	3	51.85	66	3	3	0.29	51.85	Costars family protein ABRACL	Q4KML4	Abracl	Mus musculus
Q4LDD4	3	2	2	2.55	3	1	1	1.45	6	2	2	0.95	2.55	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	Q4LDD4	Arap1	Mus musculus
Q4QRL3	0	0	0		28	7	7	9.52	28	7	7	0	9.52	Coiled-coil domain-containing protein 88B	Q4QRL3	Ccdc88b	Mus musculus
Q501J6	23	3	2	6.92	22	2	0	3.85	45	4	2	0.95	8.77	Probable ATP-dependent RNA helicase DDX17	Q501J6	Ddx17	Mus musculus
Q52KI8	2	1	1	3.59	55	2	2	5.39	57	2	2	0.95	5.39	Serine/arginine repetitive matrix protein 1	Q52KI8	Srrm1	Mus musculus
Q569Z6	7	1	1	3.15	62	2	2	5.99	69	2	2	0.95	5.99	Thyroid hormone receptor-associated protein 3	Q569Z6	Thrap3	Mus musculus
Q571E4	50	4	4	16.15	67	5	5	17.69	117	5	5	0	17.69	N-acetylgalactosamine-6-sulfatase	Q571E4	Galns	Mus musculus
Q571I9	161	7	7	17.71	86	4	4	8.98	247	7	7	0	17.71	Aldehyde dehydrogenase family 16 member A1	Q571I9	Aldh16a1	Mus musculus
Q5EG47	13	1	1	3.76	27	2	2	6.44	40	2	2	0.95	6.44	5'-AMP-activated protein kinase catalytic subunit alpha-1	Q5EG47	Prkaa1	Mus musculus
Q5FWK3	18	2	2	10.02	48	4	4	18.45	66	4	4	0.19	18.45	Rho GTPase-activating protein 1	Q5FWK3	Arhgap1	Mus musculus
Q5RKN9	237	10	8	51.75	199	11	9	52.8	436	11	9	0	52.8	Capping protein (Actin filament) muscle Z-line, alpha 1	Q5RKN9	Capza1	Mus musculus
Q5SFM8	0	0	0		18	3	3	5.85	18	3	3	0.29	5.85	RNA-binding protein 27	Q5SFM8	Rbm27	Mus musculus
Q5SQX6	9	3	3	3.03	4	2	1	1.84	13	4	3	0.29	3.99	Cytoplasmic FMR1-interacting protein 2	Q5SQX6	Cyfip2	Mus musculus
Q5SSL4	3	2	2	3.96	0	0	0		3	2	2	0.95	3.96	Active breakpoint cluster region-related protein	Q5SSL4	Abr	Mus musculus
Q5SUA5	4	2	2	3.71	36	7	7	11.52	40	8	8	0	13.38	Unconventional myosin-Ig	Q5SUA5	Myo1g	Mus musculus
Q5SUH6	1	1	1	2.96	18	4	4	14.98	19	5	5	0	17.94	Clathrin interactor 1	Q5SUH6	Clint1	Mus musculus
Q5SUR0	299	22	22	33.88	73	12	12	21.77	372	22	22	0	33.88	Phosphoribosylformylglycinamidine synthase	Q5SUR0	Pfas	Mus musculus
Q5SVD0	6	2	2	24.07	64	3	3	30.09	70	3	3	0.29	30.09	Filamin-interacting protein FAM101B	Q5SVD0	Fam101b	Mus musculus
Q5XJF6	56	2	2	13.36	14	1	1	7.37	70	2	2	0.95	13.36	Ribosomal protein	Q5XJF6	Rpl10a	Mus musculus
Q5XJY5	4	2	2	4.5	34	3	3	10.18	38	4	4	0.19	10.18	Coatomer subunit delta	Q5XJY5	Arcn1	Mus musculus
Q60597	4	1	1	1.76	10	3	3	4.99	14	3	3	0.29	4.99	2-oxoglutarate dehydrogenase, mitochondrial	Q60597	Ogdh	Mus musculus
Q60605-2	242	8	8	70.2	353	8	8	65.56	595	9	9	0	70.86	Isoform Smooth muscle of Myosin light polypeptide 6	Q60605	Myl6	Mus musculus
Q60631	35	4	4	25.35	38	4	4	30.88	73	5	5	0	30.88	Growth factor receptor-bound protein 2	Q60631	Grb2	Mus musculus
Q60634	0	0	0		38	6	6	18.69	38	6	6	0	18.69	Flotillin-2	Q60634	Flot2	Mus musculus
Q60648	14	1	1	11.4	46	3	3	21.24	60	3	3	0.29	21.24	Ganglioside GM2 activator	Q60648	Gm2a	Mus musculus
Q60664	0	0	0		29	2	2	7.79	29	2	2	0.95	7.79	Lymphoid-restricted membrane protein	Q60664	Lrmp	Mus musculus
Q60668	14	3	3	19.72	101	5	5	14.37	115	6	6	0	24.23	Heterogeneous nuclear ribonucleoprotein D0	Q60668	Hnrnpd	Mus musculus
Q60675	2	2	2	0.93	0	0	0		2	2	2	0.95	0.93	Laminin subunit alpha-2	Q60675	Lama2	Mus musculus
Q60676	16	2	2	6.41	0	0	0		16	2	2	0.95	6.41	Serine/threonine-protein phosphatase 5	Q60676	Ppp5c	Mus musculus
Q60692	138	5	5	31.93	26	4	4	27.31	164	5	5	0	31.93	Proteasome subunit beta type-6	Q60692	Psmb6	Mus musculus
Q60737	19	2	2	11	27	3	3	14.83	46	3	3	0.29	14.83	Casein kinase II subunit alpha	Q60737	Csnk2a1	Mus musculus
Q60739	1	1	1	9.86	17	2	2	14.65	18	2	2	0.95	14.65	BAG family molecular chaperone regulator 1	Q60739	Bag1	Mus musculus
Q60767	61	6	6	7.14	23	4	4	4.76	84	7	7	0	8.76	Lymphocyte antigen 75	Q60767	Ly75	Mus musculus
Q60790	0	0	0		19	3	3	8.39	19	3	3	0.29	8.39	Ras GTPase-activating protein 3	Q60790	Rasa3	Mus musculus
Q60864	78	5	5	14	76	10	10	23.02	154	10	10	0	23.02	Stress-induced-phosphoprotein 1	Q60864	Stip1	Mus musculus
Q60865	17	3	3	7.5	82	6	6	15.28	99	7	7	0	15.28	Caprin-1	Q60865	Caprin1	Mus musculus
Q60875	1	1	1	2.34	33	4	4	6.6	34	5	5	0	8.93	Rho guanine nucleotide exchange factor 2	Q60875	Arhgef2	Mus musculus
Q60902	0	0	0		32	4	4	9.04	32	4	4	0.19	9.04	Epidermal growth factor receptor substrate 15-like 1	Q60902	Eps15l1	Mus musculus
Q60930	1	1	1	7.46	37	5	5	30.51	38	5	5	0	30.51	Voltage-dependent anion-selective channel protein 2	Q60930	Vdac2	Mus musculus
Q60931	1	1	1	3.53	7	2	2	11.31	8	2	2	0.95	11.31	Voltage-dependent anion-selective channel protein 3	Q60931	Vdac3	Mus musculus
Q60932	0	0	0		60	5	5	27.03	60	5	5	0	27.03	Voltage-dependent anion-selective channel protein 1	Q60932	Vdac1	Mus musculus
Q60953	1	1	1	2.03	39	7	7	13.45	40	7	7	0	13.45	Protein PML	Q60953	Pml	Mus musculus
Q60960	3	2	2	9.48	25	3	3	12.08	28	3	3	0.29	12.08	Importin subunit alpha-5	Q60960	Kpna1	Mus musculus
Q60963	26	4	4	12.95	0	0	0		26	4	4	0.19	12.95	Platelet-activating factor acetylhydrolase	Q60963	Pla2g7	Mus musculus
Q60972	88	6	4	32.47	142	5	4	28.47	230	6	4	0.19	32.47	Histone-binding protein RBBP4	Q60972	Rbbp4	Mus musculus
Q60973	59	8	6	46.35	43	7	6	41.41	102	9	7	0	54.35	Histone-binding protein RBBP7	Q60973	Rbbp7	Mus musculus
Q61024	13	2	2	6.77	8	1	1	3.57	21	2	2	0.95	6.77	Asparagine synthetase [glutamine-hydrolyzing]	Q61024	Asns	Mus musculus
Q61029	69	8	1	30.09	390	15	6	38.5	459	16	6	0	41.59	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	Q61029	Tmpo	Mus musculus
Q61033	78	9	2	25.54	405	16	7	34.34	483	17	7	0	36.36	Lamina-associated polypeptide 2, isoforms alpha/zeta	Q61033	Tmpo	Mus musculus
Q61035	172	9	9	28.88	30	2	2	10.22	202	9	9	0	28.88	Histidine--tRNA ligase, cytoplasmic	Q61035	Hars	Mus musculus
Q61074	1	1	1	2.21	71	3	3	13.84	72	4	4	0.19	16.05	Protein phosphatase 1G	Q61074	Ppm1g	Mus musculus
Q61081	27	3	3	15.3	100	4	4	15.83	127	4	4	0.19	15.83	Hsp90 co-chaperone Cdc37	Q61081	Cdc37	Mus musculus
Q61093	46	8	8	20.88	310	18	18	32.81	356	20	20	0	32.81	Cytochrome b-245 heavy chain	Q61093	Cybb	Mus musculus
Q61096	303	11	11	55.91	1142	28	28	64.17	1445	28	28	0	64.17	Myeloblastin	Q61096	Prtn3	Mus musculus
Q61103	2	1	1	5.63	28	3	3	13.3	30	3	3	0.29	13.3	Zinc finger protein ubi-d4	Q61103	Dpf2	Mus musculus
Q61147	98	11	11	17.25	0	0	0		98	11	11	0	17.25	Ceruloplasmin	Q61147	Cp	Mus musculus
Q61152	0	0	0		49	2	2	10.38	49	2	2	0.95	10.38	Tyrosine-protein phosphatase non-receptor type 18	Q61152	Ptpn18	Mus musculus
Q61166	29	3	3	12.31	62	5	5	35.45	91	6	6	0	36.19	Microtubule-associated protein RP/EB family member 1	Q61166	Mapre1	Mus musculus
Q61171	389	22	22	81.82	85	10	10	80.3	474	22	22	0	81.82	Peroxiredoxin-2	Q61171	Prdx2	Mus musculus
Q61176	19	5	5	27.24	10	5	5	30.96	29	8	8	0	46.44	Arginase-1	Q61176	Arg1	Mus musculus
Q61191	24	3	3	3.42	26	3	3	4.21	50	4	4	0.19	4.74	Host cell factor 1	Q61191	Hcfc1	Mus musculus
Q61206	12	1	1	8.3	9	2	2	22.27	21	2	2	0.95	22.27	Platelet-activating factor acetylhydrolase IB subunit beta	Q61206	Pafah1b2	Mus musculus
Q61207	47	5	5	15.8	101	8	8	16.7	148	9	9	0	19.93	Prosaposin	Q61207	Psap	Mus musculus
Q61210-5	23	9	9	16.24	158	13	13	22.78	181	15	15	0	26.86	Isoform 5 of Rho guanine nucleotide exchange factor 1	Q61210	Arhgef1	Mus musculus
Q61233	2400	52	50	73.21	2060	52	50	70.49	4460	60	58	0	75.28	Plastin-2	Q61233	Lcp1	Mus musculus
Q61362	153	7	7	23.14	110	9	9	26.22	263	10	10	0	29.05	Chitinase-3-like protein 1	Q61362	Chi3l1	Mus musculus
Q61508	60	6	6	19.86	3	3	3	7.69	63	7	7	0	19.86	Extracellular matrix protein 1	Q61508	Ecm1	Mus musculus
Q61543	37	6	6	9.87	19	4	4	6.98	56	6	6	0	9.87	Golgi apparatus protein 1	Q61543	Glg1	Mus musculus
Q61545	7	3	3	7.94	65	4	4	10.08	72	4	4	0.19	10.08	RNA-binding protein EWS	Q61545	Ewsr1	Mus musculus
Q61550	11	2	2	5.51	24	4	4	15.12	35	4	4	0.19	15.12	Double-strand-break repair protein rad21 homolog	Q61550	Rad21	Mus musculus
Q61578	5	2	2	8.91	0	0	0		5	2	2	0.95	8.91	NADPH:adrenodoxin oxidoreductase, mitochondrial	Q61578	Fdxr	Mus musculus
Q61598	558	21	15	51.69	276	13	9	28.09	834	24	17	0	52.36	Rab GDP dissociation inhibitor beta	Q61598	Gdi2	Mus musculus
Q61599	264	9	9	60.5	679	16	16	67	943	17	17	0	67	Rho GDP-dissociation inhibitor 2	Q61599	Arhgdib	Mus musculus
Q61635	64	10	10	31.19	8	4	4	17.62	72	11	11	0	35	GTP-binding protein	Q61635	Ifi47	Mus musculus
Q61646	1552	16	16	58.79	1067	15	15	54.18	2619	18	18	0	58.79	Haptoglobin	Q61646	Hp	Mus musculus
Q61655	21	2	2	9.21	16	4	4	14.44	37	4	4	0.19	14.44	ATP-dependent RNA helicase DDX19A	Q61655	Ddx19a	Mus musculus
Q61656	25	8	7	16.78	106	8	6	19.22	131	12	10	0	26.71	Probable ATP-dependent RNA helicase DDX5	Q61656	Ddx5	Mus musculus
Q61687	0	0	0		7	2	2	1.25	7	2	2	0.95	1.25	Transcriptional regulator ATRX	Q61687	Atrx	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q61704	5	2	2	5.74	9	2	2	5.74	14	2	2	0.95	5.74	Inter-alpha-trypsin inhibitor heavy chain H3	Q61704	Itih3	Mus musculus
Q61739	14	4	4	6.87	2	2	2	3.21	16	5	5	0	8.34	Integrin alpha-6	Q61739	Itga6	Mus musculus
Q61749	6	2	2	8.02	6	1	1	4.58	12	3	3	0.29	12.6	Translation initiation factor eIF-2B subunit delta	Q61749	Eif2b4	Mus musculus
Q61753	47	7	7	22.33	71	9	9	32.65	118	10	10	0	34.9	D-3-phosphoglycerate dehydrogenase	Q61753	Phgdh	Mus musculus
Q61768	23	5	5	8.52	72	6	6	8	95	9	9	0	12.46	Kinesin-1 heavy chain	Q61768	Kif5b	Mus musculus
Q61792	3	1	1	5.32	31	4	4	17.11	34	4	4	0.19	17.11	LIM and SH3 domain protein 1	Q61792	Lasp1	Mus musculus
Q61805	32	1	1	7.48	55	3	3	10.81	87	3	3	0.29	10.81	Lipopolysaccharide-binding protein	Q61805	Lbp	Mus musculus
Q61838	148	21	21	28.23	0	0	0		148	21	21	0	28.23	Alpha-2-macroglobulin	Q61838	A2m	Mus musculus
Q61878	28	3	3	24.66	101	6	6	26.01	129	7	7	0	30.04	Bone marrow proteoglycan	Q61878	Prg2	Mus musculus
Q61881	9	6	6	15.72	43	7	7	16.13	52	8	8	0	18.22	DNA replication licensing factor MCM7	Q61881	Mcm7	Mus musculus
Q61937	94	3	3	21.58	103	6	6	24.32	197	7	7	0	33.9	Nucleophosmin	Q61937	Npm1	Mus musculus
Q61990	35	6	5	31.49	76	4	4	21.55	111	7	6	0	34.53	Poly(rC)-binding protein 2	Q61990	Pcbp2	Mus musculus
Q62059	13	4	4	2.5	0	0	0		13	4	4	0.19	2.5	Versican core protein	Q62059	Vcan	Mus musculus
Q62086	0	0	0		19	2	2	13.28	19	2	2	0.95	13.28	Serum paraoxonase/arylesterase 2	Q62086	Pon2	Mus musculus
Q62167	53	8	8	15.86	89	9	9	16.47	142	12	12	0	22.36	ATP-dependent RNA helicase DDX3X	Q62167	Ddx3x	Mus musculus
Q62178	91	6	6	15	28	5	5	13.16	119	6	6	0	15	Semaphorin-4A	Q62178	Sema4a	Mus musculus
Q62186	0	0	0		20	3	3	34.3	20	3	3	0.29	34.3	Translocon-associated protein subunit delta	Q62186	Ssr4	Mus musculus
Q62193	14	2	2	16.67	13	2	2	16.67	27	2	2	0.95	16.67	Replication protein A 32 kDa subunit	Q62193	Rpa2	Mus musculus
Q62219	0	0	0		7	2	2	8.03	7	2	2	0.95	8.03	Transforming growth factor beta-1-induced transcript 1 protein	Q62219	Tgfb1i1	Mus musculus
Q62261	339	26	25	18.71	538	32	32	21.88	877	35	34	0	24.25	Spectrin beta chain, non-erythrocytic 1	Q62261	Sptbn1	Mus musculus
Q62318	7	2	2	6.35	97	10	10	26.14	104	10	10	0	26.14	Transcription intermediary factor 1-beta	Q62318	Trim28	Mus musculus
Q62348	48	5	5	33.33	0	0	0		48	5	5	0	33.33	Translin	Q62348	Tsn	Mus musculus
Q62376	4	2	2	5.58	25	2	2	6.7	29	3	3	0.29	9.82	U1 small nuclear ribonucleoprotein 70 kDa	Q62376	Snrnp70	Mus musculus
Q62383	0	0	0		2	2	2	2.03	2	2	2	0.95	2.03	Transcription elongation factor SPT6	Q62383	Supt6h	Mus musculus
Q62393	26	2	2	22.32	68	2	2	14.73	94	3	3	0.29	28.57	Tumor protein D52	Q62393	Tpd52	Mus musculus
Q62418	59	5	5	16.97	188	9	9	32.34	247	9	9	0	32.34	Drebrin-like protein	Q62418	Dbnl	Mus musculus
Q62419	7	2	2	8.15	18	2	2	8.15	25	2	2	0.95	8.15	Endophilin-A2	Q62419	Sh3gl1	Mus musculus
Q62422	118	6	6	32.09	146	8	8	39.07	264	8	8	0	39.07	Osteoclast-stimulating factor 1	Q62422	Ostf1	Mus musculus
Q62431	0	0	0		13	2	2	9.98	13	2	2	0.95	9.98	AT-rich interactive domain-containing protein 3A	Q62431	Arid3a	Mus musculus
Q62448	0	0	0		10	2	2	5.96	10	2	2	0.95	5.96	Eukaryotic translation initiation factor 4 gamma 2	Q62448	Eif4g2	Mus musculus
Q62465	60	6	6	23.65	37	7	7	24.14	97	7	7	0	24.14	Synaptic vesicle membrane protein VAT-1 homolog	Q62465	Vat1	Mus musculus
Q62469	6	3	3	4.75	5	1	1	3.23	11	4	4	0.19	7.98	Integrin alpha-2	Q62469	Itga2	Mus musculus
Q62523	30	4	4	17.91	163	10	10	27.48	193	10	10	0	27.48	Zyxin	Q62523	Zyx	Mus musculus
Q63810	66	3	3	27.06	38	2	2	27.06	104	3	3	0.29	27.06	Calcineurin subunit B type 1	Q63810	Ppp3r1	Mus musculus
Q63844	52	9	8	33.95	0	0	0		52	9	8	0	33.95	Mitogen-activated protein kinase 3	Q63844	Mapk3	Mus musculus
Q64012	0	0	0		28	2	2	12.82	28	2	2	0.95	12.82	RNA-binding protein Raly	Q64012	Raly	Mus musculus
Q640N3	4	2	2	2.63	0	0	0		4	2	2	0.95	2.63	Rho GTPase-activating protein 30	Q640N3	Arhgap30	Mus musculus
Q64152	12	1	1	9.31	61	2	2	23.53	73	2	2	0.95	23.53	Transcription factor BTF3	Q64152	Btf3	Mus musculus
Q64277	7	1	1	4.18	15	3	3	15.11	22	3	3	0.29	15.11	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2	Q64277	Bst1	Mus musculus
Q64324	82	10	10	31.2	120	12	12	31.7	202	12	12	0	31.7	Syntaxin-binding protein 2	Q64324	Stxbp2	Mus musculus
Q64433	1	1	1	11.76	57	4	4	25.49	58	4	4	0.19	25.49	10 kDa heat shock protein, mitochondrial	Q64433	Hspe1	Mus musculus
Q64442	35	3	3	17.37	4	1	1	5.88	39	3	3	0.29	17.37	Sorbitol dehydrogenase	Q64442	Sord	Mus musculus
Q64455	34	3	3	6.54	43	3	3	6.38	77	4	4	0.19	8.4	Receptor-type tyrosine-protein phosphatase eta	Q64455	Ptprj	Mus musculus
Q64511	11	4	2	3.85	16	4	3	4.16	27	6	4	0.19	5.77	DNA topoisomerase 2-beta	Q64511	Top2b	Mus musculus
Q64514	107	10	10	17.99	44	6	6	10.62	151	12	12	0	18.78	Tripeptidyl-peptidase 2	Q64514	Tpp2	Mus musculus
Q64516	5	2	2	8.59	0	0	0		5	2	2	0.95	8.59	Glycerol kinase	Q64516	Gk	Mus musculus
Q64521	0	0	0		80	8	8	19.39	80	8	8	0	19.39	Glycerol-3-phosphate dehydrogenase, mitochondrial	Q64521	Gpd2	Mus musculus
Q64523	13444	35	7	62.79	10900	28	2	58.91	24344	36	7	0	63.57	Histone H2A type 2-C	Q64523	Hist2h2ac	Mus musculus
Q64674	35	5	5	27.15	7	1	1	7.95	42	5	5	0	27.15	Spermidine synthase	Q64674	Srm	Mus musculus
Q64727	527	23	23	33.21	127	14	14	24.58	654	26	26	0	36.4	Vinculin	Q64727	Vcl	Mus musculus
Q64737	20	4	4	8.71	20	4	4	6.44	40	5	5	0	9.01	Trifunctional purine biosynthetic protein adenosine-3	Q64737	Gart	Mus musculus
Q65Z40	0	0	0		15	4	4	7.17	15	4	4	0.19	7.17	Wings apart-like protein homolog	Q65Z40	Wapal	Mus musculus
Q66JX5	1	1	1	7.27	4	2	2	6.77	5	3	3	0.29	14.04	FGFR1 oncogene partner	Q66JX5	Fgfr1op	Mus musculus
Q68FD5	608	42	42	35.64	928	47	47	38.81	1536	52	52	0	41.31	Clathrin heavy chain 1	Q68FD5	Cltc	Mus musculus
Q68FL6	8	4	4	9.53	15	5	5	11.2	23	5	5	0	11.2	Methionine--tRNA ligase, cytoplasmic	Q68FL6	Mars	Mus musculus
Q69ZK0	7	3	3	3.64	15	6	6	8.73	22	7	7	0	10	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	Q69ZK0	Prex1	Mus musculus
Q6A026	3	2	2	2.03	22	5	5	6.38	25	6	6	0	7.43	Sister chromatid cohesion protein PDS5 homolog A	Q6A026	Pds5a	Mus musculus
Q6A068	0	0	0		28	6	6	14.84	28	6	6	0	14.84	Cell division cycle 5-like protein	Q6A068	Cdc5l	Mus musculus
Q6A4J8	64	7	7	14.23	36	5	5	10.06	100	8	8	0	15.78	Ubiquitin carboxyl-terminal hydrolase 7	Q6A4J8	Usp7	Mus musculus
Q6BCL1	0	0	0		53	9	9	25.78	53	9	9	0	25.78	PML-RARA-regulated adapter molecule 1	Q6BCL1	Pram1	Mus musculus
Q6DFW4	0	0	0		28	2	2	5.04	28	2	2	0.95	5.04	Nucleolar protein 58	Q6DFW4	Nop58	Mus musculus
Q6DFZ1	0	0	0		6	3	3	4.19	6	3	3	0.29	4.19	Golgi-specific brefeldin A-resistance factor 1	Q6DFZ1	Gbf1	Mus musculus
Q6DTY7	5	3	3	10.45	13	4	4	16.84	18	6	6	0	23.88	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	Q6DTY7	Pfkfb4	Mus musculus
Q6GQT9	0	0	0		22	5	5	8.07	22	5	5	0	8.07	Nodal modulator 1	Q6GQT9	Nomo1	Mus musculus
Q6IRU2	181	9	9	38.71	181	9	9	38.71	362	9	9	0	38.71	Tropomyosin alpha-4 chain	Q6IRU2	Tpm4	Mus musculus
Q6NSR8	5	4	4	16.41	0	0	0		5	4	4	0.19	16.41	Probable aminopeptidase NPEPL1	Q6NSR8	Npepl1	Mus musculus
Q6NVF9	28	1	1	4.54	67	2	2	9.8	95	2	2	0.95	9.8	Cleavage and polyadenylation specificity factor subunit 6	Q6NVF9	Cpsf6	Mus musculus
Q6NZB0	12	1	1	11.46	38	3	3	24.51	50	3	3	0.29	24.51	DnaJ homolog subfamily C member 8	Q6NZB0	Dnajc8	Mus musculus
Q6NZC7	2	1	1	2.51	15	2	2	4.61	17	2	2	0.95	4.61	SEC23-interacting protein	Q6NZC7	Sec23ip	Mus musculus
Q6NZJ6	13	3	3	3.44	43	5	5	6.75	56	6	6	0	8	Eukaryotic translation initiation factor 4 gamma 1	Q6NZJ6	Eif4g1	Mus musculus
Q6P069-2	206	14	14	69.4	155	7	7	50.82	361	15	15	0	70.49	Isoform 2 of Sorcin	Q6P069	Sri	Mus musculus
Q6P1B1	100	10	10	32.42	50	6	6	24.4	150	10	10	0	32.42	Xaa-Pro aminopeptidase 1	Q6P1B1	Xpnpep1	Mus musculus
Q6P1F6	8	2	2	7.61	6	3	3	12.3	14	4	4	0.19	16.78	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	Q6P1F6	Ppp2r2a	Mus musculus
Q6P2B1	8	3	3	6.5	8	1	1	2.71	16	3	3	0.29	6.5	Transportin-3	Q6P2B1	Tnpo3	Mus musculus
Q6P4S8	3	2	2	2.64	0	0	0		3	2	2	0.95	2.64	Integrator complex subunit 1	Q6P4S8	Ints1	Mus musculus
Q6P4T2	102	14	14	13.76	118	12	12	11	220	16	16	0	15.64	U5 small nuclear ribonucleoprotein 200 kDa helicase	Q6P4T2	Snrnp200	Mus musculus
Q6P542	2	2	2	5.97	30	4	4	12.78	32	5	5	0	16.49	ATP-binding cassette sub-family F member 1	Q6P542	Abcf1	Mus musculus
Q6P5E4	332	24	24	27.08	174	13	13	16.38	506	25	25	0	28.5	UDP-glucose:glycoprotein glucosyltransferase 1	Q6P5E4	Uggt1	Mus musculus
Q6P5F9	184	8	8	12.79	83	7	7	11.11	267	9	9	0	13.54	Exportin-1	Q6P5F9	Xpo1	Mus musculus
Q6P8X1	28	4	4	16.5	34	3	3	12.56	62	5	5	0	16.75	Sorting nexin-6	Q6P8X1	Snx6	Mus musculus
Q6P9Q4	13	2	2	2.92	2	1	1	1.59	15	2	2	0.95	2.92	FH1/FH2 domain-containing protein 1	Q6P9Q4	Fhod1	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q6P9Q6	0	0	0		21	4	4	7.89	21	4	4	0.19	7.89	FK506-binding protein 15	Q6P9Q6	Fkbp15	Mus musculus
Q6PAV2	9	4	4	8.33	0	0	0		9	4	4	0.19	8.33	Probable E3 ubiquitin-protein ligase HERC4	Q6PAV2	Herc4	Mus musculus
Q6PCP5	0	0	0		4	2	2	20.27	4	2	2	0.95	20.27	Mitochondrial fission factor	Q6PCP5	Mff	Mus musculus
Q6PD03	12	4	4	12.76	8	1	1	2.88	20	4	4	0.19	12.76	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	Q6PD03	Ppp2r5a	Mus musculus
Q6PDG5	28	4	4	7.17	51	5	5	10.31	79	5	5	0	10.31	SWI/SNF complex subunit SMARCC2	Q6PDG5	Smarcc2	Mus musculus
Q6PDI5	19	6	6	6.52	36	8	8	8.32	55	10	10	0	10.43	Proteasome-associated protein ECM29 homolog	Q6PDI5	Ecm29	Mus musculus
Q6PDM2	35	2	2	13.31	115	7	7	26.61	150	7	7	0	26.61	Serine/arginine-rich splicing factor 1	Q6PDM2	Srsf1	Mus musculus
Q6PDQ2	1	1	1	1.88	33	6	6	5.95	34	6	6	0	5.95	Chromodomain-helicase-DNA-binding protein 4	Q6PDQ2	Chd4	Mus musculus
Q6PE01	10	4	4	19.55	8	1	1	8.66	18	4	4	0.19	19.55	U5 small nuclear ribonucleoprotein 40 kDa protein	Q6PE01	Snrnp40	Mus musculus
Q6PEB6	24	3	3	24.89	29	1	1	9.78	53	3	3	0.29	24.89	MOB-like protein phocein	Q6PEB6	Mob4	Mus musculus
Q6PFD9	0	0	0		20	5	5	5.07	20	5	5	0	5.07	Nuclear pore complex protein Nup98-Nup96	Q6PFD9	Nup98	Mus musculus
Q6PFR5	0	0	0		24	2	2	12.46	24	2	2	0.95	12.46	Transformer-2 protein homolog alpha	Q6PFR5	Tra2a	Mus musculus
Q6PGG2	0	0	0		11	4	4	8.96	11	4	4	0.19	8.96	GEM-interacting protein	Q6PGG2	Gmip	Mus musculus
Q6PHU5	41	4	4	10.3	48	4	4	10.55	89	6	6	0	12.48	Sortilin	Q6PHU5	Sort1	Mus musculus
Q6PHZ2	11	2	2	7.62	42	2	2	7.62	53	2	2	0.95	7.62	Calcium/calmodulin-dependent protein kinase type II subunit delta	Q6PHZ2	Camk2d	Mus musculus
Q6SJQ7	0	0	0		29	3	3	13.35	29	3	3	0.29	13.35	CMRF35-like molecule 1	Q6SJQ7	Cd300lf	Mus musculus
Q6URW6	105	6	2	4.2	181	8	2	3.7	286	9	3	0.29	4.65	Myosin-14	Q6URW6	Myh14	Mus musculus
Q6WVG3	57	6	6	33.64	41	6	6	25.08	98	9	9	0	36.09	BTB/POZ domain-containing protein KCTD12	Q6WVG3	Kctd12	Mus musculus
Q6ZPJ3	7	2	2	4.11	1	1	1	1.71	8	3	3	0.29	5.82	E2/E3 hybrid ubiquitin-protein ligase UBE2O	Q6ZPJ3	Ube2o	Mus musculus
Q6ZQ38	98	8	8	11.22	29	7	7	11.14	127	10	10	0	14.23	Cullin-associated NEDD8-dissociated protein 1	Q6ZQ38	Cand1	Mus musculus
Q6ZQA0	6	2	2	1.79	40	9	9	7	46	9	9	0	7	Neurobeachin-like protein 2	Q6ZQA0	Nbeal2	Mus musculus
Q6ZQI3	0	0	0		45	2	2	12.37	45	2	2	0.95	12.37	Malectin	Q6ZQI3	Mlec	Mus musculus
Q6ZQK5	1	1	1	2.47	11	3	3	8.96	12	3	3	0.29	8.96	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	Q6ZQK5	Acap2	Mus musculus
Q6ZWM4	29	3	3	61.46	32	4	4	70.83	61	4	4	0.19	70.83	U6 snRNA-associated Sm-like protein LSm8	Q6ZWM4	Lsm8	Mus musculus
Q6ZWQ0	3	3	3	1.08	26	7	7	2.17	29	9	9	0	3	Nesprin-2	Q6ZWQ0	Syne2	Mus musculus
Q6ZWQ9	223	10	3	45.93	470	9	3	37.21	693	13	4	0.19	47.67	MCG5400	Q6ZWQ9	Myl12a	Mus musculus
Q6ZWR6	109	20	20	4.42	564	63	63	13.32	673	66	66	0	13.8	Nesprin-1	Q6ZWR6	Syne1	Mus musculus
Q6ZWV3	7	2	2	13.55	0	0	0		7	2	2	0.95	13.55	60S ribosomal protein L10	Q6ZWV3	Rpl10	Mus musculus
Q6ZWX6	21	2	2	14.29	44	3	3	20.63	65	3	3	0.29	20.63	Eukaryotic translation initiation factor 2 subunit 1	Q6ZWX6	Eif2s1	Mus musculus
Q6ZWZ6	0	0	0		34	5	5	56.82	34	5	5	0	56.82	40S ribosomal protein S12	Q6ZWZ6	Rps12	Mus musculus
Q76MZ3	246	13	8	34.97	243	12	8	32.6	489	16	11	0	41.43	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	Q76MZ3	Ppp2r1a	Mus musculus
Q78PY7	148	16	16	27.47	161	16	16	32.75	309	21	21	0	36.04	Staphylococcal nuclease domain-containing protein 1	Q78PY7	Snd1	Mus musculus
Q78ZA7	24	3	3	14.13	2	1	1	4.8	26	4	4	0.19	14.13	Nucleosome assembly protein 1-like 4	Q78ZA7	Nap1l4	Mus musculus
Q7M6Y3	16	3	3	8.48	46	5	5	20.3	62	6	6	0	20.3	Phosphatidylinositol-binding clathrin assembly protein	Q7M6Y3	Picalm	Mus musculus
Q7TMB8	2	2	2	2	2	1	0	0.96	4	3	2	0.95	2.95	Cytoplasmic FMR1-interacting protein 1	Q7TMB8	Cyfip1	Mus musculus
Q7TMK9	33	3	3	7.54	84	8	7	17.01	117	8	7	0	17.01	Heterogeneous nuclear ribonucleoprotein Q	Q7TMK9	Syncrip	Mus musculus
Q7TMY8	1	1	1	0.73	9	3	3	1.96	10	3	3	0.29	1.96	E3 ubiquitin-protein ligase HUWE1	Q7TMY8	Huwe1	Mus musculus
Q7TNC4	3	1	1	3.83	26	4	4	15.31	29	4	4	0.19	15.31	Putative RNA-binding protein Luc7-like 2	Q7TNC4	Luc7l2	Mus musculus
Q7TNG5	71	5	5	14.64	14	6	6	21.73	85	8	8	0	25.73	Echinoderm microtubule-associated protein-like 2	Q7TNG5	Eml2	Mus musculus
Q7TNP2	91	6	1	13.81	124	7	3	16.47	215	8	3	0.29	18.64	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	Q7TNP2	Ppp2r1b	Mus musculus
Q7TNV0	0	0	0		61	3	3	9.47	61	3	3	0.29	9.47	Protein DEK	Q7TNV0	Dek	Mus musculus
Q7TPD0	1	1	1	1.63	27	3	3	6.34	28	3	3	0.29	6.34	Integrator complex subunit 3	Q7TPD0	Ints3	Mus musculus
Q7TPR4	1191	44	30	61.21	747	38	25	46.52	1938	48	33	0	61.77	Alpha-actinin-1	Q7TPR4	Actn1	Mus musculus
Q7TPV4	22	9	9	12.05	41	6	6	7.96	63	10	10	0	13.02	Myb-binding protein 1A	Q7TPV4	Mybbp1a	Mus musculus
Q7TQI3	65	4	4	21.77	19	1	1	7.01	84	4	4	0.19	21.77	Ubiquitin thioesterase OTUB1	Q7TQI3	Otub1	Mus musculus
Q7TSI3	25	2	2	6.07	37	5	5	15.3	62	5	5	0	15.3	Serine/threonine-protein phosphatase 6 regulatory subunit 1	Q7TSI3	Ppp6r1	Mus musculus
Q7TSS2	0	0	0		19	2	2	15.4	19	2	2	0.95	15.4	Ubiquitin-conjugating enzyme E2 Q1	Q7TSS2	Ube2q1	Mus musculus
Q7TSV4	88	5	5	15.32	27	4	4	11.13	115	6	6	0	18.55	Phosphoglucomutase-2	Q7TSV4	Pgm2	Mus musculus
Q80T06	52	4	4	18.51	122	6	6	28.47	174	6	6	0	28.47	Elongation factor 1-delta	Q80T06	Eef1d	Mus musculus
Q80TH2	6	1	1	1.57	19	2	2	3.14	25	2	2	0.95	3.14	Protein LAP2	Q80TH2	Erbb2ip	Mus musculus
Q80TP3	0	0	0		3	3	3	2.18	3	3	3	0.29	2.18	E3 ubiquitin-protein ligase UBR5	Q80TP3	Ubr5	Mus musculus
Q80TY0	0	0	0		37	2	2	9.25	37	2	2	0.95	9.25	Formin-binding protein 1	Q80TY0	Fnbp1	Mus musculus
Q80U16-5	0	0	0		96	5	5	15.96	96	5	5	0	15.96	Isoform 5 of Protein FAM65B	Q80U16	Fam65b	Mus musculus
Q80U93	1	1	1	0.62	15	3	3	3.5	16	3	3	0.29	3.5	Nuclear pore complex protein Nup214	Q80U93	Nup214	Mus musculus
Q80UM3	11	3	3	7.63	3	1	1	2.89	14	4	4	0.19	7.63	N-alpha-acetyltransferase 15, NatA auxiliary subunit	Q80UM3	Naa15	Mus musculus
Q80UP5	4	2	2	4.93	2	1	1	4.25	6	3	3	0.29	9.18	Ankyrin repeat domain-containing protein 13A	Q80UP5	Ankrd13a	Mus musculus
Q80UR4	8	3	3	17.61	3	3	3	17.61	11	3	3	0.29	17.61	Mast cell protease-11	Q80UR4	Prss34	Mus musculus
Q80VD1	6	2	2	8.16	56	3	3	16.55	62	4	4	0.19	20.28	Protein FAM98B	Q80VD1	Fam98b	Mus musculus
Q80VP1	0	0	0		13	2	2	10.09	13	2	2	0.95	10.09	Epsin-1	Q80VP1	Epn1	Mus musculus
Q80VQ0	3	1	1	2.99	18	4	4	12.18	21	4	4	0.19	12.18	Aldehyde dehydrogenase family 3 member B1	Q80VQ0	Aldh3b1	Mus musculus
Q80WJ7	0	0	0		6	2	2	11.57	6	2	2	0.95	11.57	Protein LYRIC	Q80WJ7	Mtdh	Mus musculus
Q80WQ2	2	2	2	4.22	2	2	2	5.75	4	3	3	0.29	7.8	Protein VAC14 homolog	Q80WQ2	Vac14	Mus musculus
Q80X41	43	7	7	23.86	33	4	4	12.95	76	7	7	0	23.86	Serine/threonine-protein kinase VRK1	Q80X41	Vrk1	Mus musculus
Q80X50	0	0	0		10	3	3	4.34	10	3	3	0.29	4.34	Ubiquitin-associated protein 2-like	Q80X50	Ubap2l	Mus musculus
Q80X90	44	4	3	2.73	82	12	11	10.45	126	12	11	0	10.45	Filamin-B	Q80X90	Flnb	Mus musculus
Q80XU3	0	0	0		2	2	2	11.54	2	2	2	0.95	11.54	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	Q80XU3	Nucks1	Mus musculus
Q80Y14	0	0	0		43	2	2	21.71	43	2	2	0.95	21.71	Glutaredoxin-related protein 5, mitochondrial	Q80Y14	Glrx5	Mus musculus
Q80ZJ2	43	4	4	25	16	3	3	21.01	59	4	4	0.19	25	Impa1 protein	Q80ZJ2	Impa1	Mus musculus
Q80ZX0	8	2	2	3.36	0	0	0		8	2	2	0.95	3.36	Protein Sec24b	Q80ZX0	Sec24b	Mus musculus
Q810A7	2	1	1	2.26	7	2	2	4.63	9	2	2	0.95	4.63	ATP-dependent RNA helicase DDX42	Q810A7	Ddx42	Mus musculus
Q810B6	25	2	2	4.11	27	5	5	9.32	52	5	5	0	9.32	Rabankyrin-5	Q810B6	Ankfy1	Mus musculus
Q8BFQ8	0	0	0		6	2	2	22.27	6	2	2	0.95	22.27	Parkinson disease 7 domain-containing protein 1	Q8BFQ8	Pddc1	Mus musculus
Q8BFR5	7	2	2	7.3	31	3	3	13.27	38	3	3	0.29	13.27	Elongation factor Tu, mitochondrial	Q8BFR5	Tufm	Mus musculus
Q8BFY6	20	2	2	8.73	12	2	2	8.73	32	2	2	0.95	8.73	Peflin	Q8BFY6	Pef1	Mus musculus
Q8BFY9	80	8	8	16.04	108	11	11	23.16	188	14	14	0	27.84	Transportin-1	Q8BFY9	Tnpo1	Mus musculus
Q8BFZ3	3512	38	6	42.02	3725	20	4	39.36	7237	40	7	0	48.94	Beta-actin-like protein 2	Q8BFZ3	Actbl2	Mus musculus
Q8BG05	117	7	7	21.11	206	8	8	21.11	323	8	8	0	21.11	Heterogeneous nuclear ribonucleoprotein A3	Q8BG05	Hnrnpa3	Mus musculus
Q8BG32	20	4	4	14.22	14	4	4	15.88	34	6	6	0	22.27	26S proteasome non-ATPase regulatory subunit 11	Q8BG32	Psmd11	Mus musculus
Q8BGD9	51	2	2	8.67	60	5	5	11.95	111	5	5	0	11.95	Eukaryotic translation initiation factor 4B	Q8BGD9	Eif4b	Mus musculus
Q8BGE6	15	2	2	8.65	7	1	1	4.83	22	2	2	0.95	8.65	Cysteine protease ATG4B	Q8BGE6	Atg4b	Mus musculus
Q8BGG7	1	1	1	3.61	6	2	2	7.37	7	2	2	0.95	7.37	Ubiquitin-associated and SH3 domain-containing protein B	Q8BGG7	Ubash3b	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q8BGJ5	153	8	8	27.41	181	9	9	31	334	9	9	0	31	MCG13402, isoform CRA_a	Q8BGJ5	Ptbp1	Mus musculus
Q8BGQ7	93	10	10	18.39	91	11	11	22.93	184	13	13	0	26.24	Alanine--tRNA ligase, cytoplasmic	Q8BGQ7	Aars	Mus musculus
Q8BGT7	0	0	0		25	3	3	24.37	25	3	3	0.29	24.37	Survival of motor neuron-related-splicing factor 30	Q8BGT7	Smndc1	Mus musculus
Q8BH04	28	8	8	21.56	12	3	3	8.59	40	10	10	0	24.84	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	Q8BH04	Pck2	Mus musculus
Q8BH43	27	3	3	10.26	22	3	3	9.05	49	4	4	0.19	12.88	Wiskott-Aldrich syndrome protein family member 2	Q8BH43	Wasf2	Mus musculus
Q8BH59	0	0	0		14	3	3	8.27	14	3	3	0.29	8.27	Calcium-binding mitochondrial carrier protein Aralar1	Q8BH59	Slc25a12	Mus musculus
Q8BH61	128	13	13	21.86	7	3	3	5.6	135	13	13	0	21.86	Coagulation factor XIII A chain	Q8BH61	F13a1	Mus musculus
Q8BH69	16	2	2	9.18	2	1	1	5.36	18	2	2	0.95	9.18	Selenide, water dikinase 1	Q8BH69	Sephs1	Mus musculus
Q8BH74	1	1	1	3.24	13	4	4	8.42	14	5	5	0	11.66	Nuclear pore complex protein Nup107	Q8BH74	Nup107	Mus musculus
Q8BH78	1	1	1	3.65	23	2	2	17.98	24	3	3	0.29	21.63	Reticulon	Q8BH78	Rtn4	Mus musculus
Q8BH95	8	2	2	16.9	35	2	2	19.66	43	3	3	0.29	24.14	Enoyl-CoA hydratase, mitochondrial	Q8BH95	Echs1	Mus musculus
Q8BHD7	32	4	4	21.61	89	6	6	29.45	121	6	6	0	29.45	Polypyrimidine tract-binding protein 3	Q8BHD7	Ptbp3	Mus musculus
Q8BHG1	136	11	11	18.26	36	4	4	7.58	172	11	11	0	18.26	Nardilysin	Q8BHG1	Nrd1	Mus musculus
Q8BHJ5	19	2	2	8.95	46	2	2	8.95	65	2	2	0.95	8.95	F-box-like/WD repeat-containing protein TBL1XR1	Q8BHJ5	Tbl1xr1	Mus musculus
Q8BHN3	88	10	10	21.4	98	9	9	19.39	186	13	13	0	26.38	Neutral alpha-glucosidase AB	Q8BHN3	Ganab	Mus musculus
Q8BIJ6	13	2	2	3.36	6	1	1	1.48	19	2	2	0.95	3.36	Isoleucine--tRNA ligase, mitochondrial	Q8BIJ6	Iars2	Mus musculus
Q8BIQ5	0	0	0		29	4	4	12.59	29	4	4	0.19	12.59	Cleavage stimulation factor subunit 2	Q8BIQ5	Cstf2	Mus musculus
Q8BIW1	1	1	1	3.74	3	2	2	7.05	4	2	2	0.95	7.05	Protein prune homolog	Q8BIW1	Prune	Mus musculus
Q8BJ71	6	2	2	7.08	81	3	3	9.16	87	3	3	0.29	9.16	Nuclear pore complex protein Nup93	Q8BJ71	Nup93	Mus musculus
Q8BJS4	18	4	4	10.4	113	10	10	22.71	131	10	10	0	22.71	SUN domain-containing protein 2	Q8BJS4	Sun2	Mus musculus
Q8BJU0	0	0	0		4	2	2	9.21	4	2	2	0.95	9.21	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	Q8BJU0	Sgta	Mus musculus
Q8BJW6	2	2	2	7.06	1	1	1	3.1	3	3	3	0.29	10.15	Eukaryotic translation initiation factor 2A	Q8BJW6	Eif2a	Mus musculus
Q8BJY1	46	4	4	17.86	46	3	3	14.88	92	4	4	0.19	17.86	26S proteasome non-ATPase regulatory subunit 5	Q8BJY1	Psmd5	Mus musculus
Q8BK64	29	1	1	6.51	11	2	2	11.24	40	2	2	0.95	11.24	Activator of 90 kDa heat shock protein ATPase homolog 1	Q8BK64	Ahsa1	Mus musculus
Q8BK67	130	10	10	31.15	7	3	3	10.96	137	10	10	0	31.15	Protein RCC2	Q8BK67	Rcc2	Mus musculus
Q8BKC5	236	13	13	23.15	28	5	5	10.67	264	13	13	0	23.15	Importin-5	Q8BKC5	Ipo5	Mus musculus
Q8BL97	47	2	2	14.23	77	4	3	17.6	124	4	3	0.29	17.6	Serine/arginine-rich splicing factor 7	Q8BL97	Srsf7	Mus musculus
Q8BMA6	3	2	2	5.92	22	4	4	12	25	5	5	0	12.64	Signal recognition particle subunit SRP68	Q8BMA6	Srp68	Mus musculus
Q8BMD8	0	0	0		13	2	2	9.47	13	2	2	0.95	9.47	Calcium-binding mitochondrial carrier protein SCaMC-1	Q8BMD8	Slc25a24	Mus musculus
Q8BMJ2	16	2	2	4.07	43	3	3	5.77	59	4	4	0.19	7.22	Leucine--tRNA ligase, cytoplasmic	Q8BMJ2	Lars	Mus musculus
Q8BMJ3	0	0	0		13	2	2	30.56	13	2	2	0.95	30.56	Eukaryotic translation initiation factor 1A, X-chromosomal	Q8BMJ3	Eif1ax	Mus musculus
Q8BMK4	2	1	1	6.78	90	8	8	21.22	92	8	8	0	21.22	Cytoskeleton-associated protein 4	Q8BMK4	Ckap4	Mus musculus
Q8BML9	0	0	0		3	2	2	5.29	3	2	2	0.95	5.29	Glutaminyl-tRNA synthetase	Q8BML9	Qars	Mus musculus
Q8BMS1	13	2	2	7.47	145	10	10	21.49	158	10	10	0	21.49	Trifunctional enzyme subunit alpha, mitochondrial	Q8BMS1	Hadha	Mus musculus
Q8BND5	113	10	10	21.39	92	7	7	16.31	205	11	11	0	23.66	Sulfhydryl oxidase 1	Q8BND5	Qsox1	Mus musculus
Q8BP47	38	5	5	15.92	50	10	10	27.37	88	12	12	0	30.77	Asparagine--tRNA ligase, cytoplasmic	Q8BP47	Nars	Mus musculus
Q8BP56	12	2	2	6.67	0	0	0		12	2	2	0.95	6.67	Acid trehalase-like protein 1	Q8BP56	Athl1	Mus musculus
Q8BPU7	19	3	3	11.42	44	5	5	13.76	63	5	5	0	13.76	Engulfment and cell motility protein 1	Q8BPU7	Elmo1	Mus musculus
Q8BQ30	0	0	0		7	2	2	10.44	7	2	2	0.95	10.44	Phostensin	Q8BQ30	Ppp1r18	Mus musculus
Q8BQ46	20	1	1	7	51	4	2	12.57	71	4	2	0.95	12.57	Protein Taf15	Q8BQ46	Taf15	Mus musculus
Q8BQ47	0	0	0		12	2	2	17.14	12	2	2	0.95	17.14	Protein canopy homolog 4	Q8BQ47	Cnpy4	Mus musculus
Q8BRF7	19	4	4	12.52	10	4	4	12.21	29	5	5	0	15.49	Sec1 family domain-containing protein 1	Q8BRF7	Scfd1	Mus musculus
Q8BRN9	0	0	0		4	2	2	5.66	4	2	2	0.95	5.66	Coiled-coil and C2 domain-containing protein 1B	Q8BRN9	Cc2d1b	Mus musculus
Q8BT60	268	12	11	33.4	395	20	18	41.84	663	20	18	0	41.84	Copine-3	Q8BT60	Cpne3	Mus musculus
Q8BTE6	34	4	4	52.38	394	13	13	61.9	428	13	13	0	61.9	Protein Wfdc21	Q8BTE6	Wfdc21	Mus musculus
Q8BTI8	0	0	0		7	3	3	2.77	7	3	3	0.29	2.77	Serine/arginine repetitive matrix protein 2	Q8BTI8	Srrm2	Mus musculus
Q8BTM8	2500	86	85	45.56	5047	129	128	54.02	7547	137	136	0	57.95	Filamin-A	Q8BTM8	Flna	Mus musculus
Q8BTS4	0	0	0		4	2	2	7.06	4	2	2	0.95	7.06	Nuclear pore complex protein Nup54	Q8BTS4	Nup54	Mus musculus
Q8BTZ7	21	5	5	20	4	2	2	12.5	25	5	5	0	20	Mannose-1-phosphate guanyltransferase beta	Q8BTZ7	Gmppb	Mus musculus
Q8BU30	5	2	2	2.14	6	3	3	5.63	11	5	5	0	7.77	Isoleucine--tRNA ligase, cytoplasmic	Q8BU30	Iars	Mus musculus
Q8BUK6	0	0	0		24	4	4	11.7	24	4	4	0.19	11.7	Protein Hook homolog 3	Q8BUK6	Hook3	Mus musculus
Q8BUM3	11	3	3	17.83	0	0	0		11	3	3	0.29	17.83	Tyrosine-protein phosphatase non-receptor type 7	Q8BUM3	Ptpn7	Mus musculus
Q8BV13	5	2	2	15.15	0	0	0		5	2	2	0.95	15.15	COP9 signalosome complex subunit 7b	Q8BV13	Cops7b	Mus musculus
Q8BVE3	43	2	2	8.7	41	2	2	8.7	84	2	2	0.95	8.7	V-type proton ATPase subunit H	Q8BVE3	Atp6v1h	Mus musculus
Q8BVG4	42	2	2	5.68	5	2	2	5.68	47	2	2	0.95	5.68	Dipeptidyl peptidase 9	Q8BVG4	Dpp9	Mus musculus
Q8BWT1	44	8	8	32.49	39	4	4	22.42	83	8	8	0	32.49	3-ketoacyl-CoA thiolase, mitochondrial	Q8BWT1	Acaa2	Mus musculus
Q8BWY3	26	3	3	15.56	12	2	2	10.98	38	3	3	0.29	15.56	Eukaryotic peptide chain release factor subunit 1	Q8BWY3	Etf1	Mus musculus
Q8BX94	3	3	3	11.98	1	1	1	4.96	4	3	3	0.29	11.98	Oxysterol-binding protein-related protein 2	Q8BX94	Osbpl2	Mus musculus
Q8BXK9	4	2	2	7.17	3	2	2	7.17	7	2	2	0.95	7.17	Chloride intracellular channel protein 5	Q8BXK9	Clic5	Mus musculus
Q8BY71	7	2	2	8.17	11	3	3	15.62	18	3	3	0.29	15.62	Histone acetyltransferase type B catalytic subunit	Q8BY71	Hat1	Mus musculus
Q8BYA0	3	3	3	5.02	1	1	1	2.68	4	4	4	0.19	7.69	Tubulin-specific chaperone D	Q8BYA0	Tbcd	Mus musculus
Q8BYC6	0	0	0		3	3	3	6.46	3	3	3	0.29	6.46	Serine/threonine-protein kinase TAO3	Q8BYC6	Taok3	Mus musculus
Q8BYI6	2	1	1	3.86	8	2	2	10.29	10	2	2	0.95	10.29	Lysophosphatidylcholine acyltransferase 2	Q8BYI6	Lpcat2	Mus musculus
Q8BYW1	1	1	1	4.01	15	6	6	17.13	16	6	6	0	17.13	Rho GTPase-activating protein 25	Q8BYW1	Arhgap25	Mus musculus
Q8BZA9	10	3	3	18.59	0	0	0		10	3	3	0.29	18.59	Fructose-2,6-bisphosphatase TIGAR	Q8BZA9	Tigar	Mus musculus
Q8C079	0	0	0		8	3	3	8.96	8	3	3	0.29	8.96	Striatin-interacting protein 1	Q8C079	Strip1	Mus musculus
Q8C0C7	26	1	1	2.76	24	2	2	8.66	50	2	2	0.95	8.66	Phenylalanine--tRNA ligase alpha subunit	Q8C0C7	Farsa	Mus musculus
Q8C0D5	2	2	2	4.7	2	1	1	3.55	4	3	3	0.29	8.25	Elongation factor Tu GTP-binding domain-containing protein 1	Q8C0D5	Eftud1	Mus musculus
Q8C0E2	7	2	2	13.99	0	0	0		7	2	2	0.95	13.99	Vacuolar protein sorting-associated protein 26B	Q8C0E2	Vps26b	Mus musculus
Q8C0G2	2	1	1	5.07	18	2	2	9.75	20	2	2	0.95	9.75	TRAF3-interacting JNK-activating modulator	Q8C0G2	Traf3ip3	Mus musculus
Q8C0I1	5	2	2	6.05	67	9	9	25.27	72	9	9	0	25.27	Alkyldihydroxyacetonephosphate synthase, peroxisomal	Q8C0I1	Agps	Mus musculus
Q8C0L0	0	0	0		20	4	4	15.52	20	4	4	0.19	15.52	Thioredoxin-related transmembrane protein 4	Q8C0L0	Tmx4	Mus musculus
Q8C147	9	4	4	4.67	60	8	8	9.24	69	8	8	0	9.24	Dedicator of cytokinesis protein 8	Q8C147	Dock8	Mus musculus
Q8C166	42	5	5	19.78	107	9	8	26.87	149	10	9	0	29.85	Copine-1	Q8C166	Cpne1	Mus musculus
Q8C1A5	15	5	5	10.77	0	0	0		15	5	5	0	10.77	Thimet oligopeptidase	Q8C1A5	Thop1	Mus musculus
Q8C1B7	32	3	3	13.69	32	3	3	13.69	64	3	3	0.29	13.69	Septin-11	Q8C1B7	Sept11	Mus musculus
Q8C2Q3	0	0	0		36	4	4	11.51	36	4	4	0.19	11.51	RNA-binding protein 14	Q8C2Q3	Rbm14	Mus musculus
Q8C3J5	10	4	4	3.45	27	6	6	6.07	37	6	6	0	6.07	Dedicator of cytokinesis protein 2	Q8C3J5	Dock2	Mus musculus
Q8C4Y3	2	2	2	6.03	0	0	0		2	2	2	0.95	6.03	Negative elongation factor B	Q8C4Y3	Nelfb	Mus musculus
Q8C570	15	3	3	21.47	0	0	0		15	3	3	0.29	21.47	mRNA export factor	Q8C570	Rae1	Mus musculus
Q8C5P5	20	4	4	12.42	11	1	1	4.07	31	4	4	0.19	12.42	5'-nucleotidase domain-containing protein 1	Q8C5P5	Nt5dc1	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q8C6G8	2	2	2	5.93	24	2	2	5.93	26	3	3	0.29	8.74	WD repeat-containing protein 26	Q8C6G8	Wdr26	Mus musculus
Q8C708	20	2	2	14.22	1	1	1	4.89	21	2	2	0.95	14.22	Transmembrane protein C16orf54 homolog	Q8C708		Mus musculus
Q8CAQ8	0	0	0		33	6	6	12.02	33	6	6	0	12.02	MICOS complex subunit Mic60	Q8CAQ8	Immt	Mus musculus
Q8CB87	1	1	1	2.62	19	6	6	16.14	20	7	7	0	18.76	Ras-related protein Rab-44	Q8CB87	Rab44	Mus musculus
Q8CBW3	5	2	2	9.98	6	4	4	13.1	11	4	4	0.19	13.1	Abl interactor 1	Q8CBW3	Abi1	Mus musculus
Q8CBY8	1	1	1	7.71	16	2	2	14.13	17	2	2	0.95	14.13	Dynactin subunit 4	Q8CBY8	Dctn4	Mus musculus
Q8CC86	56	6	6	18.77	11	3	3	8.74	67	6	6	0	18.77	Nicotinate phosphoribosyltransferase	Q8CC86	Naprt	Mus musculus
Q8CCF0	1	1	1	4.21	8	2	2	9.42	9	2	2	0.95	9.42	U4/U6 small nuclear ribonucleoprotein Prp31	Q8CCF0	Prpf31	Mus musculus
Q8CCJ3	0	0	0		4	2	2	4.92	4	2	2	0.95	4.92	E3 UFM1-protein ligase 1	Q8CCJ3	Ufl1	Mus musculus
Q8CCK0	263	7	3	12.37	218	7	1	10.22	481	9	3	0.29	12.37	Core histone macro-H2A.2	Q8CCK0	H2afy2	Mus musculus
Q8CCS6	0	0	0		10	2	2	20.86	10	2	2	0.95	20.86	Polyadenylate-binding protein 2	Q8CCS6	Pabpn1	Mus musculus
Q8CD10	0	0	0		2	2	2	9.95	2	2	2	0.95	9.95	Calcium uptake protein 2, mitochondrial	Q8CD10	Micu2	Mus musculus
Q8CDN6	61	8	8	35.99	65	7	7	35.99	126	8	8	0	35.99	Thioredoxin-like protein 1	Q8CDN6	Txnl1	Mus musculus
Q8CEC0	0	0	0		14	3	3	9.96	14	3	3	0.29	9.96	Nuclear pore complex protein Nup88	Q8CEC0	Nup88	Mus musculus
Q8CEC6	9	1	1	4.02	2	2	2	7.89	11	2	2	0.95	7.89	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	Q8CEC6	Ppwd1	Mus musculus
Q8CFI7	2	2	2	5.2	7	1	1	2.21	9	2	2	0.95	5.2	DNA-directed RNA polymerase II subunit RPB2	Q8CFI7	Polr2b	Mus musculus
Q8CFQ3	2	2	2	3.92	0	0	0		2	2	2	0.95	3.92	Intron-binding protein aquarius	Q8CFQ3	Aqr	Mus musculus
Q8CFV9	4	2	2	38.71	0	0	0		4	2	2	0.95	38.71	Riboflavin kinase	Q8CFV9	Rfk	Mus musculus
Q8CFX1	3	3	3	8.62	0	0	0		3	3	3	0.29	8.62	GDH/6PGL endoplasmic bifunctional protein	Q8CFX1	H6pd	Mus musculus
Q8CG03	90	9	9	18.73	10	2	2	4.97	100	9	9	0	18.73	cGMP-specific 3',5'-cyclic phosphodiesterase	Q8CG03	Pde5a	Mus musculus
Q8CG19	47	5	5	7.13	7	2	2	4.09	54	6	6	0	9	Latent-transforming growth factor beta-binding protein 1	Q8CG19	Ltbp1	Mus musculus
Q8CG29	52	4	4	5.65	157	12	12	17.03	209	12	12	0	17.03	Myosin IF	Q8CG29	Myo1f	Mus musculus
Q8CGC7	56	9	9	10.78	76	12	12	14.55	132	16	16	0	18.12	Bifunctional glutamate/proline--tRNA ligase	Q8CGC7	Eprs	Mus musculus
Q8CGP4	6824	20	5	58.14	5090	19	5	58.91	11914	22	6	0	58.91	Histone H2A	Q8CGP4	Hist1h2aa	Mus musculus
Q8CH18	0	0	0		10	2	2	2.53	10	2	2	0.95	2.53	Cell division cycle and apoptosis regulator protein 1	Q8CH18	Ccar1	Mus musculus
Q8CHC4	0	0	0		4	2	2	1.84	4	2	2	0.95	1.84	Synaptojanin-1	Q8CHC4	Synj1	Mus musculus
Q8CHG3	0	0	0		7	2	2	2.32	7	2	2	0.95	2.32	GRIP and coiled-coil domain-containing protein 2	Q8CHG3	Gcc2	Mus musculus
Q8CHK3	0	0	0		8	2	2	10.78	8	2	2	0.95	10.78	Lysophospholipid acyltransferase 7	Q8CHK3	Mboat7	Mus musculus
Q8CHP8	56	4	4	23.99	23	4	4	22.12	79	5	5	0	24.3	Phosphoglycolate phosphatase	Q8CHP8	Pgp	Mus musculus
Q8CI94	97	8	5	15.18	8	4	2	5.34	105	9	5	0	15.54	Glycogen phosphorylase, brain form	Q8CI94	Pygb	Mus musculus
Q8CI95	0	0	0		6	3	3	11.85	6	3	3	0.29	11.85	Oxysterol-binding protein-related protein 11	Q8CI95	Osbpl11	Mus musculus
Q8CIE6	36	11	11	12.5	51	9	9	13.07	87	14	14	0	18.14	Coatomer subunit alpha	Q8CIE6	Copa	Mus musculus
Q8CIH5	264	22	22	33.12	148	11	11	16.05	412	23	23	0	33.12	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	Q8CIH5	Plcg2	Mus musculus
Q8CIM3	11	3	3	10.84	0	0	0		11	3	3	0.29	10.84	D-2-hydroxyglutarate dehydrogenase, mitochondrial	Q8CIM3	D2hgdh	Mus musculus
Q8CIN4	85	6	6	20.42	160	7	7	26.53	245	9	9	0	28.44	Serine/threonine-protein kinase PAK 2	Q8CIN4	Pak2	Mus musculus
Q8CIS0	0	0	0		3	2	2	2.33	3	2	2	0.95	2.33	Caspase recruitment domain-containing protein 11	Q8CIS0	Card11	Mus musculus
Q8CJG0	21	4	4	8.14	0	0	0		21	4	4	0.19	8.14	Protein argonaute-2	Q8CJG0	Ago2	Mus musculus
Q8JZQ9	65	11	11	24.91	129	11	11	26.53	194	15	15	0	35.74	Eukaryotic translation initiation factor 3 subunit B	Q8JZQ9	Eif3b	Mus musculus
Q8JZV7	4	2	2	10.51	2	1	1	5.13	6	3	3	0.29	15.65	Putative N-acetylglucosamine-6-phosphate deacetylase	Q8JZV7	Amdhd2	Mus musculus
Q8K0C9	16	4	4	19.35	0	0	0		16	4	4	0.19	19.35	GDP-mannose 4,6 dehydratase	Q8K0C9	Gmds	Mus musculus
Q8K0E8	393	21	21	43.04	177	14	14	46.36	570	25	25	0	49.9	Fibrinogen beta chain	Q8K0E8	Fgb	Mus musculus
Q8K124	7	1	1	6.06	105	6	6	26.87	112	6	6	0	26.87	Pleckstrin homology domain-containing family O member 2	Q8K124	Plekho2	Mus musculus
Q8K183	5	2	2	7.37	0	0	0		5	2	2	0.95	7.37	Pyridoxal kinase	Q8K183	Pdxk	Mus musculus
Q8K1B8	484	21	21	46.62	135	15	15	33.83	619	25	25	0	49.02	Fermitin family homolog 3	Q8K1B8	Fermt3	Mus musculus
Q8K1M6	41	4	4	10.92	23	4	4	12.8	64	5	5	0	14.69	Dynamin-1-like protein	Q8K1M6	Dnm1l	Mus musculus
Q8K1T1	0	0	0		31	3	3	15.82	31	3	3	0.29	15.82	Leucine-rich repeat-containing protein 25	Q8K1T1	Lrrc25	Mus musculus
Q8K1X4	7	3	3	5.91	16	5	5	8.55	23	5	5	0	8.55	NCK associated protein 1 like	Q8K1X4	Nckap1l	Mus musculus
Q8K274	2	2	2	13.59	0	0	0		2	2	2	0.95	13.59	Ketosamine-3-kinase	Q8K274	Fn3krp	Mus musculus
Q8K296	5	3	3	5.35	25	3	3	5.77	30	5	5	0	8.86	Myotubularin-related protein 3	Q8K296	Mtmr3	Mus musculus
Q8K2B3	28	5	5	16.57	29	3	3	9.64	57	5	5	0	16.57	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Q8K2B3	Sdha	Mus musculus
Q8K2H4	3	2	2	6.89	1	1	1	2.43	4	3	3	0.29	9.32	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1	Q8K2H4	Acap1	Mus musculus
Q8K2K6	0	0	0		15	2	2	10.52	15	2	2	0.95	10.52	Arf-GAP domain and FG repeat-containing protein 1	Q8K2K6	Agfg1	Mus musculus
Q8K2T1	10	2	2	11	0	0	0		10	2	2	0.95	11	NmrA-like family domain-containing protein 1	Q8K2T1	Nmral1	Mus musculus
Q8K2Z4	4	1	1	1.29	15	2	2	2.59	19	2	2	0.95	2.59	Condensin complex subunit 1	Q8K2Z4	Ncapd2	Mus musculus
Q8K310	7	1	1	2.48	38	4	4	8.27	45	4	4	0.19	8.27	Matrin-3	Q8K310	Matr3	Mus musculus
Q8K352	9	3	3	10.79	68	8	8	46.84	77	9	9	0	46.84	SAM and SH3 domain-containing protein 3	Q8K352	Sash3	Mus musculus
Q8K354	17	4	4	25.27	1	1	1	10.11	18	4	4	0.19	25.27	Carbonyl reductase [NADPH] 3	Q8K354	Cbr3	Mus musculus
Q8K3K8	0	0	0		7	2	2	5.65	7	2	2	0.95	5.65	Optineurin	Q8K3K8	Optn	Mus musculus
Q8K411	29	5	5	11	1	1	1	2.41	30	5	5	0	11	Presequence protease, mitochondrial	Q8K411	Pitrm1	Mus musculus
Q8K426	93	4	4	47.86	283	6	6	58.12	376	6	6	0	58.12	Myeloid cysteine-rich protein	Q8K426	Retnlg	Mus musculus
Q8K482	172	11	11	18.72	77	5	5	9.4	249	11	11	0	18.72	EMILIN-2	Q8K482	Emilin2	Mus musculus
Q8K4I3	15	1	1	2.59	50	5	5	14.14	65	5	5	0	14.14	Rho guanine nucleotide exchange factor 6	Q8K4I3	Arhgef6	Mus musculus
Q8K4L3	26	3	3	3.64	111	8	8	7.42	137	8	8	0	7.42	Supervillin	Q8K4L3	Svil	Mus musculus
Q8K4Z3	11	4	4	28.72	1	1	1	8.16	12	4	4	0.19	28.72	NAD(P)H-hydrate epimerase	Q8K4Z3	Apoa1bp	Mus musculus
Q8K4Z5	3	1	1	3.03	25	7	7	11.63	28	7	7	0	11.63	Splicing factor 3A subunit 1	Q8K4Z5	Sf3a1	Mus musculus
Q8K558	29	4	4	23.34	20	4	4	23.34	49	4	4	0.19	23.34	Trem-like transcript 1 protein	Q8K558	Treml1	Mus musculus
Q8QZT1	21	4	4	18.4	31	5	5	13.21	52	6	6	0	21.46	Acetyl-CoA acetyltransferase, mitochondrial	Q8QZT1	Acat1	Mus musculus
Q8QZW8	4	1	1	3.38	34	5	5	16.28	38	5	5	0	16.28	Protein Arhgap9	Q8QZW8	Arhgap9	Mus musculus
Q8QZY1	139	8	8	23.94	75	7	7	21.63	214	8	8	0	23.94	Eukaryotic translation initiation factor 3 subunit L	Q8QZY1	Eif3l	Mus musculus
Q8QZY6	53	2	2	11.85	0	0	0		53	2	2	0.95	11.85	Tetraspanin-14	Q8QZY6	Tspan14	Mus musculus
Q8QZY9	19	2	2	8.96	37	4	4	17.69	56	4	4	0.19	17.69	Splicing factor 3B subunit 4	Q8QZY9	Sf3b4	Mus musculus
Q8R010	13	3	3	30.31	36	1	1	11.25	49	3	3	0.29	30.31	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	Q8R010	Aimp2	Mus musculus
Q8R016	197	11	11	32.31	15	2	2	10.99	212	11	11	0	32.31	Bleomycin hydrolase	Q8R016	Blmh	Mus musculus
Q8R050	15	3	3	7.86	32	5	5	11.95	47	5	5	0	11.95	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	Q8R050	Gspt1	Mus musculus
Q8R081	115	9	9	26.96	288	11	11	32.59	403	12	12	0	32.59	Heterogeneous nuclear ribonucleoprotein L	Q8R081	Hnrnpl	Mus musculus
Q8R0G9	1	1	1	1.39	23	7	7	11.95	24	7	7	0	11.95	Nuclear pore complex protein Nup133	Q8R0G9	Nup133	Mus musculus
Q8R0H9	0	0	0		46	3	3	8.98	46	3	3	0.29	8.98	ADP-ribosylation factor-binding protein GGA1	Q8R0H9	Gga1	Mus musculus
Q8R0J7	11	2	2	12.28	0	0	0		11	2	2	0.95	12.28	Vacuolar protein sorting-associated protein 37B	Q8R0J7	Vps37b	Mus musculus
Q8R0T6	12	1	1	2.77	41	3	3	6.27	53	3	3	0.29	6.27	Probable G-protein coupled receptor 97	Q8R0T6	Gpr97	Mus musculus
Q8R146	218	13	13	30.33	9	2	2	6.56	227	13	13	0	30.33	Acylamino-acid-releasing enzyme	Q8R146	Apeh	Mus musculus
Q8R180	75	8	8	32.33	93	6	6	24.57	168	8	8	0	32.33	ERO1-like protein alpha	Q8R180	Ero1l	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q8R1B4	24	4	4	6.26	26	6	6	9.33	50	7	7	0	9.33	Eukaryotic translation initiation factor 3 subunit C	Q8R1B4	Eif3c	Mus musculus
Q8R1G6	0	0	0		22	5	5	26.93	22	5	5	0	26.93	PDZ and LIM domain protein 2	Q8R1G6	Pdlim2	Mus musculus
Q8R1Q8	7	3	3	17.4	16	7	7	30.98	23	7	7	0	30.98	Cytoplasmic dynein 1 light intermediate chain 1	Q8R1Q8	Dync1li1	Mus musculus
Q8R2S8	564	20	20	40.27	1049	31	31	51.53	1613	31	31	0	51.53	CD177 antigen	Q8R2S8	Cd177	Mus musculus
Q8R2Y8	0	0	0		7	2	2	19.89	7	2	2	0.95	19.89	Peptidyl-tRNA hydrolase 2, mitochondrial	Q8R2Y8	Ptrh2	Mus musculus
Q8R307	0	0	0		2	2	2	4.32	2	2	2	0.95	4.32	Vacuolar protein sorting-associated protein 18 homolog	Q8R307	Vps18	Mus musculus
Q8R326	0	0	0		8	2	2	11.47	8	2	2	0.95	11.47	Paraspeckle component 1	Q8R326	Pspc1	Mus musculus
Q8R3G1	9	2	2	6.27	10	1	1	6.27	19	2	2	0.95	6.27	Nuclear inhibitor of protein phosphatase 1	Q8R3G1	Ppp1r8	Mus musculus
Q8R460	1	1	1	9.15	24	2	2	24.39	25	3	3	0.29	24.39	Interleukin-36 gamma	Q8R460	Il36g	Mus musculus
Q8R4R6	0	0	0		17	2	2	12	17	2	2	0.95	12	Nucleoporin NUP53	Q8R4R6	Nup35	Mus musculus
Q8R550	9	2	2	5.22	59	4	4	10.72	68	5	5	0	13.26	SH3 domain-containing kinase-binding protein 1	Q8R550	Sh3kbp1	Mus musculus
Q8R574	0	0	0		5	2	2	6.78	5	2	2	0.95	6.78	Phosphoribosyl pyrophosphate synthase-associated protein 2	Q8R574	Prpsap2	Mus musculus
Q8R5A3	54	3	3	7.16	75	3	3	7.16	129	3	3	0.29	7.16	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	Q8R5A3	Apbb1ip	Mus musculus
Q8R5H1	9	3	3	4.59	44	4	4	4.79	53	4	4	0.19	4.79	Ubiquitin carboxyl-terminal hydrolase 15	Q8R5H1	Usp15	Mus musculus
Q8R5L1	154	7	7	37.28	169	8	8	38.71	323	8	8	0	38.71	Complement component 1 Q subcomponent-binding protein, mitochondrial	Q8R5L1	C1qbp	Mus musculus
Q8VBT6	0	0	0		227	15	15	31.21	227	15	15	0	31.21	Apolipoprotein B receptor	Q8VBT6	Apobr	Mus musculus
Q8VBT9	8	2	2	8	6	1	1	2.55	14	3	3	0.29	10.55	Tether containing UBX domain for GLUT4	Q8VBT9	Aspscr1	Mus musculus
Q8VBV7	44	5	5	38.28	21	3	3	24.4	65	5	5	0	38.28	COP9 signalosome complex subunit 8	Q8VBV7	Cops8	Mus musculus
Q8VBW6	15	3	3	11.61	5	1	1	5.81	20	3	3	0.29	11.61	NEDD8-activating enzyme E1 regulatory subunit	Q8VBW6	Nae1	Mus musculus
Q8VC03	9	2	2	4.57	0	0	0		9	2	2	0.95	4.57	Echinoderm microtubule-associated protein-like 3	Q8VC03	Eml3	Mus musculus
Q8VC30	9	3	3	12.11	0	0	0		9	3	3	0.29	12.11	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	Q8VC30	Dak	Mus musculus
Q8VC88	88	7	7	30.45	41	5	5	27.27	129	7	7	0	30.45	Grancalcin	Q8VC88	Gca	Mus musculus
Q8VCI0	160	11	11	24.18	148	8	8	22	308	11	11	0	24.18	Phospholipase B-like 1	Q8VCI0	Plbd1	Mus musculus
Q8VCI5	0	0	0		13	2	2	12.71	13	2	2	0.95	12.71	Peroxisomal biogenesis factor 19	Q8VCI5	Pex19	Mus musculus
Q8VCM7	517	21	21	56.42	146	12	12	43.12	663	22	22	0	57.57	Fibrinogen gamma chain	Q8VCM7	Fgg	Mus musculus
Q8VCN9	8	2	2	17.6	0	0	0		8	2	2	0.95	17.6	Tubulin-specific chaperone C	Q8VCN9	Tbcc	Mus musculus
Q8VCT3	186	16	16	39.23	59	7	7	20.62	245	16	16	0	39.23	Aminopeptidase B	Q8VCT3	Rnpep	Mus musculus
Q8VD04	0	0	0		14	3	3	8.56	14	3	3	0.29	8.56	GRIP1-associated protein 1	Q8VD04	Gripap1	Mus musculus
Q8VD58	0	0	0		14	2	2	5.86	14	2	2	0.95	5.86	Protein EVI2B	Q8VD58	Evi2b	Mus musculus
Q8VDD5	1620	64	60	36.38	3382	83	77	43.57	5002	92	86	0	45.82	Myosin-9	Q8VDD5	Myh9	Mus musculus
Q8VDJ3	0	0	0		32	3	3	4.26	32	3	3	0.29	4.26	Vigilin	Q8VDJ3	Hdlbp	Mus musculus
Q8VDK1	29	4	4	26.93	0	0	0		29	4	4	0.19	26.93	Nitrilase homolog 1	Q8VDK1	Nit1	Mus musculus
Q8VDL4	42	3	3	14.52	279	17	17	55.44	321	17	17	0	55.44	ADP-dependent glucokinase	Q8VDL4	Adpgk	Mus musculus
Q8VDM4	203	10	10	18.5	153	11	11	18.06	356	12	12	0	20.15	26S proteasome non-ATPase regulatory subunit 2	Q8VDM4	Psmd2	Mus musculus
Q8VDM6	87	12	12	20.49	101	13	13	28.99	188	16	16	0	29.57	Heterogeneous nuclear ribonucleoprotein U-like protein 1	Q8VDM6	Hnrnpul1	Mus musculus
Q8VDN2	16	3	3	5.96	39	5	5	10.65	55	6	6	0	10.65	Sodium/potassium-transporting ATPase subunit alpha-1	Q8VDN2	Atp1a1	Mus musculus
Q8VDP3	55	3	3	6.11	20	3	3	6.68	75	4	4	0.19	8.11	Protein-methionine sulfoxide oxidase MICAL1	Q8VDP3	Mical1	Mus musculus
Q8VDP4	43	5	5	14.1	154	9	9	21.69	197	9	9	0	21.69	Cell cycle and apoptosis regulator protein 2	Q8VDP4	Ccar2	Mus musculus
Q8VDQ8	10	2	2	11.83	14	3	3	13.37	24	3	3	0.29	13.37	NAD-dependent protein deacetylase sirtuin-2	Q8VDQ8	Sirt2	Mus musculus
Q8VDW0	23	5	3	17.8	25	8	4	24.82	48	10	5	0	31.62	ATP-dependent RNA helicase DDX39A	Q8VDW0	Ddx39a	Mus musculus
Q8VE11	11	2	2	5.02	0	0	0		11	2	2	0.95	5.02	Myotubularin-related protein 6	Q8VE11	Mtmr6	Mus musculus
Q8VE37	21	4	4	19.24	62	3	3	11.4	83	4	4	0.19	19.24	Regulator of chromosome condensation	Q8VE37	Rcc1	Mus musculus
Q8VE47	6	1	1	6.2	5	2	2	15.63	11	2	2	0.95	15.63	Ubiquitin-like modifier-activating enzyme 5	Q8VE47	Uba5	Mus musculus
Q8VEE0	32	2	2	17.54	27	2	2	17.54	59	2	2	0.95	17.54	Ribulose-phosphate 3-epimerase	Q8VEE0	Rpe	Mus musculus
Q8VEE4	4	2	2	6.74	3	2	2	7.87	7	3	3	0.29	10.91	Replication protein A 70 kDa DNA-binding subunit	Q8VEE4	Rpa1	Mus musculus
Q8VEH3	9	2	2	22.04	19	1	1	9.14	28	2	2	0.95	22.04	ADP-ribosylation factor-like protein 8A	Q8VEH3	Arl8a	Mus musculus
Q8VEK3	129	11	11	27.62	430	19	19	33.25	559	21	21	0	34.5	Heterogeneous nuclear ribonucleoprotein U	Q8VEK3	Hnrnpu	Mus musculus
Q8VEM8	1	1	1	7.56	29	2	2	12.04	30	2	2	0.95	12.04	Phosphate carrier protein, mitochondrial	Q8VEM8	Slc25a3	Mus musculus
Q8VH51	1	1	1	3.21	85	5	5	13.96	86	5	5	0	13.96	RNA-binding protein 39	Q8VH51	Rbm39	Mus musculus
Q8VHM5	10	2	2	5.38	13	3	2	6.01	23	4	3	0.29	9.34	Heterogeneous nuclear ribonucleoprotein R	Q8VHM5	Hnrnpr	Mus musculus
Q8VHX6	45	3	2	1.61	49	2	1	1.61	94	3	2	0.95	1.61	Filamin-C	Q8VHX6	Flnc	Mus musculus
Q8VI36	36	3	3	9.98	107	10	10	30.12	143	10	10	0	30.12	Paxillin	Q8VI36	Pxn	Mus musculus
Q8VI93	16	6	6	10.28	0	0	0		16	6	6	0	10.28	2'-5'-oligoadenylate synthase 3	Q8VI93	Oas3	Mus musculus
Q8VIJ6	49	5	5	10.3	215	10	10	11.02	264	10	10	0	11.02	Splicing factor, proline- and glutamine-rich	Q8VIJ6	Sfpq	Mus musculus
Q91UZ5	9	2	2	15.86	7	2	2	15.86	16	2	2	0.95	15.86	Inositol monophosphatase 2	Q91UZ5	Impa2	Mus musculus
Q91V12	13	2	2	5.77	0	0	0		13	2	2	0.95	5.77	Cytosolic acyl coenzyme A thioester hydrolase	Q91V12	Acot7	Mus musculus
Q91V41	58	6	5	41.4	36	5	4	33.02	94	7	5	0	41.4	Ras-related protein Rab-14	Q91V41	Rab14	Mus musculus
Q91V55	24	3	3	23.53	130	5	5	28.92	154	6	6	0	35.29	40S ribosomal protein S5	Q91V55	Rps5	Mus musculus
Q91V92	296	19	19	31.9	160	10	10	18.52	456	19	19	0	31.9	ATP-citrate synthase	Q91V92	Acly	Mus musculus
Q91VC3	91	6	4	17.76	91	4	3	14.84	182	7	5	0	18.49	Eukaryotic initiation factor 4A-III	Q91VC3	Eif4a3	Mus musculus
Q91VD9	4	3	3	7.15	45	3	3	7.7	49	4	4	0.19	9.63	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Q91VD9	Ndufs1	Mus musculus
Q91VE0	0	0	0		5	3	3	7.62	5	3	3	0.29	7.62	Long-chain fatty acid transport protein 4	Q91VE0	Slc27a4	Mus musculus
Q91VH2	7	2	2	7.23	0	0	0		7	2	2	0.95	7.23	Sorting nexin-9	Q91VH2	Snx9	Mus musculus
Q91VH6	35	4	4	26.94	0	0	0		35	4	4	0.19	26.94	Protein MEMO1	Q91VH6	Memo1	Mus musculus
Q91VI7	358	18	18	70.61	449	21	21	67.98	807	22	22	0	72.81	Ribonuclease inhibitor	Q91VI7	Rnh1	Mus musculus
Q91VJ4	19	3	3	14.19	4	1	1	6.88	23	3	3	0.29	14.19	Serine/threonine-protein kinase 38	Q91VJ4	Stk38	Mus musculus
Q91VJ5	0	0	0		35	5	5	35.74	35	5	5	0	35.74	Polyglutamine-binding protein 1	Q91VJ5	Pqbp1	Mus musculus
Q91VR2	0	0	0		42	2	2	17.45	42	2	2	0.95	17.45	ATP synthase subunit gamma, mitochondrial	Q91VR2	Atp5c1	Mus musculus
Q91VR5	23	2	2	5	31	2	2	5.41	54	3	3	0.29	7.57	ATP-dependent RNA helicase DDX1	Q91VR5	Ddx1	Mus musculus
Q91VW3	34	1	1	35.48	107	7	7	58.06	141	7	7	0	58.06	SH3 domain-binding glutamic acid-rich-like protein 3	Q91VW3	Sh3bgrl3	Mus musculus
Q91W50	0	0	0		10	2	2	3.88	10	2	2	0.95	3.88	Cold shock domain-containing protein E1	Q91W50	Csde1	Mus musculus
Q91W89	5	3	3	5.97	0	0	0		5	3	3	0.29	5.97	Alpha-mannosidase 2C1	Q91W89	Man2c1	Mus musculus
Q91W90	0	0	0		12	4	4	13.91	12	4	4	0.19	13.91	Thioredoxin domain-containing protein 5	Q91W90	Txndc5	Mus musculus
Q91WJ8	0	0	0		14	2	2	4.92	14	2	2	0.95	4.92	Far upstream element-binding protein 1	Q91WJ8	Fubp1	Mus musculus
Q91WK0	0	0	0		8	3	3	8.19	8	3	3	0.29	8.19	Leucine-rich repeat flightless-interacting protein 2	Q91WK0	Lrrfip2	Mus musculus
Q91WK2	1	1	1	5.68	14	3	3	22.16	15	3	3	0.29	22.16	Eukaryotic translation initiation factor 3 subunit H	Q91WK2	Eif3h	Mus musculus
Q91WN1	1	1	1	10.42	35	4	4	23.55	36	4	4	0.19	23.55	DnaJ homolog subfamily C member 9	Q91WN1	Dnajc9	Mus musculus
Q91WQ3	32	4	4	15.34	5	2	2	6.63	37	5	5	0	17.42	Tyrosine--tRNA ligase, cytoplasmic	Q91WQ3	Yars	Mus musculus
Q91WU5	13	1	1	5.32	23	2	2	11.17	36	2	2	0.95	11.17	Arsenite methyltransferase	Q91WU5	As3mt	Mus musculus
Q91WV0	29	3	3	34.66	20	2	2	31.25	49	4	4	0.19	38.64	Protein Dr1	Q91WV0	Dr1	Mus musculus
Q91X72	220	12	12	34.78	192	11	11	33.91	412	14	14	0	38.26	Hemopexin	Q91X72	Hpx	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q91XL1	60	5	5	18.71	138	9	9	28.07	198	11	11	0	33.92	Leucine-rich HEV glycoprotein	Q91XL1	Lrg1	Mus musculus
Q91YI4	56	7	7	27.8	145	9	9	31.95	201	10	10	0	35.37	Beta-arrestin-2	Q91YI4	Arrb2	Mus musculus
Q91YP3	32	6	6	31.45	0	0	0		32	6	6	0	31.45	Deoxyribose-phosphate aldolase	Q91YP3	Dera	Mus musculus
Q91YQ5	2	1	1	2.47	105	9	9	22.2	107	9	9	0	22.2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Q91YQ5	Rpn1	Mus musculus
Q91YR9	146	7	7	31.61	71	6	6	28.57	217	8	8	0	31.61	Prostaglandin reductase 1	Q91YR9	Ptgr1	Mus musculus
Q91YT0	6	2	2	10.13	18	4	4	20.26	24	4	4	0.19	20.26	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	Q91YT0	Ndufv1	Mus musculus
Q91YW3	15	1	1	5.95	39	3	3	9.33	54	3	3	0.29	9.33	DnaJ homolog subfamily C member 3	Q91YW3	Dnajc3	Mus musculus
Q91YX0	5	2	2	9.8	21	5	5	14.78	26	6	6	0	14.93	Protein THEMIS2	Q91YX0	Themis2	Mus musculus
Q91Z50	58	4	4	19.74	64	5	5	23.95	122	5	5	0	23.95	Flap endonuclease 1	Q91Z50	Fen1	Mus musculus
Q91ZJ5	111	6	6	18.11	17	3	3	9.84	128	7	7	0	18.11	UTP--glucose-1-phosphate uridylyltransferase	Q91ZJ5	Ugp2	Mus musculus
Q91ZR1	5	3	3	20.19	5	2	1	11.74	10	4	3	0.29	25.35	Ras-related protein Rab-4B	Q91ZR1	Rab4b	Mus musculus
Q91ZU6	5	1	1	0.27	4	2	2	0.43	9	2	2	0.95	0.43	Dystonin	Q91ZU6	Dst	Mus musculus
Q91ZW3	11	2	2	2.57	16	4	4	4.85	27	5	5	0	6.28	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	Q91ZW3	Smarca5	Mus musculus
Q91ZX7	20	7	7	3.85	1	1	1	0.33	21	8	8	0	4.18	Prolow-density lipoprotein receptor-related protein 1	Q91ZX7	Lrp1	Mus musculus
Q920B9	11	2	2	2.2	35	4	4	8.6	46	5	5	0	8.88	FACT complex subunit SPT16	Q920B9	Supt16h	Mus musculus
Q920E5	203	9	9	37.68	111	10	10	37.39	314	11	11	0	40.79	Farnesyl pyrophosphate synthase	Q920E5	Fdps	Mus musculus
Q921F2	101	8	8	37.92	197	10	10	38.65	298	10	10	0	38.65	TAR DNA-binding protein 43	Q921F2	Tardbp	Mus musculus
Q921F4	36	6	6	18.1	48	4	4	14.04	84	7	7	0	21.66	Heterogeneous nuclear ribonucleoprotein L-like	Q921F4	Hnrnpll	Mus musculus
Q921G6	13	2	2	6.91	63	6	6	19.71	76	7	7	0	20.44	Leucine-rich repeat and calponin homology domain-containing protein 4	Q921G6	Lrch4	Mus musculus
Q921G7	0	0	0		4	2	2	6.49	4	2	2	0.95	6.49	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	Q921G7	Etfdh	Mus musculus
Q921H8	35	5	5	18.4	66	6	6	22.88	101	7	7	0	22.88	3-ketoacyl-CoA thiolase A, peroxisomal	Q921H8	Acaa1a	Mus musculus
Q921I1	1883	27	27	47.2	431	22	22	43.62	2314	30	30	0	52.08	Serotransferrin	Q921I1	Tf	Mus musculus
Q921M3	246	15	15	21.36	150	13	13	17.58	396	18	18	0	22.6	Splicing factor 3B subunit 3	Q921M3	Sf3b3	Mus musculus
Q921M7	144	8	8	39.81	141	7	7	36.42	285	8	8	0	39.81	Protein FAM49B	Q921M7	Fam49b	Mus musculus
Q921W4	16	3	3	20.11	11	1	1	8.33	27	3	3	0.29	20.11	Quinone oxidoreductase-like protein 1	Q921W4	Cryzl1	Mus musculus
Q921Z5	30	2	2	21.72	28	2	2	21.72	58	2	2	0.95	21.72	Tumor necrosis factor alpha-induced protein 8	Q921Z5	Tnfaip8	Mus musculus
Q922B2	22	5	5	15.17	9	2	2	5.59	31	5	5	0	15.17	Aspartate--tRNA ligase, cytoplasmic	Q922B2	Dars	Mus musculus
Q922D4	17	3	3	5.45	22	5	5	9.24	39	6	6	0	10.55	Serine/threonine-protein phosphatase 6 regulatory subunit 3	Q922D4	Ppp6r3	Mus musculus
Q922D8	10	5	5	8.13	1	1	1	1.28	11	5	5	0	8.13	C-1-tetrahydrofolate synthase, cytoplasmic	Q922D8	Mthfd1	Mus musculus
Q922F4	175	7	2	21.48	443	11	2	22.82	618	12	2	0.95	26.17	Tubulin beta-6 chain	Q922F4	Tubb6	Mus musculus
Q922P9	4	1	1	3.66	33	4	4	12.09	37	4	4	0.19	12.09	Putative oxidoreductase GLYR1	Q922P9	Glyr1	Mus musculus
Q922Q8	1	1	1	3.91	39	5	5	19.87	40	5	5	0	19.87	Leucine-rich repeat-containing protein 59	Q922Q8	Lrrc59	Mus musculus
Q922R8	203	11	11	34.55	436	18	18	55.45	639	18	18	0	55.45	Protein disulfide-isomerase A6	Q922R8	Pdia6	Mus musculus
Q922S4	42	6	6	15.39	81	11	11	25.98	123	11	11	0	25.98	cGMP-dependent 3',5'-cyclic phosphodiesterase	Q922S4	Pde2a	Mus musculus
Q923B6	6	2	2	7.02	50	7	7	22.55	56	7	7	0	22.55	Metalloreductase STEAP4	Q923B6	Steap4	Mus musculus
Q923L7	84	2	2	20.65	25	2	2	20.65	109	2	2	0.95	20.65	Ear6 protein	Q923L7	Ear6	Mus musculus
Q93092	96	4	4	11.87	43	3	3	8.01	139	4	4	0.19	11.87	Transaldolase	Q93092	Taldo1	Mus musculus
Q99J09	29	3	3	22.22	21	2	2	17.25	50	3	3	0.29	22.22	Methylosome protein 50	Q99J09	Wdr77	Mus musculus
Q99J45	12	2	2	7.1	6	2	2	7.1	18	2	2	0.95	7.1	Nuclear receptor-binding protein	Q99J45	Nrbp1	Mus musculus
Q99J62	0	0	0		2	2	2	16.21	2	2	2	0.95	16.21	Replication factor C subunit 4	Q99J62	Rfc4	Mus musculus
Q99J77	101	8	8	39.28	22	2	2	16.71	123	8	8	0	39.28	N-acetylneuraminic acid synthase (Sialic acid synthase)	Q99J77	Nans	Mus musculus
Q99J99	90	9	9	35.69	0	0	0		90	9	9	0	35.69	3-mercaptopyruvate sulfurtransferase	Q99J99	Mpst	Mus musculus
Q99JB2	0	0	0		23	4	4	23.8	23	4	4	0.19	23.8	Stomatin-like protein 2, mitochondrial	Q99JB2	Stoml2	Mus musculus
Q99JI4	32	4	4	16.97	22	3	3	12.34	54	4	4	0.19	16.97	26S proteasome non-ATPase regulatory subunit 6	Q99JI4	Psmd6	Mus musculus
Q99JR1	0	0	0		52	6	6	29.19	52	6	6	0	29.19	Sideroflexin-1	Q99JR1	Sfxn1	Mus musculus
Q99JT2	23	3	2	14.66	93	4	2	18.75	116	4	2	0.95	18.75	Serine/threonine-protein kinase 26	Q99JT2	Stk26	Mus musculus
Q99JW2	19	2	2	10.54	1	1	1	4.9	20	2	2	0.95	10.54	Aminoacylase-1	Q99JW2	Acy1	Mus musculus
Q99JW4	40	3	3	19.69	97	5	5	32.92	137	5	5	0	32.92	LIM and senescent cell antigen-like-containing domain protein 1	Q99JW4	Lims1	Mus musculus
Q99JX3	0	0	0		47	7	7	27.05	47	7	7	0	27.05	Golgi reassembly-stacking protein 2	Q99JX3	Gorasp2	Mus musculus
Q99JX4	22	5	5	23.8	13	4	4	15.51	35	6	6	0	24.06	Eukaryotic translation initiation factor 3 subunit M	Q99JX4	Eif3m	Mus musculus
Q99JX7	9	2	2	5.5	15	2	2	7.93	24	3	3	0.29	9.87	Nuclear RNA export factor 1	Q99JX7	Nxf1	Mus musculus
Q99JY0	1	1	1	3.37	14	3	3	9.26	15	3	3	0.29	9.26	Trifunctional enzyme subunit beta, mitochondrial	Q99JY0	Hadhb	Mus musculus
Q99JY9	1232	26	26	73.92	718	21	21	59.33	1950	30	30	0	75.84	Actin-related protein 3	Q99JY9	Actr3	Mus musculus
Q99K01	0	0	0		4	3	3	8.13	4	3	3	0.29	8.13	Pyridoxal-dependent decarboxylase domain-containing protein 1	Q99K01	Pdxdc1	Mus musculus
Q99K41	59	7	7	12.98	26	4	4	8.75	85	7	7	0	12.98	EMILIN-1	Q99K41	Emilin1	Mus musculus
Q99K48	63	2	2	11.63	72	2	2	4.86	135	3	3	0.29	11.63	Non-POU domain-containing octamer-binding protein	Q99K48	Nono	Mus musculus
Q99K85	40	3	3	13.51	2	2	2	13.51	42	4	4	0.19	23.24	Phosphoserine aminotransferase	Q99K85	Psat1	Mus musculus
Q99KE1	221	15	15	43.8	111	8	8	29.54	332	15	15	0	43.8	NAD-dependent malic enzyme, mitochondrial	Q99KE1	Me2	Mus musculus
Q99KH8	35	4	3	18.56	92	6	4	22.74	127	6	4	0.19	22.74	Serine/threonine-protein kinase 24	Q99KH8	Stk24	Mus musculus
Q99KI0	108	12	12	22.31	54	7	7	15.64	162	13	13	0	24.23	Aconitate hydratase, mitochondrial	Q99KI0	Aco2	Mus musculus
Q99KJ8	25	4	4	15.92	79	6	6	19.65	104	6	6	0	19.65	Dynactin subunit 2	Q99KJ8	Dctn2	Mus musculus
Q99KK2	7	3	3	12.5	2	2	2	6.71	9	3	3	0.29	12.5	N-acylneuraminate cytidylyltransferase	Q99KK2	Cmas	Mus musculus
Q99KK7	316	15	15	38.75	109	14	14	31.17	425	17	17	0	40.38	Dipeptidyl peptidase 3	Q99KK7	Dpp3	Mus musculus
Q99KN1	24	5	5	29.03	0	0	0		24	5	5	0	29.03	Arrestin domain-containing protein 1	Q99KN1	Arrdc1	Mus musculus
Q99KP6	63	7	7	30.36	79	4	4	17.26	142	8	8	0	33.93	Pre-mRNA-processing factor 19	Q99KP6	Prpf19	Mus musculus
Q99KQ4	31	4	4	15.89	0	0	0		31	4	4	0.19	15.89	Nicotinamide phosphoribosyltransferase	Q99KQ4	Nampt	Mus musculus
Q99KV1	8	2	2	8.94	0	0	0		8	2	2	0.95	8.94	DnaJ homolog subfamily B member 11	Q99KV1	Dnajb11	Mus musculus
Q99KY4	0	0	0		21	2	2	5.36	21	2	2	0.95	5.36	Cyclin-G-associated kinase	Q99KY4	Gak	Mus musculus
Q99L04	11	3	3	18.21	34	4	4	23.64	45	4	4	0.19	23.64	Dehydrogenase/reductase SDR family member 1	Q99L04	Dhrs1	Mus musculus
Q99L13	5	2	2	9.25	0	0	0		5	2	2	0.95	9.25	3-hydroxyisobutyrate dehydrogenase, mitochondrial	Q99L13	Hibadh	Mus musculus
Q99L45	1	1	1	5.44	14	3	3	15.11	15	4	4	0.19	20.54	Eukaryotic translation initiation factor 2 subunit 2	Q99L45	Eif2s2	Mus musculus
Q99LB4	158	10	10	41.55	160	10	10	37.82	318	12	12	0	49.57	Capping protein (Actin filament), gelsolin-like	Q99LB4	Capg	Mus musculus
Q99LC3	0	0	0		29	2	2	9.3	29	2	2	0.95	9.3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	Q99LC3	Ndufa10	Mus musculus
Q99LC5	106	10	10	42.34	105	9	9	43.24	211	12	12	0	50.75	Electron transfer flavoprotein subunit alpha, mitochondrial	Q99LC5	Etfa	Mus musculus
Q99LD4	15	2	2	13.38	2	1	1	5.94	17	2	2	0.95	13.38	COP9 signalosome complex subunit 1	Q99LD4	Gps1	Mus musculus
Q99LF4	13	3	3	13.27	20	3	3	12.48	33	4	4	0.19	17.03	tRNA-splicing ligase RtcB homolog	Q99LF4	Rtcb	Mus musculus
Q99LL3	32	4	4	19.57	38	4	4	19.09	70	5	5	0	23.87	Carbohydrate sulfotransferase 12	Q99LL3	Chst12	Mus musculus
Q99LP6	6	1	1	5.07	21	2	2	9.22	27	2	2	0.95	9.22	GrpE protein homolog 1, mitochondrial	Q99LP6	Grpel1	Mus musculus
Q99LT0	57	2	2	36.36	98	3	3	36.36	155	3	3	0.29	36.36	Protein dpy-30 homolog	Q99LT0	Dpy30	Mus musculus
Q99LX0	89	4	4	39.15	140	5	5	31.22	229	6	6	0	39.15	Protein deglycase DJ-1	Q99LX0	Park7	Mus musculus
Q99M15	7	2	2	8.98	15	2	2	8.98	22	2	2	0.95	8.98	Proline-serine-threonine phosphatase-interacting protein 2	Q99M15	Pstpip2	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q99M31	4	1	1	5.7	18	2	2	11.2	22	2	2	0.95	11.2	Heat shock 70 kDa protein 14	Q99M31	Hspa14	Mus musculus
Q99M46	1	1	1	6.55	17	2	2	15.64	18	2	2	0.95	15.64	DNA-directed RNA polymerase II subunit RPB3	Q99M46	Polr2c	Mus musculus
Q99MD9	0	0	0		46	3	3	10.22	46	3	3	0.29	10.22	Nuclear autoantigenic sperm protein	Q99MD9	Nasp	Mus musculus
Q99MK8	25	5	5	12.92	16	3	3	8.56	41	6	6	0	15.82	Beta-adrenergic receptor kinase 1	Q99MK8	Adrbk1	Mus musculus
Q99MN1	39	3	3	9.41	51	2	2	7.56	90	3	3	0.29	9.41	Lysine--tRNA ligase	Q99MN1	Kars	Mus musculus
Q99MR6	0	0	0		2	2	2	3.66	2	2	2	0.95	3.66	Serrate RNA effector molecule homolog	Q99MR6	Srrt	Mus musculus
Q99N15	95	7	7	49.04	45	3	3	28.35	140	7	7	0	49.04	17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase	Q99N15	Hsd17b10	Mus musculus
Q99N16	0	0	0		3	2	2	3.24	3	2	2	0.95	3.24	Leukotriene-B(4) omega-hydroxylase 2	Q99N16	Cyp4f3	Mus musculus
Q99N80	0	0	0		12	2	2	6	12	2	2	0.95	6	Synaptotagmin-like protein 1	Q99N80	Sytl1	Mus musculus
Q99NB9	95	11	11	13.73	147	12	12	18.25	242	15	15	0	21.01	Splicing factor 3B subunit 1	Q99NB9	Sf3b1	Mus musculus
Q99P88	0	0	0		50	7	7	9.49	50	7	7	0	9.49	Nuclear pore complex protein Nup155	Q99P88	Nup155	Mus musculus
Q99PL5	0	0	0		103	7	7	6.6	103	7	7	0	6.6	Ribosome-binding protein 1	Q99PL5	Rrbp1	Mus musculus
Q99PT1	107	4	4	27.94	188	4	4	27.94	295	4	4	0.19	27.94	Rho GDP-dissociation inhibitor 1	Q99PT1	Arhgdia	Mus musculus
Q99PV0	41	8	8	6.42	41	9	9	7.45	82	13	13	0	10.62	Pre-mRNA-processing-splicing factor 8	Q99PV0	Prpf8	Mus musculus
Q9CPR4	1	1	1	8.7	29	5	5	20.11	30	5	5	0	20.11	60S ribosomal protein L17	Q9CPR4	Rpl17	Mus musculus
Q9CPV4	1	1	1	5.03	12	3	3	16.78	13	3	3	0.29	16.78	Glyoxalase domain-containing protein 4	Q9CPV4	Glod4	Mus musculus
Q9CPW4	291	10	10	43.05	149	4	4	45.7	440	11	11	0	45.7	Actin-related protein 2/3 complex subunit 5	Q9CPW4	Arpc5	Mus musculus
Q9CPX6	19	2	2	8.92	6	3	3	13.06	25	3	3	0.29	13.06	Ubiquitin-like-conjugating enzyme ATG3	Q9CPX6	Atg3	Mus musculus
Q9CPY7	15	2	2	7.32	13	2	2	9.83	28	3	3	0.29	9.83	Cytosol aminopeptidase	Q9CPY7	Lap3	Mus musculus
Q9CQ19	105	6	1	38.95	107	5	2	36.05	212	8	2	0.95	46.51	Myosin regulatory light polypeptide 9	Q9CQ19	Myl9	Mus musculus
Q9CQ60	60	4	4	38.91	215	8	8	64.2	275	8	8	0	64.2	6-phosphogluconolactonase	Q9CQ60	Pgls	Mus musculus
Q9CQ80	16	2	2	27.84	18	1	1	19.32	34	2	2	0.95	27.84	Vacuolar protein-sorting-associated protein 25	Q9CQ80	Vps25	Mus musculus
Q9CQ92	0	0	0		10	2	2	15.79	10	2	2	0.95	15.79	Mitochondrial fission 1 protein	Q9CQ92	Fis1	Mus musculus
Q9CQC6	34	3	3	6.68	28	6	6	15.75	62	6	6	0	15.75	Basic leucine zipper and W2 domain-containing protein 1	Q9CQC6	Bzw1	Mus musculus
Q9CQE1	69	4	4	33.2	14	1	1	9.31	83	4	4	0.19	33.2	Protein NipSnap homolog 3B	Q9CQE1	Nipsnap3b	Mus musculus
Q9CQE8	35	4	4	21.72	83	5	5	28.28	118	5	5	0	28.28	UPF0568 protein C14orf166 homolog	Q9CQE8		Mus musculus
Q9CQF3	7	1	1	12.78	23	3	3	20.7	30	3	3	0.29	20.7	Cleavage and polyadenylation specificity factor subunit 5	Q9CQF3	Nudt21	Mus musculus
Q9CQF9	0	0	0		22	2	2	8.32	22	2	2	0.95	8.32	Prenylcysteine oxidase	Q9CQF9	Pcyox1	Mus musculus
Q9CQI6	117	4	4	40.14	178	8	8	52.82	295	8	8	0	52.82	Coactosin-like protein	Q9CQI6	Cotl1	Mus musculus
Q9CQI7	0	0	0		3	2	2	10.22	3	2	2	0.95	10.22	U2 small nuclear ribonucleoprotein B"	Q9CQI7	Snrpb2	Mus musculus
Q9CQK7	0	0	0		10	2	2	19.75	10	2	2	0.95	19.75	RWD domain-containing protein 1	Q9CQK7	Rwdd1	Mus musculus
Q9CQM9	7	1	1	7.42	49	7	7	35.91	56	7	7	0	35.91	Glutaredoxin-3	Q9CQM9	Glrx3	Mus musculus
Q9CQR6	57	5	5	28.85	38	3	3	24.59	95	5	5	0	28.85	Serine/threonine-protein phosphatase 6 catalytic subunit	Q9CQR6	Ppp6c	Mus musculus
Q9CQV8	311	14	12	54.47	350	18	15	65.85	661	20	16	0	65.85	14-3-3 protein beta/alpha	Q9CQV8	Ywhab	Mus musculus
Q9CR16	25	1	1	3.24	21	2	2	8.92	46	2	2	0.95	8.92	Peptidyl-prolyl cis-trans isomerase D	Q9CR16	Ppid	Mus musculus
Q9CR68	0	0	0		8	2	2	17.52	8	2	2	0.95	17.52	Cytochrome b-c1 complex subunit Rieske, mitochondrial	Q9CR68	Uqcrfs1	Mus musculus
Q9CR86	0	0	0		6	3	3	25.68	6	3	3	0.29	25.68	Calcium-regulated heat stable protein 1	Q9CR86	Carhsp1	Mus musculus
Q9CRA5	44	3	3	17.79	24	3	3	17.79	68	4	4	0.19	17.79	Golgi phosphoprotein 3	Q9CRA5	Golph3	Mus musculus
Q9CRA8	6	3	3	25.53	0	0	0		6	3	3	0.29	25.53	Exosome complex component RRP46	Q9CRA8	Exosc5	Mus musculus
Q9CRB2	0	0	0		16	2	2	25.49	16	2	2	0.95	25.49	H/ACA ribonucleoprotein complex subunit 2	Q9CRB2	Nhp2	Mus musculus
Q9CRC8	5	2	2	6.15	0	0	0		5	2	2	0.95	6.15	Leucine-rich repeat-containing protein 40	Q9CRC8	Lrrc40	Mus musculus
Q9CSU0	10	2	2	14.42	68	4	4	23.93	78	4	4	0.19	23.93	Regulation of nuclear pre-mRNA domain-containing protein 1B	Q9CSU0	Rprd1b	Mus musculus
Q9CU62	41	4	4	6.89	65	5	5	8.52	106	5	5	0	8.52	Structural maintenance of chromosomes protein 1A	Q9CU62	Smc1a	Mus musculus
Q9CVB6	1207	22	22	60.33	371	14	14	50.33	1578	24	24	0	60.33	Actin-related protein 2/3 complex subunit 2	Q9CVB6	Arpc2	Mus musculus
Q9CW03	0	0	0		10	3	3	4.68	10	3	3	0.29	4.68	Structural maintenance of chromosomes protein 3	Q9CW03	Smc3	Mus musculus
Q9CWF2	318	14	2	47.19	928	23	3	55.06	1246	23	3	0.29	55.06	Tubulin beta-2B chain	Q9CWF2	Tubb2b	Mus musculus
Q9CWJ9	129	14	14	39.36	59	8	8	30.07	188	16	16	0	45.61	Bifunctional purine biosynthesis protein PURH	Q9CWJ9	Atic	Mus musculus
Q9CWK3	0	0	0		7	2	2	8.77	7	2	2	0.95	8.77	CD2 antigen cytoplasmic tail-binding protein 2	Q9CWK3	Cd2bp2	Mus musculus
Q9CWK8	0	0	0		4	2	2	6.74	4	2	2	0.95	6.74	Sorting nexin-2	Q9CWK8	Snx2	Mus musculus
Q9CWZ3	4	1	1	10.92	7	2	2	24.71	11	2	2	0.95	24.71	RNA-binding protein 8A	Q9CWZ3	Rbm8a	Mus musculus
Q9CWZ7	0	0	0		11	2	2	8.33	11	2	2	0.95	8.33	Gamma-soluble NSF attachment protein	Q9CWZ7	Napg	Mus musculus
Q9CX34	13	2	2	11.31	59	3	3	11.31	72	3	3	0.29	11.31	Protein SGT1 homolog	Q9CX34	Sugt1	Mus musculus
Q9CX56	7	1	1	8.78	34	3	3	17	41	3	3	0.29	17	26S proteasome non-ATPase regulatory subunit 8	Q9CX56	Psmd8	Mus musculus
Q9CX86	3	2	2	11.8	69	3	3	14.1	72	3	3	0.29	14.1	Heterogeneous nuclear ribonucleoprotein A0	Q9CX86	Hnrnpa0	Mus musculus
Q9CXF4	6	2	2	4.02	11	2	2	5.07	17	3	3	0.29	7	TBC1 domain family member 15	Q9CXF4	Tbc1d15	Mus musculus
Q9CXI5	38	4	4	26.82	46	5	5	35.2	84	5	5	0	35.2	Mesencephalic astrocyte-derived neurotrophic factor	Q9CXI5	Manf	Mus musculus
Q9CXR1	0	0	0		5	2	2	12.43	5	2	2	0.95	12.43	Dehydrogenase/reductase SDR family member 7	Q9CXR1	Dhrs7	Mus musculus
Q9CXT8	4	2	2	9.82	2	1	1	4.7	6	2	2	0.95	9.82	Mitochondrial-processing peptidase subunit beta	Q9CXT8	Pmpcb	Mus musculus
Q9CXW4	10	1	1	7.87	31	3	3	15.73	41	3	3	0.29	15.73	60S ribosomal protein L11	Q9CXW4	Rpl11	Mus musculus
Q9CXY6	49	5	5	28.72	30	3	3	18.21	79	5	5	0	28.72	Interleukin enhancer-binding factor 2	Q9CXY6	Ilf2	Mus musculus
Q9CY50	16	2	2	18.53	63	3	3	22.38	79	3	3	0.29	22.38	Translocon-associated protein subunit alpha	Q9CY50	Ssr1	Mus musculus
Q9CY58	11	2	2	3.93	17	4	4	12.78	28	5	5	0	12.78	Plasminogen activator inhibitor 1 RNA-binding protein	Q9CY58	Serbp1	Mus musculus
Q9CY64	16	3	3	16.61	0	0	0		16	3	3	0.29	16.61	Biliverdin reductase A	Q9CY64	Blvra	Mus musculus
Q9CYA0	0	0	0		115	5	5	28.86	115	5	5	0	28.86	Cysteine-rich with EGF-like domain protein 2	Q9CYA0	Creld2	Mus musculus
Q9CYA6	1	1	1	2.82	17	3	3	9.17	18	3	3	0.29	9.17	Zinc finger CCHC domain-containing protein 8	Q9CYA6	Zcchc8	Mus musculus
Q9CYG7	1	1	1	5.83	18	2	2	10.68	19	2	2	0.95	10.68	Mitochondrial import receptor subunit TOM34	Q9CYG7	Tomm34	Mus musculus
Q9CYL5	32	5	5	45.45	45	4	4	40.26	77	6	6	0	57.14	Golgi-associated plant pathogenesis-related protein 1	Q9CYL5	Glipr2	Mus musculus
Q9CZ04	47	4	4	28.36	19	2	2	16.73	66	4	4	0.19	28.36	COP9 signalosome complex subunit 7a	Q9CZ04	Cops7a	Mus musculus
Q9CZ13	18	5	5	21.46	205	9	9	26.88	223	9	9	0	26.88	Cytochrome b-c1 complex subunit 1, mitochondrial	Q9CZ13	Uqcrc1	Mus musculus
Q9CZ30	84	5	5	20.96	14	2	2	9.85	98	6	6	0	20.96	Obg-like ATPase 1	Q9CZ30	Ola1	Mus musculus
Q9CZ42	28	6	6	37.32	1	1	1	6.71	29	6	6	0	37.32	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	Q9CZ42	Carkd	Mus musculus
Q9CZ44	104	6	6	25.95	108	5	5	24.59	212	7	7	0	30.81	NSFL1 cofactor p47	Q9CZ44	Nsfl1c	Mus musculus
Q9CZD3	53	4	4	9.33	25	4	4	9.33	78	4	4	0.19	9.33	Glycine--tRNA ligase	Q9CZD3	Gars	Mus musculus
Q9CZE3	10	2	2	16.14	5	1	1	8.52	15	2	2	0.95	16.14	Ras-related protein Rab-32	Q9CZE3	Rab32	Mus musculus
Q9CZM2	23	3	3	12.75	2	1	1	5.39	25	3	3	0.29	12.75	60S ribosomal protein L15	Q9CZM2	Rpl15	Mus musculus
Q9CZN7	122	9	9	22.02	92	9	9	20.83	214	11	11	0	23.41	Serine hydroxymethyltransferase	Q9CZN7	Shmt2	Mus musculus
Q9CZU3	2	2	2	3.17	4	1	1	2.12	6	2	2	0.95	3.17	Superkiller viralicidic activity 2-like 2	Q9CZU3	Skiv2l2	Mus musculus
Q9CZU6	107	8	8	21.34	26	4	4	12.93	133	9	9	0	21.55	Citrate synthase, mitochondrial	Q9CZU6	Cs	Mus musculus
Q9CZX8	0	0	0		18	2	2	17.93	18	2	2	0.95	17.93	40S ribosomal protein S19	Q9CZX8	Rps19	Mus musculus
Q9D020	60	9	9	34.14	25	4	4	26.89	85	9	9	0	34.14	Cytosolic 5'-nucleotidase 3A	Q9D020	Nt5c3a	Mus musculus
Q9D071	4	2	2	4.07	2	1	1	2.23	6	2	2	0.95	4.07	MMS19 nucleotide excision repair protein homolog	Q9D071	Mms19	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9D0E1	4	1	1	3.16	38	4	4	8.09	42	4	4	0.19	8.09	Heterogeneous nuclear ribonucleoprotein M	Q9D0E1	Hnrnpm	Mus musculus
Q9D0F3	2	1	1	6.19	23	2	2	10.06	25	2	2	0.95	10.06	Protein ERGIC-53	Q9D0F3	Lman1	Mus musculus
Q9D0F9	55	5	5	17.79	22	6	6	18.51	77	8	8	0	19.93	Phosphoglucomutase-1	Q9D0F9	Pgm1	Mus musculus
Q9D0I9	36	6	6	15.3	49	3	3	9.09	85	6	6	0	15.3	Arginine--tRNA ligase, cytoplasmic	Q9D0I9	Rars	Mus musculus
Q9D0K2	56	5	5	19.23	32	5	5	16.92	88	6	6	0	20.77	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	Q9D0K2	Oxct1	Mus musculus
Q9D0L8	12	1	1	4.09	18	4	4	16.56	30	4	4	0.19	16.56	mRNA cap guanine-N7 methyltransferase	Q9D0L8	Rnmt	Mus musculus
Q9D0M1	0	0	0		2	2	2	7.02	2	2	2	0.95	7.02	Phosphoribosyl pyrophosphate synthase-associated protein 1	Q9D0M1	Prpsap1	Mus musculus
Q9D0M3	0	0	0		86	5	5	18.46	86	5	5	0	18.46	Cytochrome c1, heme protein, mitochondrial	Q9D0M3	Cyc1	Mus musculus
Q9D0R2	61	7	7	16.07	1	1	1	2.77	62	7	7	0	16.07	Threonine--tRNA ligase, cytoplasmic	Q9D0R2	Tars	Mus musculus
Q9D0T1	0	0	0		6	2	2	18.75	6	2	2	0.95	18.75	NHP2-like protein 1	Q9D0T1	Nhp2l1	Mus musculus
Q9D154	230	10	10	29.02	316	17	17	54.88	546	18	18	0	54.88	Leukocyte elastase inhibitor A	Q9D154	Serpinb1a	Mus musculus
Q9D1A2	50	8	8	26.11	29	2	2	9.89	79	8	8	0	26.11	Cytosolic non-specific dipeptidase	Q9D1A2	Cndp2	Mus musculus
Q9D1G1	38	5	4	37.31	35	4	3	26.87	73	7	5	0	41.29	Ras-related protein Rab-1B	Q9D1G1	Rab1b	Mus musculus
Q9D1K2	44	2	2	30.25	37	2	2	21.85	81	3	3	0.29	31.93	V-type proton ATPase subunit F	Q9D1K2	Atp6v1f	Mus musculus
Q9D1L9	0	0	0		22	2	2	43.96	22	2	2	0.95	43.96	Ragulator complex protein LAMTOR5	Q9D1L9	Lamtor5	Mus musculus
Q9D1M0	24	2	2	12.42	9	2	2	11.8	33	3	3	0.29	17.08	Protein SEC13 homolog	Q9D1M0	Sec13	Mus musculus
Q9D1P4	1	1	1	4.53	16	2	2	9.06	17	2	2	0.95	9.06	Cysteine and histidine-rich domain-containing protein 1	Q9D1P4	Chordc1	Mus musculus
Q9D1Q6	72	4	4	20.94	76	6	6	32.76	148	6	6	0	32.76	Endoplasmic reticulum resident protein 44	Q9D1Q6	Erp44	Mus musculus
Q9D2C2	1	1	1	5.06	19	3	3	12.03	20	3	3	0.29	12.03	Protein SAAL1	Q9D2C2	Saal1	Mus musculus
Q9D2G2	2	1	1	4.63	2	2	2	9.69	4	3	3	0.29	9.91	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	Q9D2G2	Dlst	Mus musculus
Q9D2V7	341	27	27	53.04	259	17	17	36.33	600	29	29	0	53.69	Coronin-7	Q9D2V7	Coro7	Mus musculus
Q9D3D9	0	0	0		12	2	2	35.71	12	2	2	0.95	35.71	ATP synthase subunit delta, mitochondrial	Q9D3D9	Atp5d	Mus musculus
Q9D4D4	20	2	2	4.78	3	1	1	4.15	23	2	2	0.95	4.78	Transketolase-like protein 2	Q9D4D4	Tktl2	Mus musculus
Q9D554	9	4	4	11.78	53	8	8	29.34	62	8	8	0	29.34	Splicing factor 3A subunit 3	Q9D554	Sf3a3	Mus musculus
Q9D5T0	0	0	0		2	2	2	11.63	2	2	2	0.95	11.63	ATPase family AAA domain-containing protein 1	Q9D5T0	Atad1	Mus musculus
Q9D5V6	0	0	0		19	3	3	25.21	19	3	3	0.29	25.21	Synapse-associated protein 1	Q9D5V6	Syap1	Mus musculus
Q9D662	4	2	2	4.56	1	1	1	2.35	5	2	2	0.95	4.56	Protein transport protein Sec23B	Q9D662	Sec23b	Mus musculus
Q9D6F9	307	16	2	51.8	856	21	2	52.48	1163	24	2	0.95	59.23	Tubulin beta-4A chain	Q9D6F9	Tubb4a	Mus musculus
Q9D6J6	3	1	1	4.03	27	5	5	31.05	30	5	5	0	31.05	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	Q9D6J6	Ndufv2	Mus musculus
Q9D6R2	20	4	4	14.75	16	4	4	12.3	36	6	6	0	17.49	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Q9D6R2	Idh3a	Mus musculus
Q9D6Y7	0	0	0		17	4	4	27.47	17	4	4	0.19	27.47	Mitochondrial peptide methionine sulfoxide reductase	Q9D6Y7	Msra	Mus musculus
Q9D6Y9	20	2	2	4.27	12	2	2	5.41	32	3	3	0.29	7.26	1,4-alpha-glucan-branching enzyme	Q9D6Y9	Gbe1	Mus musculus
Q9D6Z1	12	2	2	9.31	30	3	3	9.83	42	4	4	0.19	13.97	Nucleolar protein 56	Q9D6Z1	Nop56	Mus musculus
Q9D7G0	10	3	3	16.04	1	1	1	5.35	11	3	3	0.29	16.04	Ribose-phosphate pyrophosphokinase 1	Q9D7G0	Prps1	Mus musculus
Q9D7M8	0	0	0		3	2	2	21.83	3	2	2	0.95	21.83	DNA-directed RNA polymerase II subunit RPB4	Q9D7M8	Polr2d	Mus musculus
Q9D7S9	1	1	1	8.22	5	2	2	15.53	6	2	2	0.95	15.53	Charged multivesicular body protein 5	Q9D7S9	Chmp5	Mus musculus
Q9D819	12	4	4	23.88	1	1	1	6.57	13	4	4	0.19	23.88	Inorganic pyrophosphatase	Q9D819	Ppa1	Mus musculus
Q9D824	0	0	0		23	3	3	16.7	23	3	3	0.29	16.7	Pre-mRNA 3'-end-processing factor FIP1	Q9D824	Fip1l1	Mus musculus
Q9D855	0	0	0		12	2	2	25.23	12	2	2	0.95	25.23	Cytochrome b-c1 complex subunit 7	Q9D855	Uqcrb	Mus musculus
Q9D883	3	1	1	7.53	24	3	3	15.06	27	3	3	0.29	15.06	Splicing factor U2AF 35 kDa subunit	Q9D883	U2af1	Mus musculus
Q9D892	38	2	2	25.25	22	2	2	25.25	60	2	2	0.95	25.25	Inosine triphosphate pyrophosphatase	Q9D892	Itpa	Mus musculus
Q9D8B3	28	2	2	13.39	21	2	2	13.39	49	2	2	0.95	13.39	Charged multivesicular body protein 4b	Q9D8B3	Chmp4b	Mus musculus
Q9D8E6	9	3	3	11.22	51	5	5	12.65	60	6	6	0	17.18	60S ribosomal protein L4	Q9D8E6	Rpl4	Mus musculus
Q9D8N0	205	12	12	42.11	149	10	10	36.84	354	12	12	0	42.11	Elongation factor 1-gamma	Q9D8N0	Eef1g	Mus musculus
Q9D8N2	8	2	2	13.17	1	1	1	7.56	9	2	2	0.95	13.17	Protein FAM45A	Q9D8N2	Fam45a	Mus musculus
Q9D8T2	0	0	0		7	3	3	11.5	7	3	3	0.29	11.5	Gasdermin-D	Q9D8T2	Gsdmdc1	Mus musculus
Q9D8W5	36	3	3	11.84	19	2	2	7.46	55	3	3	0.29	11.84	26S proteasome non-ATPase regulatory subunit 12	Q9D8W5	Psmd12	Mus musculus
Q9D8Y0	0	0	0		20	2	2	6.67	20	2	2	0.95	6.67	EF-hand domain-containing protein D2	Q9D8Y0	Efhd2	Mus musculus
Q9D8Y7	20	3	3	32.61	7	2	2	21.74	27	3	3	0.29	32.61	Tumor necrosis factor alpha-induced protein 8-like protein 2	Q9D8Y7	Tnfaip8l2	Mus musculus
Q9D906	34	6	6	15.47	20	5	5	14.47	54	7	7	0	18.48	Ubiquitin-like modifier-activating enzyme ATG7	Q9D906	Atg7	Mus musculus
Q9D964	13	3	3	12.77	16	2	2	8.75	29	3	3	0.29	12.77	Glycine amidinotransferase, mitochondrial	Q9D964	Gatm	Mus musculus
Q9DAR7	21	4	4	19.23	24	4	4	19.53	45	5	5	0	24.26	m7GpppX diphosphatase	Q9DAR7	Dcps	Mus musculus
Q9DAU1	0	0	0		15	2	2	13.41	15	2	2	0.95	13.41	Protein canopy homolog 3	Q9DAU1	Cnpy3	Mus musculus
Q9DB05	28	5	5	30.85	54	4	4	25.42	82	6	6	0	34.92	Alpha-soluble NSF attachment protein	Q9DB05	Napa	Mus musculus
Q9DB15	0	0	0		24	2	2	12.44	24	2	2	0.95	12.44	39S ribosomal protein L12, mitochondrial	Q9DB15	Mrpl12	Mus musculus
Q9DB20	8	1	1	10.33	50	2	2	12.21	58	2	2	0.95	12.21	ATP synthase subunit O, mitochondrial	Q9DB20	Atp5o	Mus musculus
Q9DB77	0	0	0		68	5	5	22.08	68	5	5	0	22.08	Cytochrome b-c1 complex subunit 2, mitochondrial	Q9DB77	Uqcrc2	Mus musculus
Q9DBC7	9	2	2	10.76	11	3	3	13.91	20	3	3	0.29	13.91	cAMP-dependent protein kinase type I-alpha regulatory subunit	Q9DBC7	Prkar1a	Mus musculus
Q9DBG3	289	17	12	27.43	155	13	10	26.15	444	19	14	0	32.12	AP-2 complex subunit beta	Q9DBG3	Ap2b1	Mus musculus
Q9DBG5	4	1	1	6.41	70	8	8	34.78	74	8	8	0	34.78	Perilipin-3	Q9DBG5	Plin3	Mus musculus
Q9DBG6	17	7	7	20.92	230	14	14	39.78	247	14	14	0	39.78	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	Q9DBG6	Rpn2	Mus musculus
Q9DBJ1	230	10	10	40.94	159	10	10	40.94	389	10	10	0	40.94	Phosphoglycerate mutase 1	Q9DBJ1	Pgam1	Mus musculus
Q9DBK7	34	4	4	9.21	2	1	1	3.79	36	4	4	0.19	9.21	MCG18845, isoform CRA_d	Q9DBK7	Uba7	Mus musculus
Q9DBL1	18	3	3	14.12	9	3	3	14.12	27	3	3	0.29	14.12	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Q9DBL1	Acadsb	Mus musculus
Q9DBL9	1	1	1	4.84	10	2	2	10.54	11	2	2	0.95	10.54	1-acylglycerol-3-phosphate O-acyltransferase ABHD5	Q9DBL9	Abhd5	Mus musculus
Q9DBR0	0	0	0		15	2	2	7.28	15	2	2	0.95	7.28	A-kinase anchor protein 8	Q9DBR0	Akap8	Mus musculus
Q9DBR1	18	2	2	4.1	10	2	2	4.1	28	2	2	0.95	4.1	5'-3' exoribonuclease 2	Q9DBR1	Xrn2	Mus musculus
Q9DBR7	12	3	3	4.28	25	4	4	6.03	37	5	5	0	6.71	Protein phosphatase 1 regulatory subunit 12A	Q9DBR7	Ppp1r12a	Mus musculus
Q9DBS1	2	1	1	6.5	19	2	2	10.25	21	2	2	0.95	10.25	Transmembrane protein 43	Q9DBS1	Tmem43	Mus musculus
Q9DBT5	12	1	1	2.26	20	2	2	5.64	32	2	2	0.95	5.64	AMP deaminase 2	Q9DBT5	Ampd2	Mus musculus
Q9DBZ5	8	4	4	31.19	7	4	4	26.61	15	5	5	0	33.03	Eukaryotic translation initiation factor 3 subunit K	Q9DBZ5	Eif3k	Mus musculus
Q9DC23	5	3	3	7.06	0	0	0		5	3	3	0.29	7.06	DnaJ homolog subfamily C member 10	Q9DC23	Dnajc10	Mus musculus
Q9DC50	32	3	3	9.64	0	0	0		32	3	3	0.29	9.64	Peroxisomal carnitine O-octanoyltransferase	Q9DC50	Crot	Mus musculus
Q9DC51	21	4	2	17.23	704	10	4	35.31	725	11	5	0	35.31	Guanine nucleotide-binding protein G(k) subunit alpha	Q9DC51	Gnai3	Mus musculus
Q9DC61	24	3	3	10.88	12	1	1	3.24	36	3	3	0.29	10.88	Mitochondrial-processing peptidase subunit alpha	Q9DC61	Pmpca	Mus musculus
Q9DCC5	122	5	5	38.25	334	8	8	44.81	456	8	8	0	44.81	Cbx3 protein	Q9DCC5	Cbx3	Mus musculus
Q9DCD0	1093	25	25	47.41	521	20	20	39.75	1614	28	28	0	47.41	6-phosphogluconate dehydrogenase, decarboxylating	Q9DCD0	Pgd	Mus musculus
Q9DCH4	76	3	3	14.13	74	3	3	12.47	150	4	4	0.19	16.62	Eukaryotic translation initiation factor 3 subunit F	Q9DCH4	Eif3f	Mus musculus
Q9DCJ5	0	0	0		9	2	2	22.67	9	2	2	0.95	22.67	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	Q9DCJ5	Ndufa8	Mus musculus
Q9DCL9	52	3	3	14.82	26	4	4	18.12	78	4	4	0.19	18.12	Multifunctional protein ADE2	Q9DCL9	Paics	Mus musculus
Q9DCM0	5	2	2	19.29	45	4	4	31.5	50	4	4	0.19	31.5	Persulfide dioxygenase ETHE1, mitochondrial	Q9DCM0	Ethe1	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9DCR2	2	1	1	7.77	20	2	2	17.1	22	2	2	0.95	17.1	AP-3 complex subunit sigma-1	Q9DCR2	Ap3s1	Mus musculus
Q9DCS2	12	3	3	31.37	0	0	0		12	3	3	0.29	31.37	UPF0585 protein C16orf13 homolog	Q9DCS2		Mus musculus
Q9DCS3	8	3	3	20.91	0	0	0		8	3	3	0.29	20.91	Trans-2-enoyl-CoA reductase, mitochondrial	Q9DCS3	Mecr	Mus musculus
Q9DCS9	0	0	0		10	3	3	16.48	10	3	3	0.29	16.48	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Q9DCS9	Ndufb10	Mus musculus
Q9DCW4	32	3	3	19.61	50	4	4	24.31	82	4	4	0.19	24.31	Electron transfer flavoprotein subunit beta	Q9DCW4	Etfb	Mus musculus
Q9DCZ1	4	2	2	6.38	2	1	1	6.38	6	2	2	0.95	6.38	GMP reductase 1	Q9DCZ1	Gmpr	Mus musculus
Q9EPB4	25	2	2	21.76	35	4	4	31.61	60	4	4	0.19	31.61	Apoptosis-associated speck-like protein containing a CARD	Q9EPB4	Pycard	Mus musculus
Q9EPJ9	0	0	0		23	2	2	12.56	23	2	2	0.95	12.56	ADP-ribosylation factor GTPase-activating protein 1	Q9EPJ9	Arfgap1	Mus musculus
Q9EPK2	11	2	2	7.49	9	2	2	7.49	20	2	2	0.95	7.49	Protein XRP2	Q9EPK2	Rp2	Mus musculus
Q9EPK7	8	2	2	4.6	5	1	1	1.47	13	2	2	0.95	4.6	Exportin-7	Q9EPK7	Xpo7	Mus musculus
Q9EPL4	0	0	0		7	2	2	13.84	7	2	2	0.95	13.84	Methyltransferase-like protein 9	Q9EPL4	Mettl9	Mus musculus
Q9EPL8	42	6	6	10.98	15	3	3	4.72	57	7	7	0	10.98	Importin-7	Q9EPL8	Ipo7	Mus musculus
Q9EPU0	17	4	4	5.78	18	4	4	5.25	35	5	5	0	6.67	Regulator of nonsense transcripts 1	Q9EPU0	Upf1	Mus musculus
Q9EQ06	1	1	1	3.69	38	3	3	13.09	39	3	3	0.29	13.09	Estradiol 17-beta-dehydrogenase 11	Q9EQ06	Hsd17b11	Mus musculus
Q9EQ32	0	0	0		30	3	3	7.89	30	3	3	0.29	7.89	Phosphoinositide 3-kinase adapter protein 1	Q9EQ32	Pik3ap1	Mus musculus
Q9EQG9	24	5	5	13.78	39	7	7	19.39	63	9	9	0	23.88	Collagen type IV alpha-3-binding protein	Q9EQG9	Col4a3bp	Mus musculus
Q9EQH2	24	2	2	3.01	6	2	2	3.01	30	2	2	0.95	3.01	Endoplasmic reticulum aminopeptidase 1	Q9EQH2	Erap1	Mus musculus
Q9EQH3	172	15	15	26.51	116	11	11	20.23	288	15	15	0	26.51	Vacuolar protein sorting-associated protein 35	Q9EQH3	Vps35	Mus musculus
Q9EQI5	39	3	3	40.71	14	2	2	30.97	53	4	4	0.19	40.71	Chemokine (C-X-C motif) ligand 7, isoform CRA_b	Q9EQI5	Ppbp	Mus musculus
Q9EQK5	494	28	28	49.71	225	19	19	39.14	719	30	30	0	50.29	Major vault protein	Q9EQK5	Mvp	Mus musculus
Q9EQP2	9	2	2	4.62	0	0	0		9	2	2	0.95	4.62	EH domain-containing protein 4	Q9EQP2	Ehd4	Mus musculus
Q9EQU5	98	6	6	27.34	120	8	8	32.18	218	9	9	0	32.18	Protein SET	Q9EQU5	Set	Mus musculus
Q9ER72	58	4	4	8.18	20	2	2	3.85	78	4	4	0.19	8.18	Cysteine--tRNA ligase, cytoplasmic	Q9ER72	Cars	Mus musculus
Q9ERB0	0	0	0		61	5	5	27.69	61	5	5	0	27.69	Synaptosomal-associated protein 29	Q9ERB0	Snap29	Mus musculus
Q9ERD8	5	1	1	4.23	10	4	4	17.22	15	4	4	0.19	17.22	Gamma-parvin	Q9ERD8	Parvg	Mus musculus
Q9ERF3	50	4	4	24.26	24	2	2	13.44	74	4	4	0.19	24.26	WD repeat-containing protein 61	Q9ERF3	Wdr61	Mus musculus
Q9ERI2	0	0	0		13	2	2	13.12	13	2	2	0.95	13.12	Ras-related protein Rab-27A	Q9ERI2	Rab27a	Mus musculus
Q9ERK4	149	13	13	21.32	49	4	4	8.65	198	13	13	0	21.32	Exportin-2	Q9ERK4	Cse1l	Mus musculus
Q9ERL7	13	3	3	26.06	21	2	2	9.15	34	3	3	0.29	26.06	Glia maturation factor gamma	Q9ERL7	Gmfg	Mus musculus
Q9ERR7	55	3	3	37.65	50	4	4	37.65	105	4	4	0.19	37.65	15 kDa selenoprotein	Q9ERR7	Sep15	Mus musculus
Q9ERU9	5	1	1	0.75	12	4	4	2.98	17	4	4	0.19	2.98	E3 SUMO-protein ligase RanBP2	Q9ERU9	Ranbp2	Mus musculus
Q9ES46	28	3	3	12.6	10	1	1	3.84	38	3	3	0.29	12.6	Beta-parvin	Q9ES46	Parvb	Mus musculus
Q9ES52	62	5	5	5.63	54	5	5	7.39	116	6	6	0	7.39	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	Q9ES52	Inpp5d	Mus musculus
Q9ESP1	37	3	3	36.65	52	3	3	36.65	89	3	3	0.29	36.65	Stromal cell-derived factor 2-like protein 1	Q9ESP1	Sdf2l1	Mus musculus
Q9EST5	51	2	2	11.4	197	6	6	36.4	248	6	6	0	36.4	Acidic leucine-rich nuclear phosphoprotein 32 family member B	Q9EST5	Anp32b	Mus musculus
Q9ESU7	4	2	2	6.49	1	1	1	3.06	5	3	3	0.29	9.55	Amino acid transporter	Q9ESU7	Slc1a5	Mus musculus
Q9ESX5	12	2	2	5.89	5	1	1	4.32	17	3	3	0.29	10.22	H/ACA ribonucleoprotein complex subunit 4	Q9ESX5	Dkc1	Mus musculus
Q9ET01	1657	48	45	52.71	345	25	23	31.29	2002	52	48	0	53.88	Glycogen phosphorylase, liver form	Q9ET01	Pygl	Mus musculus
Q9ET66	9	2	2	8.79	46	3	3	14.11	55	3	3	0.29	14.11	Peptidase inhibitor 16	Q9ET66	Pi16	Mus musculus
Q9JHF5	1	1	1	3.84	35	7	7	12.11	36	7	7	0	12.11	V-type proton ATPase subunit a	Q9JHF5	Tcirg1	Mus musculus
Q9JHI5	6	2	2	9.91	0	0	0		6	2	2	0.95	9.91	Isovaleryl-CoA dehydrogenase, mitochondrial	Q9JHI5	Ivd	Mus musculus
Q9JHJ0	45	1	1	5.97	135	6	6	21.02	180	6	6	0	21.02	Tropomodulin-3	Q9JHJ0	Tmod3	Mus musculus
Q9JHK4	10	3	3	12.17	3	1	1	5.47	13	4	4	0.19	17.64	Geranylgeranyl transferase type-2 subunit alpha	Q9JHK4	Rabggta	Mus musculus
Q9JHK5	188	5	5	23.71	149	7	7	29.71	337	8	8	0	29.71	Pleckstrin	Q9JHK5	Plek	Mus musculus
Q9JHS3	2	1	1	30.4	32	2	2	45.6	34	2	2	0.95	45.6	Ragulator complex protein LAMTOR2	Q9JHS3	Lamtor2	Mus musculus
Q9JHU4	90	20	20	8.35	206	21	21	8.48	296	26	26	0	9.75	Cytoplasmic dynein 1 heavy chain 1	Q9JHU4	Dync1h1	Mus musculus
Q9JHU9	40	3	3	9.87	1	1	1	4.67	41	3	3	0.29	9.87	Inositol-3-phosphate synthase 1	Q9JHU9	Isyna1	Mus musculus
Q9JHW4	4	2	2	8.92	0	0	0		4	2	2	0.95	8.92	Selenocysteine-specific elongation factor	Q9JHW4	Eefsec	Mus musculus
Q9JIF0	19	3	3	11.32	3	3	3	11.32	22	4	4	0.19	15.36	Protein arginine N-methyltransferase 1	Q9JIF0	Prmt1	Mus musculus
Q9JIF7	14	4	4	7.14	76	7	7	15.95	90	9	9	0	18.36	Coatomer subunit beta	Q9JIF7	Copb1	Mus musculus
Q9JIX8	2	2	2	2.77	67	6	6	6.73	69	8	8	0	9.49	Apoptotic chromatin condensation inducer in the nucleus	Q9JIX8	Acin1	Mus musculus
Q9JIY5	4	1	1	2.62	4	2	2	5.46	8	2	2	0.95	5.46	Serine protease HTRA2, mitochondrial	Q9JIY5	Htra2	Mus musculus
Q9JIZ9	36	3	3	19.59	1	1	1	6.76	37	3	3	0.29	19.59	Phospholipid scramblase 3	Q9JIZ9	Plscr3	Mus musculus
Q9JJ00	13	2	2	17.07	25	3	3	21.04	38	3	3	0.29	21.04	Phospholipid scramblase 1	Q9JJ00	Plscr1	Mus musculus
Q9JJ28	52	10	10	13.14	114	13	13	18.96	166	17	17	0	23.29	Protein flightless-1 homolog	Q9JJ28	Flii	Mus musculus
Q9JJK2	10	3	3	14.44	1	1	1	3.78	11	3	3	0.29	14.44	LanC-like protein 2	Q9JJK2	Lancl2	Mus musculus
Q9JJU8	8	2	2	38.6	27	3	3	47.37	35	3	3	0.29	47.37	SH3 domain-binding glutamic acid-rich-like protein	Q9JJU8	Sh3bgrl	Mus musculus
Q9JKC8	11	2	2	7.18	19	5	5	15.55	30	5	5	0	15.55	AP-3 complex subunit mu-1	Q9JKC8	Ap3m1	Mus musculus
Q9JKF1	961	48	48	40.13	1315	53	53	37.48	2276	61	61	0	43.09	Ras GTPase-activating-like protein IQGAP1	Q9JKF1	Iqgap1	Mus musculus
Q9JKR6	81	6	6	11.01	165	10	10	15.72	246	11	11	0	15.72	Hypoxia up-regulated protein 1	Q9JKR6	Hyou1	Mus musculus
Q9JKV1	1	1	1	4.91	20	2	2	4.91	21	2	2	0.95	4.91	Proteasomal ubiquitin receptor ADRM1	Q9JKV1	Adrm1	Mus musculus
Q9JKY5	0	0	0		14	2	2	5.43	14	2	2	0.95	5.43	Huntingtin-interacting protein 1-related protein	Q9JKY5	Hip1r	Mus musculus
Q9JL26	29	8	8	12.52	176	10	10	11.88	205	11	11	0	13.16	Formin-like protein 1	Q9JL26	Fmnl1	Mus musculus
Q9JL62	5	1	1	14.35	13	2	2	18.66	18	2	2	0.95	18.66	Glycolipid transfer protein	Q9JL62	Gltp	Mus musculus
Q9JLF6	4	1	1	4.54	26	3	3	11.66	30	3	3	0.29	11.66	Protein-glutamine gamma-glutamyltransferase K	Q9JLF6	Tgm1	Mus musculus
Q9JLJ2	58	9	9	29.96	12	3	3	8.91	70	9	9	0	29.96	4-trimethylaminobutyraldehyde dehydrogenase	Q9JLJ2	Aldh9a1	Mus musculus
Q9JLQ2	49	6	6	18.79	87	5	5	14.41	136	7	7	0	18.93	ARF GTPase-activating protein GIT2	Q9JLQ2	Git2	Mus musculus
Q9JLT4-2	9	4	3	17.92	2	2	2	8.55	11	5	4	0.19	24.03	Isoform 2 of Thioredoxin reductase 2, mitochondrial	Q9JLT4	Txnrd2	Mus musculus
Q9JLV6	224	17	17	36.97	161	13	13	31.99	385	22	22	0	42.53	Bifunctional polynucleotide phosphatase/kinase	Q9JLV6	Pnkp	Mus musculus
Q9JM14	34	3	3	28	19	2	2	23	53	4	4	0.19	38.5	5'(3')-deoxyribonucleotidase, cytosolic type	Q9JM14	Nt5c	Mus musculus
Q9JM76	165	8	8	44.94	113	6	6	40.45	278	9	9	0	44.94	Actin-related protein 2/3 complex subunit 3	Q9JM76	Arpc3	Mus musculus
Q9JMA1	103	8	8	23.94	66	3	3	14.4	169	8	8	0	23.94	Ubiquitin carboxyl-terminal hydrolase 14	Q9JMA1	Usp14	Mus musculus
Q9JMH6	393	15	14	38.01	46	6	6	23.98	439	15	14	0	38.01	Thioredoxin reductase 1, cytoplasmic	Q9JMH6	Txnrd1	Mus musculus
Q9JMH9	7	4	4	4.2	90	8	8	6.44	97	8	8	0	6.44	Unconventional myosin-XVIIIa	Q9JMH9	Myo18a	Mus musculus
Q9QUG9	1	1	1	3.12	5	2	2	3.95	6	3	3	0.29	7.07	RAS guanyl-releasing protein 2	Q9QUG9	Rasgrp2	Mus musculus
Q9QUH0	56	3	3	38.32	134	7	7	48.6	190	7	7	0	48.6	Glutaredoxin-1	Q9QUH0	Glrx	Mus musculus
Q9QUI0	175	10	8	58.03	176	10	7	45.08	351	14	11	0	58.03	Transforming protein RhoA	Q9QUI0	Rhoa	Mus musculus
Q9QUM0	494	20	20	33.59	350	22	22	34.56	844	25	25	0	35.91	Integrin alpha-IIb	Q9QUM0	Itga2b	Mus musculus
Q9QUM9	143	6	6	29.67	7	2	2	12.2	150	6	6	0	29.67	Proteasome subunit alpha type-6	Q9QUM9	Psma6	Mus musculus
Q9QUN7	1	1	1	3.32	3	3	3	7.27	4	3	3	0.29	7.27	Toll-like receptor 2	Q9QUN7	Tlr2	Mus musculus
Q9QUR6	232	17	17	38.03	34	5	5	12.54	266	17	17	0	38.03	Prolyl endopeptidase	Q9QUR6	Prep	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9QWK4	26	4	4	18.75	0	0	0		26	4	4	0.19	18.75	CD5 antigen-like	Q9QWK4	Cd5l	Mus musculus
Q9QWR8	15	2	2	7.23	11	4	4	14.46	26	4	4	0.19	14.46	Alpha-N-acetylgalactosaminidase	Q9QWR8	Naga	Mus musculus
Q9QX47	0	0	0		29	5	5	4.79	29	5	5	0	4.79	Protein SON	Q9QX47	Son	Mus musculus
Q9QXD6	9	2	2	14.79	0	0	0		9	2	2	0.95	14.79	Fructose-1,6-bisphosphatase 1	Q9QXD6	Fbp1	Mus musculus
Q9QXG4	4	2	2	5.14	0	0	0		4	2	2	0.95	5.14	Acetyl-coenzyme A synthetase, cytoplasmic	Q9QXG4	Acss2	Mus musculus
Q9QXK3	64	7	4	12.63	157	9	7	18.94	221	10	7	0	18.94	Coatomer subunit gamma-2	Q9QXK3	Copg2	Mus musculus
Q9QXS1	188	21	21	9.21	575	54	54	18.61	763	55	55	0	18.84	Plectin	Q9QXS1	Plec	Mus musculus
Q9QXT0	0	0	0		12	3	3	26.37	12	3	3	0.29	26.37	Protein canopy homolog 2	Q9QXT0	Cnpy2	Mus musculus
Q9QXZ0	3	1	1	0.46	25	6	6	2.16	28	6	6	0	2.16	Microtubule-actin cross-linking factor 1	Q9QXZ0	Macf1	Mus musculus
Q9QY06	0	0	0		11	2	2	2.37	11	2	2	0.95	2.37	Unconventional myosin-IXb	Q9QY06	Myo9b	Mus musculus
Q9QYB5	25	3	3	9.92	10	4	4	15.44	35	5	5	0	17.71	Gamma-adducin	Q9QYB5	Add3	Mus musculus
Q9QYC0	75	5	5	16.6	70	7	7	21.77	145	8	8	0	25.58	Alpha-adducin	Q9QYC0	Add1	Mus musculus
Q9QYJ0	11	2	2	11.41	10	3	3	11.41	21	3	3	0.29	11.41	DnaJ homolog subfamily A member 2	Q9QYJ0	Dnaja2	Mus musculus
Q9QZ06	3	1	1	5.11	11	4	4	28.83	14	5	5	0	33.94	Toll-interacting protein	Q9QZ06	Tollip	Mus musculus
Q9QZ88	12	2	2	14.84	0	0	0		12	2	2	0.95	14.84	Vacuolar protein sorting-associated protein 29	Q9QZ88	Vps29	Mus musculus
Q9QZD9	55	4	4	24.31	59	4	4	24.31	114	4	4	0.19	24.31	Eukaryotic translation initiation factor 3 subunit I	Q9QZD9	Eif3i	Mus musculus
Q9QZE5	73	9	6	18.31	240	16	14	31.81	313	17	14	0	31.81	Coatomer subunit gamma-1	Q9QZE5	Copg1	Mus musculus
Q9QZF2	13	2	2	5.92	2	1	1	3.05	15	2	2	0.95	5.92	Glypican-1	Q9QZF2	Gpc1	Mus musculus
Q9QZK7	66	8	8	33.78	77	8	8	34.68	143	10	10	0	41.44	Docking protein 3	Q9QZK7	Dok3	Mus musculus
Q9QZQ8	8169	31	17	59.14	6479	29	14	51.61	14648	36	20	0	59.14	Core histone macro-H2A.1	Q9QZQ8	H2afy	Mus musculus
Q9QZS3	0	0	0		2	2	2	5.97	2	2	2	0.95	5.97	Protein numb homolog	Q9QZS3	Numb	Mus musculus
Q9QZU3	98	8	8	24.51	11	4	4	11.99	109	10	10	0	24.51	Platelet glycoprotein V (Fragment)	Q9QZU3	Gp5	Mus musculus
Q9R059	0	0	0		47	4	4	30.45	47	4	4	0.19	30.45	Four and a half LIM domains protein 3	Q9R059	Fhl3	Mus musculus
Q9R062	145	11	11	48.95	23	3	3	25.53	168	11	11	0	48.95	Glycogenin-1	Q9R062	Gyg1	Mus musculus
Q9R078	1	1	1	7.04	33	2	2	18.15	34	2	2	0.95	18.15	5'-AMP-activated protein kinase subunit beta-1	Q9R078	Prkab1	Mus musculus
Q9R0C8	21	4	4	8.85	3	1	1	2.24	24	4	4	0.19	8.85	Guanine nucleotide exchange factor VAV3	Q9R0C8	Vav3	Mus musculus
Q9R0E1	8	4	4	9.99	1	1	1	2.29	9	5	5	0	12.28	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	Q9R0E1	Plod3	Mus musculus
Q9R0N0	41	7	7	26.53	0	0	0		41	7	7	0	26.53	Galactokinase	Q9R0N0	Galk1	Mus musculus
Q9R0P3	357	14	14	64.89	130	9	9	54.61	487	15	15	0	69.5	S-formylglutathione hydrolase	Q9R0P3	Esd	Mus musculus
Q9R0P5	458	7	7	57.58	384	6	6	47.27	842	8	8	0	57.58	Destrin	Q9R0P5	Dstn	Mus musculus
Q9R0Q7	40	4	4	27.5	51	5	5	27.5	91	5	5	0	27.5	Prostaglandin E synthase 3	Q9R0Q7	Ptges3	Mus musculus
Q9R0U0	2	1	1	6.11	25	2	2	10.31	27	2	2	0.95	10.31	Serine/arginine-rich splicing factor 10	Q9R0U0	Srsf10	Mus musculus
Q9R0X4	6	2	2	7.06	0	0	0		6	2	2	0.95	7.06	Acyl-coenzyme A thioesterase 9, mitochondrial	Q9R0X4	Acot9	Mus musculus
Q9R111	686	17	17	52.2	318	14	14	45.37	1004	18	18	0	52.2	Guanine deaminase	Q9R111	Gda	Mus musculus
Q9R112	0	0	0		57	7	7	18.44	57	7	7	0	18.44	Sulfide:quinone oxidoreductase, mitochondrial	Q9R112	Sqrdl	Mus musculus
Q9R190	9	1	1	2.69	48	4	4	12.72	57	4	4	0.19	12.72	Metastasis-associated protein MTA2	Q9R190	Mta2	Mus musculus
Q9R1C7	1	1	1	1.89	40	5	5	9.76	41	5	5	0	9.76	Pre-mRNA-processing factor 40 homolog A	Q9R1C7	Prpf40a	Mus musculus
Q9R1P0	170	8	8	57.47	65	6	6	28.74	235	10	10	0	57.47	Proteasome subunit alpha type-4	Q9R1P0	Psma4	Mus musculus
Q9R1P1	107	2	2	16.59	26	3	3	16.59	133	3	3	0.29	16.59	Proteasome subunit beta type-3	Q9R1P1	Psmb3	Mus musculus
Q9R1P3	172	8	8	41.29	16	4	4	25.87	188	9	9	0	49.25	Proteasome subunit beta type-2	Q9R1P3	Psmb2	Mus musculus
Q9R1P4	149	7	7	44.11	35	2	2	15.59	184	7	7	0	44.11	Proteasome subunit alpha type-1	Q9R1P4	Psma1	Mus musculus
Q9R1T2	65	4	4	16.29	43	5	5	23.71	108	5	5	0	23.71	SUMO-activating enzyme subunit 1	Q9R1T2	Sae1	Mus musculus
Q9R1T4	13	2	2	11.52	18	2	2	11.52	31	2	2	0.95	11.52	Septin-6	Q9R1T4	Sept6	Mus musculus
Q9R257	24	3	3	23.16	20	1	1	14.74	44	3	3	0.29	23.16	Heme-binding protein 1	Q9R257	Hebp1	Mus musculus
Q9WTI7	0	0	0		3	2	2	3.57	3	2	2	0.95	3.57	Unconventional myosin-Ic	Q9WTI7	Myo1c	Mus musculus
Q9WTL7	15	2	2	21.21	1	1	1	11.26	16	2	2	0.95	21.21	Acyl-protein thioesterase 2	Q9WTL7	Lypla2	Mus musculus
Q9WTM5	3	2	2	6.7	2	2	2	4.75	5	3	3	0.29	9.07	RuvB-like 2	Q9WTM5	Ruvbl2	Mus musculus
Q9WTP6	30	2	2	17.15	65	5	5	23.85	95	5	5	0	23.85	Adenylate kinase 2, mitochondrial	Q9WTP6	Ak2	Mus musculus
Q9WTX5	40	1	1	11.66	54	2	2	19.63	94	2	2	0.95	19.63	S-phase kinase-associated protein 1	Q9WTX5	Skp1	Mus musculus
Q9WTX6	2	2	2	4.51	1	1	1	2.71	3	3	3	0.29	5.67	Cullin-1	Q9WTX6	Cul1	Mus musculus
Q9WU28	47	2	2	24.03	7	2	2	22.08	54	3	3	0.29	34.42	Prefoldin subunit 5	Q9WU28	Pfdn5	Mus musculus
Q9WU78	341	16	16	33.14	214	13	13	22.78	555	20	20	0	36.48	Programmed cell death 6-interacting protein	Q9WU78	Pdcd6ip	Mus musculus
Q9WUA2	24	3	3	6.79	13	2	2	3.74	37	3	3	0.29	6.79	Phenylalanine--tRNA ligase beta subunit	Q9WUA2	Farsb	Mus musculus
Q9WUA3	23	5	5	13.52	25	7	7	16.71	48	7	7	0	16.71	ATP-dependent 6-phosphofructokinase, platelet type	Q9WUA3	Pfkp	Mus musculus
Q9WUK2	18	1	1	11.69	91	7	7	35.08	109	7	7	0	35.08	Eukaryotic translation initiation factor 4H	Q9WUK2	Eif4h	Mus musculus
Q9WUM3	131	9	8	32.44	71	8	8	25.21	202	12	11	0	35.74	Coronin-1B	Q9WUM3	Coro1b	Mus musculus
Q9WUM4	133	6	5	18.57	34	6	6	14.35	167	8	7	0	18.57	Coronin-1C	Q9WUM4	Coro1c	Mus musculus
Q9WUP7	11	2	2	10.03	33	5	5	33.74	44	5	5	0	33.74	Ubiquitin carboxyl-terminal hydrolase isozyme L5	Q9WUP7	Uchl5	Mus musculus
Q9WUU7	2	1	1	11.76	104	6	6	24.84	106	6	6	0	24.84	Cathepsin Z	Q9WUU7	Ctsz	Mus musculus
Q9WV02	15	3	3	11	17	3	3	9.46	32	4	4	0.19	13.04	RNA-binding motif protein, X chromosome	Q9WV02	Rbmx	Mus musculus
Q9WV32	501	15	15	48.12	319	16	16	48.12	820	20	20	0	53.49	Actin-related protein 2/3 complex subunit 1B	Q9WV32	Arpc1b	Mus musculus
Q9WV60	10	2	2	12.62	9	3	3	21.43	19	3	3	0.29	21.43	Glycogen synthase kinase-3 beta	Q9WV60	Gsk3b	Mus musculus
Q9WV98	0	0	0		11	2	2	35.96	11	2	2	0.95	35.96	Mitochondrial import inner membrane translocase subunit Tim9	Q9WV98	Timm9	Mus musculus
Q9WVA3	23	3	3	18.71	39	1	1	5.83	62	3	3	0.29	18.71	Mitotic checkpoint protein BUB3	Q9WVA3	Bub3	Mus musculus
Q9WVA4	143	6	6	38.69	224	9	9	46.23	367	9	9	0	46.23	Transgelin-2	Q9WVA4	Tagln2	Mus musculus
Q9WVE8	0	0	0		7	2	2	7.41	7	2	2	0.95	7.41	Protein kinase C and casein kinase substrate in neurons protein 2	Q9WVE8	Pacsin2	Mus musculus
Q9WVG5	105	8	8	23.6	50	4	4	15.2	155	9	9	0	23.6	Endothelial lipase	Q9WVG5	Lipg	Mus musculus
Q9WVJ2	22	4	4	16.49	6	4	4	21.28	28	6	6	0	24.47	26S proteasome non-ATPase regulatory subunit 13	Q9WVJ2	Psmd13	Mus musculus
Q9WVK4	119	11	11	28.84	74	5	5	14.23	193	11	11	0	28.84	EH domain-containing protein 1	Q9WVK4	Ehd1	Mus musculus
Q9Z0H3	3	3	3	15.58	36	3	3	15.58	39	3	3	0.29	15.58	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	Q9Z0H3	Smarcb1	Mus musculus
Q9Z0H4	13	3	3	5.71	13	1	1	3.15	26	3	3	0.29	5.71	CUGBP Elav-like family member 2	Q9Z0H4	Celf2	Mus musculus
Q9Z0I7	28	4	4	20.77	5	3	3	13.06	33	5	5	0	24.33	Protein Slfn1	Q9Z0I7	Slfn1	Mus musculus
Q9Z0J0	0	0	0		43	4	4	31.54	43	4	4	0.19	31.54	Epididymal secretory protein E1	Q9Z0J0	Npc2	Mus musculus
Q9Z0N1	71	6	6	23.09	68	4	4	16.1	139	7	7	0	26.91	Eukaryotic translation initiation factor 2 subunit 3, X-linked	Q9Z0N1	Eif2s3x	Mus musculus
Q9Z0P4	0	0	0		8	2	2	8.36	8	2	2	0.95	8.36	Paralemmin-1	Q9Z0P4	Palm	Mus musculus
Q9Z0P5	138	8	8	37.82	200	13	13	46.13	338	13	13	0	46.13	Twinfilin-2	Q9Z0P5	Twf2	Mus musculus
Q9Z0W3	0	0	0		6	3	3	3.28	6	3	3	0.29	3.28	Nuclear pore complex protein Nup160	Q9Z0W3	Nup160	Mus musculus
Q9Z0X1	0	0	0		9	3	3	10.29	9	3	3	0.29	10.29	Apoptosis-inducing factor 1, mitochondrial	Q9Z0X1	Aifm1	Mus musculus
Q9Z126	469	5	5	38.1	97	3	3	29.52	566	5	5	0	38.1	Platelet factor 4	Q9Z126	Pf4	Mus musculus
Q9Z130	0	0	0		30	3	2	11.63	30	3	2	0.95	11.63	Heterogeneous nuclear ribonucleoprotein D-like	Q9Z130	Hnrnpdl	Mus musculus
Q9Z183	134	12	12	30.63	196	18	18	33.78	330	20	20	0	36.94	Protein-arginine deiminase type-4	Q9Z183	Padi4	Mus musculus

Protein	Exosome Spectral Counts	Exosome Distinct Peptides	Exosome Unshared Peptides	Exosome Protein Coverage %	Parental Spectral Counts	Parental Distinct Peptides	Parental Unshared Peptides	Parental Protein Coverage %	Spectral Counts	Distinct Peptides	Unshared Peptides	Protein FDR %	Protein Coverage %	Description	Entry	Gene	Organism
Q9Z1B7	18	3	3	7.92	0	0	0		18	3	3	0.29	7.92	Mitogen-activated protein kinase 13	Q9Z1B7	Mapk13	Mus musculus
Q9Z1D1	15	2	2	15.31	21	3	3	18.12	36	3	3	0.29	18.12	Eukaryotic translation initiation factor 3 subunit G	Q9Z1D1	Eif3g	Mus musculus
Q9Z1E4	63	6	6	18.56	75	5	5	15.58	138	7	7	0	21.68	Glycogen [starch] synthase, muscle	Q9Z1E4	Gys1	Mus musculus
Q9Z1F9	37	7	7	22.41	37	6	6	19.91	74	9	9	0	26.33	SUMO-activating enzyme subunit 2	Q9Z1F9	Uba2	Mus musculus
Q9Z1G3	0	0	0		10	2	2	6.81	10	2	2	0.95	6.81	V-type proton ATPase subunit C 1	Q9Z1G3	Atp6v1c1	Mus musculus
Q9Z1N5	141	7	5	27.1	128	9	5	33.88	269	12	7	0	40.89	Spliceosome RNA helicase Ddx39b	Q9Z1N5	Ddx39b	Mus musculus
Q9Z1Q5	322	16	16	56.43	202	8	8	40.66	524	16	16	0	56.43	Chloride intracellular channel protein 1	Q9Z1Q5	Clic1	Mus musculus
Q9Z1Q9	104	13	13	22.33	97	12	12	22.41	201	15	15	0	24.39	Valine--tRNA ligase	Q9Z1Q9	Vars	Mus musculus
Q9Z1R2	5	1	1	2.69	31	3	3	7.28	36	3	3	0.29	7.28	Large proline-rich protein BAG6	Q9Z1R2	Bag6	Mus musculus
Q9Z1T1	0	0	0		22	2	2	3.53	22	2	2	0.95	3.53	AP-3 complex subunit beta-1	Q9Z1T1	Ap3b1	Mus musculus
Q9Z1X4	12	1	1	2	28	3	3	9.91	40	4	4	0.19	11.92	Interleukin enhancer-binding factor 3	Q9Z1X4	Ilf3	Mus musculus
Q9Z1Z0	3	3	3	6.15	28	7	7	13.87	31	7	7	0	13.87	General vesicular transport factor p115	Q9Z1Z0	Uso1	Mus musculus
Q9Z1Z2	76	4	4	18.29	30	5	5	27.14	106	5	5	0	27.14	Serine-threonine kinase receptor-associated protein	Q9Z1Z2	Strap	Mus musculus
Q9Z204-2	3	1	1	3.67	9	3	3	13.33	12	4	4	0.19	17	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	Q9Z204	Hnrnpc	Mus musculus
Q9Z277	0	0	0		9	2	2	3.31	9	2	2	0.95	3.31	Tyrosine-protein kinase BAZ1B	Q9Z277	Baz1b	Mus musculus
Q9Z2D3	3	1	1	5.66	25	3	3	15.23	28	3	3	0.29	15.23	Non-syndromic hearing impairment protein 5 homolog	Q9Z2D3	Dfna5	Mus musculus
Q9Z2E1	0	0	0		20	2	2	11.84	20	2	2	0.95	11.84	Methyl-CpG-binding domain protein 2	Q9Z2E1	Mbd2	Mus musculus
Q9Z2G9	3	2	2	9.5	0	0	0		3	2	2	0.95	9.5	Oxidoreductase HTATIP2	Q9Z2G9	Htatip2	Mus musculus
Q9Z2I8	2	2	2	12.7	15	5	5	23.09	17	5	5	0	23.09	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Q9Z2I8	Suclg2	Mus musculus
Q9Z2L7	97	5	5	31.22	83	8	8	41.63	180	8	8	0	41.63	Cytokine receptor-like factor 3	Q9Z2L7	Crlf3	Mus musculus
Q9Z2M7	11	1	1	11.16	10	3	3	12.4	21	3	3	0.29	12.4	Phosphomannomutase 2	Q9Z2M7	Pmm2	Mus musculus
Q9Z2R6	7	3	3	17.92	0	0	0		7	3	3	0.29	17.92	Protein unc-119 homolog A	Q9Z2R6	Unc119	Mus musculus
Q9Z2U0	251	10	10	51.21	11	3	3	22.58	262	10	10	0	51.21	Proteasome subunit alpha type-7	Q9Z2U0	Psma7	Mus musculus
Q9Z2U1	134	5	5	31.12	61	2	2	12.86	195	5	5	0	31.12	Proteasome subunit alpha type-5	Q9Z2U1	Psma5	Mus musculus
Q9Z2W0	189	10	10	39.96	18	2	2	11.42	207	10	10	0	39.96	Aspartyl aminopeptidase	Q9Z2W0	Dnpep	Mus musculus
Q9Z2X1	216	9	8	35.42	510	20	17	46.27	726	20	17	0	46.27	Heterogeneous nuclear ribonucleoprotein F	Q9Z2X1	Hnrnpf	Mus musculus
Q9Z315	0	0	0		6	2	2	5.33	6	2	2	0.95	5.33	U4/U6.U5 tri-snRNP-associated protein 1	Q9Z315	Sart1	Mus musculus

Peptide identifications for the comparison Exosome Infl. vs. Exosome Conv.

Peptide FDR ≤ 0.31%

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A075B5R8	Conv	KDVQC	EVQLLETGGGLVQPGGSR	GLSCE	2		898.9792115	1795.942823	0.000451244	6	N	19	37
A0A075B5R8	Conv	QTPGK	TLEWIGDINSDGSAINYAPSIKDR	FTIFR	2		1318.154079	2634.292557	0.000451244	5	N	62	86
A0A075B5R8	Conv	QTPGK	TLEWIGDINSDGSAINYAPSIK	DRFTI	2		1182.590052	2363.164503	0.000451244	6	N	62	84
A0A075B5U4	Conv	SHGKS	LEWIGDINPNNGGTIYNQKFK	GKATL	3		807.7452854	2420.212456	0.002981883	1	N	62	83
A0A075B5U4	Conv	TAVLS	EVQLQQSGPELVKPGASVK	IPCKA	2		997.550001	1993.084402	0.000823681	1	N	18	37
A0A087WR50	Conv	NDNAR	SSPVIIDASTAIDAPSNLR	FLTTT	2		964.0107086	1926.005817	0.000451244	22	N	1890	1909
A0A087WR50	Conv	PDTMR	VTWAPPPSIELTNLLVR	YSPVK	2		953.5439903	1905.072381	0.000451244	7	N	1283	1300
A0A087WR50	Conv	CDNCR	RPGAAEPSPDGTTGHTYNQYTQR	YNQRT	3		835.3903414	2503.147624	0.000451244	4	N	2333	2356
A0A087WR50	Conv	QGRGR	WKCDPIDQCQDSETR	TFYQI	2	C3:+57.021,C9:+57.021	969.4095158	1936.803432	0.000451244	5	N	552	567
A0A087WR50	Conv	DAGFK	LTCQCLGFGSGHFR	CDSSK	2	C3:+57.021,C5:+57.021	820.3770933	1638.738587	0.000451244	22	N	2229	2243
A0A087WR50	Conv	YGGSR	GFNCESKPEPEETCFDKYTGNTYK	VGDTY	2	C4:+57.021,C14:+57.021	1451.120798	2900.225997	0.001162105	1	N	84	108
A0A087WR50	Conv	VSGYR	VEVLPVSLPGEHGQR	LPVNR	2		808.9419006	1615.868201	0.000451244	14	N	937	952
A0A087WR50	Conv	TISWR	TKTETITGFQVDAIPANGQTPVQR	SISPD	2		1286.672439	2571.329277	0.000451244	21	N	1834	1858
A0A087WR50	Conv	DADQK	FGFCPMAAHEEICTTNEGVMYR	IGDQW	2	C4:+57.021,M6:+15.995,C13:+57.021,M20:+15.995	1326.553072	2651.090544	0.000662267	1	N	457	479
A0A087WR50	Conv	QQWER	TYLGNALVCTCYGGSR	GFNCE	2	C9:+57.021,C11:+57.021	896.4113301	1790.80706	0.000451244	17	N	68	84
A0A087WR50	Conv	VRYYR	ITYGETGGNSPVQEFTVPGSK	STATI	2		1084.529463	2167.043325	0.000451244	20	N	1478	1499
A0A087WR50	Conv	KYPLR	NLQPGSEYTVTLVAVK	GNQQS	2		859.9703238	1717.925048	0.000451244	8	N	1053	1069
A0A087WR50	Conv	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3		1045.511296	3133.510489	0.000451244	6	N	1352	1381
A0A087WR50	Conv	TGTPR	SDNVPPPTDLQFVELTDVK	VTIMW	2		1057.536756	2113.057912	0.000451244	16	N	902	921
A0A087WR50	Conv	RGRQK	TGLDSPTGFDSSDITANSFTVHWVAPR	APITG	2		1439.686274	2877.356949	0.002296037	2	N	1354	1381
A0A087WR50	Conv	TGLTR	GVTYNIIVEALQNQR	RHKVR	2		859.4657399	1716.91588	0.000451244	21	N	2163	2178
A0A087WR50	Conv	PSNLR	FLTTTPNSLLVSWQAPR	ARITG	2		966.023422	1930.031244	0.000451244	12	N	1909	1926
A0A087WR50	Conv	PIVNR	VVTPLSPPTNLHLEANPDTGVLTVSWER	STTPD	3		1014.868533	3041.582198	0.000451244	20	N	1168	1196
A0A087WR50	Conv	RHKVR	EEVVTVGNAVSEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C22:+57.021	1467.32428	4398.949441	0.000451244	16	N	2183	2222
A0A087WR50	Conv	EVVPR	PRPGVTEATITGLEPGTEYTIYVIALK	NNQKS	3		963.8589744	2888.553523	0.000451244	13	N	1949	1976
A0A087WR50	Conv	VSGFR	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK	YIVNV	3		1258.958581	3773.852344	0.000451244	27	N	750	784
A0A087WR50	Conv	PTNLK	FSQVTPTSFTAQWIAPSVQLTGYR	VRVNP	2		1343.187724	2684.359849	0.000451244	13	N	1728	1752
A0A087WR50	Conv	GEAPR	EVTSDSGSIVVSGLTPGVEYTYTIQVLR	DGQER	3		990.8489152	2969.523345	0.000451244	23	N	1128	1156
A0A087WR50	Conv	LPVNR	NTFAEITGLSPGVTYLFK	VFAVH	2		979.5176382	1957.019676	0.000451244	19	N	957	975
A0A087WR50	Conv	VPPSR	NSITLTNLNPGTEYVVSIIAVNGR	EESPP	2		1273.185182	2544.354764	0.000451244	20	N	1409	1433
A0A087WR50	Conv	VSGFR	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR	KYIVN	3		1216.26026	3645.757381	0.000451244	6	N	750	783
A0A087WR50	Conv	SDIPR	DLEVIASTPTSLLISWEPPAVSVR	YYRIT	2		1290.700133	2579.384667	0.000451244	17	N	1451	1475
A0A087WR50	Conv	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	2	C7:+57.021	1098.966472	2195.917344	0.000451244	15	N	379	397
A0A087WR50	Conv	SEEGK	QSLILSTSQTTAPDAPPDPTVDQVDDTSIVVR	WSRPQ	3		1122.902407	3365.683822	0.000451244	5	N	797	829
A0A087WR50	Conv	NRVVT	PLSPPTNLHLEANPDTGVLTVSWER	STTPD	3		915.1403637	2742.397691	0.0007646	1	N	1171	1196
A0A087WR50	Conv	QQSPK	ATGVFTTLQPLR	SIPPY	2		652.3725911	1302.729582	0.000622848	1	N	1076	1088
A0A087WR50	Conv	RGRQK	TGLDSPTGFDSSDITANSFTVH	WVAPR	2		1135.016916	2268.018233	0.000698008	2	N	1354	1376
A0A087WR50	Conv	LQPLR	SIPPYNTEVTETTIVITWTPAPR	IGFKL	2		1293.676658	2585.337717	0.000451244	3	N	1088	1111
A0A087WR50	Conv	SWTPF	QESSEYIISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	C10:+57.021	1376.330595	4125.968385	0.000451244	2	N	2125	2163
A0A087WR50	Conv	WKCER	HALQSASAGSGSFTDVR	TAIYQ	2		845.9113288	1689.807058	0.001871652	2	N	273	290
A0A087WR50	Conv	EQWQK	EYLGAICSCTCFGGQR	GWRCD	2	C7:+57.021,C9:+57.021,C11:+57.021	939.900041	1877.784482	0.000451244	11	N	2309	2325
A0A087WR50	Conv	SIVVR	WSRPQAPITGYR	IVYSP	3		477.9217594	1430.741878	0.000451244	12	N	829	841
A0A087WR50	Conv	EQDQK	YSFCTDHAVLVQTR	GGNSN	2	C4:+57.021	848.9095119	1695.803424	0.000451244	27	N	397	411
A0A087WR50	Conv	AVNGR	EESPPLIGQQATVSDIPR	DLEVI	2		969.0028836	1935.990167	0.000451244	12	N	1433	1451
A0A087WR50	Conv	LTDVK	VTIMWTPPDSVVSGYR	VEVLP	2	M4:+15.995	912.4540268	1822.892454	0.000451244	9	N	921	937
A0A087WR50	Conv	VPRPR	PGVTEATITGLEPGTEYTIYVIALK	NNQKS	3		879.4743494	2635.399648	0.002145581	1	N	1951	1976
A0A087WR50	Conv	SINYK	TEIDKPSQMQVTDVQDNSISVR	WLPST	3	M9:+15.995	836.0750599	2505.20178	0.000451244	6	N	1538	1560
A0A087WR50	Conv	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	3	C1:+39.994,C8:+57.021	936.3869331	2806.137399	0.001699387	4	N	2286	2309
A0A087WR50	Conv	KKDNR	GNLLQCVCTGNGR	GEWKC	2	C6:+57.021,C8:+57.021	724.8403436	1447.665087	0.000451244	13	N	253	266
A0A087WR50	Conv	NITIY	AVEENQESTPVFIQQETTGTPR	SDNVP	2		1231.096229	2460.176859	0.000451244	4	N	880	902
A0A087WR50	Conv	PRRAR	VTDATETTITISWR	TKTET	2		797.410099	1592.804598	0.000451244	3	N	1820	1834
A0A087WR50	Conv	LVQTR	GGNSNGALCHFPFLYNNR	NYTDC	2	C9:+57.021	1019.471331	2036.927061	0.000451244	9	N	411	429
A0A087WR50	Conv	SWRTK	TETITGFQVDAIPANGQTPVQR	SISPD	2		1172.101118	2342.186635	0.00091018	1	N	1836	1858
A0A087WR50	Conv	VGNGR	GEWACIPYSQLR	DQCIV	2	C5:+57.021	740.3563838	1478.697168	0.000451244	5	N	503	515
A0A087WR50	Conv	VPGSK	STATINNIKPGADYTITLYAVTGR	GDSPA	2		1270.671907	2539.328214	0.000451244	6	N	1499	1523
A0A087WR50	Conv	STVQK	TPFITNPGYDTENGIQLPGTTHQQPSVGQQMIFEEHGFR	RTTPP	4	M31:+15.995	1097.772921	4387.060484	0.000870037	2	N	2018	2057
A0A087WR50	Conv	SYTIK	GLTPGVIYEGQLISIQQYGHR	EVTRF	2		1165.119113	2328.222627	0.000451244	10	N	669	690
A0A087WR50	Conv	NETDR	TVLVTWTPPR	ARIAG	2		585.3380199	1168.66044	0.001839721	4	N	1010	1020
A0A087WR50	Conv	YERPK	DSMIWDCTCIGAGR	GRISC	2	M3:+15.995,C7:+57.021,C9:+57.02	829.3421021	1656.668604	0.000451244	8	N	117	131
A0A087WR50	Conv	VGNAV	SEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C12:+57.021	1134.821605	3401.441414	0.000451244	6	N	2193	2222
A0A087WR50	Conv	VKDDK	ESAPISDTVVPAVPPPTDLR	FTNIG	2		1031.047291	2060.078982	0.00307782	1	N	1253	1273

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A087WR50	Conv	GSPPR	EVVPRPRPGVTEATITGLEPGTEYTIYVIALK	NNQKS	4		868.2295049	3468.88682	0.002519933	2	N	1944	1976
A0A087WR50	Conv	PSKTK	TASPDQTEMTIEGLQPTVEYVVSVYAQNR	NGESQ	3		1076.191124	3225.549972	0.000451244	14	N	1587	1616
A0A087WR50	Conv	NLLVR	YSPVKNEEDVAELSISPSDNAVVL	TNLLP	2		1288.142845	2574.270091	0.001654178	2	N	1300	1324
A0A087WR50	Conv	TGLTR	GVTYNIIVEALQNQRR	HKVRE	3		625.346797	1873.016991	0.000870037	6	N	2163	2179
A0A087WR50	Conv	AVSEG	LNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C9:+57.021	1043.789576	3128.345329	0.002145581	2	N	2196	2222
A0A087WR50	Conv	YGGSR	GFNCESKPEPEETCFDK	YTGNT	3	C4:+57.021,C14:+57.021	691.9560093	2072.844628	0.000451244	3	N	84	101
A0A087WR50	Conv	NLLVR	YSPVKNEEDVAELSISPSDNAVVLTN	LLPGT	2		1395.688148	2789.360697	0.000979378	1	N	1300	1326
A0A087WR50	Conv	QRRHK	VREEVVTVGNAVSEGLNQPTDDSCFDPYTVSHY	AIGEE	3	C24:+57.021	1228.897173	3683.66812	0.000451244	1	N	2181	2214
A0A087WSP5	Conv	EWKRR	QQSACIGGPPNACLDQLQSWFTIVAETLQQIR	QQLKK	3	C5:+57.021,C13:+57.021	1210.599703	3628.775709	0.000870037	2	N	242	274
A0A087WSP5	Conv	PYTKK	ELSAVTFPDIIR	NYKVM	2		680.8777063	1359.739813	0.000979378	2	N	643	655
A0A087WSP5	Conv	MLGEK	LLGPNAGPDGLIPWTR	FCKEN	2		838.9600934	1675.904587	0.000622848	1	N	531	547
A0A0D9SEG8	Conv	SVSLK	LLSNINSVFLTNTNTEK	LASNV	2		954.5078018	1907.000004	0.000451244	13	N	346	363
A0A0D9SEG8	Conv	LEQRR	ASLEDFYGSPIPSVSLK	LLSNI	2		905.4676139	1808.919628	0.000451244	2	N	329	346
A0A0D9SEG8	Conv	SGSLR	GPDTICQEPPFPTWTLLPTAHSQTLLR	FSVEV	3	C6:+57.021	1026.190575	3075.548326	0.000451244	7	N	160	187
A0A0D9SEG8	Conv	EAVDK	LLEDPMETETQQVAAQLLSNLEQSLR	TLAQF	3	M6:+15.995	991.5014384	2971.480915	0.001763695	1	N	217	243
A0A0D9SEG8	Conv	YTIQK	LIEAVDKLLEDPMETETQQVAAQLLSNLEQSLR	TLAQF	3	M13:+15.995	1247.64749	3739.919071	0.000698008	1	N	210	243
A2AFG7	Conv	NSSSR	LVALQGQSLILECIAEGFPTPTIK	WLHPS	3	C13:+57.021	866.8122653	2597.413396	0.000622848	3	N	245	269
A2AFG7	Conv	YLLCK	AFGAPVPSVQWLDEEGTTVLQDER	FFPYA	2		1322.648629	2643.281658	0.000451244	10	N	443	467
A2AFG7	Conv	PKWPK	ETVKPVEVEEGESVVLPCNPPPSAAPLR	IYWMN	3	C18:+57.021	1000.850107	2999.526922	0.001395409	1	N	134	162
A2AIV8	Conv	LRQCK	VLNPDDEEQVLSDPNLVIR	KRKVG	2		1083.058387	2164.101174	0.000451244	2	N	38	57
A2AN08	Conv	NLLCK	VNEAAPEKPQEDSGTAGGISSTSASVNR	YILQL	3		920.4413187	2758.300556	0.0025889	1	N	3763	3791
A2AQ07	Conv	QIGAK	FWEVIGEEHGIDCAGSYCGTSALQLER	ISVYY	3	C13:+57.021,C18:+57.021	1028.799264	3083.374392	0.000451244	17	N	19	46
A2AQ07	Conv	SIQTR	NSNCFVEWIPNNVK	VAVCD	2	C4:+57.021	860.9095119	1719.803424	0.000451244	15	N	336	350
A2AQ07	Conv	IRSSR	LGVLFQPDSFVHGNSGAGNNWAK	GHYTE	2		1208.09617	2414.176739	0.000622848	2	N	80	103
A2AQ07	Conv	PRRGR	YLTVACIFR	GKMST	2	C6:+57.021	571.805267	1141.594934	0.001591523	7	N	309	318
A2AQ07	Conv	DIPPR	GLNMAATFLGNNTAIQELFTR	VSEHF	3		761.3919665	2281.1525	0.001329271	1	N	359	380
A2ASS6	Conv	KTSFR	VENLTEGAIYYFR	VMAEN	2		787.8966274	1573.777655	0.001352548	1	N	25964	25977
A2ASS6	Conv	PALKK	GSGEEEEIDIMELLK	NVDPK	3		564.6068435	1690.79713	0.001463592	1	N	9457	9472
A2AUR7	Conv	KQVFK	AENNPWVTPIADQFQLGVSHVFEYIR	SETYK	3		1010.842318	3029.503553	0.000622848	13	N	195	221
A2AUR7	Conv	VAELK	NLEVLNFFNNQIEELPTQISSLQK	LKHLN	2		1409.735236	2817.454872	0.000451244	5	N	46	70
A2AUR7	Conv	NTLPR	GFGSLPALEVLDLTYNNLNEHSLPGNFFYLTTLR	ALYLS	3		1275.988258	3824.941375	0.000823681	8	N	86	120
A2AUR7	Conv	IQGNR	LTVLPPELGNLDLTGQK	QVFKA	2		904.5123558	1807.009112	0.000735798	3	N	174	191
A2AUR7	Conv	LTTLR	ALYLSDNDFEILPPDIGK	LTKLQ	2		1010.517835	2019.02007	0.001839721	1	N	120	138
A6H630	Conv	SSSQK	ANIINCLQDLKPFILINDTESLWALLSK	LKKTV	3	C6:+57.021	1081.588336	3241.741607	0.000823681	2	N	206	234
A6X935	Conv	RQTEK	FEVSVNVAPGSKITFELIYQE	LLQRR	3		790.746292	2369.215476	0.001162105	1	N	127	148
A6X935	Conv	ASRIR	AHGGTNINNAVLLAVELLDR	SNQAE	3		697.3837994	2089.127998	0.000451244	16	N	345	365
A6X935	Conv	LLPSK	SVSLIILLTDGDPTVGETNPTIIQNNVR	EAING	3		993.8719427	2978.592428	0.000451244	7	N	375	403
A6X935	Conv	VKILK	DLSPQDQFNLIEFSGEANQWK	QSLVQ	2		1233.582758	2465.149916	0.000451244	12	N	302	323
A6X935	Conv	APGSK	ITFELIYQELLQR	RLGMY	2		833.4646772	1664.913754	0.000451244	9	N	139	152
A6X935	Conv	SQQQK	SQSEQDTVLNGDFIVR	YDVNR	2		904.4452014	1806.874803	0.000451244	11	N	224	240
A6X935	Conv	EALVK	ILKDLSPQDQFNLIEFSGEANQWK	QSLVQ	3		940.8121356	2819.413007	0.001162105	3	N	299	323
A6ZI44	Conv	VAPGK	GILAADESTGSIAKR	LQSIG	2		744.9049838	1487.794368	0.000451244	13	N	82	97
A6ZI44	Conv	VAPGK	GILAADESTGSIAK	RLQSI	2		666.8544282	1331.693256	0.000451244	9	N	82	96
A6ZI44	Conv	ACQGK	YTPSGQSGAAASESLFISNHAY	-	2		1129.522169	2257.028738	0.000451244	40	N	396	418
A6ZI44	Conv	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLKR	CQYVT	3	C5:+57.021	1059.540044	3175.596733	0.000451244	57	N	227	255
A6ZI44	Conv	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	2		1054.052385	2106.089171	0.000451244	20	N	207	227
A6ZI44	Conv	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	3	C13:+57.021	1038.553625	3112.637476	0.000451244	22	N	114	141
A6ZI44	Conv	TALRR	TVPPAVTGVTFLSGGQSEEEASINLNAINK	CPLLK	3		1015.191452	3042.550957	0.000451244	475	N	313	343
A6ZI44	Conv	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLK	RCQYV	3	C5:+57.021	1007.506341	3019.495622	0.000451244	18	N	227	254
A6ZI44	Conv	ATGTM	PHPYPALTPEQK	KELSD	3		459.9107489	1376.708847	0.000979378	3	N	55	67
A6ZI44	Conv	TADDR	VNPCIGGVILFHETLYQK	ADDGR	2	C4:+57.021	1044.551258	2087.086916	0.000451244	13	N	123	141
A6ZI44	Conv	FSFPP	VASEQPHSELGNTQQQTELGK	ESTAT	3		761.0405381	2280.098214	0.001463592	2	N	26	47
A6ZI44	Conv	VTALR	RTVPPAVTGVTFLSGGQSEEEASINLNAINK	CPLLK	3		1067.225156	3198.652068	0.000451244	13	N	312	343
A6ZI44	Conv	YASIC	QQNGIVPIVEPEILPDGDHDLKR	CQYVT	3		861.4578042	2581.350013	0.001591523	1	N	232	255
A6ZI44	Conv	ACQGK	YTPSGQSGAAASESL	FISNH	2		713.3287745	1424.641949	0.000451244	1	N	396	411
A6ZI46	Conv	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	3	C13:+57.021	1038.88163	3113.621491	0.000451244	10	N	115	142
A6ZI46	Conv	TADDR	VNPCIGGVILFHETLYEK	ADDGR	2	C4:+57.021	1045.043266	2088.070932	0.000451244	4	N	124	142
A8E0Y8	Conv	TFSLK	IFSVGPEDVGTYSCEVAEVAR	TQMGS	2	C14:+57.021	1143.041649	2284.067697	0.001943752	2	N	363	384
A8E0Y8	Conv	LSVGK	LQPSDQGQVFCEATEWIQDPDETWTLITR	KQTDQ	3	C11:+57.021	1155.208912	3462.603335	0.002663018	1	N	238	267
B2RPV6	Conv	TVTRR	ELQNLIGAINQLNVLTK	ELTKR	2		941.0443545	1880.073109	0.000823681	1	N	659	676
B2RPV6	Conv	QSSQK	SLTELVESIVEIK	TQAAL	2		730.4168613	1458.818123	0.000451244	5	N	943	956
B2RV77	Conv	AVEYK	SQVVAGQNYFIK	MDVGG	2		677.3622234	1352.708847	0.000451244	13	N	44	56
B2RV77	Conv	LSRAR	SATPEIQEIADKVK	SLLEE	2		764.9150171	1527.814434	0.000451244	4	N	10	24
B2RXR6	Conv	MAVLK	LCEQPPLVQAIFSGDPEEIR	MLIHK	2	C2:+57.021	1149.575659	2297.135717	0.000451244	5	N	5	25
B2RXR6	Conv	DTFGR	TCLHAAAAGGNVECIK	LLQSS	3	C2:+57.021,C14:+57.021	557.9364436	1670.785931	0.000823681	1	N	406	422

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
B2RY50	Conv	RDLVR	LHGGLKPLASLLNNTDNK	ERLAA	2		953.0317784	1904.047957	0.001329271	1	N	704	722
B5THE2	Conv	GLHLR	GGYIFPTQQPATTTEASR	KNPLG	2		962.9741261	1923.932652	0.000622848	2	N	790	808
B5THE2	Conv	TGEWK	TLEAPLEYINLHIR	GGYIL	3		561.3144342	1680.919902	0.002727428	1	N	1672	1686
B5THE2	Conv	TATLK	NLPSAPVFGNSIENILLTAEYQTSNR	FHFKL	3		950.1545615	2847.440284	0.000451244	3	N	130	156
B5THE2	Conv	WGIDR	QFLWGPGLLITPVLDQGAEK	VKAYV	2		1091.599494	2181.183388	0.000451244	9	N	730	750
B5THE2	Conv	TCDER	GCCWDPQGSISVPCYYSR	NHGYK	2	C2:+57.021,C3:+57.021,C14:+57.021	1096.453169	2190.890738	0.000451244	3	N	90	108
B5THE2	Conv	WNIDK	QFLLGPAFLVSPVLEPNAR	KVEAY	2		1034.583647	2067.151694	0.000451244	14	N	1626	1645
B5THE2	Conv	VKQNG	NLLQMSPQVTYNPNLK	VATIT	3		620.6615055	1858.961117	0.000998612	1	N	893	909
B5THE2	Conv	DISLK	ASTYSNAFPSTPVNK	LKLQV	2		792.3891665	1582.762733	0.000622848	3	N	996	1011
B5THE2	Conv	PSSGR	WGGHWLGDNTAAWDQLGK	SIIGM	2		1006.474628	2010.933655	0.001699387	1	N	1492	1510
B5THE2	Conv	RISTR	LPSTYIYGFGETEHTTFK	IDMNW	3		697.6743564	2089.999669	0.002019181	1	N	1099	1117
D3Z6Q9	Conv	LYNSR	IGCYVTVFQNISNLR	DVFYR	2	C3:+57.021	892.4619116	1782.908223	0.000451244	21	N	202	217
D3Z6Q9	Conv	HEDLK	AIVGNNDLLWEDYEEKLADQALR	TMENY	2		1338.169729	2674.323857	0.001329271	1	N	100	123
D3Z6Q9	Conv	EDFSK	AQIVFEDLNQELLEELPILYNSR	IGCYV	2		1373.719054	2745.422509	0.000451244	22	N	179	202
D3Z6Q9	Conv	EDFSK	AQIVFEDLNQELLEELPILY	NSRIG	2		1195.131021	2388.246442	0.000823681	2	N	179	199
D3Z6Q9	Conv	PPPPR	ASGSGSCNAPGSPEGSSQLCSPR	ASPDA	2	C7:+57.021,C20:+57.021	1125.479189	2248.942779	0.000451244	5	N	418	441
D3Z6Q9	Conv	HEDLK	AIVGNNDLLWEDYEEK	LADQA	2		954.4552348	1906.89487	0.000451244	13	N	100	116
D3Z6Q9	Conv	TKDER	FEQSASNFYQQQAEGHK	LYKDL	2		999.9511823	1997.886765	0.000451244	4	N	42	59
D3Z6Q9	Conv	ESSKR	VSETLQEVYSSDWDGHEDLK	AIVGN	2		1169.030024	2336.044447	0.000698008	1	N	80	100
E9PUM5	Conv	KGPNK	IQCVDGMWTTLPVCVEEER	TCGDI	2	C3:+57.021,M7:+15.995,C14:+57.021	1169.529348	2337.043097	0.000622848	4	N	372	391
E9PUM5	Conv	CIRIK	TCSVSDIEIENGFFSESFR	TYALN	2	C2:+57.021	1112.497074	2222.978548	0.000637154	1	N	149	168
E9PV24	Conv	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	2		1408.647012	2815.278424	0.000451244	12	N	485	511
E9PV24	Conv	GCRMK	GLIDEANQDFTNR	INKLK	2		746.8554908	1491.695382	0.000451244	12	N	72	85
E9PV24	Conv	MEYLR	GDFANANNFDNTYGQVSEDLRR	RIEIL	3		835.0464632	2502.11599	0.000451244	6	N	115	137
E9PV24	Conv	MEYLR	GDFANANNFDNTYGQVSEDLR	RRIEI	2		1174.015239	2346.014879	0.000451244	24	N	115	136
E9PV24	Conv	ELSER	HPDLSGFFDNHFGLISPNFK	EFGSK	2		1145.058525	2288.101449	0.000622848	5	N	460	480
E9PV24	Conv	KVIEK	AQQIQALQSNVR	AQLID	2		678.3736538	1354.731708	0.000622848	1	N	149	161
E9PV24	Conv	RAVNR	EINLQDYEGHQK	QLQQV	2		737.352584	1472.689568	0.000451244	4	N	191	203
E9PV24	Conv	REVVK	EVITSDDGSDCGDATELDISHSFSGSLDELSER	HPDLS	3	C11:+57.021	1181.844804	3542.511011	0.000451244	8	N	427	460
E9PV24	Conv	SDGNR	NPGTTGSDGTGDWGTGSPRPGSDSGNFRPANPNWGVF	SEFGD	3		1240.555175	3718.642126	0.000451244	9	N	323	360
E9PV24	Conv	STVWT	TDTEDKGEFLSEGGGVR	GPRVV	2		898.9190165	1795.822433	0.000451244	3	N	19	36
E9PV24	Conv	REVVK	EVITSDDGSDCGDATELDISHSFSGSLDELSERHPDLSGF	FDNHF	4	C11:+57.021	1074.9717	4295.8556	0.002019181	1	N	427	467
E9PV24	Conv	DELSE	RHPDLSGFFDNHFGLISPNFK	EFGSK	4		612.05844	2444.20256	0.000451244	6	N	459	480
E9PYK3	Conv	NLFKK	DFSLTEAPPGYDSVHGVSETTSVPTDFQDDEFVVYK	TNQVK	3		1326.941368	3977.800703	0.000451244	2	N	509	545
E9PYK3	Conv	AVEKR	DVNEIPFANVPNISELVAK	EDVDF	2		1035.049834	2068.084068	0.000979378	1	N	1174	1193
E9PZF0	Conv	ESAEK	EIHLWFKPEELIDYK	SCAHD	2		980.5148985	1959.014197	0.00091018	1	N	243	258
E9PZF0	Conv	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDYK	SCAHD	3		1142.912578	3425.714334	0.000823681	4	N	229	258
E9Q070	Conv	PAAAR	AGAIAPCEVTVPAQNTGLGPEK	TSFFQ	2	C7:+57.021	1090.554726	2179.093852	0.000451244	11	N	112	134
E9Q070	Conv	LGPEK	TSFFQALGITTK	ISSGT	2		657.3591494	1312.702699	0.000451244	4	N	134	146
E9Q070	Conv	NGYKR	VLALSVETEYTFPLAEK	VKAFL	2		955.5120215	1909.008443	0.000451244	10	N	247	264
E9Q070	Conv	NISPF	SFGLIIQQVFDNGSIYNPEVLDITEQALHSR	FLEGV	3		1168.598882	3502.773246	0.000451244	7	N	183	214
E9Q070	Conv	TKISS	GTIEILSDVQLIK	TGDKV	2		714.9195712	1427.823542	0.001591523	5	N	149	162
E9Q070	Conv	LEGVR	NVASVCLQIGYPTVASVPHSIINGYK	RVLAL	3	C6:+57.021	929.8218234	2786.44207	0.000451244	3	N	220	246
E9Q0F0	Conv	TREIR	SLNNQFASFIDKVR	FLEQQ	2		819.9340756	1637.852551	0.000451244	5	N	110	124
E9Q0F0	Conv	TREIR	SLNNQFASFIDK	VRFLE	2		692.349313	1382.683026	0.000451244	3	N	110	122
E9Q0K6	Conv	NTDLR	TWEPEDVCSFLENR	GFREK	2	C8:+57.021	891.3938916	1780.772183	0.000451244	17	N	75	89
E9Q0K6	Conv	FRDNK	IAGSFLPFLDEDRLEDLGVSSLEER	KKMIE	2		1404.209051	2806.402502	0.000622848	2	N	104	129
E9Q0K6	Conv	EAFTK	LTDNIFLEVLHSTDPQLSEAQSILR	NIECR	2		1420.245968	2838.476336	0.000451244	10	N	464	489
E9Q0K6	Conv	IDLMK	VFNDPIHGHIEFHPLLIR	IIDTP	3		718.7256083	2153.153425	0.000451244	8	N	148	166
E9Q0K6	Conv	DYFAR	DCHHLGIQNNFDYKR	FIKFA	4	C2:+57.021	479.9763743	1915.874297	0.000451244	11	N	350	365
E9Q0K6	Conv	KQAVR	INKEQVSQLLPEK	FAEQL	2		763.4333771	1524.851154	0.000451244	3	N	573	586
E9Q0K6	Conv	ASHNR	FEHSLGVGYLAGCLVR	ALAEK	3	C13:+57.021	593.3070195	1776.897659	0.000451244	11	N	196	212
E9Q0K6	Conv	DVELK	AEDFIVDVINVDYGMEDKNPIDR	VHFYC	3	M15:+15.995	895.0905986	2682.248396	0.000451244	2	N	536	559
E9Q0K6	Conv	KLVMK	NYGLVPEEDITFIK	EQIMG	2		819.4252177	1636.834835	0.001329271	1	N	287	301
E9Q0K6	Conv	RPATK	SFLYEIVSNKR	NGIDV	2		678.3700484	1354.724497	0.002019181	1	N	326	337
E9Q0K6	Conv	WCALR	DFTKPQQCGAGEMAEDPDSIPSTQQPHAAHNQL	-	3	C8:+57.021,M13:+15.995	1207.870882	3620.589245	0.000637154	5	N	618	651
E9Q0K6	Conv	LRYIK	QLGGGYYVFPGASHNR	FEHSL	3		574.9502663	1721.827399	0.000451244	3	N	180	196
E9Q0K6	Conv	VSNKR	NGIDVDKWDYFAR	DCHHL	2		799.8840513	1597.752503	0.000451244	1	N	337	350
E9Q0K6	Conv	AYQHK	ISNLIDIMITDAFLK	ADPYV	2		853.9740211	1705.932442	0.000451244	3	N	420	435
E9Q0K6	Conv	EERKK	MIECIQQLSQSR	IDLMK	2	C4:+57.021	746.866259	1491.716918	0.001871652	1	N	131	143
E9Q0K6	Conv	VRINK	EQVSQLLPEKFAEQLIR	VYCKK	3		676.7095125	2027.105137	0.002212458	3	N	576	593
E9Q397	Conv	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	4		899.4141681	3593.625473	0.000451244	15	N	2079	2112
E9Q397	Conv	ASGEK	VIEGQTDPDYQLLGQR	LEGLD	2		916.4633942	1830.911188	0.000451244	18	N	1126	1142

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q397	Conv	QERPR	DVSSVELLLK	YHQGI	2		551.8218684	1101.628137	0.000451244	11	N	1933	1943
E9Q397	Conv	QKDAK	QAEAILSNQEYTLAHLEPPDSLAAAEAGIR	KFEDF	3		1060.205873	3177.594219	0.000451244	26	N	1178	1208
E9Q397	Conv	VESTK	DLGQDLAGVIAIQR	KLSGL	2		734.9100691	1467.804538	0.000451244	17	N	981	995
E9Q397	Conv	AFRKK	DLQDAENFFQFQGDADDLKAWLQDAHR	LLSGE	3		1065.159034	3192.453703	0.000451244	9	N	737	764
E9Q397	Conv	QLAGR	AQSLLSAGHPEGEQIIR	LQGQV	2		903.4793786	1804.943157	0.000451244	18	N	1646	1663
E9Q397	Conv	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVH	HAATE	3		977.1081167	2928.30095	0.000451244	28	N	2079	2106
E9Q397	Conv	QELVK	AAEIDCQDIEER	LGHLQ	2	C6:+57.021	724.8200281	1447.624456	0.000451244	7	N	1546	1558
E9Q397	Conv	RLNKR	WQAFQAVVSEQR	EAVDS	2		724.8682042	1447.720808	0.000451244	13	N	935	947
E9Q397	Conv	CQFSR	DASVAEAWLIAQEPYLASR	DFGHT	2		1045.531808	2089.048016	0.000451244	18	N	2016	2035
E9Q397	Conv	LNSRK	FANSLSGVQQQLQAFSTYR	TVEKP	2		1073.040332	2144.065063	0.000451244	21	N	329	348
E9Q397	Conv	SIEKR	FLDLLEPLGR	RKKQL	2		586.8378528	1171.660106	0.000979378	4	N	1459	1469
E9Q397	Conv	QDAHR	LLSGEDVGQDEGATR	ALGKK	2		773.8713379	1545.727076	0.000451244	5	N	764	779
E9Q397	Conv	CAGRR	AQLVDTADKFR	FFSMV	2		632.3387483	1262.661897	0.000637154	4	N	1896	1907
E9Q397	Conv	IGQER	VDNVNTIIER	LIDAG	2		586.8176487	1171.619697	0.000451244	10	N	1746	1756
E9Q397	Conv	LQALR	KLYQQVLTQAELR	GHKLQ	2		795.4546438	1588.893688	0.000451244	15	N	827	840
E9Q397	Conv	GDKVK	AITAATLQFAEGK	GYQPC	2		660.8620562	1319.708512	0.000451244	11	N	585	598
E9Q397	Conv	AEFGK	HLLEVEDLLQK	HKLME	2		668.8777063	1335.739813	0.000735798	5	N	558	569
E9Q397	Conv	MWESR	GNTLTQCLGFQEFQK	DAKQA	2	C7:+57.021	885.9279016	1769.840203	0.000451244	14	N	1160	1175
E9Q397	Conv	TIILR	FQIQDIVVQTQEGR	ETRSA	2		830.9368152	1659.85803	0.000451244	13	N	156	170
E9Q397	Conv	TAFER	ELHLLGVQVQQFQDVATR	LQTAY	2		1041.061067	2080.106534	0.000451244	19	N	1843	1861
E9Q397	Conv	NENQR	LVTQDNFGYDLAAVEAAK	KKHEA	2		962.9867022	1923.957804	0.000451244	16	N	443	461
E9Q397	Conv	VLNSR	KFANSLSGVQQQLQAFSTYR	TVEKP	2		1137.087813	2272.160027	0.000451244	16	N	328	348
E9Q397	Conv	LDYGK	DLTSVLILQR	KHKAF	2		579.3485847	1156.681569	0.000622848	12	N	667	677
E9Q397	Conv	KNNEK	AQEATVLLKDNLELQNFLQNCK	ELTLW	2	C21:+57.021	1295.170986	2588.326372	0.000451244	9	N	1262	1284
E9Q397	Conv	NTRAK	NFSTCLELGESLLQR	QHQAS	2	C5:+57.021	883.941009	1765.866418	0.000451244	19	N	1957	1972
E9Q397	Conv	WIKEK	EQIYSSLDYGKDLTSVLILQR	KHKAF	2		1221.150276	2440.284953	0.000451244	7	N	656	677
E9Q397	Conv	AIQSK	EQEVSAAWQALLDACAGR	RAQLV	2	C15:+57.021	987.9708292	1973.926058	0.000451244	16	N	1877	1895
E9Q397	Conv	KFQEK	GNLEVLLFTIQSR	MRANN	2		745.4228124	1488.830025	0.000451244	17	N	359	372
E9Q397	Conv	KMIEK	YSGLASDLLTWIEQTISVLNSR	KFANS	2		1233.647901	2465.280202	0.000451244	7	N	306	328
E9Q397	Conv	DSNAR	HNLEHAFDVAER	QLGII	2		719.347636	1436.679672	0.000451244	1	N	231	243
E9Q397	Conv	EDQLR	SDDLGKDLTTVNR	MLAKL	2		717.3656914	1432.715783	0.000451244	7	N	1403	1416
E9Q397	Conv	WIKEK	EQIYSSLDYGK	DLTSV	2		651.8147717	1301.613943	0.000622848	4	N	656	667
E9Q397	Conv	EALHK	LWEELQSTAK	AKAEQ	2		602.8145747	1203.613549	0.000451244	6	N	1359	1369
E9Q397	Conv	TIIER	LIDAGHSEAATIAEWK	DGLND	2		856.4366481	1710.857696	0.000451244	12	N	1756	1772
E9Q397	Conv	SDINR	AWESLEEAEYQR	ELALR	2		755.8445918	1509.673584	0.000735798	6	N	394	406
E9Q397	Conv	EKLWK	GLQDALQGQELSLGEASK	LQAFL	2		922.4739589	1842.932318	0.000451244	27	N	1044	1062
E9Q397	Conv	LQISR	DLEDETLWVEER	LPLAQ	2		767.357532	1532.699464	0.000451244	10	N	1485	1497
E9Q397	Conv	AFRKK	DLQDAENFFQFQGDADDLK	AWLQD	2		1108.493077	2214.970554	0.000451244	14	N	737	756
E9Q397	Conv	DNILR	LWSYLQELLR	SRRQR	2		660.8696843	1319.723769	0.000451244	9	N	508	518
E9Q397	Conv	LFMKK	NQTLQNEILGHAPR	VEDVL	2		795.9214995	1589.827399	0.000451244	12	N	1519	1533
E9Q397	Conv	QALRK	LYQQVLTQAELR	GHKLQ	2		731.4071623	1460.798725	0.000451244	5	N	828	840
E9Q397	Conv	FQLKR	EADDLEQWITEK	EMVAS	2		738.8468001	1475.678	0.000451244	8	N	1697	1709
E9Q397	Conv	TVLLK	DNLELQNFLQNCK	ELTLW	2	C12:+57.021	818.3936946	1634.771789	0.000451244	16	N	1271	1284
E9Q397	Conv	YDLHR	YFYTGTEILGLIDEK	HRELP	2		881.4514325	1760.887265	0.000451244	11	N	1801	1816
E9Q397	Conv	ALGKK	HKEFLEELEESR	GVMEH	2		773.3813415	1544.747083	0.001871652	1	N	784	796
E9Q397	Conv	WCQMK	TAGYPHVNVTNFTSSWK	DGLAF	3		636.9800027	1907.916608	0.000451244	8	N	186	203
E9Q397	Conv	DVAER	QLGIIPLLDPEDVFTENPDEK	SIITY	2		1191.60791	2381.20022	0.001162105	1	N	243	264
E9Q397	Conv	WINDK	LLTSPDVSYDEAR	NLHNK	2		733.3626174	1464.709635	0.000451244	7	N	1293	1306
E9Q397	Conv	GEASK	LQAFLQDLDDFKAWLSMAQK	AVASE	3		790.0722339	2367.193302	0.001162105	1	N	1062	1082
E9Q397	Conv	LIDEK	HRELPEDVGLDASTAESFHR	VHTAF	3		756.0336064	2265.077419	0.000451244	8	N	1816	1836
E9Q397	Conv	RMLIK	LLEVLSGEMLPRPTK	GKMRI	3	M9:+15.995	566.9873585	1697.938676	0.000451244	6	N	90	105
E9Q397	Conv	LLGQR	LEGLDTDWDALRR	MWESR	2		780.3947832	1558.773966	0.002884417	1	N	1142	1155
E9Q397	Conv	DQEMK	TLMAQIDGVNLAANNLVESGHPR	SGEVK	3	M3:+15.995	812.74873	2435.22279	0.0007646	2	N	898	921
E9Q397	Conv	LQNCK	ELTLWINDK	LLTSP	2		566.3063854	1130.597171	0.001839721	3	N	1284	1293
E9Q397	Conv	AIQSK	EQEVSAAWQALLDACAGRR	AQLVD	3	C15:+57.021	711.0168565	2130.027169	0.000451244	6	N	1877	1896
E9Q397	Conv	TEKGK	WLDQMDIPNTLEDLEVVQHR	FDILD	3	M5:+15.995	823.0694691	2466.185007	0.000451244	5	N	869	889
E9Q397	Conv	WVEER	LPLAQSADYGTNLQTVQLFMK	KNQTL	2		1169.609733	2337.203866	0.000451244	5	N	1497	1518
E9Q397	Conv	FSMVR	DLLSWMESIIR	QIETQ	2		681.8584598	1361.70132	0.000451244	14	N	1913	1924
E9Q397	Conv	KMIEK	YSGLASDLLTWIEQTISVLNSRK	FANSL	3		865.4661882	2593.375165	0.0025889	1	N	306	329
E9Q397	Conv	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHH	AATER	4		767.3477655	3065.359862	0.001162105	2	N	2079	2107
E9Q397	Conv	QLFMK	KNQTLQNEILGHAPR	VEDVL	3		573.6485874	1717.922362	0.000451244	4	N	1518	1533
E9Q397	Conv	MDKTK	VVESTKDLGQDLAGVIAIQR	KLSGL	2		1056.587115	2111.15863	0.000735798	1	N	975	995
E9Q397	Conv	DIEER	LGHLQSSWDTLR	EAAAG	3		471.5814028	1411.720808	0.000451244	3	N	1558	1570
E9Q397	Conv	SWAER	FAALEKPTTLELK	ERQTP	3		487.6173426	1459.828628	0.000451244	3	N	2064	2077
E9Q397	Conv	NNRDK	ILSPVDSGNKLVAEGNLYSNK	IMEKV	2		1109.589855	2217.164109	0.000823681	1	N	1223	1244

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q397	Conv	DAHLK	QIFQEADDMVAQK	QFGHP	2		761.8644705	1521.713341	0.000622848	2	N	694	707
E9Q397	Conv	LKERQ	TPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	4		867.3995237	3465.566895	0.002663018	1	N	2080	2112
E9Q586	Conv	ALKER	VDELTTDLEILKAEIEEK	GSDGA	3		696.7039813	2087.088544	0.00091018	3	N	294	312
E9Q586	Conv	VGRLR	AFLQGGQEATDIALLLR	DLETS	2		908.5023224	1814.989045	0.002374549	1	N	731	748
E9Q586	Conv	RPGLR	GAAGEQLSFAAGLVYSLSLLQATLHR	YEHAL	3		891.8173324	2672.428597	0.001162105	1	N	606	632
E9Q604	Conv	NPLTK	KPWFVKPAESSSSSEGHGALK	STTWN	3		743.7153262	2228.122578	0.000451244	10	N	841	862
E9Q604	Conv	EMTSK	VIQHQYQFNNLGQR	SLPVS	2		872.9480486	1743.880497	0.000451244	15	N	951	965
E9Q604	Conv	KKVAR	SVFACQEQVLK	NKDAG	2	C5:+57.021	654.8347528	1307.653906	0.000451244	47	N	634	645
E9Q604	Conv	SVTLR	NDGEDSYGTQVTVYYPSGLSYRK	DSASQ	3		867.0702745	2598.187423	0.001162105	1	N	808	831
E9Q604	Conv	NTKDR	LREGDIQSTVTYDLALDPGR	SRIRA	3		740.3821242	2218.122972	0.000451244	11	N	665	685
E9Q604	Conv	QENAK	GFGQSVVQLGGTSVVVAAPQEAK	AVNQT	2		1115.097847	2228.180093	0.000451244	33	N	32	55
E9Q604	Conv	SVTLR	NDGEDSYGTQVTVYYPSGLSYR	KDSAS	2		1236.05403	2470.09246	0.000451244	24	N	808	830
E9Q604	Conv	SHSQR	IIGAHFSPGLQYFGQSLSGGK	DLTMD	2		1082.563443	2163.111285	0.000451244	13	N	571	592
E9Q604	Conv	KDRLR	EGDIQSTVTYDLALDPGR	SRIRA	2		975.4766986	1948.937797	0.000622848	16	N	667	685
E9Q604	Conv	KPQSR	RELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1294.992731	3881.954793	0.000451244	21	N	297	331
E9Q604	Conv	MDAQR	FFTAMFPFEK	NCGND	2	M5:+15.995	640.8052073	1279.594815	0.000451244	8	N	759	769
E9Q604	Conv	ELPVK	YAIYMIVTSDESSIR	YLNFT	2		874.4327174	1746.849835	0.000451244	5	N	924	939
E9Q604	Conv	PQSRR	ELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1242.959027	3725.853682	0.000451244	18	N	298	331
E9Q604	Conv	CETLK	LILPDCVDDSVSPIILR	LNYTL	2	C6:+57.021	963.0245418	1924.033484	0.000451244	29	N	716	733
E9Q604	Conv	PEALR	ECPQQESDIVFLIDGSGSINNIDFQK	MKEFV	2	C2:+57.021	1477.198126	2952.380652	0.000451244	20	N	142	168
E9Q604	Conv	HQNCK	ENTYVNGLCYLFGSNLLRPPQQFPEALR	ECPQQ	3	C9:+57.021	1099.555917	3295.644352	0.000451244	26	N	114	142
E9Q604	Conv	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	2	C3:+57.021	1023.971498	2045.927396	0.000451244	11	N	503	520
E9Q604	Conv	HTSIK	GSQIGSYFGASLCSVDMDADGNTNLILIGAPHYYEK	TRGGQ	3	C13:+57.021	1288.601592	3862.781377	0.000451244	5	N	449	485
E9Q604	Conv	YEKTR	GGQVSVCPLPR	GQRAR	2	C7:+57.021	585.3087052	1168.60181	0.000451244	3	N	487	498
E9Q604	Conv	ALCHG	FNLDTEHPMTFQENAK	GFGQS	2	M9:+15.995	969.4391051	1936.86261	0.000451244	8	N	16	32
E9Q604	Conv	TDGEK	FGDPLDYKDVIPEADR	AGVIR	2		925.4524952	1848.88939	0.000451244	8	N	261	277
E9Q604	Conv	VNGDK	LTDVAIGAPGEQENQGAVYIFYGASIASLSASHSQR	IIGAH	3		1236.615372	3706.822716	0.000451244	14	N	535	571
E9Q604	Conv	AGVIR	YVIGVGNAFNKPQSR	RELDT	2		825.4420678	1648.868536	0.000451244	15	N	282	297
E9Q604	Conv	GEPLR	SFGNLRPVLAMDAQR	FFTAM	3	M11:+15.995	564.2951855	1689.862156	0.000451244	19	N	744	759
E9Q604	Conv	INTTR	VDSDMNDAYLGYASAVILR	NRVQS	2	M5:+15.995	1044.999527	2087.983454	0.000451244	18	N	394	413
E9Q604	Conv	LSGGK	DLTMDGLMDLAVGAQGHLLLLR	AQPVL	2	M4:+15.995,M8:+15.995	1192.619861	2383.224122	0.000823681	2	N	592	614
E9Q604	Conv	LKLIL	PDCVDDSVSPIILR	LNYTL	2	C3:+57.021	793.3984456	1584.781291	0.000451244	1	N	719	733
E9Q604	Conv	VVMFR	ENFGTWEPHTSIK	GSQIG	2		773.3707768	1544.725954	0.000451244	16	N	436	449
E9Q604	Conv	HPWGR	FGAALTVLGDVNGDK	LTDVA	2		738.8888023	1475.762005	0.000823681	1	N	520	535
E9Q604	Conv	SDEFR	IHFTFNDFKR	NPSPR	3		442.2319339	1323.672402	0.002727428	4	N	197	207
E9Q604	Conv	FKKSK	TLFSLMQYSDEFR	IHFTF	2		818.8879456	1635.760291	0.000451244	4	N	184	197
E9Q6U4	Conv	ATMKK	AAAEDVNVTFEDQQK	INKFA	2		832.8922704	1663.768941	0.000451244	10	N	7	22
E9Q6U4	Conv	EDAKK	TLQEEIDALESR	VASIQ	2		702.3547923	1402.693985	0.000823681	3	N	88	100
E9QNN1	Conv	TGCGK	TTQVPQYILDDFIQNDR	AAECN	2		1033.513615	2065.011631	0.000451244	11	N	420	437
E9QNN1	Conv	EIHER	DINTDFLLVVLR	DVVLA	2		709.4066309	1416.797662	0.000451244	11	N	519	531
E9QNN1	Conv	FASKK	VQSDGQIVFIDDWIR	LQISH	2		895.9577477	1789.899895	0.002212458	1	N	1077	1092
E9QNN1	Conv	EHTLR	ELDALDANDELTPLGR	ILAKL	2		871.4343024	1740.853005	0.000451244	6	N	840	856
E9QNN1	Conv	QFLAK	AIEPPPLDAVIEAEHTLR	ELDAL	3		657.6902294	1970.047288	0.001839721	1	N	822	840
E9QPU1	Conv	GKIVK	IPGTCCDTCEEPDCKDITAK	VQYIK	2	C5:+57.021,C6:+57.021,C9:+57.021,C14:+57.021	1185.489057	2368.962514	0.002296037	1	N	2713	2733
E9QPU1	Conv	VVGLR	VVQCSQRPCEDSCQPGFSYVLHEGECCGR	CLPSA	3	C4:+57.021,C9:+57.021,C13:+57.021,C26:+57.021,C27:+57.021	1167.821177	3500.440131	0.000451244	17	N	2467	2496
E9QPU1	Conv	KCASK	AVYSIDIEDVQEQCSCCLPSR	TEPMR	2	C14:+57.021,C16:+57.021,C17:+57.021	1265.056184	2528.096768	0.000451244	13	N	2760	2781
E9QPU1	Conv	CPPGR	ILDELLQTCVDPQDCPVCEVAGRR	LAPGK	3	C9:+57.021,C15:+57.021,C18:+57.021	948.4543976	2842.339793	0.000451244	12	N	1184	1208
E9QPU1	Conv	AFISK	ANIGPHLTQVSVIQYGSINTIDVPWNVVQEK	AHLQS	3		1140.603967	3418.788502	0.000451244	19	N	1723	1754
E9QPU1	Conv	FDGLK	YLFPGECQYVLVQDYCGSNPGTFQILVGNEGCSYPSVK	CRKRV	3	C7:+57.021,C16:+57.021,C32:+57.021	1449.334209	4344.979227	0.000451244	14	N	885	923
E9QPU1	Conv	SEVLK	YTLFQIFGK	IDRPE	2		558.808564	1115.601528	0.000451244	14	N	1365	1374
E9QPU1	Conv	DSACR	ILTSDVFQGCNR	LVDPE	2	C10:+57.021	705.346016	1408.676432	0.000451244	10	N	1064	1076
E9QPU1	Conv	ALCEK	ILCTCATGPECACPVLLEYAR	TCAQE	2	C3:+57.021,C5:+57.021,C11:+57.021,C13:+57.021	1227.567445	2453.119289	0.000622848	1	N	255	276
E9QPU1	Conv	VYSGK	TCGLCGNYNGNKGDDFLTPAGLVEPLVVDFGNAWK	LQGDC	3	C2:+57.021,C5:+57.021	1266.934751	3797.780854	0.000622848	11	N	522	557
E9QPU1	Conv	AECHK	VIAPATFHTICQQDSCHQER	VCEVI	3	C11:+57.021,C16:+57.021	800.0392897	2397.094469	0.000451244	3	N	2155	2175
E9QPU1	Conv	PRLTR	FAEEACALLTSSK	FEACH	2	C6:+57.021	713.8480572	1425.680514	0.000451244	8	N	581	594
E9QPU1	Conv	QGGNR	TNTGQALQYLSEHSFSPSQGDR	VEAPN	2		1212.065264	2422.114927	0.001229886	1	N	1578	1600
E9QPU1	Conv	SVGSR	WAVPENPCLVNECVR	VEDAV	2	C8:+57.021,C13:+57.021	921.9349724	1841.854345	0.000451244	17	N	2523	2538
E9QPU1	Conv	MYEVR	FTHLGHILTYTPQNNEFQLQLSPK	TFASK	3		942.824487	2825.450061	0.000451244	7	N	2054	2078
E9QPU1	Conv	APENK	AFLLSGVDELEQR	RDEIV	2		738.8888023	1475.762005	0.000451244	5	N	1439	1452

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9QPU1	Conv	LVKLK	HGGAVGIDGQDVQLPFLQGDLR	IQHTV	2		1146.59072	2291.16584	0.000622848	4	N	462	484
E9QPU1	Conv	CPPGR	ILDELLQTCVDPQDCPVCEVAGR	RLAPG	2	C9:+57.021,C15:+57.021,C18:+57.021	1344.127141	2686.238682	0.000451244	17	N	1184	1207
E9QPU1	Conv	YNGNK	GDDFLTPAGLVEPLVVDFGNAWK	LQGDC	2		1230.626437	2459.237274	0.000451244	16	N	534	557
E9QPU1	Conv	IMTLK	QDETFQDGCDSHLCR	VNERG	2	C9:+57.021,C14:+57.021	934.3703906	1866.725181	0.000451244	1	N	2665	2680
E9QPU1	Conv	EAQLR	ILAGPGASSNVVK	LQQVE	2		606.8514915	1211.687383	0.001943752	2	N	1840	1853
E9QPU1	Conv	VALER	CPCFHQGAEYAPGDTVK	IGCNT	2	C1:+57.021,C3:+57.021	968.9195193	1935.823439	0.002019181	1	N	829	846
E9QPU1	Conv	TCGCR	WTCPCVCTGSSTR	HIVTF	2	C3:+57.021,C5:+57.021,C7:+57.02	786.3234378	1570.631276	0.000735798	4	N	1946	1959
E9QPU1	Conv	NECVR	VEDAVFVQQR	NISCP	2		595.8123663	1189.609133	0.001591523	1	N	2538	2548
E9QPU1	Conv	VCVHR	GTVYPVGQFWEEGCDTCTCTDMEDTVVGLR	VVQCS	3	C14:+57.021,C17:+57.021,C19:+57.021,M22:+15.995	1166.824696	3497.450688	0.000451244	13	N	2437	2467
E9QPU1	Conv	TSQIK	YTGSQVASTSEVLK	YTLFQ	2		735.3782675	1468.740935	0.000451244	14	N	1351	1365
E9QPU1	Conv	CSDSR	DCLCNAVANYAAECAR	KGVHI	2	C2:+57.021,C4:+57.021,C14:+57.021	929.3872977	1856.758995	0.000451244	7	N	622	638
E9QPU1	Conv	SPCPR	TCQSLSINEVCQQQCVDGCSCPEGELLDEDR	CVQSS	3	C2:+57.021,C11:+57.021,C15:+57.021,C19:+57.021,C21:+57.021	1229.508993	3685.503579	0.000451244	13	N	313	344
E9QPU1	Conv	NLTCR	SLSLPDEECSEVCLEGCYCPPGLYQDER	GDCVP	3	C9:+57.021,C13:+57.021,C17:+57.021,C19:+57.021	1121.469959	3361.386476	0.000451244	8	N	673	701
E9QPU1	Conv	KCRKR	VTILVDGGELELFDGEVNVK	RPLRD	2		1073.568056	2145.120513	0.000451244	6	N	927	947
E9QPU1	Conv	TCICR	NSLWICSNEECPGECLVTGQSHFK	SFDNR	2	C6:+57.021,C11:+57.021,C15:+57.021	1426.625297	2851.234993	0.000622848	4	N	376	400
E9QPU1	Conv	ETLPR	EAPDLVLQTCCSK	EGLQL	2	C10:+57.021,C11:+57.021	760.8578677	1519.700135	0.000622848	7	N	1662	1675
E9QPU1	Conv	CHQER	VCEVIASYAHLCR	TSGVC	2	C2:+57.021,C12:+57.021	789.3818443	1576.748089	0.001763695	1	N	2175	2188
E9QPU1	Conv	ARSNR	VAVFPVGVGDRYDEAQLR	ILAGP	2		996.0214107	1990.027221	0.000622848	3	N	1822	1840
E9QPU1	Conv	SVFAR	CHPLVDPESFVALCEK	ILCTC	2	C1:+39.994,C14:+57.021	942.4367882	1882.857976	0.000451244	6	N	239	255
E9QPU1	Conv	HCPPG	RILDELLQTCVDPQDCPVCEVAGR	RLAPG	3	C10:+57.021,C16:+57.021,C19:+57.021	948.4543976	2842.339793	0.000451244	5	N	1183	1207
E9QPU1	Conv	HAGKR	YPPGTSLSQDCNTCICR	NSLWI	2	C11:+57.021,C14:+57.021,C16:+57.021	1014.932069	2027.848539	0.000451244	19	N	359	376
E9QPU1	Conv	EDDFR	TQEGTLTSDPYDFANSWALSSEEQR	CKRAS	2		1416.633904	2831.252209	0.000451244	14	N	177	202
E9QPU1	Conv	VHAGK	RYPPGTSLSQDCNTCICR	NSLWI	3	C12:+57.021,C15:+57.021,C17:+57.021	728.9910167	2183.94965	0.000451244	19	N	358	376
E9QPU1	Conv	NLTCR	SLSLPDEECSEVCLEGCYCPPGLYQDERGDCVPK	AQCPC	3	C9:+57.021,C13:+57.021,C17:+57.021,C19:+57.021,C31:+57.021	1340.23487	4017.68121	0.000451244	10	N	673	707
E9QPU1	Conv	LQNCR	YDVCSCSDSRDCLCNAVANYAAECAR	KGVHI	3	C4:+57.021,C6:+57.021,C12:+57.021,C14:+57.021,C24:+57.021	1029.741864	3086.202192	0.000451244	5	N	612	638
E9QPU1	Conv	VVQEK	AHLQSLVDLMQQEGGPSQIGDALAFAVR	YVTSQ	3		984.5068296	2950.497089	0.000451244	3	N	1754	1782
E9QPU1	Conv	DFTTS	SLQVEEDPVNFGNSWK	VSSQC	2		924.9422946	1847.868989	0.000451244	5	N	1013	1029
E9QPU1	Conv	DFNIF	AEDDFRTQEGTLTSDPYDFANSWALSSEEQR	CKRAS	3		1189.192909	3564.555327	0.000451244	1	N	171	202
F6RPJ9	Conv	KLPTK	NEFIPTNFEILSLEK	DATPY	2		897.4701566	1792.924713	0.001162105	5	N	495	510
F6RPJ9	Conv	IKDIR	NLYVTFPIPDLQQYYK	SNPGH	2		1001.520181	2001.024762	0.000823681	2	N	279	295
F6RPJ9	Conv	GALDR	FAQFFLCPLFDASCK	DREVN	2	C7:+57.021,C14:+57.021	925.9339097	1849.852219	0.000451244	4	N	132	147
F6RPJ9	Conv	GALDR	FAQFFLCPLFDASCKDR	EVNAV	3	C7:+57.021,C14:+57.021	708.0012246	2120.980274	0.002813207	1	N	132	149
F6ZDS4	Conv	SELKK	TLSTVQNEVQEALQR	ASTAL	2		858.4502868	1714.884974	0.001329271	2	N	1112	1127
F6ZDS4	Conv	IRDEE	VSSADISSSSEVISQHLVSYR	NIEEL	4		563.5360004	2250.112802	0.001763695	2	N	594	615
F8VPN4	Conv	TLQGK	AVTVYTNYPLPGEAFNR	EKFRS	2		956.4841296	1910.952659	0.001162105	2	N	42	59
F8VPN4	Conv	SIASK	LTLAELNQVLYR	CESEE	2		716.9120805	1431.808561	0.000622848	1	N	898	910
F8WI35	Conv	FKTDL	RFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1155.59292	3463.755359	0.000451244	21	N	83	115
F8WI35	Conv	SAAIG	ALQASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C19:+57.021	1317.665536	2633.315473	0.00091018	2	N	91	115
F8WI35	Conv	AAIGA	LQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C18:+57.021	855.1005862	2562.278359	0.001463592	2	N	92	115
F8WI35	Conv	DFKTD	LRFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C28:+57.021	895.2176559	3576.839423	0.00307782	2	N	82	115
F8WI35	Conv	KTDLR	FQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C26:+57.021	827.9213621	3307.654248	0.000451244	6	N	84	115
G3UWD6	Conv	GPIWN	GDNIACVILTFK	EPFGT	2	C6:+57.021	675.858228	1349.700856	0.000451244	4	N	226	238
G3UWD6	Conv	GPIWN	GDNIACVILTFKEPFGTEGR	GGYFD	2	C6:+57.021	1112.557269	2223.098938	0.000451244	7	N	226	246
G3X8U3	Conv	AAVNR	ALDQGIPITSASYYATVSLEQVR	DIFRS	2		1241.645358	2481.275116	0.000451244	2	N	106	129
G3X8U3	Conv	EGVRR	AAELLLPAAAAWR	VEQWK	2		676.8884083	1351.761217	0.002453667	1	N	30	43
G3X972	Conv	QTLAK	ECVAQGCCVDLFLFPNQYVDVATLSVVPQLTGGSVYK	YACFQ	3	C2:+57.021,C7:+57.021,C8:+57.02	1378.672274	4132.993421	0.001162105	1	N	687	724
G3X972	Conv	VKTVR	DTLITQCAQILACYR	KNCAS	2	C7:+57.021,C13:+57.021	913.4504553	1824.885311	0.001264573	1	N	870	885
G5E8K5	Conv	ETVKK	ILGNKATFSPIVTVEPR	RRKFH	2		921.5283402	1841.04108	0.001871652	1	N	1192	1209
G5E8K5	Conv	AIARR	LGYISVVDTLK	VVTEE	2		604.350793	1206.685986	0.002080925	2	N	788	799
O08553	Conv	EEQQR	ILDLGITGPEGHVLSRPEEVEAEAVNR	SITIA	3		967.5091158	2899.503947	0.000451244	2	N	211	238
O08553	Conv	RGVPR	GLYDGPVCEVSVTPK	TVTPA	2	C8:+57.021	810.9008212	1619.786042	0.000823681	1	N	496	511
O08582	Conv	DLTSK	LVLVSPTSEQYDSLLR	QMWER	2		910.494163	1818.972726	0.000823681	2	N	64	80
O08582	Conv	RGLIK	LNDTLLLGPDPLGNFLSIAVK	SIHRK	2		1105.625709	2209.235817	0.000451244	4	N	422	443
O08583	Conv	GRNSK	QQLSAEELDAQLDAYNAR	MDTS-	2		1017.990505	2033.965409	0.000451244	8	N	233	251

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O08583	Conv	ETGGK	LLVSNLDFGVSDADIQELFAEFGTLKK	AAVHY	3		990.5222509	2968.543353	0.000451244	14	N	106	133
O08583	Conv	DRSGR	SLGTADVHFER	KADAL	3		411.2075654	1230.599296	0.002727428	2	N	143	154
O08585	Conv	LIGYV	AAEEAFVNDIDESSPGTEWER	VARLC	2		1176.51728	2351.018961	0.000451244	17	N	179	200
O08663	Conv	HISGR	IIDCAFTVTFNPK	YDILL	2	C4:+57.021	763.3898923	1524.764185	0.000451244	7	N	259	272
O08663	Conv	KKKGK	GAVSAVQQELDKESGALVDEVAK	QLESQ	3		781.7399772	2342.196531	0.000451244	10	N	46	69
O08691	Conv	GCHLK	DFGDLSFTNVPQDDPYNNLVVYPR	SVGLA	3		929.1088407	2784.303122	0.001329271	1	N	66	90
O08692	Conv	DVSEK	EKFEDVPPHIR	NIYED	3		456.2424986	1365.704096	0.000451244	19	N	138	149
O08692	Conv	STQER	QPKDCDFLEDGEER	NCTGK	2	C5:+57.021	869.3731562	1736.730712	0.000622848	5	N	82	96
O08692	Conv	ERQPK	DCDFLEDGEERNCTGK	FFRRR	2	C2:+57.021,C13:+57.021	972.8886132	1943.761626	0.000451244	65	N	85	101
O08692	Conv	FFRRR	QSTSLTLTCDRDCSR	EDTQE	2	C9:+57.021,C13:+57.021	900.4042334	1798.792867	0.000451244	9	N	106	121
O08692	Conv	ERQPK	DCDFLEDGEER	NCTGK	2	C2:+57.021	692.7700038	1383.524408	0.000451244	106	N	85	96
O08692	Conv	LFRLL	SATPPSSQNPATNIPLQFR	IKETE	2		1013.521775	2025.02795	0.000451244	28	N	51	70
O08692	Conv	FRLLS	ATPPSSQNPATNIPLQFR	IKETE	2		970.0057606	1937.995921	0.000870037	1	N	52	70
O08692	Conv	RPLFR	LLSATPPSSQNPATNIPLQFR	IKETE	2		1126.605839	2251.196078	0.000451244	305	N	49	70
O08692	Conv	LLSAT	PPSSQNPATNIPLQFR	IKETE	2		883.9633644	1765.911129	0.000451244	5	N	54	70
O08692	Conv	YEDAK	YDIIGNILK	NF-	2		524.8060213	1047.596443	0.000451244	27	N	156	165
O08692	Conv	PPHIR	NIYEDAKYDIIGNILK	NF-	2		941.5019881	1880.988376	0.000451244	17	N	149	165
O08692	Conv	PPHIR	NIYEDAKYDIIGNIL	KNF-	2		877.4545065	1752.893413	0.001162105	2	N	149	164
O08692	Conv	KFFRR	RQSTSLTLTCDR	DCSRE	3	C10:+57.021	479.9090365	1436.70371	0.000823681	1	N	105	117
O08692	Conv	FFRRR	QSTSLTLTCDR	DCSRE	2	C9:+57.021	641.3090992	1280.602598	0.000451244	10	N	106	117
O08692	Conv	PLQFR	IKETECTSTQER	QPKDC	3	C6:+57.021	494.5685685	1480.682305	0.000622848	2	N	70	82
O08692	Conv	RLLSA	TPPSSQNPATNIPLQFR	IKETE	2		934.4872037	1866.958807	0.001329271	1	N	53	70
O08692	Conv	PPSSQ	NPATNIPLQFR	IKETE	2		635.8492831	1269.682966	0.001162105	1	N	59	70
O08709	Conv	FSHPR	DFTPVCTTELGR	AAKLA	2	C6:+57.021	698.3325743	1394.649549	0.000451244	6	N	41	53
O08709	Conv	DEILR	VVDSLQLTGTKPVATPVDWK	KGESV	2		1077.594409	2153.173217	0.000451244	11	N	162	182
O08709	Conv	-M	PGGLLLGDEAPNFEANTTIGR	IRFHD	2		1071.545447	2141.075294	0.000451244	13	N	1	22
O08709	Conv	KRNVK	LIALSIDSVEDHLAWSK	DINAY	2		949.0074376	1895.999275	0.000451244	11	N	67	84
O08709	Conv	IGRIR	FHDFLGDSWGILFSHPR	DFTPV	3		677.667759	2029.979877	0.000451244	20	N	24	41
O08709	Conv	LAWSK	DINAYNGETPTEK	LPFPI	2		726.3365996	1450.657599	0.000451244	2	N	84	97
O08709	Conv	LAWSK	DINAYNGETPTEKLPFPIIDDK	GRDLA	3		830.7519942	2489.232583	0.00091018	2	N	84	106
O08738	Conv	AYDAK	IEIQTLTGLFK	GDKCQ	2		631.8718926	1261.728185	0.002145581	1	N	116	127
O08749	Conv	PLRTY	ADQPIEADVTVIGSGPGGYVAAIK	SAQLG	2		1164.608244	2327.200889	0.000451244	17	N	35	59
O08749	Conv	SEAFR	EANLAAAFGKPINF	-	2		731.8886053	1461.761611	0.000451244	13	N	495	509
O08749	Conv	QLGFK	TVCIEKNETLGGTCLNVGCIPSK	ALLNN	3	C3:+57.021,C14:+57.021,C19:+57.021	850.7502628	2549.227388	0.000662267	2	N	66	89
O08749	Conv	VCIGR	RPFTQNLGLEELGIELDPK	GRIPV	2		1085.081665	2168.147731	0.000823681	2	N	315	334
O08749	Conv	EDIAR	VCHAHPTLSEAFR	EANLA	3	C2:+57.021	508.9177549	1523.729865	0.000823681	3	N	482	495
O08749	Conv	VCIEK	NETLGGTCLNVGCIPSK	ALLNN	2	C8:+57.021,C13:+57.021	910.4375449	1818.85949	0.000451244	5	N	72	89
O08749	Conv	AWVGK	SEEQLKEEGIEFK	IGKFP	3		522.5951548	1564.762064	0.000823681	3	N	404	417
O08749	Conv	SVWQR	LGADVTAVEFLGHVGGIGIDMEISK	NFQRI	3	M21:+15.995	848.7725412	2543.294224	0.000451244	5	N	234	259
O08795	Conv	ILSSR	VNDGVCDCCDGTDEYNSGTVCENTCR	EKGRK	3	C6:+57.021,C8:+57.021,C9:+57.021,C21:+57.021,C25:+57.021	1019.705256	3056.092367	0.000451244	8	N	91	117
O08795	Conv	MVSLA	ELQTHPELDTDGDGALSEEEAQALLSGDTQTDTTSFYDR	VWAAI	3		1419.302352	4254.883657	0.001463592	1	N	232	271
O08808	Conv	SIALK	VGCLQLINALITPAEELDFR	VHIRS	2	C3:+57.021	1136.604219	2271.192838	0.000451244	22	N	302	322
O08808	Conv	LESLR	VSLNNNPVSWVQTFGAEGLASLLDILKR	LHDEK	3		1014.552656	3040.634568	0.000451244	7	N	160	188
O08808	Conv	NAGSR	NAGAFGFNISFLCK	LRDTK	2	C13:+57.021	773.3798589	1544.744118	0.000451244	1	N	975	989
O08808	Conv	NEDMK	VQLCVFDEQGDEDFFDLK	GRLDD	2	C4:+57.021	1102.496542	2202.977485	0.000622848	5	N	350	368
O08808	Conv	QVNRK	AGCAVTSLLASELTK	DDAMA	2	C3:+57.021	760.9033638	1519.791128	0.000622848	1	N	1207	1222
O08808	Conv	LNTVK	DSKAEPHFLSILQHLLLVR	NDYEA	4		554.8197299	2215.247719	0.000451244	1	N	393	412
O08808	Conv	SELMR	LGLHQVLQELR	EIENE	3		435.9266219	1304.756466	0.002519933	1	N	331	342
O08808	Conv	ETLYK	ELGDYFVFDPK	KLSVE	2		665.3222325	1328.628865	0.001591523	2	N	1099	1110
O08810	Conv	LHHGK	TCFVDCLIEQTHPEIR	KRYDQ	3	C2:+57.021,C6:+57.021	673.3207343	2016.938803	0.000451244	3	N	141	157
O08810	Conv	LYTIK	AFIPAIDSFGFETDLR	THTQG	2		899.9546737	1797.893747	0.000451244	8	N	871	887
O08810	Conv	EPLEK	GLAEDIENEVVQITWNR	KKLGE	3		662.6696054	1984.985416	0.000451244	11	N	693	710
O08810	Conv	SSSQR	SFVEFILEPLYK	ILAQV	2		742.9059325	1483.796265	0.000451244	1	N	366	378
O08810	Conv	GSFAK	IYADTFGDINYQEFAK	RLWGD	2		947.9470456	1893.878491	0.000451244	7	N	324	340
O08810	Conv	LLAAR	SIWAFGPDATGPNILVDDTLPSEVDK	ALLGS	2		1379.185044	2756.354489	0.000622848	6	N	729	755
O08810	Conv	EIDIK	VADPVVTFCETVVETSSLK	CFAET	2	C9:+57.021	1041.027478	2080.039357	0.000451244	2	N	653	672
O08810	Conv	TSVIK	IAVEPVNPSELPK	MLDGL	2		696.8908137	1391.766027	0.001763695	1	N	588	601
O08992	Conv	GLRLK	SIDNGIFVQLVQANSPASLVGLR	FGDQV	2		1199.658603	2397.301606	0.000451244	25	N	131	154
O08992	Conv	VIGLK	DAQIADILSTAGTVVTITIMPTFIFEHIIK	RMAPS	3		1086.928512	3257.762137	0.000451244	7	N	251	281
O08992	Conv	LKVDK	VIQAQTAYSANPASQAFVLVDASAALPPDGNLYPK	LYPEL	3		1196.618054	3586.830761	0.000451244	10	N	14	49
O08992	Conv	LVGLR	FGDQVLQINGENCAGWSSDK	AHKVL	2	C13:+57.021	1113.000315	2223.98503	0.000451244	18	N	154	174
O08992	Conv	KIGLR	LKSIDNGIFVQLVQANSPASLVGLR	FGDQV	3		880.5013443	2638.480633	0.000451244	6	N	129	154
O08992	Conv	LEDLK	VDKVIQAQTAYSANPASQAFVLVDASAALPPDGNLYPK	LYPEL	3		1310.681494	3929.021082	0.002374549	1	N	11	49

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O09043	Conv	RALNK	AIGGYPFLNGQYFIQCSK	TPTLP	2	C16:+57.021	1032.006683	2061.997767	0.000451244	8	N	296	314
O09043	Conv	MESVK	VGTGLSLCAQGCSAILDTGTSLITGPSEEIR	ALNKA	3	C8:+57.021,C12:+57.021	1055.19205	3162.552751	0.000451244	17	N	261	292
O09043	Conv	HLGHR	ILNPLNGWEQLAELSR	TSTSG	2		926.9999469	1851.984294	0.000698008	2	N	36	52
O09061	Conv	GPVQL	RFSPYAFNGGTVLAIAGEDFSIVASDTR	LSEGF	3		987.8300778	2960.466833	0.000451244	10	N	27	55
O09061	Conv	PKCYK	LTDKTVIGCSGFHGDCLTLTK	IIEAR	3	C9:+57.021,C16:+57.021	775.0524247	2322.133874	0.000451244	6	N	72	93
O09061	Conv	LYSRR	FFPYYVYNIIGGLDEEGKGAVYSFDPVGSYQR	DSFKA	3		1217.587983	3649.740549	0.000451244	21	N	127	159
O09061	Conv	DEEGK	GAVYSFDPVGSYQR	DSFKA	2		773.3707768	1544.725954	0.000451244	20	N	145	159
O09061	Conv	ILYSR	RFFPYYVYNIIGGLDEEGK	GAVYS	2		1140.570933	2279.126267	0.000451244	11	N	126	145
O09061	Conv	RFSPY	AFNGGTVLAIAGEDFSIVASDTR	LSEGF	2		1156.082394	2310.149187	0.000451244	3	N	32	55
O09061	Conv	LYSRR	FFPYYVYNIIGGLDEEGK	GAVYS	2		1062.520378	2123.025156	0.000451244	13	N	127	145
O09061	Conv	KLTDK	TVIGCSGFHGDCLTLTK	IIEAR	2	C5:+57.021,C12:+57.021	933.4479126	1864.880225	0.000451244	13	N	76	93
O09061	Conv	PVQLR	FSPYAFNGGTVLAIAGEDFSIVASDTR	LSEGF	2		1403.190661	2804.365722	0.000735798	1	N	28	55
O09061	Conv	MRLVK	DVFISAAERDVYTGDALR	ICIVT	3		666.6696054	1996.985416	0.000451244	2	N	203	221
O09061	Conv	HSNNK	AMTTGAIAAMLSTILYSR	RFFPY	2		935.9924198	1869.96924	0.000451244	3	N	108	126
O09106	Conv	KQMQR	FNVGEDCPVFDGLFEFCQLSTGGSVASAVK	LNKQQ	3	C7:+57.021,C17:+57.021	1079.833974	3236.478523	0.000451244	4	N	93	123
O09126	Conv	FLKAR	LICSKPDSGLVFNILQDVFVLR	APGLK	3	C3:+57.021	845.1334502	2532.376951	0.000451244	8	N	278	300
O09126	Conv	HSPLR	TEYAIPWLNEPSFVFADVIQK	SPDGP	3		823.0901701	2466.24711	0.000451244	2	N	198	219
O09159	Conv	AARHR	LLAEQEVLAPQVVLSLGGSSPYHSR	ATPKT	3		884.1453376	2649.412613	0.000451244	22	N	858	883
O09159	Conv	EELWR	ASDSLEPPAADLFTGVLPNNYNPPK	YLCWD	2		1314.153547	2626.291495	0.000451244	6	N	240	265
O09159	Conv	NDYAR	QLAAGWGPCEVLVSNALAR	LSHYK	2	C9:+57.021	1006.523032	2011.030464	0.000451244	15	N	463	482
O09159	Conv	TLGLR	FLQDTFGSDGLPR	VAWHI	2		726.8600449	1451.70449	0.000451244	11	N	177	190
O09159	Conv	QTSER	FQVTLYNPLGR	KVDQM	2		654.3594837	1306.703367	0.000451244	10	N	509	520
O09159	Conv	YNPPK	YLCWDVLCTDPPVVDNPR	SPEFN	2	C3:+57.021,C8:+57.021	1110.016691	2218.017782	0.000451244	23	N	265	283
O09159	Conv	YKGQR	HLELEWTVGPIPVRDDWGK	EVISR	3		749.7239331	2246.148399	0.000451244	1	N	709	728
O09159	Conv	KVRGR	HLVLLSSVSDAAAR	HRLLA	2		719.9047868	1437.793974	0.001229886	2	N	842	856
O09159	Conv	FSGLR	QELPPQVHLLTLAR	WGPKM	3		538.9829074	1613.925322	0.000451244	3	N	894	908
O09159	Conv	RATPK	TQFSGLRQELPPQVHLLTLAR	WGPKM	3		802.1206866	2403.33866	0.000451244	5	N	887	908
O09159	Conv	YKGQR	HLELEWTVGPIPVR	DDWGK	3		549.307391	1644.898773	0.002296037	3	N	709	723
O09159	Conv	PMEIR	TFLASVQWQE	HRPA-	2		604.8014673	1207.587335	0.002663018	1	N	999	1009
O09172	Conv	DCIQK	TLNEWSSQISPDLVR	EFPDV	2		872.94738	1743.87916	0.000451244	22	N	49	64
O09172	Conv	ALLAR	ASTLHLQTGNLLNWGR	LRKKC	3		594.3204707	1779.938012	0.001699387	2	N	14	30
O35286	Conv	EAKMR	FAHIDGDHLTLLNVYHAFK	QNHES	3		737.7168899	2210.12727	0.00091018	2	N	616	635
O35343	Conv	TAALR	AVGNIVTGTDEQTQVVLNCDALSHFPALLTHPK	EKINK	4	C19:+57.021	887.2072882	3544.797953	0.000451244	2	N	306	339
O35343	Conv	LLTVK	DAQVVQVVLDGLSNILK	MAEDQ	2		906.0178053	1810.020011	0.000451244	14	N	423	440
O35350	Conv	FSEKK	AGTQELDDQIQANLPDEK	VLSEE	2		992.9770628	1983.938526	0.000451244	16	N	517	535
O35350	Conv	FSEKK	AGTQELDDQIQANLPDEKVLSEEEIDDNFK	TLFSK	3		1135.206156	3402.595067	0.000451244	2	N	517	547
O35350	Conv	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	2	C1:+39.994	1273.622915	2545.230229	0.001839721	2	N	48	71
O35350	Conv	KALER	GSLLGCSINISDIRDLEAITFK	NLVRG	3	C6:+57.021	808.0934317	2421.256895	0.000451244	8	N	244	266
O35350	Conv	AGGCR	NYPATFWVNPQFK	IRLEE	2		806.4018799	1610.78816	0.000451244	9	N	385	398
O35350	Conv	DGATR	TDICQGALGDCWLLAAIASLTLNETILHR	VVPYG	3	C4:+57.021,C11:+57.021	1075.884892	3224.631276	0.000451244	15	N	104	133
O35350	Conv	LPDEK	VLSEEEIDDNFK	TLFSK	2		719.3413506	1436.667101	0.000622848	11	N	535	547
O35350	Conv	DGNGK	LGLVEFNILWNR	IRNYL	2		737.4147903	1472.813981	0.000451244	12	N	603	615
O35350	Conv	LIITR	YSEPDLAVDFDNFVCCLVR	LETMF	2	C15:+57.021,C16:+57.021	1160.024713	2318.033826	0.000451244	11	N	661	680
O35350	Conv	REFTK	LEICNLTPDALK	SRTLR	2	C4:+57.021	693.8687927	1385.721985	0.000735798	1	N	347	359
O35350	Conv	KAYAK	VNGSYEALSGGCTSEAFEDFTGGVTEWYDLQK	APSDL	3	C12:+57.021	1173.184432	3516.529895	0.000622848	3	N	197	229
O35350	Conv	SNRIR	LPPGEYIVVPSTFEPNKEGDFLLR	FFSEK	3		906.4782053	2716.411216	0.000451244	2	N	487	511
O35350	Conv	SRTLR	NWNTTFYEGTWR	RGSTA	2		787.8552938	1573.694988	0.000451244	9	N	364	376
O35350	Conv	FFSEK	KAGTQELDDQIQANLPDEK	VLSEE	2		1057.024544	2112.033489	0.002663018	3	N	516	535
O35350	Conv	TKDGK	LVFVHSAQGNEFWSALLEK	AYAKV	3		725.7131455	2174.116036	0.000451244	2	N	174	193
O35381	Conv	LENLK	SLDLFNCEVTNLNAYR	ENVFK	2	C7:+57.021	964.9624728	1927.909346	0.000451244	2	N	116	132
O35381	Conv	SIEGK	IEGLTDEFEELEFLSTINVGLTSISNLPK	LNKLK	3		1070.222418	3207.643855	0.000451244	8	N	33	62
O35459	Conv	QRLPK	VIGNQSLVNELTFSAR	KMMAD	2		874.4710222	1746.926444	0.000451244	10	N	213	229
O35598	Conv	TDCNR	HTQVCINGQCAGSICEK	YDLEE	3	C5:+57.021,C10:+57.021,C15:+57.021	654.6257862	1960.853959	0.000637154	4	N	558	575
O35598	Conv	LKPGK	QCSPSQGPCCTAQCAFK	SKSEK	2	C2:+57.021,C9:+57.021,C10:+57.021,C14:+57.021	993.8994837	1985.783367	0.000451244	10	N	502	519
O35598	Conv	QFSGR	TITLQPGSPCNDFR	GYCDV	2	C10:+57.021	803.3884123	1604.761225	0.001162105	5	N	623	637
O35598	Conv	HVPPK	VSHITFAHEVGHNFGSPHDSGTECTPGESK	NLGQK	4	C24:+57.021	806.1143934	3220.426373	0.000451244	10	N	376	406
O35598	Conv	TLAER	NTCQLYIQTDHLFFK	YYGTR	3	C3:+57.021	643.3175842	1926.929353	0.002453667	1	N	220	235
O35638	Conv	YKHDR	DIALLDLINFFIQCSGCK	GVVTA	2	C14:+57.021,C17:+57.021	1064.034352	2126.053104	0.000451244	2	N	110	128
O35638	Conv	DKFNR	LLEDFLQEGEEPDEDDAYQVLSTLKR	ITAFH	3		1018.159818	3051.456054	0.000451244	4	N	667	693
O35639	Conv	KKSMK	GTGTDEDALIEILTTR	SSRQM	2		852.9366779	1703.857756	0.000451244	17	N	104	120
O35639	Conv	NISQK	DIEDSIKGELSGHFEDLLLAIVHCAR	NTPAF	3	C24:+57.021	979.8310472	2936.469742	0.000451244	5	N	222	248
O35639	Conv	HEFKK	HYGYSLYSAIQSDTSGDYR	TVLLK	2		1091.987962	2181.960324	0.000451244	25	N	293	312
O35639	Conv	GTDEK	TLINILTER	SNAQR	2		536.8222027	1071.628805	0.001763695	4	N	39	48

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O35639	Conv	TVYKK	SLGDDISSETSGDFR	KALLT	2		793.352978	1584.690356	0.000451244	2	N	138	153
O35639	Conv	IMVSR	SEIDLLDIR	HEFKK	2		537.2960177	1072.576435	0.000451244	15	N	279	288
O35639	Conv	EDSIK	GELSGHFEDLLLAIVHCAR	NTPAF	3	C17:+57.021	713.0338475	2136.078142	0.000451244	10	N	229	248
O35639	Conv	KSLGD	DISSETSGDFRK	ALLTL	2		671.3182098	1340.62082	0.000823681	1	N	142	154
O35639	Conv	TVYKK	SLGDDISSETSGDFRK	ALLTL	2		857.4004596	1712.785319	0.000451244	6	N	138	154
O35639	Conv	AGENK	WGTDEDKFTEVLCLR	SFPQL	3	C13:+57.021	623.6334609	1867.876983	0.000451244	17	N	189	204
O35643	Conv	PAPAR	LGAPISSGLSDLFDLTSGVGTLSGSYVAPK	AVWLP	3		970.5101223	2908.506967	0.001943752	2	N	687	717
O35643	Conv	EYAER	IDNADELLESFLEGFHDESTQVQLQLLTAIVK	LFLKK	3		1205.952991	3614.835572	0.000451244	14	N	458	490
O35643	Conv	KLFLK	KPTETQELVQQVLSLATQDSDNPDLR	DRGYI	3		975.8320356	2924.472707	0.000451244	8	N	494	520
O35643	Conv	TLLKK	LAPPLVTLLSAEPELQYVALR	NINLI	2		1147.162458	2292.309317	0.000451244	10	N	283	304
O35643	Conv	QSINK	LLTALNECTEWGQIFILDCLANYMPK	DDREA	3	C8:+57.021,C19:+57.021,M24:+15.995	1043.841553	3128.501259	0.000451244	6	N	206	232
O35643	Conv	LIQTK	VNYVVQEAIVVIK	DIFRK	2		737.4379311	1472.860262	0.000451244	3	N	402	415
O35643	Conv	DIFRK	YPNKYESVIATLCENLDSLDEPEAR	AAMIW	3	C13:+57.021	976.1310509	2925.369753	0.000451244	5	N	420	445
O35643	Conv	KLFLK	KPTETQELVQQVLSLATQDSDNPDLRDR	GYIYW	3		1066.208054	3195.600761	0.001699387	3	N	494	522
O35737	Conv	DFQGR	STGEAFVQFASQEIAEK	ALKKH	2		921.4499525	1840.884305	0.000451244	12	N	150	167
O35744	Conv	KEMRK	AFEEESVEKDIPR	LLLTS	2		774.8811743	1547.746749	0.001943752	6	N	164	177
O35744	Conv	AASEK	LIVGFPAYGHTFILSDPSK	TGIGA	2		1031.554555	2061.09351	0.000451244	20	N	259	278
O35744	Conv	YDIGK	SADLNVDSIISYWKDHGAASEK	LIVGF	4		602.2952789	2405.149916	0.000662267	5	N	237	259
O35744	Conv	KDIPR	LLLTSTGAGIIDVIK	SGYKI	2		757.4641459	1512.912692	0.000451244	25	N	177	192
O35744	Conv	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2		1036.9772	2071.9388	0.000451244	17	N	128	145
O35744	Conv	EVCTF	LNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1190.546847	3568.61714	0.000451244	5	N	309	340
O35744	Conv	YDIGK	SADLNVDSIISYWK	DHGAA	2		805.9071921	1609.798784	0.000451244	25	N	237	251
O35744	Conv	NTELK	TLLAIGGWK	FGPAP	2		479.7901742	957.5647484	0.000451244	8	N	91	100
O35744	Conv	EQDLR	DYEALNGLKDK	NTELK	2		633.3227639	1264.629928	0.000451244	2	N	75	86
O35744	Conv	LHDPK	DGYTGENSPLYK	SPYDI	2		672.3098535	1342.604107	0.000451244	4	N	218	230
O35744	Conv	KSGYK	IPELSQSLDYIQVMTYDLHDPK	DGYTG	3		869.100518	2604.278154	0.002453667	1	N	196	218
O35744	Conv	SDPSK	TGIGAPTISTGPPGK	YTDES	2		677.3727881	1352.729976	0.000451244	5	N	278	293
O35744	Conv	IGGWK	FGPAPFSAMVSTPQNR	QIFIQ	2		853.9201115	1705.824623	0.000662267	1	N	100	116
O35744	Conv	AQWLK	DNNLGGAVVWPLDMDDFSGSFCHQR	HFPLT	3	C22:+57.021	946.418761	2836.232883	0.000823681	1	N	350	375
O35744	Conv	YYEVC	TFLNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1273.252211	3816.733232	0.000451244	3	N	307	340
O35841	Conv	EELYR	NYGILADATEQVGQHKDAYQVILDGVK	GGTKE	3		982.5054828	2944.493048	0.000451244	2	N	9	36
O35841	Conv	TVSGR	QQLVELVAEQADLEQAFSPSDPDCVDR	LLQCT	3	C24:+57.021	1020.480631	3058.418494	0.000622848	2	N	210	237
O35841	Conv	KMDAK	GTLGGLFSQILQGEDIVR	ERAIK	2		952.0183367	1902.021073	0.000451244	10	N	130	148
O35841	Conv	ENLPR	VADILTQLLQTDDSAEFNLVNNALLSIFK	MDAKG	3		1069.238403	3204.691808	0.000451244	12	N	97	126
O35855	Conv	RSARR	LCLPDFDKQELLECIR	QLIEV	3	C2:+57.021,C14:+57.021	683.6765181	2048.006154	0.002080925	2	N	134	150
O35855	Conv	EGRVR	EVFGSGTACQVCPVHQILYEGK	QLHIP	3	C9:+57.021,C12:+57.021	827.0632123	2478.166237	0.000870037	2	N	334	356
O35900	Conv	GSVVR	YVQLPADEVDTQLLQDAAR	KEALQ	2		1073.04528	2144.07496	0.000451244	16	N	68	87
O35900	Conv	VVELK	NDLSICGTLHSVDQYLNIK	LTDIS	3	C6:+57.021	730.700534	2189.078202	0.000662267	1	N	20	39
O35930	Conv	NNKLR	ELPSGLLDGLEDLDTLYLQR	NWLRT	2		1130.58952	2259.16344	0.000451244	29	N	177	197
O35930	Conv	HNNLK	SLPSLGWALPALTTLDVSFNK	LGSLS	2		1115.610059	2229.204517	0.000451244	23	N	106	127
O35930	Conv	GKLIK	LENLDLSHNNLK	SLPSL	2		705.3733194	1408.731039	0.001463592	2	N	94	106
O35930	Conv	VSFNK	LGSLSPGVLDGLSQLQELYLQNNDLK	SLPPG	2		1407.748343	2813.481087	0.000451244	21	N	127	153
O35930	Conv	VASVR	CANLDNAPVSYSPGK	GCPTS	2	C1:+57.021	834.8882451	1667.76089	0.000451244	17	N	263	278
O35930	Conv	VYLWK	QGVDVKDTTPNVASVR	CANLD	3		562.632603	1684.874409	0.000451244	7	N	247	263
O35930	Conv	LANNK	LRELPSGLLDGLEDLDTLYLQR	NWLRT	3		843.7906719	2528.348616	0.000451244	8	N	175	197
O35930	Conv	VTMPR	AWLLFLQGSLPTFR	SSLFL	2		824.9646474	1647.913695	0.000451244	5	N	674	688
O35930	Conv	QTNGK	LIKLENLDLSHNNLK	SLPSL	4		441.7563325	1762.99413	0.000698008	1	N	91	106
O35955	Conv	GSYSR	LPFTALGSGQGAAVALLEDR	FQPNM	2		993.5368936	1985.058187	0.000451244	18	N	160	180
O35955	Conv	PVLTR	EVRPLTLELLEETVQAMEVE	-	2	M17:+15.995	1172.601814	2343.188027	0.000451244	2	N	253	273
O35955	Conv	ARKTG	TTIAGLVFR	DGVIL	2		489.293081	976.5705621	0.002813207	1	N	39	48
O54824	Conv	SAVMK	SLLCLPSSVSCGQITCIPK	ERVSP	2	C4:+57.021,C11:+57.021,C16:+57.021	1060.530888	2119.046176	0.000451244	1	N	993	1012
O54824	Conv	AADGR	LQEGDEILELNGESMAGLTHQDALQKF	KQAKK	4		747.3675412	2985.438965	0.002296037	1	N	257	284
O54879	Conv	PNAPK	RPPSGFFLFCSEFRPK	IKSTN	3	C10:+57.021	658.001819	1970.982057	0.000622848	3	N	94	110
O54879	Conv	KPKGK	MSAYAFFVQTCR	EEHKK	2	M1:+15.995,C11:+57.021	748.8370128	1495.658426	0.000451244	6	N	12	24
O54890	Conv	KITGK	YCECDDFSCVR	YKGEM	2	C2:+57.021,C4:+57.021,C9:+57.02	755.7732464	1509.530893	0.000451244	7	N	544	555
O54890	Conv	ENLLK	DNCAPESIEFPVSEAQILEAR	PLSSK	2	C3:+57.021	1188.063112	2374.110625	0.000451244	11	N	71	92
O54890	Conv	LCSGR	GNCECGSCVCVQPGSYGDTCEK	CPTCP	2	C3:+57.021,C5:+57.021,C8:+57.021,C10:+57.021,C20:+57.021	1262.468099	2522.920597	0.000451244	9	N	603	625
O54890	Conv	ICSQR	GECLCGQCVCHSSDFGK	ITGKY	2	C3:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	1000.889116	1999.762632	0.000622848	2	N	523	540
O54890	Conv	ENLLK	DNCAPESIEFPVSEAQILEARPLSSK	GSGSS	3	C3:+57.021	963.1432909	2886.406473	0.000823681	5	N	71	97
O54890	Conv	ICTTR	GVNSCQQCLAVSPVCAWCSDETLSQGSPR	CNLKE	3	C5:+57.021,C8:+57.021,C15:+57.021,C18:+57.021	1085.142399	3252.403798	0.000451244	4	N	33	62

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O54890	Conv	CGVCR	CDQGWLGSMCECSEEDYRPSQQEECSPK	EGQPI	3	C1:+57.021,M9:+15.995,C10:+57.021,C12:+57.021,C25:+57.021	1156.777374	3467.308723	0.000451244	13	N	486	514
O54890	Conv	RCNLK	ENLLKDNCAPESIEFPVSEAQILEARPLSSK	GSGSS	4	C8:+57.021	871.9465712	3483.755085	0.000979378	3	N	66	97
O55029	Conv	LLGVR	SVNGLAFYDWENTELIR	RIEIQ	2		1013.997601	2025.979602	0.001463592	1	N	442	459
O55029	Conv	YLSEK	VLAAQETHEGVTEDGIEDAFEVLGEIQEIVK	TGLWV	3		1123.563503	3367.667109	0.002145581	1	N	494	525
O55029	Conv	VASLR	GSNNVALGYDEGSIIVK	LGREE	2		868.4472128	1734.878826	0.000451244	2	N	281	298
O55106	Conv	ETQQR	VLTLESNVDSTSSSSCQINR	VISHP	2	C16:+57.021	1099.023987	2196.032374	0.001162105	3	N	649	669
O55106	Conv	GTDGR	IQSWSTTNPNVDPYDAYDPSVLR	GPLLG	2		1319.625154	2637.234708	0.000637154	4	N	539	562
O55106	Conv	AGGAK	GLGPLAEAAAAGDGAAAAGAAR	AQYSL	2		904.9666354	1807.917671	0.001329271	2	N	22	44
O55131	Conv	SGLGK	STLINSLFLTDLYSPEYPGPSHR	IKKTV	3		869.7750218	2606.301665	0.000451244	11	N	62	85
O55131	Conv	MAQPK	NLEGYVGFANLPNQVYR	KSVKR	2		977.4950287	1952.974457	0.000451244	4	N	24	41
O55135	Conv	VEVFR	QTVADQVLVGSYCVFSNQGGLVHPK	TSIED	3	C13:+57.021	901.7905232	2702.34817	0.00091018	5	N	139	164
O55135	Conv	LVHPK	TSIEDQDELSSLLQVPLVAGTVNR	GSEVI	2		1292.677387	2583.339173	0.000451244	3	N	164	188
O55222	Conv	AVAVR	LWLDNTENDLNQGDDHGFSPLHWACR	EGRSA	4	C25:+57.021	778.3511039	3109.373215	0.000451244	7	N	17	43
O55222	Conv	EIGMK	VALEGLRPTIPPGISPHVCK	LMKIC	4	C19:+57.021	536.0533534	2140.182214	0.000622848	1	N	403	423
O70138	Conv	YGFPR	SVQAIDAAVSYNGK	TYFFI	2		711.8653272	1421.715054	0.000451244	22	N	372	386
O70138	Conv	MEMPR	CGVPDSGDFLLTPGSPK	WTHTN	2	C1:+57.021	873.9222849	1745.82897	0.000451244	20	N	90	107
O70138	Conv	LFKGR	QYWALSGYDLQQGYPR	DISNY	2		972.9661041	1943.916608	0.000451244	18	N	347	363
O70138	Conv	SYNGK	TYFFINNQCWR	YDNQR	2	C9:+57.021	774.8565509	1547.697502	0.000451244	15	N	386	397
O70138	Conv	QGYPR	DISNYGFPR	SVQAI	2		534.7596024	1067.503605	0.000451244	21	N	363	372
O70138	Conv	NYAYR	EPSTYSLPQDDINGIQTIYGPSDNPIQPTGPSTPK	ACDPH	3		1243.271159	3726.790078	0.000451244	11	N	242	277
O70138	Conv	TAIEK	AFHVWSVASPLTFTEILQGEADINIAFVSR	DHGDN	3		1106.91062	3317.708461	0.000451244	1	N	135	165
O70138	Conv	HPQLR	TVDLNFISLFWPFLPNGLQAAYEDFDRDLVFLFK	GRQYW	4		1013.52299	4050.060761	0.002080925	1	N	311	345
O70138	Conv	GVNCR	VDAVFLQDSFFLFFSGPQYFAFNFVSHR	VTRVA	3		1111.545501	3331.613104	0.000451244	4	N	423	451
O70145	Conv	PVELR	IHPQSQPQEDTSPESDIPPPPNSSPPGR	LQLSP	3		997.8080015	2990.400604	0.000451244	27	N	300	328
O70145	Conv	IWKQK	LFEPVVIPVGR	LFRPN	2		613.3693201	1224.72304	0.000698008	6	N	170	181
O70145	Conv	FNGQK	GLVPCNYLEPVELR	IHPQS	2	C5:+57.021	829.9324557	1657.849311	0.000451244	11	N	286	300
O70145	Conv	WGQVK	NYCLTLWCEHTVGDQGLIDEPIQR	ENSDA	2	C3:+57.021,C8:+57.021	1459.184067	2916.352535	0.001395409	1	N	417	441
O70145	Conv	DPHSR	ICFNIGCVNTILENLQAAEQAFTK	SINRD	2	C2:+57.021,C7:+57.021	1377.683172	2753.350744	0.000451244	14	N	38	62
O70145	Conv	KKDWK	GALEAFSEVQDPHSR	ICFNI	2		821.8951474	1641.774695	0.000451244	9	N	23	38
O70145	Conv	RICFN	IGCVNTILENLQAAEQAFTK	SINRD	3	C3:+57.021	740.7161841	2219.125152	0.002212458	1	N	42	62
O70194	Conv	FFDKR	DNSDFDLLTVSETANEPPQDEGNSFNSPR	NLAME	3		1065.804874	3194.391222	0.001162105	1	N	281	310
O70251	Conv	FGDLK	TPAGLQVLNDYLADK	SYIEG	2		809.4282917	1616.840983	0.000451244	15	N	7	22
O70251	Conv	YLADK	SYIEGYVPSQADVAVFEAVSGPPPADLCHALR	WYNHI	3	C28:+57.021	1139.226126	3414.654977	0.000451244	16	N	22	54
O70251	Conv	KSLGK	YGPSSVEDTTGSGAADAKDDDDIDLFGSDDEEESEEAK	KLREE	3		1322.877597	3965.609392	0.001763695	1	N	78	116
O70310	Conv	LEKLK	FGIGDGNLQYYLYNWK	CPSMG	2		975.9733978	1949.931196	0.000451244	7	N	466	482
O70310	Conv	QPVPK	LGEVVNTHGPVEPDKDNIR	QEPYT	3		697.0277927	2088.059978	0.000451244	13	N	127	146
O70435	Conv	EYAMK	AVENSSTAIGIR	CKDGV	2		609.3283805	1216.641161	0.000622848	7	N	29	41
O70435	Conv	KEVAK	IIYIVHDEVKDK	AFELE	2		736.4119133	1470.808227	0.000451244	5	N	196	208
O70435	Conv	ASNFR	SNFGYNIPLK	HLADR	2		576.8065526	1151.597505	0.000698008	15	N	100	110
O70435	Conv	EVKDK	AFELELSWVGELTK	GRHEI	2		811.4277604	1620.839921	0.000451244	8	N	208	222
O70435	Conv	LADAR	SLADIAREEASNFR	SNFGY	2		789.89769	1577.77978	0.000451244	4	N	86	100
O70497	Conv	AEKYK	LILGNFLGGGAGDSLTPHNNR	LFSTK	3		708.3717823	2122.091947	0.000451244	12	N	221	242
O70497	Conv	TSYKR	GFGSQLGEFWLGNDNIHALTTQGTSELR	VDLSD	3		1016.83237	3047.47371	0.000451244	19	N	165	193
O88307	Conv	IPSSK	HCDGLRDCPDGSDEQHCEPFCTR	FMDFV	3	C2:+57.021,C8:+57.021,C17:+57.021,C21:+57.021	950.035642	2847.083526	0.002813207	2	N	1254	1277
O88307	Conv	SAWAK	TDLGDSPLAFEHILTR	GSSPP	2		892.96303	1783.91046	0.000622848	2	N	1824	1840
O88307	Conv	FFQSR	ENQEVILEEVRDFQLR	DKYMF	2		1009.021608	2016.027615	0.002212458	1	N	287	303
O88307	Conv	CIPQR	WACDGDADCQDGSDEDPVSCEK	KCNGF	2	C3:+57.021,C9:+57.021,C20:+57.021	1258.449403	2514.883206	0.000451244	8	N	1215	1237
O88307	Conv	PILSK	ESAPGLIIATGSVGK	NLASK	2		700.3937205	1398.771841	0.000451244	10	N	497	512
O88307	Conv	QEHVK	SFSWGIDPYDQPNAIYIER	HEPFG	2		1136.039997	2270.064395	0.000451244	17	N	249	268
O88307	Conv	STEIK	NLLLNALYTVR	VAAVT	2		645.3829588	1288.750318	0.000451244	9	N	1711	1722
O88307	Conv	AEGLK	FSLSLENVLYYSPGGAGSDTLVR	YFANE	2		1223.118976	2444.222352	0.000451244	17	N	381	404
O88307	Conv	MSDER	NCPTTVCDADTQFR	CQESG	2	C2:+57.021,C7:+57.021	842.8563877	1683.697175	0.000451244	14	N	1110	1124
O88307	Conv	SGQQR	SVILDSLPHPYAIAVFK	NEIYW	2		935.5278089	1869.040018	0.000451244	3	N	953	970
O88307	Conv	ITFDK	GGTWEFLQAPAFTGYGEK	INCEL	2		979.9683124	1957.921025	0.000451244	11	N	446	464
O88307	Conv	GETWK	TFVFSEKPVFVYGLLTEPGEK	STVFT	2		1194.130824	2386.246048	0.000451244	6	N	572	593
O88307	Conv	IAVFK	NEIYWDDWSQLSIFR	ASKHS	2		986.4659369	1970.916274	0.000698008	2	N	970	985
O88307	Conv	PNWKR	CDGHQDCQDGQDEANCPTHSTLTCTSR	EFKCE	4	C1:+57.021,C7:+57.021,C16:+57.021,C24:+57.021	788.3055261	3149.190904	0.002296037	2	N	1490	1517
O88307	Conv	AGFKK	IEVANPDGDFR	LTIVN	2		616.7994559	1231.583312	0.000451244	1	N	855	866
O88307	Conv	FYKGK	NAGSNACVPQPCSLLCLPK	ANNSK	2	C7:+57.021,C12:+57.021,C16:+57.021	1043.49738	2084.979159	0.000870037	5	N	1014	1033

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88307	Conv	DFGFK	MSEDLSLEVCVPDPEFSGKPYSPPVPCPVGSSYR	RTRGY	3	M1:+15.995,C10:+57.021,C27:+57.021	1266.916286	3797.725459	0.000451244	11	N	689	723
O88307	Conv	FDYER	NCLYWSDLALDTIQR	LCLNG	2	C2:+57.021	934.4542836	1866.892967	0.000451244	9	N	799	814
O88307	Conv	GYGEK	INCELSQGCSLHLAQR	LSQLL	2	C3:+57.021,C9:+57.021	943.4540607	1884.892521	0.000451244	10	N	464	480
O88307	Conv	DTQFR	CQESGTCIPLSYK	CDLED	2	C1:+57.021,C7:+57.021	771.8500427	1541.684485	0.000451244	2	N	1124	1137
O88307	Conv	LSGLR	AAVALDFDYER	NCLYW	2		635.3096565	1268.603713	0.000823681	6	N	788	799
O88307	Conv	VLSER	CDGFLDCSDESDEKACSDELTVYK	VQNLQ	3	C1:+57.021,C7:+57.021,C16:+57.021	948.3825217	2842.124165	0.000622848	3	N	1533	1557
O88307	Conv	LFLVR	VLIPYQGPSSDYVVVK	MIPDS	2		882.483067	1762.950534	0.000735798	8	N	1911	1927
O88307	Conv	EPGEK	STVFTIFGSNK	ESVHS	2		600.8171173	1199.618635	0.000451244	4	N	593	604
O88307	Conv	SALIK	WESPYDSPDQDLFYAIAVK	DLIRK	2		1122.528931	2243.042262	0.000451244	2	N	1952	1971
O88307	Conv	KSIYR	YDLASGATEQLPLSGLR	AAVAL	2		895.9683124	1789.921025	0.000451244	4	N	771	788
O88307	Conv	LLHSK	ASNLLLGFDR	SHPNK	2		553.3041771	1104.592754	0.000451244	7	N	214	224
O88307	Conv	MFATK	VVHLPGSQQQSSVQLWVSFGR	KPMRA	3		780.4138701	2338.21821	0.001763695	1	N	311	332
O88307	Conv	NLASK	TNVYISSSAGAR	WREAL	2		613.3127305	1224.609861	0.000870037	1	N	517	529
O88342	Conv	DGNVR	VYSILASTLKDEGK	LLEAK	2		762.4199353	1522.824271	0.000451244	22	N	470	484
O88342	Conv	RNGGK	SYIYSGSHDGHINYWDSETGENDSFSGK	GHTNQ	3		1051.443388	3151.306764	0.000622848	28	N	334	362
O88342	Conv	LKDQK	KCFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C2:+57.021	1171.895327	3512.662581	0.000451244	18	N	436	470
O88342	Conv	LLEAK	GPVTDVAYSHDGAFLAVCDASK	VVTVF	2	C18:+57.021	1140.533991	2279.052381	0.000451244	17	N	489	511
O88342	Conv	CDASK	VVTVFSVADGYSENNVFYGHHAK	IVCLA	2		1270.614392	2539.213185	0.000451244	6	N	511	534
O88342	Conv	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C1:+39.994	1123.521339	3367.540618	0.000823681	3	N	437	470
O88342	Conv	TRPYR	LATGSDDNCAAFFEGPPFK	FKFTI	2	C9:+57.021	1022.459763	2042.903926	0.000451244	42	N	161	180
O88342	Conv	EGREK	FGAVFLWDTGSSVGEITGHNK	VINSV	2		1111.54799	2221.080379	0.000451244	17	N	126	147
O88342	Conv	LGESK	AHDGGIYAISWSPDSTHLLSASGDKTSK	IWDVN	3		967.8058208	2900.394062	0.000451244	7	N	231	259
O88342	Conv	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	2		1209.62476	2417.23392	0.000662267	4	N	43	65
O88342	Conv	PDGNR	FATASADGQIFIYDGK	TGEKV	2		852.417924	1702.820248	0.000451244	16	N	203	219
O88342	Conv	VVVAK	YAPSGFYIASGDISGK	LRIWD	2		816.8993671	1631.783134	0.000451244	11	N	65	81
O88342	Conv	QDAHR	LHHVSSLAWLDEHTLVTTSHDASVK	EWTIT	4		696.6087598	2782.403839	0.000451244	20	N	575	600
O88342	Conv	LGESK	AHDGGIYAISWSPDSTHLLSASGDK	TSKIW	2		1293.117496	2584.219392	0.000451244	12	N	231	256
O88342	Conv	CLWQK	DHLLSISLSGYINYLDKNNPSKPLR	VIKGH	4		715.1361474	2856.51339	0.000451244	5	N	289	314
O88342	Conv	DVQPK	CVAVGPGGYTVVVCIGQIVLLK	DQKKC	2	C1:+57.021,C14:+57.021	1151.636776	2301.257953	0.000451244	8	N	411	433
O88342	Conv	DKTSK	IWDVNVNSVVSTFPMGSNVLDQQLGCLWQK	DHLLS	3	C26:+57.021	1145.567606	3433.679418	0.000451244	5	N	259	289
O88342	Conv	SGKLR	IWDTTQKEHLLK	YEYQP	2		756.4149873	1510.814375	0.001463592	1	N	83	95
O88456	Conv	FVQLA	GDDMEVSATELMNILNKVVTR	HPDLK	3	M4:+15.995,M12:+15.995	789.7231104	2366.145931	0.0025889	1	N	110	131
O88456	Conv	MIIRR	YADESGNMDFDNFISCLVR	LDAMF	2	C16:+57.021	1126.983277	2251.950954	0.002145581	1	N	217	236
O88487	Conv	THSGR	EIAVGDSEGQIVIYDVGEQIAVPR	NDEWA	2		1279.161372	2556.307145	0.000451244	4	N	557	581
O88487	Conv	DGMGR	LDLWNLNNDTEVPTASISVEGNPALNR	VRWTH	3		984.8286255	2951.462476	0.001329271	1	N	522	549
O88520	Conv	EHLPK	EIGNCTQITNLDLQHNDLLDLPDTIGNLSSLNR	LGLRY	3	C5:+57.021	1236.283251	3705.826352	0.000622848	1	N	255	288
O88544	Conv	LSASK	LYNNITFEELGALLEIPAAK	AEKIA	2		1110.102066	2218.188533	0.000451244	17	N	314	334
O88544	Conv	KIQPR	VISFEEQVASIR	QHLAS	2		689.3727881	1376.729976	0.000823681	3	N	95	107
O88544	Conv	LVISR	QLLTDFCTHLPNLPDSTAK	EVYHF	3	C7:+57.021	724.3652628	2170.072388	0.000451244	4	N	63	82
O88544	Conv	QILEK	AIQLSGTEQLEALK	AFVEA	2		750.9175598	1499.81952	0.000662267	2	N	32	46
O88569	Conv	FGDSR	GGGGNFGPGPGSNFR	GGSDG	2		689.3188785	1376.622157	0.000451244	5	N	213	228
O88569	Conv	FGGSR	NMGGPYGGGNYGPGGSGGSGGYGGR	SRY-	2	M2:+15.995	1103.454338	2204.893076	0.000451244	3	N	325	350
O88569	Conv	YGSGR	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	GGYGG	2		1248.02393	2494.03226	0.001839721	1	N	238	266
O88569	Conv	SGKKR	GFGFVTFDDHDPVDK	IVLQK	2		848.3866238	1694.757648	0.000637154	2	N	153	168
O88569	Conv	KEQFR	KLFIGGLSFETTEESLR	NYYEQ	2		964.01272	1926.00984	0.000622848	2	N	21	38
O88569	Conv	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	2		1139.081665	2276.147731	0.000451244	9	N	153	173
O88569	Conv	EHHLR	DYFEEYGKIDTIEIITDR	QSGKK	2		1110.539496	2219.063392	0.000622848	1	N	129	147
O88569	Conv	EQFRK	LFIGGLSFETTEESLRNYYEQWGK	LTDCV	3		956.4682575	2866.381372	0.000622848	2	N	22	46
O88569	Conv	VTVKK	LFVGGIKEDTEEHHLR	DYFEE	3		627.3274024	1878.958807	0.000451244	9	N	113	129
O88569	Conv	EEYGK	IDTIEIITDR	QSGKK	2		594.8276821	1187.639764	0.000451244	17	N	137	147
O88569	Conv	EQFRK	LFIGGLSFETTEESLR	NYYEQ	2		899.9652384	1797.914877	0.000451244	29	N	22	38
O88593	Conv	GHPVR	YVVISHTAGSFCNSPDSCEQQAR	NVQHY	2	C12:+57.021,C18:+57.021	1307.076528	2612.137456	0.000451244	59	N	42	65
O88593	Conv	KRALR	AALNLLECGVSR	GFLRS	2	C8:+57.021	651.8456519	1301.675704	0.000451244	25	N	133	145
O88593	Conv	EQQAR	NVQHYHKNELGWCDVAYNFLIGEDGHVYEGR	GWNIK	4	C13:+57.021	930.6829745	3718.700698	0.000451244	6	N	65	96
O88593	Conv	QHYHK	NELGWCDVAYNFLIGEDGHVYEGRG	WNIKG	3	C6:+57.021	957.4331757	2869.276127	0.000451244	12	N	72	97
O88593	Conv	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	2	C6:+57.021	1407.135132	2812.254663	0.000451244	18	N	72	96
O88593	Conv	VKGHR	DVQSTLSPGDQLYQVIQSWEHYRE	-	2		1439.686274	2877.356949	0.000451244	21	N	158	182
O88593	Conv	VKGHR	DVQSTLSPGDQLYQVIQSWEHYR	E-	3		917.1125851	2748.314355	0.000451244	9	N	158	181
O88685	Conv	VDAEK	LKPGDLVGVNKDSYLILETLPTEYDSR	VKAME	3		1012.53656	3034.58628	0.000451244	4	N	147	174
O88685	Conv	FALAK	EKAPSIIFIDELDAIGTK	RFDSE	3		654.0266186	1959.056456	0.000451244	11	N	279	297
O88685	Conv	KTSTR	QTYFLPVIGLVDAEK	LKPGD	2		846.9645101	1691.91342	0.000622848	9	N	132	147
O88685	Conv	IKVNK	TLPYLVSNVIELLDVDPNDQEEDGANIDLDSQR	KGKCA	3		1233.934436	3698.779908	0.000823681	4	N	87	120
O88685	Conv	VGVNK	DSYLILETLPTEYDSR	VKAME	2		957.9707178	1913.925836	0.000451244	21	N	158	174

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88712	Conv	ALRAK	AFGFNVLFYDPYLSDGIER	ALGLQ	2		1112.042009	2222.068418	0.000735798	2	N	194	213
O88712	Conv	NIDIK	SAGDLGIAVCNVPAASVEETADSTLCHILNLYR	RTTWL	3	C10:+57.021,C26:+57.021	1172.908314	3515.701541	0.000451244	1	N	108	141
O88783	Conv	VNVER	DIHSGLIGPLLICR	KGTLH	3	C13:+57.021	521.9610721	1562.859816	0.000451244	13	N	1698	1712
O88783	Conv	TFTYK	WNILEFDEPTENDAQCLTRPYYSDVDVTR	DIASG	3	C16:+57.021	1182.875821	3545.604063	0.000451244	16	N	482	511
O88783	Conv	VDVTR	DIASGLIGLLLICK	SRSLD	2	C13:+57.021	743.4393852	1484.86317	0.000451244	17	N	511	525
O88783	Conv	RGVQR	VADIEQQAVFAVFDENKSWYIEDNINK	FCENP	3		1062.519569	3184.535307	0.001839721	1	N	536	563
O88783	Conv	RGVQR	VADIEQQAVFAVFDENK	SWYIE	2		961.9788771	1921.942154	0.000451244	15	N	536	553
O88783	Conv	AAQLR	QFYVAAQGILWNYHPEPTDPSLNSIPSFK	KIVYR	3		1107.219454	3318.634962	0.000451244	13	N	32	61
O88783	Conv	KMFDK	QHVLLFAVFDESK	SRSQS	3		511.6089585	1531.803476	0.000870037	7	N	208	221
O88783	Conv	RPTLR	LELQGCEVNGCSTPLGLEDGR	IQDKQ	2	C6:+57.021,C11:+57.021	1152.533433	2303.051267	0.001699387	1	N	2014	2035
O88783	Conv	KEKPR	SSNSGLLGPTLYAEVGDVIK	VHFRN	2		1010.534017	2019.052433	0.000451244	11	N	78	98
O88783	Conv	SSFKK	SWWGDYWEPSLAR	LNAQG	2		826.878769	1651.741938	0.000870037	2	N	2048	2061
O88844	Conv	LIKEK	LILPYVELDLHSYDLGIENR	DATND	3		791.4219198	2371.242359	0.000451244	7	N	29	49
O88844	Conv	RMYQK	GQETSTNPIASIFAWSR	GLAHR	2		932.9635614	1863.911523	0.000451244	13	N	321	338
O88844	Conv	GDQYR	ATDFVVPGPGKVEITYTPK	DGTQK	3		673.6986134	2018.07244	0.000823681	1	N	140	159
O88844	Conv	KNIPR	LVTGWVKPIIIGR	HAYGD	3		484.6419339	1450.902402	0.001264573	5	N	119	132
O88879	Conv	IKECK	GSPLVVSLIGALLR	DFPNR	2		697.9406409	1393.865682	0.001162105	1	N	318	332
O88879	Conv	DKTAK	IWSFDLLSPLHELK	GHNGC	3		566.6474133	1696.91884	0.000823681	1	N	1110	1124
O88947	Conv	NKFQR	DTYDYDIAVLR	LKTPI	2		672.3280462	1342.640492	0.000622848	4	N	313	324
O88947	Conv	RKLCR	LDNGDCDQFCREEQNSVVCSCASGYFLGNDGK	SCIST	3	C6:+57.021,C10:+57.021,C19:+57.021,C21:+57.021	1234.504614	3700.490441	0.000451244	16	N	130	162
O88947	Conv	DQFCR	EEQNSVVCSCASGYFLGNDGK	SCIST	2	C8:+57.021,C10:+57.021	1160.994141	2319.972682	0.000451244	4	N	141	162
O88958	Conv	AFEEK	IQAAGGIELFVGGIGPDGHIAFNEPGSSLVSR	TRVKT	3		1055.882953	3164.62546	0.000451244	9	N	124	156
O88958	Conv	NNFFK	HIDIHPENTHILDGNAADLQAECDAFEEK	IQAAG	3	C23:+57.021	1101.50584	3301.494119	0.000451244	4	N	95	124
O88968	Conv	PWMDR	LSSEQLNPSVFVGLR	LSSMQ	2		823.4495585	1644.883517	0.000451244	16	N	44	59
O88968	Conv	WQLLR	APDTPLLQGIADYKPQDGETIELR	LVRW-	3		880.7892195	2639.344259	0.000451244	17	N	402	426
O88968	Conv	SVTLK	VASALSPYEQTFFVFAGSSLEDVLK	LAQDG	2		1353.189599	2704.363597	0.000451244	16	N	338	363
O88968	Conv	EDVLK	LAQDGGGFTYGTQASLSGPYLTSVLGK	DAGDR	2		1344.679929	2687.344259	0.000451244	12	N	363	390
O88968	Conv	SCQPK	LSGGSLALYLLALR	ANCEF	2		723.9380983	1445.860597	0.000451244	15	N	99	113
O88968	Conv	TACIK	AGTSLLLSLQDGAFQNPLMISQLLPILNHK	TYLDL	3		1078.264118	3231.768954	0.000823681	2	N	272	302
O88968	Conv	ILNHK	TYLDLIFPDCQASR	VMLVP	2	C10:+57.021	849.9117202	1697.80784	0.000823681	4	N	302	316
O89023	Conv	GTSFK	NPFLITDEVVDYISGGGFSNVFPRPPYQEEAVAQFLK	SSSHL	3		1382.028782	4143.062946	0.000451244	12	N	393	430
O89051	Conv	VMPPK	NLLELLINIK	AGTYL	2		591.876978	1181.738356	0.000622848	7	N	178	188
O89053	Conv	YEDVR	VSQTTWDSGFCAVNPK	FMALI	2	C11:+57.021	898.9175339	1795.819468	0.000451244	44	N	29	45
O89053	Conv	WLGGR	DAGPLLISLK	DGYVP	2		513.8138463	1025.612093	0.000622848	16	N	383	393
O89053	Conv	MTVPR	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1058.519569	3172.535307	0.000451244	45	N	354	383
O89053	Conv	AVNPK	FMALICEASGGGAFLVLPLGK	TGRVD	2	C6:+57.021	1076.07097	2150.126339	0.000451244	8	N	45	66
O89053	Conv	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C32:+57.021	1282.976765	3845.906894	0.000451244	33	N	253	287
O89053	Conv	DSSIR	YFEITSEAPFLHYLSMFSSK	ESQRG	3		799.7210897	2396.139869	0.000451244	14	N	293	313
O89053	Conv	KLQER	LDRLEETVQAK	-	2		651.357138	1300.698676	0.000451244	2	N	450	461
O89053	Conv	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	2		1292.122247	2582.228894	0.000451244	11	N	359	383
O89053	Conv	LEEPL	SLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C26:+57.021	1043.521768	3127.541904	0.000451244	4	N	259	287
O89053	Conv	EPLSL	QELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	Q1:-17.027,C24:+57.021	971.1407371	2910.398811	0.000662267	2	N	261	287
O89053	Conv	SARRR	ATPEPSGTPSSDTVSRLEEDVR	NLNAI	3		777.3755864	2329.103359	0.002884417	1	N	416	438
O89053	Conv	TVPRK	SDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1015.821248	3044.440344	0.000451244	5	N	355	383
O89053	Conv	EEPLS	LQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C25:+57.021	1014.511092	3040.509875	0.000622848	5	N	260	287
O89053	Conv	KFMAL	ICEASGGGAFLVLPLGK	TGRVD	2	C2:+57.021	844.9559308	1687.896262	0.000451244	2	N	49	66
O89053	Conv	DSSIR	YFEITSEAPFLHYL	SMFSS	2		865.4277604	1728.839921	0.001463592	3	N	293	307
O89053	Conv	GAAVL	TLGPDVHPDTIYSVDWSR	DGALI	2		1029.500508	2056.985416	0.001162105	1	N	168	186
O89053	Conv	DNVIL	VWDVGTGAAVLTLGPDVHPDTIYSVDWSR	DGALI	3		1042.856404	3125.545812	0.000451244	2	N	157	186
O89053	Conv	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLC	GKGDS	3	C32:+57.021	1221.271289	3660.790467	0.000637154	1	N	253	285
O89079	Conv	LFDVK	NAFYIGSYQQCINEAQR	VKLSS	2	C11:+57.021	1031.476279	2060.936957	0.000451244	9	N	23	40
O89079	Conv	VGGEK	LQEAYYIFQELADK	CSPTL	2		865.9359496	1729.856299	0.000451244	3	N	197	211
O89086	Conv	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVKDR	ETQRS	4		942.2249509	3764.868603	0.0007646	4	N	7	41
O89086	Conv	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	3		1165.587983	3493.740549	0.000451244	16	N	7	39
P00493	Conv	-MPTR	SPSVVISDDEPGYDLDLFCIPNHYAEDLEK	VFIPH	3	C19:+57.021	1146.529539	3436.565218	0.000451244	17	N	4	34
P00493	Conv	TLTGK	NVLIVEDIIDTGK	TMQTL	2		714.9013784	1427.787157	0.000451244	9	N	128	141
P00493	Conv	EIPDK	FVVGYALDYNEYFR	DLNHV	2		878.4230094	1754.830419	0.000870037	1	N	186	200
P00493	Conv	KGGYK	FFADLLDYIK	ALNRN	2		622.8322361	1243.648872	0.000451244	9	N	73	83
P00493	Conv	NEYFR	DLNHVCVISETGK	AKYKA	3	C6:+57.021	491.2455372	1470.713212	0.000622848	2	N	200	213
P01027	Conv	GNLLR	SEETKQNEAFSLTAK	GKGRG	2		841.9157455	1681.815891	0.000451244	4	N	1320	1335
P01027	Conv	LQEAR	DICEGQVNSLPGSINK	AGEYI	2	C3:+57.021	865.9228163	1729.830033	0.000451244	43	N	1155	1171
P01027	Conv	PGSVK	VYSYYNLEESCTR	FYHPE	2	C11:+57.021	842.3698852	1682.72417	0.000451244	42	N	1478	1491
P01027	Conv	LDPEK	LGQGGVQKVDVPAADLSDQVPDTDSETR	IILQG	3		966.4761404	2896.405021	0.000451244	11	N	951	979
P01027	Conv	GGVQK	VDVPAADLSDQVPDTDSETR	IILQG	2		1065.495817	2128.976033	0.000451244	46	N	959	979

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01027	Conv	IPSFR	LVAYYTLIGASGQR	EVVAD	2		756.4149873	1510.814375	0.000451244	13	N	530	544
P01027	Conv	FLYGK	NVDGTAFVIFGVQDGDKK	ISLAH	2		955.4868693	1908.958139	0.000451244	17	N	264	282
P01027	Conv	KIPPK	SSVAVPYVIVPLK	IGQQE	2		686.4164673	1370.817335	0.000451244	14	N	891	904
P01027	Conv	LGLAR	SELEEDIIPEEDIISR	SHFPQ	2		943.9656324	1885.915665	0.000451244	14	N	748	764
P01027	Conv	ASGQR	EVVADSVWVDVKDSCIGTLVVK	GDPRD	3	C15:+57.021	806.758049	2417.250747	0.000451244	10	N	544	566
P01027	Conv	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLKR	QVLTS	3		1118.247738	3351.719814	0.000451244	9	N	37	67
P01027	Conv	SFEVR	VEPTETFYYIDDPNGLEVSIIAK	FLYGK	2		1307.152682	2612.289763	0.000451244	30	N	236	259
P01027	Conv	LKAGR	QVREPGQDLVVLSLPITPEFIPSFR	LVAYY	3		946.5240375	2836.548713	0.000451244	14	N	505	530
P01027	Conv	GRQVR	EPGQDLVVLSLPITPEFIPSFR	LVAYY	2		1227.668105	2453.32061	0.000451244	28	N	508	530
P01027	Conv	FRNAK	EADVSLTAFVLIALQEAR	DICEG	2		973.5338196	1945.052039	0.000451244	30	N	1137	1155
P01027	Conv	FRNAK	EADVSLTAFVLIALQEARDICEGQVNSLPGSINK	AGEYI	3	C21:+57.021	1219.964971	3656.871512	0.000451244	1	N	1137	1171
P01027	Conv	TAKDR	NRWEEPDQQLYNVEATSYALLALLLLK	DFDSV	3		1064.231471	3189.671013	0.000451244	16	N	1217	1244
P01027	Conv	IPVKR	DILSSNNQHGILPLSWNIPELVNMGQWK	IRAFY	3		1068.548917	3202.623352	0.000451244	9	N	178	206
P01027	Conv	KDRNR	WEEPDQQLYNVEATSYALLALLLLKDFDSVPPVVR	WLNEQ	3		1344.705528	4031.093184	0.000451244	4	N	1219	1254
P01027	Conv	MRINK	TVAIHTLDPEKLGQGGVQK	VDVPA	2		996.0501681	1990.084736	0.000451244	8	N	940	959
P01027	Conv	YIIGK	DTWVEHWPEAEECQDQKYQK	QCEEL	3	C13:+57.021	869.3803003	2605.117501	0.000451244	10	N	1624	1644
P01027	Conv	IQTDK	TIYTPGSTVLYR	IFTVD	2		685.8698813	1369.724163	0.000451244	19	N	137	149
P01027	Conv	LSDKK	GICVADPYEIR	VMQDF	2	C3:+57.021	646.8191028	1291.622606	0.000622848	5	N	813	824
P01027	Conv	HSLTR	VVIEDGVGDAVLTR	KVLME	2		721.8966274	1441.777655	0.000451244	16	N	291	305
P01027	Conv	MRINK	TVAIHTLDPEK	LGQGG	2		612.3356743	1222.655749	0.000622848	6	N	940	951
P01027	Conv	ENCIK	AFIDCCNHITK	LREQH	2	C5:+57.021,C6:+57.021	689.8158058	1377.616012	0.000451244	3	N	722	733
P01027	Conv	IYLEK	ISHTEEDCLTFK	VHQYF	2	C8:+57.021	740.343139	1478.670678	0.000451244	5	N	1450	1462
P01027	Conv	KGKGR	GTLSVVAVYHAK	LKSKV	2		622.8540342	1243.692468	0.00091018	3	N	1339	1351
P01027	Conv	VRLDK	ACEPGVDYVYK	TELTN	2	C2:+57.021	650.797836	1299.580072	0.000451244	7	N	1535	1546
P01027	Conv	WVDVK	DSCIGTLVVK	GDPRD	2	C3:+57.021	546.2921895	1090.568779	0.000451244	7	N	556	566
P01027	Conv	LPVGK	TVVILIETPDGIPVKR	DILSS	2		875.5278089	1749.040018	0.000451244	14	N	162	178
P01027	Conv	APDTK	DLELLASGVDR	YISKY	2		594.3174815	1186.619363	0.000622848	15	N	1416	1427
P01027	Conv	KEGHK	YVTVVANFGETVVEK	AVMVS	2		827.9384923	1653.861385	0.000451244	10	N	105	120
P01027	Conv	TVLYR	IFTVDNNLLPVGK	TVVIL	2		715.4066309	1428.797662	0.000451244	13	N	149	162
P01027	Conv	QLAFK	QPSSAYAAFNNRPPSTWLTAYVVK	VFSLA	3		890.1226444	2667.344533	0.000451244	10	N	1060	1084
P01027	Conv	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLK	RQVLT	3		1066.214034	3195.618703	0.000451244	26	N	37	66
P01027	Conv	KDRNR	WEEPDQQLYNVEATSYALLALLLLK	DFDSV	2		1460.771287	2919.526974	0.000451244	12	N	1219	1244
P01027	Conv	YIIGK	DTWVEHWPEAEECQDQK	YQKQC	2	C13:+57.021	1093.958116	2185.900632	0.000451244	16	N	1624	1641
P01027	Conv	CLTFK	VHQYFNVGLIQPGSVK	VYSYY	2		893.4864753	1784.957351	0.000451244	8	N	1462	1478
P01027	Conv	ASGQR	EVVADSVWVDVK	DSCIG	2		673.354064	1344.692528	0.000451244	3	N	544	556
P01027	Conv	DSETR	IILQGSPVVQMAEDAVDGER	LKHLI	2		1064.041683	2126.067767	0.000451244	8	N	979	999
P01027	Conv	AYVVK	VFSLAANLIAIDSHVLCGAVK	WLILE	2	C17:+57.021	1099.604022	2197.192444	0.000622848	10	N	1084	1105
P01027	Conv	EVEVK	AAVFNHFISDGVK	KTLKV	2		702.8676729	1403.719746	0.000451244	7	N	913	926
P01027	Conv	EHAPK	QIFSAEFEVK	EYVLP	2		599.3116678	1196.607736	0.000823681	7	N	216	226
P01027	Conv	PYEIR	VMQDFFIDLR	LPYSV	2		642.3267955	1282.637991	0.001352548	3	N	824	834
P01027	Conv	VEAER	SGIPIVTSPYQIHFTK	TPKFF	2		894.4886837	1786.961767	0.000451244	10	N	344	360
P01027	Conv	NIFLK	DSITTWEILAVSLSDKK	GICVA	2		953.5125528	1905.009506	0.000451244	8	N	796	813
P01027	Conv	PGSGK	NYAGVFMDAGLAFK	TSQGL	2	M7:+15.995	760.3666917	1518.717783	0.000451244	8	N	632	646
P01027	Conv	NLNVR	LDKACEPGVDYVYK	TELTN	2	C5:+57.021	828.9008212	1655.786042	0.000451244	11	N	1532	1546
P01027	Conv	DIISR	SHFPQSWLWTIEELKEPEK	NGIST	3		795.4027481	2383.184844	0.000451244	11	N	764	783
P01027	Conv	ATTFR	LLWENGNLLR	SEETK	2		614.3463763	1226.677153	0.001329271	3	N	1310	1320
P01027	Conv	DYVYK	TELTNIELLDDFDEYTMTIQQVIK	SGSDE	2		1436.712778	2871.409956	0.000451244	9	N	1546	1570
P01027	Conv	NQGAR	VGLVAVDKGVFVLNK	KNKLT	3		519.9841368	1556.929011	0.001229886	4	N	591	606
P01027	Conv	ERSGI	PIVTSPYQIHFTK	TPKFF	2		765.9199055	1529.824211	0.0007646	1	N	347	360
P01027	Conv	QKGKK	YLMWGLSSDLWGEKPNTSYIIGK	DTWVE	3		886.7811197	2657.319959	0.000451244	14	N	1601	1624
P01027	Conv	EFEVK	EYVLPSFEVR	VEPTE	2		619.8249424	1237.634285	0.001763695	4	N	226	236
P01027	Conv	GSINK	AGEYIEASYMNLQRPYTVAIAGYALALMNKLEEPYLGK	FLNTA	4		1063.543597	4250.14319	0.001162105	1	N	1171	1209
P01027	Conv	TAKGK	GRGTLSVVAVYHAK	LKSKV	3		486.6128144	1456.815043	0.000451244	1	N	1337	1351
P01027	Conv	NVEAT	SYALLALLLLK	DFDSV	2		609.3975462	1216.779492	0.000851441	1	N	1233	1244
P01027	Conv	FLYGK	NVDGTAFVIFGVQDGDK	KISLA	2		891.4393878	1780.863176	0.0025889	1	N	264	281
P01027	Conv	RQATK	TMEAHPYSTMHNSNNYLHLSVSR	MELKP	4	M2:+15.995,M10:+15.995	681.0596257	2720.207303	0.00091018	1	N	439	462
P01029	Conv	AWLHR	DSSTWLTAFVLK	ILSLA	2		684.3644317	1366.713263	0.000451244	7	N	1068	1080
P01029	Conv	NSPEK	LQETASWLLAQQLGDGSFHDPCPVIHR	AMQGG	3	C22:+57.021	1025.842058	3074.502773	0.001654178	1	N	1095	1122
P01029	Conv	HGAFR	STQDTVVTLDALSAYWIASHTTEEK	ALNVT	3		922.7876557	2765.339567	0.000451244	4	N	1296	1321
P01029	Conv	LQKPR	LLLFSPSVVNLGTPLSVGVQLLDAPPGQEVK	GSVFL	3		1063.271267	3186.7904	0.000451244	1	N	22	53
P01029	Conv	FLGQK	ASAGLLGAHAAAITAYALTLTK	ASEDL	3		695.7287956	2084.162987	0.000451244	2	N	1178	1200
P01029	Conv	AAPTK	SQLLATLCSGDVCQCAEGK	CPRLL	2	C8:+57.021,C13:+57.021,C15:+57.021	1048.973934	2095.932269	0.002019181	1	N	1569	1588
P01029	Conv	PTAPR	SPTEPVPQAPALWIETTAYALLHLLLR	EGKGK	3		1000.890609	2999.648427	0.00091018	1	N	1244	1271
P01326	Conv	HPTQA	FVKQHLCGSHLVEALYLVCGER	GFFYT	3	C7:+57.021,C19:+57.021	872.4457681	2614.313904	0.000622848	5	N	24	46

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01326	Conv	HLCGS	HLVEALYLVCGER	GFFYT	2	C10:+57.021	779.9062409	1557.796882	0.000451244	14	N	33	46
P01326	Conv	LCGSH	LVEALYLVCGER	GFFYT	2	C9:+57.021	711.3767849	1420.73797	0.000451244	17	N	34	46
P01326	Conv	CGSHL	VEALYLVCGER	GFFYT	2	C8:+57.021	654.8347528	1307.653906	0.000451244	13	N	35	46
P01326	Conv	SHLVE	ALYLVCGER	GFFYT	2	C6:+57.021	540.7792492	1079.542898	0.000451244	9	N	37	46
P01326	Conv	FVKQH	LCGSHLVEALYLVCGER	GFFYT	3	C2:+57.021,C14:+57.021	659.3293412	1974.964624	0.000451244	1	N	29	46
P01326	Conv	RGIVD	QCCTSICSLYQLENYCN	-	2	C2:+57.021,C3:+57.021,C7:+57.021,C16:+57.021	1106.941546	2211.867491	0.000622848	6	N	93	110
P01326	Conv	QAFVK	QHLCGSHLVEALYLVCGER	GFFYT	3	[0:-C1:+57.021,C5:+57.021,C14:+57.021	742.0261711	2223.055113	0.000979378	1	N	27	46
P01326	Conv	IVDQC	CTSICSLYQLENYCN	-	2	C1:+57.021,C5:+57.021,C14:+57.021	962.897164	1923.778728	0.000622848	3	N	95	110
P01639	Conv	SLTCR	ASQDIGSSLNWLQQEPDGTIKR	LIYAT	3		815.0791043	2442.213913	0.002727428	1	N	46	68
P01723	Conv	GGAIS	QAVVTQESALTTSPGETVTLTCR	SSTGA	2	[0:-17.027,C22:+57.021	1216.602376	2431.189152	0.002884417	1	N	20	43
P01786	Conv	QPPGK	ALEWLGFIR	NKABG	2		552.8141807	1103.612761	0.000622848	5	N	43	52
P01786	Conv	-EVK	LVESGGGLVQPGGSLR	LSCAT	2		763.420801	1524.826002	0.000451244	9	N	3	19
P01812	Conv	QAPGK	GLEWIGEIDPNSSTINYTPSLK	DKFII	2		1217.610984	2433.206368	0.0025889	1	N	43	65
P01837	Conv	-	ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPK	DINVK	3	C26:+57.021	1191.25234	3570.733621	0.000451244	30	N	0	34
P01837	Conv	DGSER	QNGVLNSWTDQDSK	DSTYS	2		796.3715051	1590.72741	0.000622848	3	N	47	61
P01868	Conv	PPKPK	DVLTITLTPK	VTCVV	2		550.8322361	1099.648872	0.000451244	9	N	125	135
P01868	Conv	TLTPK	VTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR	EEQFN	4	C3:+57.021	987.2299546	3944.888618	0.000451244	5	N	135	169
P01868	Conv	LNVQK	SNWEAGNTFTCSVLHEGLHNHHTEK	SLSHS	3	C11:+57.021	969.107574	2904.299322	0.001463592	2	N	291	316
P01872	Conv	LKDGK	LVESGFTTDPVTIENK	GSTPQ	2		875.4494212	1748.883242	0.000451244	64	N	154	170
P01872	Conv	LLSPK	SILEGSDEYLVCK	IHYGG	2	C12:+57.021	756.866447	1511.717294	0.000451244	12	N	76	89
P01872	Conv	PRKSK	LICEATNFTPKPITVSWLK	DGKLV	2	C3:+57.021	1109.600948	2217.186296	0.000451244	18	N	132	151
P01872	Conv	GGKNR	DLHVPIPAVAEMNPNVNVFVPPR	DGFSG	3		842.4498158	2524.326047	0.000451244	5	N	97	120
P01872	Conv	TCLVK	GFSPADISVQWLQR	GQLLP	2		802.4155186	1602.815437	0.000451244	20	N	355	369
P01872	Conv	TFSAK	GVASVCVEDWNNRK	EFVCT	2	C6:+57.021	817.3914863	1632.767373	0.000451244	12	N	286	300
P01872	Conv	TFSAK	GVASVCVEDWNNR	KEFVC	2	C6:+57.021	753.3440047	1504.672409	0.000451244	9	N	286	299
P01872	Conv	RTGGK	YLATSQVLLSPK	SILEG	2		660.3826245	1318.749649	0.000451244	23	N	64	76
P01872	Conv	FYFTH	SILTVTEEEWNSGETYTCVVGHEALPHLVTER	TVDKS	4	C18:+57.021	914.9442942	3655.745977	0.000622848	3	N	396	428
P01872	Conv	HYGGK	NRDLHVPIPAVAEMNPNVNVFVPPR	DGFSG	4	M14:+15.995	703.6240715	2810.465086	0.000622848	3	N	95	120
P01872	Conv	PAPRK	SKLICEATNFTPKPITVSWLK	DGKLV	3	C5:+57.021	811.7788959	2432.313288	0.001162105	4	N	130	151
P01872	Conv	RTVDK	STGKPTLYNVSLIMSDTGGTCY	-	2	C21:+57.021	1183.056442	2364.097284	0.000451244	7	N	432	454
P01872	Conv	SPQKK	FISKPNEVHKHPPAVYLLPPAR	EQLNL	3		837.4730603	2509.395781	0.000698008	2	N	317	339
P01872	Conv	VSWLK	DGKLVESGFTTDPVTIENK	GSTPQ	2		1025.521106	2049.026612	0.000451244	4	N	151	170
P01872	Conv	PQTYK	VISTLTISEIDWLNLNVYTCR	VDHRG	3	C20:+57.021	837.4371984	2509.288195	0.002884417	1	N	178	199
P01872	Conv	LRESA	TVTCLVKGFSPADISVQWLQR	GQLLP	3	C4:+57.021	802.4267451	2404.256835	0.001463592	1	N	348	369
P01872	Conv	VISTL	TISEIDWLNLNVYTCR	VDHRG	2	C15:+57.021	998.9937729	1995.971946	0.000451244	6	N	183	199
P01872	Conv	LPQEK	YVTSAPMPEPGAPGFYFTH	SILTV	2	M7:+15.995	1042.975323	2083.935047	0.001699387	2	N	377	396
P01878	Conv	AVQKK	AVQNSCGCYSVSSVLPGCAER	WNSGA	2	C6:+57.021,C8:+57.021,C18:+57.021	1151.006297	2299.996994	0.000451244	14	N	165	186
P01878	Conv	GASFK	CTVTHPESGTLTGTIAK	VTVNT	3	C1:+57.021	591.6334609	1771.876983	0.000622848	1	N	194	211
P01887	Conv	MSFSK	DWSFYILAHTEFTPTETDTYACR	VKHAS	3	C22:+57.021	942.090527	2823.248181	0.000451244	10	N	78	101
P01887	Conv	SFYIL	AHTEFTPTETDTYACR	VKHAS	2	C15:+57.021	950.4128127	1898.810025	0.002981883	1	N	85	101
P01900	Conv	SHSLR	YFVTAVSRPGFGEPR	YMEVG	3		561.6270122	1681.857636	0.000451244	6	N	30	45
P01942	Conv	AAWGK	IGGHGAEYGAEALER	MFASF	2		765.3713081	1528.727016	0.000451244	54	N	17	32
P01942	Conv	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	2		910.4422648	1818.86893	0.000451244	49	N	41	57
P01942	Conv	ASLDK	FLASVSTVLTSK	YR-	2		626.8615249	1251.70745	0.000451244	146	N	128	140
P01942	Conv	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHKLR	VDPVN	4		777.1669732	3104.636693	0.000622848	9	N	62	93
P01942	Conv	KGHGK	KVADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		988.856627	2963.546481	0.000451244	20	N	61	91
P01942	Conv	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	2		1418.733559	2835.451518	0.000451244	15	N	62	91
P01942	Conv	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDKFLASVSTVLTSK	YR-	3	C5:+57.021	1428.766862	4283.277185	0.000451244	5	N	100	140
P01942	Conv	PAVHA	SLDKFLASVSTVLTSK	YR-	2		848.4805243	1694.945449	0.001463592	1	N	124	140
P01942	Conv	EALER	MFASFPTTK	TYFPH	2		515.2578502	1028.5001	0.000451244	24	N	32	41
P01942	Conv	LLVTL	ASHHPADFTPAVHASLDK	FLASV	2		950.9691781	1899.922756	0.002981883	1	N	110	128
P01942	Conv	LVTLA	SHHPADFTPAVHASLDK	FLASV	3		610.6363474	1828.885642	0.000662267	2	N	111	128
P01942	Conv	AWGKI	GGHGAEYGAEALER	MFASF	2		708.829276	1415.642952	0.000451244	11	N	18	32
P01942	Conv	HCLLV	TLASHHPADFTPAVHASLDK	FLASV	3		705.6926329	2114.054499	0.000451244	9	N	108	128
P01942	Conv	TKTYF	PHFDVSHGSAQVK	GHGKK	2		704.8525542	1407.689508	0.000451244	3	N	44	57
P01942	Conv	FPTTK	TYFPHFDVSHGSAQVKG	HGKKV	2		938.9529967	1875.890393	0.000451244	11	N	41	58
P01942	Conv	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDK	FLASV	3	C5:+57.021	1017.534565	3049.580295	0.000451244	21	N	100	128
P01942	Conv	KLLSH	CLLVTLASHHPADFTPAVHASLDK	FLASV	4	[0:-17.027,C1:+57.021	646.5813567	2582.294227	0.001395409	3	N	104	128
P01942	Conv	HGKKV	ADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		913.1355012	2736.383104	0.000451244	6	N	63	91
P01942	Conv	HLDDL	PGALSALSDLHAHK	LRVDP	2		708.8838543	1415.752109	0.000823681	1	N	77	91
P01942	Conv	GKKVA	DALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		889.4564633	2665.34599	0.0007646	1	N	64	91
P01942	Conv	VADAL	ASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		789.7404229	2366.197869	0.002212458	2	N	67	91

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01942	Conv	LPGAL	SALSDLHAHK	LRVDP	2		539.7861515	1077.556703	0.002145581	3	N	81	91
P01942	Conv	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHKL	RVDPV	4		738.1416955	2948.535582	0.000622848	3	N	62	92
P01942	Conv	ASHHP	ADFTPAVHASLDKFLASVSTVLTSK	YR-	3		869.1344386	2604.379916	0.000622848	12	N	115	140
P01942	Conv	ASLDK	FLASVSTVLTSKY	R-	2		708.3931892	1414.770778	0.000451244	8	N	128	141
P01942	Conv	ADALA	SAAGHLDDLPGALSALSDLHAHK	LRVDP	3		766.061385	2295.160755	0.000622848	3	N	68	91
P01942	Conv	GHGKK	VADALASAAGHLDDLPGALSAL	SDLHA	2		1024.537091	2047.058581	0.001463592	1	N	62	84
P01942	Conv	PVNFK	LLSHCLLVTLASHHPADFTPAVH	ASLDK	4	C5:+57.021	634.8340956	2535.305183	0.000622848	1	N	100	123
P01942	Conv	LASAA	GHLDDLPGALSALSDLHAHK	LRVDP	2		1034.035049	2066.054499	0.001463592	1	N	71	91
P01942	Conv	PVNFK	LLSHCLLVTLASHHPADFTPAVHA	SLDKF	4	C5:+57.021	652.5933741	2606.342296	0.000823681	1	N	100	124
P01942	Conv	GHGKK	VADALASAAGHLDDLPGALSALSDLHAH	KLRVD	3		903.4599849	2707.356555	0.002519933	1	N	62	90
P01942	Conv	KGHGK	KVADALASAAGHLDDLPGALSAL	SDLHA	2		1088.584572	2175.153544	0.002145581	1	N	61	84
P01942	Conv	GHGKK	VADALASAAGHLDDLPGALSALSDLH	AHKLR	3		834.0946429	2499.260529	0.0025889	1	N	62	88
P01942	Conv	DFTPA	VHASLDKFLASVSTVLTSK	YR-	3		668.3777628	2002.109888	0.001329271	1	N	121	140
P01942	Conv	GHGKK	VADALASAAGHLDDLPGALSALSDL	HAHKL	3		788.408339	2362.201617	0.002884417	2	N	62	87
P01942	Conv	LVTLA	SHHPADFTPAVHASLDKFLASVSTVLTSK	YR-	4		766.653433	3062.582532	0.000451244	1	N	111	140
P01942	Conv	KGHGK	KVADALASAAGHLDDLPGALSALSDL	HAHKL	3		831.10666	2490.29658	0.0025889	1	N	61	87
P02088	Conv	-M	VHLTDAEKAAVSCLWGK	VNSDE	3	C13:+57.021	628.9931006	1883.955902	0.000451244	6	N	1	18
P02088	Conv	PWTQR	YFDSFGDLSSASAIMGNAK	VKAHG	2		990.9545453	1979.893491	0.000451244	37	N	41	60
P02088	Conv	CLWGK	VNSDEVGGEALGR	LLVVY	2		651.818377	1301.621154	0.000451244	23	N	18	31
P02088	Conv	TDAEK	AAVSCLWGK	VNSDE	2	C5:+57.021	496.2554099	990.4952199	0.000451244	61	N	9	18
P02088	Conv	KAHGK	KVITAFNDGLNHLDSLK	GTFAS	2		943.0130543	1884.010509	0.000451244	2	N	66	83
P02088	Conv	VITAF	NDGLNHLDSLK	GTFAS	2		613.3127305	1224.609861	0.000451244	10	N	72	83
P02088	Conv	AHGKK	VITAFNDGLNHLDSLKG	TFASL	2		907.4763046	1812.937009	0.000451244	14	N	67	84
P02088	Conv	GKKVI	TAFNDGLNHLDSLK	GTFAS	2		772.8893337	1543.763067	0.000451244	9	N	69	83
P02088	Conv	AHGKK	VITAFNDGLNHLDSLK	GTFAS	2		878.9655727	1755.915545	0.000451244	57	N	67	83
P02088	Conv	WTQRY	FDSFGDLSSASAIMGNAK	VKAHG	2		909.422881	1816.830162	0.000451244	6	N	42	60
P02088	Conv	PENFR	LLGNMIVIVLGHHLGK	DFTPA	2		857.5139821	1713.012364	0.000622848	8	N	105	121
P02088	Conv	HGKKV	ITAFNDGLNHLDSLK	GTFAS	2		829.4313657	1656.847131	0.000451244	4	N	68	83
P02088	Conv	AHGKK	VITAFNDGLNHLDSLKGTFA	SLSEL	2		1067.052908	2132.090216	0.000451244	2	N	67	87
P02088	Conv	AHGKK	VITAFNDGLNHLDSLKGTFASLSELHCDK	LHVDP	3	C27:+57.021	1068.199799	3201.575998	0.000451244	4	N	67	96
P02088	Conv	PENFR	LLGNMIVIVLGHHLGKDFTPAAQAAFQK	VVAGV	3		997.2201839	2988.637152	0.000451244	4	N	105	133
P02088	Conv	AHGKK	VITAFNDGLNHLDSLKGTFASL	SELHC	3		778.4099027	2332.206308	0.000823681	3	N	67	89
P02089	Conv	PENFR	LLGNAIVIVLGHHLGK	DFTPA	2		827.5122961	1653.008992	0.000451244	12	N	105	121
P02089	Conv	PWTQR	YFDSFGDLSSASAIMGNPK	VKAHG	2		1003.96237	2005.909141	0.000451244	19	N	41	60
P02089	Conv	CLWAK	VNPDEVGGEALGR	LLVVY	2		656.8287447	1311.641889	0.000451244	40	N	18	31
P02089	Conv	KAHGK	KVITAFNEGLK	NLDNL	2		610.3564097	1218.697219	0.000998612	4	N	66	77
P02089	Conv	TDAEK	SAVSCLWAK	VNPDE	2	C5:+57.021	511.2606923	1020.505785	0.000451244	33	N	9	18
P02089	Conv	AHGKK	VITAFNEGLK	NLDNL	2		546.3089281	1090.602256	0.000823681	21	N	67	77
P02089	Conv	WAKVN	PDEVGGEALGR	LLVVY	2		550.2730739	1098.530548	0.002212458	2	N	20	31
P02089	Conv	PENFR	LLGNAIVIVLGH	HLGKD	2		609.8825947	1217.749589	0.002453667	1	N	105	117
P02089	Conv	PENFR	LLGNAIVIVLGHHLGKDFTPAAQAAFQK	VVAGV	3		977.2190599	2928.63378	0.000451244	5	N	105	133
P02535	Conv	EVTLR	QSVEADINGLRR	VLDEL	3		453.2447907	1356.710972	0.002019181	2	N	243	255
P02535	Conv	QLALK	QSLEASLAETEGR	YCVQL	2		695.8445918	1389.673584	0.000451244	4	N	384	397
P02535	Conv	MDKVR	ALEESNYELEGK	IKEWY	2		691.3282432	1380.640886	0.000451244	3	N	163	175
P04104	Conv	IDKVR	FLEQQNQVLQTK	WELLQ	2		738.3967946	1474.777989	0.000451244	18	N	207	219
P04104	Conv	EINKR	TNAENEFVTIKK	DVDSA	3		465.2494303	1392.724891	0.000622848	3	N	285	297
P04104	Conv	EINKR	TNAENEFVTIK	KDVDS	2		633.3227639	1264.629928	0.002374549	1	N	285	296
P04202	Conv	YLGNR	LLTPTDTPEWLSFDVTGVVR	QWLNQ	2		1123.589323	2245.163046	0.000451244	14	N	185	205
P04202	Conv	STRDR	VAGESADPEPEPEADYYAK	EVTRV	2		1019.450346	2036.885093	0.000451244	22	N	87	106
P04202	Conv	TGVVR	QWLNQGDGIQGFR	FSAHC	2		759.8765606	1517.737521	0.000451244	6	N	205	218
P04202	Conv	TQYSK	VLALYNQHNPGASASPCCVPQALEPLPIVYYVGR	KPKVE	3	C17:+57.021,C18:+57.021	1251.967727	3752.87978	0.000451244	10	N	338	372
P04202	Conv	IHEPK	GYHANFCLGPCPYIWSLDTQYSK	VLALY	3	C7:+57.021,C11:+57.021	926.4212882	2776.240465	0.000451244	5	N	315	338
P04202	Conv	LRLQR	LKSSVEQHVELYQK	YSNNS	3		563.3058272	1686.894082	0.001162105	1	N	159	173
P04919	Conv	LLLKR	SHAEDLGNLEGVKPAVLTR	SGGAS	2		1003.537425	2005.05925	0.000451244	22	N	175	194
P04919	Conv	AVLTR	SGGASEPLLPHQPSLETQLYCGQAEGGSEGPSTSGTLK	IPPDS	3	C21:+57.021	1276.606171	3826.795112	0.000451244	73	N	194	232
P04919	Conv	VLVGR	ANFLEKPVLGFVR	LKEAV	2		745.4304404	1488.845281	0.000451244	8	N	246	259
P04919	Conv	LGFVR	LKEAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1346.41743	4036.22889	0.000451244	22	N	259	296
P04919	Conv	LGFVR	LKEAVPLEDLVLPEPVGF	LLVLL	2		983.0513138	1964.087028	0.000870037	7	N	259	277
P04919	Conv	FVRLK	EAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1266.024421	3795.049862	0.000451244	24	N	261	296
P04919	Conv	EELLR	SLESFLDCSLVLPPTDAPSEK	ALLNL	2	C8:+57.021	1153.067332	2304.119064	0.000451244	25	N	322	343
P04919	Conv	TVMGK	ASGPGAAAQIQEVK	EQRIS	2		663.8547625	1325.693925	0.000622848	3	N	761	775
P04919	Conv	ALLLK	RSHAEDLGNLEGVKPAVLTR	SGGAS	3		721.394587	2161.160361	0.000451244	1	N	174	194
P04919	Conv	SGTLK	IPPDSETTLVLVGR	ANFLE	2		748.9201025	1495.824605	0.000451244	24	N	232	246
P04919	Conv	APSEK	ALLNLVPVQK	ELLRR	2		547.8507632	1093.685926	0.000451244	31	N	343	353
P04919	Conv	AVLTR	SGGASEPLLPHQPSLETQLY	CGQAE	2		1062.534548	2123.053496	0.000451244	8	N	194	214

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P04919	Conv	MMDQR	NQELQWVEAAHWIGLEENLR	EDGVW	2		1218.109277	2434.202954	0.000451244	14	N	83	103
P04919	Conv	GVWGR	PHLSYLTFWSLLELQK	VFSKG	3		659.0282938	1974.061482	0.001395409	3	N	110	126
P04919	Conv	KVFSK	GTFLLGLAETSLAGVANHLLDCFIYEDQIRPQDREELLR	ALLLK	4	C22:+57.021	1119.077642	4472.27937	0.000823681	8	N	130	169
P04919	Conv	KVFSK	GTFLLGLAETSLAGVANHLLDCFIYEDQIRPQDR	EELLR	3	C22:+57.021	1278.316115	3831.924944	0.000451244	22	N	130	164
P04919	Conv	GKLRR	VIGDFGVPISILIMVLVDSFIK	GTYTQ	2		1188.187088	2374.358576	0.000451244	2	N	621	643
P04919	Conv	EPVGF	LLVLLGPEAPHVDYTQLGR	AAATL	2		1046.084011	2090.152422	0.000451244	3	N	277	296
P04919	Conv	MMDQR	NQELQWVEAAHWIGLEENLREDGVWGR	PHLSY	3		1078.862552	3233.564256	0.001463592	4	N	83	110
P04919	Conv	EAVPL	EDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1096.262771	3285.764913	0.000622848	1	N	266	296
P04919	Conv	LLVLL	GPEAPHVDYTQLGR	AAATL	2		770.3816758	1538.747752	0.002212458	1	N	282	296
P04919	Conv	LGFVR	LKEAVPLEDLVLPEPVGFLLV	LLGPE	2		1145.669585	2289.32357	0.002296037	1	N	259	280
P04919	Conv	LGFVR	LKEAVPLEDLVLPEPVGFL	LVLLG	2		1039.593346	2077.171092	0.000622848	6	N	259	278
P04919	Conv	LGFVR	LKEAVPLEDLVLPEPVGFLL	VLLGP	2		1096.135378	2190.255156	0.001229886	2	N	259	279
P04919	Conv	SLETQ	LYCGQAEGGSEGPSTSGTLK	IPPDS	2	C3:+57.021	999.9575844	1997.899569	0.000451244	3	N	212	232
P04919	Conv	AVLTR	SGGASEPLLPHQPSLETQ	LYCGQ	2		924.4608515	1846.906103	0.000451244	2	N	194	212
P04919	Conv	FVRLK	EAVPLEDLVLPEPVGFL	LVLLG	2		919.0038323	1835.992065	0.001463592	1	N	261	278
P05201	Conv	KVEQK	IANDNSLNHEYLPILGLAEFR	SCASR	2		1200.121853	2398.228106	0.000451244	7	N	60	81
P05201	Conv	-M	APPSVFAQVPQAPPVLVFK	LTADF	2		996.5700081	1991.124416	0.000451244	13	N	1	20
P05201	Conv	VMQRR	FLFPFFDSAYQGFASGDLEK	DAWAI	2		1143.541842	2285.068083	0.000451244	11	N	216	236
P05201	Conv	VGAYR	TDESQPWVLPVVR	KVEQK	2		763.4046196	1524.793639	0.000451244	11	N	42	55
P05201	Conv	AQGAR	IVAATLSDPELFK	EWKGN	2		702.3931892	1402.770778	0.001162105	1	N	305	318
P05201	Conv	GLTTK	NLDYVATSIHEAVTK	IQ-	3		554.2900657	1659.846797	0.0007646	2	N	396	411
P05201	Conv	AQGAR	IVAATLSDPELFKEWK	GNVKT	3		616.3370159	1845.987648	0.000622848	3	N	305	321
P05202	Conv	TKDGR	ISVAGVTSGNVGYLAHAIHQVTK	-	3		774.7575254	2321.249176	0.000823681	2	N	407	430
P05202	Conv	QIAAK	NLDKEYLPIGGLAEFCK	ASAEL	2	C16:+57.021	984.0010667	1965.986533	0.000451244	19	N	90	107
P05202	Conv	LKSGR	FVTVQTISGTGALR	VGASF	2		725.4071623	1448.798725	0.002080925	1	N	125	139
P05202	Conv	AEFCK	ASAELALGENNEVLK	SGRFV	2		779.410099	1556.804598	0.000451244	8	N	107	122
P05202	Conv	YYDPK	TCGFDFSGALEDISK	IPEQS	2	C2:+57.021	823.8722607	1645.728921	0.000451244	13	N	185	200
P05202	Conv	LNGAR	IAATILTSPDLR	KQWLQ	2		635.8724239	1269.729248	0.000451244	3	N	325	337
P06151	Conv	LMGER	LGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	3	C8:+57.021	1204.279335	3609.814606	0.000451244	16	N	177	212
P06151	Conv	SPHCK	LLIVSNPVDILTY	VAWKI	2		730.4244894	1458.833379	0.000662267	7	N	132	145
P06151	Conv	STMIK	GLYGINEDVFLSVPCILGQNGISDVVK	VTLTP	2	C15:+57.021	1453.75234	2905.48908	0.000451244	46	N	278	305
P06151	Conv	SPHCK	LLIVSNPVDILTYVAWK	ISGFP	2		972.5643914	1943.113183	0.000451244	45	N	132	149
P06151	Conv	GVSLK	SLNPELGTDADKEQWK	EVHKQ	2		915.947577	1829.879554	0.000451244	38	N	212	228
P06151	Conv	ARLKK	SADTLWGIQK	ELQF-	2		559.7961849	1117.57677	0.000451244	29	N	318	328
P06151	Conv	MATLK	DQLIVNLLKEEQAPQNK	ITVVG	2		990.5421759	1979.068752	0.000451244	19	N	5	22
P06151	Conv	SILMK	DLADELALVDVMEDK	LKGEM	2		838.4089079	1674.802216	0.000622848	2	N	42	57
P06151	Conv	VIKLK	GYTSWAIGLSVADLAESIMK	NLRRV	2		1056.538245	2111.06089	0.000451244	15	N	245	265
P06151	Conv	VFLSV	PCILGQNGISDVVK	VTLTP	2	C2:+57.021	750.3982486	1498.780897	0.001162105	3	N	291	305
P06151	Conv	KEVHK	QVVDSAYEVIK	LKGYT	2		625.8355071	1249.655414	0.000451244	18	N	232	243
P06151	Conv	GVHAL	SCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	3	C2:+57.021	1007.494658	3019.460574	0.000451244	2	N	183	212
P06151	Conv	KEQWK	EVHKQVVDSAYEVIK	LKGYT	2		872.4679482	1742.920296	0.000451244	8	N	228	243
P06151	Conv	RLGVH	ALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	4	C4:+57.021	801.903238	3203.581752	0.000823681	1	N	181	212
P06151	Conv	SPHCK	LLIVSNPVDIL	TYVAW	2		598.3689858	1194.722372	0.002296037	2	N	132	143
P06336	Conv	SEDKR	TLTCLIQNFFPEDISVQWLGDGK	LISNS	2	C4:+57.021	1341.167912	2680.320224	0.00091018	1	N	326	349
P06336	Conv	PVVAK	DWIEGYGYQCIVDHPDFPKPIVR	SITKT	3	C10:+57.021	935.455252	2803.342356	0.000451244	7	N	275	298
P06745	Conv	KGGPR	VWFVSNIDGTHIAK	TLASL	2		793.9204368	1585.825274	0.000451244	30	N	180	194
P06745	Conv	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	2		1423.725065	2845.43453	0.000451244	24	N	523	550
P06745	Conv	KSGAR	VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	MIPCD	3		1105.881835	3314.622106	0.000451244	28	N	370	400
P06745	Conv	NLKLR	ELFEADPERFNNFSLNLNTNHGHILVDYSK	NLVNK	3		1178.574848	3532.701144	0.000451244	11	N	27	57
P06745	Conv	IIASK	TFTTQETITNAETAKEWFLEAAK	DPSAV	2		1315.65338	2629.29116	0.000451244	21	N	211	234
P06745	Conv	THIAK	TLASLSPETSLFIIASK	TFTTQ	2		889.5014568	1776.987314	0.000451244	41	N	194	211
P06745	Conv	VDYSK	NLVNKEVMQMLVELAK	SRGVE	3		620.3430084	1858.005625	0.000451244	11	N	57	73
P06745	Conv	GLHHK	ILLANFLAQTEALMK	GKLPE	2		838.4767309	1674.937862	0.000451244	23	N	423	438
P06745	Conv	GYTGK	SITDIINIGIGGSDLGPLMVTEALKPYSK	GGPRV	3		1001.542658	3001.604574	0.000451244	28	N	147	176
P06745	Conv	LLPHK	VFEGNRPTNSIVFTK	LTPFI	2		854.955008	1707.894416	0.000451244	21	N	466	481
P06745	Conv	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	2		1224.109277	2446.202954	0.000451244	23	N	36	57
P06745	Conv	IIASK	TFTTQETITNAETAK	EWFLE	2		828.410296	1654.804992	0.000451244	42	N	211	226
P06745	Conv	QLAKK	IEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	2		1359.677584	2717.339567	0.000451244	15	N	524	550
P06745	Conv	AETAK	EWFLEAAKDPSAVAK	HFVAL	2		831.4308344	1660.846069	0.000451244	20	N	226	241
P06745	Conv	SANLK	LRELFEADPER	FNNFS	3		458.905775	1373.693925	0.001591523	6	N	25	36
P06745	Conv	RFNNF	SLNLNTNHGHILVDYSK	NLVNK	2		962.9979355	1923.980271	0.000451244	5	N	40	57
P06745	Conv	NLVNK	EVMQMLVELAK	SRGVE	2		645.8439644	1289.672329	0.001162105	2	N	62	73
P06745	Conv	IVFTK	LTPFILGALIAMYEHK	IFVQG	2		909.0056556	1815.995711	0.000823681	4	N	481	497
P06745	Conv	TPLEK	NAPVLLALLGIWYINCYGCETHALLPYDQYMHR	FAAYF	3	C16:+57.021,C19:+57.021	1322.31625	3963.925351	0.000451244	5	N	314	347
P06745	Conv	HQGTK	MIPCDFLIPVQTQHPIRK	GLHHK	4	C4:+57.021	549.0476427	2192.159371	0.001162105	1	N	400	418

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P06745	Conv	TNTAK	VKEFGIDPQNMFEFWDWVGGR	YSLWS	3		853.0710045	2556.189613	0.002296037	1	N	252	273
P06745	Conv	GLHHK	ILLANFLAQTEAL	MKGKL	2		708.9090065	1415.802413	0.000823681	1	N	423	436
P06745	Conv	SAVAK	HFVALSTNTAK	VKEFG	2		594.822734	1187.629868	0.002080925	1	N	241	252
P06800	Conv	QEDSR	GVGTPEPTNSAEEPEHAANGSASPAPTQSS	-	3		959.7643499	2876.26965	0.000851441	3	N	1261	1291
P06800	Conv	RKEPR	TVYQYQCTTWKGEELPAEPK	DLVSM	3	C7:+57.021	810.0548655	2427.141196	0.000451244	12	N	1102	1122
P06800	Conv	VKLVK	NVINVQTDLGIPETPKPSCGDPAAR	KTLVS	3	C19:+57.021	883.7819163	2648.322349	0.000451244	17	N	363	388
P06800	Conv	KLRRR	VNAFSNFFSGPIVVHCSAGVGR	TGTYI	3	C16:+57.021	774.7201515	2321.137054	0.001463592	2	N	824	846
P06800	Conv	ADEGR	LFLAEFQSIPR	VFSKF	2		660.8696843	1319.723769	0.000451244	5	N	638	649
P06800	Conv	LVHCR	DGSQQTGLFCALFNLLESAETEDVVDVFQVVK	SLRKA	3	C10:+57.021	1186.915505	3557.723116	0.000451244	7	N	1156	1188
P06909	Conv	EIDYR	ECGADGWINDIPLCEVVK	CLPVT	2	C2:+57.021,C14:+57.021	1037.982317	2073.949033	0.000451244	6	N	127	145
P06909	Conv	GPPPR	ENSEILSGSWSEQLYPEGTQATYK	CRPGY	2		1359.133009	2716.250418	0.000451244	3	N	27	51
P06909	Conv	NCTSK	TSCPPPPQIPNTQVIETTVK	YLDGE	2	C3:+57.021	1104.072752	2206.129903	0.000622848	10	N	805	825
P06909	Conv	RIIHR	SDDEIRYECNYGFYPVTGSTVSK	CTPTG	2	C9:+57.021	1344.100423	2686.185246	0.000823681	2	N	285	308
P06909	Conv	CIRIK	TCSASDIHIDNGFLSESSSIYALNR	ETSYR	3	C2:+57.021	919.7647024	2756.270707	0.000451244	7	N	446	471
P06909	Conv	LENGR	IVSGAAETDQEYYFGQVVR	FECNS	2		1066.518898	2131.022196	0.000451244	4	N	156	175
P06909	Conv	KYSYK	CDNGFSPPSGYSWDYLR	CTAQG	2	C1:+57.021	1010.92863	2019.84166	0.000637154	3	N	356	373
P06909	Conv	FPTCK	GQVASCAPPLEILNGEINGAK	KVEYS	2	C6:+57.021	1069.549444	2137.083287	0.001699387	1	N	623	644
P06909	Conv	FKYGR	LYYEESLRPNFPVSIGNK	YSYKC	3		709.3692673	2125.084402	0.000451244	1	N	334	352
P07356	Conv	LAKGR	RAEDGSVIDYELIDQDAR	ELYDA	2		1032.995787	2063.975974	0.000451244	14	N	178	196
P07356	Conv	AKGRR	AEDGSVIDYELIDQDAR	ELYDA	2		954.9452313	1907.874863	0.000451244	26	N	179	196
P07356	Conv	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAERDALNIETAVK	TKGVD	3		1331.655784	3991.943953	0.000451244	3	N	10	47
P07356	Conv	ETAVK	TKGVDEVTIVNILTNR	SNVQR	2		886.4997797	1770.983959	0.000451244	9	N	47	63
P07356	Conv	AVKTK	GVDEVTIVNILTNR	SNVQR	2		771.9284589	1541.841318	0.000451244	16	N	49	63
P07356	Conv	KASMK	GLGTDEDSLIEIICSR	TNQEL	2	C14:+57.021	889.4357565	1776.855913	0.000451244	20	N	119	135
P07356	Conv	PSALK	SALSGHLETVILGLLK	TPAQY	2		825.9936019	1649.971604	0.000451244	19	N	88	104
P07356	Conv	ESIKK	EVKGDLENAFLNLVQCIQNKPLYFADR	LYDSM	3	C16:+57.021	1065.548651	3193.622554	0.000451244	10	N	246	273
P07356	Conv	KKEVK	GDLENAFLNLVQCIQNKPLYFADR	LYDSM	2	C13:+57.021	1419.716092	2837.416584	0.000451244	5	N	249	273
P07356	Conv	KKEVK	GDLENAFLNLVQCIQNKPLYF	ADRLY	2	C13:+57.021	1248.633508	2495.251416	0.000451244	1	N	249	270
P07356	Conv	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAER	DALNI	3		980.133826	2937.378078	0.000823681	6	N	10	37
P07356	Conv	KEMYK	TDLEKDIISDTSGDFR	KLMVA	2		906.4370421	1810.858484	0.000451244	14	N	152	168
P07356	Conv	LGLLK	TPAQYDASELK	ASMKG	2		611.8016643	1221.587729	0.001943752	3	N	104	115
P07356	Conv	RKYGK	SLYYYIQQDTK	GDYQK	2		711.3515213	1420.687443	0.000622848	6	N	313	324
P07356	Conv	KKEVK	GDLENAFLNLVQ	CIQNK	2		666.8438635	1331.672127	0.002727428	1	N	249	261
P07724	Conv	AILVR	YTQKAPQVSTPTLVEAAR	NLGRV	2		980.5290685	1959.042537	0.000451244	1	N	434	452
P07724	Conv	DTCCK	AADKDTCFSTEGPNLVTR	CKDAL	2	C7:+57.021	991.4681193	1980.920639	0.000451244	71	N	584	602
P07724	Conv	RYTQK	APQVSTPTLVEAAR	NLGRV	2		720.3967946	1438.777989	0.000451244	43	N	438	452
P07724	Conv	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	2	C11:+57.021	1077.014902	2152.014205	0.000451244	27	N	527	545
P07724	Conv	SLVER	RPCFSALTVDETYVPK	EFKAE	2	C3:+57.021	941.9723092	1881.929018	0.000451244	7	N	508	524
P07724	Conv	LFGDK	LCAIPNLRENYGELADCCTK	QEPER	2	C2:+57.021,C17:+57.021,C18:+57.021	1199.053247	2396.090895	0.000451244	11	N	97	117
P07724	Conv	SLVER	RPCFSALTVDETYVPKEFK	AETFT	3	C3:+57.021	763.0527962	2286.134989	0.000451244	9	N	508	527
P07724	Conv	ANCDK	SLHTLFGDKLCAIPNLR	ENYGE	2	C11:+57.021	978.0304928	1954.045386	0.000622848	1	N	88	105
P07724	Conv	WAVAR	LSQTFPNADFAEITK	LATDL	2		841.425749	1680.835898	0.000451244	31	N	242	257
P07724	Conv	DLYEK	LGEYGFQNAILVR	YTQKA	2		740.4018799	1478.78816	0.000451244	73	N	421	434
P07724	Conv	KNLVK	TNCDLYEKLGEYGFQNAILVR	YTQKA	3	C3:+57.021	835.0814146	2502.220844	0.000451244	1	N	413	434
P07724	Conv	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	3	C1:+39.994,C2:+57.021,C10:+57.021	978.4432368	2932.30631	0.00091018	4	N	383	409
P07724	Conv	EQHFK	GLVLIAFSQYLQK	CSYDE	2		740.4326487	1478.849697	0.000451244	23	N	44	57
P07724	Conv	AEQLK	TVMDDFAQFLDTCCK	AADKD	2	C13:+57.021,C14:+57.021	925.8915822	1849.767564	0.000451244	17	N	569	584
P07724	Conv	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	2	C1:+39.994,C2:+57.021,C12:+57.021	1403.153464	2804.291329	0.00091018	1	N	460	483
P07724	Conv	YAEAK	DVFLGTFLYEYSR	RHPDY	2		805.3990029	1608.782406	0.000451244	46	N	347	360
P07724	Conv	PEDQR	LPCVEDYLSAILNR	VCLLH	2	C3:+57.021	831.929913	1661.844226	0.000451244	38	N	469	483
P07724	Conv	EVARR	HPYFYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C23:+57.021,C24:+57.021,C32:+57.021	1472.337619	4413.989458	0.000622848	2	N	169	205
P07724	Conv	IPNLR	ENYGELADCCTK	QEPER	2	C9:+57.021,C10:+57.021	730.2951002	1458.5746	0.000451244	13	N	105	117
P07724	Conv	DEHAK	LVQEVTDFAK	TCVAD	2		575.3116678	1148.607736	0.000451244	28	N	65	75
P07724	Conv	TKVNK	ECCHGDLLECADDR	AELAK	2	C2:+57.021,C3:+57.021,C10:+57.021	875.3347308	1748.653862	0.000451244	8	N	267	281
P07724	Conv	YEYSR	RHPDYSVSLLLR	LAKKY	3		485.9409311	1454.799393	0.000451244	39	N	360	372
P07724	Conv	PKEFK	AETFTFHSDICTLPEK	EKQIK	2	C11:+57.021	948.4461242	1894.876648	0.000451244	6	N	527	543
P07724	Conv	RRHPY	FYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C20:+57.021,C21:+57.021,C29:+57.021	1339.945951	4016.814453	0.000451244	10	N	172	205
P07724	Conv	TDLTK	VNKECCHGDLLECADDR	AELAK	3	C5:+57.021,C6:+57.021,C13:+57.021	697.6278554	2089.860166	0.000451244	2	N	264	281

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P07724	Conv	TKVNK	ECCHGDLLECADDRAELAK	YMCEN	2	C2:+57.021,C3:+57.021,C10:+57.021	1131.482655	2260.94971	0.000451244	17	N	267	286
P07724	Conv	DCCTK	QEPERNECFLQHK	DDNPS	3	[0:-17.027,C8:+57.021	566.5950788	1696.761836	0.001463592	2	N	117	130
P07724	Conv	PLLKK	AHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAK	DVFLG	4	C3:+57.021,M12:+15.995,C30:+57.021	1048.225455	4188.87062	0.000451244	4	N	310	347
P07724	Conv	PLLKK	AHCLSEVEHDTMPADLPAIAADFVEDQEVCK	NYAEA	3	C3:+57.021,C30:+57.021	1166.526993	3496.55758	0.000451244	7	N	310	341
P07742	Conv	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTK	HPDYA	3		956.1818943	2865.522283	0.000451244	11	N	42	70
P07742	Conv	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	C15:+57.021	1103.540753	2205.065906	0.000451244	5	N	529	548
P07759	Conv	HEKTR	ALYQTEAFTADFQQPTEAK	NLIND	2		1080.018731	2158.021861	0.000451244	13	N	157	176
P07759	Conv	QVVHK	AVLDVAETGTEAAAATGVIGGIR	KAILP	2		1071.574204	2141.132809	0.000451244	26	N	360	383
P07759	Conv	SLYKK	LALKNPDTNIVFSPLSISAALALVSLGAK	GKTME	3		975.2342642	2922.679393	0.000823681	1	N	62	91
P07759	Conv	KGKWK	ISFDPQDTFESEFYLDEK	RSVKV	2		1105.494754	2208.973908	0.000622848	7	N	217	235
P07759	Conv	KLALK	NPDTNIVFSPLSISAALALVSLGAK	GKTME	2		1249.697394	2497.379187	0.001162105	1	N	66	91
P07759	Conv	MFIEK	DLQILAEFHEK	TRALY	2		671.8542312	1341.692862	0.000735798	2	N	144	155
P07901	Conv	MAAKK	HLEINPDHSIIETLR	QKAEA	3		596.3202478	1785.937344	0.000451244	2	N	633	648
P07901	Conv	PIWTR	NPDDITNEEYGEFYK	SLTND	2		917.3948429	1832.774086	0.000451244	5	N	300	315
P07901	Conv	EIVKK	HSQFIGYPITLFVEKER	DKEVS	3		688.7024693	2063.084008	0.002080925	1	N	209	226
P07901	Conv	EIVKK	HSQFIGYPITLFVEK	ERDKE	2		889.9779518	1777.940304	0.000622848	7	N	209	224
P07901	Conv	VVSNR	LVTSPCCIVTSTYGWTANMER	IMKAQ	2	C6:+57.021,C7:+57.021,M19:+15.995	1231.56118	2461.10676	0.000451244	3	N	592	613
P07901	Conv	DKNDK	SVKDLVILLYETALLSSGFSLEDPQTHANR	IYRMI	3		1106.252823	3315.73507	0.000451244	3	N	658	688
P07901	Conv	DKSVK	DLVILLYETALLSSGFSLEDPQTHANR	IYRMI	3		1001.521021	3001.539664	0.000451244	11	N	661	688
P07901	Conv	EIFLR	ELISNSSDALDKIR	YESLT	2		780.9155485	1559.815497	0.000451244	11	N	46	60
P07901	Conv	EIFLR	ELISNSSDALDK	IRYES	2		646.3229609	1290.630322	0.000451244	2	N	46	58
P08003	Conv	VAKVR	EVSQPDWTPPPEVTLSLTK	DNFDD	2		1062.547124	2123.078648	0.00091018	11	N	158	177
P08003	Conv	ILTLK	QVQEFLKDGDDVVIIGLFQGDGDPAYLQYQDAANNLR	EDYKF	3		1375.678701	4124.012702	0.000451244	17	N	287	324
P08003	Conv	DLAKR	FDVSGYPTLK	IFRKG	2		563.7931109	1125.570622	0.000622848	1	N	239	249
P08003	Conv	LEVAK	DFPEYTFAIADEEDYATEVK	DLGLS	2		1177.023876	2352.032151	0.000451244	5	N	436	456
P08003	Conv	ATEVK	DLGLSESGEDVNAAILDESGKK	FAMEP	3		749.7049325	2246.091398	0.000451244	11	N	456	478
P08003	Conv	MLASK	FDVSGYPTIK	ILKKG	2		563.7931109	1125.570622	0.000451244	5	N	124	134
P08003	Conv	PEYEK	IASTLKDNDPPIAVAK	IDATS	3		551.6459609	1651.914483	0.000451244	6	N	96	112
P08030	Conv	GLDSR	GFLFGPSLAQELGVGCVLIR	KQGKL	2	C16:+57.021	1067.080183	2132.144765	0.000451244	16	N	67	87
P08030	Conv	KGRER	LGPIPFFSLLQYD	-	2		755.4035569	1508.791514	0.000451244	11	N	167	180
P08030	Conv	LHQLR	AEVVECVSLVELTSLK	GRERL	2	C6:+57.021	888.476893	1774.938186	0.000451244	26	N	147	163
P08030	Conv	THSGK	IDYIAGLDSR	GFLFG	2		561.7936422	1121.571684	0.000622848	6	N	57	67
P08030	Conv	LEYGK	AELEIQKDALEPGQR	VVIVD	2		848.94738	1695.87916	0.000451244	4	N	107	122
P08030	Conv	GLDSR	GFLFGPSLAQELGVGCVLIRK	QGKLP	3	C16:+57.021	754.4210429	2260.239729	0.00091018	5	N	67	88
P08030	Conv	EPGQR	VVIVDDLLATGGTMFAACDLLHQLR	AEVVE	3	C18:+57.021	910.1439094	2727.408328	0.000451244	5	N	122	147
P08030	Conv	ARRIR	SFPDFPIPGVLFR	DISPL	2		746.4038913	1490.792183	0.000622848	2	N	14	27
P08032	Conv	ENSIK	ALRDQAEVCQQQQAAPVDEAGR	EARVI	2	C9:+57.021	1220.585609	2439.155618	0.000451244	9	N	954	976
P08032	Conv	DKKCR	ALNAADPGSDLLSVQALQR	QHEVF	2		970.0163253	1938.017051	0.000451244	23	N	1202	1221
P08032	Conv	ATAQK	GTQLYEANQLLQFENNAEDLKR	WLEEV	2		1297.646421	2593.277242	0.000451244	23	N	677	699
P08032	Conv	LQKQR	TELNEAWDTLQGLTSDRK	ESLNE	2		1039.01398	2076.012359	0.000451244	16	N	1262	1280
P08032	Conv	WMKEK	TALINADELPTDVASGEALLAR	HQQHK	2		1120.592594	2239.169588	0.000451244	29	N	387	409
P08032	Conv	KDINK	VADELLFEELLTPEGAHIR	QELNT	2		1076.568391	2151.121181	0.000451244	16	N	1137	1156
P08032	Conv	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQEEK	IITLD	3		1389.649135	4165.924006	0.000451244	10	N	492	529
P08032	Conv	EIKAK	QDEVNAAWDRLWSLALK	RRESL	3		672.3502071	2014.027221	0.000451244	3	N	236	253
P08032	Conv	DPRGR	SQPAGYDYVGFTNSFFGN	-	2		985.9319269	1969.848254	0.000451244	15	N	2397	2415
P08032	Conv	ENWIK	TIGGVISSPELAEDLTGTEILLER	HQEHH	2		1257.171406	2512.327211	0.000451244	23	N	1304	1328
P08032	Conv	DKQIK	ALNVPSSPYTWLTVDVLGR	IWNHL	2		1044.560369	2087.105137	0.000451244	15	N	2106	2125
P08032	Conv	ATRRK	LLVDSQLLQQLYQDSDDLKTWINK	KKKLA	3		959.5067122	2875.496737	0.000451244	18	N	574	598
P08032	Conv	SLKTK	SNGADLTAFLTLLAK	HDTLD	2		767.9279275	1533.840255	0.000451244	51	N	1950	1965
P08032	Conv	LKQLR	LLWDLLLELTQEKSDVLLR	ALKFY	3		766.4425438	2296.304231	0.000451244	14	N	135	154
P08032	Conv	VSMKK	NDVLTLLSSINKDWWK	VEADD	2		966.5154298	1931.01526	0.000622848	2	N	998	1014
P08032	Conv	EMLAR	EDPLKDLNDLAQELISSGTFNIDQIEEK	MNGVN	3		1058.861661	3173.561582	0.000451244	48	N	1657	1685
P08032	Conv	FQQER	LSEIAELKDQLVAGEHSQAK	AIEEQ	2		1083.574204	2165.132809	0.000451244	4	N	1980	2000
P08032	Conv	EVNGR	AEQVDGVINLGNSLIER	RVCDG	2		913.9844938	1825.953388	0.000451244	18	N	1549	1566
P08032	Conv	AHHEK	LKETYALFQFFQDLDDEEAWIEEK	LLRVS	3		1003.146961	3006.417483	0.000622848	5	N	1706	1730
P08032	Conv	ETAER	LCESHPDATEDLQK	QRTEL	2	C2:+57.021	821.872792	1641.729984	0.000451244	1	N	1246	1260
P08032	Conv	SSGPK	VLETAEEIQHR	RAEVL	2		662.8469375	1323.678275	0.000622848	1	N	15	26
P08032	Conv	GKYQK	HESFVSEVQAK	SRVLP	2		630.815106	1259.614612	0.001162105	1	N	91	102
P08032	Conv	IKALR	DQAEVCQQQQAAPVDEAGR	EARVI	2	C6:+57.021	1050.474464	2098.933329	0.000451244	7	N	957	976
P08032	Conv	ALKRR	ESLSNAADLQR	FKRDV	2		602.3023627	1202.589125	0.000622848	4	N	255	266
P08032	Conv	HRNRR	EIDNTLQNINSK	RDNLE	2		694.8549595	1387.694319	0.000451244	12	N	1362	1374
P08032	Conv	NKKKK	LADDDDYKDVQNLK	SRVQK	2		826.3946459	1650.773692	0.000451244	21	N	601	615

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08032	Conv	ERGQK	LEESYHYQVFR	RDADD	2		735.8547625	1469.693925	0.002663018	2	N	47	58
P08032	Conv	NLLNR	HEVILADIASHEPR	IQVIT	2		793.9184255	1585.821251	0.000823681	9	N	832	846
P08032	Conv	VHKNR	VQDVCAQGEDILNKEETQNK	DKIST	3	C5:+57.021	773.3695127	2317.085138	0.000451244	6	N	1872	1892
P08032	Conv	EVLHK	KFEEFQEELTAR	KGKVD	2		763.8784346	1525.741269	0.000451244	16	N	196	208
P08032	Conv	TLLAK	HDTLDASLQSFQQER	LSEIA	2		887.9218935	1773.828187	0.000451244	28	N	1965	1980
P08032	Conv	LDRWK	ALKEQLLTELGK	LGDYA	3		448.2700543	1341.786763	0.000451244	11	N	1481	1493
P08032	Conv	ALVSR	GDSGDTLAATQSLLK	KHEAL	2		738.8811743	1475.746749	0.000451244	14	N	1842	1857
P08032	Conv	LFLSK	ASDLENWIK	TIGGV	2		538.2750853	1074.534571	0.000823681	10	N	1295	1304
P08032	Conv	QQICR	DSEDEEAWIQETEPSAASTHLGK	DLVAA	2		1265.564959	2529.114318	0.000451244	19	N	798	821
P08032	Conv	GREAR	VIALYDFEAR	SRREV	2		598.81966	1195.62372	0.000698008	8	N	979	989
P08032	Conv	LAAWK	SQLDDVHAFQQFNWK	ADVVE	2		931.9451716	1861.874743	0.000451244	18	N	1917	1932
P08032	Conv	QIQAK	DTIGVSEETLKEFSTTYK	HFDEN	2		1024.507664	2046.999729	0.000451244	15	N	2259	2277
P08032	Conv	LKKHK	RLEGELVAHEPAVQNVLDTAESLR	DKAAV	3		882.80023	2645.37729	0.000451244	13	N	1754	1778
P08032	Conv	GALLK	KHEAFLVDLNAFENSIK	ALRDQ	2		988.0183367	1974.021073	0.000451244	14	N	937	954
P08032	Conv	KKHKR	LEGELVAHEPAVQNVLDTAESLR	DKAAV	3		830.7665263	2489.276179	0.000451244	20	N	1755	1778
P08032	Conv	SENIK	TSDDIESAFQALAEGK	AYITK	2		841.3999282	1680.784256	0.000451244	16	N	2348	2364
P08032	Conv	AATRR	KLLVDSQLLQQLYQDSDDLK	TWINK	3		788.0887178	2361.242753	0.000451244	7	N	573	593
P08032	Conv	LRALK	FYQYSQECEDILEWVK	EKEAI	2	C8:+57.021	1068.983071	2135.950542	0.000451244	15	N	157	173
P08032	Conv	LQKQR	TELNEAWDTLQGLTSDR	KESLN	2		974.9664981	1947.917396	0.000451244	16	N	1262	1279
P08032	Conv	WVKEK	EAIVTLVELGDDWER	TEVLH	2		872.9417633	1743.867927	0.000451244	17	N	175	190
P08032	Conv	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	2		1245.62208	2489.22856	0.000451244	22	N	492	515
P08032	Conv	ATRRK	LLVDSQLLQQLYQDSDDLK	TWINK	2		1117.581695	2233.14779	0.000451244	19	N	574	593
P08032	Conv	DDIKR	EDPTFQALEDFGTELIDSGHR	NRREI	2		1189.05129	2376.086981	0.000451244	9	N	1338	1359
P08032	Conv	IKRED	PTFQALEDFGTELIDSGHR	NRREI	3		711.6802815	2132.017445	0.000451244	6	N	1340	1359
P08032	Conv	PQHRQ	EEPVNIPQLQQQVETLYHSLLDR	AEERR	2		1375.211928	2748.408256	0.000622848	2	N	1045	1068
P08032	Conv	NTSIR	DFEFWLSEAEGLLAMKDQAR	DLTSA	3		786.0479769	2355.120531	0.001264573	2	N	1615	1635
P08032	Conv	LKQLR	LLWDLLLELTQEK	SDVLL	2		807.4616032	1612.907606	0.000451244	21	N	135	148
P08032	Conv	NTSIR	DFEFWLSEAEGLLAMK	DQARD	2	M15:+15.995	951.4536925	1900.891785	0.000823681	2	N	1615	1631
P08032	Conv	GVNER	FENVQSLAAAHHEK	LKETY	2		790.8949504	1579.774301	0.000451244	1	N	1692	1706
P08032	Conv	NVATR	LIDNDHYAKEEIAAR	LQRVL	2		879.4450044	1756.874409	0.000451244	4	N	1457	1472
P08032	Conv	AQEGK	ISDLENVATR	LIDND	2		559.2965491	1116.577498	0.002884417	1	N	1447	1457
P08032	Conv	ALLQK	HDDFEEAFTAQEEK	IITLD	2		848.360803	1694.706006	0.000451244	16	N	515	529
P08032	Conv	SYDDR	FQSADATGQELLDGNHEASEEIREK	MTILA	3		925.4341641	2773.279092	0.000451244	7	N	423	448
P08032	Conv	KDWWK	VEADDHQGFVPAVYVR	KLAPD	2		901.4475471	1800.879494	0.000451244	20	N	1014	1030
P08032	Conv	DVLGR	IWNHLPDIIK	EREQE	3		416.9086797	1247.702639	0.000823681	7	N	2125	2135
P08032	Conv	WIQEK	KTENTGVELDDVWELQK	KFDEF	2		1002.500174	2002.984747	0.000451244	16	N	1099	1116
P08032	Conv	QDYGR	DLQSVQNLLK	KHKRL	2		579.3303919	1156.645184	0.000451244	10	N	1741	1751
P08032	Conv	EDYGK	GLADVQNLLR	KHGLL	2		549.8174517	1097.619303	0.000451244	13	N	715	725
P08032	Conv	IQEKK	TENTGVELDDVWELQK	KFDEF	2		938.4526922	1874.889784	0.000451244	14	N	1100	1116
P08032	Conv	DPGRK	GYVSLEDYTSFLIDKESENIK	TSDDI	3		817.4044831	2449.190049	0.000451244	11	N	2327	2348
P08032	Conv	ENDLK	ANVQLQQYLADLHEAEAWIK	EKEPI	2		1170.603296	2339.190992	0.000451244	5	N	894	914
P08032	Conv	RQLQK	EHEAFLASLAGAQEDFNYLLELDK	QIKAL	2		1362.164112	2722.312624	0.000451244	10	N	2079	2103
P08032	Conv	HRQEE	PVNIPQLQQQVETLYHSLLDR	AEERR	3		831.1154898	2490.323069	0.001395409	1	N	1047	1068
P08032	Conv	LKETY	ALFQFFQDLDDEEAWIEEK	LLRVS	2		1187.050228	2372.084856	0.000451244	2	N	1711	1730
P08032	Conv	HSQAK	AIEEQHAALLR	HWEQL	2		625.8467405	1249.677881	0.001229886	1	N	2000	2011
P08032	Conv	QHQYR	QCLDFHLFYR	DSEQV	3	C2:+57.021	466.8926581	1397.654574	0.000451244	13	N	471	481
P08032	Conv	KKHKR	LEGELVAHEPAVQNVLDTAESLRDK	AAVGK	3		911.8071617	2732.398085	0.000451244	15	N	1755	1780
P08032	Conv	ENRKK	MLDQCLELQLFR	GKCDQ	2	M1:+15.995,C5:+57.021	791.3921523	1580.768705	0.000451244	11	N	1387	1399
P08032	Conv	LEWVK	EKEAIVTLVELGDDWER	TEVLH	2		1001.510541	2001.005483	0.000622848	3	N	173	190
P08032	Conv	EDPLK	DLNDLAQELISSGTFNIDQIEEK	MNGVN	2		1296.637927	2591.260254	0.0025889	1	N	1662	1685
P08032	Conv	EVSMK	KNDVLTLLSSINK	DWWKV	2		722.9226452	1443.82969	0.000451244	6	N	997	1010
P08032	Conv	TYALF	QFFQDLDDEEAWIEEK	LLRVS	2		1021.455432	2040.895264	0.0025889	1	N	1714	1730
P08032	Conv	HDDIK	REDPTFQALEDFGTELIDSGHR	NRREI	3		845.0704974	2532.188092	0.000622848	3	N	1337	1359
P08032	Conv	KDQAR	DLTSAGNLLK	KHQLL	2		516.2907354	1030.565871	0.002019181	1	N	1635	1645
P08032	Conv	ALLKK	HEAFLVDLNAFENSIK	ALRDQ	2		923.9708551	1845.92611	0.001162105	1	N	938	954
P08032	Conv	ERGNK	MVEEGHFAAEDIASR	VESLN	3		554.5916392	1660.751518	0.000451244	17	N	856	871
P08032	Conv	ETATK	LIDNDHYDSENIAAIR	DGLLA	3		620.303034	1857.885702	0.000622848	8	N	539	555
P08032	Conv	SYDDR	FQSADATGQELLDGNHEASEEIR	EKMTI	2		1259.078568	2516.141536	0.002374549	1	N	423	446
P08032	Conv	VLHKK	FEEFQEELTAR	KGKVD	2		699.8309531	1397.646306	0.001162105	7	N	197	208
P08032	Conv	AVAAR	LSEVANLWK	ELLEA	2		530.2958207	1058.576041	0.000451244	7	N	659	668
P08032	Conv	NSLKR	LADEQYQLLSSAHAVEMFHR	EADDV	4	M17:+15.995	591.0383033	2360.122013	0.000451244	9	N	1168	1188
P08032	Conv	ETATK	LIDNDHYDSENIAAIRDGLLAR	RDALR	3		828.7546207	2483.240462	0.000451244	11	N	539	561
P08032	Conv	RSCLR	GLNYYLPMVEEGEPEPK	FEKFL	2	M8:+15.995	990.9671641	1979.918728	0.000451244	6	N	2297	2314
P08032	Conv	QQICR	DSEDEEAWIQETEPSAASTHLGKDLVAAK	NLLNR	3		1043.16211	3126.46293	0.000451244	10	N	798	827
P08032	Conv	TSDRK	ESLNEAHKFFLFLSK	ASDLE	3		603.9898391	1808.946117	0.000451244	8	N	1280	1295

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08032	Conv	IQETR	AYFLDGSLLK	ETGTL	2		563.8113036	1125.607007	0.000451244	5	N	2173	2183
P08032	Conv	SGWMK	EKTALINADELPTDVASGEALLAR	HQQHK	3		833.1101816	2496.307145	0.000451244	5	N	385	409
P08032	Conv	EDLKR	WLEEVEWQVTSEDYGK	GLADV	2		999.4605172	1996.905434	0.000451244	6	N	699	715
P08032	Conv	FLIDK	ESENIKTSDDIESAFQALAEGK	AYITK	3		794.7156087	2381.123426	0.000622848	4	N	2342	2364
P08032	Conv	LRALK	FYQYSQECEDILEWVKEK	EAIVT	3	C8:+57.021	798.7038327	2393.088098	0.000451244	6	N	157	175
P08032	Conv	YGYHR	FLSDYDELSGWMK	EKTAL	2		795.8613965	1589.707193	0.000451244	3	N	372	385
P08032	Conv	SRVQK	QQDFEEELAVNEIMLNNLEK	TGQEM	2		1203.578827	2405.142054	0.000451244	7	N	620	640
P08032	Conv	WVKEK	EAIVTLVELGDDWERTEVLHK	KFEEF	3		818.0959838	2451.264552	0.000451244	12	N	175	196
P08032	Conv	RAIRR	ENDLKANVQLQQYLADLHEAEAWIK	EKEPI	3		980.5019612	2938.482484	0.000622848	3	N	889	914
P08032	Conv	EASLK	TKSNGADLTAFLTLLAK	HDTLD	3		588.6687656	1762.982897	0.000451244	10	N	1948	1965
P08032	Conv	LNEIR	QLQKEHEAFLASLAGAQEDFNYLLELDK	QIKAL	3		1074.210736	3219.608807	0.000451244	5	N	2075	2103
P08032	Conv	RQLQK	EHEAFLASLAGAQEDFNYLLELDKQIK	ALNVP	3		1031.524543	3091.550229	0.000451244	10	N	2079	2106
P08032	Conv	KQFYR	DLEDLEEWINEMLPIACDESYKDPTNIQR	KYLKH	3	C17:+57.021	1179.545084	3535.611852	0.000451244	2	N	1505	1534
P08032	Conv	ARQIK	NFEMCQEFEQNASAFLQWIQETR	AYFLD	3	M4:+15.995,C5:+57.021	974.7659663	2921.274499	0.000451244	3	N	2150	2173
P08032	Conv	LAKTR	GVNLEESLEYLQFMENAEEEEAWLGEK	CALVS	3		1062.820697	3185.43869	0.000451244	7	N	1809	1836
P08032	Conv	SRQQR	FNTSIRDFEFWLSEAEGLLAMK	DQARD	3	M21:+15.995	874.0971363	2619.268009	0.000823681	1	N	1609	1631
P08032	Conv	EIREK	MTILANDWAALLELWDK	CQHQY	2		1002.019491	2002.023383	0.000451244	9	N	448	465
P08032	Conv	RVAER	GQKLEESYHYQVFR	RDADD	2		892.4422648	1782.86893	0.000451244	2	N	44	58
P08032	Conv	SLLSR	FEALKEPLAIR	KKKLI	2		643.8775093	1285.739419	0.001329271	1	N	772	783
P08032	Conv	KDINK	VADELLFEELLTPEGAHIRQELNTR	WNSLK	4		724.1323334	2892.498134	0.002019181	1	N	1137	1162
P08032	Conv	IQQMK	LDLVSNWER	IRALA	2		566.2938094	1130.572019	0.000823681	4	N	343	352
P08032	Conv	QIQAK	DTIGVSEETLKEFSTTY	KHFDE	2		960.4601829	1918.904766	0.000451244	3	N	2259	2276
P08032	Conv	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQ	EEKII	3		1260.922419	3779.743856	0.002080925	1	N	492	526
P08032	Conv	PQHRQ	EEPVNIPQLQQQVETLYHSLLDRAEER	RRRLL	4		809.4157168	3233.631667	0.00091018	2	N	1045	1072
P08032	Conv	KMTIL	ANDWAALLELWDK	CQHQY	2		772.891345	1543.76709	0.000622848	3	N	452	465
P08032	Conv	IKALR	DQAEVCQQQQAAPVDEAGREAR	VIALY	3	C6:+57.021	819.3791823	2455.114147	0.000451244	3	N	957	979
P08032	Conv	GSLLK	ETGTLESQLEANK	RKQKE	2		710.3522497	1418.688899	0.000451244	1	N	2183	2196
P08071	Conv	VTEAK	NCHLAIAPNHAVVSR	TDKVE	2	C2:+57.021	829.931113	1657.846626	0.000451244	17	N	603	618
P08071	Conv	VTEYK	ECHLAQVPSHAVVSR	STNDK	2	C2:+57.021	845.4284031	1688.841206	0.000451244	7	N	261	276
P08071	Conv	KPPYK	LRPVAAEVYGTK	EQPRT	2		652.3725911	1302.729582	0.001162105	2	N	91	103
P08071	Conv	ASKAR	VTWCAVGSEEKR	KCDQW	2	C4:+57.021	711.346016	1420.676432	0.000451244	9	N	362	374
P08071	Conv	ATTVQ	WCAVSNSEEEKCLR	WQNEM	2	C2:+57.021,C12:+57.021	884.3931374	1766.770675	0.001591523	1	N	25	39
P08071	Conv	AGALR	CLRDNAGDVAFTR	GSTVF	2	C1:+57.021	747.8598219	1493.704044	0.000451244	1	N	215	228
P08071	Conv	PGAQK	DRFPNLCSSCAGTGANK	CASSP	2	C7:+57.021,C10:+57.021	927.9147683	1853.813937	0.000451244	41	N	181	198
P08071	Conv	GADPK	SNLCALCIGDEKGENK	CAPNS	2	C4:+57.021,C7:+57.021	904.4193522	1806.823104	0.000451244	161	N	516	532
P08071	Conv	TTSEK	YLGKEYVIATER	LKQCS	2		721.3884382	1440.761276	0.000451244	37	N	677	689
P08071	Conv	ASKAR	VTWCAVGSEEK	RKCDQ	2	C4:+57.021	633.2954605	1264.575321	0.000451244	67	N	362	373
P08071	Conv	AQKDR	FPNLCSSCAGTGANK	CASSP	2	C5:+57.021,C8:+57.021	792.3507412	1582.685882	0.000451244	36	N	183	198
P08071	Conv	VAFTR	GSTVFEELPNKAER	DQYKL	2		788.9024411	1575.789282	0.000451244	54	N	228	242
P08071	Conv	VAFLK	DSTVLQNTDGKNTEEWAR	NLKLK	2		1032.485586	2062.955573	0.000451244	114	N	562	580
P08071	Conv	RSCKF	NEFFSQSCAPGADPK	SNLCA	2	C8:+57.021	827.8622273	1653.708855	0.000451244	67	N	501	516
P08071	Conv	LFQSK	TKNLLFNDNTECLAK	IPGKT	2	C12:+57.021	890.9488341	1779.882068	0.000451244	75	N	653	668
P08071	Conv	GADPK	SNLCALCIGDEK	GENKC	2	C4:+57.021,C7:+57.021	690.3183783	1378.621157	0.000451244	21	N	516	528
P08071	Conv	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	C1:+39.994	899.3911235	1796.766647	0.000451244	3	N	198	215
P08071	Conv	ANQTR	SCKFNEFFSQSCAPGADPK	SNLCA	2	C2:+57.021,C12:+57.021	1088.975023	2175.934446	0.000451244	6	N	497	516
P08071	Conv	CLAEK	AGNVAFLKDSTVLQNTDGK	NTEEW	2		989.5161581	1977.016716	0.000451244	11	N	554	573
P08071	Conv	YTAGK	CGLVPVLAENQK	SSKSN	2	C1:+39.994	655.8423524	1309.669105	0.0025889	1	N	422	434
P08071	Conv	RDQYK	LLCPDNTWKPVTEYK	ECHLA	2	C3:+57.021	932.4694023	1862.923205	0.000451244	17	N	246	261
P08071	Conv	VAAVR	REDAGFTWSSLR	GKKSC	2		712.8500115	1423.684423	0.000451244	50	N	458	470
P08071	Conv	RDQYK	LLCPDNTWKPVTEYKECHLAQVPSHAVVSR	STNDK	3	C3:+57.021,C17:+57.021	1178.92575	3533.753851	0.000451244	17	N	246	276
P08071	Conv	TRSCK	FNEFFSQSCAPGADPK	SNLCA	2	C9:+57.021	901.3964343	1800.777269	0.000451244	356	N	500	516
P08071	Conv	QKSSK	SNGLDCVNRPVEGYLAVAAVRR	EDAGF	3	C6:+57.021	806.089015	2415.243645	0.000823681	4	N	437	459
P08071	Conv	KFGKK	QASGFQLFASPSGQK	DLLFK	2		776.8918764	1551.768153	0.000451244	30	N	299	314
P08071	Conv	GQRCP	GEFCLFQSK	TKNLL	2	C4:+57.021	558.263432	1114.511264	0.000451244	17	N	644	653
P08071	Conv	QSKTK	NLLFNDNTECLAK	IPGKT	2	C10:+57.021	776.3775132	1550.739426	0.000451244	388	N	655	668
P08071	Conv	NLKLK	DFELLCLDDTRKPVTEAK	NCHLA	2	C6:+57.021	1075.543827	2149.072054	0.000451244	23	N	585	603
P08071	Conv	RNGQR	CPGEFCLFQSK	TKNLL	2	C1:+57.021,C6:+57.021	686.8049068	1371.594214	0.000451244	250	N	642	653
P08071	Conv	VAIMK	GDADAMSLDGGYIYTAGK	CGLVP	2		902.9070637	1803.798527	0.000451244	17	N	404	422
P08071	Conv	AAVRR	EDAGFTWSSLR	GKKSC	2		634.7994559	1267.583312	0.000823681	31	N	459	470
P08071	Conv	QKSSK	SNGLDCVNRPVEGYLAVAAVR	REDAG	2	C6:+57.021	1130.579067	2259.142534	0.000451244	22	N	437	458
P08071	Conv	RDQYK	LLCPDNTWKPVTEY	KECHL	2	C3:+57.021	868.4219208	1734.828242	0.000451244	3	N	246	260
P08071	Conv	ARNLK	LKDFELLCLDDTR	KPVTE	2	C8:+57.021	819.4140957	1636.812591	0.000451244	28	N	583	596
P08071	Conv	PSGQK	DLLFKESAIGFVR	VPQKV	3		498.9492037	1493.824211	0.0025889	1	N	314	327
P08071	Conv	AVVSR	STNDKEEAIWELLR	QSQEK	2		852.4341054	1702.852611	0.000451244	32	N	276	290
P08071	Conv	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2		1085.071101	2168.126601	0.000622848	8	N	299	319

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08071	Conv	KVEVL	QQVLLDQQVQFGR	NGQRC	2		779.9209682	1557.826336	0.000451244	7	N	625	638
P08071	Conv	NRASR	GRVTCISFPTTEDCIVAIMK	GDADA	2	C5:+57.021,C14:+57.021	1149.568234	2297.120868	0.000451244	7	N	384	404
P08071	Conv	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	2		1172.137503	2342.259406	0.000451244	1103	N	618	638
P08071	Conv	IATER	LKQCSSSPLLEACAFLTQ	-	2	C4:+57.021,C13:+57.021	1027.008334	2052.001069	0.000451244	115	N	689	707
P08071	Conv	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	2		1361.732299	2721.448998	0.000451244	12	N	144	169
P08071	Conv	TERLK	QCSSSPLLEACAFLTQ	-	2	C2:+57.021,C11:+57.021	906.4188208	1810.822042	0.000451244	92	N	691	707
P08071	Conv	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKF	FSKSC	3		957.1802708	2868.517412	0.000451244	3	N	144	170
P08071	Conv	ASRGR	VTCISFPTTEDCIVAIMKGDADAMSLDGGYIYTAGK	CGLVP	3	C3:+57.021,C12:+57.021	1290.936553	3869.78626	0.000870037	3	N	386	422
P08071	Conv	QKSSK	SNGLDCVNRPVEGY	LAVAA	2	C6:+57.021	790.3623945	1578.709189	0.000451244	10	N	437	451
P08071	Conv	SRTDK	VEVLQQVLLDQQVQFGR	NGQRC	2		1000.052711	1998.089822	0.000451244	24	N	621	638
P08071	Conv	ASRGR	VTCISFPTTEDCIVAIMK	GDADA	2	C3:+57.021,C12:+57.021	1043.006946	2083.998293	0.000451244	32	N	386	404
P08071	Conv	DPKSN	LCALCIGDEKGENK	CAPNS	2	C2:+57.021,C5:+57.021	803.8818741	1605.748148	0.000451244	23	N	518	532
P08071	Conv	EKFGK	KQASGFQLFASPSGQK	DLLFK	2		840.9393579	1679.863116	0.000451244	16	N	298	314
P08071	Conv	VAFTR	GSTVFEELPNK	AERDQ	2		610.812032	1219.608464	0.000451244	17	N	228	239
P08071	Conv	GWKIP	IGTLRPYLNWNGPPASLEEAVSK	FFSKS	3		838.1118568	2511.31217	0.001943752	1	N	146	169
P08071	Conv	PVTEY	KECHLAQVPSHAVVSR	STNDK	3	C3:+57.021	606.6531898	1816.936169	0.000823681	1	N	260	276
P08071	Conv	EAKNC	HLAIAPNHAVVSR	TDKVE	3		462.2656376	1383.773513	0.001229886	1	N	605	618
P08071	Conv	TEAKN	CHLAIAPNHAVVSR	TDKVE	3	C1:+57.021	515.6090328	1543.803698	0.000451244	5	N	604	618
P08071	Conv	ATTVQ	WCAVSNSEEEK	CLRWQ	2	C2:+57.021	669.7854569	1337.555314	0.001395409	1	N	25	36
P08071	Conv	KEQPR	THYYAVAVVK	NSSNF	2		575.8169203	1149.618241	0.000637154	14	N	107	117
P08071	Conv	NEMRK	VGGPPLSCVK	KSSTR	2	C8:+57.021	507.2763424	1012.537085	0.000622848	10	N	46	56
P08071	Conv	PKSNL	CALCIGDEKGENK	CAPNS	2	C1:+57.021,C4:+57.021	747.3398421	1492.664084	0.000451244	17	N	519	532
P08071	Conv	SSKSN	GLDCVNRPVEGYLAVAAVR	REDAG	3	C4:+57.021	687.0303259	2058.067578	0.000451244	5	N	439	458
P08071	Conv	NLKLK	DFELLCLDDTR	KPVTE	2	C6:+57.021	698.8245821	1395.633564	0.000451244	20	N	585	596
P08071	Conv	AVVSR	TDKVEVLQQVLLDQQVQF	GRNGQ	2		1065.576216	2129.136832	0.000451244	1	N	618	636
P08071	Conv	RVPQK	VDVGLYLTFSYTTSIQNLNK	KQQDV	2		1138.594606	2275.173611	0.000451244	22	N	331	351
P08071	Conv	NSKER	YQGYTGALR	CLAEK	2		514.7621451	1027.50869	0.001871652	2	N	540	549
P08071	Conv	KSSTR	QCIQAIVTNR	ADAMT	2	C2:+57.021	601.8194371	1201.623274	0.000662267	3	N	61	71
P08071	Conv	IATER	LKQCSSSPLLEAC	AFLTQ	2	C4:+57.021,C13:+57.021	746.8604104	1491.705221	0.000451244	7	N	689	702
P08071	Conv	IGTLR	PYLNWNGPPASLEEAVSK	FFSKS	2		986.4946944	1970.973789	0.000823681	2	N	151	169
P08071	Conv	RVPQK	VDVGLYLTFSYTTSIQNLNKK	QQDVI	3		802.0973247	2403.268574	0.000451244	5	N	331	352
P08071	Conv	LYLTF	SYTTSIQNLNKK	QQDVI	2		698.8756949	1395.73579	0.002663018	1	N	340	352
P08071	Conv	TLRPY	LNWNGPPASLEEAVSK	FFSKS	2		856.4366481	1710.857696	0.000451244	3	N	153	169
P08071	Conv	DADAM	SLDGGYIYTAGK	CGLVP	2		622.812032	1243.608464	0.000622848	3	N	410	422
P08071	Conv	QYKLL	CPDNTWKPVTEYK	ECHLA	2	C1:+57.021	819.3853382	1636.755076	0.001162105	1	N	248	261
P08071	Conv	NGQRC	PGEFCLFQSK	TKNLL	2	C5:+57.021	606.7898139	1211.564028	0.001699387	1	N	643	653
P08071	Conv	RLKQC	SSSPLLEACAFLTQ	-	2	C9:+57.021	762.3744392	1522.733278	0.000622848	13	N	693	707
P08071	Conv	IATER	LKQCSSSPLLEACAF	LTQ-	2	C4:+57.021,C13:+57.021	855.9131743	1709.810749	0.000451244	7	N	689	704
P08071	Conv	LKQCS	SSPLLEACAFLTQ	-	2	C8:+57.021	718.858425	1435.70125	0.002453667	1	N	694	707
P08071	Conv	VAFLK	DSTVLQNTDGK	NTEEW	2		589.288921	1176.562242	0.001162105	7	N	562	573
P08071	Conv	LKDST	VLQNTDGKNTEEWAR	NLKLK	2		880.9322612	1759.848922	0.000451244	6	N	565	580
P08071	Conv	KDSTV	LQNTDGKNTEEWAR	NLKLK	2		831.3980542	1660.780508	0.000451244	10	N	566	580
P08071	Conv	AENQK	SSKSNGLDCVNRPVEGYLAVAAVR	REDAG	3	C9:+57.021	854.7749846	2561.301554	0.0007646	2	N	434	458
P08071	Conv	TRSCK	FNEFFSQSCAPGAD	PKSNL	2	C9:+57.021	788.8225708	1575.629542	0.002727428	1	N	500	514
P08071	Conv	QKSSK	SNGLDCVNRPVEGYLAVA	AVRRE	2	C6:+57.021	967.4757474	1932.935895	0.000622848	4	N	437	455
P08113	Conv	AKLLR	FQSSHHSTDITSLDQYVER	MKEKQ	2		1125.525243	2249.034886	0.000451244	2	N	511	530
P08113	Conv	REGSR	TDDEVVQREEEAIQLDGLNASQIR	ELREK	3		910.1181759	2727.331128	0.000451244	5	N	43	67
P08113	Conv	RLLKK	GYEVIYLTEPVDEYCIQALPEFDGKR	FQNVA	3	C15:+57.021	1035.502596	3103.484389	0.000451244	18	N	561	587
P08113	Conv	LDKIR	LISLTDENALAGNEELTVK	IKCDK	2		1015.536756	2029.057912	0.000823681	4	N	116	135
P08113	Conv	KNLVR	KYSQFINFPIYVWSSK	TETVE	3		669.6845271	2006.030181	0.000451244	8	N	269	285
P08113	Conv	TLVLK	EEASDYLELDTIK	NLVRK	2		763.3675654	1524.719531	0.001943752	1	N	252	265
P08113	Conv	GFVRA	DDEVDVDGTVEEDLGK	SREGS	2		867.8817653	1733.747931	0.002374549	1	N	21	37
P08226	Conv	NLMEK	IQASVATNPIITPVAQENQ	-	2		997.5318082	1993.048016	0.001763695	2	N	292	311
P08226	Conv	TGCLA	EGEPEVTDQLEWQSNQPWEQALNR	FWDYL	2		1442.163163	2882.310727	0.000451244	6	N	18	42
P08226	Conv	QGRQR	TANLGAGAAQPLR	DRAQA	2		620.344365	1238.67313	0.002453667	1	N	201	214
P08226	Conv	KAYKK	ELEEQLGPVAEETR	ARLGK	2		800.3971886	1598.778777	0.000451244	15	N	86	100
P08228	Conv	ADEER	HVGDLGNVTAGKDGVANVSIEDR	VISLS	2		1162.085999	2322.156398	0.000451244	5	N	80	103
P08228	Conv	-MAMK	AVCVLKGDGPVQGTIHFEQK	ASGEP	2	C3:+57.021	1092.067804	2182.120007	0.001329271	1	N	4	24
P08228	Conv	SIEDR	VISLSGEHSIIGR	TMVVH	3		456.5934199	1366.75686	0.001763695	1	N	103	116
P08228	Conv	VCVLK	GDGPVQGTIHFEQK	ASGEP	2		756.8762263	1511.736853	0.000662267	3	N	10	24
P08228	Conv	VTAGK	DGVANVSIEDR	VISLS	2		587.7890882	1173.562576	0.002981883	1	N	92	103
P08249	Conv	GHAGK	TIIPLISQCTPK	VDFPQ	2	C9:+57.021	685.8895281	1369.763456	0.000451244	10	N	203	215
P08249	Conv	QCTPK	VDFPQDQLATLTGR	IQEAG	2		780.9049838	1559.794368	0.000451244	13	N	215	229
P08249	Conv	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	2		1197.127136	2392.238671	0.000451244	9	N	52	74
P08249	Conv	FVQSK	ETECTYFSTPLLLGK	KGLEK	2	C4:+57.021	879.934861	1757.854122	0.000451244	14	N	281	296

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08249	Conv	RANVK	GYLGPEQLPDCLKGCDVVVIPAGVPR	KPGMT	3	C11:+57.021,C15:+57.021	937.1509094	2808.429328	0.000451244	10	N	78	104
P08249	Conv	QNNAK	VAVLGASGGIGQPLSLLLK	NSPLV	2		897.0489085	1792.082217	0.000451244	15	N	26	45
P08249	Conv	PDCLK	GCDVVVIPAGVPR	KPGMT	2	C2:+57.021	669.8638446	1337.712089	0.001162105	4	N	91	104
P08249	Conv	AMNGK	EGVVECSFVQSK	ETECT	2	C6:+57.021	684.8271248	1367.63865	0.000451244	8	N	269	281
P08249	Conv	YNPNK	IFGVTTLDIVR	ANTFV	2		617.3642347	1232.712869	0.002813207	3	N	165	176
P08249	Conv	RANVK	GYLGPEQLPDCLK	GCDVV	2	C11:+57.021	745.3716995	1488.727799	0.001871652	2	N	78	91
P08607	Conv	TVVNK	TVPVWSSSPPTCEK	IICSQ	2	C12:+57.021	787.8798887	1573.744177	0.000451244	3	N	228	242
P08607	Conv	PTCEK	IICSQPNILHGVIVSGYK	ATYTH	2	C3:+57.021	999.5459757	1997.076351	0.000451244	1	N	242	260
P08607	Conv	LEIYK	LTLEVELLQLQIQK	EKHTE	2		834.5012598	1666.98692	0.001943752	1	N	448	462
P08607	Conv	MVYSK	ITLVTYECDKGYR	LVGKA	2	C8:+57.021	809.4009883	1616.786377	0.002080925	1	N	321	334
P08607	Conv	EVRGK	GVAWSNPFPECVIVK	CGPPP	2	C11:+57.021	851.9349983	1701.854397	0.000451244	2	N	165	180
P08752	Conv	NDLER	IAQSDYIPTQQDVLR	TRVKT	2		873.955205	1745.89481	0.000823681	1	N	162	177
P08752	Conv	LFEEK	ITQSSLTICFPEYTGANKYDEAASYIQSK	FEDLN	3	C9:+57.021	1095.85922	3284.554259	0.000637154	6	N	278	307
P08752	Conv	FGRSR	EYQLNDSAAYYLNDLER	IAQSD	2		1038.979605	2075.943611	0.000451244	4	N	145	162
P08752	Conv	LFEEK	ITQSSLTICFPEYTGANKY	DEAAS	2	C9:+57.021	1097.030552	2192.045505	0.000622848	1	N	278	297
P08905	Conv	NYNTR	ATNYNRGDQSTDYGIFQINSR	YWCND	2		1210.565431	2419.115261	0.000451244	19	N	59	80
P08905	Conv	TNYNR	GDQSTDYGIFQINSR	YWCND	2		850.897887	1699.780174	0.000451244	22	N	65	80
P08905	Conv	NYNTR	ATNYNRGDQSTDYGIFQIN	SRYWC	2		1088.998861	2175.982122	0.000622848	5	N	59	78
P08905	Conv	DGKTP	RAVNACGINCSALLQDDITAAIQCAK	RVVRD	3	C6:+57.021,C10:+57.021,C24:+57.021	945.1300254	2832.366676	0.000451244	3	N	89	115
P08905	Conv	GKTPR	AVNACGINCSALLQDDITAAIQCAKR	VVRDP	3	C5:+57.021,C9:+57.021,C23:+57.021	945.1300254	2832.366676	0.000451244	5	N	90	116
P08905	Conv	GKTPR	AVNACGINCSALLQDDITAAIQCAK	RVVRD	2	C5:+57.021,C9:+57.021,C23:+57.021	1339.140583	2676.265565	0.000451244	63	N	90	115
P08905	Conv	RTLKR	NGMAGYYGVSLADWVCLAQHESNYNTR	ATNYN	3	C16:+57.021	1026.127758	3075.359875	0.000451244	10	N	32	59
P08905	Conv	AVNAC	GINCSALLQDDITAAIQCAK	RVVRD	2	C4:+57.021,C18:+57.021	1081.532705	2161.04981	0.000451244	7	N	95	115
P08905	Conv	GMAGY	YGVSLADWVCLAQHESNYNTR	ATNYN	3	C10:+57.021	828.3854971	2482.133091	0.002884417	1	N	38	59
P08905	Conv	TNYNR	GDQSTDYGIFQIN	SRYWC	2		729.3313172	1456.647034	0.001162105	1	N	65	78
P09055	Conv	HLVQK	LSENNIQTIFAVTEEFQPVYK	ELKNL	2		1235.629177	2469.242753	0.000451244	9	N	325	346
P09055	Conv	CTDPK	FQGPTCETCQTCLGVCAEHKECVQCR	AFNKG	4	C6:+57.021,C9:+57.021,C12:+57.021,C16:+57.021,C22:+57.021,C25:+57.021	804.5866299	3214.31532	0.000823681	4	N	624	650
P09055	Conv	GMAEK	LRPEDITQIQPQQLLLK	LRSGE	3		678.3971573	2032.168072	0.002374549	1	N	105	122
P09055	Conv	PFSYK	NVLSLTDRGEFFNELVGQQR	ISGNL	3		774.7332683	2321.176405	0.000451244	9	N	220	240
P09055	Conv	KVESR	EKLPQPVQVDPVTHCK	EKDID	3	C15:+57.021	625.664984	1873.971552	0.001162105	3	N	676	692
P09103	Conv	EEMTK	YKPESDELTAEKITEFCHR	FLEGK	4	C17:+57.021	589.0340863	2352.105145	0.001162105	4	N	328	347
P09103	Conv	ARVGA	DALEEEDNVLVLKK	SNFEE	2		807.9334069	1613.851214	0.002296037	1	N	19	33
P09103	Conv	IRLAK	VDATEESDLAQQYGVR	GYPTI	2		890.9215592	1779.827518	0.000451244	42	N	83	99
P09103	Conv	ARVGA	DALEEEDNVLVLK	KSNFE	2		743.8859253	1485.756251	0.000451244	14	N	19	32
P09103	Conv	GFKGK	ILFIFIDSDHTDNQR	ILEFF	2		917.4606545	1832.905709	0.000622848	3	N	287	302
P09103	Conv	KQPVK	VLVGANFEEVAFDEK	KNVFV	2		833.9202995	1665.824999	0.000451244	16	N	372	387
P09103	Conv	YTAGR	EADDIVNWLK	KRTGP	2		601.8067496	1201.597899	0.000451244	9	N	122	132
P09103	Conv	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3		880.7905604	2639.348281	0.000451244	29	N	172	197
P09103	Conv	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	DVESD	3		995.8366752	2984.486626	0.000451244	16	N	134	164
P09103	Conv	IGFFK	DVESDSAKQFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3		1157.910903	3470.709309	0.000622848	3	N	164	197
P09103	Conv	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	3		1272.957018	3815.847653	0.000451244	24	N	134	172
P09103	Conv	GGEIK	THILLFLPK	SVSDY	2		541.342574	1080.669548	0.001871652	2	N	256	265
P09103	Conv	LDFIK	HNQLPLVIEFTEQTAPK	IFGGE	2		983.0261617	1964.036723	0.000451244	14	N	232	249
P09103	Conv	PIWDK	LGETYKDHENIIIAK	MDSTA	2		872.4679482	1742.920296	0.000622848	2	N	411	426
P09103	Conv	FLEGK	IKPHLMSQEVPEDWDKQPVK	VLVGA	4	M6:+15.995	605.8129661	2419.220665	0.000622848	2	N	352	372
P09405	Conv	TGSSK	GFGFVDFNSEEDAK	AAKEA	2		781.3444246	1560.673249	0.000451244	12	N	607	621
P09405	Conv	GTNRK	FGYVDFESAEDLEK	ALELT	2		824.8730149	1647.73043	0.000451244	8	N	350	364
P09405	Conv	VNELK	FAISELFAK	NDLAV	2		513.2874644	1024.559329	0.000698008	9	N	326	335
P09405	Conv	HGKPK	GYAFIEFASFEDAKEALNSCNK	MEIEG	3	C20:+57.021	837.7217749	2510.141925	0.002663018	1	N	524	546
P09405	Conv	GTNRK	FGYVDFESAEDLEKALELTGLK	VFGNE	3		825.4166116	2473.226435	0.000823681	4	N	350	372
P09405	Conv	TLLAK	NLSFNITEDELKEVFEDAMEIR	LVSQD	3		881.4271822	2641.258147	0.000451244	3	N	400	422
P09405	Conv	SGESK	TLVLSNLSYSATK	ETLEE	2		698.888271	1395.760942	0.000451244	17	N	487	500
P09405	Conv	AKKQK	VEGSEPTTPFNLFIGNLNPNK	SVNEL	2		1144.582029	2287.148459	0.000451244	9	N	299	320
P09405	Conv	PEAKK	QKVEGSEPTTPFNLFIGNLNPNK	SVNEL	3		848.7751332	2543.302	0.000823681	4	N	297	320
P09405	Conv	AKAAK	EAMEDGEIDGNKVTLDWAKPK	GEGGF	3	M3:+15.995	788.0464416	2361.115925	0.000823681	1	N	624	645
P09411	Conv	KATSR	GCITIIGGGDTATCCAK	WNTED	2	C2:+57.021,C14:+57.021,C15:+57.021	877.896967	1753.778334	0.000451244	40	N	365	382
P09411	Conv	ASLSK	LGDVYVNDAFGTAHR	AHSSM	2		817.9002327	1633.784865	0.000451244	5	N	156	171
P09411	Conv	TCCAK	WNTEDKVSHVSTGGGASLELLEGK	VLPGV	2		1257.627697	2513.239793	0.000451244	10	N	382	406
P09411	Conv	KNGVK	ITLPVDFVTADKFDENAK	TGQAT	2		1012.023285	2022.030969	0.000451244	20	N	279	297

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P09411	Conv	NYFAK	ALESPERPFLAILGGAK	VADKI	2		885.0019582	1767.988316	0.000451244	10	N	199	216
P09411	Conv	VLFLK	DCVGPEVENACANPAAGTVILLENLR	FHVEE	2	C2:+57.021,C11:+57.021	1391.678618	2781.341636	0.000451244	26	N	97	123
P09411	Conv	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2		1053.034321	2104.053042	0.000451244	33	N	332	350
P09411	Conv	SLLGK	DVLFLKDCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C8:+57.021,C17:+57.021	1166.597299	3496.768498	0.000451244	15	N	91	123
P09411	Conv	LLEGK	VLPGVDALSNV	-	2		542.3063854	1082.597171	0.001329271	7	N	406	417
P09411	Conv	DVLFL	KDCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C3:+57.021,C12:+57.021	970.8199996	2909.436599	0.002663018	1	N	96	123
P09411	Conv	NTEDK	VSHVSTGGGASLELLEGK	VLPGV	2		870.9604874	1739.905375	0.000451244	9	N	388	406
P09411	Conv	PMPDK	YSLEPVAAELK	SLLGK	2		610.3326002	1218.6496	0.001871652	2	N	75	86
P09411	Conv	FTFLK	VLNNMEIGTSLYDEEGAK	IVKDL	2		991.9729351	1981.93027	0.000451244	2	N	246	264
P09528	Conv	LELHK	LATDKNDPHLCDFIETYYLSEQVK	SIKEL	2	C11:+57.021	1450.194855	2898.37411	0.000451244	12	N	120	144
P09528	Conv	LHLEK	SVNQSLLELHK	LATDK	3		423.2388656	1266.693197	0.000870037	3	N	109	120
P09528	Conv	VTNLR	KMGAPEAGMAEYLFDK	HTLGH	3		586.6132757	1756.816427	0.002145581	1	N	157	173
P09528	Conv	SEQVK	SIKELGDHVTNLR	KMGAP	3		494.6077291	1480.799787	0.000451244	1	N	144	157
P09581	Conv	WHGQG	APVIEPSGPELVVEPGETVTLR	CVSNG	2		1145.120988	2288.226375	0.000823681	17	N	19	41
P09581	Conv	HLYVK	DPAHSWNLLAQEVTVVEGQEAVLPCLITDPALK	DSVSL	3	C25:+57.021	1205.290907	3612.84932	0.000979378	6	N	102	135
P0C0S6	Conv	DSLIK	ATIAGGGVIPHIHK	SLIGK	2		685.8993074	1369.783015	0.000451244	18	N	102	116
P0C0S6	Conv	RITPR	HLQLAIRGDEELDSLIK	ATIAG	2		975.5368936	1949.058187	0.000451244	2	N	85	102
P0C0S6	Conv	AVYSA	AILEYLTAEVLELAGNASK	DLKVK	2		1003.04676	2004.07792	0.000451244	4	N	56	75
P0C0S6	Conv	TAAVY	SAAILEYLTAEVLELAGNASK	DLKVK	2		1082.081331	2162.147062	0.000451244	112	N	54	75
P0C0S6	Conv	AILEY	LTAEVLELAGNASK	DLKVK	2		708.3911779	1414.766756	0.00091018	4	N	61	75
P0C0S6	Conv	DSLIK	ATIAGGGVIPH	IHKSL	2		496.7803378	991.5450756	0.000451244	5	N	102	113
P0C0S6	Conv	QLAIR	GDEELDSLIK	ATIAG	2		559.7829402	1117.55028	0.000451244	22	N	92	102
P0C0S6	Conv	TSHGR	VGATAAVYSAAILEYLTAEVLELAGNASK	DLKVK	2		1448.271651	2894.527702	0.000451244	17	N	46	75
P0C0S6	Conv	VYSAA	ILEYLTAEVLELAGNASK	DLKVK	2		967.5282029	1933.040806	0.000451244	14	N	57	75
P0C0S6	Conv	YSAAI	LEYLTAEVLELAGNASK	DLKVK	2		910.9861708	1819.956742	0.000451244	6	N	58	75
P0C0S6	Conv	SAAIL	EYLTAEVLELAGNASK	DLKVK	2		854.4441388	1706.872678	0.000451244	6	N	59	75
P0C0S6	Conv	AAVYS	AAILEYLTAEVLELAGNASK	DLKVK	3		692.7128112	2075.115033	0.000451244	2	N	55	75
P0C0S6	Conv	GATAA	VYSAAILEYLTAEVLELAGNASK	DLKVK	2		1213.147202	2424.278805	0.000451244	3	N	52	75
P0C0S6	Conv	RVGAT	AAVYSAAILEYLTAEVLELAGNASK	DLKVK	2		1284.184316	2566.353032	0.000451244	1	N	50	75
P0CW02	Conv	KLKTR	QCLSFCPAGVPIRDPNIR	ERTSC	3	C2:+57.021,C6:+57.021	700.68764	2099.03952	0.000451244	2	N	72	90
P0CW02	Conv	ERAQG	LQCYECYGVPIETSCPAVTCR	ASDGF	2	C3:+57.021,C6:+57.021,C15:+57.021,C20:+57.021	1282.057441	2562.099282	0.0007646	1	N	26	47
P10107	Conv	LALAK	GDRCQDLSVNQDLADTDAR	ALYEA	2	C4:+57.021	1074.982654	2147.949707	0.000451244	6	N	185	204
P10107	Conv	RDLAK	DITSDTSGDFR	KALLA	2		607.2707283	1212.525857	0.000451244	6	N	166	177
P10107	Conv	LAMLK	TPAQFDADELR	GAMKG	2		631.8047383	1261.593877	0.000451244	50	N	113	124
P10107	Conv	AKGDR	CQDLSVNQDLADTDAR	ALYEA	2	C1:+57.021	910.9078945	1819.800189	0.000451244	35	N	188	204
P10107	Conv	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	2		972.5316112	1943.047622	0.000823681	5	N	81	98
P10107	Conv	TTIVK	CATSTPAFFAEK	LYEAM	2	C1:+57.021	665.3111106	1328.606621	0.000451244	9	N	269	281
P10107	Conv	HDMNK	ALDLELKGDIEK	CLTTI	2		672.3749965	1342.734393	0.000451244	4	N	250	262
P10107	Conv	RQQIK	AAYLQENGKPLDEVLR	KALTG	2		908.4841296	1814.952659	0.000451244	39	N	81	97
P10107	Conv	EELKR	DLAKDITSDTSGDFR	KALLA	2		820.8922704	1639.768941	0.000451244	3	N	162	177
P10107	Conv	GDYEK	ILVALCGGN	-	2	C6:+57.021	458.7499604	915.4843208	0.000870037	1	N	337	346
P10107	Conv	VKSYK	GGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1172.582561	2343.149522	0.002080925	1	N	29	53
P10107	Conv	AGERR	KGTDVNVFTTILTSR	SFPHL	2		826.4548408	1650.894082	0.000451244	3	N	213	228
P10107	Conv	FYQKK	YGISLCQAILDETKGDYEK	ILVAL	2	C6:+57.021	1102.033292	2202.050984	0.000451244	21	N	318	337
P10107	Conv	FYQKK	YGISLCQAILDETK	GDYEK	2	C6:+57.021	805.9086462	1609.801692	0.000451244	12	N	318	332
P10107	Conv	DEVLR	KALTGHLEEVVLAMLK	TPAQF	2		876.5085624	1751.001525	0.001162105	2	N	97	113
P10107	Conv	AIMVK	GVDEATIIDILTKR	TNAQR	2		772.4386594	1542.861719	0.000451244	17	N	58	72
P10107	Conv	MVKGV	DEATIIDILTKR	TNAQR	2		694.3937205	1386.771841	0.000451244	1	N	60	72
P10107	Conv	GERRK	GTDVNVFTTILTSR	SFPHL	2		762.4073593	1522.799119	0.000451244	19	N	214	228
P10107	Conv	AIMVK	GVDEATIIDILTK	RTNAQ	2		694.3881039	1386.760608	0.000451244	20	N	58	71
P10107	Conv	EVLRK	ALTGHLEEVVLAMLK	TPAQF	2		812.4610809	1622.906562	0.000451244	12	N	98	113
P10107	Conv	RGAMK	GLGTDEDTLIEILTTR	SNEQI	2		873.960153	1745.904706	0.000451244	67	N	128	144
P10107	Conv	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1236.630042	2471.244485	0.000451244	2	N	28	53
P10107	Conv	RDLAK	DITSDTSGDFRK	ALLAL	2		671.3182098	1340.62082	0.001463592	1	N	166	178
P10107	Conv	MVKGV	DEATIIDILTK	RTNAQ	2		616.343165	1230.67073	0.000823681	1	N	60	71
P10126	Conv	MGKEK	THINIVVIGHVDSGK	STTTG	2		794.9444433	1587.873287	0.000451244	6	N	5	20
P10126	Conv	QDVYK	IGGIGTVPVGR	VETGV	2		513.3092625	1024.602925	0.001463592	6	N	255	266
P10126	Conv	NGQTR	EHALLAYTLGVK	QLIVG	2		657.8749666	1313.734333	0.000451244	14	N	134	146
P10126	Conv	VPVGR	VETGVLKPGMVVTFAPVNVTTEVK	SVEMH	3		839.1333819	2514.376746	0.000998612	1	N	266	290
P10126	Conv	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C16:+57.021	1041.555695	3121.643684	0.000451244	8	N	218	247
P10126	Conv	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C15:+57.021	998.8573735	2993.54872	0.000451244	19	N	219	247
P10126	Conv	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK	IGGIG	3	C15:+57.021	1317.701746	3950.081839	0.001395409	3	N	219	255
P10126	Conv	FETSK	YYVTIIDAPGHR	DFIKN	2		702.8676729	1403.719746	0.000451244	19	N	84	96
P10126	Conv	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPLQDVY	KIGGI	3	C15:+57.021	1275.003425	3821.986876	0.001329271	1	N	219	254

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10126	Conv	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPL	RLPLQ	3	C15:+57.021	946.8236697	2837.447609	0.000451244	8	N	219	246
P10126	Conv	RDFIK	NMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	3	M2:+15.995,C11:+57.021	975.8163267	2924.42558	0.000451244	8	N	100	129
P10126	Conv	QVIIL	NHPGQISAGYAPVLDCHTAHIACK	FAELK	4	C16:+57.021,C23:+57.021	655.0657078	2616.231631	0.001463592	3	N	347	371
P10518	Conv	GVPSR	VPKDEQGSAADSEDSPTIEAVR	LLRKT	2		1151.046205	2300.07681	0.000451244	1	N	84	106
P10518	Conv	SRVPK	DEQGSAADSEDSPTIEAVR	LLRKT	2		988.9381346	1975.860669	0.000451244	20	N	87	106
P10518	Conv	RLLRK	TFPSLLVACDVCLCPYTSHGHCGLLSENGAFLAEESR	QRLAE	4	C9:+57.021,C12:+57.021,C14:+57.021,C22:+57.021	1042.731297	4166.893989	0.000634081	2	N	110	147
P10518	Conv	TAFRR	AGADIIITYFAPQLLK	WLKEE	2		867.4959774	1732.976355	0.000451244	15	N	309	325
P10518	Conv	HPLLR	SWQTAASTVSASNLIYPIFVTDVPDDVQPIASLPGVAR	YGVNQ	3		1329.356899	3985.047296	0.000451244	16	N	17	55
P10518	Conv	EAGLR	CVLIFGVPSR	VPKDE	2	C1:+57.021	574.3185416	1146.621483	0.000823681	11	N	74	84
P10518	Conv	MTAFR	RAGADIIITYFAPQLLK	WLKEE	3		630.7002886	1889.077466	0.000622848	2	N	308	325
P10605	Conv	TFDAR	EQWSNCPTIGQIR	DQGSC	2	C6:+57.021	794.8807544	1587.745909	0.000451244	2	N	87	100
P10605	Conv	IGQIR	DQGSCGSCWAFGAVEAISDR	TCIHT	2	C5:+57.021,C8:+57.021	1086.957362	2171.899123	0.000451244	6	N	100	120
P10605	Conv	AEIYK	NGPVEGAFTVFSDFLTYK	SGVYK	2		996.4916204	1990.967641	0.000451244	14	N	245	263
P10605	Conv	WQAGR	NFYNVDISYLK	KLCGT	2		688.3487817	1374.681963	0.000451244	2	N	45	56
P10639	Conv	LIESK	EAFQEALAAAGDK	LVVVD	2		660.8256707	1319.635741	0.000451244	12	N	8	21
P10639	Conv	LIESK	EAFQEALAAAGDKLVVVDFSATWCGPCK	MIKPF	3	C24:+57.021,C27:+57.021	1014.1565	3039.446101	0.000451244	21	N	8	36
P10639	Conv	AAGDK	LVVVDFSATWCGPCK	MIKPF	2	C11:+57.021,C14:+57.021	869.9182597	1737.820919	0.000451244	4	N	21	36
P10639	Conv	NVVFL	EVDVDDCQDVAADCEVK	CMPTF	2	C7:+57.021,C14:+57.021	983.9039289	1965.792258	0.000451244	4	N	55	72
P10649	Conv	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	3		725.3935243	2173.157173	0.000451244	4	N	50	69
P10649	Conv	NEKFK	LGLDFPNLPYLIDGSHK	ITQSN	2		950.0046979	1897.993796	0.000698008	2	N	52	69
P10649	Conv	FAGDK	VTYVDFLAYDILDQYR	MFEPK	2		997.4994454	1992.983291	0.000451244	12	N	152	168
P10649	Conv	MFEPK	CLDAFPNLR	DFLAR	2	C1:+57.021	553.2768737	1104.538147	0.001871652	1	N	173	182
P10810	Conv	CEQVR	VFPALSTLDLSDNPELGER	GLISA	2		1037.029098	2072.042597	0.000451244	8	N	187	206
P10810	Conv	ELGER	GLISALCPLKFPTLQVLALR	NAGME	3	C7:+57.021	737.4416669	2209.301601	0.000451244	6	N	206	226
P10810	Conv	FGALR	VLGISGLQELTLENLEVTGTAPPPLLEATGPDLNILNLR	NVSWA	3		1361.086409	4080.235826	0.000451244	6	N	107	146
P10810	Conv	SWATR	DAWLAELQQWLKPGLK	VLSIA	3		632.6846386	1895.030516	0.000622848	3	N	153	169
P10853	Conv	GISSK	AMGIMNSFVNDIFER	IASEA	2		872.4138052	1742.81201	0.000451244	28	N	58	73
P10853	Conv	RKRSR	KESYSVYVYK	VLKQV	2		633.3247752	1264.63395	0.000622848	28	N	34	44
P10853	Conv	SSKAM	GIMNSFVNDIFER	IASEA	2		771.3750054	1540.734411	0.000451244	8	N	60	73
P10853	Conv	ISSKA	MGIMNSFVNDIFER	IASEA	3	M1:+15.995,M4:+15.995	568.9294322	1703.764897	0.002813207	2	N	59	73
P10853	Conv	AMGIM	NSFVNDIFER	IASEA	2		620.8019986	1239.588397	0.000698008	22	N	63	73
P10853	Conv	KRSRK	ESYSVYVYK	VLKQV	2		569.2772936	1136.538987	0.000622848	10	N	35	44
P10853	Conv	MGIMN	SFVNDIFER	IASEA	2		563.7805348	1125.54547	0.002884417	2	N	64	73
P11031	Conv	WSQLK	EQISDIDDAVR	KL-	2		630.8074779	1259.599356	0.000451244	11	N	114	125
P11031	Conv	KPGRK	GISLNMEQWSQLKEQISDIDDAVR	KL-	3		925.7926356	2774.354507	0.000451244	2	N	101	125
P11152	Conv	KKVNR	ITGLDPAGPNFEYAEAPSR	LSPDD	2		1002.987233	2003.958867	0.000451244	7	N	178	197
P11152	Conv	EAPSR	LSPDDADFVDVLHTFTR	GSPGR	2		974.4765016	1946.937403	0.000451244	5	N	197	214
P11152	Conv	ALYKR	EPDSNVIVVDWLYR	AQQHY	2		852.9337412	1703.851882	0.002296037	1	N	102	116
P11247	Conv	ISLPR	IICDNTGITTVSK	NNIFM	2	C3:+57.021	711.3691568	1420.722714	0.000451244	28	N	675	688
P11247	Conv	AKLNR	QNQIVVDEIRER	LFEQV	3		500.2711169	1497.789951	0.000451244	12	N	533	545
P11247	Conv	TTVSK	NNIFMSNTYPR	DFVSC	2	M5:+15.995	686.8199086	1371.624217	0.000451244	23	N	688	699
P11247	Conv	ALTSF	VDASGVYGSEDPLAR	KLRNL	2		768.3709738	1534.726348	0.000451244	3	N	310	325
P11247	Conv	SVDPR	IANVFTNAFR	YGHTL	2		576.8121693	1151.608739	0.000451244	30	N	463	473
P11247	Conv	FSFFT	GLNCETSCLQQPPCFPLK	IPPND	2	C4:+57.021,C8:+57.021,C14:+57.021	1074.997212	2147.978825	0.000451244	12	N	251	269
P11247	Conv	SFFTG	LNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C3:+57.021,C7:+57.021,C13:+57.021	961.1313663	2880.370699	0.000622848	7	N	252	276
P11247	Conv	FASWR	VVLEGGIDPILR	GLMAT	2		640.8827917	1279.749983	0.000451244	21	N	510	522
P11247	Conv	FSFFT	GLNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C4:+57.021,C8:+57.021,C14:+57.021	980.1385209	2937.392163	0.001463592	1	N	251	276
P11247	Conv	YNAWR	RFCGLPQPSTVGELGTVLK	NLELA	2	C3:+57.021	1030.054165	2058.09273	0.000451244	15	N	577	596
P11247	Conv	EQVMR	IGLDLPALNMQR	SRDHG	2		670.8719016	1339.728203	0.000637154	8	N	552	564
P11247	Conv	NAWRR	FCGLPQPSTVGELGTVLK	NLELA	2	C2:+57.021	952.0036093	1901.991619	0.000451244	26	N	578	596
P11247	Conv	FRKLR	DGDRFWWENPGVFSK	QQRQA	2		920.4266147	1838.837629	0.001839721	2	N	647	662
P11247	Conv	NITIR	NQINALTSFVDASGVYGSEDPLARK	LRNLT	3		884.7808355	2651.319106	0.000451244	12	N	301	326
P11247	Conv	RDGDR	FWWENPGVFSK	QQRQA	2		698.8383841	1395.661168	0.000451244	18	N	651	662
P11247	Conv	RAFVR	WLPAEYEDGVSMPFGWTPGVNR	NGFKV	2	M12:+15.995	1262.584289	2523.152979	0.000451244	41	N	171	193
P11247	Conv	EPNGR	VGQLLACLIGTQFR	KLRDG	2	C7:+57.021	788.4377082	1574.859816	0.000451244	37	N	630	644
P11247	Conv	NITIR	NQINALTSFVDASGVYGSEDPLAR	KLRNL	2		1262.619872	2523.224143	0.000451244	46	N	301	325
P11247	Conv	SKQQR	QALASISLPR	IICDN	2		528.3145448	1054.61349	0.000451244	10	N	665	675
P11247	Conv	SFFTG	LNCETSCLQQPPCFPLK	IPPND	2	C3:+57.021,C7:+57.021,C13:+57.021	1046.486481	2090.957361	0.000451244	20	N	252	269
P11247	Conv	QINAL	TSFVDASGVYGSEDPLAR	KLRNL	2		935.9450343	1869.874469	0.000451244	7	N	307	325
P11247	Conv	EPNGR	VGQLLACLIGTQFRK	LRDGD	2	C7:+57.021	852.4851897	1702.954779	0.000451244	4	N	630	645

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P11247	Conv	ESIKR	SLQSGSASPTELLFYFK	QPVAG	2		937.9808885	1873.946177	0.001699387	1	N	60	77
P11247	Conv	AKLNR	QNQIVVDEIR	ERLFE	2		607.3309232	1212.646246	0.000451244	23	N	533	543
P11247	Conv	NRSAR	IPCFLAGDMR	SSEMP	2	C3:+57.021,M9:+15.995	598.2838847	1194.552169	0.000735798	5	N	369	379
P11247	Conv	IITYR	DYLPLVLGPAAMK	KYLPQ	2	M12:+15.995	702.3843532	1402.753106	0.001591523	3	N	434	447
P11247	Conv	NTYPR	DFVSCNTLPK	LNLTS	2	C5:+57.021	590.7872713	1179.558943	0.001699387	2	N	699	709
P11247	Conv	EPATR	FSFFTGLNCETSCLQQPPCFPLK	IPPND	3	C9:+57.021,C13:+57.021,C19:+57.021	926.7623913	2777.263774	0.001329271	1	N	246	269
P11247	Conv	ALMFM	QWGQFLDHDITLTPEPATR	FSFFT	2		1113.053439	2224.091278	0.001839721	2	N	227	246
P11352	Conv	LNSLK	YVRPGGGFEPNFTLFEK	CEVNG	2		979.4944974	1956.973395	0.000451244	7	N	95	112
P11352	Conv	MCAAR	LSAAAQSTVYAFSARPLTGGEPVSLGSLR	GKVLL	3		969.5177227	2905.529768	0.000451244	16	N	5	34
P11352	Conv	SRRFR	TIDIEPDIETLLSQQSGNS	-	2		1030.505653	2058.995706	0.000451244	10	N	182	201
P11352	Conv	RLGPR	GLVVLGFPCNQFGHQENGKNEEILNSLK	YVRPG	3	C9:+57.021	1047.864751	3140.570853	0.000451244	9	N	67	95
P11352	Conv	WNFEK	FLVGPDGVPVR	RYSRR	2		578.3301949	1154.64479	0.001871652	1	N	164	175
P11499	Conv	PIWTR	NPDDITQEEYGEFYK	SLTND	2		924.4026679	1846.789736	0.000451244	19	N	291	306
P11499	Conv	YRMIK	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	MEEVD	3		1179.220242	3534.637326	0.000451244	3	N	685	719
P11499	Conv	DKAVK	DLVVLLFETALLSSGFSLEDPQTHSNR	IYRMI	3		996.849138	2987.524014	0.000451244	9	N	652	679
P11499	Conv	EVVKK	HSQFIGYPITLYLEK	EREKE	3		603.6580894	1807.950868	0.000823681	6	N	204	219
P11672	Conv	QFRGR	WYVVGLAGNAVQK	KTEGS	2		702.8858657	1403.756131	0.000451244	20	N	50	63
P11672	Conv	TRFAK	SLGLKDDNIIFSVPTDQCIDN	-	2	C18:+57.021	1182.573313	2363.131026	0.000451244	17	N	179	200
P11672	Conv	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2		1275.682275	2549.34895	0.000622848	4	N	20	43
P11672	Conv	TQNLI	PAPSLLTVPLQPDFR	SDQFR	2		825.9648444	1649.914089	0.000823681	1	N	28	43
P11680	Conv	GRDIR	VEDCCLNAAYAFQEHDGGLCQACR	SPQWS	2	C4:+57.021,C5:+57.021,C20:+57.021,C23:+57.021	1422.582874	2843.150149	0.00091018	1	N	48	72
P11680	Conv	VEEKR	SCLHVPVCKDPEEK	KP-	4	C2:+57.021,C8:+57.021	425.2053869	1696.790348	0.000622848	3	N	448	462
P11680	Conv	PATGS	DPVLCFTQYEESSGR	CKGLL	2	C5:+57.021	894.399174	1786.782748	0.000451244	2	N	23	38
P11835	Conv	RHVLK	LTDNSNQFQTEVGK	QLISG	2		790.8817056	1579.747811	0.000451244	25	N	210	224
P11835	Conv	VSSCR	DCIQSGPGCSWCQK	LNFTG	2	C2:+57.021,C9:+57.021,C12:+57.021	841.839452	1681.663304	0.000451244	16	N	35	49
P11835	Conv	NMYKR	SNEFDYPSVGQLAHK	LSESN	2		846.4053479	1690.795096	0.000451244	20	N	296	311
P11835	Conv	SSIGK	SRGDCDGVQINNPVTFQVK	VMASE	2	C5:+57.021	1067.521218	2133.026835	0.000451244	19	N	396	415
P11835	Conv	SFVIR	ALGFTDTVTVQVRPQCECQCR	DQSRE	2	C16:+57.021,C18:+57.021,C20:+57.021	1263.088153	2524.160706	0.001463592	1	N	430	451
P11835	Conv	KLSSR	VFLDHSTLPDTLK	VTYDS	3		495.9369637	1484.787491	0.000451244	10	N	367	380
P11835	Conv	EIIPK	SAVGELSDDSSNVVQLIK	NAYYK	2		930.9816168	1859.947634	0.000451244	16	N	340	358
P11835	Conv	PCKER	DSEGCWITYTLQQK	DGRNI	2	C5:+57.021	864.8988098	1727.78202	0.000451244	14	N	667	681
P11835	Conv	RNVTR	LLVFATDDGFHFAGDGK	LGAIL	2		905.4444731	1808.873346	0.000451244	20	N	258	275
P11835	Conv	TESGR	IGFGSFVDKTVLPFVNTHPEK	LRNPC	3		778.0832384	2331.226315	0.000451244	11	N	166	187
P11835	Conv	LNNVK	KLGGDLLQALNEITESGR	IGFGS	2		957.5187008	1913.021802	0.000451244	11	N	148	166
P11835	Conv	NNVKK	LGGDLLQALNEITESGR	IGFGS	2		893.4712192	1784.926838	0.000451244	25	N	149	166
P11835	Conv	TEVGK	QLISGNLDAPEGGLDAIMQVAACPEEIGWR	NVTRL	3	C23:+57.021	1070.857157	3209.54807	0.000451244	19	N	224	254
P11835	Conv	QLAHK	LSESNIQPIFAVTK	KMVKT	2		773.9279275	1545.840255	0.001229886	4	N	311	325
P11835	Conv	PDTLK	VTYDSFCSNGASSIGK	SRGDC	2	C7:+57.021	846.8806171	1691.745634	0.000451244	39	N	380	396
P11835	Conv	IGKSR	GDCDGVQINNPVTFQVK	VMASE	2	C3:+57.021	945.9546477	1889.893695	0.000451244	9	N	398	415
P11835	Conv	CQCNR	CICDEGYQPPMCEDCPSCGSHCR	DNHTS	2	C1:+57.021,C3:+57.021,M11:+15.995,C12:+57.021,C15:+57.021,C18:+57.021,C22:+57.021	1446.006551	2889.997502	0.000735798	2	N	601	624
P11835	Conv	TFQVK	VMASECIQEQSFVIR	ALGFT	2	M2:+15.995,C6:+57.021	906.9349126	1811.854225	0.000451244	41	N	415	430
P11835	Conv	QKDGR	NIYNIHVEDSLECVKGPNVAA	IVGGT	2	C13:+57.021	1171.57619	2341.13678	0.000451244	12	N	684	705
P11835	Conv	QKDGR	NIYNIHVEDSLECVK	GPNVA	2	C13:+57.021	916.9462914	1831.876983	0.002374549	1	N	684	699
P11835	Conv	TESGR	IGFGSFVDK	TVLPF	2		485.2561642	968.4967284	0.002453667	1	N	166	175
P11835	Conv	DVPNK	EIFGQYCECDNVNCER	YNSQV	2	C7:+57.021,C9:+57.021,C14:+57.021	1046.911334	2091.807068	0.000451244	13	N	528	544
P11983	Conv	AEFAR	SLLVIPNTLAVNAAQDSTDLVAK	LRAFH	2		1177.152819	2352.290038	0.000451244	19	N	443	466
P11983	Conv	HPAAK	VLCELADLQDKEVGDGTTSVVIIAAELLK	NADEL	3	C3:+57.021	1033.888339	3098.641618	0.000451244	11	N	73	102
P12023	Conv	CIGTK	EGILQYCQEVYPELQITNVVEANQPVTIQNWCK	RGRKQ	3	C7:+57.021,C32:+57.021	1321.980249	3962.917347	0.000451244	11	N	66	99
P12023	Conv	VIPYR	CLVGEFVSDALLVPDKCK	FLHQE	3	C1:+57.021,C17:+57.021	684.0166518	2049.026555	0.001329271	2	N	116	134
P12023	Conv	VIPYR	CLVGEFVSDALLVPDK	CKFLH	2	C1:+57.021	881.4585033	1760.901407	0.000451244	3	N	116	132
P12246	Conv	EYTVK	APPSIVLGQEQDNYGGGFQR	SQSFV	2		1067.022139	2132.028678	0.000451244	42	N	146	166
P12246	Conv	LFVYR	DSPVNPNILNWQALNYEINGYVVIRPR	VWD-	3		1052.219788	3153.635965	0.002884417	1	N	194	221
P12265	Conv	SMYPK	GYFVQDTSFDFFNYAGLHR	SVVLY	3		762.0206381	2283.038514	0.001463592	9	N	196	215
P12265	Conv	EAALR	DFIGWVWYER	EAILP	2		685.8305591	1369.645518	0.000622848	12	N	93	103
P12265	Conv	ADISK	LVQSGPLTTCR	ITIAI	2	C10:+57.021	616.327095	1230.63859	0.002981883	1	N	155	166
P12265	Conv	ENWYK	THQKPIIQSEYGADAIPGIHEDPPR	MFSEE	3		923.803863	2768.388189	0.000451244	5	N	526	551
P12265	Conv	ANSFR	TSHYPYSEEVLQLCDR	YGIVV	2	C14:+57.021	998.9573874	1995.899175	0.000451244	2	N	378	394
P12265	Conv	ITHTK	ALDLTRPVTFVSNAK	YDADL	2		816.4599262	1630.904252	0.001329271	1	N	467	482

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P12815	Conv	-MAAY	SYRPGPGGGPGPAAGAALPDQSFLWNVFQR	VDKDR	3		1024.181445	3069.520935	0.000451244	10	N	4	34
P12815	Conv	VDKDR	SGVISDNELQQALSNGTWTPFNPVTVR	SIISM	3		977.4934657	2929.456997	0.000451244	8	N	39	66
P12815	Conv	DRENK	AGVNFSEFTGVWK	YITDW	2		721.3596807	1440.703761	0.000451244	1	N	77	90
P12815	Conv	TGVWK	YITDWQNVFR	TYDRD	2		671.3334659	1340.651332	0.001264573	5	N	90	100
P12815	Conv	GFGYR	LSDQFHDILIR	KFDRQ	3		452.9143819	1355.719746	0.000998612	2	N	125	136
P13020	Conv	KQFFK	NWRDPDQTDGPGLGYLSSHIANVER	VPFDA	3		933.1149887	2796.321566	0.000451244	14	N	392	417
P13020	Conv	MQYPR	QTQVSVLPEGGETPLFK	QFFKN	2		915.486338	1828.957076	0.000451244	21	N	371	388
P13020	Conv	LKVLR	SQHVQVEEGSEPDAFWEALGGK	TAYRT	2		1200.559283	2399.102965	0.000451244	15	N	624	646
P13020	Conv	AVQHR	EVQGFESSTFSGYFK	SGLKY	2		856.8942817	1711.772963	0.000451244	21	N	145	160
P13020	Conv	AFVLK	TPSAAYLWVGAGASEAEKTGAQELLK	VLRSQ	2		1324.682472	2647.349344	0.000451244	3	N	595	621
P13020	Conv	KQIWR	IEGSNKVPVDPATYGQFYGGDSYIILYNYR	HGGRQ	3		1133.889773	3398.64592	0.000451244	29	N	449	479
P13020	Conv	EGSNK	VPVDPATYGQFYGGDSYIILYNYR	HGGRQ	2		1386.17174	2770.32788	0.000451244	18	N	455	479
P13020	Conv	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3		1425.038957	4272.093472	0.000451244	10	N	483	523
P13020	Conv	LQIWR	VEKFDLVPVPPNLYGDFFTGDAYVILK	TVQLR	3		1019.539353	3055.59466	0.000451244	35	N	70	97
P13020	Conv	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNKFER	LKATQ	3	C16:+57.021,C29:+57.021	1466.327148	4395.958043	0.000451244	46	N	197	235
P13020	Conv	WRVEK	FDLVPVPPNLYGDFFTGDAYVILK	TVQLR	2		1350.702145	2699.388689	0.000451244	12	N	73	97
P13020	Conv	ITVVR	QGFEPPSFVGWFLGWDDNYWSVDPLDR	ALAEL	3		1077.161716	3228.461748	0.000451244	6	N	746	773
P13020	Conv	AFVLK	TPSAAYLWVGAGASEAEK	TGAQE	2		904.4472128	1806.878826	0.000451244	9	N	595	613
P13020	Conv	EVMPK	SGALNSNDAFVLK	TPSAA	2		668.349313	1334.683026	0.000451244	18	N	582	595
P13020	Conv	ASGFK	HVVPNEVVVQR	LFQVK	2		638.3625577	1274.709515	0.001943752	1	N	175	186
P13020	Conv	QGALR	SEDCFILDHGR	DGKIF	2	C4:+57.021	674.8014413	1347.587283	0.000451244	11	N	325	336
P13020	Conv	PEFLK	AGKEPGLQIWR	VEKFD	3		418.9038172	1253.688052	0.000451244	14	N	59	70
P13020	Conv	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNK	FERLK	3	C16:+57.021,C29:+57.021	1322.256442	3963.745925	0.000451244	22	N	197	232
P13020	Conv	ANVER	VPFDAATLHTSTAMAAQHGMDDDDGTGQK	QIWRI	3	M14:+15.995,M20:+15.995	969.0963352	2904.265606	0.000451244	7	N	417	445
P13439	Conv	YGTKR	LVEGEINPGQTCLVIEDVVTSGASVLETVEVLQK	EGLKV	3	C12:+57.021	1209.301248	3624.880345	0.000451244	3	N	107	141
P13609	Conv	CIEEK	GPQFDLIDESNNIGPPMNNPVLMEGPSK	DFISN	3	M17:+15.995,M23:+15.995	1014.811536	3041.411207	0.002080925	1	N	51	79
P13609	Conv	CIEEK	GPQFDLIDESNNIGPPMNNPV	LMEGP	2	M17:+15.995	1142.531723	2283.047845	0.001352548	1	N	51	72
P13634	Conv	PIDIK	TSEANHDSSLKPLSISYNPATAK	EIVNV	3		811.0753598	2430.20268	0.000451244	4	N	35	58
P13634	Conv	PATAK	EIVNVGHSFHVIFDDSSNQSVLK	GGPLA	3		857.7666377	2570.276513	0.000451244	1	N	58	81
P14069	Conv	NFQEY	VAFLGALALIYNEALK	-	2		853.4985201	1704.98144	0.000622848	4	N	73	89
P14069	Conv	DDLDR	NKDQEVNFQEYVAFLGALALIYNEALK	-	3		1034.205033	3099.5917	0.000451244	35	N	62	89
P14069	Conv	-MA	CPLDQAIGLLVAIFHK	YSGKE	3	C1:+57.021	599.0030484	1793.985745	0.000451244	11	N	2	18
P14069	Conv	-MAC	PLDQAIGLLVAIFHK	YSGKE	2		817.9855798	1633.95556	0.000451244	13	N	3	18
P14069	Conv	LDRNK	DQEVNFQEYVAFLGALALIYNEALK	-	2		1429.734705	2857.453809	0.000451244	22	N	64	89
P14069	Conv	EYVAF	LGALALIYNEALK	-	2		694.9115491	1387.807498	0.000451244	8	N	76	89
P14069	Conv	DDLDR	NKDQEVNFQEYVAFLGAL	ALIYN	2		1043.018534	2084.021467	0.002727428	1	N	62	80
P14069	Conv	EVNFQ	EYVAFLGALALIYNEALK	-	2		999.551481	1997.087362	0.000451244	6	N	71	89
P14152	Conv	KKSVK	VIVVGNPANTNCLTASK	SAPSI	2	C12:+57.021	879.4646513	1756.913703	0.000451244	31	N	125	142
P14152	Conv	DLTAK	ELTEEKETAFEFLSSA	-	2		915.9363436	1829.857087	0.000451244	7	N	318	334
P14152	Conv	NKTWK	FVEGLPINDFSR	EKMDL	2		697.3596807	1392.703761	0.000451244	9	N	298	310
P14152	Conv	KLQGK	EVGVYEALKDDSWLK	GEFIT	2		876.4466815	1750.877763	0.000662267	2	N	205	220
P14152	Conv	SEPIR	VLVTGAAGQIAYSLLYSIGNGSVFGK	DQPII	3		862.4711622	2584.390086	0.000622848	2	N	6	32
P14152	Conv	ADDVK	NVIIWGNHSSTQYPDVNHAK	VKLQG	3		760.7105751	2279.108325	0.000451244	10	N	179	199
P14152	Conv	EFVSM	GVISDGNSYGVPDDLLYSFPVVIK	NKTWK	2		1277.657934	2553.300268	0.000451244	1	N	269	293
P14206	Conv	VTDPR	ADHQPLTEASYVNLPTIALCNTDSPLR	YVDIA	3	C20:+57.021	999.4979567	2995.47047	0.000451244	25	N	128	155
P14206	Conv	RAVLK	FAAATGATPIAGR	FTPGT	2		602.3281835	1202.640767	0.002813207	1	N	89	102
P14206	Conv	PIAGR	FTPGTFTNQIQAAFR	EPRLL	2		849.9340756	1697.852551	0.000823681	5	N	102	117
P14206	Conv	LLAAR	AIVAIENPADVSVISSR	NTGQR	2		870.9786801	1739.94176	0.000451244	8	N	63	80
P14206	Conv	AAAEK	AVTKEEFQGEWTAPAPEFT	AAQPE	2		1069.507999	2137.000398	0.001943752	4	N	220	239
P14211	Conv	LPPKK	IKDPDAAKPEDWDER	AKIDD	3		595.620363	1783.837689	0.000823681	7	N	207	222
P14211	Conv	AIYFK	EQFLDGDAWTNR	WVESK	2		726.3316516	1450.647703	0.000451244	15	N	24	36
P14211	Conv	TYEVK	IDNSQVESGSLEDDWDFLPPKK	IKDPD	2		1260.10098	2518.186361	0.000451244	21	N	185	207
P14211	Conv	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	C1:+39.994	947.1253099	2838.35253	0.000451244	2	N	162	185
P14211	Conv	NPDYK	GTWIHPEIDNPEYSPDANIY	AYDSF	2		1166.032369	2330.049139	0.002727428	1	N	286	306
P14211	Conv	TYEVK	IDNSQVESGSLEDDWDFLPPK	KIKDP	2		1196.053499	2390.091398	0.000451244	5	N	185	206
P14211	Conv	GLAAA	DPAIYFKEQFLDGDAWTNR	WVESK	2		1143.545447	2285.075294	0.000451244	3	N	17	36
P14211	Conv	DANIY	AYDSFAVLGLDLWQVK	SGTIF	2		912.9806915	1823.945783	0.000451244	2	N	306	322
P14211	Conv	LWQVK	SGTIFDNFLITNDEAYAEEFGNETWGVTK	AAEKQ	3		1090.170606	3267.488417	0.000451244	25	N	322	351
P14211	Conv	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVK	SGTIF	3		1379.669254	4135.984362	0.000451244	16	N	286	322
P14211	Conv	DWDER	AKIDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	4		740.6048771	2958.388308	0.000451244	7	N	222	248
P14211	Conv	PFSNK	GQTLVVQFTVK	HEQNI	2		610.3564097	1218.697219	0.000622848	10	N	87	98
P14211	Conv	DERAK	IDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	3		920.7598771	2759.256231	0.000698008	8	N	224	248
P14211	Conv	DPDAK	KPEDWDEEMDGEWEPPVIQNPEYK	GEWKP	3	M9:+15.995	992.7680727	2975.280818	0.000451244	6	N	248	272
P14234	Conv	SSGHR	GYVPSNYVAPVDSIQAEEWYFGK	ISRKD	2		1310.124259	2618.232917	0.000622848	2	N	113	136
P14685	Conv	RGADK	AKPPPGGEQEPPPPAPQDVEMKEEAAAGSGSTGEGDGK	AAATE	4	M21:+15.995	929.6817031	3714.695613	0.000451244	8	N	14	52

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P14685	Conv	DIAQK	LQLDSPEDAEFIVAK	AIRDG	2		837.9334069	1673.851214	0.000451244	6	N	421	436
P14685	Conv	TATLR	HDADGQATLLNLLLR	NYLHY	2		825.4526325	1648.889665	0.001839721	1	N	237	252
P14685	Conv	YYHAR	VYEFLDKLDVVR	SFLHA	3		499.2772089	1494.808227	0.000735798	1	N	212	224
P14685	Conv	NNATR	DFLLPFLEEPMDTEADLQFRPR	TGKAA	3	M11:+15.995	899.1078124	2694.300037	0.002663018	1	N	124	146
P14733	Conv	STVFK	TTIPEEEEEEEEEPIGVAVEEER	FHQQG	2		1336.601404	2671.187208	0.000451244	12	N	548	571
P14733	Conv	RYVLK	AGQTVTVWAANAGVTASPPTDLIWK	NQNSW	2		1277.669168	2553.322735	0.000451244	21	N	492	517
P14733	Conv	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	2		1272.65612	2543.29664	0.000451244	1	N	158	182
P14733	Conv	LENAR	LSSEMNTSTVNSAREELMESR	MRIES	3	M5:+15.995,M18:+15.995	801.6975125	2402.069137	0.000451244	2	N	277	298
P14733	Conv	IDKVR	SLETENSALQLQVTER	EEVRG	2		909.4661339	1816.916668	0.000451244	1	N	52	68
P14733	Conv	STVFK	TTIPEEEEEEEEEPIGVAVEEERF	HQQGA	2		1410.135611	2818.255622	0.000823681	11	N	548	572
P14824	Conv	YTAMK	GFGSDKESILELITSR	SNKQR	2		876.4628629	1750.910126	0.000451244	9	N	34	50
P14824	Conv	VMVSR	SEIDLLNIR	REFIE	2		536.8040099	1071.59242	0.000622848	11	N	629	638
P14824	Conv	DAYER	DLESDIIGDTSGHFQK	MLVVL	3		587.9483682	1760.821705	0.000451244	12	N	140	156
P14824	Conv	RVELK	GTVCAANDFNPDADAK	ALRKA	2	C4:+57.021	833.3625915	1664.709583	0.000451244	10	N	354	370
P14824	Conv	AGELK	WGTDEAQFIYILGNR	SKQHL	2		891.9446403	1781.873681	0.000451244	10	N	191	206
P14824	Conv	SLYGK	DLIEDLKYELTGK	FERLI	2		768.9119431	1535.808286	0.000451244	6	N	68	81
P14824	Conv	GGENR	DQAQEDAQVAAEILEIADTPSGDKTSLETR	FMTVL	3		1067.851824	3200.532072	0.000451244	9	N	516	546
P14824	Conv	EDYHK	SLEDALSSDTSGHFR	RILIS	2		811.3767874	1620.737975	0.000451244	2	N	483	498
P14824	Conv	RKAMK	GIGTDEATIIDIVTHR	SNAQR	2		855.955205	1709.89481	0.000451244	6	N	377	393
P14824	Conv	LQGTR	ENDDVVSEDLVQQDVQDLYEAGELK	WGTDE	2		1425.662328	2849.309055	0.000451244	16	N	166	191
P14824	Conv	SGDVK	DAFVAIVQSVK	NKPLF	2		588.8353101	1175.65502	0.001162105	3	N	587	598
P15532	Conv	SDSVK	SAEKEISLWFQPEELVEYK	SCAQN	2		1163.086613	2324.157627	0.000451244	14	N	124	143
P15532	Conv	KSAEK	EISLWFQPEELVEYK	SCAQN	2		955.483264	1908.950928	0.000451244	24	N	128	143
P15864	Conv	MSEAA	PAAPAAAPPAEKAPAK	KKAAK	2		729.409705	1456.80381	0.000451244	2	N	5	21
P15864	Conv	-M	SEAAPAAPAAAPPAEK	APAKK	2		724.8731523	1447.730705	0.000451244	4	N	1	17
P16110	Conv	ADHFK	VAVNDAHLLQYNHR	MKNLR	2		825.4294917	1648.843383	0.000451244	4	N	224	238
P16110	Conv	GKPFK	IQVLVEADHFK	VAVND	2		649.8593165	1297.703033	0.000451244	12	N	213	224
P16110	Conv	VLDFR	RGNDVAFHFNPR	FNENN	3		477.241492	1428.701076	0.001264573	2	N	164	176
P16110	Conv	GKEER	QSAFPFESGKPFK	IQVLV	2		735.3753308	1468.735062	0.000451244	7	N	200	213
P16125	Conv	SILGK	SLADELALVDVLEDK	LKGEM	2		815.4332397	1628.850879	0.000451244	2	N	43	58
P16125	Conv	PQIVK	YSPDCTIIVVSNPVDILTYVTWK	LSGLP	2	C5:+57.021	1342.188313	2682.361026	0.000451244	3	N	127	150
P16546	Conv	ESAFR	ALSSEGKPYVTKEELYQNLTR	EQADY	3		809.4241005	2425.248901	0.000451244	14	N	2414	2435
P16546	Conv	WIEEK	NQALNTDNYGHDLASVQALQR	KHEGF	2		1164.570516	2327.125432	0.000451244	6	N	1252	1273
P16546	Conv	HDAFR	SSLSSAQADFNQLAELDR	QIKSF	2		976.4719476	1950.928295	0.000451244	6	N	2137	2155
P16546	Conv	WMAAR	EAFLNTEDKGDSLDSVEALIK	KHEDF	2		1147.574067	2293.132534	0.000451244	13	N	1464	1485
P16546	Conv	EIDAR	AGTFQAFEQFGQQLLAHGHYASPEIK	EKLDI	3		959.1441082	2874.408925	0.000451244	10	N	1391	1417
P16546	Conv	INGIR	GLVSSDELAKDVTGAEALLER	HQEHR	2		1087.071495	2172.127389	0.000451244	11	N	1359	1380
P16546	Conv	LAAAR	GQRLEESLEYQQFVANVEEEEAWINEK	MTLVA	3		1089.853388	3266.536764	0.00091018	7	N	1862	1889
P16546	Conv	VQEEK	IAALQAFADQLIAVDHYAK	GDIAN	3		686.7059909	2057.094573	0.000451244	14	N	1500	1519
P16546	Conv	TFAKK	ASAFNSWFENAEEDLTDPVR	CNSLE	2		1149.519626	2297.023652	0.000451244	14	N	2099	2119
P16546	Conv	WINEK	MTLVASEDYGDTLAAIQGLLK	KHEAF	2		1105.075192	2208.134784	0.000451244	3	N	1889	1910
P16546	Conv	VTEMK	ALINADELANDVAGAEALLDR	HQEHK	3		718.7066078	2153.096423	0.000451244	11	N	381	402
P16546	Conv	QQFNR	NVEDIELWLYEVEGHLASDDYGKDLTNVQNLQK	KHALL	3		1283.294076	3846.858827	0.000622848	4	N	685	718
P16546	Conv	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3		1078.233652	3231.677555	0.000451244	19	N	2017	2047
P16546	Conv	EGFER	DLAALGDKVNSLGETAQR	LIQSH	2		929.4874007	1856.959201	0.000451244	6	N	1280	1298
P16546	Conv	NLLKK	HQALQAEIAGHEPR	IKAVT	3		519.602978	1555.785534	0.001329271	1	N	825	839
P16546	Conv	SKHQK	HQAFEAELHANADR	IRGVI	3		536.9224877	1607.744063	0.000451244	6	N	1591	1605
P16546	Conv	AVKAR	LAALADQWQFLVQK	SAEKS	2		815.951737	1629.887874	0.000451244	19	N	1632	1646
P16546	Conv	QQFSR	DVDEIEAWISEK	LQTAS	2		717.3438933	1432.672187	0.000451244	12	N	1558	1570
P16546	Conv	NLLKK	HQLLEADISAHEDR	LKDLN	3		545.2696646	1632.785594	0.000698008	4	N	1699	1713
P16546	Conv	LTFAK	KASAFNSWFENAEEDLTDPVR	CNSLE	2		1213.567108	2425.118615	0.000451244	1	N	2098	2119
P16546	Conv	WISEK	LQTASDESYKDPTNIQSK	HQKHQ	2		1012.992713	2023.969826	0.000451244	4	N	1570	1588
P16546	Conv	EVLQK	KFEEFQTDLAAHEER	VNEVS	3		617.2958794	1848.864238	0.000451244	4	N	189	204
P16546	Conv	ARGQR	LEESLEYQQFVANVEEEEAWINEK	MTLVA	2		1463.685606	2925.355611	0.00091018	5	N	1865	1889
P16546	Conv	KSCLR	SLGYDLPMVEEGEPDPEFEAILDTVDPNR	DGHVS	3	M8:+15.995	1088.503285	3262.486454	0.000451244	2	N	2353	2382
P16546	Conv	DDFGR	DLASVQALLR	KHEGL	2		543.3198272	1084.624054	0.002145581	1	N	285	295
P16546	Conv	NWMSK	QEAFLLNEDLGDSLDSVEALLK	KHEDF	2		1210.116099	2418.216598	0.000451244	8	N	485	507
P16546	Conv	SLRMK	QVEELYQSLLELGEK	RKGML	2		889.4650712	1776.914542	0.000451244	5	N	1067	1082
P16546	Conv	FMLFR	EANELQQWITEK	EAALT	2		744.8706096	1487.725619	0.001699387	3	N	1098	1110
P16546	Conv	DLKEK	CTELNQAWTSLGK	RADQR	2	C1:+57.021	754.3644058	1506.713212	0.000451244	2	N	1313	1326
P16546	Conv	WITEK	EAALTNEEVGADLEQVEVLQK	KFDDF	2		1143.079517	2284.143433	0.000451244	3	N	1110	1131
P16546	Conv	QRKAK	LDENSAFLQFNWK	ADVVE	2		806.3942519	1610.772904	0.000451244	6	N	1971	1984
P16546	Conv	LDTGK	KLSDDNTIGQEEIQQR	LAQFV	3		625.3137101	1872.91773	0.001162105	1	N	1828	1844
P16546	Conv	QQFNR	NVEDIELWLYEVEGHLASDDYGK	DLTNV	3		898.7576965	2693.249689	0.000622848	2	N	685	708
P16546	Conv	QSHFR	KVEDLFLTFAK	KASAF	2		655.8718926	1309.728185	0.000451244	3	N	2087	2098

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P16546	Conv	AQSCR	QQVAPMDDETGKELVLALYDYQEK	SPREV	3	M6:+15.995	933.7851752	2798.332125	0.000451244	6	N	957	981
P16546	Conv	NDKLR	QEFAQHANAFHQWIQETR	TYLLD	4		561.0205862	2240.051145	0.002727428	1	N	2207	2225
P16546	Conv	DGKGR	ELPTAFDYVEFTR	SLFVN	2		794.3886352	1586.76167	0.000451244	2	N	2454	2467
P16546	Conv	YVDGK	GRELPTAFDYVEFTR	SLFVN	3		600.9692151	1799.884245	0.001463592	5	N	2452	2467
P16546	Conv	DTGKK	LSDDNTIGQEEIQQR	LAQFV	2		873.4191836	1744.822767	0.001162105	1	N	1829	1844
P16546	Conv	WIQEK	LQVASDENYKDPTNLQGK	LQKHQ	3		674.0047652	2018.990895	0.000662267	1	N	63	81
P16675	Conv	CAQNK	CNFYDNKDPECVNNLLEVSR	IVGKS	3	C1:+57.021,C11:+57.021	829.3742266	2485.09928	0.000451244	8	N	240	260
P16675	Conv	RIVGK	SGLNIYNLYAPCAGGVPGR	HRYED	2	C12:+57.021	989.9941073	1977.972615	0.000451244	9	N	264	283
P16858	Conv	WRDGR	GAAQNIIPASTGAAK	AVGKV	2		685.3758621	1368.736124	0.000823681	1	N	198	213
P16858	Conv	DNSLK	IVSNASCTTNCLAPLAK	VIHDN	2	C7:+57.021,C11:+57.021	910.4557377	1818.895875	0.000451244	25	N	143	160
P16858	Conv	GMAFR	VPTPNVSVVDLTCRLEKPAK	YDDIK	4	C13:+57.021	556.5600056	2222.208822	0.000451244	5	N	232	252
P16858	Conv	GMAFR	VPTPNVSVVDLTCR	LEKPA	2	C13:+57.021	778.9089805	1555.802361	0.000451244	29	N	232	246
P16858	Conv	DNFVK	LISWYDNEYGYSNR	VVDLM	2		890.4028052	1778.79001	0.000451244	21	N	307	321
P16858	Conv	GILGY	TEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C8:+57.021	1182.862352	3545.563655	0.000451244	7	N	274	307
P16858	Conv	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C13:+57.021	1350.62048	4048.838039	0.000451244	218	N	269	307
P16858	Conv	PTNIK	WGEAGAEYVVESTGVFTTMEK	AGAHL	2		1146.030981	2290.046363	0.000451244	9	N	84	105
P16858	Conv	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	3		865.7920187	2594.352656	0.000451244	11	N	160	184
P16858	Conv	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	2		1148.655332	2295.295064	0.000823681	2	N	64	84
P16858	Conv	TGMAF	RVPTPNVSVVDLTCR	LEKPA	2	C14:+57.021	856.9595361	1711.903472	0.000451244	5	N	231	246
P16858	Conv	AENGK	LVINGKPITIFQER	DPTNI	2		814.4806616	1626.945723	0.002453667	1	N	64	78
P16858	Conv	EGPLK	GILGYTEDQVVSCDFNSNSHSSTF	DAGAG	2	C13:+57.021	1332.579855	2663.14411	0.000451244	5	N	269	293
P16858	Conv	ICSGK	VEIVAINDPF	IDLNY	2		558.8009359	1115.586272	0.002884417	1	N	25	35
P16858	Conv	ICSGK	VEIVAINDPFIDLNYMVYMFQYDSTHGK	FNGTV	3		1108.198674	3321.572623	0.000451244	1	N	25	53
P17182	Conv	CLLLK	VNQIGSVTESLQACK	LAQSN	2	C14:+57.021	817.4146271	1632.813654	0.000451244	29	N	343	358
P17182	Conv	IFDSR	GNPTVEVDLYTAK	GLFRA	2		703.8622532	1405.708906	0.000451244	16	N	15	28
P17182	Conv	GAWQK	FTASAGIQVVGDDLTVTNPKR	IAKAA	2		1095.082197	2188.148793	0.000451244	25	N	306	327
P17182	Conv	GAWQK	FTASAGIQVVGDDLTVTNPK	RIAKA	2		1017.031641	2032.047682	0.000451244	62	N	306	326
P17182	Conv	KGLFR	AAVPSGASTGIYEALELR	DNDKT	2		902.9761374	1803.936675	0.000451244	17	N	32	50
P17182	Conv	ENKSK	FGANAILGVSLAVCK	AGAVE	2	C14:+57.021	760.4189841	1518.822368	0.000451244	26	N	105	120
P17182	Conv	VPLYR	HIADLAGNPEVILPVPAFNVINGGSHAGNK	LAMQE	3		1007.868867	3020.583201	0.000451244	45	N	132	162
P17182	Conv	EKYGK	DATNVGDEGGFAPNILENKEALELLK	TAIAK	2		1379.201226	2756.386852	0.000451244	10	N	202	228
P17182	Conv	LADLY	KSFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		1033.489721	3097.445764	0.000622848	7	N	280	306
P17182	Conv	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	2		1485.6832	2969.350801	0.000451244	14	N	281	306
P17182	Conv	MVSHR	SGETEDTFIADLVVGLCTGQIK	TGAPC	2	C17:+57.021	1177.083513	2352.151427	0.000451244	62	N	372	394
P17182	Conv	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQKF	TASAG	3		1039.814205	3116.419215	0.000622848	3	N	281	307
P17182	Conv	TAIAK	AGYTDQVVIGMDVAASEFYR	SGKYD	2		1096.520584	2191.025568	0.000622848	4	N	233	253
P17182	Conv	VPLYR	HIADLAGNPEVILPVPAFNV	INGGS	2		1043.570736	2085.125873	0.000622848	3	N	132	152
P17182	Conv	QKFTA	SAGIQVVGDDLTVTNPK	RIAKA	2		857.4550378	1712.894476	0.000451244	4	N	309	326
P17182	Conv	AWQKF	TASAGIQVVGDDLTVTNPK	RIAKA	2		943.497434	1884.979268	0.000979378	3	N	307	326
P17182	Conv	EKYGK	DATNVGDEGGFAPNILENK	EALEL	2		980.9664981	1959.917396	0.000451244	40	N	202	221
P17182	Conv	FRAAV	PSGASTGIYEALELR	DNDKT	2		782.4048166	1562.794033	0.000823681	1	N	35	50
P17182	Conv	DDPSR	YITPDQLADLYK	SFVQN	2		720.3749965	1438.734393	0.000451244	10	N	269	281
P17182	Conv	YPVVS	IEDPFDQDDWGAWQK	FTASA	2		925.4055449	1848.79549	0.001463592	1	N	291	306
P17182	Conv	QNYPV	VSIEDPFDQDDWGAWQK	FTASA	2		1018.455766	2034.895932	0.000451244	5	N	289	306
P17182	Conv	HAGNK	LAMQEFMILPVGASSFR	EAMRI	2	M3:+15.995	956.9871801	1911.95876	0.000451244	1	N	162	179
P17182	Conv	KSFVQ	NYPVVSIEDPFDQDDWGAWQK	FTASA	2		1255.069483	2508.123366	0.001352548	1	N	285	306
P17426-2	Conv	FYGNK	TSVQFQNFLPTVVHPGDLQTQLAVQTK	RVAAQ	3		999.5333728	2995.576718	0.000622848	3	N	761	788
P17426-2	Conv	VTKAK	LLGFGSALLDNVDPNPENFVGAGIIQTK	ALQVG	2		1450.264161	2898.512721	0.000662267	2	N	885	913
P17427	Conv	ITKAK	IIGFGSALLEEVDPNPANFVGAGIIHTK	TTQIG	3		960.5154306	2878.522892	0.000451244	16	N	868	896
P17427	Conv	HSNAK	NAVLFEAISLIIHHDSEPNLLVR	ACNQL	3		867.4785396	2599.412219	0.001654178	1	N	305	328
P17427	Conv	SRLSR	IVTSASTDLQDYTYYFVPAPWLSVK	LLRLL	2		1432.723806	2863.432011	0.000622848	2	N	235	260
P17710	Conv	IFETK	FLSQIESDRLALLQVR	AILQQ	3		630.0270644	1887.057793	0.000622848	2	N	841	857
P17710	Conv	LLQVR	AILQQLGLNSTCDDSILVK	TVCGV	2	C12:+57.021	1044.554195	2087.09279	0.000451244	6	N	857	876
P17710	Conv	LYAMR	LSDEILIDILTR	FKKEM	2		700.9039211	1399.792242	0.000451244	14	N	86	98
P17710	Conv	IVSFR	SANLVAATLGAILNR	LRDNK	3		495.2917409	1482.851823	0.000451244	3	N	437	452
P17710	Conv	DGSEK	GDFIALDLGGSSFR	ILRVQ	2		727.8678699	1453.72014	0.001162105	1	N	133	147
P17710	Conv	PSYVR	SIPDGTEHGDFLALDLGGTNFR	VLLVK	3		778.045512	2331.113136	0.000451244	5	N	573	595
P17742	Conv	GKTSK	KITISDCGQL	-	2	C7:+57.021	567.7950963	1133.574593	0.000451244	8	N	154	164
P17742	Conv	EPLGR	VSFELFADKVPK	TAENF	2		690.3826245	1378.749649	0.000451244	12	N	19	31
P17742	Conv	GTGGR	SIYGEKFEDENFILK	HTGPG	2		916.4597889	1830.903978	0.000451244	16	N	76	91
P17742	Conv	EPLGR	VSFELFADK	VPKTA	2		528.274554	1054.533508	0.000451244	15	N	19	28
P17742	Conv	NFILK	HTGPGILSMANAGPNTNGSQFFICTAK	TEWLD	3	C24:+57.021	931.1149014	2790.321304	0.000451244	10	N	91	118
P17742	Conv	-M	VNPTVFFDITADDEPLGR	VSFEL	2		1003.497434	2004.979268	0.000451244	48	N	1	19
P17742	Conv	IYGEK	FEDENFILK	HTGPG	2		577.7905682	1153.565536	0.001329271	9	N	82	91
P17742	Conv	MVNPT	VFFDITADDEPLGR	VSFEL	2		797.891542	1593.767484	0.001162105	3	N	5	19

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P17742	Conv	PLGRV	SFELFADKVPK	TAENF	2		640.8484175	1279.681235	0.000451244	1	N	20	31
P17751	Conv	GHSER	RHVFGESDELIGQK	VSHAL	3		538.9465219	1613.816166	0.000451244	6	N	149	163
P17751	Conv	LIGQK	VSHALAEGLGVIACIGEK	LDERE	2	C14:+57.021	912.4881264	1822.960653	0.000451244	14	N	163	181
P17751	Conv	KDWSK	VVLAYEPVWAIGTGK	TATPQ	2		801.948663	1601.881726	0.000451244	15	N	210	225
P17751	Conv	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAKQ	-	3		1053.219231	3156.634293	0.000451244	10	N	269	299
P17751	Conv	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAK	Q-	3		1010.533038	3028.575715	0.000451244	16	N	269	298
P17751	Conv	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	C1:+39.994,C7:+57.021,C22:+57.021	1182.906952	3545.697456	0.000451244	3	N	70	103
P17751	Conv	PGMIK	DLGATWVVLGHSER	RHVFG	2		770.3998686	1538.784137	0.000451244	7	N	135	149
P17751	Conv	HSERR	HVFGESDELIGQK	VSHAL	2		729.8653272	1457.715054	0.000622848	9	N	150	163
P18242	Conv	LTLCK	GGCEAIVDTGTSLLVGPVEEVKELQK	AIGAV	3	C3:+57.021	910.1409988	2727.399596	0.000451244	12	N	285	311
P18242	Conv	KELQK	AIGAVPLIQGEYMIPCEK	VSSLP	2	M13:+15.995,C16:+57.021	1003.01062	2004.005641	0.000451244	6	N	311	329
P18242	Conv	LTLCK	GGCEAIVDTGTSLLVGPVEEVK	ELQKA	2	C3:+57.021	1115.567499	2229.119398	0.000451244	6	N	285	307
P18242	Conv	KLGGK	NYELHPDKYILK	VSQGG	2		766.9095378	1531.803476	0.000979378	1	N	343	355
P18337	Conv	CHKRK	AALCYTASCQPGSCNGR	GECVE	2	C4:+57.021,C9:+57.021,C14:+57.021	936.8927473	1871.769895	0.001162105	2	N	151	168
P18337	Conv	NTLPK	SPYYYWIGIR	KIGKM	2		659.3354773	1316.655355	0.000823681	3	N	82	92
P18572-2	Conv	DLHTK	YIVDADDRSGEYSCIFLPEPVGR	SEINV	3	C14:+57.021	886.7553672	2657.242702	0.000451244	7	N	73	96
P18572-2	Conv	DADDR	SGEYSCIFLPEPVGR	SEINV	2	C6:+57.021	855.9117202	1709.80784	0.000451244	7	N	81	96
P18572-2	Conv	GQGAC	AAAGTIQTSVQEVNSK	TQLTC	2		802.4184553	1602.821311	0.000622848	1	N	20	36
P18760	Conv	KKRKK	AVLFCLSEDKK	NIILE	2	C5:+57.021	655.3449534	1308.674307	0.000622848	5	N	34	45
P18760	Conv	DKDCR	YALYDATYETK	ESKKE	2		669.3171472	1336.618694	0.000451244	10	N	81	92
P18760	Conv	TLAEK	LGGSAVISLEGKPL	-	2		670.8933564	1339.771113	0.000698008	1	N	152	166
P18760	Conv	LEEGK	EILVGDVGQTVDDPYTTFVK	MLPDK	2		1098.557689	2195.099777	0.000451244	17	N	53	73
P18760	Conv	TKESK	KEDLVFIFWAPENAPLK	SKMIY	2		1009.043823	2016.072046	0.000451244	18	N	95	112
P18760	Conv	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFVK	MLPDK	3		1031.53997	3091.59651	0.000451244	47	N	45	73
P18760	Conv	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTF	VKMLP	2		1433.224367	2864.433133	0.000451244	13	N	45	71
P18760	Conv	LTGIK	HELQANCYEEVKDR	CTLAE	3	C7:+57.021	597.6094268	1789.80488	0.000451244	17	N	132	146
P18760	Conv	SEDKK	NIILEEGKEILVGDVGQTV	DDPYT	2		1013.557492	2025.099383	0.000622848	11	N	45	64
P18760	Conv	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFV	KMLPD	3		988.8416491	2963.501547	0.000451244	9	N	45	72
P19096	Conv	DRATR	EACPELDYFVAFSSVSCGR	GNAGQ	2	C3:+57.021,C17:+57.021	1097.482681	2192.949762	0.000451244	8	N	2000	2019
P19096	Conv	TNLGK	VHLTGINVNPNALFPPVEFPAPR	GTPLI	3		833.788937	2498.343411	0.002519933	1	N	802	825
P19096	Conv	LAQER	LLLPEDPLISGLLNSQALK	ACVDT	2		1017.59642	2033.17724	0.000451244	11	N	1201	1220
P19096	Conv	EGDHR	TLLEGSGLESIINIIHSSLAEPR	VSVRE	3		817.1152669	2448.322401	0.000451244	14	N	2475	2498
P19096	Conv	HTVLK	GHALGETLACLPSEVQPAPSLLSQEEWESLFSR	KALHL	3	C10:+57.021	1213.598399	3637.771797	0.000451244	6	N	1344	1377
P19096	Conv	SLAAK	LSVPTYGLQCTQAAPLDSIPNLAAYYIDCIK	QVQPE	3	C10:+57.021,C29:+57.021	1152.579246	3454.714337	0.000451244	7	N	2256	2287
P19096	Conv	LVQVR	EEEPEAVLPGAQPTLISAISK	TFCPA	2		1090.078788	2178.141977	0.001839721	1	N	1850	1871
P19096	Conv	PRSAR	WLSTSIPEAQWQSSLAR	TSSAE	2		980.5003111	1958.985022	0.00307782	1	N	711	728
P19096	Conv	KTLAR	SLGLSLEETPVVFENVSFHQATILPK	TGTVA	3		952.5116861	2854.511658	0.000451244	3	N	901	927
P19096	Conv	VGLKR	SFYGTALFLCR	RAIPQ	2	C10:+57.021	667.8320132	1333.648426	0.00307782	1	N	1387	1398
P19096	Conv	SQALK	ACVDTALENLSTLK	MKVAE	2	C2:+57.021	767.8929961	1533.770392	0.002080925	1	N	1220	1234
P19096	Conv	FLCRR	AIPQEKPIFLSVEDTSFQWVDSLK	STLAT	3		926.4852485	2776.432345	0.000451244	1	N	1399	1423
P19157	Conv	GQLPK	FEDGDLTLYQSNAILR	HLGRS	2		927.9657697	1853.915939	0.000451244	8	N	55	71
P19221	Conv	ENFCR	NPDSSTTGPWCYTTDPTVR	REECS	2	C11:+57.021	1077.973766	2153.931932	0.002813207	1	N	159	178
P19221	Conv	WGNLR	ETWTTNINEIQPSVLQVVNLPIVERPVCK	ASTRI	3	C28:+57.021	1126.269666	3375.785597	0.000823681	1	N	505	534
P19973	Conv	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	3		907.739476	2720.195028	0.000451244	19	N	96	120
P19973	Conv	VASTK	TLWETGEVQSQSASK	TPSCQ	2		825.9026381	1649.789676	0.000451244	7	N	255	270
P19973	Conv	LISLK	SSELDEDEGFGDWSQKPEPR	QQFWG	2		1154.504173	2306.992746	0.002813207	1	N	76	96
P19973	Conv	SHQAK	VHLEESNLSYREPDPEDAVGGSGEAEEHLIR	HQVRT	3		1145.541873	3433.602218	0.001162105	3	N	130	161
P19973	Conv	RHQVR	TPSPLALEDTVELSSPPLSPTTK	LADRT	2		1190.628842	2379.242085	0.002519933	2	N	165	188
P19973	Conv	NSVKK	SQPTLPISTIDER	LQQYT	2		728.8862597	1455.756919	0.00307782	1	N	208	221
P20029	Conv	VVEKK	TKPYIQVDIGGGQTK	TFAPE	2		802.9362839	1603.856968	0.000451244	17	N	124	139
P20029	Conv	GDAAK	NQLTSNPENTVFDAKR	LIGRT	2		917.4586432	1832.901686	0.000451244	9	N	82	98
P20029	Conv	RLIGR	TWNDPSVQQDIK	FLPFK	2		715.8496771	1429.683754	0.000451244	17	N	102	114
P20029	Conv	PIISK	LYGSGGPPPTGEEDTSEKDEL	-	2		1089.4902	2176.9648	0.000451244	48	N	634	655
P20029	Conv	GDAAK	NQLTSNPENTVFDAK	RLIGR	2		839.4080876	1676.800575	0.000451244	38	N	82	97
P20029	Conv	YLGKK	VTHAVVTVPAYFNDAQR	QATKD	3		629.9957642	1886.963893	0.000451244	9	N	165	182
P20029	Conv	DSDLK	KSDIDEIVLVGGSTR	IPKIQ	2		794.9311986	1587.846797	0.000451244	20	N	353	368
P20029	Conv	DQGNR	ITPSYVAFTPEGER	LIGDA	2		783.8940847	1565.772569	0.000451244	17	N	61	75
P20029	Conv	LNVMR	IINEPTAAAIAYGLDKR	EGEKN	2		908.5023224	1814.989045	0.000451244	16	N	198	215
P20029	Conv	ETLTR	AKFEELNMDLFR	STMKP	3		504.9225491	1511.744247	0.000451244	6	N	325	337
P20029	Conv	RPLTK	DNHLLGTFDLTGIPPAPR	GVPQI	2		967.5106788	1933.005758	0.000451244	15	N	475	493
P20029	Conv	QHQAR	IEIESFFEGEDFSETLTR	AKFEE	2		1075.002746	2147.989892	0.000451244	37	N	307	325
P20029	Conv	GGQTK	TFAPEEISAMVLTK	MKETA	2		768.9030644	1535.790529	0.000451244	7	N	139	153
P20029	Conv	AVEEK	IEWLESHQDADIEDFKAK	KKELE	3		725.3520535	2173.03276	0.000451244	9	N	602	620

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P20029	Conv	RIDTR	NELESYAYSLK	NQIGD	2		658.8225967	1315.629593	0.00091018	3	N	563	574
P20029	Conv	KAKKK	ELEEIVQPIISK	LYGSG	2		699.3984716	1396.781343	0.000451244	7	N	622	634
P20029	Conv	SDLKK	SDIDEIVLVGGSTR	IPKIQ	2		730.883717	1459.751834	0.000622848	9	N	354	368
P20029	Conv	AVEEK	IEWLESHQDADIEDFK	AKKKE	2		987.9581417	1973.900683	0.000451244	12	N	602	618
P20029	Conv	KLKER	IDTRNELESYAYSLK	NQIGD	2		901.4524952	1800.88939	0.000823681	1	N	559	574
P20029	Conv	VVPTK	KSQIFSTASDNQPTVTIK	VYEGE	2		983.0185337	1964.021467	0.000451244	3	N	447	465
P20029	Conv	RQATK	DAGTIAGLNVMR	IINEP	2		609.3195018	1216.623404	0.002663018	1	N	186	198
P20029	Conv	KVVEK	KTKPYIQVDIGGGQTK	TFAPE	3		578.3251103	1731.951931	0.000622848	2	N	123	139
P20029	Conv	DVSLL	TIDNGVFEVVATNGDTHLGGEDFDQR	VMEHF	2		1403.649889	2805.284178	0.000622848	4	N	236	262
P20029	Conv	REGEK	NILVFDLGGGTFDVSLL	TIDNG	2		890.4805243	1778.945449	0.000451244	2	N	219	236
P20060	Conv	SYELK	QVTGSGFPAILSAPWYLDLISYGQDWK	NYYKV	3		1004.843436	3011.506907	0.000451244	9	N	413	440
P20060	Conv	ELSNK	GSYSLSHVYTPNDVR	MVLEY	2		847.9107974	1693.805995	0.000451244	11	N	236	251
P20060	Conv	EAFRR	YYNYVFGFYK	RHHGP	2		682.3220355	1362.628471	0.000451244	8	N	79	89
P20060	Conv	SSLKK	NSIVWQEVFDDKVELQPGTVVEVWK	SEHYS	3		982.175074	2943.501822	0.000451244	6	N	379	404
P20060	Conv	RMVSR	GIAAQPLYTGYCNYENKI	-	2	C12:+57.021	1037.999055	2073.982511	0.000451244	10	N	518	536
P20060	Conv	MAFNK	FNVLHWHIVDDQSFPYQSTTFPELSNK	GSYSL	3		1083.860037	3248.556711	0.000451244	5	N	209	236
P20060	Conv	LRGIR	VIPEFDTPGHTQSWGK	GQKNL	2		899.9420976	1797.868595	0.000451244	3	N	263	279
P20108	Conv	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASK	EYFEK	4	C12:+57.021	854.1676316	3412.639327	0.002145581	1	N	218	249
P20108	Conv	KQISR	DYGVLLESAGIALR	GLFII	2		738.9069951	1475.79839	0.000451244	7	N	171	185
P20108	Conv	GIALR	GLFIIDPNGVVK	HLSVN	2		636.3720598	1270.72852	0.000979378	6	N	185	197
P20108	Conv	DFKGK	YLVLFFYPLDFTFVCPTEIVAFSDK	ANEFH	3	C15:+57.021	1011.178614	3030.512441	0.000622848	1	N	94	119
P20152	Conv	SVAAK	NLQEAEEWYK	SKFAD	2		655.3071138	1308.598628	0.001229886	2	N	282	292
P20152	Conv	NDKAR	VEVERDNLAEDIMR	LREKL	2	M13:+15.995	852.9152658	1703.814932	0.002145581	1	N	170	184
P20152	Conv	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	C7:+57.021	1189.087119	2376.158637	0.000451244	15	N	321	342
P20152	Conv	LDLER	KVESLQEEIAFLK	KLHDE	2		767.4303031	1532.845006	0.000451244	17	N	222	235
P20152	Conv	EQQNK	ILLAELEQLK	GQGKS	2		585.3611607	1168.706721	0.000451244	10	N	129	139
P20152	Conv	GEESR	ISLPLPTFSSLNLR	ETNLE	2		779.4541125	1556.892625	0.000451244	7	N	410	424
P20152	Conv	EMLQR	EEAESTLQSFRQDVDNASLAR	LDLER	3		789.3793309	2365.114593	0.000451244	7	N	196	217
P20152	Conv	ERQMR	EMEENFALEAANYQDTIGR	LQDEI	2		1100.99493	2199.97426	0.000451244	3	N	345	364
P20152	Conv	QDSVD	FSLADAINTEFK	NTRTN	2		678.346239	1354.676878	0.000451244	20	N	85	97
P20152	Conv	AFLKK	LHDEEIQELQAQIQEQHVQID	VDVSK	2		1272.122778	2542.229957	0.000823681	10	N	236	257
P20152	Conv	IAFLK	KLHDEEIQELQAQIQEQHVQID	VDVSK	3		891.1161067	2670.32492	0.002296037	1	N	235	257
P20152	Conv	AFLKK	LHDEEIQELQAQIQEQHVQIDVD	VSKPD	3		919.7829047	2756.325314	0.001329271	2	N	236	259
P20918	Conv	DYRGK	TAVTAAGTPCQGWAAQEPHR	HSIFT	3	C10:+57.021	703.6695682	2107.985305	0.000451244	11	N	492	512
P20918	Conv	KNYCR	NPDGDVNGPWCYTTNPR	KLYDY	2	C11:+57.021	981.9238789	1961.832158	0.000451244	10	N	532	549
P20918	Conv	TTNPR	KLYDYCDIPLCASASSFECGKPQVEPK	KCPGR	4	C6:+57.021,C11:+57.021,C19:+57.021	791.3701507	3161.449403	0.000451244	6	N	549	576
P20918	Conv	SLRTR	FTGQHFCGGTLIAPEWVLTAAHCLEK	SSRPE	3	C7:+57.021,C23:+57.021	981.8144088	2942.419826	0.000451244	1	N	602	628
P20918	Conv	ENYCR	NPDGETAPWCYTTDSQLR	WEYCE	2	C10:+57.021	1055.960658	2109.905717	0.000451244	6	N	325	343
P20918	Conv	NNRVK	STELCAGQLAGGVDSCQGDSGGPLVCFEKDK	YILQG	3	C5:+57.021,C16:+57.021,C26:+57.021	1081.484862	3241.431187	0.000662267	2	N	742	773
P20918	Conv	NFPCK	NLEENYCRNPDGETAPWCYTTDSQLR	WEYCE	3	C7:+57.021,C18:+57.021	1063.792949	3188.355448	0.000451244	3	N	317	343
P20918	Conv	KPGQG	DSLDGYISTQGASLFSLTK	KQLAA	2		1002.002549	2001.989498	0.000622848	1	N	19	38
P20918	Conv	NNRVK	STELCAGQLAGGVDSCQGDSGGPLVCFEK	DKYIL	3	C5:+57.021,C16:+57.021,C26:+57.021	1000.444227	2998.309281	0.001654178	1	N	742	771
P20918	Conv	CDIPR	CTTPPPPPSPTYQCLK	GRGEN	2	C1:+57.021,C14:+57.021	922.4395563	1842.863513	0.002727428	2	N	261	277
P21107	Conv	LAEKK	AADAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	6	N	78	91
P21107	Conv	AKLEK	TIDDLEDELYAQK	LKYKA	2		776.8730149	1551.73043	0.000451244	5	N	252	265
P21107-2	Conv	EAVKR	KIQVLQQQADDAEER	AERLQ	2		885.9531937	1769.890787	0.000451244	7	N	12	27
P21107-2	Conv	AVKRK	IQVLQQQADDAEER	AERLQ	2		821.9057121	1641.795824	0.000451244	23	N	13	27
P21107-2	Conv	AVKRK	IQVLQQQADDAEERAER	LQREV	2		999.9961212	1997.976642	0.000451244	7	N	13	30
P21107-2	Conv	AKLEK	TIDDLEDKLK	CTKEE	2		595.3196898	1188.62378	0.001162105	8	N	215	225
P21107-2	Conv	ERRAR	EQAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	2	N	42	54
P21107-2	Conv	EGERR	AREQAEAEVASLNR	RIQLV	2		772.3953145	1542.775029	0.000622848	1	N	40	54
P21107-2	Conv	ERRAR	EQAEAEVASLNRR	IQLVE	3		491.5871051	1471.737915	0.00091018	1	N	42	55
P21107-2	Conv	LCTQR	MLDQTLLDLNEM	-	2	M1:+15.995,M12:+15.995	734.3395256	1466.663451	0.001463592	2	N	236	248
P21614	Conv	SHLIK	LAQKVPTANLENVLPLAEDFTEILSR	CCEST	3		961.1943571	2880.559671	0.000451244	8	N	238	264
P21614	Conv	RRDPK	GFADQFLYEYSSNYGQAPLPLLVAYTK	NYLSM	3		1019.174963	3054.501488	0.000451244	19	N	153	180
P21614	Conv	KLAQK	VPTANLENVLPLAEDFTEILSR	CCEST	3		814.4361175	2440.284953	0.000451244	9	N	242	264
P21614	Conv	NQLVK	EVVSLTEECCAEGADPTCYDTR	TSELS	2	C9:+57.021,C10:+57.021,C18:+57.021	1281.524914	2561.034228	0.000451244	2	N	65	87
P22366	Conv	ASVGR	LLELLALLDREDILK	ELKSR	3		589.6929112	1766.055334	0.001352548	1	N	88	103
P22599	Conv	PPILR	FDHPFLFIIFEEHTQSPIFVGK	VVDPT	4		662.8446733	2647.347493	0.000823681	1	N	384	406
P22599	Conv	VEAVK	ELDQDTVFALANYILFK	GKWKK	2		1000.522921	1999.030241	0.001943752	1	N	192	209
P22892	Conv	AAVPK	TFQLQLLSPSSSVVPAFNTGTITQVIK	VLNPQ	2		1438.792554	2875.569508	0.001591523	1	N	756	783

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P22892	Conv	RGMMK	ELLYFLDSCEPEFK	ADCAS	2	C9:+57.021	895.4215864	1788.827573	0.000622848	3	N	383	397
P22892	Conv	VQRHR	STIVDCLKDLDVSIK	RRAME	2	C6:+57.021	853.4559606	1704.896321	0.001329271	1	N	347	362
P23116	Conv	VPEVK	DLYNWLEVEFNPLK	LCERV	2		890.4517668	1778.887934	0.000451244	13	N	388	402
P23116	Conv	LNWVR	EQPEKEPELQQYVPQLQNNTILR	LLQQV	3		932.1510399	2793.42972	0.0025889	1	N	415	438
P23116	Conv	IEFSR	LTSLVPFVDAFQLER	AIVDA	2		867.9754091	1733.935218	0.00091018	1	N	454	469
P23116	Conv	NTILR	LLQQVAQIYQSIEFSR	LTSLV	2		962.0208793	1922.026159	0.000451244	7	N	438	454
P23116	Conv	NDMVR	FSVLQYVVPEVK	DLYNW	2		704.3982746	1406.780949	0.002453667	1	N	376	388
P23249	Conv	PFPAK	LDLQQGQDLLQGLSK	LSPST	2		828.4522982	1654.888996	0.000451244	1	N	953	968
P23249	Conv	GKDER	EGNSPSFFNPEEAATVTSYLK	QLLAP	2		1144.540027	2287.064455	0.000622848	2	N	788	809
P23249	Conv	LMDVK	ETGNPGGQLVLAGDPR	QLGPV	2		790.9055151	1579.79543	0.000622848	1	N	667	683
P23492	Conv	TAHLK	EAQIFDYNEIPNFPQSTVQGHAGR	LVFGL	2		1359.649495	2717.28339	0.000451244	5	N	43	67
P23492	Conv	HCGLR	VFGFSLITNK	VVMDY	2		563.3192958	1124.622992	0.000451244	15	N	234	244
P23492	Conv	IMLIR	DHINLPGFCGQNPLR	GPNDE	3	C9:+57.021	579.9548687	1736.841206	0.000451244	19	N	133	148
P23492	Conv	IMLIR	DHINLPGFCGQNPLRGPNDER	FGVRF	3	C9:+57.021	802.7174696	2405.129009	0.000451244	12	N	133	154
P23492	Conv	GHAGR	LVFGLLNGR	CCVMM	2		494.8010733	987.5865465	0.001943752	3	N	67	76
P23492	Conv	ETTAK	WLLQHTEYRPQVAVICGSGLGGLTAHLK	EAQIF	3	C16:+57.021	1035.55396	3103.638479	0.001162105	2	N	15	43
P23492	Conv	MGEQR	KLQEGTYVMLAGPNFETVAESR	LLKML	3		814.0779362	2439.210409	0.000622848	3	N	185	207
P23492	Conv	QTLER	FVSILMESIPLPDRGS	-	2		880.9667274	1759.917855	0.000622848	4	N	273	289
P23591	Conv	RAIQK	VVADGAGLPGEEWVFVSSK	DADLT	2		973.9970699	1945.97854	0.000870037	5	N	25	44
P23953	Conv	KVLGK	YISLEGFEQPVAVFLGVPFAKPPLGSLR	FAPPQ	3		1011.227221	3030.658263	0.000451244	14	N	36	64
P23953	Conv	ILPLK	ISEDCLYLNIYSPADLTK	SSQLP	2	C5:+57.021	1058.019653	2114.023707	0.000451244	1	N	111	129
P24063	Conv	GAEGR	VVVLSSRPVVDVVTELSFSPEEIPVHEVECSYSAR	EEQKH	4	C30:+57.021	979.5019763	3913.976705	0.000451244	6	N	604	639
P24063	Conv	FLDLR	EDLQGATFVGQEPLTSDVR	GGYLG	2		1031.50853	2061.00146	0.000451244	2	N	379	398
P24063	Conv	TYQRR	QSLFEMVSELQGDPGYPLGR	FGAAI	2	M6:+15.995	1120.039183	2238.062767	0.000823681	3	N	498	518
P24063	Conv	VLSSR	PVVDVVTELSFSPEEIPVHEVECSYSAR	EEQKH	3	C23:+57.021	1058.848544	3173.522231	0.000735798	2	N	611	639
P24063	Conv	VQKQK	TLHIFASEPVEEFVK	ILDTF	3		582.6423279	1744.903584	0.001395409	1	N	295	310
P24270	Conv	GFAVK	FYTEDGNWDLVGNNTPIFFIR	DAILF	2		1259.606036	2517.196472	0.000451244	20	N	135	156
P24270	Conv	EERKR	LCENIAGHLK	DAQLF	2	C2:+57.021	577.8032557	1153.590911	0.001395409	1	N	458	468
P24270	Conv	VDVKR	FNSANEDNVTQVR	TFYTK	2		747.3531153	1492.690631	0.000451244	5	N	431	444
P24270	Conv	SHTFK	LVNADGEAVYCK	FHYKT	2	C11:+57.021	669.8218424	1337.628085	0.000451244	7	N	221	233
P24270	Conv	VVHAK	GAGAFGYFEVTHDITR	YSKAK	2		870.9211652	1739.82673	0.000451244	18	N	77	93
P24270	Conv	VMTFK	EAETFPFNPFDLTK	VWPHK	2		828.4017426	1654.787885	0.000622848	3	N	287	301
P24270	Conv	WKEQR	ASQRPDVLTTGGGNPIGDK	LNIMT	2		941.9850251	1881.95445	0.000451244	2	N	19	38
P24270	Conv	THRHR	LGPNYLQIPVNCPYR	ARVAN	2	C12:+57.021	902.4644543	1802.913309	0.000451244	15	N	365	380
P24270	Conv	PEQQR	SALEHSVQCAVDVK	RFNSA	2	C9:+57.021	771.8829627	1541.750325	0.001395409	2	N	416	430
P24270	Conv	VWDFW	SLRPESLHQVSFLFSDR	GIPDG	3		673.3538401	2017.03812	0.000451244	2	N	186	203
P24270	Conv	IFFIR	DAILFPSFIHSQK	RNPQT	2		751.9042554	1501.792911	0.000451244	9	N	156	169
P24270	Conv	TAGSR	GPLLVQDVVFTDEMAHFDR	ERIPE	2		1095.038944	2188.062287	0.000451244	3	N	47	66
P24270	Conv	IFFIR	DAILFPSFIHSQKR	NPQTH	2		829.954811	1657.894022	0.000622848	1	N	156	170
P24270	Conv	TAGSR	GPLLVQDVVFTDEMAHFDRER	IPERV	3		825.4097973	2473.205992	0.000451244	4	N	47	68
P24270	Conv	EERKR	LCENIAGHLKDAQLFIQK	KAVKN	2	C2:+57.021	1049.559614	2097.103629	0.000451244	11	N	458	476
P24270	Conv	LVLNK	NPVNYFAEVEQMAFDPSNMPPGIEPSPDK	MLQGR	3		1074.158767	3219.452902	0.001871652	6	N	320	349
P24270	Conv	HSQKR	NPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDR	GIPDG	4		1007.744685	4026.94754	0.000979378	1	N	170	203
P24369	Conv	KTVPK	TVDNFVALATGEK	GFGYK	2		682.8569709	1363.698342	0.000451244	5	N	71	84
P24369	Conv	KVTVK	VYFDLQIGDESVGR	VVFGL	2		799.3969916	1596.778383	0.000451244	4	N	45	59
P24369	Conv	GTGGK	SIYGERFPDENFK	LKHYG	2		801.3838842	1600.752168	0.000451244	5	N	116	129
P24369	Conv	ANAGK	DTNGSQFFITTVK	TSWLD	2		729.3677027	1456.719805	0.000451244	7	N	145	158
P24527	Conv	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	2		1204.122384	2406.229169	0.000622848	8	N	288	310
P24527	Conv	IADLK	DLSSHQLNEFLAQVLQK	APLPL	2		985.5212435	1969.026887	0.000451244	11	N	493	510
P24527	Conv	RFNQR	VPIPCYLIALVVGALESR	QIGPR	2	C5:+57.021	985.5610945	1969.106589	0.000451244	13	N	195	213
P24527	Conv	DFARR	TLTGTAALTVQSQEENLR	SLTLD	2		966.5057904	1930.995981	0.000451244	30	N	33	51
P24527	Conv	GEKFR	HFHALGGWGELQNTIK	TFGES	2		904.4660742	1806.916548	0.000698008	1	N	339	355
P24527	Conv	TPSVK	LTYTAEVSVPK	ELVAL	2		604.3326002	1206.6496	0.000451244	15	N	154	165
P24527	Conv	VPIPC	YLIALVVGALESR	QIGPR	2		702.4169987	1402.818397	0.000451244	8	N	200	213
P24527	Conv	WVTAK	EEDLSSFSIADLKDLSSHQLNEFLAQVLQK	APLPL	3		1135.579376	3403.714728	0.000451244	5	N	480	510
P24527	Conv	IPYEK	GFALLFYLEQLLGGPEVFLGFLK	AYVKK	2		1286.217234	2570.418867	0.000451244	10	N	386	409
P24527	Conv	VVDLK	DVDPDVAYSSIPYEK	GFALL	2		849.3993969	1696.783194	0.000451244	16	N	371	386
P24527	Conv	AYVKK	FSYQSVTTDDWK	SFLYS	2		738.8362354	1475.656871	0.001162105	5	N	414	426
P24527	Conv	WVTAK	EEDLSSFSIADLK	DLSSH	2		727.3570007	1452.698401	0.000622848	5	N	480	493
P24527	Conv	LVTNK	TWDHFWLNEGHTVYLER	HICGR	2		1102.021942	2202.028284	0.001699387	1	N	310	327
P24527	Conv	ALSQR	WVTAKEEDLSSFSIADLK	DLSSH	2		1020.020742	2038.025884	0.001264573	1	N	475	493
P24527	Conv	HPFTK	LVVDLKDVDPDVAYSSIPYEK	GFALL	2		1183.112828	2364.210056	0.000451244	4	N	365	386
P24527	Conv	VDFAR	RTLTGTAALTVQSQEENLR	SLTLD	2		1044.556346	2087.097092	0.001162105	2	N	32	51
P24527	Conv	RPLFK	DLAAFDKSHDQAVHTYQEHK	ASMHP	3		780.7054898	2339.093069	0.000451244	6	N	573	593
P24527	Conv	QIGPR	TLVWSEKEQVEK	SANEF	2		738.3911779	1474.766756	0.0007646	4	N	218	230

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P24527	Conv	QTSGK	QHPYLFSQCQAIHCR	AILPC	3	[0:-	643.2945921	1926.860376	0.001162105	1	N	127	142
P24527	Conv	GHIKR	MQEVYNFNAINNSEIR	FRWLR	2		971.4603292	1940.905058	0.000451244	4	N	520	536
P24549	Conv	ANNTT	YGLAAGLFTK	DLDKA	2		520.7929139	1039.570228	0.000622848	3	N	425	435
P24549	Conv	VKAAR	QAFQIGSPWR	TMDAS	2		595.3097938	1188.603988	0.002727428	1	N	68	78
P24549	Conv	MFIWK	IGPALSCGNTVVVKPAEQTPLTALHLASLIK	EAGFP	3	C7:+57.021	1066.935847	3197.78414	0.001763695	1	N	179	210
P25444	Conv	SLPIK	ESEIIDFFLGASLKDEVLK	IMPVQ	3		718.3845831	2152.130349	0.000451244	1	N	89	108
P25911	Conv	CWKEK	AEERPTFDYLQSVLDDFYTATEGQYQQQP	-	3		1147.192069	3438.552808	0.002727428	1	N	483	512
P25911	Conv	LPGQR	FQTKDPEEQGDIVVALYPYDGIHPDDLSFK	KGEKM	4		859.9205664	3435.651065	0.000451244	10	N	55	85
P25911	Conv	RFQTK	DPEEQGDIVVALYPYDGIHPDDLSFK	KGEKM	3		978.134944	2931.381432	0.000451244	11	N	59	85
P25911	Conv	KFPIK	WTAPEAINFGCFTIK	SDVWS	2	C11:+57.021	877.9324557	1753.849311	0.000451244	1	N	408	423
P25911	Conv	KDAER	QLLAPGNSAGAFLIR	ESETL	2		764.4362541	1526.856908	0.001162105	1	N	141	156
P25911	Conv	NYVAK	VNTLETEEWFFKDITR	KDAER	3		676.6744678	2027.000004	0.000622848	4	N	120	136
P26039	Conv	SDYGR	LASQAKPAAVAAENEEIGAHIK	HRVQE	3		740.0662475	2217.175342	0.000451244	19	N	1895	1917
P26039	Conv	ASAPK	ASAGPQPLLVQSCK	AVAEQ	2	C13:+57.021	728.3851412	1454.754682	0.000451244	15	N	943	957
P26039	Conv	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2		983.0115743	1964.007549	0.000451244	4	N	922	943
P26039	Conv	KAAQK	AAAFEDQENETVVVK	EKMVG	2		825.4050136	1648.794427	0.000451244	23	N	2476	2491
P26039	Conv	ISSAK	QVAASTAQLLVACK	VKADQ	2	C13:+57.021	730.4007913	1458.785983	0.000451244	15	N	2429	2443
P26039	Conv	RLVAK	AVEGCVSASQAATEDGQLLR	GVGAA	2	C5:+57.021	1031.497408	2060.979216	0.000451244	36	N	745	765
P26039	Conv	SQNAK	NGNLPEFGDAIATASK	ALCGF	2		802.8998984	1603.784197	0.000451244	7	N	1415	1431
P26039	Conv	VACTK	VVAPTISSPVCQEQLVEAGR	LVAKA	2	C11:+57.021	1070.557269	2139.098938	0.000451244	21	N	721	741
P26039	Conv	TKGTR	ALEATTEHIRQELAVFCSPEPPAK	TSTPE	3	C17:+57.021	898.7904118	2693.347835	0.000451244	12	N	2144	2168
P26039	Conv	SRGVK	LLAALLEDEGGNGRPLLQAAK	GLAGA	2		1075.102932	2148.190264	0.000451244	16	N	592	613
P26039	Conv	VQSCK	AVAEQIPLLVQGVR	GSQAQ	2		746.9464546	1491.877309	0.000451244	15	N	957	971
P26039	Conv	ITSMR	DKAPGQLECETAIAALNSCLR	DLDQA	2	C9:+57.021,C19:+57.021	1159.067443	2316.119287	0.000451244	15	N	1652	1673
P26039	Conv	LQAAK	GLAGAVSELLR	SAQPA	2		543.3198272	1084.624054	0.000451244	10	N	613	624
P26039	Conv	EMVTK	SNTSPEELGPLANQLTSDYGR	LASQA	2		1125.038183	2248.060766	0.000451244	14	N	1874	1895
P26039	Conv	EAQSR	LNEAAAGLNQAATELVQASR	GTPQD	2		1014.029964	2026.044328	0.000451244	21	N	1241	1261
P26039	Conv	ADVVK	LGAASLGAEDPETQVVLINAVK	DVAKA	2		1098.100055	2194.18451	0.000451244	17	N	2063	2085
P26039	Conv	NSCLR	DLDQASLAAVSQQLAPR	EGISQ	2		891.9713864	1781.927173	0.000451244	16	N	1673	1690
P26039	Conv	VAQGK	VGAIPANALDDGQWSQGLISAAR	MVAAA	2		1155.596003	2309.176405	0.000451244	20	N	2375	2398
P26039	Conv	ADVVK	LGAASLGAEDPETQVVLINAVKDVAK	ALGDL	3		870.1451147	2607.411944	0.000622848	5	N	2063	2089
P26039	Conv	VRQAR	ILAQATSDLVNAIKADAEGESDLENSR	KLLSA	2		1415.707404	2829.399207	0.000451244	1	N	827	854
P26039	Conv	EQKHK	AGFLDLKDFLPK	EYVKQ	2		682.3851672	1362.754734	0.0007646	7	N	256	268
P26039	Conv	LDQTK	TLAESALQLLYTAK	EAGGN	2		761.4303031	1520.845006	0.000451244	7	N	1766	1780
P26039	Conv	VQGVR	GSQAQPDSPSAQLALIAASQSFLQPGGK	MVAAA	2		1377.70701	2753.398419	0.000622848	8	N	971	999
P26039	Conv	SVAQR	TEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	3	C17:+57.021,C27:+57.021	1018.169246	3051.484337	0.000823681	21	N	692	721
P26039	Conv	ATASK	ALCGFTEAAAQAAYLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	3	C3:+57.021	1308.306167	3921.895101	0.000451244	24	N	1431	1469
P26039	Conv	LHYGR	ECANGYLELLDHVLLTLQKPNPDLK	QQLTG	3	C2:+57.021	965.1761548	2892.505065	0.000451244	9	N	2241	2266
P26039	Conv	GQLLR	GVGAAATAVTQALNELLQHVK	AHATG	2		1046.082	2090.148399	0.000451244	20	N	765	786
P26039	Conv	RAQCR	AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR	AAMEP	3		1152.914759	3455.720876	0.000451244	25	N	1559	1593
P26039	Conv	QLAPR	EGISQEALHTQMLTAVQEISHLIEPLASAAR	AEASQ	4		836.6888472	3342.724189	0.000451244	3	N	1690	1721
P26039	Conv	AEAMK	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1017.843941	3050.508424	0.000451244	14	N	2291	2321
P26039	Conv	AQAAR	GVAALTSDPAVQAIVLDTASDVLDKASSLIEEAK	KASGH	3		1133.27032	3396.787559	0.000451244	10	N	1136	1170
P26039	Conv	LRACK	EAAFHPEVAPDVR	LRALH	2		719.360212	1436.704824	0.000622848	3	N	2220	2233
P26039	Conv	VAAAK	ASVPTIQDQASAMQLSQCAK	NLGTA	2	M13:+15.995,C18:+57.021	1075.514787	2149.013974	0.000451244	12	N	1005	1025
P26039	Conv	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	3		1388.694245	4163.059336	0.000451244	15	N	634	673
P26039	Conv	GSQEK	LAQAAQSSVATITR	LADVV	2		708.894419	1415.773238	0.000451244	17	N	2043	2057
P26039	Conv	ALVTK	AGALQCSPSDVYTK	KELIE	2	C6:+57.021	748.8564136	1495.697227	0.000451244	6	N	1933	1947
P26039	Conv	MQLAK	AVASAAAALVLK	AKSVA	2		542.8403955	1083.665191	0.000823681	1	N	673	685
P26039	Conv	RAKPK	EADESLNFEEQILEAAK	SIAAA	2		968.4632569	1934.910914	0.000451244	13	N	2333	2350
P26039	Conv	YVQAR	DDILNGSHPVSFDK	ACEFA	2		772.3735164	1542.731433	0.000451244	11	N	220	234
P26039	Conv	TEHIR	QELAVFCSPEPPAK	TSTPE	2	C7:+57.021	786.8902564	1571.764913	0.000451244	15	N	2154	2168
P26039	Conv	VRQAR	ILAQATSDLVNAIK	ADAEG	2		728.9226452	1455.82969	0.000451244	16	N	827	841
P26039	Conv	SMRDK	APGQLECETAIAALNSCLR	DLDQA	2	C7:+57.021,C17:+57.021	1037.50649	2072.997381	0.000451244	7	N	1654	1673
P26039	Conv	MIRER	IPEALAGPPNDFGLFLSDDDPKK	GIWLE	3		819.4168344	2455.227103	0.000451244	13	N	35	58
P26039	Conv	CRMIR	ERIPEALAGPPNDFGLFLSDDDPK	KGIWL	3		871.7664149	2612.275845	0.000451244	5	N	33	57
P26039	Conv	AQAAR	GVAALTSDPAVQAIVLDTASDVLDK	ASSLI	2		1235.158298	2468.300997	0.000451244	3	N	1136	1161
P26039	Conv	AAEAM	KGTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1060.542262	3178.603387	0.000698008	4	N	2290	2321
P26039	Conv	HIKHR	VQELGHGCSALVTK	AGALQ	2	C8:+57.021	749.8880481	1497.760496	0.001699387	1	N	1919	1933
P26039	Conv	ASQAK	PAAVAAENEEIGAHIK	HRVQE	3		540.6182938	1618.831481	0.000451244	4	N	1901	1917
P26039	Conv	SQCAK	NLGTALAELR	TAAQK	2		529.3041771	1056.592754	0.001162105	2	N	1025	1035
P26039	Conv	VSFDK	ACEFAGFQCQIQFGPHNEQK	HKAGF	2	C2:+57.021,C9:+57.021	1198.531028	2395.046456	0.000451244	12	N	234	254
P26039	Conv	LLRRK	FFYSDQNVDSRDPVQLNLLYVQAR	DDILN	3		963.1511513	2886.430054	0.000451244	18	N	196	220
P26039	Conv	LLAAK	ALSTDPASPNLK	SQLAA	2		607.3253065	1212.635013	0.000451244	2	N	1320	1332
P26039	Conv	NVDSR	DPVQLNLLYVQAR	DDILN	2		764.9282619	1527.840924	0.000451244	3	N	207	220

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26039	Conv	ARSLK	TYGVSFFLVK	EKMKG	2		580.8216714	1159.627743	0.000451244	8	N	306	316
P26039	Conv	QAGNR	GTQACITAASAVSGIIADLDTTIMFATAGTLNR	EGAET	3	C5:+57.021,M24:+15.995	1109.890554	3326.648263	0.002080925	1	N	1973	2006
P26039	Conv	LDHGR	TLREQGVEEHETLLLR	RKFFY	3		641.6818453	1922.022136	0.000622848	3	N	178	194
P26039	Conv	ISAAR	MVAAATNNLCEAANAAVQGHASQEK	LISSA	3	C10:+57.021	852.7362015	2555.185205	0.001162105	1	N	2398	2423
P26039	Conv	MIRER	IPEALAGPPNDFGLFLSDDDPK	KGIWL	2		1164.57387	2327.13214	0.001839721	2	N	35	57
P26039	Conv	QLGHK	VSQMAQYFEPLTLAAVGAASK	TLSHP	2		1091.564794	2181.113989	0.000823681	2	N	1730	1751
P26039	Conv	AAAAR	AVTDSINQLITMCTQQAPGQKECDNALR	QLETV	3	C13:+57.021,C23:+57.021	1054.837613	3161.48944	0.000735798	1	N	1340	1368
P26039	Conv	TAAQK	AQEACGPLEMDSALSVVQNLEKDLQEIK	AAARD	3	C5:+57.021	1039.181417	3114.520852	0.000451244	3	N	1040	1068
P26039	Conv	PAIMR	SGASGPENFQVGSMPPAQQQITSGQMHR	GHMPP	3	M14:+15.995,M26:+15.995	987.1194742	2958.335023	0.000622848	1	N	454	482
P26039	Conv	YYSVQ	TTEGEQIAQLIAGYIDIILK	KKKSK	2		1095.107349	2188.199098	0.001654178	1	N	381	401
P26039	Conv	AAQAA	YLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	2		1331.16752	2660.319441	0.000622848	1	N	1444	1469
P26039	Conv	GTLNR	EGAETFADHREGILK	TAKVL	3		558.2816817	1671.821645	0.0007646	1	N	2006	2021
P26040	Conv	QDQIK	SQEQLAAELAEYTAK	IALLE	2		826.4128386	1650.810077	0.000451244	1	N	412	427
P26040	Conv	FLQVK	DGILSDEIYCPPETAVLLGSYAVQAK	FGDYN	2	C10:+57.021	1405.202149	2808.388697	0.000451244	16	N	107	133
P26040	Conv	KFRAK	FYPEDVAEELIQDITQK	LFFLQ	2		1019.504925	2036.99425	0.000451244	15	N	83	100
P26040	Conv	ERVQR	QLLTLSNELSQAR	DENKR	2		736.9075264	1471.799453	0.000451244	11	N	529	542
P26040	Conv	TIGLR	EVWYFGLQYVDNK	GFPTW	2		830.9044524	1659.793305	0.000451244	7	N	40	53
P26040	Conv	QFKFR	AKFYPEDVAEELIQDITQK	LFFLQ	2		1119.070963	2236.126327	0.000451244	7	N	81	100
P26041	Conv	KEVHK	SGYLAGDKLLPQR	VLEQH	2		709.3940549	1416.77251	0.000662267	1	N	143	156
P26041	Conv	TIGLR	EVWFFGLQYQDTK	AFSTW	2		830.9044524	1659.793305	0.000451244	16	N	40	53
P26041	Conv	LFKFR	AKFYPEDVSEELIQDITQR	LFFLQ	2		1141.071495	2280.127389	0.000451244	13	N	81	100
P26041	Conv	IKNKK	GSELWLGVDALGLNIYEQNDRLTPK	IGFPW	2		1401.227578	2800.439556	0.000451244	3	N	212	237
P26041	Conv	IKNKK	GSELWLGVDALGLNIYEQNDR	LTPKI	2		1181.587843	2361.160086	0.000451244	30	N	212	233
P26041	Conv	KFRAK	FYPEDVSEELIQDITQR	LFFLQ	2		1041.505456	2080.995312	0.000451244	21	N	83	100
P26041	Conv	FLQVK	EGILNDDIYCPPETAVLLASYAVQSK	YGDFN	2	C10:+57.021	1433.712881	2865.410161	0.000451244	45	N	107	133
P26041	Conv	QKHLK	ALTSELANAR	DESKK	2		523.2859843	1044.556369	0.001162105	2	N	523	533
P26041	Conv	LAKER	QEAEEAKEALLQASR	DQKKT	2		836.9291872	1671.842774	0.000451244	9	N	393	408
P26041	Conv	SIKNK	KGSELWLGVDALGLNIYEQNDR	LTPKI	2		1245.635325	2489.255049	0.000870037	3	N	211	233
P26041	Conv	RAELK	TAMSTPHVAEPAENEHDEQDENGAE	ASAEL	3	M3:+15.995	908.7041315	2723.088995	0.001654178	1	N	464	489
P26041	Conv	RAELK	TAMSTPHVAEPAENEHDEQDENGAEASAELR	ADAMA	3	M3:+15.995	1117.815473	3350.423019	0.000451244	17	N	464	495
P26041	Conv	LEYLK	IAQDLEMYGVNYFSIK	NKKGS	2		945.9694671	1889.923334	0.000451244	10	N	193	209
P26043	Conv	FLQVK	EAILNDEIYCPPETAVLLASYAVQAK	YGDYN	2	C10:+57.021	1439.731073	2877.446547	0.000451244	11	N	107	133
P26043	Conv	KFRAK	FFPEDVSEELIQEITQR	LFFLQ	2		1040.515824	2079.016048	0.000451244	7	N	83	100
P26043	Conv	ADQMK	NQEQLAAELAEFTAK	IALLE	2		831.9208308	1661.826062	0.000451244	8	N	412	427
P26043	Conv	TVGLR	EVWFFGLQYVDSK	GYSTW	2		809.4015456	1616.787491	0.000451244	7	N	40	53
P26043	Conv	QFKFR	AKFFPEDVSEELIQEITQR	LFFLQ	3		760.3905082	2278.148125	0.000622848	5	N	81	100
P26043	Conv	AVQAK	YGDYNKEIHKPGYLANDR	LLPQR	4		539.0162408	2152.033763	0.001264573	5	N	133	151
P26369	Conv	PGCGK	IFVEFTSVFDCQK	AMQGL	2	C11:+57.021	810.392632	1618.769664	0.000451244	2	N	431	444
P26369	Conv	DSAHK	LFIGGLPNYLNDDQVKELLTSFGPLK	AFNLV	3		964.5238146	2890.548044	0.000451244	12	N	260	286
P26369	Conv	NAQMR	LGGLTQAPGNPVLAVQINQDKNFAFLEFR	SVDET	3		1053.231805	3156.672016	0.000823681	4	N	174	203
P26443	Conv	RVKAK	IIAEGANGPTTPEADKIFLER	NIMVI	2		1121.589855	2241.164109	0.000451244	10	N	399	420
P26443	Conv	FPKAK	VYEGSILEADCDILIPAASEK	QLTKS	2	C11:+57.021	1147.067332	2292.119064	0.000451244	19	N	365	386
P26443	Conv	RFGAK	CVGVGESDGSIWNPDGIDPK	ELEDF	2	C1:+57.021	1051.478684	2100.941768	0.000451244	20	N	326	346
P26443	Conv	ARRHY	SEAAADREDDPNFFK	MVEGF	2		856.3820698	1710.74854	0.000451244	4	N	53	68
P26443	Conv	RKFGK	HGGTIPVVPTAEFQDR	ISGAS	2		862.4422648	1722.86893	0.000451244	2	N	480	496
P26443	Conv	FPIRR	DDGSWEVIEGYR	AQHSQ	2		713.3182098	1424.62082	0.002374549	1	N	124	136
P26443	Conv	GIDPK	ELEDFKLQHGSILGFPK	AKVYE	3		653.3514366	1957.03091	0.000451244	3	N	346	363
P26443	Conv	ELAKK	GFIGPGIDVPAPDMSTGER	EMSWI	2	M14:+15.995	966.4625802	1930.90956	0.000451244	7	N	212	231
P26450	Conv	HRDGK	YGFSDPLTFNSVVELINHYR	NESLA	3		791.0626144	2370.164443	0.000451244	5	N	389	409
P26450	Conv	LTVNK	GSLVALGFSDGQEARPEDIGWLNGYNETTGER	GDFPG	3		1146.878596	3437.612388	0.000622848	1	N	34	66
P26450	Conv	PGSSK	TEADTEQQALPLPDLAEQFAPPDVAPPLLIK	LLEAI	3		1109.917329	3326.728587	0.00091018	2	N	103	134
P26516	Conv	TPTSK	TFEHVTSEIGAEEAEEVGVEHLLR	DIKDT	4		671.0823092	2680.298037	0.001162105	4	N	153	177
P26516	Conv	DVKPK	DLGLPTEAYISVEEVHDDGTPTSK	TFEHV	2		1287.116827	2572.218055	0.000451244	3	N	129	153
P26516	Conv	LAVQK	VVVHPLVLLSVVDHFNR	IGKVG	3		648.3795495	1942.115248	0.000451244	2	N	8	25
P26516	Conv	VASGK	LPINHQIIYQLQDVFNLLPDASLQEFVK	AFYLK	3		1099.262883	3294.765248	0.000823681	6	N	219	247
P26516	Conv	GNQKR	VVGVLLGSWQK	KVLDV	2		593.35367	1184.69174	0.001463592	3	N	34	45
P26516	Conv	ELMKR	YCPNSVLVIIDVKPK	DLGLP	3	C2:+57.021	582.3274206	1743.958862	0.000451244	2	N	114	129
P26638	Conv	KMKKK	EAVGDDESVPENVLNFDDLTADALAALK	VSQIK	3		977.8088966	2930.40329	0.000870037	3	N	71	99
P27005	Conv	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	2		1392.696779	2783.377959	0.000451244	15	N	7	31
P27005	Conv	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	3		886.1021319	2655.282996	0.002296037	1	N	7	30
P27005	Conv	KNDFK	KMVTTECPQFVQNINIENLFR	ELDIN	3	C7:+57.021	861.1019331	2580.282399	0.000451244	12	N	35	56
P27005	Conv	KMVTT	ECPQFVQNINIENLFR	ELDIN	2	C2:+57.021	1010.99939	2019.983179	0.000698008	6	N	40	56
P27005	Conv	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	2	C6:+57.021	1227.101518	2452.187436	0.000451244	46	N	36	56
P27005	Conv	DFKKM	VTTECPQFVQNINIENLFR	ELDIN	2	C5:+57.021	1161.581275	2321.14695	0.000451244	11	N	37	56
P27005	Conv	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2		1213.101938	2424.188276	0.000451244	93	N	56	77

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27005	Conv	SELEK	ALSNLIDVYHNY	SNIQG	2		711.357138	1420.698676	0.002519933	2	N	7	19
P27005	Conv	SELEK	ALSNLIDVYHNYSNIQGN	HHALY	2		1017.998133	2033.980665	0.001329271	4	N	7	25
P27005	Conv	LEKAL	SNLIDVYHNYSNIQGNHHALYK	NDFKK	3		867.4267269	2599.256781	0.00091018	4	N	9	31
P27005	Conv	-M	PSELEKALSNLIDVYHNYSNIQGNHHALYK	NDFKK	4		867.6895412	3466.726965	0.000451244	3	N	1	31
P27005	Conv	SELEK	ALSNLIDVYHNYSNIQ	GNHHA	2		932.4659369	1862.916274	0.000451244	1	N	7	23
P27612	Conv	NIEGK	AQCLSVISTILEVVQDLEATFR	LLVAL	3	C3:+57.021	831.44072	2491.29876	0.000735798	1	N	721	743
P27612	Conv	VLLEK	ILSLICNNSSEKPTAQQLQILWK	AINWP	3	C6:+57.021	895.4865522	2683.436257	0.000870037	2	N	578	601
P27612	Conv	EATFR	LLVALGTLISDDSNAIQLAK	SLGVD	2		1028.088959	2054.162318	0.000451244	8	N	743	763
P27612	Conv	QILWK	AINWPEDIVFPALDILR	LSIKH	2		991.5414476	1981.067295	0.001162105	3	N	601	618
P27661	Conv	NKLLG	GVTIAQGGVLPNIQAVLLPK	KSSAT	2		994.5992969	1987.182994	0.000451244	68	N	99	119
P27661	Conv	EELNK	LLGGVTIAQGGVLPNIQAV	LLPKK	2		910.5361652	1819.05673	0.000451244	42	N	96	115
P27661	Conv	EELNK	LLGGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1136.194093	2270.372586	0.000451244	43	N	96	119
P27661	Conv	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAV	LLPKK	2		1331.724671	2661.433742	0.000451244	105	N	89	115
P27661	Conv	HYAER	VGAGAPVYLAAVLEY	LTAEI	2		746.9064638	1491.797328	0.000451244	34	N	43	58
P27661	Conv	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		1038.590999	3112.749598	0.000451244	59	N	89	119
P27661	Conv	GAPVY	LAAVLEYLTAEILELAGNAAR	DNKKT	2		1101.112965	2200.210331	0.000451244	51	N	51	72
P27661	Conv	AGAPV	YLAAVLEYLTAEILELAGNAAR	DNKKT	2		1182.64463	2363.27366	0.000451244	11	N	50	72
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAARDNK	KTRII	3		1091.589547	3271.745241	0.000451244	11	N	43	75
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1458.298003	2914.580407	0.000451244	256	N	43	72
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILELAGN	AARDN	2		1309.210334	2616.405068	0.000451244	16	N	43	69
P27661	Conv	LNKLL	GGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1023.110029	2044.204458	0.000622848	8	N	98	119
P27661	Conv	HYAER	VGAGAPVYLAAVLEYL	TAEIL	2		803.4484958	1604.881392	0.000451244	10	N	43	59
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLT	AEILE	2		853.9723351	1705.92907	0.000451244	14	N	43	60
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEIL	ELAGN	2		1067.096253	2132.176905	0.00091018	5	N	43	64
P27661	Conv	EELNK	LLGGVTIAQGGVLPNIQ	AVLLP	2		825.4834013	1648.951203	0.000451244	5	N	96	113
P27661	Conv	QLAIR	NDEELNKLLGGVTIAQGGVLPN	IQAVL	2		1126.100586	2250.185573	0.000451244	10	N	89	111
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTA	EILEL	2		889.490892	1776.966184	0.000451244	7	N	43	61
P27661	Conv	ERVGA	GAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1344.734508	2687.453415	0.000823681	2	N	46	72
P27661	Conv	AERVG	AGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1380.253064	2758.490529	0.000451244	5	N	45	72
P27661	Conv	VGAGA	PVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1280.705219	2559.394838	0.000451244	22	N	48	72
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILEL	AGNAA	2		1188.159581	2374.303563	0.000451244	9	N	43	66
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAA	RDNKK	2		1380.247448	2758.479296	0.000451244	12	N	43	71
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILELA	GNAAR	2		1223.678138	2445.340677	0.001162105	10	N	43	67
P27661	Conv	YAERV	GAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		939.5117976	2815.511993	0.000451244	7	N	44	72
P27661	Conv	EELNK	LLGGVTIAQGGVLPN	IQAVL	2		704.9120805	1407.808561	0.00091018	3	N	96	111
P27661	Conv	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQ	AVLLP	2		1246.671907	2491.328214	0.000451244	17	N	89	113
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAE	ILELA	3		636.3440591	1906.008777	0.002019181	1	N	43	62
P27661	Conv	RVGAG	APVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		877.8184505	2630.431951	0.000662267	2	N	47	72
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNA	ARDNK	2		1344.728891	2687.442182	0.002374549	1	N	43	70
P27661	Conv	GHYAE	RVGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		1024.568306	3070.681518	0.001871652	1	N	42	72
P27661	Conv	QLAIR	NDEELNKLLGGV	TIAQG	2		650.8413208	1299.667042	0.000622848	1	N	89	101
P27661	Conv	HYAER	VGAGAPVYLAAV	LEYLT	2		544.3114708	1086.607342	0.002453667	1	N	43	55
P27661	Conv	EELNK	LLGGVTIAQGGVLPNIQA	VLLPK	2		861.0019582	1719.988316	0.00091018	4	N	96	114
P27661	Conv	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQA	VLLPK	2		1282.190464	2562.365328	0.000451244	15	N	89	114
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILE	LAGNA	3		754.7476329	2261.219499	0.001591523	1	N	43	65
P27661	Conv	QLAIR	NDEELNKLLGGVTIAQ	GGVLP	2		857.4550378	1712.894476	0.0007646	2	N	89	105
P27661	Conv	HYAER	VGAGAPVYLAAVLEYLTAEILELAG	NAARD	3		835.1285135	2502.36214	0.000451244	1	N	43	68
P27773	Conv	YPTLK	IFRDGEEAGAYDGPR	TADGI	2		826.8873223	1651.759045	0.000451244	11	N	104	119
P27773	Conv	NTCNK	YGVSGYPTLK	IFRDG	2		542.7878285	1083.560057	0.000451244	12	N	94	104
P27773	Conv	IVIAK	MDATANDVPSPYEVK	GFPTI	2		818.8803176	1635.745035	0.000451244	9	N	433	448
P27773	Conv	RLAAA	SDVLELTDENFESR	VSDTG	2		827.3842782	1652.752956	0.000451244	14	N	24	38
P27773	Conv	EEFKK	FISDKDASVVGFFR	DLFSD	2		794.4124446	1586.809289	0.000451244	10	N	147	161
P27773	Conv	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1360.201029	2718.386458	0.000451244	13	N	304	329
P27773	Conv	GKIKK	FIQDSIFGLCPHMTEDNKDLIQGK	DLLTA	3	C10:+57.021	936.123174	2805.346122	0.000451244	2	N	234	258
P27773	Conv	LIQGK	DLLTAYYDVDYEK	NAKGS	2		804.3779331	1606.740266	0.000451244	25	N	258	271
P27773	Conv	VASRK	TFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1296.153547	2590.291495	0.000451244	22	N	305	329
P27773	Conv	YEGGR	ELNDFISYLQR	EATNP	2		699.357138	1396.698676	0.000451244	14	N	471	482
P27773	Conv	SRDGK	ALEQFLQEYFDGNLKR	YLKSE	2		986.0026866	1969.989773	0.000451244	17	N	347	363
P27773	Conv	SRDGK	ALEQFLQEYFDGNLK	RYLKS	2		907.952131	1813.888662	0.000451244	12	N	347	362
P27773	Conv	PYEVK	GFPTIYFSPANK	KLTPK	2		671.346042	1340.676484	0.002453667	1	N	448	460
P27773	Conv	SYLQR	EATNPPIIQEEKPK	KKKKA	2		797.4282917	1592.840983	0.000622848	3	N	482	496
P27773	Conv	RDNYR	FAHTNIESLVK	EYDDN	2		629.8436665	1257.671733	0.000662267	1	N	183	194
P27773	Conv	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	2		1151.577278	2301.138957	0.000823681	2	N	194	214
P27773	Conv	ESLVK	EYDDNGEGITIFRPLHLANKFEDK	TVAYT	3		941.1317568	2820.37187	0.000451244	16	N	194	218
P27773	Conv	ELGEK	LSKDPNIVIAK	MDATA	3		399.9120898	1196.712869	0.000622848	1	N	422	433

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27773	Conv	GHCKR	LAPEYEAAATR	LKGIV	2		596.3043741	1190.593148	0.002453667	1	N	62	73
P27773	Conv	FISDK	DASVVGFFR	DLFSD	2		499.2592382	996.5028764	0.001871652	2	N	152	161
P27773	Conv	GNLKR	YLKSEPIPESNEGPVK	VVVAE	2		893.9652384	1785.914877	0.001162105	3	N	363	379
P27870	Conv	FGLKR	SELFEAFDLFDVQDFGK	VIYTL	2		1003.97326	2005.930921	0.000451244	3	N	90	107
P27870	Conv	QDFGK	VIYTLSALSWTPIAQNK	GIMPF	2		953.028173	1904.040746	0.0025889	1	N	107	124
P27870	Conv	AQALR	DGVLLCQLLNNLLPQAINLR	EVNLR	3	C6:+57.021	759.7634687	2276.267006	0.001329271	4	N	38	58
P27870	Conv	NETLR	QITNFQLSIENLDQSLANYGRPK	IDGEL	3		883.7930754	2648.355826	0.000823681	1	N	381	404
P27931	Conv	NIELR	VKGTTTEPIPVIISPLETIPASLGSR	LIVPC	3		892.8447767	2675.51093	0.00307782	1	N	239	265
P27931	Conv	ELRVK	GTTTEPIPVIISPLETIPASLGSR	LIVPC	2		1225.181576	2448.347553	0.000451244	2	N	241	265
P27931	Conv	RMWVK	GNILWILPAVQQDSGTYICTFR	NASHC	2	C19:+57.021	1276.652232	2551.288864	0.000451244	5	N	101	123
P28063	Conv	AVDSR	ATAGSYISSLR	MNKVI	2		563.2990917	1124.582583	0.000637154	5	N	91	102
P28063	Conv	CGWDK	KGPGLYYVDDNGTR	LSGQM	2		777.8815086	1553.747417	0.000451244	2	N	178	192
P28063	Conv	DGWVK	VESSDVSDLLYK	YGEAA	2		677.8409865	1353.666373	0.000451244	7	N	258	270
P28063	Conv	MYHMK	EDGWVKVESSDVSDLLYK	YGEAA	2		1035.007832	2068.000063	0.0007646	3	N	252	270
P28076	Conv	LAMNR	DGSSGGVIYLVTITAAGVDHR	VILGD	3		696.6960431	2087.064729	0.000451244	3	N	185	206
P28076	Conv	NISYK	YREDLLAHLIVAGWDQR	EGGQV	3		685.6977183	2054.069755	0.000451244	12	N	109	126
P28293	Conv	MCANR	FQFYNSQTQICVGNPR	ERKSA	2	C11:+57.021	979.9628071	1957.910014	0.000451244	21	N	175	191
P28293	Conv	PRERK	SAFRGDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C13:+57.021	1208.921876	3623.742229	0.000637154	2	N	194	230
P28293	Conv	PYMAF	LLIQSPEGLSACGGFLVR	EDFVL	2	C12:+57.021	959.0170511	1916.018502	0.000451244	5	N	37	55
P28293	Conv	QASKK	LQPGDLCTVAGWGR	VSQSR	2	C7:+57.021	765.3803902	1528.74518	0.000451244	7	N	135	149
P28293	Conv	PQASK	KLQPGDLCTVAGWGR	VSQSR	2	C8:+57.021	829.4278718	1656.840144	0.000451244	3	N	134	149
P28293	Conv	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C9:+57.021	1055.175654	3162.503561	0.000451244	3	N	198	230
P28352	Conv	WIKKK	GLDWVKEEAPDILCLQETK	CSENK	3	C14:+57.021	748.7124396	2243.113919	0.000451244	11	N	78	97
P28352	Conv	DLASR	KPLVLCGDLNVAHEEIDLR	NPKGN	3	C6:+57.021	731.0565407	2190.146222	0.000451244	2	N	201	220
P28352	Conv	TPQER	QGFGELLQAVPLADSFR	HLYPN	2		924.4866723	1846.957745	0.000451244	18	N	236	253
P28352	Conv	NVGWR	LDYFLLSHSLLPALCDSK	IRSKA	2	C15:+57.021	1046.543099	2091.070597	0.001329271	1	N	280	298
P28352	Conv	KKTEK	EAAGEGPVLYEDPPDQK	TSPSG	2		907.9263102	1813.83702	0.000451244	12	N	34	51
P28474	Conv	APLDK	VCLLGCGISTGYGAAVNTAK	VEPGS	2	C2:+57.021,C6:+57.021	1006.500677	2010.985753	0.000451244	7	N	168	188
P28474	Conv	VTKLK	AGDTVIPLYIPQCGECK	FCLNP	2	C13:+57.021,C16:+57.021	960.9633956	1919.911191	0.000622848	2	N	84	101
P28650	Conv	RTGLR	ICDLLSDFDEFSAR	FKNLA	2	C2:+57.021	844.3855352	1686.75547	0.000451244	17	N	181	195
P28650	Conv	AYTTR	VGIGAFPTEQINEIGDLLQNR	GHEWG	2		1142.600754	2283.185907	0.000451244	9	N	304	325
P28650	Conv	IINTK	AVSFIGNGVVIHLPGLFEEAEKNEK	KGLKD	3		899.813588	2696.417364	0.000451244	8	N	93	118
P28650	Conv	EGKGK	VVDLLATDADIVSR	CQGGN	2		743.9097348	1485.80387	0.000451244	17	N	48	62
P28650	Conv	VVDGK	EYDFHLLPSGIINTK	AVSFI	2		873.9572164	1745.898833	0.000622848	2	N	78	93
P28650	Conv	IISDR	AHLVFDFHQAVDGLQEVQR	QAQEG	2		1105.061599	2208.107597	0.000451244	2	N	133	152
P28650	Conv	EILQK	VEVEYETLPGWK	ADTTG	2		725.3671714	1448.718743	0.000451244	5	N	398	410
P28656	Conv	ALQER	LDGLVDTPTGYIESLPK	VVKRR	2		909.4807213	1816.945843	0.000451244	13	N	55	72
P28656	Conv	LFDKR	FEIINAIYEPTEEECEWKPDEEDEVSEELKEK	AKIED	4	C15:+57.021	989.9507105	3955.771642	0.000451244	6	N	117	149
P28656	Conv	KEDPK	GIPEFWLTVFK	NVDLL	2		668.8691529	1335.722706	0.000451244	5	N	165	176
P28665	Conv	QSGRK	NLFDELVLDKDLFQCVSFIIPR	LSSSD	3	C15:+57.021	894.4721316	2680.392995	0.000451244	9	N	71	93
P28665	Conv	VPSSR	LSEDQEDCILYSSWLAEK	HTNLV	2	C8:+57.021	1093.501825	2184.98805	0.000451244	11	N	626	644
P28665	Conv	AVLVK	NKESVVFVQTDKPVYKPGQSVK	FRVVS	3		826.4519905	2476.332572	0.000451244	5	N	123	145
P28665	Conv	ASQTR	LQVTASPQSLCGLR	AVDQS	2	C11:+57.021	765.4091477	1528.802695	0.000823681	1	N	576	590
P28665	Conv	MWLTK	QQNSNGGFSSTQDTVVALDALSK	YGAVT	2		1184.075297	2366.134994	0.000451244	7	N	1242	1265
P28665	Conv	MHLEK	QLSAFAIWVQTVPLTCNNPK	GHNSF	2	C16:+57.021	1144.099104	2286.182608	0.000451244	6	N	1338	1358
P28665	Conv	QNGER	EGNTWLTAFVLK	SFAQA	2		689.8724239	1377.729248	0.000451244	9	N	1037	1049
P28665	Conv	DTVVK	VLIVEPEGIKQEHTFSSLFCASDAEISEK	MSLVL	3	C20:+57.021	1088.543232	3262.606295	0.000622848	2	N	903	932
P28665	Conv	SRSQK	TTLVTIQSTGSFSQK	FQVEN	2		799.425749	1596.835898	0.000451244	11	N	1276	1291
P28665	Conv	LCGLR	AVDQSVLLLKPESELSPSWIYNLPGMQQNK	FVPSS	3		1128.922309	3383.743527	0.000698008	3	N	590	620
P28665	Conv	FIIPR	LSSSDEEDFLYVDIKGPTHEFSK	RKAVL	4		661.5674976	2642.23879	0.000451244	5	N	93	116
P28665	Conv	FAQAR	AFIFIDESHITHAFTWLSQK	QKDNG	3		797.7431047	2390.205914	0.000622848	5	N	1055	1075
P28665	Conv	LVKNK	ESVVFVQTDKPVYKPGQSVK	FRVVS	3		745.7393603	2234.194681	0.001229886	1	N	125	145
P28665	Conv	VSMDK	MLRPLNELLPLAYIEDPKK	NRIMQ	4	M1:+15.995	568.0716148	2268.255259	0.002663018	1	N	153	172
P28798	Conv	CPFAK	AVCCEDHIHCCPAGFQCHTEK	GTCEM	3	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021	872.6814401	2615.02092	0.000451244	4	N	309	330
P28798	Conv	LQIGD	IGCDQHTSCPVGQTCCPSLK	GSWAC	3	C3:+57.021,C9:+57.021,C15:+57.021,C16:+57.021	768.9990292	2303.973688	0.000451244	12	N	439	459
P28798	Conv	CPDAK	TQCPDDSTCCELPTGK	YGCCP	2	C3:+57.021,C9:+57.021,C10:+57.021	934.8764285	1867.737257	0.000451244	12	N	211	227
P28798	Conv	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	C1:+57.021,M3:+15.995,C7:+57.021,C13:+57.021,C14:+57.021	970.3406533	1938.665707	0.000451244	18	N	281	296
P28798	Conv	PLQIG	DIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C4:+57.021,C10:+57.021,C16:+57.021,C17:+57.021	807.3413436	2419.000631	0.001463592	2	N	438	459
P28798	Conv	CPSLK	GSWACCQLPHAVCCEDR	QHCCP	2	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021	1053.423657	2104.831715	0.000451244	5	N	459	476

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P28798	Conv	YTCCR	LNTGAWGCCPFAK	AVCCE	2	C8:+57.021,C9:+57.021	741.3369054	1480.658211	0.000451244	3	N	296	309
P28798	Conv	LPTGK	YGCCPMPNAICCSDHLHCCPQDTVCDLIQSK	CLSKN	4	C3:+57.021,C4:+57.021,M6:+15.995,C11:+57.021,C12:+57.021,C18:+57.021,C19:+57.021,C25:+57.021	953.8847121	3811.507648	0.002727428	1	N	227	258
P28798	Conv	NTCCK	LNSGDWGCCPIPEAVCCSDNQHCCPQGFTCLAQGYCQK	GDTMV	4	C8:+57.021,C9:+57.021,C16:+57.021,C17:+57.021,C23:+57.021,C24:+57.021,C30:+57.021,C36:+57.021	1134.453884	4533.784337	0.000451244	14	N	378	416
P28798	Conv	KIPAR	QTTPLQIGDIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C12:+57.021,C18:+57.021,C24:+57.021,C25:+57.021	1086.8263	3257.455499	0.000622848	3	N	430	459
P28867	Conv	APFLR	ISFNSYELGSLQVEDEASQPFCAVK	MKEAL	2	C22:+57.021	1409.66593	2817.316261	0.000451244	1	N	6	31
P28867	Conv	FELYR	ATFYAAEIICGLQFLHSK	GIIYR	3	C10:+57.021	690.356039	2068.044717	0.000451244	8	N	447	465
P28867	Conv	IHYIK	NHEFIATFFGQPTFCSVCK	EFVWG	3	C15:+57.021,C18:+57.021	764.0190553	2289.033766	0.002080925	3	N	157	176
P28867	Conv	HPFFK	TINWSLLEK	RKVEP	2		552.3089281	1102.602256	0.000823681	4	N	602	611
P29341	Conv	MITRR	SLGYAYVNFQQPADAER	ALDTM	2		964.9610187	1927.906437	0.000451244	18	N	50	67
P29341	Conv	SGKSK	GFGFVSFER	HEDAQ	2		523.2592382	1044.502876	0.002145581	1	N	231	240
P29341	Conv	SIDNK	ALYDTFSAFGNILSCK	VVCDE	2	C15:+57.021	903.9404777	1805.865355	0.000451244	12	N	113	129
P29341	Conv	ENGSK	GYGFVHFETQEAAER	AIEKM	2		870.9029724	1739.790345	0.000451244	5	N	138	153
P29341	Conv	MLYEK	FSPAGPILSIR	VCRDM	2		579.3380199	1156.66044	0.000451244	8	N	30	41
P29341	Conv	GGRSK	GFGFVCFSSPEEATK	AVTEM	2	C6:+57.021	831.877346	1661.739092	0.000451244	15	N	333	348
P29351	Conv	RWFHR	DLSGPDAETLLK	GRGVP	2		629.8304217	1257.645243	0.000622848	5	N	7	19
P29351	Conv	EYKLR	TLQISPLDNGDLVR	EIWHY	2		770.9206338	1539.825668	0.000451244	5	N	393	407
P29351	Conv	EDTAK	AGFWEEFESLQKQEVK	NLHQR	3		652.3235465	1953.94724	0.000698008	1	N	241	257
P29351	Conv	CEGGR	YTVGGSETFDSLTDLVEHFKK	TGIEE	3		791.725668	2372.153604	0.000451244	8	N	175	196
P29351	Conv	EDTAK	AGFWEEFESLQK	QEVKN	2		735.8491458	1469.682692	0.000451244	15	N	241	253
P29351	Conv	TFLVR	ESLSQPGDFVLSVLNDQPK	AGPGS	2		1037.029098	2072.042597	0.000451244	15	N	136	155
P29351	Conv	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSFLDQINQR	QESLP	3		1256.613414	3766.816843	0.000451244	9	N	407	439
P29351	Conv	VGTQR	VYGLYSVTNSR	EHDTA	2		629.8254737	1257.635347	0.000451244	5	N	372	383
P29351	Conv	IIHLK	YPLNCSDPTSER	WYHGH	2	C5:+57.021	719.8172884	1437.618977	0.00091018	5	N	97	109
P29351	Conv	CEGGR	YTVGGSETFDSLTDLVEHFK	KTGIE	3		749.0273469	2244.058641	0.000451244	18	N	175	195
P29351	Conv	YGGEK	FATLTELVEYYTQQQGILQDR	DGTII	2		1258.637533	2515.259466	0.000451244	13	N	68	89
P29351	Conv	SISTK	GLDCDIDIQK	TIQMV	2	C4:+57.021	588.7821859	1175.548772	0.000735798	2	N	476	486
P29351	Conv	VTHIR	IQNSGDFYDLYGGEK	FATLT	2		853.3893635	1704.763127	0.000451244	14	N	53	68
P29351	Conv	PTSER	WYHGHISGGQAESLLQAK	GEPWT	2		991.4981027	1980.980605	0.000451244	2	N	109	127
P29351	Conv	YGGEK	FATLTELVEYYTQQQGILQDRDGTIIHLK	YPLNC	3		1131.92834	3392.761619	0.000451244	1	N	68	97
P29351	Conv	IQSQK	GQESEYGNITYPPAVR	SAHAK	2		890.9291872	1779.842774	0.002080925	1	N	530	546
P29351	Conv	ILQGR	DSNIPGSDYINANYVK	NQLLG	2		885.421195	1768.82679	0.000451244	5	N	292	308
P29391	Conv	TSQIR	QNYSTEVEAAVNR	LVNLH	2		740.8554908	1479.695382	0.000451244	20	N	6	19
P29391	Conv	LAMEK	NLNQALLDLHALGSAR	TDPHL	2		853.4713566	1704.927113	0.000451244	15	N	105	121
P29391	Conv	TNLRR	VAGPQPAQTGAPQGSLGEYLFER	LTLKH	2		1187.095835	2372.176071	0.000451244	15	N	154	177
P29391	Conv	DRGGR	ALFQDVQKPSQDEWGK	TQEAM	2		938.4659369	1874.916274	0.000451244	9	N	76	92
P29391	Conv	TYLSL	GFFFDRDDVALEGVGHFFR	ELAEE	3		744.3609947	2230.059584	0.000823681	3	N	34	53
P29391	Conv	NLHLR	ASYTYLSLGFFFDRDDVALEGVGHFFR	ELAEE	3		1043.842206	3128.503219	0.002663018	1	N	26	53
P29391	Conv	TNLRR	VAGPQPAQTGAPQGSLGEYL	FERLT	2		970.9897762	1939.963952	0.002374549	2	N	154	174
P29416	Conv	WGALR	GLETFSQLVWK	SAEGT	2		654.353867	1306.692134	0.000451244	11	N	137	148
P29416	Conv	KDMYK	VEPLAFHGTPEQK	ALVIG	2		726.8782376	1451.740875	0.001654178	1	N	435	448
P29416	Conv	CELVR	RGIQAQPISVGYCEQEFEQT	-	2	C13:+57.021	1170.550172	2339.084744	0.001591523	1	N	508	528
P29416	Conv	ELVRR	GIQAQPISVGYCEQEFEQT	-	2	C12:+57.021	1092.499616	2182.983633	0.000622848	11	N	509	528
P29416	Conv	FTDFK	QLESFYIQTLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		1252.289603	3753.845408	0.000622848	1	N	348	379
P29416	Conv	RAGFR	ALLSAPWYLNR	VKYGP	2		652.3620264	1302.708453	0.00307782	1	N	412	423
P29416	Conv	TYHRR	YTLYPNNFQFR	YHVSS	2		731.8598479	1461.704096	0.002884417	1	N	36	47
P29416	Conv	FRRYR	NLLFGSGSWPRPS	FSNKQ	2		709.3652974	1416.714995	0.0025889	1	N	69	82
P29416	Conv	PELTR	KGSFNPVTHIYTAQDVK	EVIEY	3		635.6675361	1903.979208	0.000451244	2	N	223	240
P29416	Conv	NFQFR	YHVSSAAQAGCVVLDEAFRR	YRNLL	3	C11:+57.021	746.0361396	2235.085019	0.001591523	1	N	47	67
P29416	Conv	SFYIQ	TLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		916.1257202	2745.353761	0.000622848	3	N	356	379
P29621	Conv	KLALK	NPDTNIVFSPLSISAALAIVSLGAK	GNTLE	2		1249.697394	2497.379187	0.000451244	8	N	65	90
P29621	Conv	SLYKK	LALKNPDTNIVFSPLSISAALAIVSLGAK	GNTLE	3		975.2342642	2922.679393	0.000451244	4	N	61	90
P29699	Conv	VEISR	AQNVPLPVSTLVEFVIAATDCTAK	EVTDP	2	C21:+57.021	1272.67283	2543.33006	0.000451244	18	N	187	211
P29699	Conv	GLGFR	ELACDDPEAEQVALLAVDYLNNHLLQGFK	QVLNQ	3	C4:+57.021	1095.875093	3284.601878	0.000451244	20	N	28	57
P29699	Conv	NCSVR	QLTEHAVEGDCDFHILK	QDGQF	3	C11:+57.021	671.3232865	2010.946459	0.00091018	1	N	103	120
P29699	Conv	YHDLR	HAFSPVASVESASGETLHSPK	VGQPG	3		713.3557979	2137.043994	0.000451244	4	N	301	322
P29758	Conv	PLGCR	IAIAALEVLEEENLAENADK	MGAIL	2		1078.060596	2154.105591	0.000451244	2	N	331	351
P29758	Conv	TLTSR	AFYNNVLGEYEEYITK	LFNYN	2		976.9679781	1951.920356	0.000735798	5	N	113	129
P29758	Conv	KVCLR	LRDNGLLAKPTHGDIIR	LAPPL	4		473.0238689	1888.064275	0.001463592	2	N	396	413
P30416	Conv	VATMK	VGEVCHITCKPEYAYGAAGSPPK	IPPNA	3	C5:+57.021,C9:+57.021	831.0632123	2490.166237	0.000622848	1	N	98	121
P30681	Conv	RPKIK	IEHPGLSIGDTAK	KLGEM	2		669.357138	1336.698676	0.00091018	2	N	114	127

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P30681	Conv	ENRPK	IKIEHPGLSIGDTAK	KLGEM	2		789.9466516	1577.877703	0.000451244	33	N	112	127
P30681	Conv	TGSKK	KNEPEDEEEEEEEEEEDDEEEEEDEE	-	3		1133.728084	3398.160851	0.001763695	8	N	183	210
P30681	Conv	PNAPK	RPPSAFFLFCSENRPK	IKIEH	3	C10:+57.021	651.6652069	1951.972221	0.000451244	1	N	96	112
P30681	Conv	EEHKK	KHPDSSVNFAEFSK	KCSER	2		796.8893337	1591.763067	0.000451244	6	N	29	43
P30681	Conv	EHKKK	HPDSSVNFAEFSK	KCSER	2		732.8418521	1463.668104	0.00091018	1	N	30	43
P31725	Conv	SQMER	SITTIIDTFHQYSRK	EGHPD	2		905.4788473	1808.942095	0.000451244	7	N	11	26
P31725	Conv	SQMER	SITTIIDTFHQYSR	KEGHP	2		841.4313657	1680.847131	0.000451244	59	N	11	25
P31725	Conv	MERSI	TTIIDTFHQYSR	KEGHP	2		741.3733194	1480.731039	0.000451244	11	N	13	25
P31725	Conv	ERSIT	TIIDTFHQYSR	KEGHP	2		690.8494801	1379.68336	0.000451244	14	N	14	25
P31725	Conv	SQMER	SITTIIDTFHQY	SRKEG	2		719.8647959	1437.713992	0.000451244	10	N	11	23
P31725	Conv	MLMAK	LIFACHEKLHENNPR	GHGHS	2	C5:+57.021	939.4758847	1876.936169	0.000451244	2	N	86	101
P31725	Conv	MAKLI	FACHEKLHENNPR	GHGHS	3	C3:+57.021	551.2638137	1650.768041	0.002212458	1	N	88	101
P31750	Conv	GATMK	TFCGTPEYLAPEVLEDNDYGR	AVDWW	2	C3:+57.021	1223.547295	2445.07899	0.000451244	7	N	307	328
P31938	Conv	EPPPK	LPSGVFSLEFQDFVNK	CLIKN	2		913.9703238	1825.925048	0.001463592	2	N	324	340
P32067	Conv	HKTFK	GSIFAVFDSIQSAK	KFVEI	2		735.3858955	1468.756191	0.000451244	5	N	151	165
P32921	Conv	GELKK	TLIDVLQPLIAEHQAR	RKAVT	3		606.3480264	1816.020679	0.000451244	7	N	436	452
P32921	Conv	DCIGK	ISFPAVQAAPSFSNSFPK	IFRDR	2		947.9890478	1893.962496	0.001463592	3	N	281	299
P34022	Conv	AGSDR	AWVWNTHADFADECPKPELLAIR	FLNAE	3	C14:+57.021	913.7834801	2738.32704	0.000451244	1	N	118	141
P34022	Conv	DTSTE	NADESNHDPQFEPIVSLPEQEIK	TLEED	3		879.4211958	2635.240187	0.000622848	3	N	16	39
P34022	Conv	EQEIK	TLEEDEEELFK	MRAKL	2		691.3226265	1380.629653	0.002453667	1	N	39	50
P34884	Conv	TNVPR	ASVPEGFLSELTQQLAQATGK	PAQYI	2		1088.068755	2174.12191	0.000451244	8	N	12	33
P35174-2	Conv	AIEYK	VQVVQGLNYFIK	MNVGR	2		704.4038913	1406.792183	0.000451244	13	N	50	62
P35174-2	Conv	-MTEY	TIEIIGGLSEARPATSEIQEIADK	VRPLL	2		1271.17448	2540.33336	0.000451244	4	N	4	28
P35174-2	Conv	MNVGR	GCYLHINVLSGISSENDLELTGYQTNK	AKNDE	3	C2:+57.021	1009.1576	3024.4494	0.001839721	1	N	67	94
P35174-2	Conv	MTEYT	IEIIGGLSEARPATSEIQEIADK	VRPLL	3		814.103027	2439.285681	0.001162105	2	N	5	28
P35343	Conv	RNPVK	VNLSTLVCYEDVGNNTSR	LRVVL	2	C8:+57.021	1020.986676	2039.957752	0.001162105	1	N	187	205
P35343	Conv	EFLAK	EGRPSFVSSSSANTSTTL	-	2		914.4401161	1826.864632	0.000823681	2	N	341	359
P35441	Conv	GVQYK	NNEEWTVDSCTECHCQNSVTICKK	VSCPI	3	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	1000.417641	2998.229522	0.000451244	63	N	326	350
P35441	Conv	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	2	C1:+57.021,C10:+57.021,C13:+57.021	974.9265901	1947.83758	0.000451244	22	N	607	623
P35441	Conv	LQNVR	FVFGTTPEDILR	NKGCS	2		697.8698813	1393.724163	0.000451244	31	N	216	228
P35441	Conv	VSNGK	AGTLDLSLSLPGKQQVVSVEEALLATGQWK	SITLF	3		1046.906876	3137.697228	0.000451244	7	N	124	154
P35441	Conv	VARLR	VAKGDVNDNFQGVLQNVR	FVFGT	2		987.0141169	1972.012634	0.000451244	15	N	198	216
P35441	Conv	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDF	SGTFF	2	C8:+57.021	1336.613166	2671.210733	0.000622848	8	N	984	1008
P35441	Conv	QRRSR	LCNNPTPQFGGKDCVGDVTENQVCNK	QDCPI	2	C2:+57.021,C14:+57.021,C24:+57.021	1476.157492	2950.299384	0.000451244	19	N	517	543
P35441	Conv	SPAFR	IENANLIPAVPDDKFQDLLDAVWADK	GFIFL	2		1455.748343	2909.481087	0.000451244	11	N	60	86
P35441	Conv	GIQCK	DVDECKEVPDACFNHNGEHR	CKNTD	2	C5:+57.021,C12:+57.021	1214.505739	2426.995877	0.000451244	5	N	587	607
P35441	Conv	DGSWK	CGACPPGYSGNGIQCK	DVDEC	2	C1:+57.021,C4:+57.021,C15:+57.021	863.3605516	1724.705503	0.000451244	11	N	571	587
P35441	Conv	QFGGK	DCVGDVTENQVCNK	QDCPI	2	C2:+57.021,C12:+57.021	819.3483955	1636.681191	0.000451244	14	N	529	543
P35441	Conv	QRRSR	LCNNPTPQFGGK	DCVGD	2	C2:+57.021	666.8221768	1331.628754	0.000451244	5	N	517	529
P35441	Conv	GEHLR	NALWHTGNTPGQVR	TLWHD	2		775.8952847	1549.774969	0.000451244	21	N	1077	1091
P35441	Conv	PLDPK	GTSQNDPNWVVR	HQGKE	2		686.8343614	1371.653123	0.000451244	17	N	968	980
P35441	Conv	ILNER	DNCQYVYNVDQR	DTDMD	2	C3:+57.021	787.3389193	1572.662239	0.000451244	66	N	810	822
P35441	Conv	EHRCK	NTDPGYNCLPCPPR	FTGSQ	2	C8:+57.021,C11:+57.021	830.8640157	1659.712431	0.000451244	125	N	609	623
P35441	Conv	GVQYK	NNEEWTVDSCTECHCQNSVTICK	KVSCP	2	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	1436.075079	2870.134558	0.000451244	30	N	326	349
P35441	Conv	TGQWK	SITLFVQEDR	AQLYI	2		604.3200242	1206.624448	0.000451244	18	N	154	164
P35441	Conv	LKGLR	TIVTTLQDSIR	KVTEE	2		623.8542312	1245.692862	0.000451244	109	N	288	299
P35441	Conv	VSNGK	AGTLDLSLSLPGK	QQVVS	2		636.3644317	1270.713263	0.000451244	17	N	124	137
P35441	Conv	INTER	DDDYAGFVFGYQSSSR	FYVVM	2		907.3873522	1812.759104	0.000451244	13	N	1018	1034
P35441	Conv	SLPGK	QQVVSVEEALLATGQWK	SITLF	2		943.5050621	1884.994524	0.000451244	37	N	137	154
P35441	Conv	YIGHK	TKDLQAICGLSCDELSSMVLELK	GLRTI	3	C8:+57.021,C12:+57.021	870.7658446	2609.274134	0.000451244	11	N	262	285
P35441	Conv	HMCGS	NRIPESGGDNGVFDIFELIGGAR	RGPGR	2		1217.112017	2432.208434	0.000451244	7	N	18	41
P35441	Conv	CGSNR	IPESGGDNGVFDIFELIGGAR	RGPGR	2		1082.039997	2162.064395	0.000451244	36	N	20	41
P35441	Conv	ITRIR	LCNSPSPQMNGKPCEGEAR	ETKAC	3	C2:+57.021,C14:+57.021	711.3156549	2130.923565	0.000851441	1	N	460	479
P35441	Conv	VSELK	RPPLCFHNGVQYK	NNEEW	3	C5:+57.021	539.2772831	1614.808449	0.000451244	13	N	313	326
P35441	Conv	RRLVK	GQDLSSPAFR	IENAN	2		539.2703343	1076.525069	0.000823681	4	N	50	60
P35441	Conv	NKNAK	CNYLGHYSDPMYR	CECKP	2	C1:+57.021	838.3535157	1674.691431	0.000451244	3	N	662	675
P35441	Conv	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	3	C1:+39.994,C4:+57.021,C24:+57.021	1373.220263	4116.637388	0.000451244	11	N	773	810
P35441	Conv	LAVER	KDNTGQIFSVVSNGK	AGTLD	2		797.4157156	1592.815831	0.000622848	1	N	109	124
P35441	Conv	AVERK	DNTGQIFSVVSNGK	AGTLD	2		733.3682341	1464.720868	0.001162105	2	N	110	124

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P35441	Conv	VVMWK	QVTQSYWDTNPTR	AQGYS	2		798.3765904	1594.737581	0.000451244	59	N	1041	1054
P35441	Conv	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTER	DDDYA	3	C8:+57.021	1275.596835	3823.767106	0.001264573	2	N	984	1018
P35441	Conv	DNCPY	NHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	3	C18:+57.021	1109.147151	3324.418053	0.000451244	27	N	779	810
P35441	Conv	ADTDK	NGEGDACAVDIDGDGILNER	DNCQY	2	C7:+57.021	1045.45848	2088.90136	0.000451244	16	N	790	810
P35441	Conv	DGDGR	GDACKDDFDHDNVPDIDDICPENFDISETDFR	RFQMI	3	C4:+57.021,C20:+57.021	1262.85315	3785.536051	0.000451244	13	N	926	958
P35441	Conv	GDACK	DDFDHDNVPDIDDICPENFDISETDFR	RFQMI	3	C15:+57.021	1085.782927	3254.325382	0.000451244	11	N	931	958
P35441	Conv	KACKK	DACPINGGWGPWSPWDICSVTCGGGVQR	RSRLC	3	C3:+57.021,C18:+57.021,C22:+57.021	1030.45328	3088.336439	0.000622848	6	N	486	514
P35441	Conv	TEENR	ELVSELKRPPLCFHNGVQYK	NNEEW	3	C12:+57.021	805.4268565	2413.25717	0.000451244	10	N	306	326
P35441	Conv	IPDDR	DNCPFHYNPAQYDYDRDDVGDR	CDNCP	3	C3:+57.021	911.3740969	2731.098891	0.000451244	6	N	751	773
P35441	Conv	SGTFF	INTERDDDYAGFVFGYQSSSR	FYVVM	2		1214.046539	2426.077479	0.000451244	4	N	1013	1034
P35441	Conv	ADTDK	NGEGDACAVDIDGDGILNERDNCQYVYNVDQR	DTDMD	3	C7:+57.021,C23:+57.021	1215.52548	3643.553039	0.000451244	5	N	790	822
P35441	Conv	VQEDR	AQLYIDCDKMESAELDVPIQSIFTR	DLASV	3	C7:+57.021	981.481027	2941.419681	0.000451244	12	N	164	189
P35441	Conv	GDACK	DDFDHDNVPDIDDICPENFDISETDFRR	FQMIP	3	C15:+57.021	1137.816631	3410.426493	0.000451244	7	N	931	959
P35441	Conv	GHKTK	DLQAICGLSCDELSSMVLELK	GLRTI	2	C6:+57.021,C10:+57.021	1191.073546	2380.131492	0.000451244	5	N	264	285
P35441	Conv	LRVAK	GDVNDNFQGVLQNVR	FVFGT	2		837.9138715	1673.812143	0.000451244	6	N	201	216
P35441	Conv	IDCDK	MESAELDVPIQSIFTR	DLASV	2		918.4645489	1834.913498	0.000622848	6	N	173	189
P35441	Conv	AVERK	DNTGQIFSVVSNGKAGTLDLSLSLPGK	QQVVS	3		906.8156572	2717.423572	0.0025889	1	N	110	137
P35441	Conv	MCGSN	RIPESGGDNGVFDIFELIGGAR	RGPGR	3		773.7296353	2318.165506	0.000451244	2	N	19	41
P35441	Conv	DACAV	DIDGDGILNERDNCQYVYNVDQR	DTDMD	3	C14:+57.021	924.4160733	2770.22482	0.001463592	1	N	799	822
P35441	Conv	LKGLR	TIVTTLQDSIRK	VTEEN	2		687.9017127	1373.787825	0.000870037	1	N	288	300
P35461	Conv	RSKVK	SNLCLPICPTTLDNTEITGNAVNVK	TYCCK	2	C4:+57.021,C8:+57.021	1372.683369	2743.351138	0.000451244	19	N	47	72
P35505	Conv	NPKPR	IGVAIGDQILDLSVIK	HLFTG	2		827.4934347	1652.971269	0.000451244	22	N	31	47
P35505	Conv	DWSAR	DIQQWEYVPLGPFLGK	SFGTT	2		945.493966	1888.972332	0.000451244	16	N	237	253
P35505	Conv	QGQTR	TFLLDGDEVIITGHCQGDGYR	VGFGQ	2	C15:+57.021	1183.557997	2365.100394	0.000451244	9	N	381	402
P35505	Conv	GIMFR	GKENALLPNWLHLPVGYHGR	ASSIV	4		568.5596129	2270.207252	0.000451244	3	N	142	162
P35564	Conv	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSKSK	SDAST	4		792.8462583	3167.353833	0.001871652	2	N	20	48
P35564	Conv	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSK	SKSDA	3		985.0834139	2952.226842	0.001463592	1	N	20	46
P35564	Conv	VNPSR	EIEDPEDRKPEDWDERPK	IADPD	4		571.519079	2282.045116	0.000698008	1	N	275	293
P35585	Conv	PISVK	FEIPYFTTSGIQVR	YLKII	2		829.4333771	1656.851154	0.000451244	12	N	379	393
P35585	Conv	LMSYR	LNTHVKPLIWIESVIEK	HSHSR	3		673.7266149	2018.156445	0.001329271	1	N	268	285
P35700	Conv	GISFR	GLFIIDDKGILR	QITIN	3		453.9385275	1358.792183	0.000662267	4	N	128	140
P35700	Conv	QFTDK	HGEVCPAGWKPGSDTIKPDVNK	SKEYF	3	C5:+57.021	798.0623544	2391.163663	0.000998612	7	N	168	190
P35700	Conv	EYKGK	YVVFFFYPLDFTFVCPTEIIAFSDR	ADEFK	3	C15:+57.021	1031.842113	3092.502939	0.000451244	7	N	37	62
P35700	Conv	KGILR	QITINDLPVGR	SVDEI	2	[0:-17.027	604.835616	1207.655632	0.00307782	1	N	140	151
P35700	Conv	DEFKK	LNCQVIGASVDSHFCHLAWINTPK	KQGGL	3	C3:+57.021,C15:+57.021	923.1198322	2766.336097	0.00091018	2	N	68	92
P35700	Conv	YVVFF	FYPLDFTFVCPTEIIAFSDR	ADEFK	2	C10:+57.021	1219.590777	2437.165955	0.00091018	1	N	42	62
P35700	Conv	ADEFK	KLNCQVIGASVDSHFCHLAWINTPK	KQGGL	4	C4:+57.021,C16:+57.021	724.6155649	2894.43106	0.001591523	2	N	67	92
P35979	Conv	SGTIK	EILGTAQSVGCNVDGR	HPHDI	2	C11:+57.021	838.4073333	1674.799067	0.000451244	11	N	130	146
P35979	Conv	TIQNR	QAQIEVVPSASALIIK	ALKEP	2		833.9910592	1665.966518	0.000851441	4	N	67	83
P35979	Conv	QKNIK	HSGNITFDEIVNIAR	QMRHR	3		562.6255598	1684.853279	0.000451244	5	N	99	114
P35979	Conv	VVYLR	CTGGEVGATSALAPK	IGPLG	2	C1:+57.021	709.8511312	1417.686662	0.002212458	1	N	16	31
P38060	Conv	AAGAK	EVSVFGAVSELFTR	KNANC	2		770.9044524	1539.793305	0.001591523	1	N	122	136
P38647	Conv	MKLTR	AQFEGIVTDLIKR	TIAPC	3		497.2844749	1488.830025	0.000851441	1	N	348	361
P38647	Conv	MKLTR	AQFEGIVTDLIK	RTIAP	2		667.3722568	1332.728914	0.002145581	1	N	348	360
P39039	Conv	AEENK	AIQEVATGIAFLGITDEATEGQFMYVTGGR	LTYSN	3	M24:+15.995	1054.520721	3160.538764	0.000451244	4	N	163	193
P39039	Conv	YSNWK	KDEPNNHGSGEDCVIILDNGLWNDISCQASFK	AVCEF	3	C13:+57.021,C27:+57.021	1211.551077	3631.629832	0.000451244	2	N	200	232
P39039	Conv	FSKVK	SLCTELQGTVAIPR	NAEEN	3	C3:+57.021	515.608587	1543.802361	0.000823681	1	N	143	157
P39054	Conv	EPCLK	CVDLVIQELISTVR	QCTSK	2	C1:+57.021	822.9533881	1643.891176	0.000451244	4	N	426	440
P39054	Conv	PLVNK	LQDAFSSIGQSCHLDLPQIAVVGGQSAGK	SSVLE	3	C12:+57.021	995.1699515	2982.486454	0.000451244	7	N	15	44
P39054	Conv	YKDLR	QIELACDSQEDVDSWK	ASFLR	2	C6:+57.021	961.9257529	1921.835906	0.000622848	2	N	601	617
P39054	Conv	PGITK	VPVGDQPPDIEYQIK	DMILQ	2		849.4413991	1696.867198	0.000451244	3	N	142	157
P39054	Conv	VETIR	NLVDSYVAIINK	SIRDL	2		674.8777063	1347.739813	0.000451244	4	N	657	669
P39054	Conv	PINLR	VYSPHVLNLTLIDLPGITK	VPVGD	3		698.4055414	2092.193224	0.000622848	4	N	123	142
P39054	Conv	YHALK	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	RPVSS	3		1376.689377	4127.04473	0.001352548	3	N	730	769
P39054	Conv	IHGVR	TGLFTPDLAFEAIVK	KQVVK	2		811.4459531	1620.876306	0.001839721	3	N	399	414
P39654	Conv	WGNWK	DGTILNVAATSISDLPVDQR	FREDK	2		1043.04528	2084.07496	0.000451244	13	N	146	166
P39654	Conv	EIRNK	SLDIPYEYLRPSLVENSVAI	-	2		1139.602431	2277.189261	0.000823681	4	N	643	663
P39654	Conv	WISVK	GPGDQGSEYTFPCYR	WVQGT	2	C13:+57.021	867.3651341	1732.714668	0.000451244	8	N	84	99
P39654	Conv	LDLLK	QAGAFLTYSSLCPPDDLAER	GLLDI	2	C12:+57.021	1106.023259	2210.030918	0.000451244	4	N	431	451
P39654	Conv	VYRIR	VSTGDSVYAGSNNEVYLWLIGQHGEASLGK	LFRPC	3		1051.183068	3150.525805	0.000451244	4	N	7	37
P39654	Conv	FPCYR	WVQGTSILNLPEGTGCTVVEDSQGLFR	NHREE	3	C16:+57.021	988.4908021	2962.449006	0.000451244	14	N	99	126
P39654	Conv	LVMLK	LQPDGQLLPIAIQLELPK	TGSTP	2		993.5858552	1985.15611	0.000451244	6	N	305	323
P39654	Conv	DLYYK	TDQAVQDDYELQSWCQEITEIGLQGAQDR	GFPTS	3	C15:+57.021	1132.848043	3395.520728	0.000451244	7	N	485	514
P39654	Conv	EAEFK	VDVSEYLGPLLFVR	VQKWH	2		803.9461203	1605.876641	0.000451244	1	N	50	64

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P39654	Conv	EELKK	GTLFEADFFLLDGIK	ANVIL	2		843.4434105	1684.871221	0.000451244	4	N	271	286
P39654	Conv	VTCWK	SLDDFNYVFK	SGHTK	2		624.3013001	1246.587	0.000735798	4	N	199	209
P39655	Conv	DPRTK	AVLSQFQADLDNLEKEITAR	NEQLD	2		1131.092761	2260.169923	0.000451244	9	N	621	641
P39655	Conv	FPCYR	WVQGEGILSLPEGTAR	LAGDN	2		856.9524653	1711.889331	0.000451244	19	N	98	114
P39655	Conv	ALYAR	DALQLWEVTAR	YVKGM	2		651.3465733	1300.677547	0.000735798	3	N	462	473
P39655	Conv	DPRTK	AVLSQFQADLDNLEK	EITAR	2		845.9364809	1689.857362	0.000451244	3	N	621	636
P39655	Conv	NTRSR	TQLISDGGIFDQVVSTGGGGHVQLLTR	AVAQL	3		919.1511513	2754.430054	0.000451244	1	N	404	431
P39655	Conv	EKELK	NGSLFEADFILLDGIPANVIR	GEPQY	2		1137.61059	2273.20558	0.000451244	4	N	269	290
P39655	Conv	LRPAR	GKEEEFDFDVPEDLGPLQFVK	LHKQH	2		1219.59226	2437.16892	0.000451244	14	N	43	64
P39655	Conv	EITAR	NEQLDLPYEYLKPSR	IENSI	2		932.9761374	1863.936675	0.000451244	8	N	641	656
P39655	Conv	QLLTR	AVAQLTYHSLCPPDDLANR	GLLRI	2	C11:+57.021	1071.026136	2140.036672	0.000451244	4	N	431	450
P39655	Conv	YTLLR	SWNHLEDFDQIFWGQK	SALAE	3		683.9871573	2048.938072	0.000451244	10	N	195	211
P39655	Conv	RYRVR	VVTGAWLFSGSLNLVR	LWLVG	2		859.9835685	1717.951537	0.001943752	1	N	7	23
P39655	Conv	VKLHK	QHTVVDDAWFCNLITVQGPGTSAEAVFPCYR	WVQGE	3	C11:+57.021,C29:+57.021	1180.222344	3537.643632	0.000451244	12	N	67	98
P40124	Conv	AYLSK	NSLDCEIVSAK	SSEMN	2	C5:+57.021	618.3007428	1234.585886	0.000451244	13	N	421	432
P40124	Conv	DSASR	SALFAQINQGESITHALK	HVSDD	2		964.5159611	1927.016322	0.000451244	14	N	253	271
P40124	Conv	GKKWR	VENQENVSNLVIDDTELK	QVAYI	2		1030.013645	2058.011691	0.000451244	28	N	329	347
P40124	Conv	GKKWR	VENQENVSNLVIDDTELKQVAYIYK	CVNTT	3		975.5016269	2923.481481	0.000451244	12	N	329	354
P40124	Conv	YVQAF	DSLLANPVAEYLK	MSKEI	2		716.888271	1431.760942	0.001162105	3	N	46	59
P40124	Conv	GAVPY	VQAFDSLLANPVAEYLK	MSKEI	2		939.5045308	1876.993462	0.000451244	13	N	42	59
P40124	Conv	NRGSK	FFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	3		1028.894353	3083.65966	0.000451244	14	N	125	154
P40124	Conv	DSPSK	GAVPYVQAFDSLLANPVAEYLK	MSKEI	2		1183.126073	2364.236546	0.000451244	50	N	37	59
P40124	Conv	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITFR	EKNRG	3	C9:+57.021	1271.00717	3809.998109	0.000451244	9	N	83	118
P40124	Conv	PAGNK	LSDLLAPISEQIQEVITFR	EKNRG	2		1086.599691	2171.183782	0.000451244	43	N	99	118
P40124	Conv	DNCKK	LGLVFDDVVGIVEIINSR	DVKVQ	2		979.5520123	1957.088425	0.000451244	42	N	376	394
P40124	Conv	IVSAK	SSEMNVLIPTEGGDFNEFPVPEQFK	TLWNG	2		1406.163255	2810.310911	0.001654178	1	N	432	457
P40124	Conv	VDNCK	KLGLVFDDVVGIVEIINSR	DVKVQ	2		1043.599494	2085.183388	0.000451244	9	N	375	394
P40124	Conv	VDWVR	AYLSIWTELQAYIK	EFHTT	2		849.9592277	1697.902855	0.000451244	27	N	183	197
P40124	Conv	SGPVR	SGPKPFSAPKPQTSPSPKPATK	KEPAL	4		559.5592786	2234.205914	0.000451244	3	N	293	315
P40124	Conv	LKLER	ALLATASQCQQPAGNK	LSDLL	2	C9:+57.021	829.4202437	1656.824887	0.000451244	3	N	83	99
P40124	Conv	AYIYK	CVNTTLQIK	GKINS	2	C1:+57.021	538.7923566	1075.569113	0.001162105	2	N	354	363
P40124	Conv	KPATK	KEPALLELEGK	KWRVE	2		613.8536999	1225.6918	0.000823681	9	N	315	326
P40124	Conv	NRGSK	FFNHLSAVSESIQALGWVALAAK	PGPFV	2		1230.158239	2458.300877	0.000451244	9	N	125	148
P40124	Conv	RAVGR	LEAVSHTSDMHCGYGDSPSK	GAVPY	3	C12:+57.021	726.6461008	2176.914903	0.000823681	3	N	17	37
P40124	Conv	QAYIK	EFHTTGLAWSK	TGPVA	3		426.2160609	1275.624783	0.001699387	1	N	197	208
P40124	Conv	LEGKK	WRVENQENVSNLVIDDTELK	QVAYI	3		801.0718383	2400.192115	0.000451244	13	N	327	347
P40124	Conv	AGNKL	SDLLAPISEQIQEVITFR	EKNRG	2		1030.057659	2058.099718	0.000451244	2	N	100	118
P40124	Conv	LSDLL	APISEQIQEVITFR	EKNRG	2		815.944109	1629.872618	0.000451244	1	N	104	118
P40124	Conv	SKGAV	PYVQAFDSLLANPVAEYLK	MSKEI	2		1069.562577	2137.109554	0.000823681	2	N	40	59
P40124	Conv	QVMGK	VPTISINKTDGCHAYLSK	NSLDC	3	C12:+57.021	668.6791817	2003.014145	0.000451244	4	N	403	421
P40124	Conv	PATKK	EPALLELEGK	KWRVE	2		549.8062183	1097.596837	0.002981883	1	N	316	326
P40124	Conv	FFNHL	SAVSESIQALGWVALAAKPGPFVK	EMNDA	3		809.4534428	2425.336929	0.000622848	5	N	130	154
P40124	Conv	VPYVQ	AFDSLLANPVAEYLK	MSKEI	2		825.9410349	1649.86647	0.001229886	4	N	44	59
P40142	Conv	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	2		1097.074706	2192.133812	0.000451244	6	N	186	205
P40142	Conv	FDINR	LGQSDPAPLQHQVDIYQK	RCEAF	2		1019.02415	2036.032701	0.000451244	40	N	186	204
P40142	Conv	ICFIR	TSRPENAIIYSNNEDFQVGQAK	VVLKS	2		1241.104389	2480.193177	0.000451244	57	N	471	493
P40142	Conv	DIYQK	RCEAFGWHTIIVDGHSVEELCK	AFGQA	3	C2:+57.021,C21:+57.021	881.7531493	2642.236048	0.000622848	2	N	204	226
P40142	Conv	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	2	C1:+39.994,C20:+57.021	1235.561768	2469.107937	0.000451244	3	N	205	226
P40142	Conv	QSKKK	ILATPPQEDAPSVDIANIR	MPTPP	2		1010.539633	2019.063667	0.000451244	61	N	283	302
P40142	Conv	GCATR	DRTVPFCSTFAAFFTR	AFDQI	2	C7:+57.021	961.9648185	1921.914037	0.001699387	4	N	379	395
P40142	Conv	EAMAF	AGIYKLDNLVAIFDINR	LGQSD	3		645.6953147	1934.062544	0.000451244	2	N	169	186
P40142	Conv	RDRTV	PFCSTFAAFFTR	AFDQI	2	C3:+57.021	726.342745	1450.66989	0.000451244	13	N	383	395
P40142	Conv	ATRDR	TVPFCSTFAAFFTR	AFDQI	2	C5:+57.021	826.4007913	1650.785983	0.000451244	26	N	381	395
P40142	Conv	APILY	AVWAEAGFLPEAELLNLR	KISSD	2		1000.036529	1998.057459	0.000451244	19	N	83	101
P40142	Conv	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	2		1475.303423	2948.591246	0.000451244	4	N	75	102
P40142	Conv	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	2		1005.00457	2007.993539	0.000451244	9	N	264	281
P40142	Conv	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	2		1411.255941	2820.496283	0.000451244	21	N	75	101
P40142	Conv	AELLK	MFGIDKDAIVQAVK	GLVTK	2		767.9190488	1533.822498	0.000451244	10	N	603	617
P40142	Conv	AGIYK	LDNLVAIFDINR	LGQSD	2		701.8886053	1401.761611	0.000451244	37	N	174	186
P40142	Conv	ATKGR	ILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	3		1063.542374	3187.603721	0.000451244	198	N	555	586
P40142	Conv	APILY	AVWAEAGFLPEAELLNLRK	ISSDL	3		709.725274	2126.152422	0.000662267	1	N	83	102
P40142	Conv	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	2		988.5341539	1975.052708	0.000451244	6	N	246	264
P40142	Conv	LLNLR	KISSDLDGHPVPK	QAFTD	3		464.9214251	1391.740875	0.000451244	1	N	101	114
P40142	Conv	LNLRK	ISSDLDGHPVPK	QAFTD	2		632.8307561	1263.645912	0.000622848	2	N	102	114
P40142	Conv	LAMFR	SVPMSTVFYPSDGVATEK	AVELA	2		957.961839	1913.908078	0.001943752	1	N	438	456

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P40142	Conv	QVTVI	GAGVTLHEALAAAESLKK	DKISI	2		883.4944974	1764.973395	0.001395409	1	N	506	524
P40142	Conv	KVVLK	SKDDQVTVIGAGVTLHEALAAAESLK	KDKIS	3		875.1366193	2622.386458	0.000451244	16	N	497	523
P40142	Conv	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021	1266.596797	2531.177994	0.000451244	8	N	114	140
P40142	Conv	VLKSK	DDQVTVIGAGVTLHEALAAAESLKK	DKISI	3		846.1259431	2535.354429	0.000622848	8	N	499	524
P40142	Conv	KKILA	TPPQEDAPSVDIANIR	MPTPP	2		861.9370122	1721.858424	0.001162105	1	N	286	302
P40142	Conv	KISIR	VLDPFTIKPLDR	KLILD	2		707.4091736	1412.802747	0.000451244	11	N	530	542
P40142	Conv	VQSKK	KILATPPQEDAPSVDIANIR	MPTPP	2		1074.587115	2147.15863	0.000451244	7	N	282	302
P40142	Conv	IFDIN	RLGQSDPAPLQHQVDIYQK	RCEAF	3		731.7190706	2192.133812	0.000698008	8	N	185	204
P40142	Conv	KGRGI	TGIEDKEAWHGKPLPK	NMAEQ	3		602.65686	1804.94718	0.000451244	3	N	248	264
P40142	Conv	TVIGA	GVTLHEALAAAESLKK	DKISI	3		546.6460724	1636.914817	0.000451244	3	N	508	524
P40142	Conv	PILYA	VWAEAGFLPEAELLNLR	KISSD	2		964.5179725	1927.020345	0.000662267	4	N	84	101
P40142	Conv	VWEAM	AFAGIYKLDNLVAIFDINR	LGQSD	3		718.3971573	2152.168072	0.002519933	1	N	167	186
P40142	Conv	RFVLS	KGHAAPILYAVWAEAGFLPEAELLNLR	KISSD	4		738.1556115	2948.591246	0.000823681	1	N	74	101
P40142	Conv	FVLSK	GHAAPILYAVWAEAGFLPEAELL	NLRKI	2		1219.64189	2437.26818	0.000823681	3	N	75	98
P40142	Conv	LSKGH	AAPILYAVWAEAGFLPEAELLNLRK	ISSDL	3		919.1780901	2754.51087	0.000622848	1	N	77	102
P40142	Conv	FVLSK	GHAAPILYAVWAEAGFLPEAELLNL	RKISS	2		1333.205386	2664.395172	0.001463592	1	N	75	100
P40142	Conv	QSKKK	ILATPPQEDAPSVDIAN	IRMPT	2		875.9470456	1749.878491	0.001943752	1	N	283	300
P40142	Conv	GIYKL	DNLVAIFDINR	LGQSD	2		645.3465733	1288.677547	0.000451244	1	N	175	186
P40142	Conv	IGEAV	SAAVVGEPGVTVTR	LAVSQ	2		671.8704126	1341.725225	0.002663018	1	N	572	586
P40240	Conv	RETLK	AIHMALDCCGIAGPLEQFISDTCPK	KQLLE	2	M4:+15.995,C8:+57.021,C9:+57.021,C23:+57.021	1410.644687	2819.273773	0.000451244	11	N	142	167
P40240	Conv	DEVIK	ELQEFYKDTYQK	LRSKD	2		796.3860925	1590.756585	0.000451244	3	N	117	129
P40240	Conv	RETLK	AIHMALDCCGIAGPLEQFISDTCPKK	QLLES	3	M4:+15.995,C8:+57.021,C9:+57.021,C23:+57.021	983.4640455	2947.368736	0.001162105	1	N	142	168
P41241	Conv	MTQLR	HSNLVQLLGVIVEEK	GGLYI	3		559.9898391	1676.946117	0.000451244	13	N	244	259
P41241	Conv	EQAER	LLYPPETGLFLVR	ESTNY	2		759.4404738	1516.865348	0.002884417	1	N	94	107
P41245	Conv	RRDGR	LWCATTSNFDTDKK	WGFCP	2	C3:+57.021	843.8935275	1685.771455	0.000451244	56	N	370	384
P41245	Conv	FLNHR	GSPLQGPFLTAR	TWPAL	2		622.3438336	1242.672067	0.000451244	46	N	564	576
P41245	Conv	LMLQK	QLSLPQTGELDSQTLK	AIRTP	2		879.4681452	1756.92069	0.000451244	36	N	77	93
P41245	Conv	SDGYR	WCATTANYDQDKLYGFCPTR	VDATV	2	C2:+57.021,C17:+57.021	1234.043968	2466.072337	0.000451244	29	N	312	332
P41245	Conv	QSVIR	VDKEFSGVPWNSHDIFQYQDK	AYFCH	2		1270.098575	2538.18155	0.000451244	13	N	667	688
P41245	Conv	RSLDK	LGLGPEVTHVSGLLPR	RLGKA	2		822.9757434	1643.935887	0.000451244	10	N	621	637
P41245	Conv	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	2		1044.594743	2087.173886	0.000451244	18	N	617	637
P41245	Conv	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	2	C13:+57.021	1277.613107	2553.210613	0.000451244	25	N	275	297
P41245	Conv	TARTW	PALPATLDSAFEDPQTKR	VFFFS	2		979.0054263	1955.995253	0.000451244	8	N	578	596
P41245	Conv	FLTAR	TWPALPATLDSAFEDPQTKR	VFFFS	2		1122.568922	2243.122244	0.000451244	11	N	576	596
P41245	Conv	WSLGK	GVVIPTYYGNSNGAPCHFPFTFEGR	SYSAC	2	C16:+57.021	1394.153127	2786.290655	0.000451244	16	N	214	239
P41245	Conv	PFDGK	DGLLAHAFPPGAGVQGDAHFDDDELWSLGK	GVVIP	3		1045.832258	3134.473375	0.000451244	59	N	184	214
P41245	Conv	DAFAR	AFAVWGEVAPLTFTR	VYGPE	2		832.943912	1663.872224	0.000451244	63	N	143	158
P41245	Conv	FCPTR	VDATVVGGNSAGELCVFPFVFLGK	QYSSC	2	C15:+57.021	1242.135883	2482.256167	0.000451244	91	N	332	356
P41245	Conv	FLTAR	TWPALPATLDSAFEDPQTK	RVFFF	2		1044.518366	2087.021133	0.000451244	16	N	576	595
P41245	Conv	SDGYR	WCATTANYDQDK	LYGFC	2	C2:+57.021	736.8094634	1471.603327	0.000823681	2	N	312	324
P41245	Conv	TTDGR	NDGTPWCSTTADYDKDGK	FGFCP	2	C7:+57.021	1015.923742	2029.831883	0.000451244	31	N	249	267
P41245	Conv	LTFTR	VYGPEADIVIQFGVAEHGDGYPFDGK	DGLLA	3		927.4454528	2779.312958	0.000451244	98	N	158	184
P41245	Conv	IRVDK	EFSGVPWNSHDIFQYQDK	AYFCH	2		1099.003415	2195.99123	0.000823681	10	N	670	688
P41245	Conv	FPLNK	DDIDGIQYLYGR	GSKPD	2		714.3442276	1426.672855	0.000451244	8	N	433	445
P41245	Conv	VVGGN	SAGELCVFPFVFLGK	QYSSC	2	C6:+57.021	835.934467	1669.853334	0.000451244	7	N	341	356
P41245	Conv	TTDGR	NDGTPWCSTTADYDK	DGKFG	2	C7:+57.021	865.8520566	1729.688513	0.000823681	1	N	249	264
P41245	Conv	FCPTR	VDATVVGGNSAGELCVFPF	VFLGK	2	C15:+57.021	969.9672238	1937.918848	0.000451244	7	N	332	351
P41245	Conv	DAFAR	AFAVWGEVAPLTF	TRVYG	2		704.3695171	1406.723434	0.000622848	3	N	143	156
P41245	Conv	RRDGR	LWCATTSNFDTDK	KWGFC	2	C3:+57.021	779.8460459	1557.676492	0.000451244	6	N	370	383
P41245	Conv	RVDAT	VVGGNSAGELCVFPFVFLGK	QYSSC	2	C11:+57.021	1049.045809	2096.076017	0.000451244	7	N	336	356
P42208	Conv	TRLLK	ASIPFSVVGSNQLIEAK	GKKVR	2		880.4835983	1758.951597	0.000451244	9	N	232	249
P42208	Conv	GVKLR	LTVVDTPGYGDAINCR	DCFKT	2	C15:+57.021	875.9253589	1749.835118	0.000451244	1	N	96	112
P42208	Conv	SGLGK	STLINSLFLTDLYPER	IIPGA	2		941.5019881	1880.988376	0.000451244	1	N	50	66
P42227	Conv	DWKRR	QQIACIGGPPNICLDRLENWITSLAESQLQTR	QQIKK	3	C5:+57.021,C13:+57.021	1227.954257	3680.839372	0.001943752	1	N	246	278
P42227	Conv	WEESR	LLQTAATAAQQGGQANHPTAAVVTEK	QQMLE	3		859.4529417	2575.335425	0.000451244	22	N	114	140
P42567	Conv	ISSLK	AEITSQESQISSYEEELLK	AREEL	2		1092.531868	2183.048136	0.000451244	4	N	430	449
P42567	Conv	EELSR	LQQETAQLEESVESGK	AQLEP	2		888.4370421	1774.858484	0.000451244	1	N	456	472
P42669	Conv	DALAK	LIDDYGVEEEPAELPEGTSLTVDNKR	FFFDV	3		963.805375	2888.392725	0.000451244	18	N	203	229
P42669	Conv	QTVNR	GPGLGSTQGQTIALPAQGLIEFR	DALAK	2		1156.124396	2310.233192	0.000451244	8	N	175	198
P42669	Conv	AVEFR	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	RALKS	3		1090.849978	3269.526533	0.001943752	1	N	110	139
P42932	Conv	FVLVF	AGALLELAEELLR	IGLSV	2		699.4040883	1396.792577	0.00091018	1	N	107	120
P42932	Conv	TFLAK	LIAQACVSIFPDSGNFNVDNIR	VCKIL	2	C6:+57.021	1225.610564	2449.205528	0.000451244	12	N	181	203
P42932	Conv	NRLEK	LFVTNDAATILR	ELEVQ	2		667.3778735	1332.740147	0.000451244	7	N	62	74

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P43274	Conv	GGAKR	KTSGPPVSELITK	AVAAS	2		678.8908137	1355.766027	0.000451244	6	N	33	46
P43274	Conv	GAKRK	TSGPPVSELITK	AVAAS	2		614.8433321	1227.671064	0.000451244	59	N	34	46
P43274	Conv	-M	SETAPAAPAAPAPAEK	TPVKK	2		739.8784346	1477.741269	0.000451244	1	N	1	17
P43275	Conv	AALKK	SLAAAGYDVEK	NNSRI	2		562.28565	1122.5557	0.000823681	2	N	66	77
P43275	Conv	AAAPR	KKPAGPSVSELIVQAVSSSK	ERSGV	2		1006.573476	2011.131352	0.000451244	8	N	34	54
P43275	Conv	-MSE	TAPVAQAASTATEKPAAAK	KTKKP	2		892.481587	1782.947574	0.000451244	1	N	3	22
P43276	Conv	GAAKR	KATGPPVSELITK	AVSAS	2		670.8933564	1339.771113	0.000451244	10	N	33	46
P43276	Conv	AAKRK	ATGPPVSELITK	AVSAS	2		606.8458748	1211.67615	0.000451244	7	N	34	46
P43276	Conv	-M	SETAPAETAAPAPVEK	SPAKK	2		784.8942817	1567.772963	0.000451244	4	N	1	17
P43276	Conv	PALKK	ALAAGGYDVEK	NNSRI	2		547.2803676	1092.545135	0.001763695	1	N	64	75
P43277	Conv	-M	SETAPAAPAAPAPVEK	TPVKK	2		753.8940847	1505.772569	0.000451244	9	N	1	17
P43277	Conv	MSETA	PAAPAAPAPVEK	TPVKK	2		559.8143777	1117.613155	0.000451244	1	N	5	17
P43277	Conv	-MSE	TAPAAPAAPAPVEK	TPVKK	2		645.8567739	1289.697948	0.000451244	3	N	3	17
P45376	Conv	YCHSK	GIVVTAYSPLGSPDRPWAKPEDPSLLEDPR	IKAIA	3		1088.23013	3261.66699	0.000622848	6	N	203	233
P45376	Conv	KPGLK	YKPAVNQIECHPYLTQEK	LIEYC	3	C10:+57.021	740.0372576	2217.088373	0.001162105	2	N	177	195
P45376	Conv	EGLVK	TIGVSNFNPLQIER	ILNKP	2		794.428626	1586.841652	0.000451244	2	N	155	169
P46467	Conv	AQEDK	AGNYEEALQLYQHAVQYFLHVVK	YEAQG	4		680.8517583	2719.375833	0.000979378	8	N	23	46
P46467	Conv	RTPWR	GILLFGPPGTGK	SYLAK	2		578.8403955	1155.665191	0.0025889	1	N	168	180
P46471	Conv	ARTKK	ACLIFFDEIDAIGGAR	FDDGA	2	C2:+57.021	884.4406449	1766.86569	0.000451244	6	N	268	284
P46471	Conv	DKPIR	ALDEGDIALLK	TYGQS	2		579.3247752	1156.63395	0.000979378	5	N	23	34
P46471	Conv	LTGIK	ESDTGLAPPALWDLAADKQTLQSEQPLQVAR	CTKII	3		1116.907716	3347.699747	0.000451244	12	N	66	97
P46638	Conv	AFAEK	NNLSFIETSALDSTNVEEAFKNILTEIYR	IVSQK	3		1111.228455	3330.661964	0.000735798	1	N	145	174
P46638	Conv	AFAEK	NNLSFIETSALDSTNVEEAFK	NILTE	2		1165.063867	2328.112133	0.000451244	22	N	145	166
P46638	Conv	SAYYR	GAVGALLVYDIAK	HLTYE	2		645.3773421	1288.739084	0.000451244	7	N	82	95
P46664	Conv	ANQYK	SIYPTLEIDIEGELQQLK	GYMER	2		1045.057325	2088.099049	0.000451244	5	N	203	221
P46664	Conv	AYTTR	VGIGAFPTEQDNEIGELLQTR	GREFG	3		763.0575291	2286.149187	0.000451244	6	N	303	324
P46664	Conv	GRKRR	CGWLDLVSLK	YAHMI	2	C1:+57.021	595.8158317	1189.616063	0.002663018	1	N	337	347
P47738	Conv	PFDSR	TEQGPQVDETQFK	KILGY	2		753.8576992	1505.699798	0.000451244	15	N	357	370
P47738	Conv	SGSGR	ELGEYGLQAYTEVK	TVTVK	2		800.3991999	1598.7828	0.000451244	19	N	494	508
P47738	Conv	VKAAR	AAFQLGSPWR	RMDAS	2		566.7990619	1131.582524	0.000622848	8	N	86	96
P47738	Conv	LSRLL	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	3	C19:+57.021	1259.932775	3776.774926	0.000451244	17	N	19	53
P47738	Conv	EGVDK	VAFTGSTEVGHLIQVAAGSSNLKR	VTLEL	3		814.7753561	2441.302668	0.000451244	13	N	259	283
P47738	Conv	CAGSR	TFVQENVYDEFVER	SVARA	2		887.9182882	1773.820976	0.000451244	17	N	326	340
P47738	Conv	KYHGK	TIPIDGDFFSYTR	HEPVG	2		766.3755278	1530.735456	0.000637154	5	N	161	174
P47738	Conv	ANLIK	EAGFPPGVVNIVPGFGPTAGAAIASHEGVDK	VAFTG	3		987.8422063	2960.503219	0.000451244	40	N	228	259
P47738	Conv	VVVMK	VAEQTPLTALYVANLIK	EAGFP	2		922.5305486	1843.045497	0.000451244	27	N	211	228
P47738	Conv	AVFTK	DLDKANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C21:+57.021	1299.624837	3895.851111	0.000451244	24	N	453	488
P47738	Conv	ANDSK	YGLAAAVFTK	DLDKA	2		520.7929139	1039.570228	0.000451244	9	N	443	453
P47738	Conv	AVSRK	TFPTVNPSTGEVICQVAEGNKEDVDK	AVKAA	3	C14:+57.021	945.455646	2833.343538	0.001162105	1	N	54	80
P47738	Conv	KDLDK	ANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C17:+57.021	1142.547199	3424.618197	0.000622848	16	N	457	488
P47738	Conv	EGVDK	VAFTGSTEVGHLIQVAAGSSNLK	RVTLE	2		1143.608579	2285.201557	0.000451244	5	N	259	282
P47738	Conv	SRKTF	PTVNPSTGEVICQVAEGNKEDVDK	AVKAA	3	C12:+57.021	862.7502818	2585.227445	0.001839721	1	N	56	80
P47738	Conv	AAADR	GYFIQPTVFGDVK	DGMTI	2		735.8855313	1469.755463	0.000451244	10	N	396	409
P47738	Conv	IERDR	TYLAALETLDNGKPYVISYLVDLDMVLK	CLRYY	3		1053.23008	3156.66684	0.00091018	1	N	118	146
P47738	Conv	SRLLS	AAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	4	C18:+57.021	923.4435243	3689.742897	0.002813207	1	N	20	53
P47738	Conv	TVWIN	CYDVFGAQSPFGGYK	MSGSG	2	C1:+57.021	848.3775132	1694.739426	0.002019181	1	N	473	488
P47754	Conv	RIAAK	FIIHAPPGEFNEVFNDVR	LLLNN	2		1051.029236	2100.042871	0.00091018	8	N	19	37
P47754	Conv	TVYGK	KVDGQQTIIACIESHQFQAK	NFWNG	3	C11:+57.021	767.7270832	2300.157849	0.000451244	1	N	146	166
P47754	Conv	RSEWK	FTVTPSTTQVVGILK	IQVHY	2		795.9592277	1589.902855	0.000451244	14	N	178	193
P47754	Conv	LVSHK	DIQDSLTVSNEVQTAK	EFIKI	2		874.4395848	1746.86357	0.000451244	6	N	210	226
P47757	Conv	SARLR	KLEVEANNAFDQYR	DLYFE	2		848.9186225	1695.821645	0.000451244	28	N	94	108
P47757	Conv	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLK	IARDK	2	C13:+57.021	1392.223081	2782.430562	0.000622848	4	N	23	48
P47757	Conv	LIDLV	PSLCEDLLSSVDQPLK	IARDK	2	C4:+57.021	900.9563248	1799.89705	0.000451244	2	N	32	48
P47757	Conv	SKKIK	GCWDSIHVVEVQEK	SSGRT	2	C2:+57.021	843.4015197	1684.787439	0.000451244	13	N	145	159
P47757	Conv	ENKIR	STLNEIYFGK	TKDIV	2		586.3038428	1170.592086	0.000451244	2	N	225	235
P47757	Conv	ARLRK	LEVEANNAFDQYR	DLYFE	2		784.8711409	1567.726682	0.000451244	8	N	95	108
P47757	Conv	KVVGK	DYLLCDYNR	DGDSY	2	C5:+57.021	616.274528	1230.533456	0.002813207	1	N	57	66
P47757	Conv	GDSYR	SPWSNKYDPPLEDGAMPSAR	LRKLE	3	M16:+15.995	745.3448218	2233.011066	0.000451244	17	N	72	92
P47791	Conv	VESHK	LGGTCVNVGCVPK	KVMWN	2	C5:+57.021,C10:+57.021	680.8392809	1359.662962	0.000451244	9	N	75	88
P47791	Conv	LNLNK	VGIQTDEKGHILVDEFQNTNVK	GVYAV	2		1242.640607	2483.265614	0.000451244	4	N	324	346
P47791	Conv	MGATK	ADFDNTVAIHPTSSEELVTLR	-	2		1158.079851	2314.144102	0.000451244	16	N	479	500
P47791	Conv	DKVLR	NFDSLISSNCTEELENAGVEVLK	FTQVK	2	C10:+57.021	1284.610624	2567.205647	0.000451244	19	N	246	269
P47791	Conv	DLPSR	SVIVGAGYIAVEIAGILSALGSK	TSLMI	2		1094.633534	2187.251467	0.000451244	21	N	211	234
P47791	Conv	AYVSR	LNTIYQNNLTK	SHIEI	2		661.3596807	1320.703761	0.00091018	8	N	131	142
P47791	Conv	QTDEK	GHILVDEFQNTNVK	GVYAV	2		807.4182583	1612.820917	0.000451244	8	N	332	346

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P47791	Conv	NNLTK	SHIEIIHGYATFADGPRPTVEVNGK	KFTAP	3		903.4650702	2707.371811	0.000451244	9	N	142	167
P47791	Conv	KEVKK	TSSGLELQVVTSVPGR	KPTTT	2		815.4444731	1628.873346	0.000451244	11	N	278	294
P47791	Conv	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	3		1055.203581	3162.587343	0.000451244	30	N	383	412
P47791	Conv	FTAPH	ILIATGGVPTVPHESQIPGASLGITSDGFFQLEDLPSR	SVIVG	3		1307.353377	3919.036732	0.000451244	8	N	173	211
P47791	Conv	DVCGK	ALLTPVAIAAGR	KLAHR	2		576.8591195	1151.702639	0.000451244	16	N	357	369
P47791	Conv	LFECK	QDSKLDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	3		1207.941085	3620.799855	0.000622848	8	N	379	412
P47791	Conv	VKEVK	KTSSGLELQVVTSVPGR	KPTTT	2		879.4919547	1756.968309	0.000451244	11	N	277	294
P47791	Conv	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHKYGK	DNVKI	4		878.6995746	3510.767098	0.000637154	2	N	383	415
P47791	Conv	MGATK	ADFDNTVAIHPTSSEEL	VTLR-	2		923.429217	1844.842834	0.000622848	4	N	479	496
P47809	Conv	SGNIK	LCDFGISGQLVDSIAK	TRDAG	2	C2:+57.021	861.9404777	1721.865355	0.000662267	2	N	242	258
P47809	Conv	DKFYK	YVYSVLDDVIPEEILGK	ITLAT	2		976.5173038	1951.019008	0.0025889	1	N	188	205
P47811	Conv	VKCQK	LTDDHVQFLIYQILR	GLKYI	3		625.3443934	1873.00978	0.000451244	8	N	121	136
P47811	Conv	LKHMK	HENVIGLLDVFTPAR	SLEEF	3		560.9743005	1679.899501	0.000451244	6	N	79	94
P47811	Conv	EVPER	YQNLSPVGSGAYGSVCAAFDTK	TGHRV	2	C16:+57.021	1146.533991	2291.052381	0.000451244	8	N	23	45
P47811	Conv	AQMPK	MNFANVFIGANPLAVDLLEK	MLVLD	2		1088.577705	2175.13981	0.000451244	4	N	267	287
P47811	Conv	DSDKR	ITAAQALAHAYFAQYHDPDDEPVADPYDQSFESR	DLLID	3		1280.247237	3837.71831	0.000451244	1	N	296	330
P47811	Conv	DIIHR	DLKPSNLAVNEDCELK	ILDFG	2	C13:+57.021	922.9568561	1843.898112	0.000698008	1	N	149	165
P47911	Conv	VVFLK	QLDSGLLLVTGPLVINR	VPLRR	2		904.5361652	1807.05673	0.000451244	4	N	174	191
P47911	Conv	VRRLR	SSITPGTVLIILTGR	HRGKR	2		764.4593949	1526.90319	0.000622848	3	N	149	164
P47955	Conv	NALIK	AAGVSVEPFWPGLFAK	ALANV	2		838.4462875	1674.876975	0.000451244	11	N	33	49
P47955	Conv	KVEAK	KEESEESEDDMGFGLFD	-	2	M11:+15.995	990.3891405	1978.762681	0.000451244	3	N	97	114
P47962	Conv	KYGVK	VGLTNYAAAYCTGLLLAR	RLLNR	2	C11:+57.021	964.009226	1926.002852	0.000451244	3	N	89	107
P47968	Conv	MAVNK	AGPVVTDNGNFILDWK	FDRVH	2		873.4470158	1744.878432	0.000451244	6	N	238	254
P47968	Conv	RIAER	VKQENLDLICIPTSFQAR	QLILQ	2	C10:+57.021	1066.562354	2131.109108	0.000451244	1	N	111	129
P48025	Conv	VYLDR	SLLTLEDNELGSGNFGTVK	KGYYQ	2		997.5079988	1993.000398	0.000451244	8	N	361	380
P48025	Conv	REYVK	QTWNLQGQALEQAIISQKPQLEK	LIATT	3		884.4770873	2650.407862	0.000823681	7	N	132	155
P48036	Conv	AGELK	WGTDEEKFITIFGTR	SVSHL	2		900.4522982	1798.888996	0.000451244	3	N	184	199
P48036	Conv	IIASR	TPEELSAIKQVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	3		1295.260989	3882.759566	0.000451244	14	N	115	149
P48036	Conv	-MATR	GTVTDFPGFDGR	ADAEV	2		634.7994559	1267.583312	0.000451244	13	N	4	16
P48036	Conv	RKAMK	GLGTDEDSILNLLTSR	SNAQR	2		852.4446701	1702.87374	0.000451244	7	N	27	43
P48036	Conv	LSAIK	QVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	2		1458.128652	2914.241704	0.000451244	19	N	124	149
P48036	Conv	ETIDR	ETSGNLEQLLLAVVK	SIRSI	2		807.4595919	1612.903584	0.000451244	7	N	225	240
P48036	Conv	TLFGR	DLVDDLKSELTGK	FEKLI	2		716.880643	1431.745686	0.000451244	6	N	61	74
P48036	Conv	VVVSR	SEIDLFNIR	KEFRK	2		553.7961849	1105.57677	0.001763695	2	N	274	283
P48036	Conv	YMTIS	GFQIEETIDRETSGNLEQLLLAVVK	SIRSI	3		934.8348289	2801.481087	0.002296037	1	N	215	240
P48193	Conv	NMHCK	VSLLDDTVYECVVEK	HAKGQ	2	C11:+57.021	884.9376007	1767.859601	0.000451244	10	N	214	229
P48193	Conv	SFFIK	IRPGEQEHYESTIGFK	LPSYR	3		630.9835243	1889.927173	0.000451244	2	N	451	467
P48193	Conv	TFNVK	FYPPDPAQLTEDITR	YYLCL	2		881.9364809	1761.857362	0.000698008	3	N	288	303
P48193	Conv	ESTDR	SPRPTSAPAIAQSQVTEGPGAPIKK	TPKEA	3		830.1226444	2487.344533	0.000451244	10	N	555	580
P48193	Conv	KVEEK	RGEEPAEPAEPEPTEAWK	VEKTH	2		1011.974323	2021.933046	0.000451244	10	N	591	609
P48193	Conv	HSPFR	TLNINGQVPTGDGPPLVK	TQTVT	2		910.4997797	1818.983959	0.000870037	4	N	709	727
P48193	Conv	RKKKR	ERLDGENIYIR	HSNLM	3		459.909408	1376.704824	0.001463592	1	N	645	656
P48193	Conv	VEEKR	GEEPAEPAEPEPTEAWK	VEKTH	2		933.9237675	1865.831935	0.000637154	1	N	592	609
P48193	Conv	ANAVK	SEIPTKDVPIVHTETK	TITYE	4		449.247069	1792.957076	0.00307782	1	N	741	757
P48193	Conv	RIEKR	IVITGDADIDHDQVLVQAIK	EAKEQ	2		1082.086948	2162.158295	0.001329271	1	N	813	833
P49138	Conv	FGFAK	ETTSHNSLTTPCYTPYYVAPEVLGPEK	YDKSC	3	C12:+57.021	1018.818584	3053.432353	0.002981883	1	N	198	225
P49222	Conv	VRAVK	EGELQLDPAVPELFAAVNASCVVWK	CCEDG	3	C21:+57.021	914.7987959	2741.372988	0.000451244	9	N	372	397
P49222	Conv	NQVMR	LSTNLSFSCFEQTPPENSFLR	VTAMA	2	C9:+57.021	1237.586755	2473.157909	0.000637154	3	N	542	563
P49222	Conv	TGQGR	AVYETQAWVSAAVACTVLR	CLGIP	2	C15:+57.021	1048.035972	2094.056344	0.002663018	1	N	261	280
P49222	Conv	ALKKK	SVLPISQTQAAQEGALLYK	RRGSV	2		1009.052376	2016.089153	0.000451244	4	N	225	244
P49290	Conv	LRLYK	TPDNIDIWVGAIAEPLLPGAR	VGPLL	2		1109.597483	2217.179365	0.000451244	5	N	608	629
P49290	Conv	LPGAR	VGPLLACLFENQFR	RARDG	2	C7:+57.021	832.4351655	1662.854731	0.002080925	1	N	629	643
P49312	Conv	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	2		940.4872037	1878.958807	0.000622848	1	N	106	122
P49312	Conv	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	2		1141.079123	2280.142645	0.001395409	1	N	146	166
P49312	Conv	EQLRK	LFIGGLSFETTDESLR	SHFEQ	2		892.9574134	1783.899227	0.000451244	12	N	15	31
P49312	Conv	PEQLR	KLFIGGLSFETTDESLR	SHFEQ	2		957.0048949	1911.99419	0.000451244	6	N	14	31
P49710	Conv	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEK	EQRWG	3		1131.174855	3390.501166	0.000451244	2	N	3	34
P49722	Conv	SPSGK	LVQIEYALAAVAGGAPSVGIK	AANGV	2		1014.080937	2026.146274	0.000451244	21	N	18	39
P49722	Conv	FLEKR	YNEDLELEDAIHTAILTLK	ESFEG	2		1101.070963	2200.126327	0.000451244	19	N	177	196
P49722	Conv	HRARK	LAQQYYLVYQEPIPTAQLVQR	VASVM	2		1261.176628	2520.337657	0.000637154	17	N	92	113
P49722	Conv	TFLEK	RYNEDLELEDAIHTAILTLK	ESFEG	3		786.4169459	2356.227438	0.000451244	21	N	176	196
P49722	Conv	-MAER	GYSFSLTTFSPSGK	LVQIE	2		739.8622532	1477.708906	0.000451244	11	N	4	18
P49722	Conv	LAQQY	YLVYQEPIPTAQLVQR	VASVM	2		959.5257975	1917.035995	0.000823681	1	N	97	113
P49722	Conv	VHRAR	KLAQQYYLVYQEPIPTAQLVQR	VASVM	2		1325.22411	2648.43262	0.001264573	9	N	91	113
P49813	Conv	NKVLK	TLNVESNFISGAGILR	LVEAL	2		845.9602904	1689.904981	0.000451244	8	N	255	271

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P49813	Conv	LEKYR	DLDEDEILGALTEEELR	TLENE	2		980.4738216	1958.932043	0.002813207	1	N	11	28
P49813	Conv	RELEK	YRDLDEDEILGALTEEELR	TLENE	2		1140.056042	2278.096483	0.001162105	1	N	9	28
P50247	Conv	LSGIR	GISEETTTGVHNLYK	MMSNG	2		824.9130058	1647.810412	0.000451244	11	N	151	166
P50247	Conv	HFLPK	KLDEAVAEAHLGK	LNVKL	3		460.9214251	1379.740875	0.002519933	1	N	388	401
P50247	Conv	VFAWK	GETDEEYLWCIEQTLHFK	DGPLN	3	C10:+57.021	766.6846611	2297.030583	0.000622848	3	N	103	121
P50396	Conv	AAQGK	YIAIASTTVETAEPEKEVEPALELLEPIDQK	FVAIS	3		1142.931304	3425.770512	0.000451244	34	N	348	379
P50396	Conv	RDVYR	KFDLGQDVIDFTGHALALYR	TDDYL	3		760.399338	2278.174614	0.000451244	18	N	173	193
P50396	Conv	LALYR	TDDYLDQPCLETINR	IKLYS	2	C9:+57.021	926.9230133	1851.830427	0.000451244	8	N	193	208
P50396	Conv	LHMDR	NPYYGGESSSITPLEELYK	RFQIL	2		1074.013114	2146.010628	0.000451244	18	N	35	54
P50396	Conv	RRFRK	FLVFVANFDENDPK	TFEGV	2		827.9097348	1653.80387	0.000451244	8	N	142	156
P50396	Conv	LHMDR	NPYYGGESSSITPLEELYKR	FQILE	2		1152.06367	2302.111739	0.002212458	1	N	35	55
P50396	Conv	VARCK	QLICDPSYIPDR	VQKAG	2	C4:+57.021	738.861499	1475.707398	0.0025889	2	N	278	290
P50396	Conv	DVYRK	FDLGQDVIDFTGHALALYR	TDDYL	3		717.701017	2150.079651	0.000451244	5	N	174	193
P50429	Conv	ARASG	ATQPPHVVFVLADDLGWNDLGFHGSVIR	TPHLD	4		765.8982342	3059.561737	0.000451244	3	N	41	69
P50429	Conv	GPPTK	TLWLFDINQDPEER	HDVSR	2		888.4341054	1774.852611	0.000451244	7	N	471	485
P50429	Conv	HPSPR	VELLHNIDQDFFDGLPCPG	KNMTP	2	C17:+57.021	1093.51507	2185.014539	0.001463592	1	N	389	408
P50431	Conv	LCQKR	ALQAYHLDPQCWGVNVQPYSGSPANFAVYTALVEPHGR	IMGLD	4	C11:+57.021	1054.01458	4212.027118	0.002145581	1	N	93	131
P50446	Conv	MDNNR	SLDLDSIIAEVK	AQYED	2		651.8617219	1301.707844	0.000451244	17	N	315	327
P50446	Conv	LMNVK	LALDVEIATYR	KLLEG	2		632.3513243	1262.687049	0.001591523	2	N	444	455
P50516	Conv	SKNLR	VGSHITGGDIYGIVNENSLIK	HKIML	2		1093.576747	2185.137894	0.000451244	12	N	142	163
P50516	Conv	PLRTK	AKEILQEEEDLAEIVQLVGK	ASLAE	3		752.0779302	2253.210391	0.000451244	8	N	478	498
P50516	Conv	RTKAK	EILQEEEDLAEIVQLVGK	ASLAE	2		1028.046957	2054.078314	0.001654178	1	N	480	498
P50516	Conv	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDKK	LAQRK	3		1272.99519	3815.96217	0.000451244	24	N	400	438
P50516	Conv	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDK	KLAQR	3		1230.296869	3687.867206	0.000823681	3	N	400	437
P50516	Conv	PVAAR	EASIYTGITLSEYFR	DMGYH	2		875.4388564	1748.862113	0.000451244	3	N	323	338
P50516	Conv	QSLSK	YSNSDVIIYVGCGER	GNEMS	2	C12:+57.021	866.4042593	1730.792919	0.000451244	9	N	265	280
P50516	Conv	YELVR	VGHSELVGEIIR	LEGDM	2		654.8676729	1307.719746	0.001329271	1	N	44	56
P50516	Conv	LEVAK	LIKDDFLQQNGYTPYDR	FCPFY	2		1043.516158	2085.016716	0.000823681	2	N	513	530
P50516	Conv	PPRNR	GSVTYIAPPGNYDASDVVLELEFEGVKEK	FSMVQ	3		1042.855958	3125.544475	0.002663018	1	N	173	202
P50518	Conv	IATKK	DVDVQIDQEAYLPEEIAGGVEIYNGDRK	IKVSN	3		1045.8426	3134.504401	0.000451244	5	N	161	189
P50518	Conv	KDTTR	YQVLLDGLVLQGLYQLLEPR	MIVRC	2		1165.660083	2329.304566	0.000451244	4	N	111	131
P50518	Conv	LKVLR	ARDDLITDLLNEAK	QRLSK	2		793.9233735	1585.831147	0.000451244	3	N	85	99
P50543	Conv	TQLSK	TEFLSFMNTELAAFTK	NQKDP	2		925.4561925	1848.896785	0.000451244	2	N	31	47
P50543	Conv	TETER	CIESLIAVFQK	YSGKD	2	C1:+39.994	645.8418211	1289.668042	0.000451244	1	N	7	18
P50543	Conv	DRMMK	KLDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C6:+57.021,C26:+57.021	1370.341958	4108.002474	0.000451244	9	N	60	96
P50543	Conv	RMMKK	LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C5:+57.021,C25:+57.021	1327.643637	3979.907511	0.000451244	10	N	61	96
P50580	Conv	EAALR	LVKPGNQNTQVTEAWNK	VAHSF	3		643.0064404	1925.995921	0.000451244	7	N	155	172
P50580	Conv	KEMKK	GIAFPTSISVNNCVCHFSPLK	SDQDY	2	C13:+57.021,C15:+57.021	1174.57999	2347.144379	0.000622848	4	N	72	93
P50580	Conv	NRVLR	SLVEASSSGVSVLSLCEK	GDAMI	2	C16:+57.021	926.472339	1850.929078	0.000451244	8	N	33	51
P50580	Conv	VECAK	HELLQPFNVLYEK	EGEFV	2		815.4359198	1628.85624	0.000451244	5	N	298	311
P50580	Conv	VECAK	HELLQPFNVLYEKEGEFVAQFK	FTVLL	3		889.1273954	2664.358786	0.000451244	4	N	298	320
P51125	Conv	PLLPK	ESQEQLAPLSDDFLLDALSQDFSSPANISSLEFEDAK	LSAAI	3		1352.974848	4055.901145	0.000451244	4	N	575	612
P51125	Conv	EETSK	SLSESELIGELSADFDR	STYQD	2		934.4501495	1866.884699	0.0025889	1	N	441	458
P51125	Conv	ESKTK	FQDVPSAGGESVAGGGTVATALDK	VVGKK	2		1117.550926	2233.086253	0.000622848	3	N	180	204
P51125	Conv	KEKKR	KVEEEVINDQALQALSDSLGTR	QPDPP	3		805.7507648	2414.228894	0.000451244	7	N	359	381
P51150	Conv	ETSAK	EAINVEQAFQTIAR	NALKQ	2		795.4182583	1588.820917	0.000451244	7	N	157	171
P51150	Conv	VAFYR	GADCCVLVFDVTAPNTFK	TLDSW	2	C4:+57.021,C5:+57.021	1007.474127	2012.932655	0.000451244	4	N	79	97
P51150	Conv	PNTFK	TLDSWRDEFLIQASPR	DPENF	3		645.330924	1932.969372	0.000451244	10	N	97	113
P51150	Conv	AGQER	FQSLGVAFYR	GADCC	2		594.3145448	1186.61349	0.001871652	1	N	69	79
P51174	Conv	EKAGK	QGLLGINIAEK	HGGIG	2		578.3407596	1154.665919	0.000662267	2	N	95	106
P51174	Conv	KMGMK	AQDTAELFFEDVR	LPANA	2		770.8680669	1539.720534	0.000451244	5	N	254	267
P51174	Conv	KMGMK	AQDTAELFFEDVRLPANALLGEENK	GFYYL	3		930.8035287	2789.387186	0.000451244	6	N	254	279
P51410	Conv	-MK	TILSNQTVDIPENVEITLK	GRTVI	2		1064.081331	2126.147062	0.000451244	6	N	2	21
P51437	Conv	GKAER	QLPEQCAFKEQGVVK	QCMGA	2	[0:-17.027,C6:+57.021	872.4404194	1742.865239	0.001463592	3	N	88	103
P51437	Conv	DTNLY	RLLDLDPEPQGDEDPDTPK	SVRFR	3		717.3469681	2149.017504	0.002296037	1	N	53	72
P51437	Conv	TNLYR	LLDLDPEPQGDEDPDTPK	SVRFR	2		997.4659966	1992.916393	0.000451244	36	N	54	72
P51437	Conv	DAVLR	AVDDFNQQSLDTNLYR	LLDLD	2		949.9481083	1897.880617	0.000451244	46	N	38	54
P51437	Conv	CMGAV	TLNPAADSFDISCNEPGAQPFR	FKKIS	2	C13:+57.021	1204.053079	2406.090558	0.001329271	1	N	109	131
P51437	Conv	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	C2:+57.021,C19:+57.021	1018.456733	3052.346798	0.00091018	3	N	103	131
P51437	Conv	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQP	FRFKK	2	C2:+57.021,M3:+15.995,C19:+57.021	1383.593937	2765.172273	0.00091018	3	N	103	129
P51859	Conv	PNKRK	GFSEGLWEIENNPTVK	ASGYQ	2		910.4472128	1818.878826	0.000451244	11	N	80	96
P51859	Conv	PKRPK	ESGDHEEEDKEIAALEGERPLPVEVEK	NSTPS	4		759.3681666	3033.441466	0.001162105	1	N	170	197
P51859	Conv	STANK	YQVFFFGTHETAFLGPK	DLFPY	2		994.9994156	1987.983231	0.0025889	1	N	44	61
P52480	Conv	PITAR	NTGIICTIGPASR	SVEML	2	C6:+57.021	680.3563838	1358.697168	0.000451244	31	N	43	56

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P52480	Conv	EASFK	CCSGAIIVLTK	SGRSA	2	C1:+57.021,C2:+57.021	611.3201927	1220.624785	0.000622848	13	N	422	433
P52480	Conv	EHMCR	LDIDSAPITAR	NTGII	2		586.3200242	1170.624448	0.000451244	19	N	32	43
P52480	Conv	QVKEK	GADFLVTEVENGGSLGSKK	GVNLP	2		954.489609	1906.963618	0.000451244	2	N	188	207
P52480	Conv	SLQVK	EKGADFLVTEVENGGSLGSK	KGVNL	2		1019.010906	2036.006211	0.000451244	16	N	186	206
P52480	Conv	QVKEK	GADFLVTEVENGGSLGSK	KGVNL	2		890.4421274	1778.868655	0.000451244	28	N	188	206
P52480	Conv	HLIAR	EAEAAIYHLQLFEELRR	LAPIT	3		696.7011284	2087.079985	0.000451244	18	N	383	400
P52480	Conv	EVGSK	IYVDDGLISLQVK	EKGAD	2		731.9117461	1461.807892	0.000451244	20	N	173	186
P52480	Conv	FEELR	RLAPITSDPTEAAAVGAVEASFK	CCSGA	2		1151.108411	2300.201223	0.000451244	6	N	399	422
P52480	Conv	AYMEK	CDENILWLDYK	NICKV	2	C1:+57.021	734.8427749	1467.66995	0.000451244	21	N	151	162
P52480	Conv	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	3		1015.868421	3044.581863	0.000451244	14	N	92	120
P52480	Conv	IKNVR	EATESFASDPILYRPVAV	ALDTK	2		983.0023522	1963.989104	0.000451244	21	N	92	110
P52480	Conv	IKNVR	EATESFASDPILYRPVAVALDTK	GPEIR	2		1247.147734	2492.279867	0.000451244	9	N	92	115
P52480	Conv	HLIAR	EAEAAIYHLQLFEELR	RLAPI	2		966.497237	1930.978874	0.000451244	4	N	383	399
P52480	Conv	PVLCK	DAVLNAWAEDVDLR	VNLAM	2		793.894616	1585.773632	0.000451244	32	N	475	489
P52480	Conv	EELRR	LAPITSDPTEAAAVGAVEASFK	CCSGA	2		1073.057856	2144.100112	0.000451244	37	N	400	422
P52480	Conv	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	3	C16:+57.021	1165.55235	3493.63365	0.000451244	12	N	342	376
P52480	Conv	AHLYR	GIFPVLCKDAVLNAWAEDVDLR	VNLAM	3	C7:+57.021	834.4337882	2500.277965	0.000451244	3	N	467	489
P52480	Conv	IQDLK	FGVEQDVDMVFASFIR	KAADV	2		930.4539841	1858.892368	0.000451244	6	N	230	246
P52480	Conv	MNVAR	LNFSHGTHEYHAETIK	NVREA	2		942.4559035	1882.896207	0.001839721	3	N	73	89
P52480	Conv	LGSKK	GVNLPGAAVDLPAVSEKDIQDLK	FGVEQ	2		1175.137169	2348.258738	0.000451244	18	N	207	230
P52480	Conv	SLGSK	KGVNLPGAAVDLPAVSEK	DIQDL	2		882.9968729	1763.978146	0.000451244	12	N	206	224
P52480	Conv	IMVAR	GDLGIEIPAEK	VFLAQ	2		571.3091251	1140.60265	0.000622848	24	N	294	305
P52480	Conv	RGFFK	KGDVVIVLTGWRPGSGFTN	TMRVV	2		1002.039603	2002.063607	0.000451244	3	N	504	523
P52480	Conv	LGSKK	GVNLPGAAVDLPAVSEK	DIQDL	2		818.9493913	1635.883183	0.000451244	4	N	207	224
P52480	Conv	GETAK	GDYPLEAVR	MQHLI	2		510.2619779	1018.508356	0.002884417	1	N	367	376
P52480	Conv	GSKIY	VDDGLISLQVK	EKGAD	2		593.8380498	1185.6605	0.000823681	2	N	175	186
P52480	Conv	SKKGV	NLPGAAVDLPAVSEKDIQDLK	FGVEQ	2		1097.09223	2192.16886	0.000698008	1	N	209	230
P52480	Conv	PRPTR	AEGSDVANAVLDGADCIMLSGETAK	GDYPL	2	C16:+57.021	1247.575727	2493.135854	0.000451244	4	N	342	367
P52480	Conv	GATLK	ITLDNAYMEKCDENILWLDYK	NICKV	3	M8:+15.995,C11:+57.021	888.4175039	2662.229112	0.000662267	1	N	141	162
P52480	Conv	RGFFK	KGDVVIVLTGWRPGSGFTNTMR	VVPVP	4	M21:+15.995	602.5697706	2406.247882	0.002145581	1	N	504	526
P52480	Conv	HEGVR	RFDEILEASDGIMVAR	GDLGI	3		607.9774937	1820.909081	0.000451244	9	N	278	294
P52480	Conv	IKNVR	EATESFASDPILYRPVAVA	LDTKG	2		1018.520909	2035.026218	0.000451244	9	N	92	111
P52480	Conv	IKNVR	EATESFASDPILYRPVAVAL	DTKGP	2		1075.062941	2148.110282	0.000622848	1	N	92	112
P52624	Conv	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGK	RVIRN	3	C24:+57.021	1267.996271	3800.965412	0.000451244	10	N	139	175
P52624	Conv	TLLDR	LQGDQINTPHDVLVEYQQRPQR	LVGHF	3		878.7848028	2633.331008	0.002296037	2	N	276	298
P54071	Conv	DVQLK	YFDLGLPNRDQTNDQVTIDSALATQK	YSVAV	3		975.1531091	2922.435927	0.000451244	4	N	80	106
P54071	Conv	LSNVK	LNEHFLNTTDFLDTIK	SNLDR	3		640.9954299	1919.96289	0.000451244	18	N	426	442
P54071	Conv	AYDGR	FKDIFQEIFDK	HYKTD	3		477.2507712	1428.728914	0.000622848	1	N	261	272
P54775	Conv	SRYKK	LQQELEFLEVQEEYIKDEQK	NLKKE	3		846.7590374	2537.253712	0.000451244	13	N	46	66
P54775	Conv	ILVEK	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	YKKLQ	3		1224.620012	3670.836635	0.000451244	20	N	10	43
P54775	Conv	FRLAK	ENAPAIIFIDEIDAIATK	RFDAQ	2		972.5203778	1943.025156	0.000622848	4	N	255	273
P54775	Conv	EEVKR	IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	ILSTI	3		1185.289937	3552.846411	0.000451244	27	N	81	114
P54775	Conv	KNLKK	EFLHAQEEVKR	IQSIP	3		462.5777698	1384.709909	0.001162105	1	N	70	81
P54775	Conv	TGLSF	LGPEPEDLEDLYSR	YKKLQ	2		816.891739	1631.767878	0.002080925	1	N	29	43
P54822	Conv	SANRR	ICLAEAFLTADTILNTLQNISEGLVVYPK	VIERR	3	C2:+57.021	1069.572463	3205.693988	0.000451244	10	N	338	367
P54822	Conv	LIILR	NAFDLLLPK	LARVI	2		515.8007389	1029.585878	0.000451244	12	N	125	134
P54822	Conv	HCCPK	AAGIIHLGATSCYVGDNTDLIILR	NAFDL	3	C12:+57.021	848.4480974	2542.320892	0.002981883	1	N	101	125
P54822	Conv	IERIR	ADAYFSPIHSQLEHLLDPSSFTGR	APQQV	3		896.7737923	2687.297977	0.001654178	1	N	428	452
P54823	Conv	RGPVK	ASAGPGGGGTQPQPQLNQLK	NTSTI	2		953.4930173	1904.970435	0.000870037	2	N	26	46
P54823	Conv	LPKNR	QILLYSATFPLSVQK	FMNSH	2		854.4881524	1706.960705	0.000451244	12	N	271	286
P54923	Conv	YLELR	GILDGNSAPVFPQPFGVK	ERDQF	2		921.9915905	1841.967581	0.000823681	1	N	239	257
P55264	Conv	AENNR	VFTLNLSAPFISQFFK	EALMD	2		930.009252	1858.002904	0.000451244	8	N	207	223
P55264	Conv	TAFPV	LDQNQEEIIDTNGAGDAFVGGFLSQLVSDKPLTECIR	AGHYA	3	C35:+57.021	1350.663908	4048.968325	0.002884417	2	N	300	337
P55264	Conv	ILKRK	AADAHVDAHYYEQNEQPTGTCAACITGGNR	SLVAN	4	C21:+57.021,C24:+57.021	820.1062897	3276.393959	0.000698008	2	N	118	148
P56391	Conv	QNQTK	NCWQNYLDFHR	CEKAM	3	C2:+57.021	518.2302215	1551.667264	0.001329271	1	N	28	39
P56391	Conv	RRVYK	SLCPVSWVSAWDDR	IAEGT	2	C3:+57.021	839.3884123	1676.761225	0.000451244	1	N	62	76
P56399	Conv	DKLEK	IFQNAPTDPTQDFSTQVAK	LGHGL	2		1054.518898	2107.022196	0.000451244	10	N	360	379
P56399	Conv	DMNQR	IGEWELIQESGVPLKPLFGPGYTGIR	NLGNS	3		952.8485212	2855.522163	0.000451244	13	N	303	329
P56399	Conv	YTGIR	NLGNSCYLNSVVQVLFSIPDFQR	KYVDK	2	C6:+57.021	1335.671153	2669.326706	0.000451244	5	N	329	352
P56399	Conv	PELVR	AQVPFSSCLEAYGAPEQVDDFWSTALQAK	SVAVK	3	C8:+57.021	1072.504888	3214.491265	0.000451244	8	N	524	553
P56399	Conv	IQIKK	FTFGLDWVPK	KLDVS	2		605.3192958	1208.622992	0.001763695	1	N	575	585
P56399	Conv	VKTTR	FASFPDYLVIQIK	KFTFG	2		770.9246565	1539.833713	0.001329271	1	N	561	574
P56399	Conv	ISQLR	GTGLQPGEEELPDIAPPLVTPDEPK	GSLGF	2		1300.161038	2598.306476	0.000622848	3	N	603	628
P56399	Conv	KCDMR	ENLWLNLTDGSILCGR	RYFDG	2	C14:+57.021	930.9675581	1859.919516	0.000451244	8	N	205	221
P56399	Conv	TQVAK	LGHGLLSGEYSKPALESGDGEQVPEQK	EVQDG	3		942.4704381	2824.387914	0.000823681	2	N	379	406

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P56399	Conv	FSTNR	QQDAQEFFLHLINMVER	NCRSS	3		706.6866023	2117.036407	0.002884417	1	N	432	449
P56399	Conv	-MAE	LSEEALLSVLPTIR	VPKAG	2		770.9514027	1539.887205	0.001943752	1	N	3	17
P56480	Conv	VRGQK	VLDSGAPIKIPVGPETLGR	IMNVI	2		960.0521795	1918.088759	0.000823681	1	N	124	143
P56480	Conv	DNIFR	FTQAGSEVSALLGR	IPSAV	2		718.3811445	1434.746689	0.000451244	5	N	310	324
P56480	Conv	TVLSR	AIAELGIYPAVDPLDSTSR	IMDPN	2		994.5209092	1987.026218	0.000451244	17	N	387	406
P56480	Conv	GARAR	VALTGLTVAEYFR	DQEGQ	2		720.3988059	1438.782012	0.000451244	11	N	281	294
P56480	Conv	ITTTK	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1281.665732	3841.973797	0.000451244	6	N	350	387
P56480	Conv	TTTKK	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1238.967411	3713.878834	0.000451244	10	N	351	387
P56480	Conv	AGVGK	TVLIMELINNVAK	AHGGY	2		729.423967	1456.832334	0.001871652	1	N	212	225
P56480	Conv	AEYFR	DQEGQDVLLFIDNIFR	FTQAG	2		961.4868693	1920.958139	0.000451244	18	N	294	310
P56959	Conv	RETGK	LKGEATVSFDDPPSAK	AAIDW	3		554.6180709	1660.830813	0.001264573	1	N	325	341
P56959	Conv	PPSAK	AAIDWFDGKEFSGNPIK	VSFAT	2		947.9708551	1893.92611	0.000451244	6	N	341	358
P56959	Conv	DQGSR	HDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	3		1195.880443	3584.617928	0.000451244	9	N	267	299
P57716	Conv	RLDSR	SFFWNVAPGAESAVASFVTQLAAAEALHK	APDVT	3		1007.182451	3018.523954	0.001162105	2	N	284	313
P57780	Conv	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	2		1102.014314	2202.013028	0.000451244	7	N	772	792
P57780	Conv	EKTEK	QLETIDQLHLEYAKR	AAPFN	3		619.6675361	1855.979208	0.000451244	3	N	522	537
P57780	Conv	YCIAR	MAPYQGPDAAPGALDYK	SFSTA	2		882.9172345	1763.818869	0.000622848	5	N	883	900
P57780	Conv	SNHIK	LSGSNPYTTVTPQIINSK	WEKVQ	2		960.5078018	1919.000004	0.000451244	39	N	605	623
P57780	Conv	YDKLR	KDDPVTNLNNAFEVAEK	YLDIP	2		952.4739589	1902.932318	0.000451244	3	N	217	234
P57780	Conv	DFMSR	ETTDTDTADQVIASFK	VLAGD	2		871.410493	1740.805386	0.000451244	15	N	838	854
P57780	Conv	KQYER	SIVDYKPSLDLLEQQHQLIQEALIFDNK	HTNYT	3		1099.917552	3296.729256	0.000451244	17	N	696	724
P57780	Conv	AHQDR	VEQIAAIAQELNELDYYDSHNVNTR	CQKIC	3		969.137459	2904.388977	0.000451244	20	N	470	495
P57780	Conv	LDIPK	MLDAEDIVNTARPDEK	AIMTY	3		606.2968919	1815.867276	0.000637154	6	N	240	256
P57780	Conv	SKGVK	LVSIGAEEIVDGNAK	MTLGM	2		757.9071921	1513.798784	0.000698008	1	N	126	141
P57780	Conv	TRCQK	ICDQWDNLGSLTHSR	REALE	3	C2:+57.021	601.2814216	1800.820865	0.000451244	8	N	498	513
P57780	Conv	EKTEK	QLETIDQLHLEYAK	RAAPF	2		850.9468486	1699.878097	0.000451244	12	N	522	536
P57780	Conv	HISWK	DGLAFNALIHR	HRPEL	2		613.8361757	1225.656751	0.000451244	11	N	194	205
P57780	Conv	IASFK	VLAGDKNFITAEELR	RELPP	2		838.4548408	1674.894082	0.000451244	4	N	854	869
P57780	Conv	SHLRK	AGTQIENIDEDFRDGLK	LMLLL	2		960.9690407	1919.922481	0.000451244	8	N	67	84
P57780	Conv	EHLRR	QFASQANMVGPWIQTK	MEEIG	2		903.4543185	1804.893037	0.000622848	1	N	653	669
P57780	Conv	DKLRK	DDPVTNLNNAFEVAEK	YLDIP	2		888.4264774	1774.837355	0.00091018	1	N	218	234
P57780	Conv	PEEFK	ACLISLGYDVENDRQGDAEFNR	IMSVV	3	C2:+57.021	848.0594497	2541.154949	0.000451244	2	N	792	814
P57780	Conv	PSEGR	MVSDINNGWQHLEQAEKGYEEWLLNEIR	RLERL	4	M1:+15.995	855.1602095	3416.609638	0.001264573	1	N	379	407
P57780	Conv	MFIVH	TIEEIEGLISAHDQFK	STLPD	2		915.4681452	1828.92069	0.000451244	4	N	559	575
P57784	Conv	NRICR	IGEGLDQALPCLTELILTNNSLVELGDLDPLASLK	SLTYL	3	C11:+57.021	1245.664298	3733.969495	0.000823681	9	N	78	113
P57784	Conv	-MVK	LTAELIEQAAQYTNAVR	DRELD	2		946.0001439	1889.984688	0.001943752	1	N	3	20
P58058	Conv	RQEIR	HGDSISITTSCYPLPSICVCDPVSDWFESLAQCLHWNVR	KKQAH	4	C11:+57.021,C18:+57.021,C20:+57.021,C33:+57.021	1152.52769	4606.079558	0.000823681	3	N	387	426
P58058	Conv	YVEKK	VLEDPAIVSDENFGPVK	KKFCT	2		914.9705208	1827.925442	0.000622848	13	N	142	159
P58058	Conv	PICPH	SLSFRPIVVPAGVELK	IMLSP	3		571.3422127	1711.003238	0.000870037	3	N	347	363
P58058	Conv	SITTS	CYPLPSICVCDPVSDWFESLAQCLHWNVR	KKQAH	3	C1:+57.021,C8:+57.021,C10:+57.021,C23:+57.021	1203.545356	3607.612669	0.002727428	1	N	397	426
P58252	Conv	VVSYR	ETVSEESNVLCLSK	SPNKH	2	C11:+57.021	797.8853681	1593.755136	0.000451244	24	N	580	594
P58252	Conv	KARAR	YLAEKYEWDVAEAR	KIWCF	2		871.9233735	1741.831147	0.000451244	7	N	633	647
P58252	Conv	PTARR	CLYASVLTAQPR	LMEPI	2	C1:+57.021	689.861302	1377.707004	0.000451244	2	N	727	739
P58252	Conv	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	3		715.0313143	2142.070543	0.001329271	2	N	605	625
P58252	Conv	MFVVK	AYLPVNESFGFTADLR	SNTGG	2		900.4522982	1798.888996	0.000451244	24	N	785	801
P58252	Conv	VAEAR	KIWCFGPDGTGPNILTDITK	GVQYL	2	C4:+57.021	1117.070012	2232.124424	0.000451244	15	N	647	667
P58252	Conv	TADLR	SNTGGQAFPQCVFDHWQILPGDPFDNSSRPSQVVAETR	KRKGL	3	C11:+57.021	1415.666646	4243.976539	0.000451244	10	N	801	839
P58252	Conv	KKLPR	TFCQLILDPIFK	VFDAI	2	C3:+57.021	747.9051782	1493.794756	0.000451244	30	N	287	299
P58252	Conv	AEARK	IWCFGPDGTGPNILTDITK	GVQYL	2	C3:+57.021	1053.02253	2104.029461	0.000451244	15	N	648	667
P58252	Conv	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	2		1177.113497	2352.211394	0.000451244	16	N	667	688
P58252	Conv	NKMDR	ALLELQLEPEELYQTFQR	IVENV	2		1110.581498	2219.147396	0.000451244	18	N	162	180
P58252	Conv	LMMGR	YVEPIEDVPCGNIVGLVGVDQFLVK	TGTIT	2	C10:+57.021	1380.220144	2758.424689	0.000451244	24	N	456	481
P58252	Conv	RKGLK	EGIPALDNFLDKL	-	2		722.888271	1443.760942	0.000451244	14	N	845	858
P58252	Conv	IKQSK	DGSGFLINLIDSPGHVDFSSEVTAALR	VTDGA	2		1409.206843	2816.398085	0.000451244	7	N	93	120
P58252	Conv	CITIK	STAISLFYELSENDLNFIK	QSKDG	2		1102.560231	2203.104863	0.000451244	27	N	71	90
P58252	Conv	TAQPR	LMEPIYLVEIQCPEQVVGGIYGVLNR	KRGHV	3	C12:+57.021	997.1894073	2988.544822	0.000451244	11	N	739	765
P58252	Conv	VDHGK	STLTDSLVCK	AGIIA	2	C9:+57.021	562.2871041	1122.558608	0.000451244	2	N	32	42
P58252	Conv	TAALR	VTDGALVVVDCVSGVCVQTETVLR	QAIAE	2	C11:+57.021,C16:+57.021	1288.656623	2575.297645	0.000451244	14	N	120	144
P58252	Conv	VPCGN	IVGLVGVDQFLVK	TGTIT	2		693.9219169	1385.828234	0.001162105	1	N	468	481
P58252	Conv	AVMRR	WLPAGDALLQMITIHLPSPVTAQK	YRCEL	3		867.4810045	2599.419614	0.000622848	4	N	342	366
P58389	Conv	TWYAK	LDQEAENLVATVVPTHLAAAVPEVAVYLK	EAVGN	3		1020.892567	3059.6543	0.000451244	19	N	111	140
P59108	Conv	ETLAK	AVLAELPQQVVQYFK	HKNLP	2		866.9857768	1731.955954	0.000451244	6	N	521	536
P59999	Conv	VRSSK	ELLLQPVTISR	NEKEK	2		634.8827917	1267.749983	0.001162105	11	N	44	55

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P59999	Conv	LSAVR	ATLQAALCLENFSSQVVER	HNKPE	2	C8:+57.021	1068.541619	2135.067637	0.000451244	84	N	13	32
P60122	Conv	TYLHR	ALESSIAPIVIFASNR	GNCVI	3		563.3179557	1686.930467	0.000451244	5	N	317	333
P60122	Conv	IIKIR	AQTEGINISEEALNHLGEIGTK	TTLRY	3		775.3963219	2323.165566	0.002981883	1	N	378	400
P60122	Conv	KTTLR	YSVQLLTPANLLAK	INGKD	2		765.948663	1529.881726	0.001395409	1	N	404	418
P60122	Conv	PGTGK	TALALAIAQELGSK	VPFCP	2		693.4040883	1384.792577	0.000451244	8	N	76	90
P60229	Conv	YRYAK	FQYECGNYSGAAEYLYFFR	VLVPA	2	C5:+57.021	1193.017976	2384.020353	0.000622848	2	N	136	155
P60229	Conv	HFLDR	HLVFPLLEFLSVK	EIYNE	3		514.641711	1540.901733	0.002727428	1	N	16	29
P60335	Conv	NSTER	AITIAGVPQSVTECVK	QICLV	2	C14:+57.021	836.9508454	1671.886091	0.000451244	2	N	144	160
P60335	Conv	NCPER	IITLTGPTNAIFK	AFAMI	2		694.9115491	1387.807498	0.0025889	1	N	57	70
P60335	Conv	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	2		1089.100389	2176.185179	0.001329271	1	N	325	346
P60670	Conv	SVGLK	AFGAPNVVEDEIDQYLSK	QDGKI	2		997.9894418	1993.963284	0.000451244	5	N	98	116
P60710	Conv	MWISK	QEYDESGPSIVHR	KCF-	2		758.8554908	1515.695382	0.000451244	12	N	359	372
P60710	Conv	ILTER	GYSFTTTAER	EIVRD	2		566.7676244	1131.519649	0.000451244	26	N	196	206
P60710	Conv	ILTER	GYSFTTTAEREIVR	DIKEK	2		815.4157156	1628.815831	0.000662267	7	N	196	210
P60710	Conv	YNELR	VAPEEHPVLLTEAPLNPK	ANREK	2		977.5363622	1953.057124	0.000451244	62	N	95	113
P60710	Conv	ELRVA	PEEHPVLLTEAPLNPK	ANREK	2		892.4835983	1782.951597	0.000451244	51	N	97	113
P60710	Conv	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	2		1108.039141	2214.062681	0.000451244	52	N	291	312
P60710	Conv	IGNER	FRCPEALFQPSFLGMESCGIHETTF	NSIMK	3	C3:+57.021,C18:+57.021	987.7840097	2960.328629	0.000451244	10	N	254	279
P60710	Conv	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	2	C4:+57.021	1404.159624	2806.303648	0.000451244	6	N	213	238
P60710	Conv	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	2	C2:+57.021	1275.590846	2549.166092	0.000451244	400	N	215	238
P60710	Conv	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	KCF-	4		1025.761538	4099.014951	0.000622848	3	N	336	372
P60710	Conv	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3		1085.208517	3252.60215	0.000451244	7	N	118	147
P60710	Conv	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	2		1172.086622	2342.157645	0.000451244	8	N	290	312
P60710	Conv	QQMWI	SKQEYDESGPSIVHR	KCF-	3		577.9485911	1730.822373	0.001654178	1	N	357	372
P60710	Conv	FYNEL	RVAPEEHPVLLTEAPLNPK	ANREK	2		1055.586918	2109.158236	0.000823681	1	N	94	113
P60710	Conv	YNELR	VAPEEHPVLL	TEAPL	2		552.3089281	1102.602256	0.001463592	3	N	95	105
P60710	Conv	RKDLY	ANTVLSGGTTMYPGIADR	MQKEI	2		912.4519728	1822.888346	0.000451244	1	N	294	312
P60710	Conv	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,C16:+57.021	1077.825658	3230.453573	0.000451244	6	N	256	284
P60710	Conv	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	2	C1:+39.994,M13:+15.995,C16:+57.021	1329.071352	2656.127104	0.001943752	1	N	256	279
P60710	Conv	WISKQ	EYDESGPSIVHR	KCF-	2		694.826202	1387.636804	0.002296037	1	N	360	372
P60710	Conv	KLCYV	ALDFEQEMATAASSSSLEK	SYELP	2		1007.96785	2013.920099	0.000451244	3	N	219	238
P60710	Conv	EKLCY	VALDFEQEMATAASSSSLEK	SYELP	2	M9:+15.995	1065.499557	2128.983513	0.000451244	3	N	218	238
P60710	Conv	FQQMW	ISKQEYDESGPSIVHR	KCF-	3		615.6432791	1843.906437	0.000451244	2	N	356	372
P60710	Conv	YNELR	VAPEEHPVLLTEAPLN	PKANR	2		864.9624987	1727.909397	0.001463592	3	N	95	111
P60710	Conv	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C3:+57.021,C18:+57.021	1178.882166	3533.623098	0.001329271	1	N	254	284
P60710	Conv	CYVAL	DFEQEMATAASSSSLEK	SYELP	2		915.9072607	1829.798921	0.000451244	3	N	221	238
P60710	Conv	DLYAN	TVLSGGTTMYPGIADR	MQKEI	2		819.9119521	1637.808304	0.00307782	1	N	296	312
P60766	Conv	HHCPK	TPFLLVGTQIDLRDDPSTIEK	LAKNK	2		1179.631719	2357.247839	0.000451244	8	N	107	128
P60766	Conv	QKGLK	NVFDEAILAALEPPEPK	KSRRC	2		926.9887135	1851.961827	0.000451244	12	N	166	183
P60766	Conv	ALTQK	GLKNVFDEAILAALEPPEPK	KSRRC	3		717.7285727	2150.162318	0.002212458	1	N	163	183
P60766	Conv	EDYDR	LRPLSYPQTDVFLVCFSVVSPSSFENVK	EKWVP	3	C15:+57.021	1072.553402	3214.636807	0.000622848	5	N	66	94
P60766	Conv	GAVGK	TCLLISYTTNKFPSEYVPTVF	DNYAV	2	C2:+57.021	1240.624817	2479.234034	0.002727428	1	N	16	37
P60766	Conv	HHCPK	TPFLLVGTQIDLR	DDPST	2		736.9277305	1471.839861	0.000451244	3	N	107	120
P60766	Conv	AVTVM	IGGEPYTLGLFDTAGQEDYDR	LRPLS	2		1159.035109	2316.054618	0.000451244	2	N	45	66
P60843	Conv	SGTGK	TATFAISILQQIELDLK	ATQAL	2		952.5411133	1903.066627	0.000451244	11	N	82	99
P60843	Conv	LPCIK	GYDVIAQAQSGTGK	TATFA	2		697.8496771	1393.683754	0.000451244	4	N	68	82
P60843	Conv	EMLSR	GFKDQIYDIFQK	LNSNT	2		751.3884382	1500.761276	0.001395409	1	N	190	202
P60843	Conv	DLLAR	GIDVQQVSLVINYDLPTNR	ENYIH	2		1072.571465	2143.127329	0.000451244	10	N	334	353
P61022	Conv	SIADR	TIQEADQDGDSAISFTEFVK	VLEKV	2		1101.016385	2200.01717	0.002080925	1	N	158	178
P61079	Conv	LTISK	VLLSICSLLCDPNPDDPLVPEIAR	IYKTD	2	C6:+57.021,C10:+57.021	1353.695748	2705.375896	0.000451244	11	N	101	125
P61079	Conv	AFTTR	IYHPNINSNGSICLDILR	SQWSP	3	C13:+57.021	700.3619641	2098.062492	0.002019181	1	N	72	90
P61089	Conv	ALQIR	TVLLSIQALLSAPNPDDPLANDVAEQWK	TNEAQ	3		1006.864788	3017.570964	0.000451244	2	N	102	130
P61089	Conv	ESNAR	YFHVVIAGPQDSPFEGGTFK	LELFL	3		732.697384	2195.068752	0.000451244	10	N	33	53
P61161	Conv	MIKEK	LCYVGYNIEQEQK	LALET	2	C2:+57.021	822.3906206	1642.765641	0.000451244	49	N	219	232
P61161	Conv	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	3	C1:+39.994	852.1058556	2553.294167	0.0025889	1	N	19	42
P61161	Conv	EQEQK	LALETTVLVESYTLPDGR	IIKVG	2		989.0311097	1976.046619	0.000451244	37	N	232	250
P61161	Conv	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		1313.349856	3937.026167	0.000451244	98	N	258	294
P61161	Conv	LLLLR	GYAFNHSADFETVR	MIKEK	2		807.3713081	1612.727016	0.000451244	28	N	200	214
P61161	Conv	DSQGR	KVVVCDNGTGFVK	CGYAG	2	C5:+57.021	711.8744094	1421.733219	0.001229886	2	N	6	19
P61161	Conv	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	C1:+39.994	1037.993882	2073.972164	0.000823681	3	N	19	38
P61161	Conv	LFQPH	LINVEGVGVAELLFNTIQAADIDTR	SEFYK	2		1336.219222	2670.422843	0.000451244	11	N	269	294
P61161	Conv	SQGRK	VVVCDNGTGFVK	CGYAG	2	C4:+57.021	647.8269278	1293.638256	0.000451244	3	N	7	19
P61161	Conv	VRMIK	EKLCYVGYNIEQEQK	LALET	2	C4:+57.021	950.9593988	1899.903198	0.000451244	12	N	217	232
P61161	Conv	SEFYK	HIVLSGGSTMYPGLPSR	LEREL	2	M10:+15.995	894.4596435	1786.903687	0.000451244	10	N	299	316

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P61161	Conv	VGGER	FEAPEALFQPHLINVEGVGVAELL	FNTIQ	2		1296.689569	2591.363537	0.001871652	1	N	258	282
P61161	Conv	WDDMK	HLWDYTFGPEK	LNIDT	2		696.8332987	1391.650997	0.000622848	11	N	86	97
P61161	Conv	RSTTK	VGNIEIKDLMVGDEASELR	SMLEV	3		696.6934226	2087.056868	0.002519933	1	N	46	65
P61161	Conv	HICPV	YEGFSLPHLTR	RLDIA	3		440.5634606	1318.666982	0.001591523	1	N	169	180
P61161	Conv	GVGVA	ELLFNTIQAADIDTR	SEFYK	2		860.4497555	1718.883911	0.000622848	4	N	279	294
P61161	Conv	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAA	DIDTR	3		1113.254276	3336.739427	0.001763695	1	N	258	289
P61164	Conv	MDLRR	TLFSNIVLSGGSTLFK	GFGDR	2		842.4699596	1682.924319	0.000451244	14	N	292	308
P61164	Conv	APQER	LYSTWIGGSILASLDTFKK	MWVSK	3		700.7178965	2099.13029	0.000979378	9	N	336	355
P61164	Conv	LETEK	AQYYLPDGSTIEIGPSR	FRAPE	2		933.9657697	1865.915939	0.000451244	10	N	238	255
P61164	Conv	APQER	LYSTWIGGSILASLDTFK	KMWVS	2		986.5254632	1971.035326	0.002453667	1	N	336	354
P61164	Conv	AIKER	ACYLSINPQKDETLETEK	AQYYL	2	C2:+57.021	1070.017642	2138.019684	0.000622848	2	N	220	238
P61164	Conv	YVYSK	DQLQTFSEEHPVLLTEAPLNPR	KNRER	2		1267.648432	2533.281264	0.000451244	2	N	96	118
P61202	Conv	PFISK	ELNIDVADVESLLVQCILDNTIHGR	IDQVN	3	C16:+57.021	946.1555308	2835.443193	0.000823681	1	N	376	401
P61202	Conv	RGGAR	YTALDKWTNQLNSLNQAVVSK	LA-	3		798.4206903	2392.238671	0.000823681	1	N	420	441
P61327	Conv	VQDLK	CLVFSLIGLHFK	IKPI-	3	C1:+57.021	478.6043371	1432.789611	0.000735798	3	N	130	142
P61327	Conv	EELKR	IIDDSEITKEDDALWPPPDR	VGRQE	2		1163.066409	2324.117218	0.000451244	1	N	62	82
P61965	Conv	SPNGK	YILAATLDNTLK	LWDYS	2		668.3800818	1334.744564	0.000698008	1	N	227	239
P61965	Conv	ISGHK	LGISDVAWSSDSNLLVSASDDKTLK	IWDVS	3		874.4488629	2620.323189	0.002212458	1	N	87	112
P61979	Conv	VECIK	IILDLISESPIKGR	AQPYD	3		518.6474133	1552.91884	0.001329271	1	N	207	221
P61979	Conv	YAGGR	GSYGDLGGPIITTQVTIPK	DLAGS	2		959.020545	1916.02549	0.000451244	12	N	377	396
P61979	Conv	VECIK	IILDLISESPIK	GRAQP	2		670.9059325	1339.796265	0.000451244	16	N	207	219
P61979	Conv	GSEDR	IITITGTQDQIQNAQYLLQNSVK	QYSGK	2		1295.198289	2588.380978	0.000451244	12	N	433	456
P61979	Conv	GASIK	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	QYSGK	3		1277.320513	3828.93814	0.000451244	5	N	422	456
P61979	Conv	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	3	C29:+57.021	1352.34915	4054.024049	0.000451244	18	N	103	139
P61979	Conv	SGPER	ILSISADIETIGEILK	KIIPT	2		857.9960072	1713.976414	0.002019181	1	N	86	102
P61979	Conv	SGPER	ILSISADIETIGEILKK	IIPTL	3		615.0315925	1842.071378	0.001763695	1	N	86	103
P61982	Conv	AAAMK	NVTELNEPLSNEER	NLLSV	2		822.3977199	1642.77984	0.000451244	28	N	28	42
P61982	Conv	THPIR	LGLALNYSVFYYEIQNAPEQACHLAK	TAFDD	3	C22:+57.021	1004.836021	3011.484663	0.000451244	18	N	172	198
P61982	Conv	EKIEK	ELEAVCQDVLSLLDNYLIK	NCSET	2	C6:+57.021	1118.082785	2234.14997	0.000451244	16	N	91	110
P61982	Conv	CHLAK	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1101.210184	3300.607153	0.000451244	12	N	198	227
P61982	Conv	CHLAK	TAFDDAIAELDTLNEDSYK	DSTLI	2		1065.989836	2129.964072	0.000451244	16	N	198	217
P61982	Conv	AYREK	IEKELEAVCQDVLSLLDNYLIK	NCSET	3	C9:+57.021	869.1316635	2604.371591	0.000451244	3	N	88	110
P61982	Conv	MQLLR	DNLTLWTSDQQDDDGGEGNN	-	2		1097.444312	2192.873025	0.000451244	3	N	227	247
P62082	Conv	GGGRK	AIIIFVPVPQLK	SFQKI	2		669.4319204	1336.848241	0.000451244	4	N	58	70
P62137	Conv	YDLLR	LFEYGGFPPESNYLFLGDYVDR	GKQSL	2		1299.613527	2597.211453	0.002519933	2	N	74	96
P62137	Conv	LLAYK	IRYPENFFLLR	GNHEC	3		489.942272	1466.803416	0.000451244	9	N	111	122
P62137	Conv	EAPLK	ICGDIHGQYYDLLR	LFEYG	3	C2:+57.021	574.9474913	1721.819074	0.000735798	2	N	60	74
P62141	Conv	TDLLR	LFEYGGFPPEANYLFLGDYVDR	GKQSL	2		1291.616069	2581.216539	0.000451244	6	N	73	95
P62141	Conv	LLAYK	IKYPENFFLLR	GNHEC	3		480.6068893	1438.797268	0.000451244	13	N	110	121
P62196	Conv	NAKVR	LLREELQLLQEQGSYVGEVVR	AMDKK	3		820.1153784	2457.322735	0.000451244	14	N	57	78
P62196	Conv	VRLLR	EELQLLQEQGSYVGEVVR	AMDKK	2		1038.534548	2075.053496	0.000622848	2	N	60	78
P62196	Conv	IKEIK	EVIELPVKHPELFEALGIAQPK	GVLLY	3		819.7970981	2456.367894	0.001352548	2	N	162	184
P62196	Conv	HPEGK	FVVDVDKNIDINDVTPNCR	VALRN	2	C18:+57.021	1117.049808	2232.084016	0.002981883	1	N	94	113
P62204	Conv	REAFR	VFDKDGNGYISAAELR	HVMTN	2		877.9395549	1753.86351	0.000451244	55	N	91	107
P62204	Conv	IAEFK	EAFSLFDKDGDGTITTK	ELGTV	2		922.9497853	1843.883971	0.000451244	43	N	14	31
P62204	Conv	ARKMK	DTDSEEEIREAFR	VFDKD	3		532.9099135	1595.70634	0.002212458	1	N	78	91
P62204	Conv	DEMIR	EADIDGDGQVNYEEFVQMMTAK	-	2	M18:+15.995,M19:+15.995	1261.539128	2521.062655	0.002212458	1	N	127	149
P62259	Conv	ETELK	LICCDILDVLDKHLIPAANTGESK	VFYYK	2	C3:+57.021,C4:+57.021	1348.193372	2694.371145	0.000698008	2	N	94	118
P62259	Conv	CRLAK	AAFDDAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1086.874913	3257.601339	0.000451244	16	N	196	225
P62259	Conv	CRLAK	AAFDDAIAELDTLSEESYK	DSTLI	2		1044.486929	2086.958258	0.000451244	19	N	196	215
P62259	Conv	ETELK	LICCDILDVLDK	HLIPA	2	C3:+57.021,C4:+57.021	738.8755291	1475.735458	0.000451244	13	N	94	106
P62259	Conv	MQLLR	DNLTLWTSDMQGDGEEQNKEALQDVEDENQ	-	3	M10:+15.995	1156.494177	3466.45913	0.000451244	7	N	225	255
P62259	Conv	LVAYK	AASDIAMTELPPTHPIR	LGLAL	2	M7:+15.995	918.4702082	1834.924816	0.000622848	1	N	153	170
P62315	Conv	KMTLK	NREPVQLETLSIR	GNNIR	3		518.9586504	1553.852551	0.001943752	1	N	48	61
P62315	Conv	GNNIR	YFILPDSLPLDTLLVDVEPK	VKSKK	2		1144.12775	2286.2399	0.000451244	14	N	66	86
P62315	Conv	RYFIL	PDSLPLDTLLVDVEPK	VKSKK	2		875.9778145	1749.940029	0.000622848	2	N	70	86
P62317	Conv	ELQKR	EEEEFNTGPLSVLTQSVK	NNTQV	2		1004.000007	2005.984413	0.000451244	17	N	19	37
P62317	Conv	EELQK	REEEEFNTGPLSVLTQSVK	NNTQV	2		1082.050562	2162.085524	0.000451244	3	N	18	37
P62320	Conv	GVPIK	VLHEAEGHIVTCETNTGEVYR	GKLIE	2	C12:+57.021	1207.574178	2413.132757	0.000451244	21	N	8	29
P62320	Conv	YRDGR	VAQLEQVYIR	GSKIR	2		609.8462091	1217.676818	0.002374549	2	N	54	64
P62331	Conv	DREMR	DAIILIFANK	QDLPD	2		559.3349459	1116.654292	0.001395409	4	N	113	123
P62334	Conv	ENDLK	ALQSVGQIVGEVLK	QLTEE	2		720.9251879	1439.834776	0.000451244	11	N	48	62
P62334	Conv	IRELR	EVIELPLTNPELFQR	VGIIP	2		899.4914234	1796.967247	0.000622848	2	N	146	161
P62482	Conv	AIAER	LGCTLPQLAIAWCLR	NEGVS	2	C3:+57.021,C13:+57.021	886.4709938	1770.926388	0.001162105	4	N	298	313
P62702	Conv	TGPHK	LRECLPLIIFLR	NRLKY	3	C4:+57.021	514.9781745	1541.911124	0.002374549	2	N	37	49

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62715	Conv	GISPR	GAGYTFGQDISETFNHANGLTLVSR	AHQLV	3		885.7652968	2654.272491	0.000451244	9	N	214	239
P62715	Conv	WCHDR	NVVTIFSAPNYCYR	CGNQA	2	C12:+57.021	852.4144301	1702.81326	0.000451244	8	N	254	268
P62715	Conv	DDTLK	YSFLQFDPAPR	RGEPH	2		670.8358414	1339.656083	0.000451244	1	N	283	294
P62715	Conv	ANVWK	YFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIR	ALDRL	4	C21:+57.021	1056.534813	4222.108054	0.001871652	2	N	144	181
P62715	Conv	NHESR	QITQVYGFYDECLR	KYGNA	2	C12:+57.021	896.4224521	1790.829304	0.000851441	2	N	121	135
P62774	Conv	DKTVK	GPDGLTALEATDNQAIK	ALLQ-	2		857.4368451	1712.85809	0.000622848	6	N	97	114
P62774	Conv	LEGGR	KPLHYAADCGQLEILEFLLLK	GADIN	3	C9:+57.021	824.4507792	2470.328938	0.000698008	1	N	36	57
P62806	Conv	RKVLR	DNIQGITKPAIR	RLARR	2		663.3809475	1324.746295	0.000451244	75	N	24	36
P62806	Conv	KRKTV	TAMDVVYALKR	QGRTL	2		633.8478951	1265.68019	0.000451244	5	N	82	93
P62806	Conv	GGVKR	ISGLIYEETRGVLK	VFLEN	2		789.4490272	1576.882454	0.000451244	8	N	46	60
P62806	Conv	VLKVF	LENVIRDAVTYTEHAK	RKTVT	2		929.9870365	1857.958473	0.000451244	4	N	62	78
P62806	Conv	RGVLK	VFLENVIR	DAVTY	2		495.293081	988.5705621	0.000451244	651	N	60	68
P62806	Conv	HAKRK	TVTAMDVVYALKR	QGRTL	2		733.9059414	1465.796283	0.000451244	16	N	80	93
P62806	Conv	GVLKV	FLENVIRDAVTYTEHAK	RKTVT	2		1003.521243	2005.026887	0.000622848	4	N	61	78
P62806	Conv	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	2		1053.055451	2104.095301	0.000451244	19	N	60	78
P62806	Conv	GGVKR	ISGLIYEETR	GVLKV	2		590.8145747	1179.613549	0.000451244	390	N	46	56
P62806	Conv	YEETR	GVLKVFLENVIR	DAVTY	2		693.9275335	1385.839467	0.000622848	5	N	56	68
P62806	Conv	ENVIR	DAVTYTEHAK	RKTVT	2		567.7754495	1133.535299	0.000451244	67	N	68	78
P62806	Conv	HRKVL	RDNIQGITKPAIR	RLARR	2		741.431503	1480.847406	0.000662267	6	N	23	36
P62806	Conv	RGGVK	RISGLIYEETR	GVLKV	2		668.8651302	1335.71466	0.000451244	12	N	45	56
P62806	Conv	GGVKR	ISGLIYEETRG	VLKVF	2		619.3253065	1236.635013	0.000451244	10	N	46	57
P62806	Conv	EHAKR	KTVTAMDVVYALK	RQGRT	2		719.9028674	1437.790135	0.000451244	2	N	79	92
P62806	Conv	HAKRK	TVTAMDVVYALK	RQGRT	2		655.8553858	1309.695172	0.000451244	13	N	80	92
P62806	Conv	RKTVT	AMDVVYALK	RQGRT	2	M2:+15.995	513.2710003	1024.526401	0.002981883	1	N	83	92
P62806	Conv	RGVLK	VFLENVIRDAVTYTEH	AKRKT	2		953.489412	1904.963224	0.000622848	6	N	60	76
P62806	Conv	RHRKV	LRDNIQGITKPAIR	RLARR	3		532.3182901	1593.93147	0.001463592	2	N	22	36
P62806	Conv	KRKTV	TAMDVVYALK	RQGRT	2		555.7973395	1109.579079	0.002374549	1	N	82	92
P62806	Conv	KRHRK	VLRDNIQGITKPAIR	RLARR	2		847.5077421	1692.999884	0.000998612	1	N	21	36
P62806	Conv	LKVFL	ENVIRDAVTYTEHAK	RKTVT	2		873.4450044	1744.874409	0.000851441	1	N	63	78
P62814	Conv	RLTYK	TVSGVNGPLVILDHVK	FPRYA	3		549.9863175	1646.935553	0.002453667	2	N	48	64
P62814	Conv	ARGQK	IPIFSAAGLPHNEIAAQICR	QAGLV	2	C19:+57.021	1089.578339	2177.141077	0.000451244	12	N	188	208
P62814	Conv	PYENR	TVYETLDIGWQLLR	IFPKE	2		853.959759	1705.903918	0.000451244	8	N	471	485
P62814	Conv	VQAMK	AVVGEEALTSDDLLYLEFLQKFEK	NFITQ	3		919.8131422	2756.416027	0.000451244	7	N	436	460
P62814	Conv	VSGSK	AVVQVFEGTSGIDAK	KTSCE	2		760.9019097	1519.788219	0.000451244	9	N	93	108
P62814	Conv	IITPR	LALTTAEFLAYQCEK	HVLVI	2	C13:+57.021	879.4428532	1756.870106	0.000451244	15	N	276	291
P62814	Conv	VQAMK	AVVGEEALTSDDLLYLEFLQK	FEKNF	2		1177.112828	2352.210056	0.000451244	9	N	436	457
P62814	Conv	QLHNR	QIYPPINVLPSLSR	LMKSA	2		798.959562	1595.903524	0.002212458	1	N	386	400
P62814	Conv	GIDAK	KTSCEFTGDILR	TPVSE	3	C4:+57.021	476.2383826	1425.691748	0.001352548	2	N	108	120
P62827	Conv	DISAK	SNYNFEKPFLWLAR	KLIGD	2		892.9600934	1783.904587	0.000451244	15	N	152	166
P62827	Conv	FHTNR	GPIKFNVWDTAGQEK	FGGLR	3		563.9585389	1688.852217	0.001654178	1	N	56	71
P62827	Conv	RGPIK	FNVWDTAGQEK	FGGLR	2		647.8072809	1293.598962	0.000823681	6	N	60	71
P62827	Conv	RDLVR	VCENIPIVLCGNK	VDIKD	2	C2:+57.021,C10:+57.021	758.3865953	1514.757591	0.000451244	7	N	110	123
P62827	Conv	EFEKK	YVATLGVEVHPLVFHTNR	GPIKF	2		1026.555421	2051.095241	0.000451244	4	N	38	56
P62827	Conv	FHRKK	NLQYYDISAK	SNYNF	2		607.8067496	1213.597899	0.000823681	1	N	142	152
P62827	Conv	RDLVR	VCENIPIVLCGNKVDIK	DRKVK	2	C2:+57.021,C10:+57.021	986.0237875	1970.031975	0.000451244	8	N	110	127
P62827	Conv	AAQYE	HDLEVAQTTALPDEDDDL	-	2		998.9532533	1995.890907	0.001763695	2	N	198	216
P62827	Conv	PPEVV	MDPALAAQYEHDLEVAQTTALPDEDDDL	-	3		1029.464802	3085.371005	0.000451244	10	N	188	216
P62827	Conv	LWLAR	KLIGDPNLEFVAMPALAPPEVV	MDPAL	2	M13:+15.995	1168.63272	2335.249839	0.0025889	1	N	166	188
P62835	Conv	ESSAK	SKINVNEIFYDLVR	QINRK	3		570.6460724	1708.914817	0.000451244	14	N	149	163
P62835	Conv	GGVGK	SALTVQFVQGIFVEK	YDPTI	2		833.4646772	1664.913754	0.000451244	17	N	16	31
P62835	Conv	DLYMK	NGQGFALVYSITAQSTFNDLQDLREQILR	VKDTE	3		1099.900784	3296.678952	0.000451244	15	N	73	102
P62835	Conv	SAKSK	INVNEIFYDLVR	QINRK	2		747.9017127	1493.787825	0.000451244	16	N	151	163
P62835	Conv	DLYMK	NGQGFALVYSITAQSTFNDLQDLR	EQILR	3		886.7773139	2657.308542	0.000823681	1	N	73	97
P62874	Conv	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	C14:+57.021,C31:+57.021	1174.509101	3520.503903	0.000451244	21	N	219	251
P62874	Conv	SKSGR	LLLAGYDDFNCNVWDALKADR	AGVLA	3	C11:+57.021	823.7341263	2468.178979	0.000637154	5	N	283	304
P62874	Conv	SKSGR	LLLAGYDDFNCNVWDALK	ADRAG	2	C11:+57.021	1064.014705	2126.013811	0.000451244	10	N	283	301
P62880	Conv	DSMCR	QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	3	C31:+57.021	1170.528644	3508.562533	0.000451244	11	N	219	251
P62880	Conv	RDARK	ACGDSTLTQITAGLDPVGR	IQMRT	2	C2:+57.021	966.478487	1930.941374	0.000451244	3	N	23	42
P62889	Conv	GKYYR	VCTLAIIDPGDSDIIR	SMPEQ	2	C2:+57.021	879.4590346	1756.902469	0.000622848	8	N	90	106
P62908	Conv	KVATR	GLCAIAQAESLR	YKLLG	2	C3:+57.021	644.8378268	1287.660054	0.000451244	1	N	94	106
P62960	Conv	RKYLR	SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	YAADR	3		1158.229183	3471.664149	0.000662267	3	N	99	135
P62960	Conv	RGPPR	NYQQNYQNSESGEKNEGSESAPEGQAQQR	RPYRR	3		1086.470777	3256.38893	0.001162105	2	N	154	183
P62960	Conv	RPYAR	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	QNMYR	4	M14:+15.995	810.6371672	3238.517469	0.000451244	9	N	202	232
P62960	Conv	VEGEK	GAEAANVTGPGGVPVQGSK	YAADR	2		848.4371794	1694.858759	0.000451244	6	N	116	135
P62960	Conv	RKYLR	SVGDGETVEFDVVEGEK	GAEAA	2		898.4157753	1794.815951	0.001329271	3	N	99	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62962	Conv	AVPGK	TFVSITPAEVGVLVGKDR	SSFFV	2		944.5310799	1887.04656	0.000451244	4	N	38	56
P62962	Conv	VGKDR	SSFFVNGLTLGGQK	CSVIR	2		727.8860627	1453.756525	0.000451244	23	N	56	70
P62962	Conv	AVPGK	TFVSITPAEVGVLVGK	DRSSF	2		808.9670527	1615.918505	0.000451244	16	N	38	54
P62962	Conv	IVGYK	DSPSVWAAVPGK	TFVSI	2		607.3147418	1212.613884	0.000823681	1	N	26	38
P62962	Conv	CSVIR	DSLLQDGEFTMDLR	TKSTG	2		820.3857671	1638.755934	0.000451244	9	N	75	89
P62996	Conv	EVFSK	YGPIADVSIVYDQQSR	RSRGF	2		905.9526623	1809.889725	0.000451244	14	N	140	156
P62996	Conv	SRRSR	GFAFVYFENVDDAK	EAKER	2		811.3808101	1620.74602	0.00091018	3	N	159	173
P63005	Conv	DMTIK	LWDFQGFECIR	TMHGH	2	C9:+57.021	735.8456519	1469.675704	0.000451244	11	N	175	186
P63005	Conv	LDFHK	TAPYVVTGSVDQTVK	VWECR	2		782.9150171	1563.814434	0.000451244	9	N	390	405
P63017	Conv	IFEVK	STAGDTHLGGEDFDNR	MVNHF	2		846.366951	1690.718302	0.000451244	5	N	220	236
P63017	Conv	AKLDK	SQIHDIVLVGGSTR	IPKIQ	2		741.4076936	1480.799787	0.000451244	38	N	328	342
P63017	Conv	LRDAK	LDKSQIHDIVLVGGSTR	IPKIQ	2		919.5106788	1837.005758	0.000451244	15	N	325	342
P63017	Conv	DQGNR	TTPSYVAFTDTER	LIGDA	2		744.3547923	1486.693985	0.000451244	30	N	36	49
P63017	Conv	LNVLR	IINEPTAAAIAYGLDKK	VGAER	2		894.4992484	1786.982897	0.000451244	17	N	171	188
P63017	Conv	AYLGK	TVTNAVVTVPAYFNDSQR	QATKD	2		991.5030507	1980.990501	0.000451244	32	N	137	155
P63017	Conv	KGETK	SFYPEEVSSMVLTK	MKEIA	2		808.897979	1615.780358	0.000451244	10	N	112	126
P63017	Conv	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2		1387.66755	2773.3195	0.000451244	25	N	423	447
P63017	Conv	KELNK	SINPDEAVAYGAAVQAAILSGDK	SENVQ	2		1130.576944	2259.138288	0.000451244	15	N	361	384
P63017	Conv	ERAKR	TLSSSTQASIEIDSLYEGIDFYTSITR	ARFEE	3		999.8245467	2996.45024	0.000451244	4	N	272	299
P63017	Conv	VGAER	NVLIFDLGGGTFDVSILTIEDGIFEVK	STAGD	2		1456.27112	2910.52664	0.000823681	5	N	193	220
P63017	Conv	TSITR	ARFEELNADLFR	GTLDP	2		740.8813116	1479.747023	0.000451244	7	N	299	311
P63017	Conv	PKIQK	LLQDFFNGKELNK	SINPD	2		783.4202697	1564.824939	0.000662267	6	N	348	361
P63017	Conv	TFTTY	SDNQPGVLIQVYEGER	AMTKD	2		902.4477441	1802.879888	0.002080925	1	N	431	447
P63017	Conv	RQATK	DAGTIAGLNVLR	IINEP	2		600.3412909	1198.666982	0.001463592	8	N	159	171
P63017	Conv	KELNK	SINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPL	SLGIE	3		1304.016431	3909.025892	0.002019181	1	N	361	399
P63017	Conv	LSGDK	SENVQDLLLLDVTPLSLGIETAGGVMTVLIK	RNTTI	3		1080.267194	3237.778181	0.000451244	8	N	384	415
P63017	Conv	EDKQK	ILDKCNEIISWLDK	NQTAE	2	C5:+57.021	873.9586705	1745.901741	0.000451244	5	N	569	583
P63017	Conv	-MSK	GPAVGIDLGTTYSCVGVFQHGK	VEIIA	2	C14:+57.021	1132.062718	2262.109837	0.000451244	3	N	3	25
P63017	Conv	KILDK	CNEIISWLDK	NQTAE	2	C1:+57.021	639.3136532	1276.611706	0.000823681	2	N	573	583
P63017	Conv	GDAAK	NQVAMNPTNTVFDAK	RLIGR	2	M5:+15.995	833.3992515	1664.782903	0.000451244	23	N	56	71
P63017	Conv	PKIQK	LLQDFFNGK	ELNKS	2		541.2879957	1080.560391	0.000451244	10	N	348	357
P63017	Conv	ITRAR	FEELNADLFR	GTLDP	2		627.3121991	1252.608798	0.002212458	2	N	301	311
P63017	Conv	QSDMK	HWPFMVVNDAGRPK	VQVEY	3	M5:+15.995	557.2809878	1668.819563	0.000451244	6	N	88	102
P63017	Conv	LSGDK	SENVQDLLLLDVTPLSLGIETAGGVMTVLIKR	NTTIP	3		1132.300898	3393.879293	0.000622848	1	N	384	416
P63017	Conv	KVSSK	NSLESYAFNMK	ATVED	2	M10:+15.995	660.3010174	1318.586435	0.000451244	6	N	539	550
P63017	Conv	DVSIL	TIEDGIFEVK	STAGD	2		575.8036756	1149.591751	0.001162105	1	N	210	220
P63017	Conv	TIPTK	QTQTFTTYSDNQPGVLIQ	VYEGE	2		1020.997798	2039.979996	0.000622848	2	N	423	441
P63017	Conv	VGAER	NVLIFDLGGGTFDVSIL	TIEDG	2		890.4805243	1778.945449	0.0007646	3	N	193	210
P63017	Conv	KELNK	SINPDEAVAYGAAVQAA	ILSGD	2		823.9051808	1645.794762	0.002727428	1	N	361	378
P63028	Conv	MIIYR	DLISHDELFSDIYK	IREIA	2		847.9177568	1693.819914	0.000451244	3	N	5	19
P63073	Conv	KQQRR	SDLDRFWLETLLCLIGESFDDYSDDVCGAVVNVR	AKGDK	3	C13:+57.021,C27:+57.021	1326.955881	3977.844242	0.002145581	1	N	123	157
P63073	Conv	SDLDR	FWLETLLCLIGESFDDYSDDVCGAVVNVR	AKGDK	3	C8:+57.021,C22:+57.021	1131.532184	3391.573152	0.000622848	1	N	128	157
P63085	Conv	IFPGK	HYLDQLNHILGILGSPSQEDLNCIINLK	ARNYL	4	C23:+57.021	805.172717	3216.659668	0.000622848	1	N	229	257
P63085	Conv	LPKEK	LKELIFEETAR	FQPGY	3		450.2544042	1347.739813	0.002080925	2	N	340	351
P63085	Conv	NVLHR	DLKPSNLLLNTTCDLK	ICDFG	2	C13:+57.021	922.9932416	1843.970883	0.000451244	1	N	146	162
P63101	Conv	GDDKK	GIVDQSQQAYQEAFEISKK	EMQPT	2		1085.04528	2168.07496	0.000451244	11	N	139	158
P63101	Conv	GDDKK	GIVDQSQQAYQEAFEISK	KEMQP	2		1020.997798	2039.979996	0.000451244	24	N	139	157
P63101	Conv	MQLLR	DNLTLWTSDTQGDEAEAGEGGEN	-	2		1205.002192	2407.988783	0.000451244	19	N	222	245
P63101	Conv	ETELR	DICNDVLSLLEK	FLIPN	2	C3:+57.021	709.8637073	1417.711815	0.000451244	26	N	91	103
P63101	Conv	EYREK	IETELRDICNDVLSLLEK	FLIPN	2	C9:+57.021	1080.564759	2159.113919	0.000451244	12	N	85	103
P63101	Conv	CSLAK	TAFDEAIAELDTLSEESYK	DSTLI	2		1066.500036	2130.984473	0.000451244	21	N	193	212
P63101	Conv	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1101.550318	3301.627554	0.000451244	27	N	193	222
P63101	Conv	AACMK	SVTEQGAELSNEER	NLLSV	2		774.8609702	1547.70634	0.000451244	9	N	27	41
P63101	Conv	AGDDK	KGIVDQSQQAYQEAFEISK	KEMQP	2		1085.04528	2168.07496	0.000451244	7	N	138	157
P63158	Conv	EYRPK	IKGEHPGLSIGDVAK	KLGEM	2		760.9257192	1519.835838	0.000451244	4	N	112	127
P63158	Conv	EEHKK	KHPDASVNFSEFSK	KCSER	2		796.8893337	1591.763067	0.001162105	1	N	29	43
P63158	Conv	DVAKK	LGEMWNNTAADDKQPYEK	KAAKL	3	M4:+15.995	709.3219057	2124.942317	0.001162105	2	N	128	146
P63158	Conv	PNAPK	RPPSAFFLFCSEYRPK	IKGEH	3	C10:+57.021	668.0053406	2000.992622	0.000451244	2	N	96	112
P63242	Conv	HGHAK	VHLVGIDIFTGK	KYEDI	2		649.8775093	1297.739419	0.000451244	9	N	55	67
P63242	Conv	VPNIK	RNDFQLIGIQDGYLSLLQDSGEVR	EDLRL	3		912.8037516	2735.387855	0.000451244	19	N	85	109
P63242	Conv	PNIKR	NDFQLIGIQDGYLSLLQDSGEVREDLR	LPEGD	3		1031.854952	3092.541455	0.000622848	3	N	86	113
P63242	Conv	PNIKR	NDFQLIGIQDGYLSLLQDSGEVR	EDLRL	2		1290.651172	2579.286744	0.000451244	15	N	86	109
P63242	Conv	IFTGK	KYEDICPSTHNMDVPNIK	RNDFQ	3	C6:+57.021,M12:+15.995	726.3386367	2175.99251	0.001162105	2	N	67	85
P63325	Conv	PKKNR	IAIYELLFK	EGVMV	2		555.3344146	1108.653229	0.001352548	6	N	8	17
P63328	Conv	RMYRK	SQTTGFPSLITIFSAPNYLDVYNNK	AAVLK	3		930.8048696	2789.391209	0.000823681	3	N	293	318

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63328	Conv	HNTVR	GCSYFYSYPAVCDFLQHNNLLSILR	AHEAQ	3	C2:+57.021,C12:+57.021	1013.149569	3036.425306	0.000622848	4	N	254	279
P67778	Conv	EGDSK	AAELIANSLATAGDGLIELR	KLEAA	2		999.5474583	1997.079317	0.000451244	4	N	219	239
P68033	Conv	YNELR	VAPEEHPTLLTEAPLNPK	ANREK	2		978.5259945	1955.036389	0.000451244	4	N	97	115
P68033	Conv	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	3		1153.21946	3456.63498	0.001162105	4	N	70	97
P68033	Conv	DIKEK	LCYVALDFENEMATAASSSSLEK	SYELP	2	C2:+57.021,M12:+15.995	1276.580521	2551.145442	0.000451244	7	N	217	240
P68033	Conv	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHR	KCF-	3	M19:+15.995	1367.346146	4099.015037	0.001463592	1	N	338	374
P68033	Conv	ILTLK	YPIEHGIITNWDDMEK	IWHHT	2		980.9596307	1959.903661	0.000451244	18	N	70	86
P68033	Conv	VRDIK	EKLCYVALDFENEMATAASSSSLEK	SYELP	3	C4:+57.021,M14:+15.995	937.1021327	2808.282998	0.000451244	4	N	215	240
P68033	Conv	ELRVA	PEEHPTLLTEAPLNPK	ANREK	2		893.4732306	1784.930861	0.001329271	1	N	99	115
P68033	Conv	IDIRK	DLYANNVLSGGTTMYPGIADR	MQKEI	2	M14:+15.995	1122.534265	2243.05293	0.001463592	1	N	293	314
P68037	Conv	KPATK	TDQVIQSLIALVNDPQPEHPLRADLAEEYSK	DRKKF	3		1163.934042	3488.778726	0.002519933	1	N	100	131
P68037	Conv	KGAFR	IEINFPAEYPFKPPK	ITFKT	3		597.3228182	1788.945055	0.000662267	2	N	52	67
P68037	Conv	KPATK	TDQVIQSLIALVNDPQPEHPLR	ADLAE	3		828.447128	2482.317984	0.002080925	1	N	100	122
P68037	Conv	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDKGAFR	IEINF	3		1095.230241	3282.667324	0.000451244	8	N	23	52
P68040	Conv	VSCVR	FSPNSSNPIIVSCGWDK	LVKVW	2	C13:+57.021	954.4517409	1906.887882	0.000451244	18	N	155	172
P68040	Conv	STSSK	AEPPQCTSLAWSADGQTLFAGYTDNLVR	VWQVT	3	C6:+57.021	1023.485828	3067.434084	0.000451244	11	N	280	308
P68040	Conv	VGHTK	DVLSVAFSSDNR	QIVSG	2		655.3232952	1308.63099	0.000451244	10	N	106	118
P68040	Conv	DLEGK	IIVDELKQEVISTSSK	AEPPQ	2		895.0018209	1787.988042	0.000451244	4	N	264	280
P68040	Conv	LGVCK	YTVQDESHSEWVSCVR	FSPNS	2	C14:+57.021	991.4393618	1980.863124	0.000451244	5	N	139	155
P68040	Conv	LNEGK	HLYTLDGGDIINALCFSPNR	YWLCA	2	C15:+57.021	1138.560343	2275.105086	0.000451244	13	N	225	245
P68040	Conv	NCKLK	TNHIGHTGYLNTVTVSPDGSLCASGGK	DGQAM	3	C22:+57.021	915.1086921	2742.302676	0.000662267	8	N	185	212
P68040	Conv	FSPNR	YWLCAATGPSIK	IWDLE	2	C4:+57.021	683.8451206	1365.674641	0.000622848	4	N	245	257
P68254	Conv	GDDRK	QTIENSQGAYQEAFDISKK	EMQPT	2		1079.027087	2156.038574	0.000662267	1	N	139	158
P68254	Conv	ESELR	SICTTVLELLDKYLIANATNPESK	VFYLK	2	C3:+57.021	1347.207234	2692.398868	0.000622848	2	N	91	115
P68254	Conv	THPIR	LGLALNFSVFYYEILNNPELACTLAK	TAFDE	3	C22:+57.021	991.8529007	2972.535302	0.0025889	1	N	167	193
P68254	Conv	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1105.882068	3314.622803	0.000451244	17	N	193	222
P68254	Conv	ATCMK	AVTEQGAELSNEER	NLLSV	2		766.8635129	1531.711426	0.001162105	3	N	27	41
P68254	Conv	ELLDK	YLIANATNPESK	VFYLK	2		660.8438635	1319.672127	0.000451244	4	N	103	115
P68254	Conv	ESELR	SICTTVLELLDK	YLIAN	2	C3:+57.021	696.3764506	1390.737301	0.000451244	15	N	91	103
P68254	Conv	CTLAK	TAFDEAIAELDTLNEDSYK	DSTLI	2		1072.997661	2143.979722	0.000451244	10	N	193	212
P68368	Conv	DVVPK	DVNAAIAAIK	TKRSI	2		493.2879957	984.5603914	0.002884417	1	N	326	336
P68368	Conv	IKTKR	SIQFVDWCPTGFK	VGINY	2	C8:+57.021	792.8796917	1583.743783	0.000451244	13	N	339	352
P68368	Conv	MPSDK	TIGGGDDSFTTFFCETGAGK	HVPRA	2	C14:+57.021	1034.452135	2066.88867	0.000451244	13	N	40	60
P68368	Conv	KHVPR	AVFVDLEPTVIDEIR	NGPYR	2		858.4648742	1714.914148	0.000451244	16	N	64	79
P68368	Conv	TNLNR	LISQIVSSITASLR	FDGAL	2		744.4437448	1486.87189	0.000451244	25	N	229	243
P68368	Conv	YTIGK	EIIDPVLDR	IRKLS	2		535.2985604	1068.581521	0.002296037	1	N	112	121
P68369	Conv	MPSDK	TIGGGDDSFNTFFSETGAGK	HVPRA	2		1004.450681	2006.885762	0.000451244	18	N	40	60
P68369	Conv	IKTKR	TIQFVDWCPTGFK	VGINY	2	C8:+57.021	799.8875168	1597.759434	0.000622848	1	N	339	352
P68369	Conv	KHVPR	AVFVDLEPTVIDEVR	TGTYR	2		851.4570492	1700.898498	0.000451244	14	N	64	79
P68369	Conv	TNLNR	LIGQIVSSITASLR	FDGAL	2		729.4384624	1456.861325	0.000451244	9	N	229	243
P68369	Conv	YTIGK	EIIDLVLDR	IRKLA	2		543.3142105	1084.612821	0.001763695	5	N	112	121
P68433	Conv	KTDLR	FQSSAVMALQEACEAY	LVGLF	2	M7:+15.995,C13:+57.021	910.8954531	1819.775306	0.000451244	4	N	84	100
P68433	Conv	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	2	C4:+57.021,C18:+57.021	1326.625323	2651.235045	0.000451244	12	N	93	116
P68433	Conv	SSAVM	ALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C6:+57.021,C20:+57.021	946.126541	2835.356223	0.000451244	15	N	91	116
P68433	Conv	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C13:+57.021,C27:+57.021	936.4563991	3741.794396	0.0025889	1	N	84	117
P68433	Conv	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C13:+57.021,C27:+57.021	1196.238895	3585.693285	0.000451244	127	N	84	116
P68433	Conv	MALQE	ACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C2:+57.021,C16:+57.021	799.0524247	2394.133874	0.000622848	4	N	95	116
P68433	Conv	VMALQ	EACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C3:+57.021,C17:+57.021	842.0666225	2523.176467	0.000823681	3	N	94	116
P68433	Conv	FKTDL	RFQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	M8:+15.995,C14:+57.021,C28:+57.021	940.4551491	3757.789396	0.000451244	5	N	83	116
P68433	Conv	DLRFQ	SSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	M5:+15.995,C11:+57.021,C25:+57.021	1109.861565	3326.561294	0.000451244	8	N	86	116
P68433	Conv	ALQEA	CEAYLVGLFEDTNLCAIHAK	RVTIM	2	C1:+57.021,C15:+57.021	1162.55618	2323.09676	0.000662267	2	N	96	116
P68433	Conv	TDLRF	QSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	C12:+57.021,C26:+57.021	860.6640178	3438.624871	0.000622848	1	N	85	116
P68433	Conv	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIH	AKRVT	3	C13:+57.021,C27:+57.021	1129.861536	3386.561208	0.001162105	4	N	84	114
P68433	Conv	SAVMA	LQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C5:+57.021,C19:+57.021	922.447503	2764.319109	0.000451244	12	N	92	116
P68433	Conv	QSSAV	MALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C7:+57.021,C21:+57.021	989.8067029	2966.396709	0.000451244	4	N	90	116
P68433	Conv	RFQSS	AVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C9:+57.021,C23:+57.021	1046.508546	3136.502237	0.000451244	3	N	88	116
P68433	Conv	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLC	AIHAK	3	M7:+15.995,C13:+57.021,C27:+57.021	1028.133173	3081.376118	0.002080925	1	N	84	111
P68433	Conv	KTDLR	FQSSAVMALQEACEAYLV	GLFED	2	M7:+15.995,C13:+57.021	1016.971692	2031.927784	0.002374549	1	N	84	102
P68510	Conv	ASAMK	AVTELNEPLSNEDRNLLSVAYK	NVVGA	2		1238.14044	2474.26528	0.0007646	6	N	28	50
P68510	Conv	SGEKK	NSVVEASEAAYKEAFEISK	EHMQP	2		1036.513281	2071.010962	0.000451244	15	N	143	162
P68510	Conv	THPIR	LGLALNFSVFYYEIQNAPEQACLLAK	QAFDD	3	C22:+57.021	991.512767	2971.514901	0.000451244	11	N	172	198
P68510	Conv	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1110.213817	3327.618052	0.000451244	8	N	198	227

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68510	Conv	ASAMK	AVTELNEPLSNEDR	NLLSV	2		793.886988	1585.758376	0.000451244	26	N	28	42
P68510	Conv	EKIEK	ELETVCNDVLALLDK	FLIKN	2	C6:+57.021	866.4455929	1730.875586	0.000451244	16	N	91	106
P68510	Conv	AYREK	IEKELETVCNDVLALLDK	FLIKN	2	C9:+57.021	1051.556403	2101.097206	0.000451244	2	N	88	106
P68510	Conv	EKIEK	ELETVCNDVLALLDKFLIK	NCNDF	2	C6:+57.021	1117.111346	2232.207091	0.000451244	1	N	91	110
P70168	Conv	KFLER	AAVENLPTFLVELSR	VLANP	2		829.959759	1657.903918	0.000451244	11	N	27	42
P70168	Conv	KFYAK	GALQYLVPILTQTLTKQDENDDDDDWNPCK	AAGVC	3	C29:+57.021	1169.219476	3504.635029	0.000622848	1	N	316	346
P70168	Conv	KFYAK	GALQYLVPILTQTLTK	QDEND	2		880.0223594	1758.029119	0.000622848	10	N	316	332
P70168	Conv	GDLCR	ALQSNILPFCDEVMQLLLENLGNENVHR	SVKPQ	3	C10:+57.021	1089.548434	3265.621903	0.000451244	3	N	679	707
P70168	Conv	WTVGR	ICELLPEAAINDVYLAPLLQCLIEGLSAEPR	VASNV	3	C2:+57.021,C21:+57.021	1160.942296	3479.803487	0.000451244	11	N	434	465
P70168	Conv	SNNVK	LAATNALLNSLEFTK	ANFDK	2		803.4464845	1604.877369	0.000451244	11	N	191	206
P70168	Conv	LIVQK	LLETTDRPDGHQNNLR	SSAYE	3		626.9859278	1877.934383	0.001162105	3	N	509	525
P70168	Conv	GEFKK	YLEVVLNTLQQASQAQVDK	SDFDM	2		1074.071298	2146.126995	0.000451244	11	N	730	749
P70168	Conv	TEHMK	ESTLEAIGYICQDIDPEQLQDK	SNEIL	2	C11:+57.021	1283.105174	2564.194748	0.000451244	18	N	147	169
P70168	Conv	ENVHR	SVKPQILSVFGDIALAIGGEFK	KYLEV	3		763.7671389	2288.278017	0.000451244	2	N	707	729
P70168	Conv	GIGLK	NYAEYQVCLAAVGLVGDLCR	ALQSN	3	C8:+57.021,C19:+57.021	757.7016149	2270.081445	0.000451244	11	N	659	679
P70168	Conv	STSDR	IQFNDLQSLLCATLQNVLR	KVQHQ	2	C11:+57.021	1123.602011	2245.188421	0.000451244	5	N	574	593
P70168	Conv	ENVHR	SVKPQILSVFGDIALAIGGEFKK	YLEVV	4		605.1010449	2416.37298	0.000451244	7	N	707	730
P70168	Conv	WTVGR	ICELLPEAAINDVYLAPLLQ	CLIEG	2	C2:+57.021	1128.103521	2254.191441	0.001763695	1	N	434	454
P70195	Conv	KNCSK	IHFISPNIYCCGAGTAADTDMTTQLISSNLELHSLTTGR	LPRVV	4	C10:+57.021,C11:+57.021	1067.26235	4265.018202	0.0007646	5	N	76	115
P70195	Conv	QMLFR	YQGYIGAALVLGGVDVTGPHLYSIYPHGSTDK	LPYVT	3		1116.902013	3347.68264	0.000451244	7	N	132	164
P70195	Conv	EEEAK	KLVSEAIAAGIFNDLGSGSNIDLCVISK	SKLDF	3	C24:+57.021	964.5113146	2890.510544	0.000622848	1	N	195	223
P70195	Conv	VLTEK	VTPLEIEVLEETVQTMDTS	-	3		712.0210935	2133.03988	0.002663018	1	N	258	277
P70195	Conv	EEAKK	LVSEAIAAGIFNDLGSGSNIDLCVISK	SKLDF	2	C23:+57.021	1382.21559	2762.415581	0.000451244	15	N	196	223
P70195	Conv	FISPN	IYCCGAGTAADTDMTTQLISSNLELHSLTTGR	LPRVV	3	C3:+57.021,C4:+57.021,M14:+15.995	1158.537809	3472.590028	0.001591523	1	N	83	115
P70195	Conv	ARKTG	TTIAGVVYKDGIVLGADTR	ATEGM	2		975.0392691	1948.062938	0.000451244	2	N	43	62
P70268	Conv	QSEPR	SWSLLEQLGLAGADLAAPGVQQQLELERER	LKREI	3		1093.244551	3276.710252	0.000451244	1	N	11	41
P70290	Conv	HKQDK	IAILDIEPQTLK	TVRTA	2		677.4035569	1352.791514	0.000451244	19	N	374	386
P70290	Conv	LKTVR	TAELSPFIVFIAPTDQGTQTEALQQLQK	DSEAI	3		1025.540193	3073.597179	0.000451244	23	N	389	417
P70290	Conv	EAGLK	FVTGDIIQIINKDDSNWWQGR	VEGSS	3		835.756073	2504.244819	0.000451244	13	N	185	206
P70290	Conv	EGSSK	ESAGLIPSPELQEWR	VASVA	2		856.4366481	1710.857696	0.000622848	4	N	212	227
P70290	Conv	EAGLK	FVTGDIIQIINK	DDSNW	2		680.8958991	1359.776198	0.000979378	1	N	185	197
P70296	Conv	TGLHR	YVWLVYEQEQPLSCDEPILSNK	SGDNR	2	C14:+57.021	1355.657377	2709.299154	0.000451244	16	N	119	141
P70296	Conv	LDPGK	LYTLVLTDPDAPSR	KDPKF	2		780.9175598	1559.81952	0.000823681	2	N	62	76
P70315	Conv	PSGFK	HVSHVGWDPQNGFDVNNLDPDLR	SLFSR	4		658.5643522	2630.226209	0.001699387	1	N	247	270
P70335	Conv	LRDPK	SEVNSDCLLDGLDALVYDLDFPALRK	NKNID	3	C7:+57.021	980.155308	2937.442524	0.000451244	1	N	22	48
P70335	Conv	LEAKR	LLEFELAQLTK	QYRGN	2		652.877175	1303.73875	0.002884417	1	N	819	830
P70335	Conv	WETLR	DTVAPVVPDLSSDIDTSNFDDLEEDKGDEETFPIPK	AFVGN	3		1317.279938	3948.816413	0.000622848	3	N	349	385
P70441	Conv	DSPKR	QVSTEPSSTSSSSSDPILDLNISLAVAK	ERAHQ	2		1417.219813	2832.424025	0.001162105	2	N	300	328
P70441	Conv	LAGDR	LVEVNGENVEKETHQQVVSR	IRAAL	3		765.3965448	2293.166234	0.000451244	7	N	58	78
P70460	Conv	LPRMK	SSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	2	C16:+57.021	1320.054398	2638.093196	0.000662267	2	N	316	341
P70460	Conv	IRGVK	YNQATPIFHQWR	DARQV	3		520.928914	1559.763342	0.002981883	1	N	71	83
P70460	Conv	PRMKS	SSSVTTSEAHPSTPCSSDDSDLER	VKQEL	3	C15:+57.021	851.3615227	2551.061168	0.0025889	1	N	317	341
P70670	Conv	FGEAK	IEDLSQQAQLAAAEK	FKVQG	2		807.9208308	1613.826062	0.000451244	14	N	2099	2114
P70677	Conv	MACQK	IPVEADFLYAYSTAPGYYSWR	NSKDG	2		1235.09223	2468.16886	0.000451244	11	N	186	207
P70677	Conv	DSSYK	MDYPEMGICIIINNK	NFHKS	3	M1:+15.995,C9:+57.021	609.6214282	1825.840885	0.001763695	1	N	38	53
P70698	Conv	SSIYR	VPLLLEEQGVVDYFLR	RLDLP	3		630.6844157	1889.029847	0.002813207	1	N	252	268
P80313	Conv	EIIPR	QLCDNAGFDATNILNK	LRARH	2	C3:+57.021	897.4282658	1792.840932	0.000451244	6	N	447	463
P80313	Conv	NAEIR	VHTVEDYQAIVDAEWNILYDKLEK	IHQSG	4		723.6175218	2890.438887	0.002884417	1	N	256	280
P80313	Conv	VDIAK	SQDAEVGDGTTSVTLLAAEFLK	QVKPY	2		1126.568785	2251.121969	0.000451244	17	N	84	106
P80313	Conv	PAMVR	INALTAASEAACLIVSVDETIKNPR	STVDP	3	C12:+57.021	886.1377001	2655.3897	0.000451244	15	N	499	524
P80313	Conv	PAMVR	INALTAASEAACLIVSVDETIK	NPRST	3	C12:+57.021	763.7387659	2288.192898	0.000451244	6	N	499	521
P80314	Conv	VDMSR	VQDDEVGDGTTSVTVLAAELLR	EAESL	2		1144.584966	2287.154332	0.000451244	21	N	89	111
P80314	Conv	AETAR	LSSFIGAIAIGDLVK	STLGP	2		752.4432135	1502.870827	0.000451244	13	N	25	40
P80314	Conv	AGVER	LALVTGGEIASTFDHPELVK	LGSCK	2		1049.065484	2096.115368	0.000451244	3	N	322	342
P80314	Conv	FQVKR	QVLLSAAEAAEVILR	VDNII	2		791.9623017	1581.909003	0.000451244	6	N	501	516
P80314	Conv	TKAAR	EALLSSAVDHGSDEAR	FWQDL	2		828.8953444	1655.775089	0.002374549	1	N	138	154
P80315	Conv	LVKKR	ALIAGGGAPEIELALR	LTEYS	2		775.9491943	1549.882789	0.000451244	2	N	419	435
P80315	Conv	KSILR	DALSDLALHFLNK	MKIMV	2		728.8938877	1455.772175	0.000451244	12	N	306	319
P80315	Conv	VEKAK	IGLIQFCLSAPK	TDMDN	2	C7:+57.021	673.8789634	1345.742327	0.000451244	5	N	245	257
P80315	Conv	KIVKK	LGGTIDDCELVEGLVLTQK	VANSG	2	C8:+57.021	1030.532928	2059.050256	0.000451244	4	N	213	232
P80316	Conv	LTSEK	LGFAGVVQEISFGTTK	DKMLV	2		827.4464845	1652.877369	0.000451244	8	N	352	368
P80316	Conv	IKQIK	ETGANLAICQWGFDDEANHLLLQNGLPAVR	WVGGP	3	C9:+57.021	1108.214331	3321.619594	0.000451244	9	N	293	323
P80316	Conv	LPAVR	WVGGPEIELIAIATGGR	IVPRF	2		869.9784831	1737.941366	0.000451244	7	N	323	340
P80316	Conv	VELSK	SQDDEIGDGTTGVVVLAGALLEEAEQLLDR	GIHPI	3		1038.521527	3112.541181	0.000451244	12	N	96	126

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P80316	Conv	VVDAK	IAILTCPFEPPKPK	TKHKL	3	C6:+57.021	537.6377065	1609.88972	0.002884417	1	N	247	261
P80316	Conv	KISDK	VLVDINNPEPLIQTAK	TTLGS	2		882.4992484	1762.982897	0.000451244	5	N	154	170
P80317	Conv	LIIPK	VLAQNSGFDLQETLVK	VQAEH	2		881.4732306	1760.930861	0.000451244	6	N	449	465
P80317	Conv	SLIAK	VATAQDDITGDGTTSNVLIIGELLK	QADLY	2		1272.674313	2543.333025	0.000451244	10	N	79	104
P80317	Conv	LRAVK	NAIDDGCVVPGAGAVEVALAEALIK	YKPSV	2	C7:+57.021	1226.64153	2451.26746	0.002374549	1	N	399	424
P80317	Conv	SLRTK	VHAELADVLTEAVVDSILAIR	KKDEP	3		745.4183982	2233.231795	0.000637154	5	N	159	180
P80317	Conv	RTSLR	TKVHAELADVLTEAVVDSILAIR	KKDEP	3		821.7992788	2462.374436	0.000451244	4	N	157	180
P80317	Conv	SVKGR	AQLGVQAFADALLIIPK	VLAQN	2		884.5225265	1767.029453	0.000451244	11	N	432	449
P80317	Conv	VINQK	GIDPFSLDALAK	EGIVA	2		623.8380498	1245.6605	0.000622848	2	N	295	307
P80318	Conv	LQTYK	TAVETAVLLLR	IDDIV	2		593.3642347	1184.712869	0.001463592	1	N	507	518
P80318	Conv	KVISR	WSSLACNIALDAVK	TVQFE	2	C6:+57.021	774.3982486	1546.780897	0.000622848	1	N	167	181
P82198	Conv	RPQER	GDELADSALEIFK	QASAY	2		704.354261	1406.692922	0.000451244	10	N	642	655
P82198	Conv	PDSAK	TLLELAGESDVSTAIDILK	QAGLD	2		994.54405	1987.0725	0.000451244	69	N	377	396
P82198	Conv	TINGK	AVISNKDILATNGVIHFIDELLIPDSAK	TLLEL	3		1002.889045	3005.643735	0.000451244	7	N	349	377
P82198	Conv	KICGK	STVISYECCPGYEK	VPGEK	2	C8:+57.021,C9:+57.021	846.8658897	1691.716179	0.000451244	45	N	76	90
P82198	Conv	TNILK	YHIGDEILVSGGIGALVR	LKSLQ	3		623.6796646	1868.015594	0.000451244	17	N	570	588
P82198	Conv	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEK	IPAET	3		1012.184298	3033.529493	0.000451244	16	N	257	287
P82198	Conv	HLIDK	VISTITNNIQQIIEIEDTFETLR	AAVAA	2		1345.716512	2689.417424	0.000451244	20	N	234	257
P82198	Conv	VFVYR	NSLCIENSCIAAHDKR	GRFGT	3	C4:+57.021,C9:+57.021	629.965062	1886.871786	0.000451244	2	N	469	485
P82198	Conv	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEKIPAETLNR	ILGDP	3		1310.348403	3928.02181	0.000451244	15	N	257	295
P82198	Conv	VISNK	DILATNGVIHFIDELLIPDSAK	TLLEL	2		1197.649912	2393.284224	0.000451244	10	N	355	377
P82198	Conv	HLSGK	EQLTFLAPLNSVFK	DGVPR	2		803.9461203	1605.876641	0.001839721	7	N	407	421
P82198	Conv	KGDNR	FSMLVAAIQSAGLMEILNR	EGVYT	3	M3:+15.995,M14:+15.995	699.3680506	2095.080752	0.000622848	9	N	514	533
P82198	Conv	QLASK	YLYSGQTLDTLGGK	KLRVF	2		758.3886352	1514.76167	0.002145581	1	N	447	461
P82198	Conv	ETLNR	ILGDPEALRDLLNNHILK	SAMCA	3		682.0570236	2043.147671	0.000979378	5	N	295	313
P82198	Conv	QLASK	YLYSGQTLDTLGGKK	LRVFV	2		822.4361168	1642.856634	0.000622848	3	N	447	462
P82198	Conv	IDILK	QAGLDTHLSGKEQLTFLAPLNSVFK	DGVPR	3		905.4891044	2713.443913	0.000451244	4	N	396	421
P82198	Conv	KICGK	STVISYECCPGYEKVPGEK	GCPAA	2	C8:+57.021,C9:+57.021	1102.005989	2201.996378	0.000451244	7	N	76	95
P83917	Conv	LLKWK	GFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	3	C17:+57.021	1142.837032	3425.487696	0.000451244	2	N	43	72
P84078	Conv	SLRHR	NWYIQATCATSGDGLYEGLDWLSNQLR	NQK-	3	C8:+57.021	1044.489461	3130.444984	0.000451244	15	N	151	178
P84078	Conv	EELMR	MLAEDELRDAVLLVFANK	QDLPN	2		1024.04878	2046.08196	0.001162105	4	N	109	127
P84078	Conv	TVEYK	NISFTVWDVGGQDK	IRPLW	2		783.3838842	1564.752168	0.000451244	6	N	59	73
P84078	Conv	YIQAT	CATSGDGLYEGLDWLSNQLR	NQK-	2	C1:+57.021	1128.02379	2254.03198	0.000451244	5	N	158	178
P84084	Conv	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSKR	-	4	C8:+57.021	839.9059776	3355.592711	0.000823681	1	N	151	180
P84084	Conv	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSK	R-	3	C8:+57.021	1067.505	3199.491599	0.000451244	19	N	151	179
P84084	Conv	DELQK	MLQEDELRDAVLLVFANK	QDMPN	3		702.0422747	2103.103424	0.000979378	1	N	109	127
P84091	Conv	EENIK	NNFVLIYELLDEILDFGYPQNSETGALK	TFITQ	3		1072.543603	3214.60741	0.000622848	1	N	102	130
P84096	Conv	DTLRR	LKEQGQAPITPQQGQALAK	QIHAV	2		1003.555618	2005.095635	0.001463592	1	N	128	147
P84096	Conv	IHAVR	YLECSALQQDGVKEVFAEAVR	AVLNP	2	C4:+57.021	1206.597122	2411.178645	0.000622848	2	N	153	174
P84096	Conv	AVDGR	TVNLNLWDTAGQEEYDR	LRTLS	2		1012.471948	2022.928295	0.000451244	27	N	49	66
P84096	Conv	NAFPK	EYIPTVFDNYSAQSAVDGR	TVNLN	2		1066.500705	2130.98581	0.000451244	13	N	30	49
P84096	Conv	AVDGR	TVNLNLWDTAGQEEYDRLR	TLSYP	3		765.0456235	2292.11347	0.000451244	10	N	49	68
P84096	Conv	GAVGK	TCLLICYTTNAFPK	EYIPT	2	C2:+57.021,C6:+57.021	851.4206352	1700.82567	0.000451244	13	N	16	30
P84096	Conv	LRRLK	EQGQAPITPQQGQALAK	QIHAV	2		882.9661041	1763.916608	0.002296037	1	N	130	147
P84096	Conv	IHAVR	YLECSALQQDGVK	EVFAE	2	C4:+57.021	755.8642386	1509.712877	0.000451244	11	N	153	166
P84096	Conv	YDRLR	TLSYPQTNVFVICFSIASPPSYENVR	HKWHP	3	C13:+57.021	997.1640263	2988.468679	0.000823681	1	N	68	94
P84104	Conv	VWVAR	NPPGFAFVEFEDPRDAADAVR	ELDGR	3		774.0384689	2319.092007	0.000451244	8	N	43	64
P84228	Conv	KTDLR	FQSSAVMALQEASEAY	LVGLF	2	M7:+15.995	874.3963745	1746.777149	0.000451244	17	N	84	100
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	C27:+57.021	1223.93988	3668.796239	0.000451244	1	N	84	117
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1171.906176	3512.695128	0.000451244	164	N	84	116
P84228	Conv	AQDFK	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C31:+57.021	1000.496531	3997.954925	0.000622848	1	N	80	116
P84228	Conv	TDLRF	QSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M6:+15.995,C26:+57.021	1128.215038	3381.621714	0.000451244	7	N	85	116
P84228	Conv	RFQSS	AVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C23:+57.021	1022.175826	3063.504079	0.000451244	4	N	88	116
P84228	Conv	LRFQS	SAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M4:+15.995,C24:+57.021	1056.518169	3166.531108	0.000662267	7	N	87	116
P84228	Conv	DLRFQ	SSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C25:+57.021	1080.197179	3237.568136	0.000662267	1	N	86	116
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIH	AKRVT	3	M7:+15.995,C27:+57.021	1110.860484	3329.558051	0.000451244	14	N	84	114
P84228	Conv	QSSAV	MALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C21:+57.021	965.4739839	2893.398552	0.000451244	9	N	90	116
P84228	Conv	FKTDL	RFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M8:+15.995,C28:+57.021	922.2056098	3684.791239	0.000451244	13	N	83	116
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLVGLF	EDTNL	2	M7:+15.995	1139.059585	2276.103569	0.001463592	1	N	84	105
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLC	AIHAK	3	M7:+15.995,C27:+57.021	1003.800454	3008.377961	0.000451244	6	N	84	111
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLV	GLFED	2	M7:+15.995	980.4726136	1958.929627	0.001871652	3	N	84	102
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAI	HAKRV	3	M7:+15.995,C27:+57.021	1065.17418	3192.499139	0.001699387	1	N	84	113
P84228	Conv	KTDLR	FQSSAVMALQEASEAYLVGL	FEDTN	2	M7:+15.995	1065.525378	2129.035155	0.001943752	1	N	84	104
P84228	Conv	RFQSS	AVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	M3:+15.995,C23:+57.021	809.9078477	3235.600191	0.00091018	4	N	88	117
P84244	Conv	KTDLR	FQSAAIGALQEASEAY	LVGLF	2		828.3997312	1654.783862	0.000451244	9	N	84	100

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P84244	Conv	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	C27:+57.021	1198.607118	3592.797953	0.000451244	7	N	84	117
P84244	Conv	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1146.573414	3436.696841	0.000451244	269	N	84	116
P84244	Conv	FKTDL	RFQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C28:+57.021	1198.607118	3592.797953	0.000451244	4	N	83	116
P84244	Conv	RFQSA	AIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C23:+57.021	1002.174703	3003.500708	0.000451244	9	N	88	116
P84244	Conv	QSAAI	GALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C21:+57.021	940.8009765	2819.37953	0.000451244	2	N	90	116
P84244	Conv	DLRFQ	SAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C25:+57.021	1054.864417	3161.56985	0.000451244	5	N	86	116
P84244	Conv	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIH	AKRVT	3	C27:+57.021	1080.196055	3237.564764	0.000823681	1	N	84	114
P84244	Conv	FQSAA	IGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C22:+57.021	978.4956646	2932.463594	0.000622848	2	N	89	116
P84244	Conv	KTDLR	FQSAAIGALQEASEAYLV	GLFED	2		934.4759703	1866.936341	0.000451244	2	N	84	102
P85094	Conv	LKVAR	LLDVPILLTEQYPEGLGPTVPELGAQGIRPVSK	TCFSM	3		1167.319057	3498.93377	0.000622848	2	N	49	82
P97315	Conv	AKCGK	GLESTTLADKDGEIYCK	GCYAK	2	C16:+57.021	950.4541463	1898.892693	0.000451244	1	N	151	168
P97364	Conv	WSAGR	SFSNYRPFEPQTLGFSPSWR	LTSFS	3		801.7225922	2402.144377	0.002663018	1	N	33	53
P97369	Conv	ALMRR	EFQREDIALSYQDAEGDLVR	LLSDE	2		1177.567108	2353.118615	0.000622848	5	N	276	296
P97369	Conv	ELSFK	AGDVIFLLSK	INKDW	2		531.8138463	1061.612093	0.000451244	10	N	192	202
P97369	Conv	EDTGK	TIKDIAVEEDLSSTPLFK	DLLAL	2		1003.538768	2005.061935	0.000451244	5	N	250	268
P97369	Conv	FLLSK	INKDWLEGTSQGATGIFPGSFVK	ILKDF	2		1226.629511	2451.243422	0.000451244	7	N	202	225
P97369	Conv	AQQLR	SESDFEQLPDDVAVSANIADIEEKR	GFTSH	3		926.4424367	2776.30391	0.001162105	1	N	8	33
P97369	Conv	GKTIK	DIAVEEDLSSTPLFK	DLLAL	2		832.4254147	1662.835229	0.001463592	1	N	253	268
P97369	Conv	AQQLR	SESDFEQLPDDVAVSANIADIEEK	RGFTS	2		1311.109199	2620.202799	0.000451244	7	N	8	32
P97369	Conv	DPDVR	IFFYQSAYDAEQVPQALR	RLRPR	2		1073.534351	2145.053102	0.000451244	21	N	130	148
P97369	Conv	NAYMK	NLLSLPVCVLMDPDVR	IFFYQ	2	C8:+57.021	920.9869056	1839.958211	0.001463592	1	N	114	130
P97371	Conv	VGDYR	QLVHELDEAEYQEIR	LMVME	2		936.4608515	1870.906103	0.000622848	3	N	198	213
P97371	Conv	VMEIR	NAYAVLYDIILK	NFEKL	2		698.3982746	1394.780949	0.000451244	15	N	220	232
P97371	Conv	VLLQR	LKPEIKDVTEQLNLVTTWLQLQIPR	IEDGN	4		744.6791852	2974.685541	0.001352548	1	N	116	141
P97371	Conv	KPEIK	DVTEQLNLVTTWLQLQIPR	IEDGN	2		1134.123865	2266.232129	0.000451244	16	N	122	141
P97372	Conv	VLDLR	AFYAELYHIISSNLEK	IVNPK	3		633.3285205	1896.962161	0.000451244	10	N	210	226
P97372	Conv	VDVFR	QNLFQEADDFLCTFLPR	KIISL	2	C12:+57.021	1057.504505	2112.99341	0.000451244	4	N	21	38
P97372	Conv	PGNEK	LLALLALVKPEVWTLK	EKCIL	3		603.0538918	1806.138275	0.001162105	6	N	99	115
P97372	Conv	HLIPK	IEDGNDFGVAIQEK	VLERV	2		767.8733493	1533.731099	0.000622848	6	N	131	145
P97372	Conv	TFLPR	KIISLSQLLQEDSLNVADLSSLR	APLDI	2		1271.70849	2541.40138	0.000451244	1	N	38	61
P97372	Conv	FLPRK	IISLSQLLQEDSLNVADLSSLR	APLDI	2		1207.661008	2413.306416	0.000451244	5	N	39	61
P97372	Conv	TLKEK	CILVITWIQHLIPK	IEDGN	3	C1:+57.021	578.6763841	1733.005752	0.002727428	1	N	117	131
P97384	Conv	RMYGK	SLYHDITGDTSGDYRK	ILLKI	2		914.4295514	1826.843503	0.000451244	8	N	477	493
P97384	Conv	IMVSR	SELDLLDIR	AEYKR	2		537.2960177	1072.576435	0.000451244	18	N	459	468
P97384	Conv	QFGNR	GTITAASGFDPLRDAEVLR	KAMKG	2		995.0241503	1988.032701	0.000451244	7	N	189	208
P97384	Conv	RKAMK	GFGTDEQAIIDCLGSR	SNKQR	2	C12:+57.021	869.9071662	1737.798732	0.000451244	14	N	212	228
P97384	Conv	LALMK	TPVLFDVYEIK	EAIKG	2		662.3639004	1322.712201	0.000451244	9	N	269	280
P97384	Conv	LALMK	TPVLFDVYEIKEAIK	GAGTD	3		588.9981117	1763.970935	0.000622848	2	N	269	284
P97384	Conv	VYEIK	EAIKGAGTDEACLIEIFASR	SNEHI	3	C12:+57.021	717.696901	2150.067303	0.000451244	8	N	280	300
P97384	Conv	KEAIK	GAGTDEACLIEIFASR	SNEHI	2	C8:+57.021	855.4120844	1708.808569	0.000451244	17	N	284	300
P97384	Conv	SLVQR	DVQELYAAGENR	LGTDE	2		682.826202	1363.636804	0.000451244	4	N	357	369
P97384	Conv	CSRSR	AHLVAVFNEYQR	MTGRD	2		723.878572	1445.741544	0.000451244	2	N	386	398
P97384	Conv	RMYGK	SLYHDITGDTSGDYR	KILLK	2		850.3820698	1698.74854	0.000451244	6	N	477	492
P97425	Conv	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDNISR	NCHNS	3	C17:+57.021,C24:+57.021	1055.833079	3164.475838	0.000451244	27	N	62	92
P97425	Conv	YQPRR	SLEYYTVACNPR	TPQDS	2	C9:+57.021	736.8458489	1471.676098	0.000451244	10	N	125	137
P97426	Conv	YQSRR	SLEYYTVACDPR	TPQDS	2	C9:+57.021	737.3378567	1472.660113	0.000451244	31	N	124	136
P97426	Conv	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDKR	SQNCH	3	C17:+57.021,C24:+57.021	993.811727	2978.411781	0.000451244	16	N	62	90
P97426	Conv	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDK	RSQNC	3	C17:+57.021,C24:+57.021	941.7780232	2822.31067	0.000622848	1	N	62	89
P97426	Conv	NSSSR	VHITVCNITSR	ATNYT	3	C6:+57.021	433.8998127	1298.676038	0.001943752	2	N	100	111
P97429	Conv	EQSIK	SETSGSFEDALLAIVK	CMRSK	2		833.9308642	1665.846128	0.000451244	3	N	225	241
P97807	Conv	AAMPR	IYELAAGGTAVGTGLNTR	IGFAE	2		882.4684796	1762.921359	0.000451244	19	N	265	283
P97807	Conv	GSTLK	ETAIELGYLTAEQFDEWVKPK	DMLGP	2		1234.123727	2466.231854	0.000622848	9	N	480	501
P97807	Conv	GILKR	AAAEVNQEYGLDPK	IASAI	2		752.8680669	1503.720534	0.000451244	13	N	98	112
P97821	Conv	LIAGK	YAQDFGVVEESCFPYTAK	DSPCK	2	C12:+57.021	1055.975246	2109.934892	0.000451244	23	N	308	326
P97821	Conv	HTGLS	DPFNPFELTNHAVLLVGYGRDPVTGIEYWIIK	NSWGS	4		919.2323132	3672.898053	0.001591523	2	N	393	425
P97821	Conv	FRIRR	GTDECAIESIAVAAIPIPK	L-	2	C5:+57.021	978.0116314	1954.007663	0.000451244	5	N	442	461
P97821	Conv	VGYGR	DPVTGIEYWIIK	NSWGS	2		717.3879069	1432.760214	0.001463592	2	N	413	425
P97823	Conv	TTQQK	LAGVTALSCWLPLR	ASFSQ	2	C9:+57.021	778.9348013	1555.854003	0.000451244	9	N	135	149
P97823	Conv	IPSNR	IILGGFSQGGALSLYTALTTQQK	LAGVT	2		1184.150079	2366.284559	0.001162105	2	N	112	135
P97855	Conv	NSGGK	LPNFGFVVFDDSEPVQK	VLSNR	2		969.486338	1936.957076	0.000451244	4	N	374	391
P97864	Conv	RNPGK	GSWFVQALCSILNEHGK	DLEIM	3	C9:+57.021	649.3248503	1944.951151	0.000451244	2	N	237	254
P99024	Conv	LQLDR	ISVYYNEATGGK	YVPRA	2		651.3227639	1300.629928	0.000451244	1	N	46	58
P99024	Conv	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	3		1034.80789	3101.40027	0.000451244	4	N	19	46
P99024	Conv	SQQYR	ALTVPELTQQVFDAK	NMMAA	2		830.4517668	1658.887934	0.000823681	2	N	282	297
P99026	Conv	VLGVK	FDGGVVIAADMLGSYGSLAR	FRNIS	2		1000.00183	1997.98806	0.000451244	12	N	60	80

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P99026	Conv	TVTEK	GVEIEGPLSAQTNWDIAH	MISGF	2		968.9741261	1935.932652	0.002374549	1	N	240	258
P99026	Conv	QPLLR	EVLEKQPVLSQTEAR	ELVER	3		576.3165034	1725.92611	0.000451244	2	N	196	211
P99026	Conv	SRIMR	VNDSTMLGASGDYADFQYLK	QVLGQ	2		1098.002224	2193.988848	0.000622848	8	N	89	109
P99026	Conv	TVTEK	GVEIEGPLSAQTNWDIAHMISGFE	-	2		1301.118651	2600.221702	0.000451244	2	N	240	264
P99026	Conv	YVDML	GVAYEAPSLATGYGAYLAQPLLR	EVLEK	2		1191.129147	2380.242694	0.000451244	5	N	173	196
P99027	Conv	KDIKK	ILDSVGIEADDDRLNK	VISEL	2		886.955402	1771.895204	0.000451244	6	N	25	41
P99027	Conv	ELNGK	NIEDVIAQGVGK	LASVP	2		621.8385811	1241.661562	0.000451244	12	N	49	61
P99027	Conv	-MR	YVASYLLAALGGNSSPSAK	DIKKI	2		934.9917875	1867.967975	0.000451244	21	N	2	21
P99027	Conv	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	2		1387.720117	2773.424634	0.000622848	7	N	61	94
P99029	Conv	PGCSK	THLPGFVEQAGALK	AKGAQ	2		734.4018799	1466.78816	0.001839721	1	N	98	112
P99029	Conv	EGKVR	LLADPTGAFGK	ATDLL	2		545.3011031	1088.586606	0.001699387	4	N	144	155
P99029	Conv	LFKGK	KGVLFGVPGAFTPGCSK	THLPG	2	C15:+57.021	861.4560979	1720.896596	0.001463592	1	N	81	98
P99029	Conv	GAFGK	ATDLLLDDSLVSLFGNR	RLKRF	2		924.9892448	1847.96289	0.000451244	18	N	155	172
P99029	Conv	NGIVK	ALNVEPDGTGLTCSLAPNILSQL	-	2	C13:+57.021	1192.112605	2382.20961	0.000451244	9	N	187	210
P99029	Conv	GAFGK	ATDLLLDDSLVSLFGNRR	LKRFS	3		669.0291336	2004.064001	0.000451244	10	N	155	173
P99029	Conv	MAPIK	VGDAIPSVEVFEGEPGK	KVNLA	2		865.4363138	1728.857028	0.000637154	2	N	53	70
Q00519	Conv	MSQTK	DQTIAPSSSLFNPEDFKPLDPTQEPIFPPELLR	LKDTP	3		1246.968752	3737.882857	0.000451244	37	N	187	220
Q00519	Conv	PGYRR	TLLSPEEILVSIVIPYSR	KGEFF	2		1015.083145	2028.150691	0.000451244	6	N	397	415
Q00519	Conv	PEKIR	NACVDQFTTLCATGTPENCK	SWSVR	2	C3:+57.021,C11:+57.021,C19:+57.021	1143.992855	2285.970111	0.000451244	30	N	1309	1329
Q00519	Conv	YTLLR	NKPEPTVEEIENAFQGNLCR	CTGYR	2	C19:+57.021	1173.063447	2344.111293	0.000451244	16	N	131	151
Q00519	Conv	IPTSK	IHITETSTNTVPNTSPTAASASADLNGQAIYEACQTILK	RLEPF	3	C34:+57.021	1363.674585	4088.000354	0.000451244	34	N	1063	1102
Q00519	Conv	GKETR	STLISTAVALAAYK	TGRPV	2		704.9064638	1407.797328	0.000451244	19	N	807	821
Q00519	Conv	KVVEK	NADPETTLLVYLR	RKLGL	2		752.9044524	1503.793305	0.000451244	20	N	21	34
Q00519	Conv	GMCGK	LDPTFASATLLFQK	DPPAN	2		776.4250207	1550.834441	0.000451244	12	N	540	554
Q00519	Conv	GMCGK	LDPTFASATLLFQKDPPANVQLFQEVPK	GQSEE	3		1038.889045	3113.643735	0.000451244	19	N	540	568
Q00519	Conv	ARGVK	ITYEDLPAIITIQDAIK	NNSFY	2		959.0331211	1916.050642	0.000451244	19	N	689	706
Q00519	Conv	TGFYK	TPNLGYSFETNSGNPFHYFSYGVACSEVEIDCLTGDHK	NLRTD	3	C25:+57.021,C32:+57.021	1438.300487	4311.878061	0.0007646	2	N	1137	1175
Q00519	Conv	TSEAK	KVPGFVCFLTSEDVPGSNITGIFNDETVFAK	DEVTC	3	C7:+57.021	1130.230877	3387.66923	0.000451244	14	N	629	660
Q00519	Conv	IYASK	AVGEPPLFLASSIFFAIK	DAIRA	2		954.0380094	1906.060419	0.000451244	12	N	1260	1278
Q00519	Conv	KAVGE	PPLFLASSIFFAIK	DAIRA	2		775.953217	1549.890834	0.002813207	1	N	1264	1278
Q00519	Conv	PSTYK	IPAFGSIPIEFR	VSLLR	2		673.8775093	1345.739419	0.000451244	16	N	1231	1243
Q00519	Conv	FEGER	VTWIQVSTMEELLDLK	AQHPD	2		953.0060496	1903.996499	0.000451244	4	N	235	251
Q00519	Conv	LLFQK	DPPANVQLFQEVPK	GQSEE	2		791.417727	1580.819854	0.000698008	5	N	554	568
Q00519	Conv	FTLPR	CWDECIASSQYQAR	KMEVE	2	C1:+57.021,C5:+57.021	887.3696622	1772.723724	0.000451244	11	N	969	983
Q00519	Conv	VGFMK	TGTIVALEVAHFSNGGNSEDLSR	SIMER	2		1187.585832	2373.156064	0.000451244	13	N	855	878
Q00519	Conv	-MTR	TTVDELVFFVNGK	KVVEK	2		734.888271	1467.760942	0.000451244	12	N	3	16
Q00519	Conv	KQLSK	SWNEELLQDVCAGLAEELHLAPDAPGGMVEFR	RTLTL	3	C11:+57.021	1185.22943	3552.664891	0.000451244	3	N	478	510
Q00519	Conv	TVFAK	DEVTCVGHIIGAVVADTPEHAHR	AARGV	4	C5:+57.021	621.5582599	2482.20184	0.000451244	7	N	660	683
Q00519	Conv	GNLCR	CTGYRPILQGFR	TFAKD	3	C1:+57.021	489.9227288	1466.744786	0.001699387	4	N	151	163
Q00519	Conv	DSNAK	QLFQLDSPATPEK	IRNAC	2		737.3833528	1472.751106	0.000451244	11	N	1294	1307
Q00519	Conv	IPTSK	IHITETSTNTVPNTSPTAASASADLNGQAIYEACQTILKR	LEPFK	4	C34:+57.021	1062.033166	4244.101465	0.000823681	3	N	1063	1103
Q00612	Conv	HKIDR	EKPQPIPYVYGSR	GPTEA	2		767.4071623	1532.798725	0.000451244	13	N	474	487
Q00612	Conv	EFFAR	NSYVAGQYDDAASYK	HLNSH	2		826.3658884	1650.716177	0.000451244	29	N	104	119
Q00612	Conv	WWLFR	DGLLPEDTFIVGYAR	SRLTV	2		833.4282917	1664.840983	0.000451244	14	N	57	72
Q00612	Conv	KMMTK	KPGMFFNPEESELDLTYGNR	YKNVK	2	M4:+15.995	1180.547373	2359.079145	0.000451244	7	N	407	427
Q00612	Conv	RDGLL	PEDTFIVGYAR	SRLTV	2		634.3200242	1266.624448	0.001463592	1	N	61	72
Q00612	Conv	ELMKR	VGFQYEGTYK	WVNPH	2		596.2881927	1190.560785	0.001463592	2	N	498	508
Q00612	Conv	TFAAA	VLYVENERWDGVPFILR	CGKAL	3		702.3779857	2104.110557	0.000823681	3	N	340	357
Q00612	Conv	TATFA	AAVLYVENERWDGVPFILR	CGKAL	3		749.7360616	2246.184785	0.000622848	2	N	338	357
Q00612	Conv	TTATF	AAAVLYVENERWDGVPFILR	CGKAL	3		773.4150995	2317.221899	0.000622848	2	N	337	357
Q00612	Conv	ATFAA	AVLYVENERWDGVPFILR	CGKAL	3		726.0570236	2175.147671	0.000451244	1	N	339	357
Q00623	Conv	KDSGR	DYVSQFESSSLGQQLNLNLLENWDTLGSTVSQLQER	LGPLT	3		1367.001732	4097.981796	0.000451244	7	N	50	86
Q00896	Conv	VEAVK	KLDQDTVFALANYILFK	GKWKK	3		667.035337	1998.082611	0.000451244	2	N	192	209
Q00896	Conv	PPILR	FDHPFLFIIFEEHTQSPLFVGK	VVDPT	4		662.8446733	2647.347493	0.000823681	1	N	384	406
Q01102	Conv	GFVLK	GNDAIQCADSGQWTAPAPFCEALQCPEFPVPSK	AQVNC	3	C7:+57.021,C20:+57.021,C25:+57.021	1216.877983	3647.610548	0.000451244	11	N	361	394
Q01102	Conv	NSTYK	STCQFMCDEGFYLSGPER	LDCSP	2	C3:+57.021,M6:+15.995,C7:+57.02	1100.442742	2198.869883	0.000451244	8	N	471	489
Q01102	Conv	VGTNK	TLTEEAENWADNEPNNKK	NNQDC	3		701.6595461	2101.955238	0.000451244	3	N	108	126
Q01339	Conv	AIAGR	ICPKPDDLPFATVVPLK	TSYDP	3	C2:+57.021	637.3537469	1909.037841	0.000451244	13	N	21	38
Q01339	Conv	LYKDK	ATFGCHETYKLDGPEEAECTK	TGTWS	3	C5:+57.021,C19:+57.021	815.0230824	2442.045847	0.000451244	6	N	229	250
Q01339	Conv	RCVPR	VCPFAGILENGIVR	YTSFE	3	C2:+57.021	515.6136724	1543.817617	0.001654178	1	N	82	96
Q01339	Conv	GGMRR	FTCPLTGMWPINTLR	CVPRV	2	C3:+57.021,M8:+15.995	911.9529084	1821.890217	0.002727428	1	N	63	78
Q01339	Conv	TSSSK	CTEEGKWSPDIPACAR	ITCPP	3	C1:+57.021,C14:+57.021	626.2822795	1875.823439	0.000823681	1	N	123	139
Q01339	Conv	VVPLK	TSYDPGEQIVYSCKPGYVSR	GGMRR	3	C13:+57.021	769.3638105	2305.068031	0.002145581	1	N	38	58

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q01514	Conv	LIKSK	SSPDQSDVDNSANFVGFPPIFVWTLR	DFSLD	3		982.4755235	2944.403171	0.000451244	8	N	155	181
Q01853	Conv	GKKRR	EAVCIVLSDDTCSDEKIR	MNRVV	2	C4:+57.021,C12:+57.021	1055.493246	2108.970891	0.000451244	18	N	65	83
Q01853	Conv	TLLAK	AIANECQANFISIK	GPELL	2	C6:+57.021	789.9011555	1577.786711	0.000451244	37	N	529	543
Q01853	Conv	NLRVR	LGDVISIQPCPDVK	YGKRI	2	C10:+57.021	770.9059065	1539.796213	0.000451244	41	N	95	109
Q01853	Conv	RNNLR	VRLGDVISIQPCPDVK	YGKRI	2	C12:+57.021	898.4906691	1794.965738	0.000451244	7	N	93	109
Q01853	Conv	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	2		1106.586583	2211.157567	0.000451244	20	N	487	505
Q01853	Conv	NRPNR	LIVDEAINEDNSVVSLSQPK	MDELQ	2		1085.566045	2169.11649	0.000451244	37	N	25	45
Q01853	Conv	SPVAK	DVDLEFLAK	MTNGF	2		525.2798363	1048.544073	0.000451244	17	N	668	677
Q01853	Conv	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	2		1159.639879	2317.264158	0.000451244	4	N	365	386
Q01853	Conv	LSQPK	MDELQLFRGDTVLLK	GKKRR	3		593.3226013	1776.944404	0.001162105	1	N	45	60
Q01853	Conv	PSALR	ETVVEVPQVTWEDIGGLEDVKR	ELQEL	2		1249.642815	2497.270031	0.000451244	13	N	465	487
Q01853	Conv	LRPGR	LDQLIYIPLPDEK	SRVAI	2		778.9326786	1555.849757	0.000823681	10	N	638	651
Q01853	Conv	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	KKMDL	3	C26:+57.021	1224.935963	3671.784488	0.000451244	27	N	389	424
Q01853	Conv	EVERR	IVSQLLTLMDGLK	QRAHV	2		715.9185175	1429.821435	0.000451244	20	N	323	336
Q01853	Conv	EEAEK	NAPAIIFIDELDAIAPKR	EKTHG	2		984.0521795	1966.088759	0.000451244	6	N	295	313
Q01853	Conv	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	C5:+57.021	962.4799671	1922.944334	0.000451244	35	N	567	584
Q01853	Conv	TLIAR	AVANETGAFFFLINGPEIMSK	LAGES	2		1128.572619	2255.129639	0.000451244	16	N	256	277
Q01853	Conv	SNLRK	AFEEAEKNAPAIIFIDELDAIAPK	REKTH	2		1308.184316	2614.353032	0.000451244	4	N	288	312
Q01853	Conv	EEAEK	NAPAIIFIDELDAIAPK	REKTH	2		906.0016239	1809.987648	0.000451244	59	N	295	312
Q01853	Conv	EPIKR	EDEEESLNEVGYDDIGGCRK	QLAQI	2	C18:+57.021	1157.492717	2312.969834	0.000451244	12	N	191	211
Q01853	Conv	VKPPR	GILLYGPPGTGK	TLIAR	2		586.8378528	1171.660106	0.000451244	9	N	239	251
Q01853	Conv	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIRK	KMDLI	3	C26:+57.021	1267.634284	3799.879451	0.000451244	1	N	389	425
Q01853	Conv	KYGKR	IHVLPIDDTVEGITGNLFEVY	LKPYF	2		1172.607713	2343.199826	0.000622848	2	N	113	134
Q01853	Conv	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIR	KGDIF	3		1331.05097	3990.12951	0.000451244	5	N	113	147
Q01853	Conv	MDDFR	WALSQSNPSALR	ETVVE	2		665.3496473	1328.683695	0.000662267	16	N	453	465
Q01853	Conv	EDVKR	ELQELVQYPVEHPDK	FLKFG	2		912.4628629	1822.910126	0.000451244	9	N	487	502
Q01853	Conv	GKKRR	EAVCIVLSDDTCSDEK	IRMNR	2	C4:+57.021,C12:+57.021	920.9006579	1839.785716	0.000451244	19	N	65	81
Q01853	Conv	RERER	QTNPSAMEVEEDDPVPEIR	RDHFE	2		1078.494763	2154.973926	0.000451244	5	N	713	732
Q01853	Conv	AVEFK	VVETDPSPYCIVAPDTVIHCEGEPIKR	EDEEE	3	C10:+57.021,C20:+57.021	1027.83906	3080.493779	0.000451244	25	N	164	191
Q01853	Conv	MSTKK	NVFIIGATNRPDIIDPAILRPGR	LDQLI	3		840.1471243	2517.417973	0.000451244	11	N	615	638
Q01853	Conv	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPY	FLEAY	3		949.1727819	2844.494946	0.000622848	4	N	113	138
Q01853	Conv	EFLAK	MTNGFSGADLTEICQR	ACKLA	2	C14:+57.021	900.4064766	1798.797353	0.000451244	1	N	677	693
Q01853	Conv	EPIKR	EDEEESLNEVGYDDIGGCR	KQLAQ	2	C18:+57.021	1093.445235	2184.87487	0.000451244	16	N	191	210
Q01853	Conv	PSALR	ETVVEVPQVTWEDIGGLEDVK	RELQE	2		1171.59226	2341.16892	0.000451244	5	N	465	486
Q01853	Conv	RRFGR	FDREVDIGIPDATGR	LEILQ	2		830.9186225	1659.821645	0.002296037	2	N	362	377
Q01853	Conv	QAAPC	VLFFDELDSIAK	ARGGN	2		698.8720896	1395.728579	0.001162105	5	N	572	584
Q01853	Conv	AVEFK	VVETDPSPYCIVAPDTVIHCEGEPIK	REDEE	3	C10:+57.021,C20:+57.021	975.8053561	2924.392668	0.000662267	2	N	164	190
Q01853	Conv	AEKNA	PAIIFIDELDAIAPK	REKTH	2		813.4616032	1624.907606	0.000637154	1	N	297	312
Q01853	Conv	DNDIR	KYEMFAQTLQQSR	GFGSF	2	M4:+15.995	823.4043369	1644.793074	0.000823681	5	N	753	766
Q01853	Conv	RERER	QTNPSAMEVEEDDPVPEIRR	DHFEE	3	M7:+15.995	776.6978124	2327.070037	0.000451244	11	N	713	733
Q01853	Conv	GMSTK	KNVFIIGATNRPDIIDPAILRPGR	LDQLI	3		882.8454453	2645.512936	0.00091018	4	N	614	638
Q01853	Conv	FISIK	GPELLTMWFGESEANVR	EIFDK	2	M7:+15.995	976.4651229	1950.914646	0.000451244	6	N	543	560
Q01853	Conv	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIRK	GDIFL	4		1030.563918	4118.224473	0.000622848	1	N	113	148
Q01853	Conv	GLKQR	AHVIVMAATNRPNSIDPALRR	FGRFD	3		768.0907333	2301.2488	0.000823681	4	N	338	359
Q01853	Conv	GEVER	RIVSQLLTLMDGLK	QRAHV	2		793.9690731	1585.922546	0.000622848	2	N	322	336
Q01853	Conv	IRRER	ERQTNPSAMEVEEDDPVPEIR	RDHFE	3	M9:+15.995	819.7120101	2456.11263	0.000823681	3	N	711	732
Q01853	Conv	LRETV	VEVPQVTWEDIGGLEDVKR	ELQEL	2		1085.063473	2168.111345	0.000451244	5	N	468	487
Q01853	Conv	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQ	AIRKK	3	C26:+57.021	1111.528533	3331.562198	0.001943752	2	N	389	421
Q02053	Conv	SMVTK	DNPGVVTCLDEAR	HGFET	2	C8:+57.021	723.338388	1444.661176	0.000451244	5	N	226	239
Q02053	Conv	KSGVK	IHVSDQELQSANASVDDSRLEELK	ATLPS	3		895.1110213	2682.309664	0.000451244	17	N	806	830
Q02053	Conv	ERTLR	LAGTQPLEVLEAVQR	SLVLQ	2		812.4573835	1622.899167	0.000451244	15	N	678	693
Q02053	Conv	PPRPR	NEEDATELVGLAQAVNAR	SPPSV	2		950.4744903	1898.933381	0.000451244	15	N	350	368
Q02053	Conv	GSQDR	AAVASLLQSVQVPEFTPK	SGVKI	2		943.0256304	1884.035661	0.000451244	19	N	784	802
Q02053	Conv	PMEIK	VLGPYTFSICDTSNFSDYIR	GGIVS	2	C10:+57.021	1178.052016	2354.088432	0.000451244	21	N	268	288
Q02053	Conv	PDTER	IYDDDFFQNLDGVANALDNIDAR	MYMDR	2		1307.606961	2613.198322	0.000451244	22	N	558	581
Q02053	Conv	LDSYK	NGFLNLALPFFGFSEPLAAPR	HQYYN	2		1139.605111	2277.194621	0.000451244	5	N	923	944
Q02053	Conv	LIAGK	IIPAIATTTAAVVGLVCLELYK	VVQGH	2	C17:+57.021	1158.666288	2315.316976	0.000451244	16	N	889	911
Q02053	Conv	PVTAY	TGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		987.1978787	2958.570236	0.000451244	2	N	147	174
Q02053	Conv	VSQPR	LAELNSYVPVTAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		1460.77249	4379.294069	0.000451244	14	N	134	174
Q02053	Conv	LGGVK	AVTLHDQGTTQWADLSSQFYLR	EEDIG	2		1269.125124	2536.234648	0.000451244	1	N	97	119
Q02053	Conv	LSKQK	YFLVGAGAIGCELLK	NFAMI	2	C11:+57.021	805.934467	1609.853334	0.000451244	26	N	470	485
Q02053	Conv	ASNLR	AENYDISPADR	HKSKL	2		625.7865455	1249.557491	0.002212458	1	N	869	880
Q02053	Conv	TERIY	DDDFFQNLDGVANALDNIDAR	MYMDR	2		1169.533265	2337.05093	0.002813207	1	N	560	581
Q02053	Conv	SYVPV	TAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		1098.913919	3293.718357	0.000823681	2	N	144	174
Q02053	Conv	GRHVR	ALVLELCCNDESGEDVEVPYVR	YTIR-	2	C7:+57.021,C8:+57.021	1283.593688	2565.171776	0.001871652	2	N	1032	1054

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q02053	Conv	ICTLK	NFPNAIEHTLQWAR	DEFEG	2		848.9318672	1695.848134	0.000451244	6	N	635	649
Q02053	Conv	CNNIR	QLLHNFPPDQLTSSGAPFWSGPK	RCPHP	3		842.0926851	2523.254655	0.000979378	3	N	723	746
Q02053	Conv	LGGVK	AVTLHDQGTTQWADLSSQFYLREEDIGK	NRAEV	3		1070.190223	3207.547269	0.000622848	5	N	97	125
Q02053	Conv	EGLFK	QPAENVNQYLTDSK	FVERT	2		803.8895307	1605.763461	0.000451244	11	N	657	671
Q02053	Conv	NGMAK	NGSEADIDESLYSR	QLYVL	2		778.3476956	1554.679791	0.000622848	1	N	43	57
Q02053	Conv	LQWAR	DEFEGLFKQPAENVNQYLTDSK	FVERT	3		858.07877	2571.21291	0.000451244	12	N	649	671
Q02053	Conv	EKLSK	QKYFLVGAGAIGCELLK	NFAMI	3	C13:+57.021	623.0100916	1866.006875	0.000622848	10	N	468	485
Q02053	Conv	TLGTK	GNVQVVIPFLTESYSSSQDPPEK	SIPIC	3		841.0872655	2520.238396	0.001463592	2	N	604	627
Q02053	Conv	PRQNR	YDGQVAVFGSDFQEK	LSKQK	2		845.3919062	1688.768212	0.000451244	2	N	450	465
Q02357	Conv	GLASR	IIALGPTGAQFLSPVIVEIPHFASHGR	GDREL	3		943.1926222	2826.554467	0.000451244	7	N	970	997
Q02357	Conv	VIMSR	LCQDYDTIGPEGGSLR	SKLVP	2	C2:+57.021	890.9124485	1779.809297	0.002080925	1	N	1064	1080
Q02357	Conv	YGKVR	LAELLLEHDAHPNAAGK	NGLTP	3		600.3202478	1797.937344	0.000451244	22	N	546	563
Q02357	Conv	SLRSK	LVPLVQATFPENAVTK	KVKLA	2		863.9910592	1725.966518	0.000451244	7	N	1082	1098
Q02357	Conv	NAKTK	LGYSPLHQAAQQGHTDIVTLLLK	NGASP	3		835.1276183	2502.359455	0.000451244	9	N	728	751
Q02357	Conv	TTSLR	LLCSVIGGTDQAQWEDITGTTK	LIYAN	2	C3:+57.021	1197.086587	2392.157575	0.000451244	22	N	1167	1189
Q02357	Conv	TLLLK	NGASPNEVSSNGTTPLAIAK	RLGYI	2		964.4901403	1926.964681	0.000451244	15	N	751	771
Q02357	Conv	TKKVK	LALQAQPVPDELVTK	LLGNQ	2		811.4621346	1620.908669	0.000451244	6	N	1101	1116
Q02357	Conv	AELAR	ELQFSVEDINR	IRVEN	2		675.3389453	1348.662291	0.000451244	10	N	1419	1430
Q02357	Conv	NLGNK	SGLTPLHLVSQEGHVPVADVLIK	HGVTV	3		803.7887141	2408.342742	0.000451244	14	N	662	685
Q02357	Conv	DVLSK	TGFTPLHIAAHYENLNVAQLLLNR	GASVN	3		902.4894387	2704.444916	0.000622848	5	N	200	224
Q02357	Conv	AIAKR	LGYISVTDVLK	VVTDE	2		604.350793	1206.685986	0.000622848	9	N	772	783
Q02357	Conv	TDVLK	VVTDETSVVLVSDK	HRMSY	2		745.9015754	1489.787551	0.000451244	6	N	783	797
Q02357	Conv	INRIR	VENPNSLLDQSTALLTLWVDR	EGENA	2		1192.626968	2383.238337	0.000451244	1	N	1432	1453
Q02357	Conv	DFVPK	LDQVVESPAIPR	IPCVT	2		662.3675057	1322.719411	0.001229886	2	N	845	857
Q02357	Conv	NDDTR	TAAVLLQNDPNPDVLSK	TGFTP	2		897.9839625	1793.952325	0.000451244	7	N	183	200
Q02357	Conv	EDINR	IRVENPNSLLDQSTALLTLWVDR	EGENA	3		885.1489706	2652.423512	0.000451244	9	N	1430	1453
Q02357	Conv	KRVCR	IITTDFPLYFVIMSR	LCQDY	2		908.4898383	1814.964077	0.002019181	1	N	1049	1064
Q02357	Conv	DMQVW	SAGLTPSLVTAEDSSLECSKAEDSDAIPEWK	LEGAH	3	C18:+57.021	1098.517411	3292.528833	0.001463592	3	N	1565	1596
Q02357	Conv	HTAAR	EGHVDTALALLEK	EASQA	2		698.3780705	1394.740541	0.000823681	4	N	508	521
Q02357	Conv	INRIR	VENPNSLLDQSTALLTLWVDREGENAK	MENLY	3		1004.847797	3011.519991	0.000451244	4	N	1432	1459
Q02357	Conv	PAIPR	IPCVTPETVVIR	SEDQE	2	C3:+57.021	692.3871526	1382.758705	0.002212458	1	N	857	869
Q02819	Conv	TFEAR	DLELLIQTATR	DLAQY	2		636.8620562	1271.708512	0.000451244	2	N	151	162
Q03265	Conv	DVVKR	TGAIVDVPVGEELLGR	VVDAL	2		812.9493913	1623.883183	0.000451244	5	N	133	149
Q03265	Conv	SKITK	FENAFLSHVISQHQSLLGNIR	SDGKI	3		804.092908	2409.255324	0.000451244	5	N	506	527
Q03265	Conv	LAQYR	EVAAFAQFGSDLDAATQQLLSR	GVRLT	2		1169.587843	2337.160086	0.000451244	5	N	441	463
Q04750	Conv	CCSLR	VEHINLHPELDGQEYVVEFDFPGKDSIR	YYNKV	3		1094.874235	3281.599304	0.000451244	16	N	510	538
Q04750	Conv	KLALR	AGNEKEEGETADTVGCCSLR	VEHIN	2	C16:+57.021,C17:+57.021	1091.970666	2181.925732	0.000451244	9	N	490	510
Q04750	Conv	CCSLR	VEHINLHPELDGQEYVVEFDFPGK	DSIRY	3		937.7928525	2810.355158	0.000451244	8	N	510	534
Q04750	Conv	AKVFR	TYNASITLQQQLK	ELTAP	2		754.409902	1506.804204	0.000451244	12	N	592	605
Q04750	Conv	FLEHK	GPVFAPPYEPLPESVK	FYYDG	2		863.956685	1725.89777	0.000451244	9	N	225	241
Q04750	Conv	RHDNK	VTWLVSWTENIQGSIK	YIMLN	2		930.9968729	1859.978146	0.001591523	2	N	411	427
Q04750	Conv	QQQLK	ELTAPDENVPAK	ILSYN	2		642.3280462	1282.640492	0.000622848	2	N	605	617
Q05144	Conv	EDYDR	LRPLSYPQTDVFLICFSLVSPASYENVR	AKWFP	3	C15:+57.021	1091.232552	3270.674255	0.000622848	6	N	66	94
Q05144	Conv	KLKEK	KLAPITYPQGLALAK	DIDSV	2		792.4801303	1582.944661	0.001463592	4	N	132	147
Q05144	Conv	LKEKK	LAPITYPQGLALAK	DIDSV	2		728.4326487	1454.849697	0.000451244	10	N	133	147
Q05144	Conv	FPEVR	HHCPSTPIILVGTK	LDLRD	2	C3:+57.021	780.4220581	1558.828516	0.00091018	3	N	102	116
Q05144	Conv	SANVM	VDSKPVNLGLWDTAGQEDYDR	LRPLS	3		793.3806718	2377.118615	0.000451244	3	N	45	66
Q06890	Conv	GMVLG	EQEVSDNELQELSTQGSR	YINKE	2		1024.972509	2047.929417	0.000622848	12	N	21	39
Q06890	Conv	GQCEK	CQEILSVDCSTNNPAQANLR	QELND	2	C1:+57.021,C9:+57.021	1145.531225	2289.04685	0.000451244	10	N	303	323
Q06890	Conv	QVAER	LTEQYKELLQSFQSK	MLNTS	3		614.6601587	1840.957076	0.000851441	3	N	335	350
Q06890	Conv	EVVVK	LFDSDPITVVLPEEVSKDNPK	FMDTV	2		1171.610453	2341.205305	0.000451244	12	N	407	428
Q06890	Conv	DSFAR	ASGIIDTLFQDR	FFARE	2		668.349313	1334.683026	0.000698008	9	N	181	193
Q07076	Conv	RKAMK	GFGTDEQAIVDVVSNR	SNDQR	2		853.9213622	1705.827124	0.000451244	7	N	174	190
Q07076	Conv	ESGLK	TILQCALNRPAFFAER	LYYSM	3	C5:+57.021	636.3370902	1905.987871	0.000451244	10	N	383	399
Q07076	Conv	IVVTR	SEIDLVQIK	QMFTQ	2		522.8009359	1043.586272	0.000451244	8	N	421	430
Q07076	Conv	GTQER	VLIEILCTR	TNQEI	2	C7:+57.021	558.8261995	1115.636799	0.002080925	6	N	253	262
Q07076	Conv	AGEGR	LGTDESCFNMILATR	SFPQL	2	C7:+57.021	864.408488	1726.801376	0.000637154	1	N	331	346
Q07797	Conv	FYRGR	WGTVCDNLWNLLDAHVVCR	ALGYE	3	C5:+57.021,C18:+57.021	776.7054708	2327.093012	0.000451244	23	N	44	63
Q07797	Conv	LDLLK	AVDQWSTETIASHEDIER	LVEQV	2		1043.987962	2085.960324	0.000451244	16	N	323	341
Q07797	Conv	KCLHK	LASAYGATELQDYCGR	LFATL	2	C14:+57.021	887.9071662	1773.798732	0.000451244	13	N	229	245
Q07797	Conv	ALLPK	SELAVSSELDLLK	AVDQW	2		702.3855612	1402.755522	0.000823681	4	N	310	323
Q07797	Conv	DYCGR	LFATLLPQDPTFHTPLDLYAYAR	ATGDS	2		1332.197561	2662.379522	0.000451244	5	N	245	268
Q07797	Conv	TNSSK	TPSLFPCASGAFSSFR	VVIRP	2	C7:+57.021	866.4118874	1730.808175	0.000451244	11	N	546	562
Q07797	Conv	TYKPR	LYTSSTWSSLVMASTWR	AQRYE	2	M12:+15.995	996.4807729	1990.945946	0.001162105	2	N	407	424
Q07797	Conv	GYENR	VLILCGGYSVVDVTSFEGSK	APIPT	2	C5:+57.021	1065.543296	2129.070991	0.000823681	5	N	513	533

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q07797	Conv	GSVAR	YNSYQSFQTPQHPSFLFK	DKQIS	3		740.3572503	2218.048351	0.000451244	8	N	446	464
Q07797	Conv	TLILR	TNPEAQALWQVVGSSVIMR	VDAEC	3		696.030369	2085.067707	0.001162105	1	N	177	196
Q08761	Conv	SVVAR	LEAVSLCSDQQSQLK	CNVNR	2	C7:+57.021	853.4251918	1704.834784	0.000451244	9	N	560	575
Q08761	Conv	LVDSR	SGTSQDIVVFVENSVVAR	LEAVS	2		953.9976012	1905.979602	0.000979378	1	N	542	560
Q08761	Conv	AQDQK	SCEGIPVCLSLDLDKNYELLYLAEQFAGVVLYLK	FRLPD	3	C2:+57.021,C8:+57.021	1311.673875	3931.998224	0.001871652	2	N	280	314
Q08943	Conv	PVHIR	FDEISFVNFAR	GTTTT	2		672.8332987	1343.650997	0.000622848	2	N	370	381
Q08943	Conv	NVLSK	ADVIQATGDAICIFR	ELQCL	2	C12:+57.021	825.4197124	1648.823825	0.000451244	4	N	188	203
Q08943	Conv	WGTVK	FGGQLLSFDIGDQPVFEIPLSNVSQCTTGK	NEVTL	3	C26:+57.021	1085.539822	3253.596065	0.000451244	2	N	113	143
Q09014	Conv	YLVPK	DGKNNVADITGPIILQTYR	AIADY	2		1044.558357	2087.101115	0.000451244	3	N	143	162
Q09014	Conv	PKDGK	NNVADITGPIILQTYR	AIADY	2		894.4866723	1786.957745	0.000451244	5	N	146	162
Q09014	Conv	EVIHK	LLDGWWVVR	KGDIT	2		572.3196302	1142.62366	0.001162105	4	N	258	267
Q09014	Conv	QMKTK	RGWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1264.264005	3789.768615	0.000451244	24	N	201	235
Q09014	Conv	MKTKR	GWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1212.230301	3633.667503	0.000451244	22	N	202	235
Q09200	Conv	LARSR	SLADQLLIAPANSPLQYPLQGVEVQPLR	SILVP	3		1010.89279	3029.654969	0.002663018	1	N	130	158
Q09PK2	Conv	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	2		1260.145663	2518.275725	0.000622848	5	N	96	118
Q09PK2	Conv	GAEMK	ILGVWDTEISLGK	TKLKA	2		715.8986387	1429.781677	0.000451244	8	N	250	263
Q09PK2	Conv	LRFLK	ESLKGDALDVYNGLSSQAQGDFSFVK	QALLR	2		1388.177751	2774.339902	0.000451244	14	N	138	164
Q09PK2	Conv	LGKTK	LKAEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	4		934.7304004	3734.890402	0.000622848	12	N	265	299
Q09PK2	Conv	QALLR	AFGAPGEAFSEPEEILFANSMGK	GYYLK	2	M21:+15.995	1208.062856	2414.110111	0.000451244	18	N	169	192
Q09PK2	Conv	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPFNNVVK	VANGA	3		1323.013244	3966.016331	0.000451244	20	N	206	242
Q09PK2	Conv	GKKFR	LLPVGSSLEDEFDLELIEEEEGSSAPEGSH	-	3		1072.165297	3213.472492	0.000451244	14	N	309	339
Q09PK2	Conv	KTKLK	AEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		1165.578258	3493.711374	0.000979378	1	N	267	299
Q09PK2	Conv	KESLK	GDALDVYNGLSSQAQGDFSFVK	QALLR	2		1159.550926	2317.086253	0.000451244	4	N	142	164
Q09PK2	Conv	LWLHR	FEVIDDLNHWDHATK	LRFLK	3		613.9607196	1838.858759	0.001763695	1	N	118	133
Q09PK2	Conv	SKEGR	REHAFVPEPFTGTNLAPSLWLHR	FEVID	3		892.4667455	2674.376836	0.001699387	1	N	95	118
Q09PK2	Conv	EFLVA	NASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		955.4656871	2863.373661	0.002884417	1	N	273	299
Q11011	Conv	ELIQK	VLTFALSEEVRPQDTVSVIGGVAGGSK	HGRKA	3		906.1559024	2715.444307	0.000451244	17	N	795	822
Q11011	Conv	ADYTR	AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	GASVI	3		1237.927393	3710.758778	0.000451244	17	N	407	441
Q11011	Conv	PSAER	TIQQCCENILLNAAWLK	RDADS	2	C5:+57.021,C6:+57.021	1038.024319	2074.033038	0.000451244	14	N	883	900
Q11011	Conv	PPVDR	LGLQNDLFSLAR	AGIIS	2		673.8754979	1345.735396	0.000451244	18	N	616	628
Q11011	Conv	RPFER	LPAEVSPINYSLCLKPDLLDFTFEGK	LEAAA	3	C13:+57.021	989.5125441	2965.514232	0.000451244	13	N	54	80
Q11011	Conv	NVIDR	KPYPDDENLVEVK	FARTP	2		773.3939175	1544.772235	0.000451244	4	N	222	235
Q11011	Conv	NEDEK	VTLSFPSTLQTGTGTLK	IDFVG	2		875.9834312	1749.951262	0.000823681	2	N	129	146
Q11011	Conv	LPFYK	DYFNVPYPLPK	IDLIA	2		676.8484175	1351.681235	0.000451244	7	N	294	305
Q11011	Conv	TGTLK	IDFVGELNDK	MKGFY	2		575.293475	1148.57135	0.000451244	8	N	146	156
Q11011	Conv	DQWVK	LNLGTVGFYR	TQYSS	2		570.3145448	1138.61349	0.000451244	3	N	581	591
Q11011	Conv	NRIER	VLGATLSPELIQK	VLTFA	2		684.9090065	1367.802413	0.000451244	10	N	782	795
Q11011	Conv	PIGER	LGWDPKPGEGHLDALLR	GLVLG	2		937.5001141	1872.984628	0.000622848	3	N	690	707
Q11011	Conv	EPAIK	ATFDISLVVPK	DRVAL	2		595.3455106	1188.675421	0.000998612	2	N	198	209
Q11011	Conv	KFQQK	NAATEDLWESLESASGKPIAAVMNTWTK	QMGFP	3		1007.494367	3019.4597	0.000451244	6	N	472	500
Q11011	Conv	PSAER	TIQQCCENILLNAAWLKR	DADSI	3	C5:+57.021,C6:+57.021	744.3858496	2230.134149	0.002519933	2	N	883	901
Q11011	Conv	AGEVR	YAAVTQFEATDAR	RAFPC	2		721.8496771	1441.683754	0.001654178	1	N	173	186
Q11011	Conv	KAAWK	FIKDNWEELHNR	YQGGF	4		400.9526465	1599.779386	0.000451244	1	N	830	842
Q11011	Conv	SADLR	SPVYLTVLK	HGDGA	2		510.3109395	1018.606279	0.001943752	1	N	745	754
Q11136	Conv	YFKEK	YAVDDVQYTDEIASVLTSR	NPSVL	2		1073.02147	2144.027341	0.000451244	9	N	120	139
Q11136	Conv	NETLK	VPLALFALNR	QRLCE	2		557.3431053	1112.670611	0.002145581	2	N	17	27
Q20BD0	Conv	DPVKK	IFVGGLNPEATEEK	IREYF	2		752.3886352	1502.76167	0.001463592	4	N	160	174
Q20BD0	Conv	ATEEK	IREYFGQFGEIEAIELPIDPK	LNKRR	3		822.0973247	2463.268574	0.000451244	11	N	174	195
Q20BD0	Conv	EEKIR	EYFGQFGEIEAIELPIDPK	LNKRR	2		1098.049499	2194.083399	0.000451244	13	N	176	195
Q3TBD2	Conv	LVRGY	RSPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1151.590164	3451.747091	0.000451244	4	N	90	124
Q3TBD2	Conv	VRGYR	SPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1099.55646	3295.64598	0.000451244	8	N	91	124
Q3TBD2	Conv	HQVHK	SWPISISDTEVGLDTSSGDLK	KFDRT	2		1104.03986	2206.06412	0.001871652	1	N	617	638
Q3TBD2	Conv	KLQGR	LQLFGQDFSQAALSTPDGVPFIVK	KCVCE	2		1289.681744	2577.347887	0.000451244	3	N	752	776
Q3THK7	Conv	KVILK	NFLYDIAGCSGNFTVQNR	ELECI	2	C9:+57.021	1038.484104	2074.952607	0.000451244	5	N	204	222
Q3THK7	Conv	HNINR	VVYIFGPPVKEPPTDVTPTFLTTGVLSTLR	QADFE	3		1082.267634	3243.779501	0.000823681	6	N	559	589
Q3THK7	Conv	QGDCR	SYSYVCGISSKDEPDWESLIFLAR	LIPRM	3	C6:+57.021	941.4499438	2821.326431	0.001329271	1	N	524	548
Q3THK7	Conv	DRRVR	ELFVQSEIFPLETPAFAIK	EQGFR	2		1090.088428	2178.161255	0.000451244	3	N	46	65
Q3TIU4	Conv	DSFIR	TVSYNILADTYAQTEFSR	TVLYP	2		1040.005623	2077.995647	0.001943752	1	N	295	313
Q3TRM8	Conv	HPGER	ASVCPHEGVPRPSGSLELECLQQFK	VTRTQ	4	C4:+57.021,C20:+57.021	707.0984763	2824.362705	0.000622848	4	N	14	39
Q3TRM8	Conv	TKGFR	CSGVEGQDVVQLLR	DAIQR	2	C1:+57.021	780.3962373	1558.776875	0.000451244	1	N	187	201
Q3TRM8	Conv	NQGLK	LGFNFSFPCHQTGLDR	STLIS	2	C9:+57.021	948.4467929	1894.877986	0.001839721	2	N	160	176
Q3TRM8	Conv	LNWTK	GFNASGCEGQDVVYLLR	EAIRR	2	C7:+57.021	942.9493654	1883.883131	0.000451244	24	N	626	643
Q3TRM8	Conv	VLLVR	VAEGSVQIINQVYSIPECR	AQGSG	2	C18:+57.021	1081.549444	2161.083287	0.000451244	20	N	552	571
Q3TRM8	Conv	TGTAR	VHTILQDLGLSPR	ASDAE	2		724.9151545	1447.814709	0.000451244	17	N	362	375
Q3TRM8	Conv	PTYVR	ATPDGSERGDFLALDLGGTNFR	VLLVR	3		770.3772617	2308.108385	0.000451244	9	N	525	547

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3TRM8	Conv	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	C1:+39.994	983.4668312	1964.918062	0.000451244	5	N	143	160
Q3TRM8	Conv	PTYVR	STPHGTEQGDFLVLELGATGASLR	VLWVT	2		1228.624957	2455.234314	0.000451244	4	N	78	102
Q3TRM8	Conv	GSGQK	LFDHIVDCIVDFQKR	QGLSG	3	C8:+57.021	635.6614624	1903.960987	0.000451244	12	N	578	593
Q3TRM8	Conv	AVCTR	AAQLCAAALAAVLSR	LQHSR	2	C5:+57.021	743.4142331	1484.812866	0.000451244	17	N	392	407
Q3TRM8	Conv	SFPCK	QLGLDQGILLNWTK	GFNAS	2		799.9491943	1597.882789	0.000451244	10	N	612	626
Q3TRM8	Conv	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	2	C18:+57.021	1036.019791	2070.023981	0.000451244	14	N	593	612
Q3TRM8	Conv	RVEPR	SREFVIPQEVILGAGQQLFDFAAR	CLSEF	3		897.8138109	2690.418033	0.000451244	13	N	119	143
Q3TRM8	Conv	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDRESLTPGAQR	FEKMI	3	C2:+57.021	1401.999068	4202.973805	0.000451244	14	N	265	303
Q3TRM8	Conv	EPRSR	EFVIPQEVILGAGQQLFDFAAR	CLSEF	2		1224.650246	2447.284893	0.000451244	25	N	121	143
Q3TRM8	Conv	TLSTR	FDTSVDQASINPGK	QRFEK	2		739.8602419	1477.704884	0.000451244	12	N	729	743
Q3TRM8	Conv	AVSRR	AAQLCGAGVAAVVEK	IRENR	2	C5:+57.021	722.3851412	1442.754682	0.000622848	9	N	834	849
Q3TRM8	Conv	GSGQK	LFDHIVDCIVDFQK	RQGLS	2	C8:+57.021	874.937738	1747.859876	0.000451244	15	N	578	592
Q3TRM8	Conv	LQHSR	EQQTLQVAVATGGR	VFERH	2		729.3895008	1456.763402	0.000451244	13	N	412	426
Q3TRM8	Conv	DGSGK	GAALVTAVACR	LTQMA	2	C10:+57.021	544.7979733	1087.580347	0.000622848	4	N	904	915
Q3TRM8	Conv	GEIVR	HILLHLTNLGVLFR	GQKTQ	3		549.3353925	1644.982777	0.000451244	3	N	760	774
Q3TRM8	Conv	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDR	ESLTP	3	C2:+57.021	1088.839937	3263.49641	0.000451244	3	N	265	294
Q3TRM8	Conv	ATVRK	LAPQCTVTFLQSEDGSGK	GAALV	2	C5:+57.021	969.467588	1936.919576	0.000451244	3	N	886	904
Q3TRM8	Conv	GASLR	VLWVTLTGTK	ECRVE	2		559.3349459	1116.654292	0.000451244	5	N	102	112
Q3TRM8	Conv	SATVR	KLAPQCTVTFLQSEDGSGK	GAALV	2	C6:+57.021	1033.51507	2065.014539	0.000451244	6	N	885	904
Q3TRM8	Conv	QRFEK	MIGGLYLGELVR	LVLVH	2		660.8713702	1319.72714	0.000451244	5	N	306	318
Q3TRM8	Conv	IFKTK	FLSEIESDSLALR	QVRAI	2		740.3886352	1478.76167	0.000451244	3	N	790	803
Q3TRM8	Conv	FKVTR	TQLQQIQASLLCSMEQALK	GQDSP	2	C12:+57.021	1095.56678	2189.11796	0.000622848	4	N	42	61
Q3TW96	Conv	APEAR	AALLAELASLEADALR	EHCQR	2		813.9572164	1625.898833	0.000451244	9	N	31	47
Q3TW96	Conv	NILVR	LADPVFIGFCVLQGADCGAK	VVEKA	2	C10:+57.021,C17:+57.021	1069.524152	2137.032703	0.00091018	12	N	261	281
Q3TXS7	Conv	FILFR	TPEQCPSVVSLLSESYNPHVR	YGAAM	3	C5:+57.021	800.3938812	2398.158243	0.000451244	4	N	628	649
Q3TXS7	Conv	TYLPK	DTSPGSAYQEGGGLYALGLIHANHGGDIIDYLLNQLK	NASND	4		968.4884075	3869.92243	0.000622848	4	N	429	466
Q3TXS7	Conv	FALHK	LNAVVNDFWAEISESVDKIEVLYEDEGFR	SRQFA	3		1129.552938	3385.635415	0.00091018	1	N	26	55
Q3TXS7	Conv	DHYTK	QCVENADLPEGEKKPIDQR	LEGIV	4	C2:+57.021	557.2763448	2225.074179	0.000622848	2	N	110	129
Q3TXS7	Conv	IQNLR	TVGTPIASVPGSTNTGTVPGSEKDSDPMETEEK	TASAV	3	M28:+15.995	1112.188025	3333.540675	0.001463592	1	N	269	302
Q3U0V1	Conv	EYYKK	IGQQPQQPGAPPQQDYTK	AWEEY	2		990.9928502	1979.9701	0.0025889	1	N	629	647
Q3U0V1	Conv	EHAAR	IINDLLQSLR	SGPPG	2		592.8540342	1183.692468	0.000823681	1	N	385	395
Q3U1J4	Conv	VLSSR	IEVQDSSGGTTALRPSASTQALSSSVSSSK	LFSSS	3		980.1586999	2937.4527	0.000451244	16	N	739	769
Q3U1J4	Conv	FHTER	KTEPATGFIDGDLIESFLDISRPK	MQEVV	3		883.797715	2648.369745	0.000451244	22	N	1080	1104
Q3U1J4	Conv	KGESK	DLLFILTAK	YNACI	2		517.3187645	1032.621929	0.002145581	2	N	74	83
Q3U1J4	Conv	LWPLR	SDPGRETDDTLVLSFVGQTR	VLMLN	3		731.6981123	2192.070937	0.000451244	5	N	414	434
Q3U1J4	Conv	NVQDR	IGRPSETGIIGIIDPECR	MIGLR	3	C17:+57.021	661.6828147	1982.025044	0.000622848	9	N	111	129
Q3U1J4	Conv	VIDVK	FLYGCQAPTICFVYQDPQGR	HVKTY	2	C5:+57.021,C11:+57.021	1210.561797	2419.107994	0.000451244	8	N	168	188
Q3U1J4	Conv	GDLMR	SVLLLAYKPMEGNFEEIAR	DFNPN	3	M10:+15.995	732.7177081	2195.129724	0.001654178	3	N	928	947
Q3U1J4	Conv	DISAR	ILKLPSFELLHK	EMLGG	3		479.9663061	1436.875518	0.002019181	1	N	567	579
Q3U2G2	Conv	PISLR	WNSPAEEGLSDCEVFPK	NHAAP	2	C12:+57.021	982.9386633	1963.861727	0.000622848	6	N	405	422
Q3U2G2	Conv	LTFYR	KEPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1143.901679	3428.681637	0.000451244	7	N	436	466
Q3U2G2	Conv	TFYRK	EPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1101.203358	3300.586674	0.000451244	13	N	437	466
Q3U2G2	Conv	VEAEK	SNLAYDIVQLPTGLTGIK	VTYME	2		952.0309127	1902.046225	0.000451244	19	N	84	102
Q3U2G2	Conv	VAVAR	AGGIETIANEYSDR	CTPAC	2		748.3553237	1494.695047	0.000451244	3	N	19	33
Q3U2G2	Conv	KGKLK	VLATAFDTTLGGR	KFDEV	2		661.3596807	1320.703761	0.001463592	4	N	221	234
Q3U2G2	Conv	KAKVK	TSTVDLPIESQLLWQLDR	EMLGL	2		1057.560566	2113.105531	0.000451244	15	N	575	593
Q3U2G2	Conv	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDK	KLPEM	3		1110.149815	3327.426044	0.000451244	6	N	800	834
Q3U2G2	Conv	ISSFK	NKEDQYEHLDAADVTK	VEKST	3		625.9626774	1874.864632	0.000823681	4	N	719	735
Q3U2G2	Conv	TFTLK	LEDTENWLYEDGEDQPK	QVYVD	2		1040.953253	2079.890907	0.000451244	17	N	653	670
Q3U2G2	Conv	SKLKK	EDIYAVEIVGGATR	IPAVK	2		746.8862597	1491.756919	0.000451244	1	N	332	346
Q3U2G2	Conv	KFFGK	ELSTTLNADEAVTR	GCALQ	2		760.3840812	1518.752562	0.001943752	2	N	360	374
Q3U2G2	Conv	KEEEK	MQVDQEEPHTEEQQQQPQTPAENKAESEEMETSQAGSK	DKKTD	4	M1:+15.995,M30:+15.995	1087.220508	4344.850833	0.002663018	1	N	521	559
Q3U2G2	Conv	ESVLK	KPVVDCVVSVPSFYTDAERR	SVMDA	3	C6:+57.021	775.3953335	2323.1626	0.002296037	1	N	134	154
Q3U5Q7	Conv	PDTRR	DLLQLLGSCQEAARPQLAEFQADSQGLLWQR	LWELQ	3	C9:+57.021	1181.267095	3540.777886	0.000451244	6	N	144	175
Q3U7R1	Conv	LRLER	LTPRPTAAELEEVLQVNSLIQTQK	SSELA	3		893.4961475	2677.465042	0.000451244	3	N	754	778
Q3U7R1	Conv	QVHLR	LEWLSLLPDAEKLDQVLQWNR	GITSR	3		856.1275069	2565.359121	0.000451244	9	N	435	456
Q3U7R1	Conv	LGRYK	VSLTTVLNSGFLDEWLTLEDVPSGR	LHLRL	2		1374.708687	2747.401774	0.000662267	1	N	722	747
Q3U7R1	Conv	SHKTK	TVSQSSAPVWEESASFLIR	KPHAE	2		1047.529266	2093.042931	0.000622848	3	N	822	841
Q3U7R1	Conv	KDDSR	ALTLGALTLPLAR	LLTAS	2		655.414259	1308.812918	0.000451244	5	N	540	553
Q3U7R1	Conv	IQTQK	SSELAAALLSVFLER	AEDLP	2		803.4464845	1604.877369	0.000451244	8	N	778	793
Q3UDE2	Conv	KDYMK	LSQESPQVLLNQFPCENLLTVK	DCLAS	2	C15:+57.021	1279.170454	2556.325309	0.000451244	1	N	341	363
Q3UM45	Conv	SNRIR	AIENIDTLTNLESLFLGK	NKITK	2		996.0389348	1990.06227	0.000451244	9	N	200	218
Q3UM45	Conv	NKITK	LQNLDALTNLTVLSVQSNR	LAKIE	2		1050.076914	2098.138229	0.000451244	8	N	223	242
Q3UM45	Conv	LVNLR	ELYLSNNGIEVIEGLENNNK	LTMLD	2		1131.566576	2261.117553	0.000622848	3	N	256	276
Q3UND0	Conv	SSPQR	SQPIDDEIYEELPEEEEDTASVK	MDEQG	2		1333.098497	2664.181395	0.000451244	7	N	251	274

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3UND0	Conv	IKDVK	SVYLQEFQDKGDAEDGDEYDDPFAGPADTISLASER	YDKDD	3		1317.584131	3949.728994	0.001162105	2	N	56	92
Q3UND0	Conv	LASER	YDKDDDGPSDGNQFPPIAAQDLPFVIK	AGYLE	3		988.1422101	2961.40323	0.000870037	2	N	92	119
Q3UND0	Conv	TSGDK	STDYANFYQGLWDCTGALSDELSFK	RGDVI	2	C14:+57.021	1444.639912	2887.264225	0.000451244	3	N	293	318
Q3UND0	Conv	-M	PNPSCTSSPGPLPEEIR	NLLAD	2	C5:+57.021	919.4413732	1836.867146	0.001763695	1	N	1	18
Q3UND0	Conv	PEEIR	NLLADVETFVADTLKGENLSK	KAKEK	3		759.7377965	2276.189989	0.002212458	1	N	18	39
Q3UP87	Conv	GLNFR	SVQVVLGAHDLR	RQERT	2		647.3678401	1292.72008	0.000451244	13	N	77	89
Q3UP87	Conv	MCRRR	VNVCTLVPR	RQAGI	2	C4:+57.021	529.2950665	1056.574533	0.000451244	12	N	183	192
Q3UP87	Conv	TLVPR	RQAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C6:+57.021,C16:+57.021	1017.502893	3049.48528	0.000451244	20	N	192	220
Q3UP87	Conv	AGICF	GDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C9:+57.021	1109.549975	2217.08435	0.000622848	6	N	199	220
Q3UP87	Conv	AFAPV	AEFADWINSIIR	SHNDH	2		717.8729553	1433.730311	0.000823681	2	N	235	247
Q3UP87	Conv	RRQAG	ICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C2:+57.021,C12:+57.021	1319.641307	2637.267014	0.000451244	5	N	196	220
Q3UP87	Conv	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C5:+57.021,C15:+57.021	1447.699885	2893.384169	0.000451244	22	N	193	220
Q3UP87	Conv	PRRQA	GICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C3:+57.021,C13:+57.021	1348.152039	2694.288478	0.000451244	18	N	195	220
Q3UP87	Conv	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIR	SHNDH	2	C3:+57.021	1442.19245	2882.369299	0.000451244	23	N	220	247
Q3UP87	Conv	SLQRR	GGHFCGATLIAR	NFVMS	2	C5:+57.021	630.3196042	1258.623608	0.002212458	1	N	49	61
Q3UP87	Conv	GLNFR	SVQVVLGAHDLRR	QERTR	3		483.9481971	1448.821191	0.002145581	1	N	77	90
Q3UQ44	Conv	LLYYR	YMNPAIVAPDGFDIIDMTAGGQINSNQR	RNLGS	3		1003.480064	3007.416791	0.002374549	1	N	1107	1135
Q3UW53	Conv	LPEGR	GSTSQSTSGGLTENTSCPGPIEEPFEAQEPAEK	VLPAI	3	C17:+57.021	1141.511096	3421.509888	0.002663018	1	N	785	818
Q3UW53	Conv	EREVR	EKEAQPLEAEAPGVDLGILPEGR	GSTSQ	3		806.7557387	2417.243816	0.000451244	2	N	762	785
Q3UW53	Conv	VLLPK	AFPVYLWQPYLR	HGYFC	2		776.9197085	1551.823817	0.000451244	1	N	159	171
Q3UW53	Conv	HDYMK	QTTFEAQAFLEAVQFFR	QEKGH	3		678.3429411	2032.005423	0.000637154	3	N	203	220
Q3UW53	Conv	EVREK	EAQPLEAEAPGVDLGILPEGR	GSTSQ	2		1081.06093	2160.10626	0.001463592	2	N	764	785
Q3UW53	Conv	TIRKK	IFQEALIQITLPTVQK	ALAST	2		921.5409163	1841.066233	0.000451244	9	N	493	509
Q3UW53	Conv	FSEVR	ALFEKEVDELSQSFHATQDSAQLK	EGLQQ	3		907.7842456	2720.329337	0.000451244	5	N	365	389
Q3UYV9	Conv	KVGEK	SACSLESNLEGLAGVLEADLPNYK	SKILR	2	C3:+57.021	1275.623534	2549.231468	0.000451244	2	N	41	65
Q3UZ39	Conv	KSDSR	ASNSPEQSSCLEGLDSEVPGPTEDLKTDLGK	GSFEP	3	C10:+57.021	1087.508915	3259.503346	0.000622848	8	N	344	375
Q3UZ39	Conv	LAGAK	CEQQVQSQDQENTSDLKNSEQIESHK	VTNKS	4	C1:+57.021	773.0986746	3088.363498	0.000451244	3	N	310	336
Q3UZ39	Conv	CTDSR	GTGGNQREDEVQAGDTTVEDQVGTVASGPAK	QSKGT	3		1025.148864	3072.423191	0.000451244	7	N	401	432
Q3UZA1	Conv	EPDTK	QKEEAPLEPSCSPGADHAAGEITSEIQNEK	AVSMD	4	C11:+57.021	806.37725	3221.4778	0.000851441	1	N	368	398
Q3UZA1	Conv	NAGEK	VGQNPDTASQGHPEVQAPSQTGSPEAENGCGSPR	EETTP	3	C30:+57.021	1149.513945	3445.518436	0.000451244	6	N	265	299
Q3UZZ4	Conv	QHPER	TLYWVAPLNTDAR	ALEYY	2		760.3993372	1518.783074	0.000451244	15	N	277	290
Q3UZZ4	Conv	DYRIR	YGQGGGTVAFNNNLYVNWYNGGNIAK	INLTT	2		1396.165312	2790.315024	0.001162105	8	N	316	342
Q3UZZ4	Conv	LEYYR	LYDSLDNLLIYSHFR	DYRIR	2		934.9812228	1867.946846	0.000451244	10	N	296	311
Q3UZZ4	Conv	PFDQK	LYVYNDGYLLNYDLVFLQTPR	QPV-	2		1290.163187	2578.310773	0.000451244	30	N	481	502
Q3UZZ4	Conv	KMQER	IQSINYHPFDQK	LYVYN	2		745.3758621	1488.736124	0.000451244	13	N	469	481
Q3UZZ4	Conv	TLNTK	TEEIFYYYDTNTER	EGNLG	2		922.4052106	1842.794821	0.000451244	20	N	441	455
Q3UZZ4	Conv	EVMEK	DSISYTELDFELIK	LEVKE	2		836.9199652	1671.82433	0.000451244	4	N	138	152
Q3UZZ4	Conv	DRVER	LEYTAHILSQK	FEREF	2		651.8567739	1301.697948	0.000451244	10	N	93	104
Q3UZZ4	Conv	LLVEK	LESLDQNNVLSIR	RQILA	2		750.9049838	1499.794368	0.000451244	7	N	192	205
Q3UZZ4	Conv	AYNNR	FSYANVNWQDIDLAVDEQALWAIYATEASTGNIVISK	LNDTT	3		1372.67993	4115.01639	0.000870037	6	N	364	401
Q3UZZ4	Conv	KLYVY	NDGYLLNYDLVFLQTPR	QPV-	2		1021.023619	2040.031638	0.002374549	1	N	485	502
Q3V0K9	Conv	SFKDK	SISTSLPVLDLIDAIAPNAVR	QEMIK	2		1083.112965	2164.210331	0.000451244	8	N	546	567
Q3V1G4	Conv	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	2	C1:+57.021	1057.513058	2113.010516	0.000451244	2	N	489	508
Q3V1G4	Conv	QGASR	KEDFYTVETITSGSSCK	CACVA	2	C16:+57.021	976.4516036	1950.887607	0.000451244	14	N	98	115
Q3V1G4	Conv	GSSCK	CACVAPPSAVNPCEGDFR	LQKLR	2	C1:+57.021,C3:+57.021,C13:+57.021	1003.92933	2005.84306	0.000451244	8	N	115	133
Q3V1G4	Conv	EYEER	FLQEETVSQQINSIELLR	TQPLV	2		1074.071298	2146.126995	0.000451244	1	N	245	263
Q3V1G4	Conv	SRDLK	LSTIIDLLEGAFYGLDLLK	LHSVT	2		1047.590803	2093.166006	0.000451244	11	N	146	165
Q3V1G4	Conv	QIVPR	LLFENEYSYTTQIDYNPK	DRLLY	2		1119.534214	2237.052827	0.001699387	1	N	707	725
Q3V1L4	Conv	TGKLK	IGTYTGPLQHGIVYSGGSSDTICDLLGAK	GKDIL	3	C23:+57.021	994.162574	2979.464322	0.000451244	15	N	313	342
Q3V1L4	Conv	GNLLK	VDAYGNLLVCAHGFNFIR	GPETR	3	C10:+57.021	689.3477664	2065.019899	0.000735798	4	N	111	129
Q3V1L4	Conv	LLGAK	GKDILYIGDHIFGDILK	SKKRQ	3		639.6880487	1916.040746	0.000451244	12	N	342	359
Q3V1L4	Conv	LTVER	LVSIGYPQELLSFAYDSTFPTR	GLVFD	2		1252.639544	2503.263489	0.000451244	11	N	76	98
Q3V1L4	Conv	DDTER	FYILNTLFNLPETYLLACLVDFFTNCPR	YTSCD	3	C18:+57.021,C26:+57.021	1152.245538	3453.713215	0.000451244	7	N	149	177
Q3V1L4	Conv	AELYK	HLDSSSNERPDISSIQR	RIKKV	3		647.6527258	1939.934777	0.000451244	1	N	404	421
Q3V1L4	Conv	RQGWR	TFLVIPELAQELHVWTDK	SSLFE	3		713.7215295	2138.141189	0.002981883	1	N	367	385
Q3V1L4	Conv	VWTDK	SSLFEELQSLDIFLAELYK	HLDSS	2		1123.086082	2244.156564	0.000451244	2	N	385	404
Q3V1L4	Conv	LAVYK	SPEYESLGFELTVER	LVSIG	2		878.425946	1754.836292	0.000622848	2	N	61	76
Q3V1L4	Conv	SQVMR	YADLYAASFINLLYYPFSYLFR	AAHVL	2		1355.683755	2709.35191	0.000823681	2	N	456	478
Q3V3R1	Conv	VPVDK	LIAEESVSLLAAALR	IQNMV	2		778.4568522	1554.898104	0.001463592	1	N	310	325
Q571E4	Conv	LGISK	NTFVFFTSDNGAALISAPNEGGSNGPFLCGK	QTTFE	3	C29:+57.021	1063.836749	3188.486848	0.000451244	7	N	277	308
Q571E4	Conv	TQHAR	QSPFFLYWAIDATHAPVYASR	QFLGT	3		814.0748544	2439.201163	0.000451244	9	N	220	241
Q571E4	Conv	DSVGK	ILSLLQNLGISK	NTFVF	2		649.9062668	1297.796934	0.000451244	10	N	265	277
Q571E4	Conv	FHPLK	HGFDEWFGSPNCHFGPYDNK	AKPNI	3	C12:+57.021	804.3363662	2409.985699	0.001162105	1	N	150	170
Q571I9	Conv	QKHQR	LLWTLESLVTGR	AVREV	2		694.4013486	1386.787097	0.000451244	15	N	117	129

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q571I9	Conv	SPRAR	AGLLWALAAALER	RKPVL	2		677.8962334	1353.776867	0.000451244	15	N	588	601
Q571I9	Conv	KPEHR	NPAPCQDPITGENLASCLQAEAEDIAAAVEAAK	IAFKA	3	C5:+57.021,C17:+57.021	1142.204907	3423.591321	0.000451244	10	N	54	87
Q571I9	Conv	AKDIR	GAVEAAHQAAPGWGAQSPR	ARAGL	2		930.9591447	1859.902689	0.000823681	1	N	567	586
Q571I9	Conv	VWSER	LGQALELGYGLQVGTVWINAHGLR	DPAVP	3		855.8032461	2564.386338	0.000451244	5	N	434	458
Q571I9	Conv	TWGTR	VQDQGQTLQVTGLR	GPVLR	2		771.9158828	1541.816166	0.000451244	9	N	637	651
Q571I9	Conv	QPSTR	EIFTTLEYGPVPESHACALAWLDTHNR	LLGHH	3	C17:+57.021	1043.169951	3126.486454	0.000451244	6	N	11	38
Q5FWK3	Conv	KTFLR	ELPEPLLTFDLYPHVVGFLNIDESQR	VEVTQ	3		1014.525995	3040.554586	0.000451244	7	N	323	349
Q5RKN9	Conv	RIAAK	FITHAPPGEFNEVFNDVR	LLLNN	2		1045.011043	2088.006486	0.000979378	3	N	19	37
Q5RKN9	Conv	TVYAK	TIDGQQTIIACIESHQFQPK	NFWNG	2	C11:+57.021	1157.578733	2313.141865	0.000451244	13	N	146	166
Q5RKN9	Conv	DSALR	AYVKDHYSNGFCTVYAK	TIDGQ	3	C12:+57.021	674.9844937	2021.930081	0.000451244	7	N	129	146
Q5RKN9	Conv	DHLRK	EASDPQPEDVDGGLK	SWRES	2		778.8578962	1555.700192	0.000622848	8	N	103	118
Q5RKN9	Conv	LVSHK	DVQDSVTVSNEIQTTK	EFIKI	2		882.4370421	1762.858484	0.000451244	18	N	210	226
Q5RKN9	Conv	RSEWK	FTITPPSAQVVGVLK	IQVHY	2		778.956488	1555.897376	0.000451244	15	N	178	193
Q5RKN9	Conv	RAYVK	DHYSNGFCTVYAK	TIDGQ	2	C8:+57.021	781.3409307	1560.666261	0.000451244	5	N	133	146
Q5SQX6	Conv	VRKKK	NVLISVLQAIR	KTICD	2		613.3855015	1224.755403	0.001654178	5	N	503	514
Q5SUR0	Conv	PGQHR	LGGTALAQCFSQLGEHPPDLDLPENLVR	AFHIT	3	C9:+57.021	1016.513718	3046.517755	0.000451244	22	N	861	889
Q5SUR0	Conv	EVGPR	LNFSTPASTNIVSVCQAAGLR	AVDRV	2	C15:+57.021	1103.568168	2205.120736	0.000451244	10	N	93	114
Q5SUR0	Conv	LDTFR	GVAFVGGFSYADVLGSAK	GWAAA	2		872.9493913	1743.883183	0.000451244	8	N	1108	1126
Q5SUR0	Conv	KAAAR	LAVSEALTNLVFALVTDLR	DVKCS	2		1023.086219	2044.156839	0.000451244	14	N	740	759
Q5SUR0	Conv	KIEAK	GLVPLHWADDDGNPTEQYPLNPNGSPGGIAGICSQDGR	HLALM	3	C33:+57.021	1325.617293	3973.828478	0.000451244	15	N	1251	1289
Q5SUR0	Conv	SMAAR	VGTETVQAPGSLVISAYAVCPDITATVTPDLK	HPGGK	3	C20:+57.021	1091.902648	3272.684545	0.000451244	9	N	810	842
Q5SUR0	Conv	IYTSR	FQLGDPTLNALEIWGAEYQESNALLLRPSDR	DFLSR	3		1172.930632	3515.768495	0.001162105	1	N	541	572
Q5SUR0	Conv	VGELR	ALWEETSFQLDLLQAEPR	CVIEE	2		1073.544916	2145.074231	0.000622848	2	N	1007	1025
Q5SUR0	Conv	CPLVR	DDVAQEPWLVPGSNDLLLEVGPR	LNFST	2		1260.142983	2518.270365	0.000451244	8	N	70	93
Q5SUR0	Conv	QELQR	NPSTVEVFDLAQSNSEHSR	HWFFK	2		1058.998861	2115.982122	0.000451244	3	N	212	231
Q5SUR0	Conv	DYGNK	FGEPVLAGFAR	SLGLQ	2		582.3145448	1162.61349	0.000451244	3	N	395	406
Q5SUR0	Conv	PALEK	ANQELGLALDSWDLDFYTK	RFQEL	2		1100.034381	2198.053161	0.000622848	4	N	186	205
Q5SUR0	Conv	SMAAR	VGTETVQAPGSLVISAYAVCPDITATVTPDLKHPGGK	GHLLY	4	C20:+57.021	938.241328	3748.934112	0.000451244	5	N	810	847
Q5SUR0	Conv	CLVGK	TGQGDAPLTPPTPVDLDLDWVLGK	MPQKE	3		835.7677558	2504.279867	0.000451244	2	N	610	634
Q5SUR0	Conv	NRVIR	ACVEAPGGNPICSLHDQGAGGNGNVLK	ELSDP	3	C2:+57.021,C12:+57.021	898.0906012	2691.248404	0.001162105	2	N	500	527
Q5SUR0	Conv	KAAAR	LAVSEALTNLVFALVTDLRDVK	CSGNW	3		796.456853	2386.347159	0.000451244	3	N	740	762
Q5SUR0	Conv	IYTSR	FQLGDPTLNALEIWGAEYQESNALLLRPSDRDFLSR	ASARE	4		1034.528064	4134.081056	0.001871652	2	N	541	577
Q5SUR0	Conv	GKKVK	FLRPEDSTRPSCFQQQQGLR	HVVFT	3	C12:+57.021	817.4050031	2449.191609	0.001699387	1	N	282	302
Q5SUR0	Conv	QCTGR	GAHVVAGTAGYCFGNLHIPDYNLPWEDPSFQYPGNFAR	PLEVA	4	C12:+57.021	1060.246205	4236.953619	0.000870037	1	N	339	377
Q5SVD0	Conv	ICSPR	LCPLSFGEGVEFDPLPPK	EIKYT	2	C2:+57.021	1001.503442	2000.991284	0.002374549	1	N	86	104
Q5XJF6	Conv	TPRPK	FSVCVLGDQQHCDEAK	AVDIP	2	C4:+57.021,C12:+57.021	946.9169766	1891.818353	0.000451244	16	N	62	78
Q5XJF6	Conv	KKLAK	KYDAFLASESLIK	QIPRI	2		742.9039211	1483.792242	0.002981883	1	N	105	118
Q5XJY5	Conv	NVDKK	LFTAESLIGLK	NPEKS	2		596.3533357	1190.691071	0.002296037	1	N	336	347
Q60605-2	Conv	GDVMR	ALGQNPTNAEVLK	VLGNP	2		677.8704126	1353.725225	0.000451244	21	N	37	50
Q60605-2	Conv	QTVAK	NKDQGTYEDYVEGLR	VFDKE	2		893.9162768	1785.816954	0.000451244	23	N	79	94
Q60605-2	Conv	EMNVK	VLDFEHFLPMLQTVAK	NKDQG	3		630.0066132	1886.996439	0.000451244	12	N	63	79
Q60605-2	Conv	TLGEK	MTEEEVEMLVAGHEDSNGCINYEELVR	MVLNG	3	M1:+15.995,C19:+57.021	1057.130534	3168.368202	0.000451244	13	N	119	146
Q60605-2	Conv	VEGLR	VFDKEGNGTVMGAEIR	HVLVT	3	M11:+15.995	580.2863557	1737.835667	0.000622848	5	N	94	110
Q60605-2	Conv	TAEFK	EAFQLFDR	TGDGK	2		513.2566955	1024.497791	0.002519933	1	N	13	21
Q60631	Conv	QIFLR	DIEQMPQQPTYVQALFDFDPQEDGELGFR	RGDFI	3	M5:+15.995	1143.858062	3428.550786	0.000451244	2	N	149	178
Q60631	Conv	GDILK	VLNEECDQNWYK	AELNG	2	C6:+57.021	799.3514954	1596.687391	0.000451244	10	N	26	38
Q60631	Conv	AFLIR	ESESAPGDFSLSVK	FGNDV	2		726.8468001	1451.678	0.002374549	1	N	86	100
Q60631	Conv	YVQAL	FDFDPQEDGELGFR	RGDFI	2		836.3684311	1670.721262	0.000979378	1	N	164	178
Q60668	Conv	DYFSK	FGEVVDCTLKLDPITGR	SRGFG	3	C7:+57.021	640.6683941	1918.981782	0.000451244	2	N	119	136
Q60675	Conv	FRTTR	PTGVLLGVSSQK	MDGMG	2		593.346042	1184.676484	0.001395409	1	N	2968	2980
Q60675	Conv	STAYK	EVYLEPSEEHIEEVSLK	EEAFT	3		677.3375214	2028.989164	0.002663018	1	N	635	652
Q60676	Conv	PDVTK	AFLEENQLDYIIR	SHEVK	2		812.4230094	1622.830419	0.000622848	3	N	412	425
Q60676	Conv	ENAIK	FYSQAIELNPGNAIYYGNR	SLAYL	2		1095.534882	2189.054164	0.000451244	3	N	49	68
Q60692	Conv	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK	EMCYR	3		1352.683675	4055.027624	0.000451244	22	N	78	117
Q60692	Conv	YIANR	VTDKLTPIHDHIFCCR	SGSAA	2	C14:+57.021,C15:+57.021	1006.495729	2010.975857	0.000451244	1	N	62	78
Q60692	Conv	GGVIR	LAAIQESGVER	QVLLG	2		586.8176487	1171.619697	0.000622848	5	N	208	219
Q60692	Conv	SGVER	QVLLGDQIPK	FTIAT	2		555.8300277	1109.644455	0.000451244	3	N	219	229
Q60737	Conv	VRIAK	VLGTEDLYDYIDKYNIELDPR	FNDIL	3		848.7555158	2543.243147	0.000823681	4	N	247	268
Q60767	Conv	KEKMR	LVSITDPYQQAFLAVQATLR	NSSFW	2		1117.613133	2233.210665	0.000451244	11	N	1138	1158
Q60767	Conv	FRPLK	FLNWDPGTPVAPVIGGSSCAR	MDTES	2	C19:+57.021	1101.044329	2200.073057	0.000622848	4	N	298	319
Q60767	Conv	EDIAR	LVWLGLNQLYSAR	GWEWS	2		766.9333472	1531.851094	0.000451244	8	N	274	287
Q60767	Conv	SDVWK	KGGSEENLCAQPYHEIYTR	DGNSY	3	C9:+57.021	751.3519048	2251.032314	0.000451244	2	N	141	160
Q60864	Conv	KEQER	LAYINPDLALEEK	NKGNE	2		744.9013784	1487.787157	0.000451244	4	N	351	364
Q60864	Conv	EKGNK	ALSAGNIDDALQCYSEAIKLDPQNHVLYSNR	SAAYA	4	C13:+57.021	869.6786292	3474.683317	0.000622848	2	N	13	44
Q60864	Conv	EKGNK	ALSAGNIDDALQCYSEAIK	LDPQN	2	C13:+57.021	1019.991427	2037.967255	0.000451244	17	N	13	32

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q60864	Conv	EEAKR	TYEEGLKHEANNLQLK	EGLQN	3		629.6589292	1885.953388	0.000451244	8	N	93	109
Q60864	Conv	DPTYR	ELIEQLQNKPSDLGTK	LQDPR	2		906.9892448	1811.96289	0.000451244	5	N	153	169
Q60865	Conv	DMSLR	LNEQYEHASIHLWDLLEGK	EKPVC	4		574.5410858	2294.133143	0.001264573	2	N	200	219
Q60865	Conv	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	2		1233.636667	2465.257735	0.000451244	9	N	167	189
Q60963	Conv	RTGEK	YPLIVFSHGLGAFR	TIYSA	3		526.2931933	1575.85618	0.000451244	9	N	142	156
Q60963	Conv	MITIK	GSVHQNFDDFTFVTGK	IIGNK	3		600.2852032	1797.83221	0.001264573	1	N	346	362
Q60972	Conv	IIATK	TPSSDVLVFDYTKHPSKPDPSGECNPDLR	LRGHQ	4	C24:+57.021	815.3901604	3257.529442	0.000451244	5	N	143	172
Q60972	Conv	WDLSK	IGEEQSPEDAEDGPPELLFIHGGHTAK	ISDFS	3		958.4583096	2872.351529	0.000451244	7	N	349	376
Q60972	Conv	RGHQK	EGYGLSWNPNLSGHLLSASDDHTICLWDISAVPK	EGKVV	3	C25:+57.021	1251.605665	3751.793596	0.000451244	5	N	178	212
Q60972	Conv	VVDAK	TIFTGHTAVVEDVSWHLLHESLFGSVADDQK	LMIWD	4		860.4300956	3437.689182	0.001463592	3	N	220	251
Q60973	Conv	IIATK	TPSSDVLVFDYTKHPAKPDPSGECNPDLR	LRGHQ	4	C24:+57.021	811.3914317	3241.534527	0.001229886	1	N	142	171
Q60973	Conv	IVDAK	AIFTGHSAVVEDVAWHLLHESLFGSVADDQK	LMIWD	4		845.4248132	3377.668053	0.000622848	2	N	219	250
Q60973	Conv	KPEGK	DYALHWLVLGTHTSDEQNHLVVAR	VHIPN	4		694.3562022	2773.393609	0.002519933	1	N	58	82
Q61024	Conv	MTDRR	IGCLLSGGLDSSLVAASLLK	QLKEA	2	C3:+57.021	987.5509237	1973.086247	0.000451244	2	N	252	272
Q61033	Conv	GTESR	SSTPLPTVSSSAENTR	QNGSN	2		817.4055449	1632.79549	0.000823681	7	N	156	172
Q61033	Conv	DQLVR	YGVNPGPIVGTTR	KLYEK	2		665.8598479	1329.704096	0.000451244	4	N	125	138
Q61033	Conv	TDKPR	LEDKDDLDVTELSNEELLDQLVR	YGVNP	3		901.1191825	2700.334148	0.000451244	15	N	102	125
Q61033	Conv	AQAIR	DYVNSLLVQGGVGSLPGTSDSVPTLDVENICKR	LSQSS	3	C31:+57.021	1163.922883	3488.745248	0.002374549	1	N	376	409
Q61033	Conv	-M	PEFLEDPSVLTK	DKLKS	2		687.8617219	1373.707844	0.001591523	1	N	1	13
Q61033	Conv	GEQRK	DVYVQLYLQHLTAR	NRPPL	3		573.6461838	1717.915151	0.001839721	1	N	34	48
Q61035	Conv	KKNPK	LLNQLQYCEEAGIPLVAIIGEQELKDGVIK	LRSVA	3	C8:+57.021	1118.606055	3352.794765	0.000451244	24	N	447	477
Q61035	Conv	EVADR	IGDYVQQHGGVSLVEQLLQDPK	LSQNK	3		808.4242119	2422.249236	0.000451244	15	N	266	288
Q61035	Conv	KKNPK	LLNQLQYCEEAGIPLVAIIGEQELK	DGVIK	2	C8:+57.021	1421.257258	2840.498917	0.000451244	9	N	447	472
Q61035	Conv	LSLAR	GLDYYTGVIYEAVLLQMPTQAGEEPLGVGSIAAGGR	YDGLV	3	M17:+15.995	1237.957888	3710.850263	0.000451244	12	N	326	362
Q61035	Conv	LGDLK	LLFEYLILFGIDDK	ISFDL	2		849.9718038	1697.928008	0.000622848	2	N	303	317
Q61035	Conv	GIDDK	ISFDLSLAR	GLDYY	2		511.2879957	1020.560391	0.001654178	2	N	317	326
Q61035	Conv	LLSLR	YDLTVPFAR	YLAMN	2		541.2879957	1080.560391	0.000451244	8	N	128	137
Q61035	Conv	LLEER	LKLVSELWDAGIK	AELLY	3		491.2893374	1470.844612	0.002981883	1	N	424	437
Q61081	Conv	ERKKR	LGPGGLDPVEVYESLPEELQK	CFDVK	2		1135.084071	2268.152541	0.001162105	2	N	287	308
Q61093	Conv	DNEFK	TIASEHPNTTIGVFLCGPEALAETLSK	QSISN	3	C16:+57.021	952.8201482	2855.437045	0.000451244	4	N	521	548
Q61096	Conv	LQLSR	FPGSHFCGGTLIHPR	FVLTA	2	C7:+57.021	841.9149315	1681.814263	0.000451244	1	N	51	66
Q61096	Conv	TLVPR	RAAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	4	C6:+57.021,C16:+57.021	765.3894878	3057.526751	0.000622848	3	N	195	224
Q61096	Conv	SFVIR	ECASLQFPDFFAR	VSMYV	2	C2:+57.021	794.3669485	1586.718297	0.000451244	16	N	224	237
Q61096	Conv	DFFAR	VSMYVDWIQNVLR	GAEP-	2	M3:+15.995	819.9196228	1637.823646	0.000451244	16	N	237	250
Q61096	Conv	RRAAG	ICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C2:+57.021,C12:+57.021	901.7844495	2702.329948	0.000451244	14	N	199	224
Q61096	Conv	PRRAA	GICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C3:+57.021,C13:+57.021	1380.683506	2759.351412	0.001329271	2	N	198	224
Q61096	Conv	LVPRR	AAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C5:+57.021,C15:+57.021	968.14968	2901.42564	0.000451244	31	N	196	224
Q61096	Conv	LIHPR	FVLTAAHCLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C8:+57.021	1311.679053	3932.013759	0.000451244	7	N	66	101
Q61096	Conv	TFLCR	EHNVCTLVPR	RAAGI	2	C5:+57.021	612.811612	1223.607624	0.0025889	1	N	185	195
Q61147	Conv	GTFSK	TIDKPAWLGFLGPVIK	AEVED	3		585.6788249	1754.013075	0.000870037	11	N	82	98
Q61147	Conv	DDNIR	MFTTAPDQVDKEDEDFQESNK	MHSMN	3	M1:+15.995	830.6925041	2489.054112	0.000451244	8	N	593	614
Q61147	Conv	AHGVK	TESSTVVPTLPGEVR	TYTWQ	2		786.417924	1570.820248	0.000451244	8	N	835	850
Q61147	Conv	LNHLK	AGLQAFFQVR	DCNKP	2		568.814712	1135.613824	0.000622848	6	N	344	354
Q61147	Conv	VDAPK	DIASGLIGPLILCK	KGSLY	2	C13:+57.021	735.4237351	1468.83187	0.000451244	6	N	186	200
Q61147	Conv	VDRVK	DLYSGLIGPLIVCR	KSYVK	2	C13:+57.021	788.4320915	1574.848583	0.000451244	11	N	882	896
Q61147	Conv	TDFQR	ADDKVLPGQQYVYVLHANEPSPGEGDSNCVTR	IYHSH	3	C29:+57.021	1172.555082	3514.641846	0.000698008	1	N	144	176
Q61147	Conv	DGRQK	DVDKEFYLFPTVFDENESLLLDDNIR	MFTTA	3		1049.512192	3145.513175	0.000622848	12	N	567	593
Q61147	Conv	GPVIK	AEVEDKVYVHLK	NLASR	3		477.2615588	1428.761276	0.000451244	1	N	98	110
Q61166	Conv	FGKLR	NIELICQENEGENDPVLQR	IVDIL	2	C6:+57.021	1135.539804	2269.064009	0.000451244	9	N	222	241
Q61166	Conv	DKLVK	GKFQDNFEFVQWFK	KFFDA	3		607.2987841	1818.872952	0.000823681	1	N	98	112
Q61171	Conv	ADVTK	SLSQNYGVLKNDEGIAYR	GLFII	3		676.3451217	2026.011965	0.000451244	3	N	109	127
Q61171	Conv	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSK	HN-	4	C15:+57.021	1111.527717	4442.079667	0.000451244	20	N	157	196
Q61171	Conv	AQIGK	SAPDFTATAVVDGAFKEIK	LSDYR	2		984.0101773	1966.004755	0.000451244	12	N	10	29
Q61171	Conv	AEDFR	KLGCEVLGVSVDSQFTHLAWINTPR	KEGGL	3	C4:+57.021	943.1572061	2826.448218	0.000451244	8	N	66	91
Q61171	Conv	EDFRK	LGCEVLGVSVDSQFTHLAWINTPR	KEGGL	2	C3:+57.021	1350.184428	2698.353255	0.000979378	1	N	67	91
Q61171	Conv	YVVLF	FYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C10:+57.021	1013.14111	3036.399931	0.000979378	4	N	41	66
Q61171	Conv	DYRGK	YVVLFFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C15:+57.021	1220.258655	3657.752565	0.000451244	12	N	36	66
Q61171	Conv	ADVTK	SLSQNYGVLK	NDEGI	2		554.8040099	1107.59242	0.000451244	6	N	109	119
Q61171	Conv	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSK	EYFSK	4	C15:+57.021	947.9523849	3787.77834	0.002080925	1	N	157	191
Q61171	Conv	INTPR	KEGGLGPLNIPLLADVTK	SLSQN	2		918.0359981	1834.056396	0.000451244	11	N	91	109
Q61171	Conv	NTPRK	EGGLGPLNIPLLADVTK	SLSQN	2		853.9885165	1705.961433	0.000451244	15	N	92	109
Q61171	Conv	YVVLF	FYPLDFTFVCPTEIIAFSDHAEDFRK	LGCEV	4	C10:+57.021	792.1315235	3164.494894	0.000622848	5	N	41	67
Q61171	Conv	KGVLR	QITVNDLPVGR	SVDEA	2		606.3412909	1210.666982	0.000451244	18	N	139	150
Q61171	Conv	AQIGK	SAPDFTATAVVDGAFK	EIKLS	2		798.8993671	1595.783134	0.000451244	5	N	10	26
Q61171	Conv	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYF	SKHN-	3	C15:+57.021	1409.992025	4226.952675	0.000451244	9	N	157	194

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61171	Conv	DYRGK	YVVLFFYPLDFTFVCPTEIIAFSDHAEDFRK	LGCEV	3	C15:+57.021	1262.956976	3785.847529	0.001591523	2	N	36	67
Q61171	Conv	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDS	KEYFS	3	C15:+57.021	1220.902259	3659.683376	0.000451244	1	N	157	190
Q61171	Conv	LSDYR	GKYVVLFFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C17:+57.021	1281.964131	3842.868992	0.000451244	5	N	34	66
Q61171	Conv	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEY	FSKHN	3	C15:+57.021	1360.96922	4079.884261	0.000451244	5	N	157	193
Q61171	Conv	KYVVL	FFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C11:+57.021	1062.163915	3183.468345	0.001162105	1	N	40	66
Q61171	Conv	DEALR	LVQAFQYTDEHGEVCPA	GWKPG	2	C15:+57.021	982.4466555	1962.877711	0.002981883	1	N	157	174
Q61171	Conv	FFYPL	DFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C6:+57.021	839.7182533	2516.13136	0.001839721	1	N	45	66
Q61191	Conv	MSGCR	LGDLWTLDIETLTWNKPSLSGVAPLPR	SLHSA	3		998.2101186	2991.606956	0.000451244	8	N	228	255
Q61207	Conv	DPYQK	QCDDFVAEYEPLLLEILVEVMDPGFVCSK	IGVCP	3	C2:+57.021,M21:+15.995,C27:+57.021	1144.541609	3430.601427	0.000823681	2	N	482	511
Q61207	Conv	AALEK	GCSFLPDPYQK	QCDDF	2	C2:+57.021	656.3058282	1310.596056	0.002981883	1	N	471	482
Q61207	Conv	SASCK	EVVDSYLPVILDMIK	GEMSN	2		867.4738539	1732.932108	0.000823681	4	N	107	122
Q61233	Conv	AGCTK	ITNFSTDIKDSK	AYYHL	2		684.8544282	1367.693256	0.000451244	5	N	285	297
Q61233	Conv	GGNMK	KLENCNYAVDLGK	NQAKF	2	C5:+57.021	762.3800559	1522.744512	0.000451244	9	N	455	468
Q61233	Conv	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEK	YAFVN	2	C4:+57.021	1385.609341	2769.203081	0.000451244	13	N	97	123
Q61233	Conv	RLGCR	QFVTATDVVR	GNPKL	2		568.3094595	1134.603319	0.000698008	10	N	347	357
Q61233	Conv	IKDSK	AYYHLLEQVAPK	GDEEG	2		716.3856985	1430.755797	0.000451244	16	N	297	309
Q61233	Conv	IVLCK	MINLSVPDTIDER	TINKK	2		751.8801206	1501.744641	0.000451244	8	N	165	178
Q61233	Conv	WQLMR	RYTLNILEDIGGGQK	VNDDI	2		838.9524653	1675.889331	0.000451244	15	N	500	515
Q61233	Conv	KIGAR	VYALPEDLVEVNPK	MVMTV	2		793.4277604	1584.839921	0.000451244	15	N	596	610
Q61233	Conv	KNQAK	FSLVGIAGQDLNEGNR	TLTLA	2		845.431897	1688.848194	0.000451244	29	N	472	488
Q61233	Conv	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVNWINK	ALEND	3	C4:+57.021	1302.602649	3904.784547	0.000451244	29	N	97	132
Q61233	Conv	MMELR	EAFAKVDTDGNGYISCNELNDLFK	AACLP	2	C16:+57.021	1360.629348	2719.243096	0.000451244	1	N	15	39
Q61233	Conv	QLMRR	YTLNILEDIGGGQK	VNDDI	2		760.9019097	1519.788219	0.000451244	10	N	501	515
Q61233	Conv	EAFAK	VDTDGNGYISCNELNDLFK	AACLP	2	C11:+57.021	1087.489249	2172.962898	0.000451244	65	N	20	39
Q61233	Conv	DPDCR	HVIPMNPNTDDLFNAVGDGIVLCK	MINLS	2	C23:+57.021	1320.151739	2638.287879	0.000622848	9	N	141	165
Q61233	Conv	IKDSK	AYYHLLEQVAPKGDEEGIPAVVIDMSGLR	EKDDI	3		1057.545061	3169.611784	0.000451244	10	N	297	326
Q61233	Conv	GGGQK	VNDDIIVNWVNTTLK	EAQKS	2		872.4679482	1742.920296	0.000451244	30	N	515	530
Q61233	Conv	GGGQK	VNDDIIVNWVNTTLKEAQK	SSSIA	3		734.0589814	2199.153544	0.000451244	7	N	515	534
Q61233	Conv	RGNPK	LNLAFIANLFNKYPALHKPENQDIDWGALEGETR	EERTF	3		1300.00279	3896.984971	0.000451244	10	N	361	395
Q61233	Conv	RGNPK	LNLAFIANLFNK	YPALH	2		689.3986089	1376.781618	0.000451244	36	N	361	373
Q61233	Conv	GVNPR	VNHLYSDLSDALVIFQLYEK	IKVPV	2		1184.115705	2366.21581	0.000451244	17	N	412	432
Q61233	Conv	AEDLK	EGKPYLVLGLLWQVIK	IGLFA	2		928.5563694	1855.097139	0.000451244	8	N	217	233
Q61233	Conv	QLMRR	YTLNILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		1082.573785	3244.697956	0.000451244	39	N	501	530
Q61233	Conv	INKKK	LTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C22:+57.021	1174.947251	3521.818354	0.000451244	32	N	184	217
Q61233	Conv	PKIST	SLPVLDLIDAIQPGSINYDLLK	TENLD	2		1199.167938	2396.320275	0.002663018	1	N	548	570
Q61233	Conv	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLK	TENLD	2		1349.749823	2697.484047	0.000451244	68	N	545	570
Q61233	Conv	IDAIQ	PGSINYDLLK	TENLD	2		560.3063854	1118.597171	0.002884417	1	N	560	570
Q61233	Conv	TINKK	KLTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C23:+57.021	1217.645572	3649.913317	0.000451244	16	N	183	217
Q61233	Conv	YDLLK	TENLDDEEKLNNAK	YAISM	2		816.8897277	1631.763855	0.000622848	1	N	570	584
Q61233	Conv	ELLLR	WANYHLENAGCTK	ITNFS	2	C11:+57.021	782.3543724	1562.693145	0.000451244	1	N	272	285
Q61233	Conv	NLFNK	YPALHKPENQDIDWGALEGETREER	TFRNW	3		985.1412035	2952.40021	0.000451244	22	N	373	398
Q61233	Conv	NLFNK	YPALHKPENQDIDWGALEGETR	EERTF	2		1270.114756	2538.213913	0.000451244	7	N	373	395
Q61233	Conv	SEEEK	YAFVNWINK	ALEND	2		577.8038129	1153.592026	0.000451244	9	N	123	132
Q61233	Conv	WQVIK	IGLFADIELSR	NEALI	2		617.346042	1232.676484	0.001162105	8	N	233	244
Q61233	Conv	KLTPF	TIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C18:+57.021	1022.196278	3063.565433	0.000451244	17	N	188	217
Q61233	Conv	AGCTK	ITNFSTDIK	DSKAY	2		519.7774608	1037.539322	0.001162105	3	N	285	294
Q61233	Conv	GNMKK	LENCNYAVDLGK	NQAKF	2	C4:+57.021	698.3325743	1394.649549	0.000451244	7	N	456	468
Q61233	Conv	QVAPK	GDEEGIPAVVIDMSGLR	EKDDI	2		879.4410737	1756.866547	0.000451244	10	N	309	326
Q61233	Conv	WQVIK	IGLFADIELSRNEALIALLR	EGESL	3		743.099	2226.2736	0.000823681	2	N	233	253
Q61233	Conv	IELSR	NEALIALLR	EGESL	2		506.811638	1011.607676	0.000451244	4	N	244	253
Q61233	Conv	NDLFK	AACLPLPGYR	VREIT	2	C3:+57.021	559.2950665	1116.574533	0.000451244	4	N	39	49
Q61233	Conv	RYTLN	ILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		918.8277857	2753.459957	0.000451244	9	N	505	530
Q61233	Conv	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVN	WINKA	3	C4:+57.021	1122.168893	3363.483279	0.000662267	3	N	97	128
Q61233	Conv	PFTIQ	ENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C15:+57.021	908.1328376	2721.375113	0.000451244	5	N	191	217
Q61233	Conv	INKKK	LTPFTIQENLNLALNSASAIGCHVV	NIGAE	2	C22:+57.021	1341.69991	2681.384221	0.000870037	1	N	184	209
Q61233	Conv	GVNPR	VNHLYSDLSDALVIFQ	LYEKI	2		917.4732306	1832.930861	0.000451244	4	N	412	428
Q61362	Conv	PTFGK	SFTLASSENQLGAPISGEGLPGR	FTKEA	2		1144.580018	2287.144436	0.000451244	23	N	272	295
Q61362	Conv	APFLR	SYGFDGLDLAWLYPR	LRDKQ	2		886.9362839	1771.856968	0.000451244	11	N	137	152
Q61362	Conv	GRFTK	EAGTLAYYEICDFLK	GAEVH	2	C11:+57.021	896.927036	1791.838472	0.000451244	16	N	298	313
Q61362	Conv	TCQPK	EFFPLTNAIKDALA	-	2		775.4171957	1548.818791	0.000823681	3	N	375	389
Q61362	Conv	CSAYK	LVCYFTSWSQYR	EGVGS	2	C3:+57.021	805.3773162	1608.739032	0.000451244	12	N	31	43
Q61362	Conv	TCQPK	EFFPLTNAIK	DALA-	2		590.3245782	1178.633556	0.002212458	4	N	375	385
Q61362	Conv	PGREK	LLLSAALSAGK	VAIDT	2		522.3271209	1042.638642	0.001763695	1	N	180	191

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61508	Conv	NMTIR	CCELPYPEQACCGEEEKLAFIENLCGPR	RNSWK	3	C1:+57.021,C2:+57.021,C11:+57.021,C12:+57.021,C25:+57.021	1143.827158	3428.458073	0.000451244	14	N	467	495
Q61543	Conv	YRIDR	ALNEACESVIQTACK	HIRSG	2	C6:+57.021,C14:+57.021	847.3978884	1692.780177	0.000622848	2	N	497	512
Q61543	Conv	DCEHR	LLELQYFISR	DWKLD	2		641.3642347	1280.712869	0.001264573	2	N	541	551
Q61543	Conv	WCSEK	TETGQELECLQDHLDDLAVECR	DIVGN	3	C9:+57.021,C21:+57.021	877.7271057	2630.157917	0.000451244	3	N	646	668
Q61543	Conv	LKESK	ADIFVDPVLHTACALDIK	HHCAA	3	C13:+57.021	666.6840442	1997.028733	0.001871652	2	N	1054	1072
Q61550	Conv	RALAK	TGAESISLLELCR	NTNRK	2	C12:+57.021	724.8746064	1447.733613	0.000451244	5	N	577	590
Q61550	Conv	LVLKK	QQAIELTQEEPYSDIIATPGPR	FHII-	2		1228.61934	2455.223081	0.000823681	2	N	609	631
Q61598	Conv	LALYR	TDDYLDQPCCETINR	IKLYS	2	C9:+57.021,C10:+57.021	950.396074	1898.776548	0.000451244	32	N	193	208
Q61598	Conv	LFVPK	DLGTDSQIFISR	AYDAT	2		676.3467703	1350.677941	0.000451244	15	N	390	402
Q61598	Conv	PIEQK	FVSISDLFVPK	DLGTD	2		626.3533357	1250.691071	0.000451244	18	N	379	390
Q61598	Conv	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	2		1148.092564	2294.169529	0.001162105	1	N	173	193
Q61598	Conv	DVYKK	FDLGQDVIDFTGHSLALYR	TDDYL	2		1084.045083	2166.074566	0.000451244	16	N	174	193
Q61598	Conv	GQVIR	VICILSHPIKNTNDANSCQIIIPQNQVNR	KSDIY	3	C3:+57.021,C18:+57.021	1120.582095	3358.722885	0.002663018	1	N	299	328
Q61598	Conv	GKIYK	VPSTEAEALASSLMGLFEK	RRFRK	3		660.6718474	1978.992142	0.000451244	16	N	118	137
Q61598	Conv	KEPEK	EIRPALELLEPIEQK	FVSIS	2		889.5070734	1776.998547	0.001463592	1	N	364	379
Q61598	Conv	IFISR	AYDATTHFETTCDDIKDIYK	RMTGS	3	C12:+57.021	803.030497	2406.068091	0.000451244	13	N	402	422
Q61598	Conv	RRFRK	FLVYVANFDEKDPR	TFEGV	2		856.9362839	1711.856968	0.000622848	4	N	142	156
Q61598	Conv	IARCK	QLICDPSYVK	DRVEK	2	C4:+57.021	611.8107464	1221.605893	0.002727428	1	N	278	288
Q61598	Conv	QGFAR	LSAIYGGTYMLNKPIEEIIVQNGK	VVGVK	3		884.4758077	2650.404023	0.000451244	1	N	240	264
Q61598	Conv	YKGGK	IYKVPSTEAEALASSLMGLFEK	RRFRK	3		795.4192993	2383.234498	0.000451244	10	N	115	137
Q61598	Conv	GQLVK	MLLFTEVTR	YMDFK	2		555.3053317	1108.595063	0.001839721	1	N	89	98
Q61598	Conv	EKEIR	PALELLEPIEQK	FVSIS	2		690.3931892	1378.770778	0.000451244	4	N	367	379
Q61599	Conv	-MTEK	DAQPQLEEADDDLDSKLNYKPPPQK	SLKEL	3		952.1300816	2853.366845	0.0007646	7	N	4	29
Q61599	Conv	MRVDK	ATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		982.1411534	2943.40006	0.002019181	1	N	137	163
Q61599	Conv	TKYKK	TLLGDVPVVADPTVPNVTVTR	LSLVC	2		1082.10514	2162.194681	0.000451244	18	N	49	70
Q61599	Conv	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	2		1305.119507	2608.223415	0.0007646	1	N	174	195
Q61599	Conv	TKYKK	TLLGDVPVVADPTVPNVTVTRL	SLVCD	2		1138.647172	2275.278745	0.002145581	2	N	49	71
Q61599	Conv	VTVTR	LSLVCDSAPGPITMDLTGDLEALKK	DTFVL	3	C5:+57.021	882.124292	2643.349476	0.000451244	19	N	70	95
Q61599	Conv	-MTEK	DAQPQLEEADDDLDSK	LNYKP	2		894.8926644	1787.769729	0.000451244	4	N	4	20
Q61599	Conv	RTGMR	VDKATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	4	M7:+15.995	826.4041451	3301.58538	0.001264573	1	N	134	163
Q61599	Conv	YKKTL	LGDVPVVADPTVPNVTVTR	LSLVC	2		975.0392691	1948.062938	0.000451244	12	N	51	70
Q61635	Conv	WSLVK	DNSIIAQATSAAEAFCAVK	GGPES	2	C16:+57.021	983.9808625	1965.946125	0.000451244	14	N	360	379
Q61635	Conv	TNLIK	TGVTEPCIFLISNLDLGAFDFPK	LEETL	2	C7:+57.021	1277.648824	2553.282047	0.000451244	4	N	224	247
Q61635	Conv	KGELK	CLDFWSLVK	DNSII	2	C1:+57.021	584.2972748	1166.57895	0.001871652	4	N	351	360
Q61635	Conv	TNLIK	TGVTEPCIFLISNLDLGAFDFPKLEETLLK	ELPGH	3	C7:+57.021	1127.595156	3379.762068	0.000451244	4	N	224	254
Q61646	Conv	RQFYR	LRAEGDGVYTLNDEK	QWVNT	2		840.4159126	1678.816225	0.000451244	26	N	57	72
Q61646	Conv	IAPGR	VGYVSGWGR	NANFR	2		490.7515803	979.4875607	0.000451244	34	N	218	227
Q61646	Conv	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	2	C14:+57.021,C18:+57.021	1250.619843	2499.224086	0.000451244	16	N	72	94
Q61646	Conv	LSFDK	SCAVAEYGVYVR	ATDLK	2	C2:+57.021	687.3298346	1372.644069	0.000451244	58	N	320	332
Q61646	Conv	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	C15:+57.021	1172.873424	3515.596871	0.000451244	7	N	18	49
Q61646	Conv	KMISR	HGLTTGATLISDQWLLTTAK	NLFLN	2		1064.076383	2126.137166	0.000451244	52	N	123	143
Q61646	Conv	TASAK	DITPTLTLYVGKNQLVEIEK	VVLHP	2		1137.633731	2273.251861	0.000451244	1	N	156	176
Q61646	Conv	AGLTK	YQEDTCYGDAGSAFAIHDMEEDTWYAAGILSFDK	SCAVA	3	C6:+57.021	1292.882424	3875.623873	0.000451244	7	N	286	320
Q61646	Conv	TDRLK	YVMLPVADQDK	CVVHY	2	M3:+15.995	647.8215857	1293.627571	0.000451244	33	N	238	249
Q61646	Conv	FYRLR	AEGDGVYTLNDEK	QWVNT	2		705.823325	1409.63105	0.000451244	14	N	59	72
Q61646	Conv	TASAK	DITPTLTLYVGK	NQLVE	2		660.8746323	1319.733665	0.000451244	20	N	156	168
Q61646	Conv	QLFAV	ELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	M7:+15.995,C14:+57.021	1145.182286	3432.523457	0.000451244	8	N	19	49
Q61646	Conv	GVYVR	ATDLKDWVQETMAK	N-	3		545.9402684	1634.797405	0.000451244	8	N	332	346
Q61646	Conv	FYRLR	AEGDGVYTLNDEKQWVNTVAGEK	LPECE	2		1262.104054	2522.192509	0.000451244	3	N	59	82
Q61646	Conv	LVTER	VMPICLPSKDYIAPGR	VGYVS	2	C5:+57.021	908.9763408	1815.937082	0.000451244	4	N	202	218
Q61656	Conv	LAPTR	ELAQQVQQVAAEYCR	ACRLK	2	C14:+57.021	896.936258	1791.856916	0.000622848	1	N	177	192
Q61704	Conv	AIGGK	FPLYNLGFGNNLNYNFLETLALENHGLAR	RIYED	3		1108.898715	3323.672744	0.000451244	4	N	419	448
Q61704	Conv	LDQQR	SCPTCTDSLLNGDFTIVYDVNR	ESPGN	2	C2:+57.021,C5:+57.021	1274.078205	2546.14081	0.000451244	1	N	234	256
Q61739	Conv	MDLDR	NSYPDLAVGSLSDSVTIFR	SRPVI	2		1021.015991	2040.016382	0.000451244	8	N	444	463
Q61739	Conv	SSRRR	VNSLPEVLPILNSNEAK	TVQTD	2		919.0074376	1835.999275	0.000662267	1	N	596	613
Q61739	Conv	AHEAK	LIATFPDTLTYSAYR	ELRAF	2		866.4517668	1730.887934	0.002884417	1	N	699	714
Q61749	Conv	HSLVR	AGVPTSYLLIPAASYVLPEVSK	VLLGA	2		1138.133367	2274.251133	0.001463592	1	N	379	401
Q61753	Conv	GTSLK	NAGTCLSPAVIVGLLR	EASKQ	2	C5:+57.021	820.9615475	1639.907495	0.000451244	5	N	364	380
Q61768	Conv	EQKKR	QLEESVDSLGEELVQLR	AQEKV	2		972.5001737	1942.984747	0.000622848	3	N	658	675
Q61838	Conv	LKFTK	VNTNYRPGLPFSGQVLLVDEK	GKPIP	2		1173.626771	2345.237943	0.002296037	1	N	353	374
Q61838	Conv	HLKVK	AAPLSLCALTAVDQSVLLLKPEAK	LSPQS	3	C7:+57.021	836.8087437	2507.402831	0.000451244	14	N	587	611
Q61838	Conv	VADGK	APFALQVNTLPLNFDK	AGDHR	2		894.4886837	1786.961767	0.000451244	16	N	1357	1373
Q61838	Conv	PNIQR	TEVNTNHVLIYIEK	LTNQT	2		836.9493913	1671.883183	0.000451244	10	N	1426	1440
Q61838	Conv	HVYTK	ALLAYAFALAGNK	AKRSE	2		661.8775093	1321.739419	0.000451244	1	N	1159	1172

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61838	Conv	TFGNH	GGGNTPGNTWLTAFVLK	AFAQA	2		866.955008	1731.894416	0.000451244	6	N	1043	1060
Q61838	Conv	KWISK	QQNSHGGFSSTQDTVVALQALSK	YGAAT	2		1202.099106	2402.182613	0.000851441	2	N	1258	1281
Q61838	Conv	PKRNR	IFQWQNIHLAGGLHQLSFPLSVEPALGIYK	VVVQK	3		1126.278867	3375.813201	0.002374549	3	N	172	202
Q61838	Conv	CIQIR	VDLEISPDFLAVPVGGHENSHCICGNER	KTVSW	3	C22:+57.021,C24:+57.021	1041.15393	3120.43839	0.000451244	8	N	837	865
Q61838	Conv	VYTPK	HSLGDNDAHSIFQSVGINIFTNSK	IHKPR	2		1301.138763	2600.261926	0.000622848	2	N	658	682
Q61838	Conv	RETVR	KYFPETWIWDLVPLDVSGDGELAVK	VPDTI	3		959.8290152	2876.463646	0.000451244	2	N	744	769
Q61838	Conv	IHKPR	FCQEFQHYPAMGGVAPQALAVAASGPGSSFR	AMGVP	3	C2:+57.021,M11:+15.995	1085.51012	3253.506959	0.000451244	4	N	687	718
Q61838	Conv	LLPGK	TVQGAFFGVPVYK	DHENC	2		706.8827917	1411.749983	0.000451244	5	N	624	637
Q61838	Conv	KPEAK	LSPQSIYNLLPGK	TVQGA	2		715.4066309	1428.797662	0.002813207	1	N	611	624
Q61838	Conv	HSAVR	NALFCLETAWASISQSQESHVYTK	ALLAY	3	C5:+57.021	924.1099215	2769.306365	0.000451244	9	N	1135	1159
Q61838	Conv	LLPGK	TVQGAFFGVPVYKDHENCISGEDITHNGIVYTPK	HSLGD	4	C18:+57.021	948.9640239	3791.824896	0.001943752	2	N	624	658
Q61838	Conv	EVEAK	IKEEGTGIELTGIGSCEIANALSK	LKFTK	2	C16:+57.021	1245.641727	2489.267854	0.001264573	3	N	324	348
Q61838	Conv	IQIIK	AESPVFVQTDKPIYKPGQIVK	FRVVS	3		782.1024101	2343.28383	0.002663018	1	N	122	143
Q61838	Conv	YSRYR	STCHNQNSMSICEEFSQQADDKGCFR	QVVKT	4	C3:+57.021,M9:+15.995,C12:+57.021,C24:+57.021	788.819678	3151.247512	0.000622848	1	N	274	300
Q61838	Conv	NYVTK	GSGSGCVYLQTSLK	YNILP	2	C6:+57.021	728.8589563	1455.702313	0.000622848	1	N	1333	1347
Q61838	Conv	VPVYK	DHENCISGEDITHNGIVYTPK	HSLGD	3	C5:+57.021	800.3696241	2398.085472	0.000622848	1	N	637	658
Q61878	Conv	CKRFR	WVDGSSWNFAYWAAGQPCPGGGR	CVTLC	2	C18:+57.021	1263.556123	2525.096646	0.000451244	8	N	174	197
Q61878	Conv	RRCYR	GTLASIHSFSVNFGIQSAVR	GINQG	3		697.7047614	2090.090884	0.000622848	1	N	131	151
Q61937	Conv	KNCFR	MTDQEAIQDLWQWR	KSL-	2		910.425758	1818.835916	0.000451244	7	N	275	289
Q61937	Conv	LATLK	MSVQPTVSLGGFEITPPVVLR	LKCGS	2		1114.111912	2226.208224	0.000451244	15	N	80	101
Q61937	Conv	QLSLR	TVSLGAGAKDELHIVEAEAMNYEGSPIK	VTLAT	3	M20:+15.995	982.4907622	2944.448887	0.000451244	18	N	45	73
Q61990	Conv	NSTER	AITIAGIPQSIIECVK	QICVV	2	C14:+57.021	856.9846883	1711.953777	0.0025889	1	N	144	160
Q61990	Conv	NCPER	IITLAGPTNAIFK	AFAMI	2		679.9062668	1357.796934	0.000823681	1	N	57	70
Q62059	Conv	PTEAR	DVEEMTTLTRLETDV	TKSDK	3		584.6176311	1750.829493	0.001591523	1	N	759	774
Q62167	Conv	INITK	DLLDLLVEAK	QEVPS	2		564.8296934	1127.643787	0.000622848	2	N	554	564
Q62167	Conv	EIDKR	SFLLDLLNATGK	DSLTL	2		646.3669744	1290.718349	0.000451244	2	N	428	440
Q62167	Conv	TGSGK	TAAFLLPILSQIYADGPGEALR	AMKEN	2		1158.634065	2315.25253	0.000662267	1	N	230	252
Q62178	Conv	SEPVR	NLQLAPAQGAVFAGFSGGIWR	VPRAN	2		1080.571602	2159.127604	0.000451244	8	N	470	491
Q62178	Conv	FFQQK	GLRDFDTLLLSDDGNTLYVGAR	EAVLA	3		804.4120834	2410.21285	0.000451244	6	N	59	81
Q62178	Conv	GSLHK	AVVPQDSSAYLVEEIQLSPDSEPVR	NLQLA	3		910.1279009	2727.360303	0.000698008	3	N	445	470
Q62178	Conv	YVGAR	EAVLALNIQNPGIPR	LKNMI	2		802.9600934	1603.904587	0.000451244	6	N	81	96
Q62178	Conv	TTFLK	AQLLCAQPGQLPFNIIR	HAVLL	2	C5:+57.021	970.0330355	1938.050471	0.000451244	8	N	288	305
Q62178	Conv	VGGTR	SSAVCAFSLTDIER	VFKGK	2	C5:+57.021	778.3749705	1554.734341	0.000622848	2	N	334	348
Q62193	Conv	KSRVR	AQHIVPCTISQLLSATLTDEVFR	IGDVE	3	C7:+57.021	867.1235024	2598.347107	0.000451244	1	N	42	65
Q62261	Conv	LDILK	IVSSNDVGHDEYSTQSLVK	KHKDV	2		1039.505987	2076.996375	0.000451244	2	N	765	784
Q62261	Conv	SALER	LTTLELLEVR	RQQEE	2		593.8562425	1185.696885	0.001162105	6	N	2078	2088
Q62261	Conv	LADLK	QLWGLLIEETEKR	HRRLE	3		538.9670344	1613.877703	0.000622848	7	N	1571	1584
Q62261	Conv	DKLKK	SNAHYNLQNAFNLAEQHLGLTK	LLDPE	3		828.4195723	2482.235317	0.000622848	4	N	227	249
Q62261	Conv	SMLKK	HQILEQAVEDYAETVHQLSK	TSRAL	3		780.0611621	2337.160086	0.000451244	16	N	1633	1653
Q62261	Conv	FQLNR	EVDDLEQWIAER	EVVAG	2		751.8602419	1501.704884	0.000451244	7	N	1705	1717
Q62261	Conv	SENQR	LVSQDNFGFDLPAVEAATK	KHEAI	2		1011.513084	2021.010568	0.000451244	13	N	443	462
Q62261	Conv	RDLQK	FLQDCQELSLWINEK	MLTAQ	2	C5:+57.021	961.9697665	1921.923933	0.000451244	5	N	1279	1294
Q62261	Conv	QQFLR	DLDDFQSWLSR	TQTAI	2		691.3232952	1380.63099	0.000451244	7	N	1069	1080
Q62261	Conv	HQFSR	DASVAEAWLLGQEPYLSSR	EIGQS	2		1046.52144	2091.027281	0.000451244	7	N	2024	2043
Q62261	Conv	IAEWK	DGLNEAWADLLELIDTR	TQILA	2		972.489609	1942.963618	0.000451244	16	N	1780	1797
Q62261	Conv	SDLQK	EAEKLESEHPDQAQAILSR	LAEIS	3		717.6945907	2150.060372	0.000451244	9	N	1017	1036
Q62261	Conv	DIFER	SQNIITDSSSLNAEAIR	QRLAD	2		909.9637584	1817.911917	0.000451244	13	N	1547	1564
Q62261	Conv	LNNRK	FANSLVGVQQQLQAFNTYR	TVEKP	2		1092.563974	2183.112348	0.000451244	9	N	329	348
Q62261	Conv	DPNTK	VSEEAESQQWDTSKGDQVSQNGLPAEQGSPR	MAGTM	3		1115.514094	3343.518882	0.000622848	8	N	2108	2139
Q62261	Conv	DNVIR	LWEYLLELLR	ARRQR	2		674.3877099	1346.75982	0.000451244	15	N	508	518
Q62261	Conv	KFTEK	GNLEVLLFTIQSK	MRANN	2		731.4197383	1460.823877	0.000451244	9	N	359	372
Q62261	Conv	ASAQK	FATDGEGYKPCDPQVIR	DRVAH	2	C11:+57.021	976.9624728	1951.909346	0.000451244	4	N	593	610
Q62261	Conv	IIYIR	EQWANLEQLSAIR	KKRLE	2		779.4051509	1556.794702	0.000451244	6	N	723	736
Q62261	Conv	KMIEK	YESLASDLLEWIEQTIIILNNRK	FANSL	3		921.1643978	2760.469794	0.001463592	1	N	306	329
Q62261	Conv	HQFNR	DVEDEILWVGER	MPLAT	2		730.357335	1458.69907	0.000622848	1	N	1492	1504
Q62261	Conv	EAATK	KHEAIETDIAAYEER	VQAVV	2		887.9344696	1773.853339	0.000451244	1	N	462	477
Q62348	Conv	GDYSR	PLHISTFINELDSGFR	LLNLK	3		615.9884982	1844.942095	0.000451244	11	N	166	182
Q62348	Conv	EQTAR	EILTLLQGVHQGTGFQDIPK	RCLKA	3		732.0675884	2193.179365	0.000622848	3	N	36	56
Q62348	Conv	SELSR	LSVNSVTAGDYSRPLHISTFINELDSGFR	LLNLK	3		1065.874346	3194.599639	0.000451244	8	N	153	182
Q62348	Conv	TLVTR	EAVTEILGIEPDREK	GFHLD	2		849.9495883	1697.883577	0.000698008	4	N	116	131
Q62376	Conv	LFAPR	DPIPYLPPLEK	LPHEK	2		641.358618	1280.701636	0.002019181	1	N	16	27
Q62393	Conv	EELRR	ELTKVEEEIQTLSQVLAAK	EKHLA	2		1065.089156	2128.162712	0.000451244	1	N	80	99
Q62418	Conv	YSFHK	ESTSFQDVGPQAPVGSVYQK	TNAIS	2		1062.516355	2123.01711	0.000451244	9	N	144	164
Q62418	Conv	VVTEK	SPTDWALFTYEGNSNDIR	VAGTG	2		1043.479773	2084.943945	0.000451244	6	N	23	41

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q62418	Conv	SNDIR	VAGTGEGGLEELVEELNSGK	VMYAF	2		994.4950884	1986.974577	0.000451244	9	N	41	61
Q62418	Conv	SGLPK	FVLINWTGEGVNDVR	KGACA	2		859.947183	1717.878766	0.000451244	3	N	78	93
Q62422	Conv	NQQNK	LGDTALHAAAWK	GYADI	3		418.5599391	1252.656417	0.002884417	2	N	138	150
Q62422	Conv	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAKR	GNLSW	4		706.6127708	2822.419883	0.000451244	8	N	57	83
Q62422	Conv	AAAWK	GYADIVQLLLAK	GARTD	2		652.3851672	1302.754734	0.000451244	12	N	150	162
Q62422	Conv	HGGHK	DIVEVLFTQPNVELNQQNK	LGDTA	2		1114.582029	2227.148459	0.000451244	19	N	119	138
Q62465	Conv	YDKVK	LQSRPAVPPAPGPGQLTLR	VRACG	3		652.3782086	1954.111226	0.000451244	4	N	76	95
Q62465	Conv	LQANR	AVCGFHLGYLDGEVELVNSVVTR	LVALY	3	C3:+57.021	845.4288143	2533.263043	0.000622848	2	N	334	357
Q62465	Conv	MAMAR	TWWNQFSVTALQLLQANR	AVCGF	2		1088.569059	2175.122519	0.000451244	9	N	316	334
Q62465	Conv	HIKPR	IDSVWPFEK	VADAM	2		560.7878285	1119.560057	0.001329271	2	N	370	379
Q62465	Conv	APPLR	CLVLTGFGGYDK	VKLQS	2	[0:-17.027,C1:+57.021	656.8158033	1311.616007	0.001229886	1	N	62	74
Q62469	Conv	TPTER	YFFNVADEAALLEK	AGTLG	2		815.4121103	1628.808621	0.002212458	1	N	336	350
Q62469	Conv	LHLTR	STNINFYEISSDENAPSVIK	SVEDI	2		1114.540027	2227.064455	0.001763695	1	N	939	959
Q62469	Conv	PLDLR	VDISLENPGTSPALEAYSETVK	VFSIP	2		1160.581892	2319.148184	0.001352548	1	N	754	776
Q62523	Conv	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	C1:+39.994,C4:+57.021,C17:+57.021,C26:+57.021	1039.776907	3116.307321	0.000451244	1	N	528	555
Q62523	Conv	RATGK	AYHPQCFTCVVCACPLEGTSFIVDQANQPHCVPDYHK	QYAPR	4	C6:+57.021,C9:+57.021,C12:+57.021,C14:+57.021,C31:+57.021	1102.239011	4404.924843	0.000451244	5	N	453	490
Q62523	Conv	QYAPR	CSVCSEPIMPEPGRDETVR	VVALD	3	C1:+57.021,C4:+57.021,M9:+15.99	745.6663818	2233.975745	0.000622848	4	N	495	514
Q63810	Conv	PLVQR	VIDIFDTDGNGEVDFKEFIEGVSQFSVK	GDKEQ	3		1045.512192	3133.513175	0.000451244	17	N	57	85
Q63810	Conv	DGDGR	ISFEEFCAVVGGLDIHKK	MVVDV	4	C7:+57.021	513.0177079	2048.039632	0.000451244	12	N	147	165
Q63810	Conv	DGDGR	ISFEEFCAVVGGLDIHK	KMVVD	3	C7:+57.021	640.9893561	1919.944668	0.001871652	1	N	147	164
Q63844	Conv	NVLHR	DLKPSNLLINTTCDLK	ICDFG	3	C13:+57.021	615.6647611	1843.970883	0.001162105	1	N	166	182
Q63844	Conv	YKLLK	SQQLSNDHICYFLYQILR	GLKYI	3	C10:+57.021	766.716407	2297.125821	0.002374549	1	N	135	153
Q63844	Conv	LPKER	LKELIFQETAR	FQPGA	3		449.926399	1346.755797	0.001943752	1	N	360	371
Q64324	Conv	SSLIR	NLEQLGGTVTNSAGSGTSSR	LERRE	2		968.4724789	1934.929358	0.000451244	11	N	439	459
Q64324	Conv	DINKR	REPIPSLEAIYLLSPTEK	SVQAL	3		686.0495347	2055.125204	0.002813207	1	N	64	82
Q64324	Conv	SPTEK	SVQALIADFQGTPTFTYK	AAHIF	2		994.01272	1986.00984	0.000451244	3	N	82	100
Q64324	Conv	VKTLK	EIHLAFLPYEAQVFSLDAPHSTYNLYCPFR	AGERG	4	C27:+57.021	900.4424617	3597.738647	0.000622848	1	N	131	161
Q64324	Conv	GERGR	QLDALAQQIATLCATLQEYPSIR	YRKGP	3	C13:+57.021	868.4551406	2602.342022	0.000622848	2	N	167	190
Q64324	Conv	INKRR	EPIPSLEAIYLLSPTEK	SVQAL	2		950.5198465	1899.024093	0.000622848	1	N	65	82
Q64442	Conv	CKIGR	YNLTPTIFFCATPPDDGNLCR	FYKHN	2	C10:+57.021,C20:+57.021	1236.569819	2471.124038	0.000622848	14	N	110	131
Q64442	Conv	PGDIR	LENYPIPELGPNDVLLK	MHSVG	2		962.5254632	1923.035326	0.000451244	12	N	21	38
Q64455	Conv	HGPIK	AYAVILTTGEAAQPSADVLK	YTYED	2		1009.544384	2017.073169	0.000662267	7	N	749	769
Q64455	Conv	SYTVK	ILTQVGDGTTSLVPGWNLFCTEPEPVTSFHCEVVPK	EPALV	3	C20:+57.021,C31:+57.021	1338.992266	4013.953399	0.000451244	15	N	597	633
Q64455	Conv	GQVLC	AGAAPNPIFDIEAVVSPTSVLLTWK	HNDSG	3		866.1394125	2595.394838	0.002019181	1	N	35	60
Q64514	Conv	DGKPK	IIDIIDTTGSGDVNTATEVEPK	DGEII	2		1144.579349	2287.143099	0.000451244	17	N	63	85
Q64514	Conv	PRGLR	EGLHYTEVCGYDIASPNAGPLFR	VPITA	3	C9:+57.021	856.0729191	2565.195357	0.000451244	5	N	605	628
Q64514	Conv	QWMTK	LDSTDIYNELKETYPAYLPLYVAR	LHQLD	3		949.8204082	2846.437825	0.000451244	12	N	1048	1072
Q64514	Conv	TWSSR	GPSADGALGVSISAPGGAIASVPNWTLR	GTQLM	2		1311.188256	2620.360912	0.000735798	5	N	412	440
Q64514	Conv	ERMKR	LNEIVDAANAVISHIDQTALAVYIAMK	TDPRP	3	M26:+15.995	967.1798595	2898.516178	0.000622848	3	N	1085	1112
Q64514	Conv	VINHK	CDLVNYSYGEATHWPNSGR	ICEVI	2	C1:+57.021	1113.487375	2224.959149	0.00091018	1	N	321	340
Q64514	Conv	VGNNR	GIYLRDPVQVAAPSDHGVGIEPVFPENTENSEK	ISFQL	4		891.9461098	3563.753239	0.000451244	10	N	531	564
Q64514	Conv	SQANK	LIKEELQSQVELLNSFEK	KYSDP	2		1074.083874	2146.152147	0.002080925	1	N	168	186
Q64514	Conv	SLPEK	GTLIEAFPVLGGK	AIEFC	2		651.3773421	1300.739084	0.000451244	2	N	715	728
Q64523	Conv	QLAIR	NDEELNKLLGK	VTIAQ	2		636.8438635	1271.672127	0.000451244	91	N	89	100
Q64523	Conv	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	2		1467.276214	2932.536828	0.000451244	108	N	43	72
Q64523	Conv	NYAER	VGAGAPVYMAAVLEYLTAEILELAGN	AARDN	2		1318.188545	2634.36149	0.000622848	4	N	43	69
Q64523	Conv	NYAER	VGAGAPVYMAAVLEY	LTAEI	2		755.8846746	1509.753749	0.000622848	12	N	43	58
Q64523	Conv	RLLRK	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	3		1208.622922	3622.845367	0.002813207	1	N	37	72
Q64523	Conv	NYAER	VGAGAPVYMAAVLEYLTA	EILEL	2		898.4691029	1794.922606	0.002296037	1	N	43	61
Q64523	Conv	NYAER	VGAGAPVYMAAVLEYLTAEIL	ELAGN	2		1076.074464	2150.133327	0.002884417	1	N	43	64
Q64674	Conv	EGWFR	ETCSLWPGQALSLQVEQLLHHR	RSRYQ	4	C3:+57.021	651.3357311	2601.311725	0.001871652	1	N	22	44
Q64727	Conv	IDGSR	GILSGTSDLLLTFDEAEVR	KIIRV	2		1018.531474	2035.047348	0.000451244	14	N	113	132
Q64727	Conv	EVDGK	AIPDLTAPVAAVQAAVSNLVR	VGKET	2		1038.594743	2075.173886	0.000451244	27	N	35	56
Q64727	Conv	LEQLR	LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK	AGEVI	3		1342.684793	4025.030978	0.00307782	1	N	853	889
Q64727	Conv	LNQAK	GWLRDPNASPGDAGEQAIR	QILDE	2		1005.493549	2008.971497	0.000451244	1	N	281	300
Q64727	Conv	DLLAK	CDRVDQLTAQLADLAAR	GEGES	2	C1:+39.994	949.9731464	1897.930693	0.000451244	9	N	544	561
Q64727	Conv	DGKAI	PDLTAPVAAVQAAVSNLVR	VGKET	3		631.3587026	1891.052708	0.000451244	8	N	37	56
Q64727	Conv	VMDAK	AVAGNISDPGLQK	SFLDS	2		635.3440306	1268.672461	0.000451244	2	N	802	815
Q64727	Conv	VAMQK	AQQVSQGLDVLTAK	VENAA	2		729.4020769	1456.788554	0.000451244	36	N	352	366
Q64727	Conv	NEIIR	VLQLTSWDEDAWASK	DTEAM	2		874.9286559	1747.841712	0.000451244	14	N	246	261
Q64727	Conv	IDGSR	GILSGTSDLLLTFDEAEVRK	IIRVC	2		1082.578955	2163.142311	0.000451244	15	N	113	133
Q64727	Conv	IRVCK	GILEYLTVAEVVETMEDLVTYTK	NLGPG	2		1308.672393	2615.329186	0.000451244	7	N	139	162
Q64727	Conv	VRVGK	ETVQTTEDQILKR	DMPPA	2		780.9155485	1559.815497	0.000451244	5	N	59	72

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q64727	Conv	AKCDR	VDQLTAQLADLAAR	GEGES	2		742.9075264	1483.799453	0.000451244	4	N	547	561
Q64727	Conv	EQAIR	QILDEAGKVGELCAGK	ERREI	2	C13:+57.021	844.4381022	1686.860604	0.000451244	11	N	300	316
Q64727	Conv	EQAQR	WIDNPTVDDR	GVGQA	2		615.7916309	1229.567662	0.000451244	16	N	502	512
Q64727	Conv	TTPIK	LLAVAATAPPDAPNREEVFDER	AANFE	3		794.4085618	2380.202286	0.000870037	2	N	607	629
Q64727	Conv	SPQAR	ALASQLQDSLKDLK	AQMQE	3		510.6231563	1528.846069	0.000451244	8	N	570	584
Q64727	Conv	VFHTR	TIESILEPVAQQISHLVIMHEEGEVDGK	AIPDL	3		1034.532822	3100.575065	0.000823681	3	N	7	35
Q64727	Conv	QSIAK	KIDAAQNWLADPNGGPEGEEQIR	GALAE	3		836.7424922	2507.204076	0.000451244	1	N	386	409
Q64727	Conv	MNTVK	ELLPVLISAMK	IFVTT	2		607.3653894	1212.715179	0.002727428	1	N	199	210
Q64727	Conv	NACTK	LVQAAQMLQSDPYSVPAR	DYLID	2		987.5098221	1973.004044	0.002813207	1	N	87	105
Q64727	Conv	VAKVR	EAFQPQEPDFPPPPPDLEQLR	LTDEL	2		1224.098044	2446.180487	0.002813207	2	N	832	853
Q64737	Conv	TAQWR	AFTNPEDACSFITSANFPALVVK	ASGLA	2	C9:+57.021	1250.115148	2498.214696	0.000451244	3	N	125	148
Q68FD5	Conv	SNFGR	LASTLVHLGEYQAAVDGAR	KANST	3		657.6818453	1970.022136	0.000451244	9	N	1226	1245
Q68FD5	Conv	AKTNR	LAELEEFINGPNNAHIQQVGDR	CYDEK	2		1232.614924	2463.214247	0.001654178	2	N	1182	1204
Q68FD5	Conv	IYMNR	ISGETIFVTAPHEATAGIIGVNR	KGQVL	2		1177.129678	2352.243756	0.001463592	2	N	297	320
Q68FD5	Conv	YQALR	TSIDAYDNFDNISLAQR	LEKHE	2		971.9612157	1941.906831	0.000451244	17	N	1481	1498
Q68FD5	Conv	VAYER	GQCDLELINVCNENSLFK	SLSRY	2	C3:+57.021,C11:+57.021	1077.00378	2151.991961	0.000451244	16	N	923	941
Q68FD5	Conv	GDLVK	SVDPTLALSVYLR	ANVPN	2		717.4040883	1432.792577	0.000622848	4	N	468	481
Q68FD5	Conv	VLYAK	KVGYTPDWIFLLR	NVMRI	3		536.6368486	1606.887146	0.000451244	9	N	506	519
Q68FD5	Conv	NHNNK	SVNESLNNLFITEEDYQALR	TSIDA	2		1178.077308	2354.139017	0.000451244	17	N	1461	1481
Q68FD5	Conv	SNPYR	RPLIDQVVQTALSETQDPEEVSVTVK	AFMTA	3		961.1771432	2880.50803	0.000451244	8	N	967	993
Q68FD5	Conv	FAIFR	KFDVNTSAVQVLIEHIGNLDR	AYEFA	3		790.0926851	2367.254655	0.000451244	9	N	1073	1094
Q68FD5	Conv	LYAKK	VGYTPDWIFLLR	NVMRI	2		740.4038913	1478.792183	0.000451244	2	N	507	519
Q68FD5	Conv	IGVNR	KGQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C8:+57.021	1142.276709	3423.806726	0.000451244	11	N	320	350
Q68FD5	Conv	QEEKR	ECFGACLFTCYDLLRPDVVLETAWR	HNIMD	3	C2:+57.021,C6:+57.021,C10:+57.021	1031.15406	3090.438779	0.000451244	10	N	1563	1588
Q68FD5	Conv	EYINR	LDNYDAPDIANIAISNELFEEAFAIFR	KFDVN	3		1024.50526	3070.49238	0.000451244	7	N	1046	1073
Q68FD5	Conv	GVNRK	GQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C7:+57.021	1099.578388	3295.711763	0.000451244	3	N	321	350
Q68FD5	Conv	QAGGK	LHIIEVGTPPTGNQPFPK	KAVDV	3		649.0234314	1944.046894	0.000451244	3	N	227	245
Q68FD5	Conv	NVPNK	VIQCFAETGQVQK	IVLYA	2	C4:+57.021	754.3825986	1506.749597	0.000451244	15	N	487	500
Q68FD5	Conv	LKEAK	LTDQLPLIIVCDR	FDFVH	2	C11:+57.021	778.4295488	1554.843498	0.000451244	3	N	767	780
Q68FD5	Conv	FSEHR	NLQNLLILTAIK	ADRTR	2		677.4273664	1352.839133	0.000451244	13	N	1022	1034
Q68FD5	Conv	RKKAR	ESYVETELIFALAK	TNRLA	2		806.9275932	1611.839586	0.000451244	5	N	1165	1179
Q68FD5	Conv	QVASK	YHEQLSTQSLIELFESFK	SFEGL	3		733.7043157	2198.089547	0.001162105	4	N	688	706
Q68FD5	Conv	DTIRR	FQSVPAQPGQTSPLLQYFGILLDQGQLNK	YESLE	3		1063.231582	3186.671347	0.000451244	8	N	400	429
Q68FD5	Conv	ASESK	DTELAEELLQWFLQEEKR	ECFGA	3		759.7186248	2276.132475	0.000451244	5	N	1545	1563
Q68FD5	Conv	FESFK	SFEGLFYFLGSIVNFSQDPDVHFK	YIQAA	3		931.7906719	2792.348616	0.001162105	2	N	706	730
Q68FD5	Conv	ASESK	DTELAEELLQWFLQEEK	RECFG	2		1061.023482	2120.031363	0.000451244	7	N	1545	1562
Q68FD5	Conv	IVCDR	FDFVHDLVLYLYR	NNLQK	3		567.300125	1698.876975	0.001162105	2	N	780	793
Q68FD5	Conv	SVTVK	AFMTADLPNELIELLEK	IVLDN	2	M3:+15.995	982.0088319	1962.002064	0.002453667	2	N	993	1010
Q68FD5	Conv	DSYIK	ADDPSSYMEVVQAANASGNWEELVK	YLQMA	2	M8:+15.995	1363.616712	2725.217824	0.000451244	4	N	1130	1155
Q68FD5	Conv	VNPSR	LPVVIGGLLDVDCSEDVIK	NLILV	3	C13:+57.021	681.0347426	2040.080828	0.00307782	1	N	811	830
Q68FD5	Conv	GLLQR	ALEHFTDLYDIK	RAVVH	3		488.9176806	1463.729642	0.000870037	1	N	625	637
Q68FD5	Conv	RNRLK	LLLPWLEAR	IHEGC	2		555.8376558	1109.659712	0.000735798	2	N	856	865
Q6A4J8	Conv	VMCDR	AGFIQDTSLILYEEVKPNLTER	IQDYD	3		846.1151555	2535.322066	0.000622848	5	N	724	746
Q6A4J8	Conv	IRESK	LSEVLQAVTDHDIPQQLVER	LQEEK	3		764.0732906	2289.196472	0.000451244	12	N	524	544
Q6A4J8	Conv	DVVSR	CTKEEAIEHNYGGHDDDLSVR	HCTNA	4	C1:+57.021	612.0242499	2444.0658	0.001162105	1	N	488	509
Q6A4J8	Conv	DQNIK	INDRFEFPEQLPLDEFLQK	TDPKD	3		793.4062697	2377.195409	0.002727428	4	N	421	440
Q6IRU2	Conv	AVKRK	IQALQQQADDAEDRAQGLQR	ELDGE	2		1127.562691	2253.109782	0.000451244	9	N	13	33
Q6IRU2	Conv	VSELK	CGDLEEELKNVTNNLK	SLEAA	2	C1:+57.021	938.4597629	1874.903926	0.000622848	2	N	153	169
Q6IRU2	Conv	LAQAK	EENVGLHQTLDQTLNELNCI	-	2	C19:+57.021	1170.560737	2339.105874	0.000451244	18	N	228	248
Q6IRU2	Conv	ALNRR	IQLLEEELDRAQEQLATALQNLEEAEK	AADES	3		1042.20565	3123.59355	0.000451244	15	N	55	82
Q6IRU2	Conv	EELDR	AQEQLATALQNLEEAEKAADESER	GMKVI	3		882.0952598	2643.262379	0.000451244	21	N	65	89
Q6IRU2	Conv	DLEEK	LAQAKEENVGLHQTLDQTLNELNCI	-	3	C24:+57.021	951.1470354	2850.417706	0.000451244	5	N	223	248
Q6IRU2	Conv	AVKRK	IQALQQQADDAEDR	AQGLQ	2		800.882237	1599.748874	0.000451244	5	N	13	27
Q6IRU2	Conv	EELDR	AQEQLATALQNLEEAEK	AADES	2		943.4792413	1884.942883	0.000451244	1	N	65	82
Q6IRU2	Conv	EAVKR	KIQALQQQADDAEDR	AQGLQ	3		576.9557457	1727.843837	0.000451244	2	N	12	27
Q6NSR8	Conv	KQGFK	DNLHAVFCLAENAVGPNATRPDDIHLLYSGK	TVEIN	4	C8:+57.021	852.6758895	3406.672358	0.001591523	2	N	303	334
Q6NSR8	Conv	HAGER	ATGFGVALLLALFGR	ASEDP	2		753.4460905	1504.876581	0.001763695	1	N	474	489
Q6NSR8	Conv	PGMKR	DCGGAAAVLGAFR	AAIKQ	2	C2:+57.021	632.8090694	1263.602539	0.002884417	1	N	282	295
Q6NSR8	Conv	YGVGK	AALHPPALAILSHTPDGATQTIAWVGK	GIVYD	4		684.8767705	2735.475882	0.001329271	1	N	233	260
Q6NZJ6	Conv	RPMGK	ATSLLLEILGLLCK	SMGPK	2	C13:+57.021	772.4603176	1542.905035	0.001839721	1	N	1371	1385
Q6P069-2	Conv	LNGWR	QHFISFDSDRSGTVDPQELQK	ALTTM	3		812.0598212	2433.156064	0.000451244	8	N	91	112
Q6P069-2	Conv	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	2	C1:+39.994,C19:+57.021	1128.032647	2254.049694	0.000451244	4	N	41	61
Q6P069-2	Conv	LNGWR	QHFISFDSDR	SGTVD	2		626.291798	1250.567996	0.001763695	2	N	91	101
Q6P069-2	Conv	FNEFK	ELWAVLNGWR	QHFIS	2		622.3332689	1242.650938	0.000698008	8	N	81	91

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6P069-2	Conv	LYGYF	AAVAGQDGQIDADELQR	CLTQS	2		878.9271759	1755.838752	0.001463592	2	N	24	41
Q6P069-2	Conv	STSGK	ITFDDYIACCVK	LRALT	2	C9:+57.021,C10:+57.021	752.844229	1503.672858	0.000451244	4	N	138	150
Q6P069-2	Conv	SFRRR	DSGQQGVVNFSYDDFIQCVMTV	-	2	C18:+57.021	1255.054431	2508.093261	0.001463592	1	N	161	183
Q6P1B1	Conv	EEFRR	QQADFVDLSFPTISSTGPNGAIIHYAPVPETNR	TLSLD	3		1181.590387	3541.74776	0.000451244	8	N	371	404
Q6P1B1	Conv	NFNNR	GSLTFEPLTLVPIQTK	MIDVN	2		872.4987171	1742.981834	0.000451244	12	N	554	570
Q6P1B1	Conv	KMGLK	DTPTQEDWLVSVLPEGSR	VGVDP	2		1014.997798	2027.979996	0.000823681	1	N	98	116
Q6P1B1	Conv	RQAMR	NSEYVAEPIQAYIIPSGDAHQSEYIAPCDCR	RAFVS	3	C28:+57.021,C30:+57.021	1185.205019	3552.591656	0.000451244	3	N	18	49
Q6P1B1	Conv	RAHIK	DAVALCELFNWLEQEVPK	GGVTE	2	C6:+57.021	1081.035638	2160.055676	0.000451244	9	N	336	354
Q6P1B1	Conv	RQAMR	NSEYVAEPIQAYIIPSGDAHQSEYIAPCDCRR	AFVSG	3	C28:+57.021,C30:+57.021	1237.238722	3708.692767	0.000823681	3	N	18	50
Q6P1B1	Conv	PETNR	TLSLDEVYLIDSGAQYK	DGTTD	2		957.9889105	1913.962221	0.000823681	1	N	404	421
Q6P1F6	Conv	DPSNR	SFFSEIISSISDVK	FSHSG	2		779.9041181	1557.792636	0.002296037	1	N	278	292
Q6P2B1	Conv	VTLLR	SQVVIPILQWAIASTTLDHR	DANSS	3		750.0869829	2247.237549	0.002374549	2	N	769	789
Q6P4T2	Conv	SKLYR	AALETDENLLLCAPTGAGK	TNVAL	2	C12:+57.021	972.4910631	1942.966526	0.000451244	9	N	490	509
Q6P4T2	Conv	RKQTR	LTAIDILTTCAADIQR	QRFLH	3	C10:+57.021	592.3174728	1773.929018	0.000451244	7	N	1570	1586
Q6P4T2	Conv	TKETR	ETYEVLLSFIQAALGDQPR	DILCG	3		717.3763105	2149.105531	0.001395409	1	N	110	129
Q6P4T2	Conv	QEDVR	LIGLSATLPNYEDVATFLR	VDPAK	2		1047.068027	2092.120453	0.001463592	3	N	647	666
Q6P4T2	Conv	EDEER	NALLQLTDSQIADVAR	FCNRY	2		864.4684796	1726.921359	0.000823681	1	N	1993	2009
Q6P4T2	Conv	TELGR	IASHYYITNDTVQTYNQLLKPTLSEIELFR	VFSLS	4		893.4679494	3569.840598	0.0007646	6	N	986	1016
Q6P4T2	Conv	LLKAK	YAQDEHLITFFVPVFEPLPPQYFIR	VVSDR	3		1022.864171	3065.569114	0.000622848	4	N	1244	1269
Q6P4T2	Conv	VDPAK	GLFYFDNSFRPVPLEQTYVGITEK	KAIKR	3		940.8134765	2819.41703	0.000823681	3	N	671	695
Q6P4T2	Conv	KTKVR	GLIEIISNAAEYENIPIR	HHEDN	2		1008.044551	2014.073503	0.000622848	2	N	1843	1861
Q6P5E4	Conv	EGLHR	LGIEGLSLHNILK	LNIQP	2		703.9224482	1405.829296	0.000451244	8	N	426	439
Q6P5E4	Conv	DDIYR	IYSHDGTDSPPDANDVVVILNNFK	SKIIK	3		877.4298027	2629.266008	0.000451244	12	N	1177	1201
Q6P5E4	Conv	VAVLR	AYNYVAQEVDGYHAFQTLTQIYNK	VRTGE	2		1418.683003	2835.350407	0.002374549	1	N	553	577
Q6P5E4	Conv	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	C3:+57.021	953.5162885	2857.525466	0.000451244	4	N	156	181
Q6P5E4	Conv	ISNGR	IIGPLEDNELFNQDDFHLLENIILK	TSGQK	3		984.8504789	2951.528037	0.000451244	11	N	898	923
Q6P5E4	Conv	QVPIK	SLPQEWLWCETWCDDASK	KRAKT	2	C9:+57.021,C13:+57.021	1155.993413	2309.971225	0.000451244	6	N	1466	1484
Q6P5E4	Conv	HNILK	LNIQPSETDYAVDIR	SPAIS	2		867.4393878	1732.863176	0.000451244	13	N	439	454
Q6P5E4	Conv	LTAKR	EYLDLTASNNFYVDDFAR	FSALD	2		1076.995256	2151.974911	0.000451244	7	N	704	722
Q6P5E4	Conv	KSFYR	YVLEPEISFTADSSFAK	GPIAK	2		952.4703536	1902.925107	0.000451244	10	N	1038	1055
Q6P5E4	Conv	LKELR	DFNLDGAPYGYTPFCDSR	REMDG	2	C15:+57.021	1047.94702	2093.878439	0.000451244	16	N	1371	1389
Q6P5E4	Conv	IWGYK	ILFLDVLFPLVVDK	FLFVD	2		815.9950819	1629.974564	0.000698008	5	N	1339	1353
Q6P5E4	Conv	AVDIR	SPAISWVNNLEVDSR	YNSWP	2		843.9264475	1685.837295	0.000451244	8	N	454	469
Q6P5E4	Conv	KLKPK	EGETYYDVVAVVDPVTR	EAQRL	2		956.4708849	1910.92617	0.000451244	5	N	981	998
Q6P5E4	Conv	SKEIY	DDSFIRPVTFWIVGDFDSPSGR	QLLYD	3		838.4085618	2512.202286	0.000823681	2	N	753	775
Q6P5E4	Conv	SLTTK	WFSAPLLLEASEFLAEDSQEK	FWSFV	2		1205.594803	2409.174005	0.000622848	3	N	54	75
Q6P5E4	Conv	LVVDK	FLFVDADQIVR	TDLKE	2		661.8593165	1321.703033	0.002884417	1	N	1353	1364
Q6P5E4	Conv	REAQR	LAPLLLVLTQLINMNLR	VFMNC	2		968.0953364	1934.175073	0.000622848	1	N	1002	1019
Q6P5E4	Conv	NYVFR	HYISNPSKEPVYLSGYGVELAIK	STEYK	3		855.4518791	2563.332237	0.001162105	1	N	228	251
Q6P5E4	Conv	FQEEK	ELGTLHTEETQEGSQKHEEL	-	3		765.6965485	2294.066245	0.000451244	1	N	1531	1551
Q6P5E4	Conv	ISNGR	IIGPLEDNELFNQDDFHLL	ENIIL	2		1121.55548	2241.095361	0.002813207	1	N	898	917
Q6P5E4	Conv	FINGL	HIDLDTQDIFSLFDTLR	NEARV	3		683.6816224	2048.021467	0.002212458	1	N	398	415
Q6P5E4	Conv	QKYFK	GTIGLQPGDSALFINGLHIDLDTQDIFSLFDTLR	NEARV	3		1234.972497	3701.89409	0.000451244	1	N	381	415
Q6P5E4	Conv	EAAVR	IVPEWQDYDQEIK	QLQTL	2		831.9046494	1661.793699	0.002019181	1	N	1508	1521
Q6P5F9	Conv	MVILK	LLSEEVFDFSSGQITQVK	AKHLK	2		1014.020742	2026.025884	0.000451244	21	N	172	190
Q6P5F9	Conv	DFSQK	LDINLLDNVVNCLYHGEGAQQR	MAQEV	2	C12:+57.021	1271.129652	2540.243705	0.000451244	1	N	22	44
Q6P5F9	Conv	NMNTK	YYGLQILENVIK	TRWKI	2		726.9090065	1451.802413	0.000451244	18	N	76	88
Q6P5F9	Conv	DAQVK	LFVTGLFSLNQDIPAFK	EHLRD	2		955.5252662	1909.034932	0.000451244	8	N	995	1012
Q6P5F9	Conv	NTNIR	LAYSNGKDDEQNFIQNLSLFLCTFLK	EHGQL	3	C22:+57.021	1026.846586	3077.516358	0.000451244	5	N	305	331
Q6P5F9	Conv	LVQIK	EFAGEDTSDLFLEER	ETALR	2		879.3973856	1756.779171	0.000622848	7	N	1023	1038
Q6P5F9	Conv	EDEKR	FLVTVIKDLLGLCEQK	RGKDN	3	C13:+57.021	626.0256302	1875.053491	0.000451244	2	N	515	531
Q6P8X1	Conv	AAFRK	NLVELAELELK	HAKGN	2		635.8668073	1269.718015	0.002145581	2	N	375	386
Q6P9Q4	Conv	VVTVR	VQYLEDTDPFACANFPEPR	RAPTC	2	C12:+57.021	1135.015434	2268.015267	0.000451244	8	N	19	38
Q6PAV2	Conv	MKSLK	LVIQSTGGGESYLPVSHTCFNLLDLPK	YTEKE	3	C19:+57.021	982.5077931	2944.499979	0.001871652	1	N	1006	1033
Q6PDG5	Conv	TKVER	DIGEGNLSTAAAAALAAAAVK	AKHLA	3		629.0062175	1883.995253	0.000451244	7	N	851	872
Q6PDG5	Conv	MTIEK	SLVQNNCLSRPNIFLCPEIEPK	LLGKL	3	C7:+57.021,C16:+57.021	876.7808165	2627.319049	0.000622848	1	N	129	151
Q6PDG5	Conv	PPTNK	SLSSLVVQLLQFQEEVFGK	HVSNA	2		1076.088959	2150.162318	0.000870037	1	N	47	66
Q6PDM2	Conv	LKNRR	GGPPFAFVEFEDPRDAEDAVYGR	DGYDY	2		1271.088207	2540.160815	0.001352548	3	N	51	74
Q6PDM2	Conv	ADVYR	DGTGVVEFVR	KEDMT	2		539.7805348	1077.54547	0.000823681	2	N	154	164
Q6PEB6	Conv	NLMSK	DNLIVPILEEEVQNSVSGESEA	-	2		1186.079714	2370.143827	0.000451244	6	N	203	225
Q6PHU5	Conv	INVIK	FSTDEGQCWQSYVFTQEPIYFTGLASEPGAR	SMNIS	3	C8:+57.021	1191.208912	3570.603335	0.000451244	11	N	546	577
Q6PHU5	Conv	NGSCK	ADLGALELWR	TSDLG	2		572.3120021	1142.608404	0.000735798	3	N	276	286
Q6PHU5	Conv	SFITR	QWVSYTVDFKDILER	NCEED	3		633.6602701	1897.95741	0.001162105	3	N	593	608
Q6URW6	Conv	KAQTK	EQADFALEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	9	N	437	449
Q6URW6	Conv	DLIER	PANPPGLLALLDEECWFPK	ATDKS	2	C15:+57.021	1084.048548	2166.081496	0.000451244	1	N	547	566

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6WVG3	Conv	SRLQR	EAEYFELPELVR	RLGAP	2		747.8779033	1493.740207	0.000451244	13	N	115	127
Q6WVG3	Conv	ELVRR	LGAPQQPGPGPPPPHSR	RGVHK	3		563.9660279	1688.874684	0.000451244	1	N	128	145
Q6WVG3	Conv	TSLAK	EVFGDTLNESRDPDRPPER	YTSRY	3		743.6897282	2228.045785	0.000662267	5	N	248	267
Q6WVG3	Conv	RGVHK	EGSLGDELLPLGYAEPEPQEGASAGAPSPTLELASR	SPSGG	3		1203.592122	3607.752965	0.000451244	3	N	150	186
Q6WVG3	Conv	YVTRR	CTVVSVPDSLLWR	MFTQQ	2	C1:+57.021	766.4007913	1530.785983	0.000622848	8	N	49	62
Q6WVG3	Conv	LDYLR	DLQLVLPDYFPER	SRLQR	2		802.9201025	1603.824605	0.002663018	1	N	97	110
Q6ZPJ3	Conv	EDGAK	LYDVCPHVSDSGLFFDDSYGFYPGQVLIGPAK	IFSSV	3	C5:+57.021	1188.566148	3562.675043	0.001463592	3	N	234	266
Q6ZPJ3	Conv	VVDKR	VQSCPDPAVYGVVQSGDHVGR	TCMVK	3	C4:+57.021	743.0238996	2226.048299	0.000979378	1	N	589	610
Q6ZQ38	Conv	SEEVK	SAASYALGSISVGNLPEYLPFVLQEITSQPK	RQYLL	3		1093.910286	3278.707458	0.000451244	7	N	873	904
Q6ZQ38	Conv	EENVK	ADVFHAYLSLLK	QTRPV	3		459.5911278	1375.749983	0.000637154	3	N	391	403
Q6ZQ38	Conv	ECLGK	LTLIDPETLLPR	LKGYL	2		690.9090065	1379.802413	0.00091018	11	N	957	969
Q6ZQ38	Conv	QRALK	LGTLSALDILIK	NYSDS	2		628.8953677	1255.775135	0.001352548	2	N	667	679
Q6ZQ38	Conv	GSPLK	IDLRPVLGEGVPILASFLR	KNQRA	3		689.0776476	2064.209543	0.000622848	7	N	641	660
Q6ZQ38	Conv	SSLSK	ISGSILNELIGLVR	SPLLQ	2		742.4462875	1482.876975	0.000451244	8	N	729	743
Q6ZQ38	Conv	RACPK	EGPAVVGQFIQDVK	NSRST	2		743.8991701	1485.78274	0.000451244	4	N	812	826
Q6ZQ38	Conv	DMLSR	QGGLLVNFHPSILTCLLPQLTSPR	LAVRK	3	C15:+57.021	887.8233872	2660.446762	0.000622848	3	N	164	188
Q6ZWM4	Conv	ESHER	VFSSSQGVEQVVLGLYIVR	GDNVA	2		1040.576019	2079.136438	0.000451244	1	N	44	63
Q6ZWM4	Conv	VGTLK	GFDQTINLILDESHER	VFSSS	3		629.6468007	1885.917002	0.000451244	12	N	28	44
Q6ZWQ0	Conv	LDELR	QSSLTMDGGDVPLLEDMASGIVELFQK	KNNVT	3	M6:+15.995	966.1372205	2895.388261	0.000451244	1	N	5216	5243
Q6ZWQ0	Conv	KTKER	QYGLLSGFQDQLVMAEASLNTSLAEVESLK	IGSLD	4		811.1634022	3240.622409	0.002019181	1	N	2507	2537
Q6ZWQ9	Conv	MFGEK	LNGTDPEDVIR	NAFAC	2		614.8125633	1227.609527	0.000451244	23	N	93	104
Q6ZWQ9	Conv	PIDKK	GNFNYIEFTR	ILKHG	2		630.8045413	1259.593483	0.000451244	11	N	151	161
Q6ZWQ9	Conv	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	3	M6:+15.995	816.7132396	2447.116319	0.000622848	7	N	124	144
Q6ZWQ9	Conv	EDVIR	NAFACFDEEAIGTIQEDYLR	ELLTT	2	C5:+57.021	1181.53673	2361.057861	0.000451244	18	N	104	124
Q6ZWQ9	Conv	TMGDR	FTDEEVDELYR	EAPID	2		708.3204182	1414.625236	0.000451244	11	N	133	144
Q6ZWQ9	Conv	PQRAT	SNVFAMFDQSQIQEFK	EAFNM	2	M6:+15.995	967.9518483	1933.888097	0.000451244	5	N	19	35
Q6ZWQ9	Conv	KRPQR	ATSNVFAMFDQSQIQEFK	EAFNM	2	M8:+15.995	1053.994245	2105.972889	0.000451244	15	N	17	35
Q6ZWQ9	Conv	KRPQR	ATSNVFAMFDQSQIQEF	KEAFN	2	M8:+15.995	989.9467629	1977.877926	0.001329271	2	N	17	34
Q6ZWR6	Conv	EVSER	TAAFPSSSGVLYTVAKEELK	KFEAF	3		700.0409278	2097.099383	0.002981883	1	N	8023	8043
Q6ZWR6	Conv	SQYDK	ALQDLVDLLDTGQEK	MTGDQ	2		829.4363138	1656.857028	0.000451244	6	N	6596	6611
Q6ZWR6	Conv	MDKNK	NLFSQAFPEDSDNRDVIEDTLGCLLGR	LSLLD	3	C23:+57.021	1027.824621	3080.450463	0.000451244	11	N	6440	6467
Q6ZWR6	Conv	EKFTK	AKELISADLEHTLAELQELDGDVQEALR	TRQAT	4		777.4035464	3105.582986	0.001463592	1	N	4952	4980
Q6ZWR6	Conv	FTKAK	ELISADLEHTLAELQELDGDVQEALR	TRQAT	3		969.8247696	2906.450909	0.000451244	3	N	4954	4980
Q6ZWR6	Conv	LSRFR	LLTGSSEAVQVQVDNLQNLHDELEKQEGGLQK	FGSIT	4		880.7041169	3518.785268	0.002145581	1	N	7160	7192
Q6ZWR6	Conv	QELSR	QLEVIENSIPSVGLVEESEDRLVER	TNLYQ	3		947.1614932	2838.461079	0.000451244	10	N	6706	6731
Q6ZWR6	Conv	SNKEG	QQAIQDQLEMLK	KAWAE	2	M10:+15.995	730.8748809	1459.734162	0.002884417	2	N	2697	2709
Q6ZWX6	Conv	AVKIR	ADIEVACYGYEGIDAVK	EALRA	2	C7:+57.021	936.938132	1871.860664	0.002981883	1	N	192	209
Q76MZ3	Conv	KSLQK	IGPILDNSTLQSEVKPILEK	LTQDQ	2		1097.620623	2193.225647	0.000451244	10	N	546	566
Q76MZ3	Conv	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	2	C9:+57.021	971.5252403	1941.034881	0.000451244	14	N	381	398
Q76MZ3	Conv	PILGK	DNTIEHLLPLFLAQLKDECPEVR	LNIIS	3	C19:+57.021	917.4779452	2749.410436	0.000451244	25	N	358	381
Q76MZ3	Conv	DVDVK	YFAQEALTVLSLA	-	2		713.3853642	1424.755128	0.000698008	6	N	576	589
Q76MZ3	Conv	PILGK	DNTIEHLLPLFLAQLK	DECPE	3		622.3564105	1864.045831	0.000451244	11	N	358	374
Q76MZ3	Conv	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	3		642.3583683	1924.051705	0.001352548	1	N	398	416
Q76MZ3	Conv	NQHVK	SALASVIMGLSPILGK	DNTIE	2		778.958174	1555.900748	0.000622848	3	N	342	358
Q76MZ3	Conv	VLLAL	AEQLGTFTTLVGGPEYVHCLLPPLESLATVEETVVR	DKAVE	3	C19:+57.021	1309.347081	3925.017842	0.000451244	4	N	69	105
Q78PY7	Conv	LIGKK	VNVTVDYIRPASPATETVPAFSER	TCATV	3		873.7858094	2618.334028	0.000451244	3	N	414	438
Q78PY7	Conv	AFSTR	VLPAQATEYAFAFIQVPQDEDARTDAVDSVVR	DIQNT	4		881.1946564	3520.747426	0.000451244	2	N	787	819
Q78PY7	Conv	LYLPK	ETCLITFLLAGIECPR	GARNL	3	C3:+57.021,C14:+57.021	631.6586873	1891.952662	0.000451244	12	N	546	562
Q78PY7	Conv	IYLGK	DTNGENIAESLVAEGLATR	REGMR	2		980.485055	1958.95451	0.000451244	8	N	116	135
Q78PY7	Conv	AFSTR	VLPAQATEYAFAFIQVPQDEDAR	TDAVD	2		1290.142983	2578.270365	0.001162105	1	N	787	810
Q78ZA7	Conv	TYKMK	SEPDKADPFSFEGPEIVDCDGCTIDWK	KGKNV	3	C19:+57.021,C22:+57.021	1038.783168	3113.326105	0.000451244	2	N	228	255
Q78ZA7	Conv	ELNPK	GIPEFWFTIFR	NVDML	2		706.8722269	1411.728854	0.000451244	4	N	157	168
Q78ZA7	Conv	RTITK	QVPNESFFNFFSPLK	ASGDG	2		900.951934	1799.888268	0.001591523	2	N	282	297
Q7M6Y3	Conv	SEFLK	VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGK	KIKDS	4		943.7409651	3770.93266	0.000451244	3	N	252	288
Q7M6Y3	Conv	VGIDR	GDIPDLSQAPSSLLDALEQHLASLEGK	KIKDS	3		935.4824552	2803.423966	0.000451244	1	N	261	288
Q7TMK9	Conv	GKIPR	DLFEDELVPLFEK	AGPIW	2		797.4064936	1592.797387	0.000451244	6	N	171	184
Q7TNG5	Conv	VVDSK	CSNEAVLVATFHPTDPSLLITCGK	SHIYF	2	C1:+57.021,C22:+57.021	1315.65134	2629.287081	0.001329271	1	N	202	226
Q7TNG5	Conv	SDYSK	VQEVEVPEDFGPVR	TVAEG	2		800.4048166	1598.794033	0.001654178	2	N	327	341
Q7TNG5	Conv	PPHVR	VWDSVSLSTLHVLGLGVFDR	AVCCV	2		1100.5922	2199.1688	0.000870037	2	N	140	160
Q7TNG5	Conv	VAFSK	SNGGNLLCAVDESNDHVLSVWDWAK	ESKVV	3	C8:+57.021	929.4331757	2785.276127	0.000451244	6	N	169	194
Q7TNG5	Conv	DDFGK	VHLFSYPCCQPR	ALSHK	2	C8:+57.021,C9:+57.021	782.3634546	1562.711309	0.001162105	2	N	596	608
Q7TPR4	Conv	MASFK	ILAGDKNYITEDELR	RELPP	2		875.4550378	1748.894476	0.000451244	22	N	834	849
Q7TPR4	Conv	ARCQK	ICDQWDNLGALTQK	RREAL	2	C2:+57.021	831.4015197	1660.787439	0.000451244	16	N	478	492
Q7TPR4	Conv	SHLRK	AGTQIENIEEDFRDGLK	LMLLL	2		967.9768658	1933.938132	0.000451244	18	N	47	64
Q7TPR4	Conv	ERLRK	QFGAQANVIGPWIQTK	MEEIG	2		879.4708252	1756.92605	0.000451244	15	N	633	649

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q7TPR4	Conv	PEEFK	ACLISLGYDIGNDPQGEAEFAR	IMSIV	2	C2:+57.021	1198.563279	2395.110959	0.000451244	13	N	772	794
Q7TPR4	Conv	NYKPK	IDQLECDHQLIQEALIFDNK	HTNYN	2	C6:+57.021	1221.602405	2441.189209	0.000451244	18	N	684	704
Q7TPR4	Conv	ERTEK	LLETIDQLYLEYAKR	AAPFN	2		934.5123558	1867.009112	0.000451244	8	N	502	517
Q7TPR4	Conv	ERTEK	LLETIDQLYLEYAK	RAAPF	2		856.4618002	1710.908	0.000451244	18	N	502	516
Q7TPR4	Conv	PSEGR	MVSDINNAWGCLEQAEKGYEEWLLNEIR	RLERL	3	C11:+57.021	1123.195949	3366.564448	0.000451244	15	N	359	387
Q7TPR4	Conv	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	2		1146.027953	2290.040305	0.000451244	2	N	752	772
Q7TPR4	Conv	EAMLR	QKDYETATLSEIK	ALLKK	2		763.3913749	1524.76715	0.000662267	2	N	418	431
Q7TPR4	Conv	YGKLR	KDDPLTNLNTAFDVAER	FLDIP	2		959.9794085	1917.943217	0.000451244	18	N	197	214
Q7TPR4	Conv	ADKER	LAILGIHNEVSK	IVQTY	2		647.3804161	1292.745232	0.000451244	15	N	565	577
Q7TPR4	Conv	EEIGR	ISIEMHGTLEDQLSHLR	QYEKS	3	M5:+15.995	665.6708693	1993.989208	0.000451244	2	N	655	672
Q7TPR4	Conv	PSEGR	MVSDINNAWGCLEQAEK	GYEEW	2	C11:+57.021	982.945966	1963.876332	0.000451244	12	N	359	376
Q7TPR4	Conv	GKLRK	DDPLTNLNTAFDVAER	FLDIP	2		895.9319269	1789.848254	0.000451244	18	N	198	214
Q7TPR4	Conv	AHQDR	VEQIAAIAQELNELDYYDSPSVNAR	CQKIC	2		1404.688483	2807.361365	0.000451244	19	N	450	475
Q7TPR4	Conv	MDHYD	SQQTNDYMQPEEDWDRDLLLDPAWEK	QQRKT	3	M8:+15.995	1080.147724	3237.419772	0.000451244	9	N	5	31
Q7TPR4	Conv	VDPNR	LGVVTFQAFIDFMSR	ETADT	2		865.9508803	1729.886161	0.002884417	1	N	803	818
Q7TPR4	Conv	SHLRK	AGTQIENIEEDFR	DGLKL	2		761.3631487	1520.710697	0.002453667	1	N	47	60
Q7TPR4	Conv	HISWK	DGLGFCALIHR	HRPEL	2	C6:+57.021	629.8219798	1257.62836	0.000451244	12	N	174	185
Q7TPR4	Conv	TAPYK	NVNIQNFHISWK	DGLGF	2		750.3918465	1498.768093	0.000451244	7	N	162	174
Q7TPR4	Conv	NERLR	KQFGAQANVIGPWIQTK	MEEIG	2		943.5183068	1885.021014	0.000662267	1	N	632	649
Q7TPR4	Conv	NRICK	VLAVNQENEQLMEDYEK	LASDL	2		1026.483667	2050.951734	0.000622848	2	N	264	281
Q7TPR4	Conv	NRICK	VLAVNQENEQLMEDYEKLASDLLEWIR	RTIPW	3	M12:+15.995	1088.875164	3263.602093	0.000451244	10	N	264	291
Q7TPR4	Conv	LDIPK	MLDAEDIVGTARPDEK	AIMTY	2		880.430706	1758.845812	0.000823681	1	N	220	236
Q7TPR4	Conv	SKGVK	LVSIGAEEIVDGNVK	MTLGM	2		771.9228422	1541.830084	0.000451244	11	N	106	121
Q7TPR4	Conv	ALLKK	HEAFESDLAAHQDRVEQIAAIAQELNELDYYDSPSVNAR	CQKIC	3		1472.365733	4414.073799	0.002296037	1	N	436	475
Q7TPR4	Conv	TFIVH	TIEEIQGLTTAHEQFK	ATLPD	2		922.9735948	1843.93159	0.000451244	3	N	539	555
Q7TQI3	Conv	NCFYR	AFGFSHLEALLDDSKELQR	FKAVS	3		726.0398098	2175.096029	0.000451244	16	N	94	113
Q7TQI3	Conv	AQQDR	IQQEIAVQNPLVSER	LELSV	2		862.4710222	1722.926444	0.000451244	2	N	36	51
Q7TSI3	Conv	EERLR	YKYPSVACEILTSDVPQINDALGADESLLNR	LYGFL	3	C8:+57.021	1151.240212	3450.697235	0.000451244	4	N	74	105
Q7TSI3	Conv	SLLNR	LYGFLQSGDSLNPLLASFFSK	VMGIL	2		1152.599691	2303.183782	0.000451244	4	N	105	126
Q7TSV4	Conv	EHLKK	ELDELVGAIEEHFFQPQK	YNLQP	2		1065.031641	2128.047682	0.001264573	2	N	594	612
Q7TSV4	Conv	RRFAR	LAATAFITQGVPVYLFSDITPTPFVPYTVSHLK	LCAGI	3		1198.648514	3592.922142	0.000451244	8	N	130	163
Q7TSV4	Conv	EPKIK	YYAELCAPPGNSDPEHLKK	ELDEL	3	C6:+57.021	730.3496127	2188.025438	0.000451244	12	N	575	594
Q7TSV4	Conv	AQWLR	WDQNPLTSESVK	QLIAG	2		702.3442276	1402.672855	0.002453667	2	N	32	44
Q80T06	Conv	ENIQK	SLAGSSGPGASSGPGGDHSELIVR	ITSLE	3		732.3616116	2194.061435	0.000451244	13	N	59	83
Q80T06	Conv	ELIVR	ITSLEVENQNLR	GVVQD	2		708.3786018	1414.741604	0.000823681	3	N	83	95
Q80T06	Conv	NQNLR	GVVQDLQQAISK	LEARL	2		643.3596807	1284.703761	0.000451244	7	N	95	107
Q80UM3	Conv	QHYDK	IGQPSIALEYINTAIESTPTLIELFLVK	AKIYK	3		1025.241084	3072.699853	0.002374549	1	N	386	414
Q80UP5	Conv	YVQMK	WEFTSWVPLVSR	ICPND	2		753.891148	1505.766696	0.000451244	1	N	127	139
Q80UR4	Conv	KLDTR	VVLSEHVYPVSLPAASLR	ISSKK	3		646.3671981	1936.078194	0.002453667	1	N	140	158
Q80X41	Conv	RKEWK	LGLPIGQGGFGCIYLADTNSSKPVGSDAPCVVK	VEPSD	3	C12:+57.021,C30:+57.021	1126.56734	3376.67862	0.000451244	11	N	38	71
Q80X90	Conv	VTGQR	LVSPGSANETSSILVESVTR	SSTET	2		1023.53983	2045.064061	0.000823681	1	N	2475	2495
Q80ZJ2	Conv	AAGEK	TVFTEQPTWVIDPIDGTTNFVHR	FPFVA	2		1337.169532	2672.323463	0.000451244	3	N	78	101
Q80ZJ2	Conv	MSSIK	EKYPCHSFIGEESVAAGEK	TVFTE	3	C5:+57.021	713.3338512	2136.978154	0.001654178	1	N	59	78
Q80ZJ2	Conv	EDITK	SLLVTELGSSR	KPETL	2		581.3278492	1160.640098	0.001699387	3	N	156	167
Q810B6	Conv	HTACR	HGLANLTAELLQQGANPNLQTEEALPVPK	ESPVL	3		1022.87932	3065.614561	0.000451244	5	N	500	529
Q8BFY6	Conv	DCFIK	VCTQLQVLTEAFR	EKDTA	2	C2:+57.021	782.9115232	1563.807446	0.000451244	9	N	236	249
Q8BFY6	Conv	TKSGR	IDVAGFSALWK	FLQQW	2		603.8300277	1205.644455	0.000622848	1	N	161	172
Q8BFY9	Conv	DLLPK	LCSLLDSEDYNTCEGAFGALQK	ICEDS	2	C2:+57.021,C13:+57.021	1246.059481	2490.103362	0.000451244	6	N	140	162
Q8BFY9	Conv	TVQQK	LEQLNQYPDFNNYLIFVLTK	LKSED	2		1236.64463	2471.27366	0.000622848	1	N	44	64
Q8BFY9	Conv	YMLQR	TQDQDENVALEACEFWLTLAEQPICK	DVLVR	3	C13:+57.021,C25:+57.021	1036.814691	3107.420674	0.000451244	11	N	272	298
Q8BFY9	Conv	IILLK	GDVEEDETIPDSEQDIRPR	FHRSR	3		734.005382	2198.992746	0.002145581	1	N	327	346
Q8BFY9	Conv	MIVAL	DLLSGLAEGLGGNIEQLVAR	SNILT	3		675.7045385	2024.090216	0.000451244	1	N	653	673
Q8BFZ3	Conv	YNELR	VAPDEHPILLTEAPLNPK	INREK	2		977.5363622	1953.057124	0.000451244	30	N	96	114
Q8BFZ3	Conv	ELRVA	PDEHPILLTEAPLNPK	INREK	2		892.4835983	1782.951597	0.000451244	6	N	98	114
Q8BFZ3	Conv	INREK	MTQIMFEAFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M5:+15.995,M14:+15.995	1085.868328	3254.581585	0.001162105	1	N	119	148
Q8BG05	Conv	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	3		761.0553484	2280.142645	0.000451244	6	N	167	187
Q8BG05	Conv	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	3		814.4048174	2440.191052	0.000622848	4	N	36	57
Q8BG05	Conv	EQLRK	LFIGGLSFETTDDSLR	EHFEK	2		885.9495883	1769.883577	0.001395409	2	N	36	52
Q8BG05	Conv	SGKKR	GFAFVTFDDHDTVDK	IVVQK	3		571.9305375	1712.768212	0.001699387	3	N	167	182
Q8BG32	Conv	THLAK	LYDNLLEQNLIR	VIEPF	2		752.4124446	1502.809289	0.000451244	2	N	325	337
Q8BG32	Conv	LTDYR	AELRDDPIISTHLAK	LYDNL	3		560.3094602	1677.904981	0.001463592	7	N	310	325
Q8BGD9	Conv	SRLPK	SPPYTAFLGNLPYDVTEDSIKDFFR	GLNIS	3		964.8083912	2891.401774	0.000451244	14	N	92	117
Q8BGD9	Conv	PDRLK	GFGYAEFEDLDSLLSALSLNEESLGNRR	IRVDV	3		1034.83919	3101.494171	0.000451244	8	N	137	165
Q8BGJ5	Conv	VIHVR	KLPSDVTEGEVISLGLPFGK	VTNLL	3		696.0530563	2085.135769	0.001654178	3	N	63	83
Q8BGJ5	Conv	AAASR	IAIPGLAGAGNSVLLVSNLNPER	VTPQS	2		1138.142589	2274.269577	0.000451244	7	N	323	346

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BGJ5	Conv	LNPER	VTPQSLFILFGVYGDVQR	VKILF	2		1020.052179	2038.088759	0.001329271	1	N	346	364
Q8BGJ5	Conv	ITFTK	NNQFQALLQYADPVSAQHAK	LSLDG	3		748.3788255	2242.113076	0.000451244	5	N	217	237
Q8BGJ5	Conv	AQHAK	LSLDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	949.448444	1896.881288	0.000451244	10	N	237	253
Q8BGJ5	Conv	SPVLR	IIVENLFYPVTLDVLHQIFSK	FGTVL	3		830.1337103	2487.377731	0.002080925	2	N	184	205
Q8BGQ7	Conv	QATGK	NVGCLQEALQLATSFAQLR	LGDVK	2	C4:+57.021	1060.052154	2118.088707	0.000451244	8	N	943	962
Q8BGQ7	Conv	IPVER	LYVTYFGGDEAAGLEPDLECR	QIWQN	2	C20:+57.021	1188.046931	2374.078262	0.000451244	3	N	132	153
Q8BGQ7	Conv	DLECR	QIWQNLGLDEAR	ILPGN	2		721.8734866	1441.731373	0.001264573	2	N	153	165
Q8BH04	Conv	RIMTR	LGTPVLQALGDGDFIK	CLHSV	2		822.4543095	1642.893019	0.001264573	1	N	193	209
Q8BH43	Conv	GSLSK	YAEDIFGEICTQASAFASR	VNSLA	2	C10:+57.021	1068.489052	2134.962504	0.000622848	1	N	45	64
Q8BH61	Conv	DRSVR	LSVQSSPECIVGK	FRMYV	2	C9:+57.021	702.3638745	1402.712149	0.000451244	11	N	144	157
Q8BH61	Conv	KEFKK	ESFEETLDPFSSK	KKEVL	2		758.346633	1514.677666	0.000451244	5	N	571	584
Q8BH61	Conv	ETPVR	YGQCWVFAGVFNTFLR	CLGIP	2	C4:+57.021	982.9777289	1963.939858	0.000451244	10	N	311	327
Q8BH61	Conv	GVNLK	DYLNVTAVHLFK	ERWDS	2		710.3856985	1418.755797	0.000451244	7	N	43	55
Q8BH61	Conv	YITAK	QDGTHVVEAVDATHIGK	LIVTK	2		888.9479113	1775.880223	0.000823681	1	N	446	463
Q8BH61	Conv	GLVPR	GVNLKDYLNVTAVHLFK	ERWDS	3		644.3636765	1930.06763	0.000451244	7	N	38	55
Q8BH61	Conv	VGKFR	MYVAVWTPYGILR	TRRDP	2		784.9188518	1567.822104	0.000823681	4	N	159	172
Q8BH61	Conv	EVLVR	AGEYMSHLLEQGFLHFFVTAR	INESR	4		614.057746	2452.199784	0.002519933	1	N	591	612
Q8BH61	Conv	QEEER	LALETALMYGAK	KTLNT	2	M8:+15.995	648.8476035	1295.679607	0.001229886	2	N	492	504
Q8BH61	Conv	FGGRR	AVPPNNSNAAEVDLPTEELQGLVPR	GVNLK	2		1315.675178	2629.334756	0.002727428	1	N	13	38
Q8BH61	Conv	TFGGR	RAVPPNNSNAAEVDLPTEELQGLVPR	GVNLK	3		929.4864225	2785.435868	0.0025889	1	N	12	38
Q8BH61	Conv	SDSLR	HVYGELDLQIQR	RPTM-	2		735.8891367	1469.762673	0.000451244	3	N	716	728
Q8BH69	Conv	IDKPR	IIEVAPQVATQNVNPTPGATS	-	2		1054.055648	2106.095695	0.000451244	2	N	371	392
Q8BHD7	Conv	PNQAR	AQAALQAVSAVQSGNLSLPGATANEGTLLPGQSPVLR	IIIEN	3		1196.311624	3585.911471	0.000451244	2	N	117	154
Q8BHD7	Conv	AQYAK	MALDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	950.4291975	1898.842795	0.000451244	1	N	207	223
Q8BHG1	Conv	QLYPR	QDFLTGDQLLFEYKPEVIAEALNQLVPQK	ANLVL	3		1116.257686	3345.749657	0.000451244	11	N	588	617
Q8BHG1	Conv	YRYIK	LQNGLQALLISDLSNVEGK	TGNAT	2		1006.555283	2011.094967	0.000451244	15	N	114	133
Q8BHG1	Conv	PLIQK	SAANVVLFDIFVNILTHNLAEPAYEADVAQLEYK	LVAGE	3		1259.984514	3776.930141	0.000451244	5	N	728	762
Q8BHG1	Conv	SFEEK	IENLTEDAFNTQVTALIK	LKECE	2		1010.534017	2019.052433	0.000979378	2	N	1016	1034
Q8BHG1	Conv	ITDIR	AFTATLSLFPYHK	IVK-	3		499.2701657	1494.787097	0.000451244	3	N	1145	1158
Q8BHG1	Conv	RNKAK	STCSCPDLQPNGQDLGESGR	LARLG	2	C3:+57.021,C5:+57.021	1089.463008	2176.910416	0.000451244	16	N	56	76
Q8BHG1	Conv	TELWK	SNFDLNPDLHLPAENK	YIATD	3		608.6361245	1822.884974	0.000451244	4	N	656	672
Q8BHG1	Conv	TVDKK	IEEFLSSFEEKIENLTEDAFNTQVTALIK	LKECE	3		1120.236727	3357.686782	0.000451244	5	N	1005	1034
Q8BHG1	Conv	DLKEK	WFGTQYSIEDIENSWTELWK	SNFDL	2		1266.590052	2531.164503	0.000823681	2	N	636	656
Q8BHJ5	Conv	AVVLR	GHESEVFICAWNPVSDLLASGSGDSTAR	IWNLS	3	C9:+57.021	988.1264114	2961.355834	0.000451244	4	N	166	194
Q8BHJ5	Conv	DSTAR	IWNLSENSTSGPTQLVLR	HCIRE	2		1008.031975	2014.048351	0.001463592	1	N	194	212
Q8BHN3	Conv	LSPYR	ALLDTLQLGPDALTVHLIHEVTK	VLLVL	3		833.1395239	2496.395172	0.000698008	2	N	61	84
Q8BHN3	Conv	FDVFR	QYASLTGTQALPPLFSLGYHQSR	WNYRD	3		845.7717231	2534.291769	0.000451244	10	N	377	400
Q8BHN3	Conv	HEVTK	VLLVLELQGLQK	NMTRI	2		676.9297419	1351.843884	0.000451244	10	N	84	96
Q8BHN3	Conv	QRAPR	VPQESKDPAEGNGAQPEATPGDGDKPEETQEK	AEKDE	4		834.6346286	3334.507314	0.000622848	3	N	185	217
Q8BHN3	Conv	HSFHR	DLGIFWLNAAETWVDISSNTAGK	TLFGK	2		1254.624426	2507.233251	0.000451244	4	N	309	332
Q8BHN3	Conv	YVKTR	DGSDYEGWCWPGSASYPDFTNPR	MRAWW	2	C9:+57.021	1332.540533	2663.065465	0.000451244	10	N	493	516
Q8BHN3	Conv	FLLRR	FSFSGSTLVSSSADPK	GHLET	2		808.8942817	1615.772963	0.000622848	3	N	864	880
Q8BHN3	Conv	GLYVK	TRDGSDYEGWCWPGSASYPDFTNPR	MRAWW	3	C11:+57.021	974.4125517	2920.214255	0.002453667	1	N	491	516
Q8BHN3	Conv	LIHPV	SDAGAHGVQVYLPGQEEVWYDIQSYQK	HHGPQ	3		1023.153109	3066.435927	0.002813207	1	N	757	784
Q8BJ71	Conv	HISQR	LESLSAATTFEPLEPVKDTDIQGFLK	NEKDN	3		950.4993347	2848.474604	0.002813207	1	N	77	103
Q8BJS4	Conv	SQSPR	VILQPDVHPGNCWAFQGPQGFAVVR	LSARI	3	C12:+57.021	931.4748694	2791.401208	0.000451244	3	N	603	628
Q8BJY1	Conv	THHGR	QYLAQEGVIDQISNIIVGADSDPFSGFYLPGFVK	FFGNL	3		1229.958076	3686.850828	0.000451244	6	N	241	275
Q8BJY1	Conv	SQIGR	IVENSEAVTEILNNAELLK	QIVYC	2		1050.065681	2098.115762	0.000451244	13	N	109	128
Q8BK67	Conv	VEAPR	LIEALSHEAIVLAACGR	NHTLA	2	C15:+57.021	911.9961186	1821.976637	0.000451244	5	N	192	209
Q8BK67	Conv	ATAGK	AAGAAAIITEPEHTK	ERVKL	2		740.3942519	1478.772904	0.002813207	1	N	75	90
Q8BK67	Conv	DSQKR	VFSWGFGGYGR	LGHAE	2		616.7965192	1231.577438	0.000451244	10	N	348	359
Q8BKC5	Conv	ANVVR	QVQTSGGLWTECIAQLSPEQQAAIQELLNSA	-	3	C12:+57.021	1124.224673	3369.65062	0.000451244	6	N	1066	1097
Q8BKC5	Conv	VLLRR	LLSSAFDEVYPALPSDVQTAIK	SELLM	2		1182.62082	2363.226041	0.000451244	18	N	68	90
Q8BKC5	Conv	QKGTK	LVLEQVVTSIASVADTAEEK	FVPYY	2		1051.565514	2101.115427	0.000451244	9	N	506	526
Q8BKC5	Conv	APEAK	TKENVNATENCISAVGK	IMKFK	3	C11:+57.021	612.3040034	1833.88861	0.0007646	2	N	961	978
Q8BKC5	Conv	LRQVK	RQDEDYDEQVEESLQDEDDNDVYILTK	VSDIL	3		1101.815216	3302.422247	0.000451244	11	N	814	841
Q8BKC5	Conv	PWPDR	QWGLCIFDDIVEHCSPASFK	YAEYF	3	C5:+57.021,C14:+57.021	803.7051364	2408.092009	0.000622848	2	N	881	901
Q8BKC5	Conv	AELAR	NLIDEDGNNQWPEGLK	FLFDS	2		921.4373764	1840.859153	0.000451244	8	N	118	134
Q8BKC5	Conv	LLRGK	TIECISLIGLAVGK	EKFMQ	2	C4:+57.021	737.4211924	1472.826785	0.000451244	4	N	556	570
Q8BKC5	Conv	TLSAR	ATAAFILANEHNVALFK	HFADL	3		610.6689885	1828.983565	0.001264573	6	N	195	212
Q8BL97	Conv	DSETK	VYVGNLGTGAGKGELER	AFSYY	2		860.4553722	1718.895144	0.000451244	2	N	41	58
Q8BL97	Conv	VWIAR	NPPGFAFVEFEDPRDAEDAVR	GLDGK	2		1189.556543	2377.097486	0.001162105	2	N	73	94
Q8BMJ2	Conv	DKLKR	EIELYGCPPDFPEEEEEEEESSAKPGDIVVR	DKAKG	3	C7:+57.021	1193.538652	3577.592555	0.000823681	2	N	108	139
Q8BND5	Conv	MHQVR	SPSNAILWLWTSHNR	VNARL	3		594.6414328	1780.900898	0.000451244	4	N	471	486
Q8BND5	Conv	QWPPR	ELCSACHNELNGQVPLWDLGATLNFLK	AHFSP	3	C3:+57.021,C6:+57.021	1033.839283	3098.494448	0.000451244	30	N	509	536

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BND5	Conv	LNFLK	AHFSPANIVIDSSASR	HTGRR	2		836.4266147	1670.837629	0.000451244	4	N	536	552
Q8BND5	Conv	LQAMR	SYVQFFFGCR	DCADH	2	C9:+57.021	655.8032557	1309.590911	0.000451244	5	N	443	453
Q8BND5	Conv	DLVNK	FGVTDFPSCYLLLR	NGSVS	2	C9:+57.021	844.4295488	1686.843498	0.001162105	3	N	231	245
Q8BND5	Conv	ANDVK	DWRPALNLAVLDCAEETNSAVCR	EFNIA	3	C13:+57.021,C22:+57.021	887.4235804	2659.247341	0.000451244	9	N	91	114
Q8BND5	Conv	SYLGR	EVTLDLSQYHAVAVR	RVLNT	2		850.9524653	1699.889331	0.002145581	3	N	204	219
Q8BND5	Conv	SAVCR	EFNIAGFPTVR	FFQAF	2		625.8305591	1249.645518	0.002296037	1	N	114	125
Q8BP47	Conv	HFFDR	GYCEVTTPTLVQTQVEGGATLFK	LDYFG	2	C3:+57.021	1250.125713	2498.235825	0.000451244	4	N	274	297
Q8BP47	Conv	EGYKR	EGIDPAPYYWYTDQR	KYGTC	2		937.4237377	1872.831875	0.001162105	3	N	502	517
Q8BP56	Conv	EVTAR	AEPWAPLLEAELWPSLAHLPLTPGQK	VSFPH	3		955.5168829	2863.527249	0.000823681	6	N	649	675
Q8BPU7	Conv	EIKLR	LLDLENIQIPDAPPPIPK	EPSNY	2		992.0622129	1982.108826	0.000823681	5	N	697	715
Q8BPU7	Conv	DLYQK	VAQEITIGQLIPHLQGTDQEIQTYTIAVINALFLK	APDER	3		1293.714246	3878.119339	0.001162105	1	N	218	253
Q8BRF7	Conv	LRDAR	NSLFTGDPLGTGQFSFQRPLLVLVDR	NIDLA	3		959.8472917	2876.518475	0.002519933	1	N	234	260
Q8BT60	Conv	KPAGK	GSITISAEEIKDNR	VVLFE	2		766.8998984	1531.784197	0.001162105	1	N	125	139
Q8BT60	Conv	LPQIR	LYGPTNFSPIINHVAR	FAAAA	3		600.3253332	1797.9526	0.000451244	8	N	390	406
Q8BT60	Conv	GGSLR	APSGEVAIRDIVQFVPFR	QFQNA	3		667.7025808	2000.084342	0.000451244	10	N	475	493
Q8BT60	Conv	DIDNK	TIELSDDDFLGECEVTLGQIVSSK	KLTRP	2	C13:+57.021	1328.139214	2654.262828	0.000451244	15	N	85	109
Q8BT60	Conv	QNAPK	EALAQCVLAEIPQQVVGYFNTYK	LLPPK	2	C6:+57.021	1321.170454	2640.325309	0.000451244	10	N	500	523
Q8BT60	Conv	NHVAR	FAAAATQQQTASQYFVLLIITDGVITDLDETR	QAIVN	3		1167.270543	3498.788228	0.000451244	10	N	406	438
Q8BT60	Conv	DVTSK	SDPLCVLFLNTSGHQWYEVER	TERIK	2	C5:+57.021	1275.608021	2549.200443	0.000979378	1	N	26	47
Q8BT60	Conv	QCVTK	VELNVSCNNLLDADVTSK	SDPLC	2	C7:+57.021	995.9914273	1989.967255	0.000451244	3	N	8	26
Q8BTE6	Conv	AELCR	GDWDCGPEEQCVSIGCSHICTTN	-	2	C5:+57.021,C11:+57.021,C16:+57.021,C20:+57.021	1341.519408	2681.023217	0.000823681	7	N	40	63
Q8BTM8	Conv	PSRVR	VHGPGIQSGTTNKPNKFTVETR	GAGTG	4		592.8151758	2367.229503	0.001591523	1	N	1359	1381
Q8BTM8	Conv	PGLNR	TGVELGKPTHFTVNAK	TAGKG	2		849.962833	1697.910066	0.000451244	4	N	884	900
Q8BTM8	Conv	KAPLR	VQVQDNEGCSVEATVK	DNGNG	2	C9:+57.021	881.9177309	1761.819862	0.000451244	38	N	708	724
Q8BTM8	Conv	MPSGK	VAQPSITDNKDGTVTVR	YSPSE	2		900.9766688	1799.937738	0.000451244	6	N	1814	1831
Q8BTM8	Conv	PSKVK	AFGPGLQGGNAGSPAR	FTIDT	2		728.8687356	1455.721871	0.000451244	16	N	1071	1087
Q8BTM8	Conv	GDASK	VTAQGPGLEPSGNIANK	TTYFE	2		826.9342726	1651.852945	0.000451244	26	N	383	400
Q8BTM8	Conv	QGVFR	EATTEFSVDAR	ALTQT	2		613.288921	1224.562242	0.000451244	4	N	1272	1283
Q8BTM8	Conv	PGLEK	TGVAVNKPAEFTVDAK	HAGKA	2		823.9415663	1645.867533	0.000451244	27	N	684	700
Q8BTM8	Conv	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	2		1142.054167	2282.092735	0.001162105	1	N	916	936
Q8BTM8	Conv	SILVK	YNDQHIPGSPFTAR	VTGDD	3		534.9273502	1601.758651	0.000451244	24	N	1937	1951
Q8BTM8	Conv	VPIPR	SPYTVTVGQACNPAACR	AIGRG	2	C11:+57.021,C16:+57.021	926.4275115	1850.839423	0.000451244	35	N	467	484
Q8BTM8	Conv	PGMVR	ANLPQSFQVDTSK	AGVAP	2		717.8653272	1433.715054	0.000451244	18	N	1464	1477
Q8BTM8	Conv	TVETR	GAGTGGLGLAVEGPSEAK	MSCMD	2		785.9077234	1569.799847	0.000451244	33	N	1381	1399
Q8BTM8	Conv	KVASK	IVSPSGAAVPCKVEPGLGADNSVVR	FVPRE	2	C11:+57.021	1240.152596	2478.289592	0.002374549	1	N	1007	1032
Q8BTM8	Conv	KAPLR	VQVQDNEGCSVEATVKDNGNGTYSCSYVPR	KPVKH	3	C9:+57.021,C25:+57.021	1111.829952	3332.466455	0.000451244	26	N	708	738
Q8BTM8	Conv	VTGPR	LVSNHSLHETSSVFVDSLTK	VATVP	2		1100.566379	2199.117159	0.000451244	14	N	2520	2540
Q8BTM8	Conv	HVKAR	VANPSGNLTDTYVQDCGDGTYK	VEYTP	2	C16:+57.021	1188.026727	2374.037854	0.002296037	1	N	1296	1318
Q8BTM8	Conv	TVETR	SAGQGEVLVYVEDPAGHQEEAK	VTANN	2		1157.053833	2312.092066	0.000451244	16	N	309	331
Q8BTM8	Conv	SFEDR	KDGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C5:+57.021	1193.565488	2385.115376	0.000451244	2	N	2288	2310
Q8BTM8	Conv	TYTVK	YIPVQQGPVGVNVTYGGDHIPK	SPFSV	2		1169.613664	2337.211728	0.000451244	22	N	936	958
Q8BTM8	Conv	TVKYI	PVQQGPVGVNVTYGGDHIPK	SPFSV	3		688.0292451	2061.064335	0.000622848	3	N	938	958
Q8BTM8	Conv	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	3	C11:+57.021	922.7731979	2765.296194	0.000451244	20	N	2367	2391
Q8BTM8	Conv	CVSKR	IANLQTDLSDGLR	LIALL	2		708.3786018	1414.741604	0.000451244	12	N	63	76
Q8BTM8	Conv	TIDAK	DAGEGLLAVQITDPEGKPK	KTHIQ	3		646.6779894	1937.010568	0.000451244	4	N	1573	1592
Q8BTM8	Conv	VSVKF	NEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1160.564368	2319.113136	0.000451244	9	N	2311	2333
Q8BTM8	Conv	KTGLK	AHEPTYFTVDCTEAGQGDVSIGIK	CAPGV	2	C11:+57.021	1298.105508	2594.195417	0.000451244	3	N	785	809
Q8BTM8	Conv	FEDRK	DGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C4:+57.021	1129.518006	2257.020412	0.000451244	8	N	2289	2310
Q8BTM8	Conv	NDKNR	TFSVWYVPEVTGTHK	VTVLF	2		875.944109	1749.872618	0.000662267	6	N	340	355
Q8BTM8	Conv	DHIPK	SPFSVGVSPSLDLSK	IKVSG	2		760.4042853	1518.792971	0.000451244	16	N	958	973
Q8BTM8	Conv	EVSVK	FNEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1234.098575	2466.18155	0.000451244	11	N	2310	2333
Q8BTM8	Conv	VQGPK	GLVEPVDVVDNADGTQTVNYVPSR	EGSYS	2		1272.632979	2543.250358	0.000451244	23	N	1491	1515
Q8BTM8	Conv	YVPSR	EGSYSISVLYGEEEVPR	SPFKV	2		957.4605172	1912.905434	0.000451244	23	N	1515	1532
Q8BTM8	Conv	VICVR	FGGEHVPNSPFQVTALAGDQPTVQTPLR	SQQLA	3		988.5057056	2962.493717	0.000451244	14	N	1725	1753
Q8BTM8	Conv	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	2	C14:+57.021	1382.174257	2762.332914	0.000451244	19	N	1246	1272
Q8BTM8	Conv	SDGLR	LIALLEVLSQKK	MHRKH	3		452.2943113	1353.859534	0.002813207	1	N	76	88
Q8BTM8	Conv	WQSGR	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	EAMQQ	3	C9:+57.021,C14:+57.021	1081.504851	3241.491154	0.000451244	33	N	196	226
Q8BTM8	Conv	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C26:+57.021	1345.662062	4033.962786	0.000451244	17	N	1234	1272
Q8BTM8	Conv	NSVVR	FVPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1329.014362	3984.019685	0.000451244	17	N	1032	1069
Q8BTM8	Conv	DGTYK	VEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C35:+57.021	1428.318467	4281.932	0.000451244	10	N	1318	1357
Q8BTM8	Conv	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	2	C1:+57.021	1023.004338	2043.993075	0.000451244	20	N	809	828
Q8BTM8	Conv	SIGIK	CAPGVVGPTEADIDFDIIRNDNDTFTVK	YTPCG	3	C1:+57.021	1027.161122	3078.459965	0.000451244	14	N	809	837
Q8BTM8	Conv	FEDRK	DGSCGVAYVVQEPGDYEVSVKF	NEEHI	2	C4:+57.021	1203.052213	2404.088826	0.000451244	5	N	2289	2311
Q8BTM8	Conv	SCDVR	YWPQEAGEYAVHVLCNSEDIR	LSPFM	2	C15:+57.021	1268.582004	2535.148407	0.000451244	19	N	634	655

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Conv	DVRYW	PQEAGEYAVHVLCNSEDIR	LSPFM	3	C13:+57.021	729.6763885	2186.005765	0.000451244	2	N	636	655
Q8BTM8	Conv	RFVPR	EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1162.584127	3484.728981	0.000451244	26	N	1036	1069
Q8BTM8	Conv	EERVK	QKDLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1256.284963	3765.83149	0.000451244	18	N	529	563
Q8BTM8	Conv	GIVGK	SADFVVEAIGDDVGTLGFSVEGPSQAK	IECDD	2		1348.159027	2694.302453	0.000451244	33	N	593	620
Q8BTM8	Conv	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK	RLRNG	3	C33:+57.021	1254.999681	3761.975643	0.000451244	10	N	1964	2000
Q8BTM8	Conv	RVKQK	DLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1170.90045	3509.677949	0.000451244	23	N	531	563
Q8BTM8	Conv	GDAVR	DVDIIDHHDNTYTVK	YIPVQ	3		595.620363	1783.837689	0.000451244	13	N	921	936
Q8BTM8	Conv	GIWTR	EAGAGGLAIAVEGPSKAEISFEDR	KDGSC	2		1187.598408	2373.181216	0.002453667	3	N	2264	2288
Q8BTM8	Conv	TGTHK	VTVLFAGQHIAK	SPFEV	3		428.5877176	1282.739753	0.000823681	4	N	355	367
Q8BTM8	Conv	TLVVK	WGDEHIPGSPYR	IMVP-	3		471.8902364	1412.647309	0.000451244	10	N	2631	2643
Q8BTM8	Conv	SSHSR	CGQSAAVASPGGSIDSR	DAEMP	2	C1:+57.021	810.3760332	1618.736466	0.000870037	1	N	7	24
Q8BTM8	Conv	EGPSK	AEISCTDNQDGTCSVSYLPVLPGDYSILVK	YNDQH	3	C5:+57.021,C13:+57.021	1101.191827	3300.552082	0.000451244	15	N	1907	1937
Q8BTM8	Conv	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGR	EEPCL	2		1447.280008	2892.544415	0.000451244	16	N	1964	1993
Q8BTM8	Conv	DSLTK	VATVPQHATSGPGPADVSK	VVAKG	2		909.9713864	1817.927173	0.000823681	2	N	2540	2559
Q8BTM8	Conv	PKKAR	AYGPGIEPTGNMVK	KRAEF	2	M12:+15.995	725.356324	1448.697048	0.000451244	3	N	285	299
Q8BTM8	Conv	EATVK	DNGNGTYSCSYVPR	KPVKH	2	C9:+57.021	795.3363767	1588.657153	0.000451244	5	N	724	738
Q8BTM8	Conv	GIWTR	EAGAGGLAIAVEGPSK	AEISF	2		713.8809773	1425.746355	0.000451244	17	N	2264	2280
Q8BTM8	Conv	ESGLK	VNQPASFAVSLNGAK	GAIDA	2		751.9022441	1501.788888	0.001162105	4	N	2346	2361
Q8BTM8	Conv	CMDNK	DGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFK	VPVHD	3	C4:+57.021	1193.884317	3578.62955	0.000451244	14	N	1406	1439
Q8BTM8	Conv	AVPCK	VEPGLGADNSVVR	FVPRE	2		656.8469375	1311.678275	0.000451244	5	N	1019	1032
Q8BTM8	Conv	TVNTK	DAGEGGLSLAIEGPSK	AEISC	2		750.8811743	1499.746749	0.000451244	9	N	1891	1907
Q8BTM8	Conv	KVASK	IVSPSGAAVPCK	VEPGL	2	C11:+57.021	593.3187386	1184.621877	0.000451244	1	N	1007	1019
Q8BTM8	Conv	EPTYF	TVDCTEAGQGDVSIGIK	CAPGV	2	C4:+57.021	875.4201064	1748.824613	0.000451244	1	N	792	809
Q8BTM8	Conv	AGKGK	LDVQFSGLAK	GDAVR	2		539.3011031	1076.586606	0.000451244	4	N	906	916
Q8BTM8	Conv	HVKAR	VANPSGNLTDTYVQDCGDGTY	KVEYT	2	C16:+57.021	1123.979245	2245.94289	0.002080925	2	N	1296	1317
Q8BTM8	Conv	GDARR	LTVSSLQESGLK	VNQPA	2		631.354064	1260.692528	0.001329271	2	N	2334	2346
Q8BTM8	Conv	TVTIK	YGGQPVPNFPSK	LQVEP	2		645.8280164	1289.640433	0.00307782	1	N	1234	1246
Q8BTM8	Conv	RFIPR	ENGIYLIDVK	FNGTH	2		582.3194928	1162.623386	0.000622848	5	N	2395	2405
Q8BTM8	Conv	GDGTY	KVEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C36:+57.021	1471.016788	4410.026963	0.001943752	4	N	1317	1357
Q8BTM8	Conv	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVF	REATT	3	C26:+57.021	1293.628358	3877.861675	0.000451244	5	N	1234	1271
Q8BTM8	Conv	TFTVK	YTPCGAGSYTIMVLFADQATPTSPIR	VKVEP	2	C4:+57.021	1409.183237	2816.350873	0.000451244	5	N	837	863
Q8BTM8	Conv	SPSGK	THEAEIVEGENHTYCIR	FVPAE	3	C15:+57.021	686.6500622	2056.926787	0.001329271	1	N	2184	2201
Q8BTM8	Conv	TIEIC	SEAGLPAEVYIQDHGDGTHTITYIPLCPGAYTVTIK	YGGQP	3	C27:+57.021	1296.643897	3886.908291	0.000451244	4	N	1198	1234
Q8BTM8	Conv	WIQNK	LPQLPITNFSR	DWQSG	2		643.3673087	1284.719017	0.002519933	1	N	179	190
Q8BTM8	Conv	GIVGK	SADFVVEAIGDDVGTL	GFSVE	2		804.3941145	1606.772629	0.001329271	1	N	593	609
Q8BTZ7	Conv	DAHIR	SHSWLESCIVGWR	CRVGQ	3	C8:+57.021	539.5931598	1615.756079	0.000622848	4	N	298	311
Q8BUM3	Conv	GPLLR	LVAEVETPETAANSGPIVVHCSAGIGR	TGCFI	3	C21:+57.021	912.1328376	2733.375113	0.000451244	1	N	269	296
Q8BV13	Conv	MRNLR	ELEDLIIEAVYTDIIQGK	LDQRN	3		688.0371833	2061.08815	0.000823681	2	N	126	144
Q8BVE3	Conv	FLLEK	LGESVQDLSSFDEYSSELK	SGRLE	2		1066.997661	2131.979722	0.000451244	16	N	341	360
Q8BVE3	Conv	KILTK	LLEVSDDPQVLAVAAHDVGEYVR	HYPRG	3		832.4312551	2494.270365	0.000823681	5	N	396	419
Q8BVG4	Conv	RMDPK	ICPADPAFFSFINNSDLWVANIETGEER	RLTFC	3	C2:+57.021	1071.505	3211.491599	0.000451244	4	N	191	219
Q8BVG4	Conv	RPQQR	LQLVLLPPALFIPAVESEAQR	QAAAR	2		1152.670451	2303.325301	0.001699387	1	N	374	395
Q8BWT1	Conv	LTLNR	LCGSGFQSIVSGCQEICSK	DAEVV	2	C2:+57.021,C13:+57.021,C17:+57.021	1058.976477	2115.937354	0.000622848	3	N	90	109
Q8BWT1	Conv	SVFKK	DGTVTAGNASGVSDGAGAVIIASEDAVKK	HNFTP	3		887.451155	2659.330065	0.001943752	2	N	241	270
Q8BWY3	Conv	SKVLK	LVDISYGGENGFNQAIELSTEVLSNVK	FIQEK	2		1448.73289	2895.45018	0.000662267	2	N	252	279
Q8BWY3	Conv	GKEKK	VNIDFEPFKPINTSLYLCDNK	FHTEA	3	C18:+57.021	843.0897986	2526.245996	0.000735798	1	N	109	130
Q8BXK9	Conv	GSQRK	FLDGDELTLADCNLLPK	LHVVK	2	C12:+57.021	967.4827067	1932.949813	0.002884417	1	N	174	191
Q8C0E2	Conv	GKKEK	YFLFYDGETVSGK	VSLSL	2		763.3646287	1524.713657	0.0007646	2	N	36	49
Q8C147	Conv	VCSGR	YFTESGLVGLLEQAAELFSTGGLYETVNEVYK	LVIPI	3		1176.587649	3526.739546	0.001162105	1	N	1722	1754
Q8C166	Conv	DIGSK	SDPLCVLLQDVGGAWAELCR	TERVR	2	C5:+57.021,C19:+57.021	1130.048522	2258.081445	0.000451244	15	N	25	45
Q8C1B7	Conv	QLVNK	STSQGFCFNILCVGETGIGK	STLMD	2	C7:+57.021,C12:+57.021	1088.014148	2174.012696	0.000451244	8	N	34	54
Q8C1B7	Conv	FQKKK	AAAQLLQSQAQQSGAQQTK	KDKDK	2		979.0090316	1956.002463	0.000451244	3	N	399	418
Q8C1B7	Conv	NEELR	NLSLSGHVGFDSLPDQLVNK	STSQG	2		1070.555815	2139.096029	0.000451244	2	N	14	34
Q8C708	Conv	GLQPR	VTLEQISAFWK	REGRT	2		661.3616921	1320.707784	0.000451244	4	N	205	216
Q8C708	Conv	DPSQR	APTLVWRPGGELWIEPTSSAR	ERSED	3		775.0784874	2322.212062	0.000622848	5	N	69	90
Q8CBW3	Conv	LEETK	AYTTQSLASVAYQINALANNVLQLLDIQASQLR	RMESS	3		1197.644603	3589.910409	0.001591523	1	N	51	84
Q8CC86	Conv	AFRLR	DADVQFLASVLPPDTDPAFFEHLR	ALDCS	3		900.7821764	2699.323129	0.000823681	2	N	73	97
Q8CC86	Conv	KAAFR	FLGPDGSLLLDLLQLAEEPPPK	AGQEL	2		1181.649381	2361.283162	0.001229886	1	N	425	447
Q8CCK0	Conv	GAPVY	MAAVIEYLAAEILELAGNAAR	DNKKA	2		1095.085894	2188.156188	0.0007646	1	N	48	69
Q8CCK0	Conv	TFKYR	ISVGAPVYMAAVIEYLAAEILELAGNAAR	DNKKA	3		992.5357262	2974.583779	0.000451244	2	N	40	69
Q8CDN6	Conv	RNKVR	IDQYQGADAVGLEEK	IKQHL	2		818.3971886	1634.778777	0.000451244	4	N	87	102
Q8CDN6	Conv	LRYVK	FQNVNSVTLFVQSNQGEEETTR	ISYFT	2		1264.107128	2526.198657	0.000451244	5	N	237	259
Q8CDN6	Conv	EEAER	SEPTQALELTEDDIKEDGIVPLR	YVKFQ	3		856.7733466	2567.29664	0.000823681	2	N	211	234
Q8CDN6	Conv	-M	VGVKPVGSDPDFQPELSGAGSR	LAVVK	3		733.7067192	2198.096758	0.000851441	4	N	1	23

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CDN6	Conv	PFINK	AGCECLNESDEHGFDNCLRK	DMSFL	4	C3:+57.021,C5:+57.021,C17:+57.021	603.500859	2409.972236	0.001591523	1	N	132	152
Q8CFX1	Conv	GQVRR	ELQKPDGFQSLTPTFAGVLVHIDNLR	WEGVP	4		724.64006	2894.52904	0.001264573	1	N	319	345
Q8CG03	Conv	KIQNK	LTDLETLALLIAALSHDLDHR	GVNNS	3		777.4291858	2329.264158	0.000451244	5	N	627	648
Q8CG03	Conv	AQTLK	ITDFSFSDFELSDLETALCTIR	MFTDL	2	C19:+57.021	1290.612635	2579.20967	0.000451244	18	N	545	567
Q8CG03	Conv	KEGIR	AHTESCSCSLQQSPHADNTTPGAPAR	KISAS	3	C6:+57.021,C8:+57.021	927.40877	2779.20291	0.001591523	1	N	63	89
Q8CG03	Conv	PIQQR	IAELVAAEFFDQGDR	ERKEL	2		840.9155485	1679.815497	0.000622848	5	N	767	782
Q8CG03	Conv	MQVQK	CTIFIVDEDCPDSFSR	VFHME	2	C1:+57.021,C10:+57.021	980.9244674	1959.833335	0.000451244	2	N	356	372
Q8CG03	Conv	EEETR	ELQALSAAVVPSAQTLK	ITDFS	2		863.4914234	1724.967247	0.000451244	9	N	528	545
Q8CG03	Conv	PIQQR	IAELVAAEFFDQGDRER	KELNM	2		983.4874007	1964.959201	0.000870037	1	N	767	784
Q8CG03	Conv	LENKR	NQVLLDLASLIFEEQQSLEVILKK	IAATI	3		924.192065	2769.552795	0.000870037	2	N	319	343
Q8CG03	Conv	FLISR	LFDVAEGSTLEEASNNCIR	LEWNK	2	C17:+57.021	1062.997241	2123.978882	0.000451244	5	N	193	212
Q8CG19	Conv	TPDHR	HCQDIDECQQGNLCMNGQCR	NTDGS	3	C2:+57.021,C8:+57.021,C14:+57.021,M15:+15.995,C19:+57.021	846.9926374	2537.954512	0.001162105	2	N	1067	1087
Q8CG19	Conv	CPRGK	GLVPAGESSYDTGGENYKDADECLLFGEEICK	NGYCL	3	C23:+57.021,C31:+57.021	1175.188923	3522.543368	0.000451244	15	N	1396	1428
Q8CG19	Conv	TEGFR	GWNGQCLDVDECLQPK	VCTNG	2	C6:+57.021,C12:+57.021	959.9248017	1917.834003	0.000451244	5	N	1022	1038
Q8CG19	Conv	ASEKR	CVQPTESNEQIEETDVYQDLCWEHLSEEYVCSRPLVGK	QTTYT	4	C1:+57.021,C21:+57.021,C31:+57.021	1157.52308	4626.061119	0.000823681	7	N	1496	1534
Q8CG19	Conv	EEICK	NGYCLNTQPGYECYCK	QGTYY	2	C4:+57.021,C13:+57.021,C15:+57.021	1013.908063	2025.800526	0.000451244	10	N	1428	1444
Q8CG29	Conv	GLYAR	LFDFLVEAINR	AMQKP	2		668.8671416	1335.718683	0.000622848	2	N	360	371
Q8CG29	Conv	GNYAR	VESVDLLAFPAYLLGIDSGR	LQEKL	2		1068.073309	2134.131018	0.000451244	15	N	296	316
Q8CGC7	Conv	EYKEK	TGQEYKPGNPSAAAVQTVSTK	SSSNT	3		712.0312028	2133.070209	0.000451244	6	N	794	815
Q8CGC7	Conv	QLQRR	GFFICDQPYEPVSPYSCR	EAPCI	2	C5:+57.021,C17:+57.021	1111.487766	2220.959932	0.001654178	2	N	675	693
Q8CGC7	Conv	ELYAR	VYEELLAIPVVR	GRKTE	2		700.9115491	1399.807498	0.000823681	2	N	1195	1207
Q8CGP4	Conv	QLAIR	NDEELNKLLGR	VTIAQ	2		650.8469375	1299.678275	0.000451244	39	N	89	100
Q8CGP4	Conv	APVYL	AAVLEYLTAEVLELAGNAAR	DNKKT	2		1037.563108	2073.110617	0.000451244	32	N	52	72
Q8CGP4	Conv	PVYLA	AVLEYLTAEVLELAGNAAR	DNKKT	2		1002.044551	2002.073503	0.000451244	49	N	53	72
Q8CGP4	Conv	NYAQR	IGAGAPVYLAAVLEYLTAEVLELAGNAAR	DNKKT	3		972.5346022	2914.580407	0.000451244	14	N	43	72
Q8CGP4	Conv	QRIGA	GAPVYLAAVLEYLTAEVLELAGNAAR	DNKKT	3		892.1537217	2673.437765	0.000637154	1	N	46	72
Q8CHP8	Conv	TCSLK	TILTLTGVSSLEDVK	SNQES	2		788.4461501	1574.8767	0.001943752	2	N	275	290
Q8CHP8	Conv	GKPSR	FIFDCVSQEYGINPER	TVMVG	2	C5:+57.021	987.4570233	1972.898447	0.000451244	7	N	238	254
Q8CHP8	Conv	EKLRR	LGFGGPVGPEAGLEVFGTAYCSALYLR	QRLAG	2	C21:+57.021	1401.202286	2800.388972	0.000451244	8	N	83	110
Q8CI94	Conv	IIVER	IGEGFLTDLSQLKK	LLSLV	3		516.9597684	1547.855905	0.000451244	4	N	507	521
Q8CI94	Conv	SQLKK	LLSLVDDEAFIRDVAK	VKQEN	3		602.0004038	1802.977811	0.001839721	1	N	521	537
Q8CI94	Conv	TEYAR	EIWGVEPSDLQIPPPNLPKD	-	2		1122.581498	2243.147396	0.002884417	1	N	823	843
Q8CIE6	Conv	EITKK	IQVPNCDEIFYAGTGNLLLR	DADSI	2	C6:+57.021	1147.086193	2292.156787	0.000823681	2	N	447	467
Q8CIE6	Conv	VEKFR	SILLSVPLLVVDNKQEIAEAQQLITICR	EYIVG	3	C27:+57.021	1055.263852	3162.768156	0.000979378	3	N	1030	1058
Q8CIH5	Conv	GKNQK	AFVFILEPK	KQGDP	2		532.3134822	1062.611364	0.000451244	14	N	870	879
Q8CIH5	Conv	IADAK	LSFGDDIEQAVEEEPVQDTPPTELHFGEK	WFHKK	3		1086.177649	3255.509546	0.000451244	20	N	502	531
Q8CIH5	Conv	DEFKK	DSSVFILGNTDRPDASAVYLQDFQR	FLLHE	2		1407.688817	2813.362034	0.000851441	3	N	223	248
Q8CIH5	Conv	PTQEK	VTFEIYDPNLAFLR	FVVYE	2		849.4490272	1696.882454	0.000451244	4	N	1119	1133
Q8CIH5	Conv	SNKFK	TTVVNDNGLSPVWAPTQEK	VTFEI	2		1028.52144	2055.027281	0.000451244	15	N	1100	1119
Q8CIH5	Conv	VQAIR	DHAFVTSSFPVILSIEEHCSVEQQR	HMAKV	3	C19:+57.021	972.4716304	2914.391491	0.000622848	3	N	390	415
Q8CIH5	Conv	PKLGR	SIACPFVEVEICGAEYDSNK	FKTTV	2	C4:+57.021,C12:+57.021	1144.514178	2287.012756	0.002080925	1	N	1078	1098
Q8CIH5	Conv	GSLCK	GILDLNTYNVVK	APQGK	2		674.8777063	1347.739813	0.000451244	10	N	850	862
Q8CIH5	Conv	RAGCR	CIELDCWDGPDGKPIIYHGWTR	TTKIK	4	C1:+57.021,C6:+57.021	672.8140872	2687.225149	0.000451244	6	N	354	376
Q8CIH5	Conv	QDFQR	FLLHEQQELWAQDLNK	VRERM	2		1006.515961	2011.016322	0.000451244	4	N	248	264
Q8CIH5	Conv	TFLVR	ESETFPNDYTLSFWR	SGRVQ	2		946.42902	1890.84244	0.000451244	2	N	564	579
Q8CIH5	Conv	NGVMK	YYLTDNLTFNSIYALIQHYR	EAHLR	3		836.7573025	2507.248507	0.000998612	1	N	598	618
Q8CIH5	Conv	DALVK	EFNVNENQLQLYQEK	CNRRL	2		948.4608515	1894.906103	0.002212458	1	N	1233	1248
Q8CIH5	Conv	DYGTR	IQQYFPSNYVEDISAGDAEEMEKQIIEDNPLGSLCK	GILDL	3	M21:+15.995,C35:+57.021	1382.977193	4145.908179	0.000451244	7	N	814	850
Q8CIH5	Conv	FLKDK	LVEIGAQKDELSFEQFHLFYK	KLMFD	3		847.7728411	2540.295123	0.00091018	1	N	186	207
Q8CIH5	Conv	EFELR	LTDPVPNPNPHESKPWYYDSLSR	GEAED	4		678.8322942	2711.297977	0.00307782	1	N	630	653
Q8CIN4	Conv	ALNTK	GSETSAVVTEEDDDDEDAAPPVIAPRPDHTK	SIYTR	3		1088.49945	3262.474951	0.001763695	2	N	160	191
Q8CIN4	Conv	ENPLR	ALYLIATNGTPELQNPEK	LSPIF	2		986.5234518	1971.031304	0.000451244	14	N	450	468
Q8CIN4	Conv	TRYEK	IGQGASGTVFTATDVALGQEVAIK	QINLQ	2		1167.121519	2332.227438	0.002212458	1	N	254	278
Q8CJG0	Conv	IIFYR	DGVSEGQFQQVLHHELLAIR	EACIK	4		569.8005314	2275.170926	0.001162105	1	N	669	689
Q8CJG0	Conv	WDDNR	FSSDELQILTYQLCHTYVR	CTRSV	3	C14:+57.021	791.7233387	2372.146616	0.000451244	2	N	774	793
Q8CJG0	Conv	TAFYK	AQPVIEFVCEVLDFK	SIEEQ	3	C9:+57.021	598.6432973	1792.906492	0.000451244	1	N	227	242
Q8JZQ9	Conv	EPEVR	AKPAAQSEEETATSPAASPTPQSAER	SPSQE	3		871.4198549	2611.236165	0.000451244	2	N	61	87
Q8JZQ9	Conv	QSAER	SPSQEPSAPGKAEAVGEQAR	GHPSA	3		665.9963811	1994.965743	0.001264573	1	N	87	107
Q8JZQ9	Conv	DRTPK	GTQGVVTNFEIFR	MREKQ	2		734.3836872	1466.751774	0.001329271	2	N	524	537
Q8JZQ9	Conv	WWSHK	VDNAYWLWTFQGR	LLQKN	2		828.4024112	1654.789222	0.000622848	4	N	665	678
Q8JZQ9	Conv	GDVLK	DRPQEADGIDSVIVVDNVPQVGPDRLEK	LKNVI	3		1020.858585	3059.552354	0.000451244	3	N	163	191

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8JZQ9	Conv	SPCER	YLVTFSPLMDTQDDPQAIIIWDILTGHK	KRGFH	3	M9:+15.995	1082.885112	3245.631937	0.000823681	3	N	375	403
Q8JZQ9	Conv	ISGIK	DFSWSPGGNIIAFWVPEDKDIPAR	VTLMQ	3		906.4506496	2716.328549	0.000451244	5	N	457	481
Q8K0E8	Conv	MEYCR	TPCTVSCNIPVVSGK	ECEEI	2	C3:+57.021,C7:+57.021	809.9000669	1617.784534	0.000451244	24	N	214	229
Q8K0E8	Conv	MEYCR	TPCTVSCNIPVVSGKECEEIIR	KGGET	3	C3:+57.021,C7:+57.021,C17:+57.021	850.0783795	2547.211738	0.000451244	16	N	214	236
Q8K0E8	Conv	QAQVK	ENENVINEYSSILEDQR	LYIDE	2		1026.47997	2050.944339	0.000451244	16	N	153	170
Q8K0E8	Conv	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLK	DMWKK	3		1024.863224	3071.566273	0.000451244	17	N	114	142
Q8K0E8	Conv	LEDQR	LYIDETVNDNIPLNLR	VLRSI	2		951.5025194	1900.989439	0.000451244	17	N	170	186
Q8K0E8	Conv	SKIQK	LESDISAQMEYCR	TPCTV	2	M9:+15.995,C12:+57.021	809.3481387	1616.680677	0.000662267	3	N	201	214
Q8K0E8	Conv	EDAKK	YCGLPGEYWLGNDK	ISQLT	2	C2:+57.021	836.3775132	1670.739426	0.000998612	7	N	304	318
Q8K0E8	Conv	GDKVK	AHYGGFTVQNEASK	YQVSV	2		754.8605762	1507.705552	0.000451244	2	N	343	357
Q8K0E8	Conv	ERPIK	SSIAELNNNIQSVSDTSSVTF	QYLTL	2		1107.032566	2212.049533	0.00091018	1	N	114	135
Q8K0E8	Conv	KKVER	RPPDAGGCLHADTDMGVLCPTGCTLQQTLLNQERPIK	SSIAE	4	C8:+57.021,M15:+15.995,C19:+57.021,C23:+57.021	1034.750159	4134.969434	0.000451244	5	N	77	114
Q8K0E8	Conv	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLKDMWK	KKQAQ	3	M30:+15.995	1216.942126	3647.802978	0.00091018	2	N	114	146
Q8K183	Conv	VYRDK	VVPVADIITPNQFEAELLSGR	KIHSQ	2		1134.615872	2267.216145	0.000622848	3	N	139	160
Q8K1B8	Conv	QLTPR	ILEAHQNVAQLSLTEAQLR	FIQAW	2		1067.584906	2133.154213	0.000451244	13	N	521	540
Q8K1B8	Conv	YHINK	LTLSGDVGELASGDLGLDDLDAALNNLEVK	LKGSA	3		1009.850984	3026.529553	0.000451244	11	N	303	333
Q8K1B8	Conv	SWELR	VFVGEEDPEAQSVTLR	VTGES	2		888.4446701	1774.87374	0.000451244	35	N	19	35
Q8K1B8	Conv	LSLQR	AGGSNGGSGNKPQGPEAPAEGLNPYGLVAPR	FQRKF	3		973.8168313	2918.427094	0.000451244	16	N	477	508
Q8K1B8	Conv	HDLTK	VVLAGGVAPTLFR	GMPAH	2		650.3933265	1298.771053	0.000451244	11	N	166	179
Q8K1B8	Conv	LSYYK	SQDEAPGDPTQQLNLK	GCEVV	2		870.9241018	1739.832604	0.000451244	19	N	385	401
Q8K1B8	Conv	MAGMK	TASGDYIDSSWELR	VFVGE	2		800.3684311	1598.721262	0.000451244	14	N	5	19
Q8K1B8	Conv	VLRLR	ASFSKPLFQTVAAICR	LLSIR	2	C15:+57.021	898.4801044	1794.944609	0.000451244	14	N	113	129
Q8K1B8	Conv	SVTLR	VTGESHIGGVLLK	IVEEI	2		655.3778735	1308.740147	0.001591523	2	N	35	48
Q8K1B8	Conv	VLWLR	FKYYSFFDLDPK	TDPVR	3		523.9261761	1568.755128	0.002019181	2	N	250	262
Q8K1B8	Conv	STRER	ARGEELDEDLFLQLTGGHEAF	-	2		1174.064201	2346.112802	0.001162105	2	N	644	665
Q8K1B8	Conv	ASKGR	TMADSSYASEVQAILAFLSLQR	AGGSN	2		1201.107555	2400.199509	0.000662267	5	N	455	477
Q8K1B8	Conv	KFCIK	LLVPSPEGMSEIYLR	CQDEQ	2		852.4559955	1702.896391	0.002663018	2	N	419	434
Q8K1B8	Conv	EAQLR	FIQAWQSLPDFGISYVMVR	FKGSR	2		1129.077872	2256.140144	0.001162105	1	N	540	559
Q8K1B8	Conv	QLNLK	GCEVVPDVNVSGQK	FCIKL	2	C2:+57.021	744.3618631	1486.708126	0.000451244	4	N	401	415
Q8K1B8	Conv	WLRFK	YYSFFDLDPK	TDPVR	2		647.8036756	1293.591751	0.000823681	3	N	252	262
Q8K1B8	Conv	RERAR	GEELDEDLFLQLTGGHEAF	-	2		1060.495088	2118.974577	0.000622848	5	N	646	665
Q8K1M6	Conv	ELKTR	INVLAAQYQSLLNSYGEPVDDKSATLLQLITK	FATEY	3		1169.298321	3504.871564	0.000451244	5	N	313	345
Q8K1M6	Conv	ETFGR	TLESVDPLGGLNTIDILTAIR	NATGP	2		1106.115705	2210.21581	0.000451244	5	N	382	403
Q8K1M6	Conv	LRFPK	LHDAIVEVVTCLLR	KRLPV	3	C11:+57.021	546.6399986	1636.896596	0.00091018	1	N	465	479
Q8K296	Conv	ETENK	ASEQPAGFDTLQK	YPTPN	2		696.3442276	1390.672855	0.000662267	1	N	935	948
Q8K2B3	Conv	HGANR	LGANSLLDLVVFGR	ACALS	2		737.425355	1472.83511	0.000451244	4	N	451	465
Q8K2B3	Conv	AMVTR	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	GEGGI	3	C5:+57.021,C23:+57.021,C29:+57.021	1122.861716	3365.561747	0.002519933	1	N	282	312
Q8K352	Conv	ELLER	IGLEEHTSTLLLNGYQTLEDFK	ELRET	3		841.099394	2520.274782	0.002374549	1	N	263	285
Q8K352	Conv	ELLER	IGLEEHTSTLLLNGYQTLEDFKELR	ETHLN	4		730.6334376	2918.50255	0.000979378	2	N	263	288
Q8K411	Conv	HLQNK	LLPDHTYSVVSGGDPLCIPELTWEQLK	QFHAT	3	C17:+57.021	1023.18672	3066.536759	0.000451244	4	N	224	251
Q8K411	Conv	SPFYK	ALIESGLGTDFSPDVGYNGYTR	EAYFS	2		1166.558751	2331.101903	0.000451244	3	N	363	385
Q8K426	Conv	EKKVK	ELLANRDDCPSTVTK	TFSCT	2	C9:+57.021	859.9228163	1717.830033	0.000451244	4	N	42	57
Q8K426	Conv	STVTK	TFSCTSITASGR	LASCP	2	C4:+57.021	644.3038168	1286.592034	0.000451244	9	N	57	69
Q8K426	Conv	VPVNT	EGTLESIVEKK	VKELL	3		411.5631263	1231.665979	0.000451244	3	N	29	40
Q8K482	Conv	VLFNK	VLVNDGDVYNPNTGIFTAPYDGR	YLITA	2		1249.103857	2496.192115	0.000451244	28	N	949	972
Q8K482	Conv	ISGLK	NSVQQFYSHVFQISTDLQDLVK	FQPSA	2		1298.656257	2595.296914	0.000451244	4	N	758	780
Q8K482	Conv	LDTCK	ESAHGVQSGVSAIEGR	VFQLE	2		792.3927718	1582.769944	0.001591523	1	N	688	704
Q8K482	Conv	TCEYK	LVGLQQQCDDYGSSYLGVIELIGEK	EASLK	2	C8:+57.021	1392.691948	2783.368296	0.0007646	2	N	352	377
Q8K482	Conv	EGQLK	QLQEAAQGPTVTMTTNELYQAYVDSK	IDALR	3	M13:+15.995	968.131234	2901.370302	0.000622848	2	N	300	326
Q8K482	Conv	RGLPR	GVDGQMGQGPIHSSEGYAGAPGYPK	SPPVT	3	M6:+15.995	826.0453236	2475.112571	0.000637154	4	N	887	912
Q8K4L3	Conv	KDFWK	LLGGQTSYQSAGDPKEDELYETAIIETNCVYR	LTDDK	3	C29:+57.021	1207.573919	3619.698358	0.000451244	6	N	1491	1523
Q8K4Z3	Conv	KGDVR	EPFHSILSVLSGLTVPIASIDIPSGWDVEK	GNPSG	3		1069.571493	3205.69108	0.000823681	1	N	191	221
Q8K4Z3	Conv	TSMSK	SPPTVLVICGPGNNGGDGLVCAR	HLKLF	2	C9:+57.021,C21:+57.021	1155.570153	2309.124706	0.000451244	2	N	100	123
Q8K4Z3	Conv	ARHLK	LFGYQPTIYYPK	RPNKP	2		745.3904495	1488.765299	0.002981883	1	N	126	138
Q8K558	Conv	GQGSA	DSHPEVLQAPVGSSILVQCHYR	LQDVR	3	C19:+57.021	831.4169087	2491.227326	0.000451244	7	N	20	42
Q8K558	Conv	VRALK	VWCQFLQEGCHPLVTSAVDR	RAPGN	3	C3:+57.021,C10:+57.021	801.3843973	2401.129792	0.000823681	4	N	50	70
Q8K558	Conv	QTLHR	VSLLVLPPVPGPR	EGEEA	2		672.4246267	1342.833653	0.001699387	2	N	118	131
Q8QZY1	Conv	LQQLK	VFSDEVQQQAQLSTIR	SFLKL	2		924.9766688	1847.937738	0.000451244	19	N	445	461
Q8QZY1	Conv	LRMQK	GDPQVYEELFSYACPK	FLSPV	2	C14:+57.021	951.9328497	1901.850099	0.000451244	4	N	403	419
Q8QZY1	Conv	MPVAK	LAGFLDLTEQEFR	IQLLV	2		769.8966274	1537.777655	0.001871652	1	N	474	487
Q8QZY1	Conv	RSNPK	VWNVHSVLNVLHSLVDK	SNINR	3		653.6990592	1958.073778	0.000451244	5	N	220	237
Q8QZY1	Conv	ERFFK	NTPWPEAEAIAPQVGNDAVFLILYK	ELYYR	3		919.4818383	2755.422115	0.000451244	10	N	108	133

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8QZY1	Conv	SNINR	QLEVYTSGGDPESVAGEYGR	HSLYK	2		1057.487795	2112.959989	0.000622848	12	N	242	262
Q8QZY6	Conv	ESNIK	SYRDDIDLQNLIDSLQK	ANQCC	2		1018.518898	2035.022196	0.000451244	11	N	132	149
Q8QZY6	Conv	YSREK	CGVPFSCCVPDPAQK	VVNTQ	2	C1:+57.021,C7:+57.021,C8:+57.02	861.3756704	1720.735741	0.000451244	3	N	179	194
Q8QZY9	Conv	PISER	NQDATVYVGGLDEK	VSEPL	2		754.8655242	1507.715448	0.000823681	6	N	9	23
Q8R010	Conv	SALGR	SPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQR	WLKSC	3		1246.315145	3735.922036	0.001162105	3	N	265	301
Q8R016	Conv	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLR	RATVQ	2	C23:+57.021	1420.224281	2838.432962	0.002519933	1	N	17	42
Q8R016	Conv	EEIFR	VVCICLGNPPETFTWEYR	DKDKN	2	C3:+57.021,C5:+57.021	1121.027059	2240.038517	0.000451244	31	N	218	236
Q8R016	Conv	DKVER	CYFFLNAFVDTAQK	KEPED	2	C1:+39.994	853.897856	1705.780112	0.002663018	1	N	110	124
Q8R016	Conv	ICLRR	ATVQGAQHVFQHVVPQEGKPVTNQK	SSGRC	3		909.8162144	2726.425243	0.000451244	8	N	43	68
Q8R016	Conv	VGGRK	TLYNNQPIDFLK	KMVAA	2		733.3884382	1464.761276	0.000662267	1	N	297	309
Q8R016	Conv	KNYHK	IGPITPLQFYK	EHVKP	2		638.8691529	1275.722706	0.000662267	7	N	244	255
Q8R016	Conv	AASIK	DGEAVWFGCDVGK	HFNGK	2	C9:+57.021	720.3169242	1438.618248	0.000451244	5	N	317	330
Q8R016	Conv	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLRR	ATVQG	3	C23:+57.021	999.1858244	2994.534073	0.000451244	4	N	17	43
Q8R016	Conv	DICLR	RATVQGAQHVFQHVVPQEGKPVTNQK	SSGRC	4		721.6393886	2882.526354	0.000451244	12	N	42	68
Q8R016	Conv	VVDKK	HVPEEVLAVLEQEPIVLPAWDPMGALA	E-	3		975.1811719	2922.520116	0.000622848	1	N	427	454
Q8R016	Conv	DKVER	CYFFLNAFVDTAQKK	EPEDG	3	C1:+57.021	617.9751584	1850.902075	0.000451244	1	N	110	125
Q8R050	Conv	KIRLK	GIEEEEILPGFILCDLNNLCHSGR	TFDAQ	3	C14:+57.021,C20:+57.021	929.1145239	2784.320172	0.000451244	1	N	504	528
Q8R050	Conv	GANLK	EQSDFCPWYIGLPFIPYLDNLPNFNR	SVDGP	3	C6:+57.021	1072.515059	3214.521777	0.000823681	3	N	407	433
Q8R081	Conv	LNVFK	NDQDTWDYTNPNLSGQGDPGSNPNKR	QRQPP	3		964.0928009	2889.255003	0.000451244	6	N	274	300
Q8R081	Conv	MNCDR	VFNVFCLYGNVEK	VKFMK	2	C6:+57.021	794.8953418	1587.775084	0.000451244	10	N	395	408
Q8R081	Conv	VVHIR	GLIDGVVEADLVEALQEFGPISYVVVMPK	KRQAL	3		1029.882792	3086.624975	0.000451244	1	N	104	133
Q8R081	Conv	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	C13:+57.021	1463.369496	4387.085087	0.000622848	1	N	135	175
Q8R081	Conv	SDDSR	SVNSVLLFTILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C26:+57.021,C29:+57.021	1290.005847	3866.994141	0.000451244	4	N	186	220
Q8R0J7	Conv	NMAEK	FLDGELPLDSFIDVYQSK	RKLAH	2		1043.523118	2085.030635	0.000622848	4	N	127	145
Q8R0J7	Conv	LASNR	SLAEGNLLYQPQLDAQK	ARLTQ	2		944.4946944	1886.973789	0.001162105	1	N	53	70
Q8R146	Conv	LSGGK	CELLSDESLAVCSPR	LSPDQ	2	C1:+57.021,C12:+57.021	868.4031708	1734.790742	0.000451244	15	N	291	306
Q8R146	Conv	-MER	QVLLSEPQEAAALYR	GLSRQ	2		844.4548408	1686.894082	0.000451244	4	N	3	18
Q8R146	Conv	RGLSR	QPSLSAACLGPEVTTQYGGLYR	TVHTE	2	C8:+57.021	1184.584015	2367.15243	0.000451244	17	N	22	44
Q8R146	Conv	HQDVK	DVQFAVQQVLQEEHFDAR	RVALM	2		1080.029964	2158.044328	0.000451244	7	N	561	579
Q8R146	Conv	HWGIR	VLHPPPDQENVQYADLDFEAILLQPSNSPDK	SQVPM	3		1163.911126	3488.709977	0.000451244	5	N	466	497
Q8R146	Conv	PPAGK	EQSVSWVSLEEAEPIPDIHWGIR	VLHPP	2		1339.166989	2676.318378	0.000823681	2	N	443	466
Q8R146	Conv	DIVPR	QLGESFSGIYCSLLPLGCWSADSQR	VVFDS	2	C11:+57.021,C18:+57.021	1416.160061	2830.304522	0.000451244	15	N	350	375
Q8R146	Conv	LVNYR	GSTGFGQDSILSLPGNVGHQDVK	DVQFA	2		1157.077643	2312.139685	0.000698008	3	N	538	561
Q8R146	Conv	VQRSR	QDLFAVDTQTGSVTSLTAGGSAGSWK	LLTID	2		1292.630436	2583.245273	0.000823681	1	N	385	411
Q8R146	Conv	HQDVK	DVQFAVQQVLQEEHFDARR	VALMG	3		772.3896131	2314.145439	0.000451244	2	N	561	580
Q8R146	Conv	CTNRR	SALYYVDLSGGK	CELLS	2		636.8276821	1271.639764	0.000451244	1	N	279	291
Q8R146	Conv	DWYTK	VTSLVVDIVPR	QLGES	2		599.3642347	1196.712869	0.001591523	2	N	339	350
Q8R146	Conv	CTNRR	SALYYVDLSGGKCELLSDESLAVCSPR	LSPDQ	3	C13:+57.021,C24:+57.021	997.1477819	2988.419946	0.000622848	1	N	279	306
Q8R180	Conv	EQAER	LGAVDESLSEETQK	AVLQW	2		753.3706394	1504.725679	0.000451244	6	N	135	149
Q8R180	Conv	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	C1:+57.021,C3:+57.021,C12:+57.021,C14:+57.021	1093.787622	3278.339466	0.000451244	12	N	34	60
Q8R180	Conv	QCGRR	DCAVKPCHSDEVPDGIK	SASYK	3	C2:+57.021,C7:+57.021	642.9612061	1925.860218	0.000823681	2	N	97	114
Q8R180	Conv	LQWTK	HDDSSDSFCEIDDIQSPDAEYVDLLLNPER	YTGYK	3	C9:+57.021	1165.511096	3493.509888	0.000451244	5	N	156	186
Q8R180	Conv	DAENK	ALLLEILHEIK	SFPLH	2		646.4033599	1290.79112	0.001395409	3	N	337	348
Q8R180	Conv	PDAWR	IWSVIYEENCFKPQTIQRPLASGR	GKSKE	3	C10:+57.021	964.8327225	2891.474767	0.002519933	2	N	197	221
Q8R1B4	Conv	VVMHR	TEPTAQQNLALQLAEK	LGSLV	2		877.9683124	1753.921025	0.002212458	2	N	844	860
Q8R1B4	Conv	KMNGK	VWDLFPEADKVR	TMLVR	3		492.2616702	1473.761611	0.000637154	3	N	762	774
Q8R2S8	Conv	VTCPR	GATHCYKGDIALQGGGLTTR	VSIQG	3	C5:+57.021	692.6815853	2075.021356	0.000622848	5	N	725	745
Q8R2S8	Conv	DVSER	CSPPSETTELSCYR	GVMFE	2	C1:+57.021,C12:+57.021	843.858596	1685.701592	0.000451244	3	N	579	593
Q8R2S8	Conv	VTEHR	TGPGLSVTSYTR	VCRKK	2		619.822931	1237.630262	0.000451244	1	N	468	480
Q8R2S8	Conv	THCYK	GDIALQGGGLTTR	VSIQG	2		629.8416551	1257.66771	0.000823681	8	N	732	745
Q8R2S8	Conv	LTRHR	TGPGISIVSYVHVCR	DRDFC	2	C14:+57.021	822.9302473	1643.844895	0.000451244	4	N	279	294
Q8R2S8	Conv	PGSLR	CPLCLSNDSCENAPEQVCPVGSTHCYDGVLR	LRGDG	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1198.843759	3593.507877	0.000451244	14	N	133	164
Q8R2S8	Conv	TLRCR	HCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	3	C2:+57.021,C8:+57.021,C16:+57.021,C23:+57.021	1118.177332	3351.508597	0.000451244	24	N	323	354
Q8R2S8	Conv	FLGSK	GCSSPGAQDNIGVSIFSR	LPGML	2	C2:+57.021	926.4366222	1850.857644	0.000451244	7	N	643	661
Q8R2S8	Conv	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLRG	GGIIS	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1281.221118	3840.639954	0.000451244	5	N	510	544
Q8R2S8	Conv	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C1:+39.994,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1256.538297	3766.59149	0.000451244	7	N	510	543
Q8R2S8	Conv	HGTLK	TIQDISKLPLQWTAGQK	ICNVG	2		964.0365294	1926.057459	0.000451244	8	N	408	425
Q8R2S8	Conv	VNSTK	ILEELPTPTVPGSLR	CPLCL	2		811.4621346	1620.908669	0.000451244	9	N	118	133
Q8R2S8	Conv	VHVCR	DRDFCNDLSTTDPLWTPPPDTELGTLR	CRHCL	3	C5:+57.021	1044.82451	3131.450129	0.000451244	22	N	294	321
Q8R2S8	Conv	VCRKK	DFCNDLSTTAPLWAPPPVTAPGTTR	CPLCF	2	C3:+57.021	1343.152793	2684.289986	0.001763695	2	N	485	510

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R2S8	Conv	GAGEK	TCEVSEGCQDLIMLLYNGPK	VNLVI	3	C2:+57.021,C8:+57.021	776.3622708	2326.063412	0.000451244	9	N	48	68
Q8R2S8	Conv	EEPVK	WTAPGSQVCAPDEICQETLLLIDVGQK	SAFLG	3	C9:+57.021,C15:+57.021	1010.163543	3027.46723	0.000451244	19	N	609	636
Q8R2S8	Conv	VIWLR	TGPGLSVVSYTR	VCRHG	2		618.8332987	1235.650997	0.000451244	9	N	91	103
Q8R550	Conv	SNFIK	ELSGESDELGISQDEQLSK	SRPEG	2		1032.484918	2062.954235	0.001329271	1	N	153	172
Q8R5A3	Conv	RQLAR	DVLDNLFEK	THCDC	2		546.7827432	1091.549886	0.000637154	4	N	204	213
Q8R5A3	Conv	LQIER	VFEDHENVVEVLSDWTR	DTENK	3		692.0012436	2072.980331	0.000451244	15	N	235	252
Q8R5A3	Conv	NLFEK	THCDCNVDWCLYEIYPELQIER	VFEDH	3	C3:+57.021,C5:+57.021,C10:+57.021	971.7595981	2912.255394	0.000451244	4	N	213	235
Q8R5H1	Conv	NHLKR	NDSIIVDIFHGLFK	STLVC	3		539.9598798	1616.85624	0.002981883	2	N	429	443
Q8R5H1	Conv	TQVGR	FAPQFSGYQQQDCQELLAFLLDGLHEDLNR	IRKKP	3	C13:+57.021	1184.900301	3551.677503	0.002453667	1	N	368	398
Q8R5L1	Conv	SQGQK	AEEQEPELTSTPNFVVEVTK	TDGKK	2		1124.05551	2246.09542	0.000451244	17	N	152	172
Q8R5L1	Conv	TDGKK	TLVLDCHYPEDEIGHEDEAESDIFSIK	EVSFQ	3	C6:+57.021	1054.480408	3160.417825	0.000451244	34	N	177	204
Q8R5L1	Conv	FLADR	GVDNTFADELVELSTALEHQEYITFLEDLK	SFVKN	3		1147.231754	3438.671861	0.000451244	17	N	243	273
Q8R5L1	Conv	TEGDK	AFVEFLTDEIKEEK	KIQKH	2		849.4357824	1696.855965	0.000823681	2	N	78	92
Q8VBT9	Conv	RHTVK	VTPSTVLLQVLEDTCR	RQDFN	2	C15:+57.021	915.9854166	1829.955233	0.001591523	1	N	25	41
Q8VBV7	Conv	ATRRR	AFALVSQAYTSIIADDFAAFVGLPVEEAVK	GVLEQ	3		1048.216939	3141.627417	0.000662267	6	N	116	146
Q8VBV7	Conv	VSLNR	FIPLSEPAPVPPIPNEQQLAR	LTDYV	2		1157.134232	2312.252864	0.0007646	6	N	178	199
Q8VBV7	Conv	PPAIK	SANSELGGIWSVGQR	IWQRD	2		780.8924077	1559.769215	0.000451244	1	N	65	80
Q8VBV7	Conv	EEAVK	GVLEQGWQADSTTR	MVLPR	2		774.3765904	1546.737581	0.000622848	3	N	146	160
Q8VBW6	Conv	TEILK	NLVLPGIGSFTIIDGNLVSGEDAGNNFFLQK	SSIGK	3		1083.89838	3248.671741	0.0025889	1	N	47	78
Q8VC30	Conv	RKRIR	AAPTEPPEAPEATAAGGVTSKQMALVLDR	ICTTL	4	M23:+15.995	724.3701053	2893.449221	0.001162105	1	N	351	380
Q8VC30	Conv	LVLDR	ICTTLIGLEEHLNALDR	AAGDG	3	C2:+57.021	656.6791817	1967.014145	0.001329271	3	N	380	397
Q8VC88	Conv	EELQR	CLTQSGISGTYAPFSLETCR	IMIAM	2	C1:+39.994,C19:+57.021	1116.008837	2230.002075	0.001162105	3	N	78	98
Q8VC88	Conv	SKNGR	IFFDDYVACCVK	LRALT	2	C9:+57.021,C10:+57.021	768.8467717	1535.677943	0.000451244	6	N	175	187
Q8VC88	Conv	FNEFK	ELWAALNAWK	QNFMT	2		601.3223699	1200.62914	0.000622848	5	N	118	128
Q8VC88	Conv	DYTGK	MGFNEFKELWAALNAWK	QNFMT	3		685.6772671	2054.008401	0.000451244	7	N	111	128
Q8VC88	Conv	WTYFT	AVAGQDGEVDAEELQR	CLTQS	2		843.9006267	1685.785653	0.000851441	3	N	62	78
Q8VCI0	Conv	AASQS	DPTGVHCATAYWSPESK	KVEIK	2	C7:+57.021	953.4257231	1904.835846	0.000451244	13	N	36	53
Q8VCI0	Conv	DPFWR	HTGYVVTQLDGLYLGAQKR	ASEEK	3		707.0485282	2118.122184	0.000451244	2	N	161	180
Q8VCI0	Conv	KGTLY	IVEQIPTYVEYSDQTNVLR	KGYWA	2		1134.081862	2266.148125	0.001463592	1	N	376	395
Q8VCI0	Conv	VTINR	SLDKGTLYIVEQIPTYVEYSDQTNVLR	KGYWA	3		1048.875353	3143.602659	0.000451244	20	N	368	395
Q8VCI0	Conv	TICCR	EDLNGASPSPGGCYDTK	VADIF	2	C13:+57.021	884.3784385	1766.741277	0.000451244	6	N	477	494
Q8VCI0	Conv	CYDTK	VADIFLASQYK	AYAIS	2		627.8405925	1253.665585	0.001162105	4	N	494	505
Q8VCI0	Conv	ASQYK	AYAISGPTVQDGLPPFNWNR	FNETL	2		1102.050699	2202.085799	0.000451244	8	N	505	525
Q8VCI0	Conv	RSLDK	GTLYIVEQIPTYVEYSDQTNVLR	KGYWA	2		1351.19013	2700.36466	0.000451244	11	N	372	395
Q8VCI0	Conv	NDSIK	TTGWGILEIR	AGYGS	2		573.3198272	1144.624054	0.000823681	4	N	76	86
Q8VCI0	Conv	LLVHK	LGLDYSYDLAPR	AKIFR	2		691.8516885	1381.687777	0.001763695	1	N	422	434
Q8VCI0	Conv	DPFWR	HTGYVVTQLDGLYLGAQK	RASEE	2		982.0183367	1962.021073	0.000451244	12	N	161	179
Q8VCM7	Conv	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	2	C7:+57.021	1221.59184	2441.16808	0.000451244	23	N	200	221
Q8VCM7	Conv	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLR	TLEDI	3	C5:+57.021,C9:+57.021	1029.455275	3085.342424	0.000451244	19	N	39	66
Q8VCM7	Conv	GTYSK	SSTTNGFDDGIIWATWK	SRWYS	2		949.9501196	1897.884639	0.000451244	16	N	381	398
Q8VCM7	Conv	NLKQK	VAQLEAQCQEPCKDSVQIHDTTGK	DCQEI	3	C8:+57.021,C12:+57.021	914.7657833	2741.27395	0.000451244	19	N	152	176
Q8VCM7	Conv	YVATR	DNCCILDER	FGSFC	2	C3:+57.021,C4:+57.021	597.7475888	1193.479578	0.001463592	1	N	30	39
Q8VCM7	Conv	EEIVK	YEALLLTHETSIR	YLQEI	3		515.9477513	1544.819854	0.001329271	1	N	120	133
Q8VCM7	Conv	WIQYK	EGFGHLSPTGTTEFWLGNEK	IHLIS	2		1104.024347	2206.033095	0.000451244	16	N	237	257
Q8VCM7	Conv	QEPCK	DSVQIHDTTGKDCQEIANK	GAKES	3	C13:+57.021	720.3396649	2157.995595	0.001699387	1	N	165	184
Q8VCM7	Conv	ETSIR	YLQEIYNSNNQK	ITNLK	2		757.3682341	1512.720868	0.000823681	4	N	133	145
Q8VCM7	Conv	NKGAK	ESGLYFIRPLK	AKQQF	2		661.8775093	1321.739419	0.000451244	7	N	187	198
Q8VCM7	Conv	KELIK	AIQVYYNPDQPPKPGMIDSATQK	SKKMV	3	M16:+15.995	859.7605241	2576.258172	0.001699387	1	N	87	110
Q8VCM7	Conv	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLRTLEDILFR	AENRT	3	C5:+57.021,C9:+57.021	1358.634919	4072.881356	0.000451244	3	N	39	74
Q8VCT3	Conv	RTLAK	DTFAATASQLHSNVVNYVQQILAPKDS	-	3		973.161716	2916.461748	0.001162105	3	N	623	650
Q8VCT3	Conv	LNKLR	VKIEPGVDPDDTYNETPYEK	GYCFV	2		1155.045142	2308.074685	0.001352548	1	N	396	416
Q8VCT3	Conv	YAQRR	ISTILFGAAYTCLEAATGR	ALLRQ	2	C12:+57.021	1008.017248	2014.018896	0.000451244	6	N	357	376
Q8VCT3	Conv	GPRSR	VWAEPCLIEAAKEEYSGVIEEFLATGEK	LFGPY	3	C6:+57.021	1056.853406	3167.536818	0.000451244	19	N	248	276
Q8VCT3	Conv	ISTWK	TYQLVYFLDK	ILQKS	2		645.342968	1288.670336	0.000451244	7	N	531	541
Q8VCT3	Conv	VDEFK	FQSILAEDFLEFYLEYFPELK	KKGVD	2		1321.159778	2640.303957	0.000451244	1	N	446	467
Q8VCT3	Conv	TPYEK	GYCFVSYLAHLVGDQDQFDK	FLKAY	3	C3:+57.021	788.0321722	2361.073117	0.000451244	8	N	416	436
Q8VCT3	Conv	ASELR	LDSHSCLEVTAATLR	RGQPG	2	C6:+57.021	836.9200766	1671.824553	0.002374549	1	N	79	94
Q8VCT3	Conv	ATLRR	GQPGDQQAPAEPVPFHTQPFSHYGQALCVAFR	QPCGA	3	C28:+57.021	1179.897114	3536.667941	0.002813207	1	N	95	127
Q8VCT3	Conv	KLRVK	IEPGVDPDDTYNETPYEK	GYCFV	2		1041.463454	2080.911308	0.001162105	3	N	398	416
Q8VCT3	Conv	AVLNR	AFFPCFDTPAVK	CTYSA	2	C5:+57.021	700.339671	1398.663742	0.002519933	1	N	176	188
Q8VCT3	Conv	RTLAK	DTFAATASQLHSNVVNYVQQILAPK	DS-	3		905.8087255	2714.402777	0.001162105	1	N	623	648
Q8VDD5	Conv	LEKAK	QTLENERGELANEVK	ALLQG	2		865.4399191	1728.864238	0.000451244	9	N	1219	1234
Q8VDD5	Conv	ERAKR	QAQQERDELADEIANSSGK	GALAL	2		1044.993776	2087.971951	0.000451244	18	N	1697	1716
Q8VDD5	Conv	ALEAK	IAQLEEQLDNETKER	QAASK	2		908.4583088	1814.901018	0.000451244	12	N	1815	1830

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDD5	Conv	ALEAK	IAQLEEQLDNETK	ERQAA	2		765.8864567	1529.757313	0.000451244	21	N	1815	1828
Q8VDD5	Conv	FQEFR	QRYEILTPNSIPK	GFMDG	3		520.2916295	1557.851488	0.000451244	5	N	718	731
Q8VDD5	Conv	EMRQK	HSQAVEELADQLEQTKR	VKATL	2		991.5010394	1980.986479	0.000451244	1	N	1193	1210
Q8VDD5	Conv	EFRQR	YEILTPNSIPK	GFMDG	2		637.8536999	1273.6918	0.001162105	3	N	720	731
Q8VDD5	Conv	NDRLK	KANLQIDQINTDLNLER	SHAQK	2		999.5348822	1997.054164	0.000451244	8	N	1753	1770
Q8VDD5	Conv	KKAGK	LDPHLVLDQLR	CNGVL	2		659.8780406	1317.740481	0.000451244	4	N	682	693
Q8VDD5	Conv	TAAQK	VSHLLGINVTDFTR	GILTP	2		786.4311687	1570.846737	0.000451244	9	N	373	387
Q8VDD5	Conv	MGLLR	VISGVLQLGNIAFKK	ERNTD	2		793.9855798	1585.95556	0.000451244	10	N	341	356
Q8VDD5	Conv	DRLKK	ANLQIDQINTDLNLER	SHAQK	2		935.4874007	1868.959201	0.000451244	18	N	1754	1770
Q8VDD5	Conv	RLEAR	IAQLEEELEEEQGNTELINDR	LKKAN	2		1236.590977	2471.166354	0.000451244	27	N	1730	1751
Q8VDD5	Conv	LYVDK	NFINNPLAQADWAAK	KLVWV	2		836.9262505	1671.836901	0.000451244	11	N	14	29
Q8VDD5	Conv	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	2		1167.032241	2332.048882	0.000451244	11	N	940	959
Q8VDD5	Conv	QAADK	YLYVDKNFINNPLAQADWAAK	KLVWV	3		818.7537809	2453.237943	0.000622848	3	N	8	29
Q8VDD5	Conv	DKVTK	LQVELDSVTGLLSQSDSK	SSKLT	2		960.0025492	1917.989498	0.000451244	24	N	1277	1295
Q8VDD5	Conv	MGLLR	VISGVLQLGNIAFK	KERNT	2		729.9380983	1457.860597	0.000451244	25	N	341	355
Q8VDD5	Conv	KTKTR	LQQELDDLLVDLDHQR	QSVSN	2		975.5005081	1948.985416	0.000451244	17	N	1417	1433
Q8VDD5	Conv	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	2		998.5205152	1995.02543	0.000637154	2	N	272	289
Q8VDD5	Conv	LKKIR	ELETQISELQEDLESER	ASRNK	2		1024.48746	2046.959321	0.000451244	12	N	1107	1124
Q8VDD5	Conv	LMAEK	LQLQEQLQAETELCAEAEELR	ARLTA	2	C14:+57.021	1251.113334	2500.211067	0.000451244	17	N	882	903
Q8VDD5	Conv	SKSSK	LTKDFSALESQLQDTQELLQEENR	QKLSL	3		945.8055979	2834.393394	0.000451244	7	N	1298	1322
Q8VDD5	Conv	LEKTK	TRLQQELDDLLVDLDHQR	QSVSN	3		736.3858686	2206.134206	0.000451244	14	N	1415	1433
Q8VDD5	Conv	SKLTK	DFSALESQLQDTQELLQEENRQK	LSLST	2		1375.167914	2748.320229	0.000451244	7	N	1301	1324
Q8VDD5	Conv	EKTRR	KLEGDSTDLSDQIAELQAQIAELK	MQLAK	3		872.4523845	2614.333754	0.000451244	20	N	1051	1075
Q8VDD5	Conv	SKLTK	DFSALESQLQDTQELLQEENR	QKLSL	2		1247.091144	2492.166688	0.000451244	20	N	1301	1322
Q8VDD5	Conv	GKFIR	INFDVNGYIVGANIETYLLEK	SRAIR	3		795.749925	2384.226375	0.000998612	1	N	240	261
Q8VDD5	Conv	EKQKR	DLGEELEALKTELEDTLDSTAAQQELR	SKREQ	3		1006.498611	3016.472432	0.000451244	33	N	1135	1162
Q8VDD5	Conv	MALKK	IRELETQISELQEDLESER	ASRNK	2		1159.080048	2316.144496	0.000451244	10	N	1105	1124
Q8VDD5	Conv	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	2	M10:+15.995	1017.533006	2033.050411	0.000451244	15	N	617	637
Q8VDD5	Conv	EKSKR	ALEQQVEEMKTQLEELEDELQATEDAK	LRLEV	3		1049.834895	3146.481284	0.001699387	1	N	1528	1555
Q8VDD5	Conv	DLQPC	IDLIEKPAGPPGILALLDEECWFPK	ATDKS	3	C21:+57.021	941.1667081	2820.476724	0.001463592	1	N	511	536
Q8VDD5	Conv	ENTKK	VIQYLAHVASSHK	SKKDQ	3		484.9372981	1451.788494	0.000451244	4	N	186	199
Q8VDD5	Conv	RLTAK	KQELEEICHDLEAR	VEEEE	2	C8:+57.021	885.4282658	1768.840932	0.000451244	17	N	909	923
Q8VDD5	Conv	EHKRK	KVEAQLQELQVK	FSEGE	3		471.6089585	1411.803476	0.002019181	1	N	1248	1260
Q8VDD5	Conv	KVFFR	AGVLAHLEEER	DLKIT	2		612.3230982	1222.630596	0.000451244	5	N	764	775
Q8VDD5	Conv	LLEDR	VAEFTTNLMEEEEK	SKSLA	2	M9:+15.995	843.3829328	1684.750266	0.000451244	15	N	1000	1014
Q8VDD5	Conv	GEHLK	TDLLLEPYNK	YRFLS	2		603.3247752	1204.63395	0.000451244	6	N	289	299
Q8VDD5	Conv	INPYK	NLPIYSEEIVEMYK	GKKRH	2	M12:+15.995	872.429686	1742.843772	0.000451244	15	N	125	139
Q8VDD5	Conv	VEEMK	TQLEELEDELQATEDAK	LRLEV	2		981.4634539	1960.911308	0.000451244	10	N	1538	1555
Q8VDD5	Conv	LLEDR	VAEFTTNLMEEEEKSK	SLAKL	2	M9:+15.995	950.9464286	1899.877257	0.000451244	11	N	1000	1016
Q8VDD5	Conv	KVTKL	QVELDSVTGLLSQSDSK	SSKLT	2		903.4605172	1804.905434	0.000451244	2	N	1278	1295
Q8VDD5	Conv	EKLQL	QEQLQAETELCAEAEELR	ARLTA	2	C11:+57.021	1073.999981	2145.984361	0.001395409	1	N	885	903
Q8VDD5	Conv	DLIEK	PAGPPGILALLDEECWFPK	ATDKS	2	C15:+57.021	1055.537816	2109.060033	0.000451244	4	N	517	536
Q8VDD5	Conv	ERDLK	ITDVIIGFQACCR	GYLAR	2	C11:+57.021,C12:+57.021	776.8842198	1551.75284	0.001654178	2	N	778	791
Q8VDD5	Conv	DKYLY	VDKNFINNPLAQADWAAK	KLVWV	2		1008.021411	2014.027221	0.000451244	2	N	11	29
Q8VDD5	Conv	EWLMK	NMDPLNDNIATLLHQSSDKFVSELWK	DVDRI	3	M2:+15.995	1011.16639	3030.47577	0.000662267	2	N	587	613
Q8VDD5	Conv	KAQTK	EQADFAIEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	5	N	407	419
Q8VDD5	Conv	EKQKR	DLGEELEALKTELEDTLD	STAAQ	2		1016.994587	2031.973574	0.000823681	4	N	1135	1153
Q8VDD5	Conv	DFSAL	ESQLQDTQELLQEENR	QKLSL	2		980.4668622	1958.918124	0.000823681	1	N	1306	1322
Q8VDK1	Conv	QEAAR	LGACLAFLPEAFDFIAR	NPAET	2	C4:+57.021	955.9955873	1909.975575	0.000451244	4	N	72	89
Q8VDK1	Conv	ELSLK	LAQAGAEILTYPSAFGSVTGPAHWEVLLR	ARAIE	3		1018.873618	3053.597454	0.000451244	5	N	210	239
Q8VDK1	Conv	DFIAR	NPAETLLLSEPLNGDLLGQYSQLAR	ECGIW	3		904.8121356	2711.413007	0.000622848	2	N	89	114
Q8VDK1	Conv	LLRAR	AIESQCYVIAAAQCGR	HHETR	2	C6:+57.021,C14:+57.021	898.9246047	1795.833609	0.000622848	2	N	241	257
Q8VDL4	Conv	AAAER	FFSDKETFHDIAQAASEFPGAQHYVGGNAALIGQR	FAANT	4		945.711005	3778.81282	0.000451244	5	N	131	166
Q8VDL4	Conv	KDPVR	TVGLGDAISAEGLFYSEARPD	-	2		1084.529463	2167.043325	0.000451244	8	N	475	496
Q8VDL4	Conv	AAGAR	VAGTQACATETIDTNR	VSLRA	2	C7:+57.021	854.402248	1706.788896	0.000451244	1	N	408	424
Q8VDM4	Conv	SEPFR	SFANTLVDVCAYAGSGNVLK	VQQLL	2	C10:+57.021	1043.517612	2085.019624	0.000451244	12	N	588	608
Q8VDM4	Conv	AHGER	AELATEEFLPVTPILEGFVILR	KNPNY	2		1229.186131	2456.356661	0.000451244	8	N	879	901
Q8VDM4	Conv	PTLRR	AVPLALALISVSNPR	LNILD	2		760.9621047	1519.908609	0.000451244	15	N	688	703
Q8VDM4	Conv	CLKYR	LVGSQEELASWGHEYVR	HLAGE	2		980.4821183	1958.948637	0.00091018	1	N	143	160
Q8VDM4	Conv	AHGER	AELATEEFLPVTPILEGFVILRK	NPNYD	3		862.4916747	2584.451624	0.001463592	1	N	879	902
Q8VDM4	Conv	NAYAK	VCLYLTSCVNYVPEPENSALLR	CALGV	2	C2:+57.021,C8:+57.021	1299.140608	2596.265617	0.000451244	12	N	228	250
Q8VDM4	Conv	NHLGK	GEAIEAILAALEVVSEPFR	SFANT	2		1007.546927	2013.078254	0.000451244	11	N	569	588
Q8VDM4	Conv	AGKPK	TITGFQTHTTPVLLAHGER	AELAT	2		1040.053242	2078.090884	0.000662267	1	N	860	879
Q8VDM4	Conv	VDSAR	MNLASSFVNGFVNAAFGQDK	LLTDD	2		1059.010186	2116.004772	0.002296037	1	N	369	389
Q8VDM6	Conv	NFGQR	AEPYCSVLPGFTFIQHLPLSER	IRGTI	3	C5:+57.021	854.4337882	2560.277965	0.000451244	2	N	387	409

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDM6	Conv	ARKKR	NYILDQTNVYGSAQR	RKMRP	2		871.4293544	1740.843109	0.000451244	4	N	501	516
Q8VDM6	Conv	PHVVR	IGWSLDSCSTQLGEEPFSYGYGGTGK	KSTNS	2	C8:+57.021	1398.626805	2795.23801	0.0007646	1	N	284	310
Q8VDN2	Conv	KAIAK	GVGIISEGNETVEDIAAR	LNIPV	2		915.4661339	1828.916668	0.001943752	1	N	629	647
Q8VDN2	Conv	LLHGK	EQPLDEELKDAFQNAYLELGGLGER	VLGFC	3		945.4668051	2833.377015	0.000622848	2	N	526	551
Q8VDP3	Conv	KHGAR	LLLGLVGDCLVEPFWPLGTGVAR	GFLAA	2	C9:+57.021	1241.680261	2481.344922	0.000451244	10	N	385	408
Q8VDP3	Conv	FVNGR	TVEETQVPEISGVAR	IYNQK	2		807.9208308	1613.826062	0.002080925	2	N	248	263
Q8VDP4	Conv	HHPSR	IQVSSEKEAAPDTGAEPSPEDSDPTYSSK	VLLLS	3		1008.126954	3021.357462	0.000979378	2	N	280	309
Q8VDP4	Conv	FLLGR	KEEEAVLVGGEWSPSLDGLDPQADPQVLVR	TAIRC	3		1078.549528	3232.625185	0.000451244	7	N	352	382
Q8VDP4	Conv	TYSSK	VLLLSSPGLEEFYR	CCMLF	2		811.9435776	1621.871555	0.002374549	1	N	309	323
Q8VDP4	Conv	LCQQK	ATEAAPQPHEASGEAEATEQAPDVSEQADTSK	QNTET	3		1084.819072	3251.433815	0.000622848	3	N	446	478
Q8VDQ8	Conv	DLVRR	EHANIDAQSGSQAPNPSTTISPGK	SPPPA	3		803.0548473	2406.141142	0.000998612	1	N	347	371
Q8VE11	Conv	DGWDR	TSQVCSLGSLLLDSYYR	TMKGF	2	C5:+57.021	981.4857807	1960.955961	0.002727428	1	N	342	359
Q8VE11	Conv	SKSQR	LTVLEPNTASFNFK	FWRNM	2		790.9201025	1579.824605	0.000622848	1	N	479	493
Q8VE37	Conv	KVSHR	SHNTEPGLVLTLGQGDVGQLGLGESVLER	KKPAL	3		992.5197919	2974.535976	0.000622848	2	N	28	57
Q8VEE0	Conv	VHWLR	TQFPTLDIEVDGGVGPDTVQK	CAEAG	2		1108.55822	2215.10084	0.000823681	5	N	164	185
Q8VEE0	Conv	ASGCK	IGPSILNSDLANLGAECLR	MLDSG	2	C17:+57.021	1007.025604	2012.035609	0.000451244	10	N	6	25
Q8VEH3	Conv	SISCK	EKDNIDITLQWLIQHSK	SRRS-	3		694.3729003	2080.095301	0.000451244	2	N	165	182
Q8VEK3	Conv	ARKKR	NFILDQTNVSAAAQR	RKMCL	2		824.4266147	1646.837629	0.000451244	6	N	551	566
Q8VEK3	Conv	FKISK	EVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	3	C14:+57.021,C17:+57.021	1033.176229	3096.505287	0.000451244	7	N	412	438
Q8VEK3	Conv	NFGQK	EKPYFPIPEDCTFIQNVPLEDR	VRGPK	3	C11:+57.021	903.1076294	2706.299488	0.000451244	17	N	438	460
Q8VEK3	Conv	LKGIK	TCNCETEDYGEKFDENDVITCFANFETDEVELSYAK	NGQDL	3	C2:+57.021,C4:+57.021,C21:+57.021	1448.268147	4341.781041	0.000451244	2	N	363	399
Q8VEK3	Conv	YSRAK	SPQPPVEEEDEHFDDTVVCLDTYNCDLHFK	ISRDR	4	C19:+57.021,C25:+57.021	909.6451791	3634.549516	0.000451244	1	N	246	276
Q8VHM5	Conv	VLFVR	NLATTVTEEILEK	SFSEF	2		730.8962931	1459.776986	0.000451244	1	N	346	359
Q8VHX6	Conv	GQVGK	SADFVVEAIGTEVGTLGFSIEGPSQAKIECDDK	GDGSC	3	C30:+57.021	1157.22786	3468.660181	0.002813207	1	N	589	622
Q8VHX6	Conv	GQVGK	SADFVVEAIGTEVGTL	GFSIE	2		804.4123073	1606.809015	0.001463592	3	N	589	605
Q8VI36	Conv	TAMGK	TWHPEHFVCTHCQEEIGSR	NFFER	3	C9:+57.021,C12:+57.021	804.020118	2409.036954	0.000662267	1	N	375	394
Q8VI36	Conv	GGCAR	AILENYISALNTLWHPECFVCR	ECFTP	3	C18:+57.021,C21:+57.021	902.7772949	2705.308485	0.000451244	12	N	481	503
Q8VIJ6	Conv	ALSVR	NLSPYVSNELLEEAFSQFGPIER	AVVIV	3		880.4382982	2638.291495	0.000451244	8	N	368	391
Q8VIJ6	Conv	TTTPR	PVIVEPLEQLDDEDGLPEK	LAQKN	2		1068.041871	2134.068143	0.001591523	1	N	435	454
Q91UZ5	Conv	RVSTK	TSAADLVTETDHRVEDLIVSELR	KRFPS	3		857.1088407	2568.303122	0.000451244	1	N	49	72
Q91V12	Conv	KNVDK	VLEVPPIVYLR	QEQEE	2		649.3980776	1296.780555	0.00307782	1	N	173	184
Q91V12	Conv	KLTNK	ATLWYVPLSLK	NVDKV	2		645.876978	1289.738356	0.000698008	4	N	158	169
Q91V41	Conv	EAAKK	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	3		1050.857467	3149.549	0.000451244	1	N	171	201
Q91V41	Conv	LEAAK	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	4		820.4187908	3277.643963	0.001871652	1	N	170	201
Q91V41	Conv	LTDAR	NLTNPNTVIILIGNK	ADLEA	2		812.4755763	1622.935553	0.000451244	7	N	110	125
Q91V41	Conv	YEEAK	QFAEENGLLFLEASAK	TGENV	2		883.952131	1765.888662	0.000622848	2	N	140	156
Q91V41	Conv	EASAK	TGENVEDAFLEAAKK	IYQNI	3		541.2743042	1620.799513	0.000451244	2	N	156	171
Q91V92	Conv	VDMLR	NCGSFTREEADEYVDIGALNGIFVLGR	SMGFI	3	C2:+57.021	1001.482307	3001.42352	0.000451244	1	N	1028	1055
Q91V92	Conv	VFVPR	SFDELGEIIQSVYEDLVAK	GAIVP	2		1078.044414	2154.073228	0.000451244	16	N	778	797
Q91V92	Conv	KRRGK	LGLVGVNLSLDGVK	SWLKP	2		692.414456	1382.813312	0.000451244	11	N	68	82
Q91V92	Conv	YAQIR	TIAIIAEGIPEALTR	KLIKK	2		784.4568522	1566.898104	0.000451244	16	N	582	597
Q91V92	Conv	KGFLK	NFLIEPFVPHSQAEEFYVCIYATR	EGDYV	3	C19:+57.021	977.4779452	2929.410436	0.000823681	2	N	103	127
Q91V92	Conv	GSFTR	EEADEYVDIGALNGIFVLGR	SMGFI	2		1090.547655	2179.079711	0.000451244	15	N	1035	1055
Q91V92	Conv	ARAGK	DLVSSLTSGLLTIGDR	FGGAL	2		823.952131	1645.888662	0.000451244	18	N	908	924
Q91V92	Conv	KDFVK	QHFPATPLLDYALEVEK	ITTSK	3		657.6794418	1970.014925	0.000451244	17	N	985	1002
Q91V92	Conv	PEDKK	EVLASFISGLFNFYEDLYFTYLEINPLVVTK	DGVYI	3		1215.63253	3643.874189	0.000451244	2	N	178	209
Q91V92	Conv	ADAMK	KHPEVDVLINFASLR	SAYDS	3		579.9935836	1736.957351	0.000451244	1	N	551	566
Q91V92	Conv	NIISR	TTDGVYEGVAIGGDRYPGSTF	MDHVL	2		1081.505987	2160.996375	0.002212458	1	N	666	687
Q91V92	Conv	FKYAR	VTPDTDWAHLLQDHPWLLSQSLVVKPDQLIK	RRGKL	3		1198.310784	3591.908952	0.001329271	1	N	33	64
Q91V92	Conv	KADQK	GVTIIGPATVGGIKPGCFK	IGNTG	2	C17:+57.021	936.5245119	1871.033424	0.000622848	2	N	606	625
Q91V92	Conv	PPFGR	EAYPEEAYIADLDAK	SGASL	2		849.3993969	1696.783194	0.000735798	3	N	244	259
Q91V92	Conv	IICAR	AGKDLVSSLTSGLLTIGDR	FGGAL	2		952.0289014	1902.042203	0.000451244	1	N	905	924
Q91V92	Conv	LVVTK	DGVYILDLAAK	VDATA	2		589.3273179	1176.639036	0.001162105	1	N	209	220
Q91VC3	Conv	DVWAR	GLDVPQVSLIINYDLPNNR	ELYIH	2		1070.574007	2139.132415	0.000451244	11	N	339	358
Q91VI7	Conv	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	C1:+57.021	1087.068001	2172.120401	0.000451244	2	N	39	59
Q91VI7	Conv	SLWIK	TCSLTAASCPYFCSVLTK	SRSLL	2	C2:+57.021,C9:+57.021,C13:+57.021	1033.473039	2064.930478	0.000451244	16	N	316	334
Q91VI7	Conv	ELSLR	TNELGDGGVGLVLQGLQNPTCK	IQKLS	2	C21:+57.021	1135.57619	2269.13678	0.000451244	15	N	59	81
Q91VI7	Conv	LSSNK	LGNAGIAALCPGLLLPSCK	LRTLW	2	C10:+57.021,C18:+57.021	963.0210478	1924.026496	0.000451244	9	N	233	252
Q91VI7	Conv	CRLEK	LQLEYCNLTATSCEPLASVLR	VKADF	2	C6:+57.021,C13:+57.021	1219.606401	2437.197203	0.000451244	19	N	141	162
Q91VI7	Conv	DTVLR	ELWLGDCDVTNSGCSSLANVLLANR	SLREL	2	C7:+57.021,C14:+57.021	1382.655143	2763.294685	0.000451244	11	N	368	393
Q91VI7	Conv	LSDAR	WTELLPLIQQYEVVR	LDDCG	2		944.0228907	1886.030181	0.000823681	4	N	14	29
Q91VI7	Conv	DEGAR	LLCESLLEPGCQLESLWIK	TCSLT	2	C3:+57.021,C11:+57.021	1144.586949	2287.158298	0.000451244	9	N	297	316
Q91VI7	Conv	CKIQK	LSLQNCGLTEAGCGILPGMLR	SLSTL	2	C6:+57.021,C13:+57.021	1130.566026	2259.116451	0.001463592	1	N	84	105

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91VI7	Conv	EVRCK	DISSAVQANPALTELSLR	TNELG	2		943.0054263	1883.995253	0.000451244	5	N	41	59
Q91VI7	Conv	KADFK	ELVLSNNDLHEPGVR	ILCQG	2		846.4397221	1690.863844	0.000451244	3	N	168	183
Q91VI7	Conv	VVASK	ASLQELDLSSNK	LGNAG	2		652.8387781	1303.661956	0.001591523	1	N	221	233
Q91VI7	Conv	SCKLR	TLWLWECDITAEGCKDLCR	VLRAK	3	C7:+57.021,C14:+57.021,C18:+57.021	809.3694937	2425.085081	0.000637154	2	N	254	273
Q91VR5	Conv	LSQVR	FLVLDEADGLLSQGYSDFINR	MHNQI	2		1186.592594	2371.169588	0.000451244	1	N	365	386
Q91W89	Conv	NLRGR	LFGDSCSVTLSSFLTPER	LPYEK	2	C6:+57.021	1008.491063	2014.966526	0.001395409	1	N	34	52
Q91W89	Conv	KKGNR	ECEQILHDVEVLSSLALAR	SAQFL	3	C2:+57.021	728.0443007	2181.109502	0.000451244	3	N	533	552
Q91W89	Conv	LPYEK	AVQQNFSPAQVGDSFGPTWWTCWFR	VELVI	3	C22:+57.021	991.4576556	2971.349567	0.000823681	1	N	57	82
Q91WQ3	Conv	AEVVK	QVEHPLLSGLLYPGLQALDEEYLK	VDAQF	3		909.1536102	2724.437431	0.000451244	6	N	154	178
Q91WV0	Conv	KSEKK	TISPEHVIQALESLGFGSYISEVK	EVLQE	3		868.7905604	2603.348281	0.000979378	1	N	64	88
Q91WV0	Conv	ANDAR	ELVVNCCTEFIHLISSEANEICNK	SEKKT	3	C6:+57.021,C7:+57.021,C22:+57.021	960.4506531	2878.328559	0.000451244	6	N	36	60
Q91X72	Conv	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDKLNAAK	SLPQP	3	C7:+57.021,C24:+57.021	1279.273544	3834.797232	0.000451244	6	N	409	444
Q91X72	Conv	KRLEK	ELGSPPGISLETIDAAFSCPGSSR	LYVSS	2	C19:+57.021	1224.589494	2447.163388	0.000451244	18	N	345	369
Q91X72	Conv	PMHSR	CSPDPGLTALLSDHR	GATYA	3	C1:+57.021	546.9353628	1637.782688	0.000622848	2	N	254	269
Q91X72	Conv	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDK	LNAAK	3	C7:+57.021,C24:+57.021	1113.50815	3337.50105	0.000451244	21	N	409	439
Q91X72	Conv	NGYPK	LFQEEFPGIPYPPDAAVECHR	GECQS	2	C19:+57.021	1236.586558	2471.157515	0.001162105	3	N	129	150
Q91X72	Conv	LISAR	WKNPITSVDAAFR	GPDSV	3		502.2689363	1503.783409	0.000451244	1	N	89	102
Q91X72	Conv	RWLER	YYCFQGNKFLR	FNPVT	2	C3:+57.021	748.3614691	1494.707338	0.001162105	6	N	196	207
Q91X72	Conv	WLDLK	SGAQATWTEVSWPHEKVDGALCLDK	SLGPN	3	C22:+57.021	929.1135545	2784.317264	0.000622848	6	N	384	409
Q91XL1	Conv	LSSNR	LQALSPELLAPVPR	LRALD	2		752.4488302	1502.88206	0.000451244	11	N	96	110
Q91XL1	Conv	NRLQR	LEDSLLAPQPFLR	VLFLN	2		749.9173628	1497.819126	0.000451244	10	N	219	232
Q91XL1	Conv	ALHTL	DLGYNLLESLPEGLLR	GPRRL	2		901.4888807	1800.962161	0.000451244	6	N	186	202
Q91XL1	Conv	QPFLR	VLFLNDNQLVGVATGSFQGL	QHLDM	2		1046.557826	2091.100052	0.001943752	3	N	232	252
Q91YI4	Conv	TAQYK	CPVAQLEQDDQVSPSSTFCK	VYTIT	2	C1:+57.021,C19:+57.021	1148.514709	2295.013819	0.000451244	7	N	252	272
Q91YI4	Conv	RLIIR	KVQFAPETPGPQPSAETTR	HFLMS	3		681.0170051	2040.027615	0.000823681	2	N	170	189
Q91YI4	Conv	YLGKR	DFVDHLDKVDPVDGVVLVDPDYLK	DRKVF	3		904.7976036	2711.369411	0.000451244	1	N	26	50
Q91YP3	Conv	AWLLK	AVTFIDLTTLSGDDTFSNVQR	LCYKA	2		1150.574401	2299.133203	0.000451244	5	N	49	70
Q91YP3	Conv	PDLFR	IGASSLLSDIER	QIYHH	2		630.8438635	1259.672127	0.00091018	5	N	287	299
Q91YP3	Conv	LEEIR	LAVEDGATEIDVVINR	TLVLT	2		857.4550378	1712.894476	0.000451244	1	N	144	160
Q91YP3	Conv	IRTAK	ESLAWLSLVKEELGDEWLTPDLFR	IGASS	3		949.492403	2845.453809	0.000698008	2	N	263	287
Q91YP3	Conv	AAHCR	GTELDLSWISK	VQVNH	2		624.8276821	1247.639764	0.000451244	1	N	6	17
Q91YR9	Conv	SQYNR	TGPCPQGPAPEVVIYQQLR	MEGFI	2	C4:+57.021	1055.541422	2109.067243	0.000451244	27	N	247	266
Q91YR9	Conv	KTFGR	IAICGAISQYNR	TGPCP	2	C4:+57.021	683.3511014	1364.686603	0.000451244	6	N	235	247
Q91YR9	Conv	SAFPK	GTIVAALLGWTSHSISDGNGLTK	LPVEW	2		1149.608579	2297.201557	0.000451244	11	N	81	104
Q91YR9	Conv	WTLKK	HFEGFPTDGNFELK	TTELP	2		819.3838842	1636.752168	0.000451244	2	N	11	25
Q91YR9	Conv	AYLKK	LGFDVAFNYK	TVKSL	2		587.3011031	1172.586606	0.000451244	7	N	184	194
Q91YR9	Conv	NFELK	TTELPPLNNGEVLLEALFLSVDPYMR	VAAKK	3		977.8444483	2930.509945	0.002080925	1	N	25	51
Q91YR9	Conv	NFELK	TTELPPLNNGEVLLEAL	FLSVD	2		911.9939959	1821.972392	0.002374549	1	N	25	42
Q91Z50	Conv	NWLHK	EAQQLFLEPEVLDPESVELKWSEPNEEELVK	FMCGE	3		1218.609001	3652.803603	0.000622848	2	N	277	308
Q91Z50	Conv	NWLHK	EAQQLFLEPEVLDPESVELK	WSEPN	2		1157.097178	2312.178756	0.000451244	19	N	277	297
Q91ZJ5	Conv	LIGVR	NENTFLDLTVQQIEHLNK	TYNTD	2		1078.553272	2155.090944	0.000451244	14	N	133	151
Q91ZJ5	Conv	IVNPK	TLDGGLNVIQLETAVGAAIK	SFENS	2		992.0602015	1982.104803	0.000451244	15	N	357	377
Q91ZJ5	Conv	VSKFK	IFNTNNLWISLGAVK	RLQEQ	2		845.4702939	1688.924988	0.000451244	4	N	325	340
Q91ZJ5	Conv	VDWGK	IQRPPEDSIQPYEK	IKARG	2		850.4366481	1698.857696	0.002080925	1	N	77	91
Q91ZJ5	Conv	GAAIK	SFENSLGINVPR	SRFLP	2		666.8494801	1331.68336	0.001463592	1	N	377	389
Q91ZJ5	Conv	GASQF	QEVILQELELSVK	KELEK	2	Q1:-17.027	755.9220854	1509.828571	0.002019181	1	N	20	33
Q91ZX7	Conv	GESCR	SLDPFKPFIIFSNR	HEIRR	3		560.9756414	1679.903524	0.002663018	1	N	1263	1277
Q91ZX7	Conv	PHSCK	AVTDEEPFLIFANR	YYLRK	2		811.4151843	1620.814769	0.002019181	3	N	3023	3037
Q920E5	Conv	SLTRR	GQICWYQKPGIGLDAINDALLLEASIYR	LLKFY	3	C4:+57.021	1059.885263	3176.63239	0.000451244	11	N	113	141
Q920E5	Conv	GKYNR	GLTVVQAFQELVEPK	KQDAE	2		829.4621346	1656.908669	0.000451244	17	N	60	75
Q920E5	Conv	VARVK	ALYEALDLQSAFFK	YEEDS	2		808.422478	1614.829356	0.000451244	13	N	302	316
Q920E5	Conv	IQDNK	CSWLVVQCLLR	ASPQQ	2	C1:+39.994,C8:+57.021	708.8597909	1415.703982	0.0025889	1	N	266	277
Q920E5	Conv	YNQEK	QNFIQHFSQIVK	VLTEK	2	[0:-17.027	736.3885471	1470.761494	0.000622848	7	N	14	26
Q920E5	Conv	SQIVK	VLTEKELGHPEIGDAIAR	LKEVL	3		650.021979	1947.042537	0.000451244	6	N	26	44
Q920E5	Conv	VARVK	ALYEALDLQSAFFKYEEDSYNR	LKSLI	3		891.4225367	2671.24421	0.000451244	5	N	302	324
Q921F2	Conv	RAVQK	TSDLIVLGLPWK	TTEQD	2		671.3929922	1340.770384	0.000451244	3	N	102	114
Q921F2	Conv	MRGVR	LVEGILHAPDAGWGNLVYVVNYPK	DNKRK	3		875.467752	2623.379856	0.000451244	15	N	55	79
Q921F2	Conv	PKPFR	AFAFVTFADDKVAQSLCGEDLIIK	GISVH	3	C17:+57.021	886.7880082	2657.340625	0.000451244	20	N	227	251
Q921F2	Conv	SEYIR	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR	YRNPV	3	C33:+57.021	1292.27772	3873.809759	0.000451244	3	N	6	42
Q921F4	Conv	VVHVR	GLCESVVEADLVEALEK	FGTIC	2	C3:+57.021	930.9668895	1859.918179	0.001162105	3	N	130	147
Q921G6	Conv	LGSLR	QLDVSSNELQSLPVELCSLR	SLRDL	2	C17:+57.021	1144.083848	2286.152095	0.000451244	4	N	162	182
Q921G6	Conv	ADLSR	NRFPEVPEAACQLVSLEGLSLYHNCLK	CLNPA	4	C11:+57.021,C25:+57.021	786.8958743	3143.552297	0.001839721	1	N	77	104
Q921H8	Conv	RGGFK	NTTPDELLSAVLTAVLQDVR	LKPEQ	2		1078.084405	2154.15321	0.000451244	1	N	57	77

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q921H8	Conv	AVMAR	IAQFLSGIPETVPLSTVNR	QCSSG	2		1021.568194	2041.120787	0.000735798	7	N	102	121
Q921I1	Conv	VTAIR	NQQEGVCPEGSIDNSPVK	WCALS	2	C7:+57.021	979.4499266	1956.884253	0.000451244	42	N	343	361
Q921I1	Conv	TGAFR	CLVEKGDVAFVK	HQTVL	2	C1:+57.021	682.866053	1363.716506	0.000451244	93	N	542	554
Q921I1	Conv	SPLEK	AVSSFFSGSCVPCADPVAFPK	LCQLC	2	C10:+57.021,C13:+57.021	1115.519066	2229.022533	0.000451244	16	N	167	188
Q921I1	Conv	VAFPK	LCQLCPGCGCSSTQPFFGYVGAFK	CLKDG	2	C2:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	1371.102183	2740.188766	0.000451244	11	N	188	212
Q921I1	Conv	SPLGK	DLLFKDSAFGLLR	VPPRM	2		747.9199055	1493.824211	0.002663018	1	N	310	323
Q921I1	Conv	AARVK	AVLTSQETLFGGSDCTGNFCLFK	STTKD	2	C15:+57.021,C20:+57.021	1276.593491	2551.171382	0.000451244	24	N	618	641
Q921I1	Conv	TGLGR	SAGWVIPIGLLFCK	LSEPR	2	C13:+57.021	780.93427	1559.85294	0.000622848	10	N	143	157
Q921I1	Conv	VAFVK	HQTVLDNTEGKNPAEWAK	NLKQE	2		1019.503582	2036.991564	0.000451244	10	N	554	572
Q921I1	Conv	IGPLK	CAPNNKEEYNGYTGAFR	CLVEK	2	C1:+57.021	995.939529	1989.863458	0.000451244	7	N	525	542
Q921I1	Conv	LDNTR	KPVDQYEDCYLAR	IPSHA	2	C9:+57.021	828.8882451	1655.76089	0.000451244	11	N	251	264
Q921I1	Conv	VLPEK	ADRDQYELLCLDNTR	KPVDQ	2	C10:+57.021	941.4419045	1880.868209	0.000451244	144	N	236	251
Q921I1	Conv	AEWAK	NLKQEDFELLCPDGTR	KPVKD	2	C11:+57.021	967.9677551	1933.91991	0.000451244	22	N	572	588
Q921I1	Conv	INHCK	FDEFFSQGCAPGYEK	NSTLC	2	C9:+57.021	891.3777102	1780.73982	0.000451244	13	N	497	512
Q921I1	Conv	EKADR	DQYELLCLDNTR	KPVDQ	2	C7:+57.021	770.3593204	1538.703041	0.000451244	102	N	239	251
Q921I1	Conv	ISEGK	IECESAETTEDCIEK	IVNGE	2	C3:+57.021,C12:+57.021	907.3770156	1812.738431	0.000451244	11	N	383	398
Q921I1	Conv	GIFPK	GYYAVAVVK	ASDTS	2		485.274357	968.5331139	0.002080925	2	N	446	455
Q921I1	Conv	KGKSK	DFQLFSSPLGK	DLLFK	2		619.8249424	1237.634285	0.001229886	1	N	299	310
Q921I1	Conv	PDGTR	KPVKDFASCHLAQAPNHVVVSR	KEKAA	3	C9:+57.021	820.7695052	2459.285116	0.000451244	11	N	588	610
Q921I1	Conv	FGKGK	SKDFQLFSSPLGK	DLLFK	2		727.3884382	1452.761276	0.000451244	7	N	297	310
Q921I1	Conv	RMDYR	LYLGHNYVTAIR	NQQEG	2		710.3913152	1418.76703	0.000451244	1	N	331	343
Q921I1	Conv	VVARK	NNGKEDLIWEILK	VAQEH	3		524.6196347	1570.835504	0.000451244	4	N	274	287
Q921I1	Conv	RKPVK	DFASCHLAQAPNHVVVSR	KEKAA	2	C5:+57.021	1004.494806	2006.974012	0.000451244	5	N	592	610
Q921I1	Conv	LERTK	CDEWSIISEGKIECESAETTEDCIEK	IVNGE	3	C1:+57.021,C14:+57.021,C23:+57.021	1040.110691	3117.308672	0.000451244	4	N	372	398
Q921I1	Conv	EKADR	DQYELLCLDNTRKPVDQYE	DCYLA	2	C7:+57.021	1200.063112	2398.110625	0.001352548	2	N	239	258
Q921I1	Conv	RDDTK	CFVKLPEGTTPEK	YLGAE	3	C1:+57.021	502.5941664	1504.759099	0.000451244	2	N	654	667
Q921M3	Conv	VAVCR	FSNTGEDWYVLVGVAK	DLILS	2		892.9468486	1783.878097	0.000451244	12	N	895	911
Q921M3	Conv	LALEK	LGAVFNQVAFPLQYTPR	KFVIH	2		961.0206823	1920.025765	0.000451244	17	N	769	786
Q921M3	Conv	DTYPR	WVTTASLLDYDTVAGADKFGNICVVR	LPPNT	3	C23:+57.021	957.816738	2870.426814	0.000451244	10	N	1031	1057
Q921M3	Conv	SYQSR	FHLTPLSYETLEFASGFASEQCPEGIVAISTNTLR	ILALE	3	C22:+57.021	1295.972014	3884.892641	0.000451244	22	N	728	763
Q921M3	Conv	PRPLK	NLVLVDELDSLSPILFCQIADLANEDTPQLYVACGR	GPRSS	3	C17:+57.021,C34:+57.021	1354.678347	4061.011642	0.000451244	11	N	393	429
Q921M3	Conv	GVLLR	TVLDPVTGDLSDTR	TRYLG	2		744.8811743	1487.746749	0.000451244	1	N	676	690
Q921M3	Conv	TIGHR	VIVSDVQESFIWVR	YKRNE	2		838.9544767	1675.893353	0.000451244	7	N	999	1013
Q921M3	Conv	ICVVR	LPPNTNDEVDEDPTGNK	ALWDR	2		927.9217562	1853.827912	0.000451244	4	N	1057	1074
Q921M3	Conv	EFLHK	TPVEEVPAAIAPFQGR	VLIGV	2		841.4495585	1680.883517	0.000451244	13	N	942	958
Q921M3	Conv	DTYPR	WVTTASLLDYDTVAGADK	FGNIC	2		963.47871	1924.94182	0.000451244	2	N	1031	1049
Q921M3	Conv	EQRSR	FLAVGLVDNTVR	IISLD	2		652.3725911	1302.729582	0.000622848	1	N	603	615
Q921M3	Conv	QYTPR	KFVIHPESNNLIIIETDHNAYTEATK	AQRKQ	4		750.1388871	2996.524348	0.000451244	4	N	786	812
Q921M3	Conv	KCENK	HIANYISGIQTIGHR	VIVSD	3		560.6379112	1678.890334	0.000451244	3	N	984	999
Q921M3	Conv	PRPLK	NLVLVDELDSLSPILFC	QIADL	2	C17:+57.021	974.0111001	1946.0066	0.000622848	3	N	393	410
Q921M7	Conv	LSRMR	INNVPAEGENEVNNELANR	MSLFY	2		1048.50431	2094.993021	0.000451244	13	N	167	186
Q921M7	Conv	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEKEIYNQVNVVLK	DAEGI	3	C4:+57.021	1477.056695	4428.146684	0.000451244	21	N	6	44
Q921M7	Conv	KLQEK	AWGAVVPLVGK	LKKFY	2		548.8298307	1095.644061	0.000622848	3	N	78	89
Q921M7	Conv	EAALR	GLLGALTSTPYSPTQHLER	EQALA	3		681.0291336	2040.064001	0.000451244	2	N	105	124
Q921M7	Conv	NVVLK	DAEGILEDLQSYR	GAGHE	2		754.8655242	1507.715448	0.000451244	6	N	44	57
Q921M7	Conv	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEK	EIYNQ	3	C4:+57.021	1043.817132	3128.427996	0.001871652	1	N	6	33
Q921M7	Conv	KGCIK	VLKDQPPNSVEGLLNALR	YTTKH	3		655.0377405	1962.089822	0.000451244	9	N	286	304
Q921M7	Conv	QALAK	QFAEILHFTLR	FDELK	2		687.8805833	1373.745567	0.002884417	1	N	130	141
Q921W4	Conv	LEVGR	KVTFFQPDDEVVGILPLDSEDPGLCEVIR	VHEHY	3	C25:+57.021	1096.55536	3286.642681	0.001352548	2	N	75	104
Q921Z5	Conv	KMVSK	SIATTLIDDTSSEVLDELYR	VTKEY	2		1121.060793	2240.105985	0.000451244	4	N	36	56
Q922B2	Conv	IQTPK	IISAASEGGANVFTVSYFK	NNAYL	2		981.0048949	1959.99419	0.000823681	3	N	222	241
Q922B2	Conv	KVNQK	IGSCTQQDVELHVQK	IYVIS	3	C4:+57.021	581.2898056	1740.846017	0.000622848	2	N	126	141
Q922D4	Conv	ATLEK	QEIIEQLLSNIFHK	EKNES	3		571.3179557	1710.930467	0.000451244	8	N	244	258
Q922D4	Conv	SLLMK	LYSFLLNESPLNPLLASFFSK	VLSIL	2		1200.646641	2399.277682	0.000451244	1	N	105	126
Q922R8	Conv	FPTIK	IFQKGESPVDYDGGR	TRSDI	2		834.4053479	1666.795096	0.002019181	1	N	241	256
Q922R8	Conv	LSFGR	GSTAPVGGGSFPTITPR	EPWDG	2		801.4182583	1600.820917	0.000451244	4	N	392	409
Q922R8	Conv	LAVSG	LYSSSDDVIELTPSNFNR	EVIQS	2		1028.995256	2055.974911	0.000451244	12	N	19	37
Q922R8	Conv	GAAGR	NSYLEVLLK	LADKY	2		539.8113036	1077.607007	0.000451244	15	N	313	322
Q922R8	Conv	YQGGR	TGEAIVDAALSALR	QLVKD	2		693.88352	1385.75144	0.000451244	27	N	118	132
Q922R8	Conv	DIVSR	ALDLFSDNAPPPELLEIINEDIAKK	TCEEH	3		922.4922916	2764.453475	0.000451244	12	N	264	289
Q922R8	Conv	DIVSR	ALDLFSDNAPPPELLEIINEDIAK	KTCEE	3		879.7939706	2636.358512	0.000451244	11	N	264	288
Q922R8	Conv	KGKVK	LAAVDATVNQVLASR	YGIKG	2		764.428626	1526.841652	0.000451244	12	N	216	231
Q922R8	Conv	FALLK	GSFSEQGINEFLR	ELSFG	2		742.3629517	1482.710303	0.000451244	7	N	373	386

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q922S4	Conv	LQVAK	NLFTHLDDVSVLLQEIITEAR	NLSNA	3		809.436229	2425.285287	0.001264573	1	N	377	398
Q922S4	Conv	ITEAR	NLSNAEICSVFLLDQNELVAK	VFDGG	2	C8:+57.021	1189.107323	2376.199046	0.000451244	2	N	398	419
Q922S4	Conv	SLQLK	VLQYLQQETQATHCCLLLVSEDNLQLSCK	VIGDK	3	C14:+57.021,C15:+57.021,C28:+57.021	1164.57049	3490.68807	0.000451244	5	N	223	252
Q922S4	Conv	DEYTK	LLHDGIQPVAAIDSNFANFTYTPR	SLPED	3		887.4542826	2659.339448	0.000451244	10	N	560	584
Q922S4	Conv	SYEIR	IPADQGIAGHVATTGQILNIPDAYAHPLFYR	GVDDS	4		830.6865358	3318.714943	0.001871652	1	N	434	465
Q923L7	Conv	RYQTK	GSVEYYTVACEPR	VAWDC	2	C10:+57.021	765.8485886	1529.681577	0.000451244	42	N	123	136
Q923L7	Conv	ACEPR	VAWDCPIYPVVPVHLDGTF	-	2	C5:+57.021	1093.043266	2184.070932	0.000622848	9	N	136	155
Q93092	Conv	EEQIK	NAIDKLFVLFGAEILK	KIPGR	2		896.024902	1790.034204	0.000451244	5	N	81	97
Q93092	Conv	NAIDK	LFVLFGAEILK	KIPGR	2		625.3818962	1248.748192	0.000451244	7	N	86	97
Q93092	Conv	TGEIK	ALAGCDFLTISPK	LLGEL	2	C5:+57.021	696.8635103	1391.711421	0.000451244	14	N	245	258
Q93092	Conv	TISPK	LLGELLKDNSK	LAPAL	2		615.3591494	1228.702699	0.000451244	7	N	258	269
Q99J09	Conv	QGVTR	LVFSPHSVPLLTSLSEDCSLAVLDSSLSEVFR	SRAHR	3	C18:+57.021	1168.936241	3503.785322	0.002374549	1	N	260	292
Q99J09	Conv	LNSYR	AHAGQVTCVAASPHKDSVFLSCSEDSR	ILLWD	4	C8:+57.021,C22:+57.021	729.8398277	2915.328111	0.001699387	1	N	164	191
Q99J45	Conv	RPTAR	ELLFHPALFEVPSLK	LLAAH	3		580.6630634	1738.96579	0.002813207	4	N	319	334
Q99J77	Conv	MDTMK	QVYQIVKPLNPNFCFLQCTSAYPLQPEDANLR	VISEY	3	C14:+57.021,C18:+57.021	1275.302886	3822.885259	0.000451244	17	N	166	198
Q99J77	Conv	SEYQK	LFPDIPIGYSGHETGIAISVAAVALGAK	VLERH	3		923.1730048	2766.495614	0.000662267	4	N	205	233
Q99J99	Conv	LFKEK	KVDLSKPLVATCGSGVTACHVVLGAFLCGK	SDVPV	4	C12:+57.021,C19:+57.021,C28:+57.021	786.9147941	3143.627976	0.001871652	2	N	236	266
Q99J99	Conv	PQLFR	ALVSAQWVAEALK	APRSS	2		693.3935235	1384.771447	0.000451244	10	N	8	21
Q99J99	Conv	SQPLK	LLDASWYLPK	LGRDA	2		603.3324032	1204.649206	0.000451244	4	N	30	40
Q99JI4	Conv	-M	PLENLEEEGLPKNPDLR	IAQLR	3		655.0097391	1962.005817	0.000698008	1	N	1	18
Q99JI4	Conv	RLHCK	IDKVNEIVETNRPDSK	NWQYQ	3		619.6624508	1855.963952	0.000451244	2	N	346	362
Q99JI4	Conv	EKVIK	GAEILEVLHSLPAVR	QYLFS	3		535.3109126	1602.909338	0.000622848	4	N	242	257
Q99JW2	Conv	RQYLR	ICTVQPNPDYGGAITFLEER	ARQLG	2	C2:+57.021	1140.552183	2279.088767	0.000451244	5	N	21	41
Q99JW2	Conv	FQALR	AGFALDEGLANPTDAFTVFYSER	SPWWV	2		1246.092958	2490.170317	0.000451244	7	N	168	191
Q99JW4	Conv	PECFR	CDLCQEVLADIGFVK	NAGRH	2	C1:+57.021,C4:+57.021	883.9262817	1765.836963	0.000451244	15	N	96	111
Q99JX4	Conv	RTFGK	QQWQQLYDTLNAWK	QNLNK	2		911.4500898	1820.88458	0.001352548	1	N	344	358
Q99JX4	Conv	LKPVK	FLEGELIHDLLTIFVSAK	LASYV	3		682.3826253	2044.124476	0.000622848	1	N	230	248
Q99JX4	Conv	RCIVR	ALKDPNAFLFDHLLTLKPVK	FLEGE	4		570.8338429	2279.304172	0.000451244	6	N	210	230
Q99JX7	Conv	LKHTR	LNVVAFLNELPK	TQHDV	2		678.8984417	1355.781283	0.002019181	2	N	458	470
Q99JY9	Conv	QQLLR	DREVGIPPEQSLETAK	AVKER	2		884.9579447	1767.900289	0.000451244	61	N	209	225
Q99JY9	Conv	AISKK	EFSIDVGYER	FLGPE	2		607.7885569	1213.561514	0.000451244	30	N	265	275
Q99JY9	Conv	QVIFK	YLRAEPEDHYFLLTEPPLNTPENR	EYTAE	3		972.1510399	2913.42972	0.000451244	9	N	99	123
Q99JY9	Conv	RRVMK	GVDDLDFFIGDEAIEKPTYATK	WPIRH	2		1222.597542	2443.179484	0.000451244	25	N	53	75
Q99JY9	Conv	TGYTK	LGYAGNTEPQFIIPSCIAIK	ESAKV	2	C16:+57.021	1096.57493	2191.13426	0.000451244	40	N	18	38
Q99JY9	Conv	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	HIPIA	3	C28:+57.021	1020.197396	3057.568787	0.000451244	80	N	161	191
Q99JY9	Conv	PIAGR	DITYFIQQLLR	DREVG	2		705.3935235	1408.771447	0.000451244	36	N	198	209
Q99JY9	Conv	VGYER	FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C32:+57.021	1439.372177	4315.093132	0.000451244	55	N	275	312
Q99JY9	Conv	-MAGR	LPACVVDCGTGYTK	LGYAG	2	C4:+57.021,C8:+57.021	770.8604104	1539.705221	0.000451244	65	N	4	18
Q99JY9	Conv	NAISK	KEFSIDVGYER	FLGPE	3		448.2266256	1341.656477	0.000451244	11	N	264	275
Q99JY9	Conv	CHTKK	DYEEIGPSICR	HNPVF	2	C10:+57.021	669.8036497	1337.591699	0.000451244	25	N	398	409
Q99JY9	Conv	FKYLR	AEPEDHYFLLTEPPLNTPENR	EYTAE	2		1241.598408	2481.181216	0.000451244	33	N	102	123
Q99JY9	Conv	VCHTK	KDYEEIGPSICR	HNPVF	2	C11:+57.021	733.8511312	1465.686662	0.000451244	10	N	397	409
Q99JY9	Conv	GPEIF	FHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C25:+57.021	1171.564918	3511.671355	0.000451244	7	N	282	312
Q99JY9	Conv	RRVMK	GVDDLDFFIGDEAIEKPTY	ATKWP	2		1072.507664	2142.999729	0.000622848	3	N	53	72
Q99JY9	Conv	HHMQR	YAVWFGGSMLASTPEFYQVCHTK	KDYEE	3	C20:+57.021	893.7509004	2678.229301	0.002981883	1	N	374	397
Q99JY9	Conv	TPENR	EYTAEIMFESFNVPGLYIAVQAVLALAASWTSR	QVGER	3		1216.620519	3646.838156	0.00307782	1	N	123	156
Q99JY9	Conv	KWPIR	HGIVEDWDLMER	FMEQV	2		750.3515303	1498.687461	0.000637154	5	N	79	91
Q99JY9	Conv	FTQPI	SEVVDEVIQNCPIDVR	RPLYK	2	C11:+57.021	936.4623056	1870.909011	0.000451244	8	N	296	312
Q99JY9	Conv	RRVMK	GVDDLDFFIGDEAIEKPTYA	TKWPI	2		1108.026221	2214.036843	0.000451244	7	N	53	73
Q99JY9	Conv	QAQRR	VMKGVDDLDFFIGDEAIEKPTYATK	WPIRH	4	M2:+15.995	705.3523868	2817.378347	0.000451244	6	N	50	75
Q99JY9	Conv	RPLYK	NIVLSGGSTMFR	DFGRR	2	M10:+15.995	649.3326519	1296.649704	0.000622848	3	N	317	329
Q99JY9	Conv	AKAVK	ERYSYVCPDLVK	EFNKY	2	C7:+57.021	764.877149	1527.738698	0.001463592	1	N	228	240
Q99JY9	Conv	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGS	CIKHI	2		1329.187587	2656.359574	0.00307782	1	N	161	188
Q99K41	Conv	EERFR	GLEEGQAQAGQCPSLEGR	LGRLE	2	C12:+57.021	943.9369863	1885.858373	0.000451244	8	N	709	727
Q99K41	Conv	VPFDR	VLLNDGGYYDPETGVFTAPLAGR	YLLSA	2		1213.105869	2424.196137	0.000451244	12	N	892	915
Q99K41	Conv	LLQAR	GDEGCGACGGVQEELGR	LRDGV	2	C5:+57.021,C8:+57.021	875.8596587	1749.703717	0.000451244	4	N	578	595
Q99K41	Conv	DSEGR	LQLVGSGLHEAEAAGEAQQAVLEGLQGLLSR	LRERM	3		1048.893629	3143.657488	0.000451244	8	N	511	542
Q99K41	Conv	RQLER	QLQESCSVCLTGLDGFR	QQQQE	2	C6:+57.021,C9:+57.021	985.4590087	1968.902417	0.000451244	3	N	297	314
Q99K41	Conv	ESEER	FRGLEEGQAQAGQCPSLEGR	LGRLE	3	C14:+57.021	730.6837659	2189.027898	0.000451244	1	N	707	727
Q99K41	Conv	VLSGR	RGSELGGAAGQGGHPPGYTSLASR	LSRLE	4		571.5366004	2282.115202	0.002374549	1	N	383	407
Q99K48	Conv	SLTVR	NLPQYVSNELLEEAFSVFGQVER	AVVIV	2		1334.666822	2667.318044	0.000451244	14	N	155	178
Q99K85	Conv	VGGIR	ASLYNAVTTEDVEK	LAAFM	2		770.3810071	1538.746414	0.000451244	6	N	342	356
Q99K85	Conv	PNNYK	VIFVQGGGSGQFSAVPLNLIGLK	AGRSA	2		1151.152425	2300.28925	0.000451244	3	N	71	94

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99KE1	Conv	LEAAK	ALTTQLTDAELAQGR	LYPSL	2		794.420998	1586.826396	0.000622848	1	N	496	511
Q99KE1	Conv	LVKGR	TASIDSNQEPYAHAAPESIPATFEDAVNK	LKPSV	3		1025.151545	3072.431236	0.000451244	11	N	354	383
Q99KE1	Conv	LAQGR	LYPSLANIQEVSANIAIK	LAEYL	2		972.5441873	1943.072775	0.000451244	15	N	511	529
Q99KE1	Conv	LQDGR	VFTPGQGNNAYIFPGVALAVILCEAR	HISDT	2	C23:+57.021	1389.226095	2776.436591	0.000451244	3	N	458	484
Q99KE1	Conv	KYQQK	YCTFNDDIQGTAAVALSGLLAAQR	VINKP	2	C2:+57.021	1278.131861	2554.248121	0.000451244	2	N	272	296
Q99KE1	Conv	IPVGK	LCLYTACAGIQPEK	CLPVC	2	C2:+57.021,C7:+57.021	812.3971601	1622.77872	0.00091018	3	N	183	197
Q99KE1	Conv	DAVNK	LKPSVIIGVAGAGPLFTHGVIK	AMASI	4		544.3324731	2173.298692	0.000451244	2	N	383	405
Q99KE1	Conv	LTEGR	CLFASGSPFEPVK	LQDGR	2	C1:+57.021	719.8556853	1437.695771	0.002981883	1	N	440	453
Q99KH8	Conv	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTK	YYGSY	3	C24:+57.021	1208.245357	3621.712671	0.000451244	5	N	53	84
Q99KI0	Conv	TLSEK	IVYGHLDDPANQEIER	GKTYL	2		934.9610187	1867.906437	0.001162105	1	N	68	84
Q99KI0	Conv	ANSVR	NAVTQEFGPVPDTAR	YYKKH	2		801.4000656	1600.784531	0.001162105	1	N	633	648
Q99KI0	Conv	NFTGR	NDANPETHAFVTSPEIVTALAIAGTLK	FNPET	3		927.4875406	2779.439222	0.000622848	5	N	479	506
Q99KI0	Conv	LRRAK	DINQEVYNFLATAGAK	YGVGF	2		877.4419304	1752.868261	0.000451244	2	N	144	160
Q99KJ8	Conv	SHLEK	LLGPDAAINLADPDGALAK	RLLLQ	2		917.9996126	1833.983625	0.001162105	2	N	156	175
Q99KJ8	Conv	LLQAK	VSALDLAVLDQVEAR	LQSVL	2		799.9415663	1597.867533	0.000451244	1	N	268	283
Q99KJ8	Conv	ETIQR	WSPVASTLPELVQR	LVTIK	2		791.9335442	1581.851488	0.002519933	1	N	319	333
Q99KJ8	Conv	QTTMR	ENLATVEGNFASIDAR	MKRLG	2		853.9213622	1705.827124	0.000451244	8	N	380	396
Q99KK2	Conv	GWVLR	AALDAGVFQSVWVSTDHDEIENVAK	QFGAQ	3		901.1088407	2700.303122	0.00091018	1	N	75	100
Q99KK7	Conv	AGLIR	SFCERFPEDGPELEEVLIQLAAADAR	FWRNQ	3	C3:+57.021	988.1469239	2961.417372	0.000451244	9	N	698	724
Q99KK7	Conv	HYEVR	LASVLNTDPALDSELTSK	LKRYE	2		937.4918174	1872.968035	0.000451244	18	N	215	233
Q99KK7	Conv	MEDAK	LAQDFLDSQNLSAYNTR	LFKVV	2		978.4770329	1954.938466	0.000451244	10	N	182	199
Q99KK7	Conv	TEGFK	NVSLGNVLAVAYAAK	REKLT	2		745.4228124	1488.830025	0.000451244	10	N	405	420
Q99KK7	Conv	VVAGR	ALYEGYAAVTDAPPECFLTLR	DTVLL	2	C16:+57.021	1179.078034	2356.140468	0.000451244	18	N	638	659
Q99KK7	Conv	QPNTR	LEGSEVQLVEYEASAAGLIR	SFCER	2		1067.55548	2133.095361	0.000451244	17	N	678	698
Q99KK7	Conv	FVILR	VLLEAGEGLVTVTPTTGSDGRPDAR	VRLDR	3		837.7736809	2510.297643	0.000451244	12	N	577	602
Q99KK7	Conv	VQDEK	GAFNFDKETVINPETGEQIQSWYR	SGETW	2		1415.178085	2828.34057	0.000622848	3	N	466	490
Q99KK7	Conv	LNMVR	AGLLALEFYTPEAANWR	QAHMQ	2		961.4944974	1920.973395	0.000451244	11	N	548	565
Q99KK7	Conv	SFCER	FPEDGPELEEVLIQLAAADAR	FWRNQ	2		1142.07932	2282.143039	0.000823681	1	N	703	724
Q99KK7	Conv	WIQDK	GPIVESYIGFIESYRDPFGSR	GEFEG	3		797.066136	2388.175008	0.000451244	7	N	304	325
Q99KK7	Conv	LAFEK	DKFLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1228.293347	3681.856642	0.0007646	2	N	365	399
Q99KK7	Conv	FEKDK	FLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1147.252712	3438.734735	0.001591523	2	N	367	399
Q99KK7	Conv	HHLSR	AAWYGGLAVLLQTSPEAPYIYALLSR	LFRAQ	3		941.8413666	2822.5007	0.000451244	6	N	39	65
Q99KK7	Conv	DLYIR	WKGPSFDVQVGLHELLGHGSGK	LFVQD	4		587.8096278	2347.207311	0.001839721	1	N	437	459
Q99KN1	Conv	SKDHK	CSLVFYILSPLNLNSIPDIEQPNVASTTKK	FSYKL	3	C1:+57.021	1121.262288	3360.763464	0.001943752	1	N	125	155
Q99KP6	Conv	RLIEK	YIAENGTDPINNQPLSEEQLIDIK	VAHPI	2		1357.680126	2713.344653	0.000451244	12	N	32	56
Q99KQ4	Conv	LIVSR	STEAPLIIRPDSGNPLDTVLK	VLDIL	2		1118.61333	2235.211059	0.000662267	3	N	302	323
Q99KQ4	Conv	LSLHR	TPAGNFVTLEEGKGDLEEYGHDLLHTVFK	NGKVT	4		804.9021766	3215.577506	0.000451244	6	N	434	463
Q99KV1	Conv	QAQEK	FQDLGAAYEVLSDSEK	RKQYD	2		886.4234034	1770.831207	0.000622848	3	N	66	82
Q99L04	Conv	NTTNK	SFWEVPASIWDDINNVGLR	GHYLC	2		1109.550532	2217.085465	0.001264573	1	N	106	125
Q99LB4	Conv	ISRMR	YSPNTQVEILPQGR	ESPIF	2		801.4182583	1600.820917	0.000451244	12	N	322	336
Q99LB4	Conv	MNLTK	VADSSPFASELLIPDDCFVLDNGLCGK	IYIWK	2	C17:+57.021,C25:+57.021	1470.193766	2938.371933	0.000451244	4	N	266	293
Q99LB4	Conv	RATER	ALSWDSFNTGDCFILDLGQNIFAWCGGK	SNILE	3	C12:+57.021,C25:+57.021	1064.823521	3191.447163	0.000451244	9	N	154	182
Q99LB4	Conv	NEKER	QAALQVADGFISR	MRYSP	2	Q1:-17.027	679.8570798	1357.69856	0.002374549	1	N	307	320
Q99LB4	Conv	KPALK	EGNPEEDITADQTNAQAAALYK	VSDAT	2		1175.046205	2348.07681	0.000451244	16	N	232	254
Q99LB4	Conv	QQSSR	DEQGACAVLAVHLNTLLGERPVQHR	EVQGN	4	C6:+57.021	696.6151035	2782.429214	0.002663018	1	N	71	96
Q99LC5	Conv	GENFK	LLYDLADQLHAAVGASR	AAVDA	3		604.9921312	1811.952994	0.001329271	2	N	232	249
Q99LC5	Conv	MKDSK	TIVAINKDPEAPIFQVADYGIVADLFK	VVPEM	3		983.1992196	2946.574259	0.000451244	11	N	294	321
Q99LC5	Conv	HDAYK	GLLPEELTPLILETQK	QFSYT	2		897.5171068	1793.018614	0.000451244	4	N	85	101
Q99LD4	Conv	KQAAK	CFLLASFDHCDFPELLSPSNVAVYGGLCALATFDR	QELQR	3	C1:+57.021,C10:+57.021,C28:+57.021	1321.623254	3961.846362	0.002813207	1	N	248	283
Q99LD4	Conv	SEATR	ELQNAPDAIPESGVEPPPLDTAWVEATR	KKALL	3		1001.496764	3001.466893	0.000451244	8	N	87	115
Q99LF4	Conv	LPAMK	QIGNVAALPGIVHR	SIGLP	3		482.2848092	1443.831028	0.000662267	1	N	67	81
Q99LL3	Conv	SAGLK	VSFANFIQYLLDPHTEK	LAPFN	3		674.6830748	2021.025824	0.000451244	10	N	302	319
Q99LL3	Conv	SYRNR	TASSWEEDWFANIPLAWR	QQLYK	2		1090.016325	2178.017051	0.000823681	2	N	376	394
Q99LT0	Conv	AVLAK	ERPPNPIEFLASYLLK	NKAQF	3		629.6845271	1886.030181	0.000451244	13	N	74	90
Q99LT0	Conv	SLPTR	AYLDQTVVPILLQGLAVLAK	ERPPN	2		1063.135712	2124.255825	0.000622848	4	N	54	74
Q99LX0	Conv	RAGIK	VTVAGLAGKDPVQCSR	DVMIC	2	C14:+57.021	829.4384365	1656.861273	0.001162105	2	N	32	48
Q99LX0	Conv	EQESR	KGLIAAICAGPTALLAHEVGFGCK	VTTHP	3	C8:+57.021,C23:+57.021	818.7715927	2453.291378	0.000451244	2	N	98	122
Q99LX0	Conv	ILTSR	GPGTSFEFALAIVEALVGK	DMANQ	2		953.5201808	1905.024762	0.000622848	3	N	156	175
Q99LX0	Conv	HPLAK	DKMMNGSHYSYSESR	VEKDG	3	M3:+15.995,M4:+15.995	608.5828722	1822.725217	0.002453667	3	N	130	145
Q99MK8	Conv	SPELR	SLLEGLLQR	DVNRR	2		514.8090953	1027.602591	0.002663018	1	N	422	431
Q99MN1	Conv	ELSEK	QLNQTASAPNHTADNGVGAEEETLDPNQYYK	IRSQA	3		1125.850706	3374.528718	0.000451244	4	N	45	76
Q99MN1	Conv	RYRQR	YLDLILNDFVR	QKFIV	2		690.880249	1379.744898	0.000451244	9	N	228	239
Q99N15	Conv	PFPSR	LGDPAEYAHLVQTIIENPFLNGEVIR	LDGAI	3		970.1788185	2907.513055	0.000451244	12	N	226	252
Q99N15	Conv	PTGIR	VVTIAPGLFATPLLTTLPEK	VRNFL	2		1041.116988	2080.218376	0.002080925	3	N	192	212

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99N15	Conv	ATAKR	LVGQGATAVLLDVPDSEGEAQAK	KLGES	2		1134.590052	2267.164503	0.001839721	2	N	29	52
Q99NB9	Conv	NTTAR	AFAVVASALGIPSLLPFLK	AVCKS	2		957.5773018	1913.139004	0.000823681	5	N	630	649
Q99NB9	Conv	QQKVR	TISALAIAALAEAATPYGIESFDSVLKPLWK	GIRQH	3		1082.927388	3245.758765	0.000622848	10	N	702	733
Q99NB9	Conv	PYVHK	ILVVIEPLLIDEDYYAR	VEGRE	2		1017.562046	2033.108491	0.000823681	2	N	573	590
Q99NB9	Conv	GYIAK	AIGPHDVLATLLNNLK	VQERQ	3		563.6618339	1687.962102	0.000451244	2	N	1086	1102
Q99NB9	Conv	LPHLR	SLVEIIEHGLVDEQQK	VRTIS	3		612.9954299	1835.96289	0.00307782	1	N	684	700
Q99PT1	Conv	PPAQK	SIQEIQELDKDDESLR	KYKEA	2		959.4741559	1916.932712	0.0025889	1	N	33	49
Q99PT1	Conv	ALLGR	VAVSADPNVPNVIVTR	LTLVC	2		825.962833	1649.910066	0.000451244	23	N	58	74
Q99PT1	Conv	VIVTR	LTLVCSTAPGPLELDLTGDLESFKK	QSFVL	2	C5:+57.021	1352.70961	2703.403619	0.000451244	4	N	74	99
Q99PV0	Conv	MTYFR	EAVVNTQELLDLLVK	CENKI	2		842.4805243	1682.945449	0.000622848	6	N	1275	1290
Q99PV0	Conv	STLYR	LANQLLTDLVDDNYFYLFDLK	AFFTS	2		1267.147202	2532.278805	0.000451244	4	N	240	261
Q99PV0	Conv	RHSVK	SQEPLPDDDEEFELPEFVEPFLK	DTPLY	3		917.0976073	2748.269422	0.000622848	2	N	366	389
Q9CPW4	Conv	QWHEK	ALAAGGVGSIVR	VLTAR	2		535.8199943	1069.624389	0.000451244	29	N	131	143
Q9CPW4	Conv	KYIYK	GFESPSDNSSAVLLQWHEK	ALAAG	2		1066.008697	2130.001795	0.000451244	28	N	112	131
Q9CPW4	Conv	ARFRK	VDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C32:+57.021	1253.850506	3758.528117	0.000451244	30	N	13	47
Q9CPW4	Conv	VDEED	GGDGQAGPDEGEVDSCLR	QGNMT	2	C16:+57.021	909.8818767	1817.748153	0.000451244	21	N	29	47
Q9CPW4	Conv	RFRKV	DVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C31:+57.021	1220.827701	3659.459703	0.000451244	8	N	14	47
Q9CPW4	Conv	DENKF	VDEEDGGDGQAGPDEGEVDSCLR	QGNMT	2	C21:+57.021	1203.48562	2404.95564	0.000451244	3	N	24	47
Q9CPW4	Conv	YDENK	FVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	2	C22:+57.021	1277.019827	2552.024054	0.00091018	1	N	23	47
Q9CPW4	Conv	FRKVD	VDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C30:+57.021	1182.485387	3544.43276	0.000451244	3	N	15	47
Q9CPW4	Conv	ENKFV	DEEDGGDGQAGPDEGEVDSCLR	QGNMT	2	C20:+57.021	1153.951413	2305.887226	0.000698008	1	N	25	47
Q9CPX6	Conv	LIFLK	FVQAVIPTIEYDYTR	HFTM-	2		907.9703238	1813.925048	0.000662267	5	N	295	310
Q9CQ60	Conv	LVQPR	TGALCWFLDEAAAR	LLSVP	2	C5:+57.021	790.8802231	1579.744846	0.000451244	10	N	231	245
Q9CQ60	Conv	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	4	C25:+57.021	1007.020602	4024.051208	0.000451244	5	N	131	168
Q9CQ60	Conv	HLLSK	LPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	2		1404.227244	2806.438887	0.000451244	3	N	102	128
Q9CQ80	Conv	QWVSR	SGQNNSVFTLYELTSGEDTEDEEFHGLDEATLLR	ALQAL	3		1272.917333	3815.7286	0.000451244	3	N	117	151
Q9CQC6	Conv	DEKER	FDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	2	C9:+57.021	1449.197595	2896.379589	0.000451244	5	N	26	52
Q9CQE1	Conv	VAAVR	ESVSYLESQQNTFLIPTSFSPLK	-	2		1308.166123	2614.316647	0.000451244	18	N	224	247
Q9CQE1	Conv	NAFKR	AVNAHVELGYSTLVGVFHTEYGALNR	VHVLW	3		939.8159915	2816.424575	0.001943752	1	N	167	193
Q9CQE1	Conv	EWQER	FLIPNLAFIDKQEVEITYLVPWCK	IGTPP	3	C23:+57.021	979.5262364	2935.555309	0.000622848	5	N	112	136
Q9CQE8	Conv	VALEK	HILGFDTGDAVLNEAAQILR	LLHIE	3		718.3836879	2152.127664	0.000451244	9	N	185	205
Q9CQI6	Conv	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVR	LFAFV	3	C22:+57.021	1023.793321	3068.356562	0.000451244	14	N	30	57
Q9CQI6	Conv	AMSKR	SKFALITWIGEDVSGLQR	AKTGT	2		1010.547261	2019.078923	0.000451244	9	N	73	91
Q9CQI6	Conv	SKRSK	FALITWIGEDVSGLQR	AKTGT	2		902.9837655	1803.951931	0.000451244	15	N	75	91
Q9CQI6	Conv	YNLVR	DDGSAVIWVTFR	YDGAT	2		683.3440306	1364.672461	0.001162105	3	N	18	30
Q9CQR6	Conv	EIPHK	GAFCDLVWSDPEDVDTWAISPR	GAGWL	2	C4:+57.021	1268.576387	2535.137174	0.000451244	9	N	188	210
Q9CQR6	Conv	MFDEK	LVTVWSAPNYCYR	CGNIA	2	C11:+57.021	814.8984158	1627.781232	0.000870037	6	N	251	264
Q9CQR6	Conv	-M	APLDLDKYVEIAR	QCKYL	3		501.6124801	1501.81404	0.000451244	3	N	1	14
Q9CQV8	Conv	SGENK	QTTVSNSQQAYQEAFEISKK	EMQPT	2		1144.064201	2286.112802	0.000698008	4	N	140	160
Q9CQV8	Conv	SGENK	QTTVSNSQQAYQEAFEISK	KEMQP	2		1080.016719	2158.017839	0.000451244	23	N	140	159
Q9CQV8	Conv	GDYFR	YLSEVASGENKQTTVSNSQQAYQEAFEISK	KEMQP	3		1112.867586	3335.579357	0.002519933	1	N	129	159
Q9CQV8	Conv	MQLLR	DNLTLWTSENQGDEGDAGEGEN	-	2		1175.981259	2349.946918	0.000451244	1	N	224	246
Q9CQV8	Conv	CSLAK	TAFDEAIAELDTLNEESYK	DSTLI	2		1080.005486	2157.995372	0.000451244	16	N	195	214
Q9CQV8	Conv	CSLAK	TAFDEAIAELDTLNEESYKDSTLIMQLLR	DNLTL	3		1110.553951	3328.638453	0.000451244	15	N	195	224
Q9CQV8	Conv	EYREK	IEAELQDICNDVLELLDKYLILNATQAESK	VFYLK	3	C9:+57.021	1154.595884	3460.764252	0.000451244	8	N	87	117
Q9CQV8	Conv	EYREK	IEAELQDICNDVLELLDK	YLILN	2	C9:+57.021	1065.535668	2129.055735	0.000451244	13	N	87	105
Q9CQV8	Conv	ELLDK	YLILNATQAESK	VFYLK	2		675.8673386	1349.719077	0.000622848	3	N	105	117
Q9CQV8	Conv	GKEYR	EKIEAELQDICNDVLELLDK	YLILN	3	C11:+57.021	796.4055639	2386.193292	0.000451244	1	N	85	105
Q9CRA5	Conv	VECLK	ANTNEVLWAVVAAFTK	-	3		578.6460724	1732.914817	0.000451244	8	N	282	298
Q9CU62	Conv	CVISK	VLTFDLTKYPDANPNPNEQ	-	2		1088.532005	2175.04841	0.000662267	10	N	1214	1233
Q9CU62	Conv	KALSR	NSSAQAFLGPENPEEPYLDGINYNCVAPGKR	FRPMD	3	C25:+57.021	1136.537251	3406.588354	0.000451244	6	N	1090	1121
Q9CU62	Conv	EFYTK	AESLIGVYPEQGDCVISK	VLTFD	2	C14:+57.021	982.9856136	1963.955627	0.000622848	3	N	1196	1214
Q9CVB6	Conv	SVFEK	YFQFQEEGKEGENR	AVIHY	2		880.897887	1759.780174	0.000451244	28	N	127	141
Q9CVB6	Conv	NATAR	DNTINLIHTF	RDYLH	2		594.3069168	1186.598234	0.002519933	1	N	237	247
Q9CVB6	Conv	DELLK	RVYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1085.563109	3253.665927	0.000451244	19	N	77	106
Q9CVB6	Conv	LFSHR	EPPLELKDTDAAVGDNIGYITFVLFPR	HTNAT	3		997.5223623	2989.543687	0.000451244	29	N	203	230
Q9CVB6	Conv	ELLKR	VYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1033.529405	3097.564816	0.000451244	27	N	78	106
Q9CVB6	Conv	PLELK	DTDAAVGDNIGYITFVLFPR	HTNAT	2		1092.552741	2183.089881	0.000451244	51	N	210	230
Q9CVB6	Conv	KEGRR	ASHTAPQVLFSHR	EPPLE	3		484.2570306	1449.747692	0.000698008	4	N	190	203
Q9CVB6	Conv	LKFYK	ELQAHGADELLKR	VYGSF	3		493.9358457	1478.784137	0.000451244	10	N	65	78
Q9CVB6	Conv	NATAR	DNTINLIHTFR	DYLHY	2		672.3574724	1342.699345	0.000451244	2	N	237	248
Q9CVB6	Conv	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTK	VMVSI	3		1289.294298	3864.859495	0.000451244	6	N	18	54
Q9CVB6	Conv	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK	TKVMV	3		1212.913418	3635.716854	0.000451244	11	N	18	52
Q9CVB6	Conv	SKKDR	VTVVFSTVFKDDDDVVIGK	VFMQE	2		1042.052042	2082.088484	0.001654178	1	N	160	179
Q9CVB6	Conv	ELLKR	VYGSFLVNPEPGYNVSLL	YDLEN	2		984.5098131	1967.004026	0.000870037	1	N	78	96

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CVB6	Conv	GMLKR	NCFASVFEK	YFQFQ	2	C2:+57.021	551.2556069	1100.495614	0.000622848	4	N	118	127
Q9CVB6	Conv	PPLEL	KDTDAAVGDNIGYITFVLFPR	HTNAT	3		771.4027481	2311.184844	0.001654178	1	N	209	230
Q9CVB6	Conv	KEGRR	ASHTAPQVLFSHREPPLELK	DTDAA	3		753.0749658	2256.201498	0.000451244	6	N	190	210
Q9CVB6	Conv	NATAR	DNTINLIHTFRDYLHYHIK	CSKAY	4		604.0662651	2412.23386	0.002663018	2	N	237	256
Q9CVB6	Conv	RVYGS	FLVNPEPGYNVSLLYDLENLPASK	DSIVH	2		1346.697591	2691.379581	0.001329271	2	N	82	106
Q9CVB6	Conv	SISLK	FYKELQAHGADELLK	RVYGS	3		587.9777106	1760.909732	0.000622848	1	N	62	77
Q9CVB6	Conv	PLELK	DTDAAVGDNIGYITF	VLFPR	2		786.3653571	1570.715114	0.002374549	1	N	210	225
Q9CWF2	Conv	QIGAK	FWEVISDEHGIDPTGSYHGDSDLQLER	INVYY	3		1034.80789	3101.40027	0.000451244	1	N	19	46
Q9CWF2	Conv	PRGLK	MSATFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.001591523	1	N	362	380
Q9CWJ9	Conv	DRAKR	SGVAYIVAPSGSTADKVVIEACDELGIVLAHTDLR	LFHH-	4	C22:+57.021	907.4742245	3625.865698	0.002813207	1	N	553	588
Q9CWJ9	Conv	TLKPK	LPITVLNGAPGFINLCDALNAWQLVTELR	GAVDI	3	C16:+57.021	1070.244792	3207.710975	0.000451244	9	N	225	254
Q9CWJ9	Conv	KIISR	EVSDGIVAPGYEEEALK	ILSKK	2		903.4443358	1804.873072	0.000622848	5	N	335	352
Q9CWJ9	Conv	EWVDK	LSGVSVSSDAFFPFR	DNVDR	2		808.409902	1614.804204	0.000662267	2	N	530	545
Q9CWJ9	Conv	EDLVK	WEALFEEVPELLTEAEKK	EWVDK	3		721.0408163	2160.099049	0.000451244	11	N	507	525
Q9CWJ9	Conv	KAGVK	RAEISNAIDQYVTGTIGEGEDLVK	WEALF	3		860.1052077	2577.292223	0.002296037	1	N	483	507
Q9CWJ9	Conv	YPFVK	TVASPDVTVEAAVEQIDIGGVTLLR	AAAKN	3		851.797715	2552.369745	0.001463592	2	N	108	133
Q9CWJ9	Conv	EAEKK	EWVDKLSGVSVSSDAFFPFR	DNVDR	3		758.3799435	2272.11643	0.000662267	3	N	525	545
Q9CX34	Conv	EELTK	ALEQNPDDAQYYCQR	AYCHI	2	C13:+57.021	935.9051548	1869.79471	0.000622848	3	N	36	51
Q9CX34	Conv	ASSQR	LFQSFSDALIDGDPQAALEELTK	ALEQN	3		836.7555158	2507.243147	0.000451244	2	N	13	36
Q9CXI5	Conv	GKENR	LCYYIGATDDAATK	IINEV	2	C2:+57.021	781.3640715	1560.712543	0.0025889	1	N	70	84
Q9CXI5	Conv	YQDLK	DRDVTFSPATIEEELIK	FCREA	3		655.0059946	1961.994584	0.000451244	5	N	42	59
Q9CXI5	Conv	DAATK	IINEVSKPLAHHIPVEK	ICEKL	4		481.7813447	1923.094179	0.000451244	6	N	84	101
Q9CXI5	Conv	DLKDR	DVTFSPATIEEELIK	FCREA	2		846.4410648	1690.86653	0.001162105	1	N	44	59
Q9CXY6	Conv	SLVTK	INNVIDNLIVAPGTFEVQIEEVR	QVGSY	3		861.4661882	2581.375165	0.000823681	2	N	80	103
Q9CXY6	Conv	ALLKR	NQDLAPNSAEQASILSLVTK	INNVI	2		1050.053105	2098.09061	0.000451244	8	N	60	80
Q9CXY6	Conv	VVILK	ILPTLEAVAALGNK	VVESL	2		705.422281	1408.828962	0.000451244	7	N	127	141
Q9CY58	Conv	VVTNR	FDQLFDDESDPFEVLK	AAENK	2		972.4496182	1942.883636	0.000451244	4	N	16	32
Q9CYL5	Conv	FVVAR	YFPAGNIVNQGFFEENVPPPKK	-	3		831.4256643	2491.253593	0.002884417	2	N	132	154
Q9CZ04	Conv	LRNVR	QLEDLVIEAVYADVLR	GSLDQ	2		923.5019881	1844.988376	0.000622848	2	N	126	142
Q9CZ04	Conv	RDIQR	QDLSAIAQTLQEWCVGCEVVLSGIEEQVSR	ANQHK	3	C14:+57.021,C17:+57.021	1135.553759	3403.637878	0.000451244	12	N	164	194
Q9CZ04	Conv	ASTFR	LLTVFAYGTYADYLAEAR	NLPPL	2		1019.020545	2036.02549	0.001763695	1	N	65	83
Q9CZ13	Conv	KDLPK	VVELLADIVQNSSLEDSQIEKER	DVILR	3		872.1243793	2613.349738	0.000451244	4	N	142	165
Q9CZ30	Conv	KPASK	IPAFLNVVDIAGLVK	GAHNG	2		784.9746808	1567.933762	0.000451244	17	N	83	98
Q9CZ30	Conv	PNVGK	STFFNVLTNSQASAENFPFCTIDPNESR	VPVPD	3	C20:+57.021	1065.156259	3192.445378	0.000451244	12	N	35	63
Q9CZ30	Conv	PKIIK	AGFAALQLEYFFTAGPDEVR	AWTIR	2		1101.547458	2201.079317	0.000451244	4	N	297	317
Q9CZ30	Conv	RQQGR	NYIVEDGDIIFFK	FNTPQ	2		786.9013784	1571.787157	0.000451244	3	N	373	386
Q9CZ44	Conv	GGGYR	LGAAPEEESAYVAGER	RRHSG	2		824.894813	1647.774026	0.000451244	10	N	156	172
Q9CZ44	Conv	GEGQK	LGSTAPQVLNTSSPAQQAENEAK	ASSSI	2		1171.085665	2340.155729	0.000451244	12	N	259	282
Q9CZ44	Conv	ENEAK	ASSSILINEAEPTTNIQIR	LADGG	2		1029.047822	2056.080045	0.000451244	13	N	282	301
Q9CZ44	Conv	NQTLK	EANLLNAVIVQR	LT-	2		670.3887725	1338.761945	0.000979378	4	N	356	368
Q9CZ44	Conv	NGDLR	SYQDPSNAQFLESIR	RGEVP	2		877.9213622	1753.827124	0.000451244	4	N	199	214
Q9CZ44	Conv	PPRKK	SPNELVDDLFK	GAKEH	2		638.8251394	1275.634679	0.000622848	1	N	113	124
Q9CZD3	Conv	ARKMR	LGDAVEQGVINNSVLGYFIGR	IYLYL	2		1111.084739	2220.153879	0.000451244	4	N	381	402
Q9CZD3	Conv	KRFQK	TLHVEEVVPSVIEPSFGLGR	IMYTI	3		722.392072	2164.152816	0.001943752	1	N	553	573
Q9CZD3	Conv	GDEQR	TFFSFPAVVAPFK	CSVLP	2		729.3955349	1456.77547	0.000451244	3	N	592	605
Q9CZE3	Conv	-M	AGEGLGQQGASATAAPETR	EHLFK	2		886.4326254	1770.849651	0.001591523	1	N	1	20
Q9CZN7	Conv	LCQRR	ALEAFDLDPAQWGVNVQPYSGSPANLAAYTALLQPHDR	IMGLD	3		1366.012014	4095.012642	0.000451244	17	N	122	160
Q9CZN7	Conv	YPGKR	YYGGAEVVDEIELLCQR	RALEA	2	C15:+57.021	1007.483238	2012.950876	0.000451244	11	N	104	121
Q9CZN7	Conv	SMPYK	LNPQTGLIDYDQLALTAR	LFRPR	2		1001.534351	2001.053102	0.000451244	4	N	196	214
Q9CZU6	Conv	MRGMK	GLVYETSVLDPDEGIR	FRGYS	2		881.9470456	1761.878491	0.000451244	20	N	76	92
Q9CZU6	Conv	FGVSR	ALGVLAQLIWSR	ALGFP	2		663.8987761	1325.781952	0.000451244	12	N	428	440
Q9D020	Conv	NFFGK	LQQHGIPVFIFSAGIGDVLEEVIR	QAGVY	3		879.8186733	2636.43262	0.000451244	3	N	186	210
Q9D020	Conv	LLQLK	EQYYAIEVDPVLTVEEK	FPYMV	2		1013.0073	2023.999001	0.0007646	2	N	123	140
Q9D020	Conv	DGALK	NTDYFSQLKDNSNIILLGDSQGDLR	MADGV	3		942.8021878	2825.383163	0.000823681	6	N	253	278
Q9D020	Conv	EHILK	IGYLNDRVDELLEK	YMDSY	3		559.6338324	1675.878097	0.000451244	2	N	291	305
Q9D0F9	Conv	ATMLR	NIFDFNALKELLSGPNR	LKIRI	3		650.0149359	1947.021408	0.0025889	2	N	200	217
Q9D0F9	Conv	MILGK	HGFFVNPSDSVAVIAANIFSIPYFQQTGVR	GFARS	3		1094.563443	3280.66693	0.000451244	9	N	299	329
Q9D0F9	Conv	RKRVK	VFQSNANYAENFIQSIVSTVEPALR	QEATL	2		1399.211928	2796.408256	0.000622848	3	N	27	52
Q9D0F9	Conv	YTVEK	ADNFEYSDPVDGSISK	NQGLR	2		872.3895605	1742.763521	0.000823681	3	N	470	486
Q9D0F9	Conv	RKRVK	VFQSNANYAENFIQSIVSTVEPALRQEATLVVGGDGR	FYMTE	3		1327.343652	3979.007557	0.000451244	3	N	27	64
Q9D0I9	Conv	GCAIR	AAYPDLENPPLIVTPSQQPK	FGDYQ	2		1089.576216	2177.136832	0.000451244	10	N	89	109
Q9D0I9	Conv	DDGRK	IVFVPGCSVPLTIVK	SDGGY	2	C7:+57.021	814.9761349	1627.93667	0.001463592	1	N	362	377
Q9D0I9	Conv	AVMAK	GFDILGIKPVQR	M-	3		448.2667556	1341.776867	0.000451244	2	N	647	659
Q9D0K2	Conv	AERIR	AGGAGVPAFYTSTGYGTLVQEGGSPIK	YNKDG	2		1293.148265	2584.28093	0.000622848	6	N	146	173
Q9D0K2	Conv	KTGVK	DLTAVSNNAGVDNFGLGLLLR	SKQIK	2		1080.076914	2158.138229	0.000451244	6	N	83	104

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D0K2	Conv	AEFER	QFLSGELEVELTPQGTLAER	IRAGG	2		1109.074037	2216.132475	0.001329271	2	N	124	144
Q9D0R2	Conv	AESWK	TTPYQIACGISQGLADNTVVAK	VNKVV	2	C8:+57.021	1154.08639	2306.157181	0.000451244	4	N	98	120
Q9D0R2	Conv	RKIGR	DQELYFFHELSPGSCFFLPK	GAYIY	3	C15:+57.021	821.0563178	2460.145553	0.000451244	9	N	327	347
Q9D0R2	Conv	NQAEK	QLENSLNEFGEKWELNPGDGAFYGPK	IDIQI	3		980.4669166	2938.37735	0.000451244	3	N	516	542
Q9D154	Conv	AQLSK	TFHFDSVEDIHSR	FQSLN	2		795.3713081	1588.727016	0.000451244	20	N	56	69
Q9D154	Conv	LYGEK	TYNFLPEYLASTQK	MYGAD	2		837.9228422	1673.830084	0.000451244	7	N	96	110
Q9D154	Conv	ASTQK	MYGADLAPVDFLHASEDAR	KEINQ	2		1039.486544	2076.957488	0.000451244	5	N	110	129
Q9D154	Conv	IFFIR	HNPTSNVLFLGR	VCSP-	2		677.8654646	1353.715329	0.000622848	6	N	363	375
Q9D154	Conv	VKLPR	FKIEESYTLNSNLGR	LGVQD	2		885.955205	1769.89481	0.000451244	12	N	275	290
Q9D154	Conv	ASTQK	MYGADLAPVDFLHASEDARK	EINQW	3		736.0252837	2205.052451	0.000622848	5	N	110	130
Q9D154	Conv	SNLGR	LGVQDLFSSSK	ADLSG	2		590.8145747	1179.613549	0.001463592	4	N	290	301
Q9D154	Conv	DSMTK	LVLVNAIYFK	GMWEE	2		590.3609637	1178.706327	0.000823681	5	N	158	168
Q9D154	Conv	QTEGK	IPELLSVGVVDSMTK	LVLVN	2	M13:+15.995	802.4347714	1602.853943	0.000451244	17	N	143	158
Q9D154	Conv	LPRFK	IEESYTLNSNLGR	LGVQD	2		748.3735164	1494.731433	0.00091018	1	N	277	290
Q9D1A2	Conv	DPQKK	TVCIYGHLDVQPAALEDGWDSEPFTLVER	EGKLY	3	C3:+57.021	1106.531326	3316.570578	0.000622848	7	N	92	121
Q9D1A2	Conv	DKFFK	DVDYVCISDNYWLGK	NKPCI	2	C6:+57.021	923.9197423	1845.823885	0.001264573	1	N	186	201
Q9D1A2	Conv	VDIGK	QKLPDGSEIPLPPILLGK	LGSDP	3		639.0474655	1914.118996	0.000622848	1	N	66	84
Q9D1G1	Conv	CLLLR	FADDTYTESYISTIGVDFK	IRTIE	2		1086.505122	2170.994644	0.000451244	14	N	27	46
Q9D1G1	Conv	NTTAK	EFADSLGVPFLETSAK	NATNV	2		855.9334069	1709.851214	0.000870037	1	N	137	153
Q9D1K2	Conv	AGRGK	LIAVIGDEDTVTGFLLGGIGELNK	NRHPN	2		1222.668302	2443.321004	0.000451244	16	N	6	30
Q9D1K2	Conv	LVVEK	DTTINEIEDTFR	QFLNR	2		727.3444246	1452.673249	0.000451244	2	N	41	53
Q9D1M0	Conv	SDWVR	DVAWAPSIGLPTSTIASCSQDGR	VFIWT	2	C18:+57.021	1195.076554	2388.137508	0.000637154	7	N	216	239
Q9D1M0	Conv	SQDGR	VFIWTCDDASGNMWSPK	LLHKF	2	C6:+57.021,M13:+15.995	1015.443102	2028.870604	0.001264573	4	N	239	256
Q9D1Q6	Conv	LHIQK	TPADCPVIAIDSFR	HMYVF	2	C5:+57.021	781.3878809	1560.760162	0.000823681	3	N	313	327
Q9D1Q6	Conv	RVFER	VASILHDDCAFLSAFGDLSKPER	YNGDN	3	C9:+57.021	850.0885692	2547.242308	0.000451244	10	N	180	203
Q9D1Q6	Conv	IRQQK	SNPVHEIQSLDEVTNLDR	SKRNI	2		1033.511604	2065.007608	0.000451244	10	N	140	158
Q9D1Q6	Conv	TPITA	EIASLDSENIDEILNNADVALVNFYADWCR	FSQML	3	C29:+57.021	1157.212433	3468.6139	0.000823681	3	N	29	59
Q9D2V7	Conv	VYEPR	SSPLPLQEGPGPEGGR	GARIV	2		789.4000656	1576.784531	0.000622848	6	N	664	680
Q9D2V7	Conv	AMVAK	LGNREDPLPQDSFEGVDEDEWD	-	2		1281.549309	2561.083018	0.000622848	3	N	900	922
Q9D2V7	Conv	GRGAR	IVWVCDGGCLLVSGFDSR	SERQL	2	C5:+57.021,C9:+57.021	1020.487569	2038.959538	0.000451244	14	N	683	701
Q9D2V7	Conv	PRVRK	EFFQDDVFPDTAVTWEPALSAK	AWFEG	2		1257.097709	2512.179819	0.000451244	19	N	817	839
Q9D2V7	Conv	EENKR	HVTYLGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	3	C7:+57.021	1190.88795	3569.640449	0.001839721	2	N	68	100
Q9D2V7	Conv	ITNLK	GLNLTTPGESDGFCANR	LRVAV	2	C14:+57.021	904.9155225	1807.815445	0.000451244	5	N	488	505
Q9D2V7	Conv	VLLPK	TECDIQDVEFAR	CLRLR	2	C3:+57.021	741.8303958	1481.645192	0.000451244	4	N	784	796
Q9D2V7	Conv	VLAGK	GENQLYCYEVTPQQPALSPVTQCILENVLR	GAALV	3	C7:+57.021,C23:+57.021	1173.913287	3518.716462	0.000451244	11	N	280	310
Q9D2V7	Conv	IRLWR	VPPGGLENVLTTPETVLTGHTEK	IYSLR	3		797.0923508	2388.253652	0.000979378	1	N	570	593
Q9D2V7	Conv	LWDTR	LFSSALASVTLDTSPGPLIPLLDPDSGLLVLAGK	GENQL	3		1126.632641	3376.874524	0.000637154	6	N	246	280
Q9D2V7	Conv	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHK	GFVLL	3	C16:+57.021	1028.500527	3082.478181	0.000451244	8	N	751	777
Q9D2V7	Conv	GNHIK	SSCSLIAFNSDRPGVLGVISLEGHEENKR	HVTYL	4	C3:+57.021	793.6521487	3170.577395	0.000823681	2	N	39	68
Q9D2V7	Conv	DTRLF	SSALASVTLDTSPGPLIPLLDPDSGLLVLAGK	GENQL	3		1039.915148	3116.722045	0.002145581	1	N	248	280
Q9D2V7	Conv	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHKGFVLLPK	TECDI	3	C16:+57.021	1279.991909	3836.952328	0.002296037	1	N	751	784
Q9D2V7	Conv	IKLWR	LSGTGEALPSVPGVVLGPEELPVEVL	QFHPT	2		1279.702342	2557.389083	0.002813207	1	N	106	132
Q9D4D4	Conv	HPTPR	LSFVDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021	1266.117365	2530.21913	0.000451244	9	N	116	142
Q9D4D4	Conv	HPTPR	LSFVDVATGSLGQGLGAACGMAYTGKYFDK	ASYRV	4	C19:+57.021,M21:+15.995	775.8747448	3099.467779	0.001763695	1	N	116	146
Q9D554	Conv	LLKAR	ENPSEEAQNLVEFTDEEGYGR	YLDLH	2		1207.02547	2412.035339	0.002019181	1	N	117	138
Q9D554	Conv	KASEK	LDYITYLSIFDQLFDIPK	ERKNA	2		1102.580435	2203.145271	0.000979378	1	N	157	175
Q9D662	Conv	SLNVK	GPCVSENELGVGGTSQWK	ICGLD	2	C3:+57.021	952.94428	1903.87296	0.000622848	1	N	431	449
Q9D6F9	Conv	-MR	EIVHLQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.001763695	1	N	2	19
Q9D6F9	Conv	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		1039.479773	3115.41592	0.000451244	17	N	19	46
Q9D6F9	Conv	PRGLK	MAATFIGNSTAIQELFK	RISEQ	2	M1:+15.995	929.4749593	1856.934319	0.000662267	2	N	362	379
Q9D6Y9	Conv	PELAR	LLEIDPYLKPFAADFQR	RYKKF	3		679.3670866	2035.07786	0.000622848	3	N	30	47
Q9D7G0	Conv	AGATR	VYAILTHGIFSGPAISR	INNAC	3		601.3373503	1800.988651	0.000451244	1	N	243	260
Q9D892	Conv	GFEDK	SAYALCTFALSTGDPSQPVLLFR	GQTSG	2	C6:+57.021	1257.63879	2513.26198	0.000451244	7	N	110	133
Q9D8B3	Conv	KRYEK	QLAQIDGTLSTIEFQR	EALEN	2		910.481587	1818.947574	0.00091018	1	N	77	93
Q9D8N0	Conv	QTLVR	EYFSWEGTFQHVGK	AVNQG	2		857.8971587	1713.778717	0.000823681	2	N	414	428
Q9D8N0	Conv	PNTNR	WFLTCINQPQFR	AILGE	2	C5:+57.021	805.4011257	1608.786651	0.000451244	13	N	189	201
Q9D8N0	Conv	FPAGK	VPAFEGDDGFCVFESNAIAYYVSNEELR	GSTPE	3	C11:+57.021	1066.817243	3197.42833	0.000451244	8	N	57	85
Q9D8N0	Conv	LVGER	VTLADITVVCTLLWLYK	QVLEP	2	C10:+57.021	1004.563303	2007.111006	0.001943752	2	N	156	173
Q9D8N0	Conv	SYTWR	KLDPGSEETQTLVR	EYFSW	2		786.9155485	1571.815497	0.001162105	2	N	400	414
Q9D8N0	Conv	VWVFR	GQELAFPLSPDWQVDYESYTWR	KLDPG	2		1344.12479	2686.23398	0.000451244	16	N	378	400
Q9D8N0	Conv	RKEEK	KAAAPAPEEEMDECEQALAAEPK	AKDPF	3	M11:+15.995,C14:+57.021	834.3775968	2500.109391	0.000451244	11	N	252	275
Q9D8W5	Conv	AKEGR	LQEVIETLLSLEK	QTRTA	2		757.9379609	1513.860322	0.000451244	12	N	39	52
Q9D8W5	Conv	QQALK	SVVLYVILAPFDNEQSDLVHR	ISSDK	3		805.4291858	2413.264158	0.000451244	7	N	268	289
Q9D8W5	Conv	CKHYR	AIYDTPCIQAESDKWQQALK	SVVLY	3	C7:+57.021	789.0549769	2364.141531	0.000451244	1	N	248	268
Q9D8Y7	Conv	LVECR	DILLELVEHHLTPK	SHDRI	3		552.9826845	1655.924654	0.001395409	1	N	124	138

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D8Y7	Conv	KMAGR	SVAHLFIDETSSEVLDELYR	VSKEY	3		775.0537846	2322.137954	0.000823681	1	N	24	44
Q9D906	Conv	LKKPK	QQGAGDLCPSHLVAPADLGSSLFANIPGYK	LGCYF	3	C8:+57.021	1028.513718	3082.517755	0.000622848	2	N	512	542
Q9D906	Conv	IPGYK	LGCYFCNDVVAPGDSTR	DRTLD	2	C3:+57.021,C6:+57.021	965.9248017	1929.834003	0.002145581	1	N	542	559
Q9D906	Conv	DDLCR	AEGVTALPYFLFK	YDDDT	2		728.3982746	1454.780949	0.000735798	3	N	185	198
Q9D964	Conv	HPLPK	DCPVSSYNEWDPLEEVIVGR	AENAC	2	C2:+57.021	1182.544555	2363.073511	0.000451244	3	N	62	82
Q9DAR7	Conv	AEADR	IVFENPDPSDGFVLIPDLK	WNQQQ	2		1058.054585	2114.09357	0.000823681	4	N	187	206
Q9DAR7	Conv	TFALR	TDDPLLQLLQK	AQQER	2		642.3644317	1282.713263	0.002374549	1	N	321	332
Q9DAR7	Conv	VILEK	TPFQVEHVAQLLTGSPELK	LQFSN	2		1047.565651	2093.115702	0.000451244	1	N	85	104
Q9DAR7	Conv	SGVER	AHLLAQVIENLECDPK	HYQQR	3	C13:+57.021	617.3211058	1848.939917	0.000823681	3	N	293	309
Q9DB05	Conv	VDVEK	AIAHYEQSADYYKGEESNSSANK	CLLKV	3		854.7180123	2561.130637	0.000823681	2	N	140	163
Q9DB05	Conv	ERKVK	NSQSFFSGLFGGSSK	IEEAC	2		775.3682341	1548.720868	0.000622848	1	N	22	37
Q9DBC7	Conv	EDGQK	IVVQGEPGDEFFIILEGTAAVLQR	RSENE	2		1301.200301	2600.385001	0.000451244	4	N	281	305
Q9DBG3	Conv	EYAER	IDNADELLESFLEGFHDESTQVQLTLLTAIVK	LFLKK	3		1196.949358	3587.824673	0.000451244	6	N	458	490
Q9DBG3	Conv	MLLKK	LAPPLVTLLSGEPEVQYVALR	NINLI	2		1133.146808	2264.278017	0.000451244	20	N	283	304
Q9DBG3	Conv	LIQTK	VNYVVQEAIVVIR	DIFRK	2		751.4410051	1500.86641	0.000451244	4	N	402	415
Q9DBG3	Conv	QNINK	LLTALNECTEWGQIFILDCLSNYNPK	DDREA	3	C8:+57.021,C19:+57.021	1038.175672	3111.503616	0.000451244	7	N	206	232
Q9DBG3	Conv	DIFRK	YPNKYESIIATLCENLDSLDEPDAR	AAMIW	3	C13:+57.021	976.1310509	2925.369753	0.001591523	3	N	420	445
Q9DBG3	Conv	SLKCR	APEVSQYIYQVYDSILKN	-	2		1065.541842	2129.068083	0.001943752	1	N	919	937
Q9DBG3	Conv	YQSLK	LTNGIWILAELR	IQPGN	2		699.9093408	1397.803082	0.001943752	1	N	892	904
Q9DBG3	Conv	QNINK	LLTALNECTEWGQIFILDCLSNYNPKDDR	EAQSI	3	C8:+57.021,C19:+57.021	1166.894004	3497.658613	0.001229886	2	N	206	235
Q9DBG6	Conv	IFSKK	NFESLSEAFSVASAAAALSQNR	YHVPV	3		757.3736287	2269.097486	0.000823681	1	N	244	266
Q9DBG6	Conv	TVLQK	TPFSLVGNVFELNFK	NVKLS	2		856.4568522	1710.898104	0.000662267	2	N	322	337
Q9DBG6	Conv	VERLK	ASLDRPFTDLESAFYSIVGLSSLGVQVPDVKK	ACTFI	4		860.4598587	3437.808235	0.002296037	1	N	38	70
Q9DBG6	Conv	QADLR	NIVEEIEDLVAR	LDELG	2		700.3755278	1398.735456	0.002884417	1	N	178	190
Q9DBJ1	Conv	SKDRR	YADLTEDQLPSCESLKDTIAR	ALPFW	2	C12:+57.021	1213.081502	2424.147404	0.000451244	20	N	141	162
Q9DBJ1	Conv	DTIAR	ALPFWNEEIVPQIK	EGKRV	2		842.4593949	1682.90319	0.000451244	18	N	162	176
Q9DBJ1	Conv	NLENR	FSGWYDADLSPAGHEEAK	RGGQA	2		990.4426588	1978.869718	0.001162105	3	N	21	39
Q9DBJ1	Conv	GQALR	DAGYEFDICFTSVQKR	AIRTL	3	C9:+57.021	645.9687321	1934.882796	0.001654178	4	N	46	62
Q9DBJ1	Conv	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	2		1068.493214	2134.970829	0.000451244	7	N	21	40
Q9DBJ1	Conv	IARAL	PFWNEEIVPQIK	EGKRV	2		750.3988059	1498.782012	0.000451244	3	N	164	176
Q9DBJ1	Conv	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	2		1078.58279	2155.14998	0.000451244	4	N	65	83
Q9DBJ1	Conv	GQALR	DAGYEFDICFTSVQK	RAIRT	2	C9:+57.021	890.3986426	1778.781685	0.000451244	14	N	46	61
Q9DBJ1	Conv	SKDRR	YADLTEDQLPSCESLK	DTIAR	2	C12:+57.021	934.9330467	1867.850493	0.000823681	2	N	141	157
Q9DBK7	Conv	QLHGR	LPKPWDPDDAETVVELAQDLEPLKGTEEESLDEALLR	TIALS	4		1041.02502	4160.068879	0.000451244	10	N	297	334
Q9DBK7	Conv	NPDLR	ATPYTCPLDPTTEDIYDDSFFSR	VNGVV	2	C6:+57.021	1356.094806	2710.174013	0.001162105	4	N	495	518
Q9DBK7	Conv	IQEAK	VLLCGLQGLGAEVAK	NLVLT	2	C4:+57.021	764.4320915	1526.848583	0.000451244	3	N	25	40
Q9DBL1	Conv	QFGKR	IFDFQGLQHQVAQVATQLEATR	LLTYN	3		834.1034728	2499.287018	0.000637154	2	N	325	347
Q9DBR1	Conv	VPMLR	DLTQNTAVSINFKDPQFAEDYVFK	AAMLP	3		930.7927411	2789.354823	0.000622848	5	N	743	767
Q9DBR7	Conv	ETVNK	VGQTAFDVADEDILGYLEELQKK	QTLLH	3		861.1064371	2580.295911	0.000451244	3	N	263	286
Q9DBR7	Conv	KTKVK	FDDGAVFLAACSSGDTDEVLK	LLHRG	2	C11:+57.021	1109.004732	2215.993863	0.001871652	1	N	37	58
Q9DBR7	Conv	ETVNK	VGQTAFDVADEDILGYLEELQK	KQTLL	3		818.4081161	2452.200948	0.000451244	2	N	263	285
Q9DBZ5	Conv	LAVLK	LYQFNPAFFQTTVTAQILLK	ALTNL	2		1172.141526	2342.267452	0.001463592	1	N	52	72
Q9DC23	Conv	AYSLR	SWGLGFLPQASIDLTPQTFNEK	VLQGK	2		1225.124062	2448.232523	0.001229886	2	N	661	683
Q9DC50	Conv	LLIAK	EEGLPVPELFEDPLFSR	SGGGG	2		987.4969027	1972.978205	0.000622848	4	N	515	532
Q9DC50	Conv	LCRGR	AFVFDVLHEGCLITPPELLR	QLTYI	3	C11:+57.021	776.0806863	2325.218659	0.000622848	9	N	199	219
Q9DC61	Conv	SADSK	GLDTVVDLLADVVLHPR	LTDEE	3		611.347915	1831.020345	0.000451244	6	N	157	174
Q9DCC5	Conv	NGKSK	KVEEAEPEEFVVEK	VLDRR	2		831.4175897	1660.819579	0.000451244	12	N	20	34
Q9DCC5	Conv	MFLMK	WKDSDEADLVLAK	EANMK	2		745.3808101	1488.74602	0.000451244	7	N	141	154
Q9DCC5	Conv	EANMK	CPQIVIAFYEER	LTWHS	2	C1:+39.994	754.3661917	1506.716783	0.0025889	1	N	159	171
Q9DCC5	Conv	EYFLK	WKGFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C19:+57.021	1232.898514	3695.672143	0.000451244	14	N	50	81
Q9DCC5	Conv	FLKWK	GFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C17:+57.021	1128.173756	3381.497867	0.000451244	18	N	52	81
Q9DCD0	Conv	CAFNR	TVSKVDDFLANEAK	GTKVV	2		768.8993671	1535.783134	0.000451244	43	N	34	48
Q9DCD0	Conv	ILLVK	AGQAVDDFIEK	LVPLL	2		596.7963819	1191.577164	0.000451244	26	N	76	87
Q9DCD0	Conv	CRDLK	AKGILFVGSGVSGGEEGAR	YGPSL	2		895.9739291	1789.932258	0.000451244	4	N	117	136
Q9DCD0	Conv	AIAAK	VGTGEPCCDWVGDEGAGHFVK	MVHNG	2	C7:+57.021,C8:+57.021	1138.988662	2275.961723	0.000451244	20	N	163	184
Q9DCD0	Conv	DLKAK	GILFVGSGVSGGEEGAR	YGPSL	2		796.4078906	1590.800181	0.000451244	64	N	119	136
Q9DCD0	Conv	IQAQR	DYFGAHTYELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		1310.938515	3929.792144	0.000451244	15	N	447	483
Q9DCD0	Conv	DFIEK	LVPLLDTGDIIIDGGNSEYR	DTTRR	2		1080.563305	2159.111011	0.000451244	63	N	87	107
Q9DCD0	Conv	LGKIK	DAFERNPELQNLLLDDFFK	SAVDN	2		1162.582029	2323.148459	0.000451244	16	N	377	396
Q9DCD0	Conv	DAFER	NPELQNLLLDDFFK	SAVDN	2		853.4439418	1704.872284	0.000451244	37	N	382	396
Q9DCD0	Conv	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	2		1248.154308	2494.293016	0.000451244	16	N	265	288
Q9DCD0	Conv	WPHIK	AIFQAIAAK	VGTGE	2		466.7823492	931.5490983	0.000698008	11	N	154	163
Q9DCD0	Conv	DFIEK	LVPLLDTGDIIIIDGGNSEYRDTTR	RCRDL	2		1317.175011	2632.334422	0.000870037	1	N	87	111
Q9DCD0	Conv	RTVSK	VDDFLANEAK	GTKVV	2		561.277825	1120.54005	0.000451244	6	N	38	48
Q9DCD0	Conv	IPMPC	FTTALSFYDGYR	HEMLP	2		720.8438635	1439.672127	0.000622848	2	N	422	434

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DCD0	Conv	IEKLV	PLLDTGDIIIDGGNSEYR	DTTRR	3		649.9939776	1946.958533	0.000622848	1	N	89	107
Q9DCD0	Conv	EEWNK	TELDSFLIEITANILK	YRDTD	2		910.5067391	1818.997878	0.000451244	13	N	225	241
Q9DCD0	Conv	GAHTY	ELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		992.8094538	2975.404961	0.002981883	1	N	455	483
Q9DCD0	Conv	LYASK	IISYAQGFMLLR	QAATE	2		706.3924698	1410.76934	0.000451244	8	N	331	343
Q9DCD0	Conv	IQAQR	DYFGAHTYELLTKPGEF	IHTNW	3		663.3199135	1986.936341	0.001871652	1	N	447	464
Q9DCD0	Conv	WTAIS	ALEYGMPVTLIGEAVFAR	CLSSL	2		969.0142089	1936.012818	0.001463592	1	N	270	288
Q9DCH4	Conv	GASAR	IQDALSTVLQYAEDVLSGK	VSADN	2		1025.539299	2049.062998	0.000451244	17	N	282	301
Q9DCH4	Conv	FSPNR	VIGLSSDLQQVGGASAR	IQDAL	2		829.4475471	1656.879494	0.000451244	7	N	265	282
Q9DCH4	Conv	GRVVR	LHPVILASIVDSYER	RNEGA	3		571.3179557	1710.930467	0.000662267	7	N	97	112
Q9DCL9	Conv	AISNK	ITSCIFQLLQEAGIK	TAFTK	2	C4:+57.021	860.9690382	1719.922476	0.000451244	13	N	59	74
Q9DCL9	Conv	DVTTK	EIVLADVIDNDSWR	LWPSG	2		822.9155485	1643.815497	0.000979378	3	N	201	215
Q9DCL9	Conv	WSSLR	LPSGIGCSTILSPEGSAQFAAQIFGLNNHLVWAK	LRASI	3	C7:+57.021	1195.284086	3582.828859	0.000451244	8	N	367	401
Q9DCW4	Conv	KKLVK	EIIAVSCGPSQCQETIR	TALAM	2	C7:+57.021,C12:+57.021	974.4668337	1946.918067	0.000451244	8	N	59	76
Q9DCZ1	Conv	ASEGK	TVEVPYKGDVENTILDILGGLR	STCTY	3		801.1044793	2400.290038	0.000637154	1	N	291	313
Q9EPB4	Conv	MGRAR	DAILDALENLSGDELKK	FKMKL	2		922.486535	1842.95747	0.000451244	6	N	5	22
Q9EPB4	Conv	ALIAR	VTEVDGVLDALHGSVLTEGQYQAVR	AETTS	3		886.1246022	2655.350407	0.000451244	5	N	123	148
Q9EPK2	Conv	STNIK	FGCFQWYYPELAAQFK	DAGLS	2	C3:+57.021	1027.977395	2053.939189	0.000622848	3	N	141	157
Q9EPK2	Conv	VFQEK	ASDFLLLLNK	GPVIA	2		567.3324032	1132.649206	0.000662267	5	N	281	291
Q9EPK7	Conv	TDVTR	FLQDSVEYCIIGVTILSQLTNEINQADTTHPLTK	HRKIA	3	C9:+57.021	1287.991185	3860.950156	0.000622848	1	N	139	173
Q9EPK7	Conv	ASSFR	DSSLFDIFTLSCNLLK	QASGK	2	C12:+57.021	936.9745175	1871.933435	0.000451244	2	N	182	198
Q9EPL8	Conv	RHCIR	ENIVEAIIHSPELIR	VQLTT	3		578.3251103	1731.951931	0.000451244	10	N	92	107
Q9EPL8	Conv	DDAEE	TALEGYSTIIDDEDNPVDEYQIFK	AIFQT	2		1388.148325	2774.281049	0.000451244	1	N	939	963
Q9EPL8	Conv	QCKGR	GIDQCIPLFVEAALER	LTREV	2	C5:+57.021	915.9748519	1829.934104	0.000622848	5	N	752	768
Q9EPU0	Conv	NCGCR	NVFLLGFIPAK	ADSVV	2		609.8664133	1217.717227	0.001264573	2	N	184	195
Q9EQH2	Conv	SSNDR	ASLINNAFQLVSIEK	LSIEK	2		823.959759	1645.903918	0.001329271	1	N	625	640
Q9EQH2	Conv	GEIIK	TQEFPHILTLIGR	NPVGY	3		508.9564697	1523.846009	0.000451244	7	N	817	830
Q9EQH3	Conv	IHLLR	SDDPDQQYLILNTAR	KHFGA	2		874.9266445	1747.837689	0.000451244	12	N	499	514
Q9EQH3	Conv	-M	PTTQQSPQDEQEKLLDEAIQAVK	VQSFQ	3		866.1087292	2595.302788	0.000451244	8	N	1	24
Q9EQH3	Conv	PAEIK	LFDIFSQQVATVIQSR	QDMPS	2		926.5023224	1850.989045	0.000451244	17	N	323	339
Q9EQH3	Conv	VERYK	QIVLTGILEQVVNCR	DALAQ	3	C14:+57.021	581.3261912	1740.955173	0.000451244	6	N	239	254
Q9EQH3	Conv	AKGRK	VADLYELVQYAGNIIPR	LYLLI	3		645.3514366	1933.03091	0.000451244	8	N	90	107
Q9EQH3	Conv	NVNVK	NIIIALIDR	LALFA	2		520.8272881	1039.638976	0.002813207	1	N	296	305
Q9EQH3	Conv	ISDSK	AQLAAITLIIGTFER	MKCFS	2		808.9726694	1615.929739	0.000622848	1	N	622	637
Q9EQH3	Conv	QLIQK	IREDLPNLESSEETEQINK	HFHNT	3		748.705044	2243.091732	0.002145581	2	N	749	768
Q9EQI5	Conv	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	3	C1:+39.994,C25:+57.021	1276.653546	3826.937238	0.000823681	4	N	53	88
Q9EQI5	Conv	KNGQK	TCLDPNAPGVK	RIVMK	2	C2:+57.021	586.2927208	1170.569842	0.001264573	1	N	92	103
Q9EQI5	Conv	ELRCR	CTNTISGIPFNSISLVNVYR	PGVHC	2	C1:+57.021	1128.078368	2254.141137	0.000451244	8	N	53	73
Q9EQK5	Conv	VVEER	QAIPLDQNEGIYVQDVK	TGKVR	2		965.4999767	1928.984353	0.000451244	13	N	377	394
Q9EQK5	Conv	ERLER	GIQDVYVLSEQQGLLLK	ALQPL	2		952.0309127	1902.046225	0.000451244	18	N	318	335
Q9EQK5	Conv	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGRPK	RPHAR	3		972.1907241	2913.548772	0.000451244	18	N	479	506
Q9EQK5	Conv	DQEIR	LAQDPFPLYPGELLEKDITPLQVVLPNTALHLK	ALLDF	3		1228.35399	3682.038569	0.000622848	1	N	91	124
Q9EQK5	Conv	GVAHR	TGEEWLVTVQDTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	3		1283.658466	3847.951999	0.000451244	15	N	244	279
Q9EQK5	Conv	SLGLK	STLITDGSSPINLFNTAFGLLGLGSDGQPPVQK	-	3		1115.584461	3343.729984	0.000451244	20	N	828	861
Q9EQK5	Conv	EWLVR	SVGAYLPAVFEEVLDLVDAVILTEK	TALHL	2		1345.731099	2689.446598	0.000451244	5	N	199	224
Q9EQK5	Conv	TVPPR	HYCIVANPVSR	DAQSS	2	C3:+57.021	658.3327116	1314.649823	0.000622848	8	N	56	67
Q9EQK5	Conv	RARDR	AVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	2		1285.166989	2568.318378	0.000451244	10	N	625	649
Q9EQK5	Conv	EETAK	LFSVPDFVGDACK	AIASR	2	C12:+57.021	727.8531426	1453.690685	0.000451244	4	N	560	573
Q9EQK5	Conv	ELLEK	DITPLQVVLPNTALHLK	ALLDF	2		936.5518153	1871.088031	0.000451244	12	N	107	124
Q9EQK5	Conv	DQEIR	LAQDPFPLYPGELLEK	DITPL	2		915.4883494	1828.961099	0.000451244	9	N	91	107
Q9EQK5	Conv	YIPQK	EVEVVEIIQATVIK	QNQAL	2		785.4590605	1568.902521	0.000451244	5	N	155	169
Q9EQK5	Conv	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGR	PKRPH	2		1345.208323	2688.401045	0.000662267	3	N	479	504
Q9EQK5	Conv	PHARR	ALCLLLGPDFFTDVITIETADHAR	LQLQL	3	C3:+57.021	896.7952743	2687.362423	0.000979378	4	N	512	536
Q9EQK5	Conv	VVSYR	VPHNAAVQVYDYR	AKRAR	2		766.3867612	1530.757922	0.000451244	1	N	461	474
Q9EQK5	Conv	DALQR	SVQLAIEITTNSQEAAAK	HEAQR	2		937.497434	1872.979268	0.000451244	4	N	656	674
Q9EQK5	Conv	NPVSR	DAQSSVLFDVTGQVR	LRHAD	2		811.413173	1620.810746	0.000451244	3	N	67	82
Q9EQK5	Conv	VLWEK	ELPSGVEELLNLGHDPLADR	GQKGT	2		1087.558554	2173.101509	0.000451244	8	N	417	437
Q9EQK5	Conv	AEAAR	IEGEGSVLQAK	LKAQA	2		565.8067496	1129.597899	0.002019181	1	N	734	745
Q9EQK5	Conv	QAKLK	AQALAIETEAELER	VKKVR	2		772.4022739	1542.788948	0.000451244	1	N	747	761
Q9EQK5	Conv	ARIIR	MAVFGFEMSEDAGPDGALLPR	ARDRA	2	M1:+15.995,M8:+15.995	1121.511987	2241.008375	0.001763695	1	N	600	621
Q9EQK5	Conv	EAIIR	IPPYHYIHVLDQNSNVSR	VEVGP	2		1076.550867	2151.086133	0.000451244	3	N	9	27
Q9EQK5	Conv	VLQAK	LKAQALAIETEAELER	VKKVR	3		595.6637917	1783.967975	0.000698008	1	N	745	761
Q9EQK5	Conv	LPRAR	DRAVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	3		947.4899441	2839.446432	0.000451244	3	N	623	649
Q9EQK5	Conv	LVTVQ	DTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	3		902.8048696	2705.391209	0.002981883	1	N	254	279
Q9EQP2	Conv	QRISR	GYDFCQVLQWFAER	VDRII	2	C5:+57.021	909.9173369	1817.819074	0.001162105	2	N	170	184
Q9EQU5	Conv	FEDIK	SGYRIDFYFDENPYFENK	VLSKE	3		768.6801701	2303.01711	0.001162105	1	N	131	149

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9EQU5	Conv	KSGYR	IDFYFDENPYFENK	VLSKE	2		920.9073891	1839.799178	0.000451244	16	N	135	149
Q9EQU5	Conv	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR	VEVTE	3		1242.62532	3724.852559	0.000451244	5	N	89	121
Q9EQU5	Conv	NFWVT	TFVNHPQVSALLGEEDEEALHYLTR	VEVTE	4		717.860046	2867.408984	0.002813207	1	N	96	121
Q9ER72	Conv	EVDSK	VQVLLEEAKDLLSDWLDSTGGSEVTDNSIFSK	LPKFW	3		1165.917946	3494.730438	0.000451244	12	N	265	297
Q9ER72	Conv	LEEAK	DLLSDWLDSTGGSEVTDNSIFSK	LPKFW	2		1243.58262	2485.149641	0.000451244	6	N	274	297
Q9ER72	Conv	AREKK	VLEVLQLSDALRDDILPELGVR	FEDHE	3		821.7992788	2462.374436	0.000451244	13	N	689	711
Q9ERF3	Conv	SPDGK	YLASGAIDGIINIFDIATGK	LLHTL	2		1026.554752	2051.093904	0.001463592	1	N	161	181
Q9ERF3	Conv	AMPIR	SLTFSPDSQLLVTASDDGYIK	IYDVQ	2		1129.065878	2256.116156	0.000451244	8	N	194	215
Q9ERK4	Conv	RPAEK	FLESVEGNQNYPLLLLTLLEK	SQDNV	2		1217.167938	2432.320275	0.000451244	11	N	31	52
Q9ERK4	Conv	TLDNK	LLQTDDEEEAGLLELLK	SQICD	2		965.0073003	1927.999001	0.001162105	4	N	251	268
Q9ERK4	Conv	LYCIK	YGALALQEIFDGIQPK	MFGMV	2		881.9728664	1761.930133	0.001463592	2	N	800	816
Q9ERK4	Conv	AFLER	GSSTIATAAADKIPGLLGVFQK	LIASK	3		715.7358387	2144.184116	0.000637154	2	N	714	736
Q9ERK4	Conv	WTEIK	LVLDAFALPLTNLFK	ATIEL	2		837.9956132	1673.975626	0.000451244	2	N	174	189
Q9ERK4	Conv	RPHYK	NLFEDQNTLTSICEK	VIVPN	2	C13:+57.021	906.4279315	1810.840263	0.000451244	6	N	331	346
Q9ERL7	Conv	VDKDR	QMVVLEDELQNISPEELKLELPER	QPRFV	3	M2:+15.995	956.4956247	2866.463474	0.000451244	4	N	40	64
Q9ERR7	Conv	DPVLK	LLDDNGNIAEELSILK	WNTDS	2		878.9705208	1755.925442	0.000451244	10	N	129	145
Q9ERR7	Conv	SEACR	ELGFSSNLLCSSCDLLGQFNLLPLDPVCR	GCCQE	3	C10:+57.021,C13:+57.021,C28:+57.021	1108.873621	3323.597464	0.000451244	8	N	39	68
Q9ERR7	Conv	LSILK	WNTDSVEEFLSEKLER	I-	3		661.3220942	1980.942883	0.000451244	2	N	145	161
Q9ES46	Conv	KELVK	VLLDWINDVLAEER	IIVKQ	2		842.9493913	1683.883183	0.000451244	14	N	92	106
Q9ES46	Conv	RIIVK	QLEEDLYDGQVLQK	LLEKL	2		839.4206637	1676.825727	0.000622848	1	N	110	124
Q9ES52	Conv	EEHLK	AIQDYLSTQLLLDSDFLK	TGSSN	2		1042.052042	2082.088484	0.000451244	15	N	185	203
Q9ES52	Conv	TMVAK	LSQLTSLLSSIEDK	VKSLL	2		767.422675	1532.82975	0.000823681	3	N	267	281
Q9ES52	Conv	ESFVK	SQEGENEEGSEGELVVR	FGETL	2		924.416838	1846.818076	0.001463592	1	N	765	782
Q9ESP1	Conv	SHDIK	YGSGSGQQSVTGVEESDDANSYWR	IRGGS	2		1290.050007	2578.084415	0.000451244	11	N	59	83
Q9ESP1	Conv	VLTGK	NLHTHHFPSPLSNNQEVSAFGEDGEGDDLDLWTVR	CSGQH	3		1311.940807	3932.79902	0.002019181	2	N	113	148
Q9ESP1	Conv	EASVR	FQHVGTSVFLSVTGEQYGNPIR	GQHEV	3		812.7489184	2435.223355	0.000735798	2	N	161	183
Q9EST5	Conv	LDCLK	SLDLFGCEVTNR	SDYRE	2	C7:+57.021	705.8380238	1409.660448	0.000451244	6	N	116	128
Q9EST5	Conv	GGLDR	LAEELPSLTHLNLSGNNLK	DISTL	3		688.3764219	2062.105866	0.000451244	5	N	82	101
Q9ET01	Conv	SQLTK	LHSFVSDDIFLR	EIAKV	2		724.8807803	1447.745961	0.000451244	10	N	521	533
Q9ET01	Conv	IFNQK	IREGWQVEEADDWLR	HGNPW	2		951.4611859	1900.906772	0.000451244	15	N	170	185
Q9ET01	Conv	SQLTK	LHSFVSDDIFLREIAK	VKQEN	3		630.6760316	1889.004695	0.000451244	6	N	521	537
Q9ET01	Conv	GITPR	RWLLLCNPGLADLIAEK	IGEDY	2	C6:+57.021	991.5485184	1981.081437	0.000451244	14	N	490	507
Q9ET01	Conv	ITPRR	WLLLCNPGLADLIAEK	IGEDY	2	C5:+57.021	913.4979628	1824.980326	0.000451244	32	N	491	507
Q9ET01	Conv	LWSAR	APNDFNLQDFNVGDYIQAVLDRNLAENISR	VLYPN	3		1141.231081	3420.669844	0.000451244	11	N	248	278
Q9ET01	Conv	LWSAR	APNDFNLQDFNVGDYIQAVLDR	NLAEN	2		1262.609307	2523.203014	0.000451244	62	N	248	270
Q9ET01	Conv	LIAEK	IGEDYVKDLSQLTK	LHSFV	2		804.9281245	1607.840649	0.000451244	14	N	507	521
Q9ET01	Conv	LPELK	LVIDQIDNGFFSPNQPDLF	KDIIN	2		1090.039466	2178.063332	0.000451244	6	N	740	759
Q9ET01	Conv	KLLPR	HLEIIYEINQK	HLDRI	2		700.3831558	1398.750712	0.000451244	45	N	399	410
Q9ET01	Conv	NQKIR	EGWQVEEADDWLR	HGNPW	2		816.8685982	1631.721596	0.000451244	14	N	172	185
Q9ET01	Conv	PSDLK	ISLSNESSNGVSANGK	-	2		782.3846125	1562.753625	0.000451244	6	N	834	850
Q9ET01	Conv	QISIR	GIVGVENVAELK	KGFNR	2		614.3513243	1226.687049	0.0007646	2	N	17	29
Q9ET01	Conv	EITKK	TFAYTNHTVLPEALER	WPVEL	2		931.4763046	1860.937009	0.000451244	20	N	371	387
Q9ET01	Conv	HDRFK	VFADYEAYVK	CQEKV	2		602.7983932	1203.581186	0.000451244	19	N	773	783
Q9ET01	Conv	KMIIK	LITSVAEVVNNDPMVGSK	LKVIF	2		936.9909308	1871.966262	0.000451244	13	N	622	640
Q9ET01	Conv	GKELR	LKQEYFVVAATLQDVIR	RFKAS	2		997.0600045	1992.104409	0.000451244	21	N	293	310
Q9ET01	Conv	LLLCN	PGLADLIAEK	IGEDY	2		513.7956536	1025.575707	0.002727428	1	N	497	507
Q9ET01	Conv	ELRLK	QEYFVVAATLQDVIR	RFKAS	2		876.4704909	1750.925382	0.000451244	12	N	295	310
Q9ET01	Conv	LPELK	LVIDQIDNGFFSPNQPDLFK	DIINM	2		1154.086948	2306.158295	0.000451244	30	N	740	760
Q9ET01	Conv	LWSAR	APNDFNLQDFNVGDYIQAV	LDRNL	2		1070.503248	2138.990895	0.000451244	12	N	248	267
Q9ET01	Conv	QISIR	GIVGVENVAELKK	GFNRH	2		678.3988059	1354.782012	0.000823681	2	N	17	30
Q9ET01	Conv	GYGIR	YEYGIFNQK	IREGW	2		581.2829103	1160.550221	0.000979378	20	N	161	170
Q9ET01	Conv	TQVFK	DFSELEPDKFQNK	TNGIT	2		798.8811743	1595.746749	0.000451244	6	N	470	483
Q9ET01	Conv	VATPR	DYYFALAHTVR	DHLVG	2		678.3412909	1354.666982	0.000451244	18	N	50	61
Q9ET01	Conv	GYEAK	EYYEALPELK	LVIDQ	2		627.816783	1253.617966	0.002374549	3	N	730	740
Q9ET01	Conv	PELMR	IFVDIEKLPWAK	AWEIT	2		729.9219169	1457.828234	0.000451244	18	N	352	364
Q9ET01	Conv	MVGSK	LKVIFLENYR	VSLAE	3		432.255968	1293.744504	0.000451244	9	N	640	650
Q9ET01	Conv	LPELK	LVIDQIDNGFFSPNQPDLFKDIINMLFYHDR	FKVFA	3		1242.287651	3723.839553	0.000451244	6	N	740	771
Q9ET01	Conv	VATPR	DYYFALAHTVRDHLVGR	WIRTQ	3		678.35043	2032.02789	0.000735798	8	N	50	67
Q9ET01	Conv	EITKK	TFAYTNHTVLPEALERWPVELVEK	LLPRH	3		948.1645093	2841.470128	0.000622848	3	N	371	395
Q9ET01	Conv	NPWEK	ARPEFMLPVHFYGR	VEHTQ	3		573.9649712	1718.871513	0.000451244	7	N	192	206
Q9ET01	Conv	HEYKR	QLLNCLHVITMYNR	IKKDP	2	C5:+57.021	887.9584824	1773.901365	0.002981883	1	N	576	590
Q9ET01	Conv	SLAEK	VIPATDLSEQISTAGTEASGTGNMK	FMLNG	2		1239.605573	2477.195546	0.000823681	6	N	656	681
Q9ET01	Conv	KEYAK	DIWNMEPSDLK	ISLSN	2		674.3166248	1346.61765	0.000451244	4	N	823	834
Q9ET01	Conv	PDLFK	DIINMLFYHDR	FKVFA	3		479.5717392	1435.691818	0.001699387	2	N	760	771

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9ET01	Conv	AIYQL	GLDMEELEEIEEDAGLGNGGLGR	LAACF	2		1202.053173	2402.090747	0.000451244	1	N	116	139
Q9ET01	Conv	ITPRR	WLLLCNPGLADLIAEKIGEDYVK	DLSQL	3	C5:+57.021	877.4684985	2629.382096	0.001162105	1	N	491	514
Q9ET01	Conv	DFNLQ	DFNVGDYIQAVLDR	NLAEN	2		812.9024411	1623.789282	0.000823681	2	N	256	270
Q9ET01	Conv	ENKLK	FSQFLEKEYK	VKINP	2		659.8380498	1317.6605	0.002519933	1	N	545	555
Q9ET66	Conv	MLQMR	WDDELAAFAK	AYAQK	2		583.2803676	1164.545135	0.001329271	4	N	51	61
Q9ET66	Conv	SKTER	IGCGSHFCETLQGVEEANIHLLVCNYEPPGNVK	GRKPY	4	C3:+57.021,C8:+57.021,C24:+57.021	936.1920865	3740.737146	0.000870037	1	N	132	165
Q9JHK5	Conv	EKDKK	VFNHCLTGSGVIDWLVSNK	LVRNR	2	C5:+57.021	1073.541422	2145.067243	0.000451244	15	N	150	169
Q9JHK5	Conv	SHDVK	KSDEENLFEIITADEVHYYLQAATSK	ERTEW	3		1005.49302	3013.45566	0.000870037	5	N	307	333
Q9JHK5	Conv	HDVKK	SDEENLFEIITADEVHYYLQAATSK	ERTEW	3		962.7946989	2885.360697	0.000451244	10	N	308	333
Q9JHK5	Conv	ITTTK	QQDHFFQAAFLEER	DAWVR	3		589.2817931	1764.821979	0.000451244	7	N	75	89
Q9JHK5	Conv	KFILR	EDPAYLHYYDPAGGEDPLGAVHLR	GCVVT	3		885.7545092	2654.240128	0.000451244	6	N	269	293
Q9JHU4	Conv	ESALR	FGNPLLVQDVESYDPVLNPVLNR	EVRRT	2		1299.682275	2597.34895	0.000451244	7	N	3626	3649
Q9JHU4	Conv	ELQKR	QWIVFDGDVDPEWVENLNSVLDDNKLLTLPNGER	LSLPP	3		1313.985353	3938.93266	0.000451244	1	N	2296	2330
Q9JHU4	Conv	TMVPK	LVAEDIPLLFSLLSDVFPGVQYHR	GEMTA	3		910.1623286	2727.463586	0.000637154	2	N	2146	2170
Q9JHU4	Conv	SIIMR	ENFIPTIVNFSAEEISDAIR	EKMKK	2		1133.074037	2264.132475	0.000823681	6	N	3342	3362
Q9JHU4	Conv	ELQKR	QWIVFDGDVDPEWVENLNSVLDDNK	LLTLP	3		982.7984433	2945.37193	0.000979378	1	N	2296	2321
Q9JHU4	Conv	EVKGR	ILDDDTIITTLENLKR	EAAEV	3		625.0146015	1872.020405	0.002519933	1	N	3757	3773
Q9JHU9	Conv	QTKVK	SVLVDFLIGSGLK	TMSIV	2		674.3982746	1346.780949	0.000451244	15	N	312	325
Q9JHU9	Conv	ELCQR	VSFCTDSDPEPQGFHTVLSLLSFLFK	APLVP	3	C4:+57.021	991.1567603	2970.446881	0.000451244	12	N	439	465
Q9JHU9	Conv	SLRPR	PSVYIPEFIAANQTAR	ADNLI	2		888.9681154	1775.920631	0.000823681	1	N	175	191
Q9JIF0	Conv	DLDFK	GQLCELSCSTDYR	MR-	2	C4:+57.021,C8:+57.021	794.8402063	1587.664813	0.000451244	2	N	356	369
Q9JIF0	Conv	IYTVK	VEDLTFTSPFCLQVK	RNDYV	2	C11:+57.021	892.4506782	1782.885756	0.001591523	2	N	261	276
Q9JIF7	Conv	YTIYR	NFEHLIPDAPELIHDFLVNEK	DASCK	4		623.322568	2489.259072	0.002296037	1	N	164	185
Q9JIZ9	Conv	MYELR	SGTGQQLGQAAEESNCCAR	LCCGA	2	C16:+57.021,C17:+57.021	1012.431511	2022.847422	0.000451244	2	N	110	129
Q9JIZ9	Conv	GGLLR	EALTDADDFGLQFPVDLDVK	VKAVL	2		1104.539496	2207.063392	0.000451244	6	N	246	266
Q9JJ00	Conv	SGFVR	EAFTDADNFGIQFPLDLDVK	MKAVM	2		1128.047488	2254.079376	0.001763695	2	N	277	297
Q9JJ28	Conv	TDQMK	ADLTALFLPR	QPPMP	2		558.8247454	1115.633891	0.002080925	3	N	874	884
Q9JJ28	Conv	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTRVPECLYTLPSLR	RLNLS	3	C22:+57.021,C31:+57.021	1460.056435	4377.145904	0.000979378	1	N	210	249
Q9JJ28	Conv	CFILK	VPFESEDNQGIVYAWVGR	ASDPD	2		1033.503051	2064.990501	0.000451244	9	N	1091	1109
Q9JJ28	Conv	LNKNR	LVTLPEAIHFLTEIQVLDVR	ENPSL	3		769.4426552	2305.304566	0.000823681	4	N	351	371
Q9JJ28	Conv	KPADR	TAEWYNIDFSLQNQLR	LAGAS	2		999.4899433	1996.964287	0.000622848	1	N	385	401
Q9JJ28	Conv	PKLYK	VGLGLGYLELPQINYK	LSVEH	2		888.9988842	1775.982168	0.000451244	5	N	730	746
Q9JKC8	Conv	EKHWK	SVVSQSVCDYFFEAQEK	AADVE	2	C8:+57.021	1011.959596	2021.903592	0.000823681	2	N	21	38
Q9JKF1	Conv	TTVWK	QLSSSVTGLTNIEEENCQR	YLDEL	2	C17:+57.021	1083.01088	2164.006159	0.000451244	21	N	477	496
Q9JKF1	Conv	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	C9:+57.021	674.9952813	2021.962444	0.000735798	3	N	36	52
Q9JKF1	Conv	LQQKR	QSGQTDPLQKEEVQAGVDAANSAAQQYQR	RLAAV	3		1039.833098	3116.475895	0.000451244	24	N	358	387
Q9JKF1	Conv	EIKSK	VDQIQEIVTGNPTVIK	MVVSF	2		877.4888807	1752.962161	0.000451244	10	N	1037	1053
Q9JKF1	Conv	AAYNR	EQLWLANEGLITK	LQACC	2		757.9148201	1513.81404	0.000451244	18	N	738	751
Q9JKF1	Conv	VDVIR	FQPGETLTEILETPATNEQEAEHQR	AMQRR	2		1434.686471	2867.357343	0.000698008	3	N	1397	1422
Q9JKF1	Conv	LSALR	SPDVGLYGVIPECGETYQSDLAEAK	KKRLA	2	C13:+57.021	1349.631556	2697.247512	0.000451244	14	N	647	672
Q9JKF1	Conv	QEAQR	FALGISAINEAVDSGDVGR	TLSAL	2		945.9819511	1889.948302	0.000451244	12	N	622	641
Q9JKF1	Conv	IPAAK	LEGVLAEVAQHYQDTLIR	AKREK	3		685.701017	2054.079651	0.000451244	20	N	567	585
Q9JKF1	Conv	RLHEK	GVLLEIEDLQANQFK	NVIFE	2		858.9624987	1715.909397	0.000451244	7	N	1571	1586
Q9JKF1	Conv	KNMPR	CIYCIHALSLYLFK	LGLAP	2	C1:+57.021,C4:+57.021	900.9624702	1799.90934	0.00091018	1	N	147	161
Q9JKF1	Conv	ANQFK	NVIFEIGPTEEVGDFEVK	AKFMG	2		1011.507467	2020.999335	0.000451244	17	N	1586	1604
Q9JKF1	Conv	AASNK	MFLGDNAHLSIINEYLSQSYQK	FRRFF	3		857.7569741	2570.247522	0.000622848	4	N	1239	1261
Q9JKF1	Conv	EEHER	ILAIGLINEALDEGDAQK	TLQAL	2		942.0101773	1882.004755	0.000451244	21	N	538	556
Q9JKF1	Conv	AKREK	AQETQDESAVLWLDEIQGGIWQSNKDTQEAQR	FALGI	3		1225.25087	3672.729209	0.000451244	14	N	590	622
Q9JKF1	Conv	RLHEK	GVLLEIEDLQANQF	KNVIF	2		794.9150171	1587.814434	0.001162105	1	N	1571	1585
Q9JKF1	Conv	EEHER	ILAIGLINEALDEGDAQKTLQALQIPAAK	LEGVL	3		1006.568083	3016.680849	0.000451244	11	N	538	567
Q9JKF1	Conv	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDRR	VAADT	3		1038.902236	3113.683309	0.000823681	3	N	201	231
Q9JKF1	Conv	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDR	RVAAD	3		986.8685326	2957.582198	0.000451244	3	N	201	230
Q9JKF1	Conv	VTLLK	ALQSLALGLR	GLQTQ	2		521.3249125	1040.634225	0.000622848	2	N	326	336
Q9JKF1	Conv	IRAKR	EKAQETQDESAVLWLDEIQGGIWQSNK	DTQEA	3		1034.83919	3101.494171	0.000451244	6	N	588	615
Q9JKF1	Conv	IGLPK	IFYPETTDIYDRK	NMPRC	3		554.2792781	1659.814434	0.002519933	1	N	130	143
Q9JKF1	Conv	YLLLR	LFQTALQEEIK	SKVDQ	2		660.3644317	1318.713263	0.000451244	9	N	1024	1035
Q9JKF1	Conv	QEEIK	SKVDQIQEIVTGNPTVIK	MVVSF	2		985.0523765	1968.089153	0.000451244	9	N	1035	1053
Q9JKF1	Conv	GDAQK	TLQALQIPAAK	LEGVL	2		577.3511273	1152.686655	0.000451244	11	N	556	567
Q9JKF1	Conv	VQLSR	EEIQSSISGVTAAYNR	EQLWL	2		862.9266445	1723.837689	0.000451244	19	N	722	738
Q9JKF1	Conv	KHWVK	GGYHYYHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	3		1174.215543	3519.623228	0.000451244	17	N	691	722
Q9JKF1	Conv	GNVNK	VNTSSALANISLALEQGCAVTLLK	ALQSL	2	C18:+57.021	1237.170454	2472.325309	0.000451244	14	N	302	326
Q9JKF1	Conv	FDRAK	VNVNLLIFLLNK	KFYGK	2		700.4377341	1398.859868	0.001162105	2	N	1640	1652
Q9JKF1	Conv	AIDRR	VAADTFTALKNPNAMLVNLEEGLAPTYQDVLYQAK	QDKMT	3	M15:+15.995	1275.652576	3823.934327	0.000451244	10	N	231	266
Q9JKF1	Conv	AEEVD	GLGVVRPHYGSVLDNER	LTAEE	3		623.3311469	1866.970041	0.000451244	2	N	8	25

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JKF1	Conv	DPLQK	EEVQAGVDAANSAAQQYQR	RLAAV	2		1017.977928	2033.940257	0.000451244	4	N	368	387
Q9JKF1	Conv	LYLFK	LGLAPQIQDLYGK	VDFTE	2		708.3988059	1414.782012	0.000622848	2	N	161	174
Q9JKF1	Conv	ENSDR	ERDVYEELLTQAEIQGNVNK	VNTSS	2		1174.590583	2347.165566	0.000451244	3	N	282	302
Q9JKF1	Conv	SKEKR	EKLEAYQHLFYLLQTNPTYLAK	LIFQM	3		895.1430455	2682.405737	0.000451244	1	N	966	988
Q9JKF1	Conv	DELLK	IIGNLLYYR	YMNPA	2		562.8272881	1123.638976	0.001162105	8	N	1185	1194
Q9JKF1	Conv	FDRAK	VNVNLLIFLLNKK	FYGK-	3		509.9927438	1526.954831	0.002981883	1	N	1640	1653
Q9JKF1	Conv	EKREK	LEAYQHLFYLLQTNPTYLAK	LIFQM	3		809.4305267	2425.26818	0.002813207	2	N	968	988
Q9JKF1	Conv	GLLVK	NKITLQDVVSHSK	KLTKK	3		490.2759794	1467.804538	0.000735798	1	N	922	935
Q9JKR6	Conv	MAGLK	VLQLINDNTATALSYGVFR	RKDIN	2		1048.063276	2094.110951	0.000451244	17	N	198	217
Q9JKR6	Conv	LNYSR	SLAEDFAEQPIKDAVITVPAFFNQAER	RAVLQ	3		1002.845616	3005.513449	0.002884417	1	N	158	185
Q9JKR6	Conv	PFVVR	DAVIYPILVEFTR	EVEEE	2		768.4275634	1534.839527	0.001352548	5	N	438	451
Q9JKR6	Conv	QEREK	AANSLEAFIFETQDK	LYQPE	2		842.4153813	1682.815163	0.000622848	8	N	738	753
Q9JKR6	Conv	LDRVE	SVFETLVEDSPEEESTLTK	LGNTI	2		1070.513144	2139.010688	0.000622848	3	N	557	576
Q9JL26	Conv	HFLDK	AGSVSLDSVLGDVR	SLQRG	2		687.8653272	1373.715054	0.000622848	1	N	901	915
Q9JLJ2	Conv	FGYTR	REPLGVCVGIGAWNYPFQIACWK	SAPAL	3	C7:+57.021,C21:+57.021	907.7860133	2720.33464	0.000622848	3	N	143	166
Q9JLJ2	Conv	QRAHR	VAAELQAGTCYINNYNVSPVELPFGGYKK	SGFGR	3	C10:+57.021	1068.20114	3201.580021	0.000622848	6	N	433	462
Q9JLJ2	Conv	VKLAK	EQGATVLCGGEVYVPEDPKLK	HGYYM	3	C8:+57.021	763.7195942	2288.135383	0.001162105	1	N	347	368
Q9JLJ2	Conv	EVLER	ANDTTFGLAAGVFTR	DIQRA	2		770.8918764	1539.768153	0.000662267	3	N	411	426
Q9JLQ2	Conv	QKLAR	FNAHEFATLVIDILSDAK	RRQQG	3		668.6865964	2003.036389	0.000451244	9	N	335	353
Q9JLT4-2	Conv	PKNQK	IIVDAQEATSVPHIYAIGDVAEGRPELTPTAIK	AGKLL	3		1158.954666	3473.840598	0.000998612	1	N	307	340
Q9JLT4-2	Conv	MVCMR	EPPQLVLGLHFLGPNAGEVTQGFALGIK	CGASY	3		968.1995539	2901.575262	0.000451244	3	N	421	449
Q9JLV6	Conv	GSRGR	LWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	2		1358.74521	2715.474819	0.000451244	4	N	9	35
Q9JLV6	Conv	MFSYR	KQFEPPTLAEGFLEILEIPFR	LQEHL	3		825.4496984	2473.325695	0.000622848	1	N	482	503
Q9JLV6	Conv	SCADR	LFALNVGLPFATPEEFFLK	WPAAR	2		1077.088231	2152.160861	0.000451244	10	N	310	329
Q9JLV6	Conv	FSYRK	QFEPPTLAEGFLEILEIPFR	LQEHL	2		1173.623166	2345.230732	0.000823681	10	N	483	503
Q9JLV6	Conv	EIPFR	LQEHLDPALQR	LYRQF	3		440.5742482	1318.699345	0.001352548	1	N	503	514
Q9JLV6	Conv	KPQGK	VAAFDLDGTLITTR	SGKVF	2		746.9044524	1491.793305	0.000451244	6	N	165	179
Q9JLV6	Conv	WPAAR	FELPAFDPR	TISSA	2		546.2801706	1090.544741	0.002080925	1	N	334	343
Q9JLV6	Conv	PLTLR	WEELSTSGSQPDAPPDTPGDPEEGEDTEPQKK	RVRKS	3		1151.841653	3452.50156	0.000451244	20	N	105	137
Q9JLV6	Conv	AVLEK	LGVPFQVLVATHAGLNR	KPVSG	3		598.0129781	1791.015534	0.002212458	2	N	241	258
Q9JLV6	Conv	LRWEE	LSTSGSQPDAPPDTPGDPEEGEDTEPQKK	RVRKS	3		1003.78682	3008.337061	0.000622848	1	N	108	137
Q9JM14	Conv	DLAEK	VASVYESPGFFLNLEPIPGALDALR	EMNDM	3		892.4746837	2674.400651	0.001264573	1	N	62	87
Q9JM76	Conv	RLCEK	VFDPQSDKPSKWWTCFVK	RQFMN	4	C15:+57.021	564.5297111	2254.087644	0.000998612	8	N	147	165
Q9JM76	Conv	DPDTK	LIGNMALLPLR	SQFKG	2		605.8711732	1209.726746	0.000823681	7	N	14	25
Q9JM76	Conv	GPAPR	ETKDTDIVDEAIYYFK	ANVFF	2		975.4730933	1948.930587	0.000451244	18	N	34	50
Q9JM76	Conv	PRETK	DTDIVDEAIYYFK	ANVFF	2		796.3804758	1590.745352	0.000451244	20	N	37	50
Q9JM76	Conv	KCNSK	SQGEKEMYTLGITNFPIPGEPGFPLNAIYAK	PASKQ	3		1128.239638	3381.695514	0.000622848	6	N	88	119
Q9JM76	Conv	SQGEK	EMYTLGITNFPIPGEPGFPLNAIYAK	PASKQ	3		951.823096	2852.445888	0.002453667	1	N	93	119
Q9JMA1	Conv	VLQQK	LEAIEDDSGRETDSSSAPAVTPSK	KKSLI	3		821.3896727	2461.145618	0.000451244	23	N	214	238
Q9JMA1	Conv	PKEIK	YEPFSFADDIGSNNCGYYDLQAVLTHQGR	SSSSG	3	C15:+57.021	1113.167047	3336.47774	0.000451244	18	N	399	428
Q9JMA1	Conv	EDILR	LSGGGDWHIAYVLLYGPR	RVEIM	3		658.6797761	1973.015928	0.002296037	2	N	464	482
Q9JMA1	Conv	DEWIK	FDDDKVSIVTPEDILR	LSGGG	3		621.3234351	1860.946905	0.002727428	1	N	448	464
Q9JMH6	Conv	KDDER	VVGFHVLGPNAGEVTQGFAAALK	CGLTK	2		1141.618749	2281.221899	0.000451244	8	N	548	571
Q9JMH6	Conv	CGLTK	QQLDSTIGIHPVCAEIFTTLSVTK	RSGGD	3	C13:+57.021	886.7987959	2657.372988	0.000451244	12	N	576	600
Q9JMH6	Conv	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	2	C1:+57.021,C18:+57.021,C19:+57.021	1477.62991	2953.244221	0.000451244	15	N	478	503
Q9JMH6	Conv	GERPR	YLGIPGDKEYCISSDDLFSLPYCPGK	TLVVG	3	C11:+57.021,C23:+57.021	998.801723	2993.381769	0.000451244	15	N	280	306
Q9JMH6	Conv	PGRLR	VTAQSTNSEETIEGEFNTVLLAVGR	DSCTR	2		1333.169926	2664.324251	0.000451244	18	N	382	407
Q9JMH6	Conv	KAVEK	FGEENIEVYHSFFWPLEWTVPSR	DNNKC	3		957.1260545	2868.354764	0.000451244	23	N	507	530
Q9JMH6	Conv	EKTGK	IPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGR	LLAQR	3		1309.365283	3925.072449	0.000451244	24	N	429	465
Q9JMH6	Conv	KFDKK	VLVLDFVTPTPLGTR	WGLGG	2		814.475045	1626.93449	0.000451244	12	N	151	166
Q9JMH6	Conv	IPGDK	EYCISSDDLFSLPYCPGK	TLVVG	2	C3:+57.021,C15:+57.021	1075.974157	2149.932715	0.000451244	1	N	288	306
Q9JMH6	Conv	EKTGK	IPVTDEEQTNVPYIYAIGDILEGK	LELTP	2		1339.184513	2676.353426	0.000662267	1	N	429	453
Q9JMH6	Conv	CGLTK	QQLDSTIGIHPVCAEIFTTLSVTKR	SGGDI	4	C13:+57.021	704.3763247	2813.474099	0.001162105	1	N	576	601
Q9JMH6	Conv	KINEK	TGKIPVTDEEQTNVPYIYAIGDILEGK	LELTP	3		988.5136439	2962.517532	0.000451244	4	N	426	453
Q9QUH0	Conv	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3		1060.877756	3179.609869	0.000451244	13	N	39	68
Q9QUI0	Conv	TPEVK	HFCPNVPIILVGNKK	DLRND	2	C3:+57.021	868.4877324	1734.959865	0.000451244	3	N	104	119
Q9QUI0	Conv	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2		1004.966498	2007.917396	0.000451244	10	N	51	68
Q9QUI0	Conv	IVFSK	DQFPEVYVPTVFENYVADIEVDGK	QVELA	2		1387.16632	2772.317041	0.000451244	10	N	27	51
Q9QUI0	Conv	GACGK	TCLLIVFSK	DQFPE	2	C2:+57.021	540.8100181	1079.604436	0.0007646	9	N	18	27
Q9QUM0	Conv	RRQAF	LQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	C16:+57.021,C22:+57.021,C27:+57.021	1096.188269	3285.541406	0.000451244	30	N	889	919
Q9QUM0	Conv	ANGGK	CNPLLFDLRDETR	NLGFQ	3	C1:+57.021	550.2756079	1647.803424	0.000451244	2	N	95	108
Q9QUM0	Conv	VSNQR	FTYDNSNPVFFDGYR	GYSVA	2		921.4106303	1840.805661	0.000451244	18	N	250	265
Q9QUM0	Conv	QEQTR	IILDCGEDDLCVPQLR	LTATA	2	C5:+57.021,C11:+57.021	958.4663024	1914.917005	0.000451244	17	N	627	643

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QUM0	Conv	RDETR	NLGFQIFQTFK	TGQGL	2		671.8618592	1341.708118	0.000451244	16	N	108	119
Q9QUM0	Conv	VPQLR	LTATAGDSPLLIGADNVLELK	IEAAN	2		1056.083874	2110.152147	0.000451244	21	N	643	664
Q9QUM0	Conv	FQTFK	TGQGLGASVVSWNDVIVACAPWQHWNVLEK	RDEAE	3	C19:+57.021	1107.887667	3320.639601	0.000451244	18	N	119	149
Q9QUM0	Conv	VNGLR	LLIHIPGQSQPSDLLYILDVQPQGGLLCSTQPSPK	VDWKL	3	C28:+57.021	1271.680394	3812.017782	0.000451244	23	N	828	863
Q9QUM0	Conv	GFSLR	GAVDIDDNGYPDLIVGAYGASK	VAVYR	2		1105.534745	2209.05389	0.000451244	13	N	452	474
Q9QUM0	Conv	FLQPK	GPQALSTPTLLLTGTQLYGR	FGSAI	2		1044.078926	2086.142251	0.000451244	17	N	365	385
Q9QUM0	Conv	ANGGK	CNPLLFDLR	DETRN	2	C1:+57.021	574.3003488	1146.585098	0.000622848	9	N	95	104
Q9QUM0	Conv	GLLAR	VPIENIISSYRPGTLLWHVSNQR	FTYDN	3		893.8175553	2678.429266	0.000451244	15	N	227	250
Q9QUM0	Conv	GLSPR	PSQVLDSPFPTGSGFGFSLR	GAVDI	2		1048.526526	2095.037452	0.000451244	18	N	432	452
Q9QUM0	Conv	GDLNR	DGYNDIAVAAPYGGPSGQGQVLIFLGQSEGLSPR	PSQVL	3		1145.239465	3432.694996	0.000622848	8	N	398	432
Q9QUM0	Conv	VLEKR	DEAEKTPVGGCFLAQLQSGGR	AEYSP	2	C11:+57.021	1110.539607	2219.063615	0.000622848	8	N	150	171
Q9QUM0	Conv	VDFHK	DKHGSVSIVVGAPR	ALNAS	3		474.6006859	1420.778658	0.002727428	1	N	58	72
Q9QUM0	Conv	DEAEK	TPVGGCFLAQLQSGGR	AEYSP	2	C6:+57.021	824.4175041	1646.819408	0.000622848	1	N	155	171
Q9QUM0	Conv	RWVSR	LEHTYELHNIGPGTVNGLR	LLIHI	2		1060.548324	2119.081048	0.000451244	4	N	809	828
Q9QUM9	Conv	AGFDR	HITIFSPEGR	LYQVE	2		578.8096266	1155.603653	0.000451244	9	N	11	21
Q9QUM9	Conv	KVPDK	LLDSSTVTHLFK	ITESI	2		680.8777063	1359.739813	0.000451244	7	N	59	71
Q9QUM9	Conv	NPKFR	ILTEAEIDAHLVALAERD	-	2		990.0263587	1978.037117	0.000451244	16	N	228	246
Q9QUM9	Conv	SPEGR	LYQVEYAFK	AINQG	2		580.8034786	1159.591357	0.000998612	7	N	21	30
Q9QUM9	Conv	EYAFK	AINQGGLTSVAVR	GKDCA	2		643.3652974	1284.714995	0.000451244	13	N	30	43
Q9QUM9	Conv	PQVYK	CDPAGYYCGFK	ATAAG	2	[0:-17.027,C1:+57.021,C8:+57.021	660.7546571	1319.493714	0.001162105	2	N	153	164
Q9QUR6	Conv	EGEAR	VFLDPNTLSDDGTVALR	GYAFS	2		916.9735948	1831.93159	0.000451244	14	N	111	128
Q9QUR6	Conv	ILANK	QNCFDDFQCAAEYLIK	EGYTS	2	C3:+57.021,C9:+57.021	1011.440285	2020.864969	0.000451244	18	N	523	539
Q9QUR6	Conv	LKWVK	LIDNFEGEYDYVTNEGTVFTFK	TNRNS	2		1301.105731	2600.195863	0.000451244	14	N	281	303
Q9QUR6	Conv	YHGHK	ICDPYSWLEDPDSEQTK	AFVEA	2	C2:+57.021	1041.951968	2081.888335	0.000451244	14	N	23	40
Q9QUR6	Conv	VACVR	SNFLVLCYLHDVK	NILQL	2	C7:+57.021	804.4164414	1606.817283	0.00307782	1	N	345	358
Q9QUR6	Conv	ESKWK	VLVPEHEKDVLEWVACVR	SNFLV	3	C16:+57.021	726.7177479	2177.129844	0.000451244	6	N	327	345
Q9QUR6	Conv	KKGKR	YFYFYNTGLQNQR	VLYVQ	2		857.4051509	1712.794702	0.000451244	1	N	85	98
Q9QUR6	Conv	SPNYR	LINIDFTDPDESKWK	VLVPE	2		910.9574134	1819.899227	0.000451244	2	N	312	327
Q9QUR6	Conv	LHSLK	FIATLQYIVGR	SRKQS	2		640.8722269	1279.728854	0.000823681	2	N	651	662
Q9QUR6	Conv	NLHQK	LCYHVLGTDQSEDILCAEFPDEPK	WMGGA	3	C2:+57.021,C16:+57.021	946.0985395	2835.272219	0.000451244	7	N	209	233
Q9QUR6	Conv	LQNQR	VLYVQDSLEGEAR	VFLDP	2		739.8784346	1477.741269	0.000451244	7	N	98	111
Q9QUR6	Conv	EAQNK	ITVPFLEQCPIR	GLYKE	2	C9:+57.021	736.9004272	1471.785254	0.001162105	1	N	48	60
Q9QUR6	Conv	EVTVK	GIDAADYQTIQIFYPSK	DGTKI	2		965.4837953	1928.951991	0.000451244	4	N	428	445
Q9QUR6	Conv	GALLK	TFPLDVGSVVGYSGR	KKDSE	2		777.4020769	1552.788554	0.002884417	1	N	373	388
Q9QWK4	Conv	EVLHK	GSWGSVCDDNWGEKEDQVVCK	QLGCG	2	C7:+57.021,C20:+57.021	1228.018147	2454.020695	0.000451244	1	N	264	285
Q9QWK4	Conv	PGAGR	IWLDDVNCSGKEQSLEFCR	HRLWG	2	C8:+57.021,C18:+57.021	1178.538519	2355.061437	0.000622848	1	N	309	328
Q9QWK4	Conv	AVVCR	ELNCGAVIQTPR	GASYQ	2	C4:+57.021	679.3485587	1356.681517	0.000451244	2	N	66	78
Q9QWK4	Conv	HCQGR	VEVLHQSQWSTVCK	AGWNL	2	C13:+57.021	850.9251619	1699.834724	0.001591523	1	N	153	167
Q9QWR8	Conv	IPDPK	RFPHGIAFLADYAHSLGLK	LGIYE	4		529.039519	2112.126876	0.000637154	5	N	96	115
Q9QWR8	Conv	QDSWK	SVLSILDWFVR	HQDVL	2		667.8775093	1333.739419	0.000451244	5	N	223	234
Q9QXD6	Conv	SSAVR	QAGIAQLYGIAGSTNVTGDQVK	KLDIL	2		1096.071829	2190.128058	0.000451244	7	N	50	72
Q9QXK3	Conv	GPLFK	SSEPVQLTEAETEYFVR	CVKHM	2		992.9790741	1983.942548	0.000823681	3	N	629	646
Q9QXK3	Conv	SALAK	FGAQNESLLPSILVLLQR	CMMDT	2		999.5732791	1997.130958	0.000451244	5	N	497	515
Q9QXS1	Conv	EEAER	LKQSAEEQAQAQAQAQAAAEK	LRKEA	3		733.7053783	2198.092735	0.000451244	4	N	2261	2282
Q9QXS1	Conv	EEALR	LLDAQLATGGIVDPR	LGFHL	2		769.9310016	1537.846403	0.001591523	1	N	3942	3957
Q9QXS1	Conv	ITGQR	LLEAQACTGGIIDPSTGERFPVTEAVNK	GLVDK	3	C7:+57.021	991.8380904	2972.490871	0.000622848	3	N	4454	4482
Q9QXS1	Conv	IVDPR	LGFHLPLEVAYQR	GYLNK	3		514.9529481	1541.835444	0.000451244	1	N	3957	3970
Q9QXS1	Conv	ESAWR	YLYGTGAVAGVYLPGSR	QTLTI	2		872.4573835	1742.899167	0.000451244	1	N	3828	3845
Q9QXS1	Conv	EAGQR	FLEVQYLTGGLIEPDTPGR	VSLDE	2		1053.049834	2104.084068	0.000451244	8	N	4530	4549
Q9QXS1	Conv	EALKK	DLLQPEVAVALLEAQAGTGHIIDPATSAR	LTVDE	3		986.1966492	2955.566548	0.000451244	18	N	3190	3219
Q9QXS1	Conv	TALQR	QLLSPGTALILLEAQAASGFLLDPVR	NRRLT	3		898.5132499	2692.51635	0.000451244	11	N	2862	2888
Q9QXS1	Conv	FEGLR	ALVPAAELLDSGVISHELYQQLQR	GERSV	3		884.1453376	2649.412613	0.000451244	4	N	3122	3146
Q9QXS1	Conv	SDDTK	GFFDPNTHENLTYLQLLER	CVEDP	3		769.7188477	2306.133143	0.000451244	7	N	2995	3014
Q9QXS1	Conv	YEDLR	DGHNLISLLEVLSGDSLPR	EKGRM	3		679.0326552	2034.074566	0.000451244	5	N	219	238
Q9QYB5	Conv	ASLYR	LADLFGWAHLANTYISVR	ISKEQ	3		683.0306974	2046.068692	0.000451244	11	N	146	164
Q9QYB5	Conv	VSSMK	CGILPISQESLILGDVAYYDYQGSLDEEEERIELQK	VLGPS	3	C1:+57.021	1391.679224	4172.014273	0.001591523	2	N	244	280
Q9QYC0	Conv	EDGHR	TSTSAVPNLFVPLNTNPK	EVQEM	2		950.5128871	1899.010174	0.000451244	8	N	479	497
Q9QYC0	Conv	HITTR	VNSEQEHFLIVPFGLLYSEVTASSLVK	VNLQG	3		1002.866129	3005.574987	0.000451244	10	N	172	199
Q9QYC0	Conv	VSAMK	CGLLPISPEALSLGDVAYHDYHGILVDEEEK	ILIQK	4	C1:+57.021	860.6740182	3438.664873	0.000451244	7	N	252	283
Q9QYC0	Conv	ERSKK	YSDVEVPASVTGHSFASDGDSGTCSPLR	HSFQK	3	C24:+57.021	966.7667717	2897.276915	0.000451244	6	N	406	434
Q9QYC0	Conv	AAFYR	LADLFGWSQLIYNHITTR	VNSEQ	2		1074.565985	2147.116371	0.002981883	1	N	154	172
Q9QYJ0	Conv	HMTYK	IGLVEALCGFQFTFK	HLDAR	2	C8:+57.021	865.4530239	1728.890448	0.001329271	2	N	272	287
Q9QZD9	Conv	CNDSK	ITSAVWGPLGECVIAGHESGELNQYSAK	SGEVL	3	C12:+57.021	991.8189187	2972.433356	0.000451244	7	N	148	176
Q9QZD9	Conv	KFEAR	FFHLAFEEEFGR	VKGHF	3		510.2460202	1527.71466	0.000979378	6	N	268	280
Q9QZD9	Conv	IKYNR	EGDLLFTVAKDPIVNVWYSVNGER	LGTYM	3		907.8014595	2720.380978	0.000451244	5	N	20	44

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QZD9	Conv	DGYVR	IHYFDPQYFEFEFEA	-	2		991.4363138	1980.857028	0.00307782	1	N	310	325
Q9QZE5	Conv	GPLFK	SSPEPVALTESETEYVIR	CTKHT	2		1004.000007	2005.984413	0.000451244	4	N	631	649
Q9QZE5	Conv	QKVMK	VNFEAAWDEVGDEFEKEETFTLSTIK	TLEEA	3		1012.145509	3033.413126	0.000735798	5	N	769	795
Q9QZE5	Conv	KFTVK	DCDPNTGEIDEEGYEDEYVLEDLEVTVADHIQK	VMKVN	3	C2:+57.021	1280.558552	3838.652255	0.000451244	4	N	733	766
Q9QZF2	Conv	KAQLR	DIQDFWISLPGTLCSEK	MAMSP	2	C14:+57.021	1004.988156	2007.960713	0.000622848	9	N	386	403
Q9QZK7	Conv	RRVIR	LADCVSVLPADGESCPR	DTGAF	2	C4:+57.021,C15:+57.021	923.4271772	1844.838754	0.000451244	3	N	73	90
Q9QZK7	Conv	FSSPR	APDICGVVAAAIAR	QRERL	2	C5:+57.021	692.3745765	1382.733553	0.000451244	7	N	239	253
Q9QZK7	Conv	LPTPR	KLPLTDPGPQSLPLLLSPTQEGPASGLYASVCK	QTSKH	3	C32:+57.021	1145.613209	3433.816228	0.000979378	2	N	297	330
Q9QZQ8	Conv	GLPAK	FVIHCNSPVWGADKCEELLEK	TVKNC	3	C5:+57.021,C15:+57.021	844.4069791	2530.197537	0.000451244	26	N	271	292
Q9QZQ8	Conv	NQLLK	GVTIASGGVLPNIHPELLAK	KRGSK	2		993.5732791	1985.130958	0.000451244	19	N	96	116
Q9QZQ8	Conv	TLEKK	GGKEFVEAVLELR	KKNGP	2		723.9017127	1445.787825	0.000622848	1	N	236	249
Q9QZQ8	Conv	KKGGK	EFVEAVLELR	KKNGP	2		602.8327674	1203.649935	0.000622848	9	N	239	249
Q9QZQ8	Conv	FLGQK	LNLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	4		1063.05284	4248.180161	0.000451244	7	N	196	235
Q9QZQ8	Conv	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	2		1488.299689	2974.583779	0.000451244	26	N	40	69
Q9QZQ8	Conv	GEVSK	AASADSTTEGTPTDGFTVLSTK	SLFLG	2		1079.013842	2156.012085	0.000998612	38	N	167	189
Q9QZQ8	Conv	DRKLK	SIAFPSIGSGR	NGFPK	2		546.2963521	1090.577104	0.000451244	8	N	307	318
Q9QZQ8	Conv	GEVSK	AASADSTTEGTPTDGFTVL	STKSL	2		920.9265072	1839.837414	0.001162105	4	N	167	186
Q9QZQ8	Conv	KRGSK	GKLEAIITPPPAK	KAKSP	2		667.9062668	1333.796934	0.000622848	5	N	121	134
Q9QZQ8	Conv	GSKGK	LEAIITPPPAK	KAKSP	2		575.3480533	1148.680507	0.000622848	2	N	123	134
Q9QZQ8	Conv	ELRKK	NGPLEVAGAAISAGHGLPAK	FVIHC	2		915.4975714	1828.979543	0.000451244	4	N	251	271
Q9QZQ8	Conv	NQLLK	GVTIASGGVLPNIHPELL	AKKRG	2		894.0072406	1785.998881	0.000451244	11	N	96	114
Q9QZQ8	Conv	QLILK	AISSYFVSTMSSSIK	TVYFM	2	M10:+15.995	812.4009286	1622.786257	0.000451244	10	N	332	347
Q9QZQ8	Conv	RVTPR	HILLAVANDEELNQLLKGVTIASGGVLPNIHPELLAK	KRGSK	4		975.8049054	3899.188422	0.000823681	5	N	79	116
Q9QZQ8	Conv	NQLLK	GVTIASGGVLPNIHPEL	LAKKR	2		837.4652086	1672.914817	0.000451244	6	N	96	113
Q9QZU3	Conv	GPEPR	ASLSFWELLQGDPWCPDPR	SLPLD	2	C15:+57.021	1137.536336	2273.057073	0.000451244	14	N	457	476
Q9QZU3	Conv	VKLEK	LLLYSNQLTSVDSGLLSNLGALTELR	LERNH	2		1395.766536	2789.517472	0.000451244	17	N	198	224
Q9QZU3	Conv	FQQLR	NLQELGLNQNQLSFLPANLFSSLR	ELKLL	2		1358.725005	2715.434411	0.000451244	6	N	146	170
Q9QZU3	Conv	AILDK	MVLLEQLFLDHNALR	DLDQN	2		906.4959863	1810.976373	0.002019181	3	N	120	135
Q9QZU3	Conv	VKLEK	LLLYSNQLTSVDSGLLSNLGALTELRLER	NHLRS	3		1063.589547	3187.745241	0.000451244	3	N	198	227
Q9QZU3	Conv	SSVSR	LTLFENPLEELPDVLFGEMAGLR	ELWLN	2		1302.175437	2602.335275	0.000451244	5	N	270	293
Q9QZU3	Conv	HNALR	DLDQNLFQQLR	NLQEL	2		695.360212	1388.704824	0.000698008	3	N	135	146
Q9QZU3	Conv	LRELR	VLALHTNALAELRDDALR	GLGHL	4		498.5317924	1990.09597	0.000698008	2	N	342	360
Q9R062	Conv	NPQTK	SVNCDSQDPTVSHPEFLNLWWDTFTTNVLPLLQHHGLVK	DASSY	4	C4:+57.021	1137.063264	4544.221855	0.000451244	14	N	229	268
Q9R062	Conv	DAYAK	GALVLGSSLK	QHRTT	2		472.7929139	943.5702278	0.001654178	3	N	17	27
Q9R062	Conv	HGLVK	DASSYLMMEHVSGALSDLSFGEAPAAPQPSMSSEER	KERWE	3	M7:+15.995,M8:+15.995,M31:+15.995	1278.226214	3831.655243	0.000451244	18	N	268	304
Q9R062	Conv	SIETY	NQLLHLASEQGSFDGGDQGLLNTYFSGWATTDITK	HLPFV	3		1262.275015	3783.801646	0.000451244	7	N	146	181
Q9R062	Conv	HFLGR	TKPWNYTYNPQTK	SVNCD	2		820.9075264	1639.799453	0.000622848	9	N	216	229
Q9R062	Conv	ERKER	WEQGQADYMGADSFDNIKR	KLDTY	2	M9:+15.995	1123.992764	2245.969929	0.000451244	6	N	307	326
Q9R062	Conv	ITLTK	LHCWSLTQYSK	CVFMD	2	C3:+57.021	711.8456519	1421.675704	0.001162105	5	N	86	97
Q9R062	Conv	NPQTK	SVNCDSQDPTVSHPEFLNLWWDTFTTN	VLPLL	3	C4:+57.021	1070.808859	3209.403178	0.000823681	4	N	229	256
Q9R062	Conv	MMEHV	SGALSDLSFGEAPAAPQPSMSSEER	KERWE	2	M20:+15.995	1269.077223	2536.138845	0.001654178	1	N	279	304
Q9R062	Conv	ERKER	WEQGQADYMGADSFDNIK	RKLDT	2	M9:+15.995	1045.942209	2089.868818	0.000823681	2	N	307	325
Q9R062	Conv	TYNQL	LHLASEQGSFDGGDQGLLNTYFSGWATTDITK	HLPFV	3		1143.879826	3428.616077	0.001591523	1	N	149	181
Q9R0E1	Conv	QPPPR	VLLAVFVEQPTPFLPR	FLQRL	2		913.5328942	1825.050188	0.002453667	2	N	300	316
Q9R0E1	Conv	HQIVR	QWNYKDDDDDQLFYTQLYLDPGLR	EKLKL	3		1007.802076	3020.382829	0.002813207	2	N	184	208
Q9R0N0	Conv	QVCQR	AEHSFAGVPCGIMDQLIALLGQK	GYALL	3	C10:+57.021	819.0876239	2454.239472	0.000451244	2	N	172	195
Q9R0N0	Conv	DEPQR	LQFPLPSAQWSLEPGIPQWANYVK	GVIQH	3		923.8186733	2768.43262	0.002374549	1	N	87	111
Q9R0P3	Conv	PGKYR	SVSAFAPICNPVLCSWGK	KAFSG	2	C9:+57.021,C14:+57.021	996.987205	1991.95881	0.000451244	13	N	167	185
Q9R0P3	Conv	TCLVK	AYSGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	3	C34:+57.021	1362.660164	4084.957092	0.000622848	19	N	209	246
Q9R0P3	Conv	NFISK	SGYQQAASEHGLVVIAPDTSPR	GCNIK	2		1142.07236	2282.12912	0.000451244	10	N	64	86
Q9R0P3	Conv	PVVFR	LQEGYDHSYYFIATFIADHIR	HHAKY	3		853.748807	2558.223021	0.000451244	3	N	253	274
Q9R0P3	Conv	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	C1:+39.994,C12:+57.021	1186.05833	2370.101061	0.000451244	1	N	44	64
Q9R0P3	Conv	NYRMY	SYVTEELPQLINANFPVDPQR	MSIFG	2		1215.619143	2429.222687	0.001264573	2	N	121	142
Q9R0P3	Conv	DTSPR	GCNIKGEDDSWDFGTGAGFYVNATEDPWK	ANYRM	3	C2:+57.021	1079.468614	3235.382443	0.001352548	1	N	86	115
Q9R0P3	Conv	KANYR	MYSYVTEELPQLINANFPVDPQR	MSIFG	2		1362.671051	2723.326501	0.00091018	1	N	119	142
Q9R0P5	Conv	KKRKK	AVIFCLSADKK	CIVVE	2	C5:+57.021	626.3422137	1250.668827	0.001162105	3	N	34	45
Q9R0P5	Conv	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	C1:+39.994	1286.664445	2571.31329	0.000451244	6	N	45	69
Q9R0P5	Conv	CIAEK	LGGSLIVAFEGSPV	-	2		673.3722568	1344.728914	0.000451244	21	N	151	165
Q9R0P5	Conv	VEEGK	EILVGDVGATITDPFK	HFVGM	2		837.9515997	1673.887599	0.000451244	3	N	53	69
Q9R0P5	Conv	TKESR	KEELMFFLWAPEQAPLK	SKMIY	3		693.0329394	2076.075418	0.001264573	2	N	95	112
Q9R0Q7	Conv	FEKSK	LTFSCLGGSDNFK	HLNEI	2	C5:+57.021	723.3403994	1444.665199	0.000451244	3	N	35	48
Q9R0Q7	Conv	SDNFK	HLNEIDLFHCIDPNDSK	HKRTD	3	C10:+57.021	689.6585577	2065.952273	0.001463592	1	N	48	65
Q9R0X4	Conv	PRKMR	DSYIEVLLPLGTDPELR	DKYVT	2		965.5125528	1929.009506	0.000823681	2	N	83	100
Q9R111	Conv	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	2		1256.127864	2510.240128	0.000451244	4	N	231	252

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9R111	Conv	AVIQK	FLYLGDDRNIEEVYVGGK	QVVPF	2		1044.026359	2086.037117	0.000451244	19	N	427	445
Q9R111	Conv	LINPR	ASDSPIDLFYGDFVGDISEAVIQK	FLYLG	2		1293.634656	2585.253712	0.000451244	36	N	403	427
Q9R111	Conv	RRTLK	NGTTTACYFGTIHTDSSLILAEITDKFGQR	AFVGK	3	C7:+57.021	1106.542114	3316.602941	0.000451244	6	N	133	163
Q9R111	Conv	IFSER	GASIAHCPNSNLSLSSGLLNVLEVLK	HKVKI	2	C7:+57.021	1347.218467	2692.421335	0.000451244	5	N	294	320
Q9R111	Conv	KEVFR	LATLGGSQALGLDSEIGNFEVGKEFDALLINPR	ASDSP	3		1148.939016	3443.793647	0.000451244	35	N	370	403
Q9R111	Conv	YPSYK	NYTDVYDKNNLLTNK	TVMAH	2		907.9501196	1813.884639	0.000451244	16	N	259	274
Q9R111	Conv	EQRFR	STDVAEEVYTR	VVRRT	2		635.3020284	1268.588457	0.000451244	12	N	115	126
Q9R111	Conv	SDSGK	IVFLEESSQQEK	LAKEW	2		718.8675356	1435.719471	0.000451244	42	N	41	53
Q9R111	Conv	FEVGK	EFDALLINPR	ASDSP	2		594.3251095	1186.634619	0.000735798	5	N	393	403
Q9R111	Conv	KEVFR	LATLGGSQALGLDSEIGNFEVGK	EFDAL	2		1138.592594	2275.169588	0.000451244	17	N	370	393
Q9R111	Conv	RRTLK	NGTTTACYFGTIHTDSSLILAEITDK	FGQRA	3	C7:+57.021	943.7922581	2828.353374	0.000451244	19	N	133	159
Q9R111	Conv	IVTPR	FTLSCTETLMSELGNIAK	THDLY	2	C5:+57.021	1007.995125	2013.974649	0.000451244	17	N	213	231
Q9R111	Conv	KHKVK	IGLGTDVAGGYSYSMLDAIR	RAVMV	2		1030.012395	2058.009189	0.000451244	6	N	324	344
Q9R111	Conv	GSQAL	GLDSEIGNFEVGKEFDALLINPR	ASDSP	3		845.1031384	2532.286015	0.001162105	1	N	380	403
Q9R1P0	Conv	LIAQR	YLLQYQEPIPCEQLVTALCDIK	QAYTQ	2	C11:+57.021,C19:+57.021	1347.679566	2693.343533	0.000451244	22	N	96	118
Q9R1P0	Conv	RNIHK	LLDEVFFSEK	IYKLN	2		613.8193257	1225.623051	0.000735798	14	N	54	64
Q9R1P0	Conv	QFGGK	RPFGVSLLYIGWDK	HYGFQ	2		825.9542797	1649.892959	0.000451244	5	N	127	141
Q9R1P0	Conv	SPEGR	LYQVEYAMEAIGHAGTCLGILANDGVLLAAER	RNIHK	3	C17:+57.021	1140.243011	3417.705633	0.00091018	2	N	17	49
Q9R1P0	Conv	IGWDK	HYGFQLYQSDPSGNYGGWK	ATCIG	2		1102.495757	2202.975914	0.000451244	3	N	141	160
Q9R1P0	Conv	MDVSK	LSAEKVEIATLTR	ESGKT	2		715.9148201	1429.81404	0.001329271	3	N	205	218
Q9R1P0	Conv	EKIYK	LNEDMACSVAGITSDANVLTNELR	LIAQR	2	C7:+57.021	1297.115551	2592.215502	0.000451244	5	N	67	91
Q9R1P0	Conv	YGGWK	ATCIGNNSAAAVSMLK	QDYKE	2	C3:+57.021	804.3979233	1606.780247	0.000451244	1	N	160	176
Q9R1P1	Conv	LYEKR	FGPYYTEPVIAGLDPK	TFKPF	2		883.9541423	1765.892685	0.000451244	14	N	99	115
Q9R1P1	Conv	PMGDR	LYIGLAGLATDVQTVAQR	LKFRL	2		945.0287044	1888.041809	0.000451244	18	N	48	66
Q9R1P3	Conv	KMSEK	ILLLCVGEAGDTVQFAEYIQK	NVQLY	2	C5:+57.021	1184.117159	2366.218718	0.000451244	23	N	41	62
Q9R1P3	Conv	LYKMR	NGYELSPTAAANFTR	RNLAD	2		806.3922405	1610.768881	0.000451244	19	N	70	85
Q9R1P3	Conv	AALAK	APFAAHGYGAFLTLSILDR	YYTPT	2		1010.536697	2019.057793	0.000451244	4	N	126	145
Q9R1P3	Conv	TFSVR	VIDKDGIHNLENIAFPK	RDS-	2		962.0208793	1922.026159	0.000451244	18	N	181	198
Q9R1P3	Conv	LAKAP	FAAHGYGAFLTLSILDR	YYTPT	3		617.9971051	1850.967915	0.002727428	1	N	128	145
Q9R1P3	Conv	KMSEK	ILLLCVGEAGDTVQF	AEYIQ	2	C5:+57.021	817.926839	1633.838078	0.001699387	1	N	41	56
Q9R1P3	Conv	ELQKR	FILNLPTFSVR	VIDKD	2		653.880052	1305.744504	0.000451244	5	N	170	181
Q9R1P3	Conv	KILLL	CVGEAGDTVQFAEYIQK	NVQLY	2	C1:+57.021	957.9490311	1913.882462	0.000451244	3	N	45	62
Q9R1P4	Conv	GIVGK	DLEFTIYDDDDVSPFLDGLEERPQRK	AQPSQ	3		1038.163562	3111.467287	0.000451244	14	N	217	243
Q9R1P4	Conv	-MFR	NQYDNDVTVWSPQGR	IHQIE	2		889.9087861	1777.801972	0.000451244	29	N	3	18
Q9R1P4	Conv	GIVGK	DLEFTIYDDDDVSPFLDGLEERPQR	KAQPS	3		995.4652413	2983.372324	0.000451244	11	N	217	242
Q9R1P4	Conv	LRALR	ETLPAEQDLTTK	NVSIG	2		673.346436	1344.677272	0.000622848	3	N	196	208
Q9R1P4	Conv	AHQKK	ILHVDNHIGISIAGLTADAR	LLCNF	2		1043.574342	2085.133084	0.002145581	1	N	62	82
Q9R1P4	Conv	QRYGR	RPYGVGLLIAGYDDMGPHIFQTCPSANYFDCR	AMSIG	3	M15:+15.995,C23:+57.021,C31:+57.021	1236.234284	3705.679452	0.000451244	6	N	125	157
Q9R1P4	Conv	CLDSR	FVFDRPLPVSR	LVSLI	3		444.9194673	1331.735002	0.001329271	3	N	96	107
Q9R1T2	Conv	AALKR	TAPDYFLLQVLLK	FRTDK	2		760.9403066	1519.865013	0.000451244	5	N	239	252
Q9R1T2	Conv	LLQIR	NDVFDSLGISPDLLPDDFVR	YCFSE	2		1117.552938	2233.090275	0.000451244	19	N	277	297
Q9R1T2	Conv	-M	VEKEEAGGGGGGGISEEEAAQYDR	QIRLW	3		799.0268458	2394.057137	0.000622848	4	N	1	25
Q9R1T4	Conv	QLVNK	SVSQGFCFNILCVGETGLGK	STLMD	2	C7:+57.021,C12:+57.021	1087.024516	2172.033432	0.000622848	1	N	35	55
Q9R1T4	Conv	LFNTK	FEGEPATHTQPGVQLQSNTYDLQESNVGLK	LTIVS	3		1096.532537	3286.574212	0.002019181	1	N	66	96
Q9R257	Conv	LGMIR	NSLFGSVETWPWQVLSTGGKEDVSYEER	ACEGG	3		1067.511074	3199.509821	0.000451244	4	N	6	34
Q9WTL7	Conv	SGAER	ETAAVIFLHGLGDTGHSWADALSTIR	LPHVK	3		913.4685918	2737.382375	0.000451244	2	N	22	48
Q9WTP6	Conv	YYRKR	GIHCAIDASQTPDIVFASILAAFSK	ATCKD	3	C4:+57.021	878.1198693	2631.336208	0.000451244	10	N	204	229
Q9WU28	Conv	LEMLK	NQLDQEVEFLSTSIAQLK	VVQTK	2		1032.036923	2062.058247	0.000451244	13	N	19	37
Q9WU28	Conv	YVPGK	LHDVEHVLIDVGTGYYVEK	TAEDA	3		729.3763105	2185.105531	0.001763695	1	N	75	94
Q9WU78	Conv	KPLVK	FIQQTYPSGGEEQAQYCR	AAEEL	2	C17:+57.021	1081.484301	2160.953001	0.000451244	19	N	23	41
Q9WU78	Conv	KEGTK	FYNELTEILVR	FQNKC	2		698.8777063	1395.739813	0.000451244	7	N	675	686
Q9WU78	Conv	EEVLK	NLATAYDNFVELVANLK	EGTKF	2		947.9996126	1893.983625	0.000451244	15	N	654	671
Q9WU78	Conv	IAQMR	EATTLANGVLASLNLPAAIEDVSGDTVPQSILTK	STSVV	3		1136.942315	3407.803544	0.000451244	14	N	386	420
Q9WU78	Conv	SILTK	STSVVEQGGIQTVDQLIK	ELPEL	2		951.5130841	1901.010568	0.000451244	21	N	420	438
Q9WU78	Conv	LGYEK	SCVLFNCAALASQIAAEQNLDNDEGLK	TAAKQ	3	C2:+57.021,C7:+57.021	984.4675145	2950.379143	0.000451244	5	N	120	147
Q9WU78	Conv	DMTSK	FLTALAQDGVINEEALSVTELDR	IYGGL	2		1252.648098	2503.280596	0.000451244	16	N	583	606
Q9WU78	Conv	EESLR	LLDEEEATDNDLR	AKFKD	2		766.8578962	1531.700192	0.000451244	2	N	456	469
Q9WU78	Conv	AIIAK	LANQAADYFGDAFK	QCQYK	2		765.8653272	1529.715054	0.000451244	9	N	215	229
Q9WU78	Conv	YQSHR	DTIALLCKPEPELNAAIPSANPAK	TMQGS	2	C7:+57.021	1267.170454	2532.325309	0.000451244	4	N	517	541
Q9WU78	Conv	FLTAL	AQDGVINEEALSVTELDR	IYGGL	2		979.9874305	1957.959261	0.000622848	1	N	588	606
Q9WUA2	Conv	VYYNK	TPGFEIIHGLLDR	IMQLL	3		489.9371866	1466.78816	0.000451244	6	N	504	517
Q9WUA3	Conv	YTGAK	VYFIYEGYQGLVDGGSNIVEAK	WDCVS	2		1211.102795	2420.189989	0.000451244	2	N	55	77
Q9WUM3	Conv	ASYSR	SGASTATAVTDVPSGNLAGAGEAGKLEEVMQELR	ALRML	3		1106.216221	3315.625263	0.000451244	11	N	422	456
Q9WUM3	Conv	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	3		1420.692675	4259.054626	0.000451244	13	N	354	393

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9WUM3	Conv	IRVSR	VTWDSTFCAVNPK	FLAVI	2	C8:+57.021	762.861499	1523.707398	0.000451244	4	N	33	46
Q9WUM3	Conv	ASYSR	SGASTATAVTDVPSGNLAGAGEAGK	LEEVM	2		1095.038183	2188.060766	0.001943752	1	N	422	447
Q9WUM3	Conv	TAGPE	AALEAEDWVSGQDANPILISLR	EAYVP	2		1184.611318	2367.207037	0.000451244	10	N	371	393
Q9WUM3	Conv	DSSIR	YFEITDEPPYIHFLNTFTSK	EPQRG	3		821.4025253	2461.184176	0.000870037	1	N	293	313
Q9WUM4	Conv	IRVSR	VTWDSSFCAVNPR	FVAII	2	C8:+57.021	769.8567479	1537.697896	0.000451244	6	N	31	44
Q9WUM4	Conv	ARPMR	AIFLADGNVFTTGFSR	MSERQ	2		858.4417334	1714.867867	0.000451244	14	N	223	239
Q9WUM4	Conv	MTVPR	KSDLFQDDLYPDTAGPEAALEAEEWFEGK	NADPI	3		1091.170494	3270.488082	0.000451244	22	N	352	381
Q9WUM4	Conv	DSSIR	YFEITDESPYVHYLNTFSSK	EPQRG	3		814.0501516	2439.127055	0.000451244	11	N	291	311
Q9WUM4	Conv	WFEGK	NADPILISLK	HGYIP	2		542.3245782	1082.633556	0.000998612	2	N	381	391
Q9WV32	Conv	AKWNK	VHELKEHNGQVTGIDWAPESNR	IVTCG	2		1258.617998	2515.220395	0.000662267	2	N	44	66
Q9WV32	Conv	WNKDR	TQIAICPNNHEVHIYEK	SGAKW	2	C6:+57.021	1033.510122	2065.004643	0.000451244	16	N	20	37
Q9WV32	Conv	DSLHK	NSVSQISVLSGGK	AKCSQ	2		638.349313	1274.683026	0.000451244	13	N	326	339
Q9WV32	Conv	KKPIR	STVLSLDWHPNNVLLAAGSCDFK	CRIFS	2	C20:+57.021	1272.631496	2543.247393	0.000451244	20	N	142	165
Q9WV32	Conv	GSGSR	VISICYFEQENDWWVCK	HIKKP	2	C5:+57.021,C16:+57.021	1138.511241	2275.006883	0.000451244	16	N	118	135
Q9WV32	Conv	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	2	C11:+57.021	1015.504505	2028.99341	0.000451244	18	N	216	234
Q9WV32	Conv	QNLDK	KASSEGGAATGAGLDSLHK	NSVSQ	3		586.2995124	1755.875137	0.000451244	2	N	307	326
Q9WV32	Conv	NLDKK	ASSEGGAATGAGLDSLHK	NSVSQ	2		814.897887	1627.780174	0.000451244	4	N	308	326
Q9WV32	Conv	VHELK	EHNGQVTGIDWAPESNR	IVTCG	2		955.4435244	1908.871449	0.000451244	15	N	49	66
Q9WV32	Conv	HAWNK	DRTQIAICPNNHEVHIYEK	SGAKW	3	C8:+57.021	779.7186991	2336.132697	0.000451244	1	N	18	37
Q9WV32	Conv	ARCVR	WAPNENKFAVGSGSR	VISIC	3		540.6028666	1618.7852	0.000451244	3	N	103	118
Q9WV32	Conv	GGKAK	CSQFCTTGMDGGMSIWDVK	SLESA	2	C1:+57.021,C5:+57.021,M9:+15.995,M13:+15.995	1106.44447	2210.87334	0.000451244	3	N	341	360
Q9WV32	Conv	TVLSL	DWHPNNVLLAAGSCDFK	CRIFS	2	C14:+57.021	972.4573576	1942.899115	0.001264573	1	N	148	165
Q9WV32	Conv	VISIC	YFEQENDWWVCK	HIKKP	2	C11:+57.021	852.3618631	1702.708126	0.000451244	4	N	123	135
Q9WV60	Conv	LPNGR	DTPALFNFTTQELSSNPPLATILIPPHAR	IQAAA	3		1054.559699	3160.655697	0.0025889	1	N	354	383
Q9WVA3	Conv	ISSVK	FSPNTSQFLLVSSWDTSVR	LYDVP	2		1086.04254	2170.06948	0.001162105	2	N	21	40
Q9WVA4	Conv	LAVAR	DDGLFSGDPNWFPKK	SKENP	2		861.9102661	1721.804932	0.000823681	2	N	139	154
Q9WVA4	Conv	QAAER	YGINTTDIFQTVDLWEGK	NMACV	2		1050.518366	2099.021133	0.000451244	23	N	102	120
Q9WVA4	Conv	QKIEK	QYDADLEQILIQWITTQCREDVGQPQPGR	ENFQK	3	C18:+57.021	1153.232051	3456.672752	0.000451244	2	N	20	49
Q9WVA4	Conv	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	C18:+57.021	1197.59184	2393.16808	0.000451244	9	N	20	39
Q9WVA4	Conv	TVLCK	LINSLYPEGQAPVKK	IQASS	2		828.9701268	1655.924654	0.000451244	6	N	64	79
Q9WVA4	Conv	LAVAR	DDGLFSGDPNWFPK	KSKEN	2		797.8627845	1593.709969	0.00091018	3	N	139	153
Q9WVG5	Conv	AFNIR	TSKDPEQEGCNLSLGDSK	LLENC	2	C10:+57.021	982.9472167	1963.878833	0.000622848	1	N	54	72
Q9WVG5	Conv	QPTLY	ITLYGSNADSQNLPLEIVEK	IELNA	2		1102.576413	2203.137226	0.000823681	1	N	369	389
Q9WVG5	Conv	LLKMR	LTWEGVAHSWYNLWNEFR	NYLSQ	3		770.0365111	2307.086133	0.000451244	11	N	413	431
Q9WVG5	Conv	CEHER	AVHLFVDSLVNQDKPSFAFQCTDSSR	FKRGI	3	C21:+57.021	990.1471468	2967.41804	0.000451244	7	N	276	302
Q9WVG5	Conv	GTVGR	ITGLDPAGPMFEGVDINRR	LSPDD	3	M10:+15.995	692.018269	2073.031407	0.001839721	1	N	188	207
Q9WVJ2	Conv	EFEHR	VNPLSLVEIILHVVR	QMTDP	3		567.6860909	1700.034873	0.001591523	1	N	70	85
Q9WVJ2	Conv	RDTDR	QWLIDTLYAFNSGAVDR	FQTLK	2		984.9948615	1967.974123	0.000451244	1	N	230	247
Q9WVJ2	Conv	FQTLK	CAWGQQPDLAANEAQLLR	KIQLL	2	C1:+57.021	1020.999921	2039.984242	0.000451244	2	N	252	270
Q9WVJ2	Conv	DGLIK	LYENFISEFEHR	VNPLS	3		528.5883345	1582.741604	0.001463592	1	N	58	70
Q9WVK4	Conv	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	3		852.1065486	2553.296246	0.000451244	13	N	486	509
Q9WVK4	Conv	PDNRK	LFEAEEQDLFKDIQSLPR	NAALR	2		1089.558023	2177.100446	0.000823681	1	N	269	287
Q9WVK4	Conv	WVVGK	DKPTYDEIFYTLSPVNGK	ITGAN	2		1044.020742	2086.025884	0.000622848	2	N	443	461
Q9WVK4	Conv	HGYGE	GAGEGIDDVEWVVGK	DKPTY	2		765.8758919	1529.736184	0.001162105	2	N	428	443
Q9WVK4	Conv	PEVVR	VYIGSFWSHPLLIPDNR	KLFEA	3		672.0235428	2013.047228	0.000823681	1	N	251	268
Q9Z0H3	Conv	SWHQK	TYAFSENPLPTVEIAIR	NTGDA	2		961.0074376	1919.999275	0.000823681	1	N	324	341
Q9Z0I7	Conv	EILPR	TVSAFANTDGGYLFIGLDEK	KQEIV	2		1059.523649	2117.031698	0.000451244	5	N	217	237
Q9Z0N1	Conv	PIFSK	IVSLFAEHNDLQYAAPGGLIGVGTK	IDPTL	2		1285.684818	2569.354035	0.002212458	1	N	317	342
Q9Z0N1	Conv	ESQAK	EQYEQILAFVQGTVAEGAPIIPISAQLK	YNIEV	3		1005.213529	3012.617186	0.000451244	6	N	201	229
Q9Z0P5	Conv	IRLIK	VIIEDEQLVLGASQEPVGR	WDQDY	2		1026.552741	2051.089881	0.000451244	17	N	29	48
Q9Z0P5	Conv	SCKSR	LLDSVEQDFQLEIAK	KIEIG	2		874.4597889	1746.903978	0.000451244	12	N	278	293
Q9Z0P5	Conv	QDYDR	AVLPLLDAQEPCYLLFR	LDSQN	2	C12:+57.021	1009.542902	2017.070203	0.000451244	11	N	55	72
Q9Z0P5	Conv	YLLFR	LDSQNAQGFEWLFLAWSPDNSPVR	LKMLY	2		1389.170063	2776.324526	0.000451244	4	N	72	96
Q9Z0P5	Conv	YIQLK	LDLERETIELVHTEPTNVAQLPSR	IPRDA	3		920.8229232	2759.44537	0.000451244	6	N	204	228
Q9Z0P5	Conv	AGYQK	HLSSCAAPAPLTSAER	ELQQI	2	C5:+57.021	834.4124187	1666.809237	0.000451244	2	N	136	152
Q9Z0P5	Conv	SVESK	HQTLQGLAFPLQPEAQR	ALQQL	2		967.5162955	1933.016991	0.002212458	1	N	171	188
Q9Z126	Conv	PAVVA	VTSAGPEESDGDLSCVCVK	TISSG	2	C15:+57.021,C17:+57.021	1005.443221	2008.870843	0.000451244	90	N	29	48
Q9Z126	Conv	GIHLK	HITSLEVIK	AGRHC	2		520.3114708	1038.607342	0.001395409	4	N	57	66
Q9Z126	Conv	AVVAV	TSAGPEESDGDLSCVCVK	TISSG	2	C14:+57.021,C16:+57.021	955.9090143	1909.802429	0.000451244	67	N	30	48
Q9Z126	Conv	IKAGR	HCAVPQLIATLK	NGRKI	2	C2:+57.021	675.8820374	1349.748475	0.000451244	85	N	69	81
Q9Z126	Conv	VVAVT	SAGPEESDGDLSCVCVK	TISSG	2	C13:+57.021,C15:+57.021	905.385175	1808.75475	0.000451244	3	N	31	48
Q9Z183	Conv	YPLGR	ILIGNSGYSSSESR	DMHQA	2		735.3656914	1468.715783	0.000622848	4	N	427	441
Q9Z183	Conv	SLLDK	SNPELPEALVFQDSVTFR	VAPWI	2		1025.018534	2048.021467	0.000451244	15	N	274	292
Q9Z183	Conv	QQFSY	CLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C1:+57.021	971.785215	2912.332245	0.000823681	1	N	236	262

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z183	Conv	GPQQF	SYCLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C3:+57.021	1055.150334	3162.427602	0.001329271	4	N	234	262
Q9Z183	Conv	AVLKR	ELGLAEGDIIDIPQLFK	LAGNS	2		936.0121886	1870.008777	0.000451244	13	N	554	571
Q9Z183	Conv	YYGPK	TSPVQALIYITGVELSLSADVTR	TGRVK	2		1217.165926	2432.316253	0.000451244	8	N	100	123
Q9Z183	Conv	LSSPR	ACYQLFQELQSQGHGEATLFEGLK	RKRQT	3	C2:+57.021	918.7782833	2753.31145	0.000451244	4	N	495	519
Q9Z183	Conv	LSSPR	ACYQLFQELQSQGHGEATLFEGLKR	KRQTI	4	C2:+57.021	728.3609403	2909.412561	0.0025889	4	N	495	520
Q9Z183	Conv	PSRYK	VALGPQQFSYCLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C11:+57.021	1335.30013	4002.876991	0.000451244	7	N	226	262
Q9Z1B7	Conv	KTLFK	GKDYLDQLTQILK	VTGVP	3		512.287885	1533.840255	0.000998612	1	N	224	237
Q9Z1D1	Conv	SEDTR	ETDLQELFRPFGSISR	IYLAK	3		632.327291	1893.958473	0.000451244	3	N	251	267
Q9Z1E4	Conv	DRRFR	SLDDSCSQLTSFLYSFCQQSR	RQRII	2	C6:+57.021,C17:+57.021	1265.05473	2528.09386	0.000451244	15	N	558	579
Q9Z1E4	Conv	ADRVK	VIFHPEFLSSTSPLLPVDYEEFVR	GCHLG	3		941.1536102	2820.437431	0.001699387	1	N	474	498
Q9Z1E4	Conv	EFSNK	GADVFLEALAR	LNYLL	2		581.3172845	1160.618969	0.000451244	1	N	337	348
Q9Z1E4	Conv	QTKAK	VTGDEWGDNYYLVGPYTEQGVR	TQVEL	2		1259.580215	2517.14483	0.000870037	2	N	52	74
Q9Z1E4	Conv	MPLSR	SLSVSSLPGLEDWEDEFDPENAVLFEVAWEVANK	VGGIY	3		1274.60766	3820.79958	0.000823681	1	N	5	39
Q9Z1F9	Conv	IVWAK	YLFNQLFGEEDADQEVSPDRADPEAAWEPTEAEAR	ARASN	3		1332.600116	3994.776948	0.000451244	7	N	190	225
Q9Z1F9	Conv	LWRKR	KPPVPLDWAEVQSQGEANADQQNEPQLGLK	DQQVL	3		1096.216661	3285.626582	0.00091018	1	N	276	306
Q9Z1N5	Conv	RFGTK	GLAITFVSDENDAK	ILNDV	2		740.3704424	1478.725285	0.001352548	3	N	384	398
Q9Z1N5	Conv	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	C1:+39.994	1130.617238	2259.218877	0.000622848	4	N	299	319
Q9Z1N5	Conv	MPNVK	VAVFFGGLSIK	KDEEV	2		569.3374886	1136.659377	0.002813207	1	N	144	155
Q9Z1N5	Conv	-MAE	NDVDNELLDYEDDEVETAAGADGTEAPAKK	DVKGS	3		1065.476423	3193.405869	0.000451244	11	N	3	33
Q9Z1Q5	Conv	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQRK	FLDGN	3		1045.505765	3133.493896	0.000622848	4	N	138	166
Q9Z1Q5	Conv	PRYPK	LAALNPESNTSGLDIFAK	FSAYI	2		930.9892448	1859.96289	0.000451244	7	N	95	113
Q9Z1Q5	Conv	NAYAR	EEFASTCPDDEEIELAYEQVAR	ALK-	2	C7:+57.021	1301.068789	2600.121977	0.000451244	24	N	216	238
Q9Z1Q5	Conv	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQR	KFLDG	3		1002.807444	3005.398933	0.000451244	20	N	138	165
Q9Z1Q5	Conv	ISQRK	FLDGNELTLADCNLLPK	LHIVQ	2	C12:+57.021	966.9906989	1931.965798	0.000451244	13	N	166	183
Q9Z1Q5	Conv	VLWLK	GVTFNVTTVDTK	RRTET	2		641.3384139	1280.661228	0.000451244	6	N	37	49
Q9Z1Q5	Conv	GISQR	KFLDGNELTLADCNLLPK	LHIVQ	2	C13:+57.021	1031.038181	2060.060761	0.000451244	3	N	165	183
Q9Z1Q9	Conv	RKMSK	SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDPSEVEK	AKEGQ	3		1297.672775	3889.994926	0.000451244	16	N	864	900
Q9Z1Q9	Conv	YSGAR	SVTQQPGSEVIAPQK	TPAQL	2		784.9180912	1567.820582	0.000735798	2	N	214	229
Q9Z1Q9	Conv	SFAYK	VQGSDSDEEVVVATTR	IETML	2		846.4082846	1690.800969	0.000451244	2	N	520	536
Q9Z1Q9	Conv	EDWLR	LHTYLAGDAPTLADLAAVTALLLPFR	YVLDP	3		908.5097283	2722.505785	0.002884417	1	N	147	173
Q9Z1Z0	Conv	LADSR	EIIRNDGVLLLQALTR	SNGAI	3		608.6954262	1823.062879	0.000451244	1	N	179	195
Q9Z1Z0	Conv	LQTDR	SDSEIIAYALDTLYNIISNDEEEELEENSTR	QSEDL	3		1192.55188	3574.63224	0.001839721	1	N	73	104
Q9Z1Z2	Conv	KPMLR	QGDTGDWIGTFLGHK	GAVWG	3		544.5991221	1630.773966	0.000451244	9	N	44	59
Q9Z1Z2	Conv	KHIVK	TVDFTQDSNYLLTGGQDK	LLRIY	2		1001.474156	2000.932712	0.000451244	8	N	104	122
Q9Z1Z2	Conv	IHCVR	FSPDGELYASGSEDGTLR	LWQTV	2		950.9321239	1899.848648	0.000451244	2	N	272	290
Q9Z2L7	Conv	DDLVR	EGEIAILGGIEEESDKLWNFTK	KASHI	3		826.7519942	2477.232583	0.000451244	12	N	111	133
Q9Z2L7	Conv	LLDER	LVTLLQEVDTIEQETIKPLDDCQK	LIEHG	3	C22:+57.021	943.4918087	2827.452026	0.000451244	16	N	73	97
Q9Z2L7	Conv	NFTKK	ASHIQLDSLPEVPLLVDVPCLSAQLDDSILNIVK	DHIFK	3	C20:+57.021	1238.001133	3710.98	0.000451244	13	N	134	168
Q9Z2L7	Conv	NIALR	NDAESSGVLYSSAPTYFCGQTLTFR	VETVG	2	C18:+57.021	1386.134797	2770.253995	0.000451244	7	N	295	320
Q9Z2U0	Conv	MSYDR	AITVFSPDGHLFQVEYAQEAVKK	GSTAV	2		1289.171543	2576.327486	0.000451244	7	N	5	28
Q9Z2U0	Conv	AVGVR	GKDIVVLGVEK	KSVAK	2		578.8509602	1155.68632	0.00091018	3	N	36	47
Q9Z2U0	Conv	EFLEK	NYTDDAIETDDLTIK	LVIKA	2		863.9050434	1725.794487	0.000451244	8	N	174	189
Q9Z2U0	Conv	MSYDR	AITVFSPDGHLFQVEYAQEAVK	KGSTA	2		1225.124062	2448.232523	0.000451244	17	N	5	27
Q9Z2U0	Conv	QSNGR	RPFGISALIVGFDFDGTPR	LYQTD	2		1033.047428	2064.079257	0.000451244	8	N	124	143
Q9Z2U0	Conv	KLVIK	ALLEVVQSGGK	NIELA	2		550.81966	1099.62372	0.000979378	4	N	193	204
Q9Z2U0	Conv	DGTPR	LYQTDPSGTYHAWK	ANAIG	2		833.8971587	1665.778717	0.000451244	21	N	143	157
Q9Z2U0	Conv	CQSHR	LTVEDPVTVEYITR	YIASL	2		817.9359496	1633.856299	0.000451244	15	N	95	109
Q9Z2U0	Conv	RTVRK	ICALDDNVCMAFAGLTADAR	IVINR	2	C2:+57.021,C9:+57.021	1092.497809	2182.980017	0.001329271	2	N	61	81
Q9Z2U0	Conv	PFGIS	ALIVGFDFDGTPR	LYQTD	2		704.3675057	1406.719411	0.000451244	4	N	130	143
Q9Z2U1	Conv	QCDAR	AIGSASEGAQSSLQEVYHK	SMTLK	2		981.4823153	1960.949031	0.000451244	24	N	168	187
Q9Z2U1	Conv	SPEGR	LFQVEYAIEAIK	LGSTA	2		712.3957319	1422.775864	0.000451244	18	N	20	32
Q9Z2U1	Conv	GAMSR	PFGVALLFGGVDEK	GPQLF	2		724.8933564	1447.771113	0.000451244	9	N	135	149
Q9Z2U1	Conv	IEAIK	LGSTAIGIQTSEGVCLAVEK	RITSP	2	C15:+57.021	1017.033095	2032.05059	0.000451244	6	N	32	52
Q9Z2U1	Conv	HMFTK	EELEEVIKDI	-	2		608.8195227	1215.623445	0.001329271	6	N	231	241
Q9Z2W0	Conv	DLMVR	NDSPCGTTIGPILASR	LGLRV	2	C5:+57.021	829.9122515	1657.808903	0.000451244	9	N	406	422
Q9Z2W0	Conv	MHSIR	ETACTTGVLQTLTLFK	GFFEL	2	C4:+57.021	891.9692352	1781.92287	0.000451244	16	N	441	457
Q9Z2W0	Conv	LTLFK	GFFELFPSVSR	NLLVD	2		643.3329346	1284.650269	0.000451244	15	N	457	468
Q9Z2W0	Conv	YFLTR	NSSSIIAFAVGGQYVPGNGFSLIGAHTDSPCLR	VKRKS	3	C31:+57.021	1131.56162	3391.661459	0.000451244	12	N	66	99
Q9Z2W0	Conv	IHLQR	NINENFGPNTEIHLVPILATAVQEELEK	GTPEP	3		1044.879097	3131.613892	0.000451244	19	N	171	199
Q9Z2W0	Conv	IFAPR	LDNLHSCFCALQALIDSCASPASLAR	DPHVR	3	C7:+57.021,C9:+57.021,C18:+57.021	964.1263924	2889.355777	0.000451244	15	N	260	286
Q9Z2W0	Conv	DPHVR	MVTLYDNEEVGSESAQGAQSLLTELILR	RISAS	3		1022.848698	3065.522695	0.000451244	11	N	291	319
Q9Z2W0	Conv	RKSRR	SQVGYHQVGVETYGGGIWSTWFDR	DLTLA	3		910.430137	2728.267011	0.002663018	1	N	106	130
Q9Z2W0	Conv	RKSRR	SQVGYHQVGVETYGGGIWSTWFDRDLTLAGR	VIIKC	4		864.6751624	3454.66945	0.000662267	3	N	106	137
Q9Z2X1	Conv	DPEGK	ITGEAFVQFASQELAEK	ALGKH	2		934.4759703	1866.936341	0.000451244	15	N	150	167

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z2X1	Conv	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	4	C6:+57.021,C18:+57.021	949.1991845	3792.765538	0.001162105	4	N	16	49
Q9Z2X1	Conv	FGCTK	EEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	2		1414.242362	2826.469125	0.000451244	21	N	124	150
Q9Z2X1	Conv	FVRLR	GLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	3	C6:+57.021	1229.971174	3686.890122	0.000451244	9	N	116	150
Q9Z2X1	Conv	TREGR	QSGEAFVELESEDDVK	LALKK	2		891.4079503	1780.800301	0.001943752	1	N	52	68

Peptide identifications for the comparison MDSC Infl. vs. MDSC Conv.

Peptide FDR ≤ 0.31%

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A087WR50	Infl	NDNAR	SSPVIIDASTAIDAPSNLR	FLTTT	2		964.0107086	1926.005817	0.000451244	19	N	1890	1909
A0A087WR50	Infl	PDTMR	VTWAPPPSIELTNLLVR	YSPVK	2		953.5439903	1905.072381	0.000622848	3	N	1283	1300
A0A087WR50	Infl	CDNCR	RPGAAEPSPDGTTGHTYNQYTQR	YNQRT	3		835.3903414	2503.147624	0.000451244	11	N	2333	2356
A0A087WR50	Infl	QGRGR	WKCDPIDQCQDSETR	TFYQI	2	C3:+57.021,C9:+57.021	969.4095158	1936.803432	0.000622848	5	N	552	567
A0A087WR50	Infl	DAGFK	LTCQCLGFGSGHFR	CDSSK	2	C3:+57.021,C5:+57.021	820.3770933	1638.738587	0.000451244	2	N	2229	2243
A0A087WR50	Infl	YGGSR	GFNCESKPEPEETCFDKYTGNTYK	VGDTY	3	C4:+57.021,C14:+57.021	967.7497989	2900.225997	0.000451244	7	N	84	108
A0A087WR50	Infl	VSGYR	VEVLPVSLPGEHGQR	LPVNR	2		808.9419006	1615.868201	0.000451244	5	N	937	952
A0A087WR50	Infl	TISWR	TKTETITGFQVDAIPANGQTPVQR	SISPD	2		1286.672439	2571.329277	0.000451244	9	N	1834	1858
A0A087WR50	Infl	QQWER	TYLGNALVCTCYGGSR	GFNCE	2	C9:+57.021,C11:+57.021	896.4113301	1790.80706	0.000451244	3	N	68	84
A0A087WR50	Infl	VRYYR	ITYGETGGNSPVQEFTVPGSK	STATI	2		1084.529463	2167.043325	0.000451244	6	N	1478	1499
A0A087WR50	Infl	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3		1045.511296	3133.510489	0.000451244	6	N	1352	1381
A0A087WR50	Infl	TGTPR	SDNVPPPTDLQFVELTDVK	VTIMW	2		1057.536756	2113.057912	0.000451244	4	N	902	921
A0A087WR50	Infl	TGLTR	GVTYNIIVEALQNQR	RHKVR	2		859.4657399	1716.91588	0.000451244	9	N	2163	2178
A0A087WR50	Infl	PSNLR	FLTTTPNSLLVSWQAPR	ARITG	2		966.023422	1930.031244	0.000451244	6	N	1909	1926
A0A087WR50	Infl	PIVNR	VVTPLSPPTNLHLEANPDTGVLTVSWER	STTPD	3		1014.868533	3041.582198	0.000451244	12	N	1168	1196
A0A087WR50	Infl	RHKVR	EEVVTVGNAVSEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C22:+57.021	1467.32428	4398.949441	0.000451244	22	N	2183	2222
A0A087WR50	Infl	PTNLK	FSQVTPTSFTAQWIAPSVQLTGYR	VRVNP	2		1343.187724	2684.359849	0.000451244	6	N	1728	1752
A0A087WR50	Infl	LPVNR	NTFAEITGLSPGVTYLFK	VFAVH	2		979.5176382	1957.019676	0.002080925	1	N	957	975
A0A087WR50	Infl	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	2	C7:+57.021	1098.966472	2195.917344	0.000451244	4	N	379	397
A0A087WR50	Infl	LQPLR	SIPPYNTEVTETTIVITWTPAPR	IGFKL	2		1293.676658	2585.337717	0.000735798	2	N	1088	1111
A0A087WR50	Infl	SWTPF	QESSEYIISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	C10:+57.021	1376.330595	4125.968385	0.000451244	15	N	2125	2163
A0A087WR50	Infl	EQWQK	EYLGAICSCTCFGGQR	GWRCD	2	C7:+57.021,C9:+57.021,C11:+57.021	939.900041	1877.784482	0.000451244	19	N	2309	2325
A0A087WR50	Infl	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	3	C1:+57.021,C8:+57.021	942.0625998	2823.164399	0.000823681	5	N	2286	2309
A0A087WR50	Infl	NITIY	AVEENQESTPVFIQQETTGTPR	SDNVP	2		1231.096229	2460.176859	0.000451244	7	N	880	902
A0A087WR50	Infl	VGNGR	GEWACIPYSQLR	DQCIV	2	C5:+57.021	740.3563838	1478.697168	0.001395409	2	N	503	515
A0A087WR50	Infl	PSKTK	TASPDQTEMTIEGLQPTVEYVVSVYAQNR	NGESQ	3		1076.191124	3225.549972	0.001463592	1	N	1587	1616
A0A087WR50	Infl	SPDVR	SYTITGLQPGTDYK	IHLYT	2		772.3860925	1542.756585	0.001395409	1	N	1865	1879
A0A087WR50	Infl	GGQPK	QYNVGPLASKYPLR	NLQPG	2		803.4415364	1604.867473	0.001943752	1	N	1039	1053
A0A087WR50	Infl	GHMMR	CTCVGNGRGEWACIPYSQLR	DQCIV	3	C1:+57.021,C3:+57.021,C13:+57.021	795.3613325	2383.060598	0.000622848	3	N	495	515
A0A087WR50	Infl	RGVTY	NIIVEALQNQR	RHKVR	2		649.3652974	1296.714995	0.000451244	9	N	2167	2178
A0A087WR50	Infl	QYGHR	EVTRFDFTTSASTPVTSNTVTGET	APYSP	2		1274.606627	2547.197654	0.001352548	2	N	690	714
A0A087WR50	Infl	NLLVR	YSPVKNEEDVAELSISPSDNAVVL	TNLLP	2		1288.142845	2574.270091	0.000451244	11	N	1300	1324
A0A087WR50	Infl	LPVNR	NTFAEITGLSPGVTY	LFKVF	2		785.3939175	1568.772235	0.00091018	4	N	957	972
A0A087WR50	Infl	TVSGF	RVEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR	KYIVN	3		1268.293964	3801.858492	0.000979378	1	N	749	783
A0A087WR50	Infl	RIGFK	LGVRPSQGGEAPREVTSDSGSIVVSGLTPGVEY	TYTIQ	3		1100.895587	3299.663361	0.002374549	1	N	1115	1148
A0A087WR50	Infl	QRGWR	CDNCRRPGAAEPSPDGTTGHTYNQYTQR	YNQRT	4	[0:-17.027,C1:+57.021,C4:+57.021	798.8457943	3191.351977	0.001943752	1	N	2328	2356
A0A087WR50	Infl	ESSEY	IISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	C4:+57.021	1135.240212	3402.697235	0.001871652	2	N	2131	2163
A0A087WSP5	Infl	EWKRR	QQSACIGGPPNACLDQLQSWFTIVAETLQQIR	QQLKK	3	C5:+57.021,C13:+57.021	1210.599703	3628.775709	0.000451244	7	N	242	274
A0A087WSP5	Infl	PYTKK	ELSAVTFPDIIR	NYKVM	2		680.8777063	1359.739813	0.000451244	9	N	643	655
A0A087WSP5	Infl	MLGEK	LLGPNAGPDGLIPWTR	FCKEN	2		838.9600934	1675.904587	0.000622848	5	N	531	547
A0A0D9SEG8	Infl	FAMCK	NSEGSYTCVCNLGYK	LLSGA	2	C8:+57.021,C10:+57.021	876.3718706	1750.728141	0.000451244	2	N	87	102
A0A0D9SEG8	Infl	SVSLK	LLSNINSVFLTNTNTEK	LASNV	2		954.5078018	1907.000004	0.000451244	17	N	346	363
A0A0D9SEG8	Infl	LEQRR	ASLEDFYGSPIPSVSLK	LLSNI	2		905.4676139	1808.919628	0.000451244	8	N	329	346
A0A0D9SEG8	Infl	SGSLR	GPDTICQEPPFPTWTLLPTAHSQTLLR	FSVEV	3	C6:+57.021	1026.190575	3075.548326	0.000451244	13	N	160	187
A0A0D9SEG8	Infl	NVTFK	FDFTSVESIEPR	HELIC	2		713.8466031	1425.677606	0.001871652	1	N	371	383
A2A8Z1	Infl	DFDKK	LTEADAYLQILIEQLK	LFDDK	2		931.0200137	1860.024427	0.001162105	2	N	122	138
A2A8Z1	Infl	LGEIF	QCHWTLPNDTEENAELVSEGPVPWVSK	NSVTF	3	C2:+57.021	1041.48935	3121.444649	0.001943752	4	N	462	489
A2A8Z1	Infl	NGYGR	SILTVPWVELGGECNINCSK	TGYSA	2	C14:+57.021,C18:+57.021	1138.55618	2275.09676	0.001264573	2	N	563	583
A2ADY9	Infl	YGTGR	EDIRPEEIADQELAEAIQK	SAEDA	2		1099.053302	2196.091004	0.000451244	7	N	370	389
A2ADY9	Infl	IDLKK	NVLVIGTTGSQTTFLPEGELPECAR	LAYGT	2	C23:+57.021	1345.179008	2688.342416	0.000451244	10	N	338	363
A2ADY9	Infl	SNLPR	IDFSSIAVPGTSNPQQR	QLPRT	2		908.9635614	1815.911523	0.000634081	5	N	93	110
A2ADY9	Infl	QERIR	LFSADPFDLEAQAK	IEEDI	2		776.3886352	1550.76167	0.0025889	1	N	191	205
A2AIV8	Infl	LRQCK	VLNPDDEEQVLSDPNLVIR	KRKVG	2		1083.058387	2164.101174	0.000451244	20	N	38	57
A2AIV8	Infl	RKLVR	ELGEKADELQLQLFQTESR	LLAAE	2		1117.569119	2233.122638	0.000451244	5	N	386	405
A2AIV8	Infl	IRKRK	VGVLLDILQR	TGHKG	2		563.35367	1124.69174	0.001329271	1	N	60	70
A2AIV8	Infl	DSSPR	NSQELSLPQDLEEDAQLSDK	GVLAD	2		1130.035306	2258.055012	0.000451244	6	N	433	453
A2AIV8	Infl	KLQKK	VQDLTALLSSKDDFIK	ELRVK	3		598.328409	1791.961827	0.002296037	1	N	129	145
A2AJW4	Infl	LHMPR	GECEESWIHFI	-	2	C3:+57.021	703.8061924	1405.596785	0.001162105	1	N	268	279
A2AJW4	Infl	HVLSR	LAINSDLCCSSQDLEFTLQCLVPDFSPPIETPGFGER	LARQL	3	C8:+57.021,C9:+57.021,C20:+57.021	1404.990331	4211.947593	0.001591523	4	N	114	151
A2AL36	Infl	GAGTK	GGIENVLEEIAELR	HAVSA	2		771.4126416	1540.809683	0.000735798	2	N	1108	1122

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A2AL36	Infl	EALKK	DLEGVISGLQEYLGTIK	GQATQ	2		917.9939959	1833.972392	0.000622848	1	N	613	630
A2AN08	Infl	RVYEK	LITGCYNILANHADPNSGLDESILEECLQYLEK	QLESS	3	C5:+57.021,C27:+57.021	1264.941571	3791.801314	0.000451244	15	N	1352	1385
A2AN08	Infl	SEITK	NLLPATLQLIDTYASFTR	AYLLQ	2		1019.054919	2036.094238	0.000451244	4	N	1155	1173
A2AN08	Infl	GSTLR	TSPADHGGSVGSESGGSAVDSVAGEHSVSGR	SSAYG	3		947.4279607	2839.260482	0.000451244	2	N	2880	2911
A2AN08	Infl	IGSWR	NAFANDTIPSESYISAVQAAHLGTLCGQSLPLAASLK	HTLLS	3	C26:+57.021	1272.647642	3814.919525	0.001264573	1	N	1247	1284
A2AN08	Infl	PVETF	SEFLDAAGLLSEITDPESFLK	DLLNS	2		1141.576078	2281.136557	0.000451244	6	N	5152	5173
A2AN08	Infl	ATVSR	STLEVLQLFPINIK	SSNGG	2		807.9774205	1613.939241	0.001654178	1	N	2136	2150
A2AN08	Infl	KSGSK	SSICESSSLISSATAAALLSSGAVDYCLHVLK	SLLEY	3	C4:+57.021,C27:+57.021	1099.883105	3296.625916	0.002663018	1	N	3068	3100
A2AN08	Infl	LMIEF	ADFYENYQASTETLQCPR	CSASV	2	C16:+57.021	1096.981591	2191.947582	0.000637154	1	N	3641	3659
A2AN08	Infl	VYRMR	GLLGDATEEFIESLDSTTDEEEDEEEVYR	MAGVM	3		1107.483243	3319.42633	0.001463592	1	N	4442	4471
A2AQ07	Infl	QIGAK	FWEVIGEEHGIDCAGSYCGTSALQLER	ISVYY	3	C13:+57.021,C18:+57.021	1028.799264	3083.374392	0.000735798	13	N	19	46
A2AQ07	Infl	EYPDR	ILNSFSVMPSPK	VSDTV	2	M8:+15.995	668.353053	1334.690506	0.000451244	8	N	162	174
A2AQ07	Infl	SIQTR	NSNCFVEWIPNNVK	VAVCD	2	C4:+57.021	860.9095119	1719.803424	0.000451244	4	N	336	350
A2AQ07	Infl	IRSSR	LGVLFQPDSFVHGNSGAGNNWAK	GHYTE	2		1208.09617	2414.176739	0.000451244	4	N	80	103
A2AQ07	Infl	KMSTK	EVDQQLLSIQTR	NSNCF	2		715.3864268	1428.757254	0.000451244	5	N	324	336
A2AQ07	Infl	SQQYR	ALSVAELTQQMFDAR	NIMAA	2		840.4252267	1678.834853	0.000451244	3	N	282	297
A2AQ07	Infl	NNWAK	GHYTEGAELIENVMDVVRR	ESESC	3		730.0325497	2187.074249	0.000451244	2	N	103	122
A2AQ07	Infl	-MR	EIVHIQIGQCGNQIGAK	FWEVI	2	C10:+57.021	932.9888249	1863.96205	0.000662267	1	N	2	19
A2AQ07	Infl	DIPPR	GLNMAATFLGNNTAIQELFTR	VSEHF	2		1141.58405	2281.1525	0.000735798	2	N	359	380
A2AQ07	Infl	DVVRR	ESESCDCLQGFQIVHSLG	GGTGS	2	C5:+57.021,C7:+57.021	1033.451381	2064.887161	0.002212458	1	N	122	140
A2AUR7	Infl	KQVFK	AENNPWVTPIADQFQLGVSHVFEYIR	SETYK	3		1010.842318	3029.503553	0.000451244	17	N	195	221
A2AUR7	Infl	VAELK	NLEVLNFFNNQIEELPTQISSLQK	LKHLN	2		1409.735236	2817.454872	0.000451244	17	N	46	70
A2AUR7	Infl	NTLPR	GFGSLPALEVLDLTYNNLNEHSLPGNFFYLTTLR	ALYLS	3		1275.988258	3824.941375	0.000451244	14	N	86	120
A2AUR7	Infl	IQGNR	LTVLPPELGNLDLTGQK	QVFKA	2		904.5123558	1807.009112	0.000451244	4	N	174	191
A2AUR7	Infl	VLNFF	NNQIEELPTQISSLQK	LKHLN	2		921.4843266	1840.953053	0.001162105	2	N	54	70
A2AUR7	Infl	LTGQK	QVFKAENNPWVTPIADQFQLGVSHVFEYIR	SETYK	3		1178.272441	3531.793922	0.000451244	6	N	191	221
A2AUR7	Infl	KQVFK	AENNPWVTPIADQFQLGVSHVFEYIRSETY	KYLYG	3		1170.904194	3509.689182	0.000451244	5	N	195	225
A2AUR7	Infl	ISLPK	EIGELTQLKELHIQGNR	LTVLP	3		660.0292451	1977.064335	0.000851441	1	N	157	174
A2AUR7	Infl	GKLTK	LQILSLRDNDLISLPK	EIGEL	3		613.3635651	1837.067295	0.000823681	2	N	141	157
A2AUR7	Infl	LTTLR	ALYLSDNDFEILPPDIGKLTK	LQILS	2		1181.631188	2361.246776	0.001943752	1	N	120	141
A3KGV1	Infl	ITEAK	LAECQDQLQGYER	KNIDL	2	C4:+57.021	805.3676768	1608.719754	0.000451244	2	N	609	622
A6ZI44	Infl	VAPGK	GILAADESTGSIAKR	LQSIG	2		744.9049838	1487.794368	0.000451244	16	N	82	97
A6ZI44	Infl	TLYQK	ADDGRPFPQVIK	SKGGV	2		671.8598479	1341.704096	0.000451244	8	N	141	153
A6ZI44	Infl	VAPGK	GILAADESTGSIAK	RLQSI	2		666.8544282	1331.693256	0.000451244	21	N	82	96
A6ZI44	Infl	DIAHR	IVAPGKGILAADESTGSIAK	RLQSI	2		949.5338196	1897.052039	0.000451244	5	N	76	96
A6ZI44	Infl	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1307.670093	2613.324586	0.000451244	22	N	162	188
A6ZI44	Infl	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1136.574933	2271.134266	0.000451244	104	N	165	188
A6ZI44	Infl	ACQGK	YTPSGQSGAAASESLFISNHAY	-	2		1129.522169	2257.028738	0.000451244	43	N	396	418
A6ZI44	Infl	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLKR	CQYVT	3	C5:+57.021	1059.540044	3175.596733	0.000451244	74	N	227	255
A6ZI44	Infl	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	2		1054.052385	2106.089171	0.000451244	7	N	207	227
A6ZI44	Infl	NAINK	CPLLKPWALTFSYGR	ALQAS	3	C1:+57.021	603.6557601	1807.94388	0.000451244	15	N	343	358
A6ZI44	Infl	TALRR	TVPPAVTGVTFLSGGQSEEEASINLNAINK	CPLLK	3		1015.191452	3042.550957	0.000451244	140	N	313	343
A6ZI44	Infl	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	2	C13:+57.021	1107.601479	2213.187359	0.000662267	11	N	114	134
A6ZI44	Infl	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLK	RCQYV	3	C5:+57.021	1007.506341	3019.495622	0.000451244	12	N	227	254
A6ZI44	Infl	NAINK	CPLLKPWALTF	SYGRA	2	C1:+57.021	673.3707742	1344.725948	0.000451244	4	N	343	354
A6ZI44	Infl	TGVTF	LSGGQSEEEASINLNAINK	CPLLK	2		987.49288	1972.97016	0.000451244	32	N	324	343
A6ZI44	Infl	TGVTF	LSGGQSEEEASINLNAINKCPLLKPWALTFSYGR	ALQAS	3	C20:+57.021	1255.30896	3762.90348	0.000823681	1	N	324	358
A6ZI44	Infl	GVVPL	AGTNGETTTQGLDGLSER	CAQYK	2		903.9273729	1805.839146	0.000451244	2	N	170	188
A6ZI44	Infl	ACQGK	YTPSGQSGAAASESLF	ISNHA	2		786.8629815	1571.710363	0.000823681	11	N	396	412
A6ZI44	Infl	NAINK	CPLLKPWALTFSY	GRALQ	2	C1:+57.021	798.4184528	1594.821306	0.001839721	2	N	343	356
A6ZI44	Infl	SIAKR	LQSIGTENTEENRR	FYRQL	3		549.6084574	1645.801972	0.002727428	1	N	97	111
B1AUY2	Infl	KRSGR	SALSTTTTTSATTTTTTTTVETGPHR	KSSLK	3		875.7670317	2624.277695	0.000622848	2	N	199	225
B1AUY2	Infl	GDLEK	FIQSSGQPVPLVVESCIR	FINLN	2	C16:+57.021	1008.533065	2015.050531	0.000622848	1	N	522	540
B1AUY2	Infl	VKKSK	DLVQQLQAELLEVVSELQTTK	KMYHV	3		795.4360061	2383.284618	0.000622848	5	N	148	169
B1AUY2	Infl	KATLK	ALLEAVASEDGDILDSLQASPSTESLK	STSSD	2		1380.195806	2758.376012	0.000451244	1	N	399	426
B1AVH7	Infl	LYYSR	TAQDANPLDSIDLSSAVFDCK	ADAEE	2	C20:+57.021	1134.028738	2266.041876	0.000622848	3	N	80	101
B1AVH7	Infl	KLTQK	LTEDLAQPADATNGDFLSQQER	MEHLK	2		1210.072754	2418.129908	0.000451244	1	N	427	449
B1AVH7	Infl	TLHLK	LEQEEAELEEFLCPVK	TPTGL	2	C13:+57.021	981.9721719	1961.928744	0.000451244	1	N	168	184
B2RPV6	Infl	TVTRR	ELQNLIGAINQLNVLTK	ELTKR	2		941.0443545	1880.073109	0.001264573	1	N	659	676
B2RPV6	Infl	QSSQK	SLTELVESIVEIK	TQAAL	2		730.4168613	1458.818123	0.000451244	2	N	943	956
B2RQC6	Infl	DPSYK	AQILVLTYPLIGNYGIPSDEEDEFGLSK	WFESS	3		1027.860932	3080.559397	0.001463592	1	N	46	74
B2RQC6	Infl	LPELR	NSVTGGTAAFEPSLDYCVVK	IPRWD	2	C17:+57.021	1058.007077	2113.998555	0.000451244	11	N	719	739
B2RQC6	Infl	CPAVK	QIDTVAAEWPAQTNYLYLTYWGNTHDLDFR	APHVL	3		1201.239465	3600.694996	0.002374549	1	N	901	931
B2RQC6	Infl	PVLVR	AAFALGGLGSGFASTKEELSALVAPAFAHTSQVLIDK	SLKGW	4		919.4916902	3673.935561	0.001162105	6	N	555	592
B2RQC6	Infl	RQQCR	VLGTSPEAIDSAENR	FKFSR	2		779.8895307	1557.763461	0.000622848	4	N	1033	1048

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
B2RQC6	Infl	FKFSR	LLDTIGISQPQWR	ELSDL	2		763.9204368	1525.825274	0.002519933	2	N	1053	1066
B2RQC6	Infl	VSEGR	LSLDDLLQR	LHHNP	2		536.8040099	1071.59242	0.002453667	1	N	1722	1731
B2RQC6	Infl	PFVSK	TLGVDLVALATR	IIMGE	2		614.8671416	1227.718683	0.001395409	1	N	1228	1240
B2RUP2	Infl	GELTK	HSTSAVDLSTCFAQISHTAR	QLDWP	3	C11:+57.021	730.3520163	2188.032649	0.000823681	1	N	624	644
B2RUP2	Infl	MCKMK	AFGELCPDSAPLSQLVSEALR	MGTVE	2	C6:+57.021	1130.567833	2259.120067	0.000451244	7	N	441	462
B2RUP2	Infl	LAYSR	LYQSLEFPSSCLLHPITSIEYQWIQGR	LKAEQ	3	C11:+57.021	1089.216902	3264.627305	0.001699387	1	N	358	385
B2RV77	Infl	AVEYK	SQVVAGQNYFIK	MDVGG	2		677.3622234	1352.708847	0.000451244	32	N	44	56
B2RV77	Infl	LSRAR	SATPEIQEIADKVK	SLLEE	2		764.9150171	1527.814434	0.000451244	28	N	10	24
B2RV77	Infl	HIKVF	KGISGENVLELHGYQTNK	TRKDE	2		994.0163253	1986.017051	0.000451244	5	N	70	88
B2RV77	Infl	IKVFK	GISGENVLELHGYQTNK	TRKDE	2		929.9688437	1857.922087	0.000451244	35	N	71	88
B2RV77	Infl	FLHIK	VFKGISGENVLELHGYQTNK	TRKDE	2		1117.084739	2232.153879	0.000451244	2	N	68	88
B2RV77	Infl	NYFIK	MDVGGGCFLHIK	VFKGI	2	C7:+57.021	667.3234986	1332.631397	0.000735798	2	N	56	68
B2RV77	Infl	KAVEY	KSQVVAGQNYFIK	MDVGG	2		741.409705	1480.80381	0.000451244	11	N	43	56
B2RV77	Infl	LSRAR	SATPEIQEIADK	VKSLL	2		651.3333286	1300.651057	0.000451244	3	N	10	22
B2RV77	Infl	VFKGI	SGENVLELHGYQTNK	TRKDE	2		844.9160798	1687.81656	0.000451244	16	N	73	88
B2RV77	Infl	ARSAT	PEIQEIADKVK	SLLEE	2		635.3566067	1268.697613	0.002453667	1	N	13	24
B2RXR6	Infl	MAVLK	LCEQPPLVQAIFSGDPEEIR	MLIHK	2	C2:+57.021	1149.575659	2297.135717	0.000622848	19	N	5	25
B2RXR6	Infl	GRFTR	SQTLIQNGGEIDCVDKDGNTPLHVAAR	HGHEL	3	C13:+57.021	970.1458059	2907.414018	0.000622848	2	N	321	348
B2RXR6	Infl	NKAVK	CAEVIIPLLSSVNVSDR	GGRTA	2	C1:+39.994	927.9851911	1853.954782	0.000451244	2	N	121	138
B2RXR6	Infl	DCCLK	DNQGYTPLHWACYNGNENCIEVLLEQK	CFRKF	3	C12:+57.021,C19:+57.021	1089.160973	3264.459519	0.000451244	8	N	768	795
B2RXR6	Infl	TLCLR	LLLETADNPEVVDVK	DAKGQ	2		827.949057	1653.882514	0.000979378	1	N	651	666
B2RY56	Infl	EIRQR	LLAEGHPDPDAELQR	MEQEA	3		554.2816817	1659.821645	0.002981883	1	N	544	559
B5THE2	Infl	GLHLR	GGYIFPTQQPATTTEASR	KNPLG	2		962.9741261	1923.932652	0.000735798	2	N	790	808
B5THE2	Infl	KLSPK	FSGFPALINR	MKANG	2		561.3092625	1120.602925	0.002727428	1	N	1268	1278
B5THE2	Infl	TATLK	NLPSAPVFGNSIENILLTAEYQTSNR	FHFKL	3		950.1545615	2847.440284	0.000622848	6	N	130	156
B5THE2	Infl	WGIDR	QFLWGPGLLITPVLDQGAEK	VKAYV	2		1091.599494	2181.183388	0.001871652	2	N	730	750
B5THE2	Infl	TCDER	GCCWDPQGSISVPCYYSR	NHGYK	2	C2:+57.021,C3:+57.021,C14:+57.021	1096.453169	2190.890738	0.002813207	1	N	90	108
B5THE2	Infl	VSDRE	TWNIDKQFLLGPAFLVSPVLEPNAR	KVEAY	3		942.5169944	2824.527583	0.001162105	2	N	1620	1645
B5THE2	Infl	WNIDK	QFLLGPAFLVSPVLEPNAR	KVEAY	2		1034.583647	2067.151694	0.000451244	10	N	1626	1645
B5THE2	Infl	PSSGR	WGGHWLGDNTAAWDQLGK	SIIGM	2		1006.474628	2010.933655	0.000622848	1	N	1492	1510
B9EJ54	Infl	EQLIK	EAFIISDLFDIGELSAVELLLAGEHQQPHFPGLTR	GLVAV	4		966.5063346	3861.994138	0.001943752	3	N	92	127
B9EJ54	Infl	MDLLR	ESQLALIVSPLEQLLQGINPR	TKKAD	3		773.4413143	2317.300543	0.000451244	1	N	868	889
D3YTQ8	Infl	EPDVK	KLEALLQGGEVEEVILQAEK	ELSLA	3		732.7427704	2195.204911	0.000622848	2	N	27	47
D3YTQ8	Infl	AGLLK	KTTGLVGLAVCDTPHEEPDVK	KLEAL	4	C11:+57.021	567.2904579	2265.130632	0.000823681	1	N	6	27
D3YXK2	Infl	ERLKK	AIEDEGGNPDEIEVTSECNKK	MPKRP	2	C18:+57.021	1167.524017	2333.032434	0.000451244	1	N	63	84
D3YXK2	Infl	ERLKK	AIEDEGGNPDEIEVTSECNK	KMPKR	2	C18:+57.021	1103.476535	2204.937471	0.000451244	23	N	63	83
D3YXK2	Infl	EDVKK	FAFDACNDVPAPPKESSASEGADQK	MSSVE	3	C6:+57.021	880.0627484	2637.164845	0.000451244	17	N	378	403
D3YXK2	Infl	SPSTR	CQWSEADAPLAVVK	REPAD	2	C1:+57.021	787.3878809	1572.760162	0.001943752	1	N	302	316
D3YZZ5	Infl	NGTYK	FCFSNEFSTFTHK	TVYFD	3	C2:+57.021	551.2455372	1650.713212	0.000823681	1	N	107	120
D3Z6Q9	Infl	HEDLK	AIVGNNDLLWEDYEEKLADQALR	TMENY	2		1338.169729	2674.323857	0.000451244	7	N	100	123
D3Z6Q9	Infl	EDFSK	AQIVFEDLNQELLEELPILY	NSRIG	2		1195.131021	2388.246442	0.000451244	24	N	179	199
D3Z6Q9	Infl	AKMAK	AEEDFSKAQIVFEDLNQELLEELPILY	NSRIG	3		1065.871497	3194.591091	0.000451244	5	N	172	199
D3Z6Q9	Infl	PPPPR	ASGSGSCNAPGSPEGSSQLCSPR	ASPDA	2	C7:+57.021,C20:+57.021	1125.479189	2248.942779	0.000451244	11	N	418	441
D3Z6Q9	Infl	HEDLK	AIVGNNDLLWEDYEEK	LADQA	2		954.4552348	1906.89487	0.000451244	14	N	100	116
D4AFX7	Infl	PYLLK	LLEGVGLENLDSPAATK	AQIVK	2		863.9652384	1725.914877	0.000451244	1	N	2144	2161
D4AFX7	Infl	SSTER	DSLLASLLDGVR	ASGNR	2		629.8542312	1257.692862	0.000622848	8	N	311	323
D4AFX7	Infl	LRFGK	YSTDESITSLAEFVVQK	ISPRH	2		958.9785428	1915.941486	0.000451244	3	N	225	242
D4AFX7	Infl	QSNTR	ALYQYCPIPVINYPQLENELFCNIYYLK	QLCDT	3	C6:+57.021,C22:+57.021	1180.252581	3537.734344	0.000451244	3	N	1236	1264
D4AFX7	Infl	LPSSR	QLVLETLYALASNTK	IIKEA	3		555.3142113	1662.919234	0.000451244	7	N	1835	1850
E9PV24	Infl	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	2		1408.647012	2815.278424	0.000451244	11	N	485	511
E9PV24	Infl	GCRMK	GLIDEANQDFTNR	INKLK	2		746.8554908	1491.695382	0.000451244	3	N	72	85
E9PV24	Infl	MEYLR	GDFANANNFDNTYGQVSEDLRR	RIEIL	3		835.0464632	2502.11599	0.000622848	3	N	115	137
E9PV24	Infl	RAVNR	EINLQDYEGHQK	QLQQV	2		737.352584	1472.689568	0.000451244	1	N	191	203
E9PV24	Infl	REVVK	EVITSDDGSDCGDATELDISHSFSGSLDELSER	HPDLS	3	C11:+57.021	1181.844804	3542.511011	0.000451244	4	N	427	460
E9PV24	Infl	STVWT	TDTEDKGEFLSEGGGVR	GPRVV	2		898.9190165	1795.822433	0.000451244	10	N	19	36
E9PV24	Infl	RVVER	HQSQCKDSDWPFCSDDDWNHK	CPSGC	3	C5:+57.021,C13:+57.021	898.0242565	2691.049369	0.001162105	5	N	43	64
E9PV24	Infl	PGSFK	SQLQEAPPEWK	ALTEM	2		656.8307561	1311.645912	0.001395409	3	N	239	250
E9PV24	Infl	GCRMK	GLIDEANQDFTNRINK	LKNSL	2		924.4664682	1846.917336	0.000698008	3	N	72	88
E9PV24	Infl	QSQCK	DSDWPFCSDDDWNHKCPSGCR	MKGLI	2	C7:+57.021,C16:+57.021,C20:+57.021	1320.999732	2639.983864	0.000823681	1	N	49	70
E9PVA8	Infl	AHGVK	LVLPSLLAALEEESWR	TKAGS	2		913.5070734	1824.998547	0.000451244	6	N	1496	1512
E9PVA8	Infl	QQALR	QIGSVIRNPEILAIAPVLLDALTDPSR	KTQKC	3		957.8821134	2870.62294	0.000451244	3	N	1563	1590
E9PVA8	Infl	GSVIR	NPEILAIAPVLLDALTDPSR	KTQKC	2		1059.594409	2117.173217	0.001329271	1	N	1570	1590
E9PVX6	Infl	EESAK	ISLESSQAEPVR	TRAST	2		658.3467703	1314.677941	0.000451244	2	N	2298	2310

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9PVX6	Infl	GKKTK	SPGRAPGTPAPVQEENDCTAY	METPK	2	C18:+57.021	1108.997772	2215.979945	0.000622848	7	N	1392	1413
E9PVX6	Infl	GKRTK	SPGRAPGTPAPVQEENDSTAF	METPK	2		1064.501236	2126.986873	0.000451244	5	N	1151	1172
E9PVX6	Infl	NLSER	QLQVTNSGDIPEPITTEILGEK	VLSST	2		1191.624091	2381.232583	0.000451244	7	N	726	748
E9PVX6	Infl	TPKIR	AQPLEDLDGFQELFQTPAGANDSVTVEESAK	MSLES	3		1102.86032	3305.557559	0.000622848	1	N	1319	1350
E9PVX6	Infl	EAILY	NFSSTNPTQVNGVTIDEPVR	LRHGD	2		1088.037986	2174.060372	0.000451244	13	N	61	81
E9PVX6	Infl	ASISK	IDVKEELLESEEHLQLGEGVDTF	QVSTN	2		1315.148128	2628.280655	0.001162105	2	N	1491	1514
E9PVX6	Infl	TPKIR	AQPLEDLDGFQELFQTPAGANDSVTVEESVK	MSLES	3		1112.204086	3333.588859	0.002019181	2	N	2029	2060
E9PWG6	Infl	NLAIK	ICNEILTSPCSPENR	VYTKA	2	C2:+57.021,C10:+57.021	895.4140698	1788.81254	0.000622848	8	N	831	846
E9PWG6	Infl	RILSR	LILLWYNPVTEEDVR	LRHCL	2		930.4992484	1858.982897	0.001839721	1	N	730	745
E9PWG6	Infl	LIEAK	EALENCIAVQDFDQASK	LKEEI	2	C6:+57.021	969.4493952	1936.88319	0.001162105	1	N	501	518
E9PX59	Infl	HSILR	VAETGPLNLIDPIHEFK	AFTNT	3		631.6759202	1892.004361	0.000637154	2	N	179	196
E9PX59	Infl	KLLTR	HQGSLDESYYDWYILVTNTCAPTQLEHLEFIK	EMKLF	4	C20:+57.021	968.4638568	3869.824227	0.000451244	1	N	399	431
E9PX59	Infl	LMSYK	ATSHEDFIPVLLLVDDFEEQENAYILQNAINAFIAEK	GLRYE	3		1407.374507	4219.10012	0.000451244	1	N	779	816
E9PX59	Infl	NPNHK	EANNIENIVGNYTFLLQDILNK	QLSKV	2		1268.158633	2534.301665	0.000451244	1	N	1343	1365
E9PZF0	Infl	ESAEK	EIHLWFKPEELIDYK	SCAHD	2		980.5148985	1959.014197	0.000622848	1	N	243	258
E9PZF0	Infl	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDYK	SCAHD	3		1142.912578	3425.714334	0.000451244	7	N	229	258
E9PZF0	Infl	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDY	KSCAH	3		1100.214257	3297.619371	0.000451244	2	N	229	257
E9Q070	Infl	PAAAR	AGAIAPCEVTVPAQNTGLGPEK	TSFFQ	2	C7:+57.021	1090.554726	2179.093852	0.000451244	37	N	112	134
E9Q070	Infl	AEKVK	AFLADPSAFAAAAPAAAATTAAPAAAAAPAK	AEAKE	2		1348.706281	2695.396963	0.000451244	28	N	266	297
E9Q070	Infl	LGPEK	TSFFQALGITTK	ISSGT	2		657.3591494	1312.702699	0.000451244	15	N	134	146
E9Q070	Infl	NGYKR	VLALSVETEYTFPLAEK	VKAFL	2		955.5120215	1909.008443	0.000451244	24	N	247	264
E9Q070	Infl	PAAAR	AGAIAPCEVTVPAQNTGLGPEKTSFFQALGITTK	ISSGT	3	C7:+57.021	1158.936464	3473.785991	0.000735798	4	N	112	146
E9Q070	Infl	NISPF	SFGLIIQQVFDNGSIYNPEVLDITEQALHSR	FLEGV	3		1168.598882	3502.773246	0.000451244	23	N	183	214
E9Q070	Infl	LEGVR	NVASVCLQIGYPTVASVPHSIINGYK	RVLAL	2	C6:+57.021	1394.228835	2786.44207	0.000451244	1	N	220	246
E9Q070	Infl	AEKVK	AFLADPSAFAAAAPAAAATTAAPAAAAAPAKAEAK	EESEE	3		1032.544049	3094.608747	0.0007646	3	N	266	301
E9Q070	Infl	LEGVR	NVASVCLQIGYPTVASVPHSIINGYKR	VLALS	4	C6:+57.021	736.6435953	2942.543181	0.000451244	1	N	220	247
E9Q070	Infl	SPFSF	GLIIQQVFDNGSIYNPEVLDITEQALHSR	FLEGV	3		1090.565401	3268.672804	0.000451244	9	N	185	214
E9Q070	Infl	DDYPK	CFIVGADNVGSK	QMQQI	2	C1:+57.021	633.8112777	1265.606955	0.002453667	1	N	26	38
E9Q070	Infl	LPHIR	GNVGFVFTKEDLTEIR	DMLLA	3		608.9883867	1823.94176	0.000451244	6	N	83	99
E9Q070	Infl	DPSAF	AAAAPAAAATTAAPAAAAAPAK	AEAKE	2		888.9842968	1775.952994	0.001162105	3	N	275	297
E9Q0K6	Infl	NTDLR	TWEPEDVCSFLENR	GFREK	2	C8:+57.021	891.3938916	1780.772183	0.000451244	14	N	75	89
E9Q0K6	Infl	FRDNK	IAGSFLPFLDEDRLEDLGVSSLEER	KKMIE	2		1404.209051	2806.402502	0.000451244	8	N	104	129
E9Q0K6	Infl	EAFTK	LTDNIFLEVLHSTDPQLSEAQSILR	NIECR	2		1420.245968	2838.476336	0.000451244	7	N	464	489
E9Q0K6	Infl	IDLMK	VFNDPIHGHIEFHPLLIR	IIDTP	4		539.2961562	2153.153425	0.001699387	3	N	148	166
E9Q0K6	Infl	DYFAR	DCHHLGIQNNFDYKR	FIKFA	4	C2:+57.021	479.9763743	1915.874297	0.000622848	3	N	350	365
E9Q0K6	Infl	ASHNR	FEHSLGVGYLAGCLVR	ALAEK	3	C13:+57.021	593.3070195	1776.897659	0.001162105	5	N	196	212
E9Q0K6	Infl	LRYIK	QLGGGYYVFPGASHNR	FEHSL	3		574.9502663	1721.827399	0.001699387	2	N	180	196
E9Q0K6	Infl	VSNKR	NGIDVDKWDYFAR	DCHHL	3		533.5919675	1597.752503	0.001763695	5	N	337	350
E9Q0K6	Infl	AFTKL	TDNIFLEVLHSTDPQLSEAQSILR	NIECR	3		909.4718905	2725.392271	0.000451244	14	N	465	489
E9Q0K6	Infl	AYQHK	ISNLIDIMITDAFLKADPY	VEITG	2		1077.064096	2152.112592	0.000451244	1	N	420	439
E9Q0K6	Infl	TDNIF	LEVLHSTDPQLSEAQSILR	NIECR	2		1068.568922	2135.122244	0.0007646	5	N	470	489
E9Q0Y4	Infl	ATPTR	LFTDPLALLGLPAEEPEPTFPPVLEPR	WFAHY	3		986.8674699	2957.57901	0.00091018	4	N	85	112
E9Q0Y4	Infl	PTRLF	TDPLALLGLPAEEPEPTFPPVLEPR	WFAHY	3		900.1499772	2697.426532	0.000451244	5	N	87	112
E9Q0Y4	Infl	NSISK	IMSEAGSETLEDEWQSISEIASTCNTILESLSR	EGQPI	3	C24:+57.021	1229.573479	3685.697038	0.002884417	1	N	911	944
E9Q0Y4	Infl	ATRTR	QQYLQDLATNEVTTTSLDSASR	FGLPS	2		1221.093687	2440.171773	0.000622848	2	N	528	550
E9Q0Y4	Infl	SGDPK	EALKCDSEPEPGSLSEK	VSHLE	3	C5:+57.021	625.9599023	1874.856307	0.000823681	2	N	956	973
E9Q394	Infl	DLLSR	ISAASEEEAVGNGAATPK	MKQGP	2		851.4186523	1700.821705	0.001229886	1	N	1326	1344
E9Q394	Infl	ETQER	GCEGGTTSDQSSPVLPAAAIENK	VLGGQ	2	C2:+57.021	1145.037094	2288.058589	0.000451244	2	N	571	594
E9Q394	Infl	LQCTK	DNEVEQEDLTQSLSLVK	DVIGA	2		973.9818138	1945.948028	0.000451244	4	N	2128	2145
E9Q397	Infl	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVH	HAATE	3		977.1081167	2928.30095	0.001763695	1	N	2079	2106
E9Q586	Infl	GIFVR	QSQIQVFEDGADTTSPETPDSSASK	VLKRE	2		1313.094081	2624.172561	0.000451244	6	N	73	98
E9Q586	Infl	ALKER	VDELTTDLEILKAEIEEK	GSDGA	3		696.7039813	2087.088544	0.000451244	1	N	294	312
E9Q586	Infl	VGRLR	AFLQGGQEATDIALLLR	DLETS	2		908.5023224	1814.989045	0.000451244	4	N	731	748
E9Q586	Infl	DEVLK	ETVTQRPGATVPTDFATFPSSAFLR	AKEEQ	3		899.4613258	2695.360577	0.000451244	3	N	1169	1194
E9Q586	Infl	IEGLR	GPPPSGIATLVSGIAGGGAPGQAPGALPGPGLVK	DSPLL	3		973.5419797	2917.602539	0.000622848	1	N	1012	1046
E9Q586	Infl	RPGLR	GAAGEQLSFAAGLVYSLSLLQATLHR	YEHAL	3		891.8173324	2672.428597	0.000451244	2	N	606	632
E9Q604	Infl	NPLTK	KPWFVKPAESSSSSEGHGALK	STTWN	3		743.7153262	2228.122578	0.000451244	7	N	841	862
E9Q604	Infl	EMTSK	VIQHQYQFNNLGQR	SLPVS	2		872.9480486	1743.880497	0.000451244	12	N	951	965
E9Q604	Infl	KKVAR	SVFACQEQVLK	NKDAG	2	C5:+57.021	654.8347528	1307.653906	0.000451244	17	N	634	645
E9Q604	Infl	SVTLR	NDGEDSYGTQVTVYYPSGLSYRK	DSASQ	2		1300.101512	2598.187423	0.001329271	3	N	808	831
E9Q604	Infl	QENAK	GFGQSVVQLGGTSVVVAAPQEAK	AVNQT	2		1115.097847	2228.180093	0.000451244	34	N	32	55
E9Q604	Infl	SVTLR	NDGEDSYGTQVTVYYPSGLSYR	KDSAS	2		1236.05403	2470.09246	0.000451244	29	N	808	830
E9Q604	Infl	SHSQR	IIGAHFSPGLQYFGQSLSGGK	DLTMD	2		1082.563443	2163.111285	0.000451244	9	N	571	592
E9Q604	Infl	KPQSR	RELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1294.992731	3881.954793	0.000451244	28	N	297	331
E9Q604	Infl	PQSRR	ELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1242.959027	3725.853682	0.000451244	26	N	298	331

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q604	Infl	CETLK	LILPDCVDDSVSPIILR	LNYTL	2	C6:+57.021	963.0245418	1924.033484	0.000451244	31	N	716	733
E9Q604	Infl	ENAAK	ILVVITDGEKFGDPLDY	KDVIP	2		947.4963714	1892.977143	0.000622848	1	N	251	268
E9Q604	Infl	PEALR	ECPQQESDIVFLIDGSGSINNIDFQK	MKEFV	2	C2:+57.021	1477.198126	2952.380652	0.000451244	15	N	142	168
E9Q604	Infl	HQNCK	ENTYVNGLCYLFGSNLLRPPQQFPEALR	ECPQQ	3	C9:+57.021	1099.555917	3295.644352	0.000451244	41	N	114	142
E9Q604	Infl	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	2	C3:+57.021	1023.971498	2045.927396	0.002296037	3	N	503	520
E9Q604	Infl	HTSIK	GSQIGSYFGASLCSVDMDADGNTNLILIGAPHYYEK	TRGGQ	3	C13:+57.021	1288.601592	3862.781377	0.000622848	2	N	449	485
E9Q604	Infl	YEKTR	GGQVSVCPLPR	GQRAR	2	C7:+57.021	585.3087052	1168.60181	0.001871652	2	N	487	498
E9Q604	Infl	VNGDK	LTDVAIGAPGEQENQGAVYIFYGASIASLSASHSQR	IIGAH	3		1236.615372	3706.822716	0.000735798	3	N	535	571
E9Q604	Infl	AGVIR	YVIGVGNAFNKPQSR	RELDT	3		550.6306452	1648.868536	0.002981883	1	N	282	297
E9Q604	Infl	LKLIL	PDCVDDSVSPIILR	LNYTL	2	C3:+57.021	793.3984456	1584.781291	0.000823681	3	N	719	733
E9Q604	Infl	KCETL	KLILPDCVDDSVSPIILR	LNYTL	2	C7:+57.021	1027.072023	2052.128447	0.000637154	3	N	715	733
E9Q604	Infl	DIVFL	IDGSGSINNIDFQK	MKEFV	2		754.3735164	1506.731433	0.000451244	1	N	154	168
E9Q604	Infl	CETLK	LILPDCVDDSVSPIIL	RLNYT	2	C6:+57.021	884.9739862	1767.932372	0.000451244	5	N	716	732
E9Q604	Infl	KTETK	VEPYEVHNPVPLIVGSSIGGLVLLALITAGLY	KLGFF	3		1101.9588	3302.853	0.001943752	1	N	1098	1130
E9Q604	Infl	KTETK	VEPYEVHNPVPLIVGSSIGGLVLLALITAGLYK	LGFFK	3		1144.657121	3430.947963	0.000823681	1	N	1098	1131
E9Q604	Infl	ENAAK	ILVVITDGEKF	GDPLD	2		617.358618	1232.701636	0.000823681	6	N	251	262
E9Q604	Infl	SDIVF	LIDGSGSINNIDFQK	MKEFV	2		810.9155485	1619.815497	0.002145581	1	N	153	168
E9Q616	Infl	VPGFK	AEGPEVDVNLPK	ADLDI	2		634.3305889	1266.645578	0.000622848	1	N	762	774
E9Q616	Infl	IKGPK	VDIDVPDVDVHGPDWHLK	MPKIK	4		514.7593379	2055.006152	0.000451244	3	N	2605	2623
E9Q6Q4	Infl	NEFMR	IPCVDAGLISPLVQLLNSKDQEVLLQTGR	ALGNI	3	C3:+57.021	1059.583473	3175.727019	0.000451244	3	N	82	111
E9Q6Q4	Infl	NDAIK	LQLVEAGLVECLLEIVQQK	VDSNK	2	C11:+57.021	1091.611513	2181.207425	0.001763695	1	N	209	228
E9Q6U4	Infl	ATMKK	AAAEDVNVTFEDQQK	INKFA	2		832.8922704	1663.768941	0.000451244	8	N	7	22
E9Q6U4	Infl	EDAKK	TLQEEIDALESR	VASIQ	2		702.3547923	1402.693985	0.001871652	1	N	88	100
E9Q7G0	Infl	LKGEK	TGQEVQEEAVEIHSEGQPGQQQSQLAQLHASLAK	AIQQV	3		1219.270264	3654.787393	0.000451244	9	N	836	870
E9Q7G0	Infl	EAERK	SSLISSLEEEVSILNR	QVLEK	2		888.4734276	1774.931255	0.000451244	5	N	1219	1235
E9Q7G0	Infl	LHATR	AATLLSWVNSLHVADPVETVLQLQDCSIFIK	IINTI	3	C26:+57.021	1156.613321	3466.816563	0.000451244	11	N	7	38
E9Q7G0	Infl	LNEQR	VEFAALQEALAHALTEK	EGTDQ	3		614.3321535	1839.97306	0.000451244	4	N	1029	1046
E9Q7G0	Infl	SKLPR	TQPDGTSVPGEPASPISQR	LPPKV	2		962.4744903	1922.933381	0.001699387	1	N	1725	1744
E9Q7G0	Infl	IHDTK	EGQQILQQPLPER	LDFVC	2		768.412976	1534.810352	0.002212458	1	N	47	60
E9Q7G0	Infl	EKDAK	LESLQQQLQAANDAR	DNAQT	2		842.9348039	1683.854008	0.000451244	9	N	610	625
E9Q7G0	Infl	IHDTK	EGQQILQQPLPERLDFVCSFLQK	NRKHP	3	C18:+57.021	925.14994	2772.42642	0.000823681	1	N	47	70
E9Q7G0	Infl	TAQVR	SLEAQVAHADQQLR	DLGKF	2		783.4056822	1564.795764	0.001162105	1	N	1663	1677
E9Q7G0	Infl	KFFQK	EQALSALQLEHTSTQALVSELLPAK	HLCQQ	3		893.1522693	2676.433408	0.001871652	1	N	1335	1360
E9Q8K8	Infl	PSFAR	TVLWNPEDLIPLPIPK	QDVPP	2		923.0301844	1844.044769	0.000451244	16	N	933	949
E9Q8L9	Infl	GSVLR	AGSPESPHTEGTGQEPVTAEAQPNISSEGK	CFPEG	3		998.1309213	2991.369364	0.000622848	5	N	777	807
E9QNN1	Infl	TGCGK	TTQVPQYILDDFIQNDR	AAECN	2		1033.513615	2065.011631	0.000451244	15	N	420	437
E9QNN1	Infl	HLALK	AEAENNSGVESSGYGSPGPTWDR	GANLK	2		1184.010154	2366.004708	0.000451244	27	N	121	144
E9QNN1	Infl	DKKKK	DKEDDGGEDDDANCNLICGDEYGPETK	LSMSQ	3	C14:+57.021,C18:+57.021	1011.061319	3030.160556	0.000451244	5	N	597	624
E9QNN1	Infl	DYYSR	KEEQEVQATLESEEVDLNAGLHGNWTLENAK	ARLNQ	3		1161.229295	3480.664484	0.000622848	1	N	154	185
E9QNN1	Infl	EIHER	DINTDFLLVVLR	DVVLA	2		709.4066309	1416.797662	0.000451244	9	N	519	531
E9QNN1	Infl	QLNEK	ETPFELIEALLK	YIETL	2		701.8955647	1401.775529	0.000823681	2	N	633	645
E9QNN1	Infl	EHTLR	ELDALDANDELTPLGR	ILAKL	2		871.4343024	1740.853005	0.000451244	3	N	840	856
E9QNN1	Infl	IQNDR	AAECNIVVTQPR	RISAV	2	C4:+57.021	679.3485587	1356.681517	0.000451244	33	N	437	449
E9QNN1	Infl	QFLAK	AIEPPPLDAVIEAEHTLR	ELDAL	3		657.6902294	1970.047288	0.000698008	2	N	822	840
E9QNN1	Infl	LALKA	EAENNSGVESSGYGSPGPTWDR	GANLK	2		1148.491597	2294.967594	0.001839721	1	N	122	144
E9QPU1	Infl	GKIVK	IPGTCCDTCEEPDCKDITAK	VQYIK	2	C5:+57.021,C6:+57.021,C9:+57.021,C14:+57.021	1185.489057	2368.962514	0.000451244	4	N	2713	2733
E9QPU1	Infl	VVGLR	VVQCSQRPCEDSCQPGFSYVLHEGECCGR	CLPSA	3	C4:+57.021,C9:+57.021,C13:+57.021,C26:+57.021,C27:+57.021	1167.821177	3500.440131	0.000451244	9	N	2467	2496
E9QPU1	Infl	KCASK	AVYSIDIEDVQEQCSCCLPSR	TEPMR	2	C14:+57.021,C16:+57.021,C17:+57.021	1265.056184	2528.096768	0.000451244	6	N	2760	2781
E9QPU1	Infl	CPPGR	ILDELLQTCVDPQDCPVCEVAGRR	LAPGK	3	C9:+57.021,C15:+57.021,C18:+57.021	948.4543976	2842.339793	0.000451244	9	N	1184	1208
E9QPU1	Infl	AFISK	ANIGPHLTQVSVIQYGSINTIDVPWNVVQEK	AHLQS	3		1140.603967	3418.788502	0.000451244	8	N	1723	1754
E9QPU1	Infl	FDGLK	YLFPGECQYVLVQDYCGSNPGTFQILVGNEGCSYPSVK	CRKRV	3	C7:+57.021,C16:+57.021,C32:+57.021	1449.334209	4344.979227	0.000451244	9	N	885	923
E9QPU1	Infl	DSACR	ILTSDVFQGCNR	LVDPE	2	C10:+57.021	705.346016	1408.676432	0.000451244	5	N	1064	1076
E9QPU1	Infl	ALCEK	ILCTCATGPECACPVLLEYAR	TCAQE	2	C3:+57.021,C5:+57.021,C11:+57.021,C13:+57.021	1227.567445	2453.119289	0.000451244	8	N	255	276
E9QPU1	Infl	VYSGK	TCGLCGNYNGNKGDDFLTPAGLVEPLVVDFGNAWK	LQGDC	3	C2:+57.021,C5:+57.021	1266.934751	3797.780854	0.000451244	5	N	522	557
E9QPU1	Infl	AECHK	VIAPATFHTICQQDSCHQER	VCEVI	3	C11:+57.021,C16:+57.021	800.0392897	2397.094469	0.001162105	2	N	2155	2175
E9QPU1	Infl	SVGSR	WAVPENPCLVNECVR	VEDAV	2	C8:+57.021,C13:+57.021	921.9349724	1841.854345	0.000451244	3	N	2523	2538
E9QPU1	Infl	MYEVR	FTHLGHILTYTPQNNEFQLQLSPK	TFASK	2		1413.732831	2825.450061	0.002813207	1	N	2054	2078
E9QPU1	Infl	CPPGR	ILDELLQTCVDPQDCPVCEVAGR	RLAPG	2	C9:+57.021,C15:+57.021,C18:+57.021	1344.127141	2686.238682	0.000451244	5	N	1184	1207

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9QPU1	Infl	YNGNK	GDDFLTPAGLVEPLVVDFGNAWK	LQGDC	2		1230.626437	2459.237274	0.000622848	2	N	534	557
E9QPU1	Infl	VALER	CPCFHQGAEYAPGDTVK	IGCNT	3	C1:+57.021,C3:+57.021	646.2822795	1935.823439	0.000451244	3	N	829	846
E9QPU1	Infl	TCGCR	WTCPCVCTGSSTR	HIVTF	2	C3:+57.021,C5:+57.021,C7:+57.02	786.3234378	1570.631276	0.0025889	1	N	1946	1959
E9QPU1	Infl	TCICR	NSLWICSNEECPGECLVTGQSHFK	SFDNR	2	C6:+57.021,C11:+57.021,C15:+57.021	1426.625297	2851.234993	0.000451244	1	N	376	400
E9QPU1	Infl	ETLPR	EAPDLVLQTCCSK	EGLQL	2	C10:+57.021,C11:+57.021	760.8578677	1519.700135	0.000823681	3	N	1662	1675
E9QPU1	Infl	VHAGK	RYPPGTSLSQDCNTCICR	NSLWI	3	C12:+57.021,C15:+57.021,C17:+57.021	728.9910167	2183.94965	0.001162105	2	N	358	376
E9QPU1	Infl	QELER	ISRPIAPIFIRDFETLPR	EAPDL	4		536.0617227	2140.215691	0.002519933	5	N	1644	1662
E9QPU1	Infl	NLTCR	SLSLPDEECSEVCLEGCYCPPGLYQDERGDCVPK	AQCPC	3	C9:+57.021,C13:+57.021,C17:+57.021,C19:+57.021,C31:+57.021	1340.23487	4017.68121	0.000451244	7	N	673	707
E9QPU1	Infl	GQNFK	LTGSCSYVIFQNKEQDLEVLLHNGACSPGAK	QACMK	3	C5:+57.021,C26:+57.021	1145.894116	3434.658947	0.000622848	4	N	1970	2001
F6ZDS4	Infl	SELKK	TLSTVQNEVQEALQR	ASTAL	2		858.4502868	1714.884974	0.00091018	9	N	1112	1127
F6ZDS4	Infl	LAEQR	GQNLLLTNLQTIQGILER	SETET	2		1012.579093	2023.142586	0.000451244	16	N	884	902
F6ZDS4	Infl	ETEAR	SLQEQTVQLQSELSR	LRQDL	2		873.4555692	1744.895538	0.000451244	14	N	1586	1601
F6ZDS4	Infl	QAKVR	KLELDILPLQEANAELSEK	SGMLQ	2		1077.089156	2152.162712	0.002519933	1	N	1372	1391
F6ZDS4	Infl	VTSMK	DAVQAPLNVSLNEEGKSQEQILEILR	FIRRE	3		965.1808877	2892.519263	0.000698008	3	N	1249	1275
F6ZDS4	Infl	ELLER	ELQELQDSLNVER	EKVQV	2		786.8973557	1571.779111	0.001395409	1	N	1307	1320
F6ZDS4	Infl	STPKR	SSTSQTVSTPAPEPVIDSTEAIEAK	AALKQ	2		1273.129935	2544.24427	0.002145581	1	N	718	743
F6ZDS4	Infl	ELQHK	LENSLAELEQLR	ESRQH	2		707.8809773	1413.746355	0.001395409	2	N	656	668
F8VQC1	Infl	NQIIK	LKPTDVALLAVIANNIITINKDQNVFDSK	KKVKL	4		792.6978406	3166.760162	0.002813207	1	N	254	283
F8VQC1	Infl	EQCRK	IAASLQSQSPEYLLPVLIQAAQLCR	EKQHT	3	C24:+57.021	923.8374735	2768.48902	0.000451244	12	N	325	350
F8WI35	Infl	FKTDL	RFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1155.59292	3463.755359	0.000622848	2	N	83	115
F8WI35	Infl	SAAIG	ALQASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C19:+57.021	1317.665536	2633.315473	0.000451244	6	N	91	115
G5E870	Infl	FDSFR	DGFESVFPLCHLQYFYPEELDQLLCGSK	ADTWD	3	C10:+57.021,C25:+57.021	1131.193391	3390.556774	0.000451244	9	N	1875	1903
O08528	Infl	PTFVR	STPDGTEHGEFLALDLGGTNFR	VLRVR	2		1167.554	2333.092401	0.000979378	1	N	69	91
O08528	Infl	CHQTK	LDESFLVSWTK	GFKSS	2		662.8433321	1323.671064	0.000637154	1	N	162	173
O08553	Infl	AFKDR	FQLTDSQIYEVLSVIR	DIGAI	2		956.0152626	1910.014925	0.000451244	6	N	173	189
O08553	Infl	EAVNR	SITIANQTNCPLYVTK	VMSKS	2	C10:+57.021	911.9723092	1821.929018	0.002080925	1	N	238	254
O08582	Infl	IESGR	TSSVGNDILGFDSEGNVVNKPDSHGGSLEWTK	ICEKS	3		1116.199447	3345.57494	0.000451244	5	N	207	239
O08582	Infl	DLTSK	LVLVSPTSEQYDSLLR	QMWER	2		910.494163	1818.972726	0.000622848	6	N	64	80
O08582	Infl	VDAGK	STLLGVLTHGELDNGR	GFARQ	3		561.3009648	1680.879494	0.000637154	3	N	173	189
O08583	Infl	DGRPM	NIQLVTSQIDTQR	RPAQS	2		758.4104333	1514.805267	0.001162105	13	N	175	188
O08583	Infl	YSRPK	QLPDKWQHDLFDSGFGGGAGVETGGK	LLVSN	2		1352.144045	2702.272491	0.000451244	2	N	80	106
O08583	Infl	ETGGK	LLVSNLDFGVSDADIQELFAEFGTLKK	AAVHY	3		990.5222509	2968.543353	0.000451244	20	N	106	133
O08583	Infl	ETGGK	LLVSNLDFGVSDADIQELF	AEFGT	2		1048.033849	2094.052099	0.000451244	17	N	106	125
O08583	Infl	ETGGK	LLVSNLDFGVSDADIQELFAEFGTLK	KAAVH	3		947.8239298	2840.448389	0.002453667	1	N	106	132
O08583	Infl	DRSGR	SLGTADVHFER	KADAL	2		616.3074481	1230.599296	0.000451244	2	N	143	154
O08583	Infl	RGTGR	NSKQQLSAEELDAQLDAY	NARMD	2		1011.984888	2021.954176	0.002981883	1	N	230	248
O08583	Infl	GRNSK	QQLSAEELDAQLDAY	NARMD	2		847.3999282	1692.784256	0.002145581	1	N	233	248
O08585	Infl	LIGYV	AAEEAFVNDIDESSPGTEWER	VARLC	2		1176.51728	2351.018961	0.000451244	23	N	179	200
O08585	Infl	EWKEK	AIKELEEWYAR	QDEQL	3		469.9142705	1406.719411	0.000823681	4	N	137	148
O08663	Infl	HISGR	IIDCAFTVTFNPK	YDILL	2	C4:+57.021	763.3898923	1524.764185	0.000451244	1	N	259	272
O08663	Infl	KKKGK	GAVSAVQQELDKESGALVDEVAK	QLESQ	3		781.7399772	2342.196531	0.000451244	3	N	46	69
O08663	Infl	SEEKK	ALDQASEEIWNDFREAAEAHR	QVRKY	4		615.2905279	2457.130911	0.001943752	2	N	156	177
O08663	Infl	LMALK	NLCDLGIVDPYPPLCDIK	GSYTA	2	C3:+57.021,C15:+57.021	1051.518535	2101.02147	0.000622848	11	N	433	451
O08663	Infl	RKLIK	ENGLNAGLAFPTGCSLNNCAAHYTPNAGDTTVLQYDDICK	IDFGT	3	C14:+57.021,C19:+57.021,C39:+57.021	1448.31951	4341.935131	0.000451244	9	N	209	249
O08663	Infl	KRGPK	VQTDPPSVPICDLYPNGVFPK	GQECE	2	C11:+57.021	1172.088402	2342.161204	0.000637154	1	N	110	131
O08677	Infl	APILK	AYFPCIGCVHAISTDSPDLEPVLK	HSIEH	3	C5:+57.021,C8:+57.021	897.1050772	2688.291832	0.001229886	2	N	136	160
O08692	Infl	DVSEK	EKFEDVPPHIR	NIYED	2		683.8598479	1365.704096	0.000622848	3	N	138	149
O08692	Infl	STQER	QPKDCDFLEDGEER	NCTGK	2	C5:+57.021	869.3731562	1736.730712	0.000451244	11	N	82	96
O08692	Infl	ERQPK	DCDFLEDGEERNCTGK	FFRRR	2	C2:+57.021,C13:+57.021	972.8886132	1943.761626	0.000451244	70	N	85	101
O08692	Infl	FFRRR	QSTSLTLTCDRDCSR	EDTQE	2	C9:+57.021,C13:+57.021	900.4042334	1798.792867	0.000870037	6	N	106	121
O08692	Infl	ERQPK	DCDFLEDGEER	NCTGK	2	C2:+57.021	692.7700038	1383.524408	0.000451244	78	N	85	96
O08692	Infl	LFRLL	SATPPSSQNPATNIPLQFR	IKETE	2		1013.521775	2025.02795	0.000451244	16	N	51	70
O08692	Infl	PPHIR	NIYEDAKYDIIGN	ILKNF	2		764.3704424	1526.725285	0.000451244	11	N	149	162
O08692	Infl	LRQLR	YEEIVDRAIEAYNQGR	QGRPL	2		963.4717506	1924.927901	0.000451244	9	N	26	42
O08692	Infl	RPLFR	LLSATPPSSQNPATNIPLQFR	IKETE	2		1126.605839	2251.196078	0.000451244	472	N	49	70
O08692	Infl	YEDAK	YDIIGNILK	NF-	2		524.8060213	1047.596443	0.000451244	612	N	156	165
O08692	Infl	YEDAK	YDIIGNILKN	F-	2		581.8274851	1161.63937	0.002663018	2	N	156	166
O08692	Infl	PPHIR	NIYEDAKYDIIGNILK	NF-	2		941.5019881	1880.988376	0.000451244	137	N	149	165
O08692	Infl	HIRNI	YEDAKYDIIGNILK	NF-	3		552.2949282	1653.861385	0.002080925	1	N	151	165
O08692	Infl	PPHIR	NIYEDAKYDIIGNIL	KNF-	2		877.4545065	1752.893413	0.000451244	12	N	149	164
O08692	Infl	FFRRR	QSTSLTLTCDR	DCSRE	2	C9:+57.021	641.3090992	1280.602598	0.000451244	11	N	106	117

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O08692	Infl	PLQFR	IKETECTSTQER	QPKDC	3	C6:+57.021	494.5685685	1480.682305	0.001463592	2	N	70	82
O08692	Infl	RQLRY	EEIVDRAIEAYNQGR	QGRPL	3		588.2959908	1761.864573	0.000451244	2	N	27	42
O08692	Infl	RPLFR	LLSATPPSSQNPATNIPLQF	RIKET	2		1048.555283	2095.094967	0.000451244	11	N	49	69
O08692	Infl	RPLFR	LLSATPPSSQNPATNIPL	QFRIK	2		910.9917875	1819.967975	0.000823681	1	N	49	67
O08709	Infl	FSHPR	DFTPVCTTELGR	AAKLA	2	C6:+57.021	698.3325743	1394.649549	0.000451244	7	N	41	53
O08709	Infl	DEILR	VVDSLQLTGTKPVATPVDWK	KGESV	2		1077.594409	2153.173217	0.000451244	19	N	162	182
O08709	Infl	-M	PGGLLLGDEAPNFEANTTIGR	IRFHD	2		1071.545447	2141.075294	0.000451244	18	N	1	22
O08709	Infl	KRNVK	LIALSIDSVEDHLAWSK	DINAY	2		949.0074376	1895.999275	0.000451244	6	N	67	84
O08709	Infl	TTIGR	IRFHDFLGDSWGILFSHPR	DFTPV	4		575.7990631	2299.165052	0.000451244	1	N	22	41
O08709	Infl	IGRIR	FHDFLGDSWGILFSHPR	DFTPV	3		677.667759	2029.979877	0.000451244	18	N	24	41
O08709	Infl	LAWSK	DINAYNGETPTEK	LPFPI	2		726.3365996	1450.657599	0.000451244	6	N	84	97
O08709	Infl	TPTEK	LPFPIIDDKGR	DLAIL	3		424.2438395	1269.708118	0.001591523	4	N	97	108
O08709	Infl	LAWSK	DINAYNGETPTEKLPFPIIDDK	GRDLA	2		1245.624091	2489.232583	0.001264573	1	N	84	106
O08734	Infl	PGPPK	VGCDESPSPSEQQVAQDTEEVFR	SYVFY	2	C3:+57.021	1297.569487	2593.123374	0.000451244	5	N	11	34
O08734	Infl	DINRR	YDTEFQNLLEQLQPTAGNAYELFTK	IASSL	3		978.4788222	2932.413067	0.000451244	1	N	86	111
O08738	Infl	AYDAK	IEIQTLTGLFK	GDKCQ	2		631.8718926	1261.728185	0.000823681	5	N	116	127
O08738	Infl	EMLAR	YGSSLEFTELLTLVNRK	VSQRR	3		657.3584797	1969.052039	0.001395409	2	N	220	237
O08749	Infl	PLRTY	ADQPIEADVTVIGSGPGGYVAAIK	SAQLG	2		1164.608244	2327.200889	0.000451244	21	N	35	59
O08749	Infl	SEAFR	EANLAAAFGKPINF	-	2		731.8886053	1461.761611	0.000662267	1	N	495	509
O08749	Infl	QLGFK	TVCIEKNETLGGTCLNVGCIPSK	ALLNN	3	C3:+57.021,C14:+57.021,C19:+57.021	850.7502628	2549.227388	0.000698008	1	N	66	89
O08749	Infl	VCIGR	RPFTQNLGLEELGIELDPK	GRIPV	2		1085.081665	2168.147731	0.000979378	3	N	315	334
O08749	Infl	AWVGK	SEEQLKEEGIEFK	IGKFP	3		522.5951548	1564.762064	0.001264573	1	N	404	417
O08759	Infl	HLIER	YYHQLTEGCGNEACTNEFCASCPTFLR	MDNNA	3	C9:+57.021,C14:+57.021,C19:+57.021,C22:+57.021	1095.787845	3284.340135	0.000451244	4	N	33	60
O08759	Infl	LANEK	LETAFLNALVYLSPNVECDLTYHNVYTR	DPNYL	3	C18:+57.021	1105.8837	3314.627699	0.000698008	2	N	246	274
O08795	Infl	ILSSR	VNDGVCDCCDGTDEYNSGTVCENTCREK	GRKEK	3	C6:+57.021,C8:+57.021,C9:+57.021,C21:+57.021,C25:+57.021	1105.417774	3313.229923	0.000451244	6	N	91	119
O08795	Infl	ILSSR	VNDGVCDCCDGTDEYNSGTVCENTCR	EKGRK	3	C6:+57.021,C8:+57.021,C9:+57.021,C21:+57.021,C25:+57.021	1019.705256	3056.092367	0.000451244	23	N	91	117
O08808	Infl	SIALK	VGCLQLINALITPAEELDFRVHIR	SELMR	4	C3:+57.021	695.1341348	2776.505339	0.000451244	1	N	302	326
O08808	Infl	SIALK	VGCLQLINALITPAEELDFR	VHIRS	2	C3:+57.021	1136.604219	2271.192838	0.000451244	17	N	302	322
O08808	Infl	LESLR	VSLNNNPVSWVQTFGAEGLASLLDILKR	LHDEK	3		1014.552656	3040.634568	0.000451244	10	N	160	188
O08808	Infl	NAGSR	NAGAFGFNISFLCK	LRDTK	2	C13:+57.021	773.3798589	1544.744118	0.000451244	6	N	975	989
O08808	Infl	NEDMK	VQLCVFDEQGDEDFFDLK	GRLDD	2	C4:+57.021	1102.496542	2202.977485	0.000451244	6	N	350	368
O08808	Infl	LNTVK	DSKAEPHFLSILQHLLLVR	NDYEA	4		554.8197299	2215.247719	0.002727428	1	N	393	412
O08808	Infl	LESLR	VSLNNNPVSWVQTFGAEGLASLLDILK	RLHDE	2		1443.274528	2884.533457	0.000662267	1	N	160	187
O08808	Infl	SELMR	LGLHQVLQELR	EIENE	3		435.9266219	1304.756466	0.001162105	5	N	331	342
O08808	Infl	VKDSK	AEPHFLSILQHLLLVR	NDYEA	3		629.3723949	1885.093785	0.001943752	1	N	396	412
O08810	Infl	LHHGK	TCFVDCLIEQTHPEIR	KRYDQ	3	C2:+57.021,C6:+57.021	673.3207343	2016.938803	0.000451244	6	N	141	157
O08810	Infl	HEDKK	YYPTAEEVYGPEVETIVQEEDTQPLTEPIIKPVK	TKKFT	3		1302.326382	3903.955747	0.000451244	24	N	63	97
O08810	Infl	LYTIK	AFIPAIDSFGFETDLR	THTQG	2		899.9546737	1797.893747	0.000451244	11	N	871	887
O08810	Infl	EPLEK	GLAEDIENEVVQITWNR	KKLGE	2		993.5005081	1984.985416	0.000451244	14	N	693	710
O08810	Infl	SSSQR	SFVEFILEPLYK	ILAQV	2		742.9059325	1483.796265	0.000451244	13	N	366	378
O08810	Infl	GSFAK	IYADTFGDINYQEFAK	RLWGD	2		947.9470456	1893.878491	0.000823681	1	N	324	340
O08810	Infl	LLAAR	SIWAFGPDATGPNILVDDTLPSEVDK	ALLGS	2		1379.185044	2756.354489	0.000451244	5	N	729	755
O08810	Infl	LARRR	GHVTQDAPIPGSPLYTIK	AFIPA	2		947.5076048	1892.99961	0.002453667	1	N	853	871
O08810	Infl	GQPVK	VLGENYTLEDEEDSQICTVGR	LWISV	2	C17:+57.021	1214.052942	2426.090283	0.000451244	2	N	507	528
O08917	Infl	MGAAK	VTGEVLDILSRLPESVER	LTGVS	2		1006.555283	2011.094967	0.002663018	1	N	392	410
O08917	Infl	QVVER	AQQVAVQEQEIAR	REKEL	2		735.3895008	1468.763402	0.000451244	17	N	261	274
O08917	Infl	MFLGK	TEAEIAHIALETLEGHQR	AIMAH	3		673.3487548	2017.022864	0.000451244	12	N	91	109
O08917	Infl	MLLEK	LPQVAEEISGPLTSANK	ITLVS	2		877.4706879	1752.925776	0.000451244	9	N	360	377
O08992	Infl	GLRLK	SIDNGIFVQLVQANSPASLVGLR	FGDQV	2		1199.658603	2397.301606	0.000451244	5	N	131	154
O08992	Infl	LVGLR	FGDQVLQINGENCAGWSSDK	AHKVL	2	C13:+57.021	1113.000315	2223.98503	0.001463592	1	N	154	174
O08997	Infl	LPNKK	VCIDSEHSSDTLLATLNK	TGKAV	2	C2:+57.021	1001.991427	2001.967255	0.000451244	2	N	39	57
O08997	Infl	RVLNK	LGGVEFNIDLPNKK	VCIDS	2		772.4280947	1542.840589	0.000823681	5	N	25	39
O08997	Infl	LPNKK	VCIDSEHSSDTLLATLNKTGK	AVSYL	2	C2:+57.021	1145.07348	2288.13136	0.000451244	2	N	39	60
O09043	Infl	RALNK	AIGGYPFLNGQYFIQCSK	TPTLP	2	C16:+57.021	1032.006683	2061.997767	0.000451244	15	N	296	314
O09043	Infl	MESVK	VGTGLSLCAQGCSAILDTGTSLITGPSEEIR	ALNKA	3	C8:+57.021,C12:+57.021	1055.19205	3162.552751	0.000451244	30	N	261	292
O09043	Infl	DYVIK	ILQSDVGLCLLGFQALDIPKPAGPLWILGDVF	LGPYV	3	C9:+57.021	1155.967035	3464.877706	0.000451244	4	N	340	372
O09061	Infl	GPVQL	RFSPYAFNGGTVLAIAGEDFSIVASDTR	LSEGF	3		987.8300778	2960.466833	0.000451244	1	N	27	55
O09061	Infl	PKCYK	LTDKTVIGCSGFHGDCLTLTK	IIEAR	3	C9:+57.021,C16:+57.021	775.0524247	2322.133874	0.000622848	1	N	72	93
O09061	Infl	LYSRR	FFPYYVYNIIGGLDEEGKGAVYSFDPVGSYQR	DSFKA	3		1217.587983	3649.740549	0.000451244	20	N	127	159
O09061	Infl	DEEGK	GAVYSFDPVGSYQR	DSFKA	2		773.3707768	1544.725954	0.000451244	10	N	145	159
O09061	Infl	LYSRR	FFPYYVYNIIGGLDEEGK	GAVYS	2		1062.520378	2123.025156	0.000451244	2	N	127	145

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O09061	Infl	PYYVY	NIIGGLDEEGKGAVYSFDPVGSYQR	DSFKA	2		1336.154079	2670.292557	0.000451244	6	N	134	159
O09106	Infl	KQMQR	FNVGEDCPVFDGLFEFCQLSTGGSVASAVK	LNKQQ	3	C7:+57.021,C17:+57.021	1079.833974	3236.478523	0.000451244	11	N	93	123
O09106	Infl	NELPY	NDYFEYFGPDFK	LHISP	2		771.3333286	1540.651057	0.000451244	5	N	330	342
O09106	Infl	VSFHK	YGEYFPGTGDLR	DIGAG	2		687.8203883	1373.625177	0.001763695	2	N	200	212
O09110	Infl	FQQLK	QVVEEPSPQLPADQFSPEFVDFTSQCLR	KNPAE	3	C26:+57.021	1084.183926	3249.528379	0.000451244	19	N	279	307
O09110	Infl	EKNMK	IPEDILGEIAVSIVR	ALEHL	3		541.9825731	1622.924319	0.000451244	5	N	160	175
O09130	Infl	PSTLK	LGVADIIDCVVLASSSEATETSQELR	LRVQG	3	C9:+57.021	921.7957797	2762.363939	0.000451244	4	N	316	342
O09131	Infl	ESFSK	VPPLIASFVR	SKRKE	2		549.8376558	1097.659712	0.0025889	2	N	122	132
O09131	Infl	DAKTY	REYLNLYLQDSPEACDYGL	-	2	C15:+57.021	1160.033823	2318.052047	0.000451244	3	N	221	240
O09159	Infl	YNPPK	YLCWDVLCTDPPVVDNPRSPEFNAK	TLVNY	3	C3:+57.021,C8:+57.021	998.1373286	2991.388586	0.001352548	3	N	265	290
O09159	Infl	AARHR	LLAEQEVLAPQVVLSLGGSSPYHSR	ATPKT	3		884.1453376	2649.412613	0.000451244	5	N	858	883
O09159	Infl	EELWR	ASDSLEPPAADLFTGVLPNNYNPPK	YLCWD	2		1314.153547	2626.291495	0.002663018	1	N	240	265
O09159	Infl	NDYAR	QLAAGWGPCEVLVSNALAR	LSHYK	2	C9:+57.021	1006.523032	2011.030464	0.000451244	5	N	463	482
O09159	Infl	LFQTF	TINYLQETTLAANQPLSR	ASRLK	2		1017.037258	2032.058915	0.000451244	6	N	947	965
O09159	Infl	VGWLK	TVDQYYYGILSDVQHASVQYILDSVVSSLLEKPTR	RFIYV	4		997.515628	3986.031312	0.000451244	1	N	79	114
O09159	Infl	FTINY	LQETTLAANQPLSR	ASRLK	2		771.4182583	1540.820917	0.001839721	1	N	951	965
O09172	Infl	DCIQK	TLNEWSSQISPDLVR	EFPDV	2		872.94738	1743.87916	0.000451244	16	N	49	64
O09172	Infl	ALLAR	ASTLHLQTGNLLNWGR	LRKKC	3		594.3204707	1779.938012	0.001871652	1	N	14	30
O09172	Infl	HNDPK	ELLSEASFQEALQESIPDIEAQDWVPLWLLR	YSVIV	3		1209.286193	3624.835178	0.000622848	4	N	218	249
O09172	Infl	HNDPK	ELLSEASFQEALQESIPDIEAQDWVPL	WLLRY	3		1019.836675	3056.486626	0.001654178	2	N	218	245
O35129	Infl	TSQNR	IYLTADNLVLNLQDESFTR	GSDSL	2		1113.07658	2224.13756	0.000451244	2	N	270	289
O35129	Infl	IFFNR	IGGVQQDTILAEGLHF	RIPWF	2		849.4470158	1696.878432	0.000451244	9	N	54	70
O35129	Infl	QNRIY	LTADNLVLNLQDESFTR	GSDSL	2		975.0028836	1947.990167	0.000451244	1	N	272	289
O35129	Infl	RAKDF	SLILDDVAITELSFSR	EYTAA	2		889.9808885	1777.946177	0.000637154	1	N	175	191
O35226	Infl	LKKEK	VNVDIINFGEEEVNTEK	LTAFV	2		974.9790741	1947.942548	0.000451244	3	N	135	152
O35226	Infl	LKKEK	VNVDIINFGEEEVNTEKLTAFVNTLNGK	DGTGS	3		1036.535219	3106.582257	0.000451244	8	N	135	163
O35226	Infl	HSKTR	SNPENNVGLITLANDCEVLTTLTPDTGR	ILSKL	3	C16:+57.021	1005.496393	3013.465779	0.000622848	6	N	42	70
O35226	Infl	FLPTR	LQAQQDAVNIVCHSK	TRSNP	2	C12:+57.021	855.9335183	1709.851437	0.001463592	2	N	25	40
O35226	Infl	EEARR	AAAASAAEAGIATPGTEDSDDALLK	MTINQ	2		1158.564231	2315.112861	0.000451244	3	N	237	262
O35226	Infl	EEEAR	RAAAASAAEAGIATPGTEDSDDALLK	MTINQ	3		824.7457909	2471.213973	0.000637154	1	N	236	262
O35286	Infl	PLLER	YGVIILDEAHER	TLATD	3		472.2495417	1413.725225	0.000622848	6	N	253	265
O35286	Infl	LDAGK	FQIYFDNCPLLTIPGR	THPVE	2	C8:+57.021	977.4984941	1952.981388	0.000451244	4	N	299	315
O35286	Infl	EAKMR	FAHIDGDHLTLLNVYHAFK	QNHES	3		737.7168899	2210.12727	0.001871652	1	N	616	635
O35286	Infl	YLTVK	DNQVVQLHPSTVLDHKPEWVLY	NEFVL	3		873.1190114	2616.333634	0.001463592	4	N	714	736
O35343	Infl	LLTVK	DAQVVQVVLDGLSNILK	MAEDQ	2		906.0178053	1810.020011	0.000451244	14	N	423	440
O35343	Infl	DGDYR	VQNTSLEAIVQNASSDNQGIQLSAVQAAR	KLLSS	3		1004.850201	3011.527202	0.000451244	4	N	67	96
O35344	Infl	LLSVK	DSQVVQVVLDGLK	NILIM	2		700.3937205	1398.771841	0.000823681	8	N	423	436
O35344	Infl	DADFK	AQNVTLEAILQNATSDNPVVQLSAVQAAR	KLLSS	3		1007.870825	3020.589074	0.002813207	1	N	67	96
O35350	Infl	FSEKK	AGTQELDDQIQANLPDEK	VLSEE	2		992.9770628	1983.938526	0.000451244	14	N	517	535
O35350	Infl	FSEKK	AGTQELDDQIQANLPDEKVLSEEEIDDNFK	TLFSK	3		1135.206156	3402.595067	0.00307782	1	N	517	547
O35350	Infl	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	3	C1:+57.021	855.0935431	2562.257229	0.000451244	14	N	48	71
O35350	Infl	AGGCR	NYPATFWVNPQFK	IRLEE	2		806.4018799	1610.78816	0.001463592	4	N	385	398
O35350	Infl	DGATR	TDICQGALGDCWLLAAIASLTLNETILHR	VVPYG	3	C4:+57.021,C11:+57.021	1075.884892	3224.631276	0.000451244	16	N	104	133
O35350	Infl	LPDEK	VLSEEEIDDNFK	TLFSK	2		719.3413506	1436.667101	0.000451244	5	N	535	547
O35350	Infl	DGNGK	LGLVEFNILWNR	IRNYL	2		737.4147903	1472.813981	0.000451244	4	N	603	615
O35350	Infl	LIITR	YSEPDLAVDFDNFVCCLVR	LETMF	2	C15:+57.021,C16:+57.021	1160.024713	2318.033826	0.000451244	7	N	661	680
O35350	Infl	KAYAK	VNGSYEALSGGCTSEAFEDFTGGVTEWYDLQK	APSDL	3	C12:+57.021	1173.184432	3516.529895	0.000451244	14	N	197	229
O35350	Infl	SRTLR	NWNTTFYEGTWR	RGSTA	2		787.8552938	1573.694988	0.000735798	1	N	364	376
O35350	Infl	FFSEK	KAGTQELDDQIQANLPDEK	VLSEE	2		1057.024544	2112.033489	0.000622848	1	N	516	535
O35350	Infl	TKDGK	LVFVHSAQGNEFWSALLEK	AYAKV	2		1088.065818	2174.116036	0.000451244	3	N	174	193
O35350	Infl	YDLQK	APSDLYQIILK	ALERG	2		630.8640676	1259.712535	0.000823681	3	N	229	240
O35350	Infl	KALER	GSLLGCSINISDIR	DLEAI	2	C6:+57.021	752.8933305	1503.771061	0.001699387	1	N	244	258
O35350	Infl	RVVPY	GQSFQDGYAGIFHFQLWQFGEWVDVVIDDLLPTK	DGKLV	3		1319.316375	3954.925724	0.000823681	1	N	137	171
O35381	Infl	DVSGE	EEEDEEGYNDGEVDDEEDEEEAGEEEGSQKR	KREPD	3		1192.449767	3574.3259	0.000451244	50	N	204	235
O35381	Infl	LENLK	SLDLFNCEVTNLNAYR	ENVFK	2	C7:+57.021	964.9624728	1927.909346	0.000451244	18	N	116	132
O35381	Infl	LENLK	SLDLFNCEVTNLNAYRENVFK	LLPQV	2	C7:+57.021	1273.621129	2545.226657	0.000451244	6	N	116	137
O35381	Infl	LDNCK	SIEGKIEGLTDEFEELEFLSTINVGLTSISNLPK	LNKLK	3		1241.647456	3721.918967	0.000451244	12	N	28	62
O35381	Infl	SIEGK	IEGLTDEFEELEFLSTINVGLTSISNLPK	LNKLK	3		1070.222418	3207.643855	0.000451244	66	N	33	62
O35381	Infl	LSENR	ISGDLEVLAEK	CPNLK	2		587.3222325	1172.628865	0.000451244	9	N	75	86
O35381	Infl	LSENR	ISGDLEVLAEKCPNLK	HLNLS	2	C12:+57.021	893.4746847	1784.933769	0.000451244	1	N	75	91
O35639	Infl	WVGPR	GTIKDYPGFSPSVDAEAIR	KAIRG	2		1012.010709	2022.005817	0.000451244	10	N	9	28
O35639	Infl	RKAIR	GLGTDEKTLINILTER	SNAQR	2		886.9917875	1771.967975	0.000451244	2	N	32	48
O35639	Infl	KKSMK	GTGTDEDALIEILTTR	SSRQM	2		852.9366779	1703.857756	0.000451244	15	N	104	120
O35639	Infl	NISQK	DIEDSIKGELSGHFEDLLLAIVHCAR	NTPAF	3	C24:+57.021	979.8310472	2936.469742	0.000451244	15	N	222	248
O35639	Infl	HEFKK	HYGYSLYSAIQSDTSGDYR	TVLLK	2		1091.987962	2181.960324	0.000451244	14	N	293	312

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O35639	Infl	GTDEK	TLINILTER	SNAQR	2		536.8222027	1071.628805	0.000451244	8	N	39	48
O35639	Infl	TVYKK	SLGDDISSETSGDFR	KALLT	2		793.352978	1584.690356	0.000451244	11	N	138	153
O35639	Infl	IMVSR	SEIDLLDIR	HEFKK	2		537.2960177	1072.576435	0.000451244	15	N	279	288
O35639	Infl	EDSIK	GELSGHFEDLLLAIVHCAR	NTPAF	3	C17:+57.021	713.0338475	2136.078142	0.000451244	15	N	229	248
O35639	Infl	KSLGD	DISSETSGDFRK	ALLTL	2		671.3182098	1340.62082	0.000451244	5	N	142	154
O35639	Infl	TVYKK	SLGDDISSETSGDFRK	ALLTL	2		857.4004596	1712.785319	0.000451244	5	N	138	154
O35639	Infl	AGENK	WGTDEDKFTEVLCLR	SFPQL	2	C13:+57.021	934.9462914	1867.876983	0.000451244	10	N	189	204
O35639	Infl	RGTIK	DYPGFSPSVDAEAIRK	AIRGL	2		876.4341054	1750.852611	0.000823681	5	N	13	29
O35639	Infl	FLAER	LHQALKGAGTDEFTLNR	IMVSR	2		935.9926532	1869.969706	0.000451244	5	N	257	274
O35639	Infl	IMVSR	SEIDLLDIRHEFK	KHYGY	4		404.4681294	1613.841318	0.000451244	3	N	279	292
O35639	Infl	HQALK	GAGTDEFTLNR	IMVSR	2		590.7838058	1179.552012	0.000451244	1	N	263	274
O35639	Infl	RGTIK	DYPGFSPSVDAEAIR	KAIRG	2		812.3866238	1622.757648	0.000622848	2	N	13	28
O35643	Infl	PAPAR	LGAPISSGLSDLFDLTSGVGTLSGSYVAPK	AVWLP	2		1455.261284	2908.506967	0.000451244	14	N	687	717
O35643	Infl	EYAER	IDNADELLESFLEGFHDESTQVQLQLLTAIVK	LFLKK	3		1205.952991	3614.835572	0.000451244	12	N	458	490
O35643	Infl	IQFNR	NSFGLAPAAPLQVHVPLSPNQTVEISLPLNTVGSVLK	MEPLN	3		1270.038953	3807.093459	0.000451244	11	N	765	802
O35643	Infl	KLFLK	KPTETQELVQQVLSLATQDSDNPDLR	DRGYI	3		975.8320356	2924.472707	0.000451244	5	N	494	520
O35643	Infl	TLLKK	LAPPLVTLLSAEPELQYVALR	NINLI	3		765.1109056	2292.309317	0.000451244	3	N	283	304
O35737	Infl	EIVQF	FSGLEIVPNGITLPVDFQGR	STGEA	2		1080.078926	2158.142251	0.000451244	15	N	130	150
O35737	Infl	FVRLR	GLPFGCSKEEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	3	C6:+57.021	1250.978551	3749.912254	0.000451244	12	N	116	150
O35737	Infl	FGCSK	EEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	2		1452.761254	2903.506907	0.000451244	5	N	124	150
O35737	Infl	VVKVR	GLPWSCSADEVQR	FFSDC	2	C6:+57.021	752.8463802	1503.67716	0.000451244	16	N	16	29
O35737	Infl	NMQHR	YVELFLNSTAGASGGAYEHR	YVELF	2		1071.516689	2141.017779	0.000622848	1	N	355	375
O35737	Infl	IVQFF	SGLEIVPNGITLPVDFQGR	STGEA	2		1006.544719	2011.073837	0.000451244	2	N	131	150
O35744	Infl	KEMRK	AFEEESVEKDIPR	LLLTS	2		774.8811743	1547.746749	0.000622848	13	N	164	177
O35744	Infl	QEVPY	AYQGNEWVGYDNVR	SFKLK	2		835.88204	1669.74848	0.000451244	33	N	326	340
O35744	Infl	AASEK	LIVGFPAYGHTFILSDPSK	TGIGA	2		1031.554555	2061.09351	0.000451244	25	N	259	278
O35744	Infl	YDIGK	SADLNVDSIISYWKDHGAASEK	LIVGF	2		1203.582758	2405.149916	0.000451244	5	N	237	259
O35744	Infl	KDIPR	LLLTSTGAGIIDVIK	SGYKI	2		757.4641459	1512.912692	0.000451244	49	N	177	192
O35744	Infl	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2		1036.9772	2071.9388	0.000451244	45	N	128	145
O35744	Infl	EVCTF	LNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1190.546847	3568.61714	0.000451244	18	N	309	340
O35744	Infl	YDIGK	SADLNVDSIISYWK	DHGAA	2		805.9071921	1609.798784	0.000451244	60	N	237	251
O35744	Infl	NTELK	TLLAIGGWK	FGPAP	2		479.7901742	957.5647484	0.000451244	21	N	91	100
O35744	Infl	GLLAY	YEVCTFLNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3	C4:+57.021	1456.987051	4367.937754	0.000451244	15	N	303	340
O35744	Infl	TSTLK	GDLNIHSASCKGPY	-	2	C10:+57.021	759.8542053	1517.692811	0.000622848	1	N	384	398
O35744	Infl	EQDLR	DYEALNGLKDK	NTELK	2		633.3227639	1264.629928	0.000451244	11	N	75	86
O35744	Infl	LHDPK	DGYTGENSPLYK	SPYDI	2		672.3098535	1342.604107	0.000451244	24	N	218	230
O35744	Infl	KSGYK	IPELSQSLDYIQVMTYDLHDPK	DGYTG	3	M14:+15.995	874.4321846	2620.273154	0.000637154	1	N	196	218
O35744	Infl	SDPSK	TGIGAPTISTGPPGK	YTDES	2		677.3727881	1352.729976	0.000451244	13	N	278	293
O35744	Infl	SDPSK	TGIGAPTISTGPPGKYTDESGLLAYYEVCTF	LNEGA	3	C29:+57.021	1089.192199	3264.553197	0.000451244	1	N	278	309
O35744	Infl	SDPSK	TGIGAPTISTGPPGKYTDESGLLAY	YEVCT	2		1233.624091	2465.232583	0.001943752	1	N	278	303
O35744	Infl	SFKLK	AQWLKDNNLGGAVVWPLDMDDFSGSFCHQR	HFPLT	3	C27:+57.021	1155.203438	3462.586915	0.001591523	1	N	345	375
O35744	Infl	QVMTY	DLHDPKDGYTGENSPLYK	SPYDI	2		1024.982148	2047.948696	0.000451244	9	N	212	230
O35744	Infl	EQDLR	DYEALNGLK	DKNTE	2		511.7618107	1021.508021	0.002019181	1	N	75	84
O35744	Infl	AQWLK	DNNLGGAVVWPLDMDDFSGSFCHQR	HFPLT	3	C22:+57.021	946.418761	2836.232883	0.002981883	1	N	350	375
O35744	Infl	FLRQY	NFDGLNLDWQYPGSR	GSPPK	2		891.416247	1780.816894	0.000870037	3	N	130	145
O35744	Infl	VCTFL	NEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1152.852158	3455.533075	0.000451244	2	N	310	340
O35744	Infl	APQEV	PYAYQGNEWVGYDNVR	SFKLK	2		965.9400863	1929.864573	0.000622848	3	N	324	340
O35744	Infl	GPPGK	YTDESGLLAYYEVCTF	LNEGA	2	C14:+57.021	965.9246903	1929.833781	0.000698008	1	N	293	309
O35744	Infl	GPPGK	YTDESGLLAYYEVCTFLNEGATEVWDAPQEVPY	AYQGN	3	C14:+57.021	1277.241947	3828.70244	0.001463592	1	N	293	326
O35841	Infl	EELYR	NYGILADATEQVGQHKDAYQVILDGVK	GGTKE	3		982.5054828	2944.493048	0.000451244	6	N	9	36
O35841	Infl	KMDAK	GTLGGLFSQILQGEDIVRER	AIKFL	3		730.0627259	2187.164778	0.001162105	1	N	130	150
O35841	Infl	TVSGR	QQLVELVAEQADLEQAFSPSDPDCVDR	LLQCT	3	C24:+57.021	1020.480631	3058.418494	0.000451244	12	N	210	237
O35841	Infl	KMDAK	GTLGGLFSQILQGEDIVR	ERAIK	2		952.0183367	1902.021073	0.000451244	14	N	130	148
O35841	Infl	ENLPR	VADILTQLLQTDDSAEFNLVNNALLSIFK	MDAKG	3		1069.238403	3204.691808	0.000451244	17	N	97	126
O35841	Infl	STKLK	TLPDEVLTKEVEELILTESK	KVLED	3		762.7495907	2285.225372	0.000451244	5	N	160	180
O35841	Infl	RQAIK	ELPQFATGENLPR	VADIL	2		736.3811445	1470.746689	0.001699387	4	N	84	97
O35892	Infl	QLNNR	DATPESCSLLPQNEER	AVQLN	2	C7:+57.021	923.4180951	1844.82059	0.000998612	2	N	206	222
O35892	Infl	KRGPR	IPREENADFGGAELPVVCGNAQGF	LDKEK	2	C18:+57.021	1274.10056	2546.185521	0.00091018	2	N	374	398
O35900	Infl	GSVVR	YVQLPADEVDTQLLQDAAR	KEALQ	2		1073.04528	2144.07496	0.000451244	16	N	68	87
O35900	Infl	VVELK	NDLSICGTLHSVDQYLNIK	LTDIS	3	C6:+57.021	730.700534	2189.078202	0.000451244	10	N	20	39
O35930	Infl	NNKLR	ELPSGLLDGLEDLDTLYLQR	NWLRT	2		1130.58952	2259.16344	0.000622848	6	N	177	197
O35930	Infl	HNNLK	SLPSLGWALPALTTLDVSFNK	LGSLS	2		1115.610059	2229.204517	0.000451244	4	N	106	127
O35930	Infl	VSFNK	LGSLSPGVLDGLSQLQELYLQNNDLK	SLPPG	2		1407.748343	2813.481087	0.000622848	5	N	127	153
O35930	Infl	VASVR	CANLDNAPVYSYPGK	GCPTS	2	C1:+57.021	834.8882451	1667.76089	0.000451244	8	N	263	278
O35930	Infl	VYLWK	QGVDVKDTTPNVASVR	CANLD	3		562.632603	1684.874409	0.002212458	1	N	247	263

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O54734	Infl	FDEEK	TAVIDHHNYDVSDLGQHTLIVADTENLLK	APTIV	4		808.6629921	3230.620768	0.000622848	1	N	138	167
O54774	Infl	KLQAK	GVPVAEEVSALFAGELNPVAPK	AQKKV	2		1097.591866	2193.168132	0.001943752	2	N	588	610
O54774	Infl	ILQQK	EQAADTEAAQEVTQLLVER	LPQFV	2		1051.024544	2100.033489	0.000622848	1	N	537	556
O54774	Infl	QMLGY	DISWAAFNIIEVMSASKFTFK	RVGYL	3		802.4123676	2404.213703	0.001264573	1	N	70	91
O54824	Infl	APDPR	RPPEVASAIQPTPVSRDPPGPQPQASSSIR	QRISS	3		1041.550086	3121.626857	0.000451244	2	N	804	834
O54824	Infl	DPLLR	LLTTQSEDTQGPGLK	MPSQR	2		794.4153813	1586.815163	0.000451244	10	N	936	951
O54824	Infl	LSELR	EYSEGLTEPGETEDRNHCSSQAGQSVISLLSAEELEK	LIEEV	3	C18:+57.021	1360.625959	4078.854478	0.001162105	2	N	1048	1085
O54890	Infl	LCSGR	GNCECGSCVCVQPGSYGDTCEK	CPTCP	2	C3:+57.021,C5:+57.021,C8:+57.021,C10:+57.021,C20:+57.021	1262.468099	2522.920597	0.000823681	2	N	603	625
O54890	Infl	ICTTR	GVNSCQQCLAVSPVCAWCSDETLSQGSPR	CNLKE	3	C5:+57.021,C8:+57.021,C15:+57.021,C18:+57.021	1085.142399	3252.403798	0.000451244	3	N	33	62
O54950	Infl	HDVVK	GIVSLSDILQALVLTGGEK	KP-	2		957.0518452	1912.08809	0.000451244	6	N	309	328
O54950	Infl	IETWR	EVYLQDSFKPLVCISPNASLFDAVSSLIR	NKIHR	3	C13:+57.021	1090.235962	3267.684486	0.000622848	1	N	117	146
O54988	Infl	EHVKR	DLNPEEFWEIIGELGDGAFGK	VYKAQ	2		1168.55822	2335.10084	0.000451244	13	N	26	47
O54988	Infl	AELSK	AAQSGEGDEALAPTQTLAEKPTEGPEAGGAEEEPPGGER	VEDKQ	3		1278.591509	3832.751127	0.000451244	3	N	562	601
O54988	Infl	GAEAR	ALGSEGEAAATEVDLER	KENAQ	2		859.4161096	1716.816619	0.000451244	11	N	662	679
O54988	Infl	PGGER	VEDKQPEQQPAVCEAEGQLTSTSETTR	ATLEQ	3	C13:+57.021	1006.803774	3017.387922	0.000823681	2	N	601	628
O54988	Infl	KKRPK	LENLPDTQDQQTVDVNSVSEENENNR	VTLET	3		996.454064	2986.338792	0.001463592	1	N	427	453
O55029	Infl	KVNQK	AAESLADPTEYENLFPGLK	EAFVV	2		1033.010374	2064.005149	0.000451244	12	N	783	802
O55029	Infl	KVNQK	AAESLADPTEYENLFPGLKEAFVVEEWVK	ETHAD	3		1094.547125	3280.617974	0.000451244	6	N	783	812
O55029	Infl	LLGVR	SVNGLAFYDWENTELIR	RIEIQ	2		1013.997601	2025.979602	0.000451244	13	N	442	459
O55029	Infl	YLSEK	VLAAQETHEGVTEDGIEDAFEVLGEIQEIVK	TGLWV	3		1123.563503	3367.667109	0.000451244	13	N	494	525
O55029	Infl	VASLR	GSNNVALGYDEGSIIVK	LGREE	2		868.4472128	1734.878826	0.000451244	6	N	281	298
O55029	Infl	DYQNK	TCVQTLEGHAQNVSCASFHPELPIIITGSEDGTVR	IWHSS	3	C2:+57.021,C15:+57.021	1275.284332	3822.829595	0.000451244	1	N	219	254
O55029	Infl	FKEKK	SFKPDFGAESIYGGFLLGVR	SVNGL	3		720.7095125	2159.105137	0.002813207	1	N	422	442
O55029	Infl	DRTIK	VWQLGSSSPNFTLEGHEK	GVNCI	3		672.6660838	2014.974851	0.000662267	2	N	168	186
O55029	Infl	EGHEK	GVNCIDYYSGGDKPYLISGADDR	LVKIW	2	C4:+57.021	1268.076751	2534.137902	0.000622848	3	N	186	209
O55029	Infl	FLQGK	LDACLELLIR	TGRLP	2	C4:+57.021	608.3422137	1214.668827	0.0025889	1	N	737	747
O55029	Infl	ALRNK	SFGSAQEFAWAHDSSEYAIR	ESNSI	3		753.6754191	2258.002857	0.001463592	1	N	386	406
O55098	Infl	EHVRR	DLDPNDVWEIVGELGDGAFGK	VYKAK	2		1123.534745	2245.05389	0.000451244	13	N	28	49
O55098	Infl	VIETK	SEEELEDYIVEIEILATCDHPYIVK	LLGAY	3	C18:+57.021	1003.154974	3006.441521	0.000451244	5	N	70	95
O55106	Infl	DNESR	SAGDGTDWEKEDQCLTPEAWNVDQGVISK	LKEQY	3	C14:+57.021	1079.154695	3234.440686	0.000451244	12	N	302	331
O55106	Infl	ETQQR	VLTLESNVDSTSSSSCQINR	VISHP	2	C16:+57.021	1099.023987	2196.032374	0.000823681	1	N	649	669
O55106	Infl	GTDGR	IQSWSTTNPNVDPYDAYDPSVLR	GPLLG	2		1319.625154	2637.234708	0.000451244	4	N	539	562
O55106	Infl	DRDTK	EALKEFDFLVTSEEGDNESR	SAGDG	2		1158.037849	2314.060097	0.000451244	3	N	282	302
O55106	Infl	FDGIR	ALAFHPIEPVLITASEDHTLK	MWNLQ	4		576.31702	2301.23688	0.00091018	1	N	467	488
O55131	Infl	SGLGK	STLINSLFLTDLYSPEYPGPSHR	IKKTV	2		1304.158633	2606.301665	0.000451244	2	N	62	85
O55131	Infl	MAQPK	NLEGYVGFANLPNQVYR	KSVKR	2		977.4950287	1952.974457	0.001763695	1	N	24	41
O55131	Infl	EHKIK	IYEFPETDDEEENKLVK	KIKDR	2		1049.497297	2096.978993	0.002813207	1	N	220	237
O55131	Infl	KVLIK	EGGVQLLLTIVDTPGFGDAVDNSNCWQPVIDYIDSK	FEDYL	3	C25:+57.021	1312.638812	3934.893035	0.00091018	1	N	100	136
O55135	Infl	VEVFR	QTVADQVLVGSYCVFSNQGGLVHPK	TSIED	3	C13:+57.021	901.7905232	2702.34817	0.000451244	11	N	139	164
O55135	Infl	LVHPK	TSIEDQDELSSLLQVPLVAGTVNR	GSEVI	2		1292.677387	2583.339173	0.000451244	29	N	164	188
O55135	Infl	-MAVR	ASFENNCEVGCFAK	LTNAY	2	C7:+57.021,C11:+57.021	816.8427489	1631.669898	0.000451244	14	N	4	18
O55135	Infl	RVEER	LSALGNVTTCNDYVALVHPDLDRETEEILADVLK	VEVFR	4	C10:+57.021	946.7336015	3782.903206	0.000823681	4	N	100	134
O55135	Infl	GCFAK	LTNAYCLVAIGGSENFYSVFEGELSDAIPVVHASIAGCR	IIGRM	3	C6:+57.021,C38:+57.021	1396.34548	4186.013039	0.0025889	1	N	18	57
O55201	Infl	KKYAK	SSVGETVYGGSDELSDDITQQQLLPGVKDPNLWTVK	CKIGE	3		1292.644885	3874.911256	0.000451244	13	N	145	181
O55201	Infl	KVLPR	DLQLCSETASGVDVGGQHEWGELVQLDPR	TVGVI	3	C5:+57.021	1065.83893	3194.49339	0.000735798	1	N	514	543
O55201	Infl	HDGSR	TPAQSGAWDPNNPNTPSR	AEEEY	2		955.4435244	1908.871449	0.002663018	2	N	807	825
O55201	Infl	TGKER	EHNFQPGDNVEVCEGELINLQGK	VLSVD	3	C13:+57.021	876.0786213	2625.212464	0.000451244	1	N	414	437
O55222	Infl	AVAVR	LWLDNTENDLNQGDDHGFSPLHWACR	EGRSA	3	C25:+57.021	1037.465538	3109.373215	0.000451244	18	N	17	43
O55222	Infl	YGSLY	NVLHEGTNFVVDQSQAVK	FALDM	2		993.0085003	1984.001401	0.000451244	3	N	278	296
O55222	Infl	EIGMK	VALEGLRPTIPPGISPHVCK	LMKIC	2	C19:+57.021	1071.098907	2140.182214	0.002519933	1	N	403	423
O70138	Infl	YGFPR	SVQAIDAAVSYNGK	TYFFI	2		711.8653272	1421.715054	0.000451244	28	N	372	386
O70138	Infl	MEMPR	CGVPDSGDFLLTPGSPK	WTHTN	2	C1:+57.021	873.9222849	1745.82897	0.000451244	9	N	90	107
O70138	Infl	LFKGR	QYWALSGYDLQQGYPR	DISNY	2		972.9661041	1943.916608	0.000451244	15	N	347	363
O70138	Infl	SYNGK	TYFFINNQCWR	YDNQR	2	C9:+57.021	774.8565509	1547.697502	0.000451244	5	N	386	397
O70138	Infl	NYAYR	EPSTYSLPQDDINGIQTIYGPSDNPIQPTGPSTPK	ACDPH	3		1243.271159	3726.790078	0.000451244	4	N	242	277
O70138	Infl	GVNCR	VDAVFLQDSFFLFFSGPQYFAFNFVSHR	VTRVA	3		1111.545501	3331.613104	0.000622848	1	N	423	451
O70145	Infl	PVELR	IHPQSQPQEDTSPESDIPPPPNSSPPGR	LQLSP	3		997.8080015	2990.400604	0.000451244	62	N	300	328
O70145	Infl	IWKQK	LFEPVVIPVGR	LFRPN	2		613.3693201	1224.72304	0.000698008	13	N	170	181
O70145	Infl	FNGQK	GLVPCNYLEPVELR	IHPQS	2	C5:+57.021	829.9324557	1657.849311	0.000451244	18	N	286	300
O70145	Infl	WGQVK	NYCLTLWCEHTVGDQGLIDEPIQR	ENSDA	2	C3:+57.021,C8:+57.021	1459.184067	2916.352535	0.000451244	8	N	417	441
O70145	Infl	DPHSR	ICFNIGCVNTILENLQAAEQAFTK	SINRD	2	C2:+57.021,C7:+57.021	1377.683172	2753.350744	0.000451244	21	N	38	62
O70145	Infl	KKDWK	GALEAFSEVQDPHSR	ICFNI	2		821.8951474	1641.774695	0.000451244	4	N	23	38
O70145	Infl	QVKNY	CLTLWCEHTVGDQGLIDEPIQR	ENSDA	2	C1:+39.994,C6:+57.021	1312.117439	2622.219278	0.000662267	1	N	419	441

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O70145	Infl	VVAIF	SYEAAQPEDLEFVEGDVILVLSHVNEEWLEGECKGK	VGIFP	4	C33:+57.021	1030.494348	4117.946193	0.00091018	1	N	465	501
O70145	Infl	VVAIF	SYEAAQPEDLEFVEGDVILVLSHVNEEWLEGECK	GKVGI	3	C33:+57.021	1311.951055	3932.829766	0.000622848	1	N	465	499
O70145	Infl	DYLGK	ATVVASVVHQDNFSGFAPLQPQSAEPPPRPK	TPEIF	4		818.6774395	3270.678558	0.001591523	1	N	201	232
O70194	Infl	FFDKR	DNSDFDLLTVSETANEPPQDEGNSFNSPR	NLAME	3		1065.804874	3194.391222	0.000451244	11	N	281	310
O70194	Infl	LMKMR	YLEVSEPQDIECCGALEY	YDKAF	2	C12:+57.021,C13:+57.021	1087.966529	2173.917458	0.000451244	14	N	183	201
O70251	Infl	FGDLK	TPAGLQVLNDYLADK	SYIEG	2		809.4282917	1616.840983	0.000451244	16	N	7	22
O70251	Infl	YLADK	SYIEGYVPSQADVAVFEAVSGPPPADLCHALR	WYNHI	3	C28:+57.021	1139.226126	3414.654977	0.000451244	27	N	22	54
O70251	Infl	-M	GFGDLKTPAGLQVLNDYLADK	SYIEG	3		745.7272318	2234.158295	0.000622848	5	N	1	22
O70251	Infl	AVVAK	SSILLDVKPWDDETDMTKLEECVR	SIQAD	3	C22:+57.021	960.4652655	2878.372396	0.000451244	7	N	139	163
O70251	Infl	GLQVL	NDYLADKSYIEGYVPSQADVAVFEAVSGPPPADLCHALR	WYNHI	3	C35:+57.021	1412.351553	4234.03126	0.000451244	4	N	15	54
O70252	Infl	IKDMK	YFFGENWEEQVK	CSEAA	2		788.3598777	1574.704155	0.001943752	1	N	113	125
O70252	Infl	EEMDR	NKDHPAFAPLYFPTELHR	KAALI	4		539.0291512	2152.085405	0.001162105	1	N	86	104
O70310	Infl	LEKLK	FGIGDGNLQYYLYNWK	CPSMG	2		975.9733978	1949.931196	0.001162105	1	N	466	482
O70310	Infl	QPVPK	LGEVVNTHGPVEPDKDNIR	QEPYT	3		697.0277927	2088.059978	0.001329271	1	N	127	146
O70310	Infl	KDNIR	QEPYTLPQGFTWDALDLGDR	GVLKE	2		1161.556012	2321.096423	0.000451244	3	N	146	166
O70400	Infl	AVESK	TSASGEEANSRPVVQPHPSGSLIIDKDSEVYK	MLQEK	3		1133.23438	3396.67974	0.000451244	4	N	164	196
O70400	Infl	NLKQK	GHFFVEDQIYCEK	HARER	2	C11:+57.021	836.3775132	1670.739426	0.001943752	1	N	294	307
O70400	Infl	APSTR	VITNQYNSPTGLYSSENISNFNNAVESK	TSASG	3		1030.827062	3089.457785	0.000451244	1	N	136	164
O70435	Infl	ASNFR	SNFGYNIPLK	HLADR	2		576.8065526	1151.597505	0.0025889	1	N	100	110
O70435	Infl	LADAR	SLADIAREEASNFR	SNFGY	3		526.9343934	1577.77978	0.000451244	4	N	86	100
O70492	Infl	ADTRR	LITKPQNLNDAYGPPSNFLEIDVSNPQTVGVGR	GRFTT	3		1185.281553	3552.821259	0.000451244	16	N	10	43
O70492	Infl	RHVPF	RGDDGIFDDNFIEER	KQGLE	2		899.4060762	1796.796552	0.000979378	1	N	103	118
O70497	Infl	TSYKR	GFGSQLGEFWLGNDNIHALTTQGTSELR	VDLSD	3		1016.83237	3047.47371	0.000451244	8	N	165	193
O70566	Infl	VHDDR	SLILSEKEVLDLFEK	MMEDM	3		588.3332715	1761.976414	0.000622848	1	N	89	104
O70566	Infl	LESLR	VSLTSHPVSWVNNFGYEGLGVLLDVLEK	LLDKK	3		1024.873395	3071.596785	0.000662267	1	N	186	214
O88307	Infl	CIPQR	WACDGDADCQDGSDEDPVSCEK	KCNGF	2	C3:+57.021,C9:+57.021,C20:+57.021	1258.449403	2514.883206	0.000451244	6	N	1215	1237
O88307	Infl	QEHVK	SFSWGIDPYDQPNAIYIER	HEPFG	2		1136.039997	2270.064395	0.000451244	7	N	249	268
O88307	Infl	AEGLK	FSLSLENVLYYSPGGAGSDTLVR	YFANE	2		1223.118976	2444.222352	0.000451244	3	N	381	404
O88307	Infl	MSDER	NCPTTVCDADTQFR	CQESG	2	C2:+57.021,C7:+57.021	842.8563877	1683.697175	0.000451244	7	N	1110	1124
O88307	Infl	GETWK	TFVFSEKPVFVYGLLTEPGEK	STVFT	3		796.4231493	2386.246048	0.000451244	4	N	572	593
O88307	Infl	FYKGK	NAGSNACVPQPCSLLCLPK	ANNSK	2	C7:+57.021,C12:+57.021,C16:+57.021	1043.49738	2084.979159	0.000823681	2	N	1014	1033
O88307	Infl	CIPQR	WACDGDADCQDGSDEDPVSCEKK	CNGFH	3	C3:+57.021,C9:+57.021,C20:+57.021	882.0005231	2642.978169	0.0007646	1	N	1215	1238
O88307	Infl	SALIK	WESPYDSPDQDLFYAIAVK	DLIRK	2		1122.528931	2243.042262	0.002080925	1	N	1952	1971
O88307	Infl	LLHSK	ASNLLLGFDR	SHPNK	2		553.3041771	1104.592754	0.001352548	1	N	214	224
O88342	Infl	NLTLR	DYSGQGVVKLDVQPK	CVAVG	2		816.9337412	1631.851882	0.000451244	6	N	396	411
O88342	Infl	DGNVR	VYSILASTLKDEGK	LLEAK	2		762.4199353	1522.824271	0.000451244	17	N	470	484
O88342	Infl	RNGGK	SYIYSGSHDGHINYWDSETGENDSFSGK	GHTNQ	3		1051.443388	3151.306764	0.000622848	27	N	334	362
O88342	Infl	LKDQK	KCFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C2:+57.021	1171.895327	3512.662581	0.000451244	30	N	436	470
O88342	Infl	LLEAK	GPVTDVAYSHDGAFLAVCDASK	VVTVF	2	C18:+57.021	1140.533991	2279.052381	0.000451244	19	N	489	511
O88342	Infl	CDASK	VVTVFSVADGYSENNVFYGHHAK	IVCLA	3		847.4121949	2539.213185	0.000451244	10	N	511	534
O88342	Infl	VNCVR	FSPDGNRFATASADGQIFIYDGK	TGEKV	2		1239.09075	2476.1659	0.000451244	6	N	196	219
O88342	Infl	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C1:+39.994	1123.521339	3367.540618	0.0007646	6	N	437	470
O88342	Infl	TRPYR	LATGSDDNCAAFFEGPPFK	FKFTI	2	C9:+57.021	1022.459763	2042.903926	0.000451244	37	N	161	180
O88342	Infl	EGREK	FGAVFLWDTGSSVGEITGHNK	VINSV	2		1111.54799	2221.080379	0.000451244	9	N	126	147
O88342	Infl	LGESK	AHDGGIYAISWSPDSTHLLSASGDKTSK	IWDVN	3		967.8058208	2900.394062	0.000451244	4	N	231	259
O88342	Infl	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	2		1209.62476	2417.23392	0.000451244	8	N	43	65
O88342	Infl	PDGNR	FATASADGQIFIYDGK	TGEKV	2		852.417924	1702.820248	0.000451244	8	N	203	219
O88342	Infl	VVVAK	YAPSGFYIASGDISGK	LRIWD	2		816.8993671	1631.783134	0.000451244	13	N	65	81
O88342	Infl	QDAHR	LHHVSSLAWLDEHTLVTTSHDASVK	EWTIT	4		696.6087598	2782.403839	0.000451244	9	N	575	600
O88342	Infl	LGESK	AHDGGIYAISWSPDSTHLLSASGDK	TSKIW	2		1293.117496	2584.219392	0.000451244	11	N	231	256
O88342	Infl	DVQPK	CVAVGPGGYTVVVCIGQIVLLK	DQKKC	2	C1:+57.021,C14:+57.021	1151.636776	2301.257953	0.000451244	8	N	411	433
O88342	Infl	KSYIY	SGSHDGHINYWDSETGENDSFSGK	GHTNQ	2		1313.539807	2625.064014	0.000622848	1	N	338	362
O88342	Infl	QDAHR	LHHVSSLAWLDEHTLVTTSHDASVKEWTITY	-	3		1192.930632	3575.768495	0.000735798	3	N	575	606
O88342	Infl	TRPYR	LATGSDDNCAAFFEGPPFKFK	FTIGD	2	C9:+57.021	1160.041452	2318.067303	0.000622848	4	N	161	182
O88342	Infl	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVRVY	SILAS	3	C1:+57.021	1216.574254	3646.699361	0.000662267	2	N	437	472
O88342	Infl	YEIKK	VFASLPQVER	GVSKI	2		573.3198272	1144.624054	0.001264573	3	N	7	17
O88379	Infl	DADTK	DLTEALDEDADPTKSALSAVAALAAAWPQLHQGCSLK	SLDLD	4	C34:+57.021	966.7338671	3862.904268	0.001699387	1	N	504	541
O88379	Infl	QLELR	LRDFLLDIEDR	IYQGT	3		468.9214251	1403.740875	0.001943752	2	N	980	991
O88520	Infl	EHLPK	EIGNCTQITNLDLQHNDLLDLPDTIGNLSSLNR	LGLRY	3	C5:+57.021	1236.283251	3705.826352	0.000451244	9	N	255	288
O88536	Infl	YSLER	ALSEDSGQTSDSSTSSTSPPADIELKAP	-	2		1389.644135	2777.27267	0.0025889	1	N	323	351
O88536	Infl	YSLER	ALSEDSGQTSDSSTSSTSPPADIELK	AP-	2		1305.599196	2609.182792	0.002145581	1	N	323	349
O88544	Infl	LSASK	LYNNITFEELGALLEIPAAK	AEKIA	2		1110.102066	2218.188533	0.000451244	16	N	314	334

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88544	Infl	LKIAR	LYLEDDDPVQAEAYINR	ASLLQ	2		1012.484524	2022.953447	0.000662267	1	N	153	170
O88544	Infl	LSASK	LYNNITFEELGALLEIPAAKAEK	IASQM	3		849.7955343	2546.363203	0.000662267	2	N	314	337
O88569	Infl	FGDSR	GGGGNFGPGPGSNFR	GGSDG	2		689.3188785	1376.622157	0.000451244	31	N	213	228
O88569	Infl	FGGSR	NMGGPYGGGNYGPGGSGGSGGYGGR	SRY-	2		1095.456838	2188.898076	0.000451244	5	N	325	350
O88569	Infl	YGSGR	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	GGYGG	2		1248.02393	2494.03226	0.000451244	46	N	238	266
O88569	Infl	SGKKR	GFGFVTFDDHDPVDK	IVLQK	2		848.3866238	1694.757648	0.001162105	1	N	153	168
O88569	Infl	KEQFR	KLFIGGLSFETTEESLR	NYYEQ	2		964.01272	1926.00984	0.000451244	10	N	21	38
O88569	Infl	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	2		1139.081665	2276.147731	0.000451244	16	N	153	173
O88569	Infl	EHHLR	DYFEEYGKIDTIEIITDR	QSGKK	2		1110.539496	2219.063392	0.000451244	25	N	129	147
O88569	Infl	EQFRK	LFIGGLSFETTEESLRNYYEQWGK	LTDCV	2		1434.198486	2866.381372	0.0025889	1	N	22	46
O88569	Infl	VTVKK	LFVGGIKEDTEEHHLR	DYFEE	2		940.4872037	1878.958807	0.000451244	2	N	113	129
O88569	Infl	EEYGK	IDTIEIITDR	QSGKK	2		594.8276821	1187.639764	0.000451244	16	N	137	147
O88569	Infl	EQFRK	LFIGGLSFETTEESLR	NYYEQ	2		899.9652384	1797.914877	0.000451244	44	N	22	38
O88569	Infl	GFVTF	DDHDPVDKIVLQK	YHTIN	2		761.3995342	1520.783468	0.000451244	4	N	160	173
O88569	Infl	FRKLF	IGGLSFETTEESLR	NYYEQ	2		769.8889993	1537.762399	0.000870037	1	N	24	38
O88593	Infl	GHPVR	YVVISHTAGSFCNSPDSCEQQAR	NVQHY	2	C12:+57.021,C18:+57.021	1307.076528	2612.137456	0.000451244	93	N	42	65
O88593	Infl	ECSSR	LGHPVRYVVISHTAGSFCNSPDSCEQQAR	NVQHY	3	C18:+57.021,C24:+57.021	1091.515862	3271.524185	0.000451244	10	N	36	65
O88593	Infl	KRALR	AALNLLECGVSR	GFLRS	2	C8:+57.021	651.8456519	1301.675704	0.000451244	22	N	133	145
O88593	Infl	EQQAR	NVQHYHKNELGWCDVAYNFLIGEDGHVYEGR	GWNIK	3	C13:+57.021	1240.574699	3718.700698	0.000451244	22	N	65	96
O88593	Infl	QHYHK	NELGWCDVAYNFLIGEDGHVYEGRG	WNIKG	2	C6:+57.021	1435.645864	2869.276127	0.000451244	2	N	72	97
O88593	Infl	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	2	C6:+57.021	1407.135132	2812.254663	0.000451244	26	N	72	96
O88593	Infl	VKGHR	DVQSTLSPGDQLYQVIQSWEHYRE	-	2		1439.686274	2877.356949	0.000451244	27	N	158	182
O88593	Infl	VKGHR	DVQSTLSPGDQLYQVIQSWEHYR	E-	3		917.1125851	2748.314355	0.000662267	7	N	158	181
O88593	Infl	QSTLS	PGDQLYQVIQSWEHYRE	-	3		716.6768714	2147.007214	0.000622848	2	N	165	182
O88593	Infl	HPVRY	VVISHTAGSFCNSPDSCEQQAR	NVQHY	3	C11:+57.021,C17:+57.021	817.3658425	2449.074128	0.000451244	18	N	43	65
O88593	Infl	VKGHR	DVQSTLSPGDQLYQVIQSWEHY	RE-	2		1297.114422	2592.213244	0.000451244	13	N	158	180
O88593	Infl	CDVAY	NFLIGEDGHVYEGR	GWNIK	2		803.3869582	1604.758316	0.000451244	6	N	82	96
O88593	Infl	HYHKN	ELGWCDVAYNFLIGEDGHVYEGR	GWNIK	3	C5:+57.021	900.4117119	2698.211736	0.000622848	2	N	73	96
O88593	Infl	QHYHK	NELGWCDVAYNFLIGEDGHVY	EGRGW	2	C6:+57.021	1236.052548	2470.089495	0.000622848	1	N	72	93
O88593	Infl	GWNIK	GDHTGPIWNPMSIGITF	MGNFM	2	M11:+15.995	929.9438263	1857.872053	0.002080925	1	N	101	118
O88668	Infl	LKISR	IWVLDYFGGPK	VVTPE	2		647.8456778	1293.675756	0.001699387	2	N	196	207
O88685	Infl	NTQVK	VIAATNRVDILDPALLR	SGRLD	3		617.3673095	1849.078529	0.001463592	4	N	330	347
O88685	Infl	VDAEK	LKPGDLVGVNKDSYLILETLPTEYDSR	VKAME	3		1012.53656	3034.58628	0.000451244	11	N	147	174
O88685	Infl	FALAK	EKAPSIIFIDELDAIGTK	RFDSE	2		980.5360279	1959.056456	0.000451244	7	N	279	297
O88685	Infl	KTSTR	QTYFLPVIGLVDAEK	LKPGD	2		846.9645101	1691.91342	0.000622848	7	N	132	147
O88685	Infl	IKVNK	TLPYLVSNVIELLDVDPNDQEEDGANIDLDSQR	KGKCA	3		1233.934436	3698.779908	0.000451244	8	N	87	120
O88685	Infl	VGVNK	DSYLILETLPTEYDSR	VKAME	2		957.9707178	1913.925836	0.000451244	11	N	158	174
O88685	Infl	AATNR	VDILDPALLR	SGRLD	2		562.8378528	1123.660106	0.002663018	2	N	337	347
O88712	Infl	ALRAK	AFGFNVLFYDPYLSDGIER	ALGLQ	2		1112.042009	2222.068418	0.000451244	5	N	194	213
O88712	Infl	NIDIK	SAGDLGIAVCNVPAASVEETADSTLCHILNLYR	RTTWL	3	C10:+57.021,C26:+57.021	1172.908314	3515.701541	0.000451244	10	N	108	141
O88746	Infl	NTSQR	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	LRSEL	3		1045.550981	3133.629542	0.000451244	14	N	188	219
O88746	Infl	IVHDK	VLNLIQSWADAFR	SSPDL	2		766.9151545	1531.814709	0.000451244	12	N	116	129
O88783	Infl	VNVER	DIHSGLIGPLLICR	KGTLH	3	C13:+57.021	521.9610721	1562.859816	0.000451244	10	N	1698	1712
O88783	Infl	TFTYK	WNILEFDEPTENDAQCLTRPYYSDVDVTR	DIASG	3	C16:+57.021	1182.875821	3545.604063	0.000451244	9	N	482	511
O88783	Infl	VDVTR	DIASGLIGLLLICK	SRSLD	2	C13:+57.021	743.4393852	1484.86317	0.000451244	23	N	511	525
O88783	Infl	DDNQK	TSSPDLGQVSLSPDDNQK	TSSPD	2		944.4506808	1886.885762	0.002663018	1	N	1228	1246
O88783	Infl	AAQLR	QFYVAAQGILWNYHPEPTDPSLNSIPSFK	KIVYR	3		1107.219454	3318.634962	0.001162105	2	N	32	61
O88842	Infl	EKMHK	LLEVYEQLGGEEDIVNPANELIK	EGSIQ	2		1293.171406	2584.327211	0.000451244	12	N	346	369
O88842	Infl	EPDPK	VTLFRPQEDVSLTQCSDPQK	LLHIA	3	C15:+57.021	783.3902481	2347.147344	0.001264573	1	N	133	153
O88842	Infl	QCWLK	ALGTAVHGDTAGDRPGASQPQAPAGTDTP	-	3		906.1027487	2715.284846	0.000451244	4	N	704	733
O88844	Infl	LIKEK	LILPYVELDLHSYDLGIENR	DATND	3		791.4219198	2371.242359	0.000451244	2	N	29	49
O88844	Infl	RMYQK	GQETSTNPIASIFAWSR	GLAHR	2		932.9635614	1863.911523	0.000451244	11	N	321	338
O88844	Infl	GDQYR	ATDFVVPGPGKVEITYTPK	DGTQK	2		1010.04402	2018.07244	0.000823681	2	N	140	159
O88879	Infl	RKHPR	SLLILDDVWDPWVLK	AFDNQ	2		906.5012598	1810.98692	0.000451244	10	N	237	252
O88879	Infl	DKTAK	IWSFDLLSPLHELK	GHNGC	3		566.6474133	1696.91884	0.000662267	7	N	1110	1124
O88879	Infl	LIAGK	TGQIDYLPEAQVSCCCLSPHLEYVAFGDEDGAIK	IIELP	3	C14:+57.021,C15:+57.021,C16:+57.021	1281.583124	3841.725972	0.000451244	6	N	952	986
O88879	Infl	HLLGR	QPFPNIVQLGLCEPETSEVYR	QAKLQ	2	C12:+57.021	1238.612772	2475.209945	0.000622848	5	N	557	578
O88968	Infl	PWMDR	LSSEQLNPSVFVGLR	LSSMQ	2		823.4495585	1644.883517	0.000622848	7	N	44	59
O88968	Infl	WQLLR	APDTPLLQGIADYKPQDGETIELR	LVRW-	2		1320.679929	2639.344259	0.000451244	1	N	402	426
O88968	Infl	SVTLK	VASALSPYEQTFFVFAGSSLEDVLK	LAQDG	2		1353.189599	2704.363597	0.000451244	14	N	338	363
O88968	Infl	EDVLK	LAQDGGGFTYGTQASLSGPYLTSVLGK	DAGDR	2		1344.679929	2687.344259	0.000451244	3	N	363	390
O89053	Infl	YEDVR	VSQTTWDSGFCAVNPK	FMALI	2	C11:+57.021	898.9175339	1795.819468	0.000451244	35	N	29	45
O89053	Infl	GQPAK	ADQCYEDVRVSQTTWDSGFCAVNPK	FMALI	2	C4:+57.021,C20:+57.021	1467.145139	2932.274678	0.000451244	5	N	20	45
O89053	Infl	WLGGR	DAGPLLISLK	DGYVP	2		513.8138463	1025.612093	0.000622848	15	N	383	393

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O89053	Infl	MTVPR	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1058.519569	3172.535307	0.000451244	117	N	354	383
O89053	Infl	AVNPK	FMALICEASGGGAFLVLPLGK	TGRVD	2	C6:+57.021	1076.07097	2150.126339	0.001871652	1	N	45	66
O89053	Infl	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIR	YFEIT	4	C32:+57.021	1116.308933	4461.204533	0.001591523	3	N	253	293
O89053	Infl	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C32:+57.021	1282.976765	3845.906894	0.000451244	76	N	253	287
O89053	Infl	WLGGR	DAGPLLISLKDGYVPPK	SRELR	3		595.0053777	1781.992733	0.000622848	5	N	383	400
O89053	Infl	DSSIR	YFEITSEAPF	LHYLS	2		602.282576	1202.549552	0.000622848	13	N	293	303
O89053	Infl	DSSIR	YFEITSEAPFLHYLSMFSSK	ESQRG	3		799.7210897	2396.139869	0.000451244	5	N	293	313
O89053	Infl	SGVLL	PFFDPDTNIVYLCGK	GDSSI	2	C13:+57.021	893.4297458	1784.843892	0.000451244	7	N	272	287
O89053	Infl	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	2		1292.122247	2582.228894	0.000451244	24	N	359	383
O89053	Infl	SSGVL	LPFFDPDTNIVYLCGK	GDSSI	2	C14:+57.021	949.9717779	1897.927956	0.000823681	1	N	271	287
O89053	Infl	SARRR	ATPEPSGTPSSDTVSRLEEDVR	NLNAI	2		1165.55948	2329.103359	0.001871652	1	N	416	438
O89053	Infl	TVPRK	SDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1015.821248	3044.440344	0.000451244	5	N	355	383
O89053	Infl	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVY	LCGKG	3		1130.233206	3387.676218	0.000451244	8	N	253	283
O89053	Infl	KSDLF	QEDLYPPTAGPDPALTAEEWLGGRDAGPLLISLK	DGYVP	3		1197.617942	3589.830427	0.000823681	1	N	359	393
O89053	Infl	QEDLY	PPTAGPDPALTAEEWLGGRDAGPLLISLK	DGYVP	3		981.5261068	2941.55492	0.000451244	1	N	364	393
O89053	Infl	VLLPF	FDPDTNIVYLCGK	GDSSI	2	C11:+57.021	771.3691568	1540.722714	0.000622848	7	N	274	287
O89053	Infl	DSSIR	YFEITSEAPFLHY	LSMFS	2		808.8857283	1615.755857	0.0025889	1	N	293	306
O89053	Infl	LWDTK	HLEEPLSLQELDTSSGVLLPF	FDPDT	3		775.4060468	2323.194741	0.000622848	1	N	253	274
O89053	Infl	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYL	CGKGD	3		1167.927894	3500.760282	0.000979378	1	N	253	284
O89079	Infl	LFDVK	NAFYIGSYQQCINEAQR	VKLSS	2	C11:+57.021	1031.476279	2060.936957	0.000451244	24	N	23	40
O89079	Infl	VGGEK	LQEAYYIFQELADK	CSPTL	2		865.9359496	1729.856299	0.000451244	5	N	197	211
O89079	Infl	-M	APPVPGAVSGGSGEVDELFDVK	NAFYI	2		1064.034381	2126.053161	0.000451244	5	N	1	23
O89086	Infl	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVKDR	ETQRS	3		1255.964001	3764.868603	0.000451244	9	N	7	41
O89086	Infl	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	3		1165.587983	3493.740549	0.000451244	65	N	7	39
O89086	Infl	EGKLF	VGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	3		1078.87049	3233.588071	0.000451244	10	N	9	39
P00405	Infl	ELPIR	MLISSEDVLHSWAVPSLGLK	TDAIP	2		1091.582987	2181.150374	0.000451244	5	N	151	171
P00493	Infl	-MPTR	SPSVVISDDEPGYDLDLFCIPNHYAEDLEK	VFIPH	3	C19:+57.021	1146.529539	3436.565218	0.000451244	22	N	4	34
P00493	Infl	LCVLK	GGYKFFADLLDYIK	ALNRN	3		550.6244972	1648.850091	0.001352548	3	N	69	83
P00493	Infl	TLTGK	NVLIVEDIIDTGK	TMQTL	2		714.9013784	1427.787157	0.001463592	2	N	128	141
P00493	Infl	KGGYK	FFADLLDYIK	ALNRN	2		622.8322361	1243.648872	0.000451244	2	N	73	83
P00493	Infl	-M	PTRSPSVVISDDEPGYDLDLFCIPNHYAEDLEK	VFIPH	4	C22:+57.021	948.699493	3790.766772	0.000451244	2	N	1	34
P00493	Infl	KRTSR	SVGYRPDFVGFEIPDKF	VVGYA	3		658.3321535	1971.97306	0.002884417	1	N	170	187
P00493	Infl	-MPTR	SPSVVISDDEPGYDLDLFCIPNHY	AEDLE	2	C19:+57.021	1376.626274	2751.236948	0.000451244	3	N	4	28
P01027	Infl	GLAFK	TSQGLQTEQRADLECTKPAA	RRRRS	2	C15:+57.021	1102.534522	2203.053444	0.002080925	1	N	646	666
P01027	Infl	GNLLR	SEETKQNEAFSLTAK	GKGRG	2		841.9157455	1681.815891	0.002453667	1	N	1320	1335
P01027	Infl	LQEAR	DICEGQVNSLPGSINK	AGEYI	2	C3:+57.021	865.9228163	1729.830033	0.000451244	14	N	1155	1171
P01027	Infl	PGSVK	VYSYYNLEESCTR	FYHPE	2	C11:+57.021	842.3698852	1682.72417	0.000451244	19	N	1478	1491
P01027	Infl	LDPEK	LGQGGVQKVDVPAADLSDQVPDTDSETR	IILQG	3		966.4761404	2896.405021	0.000451244	4	N	951	979
P01027	Infl	GGVQK	VDVPAADLSDQVPDTDSETR	IILQG	2		1065.495817	2128.976033	0.000451244	35	N	959	979
P01027	Infl	KIPPK	SSVAVPYVIVPLK	IGQQE	2		686.4164673	1370.817335	0.000622848	2	N	891	904
P01027	Infl	LGLAR	SELEEDIIPEEDIISR	SHFPQ	2		943.9656324	1885.915665	0.000451244	13	N	748	764
P01027	Infl	SFEVR	VEPTETFYYIDDPNGLEVSIIAK	FLYGK	2		1307.152682	2612.289763	0.000451244	25	N	236	259
P01027	Infl	GRQVR	EPGQDLVVLSLPITPEFIPSFR	LVAYY	2		1227.668105	2453.32061	0.000451244	3	N	508	530
P01027	Infl	FRNAK	EADVSLTAFVLIALQEAR	DICEG	2		973.5338196	1945.052039	0.000451244	18	N	1137	1155
P01027	Infl	FRNAK	EADVSLTAFVLIALQEARDICEGQVNSLPGSINK	AGEYI	3	C21:+57.021	1219.964971	3656.871512	0.000451244	4	N	1137	1171
P01027	Infl	TAKDR	NRWEEPDQQLYNVEATSYALLALLLLK	DFDSV	3		1064.231471	3189.671013	0.000451244	8	N	1217	1244
P01027	Infl	LTQSK	IWDVVEKADIGCTPGSGK	NYAGV	2	C12:+57.021	966.4804984	1930.945397	0.000451244	4	N	614	632
P01027	Infl	IPVKR	DILSSNNQHGILPLSWNIPELVNMGQWK	IRAFY	3		1068.548917	3202.623352	0.000622848	7	N	178	206
P01027	Infl	KDRNR	WEEPDQQLYNVEATSYALLALLLLKDFDSVPPVVR	WLNEQ	3		1344.705528	4031.093184	0.001329271	1	N	1219	1254
P01027	Infl	YIIGK	DTWVEHWPEAEECQDQKYQK	QCEEL	3	C13:+57.021	869.3803003	2605.117501	0.001591523	1	N	1624	1644
P01027	Infl	HSLTR	VVIEDGVGDAVLTR	KVLME	2		721.8966274	1441.777655	0.000451244	24	N	291	305
P01027	Infl	LPVGK	TVVILIETPDGIPVKR	DILSS	3		584.0211393	1749.040018	0.000622848	2	N	162	178
P01027	Infl	KDRNR	WEEPDQQLYNVEATSYALLALLLLK	DFDSV	3		974.1834581	2919.526974	0.000451244	6	N	1219	1244
P01027	Infl	YIIGK	DTWVEHWPEAEECQDQK	YQKQC	2	C13:+57.021	1093.958116	2185.900632	0.000823681	3	N	1624	1641
P01027	Infl	DSETR	IILQGSPVVQMAEDAVDGER	LKHLI	2		1064.041683	2126.067767	0.001329271	1	N	979	999
P01027	Infl	AYVVK	VFSLAANLIAIDSHVLCGAVK	WLILE	2	C17:+57.021	1099.604022	2197.192444	0.000823681	2	N	1084	1105
P01027	Infl	NIFLK	DSITTWEILAVSLSDKK	GICVA	3		636.0109685	1905.009506	0.000451244	3	N	796	813
P01027	Infl	HSLTR	VVIEDGVGDAVLTRK	VLMEG	3		524.2986726	1569.872618	0.00091018	1	N	291	306
P01029	Infl	AWLHR	DSSTWLTAFVLK	ILSLA	2		684.3644317	1366.713263	0.000622848	5	N	1068	1080
P01029	Infl	HGAFR	STQDTVVTLDALSAYWIASHTTEEK	ALNVT	3		922.7876557	2765.339567	0.000451244	5	N	1296	1321
P01887	Infl	DWSFY	ILAHTEFTPTETDTYACR	VKHAS	2	C17:+57.021	1063.496877	2124.978154	0.000451244	13	N	83	101
P01887	Infl	MSFSK	DWSFYILAHTEFTPTETDTYACR	VKHAS	3	C22:+57.021	942.090527	2823.248181	0.001943752	1	N	78	101
P01942	Infl	AAWGK	IGGHGAEYGAEALER	MFASF	2		765.3713081	1528.727016	0.000451244	22	N	17	32
P01942	Infl	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	4		455.7250324	1818.86893	0.000451244	6	N	41	57
P01942	Infl	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		946.1583059	2835.451518	0.000451244	14	N	62	91

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P02088	Infl	-M	VHLTDAEKAAVSCLWGK	VNSDE	2	C13:+57.021	942.9857509	1883.955902	0.001871652	2	N	1	18
P02088	Infl	PWTQR	YFDSFGDLSSASAIMGNAK	VKAHG	2		990.9545453	1979.893491	0.000451244	4	N	41	60
P02089	Infl	PENFR	LLGNAIVIVLGHHLGK	DFTPA	4		414.2600481	1653.008992	0.001591523	4	N	105	121
P03958	Infl	LKTER	VGHGYHTIEDEALYNR	LLKEN	2		937.4455358	1872.875472	0.000451244	5	N	235	251
P03958	Infl	LANSK	VDPMPWNQTEGDVTPDDVVDLVNQGLQEGEQAFGIK	VRSIL	3		1314.290226	3939.847277	0.002813207	1	N	111	147
P03958	Infl	FKNDK	ANYSLNTDDPLIFK	STLDT	2		805.9071921	1609.798784	0.001463592	1	N	287	301
P04202	Infl	YLGNR	LLTPTDTPEWLSFDVTGVVR	QWLNQ	2		1123.589323	2245.163046	0.000451244	9	N	185	205
P04202	Infl	STRDR	VAGESADPEPEPEADYYAK	EVTRV	2		1019.450346	2036.885093	0.000622848	5	N	87	106
P04919	Infl	LLLKR	SHAEDLGNLEGVKPAVLTR	SGGAS	2		1003.537425	2005.05925	0.000451244	3	N	175	194
P04919	Infl	AVLTR	SGGASEPLLPHQPSLETQLYCGQAEGGSEGPSTSGTLK	IPPDS	3	C21:+57.021	1276.606171	3826.795112	0.000451244	2	N	194	232
P04919	Infl	VLVGR	ANFLEKPVLGFVR	LKEAV	3		497.2895603	1488.845281	0.000451244	7	N	246	259
P04919	Infl	LGFVR	LKEAVPLEDLVLPEPVGF	LLVLL	2		983.0513138	1964.087028	0.000622848	1	N	259	277
P05201	Infl	KVEQK	IANDNSLNHEYLPILGLAEFR	SCASR	2		1200.121853	2398.228106	0.000451244	6	N	60	81
P05201	Infl	-M	APPSVFAQVPQAPPVLVFK	LTADF	2		996.5700081	1991.124416	0.000823681	3	N	1	20
P05201	Infl	VMQRR	FLFPFFDSAYQGFASGDLEK	DAWAI	2		1143.541842	2285.068083	0.000451244	5	N	216	236
P05201	Infl	VGAYR	TDESQPWVLPVVR	KVEQK	2		763.4046196	1524.793639	0.000622848	9	N	42	55
P05202	Infl	TKDGR	ISVAGVTSGNVGYLAHAIHQVTK	-	4		581.320094	2321.249176	0.000823681	11	N	407	430
P05202	Infl	QIAAK	NLDKEYLPIGGLAEFCK	ASAEL	2	C16:+57.021	984.0010667	1965.986533	0.000451244	11	N	90	107
P05202	Infl	LKSGR	FVTVQTISGTGALR	VGASF	2		725.4071623	1448.798725	0.000451244	9	N	125	139
P05202	Infl	AEFCK	ASAELALGENNEVLK	SGRFV	2		779.410099	1556.804598	0.000451244	6	N	107	122
P05202	Infl	YYDPK	TCGFDFSGALEDISK	IPEQS	2	C2:+57.021	823.8722607	1645.728921	0.000451244	11	N	185	200
P06151	Infl	LMGER	LGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	3	C8:+57.021	1204.279335	3609.814606	0.000451244	19	N	177	212
P06151	Infl	SPHCK	LLIVSNPVDILTY	VAWKI	2		730.4244894	1458.833379	0.000451244	16	N	132	145
P06151	Infl	STMIK	GLYGINEDVFLSVPCILGQNGISDVVK	VTLTP	2	C15:+57.021	1453.75234	2905.48908	0.000451244	48	N	278	305
P06151	Infl	SPHCK	LLIVSNPVDILTYVAWK	ISGFP	2		972.5643914	1943.113183	0.000451244	44	N	132	149
P06151	Infl	STMIK	GLYGINEDVFLSVPCILGQNGISDVVKVTLTPEEEAR	LKKSA	3	C15:+57.021	1344.693028	4031.055684	0.000451244	18	N	278	315
P06151	Infl	GVSLK	SLNPELGTDADKEQWK	EVHKQ	2		915.947577	1829.879554	0.000451244	22	N	212	228
P06151	Infl	ARLKK	SADTLWGIQK	ELQF-	2		559.7961849	1117.57677	0.002374549	1	N	318	328
P06151	Infl	MATLK	DQLIVNLLKEEQAPQNK	ITVVG	2		990.5421759	1979.068752	0.000451244	10	N	5	22
P06151	Infl	VIKLK	GYTSWAIGLSVADLAESIMK	NLRRV	2		1056.538245	2111.06089	0.000451244	5	N	245	265
P06151	Infl	KEVHK	QVVDSAYEVIK	LKGYT	2		625.8355071	1249.655414	0.000662267	7	N	232	243
P06151	Infl	NLVQR	NVNIFKFIIPNIVK	YSPHC	3		553.6717817	1657.991945	0.000451244	3	N	112	126
P06151	Infl	KEQWK	EVHKQVVDSAYEVIK	LKGYT	2		872.4679482	1742.920296	0.000637154	4	N	228	243
P06151	Infl	KLKGY	TSWAIGLSVADLAESIMKNLR	RVHPI	3	M17:+15.995	764.4075336	2290.199201	0.002374549	2	N	247	268
P06745	Infl	KGGPR	VWFVSNIDGTHIAK	TLASL	2		793.9204368	1585.825274	0.000451244	7	N	180	194
P06745	Infl	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	2		1423.725065	2845.43453	0.000451244	24	N	523	550
P06745	Infl	KSGAR	VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	MIPCD	3		1105.881835	3314.622106	0.000451244	45	N	370	400
P06745	Infl	NLKLR	ELFEADPERFNNFSLNLNTNHGHILVDYSK	NLVNK	3		1178.574848	3532.701144	0.000451244	6	N	27	57
P06745	Infl	IIASK	TFTTQETITNAETAKEWFLEAAK	DPSAV	2		1315.65338	2629.29116	0.000451244	21	N	211	234
P06745	Infl	THIAK	TLASLSPETSLFIIASK	TFTTQ	2		889.5014568	1776.987314	0.000451244	17	N	194	211
P06745	Infl	VDYSK	NLVNKEVMQMLVELAK	SRGVE	3		620.3430084	1858.005625	0.000451244	7	N	57	73
P06745	Infl	GLHHK	ILLANFLAQTEALMK	GKLPE	2		838.4767309	1674.937862	0.000451244	5	N	423	438
P06745	Infl	GYTGK	SITDIINIGIGGSDLGPLMVTEALKPYSK	GGPRV	3		1001.542658	3001.604574	0.000451244	28	N	147	176
P06745	Infl	LLPHK	VFEGNRPTNSIVFTK	LTPFI	2		854.955008	1707.894416	0.000662267	9	N	466	481
P06745	Infl	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	2		1224.109277	2446.202954	0.000451244	4	N	36	57
P06745	Infl	IIASK	TFTTQETITNAETAK	EWFLE	2		828.410296	1654.804992	0.000451244	38	N	211	226
P06745	Infl	AETAK	EWFLEAAKDPSAVAK	HFVAL	2		831.4308344	1660.846069	0.000451244	3	N	226	241
P06745	Infl	KPYSK	GGPRVWFVSNIDGTHIAK	TLASL	4		489.2633191	1953.022076	0.001162105	3	N	176	194
P06745	Infl	RFNNF	SLNLNTNHGHILVDYSK	NLVNK	3		642.334557	1923.980271	0.000662267	1	N	40	57
P06745	Infl	KSGAR	VDHQTGPIVWGEPGTNGQHAF	YQLIH	2		1124.033038	2246.050476	0.002813207	1	N	370	391
P06745	Infl	TPLEK	NAPVLLALLGIWY	INCYG	2		721.9244595	1441.833319	0.000622848	4	N	314	327
P06745	Infl	KSGAR	VDHQTGPIVWGEPGTNGQHAFY	QLIHQ	2		1205.564702	2409.113805	0.002727428	2	N	370	392
P06745	Infl	THIAK	TLASLSPETSLF	IIASK	2		633.3353399	1264.65508	0.002453667	1	N	194	206
P06800	Infl	GPLNK	AQEDSRGVGTPEPTNSAEEPEHAANGSASPAPTQSS	-	3		1188.530472	3562.568017	0.001162105	3	N	1255	1291
P06800	Infl	QEDSR	GVGTPEPTNSAEEPEHAANGSASPAPTQSS	-	2		1439.142625	2876.26965	0.000451244	24	N	1261	1291
P06800	Infl	RKEPR	TVYQYQCTTWKGEELPAEPK	DLVSM	2	C7:+57.021	1214.578398	2427.141196	0.000451244	6	N	1102	1122
P06800	Infl	VKLVK	NVINVQTDLGIPETPKPSCGDPAARK	TLVSW	3	C19:+57.021	926.4802374	2776.417312	0.000451244	7	N	363	389
P06800	Infl	VKLVK	NVINVQTDLGIPETPKPSCGDPAAR	KTLVS	2	C19:+57.021	1325.168974	2648.322349	0.000622848	15	N	363	388
P06800	Infl	KATGR	EVTHIQFTSWPDHGVPEDPHLLLK	LRRRV	4		699.6097655	2794.407862	0.001264573	2	N	796	820
P06800	Infl	QYQFL	YDIIASIYPAQNGQVK	KTNSQ	2		890.4679482	1778.920296	0.001229886	2	N	1207	1223
P06800	Infl	YDYNR	VELSEINGDAGSTYINASYIDGFKEPR	KYIAA	3		982.4774813	2944.409044	0.000451244	2	N	680	707
P06800	Infl	LKPYK	YYEVSLLAYVNGK	IQRNG	2		759.8960961	1517.776592	0.000451244	4	N	440	453
P06800	Infl	LFCAL	FNLLESAETEDVVDVFQVVK	SLRKA	2		1141.084071	2280.152541	0.000451244	1	N	1168	1188
P06800	Infl	QTGLF	CALFNLLESAETEDVVDVFQVVK	SLRKA	2	C1:+39.994	1304.646252	2607.276905	0.000662267	1	N	1165	1188
P06800	Infl	LVHCR	DGSQQTGLFCALFNLLESAETEDVVDVFQVVK	SLRKA	3	C10:+57.021	1186.915505	3557.723116	0.000451244	11	N	1156	1188

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P06800	Infl	FCALF	NLLESAETEDVVDVFQVVK	SLRKA	2		1067.549864	2133.084127	0.000451244	9	N	1169	1188
P06800	Infl	DPAAR	KTLVSWPEPVSKPESASKPHGYVLCYK	NNSEK	4	C25:+57.021	772.6551657	3086.589463	0.001871652	1	N	388	415
P06800	Infl	RVNAF	SNFFSGPIVVHCSAGVGR	TGTYI	2	C12:+57.021	945.9678925	1889.920185	0.002663018	1	N	828	846
P06800	Infl	NMKKR	DPPSDPSPLEAEYQR	LPSYR	2		850.8922704	1699.768941	0.002145581	2	N	922	937
P06800	Infl	VQNAK	CGNEDCENVLNNLEECSQIK	NISVS	2	C1:+57.021,C6:+57.021,C16:+57.021	1213.006691	2423.997782	0.000451244	3	N	232	252
P06800	Infl	KVIVM	LTELVNGDQEVCAQYWGEGK	QTYGD	2	C12:+57.021	1148.531448	2295.047296	0.000451244	2	N	1047	1067
P06800	Infl	KSLRK	ARPGVVCSYEQYQFL	YDIIA	2	C7:+57.021	908.9382693	1815.860939	0.002212458	1	N	1192	1207
P06800	Infl	VIVML	TELVNGDQEVCAQYWGEGK	QTYGD	2	C11:+57.021	1091.989416	2181.963232	0.000451244	2	N	1048	1067
P07356	Infl	ILTNR	SNVQRQDIAFAYQR	RTKKE	2		848.4322314	1694.848863	0.000451244	5	N	63	77
P07356	Infl	LAKGR	RAEDGSVIDYELIDQDAR	ELYDA	2		1032.995787	2063.975974	0.000451244	34	N	178	196
P07356	Infl	AKGRR	AEDGSVIDYELIDQDAR	ELYDA	2		954.9452313	1907.874863	0.000451244	19	N	179	196
P07356	Infl	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAERDALNIETAVK	TKGVD	3		1331.655784	3991.943953	0.000451244	29	N	10	47
P07356	Infl	ETAVK	TKGVDEVTIVNILTNR	SNVQR	3		591.3357865	1770.983959	0.000451244	12	N	47	63
P07356	Infl	AVKTK	GVDEVTIVNILTNR	SNVQR	2		771.9284589	1541.841318	0.000451244	29	N	49	63
P07356	Infl	KASMK	GLGTDEDSLIEIICSR	TNQEL	2	C14:+57.021	889.4357565	1776.855913	0.000451244	33	N	119	135
P07356	Infl	PSALK	SALSGHLETVILGLLK	TPAQY	2		825.9936019	1649.971604	0.000451244	17	N	88	104
P07356	Infl	PSALK	SALSGHLETVILGLLKTPAQYDASELK	ASMKG	3		952.1907241	2853.548772	0.000451244	1	N	88	115
P07356	Infl	KKEVK	GDLENAFLNLVQCIQNKPLYFADR	LYDSM	3	C13:+57.021	946.8133279	2837.416584	0.000451244	9	N	249	273
P07356	Infl	KKEVK	GDLENAFLNLVQCIQNKPLYF	ADRLY	2	C13:+57.021	1248.633508	2495.251416	0.000451244	20	N	249	270
P07356	Infl	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAER	DALNI	2		1469.696839	2937.378078	0.001162105	1	N	10	37
P07356	Infl	KEMYK	TDLEKDIISDTSGDFR	KLMVA	2		906.4370421	1810.858484	0.000451244	12	N	152	168
P07356	Infl	ESIKK	EVKGDLENAFLNLVQCIQNKPLYF	ADRLY	2	C16:+57.021	1426.736493	2851.457386	0.000451244	7	N	246	270
P07356	Infl	IICSR	TNQELQEINRVY	KEMYK	2		753.8815086	1505.747417	0.000451244	10	N	135	147
P07356	Infl	LGLLK	TPAQYDASELK	ASMKG	2		611.8016643	1221.587729	0.000451244	1	N	104	115
P07356	Infl	EILCK	LSLEGDHSTPPSAYGSVKPY	TNFDA	2		1053.013448	2104.011297	0.000451244	8	N	10	30
P07356	Infl	AKGRR	AEDGSVIDYELIDQDARELYDAGVK	RKGTD	2		1392.664673	2783.313746	0.000451244	1	N	179	204
P07356	Infl	TKKEL	PSALKSALSGHLETVILGLLK	TPAQY	3		716.4319791	2146.272537	0.002663018	1	N	83	104
P07356	Infl	LPSAL	KSALSGHLETVILGLLK	TPAQY	3		593.6966556	1778.066567	0.000451244	6	N	87	104
P07356	Infl	ALKSA	LSGHLETVILGLLK	TPAQY	2		746.9590307	1491.902461	0.001329271	2	N	90	104
P07724	Infl	AILVR	YTQKAPQVSTPTLVEAAR	NLGRV	2		980.5290685	1959.042537	0.000451244	6	N	434	452
P07724	Infl	DTCCK	AADKDTCFSTEGPNLVTR	CKDAL	2	C7:+57.021	991.4681193	1980.920639	0.000451244	33	N	584	602
P07724	Infl	YAEQY	NEILTQCCAEADKESCLTPK	LDGVK	2	C7:+57.021,C8:+57.021,C16:+57.021	1184.03472	2366.053841	0.000451244	8	N	185	205
P07724	Infl	RYTQK	APQVSTPTLVEAAR	NLGRV	2		720.3967946	1438.777989	0.000451244	25	N	438	452
P07724	Infl	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	2	C11:+57.021	1077.014902	2152.014205	0.000451244	7	N	527	545
P07724	Infl	SLVER	RPCFSALTVDETYVPK	EFKAE	2	C3:+57.021	941.9723092	1881.929018	0.000451244	8	N	508	524
P07724	Infl	SLVER	RPCFSALTVDETYVPKEFK	AETFT	3	C3:+57.021	763.0527962	2286.134989	0.000451244	3	N	508	527
P07724	Infl	WAVAR	LSQTFPNADFAEITK	LATDL	2		841.425749	1680.835898	0.000451244	7	N	242	257
P07724	Infl	DLYEK	LGEYGFQNAILVR	YTQKA	2		740.4018799	1478.78816	0.000451244	515	N	421	434
P07724	Infl	DLYEK	LGEYGFQNAILVRY	TQKAP	2		821.9335442	1641.851488	0.000451244	5	N	421	435
P07724	Infl	KNLVK	TNCDLYEKLGEYGFQNAILVR	YTQKA	2	C3:+57.021	1252.118222	2502.220844	0.000451244	7	N	413	434
P07724	Infl	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPKNLVK	TNCDL	3	C1:+57.021,C2:+57.021,C10:+57.021	1135.549026	3403.623679	0.000451244	5	N	383	413
P07724	Infl	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	2	C1:+57.021,C2:+57.021,C10:+57.021	1475.674455	2949.33331	0.000622848	7	N	383	409
P07724	Infl	EQHFK	GLVLIAFSQYLQK	CSYDE	2		740.4326487	1478.849697	0.000451244	15	N	44	57
P07724	Infl	AEQLK	TVMDDFAQFLDTCCK	AADKD	2	C13:+57.021,C14:+57.021	925.8915822	1849.767564	0.000451244	8	N	569	584
P07724	Infl	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	3	C1:+39.994,C2:+57.021,C12:+57.021	935.7715763	2804.291329	0.000451244	5	N	460	483
P07724	Infl	YAEAK	DVFLGTFLYEYSR	RHPDY	2		805.3990029	1608.782406	0.000451244	32	N	347	360
P07724	Infl	PEDQR	LPCVEDYLSAILNR	VCLLH	2	C3:+57.021	831.929913	1661.844226	0.000451244	13	N	469	483
P07724	Infl	EVARR	HPYFYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	4	C23:+57.021,C24:+57.021,C32:+57.021	1104.505164	4413.989458	0.000451244	18	N	169	205
P07724	Infl	IPNLR	ENYGELADCCTK	QEPER	2	C9:+57.021,C10:+57.021	730.2951002	1458.5746	0.000451244	14	N	105	117
P07724	Infl	DEHAK	LVQEVTDFAK	TCVAD	2		575.3116678	1148.607736	0.000451244	21	N	65	75
P07724	Infl	TKVNK	ECCHGDLLECADDR	AELAK	2	C2:+57.021,C3:+57.021,C10:+57.021	875.3347308	1748.653862	0.000451244	38	N	267	281
P07724	Infl	TKVNK	ECCHGDLLECADDRAELAK	YMCEN	2	C2:+57.021,C3:+57.021,C10:+57.021	1131.482655	2260.94971	0.000451244	2	N	267	286
P07724	Infl	EKLGE	YGFQNAILVR	YTQKA	2		590.8278194	1179.640039	0.000662267	10	N	424	434
P07724	Infl	EQHFK	GLVLIAFSQY	LQKCS	2		555.8138463	1109.612093	0.002374549	1	N	44	54
P07724	Infl	LYEKL	GEYGFQNAILVR	YTQKA	2		683.8598479	1365.704096	0.000698008	1	N	422	434
P07742	Infl	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTKHPDYAILAAR	IAVSN	3		1325.37607	3973.104811	0.002453667	1	N	42	80
P07742	Infl	QLLNK	QIFETIYYGALEASCELAKEYGPYETYEGSPVSK	GILQY	3	C15:+57.021	1298.27688	3891.80724	0.000451244	8	N	529	563

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P07742	Infl	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTK	HPDYA	3		956.1818943	2865.522283	0.000451244	10	N	42	70
P07742	Infl	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	C15:+57.021	1103.540753	2205.065906	0.000451244	4	N	529	548
P07742	Infl	IYTRR	VLSGEFQIVNPHLLK	DLTER	3		565.3265627	1692.956288	0.000451244	3	N	628	643
P07759	Infl	HEKTR	ALYQTEAFTADFQQPTEAK	NLIND	2		1080.018731	2158.021861	0.000451244	3	N	157	176
P07759	Infl	QVVHK	AVLDVAETGTEAAAATGVIGGIR	KAILP	2		1071.574204	2141.132809	0.000451244	7	N	360	383
P07759	Infl	SLYKK	LALKNPDTNIVFSPLSISAALALVSLGAK	GKTME	3		975.2342642	2922.679393	0.000823681	2	N	62	91
P07759	Infl	KLALK	NPDTNIVFSPLSISAALALVSLGAK	GKTME	2		1249.697394	2497.379187	0.001763695	3	N	66	91
P07901	Infl	MAAKK	HLEINPDHSIIETLR	QKAEA	2		893.9764718	1785.937344	0.000451244	5	N	633	648
P07901	Infl	PIWTR	NPDDITNEEYGEFYK	SLTND	2		917.3948429	1832.774086	0.000451244	21	N	300	315
P07901	Infl	EIVKK	HSQFIGYPITLFVEKER	DKEVS	3		688.7024693	2063.084008	0.002374549	2	N	209	226
P07901	Infl	EIVKK	HSQFIGYPITLFVEK	ERDKE	3		593.6545679	1777.940304	0.00091018	5	N	209	224
P07901	Infl	DKSVK	DLVILLYETALLSSGFSLEDPQTHANR	IYRMI	3		1001.521021	3001.539664	0.000451244	19	N	661	688
P07901	Infl	YMAAK	KHLEINPDHSIIETLR	QKAEA	2		958.0239533	1914.032307	0.000451244	7	N	632	648
P07901	Infl	LVILL	YETALLSSGFSLEDPQTHANR	IYRMI	2		1168.561825	2335.108051	0.000451244	20	N	667	688
P07901	Infl	EIFLR	ELISNSSDALDKIR	YESLT	2		780.9155485	1559.815497	0.000451244	12	N	46	60
P07901	Infl	KENQK	HIYFITGETKDQVANSAFVER	LRKHG	2		1213.111485	2424.207371	0.000451244	8	N	490	511
P07901	Infl	GEFYK	SLTNDWEEHLAVK	HFSVE	2		771.3838842	1540.752168	0.000451244	6	N	315	328
P07901	Infl	EELNK	TKPIWTRNPDDITNEEYGEFYK	SLTND	3		906.1016861	2715.281658	0.000451244	5	N	293	315
P07901	Infl	SKQDR	TLTIVDTGIGMTKADLINNLGTIAK	SGTKA	3		858.4793293	2572.414588	0.000823681	2	N	87	112
P07901	Infl	SELLR	YYTSASGDEMVSLKDYCTR	MKENQ	2	C17:+57.021	1123.490935	2244.966269	0.001591523	1	N	465	484
P08003	Infl	VAKVR	EVSQPDWTPPPEVTLSLTK	DNFDD	2		1062.547124	2123.078648	0.000622848	8	N	158	177
P08003	Infl	ILTLK	QVQEFLKDGDDVVIIGLFQGDGDPAYLQYQDAANNLR	EDYKF	3		1375.678701	4124.012702	0.001329271	3	N	287	324
P08003	Infl	LEVAK	DFPEYTFAIADEEDYATEVK	DLGLS	2		1177.023876	2352.032151	0.000622848	2	N	436	456
P08003	Infl	KILKK	GQAVDYDGSRTQEEIVAK	VREVS	2		983.4797726	1964.943945	0.000979378	1	N	138	156
P08003	Infl	LSLTK	DNFDDVVNNADIILVEF	YAPWC	2		976.4683422	1950.921084	0.000823681	3	N	177	194
P08030	Infl	GLDSR	GFLFGPSLAQELGVGCVLIR	KQGKL	2	C16:+57.021	1067.080183	2132.144765	0.000451244	18	N	67	87
P08030	Infl	KGRER	LGPIPFFSLLQYD	-	2		755.4035569	1508.791514	0.000451244	8	N	167	180
P08030	Infl	LHQLR	AEVVECVSLVELTSLK	GRERL	2	C6:+57.021	888.476893	1774.938186	0.000451244	7	N	147	163
P08030	Infl	LEYGK	AELEIQKDALEPGQR	VVIVD	2		848.94738	1695.87916	0.000823681	2	N	107	122
P08030	Infl	ARRIR	SFPDFPIPGVLF	RDISP	2		668.3533357	1334.691071	0.000998612	2	N	14	26
P08030	Infl	GLDSR	GFLFGPSLAQELGVGCVLIRK	QGKLP	3	C16:+57.021	754.4210429	2260.239729	0.001162105	2	N	67	88
P08032	Infl	ENSIK	ALRDQAEVCQQQQAAPVDEAGR	EARVI	3	C9:+57.021	814.0596726	2439.155618	0.001352548	1	N	954	976
P08032	Infl	ENWIK	TIGGVISSPELAEDLTGTEILLER	HQEHH	2		1257.171406	2512.327211	0.001329271	2	N	1304	1328
P08032	Infl	ATRRK	LLVDSQLLQQLYQDSDDLKTWINK	KKKLA	3		959.5067122	2875.496737	0.001395409	1	N	574	598
P08032	Infl	EMLAR	EDPLKDLNDLAQELISSGTFNIDQIEEK	MNGVN	3		1058.861661	3173.561582	0.000823681	3	N	1657	1685
P08071	Infl	VTEAK	NCHLAIAPNHAVVSR	TDKVE	2	C2:+57.021	829.931113	1657.846626	0.000451244	11	N	603	618
P08071	Infl	VTEYK	ECHLAQVPSHAVVSR	STNDK	2	C2:+57.021	845.4284031	1688.841206	0.000451244	7	N	261	276
P08071	Infl	KPPYK	LRPVAAEVYGTK	EQPRT	3		435.2509941	1302.729582	0.000451244	14	N	91	103
P08071	Infl	ASKAR	VTWCAVGSEEKR	KCDQW	2	C4:+57.021	711.346016	1420.676432	0.000451244	9	N	362	374
P08071	Infl	ATTVQ	WCAVSNSEEEKCLR	WQNEM	2	C2:+57.021,C12:+57.021	884.3931374	1766.770675	0.000451244	11	N	25	39
P08071	Infl	AGALR	CLRDNAGDVAFTR	GSTVF	2	C1:+57.021	747.8598219	1493.704044	0.000451244	8	N	215	228
P08071	Infl	PGAQK	DRFPNLCSSCAGTGANK	CASSP	2	C7:+57.021,C10:+57.021	927.9147683	1853.813937	0.000451244	59	N	181	198
P08071	Infl	LYLTF	SYTTSIQNLNK	KQQDV	2		634.8282134	1267.640827	0.000451244	2	N	340	351
P08071	Infl	GADPK	SNLCALCIGDEKGENK	CAPNS	2	C4:+57.021,C7:+57.021	904.4193522	1806.823104	0.000451244	77	N	516	532
P08071	Infl	TTSEK	YLGKEYVIATER	LKQCS	2		721.3884382	1440.761276	0.000451244	8	N	677	689
P08071	Infl	ASKAR	VTWCAVGSEEK	RKCDQ	2	C4:+57.021	633.2954605	1264.575321	0.000451244	34	N	362	373
P08071	Infl	AQKDR	FPNLCSSCAGTGANK	CASSP	2	C5:+57.021,C8:+57.021	792.3507412	1582.685882	0.000451244	25	N	183	198
P08071	Infl	VAFTR	GSTVFEELPNKAER	DQYKL	2		788.9024411	1575.789282	0.000451244	36	N	228	242
P08071	Infl	VAFLK	DSTVLQNTDGKNTEEWAR	NLKLK	2		1032.485586	2062.955573	0.000451244	31	N	562	580
P08071	Infl	RSCKF	NEFFSQSCAPGADPK	SNLCA	2	C8:+57.021	827.8622273	1653.708855	0.000451244	87	N	501	516
P08071	Infl	LFQSK	TKNLLFNDNTECLAK	IPGKT	2	C12:+57.021	890.9488341	1779.882068	0.000451244	27	N	653	668
P08071	Infl	GADPK	SNLCALCIGDEK	GENKC	2	C4:+57.021,C7:+57.021	690.3183783	1378.621157	0.000451244	2	N	516	528
P08071	Infl	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	C1:+39.994	899.3911235	1796.766647	0.000451244	4	N	198	215
P08071	Infl	ANQTR	SCKFNEFFSQSCAPGADPK	SNLCA	2	C2:+57.021,C12:+57.021	1088.975023	2175.934446	0.000451244	11	N	497	516
P08071	Infl	CLAEK	AGNVAFLKDSTVLQNTDGK	NTEEW	2		989.5161581	1977.016716	0.000451244	5	N	554	573
P08071	Infl	YTAGK	CGLVPVLAENQK	SSKSN	2	C1:+57.021	664.3558524	1326.696105	0.000451244	43	N	422	434
P08071	Infl	RDQYK	LLCPDNTWKPVTEYK	ECHLA	2	C3:+57.021	932.4694023	1862.923205	0.000451244	16	N	246	261
P08071	Infl	VAAVR	REDAGFTWSSLR	GKKSC	2		712.8500115	1423.684423	0.000622848	5	N	458	470
P08071	Infl	RDQYK	LLCPDNTWKPVTEYKECHLAQVPSHAVVSR	STNDK	3	C3:+57.021,C17:+57.021	1178.92575	3533.753851	0.000451244	18	N	246	276
P08071	Infl	TRSCK	FNEFFSQSCAPGADPK	SNLCA	2	C9:+57.021	901.3964343	1800.777269	0.000451244	70	N	500	516
P08071	Infl	KFGKK	QASGFQLFASPSGQK	DLLFK	2		776.8918764	1551.768153	0.000451244	25	N	299	314
P08071	Infl	QSKTK	NLLFNDNTECLAK	IPGKT	2	C10:+57.021	776.3775132	1550.739426	0.000451244	19	N	655	668
P08071	Infl	NLKLK	DFELLCLDDTRKPVTEAK	NCHLA	2	C6:+57.021	1075.543827	2149.072054	0.000451244	4	N	585	603
P08071	Infl	RNGQR	CPGEFCLFQSK	TKNLL	2	C1:+57.021,C6:+57.021	686.8049068	1371.594214	0.000451244	43	N	642	653
P08071	Infl	AAVRR	EDAGFTWSSLR	GKKSC	2		634.7994559	1267.583312	0.000823681	5	N	459	470

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08071	Infl	QKSSK	SNGLDCVNRPVEGYLAVAAVR	REDAG	2	C6:+57.021	1130.579067	2259.142534	0.000451244	7	N	437	458
P08071	Infl	RDQYK	LLCPDNTWKPVTEY	KECHL	2	C3:+57.021	868.4219208	1734.828242	0.000451244	16	N	246	260
P08071	Infl	ARNLK	LKDFELLCLDDTR	KPVTE	2	C8:+57.021	819.4140957	1636.812591	0.000451244	9	N	583	596
P08071	Infl	PSGQK	DLLFKESAIGFVR	VPQKV	3		498.9492037	1493.824211	0.000622848	5	N	314	327
P08071	Infl	AVVSR	STNDKEEAIWELLR	QSQEK	2		852.4341054	1702.852611	0.000451244	45	N	276	290
P08071	Infl	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2		1085.071101	2168.126601	0.000451244	5	N	299	319
P08071	Infl	KVEVL	QQVLLDQQVQFGR	NGQRC	2		779.9209682	1557.826336	0.000451244	1	N	625	638
P08071	Infl	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	2		1172.137503	2342.259406	0.000451244	5	N	618	638
P08071	Infl	IATER	LKQCSSSPLLEACAFLTQ	-	2	C4:+57.021,C13:+57.021	1027.008334	2052.001069	0.000451244	57	N	689	707
P08071	Infl	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	2		1361.732299	2721.448998	0.000451244	25	N	144	169
P08071	Infl	KFGKK	QASGFQLFASPSGQKDLLF	KESAI	2		1021.023619	2040.031638	0.000451244	3	N	299	318
P08071	Infl	TERLK	QCSSSPLLEACAFLTQ	-	2	C2:+57.021,C11:+57.021	906.4188208	1810.822042	0.000451244	21	N	691	707
P08071	Infl	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKF	FSKSC	2		1435.266506	2868.517412	0.00091018	1	N	144	170
P08071	Infl	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKFFSK	SCVPG	3		1077.912073	3230.712818	0.001162105	8	N	144	173
P08071	Infl	ASRGR	VTCISFPTTEDCIVAIMKGDADAMSLDGGYIYTAGK	CGLVP	3	C3:+57.021,C12:+57.021	1290.936553	3869.78626	0.000662267	1	N	386	422
P08071	Infl	QKSSK	SNGLDCVNRPVEGY	LAVAA	2	C6:+57.021	790.3623945	1578.709189	0.000451244	18	N	437	451
P08071	Infl	DVGLY	LTFSYTTSIQNLNKK	QQDVI	2		879.4757733	1756.935947	0.001699387	3	N	337	352
P08071	Infl	ASRGR	VTCISFPTTEDCIVAIMK	GDADA	2	C3:+57.021,C12:+57.021	1043.006946	2083.998293	0.000451244	7	N	386	404
P08071	Infl	EKFGK	KQASGFQLFASPSGQK	DLLFK	2		840.9393579	1679.863116	0.001654178	2	N	298	314
P08071	Infl	VAFTR	GSTVFEELPNK	AERDQ	2		610.812032	1219.608464	0.000622848	13	N	228	239
P08071	Infl	TGIGR	SAGWKIPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	3		1084.579094	3250.713881	0.000823681	2	N	139	169
P08071	Infl	IGFVR	VPQKVDVGLYLTF	SYTTS	2		739.9168315	1477.818063	0.000637154	5	N	327	340
P08071	Infl	PVTEY	KECHLAQVPSHAVVSR	STNDK	3	C3:+57.021	606.6531898	1816.936169	0.000451244	6	N	260	276
P08071	Infl	KSSTR	QCIQAIVTNR	ADAMT	2	C2:+57.021	601.8194371	1201.623274	0.000622848	9	N	61	71
P08071	Infl	LYLTF	SYTTSIQNLNKK	QQDVI	2		698.8756949	1395.73579	0.000998612	2	N	340	352
P08071	Infl	TLRPY	LNWNGPPASLEEAVSK	FFSKS	2		856.4366481	1710.857696	0.000451244	6	N	153	169
P08071	Infl	IATER	LKQCSSSPLLEACAF	LTQ-	2	C4:+57.021,C13:+57.021	855.9131743	1709.810749	0.001763695	3	N	689	704
P08071	Infl	NKAER	DQYKLLCPDNTWKPVTEY	KECHL	2	C7:+57.021	1135.543827	2269.072054	0.000451244	5	N	242	260
P08071	Infl	IGFVR	VPQKVDVGLY	LTFSY	2		559.3167532	1116.617906	0.000622848	3	N	327	337
P08071	Infl	TGIGR	SAGWKIPIGTLRPY	LNWNG	3		520.2967149	1557.866745	0.002663018	1	N	139	153
P08103	Infl	IRCWK	NRPEERPTFEYIQSVLDDFYTATESQYQQQP	-	3		1260.58737	3778.738711	0.000451244	18	N	493	524
P08103	Infl	YISPR	STFSSLQELVLHYK	KGKDG	3		551.2950396	1650.861719	0.000451244	3	N	211	225
P08113	Infl	EKSEK	FAFQAEVNR	MMKLI	2		541.2754196	1080.535239	0.000622848	4	N	75	84
P08113	Infl	AKLLR	FQSSHHSTDITSLDQYVER	MKEKQ	2		1125.525243	2249.034886	0.000451244	21	N	511	530
P08113	Infl	GVGFY	SAFLVADKVIVTSK	HNNDT	2		739.4353884	1476.855177	0.000451244	4	N	200	214
P08113	Infl	CDKEK	NLLHVTDTGVGMTREELVK	NLGTI	3		704.7092955	2111.104487	0.000451244	7	N	142	161
P08113	Infl	LNFVK	GVVDSDDLPLNVSR	ETLQQ	2		743.3813415	1484.747083	0.000451244	3	N	434	448
P08113	Infl	REGSR	TDDEVVQREEEAIQLDGLNASQIR	ELREK	2		1364.673364	2727.331128	0.000451244	10	N	43	67
P08113	Infl	VVSQR	LTESPCALVASQYGWSGNMER	IMKAQ	2	C6:+57.021	1178.538751	2355.061901	0.001264573	1	N	639	660
P08113	Infl	RLLKK	GYEVIYLTEPVDEYCIQALPEFDGKR	FQNVA	3	C15:+57.021	1035.502596	3103.484389	0.000451244	14	N	561	587
P08113	Infl	LVRKY	SQFINFPIYVWSSK	TETVE	2		858.4437448	1714.87189	0.000451244	14	N	271	285
P08113	Infl	LDKIR	LISLTDENALAGNEELTVK	IKCDK	2		1015.536756	2029.057912	0.000451244	46	N	116	135
P08113	Infl	ERIMK	AQAYQTGKDISTNYYASQK	KTFEI	2		1069.01398	2136.012359	0.000451244	4	N	663	682
P08113	Infl	KNLVR	KYSQFINFPIYVWSSK	TETVE	2		1004.022891	2006.030181	0.000451244	3	N	269	285
P08113	Infl	TLVLK	EEASDYLELDTIK	NLVRK	2		763.3675654	1524.719531	0.000451244	7	N	252	265
P08113	Infl	NLVRK	YSQFINFPIYVWSSK	TETVE	2		939.9754091	1877.935218	0.000451244	3	N	270	285
P08113	Infl	EFLNK	MTEAQEDGQSTSELIGQFGVGFY	SAFLV	2		1247.558092	2493.100583	0.000451244	1	N	177	200
P08226	Infl	TGCLA	EGEPEVTDQLEWQSNQPWEQALNR	FWDYL	2		1442.163163	2882.310727	0.000451244	2	N	18	42
P08226	Infl	KAYKK	ELEEQLGPVAEETR	ARLGK	2		800.3971886	1598.778777	0.000823681	1	N	86	100
P08228	Infl	ADEER	HVGDLGNVTAGKDGVANVSIEDR	VISLS	2		1162.085999	2322.156398	0.000451244	9	N	80	103
P08228	Infl	-MAMK	AVCVLKGDGPVQGTIHFEQK	ASGEP	2	C3:+57.021	1092.067804	2182.120007	0.000451244	5	N	4	24
P08228	Infl	SIEDR	VISLSGEHSIIGR	TMVVH	2		684.3862298	1366.75686	0.000451244	4	N	103	116
P08228	Infl	VCVLK	GDGPVQGTIHFEQK	ASGEP	2		756.8762263	1511.736853	0.000451244	1	N	10	24
P08228	Infl	VTAGK	DGVANVSIEDR	VISLS	2		587.7890882	1173.562576	0.002884417	1	N	92	103
P08249	Infl	GHAGK	TIIPLISQCTPK	VDFPQ	2	C9:+57.021	685.8895281	1369.763456	0.000451244	15	N	203	215
P08249	Infl	QCTPK	VDFPQDQLATLTGR	IQEAG	2		780.9049838	1559.794368	0.000451244	14	N	215	229
P08249	Infl	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	2		1197.127136	2392.238671	0.000451244	13	N	52	74
P08249	Infl	RANVK	GYLGPEQLPDCLKGCDVVVIPAGVPR	KPGMT	2	C11:+57.021,C15:+57.021	1405.222464	2808.429328	0.000451244	9	N	78	104
P08249	Infl	SAQNN	AKVAVLGASGGIGQPLSLLLK	NSPLV	3		664.745898	1991.214294	0.001943752	1	N	24	45
P08249	Infl	QNNAK	VAVLGASGGIGQPLSLLLK	NSPLV	2		897.0489085	1792.082217	0.000451244	15	N	26	45
P08249	Infl	PDCLK	GCDVVVIPAGVPR	KPGMT	2	C2:+57.021	669.8638446	1337.712089	0.000451244	7	N	91	104
P08249	Infl	AMNGK	EGVVECSFVQSK	ETECT	2	C6:+57.021	684.8271248	1367.63865	0.000451244	41	N	269	281
P08249	Infl	RANVK	GYLGPEQLPDCLK	GCDVV	2	C11:+57.021	745.3716995	1488.727799	0.002519933	1	N	78	91
P08249	Infl	FVQSK	ETECTYFSTPLLLGKK	GLEKN	2	C4:+57.021	943.9823426	1885.949085	0.001463592	2	N	281	297
P08249	Infl	EVFKK	HGVYNPNKIFGVTTLDIVR	ANTFV	2		1072.087085	2142.15857	0.000451244	7	N	157	176

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08556	Infl	GGVGK	SALTIQLIQNHFVDEYDPTIEDSYRK	QVVID	3		1032.516047	3094.524742	0.000451244	17	N	16	42
P08556	Infl	GGVGK	SALTIQLIQNHFVDEYDPTIEDSYR	KQVVI	3		989.8177264	2966.429779	0.00307782	1	N	16	41
P08607	Infl	TVVNK	TVPVWSSSPPTCEK	IICSQ	2	C12:+57.021	787.8798887	1573.744177	0.001943752	1	N	228	242
P08607	Infl	ISNGK	HSGTEDFYPYNHGISYTCDPGFR	LVGSP	3	C18:+57.021	907.3875663	2719.139299	0.000451244	3	N	191	214
P08752	Infl	VKQMK	IIHEDGYSEEECRQY	RAVVY	2	C12:+57.021	964.41027	1926.80494	0.000451244	9	N	54	69
P08752	Infl	SGVIR	RLWADHGVQACFGR	SREYQ	3	C11:+57.021	558.2760537	1671.804761	0.000823681	5	N	129	143
P08752	Infl	NDLER	IAQSDYIPTQQDVLR	TRVKT	2		873.955205	1745.89481	0.000451244	29	N	162	177
P08752	Infl	ACFGR	SREYQLNDSAAYYLNDLER	IAQSD	2		1160.546175	2319.076751	0.000451244	21	N	143	162
P08752	Infl	LFEEK	ITQSSLTICFPEYTGANKYDEAASYIQSK	FEDLN	3	C9:+57.021	1095.85922	3284.554259	0.000451244	28	N	278	307
P08752	Infl	FGRSR	EYQLNDSAAYYLNDLER	IAQSD	2		1038.979605	2075.943611	0.000451244	21	N	145	162
P08752	Infl	RKDTK	EIYTHFTCATDTK	NVQFV	2	C8:+57.021	793.861696	1585.707792	0.000451244	14	N	318	331
P08752	Infl	LFEEK	ITQSSLTICFPEYTGANKY	DEAAS	2	C9:+57.021	1097.030552	2192.045505	0.000451244	3	N	278	297
P08752	Infl	LNKRK	DTKEIYTHFTCATDTK	NVQFV	2	C11:+57.021	965.9464884	1929.877377	0.001943752	1	N	315	331
P08752	Infl	LFEEK	ITQSSLTICFPEYTGANKYDEAASY	IQSKF	2	C9:+57.021	1415.150113	2828.284626	0.000451244	3	N	278	303
P08775	Infl	QIAEK	INAGFGDDLNCIFNDDNAEK	LVLRI	2	C11:+57.021	1121.48978	2240.96396	0.000622848	5	N	1234	1254
P08775	Infl	VDPVR	TTSNDIVEIFTVLGIEAVR	KALER	2		1039.062941	2076.110282	0.000637154	1	N	1356	1375
P08905	Infl	NYNTR	ATNYNRGDQSTDYGIFQINSR	YWCND	2		1210.565431	2419.115261	0.000451244	26	N	59	80
P08905	Infl	TNYNR	GDQSTDYGIFQINSR	YWCND	2		850.897887	1699.780174	0.000451244	10	N	65	80
P08905	Infl	DGKTP	RAVNACGINCSALLQDDITAAIQCAK	RVVRD	3	C6:+57.021,C10:+57.021,C24:+57.021	945.1300254	2832.366676	0.001839721	1	N	89	115
P08905	Infl	GKTPR	AVNACGINCSALLQDDITAAIQCAKR	VVRDP	2	C5:+57.021,C9:+57.021,C23:+57.021	1417.191138	2832.366676	0.000451244	7	N	90	116
P08905	Infl	GKTPR	AVNACGINCSALLQDDITAAIQCAK	RVVRD	2	C5:+57.021,C9:+57.021,C23:+57.021	1339.140583	2676.265565	0.000451244	66	N	90	115
P08905	Infl	RTLKR	NGMAGYYGVSLADWVCLAQHESNYNTR	ATNYN	3	C16:+57.021	1026.127758	3075.359875	0.000451244	5	N	32	59
P08905	Infl	YGVSL	ADWVCLAQHESNYNTR	ATNYN	2	C5:+57.021	982.4396962	1962.863792	0.000451244	9	N	43	59
P08905	Infl	MAGYY	GVSLADWVCLAQHESNYNTR	ATNYN	3	C9:+57.021	774.0310542	2319.069763	0.000823681	1	N	39	59
P09103	Infl	EEMTK	YKPESDELTAEKITEFCHR	FLEGK	2	C17:+57.021	1177.060373	2352.105145	0.001352548	5	N	328	347
P09103	Infl	GSEIR	LAKVDATEESDLAQQYGVR	GYPTI	2		1047.02963	2092.043659	0.000451244	8	N	80	99
P09103	Infl	ARVGA	DALEEEDNVLVLKK	SNFEE	2		807.9334069	1613.851214	0.000662267	3	N	19	33
P09103	Infl	IRLAK	VDATEESDLAQQYGVR	GYPTI	2		890.9215592	1779.827518	0.000451244	52	N	83	99
P09103	Infl	ARVGA	DALEEEDNVLVLK	KSNFE	2		743.8859253	1485.756251	0.000451244	7	N	19	32
P09103	Infl	TASPK	EYTAGREADDIVNWLK	KRTGP	3		627.3115295	1878.911188	0.000451244	4	N	116	132
P09103	Infl	GFKGK	ILFIFIDSDHTDNQR	ILEFF	2		917.4606545	1832.905709	0.000451244	3	N	287	302
P09103	Infl	KQPVK	VLVGANFEEVAFDEK	KNVFV	2		833.9202995	1665.824999	0.000451244	12	N	372	387
P09103	Infl	YTAGR	EADDIVNWLK	KRTGP	2		601.8067496	1201.597899	0.000451244	11	N	122	132
P09103	Infl	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	2		1320.681941	2639.348281	0.000451244	22	N	172	197
P09103	Infl	AATTL	SDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	3		1035.498499	3103.472098	0.000735798	3	N	142	172
P09103	Infl	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	DVESD	3		995.8366752	2984.486626	0.000451244	27	N	134	164
P09103	Infl	IGFFK	DVESDSAKQFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3		1157.910903	3470.709309	0.000451244	8	N	164	197
P09103	Infl	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	3		1272.957018	3815.847653	0.000451244	37	N	134	172
P09103	Infl	IIIAK	MDSTANEVEAVKVHSFPTLK	FFPAS	3		735.0408223	2202.099067	0.000622848	1	N	426	446
P09103	Infl	GGEIK	THILLFLPK	SVSDY	2		541.342574	1080.669548	0.002727428	1	N	256	265
P09103	Infl	LDFIK	HNQLPLVIEFTEQTAPK	IFGGE	2		983.0261617	1964.036723	0.000451244	10	N	232	249
P09103	Infl	PIWDK	LGETYKDHENIIIAK	MDSTA	2		872.4679482	1742.920296	0.000451244	3	N	411	426
P09103	Infl	GVFSK	YQLDKDGVVLFK	KFDEG	2		712.8933564	1423.771113	0.000662267	1	N	197	209
P09103	Infl	KQPVK	VLVGANFEEVAFDEKK	NVFVE	2		897.9677811	1793.919962	0.000451244	5	N	372	388
P09103	Infl	AATTL	SDTAAAESLVDSSEVTVIGFFK	DVESD	2		1137.063335	2272.11107	0.000451244	2	N	142	164
P09405	Infl	TLFVK	GLSEDTTEETLKESFEGSVR	ARIVT	2		1107.524574	2213.033548	0.000451244	15	N	574	594
P09405	Infl	TGSSK	GFGFVDFNSEEDAK	AAKEA	2		781.3444246	1560.673249	0.000451244	12	N	607	621
P09405	Infl	GTNRK	FGYVDFESAEDLEK	ALELT	2		824.8730149	1647.73043	0.000451244	11	N	350	364
P09405	Infl	VNELK	FAISELFAK	NDLAV	2		513.2874644	1024.559329	0.001162105	4	N	326	335
P09405	Infl	VNELK	FAISELFAKNDLAVVDVR	TGTNR	2		1004.049637	2006.083674	0.000735798	2	N	326	344
P09405	Infl	SGESK	TLVLSNLSYSATKETLEEVFEK	ATFIK	2		1251.155224	2500.294849	0.000451244	4	N	487	509
P09405	Infl	GTNRK	FGYVDFESAEDLEKALELTGLK	VFGNE	2		1237.621017	2473.226435	0.000451244	3	N	350	372
P09405	Infl	TLLAK	NLSFNITEDELKEVFEDAMEIR	LVSQD	3		881.4271822	2641.258147	0.000451244	3	N	400	422
P09405	Infl	SGESK	TLVLSNLSYSATK	ETLEE	2		698.888271	1395.760942	0.000451244	2	N	487	500
P09405	Infl	HGKPK	GYAFIEFASFEDAK	EALNS	2		797.8753606	1593.735121	0.002212458	3	N	524	538
P09405	Infl	KGYAF	IEFASFEDAKEALNSCNK	MEIEG	2	C16:+57.021	1036.983602	2071.951604	0.000451244	2	N	528	546
P09405	Infl	TGTNR	KFGYVDFESAEDLEK	ALELT	2		888.9204965	1775.825393	0.000451244	3	N	349	364
P09405	Infl	EDLEK	ALELTGLKVF	GNEIK	2		545.8294964	1089.643393	0.000451244	7	N	364	374
P09405	Infl	KTLVL	SNLSYSATKETLEEVFEK	ATFIK	2		1038.013114	2074.010628	0.000823681	1	N	491	509
P09411	Infl	KATSR	GCITIIGGGDTATCCAK	WNTED	2	C2:+57.021,C14:+57.021,C15:+57.021	877.896967	1753.778334	0.000451244	52	N	365	382
P09411	Infl	ASLSK	LGDVYVNDAFGTAHR	AHSSM	2		817.9002327	1633.784865	0.000451244	2	N	156	171

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P09411	Infl	TCCAK	WNTEDKVSHVSTGGGASLELLEGK	VLPGV	2		1257.627697	2513.239793	0.000451244	22	N	382	406
P09411	Infl	KNGVK	ITLPVDFVTADKFDENAK	TGQAT	2		1012.023285	2022.030969	0.000451244	20	N	279	297
P09411	Infl	NYFAK	ALESPERPFLAILGGAK	VADKI	2		885.0019582	1767.988316	0.000870037	1	N	199	216
P09411	Infl	EAVGR	AKQIVWNGPVGVFEWEAFAR	GTKSL	3		768.736173	2303.185119	0.000451244	4	N	330	350
P09411	Infl	VLFLK	DCVGPEVENACANPAAGTVILLENLR	FHVEE	2	C2:+57.021,C11:+57.021	1391.678618	2781.341636	0.000451244	24	N	97	123
P09411	Infl	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2		1053.034321	2104.053042	0.000451244	32	N	332	350
P09411	Infl	SLLGK	DVLFLKDCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C8:+57.021,C17:+57.021	1166.597299	3496.768498	0.00091018	5	N	91	123
P09411	Infl	LLEGK	VLPGVDALSNV	-	2		542.3063854	1082.597171	0.001352548	6	N	406	417
P09411	Infl	DVLFL	KDCVGPEVENACANPAAGTVILLENLR	FHVEE	2	C3:+57.021,C12:+57.021	1455.726099	2909.436599	0.000451244	3	N	96	123
P09411	Infl	AAELK	SLLGKDVLFL	KDCVG	2		552.8373214	1103.659043	0.001591523	2	N	86	96
P09411	Infl	NTEDK	VSHVSTGGGASLELLEGK	VLPGV	2		870.9604874	1739.905375	0.000451244	7	N	388	406
P09411	Infl	PMPDK	YSLEPVAAELK	SLLGK	2		610.3326002	1218.6496	0.001463592	3	N	75	86
P09411	Infl	SLLGK	DVLFLKDCVGPEVENACANPAAGTVIL	LENLR	2	C8:+57.021,C17:+57.021	1436.714669	2871.413738	0.000451244	6	N	91	118
P09411	Infl	FTFLK	VLNNMEIGTSLYDEEGAK	IVKDL	2		991.9729351	1981.93027	0.001463592	1	N	246	264
P09411	Infl	VLFLK	DCVGPEVENACANPAAGTVIL	LENLR	2	C2:+57.021,C11:+57.021	1079.001238	2155.986875	0.001352548	1	N	97	118
P0C0S6	Infl	DSLIK	ATIAGGGVIPHIHK	SLIGK	2		685.8993074	1369.783015	0.000622848	10	N	102	116
P0C0S6	Infl	RITPR	HLQLAIRGDEELDSLIK	ATIAG	2		975.5368936	1949.058187	0.000622848	5	N	85	102
P0C0S6	Infl	TAAVY	SAAILEYLTAEVLELAGNASKDLK	VKRIT	3		840.4588108	2518.353032	0.000637154	2	N	54	78
P0C0S6	Infl	TAAVY	SAAILEYLTAEVLELAGNASK	DLKVK	2		1082.081331	2162.147062	0.000451244	81	N	54	75
P0C0S6	Infl	AILEY	LTAEVLELAGNASK	DLKVK	2		708.3911779	1414.766756	0.000451244	28	N	61	75
P0C0S6	Infl	QLAIR	GDEELDSLIK	ATIAG	2		559.7829402	1117.55028	0.000451244	7	N	92	102
P0C0S6	Infl	YSAAI	LEYLTAEVLELAGNASK	DLKVK	2		910.9861708	1819.956742	0.000451244	2	N	58	75
P0C0S6	Infl	QLAIR	GDEELDSLIKATIAGGGVIPHIHK	SLIGK	4		618.3384838	2469.322735	0.000451244	2	N	92	116
P0C0S6	Infl	ILEYL	TAEVLELAGNASK	DLKVK	2		651.8491458	1301.682692	0.001162105	1	N	62	75
P10107	Infl	LALAK	GDRCQDLSVNQDLADTDAR	ALYEA	2	C4:+57.021	1074.982654	2147.949707	0.000451244	43	N	185	204
P10107	Infl	KQARF	LENQEQEYVQAVK	SYKGG	2		789.3944489	1576.773298	0.000451244	17	N	13	26
P10107	Infl	RDLAK	DITSDTSGDFR	KALLA	2		607.2707283	1212.525857	0.000451244	28	N	166	177
P10107	Infl	LAMLK	TPAQFDADELR	GAMKG	2		631.8047383	1261.593877	0.000451244	124	N	113	124
P10107	Infl	AKGDR	CQDLSVNQDLADTDAR	ALYEA	2	C1:+39.994	902.3943945	1802.773189	0.002519933	2	N	188	204
P10107	Infl	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	2		972.5316112	1943.047622	0.000451244	41	N	81	98
P10107	Infl	TTIVK	CATSTPAFFAEK	LYEAM	2	C1:+57.021	665.3111106	1328.606621	0.000451244	5	N	269	281
P10107	Infl	HDMNK	ALDLELKGDIEK	CLTTI	2		672.3749965	1342.734393	0.000451244	13	N	250	262
P10107	Infl	RQQIK	AAYLQENGKPLDEVLR	KALTG	2		908.4841296	1814.952659	0.000451244	128	N	81	97
P10107	Infl	LKQAR	FLENQEQEYVQAVK	SYKGG	2		862.9286559	1723.841712	0.000451244	122	N	12	26
P10107	Infl	EELKR	DLAKDITSDTSGDFR	KALLA	2		820.8922704	1639.768941	0.000451244	25	N	162	177
P10107	Infl	VQAVK	SYKGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1361.677721	2721.339842	0.000451244	7	N	26	53
P10107	Infl	GDYEK	ILVALCGGN	-	2	C6:+57.021	458.7499604	915.4843208	0.000451244	26	N	337	346
P10107	Infl	VKSYK	GGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1172.582561	2343.149522	0.000451244	21	N	29	53
P10107	Infl	IMVSR	SEIDMNEIKVFYQK	KYGIS	2		872.4352601	1742.85492	0.00091018	3	N	303	317
P10107	Infl	AGERR	KGTDVNVFTTILTSR	SFPHL	2		826.4548408	1650.894082	0.000451244	1	N	213	228
P10107	Infl	YQKKY	GISLCQAILDETKGDYEK	ILVAL	2	C5:+57.021	1020.501628	2038.987656	0.000451244	17	N	319	337
P10107	Infl	FYQKK	YGISLCQAILDETKGDYEK	ILVAL	2	C6:+57.021	1102.033292	2202.050984	0.000451244	55	N	318	337
P10107	Infl	FYQKK	YGISLCQAILDETK	GDYEK	2	C6:+57.021	805.9086462	1609.801692	0.000451244	10	N	318	332
P10107	Infl	DEVLR	KALTGHLEEVVLAMLK	TPAQF	2		876.5085624	1751.001525	0.000451244	4	N	97	113
P10107	Infl	AIMVK	GVDEATIIDILTKR	TNAQR	2		772.4386594	1542.861719	0.000451244	82	N	58	72
P10107	Infl	MVKGV	DEATIIDILTKR	TNAQR	2		694.3937205	1386.771841	0.000451244	8	N	60	72
P10107	Infl	GERRK	GTDVNVFTTILTSR	SFPHL	2		762.4073593	1522.799119	0.000451244	17	N	214	228
P10107	Infl	AIMVK	GVDEATIIDILTK	RTNAQ	2		694.3881039	1386.760608	0.000451244	272	N	58	71
P10107	Infl	EVLRK	ALTGHLEEVVLAMLK	TPAQF	2		812.4610809	1622.906562	0.000451244	21	N	98	113
P10107	Infl	RGAMK	GLGTDEDTLIEILTTR	SNEQI	2		873.960153	1745.904706	0.000451244	561	N	128	144
P10107	Infl	EVLRK	ALTGHLEEVVLAMLKTPAQFDADELR	GAMKG	3		956.5044261	2866.489878	0.000451244	1	N	98	124
P10107	Infl	LRKAL	TGHLEEVVLAMLK	TPAQF	2		720.4004919	1438.785384	0.000622848	1	N	100	113
P10107	Infl	AMKGL	GTDEDTLIEILTTR	SNEQI	2		788.9073891	1575.799178	0.000451244	6	N	130	144
P10107	Infl	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1236.630042	2471.244485	0.000451244	7	N	28	53
P10107	Infl	IMVKG	VDEATIIDILTKR	TNAQR	3		496.287885	1485.840255	0.000735798	3	N	59	72
P10107	Infl	RDLAK	DITSDTSGDFRK	ALLAL	2		671.3182098	1340.62082	0.000622848	26	N	166	178
P10107	Infl	MVKGV	DEATIIDILTK	RTNAQ	2		616.343165	1230.67073	0.001699387	1	N	60	71
P10107	Infl	YGISL	CQAILDETKGDYEK	ILVAL	2	C1:+57.021	835.3908176	1668.766035	0.000451244	20	N	323	337
P10107	Infl	LAMLK	TPAQFDADELRGAMK	GLGTD	2		825.4017515	1648.787903	0.000451244	3	N	113	128
P10107	Infl	GSAVS	PYPSFNVSSDVAALHK	AIMVK	2		866.4391908	1730.862782	0.000451244	2	N	37	53
P10107	Infl	AVSPY	PSFNVSSDVAALHK	AIMVK	2		736.3811445	1470.746689	0.002519933	2	N	39	53
P10107	Infl	QARFL	ENQEQEYVQAVK	SYKGG	2		732.8524168	1463.689234	0.001699387	1	N	14	26
P10107	Infl	MKGLG	TDEDTLIEILTTR	SNEQI	2		760.3966572	1518.777714	0.00091018	4	N	131	144
P10107	Infl	QRQQI	KAAYLQENGKPLDEVLR	KALTG	2		972.5316112	1943.047622	0.000451244	12	N	80	97
P10107	Infl	VKSYK	GGPGSAVSPYPSFNVSSDVAALH	KAIMV	2		1108.535079	2215.054558	0.001839721	3	N	29	52

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10126	Infl	MGKEK	THINIVVIGHVDSGK	STTTG	2		794.9444433	1587.873287	0.000451244	26	N	5	20
P10126	Infl	QDVYK	IGGIGTVPVGR	VETGV	2		513.3092625	1024.602925	0.000451244	14	N	255	266
P10126	Infl	NGQTR	EHALLAYTLGVK	QLIVG	2		657.8749666	1313.734333	0.000451244	21	N	134	146
P10126	Infl	FETSK	YYVTIIDAPGHRDFIK	NMITG	2		954.5048651	1906.99413	0.000451244	5	N	84	100
P10126	Infl	YSQKR	YEEIVKEVSTYIK	KIGYN	3		534.2876621	1599.839586	0.000451244	2	N	166	179
P10126	Infl	VPVGR	VETGVLKPGMVVTFAPVNVTTEVK	SVEMH	2		1258.196173	2514.376746	0.000451244	4	N	266	290
P10126	Infl	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C16:+57.021	1041.555695	3121.643684	0.000451244	15	N	218	247
P10126	Infl	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C15:+57.021	998.8573735	2993.54872	0.000451244	26	N	219	247
P10126	Infl	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK	IGGIG	3	C15:+57.021	1317.701746	3950.081839	0.000451244	8	N	219	255
P10126	Infl	FETSK	YYVTIIDAPGHR	DFIKN	2		702.8676729	1403.719746	0.000451244	19	N	84	96
P10126	Infl	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPLQDVY	KIGGI	3	C15:+57.021	1275.003425	3821.986876	0.000451244	9	N	219	254
P10126	Infl	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPL	RLPLQ	3	C15:+57.021	946.8236697	2837.447609	0.000451244	8	N	219	246
P10126	Infl	RDFIK	NMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	2	C11:+57.021	1455.22309	2908.43058	0.000622848	2	N	100	129
P10126	Infl	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPL	QDVYK	3	C15:+57.021	1106.597671	3316.769613	0.002813207	1	N	219	250
P10126	Infl	ETSKY	YVTIIDAPGHR	DFIKN	2		621.3360086	1240.656417	0.001264573	2	N	85	96
P10126	Infl	QVIIL	NHPGQISAGYAPVLDCHTAHIACK	FAELK	2	C16:+57.021,C23:+57.021	1309.123616	2616.231631	0.000823681	1	N	347	371
P10126	Infl	ETSKY	YVTIIDAPGHRDFIK	NMITG	2		872.9732008	1743.930802	0.000451244	3	N	85	100
P10126	Infl	YSQKR	YEEIVKEVSTY	IKKIG	2		680.3380796	1358.660559	0.000451244	5	N	166	177
P10126	Infl	EAAGF	TAQVIILNHPGQISAGYAPVLDCHTAHIACK	FAELK	3	C23:+57.021,C30:+57.021	1119.239669	3354.695608	0.000451244	16	N	340	371
P10126	Infl	SGTTL	LEALDCILPPTRPTDKPLRLPLQDVYK	IGGIG	3	C6:+57.021	1054.584925	3160.731376	0.001162105	5	N	228	255
P10126	Infl	APGHR	DFIKNMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	3	C15:+57.021	1138.242788	3411.704964	0.000622848	1	N	96	129
P10126	Infl	MGKEK	THINIVVIGHVDSGKSTTTGHLIYK	CGGID	3		897.4928488	2689.455146	0.000451244	6	N	5	30
P10126	Infl	KVTRK	DGSASGTTLLEALDCILPPTRPTDK	PLRLP	3	C15:+57.021	876.7780604	2627.310781	0.000622848	7	N	219	244
P10126	Infl	SGTTL	LEALDCILPPTRPTDKPLR	LPLQD	3	C6:+57.021	735.7405526	2204.198258	0.001654178	1	N	228	247
P10518	Infl	HPLLR	SWQTAASTVSASNLIYPIFVTDVPDDVQPIASLPGVAR	YGVNQ	3		1329.356899	3985.047296	0.000451244	4	N	17	55
P10605	Infl	TFDAR	EQWSNCPTIGQIR	DQGSC	2	C6:+57.021	794.8807544	1587.745909	0.000451244	21	N	87	100
P10605	Infl	TFDAR	EQWSNCPTIGQIRDQGSCGSCWAFGAVEAISDR	TCIHT	3	C6:+57.021,C18:+57.021,C21:+57.021	1248.219291	3741.634472	0.000451244	3	N	87	120
P10605	Infl	IGQIR	DQGSCGSCWAFGAVEAISDR	TCIHT	2	C5:+57.021,C8:+57.021	1086.957362	2171.899123	0.000451244	19	N	100	120
P10605	Infl	HTNGR	VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTKK	GLVSG	3	C13:+57.021,C14:+57.021,C18:+57.021,C22:+57.021	1374.941051	4121.799754	0.000451244	7	N	128	165
P10605	Infl	NGVPY	WLAANSWNLDWGDNGFFK	ILRGE	2		1070.997936	2139.980271	0.000451244	9	N	293	311
P10605	Infl	HTNGR	VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTK	KGLVS	3	C13:+57.021,C14:+57.021,C18:+57.021,C22:+57.021	1332.24273	3993.704791	0.000451244	21	N	128	164
P10605	Infl	AEIYK	NGPVEGAFTVFSDFLTYK	SGVYK	2		996.4916204	1990.967641	0.000451244	11	N	245	263
P10605	Infl	GHAIR	ILGWGVENGVPYWLAANSWNLDWGDNGFFK	ILRGE	3		1142.551315	3424.630545	0.000823681	5	N	281	311
P10605	Infl	FKILR	GENHCGIESEIVAGIPR	TDQYW	2	C5:+57.021	919.4469899	1836.87838	0.000451244	6	N	314	331
P10605	Infl	YKEDK	HFGYTSYSVSNSVK	EIMAE	2		788.3760591	1574.736518	0.000451244	1	N	223	237
P10639	Infl	LIESK	EAFQEALAAAGDK	LVVVD	2		660.8256707	1319.635741	0.000451244	53	N	8	21
P10639	Infl	LIESK	EAFQEALAAAGDKLVVVDFSATWCGPCK	MIKPF	3	C24:+57.021,C27:+57.021	1014.1565	3039.446101	0.000451244	275	N	8	36
P10639	Infl	SGANK	EKLEASITEYA	-	2		627.3171472	1252.618694	0.000451244	5	N	94	105
P10639	Infl	AAGDK	LVVVDFSATWCGPCK	MIKPF	2	C11:+57.021,C14:+57.021	869.9182597	1737.820919	0.000451244	1	N	21	36
P10639	Infl	LIESK	EAFQEALAAAGDKLVVVDF	SATWC	2		997.0180023	1992.020405	0.000662267	6	N	8	27
P10639	Infl	SLCDK	YSNVVFLEVDVDDCQDVAADCEVK	CMPTF	2	C14:+57.021,C21:+57.021	1395.117724	2788.219849	0.000451244	22	N	48	72
P10639	Infl	SNVVF	LEVDVDDCQDVAADCEVK	CMPTF	2	C8:+57.021,C15:+57.021	1040.445961	2078.876322	0.002453667	1	N	54	72
P10649	Infl	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	2		1087.586386	2173.157173	0.000451244	5	N	50	69
P10649	Infl	DKVTY	VDFLAYDILDQYR	MFEPK	2		815.9097348	1629.80387	0.000451244	14	N	155	168
P10649	Infl	NEKFK	LGLDFPNLPYLIDGSHK	ITQSN	2		950.0046979	1897.993796	0.000451244	7	N	52	69
P10649	Infl	MFEPK	CLDAFPNLRDFLAR	FEGLK	3	C1:+57.021	569.9597312	1706.855794	0.001352548	2	N	173	187
P10649	Infl	MFEPK	CLDAFPNLR	DFLAR	2	C1:+57.021	553.2768737	1104.538147	0.001463592	2	N	173	182
P10711	Infl	AAALR	TGDDYVAIGADEEELGSQIEEAIYQEIR	NTDMK	3		1038.486482	3112.436047	0.000622848	5	N	153	181
P10711	Infl	AAALR	TGDDYVAIGADEEELGSQIEEAIY	QEIRN	2		1294.08265	2586.149701	0.000622848	3	N	153	177
P10810	Infl	CEQVR	VFPALSTLDLSDNPELGER	GLISA	2		1037.029098	2072.042597	0.000451244	15	N	187	206
P10810	Infl	ELGER	GLISALCPLKFPTLQVLALR	NAGME	3	C7:+57.021	737.4416669	2209.301601	0.000451244	6	N	206	226
P10810	Infl	FGALR	VLGISGLQELTLENLEVTGTAPPPLLEATGPDLNILNLR	NVSWA	3		1361.086409	4080.235826	0.000998612	2	N	107	146
P10852	Infl	DHLLR	LYQLLLFTLPGTPVFSYGDELGLQGALPGQPAK	APLMP	3		1168.632864	3502.875192	0.000451244	5	N	345	378
P10852	Infl	RGKER	SLLHGDFHALSSSPDLFSYIR	HWDQN	2		1181.595471	2361.175342	0.001395409	1	N	427	448
P10852	Infl	ATKMK	EALSSWLQDGVDGFQFR	DVGKL	2		977.9688437	1953.922087	0.000451244	5	N	225	242
P10852	Infl	GRSAR	LGASNLPAGISLPASAK	LLLST	2		783.9466516	1565.877703	0.001264573	1	N	470	487
P10852	Infl	ETDLK	QINPTLGSQEDFKDLLQSAK	KKSIH	3		744.7222579	2231.143374	0.002813207	1	N	171	191
P10852	Infl	ARQSR	EEDTSLKLENLSLNPYEGLLLQFPFVA	-	3		1027.201177	3078.580132	0.000662267	1	N	499	526
P10852	Infl	SAKKK	SIHIILDLTPNYQGQNAWFLPAQADIVATK	MKEAL	3		1113.25802	3336.75066	0.002374549	1	N	193	223
P10853	Infl	TITSR	EIQTAVRLLLPGELAK	HAVSE	2		876.0254334	1750.035267	0.00091018	4	N	93	109
P10853	Infl	GISSK	AMGIMNSFVNDIFER	IASEA	2		872.4138052	1742.81201	0.000451244	12	N	58	73
P10853	Infl	SSKAM	GIMNSFVNDIFER	IASEA	2		771.3750054	1540.734411	0.001943752	1	N	60	73

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10853	Infl	AMGIM	NSFVNDIFER	IASEA	2		620.8019986	1239.588397	0.001229886	1	N	63	73
P11247	Infl	ISLPR	IICDNTGITTVSK	NNIFM	2	C3:+57.021	711.3691568	1420.722714	0.000451244	70	N	675	688
P11247	Infl	AKLNR	QNQIVVDEIRER	LFEQV	2		749.9027754	1497.789951	0.000451244	3	N	533	545
P11247	Infl	TTVSK	NNIFMSNTYPR	DFVSC	2	M5:+15.995	686.8199086	1371.624217	0.000451244	41	N	688	699
P11247	Infl	ALTSF	VDASGVYGSEDPLAR	KLRNL	2		768.3709738	1534.726348	0.000451244	18	N	310	325
P11247	Infl	ISLPR	IICDNTGITTVSKNNIFMSNTYPR	DFVSC	2	C3:+57.021,M18:+15.995	1388.175985	2774.336371	0.000662267	5	N	675	699
P11247	Infl	SVDPR	IANVFTNAFR	YGHTL	2		576.8121693	1151.608739	0.000451244	23	N	463	473
P11247	Infl	FSFFT	GLNCETSCLQQPPCFPLK	IPPND	2	C4:+57.021,C8:+57.021,C14:+57.021	1074.997212	2147.978825	0.000451244	39	N	251	269
P11247	Infl	SFFTG	LNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C3:+57.021,C7:+57.021,C13:+57.021	961.1313663	2880.370699	0.000451244	13	N	252	276
P11247	Infl	FASWR	VVLEGGIDPILR	GLMAT	2		640.8827917	1279.749983	0.000451244	37	N	510	522
P11247	Infl	FSFFT	GLNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C4:+57.021,C8:+57.021,C14:+57.021	980.1385209	2937.392163	0.000451244	32	N	251	276
P11247	Infl	YNAWR	RFCGLPQPSTVGELGTVLK	NLELA	2	C3:+57.021	1030.054165	2058.09273	0.000451244	1	N	577	596
P11247	Infl	NAWRR	FCGLPQPSTVGELGTVLK	NLELA	2	C2:+57.021	952.0036093	1901.991619	0.000451244	52	N	578	596
P11247	Infl	FRKLR	DGDRFWWENPGVFSK	QQRQA	2		920.4266147	1838.837629	0.000622848	2	N	647	662
P11247	Infl	NITIR	NQINALTSFVDASGVYGSEDPLARK	LRNLT	2		1326.667353	2651.319106	0.000451244	6	N	301	326
P11247	Infl	RDGDR	FWWENPGVFSK	QQRQA	2		698.8383841	1395.661168	0.000451244	21	N	651	662
P11247	Infl	RAFVR	WLPAEYEDGVSMPFGWTPGVNR	NGFKV	2		1254.586789	2507.157979	0.000451244	2	N	171	193
P11247	Infl	EPNGR	VGQLLACLIGTQFR	KLRDG	2	C7:+57.021	788.4377082	1574.859816	0.000451244	33	N	630	644
P11247	Infl	RTAVR	AADYLHVALDLLK	RKLQP	3		481.2736873	1440.797662	0.000451244	3	N	88	101
P11247	Infl	NITIR	NQINALTSFVDASGVYGSEDPLAR	KLRNL	2		1262.619872	2523.224143	0.000451244	73	N	301	325
P11247	Infl	SKQQR	QALASISLPR	IICDN	2		528.3145448	1054.61349	0.000622848	17	N	665	675
P11247	Infl	SFFTG	LNCETSCLQQPPCFPLK	IPPND	2	C3:+57.021,C7:+57.021,C13:+57.021	1046.486481	2090.957361	0.000451244	25	N	252	269
P11247	Infl	EPNGR	VGQLLACLIGTQF	RKLRD	2	C7:+57.021	710.3871526	1418.758705	0.000622848	14	N	630	643
P11247	Infl	QINAL	TSFVDASGVYGSEDPLAR	KLRNL	2		935.9450343	1869.874469	0.000451244	11	N	307	325
P11247	Infl	NAWRR	FCGLPQPSTVGELGTVLKNLELAR	KLMAQ	2	C2:+57.021	1300.199546	2598.383493	0.001162105	1	N	578	602
P11247	Infl	NAWRR	FCGLPQPSTVGELGTVL	KNLEL	2	C2:+57.021	887.9561278	1773.896656	0.000451244	3	N	578	595
P11247	Infl	AKLNR	QNQIVVDEIR	ERLFE	2		607.3309232	1212.646246	0.000451244	16	N	533	543
P11247	Infl	LPAEY	EDGVSMPFGWTPGVNR	NGFKV	2	M6:+15.995	882.9047011	1763.793802	0.000451244	10	N	177	193
P11247	Infl	VPLAR	QVSNAIVRFPNDQLTK	DQERA	2		915.4975714	1828.979543	0.00091018	4	N	202	218
P11247	Infl	RALMF	MQWGQFLDHDITLTPEPATR	FSFFT	2		1178.573682	2355.131764	0.000451244	8	N	226	246
P11247	Infl	DPRIK	NQKDCIPFFR	SCPAC	2	C5:+57.021	662.8272621	1323.638924	0.001943752	1	N	278	288
P11247	Infl	RTAVR	AADYLHVALDLLKR	KLQPL	3		533.307391	1596.898773	0.000698008	2	N	88	102
P11247	Infl	RAFVR	WLPAEYEDGVSMPF	GWTPG	2	M12:+15.995	828.8667216	1655.717843	0.001699387	2	N	171	185
P11247	Infl	ISLPR	IICDNTGITTVSKN	NIFMS	2	C3:+57.021	768.3906206	1534.765641	0.002813207	1	N	675	689
P11247	Infl	QWGQF	LDHDITLTPEPATR	FSFFT	2		789.9102661	1577.804932	0.001463592	1	N	232	246
P11352	Infl	LNSLK	YVRPGGGFEPNFTLFEK	CEVNG	2		979.4944974	1956.973395	0.000451244	7	N	95	112
P11352	Infl	MCAAR	LSAAAQSTVYAFSARPLTGGEPVSLGSLR	GKVLL	2		1453.772684	2905.529768	0.002981883	1	N	5	34
P11352	Infl	RYSRR	FRTIDIEPDIETLLSQQSGNS	-	2		1182.090416	2362.165231	0.000451244	9	N	180	201
P11352	Infl	SRRFR	TIDIEPDIETLLSQQSGNS	-	2		1030.505653	2058.995706	0.000451244	16	N	182	201
P11352	Infl	RLGPR	GLVVLGFPCNQFGHQENGKNEEILNSLK	YVRPG	3	C9:+57.021	1047.864751	3140.570853	0.001699387	1	N	67	95
P11352	Infl	AFSAR	PLTGGEPVSLGSLR	GKVLL	2		691.8860627	1381.756525	0.000622848	2	N	20	34
P11352	Infl	MCAAR	LSAAAQSTVYAFSAR	PLTGG	2		771.8997014	1541.783803	0.001654178	1	N	5	20
P11499	Infl	YMMAK	KHLEINPDHPIVETLR	QKAEA	2		956.026496	1910.037392	0.000451244	5	N	623	639
P11499	Infl	KETQK	SIYYITGESKEQVANSAFVER	VRKRG	2		1196.095501	2390.175402	0.000451244	7	N	481	502
P11499	Infl	PIWTR	NPDDITQEEYGEFYK	SLTND	2		924.4026679	1846.789736	0.000451244	21	N	291	306
P11499	Infl	LVVLL	FETALLSSGFSLEDPQTHSNR	IYRMI	2		1168.561825	2335.108051	0.000451244	17	N	658	679
P11499	Infl	TISNR	LVSSPCCIVTSTYGWTANMER	IMKAQ	2	C6:+57.021,C7:+57.021	1216.555855	2431.09611	0.001162105	4	N	583	604
P11499	Infl	YRMIK	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	MEEVD	3		1179.220242	3534.637326	0.000451244	29	N	685	719
P11499	Infl	DKNDK	AVKDLVVLLFETALLSSGFSLEDPQTHSNR	IYRMI	3		1096.249302	3285.724505	0.000698008	1	N	649	679
P11499	Infl	DKAVK	DLVVLLFETALLSSGFSLEDPQTHSNR	IYRMI	3		996.849138	2987.524014	0.000451244	31	N	652	679
P11499	Infl	YRMIK	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASRMEEVD	-	3		1380.293918	4137.858355	0.000451244	6	N	685	724
P11499	Infl	GEFYK	SLTNDWEDHLAVK	HFSVE	3		509.9199727	1526.736518	0.000451244	4	N	306	319
P11499	Infl	NPQER	TLTLVDTGIGMTKADLINNLGTIAK	SGTKA	3		858.4793293	2572.414588	0.000451244	4	N	82	107
P11499	Infl	LYVRR	VFIMDSCDELIPEYLNFIR	GVVDS	2	C7:+57.021	1187.576813	2373.138026	0.000622848	2	N	359	378
P11499	Infl	YGEFY	KSLTNDWEDHLAVK	HFSVE	3		552.6182938	1654.831481	0.0007646	3	N	305	319
P11499	Infl	EELNK	TKPIWTRNPDDITQEEYGEFYK	SLTND	2		1365.656454	2729.297308	0.000622848	2	N	284	306
P11499	Infl	RVRKR	GFEVVYMTEPIDEYCVQQLK	EFDGK	2	C15:+57.021	1224.57701	2447.13842	0.001352548	1	N	506	526
P11499	Infl	MMAKK	HLEINPDHPIVETLR	QKAEA	2		891.9790145	1781.942429	0.000451244	7	N	624	639
P11499	Infl	KETQK	SIYYITGESK	EQVAN	2		580.7958506	1159.576101	0.001591523	2	N	481	491
P11672	Infl	QFRGR	WYVVGLAGNAVQKK	TEGSF	2		766.9333472	1531.851094	0.000451244	23	N	50	64
P11672	Infl	SDQFR	GRWYVVGLAGNAVQK	KTEGS	2		809.4471531	1616.878706	0.001162105	2	N	48	63

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P11672	Infl	QFRGR	WYVVGLAGNAVQK	KTEGS	2		702.8858657	1403.756131	0.000451244	99	N	50	63
P11672	Infl	TRFAK	SLGLKDDNIIFSVPTDQCIDN	-	2	C18:+57.021	1182.573313	2363.131026	0.000451244	197	N	179	200
P11672	Infl	QSQAQ	DSTQNLIPAPSLLTVPLQPDFR	SDQFR	2		1211.652986	2421.290372	0.000823681	3	N	21	43
P11672	Infl	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2		1275.682275	2549.34895	0.001763695	2	N	20	43
P11672	Infl	TQNLI	PAPSLLTVPLQPDFR	SDQFR	2		825.9648444	1649.914089	0.000622848	5	N	28	43
P11672	Infl	DSTQN	LIPAPSLLTVPLQPDFR	SDQFR	2		939.0489085	1876.082217	0.001591523	1	N	26	43
P11672	Infl	QDSTQ	NLIPAPSLLTVPLQPDFR	SDQFR	2		996.0703723	1990.125145	0.000451244	3	N	25	43
P11672	Infl	STQNL	IPAPSLLTVPLQPDFR	SDQFR	2		882.5068764	1762.998153	0.000451244	1	N	27	43
P11672	Infl	NLIPA	PSLLTVPLQPDFR	SDQFR	2		741.9199055	1481.824211	0.002296037	1	N	30	43
P11672	Infl	GNMHR	YPQVQSYNVQVATTDYNQF	AMVFF	2		1133.027087	2264.038574	0.000451244	14	N	121	140
P11672	Infl	KSLGL	KDDNIIFSVPTDQCIDN	-	2	C14:+57.021	997.4625026	1992.909405	0.000451244	12	N	183	200
P11672	Infl	VPSSR	AGQFTLGNMHRYPQVQSY	NVQVA	3	M9:+15.995	705.0027304	2111.984791	0.001463592	3	N	110	128
P11672	Infl	AQDST	QNLIPAPSLLTVPLQPDFR	SDQFR	2		1060.099661	2118.183722	0.000451244	1	N	24	43
P11680	Infl	GRDIR	VEDCCLNAAYAFQEHDGGLCQACR	SPQWS	3	C4:+57.021,C5:+57.021,C20:+57.021,C23:+57.021	948.7245163	2843.150149	0.000451244	6	N	48	72
P11835	Infl	RHVLK	LTDNSNQFQTEVGK	QLISG	2		790.8817056	1579.747811	0.000451244	8	N	210	224
P11835	Infl	VSSCR	DCIQSGPGCSWCQK	LNFTG	2	C2:+57.021,C9:+57.021,C12:+57.021	841.839452	1681.663304	0.000451244	17	N	35	49
P11835	Infl	NMYKR	SNEFDYPSVGQLAHK	LSESN	2		846.4053479	1690.795096	0.000823681	3	N	296	311
P11835	Infl	SSIGK	SRGDCDGVQINNPVTFQVK	VMASE	2	C5:+57.021	1067.521218	2133.026835	0.000451244	6	N	396	415
P11835	Infl	SFVIR	ALGFTDTVTVQVRPQCECQCR	DQSRE	3	C16:+57.021,C18:+57.021,C20:+57.021	842.3947019	2524.160706	0.000451244	8	N	430	451
P11835	Infl	EIIPK	SAVGELSDDSSNVVQLIK	NAYYK	2		930.9816168	1859.947634	0.000451244	9	N	340	358
P11835	Infl	PCKER	DSEGCWITYTLQQK	DGRNI	2	C5:+57.021	864.8988098	1727.78202	0.000451244	11	N	667	681
P11835	Infl	RNVTR	LLVFATDDGFHFAGDGK	LGAIL	3		603.9655821	1808.873346	0.000451244	9	N	258	275
P11835	Infl	TESGR	IGFGSFVDKTVLPFVNTHPEK	LRNPC	3		778.0832384	2331.226315	0.000451244	5	N	166	187
P11835	Infl	KLSSR	VFLDHSTLPDTLKVTYDSFCSNGASSIGK	SRGDC	3	C20:+57.021	1053.848655	3158.522565	0.000451244	3	N	367	396
P11835	Infl	LNNVK	KLGGDLLQALNEITESGR	IGFGS	2		957.5187008	1913.021802	0.000451244	6	N	148	166
P11835	Infl	NNVKK	LGGDLLQALNEITESGR	IGFGS	2		893.4712192	1784.926838	0.000451244	15	N	149	166
P11835	Infl	PDTLK	VTYDSFCSNGASSIGK	SRGDC	2	C7:+57.021	846.8806171	1691.745634	0.000451244	3	N	380	396
P11983	Infl	AEFAR	SLLVIPNTLAVNAAQDSTDLVAK	LRAFH	2		1177.152819	2352.290038	0.000451244	17	N	443	466
P11983	Infl	HPAAK	VLCELADLQDKEVGDGTTSVVIIAAELLK	NADEL	3	C3:+57.021	1033.888339	3098.641618	0.000451244	14	N	73	102
P11983	Infl	VGLDK	MLVDDIGDVTITNDGATILK	LLEVE	2		1052.546267	2103.076935	0.001699387	2	N	43	63
P11983	Infl	KEAVR	YINENLIINTDELGRDCLINAAK	TSMSS	2	C17:+57.021	1331.679175	2661.34275	0.000622848	5	N	130	153
P11983	Infl	SMGSR	EQLAIAEFAR	SLLVI	2		574.3094595	1146.603319	0.000451244	1	N	433	443
P12023	Infl	CIGTK	EGILQYCQEVYPELQITNVVEANQPVTIQNWCKR	GRKQC	3	C7:+57.021,C32:+57.021	1374.013953	4119.018459	0.000451244	5	N	66	100
P12023	Infl	CIGTK	EGILQYCQEVYPELQITNVVEANQPVTIQNWCK	RGRKQ	3	C7:+57.021,C32:+57.021	1321.980249	3962.917347	0.000451244	12	N	66	99
P12023	Infl	GILQY	CQEVYPELQITNVVEANQPVTIQNWCK	RGRKQ	3	C1:+57.021,C26:+57.021	1087.528885	3259.563256	0.002212458	2	N	72	99
P12023	Infl	LSLLY	NVPAVAEEIQDEVDELLQK	EQNYS	2		1070.044945	2138.074291	0.002453667	1	N	549	568
P12382	Infl	ANIFR	NEWGSLLEELVK	EGKIS	2		708.8726209	1415.729642	0.001162105	5	N	129	141
P12382	Infl	TREGR	LAAAYNLLQHGITNLCVIGGDGSLTGANIFR	NEWGS	3	C16:+57.021	1077.231434	3228.670901	0.001871652	5	N	98	129
P12787	Infl	EFDAR	WVTYFNKPDIDAWELRK	GMNTL	2		1091.060536	2180.105472	0.000451244	5	N	51	68
P12787	Infl	AGPHK	EIYPYVIQELRPTLNELGISTPEELGLDKV	-	3		1143.612017	3427.812652	0.000451244	31	N	116	146
P12787	Infl	RWVTY	FNKPDIDAWELRK	GMNTL	4		408.7194844	1630.846737	0.001654178	1	N	55	68
P12787	Infl	EIYPY	VIQELRPTLNELGISTPEELGLDKV	-	3		921.8433243	2762.506573	0.001871652	2	N	121	146
P12815	Infl	-MAAY	SYRPGPGGGPGPAAGAALPDQSFLWNVFQR	VDKDR	3		1024.181445	3069.520935	0.000451244	7	N	4	34
P12815	Infl	VDKDR	SGVISDNELQQALSNGTWTPFNPVTVR	SIISM	2		1465.736299	2929.456997	0.000451244	7	N	39	66
P12815	Infl	DRENK	AGVNFSEFTGVWK	YITDW	2		721.3596807	1440.703761	0.000622848	1	N	77	90
P12970	Infl	VENKK	AQLVVIAHDVDPIELVVFLPALCR	KMGVP	2	C23:+57.021	1344.251582	2686.487564	0.000451244	4	N	151	175
P12970	Infl	LVENK	KAQLVVIAHDVDPIELVVFLPALCR	KMGVP	2	C24:+57.021	1408.299063	2814.582527	0.001352548	1	N	150	175
P12970	Infl	EKRPK	NFGIGQDIQPK	RDLTR	2		608.8201913	1215.624783	0.000622848	5	N	37	48
P13020	Infl	KQFFK	NWRDPDQTDGPGLGYLSSHIANVER	VPFDA	4		700.0881915	2796.321566	0.000451244	11	N	392	417
P13020	Infl	MQYPR	QTQVSVLPEGGETPLFK	QFFKN	2		915.486338	1828.957076	0.000451244	17	N	371	388
P13020	Infl	LKVLR	SQHVQVEEGSEPDAFWEALGGK	TAYRT	2		1200.559283	2399.102965	0.000451244	19	N	624	646
P13020	Infl	AFVLK	TPSAAYLWVGAGASEAEKTGAQELLK	VLRSQ	2		1324.682472	2647.349344	0.000451244	9	N	595	621
P13020	Infl	KQIWR	IEGSNKVPVDPATYGQFYGGDSYIILYNYR	HGGRQ	3		1133.889773	3398.64592	0.000451244	22	N	449	479
P13020	Infl	EGSNK	VPVDPATYGQFYGGDSYIILYNYR	HGGRQ	2		1386.17174	2770.32788	0.000622848	5	N	455	479
P13020	Infl	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3		1425.038957	4272.093472	0.000451244	22	N	483	523
P13020	Infl	LQIWR	VEKFDLVPVPPNLYGDFFTGDAYVILK	TVQLR	3		1019.539353	3055.59466	0.000451244	31	N	70	97
P13020	Infl	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNKFER	LKATQ	3	C16:+57.021,C29:+57.021	1466.327148	4395.958043	0.000451244	38	N	197	235
P13020	Infl	WRVEK	FDLVPVPPNLYGDFFTGDAYVILK	TVQLR	2		1350.702145	2699.388689	0.000870037	3	N	73	97
P13020	Infl	ITVVR	QGFEPPSFVGWFLGWDDNYWSVDPLDR	ALAEL	3		1077.161716	3228.461748	0.000451244	16	N	746	773
P13020	Infl	AFVLK	TPSAAYLWVGAGASEAEK	TGAQE	2		904.4472128	1806.878826	0.000451244	15	N	595	613
P13020	Infl	EVMPK	SGALNSNDAFVLK	TPSAA	2		668.349313	1334.683026	0.000451244	15	N	582	595
P13020	Infl	QGALR	SEDCFILDHGR	DGKIF	2	C4:+57.021	674.8014413	1347.587283	0.000823681	2	N	325	336

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P13020	Infl	PEFLK	AGKEPGLQIWR	VEKFD	3		418.9038172	1253.688052	0.001463592	4	N	59	70
P13020	Infl	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNK	FERLK	3	C16:+57.021,C29:+57.021	1322.256442	3963.745925	0.000451244	10	N	197	232
P13020	Infl	NGDCF	ILDLGNNIYQWCGSGSNKFER	LKATQ	2	C12:+57.021	1236.092538	2470.169477	0.001229886	1	N	214	235
P13020	Infl	KQIWR	IEGSNKVPVDPATY	GQFYG	2		745.3808101	1488.74602	0.000622848	2	N	449	463
P13020	Infl	LKVLR	SQHVQVEEGSEPDAF	WEALG	2		829.8687952	1657.72199	0.00091018	4	N	624	639
P13020	Infl	DDVML	LDTWDQVFVWVGK	DSQEE	2		796.9095378	1591.803476	0.000823681	1	N	698	711
P13020	Infl	TVQLR	NGNLQYDLHYWLGNECSQDESGAAAIF	TVQLD	3	C16:+57.021	1024.786166	3071.335099	0.001654178	4	N	102	129
P13020	Infl	GQIIY	NWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3		1190.915599	3569.723396	0.000451244	15	N	489	523
P13020	Infl	FKNWR	DPDQTDGPGLGYLSSHIANVER	VPFDA	3		781.0405381	2340.098214	0.000823681	1	N	395	417
P13439	Infl	YGTKR	LVEGEINPGQTCLVIEDVVTSGASVLETVEVLQK	EGLKV	3	C12:+57.021	1209.301248	3624.880345	0.000451244	16	N	107	141
P13439	Infl	VSRPR	LLSQVADILFQTAK	NAGIS	2		773.9461203	1545.876641	0.0025889	1	N	48	62
P13864	Infl	DKKRR	VVDTESGAAAAVEKLEEVTAGTQLGPEEPCEQEDDNR	SLRRH	3	C30:+57.021	1315.271405	3942.790815	0.000451244	5	N	202	239
P13864	Infl	GINGK	NLGPINQWWLSGFDGGEK	VLIGF	2		1009.492486	2016.969372	0.000451244	3	N	462	480
P13864	Infl	IYISK	IVVEFLQNNPDAVYEDLINKIETTVPPSTINVNR	FTEDS	3		1285.677861	3854.010183	0.000451244	10	N	516	550
P14069	Infl	NFQEY	VAFLGALALIYNEALK	-	3		569.3349467	1704.98144	0.000823681	13	N	73	89
P14069	Infl	QEVNF	QEYVAFLGALALIYNEALK	-	3		709.3897799	2125.14594	0.001162105	2	N	70	89
P14069	Infl	DDLDR	NKDQEVNFQEYVAFLGALALIYNEALK	-	3		1034.205033	3099.5917	0.000451244	18	N	62	89
P14069	Infl	-MA	CPLDQAIGLLVAIFHK	YSGKE	2	C1:+57.021	898.0006727	1793.985745	0.000451244	6	N	2	18
P14069	Infl	-MAC	PLDQAIGLLVAIFHK	YSGKE	2		817.9855798	1633.95556	0.000451244	31	N	3	18
P14069	Infl	LDRNK	DQEVNFQEYVAFLGALALIYNEALK	-	2		1429.734705	2857.453809	0.000451244	13	N	64	89
P14069	Infl	KKELK	ELIQKELTIGSK	LQDAE	2		679.8986387	1357.781677	0.000451244	8	N	35	47
P14069	Infl	EYVAF	LGALALIYNEALK	-	2		694.9115491	1387.807498	0.000451244	9	N	76	89
P14069	Infl	ELIQK	ELTIGSKLQDAEIAR	LMDDL	3		548.6374654	1642.888996	0.000622848	3	N	40	55
P14069	Infl	MACPL	DQAIGLLVAIFHK	YSGKE	2		712.9171658	1423.818732	0.000451244	24	N	5	18
P14069	Infl	-MAC	PLDQAIGLLVAIFHKYSGK	EGDKH	3		690.7302479	2069.167344	0.000662267	1	N	3	22
P14069	Infl	DDLDR	NKDQEVNFQEYVAF	LGALA	2		865.9051808	1729.794762	0.001654178	1	N	62	76
P14069	Infl	LDRNK	DQEVNFQEYVAF	LGALA	2		744.8362354	1487.656871	0.002374549	2	N	64	76
P14069	Infl	DDLDR	NKDQEVNFQEYVAFLGALALIY	NEALK	2		1273.152819	2544.290038	0.000451244	1	N	62	84
P14069	Infl	LDRNK	DQEVNFQEYVAFLGALALIY	NEALK	2		1152.083874	2302.152147	0.000698008	2	N	64	84
P14115	Infl	YHLKR	NQSFCPTVNLDKLWTLVSEQTR	VNAAK	2	C5:+57.021	1318.660785	2635.305971	0.001329271	1	N	65	87
P14148	Infl	GIICM	EDLIHEIYTVGKR	FKEAN	3		524.9513843	1571.830753	0.0025889	1	N	209	222
P14148	Infl	GMKKK	TTHFVEGGDAGNREDQINR	LIRRM	4		529.7510385	2114.972954	0.000451244	1	N	245	264
P14152	Infl	KKSVK	VIVVGNPANTNCLTASK	SAPSI	2	C12:+57.021	879.4646513	1756.913703	0.000451244	18	N	125	142
P14152	Infl	KLQGK	EVGVYEALKDDSWLK	GEFIT	3		584.633721	1750.877763	0.000698008	4	N	205	220
P14152	Infl	ADDVK	NVIIWGNHSSTQYPDVNHAK	VKLQG	2		1140.561963	2279.108325	0.000451244	2	N	179	199
P14152	Infl	DSWLK	GEFITTVQQR	GAAVI	2		589.8123663	1177.609133	0.000622848	3	N	220	230
P14206	Infl	DSPLR	YVDIAIPCNNK	GAHSV	2	C8:+57.021	653.8269278	1305.638256	0.000870037	7	N	155	166
P14206	Infl	VTDPR	ADHQPLTEASYVNLPTIALCNTDSPLR	YVDIA	3	C20:+57.021	999.4979567	2995.47047	0.000451244	29	N	128	155
P14206	Infl	PIAGR	FTPGTFTNQIQAAFR	EPRLL	2		849.9340756	1697.852551	0.001162105	3	N	102	117
P14206	Infl	LLAAR	AIVAIENPADVSVISSR	NTGQR	2		870.9786801	1739.94176	0.000451244	14	N	63	80
P14206	Infl	VTDPR	ADHQPLTEASYVNLPTIALCNTDSPLRY	VDIAI	3	C20:+57.021	1053.8524	3158.533799	0.000451244	10	N	128	156
P14211	Infl	LPPKK	IKDPDAAKPEDWDER	AKIDD	2		892.9266445	1783.837689	0.000451244	26	N	207	222
P14211	Infl	PAIYF	KEQFLDGDAWTNR	WVESK	2		790.3791331	1578.742666	0.0025889	3	N	23	36
P14211	Infl	NDEAY	AEEFGNETWGVTK	AAEKQ	2		734.3416849	1466.66777	0.000451244	17	N	338	351
P14211	Infl	AIYFK	EQFLDGDAWTNR	WVESK	2		726.3316516	1450.647703	0.000622848	4	N	24	36
P14211	Infl	DPDAK	KPEDWDEEMDGEWEPPVIQNPEYKGEWKPR	QIDNP	4	M9:+15.995	933.1760566	3728.673026	0.002019181	1	N	248	278
P14211	Infl	ALSAK	FEPFSNKGQTLVVQFTVK	HEQNI	2		1035.057462	2068.099324	0.000451244	5	N	80	98
P14211	Infl	TYEVK	IDNSQVESGSLEDDWDFLPPKK	IKDPD	2		1260.10098	2518.186361	0.000451244	55	N	185	207
P14211	Infl	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	C1:+39.994	947.1253099	2838.35253	0.000451244	12	N	162	185
P14211	Infl	NPDYK	GTWIHPEIDNPEYSPDANIY	AYDSF	2		1166.032369	2330.049139	0.000451244	17	N	286	306
P14211	Infl	TYEVK	IDNSQVESGSLEDDWDFLPPK	KIKDP	2		1196.053499	2390.091398	0.000451244	43	N	185	206
P14211	Infl	GLAAA	DPAIYFKEQFLDGDAWTNR	WVESK	3		762.6995646	2285.075294	0.000622848	1	N	17	36
P14211	Infl	SGTIF	DNFLITNDEAYAEEFGNETWGVTK	AAEKQ	2		1382.125184	2762.234768	0.000451244	21	N	327	351
P14211	Infl	DANIY	AYDSFAVLGLDLWQVK	SGTIF	2		912.9806915	1823.945783	0.000451244	24	N	306	322
P14211	Infl	NIYAY	DSFAVLGLDLWQVK	SGTIF	2		795.9304702	1589.84534	0.000451244	16	N	308	322
P14211	Infl	LWQVK	SGTIFDNFLITNDEAYAEEFGNETWGVTK	AAEKQ	3		1090.170606	3267.488417	0.000451244	57	N	322	351
P14211	Infl	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVK	SGTIF	3		1379.669254	4135.984362	0.000451244	45	N	286	322
P14211	Infl	DWDER	AKIDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	3		987.1372361	2958.388308	0.000451244	18	N	222	248
P14211	Infl	LWQVK	SGTIFDNFLITNDEAY	AEEFG	2		910.4234034	1818.831207	0.000622848	10	N	322	338
P14211	Infl	PFSNK	GQTLVVQFTVK	HEQNI	2		610.3564097	1218.697219	0.000622848	6	N	87	98
P14211	Infl	DERAK	IDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	2		1380.635916	2759.256231	0.001463592	1	N	224	248
P14211	Infl	DPDAK	KPEDWDEEMDGEWEPPVIQNPEYK	GEWKP	3	M9:+15.995	992.7680727	2975.280818	0.000451244	9	N	248	272
P14211	Infl	FTHLY	TLIVRPDNTYEVK	IDNSQ	2		774.425552	1546.835504	0.000823681	3	N	172	185
P14211	Infl	ALSAK	FEPFSNKGQTLVVQF	TVKHE	2		870.951934	1739.888268	0.002453667	2	N	80	95
P14211	Infl	AYDSF	AVLGLDLWQVK	SGTIF	2		621.3667774	1240.717955	0.001395409	2	N	311	322

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P14211	Infl	QFTVK	HEQNIDCGGGYVK	LFPSG	3	C7:+57.021	492.8897534	1475.64586	0.001329271	1	N	98	111
P14234	Infl	ALERR	LGTGCFGDVWLGTWNCSTK	VAVKT	2	C5:+57.021,C16:+57.021	1079.987933	2157.960267	0.000451244	12	N	256	275
P14234	Infl	SSGHR	GYVPSNYVAPVDSIQAEEWYFGK	ISRKD	2		1310.124259	2618.232917	0.000451244	18	N	113	136
P14234	Infl	EQAWR	LDPEERPTFEYLQSFLEDYFTSTEPQYQPGDQT	-	3		1324.265963	3969.774488	0.000451244	16	N	484	517
P14234	Infl	RFTVK	SDVWSFGILLTELITK	GRVPY	2		911.5039994	1820.992399	0.000451244	16	N	426	442
P14234	Infl	YITTR	AQFDSIQDLVR	HYMEV	2		646.3362056	1290.656811	0.000451244	1	N	201	212
P14234	Infl	FGLAR	LIEDNEYNPQQGTK	FPIKW	2		824.894813	1647.774026	0.000622848	5	N	393	407
P14234	Infl	YLQSF	LEDYFTSTEPQYQPGDQT	-	2		1059.961078	2117.906557	0.000451244	5	N	499	517
P14234	Infl	HRDLR	AANILVGEYLICK	IADFG	2	C12:+57.021	732.40026	1462.78492	0.000451244	4	N	372	385
P14234	Infl	TKGEK	FHILNNTEYDWWEAR	SLSSG	2		997.4637285	1992.911857	0.000451244	4	N	91	106
P14685	Infl	DIAQK	LQLDSPEDAEFIVAK	AIRDG	2		837.9334069	1673.851214	0.000622848	1	N	421	436
P14685	Infl	TATLR	HDADGQATLLNLLLR	NYLHY	3		550.6376883	1648.889665	0.000451244	1	N	237	252
P14685	Infl	YYHAR	VYEFLDKLDVVR	SFLHA	3		499.2772089	1494.808227	0.000451244	1	N	212	224
P14685	Infl	KLVSK	SVFPEQANNNEWAR	YLYYT	2		831.3874895	1660.759379	0.000451244	9	N	269	283
P14685	Infl	LSYSR	ISLADIAQKLQLDSPEDAEFIVAK	AIRDG	3		872.1378487	2613.390146	0.000451244	5	N	412	436
P14733	Infl	IELGK	FKAEHDQLLLNYAK	KESDL	2		845.4521012	1688.888602	0.000451244	7	N	110	124
P14733	Infl	KHETR	LVEVDSGRQIEYEYK	LAQAL	2		914.4603202	1826.90504	0.000451244	7	N	227	242
P14733	Infl	DLENR	CQSLTEDLEFRK	NMYEE	2	C1:+57.021	763.3696882	1524.723776	0.000451244	11	N	198	210
P14733	Infl	RSTVF	KTTIPEEEEEEEEEPIGVAVEEER	FHQQG	2		1400.648886	2799.282172	0.000451244	19	N	547	571
P14733	Infl	ESRMR	IESLSSQLSNLQK	ESRAC	2		723.8940847	1445.772569	0.000451244	17	N	300	313
P14733	Infl	STVFK	TTIPEEEEEEEEEPIGVAVEEER	FHQQG	2		1336.601404	2671.187208	0.000451244	20	N	548	571
P14733	Infl	DLENR	CQSLTEDLEFR	KNMYE	2	C1:+57.021	699.3222066	1396.628813	0.000998612	5	N	198	209
P14733	Infl	RYVLK	AGQTVTVWAANAGVTASPPTDLIWK	NQNSW	2		1277.669168	2553.322735	0.000451244	23	N	492	517
P14733	Infl	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	2		1272.65612	2543.29664	0.000451244	14	N	158	182
P14733	Infl	IDKVR	SLETENSALQLQVTEREEVR	GRELT	3		777.7315931	2330.171379	0.000637154	6	N	52	72
P14733	Infl	DLIWK	NQNSWGTGEDVKVILK	NSQGE	2		894.4684796	1786.921359	0.00091018	2	N	517	533
P14733	Infl	IDKVR	SLETENSALQLQVTER	EEVRG	2		909.4661339	1816.916668	0.000451244	12	N	52	68
P14733	Infl	STVFK	TTIPEEEEEEEEEPIGVAVEEERF	HQQGA	2		1410.135611	2818.255622	0.002296037	1	N	548	572
P14733	Infl	TVTVW	AANAGVTASPPTDLIWK	NQNSW	2		856.4548408	1710.894082	0.000698008	4	N	500	517
P14824	Infl	YTAMK	GFGSDKESILELITSR	SNKQR	3		584.6445086	1750.910126	0.000451244	3	N	34	50
P14824	Infl	DAYER	DLESDIIGDTSGHFQK	MLVVL	3		587.9483682	1760.821705	0.002019181	1	N	140	156
P14824	Infl	RVELK	GTVCAANDFNPDADAK	ALRKA	2	C4:+57.021	833.3625915	1664.709583	0.001463592	1	N	354	370
P14824	Infl	AGELK	WGTDEAQFIYILGNR	SKQHL	2		891.9446403	1781.873681	0.000451244	2	N	191	206
P14824	Infl	RKAMK	GIGTDEATIIDIVTHR	SNAQR	3		570.9727367	1709.89481	0.001943752	1	N	377	393
P14824	Infl	LQGTR	ENDDVVSEDLVQQDVQDLYEAGELK	WGTDE	2		1425.662328	2849.309055	0.000451244	7	N	166	191
P15532	Infl	SDSVK	SAEKEISLWFQPEELVEYK	SCAQN	2		1163.086613	2324.157627	0.000451244	8	N	124	143
P15532	Infl	KSAEK	EISLWFQPEELVEYK	SCAQN	2		955.483264	1908.950928	0.000451244	11	N	128	143
P15532	Infl	SDSVK	SAEKEISLWFQPEELVEY	KSCAQ	2		1099.039132	2196.062664	0.000622848	4	N	124	142
P15864	Infl	MSEAA	PAAPAAAPPAEKAPAK	KKAAK	2		729.409705	1456.80381	0.000451244	7	N	5	21
P15864	Infl	-M	SEAAPAAPAAAPPAEK	APAKK	2		724.8731523	1447.730705	0.002727428	1	N	1	17
P16045	Infl	LNLGK	DSNNLCLHFNPR	FNAHG	2	C6:+57.021	743.8467145	1485.677829	0.000622848	11	N	37	49
P16045	Infl	ASDAK	SFVLNLGKDSNNLCLHFNPR	FNAHG	3	C14:+57.021	782.3991894	2344.174168	0.000451244	2	N	29	49
P16045	Infl	HFNPR	FNAHGDANTIVCNTK	EDGTW	2	C12:+57.021	831.3889436	1660.762287	0.000451244	8	N	49	64
P16045	Infl	VCNTK	EDGTWGTEHREPAFPFQPGSITEVCITFDQADLTIK	LPDGH	3	C25:+57.021	1364.981349	4091.920647	0.000451244	6	N	64	100
P16110	Infl	ADHFK	VAVNDAHLLQYNHR	MKNLR	2		825.4294917	1648.843383	0.001763695	1	N	224	238
P16110	Infl	LDFRR	GNDVAFHFNPR	FNENN	3		425.2077883	1272.599965	0.000451244	12	N	165	176
P16110	Infl	GKPFK	IQVLVEADHFK	VAVND	2		649.8593165	1297.703033	0.001943752	1	N	213	224
P16110	Infl	VLDFR	RGNDVAFHFNPR	FNENN	3		477.241492	1428.701076	0.001591523	3	N	164	176
P16110	Infl	GKEER	QSAFPFESGKPFK	IQVLV	3		490.5861539	1468.735062	0.00091018	4	N	200	213
P16110	Infl	SGKPF	KIQVLVEADHFK	VAVND	3		476.2737987	1425.797996	0.001329271	4	N	212	224
P16546	Infl	FMISR	ETENVKSSEEIESAFR	ALSSE	2		927.9399489	1853.864298	0.000451244	2	N	2398	2414
P16546	Infl	ESAFR	ALSSEGKPYVTKEELYQNLTR	EQADY	2		1213.632251	2425.248901	0.000451244	4	N	2414	2435
P16546	Infl	WIEEK	NQALNTDNYGHDLASVQALQR	KHEGF	2		1164.570516	2327.125432	0.000451244	18	N	1252	1273
P16546	Infl	HDAFR	SSLSSAQADFNQLAELDR	QIKSF	2		976.4719476	1950.928295	0.000451244	6	N	2137	2155
P16546	Infl	WMAAR	EAFLNTEDKGDSLDSVEALIK	KHEDF	2		1147.574067	2293.132534	0.000451244	14	N	1464	1485
P16546	Infl	EIDAR	AGTFQAFEQFGQQLLAHGHYASPEIK	EKLDI	3		959.1441082	2874.408925	0.002884417	1	N	1391	1417
P16546	Infl	INGIR	GLVSSDELAKDVTGAEALLER	HQEHR	2		1087.071495	2172.127389	0.000451244	8	N	1359	1380
P16546	Infl	LAAAR	GQRLEESLEYQQFVANVEEEEAWINEK	MTLVA	3		1089.853388	3266.536764	0.000451244	8	N	1862	1889
P16546	Infl	VQEEK	IAALQAFADQLIAVDHYAK	GDIAN	3		686.7059909	2057.094573	0.000451244	15	N	1500	1519
P16546	Infl	TFAKK	ASAFNSWFENAEEDLTDPVR	CNSLE	2		1149.519626	2297.023652	0.000451244	13	N	2099	2119
P16546	Infl	FMLFR	EANELQQWITEKEAALTNEEVGADLEQVEVLQK	KFDDF	3		1252.293964	3753.858492	0.000451244	12	N	1098	1131
P16546	Infl	WINEK	MTLVASEDYGDTLAAIQGLLK	KHEAF	2		1105.075192	2208.134784	0.000451244	13	N	1889	1910
P16546	Infl	VTEMK	ALINADELANDVAGAEALLDR	HQEHK	2		1077.556012	2153.096423	0.000451244	5	N	381	402
P16546	Infl	QQFNR	NVEDIELWLYEVEGHLASDDYGKDLTNVQNLQK	KHALL	3		1283.294076	3846.858827	0.000451244	11	N	685	718
P16546	Infl	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3		1078.233652	3231.677555	0.000451244	7	N	2017	2047

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P16546	Infl	EGFER	DLAALGDKVNSLGETAQR	LIQSH	2		929.4874007	1856.959201	0.000451244	7	N	1280	1298
P16546	Infl	TLLTK	QETFDAGLQAFQQEGIANITAL	KDQLL	2		1183.087676	2364.159752	0.000451244	9	N	2017	2039
P16546	Infl	SKHQK	HQAFEAELHANADR	IRGVI	3		536.9224877	1607.744063	0.000451244	1	N	1591	1605
P16546	Infl	AVKAR	LAALADQWQFLVQK	SAEKS	2		815.951737	1629.887874	0.000451244	8	N	1632	1646
P16546	Infl	QQFSR	DVDEIEAWISEK	LQTAS	2		717.3438933	1432.672187	0.000451244	7	N	1558	1570
P16546	Infl	WISEK	LQTASDESYKDPTNIQSK	HQKHQ	2		1012.992713	2023.969826	0.000451244	5	N	1570	1588
P16546	Infl	ARGQR	LEESLEYQQFVANVEEEEAWINEK	MTLVA	2		1463.685606	2925.355611	0.000451244	7	N	1865	1889
P16546	Infl	NWMSK	QEAFLLNEDLGDSLDSVEALLK	KHEDF	2		1210.116099	2418.216598	0.000451244	12	N	485	507
P16546	Infl	SLRMK	QVEELYQSLLELGEK	RKGML	2		889.4650712	1776.914542	0.000451244	6	N	1067	1082
P16546	Infl	FMLFR	EANELQQWITEK	EAALT	2		744.8706096	1487.725619	0.000979378	1	N	1098	1110
P16546	Infl	DDYGR	DLSSVQTLLTK	QETFD	2		602.8433321	1203.671064	0.000451244	4	N	2006	2017
P16546	Infl	KASAF	NSWFENAEEDLTDPVR	CNSLE	2		961.432291	1920.848982	0.000451244	18	N	2103	2119
P16546	Infl	KASAF	NSWFENAEEDLTDPVRCNSLEEIK	ALREA	3	C17:+57.021	965.7752672	2894.302401	0.000451244	2	N	2103	2127
P16546	Infl	DDYGR	DLSSVQTLLTKQETFDAGLQAFQQEGIANITAL	KDQLL	3		1184.281219	3549.820256	0.000451244	1	N	2006	2039
P16546	Infl	EKRSK	LGESQTLQQFSR	DVDEI	2		697.3576694	1392.699739	0.000451244	1	N	1546	1558
P16546	Infl	WITEK	EAALTNEEVGADLEQVEVLQK	KFDDF	2		1143.079517	2284.143433	0.000451244	19	N	1110	1131
P16546	Infl	QRKAK	LDENSAFLQFNWK	ADVVE	2		806.3942519	1610.772904	0.000451244	6	N	1971	1984
P16546	Infl	LDTGK	KLSDDNTIGQEEIQQR	LAQFV	3		625.3137101	1872.91773	0.002145581	2	N	1828	1844
P16546	Infl	DELAK	DVTGAEALLER	HQEHR	2		587.3096565	1172.603713	0.000622848	2	N	1369	1380
P16546	Infl	EDSFK	SADESGQALLAASHYASDEVR	EKLSI	3		726.3422171	2176.003251	0.001352548	1	N	418	439
P16546	Infl	QQFNR	NVEDIELWLYEVEGHLASDDYGK	DLTNV	3		898.7576965	2693.249689	0.000451244	5	N	685	708
P16546	Infl	QSASR	ENLLEEQGSIALR	QGQID	2		736.3917092	1470.767818	0.000451244	2	N	1032	1045
P16546	Infl	DGKGR	ELPTAFDYVEFTR	SLFVN	2		794.3886352	1586.76167	0.000870037	1	N	2454	2467
P16546	Infl	NTGIK	DFDFWLSEVEALLASEDYGKDLASVNNLLK	KHQLL	3		1134.564956	3400.671467	0.001329271	1	N	1668	1698
P16546	Infl	QDLED	SLQAQQYFADANEAESWMREK	EPIVG	2	M18:+15.995	1259.569368	2517.123135	0.002212458	1	N	888	909
P16675	Infl	CAQNK	CNFYDNKDPECVNNLLEVSR	IVGKS	2	C1:+39.994,C11:+57.021	1235.04394	2468.07228	0.002080925	1	N	240	260
P16675	Infl	ASDSK	HFHYWFVESQNDPK	NSPVV	3		611.9501549	1832.827065	0.002296037	1	N	55	69
P16858	Infl	WRDGR	GAAQNIIPASTGAAK	AVGKV	2		685.3758621	1368.736124	0.000451244	37	N	198	213
P16858	Infl	DNSLK	IVSNASCTTNCLAPLAK	VIHDN	2	C7:+57.021,C11:+57.021	910.4557377	1818.895875	0.000451244	16	N	143	160
P16858	Infl	GMAFR	VPTPNVSVVDLTCRLEKPAK	YDDIK	4	C13:+57.021	556.5600056	2222.208822	0.000451244	4	N	232	252
P16858	Infl	GMAFR	VPTPNVSVVDLTCR	LEKPA	2	C13:+57.021	778.9089805	1555.802361	0.000451244	31	N	232	246
P16858	Infl	DNFVK	LISWYDNEYGYSNR	VVDLM	2		890.4028052	1778.79001	0.000451244	46	N	307	321
P16858	Infl	GILGY	TEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C8:+57.021	1182.862352	3545.563655	0.000451244	47	N	274	307
P16858	Infl	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C13:+57.021	1350.62048	4048.838039	0.000451244	1196	N	269	307
P16858	Infl	PTNIK	WGEAGAEYVVESTGVFTTMEK	AGAHL	2		1146.030981	2290.046363	0.000451244	12	N	84	105
P16858	Infl	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	2		1298.184128	2594.352656	0.000451244	4	N	160	184
P16858	Infl	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	2		1148.655332	2295.295064	0.000451244	8	N	64	84
P16858	Infl	TGMAF	RVPTPNVSVVDLTCR	LEKPA	2	C14:+57.021	856.9595361	1711.903472	0.000451244	20	N	231	246
P16858	Infl	AENGK	LVINGKPITIFQER	DPTNI	3		543.3230411	1626.945723	0.000451244	6	N	64	78
P16858	Infl	EGPLK	GILGYTEDQVVSCDFNSNSHSSTF	DAGAG	2	C13:+57.021	1332.579855	2663.14411	0.000451244	15	N	269	293
P16858	Infl	ICSGK	VEIVAINDPF	IDLNY	2		558.8009359	1115.586272	0.000622848	12	N	25	35
P16858	Infl	ICSGK	VEIVAINDPFIDLN	YMVYM	2		786.4199353	1570.824271	0.000451244	6	N	25	39
P16858	Infl	FRVPT	PNVSVVDLTCR	LEKPA	2	C10:+57.021	630.3245523	1258.633505	0.001463592	3	N	235	246
P16858	Infl	AENGK	LVINGKPITIF	QERDP	2		607.8795207	1213.743441	0.000622848	10	N	64	75
P16858	Infl	APLAK	VIHDNFGIVEGLMTTVHAITATQKTVDGPSGK	LWRDG	4		834.9373938	3335.718375	0.000451244	2	N	160	192
P16858	Infl	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIAL	NDNFV	3	C13:+57.021	1111.505617	3331.49345	0.000451244	28	N	269	301
P16858	Infl	RLVTR	AAICSGKVEIVAINDPFIDLNYMVY	MFQYD	3	C4:+57.021	939.1400535	2814.396761	0.000823681	1	N	18	43
P16858	Infl	VNHEK	YDNSLKIVSNASCTTNCLAPLAK	VIHDN	2	C13:+57.021,C17:+57.021	1270.627865	2539.24013	0.000451244	3	N	137	160
P16858	Infl	KKVVK	QASEGPLKGILGYTEDQVVSCDFNSNSHSSTFDAGAGIAL	NDNFV	3	C21:+57.021	1381.646806	4141.917018	0.001329271	2	N	261	301
P16858	Infl	SLKIV	SNASCTTNCLAPLAK	VIHDN	2	C5:+57.021,C9:+57.021	804.3794986	1606.743397	0.000451244	3	N	145	160
P16858	Infl	ELNGK	LTGMAFRVPTPNVSVVDLTCR	LEKPA	3	C20:+57.021	778.4086974	2332.202692	0.002727428	1	N	225	246
P16858	Infl	RLVTR	AAICSGKVEIVAINDPFIDLNY	MVYMF	2	C4:+57.021	1211.620066	2421.224532	0.001763695	1	N	18	40
P16858	Infl	DNFVK	LISWYDNEYGY	SNRVV	2		711.8147717	1421.613943	0.000451244	2	N	307	318
P16858	Infl	NFVKL	ISWYDNEYGYSNR	VVDLM	2		833.8607732	1665.705946	0.000451244	5	N	308	321
P16858	Infl	ICSGK	VEIVAINDPFIDLNY	MVYMF	2		867.9515997	1733.887599	0.001463592	1	N	25	40
P16879	Infl	MAGIL	KDILQEYLEISSLVQDDVASIHR	ELAAA	4		668.6044144	2670.386458	0.000622848	4	N	223	246
P16879	Infl	GAIPR	AEVAELLTHSGDFLVR	ESQGK	3		586.3129818	1755.915545	0.000622848	5	N	467	483
P16879	Infl	DNLYR	LEGDGFPSIPLLITHLLSSQQPLTK	KSGVV	3		902.1693718	2703.484715	0.002453667	1	N	514	539
P17047	Infl	NSQIK	YLDFIFAVK	NEKRF	2		558.3109395	1114.606279	0.001329271	3	N	285	294
P17047	Infl	LSVSR	AFQINTFNLK	VQPFN	2		598.3276522	1194.639704	0.002727428	1	N	346	356
P17047	Infl	NQTNK	TITIAVPDKATHDGSSCGDDR	NSAKI	3	C17:+57.021	739.3468195	2215.017058	0.001395409	1	N	58	79
P17182	Infl	CLLLK	VNQIGSVTESLQACK	LAQSN	2	C14:+57.021	817.4146271	1632.813654	0.000451244	59	N	343	358
P17182	Infl	IFDSR	GNPTVEVDLYTAK	GLFRA	2		703.8622532	1405.708906	0.000451244	25	N	15	28
P17182	Infl	GAWQK	FTASAGIQVVGDDLTVTNPKR	IAKAA	2		1095.082197	2188.148793	0.000451244	20	N	306	327
P17182	Infl	RIHAR	EIFDSRGNPTVEVDLYTAK	GLFRA	2		1077.53983	2153.064061	0.000451244	5	N	9	28

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P17182	Infl	GAWQK	FTASAGIQVVGDDLTVTNPK	RIAKA	2		1017.031641	2032.047682	0.000451244	121	N	306	326
P17182	Infl	DLDFK	SPDDPSRYITPDQLADLYK	SFVQN	2		1097.537288	2193.058975	0.000451244	6	N	262	281
P17182	Infl	KGLFR	AAVPSGASTGIYEALELR	DNDKT	2		902.9761374	1803.936675	0.000451244	28	N	32	50
P17182	Infl	ENKSK	FGANAILGVSLAVCK	AGAVE	2	C14:+57.021	760.4189841	1518.822368	0.000451244	343	N	105	120
P17182	Infl	VPLYR	HIADLAGNPEVILPVPAFNVINGGSHAGNK	LAMQE	3		1007.868867	3020.583201	0.000451244	42	N	132	162
P17182	Infl	EKYGK	DATNVGDEGGFAPNILENKEALELLK	TAIAK	2		1379.201226	2756.386852	0.000451244	24	N	202	228
P17182	Infl	LADLY	KSFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		1033.489721	3097.445764	0.000451244	15	N	280	306
P17182	Infl	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	2		1485.6832	2969.350801	0.000451244	24	N	281	306
P17182	Infl	MVSHR	SGETEDTFIADLVVGLCTGQIK	TGAPC	2	C17:+57.021	1177.083513	2352.151427	0.000451244	764	N	372	394
P17182	Infl	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQKF	TASAG	3		1039.814205	3116.419215	0.000451244	9	N	281	307
P17182	Infl	ERLAK	YNQILRIEEELGSK	AKFAG	3		564.6374654	1690.888996	0.001943752	1	N	406	420
P17182	Infl	TAIAK	AGYTDQVVIGMDVAASEFYR	SGKYD	2		1096.520584	2191.025568	0.000451244	14	N	233	253
P17182	Infl	VSIED	PFDQDDWGAWQK	FTASA	2		746.8287447	1491.641889	0.002519933	2	N	294	306
P17182	Infl	VIKEK	YGKDATNVGDEGGFAPNILENK	EALEL	2		1155.056376	2308.097152	0.000451244	14	N	199	221
P17182	Infl	AWQKF	TASAGIQVVGDDLTVTNPK	RIAKA	2		943.497434	1884.979268	0.000451244	27	N	307	326
P17182	Infl	REAMR	IGAEVYHNLKNVIK	EKYGK	3		533.307391	1596.898773	0.000622848	2	N	183	197
P17182	Infl	MVSHR	SGETEDTFIADLVVGLCTGQIKTGAPCR	SERLA	3	C17:+57.021,C27:+57.021	999.1550479	2994.441744	0.000451244	4	N	372	400
P17182	Infl	AASEK	SCNCLLLKVNQIGSVTESLQACK	LAQSN	3	C2:+57.021,C4:+57.021,C22:+57.021	874.7731789	2621.296137	0.000622848	1	N	335	358
P17182	Infl	EKYGK	DATNVGDEGGFAPNILENK	EALEL	2		980.9664981	1959.917396	0.000451244	63	N	202	221
P17182	Infl	FRAAV	PSGASTGIYEALELR	DNDKT	2		782.4048166	1562.794033	0.000451244	4	N	35	50
P17182	Infl	DDPSR	YITPDQLADLYK	SFVQN	2		720.3749965	1438.734393	0.000451244	4	N	269	281
P17182	Infl	YRSGK	YDLDFKSPDDPSR	YITPD	2		777.8576992	1553.699798	0.000451244	7	N	256	269
P17182	Infl	PSRYI	TPDQLADLYK	SFVQN	2		582.3013001	1162.587	0.002019181	4	N	271	281
P17182	Infl	NYPVV	SIEDPFDQDDWGAWQK	FTASA	2		968.9215592	1935.827518	0.000451244	3	N	290	306
P17182	Infl	VVSIE	DPFDQDDWGAWQK	FTASA	2		804.3422163	1606.668833	0.001162105	2	N	293	306
P17182	Infl	AWQKF	TASAGIQVVGDDLTVTNPKR	IAKAA	2		1021.54799	2041.080379	0.000451244	8	N	307	327
P17182	Infl	HAGNK	LAMQEFMILPVGASSFR	EAMRI	3		632.9957201	1895.96376	0.001162105	2	N	162	179
P17182	Infl	DDPSR	YITPDQLADLYKSFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		1464.366011	4390.074633	0.001591523	2	N	269	306
P17182	Infl	RLAKY	NQILRIEEELGSK	AKFAG	2		764.9206338	1527.825668	0.000662267	1	N	407	420
P17182	Infl	IFDSR	GNPTVEVDLY	TAKGL	2		553.7723754	1105.529151	0.000622848	6	N	15	25
P17182	Infl	AKGLF	RAAVPSGASTGIYEALELR	DNDKT	3		654.3537287	1960.037786	0.001463592	3	N	31	50
P17182	Infl	TEDTF	IADLVVGLCTGQIK	TGAPC	2	C9:+57.021	743.9188169	1485.822034	0.000451244	2	N	380	394
P17182	Infl	DDPSR	YITPDQLADLY	KSFVQ	2		656.3275149	1310.63943	0.000451244	6	N	269	280
P17426-2	Infl	VTKAK	LLGFGSALLDNVDPNPENFVGAGIIQTK	ALQVG	3		967.178707	2898.512721	0.000451244	10	N	885	913
P17426-2	Infl	SRLSR	IVSSASTDLQDYTYYFVPAPWLSVK	LLRLL	2		1425.71598	2849.416361	0.001699387	1	N	235	260
P17426-2	Infl	VQTKR	VAAQVDGGAQVQQVLNIECLRDFLTPPLLSVR	FRYGG	3	C19:+57.021	1169.631486	3505.871058	0.000823681	1	N	789	821
P17426-2	Infl	LVDVF	SDGPTAQPSLGPTPEEAFLSPGPEDIGPPIPEADELLNK	FVCKN	3		1328.320179	3981.937137	0.000451244	8	N	685	724
P17426-2	Infl	HSNAK	NAILFETISLIIHYDSEPNLLVR	ACNQL	3		890.8220835	2669.44285	0.001591523	1	N	306	329
P17427	Infl	ITKAK	IIGFGSALLEEVDPNPANFVGAGIIHTK	TTQIG	3		960.5154306	2878.522892	0.000451244	22	N	868	896
P17427	Infl	HSNAK	NAVLFEAISLIIHHDSEPNLLVR	ACNQL	4		650.8608547	2599.412219	0.002080925	2	N	305	328
P17427	Infl	VEYLR	LSTVASTDILATVLEEMPPFPERESSILAK	LKKKK	3		1082.239415	3243.694846	0.001654178	1	N	584	614
P17427	Infl	LVDVF	SDSASAVAPLAPGSEDNFAR	FVCKN	2		981.4641225	1960.912645	0.000823681	2	N	687	707
P17439	Infl	KYGLR	FWAVTAENEPTAGLFTGYPFQCLGFTPEHQR	DFISR	3	C22:+57.021	1191.22987	3570.66621	0.000451244	7	N	245	276
P17439	Infl	VVLNR	SSEDVPLTISDPDLGFLETVSPGYSIHTYLWR	RQ-	3		1198.926664	3593.756593	0.000451244	5	N	481	513
P17710	Infl	LYAMR	LSDEILIDILTR	FKKEM	2		700.9039211	1399.792242	0.000451244	10	N	86	98
P17710	Infl	IVSFR	SANLVAATLGAILNR	LRDNK	3		495.2917409	1482.851823	0.000451244	6	N	437	452
P17710	Infl	YAMRL	SDEILIDILTR	FKKEM	2		644.3618891	1286.708178	0.000823681	4	N	87	98
P17710	Infl	PSYVR	SIPDGTEHGDFLALDLGGTNF	RVLLV	2		1088.513812	2175.012025	0.001162105	1	N	573	594
P17710	Infl	LTRGK	FTTSDVAAIETDKEGVQNAK	EILTR	3		708.6872132	2123.03824	0.000622848	1	N	389	409
P17710	Infl	CRQSK	IDEAVLITWTK	RFKAS	2		644.8615249	1287.70745	0.001162105	2	N	218	229
P17742	Infl	GKTSK	KITISDCGQL	-	2	C7:+57.021	567.7950963	1133.574593	0.000451244	23	N	154	164
P17742	Infl	NPTVF	FDITADDEPLGR	VSFEL	2		674.823128	1347.630656	0.000451244	43	N	7	19
P17742	Infl	EPLGR	VSFELFADKVPK	TAENF	2		690.3826245	1378.749649	0.000451244	13	N	19	31
P17742	Infl	GTGGR	SIYGEKFEDENFILK	HTGPG	2		916.4597889	1830.903978	0.000451244	22	N	76	91
P17742	Infl	EPLGR	VSFELFADK	VPKTA	2		528.274554	1054.533508	0.001162105	3	N	19	28
P17742	Infl	NFILK	HTGPGILSMANAGPNTNGSQFFICTAK	TEWLD	2	C24:+57.021	1396.168452	2790.321304	0.000637154	2	N	91	118
P17742	Infl	-M	VNPTVFFDITADDEPLGR	VSFEL	2		1003.497434	2004.979268	0.000451244	77	N	1	19
P17742	Infl	-MVN	PTVFFDITADDEPLGR	VSFEL	2		896.9417633	1791.867927	0.000451244	5	N	3	19
P17742	Infl	-MV	NPTVFFDITADDEPLGR	VSFEL	2		953.963227	1905.910854	0.000451244	7	N	2	19
P17742	Infl	ICTAK	TEWLDGKHVVFGK	VKEGM	2		758.4018799	1514.78816	0.000451244	6	N	118	131
P17742	Infl	IYGEK	FEDENFILK	HTGPG	2		577.7905682	1153.565536	0.000823681	10	N	82	91
P17742	Infl	FHRII	PGFMCQGGDFTR	HNGTG	2	C5:+57.021	686.7925626	1371.569525	0.00091018	1	N	57	69
P17751	Infl	GHSER	RHVFGESDELIGQK	VSHAL	3		538.9465219	1613.816166	0.000451244	10	N	149	163
P17751	Infl	LIGQK	VSHALAEGLGVIACIGEK	LDERE	2	C14:+57.021	912.4881264	1822.960653	0.000451244	18	N	163	181

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P17751	Infl	KDWSK	VVLAYEPVWAIGTGK	TATPQ	2		801.948663	1601.881726	0.000451244	19	N	210	225
P17751	Infl	LIGQK	VSHALAEGLGVIACIGEKLDER	EAGIT	3	C14:+57.021	779.7462548	2336.215364	0.000451244	2	N	163	185
P17751	Infl	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAKQ	-	3		1053.219231	3156.634293	0.000451244	14	N	269	299
P17751	Infl	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAK	Q-	3		1010.533038	3028.575715	0.000451244	23	N	269	298
P17751	Infl	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	C1:+39.994,C7:+57.021,C22:+57.021	1182.906952	3545.697456	0.000451244	2	N	70	103
P17751	Infl	PGMIK	DLGATWVVLGHSERR	HVFGE	3		565.9695494	1694.885248	0.002981883	1	N	135	150
P17751	Infl	PGMIK	DLGATWVVLGHSER	RHVFG	2		770.3998686	1538.784137	0.000451244	11	N	135	149
P17751	Infl	HSERR	HVFGESDELIGQK	VSHAL	2		729.8653272	1457.715054	0.000451244	11	N	150	163
P17751	Infl	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAY	IDFAR	2	C1:+39.994,C7:+57.021,C22:+57.021	1472.697705	2943.37981	0.002727428	1	N	70	98
P17918	Infl	ARICR	DLSHIGDAVVISCAK	NGVKF	2	C13:+57.021	792.9064379	1583.797276	0.000451244	11	N	149	164
P17918	Infl	IITLR	AEDNADTLALVFEAPNQEK	VSDYE	2		1038.000538	2073.985476	0.000451244	19	N	91	110
P17918	Infl	DYEMK	LMDLDVEQLGIPEQEYSCVIK	MPSGE	2	C18:+57.021	1240.108674	2478.201749	0.000622848	3	N	117	138
P17918	Infl	KNGVK	FSASGELGNGNIK	LSQTS	2		647.3258379	1292.636076	0.000451244	1	N	168	181
P18242	Infl	IKVEK	QIFGEATKQPGIVFVAAK	FDGIL	2		952.5361652	1903.05673	0.000451244	6	N	174	192
P18242	Infl	LTLCK	GGCEAIVDTGTSLLVGPVEEVKELQK	AIGAV	2	C3:+57.021	1364.707598	2727.399596	0.000451244	8	N	285	311
P18242	Infl	KELQK	AIGAVPLIQGEYMIPCEK	VSSLP	2	C16:+57.021	995.0131204	1988.010641	0.002884417	1	N	311	329
P18242	Infl	LTLCK	GGCEAIVDTGTSLLVGPVEEVK	ELQKA	2	C3:+57.021	1115.567499	2229.119398	0.000451244	15	N	285	307
P18242	Infl	KLGGK	NYELHPDKYILK	VSQGG	2		766.9095378	1531.803476	0.001162105	4	N	343	355
P18242	Infl	KLVDK	NIFSFYLNRDPEGQPGGELMLGGTDSK	YYHGE	3	M20:+15.995	986.8033402	2957.386621	0.000451244	1	N	224	251
P18242	Infl	DAQYY	GDIGIGTPPQCFTVVFDTGSSNLWVPSIHCK	ILDIA	3	C11:+57.021,C30:+57.021	1130.548168	3388.621105	0.002296037	1	N	80	111
P18242	Infl	SELLK	NYLDAQYYGDIGIGTPPQCF	TVVFD	2	C19:+57.021	1146.517809	2291.020018	0.001699387	3	N	72	92
P18653	Infl	GVVHR	DLKPSNILYVDESGNPECLR	ICDFG	2	C18:+57.021	1160.068198	2318.120795	0.000451244	8	N	523	543
P18653	Infl	IGSGK	FTLSGGNWNTVSETAK	DLVSK	2		856.4184553	1710.821311	0.000451244	8	N	622	638
P18653	Infl	DKSKR	DPSEEIEILLR	YGQHP	2		657.3515213	1312.687443	0.000451244	1	N	443	454
P18760	Infl	DKDCR	YALYDATYETK	ESKKE	2		669.3171472	1336.618694	0.000451244	36	N	81	92
P18760	Infl	TLAEK	LGGSAVISLEGKPL	-	2		670.8933564	1339.771113	0.000451244	48	N	152	166
P18760	Infl	LEEGK	EILVGDVGQTVDDPYTTFVK	MLPDK	2		1098.557689	2195.099777	0.000451244	27	N	53	73
P18760	Infl	TKESK	KEDLVFIFWAPENAPLK	SKMIY	2		1009.043823	2016.072046	0.000451244	18	N	95	112
P18760	Infl	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFVK	MLPDK	3		1031.53997	3091.59651	0.000451244	539	N	45	73
P18760	Infl	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTF	VKMLP	2		1433.224367	2864.433133	0.000451244	32	N	45	71
P18760	Infl	KESKK	EDLVFIFWAPENAPLK	SKMIY	2		944.9963416	1887.977083	0.000451244	15	N	96	112
P18760	Infl	LTGIK	HELQANCYEEVKDR	CTLAE	2	C7:+57.021	895.9102402	1789.80488	0.000870037	2	N	132	146
P18760	Infl	SEDKK	NIILEEGKEILVGDVGQTVDDPY	TTFVK	2		1258.642481	2515.269362	0.000451244	9	N	45	68
P18760	Infl	LVGDV	GQTVDDPYTTFVK	MLPDK	2		735.8597105	1469.703821	0.00091018	4	N	60	73
P18760	Infl	LEEGK	EILVGDVGQTVDDPYTTF	VKMLP	2		984.9760001	1967.9364	0.000451244	9	N	53	71
P18760	Infl	TKESK	KEDLVFIFWAPENAPL	KSKMI	2		944.9963416	1887.977083	0.000451244	2	N	95	111
P19096	Infl	DRATR	EACPELDYFVAFSSVSCGR	GNAGQ	2	C3:+57.021,C17:+57.021	1097.482681	2192.949762	0.000451244	26	N	2000	2019
P19096	Infl	TNLGK	VHLTGINVNPNALFPPVEFPAPR	GTPLI	3		833.788937	2498.343411	0.000622848	8	N	802	825
P19096	Infl	LAQER	LLLPEDPLISGLLNSQALK	ACVDT	2		1017.59642	2033.17724	0.000451244	21	N	1201	1220
P19096	Infl	EGDHR	TLLEGSGLESIINIIHSSLAEPR	VSVRE	2		1225.169	2448.322401	0.000451244	1	N	2475	2498
P19096	Infl	HTVLK	GHALGETLACLPSEVQPAPSLLSQEEWESLFSR	KALHL	3	C10:+57.021	1213.598399	3637.771797	0.000451244	14	N	1344	1377
P19096	Infl	SLAAK	LSVPTYGLQCTQAAPLDSIPNLAAYYIDCIK	QVQPE	3	C10:+57.021,C29:+57.021	1152.579246	3454.714337	0.000451244	11	N	2256	2287
P19096	Infl	LVQVR	EEEPEAVLPGAQPTLISAISK	TFCPA	2		1090.078788	2178.141977	0.000823681	2	N	1850	1871
P19096	Infl	LLRAK	TGGTYGEDLGADYNLSQVCDGK	VSVHI	2	C19:+57.021	1160.505627	2318.995654	0.000451244	10	N	2442	2464
P19096	Infl	KTLAR	SLGLSLEETPVVFENVSFHQATILPK	TGTVA	3		952.5116861	2854.511658	0.000622848	1	N	901	927
P19096	Infl	ECKQR	CPAGVVPACHNSEDTVTISGPQAAVNEFVEQLKQEGVFAK	EVRTG	4	C1:+57.021,C9:+57.021	1071.773245	4283.06178	0.000662267	12	N	633	673
P19096	Infl	AIFLK	NVTFHGILLDALFEEANDSWR	EVAAL	3		816.4050403	2446.191721	0.002019181	1	N	1780	1801
P19096	Infl	FFDFK	GPSIALDTACSSSLLALQNAYQAIR	SGECP	3	C10:+57.021	874.1185284	2619.332185	0.000662267	7	N	151	176
P19096	Infl	SQALK	ACVDTALENLSTLK	MKVAE	2	C2:+57.021	767.8929961	1533.770392	0.000622848	3	N	1220	1234
P19096	Infl	VEHSK	VLEALLPLK	SLEDR	2		498.3291322	994.6426645	0.002884417	1	N	2375	2384
P19096	Infl	FLCRR	AIPQEKPIFLSVEDTSFQWVDSLK	STLAT	3		926.4852485	2776.432345	0.000451244	2	N	1399	1423
P19096	Infl	YKELR	LRGYDYGPQFQGICEATLEGEQGK	LLWKD	3	C14:+57.021	906.0942714	2715.259414	0.000451244	1	N	996	1020
P19157	Infl	GQLPK	FEDGDLTLYQSNAILR	HLGRS	2		927.9657697	1853.915939	0.000451244	2	N	55	71
P19157	Infl	NDYVK	ALPGHLKPFETLLSQNQGGK	AFIVG	2		1068.084542	2134.153485	0.00307782	1	N	121	141
P19157	Infl	DQISF	ADYNLLDLLLIHQVLAPGCLDNFPLLSAYVAR	LSARP	3	C19:+57.021	1199.976482	3596.906047	0.002374549	1	N	151	183
P19221	Infl	VMLFR	KSPQELLCGASLISDR	WVLTA	2	C8:+57.021	887.4621086	1772.908617	0.000451244	4	N	380	396
P19221	Infl	MLFRK	SPQELLCGASLISDR	WVLTA	2	C7:+57.021	823.4146271	1644.813654	0.000451244	3	N	381	396
P19536	Infl	VTRSM	ASGGGVPTDEEQATGLER	EIMIA	2		887.416641	1772.817682	0.000451244	28	N	30	48
P19536	Infl	ISNKR	IVGCICEEDNCTVIWFWLHK	GESQR	3	C4:+57.021,C6:+57.021,C11:+57.021	860.4009053	2578.179316	0.000451244	2	N	86	106
P19536	Infl	AVTRS	MASGGGVPTDEEQATGLER	EIMIA	2		952.9368839	1903.858168	0.001229886	1	N	29	48
P19973	Infl	KPEPR	QQFWGNEGTAEGTEPSQSERPEEKQTEESSHQAK	VHLEE	3		1282.907831	3845.700094	0.000451244	8	N	96	130
P19973	Infl	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	2		1361.105314	2720.195028	0.000451244	18	N	96	120

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P19973	Infl	VASTK	TLWETGEVQSQSASK	TPSCQ	2		825.9026381	1649.789676	0.000451244	22	N	255	270
P19973	Infl	LISLK	SSELDEDEGFGDWSQKPEPR	QQFWG	2		1154.504173	2306.992746	0.000451244	15	N	76	96
P19973	Infl	SHQAK	VHLEESNLSYREPDPEDAVGGSGEAEEHLIR	HQVRT	3		1145.541873	3433.602218	0.000451244	25	N	130	161
P19973	Infl	AIDPR	CEEQEELHAEDSEGLTTQWREDEEEAAR	EQRQR	3	C1:+39.994	1163.481826	3487.422079	0.000870037	3	N	9	38
P19973	Infl	SNLSY	REPDPEDAVGGSGEAEEHLIR	HQVRT	3		755.024888	2262.051264	0.000451244	8	N	140	161
P20029	Infl	VVEKK	TKPYIQVDIGGGQTK	TFAPE	2		802.9362839	1603.856968	0.000451244	26	N	124	139
P20029	Infl	GDAAK	NQLTSNPENTVFDAKR	LIGRT	2		917.4586432	1832.901686	0.000451244	16	N	82	98
P20029	Infl	RLIGR	TWNDPSVQQDIK	FLPFK	2		715.8496771	1429.683754	0.000451244	29	N	102	114
P20029	Infl	PIISK	LYGSGGPPPTGEEDTSEKDEL	-	2		1089.4902	2176.9648	0.000451244	54	N	634	655
P20029	Infl	GDAAK	NQLTSNPENTVFDAK	RLIGR	2		839.4080876	1676.800575	0.000451244	24	N	82	97
P20029	Infl	YLGKK	VTHAVVTVPAYFNDAQR	QATKD	2		944.4897463	1886.963893	0.000451244	16	N	165	182
P20029	Infl	VPTKK	SQIFSTASDNQPTVTIK	VYEGE	2		918.9710521	1835.926504	0.000451244	87	N	448	465
P20029	Infl	DSDLK	KSDIDEIVLVGGSTR	IPKIQ	2		794.9311986	1587.846797	0.000451244	19	N	353	368
P20029	Infl	DQGNR	ITPSYVAFTPEGER	LIGDA	2		783.8940847	1565.772569	0.000451244	35	N	61	75
P20029	Infl	LNVMR	IINEPTAAAIAYGLDKR	EGEKN	2		908.5023224	1814.989045	0.000451244	8	N	198	215
P20029	Infl	DQGNR	ITPSYVAFTPEGERLIGDAAK	NQLTS	2		1118.086948	2234.158295	0.000622848	3	N	61	82
P20029	Infl	ETLTR	AKFEELNMDLFR	STMKP	3		504.9225491	1511.744247	0.00091018	3	N	325	337
P20029	Infl	RPLTK	DNHLLGTFDLTGIPPAPR	GVPQI	2		967.5106788	1933.005758	0.000451244	21	N	475	493
P20029	Infl	QHQAR	IEIESFFEGEDFSETLTR	AKFEE	2		1075.002746	2147.989892	0.000451244	96	N	307	325
P20029	Infl	GGQTK	TFAPEEISAMVLTK	MKETA	2		768.9030644	1535.790529	0.0007646	2	N	139	153
P20029	Infl	AVEEK	IEWLESHQDADIEDFKAK	KKELE	2		1087.52418	2173.03276	0.000451244	5	N	602	620
P20029	Infl	RIDTR	NELESYAYSLK	NQIGD	2		658.8225967	1315.629593	0.000637154	10	N	563	574
P20029	Infl	SDLKK	SDIDEIVLVGGSTR	IPKIQ	2		730.883717	1459.751834	0.001162105	6	N	354	368
P20029	Infl	AVEEK	IEWLESHQDADIEDFK	AKKKE	2		987.9581417	1973.900683	0.000451244	8	N	602	618
P20029	Infl	KLKER	IDTRNELESYAYSLK	NQIGD	2		901.4524952	1800.88939	0.000451244	1	N	559	574
P20029	Infl	VVPTK	KSQIFSTASDNQPTVTIK	VYEGE	2		983.0185337	1964.021467	0.000451244	6	N	447	465
P20029	Infl	PPAPR	GVPQIEVTFEIDVNGILR	VTAED	2		1000.047094	1998.078588	0.000451244	36	N	493	511
P20029	Infl	KVVEK	KTKPYIQVDIGGGQTK	TFAPE	3		578.3251103	1731.951931	0.00307782	1	N	123	139
P20060	Infl	SYELK	QVTGSGFPAILSAPWYLDLISYGQDWK	NYYKV	3		1004.843436	3011.506907	0.000451244	11	N	413	440
P20060	Infl	ELSNK	GSYSLSHVYTPNDVR	MVLEY	2		847.9107974	1693.805995	0.000451244	6	N	236	251
P20060	Infl	SSLKK	NSIVWQEVFDDKVELQPGTVVEVWK	SEHYS	3		982.175074	2943.501822	0.000870037	3	N	379	404
P20060	Infl	RMVSR	GIAAQPLYTGYCNYENKI	-	2	C12:+57.021	1037.999055	2073.982511	0.000451244	4	N	518	536
P20060	Infl	MAFNK	FNVLHWHIVDDQSFPYQSTTFPELSNK	GSYSL	3		1083.860037	3248.556711	0.000622848	5	N	209	236
P20108	Infl	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASKEYFEK	VHQ-	3	C12:+57.021	1370.658206	4108.951219	0.000451244	1	N	218	254
P20108	Infl	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASK	EYFEK	3	C12:+57.021	1138.554242	3412.639327	0.002519933	2	N	218	249
P20108	Infl	KQISR	DYGVLLESAGIALR	GLFII	2		738.9069951	1475.79839	0.000451244	11	N	171	185
P20152	Infl	TVETR	DGQVINETSQHHDDLE	-	2		918.9038977	1835.792195	0.000451244	42	N	450	466
P20152	Infl	FKNTR	TNEKVELQELNDR	FANYI	2		794.4028052	1586.79001	0.000451244	30	N	100	113
P20152	Infl	WYKSK	FADLSEAANR	NNDAL	2		547.2677916	1092.519983	0.000451244	28	N	294	304
P20152	Infl	WYKSK	FADLSEAANRNNDALR	QAKQE	2		888.9353352	1775.85507	0.000451244	5	N	294	310
P20152	Infl	PSTSR	SLYSSSPGGAYVTR	SSAVR	2		722.8575022	1443.699404	0.000451244	35	N	50	64
P20152	Infl	SLNLR	ETNLESLPLVDTHSKR	TLLIK	2		919.9844938	1837.953388	0.000451244	26	N	424	440
P20152	Infl	SLNLR	ETNLESLPLVDTHSK	RTLLI	2		841.9339382	1681.852276	0.000451244	34	N	424	439
P20152	Infl	SVAAK	NLQEAEEWYK	SKFAD	2		655.3071138	1308.598628	0.000451244	30	N	282	292
P20152	Infl	NDKAR	VEVERDNLAEDIMR	LREKL	2		844.9177658	1687.819932	0.000870037	2	N	170	184
P20152	Infl	ARHLR	EYQDLLNVK	MALDI	2		561.2960177	1120.576435	0.001699387	2	N	381	390
P20152	Infl	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	C7:+57.021	1189.087119	2376.158637	0.000451244	50	N	321	342
P20152	Infl	EQQNK	ILLAELEQLKGQGK	SRLGD	2		770.4593949	1538.90319	0.000451244	14	N	129	143
P20152	Infl	DLERK	VESLQEEIAFLKK	LHDEE	3		511.9561354	1532.845006	0.001162105	3	N	223	236
P20152	Infl	LDLER	KVESLQEEIAFLK	KLHDE	2		767.4303031	1532.845006	0.000451244	20	N	222	235
P20152	Infl	EQQNK	ILLAELEQLK	GQGKS	2		585.3611607	1168.706721	0.000451244	29	N	129	139
P20152	Infl	IAFLK	KLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	DVRQQ	3		1346.369979	4036.086536	0.000451244	9	N	235	270
P20152	Infl	AFLKK	LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	DVRQQ	3		1303.671657	3907.991572	0.000451244	45	N	236	270
P20152	Infl	GVRLL	QDSVDFSLADAINTEFKNTR	TNEKV	2		1136.048551	2270.081502	0.000451244	3	N	80	100
P20152	Infl	VPGVR	LLQDSVDFSLADAINTEFKNTR	TNEKV	2		1249.132615	2496.24963	0.000451244	8	N	78	100
P20152	Infl	GVRLL	QDSVDFSLADAINTEFK	NTRTN	2		950.4526922	1898.889784	0.000451244	51	N	80	97
P20152	Infl	GEESR	ISLPLPTFSSLNLR	ETNLE	2		779.4541125	1556.892625	0.000451244	33	N	410	424
P20152	Infl	VPGVR	LLQDSVDFSLADAINTEFK	NTRTN	2		1063.536756	2125.057912	0.000451244	418	N	78	97
P20152	Infl	GEESR	ISLPLPTFSSLNL	RETNL	2		701.4035569	1400.791514	0.000451244	2	N	410	423
P20152	Infl	TLLIK	TVETRDGQVINETSQHHDDLE	-	3		808.374357	2422.099671	0.000622848	3	N	445	466
P20152	Infl	EEMAR	HLREYQDLLNVK	MALDI	3		509.9479742	1526.820523	0.000823681	5	N	378	390
P20152	Infl	EMLQR	EEAESTLQSFRQDVDNASLAR	LDLER	2		1183.565096	2365.114593	0.000622848	3	N	196	217
P20152	Infl	LLNVK	MALDIEIATYR	KLLEG	2		648.3373602	1294.65912	0.000622848	4	N	390	401
P20152	Infl	NEYRR	QVQSLTCEVDALK	GTNES	2	C7:+57.021	745.8798887	1489.744177	0.000451244	19	N	321	334
P20152	Infl	ERQMR	EMEENFALEAANYQDTIGR	LQDEI	2		1100.99493	2199.97426	0.000451244	2	N	345	364

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P20152	Infl	SRISL	PLPTFSSLNLR	ETNLE	2		622.8540342	1243.692468	0.000622848	6	N	413	424
P20152	Infl	EMLQR	EEAESTLQSFR	QDVDN	2		648.8074779	1295.599356	0.000451244	17	N	196	207
P20491	Infl	EQAAA	LGEPQLCYILDAVLFLYGIVLTLLYCRLK	IQVRK	3	C7:+57.021,C26:+57.021	1152.972979	3455.895536	0.001943752	1	N	18	47
P20491	Infl	EQAAA	LGEPQLCYILDAVLFLYGIVLTLLYCR	LKIQV	3	C7:+57.021,C26:+57.021	1072.57997	3214.716509	0.000823681	4	N	18	45
P21107	Infl	LAEKK	AADAEAEVASLNRR	IQLVE	2		736.8767576	1471.737915	0.0007646	2	N	78	92
P21107	Infl	LAEKK	AADAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	19	N	78	91
P21107	Infl	AKLEK	TIDDLEDELYAQK	LKYKA	2		776.8730149	1551.73043	0.000451244	1	N	252	265
P21107-2	Infl	EAVKR	KIQVLQQQADDAEER	AERLQ	2		885.9531937	1769.890787	0.000451244	22	N	12	27
P21107-2	Infl	AVKRK	IQVLQQQADDAEER	AERLQ	2		821.9057121	1641.795824	0.000451244	53	N	13	27
P21107-2	Infl	AVKRK	IQVLQQQADDAEERAER	LQREV	2		999.9961212	1997.976642	0.000451244	18	N	13	30
P21107-2	Infl	AKLEK	TIDDLEDKLK	CTKEE	2		595.3196898	1188.62378	0.001463592	2	N	215	225
P21107-2	Infl	ERRAR	EQAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	4	N	42	54
P21107-2	Infl	EGERR	AREQAEAEVASLNR	RIQLV	3		515.266143	1542.775029	0.000451244	1	N	40	54
P21107-2	Infl	ERRAR	EQAEAEVASLNRR	IQLVE	2		736.8767576	1471.737915	0.002981883	1	N	42	55
P21614	Infl	MAALS	HQPQEFPTYVEPTNDEICEAFR	RDPKG	2	C18:+57.021	1354.108583	2706.201565	0.000451244	6	N	127	149
P21614	Infl	SHLIK	LAQKVPTANLENVLPLAEDFTEILSR	CCEST	3		961.1943571	2880.559671	0.000637154	1	N	238	264
P21619	Infl	SLFHR	SEAELATALSDKQGLETEVAELR	AQLAK	3		820.7541749	2459.239125	0.000451244	10	N	136	159
P21619	Infl	SSGSR	LAQQTVATGVVNIDEVDPEGR	FVRLK	2		1106.066744	2210.117887	0.000451244	3	N	439	460
P21619	Infl	SVQGR	ENGEEEEEEEAEFGEEDLFHQQGDPR	TTSRG	3		1026.750546	3077.228239	0.000823681	2	N	561	587
P22599	Infl	LGITR	IFNNGADLSGITEENAPLK	LSKAV	2		1002.008166	2002.000732	0.00091018	2	N	328	347
P22599	Infl	ADIHK	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	LVEKF	3		1166.937898	3497.790293	0.000637154	1	N	112	143
P22682	Infl	KLALK	NSPPYILDLLPDTYQHLR	TVLSR	2		1078.063276	2154.110951	0.002981883	1	N	76	94
P22682	Infl	INSER	KASSYQQGGGATANPVATAPSPQLSSEIER	LMSQG	3		1001.499168	3001.474104	0.000451244	12	N	840	870
P22682	Infl	RCEIK	GTEPIVVDPFDPR	GSGSL	2		721.3702454	1440.724891	0.000451244	2	N	422	435
P22682	Infl	FPDGR	NQNPDLTGLCEPTPQDHIK	VTQEQ	3	C10:+57.021	726.3482718	2176.021415	0.002453667	1	N	341	360
P22682	Infl	NSERK	ASSYQQGGGATANPVATAPSPQLSSEIER	LMSQG	2		1437.69737	2873.379141	0.000451244	1	N	841	870
P23116	Infl	VPEVK	DLYNWLEVEFNPLK	LCERV	2		890.4517668	1778.887934	0.000451244	13	N	388	402
P23116	Infl	LNWVR	EQPEKEPELQQYVPQLQNNTILR	LLQQV	3		932.1510399	2793.42972	0.000451244	9	N	415	438
P23116	Infl	NDMVR	FSVLQYVVPEVK	DLYNW	2		704.3982746	1406.780949	0.000823681	3	N	376	388
P23492	Infl	TAHLK	EAQIFDYNEIPNFPQSTVQGHAGR	LVFGL	2		1359.649495	2717.28339	0.000622848	1	N	43	67
P23492	Infl	HCGLR	VFGFSLITNK	VVMDY	2		563.3192958	1124.622992	0.000451244	7	N	234	244
P23492	Infl	IMLIR	DHINLPGFCGQNPLRGPNDER	FGVRF	3	C9:+57.021	802.7174696	2405.129009	0.000622848	1	N	133	154
P23492	Infl	GHAGR	LVFGLLNGR	CCVMM	2		494.8010733	987.5865465	0.001943752	1	N	67	76
P23492	Infl	ETTAK	WLLQHTEYRPQVAVICGSGLGGLTAHLK	EAQIF	3	C16:+57.021	1035.55396	3103.638479	0.002813207	1	N	15	43
P23591	Infl	RAIQK	VVADGAGLPGEEWVFVSSK	DADLT	2		973.9970699	1945.97854	0.000662267	5	N	25	44
P23591	Infl	RAIQK	VVADGAGLPGEEWVFVSSKDADLTDAAQTQALFQK	VQPTH	3		1221.944607	3662.81042	0.000451244	4	N	25	60
P23953	Infl	ILPLK	ISEDCLYLNIYSPADLTK	SSQLP	2	C5:+57.021	1058.019653	2114.023707	0.000451244	1	N	111	129
P23953	Infl	LPEGK	MNEETASLLLR	RFHSE	2	M1:+15.995	646.829942	1291.644284	0.002519933	1	N	359	370
P24063	Infl	GAEGR	VVVLSSRPVVDVVTELSFSPEEIPVHEVECSYSAR	EEQKH	3	C30:+57.021	1305.666702	3913.976705	0.000451244	1	N	604	639
P24063	Infl	AVGAK	DWAGGFLDLREDLQGATFVGQEPLTSDVR	GGYLG	3		1064.858585	3191.552354	0.000451244	12	N	369	398
P24063	Infl	FLDLR	EDLQGATFVGQEPLTSDVR	GGYLG	2		1031.50853	2061.00146	0.000451244	10	N	379	398
P24063	Infl	AVGAK	DWAGGFLDLR	EDLQG	2		575.288527	1148.561454	0.002374549	2	N	369	379
P24063	Infl	VQKQK	TLHIFASEPVEEFVK	ILDTF	3		582.6423279	1744.903584	0.000637154	1	N	295	310
P24063	Infl	INGDR	LTDVAVGAPLEEQGAVYIFNGKPGGLSPQPSQR	IQGAQ	3		1132.591839	3394.752117	0.000451244	5	N	533	566
P24270	Infl	GFAVK	FYTEDGNWDLVGNNTPIFFIR	DAILF	2		1259.606036	2517.196472	0.000622848	4	N	135	156
P24369	Infl	KTVPK	TVDNFVALATGEK	GFGYK	2		682.8569709	1363.698342	0.000622848	2	N	71	84
P24369	Infl	KTVPK	TVDNFVALATGEKGFGYK	NSKFH	2		958.9917875	1915.967975	0.002519933	1	N	71	89
P24369	Infl	GTGGK	SIYGERFPDENFK	LKHYG	2		801.3838842	1600.752168	0.002727428	1	N	116	129
P24369	Infl	TVKVY	FDLQIGDESVGR	VVFGL	2		668.3311202	1334.64664	0.002212458	1	N	47	59
P24527	Infl	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	2		1204.122384	2406.229169	0.000451244	8	N	288	310
P24527	Infl	IADLK	DLSSHQLNEFLAQVLQK	APLPL	2		985.5212435	1969.026887	0.000622848	2	N	493	510
P24527	Infl	RFNQR	VPIPCYLIALVVGALESR	QIGPR	2	C5:+57.021	985.5610945	1969.106589	0.000451244	13	N	195	213
P24527	Infl	DFARR	TLTGTAALTVQSQEENLR	SLTLD	2		966.5057904	1930.995981	0.000451244	38	N	33	51
P24527	Infl	GEKFR	HFHALGGWGELQNTIK	TFGES	2		904.4660742	1806.916548	0.000451244	3	N	339	355
P24527	Infl	TPSVK	LTYTAEVSVPK	ELVAL	2		604.3326002	1206.6496	0.000698008	1	N	154	165
P24527	Infl	VPIPC	YLIALVVGALESR	QIGPR	2		702.4169987	1402.818397	0.000451244	7	N	200	213
P24527	Infl	WVTAK	EEDLSSFSIADLKDLSSHQLNEFLAQVLQK	APLPL	3		1135.579376	3403.714728	0.000451244	7	N	480	510
P24527	Infl	IPYEK	GFALLFYLEQLLGGPEVFLGFLK	AYVKK	2		1286.217234	2570.418867	0.000622848	2	N	386	409
P24527	Infl	VVDLK	DVDPDVAYSSIPYEK	GFALL	2		849.3993969	1696.783194	0.000451244	8	N	371	386
P24527	Infl	AYVKK	FSYQSVTTDDWK	SFLYS	2		738.8362354	1475.656871	0.000823681	5	N	414	426
P24527	Infl	WVTAK	EEDLSSFSIADLK	DLSSH	2		727.3570007	1452.698401	0.000622848	6	N	480	493
P24527	Infl	LVTNK	TWDHFWLNEGHTVYLER	HICGR	2		1102.021942	2202.028284	0.00307782	1	N	310	327
P24527	Infl	HPFTK	LVVDLKDVDPDVAYSSIPYEK	GFALL	2		1183.112828	2364.210056	0.000451244	4	N	365	386
P24527	Infl	RPLFK	DLAAFDKSHDQAVHTY	QEHKA	2		909.4268117	1816.838023	0.001329271	2	N	573	589
P24527	Infl	VDFAR	RTLTGTAALTVQSQEENLR	SLTLD	2		1044.556346	2087.097092	0.000622848	4	N	32	51

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P24527	Infl	ETSPK	SSALQWLTPEQTSGKQHPYLFSQCQAIHCR	AILPC	3	C24:+57.021,C29:+57.021	1186.905238	3557.692313	0.000622848	10	N	112	142
P24527	Infl	RPLFK	DLAAFDKSHDQAVHTYQEHK	ASMHP	3		780.7054898	2339.093069	0.001591523	3	N	573	593
P24527	Infl	RKIYR	FNQRVPIPCYLIALVVGALESR	QIGPR	3	C9:+57.021	839.1336731	2514.377619	0.000451244	2	N	191	213
P24527	Infl	QIGPR	TLVWSEKEQVEK	SANEF	2		738.3911779	1474.766756	0.001699387	1	N	218	230
P24527	Infl	AIHCR	AILPCQDTPSVK	LTYTA	2	C5:+57.021	664.8478602	1327.68012	0.001943752	1	N	142	154
P24527	Infl	QTSGK	QHPYLFSQCQAIHCR	AILPC	2	C9:+57.021,C14:+57.021	972.9514881	1943.887376	0.001352548	1	N	127	142
P24547	Infl	KFEKR	TSSAQVEGGVHSLHSYEK	RLF-	3		639.3101886	1914.907166	0.0007646	1	N	493	511
P24547	Infl	DGLTY	NDFLILPGYIDFTADQVDLTSALTK	KITLK	3		924.1448919	2769.411276	0.001162105	5	N	32	57
P24547	Infl	AAQAK	NLIDAGVDALR	VGMGS	2		578.8201913	1155.624783	0.000998612	6	N	311	322
P25206	Infl	MHQYR	APGEQDGDALPLGSSVDILATDDPDFTQDDQQDTR	IYEKH	3		1234.889555	3701.645265	0.000451244	21	N	508	543
P25206	Infl	ARMSK	TVDLQDAEEAVELVQYAYFK	KVLEK	2		1166.073703	2330.131806	0.000451244	8	N	635	655
P25206	Infl	ARMSK	TVDLQDAEEAVELVQYAYFKK	VLEKE	3		820.416723	2458.226769	0.001162105	1	N	635	656
P25206	Infl	ESINR	NREEPFSSEEIQACLSR	MQDDN	2	C14:+57.021	1026.476476	2050.937351	0.000451244	1	N	778	795
P25206	Infl	REAQR	DYLDFLDDEEDQGIYQNK	VRELI	2		1110.484918	2218.954235	0.000451244	12	N	17	35
P25206	Infl	KRANR	LLNNAFEELVAFQR	ALKDF	2		832.4442761	1662.872952	0.000451244	3	N	64	78
P25444	Infl	TVFTK	SPYQEFTDHLVK	THTRV	3		488.5775469	1462.709241	0.000622848	3	N	263	275
P25444	Infl	SLPIK	ESEIIDFFLGASL	KDEVL	2		720.8670043	1439.718409	0.000622848	2	N	89	102
P25911	Infl	CWKEK	AEERPTFDYLQSVLDDFYTATEGQYQQQP	-	3		1147.192069	3438.552808	0.000451244	14	N	483	512
P25911	Infl	KMCWK	EKAEERPTFDYLQSVLDDFYTATEGQYQQQP	-	3		1232.904588	3695.690364	0.000823681	3	N	481	512
P26039	Infl	KAAQK	AAAFEDQENETVVVKEK	MVGGI	2		953.9737918	1905.931984	0.000451244	13	N	2476	2493
P26039	Infl	SDYGR	LASQAKPAAVAAENEEIGAHIK	HRVQE	2		1109.595471	2217.175342	0.000451244	6	N	1895	1917
P26039	Infl	ASAPK	ASAGPQPLLVQSCK	AVAEQ	2	C13:+57.021	728.3851412	1454.754682	0.000451244	22	N	943	957
P26039	Infl	MATAK	AVAAGNSCRQEDVIATANLSR	RAIAD	2	C8:+57.021	1102.048131	2202.080662	0.000823681	6	N	2188	2209
P26039	Infl	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2		983.0115743	1964.007549	0.000451244	14	N	922	943
P26039	Infl	KAAQK	AAAFEDQENETVVVK	EKMVG	2		825.4050136	1648.794427	0.000451244	16	N	2476	2491
P26039	Infl	ISSAK	QVAASTAQLLVACK	VKADQ	2	C13:+57.021	730.4007913	1458.785983	0.000451244	19	N	2429	2443
P26039	Infl	RLVAK	AVEGCVSASQAATEDGQLLR	GVGAA	2	C5:+57.021	1031.497408	2060.979216	0.000451244	15	N	745	765
P26039	Infl	SAIAK	LLGEIAQGNENYAGIAAR	DVAGG	2		930.484661	1858.953722	0.000451244	6	N	1104	1122
P26039	Infl	SQNAK	NGNLPEFGDAIATASK	ALCGF	2		802.8998984	1603.784197	0.000451244	5	N	1415	1431
P26039	Infl	VACTK	VVAPTISSPVCQEQLVEAGR	LVAKA	2	C11:+57.021	1070.557269	2139.098938	0.000451244	24	N	721	741
P26039	Infl	QLKPR	AKPKEADESLNFEEQILEAAK	SIAAA	2		1180.603159	2359.190718	0.000451244	9	N	2329	2350
P26039	Infl	TKGTR	ALEATTEHIRQELAVFCSPEPPAK	TSTPE	2	C17:+57.021	1347.681718	2693.347835	0.000451244	7	N	2144	2168
P26039	Infl	SRGVK	LLAALLEDEGGNGRPLLQAAK	GLAGA	2		1075.102932	2148.190264	0.000451244	11	N	592	613
P26039	Infl	VQSCK	AVAEQIPLLVQGVR	GSQAQ	2		746.9464546	1491.877309	0.000451244	25	N	957	971
P26039	Infl	ITSMR	DKAPGQLECETAIAALNSCLR	DLDQA	2	C9:+57.021,C19:+57.021	1159.067443	2316.119287	0.000451244	19	N	1652	1673
P26039	Infl	LQAAK	GLAGAVSELLR	SAQPA	2		543.3198272	1084.624054	0.000451244	15	N	613	624
P26039	Infl	EMVTK	SNTSPEELGPLANQLTSDYGR	LASQA	2		1125.038183	2248.060766	0.000451244	7	N	1874	1895
P26039	Infl	EAQSR	LNEAAAGLNQAATELVQASR	GTPQD	2		1014.029964	2026.044328	0.000451244	23	N	1241	1261
P26039	Infl	ADVVK	LGAASLGAEDPETQVVLINAVK	DVAKA	2		1098.100055	2194.18451	0.000451244	29	N	2063	2085
P26039	Infl	NSCLR	DLDQASLAAVSQQLAPR	EGISQ	2		891.9713864	1781.927173	0.000451244	15	N	1673	1690
P26039	Infl	VAQGK	VGAIPANALDDGQWSQGLISAAR	MVAAA	2		1155.596003	2309.176405	0.000451244	23	N	2375	2398
P26039	Infl	ADVVK	LGAASLGAEDPETQVVLINAVKDVAK	ALGDL	2		1304.713772	2607.411944	0.000451244	7	N	2063	2089
P26039	Infl	VRQAR	ILAQATSDLVNAIKADAEGESDLENSR	KLLSA	2		1415.707404	2829.399207	0.000451244	3	N	827	854
P26039	Infl	EQKHK	AGFLDLKDFLPK	EYVKQ	2		682.3851672	1362.754734	0.001654178	4	N	256	268
P26039	Infl	VLKAK	SVAQRTEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	3	C22:+57.021,C32:+57.021	1198.601661	3592.781582	0.000451244	6	N	687	721
P26039	Infl	LDQTK	TLAESALQLLYTAK	EAGGN	2		761.4303031	1520.845006	0.000451244	13	N	1766	1780
P26039	Infl	VQGVR	GSQAQPDSPSAQLALIAASQSFLQPGGK	MVAAA	2		1377.70701	2753.398419	0.000622848	11	N	971	999
P26039	Infl	SVAQR	TEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	3	C17:+57.021,C27:+57.021	1018.169246	3051.484337	0.000451244	16	N	692	721
P26039	Infl	ATASK	ALCGFTEAAAQAAYLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	3	C3:+57.021	1308.306167	3921.895101	0.000451244	43	N	1431	1469
P26039	Infl	LHYGR	ECANGYLELLDHVLLTLQKPNPDLK	QQLTG	3	C2:+57.021	965.1761548	2892.505065	0.000451244	9	N	2241	2266
P26039	Infl	GQLLR	GVGAAATAVTQALNELLQHVK	AHATG	2		1046.082	2090.148399	0.000451244	13	N	765	786
P26039	Infl	RAQCR	AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR	AAMEP	3		1152.914759	3455.720876	0.000451244	41	N	1559	1593
P26039	Infl	QLAPR	EGISQEALHTQMLTAVQEISHLIEPLASAAR	AEASQ	3		1115.249196	3342.724189	0.000451244	7	N	1690	1721
P26039	Infl	AEAMK	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1017.843941	3050.508424	0.000451244	42	N	2291	2321
P26039	Infl	AQAAR	GVAALTSDPAVQAIVLDTASDVLDKASSLIEEAK	KASGH	3		1133.27032	3396.787559	0.000637154	9	N	1136	1170
P26039	Infl	LRACK	EAAFHPEVAPDVR	LRALH	2		719.360212	1436.704824	0.000451244	5	N	2220	2233
P26039	Infl	VAAAK	ASVPTIQDQASAMQLSQCAK	NLGTA	2	C18:+57.021	1067.517287	2133.018974	0.000451244	4	N	1005	1025
P26039	Infl	VEDTK	VLVQNAAGSQEKLAQAAQSSVATITR	LADVV	3		881.1476297	2640.419489	0.000451244	3	N	2031	2057
P26039	Infl	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	3		1388.694245	4163.059336	0.000451244	10	N	634	673
P26039	Infl	GSQEK	LAQAAQSSVATITR	LADVV	2		708.894419	1415.773238	0.000451244	33	N	2043	2057
P26039	Infl	ALVTK	AGALQCSPSDVYTK	KELIE	2	C6:+57.021	748.8564136	1495.697227	0.000451244	22	N	1933	1947
P26039	Infl	GNSCR	QEDVIATANLSR	RAIAD	2		658.8443948	1315.67319	0.000622848	1	N	2197	2209
P26039	Infl	LLAAK	ALSTDPASPNLKSQLAAAAR	AVTDS	2		991.5374249	1981.05925	0.000451244	5	N	1320	1340
P26039	Infl	KLKQK	LHTDDELNWLDHGR	TLREQ	2		860.9060464	1719.796493	0.000451244	10	N	164	178
P26039	Infl	MQLAK	AVASAAAALVLK	AKSVA	2		542.8403955	1083.665191	0.000823681	7	N	673	685

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26039	Infl	RAKPK	EADESLNFEEQILEAAK	SIAAA	2		968.4632569	1934.910914	0.000451244	15	N	2333	2350
P26039	Infl	YVQAR	DDILNGSHPVSFDK	ACEFA	2		772.3735164	1542.731433	0.000451244	16	N	220	234
P26039	Infl	TEHIR	QELAVFCSPEPPAK	TSTPE	2	C7:+57.021	786.8902564	1571.764913	0.000451244	9	N	2154	2168
P26039	Infl	VRQAR	ILAQATSDLVNAIK	ADAEG	2		728.9226452	1455.82969	0.000451244	15	N	827	841
P26039	Infl	SMRDK	APGQLECETAIAALNSCLR	DLDQA	2	C7:+57.021,C17:+57.021	1037.50649	2072.997381	0.000451244	8	N	1654	1673
P26039	Infl	MIRER	IPEALAGPPNDFGLFLSDDDPKK	GIWLE	3		819.4168344	2455.227103	0.000451244	13	N	35	58
P26039	Infl	CRMIR	ERIPEALAGPPNDFGLFLSDDDPK	KGIWL	2		1307.145722	2612.275845	0.001943752	1	N	33	57
P26039	Infl	AQAAR	GVAALTSDPAVQAIVLDTASDVLDK	ASSLI	2		1235.158298	2468.300997	0.000451244	9	N	1136	1161
P26039	Infl	AAEAM	KGTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1060.542262	3178.603387	0.000735798	2	N	2290	2321
P26039	Infl	ASQAK	PAAVAAENEEIGAHIK	HRVQE	3		540.6182938	1618.831481	0.000823681	1	N	1901	1917
P26039	Infl	SQCAK	NLGTALAELR	TAAQK	2		529.3041771	1056.592754	0.000451244	12	N	1025	1035
P26039	Infl	VSFDK	ACEFAGFQCQIQFGPHNEQK	HKAGF	2	C2:+57.021,C9:+57.021	1198.531028	2395.046456	0.000451244	5	N	234	254
P26039	Infl	LLRRK	FFYSDQNVDSRDPVQLNLLYVQAR	DDILN	3		963.1511513	2886.430054	0.000451244	6	N	196	220
P26039	Infl	LLAAK	ALSTDPASPNLK	SQLAA	2		607.3253065	1212.635013	0.000451244	8	N	1320	1332
P26039	Infl	TICAR	IGITNHDEYSLVR	ELMEE	2		758.8918764	1515.768153	0.000451244	6	N	118	131
P26039	Infl	GPAGR	YDQATDTILTVTENIF	SSMGD	2		922.4521608	1842.888722	0.002727428	1	N	797	813
P26039	Infl	QAGNR	GTQACITAASAVSGIIADLDTTIMFATAGTLNR	EGAET	3	C5:+57.021	1104.558888	3310.653263	0.000622848	4	N	1973	2006
P26039	Infl	LDHGR	TLREQGVEEHETLLLR	RKFFY	2		962.018868	1922.022136	0.000451244	6	N	178	194
P26039	Infl	ISAAR	MVAAATNNLCEAANAAVQGHASQEK	LISSA	2	C10:+57.021	1278.600402	2555.185205	0.000622848	2	N	2398	2423
P26039	Infl	AAAGK	VGDDPAVWQLK	NSAKV	2		614.3225669	1226.629534	0.000622848	4	N	2104	2115
P26039	Infl	LLRRK	FFYSDQNVDSRDPVQL	NLLYV	2		965.4530265	1928.890453	0.000451244	12	N	196	212
P26039	Infl	MIRER	IPEALAGPPNDFGLFLSDDDPK	KGIWL	2		1164.57387	2327.13214	0.001162105	10	N	35	57
P26039	Infl	QLGHK	VSQMAQYFEPLTLAAVGAASK	TLSHP	2		1091.564794	2181.113989	0.000451244	4	N	1730	1751
P26039	Infl	AEAMK	GTEWVDPEDPTVIAENELLG	AAAAI	2		1092.521303	2183.027006	0.001329271	2	N	2291	2311
P26039	Infl	AEAMK	GTEWVDPEDPTVIAENELLGAAAAIEAAAKK	LEQLK	3		1060.542262	3178.603387	0.000451244	4	N	2291	2322
P26039	Infl	RAKPK	EADESLNFEEQILEAAKSIAAATSALVK	AASAA	3		983.50867	2947.50261	0.000451244	4	N	2333	2361
P26039	Infl	ADMLR	ACKEAAFHPEVAPDVR	LRALH	3	C2:+57.021	599.6301622	1795.867087	0.000451244	3	N	2217	2233
P26039	Infl	KACEF	AGFQCQIQFGPHNEQK	HKAGF	2	C5:+57.021	944.9418747	1887.868149	0.000451244	3	N	238	254
P26039	Infl	TQFAR	ANQAIQMACQSLGEPGCTQAQVLSAATIVAK	HTSAL	3	C9:+57.021,C17:+57.021	1072.865392	3215.572776	0.000451244	3	N	1469	1500
P26039	Infl	DFGDY	QDGYYSVQTTEGEQIAQLIAGYIDIILKK	KKSKD	3		1086.570041	3256.686723	0.000451244	1	N	373	402
P26039	Infl	GAASK	TLSHPQQMALLDQTK	TLAES	2		855.9463263	1709.877053	0.001162105	3	N	1751	1766
P26039	Infl	VISAK	TMLESAGGLIQTAR	ALAVN	2		724.3828305	1446.750061	0.00091018	1	N	1604	1618
P26039	Infl	YVQAR	DDILNGSHPVSFDKACEF	AGFQC	2	C16:+57.021	1025.96267	2049.90974	0.000823681	2	N	220	238
P26039	Infl	YVQAR	DDILNGSHPVSFDKACEFAGFQCQIQFGPHNEQK	HKAGF	3	C16:+57.021,C23:+57.021	1307.59691	3919.767329	0.001352548	1	N	220	254
P26039	Infl	KDVAK	ALGDLISATK	AAAGK	2		494.7878285	987.560057	0.000622848	7	N	2089	2099
P26039	Infl	AQAAY	LVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	2		1249.635856	2497.256112	0.000823681	4	N	1445	1469
P26039	Infl	QMAQY	FEPLTLAAVGAASK	TLSHP	2		687.8855313	1373.755463	0.000823681	2	N	1737	1751
P26040	Infl	QDQIK	SQEQLAAELAEYTAK	IALLE	2		826.4128386	1650.810077	0.001871652	1	N	412	427
P26040	Infl	EELER	QAQDQIKSQEQLAAELAEYTAK	IALLE	2		1232.122247	2462.228894	0.000451244	9	N	405	427
P26040	Infl	FLQVK	DGILSDEIYCPPETAVLLGSYAVQAK	FGDYN	2	C10:+57.021	1405.202149	2808.388697	0.000451244	24	N	107	133
P26040	Infl	KFRAK	FYPEDVAEELIQDITQK	LFFLQ	2		1019.504925	2036.99425	0.000451244	6	N	83	100
P26040	Infl	ERVQR	QLLTLSNELSQAR	DENKR	2		736.9075264	1471.799453	0.000451244	9	N	529	542
P26040	Infl	QFKFR	AKFYPEDVAEELIQDITQK	LFFLQ	2		1119.070963	2236.126327	0.000451244	4	N	81	100
P26041	Infl	KEVHK	SGYLAGDKLLPQR	VLEQH	2		709.3940549	1416.77251	0.000451244	4	N	143	156
P26041	Infl	TIGLR	EVWFFGLQYQDTK	AFSTW	2		830.9044524	1659.793305	0.000451244	8	N	40	53
P26041	Infl	LFKFR	AKFYPEDVSEELIQDITQR	LFFLQ	2		1141.071495	2280.127389	0.000451244	30	N	81	100
P26041	Infl	IKNKK	GSELWLGVDALGLNIYEQNDRLTPK	IGFPW	2		1401.227578	2800.439556	0.000451244	8	N	212	237
P26041	Infl	IKNKK	GSELWLGVDALGLNIYEQNDR	LTPKI	2		1181.587843	2361.160086	0.000451244	21	N	212	233
P26041	Infl	KFRAK	FYPEDVSEELIQDITQR	LFFLQ	2		1041.505456	2080.995312	0.000451244	14	N	83	100
P26041	Infl	FLQVK	EGILNDDIYCPPETAVLLASYAVQSK	YGDFN	2	C10:+57.021	1433.712881	2865.410161	0.000451244	39	N	107	133
P26041	Infl	LAKER	QEAEEAKEALLQASR	DQKKT	3		558.2887248	1671.842774	0.000698008	3	N	393	408
P26041	Infl	SIKNK	KGSELWLGVDALGLNIYEQNDR	LTPKI	2		1245.635325	2489.255049	0.000870037	1	N	211	233
P26041	Infl	RGMLR	EDAVLEYLK	IAQDL	2		540.2851187	1078.554637	0.000622848	2	N	184	193
P26043	Infl	FLQVK	EAILNDEIYCPPETAVLLASYAVQAK	YGDYN	2	C10:+57.021	1439.731073	2877.446547	0.000451244	5	N	107	133
P26043	Infl	KFRAK	FFPEDVSEELIQEITQR	LFFLQ	3		694.0131492	2079.016048	0.000451244	4	N	83	100
P26043	Infl	IKNKK	GTELWLGVDALGLNIYEHDDKLTPK	IGFPW	4		700.116152	2796.433408	0.000451244	1	N	212	237
P26350	Infl	EGGEE	EEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1003.717348	3008.128644	0.000451244	44	N	63	90
P26350	Infl	EEGGE	EEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1046.731546	3137.171237	0.000451244	29	N	62	90
P26350	Infl	EEEEE	GGEEEEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1127.760053	3380.256758	0.000451244	79	N	59	90
P26350	Infl	EEEEE	GGEEEEEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	3		1075.726349	3224.155647	0.000451244	38	N	59	89
P26350	Infl	EGGEE	EEEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	2		1427.021566	2852.027533	0.000451244	27	N	63	89
P26350	Infl	LKEKK	EVVEEAENGRDAPANGNAQNEENGEQEADNEVDEEEEE	GGEEE	3		1396.564964	4186.671492	0.000451244	25	N	21	59
P26350	Infl	DEEEE	EGGEEEEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1170.77425	3509.299351	0.000451244	10	N	58	90
P26350	Infl	EEGGE	EEEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	3		994.6978419	2981.070126	0.000451244	18	N	62	89
P26350	Infl	LKEKK	EVVEEAENGRDAPANGNAQNEENGEQE	ADNEV	2		1450.114596	2898.213591	0.000979378	1	N	21	48

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26350	Infl	GGEEE	EEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	2		1362.50027	2722.984939	0.000451244	8	N	64	89
P26350	Infl	GGEEE	EEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		960.7031502	2879.086051	0.000451244	27	N	64	90
P26350	Infl	GEEEE	EEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		917.6889525	2750.043457	0.000451244	12	N	65	90
P26350	Infl	GEEEE	EEEEGDGEEEDGDEDEEAEAPTGK	RVAED	2		1297.978973	2593.942346	0.000451244	16	N	65	89
P26369	Infl	YGLVK	SIEIPRPVDGVEVPGCGK	IFVEF	2	C16:+57.021	954.9963156	1907.977031	0.000451244	1	N	413	431
P26369	Infl	PGCGK	IFVEFTSVFDCQK	AMQGL	2	C11:+57.021	810.392632	1618.769664	0.000451244	5	N	431	444
P26369	Infl	DSAHK	LFIGGLPNYLNDDQVKELLTSFGPLK	AFNLV	2		1446.281822	2890.548044	0.000451244	2	N	260	286
P26369	Infl	NAQMR	LGGLTQAPGNPVLAVQINQDKNFAFLEFR	SVDET	3		1053.231805	3156.672016	0.000622848	10	N	174	203
P26369	Infl	NAQMR	LGGLTQAPGNPVLAVQINQDK	NFAFL	2		1067.087282	2132.158964	0.000662267	3	N	174	195
P26443	Infl	RVKAK	IIAEGANGPTTPEADKIFLER	NIMVI	2		1121.589855	2241.164109	0.000451244	1	N	399	420
P26443	Infl	FPKAK	VYEGSILEADCDILIPAASEK	QLTKS	2	C11:+57.021	1147.067332	2292.119064	0.000451244	22	N	365	386
P26443	Infl	RFGAK	CVGVGESDGSIWNPDGIDPK	ELEDF	2	C1:+57.021	1051.478684	2100.941768	0.000451244	12	N	326	346
P26443	Infl	ARRHY	SEAAADREDDPNFFK	MVEGF	2		856.3820698	1710.74854	0.000451244	5	N	53	68
P26443	Infl	RKFGK	HGGTIPVVPTAEFQDR	ISGAS	2		862.4422648	1722.86893	0.001352548	1	N	480	496
P26450	Infl	LTVNK	GSLVALGFSDGQEARPEDIGWLNGYNETTGER	GDFPG	3		1146.878596	3437.612388	0.000451244	6	N	34	66
P26450	Infl	PGSSK	TEADTEQQALPLPDLAEQFAPPDVAPPLLIK	LLEAI	3		1109.917329	3326.728587	0.000451244	14	N	103	134
P26516	Infl	TPTSK	TFEHVTSEIGAEEAEEVGVEHLLR	DIKDT	4		671.0823092	2680.298037	0.000451244	3	N	153	177
P26516	Infl	DVKPK	DLGLPTEAYISVEEVHDDGTPTSK	TFEHV	2		1287.116827	2572.218055	0.000451244	6	N	129	153
P26516	Infl	LAVQK	VVVHPLVLLSVVDHFNR	IGKVG	3		648.3795495	1942.115248	0.000451244	4	N	8	25
P26516	Infl	VASGK	LPINHQIIYQLQDVFNLLPDASLQEFVK	AFYLK	3		1099.262883	3294.765248	0.000622848	4	N	219	247
P26516	Infl	HQIIY	QLQDVFNLLPDASLQEFVK	AFYLK	2		1102.584041	2203.152482	0.001329271	1	N	228	247
P27005	Infl	SELEK	ALSNLIDVYHNYSNIQGNHHALYKNDFK	KMVTT	3		1096.878202	3287.611206	0.000451244	12	N	7	35
P27005	Infl	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	2		1392.696779	2783.377959	0.000451244	75	N	7	31
P27005	Infl	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	2		1328.649298	2655.282996	0.000451244	73	N	7	30
P27005	Infl	KNDFK	KMVTTECPQFVQNINIENLFR	ELDIN	2	C7:+57.021	1291.149	2580.282399	0.000451244	9	N	35	56
P27005	Infl	FKKMV	TTECPQFVQNINIENLFR	ELDIN	2	C4:+57.021	1112.047068	2222.078536	0.000451244	4	N	38	56
P27005	Infl	KKMVT	TECPQFVQNINIENLFR	ELDIN	2	C3:+57.021	1061.523229	2121.030858	0.000451244	14	N	39	56
P27005	Infl	KMVTT	ECPQFVQNINIENLFR	ELDIN	2	E1:-18.011,C2:+57.021	1001.99389	2001.972179	0.000823681	7	N	40	56
P27005	Infl	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	2	C6:+57.021	1227.101518	2452.187436	0.000451244	650	N	36	56
P27005	Infl	DFKKM	VTTECPQFVQNINIENLFR	ELDIN	2	C5:+57.021	1161.581275	2321.14695	0.000451244	23	N	37	56
P27005	Infl	ENLFR	ELDINSDNAINFEEF	LAMVI	2		885.3973856	1768.779171	0.000451244	55	N	56	71
P27005	Infl	NDFKK	MVTTECPQFVQNINIENLF	RELDI	2	C6:+57.021	1149.050963	2296.086325	0.000451244	27	N	36	55
P27005	Infl	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2		1213.101938	2424.188276	0.000451244	745	N	56	77
P27005	Infl	NAINF	EEFLAMVIK	VGVAS	2		540.2944327	1078.573265	0.001162105	15	N	68	77
P27005	Infl	ECPQF	VQNINIENLFR	ELDIN	2		680.3731224	1358.730645	0.000451244	19	N	45	56
P27005	Infl	ENLFR	ELDINSDNAINF	EEFLA	2		682.8205853	1363.625571	0.000451244	28	N	56	68
P27005	Infl	SELEK	ALSNLIDVYHNY	SNIQG	2		711.357138	1420.698676	0.000451244	6	N	7	19
P27005	Infl	SELEK	ALSNLIDVYHNYSNIQGN	HHALY	2		1017.998133	2033.980665	0.000451244	6	N	7	25
P27005	Infl	VTTEC	PQFVQNINIENLFR	ELDIN	2		866.4630002	1730.9104	0.000451244	18	N	42	56
P27005	Infl	LEKAL	SNLIDVYHNYSNIQGNHHALYK	NDFKK	2		1300.63619	2599.256781	0.000451244	4	N	9	31
P27005	Infl	SELEK	ALSNLIDVYHNYSNIQGNHH	ALYKN	2		1155.057044	2308.098489	0.000451244	10	N	7	27
P27005	Infl	-M	PSELEKALSNLIDVYHNYSNIQGNHHALYK	NDFKK	4		867.6895412	3466.726965	0.000622848	3	N	1	31
P27005	Infl	ENLFR	ELDINSDNAINFEEFL	AMVIK	2		941.9394176	1881.863235	0.000451244	9	N	56	72
P27005	Infl	KALSN	LIDVYHNYSNIQGNHHALYK	NDFKK	3		800.4017416	2398.181825	0.000451244	14	N	11	31
P27005	Infl	MVTTE	CPQFVQNINIENLFR	ELDIN	2	C1:+57.021	946.478093	1890.940586	0.000451244	17	N	41	56
P27005	Infl	CPQFV	QNINIENLFR	ELDIN	2		630.8389154	1259.662231	0.000451244	3	N	46	56
P27005	Infl	SDNAI	NFEEFLAMVIK	VGVAS	2		670.8501035	1339.684607	0.002145581	1	N	66	77
P27005	Infl	NDFKK	MVTTECPQFVQNINIENLFRE	LDINS	3	C6:+57.021	861.4178098	2581.230029	0.001763695	3	N	36	57
P27005	Infl	KNDFK	KMVTTECPQFVQNINIENLF	RELDI	2	C7:+57.021	1213.098444	2424.181288	0.000662267	1	N	35	55
P27005	Infl	NDFKK	MVTTECPQFVQNINIENLFRELDINSDNAINF	EEFLA	3	C6:+57.021	1266.941949	3797.802447	0.002981883	1	N	36	68
P27005	Infl	SELEK	ALSNLIDVYHNYSNIQGNHHAL	YKNDF	2		1247.117633	2492.219667	0.000637154	3	N	7	29
P27005	Infl	LIDVY	HNYSNIQGNHHALYK	NDFKK	3		599.2928036	1794.855011	0.000823681	2	N	16	31
P27005	Infl	SELEK	ALSNLIDVYHNYSNIQGNHHALYKN	DFKKM	3		966.8147621	2897.420886	0.000662267	4	N	7	32
P27005	Infl	SELEK	ALSNLIDVYHNYSN	IQGNH	2		811.894616	1621.773632	0.000637154	7	N	7	21
P27005	Infl	TECPQ	FVQNINIENLFR	ELDIN	2		753.9073294	1505.799059	0.000735798	3	N	44	56
P27005	Infl	LSNLI	DVYHNYSNIQGNHHALYK	NDFKK	3		725.0123655	2172.013697	0.000451244	3	N	13	31
P27005	Infl	SELEK	ALSNLIDVYHN	YSNIQ	2		629.8254737	1257.635347	0.001463592	1	N	7	18
P27005	Infl	EKALS	NLIDVYHNYSNIQGNHHALYK	NDFKK	3		838.4160508	2512.224752	0.000823681	3	N	10	31
P27005	Infl	ALSNL	IDVYHNYSNIQGNHHALYK	NDFKK	3		762.7070535	2285.097761	0.000622848	2	N	12	31
P27601	Infl	GESVK	YFLDNLDKLGVPDYIPSQQDILLAR	RPTKG	3		969.5153192	2905.522557	0.002813207	1	N	175	200
P27601	Infl	LPAIR	ALWEDSGIQNAYDR	RREFQ	2		819.3818728	1636.748146	0.001352548	1	N	150	164
P27659	Infl	GKLIK	NNASTDYDLSDKSINPLGGFVHY	GEVTN	2		1264.090947	2526.166294	0.000451244	6	N	300	323
P27661	Infl	NKLLG	GVTIAQGGVLPNIQAVLLPK	KSSAT	2		994.5992969	1987.182994	0.000451244	319	N	99	119
P27661	Infl	EELNK	LLGGVTIAQGGVLPNIQAV	LLPKK	2		910.5361652	1819.05673	0.000823681	4	N	96	115
P27661	Infl	EELNK	LLGGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1136.194093	2270.372586	0.000451244	131	N	96	119

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27661	Infl	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAV	LLPKK	2		1331.724671	2661.433742	0.000451244	12	N	89	115
P27661	Infl	HYAER	VGAGAPVYLAAVLEY	LTAEI	2		746.9064638	1491.797328	0.000451244	33	N	43	58
P27661	Infl	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		1038.590999	3112.749598	0.000451244	125	N	89	119
P27661	Infl	GAPVY	LAAVLEYLTAEILELAGNAAR	DNKKT	2		1101.112965	2200.210331	0.000451244	102	N	51	72
P27661	Infl	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1458.298003	2914.580407	0.000451244	19	N	43	72
P27661	Infl	HYAER	VGAGAPVYLAAVLEYLTAEILELAGN	AARDN	2		1309.210334	2616.405068	0.000823681	2	N	43	69
P27661	Infl	LAIRN	DEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		1000.57669	2998.70667	0.000451244	5	N	90	119
P27661	Infl	LNKLL	GGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1023.110029	2044.204458	0.000823681	6	N	98	119
P27661	Infl	HYAER	VGAGAPVYLAAVLEYLT	AEILE	2		853.9723351	1705.92907	0.000451244	12	N	43	60
P27661	Infl	QLAIR	NDEELNKLLGGVTIAQGGVLPN	IQAVL	2		1126.100586	2250.185573	0.000622848	11	N	89	111
P27661	Infl	HYAER	VGAGAPVYLAAVLEYLTAEILEL	AGNAA	3		792.4423209	2374.303563	0.002212458	1	N	43	66
P27661	Infl	EELNK	LLGGVTIAQGGVLPN	IQAVL	2		704.9120805	1407.808561	0.001162105	2	N	96	111
P27661	Infl	QLAIR	NDEELNKLLGGV	TIAQG	2		650.8413208	1299.667042	0.000451244	1	N	89	101
P27773	Infl	YPTLK	IFRDGEEAGAYDGPR	TADGI	2		826.8873223	1651.759045	0.000451244	22	N	104	119
P27773	Infl	VPLAK	VDCTANTNTCNKYGVSGYPTLK	IFRDG	2	C3:+57.021,C10:+57.021	1232.06764	2462.119681	0.000451244	5	N	82	104
P27773	Infl	NTCNK	YGVSGYPTLK	IFRDG	2		542.7878285	1083.560057	0.000451244	8	N	94	104
P27773	Infl	IVIAK	MDATANDVPSPYEVK	GFPTI	2		818.8803176	1635.745035	0.000622848	1	N	433	448
P27773	Infl	VGFFR	DLFSDGHSEFLK	AASNL	2		697.8334957	1393.651391	0.000451244	1	N	161	173
P27773	Infl	RLAAA	SDVLELTDENFESR	VSDTG	2		827.3842782	1652.752956	0.000451244	18	N	24	38
P27773	Infl	EEFKK	FISDKDASVVGFFR	DLFSD	2		794.4124446	1586.809289	0.000451244	8	N	147	161
P27773	Infl	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1360.201029	2718.386458	0.000451244	13	N	304	329
P27773	Infl	LIQGK	DLLTAYYDVDYEK	NAKGS	2		804.3779331	1606.740266	0.000451244	15	N	258	271
P27773	Infl	VASRK	TFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1296.153547	2590.291495	0.000451244	26	N	305	329
P27773	Infl	YEGGR	ELNDFISYLQR	EATNP	2		699.357138	1396.698676	0.000622848	4	N	471	482
P27773	Infl	SRDGK	ALEQFLQEYFDGNLKR	YLKSE	2		986.0026866	1969.989773	0.000451244	15	N	347	363
P27773	Infl	SRDGK	ALEQFLQEYFDGNLK	RYLKS	2		907.952131	1813.888662	0.000451244	14	N	347	362
P27773	Infl	SYLQR	EATNPPIIQEEKPK	KKKKA	2		797.4282917	1592.840983	0.000451244	7	N	482	496
P27773	Infl	RDNYR	FAHTNIESLVK	EYDDN	2		629.8436665	1257.671733	0.000451244	1	N	183	194
P27773	Infl	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	2		1151.577278	2301.138957	0.000451244	1	N	194	214
P27773	Infl	ESLVK	EYDDNGEGITIFRPLHLANKFEDK	TVAYT	3		941.1317568	2820.37187	0.000451244	14	N	194	218
P27773	Infl	ELGEK	LSKDPNIVIAK	MDATA	3		399.9120898	1196.712869	0.002296037	1	N	422	433
P27773	Infl	KRYLK	SEPIPESNEGPVK	VVVAE	2		691.8440605	1381.672521	0.000622848	7	N	366	379
P27773	Infl	VVGFF	RDLFSDGHSEFLK	AASNL	3		517.5919675	1549.752503	0.000622848	8	N	160	173
P27773	Infl	GNLKR	YLKSEPIPESNEGPVK	VVVAE	2		893.9652384	1785.914877	0.002374549	1	N	363	379
P27870	Infl	KKAFR	GLLELVEFYQQNSLKDCFK	SLDTT	3	C17:+57.021	777.7282012	2330.161204	0.002145581	2	N	736	755
P27870	Infl	FGLKR	SELFEAFDLFDVQDFGK	VIYTL	2		1003.97326	2005.930921	0.000451244	16	N	90	107
P27870	Infl	AQALR	DGVLLCQLLNNLLPQAINLR	EVNLR	2	C6:+57.021	1139.141303	2276.267006	0.000451244	7	N	38	58
P27870	Infl	WWEGR	NTATNEVGWFPCNR	VHPYV	2	C12:+57.021	833.3758362	1664.736072	0.000451244	14	N	640	654
P27870	Infl	EIYGR	IGWFPSNYVEEDYSEYC	-	2	C17:+57.021	1079.441236	2156.866872	0.000451244	3	N	828	845
P27870	Infl	NETLR	QITNFQLSIENLDQSLANYGRPK	IDGEL	2		1325.185713	2648.355826	0.000451244	1	N	381	404
P27870	Infl	KKAFR	GLLELVEFYQQNSLK	DCFKS	2		890.9781488	1779.940698	0.001763695	1	N	736	751
P27931	Infl	NIELR	VKGTTTEPIPVIISPLETIPASLGSR	LIVPC	3		892.8447767	2675.51093	0.002519933	1	N	239	265
P27931	Infl	RMWVK	GNILWILPAVQQDSGTYICTFR	NASHC	2	C19:+57.021	1276.652232	2551.288864	0.000451244	9	N	101	123
P28293	Infl	VSQSR	GTNVLQEVQLR	VQMDQ	2		628.8520228	1255.688446	0.000451244	5	N	154	165
P28293	Infl	MCANR	FQFYNSQTQICVGNPR	ERKSA	2	C11:+57.021	979.9628071	1957.910014	0.000451244	30	N	175	191
P28293	Infl	PRERK	SAFRGDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C13:+57.021	1208.921876	3623.742229	0.000451244	11	N	194	230
P28293	Infl	PYMAF	LLIQSPEGLSACGGFLVR	EDFVL	2	C12:+57.021	959.0170511	1916.018502	0.000451244	21	N	37	55
P28293	Infl	HSYPY	MAFLLIQSPEGLSACGGFLVR	EDFVL	2	C15:+57.021	1133.590058	2265.164516	0.000451244	8	N	34	55
P28293	Infl	EVQLR	VQMDQMCANRFQFYNSQTQICVGNPR	ERKSA	3	M3:+15.995,M6:+15.995,C7:+57.021,C21:+57.021	1075.476079	3223.404836	0.002019181	1	N	165	191
P28293	Infl	QASKK	LQPGDLCTVAGWGR	VSQSR	2	C7:+57.021	765.3803902	1528.74518	0.000622848	5	N	135	149
P28293	Infl	PQASK	KLQPGDLCTVAGWGR	VSQSR	3	C8:+57.021	553.2878479	1656.840144	0.000451244	9	N	134	149
P28293	Infl	KSAFR	GDSGGPLVCSNVAQGIVSY	GSNNG	2	C9:+57.021	940.4466555	1878.877711	0.000451244	11	N	198	217
P28293	Infl	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C9:+57.021	1055.175654	3162.503561	0.000622848	2	N	198	230
P28293	Infl	PRERK	SAFRGDSGGPLVCSNVAQGIVSYGSNNGNPPAVF	TKIQS	3	C13:+57.021	1132.540996	3394.599587	0.000451244	7	N	194	228
P28293	Infl	SKKLQ	PGDLCTVAGWGR	VSQSR	2	C5:+57.021	644.8090694	1287.602539	0.001463592	1	N	137	149
P28293	Infl	MAFLL	IQSPEGLSACGGFLVR	EDFVL	2	C10:+57.021	845.932987	1689.850374	0.000823681	5	N	39	55
P28293	Infl	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVF	TKIQS	2	C9:+57.021	1467.68826	2933.360919	0.000451244	3	N	198	228
P28293	Infl	SYPYM	AFLLIQSPEGLSACGGFLVR	EDFVL	2	C14:+57.021	1068.069815	2134.12403	0.000451244	3	N	35	55
P28293	Infl	RFQFY	NSQTQICVGNPR	ERKSA	2	C7:+57.021	687.33344	1372.65128	0.000622848	2	N	179	191
P28352	Infl	WIKKK	GLDWVKEEAPDILCLQETK	CSENK	2	C14:+57.021	1122.564759	2243.113919	0.000451244	8	N	78	97
P28352	Infl	KKTEK	EAAGEGPVLYEDPPDQK	TSPSG	2		907.9263102	1813.83702	0.000451244	8	N	34	51
P28474	Infl	APLDK	VCLLGCGISTGYGAAVNTAK	VEPGS	2	C2:+57.021,C6:+57.021	1006.500677	2010.985753	0.000451244	4	N	168	188
P28474	Infl	DKFAK	AKEFGASECISPQDFSK	SIQEV	2	C9:+57.021	950.941206	1899.866812	0.000823681	2	N	231	248
P28650	Infl	RTGLR	ICDLLSDFDEFSAR	FKNLA	2	C2:+57.021	844.3855352	1686.75547	0.000451244	2	N	181	195

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P28650	Infl	AYTTR	VGIGAFPTEQINEIGDLLQNR	GHEWG	2		1142.600754	2283.185907	0.000451244	5	N	304	325
P28650	Infl	EGKGK	VVDLLATDADIVSR	CQGGN	2		743.9097348	1485.80387	0.000622848	2	N	48	62
P28656	Infl	ALQER	LDGLVDTPTGYIESLPK	VVKRR	2		909.4807213	1816.945843	0.000451244	14	N	55	72
P28656	Infl	LFDKR	FEIINAIYEPTEEECEWKPDEEDEVSEELKEK	AKIED	3	C15:+57.021	1319.598347	3955.771642	0.000451244	19	N	117	149
P28656	Infl	KEDPK	GIPEFWLTVFK	NVDLL	2		668.8691529	1335.722706	0.001162105	2	N	165	176
P28656	Infl	QPMSF	VLEFHFEPNDYFTNEVLTK	TYRMR	3		781.3833536	2341.126661	0.000451244	12	N	212	231
P28658	Infl	FRCLR	NACIECSVNQNSIR	NLDTI	2	C3:+57.021,C6:+57.021	832.8776544	1663.739709	0.000451244	10	N	89	103
P28658	Infl	EAHQK	HPASEWPFLIISDHFLK	SPELV	3		679.6917932	2036.051979	0.001591523	5	N	209	226
P28658	Infl	VYAVR	NLTEDNSQNQDVIAK	MEEQG	2		844.9084518	1687.801304	0.000622848	3	N	423	438
P28665	Infl	QSGRK	NLFDELVLDKDLFQCVSFIIPR	LSSSD	3	C15:+57.021	894.4721316	2680.392995	0.002663018	1	N	71	93
P28667	Infl	DLTPK	GEGESPPVNGTDEAAGATGDAIEPAPPSQEAEAKGEVAPK	ETPKK	3		1277.600004	3829.776613	0.000622848	19	N	43	83
P28667	Infl	SAASK	EGDTEEEAGPQAAEPSTPSGPESGPTPASAEQNE	-	3		1118.47363	3352.397489	0.000622848	4	N	166	200
P28667	Infl	DLTPK	GEGESPPVNGTDEAAGATGDAIEPAPPSQEAEAK	GEVAP	3		1083.827567	3248.459301	0.000823681	1	N	43	77
P28798	Infl	CPFAK	AVCCEDHIHCCPAGFQCHTEK	GTCEM	3	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021	872.6814401	2615.02092	0.000451244	24	N	309	330
P28798	Infl	CPFAK	AVCCEDHIHCCPAGFQCHTEKGTCEM	GILQV	4	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021,C24:+57.021,M26:+15.995	803.3073819	3209.198327	0.001654178	2	N	309	335
P28798	Infl	GYPVK	EVKCDMEVSCPEGYTCCR	LNTGA	2	C4:+57.021,M6:+15.995,C10:+57.021,C16:+57.021,C17:+57.021	1148.443638	2294.871677	0.000451244	3	N	278	296
P28798	Infl	LQIGD	IGCDQHTSCPVGQTCCPSLK	GSWAC	2	C3:+57.021,C9:+57.021,C15:+57.021,C16:+57.021	1152.994644	2303.973688	0.000451244	8	N	439	459
P28798	Infl	CPDAK	TQCPDDSTCCELPTGK	YGCCP	2	C3:+57.021,C9:+57.021,C10:+57.021	934.8764285	1867.737257	0.000451244	62	N	211	227
P28798	Infl	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	C1:+57.021,C7:+57.021,C13:+57.021,C14:+57.021	962.3431533	1922.670707	0.002212458	1	N	281	296
P28798	Infl	PLQIG	DIGCDQHTSCPVGQTCCPSLK	GSWAC	2	C4:+57.021,C10:+57.021,C16:+57.021,C17:+57.021	1210.508115	2419.000631	0.000451244	8	N	438	459
P28798	Infl	CPSLK	GSWACCQLPHAVCCEDRQHCCPAGYTCNVK	ARTCE	3	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021,C20:+57.021,C21:+57.021,C27:+57.021	1227.830605	3680.468415	0.001162105	2	N	459	489
P28798	Infl	CPSLK	GSWACCQLPHAVCCEDR	QHCCP	2	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021	1053.423657	2104.831715	0.000451244	27	N	459	476
P28798	Infl	YTCCR	LNTGAWGCCPFAK	AVCCE	2	C8:+57.021,C9:+57.021	741.3369054	1480.658211	0.000451244	11	N	296	309
P28798	Infl	LPTGK	YGCCPMPNAICCSDHLHCCPQDTVCDLIQSK	CLSKN	3	C3:+57.021,C4:+57.021,M6:+15.995,C11:+57.021,C12:+57.021,C18:+57.021,C19:+57.021,C25:+57.021	1271.510349	3811.507648	0.000451244	11	N	227	258
P28798	Infl	NTCCK	LNSGDWGCCPIPEAVCCSDNQHCCPQGFTCLAQGYCQK	GDTMV	4	C8:+57.021,C9:+57.021,C16:+57.021,C17:+57.021,C23:+57.021,C24:+57.021,C30:+57.021,C36:+57.021	1134.453884	4533.784337	0.000451244	21	N	378	416
P28798	Infl	EKIPA	RQTTPLQIGDIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C13:+57.021,C19:+57.021,C25:+57.021,C26:+57.021	1138.860003	3413.55661	0.002145581	2	N	429	459
P28798	Infl	KIPAR	QTTPLQIGDIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C12:+57.021,C18:+57.021,C24:+57.021,C25:+57.021	1086.8263	3257.455499	0.000823681	5	N	430	459
P28798	Infl	QIGDI	GCDQHTSCPVGQTCCPSLK	GSWAC	3	C2:+57.021,C8:+57.021,C14:+57.021,C15:+57.021	731.3043412	2190.889624	0.000451244	8	N	440	459
P28798	Infl	IGDIG	CDQHTSCPVGQTCCPSLK	GSWAC	3	C1:+57.021,C7:+57.021,C13:+57.021,C14:+57.021	712.2971866	2133.86816	0.000451244	1	N	441	459
P28798	Infl	QTCCK	DSAGVWACCPYLK	GVCCR	2	C8:+57.021,C9:+57.021	763.8420206	1525.668441	0.000451244	8	N	531	544
P28798	Infl	CCEDR	VHCCPHGASCDLVHTR	CVSPT	4	C3:+57.021,C4:+57.021,C10:+57.021	477.2122619	1904.817848	0.001329271	2	N	160	176
P28867	Infl	APFLR	ISFNSYELGSLQVEDEASQPFCAVK	MKEAL	2	C22:+57.021	1409.66593	2817.316261	0.000451244	3	N	6	31
P28867	Infl	FELYR	ATFYAAEIICGLQFLHSK	GIIYR	3	C10:+57.021	690.356039	2068.044717	0.00307782	1	N	447	465
P28867	Infl	IHYIK	NHEFIATFFGQPTFCSVCK	EFVWG	3	C15:+57.021,C18:+57.021	764.0190553	2289.033766	0.000451244	7	N	157	176
P28867	Infl	HPFFK	TINWSLLEK	RKVEP	2		552.3089281	1102.602256	0.001162105	6	N	602	611
P28867	Infl	IVLMR	AAEDPVSEVTVGVSVLAER	CKKNN	2		964.5027164	1926.989833	0.000851441	2	N	75	94
P28867	Infl	RISFN	SYELGSLQVEDEASQPFCAVK	MKEAL	2	C18:+57.021	1179.052213	2356.088826	0.000451244	1	N	10	31
P29341	Infl	SGKSK	GFGFVSFER	HEDAQ	2		523.2592382	1044.502876	0.000451244	9	N	231	240
P29341	Infl	SIDNK	ALYDTFSAFGNILSCK	VVCDE	2	C15:+57.021	903.9404777	1805.865355	0.000451244	3	N	113	129
P29341	Infl	ENGSK	GYGFVHFETQEAAER	AIEKM	3		580.9379149	1739.790345	0.000451244	13	N	138	153
P29341	Infl	MLYEK	FSPAGPILSIR	VCRDM	2		579.3380199	1156.66044	0.000637154	2	N	30	41
P29341	Infl	MASVR	AVPNPVINPYQPAPPSGYF	MAAIP	2		1014.51543	2027.01526	0.001395409	2	N	390	409
P29341	Infl	PESLR	SKVDEAVAVLQAHQAK	EAAQK	3		565.3130933	1692.91588	0.000823681	1	N	604	620
P29351	Infl	RWFHR	DLSGPDAETLLK	GRGVP	2		629.8304217	1257.645243	0.000451244	2	N	7	19
P29351	Infl	EYKLR	TLQISPLDNGDLVR	EIWHY	2		770.9206338	1539.825668	0.001162105	9	N	393	407

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P29351	Infl	EDTAK	AGFWEEFESLQKQEVK	NLHQR	2		977.9814198	1953.94724	0.000451244	5	N	241	257
P29351	Infl	CEGGR	YTVGGSETFDSLTDLVEHFKK	TGIEE	3		791.725668	2372.153604	0.000870037	2	N	175	196
P29351	Infl	EDTAK	AGFWEEFESLQK	QEVKN	2		735.8491458	1469.682692	0.000451244	7	N	241	253
P29351	Infl	TFLVR	ESLSQPGDFVLSVLNDQPK	AGPGS	2		1037.029098	2072.042597	0.000451244	18	N	136	155
P29351	Infl	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSFLDQINQR	QESLP	3		1256.613414	3766.816843	0.000622848	5	N	407	439
P29351	Infl	VGTQR	VYGLYSVTNSR	EHDTA	2		629.8254737	1257.635347	0.000451244	5	N	372	383
P29351	Infl	VTHIR	IQNSGDFYDLYGGEKFATLTELVEYYTQQQGILQDR	DGTII	3		1401.678478	4202.012033	0.000823681	3	N	53	89
P29351	Infl	IIHLK	YPLNCSDPTSER	WYHGH	2	C5:+57.021	719.8172884	1437.618977	0.000451244	20	N	97	109
P29351	Infl	YGGEK	FATLTELVEYYTQQQGILQDR	DGTII	2		1258.637533	2515.259466	0.000451244	17	N	68	89
P29351	Infl	SISTK	GLDCDIDIQK	TIQMV	2	C4:+57.021	588.7821859	1175.548772	0.001654178	1	N	476	486
P29351	Infl	VTHIR	IQNSGDFYDLYGGEK	FATLT	2		853.3893635	1704.763127	0.000451244	8	N	53	68
P29351	Infl	PTSER	WYHGHISGGQAESLLQAK	GEPWT	2		991.4981027	1980.980605	0.000451244	3	N	109	127
P29351	Infl	YGGEK	FATLTELVEYYTQQQGILQDRDGTIIHLK	YPLNC	3		1131.92834	3392.761619	0.001352548	1	N	68	97
P29351	Infl	IQSQK	GQESEYGNITYPPAVR	SAHAK	2		890.9291872	1779.842774	0.000451244	31	N	530	546
P29351	Infl	QINQR	QESLPHAGPIIVHCSAGIGR	TGTII	2	C14:+57.021	1050.044663	2098.073726	0.000451244	3	N	439	459
P29351	Infl	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSF	LDQIN	2		1450.688089	2899.360577	0.000622848	2	N	407	432
P29351	Infl	ILQGR	DSNIPGSDYINANYVK	NQLLG	2		885.421195	1768.82679	0.001699387	1	N	292	308
P29416	Infl	FTDFK	QLESFYIQTLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		1252.289603	3753.845408	0.002374549	1	N	348	379
P29416	Infl	MAYNK	FNVFHWHLVDDSSFPYESFTFPELTR	KGSFN	3		1073.173845	3216.498134	0.000622848	2	N	197	223
P29416	Infl	LESFY	IQTLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		996.5066008	2986.496402	0.002981883	1	N	354	379
P29621	Infl	KLALK	NPDTNIVFSPLSISAALAIVSLGAK	GNTLE	2		1249.697394	2497.379187	0.000451244	2	N	65	90
P29621	Infl	SLYKK	LALKNPDTNIVFSPLSISAALAIVSLGAK	GNTLE	3		975.2342642	2922.679393	0.000451244	9	N	61	90
P29699	Infl	VEISR	AQNVPLPVSTLVEFVIAATDCTAK	EVTDP	2	C21:+57.021	1272.67283	2543.33006	0.000451244	14	N	187	211
P29699	Infl	GLGFR	ELACDDPEAEQVALLAVDYLNNHLLQGFK	QVLNQ	3	C4:+57.021	1095.875093	3284.601878	0.000451244	18	N	28	57
P29699	Infl	YHDLR	HAFSPVASVESASGETLHSPK	VGQPG	3		713.3557979	2137.043994	0.000823681	2	N	301	322
P29758	Infl	PLGCR	IAIAALEVLEEENLAENADK	MGAIL	2		1078.060596	2154.105591	0.000451244	13	N	331	351
P29788	Infl	PKLIQ	DVWGIEGPIDAAFTR	INCQG	2		823.9128088	1645.810018	0.000451244	4	N	196	211
P30355	Infl	-	MDQEAVGNVVLLALVTLISVVQNAFFAHKVEHESK	AHNGR	4		959.7663576	3835.03423	0.002453667	1	N	0	35
P30355	Infl	FVRQK	YFVGYLGER	TQSTP	2		552.2801706	1102.544741	0.002663018	1	N	96	105
P30355	Infl	-	MDQEAVGNVVLLALVTLISVVQNAFFAHK	VEHES	3		1042.906042	3125.694726	0.001264573	3	N	0	29
P30416	Infl	LFDQR	ELCFEVGEGESLDLPCGLEEAIQR	MEKGE	2	C3:+57.021,C16:+57.021	1375.636084	2749.256568	0.000451244	8	N	186	210
P30416	Infl	VATMK	VGEVCHITCKPEYAYGAAGSPPK	IPPNA	3	C5:+57.021,C9:+57.021	831.0632123	2490.166237	0.000451244	2	N	98	121
P30416	Infl	MIGDR	VFVHYTGWLLDGTK	FDSSL	3		545.9563583	1634.845675	0.000735798	4	N	52	66
P30681	Infl	RPKIK	IEHPGLSIGDTAK	KLGEM	3		446.5740253	1336.698676	0.000451244	18	N	114	127
P30681	Infl	ENRPK	IKIEHPGLSIGDTAK	KLGEM	2		789.9466516	1577.877703	0.000451244	38	N	112	127
P30681	Infl	TGSKK	KNEPEDEEEEEEEEEEDDEEEEEDEE	-	3		1133.728084	3398.160851	0.000451244	42	N	183	210
P31230	Infl	RLEQK	GAEADQIIEYLKQQVALLK	EKAIL	3		710.7322057	2129.173217	0.001329271	1	N	14	33
P31230	Infl	QVRVR	LSTPLQTNCTASESVVQSPSVATTASPATKEQIK	AGEEK	3	C9:+57.021	1177.933448	3530.776943	0.001943752	1	N	81	115
P31725	Infl	SQMER	SITTIIDTFHQYSRK	EGHPD	2		905.4788473	1808.942095	0.000451244	23	N	11	26
P31725	Infl	SQMER	SITTIIDTFHQYSR	KEGHP	2		841.4313657	1680.847131	0.000451244	538	N	11	25
P31725	Infl	MERSI	TTIIDTFHQYSR	KEGHP	2		741.3733194	1480.731039	0.000451244	42	N	13	25
P31725	Infl	ERSIT	TIIDTFHQYSR	KEGHP	2		690.8494801	1379.68336	0.000451244	14	N	14	25
P31725	Infl	SQMER	SITTIIDTFHQY	SRKEG	2		719.8647959	1437.713992	0.000451244	31	N	11	23
P31725	Infl	SQMER	SITTIIDTF	HQYSR	2		505.7743868	1009.533174	0.000622848	9	N	11	20
P31725	Infl	KKEFR	QMVEAQLATFMKK	EKRNE	2		762.8998023	1523.784005	0.000451244	3	N	39	52
P31725	Infl	MLMAK	LIFACHEKLHENNPR	GHGHS	3	C5:+57.021	626.6531898	1876.936169	0.000451244	7	N	86	101
P31725	Infl	MAKLI	FACHEKLHENNPR	GHGHS	3	C3:+57.021	551.2638137	1650.768041	0.000451244	6	N	88	101
P31725	Infl	SITTI	IDTFHQYSR	KEGHP	2		583.7836088	1165.551618	0.001763695	4	N	16	25
P31725	Infl	MERSI	TTIIDTFHQYSRK	EGHPD	2		805.420801	1608.826002	0.000451244	4	N	13	26
P31725	Infl	ERSIT	TIIDTFHQYSRK	EGHPD	2		754.8969617	1507.778323	0.000451244	3	N	14	26
P31725	Infl	RSITT	IIDTFHQYSR	KEGHP	2		640.3256409	1278.635682	0.000622848	12	N	15	25
P31725	Infl	KKEKR	NEALINDIMEDLDTNQDNQLSF	EECMM	2		1276.577013	2551.138425	0.000451244	9	N	55	77
P31725	Infl	KKEKR	NEALINDIMEDLDTNQDNQLSFEECMML	MAKLI	3	C25:+57.021	1115.814078	3344.418833	0.000823681	3	N	55	83
P31725	Infl	KKEKR	NEALINDIMEDLDTNQDNQLSFEECMM	LMAKL	3	C25:+57.021,M26:+15.995	1083.451056	3247.329769	0.002296037	1	N	55	82
P31725	Infl	KKEFR	QMVEAQLATFMK	KEKRN	2		698.8523208	1395.689042	0.000622848	1	N	39	51
P31725	Infl	QMERS	ITTIIDTFHQYSR	KEGHP	3		532.279501	1593.815103	0.000622848	5	N	12	25
P31750	Infl	GATMK	TFCGTPEYLAPEVLEDNDYGR	AVDWW	2	C3:+57.021	1223.547295	2445.07899	0.000451244	13	N	307	328
P31750	Infl	IMQHR	FFANIVWQDVYEK	KLSPP	2		829.9148201	1657.81404	0.001943752	1	N	406	419
P31786	Infl	YSHFK	QATVGDVNTDRPGLLDLK	GKAKW	2		956.5108758	1911.006152	0.000451244	13	N	33	51
P31786	Infl	YSHFK	QATVGDVNTDRPGLLDLKGK	AKWDS	2		1049.069089	2096.122578	0.000451244	7	N	33	53
P31938	Infl	EPPPK	LPSGVFSLEFQDFVNK	CLIKN	2		913.9703238	1825.925048	0.00091018	1	N	324	340
P31938	Infl	-MPK	KKPTPIQLNPAPDGSAVNGTSSAETNLEALQK	KLEEL	3		1092.907716	3275.699747	0.000451244	3	N	3	35
P32020	Infl	EEVMK	SKPVFDFLTILQCCPTSDGAAAAILSSEEFVQQYGLQSK	AVEIV	3	C13:+57.021,C14:+57.021	1436.039945	4305.096434	0.000451244	24	N	211	250
P32020	Infl	AQIPY	SAVEQACVGYVYGDSTSGQR	AIYHS	2	C7:+57.021	1067.479215	2132.942831	0.000451244	8	N	54	74
P32020	Infl	GPGGK	EATWVVDVK	NGKGS	2		523.7800035	1045.544407	0.002663018	1	N	470	479

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P32067	Infl	NRLNR	LTTDFNVIVQALSK	SKAKL	2		774.9357526	1547.855905	0.000451244	6	N	60	74
P34022	Infl	MAAAK	DSHEDHDTSTENADESNHDPQFEPIVSLPEQEIK	TLEED	3		1297.235614	3888.683441	0.000451244	23	N	5	39
P34022	Infl	AGSDR	AWVWNTHADFADECPKPELLAIR	FLNAE	2	C14:+57.021	1370.17132	2738.32704	0.000451244	2	N	118	141
P34022	Infl	AKLFR	FASENDLPEWKER	GTGDV	2		810.886791	1619.757982	0.002981883	2	N	57	70
P34022	Infl	AKLFR	FASENDLPEWK	ERGTG	2		668.3149388	1334.614278	0.002453667	1	N	57	68
P34022	Infl	EQEIK	TLEEDEEELFK	MRAKL	2		691.3226265	1380.629653	0.000451244	1	N	39	50
P34884	Infl	TNVPR	ASVPEGFLSELTQQLAQATGK	PAQYI	2		1088.068755	2174.12191	0.000451244	11	N	12	33
P34884	Infl	TNVPR	ASVPEGFLSELTQQLAQATGKPAQY	IAVHV	2		1317.674647	2633.333694	0.000451244	6	N	12	37
P35123	Infl	TQVGR	FAPQFSGYQQQDSQELLAFILDGLHEDLNRVK	KKPYL	4		927.4684807	3705.842723	0.000451244	2	N	381	413
P35123	Infl	TQVGR	FAPQFSGYQQQDSQELLAFILDGLHEDLNR	VKKKP	3		1160.567582	3478.679346	0.000451244	13	N	381	411
P35123	Infl	DSETR	SLYFDEQESEACEK	HLSMS	2	C12:+57.021	867.86209	1733.70858	0.000451244	8	N	746	760
P35123	Infl	EQLSK	LDNTIQDAGLYQGQVLVIEPQNEDGTWPR	QSLQS	3		1090.541144	3268.600033	0.000870037	2	N	197	226
P35123	Infl	PRHKR	LFTFSLVNSCGTADINSLATDGK	LLKLN	2	C10:+57.021	1216.094412	2430.173225	0.000622848	4	N	704	727
P35173	Infl	EAVEY	KSQVVAGQNLFIK	IDVGN	2		716.4200727	1430.824545	0.000451244	3	N	49	62
P35173	Infl	MIADK	VRPLLEEQTNEKYEK	FEAVE	2		938.4946944	1874.973789	0.000823681	4	N	28	43
P35173	Infl	MKVFR	GLSGEDDLKLK	GYQTN	2		587.819857	1173.624114	0.00091018	1	N	77	88
P35174-2	Infl	AIEYK	VQVVQGLNYFIK	MNVGR	2		704.4038913	1406.792183	0.000451244	53	N	50	62
P35174-2	Infl	-MTEY	TIEIIGGLSEARPATSEIQEIADK	VRPLL	2		1271.17448	2540.33336	0.000451244	32	N	4	28
P35174-2	Infl	MNVGR	GCYLHINVLSGISSENDLELTGYQTNK	AKNDE	3	C2:+57.021	1009.1576	3024.4494	0.000451244	1461	N	67	94
P35174-2	Infl	TIEII	GGLSEARPATSEIQEIADKVR	PLLEE	2		1114.08801	2226.160421	0.001352548	3	N	9	30
P35174-2	Infl	TIEII	GGLSEARPATSEIQEIADK	VRPLL	2		986.5032477	1970.990895	0.000451244	16	N	9	28
P35174-2	Infl	KAIEY	KVQVVQGLNYFIK	MNVGR	2		768.4513728	1534.887146	0.000451244	24	N	49	62
P35174-2	Infl	GCYLH	INVLSGISSENDLELTGYQTNK	AKNDE	2		1198.103523	2394.191446	0.000451244	29	N	72	94
P35174-2	Infl	-MTEY	TIEIIGGLSEARPATSEIQEIADKVRPLLEEK	TNEKY	3		1169.309109	3504.903926	0.000451244	14	N	4	36
P35174-2	Infl	LSEAR	PATSEIQEIADKVRPLLEEK	TNEKY	4		567.313206	2265.221624	0.000451244	4	N	16	36
P35174-2	Infl	IEIIG	GLSEARPATSEIQEIADK	VRPLL	2		957.9925159	1913.969432	0.002296037	2	N	10	28
P35174-2	Infl	YQTNK	AKNDELTYF	-	2		550.7670931	1099.518586	0.00307782	1	N	94	103
P35174-2	Infl	YLHIN	VLSGISSENDLELTGYQTNK	AKNDE	2		1084.540027	2167.064455	0.000451244	2	N	74	94
P35276	Infl	SFLFR	YADDSFTPAFVSTVGIDFK	VKTVY	2		1040.499642	2078.983685	0.000451244	9	N	41	60
P35278	Infl	PMYYR	GAQAAIVVYDITNTDTFAR	AKNWV	2		1013.516158	2025.016716	0.000451244	17	N	92	111
P35282	Infl	AKQNK	GIEELFLDLCKR	MIETA	3	C10:+57.021	498.2661612	1491.775084	0.000735798	4	N	165	177
P35282	Infl	PIYYR	DSNGAILVYDVTDEDSFQK	VKNWV	2		1058.490003	2114.964406	0.000451244	8	N	88	107
P35441	Infl	GVQYK	NNEEWTVDSCTECHCQNSVTICKK	VSCPI	3	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	1000.417641	2998.229522	0.000451244	8	N	326	350
P35441	Infl	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	2	C1:+57.021,C10:+57.021,C13:+57.021	974.9265901	1947.83758	0.000451244	1	N	607	623
P35441	Infl	LQNVR	FVFGTTPEDILR	NKGCS	2		697.8698813	1393.724163	0.000851441	4	N	216	228
P35441	Infl	VSNGK	AGTLDLSLSLPGKQQVVSVEEALLATGQWK	SITLF	3		1046.906876	3137.697228	0.000451244	5	N	124	154
P35441	Infl	VARLR	VAKGDVNDNFQGVLQNVR	FVFGT	2		987.0141169	1972.012634	0.000451244	5	N	198	216
P35441	Infl	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDF	SGTFF	2	C8:+57.021	1336.613166	2671.210733	0.000451244	5	N	984	1008
P35441	Infl	QRRSR	LCNNPTPQFGGKDCVGDVTENQVCNK	QDCPI	3	C2:+57.021,C14:+57.021,C24:+57.021	984.4409282	2950.299384	0.000451244	5	N	517	543
P35441	Infl	SPAFR	IENANLIPAVPDDKFQDLLDAVWADK	GFIFL	3		970.8348289	2909.481087	0.000451244	13	N	60	86
P35441	Infl	GIQCK	DVDECKEVPDACFNHNGEHR	CKNTD	3	C5:+57.021,C12:+57.021	810.0064257	2426.995877	0.001162105	3	N	587	607
P35441	Infl	GEHLR	NALWHTGNTPGQVR	TLWHD	2		775.8952847	1549.774969	0.000451244	6	N	1077	1091
P35441	Infl	ILNER	DNCQYVYNVDQR	DTDMD	2	C3:+57.021	787.3389193	1572.662239	0.001871652	1	N	810	822
P35441	Infl	EHRCK	NTDPGYNCLPCPPR	FTGSQ	2	C8:+57.021,C11:+57.021	830.8640157	1659.712431	0.000451244	9	N	609	623
P35441	Infl	GVQYK	NNEEWTVDSCTECHCQNSVTICK	KVSCP	3	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	957.7193195	2870.134558	0.001162105	1	N	326	349
P35441	Infl	LKGLR	TIVTTLQDSIR	KVTEE	2		623.8542312	1245.692862	0.000451244	1	N	288	299
P35441	Infl	SLPGK	QQVVSVEEALLATGQWK	SITLF	2		943.5050621	1884.994524	0.000451244	4	N	137	154
P35441	Infl	YIGHK	TKDLQAICGLSCDELSSMVLELK	GLRTI	3	C8:+57.021,C12:+57.021	870.7658446	2609.274134	0.001162105	2	N	262	285
P35441	Infl	HMCGS	NRIPESGGDNGVFDIFELIGGAR	RGPGR	2		1217.112017	2432.208434	0.000451244	3	N	18	41
P35441	Infl	VVMWK	QVTQSYWDTNPTR	AQGYS	2		798.3765904	1594.737581	0.000451244	4	N	1041	1054
P35461	Infl	RSKVK	SNLCLPICPTTLDNTEITGNAVNVK	TYCCK	2	C4:+57.021,C8:+57.021	1372.683369	2743.351138	0.000451244	16	N	47	72
P35486	Infl	VEVRK	EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR	GANQW	3		1278.267526	3831.779179	0.000451244	14	N	344	378
P35505	Infl	NPKPR	IGVAIGDQILDLSVIK	HLFTG	2		827.4934347	1652.971269	0.000451244	9	N	31	47
P35505	Infl	DWSAR	DIQQWEYVPLGPFLGK	SFGTT	2		945.493966	1888.972332	0.000451244	15	N	237	253
P35505	Infl	QGQTR	TFLLDGDEVIITGHCQGDGYR	VGFGQ	2	C15:+57.021	1183.557997	2365.100394	0.001654178	2	N	381	402
P35505	Infl	WKEAR	ASLQNLLSASQAR	LRDDK	2		679.8734866	1357.731373	0.001591523	1	N	82	95
P35550	Infl	PFRSK	LAAAILGGVDQIHIKPGAK	VLYLG	3		624.7075547	1871.099264	0.002663018	1	N	149	168
P35550	Infl	EPYER	DHAVVVGVYRPPPK	VKN-	3		511.9565811	1532.846343	0.001264573	3	N	310	324
P35550	Infl	KPGAK	VLYLGAASGTTVSHVSDIVGPDGLVY	AVEFS	2		1295.674116	2589.332631	0.002212458	3	N	168	194
P35550	Infl	VISIK	ANCIDSTASAEAVFASEVK	KMQQE	2	C3:+57.021	985.4625026	1968.909405	0.000451244	2	N	271	290
P35564	Infl	IWKPR	KIPNPDFFEDLEPFK	MTPFS	2		918.4648742	1834.914148	0.000451244	1	N	401	416

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P35564	Infl	AISAK	LNKPFLFDTKPLIVQYEVNFQNGIECGGAYVK	LLSKT	3	C26:+57.021	1234.639759	3700.895876	0.000451244	12	N	135	167
P35564	Infl	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSKSK	SDAST	3		1056.792411	3167.353833	0.000451244	6	N	20	48
P35564	Infl	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSK	SKSDA	3		985.0834139	2952.226842	0.000451244	16	N	20	46
P35564	Infl	KLLSK	TAELSLDQFHDKTPY	TIMFG	3		588.9533421	1763.836626	0.001591523	1	N	171	186
P35564	Infl	KVTYK	APVPTGEVYFADSFDRGSLSGWILSK	AKKDD	3		933.804981	2798.391543	0.000451244	3	N	62	88
P35564	Infl	DSFDR	GSLSGWILSK	AKKDD	2		524.2958207	1046.576041	0.000662267	5	N	78	88
P35564	Infl	KTHLY	TLILNPDNSFEILVDQSVVNSGNLLNDMTPPVNPSR	EIEDP	3		1308.333877	3921.978232	0.00091018	4	N	239	275
P35564	Infl	VNPSR	EIEDPEDRKPEDWDERPK	IADPD	3		761.6895054	2282.045116	0.000823681	5	N	275	293
P35700	Infl	GISFR	GLFIIDDKGILR	QITIN	3		453.9385275	1358.792183	0.000622848	5	N	128	140
P35700	Infl	DEIIR	LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVNK	SKEYF	3	C15:+57.021	1190.600074	3568.776823	0.001463592	2	N	158	190
P35700	Infl	QFTDK	HGEVCPAGWKPGSDTIKPDVNK	SKEYF	3	C5:+57.021	798.0623544	2391.163663	0.000662267	3	N	168	190
P35700	Infl	KGILR	QITINDLPVGR	SVDEI	2		613.349116	1224.682632	0.002374549	1	N	140	151
P35700	Infl	DEFKK	LNCQVIGASVDSHFCHLAWINTPK	KQGGL	4	C3:+57.021,C15:+57.021	692.5918241	2766.336097	0.000451244	6	N	68	92
P35700	Infl	YVVFF	FYPLDFTFVCPTEIIAFSDR	ADEFK	2	C10:+57.021	1219.590777	2437.165955	0.000451244	12	N	42	62
P35831	Infl	SVVDR	TSKPQELSAGALKVDDVSQNSCADCSAAHSHR	AAESS	4	C22:+57.021,C25:+57.021	857.3997751	3425.567901	0.002374549	1	N	473	505
P35831	Infl	VTRNK	TSISTASATVSPASSAESACTR	RVLPM	2	C20:+57.021	1071.502887	2140.990175	0.000451244	4	N	621	643
P35831	Infl	KKCER	YWPLYGEDPITFAPFK	ISCEN	2		972.483067	1942.950534	0.001162105	1	N	145	161
P35979	Infl	SGTIK	EILGTAQSVGCNVDGR	HPHDI	2	C11:+57.021	838.4073333	1674.799067	0.000451244	42	N	130	146
P35979	Infl	SGTIK	EILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS	-	3	C11:+57.021,C32:+57.021	1235.240903	3702.699309	0.000622848	3	N	130	165
P35979	Infl	TIQNR	QAQIEVVPSASALIIK	ALKEP	2		833.9910592	1665.966518	0.000451244	3	N	67	83
P35979	Infl	RSLAR	ELSGTIKEILGTAQSVGCNVDGR	HPHDI	2	C18:+57.021	1202.610761	2403.205922	0.000451244	5	N	123	146
P35979	Infl	VVYLR	CTGGEVGATSALAPK	IGPLG	2	C1:+57.021	709.8511312	1417.686662	0.000451244	4	N	16	31
P35979	Infl	NVDGR	HPHDIIDDINSGAVECPAS	-	2	C16:+57.021	1023.963201	2045.910802	0.000622848	12	N	146	165
P36371	Infl	VRNPR	VLILDEATSALDAQCEQALQNWR	SQGDR	2	C15:+57.021	1322.6557	2643.2958	0.000451244	10	N	625	648
P36371	Infl	NGSGK	STVAALLQNLYQPTGGQLLLDGEPLTEYDHHYLHR	QVVLV	4		991.5068659	3961.996264	0.000823681	1	N	508	543
P37040	Infl	TNPPR	TNVLYELAQYASEPSEQEHLHK	MASSS	3		862.7543978	2585.239793	0.000451244	6	N	382	404
P37040	Infl	LGAQR	IFELGLGLDDDGNLEEDFITWR	EQFWP	2		1227.577141	2453.138682	0.000451244	11	N	199	220
P37040	Infl	EHLWK	LIHEGGAHIYVCGDAR	NMAKD	4	C12:+57.021	442.7207427	1766.851771	0.001229886	2	N	618	634
P37913	Infl	RPYVR	IDGAVAPDHWLDPSIVWEVK	CADLS	3		749.7201886	2246.137166	0.000851441	2	N	823	843
P37913	Infl	LKLKK	DYLDGVGDTLDLVVIGAYLGR	GKRAG	2		1112.578955	2223.142311	0.000451244	12	N	745	766
P37913	Infl	SGRLR	LGLAEQSVLAALAQAVSLTPPGQEFPTVVVDAGK	GKTAE	3		1126.284123	3375.82897	0.000451244	2	N	449	483
P37913	Infl	SLDTK	DTEQIAEFLEQSVK	DSCEG	2		818.9073891	1635.799178	0.002019181	2	N	700	714
P38647	Infl	IPTKK	SQVFSTAADGQTQVEIK	VCQGE	2		904.955402	1807.895204	0.000451244	16	N	468	485
P38647	Infl	MKLTR	AQFEGIVTDLIKR	TIAPC	3		497.2844749	1488.830025	0.000451244	15	N	348	361
P38647	Infl	VFEVK	STNGDTFLGGEDFDQALLR	HIVKE	2		1028.485055	2054.95451	0.000451244	17	N	265	284
P38647	Infl	AEGAR	TTPSVVAFTADGER	LVGMP	2		725.8627845	1449.709969	0.000451244	6	N	85	99
P38647	Infl	MPAKR	QAVTNPNNTFYATK	RLIGR	2		784.8893337	1567.763067	0.000823681	1	N	107	121
P38647	Infl	DVTPL	SLGIETLGGVFTK	LINRN	2		661.3722568	1320.728914	0.002663018	1	N	443	456
P39054	Infl	QSAGK	SSVLENFVGRDFLPR	GSGIV	3		579.3095717	1734.905315	0.000451244	3	N	44	59
P39054	Infl	EPCLK	CVDLVIQELISTVR	QCTSK	2	C1:+39.994	814.4398881	1626.864176	0.000451244	4	N	426	440
P39054	Infl	PLVNK	LQDAFSSIGQSCHLDLPQIAVVGGQSAGK	SSVLE	3	C12:+57.021	995.1699515	2982.486454	0.000451244	22	N	15	44
P39054	Infl	DFEKR	IEGSGDQVDTLELSGGAR	INRIF	2		902.4401161	1802.864632	0.00091018	2	N	343	361
P39054	Infl	YKDLR	QIELACDSQEDVDSWK	ASFLR	2	C6:+57.021	961.9257529	1921.835906	0.000451244	17	N	601	617
P39054	Infl	PGITK	VPVGDQPPDIEYQIK	DMILQ	2		849.4413991	1696.867198	0.001329271	8	N	142	157
P39054	Infl	PINLR	VYSPHVLNLTLIDLPGITK	VPVGD	3		698.4055414	2092.193224	0.000662267	4	N	123	142
P39054	Infl	YHALK	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	RPVSS	3		1376.689377	4127.04473	0.001591523	1	N	730	769
P39054	Infl	IHGVR	TGLFTPDLAFEAIVKK	QVVKL	3		583.9982231	1748.971269	0.000451244	3	N	399	415
P39654	Infl	WGNWK	DGTILNVAATSISDLPVDQR	FREDK	2		1043.04528	2084.07496	0.000451244	10	N	146	166
P39654	Infl	EIRNK	SLDIPYEYLRPSLVENSVAI	-	2		1139.602431	2277.189261	0.000451244	5	N	643	663
P39654	Infl	WISVK	GPGDQGSEYTFPCYR	WVQGT	2	C13:+57.021	867.3651341	1732.714668	0.000451244	6	N	84	99
P39654	Infl	LDLLK	QAGAFLTYSSLCPPDDLAER	GLLDI	2	C12:+57.021	1106.023259	2210.030918	0.000451244	8	N	431	451
P39654	Infl	VYRIR	VSTGDSVYAGSNNEVYLWLIGQHGEASLGK	LFRPC	3		1051.183068	3150.525805	0.000451244	4	N	7	37
P39654	Infl	FPCYR	WVQGTSILNLPEGTGCTVVEDSQGLFR	NHREE	3	C16:+57.021	988.4908021	2962.449006	0.000451244	5	N	99	126
P39654	Infl	LVMLK	LQPDGQLLPIAIQLELPK	TGSTP	2		993.5858552	1985.15611	0.000451244	2	N	305	323
P39654	Infl	DLYYK	TDQAVQDDYELQSWCQEITEIGLQGAQDR	GFPTS	3	C15:+57.021	1132.848043	3395.520728	0.000451244	6	N	485	514
P39654	Infl	EAEFK	VDVSEYLGPLLFVR	VQKWH	2		803.9461203	1605.876641	0.001591523	2	N	50	64
P39654	Infl	EELKK	GTLFEADFFLLDGIK	ANVIL	2		843.4434105	1684.871221	0.000451244	3	N	271	286
P39654	Infl	DLAER	GLLDIDTCFYAK	DALQL	2	C8:+57.021	708.3476931	1414.679786	0.000451244	3	N	451	463
P39654	Infl	KCWVR	SSDLQLHELQAHLLR	GHLVA	4		440.7422195	1758.937678	0.000451244	1	N	349	364
P39655	Infl	DPRTK	AVLSQFQADLDNLEKEITAR	NEQLD	2		1131.092761	2260.169923	0.000451244	5	N	621	641
P39655	Infl	FPCYR	WVQGEGILSLPEGTAR	LAGDN	2		856.9524653	1711.889331	0.000451244	4	N	98	114
P39655	Infl	ALYAR	DALQLWEVTAR	YVKGM	2		651.3465733	1300.677547	0.001264573	2	N	462	473
P39655	Infl	EKELK	NGSLFEADFILLDGIPANVIR	GEPQY	2		1137.61059	2273.20558	0.000451244	5	N	269	290
P39655	Infl	LRPAR	GKEEEFDFDVPEDLGPLQFVK	LHKQH	2		1219.59226	2437.16892	0.000451244	9	N	43	64
P39655	Infl	YTLLR	SWNHLEDFDQIFWGQK	SALAE	2		1025.476836	2048.938072	0.002296037	2	N	195	211

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P40124	Infl	AYLSK	NSLDCEIVSAK	SSEMN	2	C5:+57.021	618.3007428	1234.585886	0.000451244	23	N	421	432
P40124	Infl	DSASR	SALFAQINQGESITHALK	HVSDD	2		964.5159611	1927.016322	0.000451244	19	N	253	271
P40124	Infl	GKKWR	VENQENVSNLVIDDTELK	QVAYI	2		1030.013645	2058.011691	0.000451244	74	N	329	347
P40124	Infl	GKKWR	VENQENVSNLVIDDTELKQVAY	IYKCV	2		1260.627362	2519.239125	0.000451244	7	N	329	351
P40124	Infl	GKKWR	VENQENVSNLVIDDTELKQVAYIYK	CVNTT	3		975.5016269	2923.481481	0.000451244	5	N	329	354
P40124	Infl	YVQAF	DSLLANPVAEYLK	MSKEI	2		716.888271	1431.760942	0.000451244	12	N	46	59
P40124	Infl	LGLVF	DDVVGIVEIINSR	DVKVQ	2		714.8888023	1427.762005	0.000451244	13	N	381	394
P40124	Infl	GAVPY	VQAFDSLLANPVAEYLK	MSKEI	2		939.5045308	1876.993462	0.000451244	26	N	42	59
P40124	Infl	WVRAY	LSIWTELQAYIK	EFHTT	2		732.9090065	1463.802413	0.000451244	14	N	185	197
P40124	Infl	NRGSK	FFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	3		1028.894353	3083.65966	0.000451244	16	N	125	154
P40124	Infl	DSPSK	GAVPYVQAFDSLLANPVAEYLK	MSKEI	2		1183.126073	2364.236546	0.000451244	60	N	37	59
P40124	Infl	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITFR	EKNRG	3	C9:+57.021	1271.00717	3809.998109	0.000451244	6	N	83	118
P40124	Infl	PAGNK	LSDLLAPISEQIQEVITFR	EKNRG	2		1086.599691	2171.183782	0.000451244	36	N	99	118
P40124	Infl	DNCKK	LGLVFDDVVGIVEIINSR	DVKVQ	2		979.5520123	1957.088425	0.000451244	58	N	376	394
P40124	Infl	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITF	REKNR	3	C9:+57.021	1218.973466	3653.896998	0.000451244	5	N	83	117
P40124	Infl	IVSAK	SSEMNVLIPTEGGDFNEFPVPEQFK	TLWNG	2		1406.163255	2810.310911	0.000451244	3	N	432	457
P40124	Infl	VDNCK	KLGLVFDDVVGIVEIINSR	DVKVQ	3		696.0689293	2085.183388	0.000451244	15	N	375	394
P40124	Infl	PAGNK	LSDLLAPISEQIQEVITFREK	NRGSK	3		810.448246	2428.321338	0.002453667	1	N	99	120
P40124	Infl	RGSKF	FNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	2		1469.303423	2936.591246	0.0025889	1	N	126	154
P40124	Infl	PAGNK	LSDLLAPISEQIQEVITF	REKNR	2		1008.549135	2015.082671	0.000451244	27	N	99	117
P40124	Infl	VDWVR	AYLSIWTELQAYIK	EFHTT	2		849.9592277	1697.902855	0.000622848	1	N	183	197
P40124	Infl	LKLER	ALLATASQCQQPAGNK	LSDLL	2	C9:+57.021	829.4202437	1656.824887	0.000451244	43	N	83	99
P40124	Infl	KPATK	KEPALLELEGK	KWRVE	3		409.5717332	1225.6918	0.000622848	16	N	315	326
P40124	Infl	NRGSK	FFNHLSAVSESIQALGWVALAAK	PGPFV	2		1230.158239	2458.300877	0.000451244	3	N	125	148
P40124	Infl	QAYIK	EFHTTGLAWSK	TGPVA	2		638.8201913	1275.624783	0.000451244	5	N	197	208
P40124	Infl	LEGKK	WRVENQENVSNLVIDDTELK	QVAYI	3		801.0718383	2400.192115	0.000451244	8	N	327	347
P40124	Infl	AGNKL	SDLLAPISEQIQEVITFR	EKNRG	2		1030.057659	2058.099718	0.000451244	5	N	100	118
P40124	Infl	ERLER	AVGRLEAVSHTSDMHCGYGDSPSK	GAVPY	4	C16:+57.021	641.0435513	2560.143005	0.000451244	6	N	13	37
P40124	Infl	QVMGK	VPTISINKTDGCHAYLSK	NSLDC	2	C12:+57.021	1002.514873	2003.014145	0.000451244	5	N	403	421
P40124	Infl	LKLER	ALLATASQCQQPAGNKL	SDLLA	2	C9:+57.021	885.9622758	1769.908952	0.000451244	14	N	83	100
P40124	Infl	GKKWR	VENQENVSNLVIDDTELKQVAYIY	KCVNT	2		1398.701059	2795.386517	0.000451244	4	N	329	353
P40124	Infl	REKNR	GSKFFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	4		839.9598289	3355.808116	0.001162105	2	N	122	154
P40124	Infl	DNCKK	LGLVFDDVVGIVEIINSRDVK	VQVMG	3		767.4340483	2299.278745	0.001162105	1	N	376	397
P40124	Infl	GDVQK	HAEMVHTGLKLER	ALLAT	3		507.6054429	1519.792929	0.001871652	2	N	70	83
P40124	Infl	PATKK	EPALLELEGK	KWRVE	2		549.8062183	1097.596837	0.001591523	3	N	316	326
P40124	Infl	NVLIP	TEGGDFNEFPVPEQFK	TLWNG	2		920.9235705	1839.831541	0.00091018	1	N	441	457
P40142	Infl	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	2		1097.074706	2192.133812	0.000451244	5	N	186	205
P40142	Infl	FDINR	LGQSDPAPLQHQVDIYQK	RCEAF	2		1019.02415	2036.032701	0.000451244	37	N	186	204
P40142	Infl	ICFIR	TSRPENAIIYSNNEDFQVGQAK	VVLKS	2		1241.104389	2480.193177	0.000451244	35	N	471	493
P40142	Infl	DIYQK	RCEAFGWHTIIVDGHSVEELCK	AFGQA	3	C2:+57.021,C21:+57.021	881.7531493	2642.236048	0.000451244	7	N	204	226
P40142	Infl	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	3	C1:+39.994,C20:+57.021	824.043779	2469.107937	0.000451244	5	N	205	226
P40142	Infl	QSKKK	ILATPPQEDAPSVDIANIR	MPTPP	2		1010.539633	2019.063667	0.000451244	86	N	283	302
P40142	Infl	ARATK	GRILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	3		1134.583232	3400.726296	0.000451244	3	N	553	586
P40142	Infl	GCATR	DRTVPFCSTFAAFFTR	AFDQI	3	C7:+57.021	641.6458123	1921.914037	0.000451244	8	N	379	395
P40142	Infl	EAMAF	AGIYKLDNLVAIFDINR	LGQSD	2		968.0390721	1934.062544	0.000451244	10	N	169	186
P40142	Infl	RDRTV	PFCSTFAAFFTR	AFDQI	2	C3:+57.021	726.342745	1450.66989	0.000451244	19	N	383	395
P40142	Infl	ATRDR	TVPFCSTFAAFFTR	AFDQI	3	C5:+57.021	551.2697942	1650.785983	0.000451244	15	N	381	395
P40142	Infl	APILY	AVWAEAGFLPEAELLNLR	KISSD	2		1000.036529	1998.057459	0.000451244	30	N	83	101
P40142	Infl	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	3		983.8715487	2948.591246	0.000451244	6	N	75	102
P40142	Infl	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	2		1005.00457	2007.993539	0.000451244	7	N	264	281
P40142	Infl	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	2		1411.255941	2820.496283	0.000823681	1	N	75	101
P40142	Infl	AELLK	MFGIDKDAIVQAVK	GLVTK	2		767.9190488	1533.822498	0.000451244	4	N	603	617
P40142	Infl	AGIYK	LDNLVAIFDINR	LGQSD	2		701.8886053	1401.761611	0.000451244	40	N	174	186
P40142	Infl	ATKGR	ILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	3		1063.542374	3187.603721	0.000451244	78	N	555	586
P40142	Infl	APILY	AVWAEAGFLPEAELLNLRK	ISSDL	2		1064.084011	2126.152422	0.000451244	7	N	83	102
P40142	Infl	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	2		988.5341539	1975.052708	0.000622848	3	N	246	264
P40142	Infl	KVVLK	SKDDQVTVIGAGVTLHEALAAAESLK	KDKIS	3		875.1366193	2622.386458	0.000622848	2	N	497	523
P40142	Infl	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021	1266.596797	2531.177994	0.000451244	2	N	114	140
P40142	Infl	KKILA	TPPQEDAPSVDIANIR	MPTPP	2		861.9370122	1721.858424	0.001162105	1	N	286	302
P40142	Infl	KISIR	VLDPFTIKPLDR	KLILD	2		707.4091736	1412.802747	0.001871652	1	N	530	542
P40142	Infl	VQSKK	KILATPPQEDAPSVDIANIR	MPTPP	2		1074.587115	2147.15863	0.000451244	4	N	282	302
P40142	Infl	FAGIY	KLDNLVAIFDINR	LGQSD	3		510.9599913	1529.856574	0.000451244	14	N	173	186
P40142	Infl	AGVTL	HEALAAAESLKK	DKISI	3		423.2388656	1266.693197	0.000622848	5	N	512	524
P40142	Infl	VEDHY	YEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	2		1109.571662	2217.127723	0.000451244	5	N	563	586
P40142	Infl	EAGFL	PEAELLNLR	KISSD	2		527.7987276	1053.581855	0.002981883	1	N	92	101

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P40142	Infl	KVVLK	SKDDQVTVIGAGVTL	HEALA	2		751.9071921	1501.798784	0.002981883	1	N	497	512
P41216	Infl	FEQVK	GIAVHPELFSIDNGLLTPTLK	AKRPE	3		745.7514888	2234.231066	0.000622848	1	N	655	676
P41216	Infl	WISYK	EVAELAECIGSGLIQK	GFKPC	3	C8:+57.021	572.96644	1715.87592	0.001871652	1	N	125	141
P41245	Infl	RRDGR	LWCATTSNFDTDKK	WGFCP	2	C3:+57.021	843.8935275	1685.771455	0.000451244	27	N	370	384
P41245	Infl	FLNHR	GSPLQGPFLTAR	TWPAL	2		622.3438336	1242.672067	0.000451244	8	N	564	576
P41245	Infl	LMLQK	QLSLPQTGELDSQTLK	AIRTP	2		879.4681452	1756.92069	0.000451244	6	N	77	93
P41245	Infl	SDGYR	WCATTANYDQDKLYGFCPTR	VDATV	2	C2:+57.021,C17:+57.021	1234.043968	2466.072337	0.000451244	23	N	312	332
P41245	Infl	QSVIR	VDKEFSGVPWNSHDIFQYQDK	AYFCH	2		1270.098575	2538.18155	0.000451244	1	N	667	688
P41245	Infl	RSLDK	LGLGPEVTHVSGLLPR	RLGKA	2		822.9757434	1643.935887	0.000451244	2	N	621	637
P41245	Infl	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	2		1044.594743	2087.173886	0.000451244	11	N	617	637
P41245	Infl	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	2	C13:+57.021	1277.613107	2553.210613	0.000451244	22	N	275	297
P41245	Infl	FLTAR	TWPALPATLDSAFEDPQTKR	VFFFS	2		1122.568922	2243.122244	0.000451244	8	N	576	596
P41245	Infl	WSLGK	GVVIPTYYGNSNGAPCHFPFTFEGR	SYSAC	2	C16:+57.021	1394.153127	2786.290655	0.000451244	16	N	214	239
P41245	Infl	PFDGK	DGLLAHAFPPGAGVQGDAHFDDDELWSLGK	GVVIP	3		1045.832258	3134.473375	0.000451244	25	N	184	214
P41245	Infl	DAFAR	AFAVWGEVAPLTFTR	VYGPE	2		832.943912	1663.872224	0.000451244	28	N	143	158
P41245	Infl	FCPTR	VDATVVGGNSAGELCVFPFVFLGK	QYSSC	2	C15:+57.021	1242.135883	2482.256167	0.000451244	58	N	332	356
P41245	Infl	FLTAR	TWPALPATLDSAFEDPQTK	RVFFF	2		1044.518366	2087.021133	0.000451244	9	N	576	595
P41245	Infl	SDGYR	WCATTANYDQDK	LYGFC	2	C2:+57.021	736.8094634	1471.603327	0.001463592	1	N	312	324
P41245	Infl	TTDGR	NDGTPWCSTTADYDKDGK	FGFCP	2	C7:+57.021	1015.923742	2029.831883	0.000451244	4	N	249	267
P41245	Infl	LTFTR	VYGPEADIVIQFGVAEHGDGYPFDGK	DGLLA	3		927.4454528	2779.312958	0.000451244	5	N	158	184
P41245	Infl	FCPTR	VDATVVGGNSAGELCVFPF	VFLGK	2	C15:+57.021	969.9672238	1937.918848	0.002019181	2	N	332	351
P41245	Infl	NVDVF	DAIAEIQGALHFFK	DGWYW	3		520.6125915	1558.814375	0.001264573	1	N	539	553
P41245	Infl	DTDKK	WGFCPDQGYSLF	LVAAH	2	C4:+57.021	738.8165601	1475.61752	0.000979378	5	N	384	396
P42208	Infl	SGLGK	STLINSLFLTDLYPER	IIPGA	2		941.5019881	1880.988376	0.000451244	6	N	50	66
P42208	Infl	-MSK	QQPTQFINPETPGYVGFANLPNQVHR	KSVKK	3		984.8304122	2951.467836	0.001839721	1	N	3	29
P42227	Infl	DWKRR	QQIACIGGPPNICLDRLENWITSLAESQLQTR	QQIKK	3	C5:+57.021,C13:+57.021	1227.954257	3680.839372	0.000451244	6	N	246	278
P42227	Infl	WEESR	LLQTAATAAQQGGQANHPTAAVVTEK	QQMLE	3		859.4529417	2575.335425	0.000451244	12	N	114	140
P42227	Infl	TLAEK	LLGPGVNYSGCQITWAK	FCKEN	2	C11:+57.021	932.475019	1862.934438	0.001395409	1	N	531	548
P42227	Infl	PMELR	QFLAPWIESQDWAYAASK	ESHAT	2		1056.015794	2110.015988	0.001763695	3	N	31	49
P42227	Infl	DQMRR	SIVSELAGLLSAMEYVQK	TLTDE	3		646.6804543	1937.017963	0.000451244	1	N	215	233
P42227	Infl	EAFGK	YCRPESQEHPEADPGSAAPYLK	TKFIC	3	C2:+57.021	834.7170239	2501.127672	0.000451244	1	N	685	707
P42227	Infl	EQKMK	VVENLQDDFDFNYK	TLKSQ	2		873.4050136	1744.794427	0.002145581	1	N	163	177
P42227	Infl	GNGGR	ANCDASLIVTEELHLITFETEVYHQGLK	IDLET	4	C3:+57.021	808.4068162	3229.596065	0.000451244	7	N	423	451
P42227	Infl	TNNPK	NVNFFTKPPIGTWDQVAEVLSWQFSSTTK	RGLSI	3		1109.894859	3326.661176	0.00091018	1	N	488	517
P42567	Infl	LQAQK	QQVQELLGELDEQKAQLEEQLQEVR	KKCAE	3		994.1794353	2979.514906	0.000451244	2	N	391	416
P42567	Infl	SSLQK	NITGSSPVADFSAIKELDTLNNEIVDLQR	EKNNV	3		1053.877645	3158.609535	0.000451244	5	N	318	347
P42567	Infl	EVRKK	CAEEAQLISSLKAEITSQESQISSYEEELLK	AREEL	3	C1:+39.994	1166.234642	3495.680526	0.000823681	3	N	418	449
P42567	Infl	ISSLK	AEITSQESQISSYEEELLK	AREEL	2		1092.531868	2183.048136	0.000451244	11	N	430	449
P42567	Infl	QRLAR	LNQQEQEDLELAIALSK	SEISE	2		971.5105414	1941.005483	0.000979378	1	N	874	891
P42567	Infl	EELSR	LQQETAQLEESVESGK	AQLEP	2		888.4370421	1774.858484	0.000451244	1	N	456	472
P42567	Infl	GNTGR	VLALDAAAFLK	KSGLP	2		566.342771	1130.669942	0.001591523	2	N	33	44
P42567	Infl	EDKAK	YDAIFDSLSPVDGFLSGDK	VKPVL	2		1023.489275	2044.962949	0.001162105	3	N	131	150
P42669	Infl	DALAK	LIDDYGVEEEPAELPEGTSLTVDNKR	FFFDV	3		963.805375	2888.392725	0.000451244	8	N	203	229
P42669	Infl	QREKR	AACEQLHQQQQQQQEETTAATLLLQGEEEGEED	-	3	C3:+57.021	1257.22954	3768.66522	0.000622848	2	N	288	321
P42932	Infl	FVLVF	AGALLELAEELLR	IGLSV	2		699.4040883	1396.792577	0.000451244	12	N	107	120
P42932	Infl	YAIKK	FAEAFEAIPR	ALAEN	2		575.7987276	1149.581855	0.000823681	1	N	440	450
P42932	Infl	TFLAK	LIAQACVSIFPDSGNFNVDNIR	VCKIL	2	C6:+57.021	1225.610564	2449.205528	0.000451244	14	N	181	203
P42932	Infl	IELAK	QITSYGETCPGLEQYAIKK	FAEAF	2	C9:+57.021	1093.543827	2185.072054	0.000451244	5	N	421	440
P42932	Infl	IELAK	QITSYGETCPGLEQYAIK	KFAEA	2	C9:+57.021	1029.496345	2056.977091	0.000451244	18	N	421	439
P42932	Infl	NRLEK	LFVTNDAATILR	ELEVQ	2		667.3778735	1332.740147	0.000823681	12	N	62	74
P42932	Infl	QEGNK	NVGLDIEAEVPAVK	DMLEA	2		727.3990029	1452.782406	0.000870037	2	N	476	490
P43024	Infl	NHTLF	HNPHVNPLPTGYEDE	-	2		859.8926047	1717.769609	0.000622848	5	N	96	111
P43024	Infl	HLRIR	TKPFPWGDGNHTLF	HNPHV	3		539.6005745	1615.778323	0.000851441	11	N	82	96
P43274	Infl	-M	SETAPAAPAAPAPAEKTPVK	KKARK	2		952.5103444	1903.005089	0.000823681	3	N	1	21
P43274	Infl	GAKRK	TSGPPVSELITK	AVAAS	2		614.8433321	1227.671064	0.000451244	52	N	34	46
P43274	Infl	-M	SETAPAAPAAPAPAEK	TPVKK	2		739.8784346	1477.741269	0.000451244	17	N	1	17
P43275	Infl	AALKK	SLAAAGYDVEK	NNSRI	2		562.28565	1122.5557	0.000451244	15	N	66	77
P43275	Infl	AAAPR	KKPAGPSVSELIVQAVSSSK	ERSGV	2		1006.573476	2011.131352	0.000451244	6	N	34	54
P43275	Infl	MSETA	PVAQAASTATEKPAAAKK	TKKPA	2		870.4866723	1738.957745	0.000451244	3	N	5	23
P43275	Infl	AALKK	SLAAAGYDVEKN	NSRIK	2		619.3071138	1236.598628	0.000451244	3	N	66	78
P43276	Infl	GAAKR	KATGPPVSELITK	AVSAS	2		670.8933564	1339.771113	0.000451244	14	N	33	46
P43276	Infl	AAKRK	ATGPPVSELITK	AVSAS	2		606.8458748	1211.67615	0.000451244	32	N	34	46
P43276	Infl	-M	SETAPAETAAPAPVEK	SPAKK	2		784.8942817	1567.772963	0.000451244	15	N	1	17
P43276	Infl	PALKK	ALAAGGYDVEK	NNSRI	2		547.2803676	1092.545135	0.000451244	12	N	64	75
P43277	Infl	-M	SETAPAAPAAPAPVEKTPVK	KKAKK	2		966.5259945	1931.036389	0.000451244	3	N	1	21

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P43277	Infl	-M	SETAPAAPAAPAPVEK	TPVKK	2		753.8940847	1505.772569	0.000451244	35	N	1	17
P43430	Infl	LKLER	KAQLNSAVDTIALPK	SKDWV	2		784.9544767	1567.893353	0.000451244	5	N	115	130
P43430	Infl	IALPK	SKDWVKPGQVCTVAGWGK	LANCT	2	C11:+57.021	1002.0123	2002.009	0.000451244	2	N	130	148
P45878	Infl	GYGER	GAPPKIPGGATLVFEVELLK	IERRS	3		679.3983868	2035.17176	0.001329271	2	N	113	133
P45878	Infl	HYTGK	LEDGTEFDSSLPQNQPFVF	SLGTG	2		1085.502913	2168.990227	0.00091018	1	N	57	76
P45878	Infl	LHMHY	TGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK	GWDQG	3		1113.896817	3338.66705	0.001943752	1	N	54	85
P46061	Infl	DYFPK	ALAPLLLAFVTKPNGALETCSFAR	HNLLQ	3	C20:+57.021	854.1370832	2559.38785	0.000451244	8	N	555	579
P46061	Infl	TPSRK	ILDPNSGEPAPVLSSPTPTDLSTFLSFPSPEK	LLRLG	3		1114.233206	3339.676218	0.000451244	15	N	415	447
P46061	Infl	MFTGR	LRSEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVR	GFEAL	3		1335.383336	4003.126609	0.000622848	3	N	91	130
P46061	Infl	TGRLR	SEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVR	GFEAL	3		1245.654945	3733.941434	0.000451244	3	N	93	130
P46414	Infl	KRANR	TEENVSDGSPNAGTVEQTPK	KPGLR	2		1030.474884	2058.934169	0.000451244	7	N	169	189
P46414	Infl	SQNKR	ANRTEENVSDGSPNAGTVEQTPK	KPGLR	3		801.0462403	2400.115321	0.000735798	5	N	166	189
P46460	Infl	PIGPR	FSNLVLQALLVLLK	KAPPQ	2		786.0006986	1569.985797	0.000451244	3	N	617	631
P46460	Infl	AVETK	NFSGAELEGLVR	AAQST	2		646.3362056	1290.656811	0.001352548	2	N	434	446
P46471	Infl	DKPIR	ALDEGDIALLK	TYGQS	2		579.3247752	1156.63395	0.000451244	4	N	23	34
P46471	Infl	LTGIK	ESDTGLAPPALWDLAADKQTLQSEQPLQVAR	CTKII	3		1116.907716	3347.699747	0.000451244	8	N	66	97
P46471	Infl	LHPER	FVNLGIEPPKGVLLFGPPGTGK	TLCAR	3		746.4284575	2236.261973	0.000451244	5	N	200	222
P46638	Infl	AFAEK	NNLSFIETSALDSTNVEEAFKNILTEIYR	IVSQK	3		1111.228455	3330.661964	0.000451244	10	N	145	174
P46638	Infl	AFAEK	NNLSFIETSALDSTNVEEAFK	NILTE	2		1165.063867	2328.112133	0.000451244	15	N	145	166
P46638	Infl	AFAEK	NNLSFIETSALDSTNVEEAF	KNILT	2		1101.016385	2200.01717	0.001162105	1	N	145	165
P46664	Infl	ANQYK	SIYPTLEIDIEGELQQLK	GYMER	2		1045.057325	2088.099049	0.000451244	7	N	203	221
P46664	Infl	AYTTR	VGIGAFPTEQDNEIGELLQTR	GREFG	2		1144.082394	2286.149187	0.000451244	8	N	303	324
P46935	Infl	NRLTR	DDFLGQVDVPLYPLPTENPR	MERPY	2		1143.07658	2284.13756	0.000622848	7	N	158	178
P47738	Infl	PFDSR	TEQGPQVDETQFK	KILGY	2		753.8576992	1505.699798	0.000451244	13	N	357	370
P47738	Infl	SGSGR	ELGEYGLQAYTEVK	TVTVK	2		800.3991999	1598.7828	0.000451244	12	N	494	508
P47738	Infl	VKAAR	AAFQLGSPWR	RMDAS	2		566.7990619	1131.582524	0.000451244	6	N	86	96
P47738	Infl	LSRLL	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	3	C19:+57.021	1259.932775	3776.774926	0.000451244	18	N	19	53
P47738	Infl	EGVDK	VAFTGSTEVGHLIQVAAGSSNLKR	VTLEL	3		814.7753561	2441.302668	0.000451244	9	N	259	283
P47738	Infl	CAGSR	TFVQENVYDEFVER	SVARA	2		887.9182882	1773.820976	0.000451244	2	N	326	340
P47738	Infl	KYHGK	TIPIDGDFFSYTR	HEPVG	2		766.3755278	1530.735456	0.00091018	2	N	161	174
P47738	Infl	ANLIK	EAGFPPGVVNIVPGFGPTAGAAIASHEGVDK	VAFTG	3		987.8422063	2960.503219	0.000451244	38	N	228	259
P47738	Infl	VVVMK	VAEQTPLTALYVANLIK	EAGFP	2		922.5305486	1843.045497	0.000451244	24	N	211	228
P47738	Infl	AVFTK	DLDKANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C21:+57.021	1299.624837	3895.851111	0.000451244	32	N	453	488
P47738	Infl	ANDSK	YGLAAAVFTK	DLDKA	2		520.7929139	1039.570228	0.000451244	23	N	443	453
P47738	Infl	IERDR	TYLAALETLDNGKPYVISY	LVDLD	2		1066.052042	2130.088484	0.000451244	3	N	118	137
P47738	Infl	AVSRK	TFPTVNPSTGEVICQVAEGNKEDVDK	AVKAA	3	C14:+57.021	945.455646	2833.343538	0.000451244	5	N	54	80
P47738	Infl	KDLDK	ANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C17:+57.021	1142.547199	3424.618197	0.000622848	16	N	457	488
P47738	Infl	QPEVF	CNQIFINNEWHDAVSR	KTFPT	2	C1:+39.994	993.4498384	1984.884077	0.002019181	2	N	37	53
P47738	Infl	FSYTR	HEPVGVCGQIIPWNFPLLMQAWK	LGPAL	3	C7:+57.021	907.4665467	2719.37624	0.000823681	1	N	174	197
P47738	Infl	EVVGR	ANDSKYGLAAAVFTK	DLDKA	2		778.409902	1554.804204	0.001162105	1	N	438	453
P47738	Infl	AGTVW	INCYDVFGAQSPFGGYK	MSGSG	2	C3:+57.021	961.941009	1921.866418	0.000622848	3	N	471	488
P47740	Infl	MVQER	EKEILAAIAADLSK	SELNA	3		491.284252	1470.829356	0.000662267	5	N	37	51
P47740	Infl	ENTAK	ILAELLPQYLDQDLYAIVNGGIPETTELLK	QRFDH	3		1114.941475	3341.801024	0.000451244	11	N	145	175
P47754	Infl	RIAAK	FIIHAPPGEFNEVFNDVR	LLLNN	2		1051.029236	2100.042871	0.000451244	10	N	19	37
P47754	Infl	DNLLR	EGAAHAFAQYNLDQFTPVKIEGYEDQVLITEHGDLGNGK	FLDPK	4		1069.521707	4274.055629	0.000451244	16	N	47	86
P47754	Infl	TVYGK	KVDGQQTIIACIESHQFQAK	NFWNG	3	C11:+57.021	767.7270832	2300.157849	0.000451244	16	N	146	166
P47754	Infl	RSEWK	FTVTPSTTQVVGILK	IQVHY	2		795.9592277	1589.902855	0.000451244	10	N	178	193
P47754	Infl	LVSHK	DIQDSLTVSNEVQTAK	EFIKI	2		874.4395848	1746.86357	0.000451244	2	N	210	226
P47754	Infl	DNLLR	EGAAHAFAQYNLDQFTPVK	IEGYE	2		1054.016325	2106.017051	0.000451244	3	N	47	66
P47757	Infl	SARLR	KLEVEANNAFDQYR	DLYFE	2		848.9186225	1695.821645	0.000451244	30	N	94	108
P47757	Infl	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLKIAR	DKVVG	3	C13:+57.021	1041.892084	3122.652851	0.000870037	3	N	23	51
P47757	Infl	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLK	IARDK	2	C13:+57.021	1392.223081	2782.430562	0.000451244	12	N	23	48
P47757	Infl	LIDLV	PSLCEDLLSSVDQPLK	IARDK	2	C4:+57.021	900.9563248	1799.89705	0.000451244	8	N	32	48
P47757	Infl	SKKIK	GCWDSIHVVEVQEK	SSGRT	2	C2:+57.021	843.4015197	1684.787439	0.000451244	16	N	145	159
P47757	Infl	ENKIR	STLNEIYFGK	TKDIV	2		586.3038428	1170.592086	0.000451244	5	N	225	235
P47757	Infl	ARLRK	LEVEANNAFDQYR	DLYFE	2		784.8711409	1567.726682	0.000451244	9	N	95	108
P47757	Infl	KVVGK	DYLLCDYNR	DGDSY	2	C5:+57.021	616.274528	1230.533456	0.001463592	6	N	57	66
P47757	Infl	DGSKK	IKGCWDSIHVVEVQEK	SSGRT	2	C4:+57.021	963.9910333	1925.966467	0.000451244	4	N	143	159
P47757	Infl	FDQYR	DLYFEGGVSSVYLWDLDHGFAGVILIK	KAGDG	3		1005.183569	3012.527308	0.000823681	12	N	108	135
P47757	Infl	VSSVY	LWDLDHGFAGVILIK	KAGDG	3		566.3194081	1695.934824	0.000451244	5	N	120	135
P47791	Infl	VESHK	LGGTCVNVGCVPK	KVMWN	2	C5:+57.021,C10:+57.021	680.8392809	1359.662962	0.001229886	2	N	75	88
P47791	Infl	LNLNK	VGIQTDEKGHILVDEFQNTNVK	GVYAV	2		1242.640607	2483.265614	0.000451244	7	N	324	346
P47791	Infl	MGATK	ADFDNTVAIHPTSSEELVTLR	-	2		1158.079851	2314.144102	0.000451244	22	N	479	500
P47791	Infl	DKVLR	NFDSLISSNCTEELENAGVEVLK	FTQVK	2	C10:+57.021	1284.610624	2567.205647	0.000451244	17	N	246	269
P47791	Infl	DLPSR	SVIVGAGYIAVEIAGILSALGSK	TSLMI	2		1094.633534	2187.251467	0.000451244	12	N	211	234

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P47791	Infl	ELGAR	AAVVESHKLGGTCVNVGCVPK	KVMWN	3	C13:+57.021,C18:+57.021	728.0419715	2181.102514	0.000451244	3	N	67	88
P47791	Infl	DKVLR	NFDSLISSNCTEELENAGVEVLKFTQVK	EVKKT	3	C10:+57.021	1057.855698	3170.543695	0.000870037	2	N	246	274
P47791	Infl	KEVKK	TSSGLELQVVTSVPGR	KPTTT	2		815.4444731	1628.873346	0.000451244	1	N	278	294
P47791	Infl	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	3		1055.203581	3162.587343	0.002145581	1	N	383	412
P47791	Infl	DVCGK	ALLTPVAIAAGR	KLAHR	2		576.8591195	1151.702639	0.002453667	1	N	357	369
P47811	Infl	VKCQK	LTDDHVQFLIYQILR	GLKYI	3		625.3443934	1873.00978	0.000451244	17	N	121	136
P47811	Infl	AQMPK	MNFANVFIGANPLAVDLLEK	MLVLD	2		1088.577705	2175.13981	0.000451244	11	N	267	287
P47811	Infl	DSDKR	ITAAQALAHAYFAQYHDPDDEPVADPYDQSFESR	DLLID	3		1280.247237	3837.71831	0.001654178	1	N	296	330
P47811	Infl	DIIHR	DLKPSNLAVNEDCELK	ILDFG	2	C13:+57.021	922.9568561	1843.898112	0.000451244	8	N	149	165
P47811	Infl	LAHAY	FAQYHDPDDEPVADPYDQSFESR	DLLID	2		1364.575858	2727.136116	0.000622848	1	N	307	330
P47941	Infl	MFLVR	DSSTCPGDYVLSVSENSR	VSHYI	2	C5:+57.021	986.9315666	1971.847533	0.000451244	7	N	39	57
P47941	Infl	EPAPR	YPSPPVGSVSAPNLPTAEENLEYVR	TLYDF	2		1343.672104	2685.328608	0.000451244	1	N	104	129
P47955	Infl	LACIY	SALILHDDEVTVTEDKINALIK	AAGVS	2		1219.163384	2436.311167	0.000451244	17	N	11	33
P47955	Infl	NALIK	AAGVSVEPFWPGLFAK	ALANV	2		838.4462875	1674.876975	0.000451244	14	N	33	49
P47955	Infl	LACIY	SALILHDDEVTVTEDK	INALI	2		892.9497853	1783.883971	0.000622848	2	N	11	27
P47962	Infl	KYGVK	VGLTNYAAAYCTGLLLAR	RLLNR	2	C11:+57.021	964.009226	1926.002852	0.000451244	10	N	89	107
P47962	Infl	FGMDK	IYEGQVEVNGGEYNVESIDGQPGAFTCY	LDAGL	3	C27:+57.021	1032.457715	3094.349746	0.002080925	1	N	117	145
P47968	Infl	MAVNK	AGPVVTDNGNFILDWK	FDRVH	2		873.4470158	1744.878432	0.000451244	5	N	238	254
P47968	Infl	RIAER	VKQENLDLICIPTSFQAR	QLILQ	2	C10:+57.021	1066.562354	2131.109108	0.000451244	1	N	111	129
P48024	Infl	AFKKK	FACNGTVIEHPEYGEVIQLQGDQR	KNICQ	3	C3:+57.021	920.7734208	2759.296862	0.000451244	11	N	66	90
P48024	Infl	AFKKK	FACNGTVIEHPEYGEVIQLQGDQRK	NICQF	3	C3:+57.021	963.4717419	2887.391826	0.0025889	1	N	66	91
P48036	Infl	AGELK	WGTDEEKFITIFGTR	SVSHL	3		600.6374654	1798.888996	0.000451244	10	N	184	199
P48036	Infl	IIASR	TPEELSAIKQVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	3		1295.260989	3882.759566	0.000451244	5	N	115	149
P48036	Infl	-MATR	GTVTDFPGFDGR	ADAEV	2		634.7994559	1267.583312	0.000451244	8	N	4	16
P48036	Infl	-MATR	GTVTDFPGFDGRADAEVLR	KAMKG	2		1011.998133	2021.980665	0.00091018	3	N	4	23
P48036	Infl	RKAMK	GLGTDEDSILNLLTSR	SNAQR	2		852.4446701	1702.87374	0.000451244	7	N	27	43
P48036	Infl	LSAIK	QVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	2		1458.128652	2914.241704	0.000451244	15	N	124	149
P48036	Infl	ETIDR	ETSGNLEQLLLAVVK	SIRSI	2		807.4595919	1612.903584	0.000451244	9	N	225	240
P48036	Infl	TLFGR	DLVDDLKSELTGK	FEKLI	2		716.880643	1431.745686	0.000451244	5	N	61	74
P48999	Infl	QMVQR	AVQDLTYSSLCFPEAIK	ARGMD	2	C11:+57.021	971.4852494	1940.954899	0.000451244	5	N	439	456
P48999	Infl	PPTAK	GVVTIEQIVDTLPDRGR	SCWHL	3		623.3465741	1867.016322	0.000622848	6	N	580	597
P48999	Infl	IRFRK	NLEAIVSVIAER	NKNKK	2		657.3753308	1312.735062	0.000451244	18	N	640	652
P48999	Infl	NLANK	IVPIAIQLNQTPGESNPIFLPTDSKYDWLLAK	IWVRS	3		1194.647173	3580.91812	0.000451244	15	N	320	352
P48999	Infl	NKNKK	LPYYYLSPDRIPNSVAI	-	2		991.0256304	1980.035661	0.001591523	1	N	657	674
P48999	Infl	PPTAK	GVVTIEQIVDTLPDR	GRSCW	2		827.9546737	1653.893747	0.000451244	10	N	580	595
P48999	Infl	NLANK	IVPIAIQLNQTPGESNPIFLPTDSK	YDWLL	2		1346.731965	2691.44833	0.000451244	4	N	320	345
P48999	Infl	FYFYR	DDGLLVWEAIQSF	TMEVV	2		746.8700783	1491.724557	0.001229886	1	N	472	485
P49290	Infl	ISLSR	IVCDNTGITTVSR	DIFRA	2	C3:+57.021	718.3644058	1434.713212	0.002884417	1	N	674	687
P49290	Infl	LRLYK	TPDNIDIWVGAIAEPLLPGAR	VGPLL	2		1109.597483	2217.179365	0.000823681	1	N	608	629
P49312	Infl	NFGGR	SSGPYGGGGQYFAKPR	NQGGY	2		814.8949504	1627.774301	0.001463592	1	N	284	300
P49312	Infl	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	2		940.4872037	1878.958807	0.000451244	5	N	106	122
P49312	Infl	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	3		761.0553484	2280.142645	0.000451244	4	N	146	166
P49312	Infl	EQLRK	LFIGGLSFETTDESLR	SHFEQ	2		892.9574134	1783.899227	0.000451244	22	N	15	31
P49312	Infl	PEQLR	KLFIGGLSFETTDESLR	SHFEQ	2		957.0048949	1911.99419	0.000451244	16	N	14	31
P49710	Infl	DRMDK	SAVGHEYVADVEKHSSQTDAAR	GFGGK	3		786.3759208	2356.104362	0.000451244	5	N	96	118
P49710	Infl	AQLPK	KISSEVWPPAESHLPPESQPVR	SRREY	2		1235.64041	2469.26522	0.000451244	4	N	296	318
P49710	Infl	QLPKK	ISSEVWPPAESHLPPESQPVR	SRREY	3		781.3978857	2341.170257	0.000622848	2	N	297	318
P49710	Infl	VKMSR	EVQQPSMPVEEPAAPAQLPK	KISSE	2		1073.546602	2145.077603	0.000451244	10	N	276	296
P49710	Infl	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEKEQR	WGAKT	3		1268.908949	3803.703448	0.000451244	34	N	3	37
P49710	Infl	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEK	EQRWG	3		1131.174855	3390.501166	0.000451244	19	N	3	34
P49710	Infl	DRADK	SAVGFDYKGEVEK	HASQK	2		714.8544282	1427.693256	0.001264573	2	N	133	146
P49710	Infl	RGQCR	GHFGLFPANYVK	LL-	2		675.3542013	1348.692803	0.000622848	3	N	472	484
P49710	Infl	SLPTR	QSPLQNHLEDNEEPPALPPR	TPEGL	3		761.0456235	2280.11347	0.000451244	4	N	331	351
P49710	Infl	DRMDK	SAVGHEYVADVEK	HSSQT	2		702.3442276	1402.672855	0.000451244	1	N	96	109
P49710	Infl	ALPPR	TPEGLQVVEEPVYEAAPELEPEPEPDYEPEPE	TEPDY	3		1203.217838	3606.630115	0.002813207	2	N	351	383
P49717	Infl	SLGQK	LVIWGTDVNVATCK	ENFQR	2	C13:+57.021	788.4138987	1574.812197	0.000622848	2	N	148	162
P49717	Infl	QLNAR	TSVLAAANPIESQWNPK	KTTIE	2		913.4763046	1824.937009	0.000451244	4	N	609	626
P49722	Infl	SPSGK	LVQIEYALAAVAGGAPSVGIK	AANGV	2		1014.080937	2026.146274	0.000451244	9	N	18	39
P49722	Infl	FLEKR	YNEDLELEDAIHTAILTLK	ESFEG	3		734.3832422	2200.126327	0.000451244	21	N	177	196
P49722	Infl	TFLEK	RYNEDLELEDAIHTAILTLK	ESFEG	3		786.4169459	2356.227438	0.000451244	5	N	176	196
P49722	Infl	LAQQY	YLVYQEPIPTAQLVQR	VASVM	2		959.5257975	1917.035995	0.000823681	1	N	97	113
P49722	Infl	FLEKR	YNEDLELEDAIHTAILTL	KESFE	2		1037.023482	2072.031363	0.000870037	3	N	177	195
P49722	Infl	GVRPF	GVSLLICGWNEGRPYLFQSDPSGAYFAWK	ATAMG	3	C7:+57.021	1106.873246	3317.596339	0.000451244	2	N	130	159
P50247	Infl	LSGIR	GISEETTTGVHNLYK	MMSNG	2		824.9130058	1647.810412	0.000451244	5	N	151	166
P50247	Infl	VFAWK	GETDEEYLWCIEQTLHFK	DGPLN	3	C10:+57.021	766.6846611	2297.030583	0.000637154	3	N	103	121

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P50247	Infl	GAEVR	WSSCNIFSTQDHAAAAIAK	AGIPV	3	C4:+57.021	693.3305525	2076.968258	0.001699387	1	N	75	94
P50396	Infl	AAQGK	YIAIASTTVETAEPEKEVEPALELLEPIDQK	FVAIS	3		1142.931304	3425.770512	0.000451244	25	N	348	379
P50396	Infl	RDVYR	KFDLGQDVIDFTGHALALYR	TDDYL	3		760.399338	2278.174614	0.000451244	12	N	173	193
P50396	Infl	LHMDR	NPYYGGESSSITPLEELYK	RFQIL	2		1074.013114	2146.010628	0.000622848	4	N	35	54
P50429	Infl	ARASG	ATQPPHVVFVLADDLGWNDLGFHGSVIR	TPHLD	3		1020.861712	3059.561737	0.000451244	4	N	41	69
P50429	Infl	GPPTK	TLWLFDINQDPEER	HDVSR	2		888.4341054	1774.852611	0.000451244	3	N	471	485
P50516	Infl	SKNLR	VGSHITGGDIYGIVNENSLIK	HKIML	2		1093.576747	2185.137894	0.000451244	22	N	142	163
P50516	Infl	LTGQR	VLDALFPCVQGGTTAIPGAFGCGK	TVISQ	2	C8:+57.021,C22:+57.021	1218.606204	2435.196809	0.000451244	17	N	232	256
P50516	Infl	PLRTK	AKEILQEEEDLAEIVQLVGK	ASLAE	2		1127.612995	2253.210391	0.000451244	10	N	478	498
P50516	Infl	RTKAK	EILQEEEDLAEIVQLVGK	ASLAE	2		1028.046957	2054.078314	0.000451244	10	N	480	498
P50516	Infl	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDKK	LAQRK	3		1272.99519	3815.96217	0.000451244	24	N	400	438
P50516	Infl	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDK	KLAQR	3		1230.296869	3687.867206	0.000451244	13	N	400	437
P50516	Infl	PVAAR	EASIYTGITLSEYFR	DMGYH	2		875.4388564	1748.862113	0.000823681	3	N	323	338
P50516	Infl	QSLSK	YSNSDVIIYVGCGER	GNEMS	2	C12:+57.021	866.4042593	1730.792919	0.000451244	7	N	265	280
P50516	Infl	LEVAK	LIKDDFLQQNGYTPYDR	FCPFY	2		1043.516158	2085.016716	0.000451244	16	N	513	530
P50516	Infl	PPRNR	GSVTYIAPPGNYDASDVVLELEFEGVKEK	FSMVQ	3		1042.855958	3125.544475	0.000451244	3	N	173	202
P50516	Infl	SKYMR	ALDEYYDKHFTEFVPLR	TKAKE	2		1072.028901	2142.042203	0.000451244	2	N	459	476
P50518	Infl	IATKK	DVDVQIDQEAYLPEEIAGGVEIYNGDRK	IKVSN	3		1045.8426	3134.504401	0.000451244	9	N	161	189
P50518	Infl	DTTRY	QVLLDGLVLQGLYQLLEPR	MIVRC	2		1084.128419	2166.241237	0.000451244	4	N	112	131
P50518	Infl	LKVLR	ARDDLITDLLNEAK	QRLSK	2		793.9233735	1585.831147	0.000451244	11	N	85	99
P50518	Infl	RYQVL	LDGLVLQGLYQLLEPR	MIVRC	2		914.0228907	1826.030181	0.002727428	1	N	115	131
P50543	Infl	-M	PTETERCIESLIAVFQK	YSGKD	2	C7:+57.021	1011.02253	2020.029461	0.001264573	1	N	1	18
P50543	Infl	TQLSK	TEFLSFMNTELAAFTK	NQKDP	2		925.4561925	1848.896785	0.000451244	23	N	31	47
P50543	Infl	TETER	CIESLIAVFQK	YSGKD	2	C1:+57.021	654.3553211	1306.695042	0.000451244	242	N	7	18
P50543	Infl	DRMMK	KLDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C6:+57.021,C26:+57.021	1370.341958	4108.002474	0.000451244	59	N	60	96
P50543	Infl	FLNLI	GGLAIACHDSFIQTSQK	RI-	2	C7:+57.021	916.9519081	1831.888216	0.000451244	12	N	79	96
P50543	Infl	RMMKK	LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQKR	I-	4	C5:+57.021,C25:+57.021	1035.009956	4136.008622	0.001943752	2	N	61	97
P50543	Infl	RMMKK	LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C5:+57.021,C25:+57.021	1327.643637	3979.907511	0.000451244	31	N	61	96
P50543	Infl	DRMMK	KLDLNCDGQLDFQEF	LNLIG	2	C6:+57.021	921.4226491	1840.829698	0.000451244	12	N	60	75
P50543	Infl	LNLIG	GLAIACHDSFIQTSQK	RI-	2	C6:+57.021	888.4411762	1774.866752	0.000622848	2	N	80	96
P50543	Infl	KYSGK	DGNNTQLSKTEFLSFMNTELAAFTK	NQKDP	3		936.4572529	2806.348359	0.002663018	1	N	22	47
P50543	Infl	DFQEF	LNLIGGLAIACHDSFIQTSQK	RI-	2	C11:+57.021	1143.599468	2285.183336	0.000451244	11	N	75	96
P50543	Infl	GQLDF	QEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C14:+57.021	897.4587736	2689.352921	0.000451244	4	N	72	96
P50543	Infl	PTETE	RCIESLIAVFQK	YSGKD	3	C2:+57.021	488.6065178	1462.796153	0.001395409	1	N	6	18
P50543	Infl	EFLNL	IGGLAIACHDSFIQTSQK	RI-	2	C8:+57.021	973.4939401	1944.97228	0.000451244	2	N	78	96
P50580	Infl	EAALR	LVKPGNQNTQVTEAWNK	VAHSF	2		964.0057606	1925.995921	0.000451244	11	N	155	172
P50580	Infl	KEMKK	GIAFPTSISVNNCVCHFSPLK	SDQDY	2	C13:+57.021,C15:+57.021	1174.57999	2347.144379	0.002374549	1	N	72	93
P50580	Infl	NRVLR	SLVEASSSGVSVLSLCEK	GDAMI	2	C16:+57.021	926.472339	1850.929078	0.000451244	9	N	33	51
P50580	Infl	KKASK	TVENATSGETLEENGAGD	-	2		897.3877462	1792.759892	0.002453667	1	N	376	394
P50580	Infl	EKEMK	KGIAFPTSISVNNCVCHFSPLK	SDQDY	2	C14:+57.021,C16:+57.021	1238.627471	2475.239342	0.002145581	1	N	71	93
P50580	Infl	GDLVK	IDLGVHVDGFIANVAHTFVIGVAQGTQVTGR	KADVI	4		798.6799821	3190.688729	0.002981883	1	N	107	138
P50637	Infl	PPAAR	LLYPYLAWLAFATVLNYYVWRDNSGR	RGGSR	3		1055.550587	3163.62836	0.000451244	1	N	135	161
P50637	Infl	PPAAR	LLYPYLAWLAFATVLNYYVWR	DNSGR	2		1318.209743	2634.403886	0.00307782	1	N	135	156
P51125	Infl	LASLK	GVVPEDAVETLAGSLGTR	EADPE	2		885.9657697	1769.915939	0.000662267	2	N	504	522
P51125	Infl	PLLPK	ESQEQLAPLSDDFLLDALSQDFSSPANISSLEFEDAK	LSAAI	3		1352.974848	4055.901145	0.000451244	21	N	575	612
P51125	Infl	ESKTK	FQDVPSAGGESVAGGGTVATALDKVVGK	KKEQK	3		873.1209692	2616.339508	0.000451244	1	N	180	208
P51125	Infl	EETSK	SLSESELIGELSADFDR	STYQD	2		934.4501495	1866.884699	0.000451244	10	N	441	458
P51125	Infl	ESKTK	FQDVPSAGGESVAGGGTVATALDK	VVGKK	2		1117.550926	2233.086253	0.000451244	2	N	180	204
P51125	Infl	KEKKR	KVEEEVINDQALQALSDSLGTR	QPDPP	2		1208.122247	2414.228894	0.000451244	3	N	359	381
P51125	Infl	ERQEK	CGEDEDTVPAEYR	LKPAK	2	C1:+57.021	770.8149427	1539.614285	0.000451244	3	N	407	420
P51125	Infl	FEDAK	LSAAISEVVSQTPAPSTHAAAPLPGTEQK	DKELD	3		953.5018497	2857.482149	0.000451244	4	N	612	641
P51125	Infl	QLAPL	SDDFLLDALSQDFSSPANISSLEFEDAK	LSAAI	3		1021.144056	3060.408769	0.000451244	7	N	584	612
P51125	Infl	SKTKF	QDVPSAGGESVAGGGTVATALDK	VVGKK	2		1044.016719	2086.017839	0.000823681	3	N	181	204
P51150	Infl	QASPR	DPENFPFVVLGNKIDLENR	QVATK	2		1108.571465	2215.127329	0.001229886	2	N	113	132
P51150	Infl	ETSAK	EAINVEQAFQTIAR	NALKQ	2		795.4182583	1588.820917	0.000451244	4	N	157	171
P51150	Infl	VAFYR	GADCCVLVFDVTAPNTFK	TLDSW	2	C4:+57.021,C5:+57.021	1007.474127	2012.932655	0.000451244	1	N	79	97
P51150	Infl	PNTFK	TLDSWRDEFLIQASPR	DPENF	2		967.492486	1932.969372	0.000622848	5	N	97	113
P51150	Infl	QASPR	DPENFPFVVLGNK	IDLEN	2		738.3806131	1474.745626	0.000451244	10	N	113	126
P51150	Infl	GVAFY	RGADCCVLVFDVTAPNTFK	TLDSW	2	C5:+57.021,C6:+57.021	1085.524683	2169.033766	0.002080925	1	N	78	97
P51174	Infl	RESVR	KFFQEEVIPHHTEWEK	AGEVS	3		695.3465741	2083.016322	0.001162105	2	N	65	81
P51174	Infl	EKAGK	QGLLGINIAEK	HGGIG	2		578.3407596	1154.665919	0.000998612	2	N	95	106
P51174	Infl	NIAEK	HGGIGGDLLSTAVTWEEQAYSNCTGPGFSLH	SDIVM	3	C23:+57.021	1087.835409	3260.482826	0.000622848	3	N	106	137
P51174	Infl	ESVRK	FFQEEVIPHHTEWEK	AGEVS	2		978.4684796	1954.921359	0.002884417	1	N	66	81
P51174	Infl	NIAEK	HGGIGGDLLSTAVTWEEQAY	SNCTG	2		1052.503248	2102.990895	0.000622848	2	N	106	126
P51410	Infl	GTLRR	DFNHINVELSLLGK	KKKRL	3		533.6232677	1597.846403	0.000451244	6	N	36	50

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P51410	Infl	-MK	TILSNQTVDIPENVEITLK	GRTVI	2		1064.081331	2126.147062	0.000451244	12	N	2	21
P51410	Infl	RVRMR	TGVACSVSQAQKDELILEGNDIELVSNSAALIQQATTVK	NKDIR	3	C5:+57.021	1367.705885	4100.094254	0.000451244	15	N	129	168
P51410	Infl	MRSVY	AHFPINVVIQENGSLVEIR	NFLGE	2		1068.084542	2134.153485	0.000451244	5	N	96	115
P51410	Infl	TGVAC	SVSQAQKDELILEGNDIELVSNSAALIQQATTVK	NKDIR	3		1204.970933	3611.889399	0.000451244	11	N	134	168
P51410	Infl	RYKMR	SVYAHFPINVVIQENGSLVEIR	NFLGE	2		1242.666428	2483.317256	0.000823681	2	N	93	115
P51410	Infl	SQAQK	DELILEGNDIELVSNSAALIQQATTVK	NKDIR	3		962.1770318	2883.507695	0.000451244	1	N	141	168
P51437	Infl	LYRLL	DLDPEPQGDEDPDTPK	SVRFR	2		884.3819325	1766.748265	0.000451244	9	N	56	72
P51437	Infl	GKAER	QLPEQCAFKEQGVVK	QCMGA	2	C6:+57.021	880.9539194	1759.892239	0.000451244	8	N	88	103
P51437	Infl	DTNLY	RLLDLDPEPQGDEDPDTPK	SVRFR	2		1075.516552	2149.017504	0.000451244	64	N	53	72
P51437	Infl	TNLYR	LLDLDPEPQGDEDPDTPKSVR	FRVKE	2		1168.566773	2335.117947	0.000451244	11	N	54	75
P51437	Infl	TNLYR	LLDLDPEPQGDEDPDTPK	SVRFR	2		997.4659966	1992.916393	0.000451244	69	N	54	72
P51437	Infl	DAVLR	AVDDFNQQSLDTNLYR	LLDLD	2		949.9481083	1897.880617	0.000451244	79	N	38	54
P51437	Infl	TNLYR	LLDLDPEPQGDEDPDTPKSV	RFRVK	2		1090.516218	2179.016836	0.000451244	4	N	54	74
P51437	Infl	CMGAV	TLNPAADSFDISCNEPGAQPFR	FKKIS	2	C13:+57.021	1204.053079	2406.090558	0.000451244	1	N	109	131
P51437	Infl	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	C2:+57.021,C19:+57.021	1018.456733	3052.346798	0.000823681	1	N	103	131
P51437	Infl	DAVLR	AVDDFNQQSLDTNLY	RLLDL	2		871.8975527	1741.779505	0.000823681	3	N	38	53
P51437	Infl	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPF	RFKKI	2	C2:+57.021,C19:+57.021	1449.130644	2896.245687	0.000622848	2	N	103	130
P51859	Infl	VEVEK	NSTPSEPDSGQGPPAEEEEGEEEAAKEEAEAQGVR	DHESL	3		1214.193415	3639.556844	0.000451244	27	N	197	232
P51859	Infl	PNKRK	GFSEGLWEIENNPTVK	ASGYQ	2		910.4472128	1818.878826	0.000451244	3	N	80	96
P51859	Infl	PKRPK	ESGDHEEEDKEIAALEGERPLPVEVEK	NSTPS	3		1012.154955	3033.441466	0.000823681	3	N	170	197
P51863	Infl	EQECR	NIVWIAECIAQR	HRAKI	2	C8:+57.021	736.8878511	1471.760102	0.000451244	2	N	327	339
P51863	Infl	AQLAR	ADDYEQVKNVADYYPEYK	LLFEG	2		1105.500371	2208.985141	0.000451244	3	N	257	275
P51863	Infl	EADRR	AFIITINSFGTELSKEDR	AKLFP	2		1021.034184	2040.052767	0.000622848	2	N	219	237
P51863	Infl	VRGLK	AGVLSQADYLNLVQCETLEDLK	LHLQS	2	C15:+57.021	1240.12317	2478.23074	0.000451244	13	N	24	46
P51863	Infl	EADRR	AFIITINSFGTELSK	EDRAK	2		820.94886	1639.88212	0.001395409	2	N	219	234
P51863	Infl	LEDLK	LHLQSTDYGNFLANEASPLTVSVIDDK	LKEKM	3		983.1614932	2946.461079	0.000451244	5	N	46	73
P51881	Infl	VSFAK	DFLAGGVAAAISK	TAVAP	2		610.3382169	1218.660834	0.000451244	9	N	10	23
P51881	Infl	TQFWR	YFAGNLASGGAAGATSLCFVYPLDFAR	TRLAA	2	C18:+57.021	1398.676435	2795.337271	0.000451244	21	N	111	138
P51881	Infl	DCVVR	IPKEQGVLSFWR	GNLAN	3		487.2739102	1458.798331	0.001591523	1	N	60	72
P52480	Infl	PITAR	NTGIICTIGPASR	SVEML	2	C6:+57.021	680.3563838	1358.697168	0.000451244	43	N	43	56
P52480	Infl	EASFK	CCSGAIIVLTK	SGRSA	2	C1:+57.021,C2:+57.021	611.3201927	1220.624785	0.000622848	15	N	422	433
P52480	Infl	EHMCR	LDIDSAPITAR	NTGII	2		586.3200242	1170.624448	0.000451244	37	N	32	43
P52480	Infl	QVKEK	GADFLVTEVENGGSLGSKK	GVNLP	2		954.489609	1906.963618	0.000451244	7	N	188	207
P52480	Infl	SLQVK	EKGADFLVTEVENGGSLGSK	KGVNL	2		1019.010906	2036.006211	0.000451244	26	N	186	206
P52480	Infl	QVKEK	GADFLVTEVENGGSLGSK	KGVNL	2		890.4421274	1778.868655	0.000451244	37	N	188	206
P52480	Infl	AYMEK	CDENILWLDYKNICK	VVEVG	2	C1:+57.021,C14:+57.021	992.4688451	1982.92209	0.000451244	5	N	151	166
P52480	Infl	EVGSK	IYVDDGLISLQVK	EKGAD	2		731.9117461	1461.807892	0.000451244	34	N	173	186
P52480	Infl	FEELR	RLAPITSDPTEAAAVGAVEASFK	CCSGA	2		1151.108411	2300.201223	0.000451244	8	N	399	422
P52480	Infl	AYMEK	CDENILWLDYK	NICKV	2	C1:+57.021	734.8427749	1467.66995	0.000451244	9	N	151	162
P52480	Infl	IMVAR	GDLGIEIPAEKVFLAQK	MMIGR	2		914.5148985	1827.014197	0.000451244	1	N	294	311
P52480	Infl	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	3		1015.868421	3044.581863	0.000451244	37	N	92	120
P52480	Infl	IKNVR	EATESFASDPILYRPVAV	ALDTK	2		983.0023522	1963.989104	0.000451244	15	N	92	110
P52480	Infl	IKNVR	EATESFASDPILYRPVAVALDTK	GPEIR	2		1247.147734	2492.279867	0.000451244	19	N	92	115
P52480	Infl	PVLCK	DAVLNAWAEDVDLR	VNLAM	2		793.894616	1585.773632	0.000451244	24	N	475	489
P52480	Infl	EELRR	LAPITSDPTEAAAVGAVEASFK	CCSGA	2		1073.057856	2144.100112	0.000451244	67	N	400	422
P52480	Infl	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	3	C16:+57.021	1165.55235	3493.63365	0.000451244	27	N	342	376
P52480	Infl	AHLYR	GIFPVLCKDAVLNAWAEDVDLR	VNLAM	2	C7:+57.021	1251.146782	2500.277965	0.002663018	1	N	467	489
P52480	Infl	IQDLK	FGVEQDVDMVFASFIRK	AADVH	3		663.3369105	1986.987331	0.000823681	4	N	230	247
P52480	Infl	IQDLK	FGVEQDVDMVFASFIR	KAADV	2		930.4539841	1858.892368	0.000451244	6	N	230	246
P52480	Infl	MNVAR	LNFSHGTHEYHAETIK	NVREA	3		628.639869	1882.896207	0.000451244	26	N	73	89
P52480	Infl	LGSKK	GVNLPGAAVDLPAVSEKDIQDLK	FGVEQ	2		1175.137169	2348.258738	0.000451244	17	N	207	230
P52480	Infl	MNVAR	LNFSHGTHEYHAETIKNVR	EATES	3		751.7106866	2252.10866	0.000451244	3	N	73	92
P52480	Infl	SLGSK	KGVNLPGAAVDLPAVSEK	DIQDL	2		882.9968729	1763.978146	0.000451244	21	N	206	224
P52480	Infl	IMVAR	GDLGIEIPAEK	VFLAQ	2		571.3091251	1140.60265	0.000451244	15	N	294	305
P52480	Infl	RGFFK	KGDVVIVLTGWRPGSGFTN	TMRVV	2		1002.039603	2002.063607	0.000823681	1	N	504	523
P52480	Infl	LGSKK	GVNLPGAAVDLPAVSEK	DIQDL	2		818.9493913	1635.883183	0.000451244	8	N	207	224
P52480	Infl	GETAK	GDYPLEAVR	MQHLI	2		510.2619779	1018.508356	0.001943752	4	N	367	376
P52480	Infl	PRPTR	AEGSDVANAVLDGADCIMLSGETAK	GDYPL	2	C16:+57.021	1247.575727	2493.135854	0.000451244	9	N	342	367
P52480	Infl	EELRR	LAPITSDPTEAAAVGAVEASF	KCCSG	2		1009.010374	2016.005149	0.000451244	10	N	400	421
P52480	Infl	GATLK	ITLDNAYMEKCDENILWLDYK	NICKV	2	C11:+57.021	1324.124856	2646.234112	0.002296037	1	N	141	162
P52480	Infl	LRRLA	PITSDPTEAAAVGAVEASFK	CCSGA	2		980.9972669	1959.978934	0.001162105	1	N	402	422
P52480	Infl	FPVLC	KDAVLNAWAEDVDLR	VNLAM	2		857.9420976	1713.868595	0.000451244	1	N	474	489
P52480	Infl	ATESF	ASDPILYRPVAVALDTK	GPEIR	3		610.344282	1828.009446	0.001162105	2	N	98	115
P52624	Infl	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGKR	VIRNT	4	C24:+57.021	990.2744308	3957.066523	0.000451244	4	N	139	176
P52624	Infl	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGK	RVIRN	3	C24:+57.021	1267.996271	3800.965412	0.000451244	22	N	139	175

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P52624	Infl	TLLDR	LQGDQINTPHDVLVEYQQRPQR	LVGHF	3		878.7848028	2633.331008	0.000622848	2	N	276	298
P52633	Infl	QDLTK	LLLENQGEAGGSLGSQPLLQPSPYGQSGISLSHLDLR	TNPSW	3		1278.001226	3830.980279	0.000451244	15	N	795	832
P52633	Infl	GLQER	CESLVEIYSQLQQEIGAASGELEPK	TRASL	3	C1:+57.021	926.7886251	2777.342475	0.002884417	1	N	227	252
P52633	Infl	GFISK	QYVTSLLLNEPDGTFLLR	FSDSE	2		1040.060202	2078.104803	0.001591523	1	N	544	562
P53994	Infl	ETSAK	TASNVEEAFINTAK	EIYEK	2		747.8758919	1493.736184	0.000823681	5	N	151	165
P53994	Infl	GKQIK	LQIWDTAGQESFR	SITRS	2		775.8840513	1549.752503	0.000451244	6	N	56	69
P53994	Infl	TGVGK	SCLLLQFTDKR	FQPVH	3	C2:+57.021	460.9153513	1379.722654	0.001229886	3	N	19	30
P53996-2	Infl	RSRGR	GFQFVSSSLPDICYR	CGESG	2	C13:+57.021	888.4249948	1774.83439	0.000451244	5	N	34	49
P53996-2	Infl	DICYR	CGESGHLAKDCDLQEDACYNCGR	GGHIA	3	C1:+39.994,C11:+57.021,C18:+57.021,C21:+57.021	900.017438	2697.028914	0.000979378	1	N	49	72
P53996-2	Infl	GHLAK	DCDLQEDACYNCGR	GGHIA	2	C2:+57.021,C9:+57.021,C12:+57.021	888.3243631	1774.633126	0.000451244	3	N	58	72
P54071	Infl	DVQLK	YFDLGLPNRDQTNDQVTIDSALATQK	YSVAV	3		975.1531091	2922.435927	0.001463592	1	N	80	106
P54071	Infl	LSNVK	LNEHFLNTTDFLDTIK	SNLDR	3		640.9954299	1919.96289	0.000451244	9	N	426	442
P54071	Infl	AYDGR	FKDIFQEIFDK	HYKTD	3		477.2507712	1428.728914	0.001329271	1	N	261	272
P54071	Infl	REHQK	GRPTSTNPIASIFAWTR	GLEHR	3		625.667759	1873.979877	0.001162105	7	N	360	377
P54103	Infl	KSEAK	DNFFQVFSPVFER	NSRWS	2		816.3967946	1630.777989	0.000451244	5	N	175	188
P54103	Infl	PDKRK	AAGEPIKEGDNDYFTCITK	AYEML	2	C16:+57.021	1064.99671	2127.977819	0.000662267	1	N	124	143
P54103	Infl	APSER	FEGPCIDSTPWTTEEQK	LLEQA	2	C5:+57.021	1012.949228	2023.882856	0.000851441	1	N	543	560
P54728	Infl	FQQMR	QIIQQNPSLLPALLQQIGR	ENPQL	2		1065.623835	2129.232069	0.000451244	10	N	289	308
P54728	Infl	FACEK	NENLAANFLLQQNFDED	-	2		997.958673	1993.901746	0.001162105	3	N	399	416
P54775	Infl	SRYKK	LQQELEFLEVQEEYIKDEQK	NLKKE	2		1269.634656	2537.253712	0.002080925	3	N	46	66
P54775	Infl	ILVEK	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	YKKLQ	3		1224.620012	3670.836635	0.000451244	16	N	10	43
P54775	Infl	RDVFR	LAKENAPAIIFIDEIDAIATK	RFDAQ	3		752.7548989	2255.241297	0.000451244	3	N	252	273
P54775	Infl	FRLAK	ENAPAIIFIDEIDAIATK	RFDAQ	2		972.5203778	1943.025156	0.000451244	7	N	255	273
P54775	Infl	EEVKR	IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	ILSTI	3		1185.289937	3552.846411	0.000451244	28	N	81	114
P54822	Infl	SANRR	ICLAEAFLTADTILNTLQNISEGLVVYPK	VIERR	3	C2:+57.021	1069.572463	3205.693988	0.000451244	9	N	338	367
P54822	Infl	LIILR	NAFDLLLPK	LARVI	2		515.8007389	1029.585878	0.001395409	1	N	125	134
P54822	Infl	QTYTR	KVDIEVLSVLASLGASVHK	ICTDI	3		655.718008	1964.130624	0.002080925	2	N	245	264
P54823	Infl	RGPVK	ASAGPGGGGTQPQPQLNQLK	NTSTI	2		953.4930173	1904.970435	0.000451244	17	N	26	46
P54823	Infl	RFNLK	SIEEQLGTEIKPIPSNIDK	SLYVA	2		1056.065681	2110.115762	0.000451244	21	N	447	466
P54823	Infl	SNIDK	SLYVAEYHSEPAEDEKP	-	2		982.4501495	1962.884699	0.000823681	2	N	466	483
P55937	Infl	GSLAR	LPDQQDTAQDASVEVNR	GFKEE	2		943.4484725	1884.881345	0.000451244	1	N	36	53
P56391	Infl	QNQTK	NCWQNYLDFHR	CEKAM	2	C2:+57.021	776.8414322	1551.667264	0.001463592	2	N	28	39
P56391	Infl	RRVYK	SLCPVSWVSAWDDR	IAEGT	2	C3:+57.021	839.3884123	1676.761225	0.000451244	11	N	62	76
P56391	Infl	AWDDR	IAEGTFPGKI	-	2		516.7903712	1031.565142	0.002019181	1	N	76	86
P56399	Infl	DKLEK	IFQNAPTDPTQDFSTQVAK	LGHGL	2		1054.518898	2107.022196	0.000451244	16	N	360	379
P56399	Infl	DMNQR	IGEWELIQESGVPLKPLFGPGYTGIR	NLGNS	2		1428.768882	2855.522163	0.000998612	1	N	303	329
P56399	Infl	YTGIR	NLGNSCYLNSVVQVLFSIPDFQRK	YVDKL	3	C6:+57.021	933.4816897	2797.421669	0.000451244	2	N	329	353
P56399	Infl	YTGIR	NLGNSCYLNSVVQVLFSIPDFQR	KYVDK	2	C6:+57.021	1335.671153	2669.326706	0.000451244	15	N	329	352
P56399	Infl	PELVR	AQVPFSSCLEAYGAPEQVDDFWSTALQAK	SVAVK	3	C8:+57.021	1072.504888	3214.491265	0.000451244	8	N	524	553
P56399	Infl	IQIKK	FTFGLDWVPK	KLDVS	2		605.3192958	1208.622992	0.001463592	3	N	575	585
P56399	Infl	VKTTR	FASFPDYLVIQIK	KFTFG	2		770.9246565	1539.833713	0.000622848	4	N	561	574
P56399	Infl	ISQLR	GTGLQPGEEELPDIAPPLVTPDEPK	GSLGF	2		1300.161038	2598.306476	0.000451244	9	N	603	628
P56399	Infl	KCDMR	ENLWLNLTDGSILCGR	RYFDG	2	C14:+57.021	930.9675581	1859.919516	0.000451244	5	N	205	221
P56399	Infl	TQVAK	LGHGLLSGEYSKPALESGDGEQVPEQKEVQDGIAPR	MFKAL	3		1264.301453	3789.880959	0.000451244	5	N	379	415
P56399	Infl	ISEGR	SAAESISESVPVGPK	VRDGP	2		729.3782675	1456.740935	0.000637154	3	N	778	793
P56399	Infl	AQVPF	SSCLEAYGAPEQVDDFWSTALQAK	SVAVK	2	C3:+57.021	1337.110791	2672.205982	0.002080925	1	N	529	553
P56399	Infl	TQVAK	LGHGLLSGEYSKPALESGDGEQVPEQK	EVQDG	3		942.4704381	2824.387914	0.000622848	12	N	379	406
P56399	Infl	DEDVK	IVILPDYLEIAR	DGLGG	2		707.9193742	1413.823148	0.001591523	2	N	121	133
P56480	Infl	NNVAK	AHGGYSVFAGVGER	TREGN	3		469.5657527	1405.673858	0.000451244	28	N	225	239
P56480	Infl	AKGGK	IGLFGGAGVGK	TVLIM	2		488.285256	974.554912	0.000622848	9	N	201	212
P56480	Infl	GRDSR	LVLEVAQHLGESTVR	TIAMD	2		825.962833	1649.910066	0.000451244	4	N	94	109
P56480	Infl	VTGIK	VVDLLAPYAK	GGKIG	2		544.8216714	1087.627743	0.000451244	15	N	188	198
P56480	Infl	VRGQK	VLDSGAPIKIPVGPETLGR	IMNVI	2		960.0521795	1918.088759	0.000451244	19	N	124	143
P56480	Infl	DNIFR	FTQAGSEVSALLGR	IPSAV	2		718.3811445	1434.746689	0.000451244	13	N	310	324
P56480	Infl	TVLSR	AIAELGIYPAVDPLDSTSR	IMDPN	2		994.5209092	1987.026218	0.000451244	41	N	387	406
P56480	Infl	GARAR	VALTGLTVAEYFR	DQEGQ	2		720.3988059	1438.782012	0.000451244	10	N	281	294
P56480	Infl	ITTTK	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1281.665732	3841.973797	0.000451244	31	N	350	387
P56480	Infl	TTTKK	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1238.967411	3713.878834	0.000451244	32	N	351	387
P56480	Infl	AGVGK	TVLIMELINNVAK	AHGGY	2		729.423967	1456.832334	0.000451244	7	N	212	225
P56480	Infl	KETIK	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	ADKLA	3		1117.552105	3349.632914	0.000451244	6	N	489	519
P56480	Infl	LQDYK	SLQDIIAILGMDELSEEDKLTVSR	ARKIQ	3		892.465637	2674.373511	0.000451244	4	N	432	456
P56480	Infl	TATGR	IVAVIGAVVDVQFDEGLPPILNALEVQGR	DSRLV	3		1011.232923	3030.67537	0.000451244	143	N	62	91
P56480	Infl	AEYFR	DQEGQDVLLFIDNIFR	FTQAG	2		961.4868693	1920.958139	0.000451244	16	N	294	310

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P56480	Infl	GARAR	VALTGLTVAEYFRDQEGQDVLLFIDNIFR	FTQAG	3		1114.917663	3341.72959	0.000451244	11	N	281	310
P56480	Infl	PIKTK	QFAPIHAEAPEFIEMSVEQEILVTGIKVVDLLAPYAK	GGKIG	4		1024.79886	4095.164242	0.000451244	6	N	161	198
P56480	Infl	PIKTK	QFAPIHAEAPEFIEMSVEQEILVTGIK	VVDLL	3		1009.523486	3025.547059	0.001839721	2	N	161	188
P56480	Infl	RKIQR	FLSQPFQVAEVF	TGHMG	2		706.3669744	1410.718349	0.000637154	6	N	462	474
P56480	Infl	RKIQR	FLSQPFQVAEVFTGHMGK	LVPLK	3		675.0089053	2022.003316	0.002019181	1	N	462	480
P56480	Infl	ITTTK	KGSITSVQAIYVPADDLTDPAPATTF	AHLDA	2		1339.682138	2677.348675	0.001463592	3	N	350	376
P56546	Infl	NVDIK	AAGELGIAVCNIPSAAVEETADSTVCHILNLYR	RNTWL	3	C10:+57.021,C26:+57.021	1172.248559	3513.722276	0.000451244	6	N	114	147
P56546	Infl	NCVNK	EFFVTSAPWSVIDQQAIHPELNGATYR	YPPGI	3		1026.177478	3075.509033	0.000451244	7	N	359	386
P56565	Infl	KKELK	DLLQTELSGFLDVQKDADAVDK	VMKEL	3		807.4117491	2419.211847	0.000451244	10	N	35	57
P56565	Infl	KLSKK	ELKDLLQTELSGFLDVQK	DADAV	2		1038.565317	2075.115033	0.002884417	1	N	32	50
P56565	Infl	KKELK	DLLQTELSGFLDVQK	DADAV	2		853.4545065	1704.893413	0.000451244	3	N	35	50
P56812	Infl	EAEMR	NSILAQVLDQSAR	ARLSN	2		707.886594	1413.757588	0.000622848	10	N	40	53
P56959	Infl	RETGK	LKGEATVSFDDPPSAK	AAIDW	2		831.4232064	1660.830813	0.000451244	15	N	325	341
P56959	Infl	FGGPR	DQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	3		1376.960484	4127.858052	0.000735798	3	N	262	299
P56959	Infl	DQGSR	HDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	3		1195.880443	3584.617928	0.000451244	9	N	267	299
P56959	Infl	NNTIF	VQGLGENVTIESVADYFK	QIGII	2		984.9998096	1967.984019	0.000451244	19	N	281	299
P57716	Infl	RLDSR	SFFWNVAPGAESAVASFVTQLAAAEALHKAPDVTTLSR	NVMFV	4		990.7632376	3959.02175	0.002374549	1	N	284	322
P57746	Infl	IRAKK	DNVAGVTLPVFEHYHEGTDSYELTGLAR	GGEQL	3		1030.832147	3089.473041	0.000451244	9	N	98	126
P57746	Infl	LAEAK	FTAGDFSTTVIQNVNK	AQVKI	2		871.4419304	1740.868261	0.000622848	1	N	73	89
P57759	Infl	EELQK	SLNILTAFR	KKEAE	2		517.8038129	1033.592026	0.000451244	16	N	244	253
P57759	Infl	GLHTK	GALPLDTVTF	YKVIP	2		517.282379	1032.549158	0.001329271	1	N	38	48
P57780	Infl	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	2		1102.014314	2202.013028	0.000451244	3	N	772	792
P57780	Infl	YCIAR	MAPYQGPDAAPGALDYK	SFSTA	2		882.9172345	1763.818869	0.000451244	4	N	883	900
P57780	Infl	SNHIK	LSGSNPYTTVTPQIINSK	WEKVQ	2		960.5078018	1919.000004	0.000451244	26	N	605	623
P57780	Infl	YDKLR	KDDPVTNLNNAFEVAEK	YLDIP	2		952.4739589	1902.932318	0.000451244	5	N	217	234
P57780	Infl	DFMSR	ETTDTDTADQVIASFK	VLAGD	2		871.410493	1740.805386	0.000451244	14	N	838	854
P57780	Infl	KQYER	SIVDYKPSLDLLEQQHQLIQEALIFDNK	HTNYT	3		1099.917552	3296.729256	0.000451244	19	N	696	724
P57780	Infl	AHQDR	VEQIAAIAQELNELDYYDSHNVNTR	CQKIC	3		969.137459	2904.388977	0.000451244	14	N	470	495
P57780	Infl	SKGVK	LVSIGAEEIVDGNAK	MTLGM	2		757.9071921	1513.798784	0.000451244	11	N	126	141
P57780	Infl	TRCQK	ICDQWDNLGSLTHSR	REALE	2	C2:+57.021	901.4182324	1800.820865	0.000823681	1	N	498	513
P57780	Infl	EKTEK	QLETIDQLHLEYAK	RAAPF	2		850.9468486	1699.878097	0.000451244	5	N	522	536
P57780	Infl	HISWK	DGLAFNALIHR	HRPEL	2		613.8361757	1225.656751	0.000998612	2	N	194	205
P57780	Infl	IASFK	VLAGDKNFITAEELR	RELPP	2		838.4548408	1674.894082	0.000451244	1	N	854	869
P57780	Infl	SHLRK	AGTQIENIDEDFRDGLK	LMLLL	2		960.9690407	1919.922481	0.000637154	1	N	67	84
P57780	Infl	PEEFK	ACLISLGYDVENDRQGDAEFNR	IMSVV	2	C2:+57.021	1271.585275	2541.154949	0.000451244	8	N	792	814
P57780	Infl	PEEFK	ACLISLGYDVENDR	QGDAE	2	C2:+57.021	812.8857024	1623.755805	0.000622848	1	N	792	806
P57780	Infl	TAPYK	NVNVQNFHISWK	DGLAF	2		743.3840215	1484.752443	0.001699387	1	N	182	194
P57784	Infl	NRICR	IGEGLDQALPCLTELILTNNSLVELGDLDPLASLK	SLTYL	3	C11:+57.021	1245.664298	3733.969495	0.000451244	15	N	78	113
P57784	Infl	ELDLR	GYKIPVIENLGATLDQFDAIDFSDNEIR	KLDGF	3		1051.863336	3152.566607	0.000998612	1	N	27	55
P57784	Infl	-MVK	LTAELIEQAAQYTNAVR	DRELD	2		946.0001439	1889.984688	0.000451244	8	N	3	20
P57784	Infl	-M	VKLTAELIEQAAQYTNAVR	DRELD	2		1059.581832	2117.148065	0.001162105	2	N	1	20
P57784	Infl	PGRER	RSGPSDEGEEEIEDDTVTNGS	-	2		1111.962535	2221.90947	0.000622848	3	N	234	255
P57784	Infl	LRGYK	IPVIENLGATLDQFDAIDFSDNEIR	KLDGF	2		1403.201226	2804.386852	0.000823681	1	N	30	55
P58058	Infl	RQEIR	HGDSISITTSCYPLPSICVCDPVSDWFESLAQCLHWNVR	KKQAH	4	C11:+57.021,C18:+57.021,C20:+57.021,C33:+57.021	1152.52769	4606.079558	0.00307782	1	N	387	426
P58058	Infl	YVEKK	VLEDPAIVSDENFGPVK	KKFCT	2		914.9705208	1827.925442	0.000451244	7	N	142	159
P58252	Infl	VVSYR	ETVSEESNVLCLSK	SPNKH	2	C11:+57.021	797.8853681	1593.755136	0.000451244	9	N	580	594
P58252	Infl	KARAR	YLAEKYEWDVAEAR	KIWCF	2		871.9233735	1741.831147	0.000451244	18	N	633	647
P58252	Infl	PTARR	CLYASVLTAQPR	LMEPI	2	C1:+57.021	689.861302	1377.707004	0.000451244	11	N	727	739
P58252	Infl	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	2		1072.043071	2142.070543	0.000451244	17	N	605	625
P58252	Infl	MFVVK	AYLPVNESFGFTADLR	SNTGG	2		900.4522982	1798.888996	0.000451244	34	N	785	801
P58252	Infl	VAEAR	KIWCFGPDGTGPNILTDITK	GVQYL	2	C4:+57.021	1117.070012	2232.124424	0.000451244	18	N	647	667
P58252	Infl	TADLR	SNTGGQAFPQCVFDHWQILPGDPFDNSSRPSQVVAETR	KRKGL	3	C11:+57.021	1415.666646	4243.976539	0.000451244	46	N	801	839
P58252	Infl	KKLPR	TFCQLILDPIFK	VFDAI	2	C3:+57.021	747.9051782	1493.794756	0.000451244	17	N	287	299
P58252	Infl	AEARK	IWCFGPDGTGPNILTDITK	GVQYL	2	C3:+57.021	1053.02253	2104.029461	0.000451244	20	N	648	667
P58252	Infl	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	2		1177.113497	2352.211394	0.000451244	12	N	667	688
P58252	Infl	NKMDR	ALLELQLEPEELYQTFQR	IVENV	2		1110.581498	2219.147396	0.000451244	22	N	162	180
P58252	Infl	LMMGR	YVEPIEDVPCGNIVGLVGVDQFLVK	TGTIT	2	C10:+57.021	1380.220144	2758.424689	0.000451244	27	N	456	481
P58252	Infl	RKGLK	EGIPALDNFLDKL	-	2		722.888271	1443.760942	0.000451244	18	N	845	858
P58252	Infl	IKQSK	DGSGFLINLIDSPGHVDFSSEVTAALR	VTDGA	2		1409.206843	2816.398085	0.000451244	23	N	93	120
P58252	Infl	CITIK	STAISLFYELSENDLNFIK	QSKDG	2		1102.560231	2203.104863	0.000451244	23	N	71	90
P58252	Infl	CITIK	STAISLFYELSENDLNFIKQSK	DGSGF	3		849.7712773	2546.290432	0.000451244	6	N	71	93
P58252	Infl	VKAYL	PVNESFGFTADLR	SNTGG	2		726.8600449	1451.70449	0.000451244	2	N	788	801
P58252	Infl	TAQPR	LMEPIYLVEIQCPEQVVGGIYGVLNR	KRGHV	3	C12:+57.021	997.1894073	2988.544822	0.000451244	8	N	739	765
P58252	Infl	TAALR	VTDGALVVVDCVSGVCVQTETVLR	QAIAE	2	C11:+57.021,C16:+57.021	1288.656623	2575.297645	0.000451244	52	N	120	144

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P58252	Infl	PVVSY	RETVSEESNVLCLSK	SPNKH	2	C12:+57.021	875.9359237	1749.856247	0.000451244	8	N	579	594
P58252	Infl	AISLF	YELSENDLNFIK	QSKDG	2		742.8675356	1483.719471	0.000622848	1	N	78	90
P58252	Infl	KGVQY	LNEIKDSVVAGFQWATK	EGALC	2		953.5076048	1904.99961	0.000451244	14	N	671	688
P58252	Infl	LMMGR	YVEPIEDVPCGNIVGLVGVDQF	LVKTG	2	C10:+57.021	1210.096424	2418.177248	0.000622848	12	N	456	478
P58252	Infl	MYVAK	FAAKGEGQLSAAER	AKKVE	3		478.9165626	1433.726288	0.000451244	8	N	235	249
P58252	Infl	IKQSK	DGSGFLINLIDSPGHVDF	SSEVT	2		951.9657697	1901.915939	0.000622848	3	N	93	111
P58252	Infl	YLAEK	YEWDVAEAR	KIWCF	2		569.7623421	1137.509084	0.001763695	4	N	638	647
P58252	Infl	EPIYL	VEIQCPEQVVGGIYGVLNR	KRGHV	2	C5:+57.021	1065.554529	2129.093458	0.000451244	3	N	746	765
P58252	Infl	LKEGI	PALDNFLDKL	-	2		573.3142105	1144.612821	0.000979378	4	N	848	858
P58252	Infl	LPRTF	CQLILDPIFK	VFDAI	2	C1:+57.021	623.8471319	1245.678664	0.00091018	1	N	289	299
P58389	Infl	TWYAK	LDQEAENLVATVVPTHLAAAVPEVAVYLK	EAVGN	3		1020.892567	3059.6543	0.000451244	18	N	111	140
P58389	Infl	EAIEK	LVALLDTLDRWIDETPPVDQPSR	FGNKA	3		883.8014595	2648.380978	0.000451244	7	N	76	99
P58389	Infl	DTLDR	WIDETPPVDQPSR	FGNKA	2		770.3760591	1538.736518	0.000622848	4	N	86	99
P58389	Infl	EAIEK	LVALLDTLDR	WIDET	2		564.8353101	1127.65502	0.002296037	1	N	76	86
P58742	Infl	LFRTR	NSPVFELLPCGIIQGEPGAQAQLITFHPSFNK	GALLS	3	C10:+57.021	1170.601415	3508.780846	0.000622848	5	N	434	466
P59108	Infl	ETLAK	AVLAELPQQVVQYFK	HKNLP	2		866.9857768	1731.955954	0.000451244	3	N	521	536
P59325	Infl	TVEER	VNILFDFVK	KKKEE	2		547.816389	1093.617178	0.00307782	1	N	237	246
P59325	Infl	GFIKK	FVLCPECENPETDLHVNPK	KQTIG	2	C4:+57.021,C7:+57.021	1149.530162	2297.044725	0.001654178	1	N	95	114
P59708	Infl	IFDAK	NACDHLSGFNVCNR	YLVVL	2	C3:+57.021,C12:+57.021	832.3568892	1662.698178	0.001162105	2	N	71	85
P59708	Infl	TPETR	GTAYVVYEDIFDAK	NACDH	2		795.888468	1589.761336	0.001463592	1	N	57	71
P59999	Infl	VRSSK	ELLLQPVTISR	NEKEK	2		634.8827917	1267.749983	0.001162105	4	N	44	55
P59999	Infl	LSAVR	ATLQAALCLENFSSQVVER	HNKPE	2	C8:+57.021	1068.541619	2135.067637	0.000451244	16	N	13	32
P60122	Infl	TYLHR	ALESSIAPIVIFASNR	GNCVI	3		563.3179557	1686.930467	0.000451244	8	N	317	333
P60122	Infl	KRQGR	CDTYATEFDLEAEEYVPLPK	GDVHK	2	C1:+57.021	1195.541147	2389.066694	0.000451244	8	N	205	225
P60122	Infl	NCVIR	GTEDITSPHGIPLDLLDR	VMIIR	3		650.3378557	1947.990167	0.000451244	4	N	339	357
P60122	Infl	PGTGK	TALALAIAQELGSK	VPFCP	2		693.4040883	1384.792577	0.000451244	9	N	76	90
P60229	Infl	YRYAK	FQYECGNYSGAAEYLYFFR	VLVPA	2	C5:+57.021	1193.017976	2384.020353	0.000451244	10	N	136	155
P60229	Infl	EDLTR	LKETIDNNSVSSPLQSLQQR	TWLIH	2		1129.093293	2256.170985	0.001162105	1	N	191	211
P60229	Infl	QKKLR	ECESVLVNDFFLVACLEDFIENAR	LFIFE	3	C2:+57.021,C15:+57.021	963.7861844	2888.335153	0.000451244	4	N	313	337
P60229	Infl	HFLDR	HLVFPLLEFLSVK	EIYNE	3		514.641711	1540.901733	0.001839721	2	N	16	29
P60229	Infl	GAQKK	LRECESVLVNDFFLVACLEDFIENAR	LFIFE	3	C4:+57.021,C17:+57.021	1053.514576	3157.520328	0.000622848	7	N	311	337
P60335	Infl	NSTER	AITIAGVPQSVTECVK	QICLV	2	C14:+57.021	836.9508454	1671.886091	0.000451244	16	N	144	160
P60335	Infl	GGQDR	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	LNQVA	4	C1:+39.994	982.9669166	3927.836466	0.000451244	2	N	200	237
P60335	Infl	NCPER	IITLTGPTNAIFK	AFAMI	2		694.9115491	1387.807498	0.000622848	10	N	57	70
P60335	Infl	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	2		1089.100389	2176.185179	0.000451244	16	N	325	346
P60335	Infl	SPEVK	GYWASLDASTQTTHELTIPNNLIGCIIGR	QGANI	3	C25:+57.021	1067.871794	3200.591982	0.000451244	10	N	268	297
P60335	Infl	PVTLR	LVVPATQCGSLIGK	GGCKI	2	C8:+57.021	721.9057095	1441.795819	0.000823681	1	N	101	115
P60670	Infl	PLGIR	AEVAAIYEPPQIGTQNSLELLEDPKAEVVDEIAAK	LGLRK	3		1250.982838	3749.925115	0.000979378	2	N	267	302
P60670	Infl	QTWKK	SEQWATIEQLCSTVGVQLPGLHEFGAVGGSAR	AATSA	3	C11:+57.021	1128.893258	3383.656374	0.000451244	4	N	545	577
P60670	Infl	PIENR	DVLGETQDFHSLATYLSQNTSSVF	LDTIS	2		1330.130269	2658.244938	0.002884417	1	N	476	500
P60710	Infl	MWISK	QEYDESGPSIVHR	KCF-	2		758.8554908	1515.695382	0.000451244	34	N	359	372
P60710	Infl	ILTER	GYSFTTTAER	EIVRD	2		566.7676244	1131.519649	0.000451244	61	N	196	206
P60710	Infl	ILTER	GYSFTTTAEREIVR	DIKEK	2		815.4157156	1628.815831	0.000622848	5	N	196	210
P60710	Infl	YNELR	VAPEEHPVLLTEAPLNPK	ANREK	2		977.5363622	1953.057124	0.000451244	72	N	95	113
P60710	Infl	ELRVA	PEEHPVLLTEAPLNPK	ANREK	2		892.4835983	1782.951597	0.000451244	35	N	97	113
P60710	Infl	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	2		1108.039141	2214.062681	0.000451244	60	N	291	312
P60710	Infl	IGNER	FRCPEALFQPSFLGMESCGIHETTF	NSIMK	3	C3:+57.021,C18:+57.021	987.7840097	2960.328629	0.000451244	6	N	254	279
P60710	Infl	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	2	C4:+57.021	1404.159624	2806.303648	0.000451244	5	N	213	238
P60710	Infl	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	2	C2:+57.021	1275.590846	2549.166092	0.000451244	383	N	215	238
P60710	Infl	DIKEK	LCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNER	FRCPE	3	C2:+57.021	1441.354524	4321.040171	0.000451244	15	N	215	254
P60710	Infl	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	KCF-	4		1025.761538	4099.014951	0.000662267	2	N	336	372
P60710	Infl	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3		1085.208517	3252.60215	0.000451244	12	N	118	147
P60710	Infl	NELRV	APEEHPVLLTEAPLNPK	ANREK	2		928.0021552	1853.98871	0.000451244	4	N	96	113
P60710	Infl	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	2		1172.086622	2342.157645	0.000451244	6	N	290	312
P60710	Infl	DYLMK	ILTERGYSFTTTAER	EIVRD	2		872.94738	1743.87916	0.000451244	4	N	191	206
P60710	Infl	YNELR	VAPEEHPVLLTEAPLNPKANR	EKMTQ	3		765.7538923	2294.238277	0.000451244	2	N	95	116
P60710	Infl	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,C16:+57.021	1077.825658	3230.453573	0.000451244	5	N	256	284
P60710	Infl	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	2	C1:+57.021,C16:+57.021	1329.587352	2657.159104	0.000451244	5	N	256	279
P60710	Infl	FQQMW	ISKQEYDESGPSIVHR	KCF-	3		615.6432791	1843.906437	0.000451244	8	N	356	372
P60710	Infl	YNELR	VAPEEHPVLLTEAPLN	PKANR	2		864.9624987	1727.909397	0.002813207	1	N	95	111
P60710	Infl	MWISK	QEYDESGPSIVHRK	CF-	3		548.9379149	1643.790345	0.000622848	13	N	359	373
P60710	Infl	SLSTF	QQMWISKQEYDESGPSIVHR	KCF-	2		1209.579496	2417.143391	0.000451244	4	N	352	372
P60710	Infl	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C3:+57.021,C18:+57.021	1178.882166	3533.623098	0.000451244	4	N	254	284
P60766	Infl	HHCPK	TPFLLVGTQIDLRDDPSTIEK	LAKNK	2		1179.631719	2357.247839	0.000451244	13	N	107	128
P60766	Infl	EDYDR	LRPLSYPQTDVFLVCFSVVSPSSFENVKEK	WVPEI	3	C15:+57.021	1158.265921	3471.774364	0.001943752	2	N	66	96

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P60766	Infl	QKGLK	NVFDEAILAALEPPEPK	KSRRC	2		926.9887135	1851.961827	0.000451244	14	N	166	183
P60766	Infl	ALTQK	GLKNVFDEAILAALEPPEPK	KSRRC	2		1076.088959	2150.162318	0.000451244	2	N	163	183
P60766	Infl	EDYDR	LRPLSYPQTDVFLVCF	SVVSP	2	C15:+57.021	978.0086947	1954.001789	0.000979378	1	N	66	82
P60766	Infl	EDYDR	LRPLSYPQTDVFLVCFSVVSPSSFENVK	EKWVP	3	C15:+57.021	1072.553402	3214.636807	0.000451244	10	N	66	94
P60766	Infl	GAVGK	TCLLISYTTNKFPSEYVPTVF	DNYAV	2	C2:+57.021	1240.624817	2479.234034	0.001591523	1	N	16	37
P60766	Infl	HHCPK	TPFLLVGTQIDLR	DDPST	2		736.9277305	1471.839861	0.001591523	1	N	107	120
P60766	Infl	PKTPF	LLVGTQIDLRDDPSTIEK	LAKNK	2		1007.047291	2012.078982	0.001162105	1	N	110	128
P60766	Infl	QTDVF	LVCFSVVSPSSFENVK	EKWVP	2	C3:+57.021	899.9561278	1797.896656	0.000622848	5	N	78	94
P60843	Infl	DLLAR	GIDVQQVSLVINYDLPTNRENYIHR	IGRGG	3		986.181222	2955.520266	0.000451244	4	N	334	359
P60843	Infl	SGTGK	TATFAISILQQIELDLK	ATQAL	2		952.5411133	1903.066627	0.000451244	5	N	82	99
P60843	Infl	LPCIK	GYDVIAQAQSGTGK	TATFA	2		697.8496771	1393.683754	0.000451244	20	N	68	82
P60843	Infl	EMLSR	GFKDQIYDIFQK	LNSNT	3		501.2615588	1500.761276	0.000451244	7	N	190	202
P60843	Infl	REEWK	LDTLCDLYETLTITQAVIFINTR	RKVDW	2	C5:+57.021	1357.209777	2712.403953	0.000451244	5	N	259	282
P60843	Infl	DLLAR	GIDVQQVSLVINYDLPTNR	ENYIH	2		1072.571465	2143.127329	0.000451244	6	N	334	353
P60843	Infl	REEWK	LDTLCDLYETLTITQAVIF	INTRR	2	C5:+57.021	1115.071886	2228.128172	0.001329271	3	N	259	278
P60843	Infl	KTATF	AISILQQIELDLK	ATQAL	2		742.4406708	1482.865742	0.000451244	7	N	86	99
P60867	Infl	RIHKR	LIDLHSPSEIVK	QITSI	2		675.8855313	1349.755463	0.000823681	1	N	87	99
P60867	Infl	KDTGK	TPVEPEVAIHR	IRITL	3		416.5634606	1246.666982	0.001699387	1	N	8	19
P60898	Infl	IYVNK	ITHEVDELTQIIADVSQDPTLPR	TEDHP	3		864.1173362	2589.328608	0.0025889	1	N	57	80
P60898	Infl	LYACR	NCDYQQEADNSCIYVNK	ITHEV	2	C2:+57.021,C12:+57.021	1060.936095	2119.856589	0.000823681	3	N	40	57
P61022	Infl	SIADR	TIQEADQDGDSAISFTEFVK	VLEKV	2		1101.016385	2200.01717	0.000451244	2	N	158	178
P61079	Infl	LTISK	VLLSICSLLCDPNPDDPLVPEIAR	IYKTD	2	C6:+57.021,C10:+57.021	1353.695748	2705.375896	0.000451244	18	N	101	125
P61079	Infl	AFTTR	IYHPNINSNGSICLDILR	SQWSP	2	C13:+57.021	1050.039046	2098.062492	0.000451244	8	N	72	90
P61087	Infl	AMTLR	TVLLSLQALLAAAEPDDPQDAVVANQYK	QNPEM	3		985.1892717	2952.544415	0.000451244	4	N	107	135
P61087	Infl	RFITK	IWHPNISSVTGAICLDILK	DQWAA	3	C14:+57.021	713.05436	2136.13968	0.000979378	2	N	78	97
P61089	Infl	KETQR	LLAEPVPGIKAEPDESNAR	YFHVV	2		1003.531808	2005.048016	0.000823681	1	N	14	33
P61089	Infl	ALQIR	TVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQAIETAR	AWTRL	3		1401.72431	4202.14953	0.00091018	5	N	102	141
P61089	Infl	ALQIR	TVLLSIQALLSAPNPDDPLANDVAEQWK	TNEAQ	3		1006.864788	3017.570964	0.000451244	17	N	102	130
P61089	Infl	ESNAR	YFHVVIAGPQDSPFEGGTFK	LELFL	2		1098.542176	2195.068752	0.000451244	4	N	33	53
P61089	Infl	ESNAR	YFHVVIAGPQDSPFEGGTF	KLELF	2		1034.494694	2066.973789	0.001329271	3	N	33	52
P61161	Infl	MIKEK	LCYVGYNIEQEQK	LALET	2	C2:+57.021	822.3906206	1642.765641	0.000451244	16	N	219	232
P61161	Infl	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	2	C1:+57.021	1286.168383	2570.321167	0.001871652	2	N	19	42
P61161	Infl	EQEQK	LALETTVLVESYTLPDGR	IIKVG	2		989.0311097	1976.046619	0.000451244	18	N	232	250
P61161	Infl	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		1313.349856	3937.026167	0.000451244	37	N	258	294
P61161	Infl	LLLLR	GYAFNHSADFETVR	MIKEK	2		807.3713081	1612.727016	0.000451244	8	N	200	214
P61161	Infl	WDDMK	HLWDYTFGPEKLNIDTR	NCKIL	2		1053.026693	2104.037786	0.000622848	1	N	86	103
P61161	Infl	MIKEK	LCYVGYNIEQEQKLALETTVLVESYTLPDGR	IIKVG	3	C2:+57.021	1201.275034	3600.801701	0.000823681	2	N	219	250
P61161	Infl	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	C1:+39.994	1037.993882	2073.972164	0.00091018	2	N	19	38
P61161	Infl	LFQPH	LINVEGVGVAELLFNTIQAADIDTR	SEFYK	2		1336.219222	2670.422843	0.000451244	3	N	269	294
P61161	Infl	VRMIK	EKLCYVGYNIEQEQK	LALET	2	C4:+57.021	950.9593988	1899.903198	0.000451244	4	N	217	232
P61161	Infl	VGGER	FEAPEALFQPHLINVEGVGVAELL	FNTIQ	2		1296.689569	2591.363537	0.000698008	5	N	258	282
P61161	Infl	VLTLY	AQGLLTGVVVDSGDGVTHICPVYEGFSLPHLTR	RLDIA	3	C20:+57.021	1165.596441	3493.765924	0.000451244	7	N	147	180
P61161	Infl	GRIIK	VGGERFEAPEALFQPHLINVEGVGVAELL	FNTIQ	3		1030.880661	3089.618583	0.000823681	1	N	253	282
P61161	Infl	VAELL	FNTIQAADIDTR	SEFYK	2		682.8443948	1363.67319	0.000998612	2	N	282	294
P61161	Infl	APEAL	FQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		1060.89497	3179.661511	0.000451244	8	N	265	294
P61164	Infl	MDLRR	TLFSNIVLSGGSTLFK	GFGDR	2		842.4699596	1682.924319	0.000451244	6	N	292	308
P61164	Infl	LETEK	AQYYLPDGSTIEIGPSR	FRAPE	2		933.9657697	1865.915939	0.000451244	13	N	238	255
P61164	Infl	YVYSK	DQLQTFSEEHPVLLTEAPLNPR	KNRER	2		1267.648432	2533.281264	0.001763695	3	N	96	118
P61164	Infl	QLQTF	SEEHPVLLTEAPLNPR	KNRER	2		901.4763046	1800.937009	0.000622848	6	N	102	118
P61205	Infl	SLRHR	NWYIQATCATSGDGLYEGLDWLANQLK	NKK-	3	C8:+57.021	1029.82244	3086.443921	0.000451244	6	N	151	178
P61205	Infl	LHSLR	HRNWYIQATCATSGDGLYEGLDWLANQLK	NKK-	3	C10:+57.021	1127.542448	3379.603944	0.000823681	2	N	149	178
P61219	Infl	LDDLE	NAEEEGQENVEILPSGERPQANQKR	ITTPY	3		941.4608246	2821.359074	0.000698008	3	N	26	51
P61219	Infl	LDDLE	NAEEEGQENVEILPSGERPQANQK	RITTP	3		889.4271209	2665.257963	0.001395409	2	N	26	50
P61222	Infl	GELQR	VALALCLGKPADVYLIDEPSAYLDSEQR	LMAAR	3	C6:+57.021	1036.197396	3105.568787	0.000451244	3	N	469	497
P61222	Infl	GELQR	VALALCLGKPADVYLIDEPSAY	LDSEQ	2	C6:+57.021	1189.619535	2377.22347	0.000451244	1	N	469	491
P61222	Infl	ICIKK	CPFGALSIVNLPSNLEK	ETTHR	2	C1:+57.021	929.9905019	1857.965404	0.000622848	2	N	64	81
P61290	Infl	SFRER	ITSEAEDLVANFFPK	KLLEL	3		560.954683	1679.840649	0.002296037	1	N	21	36
P61290	Infl	LLIPR	IEDGNNFGVSIQEETVAELRTVESEAASYLDQISR	YYITR	3		1290.627894	3868.860283	0.000998612	1	N	146	181
P61750	Infl	SLRNR	TWYVQATCATQGTGLYEGLDWLSNELSKR	-	3	C8:+57.021	1116.538592	3346.592376	0.000451244	5	N	151	180
P61750	Infl	SLRNR	TWYVQATCATQGTGLYEGLDWLSNELSK	R-	3	C8:+57.021	1064.504888	3190.491265	0.000451244	6	N	151	179
P61750	Infl	AVLQK	MLLEDELQDAVLLLFANK	QDLPN	2		1038.058814	2074.102027	0.002981883	1	N	109	127
P61924	Infl	QVVHR	VALRGEDVPLTEQTVSQVLQSAK	EQIKW	3		823.4505382	2467.328214	0.000662267	6	N	145	168
P61924	Infl	NVEKR	ALLENMEGLFLAVDEIVDGGVILESDPQQVVHR	VALRG	3		1202.622699	3604.844698	0.002080925	1	N	112	145
P61924	Infl	RVALR	GEDVPLTEQTVSQVLQSAK	EQIKW	2		1015.026556	2028.037511	0.001229886	1	N	149	168
P61961	Infl	TAVLK	FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK	HGSEL	3		1192.630182	3574.867147	0.000451244	17	N	34	69

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P61961	Infl	AVLKF	AAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK	HGSEL	3		1143.607378	3427.798733	0.00091018	3	N	35	69
P61961	Infl	AAEEF	KVPAATSAIITNDGIGINPAQTAGNVFLK	HGSEL	3		961.1981016	2880.570905	0.000451244	1	N	40	69
P61979	Infl	QTTIK	LFQECCPHSTDRVVLIGGKPDR	VVECI	2	C5:+57.021,C6:+57.021	1292.641641	2583.267682	0.000735798	2	N	179	201
P61979	Infl	DCELR	LLIHQSLAGGIIGVK	GAKIK	2		759.9724724	1517.929345	0.002374549	1	N	148	163
P61979	Infl	VECIK	IILDLISESPIKGR	AQPYD	2		777.4672199	1552.91884	0.000451244	5	N	207	221
P61979	Infl	YAGGR	GSYGDLGGPIITTQVTIPK	DLAGS	2		959.020545	1916.02549	0.000451244	37	N	377	396
P61979	Infl	VECIK	IILDLISESPIK	GRAQP	2		670.9059325	1339.796265	0.000451244	23	N	207	219
P61979	Infl	GSEDR	IITITGTQDQIQNAQYLLQNSVK	QYSGK	2		1295.198289	2588.380978	0.000451244	26	N	433	456
P61979	Infl	YAGGR	GSYGDLGGPIITTQVTIPKDLAGSIIGK	GGQRI	2		1386.263629	2770.511658	0.000823681	1	N	377	405
P61979	Infl	GASIK	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	QYSGK	3		1277.320513	3828.93814	0.000451244	22	N	422	456
P61979	Infl	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	3	C29:+57.021	1352.34915	4054.024049	0.000451244	35	N	103	139
P61979	Infl	PIKGR	AQPYDPNFYDETYDYGGF	TMMFD	2		1081.437239	2160.858878	0.000451244	17	N	221	239
P61979	Infl	SGPER	ILSISADIETIGEILK	KIIPT	2		857.9960072	1713.976414	0.000451244	13	N	86	102
P61979	Infl	GKNIK	ALRTDYNASVSVPDSSGPER	ILSIS	2		1061.014511	2120.013422	0.000451244	6	N	66	86
P61979	Infl	SGPER	ILSISADIETIGEILKK	IIPTL	3		615.0315925	1842.071378	0.000451244	26	N	86	103
P61979	Infl	IKALR	TDYNASVSVPDSSGPER	ILSIS	2		890.9033664	1779.791133	0.000451244	26	N	69	86
P61979	Infl	IKQIR	HESGASIKIDEPLEGSEDR	IITIT	2		1034.993244	2067.970888	0.000451244	6	N	414	433
P61979	Infl	SEWQM	AYEPQGGSGYDYSYAGGR	GSYGD	2		949.4035336	1896.791467	0.000451244	8	N	359	377
P61979	Infl	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYKG	SDFDC	3	C29:+57.021	1371.356304	4111.045513	0.000622848	3	N	103	140
P61979	Infl	GEILK	KIIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	3	C30:+57.021	1395.047471	4182.119013	0.000979378	1	N	102	139
P61982	Infl	AAAMK	NVTELNEPLSNEER	NLLSV	2		822.3977199	1642.77984	0.000451244	51	N	28	42
P61982	Infl	THPIR	LGLALNYSVFYYEIQNAPEQACHLAK	TAFDD	3	C22:+57.021	1004.836021	3011.484663	0.000451244	18	N	172	198
P61982	Infl	EKIEK	ELEAVCQDVLSLLDNYLIK	NCSET	2	C6:+57.021	1118.082785	2234.14997	0.000451244	21	N	91	110
P61982	Infl	CHLAK	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1101.210184	3300.607153	0.000451244	15	N	198	227
P61982	Infl	CHLAK	TAFDDAIAELDTLNEDSYK	DSTLI	2		1065.989836	2129.964072	0.000451244	14	N	198	217
P61982	Infl	AYREK	IEKELEAVCQDVLSLLDNYLIK	NCSET	3	C9:+57.021	869.1316635	2604.371591	0.000451244	3	N	88	110
P61982	Infl	IMQLL	RDNLTLWTSDQQDDDGGEGNN	-	2		1175.494868	2348.974136	0.000451244	16	N	226	247
P61982	Infl	EKIEK	ELEAVCQDVLSLLDNYLIKNCSETQYESK	VFYLK	3	C6:+57.021,C21:+57.021	1154.553425	3460.636875	0.000451244	3	N	91	120
P61982	Infl	NYSVF	YYEIQNAPEQACHLAK	TAFDD	2	C12:+57.021	967.9571904	1933.898781	0.000979378	2	N	182	198
P61982	Infl	THPIR	LGLALNYSVF	YYEIQ	2		548.8060213	1095.596443	0.001943752	1	N	172	182
P61982	Infl	MQLLR	DNLTLWTSDQQDDDGGEGNN	-	2		1097.444312	2192.873025	0.000622848	8	N	227	247
P62082	Infl	RPRSR	TLTAVHDAILEDLVFPSEIVGKR	IRVKL	2		1262.195018	2522.374436	0.002453667	1	N	120	143
P62082	Infl	GGGRK	AIIIFVPVPQLK	SFQKI	2		669.4319204	1336.848241	0.000451244	18	N	58	70
P62082	Infl	LTAVH	DAILEDLVFPSEIVGKR	IRVKL	3		634.3513251	1900.030575	0.0007646	5	N	126	143
P62082	Infl	GVYKK	LTGKDVNFEFPEFQL	-	2		892.4492242	1782.882848	0.000451244	6	N	179	194
P62082	Infl	RPRSR	TLTAVHDAILEDLVFPSEIVGK	RIRVK	2		1184.144463	2366.273325	0.000451244	6	N	120	142
P62082	Infl	RSRTL	TAVHDAILEDLVFPSEIVGKR	IRVKL	4		578.0684734	2308.242694	0.000451244	5	N	122	143
P62082	Infl	KLTGK	DVNFEFPEFQL	-	2		692.8251394	1383.634679	0.002080925	5	N	183	194
P62082	Infl	RSRTL	TAVHDAILEDLVFPSEIVGK	RIRVK	3		718.3883275	2152.141583	0.002519933	1	N	122	142
P62082	Infl	LTAVH	DAILEDLVFPSEIVGK	RIRVK	2		872.9725321	1743.929464	0.00307782	1	N	126	142
P62137	Infl	YDLLR	LFEYGGFPPESNYLFLGDYVDR	GKQSL	2		1299.613527	2597.211453	0.000451244	16	N	74	96
P62137	Infl	LLAYK	IRYPENFFLLR	GNHEC	3		489.942272	1466.803416	0.002080925	2	N	111	122
P62137	Infl	EAPLK	ICGDIHGQYYDLLR	LFEYG	3	C2:+57.021	574.9474913	1721.819074	0.000451244	9	N	60	74
P62137	Infl	EVVAK	FLHKHDLDLICR	AHQVV	3	C11:+57.021	522.9455335	1565.8132	0.002981883	1	N	234	246
P62137	Infl	SRPGK	NVQLTENEIR	GLCLK	2		608.3205555	1214.625511	0.002296037	1	N	26	36
P62141	Infl	TDLLR	LFEYGGFPPEANYLFLGDYVDR	GKQSL	2		1291.616069	2581.216539	0.000451244	8	N	73	95
P62141	Infl	LLAYK	IKYPENFFLLR	GNHEC	3		480.6068893	1438.797268	0.000823681	5	N	110	121
P62192	Infl	MATNR	IETLDPALIRPGR	IDRKI	3		484.2845863	1449.830359	0.000823681	3	N	333	346
P62192	Infl	MKVEK	APQETYADIGGLDNQIQEIK	ESVEL	2		1102.048019	2202.080439	0.000451244	11	N	178	198
P62196	Infl	NAKVR	LLREELQLLQEQGSYVGEVVR	AMDKK	3		820.1153784	2457.322735	0.000451244	4	N	57	78
P62196	Infl	YYLSK	IEELQLIVNDK	SQNLR	2		657.3697141	1312.723828	0.000451244	2	N	27	38
P62204	Infl	REAFR	VFDKDGNGYISAAELR	HVMTN	2		877.9395549	1753.86351	0.000451244	68	N	91	107
P62204	Infl	IAEFK	EAFSLFDKDGDGTITTK	ELGTV	2		922.9497853	1843.883971	0.000451244	29	N	14	31
P62204	Infl	ARKMK	DTDSEEEIREAFR	VFDKD	3		532.9099135	1595.70634	0.002727428	1	N	78	91
P62204	Infl	REAFR	VFDKDGNGYISAAEL	RHVMT	2		799.8889993	1597.762399	0.000637154	2	N	91	106
P62242	Infl	KKNAK	ISSLLEEQFQQGK	LLACI	2		753.8940847	1505.772569	0.000823681	9	N	157	170
P62242	Infl	KYRAL	RLDVGNFSWGSECCTR	KTRII	3	C13:+57.021,C14:+57.021	648.6212952	1942.840486	0.001871652	1	N	58	74
P62242	Infl	GQCGR	ADGYVLEGKELEFY	LRKIK	2		816.8937504	1631.771901	0.00091018	4	N	184	198
P62259	Infl	ETELK	LICCDILDVLDKHLIPAANTGESK	VFYYK	3	C3:+57.021,C4:+57.021	899.1315149	2694.371145	0.000451244	10	N	94	118
P62259	Infl	CRLAK	AAFDDAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1086.874913	3257.601339	0.000451244	17	N	196	225
P62259	Infl	CRLAK	AAFDDAIAELDTLSEESYK	DSTLI	2		1044.486929	2086.958258	0.000451244	20	N	196	215
P62259	Infl	ETELK	LICCDILDVLDK	HLIPA	2	C3:+57.021,C4:+57.021	738.8755291	1475.735458	0.000451244	12	N	94	106
P62259	Infl	CRLAK	AAFDDAIAELDTLSEESY	KDSTL	2		980.4394474	1958.863295	0.000451244	15	N	196	214
P62259	Infl	GDYHR	YLAEFATGNDRK	EAAEN	2		692.8469375	1383.678275	0.000451244	6	N	130	142
P62259	Infl	GNDRK	EAAENSLVAYK	AASDI	2		597.8042069	1193.592814	0.000451244	14	N	142	153

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62259	Infl	FSVFY	YEILNSPDR	ACRLA	2		553.7779921	1105.540384	0.001463592	1	N	181	190
P62259	Infl	ELKLI	CCDILDVLDK	HLIPA	2	C1:+57.021,C2:+57.021	625.791465	1249.56733	0.000622848	1	N	96	106
P62264	Infl	IFASF	NDTFVHVTDLSGKETICR	VTGGM	2	C17:+57.021	1046.510319	2091.005037	0.000451244	7	N	37	55
P62264	Infl	KGKEK	KEEQVISLGPQVAEGENVFGVCHIFASF	NDTFV	3	C22:+57.021	1031.178336	3090.511607	0.000451244	7	N	9	37
P62264	Infl	KGKEK	KEEQVISLGPQVAEGENVFGVCHIF	ASFND	2	C22:+57.021	1393.694825	2785.37405	0.000823681	1	N	9	34
P62264	Infl	GKEKK	EEQVISLGPQVAEGENVFGVCHIFASF	NDTFV	3	C21:+57.021	988.4800145	2962.416643	0.000662267	5	N	10	37
P62264	Infl	IFASF	NDTFVHVTDLSGK	ETICR	2		716.8575022	1431.699404	0.000451244	3	N	37	50
P62264	Infl	MKIGR	IEDVTPIPSDSTR	RKGGR	2		715.3626174	1428.709635	0.001352548	1	N	128	141
P62267	Infl	GCLNF	IEENDEVLVAGFGR	KGHAV	2		774.3891665	1546.762733	0.000451244	8	N	93	107
P62267	Infl	KNGKK	ITAFVPNDGCLNFIEENDEVLVAGFGR	KGHAV	3	C10:+57.021	999.4871691	2995.438107	0.000451244	10	N	80	107
P62267	Infl	IKNGK	KITAFVPNDGCLNFIEENDEVLVAGFGR	KGHAV	3	C11:+57.021	1042.18549	3123.53307	0.000451244	9	N	79	107
P62281	Infl	SPCFR	DVQIGDIVTVGECRPLSK	TVRFN	2	C13:+57.021	993.5201549	1985.02471	0.000451244	6	N	118	136
P62281	Infl	LSPCF	RDVQIGDIVTVGECRPLSK	TVRFN	2	C14:+57.021	1071.57071	2141.125821	0.002080925	1	N	117	136
P62315	Infl	GNNIR	YFILPDSLPLDTLL	VDVEP	2		810.4507042	1618.885808	0.000451244	4	N	66	80
P62317	Infl	ELQKR	EEEEFNTGPLSVLTQSVK	NNTQV	2		1004.000007	2005.984413	0.000451244	17	N	19	37
P62317	Infl	EELQK	REEEEFNTGPLSVLTQSVK	NNTQV	2		1082.050562	2162.085524	0.000622848	1	N	18	37
P62320	Infl	GVPIK	VLHEAEGHIVTCETNTGEVYRGK	LIEAE	4	C12:+57.021	650.570096	2598.249184	0.001763695	1	N	8	31
P62320	Infl	GVPIK	VLHEAEGHIVTCETNTGEVYR	GKLIE	2	C12:+57.021	1207.574178	2413.132757	0.000451244	25	N	8	29
P62320	Infl	GVPIK	VLHEAEGHIVTCETNTGEVY	RGKLI	2	C12:+57.021	1129.523623	2257.031646	0.001463592	7	N	8	28
P62331	Infl	RIRDR	NWYVQPSCATSGDGLYEGLTWLTSNYKS	-	3	C8:+57.021	1066.489238	3196.444315	0.000451244	6	N	147	175
P62331	Infl	RIRDR	NWYVQPSCATSGDGLYEGLTWLTSNYK	S-	3	C8:+57.021	1037.478562	3109.412286	0.000451244	10	N	147	174
P62334	Infl	ENDLK	ALQSVGQIVGEVLK	QLTEE	2		720.9251879	1439.834776	0.000451244	7	N	48	62
P62334	Infl	IRELR	EVIELPLTNPELFQR	VGIIP	2		899.4914234	1796.967247	0.000451244	5	N	146	161
P62334	Infl	CNFLK	VVSSSIVDKYIGESAR	LIREM	3		570.640987	1708.899561	0.001654178	2	N	197	213
P62492	Infl	AFAEK	NGLSFIETSALDSTNVEAAFQTILTEIYR	IVSQK	3		1068.542262	3202.603387	0.000451244	19	N	145	174
P62492	Infl	TDEAR	AFAEKNGLSFIETSALDSTNVEAAFQTILTEIYR	IVSQK	3		1250.635662	3748.883585	0.002296037	1	N	140	174
P62715	Infl	GISPR	GAGYTFGQDISETFNHANGLTLVSR	AHQLV	3		885.7652968	2654.272491	0.001162105	3	N	214	239
P62715	Infl	WCHDR	NVVTIFSAPNYCYR	CGNQA	2	C12:+57.021	852.4144301	1702.81326	0.000451244	11	N	254	268
P62715	Infl	VWKYF	TDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIR	ALDRL	4	C19:+57.021	979.0018778	3911.976311	0.002080925	1	N	146	181
P62715	Infl	DDTLK	YSFLQFDPAPR	RGEPH	2		670.8358414	1339.656083	0.000622848	1	N	283	294
P62715	Infl	NHESR	QITQVYGFYDECLR	KYGNA	2	C12:+57.021	896.4224521	1790.829304	0.000451244	5	N	121	135
P62715	Infl	KAFTK	ELDQWVEQLNECK	QLNEN	2	C12:+57.021	845.8909848	1689.76637	0.000870037	2	N	8	21
P62746	Infl	IVFSK	DEFPEVYVPTVFENYVADIEVDGK	QVELA	2		1387.658328	2773.301056	0.000451244	9	N	27	51
P62746	Infl	GACGK	TCLLIVFSKDEFPEVYVPTVFENYVADIEVDGK	QVELA	3	C2:+57.021	1279.306111	3834.894932	0.000451244	1	N	18	51
P62751	Infl	KAYVR	LAPDYDALDVANKIGII	-	2		900.9912562	1799.966912	0.000637154	3	N	139	156
P62751	Infl	KAYVR	LAPDYDALDVANK	IGII-	2		702.8544282	1403.693256	0.000622848	9	N	139	152
P62754	Infl	FYEKR	MATEVAADALGEEWKGY	VVRIS	2		920.9252565	1839.834913	0.000622848	4	N	31	48
P62754	Infl	-MK	LNISFPATGCQK	LIEVD	2	C10:+57.021	668.3402024	1334.664805	0.000451244	9	N	2	14
P62754	Infl	-	MKLNISFPATGCQK	LIEVD	2	C12:+57.021	797.9079268	1593.800254	0.0007646	4	N	0	14
P62754	Infl	KKGEK	DIPGLTDTTVPR	RLGPK	2		642.8438635	1283.672127	0.002080925	1	N	119	131
P62774	Infl	FLLLK	GADINAPDKHHITPLLSAVYEGHVSCVK	LLLSK	3	C26:+57.021	1010.182191	3027.523174	0.000451244	11	N	57	85
P62774	Infl	DKTVK	GPDGLTALEATDNQAIK	ALLQ-	2		857.4368451	1712.85809	0.000451244	11	N	97	114
P62774	Infl	LEGGR	KPLHYAADCGQLEILEFLLLK	GADIN	3	C9:+57.021	824.4507792	2470.328938	0.000451244	13	N	36	57
P62806	Infl	RKVLR	DNIQGITKPAIR	RLARR	2		663.3809475	1324.746295	0.000451244	48	N	24	36
P62806	Infl	GGVKR	ISGLIYEETRGVLK	VFLEN	2		789.4490272	1576.882454	0.00091018	4	N	46	60
P62806	Infl	RGVLK	VFLENVIR	DAVTY	2		495.293081	988.5705621	0.000451244	397	N	60	68
P62806	Infl	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	2		1053.055451	2104.095301	0.000451244	5	N	60	78
P62806	Infl	GGVKR	ISGLIYEETR	GVLKV	2		590.8145747	1179.613549	0.000451244	39	N	46	56
P62806	Infl	HRKVL	RDNIQGITKPAIR	RLARR	2		741.431503	1480.847406	0.000662267	1	N	23	36
P62814	Infl	ARGQK	IPIFSAAGLPHNEIAAQICR	QAGLV	2	C19:+57.021	1089.578339	2177.141077	0.000451244	5	N	188	208
P62814	Infl	RLTYK	TVSGVNGPLVILDHVKFPR	YAEIV	4		512.7972604	2047.157842	0.000622848	2	N	48	67
P62814	Infl	PYENR	TVYETLDIGWQLLR	IFPKE	2		853.959759	1705.903918	0.001395409	2	N	471	485
P62814	Infl	VQAMK	AVVGEEALTSDDLLYLEFLQKFEK	NFITQ	3		919.8131422	2756.416027	0.002296037	1	N	436	460
P62814	Infl	VSGSK	AVVQVFEGTSGIDAK	KTSCE	2		760.9019097	1519.788219	0.000451244	7	N	93	108
P62814	Infl	IITPR	LALTTAEFLAYQCEK	HVLVI	3	C13:+57.021	586.6311688	1756.870106	0.001352548	1	N	276	291
P62814	Infl	VQAMK	AVVGEEALTSDDLLYLEFLQK	FEKNF	2		1177.112828	2352.210056	0.000451244	9	N	436	457
P62814	Infl	VKFPR	YAEIVHLTLPDGTKR	SGQVL	4		428.989229	1711.925716	0.001329271	1	N	67	82
P62814	Infl	QLHNR	QIYPPINVLPSLSR	LMKSA	2		798.959562	1595.903524	0.001699387	2	N	386	400
P62814	Infl	VQAMK	AVVGEEALTSDDLLY	LEFLQ	2		797.8964901	1593.77738	0.001162105	2	N	436	451
P62814	Infl	QKFEK	NFITQGPYENR	TVYET	2		669.826005	1337.63641	0.001395409	1	N	460	471
P62827	Infl	DISAK	SNYNFEKPFLWLAR	KLIGD	2		892.9600934	1783.904587	0.000622848	1	N	152	166
P62827	Infl	FHTNR	GPIKFNVWDTAGQEK	FGGLR	2		845.4339084	1688.852217	0.001591523	4	N	56	71
P62827	Infl	RGPIK	FNVWDTAGQEK	FGGLR	2		647.8072809	1293.598962	0.000451244	7	N	60	71
P62827	Infl	EFEKK	YVATLGVEVHPLVFHTNR	GPIKF	4		513.7816103	2051.095241	0.000451244	8	N	38	56
P62830	Infl	SGAKF	RISLGLPVGAVINCADNTGAK	NLYII	2	C14:+57.021	1063.573253	2125.130906	0.000451244	7	N	14	35

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62830	Infl	GAKFR	ISLGLPVGAVINCADNTGAK	NLYII	2	C13:+57.021	985.5226976	1969.029795	0.000451244	8	N	15	35
P62830	Infl	GVFLY	FEDNAGVIVNNK	GEMKG	2		660.3336629	1318.651726	0.000451244	10	N	97	109
P62835	Infl	FALVY	SITAQSTFNDLQDLR	EQILR	2		854.9291872	1707.842774	0.000451244	7	N	82	97
P62835	Infl	ESSAK	SKINVNEIFYDLVR	QINRK	3		570.6460724	1708.914817	0.000451244	7	N	149	163
P62835	Infl	GGVGK	SALTVQFVQGIFVEK	YDPTI	2		833.4646772	1664.913754	0.000451244	15	N	16	31
P62835	Infl	FALVY	SITAQSTFNDLQDLREQILR	VKDTE	3		783.4121949	2347.213185	0.000451244	2	N	82	102
P62835	Infl	DLYMK	NGQGFALVYSITAQSTFNDLQDLREQILR	VKDTE	3		1099.900784	3296.678952	0.000451244	10	N	73	102
P62835	Infl	SAKSK	INVNEIFYDLVR	QINRK	2		747.9017127	1493.787825	0.000451244	11	N	151	163
P62835	Infl	GGVGK	SALTVQFVQGIFVEKYDPTIEDSYR	KQVEV	3		969.1593125	2904.454537	0.000451244	5	N	16	41
P62835	Infl	DLYMK	NGQGFALVYSITAQSTFNDLQDLR	EQILR	3		886.7773139	2657.308542	0.002981883	1	N	73	97
P62858	Infl	KGPVR	EGDVLTLLESER	EARRL	2		680.8518855	1359.688171	0.000451244	10	N	51	63
P62858	Infl	KGPVR	EGDVLTLLESEREAR	RLR-	3		572.9641297	1715.868989	0.000823681	2	N	51	66
P62869	Infl	GLAFR	ADDTFEALRIEPFSSPPELPDVMKPQDSGGSANEQAVQ	-	3		1358.308056	4071.900769	0.001699387	1	N	80	118
P62869	Infl	LDDGK	TLGECGFTSQTARPQAPATVGLAFR	ADDTF	3	C5:+57.021	879.446868	2635.317204	0.000451244	7	N	55	80
P62874	Infl	IRDAR	KACADATLSQITNNIDPVGR	IQMRT	2	C3:+57.021	1072.54215	2143.0687	0.000451244	5	N	22	42
P62874	Infl	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	C14:+57.021,C31:+57.021	1174.509101	3520.503903	0.000451244	11	N	219	251
P62874	Infl	SKSGR	LLLAGYDDFNCNVWDALKADR	AGVLA	2	C11:+57.021	1235.097289	2468.178979	0.000451244	5	N	283	304
P62874	Infl	SKSGR	LLLAGYDDFNCNVWDALK	ADRAG	2	C11:+57.021	1064.014705	2126.013811	0.000622848	4	N	283	301
P62880	Infl	IRDAR	KACGDSTLTQITAGLDPVGR	IQMRT	2	C3:+57.021	1030.525969	2059.036337	0.000451244	15	N	22	42
P62880	Infl	DSMCR	QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	3	C31:+57.021	1170.528644	3508.562533	0.000451244	38	N	219	251
P62880	Infl	LFDLR	ADQELLMYSHDNIICGITSVAFSR	SGRLL	3	C15:+57.021	914.1075239	2739.299172	0.000451244	2	N	256	280
P62880	Infl	VRVSR	ELPGHTGYLSCCR	FLDDN	2	C11:+57.021,C12:+57.021	775.3480015	1548.680403	0.000451244	1	N	137	150
P62880	Infl	APDGR	TFVSGACDASIK	LWDVR	2	C7:+57.021	628.3032855	1254.590971	0.000451244	8	N	197	209
P62880	Infl	RDARK	ACGDSTLTQITAGLDPVGR	IQMRT	2	C2:+57.021	966.478487	1930.941374	0.000451244	7	N	23	42
P62880	Infl	APDGR	TFVSGACDASIKLWDVR	DSMCR	2	C7:+57.021	962.9832082	1923.950816	0.000735798	2	N	197	214
P62880	Infl	SRSGR	LLLAGYDDFNCNIWDAMKGDR	AGVLA	3	C11:+57.021	829.7196002	2486.135401	0.000451244	1	N	283	304
P62880	Infl	AIPLR	SSWVMTCAYAPSGNFVACGGLDNICSIYSLK	TREGN	3	C7:+57.021,C18:+57.021,C25:+57.021	1143.51885	3427.533151	0.001162105	2	N	96	127
P62889	Infl	GKYYR	VCTLAIIDPGDSDIIR	SMPEQ	2	C2:+57.021	879.4590346	1756.902469	0.000451244	8	N	90	106
P62889	Infl	AMLAK	TGVHHYSGNNIELGTACGK	YYRVC	3	C17:+57.021	672.3185354	2013.932206	0.000823681	7	N	68	87
P62908	Infl	EFLTR	ELAEDGYSGVEVR	VTPTR	2		712.3391423	1422.662685	0.000451244	19	N	27	40
P62908	Infl	KVATR	GLCAIAQAESLR	YKLLG	2	C3:+57.021	644.8378268	1287.660054	0.000451244	3	N	94	106
P62908	Infl	KIGPK	KPLPDHVSIVEPKDEILPTTPISEQK	GGKPE	3		970.866129	2909.574987	0.000451244	2	N	201	227
P62908	Infl	KIGPK	KPLPDHVSIVEPK	DEILP	3		486.9492037	1457.824211	0.000451244	15	N	201	214
P62908	Infl	VVQKR	FGFPEGSVELY	AEKVA	2		622.7958506	1243.576101	0.002296037	1	N	76	87
P62960	Infl	RKYLR	SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	YAADR	3		1158.229183	3471.664149	0.000622848	3	N	99	135
P62960	Infl	RGPPR	NYQQNYQNSESGEKNEGSESAPEGQAQQR	RPYRR	3		1086.470777	3256.38893	0.001162105	1	N	154	183
P62960	Infl	RPYAR	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	QNMYR	4		806.6384172	3222.522469	0.000622848	3	N	202	232
P62960	Infl	VEGEK	GAEAANVTGPGGVPVQGSKY	AADRN	2		929.9688437	1857.922087	0.000451244	17	N	116	136
P62960	Infl	VEGEK	GAEAANVTGPGGVPVQGSK	YAADR	2		848.4371794	1694.858759	0.000451244	12	N	116	135
P62960	Infl	RKYLR	SVGDGETVEFDVVEGEK	GAEAA	2		898.4157753	1794.815951	0.000662267	6	N	99	116
P62962	Infl	AVPGK	TFVSITPAEVGVLVGKDR	SSFFV	2		944.5310799	1887.04656	0.000451244	18	N	38	56
P62962	Infl	VGKDR	SSFFVNGLTLGGQK	CSVIR	2		727.8860627	1453.756525	0.000451244	61	N	56	70
P62962	Infl	LGGQK	CSVIRDSLLQDGEFTMDLR	TKSTG	3	C1:+57.021	752.3650459	2254.071738	0.000451244	3	N	70	89
P62962	Infl	AVPGK	TFVSITPAEVGVLVGK	DRSSF	2		808.9670527	1615.918505	0.000451244	56	N	38	54
P62962	Infl	IVGYK	DSPSVWAAVPGK	TFVSI	2		607.3147418	1212.613884	0.001463592	4	N	26	38
P62962	Infl	GWNAY	IDSLMADGTCQDAAIVGYKDSPSVWAAVPGK	TFVSI	3	C10:+57.021	1074.853412	3221.536836	0.000622848	3	N	7	38
P62962	Infl	CSVIR	DSLLQDGEFTMDLR	TKSTG	2		820.3857671	1638.755934	0.000451244	8	N	75	89
P62962	Infl	AIVGY	KDSPSVWAAVPGK	TFVSI	2		671.3622234	1340.708847	0.00091018	6	N	25	38
P62962	Infl	VLVGK	DRSSFFVNGLTLGGQK	CSVIR	2		863.4500898	1724.88458	0.00307782	1	N	54	70
P62962	Infl	PGKTF	VSITPAEVGVLVGKDR	SSFFV	2		820.4730336	1638.930467	0.000451244	1	N	40	56
P62962	Infl	PGKTF	VSITPAEVGVLVGK	DRSSF	2		684.9090065	1367.802413	0.000823681	1	N	40	54
P62983	Infl	HYCGK	CCLTYCFNKPEDK	-	2	C1:+57.021,C2:+57.021,C6:+57.02	867.8676782	1733.719756	0.000451244	18	N	143	156
P62983	Infl	TLTGK	TITLEVEPSDTIENVKAK	IQDKE	2		994.0338494	1986.052099	0.000451244	6	N	11	29
P62983	Infl	TLTGK	TITLEVEPSDTIENVK	AKIQD	2		894.4678109	1786.920022	0.000451244	30	N	11	27
P62983	Infl	LEDGR	TLSDYNIQKESTL	HLVLR	2		756.3835498	1510.7515	0.000823681	4	N	54	67
P62983	Infl	NVKAK	IQDKEGIPPDQQR	LIFAG	3		508.5991221	1522.773966	0.001162105	3	N	29	42
P62996	Infl	EVFSK	YGPIADVSIVYDQQSR	RSRGF	2		905.9526623	1809.889725	0.000451244	19	N	140	156
P62996	Infl	HVGNR	ANPDPNCCLGVFGLSLYTTER	DLREV	2	C7:+57.021,C8:+57.021	1192.554169	2383.092738	0.000622848	15	N	111	132
P62996	Infl	SRRSR	GFAFVYFENVDDAK	EAKER	2		811.3808101	1620.74602	0.000979378	2	N	159	173
P63005	Infl	DMTIK	LWDFQGFECIR	TMHGH	2	C9:+57.021	735.8456519	1469.675704	0.000451244	7	N	175	186
P63005	Infl	LDFHK	TAPYVVTGSVDQTVK	VWECR	2		782.9150171	1563.814434	0.000451244	13	N	390	405
P63017	Infl	IFEVK	STAGDTHLGGEDFDNR	MVNHF	2		846.366951	1690.718302	0.000451244	28	N	220	236
P63017	Infl	AKLDK	SQIHDIVLVGGSTR	IPKIQ	2		741.4076936	1480.799787	0.000451244	16	N	328	342
P63017	Infl	LRDAK	LDKSQIHDIVLVGGSTR	IPKIQ	2		919.5106788	1837.005758	0.000451244	17	N	325	342

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63017	Infl	NDSQR	QATKDAGTIAGLNVLR	IINEP	2		814.4604575	1626.905315	0.000451244	4	N	155	171
P63017	Infl	DQGNR	TTPSYVAFTDTER	LIGDA	2		744.3547923	1486.693985	0.000451244	35	N	36	49
P63017	Infl	LNVLR	IINEPTAAAIAYGLDKK	VGAER	2		894.4992484	1786.982897	0.000451244	12	N	171	188
P63017	Infl	AYLGK	TVTNAVVTVPAYFNDSQR	QATKD	2		991.5030507	1980.990501	0.000451244	47	N	137	155
P63017	Infl	VLIKR	NTTIPTKQTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3		1177.253552	3528.737255	0.000451244	2	N	416	447
P63017	Infl	KGETK	SFYPEEVSSMVLTK	MKEIA	2		808.897979	1615.780358	0.001871652	2	N	112	126
P63017	Infl	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2		1387.66755	2773.3195	0.000451244	38	N	423	447
P63017	Infl	KELNK	SINPDEAVAYGAAVQAAILSGDK	SENVQ	2		1130.576944	2259.138288	0.000451244	20	N	361	384
P63017	Infl	GGGTF	DVSILTIEDGIFEVK	STAGD	2		839.4514325	1676.887265	0.000451244	11	N	205	220
P63017	Infl	ERAKR	TLSSSTQASIEIDSLYEGIDFY	TSITR	2		1220.07664	2438.137679	0.000451244	59	N	272	294
P63017	Infl	VGAER	NVLIFDLGGGTFDVSILTIEDGIFEVK	STAGD	2		1456.27112	2910.52664	0.000451244	7	N	193	220
P63017	Infl	TSITR	ARFEELNADLFR	GTLDP	2		740.8813116	1479.747023	0.000451244	6	N	299	311
P63017	Infl	PKIQK	LLQDFFNGKELNK	SINPD	2		783.4202697	1564.824939	0.000451244	4	N	348	361
P63017	Infl	TFTTY	SDNQPGVLIQVYEGER	AMTKD	2		902.4477441	1802.879888	0.000451244	15	N	431	447
P63017	Infl	RQATK	DAGTIAGLNVLR	IINEP	2		600.3412909	1198.666982	0.0025889	1	N	159	171
P63017	Infl	KELNK	SINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPL	SLGIE	3		1304.016431	3909.025892	0.000622848	8	N	361	399
P63017	Infl	EDKQK	ILDKCNEIISWLDK	NQTAE	2	C5:+57.021	873.9586705	1745.901741	0.000622848	3	N	569	583
P63017	Infl	-MSK	GPAVGIDLGTTYSCVGVFQHGK	VEIIA	3	C14:+57.021	755.0444122	2262.109837	0.000451244	10	N	3	25
P63017	Infl	GDAAK	NQVAMNPTNTVFDAK	RLIGR	2	M5:+15.995	833.3992515	1664.782903	0.0007646	2	N	56	71
P63017	Infl	PKIQK	LLQDFFNGK	ELNKS	2		541.2879957	1080.560391	0.000451244	6	N	348	357
P63017	Infl	PPAPR	GVPQIEVTFDIDANGILNVSAVDK	STGKE	2		1257.658466	2513.301331	0.000451244	45	N	469	493
P63017	Infl	LGTTY	SCVGVFQHGKVEIIANDQGNR	TTPSY	2	C2:+57.021	1164.579598	2327.143596	0.000451244	6	N	15	36
P63017	Infl	AYLGK	TVTNAVVTVPAYF	NDSQR	2		691.3722568	1380.728914	0.001162105	2	N	137	150
P63017	Infl	VGAER	NVLIFDLGGGTF	DVSIL	2		626.8327674	1251.649935	0.000998612	2	N	193	205
P63017	Infl	EAVAY	GAAVQAAILSGDK	SENVQ	2		600.8332987	1199.650997	0.000451244	4	N	371	384
P63017	Infl	NVLIF	DLGGGTFDVSILTIEDGIFEVK	STAGD	2		1163.097178	2324.178756	0.000451244	7	N	198	220
P63017	Infl	TSITR	ARFEELNADLF	RGTLD	2		662.8307561	1323.645912	0.002813207	1	N	299	310
P63017	Infl	-MSK	GPAVGIDLGTTY	SCVGV	2		582.3013001	1162.587	0.002453667	1	N	3	15
P63028	Infl	MIIYR	DLISHDELFSDIYK	IREIA	3		565.6144379	1693.819914	0.000823681	6	N	5	19
P63028	Infl	SDIYK	IREIADGLCLEVEGK	MVSRT	2	C9:+57.021	851.4459272	1700.876254	0.000451244	7	N	19	34
P63028	Infl	-MIIY	RDLISHDELFSDIYK	IREIA	3		617.6481416	1849.921025	0.000451244	5	N	4	19
P63028	Infl	QKPER	VKPFMTGAAEQIK	HILAN	3		473.927523	1418.759169	0.001839721	1	N	110	123
P63038	Infl	CALLR	CIPALDSLKPANEDQK	IGIEI	2	C1:+57.021	899.9541164	1797.892633	0.000451244	7	N	446	462
P63038	Infl	NIGAK	LVQDVANNTNEEAGDGTTTATVLAR	SIAKE	2		1280.628425	2559.24125	0.000451244	31	N	96	121
P63038	Infl	HIEKR	IQEITEQLDITTSEYEKEK	LNERL	2		1149.0739	2296.1322	0.000451244	4	N	370	389
P63038	Infl	SKGQK	CEFQDAYVLLSEK	KISSV	2	C1:+57.021	801.3797216	1600.743843	0.000451244	5	N	236	249
P63038	Infl	ANAHR	KPLVIIAEDVDGEALSTLVLNR	LKVGL	2		1183.171012	2364.326423	0.002663018	1	N	268	290
P63038	Infl	MTIAK	NAGVEGSLIVEK	ILQSS	2		608.3331316	1214.650663	0.000823681	1	N	481	493
P63038	Infl	MKFDR	GYISPYFINTSK	GQKCE	2		695.3566067	1388.697613	0.002519933	1	N	221	233
P63038	Infl	TKVVR	TALLDAAGVASLLTTAEAVVTEIPKEEK	DPGMG	3		947.5221394	2839.543018	0.000451244	18	N	526	554
P63038	Infl	NIGAK	LVQDVANNTNEEAGDGTTTATVL	ARSIA	2		1167.059313	2332.103025	0.000823681	3	N	96	119
P63038	Infl	LLSEK	KISSVQSIVPALEIANAHR	KPLVI	4		509.04353	2032.14292	0.002212458	1	N	249	268
P63085	Infl	PGKHY	LDQLNHILGILGSPSQEDLNCIINLK	ARNYL	3	C21:+57.021	973.1869425	2916.537427	0.000451244	3	N	231	257
P63085	Infl	LPKEK	LKELIFEETAR	FQPGY	3		450.2544042	1347.739813	0.002727428	2	N	340	351
P63094	Infl	ACYER	SNEYQLIDCAQYFLDKIDVIK	QADYV	3	C9:+57.021	859.0968418	2574.267125	0.001654178	1	N	165	186
P63094	Infl	PEFAR	YTTPEDATPEPGEDPR	VTRAK	2		887.8924674	1773.769335	0.000451244	8	N	317	333
P63101	Infl	SLLEK	FLIPNASQPESK	VFYLK	2		665.8542312	1329.692862	0.000451244	8	N	103	115
P63101	Infl	IMQLL	RDNLTLWTSDTQGDEAEAGEGGEN	-	2		1283.052747	2564.089894	0.000451244	48	N	221	245
P63101	Infl	GDDKK	GIVDQSQQAYQEAFEISKK	EMQPT	2		1085.04528	2168.07496	0.000451244	9	N	139	158
P63101	Infl	AACMK	SVTEQGAELSNEERNLLSVAYK	NVVGA	2		1219.114422	2436.213244	0.000451244	8	N	27	49
P63101	Infl	GDDKK	GIVDQSQQAYQEAFEISK	KEMQP	2		1020.997798	2039.979996	0.000451244	28	N	139	157
P63101	Infl	MQLLR	DNLTLWTSDTQGDEAEAGEGGEN	-	2		1205.002192	2407.988783	0.000451244	32	N	222	245
P63101	Infl	ETELR	DICNDVLSLLEK	FLIPN	2	C3:+57.021	709.8637073	1417.711815	0.000451244	42	N	91	103
P63101	Infl	EYREK	IETELRDICNDVLSLLEK	FLIPN	2	C9:+57.021	1080.564759	2159.113919	0.000451244	13	N	85	103
P63101	Infl	CSLAK	TAFDEAIAELDTLSEESYK	DSTLI	2		1066.500036	2130.984473	0.000451244	28	N	193	212
P63101	Infl	CSLAK	TAFDEAIAELDTLSEESY	KDSTL	2		1002.452555	2002.88951	0.000451244	17	N	193	211
P63101	Infl	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1101.550318	3301.627554	0.000451244	9	N	193	222
P63101	Infl	AACMK	SVTEQGAELSNEER	NLLSV	2		774.8609702	1547.70634	0.000451244	44	N	27	41
P63101	Infl	AGDDK	KGIVDQSQQAYQEAFEISK	KEMQP	2		1085.04528	2168.07496	0.000451244	5	N	138	157
P63101	Infl	CSLAK	TAFDEAIAELDTLSEESYKDSTL	IMQLL	2		1274.595394	2547.175187	0.000451244	5	N	193	216
P63101	Infl	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLL	RDNLT	3		1049.516614	3145.526443	0.002453667	2	N	193	221
P63101	Infl	ETELR	DICNDVLSLLEKFLIPNASQPESK	VFYLK	3	C3:+57.021	910.805839	2729.394117	0.001352548	1	N	91	115
P63139	Infl	AKDAK	ECVQECVSEFISFITSEASER	CHQEK	2	C2:+57.021,C6:+57.021	1254.056938	2506.098277	0.000451244	4	N	83	104
P63147	Infl	ILQNR	WSPTYDVSSILTSIQSLLDEPNPNSPANSQAAQLYQENKR	EYEKR	4		1116.300913	4461.17245	0.000451244	11	N	95	135
P63147	Infl	ILQNR	WSPTYDVSSILTSIQSLLDEPNPNSPANSQAAQLY	QENKR	3		1269.618559	3805.832278	0.002296037	1	N	95	130

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63242	Infl	HGHAK	VHLVGIDIFTGK	KYEDI	2		649.8775093	1297.739419	0.001463592	3	N	55	67
P63242	Infl	VPNIK	RNDFQLIGIQDGYLSLLQDSGEVR	EDLRL	2		1368.701727	2735.387855	0.000451244	7	N	85	109
P63242	Infl	PNIKR	NDFQLIGIQDGYLSLLQDSGEVREDLR	LPEGD	3		1031.854952	3092.541455	0.000451244	9	N	86	113
P63242	Infl	PNIKR	NDFQLIGIQDGYLSLLQDSGEVR	EDLRL	2		1290.651172	2579.286744	0.000451244	47	N	86	109
P63242	Infl	EIEQK	YDCGEEILITVLSAMTEEAAVAIK	AMAK-	2	C3:+57.021	1313.653446	2625.291292	0.0007646	1	N	126	150
P63276	Infl	ERERR	DNYVPEVSALDQEIIEVDPDTK	EMLKL	2		1245.100646	2488.185692	0.000451244	23	N	81	103
P63276	Infl	KEMLK	LLDFGSLSNLQVTQPTVGMNFK	TPRGA	2		1205.12829	2408.24098	0.000451244	7	N	107	129
P63276	Infl	ERERR	DNYVPEVSALDQEIIEVDPDTKEMLK	LLDFG	3		997.4903995	2989.447798	0.001162105	2	N	81	107
P63276	Infl	EERER	RDNYVPEVSALDQEIIEVDPDTK	EMLKL	3		882.4367344	2644.286803	0.000451244	4	N	80	103
P63280	Infl	AITIK	QILLGIQELLNEPNIQDPAQAEAYTIYCQNR	VEYEK	3	C28:+57.021	1205.942277	3614.803432	0.000451244	14	N	110	141
P63280	Infl	AITIK	QILLGIQELLNEPNIQDPAQAEAY	TIYCQ	2		1340.695579	2679.375559	0.000451244	17	N	110	134
P63280	Infl	AITIK	QILLGIQELLNEPNIQDPAQAEAYTIY	CQNRV	3		1019.864677	3056.57063	0.000698008	3	N	110	137
P63321	Infl	SYRKK	VVLDGEEVQIDILDTAGQEDYAAIRDNYFR	SGEGF	3		1143.227114	3426.657942	0.001162105	1	N	54	84
P67778	Infl	LIELR	KLEAAEDIAYQLSR	SRNIT	2		803.9259162	1605.836232	0.000451244	15	N	239	253
P67778	Infl	SQLPR	IYTSIGEDYDERVLPSITTEILK	SVVAR	3		885.7974921	2654.369076	0.000451244	6	N	105	128
P67778	Infl	EGDSK	AAELIANSLATAGDGLIELR	KLEAA	2		999.5474583	1997.079317	0.000451244	30	N	219	239
P67778	Infl	FDRFR	GVQDIVVGEGTHFLIPWVQKPIIFDCR	SRPRN	3	C26:+57.021	1041.886827	3122.637082	0.000451244	17	N	43	70
P67778	Infl	EQQKK	AAIISAEGDSKAAELIANSLATAGDGLIELR	KLEAA	3		1014.210736	3039.608807	0.000451244	8	N	208	239
P67778	Infl	RAATF	GLILDDVSLTHLTFGKEFTEAVEAK	QVAQQ	2		1367.22143	2732.42726	0.000451244	1	N	161	186
P67778	Infl	ESIGK	FGLALAVAGGVVNSALYNVDAGHR	AVIFD	3		791.089275	2370.244425	0.001329271	1	N	11	35
P67778	Infl	YQLSR	SRNITYLPAGQSVLLQLPQ	-	2		1049.586918	2097.158236	0.000451244	6	N	253	272
P67778	Infl	LSRSR	NITYLPAGQSVLLQLPQ	-	2		928.020348	1854.025096	0.000451244	17	N	255	272
P67778	Infl	SQLPR	IYTSIGEDYDER	VLPSI	2		730.8311501	1459.6467	0.000622848	16	N	105	117
P67778	Infl	RAATF	GLILDDVSLTHLTFGK	EFTEA	2		864.9806915	1727.945783	0.000637154	1	N	161	177
P67778	Infl	RSRPR	NVPVITGSKDLQNVNITLR	ILFRP	2		1041.089825	2080.164049	0.0025889	1	N	74	93
P67778	Infl	ITGSK	DLQNVNITLR	ILFRP	2		593.3334659	1184.651332	0.000622848	7	N	83	93
P67778	Infl	SVVAR	FDAGELITQR	ELVSR	2		575.2990917	1148.582583	0.001591523	2	N	133	143
P67871	Infl	FCGLR	GNEFFCEVDEDYIQDKFNLTGLNEQVPHYR	QALDM	3	C6:+57.021	1226.226854	3675.657162	0.000451244	5	N	17	47
P67871	Infl	FCGLR	GNEFFCEVDEDYIQDK	FNLTG	2	C6:+57.021	1004.417761	2006.819921	0.000451244	1	N	17	33
P67984	Infl	KVNGK	AGNLGGGVVTIER	SKSKI	2		621.8441978	1241.672796	0.000451244	6	N	52	65
P67984	Infl	QVLKF	TLDCTHPVEDGIMDAANFEQFLQER	IKVNG	3	C4:+57.021	979.4448644	2935.311193	0.000979378	1	N	21	46
P67984	Infl	ESYEL	RYFQINQDEEEEEDED	-	2		1044.419775	2086.823949	0.000451244	5	N	112	128
P67984	Infl	SYELR	YFQINQDEEEEEDED	-	2		966.3692191	1930.722838	0.002884417	1	N	113	128
P68033	Infl	YNELR	VAPEEHPTLLTEAPLNPK	ANREK	2		978.5259945	1955.036389	0.000451244	12	N	97	115
P68033	Infl	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	3		1153.21946	3456.63498	0.000451244	4	N	70	97
P68033	Infl	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	2		1473.189942	2944.364284	0.000622848	1	N	70	93
P68033	Infl	DIKEK	LCYVALDFENEMATAASSSSLEK	SYELP	2	C2:+57.021,M12:+15.995	1276.580521	2551.145442	0.000451244	6	N	217	240
P68033	Infl	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHR	KCF-	3	M19:+15.995	1367.346146	4099.015037	0.000451244	2	N	338	374
P68033	Infl	ILTLK	YPIEHGIITNWDDMEK	IWHHT	2		980.9596307	1959.903661	0.000451244	12	N	70	86
P68033	Infl	DIKEK	LCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNER	FRCPE	3	C2:+57.021,M12:+15.995	1442.014307	4323.019521	0.000823681	1	N	217	256
P68033	Infl	VRDIK	EKLCYVALDFENEMATAASSSSLEK	SYELP	2	C4:+57.021,M14:+15.995	1405.149299	2808.282998	0.000823681	3	N	215	240
P68033	Infl	ELRVA	PEEHPTLLTEAPLNPK	ANREK	2		893.4732306	1784.930861	0.000451244	8	N	99	115
P68033	Infl	AQSKR	GILTLKYPIEHGIITNWDDMEK	IWHHT	3		862.7811197	2585.319959	0.000451244	7	N	64	86
P68033	Infl	NELRV	APEEHPTLLTEAPLNPK	ANREK	2		928.9917875	1855.967975	0.000622848	4	N	98	115
P68037	Infl	KPATK	TDQVIQSLIALVNDPQPEHPLRADLAEEYSK	DRKKF	4		873.2024814	3488.778726	0.001654178	1	N	100	131
P68037	Infl	KPATK	TDQVIQSLIALVNDPQPEHPLR	ADLAE	2		1242.166792	2482.317984	0.00091018	1	N	100	122
P68037	Infl	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDK	GAFRI	2		1426.727411	2851.439222	0.000451244	7	N	23	48
P68037	Infl	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDKGAFR	IEINF	3		1095.230241	3282.667324	0.000451244	12	N	23	52
P68040	Infl	VSCVR	FSPNSSNPIIVSCGWDK	LVKVW	2	C13:+57.021	954.4517409	1906.887882	0.000451244	16	N	155	172
P68040	Infl	STSSK	AEPPQCTSLAWSADGQTLFAGYTDNLVR	VWQVT	3	C6:+57.021	1023.485828	3067.434084	0.000451244	20	N	280	308
P68040	Infl	VGHTK	DVLSVAFSSDNR	QIVSG	2		655.3232952	1308.63099	0.000451244	13	N	106	118
P68040	Infl	DLEGK	IIVDELKQEVISTSSK	AEPPQ	2		895.0018209	1787.988042	0.000622848	1	N	264	280
P68040	Infl	LGVCK	YTVQDESHSEWVSCVR	FSPNS	2	C14:+57.021	991.4393618	1980.863124	0.000451244	14	N	139	155
P68040	Infl	LNEGK	HLYTLDGGDIINALCFSPNR	YWLCA	2	C15:+57.021	1138.560343	2275.105086	0.000451244	13	N	225	245
P68040	Infl	NCKLK	TNHIGHTGYLNTVTVSPDGSLCASGGK	DGQAM	2	C22:+57.021	1372.159138	2742.302676	0.000451244	2	N	185	212
P68040	Infl	FSPNR	YWLCAATGPSIK	IWDLE	2	C4:+57.021	683.8451206	1365.674641	0.000622848	8	N	245	257
P68040	Infl	GVCKY	TVQDESHSEWVSCVR	FSPNS	2	C13:+57.021	909.9076975	1817.799795	0.000451244	1	N	140	155
P68040	Infl	DGTLR	LWDLTTGTTTR	RFVGH	2		632.8307561	1263.645912	0.001763695	3	N	88	99
P68254	Infl	GDDRK	QTIENSQGAYQEAFDISKK	EMQPT	3		719.6873247	2156.038574	0.000451244	9	N	139	158
P68254	Infl	FSVFY	YEILNNPELACTLAK	TAFDE	2	C11:+57.021	874.9483027	1747.881005	0.000451244	15	N	178	193
P68254	Infl	ESELR	SICTTVLELLDKYLIANATNPESK	VFYLK	3	C3:+57.021	898.4740893	2692.398868	0.000451244	15	N	91	115
P68254	Infl	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1105.882068	3314.622803	0.000451244	18	N	193	222
P68254	Infl	CTLAK	TAFDEAIAELDTLNEDSYK	DSTLI	2		1072.997661	2143.979722	0.000451244	8	N	193	212
P68254	Infl	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLL	RDNLT	3		1053.848364	3158.521692	0.002296037	2	N	193	221
P68254	Infl	MQLLR	DNLTLWTSDSAGEECDAAEGAEN	-	2	C15:+57.021	1227.995821	2453.976041	0.00307782	1	N	222	245

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68254	Infl	IMQLL	RDNLTLWTSDSAGEECDAAEGAEN	-	2	C16:+57.021	1306.046376	2610.077152	0.000451244	5	N	221	245
P68368	Infl	DVVPK	DVNAAIAAIK	TKRSI	2		493.2879957	984.5603914	0.002296037	1	N	326	336
P68368	Infl	AIKTK	RSIQFVDWCPTGFK	VGINY	3	C9:+57.021	580.9560982	1739.844895	0.000451244	5	N	338	352
P68368	Infl	IKTKR	SIQFVDWCPTGFK	VGINY	2	C8:+57.021	792.8796917	1583.743783	0.000451244	19	N	339	352
P68368	Infl	MPSDK	TIGGGDDSFTTFFCETGAGK	HVPRA	2	C14:+57.021	1034.452135	2066.88867	0.000451244	22	N	40	60
P68368	Infl	KHVPR	AVFVDLEPTVIDEIRNGPYR	QLFHP	2		1152.105672	2302.195743	0.000451244	2	N	64	84
P68368	Infl	KHVPR	AVFVDLEPTVIDEIR	NGPYR	2		858.4648742	1714.914148	0.000451244	26	N	64	79
P68368	Infl	IKTKR	SIQFVDWCPTGFKVGINYQPPTVVPGGDLAK	VQRAV	3	C8:+57.021	1130.91159	3389.711369	0.000451244	11	N	339	370
P68368	Infl	TNLNR	LISQIVSSITASLR	FDGAL	2		744.4437448	1486.87189	0.000451244	80	N	229	243
P68368	Infl	KHVPR	AVFVDLEPTVIDEIRNGPY	RQLFH	2		1074.055116	2146.094632	0.000451244	6	N	64	83
P68368	Infl	NNYAR	GHYTIGKEIIDPVLDR	IRKLS	2		913.4944974	1824.973395	0.000451244	3	N	105	121
P68368	Infl	DRIRK	LSDQCTGLQGFLVFHSFGGGTGSGFTSLLMER	LSVDY	3	C5:+57.021	1136.211711	3405.611733	0.000622848	3	N	124	156
P68368	Infl	YTIGK	EIIDPVLDR	IRKLS	2		535.2985604	1068.581521	0.0007646	14	N	112	121
P68368	Infl	MAALE	KDYEEVGIDSYEDEDEGEE	-	2		1125.44057	2248.86554	0.000451244	1	N	429	448
P68368	Infl	LDRIR	KLSDQCTGLQGFLVFHSFGGGTGSGFTSLL	MERLS	3	C6:+57.021	1040.181969	3117.522506	0.000451244	3	N	123	153
P68369	Infl	DVVPK	DVNAAIATIK	TKRTI	2		508.293278	1014.570956	0.000451244	34	N	326	336
P68369	Infl	MPSDK	TIGGGDDSFNTFFSETGAGK	HVPRA	2		1004.450681	2006.885762	0.000451244	34	N	40	60
P68369	Infl	IKTKR	TIQFVDWCPTGFK	VGINY	2	C8:+57.021	799.8875168	1597.759434	0.000451244	8	N	339	352
P68369	Infl	KHVPR	AVFVDLEPTVIDEVR	TGTYR	2		851.4570492	1700.898498	0.000451244	37	N	64	79
P68369	Infl	KHVPR	AVFVDLEPTVIDEVRTGTY	RQLFH	3		708.7006826	2123.078648	0.000451244	1	N	64	83
P68369	Infl	TNLNR	LIGQIVSSITASLR	FDGAL	2		729.4384624	1456.861325	0.000451244	12	N	229	243
P68369	Infl	NNYAR	GHYTIGKEIIDLVLDR	IRKLA	2		921.5101474	1841.004695	0.000451244	2	N	105	121
P68369	Infl	YTIGK	EIIDLVLDR	IRKLA	2		543.3142105	1084.612821	0.000823681	9	N	112	121
P68369	Infl	MPSDK	TIGGGDDSFNTFFSETGAGKHVPR	AVFVD	3		833.0634542	2496.166963	0.001264573	1	N	40	64
P68369	Infl	IKTKR	TIQFVDWCPTGFKVGINYQPPTVVPGGDLAK	VQRAV	3	C8:+57.021	1135.583473	3403.727019	0.000622848	3	N	339	370
P68369	Infl	AALEK	DYEEVGVDSVEGEGEEEGEEY	-	2		1174.956584	2347.897568	0.001162105	1	N	430	451
P68369	Infl	DRIRK	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	LSVDY	3	C5:+57.021	1130.880073	3389.616818	0.000622848	4	N	124	156
P68369	Infl	LDRIR	KLADQCTGLQGFLVFHSFGGGTGSGFTSLL	MERLS	3	C6:+57.021	1034.85033	3101.527591	0.001591523	3	N	123	153
P68369	Infl	DRIRK	LADQCTGLQGFLVFHSFGGGTGSGFTSLL	MERLS	3	C5:+57.021	992.1520093	2973.432628	0.001162105	1	N	124	153
P68372	Infl	LQLER	INVYYNEATGGK	YVPRA	2		664.8282134	1327.640827	0.000451244	15	N	46	58
P68372	Infl	LQLER	INVYYNEATGGKYVPR	AVLVD	2		922.4710222	1842.926444	0.000451244	7	N	46	62
P68372	Infl	LVSEY	QQYQDATAEEEGEFEEEAEEEVA	-	2		1330.536261	2659.056922	0.000622848	1	N	422	445
P68404-2	Infl	GVTTK	TFCGTPDYIAPEIIAYQPYGK	SVDWW	2	C3:+57.021	1202.58041	2403.145219	0.000637154	2	N	499	520
P68404-2	Infl	QEVIR	NIDQSEFEGFSFVNSEFLKPEVK	S-	2		1345.65338	2689.29116	0.000622848	1	N	649	672
P68433	Infl	KTDLR	FQSSAVMALQEACEAY	LVGLF	2	M7:+15.995,C13:+57.021	910.8954531	1819.775306	0.000451244	5	N	84	100
P68433	Infl	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	2	C4:+57.021,C18:+57.021	1326.625323	2651.235045	0.000451244	17	N	93	116
P68433	Infl	SSAVM	ALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C6:+57.021,C20:+57.021	946.126541	2835.356223	0.000451244	10	N	91	116
P68433	Infl	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C13:+57.021,C27:+57.021	1196.238895	3585.693285	0.000451244	22	N	84	116
P68433	Infl	TDLRF	QSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	Q1:-17.027,M6:+15.995,C12:+57.021,C26:+57.021	860.4060178	3437.592871	0.001264573	1	N	85	116
P68510	Infl	ASAMK	AVTELNEPLSNEDRNLLSVAYK	NVVGA	3		825.7628933	2474.26528	0.000622848	2	N	28	50
P68510	Infl	SGEKK	NSVVEASEAAYKEAFEISK	EHMQP	2		1036.513281	2071.010962	0.000451244	7	N	143	162
P68510	Infl	THPIR	LGLALNFSVFYYEIQNAPEQACLLAK	QAFDD	3	C22:+57.021	991.512767	2971.514901	0.000451244	10	N	172	198
P68510	Infl	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1110.213817	3327.618052	0.000451244	9	N	198	227
P68510	Infl	FSVFY	YEIQNAPEQACLLAK	QAFDD	2	C11:+57.021	874.4381022	1746.860604	0.000451244	7	N	183	198
P68510	Infl	ASAMK	AVTELNEPLSNEDR	NLLSV	2		793.886988	1585.758376	0.000451244	35	N	28	42
P68510	Infl	EKIEK	ELETVCNDVLALLDK	FLIKN	2	C6:+57.021	866.4455929	1730.875586	0.000451244	7	N	91	106
P68510	Infl	AYREK	IEKELETVCNDVLALLDK	FLIKN	2	C9:+57.021	1051.556403	2101.097206	0.000823681	1	N	88	106
P68510	Infl	EKIEK	ELETVCNDVLALLDKFLIK	NCNDF	2	C6:+57.021	1117.111346	2232.207091	0.000451244	6	N	91	110
P68510	Infl	IMQLL	RDNLTLWTSDQQDEEAGEGN	-	2		1139.496879	2276.978159	0.000451244	11	N	226	246
P70168	Infl	KFLER	AAVENLPTFLVELSR	VLANP	2		829.959759	1657.903918	0.000451244	16	N	27	42
P70168	Infl	KFYAK	GALQYLVPILTQTLTKQDENDDDDDWNPCK	AAGVC	3	C29:+57.021	1169.219476	3504.635029	0.000451244	2	N	316	346
P70168	Infl	KFYAK	GALQYLVPILTQTLTK	QDEND	2		880.0223594	1758.029119	0.002374549	1	N	316	332
P70168	Infl	WTVGR	ICELLPEAAINDVYLAPLLQCLIEGLSAEPR	VASNV	3	C2:+57.021,C21:+57.021	1160.942296	3479.803487	0.000451244	21	N	434	465
P70168	Infl	SNNVK	LAATNALLNSLEFTK	ANFDK	2		803.4464845	1604.877369	0.000451244	13	N	191	206
P70168	Infl	GEFKK	YLEVVLNTLQQASQAQVDK	SDFDM	2		1074.071298	2146.126995	0.000451244	11	N	730	749
P70168	Infl	TEHMK	ESTLEAIGYICQDIDPEQLQDK	SNEIL	2	C11:+57.021	1283.105174	2564.194748	0.000451244	11	N	147	169
P70168	Infl	GIGLK	NYAEYQVCLAAVGLVGDLCR	ALQSN	3	C8:+57.021,C19:+57.021	757.7016149	2270.081445	0.00307782	1	N	659	679
P70168	Infl	STSDR	IQFNDLQSLLCATLQNVLR	KVQHQ	2	C11:+57.021	1123.602011	2245.188421	0.000451244	10	N	574	593
P70168	Infl	FILSF	IDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLK	LVEAR	3	C17:+57.021,C26:+57.021	1218.590873	3652.749219	0.000622848	2	N	800	835
P70168	Infl	SAEPR	VASNVCWAFSSLAEAAYEAADVADDQEEPATY	CLSSS	3	C6:+57.021	1150.837032	3449.487696	0.00091018	1	N	465	497
P70168	Infl	FILSF	IDHIAGDEDHTDGVVACAAGLIGDLCTAFGK	DVLKL	3	C17:+57.021,C26:+57.021	1066.832745	3197.474835	0.000451244	5	N	800	831
P70168	Infl	QTLTK	QDENDDDDDWNPCK	AAGVC	2	C13:+57.021	883.3160352	1764.61647	0.000451244	9	N	332	346
P70168	Infl	ENVHR	SVKPQILSVFGDIALAIGGEFKK	YLEVV	4		605.1010449	2416.37298	0.000451244	6	N	707	730

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P70268	Infl	QSEPR	SWSLLEQLGLAGADLAAPGVQQQLELERER	LKREI	3		1093.244551	3276.710252	0.000451244	11	N	11	41
P70268	Infl	STVLK	LDNTVVGQTAWKPCGPNAWDQSFTLELER	ARELE	3	C14:+57.021	1111.538704	3331.592711	0.000451244	7	N	399	428
P70268	Infl	QSEPR	SWSLLEQLGLAGADLAAPGVQQQLELER	ERLKR	3		998.1966492	2991.566548	0.000451244	14	N	11	39
P70268	Infl	QPFFR	SLGWDVLLAR	RLPPP	2		565.3223699	1128.62914	0.000622848	5	N	879	889
P70268	Infl	KIVYR	DLKLDNLLLDTEGYVK	IADFG	3		617.0038139	1847.988042	0.001654178	1	N	743	759
P70268	Infl	MQLRR	ALQALQAGELESQAAPDEAQGDPELGAVELR	IEELR	3		1059.528904	3175.563313	0.000451244	1	N	186	217
P70268	Infl	RLLRR	LIPSAVATGTFSPNASPGAEIR	HTGDI	2		1078.571465	2155.127329	0.000451244	3	N	524	546
P70290	Infl	LKTVR	TAELSPFIVFIAPTDQGTQTEALQQLQK	DSEAI	3		1025.540193	3073.597179	0.000451244	16	N	389	417
P70290	Infl	LKTVR	TAELSPFIVFIAPTDQGTQTEALQQLQKDSEAIR	SQYAH	3		1249.314811	3744.921033	0.000451244	3	N	389	423
P70290	Infl	EAGLK	FVTGDIIQIINKDDSNWWQGR	VEGSS	3		835.756073	2504.244819	0.000451244	3	N	185	206
P70290	Infl	LQEWR	VASVAHSAPSEAPSCSPFGK	KKKCK	2	C15:+57.021	993.4732047	1984.930809	0.001162105	1	N	227	247
P70290	Infl	AGLKF	VTGDIIQIINKDDSNWWQGR	VEGSS	3		786.7332683	2357.176405	0.000662267	1	N	186	206
P70290	Infl	ETLKK	LQEAFDQACSSPQWVPVSWVY	-	2	C9:+57.021	1249.078565	2496.141531	0.000451244	2	N	445	466
P70296	Infl	VVNMK	GNDISSGTVLSDYVGSGPPSGTGLHR	YVWLV	2		1265.612578	2529.209556	0.000698008	2	N	93	119
P70296	Infl	TGLHR	YVWLVYEQEQPLSCDEPILSNK	SGDNR	2	C14:+57.021	1355.657377	2709.299154	0.000451244	23	N	119	141
P70296	Infl	QHALR	VDYAGVTVDELGK	VLTPT	2		683.3489787	1364.682357	0.000451244	16	N	26	39
P70296	Infl	SGTVL	SDYVGSGPPSGTGLHR	YVWLV	2		793.88204	1585.74848	0.002727428	2	N	103	119
P70315	Infl	SLFSR	AGISEAQLTDAETSKLIYDFIEDQGGLEAVR	QEMRR	3		1113.891731	3338.651794	0.000451244	4	N	275	306
P70315	Infl	RPGGR	GGPAVQQNIPSNLLQDHENQR	LFELL	2		1158.078508	2314.141417	0.000637154	1	N	15	36
P70315	Infl	PPPCR	GGGGGGGGGGGGGGGGGGGQPLRPPVVGSNK	GRSGP	3		773.3835211	2317.127163	0.001463592	3	N	323	353
P70315	Infl	AETSK	LIYDFIEDQGGLEAVR	QEMRR	2		919.4706879	1836.925776	0.000451244	2	N	290	306
P70315	Infl	SGGPL	SLGLVTVDIQNPDITSSR	YRGLP	2		958.0107086	1914.005817	0.000823681	1	N	195	213
P70335	Infl	LRDPK	SEVNSDCLLDGLDALVYDLDFPALRK	NKNID	3	C7:+57.021	980.155308	2937.442524	0.000451244	12	N	22	48
P70335	Infl	WETLR	DTVAPVVPDLSSDIDTSNFDDLEEDKGDEETFPIPK	AFVGN	3		1317.279938	3948.816413	0.000622848	5	N	349	385
P70349	Infl	DEIAK	AQVAQPGGDTIFGK	IIRKE	2		694.8625875	1387.709575	0.000451244	19	N	7	21
P70349	Infl	EIPAK	IIFEDDRCLAFHDISPQAPTHFLVIPK	KHISQ	4	C8:+57.021	795.6645278	3178.626911	0.000823681	2	N	30	57
P70349	Infl	FEDDR	CLAFHDISPQAPTHFLVIPK	KHISQ	3	C1:+57.021	764.4053928	2290.192778	0.000451244	4	N	37	57
P70372	Infl	RFDKR	SEAEEAITSFNGHKPPGSSEPITVK	FAANP	3		871.4333243	2611.276573	0.000451244	8	N	157	182
P70372	Infl	QEELR	SLFSSIGEVESAK	LIRDK	2		677.3489787	1352.682357	0.000622848	1	N	37	50
P70388	Infl	YKKQK	ETELNGVAVQLNECEKHR	EKINK	3	C14:+57.021	709.3483833	2125.02175	0.002813207	1	N	976	994
P70388	Infl	HIRAR	DSLIQSLATHLELDGFER	GPFSE	3		682.0168937	2043.027281	0.000622848	1	N	367	385
P70398	Infl	AGVAK	LEGDNVNPESQLIQQNEQSESEKAGSTK	YRLVG	3		1020.485364	3058.432693	0.000451244	5	N	1834	1862
P70398	Infl	RTGQR	AQENYEGGEEVSPPQTK	GSVKC	2		931.9242988	1861.832998	0.000451244	8	N	2535	2552
P70398	Infl	DLLAK	LAWDFSPEQLDHLFDCFK	ASWTN	3	C16:+57.021	756.6862248	2267.035275	0.002145581	3	N	455	473
P70398	Infl	PVNLR	EQHDALEFFNSLVDSLDEALK	ALGHP	3		807.3925774	2419.154332	0.001395409	3	N	1681	1702
P70398	Infl	DLKRK	WTWAVEWLGDELER	RPYTG	2		895.4313657	1788.847131	0.000451244	1	N	2414	2428
P70398	Infl	LKQIR	EICSLFGEAPQNLSQSQR	SPHVF	2	C3:+57.021	1032.494668	2062.973737	0.000451244	1	N	574	592
P70441	Infl	LNAVR	LLVVDPETDERLK	KLGVS	2		763.9253849	1525.83517	0.00307782	1	N	87	100
P70441	Infl	GQFIR	AVDPDSPAEASGLR	AQDRI	2		692.8393094	1383.663019	0.000451244	13	N	175	189
P70441	Infl	DSPKR	QVSTEPSSTSSSSSDPILDLNISLAVAK	ERAHQ	2		1417.219813	2832.424025	0.000451244	4	N	300	328
P70441	Infl	LAGDR	LVEVNGENVEKETHQQVVSR	IRAAL	2		1147.590917	2293.166234	0.001839721	1	N	58	78
P70441	Infl	FKKCK	VIPSQEHLDGPLPEPFSNGEIQK	ESSRE	3		844.4312551	2530.270365	0.001763695	1	N	238	261
P70444	Infl	PSLLR	DVFHTTVNFINQNLFSYVR	NLVRN	2		1157.584906	2313.154213	0.000735798	6	N	168	187
P70444	Infl	GLGAE	HITDLLVFGFLQSSGCTR	QELEV	2	C16:+57.021	1026.022865	2050.03013	0.000451244	4	N	14	32
P70444	Infl	EVLGR	ELPVQAYWEADLEDELQTDGSQASR	SFNQG	2		1425.657379	2849.299159	0.000451244	2	N	40	65
P70460	Infl	LPRMK	SSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	2	C16:+57.021	1320.054398	2638.093196	0.000451244	19	N	316	341
P70460	Infl	TTLPR	MKSSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	3	C18:+57.021	966.7506818	2897.228645	0.000622848	4	N	314	341
P70460	Infl	IRGVK	YNQATPIFHQWR	DARQV	3		520.928914	1559.763342	0.000698008	4	N	71	83
P70670	Infl	FGEAK	IEDLSQQAQLAAAEK	FKVQG	2		807.9208308	1613.826062	0.000451244	39	N	2099	2114
P70670	Infl	IRKSK	NILFVITKPDVY	KSPAS	2		711.4060996	1420.796599	0.000451244	9	N	2072	2084
P70670	Infl	IRKSK	NILFVITKPDVYK	SPASD	2		775.4535812	1548.891562	0.000451244	4	N	2072	2085
P70670	Infl	TYIVF	GEAKIEDLSQQAQLAAAEK	FKVQG	2		1000.518898	1999.022196	0.002663018	1	N	2095	2114
P70698	Infl	SSIYR	VPLLLEEQGVVDYFLR	RLDLP	2		945.5227235	1889.029847	0.000622848	1	N	252	268
P70698	Infl	KLEIK	YIDSTDLEPSTLQEEPVRY	HEAWQ	2		1128.03986	2254.06412	0.000823681	3	N	335	354
P80313	Infl	EIIPR	QLCDNAGFDATNILNK	LRARH	2	C3:+57.021	897.4282658	1792.840932	0.000451244	13	N	447	463
P80313	Infl	VILLK	EGTDSSQGIPQLVSNISACQVIAEAVR	TTLGP	2	C19:+57.021	1415.206285	2828.396971	0.000451244	16	N	10	37
P80313	Infl	NAEIR	VHTVEDYQAIVDAEWNILYDKLEK	IHQSG	3		964.4874291	2890.438887	0.000451244	8	N	256	280
P80313	Infl	VDIAK	SQDAEVGDGTTSVTLLAAEFLK	QVKPY	2		1126.568785	2251.121969	0.000451244	17	N	84	106
P80313	Infl	PAMVR	INALTAASEAACLIVSVDETIKNPR	STVDP	2	C12:+57.021	1328.70265	2655.3897	0.00307782	1	N	499	524
P80313	Infl	PAMVR	INALTAASEAACLIVSVDETIK	NPRST	3	C12:+57.021	763.7387659	2288.192898	0.000451244	7	N	499	521
P80314	Infl	VDMSR	VQDDEVGDGTTSVTVLAAELLR	EAESL	2		1144.584966	2287.154332	0.000451244	20	N	89	111
P80314	Infl	FQVKR	QVLLSAAEAAEVILRVDNIIK	AAPRK	3		755.7779265	2264.310379	0.000622848	4	N	501	522
P80314	Infl	HVIKK	LGGSLADSYLDEGFLLDKK	IGVNQ	2		1021.028567	2040.041534	0.000451244	6	N	204	223
P80314	Infl	AETAR	LSSFIGAIAIGDLVK	STLGP	2		752.4432135	1502.870827	0.000451244	18	N	25	40
P80314	Infl	AGVER	LALVTGGEIASTFDHPELVK	LGSCK	2		1049.065484	2096.115368	0.000451244	4	N	322	342

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P80314	Infl	FQVKR	QVLLSAAEAAEVILR	VDNII	2		791.9623017	1581.909003	0.000735798	3	N	501	516
P80314	Infl	TKAAR	EALLSSAVDHGSDEAR	FWQDL	2		828.8953444	1655.775089	0.000451244	11	N	138	154
P80314	Infl	DEAER	SLHDALCVLAQTVKDPR	TVYGG	4	C7:+57.021	481.5087787	1922.003915	0.001329271	1	N	388	405
P80314	Infl	TIVLR	GATQQILDEAER	SLHDA	2		665.8340271	1329.652454	0.001871652	1	N	376	388
P80315	Infl	VELSK	AQDIEAGDGTTSVVIIAGSLLDSCTK	LLQKG	2	C24:+57.021	1311.152656	2620.289711	0.000451244	17	N	96	122
P80315	Infl	LVKKR	ALIAGGGAPEIELALR	LTEYS	2		775.9491943	1549.882789	0.000823681	4	N	419	435
P80315	Infl	KSILR	DALSDLALHFLNK	MKIMV	2		728.8938877	1455.772175	0.000451244	10	N	306	319
P80315	Infl	VEKAK	IGLIQFCLSAPK	TDMDN	2	C7:+57.021	673.8789634	1345.742327	0.002080925	2	N	245	257
P80315	Infl	KIVKK	LGGTIDDCELVEGLVLTQK	VANSG	2	C8:+57.021	1030.532928	2059.050256	0.000451244	9	N	213	232
P80315	Infl	KLLQK	GIHPTIISESFQK	ALEKG	3		486.2651918	1455.772175	0.000451244	4	N	126	139
P80315	Infl	LLIQK	SILRDALSDLALHFLNK	MKIMV	3		642.6989477	1925.073443	0.001839721	2	N	302	319
P80316	Infl	LTSEK	LGFAGVVQEISFGTTK	DKMLV	2		827.4464845	1652.877369	0.000451244	9	N	352	368
P80316	Infl	IKQIK	ETGANLAICQWGFDDEANHLLLQNGLPAVR	WVGGP	3	C9:+57.021	1108.214331	3321.619594	0.000451244	22	N	293	323
P80316	Infl	LPAVR	WVGGPEIELIAIATGGR	IVPRF	2		869.9784831	1737.941366	0.000451244	10	N	323	340
P80316	Infl	VELSK	SQDDEIGDGTTGVVVLAGALLEEAEQLLDR	GIHPI	3		1038.521527	3112.541181	0.000451244	25	N	96	126
P80316	Infl	VVDAK	IAILTCPFEPPKPK	TKHKL	3	C6:+57.021	537.6377065	1609.88972	0.000622848	5	N	247	261
P80316	Infl	KISDK	VLVDINNPEPLIQTAK	TTLGS	2		882.4992484	1762.982897	0.000451244	4	N	154	170
P80316	Infl	EEMIK	QIKETGANLAICQWGFDDEANHLLLQNGLPAVR	WVGGP	3	C12:+57.021	1231.293533	3690.857199	0.000451244	4	N	290	323
P80316	Infl	VELSK	SQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIR	IADGY	4		947.4936899	3785.943559	0.000662267	2	N	96	132
P80316	Infl	ARQVK	ESNPALGIDCLHK	GSNDM	3	C10:+57.021	485.2420156	1452.702647	0.002884417	1	N	483	496
P80317	Infl	LIIPK	VLAQNSGFDLQETLVK	VQAEH	2		881.4732306	1760.930861	0.000451244	11	N	449	465
P80317	Infl	SLIAK	VATAQDDITGDGTTSNVLIIGELLK	QADLY	2		1272.674313	2543.333025	0.000451244	22	N	79	104
P80317	Infl	LRAVK	NAIDDGCVVPGAGAVEVALAEALIK	YKPSV	2	C7:+57.021	1226.64153	2451.26746	0.000622848	6	N	399	424
P80317	Infl	SLRTK	VHAELADVLTEAVVDSILAIR	KKDEP	2		1117.623697	2233.231795	0.000451244	14	N	159	180
P80317	Infl	RTSLR	TKVHAELADVLTEAVVDSILAIR	KKDEP	2		1232.195018	2462.374436	0.000979378	2	N	157	180
P80317	Infl	SLIAK	VATAQDDITGDGTTSNVLIIGELLKQADLYISEGLHPR	IITEG	4		1006.777813	4023.080053	0.000451244	2	N	79	117
P80318	Infl	KVISR	WSSLACNIALDAVK	TVQFE	2	C6:+57.021	774.3982486	1546.780897	0.000451244	7	N	167	181
P80318	Infl	EVIPR	TLIQNCGASTIR	LLTSL	2	C6:+57.021	667.3485587	1332.681517	0.000698008	5	N	449	461
P80318	Infl	ACGAR	IVSRPEELREDDVGTGAGLLEIK	KIGDE	3		832.7821764	2495.323129	0.000622848	1	N	330	353
P81117	Infl	KTFFK	LHDVNNDGFLDEQELEALFTR	ELEKV	2		1238.09349	2474.171379	0.001162105	1	N	251	272
P81117	Infl	HPGSK	DQLKEVWEETDGLDPNDFDPK	TFFKL	2		1245.569513	2489.123426	0.002145581	1	N	226	247
P81117	Infl	DEYLK	QVIEVLETDPHFR	EKLQK	3		528.279501	1581.815103	0.000451244	5	N	59	72
P82198	Infl	RPQER	GDELADSALEIFK	QASAY	2		704.354261	1406.692922	0.000451244	14	N	642	655
P82198	Infl	PDSAK	TLLELAGESDVSTAIDILK	QAGLD	2		994.54405	1987.0725	0.000451244	16	N	377	396
P82198	Infl	TINGK	AVISNKDILATNGVIHFIDELLIPDSAK	TLLEL	4		752.4187338	3005.643735	0.000451244	3	N	349	377
P82198	Infl	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEK	IPAET	3		1012.184298	3033.529493	0.000451244	8	N	257	287
P82198	Infl	HLIDK	VISTITNNIQQIIEIEDTFETLR	AAVAA	2		1345.716512	2689.417424	0.000451244	14	N	234	257
P82198	Infl	VISNK	DILATNGVIHFIDELLIPDSAK	TLLEL	3		798.7692081	2393.284224	0.000451244	13	N	355	377
P82198	Infl	ETLNR	ILGDPEALRDLLNNHILK	SAMCA	4		511.7947177	2043.147671	0.000735798	5	N	295	313
P83870	Infl	SYQGR	CVICGGPGVSDAYYCK	ECTIQ	2	C1:+57.021,C4:+57.021,C15:+57.021	903.3862351	1804.75687	0.000451244	13	N	57	73
P83870	Infl	CTLVR	ICDECNYGSYQGR	CVICG	2	C2:+57.021,C5:+57.021	811.3221807	1620.628761	0.001463592	1	N	44	57
P83917	Infl	KQNKK	KVEEVLEEEEEEYVVEK	VLDRR	2		1055.010237	2108.004874	0.000451244	7	N	8	25
P83917	Infl	EYLLK	WKGFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	3	C19:+57.021	1247.561791	3739.661972	0.000451244	19	N	41	72
P83917	Infl	LLKWK	GFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	3	C17:+57.021	1142.837032	3425.487696	0.000451244	7	N	43	72
P84078	Infl	LHSLR	HRNWYIQATCATSGDGLYEGLDWLSNQLR	NQK-	3	C10:+57.021	1142.209469	3423.605007	0.000451244	13	N	149	178
P84078	Infl	SLRHR	NWYIQATCATSGDGLYEGLDWLSNQLR	NQK-	3	C8:+57.021	1044.489461	3130.444984	0.000451244	18	N	151	178
P84084	Infl	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSKR	-	4	C8:+57.021	839.9059776	3355.592711	0.000451244	5	N	151	180
P84084	Infl	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSK	R-	3	C8:+57.021	1067.505	3199.491599	0.000451244	20	N	151	179
P84089	Infl	EHLKR	MNPNSPSITYDISQLFDFIDDLADLSCLVYR	ADTQT	3	C27:+57.021	1208.241224	3621.700273	0.000622848	2	N	42	73
P84089	Infl	DISQL	FDFIDDLADLSCLVYR	ADTQT	2	C12:+57.021	981.4695993	1960.923599	0.000451244	2	N	57	73
P84089	Infl	CLVYR	ADTQTYQPYNKDWIK	EKIYV	2		935.9526623	1869.889725	0.001329271	1	N	73	88
P84091	Infl	EENIK	NNFVLIYELLDEILDFGYPQNSETGALK	TFITQ	3		1072.543603	3214.60741	0.000451244	1	N	102	130
P84091	Infl	FVLIY	ELLDEILDFGYPQNSETGALK	TFITQ	2		1176.584435	2351.15327	0.000451244	4	N	109	130
P84096	Infl	DTLRR	LKEQGQAPITPQQGQALAK	QIHAV	2		1003.555618	2005.095635	0.001463592	3	N	128	147
P84096	Infl	IHAVR	YLECSALQQDGVKEVFAEAVR	AVLNP	2	C4:+57.021	1206.597122	2411.178645	0.001699387	2	N	153	174
P84096	Infl	AVDGR	TVNLNLWDTAGQEEYDR	LRTLS	2		1012.471948	2022.928295	0.000451244	16	N	49	66
P84096	Infl	NAFPK	EYIPTVFDNYSAQSAVDGR	TVNLN	2		1066.500705	2130.98581	0.000451244	16	N	30	49
P84096	Infl	AVDGR	TVNLNLWDTAGQEEYDRLR	TLSYP	2		1147.064535	2292.11347	0.000823681	5	N	49	68
P84096	Infl	GAVGK	TCLLICYTTNAFPK	EYIPT	2	C2:+57.021,C6:+57.021	851.4206352	1700.82567	0.000451244	7	N	16	30
P84096	Infl	GAVGK	TCLLICYTTNAFPKEYIPTVFDNYSAQSAVDGR	TVNLN	3	C2:+57.021,C6:+57.021	1272.274773	3813.80092	0.001162105	1	N	16	49
P84096	Infl	LRRLK	EQGQAPITPQQGQALAK	QIHAV	2		882.9661041	1763.916608	0.000823681	3	N	130	147
P84099	Infl	CGKKK	VWLDPNETNEIANANSR	QQIRK	2		971.9668324	1941.918065	0.000451244	15	N	21	38
P84104	Infl	PLDCK	VYVGNLGNNGNKTELER	AFGYY	2		938.9797428	1875.943886	0.000451244	15	N	11	28
P84104	Infl	VWVAR	NPPGFAFVEFEDPRDAADAVR	ELDGR	2		1160.553803	2319.092007	0.000451244	10	N	43	64

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P84104	Infl	TELER	AFGYYGPLR	SVWVA	2		522.2696059	1042.523612	0.002813207	1	N	28	37
P84228	Infl	KTDLR	FQSSAVMALQEASEAY	LVGLF	2		866.3988745	1730.782149	0.000451244	3	N	84	100
P84228	Infl	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C27:+57.021	918.2068598	3668.796239	0.000451244	4	N	84	117
P84228	Infl	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1171.906176	3512.695128	0.000451244	17	N	84	116
P84244	Infl	KTDLR	FQSAAIGALQEASEAY	LVGLF	2		828.3997312	1654.783862	0.000451244	16	N	84	100
P84244	Infl	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C27:+57.021	899.2072882	3592.797953	0.000451244	5	N	84	117
P84244	Infl	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1146.573414	3436.696841	0.000451244	43	N	84	116
P85094	Infl	ELDGR	SQLQSVLLCGIETQACILNTALDLLHR	GLQVH	3	C9:+57.021,C16:+57.021	1022.874216	3065.599247	0.000451244	9	N	98	125
P85094	Infl	LKVAR	LLDVPILLTEQYPEGLGPTVPELGAQGIRPVSK	TCFSM	3		1167.319057	3498.93377	0.000622848	3	N	49	82
P97302	Infl	DEVCR	CVEFLSVHNIEESCFQFLK	FKFLD	3	C1:+57.021,C14:+57.021	796.0452701	2385.11241	0.001654178	1	N	108	127
P97310	Infl	DGMER	DYRPIPELDVYEAEGLALDDEDVEELTASQR	EAAER	3		1184.22896	3549.663481	0.000451244	11	N	79	110
P97310	Infl	PIGGR	YDPSLTFSENVDLTEPIISR	FDVLC	2		1148.571327	2295.127055	0.000451244	2	N	636	656
P97311	Infl	EKCQK	LFLDFLEEFQGSDGEIK	YLQFA	2		993.9889105	1985.962221	0.000451244	14	N	28	45
P97311	Infl	IRPER	NTLVVSFADLEQFNQQLSTTIQEEFYR	VYPYL	3		1074.198607	3219.572421	0.000622848	3	N	58	85
P97311	Infl	GQVVR	THPVHPELVSGTFLCLDCQTVIKDVEQQFK	YTQPN	4	C15:+57.021,C18:+57.021	882.1933708	3524.742283	0.000451244	2	N	143	173
P97311	Infl	LVVSF	ADLEQFNQQLSTTIQEEFYR	VYPYL	2		1230.58804	2459.16048	0.000451244	12	N	65	85
P97311	Infl	RFDLF	FILVDECNEVTDYAIAR	RIVDL	2	C7:+57.021	1014.491063	2026.966526	0.000998612	2	N	533	550
P97311	Infl	QAGLK	GSSEGSESYEEDPYLVVNPNYLLED	-	2		1403.117221	2804.218843	0.000622848	3	N	796	821
P97311	Infl	EKCQK	LFLDFLEEFQGSDGEIKY	LQFAE	2		1075.520575	2149.02555	0.000823681	3	N	28	46
P97315	Infl	AKCGK	GLESTTLADKDGEIYCK	GCYAK	2	C16:+57.021	950.4541463	1898.892693	0.000451244	13	N	151	168
P97315	Infl	MVCKK	NLDSTTVAVHGEEIYCK	SCYGK	2	C16:+57.021	968.4597629	1934.903926	0.000451244	8	N	42	59
P97315	Infl	GVCQK	TVYFAEEVQCEGNSFHK	SCFLC	2	C10:+57.021	1022.957387	2043.899175	0.000451244	5	N	15	32
P97315	Infl	NFGPK	GFGFGQGAGALVHSE	-	2		717.344562	1432.673524	0.001943752	1	N	178	193
P97315	Infl	KYGPK	GYGYGQGAGTLSTDKGESLG	IKHEE	2		959.4453984	1916.875197	0.002374549	1	N	69	89
P97351	Infl	GLKGR	VFEVSLADLQNDEVAFRK	FKLIT	3		694.0290222	2079.063667	0.000451244	2	N	65	83
P97351	Infl	GLKGR	VFEVSLADLQNDEVAFR	KFKLI	2		976.4921517	1950.968703	0.000451244	6	N	65	82
P97351	Infl	KGRVF	EVSLADLQNDEVAFR	KFKLI	2		853.4237377	1704.831875	0.000637154	2	N	67	82
P97363	Infl	AAHTK	EILDTALKEIDEVGDLLQLK	YSRHR	3		752.4180639	2254.230792	0.000451244	12	N	516	536
P97369	Infl	ALMRR	EFQREDIALSYQDAEGDLVR	LLSDE	2		1177.567108	2353.118615	0.000451244	22	N	276	296
P97369	Infl	ELSFK	AGDVIFLLSK	INKDW	2		531.8138463	1061.612093	0.000698008	8	N	192	202
P97369	Infl	EDTGK	TIKDIAVEEDLSSTPLFK	DLLAL	2		1003.538768	2005.061935	0.000451244	6	N	250	268
P97369	Infl	FLLSK	INKDWLEGTSQGATGIFPGSFVK	ILKDF	2		1226.629511	2451.243422	0.000451244	27	N	202	225
P97369	Infl	AQQLR	SESDFEQLPDDVAVSANIADIEEKR	GFTSH	2		1389.159755	2776.30391	0.000451244	9	N	8	33
P97369	Infl	GKTIK	DIAVEEDLSSTPLFK	DLLAL	2		832.4254147	1662.835229	0.000451244	12	N	253	268
P97369	Infl	AQQLR	SESDFEQLPDDVAVSANIADIEEK	RGFTS	2		1311.109199	2620.202799	0.000451244	22	N	8	32
P97369	Infl	GKTIK	DIAVEEDLSSTPLFKDLLALMR	REFQR	3		826.1054919	2475.293076	0.001463592	1	N	253	275
P97369	Infl	GSFVK	ILKDFPEDEDTTNWLR	CYFYE	2		996.489609	1990.963618	0.000451244	11	N	225	241
P97369	Infl	EDTGK	TIKDIAVEEDLSSTPLF	KDLLA	2		939.491286	1876.966972	0.000451244	13	N	250	267
P97369	Infl	RIFFY	QSAYDAEQVPQALRR	LRPRT	3		577.9644641	1730.869992	0.000735798	1	N	134	149
P97369	Infl	REFQR	EDIALSYQDAEGDLVR	LLSDE	2		897.4317597	1792.847919	0.000698008	1	N	280	296
P97369	Infl	NAYMK	NLLSLPVCVL	MDPDV	2	C8:+57.021	564.328575	1126.64155	0.000823681	9	N	114	124
P97369	Infl	RIFFY	QSAYDAEQVPQALR	RLRPR	2		788.3922405	1574.768881	0.001162105	2	N	134	148
P97370	Infl	VKMNR	IIDLIPDGYPQISCLPK	EENAT	2	C14:+57.021	971.5216349	1941.02767	0.0025889	1	N	177	194
P97371	Infl	VGDYR	QLVHELDEAEYQEIR	LMVME	2		936.4608515	1870.906103	0.000451244	14	N	198	213
P97371	Infl	VMEIR	NAYAVLYDIILK	NFEKL	2		698.3982746	1394.780949	0.000451244	6	N	220	232
P97371	Infl	VLLQR	LKPEIKDVTEQLNLVTTWLQLQIPR	IEDGN	3		992.5696469	2974.685541	0.001162105	7	N	116	141
P97371	Infl	KPEIK	DVTEQLNLVTTWLQLQIPR	IEDGN	2		1134.123865	2266.232129	0.000451244	21	N	122	141
P97371	Infl	DLCSK	TENLLGSYFPK	KISEL	2		634.8302247	1267.644849	0.000451244	2	N	24	35
P97372	Infl	VLDLR	AFYAELYHIISSNLEK	IVNPK	2		949.4888807	1896.962161	0.000622848	5	N	210	226
P97372	Infl	VDVFR	QNLFQEADDFLCTFLPR	KIISL	2	C12:+57.021	1057.504505	2112.99341	0.000451244	14	N	21	38
P97372	Infl	PGNEK	LLALLALVKPEVWTLK	EKCIL	3		603.0538918	1806.138275	0.000451244	13	N	99	115
P97372	Infl	TFLPR	KIISLSQLLQEDSLNVADLSSLR	APLDI	2		1271.70849	2541.40138	0.000451244	6	N	38	61
P97372	Infl	FLPRK	IISLSQLLQEDSLNVADLSSLR	APLDI	2		1207.661008	2413.306416	0.000451244	3	N	39	61
P97372	Infl	QVDVF	RQNLFQEADDFLCTFLPR	KIISL	3	C13:+57.021	757.3726403	2269.094521	0.001591523	1	N	20	38
P97372	Infl	TLKEK	CILVITWIQHLIPK	IEDGN	3	C1:+57.021	578.6763841	1733.005752	0.000823681	5	N	117	131
P97372	Infl	KIISL	SQLLQEDSLNVADLSSLR	APLDI	2		994.5188978	1987.022196	0.000451244	4	N	43	61
P97376	Infl	GAPHR	EVDEGPSPPEQFTAVKL	SDSRI	2		921.960153	1841.904706	0.001463592	1	N	85	102
P97376	Infl	GAPHR	EVDEGPSPPEQFTAVK	LSDSR	2		865.418121	1728.820642	0.000622848	3	N	85	101
P97384	Infl	RMYGK	SLYHDITGDTSGDYRK	ILLKI	2		914.4295514	1826.843503	0.000451244	2	N	477	493
P97384	Infl	IMVSR	SELDLLDIR	AEYKR	2		537.2960177	1072.576435	0.000451244	18	N	459	468
P97384	Infl	RKAMK	GFGTDEQAIIDCLGSR	SNKQR	2	C12:+57.021	869.9071662	1737.798732	0.002374549	1	N	212	228
P97384	Infl	LALMK	TPVLFDVYEIK	EAIKG	2		662.3639004	1322.712201	0.000451244	8	N	269	280
P97384	Infl	LALMK	TPVLFDVYEIKEAIK	GAGTD	3		588.9981117	1763.970935	0.000451244	7	N	269	284
P97384	Infl	KEAIK	GAGTDEACLIEIFASR	SNEHI	2	C8:+57.021	855.4120844	1708.808569	0.000451244	15	N	284	300
P97384	Infl	SLVQR	DVQELYAAGENR	LGTDE	2		682.826202	1363.636804	0.000698008	3	N	357	369

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P97384	Infl	AGENR	LGTDESKFNAILCSR	SRAHL	2	C13:+57.021	855.9279016	1709.840203	0.000451244	1	N	369	384
P97425	Infl	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDNISR	NCHNS	3	C17:+57.021,C24:+57.021	1055.833079	3164.475838	0.000451244	4	N	62	92
P97425	Infl	YQPRR	SLEYYTVACNPR	TPQDS	2	C9:+57.021	736.8458489	1471.676098	0.000870037	1	N	125	137
P97426	Infl	YQSRR	SLEYYTVACDPR	TPQDS	2	C9:+57.021	737.3378567	1472.660113	0.000451244	8	N	124	136
P97426	Infl	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDKR	SQNCH	4	C17:+57.021,C24:+57.021	745.6107452	2978.411781	0.002374549	1	N	62	90
P97450	Infl	FPTFK	FDDPKFEVIDKPQS	-	2		832.9124745	1663.809349	0.000451244	6	N	94	108
P97450	Infl	YKSKR	QASGGPVDIGPEYQQDLDRELYK	LKQMY	2		1289.625154	2577.234708	0.000451244	12	N	54	77
P97450	Infl	YKSKR	QASGGPVDIGPEYQQDLDRELY	KLKQM	2		1225.577672	2449.139745	0.000451244	8	N	54	76
P97492	Infl	QGEGR	GSSLSIHSLPSGPSSPFSTEEQPVASWAQSFER	LLQDP	3		1163.890613	3488.64844	0.000451244	1	N	37	70
P97492	Infl	STGNR	QTCDIEGLVELLNR	VQSSG	2	C3:+57.021	830.4224521	1658.829304	0.000451244	5	N	495	509
P97492	Infl	SRPGK	YCCVYLPDGTASLALAR	PGLTI	2	C2:+57.021,C3:+57.021	965.4635627	1928.911525	0.000451244	4	N	303	320
P97493	Infl	TRVCL	TTFNVQDGPDFQDR	VVNSE	2		820.3715051	1638.72741	0.000622848	1	N	59	73
P97496	Infl	APTNK	TLAGLVVQLLQFQEDAFGK	HVTNP	2		1039.070569	2076.125539	0.000451244	4	N	74	93
P97496	Infl	MNIEK	TLVQNNCLTRPNIYLIPDIDLK	LANKL	3	C7:+57.021	871.8075142	2612.399143	0.000451244	2	N	156	178
P97807	Infl	AAMPR	IYELAAGGTAVGTGLNTR	IGFAE	2		882.4684796	1762.921359	0.000451244	21	N	265	283
P97807	Infl	GSTLK	ETAIELGYLTAEQFDEWVKPK	DMLGP	3		823.0850848	2466.231854	0.000622848	4	N	480	501
P97807	Infl	KTAHK	NGSTLKETAIELGYLTAEQFDEWVKPK	DMLGP	4		767.646545	3066.55498	0.000823681	3	N	474	501
P97807	Infl	GILKR	AAAEVNQEYGLDPK	IASAI	2		752.8680669	1503.720534	0.00091018	1	N	98	112
P97807	Infl	ASVSF	TDNCVVGIQANTER	INKLM	2	C4:+57.021	788.8731263	1575.730653	0.000637154	1	N	427	441
P97814	Infl	NELVY	ASIEVQATQGNLNSSAQDYR	ALYDY	2		1076.517418	2151.019236	0.000451244	14	N	344	364
P97814	Infl	YEEVR	LTLEGCDVEGDINGFIQSK	STGRE	2	C6:+57.021	1048.004535	2093.993469	0.000451244	18	N	253	272
P97814	Infl	HGSPK	TTPSAPAASTETLTPTPER	NELVY	2		964.4845236	1926.953447	0.000451244	1	N	320	339
P97821	Infl	LIAGK	YAQDFGVVEESCFPYTAK	DSPCK	2	C12:+57.021	1055.975246	2109.934892	0.000451244	25	N	308	326
P97821	Infl	FRIRR	GTDECAIESIAVAAIPIPKL	-	2	C5:+57.021	1034.553663	2067.091727	0.000622848	4	N	442	462
P97821	Infl	HTGLS	DPFNPFELTNHAVLLVGYGRDPVTGIEYWIIK	NSWGS	4		919.2323132	3672.898053	0.000451244	2	N	393	425
P97821	Infl	VGYGR	DPVTGIEYWIIK	NSWGS	2		717.3879069	1432.760214	0.002519933	1	N	413	425
P97821	Infl	SWDWR	NVQGVNYVSPVR	NQESC	2		666.3574724	1330.699345	0.000451244	1	N	237	249
P97822	Infl	LNKLR	KLELSDNIISGGLEVLAEK	CPNLT	2		1014.565317	2027.115033	0.000451244	5	N	67	86
P97822	Infl	LSGNK	IKDLSTVEALQNLK	NLKSL	2		786.4543095	1570.893019	0.000451244	11	N	99	113
P97822	Infl	LKNLK	SLDLFNCEITNLEDYR	ESIFE	2	C7:+57.021	1001.465045	2000.914491	0.000451244	2	N	116	132
P97822	Infl	GNKIK	DLSTVEALQNLK	NLKSL	2		665.8647959	1329.713992	0.000451244	7	N	101	113
P97822	Infl	LEDYR	ESIFELLQQITY	LDGFD	2		742.3881039	1482.760608	0.000823681	7	N	132	144
P97822	Infl	LKNLK	SLDLFNCEITNLEDYRESIFELLQQITY	LDGFD	3	C7:+57.021	1156.229313	3465.664538	0.002813207	1	N	116	144
P97822	Infl	VLAEK	CPNLTYLNLSGNK	IKDLS	2	C1:+57.021	747.3747735	1492.733947	0.002212458	1	N	86	99
P97823	Infl	TTQQK	LAGVTALSCWLPLR	ASFSQ	2	C9:+57.021	778.9348013	1555.854003	0.000451244	8	N	135	149
P97823	Infl	IPSNR	IILGGFSQGGALSLYTALTTQQK	LAGVT	2		1184.150079	2366.284559	0.000451244	3	N	112	135
P97823	Infl	VERLK	ALINPANVTFK	IYEGM	2		594.3433023	1186.671005	0.00091018	2	N	190	201
P97855	Infl	VVELR	INSGGKLPNFGFVVFDDSEPVQK	VLSNR	2		1247.634793	2493.253987	0.000823681	1	N	368	391
P97855	Infl	DDVQK	STSPAPADVAPAQEDLR	TFSWA	2		862.9266445	1723.837689	0.000451244	8	N	228	245
P97855	Infl	NSGGK	LPNFGFVVFDDSEPVQK	VLSNR	2		969.486338	1936.957076	0.000451244	9	N	374	391
P97855	Infl	RFYGK	NSSYAHGGLDSNGKPADAVYGQK	EIHRK	3		779.3687662	2335.082899	0.001463592	2	N	36	59
P97855	Infl	KSELK	DFFQNFGNVVELR	INSGG	2		792.894419	1583.773238	0.000451244	3	N	355	368
P97864	Infl	IQACR	GTELDDGIQADSGPINDIDANPR	NKIPV	2		1192.054561	2382.093523	0.000451244	5	N	187	210
P97864	Infl	DANPR	NKIPVEADFLFAYSTVPGYYSWR	NPGKG	3		908.4555121	2722.343136	0.001463592	1	N	210	233
P97872	Infl	LTCIK	CCLEEGLEPVCFER	SGDIG	2	C1:+57.021,C2:+57.021,C11:+57.021	899.3836924	1796.751785	0.000622848	3	N	20	34
P97872	Infl	KPKHR	ALSQHPTVNDDLPNR	IIAGL	3		559.6170643	1675.827793	0.002080925	1	N	277	292
P98083	Infl	PVNQR	ACHILECPEGLAQDVISTIGQAFELR	FKQYL	3	C2:+57.021,C7:+57.021	976.4847283	2926.430785	0.000451244	14	N	285	311
P98083	Infl	PVNQR	ACHILECPEGLAQDVISTIGQAF	ELRFK	2	C2:+57.021,C7:+57.021	1265.109308	2528.203017	0.000451244	1	N	285	308
P98083	Infl	PCPGR	ELFDDPSYVNIQNLDK	ARQAG	2		955.4630599	1908.91052	0.000451244	8	N	415	431
P99024	Infl	LQLDR	ISVYYNEATGGK	YVPRA	2		651.3227639	1300.629928	0.000451244	24	N	46	58
P99024	Infl	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	3		985.7850854	2954.331856	0.000451244	34	N	20	46
P99024	Infl	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	3		1034.80789	3101.40027	0.000451244	25	N	19	46
P99024	Infl	SQQYR	ALTVPELTQQVFDAK	NMMAA	2		830.4517668	1658.887934	0.000451244	29	N	282	297
P99024	Infl	PRGLK	MAVTFIGNSTAIQELFKR	ISEQF	3		676.0317099	2025.07173	0.000451244	6	N	362	380
P99024	Infl	RALTV	PELTQQVFDAK	NMMAA	2		638.3331316	1274.650663	0.001654178	1	N	286	297
P99024	Infl	PRGLK	MAVTFIGNSTAIQELFK	RISEQ	2		935.4931093	1868.970619	0.000451244	2	N	362	379
P99027	Infl	KDIKK	ILDSVGIEADDDRLNK	VISEL	2		886.955402	1771.895204	0.000451244	15	N	25	41
P99027	Infl	ELNGK	NIEDVIAQGVGK	LASVP	2		621.8385811	1241.661562	0.000451244	18	N	49	61
P99027	Infl	DRLNK	VISELNGKNIEDVIAQGVGK	LASVP	2		1042.07384	2082.132081	0.000451244	10	N	41	61
P99027	Infl	-MR	YVASYLLAALGGNSSPSAK	DIKKI	2		934.9917875	1867.967975	0.000451244	32	N	2	21
P99027	Infl	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	2		1387.720117	2773.424634	0.000451244	30	N	61	94
P99027	Infl	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKK	DEKKE	3		968.1809991	2901.519597	0.00091018	2	N	61	95
P99028	Infl	RVSSR	SQTEEDCTEELFDFLHAR	DHCVA	2	C7:+57.021	1113.984331	2225.953061	0.000451244	10	N	58	76
P99028	Infl	MLTGS	GDPKEEEEEELVDPLTTVR	EHCEQ	2		1093.029492	2184.043385	0.000451244	11	N	13	32

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P99029	Infl	PGCSK	THLPGFVEQAGALKAK	GAQVV	2		833.9679184	1665.920237	0.001943752	1	N	98	114
P99029	Infl	PGCSK	THLPGFVEQAGALK	AKGAQ	3		489.9371866	1466.78816	0.000451244	55	N	98	112
P99029	Infl	EGKVR	LLADPTGAFGK	ATDLL	2		545.3011031	1088.586606	0.000451244	18	N	144	155
P99029	Infl	LFKGK	KGVLFGVPGAFTPGCSK	THLPG	2	C15:+57.021	861.4560979	1720.896596	0.000451244	6	N	81	98
P99029	Infl	SAVTM	APIKVGDAIPSVEVFEGEPGK	KVNLA	2		1070.070766	2138.125933	0.000451244	5	N	49	70
P99029	Infl	ALKAK	GAQVVACLSVNDVFVIEEWGR	AHQAE	2	C7:+57.021	1174.5891	2347.1626	0.000451244	47	N	114	135
P99029	Infl	GAFGK	ATDLLLDDSLVSLFGNR	RLKRF	2		924.9892448	1847.96289	0.000451244	23	N	155	172
P99029	Infl	NGIVK	ALNVEPDGTGLTCSLAPNILSQL	-	2	C13:+57.021	1192.112605	2382.20961	0.000451244	31	N	187	210
P99029	Infl	GAFGK	ATDLLLDDSLVSLFGNRR	LKRFS	2		1003.0398	2004.064001	0.000451244	10	N	155	173
P99029	Infl	GAFGK	ATDLLLDDSLVSLF	GNRRL	2		761.4064936	1520.797387	0.000662267	3	N	155	169
P99029	Infl	MAPIK	VGDAIPSVEVFEGEPGKK	VNLAE	2		929.4837953	1856.951991	0.000451244	9	N	53	71
P99029	Infl	MAPIK	VGDAIPSVEVFEGEPGK	KVNLA	2		865.4363138	1728.857028	0.000637154	7	N	53	70
P99029	Infl	GEPGK	KVNLAELFK	GKKGV	2		531.3218385	1060.628077	0.001591523	1	N	70	79
P99029	Infl	FKGKK	GVLFGVPGAFTPGCSK	THLPG	2	C14:+57.021	797.4086164	1592.801633	0.001162105	3	N	82	98
P99029	Infl	EGKVR	LLADPTGAFGKATDLLLDDSLVSLFGNR	RLKRF	3		973.854112	2918.538936	0.001839721	1	N	144	172
Q00519	Infl	MSQTK	DQTIAPSSSLFNPEDFKPLDPTQEPIFPPELLR	LKDTP	3		1246.968752	3737.882857	0.000451244	31	N	187	220
Q00519	Infl	PGYRR	TLLSPEEILVSIVIPYSR	KGEFF	2		1015.083145	2028.150691	0.000451244	5	N	397	415
Q00519	Infl	PEKIR	NACVDQFTTLCATGTPENCK	SWSVR	2	C3:+57.021,C11:+57.021,C19:+57.021	1143.992855	2285.970111	0.000451244	1	N	1309	1329
Q00519	Infl	IPTSK	IHITETSTNTVPNTSPTAASASADLNGQAIYEACQTILK	RLEPF	3	C34:+57.021	1363.674585	4088.000354	0.000451244	9	N	1063	1102
Q00519	Infl	GMCGK	LDPTFASATLLFQK	DPPAN	2		776.4250207	1550.834441	0.000451244	5	N	540	554
Q00519	Infl	GMCGK	LDPTFASATLLFQKDPPANVQLFQEVPK	GQSEE	3		1038.889045	3113.643735	0.000451244	8	N	540	568
Q00519	Infl	ARGVK	ITYEDLPAIITIQDAIK	NNSFY	2		959.0331211	1916.050642	0.000823681	3	N	689	706
Q00519	Infl	TGFYK	TPNLGYSFETNSGNPFHYFSYGVACSEVEIDCLTGDHK	NLRTD	4	C25:+57.021,C32:+57.021	1078.977315	4311.878061	0.000451244	7	N	1137	1175
Q00519	Infl	TSEAK	KVPGFVCFLTSEDVPGSNITGIFNDETVFAK	DEVTC	3	C7:+57.021	1130.230877	3387.66923	0.000622848	2	N	629	660
Q00519	Infl	IYASK	AVGEPPLFLASSIFFAIK	DAIRA	2		954.0380094	1906.060419	0.001329271	2	N	1260	1278
Q00519	Infl	ARGVK	ITYEDLPAIITIQDAIKNNSFYGPEVK	IEKGD	3		1018.201289	3051.580466	0.000622848	3	N	689	716
Q00519	Infl	VGFMK	TGTIVALEVAHFSNGGNSEDLSR	SIMER	3		792.0598212	2373.156064	0.000698008	1	N	855	878
Q00612	Infl	HKIDR	EKPQPIPYVYGSR	GPTEA	2		767.4071623	1532.798725	0.000451244	10	N	474	487
Q00612	Infl	EFFAR	NSYVAGQYDDAASYK	HLNSH	2		826.3658884	1650.716177	0.000451244	42	N	104	119
Q00612	Infl	KAEVR	LQFRDVAGDIFHQQCK	RNELV	3	C15:+57.021	654.6602329	1960.957299	0.000451244	3	N	370	386
Q00612	Infl	IWWLF	RDGLLPEDTFIVGYAR	SRLTV	2		911.4788473	1820.942095	0.000451244	14	N	56	72
Q00612	Infl	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	3		917.4551224	2749.341967	0.000451244	9	N	175	198
Q00612	Infl	GTEGR	GGYFDEFGIIR	DVMQN	2		637.3147418	1272.613884	0.000451244	6	N	246	257
Q00612	Infl	WWLFR	DGLLPEDTFIVGYAR	SRLTV	2		833.4282917	1664.840983	0.000451244	18	N	57	72
Q00612	Infl	PIWNR	DNIACVILTFKEPFGTEGR	GGYFD	2	C5:+57.021	1084.046537	2166.077474	0.000451244	9	N	227	246
Q00612	Infl	DLAKK	KIYPTIWWLFR	DGLLP	3		508.2910126	1521.849638	0.001162105	7	N	46	57
Q00612	Infl	LAKKK	IYPTIWWLFR	DGLLP	2		697.8851373	1393.754675	0.000451244	15	N	47	57
Q00612	Infl	MQANR	LFYLALPPTVYEAVTK	NIQET	2		913.0114603	1824.007321	0.000622848	5	N	136	152
Q00612	Infl	EAVTK	NIQETCMSQTGWNR	IIVEK	2	C6:+57.021	862.8778863	1723.740173	0.000451244	5	N	152	166
Q00612	Infl	RLQFR	DVAGDIFHQQCK	RNELV	2	C11:+57.021	709.330366	1416.645132	0.001162105	20	N	374	386
Q00612	Infl	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	2		973.4904747	1944.965349	0.000451244	13	N	175	192
Q00612	Infl	PIWNR	DNIACVILTFK	EPFGT	2	C5:+57.021	647.3474961	1292.679392	0.000451244	5	N	227	238
Q00612	Infl	RDGLL	PEDTFIVGYAR	SRLTV	2		634.3200242	1266.624448	0.002080925	1	N	61	72
Q00612	Infl	FRDGL	LPEDTFIVGYAR	SRLTV	2		690.8620562	1379.708512	0.00307782	1	N	60	72
Q00612	Infl	ELMKR	VGFQYEGTYK	WVNPH	2		596.2881927	1190.560785	0.00307782	1	N	498	508
Q00612	Infl	PIWNR	DNIACVILTF	KEPFG	2	C5:+57.021	583.3000145	1164.584429	0.000451244	4	N	227	237
Q00612	Infl	FYLAL	PPTVYEAVTK	NIQET	2		552.8009359	1103.586272	0.001162105	2	N	142	152
Q00612	Infl	ANRLF	YLALPPTVYEAVTK	NIQET	2		782.9352213	1563.854843	0.002019181	1	N	138	152
Q00612	Infl	KPFGR	DLQSSNQLSNHISSLF	REDQI	2		895.4399191	1788.864238	0.000823681	5	N	175	191
Q00623	Infl	KDSGR	DYVSQFESSSLGQQLNLNLLENWDTLGSTVSQLQER	LGPLT	3		1367.001732	4097.981796	0.000451244	3	N	50	86
Q00PI9	Infl	EMDPK	SRDLLVQQASQCLSK	LVQIA	2	C12:+57.021	866.9544507	1731.893301	0.000451244	2	N	504	519
Q00PI9	Infl	HVLCK	NCVVELNFGQKEEPFFPPPEEFVFIHAVPVEER	VRTAV	3	C2:+57.021	1310.645461	3928.912983	0.000451244	11	N	404	437
Q00PI9	Infl	DPKSR	DLLVQQASQCLSK	LVQIA	2	C10:+57.021	745.3878809	1488.760162	0.001591523	2	N	506	519
Q00PI9	Infl	GRGLK	AENGQFEEFGQTFGENDVIGCFANFETEEVELSFSK	NGEDL	3	C21:+57.021	1369.269224	4104.784273	0.001699387	1	N	340	376
Q00PI9	Infl	SRSKR	NFILDQCNVYNSGQR	RKLLL	2	C7:+57.021	914.4260574	1826.836515	0.002019181	1	N	529	544
Q00PI9	Infl	TFSRK	VVVVVPNEEDWKR	RLELR	3		523.6197461	1567.835838	0.000451244	5	N	556	569
Q01102	Infl	GFVLK	GNDAIQCADSGQWTAPAPFCEALQCPEFPVPSK	AQVNC	3	C7:+57.021,C20:+57.021,C25:+57.021	1216.877983	3647.610548	0.000451244	2	N	361	394
Q01102	Infl	SGPER	LDCSPSGHWTGTPPTCEAIK	CPGIF	3	C3:+57.021,C16:+57.021	738.6702033	2212.98721	0.000662267	5	N	489	509
Q01320	Infl	KIRKK	IKSENVEGTPAEDGAEPGSLR	QRIEK	3		719.3542341	2155.039302	0.0007646	6	N	1236	1257
Q01320	Infl	RKKIK	SENVEGTPAEDGAEPGSLR	QRIEK	2		957.9379376	1913.860275	0.000451244	9	N	1238	1257
Q01320	Infl	EKFIK	AAIGCGIVESILNWVKF	KAQIQ	2	C5:+57.021	939.0034123	1875.991225	0.000622848	3	N	399	416
Q01320	Infl	SKKAK	GEEQDFPVDLEDTIAPR	AKSDR	2		965.955599	1929.895598	0.001943752	1	N	1488	1505
Q01853	Infl	TLLAK	AIANECQANFISIK	GPELL	2	C6:+57.021	789.9011555	1577.786711	0.000451244	14	N	529	543

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q01853	Infl	NLRVR	LGDVISIQPCPDVK	YGKRI	2	C10:+57.021	770.9059065	1539.796213	0.000451244	13	N	95	109
Q01853	Infl	RNNLR	VRLGDVISIQPCPDVK	YGKRI	3	C12:+57.021	599.3297127	1794.965738	0.000622848	1	N	93	109
Q01853	Infl	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	2		1106.586583	2211.157567	0.000451244	10	N	487	505
Q01853	Infl	NRPNR	LIVDEAINEDNSVVSLSQPK	MDELQ	2		1085.566045	2169.11649	0.000451244	42	N	25	45
Q01853	Infl	SPVAK	DVDLEFLAK	MTNGF	2		525.2798363	1048.544073	0.000451244	21	N	668	677
Q01853	Infl	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	2		1159.639879	2317.264158	0.000451244	6	N	365	386
Q01853	Infl	LQQSR	GFGSFRFPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG	-	3		1291.216665	3870.626595	0.000622848	4	N	766	806
Q01853	Infl	PSALR	ETVVEVPQVTWEDIGGLEDVKR	ELQEL	2		1249.642815	2497.270031	0.000451244	20	N	465	487
Q01853	Infl	LRPGR	LDQLIYIPLPDEK	SRVAI	2		778.9326786	1555.849757	0.000998612	5	N	638	651
Q01853	Infl	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	KKMDL	3	C26:+57.021	1224.935963	3671.784488	0.000451244	17	N	389	424
Q01853	Infl	EVERR	IVSQLLTLMDGLK	QRAHV	2		715.9185175	1429.821435	0.000451244	1	N	323	336
Q01853	Infl	EEAEK	NAPAIIFIDELDAIAPKR	EKTHG	2		984.0521795	1966.088759	0.000451244	2	N	295	313
Q01853	Infl	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	C5:+57.021	962.4799671	1922.944334	0.000451244	15	N	567	584
Q01853	Infl	SNLRK	AFEEAEKNAPAIIFIDELDAIAPK	REKTH	3		872.4588108	2614.353032	0.000451244	2	N	288	312
Q01853	Infl	EEAEK	NAPAIIFIDELDAIAPK	REKTH	2		906.0016239	1809.987648	0.000451244	22	N	295	312
Q01853	Infl	EPIKR	EDEEESLNEVGYDDIGGCRK	QLAQI	2	C18:+57.021	1157.492717	2312.969834	0.000823681	1	N	191	211
Q01853	Infl	VKPPR	GILLYGPPGTGK	TLIAR	2		586.8378528	1171.660106	0.002145581	1	N	239	251
Q01853	Infl	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIRK	KMDLI	4	C26:+57.021	950.9776627	3799.879451	0.000622848	4	N	389	425
Q01853	Infl	KYGKR	IHVLPIDDTVEGITGNLFEVY	LKPYF	2		1172.607713	2343.199826	0.000451244	13	N	113	134
Q01853	Infl	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIR	KGDIF	4		998.5401774	3990.12951	0.001352548	3	N	113	147
Q01853	Infl	EDVKR	ELQELVQYPVEHPDK	FLKFG	3		608.6445086	1822.910126	0.000451244	10	N	487	502
Q01853	Infl	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPY	FLEAY	3		949.1727819	2844.494946	0.001395409	1	N	113	138
Q01853	Infl	EFLAK	MTNGFSGADLTEICQR	ACKLA	2	C14:+57.021	900.4064766	1798.797353	0.001264573	1	N	677	693
Q01853	Infl	NLRVR	LGDVISIQPCPDVKY	GKRIH	2	C10:+57.021	852.4375708	1702.859542	0.001329271	2	N	95	110
Q01853	Infl	KYGKR	IHVLPIDDTVEGITGNLF	EVYLK	2		977.020545	1952.02549	0.000823681	3	N	113	131
Q02053	Infl	SMVTK	DNPGVVTCLDEAR	HGFET	2	C8:+57.021	723.338388	1444.661176	0.000451244	10	N	226	239
Q02053	Infl	KSGVK	IHVSDQELQSANASVDDSRLEELK	ATLPS	2		1342.162632	2682.309664	0.001463592	1	N	806	830
Q02053	Infl	ERTLR	LAGTQPLEVLEAVQR	SLVLQ	2		812.4573835	1622.899167	0.000451244	9	N	678	693
Q02053	Infl	PPRPR	NEEDATELVGLAQAVNAR	SPPSV	2		950.4744903	1898.933381	0.000451244	19	N	350	368
Q02053	Infl	GSQDR	AAVASLLQSVQVPEFTPK	SGVKI	2		943.0256304	1884.035661	0.000451244	14	N	784	802
Q02053	Infl	PMEIK	VLGPYTFSICDTSNFSDYIR	GGIVS	2	C10:+57.021	1178.052016	2354.088432	0.000451244	19	N	268	288
Q02053	Infl	SHQNR	VGPDTERIYDDDFFQNLDGVANALDNIDAR	MYMDR	3		1123.527563	3367.55929	0.000451244	5	N	551	581
Q02053	Infl	PDTER	IYDDDFFQNLDGVANALDNIDAR	MYMDR	2		1307.606961	2613.198322	0.000451244	24	N	558	581
Q02053	Infl	LDSYK	NGFLNLALPFFGFSEPLAAPR	HQYYN	2		1139.605111	2277.194621	0.000451244	14	N	923	944
Q02053	Infl	LIAGK	IIPAIATTTAAVVGLVCLELYK	VVQGH	2	C17:+57.021	1158.666288	2315.316976	0.000451244	12	N	889	911
Q02053	Infl	PVTAY	TGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		987.1978787	2958.570236	0.000622848	11	N	147	174
Q02053	Infl	VSQPR	LAELNSYVPVTAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		1460.77249	4379.294069	0.000451244	20	N	134	174
Q02053	Infl	KCLPR	QNRYDGQVAVFGSDFQEK	LSKQK	2		1044.493214	2086.970829	0.000451244	5	N	447	465
Q02053	Infl	LGGVK	AVTLHDQGTTQWADLSSQFYLR	EEDIG	2		1269.125124	2536.234648	0.000451244	2	N	97	119
Q02053	Infl	LSKQK	YFLVGAGAIGCELLK	NFAMI	2	C11:+57.021	805.934467	1609.853334	0.000451244	24	N	470	485
Q02053	Infl	TERIY	DDDFFQNLDGVANALDNIDAR	MYMDR	2		1169.533265	2337.05093	0.000451244	10	N	560	581
Q02053	Infl	LGGVK	AVTLHDQGTTQWADLSSQFYLREEDIGK	NRAEV	3		1070.190223	3207.547269	0.000622848	2	N	97	125
Q02053	Infl	EGLFK	QPAENVNQYLTDSK	FVERT	2		803.8895307	1605.763461	0.00091018	6	N	657	671
Q02053	Infl	NGMAK	NGSEADIDESLYSR	QLYVL	2		778.3476956	1554.679791	0.000451244	2	N	43	57
Q02053	Infl	MQWLY	FDALECLPEDKEALTEEK	CLPRQ	2	C6:+57.021	1069.0042	2135.992801	0.000451244	3	N	425	443
Q02053	Infl	LQWAR	DEFEGLFKQPAENVNQYLTDSK	FVERT	2		1286.614255	2571.21291	0.000451244	2	N	649	671
Q02053	Infl	PMEIK	VLGPYTFSICDTSNF	SDYIR	2	C10:+57.021	860.8982785	1719.780957	0.000451244	7	N	268	283
Q02053	Infl	LELYK	VVQGHQQLDSYKNGFLNLALPFFGFSEPLAAPR	HQYYN	3		1220.970762	3659.888885	0.001463592	1	N	911	944
Q02053	Infl	PRQNR	YDGQVAVFGSDFQEK	LSKQK	2		845.3919062	1688.768212	0.000451244	1	N	450	465
Q02819	Infl	TFEAR	DLELLIQTATR	DLAQY	2		636.8620562	1271.708512	0.000451244	8	N	151	162
Q02819	Infl	LYYHR	YLQEVINVLETDGHFR	EKLQA	3		644.9991744	1931.974123	0.000451244	9	N	52	68
Q02819	Infl	TNQDR	LVTLEEFLASTQR	KEFGD	2		753.9122775	1505.808955	0.000622848	4	N	309	322
Q02819	Infl	RFNPK	TFFILHDINSDGVLDEQELEALFTKELEK	VYDPK	3		1131.908722	3392.702767	0.001395409	3	N	245	274
Q02819	Infl	RFNPK	TFFILHDINSDGVLDEQELEALFTK	ELEKV	3		965.4873177	2893.438553	0.000451244	4	N	245	270
Q02819	Infl	QTATR	DLAQYDAAHHEEFKR	YEMLK	3		610.6242189	1828.849257	0.000622848	1	N	162	177
Q02819	Infl	QAQLK	EVWEELDGLDPNRFNPK	TFFIL	2		1029.500508	2056.985416	0.000451244	5	N	228	245
Q03265	Infl	RDNGK	HALIIYDDLSK	QAVAY	2		644.3513243	1286.687049	0.000451244	11	N	305	316
Q03265	Infl	ILEER	ILGADTSVDLEETGR	VLSIG	2		788.3971886	1574.778777	0.000451244	28	N	58	73
Q03265	Infl	RQTGK	TSIAIDTIINQK	RFNDG	2		658.8751636	1315.734727	0.000451244	12	N	218	230
Q03265	Infl	DVVKR	TGAIVDVPVGEELLGR	VVDAL	2		812.9493913	1623.883183	0.000451244	16	N	133	149
Q03265	Infl	SKITK	FENAFLSHVISQHQSLLGNIR	SDGKI	3		804.092908	2409.255324	0.000451244	16	N	506	527
Q03265	Infl	EVAAF	AQFGSDLDAATQQLLSR	GVRLT	2		910.9610187	1819.906437	0.000451244	12	N	446	463
Q03265	Infl	ELAQY	REVAAFAQFGSDLDAATQQLLSR	GVRLT	3		832.0948658	2493.261197	0.000451244	4	N	440	463
Q03265	Infl	LAQYR	EVAAFAQFGSDLDAATQQLLSR	GVRLT	2		1169.587843	2337.160086	0.000451244	20	N	441	463
Q03265	Infl	AGTMK	LELAQYREVAAFAQFGSDLDAATQQLLSR	GVRLT	3		1071.218113	3210.630939	0.001463592	1	N	434	463

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q03265	Infl	RPPGR	EAYPGDVFYLHSR	LLERA	2		777.3733194	1552.731039	0.000622848	5	N	334	347
Q03265	Infl	QSDAK	LKEIVTNFLAGFEP	-	2		789.4328457	1576.850091	0.000451244	3	N	539	553
Q03265	Infl	ILEER	ILGADTSVDLEETGRVLSIGDGIAR	VHGLR	3		853.1209692	2556.339508	0.000622848	2	N	58	83
Q03265	Infl	ERAAK	MNDSFGGGSLTALPVIETQAGDVSAYIPTNVISITDGQIF	LETEL	3		1367.012581	4098.014342	0.002145581	2	N	354	394
Q03265	Infl	QTGIK	AVDSLVPIGR	GQREL	2		513.8012703	1025.586941	0.001162105	1	N	194	204
Q03265	Infl	ELLGR	VVDALGNAIDGK	GPIGS	2		586.3200242	1170.624448	0.000451244	1	N	149	161
Q03265	Infl	KITKF	ENAFLSHVISQHQSLLGNIR	SDGKI	3		755.0701034	2262.18691	0.000451244	6	N	507	527
Q04750	Infl	CCSLR	VEHINLHPELDGQEYVVEFDFPGKDSIR	YYNKV	3		1094.874235	3281.599304	0.000451244	6	N	510	538
Q04750	Infl	KLALR	AGNEKEEGETADTVGCCSLR	VEHIN	2	C16:+57.021,C17:+57.021	1091.970666	2181.925732	0.000451244	12	N	490	510
Q04750	Infl	FLEHK	GPVFAPPYEPLPESVK	FYYDG	2		863.956685	1725.89777	0.001871652	2	N	225	241
Q04750	Infl	QQQLK	ELTAPDENVPAK	ILSYN	2		642.3280462	1282.640492	0.000998612	1	N	605	617
Q04998	Infl	IIVRS	SPTPGSEGHGSAPDCPSCALATLPK	DGPNS	3	C15:+57.021,C18:+57.021	832.0496315	2493.125494	0.002374549	1	N	20	45
Q05144	Infl	EDYDR	LRPLSYPQTDVFLICFSLVSPASYENVR	AKWFP	3	C15:+57.021	1091.232552	3270.674255	0.000451244	20	N	66	94
Q05144	Infl	KLKEK	KLAPITYPQGLALAK	DIDSV	2		792.4801303	1582.944661	0.001871652	1	N	132	147
Q05144	Infl	EDYDR	LRPLSYPQTDVFLICF	SLVSP	2	C15:+57.021	985.0165197	1968.017439	0.000979378	7	N	66	82
Q05144	Infl	LKEKK	LAPITYPQGLALAK	DIDSV	2		728.4326487	1454.849697	0.000451244	8	N	133	147
Q05144	Infl	FPEVR	HHCPSTPIILVGTK	LDLRD	2	C3:+57.021	780.4220581	1558.828516	0.001162105	1	N	102	116
Q05144	Infl	IDSVK	YLECSALTQR	GLKTV	2	C4:+57.021	620.8034527	1239.591305	0.000451244	19	N	153	163
Q05144	Infl	GAVGK	TCLLISYTTNAFPGEYIPTVFDNY	SANVM	2	C2:+57.021	1400.165035	2798.31447	0.002212458	2	N	16	40
Q05144	Infl	GAVGK	TCLLISYTTNAFPGEYIPTVF	DNYSA	2	C2:+57.021	1204.098435	2406.18127	0.000622848	4	N	16	37
Q05144	Infl	FLICF	SLVSPASYENVR	AKWFP	2		661.3414879	1320.667376	0.000622848	3	N	82	94
Q06890	Infl	GMVLG	EQEVSDNELQELSTQGSR	YINKE	2		1024.972509	2047.929417	0.002813207	1	N	21	39
Q07076	Infl	RKAMK	GFGTDEQAIVDVVSNR	SNDQR	2		853.9213622	1705.827124	0.000451244	11	N	174	190
Q07076	Infl	IVVTR	SEIDLVQIK	QMFTQ	2		522.8009359	1043.586272	0.002145581	1	N	421	430
Q07076	Infl	SSVSR	EFSGYVESGLK	TILQC	2		608.2987574	1214.581915	0.001654178	1	N	372	383
Q07797	Infl	FYRGR	WGTVCDNLWNLLDAHVVCR	ALGYE	3	C5:+57.021,C18:+57.021	776.7054708	2327.093012	0.000451244	6	N	44	63
Q07797	Infl	DYCGR	LFATLLPQDPTFHTPLDLYAYAR	ATGDS	2		1332.197561	2662.379522	0.001162105	2	N	245	268
Q08093	Infl	IYDPK	YCPQGSAADGAPAGDGQGEAPEYLAYCQEEAGY	-	3	C2:+57.021,C27:+57.021	1151.470201	3451.387202	0.000451244	12	N	272	305
Q08093	Infl	EAELR	SWIEGLTGLSIGPDFQK	GLKDG	2		924.4810556	1846.946511	0.000451244	20	N	35	52
Q08943	Infl	PVHIR	FDEISFVNFAR	GTTTT	2		672.8332987	1343.650997	0.000451244	5	N	370	381
Q08943	Infl	NVLSK	ADVIQATGDAICIFR	ELQCL	2	C12:+57.021	825.4197124	1648.823825	0.000451244	2	N	188	203
Q08943	Infl	WGTVK	FGGQLLSFDIGDQPVFEIPLSNVSQCTTGK	NEVTL	3	C26:+57.021	1085.539822	3253.596065	0.000451244	19	N	113	143
Q09014	Infl	YLVPK	DGKNNVADITGPIILQTYR	AIADY	2		1044.558357	2087.101115	0.000451244	19	N	143	162
Q09014	Infl	VPASY	LEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	2		1437.664339	2873.313078	0.000451244	19	N	209	235
Q09014	Infl	PKDGK	NNVADITGPIILQTYR	AIADY	2		894.4866723	1786.957745	0.000451244	1	N	146	162
Q09014	Infl	EVIHK	LLDGWWVVR	KGDIT	2		572.3196302	1142.62366	0.000698008	12	N	258	267
Q09014	Infl	QMKTK	RGWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1264.264005	3789.768615	0.000451244	29	N	201	235
Q09014	Infl	MKTKR	GWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1212.230301	3633.667503	0.000451244	22	N	202	235
Q09014	Infl	PDDLK	LPTDSQAKKPETYLVPK	DGKNN	3		639.0232085	1914.046225	0.000451244	3	N	126	143
Q09014	Infl	YLVPK	DGKNNVADITGPIILQTY	RAIAD	2		966.5078018	1931.000004	0.000451244	1	N	143	161
Q09014	Infl	PKDGK	NNVADITGPIILQTY	RAIAD	2		816.4361168	1630.856634	0.000823681	2	N	146	161
Q09014	Infl	QMKTK	RGWVPASYLEPLDSPDEAEDPDPNYAGEPY	VTIKA	3		1117.165632	3348.473495	0.000451244	1	N	201	231
Q09PK2	Infl	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	2		1260.145663	2518.275725	0.000451244	13	N	96	118
Q09PK2	Infl	GAEMK	ILGVWDTEISLGK	TKLKA	2		715.8986387	1429.781677	0.000451244	29	N	250	263
Q09PK2	Infl	LRFLK	ESLKGDALDVYNGLSSQAQGDFSFVK	QALLR	2		1388.177751	2774.339902	0.000451244	33	N	138	164
Q09PK2	Infl	LGKTK	LKAEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		1245.971267	3734.890402	0.000451244	19	N	265	299
Q09PK2	Infl	QALLR	AFGAPGEAFSEPEEILFANSMGK	GYYLK	2		1200.065356	2398.115111	0.000451244	13	N	169	192
Q09PK2	Infl	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPFNNVVK	VANGA	3		1323.013244	3966.016331	0.000451244	51	N	206	242
Q09PK2	Infl	LKGKK	FRLLPVGSSLEDEFDLELIEEEEGSSAPEGSH	-	3		1173.221806	3516.642017	0.000451244	8	N	307	339
Q09PK2	Infl	GKKFR	LLPVGSSLEDEFDLELIEEEEGSSAPEGSH	-	3		1072.165297	3213.472492	0.000451244	129	N	309	339
Q09PK2	Infl	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPF	NNVVK	3		1138.240695	3411.698684	0.000451244	9	N	206	237
Q09PK2	Infl	KTKLK	AEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		1165.578258	3493.711374	0.000451244	15	N	267	299
Q09PK2	Infl	KESLK	GDALDVYNGLSSQAQGDFSFVK	QALLR	2		1159.550926	2317.086253	0.000451244	12	N	142	164
Q09PK2	Infl	LWLHR	FEVIDDLNHWDHATK	LRFLK	2		920.4371794	1838.858759	0.000451244	19	N	118	133
Q09PK2	Infl	SKEGR	REHAFVPEPFTGTNLAPSLWLHR	FEVID	3		892.4667455	2674.376836	0.000622848	2	N	95	118
Q09PK2	Infl	QALLR	AFGAPGEAFSEPEEILF	ANSMG	2		905.9308642	1809.846128	0.001463592	4	N	169	186
Q09PK2	Infl	VPEPF	TGTNLAPSLWLHR	FEVID	3		489.2690477	1464.783743	0.000622848	4	N	105	118
Q11011	Infl	ELIQK	VLTFALSEEVRPQDTVSVIGGVAGGSK	HGRKA	3		906.1559024	2715.444307	0.000622848	4	N	795	822
Q11011	Infl	ADYTR	AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	GASVI	3		1237.927393	3710.758778	0.000451244	21	N	407	441
Q11011	Infl	PSAER	TIQQCCENILLNAAWLK	RDADS	2	C5:+57.021,C6:+57.021	1038.024319	2074.033038	0.000451244	1	N	883	900
Q11011	Infl	PPVDR	LGLQNDLFSLAR	AGIIS	2		673.8754979	1345.735396	0.000451244	4	N	616	628
Q11011	Infl	NRIER	VLGATLSPELIQK	VLTFA	2		684.9090065	1367.802413	0.001329271	3	N	782	795
Q11011	Infl	PIGER	LGWDPKPGEGHLDALLR	GLVLG	2		937.5001141	1872.984628	0.001839721	1	N	690	707
Q11011	Infl	KFQQK	NAATEDLWESLESASGKPIAAVMNTWTK	QMGFP	3		1007.494367	3019.4597	0.001943752	1	N	472	500
Q11011	Infl	VKFAR	TPVMSTYLVAFVVGEYDFVETR	SKDGV	3	M4:+15.995	847.0862372	2538.235312	0.002374549	1	N	238	260

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q1HFZ0	Infl	SVVLK	YEPDSANPDTLQCPIVLCGWR	GKASI	2	C13:+57.021,C18:+57.021	1246.072726	2490.129851	0.000451244	3	N	659	680
Q1HFZ0	Infl	ARGRR	FQQPPQPEGEEDASDGGR	KRGQA	2		972.4224547	1942.829309	0.000622848	4	N	9	27
Q20BD0	Infl	DYSPY	GYYGYGPGYDYSQGSTNYGK	SQRRG	2		1098.961413	2195.907225	0.000451244	11	N	298	318
Q20BD0	Infl	DPVKK	IFVGGLNPEATEEK	IREYF	2		752.3886352	1502.76167	0.000451244	21	N	160	174
Q20BD0	Infl	ATEEK	IREYFGQFGEIEAIELPIDPK	LNKRR	3		822.0973247	2463.268574	0.000451244	6	N	174	195
Q20BD0	Infl	KIREY	FGQFGEIEAIELPIDPK	LNKRR	2		951.9965386	1901.977477	0.000451244	27	N	178	195
Q20BD0	Infl	EEKIR	EYFGQFGEIEAIELPIDPK	LNKRR	2		1098.049499	2194.083399	0.000451244	23	N	176	195
Q20BD0	Infl	DPVKK	IFVGGLNPEATEEKIR	EYFGQ	2		886.9812228	1771.946846	0.000637154	1	N	160	176
Q2YFS3	Infl	NNIVY	ASISLSSPTSPGTAPNLPVHGNPQEETVYSIVK	AK-	3		1126.579488	3376.715063	0.001943752	1	N	267	300
Q3TBD2	Infl	LVRGY	RSPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1151.590164	3451.747091	0.000451244	20	N	90	124
Q3TBD2	Infl	WTLVR	GYRSPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1224.951761	3671.831884	0.000451244	1	N	88	124
Q3TBD2	Infl	KLQGR	LQLFGQDFSQAALSTPDGVPF	IVKKC	2		1119.558023	2237.100446	0.001352548	3	N	752	773
Q3TBD2	Infl	VRGYR	SPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1099.55646	3295.64598	0.000451244	15	N	91	124
Q3TBD2	Infl	VRGYR	SPLSAASPAELPTEGAFPDGVEDISTLLADVARF	AEGLE	3		1148.579265	3442.714394	0.000451244	3	N	91	125
Q3TBD2	Infl	EGLEK	LKECVLQDDLLEAR	RPLAH	2	C4:+57.021	851.4459272	1700.876254	0.000823681	2	N	131	145
Q3TBD2	Infl	HQVHK	SWPISISDTEVGLDTSSGDLK	KFDRT	2		1104.03986	2206.06412	0.000451244	17	N	617	638
Q3TBD2	Infl	CESSK	LYDPGQQYASHVR	QLQRG	3		511.9201956	1532.737187	0.002519933	1	N	531	544
Q3TBD2	Infl	QVISR	YPLLNTVETLTAAGTLIAK	VKAFH	2		995.0674952	1988.11939	0.000698008	4	N	166	185
Q3TGF2	Infl	LEKQK	LQEEQENAPEFVK	VKGNL	2		780.8811743	1559.746749	0.000451244	9	N	100	113
Q3TGF2	Infl	LELEK	QKLQEEQENAPEFVK	VKGNL	2		908.9579447	1815.900289	0.000662267	7	N	98	113
Q3THE2	Infl	EDVIR	NAFACFDEEATGTIQEDYLR	ELLTT	2	C5:+57.021	1175.518538	2349.021475	0.000451244	249	N	104	124
Q3THK3	Infl	NTAYY	IFTQCADGAFEAFPVQNWYNFTPLAR	HRTLT	3	C5:+57.021	1021.820483	3062.438048	0.000451244	6	N	125	151
Q3THK3	Infl	ENTAY	YIFTQCADGAFEAFPVQNWYNFTPLAR	HRTLT	3	C6:+57.021	1076.174925	3225.501376	0.002296037	2	N	124	151
Q3THK7	Infl	KVILK	NFLYDIAGCSGNFTVQNR	ELECI	2	C9:+57.021	1038.484104	2074.952607	0.000622848	1	N	204	222
Q3THK7	Infl	QGDCR	SYSYVCGISSKDEPDWESLIFLAR	LIPRM	3	C6:+57.021	941.4499438	2821.326431	0.000451244	5	N	524	548
Q3THK7	Infl	DRRVR	ELFVQSEIFPLETPAFAIK	EQGFR	2		1090.088428	2178.161255	0.000451244	8	N	46	65
Q3THK7	Infl	EQGFR	AIIISGGPNSVYAEDAPWFDPAIFTIGKPILGICY	GMQMM	3	C34:+57.021	1255.979781	3764.915943	0.00307782	1	N	70	105
Q3TIX9	Infl	LNNIK	ANDYANAVLQALSNVPPLR	NYFLE	2		1013.539968	2025.064335	0.001264573	1	N	230	249
Q3TIX9	Infl	AKLSR	AYDGTTYLPGIVGLNNIK	ANDYA	2		955.0074376	1907.999275	0.000851441	3	N	212	230
Q3TIX9	Infl	LHTLK	FYCLPDNYEIIDSSLEDITYVLKPTFTK	QQIAN	3	C3:+57.021	1128.891749	3383.651848	0.001329271	2	N	170	198
Q3TJD7	Infl	TPGGK	AAQAGVAVGDWVLNIDGENAGSLTHIEAQNK	IRACG	3		1050.193967	3147.558502	0.001463592	2	N	38	69
Q3TLH4	Infl	LKNRK	VKDAQQVEPEGQEKPSPAVVR	STDPE	4		573.5557302	2290.191721	0.002663018	1	N	2079	2100
Q3TLH4	Infl	DQDEK	QLGQDESTAITSEQNDILK	VVEKR	2		1045.516552	2089.017504	0.000622848	1	N	197	216
Q3TRM8	Infl	HPGER	ASVCPHEGVPRPSGSLELECLQQFK	VTRTQ	3	C4:+57.021,C20:+57.021	942.4620351	2824.362705	0.000451244	3	N	14	39
Q3TRM8	Infl	TKGFR	CSGVEGQDVVQLLR	DAIQR	2	C1:+57.021	780.3962373	1558.776875	0.000451244	4	N	187	201
Q3TRM8	Infl	NQGLK	LGFNFSFPCHQTGLDR	STLIS	2	C9:+57.021	948.4467929	1894.877986	0.000622848	1	N	160	176
Q3TRM8	Infl	LNWTK	GFNASGCEGQDVVYLLR	EAIRR	2	C7:+57.021	942.9493654	1883.883131	0.000451244	21	N	626	643
Q3TRM8	Infl	VLLVR	VAEGSVQIINQVYSIPECR	AQGSG	2	C18:+57.021	1081.549444	2161.083287	0.000451244	45	N	552	571
Q3TRM8	Infl	TGTAR	VHTILQDLGLSPR	ASDAE	2		724.9151545	1447.814709	0.000451244	3	N	362	375
Q3TRM8	Infl	PTYVR	ATPDGSERGDFLALDLGGTNFR	VLLVR	2		1155.061993	2308.108385	0.000870037	2	N	525	547
Q3TRM8	Infl	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	C1:+39.994	983.4668312	1964.918062	0.000451244	5	N	143	160
Q3TRM8	Infl	PTYVR	STPHGTEQGDFLVLELGATGASLR	VLWVT	2		1228.624957	2455.234314	0.000451244	16	N	78	102
Q3TRM8	Infl	GSGQK	LFDHIVDCIVDFQKR	QGLSG	3	C8:+57.021	635.6614624	1903.960987	0.000451244	5	N	578	593
Q3TRM8	Infl	AVCTR	AAQLCAAALAAVLSR	LQHSR	2	C5:+57.021	743.4142331	1484.812866	0.000451244	13	N	392	407
Q3TRM8	Infl	SFPCK	QLGLDQGILLNWTK	GFNAS	2		799.9491943	1597.882789	0.000451244	12	N	612	626
Q3TRM8	Infl	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	2	C18:+57.021	1036.019791	2070.023981	0.000451244	14	N	593	612
Q3TRM8	Infl	RVEPR	SREFVIPQEVILGAGQQLFDFAAR	CLSEF	2		1346.216816	2690.418033	0.000622848	2	N	119	143
Q3TRM8	Infl	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDRESLTPGAQR	FEKMI	3	C2:+57.021	1401.999068	4202.973805	0.000451244	24	N	265	303
Q3TRM8	Infl	EPRSR	EFVIPQEVILGAGQQLFDFAAR	CLSEF	2		1224.650246	2447.284893	0.000451244	20	N	121	143
Q3TRM8	Infl	TLSTR	FDTSVDQASINPGK	QRFEK	2		739.8602419	1477.704884	0.000451244	4	N	729	743
Q3TRM8	Infl	AVSRR	AAQLCGAGVAAVVEK	IRENR	2	C5:+57.021	722.3851412	1442.754682	0.000451244	5	N	834	849
Q3TRM8	Infl	GSGQK	LFDHIVDCIVDFQK	RQGLS	2	C8:+57.021	874.937738	1747.859876	0.000637154	1	N	578	592
Q3TRM8	Infl	LQHSR	EQQTLQVAVATGGR	VFERH	2		729.3895008	1456.763402	0.000622848	2	N	412	426
Q3TRM8	Infl	GEIVR	HILLHLTNLGVLFR	GQKTQ	3		549.3353925	1644.982777	0.000451244	2	N	760	774
Q3TRM8	Infl	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDR	ESLTP	3	C2:+57.021	1088.839937	3263.49641	0.000451244	7	N	265	294
Q3TRM8	Infl	SATVR	KLAPQCTVTFLQSEDGSGK	GAALV	2	C6:+57.021	1033.51507	2065.014539	0.000451244	5	N	885	904
Q3TVI8	Infl	EVALK	QTGDDDEVDDFEDFVFGHFF	GDKAL	2		1190.979999	2379.944399	0.00091018	1	N	669	689
Q3TW96	Infl	APEAR	AALLAELASLEADALR	EHCQR	2		813.9572164	1625.898833	0.002519933	2	N	31	47
Q3TW96	Infl	GPTIK	FFKEHDFFHLDPTNVVLFEQR	MLPAV	4		667.0859262	2664.312505	0.000823681	1	N	179	200
Q3TW96	Infl	APEAR	AALLAELASLEADALREHCQR	AAAAG	4	C19:+57.021	585.0553531	2336.190212	0.000998612	1	N	31	52
Q3TW96	Infl	IKMEK	FVFDVFQFAK	NFVAF	2		624.3271209	1246.638642	0.001463592	2	N	383	393
Q3TXS7	Infl	FILFR	TPEQCPSVVSLLSESYNPHVR	YGAAM	3	C5:+57.021	800.3938812	2398.158243	0.000451244	8	N	628	649
Q3TXS7	Infl	TYLPK	DTSPGSAYQEGGGLYALGLIHANHGGDIIDYLLNQLK	NASND	3		1290.981943	3869.92243	0.002296037	1	N	429	466
Q3TXS7	Infl	FALHK	LNAVVNDFWAEISESVDKIEVLYEDEGFR	SRQFA	3		1129.552938	3385.635415	0.000451244	11	N	26	55
Q3TXS7	Infl	DDVRR	AAVESLGFILFR	TPEQC	2		661.8775093	1321.739419	0.000451244	3	N	616	628

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3TXS7	Infl	-	MITSAAGIISLLDEEEPQLKEFALHK	LNAVV	4		721.6352863	2882.509945	0.000451244	2	N	0	26
Q3TXS7	Infl	AHGPK	IEEEEQEPEPPEPFEYIDD	-	2		1167.495148	2332.974696	0.000622848	9	N	934	953
Q3TXS7	Infl	IIILK	DTSEDVEELVEPVAAHGPK	IEEEE	2		1011.487263	2020.958927	0.000622848	3	N	915	934
Q3U0V1	Infl	EYYKK	IGQQPQQPGAPPQQDYTK	AWEEY	2		990.9928502	1979.9701	0.000451244	13	N	629	647
Q3U0V1	Infl	EYGSR	VGGGIDVPVPR	HSVGV	2		533.3067198	1064.59784	0.001162105	2	N	321	332
Q3U0V1	Infl	GENVK	AINQQTGAFVEISR	QLPPN	2		767.4051509	1532.794702	0.000451244	23	N	449	463
Q3U0V1	Infl	QIAAK	IGGDAATTVNNNTPDFGFGGQKR	QLEDG	2		1169.065067	2336.114533	0.000451244	6	N	88	111
Q3U0V1	Infl	EHAAR	IINDLLQSLR	SGPPG	2		592.8540342	1183.692468	0.000622848	18	N	385	395
Q3U0V1	Infl	EQINK	IQQDSGCKVQISPDSGGLPER	SVSLT	2	C7:+57.021	1136.055622	2270.095643	0.000851441	1	N	170	191
Q3U0V1	Infl	DSGCK	VQISPDSGGLPER	SVSLT	2		677.8522198	1353.68884	0.000451244	5	N	178	191
Q3U0V1	Infl	EYYKK	QAQVATGGGPGAPPGSQPDYSAAWAEYYR	QQAAY	2		1476.681523	2951.347447	0.000823681	3	N	655	684
Q3U0V1	Infl	QIAAK	IGGDAATTVNNNTPDFGFGGQK	RQLED	2		1091.014511	2180.013422	0.000451244	11	N	88	110
Q3U0V1	Infl	GAGDR	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	KDAFA	2		1164.047739	2326.079879	0.000622848	4	N	40	71
Q3U0V1	Infl	QPDSK	KLASQGDSIGSQLGPIHPPPR	TSMTE	3		719.0593158	2154.154547	0.001329271	1	N	122	143
Q3U0V1	Infl	EEYYK	KIGQQPQQPGAPPQQDYTK	AWEEY	3		703.6961545	2108.065063	0.001162105	3	N	628	647
Q3U0V1	Infl	GAGDR	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIRK	DAFAD	3		819.0660807	2454.174842	0.000823681	8	N	40	72
Q3U0V1	Infl	WAAYY	SHYYQQPPGPVPGPAPAPAAPPAQGEPPQPPPTGQSDYTK	AWEEY	3		1358.992731	4073.954793	0.000451244	6	N	581	621
Q3U0V2	Infl	ATLQR	LVEALEENELTSLAEDLLGQAEPDGGLA	-	2		1448.719645	2895.423691	0.000451244	9	N	282	310
Q3U0V2	Infl	VAIYK	ALQTALSESGDSSDVLQILK	IHCSD	2		1038.047488	2074.079376	0.000451244	3	N	43	63
Q3U0V2	Infl	DELCK	LTCDCTGQGGAIQVASAGSK	FPVSS	2	C3:+57.021,C5:+57.021	990.9593729	1979.903146	0.000622848	1	N	161	181
Q3U141	Infl	SLKTR	IQEDTGILETDQELLQEAGLVLLPDKPATQCISDSK	TNEGL	3	C31:+57.021	1323.340431	3966.997894	0.000451244	1	N	339	375
Q3U141	Infl	CCGLR	EGAVLTLLSDIASALR	YLHEN	2		814.9650414	1627.914483	0.000451244	2	N	118	134
Q3U1F9	Infl	PVPVK	LLDENANLPQEGGGQAEEQAAEGTGGHSK	RFSSL	3		969.7837445	2906.327833	0.000451244	14	N	260	289
Q3U1F9	Infl	HHVPK	ESDYESIGDLQQCR	DVTRL	2	C13:+57.021	850.3653311	1698.715062	0.000451244	1	N	410	424
Q3U1J4	Infl	VLSSR	IEVQDSSGGTTALRPSASTQALSSSVSSSK	LFSSS	3		980.1586999	2937.4527	0.000451244	22	N	739	769
Q3U1J4	Infl	FHTER	KTEPATGFIDGDLIESFLDISRPK	MQEVV	4		663.1002363	2648.369745	0.000451244	6	N	1080	1104
Q3U1J4	Infl	SGMKR	EATADDLIKVVEELTR	IH-	2		901.4812526	1800.946905	0.000622848	1	N	1122	1138
Q3U1J4	Infl	YESPR	KICYQEVSQCFGVLSSR	IEVQD	2	C3:+57.021,C10:+57.021	1030.998301	2059.981002	0.000451244	1	N	722	739
Q3U1J4	Infl	VDLER	QGQGQLVTCSGAFK	EGSLR	2	C9:+57.021	740.864573	1479.713546	0.001352548	1	N	369	383
Q3U1J4	Infl	VIDVK	FLYGCQAPTICFVYQDPQGR	HVKTY	2	C5:+57.021,C11:+57.021	1210.561797	2419.107994	0.000451244	3	N	168	188
Q3U1Z5	Infl	LEEQR	ATFHTPEAPPNLAPAPPR	LLEDK	2		942.492289	1882.968978	0.000622848	10	N	80	98
Q3U1Z5	Infl	PAPPR	LLEDKEQLYSTILSHQCQR	IEAQR	2	C17:+57.021	1181.097289	2360.178979	0.000622848	2	N	98	117
Q3U1Z5	Infl	IEAQR	SDPPLPPGGQELLELLLR	VQGGG	2		972.5441873	1943.072775	0.000451244	8	N	122	140
Q3U1Z5	Infl	ALGPR	SGSLLSLQTELLLDLVAEAQSR	RLEEQ	3		781.7642342	2342.269303	0.000451244	2	N	52	74
Q3U2G2	Infl	PISLR	WNSPAEEGLSDCEVFPK	NHAAP	2	C12:+57.021	982.9386633	1963.861727	0.000451244	3	N	405	422
Q3U2G2	Infl	LTFYR	KEPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1143.901679	3428.681637	0.000622848	8	N	436	466
Q3U2G2	Infl	TFYRK	EPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1101.203358	3300.586674	0.000451244	15	N	437	466
Q3U2G2	Infl	VEAEK	SNLAYDIVQLPTGLTGIK	VTYME	2		952.0309127	1902.046225	0.000451244	14	N	84	102
Q3U2G2	Infl	VAVAR	AGGIETIANEYSDR	CTPAC	2		748.3553237	1494.695047	0.000451244	3	N	19	33
Q3U2G2	Infl	EAVTR	GCALQCAILSPAFK	VREFS	2	C2:+57.021,C6:+57.021	768.389138	1534.762676	0.000451244	6	N	374	388
Q3U2G2	Infl	HGRAF	SDPFVEAEKSNLAYDIVQLPTGLTGIK	VTYME	2		1453.263826	2904.512052	0.001162105	1	N	75	102
Q3U2G2	Infl	KAKVK	TSTVDLPIESQLLWQLDR	EMLGL	2		1057.560566	2113.105531	0.000451244	10	N	575	593
Q3U2G2	Infl	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDK	KLPEM	3		1110.149815	3327.426044	0.000451244	18	N	800	834
Q3U2G2	Infl	TFTLK	LEDTENWLYEDGEDQPK	QVYVD	2		1040.953253	2079.890907	0.000451244	6	N	653	670
Q3U2G2	Infl	AFKVR	EFSITDVVPYPISLR	WNSPA	2		868.4674169	1734.919234	0.000637154	3	N	390	405
Q3U2G2	Infl	EIEAK	IKELTSICSPIISKPKPK	VEPPK	2	C8:+57.021	1020.100584	2038.185568	0.001329271	1	N	773	791
Q3U2G2	Infl	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDKK	LPEMD	4		864.8880518	3455.521007	0.000451244	1	N	800	835
Q3U7R1	Infl	LRLER	LTPRPTAAELEEVLQVNSLIQTQK	SSELA	3		893.4961475	2677.465042	0.000451244	11	N	754	778
Q3U7R1	Infl	QVHLR	LEWLSLLPDAEKLDQVLQWNR	GITSR	3		856.1275069	2565.359121	0.000451244	18	N	435	456
Q3U7R1	Infl	LGRYK	VSLTTVLNSGFLDEWLTLEDVPSGR	LHLRL	2		1374.708687	2747.401774	0.000451244	4	N	722	747
Q3U7R1	Infl	SHKTK	TVSQSSAPVWEESASFLIR	KPHAE	2		1047.529266	2093.042931	0.000451244	14	N	822	841
Q3U7R1	Infl	KDDSR	ALTLGALTLPLAR	LLTAS	2		655.414259	1308.812918	0.000451244	8	N	540	553
Q3U7R1	Infl	EFNER	FEWDLPLDGTLR	RKLDV	2		731.3727881	1460.729976	0.001162105	4	N	1028	1040
Q3U7R1	Infl	IQTQK	SSELAAALLSVFLER	AEDLP	2		803.4464845	1604.877369	0.000451244	6	N	778	793
Q3U7R1	Infl	TRESK	ATYSTNSPVWEEAFRF	FLQDP	2		952.9448373	1903.874075	0.002453667	2	N	505	521
Q3U7R1	Infl	VLPNR	LLVPLVPDLQDVAQLR	SPLPR	2		895.0332584	1788.050917	0.000451244	6	N	297	313
Q3U7R1	Infl	LDVGK	VLQAGVLDNWYPLQGGQGQVHLR	LEWLS	2		1274.675119	2547.334637	0.000451244	2	N	412	435
Q3U7R1	Infl	EVRHR	LTHGDSPSEAPVGPLGQVK	LTVWY	2		944.9923189	1887.969038	0.000451244	2	N	945	964
Q3U7R1	Infl	LPLAR	LLTASELTLDQWFQLSSSGPNSR	LYMKL	2		1275.645889	2549.276179	0.001162105	1	N	553	576
Q3U7R1	Infl	IQTQK	SSELAAALLSVF	LERAE	2		604.3326002	1206.6496	0.001871652	5	N	778	790
Q3U9G9	Infl	TPQRK	DLEFGGVPGAVLIMLGLPACVLLLLQCR	QKDPG	3	C20:+57.021,C28:+57.021	1046.581317	3136.72055	0.000823681	12	N	216	245
Q3U9G9	Infl	LRAPR	EELSPASSGNAVYDFFIGR	ELNPR	2		1029.992516	2057.969432	0.000451244	3	N	364	383
Q3U9G9	Infl	REEVK	AKEIESEEQNLVTK	GPAPL	2		809.4206637	1616.825727	0.000622848	4	N	186	200
Q3U9G9	Infl	EVKAK	EIESEEQNLVTK	GPAPL	2		709.8546252	1417.69365	0.000622848	11	N	188	200
Q3U9G9	Infl	GSSLY	YEVEILSHDNK	SQLYT	2		673.8334957	1345.651391	0.000622848	22	N	22	33

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3U9G9	Infl	NLVTK	GPAPLGTFQVTTPQR	KDLEF	2		785.4233437	1568.831087	0.000451244	4	N	200	215
Q3U9G9	Infl	TSTGK	SLLVSGWWGFVR	HPNYL	2		703.883126	1405.750652	0.000622848	3	N	543	555
Q3UEB3	Infl	RAFNR	IYVASVHQDLSDDDIKSVFEAFGK	IKSCT	4		671.5872274	2682.317709	0.000851441	1	N	232	256
Q3UEB3	Infl	AIMCR	VYVGSIYYELGEDTIR	QAFAP	2		938.9705208	1875.925442	0.000451244	5	N	135	151
Q3UEB3	Infl	STGTK	LGLPPLTPEQQEALQK	AKKYA	2		881.4914234	1760.967247	0.001943752	1	N	58	74
Q3UEB3	Infl	GRNIK	VGRPSNIGQAQPIIDQLAEEAR	AFNRI	3		788.0878227	2361.240068	0.000451244	2	N	206	228
Q3UI43	Infl	SVGSR	SEGEGEAATADGGAASVPGAGPKPWQVPASASEVQIR	TPRVN	3		1178.908555	3533.702266	0.000451244	18	N	52	89
Q3UI43	Infl	TSDPR	ELCSCLYDLETASCSTFNLEGLFSLIQQK	TELPV	3	C3:+57.021,C5:+57.021,C14:+57.021	1142.868313	3425.58154	0.000451244	6	N	168	197
Q3UJB0	Infl	KDSGR	SRGSDPPAADVEIEYVTEEPEIYEPNFIFF	KRIFE	3		1154.208949	3459.603447	0.001699387	1	N	339	369
Q3UJB0	Infl	ETDTR	SSLGQSASETEEDTVSISKK	EKNRK	2		1042.006017	2081.996435	0.000622848	1	N	284	304
Q3UJB0	Infl	SGRSR	GSDPPAADVEIEYVTEEPEIYEPNFIFF	KRIFE	3		1073.164569	3216.470307	0.000823681	1	N	341	369
Q3UJB9	Infl	PCVSR	SLEPVAGQLSNSVATK	LTAVE	2		800.9311986	1599.846797	0.000622848	6	N	1062	1078
Q3UJB9	Infl	EGQQR	GGQLQEQLTQQLSQALSSAVAGR	LERSV	2		1185.622749	2369.229897	0.002080925	1	N	1020	1043
Q3UJB9	Infl	ELLQR	LCAQLEGLQSTVTDHVER	ALETR	3	C2:+57.021	686.009479	2055.005037	0.002296037	1	N	979	997
Q3ULJ0	Infl	LPGHK	LPENVVAVPNLSEAVQDADLLVFVIPHQFIHK	ICDEI	3		1184.647396	3550.918788	0.002884417	1	N	70	102
Q3ULJ0	Infl	LPGHK	LPENVVAVPNLSEAVQDADLLVFVIPHQF	IHKIC	3		1058.568083	3172.680849	0.000451244	7	N	70	99
Q3ULJ0	Infl	ITLIK	GIDEGPDGLKLISDIIR	EKMGI	3		604.335675	1809.983625	0.001839721	1	N	122	139
Q3ULJ0	Infl	KIFCK	GQVSTATFLESCGVADLITTCYGGR	NRRVA	2	C12:+57.021,C21:+57.021	1332.125687	2662.235773	0.000451244	1	N	246	271
Q3ULJ0	Infl	STATF	LESCGVADLITTCYGGR	NRRVA	2	C4:+57.021,C13:+57.021	936.4350022	1870.854404	0.000451244	2	N	254	271
Q3ULJ0	Infl	TPNFR	ITVVDDADTVELCGALK	NIVAV	2	C13:+57.021	909.9616071	1817.907614	0.001943752	2	N	189	206
Q3UM45	Infl	SNRIR	AIENIDTLTNLESLFLGK	NKITK	2		996.0389348	1990.06227	0.000451244	17	N	200	218
Q3UM45	Infl	NKITK	LQNLDALTNLTVLSVQSNR	LAKIE	2		1050.076914	2098.138229	0.000451244	13	N	223	242
Q3UM45	Infl	LVNLR	ELYLSNNGIEVIEGLENNNK	LTMLD	2		1131.566576	2261.117553	0.000451244	8	N	256	276
Q3UND0	Infl	SSPQR	SQPIDDEIYEELPEEEEDTASVK	MDEQG	2		1333.098497	2664.181395	0.000451244	20	N	251	274
Q3UND0	Infl	VQQLK	FILQDLGSDVIPEDDEERGELYDDVDHPAAVSSPQR	SQPID	3		1342.966687	4025.876662	0.000451244	23	N	215	251
Q3UND0	Infl	IKDVK	SVYLQEFQDKGDAEDGDEYDDPFAGPADTISLASER	YDKDD	3		1317.584131	3949.728994	0.000451244	24	N	56	92
Q3UND0	Infl	LASER	YDKDDDGPSDGNQFPPIAAQDLPFVIK	AGYLE	3		988.1422101	2961.40323	0.000451244	32	N	92	119
Q3UND0	Infl	GKGSR	DSVHHTSGDKSTDYANFYQGLWDCTGALSDELSFK	RGDVI	3	C24:+57.021	1317.918637	3950.732512	0.002663018	1	N	283	318
Q3UND0	Infl	TSGDK	STDYANFYQGLWDCTGALSDELSFK	RGDVI	2	C14:+57.021	1444.639912	2887.264225	0.000451244	15	N	293	318
Q3UND0	Infl	-M	PNPSCTSSPGPLPEEIR	NLLAD	2	C5:+57.021	919.4413732	1836.867146	0.000451244	4	N	1	18
Q3UND0	Infl	PEEIR	NLLADVETFVADTLKGENLSK	KAKEK	2		1139.102795	2276.189989	0.000451244	1	N	18	39
Q3UND0	Infl	EKRRK	DHSFLGFEWQKR	WCALS	3		517.2569192	1548.747358	0.001162105	2	N	128	140
Q3UND0	Infl	PEEIR	NLLADVETFVADTLK	GENLS	2		824.9437746	1647.871949	0.000451244	7	N	18	33
Q3UND0	Infl	DKQQK	GEFAIDGYDVR	MNNTL	2		621.2940064	1240.572413	0.000451244	4	N	161	172
Q3UND0	Infl	APDKR	IYQFTAASPKDAEEWVQQLK	FILQD	2		1176.59768	2351.179759	0.000451244	3	N	195	215
Q3UND0	Infl	QQLKF	ILQDLGSDVIPEDDEERGELYDDVDHPAAVSSPQR	SQPID	3		1293.943883	3878.808248	0.000451244	8	N	216	251
Q3UND0	Infl	KDGKK	DCCFEICAPDKR	IYQFT	2	C2:+57.021,C3:+57.021,C7:+57.02	785.8258133	1569.636027	0.000451244	5	N	183	195
Q3UND0	Infl	AASPK	DAEEWVQQLK	FILQD	2		623.3096565	1244.603713	0.001699387	2	N	205	215
Q3UND0	Infl	EKRRK	DHSFLGFEWQK	RWCAL	3		465.2232155	1392.646246	0.002374549	1	N	128	139
Q3UND0	Infl	VKSVY	LQEFQDKGDAEDGDEYDDPFAGPADTISLASER	YDKDD	3		1201.196208	3600.565223	0.000451244	9	N	59	92
Q3UP87	Infl	GLNFR	SVQVVLGAHDLR	RQERT	2		647.3678401	1292.72008	0.000451244	13	N	77	89
Q3UP87	Infl	MCRRR	VNVCTLVPR	RQAGI	2	C4:+57.021	529.2950665	1056.574533	0.000622848	9	N	183	192
Q3UP87	Infl	TLVPR	RQAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C6:+57.021,C16:+57.021	1017.502893	3049.48528	0.000451244	18	N	192	220
Q3UP87	Infl	AGICF	GDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C9:+57.021	1109.549975	2217.08435	0.000451244	58	N	199	220
Q3UP87	Infl	DSFIR	GGCGSGLYPDAFAPVAEF	ADWIN	2	C3:+57.021	907.9066349	1813.79767	0.000622848	21	N	220	238
Q3UP87	Infl	RRQAG	ICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C2:+57.021,C12:+57.021	1319.641307	2637.267014	0.000451244	10	N	196	220
Q3UP87	Infl	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C5:+57.021,C15:+57.021	1447.699885	2893.384169	0.000451244	25	N	193	220
Q3UP87	Infl	PRRQA	GICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C3:+57.021,C13:+57.021	1348.152039	2694.288478	0.000451244	55	N	195	220
Q3UP87	Infl	GGPLV	CNNLVQGIDSFIR	GGCGS	2	C1:+57.021	768.3856726	1534.755745	0.001329271	3	N	207	220
Q3UP87	Infl	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIR	SHNDH	2	C3:+57.021	1442.19245	2882.369299	0.000451244	9	N	220	247
Q3UP87	Infl	PVAEF	ADWINSIIR	SHNDH	2		544.2988947	1086.582189	0.000998612	4	N	238	247
Q3UP87	Infl	SLQRR	GGHFCGATLIAR	NFVMS	2	C5:+57.021	630.3196042	1258.623608	0.001395409	1	N	49	61
Q3UP87	Infl	SATIN	ANVQVAQLPAQGQGVGDR	TPCLA	2		904.4746276	1806.933655	0.000451244	8	N	129	147
Q3UP87	Infl	FSVQR	IFENGFDPSQLL	NDIVI	2		690.346239	1378.676878	0.001591523	3	N	102	114
Q3UP87	Infl	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIRS	HNDHL	3	C3:+57.021	990.8082426	2969.401328	0.001591523	1	N	220	248
Q3UP87	Infl	TLIAR	NFVMSAAHCVNGLNFR	SVQVV	2	C9:+57.021	918.9355386	1835.855477	0.000451244	2	N	61	77
Q3UP87	Infl	SGGPL	VCNNLVQGIDSFIR	GGCGS	2	C2:+57.021	817.9198796	1633.824159	0.000823681	4	N	206	220
Q3UPH1	Infl	VAAVR	DAFQEVFGLAVVVGEAGQSNIAPQPVGYAAGLK	GAQER	3		1101.573897	3301.69829	0.000451244	17	N	272	305
Q3UPH1	Infl	VHGIR	LEAFTQATPVPLEFVQQAQSLTPQDYNLR	WSGLL	3		1102.233652	3303.677555	0.000451244	20	N	357	386
Q3UPH1	Infl	DYNLR	WSGLLVTVGEVLEK	SLLNV	2		765.4328457	1528.850091	0.001871652	1	N	386	400
Q3UPH1	Infl	AIHEK	QTAVSVENFIAELLPDKWFDIGCLVVEDPVHGIR	LEAFT	4	C23:+57.021	967.500508	3865.970832	0.000622848	2	N	323	357
Q3UQ44	Infl	PAFSK	IGGILANELSVDEAALHAAVIAINEAIEK	GVAKQ	3		982.2050333	2943.5917	0.000451244	16	N	198	227
Q3UQ44	Infl	SAKLK	NSCISEEERDAYEELLTQAEIQSNISTVNR	MAAVD	3	C3:+57.021	1166.881523	3497.62117	0.000451244	11	N	273	303
Q3UQ44	Infl	PAFSK	IGGILANELSVDEAALHAAVIAINEAIEKGVAK	QTIIT	4		825.7112136	3298.813655	0.000622848	2	N	198	231

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3UQ44	Infl	KNVSK	VLWLDEIQQAINEANVDENR	AKQWV	2		1185.09075	2368.1659	0.000451244	14	N	514	534
Q3UQ44	Infl	IITLR	NPNAVLTCVDDSLSQEYQK	ELWEA	2	C8:+57.021	1091.010348	2180.005097	0.001871652	3	N	238	257
Q3UQ44	Infl	KVTDK	VLGSIISSLDLLPYGLR	YIAKV	2		908.5330912	1815.050582	0.002981883	1	N	1057	1074
Q3UQ44	Infl	VEVYK	AWVNQLETQTGEASKLPYDVTTEQALTYPEVK	NKLEA	3		1203.937341	3608.788622	0.000451244	1	N	1009	1041
Q3UQ44	Infl	LCLSK	ESWLTGEEIEDIVEEVTSDYIR	EKLWS	2		1306.61666	2611.217721	0.000662267	2	N	631	653
Q3UW53	Infl	LPEGR	GSTSQSTSGGLTENTSCPGPIEEPFEAQEPAEK	VLPAI	3	C17:+57.021	1141.511096	3421.509888	0.000451244	22	N	785	818
Q3UW53	Infl	EREVR	EKEAQPLEAEAPGVDLGILPEGR	GSTSQ	2		1209.629708	2417.243816	0.000451244	4	N	762	785
Q3UW53	Infl	VLLPK	AFPVYLWQPYLR	HGYFC	2		776.9197085	1551.823817	0.000451244	6	N	159	171
Q3UW53	Infl	EVREK	EAQPLEAEAPGVDLGILPEGR	GSTSQ	2		1081.06093	2160.10626	0.000451244	16	N	764	785
Q3UW53	Infl	TIRKK	IFQEALIQITLPTVQK	ALAST	2		921.5409163	1841.066233	0.000870037	1	N	493	509
Q3UW53	Infl	FSEVR	ALFEKEVDELSQSFHATQDSAQLK	EGLQQ	3		907.7842456	2720.329337	0.000451244	8	N	365	389
Q3UW53	Infl	ALFEK	EVDELSQSFHATQDSAQLK	EGLQQ	2		1067.008894	2132.002189	0.000451244	10	N	370	389
Q3UW53	Infl	CNHVR	SEVEQQRDLTSQFLK	TKPPL	2		904.4633942	1806.911188	0.000870037	1	N	45	60
Q3UW53	Infl	KELKK	LLTVTVSVESAPVVENDIHNGTPVPQENIKEEESK	IHPEA	4		951.2407979	3800.931992	0.000451244	1	N	705	740
Q3UYV9	Infl	KVGEK	SACSLESNLEGLAGVLEADLPNYK	SKILR	2	C3:+57.021	1275.623534	2549.231468	0.000451244	15	N	41	65
Q3UYV9	Infl	LLPEK	LTIYTTLVGLLNAR	NYNFG	3		516.6438917	1546.908275	0.002374549	1	N	82	96
Q3UZ39	Infl	KSDSR	ASNSPEQSSCLEGLDSEVPGPTEDLKTDLGK	GSFEP	3	C10:+57.021	1087.508915	3259.503346	0.000451244	28	N	344	375
Q3UZ39	Infl	TDLGK	GSFEPCPDYILGQTAEIDKVTCTDSR	GTGGN	3	C6:+57.021,C22:+57.021	987.1200033	2958.33661	0.000451244	11	N	375	401
Q3UZ39	Infl	EMLEK	HGIILNSEIATNGETSDTVNDVGYQAPTK	ITKEE	3		1015.498945	3043.473435	0.000451244	2	N	194	223
Q3UZ39	Infl	LAGAK	CEQQVQSQDQENTSDLKNSEQIESHK	VTNKS	3	C1:+57.021	1030.462299	3088.363498	0.000451244	4	N	310	336
Q3UZ39	Infl	CTDSR	GTGGNQREDEVQAGDTTVEDQVGTVASGPAK	QSKGT	3		1025.148864	3072.423191	0.000451244	23	N	401	432
Q3UZ39	Infl	HPGEK	AENQRPAEDSALSPGPLAGAK	CEQQV	2		1040.027421	2078.039243	0.000451244	6	N	289	310
Q3UZ39	Infl	GSSGK	QNKVEEDGPTEGPTDILDQNSPQCEDR	EISPV	3	C24:+57.021	1024.455033	3070.3417	0.000451244	9	N	628	655
Q3UZ39	Infl	TDLGK	GSFEPCPDYILGQTAEIDK	VTCTD	2	C6:+57.021	1070.499085	2138.98257	0.000451244	2	N	375	394
Q3UZ39	Infl	GKQNK	VEEDGPTEGPTDILDQNSPQCEDREISPVGEK	GPQCD	3	C21:+57.021	1180.869172	3539.584116	0.000451244	4	N	631	663
Q3UZ39	Infl	GKQNK	VEEDGPTEGPTDILDQNSPQCEDR	EISPV	2	C21:+57.021	1351.080416	2700.145232	0.002145581	1	N	631	655
Q3UZA1	Infl	FRDYR	AVEPSQENGAREENGDDVFASK	SKDPG	2		1175.033629	2348.051658	0.000698008	1	N	188	210
Q3UZA1	Infl	EPDTK	QKEEAPLEPSCSPGADHAAGEITSEIQNEK	AVSMD	3	C11:+57.021	1074.833733	3221.4778	0.000451244	22	N	368	398
Q3UZA1	Infl	PLIEK	LQANLAFDPAALLPGASPK	SPGLK	2		947.5257975	1893.035995	0.000451244	22	N	88	107
Q3UZA1	Infl	NAGEK	VGQNPDTASQGHPEVQAPSQTGSPEAENGCGSPR	EETTP	3	C30:+57.021	1149.513945	3445.518436	0.000451244	35	N	265	299
Q3UZA1	Infl	SPGIR	SHPSEAEEVPVSFDQPPEGTHLPSYNK	VRTRG	3		993.4654642	2977.372993	0.000451244	4	N	131	158
Q3UZZ4	Infl	QHPER	TLYWVAPLNTDAR	ALEYY	2		760.3993372	1518.783074	0.000451244	13	N	277	290
Q3UZZ4	Infl	LEYYR	LYDSLDNLLIYSHFRDYR	IRYGQ	4		576.5423571	2302.138229	0.0025889	1	N	296	314
Q3UZZ4	Infl	DYRIR	YGQGGGTVAFNNNLYVNWYNGGNIAK	INLTT	2		1396.165312	2790.315024	0.000451244	5	N	316	342
Q3UZZ4	Infl	LEYYR	LYDSLDNLLIYSHFR	DYRIR	2		934.9812228	1867.946846	0.000622848	1	N	296	311
Q3UZZ4	Infl	PFDQK	LYVYNDGYLLNYDLVFLQTPR	QPV-	2		1290.163187	2578.310773	0.000451244	11	N	481	502
Q3UZZ4	Infl	TLNTK	TEEIFYYYDTNTER	EGNLG	2		922.4052106	1842.794821	0.000451244	14	N	441	455
Q3UZZ4	Infl	LLVEK	LESLDQNNVLSIR	RQILA	2		750.9049838	1499.794368	0.000451244	2	N	192	205
Q3UZZ4	Infl	AYNNR	FSYANVNWQDIDLAVDEQALWAIYATEASTGNIVISK	LNDTT	3		1372.67993	4115.01639	0.000870037	8	N	364	401
Q3UZZ4	Infl	KLYVY	NDGYLLNYDLVFLQTPR	QPV-	2		1021.023619	2040.031638	0.000451244	18	N	485	502
Q3UZZ4	Infl	REFSK	VKEYVQLISVYEK	RLLNL	2		799.4459531	1596.876306	0.000451244	7	N	111	124
Q3UZZ4	Infl	EVEIR	NMTLLVEKLESLDQNNVLSIR	RQILA	2	M2:+15.995	1223.155079	2444.294558	0.002019181	1	N	184	205
Q3V1G4	Infl	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	2	C1:+57.021	1057.513058	2113.010516	0.000451244	10	N	489	508
Q3V1G4	Infl	QGASR	KEDFYTVETITSGSSCK	CACVA	2	C16:+57.021	976.4516036	1950.887607	0.000451244	14	N	98	115
Q3V1G4	Infl	GSSCK	CACVAPPSAVNPCEGDFR	LQKLR	2	C1:+57.021,C3:+57.021,C13:+57.021	1003.92933	2005.84306	0.000451244	23	N	115	133
Q3V1G4	Infl	EYEER	FLQEETVSQQINSIELLR	TQPLV	2		1074.071298	2146.126995	0.000451244	3	N	245	263
Q3V1G4	Infl	SRDLK	LSTIIDLLEGAFY	GLDLL	2		727.8930221	1453.770444	0.000451244	8	N	146	159
Q3V1G4	Infl	SRDLK	LSTIIDLLEGAFYGLDLLK	LHSVT	2		1047.590803	2093.166006	0.000451244	11	N	146	165
Q3V1G4	Infl	SALQR	DAAAAYAHPEYEER	FLQEE	2		796.8529482	1591.690296	0.000637154	2	N	231	245
Q3V1L4	Infl	LLGAK	GKDILYIGDHIFGDILK	SKKRQ	3		639.6880487	1916.040746	0.00307782	1	N	342	359
Q3V1L4	Infl	LTVER	LVSIGYPQELLSFAYDSTFPTR	GLVFD	2		1252.639544	2503.263489	0.000451244	17	N	76	98
Q3V1L4	Infl	RQGWR	TFLVIPELAQELHVWTDK	SSLFE	3		713.7215295	2138.141189	0.002813207	1	N	367	385
Q3V1L4	Infl	VWTDK	SSLFEELQSLDIFLAELYK	HLDSS	2		1123.086082	2244.156564	0.000451244	1	N	385	404
Q3V1L4	Infl	LPETY	LLACLVDFFTNCPR	YTSCD	2	C4:+57.021,C12:+57.021	863.4262519	1724.836904	0.000451244	6	N	163	177
Q3V3R1	Infl	FLSGK	LSGGSPGVPVDKLIAEESVSLLAAALR	IQNMV	3		883.8327596	2648.474879	0.000451244	3	N	298	325
Q3V3R1	Infl	VPVDK	LIAEESVSLLAAALR	IQNMV	2		778.4568522	1554.898104	0.000823681	1	N	310	325
Q497J0	Infl	AVEYK	TQAVAGENIFIK	MDVGH	2		645.8567739	1289.697948	0.000451244	25	N	44	56
Q497J0	Infl	FIHIK	VFNGPTGKDNYELHGYQTDK	TKDDE	2		1142.037986	2282.060372	0.001352548	1	N	68	88
Q497J0	Infl	EAVEY	KTQAVAGENIFIK	MDVGH	2		709.9042554	1417.792911	0.000451244	26	N	43	56
Q497J0	Infl	GPTGK	DNYELHGYQTDK	TKDDE	2		741.8289417	1481.642283	0.000451244	4	N	76	88
Q4KML4	Infl	FQDDR	CANLFEALVGTLK	AAKRR	2	C1:+39.994	709.8711099	1417.72662	0.000870037	3	N	38	51
Q4KML4	Infl	KIVTY	AGELLLQGVHDDVDIVLLQD	-	2		1081.57113	2161.126661	0.00307782	2	N	61	81
Q4QRL3	Infl	KAVLR	GQELGDRLEHLQEELEQAALER	QKFLQ	3		855.096935	2562.267405	0.000451244	2	N	885	907
Q4QRL3	Infl	GPRLR	AQVEAAEQQVQALESQVR	CHLEE	2		992.5088644	1983.002129	0.001699387	1	N	841	859

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q4QRL3	Infl	ELKAR	ALQLEEELIQLR	QYPVD	2		727.9148201	1453.81404	0.00091018	1	N	949	961
Q4QRL3	Infl	DAWSR	EEPTPGETLVSAIPEEQALRDEVAQLR	REVAG	3		993.1758023	2976.504007	0.000451244	7	N	716	743
Q4QRL3	Infl	EVEEK	AEQLLDSQAEVQGLEAEIR	RLRQE	2		1050.034912	2098.054224	0.000451244	1	N	282	301
Q4QRL3	Infl	HGGPR	LGADGAGSTESLGGPLETELPEGR	EADGT	2		1157.064398	2312.113196	0.001463592	1	N	1342	1366
Q52KI8	Infl	HKKEK	AVTIATPATAAPAAVSAATTTSAQEEPAAAPEPR	KETES	3		1064.212916	3189.615349	0.000451244	25	N	876	910
Q569Z6	Infl	KSSSK	DSRPSQAAGDNQGDEAKEQTFSGGTSQDIK	GSESS	3		1042.140368	3123.397704	0.000451244	15	N	185	215
Q569Z6	Infl	SPVGK	SPPATGSAYGSSQKEESAASGGAAYSK	RYLEE	3		849.3934172	2545.156852	0.000622848	8	N	319	346
Q571E4	Infl	LGISK	NTFVFFTSDNGAALISAPNEGGSNGPFLCGK	QTTFE	3	C29:+57.021	1063.836749	3188.486848	0.000622848	9	N	277	308
Q571E4	Infl	TQHAR	QSPFFLYWAIDATHAPVYASR	QFLGT	2		1220.608382	2439.201163	0.001839721	1	N	220	241
Q571E4	Infl	DSVGK	ILSLLQNLGISK	NTFVF	2		649.9062668	1297.796934	0.000451244	7	N	265	277
Q571E4	Infl	GDAVR	EIDDSVGKILSLLQNLGISK	NTFVF	3		714.7392488	2141.194347	0.000451244	3	N	257	277
Q571E4	Infl	FHPLK	HGFDEWFGSPNCHFGPYDNK	AKPNI	3	C12:+57.021	804.3363662	2409.985699	0.002453667	1	N	150	170
Q571I9	Infl	QKHQR	LLWTLESLVTGR	AVREV	2		694.4013486	1386.787097	0.000451244	13	N	117	129
Q571I9	Infl	SPRAR	AGLLWALAAALER	RKPVL	2		677.8962334	1353.776867	0.000451244	14	N	588	601
Q571I9	Infl	KPEHR	NPAPCQDPITGENLASCLQAEAEDIAAAVEAAK	IAFKA	3	C5:+57.021,C17:+57.021	1142.204907	3423.591321	0.000451244	21	N	54	87
Q571I9	Infl	TWGTR	VQDQGQTLQVTGLR	GPVLR	2		771.9158828	1541.816166	0.000451244	1	N	637	651
Q5EG47	Infl	TLFKK	ICDGIFYTPQYLNPSVISLLK	HMLQV	2	C2:+57.021	1221.143177	2440.270754	0.000451244	10	N	236	257
Q5EG47	Infl	EVCEK	FECSEEEVLSCLYNR	NHQDP	2	C3:+57.021,C11:+57.021	967.9166423	1933.817685	0.000622848	1	N	310	325
Q5FWK3	Infl	KTFLR	ELPEPLLTFDLYPHVVGFLNIDESQR	VEVTQ	3		1014.525995	3040.554586	0.000451244	22	N	323	349
Q5FWK3	Infl	NTFTK	FLLDHQGELFPSTDAQGV	-	2		987.4843266	1972.953053	0.000451244	4	N	421	439
Q5FWK3	Infl	DESQR	VEVTQQVLQTLPEENYQVLHFLTAFLVQISAHCDQNK	MTNTN	4	C33:+57.021	1085.806361	4339.194243	0.000823681	4	N	349	386
Q5FWK3	Infl	DESQR	VEVTQQVLQTLPEENYQVLHFLTAF	LVQIS	3		982.8469574	2945.517472	0.001162105	2	N	349	374
Q5RKN9	Infl	DHLRK	EASDPQPEDVDGGLKSWR	ESCDS	2		993.4641225	1984.912645	0.000451244	6	N	103	121
Q5RKN9	Infl	RIAAK	FITHAPPGEFNEVFNDVR	LLLNN	2		1045.011043	2088.006486	0.000823681	6	N	19	37
Q5RKN9	Infl	TVYAK	TIDGQQTIIACIESHQFQPK	NFWNG	2	C11:+57.021	1157.578733	2313.141865	0.000451244	17	N	146	166
Q5RKN9	Infl	DSALR	AYVKDHYSNGFCTVYAK	TIDGQ	2	C12:+57.021	1011.972841	2021.930081	0.000622848	7	N	129	146
Q5RKN9	Infl	DHLRK	EASDPQPEDVDGGLK	SWRES	2		778.8578962	1555.700192	0.000451244	18	N	103	118
Q5RKN9	Infl	LVSHK	DVQDSVTVSNEIQTTK	EFIKI	2		882.4370421	1762.858484	0.000451244	8	N	210	226
Q5RKN9	Infl	RSEWK	FTITPPSAQVVGVLK	IQVHY	2		778.956488	1555.897376	0.000451244	7	N	178	193
Q5RKN9	Infl	RAYVK	DHYSNGFCTVYAK	TIDGQ	2	C8:+57.021	781.3409307	1560.666261	0.000451244	3	N	133	146
Q5RKN9	Infl	FTPVK	IEGYDDQVLITEHGDLGNSR	FLDPR	2		1116.032901	2230.050201	0.00091018	5	N	66	86
Q5SFM8	Infl	WHKPK	VPSISTETEEEEVKEEETETSDLFLHDDDDEDEDEYESR	SWRR-	4		1155.732854	4618.900215	0.000823681	2	N	1017	1056
Q5SFM8	Infl	SWLAK	LLEPICDADPSALANYVVALVK	KDKPE	2	C6:+57.021	1186.132809	2370.250019	0.000451244	9	N	15	37
Q5SFM8	Infl	SWLAK	LLEPICDADPSALANYVVALVKK	DKPEK	3	C6:+57.021	833.7894606	2498.344982	0.000451244	2	N	15	38
Q5SUA5	Infl	RGARR	LISVEPRPEQPEPDFQSSR	STFTL	3		737.7067192	2210.096758	0.001329271	1	N	995	1014
Q5SUA5	Infl	RIYTY	IGEVLVSVNPYQELPLYGPEAIAK	YQGRE	2		1300.205052	2598.394503	0.000451244	12	N	47	71
Q5SUA5	Infl	EQPHR	GILAVLDEACSTAGPITDR	IFLQT	2	C10:+57.021	979.9965126	1957.977425	0.000451244	7	N	468	487
Q5SUH6	Infl	TVQPK	QDAFANFANFSK	-	2		680.3205555	1358.625511	0.000622848	3	N	629	641
Q5SUH6	Infl	ANPSK	TIDLGAAAHYTGDKASPDQNASTHTPQSSAKPSVPSSK	SSGDL	3		1274.956345	3821.845636	0.000823681	1	N	283	321
Q5SUH6	Infl	IYDLR	SLENYHFVDEHGKDQGINIR	QKVKE	3		791.0528895	2370.135268	0.000451244	1	N	109	129
Q5SUR0	Infl	PGQHR	LGGTALAQCFSQLGEHPPDLDLPENLVR	AFHIT	3	C9:+57.021	1016.513718	3046.517755	0.000451244	26	N	861	889
Q5SUR0	Infl	EVGPR	LNFSTPASTNIVSVCQAAGLR	AVDRV	2	C15:+57.021	1103.568168	2205.120736	0.000451244	3	N	93	114
Q5SUR0	Infl	KAAAR	LAVSEALTNLVFALVTDLR	DVKCS	2		1023.086219	2044.156839	0.000451244	2	N	740	759
Q5SUR0	Infl	KIEAK	GLVPLHWADDDGNPTEQYPLNPNGSPGGIAGICSQDGR	HLALM	3	C33:+57.021	1325.617293	3973.828478	0.001162105	3	N	1251	1289
Q5SUR0	Infl	SMAAR	VGTETVQAPGSLVISAYAVCPDITATVTPDLK	HPGGK	3	C20:+57.021	1091.902648	3272.684545	0.000823681	3	N	810	842
Q5SUR0	Infl	QELQR	NPSTVEVFDLAQSNSEHSR	HWFFK	2		1058.998861	2115.982122	0.000451244	1	N	212	231
Q5SUR0	Infl	PALEK	ANQELGLALDSWDLDFYTK	RFQEL	2		1100.034381	2198.053161	0.001229886	1	N	186	205
Q5SUR0	Infl	CLVGK	TGQGDAPLTPPTPVDLDLDWVLGK	MPQKE	2		1253.147734	2504.279867	0.001162105	3	N	610	634
Q5SUR0	Infl	NRVIR	ACVEAPGGNPICSLHDQGAGGNGNVLK	ELSDP	3	C2:+57.021,C12:+57.021	898.0906012	2691.248404	0.001395409	1	N	500	527
Q5SUR0	Infl	KAAAR	LAVSEALTNLVFALVTDLRDVK	CSGNW	3		796.456853	2386.347159	0.001264573	1	N	740	762
Q5SUR0	Infl	QCTGR	GAHVVAGTAGYCFGNLHIPDYNLPWEDPSFQYPGNFAR	PLEVA	4	C12:+57.021	1060.246205	4236.953619	0.000698008	2	N	339	377
Q5SVD0	Infl	-MVGR	LSLQDVPELVDTK	KKGDG	2		728.8988357	1455.782071	0.001463592	1	N	4	17
Q5SVD0	Infl	GGGER	APVAGTLEPDAAVTPIVPNPASLTHSLAAICSPR	LCPLS	3	C31:+57.021	1131.933054	3392.775761	0.000451244	22	N	52	86
Q5SVD0	Infl	ICSPR	LCPLSFGEGVEFDPLPPK	EIKYT	2	C2:+57.021	1001.503442	2000.991284	0.000451244	4	N	86	104
Q5XJY5	Infl	LITTK	NSNILEDLETLR	LFSRV	2		708.8706096	1415.725619	0.000451244	12	N	72	84
Q5XJY5	Infl	DAKNK	SGSLEFSIPGQPNDFFPVQVSFISK	KNYCN	2		1364.18739	2726.35918	0.000451244	3	N	450	475
Q60597	Infl	ILHIK	HWLDSPWPGFFTLDGQPR	SMTCP	3		719.3503185	2155.027556	0.000451244	4	N	582	600
Q60597	Infl	DIFFR	NTNAGAPPGTAYQSPLSLSR	SSLAT	2		1001.503582	2000.991564	0.001463592	3	N	81	101
Q60597	Infl	TELQR	FLDTAFDLDAFKK	FS-	3		510.9333307	1529.776592	0.001654178	2	N	1008	1021
Q60605-2	Infl	GDVMR	ALGQNPTNAEVLK	VLGNP	2		677.8704126	1353.725225	0.000451244	41	N	37	50
Q60605-2	Infl	QTVAK	NKDQGTYEDYVEGLR	VFDKE	2		893.9162768	1785.816954	0.000451244	39	N	79	94
Q60605-2	Infl	EMNVK	VLDFEHFLPMLQTVAK	NKDQG	2		944.5060197	1886.996439	0.001352548	1	N	63	79
Q60605-2	Infl	TLGEK	MTEEEVEMLVAGHEDSNGCINYEELVR	MVLNG	3	M1:+15.995,C19:+57.021	1057.130534	3168.368202	0.000451244	1	N	119	146
Q60605-2	Infl	VEGLR	VFDKEGNGTVMGAEIR	HVLVT	2		861.9281335	1721.840667	0.000451244	6	N	94	110
Q60605-2	Infl	TGDGK	ILYSQCGDVMR	ALGQN	2	C6:+57.021	671.3184132	1340.621226	0.002813207	1	N	26	37

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q60605-2	Infl	VAKNK	DQGTYEDYVEGLR	VFDKE	2		772.8473315	1543.679063	0.000451244	8	N	81	94
Q60631	Infl	QIFLR	DIEQMPQQPTYVQALFDFDPQEDGELGFR	RGDFI	3		1138.526395	3412.555786	0.000451244	1	N	149	178
Q60631	Infl	GDILK	VLNEECDQNWYK	AELNG	2	C6:+57.021	799.3514954	1596.687391	0.000451244	13	N	26	38
Q60634	Infl	SEVNR	LLAELPASVHALTGVDLSKIPLIK	NATGA	3		833.5039147	2497.488344	0.002374549	1	N	397	421
Q60634	Infl	SEVNR	LLAELPASVHALTGVDLSK	IPLIK	2		967.5520123	1933.088425	0.000451244	6	N	397	416
Q60648	Infl	PAVIK	SLTIQPDPIVVPGDVVVSLEGK	TSVPL	2		1131.633731	2261.251861	0.000451244	18	N	49	71
Q60664	Infl	TNCLK	LLESLTPLCEEDNQAQEIVK	KLEKS	2	C9:+57.021	1165.083513	2328.151427	0.000451244	11	N	239	259
Q60668	Infl	DYTGY	NNYYGYGDYSNQQSGYGK	VSRRG	2		1039.43028	2076.844959	0.000451244	13	N	323	341
Q60668	Infl	DYFSK	FGEVVDCTLK	LDPIT	2	C7:+57.021	584.2896468	1166.563694	0.000451244	10	N	119	129
Q60668	Infl	DYFSK	FGEVVDCTLKLDPITGR	SRGFG	3	C7:+57.021	640.6683941	1918.981782	0.000451244	8	N	119	136
Q60668	Infl	EPVKK	IFVGGLSPDTPEEK	IREYF	2		744.8831857	1487.750771	0.000451244	33	N	183	197
Q60692	Infl	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK	EMCYR	4		1014.764706	4055.027624	0.000823681	7	N	78	117
Q60692	Infl	YIANR	VTDKLTPIHDHIFCCR	SGSAA	2	C14:+57.021,C15:+57.021	1006.495729	2010.975857	0.000451244	2	N	62	78
Q60692	Infl	SGVER	QVLLGDQIPK	FTIAT	2		555.8300277	1109.644455	0.002813207	1	N	219	229
Q60692	Infl	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLF	KEMCY	3		1309.985353	3926.93266	0.002374549	1	N	78	116
Q60737	Infl	VRIAK	VLGTEDLYDYIDKYNIELDPR	FNDIL	3		848.7555158	2543.243147	0.000451244	7	N	247	268
Q60737	Infl	THRPR	EYWDYESHVVEWGNQDDYQLVR	KLGRG	3		944.0846951	2829.230685	0.000451244	5	N	21	43
Q60737	Infl	DPVSR	TPALVFEHVNNTDFK	QLYQT	3		577.9620605	1730.862782	0.00091018	2	N	107	122
Q60739	Infl	HSNER	YDLLVTPQQGNSEPVVQDLAQLVEEATGVPLPFQK	LIFKG	3		1274.998711	3821.972734	0.000451244	10	N	164	199
Q60739	Infl	KVQVF	LAECDTVEQYICQETER	LQSTN	2	C4:+57.021,C12:+57.021	1072.467228	2142.918855	0.0007646	3	N	328	345
Q60767	Infl	KEKMR	LVSITDPYQQAFLAVQATLR	NSSFW	2		1117.613133	2233.210665	0.000451244	9	N	1138	1158
Q60767	Infl	ILSWK	EAYVSCQNQGADLLSIHSAAELAYITGK	EDIAR	3	C6:+57.021	1003.825962	3008.454486	0.001699387	1	N	241	269
Q60790	Infl	ACGSK	SVYDGPEQEEYSTFVIDDPQETYK	TLKQV	2		1420.127589	2838.239578	0.000451244	6	N	754	778
Q60790	Infl	ASNLK	FGDEFLGELRLPLK	ILRHS	3		545.3036466	1632.88754	0.001591523	1	N	237	251
Q60864	Infl	DVYQK	ALDLDSSCKEAADGYQR	CMMAQ	2	C8:+57.021	949.9313696	1897.847139	0.000451244	9	N	453	470
Q60864	Infl	KEQER	LAYINPDLALEEK	NKGNE	2		744.9013784	1487.787157	0.000622848	10	N	351	364
Q60864	Infl	EKGNK	ALSAGNIDDALQCYSEAIKLDPQNHVLYSNR	SAAYA	3	C13:+57.021	1159.235572	3474.683317	0.000451244	1	N	13	44
Q60864	Infl	ACYTK	LLEFQLALKDCEECIQLEPTFIK	GYTRK	3	C11:+57.021,C14:+57.021	946.4871872	2836.438162	0.002663018	1	N	406	429
Q60864	Infl	EKGNK	ALSAGNIDDALQCYSEAIK	LDPQN	2	C13:+57.021	1019.991427	2037.967255	0.002519933	1	N	13	32
Q60864	Infl	EEAKR	TYEEGLKHEANNLQLK	EGLQN	2		943.9844938	1885.953388	0.000451244	2	N	93	109
Q60864	Infl	DPTYR	ELIEQLQNKPSDLGTK	LQDPR	3		604.9954299	1811.96289	0.00091018	3	N	153	169
Q60864	Infl	ALQCY	SEAIKLDPQNHVLYSNR	SAAYA	2		992.5164925	1983.017385	0.001463592	1	N	27	44
Q60864	Infl	DPRTR	SLLSDPTYRELIEQLQNKPSDLGTK	LQDPR	3		949.1701001	2844.4869	0.002981883	1	N	144	169
Q60864	Infl	EKGNK	ALSAGNIDDALQCY	SEAIK	2	C13:+57.021	755.8460459	1509.676492	0.002374549	2	N	13	27
Q60865	Infl	DMSLR	LNEQYEHASIHLWDLLEGK	EKPVC	2		1148.074372	2294.133143	0.001229886	1	N	200	219
Q60865	Infl	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	2		1233.636667	2465.257735	0.000451244	24	N	167	189
Q60865	Infl	NKGER	LNQDQLDAVSKY	QEVTN	2		697.3520527	1392.688505	0.002663018	1	N	85	97
Q60865	Infl	VVGTY	HGSQDQPHQVPGNHQQPPQQNTGFPR	SSQPY	4		729.8467986	2915.355995	0.000622848	1	N	571	597
Q60865	Infl	QKRLK	TVLELQYVLDKLGDDDVR	TDLKQ	3		697.7043157	2090.089547	0.001162105	1	N	145	163
Q60875	Infl	GNQLR	SPQEEVLQPLINLYGLLHGLQAVVVQQER	LMEAL	3		1090.933536	3269.777209	0.000451244	12	N	731	760
Q60875	Infl	EEIRR	QLAALGQNEPLPAEAPWAR	RPLDP	2		1016.534685	2031.05377	0.000622848	2	N	857	876
Q60875	Infl	KEVMK	KQDVIYELIQTELHHVR	TLKIM	4		531.0422586	2120.137835	0.000622848	2	N	236	253
Q60875	Infl	EVMKK	QDVIYELIQTELHHVR	TLKIM	4		499.0185179	1992.042871	0.000451244	2	N	237	253
Q60902	Infl	LEAHR	SLEQYDQVPDGVSGTSLPDLATLNEGILLAER	GGFGA	3		1134.242653	3399.704558	0.000451244	12	N	557	589
Q60930	Infl	SISAK	VNNSSLIGVGYTQTLRPGVK	LTLSA	2		1052.082	2102.148399	0.000451244	3	N	248	268
Q60930	Infl	TFTEK	WNTDNTLGTEIAIEDQICQGLK	LTFDT	2	C18:+57.021	1260.108051	2518.200502	0.000451244	9	N	86	108
Q60930	Infl	DVKTK	SCSGVEFSTSGSSNTDTGKVSGTLETK	YKWCE	3	C2:+57.021	908.4156275	2722.223482	0.001162105	1	N	46	73
Q60930	Infl	DVKTK	SCSGVEFSTSGSSNTDTGK	VSGTL	2	C2:+57.021	954.4000993	1906.784599	0.000451244	2	N	46	65
Q60930	Infl	SIYQK	VCEDFDTSVNLAWTSGTNCTR	FGIAA	2	C2:+57.021,C19:+57.021	1217.025973	2432.036345	0.000622848	2	N	209	230
Q60931	Infl	RPGVK	LTLSALIDGK	NFNAG	2		515.8113036	1029.607007	0.001264573	4	N	256	266
Q60931	Infl	TFTQK	WNTDNTLGTEISWENKLAEGLK	LTLDT	2		1260.12479	2518.23398	0.001654178	1	N	74	96
Q60932	Infl	CFSAK	VNNSSLIGLGYTQTLKPGIK	LTLSA	2		1052.094576	2102.173551	0.000622848	1	N	249	269
Q60932	Infl	TFTEK	WNTDNTLGTEITVEDQLAR	GLKLT	2		1088.529994	2175.044388	0.000451244	19	N	87	106
Q60932	Infl	KPGIK	LTLSALLDGK	NVNAG	2		515.8113036	1029.607007	0.000622848	3	N	269	279
Q60953	Infl	DRYQR	DYQEIAGQLSCLEAVLQR	IRTSG	2	C11:+57.021	1047.020519	2092.025438	0.000662267	1	N	311	329
Q60960	Infl	SPALR	AVGNIVTGDDIQTQVILNCSALQSLLHLLSSPK	ESIKK	3	C19:+57.021	1168.962901	3503.865304	0.000622848	11	N	318	351
Q60960	Infl	VMDAK	IVQVALNGLENILR	LGEQE	2		776.4650116	1550.914423	0.000451244	6	N	438	452
Q60972	Infl	IIATK	TPSSDVLVFDYTKHPSKPDPSGECNPDLR	LRGHQ	3	C24:+57.021	1086.850947	3257.529442	0.000451244	13	N	143	172
Q60972	Infl	WDLSK	IGEEQSPEDAEDGPPELLFIHGGHTAK	ISDFS	3		958.4583096	2872.351529	0.000451244	19	N	349	376
Q60972	Infl	RGHQK	EGYGLSWNPNLSGHLLSASDDHTICLWDISAVPK	EGKVV	3	C25:+57.021	1251.605665	3751.793596	0.000451244	18	N	178	212
Q60972	Infl	VVDAK	TIFTGHTAVVEDVSWHLLHESLFGSVADDQK	LMIWD	3		1146.904194	3437.689182	0.001264573	1	N	220	251
Q60973	Infl	IIATK	TPSSDVLVFDYTKHPAKPDPSGECNPDLR	LRGHQ	4	C24:+57.021	811.3914317	3241.534527	0.000622848	3	N	142	171
Q60973	Infl	WDLSK	IGEEQSAEDAEDGPPELLFIHGGHTAK	ISDFS	3		949.7864263	2846.335879	0.000451244	10	N	348	375
Q60973	Infl	IVDAK	AIFTGHSAVVEDVAWHLLHESLFGSVADDQK	LMIWD	4		845.4248132	3377.668053	0.000662267	1	N	219	250
Q60973	Infl	KPEGK	DYALHWLVLGTHTSDEQNHLVVAR	VHIPN	4		694.3562022	2773.393609	0.001763695	1	N	58	82

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q60973	Infl	RGHQK	EGYGLSWNSNLSGHLLSASDDHTVCLWDINAGPK	EGKIV	3	C25:+57.021	1238.58152	3712.721159	0.0025889	1	N	177	211
Q61029	Infl	HNQSY	SQAGVTETEWTSGSSTGGPLQALTR	ESTRG	2		1261.112411	2520.209222	0.000451244	23	N	222	247
Q61029	Infl	SQHFR	IDGAVISESTPIAETIK	ASSNE	2		872.4728963	1742.930193	0.000637154	10	N	268	285
Q61029	Infl	TLKQR	RTEHNQSYSQAGVTETEWTSGSSTGGPLQALTR	ESTRG	3		1179.559926	3535.656379	0.000622848	2	N	214	247
Q61029	Infl	TSQHF	RIDGAVISESTPIAETIK	ASSNE	2		950.5234518	1899.031304	0.000451244	3	N	267	285
Q61033	Infl	AFVAK	SLQADISQAAQIINSDPSDAQQALR	ILNRT	2		1320.665342	2639.315084	0.000451244	7	N	590	615
Q61033	Infl	AQAIR	DYVNSLLVQGGVGSLPGTSDSVPTLDVENICKR	LSQSS	3	C31:+57.021	1163.922883	3488.745248	0.000451244	23	N	376	409
Q61033	Infl	IEAAR	ILSVPKVDDEILGFISEATPR	AATQA	3		767.0901701	2298.24711	0.000451244	4	N	528	549
Q61033	Infl	EATPR	AATQASSTESCDKHLDLALCR	SYEAA	3	C11:+57.021,C20:+57.021	778.6988216	2333.073065	0.000622848	4	N	549	570
Q61033	Infl	LSVPK	VDDEILGFISEATPR	AATQA	2		831.4232064	1660.830813	0.001463592	1	N	534	549
Q61033	Infl	AQAIR	DYVNSLLVQGGVGSLPGTSDSVPTLDVENICK	RLSQS	3	C31:+57.021	1111.889179	3332.644137	0.002374549	1	N	376	408
Q61035	Infl	KKNPK	LLNQLQYCEEAGIPLVAIIGEQELKDGVIK	LRSVA	3	C8:+57.021	1118.606055	3352.794765	0.000451244	14	N	447	477
Q61035	Infl	EVADR	IGDYVQQHGGVSLVEQLLQDPK	LSQNK	3		808.4242119	2422.249236	0.000451244	9	N	266	288
Q61074	Infl	PPHTK	SGIGTGDEPGPQGLNGEAGPEDPSRETPSQENGPTAK	GHTGF	3		1211.889889	3632.646268	0.000451244	38	N	172	209
Q61074	Infl	GPTAK	GHTGFSSNSEHGTEAGQISEPGTATGEAGPSCSSASDK	LPRVA	4	C32:+57.021	923.8968009	3691.556004	0.000451244	2	N	209	247
Q61074	Infl	PPHTK	SGIGTGDEPGPQGLNGEAGPEDPSR	ETPSQ	2		1197.544361	2393.073122	0.00091018	2	N	172	197
Q61081	Infl	ERKKR	LGPGGLDPVEVYESLPEELQK	CFDVK	2		1135.084071	2268.152541	0.000451244	23	N	287	308
Q61081	Infl	VPNSK	SGEAKEGEEAGPGDPLLEAVPK	AGNEK	2		1090.540027	2179.064455	0.000451244	12	N	348	370
Q61081	Infl	QRKLK	ELEVAESDGQVELER	LRAEA	2		851.9106601	1701.80572	0.000451244	9	N	69	84
Q61093	Infl	NFLSY	NIYLTGWDESQANHFAVHHDEEKDVITGLK	QKTLY	3		1156.227448	3465.658945	0.000451244	12	N	476	506
Q61093	Infl	CVNAR	VGISDRYSIALSDIGDNENEEYLNFAR	EKIKN	3		1020.82354	3059.44722	0.000622848	6	N	130	157
Q61093	Infl	GISDR	YSIALSDIGDNENEEYLNFAR	EKIKN	2		1217.064398	2432.113196	0.000451244	18	N	136	157
Q61093	Infl	SIHIR	IVGDWTEGLFNACGCDKQEFQDAWK	LPKIA	3	C13:+57.021,C15:+57.021	992.10955	2973.30525	0.000451244	9	N	356	381
Q61093	Infl	PKVSK	LEWHPFTLTSAPEEDFFSIHIR	IVGDW	4		668.8345713	2671.307085	0.000451244	9	N	334	356
Q61093	Infl	DNEFK	TIASEHPNTTIGVFLCGPEALAETLSK	QSISN	2	C16:+57.021	1428.726322	2855.437045	0.000451244	17	N	521	548
Q61093	Infl	QMQER	NNANFLSYNIYLTGWDESQANHFAVHHDEEKDVITGLK	QKTLY	4		1098.275969	4389.072676	0.000622848	2	N	468	506
Q61093	Infl	SYNIY	LTGWDESQANHFAVHHDEEKDVITGLK	QKTLY	3		1026.164008	3075.468624	0.000698008	3	N	479	506
Q61093	Infl	ESGPR	GVHFIFNKENF	-	2		676.3438336	1350.672067	0.002374549	1	N	559	570
Q61093	Infl	SIHIR	IVGDWTEGLFNACGCDK	QEFQD	2	C13:+57.021,C15:+57.021	971.4271772	1940.838754	0.001329271	2	N	356	373
Q61096	Infl	LQLSR	FPGSHFCGGTLIHPR	FVLTA	2	C7:+57.021	841.9149315	1681.814263	0.000451244	6	N	51	66
Q61096	Infl	LQLNR	TASLGKEVAVASLPQQDQTLSQGTQCLAMGWGR	LGTQA	3	C26:+57.021	1163.580574	3487.718323	0.000451244	10	N	128	161
Q61096	Infl	ASLGK	EVAVASLPQQDQTLSQGTQCLAMGWGR	LGTQA	2	C20:+57.021	1466.208306	2930.401011	0.000451244	8	N	134	161
Q61096	Infl	IRECA	SLQFPDFFAR	VSMYV	2		614.3120021	1226.608404	0.002663018	1	N	227	237
Q61096	Infl	TLVPR	RAAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C6:+57.021,C16:+57.021	1020.183384	3057.526751	0.000451244	3	N	195	224
Q61096	Infl	SFVIR	ECASLQFPDFFAR	VSMYV	2	C2:+57.021	794.3669485	1586.718297	0.000451244	22	N	224	237
Q61096	Infl	DFFAR	VSMYVDWIQNVLR	GAEP-	2	M3:+15.995	819.9196228	1637.823646	0.000451244	9	N	237	250
Q61096	Infl	RRAAG	ICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C2:+57.021,C12:+57.021	1352.172774	2702.329948	0.000451244	2	N	199	224
Q61096	Infl	PRRAA	GICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C3:+57.021,C13:+57.021	1380.683506	2759.351412	0.000451244	21	N	198	224
Q61096	Infl	LVPRR	AAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C5:+57.021,C15:+57.021	1451.72062	2901.42564	0.000451244	6	N	196	224
Q61096	Infl	VPRRA	AGICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C4:+57.021,C14:+57.021	1416.202063	2830.388526	0.00091018	2	N	197	224
Q61096	Infl	LTAAH	CLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C1:+39.994	1059.53615	3175.585049	0.000451244	5	N	73	101
Q61096	Infl	LIHPR	FVLTAAHCLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C8:+57.021	1311.679053	3932.013759	0.000451244	20	N	66	101
Q61096	Infl	TFLCR	EHNVCTLVPR	RAAGI	2	C5:+57.021	612.811612	1223.607624	0.002813207	1	N	185	195
Q61096	Infl	AGICF	GDSGGPLICNGILHGVDSFVIR	ECASL	2	C9:+57.021	1142.081442	2282.147285	0.000451244	9	N	202	224
Q61096	Infl	AAHCL	QDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3		974.1737331	2919.497799	0.000451244	11	N	75	101
Q61096	Infl	RECAS	LQFPDFFAR	VSMYV	2		570.7959879	1139.576376	0.0025889	1	N	228	237
Q61096	Infl	LVTVV	LGAHDLLSSEPEQQK	FTISQ	2		826.4184553	1650.821311	0.001943752	1	N	86	101
Q61096	Infl	ASLGK	EVAVASLPQQDQTLSQGTQCL	AMGWG	2	C20:+57.021	1137.05783	2272.10006	0.000451244	2	N	134	155
Q61096	Infl	RPHSR	PYVASLQLSR	FPGSH	2		567.3198272	1132.624054	0.00091018	2	N	41	51
Q61103	Infl	KINKK	TGQPEELVSCSDCGR	SGHPS	2	C10:+57.021,C13:+57.021	847.8591274	1693.702655	0.000823681	2	N	285	300
Q61103	Infl	RARKR	IIEPDDFLDDLDDEDYEEDTPK	RRGKG	2		1321.064123	2640.112646	0.000451244	11	N	156	178
Q61152	Infl	TTALR	RVPADQNSSGPDAYEEVTDGAQTGGLGFNLR	IGRPK	3		1074.508503	3220.50211	0.000451244	10	N	405	436
Q61152	Infl	GPGPR	APTSTDTPIYSQVAPR	AQRPV	2		852.4341054	1702.852611	0.000451244	14	N	371	387
Q61166	Infl	FGKLR	NIELICQENEGENDPVLQR	IVDIL	2	C6:+57.021	1135.539804	2269.064009	0.000451244	24	N	222	241
Q61166	Infl	PVAAR	QGQETAVAPSLVAPALSKPK	KPLGS	2		996.5603687	1991.105137	0.000451244	9	N	130	150
Q61166	Infl	QWFKK	FFDANYDGKEYDPVAAR	QGQET	2		989.4530265	1976.890453	0.002019181	1	N	113	130
Q61166	Infl	PVLQR	IVDILYATDEGFVIPDEGGPQEEQEEY	-	3		1019.13679	3054.386971	0.000622848	3	N	241	268
Q61171	Infl	ADVTK	SLSQNYGVLKNDEGIAYR	GLFII	2		1014.013783	2026.011965	0.001162105	2	N	109	127
Q61171	Infl	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSK	HN-	4	C15:+57.021	1111.527717	4442.079667	0.001162105	14	N	157	196
Q61171	Infl	AQIGK	SAPDFTATAVVDGAFKEIK	LSDYR	2		984.0101773	1966.004755	0.000622848	1	N	10	29
Q61171	Infl	AEDFR	KLGCEVLGVSVDSQFTHLAWINTPR	KEGGL	3	C4:+57.021	943.1572061	2826.448218	0.000622848	1	N	66	91
Q61171	Infl	EDFRK	LGCEVLGVSVDSQFTHLAWINTPR	KEGGL	3	C3:+57.021	900.458885	2698.353255	0.000451244	14	N	67	91
Q61171	Infl	YVVLF	FYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C10:+57.021	1013.14111	3036.399931	0.000823681	1	N	41	66
Q61171	Infl	AQIGK	SAPDFTATAVVDGAFK	EIKLS	2		798.8993671	1595.783134	0.000451244	1	N	10	26
Q61176	Infl	EYDVR	DHGDLAFVDVPNDSSFQIVK	NPRSV	2		1102.037455	2202.059309	0.000451244	2	N	48	68

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61176	Infl	AEEVK	STVNTAVALTLACFGTQR	EGNHK	2	C13:+57.021	955.4939401	1908.97228	0.000451244	3	N	290	308
Q61176	Infl	SSKPK	SLEIIGAPFSK	GQPRG	2		581.3298606	1160.644121	0.000823681	2	N	6	17
Q61176	Infl	SGHAR	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVSFLLK	ELKGK	4	C6:+57.021	1021.275968	4081.072671	0.001591523	1	N	113	150
Q61176	Infl	RSVGK	ANEELAGVVAEVQK	NGRVS	2		728.8862597	1455.756919	0.000698008	2	N	75	89
Q61191	Infl	MSGCR	LGDLWTLDIETLTWNKPSLSGVAPLPR	SLHSA	3		998.2101186	2991.606956	0.000451244	6	N	228	255
Q61191	Infl	LIVVF	GGGNEGIVDELHVYNTATNQWFIPAVR	GDIPP	3		986.4900556	2956.446767	0.000451244	8	N	48	75
Q61206	Infl	YEIWR	ELFSPLHALNFGIGGDTTR	HVLWR	2		1023.026693	2044.037786	0.000451244	1	N	60	79
Q61207	Infl	HYLEK	TCEWIHDSSLSASCK	EVVDS	3	C2:+57.021,C14:+57.021	594.2593634	1779.75469	0.000451244	14	N	92	107
Q61207	Infl	DQQPK	EICVLAGFCNE	VKRVP	2	C3:+57.021,C9:+57.021	656.2890895	1310.562579	0.001839721	3	N	264	275
Q61207	Infl	DQQPK	EICVLAGFCNEV	KRVPM	2	C3:+57.021,C9:+57.021	705.8232965	1409.630993	0.000698008	2	N	264	276
Q61207	Infl	DPYQK	QCDDFVAEYEPLLLEILVEVMDPGFVCSK	IGVCP	3	C2:+57.021,C27:+57.021	1139.209942	3414.606427	0.000451244	7	N	482	511
Q61207	Infl	AALEK	GCSFLPDPYQK	QCDDF	2	C2:+57.021	656.3058282	1310.596056	0.001264573	4	N	471	482
Q61207	Infl	SASCK	EVVDSYLPVILDMIK	GEMSN	2		867.4738539	1732.932108	0.001329271	1	N	107	122
Q61210-5	Infl	VLSLK	QILLSTEEDSGAGPPRDGDGVPGGR	APGPV	3		827.4057686	2479.193906	0.001329271	1	N	893	918
Q61210-5	Infl	DVQRR	FIQEVVQSQQAAVSR	QLEDF	2		845.4500898	1688.88458	0.000451244	8	N	135	150
Q61210-5	Infl	RLMKR	RQESGYLIEEIGDVLLAR	FDGAE	3		687.7045385	2060.090216	0.001162105	2	N	539	557
Q61210-5	Infl	PGPPR	SGLVSIIIGAEDEDFENELEANSEDQNSQFQSLEQVKR	RPAHL	3		1423.342482	4267.004047	0.000451244	21	N	14	52
Q61210-5	Infl	PGPPR	SGLVSIIIGAEDEDFENELEANSEDQNSQFQSLEQVK	RRPAH	3		1371.308779	4110.902936	0.000451244	22	N	14	51
Q61210-5	Infl	HVAER	LLSHLEETQHTISTDEEK	SAAVV	2		1055.519095	2109.02259	0.000622848	2	N	194	212
Q61210-5	Infl	EEFCR	LRPLLSQLGGTLSPNLAAPER	SAQTG	3		735.0906159	2202.248448	0.002374549	1	N	951	972
Q61210-5	Infl	ARTER	LLNDLLPFCRPGPEGQLAATALQK	VLSLK	2	C9:+57.021	1311.707539	2621.399477	0.002663018	1	N	864	888
Q61210-5	Infl	VLSLK	QILLSTEEDSGAGPPR	DGDGV	2		835.4237377	1668.831875	0.000451244	5	N	893	909
Q61210-5	Infl	QRLTK	YPLLLQSIGQNTEESTER	GKVEL	2		1039.52418	2077.03276	0.000451244	4	N	625	643
Q61210-5	Infl	PKEAK	KAFLDFYHSFLEK	TAVLR	3		548.9527252	1643.834776	0.000735798	2	N	91	104
Q61210-5	Infl	EVAIR	QLEELEEEFCR	LRPLL	2	C10:+57.021	741.3327713	1480.649943	0.001162105	3	N	940	951
Q61233	Infl	AGCTK	ITNFSTDIKDSK	AYYHL	2		684.8544282	1367.693256	0.000451244	5	N	285	297
Q61233	Infl	GGNMK	KLENCNYAVDLGK	NQAKF	2	C5:+57.021	762.3800559	1522.744512	0.000451244	26	N	455	468
Q61233	Infl	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEK	YAFVN	2	C4:+57.021	1385.609341	2769.203081	0.000451244	12	N	97	123
Q61233	Infl	RLGCR	QFVTATDVVR	GNPKL	2		568.3094595	1134.603319	0.000451244	20	N	347	357
Q61233	Infl	IKDSK	AYYHLLEQVAPK	GDEEG	2		716.3856985	1430.755797	0.000451244	11	N	297	309
Q61233	Infl	IVLCK	MINLSVPDTIDER	TINKK	2		751.8801206	1501.744641	0.001162105	2	N	165	178
Q61233	Infl	WQLMR	RYTLNILEDIGGGQK	VNDDI	2		838.9524653	1675.889331	0.000622848	7	N	500	515
Q61233	Infl	KIGAR	VYALPEDLVEVNPK	MVMTV	2		793.4277604	1584.839921	0.000451244	25	N	596	610
Q61233	Infl	KNQAK	FSLVGIAGQDLNEGNR	TLTLA	2		845.431897	1688.848194	0.000451244	25	N	472	488
Q61233	Infl	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVNWINK	ALEND	3	C4:+57.021	1302.602649	3904.784547	0.000451244	59	N	97	132
Q61233	Infl	MMELR	EAFAKVDTDGNGYISCNELNDLFK	AACLP	2	C16:+57.021	1360.629348	2719.243096	0.000451244	8	N	15	39
Q61233	Infl	QLMRR	YTLNILEDIGGGQK	VNDDI	2		760.9019097	1519.788219	0.000451244	8	N	501	515
Q61233	Infl	EAFAK	VDTDGNGYISCNELNDLFK	AACLP	2	C11:+57.021	1087.489249	2172.962898	0.000451244	97	N	20	39
Q61233	Infl	DPDCR	HVIPMNPNTDDLFNAVGDGIVLCK	MINLS	2	C23:+57.021	1320.151739	2638.287879	0.000451244	9	N	141	165
Q61233	Infl	IKDSK	AYYHLLEQVAPKGDEEGIPAVVIDMSGLR	EKDDI	3		1057.545061	3169.611784	0.000451244	7	N	297	326
Q61233	Infl	GGGQK	VNDDIIVNWVNTTLK	EAQKS	2		872.4679482	1742.920296	0.000451244	42	N	515	530
Q61233	Infl	GGGQK	VNDDIIVNWVNTTLKEAQK	SSSIA	2		1100.584572	2199.153544	0.000451244	6	N	515	534
Q61233	Infl	RGNPK	LNLAFIANLFNKYPALHKPENQDIDWGALEGETR	EERTF	3		1300.00279	3896.984971	0.000451244	13	N	361	395
Q61233	Infl	RGNPK	LNLAFIANLFNK	YPALH	2		689.3986089	1376.781618	0.000451244	56	N	361	373
Q61233	Infl	GVNPR	VNHLYSDLSDALVIFQLYEK	IKVPV	2		1184.115705	2366.21581	0.000451244	20	N	412	432
Q61233	Infl	AEDLK	EGKPYLVLGLLWQVIK	IGLFA	2		928.5563694	1855.097139	0.000451244	12	N	217	233
Q61233	Infl	LMRRY	TLNILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		1028.219342	3081.634627	0.000451244	37	N	502	530
Q61233	Infl	NEGNR	TLTLALVWQLMR	RYTLN	3		482.2835297	1443.827189	0.000451244	2	N	488	500
Q61233	Infl	QLMRR	YTLNILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		1082.573785	3244.697956	0.000451244	31	N	501	530
Q61233	Infl	INKKK	LTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C22:+57.021	1174.947251	3521.818354	0.000451244	31	N	184	217
Q61233	Infl	PKIST	SLPVLDLIDAIQPGSINYDLLK	TENLD	2		1199.167938	2396.320275	0.000451244	9	N	548	570
Q61233	Infl	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLK	TENLD	2		1349.749823	2697.484047	0.000451244	37	N	545	570
Q61233	Infl	IDAIQ	PGSINYDLLK	TENLD	2		560.3063854	1118.597171	0.000451244	3	N	560	570
Q61233	Infl	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLKTENLDDEEK	LNNAK	3		1257.986249	3770.935346	0.000823681	6	N	545	579
Q61233	Infl	TINKK	KLTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C23:+57.021	1217.645572	3649.913317	0.000451244	13	N	183	217
Q61233	Infl	ELLLR	WANYHLENAGCTK	ITNFS	2	C11:+57.021	782.3543724	1562.693145	0.000451244	5	N	272	285
Q61233	Infl	NLFNK	YPALHKPENQDIDWGALEGETREER	TFRNW	3		985.1412035	2952.40021	0.000451244	28	N	373	398
Q61233	Infl	NLFNK	YPALHKPENQDIDWGALEGETR	EERTF	2		1270.114756	2538.213913	0.000451244	8	N	373	395
Q61233	Infl	SEEEK	YAFVNWINK	ALEND	2		577.8038129	1153.592026	0.000451244	7	N	123	132
Q61233	Infl	WQVIK	IGLFADIELSR	NEALI	2		617.346042	1232.676484	0.001943752	2	N	233	244
Q61233	Infl	KLTPF	TIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C18:+57.021	1022.196278	3063.565433	0.000451244	39	N	188	217
Q61233	Infl	AGCTK	ITNFSTDIK	DSKAY	2		519.7774608	1037.539322	0.002212458	2	N	285	294
Q61233	Infl	GNMKK	LENCNYAVDLGK	NQAKF	2	C4:+57.021	698.3325743	1394.649549	0.000451244	6	N	456	468
Q61233	Infl	WQVIK	IGLFADIELSRNEALIALLR	EGESL	3		743.099	2226.2736	0.000451244	2	N	233	253
Q61233	Infl	IELSR	NEALIALLR	EGESL	2		506.811638	1011.607676	0.000451244	11	N	244	253

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61233	Infl	ISTSL	PVLDLIDAIQPGSINYDLLK	TENLD	2		1099.109891	2196.204183	0.000451244	1	N	550	570
Q61233	Infl	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKY	AFVNW	3	C4:+57.021	978.4299367	2932.26641	0.000637154	3	N	97	124
Q61233	Infl	LMRRY	TLNILEDIGGGQK	VNDDI	2		679.3702454	1356.724891	0.000451244	9	N	502	515
Q61233	Infl	VNHLY	SDLSDALVIFQLYEK	IKVPV	2		870.956882	1739.898164	0.000451244	12	N	417	432
Q61233	Infl	NWINK	ALENDPDCRHVIPMNPNTDDLFNAVGDGIVLCK	MINLS	3	C8:+57.021,C32:+57.021	1237.251975	3708.732524	0.001162105	1	N	132	165
Q61233	Infl	GNMKK	LENCNYAVDLGKNQAK	FSLVG	2	C4:+57.021	918.9493654	1835.883131	0.000451244	1	N	456	472
Q61233	Infl	AINKK	EGICAIGGTSEQSSVGTQHSY	SEEEK	2	C4:+57.021	1084.481955	2166.94831	0.000622848	7	N	97	118
Q61233	Infl	EDLMK	LSPEELLLR	WANYH	2		535.3167532	1068.617906	0.001264573	2	N	263	272
Q61233	Infl	NQAKF	SLVGIAGQDLNEGNR	TLTLA	2		771.89769	1541.77978	0.000622848	2	N	473	488
Q61233	Infl	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAF	VNWIN	3	C4:+57.021	1051.131779	3150.371938	0.001162105	3	N	97	126
Q61362	Infl	PTFGK	SFTLASSENQLGAPISGEGLPGR	FTKEA	2		1144.580018	2287.144436	0.000451244	23	N	272	295
Q61362	Infl	APFLR	SYGFDGLDLAWLYPR	LRDKQ	2		886.9362839	1771.856968	0.000451244	13	N	137	152
Q61362	Infl	GRFTK	EAGTLAYYEICDFLK	GAEVH	2	C11:+57.021	896.927036	1791.838472	0.000451244	2	N	298	313
Q61362	Infl	TCQPK	EFFPLTNAIK	DALA-	2		590.3245782	1178.633556	0.001352548	1	N	375	385
Q61508	Infl	HIEQK	EIDPPAQPQEEIVQK	EVKPH	2		860.9417633	1719.867927	0.001162105	1	N	132	147
Q61508	Infl	NMTIR	CCELPYPEQACCGEEEK	LAFIE	2	C1:+57.021,C2:+57.021,C11:+57.021,C12:+57.021	1079.912454	2157.809308	0.001162105	1	N	467	484
Q61543	Infl	YRIDR	ALNEACESVIQTACK	HIRSG	2	C6:+57.021,C14:+57.021	847.3978884	1692.780177	0.000451244	1	N	497	512
Q61543	Infl	ALDYR	LDPQLQLHCSDEIANLCAEEAAAQEQTGQVEECLK	VNLLK	3	C9:+57.021,C17:+57.021,C33:+57.021	1333.278652	3996.812556	0.000451244	1	N	996	1031
Q61545	Infl	NVQHR	AGDWQCPNPGCGNQNFAWR	TECNQ	2	C6:+57.021,C11:+57.021	1117.965855	2233.91611	0.000451244	18	N	517	536
Q61545	Infl	NSAIY	VQGLNDNVTLDDLADFFK	QCGVV	2		1012.502716	2022.989833	0.000451244	14	N	363	381
Q61545	Infl	TGKPK	GDATVSYEDPPTAK	AAVEW	2		725.8389751	1449.66235	0.000622848	4	N	409	423
Q61550	Infl	RALAK	TGAESISLLELCR	NTNRK	2	C12:+57.021	724.8746064	1447.733613	0.000451244	2	N	577	590
Q61550	Infl	DEFLK	EFENPEVPREEQQPQQQQPQPQR	DVIDE	3		949.4537815	2845.337944	0.000823681	3	N	418	441
Q61550	Infl	PEENR	EAAYNAITLPEEFHDFDQPLPDLDDIDVAQQFSLNQSR	VEEIT	3		1454.687813	4361.040039	0.001395409	1	N	101	139
Q61598	Infl	LALYR	TDDYLDQPCCETINR	IKLYS	2	C9:+57.021,C10:+57.021	950.396074	1898.776548	0.000451244	24	N	193	208
Q61598	Infl	LFVPK	DLGTDSQIFISR	AYDAT	2		676.3467703	1350.677941	0.000451244	1	N	390	402
Q61598	Infl	PIEQK	FVSISDLFVPK	DLGTD	2		626.3533357	1250.691071	0.000451244	14	N	379	390
Q61598	Infl	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	2		1148.092564	2294.169529	0.000451244	7	N	173	193
Q61598	Infl	DVYKK	FDLGQDVIDFTGHSLALYR	TDDYL	2		1084.045083	2166.074566	0.000451244	13	N	174	193
Q61598	Infl	PIEQK	FVSISDLFVPKDLGTDSQIFISR	AYDAT	2		1292.687026	2583.358452	0.002212458	1	N	379	402
Q61598	Infl	GQVIR	VICILSHPIKNTNDANSCQIIIPQNQVNR	KSDIY	3	C3:+57.021,C18:+57.021	1120.582095	3358.722885	0.000451244	2	N	299	328
Q61598	Infl	KEPEK	EIRPALELLEPIEQK	FVSIS	3		593.340649	1776.998547	0.001943752	1	N	364	379
Q61598	Infl	SLALY	RTDDYLDQPCCETINR	IKLYS	2	C10:+57.021,C11:+57.021	1028.44663	2054.877659	0.000451244	13	N	192	208
Q61599	Infl	EALKK	DTFVLKEGIEYR	VKINF	2		735.3858955	1468.756191	0.00091018	1	N	95	107
Q61599	Infl	-MTEK	DAQPQLEEADDDLDSKLNYKPPPQK	SLKEL	2		1427.691222	2853.366845	0.000451244	5	N	4	29
Q61599	Infl	KATFM	VGSYGPRPEEYEFLTPVEEAPK	GMLAR	2		1247.610984	2493.206368	0.000451244	15	N	141	163
Q61599	Infl	MRVDK	ATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		982.1411534	2943.40006	0.000451244	4	N	137	163
Q61599	Infl	TKYKK	TLLGDVPVVADPTVPNVTVTR	LSLVC	2		1082.10514	2162.194681	0.000451244	242	N	49	70
Q61599	Infl	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	2		1305.119507	2608.223415	0.000451244	26	N	174	195
Q61599	Infl	TKYKK	TLLGDVPVVADPTVPNVTVTRL	SLVCD	2		1138.647172	2275.278745	0.000451244	16	N	49	71
Q61599	Infl	VTVTR	LSLVCDSAPGPITMDLTGDLEALKK	DTFVL	2	C5:+57.021	1322.682538	2643.349476	0.000451244	7	N	70	95
Q61599	Infl	LTKYK	KTLLGDVPVVADPTVPNVTVTR	LSLVC	2		1146.152622	2290.289644	0.000451244	23	N	48	70
Q61599	Infl	-MTEK	DAQPQLEEADDDLDSK	LNYKP	2		894.8926644	1787.769729	0.000451244	21	N	4	20
Q61599	Infl	EALKK	DTFVLKEGIEY	RVKIN	2		657.3353399	1312.65508	0.000735798	4	N	95	106
Q61599	Infl	RTGMR	VDKATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		1096.204593	3285.59038	0.000451244	7	N	134	163
Q61599	Infl	KTLLG	DVPVVADPTVPNVTVTR	LSLVC	2		889.9865052	1777.95741	0.000823681	2	N	53	70
Q61599	Infl	DKATF	MVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		875.7567512	2624.246854	0.002884417	1	N	140	163
Q61635	Infl	WSLVK	DNSIIAQATSAAEAFCAVK	GGPES	2	C16:+57.021	983.9808625	1965.946125	0.000451244	1	N	360	379
Q61635	Infl	KGELK	CLDFWSLVK	DNSII	2	C1:+57.021	584.2972748	1166.57895	0.002663018	1	N	351	360
Q61635	Infl	TNLIK	TGVTEPCIFLISNLDLGAFDFPKLEETLLK	ELPGH	3	C7:+57.021	1127.595156	3379.762068	0.001162105	2	N	224	254
Q61635	Infl	VYYRR	TQFLNIVVDDAKHLLR	KIETV	4		471.2696071	1881.047228	0.000451244	4	N	396	412
Q61646	Infl	RQFYR	LRAEGDGVYTLNDEK	QWVNT	2		840.4159126	1678.816225	0.000451244	36	N	57	72
Q61646	Infl	IAPGR	VGYVSGWGR	NANFR	2		490.7515803	979.4875607	0.000451244	35	N	218	227
Q61646	Infl	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	2	C14:+57.021,C18:+57.021	1250.619843	2499.224086	0.000451244	7	N	72	94
Q61646	Infl	LSFDK	SCAVAEYGVYVR	ATDLK	2	C2:+57.021	687.3298346	1372.644069	0.000451244	42	N	320	332
Q61646	Infl	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	M8:+15.995,C15:+57.021	1178.20509	3531.591871	0.000451244	15	N	18	49
Q61646	Infl	KMISR	HGLTTGATLISDQWLLTTAK	NLFLN	2		1064.076383	2126.137166	0.000451244	51	N	123	143
Q61646	Infl	TASAK	DITPTLTLYVGKNQLVEIEK	VVLHP	2		1137.633731	2273.251861	0.000451244	4	N	156	176
Q61646	Infl	AGLTK	YQEDTCYGDAGSAFAIHDMEEDTWYAAGILSFDK	SCAVA	3	C6:+57.021	1292.882424	3875.623873	0.000451244	4	N	286	320
Q61646	Infl	FYRLR	AEGDGVYTLNDEK	QWVNT	2		705.823325	1409.63105	0.000451244	13	N	59	72
Q61646	Infl	TASAK	DITPTLTLYVGK	NQLVE	2		660.8746323	1319.733665	0.000451244	9	N	156	168
Q61655	Infl	NKLIR	SNLVDNTNQVEVLQRDPSSPLYSVK	SFEEL	3		934.8143163	2801.419549	0.000451244	4	N	66	91
Q61655	Infl	ERGQK	VSEQIVIGTPGTVLDWCSK	LKFID	2	C17:+57.021	1045.035638	2088.055676	0.000451244	5	N	207	226

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61655	Infl	NKLIR	SNLVDNTNQVEVLQR	DPSSP	2		864.9479113	1727.880223	0.000451244	3	N	66	81
Q61656	Infl	LAPTR	ELAQQVQQVAAEYCR	ACRLK	2	C14:+57.021	896.936258	1791.856916	0.000451244	21	N	177	192
Q61656	Infl	EDVKF	VINYDYPNSSEDYIHR	IGRTA	2		992.9559333	1983.896267	0.000451244	15	N	412	428
Q61656	Infl	DVASR	GLDVEDVKFVINYDYPNSSEDYIHR	IGRTA	3		996.4739597	2986.398479	0.000451244	2	N	403	428
Q61656	Infl	FKHGK	APILIATDVASR	GLDVE	2		613.8593165	1225.703033	0.000823681	9	N	391	403
Q61656	Infl	PFLER	GDGPICLVLAPTR	ELAQQ	2	C6:+57.021	684.869127	1367.722654	0.001264573	6	N	164	177
Q61656	Infl	ATPGR	LIDFLECGK	TNLRR	2	C7:+57.021	547.7814576	1093.547315	0.000451244	6	N	227	236
Q61656	Infl	TGSGK	TLSYLLPAIVHINHQPFLER	GDGPI	4		591.0829208	2360.300483	0.002727428	1	N	144	164
Q61656	Infl	QNGVY	SAANYTNGSFGSNFVSAGIQTSFR	TGNPT	2		1242.083456	2482.151313	0.000622848	2	N	535	559
Q61687	Infl	KVLVF	SQSLISLDLIEDFLELASR	EKTED	2		1075.073506	2148.131412	0.000451244	6	N	2023	2042
Q61687	Infl	PMLPK	DTILAELLQIHK	EHIVG	3		465.2736873	1392.797662	0.001943752	1	N	2216	2228
Q61753	Infl	PPRDR	ALVDHENVISCPHLGASTK	EAQSR	2	C11:+57.021	1024.515404	2047.015208	0.000451244	5	N	270	289
Q61753	Infl	QVVGR	AGTGVDNVDLEAATR	KGILV	2		744.8685982	1487.721596	0.000451244	16	N	75	90
Q61753	Infl	GALLR	ALQSGQCAGAALDVFTEEPPRDR	ALVDH	3	C7:+57.021	830.0680566	2487.18077	0.000451244	4	N	247	270
Q61753	Infl	QVVEK	QNLSKEELIAELQDCEGLIVR	SATKV	3	C15:+57.021	819.7603411	2456.257623	0.000451244	7	N	33	54
Q61753	Infl	EIWPL	CDFITVHTPLLPSTTGLLNDSTFAQCK	KGVRV	3	C1:+39.994,C26:+57.021	1007.156239	3018.445316	0.001395409	1	N	199	226
Q61753	Infl	SFGMK	TVGYDPIISPEVAASFGVQQLPLEEIWPL	CDFIT	3		1056.888822	3167.643067	0.001162105	7	N	170	199
Q61753	Infl	GTSLK	NAGTCLSPAVIVGLLR	EASKQ	2	C5:+57.021	820.9615475	1639.907495	0.000451244	3	N	364	380
Q61753	Infl	AGSPK	GTIQVVTQGTSLK	NAGTC	2		666.3806131	1330.745626	0.000622848	1	N	351	364
Q61768	Infl	KNINK	SLSALGNVISALAEGSTYVPYRDSK	MTRIL	3		866.7856979	2597.333694	0.001162105	3	N	256	281
Q61768	Infl	EQKKR	QLEESVDSLGEELVQLR	AQEKV	2		972.5001737	1942.984747	0.000451244	7	N	658	675
Q61768	Infl	YAFDR	VFQSSTSQEQVYNDCAK	KIVKD	2	C15:+57.021	995.944477	1989.873354	0.000451244	14	N	50	67
Q61768	Infl	KNINK	SLSALGNVISALAEGSTYVPYR	DSKMT	2		1134.59768	2267.179759	0.000451244	8	N	256	278
Q61768	Infl	KNINK	SLSALGNVISALAEGSTYVPY	RDSKM	2		1056.547124	2111.078648	0.000451244	5	N	256	277
Q61792	Infl	FEKNK	GKGFSVVADTPELQR	IKKTQ	2		802.4260834	1602.836567	0.000451244	4	N	94	109
Q61792	Infl	KNKGK	GFSVVADTPELQR	IKKTQ	2		709.8678699	1417.72014	0.000451244	10	N	96	109
Q61792	Infl	QRIKK	TQDQISNIKYHEEFEK	SRMGP	2		1004.984691	2007.953782	0.000451244	4	N	112	128
Q61805	Infl	DLQPY	LQTLPVTAEIDNVLGIDYSLVAAPQAK	AQVLD	2		1420.276737	2838.537873	0.000637154	2	N	212	239
Q61805	Infl	EMIQK	SVTSDLQPYLQTLPVTAEIDNVLGIDYSLVAAPQAK	AQVLD	3		1277.342367	3829.0037	0.000451244	21	N	203	239
Q61805	Infl	KAVGR	GQYEFHSLEIQNCELR	GSSLK	2	C13:+57.021	1011.970829	2021.926058	0.000451244	3	N	73	89
Q61878	Infl	SIHSF	SVNFGIQSAVR	GINQG	2		589.3203585	1176.625117	0.000451244	2	N	140	151
Q61878	Infl	PGGGR	CVTLCTQGGHWR	LSHCV	2	C1:+57.021,C5:+57.021	737.8376039	1473.659608	0.000622848	4	N	197	209
Q61878	Infl	CKRFR	WVDGSSWNFAYWAAGQPCPGGGR	CVTLC	2	C18:+57.021	1263.556123	2525.096646	0.000451244	19	N	174	197
Q61878	Infl	DGSSW	NFAYWAAGQPCPGGGR	CVTLC	2	C11:+57.021	854.8863711	1707.757142	0.001699387	2	N	181	197
Q61881	Infl	GENTR	IAQPGDHVSVTGIFLPVLR	TGFQQ	3		673.7182308	2018.131293	0.000451244	7	N	263	282
Q61881	Infl	RCISR	GFTPAQFQAALDEYEELNVWQVNTSR	TRITF	3		1005.149588	3012.425363	0.000451244	5	N	687	713
Q61881	Infl	QVALY	VDLDDIAEDDPELVDSICENAK	RYSRL	2	C18:+57.021	1238.05789	2474.100179	0.000451244	11	N	49	71
Q61881	Infl	VKMTK	SDDDVSGAGELSSEELK	QIAEE	2		869.3872148	1736.75883	0.000451244	8	N	308	325
Q61881	Infl	KRYSR	LFGDVVQELLPEYK	EKEVV	2		825.4434105	1648.871221	0.000451244	1	N	75	89
Q61881	Infl	ALLSR	FDLLWLIQDRPDRDNDLR	LAQHI	4		575.8005314	2299.170926	0.00307782	1	N	514	532
Q61881	Infl	ALLSR	FDLLWLIQDRPDR	DNDLR	3		562.9707789	1685.888937	0.001329271	1	N	514	527
Q61937	Infl	KNCFR	MTDQEAIQDLWQWR	KSL-	2		910.425758	1818.835916	0.000451244	14	N	275	289
Q61937	Infl	LATLK	MSVQPTVSLGGFEITPPVVLR	LKCGS	2		1114.111912	2226.208224	0.000451244	20	N	80	101
Q61937	Infl	LATLK	MSVQPTVSLGGFEITPPVVL	RLKCG	2		1036.061356	2070.107112	0.000451244	16	N	80	100
Q61937	Infl	QKKVK	LDEDDEDDDEDDEDDEDDDDDDFDEEETEEKVPVK	KSVRD	3		1393.165867	4176.4742	0.001329271	1	N	157	192
Q61990	Infl	GAQIK	IANPVEGSTDRQVTITGSAASISLAQYLINVR	LSSET	3		1115.598994	3343.773581	0.001162105	1	N	319	351
Q61990	Infl	GSTDR	QVTITGSAASISLAQYLINVR	LSSET	2		1103.116039	2204.216479	0.000451244	13	N	330	351
Q61990	Infl	SPEVK	GYWAGLDASAQTTSHELTIPNDLIGCIIGR	QGAKI	3	C26:+57.021	1077.203432	3228.586897	0.000451244	26	N	272	302
Q61990	Infl	NSTER	AITIAGIPQSIIECVK	QICVV	2	C14:+57.021	856.9846883	1711.953777	0.000451244	9	N	144	160
Q62086	Infl	LTQLK	VLQLGTLVDNLSIDPSSGDIWVGCHPNGQR	LFVYH	3	C24:+57.021	1083.210698	3246.608695	0.000698008	3	N	259	289
Q62086	Infl	SPDKK	YVYVADILAHEIHVLEK	QPNMN	4		503.777265	2011.07786	0.000451244	3	N	232	249
Q62167	Infl	FFNER	NINITKDLLDLLVEAK	QEVPS	2		906.5280059	1811.040412	0.000451244	2	N	548	564
Q62167	Infl	QMLAR	DFLDEYIFLAVGR	VGSTS	2		779.4015456	1556.787491	0.000622848	11	N	394	407
Q62167	Infl	INITK	DLLDLLVEAK	QEVPS	2		564.8296934	1127.643787	0.000662267	10	N	554	564
Q62167	Infl	EIDKR	SFLLDLLNATGK	DSLTL	2		646.3669744	1290.718349	0.000451244	8	N	428	440
Q62167	Infl	ISNVK	HVINFDLPSDIEEYVHR	IGRTG	3		695.0134835	2082.017051	0.000451244	3	N	511	528
Q62167	Infl	PPSER	LEQELFSGGNTGINFEKYDDIPVEATGNNCPPHIESF	SDVEM	3	C30:+57.021	1380.30438	4137.889741	0.000451244	4	N	145	182
Q62167	Infl	PPSER	LEQELFSGGNTGINFEK	YDDIP	2		941.963227	1881.910854	0.000451244	6	N	145	162
Q62167	Infl	PPSER	LEQELFSGGNTGINFEKY	DDIPV	2		1023.494891	2044.974183	0.000622848	1	N	145	163
Q62178	Infl	SEPVR	NLQLAPAQGAVFAGFSGGIWR	VPRAN	2		1080.571602	2159.127604	0.000451244	9	N	470	491
Q62186	Infl	SVDHR	GTWNGPWVSTEVLAAVIGIVIYYLAFSAK	SHIQA	3		1042.562381	3124.663743	0.00091018	5	N	138	167
Q62193	Infl	KSRVR	AQHIVPCTISQLLSATLTDEVFR	IGDVE	3	C7:+57.021	867.1235024	2598.347107	0.000451244	4	N	42	65
Q62219	Infl	PYCRR	DFLQLFAPR	CQGCQ	2		553.8038129	1105.592026	0.001395409	3	N	336	345
Q62219	Infl	LFAPR	CQGCQGPILDNYISALSALWHPDCFVCR	ECLAP	3	C1:+57.021,C4:+57.021,C24:+57.021,C27:+57.021	1113.171742	3336.491825	0.000451244	4	N	345	373

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q62261	Infl	LDILK	IVSSNDVGHDEYSTQSLVK	KHKDV	2		1039.505987	2076.996375	0.000451244	7	N	765	784
Q62261	Infl	SALER	LTTLELLEVR	RQQEE	2		593.8562425	1185.696885	0.001162105	11	N	2078	2088
Q62261	Infl	LADLK	QLWGLLIEETEKR	HRRLE	3		538.9670344	1613.877703	0.000451244	9	N	1571	1584
Q62261	Infl	DKLKK	SNAHYNLQNAFNLAEQHLGLTK	LLDPE	3		828.4195723	2482.235317	0.001162105	3	N	227	249
Q62261	Infl	SMLKK	HQILEQAVEDYAETVHQLSK	TSRAL	3		780.0611621	2337.160086	0.000451244	15	N	1633	1653
Q62261	Infl	FQLNR	EVDDLEQWIAER	EVVAG	2		751.8602419	1501.704884	0.000451244	4	N	1705	1717
Q62261	Infl	SENQR	LVSQDNFGFDLPAVEAATK	KHEAI	2		1011.513084	2021.010568	0.000451244	18	N	443	462
Q62261	Infl	QQFLR	DLDDFQSWLSR	TQTAI	2		691.3232952	1380.63099	0.000451244	3	N	1069	1080
Q62261	Infl	HQFSR	DASVAEAWLLGQEPYLSSR	EIGQS	2		1046.52144	2091.027281	0.000451244	16	N	2024	2043
Q62261	Infl	IAEWK	DGLNEAWADLLELIDTR	TQILA	2		972.489609	1942.963618	0.000451244	15	N	1780	1797
Q62261	Infl	SDLQK	EAEKLESEHPDQAQAILSR	LAEIS	2		1076.037986	2150.060372	0.000451244	2	N	1017	1036
Q62261	Infl	EVRKK	EIEELQSQAQALSQEGK	STDEV	2		944.4688736	1886.922147	0.001162105	1	N	1434	1451
Q62261	Infl	DIFER	SQNIITDSSSLNAEAIR	QRLAD	2		909.9637584	1817.911917	0.000451244	2	N	1547	1564
Q62261	Infl	LNNRK	FANSLVGVQQQLQAFNTYR	TVEKP	2		1092.563974	2183.112348	0.000451244	15	N	329	348
Q62261	Infl	DPNTK	VSEEAESQQWDTSKGDQVSQNGLPAEQGSPR	MAGTM	3		1115.514094	3343.518882	0.000451244	33	N	2108	2139
Q62261	Infl	PASSR	AQTLPTSVVTITSESSPGKR	EKDKE	2		1030.055648	2058.095695	0.000451244	6	N	2324	2344
Q62261	Infl	DNVIR	LWEYLLELLR	ARRQR	2		674.3877099	1346.75982	0.001162105	8	N	508	518
Q62261	Infl	ASAQK	FATDGEGYKPCDPQVIRDR	VAHME	4	C11:+57.021	556.76715	2223.0374	0.0007646	2	N	593	612
Q62261	Infl	KFTEK	GNLEVLLFTIQSK	MRANN	2		731.4197383	1460.823877	0.001162105	1	N	359	372
Q62261	Infl	IIYIR	EQWANLEQLSAIR	KKRLE	2		779.4051509	1556.794702	0.000451244	6	N	723	736
Q62261	Infl	KMIEK	YESLASDLLEWIEQTIIILNNRK	FANSL	3		921.1643978	2760.469794	0.000451244	2	N	306	329
Q62261	Infl	VDRKK	DALLSALSIQNYHLECNETK	SWIRE	2	C16:+57.021	1160.068198	2318.120795	0.000451244	6	N	948	968
Q62261	Infl	IRKKR	LEEASLLHQFQADADDIDAWMLDILK	IVSSN	3		1000.827346	2999.458638	0.000622848	1	N	739	765
Q62261	Infl	TEAEK	LLTQHENIKNEIDNYEEDYQK	MRDMG	3		879.4211958	2635.240187	0.000698008	6	N	1099	1120
Q62261	Infl	HQFNR	DVEDEILWVGER	MPLAT	2		730.357335	1458.69907	0.0025889	1	N	1492	1504
Q62318	Infl	RLQEK	LSPPYSSPQEFAQDVGR	MFKQF	2		939.4555692	1876.895538	0.000451244	6	N	750	767
Q62318	Infl	AEGPR	LASPSGSTSSGLEVVAPEVTSAPVSGPGILDDSATICR	VCQKP	3	C37:+57.021	1228.947645	3683.819536	0.000622848	15	N	591	629
Q62318	Infl	TLTCR	DCQLNAHKDHQYQFLEDAVR	NQRKL	3	C2:+57.021	829.7208798	2486.139239	0.001591523	2	N	231	251
Q62318	Infl	PPVFK	VFPGSTTEDYNLIVIER	GAAAA	2		977.0023522	1951.989104	0.000451244	1	N	507	524
Q62318	Infl	VSLER	LDLDLTSDSQPPVFK	VFPGS	2		837.9334069	1673.851214	0.000451244	10	N	492	507
Q62318	Infl	AGGEK	RPAASSAAAASAAASSPAGGGGEAQELLEHCGVCR	ERLRP	3	C31:+57.021,C34:+57.021	1108.853202	3323.536206	0.000451244	5	N	35	70
Q62318	Infl	KQFNK	LTEDKADVQSIIGLQR	FFETR	2		893.489412	1784.963224	0.000870037	2	N	774	790
Q62376	Infl	RDEAR	GGGGSGQDNGLEGLGSDGR	DMYME	2		845.3753074	1688.735015	0.000622848	6	N	403	422
Q62393	Infl	QAGQK	ASAAFSSVGSVITK	KLEDV	2		662.8595135	1323.703427	0.000451244	15	N	148	162
Q62393	Infl	EELRR	ELTKVEEEIQTLSQVLAAK	EKHLA	2		1065.089156	2128.162712	0.000451244	13	N	80	99
Q62418	Infl	EKVAK	ASGANYSFHKESTSFQDVGPQAPVGSVYQK	TNAIS	3		1062.842935	3185.505404	0.000451244	8	N	134	164
Q62418	Infl	YSFHK	ESTSFQDVGPQAPVGSVYQK	TNAIS	2		1062.516355	2123.01711	0.000451244	35	N	144	164
Q62418	Infl	VVTEK	SPTDWALFTYEGNSNDIR	VAGTG	2		1043.479773	2084.943945	0.000451244	20	N	23	41
Q62418	Infl	SNDIR	VAGTGEGGLEELVEELNSGK	VMYAF	2		994.4950884	1986.974577	0.000451244	17	N	41	61
Q62418	Infl	GLCAR	ALYDYQAADDTEISFDPENLITGIEVIDEGWWR	GYGPD	3		1282.267526	3843.779179	0.000451244	17	N	383	416
Q62418	Infl	EAYVR	VVTEKSPTDWALFTYEGNSNDIR	VAGTG	2		1321.640804	2641.266008	0.001162105	1	N	18	41
Q62418	Infl	SGLPK	FVLINWTGEGVNDVR	KGACA	2		859.947183	1717.878766	0.000451244	3	N	78	93
Q62418	Infl	PFLQK	QLTQPETSYGREPTAPVSR	PAAGV	3		706.3594309	2116.054893	0.001654178	3	N	296	315
Q62419	Infl	LDYHR	QAVQILEELADKLK	RRVRE	3		533.3106897	1596.908669	0.000451244	7	N	227	241
Q62422	Infl	NQQNK	LGDTALHAAAWK	GYADI	2		627.3360086	1252.656417	0.000451244	8	N	138	150
Q62422	Infl	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAKR	GNLSW	2		1412.217742	2822.419883	0.000823681	1	N	57	83
Q62422	Infl	NGLDK	AGSTALYWACHGGHKDIVEVLFTQPNVELNQQNK	LGDTA	3	C10:+57.021	1275.632326	3823.873577	0.000451244	8	N	104	138
Q62422	Infl	AAAWK	GYADIVQLLLAK	GARTD	2		652.3851672	1302.754734	0.000451244	13	N	150	162
Q62422	Infl	HGGHK	DIVEVLFTQPNVELNQQNK	LGDTA	2		1114.582029	2227.148459	0.000451244	14	N	119	138
Q62422	Infl	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAK	RGNLS	2		1334.167186	2666.318772	0.000451244	10	N	57	82
Q62422	Infl	AWKGY	ADIVQLLLAK	GARTD	2		542.342771	1082.669942	0.001162105	5	N	152	162
Q62431	Infl	LPSPK	LPVTPLGLAASTNGSSITPAPK	IKKEE	2		1046.586583	2091.157567	0.000451244	2	N	379	401
Q62431	Infl	TVPGR	LPVSLAGHPVVAAQAAAVQAAAAQAAVAAQAAALEQLR	EKLES	3		1192.332582	3573.974346	0.000451244	6	N	417	455
Q62448	Infl	QLCLR	LAEDAPNFDGPAAEGQPGQK	QSTTF	2		1006.471948	2010.928295	0.000451244	8	N	138	158
Q62448	Infl	QFAAR	AIISELVSISELAQPLESGTHFPLFLLCLQQLAK	LQDRE	3	C28:+57.021	1256.021869	3765.042206	0.001839721	1	N	648	682
Q62465	Infl	YDKVK	LQSRPAVPPAPGPGQLTLR	VRACG	3		652.3782086	1954.111226	0.000451244	5	N	76	95
Q62465	Infl	LQANR	AVCGFHLGYLDGEVELVNSVVTR	LVALY	3	C3:+57.021	845.4288143	2533.263043	0.000451244	5	N	334	357
Q62465	Infl	MAMAR	TWWNQFSVTALQLLQANR	AVCGF	2		1088.569059	2175.122519	0.000451244	1	N	316	334
Q62465	Infl	HIKPR	IDSVWPFEK	VADAM	2		560.7878285	1119.560057	0.002981883	1	N	370	379
Q62465	Infl	APPLR	CLVLTGFGGYDKVK	LQSRP	3	C1:+57.021	519.6099279	1555.806384	0.000451244	3	N	62	76
Q62465	Infl	LQLCR	TVENVTVFGTASASK	HEVLK	2		755.891542	1509.767484	0.000622848	2	N	223	238
Q62465	Infl	APPLR	CLVLTGFGGYDK	VKLQS	2	C1:+57.021	665.3293033	1328.643007	0.002663018	1	N	62	74
Q62523	Infl	APKPK	VNPFRPGDSEPPVAAGAQR	AQMGR	2		983.0010095	1963.986419	0.000451244	13	N	35	54
Q62523	Infl	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	C1:+39.994,C4:+57.021,C17:+57.021,C26:+57.021	1039.776907	3116.307321	0.000451244	9	N	528	555

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q62523	Infl	RATGK	AYHPQCFTCVVCACPLEGTSFIVDQANQPHCVPDYHK	QYAPR	3	C6:+57.021,C9:+57.021,C12:+57.021,C14:+57.021,C31:+57.021	1469.316081	4404.924843	0.000451244	14	N	453	490
Q62523	Infl	NFHMK	CYKCEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	C1:+57.021,C4:+57.021,C7:+57.021,C20:+57.021,C29:+57.021	1195.848733	3584.522799	0.000451244	3	N	525	555
Q62523	Infl	QYAPR	CSVCSEPIMPEPGRDETVR	VVALD	3	C1:+57.021,C4:+57.021	740.3347151	2217.980745	0.000622848	3	N	495	514
Q62523	Infl	RATGK	AYHPQCFTCVVCACPLEGTSFIVDQANQPH	CVPDY	3	C6:+57.021,C9:+57.021,C12:+57.021,C14:+57.021	1169.517578	3505.529333	0.000622848	4	N	453	483
Q62523	Infl	GQQFY	SLEGAPYCEGCYTDTLEK	CNTCG	2	C8:+57.021,C11:+57.021	1046.945597	2091.875594	0.000622848	3	N	417	435
Q62523	Infl	PVVSK	FSPGAPSGPGPQPNQK	MVPPD	2		783.3895008	1564.763402	0.000451244	10	N	270	286
Q62523	Infl	HITCF	TCHQCQQQLQGQQFYSLEGAPYCEGCYTDTLEK	CNTCG	3	C2:+57.021,C5:+57.021,C23:+57.021,C26:+57.021	1343.237756	4026.689869	0.000823681	2	N	402	435
Q63810	Infl	PLVQR	VIDIFDTDGNGEVDFKEFIEGVSQFSVK	GDKEQ	3		1045.512192	3133.513175	0.000451244	21	N	57	85
Q63810	Infl	DGDGR	ISFEEFCAVVGGLDIHKK	MVVDV	4	C7:+57.021	513.0177079	2048.039632	0.000662267	1	N	147	165
Q64012	Infl	SSSSR	LPAPQEDTASEAGTPQGEVQTR	DDGDE	2		1141.548915	2281.08223	0.000451244	17	N	260	282
Q64152	Infl	FNNPK	VQASLAANTFTITGHAETK	QLTEM	2		980.5108758	1959.006152	0.000451244	24	N	120	139
Q64152	Infl	SVDGK	APLATGEDDDDEVPDLVENFDEASKNEAN	-	3		1040.453618	3118.337455	0.000622848	13	N	175	204
Q64324	Infl	SSLIR	NLEQLGGTVTNSAGSGTSSR	LERRE	2		968.4724789	1934.929358	0.000451244	13	N	439	459
Q64324	Infl	DRLDR	KLWPFVSDPAPVPSSQAAVSAR	FGHWH	2		1155.616207	2309.216813	0.001162105	2	N	493	515
Q64324	Infl	DINKR	REPIPSLEAIYLLSPTEK	SVQAL	2		1028.570402	2055.125204	0.0007646	3	N	64	82
Q64324	Infl	SPTEK	SVQALIADFQGTPTFTYK	AAHIF	2		994.01272	1986.00984	0.000451244	12	N	82	100
Q64324	Infl	AKAVK	TLKEIHLAFLPYEAQVFSLDAPHSTYNLYCPFR	AGERG	4	C30:+57.021	985.9991381	3939.965352	0.001162105	2	N	128	161
Q64324	Infl	SSCCK	MSDILAEGITIVEDINKR	REPIP	3		673.0265131	2016.056139	0.000451244	4	N	46	64
Q64324	Infl	GERGR	QLDALAQQIATLCATLQEYPSIR	YRKGP	2	C13:+57.021	1302.178811	2602.342022	0.000451244	4	N	167	190
Q64324	Infl	SIRYR	KGPEDTAQLAHAVLAK	LNAFK	3		550.3059387	1647.894416	0.000622848	2	N	192	208
Q64324	Infl	SPTEK	SVQALIADFQGTPTFTY	KAAHI	2		929.9652384	1857.914877	0.000622848	2	N	82	99
Q64324	Infl	INKRR	EPIPSLEAIYLLSPTEK	SVQAL	2		950.5198465	1899.024093	0.000451244	2	N	65	82
Q64433	Infl	KSQGK	VLQATVVAVGSGGK	GKSGE	2		643.3778735	1284.740147	0.000451244	8	N	40	54
Q64433	Infl	YGGTK	VVLDDKDYFLFR	DSDIL	2		765.4040883	1528.792577	0.000451244	2	N	80	92
Q64433	Infl	YGGTK	VVLDDKDYFLF	RDSDI	2		687.3535327	1372.691465	0.001699387	2	N	80	91
Q64455	Infl	HGPIK	AYAVILTTGEAAQPSADVLK	YTYED	2		1009.544384	2017.073169	0.000979378	1	N	749	769
Q64455	Infl	SYTVK	ILTQVGDGTTSLVPGWNLFCTEPEPVTSFHCEVVPK	EPALV	3	C20:+57.021,C31:+57.021	1338.992266	4013.953399	0.000451244	15	N	597	633
Q64511	Infl	PSLLK	HGFLEEFITPIVK	ASKNK	3		510.617454	1528.828962	0.000870037	5	N	575	588
Q64514	Infl	DGKPK	IIDIIDTTGSGDVNTATEVEPKDGEIIGLSGR	VLKIP	3		1095.895253	3284.662358	0.000451244	3	N	63	95
Q64514	Infl	DGKPK	IIDIIDTTGSGDVNTATEVEPK	DGEII	2		1144.579349	2287.143099	0.000451244	15	N	63	85
Q64514	Infl	PRGLR	EGLHYTEVCGYDIASPNAGPLFR	VPITA	3	C9:+57.021	856.0729191	2565.195357	0.000451244	5	N	605	628
Q64514	Infl	QWMTK	LDSTDIYNELKETYPAYLPLYVAR	LHQLD	3		949.8204082	2846.437825	0.000637154	9	N	1048	1072
Q64514	Infl	ERMKR	LNEIVDAANAVISHIDQTALAVYIAMK	TDPRP	3		961.8481928	2882.521178	0.001699387	1	N	1085	1112
Q64514	Infl	GIYLR	DPVQVAAPSDHGVGIEPVFPENTENSEK	ISFQL	3		988.1408692	2961.399207	0.000622848	1	N	536	564
Q64521	Infl	DVRAK	CVINASGPFTDSVR	KMDDK	2	C1:+57.021	761.8698553	1521.724111	0.000451244	3	N	284	298
Q64521	Infl	LMTLK	NTPEFDILVIGGGATGCGCALDAVTR	GLKTA	2	C17:+57.021,C19:+57.021	1332.641504	2663.267408	0.000451244	9	N	65	91
Q64521	Infl	VVGVR	LVSEFPYIEAEVK	YGIKE	2		762.4037539	1522.791908	0.00091018	1	N	525	538
Q64521	Infl	GYKSR	TEQLTDSTEISLLPSDIDR	YKKRF	2		1067.032035	2132.04847	0.000622848	9	N	608	627
Q64521	Infl	SRRTR	LAFLNVQAAEEALPR	IVELM	2		821.4521012	1640.888602	0.000622848	3	N	557	572
Q64523	Infl	QLAIR	NDEELNKLLGK	VTIAQ	2		636.8438635	1271.672127	0.000451244	57	N	89	100
Q64523	Infl	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	2		1467.276214	2932.536828	0.000451244	2	N	43	72
Q64727	Infl	IDGSR	GILSGTSDLLLTFDEAEVR	KIIRV	2		1018.531474	2035.047348	0.000451244	8	N	113	132
Q64727	Infl	EVDGK	AIPDLTAPVAAVQAAVSNLVR	VGKET	2		1038.594743	2075.173886	0.000451244	10	N	35	56
Q64727	Infl	LEQLR	LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK	AGEVI	3		1342.684793	4025.030978	0.000622848	5	N	853	889
Q64727	Infl	EQAQR	WIDNPTVDDRGVGQAAIR	GLVAE	2		992.0062919	1981.996984	0.000451244	5	N	502	520
Q64727	Infl	LNQAK	GWLRDPNASPGDAGEQAIR	QILDE	2		1005.493549	2008.971497	0.000698008	1	N	281	300
Q64727	Infl	DLLAK	CDRVDQLTAQLADLAAR	GEGES	2	C1:+57.021	958.4866464	1914.957693	0.000451244	4	N	544	561
Q64727	Infl	VAMQK	AQQVSQGLDVLTAK	VENAA	2		729.4020769	1456.788554	0.000451244	6	N	352	366
Q64727	Infl	NEIIR	VLQLTSWDEDAWASK	DTEAM	2		874.9286559	1747.841712	0.000451244	10	N	246	261
Q64727	Infl	IDGSR	GILSGTSDLLLTFDEAEVRK	IIRVC	2		1082.578955	2163.142311	0.000451244	8	N	113	133
Q64727	Infl	SPQAR	ALASQLQDSLKDLK	AQMQE	3		510.6231563	1528.846069	0.001943752	1	N	570	584
Q64727	Infl	DKRIR	TNLLQVCERIPTISTQLK	ILSTV	2	C7:+57.021	1057.585829	2113.156058	0.001329271	1	N	978	996
Q64727	Infl	NACTK	LVQAAQMLQSDPYSVPARDYLIDGSR	GILSG	3		965.1557969	2892.443991	0.000451244	2	N	87	113
Q64727	Infl	VFHTR	TIESILEPVAQQISHLVIMHEEGEVDGK	AIPDL	3		1034.532822	3100.575065	0.001162105	1	N	7	35
Q64737	Infl	TAQWR	AFTNPEDACSFITSANFPALVVK	ASGLA	2	C9:+57.021	1250.115148	2498.214696	0.000451244	7	N	125	148
Q64737	Infl	GAYTK	GVEITGFPEAQALGLQVFHAGTALK	DGKVV	3		852.1275069	2553.359121	0.001763695	1	N	350	375
Q64737	Infl	EFNCR	FGDPECQVILPLLK	SDLYE	2	C6:+57.021	814.9397494	1627.863899	0.001943752	4	N	292	306
Q64737	Infl	GAYTK	GVEITGFPEAQALGLQVFHAGTALKDGK	VVTSG	4		714.3834227	2853.502491	0.001229886	1	N	350	378
Q65Z40	Infl	DLKNR	IGGLENLNETFEEDIIQSVLRPSNCR	TYCRA	3	C25:+57.021	1001.833228	3002.476284	0.000451244	2	N	276	302
Q65Z40	Infl	DHSLR	LAGQVHAVQALVQLFLER	ERAAQ	3		664.7183423	1991.131627	0.000870037	2	N	1035	1053
Q65Z40	Infl	VTTVR	EYLPEGDFSIMTEMLK	KFLSF	2	[0:-18.011,M14:+15.995	950.9393436	1899.863087	0.001229886	1	N	1154	1170

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q66JX5	Infl	GLEGR	ENLAQDLGIIEAEGTVGGPLLLEVIRR	CQQKE	3		959.2016231	2874.581469	0.00091018	1	N	107	134
Q66JX5	Infl	GLEGR	ENLAQDLGIIEAEGTVGGPLLLEVIR	RCQQK	3		907.1679194	2718.480358	0.000451244	3	N	107	133
Q68FD5	Infl	ELFAR	KFNALFAQGNYSEAAK	VAANA	2		879.9446403	1757.873681	0.000451244	7	N	366	382
Q68FD5	Infl	SNFGR	LASTLVHLGEYQAAVDGAR	KANST	2		986.018868	1970.022136	0.000451244	4	N	1226	1245
Q68FD5	Infl	AKTNR	LAELEEFINGPNNAHIQQVGDR	CYDEK	2		1232.614924	2463.214247	0.000451244	14	N	1182	1204
Q68FD5	Infl	IYMNR	ISGETIFVTAPHEATAGIIGVNR	KGQVL	2		1177.129678	2352.243756	0.000451244	16	N	297	320
Q68FD5	Infl	YQALR	TSIDAYDNFDNISLAQR	LEKHE	2		971.9612157	1941.906831	0.000451244	17	N	1481	1498
Q68FD5	Infl	DAKQK	WLLLTGISAQQNR	VVGAM	2		750.420604	1498.825608	0.000451244	6	N	163	176
Q68FD5	Infl	VAYER	GQCDLELINVCNENSLFK	SLSRY	2	C3:+57.021,C11:+57.021	1077.00378	2151.991961	0.000451244	21	N	923	941
Q68FD5	Infl	EKRNR	LKLLLPWLEAR	IHEGC	3		451.2873796	1350.838739	0.001162105	6	N	854	865
Q68FD5	Infl	GDLVK	SVDPTLALSVYLR	ANVPN	2		717.4040883	1432.792577	0.000451244	11	N	468	481
Q68FD5	Infl	VLYAK	KVGYTPDWIFLLR	NVMRI	3		536.6368486	1606.887146	0.000622848	11	N	506	519
Q68FD5	Infl	NHNNK	SVNESLNNLFITEEDYQALR	TSIDA	2		1178.077308	2354.139017	0.000451244	24	N	1461	1481
Q68FD5	Infl	SNPYR	RPLIDQVVQTALSETQDPEEVSVTVK	AFMTA	2		1441.261815	2880.50803	0.000451244	3	N	967	993
Q68FD5	Infl	FAIFR	KFDVNTSAVQVLIEHIGNLDR	AYEFA	2		1184.635128	2367.254655	0.000451244	3	N	1073	1094
Q68FD5	Infl	LYAKK	VGYTPDWIFLLR	NVMRI	2		740.4038913	1478.792183	0.000451244	2	N	507	519
Q68FD5	Infl	YDIKR	AVVHTHLLNPEWLVNYFGSLSVEDSLECLR	AMLSA	4	C28:+57.021	875.1939151	3496.74446	0.000622848	2	N	638	668
Q68FD5	Infl	IGVNR	KGQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C8:+57.021	1142.276709	3423.806726	0.000451244	12	N	320	350
Q68FD5	Infl	QEEKR	ECFGACLFTCYDLLRPDVVLETAWR	HNIMD	3	C2:+57.021,C6:+57.021,C10:+57.021	1031.15406	3090.438779	0.000451244	13	N	1563	1588
Q68FD5	Infl	EYINR	LDNYDAPDIANIAISNELFEEAFAIFR	KFDVN	3		1024.50526	3070.49238	0.000451244	15	N	1046	1073
Q68FD5	Infl	GLLQR	ALEHFTDLYDIKR	AVVHT	3		540.9513843	1619.830753	0.000451244	9	N	625	638
Q68FD5	Infl	YDAAK	LLYNNVSNFGR	LASTL	2		648.8389154	1295.662231	0.000823681	4	N	1215	1226
Q68FD5	Infl	GVNRK	GQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C7:+57.021	1099.578388	3295.711763	0.000451244	4	N	321	350
Q68FD5	Infl	RVMEY	INRLDNYDAPDIANIAISNELFEEAFAIFR	KFDVN	3		1152.247961	3453.720482	0.000451244	13	N	1043	1073
Q68FD5	Infl	SVYLR	ANVPNKVIQCFAETGQVQK	IVLYA	2	C10:+57.021	1066.052154	2130.088707	0.000451244	5	N	481	500
Q68FD5	Infl	QAGGK	LHIIEVGTPPTGNQPFPK	KAVDV	2		973.0312471	1944.046894	0.000451244	12	N	227	245
Q68FD5	Infl	NVPNK	VIQCFAETGQVQK	IVLYA	2	C4:+57.021	754.3825986	1506.749597	0.000451244	27	N	487	500
Q68FD5	Infl	LKEAK	LTDQLPLIIVCDR	FDFVH	2	C11:+57.021	778.4295488	1554.843498	0.000698008	3	N	767	780
Q68FD5	Infl	FSEHR	NLQNLLILTAIK	ADRTR	2		677.4273664	1352.839133	0.000451244	9	N	1022	1034
Q68FD5	Infl	RKKAR	ESYVETELIFALAK	TNRLA	2		806.9275932	1611.839586	0.000870037	2	N	1165	1179
Q68FD5	Infl	QVASK	YHEQLSTQSLIELFESFK	SFEGL	3		733.7043157	2198.089547	0.000451244	9	N	688	706
Q68FD5	Infl	DTIRR	FQSVPAQPGQTSPLLQYFGILLDQGQLNK	YESLE	3		1063.231582	3186.671347	0.000451244	11	N	400	429
Q68FD5	Infl	ASESK	DTELAEELLQWFLQEEKR	ECFGA	3		759.7186248	2276.132475	0.000622848	9	N	1545	1563
Q68FD5	Infl	FESFK	SFEGLFYFLGSIVNFSQDPDVHFK	YIQAA	3		931.7906719	2792.348616	0.000451244	11	N	706	730
Q68FD5	Infl	ASESK	DTELAEELLQWFLQEEK	RECFG	2		1061.023482	2120.031363	0.000451244	11	N	1545	1562
Q68FD5	Infl	IVCDR	FDFVHDLVLYLYR	NNLQK	3		567.300125	1698.876975	0.000823681	8	N	780	793
Q68FD5	Infl	VNPSR	LPVVIGGLLDVDCSEDVIK	NLILV	2	C13:+57.021	1021.048214	2040.080828	0.000451244	8	N	811	830
Q68FD5	Infl	GLLQR	ALEHFTDLYDIK	RAVVH	3		488.9176806	1463.729642	0.000451244	10	N	625	637
Q68FD5	Infl	NIIPY	ITNVLQNPDLALR	MAVRN	2		733.9204368	1465.825274	0.000622848	8	N	337	350
Q68FD5	Infl	VNPSR	LPVVIGGLLDVDCSEDVIKNLILVVR	GQFST	3	C13:+57.021	950.2124289	2847.613887	0.000451244	2	N	811	837
Q68FD5	Infl	YSVDR	KVSQPIEGHAASFAQFK	MEGNA	3		615.660493	1843.958079	0.002981883	1	N	188	205
Q68FD5	Infl	ELLEK	IVLDNSVFSEHR	NLQNL	2		708.3680371	1414.720474	0.000451244	1	N	1010	1022
Q68FD5	Infl	EFAER	CNEPAVWSQLAK	AQLQK	2	C1:+57.021	701.8431092	1401.670618	0.001463592	2	N	1101	1113
Q68FD5	Infl	AIFRK	FDVNTSAVQVLIEHIGNLDR	AYEFA	3		747.3943641	2239.159692	0.001654178	1	N	1074	1094
Q68FD5	Infl	PDTIR	RFQSVPAQPGQTSPLLQYFGILLDQGQLNK	YESLE	3		1115.265286	3342.772458	0.000622848	13	N	399	429
Q68FD5	Infl	IYVQK	VNPSRLPVVIGGLLDVDCSEDVIK	NLILV	3	C18:+57.021	865.4671576	2593.378073	0.000451244	3	N	806	830
Q68FD5	Infl	RMAVR	NNLAGAEELFAR	KFNAL	2		652.8338301	1303.65206	0.000451244	4	N	354	366
Q68FD5	Infl	FLITK	YGYIHLYDLETGTCIY	MNRIS	2	C14:+57.021	990.9563248	1979.89705	0.002374549	1	N	278	294
Q68FD5	Infl	LFARK	FNALFAQGNYSEAAK	VAANA	2		815.8971587	1629.778717	0.000698008	1	N	367	382
Q68FL6	Infl	LTRPK	VPVLQLDSGNYLFSASAICR	YFFLL	2	C19:+57.021	1105.567636	2209.119673	0.000451244	1	N	47	67
Q68FL6	Infl	QFMAK	DNVPFHGLVFPCSVLGAEDNYTLVK	HIIAT	3	C12:+57.021	931.1305455	2790.368237	0.000451244	9	N	556	581
Q68FL6	Infl	RARGR	AELLISTVGPEECVVPFLTRPK	VPVLQ	3	C13:+57.021	819.1140557	2454.318767	0.000451244	1	N	25	47
Q68FL6	Infl	DLLIK	NNSELLNNLGNFINR	AGMFV	2		866.4427961	1730.869992	0.002453667	1	N	643	658
Q69ZK0	Infl	PSSIR	TLVDNIQQYVEDGKNQLLLALLK	CTDTE	3		876.825605	2627.453415	0.000451244	7	N	1281	1304
Q69ZK0	Infl	ATAVK	IDQLIRPINALDELYR	LMKTF	3		648.030586	1941.068358	0.002145581	1	N	1519	1535
Q69ZK0	Infl	APSWK	CSPAVDEDSQGQGLNDSSYGSASGAPSQQDR	GLSFL	3	C1:+57.021	1057.445197	3169.312191	0.000622848	2	N	1020	1051
Q69ZK0	Infl	VLFTK	ALESVEGPPPPGNQAAEELQQEINAQSLEK	VQQYY	3		1058.525271	3172.552414	0.002453667	1	N	1461	1491
Q69ZK0	Infl	LGGRK	TTDIPLEGYLLSPIQR	ICKYP	2		908.4967057	1814.977811	0.000451244	1	N	177	193
Q69ZK0	Infl	QAGRK	IYSINEDLVFLRPFSEVETILNQFFCSR	RPLRL	3	C26:+57.021	1146.24675	3435.716849	0.000823681	1	N	662	690
Q6A026	Infl	KPYVR	SAGTETGSNINANSELSPSAGSR	SREQS	2		1104.012697	2206.009793	0.000451244	7	N	1157	1180
Q6A026	Infl	NKDVR	LLVACCLADIFR	IYAPE	2	C5:+57.021,C6:+57.021	725.8809488	1449.746298	0.000451244	4	N	86	98
Q6A026	Infl	KTNEK	LYTVCDVALCVINSK	SALCN	3	C5:+57.021,C10:+57.021	585.6322496	1753.873349	0.000622848	3	N	1073	1088
Q6A026	Infl	SAGSR	SREQSSEASETGVSENEENPVR	IISVT	3		807.6973883	2420.068765	0.002145581	1	N	1180	1202
Q6A026	Infl	IFSNK	EVQLAQIFEPLSR	SLNAD	2		765.4202697	1528.824939	0.001162105	1	N	749	762

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6A068	Infl	LKRKK	ESDLPSAILQTSGVSEFTK	KRSKL	2		1005.007832	2008.000063	0.000451244	2	N	271	290
Q6A068	Infl	KAVQK	DLPRPSEVNETILRPLNVEPPLTDLQK	SEELI	4		771.6743655	3082.666262	0.000451244	6	N	543	570
Q6A4J8	Infl	VMCDR	AGFIQDTSLILYEEVKPNLTER	IQDYD	3		846.1151555	2535.322066	0.000451244	10	N	724	746
Q6A4J8	Infl	IRESK	LSEVLQAVTDHDIPQQLVER	LQEEK	3		764.0732906	2289.196472	0.000451244	2	N	524	544
Q6A4J8	Infl	DQNIK	INDRFEFPEQLPLDEFLQK	TDPKD	3		793.4062697	2377.195409	0.000451244	7	N	421	440
Q6A4J8	Infl	IKGKK	NIFESFVDYVAVEQLDGDNKYDAGEHGLQEAEK	GVKFL	3		1243.911743	3728.711828	0.000622848	1	N	359	392
Q6A4J8	Infl	PWTIF	LETVDPELAASGATLPK	FDKDH	2		856.4597889	1710.903978	0.000451244	1	N	662	679
Q6BCL1	Infl	EIYEL	YDAVEATDDSSISPR	GRDEM	2		813.3686281	1624.721656	0.000451244	2	N	516	531
Q6BCL1	Infl	PRKPK	LPGSVSECSLPSASAGSSPQCPLSPGLIVPGIPR	WRSED	3	C8:+57.021,C21:+57.021	1125.574495	3373.700084	0.000622848	1	N	401	435
Q6BCL1	Infl	KCGSR	ELDSHSPQPDISTFPK	NNENF	2		899.4368451	1796.85809	0.002374549	1	N	246	262
Q6BCL1	Infl	GELSK	RPPQLETPQEPSAPPAQK	LLKPE	2		986.018868	1970.022136	0.001162105	1	N	150	168
Q6BCL1	Infl	NLQAK	FQTSQPELGELFR	KTPKP	2		776.3942519	1550.772904	0.00091018	4	N	13	26
Q6BCL1	Infl	GYVPR	TALLPLETEVYDDVSF	GDPLD	2		906.4516295	1810.887659	0.000622848	3	N	648	664
Q6BCL1	Infl	QTPPR	KPESCNPQSHSPLPDFNAFPK	KHPQL	3	C5:+57.021	799.7149546	2396.121464	0.000451244	9	N	296	317
Q6BCL1	Infl	GFSRK	SQPQSESIEVSQTSPSK	CGSRE	2		909.9399489	1817.864298	0.000823681	2	N	225	242
Q6DFW4	Infl	KSEVK	TYDPSGDSTLPTCSK	KRKIE	2	C13:+57.021	814.8593503	1627.703101	0.000451244	13	N	426	441
Q6DFW4	Infl	IMRCR	EWYGWHFPELGK	IISDN	3		516.9143819	1547.719746	0.000823681	1	N	184	196
Q6DFZ1	Infl	FSNLK	EVLNSVTELSEIEPNVFLRPFLEVIR	SEDTT	3		1014.889045	3041.643735	0.000622848	4	N	47	73
Q6DTY7	Infl	QAVMR	CLLAYFLDKAAEELPYLK	CPLHT	3	C1:+57.021	719.7152329	2156.122299	0.000451244	4	N	396	414
Q6DTY7	Infl	SQMKR	TIQTAEALSVPYEQWK	VLNEI	2		932.478513	1862.941426	0.001162105	3	N	306	322
Q6DTY7	Infl	DFMRR	IECYENSYESLDEDLDRDLSYIK	IMDVG	3	C3:+57.021	957.0958949	2868.264285	0.000979378	2	N	194	217
Q6DTY7	Infl	QNGYK	TFFVESICVDPEVVAANIVQVK	LGSPD	3	C8:+57.021	822.0982941	2463.271482	0.000622848	1	N	151	173
Q6GQT9	Infl	SVSGK	VSCLDTCGDLLVTLQSLSR	QGEKR	2	C3:+57.021,C7:+57.021	1069.035081	2136.054561	0.000451244	1	N	500	519
Q6GQT9	Infl	RSCHR	FEQAFYTYDTSSPSILTLTAIR	HHVLG	2		1262.634459	2523.253318	0.000451244	2	N	635	657
Q6GQT9	Infl	YAVSK	EDGSFSFYSLPSGGYTVVPFYR	GERIT	2		1238.07932	2474.143039	0.000698008	4	N	266	288
Q6IRU2	Infl	AVKRK	IQALQQQADDAEDRAQGLQR	ELDGE	2		1127.562691	2253.109782	0.000451244	4	N	13	33
Q6IRU2	Infl	VSELK	CGDLEEELKNVTNNLK	SLEAA	2	C1:+57.021	938.4597629	1874.903926	0.000622848	1	N	153	169
Q6IRU2	Infl	LAQAK	EENVGLHQTLDQTLNELNCI	-	2	C19:+57.021	1170.560737	2339.105874	0.000451244	14	N	228	248
Q6IRU2	Infl	ALNRR	IQLLEEELDRAQEQLATALQNLEEAEK	AADES	3		1042.20565	3123.59355	0.000451244	16	N	55	82
Q6IRU2	Infl	EELDR	AQEQLATALQNLEEAEKAADESER	GMKVI	3		882.0952598	2643.262379	0.000622848	4	N	65	89
Q6IRU2	Infl	DLEEK	LAQAKEENVGLHQTLDQTLNELNCI	-	2	C24:+57.021	1426.216653	2850.417706	0.000451244	7	N	223	248
Q6IRU2	Infl	AVKRK	IQALQQQADDAEDR	AQGLQ	2		800.882237	1599.748874	0.001162105	1	N	13	27
Q6NVF9	Infl	SAISR	AVSDASAGDYGSAIETLVTAISLIK	QSKVS	2		1226.645024	2451.274448	0.000451244	19	N	431	456
Q6NVF9	Infl	RIALY	IGNLTWWTTDEDLTEAVHSLGVNDILEIK	FFENR	3		1094.889662	3281.645586	0.000622848	4	N	84	113
Q6NZB0	Infl	NQIER	LTRPGSSYFNLNPFEVLQIDPEVTDEEIK	KRFRQ	3		1117.565067	3349.671801	0.000451244	17	N	45	74
Q6NZB0	Infl	KKRFR	QLSILVHPDKNQDDADR	AQKAF	4		491.7517785	1962.975914	0.000851441	2	N	78	95
Q6NZC7	Infl	MHNPK	VIVQFQPSSVPDEWGTTQDGQTRPR	VVKRG	3		943.4707725	2827.388917	0.000451244	9	N	393	418
Q6NZJ6	Infl	RPMGK	ATSLLLEILGLLCK	SMGPK	2	C13:+57.021	772.4603176	1542.905035	0.000451244	6	N	1371	1385
Q6NZJ6	Infl	EERLK	GVIDLIFEK	AISEP	2		517.3005718	1032.585544	0.000735798	4	N	799	808
Q6NZJ6	Infl	RLLQK	YLCDEQKELQALYALQALVVTLEQPANLLR	MFFDA	3	C3:+57.021	1168.292359	3501.853677	0.001591523	1	N	1513	1543
Q6NZJ6	Infl	GSNQR	VFDWIDANLNEQQIASNTLVR	ALMTT	2		1223.622217	2445.228835	0.000451244	6	N	1459	1480
Q6NZJ6	Infl	MSGAR	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	SQGAA	3		1171.592567	3511.754302	0.000451244	4	N	208	242
Q6P069-2	Infl	LNGWR	QHFISFDSDRSGTVDPQELQK	ALTTM	2		1217.585832	2433.156064	0.000451244	6	N	91	112
Q6P069-2	Infl	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	3	C1:+39.994,C19:+57.021	752.3576979	2254.049694	0.000735798	2	N	41	61
Q6P069-2	Infl	AFPGQ	TQDPLYGYFAAVAGQDGQIDADELQR	CLTQS	2		1421.170457	2840.325314	0.000698008	1	N	15	41
Q6P069-2	Infl	LYGYF	AAVAGQDGQIDADELQR	CLTQS	2		878.9271759	1755.838752	0.001162105	1	N	24	41
Q6P069-2	Infl	STSGK	ITFDDYIACCVK	LRALT	2	C9:+57.021,C10:+57.021	752.844229	1503.672858	0.000451244	5	N	138	150
Q6P1B1	Infl	EEFRR	QQADFVDLSFPTISSTGPNGAIIHYAPVPETNR	TLSLD	3		1181.590387	3541.74776	0.000451244	11	N	371	404
Q6P1B1	Infl	NFNNR	GSLTFEPLTLVPIQTK	MIDVN	2		872.4987171	1742.981834	0.000622848	5	N	554	570
Q6P1B1	Infl	RQAMR	NSEYVAEPIQAYIIPSGDAHQSEYIAPCDCR	RAFVS	3	C28:+57.021,C30:+57.021	1185.205019	3552.591656	0.000451244	11	N	18	49
Q6P1B1	Infl	RAHIK	DAVALCELFNWLEQEVPK	GGVTE	2	C6:+57.021	1081.035638	2160.055676	0.000451244	7	N	336	354
Q6P1B1	Infl	DSFAR	SALWDSGLDYLHGTGHGVGSFLNVHEGPCGISYK	TFSDE	3	C29:+57.021	1210.907567	3629.699301	0.000735798	2	N	473	507
Q6P1B1	Infl	KMAER	SIAWFVVTALDEIAWLFNLR	GSDVE	3		788.7637287	2363.267786	0.002145581	1	N	192	212
Q6P1F6	Infl	DPSNR	SFFSEIISSISDVK	FSHSG	2		779.9041181	1557.792636	0.000451244	4	N	278	292
Q6P1F6	Infl	FSQVK	GAVDDDVAEADIISTVEFNHSGELLATGDK	GGRVV	3		1030.158477	3087.452031	0.000622848	1	N	18	48
Q6P1F6	Infl	ADDLR	INLWHLEITDR	SFNIV	3		470.5898983	1408.746295	0.002981883	1	N	199	210
Q6P4T2	Infl	SKLYR	AALETDENLLLCAPTGAGK	TNVAL	2	C12:+57.021	972.4910631	1942.966526	0.000451244	10	N	490	509
Q6P4T2	Infl	RKQTR	LTAIDILTTCAADIQR	QRFLH	3	C10:+57.021	592.3174728	1773.929018	0.000451244	4	N	1570	1586
Q6P4T2	Infl	LEILK	TASDDRECENQLVLLLGFNTFDFIK	VLRQH	3	C8:+57.021	982.483536	2944.427208	0.000451244	8	N	294	319
Q6P4T2	Infl	TKETR	ETYEVLLSFIQAALGDQPR	DILCG	2		1075.560566	2149.105531	0.000451244	20	N	110	129
Q6P4T2	Infl	QEDVR	LIGLSATLPNYEDVATFLR	VDPAK	2		1047.068027	2092.120453	0.000451244	7	N	647	666
Q6P4T2	Infl	LLKAK	YAQDEHLITFFVPVFEPLPPQYFIR	VVSDR	3		1022.864171	3065.569114	0.001162105	2	N	1244	1269
Q6P4T2	Infl	VDPAK	GLFYFDNSFRPVPLEQTYVGITEK	KAIKR	3		940.8134765	2819.41703	0.000451244	1	N	671	695
Q6P4T2	Infl	KTKVR	GLIEIISNAAEYENIPIR	HHEDN	3		672.3656343	2014.073503	0.000451244	1	N	1843	1861
Q6P4T2	Infl	GDQPR	DILCGAADEVLAVLK	NEKLR	3	C4:+57.021	529.6204926	1585.838078	0.000451244	2	N	129	144

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6P4T2	Infl	QTQVF	NTVYNSDDNVFVGAPTGSGK	TICAE	2		1021.47723	2040.93886	0.002663018	2	N	1336	1356
Q6P542	Infl	VESLK	AANAAENDFSVSQAEVSSR	QAMLE	2		976.9513793	1951.887159	0.000451244	14	N	267	286
Q6P542	Infl	GQKAR	VVFAELACREPDVLILDEPTNNLDIESIDALGEAINDYK	GAVIV	3	C8:+57.021	1458.728467	4373.162	0.000823681	2	N	742	781
Q6P5E4	Infl	EGLHR	LGIEGLSLHNILK	LNIQP	3		469.6175655	1405.829296	0.000622848	7	N	426	439
Q6P5E4	Infl	VAVLR	AYNYVAQEVDGYHAFQTLTQIYNK	VRTGE	3		946.1246022	2835.350407	0.000622848	4	N	553	577
Q6P5E4	Infl	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	C3:+57.021	953.5162885	2857.525466	0.000622848	2	N	156	181
Q6P5E4	Infl	ISNGR	IIGPLEDNELFNQDDFHLLENIILK	TSGQK	3		984.8504789	2951.528037	0.000451244	14	N	898	923
Q6P5E4	Infl	QVPIK	SLPQEWLWCETWCDDASK	KRAKT	2	C9:+57.021,C13:+57.021	1155.993413	2309.971225	0.000451244	5	N	1466	1484
Q6P5E4	Infl	KSFYR	YVLEPEISFTADSSFAK	GPIAK	2		952.4703536	1902.925107	0.001352548	4	N	1038	1055
Q6P5E4	Infl	LKELR	DFNLDGAPYGYTPFCDSR	REMDG	2	C15:+57.021	1047.94702	2093.878439	0.001699387	2	N	1371	1389
Q6P5E4	Infl	IWGYK	ILFLDVLFPLVVDK	FLFVD	2		815.9950819	1629.974564	0.000662267	1	N	1339	1353
Q6P5E4	Infl	SLTTK	WFSAPLLLEASEFLAEDSQEK	FWSFV	2		1205.594803	2409.174005	0.000823681	2	N	54	75
Q6P5E4	Infl	IQQLR	VEEDVASDLVMKVDALLSAQPK	GEARI	3		786.4143254	2356.219576	0.002519933	1	N	937	959
Q6P5F9	Infl	MVILK	LLSEEVFDFSSGQITQVK	AKHLK	2		1014.020742	2026.025884	0.000451244	15	N	172	190
Q6P5F9	Infl	DHAAR	QLLDFSQKLDINLLDNVVNCLYHGEGAQQR	MAQEV	3	C20:+57.021	1167.591579	3499.751337	0.000735798	4	N	14	44
Q6P5F9	Infl	DFSQK	LDINLLDNVVNCLYHGEGAQQR	MAQEV	3	C12:+57.021	847.7557015	2540.243705	0.000451244	15	N	22	44
Q6P5F9	Infl	NMNTK	YYGLQILENVIK	TRWKI	2		726.9090065	1451.802413	0.000451244	14	N	76	88
Q6P5F9	Infl	DAQVK	LFVTGLFSLNQDIPAFK	EHLRD	2		955.5252662	1909.034932	0.000823681	2	N	995	1012
Q6P5F9	Infl	NTNIR	LAYSNGKDDEQNFIQNLSLFLCTFLK	EHGQL	3	C22:+57.021	1026.846586	3077.516358	0.000823681	3	N	305	331
Q6P8X1	Infl	KNMVK	SADGVIVSGVKDVDDFFEHER	TFLLE	3		774.3735172	2320.097152	0.000451244	3	N	193	214
Q6P8X1	Infl	AAFRK	NLVELAELELK	HAKGN	2		635.8668073	1269.718015	0.000451244	7	N	375	386
Q6P8X1	Infl	DDYNR	IGSSLYALGTQDSTDICKF	FLKVS	2	C17:+57.021	1038.501628	2074.987656	0.000451244	11	N	247	266
Q6P9Q6	Infl	LKKAR	VSTDQAAAEQLTLAQAELQSQWEAK	CEQLL	2		1358.675375	2715.33515	0.002145581	2	N	781	806
Q6P9Q6	Infl	SVSSR	DSAAPSPIPASDSLSADPVVTPLPLPLKPGEPGLR	SKSNS	3		1154.622916	3460.845349	0.000622848	8	N	304	339
Q6PCP5	Infl	QVPER	IVVTGNNEDISFSRPADLDLIQSTPFKPLALK	TPPRV	3		1166.966794	3497.876983	0.001871652	1	N	56	88
Q6PDG5	Infl	TKVER	DIGEGNLSTAAAAALAAAAVK	AKHLA	2		943.0054263	1883.995253	0.000451244	13	N	851	872
Q6PDG5	Infl	PPTNK	SLSSLVVQLLQFQEEVFGK	HVSNA	2		1076.088959	2150.162318	0.001943752	1	N	47	66
Q6PDG5	Infl	LHFLR	LPIEDPYLEDSEASLGPLAYQPIPF	SQSGN	3		925.4657425	2773.373827	0.000451244	3	N	641	666
Q6PDI5	Infl	EEIIR	SATETIGSFLDSTSPLLAIAACTALGEIGR	NGPLP	3	C22:+57.021	1008.185267	3021.532402	0.000451244	7	N	787	817
Q6PDI5	Infl	PHAPK	LIPALLESLSVLEPQVLNYLSLR	ATEQE	2		1290.754712	2579.493823	0.001943752	1	N	1290	1313
Q6PDI5	Infl	YSSVR	TEALSVVELLLK	KLEEA	2		657.8981074	1313.780615	0.00091018	3	N	1779	1791
Q6PDI5	Infl	PAGAK	VNDVVPWVLDVILNK	HIISP	3		574.9983346	1721.971604	0.000451244	10	N	929	944
Q6PDI5	Infl	YAAKR	VIGDNPWTPEQLEQCK	LGIVK	2	C15:+57.021	957.4570233	1912.898447	0.00091018	1	N	223	239
Q6PDI5	Infl	LSTYK	ELCSLASDLSQPDLVYK	FMNLA	2	C3:+57.021	969.4801641	1936.944728	0.001654178	1	N	1062	1079
Q6PDI5	Infl	NEKER	ELQLESLLGAFESLGK	AWPRN	3		578.6493711	1732.924713	0.000451244	1	N	1680	1696
Q6PDM2	Infl	LKNRR	GGPPFAFVEFEDPRDAEDAVYGR	DGYDY	2		1271.088207	2540.160815	0.001463592	3	N	51	74
Q6PDM2	Infl	ADVYR	DGTGVVEFVR	KEDMT	2		539.7805348	1077.54547	0.000622848	7	N	154	164
Q6PDM2	Infl	GDVCY	ADVYRDGTGVVEFVR	KEDMT	2		841.9289902	1681.84238	0.000451244	1	N	149	164
Q6PDQ2	Infl	ALNTR	FAEVECLAESHQHLSK	ESMAG	3	C6:+57.021	628.9688436	1883.883131	0.000451244	1	N	1824	1840
Q6PDQ2	Infl	EGHSK	GPFLVSAPLSTIINWER	EFEMW	2		950.5205152	1899.02543	0.000622848	8	N	768	785
Q6PDQ2	Infl	SLFMR	HLCEPGADGAETFADGVPR	EGLSR	2	C3:+57.021	999.9526364	1997.889673	0.000622848	5	N	1458	1477
Q6PDQ2	Infl	ARRFK	LLEQALVIEEQLR	RAAYL	2		777.4490272	1552.882454	0.001352548	2	N	1790	1803
Q6PDQ2	Infl	CRVCK	DGGELLCCDTCPSSYHIHCLNPPLPEIPNGEWLCPR	CTCPA	3	C7:+57.021,C8:+57.021,C11:+57.021,C19:+57.021,C34:+57.021	1421.965048	4262.871745	0.001329271	2	N	449	485
Q6PDQ2	Infl	PLLAR	VGGNIEVLGFNAR	QRKAF	2		673.3652974	1344.714995	0.001162105	2	N	1399	1412
Q6PFD9	Infl	APPER	SSLIQDWETSGLVYLDYIR	VIEML	2		1129.57113	2257.126661	0.001463592	2	N	1678	1697
Q6PFD9	Infl	LLQSK	FASGTFLSPSASVQECR	TPRTS	2	C16:+57.021	922.4360908	1842.856582	0.000451244	4	N	1051	1068
Q6PFD9	Infl	NGERF	SFLSKPVDENNQQDGEDDSLVSR	FYTNP	3		860.4005718	2578.178315	0.000622848	1	N	634	657
Q6PFR5	Infl	EVFSR	YGPLSGVNVVYDQR	TGRSR	2		783.8997014	1565.783803	0.000451244	1	N	139	153
Q6PFR5	Infl	HTGSR	ANPDPNTCLGVFGLSLYTTER	DLREV	2	C8:+57.021	1163.062915	2324.110231	0.000451244	3	N	110	131
Q6PGG2	Infl	SVLKR	FLQELTDPVVPFHLYDAFISLAK	TLHAD	3		888.4760246	2662.404674	0.000823681	3	N	624	647
Q6PGG2	Infl	ASSWR	DLSPEGPAPLTEEELDLR	LIRTK	2		990.9921815	1979.968763	0.002519933	1	N	72	90
Q6PGG2	Infl	EGRKR	YSDIFQSLDNLEISLGNVTFDPLAGDPVRR	EDLEP	3		1117.900561	3350.678283	0.000979378	2	N	17	47
Q6PHU5	Infl	DILER	NCEEDDYTTWLAHSTDPGDYKDGCILGY	KEQFL	3	C2:+57.021,C24:+57.021	1099.12062	3294.338461	0.000637154	3	N	608	636
Q6PHU5	Infl	INVIK	FSTDEGQCWQSYVFTQEPIYFTGLASEPGAR	SMNIS	3	C8:+57.021	1191.208912	3570.603335	0.000451244	20	N	546	577
Q6PHU5	Infl	GRWRR	GAPAEDQDCGRLPDFIAK	LTNNT	2	C9:+57.021	980.4653796	1958.915159	0.000622848	1	N	75	93
Q6PHZ2	Infl	YQQIK	AGAYDFPSPEWDTVTPEAK	DLINK	2		1040.979074	2079.942548	0.000451244	21	N	227	246
Q6PHZ2	Infl	QEIIK	VTEQLIEAINNGDFEAYTK	ICDPG	2		1078.031838	2154.048076	0.000823681	5	N	352	371
Q6SJQ7	Infl	THVPR	TGLEEETTEYSSIR	RPLPA	2		807.8788286	1613.742057	0.000622848	2	N	315	329
Q6SJQ7	Infl	APFPR	EEVSYAALTLAGLGQEPTYGNTGCPITHVPR	TGLEE	3	C24:+57.021	1101.210475	3300.608026	0.000451244	11	N	284	315
Q6URW6	Infl	DYVQK	AQTKEQADFALEALAK	ATYER	2		867.4575805	1732.899561	0.000451244	2	N	433	449
Q6URW6	Infl	KAQTK	EQADFALEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	4	N	437	449
Q6WVG3	Infl	SRLQR	EAEYFELPELVRR	LGAPQ	3		550.9549059	1649.841318	0.002453667	2	N	115	128
Q6WVG3	Infl	SRLQR	EAEYFELPELVR	RLGAP	2		747.8779033	1493.740207	0.000451244	12	N	115	127
Q6WVG3	Infl	RGVHK	EGSLGDELLPLGYAEPEPQEGASAGAPSPTLELASR	SPSGG	3		1203.592122	3607.752965	0.000451244	6	N	150	186

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6WVG3	Infl	LPLGY	AEPEPQEGASAGAPSPTLELASR	SPSGG	2		1133.053833	2264.092066	0.002145581	2	N	163	186
Q6WVG3	Infl	YVTRR	CTVVSVPDSLLWR	MFTQQ	2	C1:+57.021	766.4007913	1530.785983	0.000979378	1	N	49	62
Q6ZQ38	Infl	SEEVK	SAASYALGSISVGNLPEYLPFVLQEITSQPK	RQYLL	3		1093.910286	3278.707458	0.000451244	7	N	873	904
Q6ZQ38	Infl	EENVK	ADVFHAYLSLLK	QTRPV	3		459.5911278	1375.749983	0.000637154	2	N	391	403
Q6ZQ38	Infl	SSLSK	ISGSILNELIGLVR	SPLLQ	2		742.4462875	1482.876975	0.000451244	10	N	729	743
Q6ZQ38	Infl	DMLSR	QGGLLVNFHPSILTCLLPQLTSPR	LAVRK	3	C15:+57.021	887.8233872	2660.446762	0.000622848	2	N	164	188
Q6ZQ38	Infl	PSLIR	DLLDSVLPHLYNETK	VRKEL	3		586.3092374	1755.904312	0.000622848	4	N	1042	1057
Q6ZQ38	Infl	PLVVK	FCNVDDDELREYCIQAFESFVR	RCPKE	3	C2:+57.021,C13:+57.021	938.0831123	2811.225937	0.001699387	1	N	262	284
Q6ZQA0	Infl	CPASR	TTCVQAGLVGYLLETLNTGTALGAR	CQEQL	2	C3:+57.021	1290.178811	2578.342022	0.000823681	3	N	485	510
Q6ZQA0	Infl	AGRTY	NDLSQYPVFPWVLQDYVSPVLDLSNPAVFR	DLSKP	3		1160.26143	3477.760891	0.000823681	3	N	2078	2108
Q6ZQA0	Infl	TIAGR	TYNDLSQYPVFPWVLQDYVSPVLDLSNPAVFR	DLSKP	3		1248.298433	3741.871898	0.000451244	6	N	2076	2108
Q6ZQA0	Infl	PKVQK	LLSGPWVSDSGVSAQALAVAPDGK	LLFSG	2		1163.108411	2324.201223	0.000451244	5	N	2436	2460
Q6ZQA0	Infl	LNQLK	AFFAEVVSEAVPLVLALVPHR	QSHSF	3		755.4320905	2263.272872	0.000451244	7	N	2361	2382
Q6ZQA0	Infl	LLMLR	NFLQNHTVNQESLVQCQGPAIIGALLR	KVPSS	3	C16:+57.021	1007.529703	3019.565708	0.002019181	1	N	957	984
Q6ZQA0	Infl	RQRIR	LHDCGLQGLVASLSEESISPQLCQGLYK	LFVGT	3	C4:+57.021,C23:+57.021	1034.846214	3101.515243	0.000662267	5	N	1197	1225
Q6ZQA0	Infl	ALGAR	CQEQLLALLQALGR	VSLRP	2	C1:+57.021	806.9458974	1611.876195	0.001352548	2	N	510	524
Q6ZQI3	Infl	LPILR	STPEDQILYQTER	YNEET	2		790.3840812	1578.752562	0.000622848	9	N	89	102
Q6ZQI3	Infl	YQTER	YNEETFGYEVPVKEEGDYVLVLK	FAEVY	3		907.4500924	2719.326877	0.000622848	3	N	102	125
Q6ZQK5	Infl	LFLKR	GANQHATDEEGKDPLSIAVEAANADIVTLLR	LARMN	4		805.4131741	3217.621497	0.000823681	3	N	688	719
Q6ZQK5	Infl	SALQR	VQCIPGNTSCCDCGLADPR	WASIN	2	C3:+57.021,C10:+57.021,C11:+57.021,C13:+57.021	1090.452612	2178.889624	0.000451244	5	N	404	423
Q6ZQK5	Infl	SPRFR	AALEEVEGDVAELELKLDK	LVKLC	3		691.0322094	2070.073228	0.002813207	1	N	18	37
Q6ZWM4	Infl	ESHER	VFSSSQGVEQVVLGLYIVR	GDNVA	2		1040.576019	2079.136438	0.000451244	13	N	44	63
Q6ZWM4	Infl	VGTLK	GFDQTINLILDESHER	VFSSS	3		629.6468007	1885.917002	0.000451244	2	N	28	44
Q6ZWM4	Infl	LYIVR	GDNVAVIGEIDEETDSALDLGNIR	AEPLN	2		1258.112076	2514.208553	0.000451244	7	N	63	87
Q6ZWQ0	Infl	EIEYK	VASLLETCKDQGLGDCGTTQQEAEALSWK	LKTVK	3	C8:+57.021,C16:+57.021	1065.836155	3194.485065	0.000451244	1	N	4278	4307
Q6ZWQ0	Infl	LPLEK	ECSLLCASDLPLCTVAVQDLHPVEIDGVYQNLR	DIRDS	3	C2:+57.021,C6:+57.021,C13:+57.021	1262.283009	3783.825627	0.000451244	8	N	1228	1261
Q6ZWQ0	Infl	EEIER	EAIILETLQEDLPEISK	TNAAP	2		971.025493	1940.035386	0.000622848	1	N	3471	3488
Q6ZWQ9	Infl	EDVIR	NAFACFDEEAIGTIQEDYLR	ELLTT	2	C5:+57.021	1181.53673	2361.057861	0.000451244	118	N	104	124
Q6ZWR6	Infl	KAAAR	ESSNLTGDSQILEAR	LHNLQ	2		810.3977199	1618.77984	0.000451244	6	N	2428	2443
Q6ZWR6	Infl	EIEQK	VVALSQLSVHNENLLLEGK	AHTKE	2		1032.078926	2062.142251	0.001463592	2	N	6145	6164
Q6ZWR6	Infl	CLLGR	LSLLDSVVDQR	CHQMK	2		622.8464061	1243.677212	0.000451244	5	N	6467	6478
Q6ZWR6	Infl	QALCK	QQAVLQAGVVDYETFAK	SLEAL	2		933.9839625	1865.952325	0.000451244	7	N	7345	7362
Q6ZWR6	Infl	EVSER	TAAFPSSSGVLYTVAKEELK	KFEAF	3		700.0409278	2097.099383	0.000823681	2	N	8023	8043
Q6ZWR6	Infl	SAKQK	LLQNILEQEQEQVLYSSPNR	LLSGV	2		1201.12205	2400.2285	0.000451244	6	N	6314	6334
Q6ZWR6	Infl	DVEER	LFVATAPLPEETEACLFNQEALAK	DIKEM	2	C15:+57.021	1331.67557	2661.335539	0.000451244	8	N	6403	6427
Q6ZWR6	Infl	SQYDK	ALQDLVDLLDTGQEK	MTGDQ	2		829.4363138	1656.857028	0.000451244	15	N	6596	6611
Q6ZWR6	Infl	EVNMR	WNNLLEEIAEQLHSSK	ALLQL	3		637.6589292	1909.953388	0.000451244	16	N	7222	7238
Q6ZWR6	Infl	GLKEK	FSLLDHFQSIVSEAEDHTGALQQLAAK	SRELY	4		739.6271496	2954.477398	0.000451244	9	N	2767	2794
Q6ZWR6	Infl	MDKNK	NLFSQAFPEDSDNRDVIEDTLGCLLGR	LSLLD	3	C23:+57.021	1027.824621	3080.450463	0.000451244	16	N	6440	6467
Q6ZWR6	Infl	AILAR	KEYTSLIELTTQSLGDLEDQFLK	MRKMP	3		891.1291303	2670.363991	0.000451244	6	N	4671	4694
Q6ZWR6	Infl	FTKAK	ELISADLEHTLAELQELDGDVQEALR	TRQAT	3		969.8247696	2906.450909	0.000451244	11	N	4954	4980
Q6ZWR6	Infl	QELSR	QLEVIENSIPSVGLVEESEDRLVER	TNLYQ	3		947.1614932	2838.461079	0.000451244	11	N	6706	6731
Q6ZWR6	Infl	ISQIK	VTIQEIESKIDSIVGLEEEAQSFAQFVTTGESAR	IKAKL	3		1237.958693	3710.852679	0.002727428	1	N	1485	1519
Q6ZWR6	Infl	LLEEK	LSDQLEEQRQEQALQR	YRCEA	3		657.6683759	1969.981728	0.000451244	4	N	6080	6096
Q6ZWR6	Infl	KGYMK	LLGECSGSIDSVR	RLEHK	2	C5:+57.021	696.8433062	1391.671012	0.000622848	3	N	8378	8391
Q6ZWR6	Infl	EMFSR	QQILHSIIVDGQNLLEQGQVDDREEF	SLKLT	3		1008.507663	3022.49959	0.000979378	1	N	7510	7536
Q6ZWR6	Infl	RVGEK	IQMLEGLLESWSEYENSVQSLK	AWFAN	2		1292.136509	2582.257418	0.000451244	1	N	7016	7038
Q6ZWR6	Infl	TQVER	FVKDITAWLINVEESLTR	CAQTE	3		712.0568008	2133.147002	0.000637154	1	N	2309	2327
Q6ZWR6	Infl	HLEQK	LYDGVSATSTWLNDVEER	LFVAT	2		1027.98743	2053.959261	0.000451244	4	N	6385	6403
Q6ZWR6	Infl	EKLKK	DYQEEIAVAQENK	IQLQE	2		768.8629815	1535.710363	0.000622848	6	N	7823	7836
Q6ZWR6	Infl	LNHNK	IEQIIAQGEQLIEK	SEPLD	2		806.4517668	1610.887934	0.000451244	6	N	8165	8179
Q6ZWR6	Infl	NAFLK	ACDELTDILPEQEQQGLQEAVR	KLHKQ	2	C2:+57.021	1271.608415	2541.201231	0.000637154	2	N	980	1002
Q6ZWR6	Infl	RDIEK	HSTGVASVLNLCEVLLHDCDACATDAECDSIQQATR	NLDRR	3	C12:+57.021,C19:+57.021,C22:+57.021,C28:+57.021	1339.599465	4015.774996	0.000451244	5	N	7941	7977
Q6ZWR6	Infl	EGELR	NLQVALEQAQTILTSPEVGR	RSLKE	2		1084.090022	2166.164443	0.000622848	1	N	5640	5660
Q6ZWR6	Infl	PLQSK	VDDCFQLFEEASQVVER	RKLAL	2	C4:+57.021	1035.975777	2069.935954	0.000451244	4	N	1843	1860
Q6ZWR6	Infl	QTQDK	TSVTSLLDGLSQAFGEASSQSGGTDR	QSIHL	2		1286.112608	2570.209616	0.000451244	6	N	6351	6377
Q6ZWR6	Infl	DSLGK	INEILSVLEQEAQSSTLFK	QKHQE	2		1075.073506	2148.131412	0.000451244	1	N	833	852
Q6ZWR6	Infl	EIESK	IDSIVGLEEEAQSFAQFVTTGESAR	IKAKL	2		1342.656651	2683.297702	0.000451244	6	N	1494	1519
Q6ZWR6	Infl	KELTK	NPETPTELQFIEADLR	QKLEH	2		936.9710521	1871.926504	0.000662267	1	N	2264	2280
Q6ZWR6	Infl	EKLRK	WLAEVSHLPLSGLGNIPVPLQQVR	MLFDE	3		875.1626629	2622.464589	0.000451244	7	N	7580	7604
Q6ZWR6	Infl	KNTAK	DIQQTEQLIEQR	LVQAQ	2		750.886791	1499.757982	0.002296037	1	N	4107	4119
Q6ZWR6	Infl	LLGDR	NSVENALKDCQELEDLIK	AKEKE	3	C10:+57.021	706.6846611	2117.030583	0.000622848	3	N	7057	7075

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6ZWR6	Infl	QLTSR	YQALLLQVLEQIK	FFEEE	2		779.9643131	1557.913026	0.000451244	5	N	3683	3696
Q6ZWR6	Infl	EQKNK	YLGLYTVLPSEISLQLAEVALDLK	IHDQI	3		883.4986064	2647.472419	0.000451244	3	N	5382	5406
Q6ZWR6	Infl	LIEQR	LVQAQNLTQGWEEIK	SLKAE	2		878.9655727	1755.915545	0.002145581	1	N	4119	4134
Q6ZWR6	Infl	QSALR	IPEDVVASLPLCHAALR	LQEEA	3	C12:+57.021	621.0052291	1859.992287	0.001871652	1	N	5695	5712
Q6ZWR6	Infl	GQMLK	FSSLAPDLDRLNELGYR	LPLND	3		656.0063289	1964.995587	0.002663018	1	N	7405	7422
Q6ZWR6	Infl	ISADR	GKVESELQLIQALQNEVVSQASLY	SNLLQ	2		1323.703404	2645.391209	0.000662267	2	N	1687	1711
Q6ZWR6	Infl	KHWTR	YQSEAAALNHWLQCAK	DRLAF	3	C14:+57.021	630.6373168	1888.88855	0.002080925	1	N	6802	6818
Q6ZWX6	Infl	YSILR	HVAEVLEYTKDEQLESLFQR	TAWVF	2		1217.616601	2433.217601	0.000735798	1	N	113	133
Q6ZWX6	Infl	AVKIR	ADIEVACYGYEGIDAVK	EALRA	2	C7:+57.021	936.938132	1871.860664	0.000451244	16	N	192	209
Q6ZWX6	Infl	YDAFK	HAVSDPSILDSLDLNEDEREVLINNINR	RLTPQ	3		1064.204532	3189.590196	0.000851441	1	N	154	182
Q6ZWZ6	Infl	PMYVK	LVEALCAEHQINLIK	VDDNK	2	C6:+57.021	875.9799372	1749.944274	0.000451244	7	N	63	78
Q6ZWZ6	Infl	KDYGK	ESQAKDVIEEYFK	CKK-	2		793.3913749	1584.76715	0.000451244	4	N	116	129
Q6ZWZ6	Infl	DDNKK	LGEWVGLCK	IDREG	2	C8:+57.021	531.2763424	1060.537085	0.000451244	12	N	84	93
Q6ZWZ6	Infl	ALDKR	QAHLCVLASNCDEPMYVK	LVEAL	2	C5:+57.021,C11:+57.021	1067.989619	2133.963639	0.001763695	1	N	45	63
Q76MZ3	Infl	KSLQK	IGPILDNSTLQSEVKPILEK	LTQDQ	2		1097.620623	2193.225647	0.000451244	7	N	546	566
Q76MZ3	Infl	PILGK	DNTIEHLLPLFLAQLKDECPEVR	LNIIS	3	C19:+57.021	917.4779452	2749.410436	0.000451244	15	N	358	381
Q76MZ3	Infl	DVDVK	YFAQEALTVLSLA	-	2		713.3853642	1424.755128	0.002145581	2	N	576	589
Q76MZ3	Infl	PILGK	DNTIEHLLPLFLAQLK	DECPE	3		622.3564105	1864.045831	0.000451244	12	N	358	374
Q76MZ3	Infl	VESLR	AISHEHSPSDLEAHFVPLVK	RLAGG	3		738.3836879	2212.127664	0.000851441	4	N	113	133
Q76MZ3	Infl	GEFAK	VLELDNVKSEIIPMFSNLASDEQDSVR	LLAVE	3		1016.845177	3047.51213	0.002727428	1	N	194	221
Q76MZ3	Infl	SHKVK	EFCENLSADCR	ENVIM	2	C3:+57.021,C10:+57.021	700.78216	1399.54872	0.001162105	1	N	307	318
Q76MZ3	Infl	QLGTF	TTLVGGPEYVHCLLPPLESLATVEETVVR	DKAVE	3	C12:+57.021	1060.560446	3178.657937	0.000451244	4	N	76	105
Q78PY7	Infl	LIGKK	VNVTVDYIRPASPATETVPAFSER	TCATV	3		873.7858094	2618.334028	0.000451244	2	N	414	438
Q78PY7	Infl	AFSTR	VLPAQATEYAFAFIQVPQDEDARTDAVDSVVR	DIQNT	3		1174.590275	3520.747426	0.000451244	13	N	787	819
Q78PY7	Infl	EEKER	SASYKPVFVTEITDDLHFYVQDVETGTQLEK	LMENM	3		1187.25467	3558.740609	0.000451244	13	N	678	709
Q78PY7	Infl	LYLPK	ETCLITFLLAGIECPR	GARNL	2	C3:+57.021,C14:+57.021	946.984131	1891.952662	0.000451244	2	N	546	562
Q78PY7	Infl	IYLGK	DTNGENIAESLVAEGLATR	REGMR	2		980.485055	1958.95451	0.000451244	6	N	116	135
Q78PY7	Infl	AFSTR	VLPAQATEYAFAFIQVPQDEDAR	TDAVD	2		1290.142983	2578.270365	0.000451244	12	N	787	810
Q78PY7	Infl	PTFRR	ETDGSETPEPFAAEAK	FFTES	2		839.8762859	1677.736972	0.000622848	7	N	233	249
Q78PY7	Infl	DSVVR	DIQNTQCLLNVEHLSASCPHVTLQFADSK	GDVGL	3	C7:+57.021,C18:+57.021	1109.203061	3324.585782	0.000451244	9	N	819	848
Q78PY7	Infl	DSVVR	DIQNTQCLLNVEHLSASCPHVTLQFADSKGDVGLGLVK	EGLVM	4	C7:+57.021,C18:+57.021	1041.777059	4163.077036	0.001352548	2	N	819	857
Q78PY7	Infl	IENPR	HFVDSHHQKPVNAIIEHVR	DGSVV	4		566.5520535	2262.177014	0.000451244	3	N	184	203
Q78PY7	Infl	IYLGK	DTNGENIAESLVAEGLATRR	EGMRA	3		706.0263404	2115.055621	0.002145581	1	N	116	136
Q78PY7	Infl	RLLQR	DVQIILESCHNQNLLGTILHPNGNITELLLK	EGFAR	3	C9:+57.021	1170.631375	3508.870724	0.000451244	3	N	259	290
Q78PY7	Infl	MENMR	NDISSHPPVEGSYAPR	RGEFC	2		863.4137043	1724.811809	0.002813207	1	N	715	731
Q78PY7	Infl	NLARR	AAATQPDGKDTPDEPWAFPAR	EFLRK	3		747.6910691	2240.049807	0.002519933	1	N	62	83
Q78PY7	Infl	DDDQR	SSHYDELLAAEAR	AIKNG	2		731.352584	1460.689568	0.000451244	1	N	472	485
Q7M6Y3	Infl	VFGNK	STNVAVDSGGFDELGGLLKPTVASQNQSLPVAK	LPPNK	3		1100.575966	3298.704498	0.002727428	1	N	496	529
Q7M6Y3	Infl	TAASR	ATTLSNAVSSLASTGLSLTK	VDERE	2		961.5261915	1921.036783	0.000451244	5	N	298	318
Q7M6Y3	Infl	SEFLK	VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGK	KIKDS	3		1257.985353	3770.93266	0.001463592	3	N	252	288
Q7M6Y3	Infl	LPPNK	LVSDDLDSSLANLVGNLGIGNGTTK	NDVSW	2		1237.14318	2472.270759	0.000451244	12	N	534	559
Q7M6Y3	Infl	WGDPF	SATLDAVEDAIPSLNPFLTK	SSGDV	2		1051.554949	2101.094298	0.000451244	1	N	422	442
Q7TMK9	Infl	VLFVR	NLANTVTEEILEK	SFSQF	2		737.3939175	1472.772235	0.000451244	10	N	343	356
Q7TMK9	Infl	GKIPR	DLFEDELVPLFEK	AGPIW	2		797.4064936	1592.797387	0.000451244	13	N	171	184
Q7TMK9	Infl	DLDER	AIEALKEFNEDGALAVLQQF	KDSDL	2		1103.573673	2205.131746	0.000451244	10	N	60	80
Q7TMK9	Infl	DLDER	AIEALKEFNEDGALAVLQQFK	DSDLS	2		1167.621155	2333.226709	0.000451244	8	N	60	81
Q7TMK9	Infl	GLPQK	VAEKLDEIYVAGLVAHSDLDER	AIEAL	2		1221.629708	2441.243816	0.000451244	1	N	38	60
Q7TMK9	Infl	KVAEK	LDEIYVAGLVAHSDLDER	AIEAL	3		672.3413773	2014.000732	0.002884417	1	N	42	60
Q7TMK9	Infl	TGQRK	YGGPPPDSVYSGQQPSVGTEIFVGK	IPRDL	2		1283.627165	2565.238731	0.001839721	1	N	143	168
Q7TMY8	Infl	FVNQK	GLLPLVTILGLPNLPIDFPTSAACQAVAGVCK	SILTL	3	C24:+57.021,C31:+57.021	1102.605066	3304.791799	0.000622848	1	N	797	829
Q7TMY8	Infl	HIIAR	SDDELLDDFFHDQSTATSQAGTLSSIPTALTR	WTEEC	3		1147.2099	3438.6063	0.000451244	7	N	2618	2650
Q7TMY8	Infl	LILQR	LLGPSAAADILQLSSSLPLQSR	GRARL	3		746.4220312	2236.242694	0.000870037	1	N	2579	2601
Q7TNC4	Infl	VSKKR	LAETQEEISAEVAAK	AERVH	2		794.9073891	1587.799178	0.001763695	1	N	107	122
Q7TNC4	Infl	DRVCK	SHLLNCCPHDVLSGTR	MDLGE	2	C6:+57.021,C7:+57.021	933.4409533	1864.866307	0.000451244	4	N	37	53
Q7TNC4	Infl	AKAER	VHELNEEIGKLLAK	VEQLG	3		531.6389178	1591.893353	0.001871652	2	N	125	139
Q7TNC4	Infl	KLLAK	VEQLGAEGNVEESQK	VMDEV	2		808.8922704	1615.768941	0.000451244	5	N	139	154
Q7TNG5	Infl	VVDSK	CSNEAVLVATFHPTDPSLLITCGK	SHIYF	3	C1:+57.021,C22:+57.021	877.4368269	2629.287081	0.000451244	3	N	202	226
Q7TNG5	Infl	ADTVR	NVEWATATCVLGFGVFGIWPEGADGTDINAVAR	SHDGK	3	C9:+57.021	1165.233392	3492.676775	0.000622848	2	N	548	581
Q7TNG5	Infl	KGGNR	ITQEVQGAHDGGVFALCALR	DGTLV	3	C17:+57.021	714.6972353	2141.068306	0.001229886	1	N	284	304
Q7TNG5	Infl	PPHVR	VWDSVSLSTLHVLGLGVFDR	AVCCV	3		734.0640668	2199.1688	0.000622848	3	N	140	160
Q7TNG5	Infl	EDPAR	SAGFHPSGSVLAVGTVTGR	WLLLD	2		900.4740963	1798.932593	0.00091018	1	N	422	441
Q7TNG5	Infl	VAFSK	SNGGNLLCAVDESNDHVLSVWDWAK	ESKVV	3	C8:+57.021	929.4331757	2785.276127	0.000451244	4	N	169	194
Q7TNP2	Infl	AVGPK	IALSDLIPAFQSLLRDCEAEVR	AAAAH	3	C17:+57.021	839.4444644	2515.309993	0.000823681	1	N	289	311
Q7TNP2	Infl	GSGPG	AAGGDGDDSLYPIAVLIDELR	NEDVQ	2		1080.545113	2159.074625	0.00091018	4	N	12	33
Q7TNP2	Infl	GSGPG	AAGGDGDDSLYPIAVLIDELRNEDVQLR	LNSIK	3		1005.507552	3013.499256	0.000662267	1	N	12	40

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q7TNV0	Infl	KQICK	EVYENYPAYDLTER	KDFIK	2		881.4024709	1760.789342	0.000451244	17	N	353	367
Q7TNV0	Infl	NAMLK	SICEVLDLER	SGVNS	2	C3:+57.021	617.3111106	1232.606621	0.000637154	1	N	162	172
Q7TPD0	Infl	SSSSK	LAQLTLEQILEHLDNLR	LNLAN	3		673.7131455	2018.116036	0.000451244	11	N	913	930
Q7TPD0	Infl	KAHFR	GEVLPEEVTEESLEESVGKPLYLIFR	NLCQM	3		988.1818943	2961.522283	0.001699387	1	N	630	656
Q7TPD0	Infl	ELLWK	DIIHNPQALSPQFTGILQLLQSR	TSRKF	3		863.8102893	2588.407468	0.001463592	3	N	271	294
Q7TPR4	Infl	MASFK	ILAGDKNYITEDELR	RELPP	2		875.4550378	1748.894476	0.000451244	14	N	834	849
Q7TPR4	Infl	ARCQK	ICDQWDNLGALTQK	RREAL	2	C2:+57.021	831.4015197	1660.787439	0.000451244	12	N	478	492
Q7TPR4	Infl	SHLRK	AGTQIENIEEDFRDGLK	LMLLL	2		967.9768658	1933.938132	0.000451244	14	N	47	64
Q7TPR4	Infl	PEEFK	ACLISLGYDIGNDPQGEAEFAR	IMSIV	2	C2:+57.021	1198.563279	2395.110959	0.000451244	10	N	772	794
Q7TPR4	Infl	NYKPK	IDQLECDHQLIQEALIFDNK	HTNYN	2	C6:+57.021	1221.602405	2441.189209	0.000451244	25	N	684	704
Q7TPR4	Infl	ERTEK	LLETIDQLYLEYAKR	AAPFN	2		934.5123558	1867.009112	0.00091018	3	N	502	517
Q7TPR4	Infl	ERTEK	LLETIDQLYLEYAK	RAAPF	2		856.4618002	1710.908	0.000451244	21	N	502	516
Q7TPR4	Infl	PSEGR	MVSDINNAWGCLEQAEKGYEEWLLNEIR	RLERL	3	C11:+57.021	1123.195949	3366.564448	0.000451244	2	N	359	387
Q7TPR4	Infl	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	3		764.3545685	2290.040305	0.000451244	5	N	752	772
Q7TPR4	Infl	EAMLR	QKDYETATLSEIK	ALLKK	2		763.3913749	1524.76715	0.0007646	1	N	418	431
Q7TPR4	Infl	YGKLR	KDDPLTNLNTAFDVAER	FLDIP	2		959.9794085	1917.943217	0.000451244	10	N	197	214
Q7TPR4	Infl	ADKER	LAILGIHNEVSK	IVQTY	3		431.9228774	1292.745232	0.001162105	1	N	565	577
Q7TPR4	Infl	AHQDR	VEQIAAIAQELNELDYYDSPSVNAR	CQKIC	2		1404.688483	2807.361365	0.000451244	13	N	450	475
Q7TPR4	Infl	HISWK	DGLGFCALIHR	HRPEL	2	C6:+57.021	629.8219798	1257.62836	0.000451244	4	N	174	185
Q7TPR4	Infl	NERLR	KQFGAQANVIGPWIQTK	MEEIG	2		943.5183068	1885.021014	0.000451244	6	N	632	649
Q7TPR4	Infl	LDIPK	MLDAEDIVGTARPDEK	AIMTY	3		587.2897373	1758.845812	0.001591523	1	N	220	236
Q7TPR4	Infl	ALLKK	HEAFESDLAAHQDRVEQIAAIAQELNELDYYDSPSVNAR	CQKIC	4		1104.52625	4414.073799	0.001264573	1	N	436	475
Q7TPR4	Infl	GKLRK	DDPLTNLNTAFDVAERF	LDIPK	2		969.4661339	1936.916668	0.000823681	2	N	198	215
Q7TPV4	Infl	LEHSR	EFLDFFWDIAKPDQETR	LRATE	3		719.6816224	2156.021467	0.001871652	1	N	31	48
Q7TPV4	Infl	LGVGR	EAARPCYSLALAQLLQSFEDIPLCDILDQIQEK	YSLQA	3	C6:+57.021,C24:+57.021	1283.313228	3846.916285	0.000451244	5	N	83	116
Q7TPV4	Infl	ARELR	VCFEDPEWEQLITQLLGK	ATQTL	2	C2:+57.021	1103.048745	2204.08189	0.000451244	14	N	1041	1059
Q7TPV4	Infl	WRVTR	FLNAEALQSYVAWLR	DMFLQ	2		890.9732008	1779.930802	0.000451244	6	N	394	409
Q7TPV4	Infl	GEHQK	ELSILELLNTLLR	TVNHE	2		763.9617704	1525.907941	0.000451244	5	N	1078	1091
Q7TSI3	Infl	EERLR	YKYPSVACEILTSDVPQINDALGADESLLNR	LYGFL	3	C8:+57.021	1151.240212	3450.697235	0.000451244	10	N	74	105
Q7TSI3	Infl	SLLNR	LYGFLQSGDSLNPLLASFFSK	VMGIL	2		1152.599691	2303.183782	0.000451244	5	N	105	126
Q7TSI3	Infl	MTSAF	IDHFGFNDEEFGEQEESVNAPFDK	TANIT	3		934.0723437	2799.193631	0.001162105	3	N	565	589
Q7TSS2	Infl	GDPVR	IHCNITESYPAVPPIWSVESDDPNLAAVLER	LVDIK	3	C3:+57.021	1164.908685	3491.702655	0.000451244	4	N	103	134
Q7TSS2	Infl	HERFR	IASACLDELSCEFLLAGAGGAGAGAAPGPHLPSR	GSVPG	3	C5:+57.021,C11:+57.021	1098.539784	3292.595953	0.000451244	11	N	60	94
Q7TSV4	Infl	EHLKK	ELDELVGAIEEHFFQPQK	YNLQP	2		1065.031641	2128.047682	0.000451244	5	N	594	612
Q7TSV4	Infl	EPKIK	YYAELCAPPGNSDPEHLKK	ELDEL	3	C6:+57.021	730.3496127	2188.025438	0.000662267	2	N	575	594
Q7TSV4	Infl	AQWLR	WDQNPLTSESVK	QLIAG	2		702.3442276	1402.672855	0.001763695	3	N	32	44
Q7TSV4	Infl	SGEWR	VFSGNELGALLGWWLFTSWK	EKNQD	2		1156.099661	2310.183722	0.000451244	2	N	348	368
Q80T06	Infl	ENIQK	SLAGSSGPGASSGPGGDHSELIVR	ITSLE	2		1098.038517	2194.061435	0.000451244	13	N	59	83
Q80T06	Infl	ELIVR	ITSLEVENQNLR	GVVQD	2		708.3786018	1414.741604	0.000451244	14	N	83	95
Q80T06	Infl	NQNLR	GVVQDLQQAISK	LEARL	2		643.3596807	1284.703761	0.000451244	6	N	95	107
Q80T06	Infl	NQNLR	GVVQDLQQAISKLEAR	LSSLE	2		877.9921219	1753.968644	0.000451244	6	N	95	111
Q80T06	Infl	ETCVR	SIQLDGLVWGASK	LVPVG	2		687.3753308	1372.735062	0.000451244	7	N	219	232
Q80T06	Infl	EITKF	EEHVQSVDIAAFNKI	-	3		567.2936987	1698.857696	0.001352548	1	N	266	281
Q80TH2	Infl	QSLHK	LSLPDNDLTTLPASIANLINLR	ELDVS	2		1182.660811	2363.306022	0.000451244	1	N	73	95
Q80TH2	Infl	TQLER	LDLGSNEFTEVPEVLEQLSGLR	EFWMD	2		1223.129541	2444.243482	0.000451244	9	N	188	210
Q80TP3	Infl	ELFGR	VFMEDVGAEPGSILTELGGFEVKESK	FRREM	4	M3:+15.995	696.847203	2783.357612	0.000451244	1	N	2192	2218
Q80TP3	Infl	TGRDR	GSGLLGSQPQPVIPASVIPEELISQAQVVLQGK	SRSVI	3		1113.956118	3338.844955	0.002981883	1	N	167	200
Q80TP3	Infl	IRTGR	DRGSGLLGSQPQPVIPASVIPEELISQAQVVLQGK	SRSVI	3		1204.332136	3609.973009	0.002080925	1	N	165	200
Q80TY0	Infl	IGTCK	ALYTFEGQNEGTISVVEGETLSVIEEDKGDGWTR	IRRNE	3		1243.930914	3728.769343	0.000451244	11	N	555	589
Q80TY0	Infl	ESEHK	VLAPDFDDEFDDEEPLPAIGTCK	ALYTF	2	C22:+57.021	1297.08645	2592.1573	0.000451244	13	N	532	555
Q80U16-5	Infl	TESLF	LESSVAEALLQESDEASELKPVELDTFEGNITK	QLVKR	3		1197.932032	3590.772697	0.000451244	11	N	502	535
Q80U16-5	Infl	GVATR	SGTESLFLESSVAEALLQESDEASELKPVELDTFEGNITK	QLVKR	3		1438.374789	4312.100968	0.000451244	20	N	495	535
Q80U16-5	Infl	SEAGR	SFLDGSLEDAFNGLFLALDPHKK	QYKEF	4		634.3291217	2533.285287	0.000451244	21	N	567	590
Q80U16-5	Infl	TPTFK	DQSFFSNLPDDIFESGK	AAEEK	2		973.4448671	1944.874134	0.000823681	3	N	382	399
Q80U16-5	Infl	EVNGK	QSWDGAETVFLPLIVGFISIK	VTELK	2		1160.633534	2319.251467	0.001763695	1	N	273	294
Q80U93	Infl	TPPSK	LGELLFPSSLAGETLGSFSGLR	VGQAE	2		1126.102598	2250.189595	0.000451244	9	N	1328	1350
Q80U93	Infl	NSGAK	TFGGFGSSSFGEQKPAGTFSSGGGSVASQGFGFSTPNK	TGGFG	3		1221.233039	3660.675717	0.000735798	2	N	1923	1961
Q80UR4	Infl	KLDTR	VVLSEHVYPVSLPAASLR	ISSKK	2		969.0468971	1936.078194	0.002884417	1	N	140	158
Q80VD1	Infl	QALSK	AAEGGLSSPEFSELCIWLGSQIK	SLCNL	2	C15:+57.021	1240.112605	2478.20961	0.000451244	13	N	37	60
Q80VD1	Infl	GSQIK	SLCNLEESITSAGRDDLESFQLEISGFLK	EMACP	3	C3:+57.021	1086.866374	3257.575723	0.000451244	15	N	60	89
Q80VD1	Infl	SQLDK	NSEICQEVQAVCDALGVPK	SDTSD	2	C5:+57.021,C12:+57.021	1059.00378	2115.991961	0.00307782	1	N	142	161
Q80VP1	Infl	PPGSK	ASNPFLPSGAPPTGPSVTNPFQPAPPATLTLNQLR	LSPVP	3		1185.958522	3554.852165	0.000622848	4	N	498	533
Q80VP1	Infl	FDRLR	TALPTSGSSTGELELLAGEVPAR	SPGAF	2		1128.590052	2255.164503	0.000451244	7	N	410	433
Q80VQ0	Infl	NAITR	FYGDNPQTSPNLGR	IINQK	2		783.3713081	1564.727016	0.000622848	8	N	270	284
Q80VQ0	Infl	EVLPR	YLDQSCFTVVLGGR	QETGQ	2	C6:+57.021	807.9011555	1613.786711	0.000451244	1	N	156	170

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q80WJ7	Infl	NWSDR	SIFSGIGSTAEPVSQSTTSDYQWDVSR	NQPYI	2		1453.178479	2904.341358	0.000622848	1	N	340	367
Q80WJ7	Infl	RNQPY	IDDEWSGLNGLSSADPSSDWNAPAEEWGNWVDEDRASLLK	SQEPI	3		1478.00246	4430.983981	0.000451244	1	N	371	411
Q80WQ2	Infl	LLSHR	LQCVPNPELLQTEDCLK	AAPKS	2	C3:+57.021,C15:+57.021	1029.005792	2055.995984	0.000823681	1	N	716	733
Q80WQ2	Infl	EVVLK	DLEVLAEIASSPAGQTDDPGAPDGPDLR	VNHSE	3		936.117953	2805.330459	0.002453667	1	N	461	489
Q80X41	Infl	RKEWK	LGLPIGQGGFGCIYLADTNSSKPVGSDAPCVVK	VEPSD	3	C12:+57.021,C30:+57.021	1126.56734	3376.67862	0.000451244	4	N	38	71
Q80X41	Infl	FGCIY	LADTNSSKPVGSDAPCVVK	VEPSD	2	C16:+57.021	972.9886876	1943.961775	0.000451244	8	N	52	71
Q80X50	Infl	TAGQR	IDLAVLLGK	TPSSM	2		471.3056571	940.5957142	0.002663018	2	N	301	310
Q80X50	Infl	PGAWR	TATEEWGTEDWNEDLSETK	IFTAS	2		1120.977457	2239.939314	0.000451244	6	N	258	277
Q80X50	Infl	MLQTR	FPLDYYSIPFPTPTTPLTGR	DGSLA	2		1142.088959	2282.162318	0.002884417	1	N	849	869
Q80X90	Infl	KCDAR	VLSDDEEDVDFDIIHNANDTFTVK	YVPPA	3		917.7597657	2750.255897	0.00091018	1	N	786	810
Q80X90	Infl	WQDGK	ALGALVDSCAPGLCPDWESWDPR	KPVDN	2	C9:+57.021,C14:+57.021	1286.583458	2571.151315	0.000622848	2	N	169	192
Q80X90	Infl	CRDNK	DGSCSAEYIPFAPGDYDVNITYGGVHIPGSPFR	VPSKD	3	C4:+57.021	1186.880906	3557.619319	0.000698008	3	N	1379	1412
Q80X90	Infl	CSQVK	LGSAADFLLDISETDLSTLTASIK	APSGR	2		1241.152682	2480.289763	0.000451244	3	N	1919	1943
Q80X90	Infl	YDASK	VTASGPGLSAYGVPASLPVEFAIDAR	DAGEG	2		1273.169	2544.322401	0.000823681	2	N	1519	1545
Q80X90	Infl	IVDTR	DAGYGGISLAVEGPSKVDIQTEDLEDGTCK	VSYFP	3	C29:+57.021	1042.159446	3123.454939	0.002080925	1	N	2028	2058
Q80X90	Infl	LEHGK	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	AEVSI	3	C8:+57.021,C11:+57.021	982.4672916	2944.378475	0.002212458	1	N	1147	1177
Q80Y14	Infl	LHGVR	DYAAYNVLDDPELR	QGIKD	2		827.3919062	1652.768212	0.000451244	6	N	79	93
Q80Y14	Infl	VVFLK	GTPEQPQCGFSNAVVQILR	LHGVR	2	C8:+57.021	1051.028678	2100.041757	0.000451244	13	N	55	74
Q80ZJ2	Infl	AAGEK	TVFTEQPTWVIDPIDGTTNFVHR	FPFVA	2		1337.169532	2672.323463	0.000823681	1	N	78	101
Q80ZJ2	Infl	MSSIK	EKYPCHSFIGEESVAAGEK	TVFTE	2	C5:+57.021	1069.496877	2136.978154	0.000823681	1	N	59	78
Q80ZJ2	Infl	DVMIK	SSPADLVTVTDQKVEK	MLMSS	2		858.9548707	1715.894141	0.000451244	1	N	36	52
Q810A7	Infl	PPFEK	NFYNEHEEITNLTPQQLIDLR	HKLNL	3		863.0982759	2586.271428	0.001264573	1	N	215	236
Q810B6	Infl	HTACR	HGLANLTAELLQQGANPNLQTEEALPVPK	ESPVL	3		1022.87932	3065.614561	0.000451244	14	N	500	529
Q810B6	Infl	SPKKY	SADVMSEMAQIAEALLQAGANPNMQDSKGR	TPLHL	4		784.1237546	3132.463819	0.000662267	1	N	338	368
Q810B6	Infl	RQDSK	SALFLLEHQADINVR	TQDGE	3		575.981455	1724.920965	0.002019181	1	N	636	651
Q8BFQ8	Infl	VVLDR	HLVTGQNANSTVPAVQNLLFLCGSR	K-	3	C22:+57.021	899.4697841	2695.385952	0.00091018	1	N	194	219
Q8BFQ8	Infl	IDGAR	YHALLIPSCPGALTDLASSGSLAR	ILQHF	3	C9:+57.021	824.0971761	2469.268128	0.000451244	5	N	85	109
Q8BFR5	Infl	PVPTR	DLDKPFLLPVESVYSIPGR	GTVVT	3		715.7250511	2144.151753	0.000637154	1	N	252	271
Q8BFR5	Infl	KSVQK	LLDAVDTYIPVPTR	DLDKP	2		786.9357526	1571.855905	0.001699387	2	N	238	252
Q8BFR5	Infl	ELEIR	ELLTEFGYKGEETPVIVGSALCALEQR	DPELG	3	C22:+57.021	1003.846474	3008.516023	0.000451244	11	N	200	227
Q8BFY6	Infl	TKSGR	IDVAGFSALWK	FLQQW	2		603.8300277	1205.644455	0.002212458	1	N	161	172
Q8BFY9	Infl	DLLPK	LCSLLDSEDYNTCEGAFGALQK	ICEDS	2	C2:+57.021,C13:+57.021	1246.059481	2490.103362	0.000451244	14	N	140	162
Q8BFY9	Infl	SPLIR	ATVGILITTIASKGELQNWPDLLPK	LCSLL	3		893.5096169	2677.505451	0.000451244	5	N	115	140
Q8BFY9	Infl	TVQQK	LEQLNQYPDFNNYLIFVLTK	LKSED	2		1236.64463	2471.27366	0.000451244	6	N	44	64
Q8BFY9	Infl	YMLQR	TQDQDENVALEACEFWLTLAEQPICKDVLVR	HLPKL	3	C13:+57.021,C25:+57.021	1230.931007	3689.76962	0.000451244	6	N	272	303
Q8BFY9	Infl	YMLQR	TQDQDENVALEACEFWLTLAEQPICK	DVLVR	3	C13:+57.021,C25:+57.021	1036.814691	3107.420674	0.000451244	14	N	272	298
Q8BFY9	Infl	TDFIK	SECLNNIGDSSPLIR	ATVGI	2	C3:+57.021	837.9097089	1673.803818	0.002145581	1	N	100	115
Q8BFY9	Infl	FHRSR	TVAQQHEEDGIEEEDDDDDEIDDDDTISDWNLR	KCSAA	3		1292.858649	3875.552546	0.002296037	3	N	351	384
Q8BFY9	Infl	IILLK	GDVEEDETIPDSEQDIRPR	FHRSR	3		734.005382	2198.992746	0.000823681	1	N	327	346
Q8BFY9	Infl	DSNKR	VQEAACSAFATLEEEACTELVPYLAYILDTLVFAFSK	YQHKN	3	C6:+57.021,C17:+57.021	1390.682987	4169.025561	0.000451244	4	N	503	540
Q8BFY9	Infl	FHRSR	TVAQQHEEDGIEEEDDDDDEIDDDDTISDWNLRK	CSAAA	4		1001.919677	4003.647509	0.000451244	1	N	351	385
Q8BFZ3	Infl	YNELR	VAPDEHPILLTEAPLNPK	INREK	2		977.5363622	1953.057124	0.000451244	35	N	96	114
Q8BFZ3	Infl	ELRVA	PDEHPILLTEAPLNPK	INREK	2		892.4835983	1782.951597	0.000451244	8	N	98	114
Q8BFZ3	Infl	NELRV	APDEHPILLTEAPLNPK	INREK	2		928.0021552	1853.98871	0.000451244	3	N	97	114
Q8BFZ3	Infl	VDIRK	DLFANTVLSGGSTMYPGIADR	MQKEI	2		1093.033858	2184.052117	0.002519933	1	N	292	313
Q8BG05	Infl	SFGGR	SSGSPYGGGYGSGGGSGGYGSR	RF-	2		955.8991467	1909.782693	0.001329271	6	N	355	377
Q8BG05	Infl	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	2		1141.079123	2280.142645	0.000451244	7	N	167	187
Q8BG05	Infl	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	2		1221.103326	2440.191052	0.000451244	19	N	36	57
Q8BG05	Infl	EQLRK	LFIGGLSFETTDDSLR	EHFEK	2		885.9495883	1769.883577	0.000451244	10	N	36	52
Q8BG05	Infl	SGKKR	GFAFVTFDDHDTVDK	IVVQK	3		571.9305375	1712.768212	0.002080925	1	N	167	182
Q8BG05	Infl	LTVKK	IFVGGIKEDTEEY	NLRDY	2		750.3673684	1498.719137	0.000451244	10	N	127	140
Q8BG05	Infl	PEQLR	KLFIGGLSFETTDDSLR	EHFEK	2		949.9970699	1897.97854	0.000451244	3	N	35	52
Q8BG32	Infl	SIVKR	DIQENDEEAVQVKEQSILELGSLLAK	TGQAA	3		966.8367866	2897.48696	0.000451244	2	N	33	59
Q8BG32	Infl	AVQVK	EQSILELGSLLAK	TGQAA	2		700.9039211	1399.792242	0.001352548	5	N	46	59
Q8BG32	Infl	VEFQR	AQSLLSTDREASIDILHSIVK	RDIQE	3		766.0889407	2295.243422	0.000451244	6	N	11	32
Q8BGD9	Infl	SRLPK	SPPYTAFLGNLPYDVTEDSIKDFFR	GLNIS	3		964.8083912	2891.401774	0.000451244	15	N	92	117
Q8BGD9	Infl	PDRLK	GFGYAEFEDLDSLLSALSLNEESLGNRR	IRVDV	3		1034.83919	3101.494171	0.000451244	14	N	137	165
Q8BGD9	Infl	GPSRK	DGNKVDVVGATQGQAGSCSR	GPGDG	3	C18:+57.021	669.3170831	2004.927849	0.001463592	2	N	525	545
Q8BGD9	Infl	PDRLK	GFGYAEFEDLDSLLSALSLNEESLGNR	RIRVD	2		1473.70433	2945.393059	0.000451244	1	N	137	164
Q8BGD9	Infl	KGFGY	AEFEDLDSLLSALSLNEESLGNRR	IRVDV	3		893.4476335	2677.3195	0.00091018	2	N	141	165
Q8BGG7	Infl	CMQAR	LVGEALLESNTVIDHVYCSPSLR	CVQTA	3	C18:+57.021	858.1077408	2571.299823	0.001162105	2	N	439	462
Q8BGG7	Infl	STGGR	SVQAACDWLFSHVGDPFLDDPLPR	EYVLY	3	C6:+57.021	914.7712401	2741.29032	0.000451244	4	N	53	77
Q8BGJ5	Infl	VQLPR	EGQEDQGLTKDYGSSPLHR	FKKPG	3		706.3351739	2115.982122	0.000451244	3	N	416	435
Q8BGJ5	Infl	VIHVR	KLPSDVTEGEVISLGLPFGK	VTNLL	2		1043.575684	2085.135769	0.000451244	13	N	63	83
Q8BGJ5	Infl	KPGSK	NFQNIFPPSATLHLSNIPPSVSEDDLK	SLFSS	3		994.1737331	2979.497799	0.002453667	1	N	442	469

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BGJ5	Infl	AAASR	IAIPGLAGAGNSVLLVSNLNPER	VTPQS	2		1138.142589	2274.269577	0.000451244	19	N	323	346
Q8BGJ5	Infl	LNPER	VTPQSLFILFGVY	GDVQR	2		742.4139247	1482.812249	0.002727428	1	N	346	359
Q8BGJ5	Infl	ITFTK	NNQFQALLQYADPVSAQHAK	LSLDG	2		1122.064338	2242.113076	0.000451244	13	N	217	237
Q8BGJ5	Infl	AQHAK	LSLDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	949.448444	1896.881288	0.000451244	11	N	237	253
Q8BGJ5	Infl	SPVLR	IIVENLFYPVTLDVLHQIFSK	FGTVL	3		830.1337103	2487.377731	0.000622848	7	N	184	205
Q8BGQ7	Infl	QATGK	NVGCLQEALQLATSFAQLR	LGDVK	2	C4:+57.021	1060.052154	2118.088707	0.000451244	10	N	943	962
Q8BGQ7	Infl	IPVER	LYVTYFGGDEAAGLEPDLECR	QIWQN	2	C20:+57.021	1188.046931	2374.078262	0.000451244	20	N	132	153
Q8BGQ7	Infl	VVLDK	TCFYAEQGGQIYDEGYLVK	VDDSS	2	C2:+57.021	1121.01236	2240.009119	0.000451244	6	N	531	550
Q8BGQ7	Infl	KDVQR	EIADLGEALATAVIPQWQK	DEQRE	2		1027.052376	2052.089153	0.000622848	10	N	793	812
Q8BGQ7	Infl	PDPVR	VVSIGVPVSELLDDPCGPAGSLTSVEFCGGTHLR	NSSHA	3	C16:+57.021,C28:+57.021	1175.916809	3524.727027	0.000622848	2	N	695	729
Q8BGQ7	Infl	ELACK	MALELLTQEFGIPVER	LYVTY	2		923.4931093	1844.970619	0.001162105	2	N	116	132
Q8BGQ7	Infl	TAWLL	YDTYGFPVDLTGLIAEEK	GLVVD	2		1016.002018	2029.988436	0.000451244	5	N	414	432
Q8BGQ7	Infl	NEAGK	ITCLCQVPQNAANR	GLKAS	2	C3:+57.021,C5:+57.021	822.9009326	1643.786265	0.000451244	1	N	898	912
Q8BGQ7	Infl	RIGGR	DAAHLVNQDDPNVLEIWNLVFIQYNR	ESDGV	3		1032.856627	3095.546481	0.000622848	5	N	198	224
Q8BGQ7	Infl	DLECR	QIWQNLGLDEAR	ILPGN	2		721.8734866	1441.731373	0.001839721	2	N	153	165
Q8BGQ7	Infl	DDSPK	YNYQSDSSGSYVFECTVATVLALR	REKMF	2	C15:+57.021	1365.639715	2729.263831	0.000451244	1	N	486	510
Q8BGT7	Infl	LKLKK	DLQEVIELTKDLLSTQPSETLASSDSFASTQPTHSWK	VGDKC	4		1023.259453	4089.006613	0.000451244	1	N	37	74
Q8BGT7	Infl	LASYK	AQLQQVEAALSGNGENEDLLK	LKKDL	2		1114.064201	2226.112802	0.000622848	2	N	13	34
Q8BGT7	Infl	IELTK	DLLSTQPSETLASSDSFASTQPTHSWK	VGDKC	3		974.4653528	2920.372658	0.000662267	3	N	47	74
Q8BH04	Infl	VRDIR	GYLTEQVNQDLPKEVLAELEALEGR	VQKM-	3		938.8227004	2813.444701	0.001871652	1	N	611	636
Q8BH04	Infl	GLVPK	EGALDLSGLSAVDTSQLFSIPKDFWEQEVR	DIRGY	3		1113.224933	3336.6514	0.000622848	4	N	578	608
Q8BH04	Infl	GLVPK	EGALDLSGLSAVDTSQLFSIPK	DFWEQ	2		1124.58952	2247.16344	0.0025889	1	N	578	600
Q8BH43	Infl	GSLSK	YAEDIFGEICTQASAFASR	VNSLA	2	C10:+57.021	1068.489052	2134.962504	0.000451244	6	N	45	64
Q8BH43	Infl	RHLCR	QTLPSDTSELECR	TNITL	2	C12:+57.021	768.3542351	1534.69287	0.000451244	3	N	15	28
Q8BH59	Infl	QSAIR	YGQVTPLEIDILYQLADLYNASGR	LTLAD	2		1356.698122	2711.380644	0.000622848	1	N	259	283
Q8BH59	Infl	AGTRK	DIEVTKEEFAQSAIR	YGQVT	2		868.4472128	1734.878826	0.001839721	1	N	244	259
Q8BH61	Infl	GVNLK	DYLNVTAVHLF	KERWD	2		646.3382169	1290.660834	0.000622848	3	N	43	54
Q8BH74	Infl	SAHKR	VLIQANQEDNFGTATPR	SQIIP	2		937.4742933	1872.932987	0.000622848	2	N	31	48
Q8BH74	Infl	SGNLK	QLLPVCDTWEDTVWAYFR	VMVDS	2	C6:+57.021	1150.046537	2298.077474	0.000622848	2	N	437	455
Q8BH74	Infl	EDRLK	IDVIDWLVFDPAQR	AEALR	2		843.9466516	1685.877703	0.00307782	1	N	672	686
Q8BH78	Infl	PPAFK	YQFVTEPEDEEDEEDEEEEDDEDLEELEVLER	KPAAG	3		1368.552668	4102.634604	0.000998612	3	N	25	58
Q8BH95	Infl	LNRPK	ALNALCNGLIEELNQALETFEQDPAVGAIVLTGGDK	AFAAG	3	C6:+57.021	1261.975535	3782.903206	0.000451244	13	N	56	92
Q8BH95	Infl	YAGEK	AQFGQPEILLGTIPGAGGTQR	LTRAV	2		1056.06635	2110.117099	0.000451244	7	N	157	178
Q8BHD7	Infl	PNQAR	AQAALQAVSAVQSGNLSLPGATANEGTLLPGQSPVLR	IIIEN	3		1196.311624	3585.911471	0.000451244	23	N	117	154
Q8BHD7	Infl	MSSPY	AGAAGFAPAIAFPQAAGLSVPAVPGALGPLTLTSSAVSGR	MAIPG	3		1206.993455	3617.956965	0.001654178	3	N	276	316
Q8BHD7	Infl	AQYAK	MALDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	950.4291975	1898.842795	0.000823681	2	N	207	223
Q8BHD7	Infl	VLHLR	KIPCDVTEAEVISLGLPFGK	VTNLL	2	C4:+57.021	1087.082588	2172.149576	0.001943752	1	N	35	55
Q8BHD7	Infl	ITFTK	NNQFQALLQYADPVNAQYAK	MALDG	2		1148.571996	2295.128392	0.000451244	13	N	187	207
Q8BHD7	Infl	SPVLR	IIIENLFYPVTLEVLHQIFSK	FGTVL	3		839.477477	2515.409031	0.000823681	3	N	154	175
Q8BHG1	Infl	QLYPR	QDFLTGDQLLFEYKPEVIAEALNQLVPQK	ANLVL	3		1116.257686	3345.749657	0.000451244	10	N	588	617
Q8BHG1	Infl	YRYIK	LQNGLQALLISDLSNVEGK	TGNAT	2		1006.555283	2011.094967	0.000451244	2	N	114	133
Q8BHG1	Infl	RNKAK	STCSCPDLQPNGQDLGESGR	LARLG	2	C3:+57.021,C5:+57.021	1089.463008	2176.910416	0.000451244	16	N	56	76
Q8BHG1	Infl	DLKEK	WFGTQYSIEDIENSWTELWK	SNFDL	2		1266.590052	2531.164503	0.000823681	5	N	636	656
Q8BHJ5	Infl	AVVLR	GHESEVFICAWNPVSDLLASGSGDSTAR	IWNLS	3	C9:+57.021	988.1264114	2961.355834	0.000451244	9	N	166	194
Q8BHJ5	Infl	DSTAR	IWNLSENSTSGPTQLVLR	HCIRE	2		1008.031975	2014.048351	0.000451244	10	N	194	212
Q8BHN3	Infl	LSPYR	ALLDTLQLGPDALTVHLIHEVTK	VLLVL	4		625.106593	2496.395172	0.000451244	11	N	61	84
Q8BHN3	Infl	FDVFR	QYASLTGTQALPPLFSLGYHQSR	WNYRD	3		845.7717231	2534.291769	0.000979378	1	N	377	400
Q8BHN3	Infl	HEVTK	VLLVLELQGLQK	NMTRI	2		676.9297419	1351.843884	0.000451244	3	N	84	96
Q8BHN3	Infl	QRAPR	VPQESKDPAEGNGAQPEATPGDGDKPEETQEK	AEKDE	3		1112.510238	3334.507314	0.001162105	2	N	185	217
Q8BHN3	Infl	HSFHR	DLGIFWLNAAETWVDISSNTAGK	TLFGK	2		1254.624426	2507.233251	0.000451244	8	N	309	332
Q8BHN3	Infl	YVKTR	DGSDYEGWCWPGSASYPDFTNPR	MRAWW	2	C9:+57.021	1332.540533	2663.065465	0.000451244	1	N	493	516
Q8BHN3	Infl	SPESR	LSFQHDPETSVLILR	KPGVS	3		585.653227	1753.936281	0.000451244	9	N	914	929
Q8BIQ5	Infl	DRSLR	SVFVGNIPYEATEEQLKDIFSEVGPVVSFR	LVYDR	3		1119.573674	3355.697622	0.000451244	1	N	16	46
Q8BIQ5	Infl	DRSLR	SVFVGNIPYEATEEQLKDIFSEVGPVVSF	RLVYD	3		1067.53997	3199.59651	0.000451244	7	N	16	45
Q8BIW1	Infl	VSRKK	LLPVLQEALSAYLDSAK	MASGQ	2		916.0147313	1830.013863	0.000451244	1	N	350	367
Q8BIW1	Infl	FYLTK	TSEAEDIFIPVLNIK	RSELP	2		844.9594247	1687.903249	0.001699387	1	N	44	59
Q8BJ71	Infl	QVKQR	ILHTLLASGEDALDFTQESEPSYIGDVNPPGR	SSLDS	3		1147.898997	3440.673592	0.000451244	17	N	143	175
Q8BJ71	Infl	HISQR	LESLSAATTFEPLEPVKDTDIQGFLK	NEKDN	3		950.4993347	2848.474604	0.000451244	9	N	77	103
Q8BJ71	Infl	YLWLK	LNQVCFDDDGTSSPQDR	LTLSQ	2	C5:+57.021	977.4160837	1952.816567	0.000451244	11	N	417	434
Q8BJS4	Infl	SSNMK	HLSPAPQLGPSSDSHTSYY	SESVV	2		1022.47449	2042.933381	0.000622848	12	N	52	71
Q8BJS4	Infl	TAESK	ASEDFFGSSSGYSSEDDLAGYTDSDQHSSGSR	LRSAA	3		1116.782686	3347.324658	0.000451244	7	N	133	165
Q8BJS4	Infl	SQSPR	VILQPDVHPGNCWAFQGPQGFAVVR	LSARI	3	C12:+57.021	931.4748694	2791.401208	0.000622848	12	N	603	628
Q8BJS4	Infl	KELGR	LEAQLASLRQELAALTLK	QNSVA	3		656.721641	1967.141523	0.002145581	1	N	427	445
Q8BJS4	Infl	TYETK	TALLSLFGIPLWYHSQSPR	VILQP	3		729.3972688	2185.168406	0.000622848	10	N	584	603
Q8BJS4	Infl	EDLRR	DTVAHIQEELATLR	AEHHQ	3		532.6182938	1594.831481	0.000451244	5	N	363	377

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BJS4	Infl	TAESK	ASEDFFGSSSGYSSEDDLAGY	TDSDQ	2		1095.935258	2189.854915	0.001871652	1	N	133	154
Q8BJS4	Infl	VSLAR	SALLDDHLHSEPYWSGDLR	GRRRR	3		737.6875476	2210.039243	0.002212458	1	N	91	110
Q8BJY1	Infl	THHGR	QYLAQEGVIDQISNIIVGADSDPFSGFYLPGFVK	FFGNL	3		1229.958076	3686.850828	0.000451244	17	N	241	275
Q8BJY1	Infl	SQIGR	IVENSEAVTEILNNAELLK	QIVYC	2		1050.065681	2098.115762	0.000451244	11	N	109	128
Q8BJY1	Infl	YLRLR	AYLSEGPYYVKPVATTAVEGAD	-	2		1151.068421	2300.121241	0.000451244	8	N	482	504
Q8BK64	Infl	EELYR	VFTTQELVQAFTHAPAALEADR	GGKFH	3		805.748807	2414.223021	0.000451244	6	N	224	246
Q8BK67	Infl	VEAPR	LIEALSHEAIVLAACGR	NHTLA	2	C15:+57.021	911.9961186	1821.976637	0.000451244	1	N	192	209
Q8BK67	Infl	GVRVR	TVVSGSCAAHSLLITTEGK	LWSWG	2	C7:+57.021	965.9990553	1929.982511	0.002374549	1	N	149	168
Q8BK67	Infl	LMDCK	GNLYSFGCPEYGQLGHNSDGK	FIARA	3	C8:+57.021	767.3397763	2298.995929	0.002981883	1	N	270	291
Q8BKC5	Infl	ANVVR	QVQTSGGLWTECIAQLSPEQQAAIQELLNSA	-	3	C12:+57.021	1124.224673	3369.65062	0.000451244	15	N	1066	1097
Q8BKC5	Infl	VLLRR	LLSSAFDEVYPALPSDVQTAIK	SELLM	2		1182.62082	2363.226041	0.000698008	1	N	68	90
Q8BKC5	Infl	QKGTK	LVLEQVVTSIASVADTAEEK	FVPYY	3		701.3796092	2101.115427	0.002663018	1	N	506	526
Q8BKC5	Infl	APEAK	TKENVNATENCISAVGK	IMKFK	3	C11:+57.021	612.3040034	1833.88861	0.000622848	1	N	961	978
Q8BKC5	Infl	LRQVK	RQDEDYDEQVEESLQDEDDNDVYILTK	VSDIL	3		1101.815216	3302.422247	0.000979378	3	N	814	841
Q8BL97	Infl	DSETK	VYVGNLGTGAGKGELER	AFSYY	2		860.4553722	1718.895144	0.000451244	7	N	41	58
Q8BL97	Infl	VWIAR	NPPGFAFVEFEDPRDAEDAVR	GLDGK	2		1189.556543	2377.097486	0.000622848	5	N	73	94
Q8BL97	Infl	GELER	AFSYYGPLR	TVWIA	2		537.2748883	1072.534177	0.002080925	2	N	58	67
Q8BMA6	Infl	IDKVR	IFLLGLADNEAAIVQAESEETKER	LFESM	3		882.7927411	2645.354823	0.000451244	5	N	310	334
Q8BMA6	Infl	QMRLR	SGGTEGLLAEKLEALITQTR	AKQAA	3		696.3834651	2086.126995	0.001162105	4	N	265	285
Q8BMD8	Infl	RALDR	NGDGVVDIGELQQGLQSLGIPLGQDAEEK	IFTTG	3		993.8355572	2978.483272	0.000451244	5	N	33	62
Q8BMJ2	Infl	DKLKR	EIELYGCPPDFPEEEEEEEESSAKPGDIVVR	DKAKG	3	C7:+57.021	1193.538652	3577.592555	0.000451244	24	N	108	139
Q8BMJ2	Infl	GLGTR	LPWDEQWLIESLSDSTIY	MAFYT	2		1098.031307	2194.047013	0.002080925	3	N	584	602
Q8BMJ2	Infl	DIVKF	SEAEHWLDYFPPLAVQDLK	TIGLK	3		753.3763105	2257.105531	0.000451244	1	N	176	195
Q8BMJ3	Infl	PEHAK	INETDTFGPGDDDEIQFDDIGDDDEDIDDI	-	3		1120.118741	3357.332823	0.000451244	9	N	114	144
Q8BMJ3	Infl	KLRKK	VWINTSDIILVGLR	DYQDN	2		799.9673871	1597.919174	0.002884417	1	N	68	82
Q8BMK4	Infl	GVEQK	VQSLQATFGTFESLLR	NSQHK	2		898.9812228	1795.946846	0.000622848	10	N	140	156
Q8BMK4	Infl	LKELK	QSLGELPGTVESLQEQVLSLLSQDQAQAEGLPPQDFLDR	LSSLD	3		1412.715592	4235.123375	0.000451244	16	N	466	505
Q8BMK4	Infl	YTEVR	ELVSLKQEQQAFK	QAADS	2		774.425552	1546.835504	0.00091018	3	N	306	319
Q8BMK4	Infl	ASTVR	SLGETQLALSSDLK	ELKQS	2		731.3939175	1460.772235	0.000451244	2	N	449	463
Q8BMK4	Infl	LESAK	GLLDDLRNDLDR	LFLKV	3		472.2482008	1413.721202	0.001654178	1	N	551	563
Q8BML9	Infl	FQFER	LGYFSVDPDSHQGQIVFNR	TVTLK	3		727.0242711	2178.049413	0.000622848	1	N	745	764
Q8BML9	Infl	STQLR	EAATQAHQILGSTIDKATGVLL	YDLVS	2		1119.110954	2236.206308	0.001839721	1	N	34	56
Q8BMS1	Infl	IDAVK	AGLEQGSDAGYLAESQK	FGELA	2		862.4108273	1722.806055	0.000451244	19	N	309	326
Q8BMS1	Infl	GVDPK	KLDALTTGFGFPVGAATLADEVGVDVAQHVAEDLGK	AFGER	3		1204.625097	3610.851891	0.000451244	19	N	569	605
Q8BMS1	Infl	TKDRK	TVLGVPEVLLGILPGAGGTQR	LPKMV	2		1024.099661	2046.183722	0.000451244	5	N	166	187
Q8BMS1	Infl	IDAVK	AGLEQGSDAGYLAESQKFGELALTK	ESKAL	2		1292.151005	2582.286409	0.001871652	1	N	309	334
Q8BMS1	Infl	IDAVK	AGLEQGSDAGYLAESQKF	GELAL	2		935.9450343	1869.874469	0.000451244	4	N	309	327
Q8BND5	Infl	MHQVR	SPSNAILWLWTSHNR	VNARL	3		594.6414328	1780.900898	0.000451244	5	N	471	486
Q8BND5	Infl	QWPPR	ELCSACHNELNGQVPLWDLGATLNFLK	AHFSP	3	C3:+57.021,C6:+57.021	1033.839283	3098.494448	0.000451244	20	N	509	536
Q8BND5	Infl	LNFLK	AHFSPANIVIDSSASR	HTGRR	2		836.4266147	1670.837629	0.000451244	7	N	536	552
Q8BND5	Infl	LQAMR	SYVQFFFGCR	DCADH	2	C9:+57.021	655.8032557	1309.590911	0.002080925	1	N	443	453
Q8BND5	Infl	DLVNK	FGVTDFPSCYLLLR	NGSVS	2	C9:+57.021	844.4295488	1686.843498	0.002374549	1	N	231	245
Q8BND5	Infl	ANDVK	DWRPALNLAVLDCAEETNSAVCR	EFNIA	3	C13:+57.021,C22:+57.021	887.4235804	2659.247341	0.0025889	1	N	91	114
Q8BP47	Infl	EGYKR	EGIDPAPYYWYTDQR	KYGTC	2		937.4237377	1872.831875	0.000622848	5	N	502	517
Q8BP47	Infl	EEAKK	IIIKNDPSLPEPACVK	ISALE	2	C14:+57.021	897.4954201	1792.97524	0.000451244	7	N	111	127
Q8BP47	Infl	GGSMR	SWDSEEILEGYKR	EGIDP	3		537.9270159	1610.757648	0.000622848	4	N	489	502
Q8BP47	Infl	HFFDR	GYCEVTTPTLVQTQVEGGATLF	KLDYF	2	C3:+57.021	1186.078231	2370.140862	0.000451244	13	N	274	296
Q8BP47	Infl	TDQRK	YGTCPHGGYGLGLER	FLSWI	2	C4:+57.021	818.8807544	1635.745909	0.000662267	1	N	518	533
Q8BP47	Infl	SSQLY	LETCLPALGDVFCIAQSYR	AEQSR	2	C4:+57.021,C13:+57.021	1107.040166	2212.064732	0.000451244	8	N	314	333
Q8BP47	Infl	PFLTF	EDLLNRLEDLVCDVVDR	VLKSP	3	C12:+57.021	691.6812509	2072.020353	0.000622848	2	N	358	375
Q8BP47	Infl	HDVKK	EDGTFYEFGDDIPEAPER	LMTDT	2		1043.947971	2085.880342	0.000622848	2	N	418	436
Q8BP47	Infl	EHDVK	KEDGTFYEFGDDIPEAPER	LMTDT	2		1107.995453	2213.975305	0.0025889	2	N	417	436
Q8BP47	Infl	SRTRR	HLAEFTHVEAECPFLTFEDLLNRLEDLVCDVVDR	VLKSP	4	C12:+57.021,C29:+57.021	1026.247869	4100.960275	0.000451244	2	N	341	375
Q8BPU7	Infl	EIKLR	LLDLENIQIPDAPPPIPK	EPSNY	2		992.0622129	1982.108826	0.000451244	8	N	697	715
Q8BPU7	Infl	SPNHK	VLHYGDLEESPQGEVPHDSLQDKLPVADIK	AVVTG	4		832.9233747	3327.662299	0.000622848	2	N	584	614
Q8BPU7	Infl	EIKLR	LLDLENIQIPDAPPPIPKEPSNYDFVYDCN	-	3	C29:+57.021	1162.897675	3485.669624	0.000451244	1	N	697	727
Q8BPU7	Infl	DLYQK	VAQEITIGQLIPHLQGTDQEIQTYTIAVINALFLK	APDER	3		1293.714246	3878.119339	0.000451244	5	N	218	253
Q8BQ30	Infl	RRRAK	LGLPPGEGSPVPGNAEAGPPDPDESAVLLEAIGPVHQNR	FIQQE	3		1285.317215	3852.928244	0.0007646	2	N	50	89
Q8BQ30	Infl	SRPLR	AQQNLCSGPSPLPPEHSGTEGSR	QQEEE	3	C6:+57.021	802.7086398	2405.102519	0.001463592	1	N	371	394
Q8BQ46	Infl	FGGHR	DYGPRPDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFK	QIGII	3		1402.960261	4205.857383	0.000451244	22	N	214	253
Q8BQ47	Infl	TGKEK	ISDGQEEADDEEEEEEEITK	TSGNP	2		1226.996438	2451.977275	0.000451244	1	N	212	233
Q8BQ47	Infl	QKGVK	VDLGIPLELWDEPSVEVTFLK	KQCET	2		1200.141389	2398.267177	0.0025889	1	N	138	159
Q8BRF7	Infl	LRDAR	NSLFTGDPLGTGQFSFQRPLLVLVDR	NIDLA	3		959.8472917	2876.518475	0.000451244	3	N	234	260
Q8BRF7	Infl	CQDLR	NQLYESYYLNFISAISR	SKLED	2		1041.021076	2080.026553	0.000451244	4	N	104	121
Q8BRN9	Infl	ATAQK	LASEDAALVDDDEESDTPAQAPLAK	KPAQT	2		1286.101374	2570.187149	0.000451244	1	N	469	494

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BT60	Infl	KPAGK	GSITISAEEIKDNR	VVLFE	2		766.8998984	1531.784197	0.000451244	15	N	125	139
Q8BT60	Infl	LPQIR	LYGPTNFSPIINHVAR	FAAAA	2		899.9840998	1797.9526	0.000451244	14	N	390	406
Q8BT60	Infl	GGSLR	APSGEVAIRDIVQFVPFR	QFQNA	3		667.7025808	2000.084342	0.000451244	5	N	475	493
Q8BT60	Infl	DIDNK	TIELSDDDFLGECEVTLGQIVSSK	KLTRP	2	C13:+57.021	1328.139214	2654.262828	0.000451244	19	N	85	109
Q8BT60	Infl	QNAPK	EALAQCVLAEIPQQVVGY	FNTYK	2	C6:+57.021	994.5117985	1987.007997	0.000451244	2	N	500	518
Q8BT60	Infl	QNAPK	EALAQCVLAEIPQQVVGYFNTYK	LLPPK	2	C6:+57.021	1321.170454	2640.325309	0.000451244	25	N	500	523
Q8BT60	Infl	NHVAR	FAAAATQQQTASQYFVLLIITDGVITDLDETR	QAIVN	3		1167.270543	3498.788228	0.000451244	22	N	406	438
Q8BT60	Infl	DVTSK	SDPLCVLFLNTSGHQWYEVER	TERIK	2	C5:+57.021	1275.608021	2549.200443	0.000451244	10	N	26	47
Q8BT60	Infl	QCVTK	VELNVSCNNLLDADVTSK	SDPLC	2	C7:+57.021	995.9914273	1989.967255	0.000451244	2	N	8	26
Q8BT60	Infl	EVVQK	LKFGIYDIDNK	TIELS	3		442.5753663	1324.702699	0.001264573	1	N	74	85
Q8BT60	Infl	VLAEI	PQQVVGYFNTYK	LLPPK	2		722.3675057	1442.719411	0.002813207	1	N	511	523
Q8BT60	Infl	KTIEL	SDDDFLGECEVTLGQIVSSK	KLTRP	2	C9:+57.021	1100.010014	2198.004428	0.000451244	11	N	89	109
Q8BTE6	Infl	PLQLL	GTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C3:+57.021,C7:+57.021,C13:+57.021,C19:+57.021,C24:+57.021,C28:+57.021	1210.480338	3628.417613	0.001162105	1	N	32	63
Q8BTE6	Infl	AELCR	GDWDCGPEEQCVSIGCSHICTTN	-	2	C5:+57.021,C11:+57.021,C16:+57.021,C20:+57.021	1341.519408	2681.023217	0.000451244	71	N	40	63
Q8BTE6	Infl	QELQA	AVRPLQLLGTCAELCR	GDWDC	3	C11:+57.021,C15:+57.021	619.6661762	1855.975129	0.000451244	24	N	24	40
Q8BTE6	Infl	RPLQL	LGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C4:+57.021,C8:+57.021,C14:+57.021,C20:+57.021,C25:+57.021,C29:+57.021	1248.175026	3741.501677	0.000451244	18	N	31	63
Q8BTE6	Infl	VRPLQ	LLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C5:+57.021,C9:+57.021,C15:+57.021,C21:+57.021,C26:+57.021,C30:+57.021	1285.869714	3854.585741	0.000451244	10	N	30	63
Q8BTE6	Infl	AAVRP	LQLLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C7:+57.021,C11:+57.021,C17:+57.021,C23:+57.021,C28:+57.021,C32:+57.021	1366.250594	4095.728383	0.000451244	14	N	28	63
Q8BTE6	Infl	QELQA	AVRPLQLLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	4	C11:+57.021,C15:+57.021,C21:+57.021,C27:+57.021,C32:+57.021,C36:+57.021	1130.754746	4518.987786	0.001162105	2	N	24	63
Q8BTE6	Infl	AAVRP	LQLLGTCAELCR	GDWDC	2	C7:+57.021,C11:+57.021	717.3656629	1432.715726	0.000451244	7	N	28	40
Q8BTE6	Infl	VRPLQ	LLGTCAELCR	GDWDC	2	C5:+57.021,C9:+57.021	596.7943421	1191.573084	0.000823681	2	N	30	40
Q8BTM8	Infl	PSRVR	VHGPGIQSGTTNKPNKFTVETR	GAGTG	3		790.0843011	2367.229503	0.000451244	15	N	1359	1381
Q8BTM8	Infl	PGLNR	TGVELGKPTHFTVNAK	TAGKG	2		849.962833	1697.910066	0.000451244	6	N	884	900
Q8BTM8	Infl	KAPLR	VQVQDNEGCSVEATVK	DNGNG	2	C9:+57.021	881.9177309	1761.819862	0.000451244	58	N	708	724
Q8BTM8	Infl	MPSGK	VAQPSITDNKDGTVTVR	YSPSE	2		900.9766688	1799.937738	0.000451244	15	N	1814	1831
Q8BTM8	Infl	PSKVK	AFGPGLQGGNAGSPAR	FTIDT	2		728.8687356	1455.721871	0.000451244	39	N	1071	1087
Q8BTM8	Infl	GDASK	VTAQGPGLEPSGNIANK	TTYFE	2		826.9342726	1651.852945	0.000451244	62	N	383	400
Q8BTM8	Infl	QGVFR	EATTEFSVDAR	ALTQT	2		613.288921	1224.562242	0.000451244	28	N	1272	1283
Q8BTM8	Infl	PGLEK	TGVAVNKPAEFTVDAK	HAGKA	2		823.9415663	1645.867533	0.000451244	38	N	684	700
Q8BTM8	Infl	VHGPR	TPCEEILVK	HMGSR	2	C3:+57.021	544.7867399	1087.55788	0.000823681	5	N	2598	2607
Q8BTM8	Infl	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	2		1142.054167	2282.092735	0.000451244	9	N	916	936
Q8BTM8	Infl	SILVK	YNDQHIPGSPFTAR	VTGDD	2		801.8871253	1601.758651	0.001395409	3	N	1937	1951
Q8BTM8	Infl	EGKPK	KTHIQDNHDGTYTVAYVPDVPGR	YTILI	3		861.7582537	2582.251361	0.001763695	6	N	1592	1615
Q8BTM8	Infl	VPIPR	SPYTVTVGQACNPAACR	AIGRG	2	C11:+57.021,C16:+57.021	926.4275115	1850.839423	0.000451244	21	N	467	484
Q8BTM8	Infl	LISIK	YGGPYHIGGSPFK	AKVTG	3		460.5634606	1378.666982	0.000622848	15	N	2500	2513
Q8BTM8	Infl	PGMVR	ANLPQSFQVDTSK	AGVAP	2		717.8653272	1433.715054	0.000451244	27	N	1464	1477
Q8BTM8	Infl	TVETR	GAGTGGLGLAVEGPSEAK	MSCMD	2		785.9077234	1569.799847	0.000451244	48	N	1381	1399
Q8BTM8	Infl	KVASK	IVSPSGAAVPCKVEPGLGADNSVVR	FVPRE	2	C11:+57.021	1240.152596	2478.289592	0.000451244	21	N	1007	1032
Q8BTM8	Infl	KAPLR	VQVQDNEGCSVEATVKDNGNGTYSCSYVPR	KPVKH	3	C9:+57.021,C25:+57.021	1111.829952	3332.466455	0.000451244	28	N	708	738
Q8BTM8	Infl	VTGPR	LVSNHSLHETSSVFVDSLTK	VATVP	2		1100.566379	2199.117159	0.000451244	25	N	2520	2540
Q8BTM8	Infl	HVKAR	VANPSGNLTDTYVQDCGDGTYK	VEYTP	2	C16:+57.021	1188.026727	2374.037854	0.000451244	22	N	1296	1318
Q8BTM8	Infl	TVETR	SAGQGEVLVYVEDPAGHQEEAK	VTANN	3		771.7051554	2312.092066	0.001463592	1	N	309	331
Q8BTM8	Infl	SFEDR	KDGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C5:+57.021	1193.565488	2385.115376	0.000451244	10	N	2288	2310
Q8BTM8	Infl	TYTVK	YIPVQQGPVGVNVTYGGDHIPK	SPFSV	2		1169.613664	2337.211728	0.000451244	26	N	936	958
Q8BTM8	Infl	TVKYI	PVQQGPVGVNVTYGGDHIPK	SPFSV	3		688.0292451	2061.064335	0.000451244	11	N	938	958
Q8BTM8	Infl	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	2	C11:+57.021	1383.655897	2765.296194	0.000451244	1	N	2367	2391
Q8BTM8	Infl	CVSKR	IANLQTDLSDGLR	LIALL	2		708.3786018	1414.741604	0.000451244	13	N	63	76
Q8BTM8	Infl	PGMVR	ANLPQSFQVDTSKAGVAPLQVK	VQGPK	2		1149.626771	2297.237943	0.000451244	9	N	1464	1486
Q8BTM8	Infl	TIDAK	DAGEGLLAVQITDPEGKPK	KTHIQ	2		969.5130841	1937.010568	0.000451244	30	N	1573	1592
Q8BTM8	Infl	EVSVK	FNEEHIPDSPFVVPVASPSGDARR	LTVSS	3		875.1020204	2622.282661	0.000451244	3	N	2310	2334
Q8BTM8	Infl	VSVKF	NEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1160.564368	2319.113136	0.000451244	19	N	2311	2333
Q8BTM8	Infl	KTGLK	AHEPTYFTVDCTEAGQGDVSIGIK	CAPGV	3	C11:+57.021	865.7396057	2594.195417	0.000622848	5	N	785	809
Q8BTM8	Infl	FEDRK	DGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C4:+57.021	1129.518006	2257.020412	0.000451244	28	N	2289	2310
Q8BTM8	Infl	NDKNR	TFSVWYVPEVTGTHK	VTVLF	2		875.944109	1749.872618	0.000662267	8	N	340	355

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Infl	DHIPK	SPFSVGVSPSLDLSK	IKVSG	2		760.4042853	1518.792971	0.000451244	16	N	958	973
Q8BTM8	Infl	EVSVK	FNEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1234.098575	2466.18155	0.000451244	18	N	2310	2333
Q8BTM8	Infl	VQGPK	GLVEPVDVVDNADGTQTVNYVPSR	EGSYS	2		1272.632979	2543.250358	0.000451244	67	N	1491	1515
Q8BTM8	Infl	YVPSR	EGSYSISVLYGEEEVPR	SPFKV	2		957.4605172	1912.905434	0.000451244	49	N	1515	1532
Q8BTM8	Infl	YVPSR	EGSYSISVLYGEEEVPRSPFK	VKVLP	2		1187.084602	2372.153604	0.000451244	11	N	1515	1536
Q8BTM8	Infl	VICVR	FGGEHVPNSPFQVTALAGDQPTVQTPLR	SQQLA	3		988.5057056	2962.493717	0.000451244	11	N	1725	1753
Q8BTM8	Infl	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	2	C14:+57.021	1382.174257	2762.332914	0.000451244	37	N	1246	1272
Q8BTM8	Infl	TYTVK	YIPVQQGPVGVNVTYGGDHIPKSPFSVGVSPSLDLSK	IKVSG	3		1280.339179	3837.994138	0.000451244	8	N	936	973
Q8BTM8	Infl	IIDTR	DAGYGGLSLSIEGPSKVDINTEDLEDGTCR	VTYCP	3	C29:+57.021	1056.826467	3167.456002	0.000451244	15	N	2073	2103
Q8BTM8	Infl	WQSGR	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	EAMQQ	3	C9:+57.021,C14:+57.021	1081.504851	3241.491154	0.000451244	24	N	196	226
Q8BTM8	Infl	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C26:+57.021	1345.662062	4033.962786	0.000451244	31	N	1234	1272
Q8BTM8	Infl	NSVVR	FVPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1329.014362	3984.019685	0.000451244	28	N	1032	1069
Q8BTM8	Infl	DGTYK	VEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C35:+57.021	1428.318467	4281.932	0.000451244	19	N	1318	1357
Q8BTM8	Infl	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	2	C1:+39.994	1014.490838	2026.966075	0.000451244	2	N	809	828
Q8BTM8	Infl	ASKVK	ASGPGLNTTGVPASLPVEFTIDAK	DAGEG	2		1171.616069	2341.216539	0.000451244	11	N	1549	1573
Q8BTM8	Infl	SIGIK	CAPGVVGPTEADIDFDIIRNDNDTFTVK	YTPCG	3	C1:+57.021	1027.161122	3078.459965	0.000451244	18	N	809	837
Q8BTM8	Infl	FEDRK	DGSCGVAYVVQEPGDYEVSVKF	NEEHI	2	C4:+57.021	1203.052213	2404.088826	0.000622848	5	N	2289	2311
Q8BTM8	Infl	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFREATTEFSVDAR	ALTQT	3	C14:+57.021	1323.969332	3968.884596	0.000451244	3	N	1246	1283
Q8BTM8	Infl	SCDVR	YWPQEAGEYAVHVLCNSEDIR	LSPFM	2	C15:+57.021	1268.582004	2535.148407	0.000451244	19	N	634	655
Q8BTM8	Infl	DVRYW	PQEAGEYAVHVLCNSEDIR	LSPFM	3	C13:+57.021	729.6763885	2186.005765	0.000451244	15	N	636	655
Q8BTM8	Infl	RFVPR	EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1162.584127	3484.728981	0.000451244	54	N	1036	1069
Q8BTM8	Infl	EERVK	QKDLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1256.284963	3765.83149	0.000451244	9	N	529	563
Q8BTM8	Infl	GIVGK	SADFVVEAIGDDVGTLGFSVEGPSQAK	IECDD	2		1348.159027	2694.302453	0.000451244	118	N	593	620
Q8BTM8	Infl	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK	RLRNG	3	C33:+57.021	1254.999681	3761.975643	0.000451244	17	N	1964	2000
Q8BTM8	Infl	RVKQK	DLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1170.90045	3509.677949	0.000451244	15	N	531	563
Q8BTM8	Infl	GDAVR	DVDIIDHHDNTYTVK	YIPVQ	2		892.9266445	1783.837689	0.000451244	18	N	921	936
Q8BTM8	Infl	NQKVR	AWGPGLEGGIVGK	SADFV	2		620.8383841	1239.661168	0.000451244	19	N	580	593
Q8BTM8	Infl	VHVKK	NGQHVASSPIPVVISQSEIGDASR	VRVSG	3		816.7546207	2447.240462	0.000451244	7	N	2025	2049
Q8BTM8	Infl	GIWTR	EAGAGGLAIAVEGPSKAEISFEDR	KDGSC	2		1187.598408	2373.181216	0.000451244	3	N	2264	2288
Q8BTM8	Infl	TGTHK	VTVLFAGQHIAK	SPFEV	2		642.3776765	1282.739753	0.000622848	6	N	355	367
Q8BTM8	Infl	TLVVK	WGDEHIPGSPYR	IMVP-	3		471.8902364	1412.647309	0.000735798	6	N	2631	2643
Q8BTM8	Infl	QHIAK	SPFEVYVDKSQGDASK	VTAQG	2		878.9235705	1755.831541	0.000451244	4	N	367	383
Q8BTM8	Infl	SSHSR	CGQSAAVASPGGSIDSR	DAEMP	2	C1:+57.021	810.3760332	1618.736466	0.000634081	2	N	7	24
Q8BTM8	Infl	KAPLR	VQVQDNEGCSVEATVKDNGNGTY	SCSYV	2	C9:+57.021	1242.551097	2483.086595	0.000451244	7	N	708	731
Q8BTM8	Infl	EGPSK	AEISCTDNQDGTCSVSYLPVLPGDYSILVK	YNDQH	3	C5:+57.021,C13:+57.021	1101.191827	3300.552082	0.000451244	15	N	1907	1937
Q8BTM8	Infl	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGR	EEPCL	2		1447.280008	2892.544415	0.000451244	17	N	1964	1993
Q8BTM8	Infl	DSLTK	VATVPQHATSGPGPADVSK	VVAKG	2		909.9713864	1817.927173	0.000451244	12	N	2540	2559
Q8BTM8	Infl	EATVK	DNGNGTYSCSYVPR	KPVKH	2	C9:+57.021	795.3363767	1588.657153	0.002727428	1	N	724	738
Q8BTM8	Infl	GIWTR	EAGAGGLAIAVEGPSK	AEISF	2		713.8809773	1425.746355	0.000451244	21	N	2264	2280
Q8BTM8	Infl	ESGLK	VNQPASFAVSLNGAK	GAIDA	2		751.9022441	1501.788888	0.000451244	11	N	2346	2361
Q8BTM8	Infl	CMDNK	DGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFK	VPVHD	3	C4:+57.021	1193.884317	3578.62955	0.000451244	17	N	1406	1439
Q8BTM8	Infl	AVPCK	VEPGLGADNSVVR	FVPRE	2		656.8469375	1311.678275	0.000451244	11	N	1019	1032
Q8BTM8	Infl	TVNTK	DAGEGGLSLAIEGPSK	AEISC	2		750.8811743	1499.746749	0.000451244	8	N	1891	1907
Q8BTM8	Infl	KVASK	IVSPSGAAVPCK	VEPGL	2	C11:+57.021	593.3187386	1184.621877	0.002519933	1	N	1007	1019
Q8BTM8	Infl	EPTYF	TVDCTEAGQGDVSIGIK	CAPGV	2	C4:+57.021	875.4201064	1748.824613	0.000451244	4	N	792	809
Q8BTM8	Infl	AGKGK	LDVQFSGLAK	GDAVR	2		539.3011031	1076.586606	0.000451244	2	N	906	916
Q8BTM8	Infl	KNRTF	SVWYVPEVTGTHK	VTVLF	2		751.8860627	1501.756525	0.002813207	1	N	342	355
Q8BTM8	Infl	IPGTY	TVTITWGGQNIGR	SPFEV	2		701.8760293	1401.736459	0.000823681	3	N	550	563
Q8BTM8	Infl	ASRVR	VSGQGLHEGHTFEPAEFIIDTR	DAGYG	2		1220.598742	2439.181884	0.000622848	4	N	2051	2073
Q8BTM8	Infl	AEVGV	PAEFGIWTR	EAGAG	2		538.7803378	1075.545076	0.000451244	2	N	2255	2264
Q8BTM8	Infl	VTIKY	GGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C25:+57.021	1291.307619	3870.899458	0.000698008	1	N	1235	1272
Q8BTM8	Infl	SIGIK	CAPGVVGPTEADIDFDIIRNDNDTF	TVKYT	2	C1:+57.021	1376.132255	2750.248909	0.000622848	9	N	809	834
Q8BTM8	Infl	VYVDK	SQGDASKVTAQGPGLEPSGNIANK	TTYFE	2		1163.585832	2325.156064	0.000451244	4	N	376	400
Q8BTM8	Infl	TILIK	YGGDEIPFSPYR	VRAVP	2		700.8282134	1399.640827	0.002727428	1	N	1621	1633
Q8BTM8	Infl	SGLAK	GDAVRDVDIIDHHDNTY	TVKYI	2		977.9486396	1953.881679	0.002212458	1	N	916	933
Q8BTM8	Infl	EAGTY	SLNVTYGGHQVPGSPFKVPVHDVTDASK	VKCSG	3		979.5020726	2935.482818	0.000823681	1	N	1422	1450
Q8BTM8	Infl	EYTPY	EEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C29:+57.021	1177.539098	3529.593893	0.000451244	10	N	1324	1357
Q8BTM8	Infl	CVSKR	IANLQTDLSDGLRLIALLEVLSQK	KMHRK	3		875.1730048	2622.495614	0.000622848	3	N	63	87
Q8BTM8	Infl	GIVGK	SADFVVEAIGDDVGTLGF	SVEGP	2		906.4390534	1810.862507	0.002296037	1	N	593	611
Q8BTM8	Infl	KTAGK	GKLDVQFSGLAK	GDAVR	3		421.5754777	1261.703033	0.002374549	1	N	904	916
Q8BTM8	Infl	DGVPV	PGSPFPLEAVAPTKPSK	VKAFG	2		861.9754091	1721.935218	0.002981883	1	N	1052	1069
Q8BTM8	Infl	QHIAK	SPFEVYVDK	SQGDA	2		542.2720113	1082.528423	0.001329271	4	N	367	376
Q8BTM8	Infl	DGTCR	VTYCPTEPGNYIINIK	FADQH	2	C4:+57.021	941.4746847	1880.933769	0.000451244	6	N	2103	2119
Q8BTM8	Infl	GDGTY	KVEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C36:+57.021	1471.016788	4410.026963	0.000451244	4	N	1317	1357
Q8BTM8	Infl	PRSPY	TVTVGQACNPAACR	AIGRG	2	C8:+57.021,C13:+57.021	752.853451	1503.691302	0.000451244	19	N	470	484

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Infl	VTGPR	LVSNHSLHETSSVF	VDSLT	2		778.8893337	1555.763067	0.000451244	1	N	2520	2534
Q8BTM8	Infl	LIDVK	FNGTHIPGSPFK	IRVGE	3		434.5599391	1300.656417	0.002212458	1	N	2405	2417
Q8BTM8	Infl	VDVTY	DGSPVPSSPFQVPVTEGCDPSR	VRVHG	2	C18:+57.021	1158.034355	2314.05311	0.001871652	3	N	1335	1357
Q8BTM8	Infl	VEVTY	DGVPVPGSPFPLEAVAPTKPSK	VKAFG	2		1095.594409	2189.173217	0.000451244	5	N	1047	1069
Q8BTM8	Infl	PLQFY	VDYVNCGHITAYGPGLTHGVVNKPATFTVNTK	DAGEG	4	C6:+57.021	858.4361736	3429.713495	0.002374549	4	N	1859	1891
Q8BTM8	Infl	TYTVK	YIPVQQGPVGVNVTY	GGDHI	2		817.4333771	1632.851154	0.000451244	4	N	936	951
Q8BTM8	Infl	GDAVR	DVDIIDHHDNTY	TVKYI	2		728.8211167	1455.626633	0.000823681	1	N	921	933
Q8BTM8	Infl	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVF	REATT	2	C14:+57.021	1304.123701	2606.231803	0.000451244	1	N	1246	1271
Q8BTM8	Infl	RVKQK	DLGDGVYGFEYYPTIPGTY	TVTIT	2		1063.983825	2125.95205	0.002663018	1	N	531	550
Q8BTM8	Infl	NSVVR	FVPREEGPYEVEVTY	DGVPV	2		907.4363138	1812.857028	0.0025889	1	N	1032	1047
Q8BTS4	Infl	EEQLR	VQLDTIQGELNAPTQFK	GRLNE	2		951.5025194	1900.989439	0.001591523	1	N	414	431
Q8BTZ7	Infl	DPSAR	IGQNCSIGPNVSLGPGVVVEDGVCIRR	CTVLR	3	C5:+57.021,C24:+57.021	951.4885842	2851.442353	0.000823681	3	N	261	288
Q8BTZ7	Infl	KHPER	LYSGPGIVGNVLVDPSAR	IGQNC	2		907.4944974	1812.973395	0.001654178	1	N	243	261
Q8BU30	Infl	ISRNR	YWGTPIPLWVSEDLEEVVCIGSVAELEELSGTK	ISDLH	3	C19:+57.021	1235.946694	3704.816682	0.001654178	2	N	461	494
Q8BU30	Infl	VKNAK	LSVFHGETEIQNQTDLLSLSGR	TLCVT	3		815.419238	2443.234314	0.000451244	2	N	1128	1150
Q8BU30	Infl	-M	VQQVPENISFPAEEEK	ILEFW	2		922.4577775	1842.899955	0.001943752	2	N	1	17
Q8BUK6	Infl	NKMLK	LNQEDSDNEKIALLQSLLDDANLR	KNELE	3		909.7985548	2726.372264	0.000622848	3	N	478	502
Q8BUK6	Infl	ISELR	QQNDELTTLADEAQSLKDEIDVLR	HSSDK	3		915.4581982	2743.351195	0.000451244	7	N	283	307
Q8BUK6	Infl	KKILK	GILDYNHEILGQQINDFTLPDVNLIGEHSDAAELGR	MLQLI	4		994.9978681	3975.960272	0.001162105	2	N	81	117
Q8BUK6	Infl	SDNEK	IALLQSLLDDANLR	KNELE	2		777.9466516	1553.877703	0.001463592	2	N	488	502
Q8BVE3	Infl	FLLEK	LGESVQDLSSFDEYSSELK	SGRLE	2		1066.997661	2131.979722	0.000451244	16	N	341	360
Q8BVE3	Infl	KILTK	LLEVSDDPQVLAVAAHDVGEYVR	HYPRG	3		832.4312551	2494.270365	0.000823681	7	N	396	419
Q8BVG4	Infl	RMDPK	ICPADPAFFSFINNSDLWVANIETGEER	RLTFC	3	C2:+57.021	1071.505	3211.491599	0.000451244	3	N	191	219
Q8BVG4	Infl	RPQQR	LQLVLLPPALFIPAVESEAQR	QAAAR	3		768.7829004	2303.325301	0.002981883	1	N	374	395
Q8BWT1	Infl	LSVQK	ALDLDPSKTNVSGGAIALGHPLGGSGSR	ITAHL	3		883.1319797	2646.372539	0.000451244	3	N	332	360
Q8BWT1	Infl	SVFKK	DGTVTAGNASGVSDGAGAVIIASEDAVK	KHNFT	2		1266.625351	2531.235102	0.000451244	6	N	241	269
Q8BWT1	Infl	LTLNR	LCGSGFQSIVSGCQEICSK	DAEVV	2	C2:+57.021,C13:+57.021,C17:+57.021	1058.976477	2115.937354	0.000451244	13	N	90	109
Q8BWY3	Infl	SKVLK	LVDISYGGENGFNQAIELSTEVLSNVK	FIQEK	2		1448.73289	2895.45018	0.000451244	4	N	252	279
Q8BWY3	Infl	GKEKK	VNIDFEPFKPINTSLYLCDNK	FHTEA	3	C18:+57.021	843.0897986	2526.245996	0.000622848	1	N	109	130
Q8BXK9	Infl	GSQRK	FLDGDELTLADCNLLPK	LHVVK	2	C12:+57.021	967.4827067	1932.949813	0.0007646	1	N	174	191
Q8BXK9	Infl	KGSQR	KFLDGDELTLADCNLLPK	LHVVK	2	C13:+57.021	1031.530188	2061.044777	0.001871652	1	N	173	191
Q8BY71	Infl	ETVHR	YYISFPTVLDITAEDPSR	SYLKL	2		1044.020742	2086.025884	0.000451244	5	N	259	277
Q8BY71	Infl	EYSSK	VDENFDCVEADDVEGK	IRQII	2	C7:+57.021	920.8810111	1839.746422	0.000823681	5	N	91	107
Q8BY71	Infl	SLLEK	ETNFKPFGTLLHTYTVPSQTGGETFTFQIHK	ADMTC	4		882.447017	3525.756868	0.002981883	1	N	129	160
Q8BYC6	Infl	MESLR	MGFGNLVTLDFPKEDYR	-	3		667.9966653	2000.966596	0.002519933	1	N	881	898
Q8BYC6	Infl	MDLIR	LQHQTELENQLEYNK	RRERE	2		943.9663011	1885.917002	0.000823681	1	N	676	691
Q8BYC6	Infl	LAERK	PPLFNMNAMSALYHIAQNDSPTLQSR	EWTDS	3	M6:+15.995	978.1414107	2931.400832	0.002981883	1	N	218	244
Q8BYI6	Infl	EIKKR	ATSGGEWPQILVFPEGTCTNR	SCLIT	2	C18:+57.021	1160.555257	2319.094915	0.000622848	2	N	205	226
Q8BYI6	Infl	TVKGK	VASPLEAPIFVVAPHSTFFDGIACVVAGLPSLVSR	NENAQ	3	C24:+57.021	1208.648366	3622.921697	0.001463592	1	N	131	166
Q8BYW1	Infl	ILVEK	CAEFILEHGVSEEGIFRLPGQDNLVK	QLRDA	3	C1:+39.994	980.8237423	2939.447827	0.000451244	2	N	183	209
Q8BYW1	Infl	GSTVK	EIATNPEEAGKFVFEVIPASSDQNR	IGQDS	2		1374.677918	2747.340236	0.000851441	1	N	98	123
Q8BYW1	Infl	EEAGK	FVFEVIPASSDQNR	IGQDS	2		804.9049838	1607.794368	0.000622848	1	N	109	123
Q8C079	Infl	RNQRK	DSEGYSESPDLEFEYADTD	KWAAE	3		723.6154488	2167.822946	0.0025889	1	N	57	76
Q8C079	Infl	YITAK	NSISVLDYPHCVVNELPELTAESLEAGDNNQFCWR	NLFSC	3	C11:+57.021,C33:+57.021	1359.630168	4075.867103	0.000622848	3	N	628	663
Q8C079	Infl	RRYDR	THSNPDFLPVDNCLQSVLGQR	VDLPE	3	C13:+57.021	799.7257423	2396.153827	0.000622848	2	N	785	806
Q8C0C7	Infl	VGAVK	SLQALGEVIEAELR	STKCW	2		764.4230094	1526.830419	0.000451244	8	N	42	56
Q8C0C7	Infl	ELLLR	RLEVADGGLDSAELATQLGVEHQAVVGAVK	SLQAL	3		1011.539075	3031.593825	0.002296037	1	N	12	42
Q8C0G2	Infl	ELQTK	LESLQGDGEQQSSETQDLQDQLKK	SEEEK	3		902.102303	2703.283509	0.000451244	5	N	378	402
Q8C0I1	Infl	PEYQK	YGSVAFPNFEQGVACLR	EIAKQ	2	C15:+57.021	957.9622758	1913.908952	0.000451244	5	N	376	393
Q8C0I1	Infl	ECKAR	RAASAAGASPAATPAAPESGTIPK	KRQEV	3		717.378714	2149.112742	0.000823681	2	N	48	72
Q8C0I1	Infl	KTTSK	TSINPSEAPPSIVNEDFLQELK	EARIS	2		1214.616266	2427.216933	0.002019181	1	N	134	156
Q8C0I1	Infl	CKARR	AASAAGASPAATPAAPESGTIPK	KRQEV	2		997.5136155	1993.011631	0.000451244	11	N	49	72
Q8C0I1	Infl	GMFER	IPDIVVWPTCHDDVVK	IVNLA	3	C10:+57.021	631.6577179	1891.949754	0.000451244	1	N	191	207
Q8C0I1	Infl	IAYIR	DLGLEYYVIGESFETSAPWDR	VIDLC	2		1224.074234	2446.132869	0.000451244	9	N	502	523
Q8C0I1	Infl	LPTLR	DWIQNTLGVSLEHK	TTSKT	3		547.2866556	1638.836567	0.002663018	1	N	116	130
Q8C0I1	Infl	ERQLK	ESGYCTGHEPDSLEFSTVGGWISTR	ASGMK	2	C5:+57.021	1386.614229	2771.212858	0.000823681	1	N	279	304
Q8C0L0	Infl	RAVVK	EGSVSPKEDGAHPADTQDVVEDALR	QRKSQ	3		874.7479715	2621.220515	0.000451244	8	N	299	324
Q8C0L0	Infl	SVSPK	EDGAHPADTQDVVEDALR	QRKSQ	2		969.4459298	1936.87626	0.000451244	3	N	306	324
Q8C147	Infl	KTLQK	QTFESETLECSEPDTQTGPR	HPLNV	2	C10:+57.021	1156.503084	2310.990569	0.000451244	25	N	160	180
Q8C147	Infl	VCSGR	YFTESGLVGLLEQAAELFSTGGLYETVNEVYK	LVIPI	3		1176.587649	3526.739546	0.000451244	2	N	1722	1754
Q8C147	Infl	RFSDR	FKDDITTIVNVVTSEIAALLVKPQK	ESEQA	3		914.8604268	2741.55788	0.000451244	4	N	1016	1041
Q8C147	Infl	EISHR	LEGFYGQCFGAEFVEVIKDSTPVDK	TKLDP	3	C8:+57.021	945.7900775	2834.346832	0.000851441	2	N	1829	1854
Q8C147	Infl	SCQQK	QGASGESLLGYSWLPILLNER	LQTGS	2		1152.105672	2302.195743	0.000451244	4	N	658	679
Q8C147	Infl	EVKVK	IAALYLPLVGIILDALPQLYDFTDAR	SGRSR	3		958.8725553	2873.594266	0.001699387	1	N	1211	1237

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8C147	Infl	SGRSR	ASGSYEEQDVANGINQNVALAIAGNHFNLK	TSGAM	3		1048.850201	3143.527202	0.000451244	1	N	1242	1272
Q8C166	Infl	AAQQR	SASQYFVLLLLTDGAVTDVEATCK	AVVDA	2	C23:+57.021	1301.159752	2600.303905	0.000622848	2	N	408	432
Q8C166	Infl	DIGSK	SDPLCVLLQDVGGAWAELCR	TERVR	2	C5:+57.021,C19:+57.021	1130.048522	2258.081445	0.000451244	22	N	25	45
Q8C166	Infl	PTWKR	FSVSLQHFCGGDLSTPIQVR	CSDYD	3	C9:+57.021	750.0445236	2247.110171	0.002145581	1	N	190	210
Q8C166	Infl	QNAPR	ETLAQTVLAEVPTQMVSYFR	AQGWA	2		1142.088634	2282.161667	0.001162105	1	N	493	513
Q8C166	Infl	LIGTF	HTTLAQLQAVPAEFECVHPEK	QQRKK	3	C16:+57.021	802.4024881	2404.184064	0.001352548	1	N	226	247
Q8C166	Infl	DFLGK	SDPFLEFFR	QGDGK	2		579.285453	1156.555306	0.002519933	2	N	156	165
Q8C166	Infl	PIQVR	CSDYDSDGSHDLIGTFHTTLAQLQAVPAEFECVHPEK	QQRKK	4	C1:+39.994,C32:+57.021	1040.217924	4156.840497	0.001162105	1	N	210	247
Q8C1B7	Infl	QLVNK	STSQGFCFNILCVGETGIGK	STLMD	2	C7:+57.021,C12:+57.021	1088.014148	2174.012696	0.000451244	6	N	34	54
Q8C1B7	Infl	FQKKK	AAAQLLQSQAQQSGAQQTK	KDKDK	2		979.0090316	1956.002463	0.000451244	13	N	399	418
Q8C1B7	Infl	NEELR	NLSLSGHVGFDSLPDQLVNK	STSQG	2		1070.555815	2139.096029	0.0007646	1	N	14	34
Q8C2Q3	Infl	AAPYR	TQSSASLAASYAAQQHPQAAASYR	GQPGS	2		1233.094355	2464.173111	0.000451244	2	N	517	541
Q8C2Q3	Infl	RSPPR	ASYVAPLTAQPATYR	AQPSV	2		804.9231765	1607.830753	0.000451244	2	N	223	238
Q8C2Q3	Infl	GTGGF	SATFDYQQAFGNSTGGFDGQAR	QPTPP	2		1163.0125	2324.009399	0.000451244	8	N	181	203
Q8C2Q3	Infl	LNTWK	IFVGNVSAACTSQELR	SLFER	2	C10:+57.021	876.4411762	1750.866752	0.001162105	1	N	80	96
Q8C3J5	Infl	VEKRR	NIENIIPAEIPLAQEVTTTLWEWGSIWK	QLYVA	3		1084.571605	3250.691414	0.000698008	10	N	75	103
Q8C3J5	Infl	GDDVR	NAPGQYIQCFTVQPVLDEHPR	FKNKP	3	C9:+57.021	823.7378708	2468.190212	0.000451244	5	N	1398	1419
Q8C3J5	Infl	LIKHK	LSQGIFPTSFIHLK	EVTVE	3		529.9684868	1586.88206	0.001591523	4	N	53	67
Q8C3J5	Infl	MKILR	TKPDYFAVGYYGQGFPSFLR	NKVFI	2		1157.071101	2312.126601	0.00307782	1	N	1336	1356
Q8C6G8	Infl	TGGQR	GQFYQCDLDGNLLDSWEGVR	VQCLW	2	C6:+57.021	1186.534522	2371.053444	0.000451244	7	N	447	467
Q8C6G8	Infl	YHNTK	LDNNLDSVSLLIDHVCSR	RQFPC	3	C16:+57.021	690.6813624	2069.020687	0.000451244	2	N	302	320
Q8CAQ8	Infl	TAYAR	LRGIEQAVQSHAVAEEEAR	KAHQL	3		698.3631754	2092.066126	0.000622848	3	N	544	563
Q8CAQ8	Infl	DALNR	TSSVTLQTITAQNAAVQAVK	AHSNI	2		1016.05819	2030.10078	0.000451244	3	N	229	249
Q8CAQ8	Infl	VEAIR	VNCSDNEFTQALTAAIPPESLTR	GVYSE	2	C3:+57.021	1267.613501	2533.211401	0.001591523	3	N	599	622
Q8CAQ8	Infl	DLAGK	LSTDDLNSLIAHAHR	RIDQL	4		416.4699321	1661.848528	0.002884417	2	N	394	409
Q8CAQ8	Infl	DDFRK	ELDSITPDITPGWK	GMSIS	2		786.4017426	1570.787885	0.001591523	1	N	370	384
Q8CB87	Infl	DARPK	GSFLWSLPGALTAESGTVEAAF	RDQLA	2		1106.052573	2210.089547	0.000451244	4	N	229	251
Q8CB87	Infl	AEGQR	ELEAQLLHLSSTQQEANRENLQLR	EAERD	3		940.8253268	2819.45258	0.000622848	2	N	26	50
Q8CB87	Infl	ESHAK	GFQEAPGQVLSLDSLPTHLPQSLEEQLRPEEGNLGER	GQQDP	3		1357.685967	4070.0345	0.000451244	1	N	359	396
Q8CB87	Infl	DARPK	GSFLWSLPGALTAESGTVEAAFR	DQLAF	2		1184.103129	2366.190658	0.000451244	4	N	229	252
Q8CB87	Infl	LVDNK	TFALQLWDTAGQER	YHSLT	2		818.4104333	1634.805267	0.000622848	1	N	584	598
Q8CB87	Infl	ISISK	ISALQFSQEPASDPDPGPR	GSPEV	2		1006.49014	2010.964681	0.000451244	1	N	167	186
Q8CBW3	Infl	LEETK	AYTTQSLASVAYQINALANNVLQLLDIQASQLR	RMESS	3		1197.644603	3589.910409	0.000622848	1	N	51	84
Q8CBW3	Infl	QNLTR	VADYCENNYIQATDK	RKALE	2	C5:+57.021	902.3966313	1802.777663	0.000451244	1	N	28	43
Q8CBW3	Infl	QNLTR	VADYCENNYIQATDKR	KALEE	3	C5:+57.021	653.9673912	1958.878774	0.001591523	1	N	28	44
Q8CBW3	Infl	AVVQY	SDPYADGDPAWAPK	NYIEK	2		745.3338599	1488.65212	0.00307782	1	N	404	418
Q8CBY8	Infl	LRYMK	ESQVLLTLTNPVENLTHVTLLECDEGDPDNINSTAK	VVVPP	3	C23:+57.021	1327.319919	3978.936357	0.000979378	3	N	328	364
Q8CBY8	Infl	QKEVK	IEPAQAVAEVEPLPEDYYTRPVNLTEVTTL	QQRLL	3		1119.908722	3356.702767	0.000451244	7	N	222	252
Q8CC86	Infl	KAAFR	FLGPDGSLLLDLLQLAEEPPPKAGQELR	VWPRG	3		1006.217162	3015.628085	0.000451244	5	N	425	453
Q8CC86	Infl	KAAFR	FLGPDGSLLLDLLQLAEEPPPK	AGQEL	3		788.1021872	2361.283162	0.000451244	1	N	425	447
Q8CC86	Infl	YSVRR	SGLPNFLAVALALGELGYR	AVGVR	2		981.0468971	1960.078194	0.000451244	2	N	294	313
Q8CCF0	Infl	APEYR	VIVDANNLTVEIENELNIIHK	FIRDK	3		797.436229	2389.285287	0.000451244	1	N	91	112
Q8CCF0	Infl	TIRDR	SSGTASSVAFTPLQGLEIVNPQAAEK	KVAEA	2		1301.672104	2601.328608	0.002981883	1	N	444	470
Q8CCJ3	Infl	SELCK	AYDLPGDFLTQALTQR	LGRII	2		904.96303	1807.91046	0.002212458	1	N	144	160
Q8CCJ3	Infl	DCLRK	HIQDAPEEFISELAEYLIKPLNK	MYLEV	3		899.8098435	2696.406131	0.000451244	3	N	488	511
Q8CCS6	Infl	EADAR	SIYVGNVDYGATAEELEAHFHGCGSVNR	VTILC	3	C23:+57.021	1018.133677	3051.377632	0.000451244	2	N	168	196
Q8CCS6	Infl	AGEGD	PGGAGDYGNGLESEELEPGELLPEPEPEEEPPRPR	APPGA	3		1248.250535	3741.728206	0.000622848	2	N	39	74
Q8CD10	Infl	FKTVK	TNETEYQDPTVKEPGVNTTLQVR	FFGKR	3		873.7685955	2618.282387	0.000823681	1	N	211	234
Q8CD10	Infl	DTVFK	IFDLDGDECLSHGEFLGVLK	NRMHR	3	C9:+57.021	755.3686729	2263.082619	0.000622848	1	N	369	389
Q8CDN6	Infl	RNKVR	IDQYQGADAVGLEEK	IKQHL	2		818.3971886	1634.778777	0.000451244	13	N	87	102
Q8CDN6	Infl	LRYVK	FQNVNSVTLFVQSNQGEEETTR	ISYFT	2		1264.107128	2526.198657	0.000451244	7	N	237	259
Q8CDN6	Infl	FFRNK	VRIDQYQGADAVGLEEK	IKQHL	2		945.9819511	1889.948302	0.000451244	3	N	85	102
Q8CDN6	Infl	EEAER	SEPTQALELTEDDIKEDGIVPLR	YVKFQ	3		856.7733466	2567.29664	0.000622848	5	N	211	234
Q8CDN6	Infl	-M	VGVKPVGSDPDFQPELSGAGSR	LAVVK	2		1100.056179	2198.096758	0.000451244	6	N	1	23
Q8CDN6	Infl	PFINK	AGCECLNESDEHGFDNCLRK	DMSFL	4	C3:+57.021,C5:+57.021,C17:+57.021	603.500859	2409.972236	0.000451244	1	N	132	152
Q8CDN6	Infl	PFINK	AGCECLNESDEHGFDNCLR	KDMSF	3	C3:+57.021,C5:+57.021,C17:+57.021	761.6335577	2281.877273	0.001229886	2	N	132	151
Q8CEC0	Infl	IFEQK	DRDVVAYPLYILYENGETFLTYVSLLHSPGNIGK	LLGPL	4		965.0008851	3855.97234	0.000451244	4	N	259	293
Q8CEC0	Infl	ELALK	LASGEDDPFASDFSCPIK	LHRDP	2	C15:+57.021	978.4384962	1954.861392	0.001162105	2	N	377	395
Q8CEC6	Infl	EGSEK	TELSEREPALAVAGSEENDDENEER	WVGPL	3		930.4168388	2788.227116	0.001591523	1	N	24	49
Q8CEC6	Infl	INMLK	LGYFPGQCEWIYCPGDAISSVAASEK	STGKI	3	C8:+57.021,C13:+57.021	969.1107795	2904.308938	0.000622848	1	N	172	198
Q8CG03	Infl	KIQNK	LTDLETLALLIAALSHDLDHR	GVNNS	4		583.3238394	2329.264158	0.000451244	3	N	627	648
Q8CG03	Infl	AQTLK	ITDFSFSDFELSDLETALCTIR	MFTDL	2	C19:+57.021	1290.612635	2579.20967	0.000823681	3	N	545	567

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CG19	Infl	ASEKR	CVQPTESNEQIEETDVYQDLCWEHLSEEYVCSRPLVGK	QTTYT	4	C1:+57.021,C21:+57.021,C31:+57.021	1157.52308	4626.061119	0.000823681	2	N	1496	1534
Q8CG19	Infl	EGSYK	CLCLPGYIPSDKPNYCTPLNSALNLDKESDLE	-	3	C1:+57.021,C3:+57.021,C16:+57.021	1232.912582	3695.714345	0.000735798	5	N	1680	1712
Q8CG29	Infl	GLYAR	LFDFLVEAINR	AMQKP	2		668.8671416	1335.718683	0.000451244	17	N	360	371
Q8CG29	Infl	VQHVK	DIILQSNPLLEAFGNAK	TVRNN	2		922.0021552	1841.98871	0.000451244	18	N	141	158
Q8CG29	Infl	GNYAR	VESVDLLAFPAYLLGIDSGRLQEK	LTSRK	3		878.4782053	2632.411216	0.000451244	3	N	296	320
Q8CG29	Infl	GNYAR	VESVDLLAFPAYLLGIDSGR	LQEKL	2		1068.073309	2134.131018	0.000451244	9	N	296	316
Q8CG29	Infl	ELTLK	AEQEEYVQEGIR	WTPIE	2		725.8445918	1449.673584	0.000451244	3	N	420	432
Q8CG29	Infl	SRRPR	ARPPSEHSTEFLNVPDQGVAGMQRK	RSIGQ	4	M22:+15.995	692.595511	2766.350844	0.001871652	1	N	996	1021
Q8CG29	Infl	SLSTR	QDDFFILQEEAADSF	LESIF	2		887.8944787	1773.773357	0.002884417	1	N	827	842
Q8CG29	Infl	GPRCR	ALYQYIGQDVDELSFNVNEVIEILIEDSSGWWK	GRLHG	3		1291.63555	3871.883251	0.0025889	1	N	1047	1080
Q8CGC7	Infl	EYKEK	TGQEYKPGNPSAAAVQTVSTK	SSSNT	2		1067.542904	2133.070209	0.001463592	2	N	794	815
Q8CGC7	Infl	SSAPK	ERPAPAVSSTCATAEDSSVLYSR	VAVQG	3	C11:+57.021	818.724067	2453.148801	0.000622848	1	N	733	756
Q8CGC7	Infl	SSAPK	ERPAPAVSSTCATAEDSSVLY	SRVAV	2	C11:+57.021	1106.015631	2210.015661	0.000451244	6	N	733	754
Q8CGC7	Infl	LKAEK	ASKDQVDSAVQELLQLK	AQYKS	2		936.5078018	1871.000004	0.000451244	4	N	922	939
Q8CGC7	Infl	QPHPR	TGNKYNVYPTYDFACPIVDSIEGVTHALR	TTEYH	3	C15:+57.021	1100.871683	3299.591648	0.000451244	1	N	366	395
Q8CGC7	Infl	AKLEK	VLEDIQLNLFTR	ASEDL	2		730.9095378	1459.803476	0.000451244	3	N	1403	1415
Q8CGC7	Infl	TEKEK	FAGGDYTTTIEAFISASGR	AIQGA	2		982.4739589	1962.932318	0.000451244	1	N	1215	1234
Q8CGC7	Infl	AEIKK	LGVENCYFPIFVSQAALEK	EKNHI	3	C6:+57.021	729.0384871	2184.092061	0.000823681	1	N	1070	1089
Q8CGC7	Infl	RTGNK	YNVYPTYDFACPIVDSIEGVTHALR	TTEYH	3	C11:+57.021	967.4693383	2899.384615	0.000823681	4	N	370	395
Q8CGC7	Infl	QLQRR	GFFICDQPYEPVSPY	SCREA	2	C5:+57.021	909.9061035	1817.796607	0.001699387	1	N	675	690
Q8CGC7	Infl	FLRTR	EFLWQEGHSAFATFEEAADEVLQILELYAR	VYEEL	3		1171.572333	3511.693599	0.000451244	1	N	1165	1195
Q8CGP4	Infl	QLAIR	NDEELNKLLGR	VTIAQ	2		650.8469375	1299.678275	0.000451244	24	N	89	100
Q8CGP4	Infl	APVYL	AAVLEYLTAEVLELAGNAAR	DNKKT	2		1037.563108	2073.110617	0.000451244	8	N	52	72
Q8CGP4	Infl	PVYLA	AVLEYLTAEVLELAGNAAR	DNKKT	2		1002.044551	2002.073503	0.000451244	12	N	53	72
Q8CGP4	Infl	NYAQR	IGAGAPVYLAAVLEYLTAEVLELAGNAAR	DNKKT	3		972.5346022	2914.580407	0.000451244	6	N	43	72
Q8CH18	Infl	WNAQR	IQTLPNQNQSQTQPLLK	TPTAV	2		976.0345181	1950.053436	0.000451244	6	N	201	218
Q8CH18	Infl	DLYHK	SCALAEDPQDLR	DGFQH	2	C2:+57.021	687.8198311	1373.624062	0.001463592	1	N	460	472
Q8CHC4	Infl	RAPSR	TPGPPSSQGSPVDTQPAAQKDSSQTLEPK	RPPPP	3		979.1480237	2934.420671	0.000622848	1	N	1074	1103
Q8CHC4	Infl	RAPSR	TPGPPSSQGSPVDTQPAAQK	DSSQT	2		975.4823153	1948.949031	0.000451244	3	N	1074	1094
Q8CHG3	Infl	LKQLR	ASILEENEEEDVVKLIQAVGESLVK	VKEEE	3		914.4872062	2740.438219	0.000451244	4	N	758	783
Q8CHK3	Infl	FFRYR	TYLDWLEQPFPEAVPSLRPLLR	RAWPA	3		880.8115187	2639.411156	0.00091018	1	N	171	193
Q8CHK3	Infl	AAKAR	AGGGPTLQCPPPSSPEIAASLEYDYETIR	NIDCY	3	C9:+57.021	1026.157489	3075.449066	0.000451244	5	N	271	300
Q8CHP8	Infl	AERAK	LLLAEVDTLLFDCDGVLWR	GETAV	2	C13:+57.021	1124.588038	2247.160475	0.000451244	1	N	22	41
Q8CHP8	Infl	TCSLK	TILTLTGVSSLEDVK	SNQES	2		788.4461501	1574.8767	0.000622848	1	N	275	290
Q8CHP8	Infl	GKPSR	FIFDCVSQEYGINPER	TVMVG	2	C5:+57.021	987.4570233	1972.898447	0.000451244	13	N	238	254
Q8CHP8	Infl	AEKLR	RLGFGGPVGPEAGLEVFGTAY	CSALY	2		1047.536894	2093.058187	0.001264573	3	N	82	103
Q8CI94	Infl	ITPRR	WLLLCNPGLAEIIVER	IGEGF	2	C5:+57.021	948.5245119	1895.033424	0.002981883	1	N	491	507
Q8CI94	Infl	IIVER	IGEGFLTDLSQLKK	LLSLV	3		516.9597684	1547.855905	0.000451244	3	N	507	521
Q8CI95	Infl	NQKPR	GTLQLAGAVISPSDEDSHTFTVNAASGEQYK	LRATD	3		1065.181505	3192.521114	0.001329271	2	N	108	139
Q8CI95	Infl	WRMPK	SEVASGVSSSSSTPAITDHAPLPEEAPTQSVSDCYTVR	FVAEQ	3	C34:+57.021	1307.27649	3918.806071	0.000637154	1	N	470	508
Q8CIE6	Infl	EITKK	IQVPNCDEIFYAGTGNLLLR	DADSI	2	C6:+57.021	1147.086193	2292.156787	0.000451244	12	N	447	467
Q8CIE6	Infl	VEKFR	SILLSVPLLVVDNKQEIAEAQQLITICR	EYIVG	3	C27:+57.021	1055.263852	3162.768156	0.001943752	3	N	1030	1058
Q8CIE6	Infl	KPVEK	CPLSGACYSPEFK	GQICR	2	C1:+57.021,C7:+57.021	758.3340284	1514.652457	0.000451244	1	N	1184	1197
Q8CIE6	Infl	ETAMR	LLHDQVGVIQFGPY	KQLFL	2		793.4228124	1584.830025	0.001229886	2	N	941	955
Q8CIE6	Infl	KNFDK	LSFLYLITGNLEK	LRKMM	2		755.9299389	1509.844278	0.000451244	6	N	702	715
Q8CIE6	Infl	LLCTR	ASNLENSTYDLYTIPK	DADSQ	2		914.952328	1827.889056	0.000634081	3	N	382	398
Q8CIE6	Infl	DVLGK	GQEEGGGWDVEEDLELPPELDVPSGVSGSAEDGFFVPPTK	GTSPT	3		1391.31012	4170.906959	0.00091018	2	N	872	912
Q8CIE6	Infl	YQRTK	NFDKLSFLYLITGNLEK	LRKMM	3		672.3669752	2014.077526	0.002145581	3	N	698	715
Q8CIE6	Infl	VRNAK	LVGQSIIAYLQK	KGYPE	2		666.8984417	1331.781283	0.001162105	1	N	619	631
Q8CIH5	Infl	GKNQK	AFVFILEPK	KQGDP	2		532.3134822	1062.611364	0.000451244	8	N	870	879
Q8CIH5	Infl	IADAK	LSFGDDIEQAVEEEPVQDTPPTELHFGEK	WFHKK	3		1086.177649	3255.509546	0.000451244	23	N	502	531
Q8CIH5	Infl	SNKFK	TTVVNDNGLSPVWAPTQEKVTFEIYDPNLAFLR	FVVYE	3		1245.640858	3733.899175	0.000451244	6	N	1100	1133
Q8CIH5	Infl	DEFKK	DSSVFILGNTDRPDASAVYLQDFQR	FLLHE	3		938.7951447	2813.362034	0.000451244	14	N	223	248
Q8CIH5	Infl	SNKFK	TTVVNDNGLSPVWAPTQEK	VTFEI	2		1028.52144	2055.027281	0.000451244	9	N	1100	1119
Q8CIH5	Infl	VQAIR	DHAFVTSSFPVILSIEEHCSVEQQR	HMAKV	3	C19:+57.021	972.4716304	2914.391491	0.000979378	1	N	390	415
Q8CIH5	Infl	RAGCR	CIELDCWDGPDGKPIIYHGWTR	TTKIK	4	C1:+57.021,C6:+57.021	672.8140872	2687.225149	0.001463592	1	N	354	376
Q8CIH5	Infl	QDFQR	FLLHEQQELWAQDLNK	VRERM	2		1006.515961	2011.016322	0.000451244	2	N	248	264
Q8CIH5	Infl	NGVMK	YYLTDNLTFNSIYALIQHYR	EAHLR	3		836.7573025	2507.248507	0.000451244	5	N	598	618
Q8CIH5	Infl	EPFLF	VDEFLTYLFSR	ENSIW	2		695.3566067	1388.697613	0.000622848	8	N	286	297
Q8CIN4	Infl	ALNTK	GSETSAVVTEEDDDDEDAAPPVIAPRPDHTK	SIYTR	3		1088.49945	3262.474951	0.000451244	44	N	160	191
Q8CIN4	Infl	ENPLR	ALYLIATNGTPELQNPEK	LSPIF	2		986.5234518	1971.031304	0.000451244	21	N	450	468
Q8CIN4	Infl	SIYTR	SVIDPIPAPVGDSNVDSGAK	SSDKQ	2		969.4948914	1936.974183	0.000451244	12	N	196	216
Q8CIN4	Infl	SGTVF	TATDVALGQEVAIK	QINLQ	2		708.3911779	1414.766756	0.000870037	8	N	264	278

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CIN4	Infl	EGSVK	LTDFGFCAQITPEQSKR	STMVG	2	C7:+57.021	999.4913974	1996.967195	0.000451244	5	N	383	400
Q8CIN4	Infl	AAVCR	ECLQALEFLHANQVIHR	DIKSD	4	C2:+57.021	520.2708655	2077.052262	0.000622848	6	N	350	367
Q8CIN4	Infl	TVKQK	YLSFTPPEKDGFPSGTPALNTK	GSETS	2		1184.097512	2366.179425	0.000698008	7	N	138	160
Q8CIS0	Infl	MYKHR	MNTVMLQLEEVERER	DQAFH	3	M1:+15.995,M5:+15.995	636.9772222	1907.908267	0.001463592	1	N	364	379
Q8JZQ9	Infl	AEPAR	QQPASESPPTDEAAGSGGSEVGQTEDAEEDAEAGPEPEVR	AKPAA	3		1337.576364	4009.705693	0.000451244	24	N	21	61
Q8JZQ9	Infl	EPEVR	AKPAAQSEEETATSPAASPTPQSAER	SPSQE	2		1306.625882	2611.236165	0.000451244	1	N	61	87
Q8JZQ9	Infl	QSAER	SPSQEPSAPGKAEAVGEQAR	GHPSA	3		665.9963811	1994.965743	0.000451244	4	N	87	107
Q8JZQ9	Infl	GDVLK	DRPQEADGIDSVIVVDNVPQVGPDRLEK	LKNVI	3		1020.858585	3059.552354	0.000451244	11	N	163	191
Q8JZQ9	Infl	GDVLK	DRPQEADGIDSVIVVDNVPQVGPDR	LEKLK	3		897.4513779	2689.330734	0.000451244	4	N	163	188
Q8JZQ9	Infl	ESGDR	TSIFWNDVKDPVSIEER	ARWTE	2		1018.010709	2034.005817	0.000451244	2	N	304	321
Q8JZQ9	Infl	KMFDK	QQANTIFWSPQGQFVVLAGLR	SMNGA	2		1180.629648	2359.243697	0.00091018	1	N	597	618
Q8JZQ9	Infl	SKFGK	IINDYYPEEDGKTK	GYIFL	2		842.9073891	1683.799178	0.001162105	2	N	205	219
Q8K0E8	Infl	MEYCR	TPCTVSCNIPVVSGK	ECEEI	2	C3:+57.021,C7:+57.021	809.9000669	1617.784534	0.000451244	13	N	214	229
Q8K0E8	Infl	MEYCR	TPCTVSCNIPVVSGKECEEIIR	KGGET	2	C3:+57.021,C7:+57.021,C17:+57.021	1274.613669	2547.211738	0.000451244	8	N	214	236
Q8K0E8	Infl	QAQVK	ENENVINEYSSILEDQR	LYIDE	2		1026.47997	2050.944339	0.000451244	8	N	153	170
Q8K0E8	Infl	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLK	DMWKK	3		1024.863224	3071.566273	0.000451244	14	N	114	142
Q8K0E8	Infl	QAQVK	ENENVINEYSSILEDQRLYIDETVNDNIPLNLR	VLRSI	3		1312.315539	3933.923218	0.000451244	8	N	153	186
Q8K0E8	Infl	LEDQR	LYIDETVNDNIPLNLR	VLRSI	2		951.5025194	1900.989439	0.000451244	10	N	170	186
Q8K0E8	Infl	YCDMK	TENGGWTVIQNR	QDGSV	2		687.8421864	1373.668773	0.001395409	2	N	263	275
Q8K0E8	Infl	KKVER	RPPDAGGCLHADTDMGVLCPTGCTLQQTLLNQERPIK	SSIAE	4	C8:+57.021,C19:+57.021,C23:+57.021	1030.751409	4118.974434	0.000451244	2	N	77	114
Q8K0E8	Infl	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLKDMWK	KKQAQ	3		1211.610459	3631.807978	0.000451244	5	N	114	146
Q8K0E8	Infl	PVDRR	KEEPPSLRPAPPPISGGGYR	ARPAK	3		702.3766448	2104.106534	0.001839721	1	N	42	62
Q8K0E8	Infl	EDAKK	YCGLPGEYWLGNDKISQLTR	MGPTE	2	C2:+57.021	1185.581275	2369.14695	0.000451244	5	N	304	324
Q8K0E8	Infl	GDKVK	AHYGGFTVQNEASKYQVSVNK	YKGTA	2		1164.074903	2326.134206	0.000998612	1	N	343	364
Q8K0E8	Infl	EEIIR	KGGETSEMYLIQPDTSIKPYR	VYCDM	3		805.0743032	2412.199509	0.001871652	1	N	236	257
Q8K0E8	Infl	MWKKK	QAQVKENENVINEYSSILEDQR	LYIDE	2		1303.638793	2605.261985	0.000451244	5	N	148	170
Q8K124	Infl	SEKLK	VSWENPSPEKPSAPESAQLSSSETPEATPR	ESKKP	3		1065.841259	3194.500378	0.000451244	15	N	272	302
Q8K124	Infl	KQTEK	LLNQVLGSEPPPVCAESLLSQAVEQLR	QATQV	3	C14:+57.021	983.190464	2946.547992	0.000451244	11	N	430	457
Q8K124	Infl	PAGER	ALTPDSASSGANPESQEDAETPAKEDSDVK	SLPNS	3		1016.125613	3045.353439	0.000451244	7	N	230	260
Q8K124	Infl	LQEMR	DLGELNQETPGLVQK	RKELV	2		820.9286559	1639.841712	0.000622848	14	N	467	482
Q8K124	Infl	DGLSR	LDLDVPDSGPPVFAPLSDISEDQPQEPPR	ALMPP	3		1044.179212	3129.514237	0.000451244	17	N	173	202
Q8K124	Infl	TLSEK	LKVSWENPSPEKPSAPESAQLSSSETPEATPR	ESKKP	3		1146.234269	3435.679406	0.002080925	1	N	270	302
Q8K1B8	Infl	QLTPR	ILEAHQNVAQLSLTEAQLR	FIQAW	2		1067.584906	2133.154213	0.000451244	4	N	521	540
Q8K1B8	Infl	YHINK	LTLSGDVGELASGDLGLDDLDAALNNLEVK	LKGSA	3		1009.850984	3026.529553	0.000451244	17	N	303	333
Q8K1B8	Infl	SWELR	VFVGEEDPEAQSVTLR	VTGES	2		888.4446701	1774.87374	0.000451244	27	N	19	35
Q8K1B8	Infl	LSYYK	SQDEAPGDPTQQLNLKGCEVVPDVNVSGQK	FCIKL	3	C18:+57.021	1070.517857	3208.53017	0.000451244	6	N	385	415
Q8K1B8	Infl	LSLQR	AGGSNGGSGNKPQGPEAPAEGLNPYGLVAPR	FQRKF	3		973.8168313	2918.427094	0.000451244	9	N	477	508
Q8K1B8	Infl	LSYYK	SQDEAPGDPTQQLNLK	GCEVV	2		870.9241018	1739.832604	0.000451244	12	N	385	401
Q8K1B8	Infl	VLWLR	FKYYSFFDLDPK	TDPVR	3		523.9261761	1568.755128	0.001654178	1	N	250	262
Q8K1B8	Infl	VAIEF	DEHINVAFSCVSASCR	IVHEY	2	C10:+57.021,C15:+57.021	926.4093188	1850.803038	0.000622848	2	N	611	627
Q8K1B8	Infl	STRER	ARGEELDEDLFLQLTGGHEAF	-	2		1174.064201	2346.112802	0.000698008	2	N	644	665
Q8K1B8	Infl	NKLTL	SGDVGELASGDLGLDDLDAALNNLEVK	LKGSA	3		900.7790488	2699.313746	0.000451244	2	N	306	333
Q8K1B8	Infl	HDLTK	VVLAGGVAPTLF	RGMPA	2		572.342771	1142.669942	0.001162105	2	N	166	178
Q8K1B8	Infl	ASKGR	TMADSSYASEVQAILAFLSLQR	AGGSN	2		1201.107555	2400.199509	0.000451244	3	N	455	477
Q8K1B8	Infl	KFCIK	LLVPSPEGMSEIYLR	CQDEQ	2		852.4559955	1702.896391	0.0025889	1	N	419	434
Q8K1B8	Infl	RERAR	GEELDEDLFLQLTGGHEAF	-	2		1060.495088	2118.974577	0.000451244	5	N	646	665
Q8K1M6	Infl	ETFGR	TLESVDPLGGLNTIDILTAIR	NATGP	2		1106.115705	2210.21581	0.000451244	8	N	382	403
Q8K1M6	Infl	PVINK	LQDVFNTVGADIIQLPQIVVVGTQSSGK	SSVLE	3		976.2015117	2925.581135	0.000451244	6	N	10	38
Q8K1M6	Infl	LRFPK	LHDAIVEVVTCLLR	KRLPV	3	C11:+57.021	546.6399986	1636.896596	0.001763695	1	N	465	479
Q8K1T1	Infl	YMNYR	SVDQDSQPVYCNLESLGR	-	2	C11:+57.021	1033.976309	2065.937017	0.000823681	1	N	279	297
Q8K1X4	Infl	SRIVR	NALLQQTQPLDSSGEQTVTTLYTNWYLESLLR	QASSG	3		1228.292006	3681.852619	0.000451244	10	N	767	799
Q8K1X4	Infl	LAGVK	AYISFIQSLAQFLGADASR	IVRNA	2		1029.536894	2057.058187	0.000451244	3	N	745	764
Q8K1X4	Infl	GVKAY	ISFIQSLAQFLGADASR	IVRNA	3		608.6603816	1822.957745	0.002453667	1	N	747	764
Q8K1X4	Infl	DTDIK	VTLSVFELACAAGVSCDIDPALVAAIANLK	ADNSS	3	C10:+57.021,C16:+57.021	1030.206972	3087.597516	0.001699387	1	N	954	984
Q8K296	Infl	NEKYK	LCGSYPQELIVPAWITDKELESVAGFR	SWKRI	3	C2:+57.021	1026.858714	3077.552743	0.000451244	8	N	186	213
Q8K296	Infl	SVLHR	TSSPGNTLSLLQAPCALPLDK	CRQGI	2	C15:+57.021	1092.072752	2182.129903	0.002981883	2	N	898	919
Q8K296	Infl	PVDAK	VGLGISQSSSLLPSQVPFETR	GPHIN	2		1101.592397	2201.169194	0.000823681	2	N	815	836
Q8K2B3	Infl	HGANR	LGANSLLDLVVFGR	ACALS	2		737.425355	1472.83511	0.000451244	3	N	451	465
Q8K2B3	Infl	AMVTR	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	GEGGI	3	C5:+57.021,C23:+57.021,C29:+57.021	1122.861716	3365.561747	0.000637154	8	N	282	312
Q8K2K6	Infl	DNFPK	SSSADFGTFSTSQSHQTASTVSK	VSTNK	3		783.3599364	2347.056409	0.000451244	3	N	290	313
Q8K2K6	Infl	VSTNK	AGLQTADKYAALANLDNIFSAGQGGDQGSGFGTTGK	APVGS	3		1167.901401	3500.680803	0.000451244	9	N	318	354
Q8K2Z4	Infl	SICEK	ELLDGNQVLAAFVPLLLK	VCNNP	2		977.0751233	1952.134647	0.000451244	7	N	992	1010

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8K2Z4	Infl	VLVCK	NAIQLLASFLANNPFSCK	LSDID	3	C17:+57.021	670.0159053	2007.024316	0.000823681	5	N	422	440
Q8K310	Infl	PDEYR	IGPYQPNVPVGIDYVIPK	TGFYC	2		985.0438231	1968.072046	0.000451244	5	N	779	797
Q8K310	Infl	GKNLR	YQLLQLVEPFGVISNHLILNK	INEAF	3		813.4655714	2437.373314	0.001162105	4	N	412	433
Q8K310	Infl	SSQHR	GDTDQASNILASFGLSAR	DLDEL	2		911.950651	1821.885702	0.000451244	7	N	102	120
Q8K352	Infl	VDIPR	DSGCFEGSESGRDEAELAGTEEQLQGLSLSGAP	-	3	C4:+57.021	1128.499079	3382.473837	0.000622848	2	N	347	380
Q8K352	Infl	CGRAR	VHTDFTPSPYDHDSLK	LQKGD	3		620.2922464	1857.853339	0.000451244	9	N	179	195
Q8K352	Infl	ELLER	IGLEEHTSTLLLNGYQTLEDFKELR	ETHLN	3		973.8419834	2918.50255	0.000451244	7	N	263	288
Q8K352	Infl	LKLQK	GDVIQIVEKPPVGTWLGLLNGK	LGSFK	3		778.4462883	2332.315465	0.000851441	2	N	198	220
Q8K352	Infl	CGRAR	VHTDFTPSPYDHDSLKLQK	GDVIQ	3		743.371448	2227.090944	0.002884417	1	N	179	198
Q8K352	Infl	QHRAK	LLTAAELLLDYDTGSEEAEEGAESSQEPVAHTVSEPK	VDIPR	3		1305.955565	3914.843296	0.000451244	1	N	305	342
Q8K3K8	Infl	LRAEK	ADLLGIVSELQLK	LNSGG	2		699.9142888	1397.812978	0.000451244	3	N	164	177
Q8K3K8	Infl	EKVDK	MLLQELSEKLELAEQALASK	QLQMD	3		748.7438944	2243.208283	0.0025889	1	N	423	443
Q8K426	Infl	EKKVK	ELLANRDDCPSTVTK	TFSCT	2	C9:+57.021	859.9228163	1717.830033	0.000451244	41	N	42	57
Q8K426	Infl	STVTK	TFSCTSITASGR	LASCP	2	C4:+57.021	644.3038168	1286.592034	0.000451244	6	N	57	69
Q8K426	Infl	VPVNT	EGTLESIVEKK	VKELL	2		616.8407895	1231.665979	0.000823681	2	N	29	40
Q8K426	Infl	VPVNT	EGTLESIVEK	KVKEL	2		552.7933079	1103.571016	0.002080925	2	N	29	39
Q8K482	Infl	VLFNK	VLVNDGDVYNPNTGIFTAPYDGR	YLITA	2		1249.103857	2496.192115	0.000451244	22	N	949	972
Q8K482	Infl	ISGLK	NSVQQFYSHVFQISTDLQDLVK	FQPSA	3		866.1067714	2595.296914	0.000451244	13	N	758	780
Q8K482	Infl	TCEYK	LVGLQQQCDDYGSSYLGVIELIGEK	EASLK	3	C8:+57.021	928.7972321	2783.368296	0.000662267	1	N	352	377
Q8K482	Infl	NVTEK	NAEEHCFYIEETLR	GTING	2	C6:+57.021	905.9071662	1809.798732	0.000622848	1	N	467	481
Q8K4I3	Infl	GSVEK	YCLEPQTEADCIDNINDFLK	GCATL	2	C2:+57.021,C11:+57.021	1229.548749	2457.081898	0.000451244	13	N	55	75
Q8K4I3	Infl	NDFLK	GCATLQVEVFEPDDLYSGANFSK	VLNTL	2	C2:+57.021	1274.089327	2546.163054	0.000451244	12	N	75	98
Q8K4L3	Infl	KTESK	NALTVAAEDSGVQTR	GAFEE	2		766.3896978	1530.763796	0.000451244	12	N	910	925
Q8K4L3	Infl	KDFWK	LLGGQTSYQSAGDPKEDELYETAIIETNCVYR	LTDDK	3	C29:+57.021	1207.573919	3619.698358	0.000451244	16	N	1491	1523
Q8K4L3	Infl	HSIPR	SPVELEEDFDVIFDPYAPK	LTSSV	2		1105.53114	2209.046679	0.000451244	8	N	1277	1296
Q8K4L3	Infl	KFSLK	EFGETTSEQTEVAAR	KASVQ	2		827.8819026	1653.748205	0.000451244	4	N	1013	1028
Q8K4L3	Infl	GVQTR	GAFEEEEEPSYPILGR	VREGD	2		911.9288529	1821.842106	0.000451244	5	N	925	941
Q8K4L3	Infl	FQLAK	HLWNGTFDYENCDINPLDPGECNPLIPR	KGQGR	3	C12:+57.021,C22:+57.021	1119.508373	3355.501718	0.000451244	2	N	1580	1608
Q8K4Z5	Infl	QLPQK	VQAQVIQETIVPKEPPPEFEFIADPPSISAFDLDVVK	LTAQF	3		1365.052705	4092.134714	0.001943752	1	N	131	168
Q8K4Z5	Infl	DRSIR	EKQSDDEVYAPGLDIESSLK	QLAER	2		1112.037317	2222.059035	0.001162105	3	N	445	465
Q8K4Z5	Infl	SIREK	QSDDEVYAPGLDIESSLK	QLAER	2		983.4685392	1964.921478	0.001654178	2	N	447	465
Q8K4Z5	Infl	TIVPK	EPPPEFEFIADPPSISAFDLDVVK	LTAQF	3		887.1112996	2658.310499	0.000622848	2	N	144	168
Q8K4Z5	Infl	QLPQK	VQAQVIQETIVPK	EPPPE	2		726.9251879	1451.834776	0.000451244	2	N	131	144
Q8K4Z5	Infl	INNPK	FNFLNPNDPYHAYYR	HKVSE	3		644.3010762	1929.879829	0.00307782	1	N	80	95
Q8K558	Infl	GQGSA	DSHPEVLQAPVGSSILVQCHYR	LQDVR	2	C19:+57.021	1246.621463	2491.227326	0.000451244	5	N	20	42
Q8K558	Infl	VRALK	VWCQFLQEGCHPLVTSAVDR	RAPGN	3	C3:+57.021,C10:+57.021	801.3843973	2401.129792	0.001162105	2	N	50	70
Q8K558	Infl	GDKGK	IASCEPVQDPPNSQTPPSK	-	2	C4:+57.021	1026.489052	2050.962504	0.000622848	2	N	298	317
Q8K558	Infl	QTLHR	VSLLVLPPVPGPR	EGEEA	2		672.4246267	1342.833653	0.001871652	2	N	118	131
Q8QZT1	Infl	KPLAR	IAAFADAAVDPIDFPLAPAYAVPK	VLKYA	2		1222.149548	2442.283496	0.000622848	5	N	308	332
Q8QZT1	Infl	RIAAF	ADAAVDPIDFPLAPAYAVPK	VLKYA	2		1021.036195	2040.05679	0.000451244	4	N	312	332
Q8QZT1	Infl	QAPTR	QATLGAGLPISTPCTTVNK	VCASG	2	C14:+57.021	965.009423	1928.003246	0.001395409	2	N	102	121
Q8QZW8	Infl	KLFFR	ELPQPLVPALLLPDFRDALELSEPEQCLSK	IQKLI	3	C27:+57.021	1139.937693	3416.789679	0.000451244	9	N	362	392
Q8QZW8	Infl	ETLTR	DSSALQPQEWLDPQGLPSLSQSVPWLAL	SEQPG	3		1021.521021	3061.539664	0.000622848	4	N	9	37
Q8QZW8	Infl	KLFFR	ELPQPLVPALLLPDFR	DALEL	2		909.5303516	1817.045103	0.000451244	12	N	362	378
Q8QZW8	Infl	GQEGK	LDLDSAEWDDIHVVTGALK	LFFRE	3		699.6886656	2096.042597	0.000637154	2	N	339	358
Q8QZW8	Infl	LPDFR	DALELSEPEQCLSK	IQKLI	2	C11:+57.021	809.8853681	1617.755136	0.000622848	2	N	378	392
Q8QZY1	Infl	LQQLK	VFSDEVQQQAQLSTIR	SFLKL	2		924.9766688	1847.937738	0.000451244	16	N	445	461
Q8QZY1	Infl	LRMQK	GDPQVYEELFSYACPK	FLSPV	2	C14:+57.021	951.9328497	1901.850099	0.000451244	13	N	403	419
Q8QZY1	Infl	MPVAK	LAGFLDLTEQEFR	IQLLV	2		769.8966274	1537.777655	0.000979378	1	N	474	487
Q8QZY1	Infl	RSNPK	VWNVHSVLNVLHSLVDK	SNINR	3		653.6990592	1958.073778	0.000622848	8	N	220	237
Q8QZY1	Infl	ERFFK	NTPWPEAEAIAPQVGNDAVFLILYK	ELYYR	3		919.4818383	2755.422115	0.000451244	9	N	108	133
Q8QZY1	Infl	SNINR	QLEVYTSGGDPESVAGEYGR	HSLYK	2		1057.487795	2112.959989	0.001463592	1	N	242	262
Q8QZY9	Infl	PISER	NQDATVYVGGLDEK	VSEPL	2		754.8655242	1507.715448	0.000823681	4	N	9	23
Q8QZY9	Infl	MPKDR	VTGQHQGYGFVEFLSEEDADYAIK	IMNMI	3		901.7578079	2702.250024	0.000451244	8	N	48	72
Q8QZY9	Infl	SAHNK	NLDVGANIFIGNLDPEIDEK	LLYDT	2		1093.552938	2185.090275	0.000451244	4	N	94	114
Q8R016	Infl	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLR	RATVQ	3	C23:+57.021	947.1521207	2838.432962	0.000451244	11	N	17	42
Q8R016	Infl	ICLRR	ATVQGAQHVFQHVVPQEGKPVTNQK	SSGRC	4		682.6141108	2726.425243	0.000451244	1	N	43	68
Q8R050	Infl	AAFSR	QLNVNAKPFVPNVHAAEFVPSFLR	GPAQP	3		898.8225292	2693.444188	0.000823681	2	N	67	91
Q8R050	Infl	NLKIR	LKGIEEEEILPGFILCDLNNLCHSGR	TFDAQ	4	C16:+57.021,C22:+57.021	757.3825997	3025.499199	0.000622848	2	N	502	528
Q8R050	Infl	KIRLK	GIEEEEILPGFILCDLNNLCHSGR	TFDAQ	3	C14:+57.021,C20:+57.021	929.1145239	2784.320172	0.000451244	5	N	504	528
Q8R050	Infl	GANLK	EQSDFCPWYIGLPFIPYLDNLPNFNR	SVDGP	3	C6:+57.021	1072.515059	3214.521777	0.001943752	1	N	407	433
Q8R050	Infl	GANLK	EQSDFCPWYIGLPFIPY	LDNLP	2	C6:+57.021	1066.495617	2130.975634	0.000823681	7	N	407	424
Q8R081	Infl	LNVFK	NDQDTWDYTNPNLSGQGDPGSNPNKR	QRQPP	3		964.0928009	2889.255003	0.000451244	51	N	274	300
Q8R081	Infl	MNCDR	VFNVFCLYGNVEK	VKFMK	2	C6:+57.021	794.8953418	1587.775084	0.000451244	12	N	395	408
Q8R081	Infl	AAKNR	IQHPSNVLHFFNAPLEVTEENFFEICDELGVK	RPTSV	3	C26:+57.021	1258.282411	3771.823833	0.001699387	2	N	492	524

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R081	Infl	VVHIR	GLIDGVVEADLVEALQEFGPISYVVVMPK	KRQAL	3		1029.882792	3086.624975	0.000698008	5	N	104	133
Q8R081	Infl	VVHIR	GLIDGVVEADLVEALQEFGPISY	VVVMP	2		1217.62356	2433.23152	0.000823681	15	N	104	127
Q8R081	Infl	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	C13:+57.021	1463.369496	4387.085087	0.000451244	22	N	135	175
Q8R081	Infl	SDDSR	SVNSVLLFTILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C26:+57.021,C29:+57.021	1290.005847	3866.994141	0.000622848	3	N	186	220
Q8R081	Infl	SVLLF	TILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C18:+57.021,C21:+57.021	1003.512395	3007.513786	0.000451244	10	N	194	220
Q8R081	Infl	NSVLL	FTILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C19:+57.021,C22:+57.021	1052.5352	3154.5822	0.000451244	5	N	193	220
Q8R081	Infl	AQRAK	ASLNGADIYSGCCTLK	IEYAK	2	C12:+57.021,C13:+57.021	865.3978884	1728.780177	0.000451244	11	N	245	261
Q8R0G9	Infl	LPQEK	IVFDTQGDGILGAGSCAGVPILFSR	NSGLV	2	C16:+57.021	1275.654972	2549.294343	0.001162105	4	N	440	465
Q8R0G9	Infl	SVTPR	ENVSLLAEDLEESLTSSVGGR	GSESM	2		1103.048216	2204.080833	0.000622848	3	N	475	496
Q8R0G9	Infl	YLQKR	SELLSPLLTLGQYPWAASLAEK	YCDFD	2		1194.147005	2386.278411	0.000451244	4	N	842	864
Q8R0G9	Infl	NHHSR	LPDLVNSAILLALNKR	ECEVP	3		584.0248837	1749.051251	0.001763695	1	N	658	674
Q8R0G9	Infl	QKLIK	DGIQLSEYLPEVTDLLR	AEQLG	2		981.0154596	1960.015319	0.000451244	4	N	1109	1126
Q8R0G9	Infl	EKMCR	FLTAVQGGSFILSSVGSQLVR	LIPES	3		722.7359501	2165.18445	0.002663018	1	N	209	230
Q8R0H9	Infl	PTLFR	LASDTEDNDEALAEILQANDNLTQVINLYK	QLVRG	3		1111.883124	3332.625973	0.000451244	25	N	264	294
Q8R0H9	Infl	RPTLF	RLASDTEDNDEALAEILQANDNLTQVINLYK	QLVRG	3		1163.916828	3488.727084	0.000451244	1	N	263	294
Q8R0T6	Infl	RSAVR	LAITVLDIGAGNVFK	GPKLL	2		765.948663	1529.881726	0.000451244	13	N	147	162
Q8R0T6	Infl	QCFTK	CGQSEHSPCDVGNLQR	YWLNY	2	C1:+39.994,C9:+57.021	913.8807	1825.7458	0.002453667	1	N	52	68
Q8R146	Infl	PPAGK	EQSVSWVSLEEAEPIPDIHWGIR	VLHPP	3		893.113926	2676.318378	0.000451244	6	N	443	466
Q8R146	Infl	DIVPR	QLGESFSGIYCSLLPLGCWSADSQR	VVFDS	3	C11:+57.021,C18:+57.021	944.4426406	2830.304522	0.002080925	3	N	350	375
Q8R180	Infl	SASYK	YSEEANRIEECEQAER	LGAVD	2	C11:+57.021	1006.934641	2011.853681	0.000622848	3	N	119	135
Q8R180	Infl	EQAER	LGAVDESLSEETQK	AVLQW	2		753.3706394	1504.725679	0.000451244	3	N	135	149
Q8R180	Infl	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	C1:+39.994,C3:+57.021,C12:+57.021,C14:+57.021	1088.111955	3261.312466	0.000451244	1	N	34	60
Q8R180	Infl	LQWTK	HDDSSDSFCEIDDIQSPDAEYVDLLLNPER	YTGYK	3	C9:+57.021	1165.511096	3493.509888	0.000451244	12	N	156	186
Q8R180	Infl	DAENK	ALLLEILHEIK	SFPLH	3		431.2715066	1290.79112	0.001699387	2	N	337	348
Q8R1B4	Infl	VVMHR	TEPTAQQNLALQLAEK	LGSLV	2		877.9683124	1753.921025	0.000451244	4	N	844	860
Q8R1B4	Infl	RDVTK	CLEEFELLGK	AYGKA	2	[0:-17.027,C1:+57.021	610.7970792	1219.578558	0.001591523	6	N	78	88
Q8R1B4	Infl	RFYIR	ILADLEDYLNELWEDKEGK	KKMNK	2		1147.065878	2292.116156	0.00091018	2	N	108	127
Q8R1B4	Infl	KMNGK	VWDLFPEADKVR	TMLVR	3		492.2616702	1473.761611	0.000451244	3	N	762	774
Q8R1B4	Infl	QSSGR	AKELLGQGLLLR	SLQER	3		437.6105223	1309.808167	0.0025889	1	N	639	651
Q8R1B4	Infl	DRKSK	RLDEEEEDNEGGEWER	VRGGV	2		996.4148266	1990.814053	0.001162105	2	N	285	301
Q8R1G6	Infl	LQLDR	SQTASPGQTNGEGSLEVLATR	FQGSL	2		1052.019793	2102.023987	0.001162105	2	N	82	103
Q8R1G6	Infl	SSSFR	LLQEALEAEERGGTPAFVPSSLSSQASLPTSR	ALATP	3		1110.239354	3327.694662	0.001329271	1	N	240	272
Q8R1Q8	Infl	SLLSK	KTGSPGGPGVGGSPGGGAAGASPSLPPSAK	KSGQK	3		820.7546207	2459.240462	0.002519933	2	N	454	484
Q8R1Q8	Infl	QKLIR	DFQEYVEPGEDFPASPQR	RTTGA	2		1055.97178	2109.927961	0.000451244	4	N	192	210
Q8R1Q8	Infl	SPQRR	TTGAQEDRGDSVVLPLGADTLTHNLGLPVLVVCTK	CDAIS	3	C33:+57.021	1216.308849	3645.903146	0.002145581	1	N	211	246
Q8R1Q8	Infl	DDQTR	CNVWILDGDLYHK	GLLKF	3	C1:+57.021	544.9331821	1631.776146	0.001463592	2	N	116	129
Q8R2S8	Infl	VTCPR	GATHCYKGDIALQGGGLTTR	VSIQG	2	C5:+57.021	1038.518478	2075.021356	0.000451244	6	N	725	745
Q8R2S8	Infl	DVSER	CSPPSETTELSCYR	GVMFE	2	C1:+57.021,C12:+57.021	843.858596	1685.701592	0.000451244	18	N	579	593
Q8R2S8	Infl	VTEHR	TGPGLSVTSYTR	VCRKK	2		619.822931	1237.630262	0.000622848	3	N	468	480
Q8R2S8	Infl	LTRHR	TGPGISIVSYVHVCR	DRDFC	2	C14:+57.021	822.9302473	1643.844895	0.000451244	3	N	279	294
Q8R2S8	Infl	PGSLR	CPLCLSNDSCENAPEQVCPVGSTHCYDGVLR	LRGDG	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1198.843759	3593.507877	0.000451244	13	N	133	164
Q8R2S8	Infl	TLRCR	HCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	3	C2:+57.021,C8:+57.021,C16:+57.021,C23:+57.021	1118.177332	3351.508597	0.000451244	40	N	323	354
Q8R2S8	Infl	FLGSK	GCSSPGAQDNIGVSIFSR	LPGML	2	C2:+57.021	926.4366222	1850.857644	0.000451244	16	N	643	661
Q8R2S8	Infl	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLRG	GGIIS	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1281.221118	3840.639954	0.000451244	9	N	510	544
Q8R2S8	Infl	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1262.213963	3783.61849	0.000451244	64	N	510	543
Q8R2S8	Infl	HGTLK	TIQDISKLPLQWTAGQK	ICNVG	2		964.0365294	1926.057459	0.000451244	7	N	408	425
Q8R2S8	Infl	VNSTK	ILEELPTPTVPGSLR	CPLCL	2		811.4621346	1620.908669	0.001162105	3	N	118	133
Q8R2S8	Infl	VHVCR	DRDFCNDLSTTDPLWTPPPDTELGTLR	CRHCL	3	C5:+57.021	1044.82451	3131.450129	0.000451244	36	N	294	321
Q8R2S8	Infl	VCRKK	DFCNDLSTTAPLWAPPPVTAPGTTR	CPLCF	2	C3:+57.021	1343.152793	2684.289986	0.000451244	18	N	485	510
Q8R2S8	Infl	GAGEK	TCEVSEGCQDLIMLLYNGPK	VNLVI	3	C2:+57.021,C8:+57.021	776.3622708	2326.063412	0.000451244	6	N	48	68
Q8R2S8	Infl	EEPVK	WTAPGSQVCAPDEICQETLLLIDVGQK	SAFLG	3	C9:+57.021,C15:+57.021	1010.163543	3027.46723	0.000451244	9	N	609	636
Q8R2S8	Infl	LGTLR	CRHCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	4	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	917.9177735	3667.639894	0.000451244	1	N	321	354
Q8R2S8	Infl	PVDVR	EDCGLQLDALK	CQHGT	2	C3:+57.021	631.3085679	1260.601536	0.000451244	11	N	390	401
Q8R2S8	Infl	SERCS	PPSETTELSCYR	GVMFE	2	C10:+57.021	720.327489	1438.639378	0.000451244	8	N	581	593
Q8R2S8	Infl	QDISK	LPLQWTAGQK	ICNVG	2		571.3223699	1140.62914	0.002813207	1	N	415	425
Q8R2S8	Infl	CPLCF	SEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C5:+57.021,C13:+57.021,C20:+57.021	1036.458759	3106.352877	0.000735798	3	N	515	543
Q8R2Y8	Infl	EPGSR	TVLGIGPGPVELIDEVTGHLK	LY-	3		715.4040891	2143.188867	0.000451244	4	N	158	179
Q8R2Y8	Infl	KVVVK	APDEDTLIQLLTHAK	TLGLT	3		555.6338324	1663.878097	0.000451244	2	N	121	136

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R307	Infl	QFIGR	AVEDTEAQGFAGLFAAYTDHPPPFR	EFPSN	3		903.0982759	2706.271428	0.0025889	1	N	234	259
Q8R307	Infl	KPTER	TQATLLTTWLTELYLSR	LGALQ	2		1005.54947	2009.083339	0.001352548	1	N	485	502
Q8R326	Infl	ALTVK	NLSPVVSNELLEQAFSQFGPVEK	AVVVV	2		1266.653183	2531.290766	0.000451244	1	N	160	183
Q8R326	Infl	NMNNR	GTIPGPPMGPGPAMGPEGAANMGTPMIPDNGAVHNDR	FPQGP	4	M14:+15.995	900.1645412	3596.626965	0.002296037	1	N	429	466
Q8R460	Infl	HISGR	ETPDFGEVFDLDQQVWIFR	NQALV	2		1171.06093	2340.10626	0.000451244	7	N	14	33
Q8R460	Infl	FYHTR	TGGTSTFESVAFPGHYIASSK	TGNPI	2		1072.518898	2143.022196	0.000451244	5	N	118	139
Q8R4R6	Infl	VMEMR	SPLLAGGSPPQPVVPAHKDK	SGAPP	3		665.7061023	1994.094907	0.002374549	1	N	65	85
Q8R4R6	Infl	APPVR	SIYDDISSPGLGSTPLTSR	RQANI	2		983.4923487	1964.969097	0.000451244	10	N	92	111
Q8R550	Infl	SNFIK	ELSGESDELGISQDEQLSK	SRPEG	2		1032.484918	2062.954235	0.000451244	4	N	153	172
Q8R550	Infl	ELELK	VGDIIEVVGEVEEGWWEGVLNGK	TGMFP	2		1257.132084	2512.248567	0.000451244	18	N	120	143
Q8R550	Infl	RRRRR	CQVAFSYLPQNDDELELK	VGDII	2	C1:+57.021	1085.01236	2168.009119	0.000622848	1	N	102	120
Q8R574	Infl	DVGGR	IAIIVDDIIDDVDSFLAAAETLKER	GAYKI	3		915.8239298	2744.448389	0.000451244	2	N	263	288
Q8R574	Infl	DVGGR	IAIIVDDIIDDVDSFLAAAETLK	ERGAY	2		1230.660143	2459.304685	0.002080925	1	N	263	286
Q8R5A3	Infl	LQIER	VFEDHENVVEVLSDWTR	DTENK	2		1037.497965	2072.980331	0.000451244	6	N	235	252
Q8R5A3	Infl	NLFEK	THCDCNVDWCLYEIYPELQIER	VFEDH	2	C3:+57.021,C5:+57.021,C10:+57.021	1457.135497	2912.255394	0.000451244	6	N	213	235
Q8R5H1	Infl	NHLKR	NDSIIVDIFHGLFK	STLVC	3		539.9598798	1616.85624	0.000622848	8	N	429	443
Q8R5H1	Infl	TQVGR	FAPQFSGYQQQDCQELLAFLLDGLHEDLNR	IRKKP	3	C13:+57.021	1184.900301	3551.677503	0.000451244	18	N	368	398
Q8R5H1	Infl	ENHLK	RNDSIIVDIFHGLFK	STLVC	3		591.9935836	1772.957351	0.000870037	1	N	428	443
Q8R5L1	Infl	SQGQK	AEEQEPELTSTPNFVVEVTK	TDGKK	2		1124.05551	2246.09542	0.000451244	12	N	152	172
Q8R5L1	Infl	TDGKK	TLVLDCHYPEDEIGHEDEAESDIFSIK	EVSFQ	3	C6:+57.021	1054.480408	3160.417825	0.000451244	36	N	177	204
Q8R5L1	Infl	FLADR	GVDNTFADELVELSTALEHQEYITFLEDLK	SFVKN	3		1147.231754	3438.671861	0.000451244	8	N	243	273
Q8R5L1	Infl	FLADR	GVDNTFADELVELSTALEHQEYITF	LEDLK	2		1421.177416	2840.339233	0.002519933	1	N	243	268
Q8R5L1	Infl	FLADR	GVDNTFADELVELSTALEHQEY	ITFLE	2		1240.577338	2479.139076	0.000451244	12	N	243	265
Q8VBT6	Infl	QALTK	QLEEGQKGQEETSGAPDLSPER	VLSLK	2		1193.062387	2384.109173	0.000622848	2	N	465	487
Q8VBT6	Infl	AMLSR	EAWTVSDREGADSLGVQGTEYGSDPGDNFPGTTGR	VWVLE	3		1210.20733	3627.598589	0.000451244	16	N	271	306
Q8VBT6	Infl	PTVER	QTQAAEELGEVTEGKVVGEEAQEVLEGLR	SGQSE	3		1033.521638	3097.541515	0.000451244	6	N	39	68
Q8VBT6	Infl	HQALR	GALDSFSAFVSYLVGDTVPTVER	QTQAA	2		1215.613527	2429.211453	0.000451244	14	N	16	39
Q8VBT6	Infl	VLSLK	EYPGPVGFAGPELEAWGNWSR	GVDRR	2		1160.045614	2318.075628	0.000451244	11	N	492	513
Q8VBT6	Infl	IVGIR	AVDTEEGPKWEAGLAPETELGK	AWCSE	2		1164.074234	2326.132869	0.000622848	2	N	644	666
Q8VBT6	Infl	LSPER	VLSLKEYPGPVGFAGPELEAWGNWSR	GVDRR	3		953.820854	2858.439162	0.000451244	3	N	487	513
Q8VBT6	Infl	SFSAF	VSYLVGDTVPTVER	QTQAA	2		767.9097348	1533.80387	0.00091018	6	N	25	39
Q8VBT6	Infl	GEAGR	GTELEETTEKQSGQEVGLVGSAEK	VSGYD	3		836.0772062	2505.208219	0.000451244	4	N	678	702
Q8VBT6	Infl	GERAR	AQGTQCPGAESEDQAMLSR	EAWTV	2	C6:+57.021	1018.444319	2034.873038	0.001591523	1	N	252	271
Q8VBT6	Infl	SQEVK	ADAEAGKEQTATEQAVEIR	AEGGQ	3		672.9997912	2015.975974	0.000451244	2	N	524	543
Q8VBT6	Infl	THRDR	SSNTAQEIWEHGEEEASSGEPLR	TCEQK	2		1272.0682	2542.1208	0.000451244	6	N	142	165
Q8VBT6	Infl	VTEGK	VVGEEAQEVLEGLR	SGQSE	2		764.4048166	1526.794033	0.000451244	7	N	54	68
Q8VBT6	Infl	EETRR	CQEGSLAGEQTWGWR	ADSSA	2	C1:+57.021	882.8918504	1763.768101	0.000637154	1	N	83	98
Q8VBV7	Infl	ATRRR	AFALVSQAYTSIIADDFAAFVGLPVEEAVK	GVLEQ	3		1048.216939	3141.627417	0.002453667	1	N	116	146
Q8VBV7	Infl	VSLNR	FIPLSEPAPVPPIPNEQQLAR	LTDYV	2		1157.134232	2312.252864	0.000451244	8	N	178	199
Q8VBV7	Infl	VSQAY	TSIIADDFAAFVGLPVEEAVK	GVLEQ	2		1096.578424	2191.141248	0.000451244	12	N	125	146
Q8VC88	Infl	EELQR	CLTQSGISGTYAPFSLETCR	IMIAM	2	[0:-	1116.008837	2230.002075	0.0007646	1	N	78	98
Q8VC88	Infl	SKNGR	IFFDDYVACCVK	LRALT	2	C9:+57.021,C10:+57.021	768.8467717	1535.677943	0.000451244	1	N	175	187
Q8VC88	Infl	FNEFK	ELWAALNAWK	QNFMT	2		601.3223699	1200.62914	0.000451244	5	N	118	128
Q8VC88	Infl	MWTYF	TAVAGQDGEVDAEELQR	CLTQS	2		894.424466	1786.833332	0.000451244	16	N	61	78
Q8VC88	Infl	SMWTY	FTAVAGQDGEVDAEELQR	CLTQS	2		967.958673	1933.901746	0.000451244	5	N	60	78
Q8VCI0	Infl	AASQS	DPTGVHCATAYWSPESK	KVEIK	2	C7:+57.021	953.4257231	1904.835846	0.001162105	2	N	36	53
Q8VCI0	Infl	KGTLY	IVEQIPTYVEYSDQTNVLR	KGYWA	2		1134.081862	2266.148125	0.000451244	6	N	376	395
Q8VCI0	Infl	TICCR	EDLNGASPSPGGCYDTK	VADIF	2	C13:+57.021	884.3784385	1766.741277	0.000451244	30	N	477	494
Q8VCI0	Infl	ASQYK	AYAISGPTVQDGLPPFNWNR	FNETL	2		1102.050699	2202.085799	0.000622848	12	N	505	525
Q8VCI5	Infl	ASQEK	FFQELFDSELASQATAEFEK	AMKEL	2		1169.050228	2336.084856	0.000622848	2	N	69	89
Q8VCI5	Infl	SVMVK	ICEQFEAETPTDSEATQR	ARFEA	2	C2:+57.021	1056.463231	2110.910862	0.000622848	2	N	227	245
Q8VCM7	Infl	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	2	C7:+57.021	1221.59184	2441.16808	0.000451244	7	N	200	221
Q8VCM7	Infl	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLR	TLEDI	3	C5:+57.021,C9:+57.021	1029.455275	3085.342424	0.000451244	7	N	39	66
Q8VCM7	Infl	GTYSK	SSTTNGFDDGIIWATWK	SRWYS	2		949.9501196	1897.884639	0.000451244	13	N	381	398
Q8VCM7	Infl	NLKQK	VAQLEAQCQEPCKDSVQIHDTTGK	DCQEI	3	C8:+57.021,C12:+57.021	914.7657833	2741.27395	0.000451244	8	N	152	176
Q8VCM7	Infl	WIQYK	EGFGHLSPTGTTEFWLGNEK	IHLIS	3		736.3521649	2206.033095	0.000451244	4	N	237	257
Q8VCM7	Infl	KELIK	AIQVYYNPDQPPKPGMIDSATQK	SKKMV	2		1281.139386	2560.263172	0.000622848	4	N	87	110
Q8VCM7	Infl	QKSKK	MVEEIVKYEALLLTHETSIR	YLQEI	3		792.0949271	2373.261381	0.000451244	6	N	113	133
Q8VCM7	Infl	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLRTLEDILFR	AENRT	3	C5:+57.021,C9:+57.021	1358.634919	4072.881356	0.000823681	2	N	39	74
Q8VCM7	Infl	NWIQY	KEGFGHLSPTGTTEFWLGNEK	IHLIS	2		1168.071829	2334.128058	0.000451244	6	N	236	257
Q8VCM7	Infl	PLKAK	QQFLVYCEIDGSGNGWTVLQKR	IDGSL	3	C7:+57.021	866.764197	2597.269191	0.000823681	1	N	200	222
Q8VCM7	Infl	ETSIR	YLQEIYNSNNQKITNLK	QKVAQ	2		1042.045083	2082.074566	0.001162105	1	N	133	150
Q8VCT3	Infl	RTLAK	DTFAATASQLHSNVVNYVQQILAPKDS	-	3		973.161716	2916.461748	0.001591523	2	N	623	650
Q8VCT3	Infl	LNKLR	VKIEPGVDPDDTYNETPYEK	GYCFV	2		1155.045142	2308.074685	0.000451244	9	N	396	416

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VCT3	Infl	GPRSR	VWAEPCLIEAAKEEYSGVIEEFLATGEK	LFGPY	3	C6:+57.021	1056.853406	3167.536818	0.000451244	15	N	248	276
Q8VCT3	Infl	VDEFK	FQSILAEDFLEFYLEYFPELK	KKGVD	2		1321.159778	2640.303957	0.000451244	3	N	446	467
Q8VCT3	Infl	TPYEK	GYCFVSYLAHLVGDQDQFDK	FLKAY	3	C3:+57.021	788.0321722	2361.073117	0.000698008	5	N	416	436
Q8VCT3	Infl	SAAAR	RPLHSAQAVDVASASSFR	AFEIL	3		633.6664181	1897.975854	0.000823681	6	N	14	32
Q8VCT3	Infl	RTLAK	DTFAATASQLHSNVVNYVQQILAPK	DS-	3		905.8087255	2714.402777	0.001654178	1	N	623	648
Q8VD04	Infl	QEIVR	LSKECVGSPDPDLEPGEAN	-	2	C5:+57.021	1007.457417	2012.899235	0.001463592	3	N	787	806
Q8VD58	Infl	DLEVK	LFESSEHINDTSNLK	TDNVE	2		867.421195	1732.82679	0.001329271	4	N	291	306
Q8VDD5	Infl	KQLKR	QLEEAEEEAQRANASR	RKLQR	3		610.9579264	1829.850379	0.000451244	10	N	1877	1893
Q8VDD5	Infl	LEKAK	QTLENERGELANEVK	ALLQG	2		865.4399191	1728.864238	0.000451244	20	N	1219	1234
Q8VDD5	Infl	ERAKR	QAQQERDELADEIANSSGK	GALAL	2		1044.993776	2087.971951	0.000451244	44	N	1697	1716
Q8VDD5	Infl	ALEAK	IAQLEEQLDNETKER	QAASK	2		908.4583088	1814.901018	0.000451244	19	N	1815	1830
Q8VDD5	Infl	ALEAK	IAQLEEQLDNETK	ERQAA	2		765.8864567	1529.757313	0.000451244	33	N	1815	1828
Q8VDD5	Infl	FQEFR	QRYEILTPNSIPK	GFMDG	3		520.2916295	1557.851488	0.000451244	3	N	718	731
Q8VDD5	Infl	EMRQK	HSQAVEELADQLEQTKR	VKATL	2		991.5010394	1980.986479	0.000451244	25	N	1193	1210
Q8VDD5	Infl	DYVQK	AQTKEQADFAIEALAK	ATYER	2		867.4575805	1732.899561	0.000451244	3	N	403	419
Q8VDD5	Infl	EFRQR	YEILTPNSIPK	GFMDG	2		637.8536999	1273.6918	0.000451244	7	N	720	731
Q8VDD5	Infl	NDRLK	KANLQIDQINTDLNLER	SHAQK	2		999.5348822	1997.054164	0.000451244	17	N	1753	1770
Q8VDD5	Infl	QLKDK	ADFCIIHY	AGKVD	2	C4:+57.021	519.7395927	1037.463585	0.001352548	4	N	565	573
Q8VDD5	Infl	KKAGK	LDPHLVLDQLR	CNGVL	2		659.8780406	1317.740481	0.000451244	5	N	682	693
Q8VDD5	Infl	TAAQK	VSHLLGINVTDFTR	GILTP	2		786.4311687	1570.846737	0.000451244	11	N	373	387
Q8VDD5	Infl	MGLLR	VISGVLQLGNIAFKK	ERNTD	2		793.9855798	1585.95556	0.000451244	4	N	341	356
Q8VDD5	Infl	DRLKK	ANLQIDQINTDLNLER	SHAQK	2		935.4874007	1868.959201	0.000451244	52	N	1754	1770
Q8VDD5	Infl	RLEAR	IAQLEEELEEEQGNTELINDR	LKKAN	2		1236.590977	2471.166354	0.000451244	104	N	1730	1751
Q8VDD5	Infl	LYVDK	NFINNPLAQADWAAK	KLVWV	2		836.9262505	1671.836901	0.000451244	12	N	14	29
Q8VDD5	Infl	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	2		1167.032241	2332.048882	0.000451244	17	N	940	959
Q8VDD5	Infl	LMAEK	LQLQEQLQAETELCAEAEELRAR	LTAKK	3	C14:+57.021	910.1242307	2727.349292	0.000451244	14	N	882	905
Q8VDD5	Infl	QAADK	YLYVDKNFINNPLAQADWAAK	KLVWV	2		1227.626771	2453.237943	0.000451244	6	N	8	29
Q8VDD5	Infl	DKVTK	LQVELDSVTGLLSQSDSK	SSKLT	2		960.0025492	1917.989498	0.000451244	107	N	1277	1295
Q8VDD5	Infl	MGLLR	VISGVLQLGNIAFK	KERNT	2		729.9380983	1457.860597	0.000451244	15	N	341	355
Q8VDD5	Infl	KTKTR	LQQELDDLLVDLDHQR	QSVSN	2		975.5005081	1948.985416	0.000451244	26	N	1417	1433
Q8VDD5	Infl	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	3		666.0162768	1995.02543	0.002981883	2	N	272	289
Q8VDD5	Infl	LKKIR	ELETQISELQEDLESER	ASRNK	2		1024.48746	2046.959321	0.000451244	17	N	1107	1124
Q8VDD5	Infl	LMAEK	LQLQEQLQAETELCAEAEELR	ARLTA	2	C14:+57.021	1251.113334	2500.211067	0.000451244	171	N	882	903
Q8VDD5	Infl	SKSSK	LTKDFSALESQLQDTQELLQEENR	QKLSL	2		1418.204497	2834.393394	0.000451244	6	N	1298	1322
Q8VDD5	Infl	LEKTK	TRLQQELDDLLVDLDHQR	QSVSN	2		1104.074903	2206.134206	0.000451244	3	N	1415	1433
Q8VDD5	Infl	SKLTK	DFSALESQLQDTQELLQEENRQK	LSLST	2		1375.167914	2748.320229	0.000451244	11	N	1301	1324
Q8VDD5	Infl	EKTRR	KLEGDSTDLSDQIAELQAQIAELK	MQLAK	2		1308.174677	2614.333754	0.000451244	4	N	1051	1075
Q8VDD5	Infl	SKLTK	DFSALESQLQDTQELLQEENR	QKLSL	2		1247.091144	2492.166688	0.000451244	90	N	1301	1322
Q8VDD5	Infl	GKFIR	INFDVNGYIVGANIETYLLEK	SRAIR	2		1193.120988	2384.226375	0.000622848	22	N	240	261
Q8VDD5	Infl	NFIDF	GLDLQPCIDLIEKPAGPPGILALLDEECWFPK	ATDKS	3	C7:+57.021,C28:+57.021	1202.286062	3603.834787	0.000451244	4	N	504	536
Q8VDD5	Infl	EKQKR	DLGEELEALKTELEDTLDSTAAQQELR	SKREQ	3		1006.498611	3016.472432	0.000451244	121	N	1135	1162
Q8VDD5	Infl	RRLQK	DLEGLSQRLEEK	VAAYD	2		708.8706096	1415.725619	0.001463592	3	N	1392	1404
Q8VDD5	Infl	MALKK	IRELETQISELQEDLESER	ASRNK	2		1159.080048	2316.144496	0.000451244	10	N	1105	1124
Q8VDD5	Infl	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	2		1009.535506	2017.055411	0.000451244	3	N	617	637
Q8VDD5	Infl	EKSKR	ALEQQVEEMKTQLEELEDELQATEDAK	LRLEV	3		1049.834895	3146.481284	0.001463592	3	N	1528	1555
Q8VDD5	Infl	DLQPC	IDLIEKPAGPPGILALLDEECWFPK	ATDKS	3	C21:+57.021	941.1667081	2820.476724	0.000451244	3	N	511	536
Q8VDD5	Infl	ENTKK	VIQYLAHVASSHK	SKKDQ	3		484.9372981	1451.788494	0.001463592	1	N	186	199
Q8VDD5	Infl	RLTAK	KQELEEICHDLEAR	VEEEE	2	C8:+57.021	885.4282658	1768.840932	0.000451244	13	N	909	923
Q8VDD5	Infl	EMRQK	HSQAVEELADQLEQTK	RVKAT	2		913.4504838	1824.885368	0.000451244	2	N	1193	1209
Q8VDD5	Infl	NHEKK	AGKLDPHLVLDQLR	CNGVL	2		787.954811	1573.894022	0.000451244	4	N	679	693
Q8VDD5	Infl	EHKRK	KVEAQLQELQVK	FSEGE	2		706.9095378	1411.803476	0.000451244	8	N	1248	1260
Q8VDD5	Infl	GEHLK	TDLLLEPYNK	YRFLS	2		603.3247752	1204.63395	0.000451244	7	N	289	299
Q8VDD5	Infl	VEEMK	TQLEELEDELQATEDAK	LRLEV	2		981.4634539	1960.911308	0.000451244	11	N	1538	1555
Q8VDD5	Infl	DLIEK	PAGPPGILALLDEECWFPK	ATDKS	2	C15:+57.021	1055.537816	2109.060033	0.000622848	3	N	517	536
Q8VDD5	Infl	DKYLY	VDKNFINNPLAQADWAAK	KLVWV	2		1008.021411	2014.027221	0.000451244	10	N	11	29
Q8VDD5	Infl	KAQTK	EQADFAIEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	7	N	407	419
Q8VDD5	Infl	QLEEE	LEEEQGNTELINDR	LKKAN	2		830.3951772	1658.774754	0.000451244	1	N	1737	1751
Q8VDD5	Infl	EAKLK	KLEEDQIIMEDQNCK	LAKEK	2	C14:+57.021	946.9403493	1891.865099	0.000451244	6	N	974	989
Q8VDD5	Infl	RKLQR	ELEDATETADAMNR	EVSSL	2		783.3415566	1564.667513	0.000451244	10	N	1898	1912
Q8VDD5	Infl	VLMIK	ALELDSNLYR	IGQSK	2		597.3121991	1192.608798	0.000451244	8	N	745	755
Q8VDD5	Infl	EKKLK	SMEAEMIQLQEELAAAER	AKRQA	2		1024.98552	2047.95544	0.000622848	1	N	1676	1694
Q8VDD5	Infl	LEEER	DLKITDVIIGF	QACCR	2		617.358618	1232.701636	0.000622848	2	N	775	786
Q8VDD5	Infl	EEYQR	EGIEWNFIDFGLDLQPCIDLIEKPAGPPGILAL	LDEEC	3	C17:+57.021	1217.632381	3649.873743	0.000451244	6	N	494	527
Q8VDD5	Infl	IQEMR	QKHSQAVEELADQLEQTK	RVKAT	2		1041.527254	2081.038908	0.000451244	2	N	1191	1209
Q8VDD5	Infl	SILKK	TLEDEAKTHEAQIQEMR	QKHSQ	2		1014.986908	2027.958216	0.000622848	1	N	1174	1191

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDD5	Infl	VPSSK	NGFEPASLKEEVGEEAIVELVENGK	KVKVN	3		896.4523845	2686.333754	0.000451244	4	N	38	63
Q8VDD5	Infl	LSLAR	ALEEAMEQKAELER	LNKQF	2		823.9068667	1645.798133	0.001264573	1	N	1483	1497
Q8VDD5	Infl	RTEKK	LKDVLLQVEDER	RNAEQ	2		728.9044524	1455.793305	0.000823681	1	N	1843	1855
Q8VDD5	Infl	LEALK	TELEDTLDSTAAQQELR	SKREQ	2		960.4637882	1918.911976	0.000451244	8	N	1145	1162
Q8VDD5	Infl	MQLAK	KEEELQAALAR	VEEEA	3		419.8986204	1256.672461	0.002519933	1	N	1080	1091
Q8VDD5	Infl	AADKY	LYVDKNFINNPLAQADWAAK	KLVWV	3		764.399338	2290.174614	0.0007646	1	N	9	29
Q8VDD5	Infl	GKFIR	INFDVNGYIVGANIETY	LLEKS	2		951.4681452	1900.92069	0.001162105	1	N	240	257
Q8VDD5	Infl	KTRRK	LEGDSTDLSDQIAELQAQIAELK	MQLAK	2		1244.127195	2486.23879	0.001162105	1	N	1052	1075
Q8VDJ3	Infl	PLPEK	AACLESAQEPAGAWSNK	IRPIK	2	C3:+57.021	895.4126157	1788.809631	0.000451244	18	N	50	67
Q8VDJ3	Infl	CEAAK	EALEALVPVTIEVEVPFDLHR	YIIGQ	3		792.7656865	2375.27366	0.002080925	1	N	964	985
Q8VDJ3	Infl	PQQIK	VATLNSEEENDPPTYK	DAFPP	2		903.9237675	1805.831935	0.000451244	1	N	25	41
Q8VDL4	Infl	IDTNR	VSLRAPQEFTTSHLESGSR	IVLNP	3		701.3595424	2101.055227	0.002296037	1	N	424	443
Q8VDL4	Infl	WSSLR	LGPAPVPVGPLSPESR	LAAAW	2		786.9413693	1571.867139	0.00091018	4	N	40	56
Q8VDL4	Infl	VEWHR	EGITFHFTPVLVCKDPVR	TVGLG	2	C13:+57.021	1058.056708	2114.097815	0.000451244	6	N	457	475
Q8VDL4	Infl	AAAER	FFSDKETFHDIAQAASEFPGAQHYVGGNAALIGQR	FAANT	3		1260.612073	3778.81282	0.000451244	11	N	131	166
Q8VDL4	Infl	KDPVR	TVGLGDAISAEGLFYSEARPD	-	2		1084.529463	2167.043325	0.000451244	10	N	475	496
Q8VDL4	Infl	LQRKR	LLEVVTAISDIPTGIPVHLELASMTNR	ELMSS	3		963.8638429	2888.568129	0.000662267	1	N	277	304
Q8VDL4	Infl	MALWR	GSACAGFLALAVGCVFLLEPELPGTALR	SLWSS	3	C4:+57.021,C14:+57.021	963.8384429	2888.491929	0.000451244	4	N	5	33
Q8VDL4	Infl	AAGAR	VAGTQACATETIDTNR	VSLRA	2	C7:+57.021	854.402248	1706.788896	0.000451244	38	N	408	424
Q8VDL4	Infl	SPESR	LAAAWDALIAQPARR	WRRVA	3		541.6428851	1621.905255	0.002212458	1	N	56	71
Q8VDL4	Infl	RVSLR	APQEFTTSHLESGSR	IVLNP	3		549.5976698	1645.769609	0.001264573	2	N	428	443
Q8VDM4	Infl	SEPFR	SFANTLVDVCAYAGSGNVLK	VQQLL	2	C10:+57.021	1043.517612	2085.019624	0.000451244	7	N	588	608
Q8VDM4	Infl	AHGER	AELATEEFLPVTPILEGFVILR	KNPNY	2		1229.186131	2456.356661	0.000698008	12	N	879	901
Q8VDM4	Infl	PTLRR	AVPLALALISVSNPR	LNILD	2		760.9621047	1519.908609	0.001763695	2	N	688	703
Q8VDM4	Infl	AHGER	AELATEEFLPVTPILEGFVILRK	NPNYD	3		862.4916747	2584.451624	0.000870037	4	N	879	902
Q8VDM4	Infl	NAYAK	VCLYLTSCVNYVPEPENSALLR	CALGV	2	C2:+57.021,C8:+57.021	1299.140608	2596.265617	0.000451244	11	N	228	250
Q8VDM4	Infl	NHLGK	GEAIEAILAALEVVSEPFR	SFANT	2		1007.546927	2013.078254	0.000451244	4	N	569	588
Q8VDM4	Infl	DTYAR	WLPLGLGLNHLGK	GEAIE	3		473.2825171	1416.824151	0.001463592	1	N	556	569
Q8VDM4	Infl	VDSAR	MNLASSFVNGFVNAAFGQDK	LLTDD	2		1059.010186	2116.004772	0.001763695	2	N	369	389
Q8VDM4	Infl	KVCLY	LTSCVNYVPEPENSALLR	CALGV	2	C4:+57.021	1031.517612	2061.019624	0.001162105	2	N	232	250
Q8VDM4	Infl	EDYIK	SGALLACGIVNSGVR	NECDP	2	C7:+57.021	737.3960403	1472.776481	0.000823681	5	N	441	456
Q8VDM6	Infl	PHVVR	IGWSLDSCSTQLGEEPFSYGYGGTGKK	STNSR	3	C8:+57.021	975.4521244	2923.332973	0.000451244	6	N	284	311
Q8VDM6	Infl	DRRGR	SPQPPAEEDEDDFDDTLVAIDTYNCDLHFK	VARDR	3	C25:+57.021	1166.172192	3495.493175	0.000451244	5	N	194	224
Q8VDM6	Infl	STNSR	FENYGDKFAENDVIGCFADFECGNDVELSFTK	NGKWM	3	C16:+57.021,C22:+57.021	1246.539955	3736.596466	0.000451244	6	N	316	348
Q8VDM6	Infl	VARDR	SSGYPLTIEGFAYLWSGAR	ASYGV	2		1038.015794	2074.015988	0.000451244	8	N	229	248
Q8VDM6	Infl	ARKKR	NYILDQTNVYGSAQR	RKMRP	2		871.4293544	1740.843109	0.000451244	8	N	501	516
Q8VDM6	Infl	GFQRK	AIVICPTDEDLKDR	TVKRT	3	C5:+57.021	548.9472684	1643.818405	0.001395409	4	N	528	542
Q8VDM6	Infl	PHVVR	IGWSLDSCSTQLGEEPFSYGYGGTGK	KSTNS	2	C8:+57.021	1398.626805	2795.23801	0.000451244	2	N	284	310
Q8VDM6	Infl	FRIQK	EALGGQALYPHVLVK	NCAVE	3		532.303758	1593.887874	0.002813207	1	N	361	376
Q8VDM6	Infl	NFGQR	AEPYCSVLPGFTFIQHLPL	SERIR	2	C5:+57.021	1095.058916	2188.102232	0.001162105	1	N	387	406
Q8VDM6	Infl	GNYNR	APQQQPPPQQPPPPQPPPQQPPPPPSYSPAR	NPPGA	3		1110.234097	3327.678892	0.001162105	5	N	693	724
Q8VDN2	Infl	KAIAK	GVGIISEGNETVEDIAAR	LNIPV	2		915.4661339	1828.916668	0.000451244	6	N	629	647
Q8VDN2	Infl	LLHGK	EQPLDEELKDAFQNAYLELGGLGER	VLGFC	3		945.4668051	2833.377015	0.000451244	6	N	526	551
Q8VDP3	Infl	KHGAR	LLLGLVGDCLVEPFWPLGTGVAR	GFLAA	2	C9:+57.021	1241.680261	2481.344922	0.000622848	8	N	385	408
Q8VDP3	Infl	GSGWR	AQLQPNPPAQLASYEFDVLISAAGGK	FVPEG	3		895.8014595	2684.380978	0.002145581	1	N	195	221
Q8VDP3	Infl	HSAFK	NTSHSSGLVSQPSGTPSAILF	LGKLQ	2		1044.024347	2086.033095	0.0025889	1	N	611	632
Q8VDP4	Infl	HHPSR	IQVSSEKEAAPDTGAEPSPEDSDPTYSSK	VLLLS	3		1008.126954	3021.357462	0.000451244	19	N	280	309
Q8VDP4	Infl	FLLGR	KEEEAVLVGGEWSPSLDGLDPQADPQVLVR	TAIRC	3		1078.549528	3232.625185	0.000451244	29	N	352	382
Q8VDP4	Infl	TYSSK	VLLLSSPGLEEFYR	CCMLF	2		811.9435776	1621.871555	0.000823681	3	N	309	323
Q8VDP4	Infl	LQYSR	AEVLDDGLPEDVLFGNLDLLPPSGK	STKPG	2		1312.179231	2622.342862	0.001463592	2	N	762	787
Q8VDP4	Infl	LPGGR	NFSGAASTSLLGPPPGLLTPPVATDLSQNAR	HLQSG	3		1017.203804	3048.588011	0.00091018	1	N	16	47
Q8VDP4	Infl	LCQQK	ATEAAPQPHEASGEAEATEQAPDVSEQADTSK	QNTET	3		1084.819072	3251.433815	0.000451244	18	N	446	478
Q8VDP4	Infl	VSSEK	EAAPDTGAEPSPEDSDPTYSSK	VLLLS	2		1125.980196	2249.944793	0.000451244	10	N	287	309
Q8VDP4	Infl	ALGQK	QGILGAQPQLIFQPHR	IPPLF	3		601.6728444	1801.995133	0.000851441	1	N	138	154
Q8VDP4	Infl	PTEHK	GLVPHNGSLINVGSLLQRAEQQD	SGRLY	2		1223.146391	2444.277182	0.001352548	1	N	799	822
Q8VDQ8	Infl	DLVRR	EHANIDAQSGSQAPNPSTTISPGKSPPPAK	EAART	4		746.8736848	2983.463539	0.001591523	2	N	347	377
Q8VDQ8	Infl	KKAYR	DVAWLGDCDQGCLALADLLGWK	KELED	2	C8:+57.021,C12:+57.021	1238.585469	2475.155338	0.000451244	7	N	316	338
Q8VDQ8	Infl	DLVRR	EHANIDAQSGSQAPNPSTTISPGK	SPPPA	3		803.0548473	2406.141142	0.000979378	2	N	347	371
Q8VDW0	Infl	ENDAK	ILNDVQDRFEVNVAELPEEIDISTYIEQSR	-	3		1178.925324	3533.752571	0.000451244	1	N	397	427
Q8VDW0	Infl	MPSVK	VSVFFGGLSIK	KDEDV	2		577.3349459	1152.654292	0.000823681	2	N	143	154
Q8VDW0	Infl	ENDAK	ILNDVQDRFEVNVAELPEEIDISTY	IEQSR	3		974.4858653	2920.434196	0.002212458	4	N	397	422
Q8VE37	Infl	ELQEK	VVQVSAGDSHTAALTEDGR	VFLWG	2		956.9721147	1911.928629	0.000451244	2	N	120	139
Q8VE37	Infl	PGLVL	TLGQGDVGQLGLGESVLER	KKPAL	2		964.5083331	1927.001066	0.000451244	10	N	38	57
Q8VE47	Infl	HFMNR	ISNGGLEEGQPVDLVLSCVDNFEAR	MAINT	3	C18:+57.021	906.7731979	2717.296194	0.000622848	1	N	161	186
Q8VE47	Infl	EYKKR	AAALPTQEAEPQEEAEVVHEDNEWGIELVSEVSEEELK	NSSGP	3		1411.999834	4232.976101	0.000451244	4	N	316	354

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VEE0	Infl	VHWLR	TQFPTLDIEVDGGVGPDTVQK	CAEAG	2		1108.55822	2215.10084	0.000451244	4	N	164	185
Q8VEE0	Infl	ASGCK	IGPSILNSDLANLGAECLR	MLDSG	2	C17:+57.021	1007.025604	2012.035609	0.000451244	16	N	6	25
Q8VEE4	Infl	STAAK	AYGASKPFGKPAGTGLLQPSGGTQSK	VVPIA	3		835.7752447	2504.302334	0.002519933	1	N	166	192
Q8VEE4	Infl	LHEAK	SENLGQGDKADYFSTVAAVVFLR	KENCM	3		829.7558501	2486.24415	0.000979378	2	N	458	481
Q8VEK3	Infl	EDHGR	GYFEYIEENKYSR	AKSPQ	2		849.3944489	1696.773298	0.000451244	6	N	231	244
Q8VEK3	Infl	ARKKR	NFILDQTNVSAAAQR	RKMCL	2		824.4266147	1646.837629	0.000451244	17	N	551	566
Q8VEK3	Infl	VITCF	ANFETDEVELSYAK	NGQDL	2		808.3784645	1614.741329	0.000451244	26	N	385	399
Q8VEK3	Infl	GVAFK	ISKEVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	3	C17:+57.021,C20:+57.021	1142.579914	3424.716343	0.000451244	1	N	409	438
Q8VEK3	Infl	FKISK	EVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	3	C14:+57.021,C17:+57.021	1033.176229	3096.505287	0.000451244	23	N	412	438
Q8VEK3	Infl	EAAGK	SSGPTSLFAVTVAPPGAR	QGQQQ	2		857.9602904	1713.904981	0.000451244	8	N	181	199
Q8VEK3	Infl	NFGQK	EKPYFPIPEDCTFIQNVPLEDRVR	GPKGP	3	C11:+57.021	988.1641378	2961.469013	0.000451244	5	N	438	462
Q8VEK3	Infl	NFGQK	EKPYFPIPEDCTFIQNVPLEDR	VRGPK	2	C11:+57.021	1354.157544	2706.299488	0.000451244	22	N	438	460
Q8VEK3	Infl	LKGIK	TCNCETEDYGEKFDENDVITCFANFETDEVELSYAK	NGQDL	3	C2:+57.021,C4:+57.021,C21:+57.021	1448.268147	4341.781041	0.000451244	18	N	363	399
Q8VEK3	Infl	DLMDR	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	SGAGL	3		994.1446196	2979.410459	0.000451244	2	N	37	68
Q8VEK3	Infl	VLKMK	GNFTLPEVAECFDEITY	VELQK	2	C11:+57.021	1002.948697	2003.881793	0.000622848	15	N	613	630
Q8VEK3	Infl	EGEDE	LGDEEEGAGDENGHGEQQSQPPAAAAQQQPSQQR	GAGKE	3		1182.190562	3543.548285	0.000451244	47	N	138	172
Q8VEK3	Infl	QGFQE	GEDELGDEEEGAGDENGHGEQQSQPPAAAAQQQPSQQR	GAGKE	3		1325.568426	3973.681878	0.000451244	4	N	134	172
Q8VEK3	Infl	LKGIK	TCNCETEDYGEKFDENDVITCF	ANFET	2	C2:+57.021,C4:+57.021,C21:+57.021	1373.532936	2745.050272	0.000823681	7	N	363	385
Q8VEK3	Infl	RTQKK	AEVEGKDLPEHAVLK	MKGNF	4		409.4746831	1633.867533	0.002727428	1	N	596	611
Q8VEK3	Infl	FQEGE	DELGDEEEGAGDENGHGEQQSQPPAAAAQQQPSQQR	GAGKE	3		1263.547074	3787.617821	0.000451244	4	N	136	172
Q8VEK3	Infl	HGRGY	FEYIEENKYSR	AKSPQ	2		739.3520527	1476.688505	0.000735798	1	N	233	244
Q8VEK3	Infl	NFGQK	EKPYFPIPEDCTF	IQNVP	2	C11:+57.021	821.8768147	1641.738029	0.002981883	1	N	438	451
Q8VEM8	Infl	FGSMK	YYALCGFGGVLSCGLTHTAVVPLDLVK	CRMQV	3	C5:+57.021,C13:+57.021	970.8348099	2909.48103	0.000451244	9	N	58	85
Q8VH51	Infl	NVYVK	CPSIAAAIAAVNALHGR	WFAGK	3	C1:+57.021	564.6388806	1690.893242	0.000451244	12	N	477	494
Q8VH51	Infl	HVTER	TDASSASSFLDSDELERTGIDLGTTGR	LQLMA	3		934.4410958	2800.299887	0.001162105	5	N	329	356
Q8VH51	Infl	KGIAY	VEFVDVSSVPLAIGLTGQR	VLGVP	2		994.0470941	1986.078588	0.000451244	14	N	198	217
Q8VH51	Infl	HVTER	TDASSASSFLDSDELER	TGIDL	2		915.4059389	1828.796278	0.000451244	7	N	329	346
Q8VHM5	Infl	VLFVR	NLATTVTEEILEK	SFSEF	2		730.8962931	1459.776986	0.000451244	8	N	346	359
Q8VHM5	Infl	GKIPR	DLYEDELVPLFEK	AGPIW	2		805.4039509	1608.792302	0.001229886	3	N	174	187
Q8VI36	Infl	TAMGK	TWHPEHFVCTHCQEEIGSR	NFFER	2	C9:+57.021,C12:+57.021	1205.526277	2409.036954	0.000451244	3	N	375	394
Q8VI36	Infl	LFSPR	CYYCNGPILDKVVTALDR	TWHPE	2	C1:+57.021,C4:+57.021	1079.027059	2156.038517	0.000622848	1	N	416	434
Q8VI36	Infl	GGCAR	AILENYISALNTLWHPECFVCR	ECFTP	2	C18:+57.021,C21:+57.021	1353.662042	2705.308485	0.000451244	4	N	481	503
Q8VI36	Infl	KQLNK	GTFKEQNDKPYCQSCFVK	LFC-	3	C12:+57.021,C15:+57.021	746.0104484	2235.007945	0.000451244	4	N	570	588
Q8VI36	Infl	TALDR	TWHPEHFFCAQCGAFFGPEGFHEKDGK	AYCRK	3	C9:+57.021,C12:+57.021	1075.136322	3222.385566	0.000451244	4	N	434	461
Q8VI36	Infl	NFFER	DGQPYCEKDYHSLFSPR	CYYCN	2	C6:+57.021	1049.968286	2097.920973	0.000451244	6	N	399	416
Q8VI36	Infl	PSGSR	YAHQQPPSPLPVYSSSAK	NSSAS	2		978.9948615	1955.974123	0.002981883	1	N	75	93
Q8VI36	Infl	RNGGR	GLEDVRPSVESLLDELESSVPSPVPAITVNQGEMSSPQR	VTSSQ	3		1383.693911	4148.058333	0.001763695	1	N	208	247
Q8VI36	Infl	TALDR	TWHPEHFFCAQCGAFFGPEGFHEK	DGKAY	4	C9:+57.021,C12:+57.021	731.568349	2922.242196	0.000622848	3	N	434	458
Q8VI36	Infl	LFSPR	CYYCNGPILDK	VVTAL	2	C1:+57.021,C4:+57.021	701.8101891	1401.604778	0.000451244	3	N	416	427
Q8VIJ6	Infl	TQRCR	LFVGNLPADITEDEFKR	LFAKY	3		655.3428296	1963.005089	0.000451244	3	N	290	307
Q8VIJ6	Infl	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEKLAQK	NPMYQ	3	C1:+39.994	1340.689133	4019.044	0.000451244	6	N	422	458
Q8VIJ6	Infl	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3	C1:+39.994	1193.930894	3578.769281	0.000451244	3	N	422	454
Q8VIJ6	Infl	NLSPY	VSNELLEEAFSQFGPIER	AVVIV	2		1033.015991	2064.016382	0.000451244	11	N	373	391
Q8VIJ6	Infl	ALSVR	NLSPYVSNELLEEAFSQFGPIER	AVVIV	2		1320.153547	2638.291495	0.000451244	17	N	368	391
Q8VIJ6	Infl	TTTPR	PVIVEPLEQLDDEDGLPEK	LAQKN	2		1068.041871	2134.068143	0.000451244	9	N	435	454
Q8VIJ6	Infl	SEGVF	LLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3		973.1855273	2916.533182	0.000451244	5	N	428	454
Q8VIJ6	Infl	TQRCR	LFVGNLPADITEDEFK	RLFAK	2		904.4597889	1806.903978	0.000851441	1	N	290	306
Q91UZ5	Infl	ASGAK	CVLTHSPTWIIDPIDGTCNFVHR	FPTVA	3	[0:-	907.7686491	2720.282547	0.001463592	1	N	91	114
Q91UZ5	Infl	RVSTK	TSAADLVTETDHRVEDLIVSELR	KRFPS	3		857.1088407	2568.303122	0.000622848	3	N	49	72
Q91V41	Infl	EAAKK	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	3		1050.857467	3149.549	0.000451244	8	N	171	201
Q91V41	Infl	LTDAR	NLTNPNTVIILIGNK	ADLEA	2		812.4755763	1622.935553	0.000451244	3	N	110	125
Q91V41	Infl	EASAK	TGENVEDAFLEAAKK	IYQNI	3		541.2743042	1620.799513	0.000451244	5	N	156	171
Q91V55	Infl	KLFGK	WSTDDVQINDISLQDYIAVK	EKYAK	2		1162.076777	2322.137954	0.000451244	18	N	22	42
Q91V55	Infl	FRNIK	TIAECLADELINAAK	GSSNS	2	C5:+57.021	816.4193781	1630.823156	0.000451244	22	N	167	182
Q91V55	Infl	IIHLL	TGENPLQVLVNAIINSGPR	EDSTR	2		996.5477926	1991.079985	0.000451244	16	N	103	122
Q91V55	Infl	IIHLL	TGENPLQVLVNAIINSGPREDSTR	IGRAG	3		860.7845799	2579.33034	0.000823681	1	N	103	127
Q91V55	Infl	KLFGK	WSTDDVQINDISL	QDYIA	2		753.3600747	1504.704549	0.0025889	1	N	22	35
Q91V92	Infl	VDMLR	NCGSFTREEADEYVDIGALNGIFVLGR	SMGFI	3	C2:+57.021	1001.482307	3001.42352	0.000451244	10	N	1028	1055
Q91V92	Infl	VFVPR	SFDELGEIIQSVYEDLVAK	GAIVP	2		1078.044414	2154.073228	0.000451244	19	N	778	797
Q91V92	Infl	YAQIR	TIAIIAEGIPEALTR	KLIKK	2		784.4568522	1566.898104	0.000735798	2	N	582	597
Q91V92	Infl	GSFTR	EEADEYVDIGALNGIFVLGR	SMGFI	2		1090.547655	2179.079711	0.000451244	16	N	1035	1055
Q91V92	Infl	ARAGK	DLVSSLTSGLLTIGDR	FGGAL	2		823.952131	1645.888662	0.000451244	7	N	908	924
Q91V92	Infl	KDFVK	QHFPATPLLDYALEVEK	ITTSK	3		657.6794418	1970.014925	0.000451244	10	N	985	1002

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91V92	Infl	PEDKK	EVLASFISGLFNFYEDLYFTYLEINPLVVTK	DGVYI	3		1215.63253	3643.874189	0.000451244	4	N	178	209
Q91V92	Infl	NIISR	TTDGVYEGVAIGGDRYPGSTF	MDHVL	2		1081.505987	2160.996375	0.000451244	13	N	666	687
Q91V92	Infl	ASVVY	SDTICDLGGVNELANYGEYSGAPSEQQTYDYAK	TILSL	3	C5:+57.021	1205.862017	3614.562652	0.000451244	13	N	288	321
Q91V92	Infl	CATMF	SSEVQFGHAGACANQASETAVAK	NQALK	2	C12:+57.021	1160.535053	2319.054507	0.000451244	3	N	742	765
Q91VC3	Infl	DVWAR	GLDVPQVSLIINYDLPNNR	ELYIH	2		1070.574007	2139.132415	0.000451244	13	N	339	358
Q91VC3	Infl	REEWK	FDTLCDLYDTLTITQAVIFCNTK	RKVDW	3	C5:+57.021,C20:+57.021	918.1120089	2751.312627	0.000451244	11	N	264	287
Q91VC3	Infl	DVWAR	GLDVPQVSLIINYDLPNNRELY	IHRIG	2		1273.169	2544.322401	0.000870037	2	N	339	361
Q91VD9	Infl	WKIIR	ALSEIAGITLPYDTLDQVR	NRLEE	2		1038.055116	2074.094632	0.000451244	10	N	624	643
Q91VD9	Infl	SELAK	LVNQEVLADPLVPPQLTIK	DFYMT	2		1044.109694	2086.203789	0.000451244	9	N	673	692
Q91VD9	Infl	PNLVR	YDDIEETNYFQQASELAK	LVNQE	2		1082.490003	2162.964406	0.001352548	2	N	655	673
Q91VE0	Infl	HWTFR	QLDEYSSSVANFLQAR	GLASG	2		914.4477441	1826.879888	0.000451244	1	N	105	121
Q91VI7	Infl	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	C1:+39.994	1078.554501	2155.093401	0.000979378	1	N	39	59
Q91VI7	Infl	SLWIK	TCSLTAASCPYFCSVLTK	SRSLL	2	C2:+57.021,C9:+57.021,C13:+57.021	1033.473039	2064.930478	0.000451244	17	N	316	334
Q91VI7	Infl	ELSLR	TNELGDGGVGLVLQGLQNPTCK	IQKLS	2	C21:+57.021	1135.57619	2269.13678	0.000451244	27	N	59	81
Q91VI7	Infl	LSSNK	LGNAGIAALCPGLLLPSCK	LRTLW	2	C10:+57.021,C18:+57.021	963.0210478	1924.026496	0.000451244	9	N	233	252
Q91VI7	Infl	CRLEK	LQLEYCNLTATSCEPLASVLR	VKADF	2	C6:+57.021,C13:+57.021	1219.606401	2437.197203	0.000451244	25	N	141	162
Q91VI7	Infl	VVASK	ASLQELDLSSNKLGNAGIAALCPGLLLPSCK	LRTLW	3	C22:+57.021,C30:+57.021	1070.900431	3209.677892	0.000451244	7	N	221	252
Q91VI7	Infl	DTVLR	ELWLGDCDVTNSGCSSLANVLLANR	SLREL	2	C7:+57.021,C14:+57.021	1382.655143	2763.294685	0.000451244	24	N	368	393
Q91VI7	Infl	LSDAR	WTELLPLIQQYEVVR	LDDCG	2		944.0228907	1886.030181	0.000451244	14	N	14	29
Q91VI7	Infl	DEGAR	LLCESLLEPGCQLESLWIK	TCSLT	2	C3:+57.021,C11:+57.021	1144.586949	2287.158298	0.000451244	14	N	297	316
Q91VI7	Infl	KQSLK	ELSLASNELKDEGAR	LLCES	2		816.4159126	1630.816225	0.000622848	9	N	282	297
Q91VI7	Infl	CKIQK	LSLQNCGLTEAGCGILPGMLR	SLSTL	2	C6:+57.021,C13:+57.021	1130.566026	2259.116451	0.001162105	1	N	84	105
Q91VI7	Infl	EVRCK	DISSAVQANPALTELSLR	TNELG	2		943.0054263	1883.995253	0.000451244	15	N	41	59
Q91VI7	Infl	DAGLK	LLCEGLQDPQCR	LEKLQ	2	C3:+57.021,C11:+57.021	744.850377	1487.685154	0.000451244	12	N	126	138
Q91VI7	Infl	CQGLK	DSACQLESLKLENCGITAANCK	DLCDV	2	C4:+57.021,C14:+57.021,C21:+57.021	1241.572001	2481.128403	0.000451244	5	N	190	212
Q91VI7	Infl	LESLK	QPSCTLQQLVLYDIYWTNEVEEQLR	ALEEE	3	C4:+57.021	1042.513495	3124.517086	0.000451244	10	N	418	443
Q91VI7	Infl	KADFK	ELVLSNNDLHEPGVR	ILCQG	2		846.4397221	1690.863844	0.000451244	12	N	168	183
Q91VI7	Infl	VVASK	ASLQELDLSSNK	LGNAG	2		652.8387781	1303.661956	0.000451244	7	N	221	233
Q91VI7	Infl	SCKLR	TLWLWECDITAEGCKDLCR	VLRAK	2	C7:+57.021,C14:+57.021,C18:+57.021	1213.550341	2425.085081	0.000451244	5	N	254	273
Q91VI7	Infl	DEGAR	LLCESLLEPGCQLESLWIKTCSLTAASCPYFCSVLTK	SRSLL	3	C3:+57.021,C11:+57.021,C21:+57.021,C28:+57.021,C32:+57.021	1445.700539	4334.078216	0.000451244	3	N	297	334
Q91VI7	Infl	SCKLR	TLWLWECDITAEGCK	DLCRV	2	C7:+57.021,C14:+57.021	941.4291886	1880.842777	0.000451244	4	N	254	269
Q91VI7	Infl	QELCK	ALSQPDTVLR	ELWLG	2		550.3094595	1098.603319	0.002296037	1	N	358	368
Q91VJ5	Infl	RGILK	HLEPEPEEEIIAEDYDDDPVDYEATRIEGLPPSWYK	VFDPS	4		1065.742365	4258.938259	0.002296037	2	N	18	54
Q91VJ5	Infl	PSWYK	VFDPSCGLPYYWNVETDLVSWLSPHDPNFVVTK	SAKKV	3	C6:+57.021	1294.622545	3880.844234	0.000998612	5	N	54	87
Q91VJ5	Infl	RNEAK	TGADTTAAGPLFQQRPYPSPGAVLR	ANAEA	3		857.7825107	2570.324132	0.001463592	1	N	226	251
Q91VJ5	Infl	RGILK	HLEPEPEEEIIAEDYDDDPVDYEATR	IEGLP	3		1030.451438	3088.330913	0.000451244	7	N	18	44
Q91VJ5	Infl	CGLPY	YWNVETDLVSWLSPHDPNFVVTK	SAKKV	3		916.1224215	2745.343865	0.002296037	2	N	64	87
Q91VR2	Infl	KDVGR	KPPTFGDASVIALELLNSGYEFDEGSIIFNQFK	SVISY	3		1216.28256	3645.824279	0.000451244	13	N	158	191
Q91VR5	Infl	LSQVR	FLVLDEADGLLSQGYSDFINR	MHNQI	2		1186.592594	2371.169588	0.000451244	14	N	365	386
Q91VR5	Infl	GVAAR	DQLSVLDNGVDIVVGTPGR	LDDLV	2		977.5161581	1953.016716	0.000851441	2	N	330	349
Q91VW3	Infl	LDGKR	IQYQLVDISQDNALRDEMR	TLAGN	3		769.7186308	2306.132492	0.000451244	4	N	32	51
Q91VW3	Infl	DYELF	VEAVEQDTLQEFLK	LA-	2		824.9255819	1647.835564	0.000451244	13	N	77	91
Q91VW3	Infl	AGNPK	ATPPQIVNGNHYCGDYELFVEAVEQDTLQEFLK	LA-	3	C13:+57.021	1275.608964	3823.803492	0.000451244	36	N	58	91
Q91VW3	Infl	AGNPK	ATPPQIVNGNHYCGDYELFVEAVEQDTLQEFLKLA	-	3	C13:+57.021	1336.98269	4007.92467	0.000622848	1	N	58	93
Q91VW3	Infl	DYELF	VEAVEQDTLQEFLKLA	-	2		916.9861708	1831.956742	0.002374549	3	N	77	93
Q91VW3	Infl	NGNHY	CGDYELFVEAVEQDTLQEFLK	LA-	2	C1:+57.021	1267.094078	2532.172556	0.000622848	2	N	70	91
Q91VW3	Infl	AGNPK	ATPPQIVNGNHYCGDYELF	VEAVE	2	C13:+57.021	1097.997044	2193.978488	0.00307782	1	N	58	77
Q91W50	Infl	DKLER	ATNIEVLSNTFQFTNEAR	EMGVI	2		1028.01124	2054.00688	0.000451244	7	N	330	348
Q91W50	Infl	GVIEK	LLTSYGFIQCSER	QARLF	2	C10:+57.021	787.3878809	1572.760162	0.001162105	1	N	32	45
Q91W90	Infl	VYVAK	VDCTADSDVCSAQGVR	GYPTL	2	C3:+57.021,C10:+57.021	870.3698592	1738.724118	0.001162105	1	N	104	120
Q91WJ8	Infl	QIAAK	IGGDAGTSLNSNDYGYGGQKRPLEDGDQPDAK	KVPPQ	3		1099.175301	3294.502504	0.000451244	4	N	40	72
Q91WJ8	Infl	QIAAK	IGGDAGTSLNSNDYGYGGQK	RPLED	2		987.4459298	1972.87626	0.000451244	8	N	40	60
Q91WK2	Infl	ELEKK	SAVADKHELLSLASSNHLGK	SLQLL	3		693.0399212	2076.096364	0.000998612	4	N	221	241
Q91WK2	Infl	SFVTR	ALLDSQFSYQHAIEESVVLIYDPIKTAQGSLSLK	AYRLT	4		941.7508015	3762.972006	0.000451244	6	N	131	165
Q91WK2	Infl	LKIIK	HYQEEGQGTEVVQGVLLGLVVEDR	LEITN	3		885.4527188	2653.334756	0.000662267	2	N	51	75
Q91WN1	Infl	DKEQK	AVYDEQGTVDEDSAGLNQDRDWDAYWR	LLFKK	3		1058.794421	3173.359862	0.000451244	9	N	75	102
Q91WN1	Infl	-M	GLLELCEQVFGTADLYQVLGVR	REASD	2	C6:+57.021	1240.646615	2479.27763	0.001871652	1	N	1	23
Q91WN1	Infl	LLFKK	ISLEDIQAFEK	TYKGS	2		646.8407895	1291.665979	0.001871652	1	N	107	118
Q91WQ3	Infl	AEVVK	QVEHPLLSGLLYPGLQALDEEYLK	VDAQF	3		909.1536102	2724.437431	0.000451244	4	N	154	178
Q91WQ3	Infl	AEVVK	QVEHPLLSGLLYPGLQALDEEYLKVDAQFGGVDQR	KIFTF	4		975.2565167	3896.994867	0.000451244	1	N	154	189
Q91WU5	Infl	LKNSR	FAPDFLFTPVDASLPAPQGR	SELET	2		1073.552544	2145.089487	0.000451244	11	N	315	335

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91WU5	Infl	FCPPR	LVTADIITVENKELEGVLGDCR	FVSAT	3	C21:+57.021	815.4285914	2443.262374	0.000637154	3	N	230	252
Q91WV0	Infl	ANDAR	ELVVNCCTEFIHLISSEANEICNK	SEKKT	3	C6:+57.021,C7:+57.021,C22:+57.021	960.4506531	2878.328559	0.000451244	8	N	36	60
Q91WV0	Infl	KSEKK	TISPEHVIQALESLGFGSYISEVKEVLQECK	TVALK	3	C30:+57.021	1164.264357	3489.769672	0.001352548	1	N	64	95
Q91X72	Infl	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDKLNAAK	SLPQP	3	C7:+57.021,C24:+57.021	1279.273544	3834.797232	0.000451244	7	N	409	444
Q91X72	Infl	KRLEK	ELGSPPGISLETIDAAFSCPGSSR	LYVSS	2	C19:+57.021	1224.589494	2447.163388	0.000451244	17	N	345	369
Q91X72	Infl	PMHSR	CSPDPGLTALLSDHR	GATYA	3	C1:+57.021	546.9353628	1637.782688	0.000451244	14	N	254	269
Q91X72	Infl	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDK	LNAAK	3	C7:+57.021,C24:+57.021	1113.50815	3337.50105	0.000451244	19	N	409	439
Q91X72	Infl	NGYPK	LFQEEFPGIPYPPDAAVECHR	GECQS	3	C19:+57.021	824.7269717	2471.157515	0.000451244	8	N	129	150
Q91X72	Infl	WLDLK	SGAQATWTEVSWPHEK	VDGAL	2		907.4293544	1812.843109	0.000451244	2	N	384	400
Q91X72	Infl	LISAR	WKNPITSVDAAFR	GPDSV	3		502.2689363	1503.783409	0.00091018	1	N	89	102
Q91X72	Infl	VECHR	GECQSEGVLFFQGNRK	WFWDF	2	C3:+57.021	928.4417075	1854.867815	0.000451244	1	N	150	166
Q91X72	Infl	LFQEE	FPGIPYPPDAAVECHR	GECQS	3	C14:+57.021	609.294891	1824.861273	0.000451244	22	N	134	150
Q91X72	Infl	LNAAK	SLPQPQKVNSILGCSQ	-	2	C14:+57.021	878.4568263	1754.898053	0.0025889	1	N	444	460
Q91XL1	Infl	LSSNR	LQALSPELLAPVPR	LRALD	2		752.4488302	1502.88206	0.000451244	25	N	96	110
Q91XL1	Infl	NRLQR	LEDSLLAPQPFLR	VLFLN	2		749.9173628	1497.819126	0.000451244	13	N	219	232
Q91YI4	Infl	TAQYK	CPVAQLEQDDQVSPSSTFCK	VYTIT	2	C1:+39.994,C19:+57.021	1140.001209	2277.986819	0.001871652	1	N	252	272
Q91YI4	Infl	HAHPF	FFTIPQNLPCSVTLQPGPEDTGKACGVDFEIR	AFCAK	3	C10:+57.021,C25:+57.021	1198.585171	3592.732112	0.000622848	6	N	116	148
Q91YI4	Infl	LIIRK	VQFAPETPGPQPSAETTR	HFLMS	2		956.9741261	1911.932652	0.000451244	18	N	171	189
Q91YI4	Infl	RLIIR	KVQFAPETPGPQPSAETTR	HFLMS	2		1021.021608	2040.027615	0.000451244	8	N	170	189
Q91YI4	Infl	NREKR	GLALDGQLKHEDTNLASSTIVK	EGANK	3		770.7486955	2309.222687	0.000451244	6	N	287	309
Q91YI4	Infl	YLGKR	DFVDHLDKVDPVDGVVLVDPDYLK	DRKVF	3		904.7976036	2711.369411	0.000451244	14	N	26	50
Q91YI4	Infl	HAHPF	FFTIPQNLPCSVTLQPGPEDTGK	ACGVD	2	C10:+57.021	1273.633705	2545.25181	0.000451244	11	N	116	139
Q91YI4	Infl	TCAFR	YGREDLDVLGLSFR	KDLFI	3		547.2866556	1638.836567	0.001463592	1	N	63	77
Q91YQ5	Infl	SHLAK	VTAEVVLVHPGGGSTSR	ASSFV	2		833.4500898	1664.88458	0.000637154	17	N	49	66
Q91YQ5	Infl	ALKMR	FVDHVFDEQVIDSLTVK	IILPE	2		996.0101773	1990.004755	0.000451244	4	N	355	372
Q91YQ5	Infl	GSTSR	ASSFVLALEPELESR	LAHLG	2		824.4335741	1646.851548	0.000451244	9	N	66	81
Q91YQ5	Infl	FGGWK	THYIVGYNLPSYEYLYNLGDQYALK	MRFVD	3		999.8276743	2996.459623	0.000451244	8	N	328	353
Q91YQ5	Infl	YIVGY	NLPSYEYLYNLGDQYALK	MRFVD	2		1082.534017	2163.052433	0.000451244	8	N	335	353
Q91YQ5	Infl	GPFSR	YDYQRQPDSGISSIR	SFKTI	3		595.6241075	1783.848922	0.000451244	3	N	264	279
Q91YR9	Infl	SQYNR	TGPCPQGPAPEVVIYQQLR	MEGFI	2	C4:+57.021	1055.541422	2109.067243	0.000451244	21	N	247	266
Q91YR9	Infl	SAFPK	GTIVAALLGWTSHSISDGNGLTK	LPVEW	2		1149.608579	2297.201557	0.000451244	7	N	81	104
Q91YR9	Infl	WTLKK	HFEGFPTDGNFELK	TTELP	2		819.3838842	1636.752168	0.000451244	8	N	11	25
Q91YR9	Infl	NFELK	TTELPPLNNGEVLLEALFLSVDPYMR	VAAKK	3		977.8444483	2930.509945	0.000451244	1	N	25	51
Q91YR9	Infl	NFELK	TTELPPLNNGEVLLEALFLSVDPY	MRVAA	3		882.1305827	2643.368348	0.001463592	1	N	25	49
Q91YT0	Infl	VFVVR	GAGAYICGEETALIESIEGK	QGKPR	2	C7:+57.021	1034.499085	2066.98257	0.000451244	3	N	199	219
Q91YT0	Infl	ELIEK	HAGGVTGGWDNLLAVIPGGSSTPLIPK	SVCET	3		872.1382945	2613.391483	0.002145581	1	N	302	329
Q91YT0	Infl	QGKPR	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	RGGTW	3	C14:+57.021,C31:+57.021	1133.919714	3398.735741	0.000622848	6	N	224	256
Q91YT0	Infl	GLIGK	NACGSDYDFDVFVVR	GAGAY	2	C3:+57.021	882.3886093	1762.761619	0.002374549	1	N	184	199
Q91YW3	Infl	ELGKK	LLAAGQLADALSQFHAAVDGDPDNYIAYYR	RATVF	3		1080.19883	3237.57309	0.000451244	23	N	46	76
Q91YX0	Infl	EIPPR	WLDLTVVEAEGQPAQVARPLSIAPVEELSEAFYY	SLRKL	3		1264.312519	3789.914157	0.000870037	4	N	504	538
Q91YX0	Infl	VQLQK	VVCEYPETGQTLELNPNFTGLFSPLTSLR	SYRTL	3	C3:+57.021	1094.883588	3281.627365	0.000451244	9	N	59	88
Q91YX0	Infl	EIPPR	WLDLTVVEAEGQPAQVARPLSIAPVEELSEAF	YYSLR	3		1155.603633	3463.787499	0.00091018	1	N	504	536
Q91YX0	Infl	KPLRL	SEVLAGGGPFPLTTEILEVPEGPPVFLSPWVSFLR	KGQRL	3		1246.666345	3736.975635	0.000979378	1	N	248	283
Q91YX0	Infl	EIPPR	WLDLTVVEAEGQPAQVAR	PLSIA	2		991.5212435	1981.026887	0.002374549	1	N	504	522
Q91Z50	Infl	MGIPY	LDAPSEAEASCAALAK	AGKVY	2	C11:+57.021	802.3855352	1602.75547	0.000451244	13	N	152	168
Q91Z50	Infl	FHLSR	VLQELGLNQEQFVDLCILLGSDYCESIR	GIGPK	3	C16:+57.021,C24:+57.021	1104.547946	3310.620437	0.000451244	2	N	211	239
Q91Z50	Infl	HGLAK	LIADVAPSAIRENDIK	SYFGR	2		862.9812228	1723.946846	0.001329271	1	N	8	24
Q91Z50	Infl	NWLHK	EAQQLFLEPEVLDPESVELK	WSEPN	2		1157.097178	2312.178756	0.000451244	16	N	277	297
Q91ZJ5	Infl	LIGVR	NENTFLDLTVQQIEHLNK	TYNTD	2		1078.553272	2155.090944	0.000451244	2	N	133	151
Q91ZJ5	Infl	IVNPK	TLDGGLNVIQLETAVGAAIK	SFENS	2		992.0602015	1982.104803	0.000451244	5	N	357	377
Q91ZJ5	Infl	IVNPK	TLDGGLNVIQLETAVGAAIKSFENSLGINVPR	SRFLP	3		1099.600334	3295.777603	0.001264573	2	N	357	389
Q91ZW3	Infl	PGKQK	EIQEPDPTYEEK	MQTDR	2		739.3388079	1476.662016	0.000622848	4	N	70	82
Q91ZW3	Infl	VFASK	ESEITDEDIDGILER	GAKKT	2		867.4079503	1732.800301	0.000451244	3	N	664	679
Q920B9	Infl	GAPYR	STCLLQPTSSALVNATEWPPFVVTLDEVELIHFER	VQFHL	3	C3:+57.021	1333.67883	3998.013091	0.000451244	9	N	812	847
Q920B9	Infl	TYALF	IGDTVLVDEDGPATILTSVK	KKVKN	2		1022.046957	2042.078314	0.000451244	12	N	402	422
Q920B9	Infl	GIFLK	NEDDEEEEEEKDEAEDLLGR	GSRAA	3		798.3302597	2391.967379	0.000662267	2	N	433	453
Q920B9	Infl	SALGR	NEGNIFPNPEATFVK	EITYR	2		838.9180912	1675.820582	0.001699387	1	N	581	596
Q920E5	Infl	SLTRR	GQICWYQKPGIGLDAINDALLLEASIYR	LLKFY	3	C4:+57.021	1059.885263	3176.63239	0.000451244	11	N	113	141
Q920E5	Infl	GKYNR	GLTVVQAFQELVEPK	KQDAE	2		829.4621346	1656.908669	0.000451244	12	N	60	75
Q920E5	Infl	SVTGK	VGTDIQDNKCSWLVVQCLLR	ASPQQ	2	C10:+57.021,C17:+57.021	1202.609278	2403.202957	0.000451244	1	N	257	277
Q920E5	Infl	VARVK	ALYEALDLQSAFFK	YEEDS	2		808.422478	1614.829356	0.000451244	25	N	302	316
Q920E5	Infl	IQDNK	CSWLVVQCLLR	ASPQQ	2	C1:+39.994,C8:+57.021	708.8597909	1415.703982	0.0025889	1	N	266	277
Q920E5	Infl	DAIAR	LKEVLEYNALGGK	YNRGL	2		717.4040883	1432.792577	0.000451244	3	N	44	57
Q920E5	Infl	SQIVK	VLTEKELGHPEIGDAIAR	LKEVL	2		974.5290685	1947.042537	0.000451244	8	N	26	44

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q920E5	Infl	EKVAR	VKALYEALDLQSAFFK	YEEDS	3		615.0053777	1841.992733	0.000451244	4	N	300	316
Q920E5	Infl	VARVK	ALYEALDLQSAFFKYEEDSYNR	LKSLI	2		1336.629905	2671.24421	0.000451244	3	N	302	324
Q920E5	Infl	SPQQR	QILEENYGQKDPEK	VARVK	2		845.9182882	1689.820976	0.000622848	1	N	283	297
Q921F2	Infl	RAVQK	TSDLIVLGLPWK	TTEQD	2		671.3929922	1340.770384	0.000451244	15	N	102	114
Q921F2	Infl	MRGVR	LVEGILHAPDAGWGNLVYVVNYPK	DNKRK	3		875.467752	2623.379856	0.000451244	14	N	55	79
Q921F2	Infl	PKPFR	AFAFVTFADDKVAQSLCGEDLIIK	GISVH	3	C17:+57.021	886.7880082	2657.340625	0.000451244	9	N	227	251
Q921F2	Infl	SEYIR	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR	YRNPV	3	C33:+57.021	1292.27772	3873.809759	0.000451244	15	N	6	42
Q921F2	Infl	VFVGR	CTEDMTAEELQQFFCQYGEVVDVFIPKPFR	AFAFV	3	C1:+39.994,C15:+57.021	1222.891234	3665.650301	0.001162105	1	N	197	227
Q921F2	Infl	ERSGR	FGGNPGGFGNQGGFGNSR	GGGAG	2		863.888188	1725.760776	0.000451244	32	N	275	293
Q921F2	Infl	AFVTF	ADDKVAQSLCGEDLIIK	GISVH	2	C10:+57.021	937.9803312	1873.945062	0.000451244	5	N	234	251
Q921F2	Infl	GLPWK	TTEQDLKDYFSTF	GEVLM	2		797.8677326	1593.719865	0.001654178	1	N	114	127
Q921F2	Infl	MRGVR	LVEGILHAPDAGWGNLVYVVNYPKDNK	RKMDE	3		994.5226966	2980.54469	0.000823681	1	N	55	82
Q921F2	Infl	MRGVR	LVEGILHAPDAGWGNLVY	VVNYP	2		962.5023224	1922.989045	0.002727428	1	N	55	73
Q921F4	Infl	VVHVR	GLCESVVEADLVEALEK	FGTIC	2	C3:+57.021	930.9668895	1859.918179	0.000451244	2	N	130	147
Q921F4	Infl	GQASK	NIIQPPSCVLHYYNVPLCVTEETFTK	LCNDH	3	C8:+57.021,C18:+57.021	1041.515917	3121.524351	0.000622848	7	N	495	521
Q921F4	Infl	VCVSK	QHSVVPSQIFELEDGTSSY	KDFAM	2		1062.000538	2121.985476	0.000451244	7	N	457	476
Q921F4	Infl	ECVTF	AADVPVYIAGQQAFFNYSTSK	RITRP	2		1139.063473	2276.111345	0.001162105	1	N	179	200
Q921G6	Infl	LGSLR	QLDVSSNELQSLPVELCSLR	SLRDL	2	C17:+57.021	1144.083848	2286.152095	0.000451244	7	N	162	182
Q921G6	Infl	HNCLK	CLNPALGNLTALTYLNLSR	NQLSS	2	C1:+57.021	1052.564897	2103.114194	0.000451244	8	N	104	123
Q921G6	Infl	VLESR	LQQPLPEDLAEALANGVLLCQLANQLRPR	SVPFI	3	C20:+57.021	1080.9226	3239.744401	0.000451244	5	N	548	577
Q921G6	Infl	ADLSR	NRFPEVPEAACQLVSLEGLSLY	HNCLK	2	C11:+57.021	1246.628422	2491.241245	0.001654178	3	N	77	99
Q921G6	Infl	EAGRR	GAALGDLVPSRPPSFSPCPAEDLFPGR	RYDGG	3	C18:+57.021	937.4695612	2809.385284	0.002145581	1	N	265	292
Q921G6	Infl	LNVRR	NQLSTLPDELGDLPLVR	LDFSC	2		940.5103444	1879.005089	0.001463592	2	N	191	208
Q921G7	Infl	GPEQR	FCPAGVYEFVPLEQGDGFR	LQINA	2	C2:+57.021	1094.51233	2187.00906	0.002884417	1	N	558	577
Q921G7	Infl	KFDLR	ASCDAQTYGIGLKELWIIDEK	KWKPG	2	C3:+57.021	1205.601873	2409.188147	0.000637154	1	N	262	283
Q921H8	Infl	GRASR	GGFKNTTPDELLSAVLTAVLQDVR	LKPEQ	3		848.7943049	2543.359515	0.000622848	4	N	53	77
Q921H8	Infl	RGGFK	NTTPDELLSAVLTAVLQDVR	LKPEQ	2		1078.084405	2154.15321	0.000451244	9	N	57	77
Q921H8	Infl	KPAFK	DGGSTTAGNSSQVSDGAAAVLLAR	RSKAE	2		1103.041257	2204.066914	0.000451244	6	N	265	289
Q921H8	Infl	AVMAR	IAQFLSGIPETVPLSTVNR	QCSSG	2		1021.568194	2041.120787	0.000622848	5	N	102	121
Q921H8	Infl	LLARR	SKAEELGLPILGVLR	SYAVV	3		532.3229297	1593.945389	0.000823681	2	N	290	305
Q921I1	Infl	VGAFK	CLKDGGGDVAFVK	HTTIF	3	[0:-17.027,C1:+57.021	450.2239231	1347.648369	0.000451244	19	N	212	225
Q921I1	Infl	VTAIR	NQQEGVCPEGSIDNSPVK	WCALS	2	C7:+57.021	979.4499266	1956.884253	0.000451244	30	N	343	361
Q921I1	Infl	TGAFR	CLVEKGDVAFVK	HQTVL	2	C1:+57.021	682.866053	1363.716506	0.001943752	1	N	542	554
Q921I1	Infl	VTAIR	NQQEGVCPEGSIDNSPVKWCALSHLER	TKCDE	3	C7:+57.021,C20:+57.021	1037.48568	3109.433639	0.000451244	10	N	343	370
Q921I1	Infl	SPLEK	AVSSFFSGSCVPCADPVAFPK	LCQLC	2	C10:+57.021,C13:+57.021	1115.519066	2229.022533	0.000451244	20	N	167	188
Q921I1	Infl	VAFPK	LCQLCPGCGCSSTQPFFGYVGAFK	CLKDG	2	C2:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	1371.102183	2740.188766	0.000451244	15	N	188	212
Q921I1	Infl	SPLGK	DLLFKDSAFGLLR	VPPRM	3		498.9492037	1493.824211	0.000622848	4	N	310	323
Q921I1	Infl	AARVK	AVLTSQETLFGGSDCTGNFCLFK	STTKD	2	C15:+57.021,C20:+57.021	1276.593491	2551.171382	0.000451244	17	N	618	641
Q921I1	Infl	TGLGR	SAGWVIPIGLLFCK	LSEPR	2	C13:+57.021	780.93427	1559.85294	0.000998612	7	N	143	157
Q921I1	Infl	VAFVK	HQTVLDNTEGKNPAEWAK	NLKQE	2		1019.503582	2036.991564	0.000451244	2	N	554	572
Q921I1	Infl	IGPLK	CAPNNKEEYNGYTGAFR	CLVEK	2	[0:-17.027,C1:+57.021	987.426029	1972.836458	0.001229886	4	N	525	542
Q921I1	Infl	LDNTR	KPVDQYEDCYLAR	IPSHA	2	C9:+57.021	828.8882451	1655.76089	0.000451244	2	N	251	264
Q921I1	Infl	AEWAK	NLKQEDFELLCPDGTR	KPVKD	2	C11:+57.021	967.9677551	1933.91991	0.000451244	7	N	572	588
Q921I1	Infl	ISEGK	IECESAETTEDCIEK	IVNGE	2	C3:+57.021,C12:+57.021	907.3770156	1812.738431	0.000451244	10	N	383	398
Q921I1	Infl	RMDYR	LYLGHNYVTAIR	NQQEG	2		710.3913152	1418.76703	0.000622848	2	N	331	343
Q921I1	Infl	AARVK	AVLTSQETLFGGSDCTGNFCLF	KSTTK	2	C15:+57.021,C20:+57.021	1212.546009	2423.076419	0.0025889	1	N	618	640
Q921M3	Infl	VAVCR	FSNTGEDWYVLVGVAK	DLILS	2		892.9468486	1783.878097	0.000451244	4	N	895	911
Q921M3	Infl	LALEK	LGAVFNQVAFPLQYTPR	KFVIH	2		961.0206823	1920.025765	0.000451244	12	N	769	786
Q921M3	Infl	DTYPR	WVTTASLLDYDTVAGADKFGNICVVR	LPPNT	2	C23:+57.021	1436.221207	2870.426814	0.000823681	1	N	1031	1057
Q921M3	Infl	SYQSR	FHLTPLSYETLEFASGFASEQCPEGIVAISTNTLR	ILALE	3	C22:+57.021	1295.972014	3884.892641	0.000451244	9	N	728	763
Q921M3	Infl	PNKQK	NVSEELDRTPPEVSK	KLEDI	2		850.42902	1698.84244	0.000823681	3	N	1191	1206
Q921M3	Infl	PRPLK	NLVLVDELDSLSPILFCQIADLANEDTPQLYVACGR	GPRSS	3	C17:+57.021,C34:+57.021	1354.678347	4061.011642	0.000451244	17	N	393	429
Q921M3	Infl	ICVVR	LPPNTNDEVDEDPTGNK	ALWDR	2		927.9217562	1853.827912	0.000451244	2	N	1057	1074
Q921M3	Infl	DTYPR	WVTTASLLDYDTVAGADK	FGNIC	2		963.47871	1924.94182	0.000451244	1	N	1031	1049
Q921M3	Infl	PRPLK	NLVLVDELDSLSPILF	CQIAD	2		893.9960072	1785.976414	0.001162105	4	N	393	409
Q921M3	Infl	SPILF	CQIADLANEDTPQLYVACGR	GPRSS	2	C1:+57.021,C18:+57.021	1147.530694	2293.045787	0.001839721	1	N	409	429
Q921M7	Infl	LSRMR	INNVPAEGENEVNNELANR	MSLFY	2		1048.50431	2094.993021	0.000451244	44	N	167	186
Q921M7	Infl	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEKEIYNQVNVVLK	DAEGI	3	C4:+57.021	1477.056695	4428.146684	0.000451244	23	N	6	44
Q921M7	Infl	KLQEK	AWGAVVPLVGK	LKKFY	2		548.8298307	1095.644061	0.000622848	1	N	78	89
Q921M7	Infl	EAALR	GLLGALTSTPYSPTQHLER	EQALA	2		1021.0398	2040.064001	0.000662267	2	N	105	124
Q921M7	Infl	NVVLK	DAEGILEDLQSYR	GAGHE	2		754.8655242	1507.715448	0.000451244	8	N	44	57
Q921M7	Infl	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEK	EIYNQ	3	C4:+57.021	1043.817132	3128.427996	0.000823681	1	N	6	33
Q921M7	Infl	KGCIK	VLKDQPPNSVEGLLNALR	YTTKH	2		982.0527108	1962.089822	0.000451244	5	N	286	304
Q921Z5	Infl	KMVSK	SIATTLIDDTSSEVLDELYR	VTKEY	2		1121.060793	2240.105985	0.000451244	13	N	36	56

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q921Z5	Infl	KSHGR	VNNVFDHFSDCDFLAALYNPFGK	FKPHL	2	C11:+57.021	1345.621129	2689.226657	0.000823681	2	N	154	177
Q922B2	Infl	VSYFK	NNAYLAQSPQLYK	QMCIC	2		755.3889695	1508.762339	0.002019181	4	N	241	254
Q922B2	Infl	KVNQK	IGSCTQQDVELHVQK	IYVIS	3	C4:+57.021	581.2898056	1740.846017	0.000451244	3	N	126	141
Q922D4	Infl	ATLEK	QEIIEQLLSNIFHK	EKNES	3		571.3179557	1710.930467	0.000451244	7	N	244	258
Q922D4	Infl	SLLMK	LYSFLLNESPLNPLLASFFSK	VLSIL	2		1200.646641	2399.277682	0.000823681	3	N	105	126
Q922D4	Infl	SEEEK	LSTSQDAACKDAEETPEPAEAK	CTAPL	3	C9:+57.021	783.3571613	2347.048084	0.000451244	1	N	792	814
Q922D4	Infl	NIFHK	EKNESAIVSAIQILLTLLETR	RPTFE	3		781.1166078	2340.326423	0.001943752	1	N	258	279
Q922D4	Infl	FHKEK	NESAIVSAIQILLTLLETR	RPTFE	3		695.4040891	2083.188867	0.000451244	1	N	260	279
Q922F4	Infl	PRGLK	MASTFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.000622848	1	N	362	380
Q922F4	Infl	PRGLK	MASTFIGNSTAIQELFK	RISEQ	2		929.4749166	1856.934233	0.000451244	2	N	362	379
Q922P9	Infl	ARLGR	TPAEVVSTCDITFACVSDPK	AAKDL	2	C9:+57.021,C15:+57.021	1099.011271	2196.006942	0.000451244	9	N	308	328
Q922P9	Infl	FLDQK	CQNILQGNFKPDFYLK	YIQKD	3	C1:+57.021	662.3368673	1983.987202	0.001699387	1	N	478	494
Q922Q8	Infl	ADFGR	LVNLQHLDLLNNR	LVTLP	3		521.299007	1560.873621	0.000451244	7	N	83	96
Q922Q8	Infl	LKNLK	WLDLKDNPLDPVLAK	VAGDC	3		579.6580894	1735.950868	0.00091018	3	N	111	126
Q922Q8	Infl	GGNLR	DKLDGNELDLSLSDLNEVPVK	ELAAL	2		1157.095167	2312.174733	0.000451244	8	N	12	33
Q922Q8	Infl	LLNNR	LVTLPVSFAQLK	NLKWL	2		658.4033599	1314.79112	0.002080925	1	N	96	108
Q922R8	Infl	FPTIK	IFQKGESPVDYDGGR	TRSDI	2		834.4053479	1666.795096	0.000451244	12	N	241	256
Q922R8	Infl	KDVVK	VGAVNADKHQSLGGQYGVQGFPTIK	IFGAN	2		1286.169866	2570.324132	0.000451244	5	N	77	102
Q922R8	Infl	LSFGR	GSTAPVGGGSFPTITPR	EPWDG	2		801.4182583	1600.820917	0.000451244	5	N	392	409
Q922R8	Infl	CGHCK	NLEPEWAAAATEVKEQTK	GKVKL	2		1008.008166	2014.000732	0.000451244	8	N	194	212
Q922R8	Infl	LAVSG	LYSSSDDVIELTPSNFNR	EVIQS	2		1028.995256	2055.974911	0.000451244	20	N	19	37
Q922R8	Infl	GAAGR	NSYLEVLLK	LADKY	2		539.8113036	1077.607007	0.000451244	15	N	313	322
Q922R8	Infl	YQGGR	TGEAIVDAALSALR	QLVKD	2		693.88352	1385.75144	0.000451244	15	N	118	132
Q922R8	Infl	DIVSR	ALDLFSDNAPPPELLEIINEDIAKK	TCEEH	3		922.4922916	2764.453475	0.000451244	31	N	264	289
Q922R8	Infl	DIVSR	ALDLFSDNAPPPELLEIINEDIAK	KTCEE	2		1319.187056	2636.358512	0.000451244	10	N	264	288
Q922R8	Infl	KGKVK	LAAVDATVNQVLASR	YGIKG	2		764.428626	1526.841652	0.000451244	13	N	216	231
Q922R8	Infl	FLAVS	GLYSSSDDVIELTPSNFNR	EVIQS	2		1057.505987	2112.996375	0.000451244	8	N	18	37
Q922R8	Infl	ALDLF	SDNAPPPELLEIINEDIAK	KTCEE	2		1039.536756	2077.057912	0.000622848	2	N	269	288
Q922S4	Infl	LQVAK	NLFTHLDDVSVLLQEIITEAR	NLSNA	3		809.436229	2425.285287	0.000451244	12	N	377	398
Q922S4	Infl	ITEAR	NLSNAEICSVFLLDQNELVAK	VFDGG	2	C8:+57.021	1189.107323	2376.199046	0.000451244	21	N	398	419
Q922S4	Infl	SLQLK	VLQYLQQETQATHCCLLLVSEDNLQLSCK	VIGDK	3	C14:+57.021,C15:+57.021,C28:+57.021	1164.57049	3490.68807	0.000451244	6	N	223	252
Q922S4	Infl	DEYTK	LLHDGIQPVAAIDSNFANFTYTPR	SLPED	3		887.4542826	2659.339448	0.001654178	1	N	560	584
Q922S4	Infl	ELVAK	VFDGGVVDDESYEIR	IPADQ	2		850.3946459	1698.773692	0.000823681	1	N	419	434
Q922S4	Infl	SYEIR	IPADQGIAGHVATTGQILNIPDAYAHPLFYR	GVDDS	3		1107.246114	3318.714943	0.001871652	1	N	434	465
Q922S4	Infl	MYHMK	VSDDEYTKLLHDGIQPVAAIDSNFANFTYTPR	SLPED	3		1199.921913	3596.74234	0.002374549	1	N	552	584
Q922S4	Infl	GFRTR	NILCFPIKNENQEVIGVAELVNK	INGPW	3	C4:+57.021	881.1391524	2640.394057	0.000451244	5	N	476	499
Q922S4	Infl	PWFSK	FDEDLATAFSIYCGISIAHSLLYK	KVNEA	3	C13:+57.021	912.1196465	2733.335539	0.000451244	5	N	507	531
Q923B6	Infl	-MEK	AHADEFPLTTDSSEKQGVVCIFGTGDFGK	SLGLK	3	C20:+57.021	1038.489238	3112.444315	0.001162105	1	N	3	32
Q923B6	Infl	AHVVK	AFNTISAWALQSGTLDASR	QVFVC	2		1005.0085	2008.001401	0.000823681	2	N	132	151
Q923B6	Infl	LAMHR	EHYDSLTELVDYLK	GKVLV	2		862.9230392	1723.830478	0.000823681	1	N	83	97
Q923L7	Infl	RYQTK	GSVEYYTVACEPR	VAWDC	2	C10:+57.021	765.8485886	1529.681577	0.000622848	4	N	123	136
Q93092	Infl	EEQIK	NAIDKLFVLFGAEILK	KIPGR	2		896.024902	1790.034204	0.000823681	3	N	81	97
Q93092	Infl	NAIDK	LFVLFGAEILK	KIPGR	2		625.3818962	1248.748192	0.000451244	4	N	86	97
Q93092	Infl	TISPK	LLGELLKDNSK	LAPAL	2		615.3591494	1228.702699	0.001591523	2	N	258	269
Q99J09	Infl	QGVTR	LVFSPHSVPLLTSLSEDCSLAVLDSSLSEVFR	SRAHR	3	C18:+57.021	1168.936241	3503.785322	0.000451244	11	N	260	292
Q99J09	Infl	LNSYR	AHAGQVTCVAASPHKDSVFLSCSEDSR	ILLWD	4	C8:+57.021,C22:+57.021	729.8398277	2915.328111	0.000451244	1	N	164	191
Q99J62	Infl	AVLRK	SLEGADLPNLLFYGPPGTGK	TSTIL	2		1023.531277	2045.046954	0.000637154	1	N	64	84
Q99J62	Infl	LTGGK	EVSEDVITDIAGVIPAATIDGIFTACHSGSFDKLEAVVK	NLIDE	4	C26:+57.021	1019.520366	4074.050264	0.001871652	1	N	255	294
Q99J77	Infl	MDTMK	QVYQIVKPLNPNFCFLQCTSAYPLQPEDANLR	VISEY	3	C14:+57.021,C18:+57.021	1275.302886	3822.885259	0.000451244	17	N	166	198
Q99J77	Infl	SEYQK	LFPDIPIGYSGHETGIAISVAAVALGAK	VLERH	3		923.1730048	2766.495614	0.000451244	4	N	205	233
Q99JB2	Infl	AEAIR	ILAGALTQHNGDAAASLTVAEQYVSAFSK	LAKDS	3		978.5054828	2932.493048	0.001162105	4	N	259	288
Q99JB2	Infl	VFRER	ESLNANIVDAINQAADCWGIR	CLRYE	2	C17:+57.021	1165.563614	2329.111628	0.000451244	7	N	150	171
Q99JI4	Infl	-M	PLENLEEEGLPKNPDLR	IAQLR	2		982.0107086	1962.005817	0.000451244	5	N	1	18
Q99JI4	Infl	RLHCK	IDKVNEIVETNRPDSK	NWQYQ	4		464.9987881	1855.963952	0.000622848	2	N	346	362
Q99JI4	Infl	EKVIK	GAEILEVLHSLPAVR	QYLFS	3		535.3109126	1602.909338	0.000451244	5	N	242	257
Q99JR1	Infl	NYTNR	SGDAPLTVNELGTAYVSATTGAVATALGLNALTK	RVSPL	3		1083.240583	3246.69835	0.000451244	12	N	136	170
Q99JR1	Infl	NYTNR	SGDAPLTVNELGTAYVSATTGAVATALGLNALTKR	VSPLI	3		1135.274287	3402.799461	0.000451244	6	N	136	171
Q99JR1	Infl	VTDPR	NILLTNEQLENAR	KVVHD	2		764.4104333	1526.805267	0.000451244	8	N	35	48
Q99JT2	Infl	EELEK	SIAVAETACPGITDK	MVKKL	2	C9:+57.021	766.8851711	1531.754742	0.000451244	8	N	383	398
Q99JT2	Infl	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSSYVTK	YYGSY	3	C24:+57.021	1204.905112	3611.691935	0.000451244	20	N	53	84
Q99JW4	Infl	PECFR	CDLCQEVLADIGFVK	NAGRH	2	C1:+39.994,C4:+57.021	875.4127817	1748.809963	0.000451244	4	N	96	111
Q99JW4	Infl	APAEK	IVNSNGELYHEQCFVCAQCFQQFPEGLFYEFEGR	KYCEH	3	C13:+57.021,C16:+57.021,C19:+57.021	1401.620572	4201.838317	0.000451244	18	N	22	56

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99JW4	Infl	SALNK	AWCVSCFACSTCNTK	LTLKN	2	C3:+57.021,C6:+57.021,C9:+57.021,C12:+57.021	926.3672881	1850.718976	0.000451244	6	N	269	284
Q99JW4	Infl	YICQK	CHAIIDEQPLIFKNDPYHPDHFNCANCGK	ELTAD	3	C1:+57.021,C24:+57.021,C27:+57.021	1170.864119	3509.568958	0.000698008	1	N	137	166
Q99JW4	Infl	TADAR	ELKGELYCLPCHDK	MGVPI	4	C8:+57.021,C11:+57.021	441.2132119	1760.821648	0.000823681	1	N	173	187
Q99JX3	Infl	TLELR	EASVTPSNLWGGQGLLGVSIR	FCSFD	2		1071.071632	2140.127664	0.000451244	12	N	80	101
Q99JX3	Infl	SPGHR	AGLEPFFDFIVSINGSR	LNKDN	2		934.9812228	1867.946846	0.000823681	2	N	30	47
Q99JX3	Infl	TVEDR	VSDCTPAVEKPVSDADASEPS	-	2	C4:+57.021	1080.983996	2159.952392	0.002374549	1	N	430	451
Q99JX3	Infl	TDNCR	EVIITPNSAWGGEGSLGCGIGYGYLHR	IPTRP	3	C18:+57.021	955.1329491	2862.375447	0.001264573	1	N	174	201
Q99JX3	Infl	AKPLK	LYVYNTDTDNCR	EVIIT	2	C11:+57.021	767.3358453	1532.656091	0.000451244	1	N	162	174
Q99JX4	Infl	LKPVK	FLEGELIHDLLTIFVSAK	LASYV	3		682.3826253	2044.124476	0.000451244	4	N	230	248
Q99JX4	Infl	CSLIK	VAASCGAIQYIPTELDQVR	KWISD	2	C5:+57.021	1046.030887	2090.046174	0.002981883	1	N	129	148
Q99JX4	Infl	RCIVR	ALKDPNAFLFDHLLTLKPVK	FLEGE	4		570.8338429	2279.304172	0.000451244	4	N	210	230
Q99JX4	Infl	CSLIK	VAASCGAIQYIPTELDQVRK	WISDW	3	C5:+57.021	740.3881789	2218.141137	0.001329271	2	N	129	149
Q99JX7	Infl	RAFTR	TFIAVPASNSGLCIVNDELFVR	NASPE	2	C13:+57.021	1211.625683	2421.235766	0.000451244	11	N	514	536
Q99JX7	Infl	RENRR	ISIIINASAPPYTVQNELKPEQIEQLK	LIMSK	3		1012.892567	3035.6543	0.001763695	1	N	185	212
Q99JY0	Infl	GLLHR	TNIPKDVVDYIIFGTVIQEVK	TSNVA	3		797.7777036	2390.309711	0.00091018	3	N	91	112
Q99JY0	Infl	KAYLR	DFIYVSQDPKDQLLLGPTYATPK	VLEKA	2		1305.179034	2608.342468	0.001395409	1	N	339	362
Q99JY0	Infl	TNIPK	DVVDYIIFGTVIQEVK	TSNVA	2		919.5014568	1836.987314	0.002296037	1	N	96	112
Q99JY9	Infl	QQLLR	DREVGIPPEQSLETAK	AVKER	2		884.9579447	1767.900289	0.000451244	8	N	209	225
Q99JY9	Infl	AISKK	EFSIDVGYER	FLGPE	2		607.7885569	1213.561514	0.000622848	5	N	265	275
Q99JY9	Infl	QVIFK	YLRAEPEDHYFLLTEPPLNTPENR	EYTAE	3		972.1510399	2913.42972	0.000451244	6	N	99	123
Q99JY9	Infl	RRVMK	GVDDLDFFIGDEAIEKPTYATK	WPIRH	2		1222.597542	2443.179484	0.000451244	25	N	53	75
Q99JY9	Infl	TGYTK	LGYAGNTEPQFIIPSCIAIK	ESAKV	2	C16:+57.021	1096.57493	2191.13426	0.000451244	26	N	18	38
Q99JY9	Infl	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	HIPIA	3	C28:+57.021	1020.197396	3057.568787	0.000451244	93	N	161	191
Q99JY9	Infl	PIAGR	DITYFIQQLLR	DREVG	2		705.3935235	1408.771447	0.000451244	11	N	198	209
Q99JY9	Infl	VGYER	FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C32:+57.021	1439.372177	4315.093132	0.000451244	37	N	275	312
Q99JY9	Infl	-MAGR	LPACVVDCGTGYTK	LGYAG	2	C4:+57.021,C8:+57.021	770.8604104	1539.705221	0.000451244	33	N	4	18
Q99JY9	Infl	CHTKK	DYEEIGPSICR	HNPVF	2	C10:+57.021	669.8036497	1337.591699	0.000451244	13	N	398	409
Q99JY9	Infl	AGRDI	TYFIQQLLR	DREVG	2		591.3380199	1180.66044	0.001229886	3	N	200	209
Q99JY9	Infl	FKYLR	AEPEDHYFLLTEPPLNTPENR	EYTAE	2		1241.598408	2481.181216	0.000451244	33	N	102	123
Q99JY9	Infl	VCHTK	KDYEEIGPSICR	HNPVF	2	C11:+57.021	733.8511312	1465.686662	0.000622848	3	N	397	409
Q99JY9	Infl	GPEIF	FHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C25:+57.021	1171.564918	3511.671355	0.000451244	4	N	282	312
Q99JY9	Infl	RRVMK	GVDDLDFFIGDEAIEKPTY	ATKWP	2		1072.507664	2142.999729	0.000451244	8	N	53	72
Q99JY9	Infl	RRVMK	GVDDLDFFIGDEAIEKPTYATKWPIR	HGIVE	3		999.5067122	2995.496737	0.000451244	3	N	53	79
Q99JY9	Infl	TPENR	EYTAEIMFESFNVPGLYIAVQAVLALAASWTSR	QVGER	3		1216.620519	3646.838156	0.001699387	2	N	123	156
Q99JY9	Infl	AVKER	YSYVCPDLVK	EFNKY	2	C5:+57.021	622.3052969	1242.594994	0.000622848	1	N	230	240
Q99JY9	Infl	GYERF	LGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C31:+57.021	1390.349373	4168.024718	0.001839721	1	N	276	312
Q99K01	Infl	GEQLK	QLVPQCGLTVIDLEVDGTCVR	FSPLM	2	C6:+57.021,C19:+57.021	1186.601119	2371.186638	0.00307782	1	N	437	458
Q99K01	Infl	DLTAR	QTEALQNQAQHQEDDHSQVEELER	LR-	3		954.7682058	2861.281218	0.001463592	1	N	761	785
Q99K01	Infl	ADKLR	ALPLWLSLQYLGLDGIVER	IKHAC	2		1078.609862	2155.204123	0.001162105	2	N	337	356
Q99K41	Infl	EERFR	GLEEGQAQAGQCPSLEGR	LGRLE	2	C12:+57.021	943.9369863	1885.858373	0.000451244	1	N	709	727
Q99K41	Infl	VPFDR	VLLNDGGYYDPETGVFTAPLAGR	YLLSA	2		1213.105869	2424.196137	0.000451244	6	N	892	915
Q99K41	Infl	LLQAR	GDEGCGACGGVQEELGR	LRDGV	2	C5:+57.021,C8:+57.021	875.8596587	1749.703717	0.000622848	7	N	578	595
Q99K41	Infl	DSEGR	LQLVGSGLHEAEAAGEAQQAVLEGLQGLLSR	LRERM	3		1048.893629	3143.657488	0.000451244	5	N	511	542
Q99K48	Infl	SLTVR	NLPQYVSNELLEEAFSVFGQVER	AVVIV	2		1334.666822	2667.318044	0.000451244	18	N	155	178
Q99K48	Infl	SLTVR	NLPQYVSNELLEEAFSVF	GQVER	2		1050.020742	2098.025884	0.001763695	1	N	155	173
Q99K85	Infl	VGGIR	ASLYNAVTTEDVEK	LAAFM	2		770.3810071	1538.746414	0.000451244	1	N	342	356
Q99K85	Infl	GSYTK	IPDPSTWNLNPDASYVYFCANETVHGVEFDFVPDVK	GAVLV	3	C19:+57.021	1381.642445	4141.903934	0.00307782	1	N	133	169
Q99KE1	Infl	LEAAK	ALTTQLTDAELAQGR	LYPSL	2		794.420998	1586.826396	0.000451244	8	N	496	511
Q99KE1	Infl	LVKGR	TASIDSNQEPYAHAAPESIPATFEDAVNK	LKPSV	3		1025.151545	3072.431236	0.000451244	13	N	354	383
Q99KE1	Infl	LAQGR	LYPSLANIQEVSANIAIK	LAEYL	2		972.5441873	1943.072775	0.000451244	5	N	511	529
Q99KE1	Infl	ERIWR	SNYVSLLPDVYDWPESSLTPPQITEEKLPH	-	3		1152.240472	3453.698016	0.000451244	10	N	559	589
Q99KE1	Infl	LQDGR	VFTPGQGNNAYIFPGVALAVILCEAR	HISDT	2	C23:+57.021	1389.226095	2776.436591	0.000451244	4	N	458	484
Q99KE1	Infl	KYQQK	YCTFNDDIQGTAAVALSGLLAAQR	VINKP	3	C2:+57.021	852.4238404	2554.248121	0.00091018	3	N	272	296
Q99KE1	Infl	LTEGR	CLFASGSPFEPVKLQDGR	VFTPG	2	C1:+57.021	1004.501765	2006.98793	0.000451244	1	N	440	458
Q99KH8	Infl	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTK	YYGSY	3	C24:+57.021	1208.245357	3621.712671	0.000451244	20	N	53	84
Q99KH8	Infl	KDIPK	RPFSQCLSTIISPLFAELK	EKSQA	3	C6:+57.021	736.4016483	2206.181545	0.000622848	6	N	357	376
Q99KH8	Infl	ELKEK	SQACGGNLGSIEELR	GAIYL	2	C4:+57.021	795.8809514	1589.746303	0.000451244	2	N	378	393
Q99KH8	Infl	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTKY	YGSYL	3	C24:+57.021	1262.5998	3784.775999	0.001463592	1	N	53	85
Q99KI0	Infl	TLSEK	IVYGHLDDPANQEIER	GKTYL	2		934.9610187	1867.906437	0.000451244	5	N	68	84
Q99KI0	Infl	ANSVR	NAVTQEFGPVPDTAR	YYKKH	2		801.4000656	1600.784531	0.000622848	1	N	633	648
Q99KI0	Infl	NFTGR	NDANPETHAFVTSPEIVTALAIAGTLK	FNPET	3		927.4875406	2779.439222	0.000451244	7	N	479	506
Q99KI0	Infl	LRRAK	DINQEVYNFLATAGAK	YGVGF	2		877.4419304	1752.868261	0.000823681	3	N	144	160
Q99KI0	Infl	AQILR	DVGGIVLANACGPCIGQWDR	KDIKK	2	C11:+57.021,C14:+57.021	1079.512107	2157.008614	0.002296037	1	N	437	457

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99KI0	Infl	GLKCK	SQFTITPGSEQIR	ATIER	2		732.3786018	1462.741604	0.000662267	2	N	411	424
Q99KI0	Infl	KHGIR	WVVIGDENYGEGSSR	EHAAL	2		834.3871552	1666.75871	0.000451244	1	N	656	671
Q99KJ8	Infl	LLQAK	VSALDLAVLDQVEAR	LQSVL	2		799.9415663	1597.867533	0.000451244	16	N	268	283
Q99KJ8	Infl	ETIQR	WSPVASTLPELVQR	LVTIK	2		791.9335442	1581.851488	0.000823681	7	N	319	333
Q99KJ8	Infl	QKYQR	LLHEVQELTTEVEK	IKTTV	2		834.4466815	1666.877763	0.000451244	1	N	105	119
Q99KJ8	Infl	QTTMR	ENLATVEGNFASIDAR	MKRLG	2		853.9213622	1705.827124	0.000451244	7	N	380	396
Q99KK7	Infl	AGLIR	SFCERFPEDGPELEEVLIQLAAADAR	FWRNQ	3	C3:+57.021	988.1469239	2961.417372	0.000451244	18	N	698	724
Q99KK7	Infl	HYEVR	LASVLNTDPALDSELTSK	LKRYE	2		937.4918174	1872.968035	0.000451244	6	N	215	233
Q99KK7	Infl	MEDAK	LAQDFLDSQNLSAYNTR	LFKVV	2		978.4770329	1954.938466	0.000451244	3	N	182	199
Q99KK7	Infl	TEGFK	NVSLGNVLAVAYAAK	REKLT	2		745.4228124	1488.830025	0.000451244	3	N	405	420
Q99KK7	Infl	VVAGR	ALYEGYAAVTDAPPECFLTLR	DTVLL	2	C16:+57.021	1179.078034	2356.140468	0.002813207	1	N	638	659
Q99KK7	Infl	QPNTR	LEGSEVQLVEYEASAAGLIR	SFCER	2		1067.55548	2133.095361	0.000451244	14	N	678	698
Q99KK7	Infl	VQDEK	GAFNFDKETVINPETGEQIQSWYR	SGETW	2		1415.178085	2828.34057	0.000451244	1	N	466	490
Q99KK7	Infl	LNMVR	AGLLALEFYTPEAANWR	QAHMQ	2		961.4944974	1920.973395	0.000451244	14	N	548	565
Q99KK7	Infl	SFCER	FPEDGPELEEVLIQLAAADAR	FWRNQ	2		1142.07932	2282.143039	0.000622848	1	N	703	724
Q99KK7	Infl	LAFEK	DKFLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1228.293347	3681.856642	0.001264573	3	N	365	399
Q99KK7	Infl	FEKDK	FLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1147.252712	3438.734735	0.000451244	8	N	367	399
Q99KK7	Infl	LIRSF	CERFPEDGPELEEVLIQLAAADAR	FWRNQ	3	C1:+39.994	904.4377764	2710.289929	0.000451244	3	N	700	724
Q99KK7	Infl	TWDSK	FSTIASSYEECR	AESVG	2	C11:+57.021	725.3196639	1448.623728	0.001463592	2	N	498	510
Q99KK7	Infl	HHLSR	AAWYGGLAVLLQTSPEAPYIYALLSR	LFRAQ	3		941.8413666	2822.5007	0.000622848	2	N	39	65
Q99KP6	Infl	RLIEK	YIAENGTDPINNQPLSEEQLIDIK	VAHPI	2		1357.680126	2713.344653	0.000451244	40	N	32	56
Q99KP6	Infl	LSKYR	QVASHVGLHSASIPGILALDLCPSDTNK	ILTGG	3	C22:+57.021	967.503042	2899.485726	0.000662267	6	N	208	236
Q99KP6	Infl	TSIAF	SENGYYLATAADDSSVK	LWDLR	2		895.9081174	1789.800635	0.000979378	1	N	400	417
Q99KY4	Infl	PSQTK	SQNLDPFADLSDLSSSLQGLPAGLPAGGFVGAPAPTQK	SNSPW	3		1241.967523	3722.879168	0.000451244	13	N	1075	1113
Q99KY4	Infl	SGPSR	AQPPCGGTVNSSGVLALAEYDQPYGGFLDILR	GGTER	3	C5:+57.021	1122.554242	3364.639327	0.000451244	5	N	345	377
Q99L04	Infl	NTTNK	SFWEVPASIWDDINNVGLR	GHYLC	2		1109.550532	2217.085465	0.000451244	8	N	106	125
Q99L04	Infl	SLGGR	CVPVVCDSSQESEVK	SLFEQ	2	C1:+57.021,C6:+57.021	861.8873535	1721.759107	0.000451244	9	N	57	72
Q99L04	Infl	DREQK	GRLDVLVNNAYAGVQAILNTTNK	SFWEV	3		815.4472395	2443.318318	0.000451244	13	N	83	106
Q99L04	Infl	EMSGK	CVVALATDPNILNLSGK	VLPSC	2	C1:+39.994	884.4691769	1766.922754	0.001463592	1	N	234	251
Q99L45	Infl	KKTKK	IFDIDEAEEAIKDVK	IESDA	3		578.9652478	1733.872343	0.000622848	3	N	87	102
Q99L45	Infl	PSETK	EVEPEPTEEKDVDADEEDSR	KKDAS	3		773.331712	2316.971736	0.000451244	1	N	42	62
Q99LB4	Infl	ISRMR	YSPNTQVEILPQGR	ESPIF	2		801.4182583	1600.820917	0.000451244	18	N	322	336
Q99LB4	Infl	MNLTK	VADSSPFASELLIPDDCFVLDNGLCGK	IYIWK	2	C17:+57.021,C25:+57.021	1470.193766	2938.371933	0.000662267	2	N	266	293
Q99LB4	Infl	RATER	ALSWDSFNTGDCFILDLGQNIFAWCGGK	SNILE	3	C12:+57.021,C25:+57.021	1064.823521	3191.447163	0.000451244	17	N	154	182
Q99LB4	Infl	KPALK	EGNPEEDITADQTNAQAAALYK	VSDAT	2		1175.046205	2348.07681	0.000451244	16	N	232	254
Q99LB4	Infl	DSSPF	ASELLIPDDCFVLDNGLCGK	IYIWK	2	C10:+57.021,C18:+57.021	1118.534913	2235.054227	0.000622848	5	N	273	293
Q99LB4	Infl	TGDCF	ILDLGQNIFAWCGGK	SNILE	2	C12:+57.021	846.4326228	1690.849646	0.000451244	10	N	167	182
Q99LB4	Infl	RATER	ALSWDSFNTGDCF	ILDLG	2	C12:+57.021	760.3118389	1518.608078	0.001839721	1	N	154	167
Q99LB4	Infl	KPALK	EGNPEEDITADQTNAQAAALY	KVSDA	2		1110.998724	2219.981847	0.000451244	11	N	232	253
Q99LB4	Infl	HGIFF	SGDSYLVLHNGPEEASHLHLWIGQQSSR	DEQGA	3		1039.843269	3116.506407	0.001162105	1	N	43	71
Q99LC3	Infl	LYASR	LLQYADALEHLLSTGQGVVLER	SIYSD	3		809.1082238	2424.301271	0.000451244	14	N	139	161
Q99LC3	Infl	HCKLR	YGLLAAILGDK	TTKKL	2		567.3324032	1132.649206	0.000451244	7	N	37	48
Q99LC5	Infl	GENFK	LLYDLADQLHAAVGASR	AAVDA	3		604.9921312	1811.952994	0.000451244	12	N	232	249
Q99LC5	Infl	MKDSK	TIVAINKDPEAPIFQVADYGIVADLFK	VVPEM	3		983.1992196	2946.574259	0.000451244	24	N	294	321
Q99LC5	Infl	HDAYK	GLLPEELTPLILETQK	QFSYT	2		897.5171068	1793.018614	0.000451244	9	N	85	101
Q99LC5	Infl	SLLRF	QSTLVIAEHANDSLAPITLNTITAAGR	LGGEV	2	Q1:-17.027	1380.730259	2759.444919	0.000622848	3	N	19	46
Q99LC5	Infl	VFSVR	GTSFEAAATSGGSASSEKAPSSSSVGISEWLDQK	LTKSD	3		1106.187095	3315.537886	0.000451244	6	N	169	203
Q99LC5	Infl	ASSEK	APSSSSVGISEWLDQK	LTKSD	2		845.9182882	1689.820976	0.000451244	1	N	187	203
Q99LC5	Infl	VAINK	DPEAPIFQVADYGIVADLFK	VVPEM	2		1104.565317	2207.115033	0.000823681	2	N	301	321
Q99LF4	Infl	LPAMK	QIGNVAALPGIVHR	SIGLP	3		482.2848092	1443.831028	0.000451244	12	N	67	81
Q99LF4	Infl	AKSRR	NLDFQDVLDKLADMGIAIR	VASPK	3		716.3775459	2146.109238	0.000451244	2	N	441	460
Q99LF4	Infl	RAKKR	GLPQLGTLGAGNHYAEIQVVDEIFNEYAAK	KMGID	3		1073.210847	3216.609141	0.000451244	4	N	214	244
Q99LL3	Infl	SAGLK	VSFANFIQYLLDPHTEK	LAPFN	3		674.6830748	2021.025824	0.000451244	4	N	302	319
Q99LL3	Infl	RQVYR	LCHPCQIDYDFVGKLETLDEDAAQLLR	FLKVD	3	C2:+57.021,C5:+57.021	1073.853369	3218.536707	0.001763695	2	N	332	359
Q99LL3	Infl	SYRNR	TASSWEEDWFANIPLAWR	QQLYK	2		1090.016325	2178.017051	0.000622848	6	N	376	394
Q99LP6	Infl	QGFCK	DLLEVADILEK	ATQSV	2		629.35099	1256.68638	0.002296037	6	N	109	120
Q99LP6	Infl	VEEAK	LYGIQGFCKDLLEVADILEK	ATQSV	3	C8:+57.021	775.4121016	2323.212905	0.000451244	5	N	100	120
Q99LT0	Infl	AVLAK	ERPPNPIEFLASYLLK	NKAQF	2		944.0228907	1886.030181	0.001591523	1	N	74	90
Q99LT0	Infl	SLPTR	AYLDQTVVPILLQGLAVLAK	ERPPN	2		1063.135712	2124.255825	0.000451244	12	N	54	74
Q99LT0	Infl	PTRAY	LDQTVVPILLQGLAVLAK	ERPPN	3		631.059594	1890.155382	0.000451244	4	N	56	74
Q99LX0	Infl	RAGIK	VTVAGLAGKDPVQCSR	DVMIC	2	C14:+57.021	829.4384365	1656.861273	0.000451244	20	N	32	48
Q99LX0	Infl	EQESR	KGLIAAICAGPTALLAHEVGFGCK	VTTHP	2	C8:+57.021,C23:+57.021	1227.653489	2453.291378	0.000451244	2	N	98	122
Q99LX0	Infl	ILTSR	GPGTSFEFALAIVEALVGK	DMANQ	2		953.5201808	1905.024762	0.000451244	12	N	156	175
Q99LX0	Infl	QESRK	GLIAAICAGPTALLAHEVGFGCK	VTTHP	3	C7:+57.021,C22:+57.021	776.0732716	2325.196415	0.001162105	4	N	99	122
Q99LX0	Infl	TSFEF	ALAIVEALVGK	DMANQ	2		542.342771	1082.669942	0.002374549	1	N	164	175

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99M15	Infl	EQVRK	SLETCSIEKDIQYFVNQR	KTGQT	3	C5:+57.021	744.0321722	2229.073117	0.000451244	5	N	254	272
Q99M15	Infl	SEHIK	ACEVFEAQECER	INFFR	2	C2:+57.021,C10:+57.021	764.3138243	1526.612049	0.000451244	9	N	211	223
Q99M31	Infl	SGMYR	VLSTNTSDNIGGAHFTDTLAQYLASEFQR	LFKHD	3		1052.846456	3155.515969	0.000451244	6	N	216	245
Q99M31	Infl	AEVAK	HSLSTLGSANCFVDSLYEGQDFDCNVSR	ARFEL	3	C11:+57.021,C24:+57.021	1060.133083	3177.375849	0.000451244	3	N	269	297
Q99M46	Infl	KEHAK	WNPTAGVAFEYDPDNALR	HTVYP	2		1018.479576	2034.943551	0.000451244	1	N	175	193
Q99M46	Infl	GKPER	FYYNVESCGSLRPETIVLSALSGLK	KKLSD	3	C8:+57.021	935.1497172	2802.425751	0.000823681	2	N	228	253
Q99MD9	Infl	LLGKK	YGETANECGEAFFFYGK	SLLEL	2	C8:+57.021	995.4201064	1988.824613	0.001229886	1	N	76	93
Q99MD9	Infl	QAHLK	LGEVSVESENYIQAVEEFQACLSLQEQYLEAHDR	LLAET	3	C21:+57.021	1328.625342	3982.852627	0.000451244	14	N	533	567
Q99MD9	Infl	EAHDR	LLAETHYQLGLAYGYNSQYDEAVAQFGK	SIDVI	3		1050.512526	3148.514178	0.002884417	1	N	567	595
Q99MK8	Infl	TISER	WQQEVAETVFDTINAETDRLEAR	KKAKN	3		907.7758616	2720.304185	0.000451244	7	N	516	539
Q99MK8	Infl	IRGGK	QFVLQCDSDPELVQWK	KELRD	2	C6:+57.021	996.4804984	1990.945397	0.000823681	4	N	628	644
Q99MK8	Infl	LIPPR	GEVNAADAFDIGSFDEEDTK	GIKLL	2		1065.461443	2128.907285	0.000451244	3	N	474	494
Q99MN1	Infl	ELSEK	QLNQTASAPNHTADNGVGAEEETLDPNQYYK	IRSQA	3		1125.850706	3374.528718	0.000451244	34	N	45	76
Q99MN1	Infl	FVMKK	EICNAYTELNDPVR	QRQLF	2	C3:+57.021	847.3964343	1692.777269	0.000451244	3	N	491	505
Q99N15	Infl	PFPSR	LGDPAEYAHLVQTIIENPFLNGEVIR	LDGAI	3		970.1788185	2907.513055	0.000451244	13	N	226	252
Q99N15	Infl	ATAKR	LVGQGATAVLLDVPDSEGEAQAK	KLGES	2		1134.590052	2267.164503	0.000622848	3	N	29	52
Q99N15	Infl	QGGQR	GVIINTASVAAFEGQVGQAAYSASK	GGIVG	2		1220.129875	2438.24415	0.000451244	4	N	147	172
Q99N16	Infl	KAKAK	TLDFIDVLLLSKDEHGK	ALSDE	4		486.518085	1942.04114	0.000823681	1	N	294	311
Q99N16	Infl	KAKAK	TLDFIDVLLLSK	DEHGK	2		688.9059325	1375.796265	0.001763695	2	N	294	306
Q99N80	Infl	AAPER	STETQGPDLSSPYVPSK	ASEGQ	2		896.9341352	1791.85267	0.001229886	2	N	149	166
Q99N80	Infl	KATSK	ILENGEEAPGLGPSLDR	MLSSS	2		883.9501196	1765.884639	0.002727428	1	N	221	238
Q99NB9	Infl	EIQGK	KAALDEAQGVGLDSTGYYDQEIYGGSDSR	FAGYV	3		1022.471055	3064.389765	0.000451244	2	N	21	50
Q99NB9	Infl	GSDSR	FAGYVTSIAATELEDDDDDYSSSTSLLGQK	KPGYH	3		1066.821531	3197.441192	0.000451244	15	N	50	80
Q99NB9	Infl	NTTAR	AFAVVASALGIPSLLPFLK	AVCKS	2		957.5773018	1913.139004	0.000451244	8	N	630	649
Q99NB9	Infl	QQKVR	TISALAIAALAEAATPYGIESFDSVLKPLWK	GIRQH	3		1082.927388	3245.758765	0.000451244	17	N	702	733
Q99NB9	Infl	DRTMK	SVNDQPSGNLPFLKPDDIQY	FDKLL	2		1124.050562	2246.085524	0.000451244	14	N	454	474
Q99NB9	Infl	REWMR	ICFELLELLK	AHKKA	2	C2:+57.021	639.3626148	1276.70963	0.001839721	7	N	1057	1067
Q99NB9	Infl	PYVHK	ILVVIEPLLIDEDYYAR	VEGRE	2		1017.562046	2033.108491	0.000451244	5	N	573	590
Q99NB9	Infl	GYIAK	AIGPHDVLATLLNNLK	VQERQ	3		563.6618339	1687.962102	0.000451244	9	N	1086	1102
Q99NB9	Infl	QYFDK	LLVDVDESTLSPEEQKER	KIMKL	2		1044.029295	2086.042991	0.000451244	1	N	477	495
Q99NB9	Infl	LKVVK	QCCGTDGVEANYIK	TEILP	2	C2:+57.021,C3:+57.021	807.8480313	1613.680463	0.000451244	4	N	793	807
Q99NB9	Infl	LPHLR	SLVEIIEHGLVDEQQK	VRTIS	3		612.9954299	1835.96289	0.000451244	2	N	684	700
Q99P88	Infl	KEYQK	ISNQVDLPSVCAQYR	QVRFY	2	C11:+57.021	875.4333511	1748.851102	0.000662267	1	N	906	921
Q99P88	Infl	DLVIR	DKEVTGALIASLINCYIR	DNAAV	3	C15:+57.021	679.3667151	2035.076745	0.000451244	13	N	829	847
Q99P88	Infl	KSSNR	EITAIESSVPVQLLESVLQELK	GLQEF	2		1213.17596	2424.33632	0.000451244	2	N	693	715
Q99P88	Infl	EFLDR	NSQFSGGPLGNPNTTAR	VQQRL	2		859.4167783	1716.817957	0.001463592	1	N	723	740
Q99P88	Infl	NCYIR	DNAAVDGISLHLQDTCPLLYSTDDAVCSK	ANELL	3	C16:+57.021,C27:+57.021	1060.160639	3177.458516	0.000451244	6	N	847	876
Q99P88	Infl	WNRVK	SPLHLLDCIHVLLTR	YVENP	3	C8:+57.021	596.3384311	1785.991893	0.000622848	3	N	1318	1333
Q99PL5	Infl	DIVLK	LREAEETQNSLQAECDQYR	TILAE	3	C15:+57.021	780.6892453	2339.044336	0.000698008	4	N	1312	1331
Q99PL5	Infl	VLKLR	EAEETQNSLQAECDQYR	TILAE	2	C13:+57.021	1035.93738	2069.859161	0.000451244	15	N	1314	1331
Q99PL5	Infl	TERIR	SIEALLEAGQAQDTQASHAEANQQQTR	LKELE	2		1448.195526	2894.375452	0.0007646	1	N	1161	1188
Q99PL5	Infl	EAQTK	ETLLALLPGLSISAHQNYAEWLQEFKEK	GSELL	3		1076.903354	3227.686663	0.000662267	2	N	1264	1292
Q99PL5	Infl	EAQTK	ETLLALLPGLSISAHQNYAEWLQEFK	EKGSE	3		991.1908355	2970.549107	0.000622848	7	N	1264	1290
Q99PL5	Infl	NSILR	DALNQATSQVESK	QNTEL	2		695.8445918	1389.673584	0.001463592	1	N	1009	1022
Q99PT1	Infl	PPAQK	SIQEIQELDKDDESLR	KYKEA	2		959.4741559	1916.932712	0.000451244	35	N	33	49
Q99PT1	Infl	ALLGR	VAVSADPNVPNVIVTR	LTLVC	2		825.962833	1649.910066	0.000451244	33	N	58	74
Q99PT1	Infl	VIVTR	LTLVCSTAPGPLELDLTGDLESFKK	QSFVL	2	C5:+57.021	1352.70961	2703.403619	0.000451244	21	N	74	99
Q99PT1	Infl	VIVTR	LTLVCSTAPGPLELDLTGDLESFK	KQSFV	2	C5:+57.021	1288.662128	2575.308656	0.000622848	5	N	74	98
Q99PV0	Infl	MTYFR	EAVVNTQELLDLLVK	CENKI	2		842.4805243	1682.945449	0.00091018	1	N	1275	1290
Q99PV0	Infl	STLYR	LANQLLTDLVDDNYFYLFDLK	AFFTS	2		1267.147202	2532.278805	0.000451244	3	N	240	261
Q99PV0	Infl	RHSVK	SQEPLPDDDEEFELPEFVEPFLK	DTPLY	2		1375.142511	2748.269422	0.001329271	6	N	366	389
Q99PV0	Infl	EPLVR	DINLQDEDWNEFNDINK	IIIRQ	2		1061.472145	2120.928689	0.000451244	2	N	284	301
Q99PV0	Infl	PPLDY	ADNILDVEPLEAIQLELDPEEDAPVLDWFYDHQPLR	DSRKY	3		1406.690495	4217.048084	0.001699387	1	N	178	214
Q99PV0	Infl	RHSVK	SQEPLPDDDEEFELPEFVEPFLKDTPLY	TDNTA	3		1113.522533	3337.5442	0.000622848	1	N	366	394
Q99PV0	Infl	ISDLR	AQIAGYLYGVSPPDNPQVK	EIRCI	2		1009.023619	2016.031638	0.000622848	4	N	2121	2140
Q99PV0	Infl	EPFLK	DTPLYTDNTANGIALLWAPRPF	NLRSG	2		1223.624229	2445.232857	0.000451244	1	N	389	411
Q9CPR4	Infl	NAELK	GLDVDSLVIEHIQVNKAPK	MRRRT	4		519.5433628	2074.142251	0.001763695	1	N	105	124
Q9CPR4	Infl	IEMIL	TEKEQIVPKPEEEVAQK	KKISQ	2		991.5261915	1981.036783	0.002145581	1	N	150	167
Q9CPR4	Infl	NAELK	GLDVDSLVIEHIQVNK	APKMR	2		889.9865052	1777.95741	0.000622848	1	N	105	121
Q9CPV4	Infl	EEKQR	ALLGYADNQCKLELQGIQGAVDHAAAFGR	IAFSC	4	C10:+57.021	772.3927717	3085.539887	0.000451244	6	N	172	201
Q9CPV4	Infl	WPLSK	VAEGIFETEAPGGYKFYLQDR	SPSQS	2		1195.587312	2389.159024	0.00091018	1	N	109	130
Q9CPV4	Infl	WPLSK	VAEGIFETEAPGGYK	FYLQD	2		784.3860925	1566.756585	0.000451244	4	N	109	124
Q9CPW4	Infl	QWHEK	ALAAGGVGSIVR	VLTAR	2		535.8199943	1069.624389	0.000451244	13	N	131	143
Q9CPW4	Infl	KYIYK	GFESPSDNSSAVLLQWHEK	ALAAG	2		1066.008697	2130.001795	0.000451244	23	N	112	131
Q9CPW4	Infl	ARFRK	VDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C32:+57.021	1253.850506	3758.528117	0.000451244	37	N	13	47

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CPW4	Infl	DLLMK	YIYKGFESPSDNSSAVLLQWHEK	ALAAG	3		900.110293	2697.307479	0.000451244	5	N	108	131
Q9CPX6	Infl	LIFLK	FVQAVIPTIEYDYTR	HFTM-	2		907.9703238	1813.925048	0.000998612	1	N	295	310
Q9CPX6	Infl	ACKAK	ADAGGEDAILQTR	TYDLY	2		658.826202	1315.636804	0.000622848	1	N	185	198
Q9CQ19	Infl	PIDKK	GNFNYVEFTR	ILKHG	2		623.7967162	1245.577832	0.000622848	2	N	151	161
Q9CQ19	Infl	EDVIR	NAFACFDEEASGFIHEDHLR	ELLTT	2	C5:+57.021	1183.019039	2364.022478	0.000451244	8	N	104	124
Q9CQ60	Infl	LVQPR	TGALCWFLDEAAAR	LLSVP	2	C5:+57.021	790.8802231	1579.744846	0.000451244	19	N	231	245
Q9CQ60	Infl	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	3	C25:+57.021	1342.358203	4024.051208	0.000451244	8	N	131	168
Q9CQ60	Infl	PPPQR	VTLTLPVLNAAQSIIFVATGEGK	AAVLK	2		1171.670648	2341.325695	0.000451244	13	N	185	208
Q9CQ60	Infl	-MAA	PAPSLISVFSSPQELGASLAQLVAQR	AASCL	3		889.4891044	2665.443913	0.000622848	3	N	3	29
Q9CQ60	Infl	HLLSK	LPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	2		1404.227244	2806.438887	0.000451244	16	N	102	128
Q9CQ60	Infl	AVLKR	ILEDKEGTLPAALVQPR	TGALC	2		925.5232548	1849.03091	0.000451244	13	N	214	231
Q9CQ60	Infl	YGLYR	THLLSKLPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	3		1162.954666	3485.840598	0.001352548	1	N	96	128
Q9CQ60	Infl	SMLAR	DLPAAAAPAGPASFAR	WTLGF	2		741.8891367	1481.762673	0.000698008	3	N	56	72
Q9CQ92	Infl	EDIRR	GIVLLEELLPK	GSKEE	2		612.3846358	1222.753672	0.001699387	4	N	53	64
Q9CQC6	Infl	DEKER	FDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	2	C9:+57.021	1449.197595	2896.379589	0.000998612	1	N	26	52
Q9CQC6	Infl	DPTQF	QDCIIQGLTETGTDLEAVAK	FLDAS	2	C3:+57.021	1081.536199	2161.056798	0.000451244	4	N	32	52
Q9CQC6	Infl	IKHLK	QYSPLLAAFTTQGQSELTLLLK	IQEYC	2		1211.665562	2421.315524	0.000451244	2	N	322	344
Q9CQE8	Infl	ELQTK	INEAIVAVQAIIADPK	TDHRL	2		832.9832342	1663.950868	0.000451244	3	N	218	234
Q9CQE8	Infl	VALEK	HILGFDTGDAVLNEAAQILR	LLHIE	2		1077.071632	2152.127664	0.000451244	4	N	185	205
Q9CQF3	Infl	PKNYK	LVAAPLFELYDNAPGYGPIISSLPQLLSR	FNFIY	3		1038.901174	3113.680121	0.000451244	7	N	192	221
Q9CQF3	Infl	VAAPL	FELYDNAPGYGPIISSLPQLLSR	FNFIY	2		1275.666094	2549.316587	0.000451244	4	N	198	221
Q9CQF9	Infl	KRFVK	ELGLSSVPASGGLVGVYNGK	SLVFE	2		952.5103444	1903.005089	0.002453667	2	N	104	124
Q9CQF9	Infl	NITFR	NFDPPIEEFNDPYQQLVTTFIK	GELNS	2		1328.153016	2654.290432	0.002212458	2	N	327	349
Q9CQI6	Infl	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVR	LFAFV	3	C22:+57.021	1023.793321	3068.356562	0.000451244	37	N	30	57
Q9CQI6	Infl	AMSKR	SKFALITWIGEDVSGLQR	AKTGT	2		1010.547261	2019.078923	0.000451244	5	N	73	91
Q9CQI6	Infl	SKRSK	FALITWIGEDVSGLQR	AKTGT	2		902.9837655	1803.951931	0.000451244	18	N	75	91
Q9CQI6	Infl	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVRLFAFVR	FTTGD	3	C22:+57.021	1268.269165	3801.784094	0.000451244	1	N	30	63
Q9CQI6	Infl	YNLVR	DDGSAVIWVTFR	YDGAT	2		683.3440306	1364.672461	0.000451244	19	N	18	30
Q9CQI6	Infl	TGTDK	TLVKEVVQNFAK	EFVIS	2		688.4013486	1374.787097	0.002145581	2	N	98	110
Q9CQI6	Infl	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVRLF	AFVRF	3	C22:+57.021	1110.510814	3328.509041	0.000451244	7	N	30	59
Q9CQI6	Infl	IWVTF	RYDGATIVPGDQGADYQHFIQQCTDDVR	LFAFV	3	C23:+57.021	1075.827025	3224.457674	0.000451244	7	N	29	57
Q9CQI7	Infl	FKEVR	LVPGRHDIAFVEFENDGQAGAAR	DALQG	3		823.747689	2468.219667	0.000622848	1	N	181	204
Q9CQK7	Infl	QTTLK	FTYSEKYPDETPLYEIFSQENLEDNDVSDILK	LLALQ	3		1281.267192	3840.778176	0.000622848	4	N	53	85
Q9CQK7	Infl	EAEKK	LFHGTPVTIENFLSWK	AKFDA	3		630.3372388	1887.988316	0.000637154	6	N	139	155
Q9CQM9	Infl	CGFSK	QILEILNSTGVEYETFDILEDEEVRQGLK	TFSNW	3		1127.575632	3379.703495	0.000451244	19	N	267	296
Q9CQM9	Infl	VSFVK	LEAEAVPEVSEKYEISSVPTFLFFK	NSQKV	3		953.8287923	2858.462977	0.000451244	12	N	69	94
Q9CQM9	Infl	LDIIK	ELEASEELDTICPK	APKLE	2	C12:+57.021	817.3852009	1632.754802	0.000823681	3	N	219	233
Q9CQM9	Infl	QLYVR	GDLVGGLDIVK	ELKDN	2		543.3142105	1084.612821	0.002374549	1	N	310	321
Q9CQM9	Infl	EILHK	HNIQFSSFDIFSDEEVR	QGLKT	2		1035.482315	2068.949031	0.000823681	5	N	173	190
Q9CQR6	Infl	NDLKR	LCDYVCDLLLEESNVQPVSTPVTVCGDIHGQFYDLCELFR	TGGQV	4	C2:+57.021,C6:+57.021,C25:+57.021,C36:+57.021	1191.055009	4760.188834	0.000622848	4	N	26	66
Q9CQR6	Infl	EIPHK	GAFCDLVWSDPEDVDTWAISPR	GAGWL	2	C4:+57.021	1268.576387	2535.137174	0.000451244	20	N	188	210
Q9CQR6	Infl	-M	APLDLDKYVEIAR	QCKYL	3		501.6124801	1501.81404	0.002019181	2	N	1	14
Q9CQV8	Infl	SGENK	QTTVSNSQQAYQEAFEISKK	EMQPT	2		1144.064201	2286.112802	0.000451244	2	N	140	160
Q9CQV8	Infl	SGENK	QTTVSNSQQAYQEAFEISK	KEMQP	2		1080.016719	2158.017839	0.000451244	33	N	140	159
Q9CQV8	Infl	GDYFR	YLSEVASGENKQTTVSNSQQAYQEAFEISK	KEMQP	3		1112.867586	3335.579357	0.000451244	3	N	129	159
Q9CQV8	Infl	MQLLR	DNLTLWTSENQGDEGDAGEGEN	-	2		1175.981259	2349.946918	0.000451244	16	N	224	246
Q9CQV8	Infl	CSLAK	TAFDEAIAELDTLNEESYK	DSTLI	2		1080.005486	2157.995372	0.000451244	14	N	195	214
Q9CQV8	Infl	CSLAK	TAFDEAIAELDTLNEESYKDSTLIMQLLR	DNLTL	3		1110.553951	3328.638453	0.000451244	14	N	195	224
Q9CQV8	Infl	EYREK	IEAELQDICNDVLELLDKYLILNATQAESK	VFYLK	3	C9:+57.021	1154.595884	3460.764252	0.000451244	9	N	87	117
Q9CQV8	Infl	EYREK	IEAELQDICNDVLELLDK	YLILN	2	C9:+57.021	1065.535668	2129.055735	0.000451244	13	N	87	105
Q9CQV8	Infl	IMQLL	RDNLTLWTSENQGDEGDAGEGEN	-	2		1254.031815	2506.048029	0.000451244	29	N	223	246
Q9CQV8	Infl	GKEYR	EKIEAELQDICNDVLELLDK	YLILN	2	C11:+57.021	1194.104446	2386.193292	0.000451244	3	N	85	105
Q9CQV8	Infl	GDYFR	YLSEVASGENKQTTVSNSQQAY	QEAFE	2		1202.567305	2403.119009	0.000451244	4	N	129	151
Q9CQV8	Infl	CSLAK	TAFDEAIAELDTLNEESY	KDSTL	2		1015.958004	2029.900409	0.000451244	17	N	195	213
Q9CQV8	Infl	AAAMK	AVTEQGHELSNEERNLLSVAY	KNVVG	2		1180.080382	2358.145165	0.001264573	3	N	29	50
Q9CQV8	Infl	EYREK	IEAELQDICNDVLEL	LDKYL	2	C9:+57.021	887.4326825	1772.849765	0.001654178	1	N	87	102
Q9CR16	Infl	EKPAK	LCVIAECGELKEGDDWGIFPK	DGSGD	2	C2:+57.021,C7:+57.021	1218.582395	2435.14919	0.000870037	2	N	174	195
Q9CR68	Infl	HRTKK	EIDQEAAVEVSQLRDPQHDLDR	VKKPE	4		641.5655549	2562.23102	0.002296037	1	N	182	204
Q9CR86	Infl	KCFCR	SKGHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTYK	MCSIP	4		1019.496164	4073.953456	0.002981883	1	N	73	111
Q9CR86	Infl	FCRSK	GHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTY	KMCSI	3		1244.584967	3730.731501	0.001162105	2	N	75	110
Q9CR86	Infl	FCRSK	GHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTYK	MCSIP	3		1287.283288	3858.826464	0.000622848	2	N	75	111
Q9CRA5	Infl	VECLK	ANTNEVLWAVVAAFTK	-	3		578.6460724	1732.914817	0.000451244	10	N	282	298
Q9CRA5	Infl	LKHVK	ETQPPETVQNWIELLSGETWNPLK	LHYQL	3		937.1401408	2808.397022	0.000823681	2	N	141	165
Q9CRB2	Infl	MTKVK	AAPEESEAQAEGCSEERTY	KELLV	2	C13:+57.021	1057.43467	2112.853741	0.000451244	3	N	5	24

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CSU0	Infl	EELIK	ALQDLENAASGDATVR	QKIAS	2		815.9057121	1629.795824	0.000451244	7	N	182	198
Q9CSU0	Infl	PEFTR	EFESVLVDAFSHVAR	EADEG	3		569.2901771	1704.847131	0.001162105	4	N	79	94
Q9CSU0	Infl	RKELK	SHIQSLPDLSLLPNVTGGLAPLPSAGDLFSTD	-	3		1078.229907	3231.666321	0.000451244	19	N	294	326
Q9CU62	Infl	CVISK	VLTFDLTKYPDANPNPNEQ	-	2		1088.532005	2175.04841	0.000451244	17	N	1214	1233
Q9CU62	Infl	KALSR	NSSAQAFLGPENPEEPYLDGINYNCVAPGKR	FRPMD	3	C25:+57.021	1136.537251	3406.588354	0.002813207	1	N	1090	1121
Q9CU62	Infl	EFYTK	AESLIGVYPEQGDCVISK	VLTFD	2	C14:+57.021	982.9856136	1963.955627	0.000451244	6	N	1196	1214
Q9CVB6	Infl	SVFEK	YFQFQEEGKEGENR	AVIHY	2		880.897887	1759.780174	0.000451244	37	N	127	141
Q9CVB6	Infl	NATAR	DNTINLIHTF	RDYLH	2		594.3069168	1186.598234	0.000451244	13	N	237	247
Q9CVB6	Infl	DELLK	RVYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1085.563109	3253.665927	0.000451244	20	N	77	106
Q9CVB6	Infl	LFSHR	EPPLELKDTDAAVGDNIGYITFVLFPR	HTNAT	3		997.5223623	2989.543687	0.000451244	21	N	203	230
Q9CVB6	Infl	ELLKR	VYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1033.529405	3097.564816	0.000451244	18	N	78	106
Q9CVB6	Infl	PLELK	DTDAAVGDNIGYITFVLFPR	HTNAT	2		1092.552741	2183.089881	0.000451244	15	N	210	230
Q9CVB6	Infl	VTVVF	STVFKDDDDVVIGK	VFMQE	2		769.3913749	1536.76715	0.000451244	9	N	165	179
Q9CVB6	Infl	LKFYK	ELQAHGADELLKR	VYGSF	2		740.3998686	1478.784137	0.000870037	2	N	65	78
Q9CVB6	Infl	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTK	VMVSI	3		1289.294298	3864.859495	0.000451244	4	N	18	54
Q9CVB6	Infl	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK	TKVMV	3		1212.913418	3635.716854	0.000451244	9	N	18	52
Q9CVB6	Infl	ELLKR	VYGSFLVNPEPGYNVSLL	YDLEN	2		984.5098131	1967.004026	0.002145581	4	N	78	96
Q9CVB6	Infl	TLALK	FENAAAGNKPEAVEVTFADFDGVLY	HISNP	2		1337.63773	2673.25986	0.000451244	7	N	18	43
Q9CW03	Infl	FAIQK	CDPAPFYLFDEIDQALDAQHR	KAVSD	3	C1:+57.021	841.053636	2520.137508	0.000823681	1	N	1133	1154
Q9CW03	Infl	GESER	GSGSQSSVPSVDQFTGVGIR	VSFTG	2		982.9877648	1963.95993	0.001162105	3	N	1079	1099
Q9CWF2	Infl	QIGAK	FWEVISDEHGIDPTGSYHGDSDLQLER	INVYY	3		1034.80789	3101.40027	0.000451244	23	N	19	46
Q9CWF2	Infl	IGAKF	WEVISDEHGIDPTGSYHGDSDLQLER	INVYY	3		985.7850854	2954.331856	0.000451244	5	N	20	46
Q9CWF2	Infl	DVVRK	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	E1:-18.011,C5:+57.021,C7:+57.021	1103.8444	3308.5098	0.000698008	1	N	122	154
Q9CWJ9	Infl	DRAKR	SGVAYIVAPSGSTADKVVIEACDELGIVLAHTDLR	LFHH-	4	C22:+57.021	907.4742245	3625.865698	0.001162105	4	N	553	588
Q9CWJ9	Infl	TLKPK	LPITVLNGAPGFINLCDALNAWQLVTELR	GAVDI	3	C16:+57.021	1070.244792	3207.710975	0.000451244	19	N	225	254
Q9CWJ9	Infl	KIISR	EVSDGIVAPGYEEEALK	ILSKK	2		903.4443358	1804.873072	0.000451244	11	N	335	352
Q9CWJ9	Infl	EDLVK	WEALFEEVPELLTEAEKK	EWVDK	3		721.0408163	2160.099049	0.000451244	3	N	507	525
Q9CWJ9	Infl	AASFK	HVSPAGAAVGVPLSEDEAR	VCMVY	2		931.4742933	1860.932987	0.000451244	5	N	266	285
Q9CWJ9	Infl	VEFAR	SLASLGLSLVASGGTAK	AIRDA	3		511.2950396	1530.861719	0.00091018	3	N	22	39
Q9CWJ9	Infl	AGVKR	AEISNAIDQYVTGTIGEGEDLVK	WEALF	2		1211.603356	2421.191112	0.000451244	2	N	484	507
Q9CWK3	Infl	DAQIR	DSWLDNIDWVR	IKERP	2		709.8391124	1417.662625	0.000451244	2	N	115	126
Q9CWK3	Infl	MPKRK	VTFQGVGDEDGEDEISVPK	KKLVD	2		1010.971446	2019.927292	0.001162105	1	N	5	24
Q9CWK8	Infl	DSPER	ELILSSEPSPAVTPVTPTTLIAPR	IESKS	2		1245.197227	2488.378853	0.000451244	1	N	88	112
Q9CWK8	Infl	TALSR	ALSQLAEVEEK	IDQLH	2		608.8251394	1215.634679	0.002663018	1	N	362	373
Q9CWZ3	Infl	GSRAR	MREDYDSVEQDGDEPGPQR	SVEGW	3		741.6472007	2221.918202	0.000451244	5	N	49	68
Q9CWZ3	Infl	GWILF	VTGVHEEATEEDIHDKFAEYGEIK	NIHLN	3		916.1001223	2745.276967	0.000451244	1	N	76	100
Q9CWZ7	Infl	ERAGK	LIENVDPEKAVQLYQQTANVFENEER	LRQAV	3		1026.179435	3075.514906	0.001871652	1	N	123	149
Q9CWZ7	Infl	VDPEK	AVQLYQQTANVFENEER	LRQAV	2		1019.99559	2037.97558	0.000451244	1	N	132	149
Q9CX34	Infl	EELTK	ALEQNPDDAQYYCQR	AYCHI	2	C13:+57.021	935.9051548	1869.79471	0.000451244	15	N	36	51
Q9CX34	Infl	ASSQR	LFQSFSDALIDGDPQAALEELTK	ALEQN	2		1254.629374	2507.243147	0.000451244	7	N	13	36
Q9CX34	Infl	ASSQR	LFQSFSDALIDGDPQAALEELTKALEQNPDDAQYYCQR	AYCHI	3	C36:+57.021	1454.016899	4359.027297	0.000451244	8	N	13	51
Q9CX56	Infl	YAKKR	GWVLGPNNYYSFASQQQKPEDSTIPSTELAK	QVIEY	3		1152.563837	3454.668112	0.000451244	17	N	309	340
Q9CX56	Infl	SYTFF	IDILLDTIRDEIAGCIEK	AYEKI	3	C15:+57.021	696.3736468	2086.097541	0.000451244	9	N	262	280
Q9CX56	Infl	VFLAK	GNIPAESYTFFIDILLDTIRDEIAGCIEK	AYEKI	3	C26:+57.021	1105.227244	3312.658331	0.000622848	1	N	251	280
Q9CX86	Infl	AKVKK	LFVGGLKGDVAEGDLIEHFSQFGAVEK	AEIIA	3		954.8277857	2861.459957	0.000622848	4	N	99	126
Q9CX86	Infl	SQLCK	LFIGGLNVQTSESGLR	GHFEA	2		845.9602904	1689.904981	0.000451244	8	N	8	24
Q9CX86	Infl	VGGLK	GDVAEGDLIEHFSQFGAVEK	AEIIA	2		1074.516355	2147.01711	0.000451244	6	N	106	126
Q9CXF4	Infl	NCQNK	SLSQSFENLLDEPAYGLIQK	IKKDP	2		1126.576413	2251.137226	0.000622848	8	N	200	220
Q9CXF4	Infl	IPGLK	INQQEEPGFEVITR	IDLGE	2		830.420998	1658.826396	0.002727428	1	N	271	285
Q9CXI5	Infl	GKENR	LCYYIGATDDAATK	IINEV	2	C2:+57.021	781.3640715	1560.712543	0.000451244	7	N	70	84
Q9CXI5	Infl	DAATK	IINEVSKPLAHHIPVEK	ICEKL	3		642.0391929	1923.094179	0.001654178	2	N	84	101
Q9CXI5	Infl	PDSRA	LRPGDCEVCISYLGR	FYQDL	2	C6:+57.021,C9:+57.021	897.9349724	1793.854345	0.000451244	2	N	21	36
Q9CXI5	Infl	DLKDR	DVTFSPATIEEELIK	FCREA	2		846.4410648	1690.86653	0.000451244	5	N	44	59
Q9CXR1	Infl	KHALR	GFFNALHSELGQYPGITFCNVYPGPVQSDIVK	NAFTE	3	C19:+57.021	1185.585654	3553.733561	0.000823681	1	N	211	243
Q9CXW4	Infl	TRAAK	VLEQLTGQTPVFSK	ARYTV	2		773.9279275	1545.840255	0.000622848	16	N	38	52
Q9CXY6	Infl	SLVTK	INNVIDNLIVAPGTFEVQIEEVR	QVGSY	2		1291.695382	2581.375165	0.000451244	3	N	80	103
Q9CXY6	Infl	ALLKR	NQDLAPNSAEQASILSLVTK	INNVI	2		1050.053105	2098.09061	0.000451244	11	N	60	80
Q9CY50	Infl	GFTNK	GTEDFIVESLDASFR	YPQDY	2		843.4050136	1684.794427	0.000451244	7	N	110	125
Q9CY50	Infl	DEDDE	AEVEEDEPTDLAEDKEEEDVSSEPEASPSADTTILFVK	GEDFP	3		1384.296093	4149.864879	0.000451244	19	N	53	91
Q9CY58	Infl	VTNRF	DQLFDDESDPFEVLK	AAENK	2		898.9154111	1795.815222	0.000451244	3	N	17	32
Q9CY58	Infl	-M	PGHLQEGFGCVVTNRFDQLFDDESDPFEVLK	AAENK	3	C10:+57.021	1199.231828	3594.672083	0.000451244	2	N	1	32
Q9CY58	Infl	NRGSR	TDKSSASAPDVDDPEAFPALA	-	2		1052.490003	2102.964406	0.002727428	1	N	386	407
Q9CY58	Infl	FDQLF	DDESDPFEVLK	AAENK	2		647.2964117	1292.577223	0.001352548	4	N	21	32
Q9CYA0	Infl	AGYTK	ESGQCTDIDECSLEEK	ACKRK	2	C5:+57.021,C11:+57.021	950.3828293	1898.750059	0.000451244	20	N	281	297

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CYA0	Infl	VHTLK	ACCLPGTYGPDCQECQGGSERPCSGNGYCSGDGSR	QGDGS	3	C2:+57.021,C3:+57.021,C12:+57.021,C15:+57.021,C23:+57.021,C29:+57.021	1286.156694	3855.446681	0.000451244	18	N	123	158
Q9CYA0	Infl	HTGYK	GPLCIDCTDGFFSLQR	NETHS	2	C4:+57.021,C7:+57.021	943.4322626	1884.848925	0.000451244	7	N	171	187
Q9CYA6	Infl	FCLDK	LGQPLLNENPQLTEGWEIPK	YQQVF	2		1138.600222	2275.184844	0.000451244	5	N	185	205
Q9CYG7	Infl	LKDYK	SSLSDISSLLQIEPR	NGPAQ	2		822.944306	1643.873012	0.000451244	5	N	278	293
Q9CYG7	Infl	YVDYK	TVLQIDNSVASALEGINR	ITRAL	2		950.5108758	1899.006152	0.000735798	1	N	109	127
Q9CYL5	Infl	FVVAR	YFPAGNIVNQGFFEENVPPPKK	-	2		1246.634596	2491.253593	0.000451244	5	N	132	154
Q9CYL5	Infl	PESSR	GQCGENLAWASYDQTGK	DVADR	2	C3:+57.021	942.9129799	1883.81036	0.000451244	9	N	60	77
Q9CZ04	Infl	RDIQR	QDLSAIAQTLQEWCVGCEVVLSGIEEQVSR	ANQHK	3	C14:+57.021,C17:+57.021	1135.553759	3403.637878	0.000451244	13	N	164	194
Q9CZ13	Infl	KNILR	NALVSHLDGTTPVCEDIGR	SLLTY	2	C14:+57.021	1027.502493	2052.989387	0.000451244	16	N	396	415
Q9CZ13	Infl	FKGTK	NRPGNALEKEVESIGAHLNAYSTR	EHTAY	3		876.116441	2625.325923	0.002727428	2	N	102	126
Q9CZ13	Infl	DICSK	YFYDQCPAVAGYGPIEQLPDYNR	IRSGM	2	C6:+57.021	1368.623868	2735.232137	0.000451244	24	N	447	470
Q9CZ13	Infl	KDLPK	VVELLADIVQNSSLEDSQIEKER	DVILR	2		1307.682669	2613.349738	0.002145581	2	N	142	165
Q9CZ13	Infl	PALRG	TATFAQALQSVPETQVSILDNGLR	VASEQ	2		1280.174814	2558.334028	0.000451244	12	N	34	58
Q9CZ13	Infl	DICSK	YFYDQCPAVAGYGPIEQLPDYNRIR	SGMFW	3	C6:+57.021	1002.480237	3004.417312	0.001162105	1	N	447	472
Q9CZ13	Infl	NALEK	EVESIGAHLNAYSTR	EHTAY	2		823.9107974	1645.805995	0.000451244	1	N	111	126
Q9CZ13	Infl	KDLPK	VVELLADIVQNSSLEDSQIEK	ERDVI	2		1165.110817	2328.206034	0.000451244	7	N	142	163
Q9CZ30	Infl	KPASK	IPAFLNVVDIAGLVK	GAHNG	2		784.9746808	1567.933762	0.000451244	9	N	83	98
Q9CZ30	Infl	KSTFF	NVLTNSQASAENFPFCTIDPNESR	VPVPD	2	C16:+57.021	1356.122221	2710.228842	0.001162105	1	N	39	63
Q9CZ44	Infl	GGGYR	LGAAPEEESAYVAGER	RRHSG	2		824.894813	1647.774026	0.000451244	6	N	156	172
Q9CZ44	Infl	GEGQK	LGSTAPQVLNTSSPAQQAENEAK	ASSSI	2		1171.085665	2340.155729	0.000451244	24	N	259	282
Q9CZ44	Infl	ENEAK	ASSSILINEAEPTTNIQIR	LADGG	2		1029.047822	2056.080045	0.000451244	17	N	282	301
Q9CZ44	Infl	NGDLR	SYQDPSNAQFLESIR	RGEVP	2		877.9213622	1753.827124	0.000451244	12	N	199	214
Q9CZ44	Infl	RVTSF	RDLIHDQDEEEEEEEGQR	FYAGG	3		752.6602744	2254.957423	0.001162105	1	N	75	93
Q9CZD3	Infl	ARKMR	LGDAVEQGVINNSVLGYFIGR	IYLYL	2		1111.084739	2220.153879	0.002663018	1	N	381	402
Q9CZD3	Infl	KRFQK	TLHVEEVVPSVIEPSFGLGR	IMYTI	2		1083.084208	2164.152816	0.00091018	1	N	553	573
Q9CZD3	Infl	GDEQR	TFFSFPAVVAPFK	CSVLP	2		729.3955349	1456.77547	0.000622848	10	N	592	605
Q9CZD3	Infl	DAESK	TSYGWIEIVGCADR	SCYDL	2	C11:+57.021	813.8829627	1625.750325	0.000870037	2	N	440	454
Q9CZN7	Infl	LCQRR	ALEAFDLDPAQWGVNVQPYSGSPANLAAYTALLQPHDR	IMGLD	3		1366.012014	4095.012642	0.000451244	18	N	122	160
Q9CZN7	Infl	YPGKR	YYGGAEVVDEIELLCQR	RALEA	2	C15:+57.021	1007.483238	2012.950876	0.000451244	10	N	104	121
Q9CZN7	Infl	LCQRR	ALEAFDLDPAQWGVNVQPY	SGSPA	2		1067.018534	2132.021467	0.000451244	11	N	122	141
Q9CZN7	Infl	SMPYK	LNPQTGLIDYDQLALTAR	LFRPR	2		1001.534351	2001.053102	0.000451244	5	N	196	214
Q9CZN7	Infl	ARAER	VLELVSITANKNTCPGDR	SAITP	2	C14:+57.021	994.0177794	1986.019959	0.000451244	1	N	398	416
Q9CZN7	Infl	ARAER	VLELVSITANK	NTCPG	2		593.8562425	1185.696885	0.000451244	3	N	398	409
Q9CZN7	Infl	LLCQR	RALEAFDLDPAQWGVNVQPY	SGSPA	2		1145.069089	2288.122578	0.002296037	1	N	121	141
Q9CZU6	Infl	MRGMK	GLVYETSVLDPDEGIR	FRGYS	2		881.9470456	1761.878491	0.000451244	2	N	76	92
Q9CZU6	Infl	FGVSR	ALGVLAQLIWSR	ALGFP	2		663.8987761	1325.781952	0.000622848	2	N	428	440
Q9CZX8	Infl	-M	PGVTVKDVNQQEFVR	ALAAF	2		858.4579148	1714.90023	0.000451244	8	N	1	16
Q9CZX8	Infl	KKSGK	LKVPEWVDTVK	LAKHK	3		438.5874948	1312.739084	0.000451244	5	N	27	38
Q9D020	Infl	NFFGK	LQQHGIPVFIFSAGIGDVLEEVIR	QAGVY	3		879.8186733	2636.43262	0.000451244	6	N	186	210
Q9D020	Infl	LLQLK	EQYYAIEVDPVLTVEEK	FPYMV	2		1013.0073	2023.999001	0.000451244	4	N	123	140
Q9D020	Infl	DGALK	NTDYFSQLKDNSNIILLGDSQGDLR	MADGV	2		1413.699382	2825.383163	0.000451244	3	N	253	278
Q9D020	Infl	LLEKY	MDSYDIVLVKEESLEVVNSILQK	TL-	3		884.4669779	2650.377534	0.000662267	2	N	306	329
Q9D0E1	Infl	NGKSK	GCGVVKFESPEVAER	ACRMM	2	C2:+57.021	832.4093447	1662.803089	0.000451244	4	N	691	706
Q9D0E1	Infl	IEMER	GNFGGSFAGSFGGAGGHAPGVAR	KACQI	2		1017.980608	2033.945617	0.000451244	5	N	626	649
Q9D0F3	Infl	NDGKK	NNPAIVVIGNNGQINYDHQNDGATQALASCQR	DFRNK	3	C30:+57.021	1151.550554	3451.628261	0.000451244	6	N	168	200
Q9D0F3	Infl	SETVR	LVSGIQHPGSAGVYETTQHF	MDIKE	2		1064.527057	2127.038514	0.000622848	2	N	423	443
Q9D0F9	Infl	ATMLR	NIFDFNALKELLSGPNR	LKIRI	3		650.0149359	1947.021408	0.001395409	2	N	200	217
Q9D0F9	Infl	MILGK	HGFFVNPSDSVAVIAANIFSIPYFQQTGVR	GFARS	3		1094.563443	3280.66693	0.000622848	6	N	299	329
Q9D0F9	Infl	YTVEK	ADNFEYSDPVDGSISK	NQGLR	2		872.3895605	1742.763521	0.000735798	3	N	470	486
Q9D0F9	Infl	SNANY	AENFIQSIVSTVEPALRQEATLVVGGDGR	FYMTE	3		1019.539075	3055.593825	0.000451244	6	N	35	64
Q9D0F9	Infl	SNANY	AENFIQSIVSTVEPALR	QEATL	2		937.5050621	1872.994524	0.000451244	1	N	35	52
Q9D0F9	Infl	FQISK	TIEEYAICPDLK	VDLGV	2	C8:+57.021	726.3582578	1450.700916	0.001463592	1	N	152	164
Q9D0I9	Infl	VHLRK	DFVSEQLTSLLVNGVQLPVLGDKEK	VIVDF	3		910.1642864	2727.469459	0.000451244	17	N	168	193
Q9D0I9	Infl	GCAIR	AAYPDLENPPLIVTPSQQPK	FGDYQ	2		1089.576216	2177.136832	0.000451244	18	N	89	109
Q9D0I9	Infl	DDGRK	IVFVPGCSVPLTIVK	SDGGY	2	C7:+57.021	814.9761349	1627.93667	0.000662267	4	N	362	377
Q9D0K2	Infl	GALLK	TGVKDLTAVSNNAGVDNFGLGLLLR	SKQIK	3		848.7980493	2543.370748	0.000451244	4	N	79	104
Q9D0K2	Infl	AERIR	AGGAGVPAFYTSTGYGTLVQEGGSPIK	YNKDG	2		1293.148265	2584.28093	0.000823681	1	N	146	173
Q9D0K2	Infl	KTGVK	DLTAVSNNAGVDNFGLGLLLR	SKQIK	2		1080.076914	2158.138229	0.000451244	10	N	83	104
Q9D0K2	Infl	VEAVK	DIPNGATLLVGGFGLCGIPENLIGALLK	TGVKD	3	C16:+57.021	941.5213739	2821.540722	0.000451244	2	N	51	79
Q9D0K2	Infl	HTKFY	TDPVEAVKDIPNGATLLVGGFGLCGIPENLIGALLK	TGVKD	3	C24:+57.021	1221.334335	3660.979606	0.002519933	1	N	43	79
Q9D0L8	Infl	NACGR	LNPGGYFIGTTPNSFELIR	RLEAS	2		1048.544719	2095.073837	0.000451244	5	N	296	315
Q9D0L8	Infl	ASGQR	LPENTPPCQQVDQPK	MQKEF	2	C8:+57.021	875.9253589	1749.835118	0.000622848	8	N	29	44
Q9D0L8	Infl	PKMQK	EFGEDLVEQNSSYVQDSPSK	KRKLD	2		1129.508924	2257.002248	0.000998612	1	N	47	67

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D0L8	Infl	EGSAK	ASVASDPESPPGGNEPAAASGQR	LPENT	2		1076.499225	2150.98285	0.000622848	3	N	6	29
Q9D0M1	Infl	DVGGR	IAIIVDDIIDDVESFVAAAEILKER	GAYKI	3		919.8360583	2756.484775	0.001162105	1	N	250	275
Q9D0M1	Infl	DVGGR	IAIIVDDIIDDVESFVAAAEILK	ERGAY	3		824.7881569	2471.341071	0.001463592	1	N	250	273
Q9D0M3	Infl	MRPGK	LSDYFPKPYPNPEAAR	AANNG	3		622.3129818	1863.915545	0.000451244	11	N	170	186
Q9D0M3	Infl	IVRAR	HGGEDYVFSLLTGYCEPPTGVSLR	EGLYF	2	C15:+57.021	1327.631693	2653.247787	0.000451244	12	N	204	228
Q9D0T1	Infl	HLTKK	LLDLVQQSCNYK	QLRKG	2	C9:+57.021	740.877149	1479.738698	0.000451244	1	N	21	33
Q9D0T1	Infl	GSQLK	QQIQSIQQSIER	LLV-	2		729.3895008	1456.763402	0.000451244	5	N	113	125
Q9D154	Infl	AQLSK	TFHFDSVEDIHSR	FQSLN	2		795.3713081	1588.727016	0.000451244	30	N	56	69
Q9D154	Infl	EWTKR	ENLEFIDVHVKLPR	FKIEE	2		854.9732008	1707.930802	0.001763695	1	N	261	275
Q9D154	Infl	LYGEK	TYNFLPEYLASTQK	MYGAD	2		837.9228422	1673.830084	0.000451244	15	N	96	110
Q9D154	Infl	ASTQK	MYGADLAPVDFLHASEDAR	KEINQ	2		1039.486544	2076.957488	0.000451244	4	N	110	129
Q9D154	Infl	IFFIR	HNPTSNVLFLGR	VCSP-	2		677.8654646	1353.715329	0.002296037	3	N	363	375
Q9D154	Infl	VKLPR	FKIEESYTLNSNLGR	LGVQD	2		885.955205	1769.89481	0.000451244	39	N	275	290
Q9D154	Infl	ASTQK	MYGADLAPVDFLHASEDARK	EINQW	2		1103.534026	2205.052451	0.000823681	1	N	110	130
Q9D154	Infl	SNLGR	LGVQDLFSSSK	ADLSG	2		590.8145747	1179.613549	0.000451244	21	N	290	301
Q9D154	Infl	DSMTK	LVLVNAIYFK	GMWEE	2		590.3609637	1178.706327	0.002374549	1	N	158	168
Q9D154	Infl	LPRFK	IEESYTLNSNLGR	LGVQD	2		748.3735164	1494.731433	0.000451244	3	N	277	290
Q9D154	Infl	FFSPF	SISSALAMVILGAK	GSTAA	2		680.897585	1359.77957	0.001463592	1	N	33	47
Q9D154	Infl	KIVHK	SFVEVNEEGTEAAAATGGIATF	CMLLP	2		1086.011103	2170.006605	0.000451244	77	N	321	343
Q9D154	Infl	GIATF	CMLLPEEEFTVDHPFIFFIR	HNPTS	2	C1:+39.994	1262.108055	2522.20051	0.002813207	1	N	343	363
Q9D154	Infl	FALEL	FQTLNESSPTGNIFFSPFSISSALAMVILGAK	GSTAA	3		1125.583405	3373.726814	0.000622848	3	N	15	47
Q9D154	Infl	ANTLF	ALELFQTLNESSPTGNIFFSPFSISSALAMVILGAK	GSTAA	3		1267.666017	3799.97465	0.000823681	6	N	11	47
Q9D154	Infl	NQWVK	GQTEGKIPELLSVGVVDSMTK	LVLVN	2		1094.580641	2187.145683	0.000622848	1	N	137	158
Q9D154	Infl	EWTKR	ENLEFIDVHVK	LPRFK	3		448.2387541	1341.692862	0.000622848	4	N	261	272
Q9D1A2	Infl	DPQKK	TVCIYGHLDVQPAALEDGWDSEPFTLVER	EGKLY	3	C3:+57.021	1106.531326	3316.570578	0.000451244	16	N	92	121
Q9D1A2	Infl	VDIGK	QKLPDGSEIPLPPILLGK	LGSDP	3		639.0474655	1914.118996	0.000637154	4	N	66	84
Q9D1G1	Infl	CLLLR	FADDTYTESYISTIGVDFK	IRTIE	2		1086.505122	2170.994644	0.000451244	8	N	27	46
Q9D1G1	Infl	NTTAK	EFADSLGVPFLETSAK	NATNV	2		855.9334069	1709.851214	0.000735798	5	N	137	153
Q9D1K2	Infl	AGRGK	LIAVIGDEDTVTGFLLGGIGELNK	NRHPN	2		1222.668302	2443.321004	0.000451244	17	N	6	30
Q9D1L9	Infl	NLGCR	GTLSDEHAGVISVLAQQAAR	LTSDP	2		1012.032507	2022.049413	0.000451244	4	N	34	54
Q9D1M0	Infl	SDWVR	DVAWAPSIGLPTSTIASCSQDGR	VFIWT	2	C18:+57.021	1195.076554	2388.137508	0.000451244	4	N	216	239
Q9D1M0	Infl	VTLWK	ESVDGQWVCISDVNK	GQGSV	2	C9:+57.021	868.4017167	1734.787833	0.001162105	2	N	290	305
Q9D1P4	Infl	CCKRR	TTDFSDFLSIVGCTK	GRHNS	2	C13:+57.021	845.9035608	1689.791522	0.000451244	10	N	46	61
Q9D1P4	Infl	CCRRK	TSDFNTFLAQEGCTR	GKHVW	2	C13:+57.021	873.8915161	1745.767432	0.000451244	4	N	198	213
Q9D1Q6	Infl	LHSGK	LHREFHHGPDPTDTAPGEQDQDVASSPPESSFQK	LAPSE	3		1248.570602	3742.688407	0.002019181	3	N	355	389
Q9D1Q6	Infl	RVFER	VASILHDDCAFLSAFGDLSKPER	YNGDN	3	C9:+57.021	850.0885692	2547.242308	0.000823681	1	N	180	203
Q9D1Q6	Infl	IRQQK	SNPVHEIQSLDEVTNLDR	SKRNI	2		1033.511604	2065.007608	0.000451244	18	N	140	158
Q9D2C2	Infl	LQEQK	TVLASVFSVLSAISASR	AEQEH	3		569.9933607	1706.956682	0.000451244	5	N	320	337
Q9D2C2	Infl	NDTWR	LLFDLVCHEFCQPDDPPVILQEQK	TVLAS	3	C7:+57.021,C11:+57.021	980.8140744	2939.418823	0.000622848	3	N	296	320
Q9D2C2	Infl	MKILK	DISCEFLSNIFQVLTK	EKVAQ	2	C4:+57.021	957.4877921	1912.959984	0.000451244	9	N	397	413
Q9D2V7	Infl	VYEPR	SSPLPLQEGPGPEGGR	GARIV	2		789.4000656	1576.784531	0.000622848	8	N	664	680
Q9D2V7	Infl	AMVAK	LGNREDPLPQDSFEGVDEDEWD	-	2		1281.549309	2561.083018	0.000451244	20	N	900	922
Q9D2V7	Infl	GRGAR	IVWVCDGGCLLVSGFDSR	SERQL	2	C5:+57.021,C9:+57.021	1020.487569	2038.959538	0.000451244	7	N	683	701
Q9D2V7	Infl	PRVRK	EFFQDDVFPDTAVTWEPALSAK	AWFEG	2		1257.097709	2512.179819	0.000451244	19	N	817	839
Q9D2V7	Infl	ITNLK	GLNLTTPGESDGFCANR	LRVAV	2	C14:+57.021	904.9155225	1807.815445	0.000451244	15	N	488	505
Q9D2V7	Infl	VLLPK	TECDIQDVEFAR	CLRLR	2	C3:+57.021	741.8303958	1481.645192	0.000451244	17	N	784	796
Q9D2V7	Infl	VLAGK	GENQLYCYEVTPQQPALSPVTQCILENVLR	GAALV	3	C7:+57.021,C23:+57.021	1173.913287	3518.716462	0.000451244	16	N	280	310
Q9D2V7	Infl	LPRVR	KEFFQDDVFPDTAVTWEPALSAK	AWFEG	2		1321.145191	2640.274782	0.001162105	1	N	816	839
Q9D2V7	Infl	IRLWR	VPPGGLENVLTTPETVLTGHTEK	IYSLR	3		797.0923508	2388.253652	0.001699387	1	N	570	593
Q9D2V7	Infl	LWDTR	LFSSALASVTLDTSPGPLIPLLDPDSGLLVLAGK	GENQL	3		1126.632641	3376.874524	0.000622848	12	N	246	280
Q9D2V7	Infl	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHK	GFVLL	3	C16:+57.021	1028.500527	3082.478181	0.000451244	9	N	751	777
Q9D2V7	Infl	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHKGFVLLPK	TECDI	3	C16:+57.021	1279.991909	3836.952328	0.000823681	2	N	751	784
Q9D2V7	Infl	RHVTY	LGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	3	C3:+57.021	1024.141839	3069.402116	0.000451244	11	N	72	100
Q9D2V7	Infl	QLQLY	IADALAQGPSALLGLDVAPSTLLPSYDPDTGLVLLTGK	GDTRV	3		1255.019224	3762.034272	0.001162105	4	N	709	747
Q9D2V7	Infl	RKEFF	QDDVFPDTAVTWEPALSAK	AWFEG	2		1045.507999	2089.000398	0.000622848	2	N	820	839
Q9D3D9	Infl	SANVK	QVDVPTLTGAFGILASHVPTLQVLRPGLVVVHTEDGTTTK	YFVSS	3		1389.765781	4166.273942	0.000451244	6	N	56	96
Q9D554	Infl	LLKAR	ENPSEEAQNLVEFTDEEGYGR	YLDLH	2		1207.02547	2412.035339	0.000451244	11	N	117	138
Q9D554	Infl	KASER	WQPDTEEEYEDSSGNVVNKK	TYEDL	3		785.3526703	2353.034611	0.000698008	5	N	470	490
Q9D554	Infl	DGLRK	EELNAISGPNEFAEFYNR	LKQIK	2		1050.487598	2098.959595	0.000451244	6	N	69	87
Q9D554	Infl	DYITY	LSIFDQLFDIPK	ERKNA	2		718.3957319	1434.775864	0.002212458	2	N	163	175
Q9D5V6	Infl	ISLIK	QSAQLTALAAQQQASGKEEK	SSNRD	3		696.3629525	2086.065457	0.001463592	1	N	224	244
Q9D5V6	Infl	RDGDK	LSAGAAPSEESPERPVEPTEEQQQQPPTEDPQFLHQAK	GLGNY	4		1046.502243	4181.977773	0.000622848	8	N	31	69
Q9D5V6	Infl	KSQLK	SQEDEEEISTSPGVSEFVSDAFDTCSLNQEDLRK	EMEQL	3	C25:+57.021	1283.569451	3847.684952	0.000451244	6	N	272	306
Q9D6F9	Infl	PRGLK	MAATFIGNSTAIQELFK	RISEQ	2	M1:+15.995	929.4749593	1856.934319	0.000451244	5	N	362	379
Q9D6F9	Infl	PRGLK	MAATFIGNSTAIQELFKR	ISEQF	3	M1:+15.995	672.0196099	2013.03543	0.000870037	1	N	362	380

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D6J6	Infl	EAIVK	NYPEGHQAAAVLPVLDLAQR	QNGWL	3		721.3837994	2161.127998	0.002453667	1	N	67	87
Q9D6J6	Infl	PRSGR	FCCEPAGGLTSLTEPPKGPGFGVQAGL	-	2	C2:+57.021,C3:+57.021	1374.162072	2746.308544	0.000451244	5	N	221	248
Q9D6J6	Infl	DLTPK	DIEEIIDELK	AGKVP	2		608.8195227	1215.623445	0.000735798	5	N	198	208
Q9D6J6	Infl	LFVHR	DTPENNPDTPFDFTPENYKR	IEAIV	2		1199.03564	2396.055681	0.002813207	1	N	41	61
Q9D6R2	Infl	IEGYK	TPYTDVNIVTIRENTEGEYSGIEHVIVDGVVQSIK	LITEE	4		969.4987066	3873.963626	0.000823681	2	N	134	169
Q9D6R2	Infl	IVTIR	ENTEGEYSGIEHVIVDGVVQSIK	LITEE	2		1251.62208	2501.22856	0.000823681	2	N	146	169
Q9D6Y7	Infl	AEVVR	VVYRPEHISFEELLK	VFWEN	4		465.5075203	1857.998881	0.000451244	2	N	118	133
Q9D6Y7	Infl	DSASK	VISAEEALPGRTEPIPVTAK	HHVSG	2		1039.578758	2077.141917	0.000451244	9	N	27	47
Q9D6Y7	Infl	TTDIR	EGQVFYYAEDYHQQYLSK	NPDGY	2		1134.516355	2267.01711	0.000823681	3	N	194	212
Q9D6Y9	Infl	PELAR	LLEIDPYLKPFAADFQR	RYKKF	3		679.3670866	2035.07786	0.000451244	8	N	30	47
Q9D6Y9	Infl	GIYCK	EWAPGAEGVFLTGEFSGWNPF	SHPYK	2		1149.529266	2297.042931	0.001699387	3	N	89	110
Q9D6Z1	Infl	HNVVR	LVAFCPFSSSQVALENANAVSEGVVHEDLR	LLLET	3	C5:+57.021	1082.535071	3244.581812	0.000451244	12	N	47	77
Q9D6Z1	Infl	HAVGY	ALLALKEVEEISLLLPQVEECVLNLGK	FHNVV	3	C21:+57.021	1007.570282	3019.687446	0.001463592	1	N	14	41
Q9D6Z1	Infl	LLALK	EVEEISLLLPQVEECVLNLGK	FHNVV	2	C15:+57.021	1206.140831	2410.266063	0.002296037	1	N	20	41
Q9D7S9	Infl	PTDTK	NKDGVLVDEFGLPQIPAS	-	2		949.9970699	1897.97854	0.00091018	3	N	201	219
Q9D824	Infl	SDLAK	DLDENEVERPEEENASANPPSGIEEEAAENGVAKPK	VTETE	4		966.6982229	3862.761692	0.001352548	4	N	40	76
Q9D824	Infl	GTKVK	GVDLDAPGSINGVPLLEVDLDSFEDKPWR	KPGAD	3		1051.863336	3152.566607	0.000451244	4	N	136	165
Q9D855	Infl	LGLMR	DDTLHETEDVKEAIR	RLPED	3		590.9555228	1769.843168	0.002663018	1	N	34	49
Q9D883	Infl	QTIAL	LNIYRNPQNSSQSADGLR	CAVSD	3		678.3440037	2032.008611	0.002453667	1	N	48	66
Q9D883	Infl	DLNNR	WFNGQPIHAELSPVTDF	REACC	2		979.4763046	1956.937009	0.000870037	6	N	133	150
Q9D892	Infl	REAAR	QVQGPVLVEDTCLCFNALGGLPGPYIK	WFLQK	3	C12:+57.021,C14:+57.021	982.5017193	2944.481758	0.000451244	13	N	62	89
Q9D892	Infl	GFEDK	SAYALCTFALSTGDPSQPVLLFR	GQTSG	2	C6:+57.021	1257.63879	2513.26198	0.000622848	7	N	110	133
Q9D8B3	Infl	KRYEK	QLAQIDGTLSTIEFQR	EALEN	2		910.481587	1818.947574	0.000451244	5	N	77	93
Q9D8B3	Infl	IEFQR	EALENANTNTEVLK	NMGYA	2		773.3919062	1544.768212	0.000823681	4	N	93	107
Q9D8E6	Infl	TNLRK	NNRQPYAVSELAGHQTSAESWGTGR	AVARI	3		906.09945	2715.27495	0.000451244	5	N	46	71
Q9D8E6	Infl	NRQPY	AVSELAGHQTSAESWGTGR	AVARI	2		972.4644569	1942.913314	0.000451244	6	N	52	71
Q9D8E6	Infl	RKNNR	QPYAVSELAGHQTSAESWGTGR	AVARI	3		778.037128	2331.087984	0.000451244	6	N	49	71
Q9D8E6	Infl	SKGHR	IEEVPELPLVVEDKVEGY	KKTKE	2		1029.0386	2056.061601	0.00091018	2	N	143	161
Q9D8E6	Infl	GHVGR	FCIWTESAFR	KLDEL	2	C2:+57.021	658.808538	1315.601476	0.000979378	2	N	248	258
Q9D8N0	Infl	QTLVR	EYFSWEGTFQHVGK	AVNQG	3		572.2673725	1713.778717	0.001162105	5	N	414	428
Q9D8N0	Infl	PNTNR	WFLTCINQPQFR	AILGE	2	C5:+57.021	805.4011257	1608.786651	0.000451244	13	N	189	201
Q9D8N0	Infl	FPAGK	VPAFEGDDGFCVFESNAIAYYVSNEELR	GSTPE	3	C11:+57.021	1066.817243	3197.42833	0.000451244	25	N	57	85
Q9D8N0	Infl	LVGER	VTLADITVVCTLLWLYK	QVLEP	2	C10:+57.021	1004.563303	2007.111006	0.000451244	9	N	156	173
Q9D8N0	Infl	SYTWR	KLDPGSEETQTLVR	EYFSW	2		786.9155485	1571.815497	0.000851441	1	N	400	414
Q9D8N0	Infl	WRAFK	ALIAAQYSGAQVR	VLSAP	2		674.3731224	1346.730645	0.001463592	4	N	17	30
Q9D8N0	Infl	EEVKR	ILGLLDTHLK	TRTFL	2		561.8482205	1121.680841	0.000979378	1	N	137	147
Q9D8N0	Infl	VWVFR	GQELAFPLSPDWQVDYESYTWR	KLDPG	2		1344.12479	2686.23398	0.000451244	14	N	378	400
Q9D8N0	Infl	NEELR	GSTPEAAAQVVQWVSF	ADSDI	2		838.9180912	1675.820582	0.000451244	7	N	85	101
Q9D8N0	Infl	SVILF	GTNNSSSISGVWVFR	GQELA	2		805.9002327	1609.784865	0.001463592	1	N	363	378
Q9D8T2	Infl	CSIGK	QLSLLSDGIDEEELIEAADFQGLYAEVK	ACSSE	3		1032.515602	3094.523405	0.000451244	4	N	269	297
Q9D8T2	Infl	FWKPR	YSCVNLSIKDILEPSAPEPEPECFGSFK	VSDVV	3	C3:+57.021,C23:+57.021	1071.842358	3212.503675	0.000637154	1	N	54	82
Q9D8T2	Infl	NLSIK	DILEPSAPEPEPECFGSFK	VSDVV	2	C14:+57.021	1074.993636	2147.971671	0.000662267	1	N	63	82
Q9D8W5	Infl	AKEGR	LQEVIETLLSLEK	QTRTA	2		757.9379609	1513.860322	0.000451244	9	N	39	52
Q9D8W5	Infl	QQALK	SVVLYVILAPFDNEQSDLVHR	ISSDK	3		805.4291858	2413.264158	0.000451244	2	N	268	289
Q9D8Y0	Infl	KLLRR	ADLNQGIGEPQSPSR	RVFNP	2		784.8873223	1567.759045	0.000451244	14	N	62	77
Q9D8Y0	Infl	AKLLR	RADLNQGIGEPQSPSR	RVFNP	2		862.9378779	1723.860156	0.002663018	1	N	61	77
Q9D8Y7	Infl	LVECR	DILLELVEHHLTPK	SHDRI	3		552.9826845	1655.924654	0.001395409	5	N	124	138
Q9D8Y7	Infl	HDRIR	HVFDHYSDPDLLAALYGPDFTQHLGK	ICDGL	3		986.1475183	2955.419155	0.000823681	2	N	144	170
Q9D906	Infl	LKKPK	QQGAGDLCPSHLVAPADLGSSLFANIPGYK	LGCYF	3	C8:+57.021	1028.513718	3082.517755	0.000451244	7	N	512	542
Q9D906	Infl	IPGYK	LGCYFCNDVVAPGDSTR	DRTLD	2	C3:+57.021,C6:+57.021	965.9248017	1929.834003	0.001463592	1	N	542	559
Q9D906	Infl	GQRTK	ITVGVYDPCNLAQYPGWPLR	NFLVL	2	C9:+57.021	1160.083454	2318.151307	0.000451244	5	N	222	242
Q9D906	Infl	GFLSR	FDNVLPVSLAFDK	CTACS	2		732.8908137	1463.766027	0.001763695	1	N	627	640
Q9D906	Infl	PGLAK	LQFAPFNSALDVGFWHELTQK	KLNEY	3		816.7502593	2447.227378	0.002519933	1	N	8	29
Q9D964	Infl	HPLPK	DCPVSSYNEWDPLEEVIVGR	AENAC	2	C2:+57.021	1182.544555	2363.073511	0.000451244	6	N	62	82
Q9D964	Infl	KVNIR	NANSLGGGFHCWTCDVR	RRGTL	2	C11:+57.021,C14:+57.021	975.920385	1949.82517	0.000698008	1	N	396	413
Q9DAR7	Infl	AEADR	IVFENPDPSDGFVLIPDLK	WNQQQ	2		1058.054585	2114.09357	0.000451244	3	N	187	206
Q9DAR7	Infl	TFALR	TDDPLLQLLQK	AQQER	2		642.3644317	1282.713263	0.000637154	10	N	321	332
Q9DAR7	Infl	VILEK	TPFQVEHVAQLLTGSPELK	LQFSN	2		1047.565651	2093.115702	0.000451244	4	N	85	104
Q9DAR7	Infl	IPDLK	WNQQQLDDLYLIAICHR	RGIRS	3	C15:+57.021	729.3655971	2185.073391	0.000823681	5	N	206	223
Q9DAU1	Infl	SKQRK	ELGGLGEDANAEEEEGVQK	ASPLP	2		987.4508778	1972.886156	0.000823681	4	N	245	264
Q9DB05	Infl	VDVEK	AIAHYEQSADYYKGEESNSSANK	CLLKV	3		854.7180123	2561.130637	0.001329271	1	N	140	163
Q9DB05	Infl	ERKVK	NSQSFFSGLFGGSSK	IEEAC	2		775.3682341	1548.720868	0.002019181	3	N	22	37
Q9DB05	Infl	LAVQK	YEELFPAFSDSR	ECKLM	2		730.8387781	1459.661956	0.000870037	3	N	227	239
Q9DB15	Infl	EYPPK	IQQLVQDIASLTLLEISDLNELLKK	TLKIQ	3		946.5465079	2836.616124	0.000451244	11	N	64	89
Q9DB15	Infl	EYPPK	IQQLVQDIASLTLLEISDLNELLK	KTLKI	3		903.8481868	2708.52116	0.000451244	6	N	64	88

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DB20	Infl	MSVHR	GEVPCTVTTASPLDDAVLSELKTVLK	SFLSP	3	C5:+57.021	915.1530158	2742.435648	0.000451244	4	N	136	162
Q9DB20	Infl	MSVHR	GEVPCTVTTASPLDDAVLSELK	TVLKS	2	C5:+57.021	1151.578064	2301.140528	0.000451244	22	N	136	158
Q9DB77	Infl	APKVK	TSAAPGGVPLQPQDLEFTKLPNGLVIASLENYAPLSR	IGLFV	3		1288.690101	3863.046902	0.000622848	5	N	23	60
Q9DB77	Infl	DVSAF	NASYSDSGLFGIYTISQAAAAGEVINAAYNQVK	AVAQG	3		1131.891954	3392.652462	0.000451244	10	N	326	359
Q9DB77	Infl	FNASY	SDSGLFGIYTISQAAAAGEVINAAYNQVK	AVAQG	3		986.833488	2957.477064	0.000698008	10	N	330	359
Q9DB77	Infl	YNQVK	AVAQGNLSSADVQAAK	NKLKA	2		765.4000656	1528.784531	0.000622848	18	N	359	375
Q9DBC7	Infl	EDGQK	IVVQGEPGDEFFIILEGTAAVLQR	RSENE	2		1301.200301	2600.385001	0.000451244	2	N	281	305
Q9DBC7	Infl	DKWER	LTVADALEPVQFEDGQK	IVVQG	2		930.4734276	1858.931255	0.000451244	4	N	264	281
Q9DBC7	Infl	EFLSK	VSILESLDKWER	LTVAD	3		492.2687134	1473.78274	0.000637154	1	N	252	264
Q9DBG3	Infl	EYAER	IDNADELLESFLEGFHDESTQVQLTLLTAIVK	LFLKK	3		1196.949358	3587.824673	0.000451244	14	N	458	490
Q9DBG3	Infl	MLLKK	LAPPLVTLLSGEPEVQYVALR	NINLI	2		1133.146808	2264.278017	0.000451244	8	N	283	304
Q9DBG3	Infl	QNINK	LLTALNECTEWGQIFILDCLSNYNPK	DDREA	3	C8:+57.021,C19:+57.021	1038.175672	3111.503616	0.000451244	8	N	206	232
Q9DBG3	Infl	DIFRK	YPNKYESIIATLCENLDSLDEPDAR	AAMIW	3	C13:+57.021	976.1310509	2925.369753	0.000451244	3	N	420	445
Q9DBG3	Infl	SLKCR	APEVSQYIYQVYDSILKN	-	3		710.6971611	2129.068083	0.001463592	1	N	919	937
Q9DBG3	Infl	KLFLK	KPSETQELVQQVLSLATQDSDNPDLRDR	GYIYW	4		796.4040778	3181.585111	0.000451244	1	N	494	522
Q9DBG3	Infl	KLFLK	KPSETQELVQQVLSLATQDSDNPDLR	DRGYI	3		971.1601523	2910.457057	0.000851441	2	N	494	520
Q9DBG3	Infl	YQSLK	LTNGIWILAELR	IQPGN	2		699.9093408	1397.803082	0.000823681	7	N	892	904
Q9DBG3	Infl	QVAVK	NNIDVFYFSCLIPLNVLFVEDGK	MERQV	3	C10:+57.021	906.1282534	2715.36136	0.002884417	1	N	808	831
Q9DBG5	Infl	AQQAR	SQVNDLQATFSGIHSFQDLSAGVLAQTR	ERIAR	3		997.5042533	2989.48936	0.000451244	15	N	367	395
Q9DBG5	Infl	LSMFR	DITQQLQSMCVALGASIQGLPSHVR	EQAQQ	3	C10:+57.021	903.7989133	2708.37334	0.001352548	4	N	335	360
Q9DBG5	Infl	EKGVK	TLTTAAVSTAQPILSK	LEPQI	2		801.4595919	1600.903584	0.000451244	14	N	68	84
Q9DBG5	Infl	TVATR	VTGAVDVTLGAVQNSVDKTK	SAMTS	3		668.0325437	2001.074231	0.000823681	3	N	150	170
Q9DBG5	Infl	EKGVK	TLTTAAVSTAQPILSKLEPQIATASEYAHR	GLDRL	3		1056.902013	3167.68264	0.000451244	3	N	68	98
Q9DBG5	Infl	RGLDR	LQESLPILQQPTEK	VLADT	2		812.4517668	1622.887934	0.000823681	2	N	102	116
Q9DBG5	Infl	IARAR	EALDNTVEYVAQNTPAMWLVGPFAPGITEKTPEGK	-	3		1258.629742	3772.865827	0.002884417	1	N	402	437
Q9DBG5	Infl	PILSK	LEPQIATASEYAHR	GLDRL	2		793.4026082	1584.789616	0.000823681	3	N	84	98
Q9DBG6	Infl	IFSKK	NFESLSEAFSVASAAAALSQNR	YHVPV	2		1135.556543	2269.097486	0.000451244	15	N	244	266
Q9DBG6	Infl	TVLQK	TPFSLVGNVFELNFK	NVKLS	2		856.4568522	1710.898104	0.000451244	9	N	322	337
Q9DBG6	Infl	VERLK	ASLDRPFTDLESAFYSIVGLSSLGVQVPDVKK	ACTFI	3		1146.943878	3437.808235	0.000451244	1	N	38	70
Q9DBG6	Infl	ALTAR	LGKEETVLATVQALQTASHLSQQADLR	NIVEE	3		969.8565155	2906.546147	0.000451244	17	N	151	178
Q9DBG6	Infl	NFALF	FQLVDVNTGAELTPHQTFVR	LHNQK	2		1136.590189	2271.164778	0.000451244	2	N	417	437
Q9DBG6	Infl	VERLK	ASLDRPFTDLESAFYSIVGLSSLGVQVPDVK	KACTF	3		1104.245557	3309.713272	0.000622848	8	N	38	69
Q9DBG6	Infl	TIFSK	KNFESLSEAFSVASAAAALSQNR	YHVPV	3		800.0719497	2397.192449	0.001162105	1	N	243	266
Q9DBG6	Infl	QADLR	NIVEEIEDLVAR	LDELG	2		700.3755278	1398.735456	0.000451244	14	N	178	190
Q9DBG6	Infl	LHNQK	TGQEVVFVAEPDNK	NVYKF	2		766.883717	1531.751834	0.000451244	5	N	442	456
Q9DBG6	Infl	ELRVK	ISTEVGITNVDLSTVDKDQSIAPK	TTRVT	2		1265.666488	2529.317375	0.000451244	1	N	368	392
Q9DBG6	Infl	DLVAR	LDELGGVYLQFEEGLELTALFVAATYK	LMDHV	3		997.1868682	2988.537205	0.000451244	3	N	190	217
Q9DBG6	Infl	SNETK	ELLLAAVSEDSPIAQIY	HAVAA	2		916.4885464	1830.961493	0.002374549	1	N	109	126
Q9DBJ1	Infl	SKDRR	YADLTEDQLPSCESLKDTIAR	ALPFW	2	C12:+57.021	1213.081502	2424.147404	0.000451244	34	N	141	162
Q9DBJ1	Infl	DTIAR	ALPFWNEEIVPQIK	EGKRV	2		842.4593949	1682.90319	0.000451244	7	N	162	176
Q9DBJ1	Infl	RLNER	HYGGLTGLNKAETAAK	HGEAQ	3		544.2902886	1629.847466	0.000622848	3	N	90	106
Q9DBJ1	Infl	NLENR	FSGWYDADLSPAGHEEAK	RGGQA	2		990.4426588	1978.869718	0.000451244	5	N	21	39
Q9DBJ1	Infl	GQALR	DAGYEFDICFTSVQKR	AIRTL	2	C9:+57.021	968.4491982	1934.882796	0.000451244	4	N	46	62
Q9DBJ1	Infl	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	2		1068.493214	2134.970829	0.000451244	2	N	21	40
Q9DBJ1	Infl	IARAL	PFWNEEIVPQIK	EGKRV	2		750.3988059	1498.782012	0.000451244	10	N	164	176
Q9DBJ1	Infl	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	2		1078.58279	2155.14998	0.000451244	5	N	65	83
Q9DBJ1	Infl	GQALR	DAGYEFDICFTSVQK	RAIRT	2	C9:+57.021	890.3986426	1778.781685	0.000451244	6	N	46	61
Q9DBJ1	Infl	SKDRR	YADLTEDQLPSCESLK	DTIAR	2	C12:+57.021	934.9330467	1867.850493	0.001943752	5	N	141	157
Q9DBL1	Infl	FRDAK	IGTIYEGASNIQLNTIAK	HIDAE	2		953.5181695	1905.020739	0.000451244	2	N	408	426
Q9DBL1	Infl	EELAK	VDASVALLCDIQNTIINNLFR	KHASE	2	C9:+57.021	1195.131132	2388.246665	0.000451244	4	N	130	151
Q9DBL9	Infl	SSRPR	FDSDAEEVENQFVESIEEWR	CALRL	2		1229.538213	2457.060826	0.000451244	9	N	121	141
Q9DBL9	Infl	PMLQR	IGGLHPDIPVSVIFGAR	SCIDG	3		583.3338287	1746.978086	0.00091018	1	N	282	299
Q9DBR0	Infl	PHTEK	LLEEQTCEAASETR	SIEDK	2	C7:+57.021	818.8780744	1635.740549	0.000823681	4	N	619	633
Q9DBR0	Infl	TAAVK	AVEGEGEPAAAHSDVLTEVEGPVDTAEASSDPHTEK	LLEEQ	4		908.6689341	3630.644536	0.001352548	1	N	583	619
Q9DBR1	Infl	VPMLR	DLTQNTAVSINFKDPQFAEDYVFK	AAMLP	3		930.7927411	2789.354823	0.001699387	1	N	743	767
Q9DBR1	Infl	LNGKK	YAWQGVALLPFVDER	RLRAA	2		882.4599262	1762.904252	0.000451244	9	N	641	656
Q9DBR7	Infl	ETVNK	VGQTAFDVADEDILGYLEELQKK	QTLLH	3		861.1064371	2580.295911	0.000451244	7	N	263	286
Q9DBR7	Infl	ETVNK	VGQTAFDVADEDILGYLEELQK	KQTLL	2		1227.108274	2452.200948	0.000451244	1	N	263	285
Q9DBR7	Infl	DGAVF	LAACSSGDTDEVLK	LLHRG	2	C4:+57.021	733.3458787	1464.676157	0.000851441	1	N	44	58
Q9DBR7	Infl	ETYTR	YRPVSTSSSSAPSSSSLSTLGSTLY	ASSQL	2		1261.616995	2521.218389	0.000823681	3	N	766	791
Q9DBS1	Infl	VGDVR	VSFSYAGLSSDDPDLGPAHVVTVIAR	QRGDQ	3		891.789331	2672.344593	0.000451244	11	N	240	266
Q9DBS1	Infl	VQIGR	FFLSAGLIDKIDNFK	ALSLA	3		576.6509348	1726.929405	0.000979378	2	N	189	204
Q9DBT5	Infl	ESELR	SAPYEFPEESPIEQLEER	RQRLE	2		1075.500371	2148.985141	0.000451244	12	N	60	78
Q9DBT5	Infl	HVYTR	RDPDEHCPEVELPYPDLQEFVADVNVL	MALII	3	C7:+57.021	1065.836527	3194.48618	0.002453667	1	N	255	282
Q9DBZ5	Infl	LAVLK	LYQFNPAFFQTTVTAQILLK	ALTNL	2		1172.141526	2342.267452	0.001463592	2	N	52	72

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DBZ5	Infl	VWMSK	YGWSADESGQVFICSQEESIKPK	NIVEK	3	C14:+57.021	882.411489	2644.211067	0.000637154	2	N	176	199
Q9DBZ5	Infl	GKLLK	GIDRYNPENLATLER	YVETQ	2		880.950454	1759.885308	0.001352548	2	N	16	31
Q9DC51	Infl	FSRSR	EYQLNDSASYYLNDLDR	ISQTN	2		1039.969238	2077.922875	0.000735798	2	N	144	161
Q9DC51	Infl	EKIKR	SPLTICYPEYTGSNTYEEAAAYIQCQFEDLNR	RKDTK	3	C6:+57.021,C25:+57.021	1268.566393	3802.67578	0.000451244	13	N	280	312
Q9DCC5	Infl	NGKSK	KVEEAEPEEFVVEK	VLDRR	2		831.4175897	1660.819579	0.000451244	32	N	20	34
Q9DCC5	Infl	MFLMK	WKDSDEADLVLAK	EANMK	2		745.3808101	1488.74602	0.000451244	10	N	141	154
Q9DCC5	Infl	EANMK	CPQIVIAFYEER	LTWHS	2	C1:+57.021	762.8796917	1523.743783	0.001699387	1	N	159	171
Q9DCC5	Infl	EYFLK	WKGFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C19:+57.021	1232.898514	3695.672143	0.000451244	19	N	50	81
Q9DCC5	Infl	FLKWK	GFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C17:+57.021	1128.173756	3381.497867	0.000451244	30	N	52	81
Q9DCC5	Infl	FLKWK	GFTDADNTWEPEENLDCPELIEAF	LNSQK	2	C17:+57.021	1406.600453	2811.185306	0.000451244	8	N	52	76
Q9DCC5	Infl	GKSKK	VEEAEPEEFVVEK	VLDRR	2		767.3701081	1532.724616	0.000451244	3	N	21	34
Q9DCD0	Infl	CAFNR	TVSKVDDFLANEAK	GTKVV	2		768.8993671	1535.783134	0.000451244	49	N	34	48
Q9DCD0	Infl	ILLVK	AGQAVDDFIEK	LVPLL	2		596.7963819	1191.577164	0.000451244	21	N	76	87
Q9DCD0	Infl	CRDLK	AKGILFVGSGVSGGEEGAR	YGPSL	2		895.9739291	1789.932258	0.000451244	8	N	117	136
Q9DCD0	Infl	AIAAK	VGTGEPCCDWVGDEGAGHFVK	MVHNG	2	C7:+57.021,C8:+57.021	1138.988662	2275.961723	0.000451244	48	N	163	184
Q9DCD0	Infl	DLKAK	GILFVGSGVSGGEEGAR	YGPSL	2		796.4078906	1590.800181	0.000451244	38	N	119	136
Q9DCD0	Infl	IQAQR	DYFGAHTYELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		1310.938515	3929.792144	0.000451244	16	N	447	483
Q9DCD0	Infl	DFIEK	LVPLLDTGDIIIDGGNSEYR	DTTRR	2		1080.563305	2159.111011	0.000451244	22	N	87	107
Q9DCD0	Infl	LGKIK	DAFERNPELQNLLLDDFFK	SAVDN	2		1162.582029	2323.148459	0.001264573	3	N	377	396
Q9DCD0	Infl	DAFER	NPELQNLLLDDFFK	SAVDN	2		853.4439418	1704.872284	0.000451244	33	N	382	396
Q9DCD0	Infl	ILLVK	AGQAVDDFIEKLVPLLDTGDIIIDGGNSEYR	DTTRR	3		1111.900338	3332.677615	0.000451244	7	N	76	107
Q9DCD0	Infl	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	2		1248.154308	2494.293016	0.000451244	1	N	265	288
Q9DCD0	Infl	DFIEK	LVPLLDTGDIIIDGGNSEY	RDTTR	2		1002.51275	2003.0099	0.000451244	18	N	87	106
Q9DCD0	Infl	WPHIK	AIFQAIAAK	VGTGE	2		466.7823492	931.5490983	0.000698008	14	N	154	163
Q9DCD0	Infl	DFIEK	LVPLLDTGDIIIDGGNSEYRDTTR	RCRDL	3		878.4526074	2632.334422	0.000451244	6	N	87	111
Q9DCD0	Infl	EEWNK	TELDSFLIEITANILK	YRDTD	2		910.5067391	1818.997878	0.000451244	9	N	225	241
Q9DCD0	Infl	IEKLV	PLLDTGDIIIDGGNSEYRDTTR	RCRDL	3		807.7351147	2420.181944	0.000622848	2	N	89	111
Q9DCD0	Infl	KLVPL	LDTGDIIIDGGNSEYRDTTR	RCRDL	2		1106.030358	2210.045116	0.002727428	2	N	91	111
Q9DCD0	Infl	ILLVK	AGQAVDDFIEKLVPLLDTGDIIIDGGNSEY	RDTTR	3		1059.866634	3176.576503	0.000451244	3	N	76	106
Q9DCD0	Infl	GAHTY	ELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		992.8094538	2975.404961	0.000662267	4	N	455	483
Q9DCD0	Infl	KLVPL	LDTGDIIIDGGNSEYR	DTTRR	2		869.4186523	1736.821705	0.000451244	3	N	91	107
Q9DCH4	Infl	GASAR	IQDALSTVLQYAEDVLSGKVSADNTVGR	FLMSL	3		983.8441641	2948.509092	0.000451244	6	N	282	310
Q9DCH4	Infl	GASAR	IQDALSTVLQYAEDVLSGK	VSADN	2		1025.539299	2049.062998	0.000451244	16	N	282	301
Q9DCH4	Infl	FSPNR	VIGLSSDLQQVGGASAR	IQDAL	2		829.4475471	1656.879494	0.000622848	4	N	265	282
Q9DCJ5	Infl	QQQAK	FDQCVLDKLGWVRPDLGQLSK	VTKVK	4	C4:+57.021	619.3273748	2473.278299	0.002145581	1	N	106	127
Q9DCJ5	Infl	-M	PGIVELPTLEELKVEEVK	VSSAV	3		674.7176736	2021.129621	0.000622848	2	N	1	19
Q9DCL9	Infl	AISNK	ITSCIFQLLQEAGIK	TAFTK	2	C4:+57.021	860.9690382	1719.922476	0.000451244	8	N	59	74
Q9DCL9	Infl	DVTTK	EIVLADVIDNDSWR	LWPSG	2		822.9155485	1643.815497	0.00091018	2	N	201	215
Q9DCL9	Infl	WSSLR	LPSGIGCSTILSPEGSAQFAAQIFGLNNHLVWAK	LRASI	3	C7:+57.021	1195.284086	3582.828859	0.000451244	13	N	367	401
Q9DCL9	Infl	QMVKK	NFEWVADRVELLLK	SDSQC	3		577.9863175	1730.935553	0.000823681	2	N	247	261
Q9DCM0	Infl	ELGLK	LLYAVNTHCHADHITGTGVLR	SLLPG	3	C9:+57.021	783.4028224	2347.185067	0.001463592	1	N	71	92
Q9DCM0	Infl	SVHEK	IFTLPGNCLIYPAHDYHGLTVSTVEEER	TLNPR	3	C8:+57.021	1077.864528	3230.570184	0.000451244	10	N	181	209
Q9DCR2	Infl	PRLSK	FYQPYSEDTQQQIIR	ETFHL	2		958.4633942	1914.911188	0.000451244	8	N	18	33
Q9DCR2	Infl	PEIPR	NINIGDISIKVPNLPSFK	-	3		657.042603	1968.104409	0.002981883	1	N	175	193
Q9DCS9	Infl	-M	PDSWDKDVYPEPPSR	TPAPS	2		894.4159126	1786.816225	0.002145581	1	N	1	16
Q9DCS9	Infl	LTKAY	DLVVDWPVTLVR	EFIER	2		706.4013486	1410.787097	0.001943752	5	N	37	49
Q9DCW4	Infl	KKLVK	EIIAVSCGPSQCQETIR	TALAM	2	C7:+57.021,C12:+57.021	974.4668337	1946.918067	0.000451244	17	N	59	76
Q9DCW4	Infl	LETLR	LKLPAVVTADLR	LNEPR	3		432.6068893	1294.797268	0.000622848	6	N	174	186
Q9DCW4	Infl	MGADR	GIHVEIPGAQAESLGPLQVAR	VLAKL	2		1071.587449	2141.159298	0.000451244	3	N	85	106
Q9DCW4	Infl	DLTSK	VSVISVEEPPQR	SAGVK	2		670.3649631	1338.714326	0.001329271	1	N	221	233
Q9EPB4	Infl	MGRAR	DAILDALENLSGDELKK	FKMKL	2		922.486535	1842.95747	0.000451244	11	N	5	22
Q9EPB4	Infl	ALIAR	VTEVDGVLDALHGSVLTEGQYQAVR	AETTS	2		1328.683003	2655.350407	0.001352548	2	N	123	148
Q9EPB4	Infl	LQTTK	EESGAVAAAASVPAQSTAR	TGHFV	2		886.9428259	1771.870052	0.000451244	13	N	89	108
Q9EPB4	Infl	MGRAR	DAILDALENLSGDELK	KFKMK	2		858.4390534	1714.862507	0.000451244	3	N	5	21
Q9EPJ9	Infl	FTAHR	ASGQPQSAAASGDKAFEDWLNDDLGSYQGAQENR	YVGFG	3		1195.20392	3582.588359	0.000451244	7	N	148	182
Q9EPJ9	Infl	LAEGK	EWSLESSPAQNWTPPQPK	TLQFT	2		1041.500508	2080.985416	0.000451244	7	N	122	140
Q9EPL4	Infl	KKKYR	VLGINEWQNTGFQYDVISCLNLLDRCDQPLTLLK	DIRSV	3	C19:+57.021,C26:+57.021	1346.015294	4035.022481	0.001871652	2	N	189	223
Q9EPL4	Infl	EVFRK	AGFVVEAFTR	LPYLC	2		548.7934452	1095.57129	0.002080925	3	N	282	292
Q9EPL8	Infl	RHCIR	ENIVEAIIHSPELIR	VQLTT	3		578.3251103	1731.951931	0.000451244	7	N	92	107
Q9EPL8	Infl	QCKGR	GIDQCIPLFVEAALER	LTREV	3	C5:+57.021	610.9858346	1829.934104	0.000823681	6	N	752	768
Q9EPL8	Infl	ALEGY	STIIDDEDNPVDEYQIFK	AIFQT	2		1071.000204	2139.984807	0.000451244	2	N	945	963
Q9EPU0	Infl	NCGCR	NVFLLGFIPAKADSVVVLLCR	QPCAS	3	C20:+57.021	777.7804597	2330.317979	0.000451244	3	N	184	205
Q9EPU0	Infl	NCGCR	NVFLLGFIPAK	ADSVV	2		609.8664133	1217.717227	0.001264573	7	N	184	195
Q9EPU0	Infl	YHLAR	QGNGPVLVCAPSNIAVDQLTEK	IHQTG	2	C9:+57.021	1155.59184	2309.16808	0.000622848	1	N	517	539
Q9EPU0	Infl	QSSLK	DINWDSSQWQPLIQDR	CFLSW	2		1000.9772	1999.9388	0.001162105	2	N	215	231

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9EQ06	Infl	VGFHR	ALTDELAALGR	TGVRT	2		565.3147418	1128.613884	0.000823681	10	N	197	208
Q9EQ06	Infl	PQIEK	TFEVNVLAHFWTTK	AFLPV	3		564.9635129	1691.867139	0.000735798	6	N	139	153
Q9EQ32	Infl	KLDEK	VSTEAEFSPEDSPSIR	VEGTL	2		875.9106601	1749.80572	0.000870037	3	N	206	222
Q9EQ32	Infl	KYGLK	NLTALLLTCPGALQAYSVANK	HGHYP	2	C9:+57.021	1109.598937	2217.182273	0.000622848	9	N	350	371
Q9EQ32	Infl	SGWGR	GCDILIFYSPDAEEWCQYLQDLFVSCR	QVRSQ	3	C2:+57.021,C16:+57.021,C26:+57.021	1128.838577	3383.49233	0.000451244	2	N	8	35
Q9EQG9	Infl	DELQR	DKVVEDDEDDFPTTR	SDGDF	2		890.8977497	1779.779899	0.000451244	15	N	196	211
Q9EQG9	Infl	FDECR	FDISVNDSVWYLR	AQDPE	2		807.4020769	1612.788554	0.000662267	2	N	85	98
Q9EQG9	Infl	LSAIR	KIPALTENDPETWIVCNFSVDHDSAPLNNR	CVRAK	3	C16:+57.021	1151.556534	3451.646203	0.000451244	4	N	513	543
Q9EQG9	Infl	DTLQK	YFDVCADAVSKDELQR	DKVVE	2	C5:+57.021	958.4466555	1914.877711	0.000451244	1	N	180	196
Q9EQG9	Infl	LSAIR	KIPALTENDPETWIVCNF	SVDHD	2	C16:+57.021	1074.027813	2146.040026	0.000998612	1	N	513	531
Q9EQG9	Infl	WVVLK	NNTLSYYKSEDETEYGCR	GSICL	2	C17:+57.021	1114.973963	2227.932326	0.000451244	1	N	48	66
Q9EQG9	Infl	KKKPR	FGGPDYEEGPNSLINEEEFFDAVEAALDR	QDKIE	3		1077.486594	3229.436381	0.000451244	7	N	303	332
Q9EQH3	Infl	IHLLR	SDDPDQQYLILNTAR	KHFGA	2		874.9266445	1747.837689	0.000451244	7	N	499	514
Q9EQH3	Infl	-M	PTTQQSPQDEQEKLLDEAIQAVK	VQSFQ	3		866.1087292	2595.302788	0.000451244	1	N	1	24
Q9EQH3	Infl	PAEIK	LFDIFSQQVATVIQSR	QDMPS	2		926.5023224	1850.989045	0.000451244	6	N	323	339
Q9EQH3	Infl	VERYK	QIVLTGILEQVVNCR	DALAQ	3	C14:+57.021	581.3261912	1740.955173	0.000451244	8	N	239	254
Q9EQH3	Infl	AKGRK	VADLYELVQYAGNIIPR	LYLLI	3		645.3514366	1933.03091	0.000451244	4	N	90	107
Q9EQH3	Infl	NVNVK	NIIIALIDR	LALFA	2		520.8272881	1039.638976	0.002212458	2	N	296	305
Q9EQH3	Infl	ISDSK	AQLAAITLIIGTFER	MKCFS	3		539.6510463	1615.929739	0.000698008	5	N	622	637
Q9EQH3	Infl	NQRIR	FTLPPLVFAAYQLAFR	YKENS	3		618.6824579	1853.023974	0.000451244	3	N	526	542
Q9EQH3	Infl	QLIQK	IREDLPNLESSEETEQINK	HFHNT	2		1122.553666	2243.091732	0.000451244	7	N	749	768
Q9EQH3	Infl	EIFNK	LNLEHIATSSAVSK	ELTRL	2		735.4020769	1468.788554	0.001352548	1	N	382	396
Q9EQI5	Infl	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	3	C1:+39.994,C25:+57.021	1276.653546	3826.937238	0.001763695	2	N	53	88
Q9EQI5	Infl	SGIPF	NSISLVNVYRPGVHCADVEVIATLK	NGQKT	2	C15:+57.021	1377.734285	2753.452969	0.001763695	1	N	63	88
Q9EQK5	Infl	VVEER	QAIPLDQNEGIYVQDVK	TGKVR	2		965.4999767	1928.984353	0.000451244	10	N	377	394
Q9EQK5	Infl	ERLER	GIQDVYVLSEQQGLLLK	ALQPL	2		952.0309127	1902.046225	0.000451244	17	N	318	335
Q9EQK5	Infl	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGRPK	RPHAR	3		972.1907241	2913.548772	0.000451244	6	N	479	506
Q9EQK5	Infl	DQEIR	LAQDPFPLYPGELLEKDITPLQVVLPNTALHLK	ALLDF	3		1228.35399	3682.038569	0.000451244	4	N	91	124
Q9EQK5	Infl	GVAHR	TGEEWLVTVQDTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	3		1283.658466	3847.951999	0.000451244	10	N	244	279
Q9EQK5	Infl	SLGLK	STLITDGSSPINLFNTAFGLLGLGSDGQPPVQK	-	3		1115.584461	3343.729984	0.000451244	14	N	828	861
Q9EQK5	Infl	EWLVR	SVGAYLPAVFEEVLDLVDAVILTEK	TALHL	2		1345.731099	2689.446598	0.000622848	3	N	199	224
Q9EQK5	Infl	RARDR	AVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	2		1285.166989	2568.318378	0.000451244	14	N	625	649
Q9EQK5	Infl	EETAK	LFSVPDFVGDACK	AIASR	2	C12:+57.021	727.8531426	1453.690685	0.0025889	1	N	560	573
Q9EQK5	Infl	ELLEK	DITPLQVVLPNTALHLK	ALLDF	3		624.7038102	1871.088031	0.000622848	3	N	107	124
Q9EQK5	Infl	DQEIR	LAQDPFPLYPGELLEK	DITPL	2		915.4883494	1828.961099	0.001591523	4	N	91	107
Q9EQK5	Infl	NPVSR	DAQSSVLFDVTGQVR	LRHAD	3		541.2780486	1620.810746	0.001654178	1	N	67	82
Q9EQK5	Infl	VLWEK	ELPSGVEELLNLGHDPLADR	GQKGT	2		1087.558554	2173.101509	0.000451244	15	N	417	437
Q9EQK5	Infl	EAIIR	IPPYHYIHVLDQNSNVSR	VEVGP	2		1076.550867	2151.086133	0.000622848	3	N	9	27
Q9EQK5	Infl	AKRAR	VVFGPELVSLDPEEQFTVL	SLSAG	2		1059.554418	2117.093235	0.001463592	4	N	479	498
Q9EQK5	Infl	GLLLK	ALQPLEEGEGEEKVAHQAGDR	WLIRG	2		1132.051625	2262.08765	0.000979378	1	N	335	356
Q9EQK5	Infl	DALQR	SVQLAIEITTNSQEAAAKHEAQR	LEQEA	3		832.4336586	2494.277576	0.000735798	2	N	656	679
Q9EQK5	Infl	VLQAK	LKAQALAIETEAELER	VKKVR	2		892.9917875	1783.967975	0.000451244	4	N	745	761
Q9EQU5	Infl	WVTTF	VNHPQVSALLGEEDEEALHYLTR	VEVTE	2		1310.654246	2619.292892	0.000451244	1	N	98	121
Q9EQU5	Infl	KSGYR	IDFYFDENPYFENK	VLSKE	2		920.9073891	1839.799178	0.000451244	7	N	135	149
Q9EQU5	Infl	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHY	LTRVE	3		1119.214369	3354.619706	0.002296037	1	N	89	118
Q9EQU5	Infl	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR	VEVTE	4		932.2209398	3724.852559	0.000451244	11	N	89	121
Q9EQU5	Infl	PKGEK	EQQEAIEHIDEVQNEIDRLNEQASEEILK	VEQKY	3		1150.560933	3448.659398	0.001162105	3	N	38	67
Q9EQU5	Infl	NEIDR	LNEQASEEILKVEQK	YNKLR	3		586.6480302	1756.92069	0.000451244	1	N	56	71
Q9ER72	Infl	EVDSK	VQVLLEEAKDLLSDWLDSTGGSEVTDNSIFSK	LPKFW	3		1165.917946	3494.730438	0.000451244	15	N	265	297
Q9ER72	Infl	LEEAK	DLLSDWLDSTGGSEVTDNSIFSK	LPKFW	2		1243.58262	2485.149641	0.000451244	3	N	274	297
Q9ERB0	Infl	PNLRR	LQDAELDSVPKEPSSTVNTEVYPK	NSTLR	3		882.7768681	2645.307204	0.000622848	9	N	169	193
Q9ERB0	Infl	INSIK	SVFGGFINYFK	SKPVE	2		639.8300277	1277.644455	0.000451244	5	N	113	124
Q9ERB0	Infl	INYFK	SKPVEPPPEQNGSIVSQPNSR	LKEAI	3		749.7175068	2246.12912	0.000622848	2	N	124	145
Q9ERB0	Infl	TYHQK	IDSNLDELSVGLGHLK	DIALG	3		570.640987	1708.899561	0.001463592	1	N	203	219
Q9ERD8	Infl	TIFNK	DLLATLHLLVALAK	RFQPD	3		497.6488656	1489.923197	0.001352548	1	N	134	148
Q9ERD8	Infl	-	MELEFLYDLLQLPK	EVAQP	2	M1:+15.995	884.4660716	1766.916543	0.001591523	2	N	0	14
Q9ERD8	Infl	LQLPK	EVAQPTEEELPR	GGKKK	2		699.34951	1396.68342	0.000823681	1	N	14	26
Q9ERD8	Infl	SQRHK	LGVILEAVNQNLQVEEK	QAKWS	2		948.5259945	1895.036389	0.000451244	6	N	105	122
Q9ERF3	Infl	SPDGK	YLASGAIDGIINIFDIATGK	LLHTL	3		684.705768	2051.093904	0.000823681	2	N	161	181
Q9ERF3	Infl	AMPIR	SLTFSPDSQLLVTASDDGYIK	IYDVQ	2		1129.065878	2256.116156	0.000451244	13	N	194	215
Q9ERI2	Infl	DAMGF	LLLFDLTNEQSFLNVR	NWISQ	2		961.5232548	1921.03091	0.000451244	8	N	95	111
Q9ERK4	Infl	RPAEK	FLESVEGNQNYPLLLLTLLEK	SQDNV	2		1217.167938	2432.320275	0.000451244	17	N	31	52
Q9ERK4	Infl	RPHYK	NLFEDQNTLTSICEK	VIVPN	2	C13:+57.021	906.4279315	1810.840263	0.001463592	2	N	331	346
Q9ERK4	Infl	AQTQK	HGITQANELVNLTEFFVNHILPDLK	SNNVN	3		954.8436587	2861.507576	0.002884417	2	N	445	470

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9ERK4	Infl	KAIMR	SFSLLQEAIIPYIPTLITQLTQK	LLAVS	3		873.1670796	2616.477839	0.000823681	3	N	578	601
Q9ERL7	Infl	VFEIR	TTDDLTETWLKEK	LAFFR	2		790.3966572	1578.777714	0.000451244	3	N	124	137
Q9ERL7	Infl	VFEIR	TTDDLTETWLK	EKLAF	2		661.8278791	1321.640158	0.000451244	6	N	124	135
Q9ERR7	Infl	DPVLK	LLDDNGNIAEELSILK	WNTDS	2		878.9705208	1755.925442	0.000451244	5	N	129	145
Q9ERR7	Infl	SEACR	ELGFSSNLLCSSCDLLGQFNLLPLDPVCR	GCCQE	3	C10:+57.021,C13:+57.021,C28:+57.021	1108.873621	3323.597464	0.000451244	13	N	39	68
Q9ERR7	Infl	LSILK	WNTDSVEEFLSEKLER	I-	3		661.3220942	1980.942883	0.002884417	1	N	145	161
Q9ERR7	Infl	LSILK	WNTDSVEEFLSEK	LERI-	2		792.3653571	1582.715114	0.001329271	1	N	145	158
Q9ERU9	Infl	FSSEK	SKPFAFGNSSATGSLFGFSFNAPLK	NSNSE	3		860.4363404	2578.285621	0.001943752	2	N	2367	2392
Q9ERU9	Infl	KIEVK	TGEEDEEEFFCNR	AKLFR	2	C11:+57.021	831.3231319	1660.630664	0.001463592	1	N	1179	1192
Q9ERU9	Infl	SSKER	SFLGNDDIGNLDGQVPDPDDLAR	YDTGA	2		1222.072754	2442.129908	0.002453667	1	N	398	421
Q9ES52	Infl	EEHLK	AIQDYLSTQLLLDSDFLK	TGSSN	2		1042.052042	2082.088484	0.000451244	14	N	185	203
Q9ES52	Infl	TMVAK	LSQLTSLLSSIEDKVK	SLLHE	3		587.6721757	1759.993127	0.001352548	2	N	267	283
Q9ES52	Infl	LISIK	SSDSDESYGEGCIALR	LETTE	2	C12:+57.021	873.3680708	1744.720542	0.000451244	5	N	810	826
Q9ES52	Infl	ESFVK	SQEGENEEGSEGELVVR	FGETL	2		924.416838	1846.818076	0.000451244	7	N	765	782
Q9ES52	Infl	ETLPK	LKPIISDPEYLLDQHILISIK	SSDSD	3		816.8091152	2447.403946	0.001229886	1	N	789	810
Q9ESP1	Infl	SHDIK	YGSGSGQQSVTGVEESDDANSYWR	IRGGS	2		1290.050007	2578.084415	0.000451244	24	N	59	83
Q9ESP1	Infl	VLTGK	NLHTHHFPSPLSNNQEVSAFGEDGEGDDLDLWTVR	CSGQH	3		1311.940807	3932.79902	0.000823681	2	N	113	148
Q9EST5	Infl	GEEEE	FGHDGEVDEDEEDEDEDEDEEEEESGKGEK	RKRET	3		1152.759941	3455.256423	0.000451244	31	N	230	260
Q9EST5	Infl	LDCLK	SLDLFGCEVTNR	SDYRE	2	C7:+57.021	705.8380238	1409.660448	0.000451244	14	N	116	128
Q9EST5	Infl	GGLDR	LAEELPSLTHLNLSGNNLKDISTLEPLK	RLDCL	3		1020.559476	3058.655028	0.000451244	7	N	82	110
Q9EST5	Infl	GGLDR	LAEELPSLTHLNLSGNNLK	DISTL	2		1032.060733	2062.105866	0.000451244	12	N	82	101
Q9EST5	Infl	GHDGE	VDEDEEDEDEDEDEEEEESGKGEK	RKRET	3		938.6800112	2813.016634	0.000451244	4	N	236	260
Q9EST5	Infl	AMDGK	IEGLTDEFVNLEFLSLISVGLFSVSDLPK	LPKLK	3		1061.235999	3180.684597	0.000451244	8	N	33	62
Q9ET01	Infl	SQLTK	LHSFVSDDIFLR	EIAKV	3		483.5897869	1447.745961	0.000451244	26	N	521	533
Q9ET01	Infl	IFNQK	IREGWQVEEADDWLR	HGNPW	2		951.4611859	1900.906772	0.000451244	7	N	170	185
Q9ET01	Infl	SQLTK	LHSFVSDDIFLREIAK	VKQEN	3		630.6760316	1889.004695	0.000622848	4	N	521	537
Q9ET01	Infl	GITPR	RWLLLCNPGLADLIAEK	IGEDY	2	C6:+57.021	991.5485184	1981.081437	0.000451244	11	N	490	507
Q9ET01	Infl	ITPRR	WLLLCNPGLADLIAEK	IGEDY	2	C5:+57.021	913.4979628	1824.980326	0.000451244	15	N	491	507
Q9ET01	Infl	LWSAR	APNDFNLQDFNVGDYIQAVLDRNLAENISR	VLYPN	3		1141.231081	3420.669844	0.000451244	8	N	248	278
Q9ET01	Infl	LWSAR	APNDFNLQDFNVGDYIQAVLDR	NLAEN	2		1262.609307	2523.203014	0.000451244	13	N	248	270
Q9ET01	Infl	LIAEK	IGEDYVKDLSQLTK	LHSFV	2		804.9281245	1607.840649	0.000451244	2	N	507	521
Q9ET01	Infl	LPELK	LVIDQIDNGFFSPNQPDLF	KDIIN	2		1090.039466	2178.063332	0.000451244	20	N	740	759
Q9ET01	Infl	KLLPR	HLEIIYEINQK	HLDRI	2		700.3831558	1398.750712	0.000451244	11	N	399	410
Q9ET01	Infl	ALDKK	GYEAKEYYEALPELK	LVIDQ	2		901.9465143	1801.877429	0.000451244	4	N	725	740
Q9ET01	Infl	NQKIR	EGWQVEEADDWLR	HGNPW	2		816.8685982	1631.721596	0.000451244	13	N	172	185
Q9ET01	Infl	PSDLK	ISLSNESSNGVSANGK	-	2		782.3846125	1562.753625	0.000451244	5	N	834	850
Q9ET01	Infl	EITKK	TFAYTNHTVLPEALER	WPVEL	2		931.4763046	1860.937009	0.000451244	5	N	371	387
Q9ET01	Infl	LPELK	LVIDQIDNGFFSPNQPDLFK	DIINM	2		1154.086948	2306.158295	0.000451244	3	N	740	760
Q9ET01	Infl	GYGIR	YEYGIFNQK	IREGW	2		581.2829103	1160.550221	0.002212458	8	N	161	170
Q9ET01	Infl	VATPR	DYYFALAHTVR	DHLVG	2		678.3412909	1354.666982	0.000451244	6	N	50	61
Q9ET01	Infl	PELMR	IFVDIEKLPWAK	AWEIT	2		729.9219169	1457.828234	0.001463592	2	N	352	364
Q9ET01	Infl	MVGSK	LKVIFLENYR	VSLAE	3		432.255968	1293.744504	0.00091018	3	N	640	650
Q9ET01	Infl	VATPR	DYYFALAHTVRDHLVGR	WIRTQ	3		678.35043	2032.02789	0.002981883	1	N	50	67
Q9ET01	Infl	EITKK	TFAYTNHTVLPEALERWPVELVEK	LLPRH	3		948.1645093	2841.470128	0.000451244	2	N	371	395
Q9ET01	Infl	EITKK	TFAYTNHTVLPEALERWPVEL	VEKLL	2		1243.639879	2485.264158	0.001162105	1	N	371	392
Q9ET01	Infl	DEAIY	QLGLDMEELEEIEEDAGLGNGGLGR	LAACF	2		1322.624494	2643.233389	0.000823681	1	N	114	139
Q9ET66	Infl	MLQMR	WDDELAAFAK	AYAQK	2		583.2803676	1164.545135	0.001352548	7	N	51	61
Q9ET66	Infl	SKTER	IGCGSHFCETLQGVEEANIHLLVCNYEPPGNVK	GRKPY	3	C3:+57.021,C8:+57.021,C24:+57.021	1247.920182	3740.737146	0.000451244	7	N	132	165
Q9JHF5	Infl	EARFR	TLQQLQQQSQELQEVLGETDRFLSQVLGR	VQQLL	3		1124.590498	3370.748094	0.000979378	3	N	256	285
Q9JHF5	Infl	GSMFR	SEEVALVQLLLPTGSAYNCVSQLGELGLVEFR	DLNES	3	C19:+57.021	1164.608236	3490.801307	0.000451244	13	N	6	38
Q9JHJ0	Infl	VKGEK	ILPVFDEPPNPTNVEESLKR	IREND	2		1147.605505	2293.195409	0.000451244	5	N	172	192
Q9JHJ0	Infl	ESELK	QLETVLDDLDPENALLPAGFR	QKNQT	2		1163.600419	2325.185238	0.000451244	18	N	30	51
Q9JHJ0	Infl	ELLGK	LSESELKQLETVLDDLDPENALLPAGFR	QKNQT	3		1038.206991	3111.597573	0.000451244	4	N	23	51
Q9JHJ0	Infl	ENDAR	LVEVNLNNIK	NIPIP	2		578.3407596	1154.665919	0.000451244	3	N	199	209
Q9JHJ0	Infl	LPFRK	DLGDYKDLDEDELLGK	LSESE	3		613.2954336	1836.862901	0.000451244	5	N	7	23
Q9JHJ0	Infl	VKGEK	ILPVFDEPPNPTNVEESLK	RIREN	2		1069.554949	2137.094298	0.002981883	1	N	172	191
Q9JHK5	Infl	EKDKK	VFNHCLTGSGVIDWLVSNK	LVRNR	2	C5:+57.021	1073.541422	2145.067243	0.000451244	21	N	150	169
Q9JHK5	Infl	SHDVK	KSDEENLFEIITADEVHYYLQAATSK	ERTEW	3		1005.49302	3013.45566	0.000451244	20	N	307	333
Q9JHK5	Infl	HDVKK	SDEENLFEIITADEVHYYLQAATSK	ERTEW	3		962.7946989	2885.360697	0.000622848	12	N	308	333
Q9JHK5	Infl	ITTTK	QQDHFFQAAFLEER	DAWVR	2	[0:-17.027	874.9052896	1747.794979	0.000823681	1	N	75	89
Q9JHK5	Infl	KVRKF	ILREDPAYLHYYDPAGGEDPLGAVHLR	GCVVT	3		1013.177589	3036.509367	0.002727428	1	N	266	293
Q9JHK5	Infl	SHDVK	KSDEENLFEIITADEVHYY	LQAAT	2		1158.03986	2314.06412	0.001699387	3	N	307	326
Q9JHK5	Infl	GDLSK	NAADGIAENPFLDSPDAF	YYFPD	2		932.4239347	1862.832269	0.001463592	2	N	198	216

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JHS3	Infl	MLRPK	ALTQVLSQANTGGVQSTLLLNNEGSLLAYSGYGDTDAR	VTAAI	3		1299.987534	3896.939202	0.000451244	13	N	5	43
Q9JHU4	Infl	QKHLR	KLVPLLLEDGGDAPAALEAALEEK	SALEQ	2		1231.673584	2461.331569	0.000451244	3	N	33	57
Q9JHU4	Infl	GSEER	VQVALEELQDLKGVWSELSK	VWEQI	3		757.7464034	2270.21581	0.000823681	1	N	1316	1336
Q9JHU4	Infl	ESALR	FGNPLLVQDVESYDPVLNPVLNR	EVRRT	2		1299.682275	2597.34895	0.000451244	9	N	3626	3649
Q9JHU4	Infl	KHLRK	LVPLLLEDGGDAPAALEAALEEK	SALEQ	2		1167.626103	2333.236605	0.001162105	5	N	34	57
Q9JHU4	Infl	PAAVK	LALESICLLLGESTTDWK	QIRSI	2	C7:+57.021	1025.032564	2048.049528	0.000451244	6	N	3316	3334
Q9JHU4	Infl	ALFNR	CVLNWFGDWSTEALYQVGKEFTSK	MDLEK	3	C1:+57.021	955.7903004	2864.347501	0.000622848	2	N	3086	3110
Q9JHU4	Infl	ELQKR	QWIVFDGDVDPEWVENLNSVLDDNKLLTLPNGER	LSLPP	3		1313.985353	3938.93266	0.000451244	11	N	2296	2330
Q9JHU4	Infl	SSQLR	VLTLSEDSPYETLHSFISNAVAPFFK	SYIRE	3		971.4959246	2911.464374	0.000451244	17	N	134	160
Q9JHU4	Infl	SIIMR	ENFIPTIVNFSAEEISDAIREK	MKKNY	3		841.4311436	2521.270031	0.002374549	2	N	3342	3364
Q9JHU4	Infl	SIIMR	ENFIPTIVNFSAEEISDAIR	EKMKK	2		1133.074037	2264.132475	0.000451244	7	N	3342	3362
Q9JHU4	Infl	PDGIR	REEFVQWVELLPDAQTPSWLGLPNNAER	VLLTT	3		1098.890108	3293.646923	0.000451244	8	N	4299	4327
Q9JHU4	Infl	DGIRR	EEFVQWVELLPDAQTPSWLGLPNNAER	VLLTT	3		1046.856404	3137.545812	0.000622848	8	N	4300	4327
Q9JHU4	Infl	GEKPK	VTDFGDKVEDPTFLNQLQSGVNR	WIREI	3		860.4299142	2578.266342	0.002374549	1	N	226	249
Q9JHU4	Infl	LKQIR	EVWNTYELDLVNYQNK	CRLIR	2		1014.489609	2026.963618	0.000451244	1	N	1465	1481
Q9JHU4	Infl	DLIAK	VQADEQFGIWLDSSSPEQTVPYLWSEETPTTPIGQAIHR	LLLIQ	3		1471.715703	4412.123709	0.000451244	4	N	3948	3987
Q9JHU4	Infl	SSFPR	FYFVGDEDLLEIIGNSK	NVAKL	2		979.9914532	1957.967306	0.000451244	1	N	1626	1643
Q9JHU4	Infl	QKVTK	LDRDPASGTALQEISFWLNLER	ALYRI	3		844.4349995	2530.281599	0.000451244	7	N	259	281
Q9JHU4	Infl	AGLKK	EVQALIAEGIALVWESYK	LDPYV	3		673.6986134	2018.07244	0.000451244	3	N	808	826
Q9JHU4	Infl	NIYNR	LGEDLNKWQALLVQIR	KARGT	3		632.6954262	1895.062879	0.001763695	1	N	1069	1085
Q9JHU4	Infl	ALFNR	CVLNWFGDWSTEALYQVGK	EFTSK	2	C1:+57.021	1137.038712	2272.061824	0.001162105	1	N	3086	3105
Q9JIF0	Infl	DLDFK	GQLCELSCSTDYR	MR-	2	C4:+57.021,C8:+57.021	794.8402063	1587.664813	0.000451244	1	N	356	369
Q9JIF0	Infl	RCHKR	TGFSTSPESPYTHWK	QTVFY	2		862.8998984	1723.784197	0.002374549	1	N	298	313
Q9JIF7	Infl	NLYAR	SIFGEDALANVSIEKPVHQGPDAAVTGHIR	IRAKS	3		1043.542819	3127.605058	0.000451244	7	N	898	928
Q9JIF7	Infl	LGDLK	LVEKPSPLTLAPHDFANIK	ANVKV	3		697.3935243	2089.157173	0.002019181	1	N	767	786
Q9JIF7	Infl	YTIYR	NFEHLIPDAPELIHDFLVNEK	DASCK	3		830.760824	2489.259072	0.000451244	3	N	164	185
Q9JIF7	Infl	KANVK	VASTENGIIFGNIVYDVSGAASDR	NCVVL	2		1228.10914	2454.20268	0.000451244	11	N	790	814
Q9JIF7	Infl	SEIKK	EAGELKPEEEITVGPVQK	LVTEM	2		977.012917	1952.010234	0.000622848	3	N	495	513
Q9JIF7	Infl	ADQDR	ALDYLSTCIDQVQTFGDILQLVIVELIYK	VCHAN	3	C8:+57.021	1124.267039	3369.777718	0.000451244	8	N	204	233
Q9JIX8	Infl	PGVSR	DSNTSYTETKDPSCGQEAAAPSGPQLQVLEPK	EKAPT	3	C14:+57.021	1135.863581	3404.567343	0.000451244	16	N	662	694
Q9JIX8	Infl	ELLGR	TGTLVEEAFWIDKIK	SHCFV	3		583.9860946	1748.934884	0.000451244	4	N	1033	1048
Q9JIX8	Infl	QQQEK	ETQIVSLPQEENEVK	SSQSL	2		871.944503	1741.873406	0.000662267	1	N	363	378
Q9JIY5	Infl	AIGEK	LAQNAEDVYEAVR	TQSQL	2		739.3682341	1476.720868	0.000451244	1	N	419	432
Q9JJ00	Infl	SGFVR	EAFTDADNFGIQFPLDLDVK	MKAVM	2		1128.047488	2254.079376	0.000451244	9	N	277	297
Q9JJ28	Infl	TDQMK	ADLTALFLPR	QPPMP	2		558.8247454	1115.633891	0.001162105	7	N	874	884
Q9JJ28	Infl	SAEAR	EGEEAAAEAEEKQPEEDFQCIVYFWQGR	EASNM	3	C20:+57.021	1115.826579	3344.456336	0.000451244	13	N	964	992
Q9JJ28	Infl	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTRVPECLYTLPSLR	RLNLS	3	C22:+57.021,C31:+57.021	1460.056435	4377.145904	0.000451244	5	N	210	249
Q9JJ28	Infl	CFILK	VPFESEDNQGIVYAWVGR	ASDPD	2		1033.503051	2064.990501	0.000451244	9	N	1091	1109
Q9JJ28	Infl	YSEFF	TEDVGQLPGLTIWQIENFVPVLVEEAFHGK	FYEAD	3		1122.585914	3364.734341	0.000451244	8	N	491	521
Q9JJ28	Infl	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTR	VPECL	2	C22:+57.021	1475.209222	2948.402844	0.000451244	5	N	210	237
Q9JJ28	Infl	ANSLK	NSGVPDDIFKLDDLSVLDLSHNQLTECPR	ELENA	3	C27:+57.021	1099.873752	3296.597856	0.000451244	2	N	92	121
Q9JJ28	Infl	VDYTR	NAEAVLQGQGLSGK	VKRDT	2		686.3654944	1370.715389	0.000451244	1	N	848	862
Q9JJ28	Infl	PSLRR	LNLSSNQIAELSLCIDQWVHLETLNLSR	NQLTS	3	C14:+57.021	1089.566482	3265.676046	0.000451244	5	N	250	278
Q9JJ28	Infl	SAEAR	EGEEAAAEAEEKQPEEDFQCIVY	FWQGR	2	C20:+57.021	1336.071528	2670.127457	0.002453667	1	N	964	987
Q9JJU8	Infl	FFEAR	ENNAVYAFLGLTAPPGSK	EAEAQ	2		924.9786801	1847.94176	0.000451244	4	N	86	104
Q9JJU8	Infl	RKWMR	ENVPEDSRPSTGYPLPPQIFNECQYR	GDYDA	3	C23:+57.021	1031.817578	3092.429333	0.000662267	12	N	50	76
Q9JJU8	Infl	ECQYR	GDYDAFFEAR	ENNAV	2		595.7597994	1189.503999	0.000823681	4	N	76	86
Q9JKC8	Infl	EKHWK	SVVSQSVCDYFFEAQEK	AADVE	2	C8:+57.021	1011.959596	2021.903592	0.000451244	7	N	21	38
Q9JKC8	Infl	PTILR	SVVNSITGSSNVGDTLPTGQLSNIPWRR	AGVKY	3		985.8481315	2954.520994	0.000870037	3	N	141	169
Q9JKC8	Infl	RAGVK	YTNNEAYFDVVEEIDAIIDK	SGSTV	2		1181.060793	2360.105985	0.000451244	6	N	173	193
Q9JKC8	Infl	NNEAY	FDVVEEIDAIIDK	SGSTV	2		753.3908435	1504.766087	0.001162105	1	N	180	193
Q9JKC8	Infl	PTILR	SVVNSITGSSNVGDTLPTGQLSNIPWR	RAGVK	3		933.8144277	2798.419883	0.000870037	1	N	141	168
Q9JKF1	Infl	PGETL	TEILETPATNEQEAEHQR	AMQRR	2		1048.498694	2094.981787	0.000451244	25	N	1404	1422
Q9JKF1	Infl	TTVWK	QLSSSVTGLTNIEEENCQR	YLDEL	2	C17:+57.021	1083.01088	2164.006159	0.000451244	16	N	477	496
Q9JKF1	Infl	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	C9:+57.021	674.9952813	2021.962444	0.000451244	3	N	36	52
Q9JKF1	Infl	LQQKR	QSGQTDPLQKEEVQAGVDAANSAAQQYQR	RLAAV	3		1039.833098	3116.475895	0.000451244	25	N	358	387
Q9JKF1	Infl	EIKSK	VDQIQEIVTGNPTVIK	MVVSF	2		877.4888807	1752.962161	0.000451244	13	N	1037	1053
Q9JKF1	Infl	AAYNR	EQLWLANEGLITK	LQACC	2		757.9148201	1513.81404	0.000451244	11	N	738	751
Q9JKF1	Infl	QANQF	KNVIFEIGPTEEVGDFEVK	AKFMG	2		1075.554949	2149.094298	0.000451244	27	N	1585	1604
Q9JKF1	Infl	VDVIR	FQPGETLTEILETPATNEQEAEHQR	AMQRR	2		1434.686471	2867.357343	0.001463592	1	N	1397	1422
Q9JKF1	Infl	GDVGR	TLSALRSPDVGLYGVIPECGETYQSDLAEAK	KKRLA	3	C19:+57.021	1113.885657	3338.633572	0.000622848	2	N	641	672
Q9JKF1	Infl	LSALR	SPDVGLYGVIPECGETYQSDLAEAK	KKRLA	2	C13:+57.021	1349.631556	2697.247512	0.000451244	14	N	647	672
Q9JKF1	Infl	QEAQR	FALGISAINEAVDSGDVGR	TLSAL	2		945.9819511	1889.948302	0.000451244	13	N	622	641
Q9JKF1	Infl	IPAAK	LEGVLAEVAQHYQDTLIR	AKREK	3		685.701017	2054.079651	0.000451244	28	N	567	585
Q9JKF1	Infl	RLHEK	GVLLEIEDLQANQFK	NVIFE	2		858.9624987	1715.909397	0.000823681	7	N	1571	1586

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JKF1	Infl	KNMPR	CIYCIHALSLYLFK	LGLAP	2	C1:+57.021,C4:+57.021	900.9624702	1799.90934	0.002080925	1	N	147	161
Q9JKF1	Infl	ANQFK	NVIFEIGPTEEVGDFEVK	AKFMG	2		1011.507467	2020.999335	0.000451244	15	N	1586	1604
Q9JKF1	Infl	AASNK	MFLGDNAHLSIINEYLSQSYQK	FRRFF	2		1286.131561	2570.247522	0.000451244	8	N	1239	1261
Q9JKF1	Infl	VQLSR	EEIQSSISGVTAAYNREQLWLANEGLITK	LQACC	3		1074.221523	3219.641169	0.000451244	7	N	722	751
Q9JKF1	Infl	EEHER	ILAIGLINEALDEGDAQK	TLQAL	2		942.0101773	1882.004755	0.000451244	30	N	538	556
Q9JKF1	Infl	AKREK	AQETQDESAVLWLDEIQGGIWQSNKDTQEAQR	FALGI	3		1225.25087	3672.729209	0.000451244	19	N	590	622
Q9JKF1	Infl	GLHFR	HTDNVIQWLNAMDEIGLPK	IFYPE	3		732.0374122	2193.088837	0.000637154	4	N	111	130
Q9JKF1	Infl	RLHEK	GVLLEIEDLQANQF	KNVIF	2		794.9150171	1587.814434	0.000451244	16	N	1571	1585
Q9JKF1	Infl	EEHER	ILAIGLINEALDEGDAQKTLQALQIPAAK	LEGVL	3		1006.568083	3016.680849	0.000451244	13	N	538	567
Q9JKF1	Infl	GDAQK	TLQALQIPAAKLEGVLAEVAQHYQDTLIR	AKREK	3		1063.926382	3188.755746	0.002212458	1	N	556	585
Q9JKF1	Infl	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDRR	VAADT	3		1038.902236	3113.683309	0.000451244	16	N	201	231
Q9JKF1	Infl	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDR	RVAAD	3		986.8685326	2957.582198	0.000451244	5	N	201	230
Q9JKF1	Infl	TGLKK	LTELGTVDPK	NRYQE	2		536.7983932	1071.581186	0.000451244	11	N	1465	1475
Q9JKF1	Infl	VTLLK	ALQSLALGLR	GLQTQ	2		521.3249125	1040.634225	0.0007646	11	N	326	336
Q9JKF1	Infl	IRAKR	EKAQETQDESAVLWLDEIQGGIWQSNK	DTQEA	3		1034.83919	3101.494171	0.000451244	8	N	588	615
Q9JKF1	Infl	IGLPK	IFYPETTDIYDRK	NMPRC	2		830.9150171	1659.814434	0.000637154	10	N	130	143
Q9JKF1	Infl	YLLLR	LFQTALQEEIK	SKVDQ	2		660.3644317	1318.713263	0.000451244	11	N	1024	1035
Q9JKF1	Infl	QEEIK	SKVDQIQEIVTGNPTVIK	MVVSF	2		985.0523765	1968.089153	0.000451244	20	N	1035	1053
Q9JKF1	Infl	GDAQK	TLQALQIPAAK	LEGVL	2		577.3511273	1152.686655	0.000451244	22	N	556	567
Q9JKF1	Infl	EAQRF	ALGISAINEAVDSGDVGR	TLSAL	2		872.4477441	1742.879888	0.000451244	10	N	623	641
Q9JKF1	Infl	KHWVK	GGYHYYHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	3		1174.215543	3519.623228	0.000622848	3	N	691	722
Q9JKF1	Infl	GNVNK	VNTSSALANISLALEQGCAVTLLK	ALQSL	3	C18:+57.021	825.1162363	2472.325309	0.000451244	9	N	302	326
Q9JKF1	Infl	AIDRR	VAADTFTALKNPNAMLVNLEEGLAPTYQDVLYQAK	QDKMT	3	M15:+15.995	1275.652576	3823.934327	0.001654178	2	N	231	266
Q9JKF1	Infl	DPLQK	EEVQAGVDAANSAAQQYQR	RLAAV	2		1017.977928	2033.940257	0.000451244	2	N	368	387
Q9JKF1	Infl	LYLFK	LGLAPQIQDLYGK	VDFTE	2		708.3988059	1414.782012	0.000622848	5	N	161	174
Q9JKF1	Infl	SDRER	DVYEELLTQAEIQGNVNK	VNTSS	2		1032.018731	2062.021861	0.000451244	6	N	284	302
Q9JKF1	Infl	AKREK	AQETQDESAVLWLDEIQGGIWQSNK	DTQEA	2		1423.186107	2844.356614	0.000451244	11	N	590	615
Q9JKF1	Infl	SAVLW	LDEIQGGIWQSNKDTQEAQR	FALGI	2		1158.564899	2315.114199	0.000451244	5	N	602	622
Q9JKF1	Infl	GYHYY	HNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	2		1390.673501	2779.331402	0.000451244	4	N	697	722
Q9JKF1	Infl	GGYHY	YHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	3		981.8060437	2942.394731	0.000451244	13	N	696	722
Q9JKF1	Infl	GDVGR	TLSALRSPDVGLYGVIPECGETY	QSDLA	2	C19:+57.021	1249.117888	2496.220175	0.0007646	1	N	641	664
Q9JKF1	Infl	AKVLK	DSLHEKFPDAGEDELLK	IIGNL	2		971.9737918	1941.931984	0.000451244	7	N	1168	1185
Q9JKF1	Infl	DELLK	IIGNLLYYR	YMNPA	2		562.8272881	1123.638976	0.001162105	5	N	1185	1194
Q9JKF1	Infl	DERRR	QNVAYEYLCHLEEAK	RWMEA	3	C9:+57.021	622.9615776	1865.861333	0.000662267	2	N	36	51
Q9JKF1	Infl	LSALR	SPDVGLYGVIPECGETY	QSDLA	2	C13:+57.021	928.4248574	1854.834115	0.002019181	2	N	647	664
Q9JKR6	Infl	MAGLK	VLQLINDNTATALSYGVFR	RKDIN	2		1048.063276	2094.110951	0.000451244	16	N	198	217
Q9JKR6	Infl	LNYSR	SLAEDFAEQPIKDAVITVPAFFNQAER	RAVLQ	3		1002.845616	3005.513449	0.000451244	12	N	158	185
Q9JKR6	Infl	PFVVR	DAVIYPILVEFTR	EVEEE	2		768.4275634	1534.839527	0.001162105	1	N	438	451
Q9JKR6	Infl	SKGIK	AHFNLDESGVLSLDRVESVFETLVEDSPEEESTLTK	LGNTI	3		1341.318727	4020.93278	0.000451244	15	N	540	576
Q9JKR6	Infl	QEREK	AANSLEAFIFETQDK	LYQPE	2		842.4153813	1682.815163	0.000451244	2	N	738	753
Q9JKR6	Infl	PFVVR	DAVIYPILVEF	TREVE	2		639.8531685	1277.690737	0.002145581	1	N	438	449
Q9JKR6	Infl	LSLDR	VESVFETLVEDSPEEESTLTK	LGNTI	2		1184.568647	2367.121695	0.000451244	5	N	555	576
Q9JKV1	Infl	CWKDR	TSGTVEDDLIIFPDDCEFK	RVPQC	2	C16:+57.021	1101.001658	2199.987715	0.001162105	4	N	64	83
Q9JKV1	Infl	CWKDR	TSGTVEDDLIIFPDDCEFKR	VPQCP	2	C16:+57.021	1179.052213	2356.088826	0.000451244	1	N	64	84
Q9JKY5	Infl	LAVLR	SAAAEAEAILQDAVSKLDDPLHLR	CTSSP	4		634.0873945	2532.318378	0.00091018	4	N	625	649
Q9JKY5	Infl	YLVSR	AQAALDSVSGLEQGHTQYLASSEDASALVAALTR	FSHLA	3		1144.241535	3429.701204	0.000451244	6	N	660	694
Q9JL26	Infl	HFLDK	AGSVSLDSVLGDVR	SLQRG	2		687.8653272	1373.715054	0.000451244	4	N	901	915
Q9JL26	Infl	KGLIR	ILRGPGDVVSIEILPGAAATPSGDDAQAPR	VSTDS	3		981.8565155	2942.546147	0.000451244	12	N	489	519
Q9JL26	Infl	LADSK	TAQEAYESVVEYFGENPK	TTSPS	2		1030.976531	2059.937463	0.000451244	19	N	956	974
Q9JL26	Infl	RKQQK	EPLIYESDRDGAIEDIITDLR	NQPYI	3		811.7434987	2432.207096	0.000451244	1	N	1042	1063
Q9JL26	Infl	LGADR	ICQAIETYDLQTLSLDFLELLTR	FLPTD	2	C2:+57.021	1378.215059	2754.414518	0.000451244	6	N	726	749
Q9JL26	Infl	QIQAY	LDNVFDVGTLLEETETK	NAVLE	2		961.9838252	1921.95205	0.000451244	10	N	376	393
Q9JL26	Infl	AIETY	DLQTLSLDFLELLTR	FLPTD	2		888.9912562	1775.966912	0.000451244	5	N	734	749
Q9JL26	Infl	IRILR	GPGDVVSIEILPGAAATPSGDDAQAPR	VSTDS	2		1281.146254	2560.276907	0.000451244	17	N	492	519
Q9JL26	Infl	EPLIY	ESDRDGAIEDIITDLR	NQPYI	3		606.6345608	1816.880282	0.000451244	7	N	1047	1063
Q9JL62	Infl	LPADR	QIETGPFLEAVAHLPPFFDCLGSPVFTPIK	ADISG	3	C20:+57.021	1109.909298	3326.704493	0.000451244	8	N	16	46
Q9JL62	Infl	LPADR	QIETGPFLEAVAHLPPFFDCLGSPVFTPIKADISGNITK	IKAVY	4	C20:+57.021	1057.551735	4226.17574	0.00091018	5	N	16	55
Q9JLF6	Infl	RPGPR	QLIASLDSPQLSQVHGVIQVDVAPASGGSGFSDAGGDSR	SGENI	3		1274.968474	3821.882022	0.000451244	4	N	763	802
Q9JLF6	Infl	DCWMK	RPDLPSGFDGWQVVDATPQETSSGIFCCGPCSVESVK	NGLVY	3	C27:+57.021,C28:+57.021,C31:+57.021	1357.283737	4068.827812	0.001162105	3	N	443	480
Q9JLF6	Infl	GDYSR	GTNPSAWVGSVEILLSYLR	TGYSV	2		1031.552544	2061.089487	0.000622848	4	N	347	366
Q9JLJ2	Infl	FGYTR	REPLGVCVGIGAWNYPFQIACWK	SAPAL	3	C7:+57.021,C21:+57.021	907.7860133	2720.33464	0.000622848	6	N	143	166
Q9JLJ2	Infl	VKLAK	EQGATVLCGGEVYVPEDPKLK	HGYYM	3	C8:+57.021	763.7195942	2288.135383	0.001871652	1	N	347	368
Q9JLJ2	Infl	VKLAK	EQGATVLCGGEVYVPEDPK	LKHGY	2	C8:+57.021	1024.485978	2046.956355	0.001329271	2	N	347	366
Q9JLQ2	Infl	QKLAR	FNAHEFATLVIDILSDAK	RRQQG	3		668.6865964	2003.036389	0.000451244	17	N	335	353

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JLQ2	Infl	SECRK	ALPGDSSLPTDVQLVTQQVIQCAYDIAK	AAKQL	3	C22:+57.021	1010.853629	3029.537487	0.000451244	17	N	665	693
Q9JLQ2	Infl	SKRLR	SSDVCADCNGPDPSWASVNR	GTFIC	2	C5:+57.021,C8:+57.021	1097.449901	2192.884201	0.000451244	10	N	6	26
Q9JLQ2	Infl	QSECR	KALPGDSSLPTDVQLVTQQVIQCAYDIAK	AAKQL	3	C23:+57.021	1053.55195	3157.63245	0.000735798	3	N	664	693
Q9JLQ2	Infl	EVDRR	ETDAVWLATQNHSTLVTETTVVPFLPVNPEYSSTR	NQGRQ	3		1301.653604	3901.937411	0.001699387	1	N	291	326
Q9JLV6	Infl	RKCSR	NQVELIADPESR	TVAVK	2		685.8496771	1369.683754	0.000451244	3	N	48	60
Q9JLV6	Infl	QLGSR	GRLWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	3		977.2069314	2928.597394	0.000451244	5	N	7	35
Q9JLV6	Infl	AFDPR	TISSAGPLYLPESSSLLSPNPEVVVAVGFPGAGK	STFIQ	3		1114.261207	3339.760222	0.000451244	4	N	343	377
Q9JLV6	Infl	GSRGR	LWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	2		1358.74521	2715.474819	0.000451244	16	N	9	35
Q9JLV6	Infl	SCADR	LFALNVGLPFATPEEFFLK	WPAAR	2		1077.088231	2152.160861	0.001763695	3	N	310	329
Q9JLV6	Infl	KPQGK	VAAFDLDGTLITTR	SGKVF	2		746.9044524	1491.793305	0.000451244	15	N	165	179
Q9JLV6	Infl	PLTLR	WEELSTSGSQPDAPPDTPGDPEEGEDTEPQKK	RVRKS	3		1151.841653	3452.50156	0.000451244	13	N	105	137
Q9JLV6	Infl	GRKKK	DFSCADRLFALNVGLPFATPEEF	FLKWP	2	C4:+57.021	1308.62588	2615.23616	0.000451244	4	N	303	326
Q9JLV6	Infl	SCADR	LFALNVGLPFATPEEF	FLKWP	2		882.9645101	1763.91342	0.000698008	5	N	310	326
Q9JLV6	Infl	PLTLR	WEELSTSGSQPDAPPDTPGDPEEGEDTEPQK	KRVRK	3		1109.143332	3324.406597	0.000451244	8	N	105	136
Q9JLV6	Infl	PPIFL	PSDGQALVLGR	GPLTQ	2		556.8070839	1111.598568	0.001871652	1	N	24	35
Q9JM14	Infl	DLAEK	VASVYESPGFFLNLEPIPGALDALR	EMNDM	2		1338.208126	2674.400651	0.000451244	12	N	62	87
Q9JM14	Infl	KRPVR	VLVDMDGVLADFESGLLQGFR	RRFPE	2		1141.080809	2280.146017	0.000451244	1	N	8	29
Q9JM76	Infl	RLCEK	VFDPQSDKPSKWWTCFVK	RQFMN	4	C15:+57.021	564.5297111	2254.087644	0.000998612	4	N	147	165
Q9JM76	Infl	GPAPR	ETKDTDIVDEAIYYFK	ANVFF	2		975.4730933	1948.930587	0.000451244	15	N	34	50
Q9JM76	Infl	PRETK	DTDIVDEAIYYFK	ANVFF	2		796.3804758	1590.745352	0.000451244	21	N	37	50
Q9JM76	Infl	EKEMY	TLGITNFPIPGEPGFPLNAIYAKPASK	QEDEM	3		938.5132499	2812.51635	0.000451244	8	N	96	123
Q9JM76	Infl	PRETK	DTDIVDEAIYYF	KANVF	2		732.3329942	1462.650388	0.000823681	5	N	37	49
Q9JMA1	Infl	VLQQK	LEAIEDDSGRETDSSSAPAVTPSK	KKSLI	2		1231.580609	2461.145618	0.000451244	4	N	214	238
Q9JMA1	Infl	PKEIK	YEPFSFADDIGSNNCGYYDLQAVLTHQGR	SSSSG	3	C15:+57.021	1113.167047	3336.47774	0.000451244	11	N	399	428
Q9JMH6	Infl	KDDER	VVGFHVLGPNAGEVTQGFAAALK	CGLTK	3		761.4150995	2281.221899	0.000451244	2	N	548	571
Q9JMH6	Infl	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	2	C1:+57.021,C18:+57.021,C19:+57.021	1477.62991	2953.244221	0.000451244	1	N	478	503
Q9JMH6	Infl	PGRLR	VTAQSTNSEETIEGEFNTVLLAVGR	DSCTR	2		1333.169926	2664.324251	0.000451244	8	N	382	407
Q9JMH6	Infl	KAVEK	FGEENIEVYHSFFWPLEWTVPSR	DNNKC	3		957.1260545	2868.354764	0.000451244	10	N	507	530
Q9JMH6	Infl	EKTGK	IPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGR	LLAQR	3		1309.365283	3925.072449	0.000451244	13	N	429	465
Q9JMH6	Infl	KFDKK	VLVLDFVTPTPLGTR	WGLGG	2		814.475045	1626.93449	0.000451244	5	N	151	166
Q9JMH9	Infl	RLETR	ISELTSELTDERNTGESASQLLDAETAER	LRTEK	3		1055.839696	3164.495687	0.000622848	8	N	1286	1315
Q9JMH9	Infl	IAQLK	NQLEESEFTCAAAVK	ARKAM	2	C10:+57.021	848.8962671	1695.776934	0.001839721	1	N	1685	1700
Q9JMH9	Infl	ARLIR	AAEINGEVDDDDAGGEWR	LKYER	2		959.9066374	1917.797675	0.000451244	5	N	1350	1368
Q9JMH9	Infl	EKKQR	RFDSELSQAHEETQR	EKLQR	3		611.6227666	1831.8449	0.001943752	4	N	1457	1472
Q9QUG9	Infl	CHLVR	YWISAFPAEFDLNPELAEQIKELK	ALLDQ	3		951.1571318	2850.447995	0.000451244	4	N	80	104
Q9QUG9	Infl	CHLVR	YWISAFPAEFDLNPELAEQIK	ELKAL	2		1241.120988	2480.226375	0.001162105	1	N	80	101
Q9QUH0	Infl	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3		1060.877756	3179.609869	0.000451244	47	N	39	68
Q9QUH0	Infl	CPYCR	KTQEILSQLPFK	QGLLE	2		716.414456	1430.813312	0.000451244	10	N	27	39
Q9QUH0	Infl	PYCRK	TQEILSQLPFK	QGLLE	2		652.3669744	1302.718349	0.000698008	4	N	28	39
Q9QUH0	Infl	GLLEF	VDITATNNTSAIQDYLQQLTGAR	TVPRV	2		1247.133146	2492.250692	0.000451244	6	N	45	68
Q9QUH0	Infl	SQLPF	KQGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3		1103.576077	3307.704832	0.000451244	12	N	38	68
Q9QUH0	Infl	PYCRK	TQEILSQLPFKQGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	4		1117.087215	4464.317658	0.000451244	4	N	28	68
Q9QUH0	Infl	IQSGK	VVVFIKPTCPY	CRKTQ	2	C9:+57.021	661.862782	1321.709964	0.001763695	1	N	14	25
Q9QUI0	Infl	TPEVK	HFCPNVPIILVGNKK	DLRND	3	C3:+57.021	579.3277549	1734.959865	0.000451244	16	N	104	119
Q9QUI0	Infl	DVILM	CFSIDSPDSLENIPEKWTPEVK	HFCPN	2	C1:+39.994	1287.607127	2573.198654	0.001264573	3	N	82	104
Q9QUI0	Infl	GACGK	TCLLIVFSKDQFPEVYVPTVF	ENYVA	2	C2:+57.021	1251.653378	2501.291155	0.002884417	1	N	18	39
Q9QUI0	Infl	GACGK	TCLLIVFSKDQFPEVYVPTVFENYVADIEVDGK	QVELA	3	C2:+57.021	1278.978106	3833.910917	0.000622848	1	N	18	51
Q9QUI0	Infl	IVFSK	DQFPEVYVPTVFENYVADIEVDGK	QVELA	2		1387.16632	2772.317041	0.000451244	10	N	27	51
Q9QUI0	Infl	TPEVK	HFCPNVPIILVGNK	KDLRN	2	C3:+57.021	804.4402509	1606.864902	0.000622848	1	N	104	118
Q9QUM0	Infl	RRQAF	LQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	C16:+57.021,C22:+57.021,C27:+57.021	1096.188269	3285.541406	0.000451244	9	N	889	919
Q9QUM0	Infl	ANGGK	CNPLLFDLRDETR	NLGFQ	2	C1:+57.021	824.9095119	1647.803424	0.001654178	1	N	95	108
Q9QUM0	Infl	VSNQR	FTYDNSNPVFFDGYR	GYSVA	2		921.4106303	1840.805661	0.000451244	6	N	250	265
Q9QUM0	Infl	QEQTR	IILDCGEDDLCVPQLR	LTATA	2	C5:+57.021,C11:+57.021	958.4663024	1914.917005	0.000451244	9	N	627	643
Q9QUM0	Infl	RDETR	NLGFQIFQTFK	TGQGL	2		671.8618592	1341.708118	0.000622848	2	N	108	119
Q9QUM0	Infl	VPQLR	LTATAGDSPLLIGADNVLELK	IEAAN	2		1056.083874	2110.152147	0.000451244	12	N	643	664
Q9QUM0	Infl	VNGLR	LLIHIPGQSQPSDLLYILDVQPQGGLLCSTQPSPK	VDWKL	3	C28:+57.021	1271.680394	3812.017782	0.000451244	14	N	828	863
Q9QUM0	Infl	GFSLR	GAVDIDDNGYPDLIVGAYGASK	VAVYR	2		1105.534745	2209.05389	0.000451244	7	N	452	474
Q9QUM0	Infl	FLQPK	GPQALSTPTLLLTGTQLYGR	FGSAI	2		1044.078926	2086.142251	0.000451244	6	N	365	385
Q9QUM0	Infl	FQTFK	TGQGLGASVVSWNDVIVACAPWQHWNVLEKR	DEAEK	4	C19:+57.021	870.1929781	3476.740712	0.000451244	5	N	119	150
Q9QUM0	Infl	GLLAR	VPIENIISSYRPGTLLWHVSNQR	FTYDN	3		893.8175553	2678.429266	0.000451244	2	N	227	250
Q9QUM0	Infl	VLEKR	DEAEKTPVGGCFLAQLQSGGR	AEYSP	2	C11:+57.021	1110.539607	2219.063615	0.000451244	7	N	150	171
Q9QUM0	Infl	RWVSR	LEHTYELHNIGPGTVNGLR	LLIHI	2		1060.548324	2119.081048	0.000451244	6	N	809	828
Q9QUM0	Infl	SDLLY	ILDVQPQGGLLCSTQPSPK	VDWKL	2	C12:+57.021	1019.535805	2037.05601	0.000451244	9	N	844	863

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QUM0	Infl	VNGLR	LLIHIPGQSQPSDLLY	ILDVQ	2		897.493966	1792.972332	0.001264573	2	N	828	844
Q9QUM0	Infl	QRERR	QAFLQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	C19:+57.021,C25:+57.021,C30:+57.021	1211.576304	3631.705511	0.001463592	1	N	886	919
Q9QUM0	Infl	QVLIF	LGQSEGLSPRPSQVLDSPFPTGSGFGFSLR	GAVDI	3		1040.86367	3119.56761	0.002296037	1	N	422	452
Q9QUM9	Infl	KVPDK	LLDSSTVTHLFK	ITESI	3		454.2544042	1359.739813	0.002296037	1	N	59	71
Q9QUM9	Infl	NPKFR	ILTEAEIDAHLVALAERD	-	3		660.3535058	1978.037117	0.000823681	5	N	228	246
Q9QUR6	Infl	EGEAR	VFLDPNTLSDDGTVALR	GYAFS	2		916.9735948	1831.93159	0.001162105	1	N	111	128
Q9QUR6	Infl	ILANK	QNCFDDFQCAAEYLIK	EGYTS	2	C3:+57.021,C9:+57.021	1011.440285	2020.864969	0.001162105	4	N	523	539
Q9QUR6	Infl	LKWVK	LIDNFEGEYDYVTNEGTVFTFK	TNRNS	2		1301.105731	2600.195863	0.000451244	14	N	281	303
Q9QUR6	Infl	YHGHK	ICDPYSWLEDPDSEQTK	AFVEA	2	C2:+57.021	1041.951968	2081.888335	0.000451244	13	N	23	40
Q9QUR6	Infl	EVTVK	GIDAADYQTIQIFYPSK	DGTKI	2		965.4837953	1928.951991	0.000451244	2	N	428	445
Q9QWR8	Infl	IPDPK	RFPHGIAFLADYAHSLGLK	LGIYE	4		529.039519	2112.126876	0.002145581	1	N	96	115
Q9QWR8	Infl	QDSWK	SVLSILDWFVR	HQDVL	2		667.8775093	1333.739419	0.002296037	3	N	223	234
Q9QX47	Infl	AASAR	SLPNEEIVQKIEEVLSGVLDTELR	YKPDL	3		904.1556795	2709.443638	0.000451244	5	N	54	78
Q9QX47	Infl	ALSPK	ESSEDTEVPLPNKEIVPESGYSASIDEINEADLVRPLLPK	DMERL	4		1095.805496	4379.190786	0.000451244	5	N	1725	1765
Q9QX47	Infl	HLIVK	DAEHNTVCATTVGPVGEASEEK	ILPIS	2	C8:+57.021	1151.018902	2300.022203	0.000851441	1	N	1572	1594
Q9QXK3	Infl	GPLFK	SSEPVQLTEAETEYFVR	CVKHM	2		992.9790741	1983.942548	0.000451244	10	N	629	646
Q9QXK3	Infl	DHIQK	ILKPNFAAAWEEVGDAFEKEETFALSSTK	TLEEA	3		1076.875353	3227.602659	0.001162105	1	N	763	792
Q9QXK3	Infl	SALAK	FGAQNESLLPSILVLLQR	CMMDT	2		999.5732791	1997.130958	0.000451244	16	N	497	515
Q9QXK3	Infl	KFTVR	DCDPNTGVPDEDGYDDEYVLEDLEVTVSDHIQK	ILKPN	3	C2:+57.021	1261.211263	3780.61039	0.000451244	4	N	730	763
Q9QXK3	Infl	DHIQK	ILKPNFAAAWEEVGDAFEKEETF	ALSST	3		881.099394	2640.274782	0.001654178	1	N	763	786
Q9QXK3	Infl	FEYKK	AIVDCIISIVEENPESK	EAGLA	2	C5:+57.021	958.4879891	1914.960378	0.000451244	1	N	415	432
Q9QXK3	Infl	NPESK	EAGLAHLCEFIEDCEHTVLATK	ILHLL	3	C8:+57.021,C14:+57.021	848.4018937	2542.182281	0.000451244	1	N	432	454
Q9QXS1	Infl	EEAER	LKQSAEEQAQAQAQAQAAAEK	LRKEA	2		1100.054167	2198.092735	0.000622848	2	N	2261	2282
Q9QXS1	Infl	RDDAR	VYHDPSTQEPVTYSQLQQR	CRSDQ	2		1138.551261	2275.086921	0.000622848	1	N	3323	3342
Q9QXS1	Infl	EEALR	LLDAQLATGGIVDPR	LGFHL	3		513.6232677	1537.846403	0.000823681	1	N	3942	3957
Q9QXS1	Infl	ITGQR	LLEAQACTGGIIDPSTGERFPVTEAVNK	GLVDK	3	C7:+57.021	991.8380904	2972.490871	0.000451244	8	N	4454	4482
Q9QXS1	Infl	IVDPR	LGFHLPLEVAYQR	GYLNK	3		514.9529481	1541.835444	0.000979378	2	N	3957	3970
Q9QXS1	Infl	PSHWK	VLSGSSSEAAVPSVCFLVPPPNQEAQEAVAR	LEAQH	3	C15:+57.021	1066.203321	3195.586563	0.0007646	7	N	985	1016
Q9QXS1	Infl	EEMNR	VLADPSDDTKGFFDPNTHENLTYLQLLER	CVEDP	3		1116.8848	3347.630999	0.001162105	2	N	3644	3673
Q9QXS1	Infl	EEMNR	ILSDPSDDTKGFFDPNTHENLTYLQLLER	CVEDP	3		1126.888321	3377.641563	0.000451244	4	N	2985	3014
Q9QXS1	Infl	SAGPR	TQLASWSDPTEETGPVAGILDTETLEK	VSITE	2		1444.706538	2887.397476	0.000451244	4	N	4408	4435
Q9QXS1	Infl	EAGQR	FLEVQYLTGGLIEPDTPGR	VSLDE	2		1053.049834	2104.084068	0.000451244	14	N	4530	4549
Q9QXS1	Infl	QAMKK	GIIRPGTAFELLEAQAATGYVIDPIKGLK	LTVEE	4		761.1818263	3040.696105	0.000622848	2	N	4099	4128
Q9QXS1	Infl	LRALV	PAAELLDSGVISHELYQQLQR	GERSV	3		789.748807	2366.223021	0.000823681	1	N	3125	3146
Q9QXS1	Infl	DSTLR	YLQDLLAWVEENQR	RIDSA	2		888.9499226	1775.884245	0.000451244	7	N	668	682
Q9QXS1	Infl	EALKK	DLLQPEVAVALLEAQAGTGHIIDPATSAR	LTVDE	3		986.1966492	2955.566548	0.000451244	15	N	3190	3219
Q9QXS1	Infl	TALQR	QLLSPGTALILLEAQAASGFLLDPVR	NRRLT	2		1347.265975	2692.51635	0.000451244	7	N	2862	2888
Q9QXS1	Infl	LPNGR	DAPDGPSVEAEPEYTFEGLR	QKVPA	2		1089.995453	2177.975305	0.000451244	12	N	2774	2794
Q9QXS1	Infl	FEGLR	ALVPAAELLDSGVISHELYQQLQR	GERSV	2		1325.714106	2649.412613	0.000451244	1	N	3122	3146
Q9QXS1	Infl	FEGLR	QKVPAQQLQEAGILSQEELQR	LAQGH	3		798.4314779	2392.271034	0.000451244	1	N	2794	2815
Q9QXS1	Infl	AARQR	SQVEEELFSVR	VQMEE	2		661.8334957	1321.651391	0.002981883	1	N	2368	2379
Q9QXS1	Infl	EAMRR	GLLRPSTATLLLEAQAATGFLVDPVRNQR	LYVHE	4		777.6890785	3106.725114	0.000622848	1	N	3521	3550
Q9QXS1	Infl	LGVTR	LLDPEDVDVPQPDEK	SIITY	2		854.9179538	1707.820308	0.000451244	1	N	382	397
Q9QXS1	Infl	NKVYR	QTNLENLDQAFSVAER	DLGVT	2		917.950651	1833.885702	0.000451244	1	N	360	376
Q9QXS1	Infl	KNLQK	FLEGTSCIAGVFVDATK	ERLSV	2	C7:+57.021	907.9535851	1813.89157	0.000451244	12	N	4071	4088
Q9QXS1	Infl	VAYQR	GYLNKDTHDQLSEPSEVR	SYVDP	3		696.671786	2086.991958	0.002884417	1	N	3970	3988
Q9QXS1	Infl	AERLK	QSAEEQAQAQAQAQAAAEK	LRKEA	2		979.4646539	1956.913708	0.000451244	6	N	2263	2282
Q9QXS1	Infl	DAKRR	QEQIQAVPIANCQAAR	EQLRQ	2	C12:+57.021	898.9575248	1795.89945	0.000451244	1	N	1374	1390
Q9QXS1	Infl	ENQRR	IDSAEWGVDLPSVEAQLGSHR	GMHQS	3		756.0419904	2265.102571	0.000662267	3	N	683	704
Q9QXS1	Infl	QLMER	CITDPQTGLCLLPLK	EKKRE	2	C1:+57.021,C10:+57.021	864.9548422	1727.894084	0.000451244	4	N	4251	4266
Q9QXS1	Infl	KFQGR	TVTIWEIINSEYFTAEQR	RDLLQ	2		1100.550198	2199.084796	0.000451244	6	N	3064	3082
Q9QXS1	Infl	ITGQR	LLEAQACTGGIIDPSTGER	FPVTE	2	C7:+57.021	994.4915944	1986.967589	0.000622848	3	N	4454	4473
Q9QXS1	Infl	RQALR	GTNVIAGVWLEEAGQK	LSIYE	2		836.4391908	1670.862782	0.000637154	4	N	3165	3181
Q9QXS1	Infl	EAMRR	GLLRPSTATLLLEAQAATGFLVDPVR	NQRLY	3		903.8486326	2708.522498	0.001763695	5	N	3521	3547
Q9QXS1	Infl	AGQRF	LEVQYLTGGLIEPDTPGR	VSLDE	2		979.5156268	1957.015654	0.000451244	8	N	4531	4549
Q9QXS1	Infl	QAMKK	GIIRPGTAFELLEAQAATGYVIDPIK	GLKLT	3		915.1730048	2742.495614	0.000451244	15	N	4099	4125
Q9QXS1	Infl	LYEAR	IISLETYNLFR	EGTKN	2		684.880249	1367.744898	0.001591523	1	N	3800	3811
Q9QXS1	Infl	ITVTR	LEDLLQDAQDEKEQLNEYK	GHLSG	3		774.3768159	2320.107048	0.00091018	1	N	904	923
Q9QXS1	Infl	QQRCR	SDQLTGLSLLPLSEK	AVRAR	2		800.9437746	1599.871949	0.002813207	1	N	3344	3359
Q9QXS1	Infl	VGSVR	TLLQGSGCLAGIYLEDSKEK	VTIYE	3	C8:+57.021	728.0405563	2181.098269	0.001591523	1	N	3492	3512
Q9QXZ0	Infl	YRKLK	ALNDAATAAEEGEALQWIVGTEVDVINQQLADFK	LFQKD	3		1210.604361	3628.789684	0.000451244	4	N	5202	5236
Q9QXZ0	Infl	AEKRR	SLLEILNSAADILINSSEIDEDEIRDEK	AGLNQ	3		1048.865182	3143.572146	0.000451244	6	N	4920	4948
Q9QXZ0	Infl	LHCGK	FQDALEPLLSWLTDTEELIANQKPPSAEYK	VVKAQ	3		1149.584239	3445.729316	0.000823681	1	N	5307	5337
Q9QXZ0	Infl	VLQEK	TECLIQQYEAVSLLNSER	YARLE	2	C3:+57.021	1077.031084	2152.046568	0.002884417	1	N	5712	5730

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QXZ0	Infl	EKLQK	AAHDLLDIEGEPALDCRPIQETTDSISSR	FQNLS	3	C16:+57.021	1070.517857	3208.53017	0.000823681	1	N	4025	4054
Q9QY06	Infl	RLVER	GLLPRPQADFDDLCNLPELTEANLLQNLK	LRFMQ	3	C14:+57.021	1103.238254	3306.691362	0.000451244	6	N	138	167
Q9QYB5	Infl	ASLYR	LADLFGWAHLANTYISVR	ISKEQ	2		1024.042146	2046.068692	0.002019181	1	N	146	164
Q9QYB5	Infl	VSSMK	CGILPISQESLILGDVAYYDYQGSLDEEEERIELQK	VLGPS	3	C1:+57.021	1391.679224	4172.014273	0.000998612	2	N	244	280
Q9QYB5	Infl	EDSSK	VSSGTPIKIEDPNQFVPLNTNPTEVLEK	RNKIR	3		1022.871831	3065.592094	0.002663018	1	N	476	504
Q9QYC0	Infl	EDGHR	TSTSAVPNLFVPLNTNPK	EVQEM	2		950.5128871	1899.010174	0.000451244	7	N	479	497
Q9QYC0	Infl	HITTR	VNSEQEHFLIVPFGLLYSEVTASSLVK	VNLQG	3		1002.866129	3005.574987	0.000451244	4	N	172	199
Q9QYC0	Infl	VSAMK	CGLLPISPEALSLGDVAYHDYHGILVDEEEK	ILIQK	3	[0:-17.027,C1:+57.021	1141.553758	3421.637873	0.002019181	1	N	252	283
Q9QYC0	Infl	AAFYR	LADLFGWSQLIYNHITTR	VNSEQ	3		716.7132569	2147.116371	0.000451244	7	N	154	172
Q9QYC0	Infl	PHKER	YFDRVDENNPEYLR	ERNMA	2		915.4268117	1828.838023	0.001264573	1	N	23	37
Q9QYC0	Infl	EQKEK	SPPDQSAVPNTPPSTPVKLEEDLPQEPTSR	DDSDA	3		1071.869038	3212.583714	0.000622848	10	N	599	629
Q9QYC0	Infl	AIIEK	EYQPHVIVSTTGPNPFNTLTDR	ELEEY	3		829.4157164	2485.223749	0.000451244	1	N	548	570
Q9QYJ0	Infl	KHGQR	ITFTGEADQAPGVEPGDIVLLLQEKEHEVFQR	DGNDL	3		1189.277809	3564.810026	0.002019181	2	N	230	262
Q9QYJ0	Infl	HMTYK	IGLVEALCGFQFTFK	HLDAR	2	C8:+57.021	865.4530239	1728.890448	0.000451244	2	N	272	287
Q9QYJ0	Infl	KHGQR	ITFTGEADQAPGVEPGDIVLLLQEK	EHEVF	3		880.7976036	2639.369411	0.001162105	1	N	230	255
Q9QZ06	Infl	SMDDR	IAWTHITIPESLK	QGQVE	3		503.621087	1507.839861	0.000662267	4	N	130	143
Q9QZ06	Infl	PESLK	QGQVEDEWYSLSGR	QGDDK	2		827.3793301	1652.74306	0.000622848	2	N	143	157
Q9QZD9	Infl	CNDSK	ITSAVWGPLGECVIAGHESGELNQYSAK	SGEVL	3	C12:+57.021	991.8189187	2972.433356	0.000451244	9	N	148	176
Q9QZD9	Infl	KFEAR	FFHLAFEEEFGR	VKGHF	3		510.2460202	1527.71466	0.000637154	1	N	268	280
Q9QZD9	Infl	IKYNR	EGDLLFTVAKDPIVNVWYSVNGER	LGTYM	3		907.8014595	2720.380978	0.000451244	4	N	20	44
Q9QZD9	Infl	DGYVR	IHYFDPQYFEFEFEA	-	2		991.4363138	1980.857028	0.001699387	4	N	310	325
Q9QZE5	Infl	GPLFK	SSPEPVALTESETEYVIR	CTKHT	2		1004.000007	2005.984413	0.000451244	20	N	631	649
Q9QZE5	Infl	SCVMK	FTVKDCDPNTGEIDEEGYEDEYVLEDLEVTVADHIQK	VMKVN	4	C6:+57.021	1079.490731	4313.931725	0.000451244	3	N	729	766
Q9QZE5	Infl	VAATR	QEIFQEQLAAVPEFQGLGPLFK	SSPEP	2		1245.157904	2488.300209	0.000451244	13	N	609	631
Q9QZE5	Infl	PGLEK	ALQQYTLEPSEKPFDLK	SVPLA	2		1004.025827	2006.036055	0.000451244	2	N	560	577
Q9QZE5	Infl	EQKQK	ALNAGYILNGLTVSIPGLEK	ALQQY	2		1022.078394	2042.141189	0.000823681	7	N	540	560
Q9QZE5	Infl	QKVMK	VNFEAAWDEVGDEFEKEETFTLSTIK	TLEEA	3		1012.145509	3033.413126	0.000451244	12	N	769	795
Q9QZE5	Infl	QVTAR	SSEELPVDIILASVG	-	2		764.9094005	1527.803201	0.00091018	1	N	859	874
Q9QZE5	Infl	KFTVK	DCDPNTGEIDEEGYEDEYVLEDLEVTVADHIQK	VMKVN	3	C2:+57.021	1280.558552	3838.652255	0.000451244	17	N	733	766
Q9QZE5	Infl	QKVMK	VNFEAAWDEVGDEFEKEETF	TLSTI	2		1196.019125	2390.022649	0.000451244	5	N	769	789
Q9QZE5	Infl	FEYKR	AIVDCIISIIEENSESK	ETGLS	3	C5:+57.021	640.6595643	1918.955293	0.000451244	7	N	415	432
Q9QZE5	Infl	DVVKR	WVNEAQEAASSDNIMVQYHALGLLYHVR	KNDRL	3		1072.196655	3213.566566	0.000823681	1	N	176	204
Q9QZK7	Infl	RRVIR	LADCVSVLPADGESCPR	DTGAF	2	C4:+57.021,C15:+57.021	923.4271772	1844.838754	0.000622848	9	N	73	90
Q9QZK7	Infl	FSSPR	APDICGVVAAAIAR	QRERL	2	C5:+57.021	692.3745765	1382.733553	0.000622848	7	N	239	253
Q9QZK7	Infl	LPTPR	KLPLTDPGPQSLPLLLSPTQEGPASGLYASVCK	QTSKH	3	C32:+57.021	1145.613209	3433.816228	0.000451244	8	N	297	330
Q9QZK7	Infl	AAQHR	QSWVDPICQLAFPGTGECSSGSGQAESPKR	GFVPM	3	C8:+57.021,C18:+57.021	1079.496244	3235.465333	0.000451244	17	N	111	141
Q9QZK7	Infl	ESCPR	DTGAFLITTTER	SHLLA	2		662.8413208	1323.667042	0.000637154	5	N	90	102
Q9QZK7	Infl	EAGRR	CDSGEGLFAFSSPR	APDIC	2	C1:+57.021	765.338388	1528.661176	0.000622848	1	N	225	239
Q9QZQ8	Infl	GLPAK	FVIHCNSPVWGADKCEELLEK	TVKNC	2	C5:+57.021,C15:+57.021	1266.106569	2530.197537	0.000451244	10	N	271	292
Q9QZQ8	Infl	NQLLK	GVTIASGGVLPNIHPELLAK	KRGSK	2		993.5732791	1985.130958	0.000451244	16	N	96	116
Q9QZQ8	Infl	TLEKK	GGKEFVEAVLELR	KKNGP	3		482.9370752	1445.787825	0.000622848	3	N	236	249
Q9QZQ8	Infl	RVTPR	HILLAVANDEELNQLLK	GVTIA	2		967.0418118	1932.068024	0.000451244	10	N	79	96
Q9QZQ8	Infl	KKGGK	EFVEAVLELR	KKNGP	2		602.8327674	1203.649935	0.000451244	13	N	239	249
Q9QZQ8	Infl	FLGQK	LNLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	4		1063.05284	4248.180161	0.000998612	8	N	196	235
Q9QZQ8	Infl	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	2		1488.299689	2974.583779	0.002296037	1	N	40	69
Q9QZQ8	Infl	GEVSK	AASADSTTEGTPTDGFTVL	STKSL	2		920.9265072	1839.837414	0.000622848	2	N	167	186
Q9QZQ8	Infl	ELRKK	NGPLEVAGAAISAGHGLPAK	FVIHC	3		610.6676476	1828.979543	0.000823681	2	N	251	271
Q9QZQ8	Infl	RHILL	AVANDEELNQLLK	GVTIA	2		728.8862597	1455.756919	0.001463592	1	N	83	96
Q9QZU3	Infl	GPEPR	ASLSFWELLQGDPWCPDPR	SLPLD	2	C15:+57.021	1137.536336	2273.057073	0.000451244	4	N	457	476
Q9QZU3	Infl	FQQLR	NLQELGLNQNQLSFLPANLFSSLR	ELKLL	2		1358.725005	2715.434411	0.000622848	2	N	146	170
Q9QZU3	Infl	KLLLY	SNQLTSVDSGLLSNLGALTELRLER	NHLRS	3		896.1510399	2685.42972	0.000451244	3	N	202	227
Q9QZU3	Infl	FQQLR	NLQELGLNQNQLSFLPANLF	SSLRE	2		1137.100389	2272.185179	0.000851441	2	N	146	166
Q9R059	Infl	LYGRK	YIQTDSGPYCVPCYDNTFANTCAECQQLIGHDSR	ELFYE	3	C10:+57.021,C13:+57.021,C22:+57.021,C25:+57.021	1347.569506	4039.685118	0.000451244	13	N	18	52
Q9R059	Infl	CTGCK	TPLAGQQFTSRDDDPYCVACFGELFAPK	CSSCK	3	C17:+57.021,C20:+57.021	1064.158681	3189.452643	0.000823681	1	N	192	220
Q9R059	Infl	MPGSR	KLEYGGQTWHEHCFLCSGCEQPLGSR	SFVPD	3	C13:+57.021,C16:+57.021,C19:+57.021	1046.132317	3135.373552	0.000823681	1	N	113	139
Q9R059	Infl	QFTSR	DDDPYCVACFGELFAPK	CSSCK	2	C6:+57.021,C9:+57.021	1002.429386	2002.843171	0.000451244	6	N	203	220
Q9R062	Infl	NPQTK	SVNCDSQDPTVSHPEFLNLWWDTFTTNVLPLLQHHGLVK	DASSY	4	C4:+57.021	1137.063264	4544.221855	0.000823681	4	N	229	268
Q9R062	Infl	SIETY	NQLLHLASEQGSFDGGDQGLLNTYFSGWATTDITK	HLPFV	3		1262.275015	3783.801646	0.000451244	13	N	146	181
Q9R062	Infl	ITLTK	LHCWSLTQYSK	CVFMD	2	C3:+57.021	711.8456519	1421.675704	0.001162105	3	N	86	97
Q9R078	Infl	EHQYK	FFVDGQWTHDPSEPIVTSQLGTVNNIIQVK	KTDFE	3		1123.909168	3368.704104	0.000451244	14	N	126	156
Q9R078	Infl	LPLTR	SQNNFVAILDLPEGEHQYK	FFVDG	3		734.6995646	2201.075294	0.000851441	2	N	107	126
Q9R0P3	Infl	PGKYR	SVSAFAPICNPVLCSWGK	KAFSG	2	C9:+57.021,C14:+57.021	996.987205	1991.95881	0.000451244	12	N	167	185
Q9R0P3	Infl	TCLVK	AYSGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	3	C34:+57.021	1362.660164	4084.957092	0.000451244	20	N	209	246

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9R0P3	Infl	NFISK	SGYQQAASEHGLVVIAPDTSPR	GCNIK	2		1142.07236	2282.12912	0.000451244	18	N	64	86
Q9R0P3	Infl	PVVFR	LQEGYDHSYYFIATFIADHIR	HHAKY	4		640.5635552	2558.223021	0.000451244	2	N	253	274
Q9R0P3	Infl	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	C1:+39.994,C12:+57.021	1186.05833	2370.101061	0.000451244	9	N	44	64
Q9R0P3	Infl	NYRMY	SYVTEELPQLINANFPVDPQR	MSIFG	2		1215.619143	2429.222687	0.000451244	11	N	121	142
Q9R0P3	Infl	LVKAY	SGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	3	C32:+57.021	1284.626683	3850.85665	0.000451244	8	N	211	246
Q9R0P3	Infl	KANYR	MYSYVTEELPQLINANFPVDPQR	MSIFG	3		908.7833004	2723.326501	0.001654178	3	N	119	142
Q9R0P3	Infl	KCKMR	FAVYLPPQAESGKCPALYWLSGLTCTEQNFISK	SGYQQ	3	C14:+57.021,C25:+57.021	1259.288354	3774.841663	0.000698008	3	N	31	64
Q9R0P5	Infl	EKDCR	YALYDASFETK	ESRKE	2		654.3118648	1306.60813	0.000451244	14	N	81	92
Q9R0P5	Infl	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	C1:+39.994	1286.664445	2571.31329	0.000451244	9	N	45	69
Q9R0P5	Infl	CIAEK	LGGSLIVAFEGSPV	-	2		673.3722568	1344.728914	0.000622848	16	N	151	165
Q9R0P5	Infl	AIKKK	FPGIKHEYQANGPEDLNR	TCIAE	2		1043.011574	2084.007549	0.000451244	4	N	127	145
Q9R0P5	Infl	SADKK	CIVVEEGKEILVGDVGATITDPF	KHFVG	3	C1:+39.994	815.4139091	2443.218327	0.001329271	1	N	45	68
Q9R0Q7	Infl	FEKSK	LTFSCLGGSDNFK	HLNEI	2	C5:+57.021	723.3403994	1444.665199	0.000451244	7	N	35	48
Q9R0Q7	Infl	SDNFK	HLNEIDLFHCIDPNDSK	HKRTD	2	C10:+57.021	1033.983937	2065.952273	0.000451244	9	N	48	65
Q9R0Q7	Infl	VNFEK	SKLTFSCLGGSDNFK	HLNEI	2	C7:+57.021	830.9038952	1659.79219	0.000451244	6	N	33	48
Q9R0Q7	Infl	FEKSK	LTFSCLGGSDNFKHLNEIDLFHCIDPNDSK	HKRTD	3	C5:+57.021,C23:+57.021	1165.210104	3492.606912	0.000451244	3	N	35	65
Q9R0Q7	Infl	KERAK	LNWLSVDFNNWK	DWEDD	2		768.3862298	1534.75686	0.000451244	7	N	95	107
Q9R0U0	Infl	REFGR	YGPIVDVYVPLDFYTR	RPRGF	2		958.9937989	1915.971998	0.000451244	8	N	32	48
Q9R111	Infl	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	2		1256.127864	2510.240128	0.000451244	4	N	231	252
Q9R111	Infl	AVIQK	FLYLGDDRNIEEVYVGGK	QVVPF	2		1044.026359	2086.037117	0.000451244	17	N	427	445
Q9R111	Infl	LINPR	ASDSPIDLFYGDFVGDISEAVIQK	FLYLG	2		1293.634656	2585.253712	0.000451244	26	N	403	427
Q9R111	Infl	RRTLK	NGTTTACYFGTIHTDSSLILAEITDKFGQR	AFVGK	3	C7:+57.021	1106.542114	3316.602941	0.000451244	8	N	133	163
Q9R111	Infl	IFSER	GASIAHCPNSNLSLSSGLLNVLEVLK	HKVKI	3	C7:+57.021	898.4815783	2692.421335	0.000451244	15	N	294	320
Q9R111	Infl	KEVFR	LATLGGSQALGLDSEIGNFEVGKEFDALLINPR	ASDSP	3		1148.939016	3443.793647	0.000451244	50	N	370	403
Q9R111	Infl	YPSYK	NYTDVYDKNNLLTNK	TVMAH	3		605.6360131	1813.884639	0.002212458	1	N	259	274
Q9R111	Infl	SDSGK	IVFLEESSQQEK	LAKEW	2		718.8675356	1435.719471	0.000451244	19	N	41	53
Q9R111	Infl	RRTLK	NGTTTACYFGTIHTDSSLILAEITDK	FGQRA	3	C7:+57.021	943.7922581	2828.353374	0.000451244	18	N	133	159
Q9R111	Infl	IVTPR	FTLSCTETLMSELGNIAK	THDLY	2	C5:+57.021	1007.995125	2013.974649	0.000451244	2	N	213	231
Q9R111	Infl	PIDLF	YGDFVGDISEAVIQK	FLYLG	2		820.9124745	1639.809349	0.000451244	9	N	412	427
Q9R112	Infl	SLSVR	STLSVIPSGVQWIQDR	VAELN	2		893.4788473	1784.942095	0.002453667	2	N	101	117
Q9R112	Infl	TGYNR	VILAEFDYTAQPLETFPFDQSKER	ITMYL	3		948.8083912	2843.401774	0.000451244	5	N	387	411
Q9R112	Infl	TGYNR	VILAEFDYTAQPLETFPFDQSK	ERITM	2		1280.136835	2558.258069	0.000451244	12	N	387	409
Q9R112	Infl	LPTSK	TAAAVAAQSGILDR	TMCLI	2		672.3680371	1342.720474	0.000451244	2	N	344	358
Q9R112	Infl	RMKRR	VGAENVAIVEPSER	HFYQP	2		735.3838842	1468.752168	0.001871652	6	N	65	79
Q9R112	Infl	RPIKK	YDGYTSCPLVTGYNR	VILAE	2	C7:+57.021	883.3964343	1764.777269	0.001352548	1	N	372	387
Q9R190	Infl	ANMYR	VGDYVYFENSSSNPYLVR	RIEEL	2		1055.000341	2107.985082	0.000451244	12	N	7	25
Q9R190	Infl	HIRGK	CSVTLLNETDILNQYLDKEDCFFYSLVFDPVQK	TLLAD	3	C1:+57.021,C21:+57.021	1338.644644	4012.910531	0.000451244	1	N	105	138
Q9R190	Infl	EKYGK	DFNDIRQDFLPWK	SLASI	3		565.283134	1692.826002	0.000622848	5	N	285	298
Q9R1C7	Infl	WAKPK	ELEDLEGYQNTIVAGGLITK	SNLHA	2		1082.063138	2162.110676	0.000451244	1	N	213	233
Q9R1C7	Infl	KSMLK	QATPPIELDAVWEDIRER	FVKEP	3		713.3679264	2137.080379	0.000637154	3	N	751	769
Q9R1C7	Infl	DIRER	FVKEPAFEDITLESER	KRIFK	3		637.3234351	1908.946905	0.000622848	4	N	769	785
Q9R1P0	Infl	LIAQR	YLLQYQEPIPCEQLVTALCDIK	QAYTQ	2	C11:+57.021,C19:+57.021	1347.679566	2693.343533	0.000451244	15	N	96	118
Q9R1P0	Infl	RNIHK	LLDEVFFSEK	IYKLN	2		613.8193257	1225.623051	0.002080925	1	N	54	64
Q9R1P0	Infl	IGWDK	HYGFQLYQSDPSGNYGGWK	ATCIG	2		1102.495757	2202.975914	0.001699387	1	N	141	160
Q9R1P0	Infl	IAQRY	LLQYQEPIPCEQLVTALCDIK	QAYTQ	2	C10:+57.021,C18:+57.021	1266.147902	2530.280204	0.000451244	10	N	97	118
Q9R1P0	Infl	LIAQR	YLLQYQEPIPCEQLVTAL	CDIKQ	2	C11:+57.021	1089.561488	2177.107377	0.001352548	2	N	96	114
Q9R1P0	Infl	EKIYK	LNEDMACSVAGITSDANVLTNELR	LIAQR	2	C7:+57.021	1297.115551	2592.215502	0.000451244	1	N	67	91
Q9R1P1	Infl	LYEKR	FGPYYTEPVIAGLDPK	TFKPF	2		883.9541423	1765.892685	0.000451244	6	N	99	115
Q9R1P1	Infl	PMGDR	LYIGLAGLATDVQTVAQR	LKFRL	3		630.3550696	1888.041809	0.000451244	11	N	48	66
Q9R1P1	Infl	GDRLY	IGLAGLATDVQTVAQR	LKFRL	2		806.955008	1611.894416	0.000451244	4	N	50	66
Q9R1P3	Infl	KMSEK	ILLLCVGEAGDTVQF	AEYIQ	2	C5:+57.021	817.926839	1633.838078	0.000451244	7	N	41	56
Q9R1P3	Infl	-MEY	LIGIQGPDYVLVASDR	VAASN	2		858.4704909	1714.925382	0.000451244	6	N	3	19
Q9R1P4	Infl	-MFR	NQYDNDVTVWSPQGR	IHQIE	2		889.9087861	1777.801972	0.000451244	16	N	3	18
Q9R1T2	Infl	AALKR	TAPDYFLLQVLLK	FRTDK	2		760.9403066	1519.865013	0.002212458	1	N	239	252
Q9R1T2	Infl	LLQIR	NDVFDSLGISPDLLPDDFVR	YCFSE	2		1117.552938	2233.090275	0.000451244	14	N	277	297
Q9R1T2	Infl	-M	VEKEEAGGGGGGGISEEEAAQYDR	QIRLW	3		799.0268458	2394.057137	0.000451244	1	N	1	25
Q9R1T2	Infl	LKRTA	PDYFLLQVLLK	FRTDK	2		674.8979104	1347.780221	0.002145581	1	N	241	252
Q9R1T2	Infl	RNSIK	FFTGDVFGYHGYTFANLGEHEFVEEK	TKVAK	3		1014.131645	3039.371536	0.002884417	1	N	156	182
Q9R1T4	Infl	QLVNK	SVSQGFCFNILCVGETGLGK	STLMD	2	C7:+57.021,C12:+57.021	1087.024516	2172.033432	0.000451244	5	N	35	55
Q9R1T4	Infl	LFNTK	FEGEPATHTQPGVQLQSNTYDLQESNVGLK	LTIVS	3		1096.532537	3286.574212	0.000451244	6	N	66	96
Q9WTI7	Infl	KIIAK	GEELLSPLNLEQAAYAR	DALAK	2		937.4868693	1872.958139	0.001229886	2	N	361	378
Q9WTI7	Infl	EEKFK	GIISILDEECLRPGEATDLTF	LEKLE	2	C10:+57.021	1175.086056	2348.156512	0.002296037	1	N	488	509
Q9WTP6	Infl	-M	APNVLASEPEIPK	GIRAV	2		682.8751636	1363.734727	0.000451244	5	N	1	14
Q9WTP6	Infl	YYRKR	GIHCAIDASQTPDIVFASILAAFSK	ATCKD	2	C4:+57.021	1316.675904	2631.336208	0.000451244	3	N	204	229
Q9WTP6	Infl	ALKTR	LEAYHTQTTPLVEYYR	KRGIH	2		992.4946944	1982.973789	0.000451244	6	N	186	202

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9WTX5	Infl	QEFLK	VDQGTLFELILAANYLDIK	GLLDV	2		1068.583509	2135.151419	0.000451244	13	N	94	113
Q9WTX5	Infl	NKEKR	TDDIPVWDQEFLKVDQGTLF	ELILA	2		1183.581695	2365.14779	0.000698008	3	N	81	101
Q9WU78	Infl	KPLVK	FIQQTYPSGGEEQAQYCR	AAEEL	2	C17:+57.021	1081.484301	2160.953001	0.000451244	29	N	23	41
Q9WU78	Infl	KEGTK	FYNELTEILVR	FQNKC	2		698.8777063	1395.739813	0.000698008	7	N	675	686
Q9WU78	Infl	DMTSK	FLTALAQDGVINEEALSVTELDRIYGGLTSK	VQESL	3		1108.58435	3322.72965	0.000451244	5	N	583	614
Q9WU78	Infl	SILTK	STSVVEQGGIQTVDQLIKELPELLQR	NREIL	3		960.8612665	2879.5604	0.000451244	9	N	420	446
Q9WU78	Infl	EEVLK	NLATAYDNFVELVANLK	EGTKF	2		947.9996126	1893.983625	0.000451244	11	N	654	671
Q9WU78	Infl	IAQMR	EATTLANGVLASLNLPAAIEDVSGDTVPQSILTK	STSVV	3		1136.942315	3407.803544	0.000451244	16	N	386	420
Q9WU78	Infl	SILTK	STSVVEQGGIQTVDQLIK	ELPEL	2		951.5130841	1901.010568	0.000451244	13	N	420	438
Q9WU78	Infl	DMTSK	FLTALAQDGVINEEALSVTELDR	IYGGL	2		1252.648098	2503.280596	0.000451244	9	N	583	606
Q9WU78	Infl	EESLR	LLDEEEATDNDLR	AKFKD	2		766.8578962	1531.700192	0.000451244	5	N	456	469
Q9WU78	Infl	YQSHR	DTIALLCKPEPELNAAIPSANPAK	TMQGS	2	C7:+57.021	1267.170454	2532.325309	0.000451244	6	N	517	541
Q9WU78	Infl	EESLR	LLDEEEATDNDLRAK	FKDRW	2		866.4239347	1730.832269	0.000451244	2	N	456	471
Q9WU78	Infl	VSVLK	SLLSNLDEIKK	ERESL	3		420.5788878	1258.713263	0.002019181	1	N	553	564
Q9WUA2	Infl	VYYNK	TPGFEIIHGLLDR	IMQLL	3		489.9371866	1466.78816	0.000451244	8	N	504	517
Q9WUA2	Infl	VSVKR	DLLFQALGR	TYTDE	2		516.7959879	1031.576376	0.000451244	5	N	8	17
Q9WUA3	Infl	YTGAK	VYFIYEGYQGLVDGGSNIVEAK	WDCVS	2		1211.102795	2420.189989	0.000451244	6	N	55	77
Q9WUA3	Infl	IVEAK	WDCVSSILQVGGTIIGSAR	CKAFR	3	C3:+57.021	673.6828147	2018.025044	0.000622848	4	N	77	96
Q9WUA3	Infl	CNLAR	LGITNLCVIGGDGSLTGANLFR	KEWSG	2	C7:+57.021	1124.591643	2247.167686	0.000451244	8	N	115	137
Q9WUA3	Infl	NGQIK	EIGWADVGGWTGQGGSILGTK	RTLPG	2		1045.021608	2088.027615	0.002519933	1	N	458	479
Q9WUA3	Infl	GLVLR	NESCSVNYTTDFIYQLYSEEGK	GVFDC	2	C4:+57.021	1324.079156	2646.142713	0.001162105	1	N	636	658
Q9WUA3	Infl	GFEAY	LGLLELAAAR	EKHEA	2		513.819463	1025.623326	0.001591523	4	N	511	521
Q9WUA3	Infl	AVIAL	LEATPETPACVVSLR	GNQAV	2	C10:+57.021	821.9273703	1641.839141	0.001463592	1	N	332	347
Q9WUK2	Infl	GHGSR	SQKELPTEPPYTAYVGNLPFNTVQGDIDAIFK	DLSIR	3		1184.935271	3551.782414	0.000451244	3	N	31	63
Q9WUK2	Infl	SRSQK	ELPTEPPYTAYVGNLPFNTVQGDIDAIFK	DLSIR	3		1070.540082	3208.596845	0.000451244	20	N	34	63
Q9WUK2	Infl	QLKPR	TVATPLNQVANPNSAIFGGARPR	EEVVQ	3		784.4246577	2350.250573	0.001763695	3	N	216	239
Q9WUK2	Infl	PYTAY	VGNLPFNTVQGDIDAIFKDLSIR	SVRLV	3		844.7872617	2531.338385	0.000823681	2	N	45	68
Q9WUK2	Infl	SRSQK	ELPTEPPYTAYVGNLPFNTVQGDIDAIFKDLSIR	SVRLV	3		1265.316152	3792.925056	0.000451244	4	N	34	68
Q9WUK2	Infl	PYTAY	VGNLPFNTVQGDIDAIFK	DLSIR	2		974.5128871	1947.010174	0.000451244	15	N	45	63
Q9WUM3	Infl	ASYSR	SGASTATAVTDVPSGNLAGAGEAGKLEEVMQELR	ALRML	3		1106.216221	3315.625263	0.000451244	5	N	422	456
Q9WUM3	Infl	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	3		1420.692675	4259.054626	0.000451244	14	N	354	393
Q9WUM3	Infl	IRVSR	VTWDSTFCAVNPK	FLAVI	2	C8:+57.021	762.861499	1523.707398	0.000451244	5	N	33	46
Q9WUM3	Infl	ARPMR	AIFLADGKVFTTGFSR	MSERQ	3		577.3144342	1728.919902	0.001162105	3	N	225	241
Q9WUM3	Infl	ASYSR	SGASTATAVTDVPSGNLAGAGEAGK	LEEVM	2		1095.038183	2188.060766	0.000451244	3	N	422	447
Q9WUM3	Infl	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISL	REAYV	3		1368.658972	4102.953515	0.001162105	5	N	354	392
Q9WUM3	Infl	KSDLF	QDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	3		1223.923871	3668.748214	0.000451244	6	N	359	393
Q9WUM4	Infl	IRVSR	VTWDSSFCAVNPR	FVAII	2	C8:+57.021	769.8567479	1537.697896	0.000622848	5	N	31	44
Q9WUM4	Infl	ARPMR	AIFLADGNVFTTGFSR	MSERQ	2		858.4417334	1714.867867	0.000451244	6	N	223	239
Q9WUM4	Infl	MTVPR	KSDLFQDDLYPDTAGPEAALEAEEWFEGK	NADPI	3		1091.170494	3270.488082	0.000451244	3	N	352	381
Q9WUM4	Infl	KSDLF	QDDLYPDTAGPEAALEAEEWFEGKNADPILISLK	HGYIP	3		1249.276022	3744.804666	0.000451244	2	N	357	391
Q9WUM4	Infl	WFEGK	NADPILISLK	HGYIP	2		542.3245782	1082.633556	0.000451244	7	N	381	391
Q9WUM4	Infl	KSDLF	QDDLYPDTAGPEAALEAEEWFEGK	NADPI	2		1341.098635	2680.181669	0.000622848	1	N	357	381
Q9WUP7	Infl	GFGCR	GAQVEEIWSLEPESFEK	LKPVH	2		989.4761673	1976.936735	0.000451244	10	N	28	45
Q9WUP7	Infl	LDGLR	EGPIDLGACNQDDWITAVRPVIEK	RIQKY	3	C9:+57.021	899.4501667	2695.3271	0.000451244	5	N	182	206
Q9WUP7	Infl	IFFAK	QVINNACATQAIVSVLLNCTHQDVHLGETLSEFK	EFSQS	4	C7:+57.021,C19:+57.021	953.229479	3808.886716	0.000622848	4	N	81	115
Q9WUP7	Infl	EFDTK	TPAKEEDAFHFVSYVPVNGR	LYELD	3		755.0434428	2262.106928	0.000451244	1	N	154	174
Q9WUU7	Infl	INIKR	KGAWPSILLSVQNVIDCGNAGSCEGGNDLPVWEYAHK	HGIPD	4	C17:+57.021,C23:+57.021	1011.236298	4040.913993	0.000451244	11	N	111	148
Q9WUU7	Infl	NIKRK	GAWPSILLSVQNVIDCGNAGSCEGGNDLPVWEYAHK	HGIPD	3	C16:+57.021,C22:+57.021	1305.28081	3912.81903	0.000451244	18	N	112	148
Q9WUU7	Infl	NYQAK	DQDCDKFNQCGTCTEFK	ECHTI	2	C4:+57.021,C10:+57.021,C13:+57.021	1076.921899	2151.828197	0.000451244	2	N	162	179
Q9WUU7	Infl	TSTYK	GGTGDSYNLAIESACTFGDPIV	-	2	C15:+57.021	1122.510181	2243.004762	0.000451244	4	N	284	306
Q9WUU7	Infl	PSILL	SVQNVIDCGNAGSCEGGNDLPVWEYAHK	HGIPD	3	C8:+57.021,C14:+57.021	1026.122518	3075.344155	0.000823681	3	N	120	148
Q9WUU7	Infl	NYQAK	DQDCDKFNQCGTCTEF	KECHT	2	C4:+57.021,C10:+57.021,C13:+57.021	1012.874417	2023.733234	0.000451244	9	N	162	178
Q9WV02	Infl	DRPGK	LFIGGLNTETNEKALEAVFGK	YGRIV	2		1126.102598	2250.189595	0.001329271	2	N	9	30
Q9WV02	Infl	DRPGK	LFIGGLNTETNEK	ALEAV	2		718.3755278	1434.735456	0.000451244	3	N	9	22
Q9WV32	Infl	AKWNK	VHELKEHNGQVTGIDWAPESNR	IVTCG	2		1258.617998	2515.220395	0.000451244	3	N	44	66
Q9WV32	Infl	WNKDR	TQIAICPNNHEVHIYEK	SGAKW	2	C6:+57.021	1033.510122	2065.004643	0.000451244	18	N	20	37
Q9WV32	Infl	DSLHK	NSVSQISVLSGGK	AKCSQ	2		638.349313	1274.683026	0.000451244	5	N	326	339
Q9WV32	Infl	NLDKK	ASSEGGAATGAGLDSLHKNSVSQISVLSGGK	AKCSQ	2		1443.23412	2884.45264	0.000622848	1	N	308	339
Q9WV32	Infl	KKPIR	STVLSLDWHPNNVLLAAGSCDFKCR	IFSAY	3	C20:+57.021,C24:+57.021	954.1340299	2859.37869	0.002727428	1	N	142	167
Q9WV32	Infl	KKPIR	STVLSLDWHPNNVLLAAGSCDFK	CRIFS	2	C20:+57.021	1272.631496	2543.247393	0.000451244	15	N	142	165
Q9WV32	Infl	GSGSR	VISICYFEQENDWWVCK	HIKKP	2	C5:+57.021,C16:+57.021	1138.511241	2275.006883	0.000451244	11	N	118	135
Q9WV32	Infl	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	2	C11:+57.021	1015.504505	2028.99341	0.000451244	19	N	216	234
Q9WV32	Infl	NLDKK	ASSEGGAATGAGLDSLHK	NSVSQ	2		814.897887	1627.780174	0.000451244	9	N	308	326

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9WV32	Infl	VHELK	EHNGQVTGIDWAPESNR	IVTCG	2		955.4435244	1908.871449	0.000451244	23	N	49	66
Q9WV32	Infl	HAWNK	DRTQIAICPNNHEVHIYEK	SGAKW	4	C8:+57.021	585.0409743	2336.132697	0.000622848	2	N	18	37
Q9WV32	Infl	SAYIK	EVEERPAPTPWGSK	MPFGE	2		791.8971587	1581.778717	0.000451244	10	N	174	188
Q9WV32	Infl	RSTVL	SLDWHPNNVLLAAGSCDFK	CRIFS	2	C16:+57.021	1072.515404	2143.015208	0.000451244	16	N	146	165
Q9WV32	Infl	ISICY	FEQENDWWVCK	HIKKP	2	C10:+57.021	770.8301988	1539.644798	0.000451244	10	N	124	135
Q9WV32	Infl	DADKK	MAVATLASETLPLLAVTF	ITENS	2		924.5135105	1847.011421	0.001463592	3	N	234	252
Q9WV32	Infl	ARCVR	WAPNENKFAVGSGSR	VISIC	3		540.6028666	1618.7852	0.002374549	1	N	103	118
Q9WV60	Infl	PPHAR	IQAAASPPANATAASDTNAGDRGQTNNAASASASNST	-	3		1144.527174	3430.558121	0.000451244	6	N	383	420
Q9WV60	Infl	LPNGR	DTPALFNFTTQELSSNPPLATILIPPHAR	IQAAA	3		1054.559699	3160.655697	0.000451244	1	N	354	383
Q9WVA4	Infl	TVLCK	LINSLYPEGQAPVK	KIQAS	2		764.9226452	1527.82969	0.000823681	6	N	64	78
Q9WVA4	Infl	LAVAR	DDGLFSGDPNWFPKK	SKENP	2		861.9102661	1721.804932	0.000451244	15	N	139	154
Q9WVA4	Infl	QAAER	YGINTTDIFQTVDLWEGK	NMACV	2		1050.518366	2099.021133	0.000451244	25	N	102	120
Q9WVA4	Infl	EVQQK	IEKQYDADLEQILIQWITTQCR	EDVGQ	3	C21:+57.021	922.1377001	2763.3897	0.000451244	13	N	17	39
Q9WVA4	Infl	QKIEK	QYDADLEQILIQWITTQCREDVGQPQPGR	ENFQK	3	C18:+57.021	1153.232051	3456.672752	0.000451244	5	N	20	49
Q9WVA4	Infl	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	C18:+57.021	1197.59184	2393.16808	0.000451244	19	N	20	39
Q9WVA4	Infl	TVLCK	LINSLYPEGQAPVKK	IQASS	2		828.9701268	1655.924654	0.000451244	14	N	64	79
Q9WVA4	Infl	LAVAR	DDGLFSGDPNWFPK	KSKEN	2		797.8627845	1593.709969	0.000823681	6	N	139	153
Q9WVA4	Infl	ACVQR	TLMNLGGLAVARDDGLFSGDPNWFPK	KSKEN	3		931.1344446	2790.379934	0.000622848	1	N	127	153
Q9WVE8	Infl	ELSFK	AGDELTKIEDEDEQGWCK	GRLDS	2	C17:+57.021	1061.965606	2121.915613	0.000451244	4	N	448	466
Q9WVE8	Infl	WCKGR	LDSGQVGLYPANYVEAIQ	-	2		968.9867022	1935.957804	0.002374549	1	N	468	486
Q9WVG5	Infl	AVHLF	VDSLVNQDKPSFAFQCTDSSR	FKRGI	2	C16:+57.021	1201.058361	2400.101123	0.000451244	5	N	281	302
Q9WVG5	Infl	AFNIR	TSKDPEQEGCNLSLGDSK	LLENC	2	C10:+57.021	982.9472167	1963.878833	0.000622848	3	N	54	72
Q9WVG5	Infl	QPTLY	ITLYGSNADSQNLPLEIVEK	IELNA	2		1102.576413	2203.137226	0.000451244	7	N	369	389
Q9WVG5	Infl	LLKMR	LTWEGVAHSWYNLWNEF	RNYLS	2		1076.500311	2150.985022	0.002080925	1	N	413	430
Q9WVJ2	Infl	EFEHR	VNPLSLVEIILHVVR	QMTDP	3		567.6860909	1700.034873	0.000451244	1	N	70	85
Q9WVJ2	Infl	FQTLK	CAWGQQPDLAANEAQLLR	KIQLL	2	C1:+57.021	1020.999921	2039.984242	0.000870037	1	N	252	270
Q9WVJ2	Infl	LYTKK	LWHQLTLEVLDFVQDPCFAQGDGLIK	LYENF	3	C17:+57.021	1014.851671	3041.531614	0.000622848	2	N	32	58
Q9WVJ2	Infl	LESLR	DTDRQWLIDTLYAFNSGAVDR	FQTLK	3		819.4000663	2455.176799	0.002813207	1	N	226	247
Q9WVK4	Infl	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	2		1277.655923	2553.296246	0.000451244	1	N	486	509
Q9WVK4	Infl	PDNRK	LFEAEEQDLFKDIQSLPR	NAALR	3		726.7079487	2177.100446	0.000451244	5	N	269	287
Q9WVK4	Infl	QRISR	GYDFAAVLEWFAERVDR	IILLF	3		682.0028074	2042.985022	0.002374549	1	N	167	184
Q9WVK4	Infl	WVVGK	DKPTYDEIFYTLSPVNGK	ITGAN	2		1044.020742	2086.025884	0.000451244	2	N	443	461
Q9WVK4	Infl	QRISR	GYDFAAVLEWFAER	VDRII	2		837.4020769	1672.788554	0.000451244	1	N	167	181
Q9Z0H3	Infl	TPEMF	SEILCDDLDLNPLTFVPAIASAIR	QQIES	2	C5:+57.021	1322.188844	2642.362089	0.000451244	13	N	218	242
Q9Z0H3	Infl	ASAIR	QQIESYPTDSILEDQSDQR	VIIKL	2		1126.519823	2251.024046	0.000451244	13	N	242	261
Q9Z0I7	Infl	EILPR	TVSAFANTDGGYLFIGLDEK	KQEIV	2		1059.523649	2117.031698	0.000851441	2	N	217	237
Q9Z0I7	Infl	RNITK	ALCALINSGEGK	VKAHI	2	C3:+57.021	616.8191028	1231.622606	0.000622848	1	N	42	54
Q9Z0I7	Infl	PLDFK	QYQSYFFICVEK	SQSPD	2	C9:+57.021	806.3795246	1610.743449	0.002145581	1	N	91	103
Q9Z0J0	Infl	VGVIK	EVNVSPCPTDPCQLHK	GQSYS	2	C7:+57.021,C12:+57.021	940.9351694	1879.854739	0.000451244	10	N	35	51
Q9Z0J0	Infl	DCGSK	VGVIKEVNVSPCPTDPCQLHK	GQSYS	3	C12:+57.021,C17:+57.021	793.0718193	2376.192058	0.000451244	3	N	30	51
Q9Z0J0	Infl	LEGIR	VPFPIPEPDGCK	SGINC	2	C11:+57.021	678.3371284	1354.658657	0.000662267	2	N	82	94
Q9Z0N1	Infl	PIFSK	IVSLFAEHNDLQYAAPGGLIGVGTK	IDPTL	3		857.4591451	2569.354035	0.000451244	13	N	317	342
Q9Z0N1	Infl	ESQAK	EQYEQILAFVQGTVAEGAPIIPISAQLK	YNIEV	3		1005.213529	3012.617186	0.000451244	12	N	201	229
Q9Z0N1	Infl	PECYR	SCGSSTPDEFPTDIPGTK	GNFKL	2	C2:+57.021	948.4203034	1894.825007	0.000451244	15	N	103	121
Q9Z0N1	Infl	IDLVK	ESQAKEQYEQILAFVQGTVAEGAPIIPISAQLK	YNIEV	3		1186.301954	3555.882463	0.000637154	4	N	196	229
Q9Z0P4	Infl	KEEQK	SETLVNAQQTPLGTPK	ENRTS	2		842.4497555	1682.883911	0.001162105	2	N	131	147
Q9Z0P4	Infl	TRLEK	EIDVLEFGESAPAASK	ENSAA	2		831.9152141	1661.814828	0.002727428	1	N	93	109
Q9Z0P5	Infl	IRLIK	VIIEDEQLVLGASQEPVGR	WDQDY	2		1026.552741	2051.089881	0.000451244	23	N	29	48
Q9Z0P5	Infl	IRLIK	VIIEDEQLVLGASQEPVGRWDQDYDR	AVLPL	3		1010.832147	3029.473041	0.000451244	4	N	29	55
Q9Z0P5	Infl	SCKSR	LLDSVEQDFQLEIAK	KIEIG	2		874.4597889	1746.903978	0.000451244	15	N	278	293
Q9Z0P5	Infl	QDYDR	AVLPLLDAQEPCYLLFR	LDSQN	2	C12:+57.021	1009.542902	2017.070203	0.000451244	12	N	55	72
Q9Z0P5	Infl	YLLFR	LDSQNAQGFEWLFLAWSPDNSPVR	LKMLY	2		1389.170063	2776.324526	0.000451244	11	N	72	96
Q9Z0P5	Infl	YIQLK	LDLERETIELVHTEPTNVAQLPSR	IPRDA	3		920.8229232	2759.44537	0.000451244	16	N	204	228
Q9Z0P5	Infl	AGYQK	HLSSCAAPAPLTSAER	ELQQI	2	C5:+57.021	834.4124187	1666.809237	0.000451244	2	N	136	152
Q9Z0P5	Infl	SVESK	HQTLQGLAFPLQPEAQR	ALQQL	2		967.5162955	1933.016991	0.000451244	8	N	171	188
Q9Z0P5	Infl	QDYDR	AVLPLLDAQEPCYLLF	RLDSQ	2	C12:+57.021	931.4923461	1860.969092	0.000451244	8	N	55	71
Q9Z0P5	Infl	EPVGR	WDQDYDRAVLPLLDAQEPCYLLF	RLDSQ	2	C19:+57.021	1420.683926	2839.352252	0.002080925	1	N	48	71
Q9Z0P5	Infl	LEIAK	KIEIGDGAELTAEFLYDEVHPK	QHAFK	4		619.317217	2473.237668	0.000622848	3	N	293	315
Q9Z0P5	Infl	LDLER	ETIELVHTEPTNVAQLPSR	IPRDA	2		1067.561097	2133.106594	0.000451244	1	N	209	228
Q9Z0W3	Infl	FLICR	DLLILQQLLTR	LGDAV	2		663.4117163	1324.807833	0.000823681	4	N	698	709
Q9Z0X1	Infl	HQSMF	WSDLGPDVGYEAIGLVDSSLPTVGVFAK	ATAQD	2		1446.737444	2891.459288	0.000451244	5	N	481	509
Q9Z0X1	Infl	PPSFY	VSAQDLPNIENGGVAVLTGK	KVVHL	2		991.5318082	1981.048016	0.002374549	1	N	210	230
Q9Z126	Infl	PAVVA	VTSAGPEESDGDLSCVCVK	TISSG	2	C15:+57.021,C17:+57.021	1005.443221	2008.870843	0.000451244	36	N	29	48
Q9Z126	Infl	AVVAV	TSAGPEESDGDLSCVCVK	TISSG	2	C14:+57.021,C16:+57.021	955.9090143	1909.802429	0.001395409	3	N	30	48
Q9Z126	Infl	IKAGR	HCAVPQLIATLK	NGRKI	2	C2:+57.021	675.8820374	1349.748475	0.000451244	7	N	69	81

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z130	Infl	EYLSR	FGEVVDCTIKTDPVTGR	SRGFG	2	C7:+57.021	947.4726733	1892.929747	0.000662267	1	N	51	68
Q9Z130	Infl	EPPKK	VFVGGLSPDTSEEQIKEY	FGAFG	2		999.4892747	1996.962949	0.000451244	1	N	115	133
Q9Z183	Infl	YPLGR	ILIGNSGYSSSESR	DMHQA	2		735.3656914	1468.715783	0.000451244	3	N	427	441
Q9Z183	Infl	SLLDK	SNPELPEALVFQDSVTFR	VAPWI	2		1025.018534	2048.021467	0.000451244	2	N	274	292
Q9Z183	Infl	QQFSY	CLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C1:+57.021	971.785215	2912.332245	0.000451244	14	N	236	262
Q9Z183	Infl	GPQQF	SYCLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C3:+57.021	1055.150334	3162.427602	0.000451244	20	N	234	262
Q9Z183	Infl	AVLKR	ELGLAEGDIIDIPQLFK	LAGNS	2		936.0121886	1870.008777	0.000451244	14	N	554	571
Q9Z183	Infl	YYGPK	TSPVQALIYITGVELSLSADVTR	TGRVK	3		811.7798843	2432.316253	0.000451244	4	N	100	123
Q9Z183	Infl	-M	AQGAVIHVAPEQPTHAVCVVGTATPLDVR	GSAPK	3	C18:+57.021	998.5260696	2992.554809	0.000451244	12	N	1	30
Q9Z183	Infl	LSNKK	LRDQNAYVESCIDWNR	AVLKR	2	C11:+57.021	1019.973903	2037.932206	0.000998612	1	N	533	549
Q9Z183	Infl	GPQQF	SYCLELPGGQHSTDFYVEGLAFPDADFKGLIPLTISLLDK	SNPEL	4	C3:+57.021	1107.559757	4426.207828	0.000451244	2	N	234	274
Q9Z183	Infl	DADFK	GLIPLTISLLDKSNPELPEALVF	QDSVT	2		1240.207063	2478.398526	0.000622848	2	N	262	285
Q9Z183	Infl	AVLKR	ELGLAEGDIIDIPQLF	KLAGN	2		871.9647071	1741.913814	0.001329271	3	N	554	570
Q9Z183	Infl	TRKLY	MSELTGLDAFGNLEVSPPVTVR	GKEYP	2		1166.596823	2331.178046	0.000451244	2	N	397	419
Q9Z183	Infl	DADFK	GLIPLTISLLDK	SNPEL	2		641.9031928	1281.790786	0.000735798	2	N	262	274
Q9Z1D1	Infl	SEDTR	ETDLQELFRPFGSISR	IYLAK	3		632.327291	1893.958473	0.000451244	7	N	251	267
Q9Z1D1	Infl	NATIR	VTNLSEDTRETDLQELFRPFGSISR	IYLAK	3		970.8251039	2909.451912	0.002884417	1	N	242	267
Q9Z1E4	Infl	DRRFR	SLDDSCSQLTSFLYSFCQQSR	RQRII	2	C6:+57.021,C17:+57.021	1265.05473	2528.09386	0.000451244	23	N	558	579
Q9Z1E4	Infl	ADRVK	VIFHPEFLSSTSPLLPVDYEEFVR	GCHLG	2		1411.226515	2820.437431	0.000823681	1	N	474	498
Q9Z1E4	Infl	QTKAK	VTGDEWGDNYYLVGPYTEQGVR	TQVEL	2		1259.580215	2517.14483	0.000451244	13	N	52	74
Q9Z1E4	Infl	TLLGR	YLCAGAVDFYNNLENFNVDKEAGER	QIYHR	3	C3:+57.021	970.1121022	2907.312907	0.000622848	4	N	211	236
Q9Z1E4	Infl	VYFGR	WLIEGGPLVVLLDVGASAWALER	WKGEL	3		822.1253262	2463.352579	0.000451244	5	N	105	128
Q9Z1F9	Infl	IVWAK	YLFNQLFGEEDADQEVSPDRADPEAAWEPTEAEAR	ARASN	3		1332.600116	3994.776948	0.000451244	19	N	190	225
Q9Z1F9	Infl	RNGSR	LQADDFLQDYTLLINILHSEDLGKDVEFEVVGDSPEK	VGPKQ	4		1052.026291	4204.073965	0.001162105	3	N	514	551
Q9Z1F9	Infl	LWRKR	KPPVPLDWAEVQSQGEANADQQNEPQLGLK	DQQVL	3		1096.216661	3285.626582	0.000451244	2	N	276	306
Q9Z1F9	Infl	IVWAK	YLFNQLFGEEDADQEVSPDR	ADPEA	2		1186.538016	2371.060432	0.000451244	1	N	190	210
Q9Z1F9	Infl	CELLK	NLVLTGFSHIDLIDLDTIDVSNLNR	QFLFQ	3		933.1630569	2796.465771	0.000622848	4	N	34	59
Q9Z1F9	Infl	AKYLF	NQLFGEEDADQEVSPDRADPEAAWEPTEAEAR	ARASN	3		1191.52818	3571.561141	0.000451244	1	N	193	225
Q9Z1G3	Infl	IPDLK	VGTLDVLVGLSDELAKLDAFVEGVVK	KVAQY	3		896.1691489	2685.484047	0.001162105	1	N	44	70
Q9Z1G3	Infl	IPDLK	VGTLDVLVGLSDELAK	LDAFV	2		814.9594247	1627.903249	0.000735798	7	N	44	60
Q9Z1N5	Infl	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	C1:+39.994	1130.617238	2259.218877	0.000451244	2	N	299	319
Q9Z1N5	Infl	ENDAK	ILNDVQDRFEVNISELPDEIDISSYIEQTR	-	3		1184.256962	3549.747485	0.000451244	8	N	398	428
Q9Z1N5	Infl	-MAE	NDVDNELLDYEDDEVETAAGADGTEAPAKK	DVKGS	3		1065.476423	3193.405869	0.000451244	2	N	3	33
Q9Z1N5	Infl	DVQDR	FEVNISELPDEIDISSYIEQTR	-	2		1299.13502	2596.25444	0.000451244	7	N	406	428
Q9Z1Q5	Infl	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQRK	FLDGN	3		1045.505765	3133.493896	0.000451244	16	N	138	166
Q9Z1Q5	Infl	PRYPK	LAALNPESNTSGLDIFAK	FSAYI	2		930.9892448	1859.96289	0.000451244	19	N	95	113
Q9Z1Q5	Infl	NAYAR	EEFASTCPDDEEIELAYEQVAR	ALK-	2	C7:+57.021	1301.068789	2600.121977	0.000451244	47	N	216	238
Q9Z1Q5	Infl	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQR	KFLDG	3		1002.807444	3005.398933	0.000451244	19	N	138	165
Q9Z1Q5	Infl	ISQRK	FLDGNELTLADCNLLPK	LHIVQ	2	C12:+57.021	966.9906989	1931.965798	0.000451244	10	N	166	183
Q9Z1Q5	Infl	VLWLK	GVTFNVTTVDTK	RRTET	2		641.3384139	1280.661228	0.000451244	3	N	37	49
Q9Z1Q5	Infl	GISQR	KFLDGNELTLADCNLLPK	LHIVQ	2	C13:+57.021	1031.038181	2060.060761	0.000451244	14	N	165	183
Q9Z1Q5	Infl	PRYPK	LAALNPESNTSGLDIFAKF	SAYIK	2		1004.523452	2007.031304	0.000622848	2	N	95	114
Q9Z1Q9	Infl	RRTPK	APASLCVTPYPEPSECSWKDPEAEAALELALSITR	AVRSL	3	C6:+57.021,C16:+57.021	1286.957222	3857.848265	0.000451244	16	N	1080	1115
Q9Z1Q9	Infl	RKMSK	SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDPSEVEK	AKEGQ	3		1297.672775	3889.994926	0.000451244	17	N	864	900
Q9Z1Q9	Infl	YSGAR	SVTQQPGSEVIAPQK	TPAQL	2		784.9180912	1567.820582	0.000622848	8	N	214	229
Q9Z1Q9	Infl	SFAYK	VQGSDSDEEVVVATTR	IETML	2		846.4082846	1690.800969	0.000451244	8	N	520	536
Q9Z1Q9	Infl	PGGSR	AAVLVQQWVSYADTELIPAACGATLPALGLR	GPGQD	3	C21:+57.021	1085.579952	3253.716455	0.002145581	1	N	91	122
Q9Z1Q9	Infl	SYSAK	VPLEVQEADEAKLQQTEAELR	KVDEA	3		799.4154935	2395.223081	0.000451244	11	N	1229	1250
Q9Z1Q9	Infl	YNLTR	TRPDCFLEVADEATGALASAVSGY	VQALA	2	C5:+57.021	1250.586952	2499.158303	0.001395409	2	N	1128	1152
Q9Z1Q9	Infl	FPPPR	LPALEQGPGGLWVWGAPAVAQLLWPAGLGGPGGSR	AAVLV	3		1145.949521	3434.825163	0.000622848	7	N	56	91
Q9Z1Q9	Infl	RKMSK	SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDPSEVEKAK	EGQKA	4		1023.289551	4089.127003	0.002145581	1	N	864	902
Q9Z1Q9	Infl	EDWLR	LHTYLAGDAPTLADLAAVTALLLPFR	YVLDP	3		908.5097283	2722.505785	0.00307782	1	N	147	173
Q9Z1Q9	Infl	WWGHR	IPAYFITVHDPAVPPGEDPDGR	YWVSG	3		788.3942527	2362.159358	0.001264573	2	N	729	751
Q9Z1Q9	Infl	YRSTR	LVNWSCTLNSAISDIEVDKK	ELTGR	3	C6:+57.021	764.7232273	2291.146282	0.000451244	2	N	472	492
Q9Z1R2	Infl	HLVER	APPQTQLPSGASSGTGSASATHGGAPLPGTR	GPGAS	3		939.4694316	2815.384895	0.000451244	15	N	87	118
Q9Z1R2	Infl	PFLQR	YCEVLGAAATTDYNNNHEGREEDQR	LINLV	3	C2:+57.021	971.4218869	2911.242261	0.000451244	5	N	297	322
Q9Z1R2	Infl	VDIIR	TNLEFLQEQFNSIAAHVLHCTDSGFGAR	LLELC	4	C20:+57.021	791.382404	3161.498416	0.000823681	2	N	858	886
Q9Z1T1	Infl	MILQK	VVNVANLGAVPSSQDNVHR	FAART	3		659.3489776	1975.023533	0.000451244	14	N	1036	1055
Q9Z1T1	Infl	TLNIK	ASGYLELSNWPEVAPDPSVR	NVEVI	2		1094.039997	2186.064395	0.000451244	3	N	630	650
Q9Z1X4	Infl	GSGGR	SGGNSYGSSGSSSYNTGSHGGYGTGSGGSSSYQGK	QGGYS	3		1075.107616	3222.299447	0.000451244	10	N	817	852
Q9Z1X4	Infl	KFAAK	PHNPGFGMGGPMHNEVPPPPNIR	GRGRG	3	M8:+15.995,M12:+15.995	827.723779	2480.147937	0.001591523	1	N	617	640
Q9Z1Z0	Infl	NAFER	LLDIITEEGNSDGGIVVEDCLILLQNLLK	TNNSN	3	C20:+57.021	1066.239261	3195.694382	0.000451244	8	N	212	241
Q9Z1Z0	Infl	LQLVR	VLVSPTNPPGATSSCQK	AMFQC	2	C15:+57.021	871.941009	1741.866418	0.000823681	4	N	288	305
Q9Z1Z0	Infl	LQTDR	SDSEIIAYALDTLYNIISNDEEEELEENSTR	QSEDL	3		1192.55188	3574.63224	0.000622848	3	N	73	104
Q9Z1Z0	Infl	LTALK	SQLCSQSLEITR	LQTEN	2	C4:+57.021	711.3565808	1420.697562	0.000451244	3	N	798	810

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z1Z0	Infl	VSTLK	CQNEQLQTAVTQQASQIQQHK	DQYNL	3	C1:+57.021	823.4034393	2467.186918	0.001162105	1	N	677	698
Q9Z1Z2	Infl	LAKPK	IGFPETAEEELEEIASENSDSIYSSTPEVKA	-	3		1124.523262	3370.546385	0.000451244	2	N	319	350
Q9Z1Z2	Infl	KHIVK	TVDFTQDSNYLLTGGQDK	LLRIY	2		1001.474156	2000.932712	0.000451244	7	N	104	122
Q9Z1Z2	Infl	IHCVR	FSPDGELYASGSEDGTLR	LWQTV	2		950.9321239	1899.848648	0.000823681	1	N	272	290
Q9Z1Z2	Infl	FKLYK	YDYNSGEELESYK	GHFGP	2		798.8391721	1595.662744	0.000451244	3	N	249	262
Q9Z204-2	Infl	AAEMY	GSSFDLDYDFQR	DYYDR	2		725.3182098	1448.62082	0.000823681	2	N	105	117
Q9Z277	Infl	QLTHK	EAWEEEQEVAELLKEEFPNWYEK	LVLEM	3		975.7875443	2924.339233	0.001943752	1	N	63	86
Q9Z2D3	Infl	WQRPK	YQILSATLEDVLTEGHCLSPVVVESDFVK	YESKC	3	C17:+57.021	1083.551727	3247.631782	0.000451244	9	N	50	79
Q9Z2D3	Infl	RNFLK	EVDAGGDLISVSHLNDSDKLQLLSLVTK	KKRYW	4		742.3979984	2965.560794	0.000662267	2	N	11	39
Q9Z2D3	Infl	ATILK	DSCIFPLILHITLSGLSTLSK	EHEEE	3	C3:+57.021	772.4278631	2314.260189	0.000735798	6	N	475	496
Q9Z2E1	Infl	MELPK	GLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEK	NPAVW	3		1240.641587	3718.90136	0.000451244	7	N	310	349
Q9Z2I8	Infl	YEAFK	LLTSDPKVEAILVNIFGGIVNCAIIANGITK	ACREL	3	C22:+57.021	1085.279502	3252.815106	0.000451244	4	N	348	379
Q9Z2I8	Infl	HLFLK	IDATQVEVNPFGETPEGQVVCF	DAKIN	2	C21:+57.021	1218.573313	2435.131026	0.000823681	3	N	235	257
Q9Z2I8	Infl	ILMDR	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	EQIDI	3		1011.856293	3032.545478	0.002884417	1	N	161	191
Q9Z2L7	Infl	DDLVR	EGEIAILGGIEEESDKLWNFTK	KASHI	2		1239.624091	2477.232583	0.000451244	1	N	111	133
Q9Z2L7	Infl	LLDER	LVTLLQEVDTIEQETIKPLDDCQK	LIEHG	3	C22:+57.021	943.4918087	2827.452026	0.000451244	19	N	73	97
Q9Z2L7	Infl	NFTKK	ASHIQLDSLPEVPLLVDVPCLSAQLDDSILNIVK	DHIFK	3	C20:+57.021	1238.001133	3710.98	0.000698008	5	N	134	168
Q9Z2L7	Infl	NIALR	NDAESSGVLYSSAPTYFCGQTLTFR	VETVG	2	C18:+57.021	1386.134797	2770.253995	0.000451244	1	N	295	320
Q9Z2L7	Infl	NFTKK	ASHIQLDSLPEVPLLVDVPCLSAQLDDSILNIVKDHIFK	HGTVA	4	C20:+57.021	1088.836124	4351.313296	0.000870037	1	N	134	173
Q9Z2L7	Infl	RGDGR	QEWSPWSVPQTGHSTLVPHEWTTGFEGYSLSSR	RNIAL	4		944.1964591	3772.754636	0.001699387	2	N	256	289
Q9Z2L7	Infl	DDCQK	LIEHGVNTADDLVR	EGEIA	2		776.4104333	1550.805267	0.000451244	1	N	97	111
Q9Z2L7	Infl	SSNNR	EVVFDWLLEQACGPLYFGCSFFYPGWK	VLVF-	3	C12:+57.021,C19:+57.021	1105.849008	3314.523623	0.000451244	4	N	411	438
Q9Z2M7	Infl	KLLCK	QNIQGHLGEDVIQDLINYCLSYIANIK	LPKKR	3	C19:+57.021	1044.53289	3130.57527	0.000451244	8	N	80	107
Q9Z2M7	Infl	KLLCK	QNIQGHLGEDVIQDLINY	CLSYI	2		1035.019065	2068.02253	0.002296037	1	N	80	98
Q9Z2U0	Infl	MSYDR	AITVFSPDGHLFQVEYAQEAVKK	GSTAV	3		859.7836287	2576.327486	0.000451244	6	N	5	28
Q9Z2U0	Infl	QSNGR	RPFGISALIVGFDFDGTPR	LYQTD	3		689.034219	2064.079257	0.000823681	1	N	124	143
Q9Z2U0	Infl	DGTPR	LYQTDPSGTYHAWK	ANAIG	2		833.8971587	1665.778717	0.002884417	1	N	143	157
Q9Z2U1	Infl	QCDAR	AIGSASEGAQSSLQEVYHK	SMTLK	2		981.4823153	1960.949031	0.000451244	17	N	168	187
Q9Z2U1	Infl	SPEGR	LFQVEYAIEAIK	LGSTA	2		712.3957319	1422.775864	0.000451244	14	N	20	32
Q9Z2W0	Infl	IHLQR	NINENFGPNTEIHLVPILATAVQEELEK	GTPEP	3		1044.879097	3131.613892	0.000451244	12	N	171	199
Q9Z2W0	Infl	IFAPR	LDNLHSCFCALQALIDSCASPASLAR	DPHVR	3	C7:+57.021,C9:+57.021,C18:+57.021	964.1263924	2889.355777	0.000451244	2	N	260	286
Q9Z2X1	Infl	DPEGK	ITGEAFVQFASQELAEK	ALGKH	2		934.4759703	1866.936341	0.000451244	15	N	150	167
Q9Z2X1	Infl	CVHMR	GLPYKATENDIYNFFSPLNPVR	VHIEI	3		852.4363404	2554.285621	0.002080925	1	N	294	316
Q9Z2X1	Infl	EIVQF	FSGLEIVPNGITLPVDPEGK	ITGEA	2		1041.560034	2081.104469	0.000451244	26	N	130	150
Q9Z2X1	Infl	LDRMR	SGAYSAGYGGYEEYSGLSDGYGFTTDLFGR	DLSYC	3		1049.788384	3146.341752	0.000451244	27	N	232	262
Q9Z2X1	Infl	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	3	C6:+57.021,C18:+57.021	1265.262979	3792.765538	0.000451244	25	N	16	49
Q9Z2X1	Infl	FGCTK	EEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	2		1414.242362	2826.469125	0.000451244	21	N	124	150
Q9Z2X1	Infl	FVRLR	GLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	3	C6:+57.021	1229.971174	3686.890122	0.000451244	17	N	116	150
Q9Z2X1	Infl	RGLPW	SCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	3	C2:+57.021,C14:+57.021	1114.183778	3339.527933	0.000451244	18	N	20	49
Q9Z2X1	Infl	TREGR	QSGEAFVELESEDDVK	LALKK	2		891.4079503	1780.800301	0.000451244	10	N	52	68
Q9Z2X1	Infl	RSGAY	SAGYGGYEEYSGLSDGYGFTTDLFGR	DLSYC	2		1385.101709	2768.187817	0.000451244	18	N	236	262
Q9Z2X1	Infl	EYSGL	SDGYGFTTDLFGR	DLSYC	2		718.3285775	1434.641555	0.000451244	6	N	249	262
Q9Z2X1	Infl	KLRGL	PWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	4	C4:+57.021,C16:+57.021	906.6728025	3622.66001	0.001943752	2	N	18	49
Q9Z2X1	Infl	RGLPY	KATENDIYNFFSPLNPVR	VHIEI	2		1063.0398	2124.064001	0.002080925	2	N	298	316
Q9Z2X1	Infl	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHF	IYTRE	3	C6:+57.021,C18:+57.021	1087.497585	3259.469355	0.000823681	4	N	16	45

Peptide identifications for the comparison Exosomes vs. MDSC irrespective of their inflammation condition (Global comparison)

Peptide FDR ≤ 0.31%

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A075B5R8	Exosome	KDVQC	EVQLLETGGGLVQPGGSR	GLSCE	2		898.9792115	1795.942823	0.000451244	6	N	19	37
A0A075B5R8	Exosome	KDVQC	EVQLLETGGGLVQPGGSR	GLSCE	3		599.6554076	1795.942823	0.00307782	1	N	19	37
A0A075B5R8	Exosome	QTPGK	TLEWIGDINSDGSAINYAPSIKDR	FTIFR	2		1318.154079	2634.292557	0.000451244	5	N	62	86
A0A075B5R8	Exosome	QTPGK	TLEWIGDINSDGSAINYAPSIKDR	FTIFR	3		879.1053191	2634.292557	0.000451244	5	N	62	86
A0A075B5R8	Exosome	QTPGK	TLEWIGDINSDGSAINYAPSIK	DRFTI	2		1182.590052	2363.164503	0.000451244	6	N	62	84
A0A075B5R8	Exosome	QTPGK	TLEWIGDINSDGSAINYAPSIK	DRFTI	3		788.729301	2363.164503	0.000451244	4	N	62	84
A0A075B5U4	Exosome	SHGKS	LEWIGDINPNNGGTIYNQKFK	GKATL	3		807.7452854	2420.212456	0.002981883	1	N	62	83
A0A075B5U4	Exosome	TAVLS	EVQLQQSGPELVKPGASVK	IPCKA	2		997.550001	1993.084402	0.000622848	2	N	18	37
A0A087WR50	Exosome	NDNAR	SSPVIIDASTAIDAPSNLR	FLTTT	2		964.0107086	1926.005817	0.000451244	90	N	1890	1909
A0A087WR50	Exosome	NDNAR	SSPVIIDASTAIDAPSNLR	FLTTT	3		643.0097391	1926.005817	0.000451244	17	N	1890	1909
A0A087WR50	Exosome	PDTMR	VTWAPPPSIELTNLLVR	YSPVK	2		953.5439903	1905.072381	0.000451244	38	N	1283	1300
A0A087WR50	Exosome	PDTMR	VTWAPPPSIELTNLLVR	YSPVK	3		636.0319269	1905.072381	0.000451244	30	N	1283	1300
A0A087WR50	Exosome	CDNCR	RPGAAEPSPDGTTGHTYNQYTQR	YNQRT	3		835.3903414	2503.147624	0.000451244	31	N	2333	2356
A0A087WR50	Exosome	CDNCR	RPGAAEPSPDGTTGHTYNQYTQR	YNQRT	4		626.794706	2503.147624	0.000451244	16	N	2333	2356
A0A087WR50	Exosome	QGRGR	WKCDPIDQCQDSETR	TFYQI	2	C3:+57.021,C9:+57.021	969.4095158	1936.803432	0.000451244	25	N	552	567
A0A087WR50	Exosome	QGRGR	WKCDPIDQCQDSETR	TFYQI	3	C3:+57.021,C9:+57.021	646.6089438	1936.803432	0.000451244	44	N	552	567
A0A087WR50	Exosome	DAGFK	LTCQCLGFGSGHFR	CDSSK	2	C3:+57.021,C5:+57.021	820.3770933	1638.738587	0.000451244	50	N	2229	2243
A0A087WR50	Exosome	DAGFK	LTCQCLGFGSGHFR	CDSSK	3	C3:+57.021,C5:+57.021	547.2539955	1638.738587	0.000451244	43	N	2229	2243
A0A087WR50	Exosome	YGGSR	GFNCESKPEPEETCFDKYTGNTYK	VGDTY	2	C4:+57.021,C14:+57.021	1451.120798	2900.225997	0.000622848	6	N	84	108
A0A087WR50	Exosome	YGGSR	GFNCESKPEPEETCFDKYTGNTYK	VGDTY	3	C4:+57.021,C14:+57.021	967.7497989	2900.225997	0.000451244	76	N	84	108
A0A087WR50	Exosome	YGGSR	GFNCESKPEPEETCFDKYTGNTYK	VGDTY	4	C4:+57.021,C14:+57.021	726.0642992	2900.225997	0.000451244	30	N	84	108
A0A087WR50	Exosome	VSGYR	VEVLPVSLPGEHGQR	LPVNR	2		808.9419006	1615.868201	0.000451244	32	N	937	952
A0A087WR50	Exosome	VSGYR	VEVLPVSLPGEHGQR	LPVNR	3		539.6305337	1615.868201	0.000451244	46	N	937	952
A0A087WR50	Exosome	TISWR	TKTETITGFQVDAIPANGQTPVQR	SISPD	2		1286.672439	2571.329277	0.000451244	56	N	1834	1858
A0A087WR50	Exosome	TISWR	TKTETITGFQVDAIPANGQTPVQR	SISPD	3		858.117559	2571.329277	0.000622848	79	N	1834	1858
A0A087WR50	Exosome	DADQK	FGFCPMAAHEEICTTNEGVMYR	IGDQW	2	C4:+57.021,M6:+15.995,C13:+57.021,M20:+15.995	1326.553072	2651.090544	0.000451244	15	N	457	479
A0A087WR50	Exosome	DADQK	FGFCPMAAHEEICTTNEGVMYR	IGDQW	3	C4:+57.021,M6:+15.995,C13:+57.021,M20:+15.995	884.7046481	2651.090544	0.000451244	58	N	457	479
A0A087WR50	Exosome	QQWER	TYLGNALVCTCYGGSR	GFNCE	2	C9:+57.021,C11:+57.021	896.4113301	1790.80706	0.000451244	46	N	68	84
A0A087WR50	Exosome	VRYYR	ITYGETGGNSPVQEFTVPGSK	STATI	2		1084.529463	2167.043325	0.000451244	53	N	1478	1499
A0A087WR50	Exosome	KYPLR	NLQPGSEYTVTLVAVK	GNQQS	2		859.9703238	1717.925048	0.000451244	24	N	1053	1069
A0A087WR50	Exosome	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3		1045.511296	3133.510489	0.000451244	19	N	1352	1381
A0A087WR50	Exosome	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	4		784.3854223	3133.510489	0.000451244	25	N	1352	1381
A0A087WR50	Exosome	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3	Q1:-17.027	1039.83563	3116.483489	0.000735798	8	N	1352	1381
A0A087WR50	Exosome	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3	[0:-17.027	1039.83563	3116.483489	0.000870037	20	N	1352	1381
A0A087WR50	Exosome	TGTPR	SDNVPPPTDLQFVELTDVK	VTIMW	2		1057.536756	2113.057912	0.000451244	49	N	902	921
A0A087WR50	Exosome	TGTPR	SDNVPPPTDLQFVELTDVK	VTIMW	3		705.3604375	2113.057912	0.000451244	14	N	902	921
A0A087WR50	Exosome	RGRQK	TGLDSPTGFDSSDITANSFTVHWVAPR	APITG	2		1439.686274	2877.356949	0.000451244	17	N	1354	1381
A0A087WR50	Exosome	RGRQK	TGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3		960.1267829	2877.356949	0.000451244	50	N	1354	1381
A0A087WR50	Exosome	TGLTR	GVTYNIIVEALQNQR	RHKVR	2		859.4657399	1716.91588	0.000451244	52	N	2163	2178
A0A087WR50	Exosome	TGLTR	GVTYNIIVEALQNQR	RHKVR	3		573.3130933	1716.91588	0.000451244	37	N	2163	2178
A0A087WR50	Exosome	PSNLR	FLTTTPNSLLVSWQAPR	ARITG	2		966.023422	1930.031244	0.000451244	29	N	1909	1926
A0A087WR50	Exosome	PSNLR	FLTTTPNSLLVSWQAPR	ARITG	3		644.351548	1930.031244	0.000451244	27	N	1909	1926
A0A087WR50	Exosome	PIVNR	VVTPLSPPTNLHLEANPDTGVLTVSWER	STTPD	3		1014.868533	3041.582198	0.000451244	45	N	1168	1196
A0A087WR50	Exosome	PIVNR	VVTPLSPPTNLHLEANPDTGVLTVSWER	STTPD	4		761.4033494	3041.582198	0.000451244	4	N	1168	1196
A0A087WR50	Exosome	RHKVR	EEVVTVGNAVSEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C22:+57.021	1467.32428	4398.949441	0.000451244	41	N	2183	2222
A0A087WR50	Exosome	RHKVR	EEVVTVGNAVSEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	4	C22:+57.021	1100.74516	4398.949441	0.000451244	20	N	2183	2222
A0A087WR50	Exosome	EVVPR	PRPGVTEATITGLEPGTEYTIYVIALK	NNQKS	3		963.8589744	2888.553523	0.000451244	24	N	1949	1976
A0A087WR50	Exosome	VSGFR	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK	YIVNV	3		1258.958581	3773.852344	0.000451244	60	N	750	784
A0A087WR50	Exosome	VSGFR	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK	YIVNV	4		944.4708861	3773.852344	0.000451244	5	N	750	784
A0A087WR50	Exosome	PTNLK	FSQVTPTSFTAQWIAPSVQLTGYR	VRVNP	2		1343.187724	2684.359849	0.000451244	39	N	1728	1752
A0A087WR50	Exosome	PTNLK	FSQVTPTSFTAQWIAPSVQLTGYR	VRVNP	3		895.7944163	2684.359849	0.000451244	24	N	1728	1752
A0A087WR50	Exosome	GEAPR	EVTSDSGSIVVSGLTPGVEYTYTIQVLR	DGQER	3		990.8489152	2969.523345	0.000451244	61	N	1128	1156
A0A087WR50	Exosome	LPVNR	NTFAEITGLSPGVTYLFK	VFAVH	2		979.5176382	1957.019676	0.000451244	52	N	957	975
A0A087WR50	Exosome	LPVNR	NTFAEITGLSPGVTYLFK	VFAVH	3		653.3476921	1957.019676	0.000451244	12	N	957	975
A0A087WR50	Exosome	VPPSR	NSITLTNLNPGTEYVVSIIAVNGR	EESPP	2		1273.185182	2544.354764	0.000451244	48	N	1409	1433
A0A087WR50	Exosome	VPPSR	NSITLTNLNPGTEYVVSIIAVNGR	EESPP	3		849.1260545	2544.354764	0.000451244	27	N	1409	1433
A0A087WR50	Exosome	VSGFR	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR	KYIVN	3		1216.26026	3645.757381	0.000451244	24	N	750	783
A0A087WR50	Exosome	VSGFR	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR	KYIVN	4		912.4471453	3645.757381	0.001763695	1	N	750	783
A0A087WR50	Exosome	SDIPR	DLEVIASTPTSLLISWEPPAVSVR	YYRIT	2		1290.700133	2579.384667	0.000451244	51	N	1451	1475
A0A087WR50	Exosome	SDIPR	DLEVIASTPTSLLISWEPPAVSVR	YYRIT	3		860.8026889	2579.384667	0.000451244	57	N	1451	1475
A0A087WR50	Exosome	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	2	C7:+57.021	1098.966472	2195.917344	0.000451244	38	N	379	397

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A087WR50	Exosome	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	3	C7:+57.021	732.9802481	2195.917344	0.000451244	33	N	379	397
A0A087WR50	Exosome	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	2	Q1:-17.027,C7:+57.021	1090.452972	2178.890344	0.001352548	1	N	379	397
A0A087WR50	Exosome	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	2	[0:-17.027,C7:+57.021	1090.452972	2178.890344	0.000622848	36	N	379	397
A0A087WR50	Exosome	SEEGK	QSLILSTSQTTAPDAPPDPTVDQVDDTSIVVR	WSRPQ	3		1122.902407	3365.683822	0.000451244	18	N	797	829
A0A087WR50	Exosome	SEEGK	QSLILSTSQTTAPDAPPDPTVDQVDDTSIVVR	WSRPQ	3	Q1:-17.027	1117.226741	3348.656822	0.001943752	1	N	797	829
A0A087WR50	Exosome	SEEGK	QSLILSTSQTTAPDAPPDPTVDQVDDTSIVVR	WSRPQ	3	[0:-17.027	1117.226741	3348.656822	0.000622848	5	N	797	829
A0A087WR50	Exosome	NRVVT	PLSPPTNLHLEANPDTGVLTVSWER	STTPD	3		915.1403637	2742.397691	0.000451244	7	N	1171	1196
A0A087WR50	Exosome	QQSPK	ATGVFTTLQPLR	SIPPY	2		652.3725911	1302.729582	0.000451244	5	N	1076	1088
A0A087WR50	Exosome	RGRQK	TGLDSPTGFDSSDITANSFTVH	WVAPR	2		1135.016916	2268.018233	0.000451244	6	N	1354	1376
A0A087WR50	Exosome	LQPLR	SIPPYNTEVTETTIVITWTPAPR	IGFKL	2		1293.676658	2585.337717	0.000451244	31	N	1088	1111
A0A087WR50	Exosome	LQPLR	SIPPYNTEVTETTIVITWTPAPR	IGFKL	3		862.7870388	2585.337717	0.000451244	3	N	1088	1111
A0A087WR50	Exosome	SWTPF	QESSEYIISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	C10:+57.021	1376.330595	4125.968385	0.000451244	27	N	2125	2163
A0A087WR50	Exosome	SWTPF	QESSEYIISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	4	C10:+57.021	1032.499896	4125.968385	0.000698008	3	N	2125	2163
A0A087WR50	Exosome	SWTPF	QESSEYIISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	Q1:-17.027,C10:+57.021	1370.654928	4108.941385	0.000451244	14	N	2125	2163
A0A087WR50	Exosome	WKCER	HALQSASAGSGSFTDVR	TAIYQ	2		845.9113288	1689.807058	0.000451244	47	N	273	290
A0A087WR50	Exosome	WKCER	HALQSASAGSGSFTDVR	TAIYQ	3		564.2768192	1689.807058	0.000451244	12	N	273	290
A0A087WR50	Exosome	EQWQK	EYLGAICSCTCFGGQR	GWRCD	2	C7:+57.021,C9:+57.021,C11:+57.021	939.900041	1877.784482	0.000451244	94	N	2309	2325
A0A087WR50	Exosome	SIVVR	WSRPQAPITGYR	IVYSP	3		477.9217594	1430.741878	0.000451244	19	N	829	841
A0A087WR50	Exosome	EQDQK	YSFCTDHAVLVQTR	GGNSN	2	C4:+57.021	848.9095119	1695.803424	0.000451244	78	N	397	411
A0A087WR50	Exosome	EQDQK	YSFCTDHAVLVQTR	GGNSN	3	C4:+57.021	566.2756079	1695.803424	0.000451244	65	N	397	411
A0A087WR50	Exosome	AVNGR	EESPPLIGQQATVSDIPR	DLEVI	2		969.0028836	1935.990167	0.000451244	45	N	1433	1451
A0A087WR50	Exosome	LTDVK	VTIMWTPPDSVVSGYR	VEVLP	2	M4:+15.995	912.4540268	1822.892454	0.000451244	23	N	921	937
A0A087WR50	Exosome	VPRPR	PGVTEATITGLEPGTEYTIYVIALK	NNQKS	2		1318.707624	2635.399648	0.000451244	10	N	1951	1976
A0A087WR50	Exosome	VPRPR	PGVTEATITGLEPGTEYTIYVIALK	NNQKS	3		879.4743494	2635.399648	0.000451244	9	N	1951	1976
A0A087WR50	Exosome	AVTGR	GDSPASSKPVSINYK	TEIDK	2		775.3969916	1548.778383	0.000451244	3	N	1523	1538
A0A087WR50	Exosome	AVTGR	GDSPASSKPVSINYK	TEIDK	3		517.267261	1548.778383	0.000451244	2	N	1523	1538
A0A087WR50	Exosome	SINYK	TEIDKPSQMQVTDVQDNSISVR	WLPST	3		830.7433933	2489.20678	0.000823681	1	N	1538	1560
A0A087WR50	Exosome	SINYK	TEIDKPSQMQVTDVQDNSISVR	WLPST	3	M9:+15.995	836.0750599	2505.20178	0.000451244	20	N	1538	1560
A0A087WR50	Exosome	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	3	C1:+39.994,C8:+57.021	936.3869331	2806.137399	0.001699387	10	N	2286	2309
A0A087WR50	Exosome	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	3	C1:+57.021,C8:+57.021	942.0625998	2823.164399	0.000451244	27	N	2286	2309
A0A087WR50	Exosome	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	4	C1:+57.021,C8:+57.021	706.7988998	2823.164399	0.000451244	43	N	2286	2309
A0A087WR50	Exosome	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	3	[0:-17.027,C1:+57.021,C8:+57.021	936.3869331	2806.137399	0.000451244	39	N	2286	2309
A0A087WR50	Exosome	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	4	[0:-17.027,C1:+57.021,C8:+57.021	702.5421498	2806.137399	0.000662267	1	N	2286	2309
A0A087WR50	Exosome	KKDNR	GNLLQCVCTGNGR	GEWKC	2	C6:+57.021,C8:+57.021	724.8403436	1447.665087	0.000451244	22	N	253	266
A0A087WR50	Exosome	NITIY	AVEENQESTPVFIQQETTGTPR	SDNVP	2		1231.096229	2460.176859	0.000451244	28	N	880	902
A0A087WR50	Exosome	NITIY	AVEENQESTPVFIQQETTGTPR	SDNVP	3		821.0667529	2460.176859	0.000451244	2	N	880	902
A0A087WR50	Exosome	RLRPR	PYLPNVDEEVQIGHVPR	GDVDY	3		654.6746907	1961.000672	0.000662267	5	N	2073	2090
A0A087WR50	Exosome	PRRAR	VTDATETTITISWR	TKTET	2		797.410099	1592.804598	0.000451244	20	N	1820	1834
A0A087WR50	Exosome	LVQTR	GGNSNGALCHFPFLYNNR	NYTDC	2	C9:+57.021	1019.471331	2036.927061	0.000451244	27	N	411	429
A0A087WR50	Exosome	LVQTR	GGNSNGALCHFPFLYNNR	NYTDC	3	C9:+57.021	679.9834871	2036.927061	0.000451244	19	N	411	429
A0A087WR50	Exosome	VYTVK	DDKESAPISDTVVPAVPPPTDLR	FTNIG	2		1210.121716	2418.227832	0.000451244	9	N	1250	1273
A0A087WR50	Exosome	SWRTK	TETITGFQVDAIPANGQTPVQR	SISPD	2		1172.101118	2342.186635	0.000451244	21	N	1836	1858
A0A087WR50	Exosome	VGNGR	GEWACIPYSQLR	DQCIV	2	C5:+57.021	740.3563838	1478.697168	0.000451244	18	N	503	515
A0A087WR50	Exosome	VPGSK	STATINNIKPGADYTITLYAVTGR	GDSPA	2		1270.671907	2539.328214	0.000451244	21	N	1499	1523
A0A087WR50	Exosome	VPGSK	STATINNIKPGADYTITLYAVTGR	GDSPA	3		847.4505382	2539.328214	0.000451244	38	N	1499	1523
A0A087WR50	Exosome	STVQK	TPFITNPGYDTENGIQLPGTTHQQPSVGQQMIFEEHGFR	RTTPP	4	M31:+15.995	1097.772921	4387.060484	0.000451244	16	N	2018	2057
A0A087WR50	Exosome	SYTIK	GLTPGVIYEGQLISIQQYGHR	EVTRF	2		1165.119113	2328.222627	0.000451244	30	N	669	690
A0A087WR50	Exosome	SYTIK	GLTPGVIYEGQLISIQQYGHR	EVTRF	3		777.082009	2328.222627	0.000451244	19	N	669	690
A0A087WR50	Exosome	CDNCR	RPGAAEPSPDGTTGHTYNQY	TQRYN	2		1059.977928	2117.940257	0.000622848	6	N	2333	2353
A0A087WR50	Exosome	CDNCR	RPGAAEPSPDGTTGHTYNQY	TQRYN	3		706.9878856	2117.940257	0.0007646	6	N	2333	2353
A0A087WR50	Exosome	GTDYK	IHLYTLNDNAR	SSPVI	2		665.3496473	1328.683695	0.000451244	6	N	1879	1890
A0A087WR50	Exosome	GTDYK	IHLYTLNDNAR	SSPVI	3		443.9023649	1328.683695	0.000622848	3	N	1879	1890
A0A087WR50	Exosome	NETDR	TVLVTWTPPR	ARIAG	2		585.3380199	1168.66044	0.001839721	9	N	1010	1020
A0A087WR50	Exosome	YERPK	DSMIWDCTCIGAGR	GRISC	2	M3:+15.995,C7:+57.021,C9:+57.02	829.3421021	1656.668604	0.000451244	22	N	117	131
A0A087WR50	Exosome	VGNAV	SEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C12:+57.021	1134.821605	3401.441414	0.000451244	16	N	2193	2222
A0A087WR50	Exosome	RVTWA	PPPSIELTNLLVR	YSPVK	2		724.9277305	1447.839861	0.000451244	1	N	1287	1300
A0A087WR50	Exosome	TTTPN	SLLVSWQAPR	ARITG	2		578.8278194	1155.640039	0.000823681	10	N	1916	1926
A0A087WR50	Exosome	VKDDK	ESAPISDTVVPAVPPPTDLR	FTNIG	2		1031.047291	2060.078982	0.000823681	4	N	1253	1273
A0A087WR50	Exosome	VYALK	DTLTSRPAQGVITTLENVSPPR	RARVT	2		1176.630042	2351.244485	0.002296037	1	N	1795	1817
A0A087WR50	Exosome	VYALK	DTLTSRPAQGVITTLENVSPPR	RARVT	3		784.7559616	2351.244485	0.001162105	3	N	1795	1817
A0A087WR50	Exosome	TGPMK	EINLSPDSSSVIVSGLMVATK	YEVSV	2	M17:+15.995	1082.064867	2162.114134	0.000451244	10	N	1765	1786
A0A087WR50	Exosome	GSPPR	EVVPRPRPGVTEATITGLEPGTEYTIYVIALK	NNQKS	4		868.2295049	3468.88682	0.000823681	4	N	1944	1976
A0A087WR50	Exosome	PSKTK	TASPDQTEMTIEGLQPTVEYVVSVYAQNR	NGESQ	3		1076.191124	3225.549972	0.000451244	25	N	1587	1616
A0A087WR50	Exosome	LLPGR	KYIVNVYQISEEGK	QSLIL	2		835.4439418	1668.872284	0.00091018	2	N	783	797

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A087WR50	Exosome	SPDVR	SYTITGLQPGTDYK	IHLYT	2		772.3860925	1542.756585	0.000451244	29	N	1865	1879
A0A087WR50	Exosome	GHMMR	CTCVGNGRGEWACIPYSQLR	DQCIV	3	C1:+57.021,C3:+57.021,C13:+57.021	795.3613325	2383.060598	0.001871652	1	N	495	515
A0A087WR50	Exosome	RGVTY	NIIVEALQNQR	RHKVR	2		649.3652974	1296.714995	0.000451244	9	N	2167	2178
A0A087WR50	Exosome	NLLVR	YSPVKNEEDVAELSISPSDNAVVL	TNLLP	2		1288.142845	2574.270091	0.000451244	8	N	1300	1324
A0A087WR50	Exosome	LPVNR	NTFAEITGLSPGVTY	LFKVF	2		785.3939175	1568.772235	0.000451244	10	N	957	972
A0A087WR50	Exosome	TVSGF	RVEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR	KYIVN	3		1268.293964	3801.858492	0.000451244	3	N	749	783
A0A087WR50	Exosome	ESSEY	IISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	C4:+57.021	1135.240212	3402.697235	0.000451244	4	N	2131	2163
A0A087WR50	Exosome	TGLTR	GVTYNIIVEALQNQRR	HKVRE	3		625.346797	1873.016991	0.000451244	14	N	2163	2179
A0A087WR50	Exosome	AVSEG	LNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C9:+57.021	1043.789576	3128.345329	0.002145581	2	N	2196	2222
A0A087WR50	Exosome	YGGSR	GFNCESKPEPEETCFDK	YTGNT	2	C4:+57.021,C14:+57.021	1037.430114	2072.844628	0.000451244	5	N	84	101
A0A087WR50	Exosome	YGGSR	GFNCESKPEPEETCFDK	YTGNT	3	C4:+57.021,C14:+57.021	691.9560093	2072.844628	0.000451244	3	N	84	101
A0A087WR50	Exosome	NLLVR	YSPVKNEEDVAELSISPSDNAVVLTN	LLPGT	2		1395.688148	2789.360697	0.000979378	1	N	1300	1326
A0A087WR50	Exosome	QRRHK	VREEVVTVGNAVSEGLNQPTDDSCFDPYTVSHY	AIGEE	3	C24:+57.021	1228.897173	3683.66812	0.000451244	4	N	2181	2214
A0A087WR50	Exosome	APRAR	ITGYIIKYEKPGSPPR	EVVPR	3		607.0091222	1818.003967	0.002374549	1	N	1928	1944
A0A087WR50	Exosome	GDKWR	RPHETGGYMLECLCLGNGK	GEWTC	3	M9:+15.995,C12:+57.021,C14:+57.021	736.6715786	2206.991336	0.000451244	6	N	156	175
A0A087WR50	Exosome	TSTGR	WKEATIPGHLNSYTIK	GLTPG	3		620.0006267	1856.97848	0.000451244	10	N	653	669
A0A087WR50	Exosome	GNTYK	VGDTYERPKDSMIWDCTCIGAGR	GRISC	3	M12:+15.995,C16:+57.021,C18:+57.021	901.7370879	2702.187864	0.000451244	12	N	108	131
A0A087WR50	Exosome	ATPVR	LRPRPYLPNVDEEVQIGHVPR	GDVDY	4		621.8427306	2483.339723	0.000451244	10	N	2069	2090
A0A087WR50	Exosome	TIYAV	EENQESTPVFIQQETTGTPR	SDNVP	2		1146.043465	2290.071331	0.000451244	13	N	882	902
A0A087WR50	Exosome	PGTEY	LVSVSSVYEQHESIPLR	GRQKT	2		972.015794	1942.015988	0.000451244	10	N	1333	1350
A0A087WR50	Exosome	PGTEY	LVSVSSVYEQHESIPLR	GRQKT	3		648.3464626	1942.015988	0.002374549	1	N	1333	1350
A0A087WR50	Exosome	PIAEK	CFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGNGR	ITCTS	3	C1:+39.994,M24:+15.995,M25:+15.995,C28:+57.021,C30:+57.021	1428.593496	4282.757088	0.000622848	4	N	186	223
A0A087WR50	Exosome	PIAEK	CFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGNGR	ITCTS	4	C1:+57.021,M24:+15.995,M25:+15.995,C28:+57.021,C30:+57.021	1075.953822	4299.784088	0.000451244	9	N	186	223
A0A087WR50	Exosome	GSPPR	EVVPRPRPGVTEATITGLEPGTEYTIY	VIALK	3		982.5138668	2944.5182	0.000823681	8	N	1944	1971
A0A087WR50	Exosome	GEAPR	EVTSDSGSIVVSGLTPGVEY	TYTIQ	2		998.4920144	1994.968429	0.000451244	8	N	1128	1148
A0A087WR50	Exosome	NPNAS	TGQEALSQTTISWTPF	QESSE	2		883.9339382	1765.852276	0.001162105	3	N	2109	2125
A0A087WR50	Exosome	LTDVK	VTIMWTPPDSVVSGYRVEVLPVSLPGEHGQR	LPVNR	3	M4:+15.995	1141.257832	3420.750095	0.001463592	3	N	921	952
A0A087WR50	Exosome	LTDVK	VTIMWTPPDSVVSGYRVEVLPVSLPGEHGQR	LPVNR	4	M4:+15.995	856.1953237	3420.750095	0.000451244	3	N	921	952
A0A087WR50	Exosome	REVTR	FDFTTSASTPVTSNTVTGETAPYSPV	VATSE	2		1339.129935	2676.24427	0.001699387	3	N	694	720
A0A087WR50	Exosome	FDNGK	HYQINQQWER	TYLGN	2		701.3370712	1400.658542	0.002374549	2	N	58	68
A0A087WR50	Exosome	GSPPR	EVVPRPRPGVTEATITGLEPGTEY	TIYVI	3		856.7821764	2567.323129	0.0025889	1	N	1944	1968
A0A087WR50	Exosome	STVQK	TPFITNPGYDTENGIQLPGTTHQQPSVGQQMIF	EEHGF	3	M31:+15.995	1211.582932	3631.725396	0.001763695	1	N	2018	2051
A0A087WR50	Exosome	RDNMK	WCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYR	IGDQW	4	C2:+57.021,C17:+57.021,M19:+15.995,C26:+57.021,M33:+15.995	1055.68936	4218.726238	0.002080925	1	N	444	479
A0A087WR50	Exosome	PSKTK	TASPDQTEMTIEGLQPTVEY	VVSVY	2		1105.512621	2209.009643	0.001463592	1	N	1587	1607
A0A087WR50	Exosome	PGVIY	EGQLISIQQYGHR	EVTRF	2		764.897493	1527.779386	0.00091018	2	N	677	690
A0A087WR50	Exosome	FTDVR	TAIYQPQTHPQPAPY	GHCVT	2		856.4260834	1710.836567	0.001654178	3	N	290	305
A0A087WR50	Exosome	IDRPK	GLAFTDVDVDSIK	IAWES	2		690.3568037	1378.698007	0.000451244	1	N	1635	1648
A0A087WR50	Exosome	RDNMK	WCGTTQNYDADQK	FGFCP	2	C2:+57.021	793.8309271	1585.646254	0.000622848	1	N	444	457
A0A087WR50	Exosome	GEAPR	EVTSDSGSIVVSGLTPGVEYTY	TIQVL	2		1130.547518	2259.079436	0.000451244	3	N	1128	1150
A0A087WR50	Exosome	FTDVR	TAIYQPQTHPQPAPYGHCVTDSGVVY	SVGMQ	3	C18:+57.021	962.7890709	2885.343813	0.002663018	1	N	290	316
A0A087WR50	Exosome	QRRHK	VREEVVTVGNAVSEGLNQPTDDSCFDPY	TVSHY	3	C24:+57.021	1033.140386	3096.397759	0.000622848	1	N	2181	2209
A0A087WR50	Exosome	RSDNV	PPPTDLQFVELTDVK	VTIMW	2		849.9515997	1697.887599	0.000622848	1	N	906	921
A0A087WR50	Exosome	VTVGN	AVSEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C14:+57.021	1191.523447	3571.546942	0.001654178	1	N	2191	2222
A0A087WR50	Exosome	EDGIR	ELFPAPDGEDDTAELQGLRPGSEY	TVSVV	2		1303.598802	2605.182004	0.000823681	1	N	1673	1697
A0A087WR50	Parental	NDNAR	SSPVIIDASTAIDAPSNLR	FLTTT	2		964.0107086	1926.005817	0.000451244	28	N	1890	1909
A0A087WR50	Parental	PDTMR	VTWAPPPSIELTNLLVR	YSPVK	2		953.5439903	1905.072381	0.000622848	3	N	1283	1300
A0A087WR50	Parental	PDTMR	VTWAPPPSIELTNLLVR	YSPVK	3		636.0319269	1905.072381	0.000451244	13	N	1283	1300
A0A087WR50	Parental	CDNCR	RPGAAEPSPDGTTGHTYNQYTQR	YNQRT	3		835.3903414	2503.147624	0.000451244	16	N	2333	2356
A0A087WR50	Parental	CDNCR	RPGAAEPSPDGTTGHTYNQYTQR	YNQRT	4		626.794706	2503.147624	0.001162105	1	N	2333	2356
A0A087WR50	Parental	QGRGR	WKCDPIDQCQDSETR	TFYQI	2	C3:+57.021,C9:+57.021	969.4095158	1936.803432	0.000622848	5	N	552	567
A0A087WR50	Parental	QGRGR	WKCDPIDQCQDSETR	TFYQI	3	C3:+57.021,C9:+57.021	646.6089438	1936.803432	0.000823681	2	N	552	567
A0A087WR50	Parental	DAGFK	LTCQCLGFGSGHFR	CDSSK	2	C3:+57.021,C5:+57.021	820.3770933	1638.738587	0.000451244	2	N	2229	2243
A0A087WR50	Parental	DAGFK	LTCQCLGFGSGHFR	CDSSK	3	C3:+57.021,C5:+57.021	547.2539955	1638.738587	0.000451244	18	N	2229	2243
A0A087WR50	Parental	YGGSR	GFNCESKPEPEETCFDKYTGNTYK	VGDTY	3	C4:+57.021,C14:+57.021	967.7497989	2900.225997	0.000451244	7	N	84	108
A0A087WR50	Parental	YGGSR	GFNCESKPEPEETCFDKYTGNTYK	VGDTY	4	C4:+57.021,C14:+57.021	726.0642992	2900.225997	0.000622848	3	N	84	108
A0A087WR50	Parental	VSGYR	VEVLPVSLPGEHGQR	LPVNR	2		808.9419006	1615.868201	0.000451244	5	N	937	952
A0A087WR50	Parental	VSGYR	VEVLPVSLPGEHGQR	LPVNR	3		539.6305337	1615.868201	0.000622848	2	N	937	952
A0A087WR50	Parental	TISWR	TKTETITGFQVDAIPANGQTPVQR	SISPD	2		1286.672439	2571.329277	0.000451244	9	N	1834	1858
A0A087WR50	Parental	TISWR	TKTETITGFQVDAIPANGQTPVQR	SISPD	3		858.117559	2571.329277	0.000451244	4	N	1834	1858

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A087WR50	Parental	QQWER	TYLGNALVCTCYGGSR	GFNCE	2	C9:+57.021,C11:+57.021	896.4113301	1790.80706	0.000451244	3	N	68	84
A0A087WR50	Parental	VRYYR	ITYGETGGNSPVQEFTVPGSK	STATI	2		1084.529463	2167.043325	0.000451244	6	N	1478	1499
A0A087WR50	Parental	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3		1045.511296	3133.510489	0.000451244	6	N	1352	1381
A0A087WR50	Parental	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	4		784.3854223	3133.510489	0.001329271	1	N	1352	1381
A0A087WR50	Parental	PLRGR	QKTGLDSPTGFDSSDITANSFTVHWVAPR	APITG	3	[0:-17.027	1039.83563	3116.483489	0.002145581	3	N	1352	1381
A0A087WR50	Parental	TGTPR	SDNVPPPTDLQFVELTDVK	VTIMW	2		1057.536756	2113.057912	0.000451244	8	N	902	921
A0A087WR50	Parental	TGLTR	GVTYNIIVEALQNQR	RHKVR	2		859.4657399	1716.91588	0.000451244	12	N	2163	2178
A0A087WR50	Parental	PSNLR	FLTTTPNSLLVSWQAPR	ARITG	2		966.023422	1930.031244	0.000451244	6	N	1909	1926
A0A087WR50	Parental	PSNLR	FLTTTPNSLLVSWQAPR	ARITG	3		644.351548	1930.031244	0.000451244	5	N	1909	1926
A0A087WR50	Parental	PIVNR	VVTPLSPPTNLHLEANPDTGVLTVSWER	STTPD	3		1014.868533	3041.582198	0.000451244	20	N	1168	1196
A0A087WR50	Parental	RHKVR	EEVVTVGNAVSEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	3	C22:+57.021	1467.32428	4398.949441	0.000451244	27	N	2183	2222
A0A087WR50	Parental	RHKVR	EEVVTVGNAVSEGLNQPTDDSCFDPYTVSHYAIGEEWER	LSDAG	4	C22:+57.021	1100.74516	4398.949441	0.000451244	3	N	2183	2222
A0A087WR50	Parental	VSGFR	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK	YIVNV	3		1258.958581	3773.852344	0.001162105	2	N	750	784
A0A087WR50	Parental	PTNLK	FSQVTPTSFTAQWIAPSVQLTGYR	VRVNP	2		1343.187724	2684.359849	0.000451244	6	N	1728	1752
A0A087WR50	Parental	PTNLK	FSQVTPTSFTAQWIAPSVQLTGYR	VRVNP	3		895.7944163	2684.359849	0.000451244	6	N	1728	1752
A0A087WR50	Parental	LPVNR	NTFAEITGLSPGVTYLFK	VFAVH	2		979.5176382	1957.019676	0.002080925	1	N	957	975
A0A087WR50	Parental	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	2	C7:+57.021	1098.966472	2195.917344	0.000451244	4	N	379	397
A0A087WR50	Parental	TTEGR	QDGHLWCSTTSNYEQDQK	YSFCT	2	[0:-17.027,C7:+57.021	1090.452972	2178.890344	0.000622848	2	N	379	397
A0A087WR50	Parental	LQPLR	SIPPYNTEVTETTIVITWTPAPR	IGFKL	2		1293.676658	2585.337717	0.000735798	2	N	1088	1111
A0A087WR50	Parental	SWTPF	QESSEYIISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	C10:+57.021	1376.330595	4125.968385	0.000451244	15	N	2125	2163
A0A087WR50	Parental	SWTPF	QESSEYIISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	Q1:-17.027,C10:+57.021	1370.654928	4108.941385	0.000451244	7	N	2125	2163
A0A087WR50	Parental	EQWQK	EYLGAICSCTCFGGQR	GWRCD	2	C7:+57.021,C9:+57.021,C11:+57.021	939.900041	1877.784482	0.000451244	27	N	2309	2325
A0A087WR50	Parental	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	3	C1:+57.021,C8:+57.021	942.0625998	2823.164399	0.000823681	5	N	2286	2309
A0A087WR50	Parental	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	4	C1:+57.021,C8:+57.021	706.7988998	2823.164399	0.000451244	4	N	2286	2309
A0A087WR50	Parental	KGEFK	CDPHEATCYDDGKTYHVGEQWQK	EYLGA	3	[0:-17.027,C1:+57.021,C8:+57.021	936.3869331	2806.137399	0.000622848	8	N	2286	2309
A0A087WR50	Parental	NITIY	AVEENQESTPVFIQQETTGTPR	SDNVP	2		1231.096229	2460.176859	0.000451244	7	N	880	902
A0A087WR50	Parental	VGNGR	GEWACIPYSQLR	DQCIV	2	C5:+57.021	740.3563838	1478.697168	0.001395409	2	N	503	515
A0A087WR50	Parental	PSKTK	TASPDQTEMTIEGLQPTVEYVVSVYAQNR	NGESQ	3		1076.191124	3225.549972	0.001463592	1	N	1587	1616
A0A087WR50	Parental	SPDVR	SYTITGLQPGTDYK	IHLYT	2		772.3860925	1542.756585	0.001395409	1	N	1865	1879
A0A087WR50	Parental	GGQPK	QYNVGPLASKYPLR	NLQPG	2		803.4415364	1604.867473	0.001943752	1	N	1039	1053
A0A087WR50	Parental	GGQPK	QYNVGPLASKYPLR	NLQPG	3		535.9636243	1604.867473	0.001162105	4	N	1039	1053
A0A087WR50	Parental	GHMMR	CTCVGNGRGEWACIPYSQLR	DQCIV	3	C1:+57.021,C3:+57.021,C13:+57.021	795.3613325	2383.060598	0.000622848	3	N	495	515
A0A087WR50	Parental	RGVTY	NIIVEALQNQR	RHKVR	2		649.3652974	1296.714995	0.000451244	9	N	2167	2178
A0A087WR50	Parental	QYGHR	EVTRFDFTTSASTPVTSNTVTGET	APYSP	2		1274.606627	2547.197654	0.001352548	2	N	690	714
A0A087WR50	Parental	NLLVR	YSPVKNEEDVAELSISPSDNAVVL	TNLLP	2		1288.142845	2574.270091	0.000451244	15	N	1300	1324
A0A087WR50	Parental	LPVNR	NTFAEITGLSPGVTY	LFKVF	2		785.3939175	1568.772235	0.00091018	4	N	957	972
A0A087WR50	Parental	TVSGF	RVEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR	KYIVN	3		1268.293964	3801.858492	0.000979378	1	N	749	783
A0A087WR50	Parental	RIGFK	LGVRPSQGGEAPREVTSDSGSIVVSGLTPGVEY	TYTIQ	3		1100.895587	3299.663361	0.002374549	1	N	1115	1148
A0A087WR50	Parental	QRGWR	CDNCRRPGAAEPSPDGTTGHTYNQYTQR	YNQRT	4	[0:-17.027,C1:+57.021,C4:+57.021	798.8457943	3191.351977	0.001943752	1	N	2328	2356
A0A087WR50	Parental	ESSEY	IISCQPVGTDEEPLQFQVPGTSTSATLTGLTR	GVTYN	3	C4:+57.021	1135.240212	3402.697235	0.001871652	2	N	2131	2163
A0A087WSP5	Exosome	EWKRR	QQSACIGGPPNACLDQLQSWFTIVAETLQQIR	QQLKK	3	C5:+57.021,C13:+57.021	1210.599703	3628.775709	0.000451244	5	N	242	274
A0A087WSP5	Exosome	PYTKK	ELSAVTFPDIIR	NYKVM	2		680.8777063	1359.739813	0.000979378	9	N	643	655
A0A087WSP5	Exosome	MLGEK	LLGPNAGPDGLIPWTR	FCKEN	2		838.9600934	1675.904587	0.000622848	5	N	531	547
A0A087WSP5	Parental	EWKRR	QQSACIGGPPNACLDQLQSWFTIVAETLQQIR	QQLKK	3	C5:+57.021,C13:+57.021	1210.599703	3628.775709	0.000451244	13	N	242	274
A0A087WSP5	Parental	PYTKK	ELSAVTFPDIIR	NYKVM	2		680.8777063	1359.739813	0.000451244	17	N	643	655
A0A087WSP5	Parental	MLGEK	LLGPNAGPDGLIPWTR	FCKEN	2		838.9600934	1675.904587	0.000622848	5	N	531	547
A0A0B4J1J5	Exosome	DFKGR	FAFSLETSASTAYLQINNLK	NEDTA	2		1109.573673	2217.131746	0.000451244	7	N	86	106
A0A0B4J1J5	Exosome	DFKGR	FAFSLETSASTAYLQINNLK	NEDTA	3		740.0517154	2217.131746	0.000637154	1	N	86	106
A0A0B4J1J5	Exosome	QSAQA	QIQLVQSGPELK	KPGET	2	[0:-17.027	661.8696558	1321.723712	0.000451244	5	N	19	31
A0A0B4J1J5	Parental	QSAQA	QIQLVQSGPELKKPGETVK	ISCKA	3	[0:-17.027	688.0566505	2061.146551	0.001352548	1	N	19	38
A0A0D9SEG8	Exosome	SVSLK	LLSNINSVFLTNTNTEK	LASNV	2		954.5078018	1907.000004	0.000451244	30	N	346	363
A0A0D9SEG8	Exosome	LEQRR	ASLEDFYGSPIPSVSLK	LLSNI	2		905.4676139	1808.919628	0.000451244	10	N	329	346
A0A0D9SEG8	Exosome	SGSLR	GPDTICQEPPFPTWTLLPTAHSQTLLR	FSVEV	3	C6:+57.021	1026.190575	3075.548326	0.000451244	15	N	160	187
A0A0D9SEG8	Exosome	NVTFK	FDFTSVESIEPR	HELIC	2		713.8466031	1425.677606	0.000451244	5	N	371	383
A0A0D9SEG8	Exosome	EAVDK	LLEDPMETETQQVAAQLLSNLEQSLR	TLAQF	3	M6:+15.995	991.5014384	2971.480915	0.001763695	1	N	217	243
A0A0D9SEG8	Exosome	QTLLR	FSVEVQNLLR	DFNPA	2		602.8383841	1203.661168	0.000622848	2	N	187	197
A0A0D9SEG8	Exosome	YTIQK	LIEAVDKLLEDPMETETQQVAAQLLSNLEQSLR	TLAQF	3	M13:+15.995	1247.64749	3739.919071	0.000698008	1	N	210	243
A0A0D9SEG8	Parental	FAMCK	NSEGSYTCVCNLGYK	LLSGA	2	C8:+57.021,C10:+57.021	876.3718706	1750.728141	0.000451244	21	N	87	102
A0A0D9SEG8	Parental	SVSLK	LLSNINSVFLTNTNTEK	LASNV	2		954.5078018	1907.000004	0.000451244	37	N	346	363
A0A0D9SEG8	Parental	LEQRR	ASLEDFYGSPIPSVSLK	LLSNI	2		905.4676139	1808.919628	0.000451244	26	N	329	346
A0A0D9SEG8	Parental	SGSLR	GPDTICQEPPFPTWTLLPTAHSQTLLR	FSVEV	3	C6:+57.021	1026.190575	3075.548326	0.000451244	28	N	160	187
A0A0D9SEG8	Parental	PNMEK	LLGNTPLNLEQR	RASLE	2		684.3862298	1366.75686	0.0007646	6	N	316	328
A0A0D9SEG8	Parental	NVTFK	FDFTSVESIEPR	HELIC	2		713.8466031	1425.677606	0.000451244	5	N	371	383

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A0A0D9SEG8	Parental	QTLLR	FSVEVQNLLR	DFNPA	2		602.8383841	1203.661168	0.002080925	1	N	187	197
A2A8Z1	Exosome	DFDKK	LTEADAYLQILIEQLK	LFDDK	2		931.0200137	1860.024427	0.000451244	1	N	122	138
A2A8Z1	Parental	DFDKK	LTEADAYLQILIEQLK	LFDDK	2		931.0200137	1860.024427	0.000622848	6	N	122	138
A2A8Z1	Parental	LGEIF	QCHWTLPNDTEENAELVSEGPVPWVSK	NSVTF	3	C2:+57.021	1041.48935	3121.444649	0.001162105	5	N	462	489
A2A8Z1	Parental	NGYGR	SILTVPWVELGGECNINCSK	TGYSA	2	C14:+57.021,C18:+57.021	1138.55618	2275.09676	0.001264573	2	N	563	583
A2ADY9	Exosome	IDLKK	NVLVIGTTGSQTTFLPEGELPECAR	LAYGT	2	C23:+57.021	1345.179008	2688.342416	0.000622848	4	N	338	363
A2ADY9	Parental	YGTGR	EDIRPEEIADQELAEAIQK	SAEDA	2		1099.053302	2196.091004	0.000451244	14	N	370	389
A2ADY9	Parental	LLKER	NPPLAEALLSGDLEK	FSRVL	2		783.9228422	1565.830084	0.001162105	1	N	155	170
A2ADY9	Parental	IDLKK	NVLVIGTTGSQTTFLPEGELPECAR	LAYGT	2	C23:+57.021	1345.179008	2688.342416	0.000451244	10	N	338	363
A2ADY9	Parental	SNLPR	IDFSSIAVPGTSNPQQR	QLPRT	2		908.9635614	1815.911523	0.000634081	5	N	93	110
A2ADY9	Parental	QERIR	LFSADPFDLEAQAK	IEEDI	2		776.3886352	1550.76167	0.0025889	1	N	191	205
A2AFG7	Exosome	NSSSR	LVALQGQSLILECIAEGFPTPTIK	WLHPS	3	C13:+57.021	866.8122653	2597.413396	0.000451244	5	N	245	269
A2AFG7	Exosome	YLLCK	AFGAPVPSVQWLDEEGTTVLQDER	FFPYA	2		1322.648629	2643.281658	0.000451244	15	N	443	467
A2AFG7	Exosome	YLLCK	AFGAPVPSVQWLDEEGTTVLQDER	FFPYA	3		882.1016861	2643.281658	0.001162105	1	N	443	467
A2AFG7	Exosome	PKWPK	ETVKPVEVEEGESVVLPCNPPPSAAPLR	IYWMN	3	C18:+57.021	1000.850107	2999.526922	0.001395409	1	N	134	162
A2AFG7	Parental	NSSSR	LVALQGQSLILECIAEGFPTPTIK	WLHPS	2	C13:+57.021	1299.714498	2597.413396	0.00091018	1	N	245	269
A2AFG7	Parental	NSSSR	LVALQGQSLILECIAEGFPTPTIK	WLHPS	3	C13:+57.021	866.8122653	2597.413396	0.000622848	5	N	245	269
A2AFG7	Parental	DLQYR	FQLQATTQQGPGEAIVR	EGGTM	2		922.4872037	1842.958807	0.000451244	12	N	984	1001
A2AFG7	Parental	YLLCK	AFGAPVPSVQWLDEEGTTVLQDER	FFPYA	2		1322.648629	2643.281658	0.000451244	9	N	443	467
A2AFG7	Parental	YLLCK	AFGAPVPSVQWLDEEGTTVLQDER	FFPYA	3		882.1016861	2643.281658	0.000451244	5	N	443	467
A2AFG7	Parental	PKWPK	ETVKPVEVEEGESVVLPCNPPPSAAPLR	IYWMN	3	C18:+57.021	1000.850107	2999.526922	0.002663018	1	N	134	162
A2AFG7	Parental	QNHNK	TLQLLNVGEEDDGEYTCLAENSLGSAR	HAYYV	2	C17:+57.021	1477.688122	2953.360645	0.000622848	1	N	289	316
A2AFG7	Parental	TAINK	YGPGEPSPVSETVVTPEAAPEKNPVDVR	GEGNE	3		974.4896098	2920.445429	0.001463592	1	N	688	716
A2AIV8	Exosome	LRQCK	VLNPDDEEQVLSDPNLVIR	KRKVG	2		1083.058387	2164.101174	0.000451244	7	N	38	57
A2AIV8	Exosome	IRKRK	VGVLLDILQR	TGHKG	2		563.35367	1124.69174	0.002663018	1	N	60	70
A2AIV8	Parental	LRQCK	VLNPDDEEQVLSDPNLVIR	KRKVG	2		1083.058387	2164.101174	0.000451244	32	N	38	57
A2AIV8	Parental	RKLVR	ELGEKADELQLQLFQTESR	LLAAE	2		1117.569119	2233.122638	0.000451244	5	N	386	405
A2AIV8	Parental	RKLVR	ELGEKADELQLQLFQTESR	LLAAE	3		745.3820127	2233.122638	0.000622848	3	N	386	405
A2AIV8	Parental	IRKRK	VGVLLDILQR	TGHKG	2		563.35367	1124.69174	0.001329271	2	N	60	70
A2AIV8	Parental	DSSPR	NSQELSLPQDLEEDAQLSDK	GVLAD	2		1130.035306	2258.055012	0.000451244	8	N	433	453
A2AIV8	Parental	KLQKK	VQDLTALLSSKDDFIK	ELRVK	3		598.328409	1791.961827	0.002296037	1	N	129	145
A2AJW4	Exosome	HFALR	YGVAGAEYWDNNDGRDYSLTCR	SHALH	3	C21:+57.021	861.3719163	2581.092349	0.000622848	2	N	238	260
A2AJW4	Parental	LHMPR	GECEESWIHFI	-	2	C3:+57.021	703.8061924	1405.596785	0.001162105	1	N	268	279
A2AJW4	Parental	HVLSR	LAINSDLCCSSQDLEFTLQCLVPDFSPPIETPGFGER	LARQL	3	C8:+57.021,C9:+57.021,C20:+57.021	1404.990331	4211.947593	0.001591523	4	N	114	151
A2AL36	Parental	GAGTK	GGIENVLEEIAELR	HAVSA	2		771.4126416	1540.809683	0.000451244	4	N	1108	1122
A2AL36	Parental	EALKK	DLEGVISGLQEYLGTIK	GQATQ	2		917.9939959	1833.972392	0.000622848	1	N	613	630
A2AN08	Exosome	NLLCK	VNEAAPEKPQEDSGTAGGISSTSASVNR	YILQL	3		920.4413187	2758.300556	0.000451244	6	N	3763	3791
A2AN08	Exosome	RVYEK	LITGCYNILANHADPNSGLDESILEECLQYLEK	QLESS	3	C5:+57.021,C27:+57.021	1264.941571	3791.801314	0.000451244	11	N	1352	1385
A2AN08	Exosome	SEITK	NLLPATLQLIDTYASFTR	AYLLQ	2		1019.054919	2036.094238	0.000451244	1	N	1155	1173
A2AN08	Exosome	IQENR	QLLQLLTTYIVR	ENSQV	2		730.9459233	1459.876247	0.000622848	1	N	1488	1500
A2AN08	Exosome	AQVIR	TLLPLLLESSTESAAEISSNSLER	ILGPA	3		854.1171133	2559.32794	0.000451244	1	N	1311	1335
A2AN08	Exosome	ATVSR	STLEVLQLFPINIK	SSNGG	2		807.9774205	1613.939241	0.001871652	2	N	2136	2150
A2AN08	Exosome	KSGSK	SSICESSSLISSATAAALLSSGAVDYCLHVLK	SLLEY	3	C4:+57.021,C27:+57.021	1099.883105	3296.625916	0.001463592	1	N	3068	3100
A2AN08	Parental	RVYEK	LITGCYNILANHADPNSGLDESILEECLQYLEK	QLESS	3	C5:+57.021,C27:+57.021	1264.941571	3791.801314	0.000451244	21	N	1352	1385
A2AN08	Parental	SEITK	NLLPATLQLIDTYASFTR	AYLLQ	2		1019.054919	2036.094238	0.000451244	5	N	1155	1173
A2AN08	Parental	GSTLR	TSPADHGGSVGSESGGSAVDSVAGEHSVSGR	SSAYG	3		947.4279607	2839.260482	0.000451244	2	N	2880	2911
A2AN08	Parental	IGSWR	NAFANDTIPSESYISAVQAAHLGTLCGQSLPLAASLK	HTLLS	3	C26:+57.021	1272.647642	3814.919525	0.001264573	2	N	1247	1284
A2AN08	Parental	PVETF	SEFLDAAGLLSEITDPESFLK	DLLNS	2		1141.576078	2281.136557	0.000451244	9	N	5152	5173
A2AN08	Parental	QRIQR	LIDSVPLTNLLLTLLSTSYR	KACVL	2		1116.646641	2231.277682	0.000451244	1	N	523	543
A2AN08	Parental	ATVSR	STLEVLQLFPINIK	SSNGG	2		807.9774205	1613.939241	0.001654178	1	N	2136	2150
A2AN08	Parental	KSGSK	SSICESSSLISSATAAALLSSGAVDYCLHVLK	SLLEY	3	C4:+57.021,C27:+57.021	1099.883105	3296.625916	0.002663018	1	N	3068	3100
A2AN08	Parental	LMIEF	ADFYENYQASTETLQCPR	CSASV	2	C16:+57.021	1096.981591	2191.947582	0.000637154	1	N	3641	3659
A2AN08	Parental	VYRMR	GLLGDATEEFIESLDSTTDEEEDEEEVYR	MAGVM	3		1107.483243	3319.42633	0.001463592	1	N	4442	4471
A2AQ07	Exosome	QIGAK	FWEVIGEEHGIDCAGSYCGTSALQLER	ISVYY	3	C13:+57.021,C18:+57.021	1028.799264	3083.374392	0.000451244	35	N	19	46
A2AQ07	Exosome	SIQTR	NSNCFVEWIPNNVK	VAVCD	2	C4:+57.021	860.9095119	1719.803424	0.000451244	23	N	336	350
A2AQ07	Exosome	IRSSR	LGVLFQPDSFVHGNSGAGNNWAK	GHYTE	2		1208.09617	2414.176739	0.000622848	2	N	80	103
A2AQ07	Exosome	IRSSR	LGVLFQPDSFVHGNSGAGNNWAK	GHYTE	3		805.7333798	2414.176739	0.000451244	17	N	80	103
A2AQ07	Exosome	PRRGR	YLTVACIFR	GKMST	2	C6:+57.021	571.805267	1141.594934	0.001591523	8	N	309	318
A2AQ07	Exosome	DIPPR	GLNMAATFLGNNTAIQELFTR	VSEHF	3		761.3919665	2281.1525	0.001329271	1	N	359	380
A2AQ07	Parental	QIGAK	FWEVIGEEHGIDCAGSYCGTSALQLER	ISVYY	3	C13:+57.021,C18:+57.021	1028.799264	3083.374392	0.000451244	32	N	19	46
A2AQ07	Parental	EYPDR	ILNSFSVMPSPK	VSDTV	2	M8:+15.995	668.353053	1334.690506	0.000451244	28	N	162	174
A2AQ07	Parental	SIQTR	NSNCFVEWIPNNVK	VAVCD	2	C4:+57.021	860.9095119	1719.803424	0.000451244	12	N	336	350
A2AQ07	Parental	IRSSR	LGVLFQPDSFVHGNSGAGNNWAK	GHYTE	2		1208.09617	2414.176739	0.000451244	4	N	80	103
A2AQ07	Parental	IRSSR	LGVLFQPDSFVHGNSGAGNNWAK	GHYTE	3		805.7333798	2414.176739	0.000451244	11	N	80	103

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A2AQ07	Parental	KMSTK	EVDQQLLSIQTR	NSNCF	2		715.3864268	1428.757254	0.000451244	5	N	324	336
A2AQ07	Parental	SQQYR	ALSVAELTQQMFDAR	NIMAA	2		840.4252267	1678.834853	0.000451244	3	N	282	297
A2AQ07	Parental	NNWAK	GHYTEGAELIENVMDVVRR	ESESC	3		730.0325497	2187.074249	0.000451244	2	N	103	122
A2AQ07	Parental	TTSLR	FPGQLNADLRK	LAVNM	3		420.2354554	1257.682966	0.001162105	3	Y	241	252
A2AQ07	Parental	-MR	EIVHIQIGQCGNQIGAK	FWEVI	2	C10:+57.021	932.9888249	1863.96205	0.000662267	1	N	2	19
A2AQ07	Parental	TTSLR	FPGQLNADLR	KLAVN	2		565.8018016	1129.588003	0.000451244	5	Y	241	251
A2AQ07	Parental	DIPPR	GLNMAATFLGNNTAIQELFTR	VSEHF	2		1141.58405	2281.1525	0.000735798	2	N	359	380
A2AQ07	Parental	DIPPR	GLNMAATFLGNNTAIQELFTR	VSEHF	3		761.3919665	2281.1525	0.000451244	1	N	359	380
A2AQ07	Parental	DVVRR	ESESCDCLQGFQIVHSLG	GGTGS	2	C5:+57.021,C7:+57.021	1033.451381	2064.887161	0.002212458	1	N	122	140
A2ASS6	Exosome	KTSFR	VENLTEGAIYYFR	VMAEN	2		787.8966274	1573.777655	0.001352548	2	N	25964	25977
A2ASS6	Exosome	PALKK	GSGEEEEIDIMELLK	NVDPK	3		564.6068435	1690.79713	0.001463592	1	N	9457	9472
A2ASS6	Parental	KDSVH	LTWEPPDDDGGSPLTGYVVEKR	DMSRK	4		608.5503792	2430.170317	0.002212458	1	N	15294	15316
A2AUR7	Exosome	KQVFK	AENNPWVTPIADQFQLGVSHVFEYIR	SETYK	3		1010.842318	3029.503553	0.000451244	26	N	195	221
A2AUR7	Exosome	VAELK	NLEVLNFFNNQIEELPTQISSLQK	LKHLN	2		1409.735236	2817.454872	0.000451244	11	N	46	70
A2AUR7	Exosome	VAELK	NLEVLNFFNNQIEELPTQISSLQK	LKHLN	3		940.1594239	2817.454872	0.000451244	23	N	46	70
A2AUR7	Exosome	NTLPR	GFGSLPALEVLDLTYNNLNEHSLPGNFFYLTTLR	ALYLS	3		1275.988258	3824.941375	0.000451244	14	N	86	120
A2AUR7	Exosome	IQGNR	LTVLPPELGNLDLTGQK	QVFKA	2		904.5123558	1807.009112	0.000735798	4	N	174	191
A2AUR7	Exosome	LTTLR	ALYLSDNDFEILPPDIGK	LTKLQ	2		1010.517835	2019.02007	0.001162105	2	N	120	138
A2AUR7	Parental	KQVFK	AENNPWVTPIADQFQLGVSHVFEYIR	SETYK	3		1010.842318	3029.503553	0.000451244	31	N	195	221
A2AUR7	Parental	VAELK	NLEVLNFFNNQIEELPTQISSLQK	LKHLN	2		1409.735236	2817.454872	0.000451244	18	N	46	70
A2AUR7	Parental	VAELK	NLEVLNFFNNQIEELPTQISSLQK	LKHLN	3		940.1594239	2817.454872	0.000451244	23	N	46	70
A2AUR7	Parental	NTLPR	GFGSLPALEVLDLTYNNLNEHSLPGNFFYLTTLR	ALYLS	3		1275.988258	3824.941375	0.000451244	21	N	86	120
A2AUR7	Parental	NTLPR	GFGSLPALEVLDLTYNNLNEHSLPGNFFYLTTLR	ALYLS	4		957.2431436	3824.941375	0.000998612	1	N	86	120
A2AUR7	Parental	IQGNR	LTVLPPELGNLDLTGQK	QVFKA	2		904.5123558	1807.009112	0.000451244	5	N	174	191
A2AUR7	Parental	VLNFF	NNQIEELPTQISSLQK	LKHLN	2		921.4843266	1840.953053	0.001162105	2	N	54	70
A2AUR7	Parental	LTGQK	QVFKAENNPWVTPIADQFQLGVSHVFEYIR	SETYK	3		1178.272441	3531.793922	0.000451244	6	N	191	221
A2AUR7	Parental	KQVFK	AENNPWVTPIADQFQLGVSHVFEYIRSETY	KYLYG	3		1170.904194	3509.689182	0.000451244	5	N	195	225
A2AUR7	Parental	ISLPK	EIGELTQLKELHIQGNR	LTVLP	3		660.0292451	1977.064335	0.000851441	1	N	157	174
A2AUR7	Parental	GKLTK	LQILSLRDNDLISLPK	EIGEL	3		613.3635651	1837.067295	0.000823681	2	N	141	157
A2AUR7	Parental	LTTLR	ALYLSDNDFEILPPDIGKLTK	LQILS	2		1181.631188	2361.246776	0.001943752	1	N	120	141
A3KGV1	Parental	GYERK	NIDLTAIISDLR	SRIEH	2		672.3806131	1342.745626	0.000823681	7	N	623	635
A3KGV1	Parental	ITEAK	LAECQDQLQGYER	KNIDL	2	C4:+57.021	805.3676768	1608.719754	0.000451244	3	N	609	622
A6H630	Exosome	IRTLK	CELQVGLQPGQAEQLTASDPHWLTTGR	YGILQ	3	C1:+57.021	998.1579344	2991.450403	0.000451244	9	N	402	429
A6H630	Exosome	SSSQK	ANIINCLQDLKPFILINDTESLWALLSK	LKKTV	3	C6:+57.021	1081.588336	3241.741607	0.000823681	4	N	206	234
A6H630	Exosome	PLVDK	CVDTHIWNQYLEYQR	SLLNE	2	[0:-17.027,C1:+57.021	1004.454589	2006.893579	0.000451244	7	N	81	96
A6X935	Exosome	RQTEK	FEVSVNVAPGSKITFELIYQE	LLQRR	3		790.746292	2369.215476	0.001162105	2	N	127	148
A6X935	Exosome	ASRIR	AHGGTNINNAVLLAVELLDR	SNQAE	3		697.3837994	2089.127998	0.000451244	20	N	345	365
A6X935	Exosome	LLPSK	SVSLIILLTDGDPTVGETNPTIIQNNVR	EAING	3		993.8719427	2978.592428	0.000451244	7	N	375	403
A6X935	Exosome	VKILK	DLSPQDQFNLIEFSGEANQWK	QSLVQ	2		1233.582758	2465.149916	0.000451244	17	N	302	323
A6X935	Exosome	VKILK	DLSPQDQFNLIEFSGEANQWK	QSLVQ	3		822.7244385	2465.149916	0.001763695	1	N	302	323
A6X935	Exosome	APGSK	ITFELIYQELLQR	RLGMY	2		833.4646772	1664.913754	0.000451244	9	N	139	152
A6X935	Exosome	APGSK	ITFELIYQELLQR	RLGMY	3		555.9790515	1664.913754	0.000622848	2	N	139	152
A6X935	Exosome	SQQQK	SQSEQDTVLNGDFIVR	YDVNR	2		904.4452014	1806.874803	0.000451244	11	N	224	240
A6X935	Exosome	EALVK	ILKDLSPQDQFNLIEFSGEANQWK	QSLVQ	3		940.8121356	2819.413007	0.001162105	3	N	299	323
A6X935	Parental	RQTEK	FEVSVNVAPGSKITFELIYQE	LLQRR	3		790.746292	2369.215476	0.000823681	1	N	127	148
A6X935	Parental	VKILK	DLSPQDQFNLIEFSGEANQWK	QSLVQ	2		1233.582758	2465.149916	0.000451244	2	N	302	323
A6ZI44	Exosome	VAPGK	GILAADESTGSIAKR	LQSIG	2		744.9049838	1487.794368	0.000451244	32	N	82	97
A6ZI44	Exosome	VAPGK	GILAADESTGSIAKR	LQSIG	3		496.9392558	1487.794368	0.001162105	4	N	82	97
A6ZI44	Exosome	TLYQK	ADDGRPFPQVIK	SKGGV	2		671.8598479	1341.704096	0.000451244	65	Y	141	153
A6ZI44	Exosome	TLYQK	ADDGRPFPQVIK	SKGGV	3		448.2424986	1341.704096	0.000451244	97	Y	141	153
A6ZI44	Exosome	VAPGK	GILAADESTGSIAK	RLQSI	2		666.8544282	1331.693256	0.000451244	19	N	82	96
A6ZI44	Exosome	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1307.670093	2613.324586	0.000451244	48	Y	162	188
A6ZI44	Exosome	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	3		872.1159953	2613.324586	0.000451244	195	Y	162	188
A6ZI44	Exosome	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1136.574933	2271.134266	0.000451244	244	Y	165	188
A6ZI44	Exosome	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	3		758.0525552	2271.134266	0.000451244	75	Y	165	188
A6ZI44	Exosome	ACQGK	YTPSGQSGAAASESLFISNHAY	-	2		1129.522169	2257.028738	0.000451244	105	N	396	418
A6ZI44	Exosome	ACQGK	YTPSGQSGAAASESLFISNHAY	-	3		753.3507125	2257.028738	0.000451244	37	N	396	418
A6ZI44	Exosome	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLKR	CQYVT	3	C5:+57.021	1059.540044	3175.596733	0.000451244	147	N	227	255
A6ZI44	Exosome	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLKR	CQYVT	4	C5:+57.021	794.9069833	3175.596733	0.000451244	61	N	227	255
A6ZI44	Exosome	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	2		1054.052385	2106.089171	0.000451244	31	N	207	227
A6ZI44	Exosome	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	3		703.0375236	2106.089171	0.000451244	21	N	207	227
A6ZI44	Exosome	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	2	M12:+15.995	1062.049885	2122.084171	0.000622848	2	N	207	227
A6ZI44	Exosome	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	3	M12:+15.995	708.3691903	2122.084171	0.000451244	9	N	207	227
A6ZI44	Exosome	NAINK	CPLLKPWALTFSYGR	ALQAS	2	C1:+57.021	904.9797402	1807.94388	0.000451244	6	Y	343	358
A6ZI44	Exosome	NAINK	CPLLKPWALTFSYGR	ALQAS	3	C1:+57.021	603.6557601	1807.94388	0.000451244	49	Y	343	358

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	3	C13:+57.021	1038.553625	3112.637476	0.000451244	36	N	114	141
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	4	C13:+57.021	779.167169	3112.637476	0.000451244	46	N	114	141
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	3	Q1:-17.027,C13:+57.021	1032.877959	3095.610476	0.000451244	17	N	114	141
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	3	[0:-17.027,C13:+57.021	1032.877959	3095.610476	0.000451244	22	N	114	141
A6ZI44	Exosome	TALRR	TVPPAVTGVTFLSGGQSEEEASINLNAINK	CPLLK	3		1015.191452	3042.550957	0.000451244	1238	N	313	343
A6ZI44	Exosome	TALRR	TVPPAVTGVTFLSGGQSEEEASINLNAINK	CPLLK	4		761.6455393	3042.550957	0.000451244	27	N	313	343
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	2	C13:+57.021	1107.601479	2213.187359	0.000451244	26	Y	114	134
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	3	C13:+57.021	738.7369195	2213.187359	0.001229886	3	Y	114	134
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	2	Q1:-17.027,C13:+57.021	1099.087979	2196.160359	0.000451244	4	Y	114	134
A6ZI44	Exosome	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	3	Q1:-17.027,C13:+57.021	733.0612529	2196.160359	0.000451244	1	Y	114	134
A6ZI44	Exosome	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLK	RCQYV	3	C5:+57.021	1007.506341	3019.495622	0.000451244	34	N	227	254
A6ZI44	Exosome	ATGTM	PHPYPALTPEQK	KELSD	3		459.9107489	1376.708847	0.000979378	3	N	55	67
A6ZI44	Exosome	TADDR	VNPCIGGVILFHETLYQK	ADDGR	2	C4:+57.021	1044.551258	2087.086916	0.000451244	23	N	123	141
A6ZI44	Exosome	TADDR	VNPCIGGVILFHETLYQK	ADDGR	3	C4:+57.021	696.7034387	2087.086916	0.001591523	2	N	123	141
A6ZI44	Exosome	ACTQK	FSNEEIAMATVTALR	RTVPP	2		826.9197771	1651.823954	0.000451244	23	Y	297	312
A6ZI44	Exosome	ACTQK	FSNEEIAMATVTALR	RTVPP	2	M8:+15.995	834.9172771	1667.818954	0.000451244	15	Y	297	312
A6ZI44	Exosome	NAINK	CPLLKPWALTF	SYGRA	2	C1:+57.021	673.3707742	1344.725948	0.000451244	11	Y	343	354
A6ZI44	Exosome	FSFPP	VASEQPHSELGNTQQQTELGK	ESTAT	3		761.0405381	2280.098214	0.000979378	4	N	26	47
A6ZI44	Exosome	VTALR	RTVPPAVTGVTFLSGGQSEEEASINLNAINK	CPLLK	3		1067.225156	3198.652068	0.000451244	28	N	312	343
A6ZI44	Exosome	TADDR	VNPCIGGVILF	HETLY	2	C4:+57.021	594.8261995	1187.636799	0.001591523	4	Y	123	134
A6ZI44	Exosome	DDRVN	PCIGGVILFHETLYQK	ADDGR	3	C2:+57.021	625.6663249	1873.975575	0.000637154	4	N	125	141
A6ZI44	Exosome	INKCP	LLKPWALTFSYGR	ALQAS	3		517.9614436	1550.860931	0.001591523	1	Y	345	358
A6ZI44	Exosome	TGVTF	LSGGQSEEEASINLNAINK	CPLLK	2		987.49288	1972.97016	0.000451244	11	Y	324	343
A6ZI44	Exosome	QNGIV	PIVEPEILPDGDHDLKR	CQYVT	2		972.015794	1942.015988	0.000823681	2	N	238	255
A6ZI44	Exosome	QNGIV	PIVEPEILPDGDHDLKR	CQYVT	3		648.3464626	1942.015988	0.001699387	1	N	238	255
A6ZI44	Exosome	GVVPL	AGTNGETTTQGLDGLSER	CAQYK	2		903.9273729	1805.839146	0.002296037	1	Y	170	188
A6ZI44	Exosome	ACQGK	YTPSGQSGAAASESLF	ISNHA	2		786.8629815	1571.710363	0.001162105	6	N	396	412
A6ZI44	Exosome	ACTQK	FSNEEIAMATVTALRR	TVPPA	3		603.6494885	1807.925065	0.000451244	6	Y	297	313
A6ZI44	Exosome	AVTGV	TFLSGGQSEEEASINLNAINK	CPLLK	2		1111.550926	2221.086253	0.000622848	4	Y	322	343
A6ZI44	Exosome	AAVYK	ALSDHHVYLEGTLLKPNMVTPGHACTQK	FSNEE	3	C25:+57.021	1039.858832	3116.553095	0.000451244	1	Y	269	297
A6ZI44	Exosome	YASIC	QQNGIVPIVEPEILPDGDHDLKR	CQYVT	3		861.4578042	2581.350013	0.001591523	1	N	232	255
A6ZI44	Exosome	YASIC	QQNGIVPIVEPEILPDGDHDLKR	CQYVT	4		646.3453031	2581.350013	0.000823681	3	N	232	255
A6ZI44	Exosome	ACQGK	YTPSGQSGAAASESL	FISNH	2		713.3287745	1424.641949	0.000451244	2	N	396	411
A6ZI44	Exosome	NAINK	CPLLKPWALTFSY	GRALQ	2	C1:+57.021	798.4184528	1594.821306	0.002374549	1	Y	343	356
A6ZI44	Parental	VAPGK	GILAADESTGSIAKR	LQSIG	2		744.9049838	1487.794368	0.000451244	24	N	82	97
A6ZI44	Parental	VAPGK	GILAADESTGSIAKR	LQSIG	3		496.9392558	1487.794368	0.000979378	3	N	82	97
A6ZI44	Parental	TLYQK	ADDGRPFPQVIK	SKGGV	2		671.8598479	1341.704096	0.000451244	10	Y	141	153
A6ZI44	Parental	TLYQK	ADDGRPFPQVIK	SKGGV	3		448.2424986	1341.704096	0.000451244	26	Y	141	153
A6ZI44	Parental	VAPGK	GILAADESTGSIAK	RLQSI	2		666.8544282	1331.693256	0.000451244	24	N	82	96
A6ZI44	Parental	DIAHR	IVAPGKGILAADESTGSIAK	RLQSI	2		949.5338196	1897.052039	0.000451244	5	N	76	96
A6ZI44	Parental	DIAHR	IVAPGKGILAADESTGSIAK	RLQSI	3		633.3584797	1897.052039	0.000451244	9	N	76	96
A6ZI44	Parental	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1307.670093	2613.324586	0.000451244	27	Y	162	188
A6ZI44	Parental	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	3		872.1159953	2613.324586	0.000451244	47	Y	162	188
A6ZI44	Parental	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1136.574933	2271.134266	0.000451244	163	Y	165	188
A6ZI44	Parental	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	3		758.0525552	2271.134266	0.000451244	21	Y	165	188
A6ZI44	Parental	ACQGK	YTPSGQSGAAASESLFISNHAY	-	2		1129.522169	2257.028738	0.000451244	71	N	396	418
A6ZI44	Parental	ACQGK	YTPSGQSGAAASESLFISNHAY	-	3		753.3507125	2257.028738	0.000451244	8	N	396	418
A6ZI44	Parental	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLKR	CQYVT	3	C5:+57.021	1059.540044	3175.596733	0.000451244	105	N	227	255
A6ZI44	Parental	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLKR	CQYVT	4	C5:+57.021	794.9069833	3175.596733	0.000451244	22	N	227	255
A6ZI44	Parental	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	2		1054.052385	2106.089171	0.000451244	9	N	207	227
A6ZI44	Parental	RCVLK	IGEHTPSALAIMENANVLAR	YASIC	3		703.0375236	2106.089171	0.000451244	10	N	207	227
A6ZI44	Parental	NAINK	CPLLKPWALTFSYGR	ALQAS	3	C1:+57.021	603.6557601	1807.94388	0.000451244	21	Y	343	358
A6ZI44	Parental	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	3	C13:+57.021	1038.553625	3112.637476	0.000451244	4	N	114	141
A6ZI44	Parental	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	3	Q1:-17.027,C13:+57.021	1032.877959	3095.610476	0.001162105	2	N	114	141
A6ZI44	Parental	RRFYR	QLLLTADDRVNPCIGGVILFHETLYQK	ADDGR	3	[0:-17.027,C13:+57.021	1032.877959	3095.610476	0.001264573	3	N	114	141
A6ZI44	Parental	TALRR	TVPPAVTGVTFLSGGQSEEEASINLNAINK	CPLLK	3		1015.191452	3042.550957	0.000451244	164	N	313	343
A6ZI44	Parental	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	2	C13:+57.021	1107.601479	2213.187359	0.000662267	14	Y	114	134
A6ZI44	Parental	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	3	C13:+57.021	738.7369195	2213.187359	0.002212458	2	Y	114	134
A6ZI44	Parental	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	2	Q1:-17.027,C13:+57.021	1099.087979	2196.160359	0.000451244	8	Y	114	134
A6ZI44	Parental	RRFYR	QLLLTADDRVNPCIGGVILF	HETLY	3	Q1:-17.027,C13:+57.021	733.0612529	2196.160359	0.000451244	2	Y	114	134
A6ZI44	Parental	NVLAR	YASICQQNGIVPIVEPEILPDGDHDLK	RCQYV	3	C5:+57.021	1007.506341	3019.495622	0.000451244	26	N	227	254
A6ZI44	Parental	NAINK	CPLLKPWALTF	SYGRA	2	C1:+57.021	673.3707742	1344.725948	0.000451244	4	Y	343	354
A6ZI44	Parental	TGVTF	LSGGQSEEEASINLNAINK	CPLLK	2		987.49288	1972.97016	0.000451244	32	Y	324	343
A6ZI44	Parental	TGVTF	LSGGQSEEEASINLNAINKCPLLKPWALTFSYGR	ALQAS	3	C20:+57.021	1255.30896	3762.90348	0.000823681	1	Y	324	358
A6ZI44	Parental	GVVPL	AGTNGETTTQGLDGLSER	CAQYK	2		903.9273729	1805.839146	0.000451244	2	Y	170	188

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
A6ZI44	Parental	ACQGK	YTPSGQSGAAASESLF	ISNHA	2		786.8629815	1571.710363	0.000823681	11	N	396	412
A6ZI44	Parental	NAINK	CPLLKPWALTFSY	GRALQ	2	C1:+57.021	798.4184528	1594.821306	0.001839721	2	Y	343	356
A6ZI44	Parental	SIAKR	LQSIGTENTEENRR	FYRQL	3		549.6084574	1645.801972	0.002727428	1	Y	97	111
A6ZI46	Exosome	TLYEK	ADDGRPFPQVIK	SKGGV	2		671.8598479	1341.704096	0.000451244	65	Y	142	154
A6ZI46	Exosome	TLYEK	ADDGRPFPQVIK	SKGGV	3		448.2424986	1341.704096	0.000451244	97	Y	142	154
A6ZI46	Exosome	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1307.670093	2613.324586	0.000451244	48	Y	163	189
A6ZI46	Exosome	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	3		872.1159953	2613.324586	0.000451244	195	Y	163	189
A6ZI46	Exosome	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1136.574933	2271.134266	0.000451244	244	Y	166	189
A6ZI46	Exosome	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	3		758.0525552	2271.134266	0.000451244	75	Y	166	189
A6ZI46	Exosome	NAINK	CPLLKPWALTFSYGR	ALQAS	2	C1:+57.021	904.9797402	1807.94388	0.000451244	6	Y	344	359
A6ZI46	Exosome	NAINK	CPLLKPWALTFSYGR	ALQAS	3	C1:+57.021	603.6557601	1807.94388	0.000451244	49	Y	344	359
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	2	C13:+57.021	1107.601479	2213.187359	0.000451244	26	Y	115	135
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	3	C13:+57.021	738.7369195	2213.187359	0.001229886	3	Y	115	135
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	2	Q1:-17.027,C13:+57.021	1099.087979	2196.160359	0.000451244	4	Y	115	135
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	3	Q1:-17.027,C13:+57.021	733.0612529	2196.160359	0.000451244	1	Y	115	135
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	3	C13:+57.021	1038.88163	3113.621491	0.000451244	16	N	115	142
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	4	C13:+57.021	779.4131729	3113.621491	0.001352548	6	N	115	142
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	3	Q1:-17.027,C13:+57.021	1033.205964	3096.594491	0.001871652	4	N	115	142
A6ZI46	Exosome	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	3	[0:-17.027,C13:+57.021	1033.205964	3096.594491	0.000451244	10	N	115	142
A6ZI46	Exosome	ACTQK	FSNEEIAMATVTALR	RTVPP	2		826.9197771	1651.823954	0.000451244	23	Y	298	313
A6ZI46	Exosome	ACTQK	FSNEEIAMATVTALR	RTVPP	2	M8:+15.995	834.9172771	1667.818954	0.000451244	15	Y	298	313
A6ZI46	Exosome	NAINK	CPLLKPWALTF	SYGRA	2	C1:+57.021	673.3707742	1344.725948	0.000451244	11	Y	344	355
A6ZI46	Exosome	TADDR	VNPCIGGVILFHETLYEK	ADDGR	2	C4:+57.021	1045.043266	2088.070932	0.000451244	4	N	124	142
A6ZI46	Exosome	TADDR	VNPCIGGVILF	HETLY	2	C4:+57.021	594.8261995	1187.636799	0.001591523	4	Y	124	135
A6ZI46	Exosome	INKCP	LLKPWALTFSYGR	ALQAS	3		517.9614436	1550.860931	0.001591523	1	Y	346	359
A6ZI46	Exosome	PGVTF	LSGGQSEEEASINLNAINK	CPLLK	2		987.49288	1972.97016	0.000451244	11	Y	325	344
A6ZI46	Exosome	GVVPL	AGTNGETTTQGLDGLSER	CAQYK	2		903.9273729	1805.839146	0.002296037	1	Y	171	189
A6ZI46	Exosome	ACTQK	FSNEEIAMATVTALRR	TVPPA	3		603.6494885	1807.925065	0.000451244	6	Y	298	314
A6ZI46	Exosome	AVPGV	TFLSGGQSEEEASINLNAINK	CPLLK	2		1111.550926	2221.086253	0.000622848	4	Y	323	344
A6ZI46	Exosome	AAVYK	ALSDHHVYLEGTLLKPNMVTPGHACTQK	FSNEE	3	C25:+57.021	1039.858832	3116.553095	0.000451244	1	Y	270	298
A6ZI46	Exosome	NAINK	CPLLKPWALTFSY	GRALQ	2	C1:+57.021	798.4184528	1594.821306	0.002374549	1	Y	344	357
A6ZI46	Parental	TLYEK	ADDGRPFPQVIK	SKGGV	2		671.8598479	1341.704096	0.000451244	10	Y	142	154
A6ZI46	Parental	TLYEK	ADDGRPFPQVIK	SKGGV	3		448.2424986	1341.704096	0.000451244	26	Y	142	154
A6ZI46	Parental	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1307.670093	2613.324586	0.000451244	27	Y	163	189
A6ZI46	Parental	VVGIK	VDKGVVPLAGTNGETTTQGLDGLSER	CAQYK	3		872.1159953	2613.324586	0.000451244	47	Y	163	189
A6ZI46	Parental	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	2		1136.574933	2271.134266	0.000451244	163	Y	166	189
A6ZI46	Parental	IKVDK	GVVPLAGTNGETTTQGLDGLSER	CAQYK	3		758.0525552	2271.134266	0.000451244	21	Y	166	189
A6ZI46	Parental	NAINK	CPLLKPWALTFSYGR	ALQAS	3	C1:+57.021	603.6557601	1807.94388	0.000451244	21	Y	344	359
A6ZI46	Parental	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	2	C13:+57.021	1107.601479	2213.187359	0.000662267	14	Y	115	135
A6ZI46	Parental	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	3	C13:+57.021	738.7369195	2213.187359	0.002212458	2	Y	115	135
A6ZI46	Parental	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	2	Q1:-17.027,C13:+57.021	1099.087979	2196.160359	0.000451244	8	Y	115	135
A6ZI46	Parental	RRFFR	QLLLTADDRVNPCIGGVILF	HETLY	3	Q1:-17.027,C13:+57.021	733.0612529	2196.160359	0.000451244	2	Y	115	135
A6ZI46	Parental	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	3	C13:+57.021	1038.88163	3113.621491	0.000823681	1	N	115	142
A6ZI46	Parental	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	4	C13:+57.021	779.4131729	3113.621491	0.002884417	1	N	115	142
A6ZI46	Parental	RRFFR	QLLLTADDRVNPCIGGVILFHETLYEK	ADDGR	3	[0:-17.027,C13:+57.021	1033.205964	3096.594491	0.001329271	1	N	115	142
A6ZI46	Parental	NAINK	CPLLKPWALTF	SYGRA	2	C1:+57.021	673.3707742	1344.725948	0.000451244	4	Y	344	355
A6ZI46	Parental	PGVTF	LSGGQSEEEASINLNAINK	CPLLK	2		987.49288	1972.97016	0.000451244	32	Y	325	344
A6ZI46	Parental	PGVTF	LSGGQSEEEASINLNAINKCPLLKPWALTFSYGR	ALQAS	3	C20:+57.021	1255.30896	3762.90348	0.000823681	1	Y	325	359
A6ZI46	Parental	GVVPL	AGTNGETTTQGLDGLSER	CAQYK	2		903.9273729	1805.839146	0.000451244	2	Y	171	189
A6ZI46	Parental	NAINK	CPLLKPWALTFSY	GRALQ	2	C1:+57.021	798.4184528	1594.821306	0.001839721	2	Y	344	357
A6ZI46	Parental	SMGNR	LQSIGTENTEENRR	FFRQL	3		549.6084574	1645.801972	0.002727428	1	Y	98	112
A8E0Y8	Exosome	TFSLK	IFSVGPEDVGTYSCEVAEVAR	TQMGS	2	C14:+57.021	1143.041649	2284.067697	0.001943752	2	N	363	384
A8E0Y8	Exosome	LSVGK	LQPSDQGQVFCEATEWIQDPDETWTLITR	KQTDQ	3	C11:+57.021	1155.208912	3462.603335	0.002663018	1	N	238	267
A8E0Y8	Parental	VSLSK	DFVLTPGSSYADR	FVAGD	2		714.3442276	1426.672855	0.002145581	1	N	203	216
A8E0Y8	Parental	TFSLK	IFSVGPEDVGTYSCEVAEVAR	TQMGS	2	C14:+57.021	1143.041649	2284.067697	0.000823681	1	N	363	384
B1AUY2	Exosome	GDLEK	FIQSSGQPVPLVVESCIR	FINLN	2	C16:+57.021	1008.533065	2015.050531	0.001871652	2	N	522	540
B1AUY2	Parental	KRSGR	SALSTTTTTSATTTTTTTTVETGPHR	KSSLK	3		875.7670317	2624.277695	0.000622848	3	N	199	225
B1AUY2	Parental	GDLEK	FIQSSGQPVPLVVESCIR	FINLN	2	C16:+57.021	1008.533065	2015.050531	0.000622848	1	N	522	540
B1AUY2	Parental	VKKSK	DLVQQLQAELLEVVSELQTTK	KMYHV	3		795.4360061	2383.284618	0.000622848	5	N	148	169
B1AUY2	Parental	RQQSR	ESAALSEVLAGPLAQR	LSHIS	2		806.4391908	1610.862782	0.000979378	1	N	116	132
B1AUY2	Parental	KATLK	ALLEAVASEDGDILDSLQASPSTESLK	STSSD	2		1380.195806	2758.376012	0.000451244	1	N	399	426
B1AVH7	Parental	LYYSR	TAQDANPLDSIDLSSAVFDCK	ADAEE	2	C20:+57.021	1134.028738	2266.041876	0.000622848	3	N	80	101
B1AVH7	Parental	KLTQK	LTEDLAQPADATNGDFLSQQER	MEHLK	2		1210.072754	2418.129908	0.000451244	1	N	427	449
B1AVH7	Parental	TLHLK	LEQEEAELEEFLCPVK	TPTGL	2	C13:+57.021	981.9721719	1961.928744	0.000451244	1	N	168	184
B1AZI6	Exosome	CIFPR	CIFSAIDAVYCAR	FVELV	2	C1:+57.021,C11:+57.021	773.3631202	1544.71064	0.001871652	1	N	985	998

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
B1AZI6	Exosome	LCYDR	VFSDIIYTVASCTENEASR	YGRFL	2	C12:+57.021	1081.507442	2160.999283	0.000451244	3	N	1019	1038
B1AZI6	Parental	VDSLK	YLTSLNYDVLAYCIIEALANPEKER	MKHDD	3	C13:+57.021	986.8357983	2957.483995	0.002212458	1	N	602	627
B2RPV6	Exosome	TVTRR	ELQNLIGAINQLNVLTK	ELTKR	2		941.0443545	1880.073109	0.000823681	1	N	659	676
B2RPV6	Exosome	TVTRR	ELQNLIGAINQLNVLTK	ELTKR	3		627.6988363	1880.073109	0.000622848	4	N	659	676
B2RPV6	Exosome	QSSQK	SLTELVESIVEIK	TQAAL	2		730.4168613	1458.818123	0.000451244	8	N	943	956
B2RPV6	Parental	TVTRR	ELQNLIGAINQLNVLTK	ELTKR	2		941.0443545	1880.073109	0.001264573	1	N	659	676
B2RPV6	Parental	TVTRR	ELQNLIGAINQLNVLTK	ELTKR	3		627.6988363	1880.073109	0.000451244	10	N	659	676
B2RPV6	Parental	QSSQK	SLTELVESIVEIK	TQAAL	2		730.4168613	1458.818123	0.000451244	8	N	943	956
B2RPV6	Parental	QSSQK	SLTELVESIVEIK	TQAAL	3		487.2805076	1458.818123	0.000870037	2	N	943	956
B2RQC6	Exosome	DPSYK	AQILVLTYPLIGNYGIPSDEEDEFGLSK	WFESS	3		1027.860932	3080.559397	0.000451244	2	N	46	74
B2RQC6	Exosome	LPELR	NSVTGGTAAFEPSLDYCVVK	IPRWD	2	C17:+57.021	1058.007077	2113.998555	0.000451244	5	N	719	739
B2RQC6	Exosome	CPAVK	QIDTVAAEWPAQTNYLYLTYWGNTHDLDFR	APHVL	3		1201.239465	3600.694996	0.000823681	1	N	901	931
B2RQC6	Exosome	RQQCR	VLGTSPEAIDSAENR	FKFSR	2		779.8895307	1557.763461	0.000451244	2	N	1033	1048
B2RQC6	Exosome	FKFSR	LLDTIGISQPQWR	ELSDL	2		763.9204368	1525.825274	0.000451244	4	N	1053	1066
B2RQC6	Exosome	VSEGR	LSLDDLLQR	LHHNP	2		536.8040099	1071.59242	0.001229886	3	N	1722	1731
B2RQC6	Exosome	HPMPR	VNEISVEVDSDPR	AAYFR	2		729.8576992	1457.699798	0.000823681	1	N	2187	2200
B2RQC6	Parental	DPSYK	AQILVLTYPLIGNYGIPSDEEDEFGLSK	WFESS	3		1027.860932	3080.559397	0.000622848	2	N	46	74
B2RQC6	Parental	LPELR	NSVTGGTAAFEPSLDYCVVK	IPRWD	2	C17:+57.021	1058.007077	2113.998555	0.000451244	13	N	719	739
B2RQC6	Parental	CPAVK	QIDTVAAEWPAQTNYLYLTYWGNTHDLDFR	APHVL	3		1201.239465	3600.694996	0.001162105	2	N	901	931
B2RQC6	Parental	PVLVR	AAFALGGLGSGFASTKEELSALVAPAFAHTSQVLIDK	SLKGW	4		919.4916902	3673.935561	0.001162105	7	N	555	592
B2RQC6	Parental	RQQCR	VLGTSPEAIDSAENR	FKFSR	2		779.8895307	1557.763461	0.000622848	4	N	1033	1048
B2RQC6	Parental	FKFSR	LLDTIGISQPQWR	ELSDL	2		763.9204368	1525.825274	0.002519933	2	N	1053	1066
B2RQC6	Parental	VSEGR	LSLDDLLQR	LHHNP	2		536.8040099	1071.59242	0.002453667	1	N	1722	1731
B2RQC6	Parental	PFVSK	TLGVDLVALATR	IIMGE	2		614.8671416	1227.718683	0.001395409	1	N	1228	1240
B2RUP2	Parental	GELTK	HSTSAVDLSTCFAQISHTAR	QLDWP	3	C11:+57.021	730.3520163	2188.032649	0.000823681	1	N	624	644
B2RUP2	Parental	MCKMK	AFGELCPDSAPLSQLVSEALR	MGTVE	2	C6:+57.021	1130.567833	2259.120067	0.000451244	14	N	441	462
B2RUP2	Parental	LAYSR	LYQSLEFPSSCLLHPITSIEYQWIQGR	LKAEQ	3	C11:+57.021	1089.216902	3264.627305	0.001162105	2	N	358	385
B2RV77	Exosome	AVEYK	SQVVAGQNYFIK	MDVGG	2		677.3622234	1352.708847	0.000451244	32	N	44	56
B2RV77	Exosome	LSRAR	SATPEIQEIADKVK	SLLEE	2		764.9150171	1527.814434	0.000451244	18	N	10	24
B2RV77	Exosome	LSRAR	SATPEIQEIADKVK	SLLEE	3		510.2792781	1527.814434	0.000451244	7	N	10	24
B2RV77	Exosome	IKVFK	GISGENVLELHGYQTNK	TRKDE	2		929.9688437	1857.922087	0.000451244	8	N	71	88
B2RV77	Exosome	IKVFK	GISGENVLELHGYQTNK	TRKDE	3		620.3151625	1857.922087	0.00091018	5	N	71	88
B2RV77	Parental	AVEYK	SQVVAGQNYFIK	MDVGG	2		677.3622234	1352.708847	0.000451244	42	N	44	56
B2RV77	Parental	LSRAR	SATPEIQEIADKVK	SLLEE	2		764.9150171	1527.814434	0.000451244	42	N	10	24
B2RV77	Parental	LSRAR	SATPEIQEIADKVK	SLLEE	3		510.2792781	1527.814434	0.000451244	18	N	10	24
B2RV77	Parental	HIKVF	KGISGENVLELHGYQTNK	TRKDE	2		994.0163253	1986.017051	0.000451244	5	N	70	88
B2RV77	Parental	HIKVF	KGISGENVLELHGYQTNK	TRKDE	3		663.0134835	1986.017051	0.000451244	11	N	70	88
B2RV77	Parental	IKVFK	GISGENVLELHGYQTNK	TRKDE	2		929.9688437	1857.922087	0.000451244	38	N	71	88
B2RV77	Parental	IKVFK	GISGENVLELHGYQTNK	TRKDE	3		620.3151625	1857.922087	0.000851441	22	N	71	88
B2RV77	Parental	FLHIK	VFKGISGENVLELHGYQTNK	TRKDE	2		1117.084739	2232.153879	0.000451244	2	N	68	88
B2RV77	Parental	NYFIK	MDVGGGCFLHIK	VFKGI	2	C7:+57.021	667.3234986	1332.631397	0.000735798	2	N	56	68
B2RV77	Parental	NYFIK	MDVGGGCFLHIK	VFKGI	3	C7:+57.021	445.2182657	1332.631397	0.000451244	13	N	56	68
B2RV77	Parental	KAVEY	KSQVVAGQNYFIK	MDVGG	2		741.409705	1480.80381	0.000451244	11	N	43	56
B2RV77	Parental	KAVEY	KSQVVAGQNYFIK	MDVGG	3		494.60907	1480.80381	0.000451244	18	N	43	56
B2RV77	Parental	LSRAR	SATPEIQEIADK	VKSLL	2		651.3333286	1300.651057	0.000451244	4	N	10	22
B2RV77	Parental	VFKGI	SGENVLELHGYQTNK	TRKDE	2		844.9160798	1687.81656	0.000451244	16	N	73	88
B2RV77	Parental	ARSAT	PEIQEIADKVK	SLLEE	2		635.3566067	1268.697613	0.002453667	1	N	13	24
B2RXR6	Exosome	MAVLK	LCEQPPLVQAIFSGDPEEIR	MLIHK	2	C2:+57.021	1149.575659	2297.135717	0.000451244	14	N	5	25
B2RXR6	Exosome	DTFGR	TCLHAAAAGGNVECIK	LLQSS	3	C2:+57.021,C14:+57.021	557.9364436	1670.785931	0.000823681	1	N	406	422
B2RXR6	Exosome	NKAVK	CAEVIIPLLSSVNVSDR	GGRTA	2	C1:+39.994	927.9851911	1853.954782	0.000735798	3	N	121	138
B2RXR6	Exosome	NKAVK	CAEVIIPLLSSVNVSDR	GGRTA	2	C1:+57.021	936.4986911	1870.981782	0.001329271	2	N	121	138
B2RXR6	Exosome	KGHEK	CALLILDKIQDESLINAK	NSALQ	3	C1:+57.021	686.3822538	2056.123361	0.000823681	1	N	920	938
B2RXR6	Parental	DCCRK	LLSSGFEIDTPDTFGR	TCLHA	2		877.9339382	1753.852276	0.000451244	2	N	390	406
B2RXR6	Parental	MAVLK	LCEQPPLVQAIFSGDPEEIR	MLIHK	2	C2:+57.021	1149.575659	2297.135717	0.000451244	37	N	5	25
B2RXR6	Parental	FHCIK	ALVTTGANVNETDDWGR	TALHY	2		909.9350009	1817.854402	0.000662267	1	N	455	472
B2RXR6	Parental	GRFTR	SQTLIQNGGEIDCVDKDGNTPLHVAAR	HGHEL	3	C13:+57.021	970.1458059	2907.414018	0.000622848	2	N	321	348
B2RXR6	Parental	NKAVK	CAEVIIPLLSSVNVSDR	GGRTA	2	C1:+39.994	927.9851911	1853.954782	0.000451244	2	N	121	138
B2RXR6	Parental	DCCLK	DNQGYTPLHWACYNGNENCIEVLLEQK	CFRKF	3	C12:+57.021,C19:+57.021	1089.160973	3264.459519	0.000451244	13	N	768	795
B2RXR6	Parental	LAAFK	GHTECVEALVNQGASIFVK	DNVTK	3	C5:+57.021	687.0144529	2058.019959	0.001395409	1	N	610	629
B2RXR6	Parental	TLCLR	LLLETADNPEVVDVK	DAKGQ	2		827.949057	1653.882514	0.000979378	1	N	651	666
B2RY50	Exosome	RDLVR	LHGGLKPLASLLNNTDNK	ERLAA	2		953.0317784	1904.047957	0.000622848	2	N	704	722
B2RY50	Exosome	ELLKR	FSGKGEQTVLESIEYTSDYEFSNGC	RAPPW	3	C25:+57.021	949.7486066	2846.22242	0.00307782	1	N	208	233
B2RY56	Parental	EIRQR	LLAEGHPDPDAELQR	MEQEA	2		830.9186225	1659.821645	0.000823681	2	N	544	559
B2RY56	Parental	EIRQR	LLAEGHPDPDAELQR	MEQEA	3		554.2816817	1659.821645	0.000451244	3	N	544	559
B2RY56	Parental	WINKK	IIEYIGEEEATLVDFVCSK	VMAHS	3	C17:+57.021	739.0331788	2214.076136	0.002813207	1	N	773	792

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
B5THE2	Exosome	GLHLR	GGYIFPTQQPATTTEASR	KNPLG	2		962.9741261	1923.932652	0.000622848	7	N	790	808
B5THE2	Exosome	KLSPK	FSGFPALINR	MKANG	2		561.3092625	1120.602925	0.000622848	1	N	1268	1278
B5THE2	Exosome	TGEWK	TLEAPLEYINLHIR	GGYIL	3		561.3144342	1680.919902	0.00091018	3	N	1672	1686
B5THE2	Exosome	TATLK	NLPSAPVFGNSIENILLTAEYQTSNR	FHFKL	3		950.1545615	2847.440284	0.000451244	19	N	130	156
B5THE2	Exosome	WGIDR	QFLWGPGLLITPVLDQGAEK	VKAYV	2		1091.599494	2181.183388	0.000451244	23	N	730	750
B5THE2	Exosome	TCDER	GCCWDPQGSISVPCYYSR	NHGYK	2	C2:+57.021,C3:+57.021,C14:+57.021	1096.453169	2190.890738	0.000451244	5	N	90	108
B5THE2	Exosome	WNIDK	QFLLGPAFLVSPVLEPNAR	KVEAY	2		1034.583647	2067.151694	0.000451244	34	N	1626	1645
B5THE2	Exosome	WNIDK	QFLLGPAFLVSPVLEPNAR	KVEAY	3		690.0583645	2067.151694	0.000622848	11	N	1626	1645
B5THE2	Exosome	WNIDK	QFLLGPAFLVSPVLEPNAR	KVEAY	2	[0:-17.027	1026.070147	2050.124694	0.000622848	2	N	1626	1645
B5THE2	Exosome	VKQNG	NLLQMSPQVTYNPNLK	VATIT	3		620.6615055	1858.961117	0.000998612	1	N	893	909
B5THE2	Exosome	DISLK	ASTYSNAFPSTPVNK	LKLQV	2		792.3891665	1582.762733	0.000622848	7	N	996	1011
B5THE2	Exosome	PSSGR	WGGHWLGDNTAAWDQLGK	SIIGM	2		1006.474628	2010.933655	0.000451244	4	N	1492	1510
B5THE2	Exosome	RISTR	LPSTYIYGFGETEHTTFK	IDMNW	3		697.6743564	2089.999669	0.002019181	1	N	1099	1117
B5THE2	Parental	GLHLR	GGYIFPTQQPATTTEASR	KNPLG	2		962.9741261	1923.932652	0.000451244	16	N	790	808
B5THE2	Parental	KLSPK	FSGFPALINR	MKANG	2		561.3092625	1120.602925	0.000451244	8	N	1268	1278
B5THE2	Parental	TGEWK	TLEAPLEYINLHIR	GGYIL	3		561.3144342	1680.919902	0.000662267	1	N	1672	1686
B5THE2	Parental	TATLK	NLPSAPVFGNSIENILLTAEYQTSNRFHFK	LTDQT	4		852.6905469	3406.730987	0.000735798	1	N	130	160
B5THE2	Parental	TATLK	NLPSAPVFGNSIENILLTAEYQTSNR	FHFKL	3		950.1545615	2847.440284	0.000451244	14	N	130	156
B5THE2	Parental	WGIDR	QFLWGPGLLITPVLDQGAEK	VKAYV	2		1091.599494	2181.183388	0.000451244	12	N	730	750
B5THE2	Parental	TCDER	GCCWDPQGSISVPCYYSR	NHGYK	2	C2:+57.021,C3:+57.021,C14:+57.021	1096.453169	2190.890738	0.000637154	5	N	90	108
B5THE2	Parental	VSDRE	TWNIDKQFLLGPAFLVSPVLEPNAR	KVEAY	3		942.5169944	2824.527583	0.001162105	3	N	1620	1645
B5THE2	Parental	WNIDK	QFLLGPAFLVSPVLEPNAR	KVEAY	2		1034.583647	2067.151694	0.000451244	22	N	1626	1645
B5THE2	Parental	WNIDK	QFLLGPAFLVSPVLEPNAR	KVEAY	3		690.0583645	2067.151694	0.001463592	2	N	1626	1645
B5THE2	Parental	DISLK	ASTYSNAFPSTPVNK	LKLQV	2		792.3891665	1582.762733	0.002019181	1	N	996	1011
B5THE2	Parental	PSSGR	WGGHWLGDNTAAWDQLGK	SIIGM	2		1006.474628	2010.933655	0.000622848	1	N	1492	1510
B5THE2	Parental	NAEGR	AEGWLFWDDGKR	INTDQ	3		493.9058864	1478.694259	0.00091018	2	N	1719	1731
B5THE2	Parental	PNHSR	YEVPVPLNIPSAPLSTPEGR	LYDVL	2		1068.570933	2135.126267	0.000451244	4	N	1035	1055
B5THE2	Parental	VEQYR	AYVAFPDFFR	NSTAT	2		616.8090953	1231.602591	0.0025889	2	N	1351	1361
B9EJ54	Exosome	NLDFR	SGLSQVNQHDIDQLQSDAVNAFGESLQK	KLLDI	3		1010.158923	3027.453368	0.00307782	1	N	1945	1973
B9EJ54	Exosome	MDLLR	ESQLALIVSPLEQLLQGINPR	TKKAD	2		1159.658072	2317.300543	0.000451244	1	N	868	889
B9EJ54	Parental	EQLIK	EAFIISDLFDIGELSAVELLLAGEHQQPHFPGLTR	GLVAV	4		966.5063346	3861.994138	0.001943752	3	N	92	127
B9EJ54	Parental	MDLLR	ESQLALIVSPLEQLLQGINPR	TKKAD	3		773.4413143	2317.300543	0.000451244	1	N	868	889
D3YTQ8	Parental	EPDVK	KLEALLQGGEVEEVILQAEK	ELSLA	3		732.7427704	2195.204911	0.000622848	3	N	27	47
D3YTQ8	Parental	AGLLK	KTTGLVGLAVCDTPHEEPDVK	KLEAL	4	C11:+57.021	567.2904579	2265.130632	0.000823681	1	N	6	27
D3YVV0	Exosome	KNLPF	LIDGYEEQPGLQPHIR	DVLHQ	3		622.3237694	1863.947908	0.001162105	1	N	348	364
D3YVV0	Exosome	KEYDG	FTITITGDKVGNILFSVETQTTEER	TQLYH	3		933.8190673	2798.433802	0.00307782	1	N	567	592
D3YXK2	Parental	ERLKK	AIEDEGGNPDEIEVTSECNKK	MPKRP	2	C18:+57.021	1167.524017	2333.032434	0.000451244	3	N	63	84
D3YXK2	Parental	ERLKK	AIEDEGGNPDEIEVTSECNKK	MPKRP	3	C18:+57.021	778.6852779	2333.032434	0.000451244	7	N	63	84
D3YXK2	Parental	ERLKK	AIEDEGGNPDEIEVTSECNK	KMPKR	2	C18:+57.021	1103.476535	2204.937471	0.000451244	46	N	63	83
D3YXK2	Parental	EDVKK	FAFDACNDVPAPPKESSASEGADQK	MSSVE	3	C6:+57.021	880.0627484	2637.164845	0.000451244	35	N	378	403
D3YXK2	Parental	SSCGR	NFWVSGLSSTTR	ATDLK	2		677.8416551	1353.66771	0.000823681	6	N	428	440
D3YXK2	Parental	GETCK	SEPVKEEGSELEQPFAQATSSVGPDR	KLAEE	3		925.4425481	2773.304244	0.000622848	6	N	226	252
D3YXK2	Parental	EDVKK	FAFDACNDVPAPPK	ESSAS	2	C6:+57.021	774.861499	1547.707398	0.000451244	5	N	378	392
D3YXK2	Parental	SPSTR	CQWSEADAPLAVVK	REPAD	2	C1:+57.021	787.3878809	1572.760162	0.000622848	9	N	302	316
D3YXK2	Parental	PENEK	ILDILGETCK	SEPVK	2	C9:+57.021	581.3131219	1160.610644	0.001943752	1	N	216	226
D3YZZ5	Parental	PDNAK	QCFYEDITQGTK	CTLEF	2	C2:+57.021	745.335314	1488.655028	0.002453667	1	N	46	58
D3YZZ5	Parental	NGTYK	FCFSNEFSTFTHK	TVYFD	3	C2:+57.021	551.2455372	1650.713212	0.000823681	3	N	107	120
D3Z6Q9	Exosome	LYNSR	IGCYVTVFQNISNLR	DVFYR	2	C3:+57.021	892.4619116	1782.908223	0.000451244	32	N	202	217
D3Z6Q9	Exosome	HEDLK	AIVGNNDLLWEDYEEKLADQALR	TMENY	2		1338.169729	2674.323857	0.001329271	1	N	100	123
D3Z6Q9	Exosome	HEDLK	AIVGNNDLLWEDYEEKLADQALR	TMENY	3		892.4490858	2674.323857	0.000451244	3	N	100	123
D3Z6Q9	Exosome	EDFSK	AQIVFEDLNQELLEELPILYNSR	IGCYV	2		1373.719054	2745.422509	0.000451244	31	N	179	202
D3Z6Q9	Exosome	EDFSK	AQIVFEDLNQELLEELPILYNSR	IGCYV	3		916.1486363	2745.422509	0.000451244	21	N	179	202
D3Z6Q9	Exosome	EDFSK	AQIVFEDLNQELLEELPILY	NSRIG	2		1195.131021	2388.246442	0.000451244	9	N	179	199
D3Z6Q9	Exosome	PPPPR	ASGSGSCNAPGSPEGSSQLCSPR	ASPDA	2	C7:+57.021,C20:+57.021	1125.479189	2248.942779	0.000451244	8	N	418	441
D3Z6Q9	Exosome	HEDLK	AIVGNNDLLWEDYEEK	LADQA	2		954.4552348	1906.89487	0.000451244	27	N	100	116
D3Z6Q9	Exosome	TKDER	FEQSASNFYQQQAEGHK	LYKDL	2		999.9511823	1997.886765	0.000451244	10	N	42	59
D3Z6Q9	Exosome	TKDER	FEQSASNFYQQQAEGHK	LYKDL	3		666.9700549	1997.886765	0.000823681	7	N	42	59
D3Z6Q9	Exosome	ESSKR	VSETLQEVYSSDWDGHEDLK	AIVGN	2		1169.030024	2336.044447	0.000698008	1	N	80	100
D3Z6Q9	Exosome	ESSKR	VSETLQEVYSSDWDGHEDLK	AIVGN	3		779.6892825	2336.044447	0.000823681	4	N	80	100
D3Z6Q9	Parental	LYNSR	IGCYVTVFQNISNLR	DVFYR	2	C3:+57.021	892.4619116	1782.908223	0.000451244	2	N	202	217
D3Z6Q9	Parental	HEDLK	AIVGNNDLLWEDYEEKLADQALR	TMENY	2		1338.169729	2674.323857	0.000451244	7	N	100	123
D3Z6Q9	Parental	HEDLK	AIVGNNDLLWEDYEEKLADQALR	TMENY	3		892.4490858	2674.323857	0.000451244	10	N	100	123
D3Z6Q9	Parental	EDFSK	AQIVFEDLNQELLEELPILYNSR	IGCYV	2		1373.719054	2745.422509	0.000979378	3	N	179	202

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
D3Z6Q9	Parental	EDFSK	AQIVFEDLNQELLEELPILYNSR	IGCYV	3		916.1486363	2745.422509	0.000451244	8	N	179	202
D3Z6Q9	Parental	EDFSK	AQIVFEDLNQELLEELPILY	NSRIG	2		1195.131021	2388.246442	0.000451244	33	N	179	199
D3Z6Q9	Parental	EDFSK	AQIVFEDLNQELLEELPILY	NSRIG	3		797.0899473	2388.246442	0.000451244	26	N	179	199
D3Z6Q9	Parental	AKMAK	AEEDFSKAQIVFEDLNQELLEELPILY	NSRIG	3		1065.871497	3194.591091	0.000451244	7	N	172	199
D3Z6Q9	Parental	PPPPR	ASGSGSCNAPGSPEGSSQLCSPR	ASPDA	2	C7:+57.021,C20:+57.021	1125.479189	2248.942779	0.000451244	22	N	418	441
D3Z6Q9	Parental	PPPPR	ASGSGSCNAPGSPEGSSQLCSPR	ASPDA	3	C7:+57.021,C20:+57.021	750.655393	2248.942779	0.000451244	6	N	418	441
D3Z6Q9	Parental	AKMAK	AEEDFSKAQIVFEDLNQELLEELPILYNSR	IGCYV	3		1184.930186	3551.767158	0.000698008	1	N	172	202
D3Z6Q9	Parental	HEDLK	AIVGNNDLLWEDYEEK	LADQA	2		954.4552348	1906.89487	0.000451244	24	N	100	116
D3Z6Q9	Parental	TKDER	FEQSASNFYQQQAEGHK	LYKDL	3		666.9700549	1997.886765	0.002884417	1	N	42	59
D4AFX7	Exosome	SSTER	DSLLASLLDGVR	ASGNR	2		629.8542312	1257.692862	0.000823681	3	N	311	323
D4AFX7	Exosome	LPSSR	QLVLETLYALASNTK	IIKEA	3		555.3142113	1662.919234	0.000823681	2	N	1835	1850
D4AFX7	Parental	PYLLK	LLEGVGLENLDSPAATK	AQIVK	2		863.9652384	1725.914877	0.000451244	3	N	2144	2161
D4AFX7	Parental	SSTER	DSLLASLLDGVR	ASGNR	2		629.8542312	1257.692862	0.000622848	11	N	311	323
D4AFX7	Parental	HALSR	LGGYLSEDQATPENPTVR	KSLAG	2		973.9768658	1945.938132	0.000622848	1	N	1593	1611
D4AFX7	Parental	EELRR	ENGLEVLQEAFSR	CVAVL	2		746.3760591	1490.736518	0.000451244	1	N	1447	1460
D4AFX7	Parental	LRFGK	YSTDESITSLAEFVVQK	ISPRH	2		958.9785428	1915.941486	0.000451244	4	N	225	242
D4AFX7	Parental	KAMTR	SLQYGEQVSEILSR	SSVWS	2		804.9155485	1607.815497	0.000698008	1	N	2173	2187
D4AFX7	Parental	QSNTR	ALYQYCPIPVINYPQLENELFCNIYYLK	QLCDT	3	C6:+57.021,C22:+57.021	1180.252581	3537.734344	0.000451244	5	N	1236	1264
D4AFX7	Parental	LPSSR	QLVLETLYALASNTK	IIKEA	3		555.3142113	1662.919234	0.000451244	10	N	1835	1850
E9PUM5	Exosome	KGPNK	IQCVDGMWTTLPVCVEEER	TCGDI	2	C3:+57.021,M7:+15.995,C14:+57.021	1169.529348	2337.043097	0.000622848	4	N	372	391
E9PUM5	Exosome	CIRIK	TCSVSDIEIENGFFSESFR	TYALN	2	C2:+57.021	1112.497074	2222.978548	0.000637154	1	N	149	168
E9PV24	Exosome	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	2		1408.647012	2815.278424	0.000451244	17	N	485	511
E9PV24	Exosome	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	3		939.4339412	2815.278424	0.000451244	56	N	485	511
E9PV24	Exosome	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	4		704.8274059	2815.278424	0.000451244	10	N	485	511
E9PV24	Exosome	GCRMK	GLIDEANQDFTNR	INKLK	2		746.8554908	1491.695382	0.000451244	51	N	72	85
E9PV24	Exosome	MEYLR	GDFANANNFDNTYGQVSEDLRR	RIEIL	2		1252.065795	2502.11599	0.000622848	3	N	115	137
E9PV24	Exosome	MEYLR	GDFANANNFDNTYGQVSEDLRR	RIEIL	3		835.0464632	2502.11599	0.000451244	13	N	115	137
E9PV24	Exosome	MEYLR	GDFANANNFDNTYGQVSEDLR	RRIEI	2		1174.015239	2346.014879	0.000451244	51	N	115	136
E9PV24	Exosome	ELSER	HPDLSGFFDNHFGLISPNFK	EFGSK	2		1145.058525	2288.101449	0.000622848	9	N	460	480
E9PV24	Exosome	ELSER	HPDLSGFFDNHFGLISPNFK	EFGSK	3		763.708283	2288.101449	0.000451244	31	N	460	480
E9PV24	Exosome	ELSER	HPDLSGFFDNHFGLISPNFK	EFGSK	4		573.0331623	2288.101449	0.000451244	15	N	460	480
E9PV24	Exosome	KVIEK	AQQIQALQSNVR	AQLID	2		678.3736538	1354.731708	0.000451244	32	N	149	161
E9PV24	Exosome	RAVNR	EINLQDYEGHQK	QLQQV	2		737.352584	1472.689568	0.000451244	25	N	191	203
E9PV24	Exosome	RAVNR	EINLQDYEGHQK	QLQQV	3		491.9043227	1472.689568	0.001162105	10	N	191	203
E9PV24	Exosome	REVVK	EVITSDDGSDCGDATELDISHSFSGSLDELSER	HPDLS	3	C11:+57.021	1181.844804	3542.511011	0.000451244	14	N	427	460
E9PV24	Exosome	SDGNR	NPGTTGSDGTGDWGTGSPRPGSDSGNFRPANPNWGVF	SEFGD	3		1240.555175	3718.642126	0.000451244	26	N	323	360
E9PV24	Exosome	GPGSK	AENPTNPGPGGSGYWRPGNSGSGSDGNR	NPGTT	3		915.7385809	2744.192343	0.000451244	4	N	295	323
E9PV24	Exosome	DFANA	NNFDNTYGQVSEDLR	RRIEI	2		886.3982512	1770.780902	0.000451244	2	N	121	136
E9PV24	Exosome	QSQCK	DSDWPFCSDDDWNHK	CPSGC	2	C7:+57.021	962.3658625	1922.716125	0.001162105	6	N	49	64
E9PV24	Exosome	STVWT	TDTEDKGEFLSEGGGVR	GPRVV	2		898.9190165	1795.822433	0.000451244	11	N	19	36
E9PV24	Exosome	STVWT	TDTEDKGEFLSEGGGVR	GPRVV	3		599.6152777	1795.822433	0.000451244	5	N	19	36
E9PV24	Exosome	REVVK	EVITSDDGSDCGDATELDISHSFSGSLDELSE	RHPDL	3	C11:+57.021	1129.8111	3386.409899	0.000662267	2	N	427	459
E9PV24	Exosome	GPGSK	AENPTNPGPGGSGYWR	PGNSG	2		830.3796644	1658.743729	0.001352548	2	N	295	311
E9PV24	Exosome	RVVER	HQSQCKDSDWPFCSDDDWNHK	CPSGC	3	C5:+57.021,C13:+57.021	898.0242565	2691.049369	0.001162105	3	N	43	64
E9PV24	Exosome	REVVK	EVITSDDGSDCGDATELDISHSFSGSLDELSERHPDLSGF	FDNHF	4	C11:+57.021	1074.9717	4295.8556	0.002019181	2	N	427	467
E9PV24	Exosome	PGSFK	SQLQEAPPEWK	ALTEM	2		656.8307561	1311.645912	0.000451244	3	N	239	250
E9PV24	Exosome	DELSE	RHPDLSGFFDNHFGLISPNFK	EFGSK	4		612.05844	2444.20256	0.000451244	6	N	459	480
E9PV24	Parental	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	2		1408.647012	2815.278424	0.000451244	13	N	485	511
E9PV24	Parental	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	3		939.4339412	2815.278424	0.000451244	45	N	485	511
E9PV24	Parental	EFGSK	THSDSDILTNIEDPSSHVPEFSSSSK	TSTVK	4		704.8274059	2815.278424	0.000451244	8	N	485	511
E9PV24	Parental	GCRMK	GLIDEANQDFTNR	INKLK	2		746.8554908	1491.695382	0.000451244	13	N	72	85
E9PV24	Parental	MEYLR	GDFANANNFDNTYGQVSEDLRR	RIEIL	3		835.0464632	2502.11599	0.000622848	3	N	115	137
E9PV24	Parental	ELSER	HPDLSGFFDNHFGLISPNFK	EFGSK	2		1145.058525	2288.101449	0.001943752	1	N	460	480
E9PV24	Parental	ELSER	HPDLSGFFDNHFGLISPNFK	EFGSK	3		763.708283	2288.101449	0.000622848	3	N	460	480
E9PV24	Parental	ELSER	HPDLSGFFDNHFGLISPNFK	EFGSK	4		573.0331623	2288.101449	0.000451244	5	N	460	480
E9PV24	Parental	RAVNR	EINLQDYEGHQK	QLQQV	2		737.352584	1472.689568	0.000451244	1	N	191	203
E9PV24	Parental	RAVNR	EINLQDYEGHQK	QLQQV	3		491.9043227	1472.689568	0.001229886	4	N	191	203
E9PV24	Parental	REVVK	EVITSDDGSDCGDATELDISHSFSGSLDELSER	HPDLS	3	C11:+57.021	1181.844804	3542.511011	0.000451244	17	N	427	460
E9PV24	Parental	SDGNR	NPGTTGSDGTGDWGTGSPRPGSDSGNFRPANPNWGVF	SEFGD	3		1240.555175	3718.642126	0.000622848	2	N	323	360
E9PV24	Parental	STVWT	TDTEDKGEFLSEGGGVR	GPRVV	2		898.9190165	1795.822433	0.000451244	11	N	19	36
E9PV24	Parental	STVWT	TDTEDKGEFLSEGGGVR	GPRVV	3		599.6152777	1795.822433	0.000451244	6	N	19	36
E9PV24	Parental	GPGSK	AENPTNPGPGGSGYWR	PGNSG	2		830.3796644	1658.743729	0.002453667	1	N	295	311
E9PV24	Parental	RVVER	HQSQCKDSDWPFCSDDDWNHK	CPSGC	3	C5:+57.021,C13:+57.021	898.0242565	2691.049369	0.001162105	5	N	43	64
E9PV24	Parental	PGSFK	SQLQEAPPEWK	ALTEM	2		656.8307561	1311.645912	0.001395409	3	N	239	250

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9PV24	Parental	GCRMK	GLIDEANQDFTNRINK	LKNSL	2		924.4664682	1846.917336	0.000698008	3	N	72	88
E9PV24	Parental	GCRMK	GLIDEANQDFTNRINK	LKNSL	3		616.6469121	1846.917336	0.001162105	2	N	72	88
E9PV24	Parental	QSQCK	DSDWPFCSDDDWNHKCPSGCR	MKGLI	2	C7:+57.021,C16:+57.021,C20:+57.021	1320.999732	2639.983864	0.000823681	1	N	49	70
E9PV24	Parental	QSQCK	DSDWPFCSDDDWNHKCPSGCR	MKGLI	3	C7:+57.021,C16:+57.021,C20:+57.021	881.0024212	2639.983864	0.000622848	4	N	49	70
E9PVA8	Exosome	AHGVK	LVLPSLLAALEEESWR	TKAGS	3		609.340649	1824.998547	0.000451244	1	N	1496	1512
E9PVA8	Exosome	SIHVK	VDPLFTELLNGIR	AVEDP	2		743.9173628	1485.819126	0.002727428	1	N	2380	2393
E9PVA8	Exosome	SGLIR	LFNDSSPVVLEESWDALNAITK	KLDAG	2		1224.618809	2447.222018	0.000622848	1	N	2199	2221
E9PVA8	Parental	AHGVK	LVLPSLLAALEEESWR	TKAGS	2		913.5070734	1824.998547	0.000451244	7	N	1496	1512
E9PVA8	Parental	AHGVK	LVLPSLLAALEEESWR	TKAGS	3		609.340649	1824.998547	0.000451244	6	N	1496	1512
E9PVA8	Parental	QQALR	QIGSVIRNPEILAIAPVLLDALTDPSR	KTQKC	3		957.8821134	2870.62294	0.000451244	3	N	1563	1590
E9PVA8	Parental	GSVIR	NPEILAIAPVLLDALTDPSR	KTQKC	2		1059.594409	2117.173217	0.001329271	1	N	1570	1590
E9PVX6	Exosome	MLNRK	VDFSEDLSGLTEMFK	TPVKE	2		859.4036256	1716.791651	0.0025889	1	N	685	700
E9PVX6	Parental	EESAK	ISLESSQAEPVR	TRAST	2		658.3467703	1314.677941	0.000451244	4	N	2298	2310
E9PVX6	Parental	GKKTK	SPGRAPGTPAPVQEENDCTAY	METPK	2	C18:+57.021	1108.997772	2215.979945	0.000622848	10	N	1392	1413
E9PVX6	Parental	GKRTK	SPGRAPGTPAPVQEENDSTAF	METPK	2		1064.501236	2126.986873	0.000451244	7	N	1151	1172
E9PVX6	Parental	NLSER	QLQVTNSGDIPEPITTEILGEK	VLSST	2		1191.624091	2381.232583	0.000451244	15	N	726	748
E9PVX6	Parental	SRTSK	NRSQPLEDLDGFQELFQTPAGASNPVSVEESAK	ISLES	3		1187.576694	3559.706683	0.000622848	1	N	2265	2298
E9PVX6	Parental	TPKIR	AQPLEDLDGFQELFQTPAGASDSVTVEESAK	MSLES	3		1093.856687	3278.54666	0.000451244	6	N	2146	2177
E9PVX6	Parental	TSKNR	SQPLEDLDGFQELF	QTPAG	2		819.3888322	1636.762064	0.000823681	3	N	1199	1213
E9PVX6	Parental	TPKIR	AQPLEDLDGFQELFQTPAGANDSVTVEESAK	MSLES	3		1102.86032	3305.557559	0.000451244	7	N	1319	1350
E9PVX6	Parental	TSKNR	SQPLEDLDGFQELFQTPAGASNPVSVEESAK	ISLES	3		1097.528681	3289.562644	0.000451244	4	N	2267	2298
E9PVX6	Parental	TPKIR	AQPLEDLDGFQELF	QTPAG	2		811.3913749	1620.76715	0.001162105	2	N	1319	1333
E9PVX6	Parental	RVLCK	SPQVTTENITTNTKPQTSTSGK	KVDMK	3		774.0595983	2319.155395	0.000698008	5	N	999	1021
E9PVX6	Parental	EESAK	ISLESSQAEPVKTPASTK	RRSKM	3		625.002473	1871.984019	0.000451244	1	N	1230	1248
E9PVX6	Parental	GKRMK	SLGRAPGTPAPVQEENDSTAF	METPK	2		1072.516886	2143.018173	0.002145581	1	N	1981	2002
E9PVX6	Parental	EAILY	NFSSTNPTQVNGVTIDEPVR	LRHGD	2		1088.037986	2174.060372	0.000451244	24	N	61	81
E9PVX6	Parental	DLDGF	QELFQTPAGASDSVTVEESAK	ISLES	2		1097.52966	2193.043719	0.002663018	1	N	1209	1230
E9PVX6	Parental	ASISK	IDVKEELLESEEHLQLGEGVDTF	QVSTN	2		1315.148128	2628.280655	0.001162105	2	N	1491	1514
E9PVX6	Parental	ASISK	IDVKEELLESEEHLQLGEGVDTF	QVSTN	3		877.1013518	2628.280655	0.002080925	3	N	1491	1514
E9PVX6	Parental	SKPEK	LATAAEQTCSGLPGLSSVDISNF	GDSIN	2	C9:+57.021	1169.565488	2337.115376	0.002374549	1	N	426	449
E9PVX6	Parental	TPKIR	AQPLEDLDGFQELFQTPAGANDSVTVEESVK	MSLES	3		1112.204086	3333.588859	0.000451244	11	N	2029	2060
E9PVX6	Parental	DNLAK	LPSSSPPLEPTDTSVTSR	RQART	2		935.9737918	1869.931984	0.002727428	2	N	2420	2438
E9PVX6	Parental	KSPGR	APGTPAPVQEENDSTAF	METPK	2		865.8975527	1729.779505	0.002145581	1	N	1155	1172
E9PWG6	Parental	NLAIK	ICNEILTSPCSPENR	VYTKA	2	C2:+57.021,C10:+57.021	895.4140698	1788.81254	0.000451244	9	N	831	846
E9PWG6	Parental	TQKVK	GVQCEGEEINCHDKQEENDAGETDPAK	SVLKL	4	C4:+57.021,C11:+57.021	765.570477	3058.250708	0.002296037	2	N	661	688
E9PWG6	Parental	RILSR	LILLWYNPVTEEDVR	LRHCL	2		930.4992484	1858.982897	0.001591523	2	N	730	745
E9PWG6	Parental	LIEAK	EALENCIAVQDFDQASK	LKEEI	2	C6:+57.021	969.4493952	1936.88319	0.001162105	1	N	501	518
E9PX59	Exosome	AFVKR	DSFEELTTLIQQCADSPKPVFVK	VINLY	3	C13:+57.021	884.7794013	2651.314804	0.000451244	1	N	703	726
E9PX59	Exosome	LGKNK	TCGNISVDDLAYFLEVAEK	ASKAF	2	C2:+57.021	1072.514735	2143.01387	0.000451244	1	N	1130	1149
E9PX59	Exosome	HSILR	VAETGPLNLIDPIHEFK	AFTNT	3		631.6759202	1892.004361	0.001264573	1	N	179	196
E9PX59	Parental	HSILR	VAETGPLNLIDPIHEFK	AFTNT	3		631.6759202	1892.004361	0.000637154	2	N	179	196
E9PX59	Parental	KLLTR	HQGSLDESYYDWYILVTNTCAPTQLEHLEFIK	EMKLF	4	C20:+57.021	968.4638568	3869.824227	0.000451244	1	N	399	431
E9PX59	Parental	LMSYK	ATSHEDFIPVLLLVDDFEEQENAYILQNAINAFIAEK	GLRYE	3		1407.374507	4219.10012	0.000451244	1	N	779	816
E9PX59	Parental	NPNHK	EANNIENIVGNYTFLLQDILNK	QLSKV	2		1268.158633	2534.301665	0.000451244	1	N	1343	1365
E9PYK3	Exosome	LLDVR	NYDPLSPAPAAPPAER	SRSEV	2		833.4157156	1664.815831	0.000622848	1	N	90	106
E9PYK3	Exosome	NLFKK	DFSLTEAPPGYDSVHGVSETTSVPTDFQDDEFVVYK	TNQVK	3		1326.941368	3977.800703	0.000451244	2	N	509	545
E9PYK3	Exosome	AVEKR	DVNEIPFANVPNISELVAK	EDVDF	2		1035.049834	2068.084068	0.000979378	1	N	1174	1193
E9PYK3	Exosome	RHILR	TLSQCGAGVFEYFNSK	SKHSW	2	C5:+57.021	904.4199094	1806.824219	0.001264573	1	N	1007	1023
E9PYK3	Parental	LLDVR	NYDPLSPAPAAPPAER	SRSEV	2		833.4157156	1664.815831	0.0025889	1	N	90	106
E9PZF0	Exosome	ANSER	TFIAIKPDGVQR	GLVGE	2		672.8858657	1343.756131	0.000622848	6	Y	6	18
E9PZF0	Exosome	ANSER	TFIAIKPDGVQR	GLVGE	3		448.9265104	1343.756131	0.001162105	3	Y	6	18
E9PZF0	Exosome	ESAEK	EIHLWFKPEELIDYK	SCAHD	2		980.5148985	1959.014197	0.00091018	2	N	243	258
E9PZF0	Exosome	ESAEK	EIHLWFKPEELIDYK	SCAHD	3		654.0125323	1959.014197	0.000451244	3	N	243	258
E9PZF0	Exosome	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDYK	SCAHD	3		1142.912578	3425.714334	0.000451244	9	N	229	258
E9PZF0	Exosome	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDYK	SCAHD	4		857.4363836	3425.714334	0.000662267	3	N	229	258
E9PZF0	Exosome	PGTIR	GDFCIQVGR	TMANL	2	C4:+57.021	526.2533986	1050.491197	0.001162105	11	Y	105	114
E9PZF0	Exosome	LVGLK	FLQASEDLLKEHYTDLK	DRPFF	3		684.0217561	2049.041868	0.000698008	1	Y	39	56
E9PZF0	Parental	ANSER	TFIAIKPDGVQR	GLVGE	3		448.9265104	1343.756131	0.001162105	3	Y	6	18
E9PZF0	Parental	ESAEK	EIHLWFKPEELIDYK	SCAHD	2		980.5148985	1959.014197	0.000622848	1	N	243	258
E9PZF0	Parental	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDYK	SCAHD	3		1142.912578	3425.714334	0.000451244	7	N	229	258
E9PZF0	Parental	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDYK	SCAHD	4		857.4363836	3425.714334	0.002663018	2	N	229	258
E9PZF0	Parental	PGTIR	GDFCIQVGR	TMANL	2	C4:+57.021	526.2533986	1050.491197	0.000998612	4	Y	105	114
E9PZF0	Parental	IQVGR	NIIHGSDSVESAEKEIHLWFKPEELIDY	KSCAH	3		1100.214257	3297.619371	0.000451244	2	N	229	257

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q070	Exosome	PAAAR	AGAIAPCEVTVPAQNTGLGPEK	TSFFQ	2	C7:+57.021	1090.554726	2179.093852	0.000451244	32	N	112	134
E9Q070	Exosome	AEKVK	AFLADPSAFAAAAPAAAATTAAPAAAAAPAK	AEAKE	2		1348.706281	2695.396963	0.002727428	2	N	266	297
E9Q070	Exosome	AEKVK	AFLADPSAFAAAAPAAAATTAAPAAAAAPAK	AEAKE	3		899.4734543	2695.396963	0.002080925	1	N	266	297
E9Q070	Exosome	LGPEK	TSFFQALGITTK	ISSGT	2		657.3591494	1312.702699	0.000451244	9	N	134	146
E9Q070	Exosome	NGYKR	VLALSVETEYTFPLAEK	VKAFL	2		955.5120215	1909.008443	0.000451244	36	N	247	264
E9Q070	Exosome	NISPF	SFGLIIQQVFDNGSIYNPEVLDITEQALHSR	FLEGV	3		1168.598882	3502.773246	0.000451244	16	N	183	214
E9Q070	Exosome	TKISS	GTIEILSDVQLIK	TGDKV	2		714.9195712	1427.823542	0.001329271	9	N	149	162
E9Q070	Exosome	LEGVR	NVASVCLQIGYPTVASVPHSIINGYK	RVLAL	3	C6:+57.021	929.8218234	2786.44207	0.000451244	6	N	220	246
E9Q070	Exosome	AEKVK	AFLADPSAFAAAAPAAAATTAAPAA	AAAPA	2		1094.05819	2186.10078	0.000451244	4	N	266	291
E9Q070	Parental	PAAAR	AGAIAPCEVTVPAQNTGLGPEK	TSFFQ	2	C7:+57.021	1090.554726	2179.093852	0.000451244	64	N	112	134
E9Q070	Parental	NGYKR	VLALSVETEYTFPLAEKVK	AFLAD	3		713.0650734	2136.17182	0.001264573	1	N	247	266
E9Q070	Parental	AEKVK	AFLADPSAFAAAAPAAAATTAAPAAAAAPAK	AEAKE	2		1348.706281	2695.396963	0.000451244	40	N	266	297
E9Q070	Parental	AEKVK	AFLADPSAFAAAAPAAAATTAAPAAAAAPAK	AEAKE	3		899.4734543	2695.396963	0.000823681	13	N	266	297
E9Q070	Parental	LGPEK	TSFFQALGITTK	ISSGT	2		657.3591494	1312.702699	0.000451244	26	N	134	146
E9Q070	Parental	NGYKR	VLALSVETEYTFPLAEK	VKAFL	2		955.5120215	1909.008443	0.000451244	38	N	247	264
E9Q070	Parental	PAAAR	AGAIAPCEVTVPAQNTGLGPEKTSFFQALGITTK	ISSGT	3	C7:+57.021	1158.936464	3473.785991	0.000735798	8	N	112	146
E9Q070	Parental	NISPF	SFGLIIQQVFDNGSIYNPEVLDITEQALHSR	FLEGV	3		1168.598882	3502.773246	0.000451244	35	N	183	214
E9Q070	Parental	NISPF	SFGLIIQQVFDNGSIYNPEVLDITEQALHSR	FLEGV	4		876.7011116	3502.773246	0.001463592	1	N	183	214
E9Q070	Parental	TKISS	GTIEILSDVQLIK	TGDKV	2		714.9195712	1427.823542	0.000622848	6	N	149	162
E9Q070	Parental	LEGVR	NVASVCLQIGYPTVASVPHSIINGYK	RVLAL	2	C6:+57.021	1394.228835	2786.44207	0.000451244	1	N	220	246
E9Q070	Parental	LEGVR	NVASVCLQIGYPTVASVPHSIINGYK	RVLAL	3	C6:+57.021	929.8218234	2786.44207	0.000451244	19	N	220	246
E9Q070	Parental	AEKVK	AFLADPSAFAAAAPAAAATTAAPAAAAAPAKAEAK	EESEE	3		1032.544049	3094.608747	0.0007646	3	N	266	301
E9Q070	Parental	LEGVR	NVASVCLQIGYPTVASVPHSIINGYKR	VLALS	4	C6:+57.021	736.6435953	2942.543181	0.000451244	1	N	220	247
E9Q070	Parental	SPFSF	GLIIQQVFDNGSIYNPEVLDITEQALHSR	FLEGV	3		1090.565401	3268.672804	0.000451244	10	N	185	214
E9Q070	Parental	DDYPK	CFIVGADNVGSK	QMQQI	2	C1:+57.021	633.8112777	1265.606955	0.001162105	2	N	26	38
E9Q070	Parental	LPHIR	GNVGFVFTKEDLTEIR	DMLLA	3		608.9883867	1823.94176	0.000451244	10	N	83	99
E9Q070	Parental	EKVKA	FLADPSAFAAAAPAAAATTAAPAAAAAPAK	AEAKE	2		1313.187724	2624.359849	0.001871652	3	N	267	297
E9Q070	Parental	EKVKA	FLADPSAFAAAAPAAAATTAAPAAAAAPAK	AEAKE	3		875.7944163	2624.359849	0.002145581	1	N	267	297
E9Q070	Parental	DPSAF	AAAAPAAAATTAAPAAAAAPAK	AEAKE	2		888.9842968	1775.952994	0.001162105	3	N	275	297
E9Q0F0	Exosome	TREIR	SLNNQFASFIDKVR	FLEQQ	2		819.9340756	1637.852551	0.000451244	5	N	110	124
E9Q0F0	Exosome	TREIR	SLNNQFASFIDKVR	FLEQQ	3		546.9586504	1637.852551	0.000451244	5	N	110	124
E9Q0F0	Exosome	TREIR	SLNNQFASFIDK	VRFLE	2		692.349313	1382.683026	0.000451244	3	N	110	122
E9Q0K6	Exosome	NTDLR	TWEPEDVCSFLENR	GFREK	2	C8:+57.021	891.3938916	1780.772183	0.000451244	32	N	75	89
E9Q0K6	Exosome	FRDNK	IAGSFLPFLDEDRLEDLGVSSLEER	KKMIE	2		1404.209051	2806.402502	0.000451244	4	N	104	129
E9Q0K6	Exosome	FRDNK	IAGSFLPFLDEDRLEDLGVSSLEER	KKMIE	3		936.4753006	2806.402502	0.000451244	24	N	104	129
E9Q0K6	Exosome	EAFTK	LTDNIFLEVLHSTDPQLSEAQSILR	NIECR	2		1420.245968	2838.476336	0.000451244	19	N	464	489
E9Q0K6	Exosome	EAFTK	LTDNIFLEVLHSTDPQLSEAQSILR	NIECR	3		947.1665785	2838.476336	0.000451244	49	N	464	489
E9Q0K6	Exosome	EAFTK	LTDNIFLEVLHSTDPQLSEAQSILR	NIECR	4		710.6268839	2838.476336	0.000451244	6	N	464	489
E9Q0K6	Exosome	IDLMK	VFNDPIHGHIEFHPLLIR	IIDTP	3		718.7256083	2153.153425	0.000451244	9	N	148	166
E9Q0K6	Exosome	IDLMK	VFNDPIHGHIEFHPLLIR	IIDTP	4		539.2961562	2153.153425	0.000451244	14	N	148	166
E9Q0K6	Exosome	DYFAR	DCHHLGIQNNFDYKR	FIKFA	4	C2:+57.021	479.9763743	1915.874297	0.000451244	16	N	350	365
E9Q0K6	Exosome	KQAVR	INKEQVSQLLPEK	FAEQL	2		763.4333771	1524.851154	0.000451244	8	N	573	586
E9Q0K6	Exosome	KQAVR	INKEQVSQLLPEK	FAEQL	3		509.291518	1524.851154	0.001839721	1	N	573	586
E9Q0K6	Exosome	ASHNR	FEHSLGVGYLAGCLVR	ALAEK	3	C13:+57.021	593.3070195	1776.897659	0.000451244	19	N	196	212
E9Q0K6	Exosome	DVELK	AEDFIVDVINVDYGMEDKNPIDR	VHFYC	3	M15:+15.995	895.0905986	2682.248396	0.000451244	3	N	536	559
E9Q0K6	Exosome	KLVMK	NYGLVPEEDITFIK	EQIMG	2		819.4252177	1636.834835	0.001329271	1	N	287	301
E9Q0K6	Exosome	RPATK	SFLYEIVSNKR	NGIDV	2		678.3700484	1354.724497	0.002019181	1	N	326	337
E9Q0K6	Exosome	RPATK	SFLYEIVSNKR	NGIDV	3		452.5826323	1354.724497	0.002296037	1	N	326	337
E9Q0K6	Exosome	WCALR	DFTKPQQCGAGEMAEDPDSIPSTQQPHAAHNQL	-	3	C8:+57.021,M13:+15.995	1207.870882	3620.589245	0.000637154	8	N	618	651
E9Q0K6	Exosome	WCALR	DFTKPQQCGAGEMAEDPDSIPSTQQPHAAHNQL	-	4	C8:+57.021,M13:+15.995	906.1551112	3620.589245	0.000451244	21	N	618	651
E9Q0K6	Exosome	LRYIK	QLGGGYYVFPGASHNR	FEHSL	3		574.9502663	1721.827399	0.000451244	10	N	180	196
E9Q0K6	Exosome	VSNKR	NGIDVDKWDYFAR	DCHHL	2		799.8840513	1597.752503	0.000451244	1	N	337	350
E9Q0K6	Exosome	VSNKR	NGIDVDKWDYFAR	DCHHL	3		533.5919675	1597.752503	0.000451244	39	N	337	350
E9Q0K6	Exosome	AFTKL	TDNIFLEVLHSTDPQLSEAQSILR	NIECR	3		909.4718905	2725.392271	0.000451244	2	N	465	489
E9Q0K6	Exosome	AYQHK	ISNLIDIMITDAFLK	ADPYV	2		853.9740211	1705.932442	0.000451244	8	N	420	435
E9Q0K6	Exosome	AYQHK	ISNLIDIMITDAFLK	ADPYV	3		569.6519474	1705.932442	0.000451244	9	N	420	435
E9Q0K6	Exosome	EERKK	MIECIQQLSQSR	IDLMK	2	C4:+57.021	746.866259	1491.716918	0.000823681	3	N	131	143
E9Q0K6	Exosome	VRINK	EQVSQLLPEKFAEQLIR	VYCKK	3		676.7095125	2027.105137	0.000662267	7	N	576	593
E9Q0K6	Exosome	GCLVR	ALAEKQPELQISER	DILCV	3		537.9620605	1610.862782	0.001162105	4	N	212	226
E9Q0K6	Exosome	NTDLR	TWEPEDVCSFLENRGFR	EKKVL	2	C8:+57.021	1071.489386	2140.963172	0.000823681	2	N	75	92
E9Q0K6	Parental	NTDLR	TWEPEDVCSFLENR	GFREK	2	C8:+57.021	891.3938916	1780.772183	0.000451244	29	N	75	89
E9Q0K6	Parental	FRDNK	IAGSFLPFLDEDRLEDLGVSSLEER	KKMIE	2		1404.209051	2806.402502	0.000451244	8	N	104	129
E9Q0K6	Parental	FRDNK	IAGSFLPFLDEDRLEDLGVSSLEER	KKMIE	3		936.4753006	2806.402502	0.000451244	36	N	104	129
E9Q0K6	Parental	EAFTK	LTDNIFLEVLHSTDPQLSEAQSILR	NIECR	2		1420.245968	2838.476336	0.000451244	8	N	464	489
E9Q0K6	Parental	EAFTK	LTDNIFLEVLHSTDPQLSEAQSILR	NIECR	3		947.1665785	2838.476336	0.000451244	32	N	464	489

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q0K6	Parental	IDLMK	VFNDPIHGHIEFHPLLIR	IIDTP	4		539.2961562	2153.153425	0.001229886	6	N	148	166
E9Q0K6	Parental	DYFAR	DCHHLGIQNNFDYKR	FIKFA	4	C2:+57.021	479.9763743	1915.874297	0.000622848	3	N	350	365
E9Q0K6	Parental	KQAVR	INKEQVSQLLPEK	FAEQL	2		763.4333771	1524.851154	0.00091018	1	N	573	586
E9Q0K6	Parental	ASHNR	FEHSLGVGYLAGCLVR	ALAEK	3	C13:+57.021	593.3070195	1776.897659	0.001162105	5	N	196	212
E9Q0K6	Parental	LRYIK	QLGGGYYVFPGASHNR	FEHSL	3		574.9502663	1721.827399	0.000451244	3	N	180	196
E9Q0K6	Parental	VSNKR	NGIDVDKWDYFAR	DCHHL	3		533.5919675	1597.752503	0.001264573	7	N	337	350
E9Q0K6	Parental	AFTKL	TDNIFLEVLHSTDPQLSEAQSILR	NIECR	3		909.4718905	2725.392271	0.000451244	19	N	465	489
E9Q0K6	Parental	AYQHK	ISNLIDIMITDAFLKADPY	VEITG	2		1077.064096	2152.112592	0.000451244	1	N	420	439
E9Q0K6	Parental	TDNIF	LEVLHSTDPQLSEAQSILR	NIECR	2		1068.568922	2135.122244	0.0007646	5	N	470	489
E9Q0Y4	Exosome	ATRTR	QQYLQDLATNEVTTTSLDSASR	FGLPS	2		1221.093687	2440.171773	0.000451244	3	N	528	550
E9Q0Y4	Exosome	VAVSR	TQDTPAFGPALPEGGGPFAANADFR	AFLLA	2		1252.5962	2503.176799	0.000823681	4	N	475	500
E9Q0Y4	Exosome	PKVPR	TLLTLDEQVLSFQR	KVGIL	2		831.9572164	1661.898833	0.002019181	1	N	315	329
E9Q0Y4	Parental	ATPTR	LFTDPLALLGLPAEEPEPTFPPVLEPR	WFAHY	3		986.8674699	2957.57901	0.000451244	11	N	85	112
E9Q0Y4	Parental	DGQGR	LGFEVDAEGFITHVER	FTFAE	3		606.9727367	1817.89481	0.000451244	1	N	693	709
E9Q0Y4	Parental	PTRLF	TDPLALLGLPAEEPEPTFPPVLEPR	WFAHY	3		900.1499772	2697.426532	0.000451244	5	N	87	112
E9Q0Y4	Parental	NSISK	IMSEAGSETLEDEWQSISEIASTCNTILESLSR	EGQPI	3	C24:+57.021	1229.573479	3685.697038	0.002884417	1	N	911	944
E9Q0Y4	Parental	ATRTR	QQYLQDLATNEVTTTSLDSASR	FGLPS	2		1221.093687	2440.171773	0.000451244	3	N	528	550
E9Q0Y4	Parental	SGDPK	EALKCDSEPEPGSLSEK	VSHLE	3	C5:+57.021	625.9599023	1874.856307	0.000823681	3	N	956	973
E9Q0Y4	Parental	TEFLR	SHNSLSSGSSLSDEAPVLPNTTPDLLLVTTANPSAPGTDR	ETPPS	3		1340.33337	4017.97671	0.002663018	1	N	829	869
E9Q394	Parental	GVKGR	EGLPSCGNRNEVTGTNYSGVATCQQPLSSR	SSVLQ	3	C6:+57.021,C23:+57.021	1080.498536	3238.472209	0.000622848	1	N	411	441
E9Q394	Parental	DLLSR	ISAASEEEAVGNGAATPK	MKQGP	2		851.4186523	1700.821705	0.001162105	2	N	1326	1344
E9Q394	Parental	SCGNR	NEVTGTNYSGVATCQQPLSSR	SSVLQ	2	C14:+57.021	1135.029604	2268.043608	0.000698008	4	N	420	441
E9Q394	Parental	ETQER	GCEGGTTSDQSSPVLPAAAIENK	VLGGQ	2	C2:+57.021	1145.037094	2288.058589	0.000451244	4	N	571	594
E9Q394	Parental	LQCTK	DNEVEQEDLTQSLSLVK	DVIGA	2		973.9818138	1945.948028	0.000451244	14	N	2128	2145
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	4		899.4141681	3593.625473	0.000451244	19	N	2079	2112
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	4	Q1:-17.027	895.1574181	3576.598473	0.000698008	1	N	2079	2112
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	4	[0:-17.027	895.1574181	3576.598473	0.000451244	7	N	2079	2112
E9Q397	Exosome	ASGEK	VIEGQTDPDYQLLGQR	LEGLD	2		916.4633942	1830.911188	0.000451244	24	N	1126	1142
E9Q397	Exosome	QERPR	DVSSVELLLK	YHQGI	2		551.8218684	1101.628137	0.000451244	11	N	1933	1943
E9Q397	Exosome	QKDAK	QAEAILSNQEYTLAHLEPPDSLAAAEAGIR	KFEDF	3		1060.205873	3177.594219	0.000451244	46	N	1178	1208
E9Q397	Exosome	QKDAK	QAEAILSNQEYTLAHLEPPDSLAAAEAGIR	KFEDF	4		795.4063548	3177.594219	0.001943752	1	N	1178	1208
E9Q397	Exosome	QKDAK	QAEAILSNQEYTLAHLEPPDSLAAAEAGIR	KFEDF	3	Q1:-17.027	1054.530206	3160.567219	0.000451244	4	N	1178	1208
E9Q397	Exosome	QKDAK	QAEAILSNQEYTLAHLEPPDSLAAAEAGIR	KFEDF	3	[0:-17.027	1054.530206	3160.567219	0.000451244	10	N	1178	1208
E9Q397	Exosome	VESTK	DLGQDLAGVIAIQR	KLSGL	2		734.9100691	1467.804538	0.000451244	20	N	981	995
E9Q397	Exosome	VESTK	DLGQDLAGVIAIQR	KLSGL	3		490.2759794	1467.804538	0.000451244	31	N	981	995
E9Q397	Exosome	AFRKK	DLQDAENFFQFQGDADDLKAWLQDAHR	LLSGE	3		1065.159034	3192.453703	0.000451244	10	N	737	764
E9Q397	Exosome	AFRKK	DLQDAENFFQFQGDADDLKAWLQDAHR	LLSGE	4		799.1212257	3192.453703	0.000451244	20	N	737	764
E9Q397	Exosome	QLAGR	AQSLLSAGHPEGEQIIR	LQGQV	2		903.4793786	1804.943157	0.000451244	20	N	1646	1663
E9Q397	Exosome	QLAGR	AQSLLSAGHPEGEQIIR	LQGQV	3		602.6555191	1804.943157	0.000451244	13	N	1646	1663
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVH	HAATE	3		977.1081167	2928.30095	0.000451244	28	N	2079	2106
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVH	HAATE	2	Q1:-17.027	1456.644775	2911.27395	0.000998612	4	N	2079	2106
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVH	HAATE	3	Q1:-17.027	971.43245	2911.27395	0.000998612	3	N	2079	2106
E9Q397	Exosome	QELVK	AAEIDCQDIEER	LGHLQ	2	C6:+57.021	724.8200281	1447.624456	0.000451244	10	N	1546	1558
E9Q397	Exosome	RLNKR	WQAFQAVVSEQR	EAVDS	2		724.8682042	1447.720808	0.000451244	15	N	935	947
E9Q397	Exosome	CQFSR	DASVAEAWLIAQEPYLASR	DFGHT	2		1045.531808	2089.048016	0.000451244	23	N	2016	2035
E9Q397	Exosome	CQFSR	DASVAEAWLIAQEPYLASR	DFGHT	3		697.3571388	2089.048016	0.000451244	11	N	2016	2035
E9Q397	Exosome	LNSRK	FANSLSGVQQQLQAFSTYR	TVEKP	2		1073.040332	2144.065063	0.000451244	33	N	329	348
E9Q397	Exosome	SIEKR	FLDLLEPLGR	RKKQL	2		586.8378528	1171.660106	0.000979378	12	N	1459	1469
E9Q397	Exosome	QDAHR	LLSGEDVGQDEGATR	ALGKK	2		773.8713379	1545.727076	0.000451244	5	N	764	779
E9Q397	Exosome	CAGRR	AQLVDTADKFR	FFSMV	2		632.3387483	1262.661897	0.000637154	4	N	1896	1907
E9Q397	Exosome	IGQER	VDNVNTIIER	LIDAG	2		586.8176487	1171.619697	0.000451244	10	N	1746	1756
E9Q397	Exosome	LQALR	KLYQQVLTQAELR	GHKLQ	2		795.4546438	1588.893688	0.000451244	15	N	827	840
E9Q397	Exosome	LQALR	KLYQQVLTQAELR	GHKLQ	3		530.6390292	1588.893688	0.000979378	1	N	827	840
E9Q397	Exosome	GDKVK	AITAATLQFAEGK	GYQPC	2		660.8620562	1319.708512	0.000451244	11	N	585	598
E9Q397	Exosome	AEFGK	HLLEVEDLLQK	HKLME	2		668.8777063	1335.739813	0.000735798	5	N	558	569
E9Q397	Exosome	MWESR	GNTLTQCLGFQEFQK	DAKQA	2	C7:+57.021	885.9279016	1769.840203	0.000451244	24	N	1160	1175
E9Q397	Exosome	TIILR	FQIQDIVVQTQEGR	ETRSA	2		830.9368152	1659.85803	0.000451244	13	N	156	170
E9Q397	Exosome	TAFER	ELHLLGVQVQQFQDVATR	LQTAY	2		1041.061067	2080.106534	0.000451244	20	N	1843	1861
E9Q397	Exosome	TAFER	ELHLLGVQVQQFQDVATR	LQTAY	3		694.3766448	2080.106534	0.000451244	31	N	1843	1861
E9Q397	Exosome	NENQR	LVTQDNFGYDLAAVEAAK	KKHEA	2		962.9867022	1923.957804	0.000451244	24	N	443	461
E9Q397	Exosome	NENQR	LVTQDNFGYDLAAVEAAK	KKHEA	3		642.3270681	1923.957804	0.000622848	2	N	443	461
E9Q397	Exosome	VLNSR	KFANSLSGVQQQLQAFSTYR	TVEKP	2		1137.087813	2272.160027	0.000451244	16	N	328	348
E9Q397	Exosome	VLNSR	KFANSLSGVQQQLQAFSTYR	TVEKP	3		758.3944755	2272.160027	0.000451244	3	N	328	348
E9Q397	Exosome	LDYGK	DLTSVLILQR	KHKAF	2		579.3485847	1156.681569	0.000622848	15	N	667	677
E9Q397	Exosome	KNNEK	AQEATVLLKDNLELQNFLQNCK	ELTLW	2	C21:+57.021	1295.170986	2588.326372	0.000451244	9	N	1262	1284

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q397	Exosome	KNNEK	AQEATVLLKDNLELQNFLQNCK	ELTLW	3	C21:+57.021	863.7832572	2588.326372	0.000451244	15	N	1262	1284
E9Q397	Exosome	NTRAK	NFSTCLELGESLLQR	QHQAS	2	C5:+57.021	883.941009	1765.866418	0.000451244	26	N	1957	1972
E9Q397	Exosome	NTRAK	NFSTCLELGESLLQR	QHQAS	3	C5:+57.021	589.6299393	1765.866418	0.000451244	10	N	1957	1972
E9Q397	Exosome	WIKEK	EQIYSSLDYGKDLTSVLILQR	KHKAF	2		1221.150276	2440.284953	0.000451244	7	N	656	677
E9Q397	Exosome	WIKEK	EQIYSSLDYGKDLTSVLILQR	KHKAF	3		814.4361175	2440.284953	0.000451244	15	N	656	677
E9Q397	Exosome	AIQSK	EQEVSAAWQALLDACAGR	RAQLV	2	C15:+57.021	987.9708292	1973.926058	0.000451244	20	N	1877	1895
E9Q397	Exosome	AIQSK	EQEVSAAWQALLDACAGR	RAQLV	3	C15:+57.021	658.9831528	1973.926058	0.000451244	10	N	1877	1895
E9Q397	Exosome	KFQEK	GNLEVLLFTIQSR	MRANN	2		745.4228124	1488.830025	0.000451244	19	N	359	372
E9Q397	Exosome	KMIEK	YSGLASDLLTWIEQTISVLNSR	KFANS	2		1233.647901	2465.280202	0.000451244	8	N	306	328
E9Q397	Exosome	KMIEK	YSGLASDLLTWIEQTISVLNSR	KFANS	3		822.7678672	2465.280202	0.000451244	10	N	306	328
E9Q397	Exosome	DSNAR	HNLEHAFDVAER	QLGII	2		719.347636	1436.679672	0.000451244	1	N	231	243
E9Q397	Exosome	DSNAR	HNLEHAFDVAER	QLGII	3		479.901024	1436.679672	0.000637154	3	N	231	243
E9Q397	Exosome	EDQLR	SDDLGKDLTTVNR	MLAKL	2		717.3656914	1432.715783	0.000451244	7	N	1403	1416
E9Q397	Exosome	WIKEK	EQIYSSLDYGK	DLTSV	2		651.8147717	1301.613943	0.000622848	4	N	656	667
E9Q397	Exosome	EALHK	LWEELQSTAK	AKAEQ	2		602.8145747	1203.613549	0.000451244	6	N	1359	1369
E9Q397	Exosome	TIIER	LIDAGHSEAATIAEWK	DGLND	2		856.4366481	1710.857696	0.000451244	12	N	1756	1772
E9Q397	Exosome	TIIER	LIDAGHSEAATIAEWK	DGLND	3		571.2936987	1710.857696	0.000451244	7	N	1756	1772
E9Q397	Exosome	SDINR	AWESLEEAEYQR	ELALR	2		755.8445918	1509.673584	0.000735798	6	N	394	406
E9Q397	Exosome	EKLWK	GLQDALQGQELSLGEASK	LQAFL	2		922.4739589	1842.932318	0.000451244	29	N	1044	1062
E9Q397	Exosome	LQISR	DLEDETLWVEER	LPLAQ	2		767.357532	1532.699464	0.000451244	10	N	1485	1497
E9Q397	Exosome	AFRKK	DLQDAENFFQFQGDADDLK	AWLQD	2		1108.493077	2214.970554	0.000451244	17	N	737	756
E9Q397	Exosome	DNILR	LWSYLQELLR	SRRQR	2		660.8696843	1319.723769	0.000451244	14	N	508	518
E9Q397	Exosome	LFMKK	NQTLQNEILGHAPR	VEDVL	2		795.9214995	1589.827399	0.000451244	12	N	1519	1533
E9Q397	Exosome	LFMKK	NQTLQNEILGHAPR	VEDVL	3		530.9502663	1589.827399	0.000622848	6	N	1519	1533
E9Q397	Exosome	QALRK	LYQQVLTQAELR	GHKLQ	2		731.4071623	1460.798725	0.000451244	5	N	828	840
E9Q397	Exosome	FQLKR	EADDLEQWITEK	EMVAS	2		738.8468001	1475.678	0.000451244	8	N	1697	1709
E9Q397	Exosome	TVLLK	DNLELQNFLQNCK	ELTLW	2	C12:+57.021	818.3936946	1634.771789	0.000451244	16	N	1271	1284
E9Q397	Exosome	YDLHR	YFYTGTEILGLIDEK	HRELP	2		881.4514325	1760.887265	0.000451244	11	N	1801	1816
E9Q397	Exosome	YDLHR	YFYTGTEILGLIDEK	HRELP	3		587.9702217	1760.887265	0.000451244	3	N	1801	1816
E9Q397	Exosome	ALGKK	HKEFLEELEESR	GVMEH	2		773.3813415	1544.747083	0.001871652	1	N	784	796
E9Q397	Exosome	WCQMK	TAGYPHVNVTNFTSSWK	DGLAF	3		636.9800027	1907.916608	0.000451244	8	N	186	203
E9Q397	Exosome	DVAER	QLGIIPLLDPEDVFTENPDEK	SIITY	2		1191.60791	2381.20022	0.001162105	1	N	243	264
E9Q397	Exosome	DVAER	QLGIIPLLDPEDVFTENPDEK	SIITY	3		794.7412066	2381.20022	0.000451244	9	N	243	264
E9Q397	Exosome	DVAER	QLGIIPLLDPEDVFTENPDEK	SIITY	2	[0:-17.027	1183.09441	2364.17322	0.0025889	1	N	243	264
E9Q397	Exosome	WINDK	LLTSPDVSYDEAR	NLHNK	2		733.3626174	1464.709635	0.000451244	7	N	1293	1306
E9Q397	Exosome	GEASK	LQAFLQDLDDFKAWLSMAQK	AVASE	3		790.0722339	2367.193302	0.001162105	1	N	1062	1082
E9Q397	Exosome	GEASK	LQAFLQDLDDFKAWLSMAQK	AVASE	3	M17:+15.995	795.4039006	2383.188302	0.000451244	13	N	1062	1082
E9Q397	Exosome	LIDEK	HRELPEDVGLDASTAESFHR	VHTAF	3		756.0336064	2265.077419	0.000451244	8	N	1816	1836
E9Q397	Exosome	RMLIK	LLEVLSGEMLPRPTK	GKMRI	3	M9:+15.995	566.9873585	1697.938676	0.000451244	6	N	90	105
E9Q397	Exosome	LLGQR	LEGLDTDWDALRR	MWESR	2		780.3947832	1558.773966	0.002884417	1	N	1142	1155
E9Q397	Exosome	DQEMK	TLMAQIDGVNLAANNLVESGHPR	SGEVK	3	M3:+15.995	812.74873	2435.22279	0.0007646	2	N	898	921
E9Q397	Exosome	LQNCK	ELTLWINDK	LLTSP	2		566.3063854	1130.597171	0.001839721	3	N	1284	1293
E9Q397	Exosome	TRSAK	DALLLWCQMK	TAGYP	2	C7:+57.021,M9:+15.995	647.3204673	1292.625335	0.002080925	1	Y	176	186
E9Q397	Exosome	AIQSK	EQEVSAAWQALLDACAGRR	AQLVD	3	C15:+57.021	711.0168565	2130.027169	0.000451244	6	N	1877	1896
E9Q397	Exosome	TEKGK	WLDQMDIPNTLEDLEVVQHR	FDILD	3	M5:+15.995	823.0694691	2466.185007	0.000451244	5	N	869	889
E9Q397	Exosome	WVEER	LPLAQSADYGTNLQTVQLFMK	KNQTL	2		1169.609733	2337.203866	0.000451244	5	N	1497	1518
E9Q397	Exosome	FSMVR	DLLSWMESIIR	QIETQ	2		681.8584598	1361.70132	0.000451244	15	N	1913	1924
E9Q397	Exosome	KMIEK	YSGLASDLLTWIEQTISVLNSRK	FANSL	3		865.4661882	2593.375165	0.0025889	1	N	306	329
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHH	AATER	4		767.3477655	3065.359862	0.001162105	2	N	2079	2107
E9Q397	Exosome	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHH	AATER	3	Q1:-17.027	1017.118754	3048.332862	0.002145581	2	N	2079	2107
E9Q397	Exosome	QLFMK	KNQTLQNEILGHAPR	VEDVL	3		573.6485874	1717.922362	0.000451244	4	N	1518	1533
E9Q397	Exosome	QLFMK	KNQTLQNEILGHAPR	VEDVL	4		430.4883905	1717.922362	0.001943752	1	N	1518	1533
E9Q397	Exosome	MDKTK	VVESTKDLGQDLAGVIAIQR	KLSGL	2		1056.587115	2111.15863	0.000735798	1	N	975	995
E9Q397	Exosome	MDKTK	VVESTKDLGQDLAGVIAIQR	KLSGL	3		704.7273432	2111.15863	0.000451244	5	N	975	995
E9Q397	Exosome	DIEER	LGHLQSSWDTLR	EAAAG	3		471.5814028	1411.720808	0.000451244	3	N	1558	1570
E9Q397	Exosome	SWAER	FAALEKPTTLELK	ERQTP	3		487.6173426	1459.828628	0.000451244	3	N	2064	2077
E9Q397	Exosome	NNRDK	ILSPVDSGNKLVAEGNLYSNK	IMEKV	2		1109.589855	2217.164109	0.000823681	1	N	1223	1244
E9Q397	Exosome	DAHLK	QIFQEADDMVAQK	QFGHP	2		761.8644705	1521.713341	0.000622848	2	N	694	707
E9Q397	Exosome	LKERQ	TPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	4		867.3995237	3465.566895	0.002663018	1	N	2080	2112
E9Q397	Parental	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	3		1198.882958	3593.625473	0.002727428	1	N	2079	2112
E9Q397	Parental	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVHHAATER	TSPVS	4		899.4141681	3593.625473	0.000451244	14	N	2079	2112
E9Q397	Parental	ASGEK	VIEGQTDPDYQLLGQR	LEGLD	2		916.4633942	1830.911188	0.000451244	18	N	1126	1142
E9Q397	Parental	QERPR	DVSSVELLLK	YHQGI	2		551.8218684	1101.628137	0.000622848	7	N	1933	1943
E9Q397	Parental	QKDAK	QAEAILSNQEYTLAHLEPPDSLAAAEAGIR	KFEDF	3		1060.205873	3177.594219	0.000451244	21	N	1178	1208
E9Q397	Parental	QKDAK	QAEAILSNQEYTLAHLEPPDSLAAAEAGIR	KFEDF	3	Q1:-17.027	1054.530206	3160.567219	0.001229886	1	N	1178	1208

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q397	Parental	VESTK	DLGQDLAGVIAIQR	KLSGL	2		734.9100691	1467.804538	0.000451244	11	N	981	995
E9Q397	Parental	VESTK	DLGQDLAGVIAIQR	KLSGL	3		490.2759794	1467.804538	0.000451244	13	N	981	995
E9Q397	Parental	AFRKK	DLQDAENFFQFQGDADDLKAWLQDAHR	LLSGE	3		1065.159034	3192.453703	0.000451244	2	N	737	764
E9Q397	Parental	AFRKK	DLQDAENFFQFQGDADDLKAWLQDAHR	LLSGE	4		799.1212257	3192.453703	0.000622848	4	N	737	764
E9Q397	Parental	QLAGR	AQSLLSAGHPEGEQIIR	LQGQV	2		903.4793786	1804.943157	0.000451244	5	N	1646	1663
E9Q397	Parental	ELKER	QTPERPTEEPGPQEEEGETAGEAPQVH	HAATE	3		977.1081167	2928.30095	0.000451244	5	N	2079	2106
E9Q397	Parental	QELVK	AAEIDCQDIEER	LGHLQ	2	C6:+57.021	724.8200281	1447.624456	0.000451244	7	N	1546	1558
E9Q397	Parental	RDFAR	ETGAIGQERVDNVNTIIER	LIDAG	3		705.3665855	2113.076357	0.000451244	2	N	1737	1756
E9Q397	Parental	RLNKR	WQAFQAVVSEQR	EAVDS	2		724.8682042	1447.720808	0.000451244	3	N	935	947
E9Q397	Parental	CQFSR	DASVAEAWLIAQEPYLASR	DFGHT	2		1045.531808	2089.048016	0.000451244	6	N	2016	2035
E9Q397	Parental	CQFSR	DASVAEAWLIAQEPYLASR	DFGHT	3		697.3571388	2089.048016	0.000622848	2	N	2016	2035
E9Q397	Parental	LNSRK	FANSLSGVQQQLQAFSTYR	TVEKP	2		1073.040332	2144.065063	0.000451244	11	N	329	348
E9Q397	Parental	SIEKR	FLDLLEPLGR	RKKQL	2		586.8378528	1171.660106	0.001162105	4	N	1459	1469
E9Q397	Parental	QDAHR	LLSGEDVGQDEGATR	ALGKK	2		773.8713379	1545.727076	0.000451244	6	N	764	779
E9Q397	Parental	GDKVK	AITAATLQFAEGK	GYQPC	2		660.8620562	1319.708512	0.000451244	2	N	585	598
E9Q397	Parental	MWESR	GNTLTQCLGFQEFQK	DAKQA	2	C7:+57.021	885.9279016	1769.840203	0.000451244	6	N	1160	1175
E9Q397	Parental	TAFER	ELHLLGVQVQQFQDVATR	LQTAY	3		694.3766448	2080.106534	0.000451244	4	N	1843	1861
E9Q397	Parental	NENQR	LVTQDNFGYDLAAVEAAK	KKHEA	2		962.9867022	1923.957804	0.000451244	8	N	443	461
E9Q397	Parental	KNNEK	AQEATVLLKDNLELQNFLQNCK	ELTLW	3	C21:+57.021	863.7832572	2588.326372	0.000451244	3	N	1262	1284
E9Q397	Parental	NTRAK	NFSTCLELGESLLQR	QHQAS	2	C5:+57.021	883.941009	1765.866418	0.000451244	12	N	1957	1972
E9Q397	Parental	NTRAK	NFSTCLELGESLLQR	QHQAS	3	C5:+57.021	589.6299393	1765.866418	0.000451244	4	N	1957	1972
E9Q397	Parental	AIQSK	EQEVSAAWQALLDACAGR	RAQLV	2	C15:+57.021	987.9708292	1973.926058	0.000451244	2	N	1877	1895
E9Q397	Parental	EALHK	LWEELQSTAK	AKAEQ	2		602.8145747	1203.613549	0.001162105	1	N	1359	1369
E9Q397	Parental	SDINR	AWESLEEAEYQR	ELALR	2		755.8445918	1509.673584	0.000735798	5	N	394	406
E9Q397	Parental	EKLWK	GLQDALQGQELSLGEASK	LQAFL	2		922.4739589	1842.932318	0.000451244	2	N	1044	1062
E9Q397	Parental	LQISR	DLEDETLWVEER	LPLAQ	2		767.357532	1532.699464	0.000451244	7	N	1485	1497
E9Q397	Parental	AFRKK	DLQDAENFFQFQGDADDLK	AWLQD	2		1108.493077	2214.970554	0.000451244	5	N	737	756
E9Q397	Parental	DNILR	LWSYLQELLR	SRRQR	2		660.8696843	1319.723769	0.001839721	1	N	508	518
E9Q397	Parental	FQLKR	EADDLEQWITEK	EMVAS	2		738.8468001	1475.678	0.001352548	1	N	1697	1709
E9Q397	Parental	TVLLK	DNLELQNFLQNCK	ELTLW	2	C12:+57.021	818.3936946	1634.771789	0.00091018	3	N	1271	1284
E9Q397	Parental	DVAER	QLGIIPLLDPEDVFTENPDEK	SIITY	2		1191.60791	2381.20022	0.000451244	2	N	243	264
E9Q397	Parental	FAEGK	GYQPCDPQVIQDR	VSHLE	2	C5:+57.021	788.3649371	1574.714274	0.000451244	3	N	598	611
E9Q397	Parental	WINDK	LLTSPDVSYDEAR	NLHNK	2		733.3626174	1464.709635	0.000451244	1	N	1293	1306
E9Q397	Parental	GEASK	LQAFLQDLDDFKAWLSMAQK	AVASE	3	M17:+15.995	795.4039006	2383.188302	0.002981883	1	N	1062	1082
E9Q555	Exosome	HTFER	DPVLWSLVMAIGVCYHASLEEK	ASYRT	4	M9:+15.995,C14:+57.021	634.0675221	2532.238889	0.001463592	1	N	2638	2660
E9Q555	Exosome	YNSSR	AILDEVTHVQDLFLR	GAPIR	3		590.3251103	1767.951931	0.002663018	1	N	2679	2694
E9Q555	Parental	AAAVK	TQQAAAPQQAAAPEPTSAFNPR	DTVTV	2		1126.556877	2251.098155	0.000451244	1	N	323	345
E9Q555	Parental	KHSLA	GCEMTLDAFAAMACAEMLK	GDLLK	2	C2:+57.021,M4:+15.995,M12:+15.995,C14:+57.021	1076.448168	2150.880735	0.001839721	1	N	3801	3820
E9Q586	Exosome	ALKER	VDELTTDLEILKAEIEEK	GSDGA	3		696.7039813	2087.088544	0.00091018	6	N	294	312
E9Q586	Exosome	ELAFK	ASEQIYGSPSSSPYECLR	QSCTI	2	C16:+57.021	1015.960127	2029.904654	0.000451244	3	N	835	853
E9Q586	Exosome	VGRLR	AFLQGGQEATDIALLLR	DLETS	2		908.5023224	1814.989045	0.000451244	11	N	731	748
E9Q586	Exosome	DEVLK	ETVTQRPGATVPTDFATFPSSAFLR	AKEEQ	3		899.4613258	2695.360577	0.000735798	2	N	1169	1194
E9Q586	Exosome	RPGLR	GAAGEQLSFAAGLVYSLSLLQATLHR	YEHAL	3		891.8173324	2672.428597	0.001162105	1	N	606	632
E9Q586	Parental	GIFVR	QSQIQVFEDGADTTSPETPDSSASK	VLKRE	2		1313.094081	2624.172561	0.000451244	10	N	73	98
E9Q586	Parental	ALKER	VDELTTDLEILKAEIEEK	GSDGA	3		696.7039813	2087.088544	0.000451244	2	N	294	312
E9Q586	Parental	VGRLR	AFLQGGQEATDIALLLR	DLETS	2		908.5023224	1814.989045	0.000451244	4	N	731	748
E9Q586	Parental	EAQKR	VEAAQETVADYQQTIK	KYRQL	2		897.4499525	1792.884305	0.001699387	1	N	465	481
E9Q586	Parental	DEVLK	ETVTQRPGATVPTDFATFPSSAFLR	AKEEQ	3		899.4613258	2695.360577	0.000451244	10	N	1169	1194
E9Q586	Parental	IEGLR	GPPPSGIATLVSGIAGGGAPGQAPGALPGPGLVK	DSPLL	3		973.5419797	2917.602539	0.000622848	3	N	1012	1046
E9Q586	Parental	RPGLR	GAAGEQLSFAAGLVYSLSLLQATLHR	YEHAL	3		891.8173324	2672.428597	0.000451244	2	N	606	632
E9Q604	Exosome	NPLTK	KPWFVKPAESSSSSEGHGALK	STTWN	3		743.7153262	2228.122578	0.000451244	13	N	841	862
E9Q604	Exosome	NPLTK	KPWFVKPAESSSSSEGHGALK	STTWN	4		558.0384446	2228.122578	0.000451244	23	N	841	862
E9Q604	Exosome	EMTSK	VIQHQYQFNNLGQR	SLPVS	2		872.9480486	1743.880497	0.000451244	28	N	951	965
E9Q604	Exosome	EMTSK	VIQHQYQFNNLGQR	SLPVS	3		582.3012991	1743.880497	0.000823681	4	N	951	965
E9Q604	Exosome	KKVAR	SVFACQEQVLK	NKDAG	2	C5:+57.021	654.8347528	1307.653906	0.000451244	68	N	634	645
E9Q604	Exosome	SVTLR	NDGEDSYGTQVTVYYPSGLSYRK	DSASQ	3		867.0702745	2598.187423	0.000451244	2	N	808	831
E9Q604	Exosome	NTKDR	LREGDIQSTVTYDLALDPGR	SRIRA	2		1110.069286	2218.122972	0.001699387	1	N	665	685
E9Q604	Exosome	NTKDR	LREGDIQSTVTYDLALDPGR	SRIRA	3		740.3821242	2218.122972	0.000451244	13	N	665	685
E9Q604	Exosome	QENAK	GFGQSVVQLGGTSVVVAAPQEAK	AVNQT	2		1115.097847	2228.180093	0.000451244	74	N	32	55
E9Q604	Exosome	QENAK	GFGQSVVQLGGTSVVVAAPQEAK	AVNQT	3		743.7344978	2228.180093	0.000451244	34	N	32	55
E9Q604	Exosome	SVTLR	NDGEDSYGTQVTVYYPSGLSYR	KDSAS	2		1236.05403	2470.09246	0.000451244	47	N	808	830
E9Q604	Exosome	SVTLR	NDGEDSYGTQVTVYYPSGLSYR	KDSAS	3		824.3719534	2470.09246	0.000622848	2	N	808	830
E9Q604	Exosome	SHSQR	IIGAHFSPGLQYFGQSLSGGK	DLTMD	2		1082.563443	2163.111285	0.000451244	18	N	571	592
E9Q604	Exosome	SHSQR	IIGAHFSPGLQYFGQSLSGGK	DLTMD	3		722.0448951	2163.111285	0.000451244	39	N	571	592

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q604	Exosome	KDRLR	EGDIQSTVTYDLALDPGR	SRIRA	2		975.4766986	1948.937797	0.000622848	21	N	667	685
E9Q604	Exosome	KPQSR	RELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1294.992731	3881.954793	0.000451244	36	N	297	331
E9Q604	Exosome	KPQSR	RELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	4		971.4964982	3881.954793	0.000451244	1	N	297	331
E9Q604	Exosome	MDAQR	FFTAMFPFEK	NCGND	2	M5:+15.995	640.8052073	1279.594815	0.000451244	17	N	759	769
E9Q604	Exosome	ELPVK	YAIYMIVTSDESSIR	YLNFT	2		874.4327174	1746.849835	0.000451244	5	N	924	939
E9Q604	Exosome	PQSRR	ELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1242.959027	3725.853682	0.000451244	40	N	298	331
E9Q604	Exosome	PQSRR	ELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	4		932.4712204	3725.853682	0.000451244	29	N	298	331
E9Q604	Exosome	CETLK	LILPDCVDDSVSPIILR	LNYTL	2	C6:+57.021	963.0245418	1924.033484	0.000451244	59	N	716	733
E9Q604	Exosome	CETLK	LILPDCVDDSVSPIILR	LNYTL	3	C6:+57.021	642.3522945	1924.033484	0.000451244	21	N	716	733
E9Q604	Exosome	PEALR	ECPQQESDIVFLIDGSGSINNIDFQK	MKEFV	2	C2:+57.021	1477.198126	2952.380652	0.000451244	40	N	142	168
E9Q604	Exosome	PEALR	ECPQQESDIVFLIDGSGSINNIDFQK	MKEFV	3	C2:+57.021	985.134684	2952.380652	0.000451244	46	N	142	168
E9Q604	Exosome	HQNCK	ENTYVNGLCYLFGSNLLRPPQQFPEALR	ECPQQ	3	C9:+57.021	1099.555917	3295.644352	0.000451244	60	N	114	142
E9Q604	Exosome	HQNCK	ENTYVNGLCYLFGSNLLRPPQQFPEALR	ECPQQ	4	C9:+57.021	824.918888	3295.644352	0.000735798	1	N	114	142
E9Q604	Exosome	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	2	C3:+57.021	1023.971498	2045.927396	0.000451244	11	N	503	520
E9Q604	Exosome	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	3	C3:+57.021	682.9835985	2045.927396	0.001162105	9	N	503	520
E9Q604	Exosome	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	4	C3:+57.021	512.4896489	2045.927396	0.000998612	4	N	503	520
E9Q604	Exosome	HTSIK	GSQIGSYFGASLCSVDMDADGNTNLILIGAPHYYEK	TRGGQ	3	C13:+57.021	1288.601592	3862.781377	0.000451244	5	N	449	485
E9Q604	Exosome	YEKTR	GGQVSVCPLPR	GQRAR	2	C7:+57.021	585.3087052	1168.60181	0.000451244	10	N	487	498
E9Q604	Exosome	ALCHG	FNLDTEHPMTFQENAK	GFGQS	2	M9:+15.995	969.4391051	1936.86261	0.000451244	9	N	16	32
E9Q604	Exosome	TDGEK	FGDPLDYKDVIPEADR	AGVIR	2		925.4524952	1848.88939	0.000451244	8	N	261	277
E9Q604	Exosome	TDGEK	FGDPLDYKDVIPEADR	AGVIR	3		617.3042634	1848.88939	0.000451244	29	N	261	277
E9Q604	Exosome	VNGDK	LTDVAIGAPGEQENQGAVYIFYGASIASLSASHSQR	IIGAH	3		1236.615372	3706.822716	0.000451244	19	N	535	571
E9Q604	Exosome	AGVIR	YVIGVGNAFNKPQSR	RELDT	2		825.4420678	1648.868536	0.000451244	24	N	282	297
E9Q604	Exosome	AGVIR	YVIGVGNAFNKPQSR	RELDT	3		550.6306452	1648.868536	0.000622848	11	N	282	297
E9Q604	Exosome	GEPLR	SFGNLRPVLAMDAQR	FFTAM	3	M11:+15.995	564.2951855	1689.862156	0.000451244	24	N	744	759
E9Q604	Exosome	INTTR	VDSDMNDAYLGYASAVILR	NRVQS	2	M5:+15.995	1044.999527	2087.983454	0.000451244	36	N	394	413
E9Q604	Exosome	INTTR	VDSDMNDAYLGYASAVILR	NRVQS	3	M5:+15.995	697.0022846	2087.983454	0.000451244	17	N	394	413
E9Q604	Exosome	LSGGK	DLTMDGLMDLAVGAQGHLLLLR	AQPVL	2	M4:+15.995,M8:+15.995	1192.619861	2383.224122	0.000823681	2	N	592	614
E9Q604	Exosome	LSGGK	DLTMDGLMDLAVGAQGHLLLLR	AQPVL	3	M4:+15.995,M8:+15.995	795.4158406	2383.224122	0.000451244	63	N	592	614
E9Q604	Exosome	LKLIL	PDCVDDSVSPIILR	LNYTL	2	C3:+57.021	793.3984456	1584.781291	0.000451244	2	N	719	733
E9Q604	Exosome	VVMFR	ENFGTWEPHTSIK	GSQIG	2		773.3707768	1544.725954	0.000451244	18	N	436	449
E9Q604	Exosome	VVMFR	ENFGTWEPHTSIK	GSQIG	3		515.9164512	1544.725954	0.000662267	2	N	436	449
E9Q604	Exosome	HPWGR	FGAALTVLGDVNGDK	LTDVA	2		738.8888023	1475.762005	0.000823681	1	N	520	535
E9Q604	Exosome	SDEFR	IHFTFNDFKR	NPSPR	3		442.2319339	1323.672402	0.002727428	4	N	197	207
E9Q604	Exosome	FKKSK	TLFSLMQYSDEFR	IHFTF	2		818.8879456	1635.760291	0.000451244	4	N	184	197
E9Q604	Exosome	KENTY	VNGLCYLFGSNLLRPPQQFPEALR	ECPQQ	3	C5:+57.021	930.4904081	2788.447824	0.001591523	1	N	118	142
E9Q604	Parental	NPLTK	KPWFVKPAESSSSSEGHGALK	STTWN	2		1115.069089	2228.122578	0.002019181	1	N	841	862
E9Q604	Parental	NPLTK	KPWFVKPAESSSSSEGHGALK	STTWN	3		743.7153262	2228.122578	0.000451244	20	N	841	862
E9Q604	Parental	NPLTK	KPWFVKPAESSSSSEGHGALK	STTWN	4		558.0384446	2228.122578	0.000451244	33	N	841	862
E9Q604	Parental	EMTSK	VIQHQYQFNNLGQR	SLPVS	2		872.9480486	1743.880497	0.000451244	36	N	951	965
E9Q604	Parental	EMTSK	VIQHQYQFNNLGQR	SLPVS	3		582.3012991	1743.880497	0.000451244	18	N	951	965
E9Q604	Parental	KKVAR	SVFACQEQVLK	NKDAG	2	C5:+57.021	654.8347528	1307.653906	0.000451244	46	N	634	645
E9Q604	Parental	SVTLR	NDGEDSYGTQVTVYYPSGLSYRK	DSASQ	2		1300.101512	2598.187423	0.000622848	7	N	808	831
E9Q604	Parental	SVTLR	NDGEDSYGTQVTVYYPSGLSYRK	DSASQ	3		867.0702745	2598.187423	0.000451244	11	N	808	831
E9Q604	Parental	NTKDR	LREGDIQSTVTYDLALDPGR	SRIRA	3		740.3821242	2218.122972	0.002727428	1	N	665	685
E9Q604	Parental	QENAK	GFGQSVVQLGGTSVVVAAPQEAK	AVNQT	2		1115.097847	2228.180093	0.000451244	124	N	32	55
E9Q604	Parental	QENAK	GFGQSVVQLGGTSVVVAAPQEAK	AVNQT	3		743.7344978	2228.180093	0.000451244	33	N	32	55
E9Q604	Parental	SVTLR	NDGEDSYGTQVTVYYPSGLSYR	KDSAS	2		1236.05403	2470.09246	0.000451244	102	N	808	830
E9Q604	Parental	SVTLR	NDGEDSYGTQVTVYYPSGLSYR	KDSAS	3		824.3719534	2470.09246	0.000451244	8	N	808	830
E9Q604	Parental	SHSQR	IIGAHFSPGLQYFGQSLSGGK	DLTMD	2		1082.563443	2163.111285	0.000451244	23	N	571	592
E9Q604	Parental	SHSQR	IIGAHFSPGLQYFGQSLSGGK	DLTMD	3		722.0448951	2163.111285	0.000451244	42	N	571	592
E9Q604	Parental	KDRLR	EGDIQSTVTYDLALDPGR	SRIRA	2		975.4766986	1948.937797	0.000622848	3	N	667	685
E9Q604	Parental	KPQSR	RELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1294.992731	3881.954793	0.000451244	59	N	297	331
E9Q604	Parental	KPQSR	RELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	4		971.4964982	3881.954793	0.000870037	2	N	297	331
E9Q604	Parental	MDAQR	FFTAMFPFEK	NCGND	2		632.8077073	1263.599815	0.002981883	1	N	759	769
E9Q604	Parental	MDAQR	FFTAMFPFEK	NCGND	2	M5:+15.995	640.8052073	1279.594815	0.001699387	1	N	759	769
E9Q604	Parental	ELPVK	YAIYMIVTSDESSIR	YLNFT	2		874.4327174	1746.849835	0.000451244	8	N	924	939
E9Q604	Parental	PQSRR	ELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3		1242.959027	3725.853682	0.000451244	50	N	298	331
E9Q604	Parental	PQSRR	ELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	4		932.4712204	3725.853682	0.000451244	26	N	298	331
E9Q604	Parental	PQSRR	ELDTIASKPAGEHVFQVDNFEALNTIQNQLQEK	IFAIE	3	[0:-18.011	1236.955361	3707.842682	0.0007646	2	N	298	331
E9Q604	Parental	CETLK	LILPDCVDDSVSPIILR	LNYTL	2	C6:+57.021	963.0245418	1924.033484	0.000451244	68	N	716	733
E9Q604	Parental	CETLK	LILPDCVDDSVSPIILR	LNYTL	3	C6:+57.021	642.3522945	1924.033484	0.000451244	25	N	716	733
E9Q604	Parental	ENAAK	ILVVITDGEKFGDPLDY	KDVIP	2		947.4963714	1892.977143	0.000622848	2	N	251	268
E9Q604	Parental	PEALR	ECPQQESDIVFLIDGSGSINNIDFQK	MKEFV	2	C2:+57.021	1477.198126	2952.380652	0.000451244	48	N	142	168
E9Q604	Parental	PEALR	ECPQQESDIVFLIDGSGSINNIDFQK	MKEFV	3	C2:+57.021	985.134684	2952.380652	0.000451244	103	N	142	168

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q604	Parental	HQNCK	ENTYVNGLCYLFGSNLLRPPQQFPEALR	ECPQQ	3	C9:+57.021	1099.555917	3295.644352	0.000451244	106	N	114	142
E9Q604	Parental	HQNCK	ENTYVNGLCYLFGSNLLRPPQQFPEALR	ECPQQ	4	C9:+57.021	824.918888	3295.644352	0.000451244	11	N	114	142
E9Q604	Parental	GLMQK	CETLKLILPDCVDDSVSPIILR	LNYTL	2	C1:+39.994,C11:+57.021	1270.160784	2538.305968	0.000622848	4	N	711	733
E9Q604	Parental	GLMQK	CETLKLILPDCVDDSVSPIILR	LNYTL	2	C1:+57.021,C11:+57.021	1278.674284	2555.332968	0.001264573	1	N	711	733
E9Q604	Parental	GLMQK	CETLKLILPDCVDDSVSPIILR	LNYTL	3	C1:+57.021,C11:+57.021	852.7854561	2555.332968	0.000637154	2	N	711	733
E9Q604	Parental	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	2	C3:+57.021	1023.971498	2045.927396	0.000451244	15	N	503	520
E9Q604	Parental	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	3	C3:+57.021	682.9835985	2045.927396	0.000622848	10	N	503	520
E9Q604	Parental	GQRAR	WQCEALLHGDQGHPWGR	FGAAL	4	C3:+57.021	512.4896489	2045.927396	0.000870037	2	N	503	520
E9Q604	Parental	HTSIK	GSQIGSYFGASLCSVDMDADGNTNLILIGAPHYYEK	TRGGQ	3	C13:+57.021	1288.601592	3862.781377	0.000451244	8	N	449	485
E9Q604	Parental	YEKTR	GGQVSVCPLPR	GQRAR	2	C7:+57.021	585.3087052	1168.60181	0.000451244	8	N	487	498
E9Q604	Parental	SRTHK	TKFQLELPVK	YAIYM	2		601.8613279	1201.707056	0.001229886	3	N	914	924
E9Q604	Parental	ALCHG	FNLDTEHPMTFQENAK	GFGQS	2		961.4416051	1920.86761	0.000662267	2	N	16	32
E9Q604	Parental	LVVMF	RENFGTWEPHTSIK	GSQIG	3		567.9501549	1700.827065	0.000662267	1	N	435	449
E9Q604	Parental	TDGEK	FGDPLDYKDVIPEADR	AGVIR	2		925.4524952	1848.88939	0.000622848	2	N	261	277
E9Q604	Parental	TDGEK	FGDPLDYKDVIPEADR	AGVIR	3		617.3042634	1848.88939	0.000451244	7	N	261	277
E9Q604	Parental	VNGDK	LTDVAIGAPGEQENQGAVYIFYGASIASLSASHSQR	IIGAH	3		1236.615372	3706.822716	0.000451244	9	N	535	571
E9Q604	Parental	AGVIR	YVIGVGNAFNKPQSR	RELDT	3		550.6306452	1648.868536	0.002212458	2	N	282	297
E9Q604	Parental	LKLIL	PDCVDDSVSPIILR	LNYTL	2	C3:+57.021	793.3984456	1584.781291	0.000451244	8	N	719	733
E9Q604	Parental	VVMFR	ENFGTWEPHTSIK	GSQIG	2		773.3707768	1544.725954	0.001329271	1	N	436	449
E9Q604	Parental	KCETL	KLILPDCVDDSVSPIILR	LNYTL	2	C7:+57.021	1027.072023	2052.128447	0.000637154	3	N	715	733
E9Q604	Parental	KCETL	KLILPDCVDDSVSPIILR	LNYTL	3	C7:+57.021	685.0506156	2052.128447	0.002145581	1	N	715	733
E9Q604	Parental	GQSVV	QLGGTSVVVAAPQEAK	AVNQT	2		777.9284589	1553.841318	0.000451244	8	N	39	55
E9Q604	Parental	ILRNR	VQSLVLGAPR	YQHIG	2		520.3170875	1038.618575	0.000451244	8	N	415	425
E9Q604	Parental	DIVFL	IDGSGSINNIDFQK	MKEFV	2		754.3735164	1506.731433	0.000451244	3	N	154	168
E9Q604	Parental	CETLK	LILPDCVDDSVSPIIL	RLNYT	2	C6:+57.021	884.9739862	1767.932372	0.000451244	7	N	716	732
E9Q604	Parental	GVIRY	VIGVGNAFNKPQSR	RELDT	2		743.9104034	1485.805207	0.001763695	3	N	283	297
E9Q604	Parental	LSLAV	STVPQQLLACGPTVHQNCK	ENTYV	2	C10:+57.021,C18:+57.021	1069.527757	2137.039914	0.000451244	7	N	95	114
E9Q604	Parental	LSLAV	STVPQQLLACGPTVHQNCK	ENTYV	3	C10:+57.021,C18:+57.021	713.354438	2137.039914	0.002884417	1	N	95	114
E9Q604	Parental	NTKDR	LREGDIQSTVTY	DLALD	2		691.3520527	1380.688505	0.00307782	1	N	665	677
E9Q604	Parental	ENAAK	ILVVITDGEK	FGDPL	2		543.824411	1085.633222	0.001839721	1	N	251	261
E9Q604	Parental	KTETK	VEPYEVHNPVPLIVGSSIGGLVLLALITAGLYKLGFFK	RQYKD	4		1006.829121	4023.285282	0.000451244	1	N	1098	1136
E9Q604	Parental	GEHVF	QVDNFEALNTIQNQLQEK	IFAIE	2		1066.535079	2131.054558	0.000622848	3	N	313	331
E9Q604	Parental	TLKLI	LPDCVDDSVSPIILR	LNYTL	2	C4:+57.021	849.9404777	1697.865355	0.000851441	2	N	718	733
E9Q604	Parental	CETLK	LILPDCVDDSVSPI	ILRLN	2	C6:+57.021	771.8899221	1541.764244	0.001162105	1	N	716	730
E9Q604	Parental	KTETK	VEPYEVHNPVPLIVGSSIGGLVLLALITAGLY	KLGFF	3		1101.9588	3302.853	0.000451244	6	N	1098	1130
E9Q604	Parental	DGEKF	GDPLDYKDVIPEADR	AGVIR	2		851.9182882	1701.820976	0.000451244	4	N	262	277
E9Q604	Parental	HGALK	STTWNINHPIFPANSEVTF	NVTFD	2		1088.029433	2174.043265	0.002080925	1	N	862	881
E9Q604	Parental	KTETK	VEPYEVHNPVPLIVGSSIGGLVLLALITAGLYK	LGFFK	3		1144.657121	3430.947963	0.000622848	3	N	1098	1131
E9Q604	Parental	ENAAK	ILVVITDGEKF	GDPLD	2		617.358618	1232.701636	0.000823681	7	N	251	262
E9Q604	Parental	SDIVF	LIDGSGSINNIDFQK	MKEFV	2		810.9155485	1619.815497	0.002145581	1	N	153	168
E9Q616	Exosome	TSDMK	LEGPHLSLKGPGVDLPSVDLSMPK	VSGPD	4		622.3390611	2485.325044	0.001162105	1	N	5052	5076
E9Q616	Parental	VPGFK	AEGPEVDVNLPK	ADLDI	2		634.3305889	1266.645578	0.000622848	1	N	762	774
E9Q616	Parental	IKGPK	VDIDVPDVDVHGPDWHLK	MPKIK	4		514.7593379	2055.006152	0.000451244	3	N	2605	2623
E9Q6E5	Parental	VCFVK	FHDPDSAVVAQHLTNTVFVDR	ALIVV	3		790.061385	2367.160755	0.001699387	1	N	110	131
E9Q6E5	Parental	VFVDR	ALIVVPYAEGVIPDETK	ALSLL	2		907.5014568	1812.987314	0.000451244	8	N	131	148
E9Q6Q4	Exosome	DLLDR	HVEDGNVTVQHAALSALR	NLAIP	3		639.6699397	1915.986419	0.000451244	2	N	319	337
E9Q6Q4	Exosome	ESLYK	EVQDLAFLDVVSK	LRSHE	2		731.8935534	1461.771507	0.001591523	1	N	521	534
E9Q6Q4	Exosome	SEHVI	MQNEALVALALIAALELGPAEK	DLASA	3	M1:+15.995	761.087801	2280.240003	0.001763695	1	N	456	478
E9Q6Q4	Parental	NEFMR	IPCVDAGLISPLVQLLNSKDQEVLLQTGR	ALGNI	3	C3:+57.021	1059.583473	3175.727019	0.000451244	4	N	82	111
E9Q6Q4	Parental	NDAIK	LQLVEAGLVECLLEIVQQK	VDSNK	2	C11:+57.021	1091.611513	2181.207425	0.001763695	1	N	209	228
E9Q6Q4	Parental	NDAIK	LQLVEAGLVECLLEIVQQK	VDSNK	3	C11:+57.021	728.0769418	2181.207425	0.000451244	8	N	209	228
E9Q6U4	Exosome	ATMKK	AAAEDVNVTFEDQQK	INKFA	2		832.8922704	1663.768941	0.000451244	25	N	7	22
E9Q6U4	Exosome	EDAKK	TLQEEIDALESR	VASIQ	2		702.3547923	1402.693985	0.000451244	18	N	88	100
E9Q6U4	Parental	ATMKK	AAAEDVNVTFEDQQK	INKFA	2		832.8922704	1663.768941	0.000451244	14	N	7	22
E9Q6U4	Parental	EDAKK	TLQEEIDALESR	VASIQ	2		702.3547923	1402.693985	0.001871652	1	N	88	100
E9Q7G0	Exosome	LNEQR	VEFAALQEALAHALTEK	EGTDQ	3		614.3321535	1839.97306	0.001162105	1	N	1029	1046
E9Q7G0	Parental	LKGEK	TGQEVQEEAVEIHSEGQPGQQQSQLAQLHASLAK	AIQQV	3		1219.270264	3654.787393	0.000451244	15	N	836	870
E9Q7G0	Parental	LKGEK	TGQEVQEEAVEIHSEGQPGQQQSQLAQLHASLAK	AIQQV	4		914.7046483	3654.787393	0.000451244	12	N	836	870
E9Q7G0	Parental	EAERK	SSLISSLEEEVSILNR	QVLEK	2		888.4734276	1774.931255	0.000451244	14	N	1219	1235
E9Q7G0	Parental	EAERK	SSLISSLEEEVSILNR	QVLEK	3		592.6515517	1774.931255	0.000451244	7	N	1219	1235
E9Q7G0	Parental	QEAER	KSSLISSLEEEVSILNR	QVLEK	3		635.3498728	1903.026218	0.000451244	2	N	1218	1235
E9Q7G0	Parental	PTPAR	GQAPLETSLDSLGDAFPDSGR	KTRSA	2		1067.008894	2132.002189	0.00091018	4	N	1763	1784
E9Q7G0	Parental	LHATR	AATLLSWVNSLHVADPVETVLQLQDCSIFIK	IINTI	3	C26:+57.021	1156.613321	3466.816563	0.000451244	14	N	7	38
E9Q7G0	Parental	SFKVR	EFANHLQQLQGAFNDLIEEHSK	ASQEW	3		856.7546207	2567.240462	0.000998612	1	N	326	348
E9Q7G0	Parental	SFKVR	EFANHLQQLQGAFNDLIEEHSK	ASQEW	4		642.8179155	2567.240462	0.000451244	5	N	326	348

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9Q7G0	Parental	LNEQR	VEFAALQEALAHALTEK	EGTDQ	3		614.3321535	1839.97306	0.000451244	8	N	1029	1046
E9Q7G0	Parental	LLPAK	HLCQQLQAEQAAAEKR	FREEL	3	C3:+57.021	627.6517374	1879.931812	0.000451244	7	N	1360	1376
E9Q7G0	Parental	SKLPR	TQPDGTSVPGEPASPISQR	LPPKV	2		962.4744903	1922.933381	0.000451244	3	N	1725	1744
E9Q7G0	Parental	AEISK	LEQQCQQQQQQVEGLTHSLK	SERAC	3	C5:+57.021	804.0645351	2409.170205	0.000451244	2	N	1127	1147
E9Q7G0	Parental	IHDTK	EGQQILQQPLPER	LDFVC	2		768.412976	1534.810352	0.000451244	7	N	47	60
E9Q7G0	Parental	ITMTK	KLELEEPDSANSSFY	STQSA	2		864.9023037	1727.789007	0.00307782	1	N	1803	1818
E9Q7G0	Parental	LNEQR	VEFAALQEALAHALTEKEGTDQELAK	LRGQE	3		938.150817	2811.429051	0.000451244	6	N	1029	1055
E9Q7G0	Parental	EKDAK	LESLQQQLQAANDAR	DNAQT	2		842.9348039	1683.854008	0.000451244	14	N	610	625
E9Q7G0	Parental	IHDTK	EGQQILQQPLPERLDFVCSFLQK	NRKHP	3	C18:+57.021	925.14994	2772.42642	0.000823681	2	N	47	70
E9Q7G0	Parental	TAQVR	SLEAQVAHADQQLR	DLGKF	2		783.4056822	1564.795764	0.000870037	2	N	1663	1677
E9Q7G0	Parental	KFFQK	EQALSALQLEHTSTQALVSELLPAK	HLCQQ	3		893.1522693	2676.433408	0.001871652	1	N	1335	1360
E9Q8K8	Parental	PSFAR	TVLWNPEDLIPLPIPK	QDVPP	2		923.0301844	1844.044769	0.000451244	19	N	933	949
E9Q8K8	Parental	-MLR	GREDGELEEGELEDDGAEEVQDPPGGQER	SRKEK	3		1047.784138	3140.329015	0.000451244	9	N	3	32
E9Q8K8	Parental	PYDPR	VLAAGGLGQGSSSGQSSVLSGISLYDPR	TPNAG	2		1332.18591	2662.35622	0.001329271	1	N	1076	1104
E9Q8L9	Parental	GSVLR	AGSPESPHTEGTGQEPVTAEAQPNISSEGK	CFPEG	3		998.1309213	2991.369364	0.000622848	15	N	777	807
E9Q8L9	Parental	GKAEK	LVDLEAGVSPWNVSHSILETSGR	SSGRA	3		822.7594831	2465.255049	0.000451244	2	N	897	920
E9Q8L9	Parental	EFQVR	ELEDYIDNLLVR	VMEET	2		746.3886352	1490.76167	0.000451244	4	N	1132	1144
E9QL65	Exosome	YRQMR	DYLSGFQEQCDAILNDVNSALQHQESLQK	QYLFV	3	C10:+57.021	1117.525011	3349.551634	0.000451244	2	N	131	160
E9QL65	Exosome	RFFRL	NSNNALIEFLLEGTPEIR	EHYLD	3		677.3571388	2029.048016	0.001329271	3	N	661	679
E9QL65	Parental	YRQMR	DYLSGFQEQCDAILNDVNSALQHQESLQK	QYLFV	3	C10:+57.021	1117.525011	3349.551634	0.000451244	9	N	131	160
E9QNN1	Exosome	TGCGK	TTQVPQYILDDFIQNDR	AAECN	2		1033.513615	2065.011631	0.000451244	22	N	420	437
E9QNN1	Exosome	TGCGK	TTQVPQYILDDFIQNDR	AAECN	3		689.3450103	2065.011631	0.000451244	23	N	420	437
E9QNN1	Exosome	DKKKK	DKEDDGGEDDDANCNLICGDEYGPETK	LSMSQ	3	C14:+57.021,C18:+57.021	1011.061319	3030.160556	0.000451244	17	N	597	624
E9QNN1	Exosome	EIHER	DINTDFLLVVLR	DVVLA	2		709.4066309	1416.797662	0.000451244	27	N	519	531
E9QNN1	Exosome	FASKK	VQSDGQIVFIDDWIR	LQISH	2		895.9577477	1789.899895	0.000622848	4	N	1077	1092
E9QNN1	Exosome	QLNEK	ETPFELIEALLK	YIETL	2		701.8955647	1401.775529	0.000622848	2	N	633	645
E9QNN1	Exosome	EHTLR	ELDALDANDELTPLGR	ILAKL	2		871.4343024	1740.853005	0.000451244	19	N	840	856
E9QNN1	Exosome	GSNKK	LAAQSCALSLVR	QLYHL	2	C6:+57.021	644.8560196	1287.696439	0.001162105	3	N	239	251
E9QNN1	Exosome	LSLVR	QLYHLGVIEAYSGLTK	KKEGE	3		597.9933607	1790.956682	0.001264573	1	N	251	267
E9QNN1	Exosome	QFLAK	AIEPPPLDAVIEAEHTLR	ELDAL	3		657.6902294	1970.047288	0.001229886	5	N	822	840
E9QNN1	Exosome	LFASK	KVQSDGQIVFIDDWIR	LQISH	3		640.3394195	1917.994859	0.000823681	1	N	1076	1092
E9QNN1	Exosome	ALIHK	SSVNCPFSSQDMKYPSPFFVFGEK	IRTRA	3	C5:+57.021,M12:+15.995	934.42477	2800.25091	0.001329271	3	N	1027	1051
E9QNN1	Parental	TGCGK	TTQVPQYILDDFIQNDR	AAECN	2		1033.513615	2065.011631	0.000451244	33	N	420	437
E9QNN1	Parental	TGCGK	TTQVPQYILDDFIQNDR	AAECN	3		689.3450103	2065.011631	0.000451244	12	N	420	437
E9QNN1	Parental	DGVTK	VILSTNIAETSITINDVVYVIDSCKQK	VKLFT	3	C24:+57.021	1008.537529	3022.589188	0.000979378	3	N	711	738
E9QNN1	Parental	HLALK	AEAENNSGVESSGYGSPGPTWDR	GANLK	2		1184.010154	2366.004708	0.000451244	47	N	121	144
E9QNN1	Parental	DKKKK	DKEDDGGEDDDANCNLICGDEYGPETK	LSMSQ	3	C14:+57.021,C18:+57.021	1011.061319	3030.160556	0.000451244	18	N	597	624
E9QNN1	Parental	DYYSR	KEEQEVQATLESEEVDLNAGLHGNWTLENAK	ARLNQ	3		1161.229295	3480.664484	0.000622848	1	N	154	185
E9QNN1	Parental	DYYSR	KEEQEVQATLESEEVDLNAGLHGNWTLENAK	ARLNQ	4		871.1739209	3480.664484	0.000622848	3	N	154	185
E9QNN1	Parental	EIHER	DINTDFLLVVLR	DVVLA	2		709.4066309	1416.797662	0.000451244	12	N	519	531
E9QNN1	Parental	QLNEK	ETPFELIEALLK	YIETL	2		701.8955647	1401.775529	0.000823681	2	N	633	645
E9QNN1	Parental	EHTLR	ELDALDANDELTPLGR	ILAKL	2		871.4343024	1740.853005	0.000451244	5	N	840	856
E9QNN1	Parental	GSNKK	LAAQSCALSLVR	QLYHL	2	C6:+57.021	644.8560196	1287.696439	0.000823681	8	N	239	251
E9QNN1	Parental	LSLVR	QLYHLGVIEAYSGLTK	KKEGE	3		597.9933607	1790.956682	0.002519933	1	N	251	267
E9QNN1	Parental	IQNDR	AAECNIVVTQPR	RISAV	2	C4:+57.021	679.3485587	1356.681517	0.000451244	33	N	437	449
E9QNN1	Parental	QFLAK	AIEPPPLDAVIEAEHTLR	ELDAL	3		657.6902294	1970.047288	0.000698008	2	N	822	840
E9QNN1	Parental	LALKA	EAENNSGVESSGYGSPGPTWDR	GANLK	2		1148.491597	2294.967594	0.001839721	1	N	122	144
E9QPU1	Exosome	GKIVK	IPGTCCDTCEEPDCKDITAK	VQYIK	2	C5:+57.021,C6:+57.021,C9:+57.021,C14:+57.021	1185.489057	2368.962514	0.000451244	8	N	2713	2733
E9QPU1	Exosome	GKIVK	IPGTCCDTCEEPDCKDITAK	VQYIK	3	C5:+57.021,C6:+57.021,C9:+57.021,C14:+57.021	790.6619713	2368.962514	0.000451244	37	N	2713	2733
E9QPU1	Exosome	VVGLR	VVQCSQRPCEDSCQPGFSYVLHEGECCGR	CLPSA	3	C4:+57.021,C9:+57.021,C13:+57.021,C26:+57.021,C27:+57.021	1167.821177	3500.440131	0.000451244	35	N	2467	2496
E9QPU1	Exosome	VVGLR	VVQCSQRPCEDSCQPGFSYVLHEGECCGR	CLPSA	4	C4:+57.021,C9:+57.021,C13:+57.021,C26:+57.021,C27:+57.021	876.1178329	3500.440131	0.000451244	24	N	2467	2496
E9QPU1	Exosome	KCASK	AVYSIDIEDVQEQCSCCLPSR	TEPMR	2	C14:+57.021,C16:+57.021,C17:+57.021	1265.056184	2528.096768	0.000451244	26	N	2760	2781
E9QPU1	Exosome	KCASK	AVYSIDIEDVQEQCSCCLPSR	TEPMR	3	C14:+57.021,C16:+57.021,C17:+57.021	843.7067227	2528.096768	0.000451244	24	N	2760	2781
E9QPU1	Exosome	CPPGR	ILDELLQTCVDPQDCPVCEVAGRR	LAPGK	3	C9:+57.021,C15:+57.021,C18:+57.021	948.4543976	2842.339793	0.000451244	26	N	1184	1208
E9QPU1	Exosome	AFISK	ANIGPHLTQVSVIQYGSINTIDVPWNVVQEK	AHLQS	3		1140.603967	3418.788502	0.000451244	38	N	1723	1754
E9QPU1	Exosome	FDGLK	YLFPGECQYVLVQDYCGSNPGTFQILVGNEGCSYPSVK	CRKRV	3	C7:+57.021,C16:+57.021,C32:+57.021	1449.334209	4344.979227	0.000451244	26	N	885	923

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9QPU1	Exosome	FDGLK	YLFPGECQYVLVQDYCGSNPGTFQILVGNEGCSYPSVK	CRKRV	4	C7:+57.021,C16:+57.021,C32:+57.021	1087.252607	4344.979227	0.000622848	2	N	885	923
E9QPU1	Exosome	SEVLK	YTLFQIFGK	IDRPE	2		558.808564	1115.601528	0.000451244	26	N	1365	1374
E9QPU1	Exosome	DSACR	ILTSDVFQGCNR	LVDPE	2	C10:+57.021	705.346016	1408.676432	0.000451244	18	N	1064	1076
E9QPU1	Exosome	ALCEK	ILCTCATGPECACPVLLEYAR	TCAQE	2	C3:+57.021,C5:+57.021,C11:+57.021,C13:+57.021	1227.567445	2453.119289	0.000622848	1	N	255	276
E9QPU1	Exosome	ALCEK	ILCTCATGPECACPVLLEYAR	TCAQE	3	C3:+57.021,C5:+57.021,C11:+57.021,C13:+57.021	818.7142298	2453.119289	0.000451244	8	N	255	276
E9QPU1	Exosome	VYSGK	TCGLCGNYNGNKGDDFLTPAGLVEPLVVDFGNAWK	LQGDC	3	C2:+57.021,C5:+57.021	1266.934751	3797.780854	0.000451244	20	N	522	557
E9QPU1	Exosome	AECHK	VIAPATFHTICQQDSCHQER	VCEVI	2	C11:+57.021,C16:+57.021	1199.555034	2397.094469	0.000451244	2	N	2155	2175
E9QPU1	Exosome	AECHK	VIAPATFHTICQQDSCHQER	VCEVI	3	C11:+57.021,C16:+57.021	800.0392897	2397.094469	0.000451244	9	N	2155	2175
E9QPU1	Exosome	AECHK	VIAPATFHTICQQDSCHQER	VCEVI	4	C11:+57.021,C16:+57.021	600.2814172	2397.094469	0.000662267	1	N	2155	2175
E9QPU1	Exosome	PRLTR	FAEEACALLTSSK	FEACH	2	C6:+57.021	713.8480572	1425.680514	0.000451244	12	N	581	594
E9QPU1	Exosome	QGGNR	TNTGQALQYLSEHSFSPSQGDR	VEAPN	2		1212.065264	2422.114927	0.000451244	9	N	1578	1600
E9QPU1	Exosome	QGGNR	TNTGQALQYLSEHSFSPSQGDR	VEAPN	3		808.3794423	2422.114927	0.000451244	16	N	1578	1600
E9QPU1	Exosome	SVGSR	WAVPENPCLVNECVR	VEDAV	2	C8:+57.021,C13:+57.021	921.9349724	1841.854345	0.000451244	35	N	2523	2538
E9QPU1	Exosome	MYEVR	FTHLGHILTYTPQNNEFQLQLSPK	TFASK	2		1413.732831	2825.450061	0.002981883	1	N	2054	2078
E9QPU1	Exosome	MYEVR	FTHLGHILTYTPQNNEFQLQLSPK	TFASK	3		942.824487	2825.450061	0.000451244	11	N	2054	2078
E9QPU1	Exosome	MYEVR	FTHLGHILTYTPQNNEFQLQLSPK	TFASK	4		707.3703153	2825.450061	0.000823681	7	N	2054	2078
E9QPU1	Exosome	APENK	AFLLSGVDELEQR	RDEIV	2		738.8888023	1475.762005	0.000451244	18	N	1439	1452
E9QPU1	Exosome	APENK	AFLLSGVDELEQR	RDEIV	3		492.9284682	1475.762005	0.000451244	2	N	1439	1452
E9QPU1	Exosome	LVKLK	HGGAVGIDGQDVQLPFLQGDLR	IQHTV	2		1146.59072	2291.16584	0.000451244	9	N	462	484
E9QPU1	Exosome	LVKLK	HGGAVGIDGQDVQLPFLQGDLR	IQHTV	3		764.7297468	2291.16584	0.000451244	18	N	462	484
E9QPU1	Exosome	CPPGR	ILDELLQTCVDPQDCPVCEVAGR	RLAPG	2	C9:+57.021,C15:+57.021,C18:+57.021	1344.127141	2686.238682	0.000451244	33	N	1184	1207
E9QPU1	Exosome	CPPGR	ILDELLQTCVDPQDCPVCEVAGR	RLAPG	3	C9:+57.021,C15:+57.021,C18:+57.021	896.4206938	2686.238682	0.000451244	12	N	1184	1207
E9QPU1	Exosome	YNGNK	GDDFLTPAGLVEPLVVDFGNAWK	LQGDC	2		1230.626437	2459.237274	0.000451244	22	N	534	557
E9QPU1	Exosome	YNGNK	GDDFLTPAGLVEPLVVDFGNAWK	LQGDC	3		820.753558	2459.237274	0.000451244	5	N	534	557
E9QPU1	Exosome	IMTLK	QDETFQDGCDSHLCR	VNERG	2	C9:+57.021,C14:+57.021	934.3703906	1866.725181	0.000451244	4	N	2665	2680
E9QPU1	Exosome	IMTLK	QDETFQDGCDSHLCR	VNERG	3	C9:+57.021,C14:+57.021	623.249527	1866.725181	0.000622848	6	N	2665	2680
E9QPU1	Exosome	IMTLK	QDETFQDGCDSHLCR	VNERG	2	[0:-	925.8568906	1849.698181	0.001162105	7	N	2665	2680
E9QPU1	Exosome	EAQLR	ILAGPGASSNVVK	LQQVE	2		606.8514915	1211.687383	0.000698008	6	N	1840	1853
E9QPU1	Exosome	VALER	CPCFHQGAEYAPGDTVK	IGCNT	2	C1:+39.994,C3:+57.021	960.4060193	1918.796439	0.000451244	6	N	829	846
E9QPU1	Exosome	VALER	CPCFHQGAEYAPGDTVK	IGCNT	2	C1:+57.021,C3:+57.021	968.9195193	1935.823439	0.000451244	6	N	829	846
E9QPU1	Exosome	VALER	CPCFHQGAEYAPGDTVK	IGCNT	3	C1:+57.021,C3:+57.021	646.2822795	1935.823439	0.000451244	22	N	829	846
E9QPU1	Exosome	VALER	CPCFHQGAEYAPGDTVK	IGCNT	2	[0:-17.027,C1:+57.021,C3:+57.021	960.4060193	1918.796439	0.000451244	11	N	829	846
E9QPU1	Exosome	TCGCR	WTCPCVCTGSSTR	HIVTF	2	C3:+57.021,C5:+57.021,C7:+57.02	786.3234378	1570.631276	0.000451244	10	N	1946	1959
E9QPU1	Exosome	NECVR	VEDAVFVQQR	NISCP	2		595.8123663	1189.609133	0.000622848	4	N	2538	2548
E9QPU1	Exosome	VCVHR	GTVYPVGQFWEEGCDTCTCTDMEDTVVGLR	VVQCS	3	C14:+57.021,C17:+57.021,C19:+57.021,M22:+15.995	1166.824696	3497.450688	0.000451244	25	N	2437	2467
E9QPU1	Exosome	TSQIK	YTGSQVASTSEVLK	YTLFQ	2		735.3782675	1468.740935	0.000451244	19	N	1351	1365
E9QPU1	Exosome	CSDSR	DCLCNAVANYAAECAR	KGVHI	2	C2:+57.021,C4:+57.021,C14:+57.021	929.3872977	1856.758995	0.000451244	8	N	622	638
E9QPU1	Exosome	SPCPR	TCQSLSINEVCQQQCVDGCSCPEGELLDEDR	CVQSS	3	C2:+57.021,C11:+57.021,C15:+57.021,C19:+57.021,C21:+57.021	1229.508993	3685.503579	0.000451244	23	N	313	344
E9QPU1	Exosome	NLTCR	SLSLPDEECSEVCLEGCYCPPGLYQDER	GDCVP	3	C9:+57.021,C13:+57.021,C17:+57.021,C19:+57.021	1121.469959	3361.386476	0.000451244	16	N	673	701
E9QPU1	Exosome	KCRKR	VTILVDGGELELFDGEVNVK	RPLRD	2		1073.568056	2145.120513	0.000451244	20	N	927	947
E9QPU1	Exosome	TCICR	NSLWICSNEECPGECLVTGQSHFK	SFDNR	2	C6:+57.021,C11:+57.021,C15:+57.021	1426.625297	2851.234993	0.000622848	4	N	376	400
E9QPU1	Exosome	TCICR	NSLWICSNEECPGECLVTGQSHFK	SFDNR	3	C6:+57.021,C11:+57.021,C15:+57.021	951.4194644	2851.234993	0.000451244	17	N	376	400
E9QPU1	Exosome	ETLPR	EAPDLVLQTCCSK	EGLQL	2	C10:+57.021,C11:+57.021	760.8578677	1519.700135	0.000451244	23	N	1662	1675
E9QPU1	Exosome	CHQER	VCEVIASYAHLCR	TSGVC	2	C2:+57.021,C12:+57.021	789.3818443	1576.748089	0.000451244	6	N	2175	2188
E9QPU1	Exosome	QIFGK	IDRPEASHITLLLTASQEPPR	MARNL	2		1172.635128	2343.254655	0.00307782	1	N	1374	1395
E9QPU1	Exosome	QIFGK	IDRPEASHITLLLTASQEPPR	MARNL	3		782.0926851	2343.254655	0.000698008	7	N	1374	1395
E9QPU1	Exosome	ARSNR	VAVFPVGVGDRYDEAQLR	ILAGP	2		996.0214107	1990.027221	0.000622848	3	N	1822	1840
E9QPU1	Exosome	ARSNR	VAVFPVGVGDRYDEAQLR	ILAGP	3		664.3502071	1990.027221	0.000622848	8	N	1822	1840
E9QPU1	Exosome	SVFAR	CHPLVDPESFVALCEK	ILCTC	2	C1:+39.994,C14:+57.021	942.4367882	1882.857976	0.000451244	6	N	239	255
E9QPU1	Exosome	SVFAR	CHPLVDPESFVALCEK	ILCTC	3	C1:+57.021,C14:+57.021	634.3027921	1899.884976	0.000451244	15	N	239	255
E9QPU1	Exosome	SVFAR	CHPLVDPESFVALCEK	ILCTC	2	[0:-	942.4367882	1882.857976	0.000451244	1	N	239	255
E9QPU1	Exosome	HCPPG	RILDELLQTCVDPQDCPVCEVAGR	RLAPG	3	C10:+57.021,C16:+57.021,C19:+57.021	948.4543976	2842.339793	0.000451244	12	N	1183	1207
E9QPU1	Exosome	ECCGR	CLPTACTIQLR	GGRIM	2	[0:-17.027,C1:+57.021,C6:+57.021	658.3283236	1314.641047	0.000870037	5	N	2646	2657

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
E9QPU1	Exosome	FYCSK	LLDLVFLLDGSSMLSEAEFEVLK	AFVVG	3	M13:+15.995	862.1209475	2583.339443	0.000998612	1	N	1277	1300
E9QPU1	Exosome	LQSHR	VNCDHGPRPSCANSQSPVRVEETCGCR	WTCPC	4	C3:+57.021,C11:+57.021,C24:+57.021,C26:+57.021	783.0921624	3128.337449	0.001162105	4	N	1919	1946
E9QPU1	Exosome	IGPGK	SVMVDLCTTCR	CIVQT	2	M3:+15.995,C7:+57.021,C10:+57.021	679.2991746	1356.582749	0.00091018	1	N	2596	2607
E9QPU1	Exosome	HAGKR	YPPGTSLSQDCNTCICR	NSLWI	2	C11:+57.021,C14:+57.021,C16:+57.021	1014.932069	2027.848539	0.000451244	24	N	359	376
E9QPU1	Exosome	EDDFR	TQEGTLTSDPYDFANSWALSSEEQR	CKRAS	2		1416.633904	2831.252209	0.000451244	19	N	177	202
E9QPU1	Exosome	VHAGK	RYPPGTSLSQDCNTCICR	NSLWI	3	C12:+57.021,C15:+57.021,C17:+57.021	728.9910167	2183.94965	0.000451244	20	N	358	376
E9QPU1	Exosome	SFFHK	LCSGFSGVCVDEDGNEK	RPGDV	2	C2:+57.021,C9:+57.021	936.8906245	1871.765649	0.000451244	2	N	1873	1890
E9QPU1	Exosome	AGYYK	LSSETFGFAAR	IDGNG	2		593.2990917	1184.582583	0.000451244	1	N	131	142
E9QPU1	Exosome	TFASK	MHGLCGICDENGANDFTLR	DGTVT	2	C5:+57.021,C8:+57.021	1090.469582	2178.923565	0.000451244	1	N	2083	2102
E9QPU1	Exosome	NLTCR	SLSLPDEECSEVCLEGCYCPPGLYQDERGDCVPK	AQCPC	3	C9:+57.021,C13:+57.021,C17:+57.021,C19:+57.021,C31:+57.021	1340.23487	4017.68121	0.000451244	10	N	673	707
E9QPU1	Exosome	LQNCR	YDVCSCSDSRDCLCNAVANYAAECAR	KGVHI	3	C4:+57.021,C6:+57.021,C12:+57.021,C14:+57.021,C24:+57.021	1029.741864	3086.202192	0.000451244	5	N	612	638
E9QPU1	Exosome	VVQEK	AHLQSLVDLMQQEGGPSQIGDALAFAVR	YVTSQ	3		984.5068296	2950.497089	0.000451244	3	N	1754	1782
E9QPU1	Exosome	DFTTS	SLQVEEDPVNFGNSWK	VSSQC	2		924.9422946	1847.868989	0.000451244	5	N	1013	1029
E9QPU1	Exosome	DFNIF	AEDDFRTQEGTLTSDPYDFANSWALSSEEQR	CKRAS	3		1189.192909	3564.555327	0.000451244	1	N	171	202
E9QPU1	Parental	GKIVK	IPGTCCDTCEEPDCKDITAK	VQYIK	2	C5:+57.021,C6:+57.021,C9:+57.021,C14:+57.021	1185.489057	2368.962514	0.000451244	4	N	2713	2733
E9QPU1	Parental	GKIVK	IPGTCCDTCEEPDCKDITAK	VQYIK	3	C5:+57.021,C6:+57.021,C9:+57.021,C14:+57.021	790.6619713	2368.962514	0.000451244	9	N	2713	2733
E9QPU1	Parental	VVGLR	VVQCSQRPCEDSCQPGFSYVLHEGECCGR	CLPSA	3	C4:+57.021,C9:+57.021,C13:+57.021,C26:+57.021,C27:+57.021	1167.821177	3500.440131	0.000451244	20	N	2467	2496
E9QPU1	Parental	VVGLR	VVQCSQRPCEDSCQPGFSYVLHEGECCGR	CLPSA	4	C4:+57.021,C9:+57.021,C13:+57.021,C26:+57.021,C27:+57.021	876.1178329	3500.440131	0.002884417	1	N	2467	2496
E9QPU1	Parental	KCASK	AVYSIDIEDVQEQCSCCLPSR	TEPMR	2	C14:+57.021,C16:+57.021,C17:+57.021	1265.056184	2528.096768	0.000451244	8	N	2760	2781
E9QPU1	Parental	KCASK	AVYSIDIEDVQEQCSCCLPSR	TEPMR	3	C14:+57.021,C16:+57.021,C17:+57.021	843.7067227	2528.096768	0.000622848	2	N	2760	2781
E9QPU1	Parental	CPPGR	ILDELLQTCVDPQDCPVCEVAGRR	LAPGK	3	C9:+57.021,C15:+57.021,C18:+57.021	948.4543976	2842.339793	0.000451244	14	N	1184	1208
E9QPU1	Parental	AFISK	ANIGPHLTQVSVIQYGSINTIDVPWNVVQEK	AHLQS	3		1140.603967	3418.788502	0.000451244	23	N	1723	1754
E9QPU1	Parental	FDGLK	YLFPGECQYVLVQDYCGSNPGTFQILVGNEGCSYPSVK	CRKRV	3	C7:+57.021,C16:+57.021,C32:+57.021	1449.334209	4344.979227	0.000451244	21	N	885	923
E9QPU1	Parental	FDGLK	YLFPGECQYVLVQDYCGSNPGTFQILVGNEGCSYPSVK	CRKRV	4	C7:+57.021,C16:+57.021,C32:+57.021	1087.252607	4344.979227	0.00091018	3	N	885	923
E9QPU1	Parental	SEVLK	YTLFQIFGK	IDRPE	2		558.808564	1115.601528	0.001329271	1	N	1365	1374
E9QPU1	Parental	DSACR	ILTSDVFQGCNR	LVDPE	2	C10:+57.021	705.346016	1408.676432	0.000451244	7	N	1064	1076
E9QPU1	Parental	ALCEK	ILCTCATGPECACPVLLEYAR	TCAQE	2	C3:+57.021,C5:+57.021,C11:+57.021,C13:+57.021	1227.567445	2453.119289	0.000451244	18	N	255	276
E9QPU1	Parental	VYSGK	TCGLCGNYNGNKGDDFLTPAGLVEPLVVDFGNAWK	LQGDC	3	C2:+57.021,C5:+57.021	1266.934751	3797.780854	0.000451244	8	N	522	557
E9QPU1	Parental	AECHK	VIAPATFHTICQQDSCHQER	VCEVI	3	C11:+57.021,C16:+57.021	800.0392897	2397.094469	0.000451244	5	N	2155	2175
E9QPU1	Parental	SVGSR	WAVPENPCLVNECVR	VEDAV	2	C8:+57.021,C13:+57.021	921.9349724	1841.854345	0.000451244	7	N	2523	2538
E9QPU1	Parental	MYEVR	FTHLGHILTYTPQNNEFQLQLSPK	TFASK	2		1413.732831	2825.450061	0.002813207	1	N	2054	2078
E9QPU1	Parental	CPPGR	ILDELLQTCVDPQDCPVCEVAGR	RLAPG	2	C9:+57.021,C15:+57.021,C18:+57.021	1344.127141	2686.238682	0.000451244	5	N	1184	1207
E9QPU1	Parental	YNGNK	GDDFLTPAGLVEPLVVDFGNAWK	LQGDC	2		1230.626437	2459.237274	0.000622848	2	N	534	557
E9QPU1	Parental	VALER	CPCFHQGAEYAPGDTVK	IGCNT	3	C1:+57.021,C3:+57.021	646.2822795	1935.823439	0.000451244	3	N	829	846
E9QPU1	Parental	TCGCR	WTCPCVCTGSSTR	HIVTF	2	C3:+57.021,C5:+57.021,C7:+57.02	786.3234378	1570.631276	0.0025889	1	N	1946	1959
E9QPU1	Parental	TCICR	NSLWICSNEECPGECLVTGQSHFK	SFDNR	2	C6:+57.021,C11:+57.021,C15:+57.021	1426.625297	2851.234993	0.000451244	1	N	376	400
E9QPU1	Parental	TCICR	NSLWICSNEECPGECLVTGQSHFK	SFDNR	3	C6:+57.021,C11:+57.021,C15:+57.021	951.4194644	2851.234993	0.000451244	8	N	376	400
E9QPU1	Parental	ETLPR	EAPDLVLQTCCSK	EGLQL	2	C10:+57.021,C11:+57.021	760.8578677	1519.700135	0.000823681	3	N	1662	1675
E9QPU1	Parental	VHAGK	RYPPGTSLSQDCNTCICR	NSLWI	3	C12:+57.021,C15:+57.021,C17:+57.021	728.9910167	2183.94965	0.001162105	2	N	358	376
E9QPU1	Parental	QELER	ISRPIAPIFIRDFETLPR	EAPDL	4		536.0617227	2140.215691	0.002519933	5	N	1644	1662
E9QPU1	Parental	NLTCR	SLSLPDEECSEVCLEGCYCPPGLYQDERGDCVPK	AQCPC	3	C9:+57.021,C13:+57.021,C17:+57.021,C19:+57.021,C31:+57.021	1340.23487	4017.68121	0.000451244	7	N	673	707
E9QPU1	Parental	GQNFK	LTGSCSYVIFQNKEQDLEVLLHNGACSPGAK	QACMK	3	C5:+57.021,C26:+57.021	1145.894116	3434.658947	0.000622848	4	N	1970	2001
F6RPJ9	Exosome	KLPTK	NEFIPTNFEILSLEK	DATPY	2		897.4701566	1792.924713	0.000622848	7	N	495	510
F6RPJ9	Exosome	IKDIR	NLYVTFPIPDLQQYYK	SNPGH	2		1001.520181	2001.024762	0.000823681	2	N	279	295

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
F6RPJ9	Exosome	GALDR	FAQFFLCPLFDASCK	DREVN	2	C7:+57.021,C14:+57.021	925.9339097	1849.852219	0.000451244	6	N	132	147
F6RPJ9	Exosome	GALDR	FAQFFLCPLFDASCKDR	EVNAV	3	C7:+57.021,C14:+57.021	708.0012246	2120.980274	0.002813207	1	N	132	149
F6RPJ9	Exosome	CVLGR	ESLDDLTNLVVK	LFSEV	2		673.3646287	1344.713657	0.001395409	1	N	229	241
F6RPJ9	Parental	IKDIR	NLYVTFPIPDLQQYYK	SNPGH	2		1001.520181	2001.024762	0.002080925	1	N	279	295
F6ZDS4	Exosome	SELKK	TLSTVQNEVQEALQR	ASTAL	2		858.4502868	1714.884974	0.001329271	2	N	1112	1127
F6ZDS4	Exosome	LAEQR	GQNLLLTNLQTIQGILER	SETET	3		675.3886619	2023.142586	0.000622848	1	N	884	902
F6ZDS4	Exosome	IRDEE	VSSADISSSSEVISQHLVSYR	NIEEL	4		563.5360004	2250.112802	0.001763695	2	N	594	615
F6ZDS4	Parental	NKLEK	FLAEQQSEIDCLK	GRHEK	2	C11:+57.021	790.8851711	1579.754742	0.000451244	11	N	101	114
F6ZDS4	Parental	SELKK	TLSTVQNEVQEALQR	ASTAL	2		858.4502868	1714.884974	0.00091018	11	N	1112	1127
F6ZDS4	Parental	LAEQR	GQNLLLTNLQTIQGILER	SETET	2		1012.579093	2023.142586	0.000451244	29	N	884	902
F6ZDS4	Parental	LAEQR	GQNLLLTNLQTIQGILER	SETET	3		675.3886619	2023.142586	0.000451244	15	N	884	902
F6ZDS4	Parental	ETEAR	SLQEQTVQLQSELSR	LRQDL	2		873.4555692	1744.895538	0.000451244	21	N	1586	1601
F6ZDS4	Parental	ASGER	GIASTSDPPTANIKPTPVVSTPSK	VTAAA	3		789.0923508	2364.253652	0.001699387	1	N	1726	1750
F6ZDS4	Parental	LSTPK	RSSTSQTVSTPAPEPVIDSTEAIEAK	AALKQ	3		901.122927	2700.345381	0.000698008	2	N	717	743
F6ZDS4	Parental	ESHQR	AADSQNSGEGNTSAAESSFSQEVAR	EQQPT	2		1250.545089	2499.074578	0.000451244	2	N	2098	2123
F6ZDS4	Parental	LEEAR	GNHVIRDEEVSSADISSSSEVISQHLVSYR	NIEEL	3		1100.875075	3299.601824	0.002145581	1	N	585	615
F6ZDS4	Parental	LEEAR	GNHVIRDEEVSSADISSSSEVISQHLVSYR	NIEEL	4		825.9082559	3299.601824	0.000451244	6	N	585	615
F6ZDS4	Parental	QAKVR	KLELDILPLQEANAELSEK	SGMLQ	2		1077.089156	2152.162712	0.002019181	2	N	1372	1391
F6ZDS4	Parental	QAKVR	KLELDILPLQEANAELSEK	SGMLQ	3		718.3953707	2152.162712	0.000451244	12	N	1372	1391
F6ZDS4	Parental	VTSMK	DAVQAPLNVSLNEEGKSQEQILEILR	FIRRE	3		965.1808877	2892.519263	0.000698008	6	N	1249	1275
F6ZDS4	Parental	AEIAR	SNASLTNNQNLIQSLR	EDLSK	2		886.9666354	1771.917671	0.000622848	1	N	1458	1474
F6ZDS4	Parental	ELLER	ELQELQDSLNVER	EKVQV	2		786.8973557	1571.779111	0.000451244	2	N	1307	1320
F6ZDS4	Parental	STPKR	SSTSQTVSTPAPEPVIDSTEAIEAK	AALKQ	2		1273.129935	2544.24427	0.002145581	2	N	718	743
F6ZDS4	Parental	ELQHK	LENSLAELEQLR	ESRQH	2		707.8809773	1413.746355	0.001395409	4	N	656	668
F6ZDS4	Parental	KPGMK	LTELYNAYVETQDQLLLEK	QENKR	2		1142.091896	2282.168191	0.000622848	4	N	468	487
F7BJB9	Parental	TSTSR	SDPGITVSTQTDAPGLTVK	KEESM	2		943.9894418	1885.963284	0.002453667	1	N	638	657
F7BJB9	Parental	VEQLK	STGQQAAADGSTASNAEEPVSYVDGESLK	LRSLR	3		957.1043722	2868.289717	0.000451244	1	N	865	894
F8VPN4	Exosome	DPILR	IGVDNHVLPLDCVTLQTFLAK	CLGPF	3	C12:+57.021	785.0913624	2352.250687	0.000451244	5	N	114	135
F8VPN4	Exosome	TLQGK	AVTVYTNYPLPGEAFNR	EKFRS	2		956.4841296	1910.952659	0.001162105	3	N	42	59
F8VPN4	Exosome	SIASK	LTLAELNQVLYR	CESEE	2		716.9120805	1431.808561	0.000622848	5	N	898	910
F8VPN4	Parental	RYNCR	DAVWWWLQCIQDYCR	TVPNG	2	C9:+57.021,C14:+57.021	1049.966804	2097.918008	0.000637154	3	N	1151	1166
F8VQC1	Parental	NQIIK	LKPTDVALLAVIANNIITINKDQNVFDSK	KKVKL	4		792.6978406	3166.760162	0.000662267	3	N	254	283
F8VQC1	Parental	EQCRK	IAASLQSQSPEYLLPVLIQAAQLCR	EKQHT	3	C24:+57.021	923.8374735	2768.48902	0.000451244	14	N	325	350
F8WI35	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	2		668.349313	1334.683026	0.000451244	87	Y	73	84
F8WI35	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	3		445.902142	1334.683026	0.000451244	127	Y	73	84
F8WI35	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	2	[0:-18.011	659.343813	1316.672026	0.002212458	1	Y	73	84
F8WI35	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	24	Y	73	84
F8WI35	Exosome	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	205	Y	101	115
F8WI35	Exosome	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	51	Y	99	115
F8WI35	Exosome	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	68	Y	99	115
F8WI35	Exosome	QASEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	28	Y	98	115
F8WI35	Exosome	QASEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002080925	1	Y	98	115
F8WI35	Exosome	FKTDL	RFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1155.59292	3463.755359	0.000451244	61	N	83	115
F8WI35	Exosome	FKTDL	RFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C27:+57.021	866.9466399	3463.755359	0.000451244	96	N	83	115
F8WI35	Exosome	SAAIG	ALQASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C19:+57.021	1317.665536	2633.315473	0.000698008	5	N	91	115
F8WI35	Exosome	SAAIG	ALQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C19:+57.021	878.7796242	2633.315473	0.000451244	17	N	91	115
F8WI35	Exosome	SEAYL	VGLFEDTNLCAIHAK	RVTIM	2	C10:+57.021	844.4275375	1686.839475	0.000451244	56	Y	100	115
F8WI35	Exosome	AAIGA	LQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C18:+57.021	855.1005862	2562.278359	0.001463592	2	N	92	115
F8WI35	Exosome	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	56	Y	103	115
F8WI35	Exosome	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	68	Y	102	115
F8WI35	Exosome	DFKTD	LRFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C28:+57.021	895.2176559	3576.839423	0.00307782	2	N	82	115
F8WI35	Exosome	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.001699387	2	Y	104	115
F8WI35	Exosome	KTDLR	FQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C26:+57.021	827.9213621	3307.654248	0.000451244	6	N	84	115
F8WI35	Exosome	GALQA	SEAYLVGLFEDTNLCAIHAK	RVTIM	2	C15:+57.021	1126.057102	2250.098603	0.000451244	18	Y	95	115
F8WI35	Exosome	GALQA	SEAYLVGLFEDTNLCAIHAK	RVTIM	3	C15:+57.021	751.0406677	2250.098603	0.000451244	26	Y	95	115
F8WI35	Exosome	ALQAS	EAYLVGLFEDTNLCAIHAK	RVTIM	2	C14:+57.021	1082.541087	2163.066575	0.000451244	10	Y	96	115
F8WI35	Exosome	ALQAS	EAYLVGLFEDTNLCAIHAK	RVTIM	2	E1:-18.011,C14:+57.021	1073.535587	2145.055575	0.001871652	3	Y	96	115
F8WI35	Exosome	IGALQ	ASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C16:+57.021	1161.575659	2321.135717	0.000451244	2	Y	94	115
F8WI35	Exosome	IGALQ	ASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C16:+57.021	774.7197057	2321.135717	0.000451244	15	Y	94	115
F8WI35	Exosome	LQASE	AYLVGLFEDTNLCAIHAK	RVTIM	2	C13:+57.021	1018.019791	2034.023981	0.000451244	5	Y	97	115
F8WI35	Exosome	AIGAL	QASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C17:+57.021	1225.604947	2449.194295	0.002374549	1	N	93	115
F8WI35	Parental	QRLVR	EIAQDFKTDLR	FQSAA	2		668.349313	1334.683026	0.000451244	20	Y	73	84
F8WI35	Parental	QRLVR	EIAQDFKTDLR	FQSAA	3		445.902142	1334.683026	0.000451244	88	Y	73	84
F8WI35	Parental	QRLVR	EIAQDFKTDLR	FQSAA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	2	Y	73	84
F8WI35	Parental	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	49	Y	101	115

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
F8WI35	Parental	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	188	Y	99	115
F8WI35	Parental	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	307	Y	99	115
F8WI35	Parental	QASEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	7	Y	98	115
F8WI35	Parental	QASEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002727428	1	Y	98	115
F8WI35	Parental	FKTDL	RFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1155.59292	3463.755359	0.000451244	10	N	83	115
F8WI35	Parental	FKTDL	RFQSAAIGALQASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C27:+57.021	866.9466399	3463.755359	0.000451244	29	N	83	115
F8WI35	Parental	SAAIG	ALQASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C19:+57.021	1317.665536	2633.315473	0.000451244	11	N	91	115
F8WI35	Parental	SAAIG	ALQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C19:+57.021	878.7796242	2633.315473	0.000451244	16	N	91	115
F8WI35	Parental	ASEAY	LVGLFEDTNLCAIHAKR	VTIMP	2	C11:+57.021	979.0201251	1956.02465	0.001871652	2	Y	99	116
F8WI35	Parental	ASEAY	LVGLFEDTNLCAIHAKR	VTIMP	4	C11:+57.021	490.0139625	1956.02465	0.000451244	6	Y	99	116
F8WI35	Parental	SEAYL	VGLFEDTNLCAIHAK	RVTIM	3	C10:+57.021	563.287625	1686.839475	0.000998612	3	Y	100	115
F8WI35	Parental	AAIGA	LQASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C18:+57.021	1282.146979	2562.278359	0.00091018	1	N	92	115
F8WI35	Parental	AAIGA	LQASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C18:+57.021	855.1005862	2562.278359	0.000451244	1	N	92	115
F8WI35	Parental	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	2	Y	103	115
F8WI35	Parental	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	5	Y	102	115
F8WI35	Parental	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.000451244	1	Y	104	115
G3UWD6	Exosome	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	3		917.4551224	2749.341967	0.000451244	18	Y	175	198
G3UWD6	Exosome	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	4		688.3432918	2749.341967	0.000451244	7	Y	175	198
G3UWD6	Exosome	GTEGR	GGYFDEFGIIR	DVMQS	2		637.3147418	1272.613884	0.000451244	33	Y	246	257
G3UWD6	Exosome	PIWNG	DNIACVILTFKEPFGTEGR	GGYFD	2	C5:+57.021	1084.046537	2166.077474	0.000451244	40	Y	227	246
G3UWD6	Exosome	PIWNG	DNIACVILTFKEPFGTEGR	GGYFD	3	C5:+57.021	723.0336246	2166.077474	0.000451244	52	Y	227	246
G3UWD6	Exosome	DLAKK	KIYPTIWWLFR	DGLLP	3		508.2910126	1521.849638	0.001162105	7	Y	46	57
G3UWD6	Exosome	LAKKK	IYPTIWWLFR	DGLLP	2		697.8851373	1393.754675	0.000451244	37	Y	47	57
G3UWD6	Exosome	MQANH	LFYLALPPTVYEAVTK	NIQET	2		913.0114603	1824.007321	0.000451244	23	Y	136	152
G3UWD6	Exosome	MQANH	LFYLALPPTVYEAVTK	NIQET	3		609.0102402	1824.007321	0.000451244	26	Y	136	152
G3UWD6	Exosome	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	2		973.4904747	1944.965349	0.000451244	39	Y	175	192
G3UWD6	Exosome	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	3		649.3295831	1944.965349	0.000451244	18	Y	175	192
G3UWD6	Exosome	PIWNG	DNIACVILTFK	EPFGT	2	C5:+57.021	647.3474961	1292.679392	0.000451244	5	Y	227	238
G3UWD6	Exosome	GPIWN	GDNIACVILTFK	EPFGT	2	C6:+57.021	675.858228	1349.700856	0.000451244	16	N	226	238
G3UWD6	Exosome	GPIWN	GDNIACVILTFKEPFGTEGR	GGYFD	2	C6:+57.021	1112.557269	2223.098938	0.000451244	11	N	226	246
G3UWD6	Exosome	GPIWN	GDNIACVILTFKEPFGTEGR	GGYFD	3	C6:+57.021	742.0407792	2223.098938	0.001162105	6	N	226	246
G3UWD6	Exosome	PIWNG	DNIACVILTF	KEPFG	2	C5:+57.021	583.3000145	1164.584429	0.000622848	9	Y	227	237
G3UWD6	Exosome	KPFGR	DLQSSNQLSNHISSLF	REDQI	2		895.4399191	1788.864238	0.000451244	6	Y	175	191
G3UWD6	Exosome	VKNER	WDGVPFILR	CGKAL	2		551.8063556	1101.597111	0.000735798	2	Y	348	357
G3UWD6	Parental	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	3		917.4551224	2749.341967	0.000451244	14	Y	175	198
G3UWD6	Parental	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	4		688.3432918	2749.341967	0.001463592	2	Y	175	198
G3UWD6	Parental	GTEGR	GGYFDEFGIIR	DVMQS	2		637.3147418	1272.613884	0.000451244	15	Y	246	257
G3UWD6	Parental	PIWNG	DNIACVILTFKEPFGTEGR	GGYFD	2	C5:+57.021	1084.046537	2166.077474	0.000451244	19	Y	227	246
G3UWD6	Parental	PIWNG	DNIACVILTFKEPFGTEGR	GGYFD	3	C5:+57.021	723.0336246	2166.077474	0.000451244	37	Y	227	246
G3UWD6	Parental	DLAKK	KIYPTIWWLFR	DGLLP	3		508.2910126	1521.849638	0.001162105	12	Y	46	57
G3UWD6	Parental	LAKKK	IYPTIWWLFR	DGLLP	2		697.8851373	1393.754675	0.000451244	26	Y	47	57
G3UWD6	Parental	MQANH	LFYLALPPTVYEAVTK	NIQET	2		913.0114603	1824.007321	0.000622848	9	Y	136	152
G3UWD6	Parental	MQANH	LFYLALPPTVYEAVTK	NIQET	3		609.0102402	1824.007321	0.001229886	8	Y	136	152
G3UWD6	Parental	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	2		973.4904747	1944.965349	0.000451244	21	Y	175	192
G3UWD6	Parental	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	3		649.3295831	1944.965349	0.000451244	14	Y	175	192
G3UWD6	Parental	PIWNG	DNIACVILTFK	EPFGT	2	C5:+57.021	647.3474961	1292.679392	0.000451244	6	Y	227	238
G3UWD6	Parental	GPIWN	GDNIACVILTFKEPFGTEGR	GGYFD	3	C6:+57.021	742.0407792	2223.098938	0.001654178	1	N	226	246
G3UWD6	Parental	PIWNG	DNIACVILTF	KEPFG	2	C5:+57.021	583.3000145	1164.584429	0.000451244	4	Y	227	237
G3UWD6	Parental	FYLAL	PPTVYEAVTK	NIQET	2		552.8009359	1103.586272	0.001162105	2	Y	142	152
G3UWD6	Parental	ANHLF	YLALPPTVYEAVTK	NIQET	2		782.9352213	1563.854843	0.002019181	1	Y	138	152
G3UWD6	Parental	KPFGR	DLQSSNQLSNHISSLF	REDQI	2		895.4399191	1788.864238	0.000823681	5	Y	175	191
G3X8U3	Exosome	AAVNR	ALDQGIPITSASYYATVSLEQVR	DIFRS	2		1241.645358	2481.275116	0.000451244	16	N	106	129
G3X8U3	Exosome	AAVNR	ALDQGIPITSASYYATVSLEQVR	DIFRS	3		828.0995054	2481.275116	0.001699387	1	N	106	129
G3X8U3	Exosome	EGVRR	AAELLLPAAAAWR	VEQWK	2		676.8884083	1351.761217	0.000451244	7	N	30	43
G3X8U3	Exosome	KCAVR	YGGTPYTGYWALCAAVNR	ALDQG	2	C13:+57.021	1010.473008	2018.930415	0.000622848	7	N	88	106
G3X8U3	Exosome	ELLEK	GENSPVEINSVLLDYHLWDYAR	EHRED	3		864.0911214	2589.249964	0.000451244	2	N	297	319
G3X972	Exosome	QTLAK	ECVAQGCCVDLFLFPNQYVDVATLSVVPQLTGGSVYK	YACFQ	3	C2:+57.021,C7:+57.021,C8:+57.02	1378.672274	4132.993421	0.001162105	2	N	687	724
G3X972	Exosome	VKTVR	DTLITQCAQILACYR	KNCAS	2	C7:+57.021,C13:+57.021	913.4504553	1824.885311	0.000622848	3	N	870	885
G3X972	Exosome	ECAGK	LFLFHTSLPIAEAPGK	LKNRD	3		580.994813	1739.961039	0.000622848	7	N	640	656
G3X972	Parental	QTLAK	ECVAQGCCVDLFLFPNQYVDVATLSVVPQLTGGSVYK	YACFQ	3	C2:+57.021,C7:+57.021,C8:+57.02	1378.672274	4132.993421	0.002019181	2	N	687	724
G5E870	Exosome	FDSFR	DGFESVFPLCHLQYFYPEELDQLLCGSK	ADTWD	3	C10:+57.021,C25:+57.021	1131.193391	3390.556774	0.000823681	4	N	1875	1903
G5E870	Exosome	TELGK	TCPFFFPFDTR	QMLFY	2	C2:+57.021	717.8294705	1433.643341	0.001229886	1	N	1569	1580
G5E870	Parental	SIGGR	SCSSSSAVIVPQPEDPDRANTSER	QKTGQ	3	C2:+57.021	863.7334023	2588.176807	0.000823681	3	N	33	57
G5E870	Parental	FDSFR	DGFESVFPLCHLQYFYPEELDQLLCGSK	ADTWD	3	C10:+57.021,C25:+57.021	1131.193391	3390.556774	0.000451244	12	N	1875	1903
G5E8K5	Exosome	ETVKK	ILGNKATFSPIVTVEPR	RRKFH	2		921.5283402	1841.04108	0.000851441	2	N	1192	1209

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
G5E8K5	Exosome	AIARR	LGYISVVDTLK	VVTEE	2		604.350793	1206.685986	0.002080925	2	N	788	799
O08528	Exosome	DGTEK	GDFLALDLGGTNFR	VLLVR	2		748.3811445	1494.746689	0.000451244	9	Y	525	539
O08528	Exosome	YMGMK	GVSLPLGFTFSFPCQQNSLDQSILLK	WTKGF	3	C14:+57.021	966.1690003	2895.483601	0.001162105	2	N	592	618
O08528	Exosome	CHQTK	LDESFLVSWTK	GFKSS	2		662.8433321	1323.671064	0.000451244	2	N	162	173
O08528	Exosome	IFETK	FLSQIESDCLALLQVR	AILRH	2	C9:+57.021	946.5012338	1890.986868	0.001162105	1	N	785	801
O08528	Parental	DLAPK	CDVSFLESEDGSGKGAALITAVACR	IREAG	3	C1:+57.021,C24:+57.021	871.7478411	2612.220123	0.000451244	3	N	885	910
O08528	Parental	DGTEK	GDFLALDLGGTNFR	VLLVR	2		748.3811445	1494.746689	0.000451244	14	Y	525	539
O08528	Parental	PTFVR	STPDGTEHGEFLALDLGGTNFR	VLRVR	2		1167.554	2333.092401	0.000979378	1	N	69	91
O08528	Parental	CHQTK	LDESFLVSWTK	GFKSS	2		662.8433321	1323.671064	0.000451244	2	N	162	173
O08528	Parental	TEFDR	EIDMGSLNPGKQLFEK	MISGM	2	[0:-18.011,M4:+15.995	902.4512665	1802.886933	0.001329271	1	N	279	295
O08553	Exosome	AFKDR	FQLTDSQIYEVLSVIR	DIGAI	2		956.0152626	1910.014925	0.000451244	7	N	173	189
O08553	Exosome	AFKDR	FQLTDSQIYEVLSVIR	DIGAI	3		637.6794418	1910.014925	0.000735798	1	N	173	189
O08553	Exosome	EEQQR	ILDLGITGPEGHVLSRPEEVEAEAVNR	SITIA	3		967.5091158	2899.503947	0.000451244	3	N	211	238
O08553	Exosome	EEQQR	ILDLGITGPEGHVLSRPEEVEAEAVNR	SITIA	4		725.8837868	2899.503947	0.000451244	3	N	211	238
O08553	Exosome	RGVPR	GLYDGPVCEVSVTPK	TVTPA	2	C8:+57.021	810.9008212	1619.786042	0.000451244	4	N	496	511
O08553	Parental	AFKDR	FQLTDSQIYEVLSVIR	DIGAI	2		956.0152626	1910.014925	0.000451244	6	N	173	189
O08553	Parental	EAVNR	SITIANQTNCPLYVTK	VMSKS	2	C10:+57.021	911.9723092	1821.929018	0.000698008	2	N	238	254
O08582	Exosome	DLTSK	LVLVSPTSEQYDSLLR	QMWER	2		910.494163	1818.972726	0.000451244	13	N	64	80
O08582	Exosome	RGLIK	LNDTLLLGPDPLGNFLSIAVK	SIHRK	2		1105.625709	2209.235817	0.000451244	14	N	422	443
O08582	Exosome	RGLIK	LNDTLLLGPDPLGNFLSIAVK	SIHRK	3		737.4197391	2209.235817	0.000451244	2	N	422	443
O08582	Parental	IESGR	TSSVGNDILGFDSEGNVVNKPDSHGGSLEWTK	ICEKS	3		1116.199447	3345.57494	0.000451244	6	N	207	239
O08582	Parental	IESGR	TSSVGNDILGFDSEGNVVNKPDSHGGSLEWTK	ICEKS	4		837.4015351	3345.57494	0.000451244	4	N	207	239
O08582	Parental	DLTSK	LVLVSPTSEQYDSLLR	QMWER	2		910.494163	1818.972726	0.000451244	21	N	64	80
O08582	Parental	GLIKL	NDTLLLGPDPLGNFLSIAVK	SIHRK	2		1049.083677	2096.151753	0.000451244	1	N	423	443
O08582	Parental	VDAGK	STLLGVLTHGELDNGR	GFARQ	3		561.3009648	1680.879494	0.000637154	4	N	173	189
O08583	Exosome	GRNSK	QQLSAEELDAQLDAYNAR	MDTS-	2		1017.990505	2033.965409	0.000451244	20	N	233	251
O08583	Exosome	ETGGK	LLVSNLDFGVSDADIQELFAEFGTLKK	AAVHY	3		990.5222509	2968.543353	0.000451244	32	N	106	133
O08583	Exosome	ETGGK	LLVSNLDFGVSDADIQELFAEFGTLK	KAAVH	3		947.8239298	2840.448389	0.001162105	1	N	106	132
O08583	Exosome	DRSGR	SLGTADVHFER	KADAL	3		411.2075654	1230.599296	0.002374549	6	N	143	154
O08583	Parental	DGRPM	NIQLVTSQIDTQR	RPAQS	2		758.4104333	1514.805267	0.001162105	30	N	175	188
O08583	Parental	YSRPK	QLPDKWQHDLFDSGFGGGAGVETGGK	LLVSN	2		1352.144045	2702.272491	0.000451244	3	N	80	106
O08583	Parental	YSRPK	QLPDKWQHDLFDSGFGGGAGVETGGK	LLVSN	4		676.5759226	2702.272491	0.000622848	5	N	80	106
O08583	Parental	GRNSK	QQLSAEELDAQLDAYNAR	MDTS-	2		1017.990505	2033.965409	0.001264573	1	N	233	251
O08583	Parental	ETGGK	LLVSNLDFGVSDADIQELFAEFGTLKK	AAVHY	3		990.5222509	2968.543353	0.000451244	37	N	106	133
O08583	Parental	ETGGK	LLVSNLDFGVSDADIQELF	AEFGT	2		1048.033849	2094.052099	0.000451244	31	N	106	125
O08583	Parental	ETGGK	LLVSNLDFGVSDADIQELF	AEFGT	3		699.0251663	2094.052099	0.002453667	1	N	106	125
O08583	Parental	ETGGK	LLVSNLDFGVSDADIQELFAEFGTLK	KAAVH	3		947.8239298	2840.448389	0.000451244	5	N	106	132
O08583	Parental	GKLLV	SNLDFGVSDADIQELFAEFGTLKK	AAVHY	3		882.1100701	2643.30681	0.000451244	10	N	109	133
O08583	Parental	DRSGR	SLGTADVHFER	KADAL	2		616.3074481	1230.599296	0.000451244	5	N	143	154
O08583	Parental	DRSGR	SLGTADVHFER	KADAL	3		411.2075654	1230.599296	0.001162105	9	N	143	154
O08583	Parental	RGTGR	NSKQQLSAEELDAQLDAY	NARMD	2		1011.984888	2021.954176	0.000622848	3	N	230	248
O08583	Parental	GRNSK	QQLSAEELDAQLDAY	NARMD	2		847.3999282	1692.784256	0.001329271	3	N	233	248
O08583	Parental	GGKLL	VSNLDFGVSDADIQELFAEFGTLKK	AAVHY	3		915.1328748	2742.375224	0.000622848	1	N	108	133
O08583	Parental	GKLLV	SNLDFGVSDADIQELFAEFGTLK	KAAVH	2		1258.613724	2515.211847	0.000451244	9	N	109	132
O08585	Exosome	LIGYV	AAEEAFVNDIDESSPGTEWER	VARLC	2		1176.51728	2351.018961	0.000451244	35	N	179	200
O08585	Exosome	EWKEK	AIKELEEWYAR	QDEQL	3		469.9142705	1406.719411	0.001763695	1	N	137	148
O08585	Parental	LIGYV	AAEEAFVNDIDESSPGTEWER	VARLC	2		1176.51728	2351.018961	0.000451244	60	N	179	200
O08585	Parental	LIGYV	AAEEAFVNDIDESSPGTEWER	VARLC	3		784.680787	2351.018961	0.000451244	15	N	179	200
O08585	Parental	EWKEK	AIKELEEWYAR	QDEQL	2		704.3675057	1406.719411	0.00307782	1	N	137	148
O08585	Parental	EWKEK	AIKELEEWYAR	QDEQL	3		469.9142705	1406.719411	0.000823681	5	N	137	148
O08585	Parental	NGEYY	QESNGPTDSYAAISEVDR	LQSEP	2		969.9379376	1937.860275	0.001654178	1	N	83	101
O08663	Exosome	HISGR	IIDCAFTVTFNPK	YDILL	2	C4:+57.021	763.3898923	1524.764185	0.000451244	16	N	259	272
O08663	Exosome	KKKGK	GAVSAVQQELDKESGALVDEVAK	QLESQ	3		781.7399772	2342.196531	0.000451244	23	N	46	69
O08663	Exosome	SEEKK	ALDQASEEIWNDFREAAEAHR	QVRKY	4		615.2905279	2457.130911	0.001463592	1	N	156	177
O08663	Exosome	LMALK	NLCDLGIVDPYPPLCDIK	GSYTA	2	C3:+57.021,C15:+57.021	1051.518535	2101.02147	0.001162105	7	N	433	451
O08663	Exosome	RKLIK	ENGLNAGLAFPTGCSLNNCAAHYTPNAGDTTVLQYDDICK	IDFGT	3	C14:+57.021,C19:+57.021,C39:+57.021	1448.31951	4341.935131	0.000451244	12	N	209	249
O08663	Exosome	TFNPK	YDILLTAVK	DATNT	2		518.3083968	1034.601194	0.001162105	1	N	272	281
O08663	Parental	HISGR	IIDCAFTVTFNPK	YDILL	2	C4:+57.021	763.3898923	1524.764185	0.000451244	2	N	259	272
O08663	Parental	KKKGK	GAVSAVQQELDKESGALVDEVAK	QLESQ	3		781.7399772	2342.196531	0.000451244	18	N	46	69
O08663	Parental	SEEKK	ALDQASEEIWNDFREAAEAHR	QVRKY	4		615.2905279	2457.130911	0.000622848	5	N	156	177
O08663	Parental	QAASF	GGHLNGDLDPDDREEGTSSTAEEAAK	KKRRK	3		891.0625073	2670.164122	0.000979378	1	N	10	36
O08663	Parental	LMALK	NLCDLGIVDPYPPLCDIK	GSYTA	2	C3:+57.021,C15:+57.021	1051.518535	2101.02147	0.000622848	12	N	433	451
O08663	Parental	RKLIK	ENGLNAGLAFPTGCSLNNCAAHYTPNAGDTTVLQYDDICK	IDFGT	3	C14:+57.021,C19:+57.021,C39:+57.021	1448.31951	4341.935131	0.000451244	9	N	209	249

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O08663	Parental	SEEKK	ALDQASEEIWNDFR	EAAEA	2		847.3949802	1692.77436	0.000451244	1	N	156	170
O08663	Parental	KRGPK	VQTDPPSVPICDLYPNGVFPK	GQECE	2	C11:+57.021	1172.088402	2342.161204	0.000637154	1	N	110	131
O08677	Exosome	TLTQG	EEAQEIDCNDEAVFQAVDFSLK	QFNPG	2	C8:+57.021	1279.073874	2556.132148	0.000451244	9	N	20	42
O08677	Parental	APILK	AYFPCIGCVHAISTDSPDLEPVLK	HSIEH	3	C5:+57.021,C8:+57.021	897.1050772	2688.291832	0.000451244	8	N	136	160
O08677	Parental	TVGKR	ENEFFIVTQTCK	IAPSK	2	C11:+57.021	758.3613318	1514.707064	0.000451244	3	N	114	126
O08677	Parental	TLTQG	EEAQEIDCNDEAVFQAVDFSLK	QFNPG	2	C8:+57.021	1279.073874	2556.132148	0.000451244	5	N	20	42
O08691	Exosome	GCHLK	DFGDLSFTNVPQDDPYNNLVVYPR	SVGLA	3		929.1088407	2784.303122	0.000451244	7	N	66	90
O08691	Exosome	VVYPR	SVGLANQELAEVVSR	AVSGG	2		786.4235407	1570.831481	0.000634081	1	N	90	105
O08691	Exosome	KATAR	LAVDVIASSFGQTR	EGGHI	2		732.3967946	1462.777989	0.000823681	1	N	313	327
O08692	Exosome	DVSEK	EKFEDVPPHIR	NIYED	3		456.2424986	1365.704096	0.000451244	47	N	138	149
O08692	Exosome	STQER	QPKDCDFLEDGEER	NCTGK	2	C5:+57.021	869.3731562	1736.730712	0.000451244	29	N	82	96
O08692	Exosome	STQER	QPKDCDFLEDGEER	NCTGK	3	C5:+57.021	579.9180375	1736.730712	0.000622848	4	N	82	96
O08692	Exosome	STQER	QPKDCDFLEDGEER	NCTGK	2	[0:-17.027,C5:+57.021	860.8596562	1719.703712	0.000823681	5	N	82	96
O08692	Exosome	ERQPK	DCDFLEDGEERNCTGK	FFRRR	2	C2:+57.021,C13:+57.021	972.8886132	1943.761626	0.000451244	120	N	85	101
O08692	Exosome	ERQPK	DCDFLEDGEERNCTGK	FFRRR	3	C2:+57.021,C13:+57.021	648.9283421	1943.761626	0.000451244	46	N	85	101
O08692	Exosome	FFRRR	QSTSLTLTCDRDCSR	EDTQE	2	C9:+57.021,C13:+57.021	900.4042334	1798.792867	0.000451244	9	N	106	121
O08692	Exosome	FFRRR	QSTSLTLTCDRDCSR	EDTQE	3	C9:+57.021,C13:+57.021	600.6054223	1798.792867	0.000451244	47	N	106	121
O08692	Exosome	FFRRR	QSTSLTLTCDRDCSR	EDTQE	2	[0:-	891.8907334	1781.765867	0.000622848	6	N	106	121
O08692	Exosome	FFRRR	QSTSLTLTCDRDCSR	EDTQE	3	[0:-	594.9297556	1781.765867	0.000451244	3	N	106	121
O08692	Exosome	ERQPK	DCDFLEDGEER	NCTGK	2	C2:+57.021	692.7700038	1383.524408	0.000451244	213	N	85	96
O08692	Exosome	LFRLL	SATPPSSQNPATNIPLQFR	IKETE	2		1013.521775	2025.02795	0.000451244	58	N	51	70
O08692	Exosome	FRLLS	ATPPSSQNPATNIPLQFR	IKETE	2		970.0057606	1937.995921	0.000870037	1	N	52	70
O08692	Exosome	RPLFR	LLSATPPSSQNPATNIPLQFR	IKETE	2		1126.605839	2251.196078	0.000451244	749	N	49	70
O08692	Exosome	RPLFR	LLSATPPSSQNPATNIPLQFR	IKETE	3		751.4064926	2251.196078	0.000451244	434	N	49	70
O08692	Exosome	LLSAT	PPSSQNPATNIPLQFR	IKETE	2		883.9633644	1765.911129	0.000451244	7	N	54	70
O08692	Exosome	YEDAK	YDIIGNILK	NF-	2		524.8060213	1047.596443	0.000451244	75	N	156	165
O08692	Exosome	YEDAK	YDIIGNILKN	F-	2		581.8274851	1161.63937	0.001463592	1	N	156	166
O08692	Exosome	PPHIR	NIYEDAKYDIIGNILK	NF-	2		941.5019881	1880.988376	0.000451244	39	N	149	165
O08692	Exosome	PPHIR	NIYEDAKYDIIGNILK	NF-	3		628.0039254	1880.988376	0.000451244	54	N	149	165
O08692	Exosome	HIRNI	YEDAKYDIIGNILK	NF-	2		827.9384923	1653.861385	0.000451244	4	N	151	165
O08692	Exosome	PPHIR	NIYEDAKYDIIGNIL	KNF-	2		877.4545065	1752.893413	0.000451244	15	N	149	164
O08692	Exosome	KFFRR	RQSTSLTLTCDR	DCSRE	3	C10:+57.021	479.9090365	1436.70371	0.000823681	1	N	105	117
O08692	Exosome	FFRRR	QSTSLTLTCDR	DCSRE	2	C9:+57.021	641.3090992	1280.602598	0.000451244	23	N	106	117
O08692	Exosome	PLQFR	IKETECTSTQER	QPKDC	3	C6:+57.021	494.5685685	1480.682305	0.000622848	2	N	70	82
O08692	Exosome	RLLSA	TPPSSQNPATNIPLQFR	IKETE	2		934.4872037	1866.958807	0.001329271	3	N	53	70
O08692	Exosome	PPSSQ	NPATNIPLQFR	IKETE	2		635.8492831	1269.682966	0.001162105	2	N	59	70
O08692	Exosome	RPLFR	LLSATPPSSQNPATNIPLQF	RIKET	2		1048.555283	2095.094967	0.000451244	3	N	49	69
O08692	Parental	DVSEK	EKFEDVPPHIR	NIYED	2		683.8598479	1365.704096	0.000451244	27	N	138	149
O08692	Parental	DVSEK	EKFEDVPPHIR	NIYED	3		456.2424986	1365.704096	0.000451244	220	N	138	149
O08692	Parental	STQER	QPKDCDFLEDGEER	NCTGK	2	C5:+57.021	869.3731562	1736.730712	0.000451244	29	N	82	96
O08692	Parental	STQER	QPKDCDFLEDGEER	NCTGK	3	C5:+57.021	579.9180375	1736.730712	0.002145581	1	N	82	96
O08692	Parental	STQER	QPKDCDFLEDGEER	NCTGK	2	[0:-17.027,C5:+57.021	860.8596562	1719.703712	0.000622848	12	N	82	96
O08692	Parental	ERQPK	DCDFLEDGEERNCTGK	FFRRR	2	C2:+57.021,C13:+57.021	972.8886132	1943.761626	0.000451244	147	N	85	101
O08692	Parental	ERQPK	DCDFLEDGEERNCTGK	FFRRR	3	C2:+57.021,C13:+57.021	648.9283421	1943.761626	0.000451244	58	N	85	101
O08692	Parental	FFRRR	QSTSLTLTCDRDCSR	EDTQE	2	C9:+57.021,C13:+57.021	900.4042334	1798.792867	0.000637154	9	N	106	121
O08692	Parental	FFRRR	QSTSLTLTCDRDCSR	EDTQE	3	C9:+57.021,C13:+57.021	600.6054223	1798.792867	0.000451244	50	N	106	121
O08692	Parental	FFRRR	QSTSLTLTCDRDCSR	EDTQE	2	[0:-	891.8907334	1781.765867	0.000451244	13	N	106	121
O08692	Parental	ERQPK	DCDFLEDGEER	NCTGK	2	C2:+57.021	692.7700038	1383.524408	0.000451244	153	N	85	96
O08692	Parental	LFRLL	SATPPSSQNPATNIPLQFR	IKETE	2		1013.521775	2025.02795	0.000451244	52	N	51	70
O08692	Parental	FRLLS	ATPPSSQNPATNIPLQFR	IKETE	2		970.0057606	1937.995921	0.000451244	5	N	52	70
O08692	Parental	PPHIR	NIYEDAKYDIIGN	ILKNF	2		764.3704424	1526.725285	0.000451244	23	N	149	162
O08692	Parental	LRQLR	YEEIVDRAIEAYNQGR	QGRPL	2		963.4717506	1924.927901	0.000451244	39	N	26	42
O08692	Parental	LRQLR	YEEIVDRAIEAYNQGR	QGRPL	3		642.6504337	1924.927901	0.000451244	58	N	26	42
O08692	Parental	RPLFR	LLSATPPSSQNPATNIPLQFR	IKETE	2		1126.605839	2251.196078	0.000451244	1147	N	49	70
O08692	Parental	RPLFR	LLSATPPSSQNPATNIPLQFR	IKETE	3		751.4064926	2251.196078	0.000451244	749	N	49	70
O08692	Parental	LLSAT	PPSSQNPATNIPLQFR	IKETE	2		883.9633644	1765.911129	0.000451244	7	N	54	70
O08692	Parental	YEDAK	YDIIGNILK	NF-	2		524.8060213	1047.596443	0.000451244	1446	N	156	165
O08692	Parental	YEDAK	YDIIGNILKN	F-	2		581.8274851	1161.63937	0.000823681	14	N	156	166
O08692	Parental	PPHIR	NIYEDAKYDIIGNILK	NF-	2		941.5019881	1880.988376	0.000451244	258	N	149	165
O08692	Parental	PPHIR	NIYEDAKYDIIGNILK	NF-	3		628.0039254	1880.988376	0.000451244	800	N	149	165
O08692	Parental	PPHIR	NIYEDAKYDIIGNI	LKNF-	2		820.9124745	1639.809349	0.002374549	1	N	149	163
O08692	Parental	HIRNI	YEDAKYDIIGNILK	NF-	2		827.9384923	1653.861385	0.000451244	11	N	151	165
O08692	Parental	HIRNI	YEDAKYDIIGNILK	NF-	3		552.2949282	1653.861385	0.001463592	2	N	151	165
O08692	Parental	IRNIY	EDAKYDIIGNILK	NF-	2		746.4068279	1490.798056	0.000451244	3	N	152	165
O08692	Parental	NIYED	AKYDIIGNILK	NF-	2		624.3720598	1246.72852	0.002019181	1	N	154	165

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O08692	Parental	PPHIR	NIYEDAKYDIIGNIL	KNF-	2		877.4545065	1752.893413	0.000451244	19	N	149	164
O08692	Parental	YEDAK	YDIIGNILKNF	-	2		655.3616921	1308.707784	0.001871652	1	N	156	167
O08692	Parental	FFRRR	QSTSLTLTCDR	DCSRE	2	C9:+57.021	641.3090992	1280.602598	0.000451244	21	N	106	117
O08692	Parental	PLQFR	IKETECTSTQER	QPKDC	3	C6:+57.021	494.5685685	1480.682305	0.001463592	2	N	70	82
O08692	Parental	RQLRY	EEIVDRAIEAYNQGR	QGRPL	3		588.2959908	1761.864573	0.000451244	2	N	27	42
O08692	Parental	RPLFR	LLSATPPSSQNPATNIPLQF	RIKET	2		1048.555283	2095.094967	0.000451244	16	N	49	69
O08692	Parental	RDCSR	EDTQETSFNDKQDV	SEKEK	2		828.3557177	1654.695835	0.001943752	2	N	121	135
O08692	Parental	RPLFR	LLSATPPSSQNPATNIPL	QFRIK	2		910.9917875	1819.967975	0.000823681	1	N	49	67
O08709	Exosome	FSHPR	DFTPVCTTELGR	AAKLA	2	C6:+57.021	698.3325743	1394.649549	0.000451244	13	N	41	53
O08709	Exosome	DEILR	VVDSLQLTGTKPVATPVDWK	KGESV	2		1077.594409	2153.173217	0.000451244	20	N	162	182
O08709	Exosome	DEILR	VVDSLQLTGTKPVATPVDWK	KGESV	3		718.7322057	2153.173217	0.000451244	28	N	162	182
O08709	Exosome	-M	PGGLLLGDEAPNFEANTTIGR	IRFHD	2		1071.545447	2141.075294	0.000451244	28	N	1	22
O08709	Exosome	-M	PGGLLLGDEAPNFEANTTIGR	IRFHD	3		714.6995646	2141.075294	0.00091018	1	N	1	22
O08709	Exosome	KRNVK	LIALSIDSVEDHLAWSK	DINAY	2		949.0074376	1895.999275	0.000451244	23	N	67	84
O08709	Exosome	KRNVK	LIALSIDSVEDHLAWSK	DINAY	3		633.0075584	1895.999275	0.000451244	23	N	67	84
O08709	Exosome	IGRIR	FHDFLGDSWGILFSHPR	DFTPV	3		677.667759	2029.979877	0.000451244	38	N	24	41
O08709	Exosome	IGRIR	FHDFLGDSWGILFSHPR	DFTPV	4		508.5027693	2029.979877	0.000451244	26	N	24	41
O08709	Exosome	LAWSK	DINAYNGETPTEK	LPFPI	2		726.3365996	1450.657599	0.000451244	6	N	84	97
O08709	Exosome	TPTEK	LPFPIIDDKGR	DLAIL	3		424.2438395	1269.708118	0.001463592	4	N	97	108
O08709	Exosome	LAWSK	DINAYNGETPTEKLPFPIIDDK	GRDLA	2		1245.624091	2489.232583	0.002981883	1	N	84	106
O08709	Exosome	LAWSK	DINAYNGETPTEKLPFPIIDDK	GRDLA	3		830.7519942	2489.232583	0.00091018	2	N	84	106
O08709	Parental	FSHPR	DFTPVCTTELGR	AAKLA	2	C6:+57.021	698.3325743	1394.649549	0.000451244	16	N	41	53
O08709	Parental	DEILR	VVDSLQLTGTKPVATPVDWK	KGESV	2		1077.594409	2153.173217	0.000451244	36	N	162	182
O08709	Parental	DEILR	VVDSLQLTGTKPVATPVDWK	KGESV	3		718.7322057	2153.173217	0.000451244	35	N	162	182
O08709	Parental	-M	PGGLLLGDEAPNFEANTTIGR	IRFHD	2		1071.545447	2141.075294	0.000451244	31	N	1	22
O08709	Parental	-M	PGGLLLGDEAPNFEANTTIGR	IRFHD	3		714.6995646	2141.075294	0.000735798	2	N	1	22
O08709	Parental	KRNVK	LIALSIDSVEDHLAWSK	DINAY	2		949.0074376	1895.999275	0.000451244	12	N	67	84
O08709	Parental	KRNVK	LIALSIDSVEDHLAWSK	DINAY	3		633.0075584	1895.999275	0.000451244	14	N	67	84
O08709	Parental	TTIGR	IRFHDFLGDSWGILFSHPR	DFTPV	4		575.7990631	2299.165052	0.000451244	6	N	22	41
O08709	Parental	IGRIR	FHDFLGDSWGILFSHPR	DFTPV	2		1015.997739	2029.979877	0.000451244	3	N	24	41
O08709	Parental	IGRIR	FHDFLGDSWGILFSHPR	DFTPV	3		677.667759	2029.979877	0.000451244	35	N	24	41
O08709	Parental	IGRIR	FHDFLGDSWGILFSHPR	DFTPV	4		508.5027693	2029.979877	0.000451244	34	N	24	41
O08709	Parental	ATTGR	NFDEILRVVDSLQLTGTKPVATPVDWK	KGESV	4		761.1636336	3040.623334	0.00091018	1	N	155	182
O08709	Parental	LAWSK	DINAYNGETPTEK	LPFPI	2		726.3365996	1450.657599	0.000451244	14	N	84	97
O08709	Parental	TPTEK	LPFPIIDDKGR	DLAIL	3		424.2438395	1269.708118	0.001591523	6	N	97	108
O08709	Parental	LAWSK	DINAYNGETPTEKLPFPIIDDK	GRDLA	2		1245.624091	2489.232583	0.001264573	1	N	84	106
O08709	Parental	LAWSK	DINAYNGETPTEKLPFPIIDDK	GRDLA	3		830.7519942	2489.232583	0.000622848	2	N	84	106
O08734	Parental	PGPPK	VGCDESPSPSEQQVAQDTEEVFR	SYVFY	2	C3:+57.021	1297.569487	2593.123374	0.000451244	19	N	11	34
O08734	Parental	PGPPK	VGCDESPSPSEQQVAQDTEEVFR	SYVFY	3	C3:+57.021	865.3822581	2593.123374	0.000622848	4	N	11	34
O08734	Parental	PGPPK	VGCDESPSPSEQQVAQDTEEVF	RSYVF	2	C3:+57.021	1219.518932	2437.022263	0.000637154	3	N	11	33
O08734	Parental	DINRR	YDTEFQNLLEQLQPTAGNAYELFTK	IASSL	3		978.4788222	2932.413067	0.000451244	1	N	86	111
O08738	Exosome	AYDAK	IEIQTLTGLFK	GDKCQ	2		631.8718926	1261.728185	0.000622848	9	N	116	127
O08738	Exosome	EMLAR	YGSSLEFTELLTLVNRK	VSQRR	3		657.3584797	1969.052039	0.000823681	9	N	220	237
O08738	Exosome	GFEVK	CFNDLRAEELLLK	IHEVS	3	C1:+57.021	540.9523537	1619.833661	0.002296037	1	N	69	82
O08738	Exosome	FNHER	FFWHLTLPER	RGTNA	3		449.2404293	1344.697888	0.002296037	3	N	37	47
O08738	Exosome	AYDAK	IEIQTLTGLFKGDK	CQSLV	3		521.6316518	1561.871555	0.000870037	5	N	116	130
O08738	Parental	AYDAK	IEIQTLTGLFK	GDKCQ	2		631.8718926	1261.728185	0.000823681	5	N	116	127
O08738	Parental	EMLAR	YGSSLEFTELLTLVNRK	VSQRR	3		657.3584797	1969.052039	0.001395409	2	N	220	237
O08749	Exosome	PLRTY	ADQPIEADVTVIGSGPGGYVAAIK	SAQLG	2		1164.608244	2327.200889	0.000451244	35	N	35	59
O08749	Exosome	PLRTY	ADQPIEADVTVIGSGPGGYVAAIK	SAQLG	3		776.7414295	2327.200889	0.000451244	7	N	35	59
O08749	Exosome	SEAFR	EANLAAAFGKPINF	-	2		731.8886053	1461.761611	0.000451244	27	N	495	509
O08749	Exosome	QLGFK	TVCIEKNETLGGTCLNVGCIPSK	ALLNN	3	C3:+57.021,C14:+57.021,C19:+57.021	850.7502628	2549.227388	0.000622848	4	N	66	89
O08749	Exosome	VCIGR	RPFTQNLGLEELGIELDPK	GRIPV	2		1085.081665	2168.147731	0.000823681	4	N	315	334
O08749	Exosome	VCIGR	RPFTQNLGLEELGIELDPK	GRIPV	3		723.7237102	2168.147731	0.000451244	20	N	315	334
O08749	Exosome	EDIAR	VCHAHPTLSEAFR	EANLA	3	C2:+57.021	508.9177549	1523.729865	0.000823681	3	N	482	495
O08749	Exosome	VCIEK	NETLGGTCLNVGCIPSK	ALLNN	2	C8:+57.021,C13:+57.021	910.4375449	1818.85949	0.000451244	17	N	72	89
O08749	Exosome	AWVGK	SEEQLKEEGIEFK	IGKFP	2		783.3888322	1564.762064	0.000451244	8	N	404	417
O08749	Exosome	AWVGK	SEEQLKEEGIEFK	IGKFP	3		522.5951548	1564.762064	0.000451244	9	N	404	417
O08749	Exosome	SVWQR	LGADVTAVEFLGHVGGIGIDMEISK	NFQRI	3	M21:+15.995	848.7725412	2543.294224	0.000451244	9	N	234	259
O08749	Exosome	ASGGK	AEVITCDVLLVCIGR	RPFTQ	2	C6:+57.021,C12:+57.021	859.4524667	1716.889333	0.001463592	1	N	300	315
O08749	Parental	PLRTY	ADQPIEADVTVIGSGPGGYVAAIK	SAQLG	2		1164.608244	2327.200889	0.000451244	41	N	35	59
O08749	Parental	SEAFR	EANLAAAFGKPINF	-	2		731.8886053	1461.761611	0.000451244	13	N	495	509
O08749	Parental	QLGFK	TVCIEKNETLGGTCLNVGCIPSK	ALLNN	2	C3:+57.021,C14:+57.021,C19:+57.021	1275.621494	2549.227388	0.001162105	1	N	66	89

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O08749	Parental	QLGFK	TVCIEKNETLGGTCLNVGCIPSK	ALLNN	3	C3:+57.021,C14:+57.021,C19:+57.021	850.7502628	2549.227388	0.000622848	4	N	66	89
O08749	Parental	VCIGR	RPFTQNLGLEELGIELDPK	GRIPV	2		1085.081665	2168.147731	0.000451244	5	N	315	334
O08749	Parental	VCIGR	RPFTQNLGLEELGIELDPK	GRIPV	3		723.7237102	2168.147731	0.000451244	21	N	315	334
O08749	Parental	AWVGK	SEEQLKEEGIEFK	IGKFP	2		783.3888322	1564.762064	0.000823681	1	N	404	417
O08749	Parental	AWVGK	SEEQLKEEGIEFK	IGKFP	3		522.5951548	1564.762064	0.000451244	5	N	404	417
O08759	Exosome	ICGSR	NLDFQALEETTEYDGGYTR	ESVVI	2		1111.498359	2220.981119	0.000823681	3	N	758	777
O08759	Parental	HLIER	YYHQLTEGCGNEACTNEFCASCPTFLR	MDNNA	3	C9:+57.021,C14:+57.021,C19:+57.021,C22:+57.021	1095.787845	3284.340135	0.000451244	5	N	33	60
O08759	Parental	LANEK	LETAFLNALVYLSPNVECDLTYHNVYTR	DPNYL	3	C18:+57.021	1105.8837	3314.627699	0.000698008	2	N	246	274
O08795	Exosome	ILSSR	VNDGVCDCCDGTDEYNSGTVCENTCR	EKGRK	3	C6:+57.021,C8:+57.021,C9:+57.021,C21:+57.021,C25:+57.021	1019.705256	3056.092367	0.000451244	19	N	91	117
O08795	Exosome	MVSLA	ELQTHPELDTDGDGALSEEEAQALLSGDTQTDTTSFYDR	VWAAI	3		1419.302352	4254.883657	0.001463592	1	N	232	271
O08795	Parental	ILSSR	VNDGVCDCCDGTDEYNSGTVCENTCREK	GRKEK	3	C6:+57.021,C8:+57.021,C9:+57.021,C21:+57.021,C25:+57.021	1105.417774	3313.229923	0.000451244	12	N	91	119
O08795	Parental	ILSSR	VNDGVCDCCDGTDEYNSGTVCENTCR	EKGRK	3	C6:+57.021,C8:+57.021,C9:+57.021,C21:+57.021,C25:+57.021	1019.705256	3056.092367	0.000451244	52	N	91	117
O08795	Parental	EESIR	SLEQEISFDFGPSGEFAYLYSQCYELTTNEYVYR	LCPFK	3	C23:+57.021	1369.282694	4104.824681	0.000823681	2	N	385	419
O08795	Parental	GRKEK	ESLQQLAEVTR	EGFRL	2		637.3414879	1272.667376	0.000451244	9	N	124	135
O08795	Parental	FAYLY	SQCYELTTNEYVYR	LCPFK	2	C3:+57.021	913.406999	1824.798398	0.000698008	2	N	405	419
O08795	Parental	EESIR	SLEQEISFDFGPSGEFAYLY	SQCYE	2		1150.026221	2298.036843	0.002663018	1	N	385	405
O08795	Parental	EKGRK	EKESLQQLAEVTR	EGFRL	2		765.9102661	1529.804932	0.000735798	4	N	122	135
O08807	Exosome	IEEFK	SINTEVVACSVDSQFTHLAWINTPR	RQGGL	3	C9:+57.021	949.1364706	2844.386012	0.000451244	3	N	142	167
O08807	Parental	KGVLR	QITLNDLPVGR	SVDET	2		613.349116	1224.682632	0.000451244	3	N	215	226
O08807	Parental	IEEFK	SINTEVVACSVDSQFTHLAWINTPR	RQGGL	3	C9:+57.021	949.1364706	2844.386012	0.000451244	1	N	142	167
O08808	Exosome	SIALK	VGCLQLINALITPAEELDFR	VHIRS	2	C3:+57.021	1136.604219	2271.192838	0.000451244	47	N	302	322
O08808	Exosome	SIALK	VGCLQLINALITPAEELDFR	VHIRS	3	C3:+57.021	758.0720793	2271.192838	0.000451244	34	N	302	322
O08808	Exosome	LESLR	VSLNNNPVSWVQTFGAEGLASLLDILKR	LHDEK	3		1014.552656	3040.634568	0.000451244	10	N	160	188
O08808	Exosome	NAGSR	NAGAFGFNISFLCK	LRDTK	2	C13:+57.021	773.3798589	1544.744118	0.000451244	2	N	975	989
O08808	Exosome	NEDMK	VQLCVFDEQGDEDFFDLK	GRLDD	2	C4:+57.021	1102.496542	2202.977485	0.000622848	10	N	350	368
O08808	Exosome	QVNRK	AGCAVTSLLASELTK	DDAMA	2	C3:+57.021	760.9033638	1519.791128	0.000622848	3	N	1207	1222
O08808	Exosome	LNTVK	DSKAEPHFLSILQHLLLVR	NDYEA	4		554.8197299	2215.247719	0.000451244	1	N	393	412
O08808	Exosome	SELMR	LGLHQVLQELR	EIENE	3		435.9266219	1304.756466	0.002519933	1	N	331	342
O08808	Exosome	VKDSK	AEPHFLSILQHLLLVR	NDYEA	3		629.3723949	1885.093785	0.000451244	3	N	396	412
O08808	Exosome	ETLYK	ELGDYFVFDPK	KLSVE	2		665.3222325	1328.628865	0.001591523	2	N	1099	1110
O08808	Exosome	AILFK	LQFSEQVENIKPEIVSVTAACEELR	KSENF	3	C21:+57.021	963.8273028	2888.458508	0.000735798	2	N	926	951
O08808	Parental	SIALK	VGCLQLINALITPAEELDFRVHIR	SELMR	4	C3:+57.021	695.1341348	2776.505339	0.000451244	3	N	302	326
O08808	Parental	SIALK	VGCLQLINALITPAEELDFR	VHIRS	2	C3:+57.021	1136.604219	2271.192838	0.000451244	20	N	302	322
O08808	Parental	SIALK	VGCLQLINALITPAEELDFR	VHIRS	3	C3:+57.021	758.0720793	2271.192838	0.000451244	37	N	302	322
O08808	Parental	LESLR	VSLNNNPVSWVQTFGAEGLASLLDILKR	LHDEK	3		1014.552656	3040.634568	0.000451244	19	N	160	188
O08808	Parental	NAGSR	NAGAFGFNISFLCK	LRDTK	2	C13:+57.021	773.3798589	1544.744118	0.000451244	6	N	975	989
O08808	Parental	NEDMK	VQLCVFDEQGDEDFFDLK	GRLDD	2	C4:+57.021	1102.496542	2202.977485	0.000451244	18	N	350	368
O08808	Parental	LNTVK	DSKAEPHFLSILQHLLLVR	NDYEA	4		554.8197299	2215.247719	0.000451244	2	N	393	412
O08808	Parental	LESLR	VSLNNNPVSWVQTFGAEGLASLLDILK	RLHDE	2		1443.274528	2884.533457	0.000662267	1	N	160	187
O08808	Parental	LESLR	VSLNNNPVSWVQTFGAEGLASLLDILK	RLHDE	3		962.5189522	2884.533457	0.000451244	4	N	160	187
O08808	Parental	PNWSK	FVAEDLSQDCFWTK	VKEDR	2	C10:+57.021	873.395903	1744.776206	0.000662267	2	N	769	783
O08808	Parental	SELMR	LGLHQVLQELR	EIENE	3		435.9266219	1304.756466	0.001162105	9	N	331	342
O08808	Parental	VKDSK	AEPHFLSILQHLLLVR	NDYEA	3		629.3723949	1885.093785	0.000451244	2	N	396	412
O08810	Exosome	LHHGK	TCFVDCLIEQTHPEIR	KRYDQ	2	C2:+57.021,C6:+57.021	1009.477201	2016.938803	0.001463592	2	N	141	157
O08810	Exosome	LHHGK	TCFVDCLIEQTHPEIR	KRYDQ	3	C2:+57.021,C6:+57.021	673.3207343	2016.938803	0.000451244	11	N	141	157
O08810	Exosome	LYTIK	AFIPAIDSFGFETDLR	THTQG	2		899.9546737	1797.893747	0.000451244	23	N	871	887
O08810	Exosome	EPLEK	GLAEDIENEVVQITWNR	KKLGE	2		993.5005081	1984.985416	0.000451244	2	N	693	710
O08810	Exosome	EPLEK	GLAEDIENEVVQITWNR	KKLGE	3		662.6696054	1984.985416	0.000451244	27	N	693	710
O08810	Exosome	SSSQR	SFVEFILEPLYK	ILAQV	2		742.9059325	1483.796265	0.000451244	10	N	366	378
O08810	Exosome	GSFAK	IYADTFGDINYQEFAK	RLWGD	2		947.9470456	1893.878491	0.000451244	16	N	324	340
O08810	Exosome	LLAAR	SIWAFGPDATGPNILVDDTLPSEVDK	ALLGS	2		1379.185044	2756.354489	0.000451244	16	N	729	755
O08810	Exosome	LLAAR	SIWAFGPDATGPNILVDDTLPSEVDK	ALLGS	3		919.7926297	2756.354489	0.000451244	14	N	729	755
O08810	Exosome	EIDIK	VADPVVTFCETVVETSSLK	CFAET	2	C9:+57.021	1041.027478	2080.039357	0.000451244	12	N	653	672
O08810	Exosome	EPLYK	ILAQVVGDVDTSLPR	TLDEL	2		791.944109	1581.872618	0.000451244	8	N	378	393
O08810	Exosome	GQPVK	VLGENYTLEDEEDSQICTVGR	LWISV	2	C17:+57.021	1214.052942	2426.090283	0.000451244	6	N	507	528
O08810	Exosome	TSVIK	IAVEPVNPSELPK	MLDGL	2		696.8908137	1391.766027	0.001763695	1	N	588	601
O08810	Exosome	ETDLR	THTQGQAFSLSVFHHWQIVPGDPLDK	SIVIR	4		737.1233057	2944.462023	0.00307782	1	N	887	913
O08810	Exosome	LLAAR	SIWAFGPDATGPNILVDDTLPSEVDKALLGSVK	DSIVQ	3		1142.6	3424.7766	0.000622848	8	N	729	762
O08810	Exosome	LGSVK	DSIVQGFQWGTR	EGPLC	2		697.3471046	1392.678609	0.000451244	3	N	762	774
O08810	Exosome	EIRKR	YDQDLCYTDILFTEQER	GVGIK	2	C6:+57.021	1104.991624	2207.967649	0.002374549	2	N	159	176

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O08810	Parental	LHHGK	TCFVDCLIEQTHPEIR	KRYDQ	2	C2:+57.021,C6:+57.021	1009.477201	2016.938803	0.001162105	1	N	141	157
O08810	Parental	LHHGK	TCFVDCLIEQTHPEIR	KRYDQ	3	C2:+57.021,C6:+57.021	673.3207343	2016.938803	0.000451244	16	N	141	157
O08810	Parental	HEDKK	YYPTAEEVYGPEVETIVQEEDTQPLTEPIIKPVK	TKKFT	3		1302.326382	3903.955747	0.000451244	44	N	63	97
O08810	Parental	LYTIK	AFIPAIDSFGFETDLR	THTQG	2		899.9546737	1797.893747	0.000451244	23	N	871	887
O08810	Parental	EPLEK	GLAEDIENEVVQITWNR	KKLGE	2		993.5005081	1984.985416	0.000451244	28	N	693	710
O08810	Parental	EPLEK	GLAEDIENEVVQITWNR	KKLGE	3		662.6696054	1984.985416	0.000451244	28	N	693	710
O08810	Parental	SSSQR	SFVEFILEPLYK	ILAQV	2		742.9059325	1483.796265	0.000451244	24	N	366	378
O08810	Parental	GSFAK	IYADTFGDINYQEFAK	RLWGD	2		947.9470456	1893.878491	0.000823681	4	N	324	340
O08810	Parental	LLAAR	SIWAFGPDATGPNILVDDTLPSEVDK	ALLGS	2		1379.185044	2756.354489	0.000451244	8	N	729	755
O08810	Parental	LLAAR	SIWAFGPDATGPNILVDDTLPSEVDK	ALLGS	3		919.7926297	2756.354489	0.000451244	12	N	729	755
O08810	Parental	EIDIK	VADPVVTFCETVVETSSLK	CFAET	2	C9:+57.021	1041.027478	2080.039357	0.000451244	1	N	653	672
O08810	Parental	LARRR	GHVTQDAPIPGSPLYTIK	AFIPA	2		947.5076048	1892.99961	0.002453667	1	N	853	871
O08810	Parental	EPLYK	ILAQVVGDVDTSLPR	TLDEL	2		791.944109	1581.872618	0.000823681	1	N	378	393
O08810	Parental	GQPVK	VLGENYTLEDEEDSQICTVGR	LWISV	2	C17:+57.021	1214.052942	2426.090283	0.000451244	7	N	507	528
O08917	Exosome	QVVER	AQQVAVQEQEIAR	REKEL	2		735.3895008	1468.763402	0.000622848	1	N	261	274
O08917	Exosome	MFLGK	TEAEIAHIALETLEGHQR	AIMAH	3		673.3487548	2017.022864	0.000622848	3	N	91	109
O08917	Parental	VNTRR	AQADLAYQLQVAK	TKQQI	2		709.8860627	1417.756525	0.001329271	2	N	231	244
O08917	Parental	MGAAK	VTGEVLDILSRLPESVER	LTGVS	2		1006.555283	2011.094967	0.002663018	1	N	392	410
O08917	Parental	MGAAK	VTGEVLDILSRLPESVER	LTGVS	3		671.3727889	2011.094967	0.000451244	5	N	392	410
O08917	Parental	QVVER	AQQVAVQEQEIAR	REKEL	2		735.3895008	1468.763402	0.000451244	35	N	261	274
O08917	Parental	GAAKV	TGEVLDILSR	LPESV	2		551.8092923	1101.602985	0.001463592	2	N	393	403
O08917	Parental	MFLGK	TEAEIAHIALETLEGHQR	AIMAH	3		673.3487548	2017.022864	0.000451244	26	N	91	109
O08917	Parental	MFLGK	TEAEIAHIALETLEGHQR	AIMAH	4		505.2635161	2017.022864	0.000622848	3	N	91	109
O08917	Parental	SYTLK	DIHDDQDYLHSLGK	ARTAQ	3		552.5940368	1654.75871	0.000622848	1	N	152	166
O08917	Parental	MLLEK	LPQVAEEISGPLTSANK	ITLVS	2		877.4706879	1752.925776	0.000451244	9	N	360	377
O08992	Exosome	GLRLK	SIDNGIFVQLVQANSPASLVGLR	FGDQV	2		1199.658603	2397.301606	0.000451244	65	N	131	154
O08992	Exosome	GLRLK	SIDNGIFVQLVQANSPASLVGLR	FGDQV	3		800.1083352	2397.301606	0.000451244	52	N	131	154
O08992	Exosome	VIGLK	DAQIADILSTAGTVVTITIMPTFIFEHIIK	RMAPS	3		1086.928512	3257.762137	0.000451244	14	N	251	281
O08992	Exosome	LKVDK	VIQAQTAYSANPASQAFVLVDASAALPPDGNLYPK	LYPEL	3		1196.618054	3586.830761	0.000451244	35	N	14	49
O08992	Exosome	LKVDK	VIQAQTAYSANPASQAFVLVDASAALPPDGNLYPK	LYPEL	4		897.7154903	3586.830761	0.001162105	1	N	14	49
O08992	Exosome	LVGLR	FGDQVLQINGENCAGWSSDK	AHKVL	2	C13:+57.021	1113.000315	2223.98503	0.000451244	55	N	154	174
O08992	Exosome	VTMHK	DSSGHVGFIFK	SGKIT	2		597.3016344	1192.587669	0.000451244	11	N	204	215
O08992	Exosome	SSAAR	NGLLTDHHICEINGQNVIGLK	DAQIA	2	C10:+57.021	1173.105449	2344.195298	0.000622848	1	N	230	251
O08992	Exosome	SSAAR	NGLLTDHHICEINGQNVIGLK	DAQIA	3	C10:+57.021	782.4062325	2344.195298	0.001871652	1	N	230	251
O08992	Exosome	KIGLR	LKSIDNGIFVQLVQANSPASLVGLR	FGDQV	3		880.5013443	2638.480633	0.000451244	12	N	129	154
O08992	Exosome	LEDLK	VDKVIQAQTAYSANPASQAFVLVDASAALPPDGNLYPK	LYPEL	3		1310.681494	3929.021082	0.002374549	1	N	11	49
O08992	Exosome	AQTAY	SANPASQAFVLVDASAALPPDGNLYPK	LYPEL	3		905.1330977	2712.375893	0.001763695	1	N	22	49
O08992	Exosome	LVGLR	FGDQVLQINGENCAGWSSDKAHK	VLKQA	4	C13:+57.021	641.0518047	2560.176019	0.001162105	2	N	154	177
O08992	Parental	GLRLK	SIDNGIFVQLVQANSPASLVGLR	FGDQV	2		1199.658603	2397.301606	0.000451244	16	N	131	154
O08992	Parental	GLRLK	SIDNGIFVQLVQANSPASLVGLR	FGDQV	3		800.1083352	2397.301606	0.000451244	15	N	131	154
O08992	Parental	LVGLR	FGDQVLQINGENCAGWSSDK	AHKVL	2	C13:+57.021	1113.000315	2223.98503	0.001329271	2	N	154	174
O08997	Exosome	LPNKK	VCIDSEHSSDTLLATLNK	TGKAV	2	C2:+57.021	1001.991427	2001.967255	0.002981883	1	N	39	57
O08997	Exosome	RVLNK	LGGVEFNIDLPNKK	VCIDS	3		515.2879965	1542.840589	0.002374549	1	N	25	39
O08997	Parental	LPNKK	VCIDSEHSSDTLLATLNK	TGKAV	2	C2:+57.021	1001.991427	2001.967255	0.000451244	2	N	39	57
O08997	Parental	LPNKK	VCIDSEHSSDTLLATLNK	TGKAV	3	C2:+57.021	668.3302182	2001.967255	0.000451244	20	N	39	57
O08997	Parental	RVLNK	LGGVEFNIDLPNKK	VCIDS	2		772.4280947	1542.840589	0.000698008	10	N	25	39
O08997	Parental	RVLNK	LGGVEFNIDLPNKK	VCIDS	3		515.2879965	1542.840589	0.000622848	4	N	25	39
O08997	Parental	LPNKK	VCIDSEHSSDTLLATLNKTGK	AVSYL	2	C2:+57.021	1145.07348	2288.13136	0.000451244	2	N	39	60
O08997	Parental	LPNKK	VCIDSEHSSDTLLATLNKTGK	AVSYL	3	C2:+57.021	763.7182533	2288.13136	0.000451244	2	N	39	60
O09043	Exosome	RALNK	AIGGYPFLNGQYFIQCSK	TPTLP	2	C16:+57.021	1032.006683	2061.997767	0.000451244	26	N	296	314
O09043	Exosome	RALNK	AIGGYPFLNGQYFIQCSK	TPTLP	3	C16:+57.021	688.3403889	2061.997767	0.000451244	1	N	296	314
O09043	Exosome	MESVK	VGTGLSLCAQGCSAILDTGTSLITGPSEEIR	ALNKA	3	C8:+57.021,C12:+57.021	1055.19205	3162.552751	0.000451244	43	N	261	292
O09043	Exosome	VPSTR	CHFFSLACWFHHR	FNPKA	3	[0:-17.027,C1:+57.021,C8:+57.021	596.5943133	1786.75954	0.001699387	2	N	103	116
O09043	Exosome	HLGHR	ILNPLNGWEQLAELSR	TSTSG	2		926.9999469	1851.984294	0.000451244	6	N	36	52
O09043	Exosome	AELSR	TSTSGGNPSFVPLSK	FMNTQ	2		739.8784346	1477.741269	0.00091018	1	N	52	67
O09043	Parental	RALNK	AIGGYPFLNGQYFIQCSK	TPTLP	2	C16:+57.021	1032.006683	2061.997767	0.000451244	22	N	296	314
O09043	Parental	MESVK	VGTGLSLCAQGCSAILDTGTSLITGPSEEIR	ALNKA	3	C8:+57.021,C12:+57.021	1055.19205	3162.552751	0.000451244	51	N	261	292
O09043	Parental	VPSTR	CHFFSLACWFHHR	FNPKA	3	[0:-17.027,C1:+57.021,C8:+57.021	596.5943133	1786.75954	0.001654178	2	N	103	116
O09043	Parental	DYVIK	ILQSDVGLCLLGFQALDIPKPAGPLWILGDVF	LGPYV	3	C9:+57.021	1155.967035	3464.877706	0.000451244	5	N	340	372
O09061	Exosome	GPVQL	RFSPYAFNGGTVLAIAGEDFSIVASDTR	LSEGF	3		987.8300778	2960.466833	0.000451244	17	N	27	55
O09061	Exosome	PKCYK	LTDKTVIGCSGFHGDCLTLTK	IIEAR	3	C9:+57.021,C16:+57.021	775.0524247	2322.133874	0.000451244	8	N	72	93
O09061	Exosome	LYSRR	FFPYYVYNIIGGLDEEGKGAVYSFDPVGSYQR	DSFKA	3		1217.587983	3649.740549	0.000451244	40	N	127	159
O09061	Exosome	LYSRR	FFPYYVYNIIGGLDEEGKGAVYSFDPVGSYQR	DSFKA	4		913.4429373	3649.740549	0.000622848	14	N	127	159
O09061	Exosome	DEEGK	GAVYSFDPVGSYQR	DSFKA	2		773.3707768	1544.725954	0.000451244	32	N	145	159
O09061	Exosome	ILYSR	RFFPYYVYNIIGGLDEEGK	GAVYS	2		1140.570933	2279.126267	0.000451244	15	N	126	145

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O09061	Exosome	ILYSR	RFFPYYVYNIIGGLDEEGK	GAVYS	3		760.7165556	2279.126267	0.000451244	31	N	126	145
O09061	Exosome	RFSPY	AFNGGTVLAIAGEDFSIVASDTR	LSEGF	2		1156.082394	2310.149187	0.000451244	6	N	32	55
O09061	Exosome	RFSPY	AFNGGTVLAIAGEDFSIVASDTR	LSEGF	3		771.0575291	2310.149187	0.000451244	8	N	32	55
O09061	Exosome	LYSRR	FFPYYVYNIIGGLDEEGK	GAVYS	2		1062.520378	2123.025156	0.000451244	26	N	127	145
O09061	Exosome	LYSRR	FFPYYVYNIIGGLDEEGK	GAVYS	3		708.6828519	2123.025156	0.000622848	5	N	127	145
O09061	Exosome	KLTDK	TVIGCSGFHGDCLTLTK	IIEAR	2	C5:+57.021,C12:+57.021	933.4479126	1864.880225	0.000451244	18	N	76	93
O09061	Exosome	PVQLR	FSPYAFNGGTVLAIAGEDFSIVASDTR	LSEGF	2		1403.190661	2804.365722	0.000735798	1	N	28	55
O09061	Exosome	PVQLR	FSPYAFNGGTVLAIAGEDFSIVASDTR	LSEGF	3		935.7963741	2804.365722	0.000451244	8	N	28	55
O09061	Exosome	MRLVK	DVFISAAERDVYTGDALR	ICIVT	3		666.6696054	1996.985416	0.000451244	2	N	203	221
O09061	Exosome	HSNNK	AMTTGAIAAMLSTILYSR	RFFPY	2		935.9924198	1869.96924	0.000451244	3	N	108	126
O09061	Exosome	HSNNK	AMTTGAIAAMLSTILYSR	RFFPY	3		624.3308799	1869.96924	0.002519933	1	N	108	126
O09061	Parental	GPVQL	RFSPYAFNGGTVLAIAGEDFSIVASDTR	LSEGF	3		987.8300778	2960.466833	0.000451244	3	N	27	55
O09061	Parental	PKCYK	LTDKTVIGCSGFHGDCLTLTK	IIEAR	3	C9:+57.021,C16:+57.021	775.0524247	2322.133874	0.000622848	1	N	72	93
O09061	Parental	PKCYK	LTDKTVIGCSGFHGDCLTLTK	IIEAR	4	C9:+57.021,C16:+57.021	581.5412686	2322.133874	0.000662267	2	N	72	93
O09061	Parental	LYSRR	FFPYYVYNIIGGLDEEGKGAVYSFDPVGSYQR	DSFKA	3		1217.587983	3649.740549	0.000451244	27	N	127	159
O09061	Parental	DEEGK	GAVYSFDPVGSYQR	DSFKA	2		773.3707768	1544.725954	0.000451244	12	N	145	159
O09061	Parental	LYSRR	FFPYYVYNIIGGLDEEGK	GAVYS	2		1062.520378	2123.025156	0.000451244	2	N	127	145
O09061	Parental	PYYVY	NIIGGLDEEGKGAVYSFDPVGSYQR	DSFKA	2		1336.154079	2670.292557	0.000451244	6	N	134	159
O09106	Exosome	KQMQR	FNVGEDCPVFDGLFEFCQLSTGGSVASAVK	LNKQQ	3	C7:+57.021,C17:+57.021	1079.833974	3236.478523	0.000451244	14	N	93	123
O09106	Exosome	NELPY	NDYFEYFGPDFK	LHISP	2		771.3333286	1540.651057	0.000451244	2	N	330	342
O09106	Exosome	VSFHK	YGEYFPGTGDLR	DIGAG	2		687.8203883	1373.625177	0.000823681	3	N	200	212
O09106	Exosome	LHHAK	KSEASGFCYVNDIVLAILELLK	YHQRV	3	C8:+57.021	828.1139442	2481.318433	0.001162105	1	N	143	165
O09106	Parental	KQMQR	FNVGEDCPVFDGLFEFCQLSTGGSVASAVK	LNKQQ	3	C7:+57.021,C17:+57.021	1079.833974	3236.478523	0.000451244	26	N	93	123
O09106	Parental	NELPY	NDYFEYFGPDFK	LHISP	2		771.3333286	1540.651057	0.000451244	15	N	330	342
O09106	Parental	VSFHK	YGEYFPGTGDLR	DIGAG	2		687.8203883	1373.625177	0.000662267	4	N	200	212
O09110	Exosome	FQQLK	QVVEEPSPQLPADQFSPEFVDFTSQCLR	KNPAE	3	C26:+57.021	1084.183926	3249.528379	0.000451244	6	N	279	307
O09110	Exosome	EKNMK	IPEDILGEIAVSIVR	ALEHL	3		541.9825731	1622.924319	0.001463592	1	N	160	175
O09110	Parental	FQQLK	QVVEEPSPQLPADQFSPEFVDFTSQCLR	KNPAE	3	C26:+57.021	1084.183926	3249.528379	0.000451244	22	N	279	307
O09110	Parental	EKNMK	IPEDILGEIAVSIVR	ALEHL	3		541.9825731	1622.924319	0.000451244	5	N	160	175
O09126	Exosome	FLKAR	LICSKPDSGLVFNILQDVFVLR	APGLK	3	C3:+57.021	845.1334502	2532.376951	0.000451244	10	N	278	300
O09126	Exosome	HSPLR	TEYAIPWLNEPSFVFADVIQK	SPDGP	2		1234.131355	2466.24711	0.002296037	1	N	198	219
O09126	Exosome	HSPLR	TEYAIPWLNEPSFVFADVIQK	SPDGP	3		823.0901701	2466.24711	0.000451244	4	N	198	219
O09130	Parental	PSTLK	LGVADIIDCVVLASSSEATETSQELR	LRVQG	3	C9:+57.021	921.7957797	2762.363939	0.000451244	5	N	316	342
O09130	Parental	VSPNR	ILLLFGESELSPTATPSTLK	LGVAD	2		1059.091167	2116.166735	0.000823681	1	N	296	316
O09131	Exosome	AKTYR	EYLNLYLQDSPEACDYGL	-	2	C14:+57.021	1081.983268	2161.950936	0.000451244	8	N	222	240
O09131	Exosome	ESFSK	VPPLIASFVR	SKRKE	2		549.8376558	1097.659712	0.0007646	2	N	122	132
O09131	Exosome	DAKTY	REYLNLYLQDSPEACDYGL	-	2	C15:+57.021	1160.033823	2318.052047	0.000451244	5	N	221	240
O09131	Exosome	WFFEK	NPLGLVPVLENSQGHLVTESVITCEYLDEAYPEKK	LFPDD	4	C24:+57.021	986.2518927	3940.976371	0.000451244	2	N	66	101
O09131	Parental	ESFSK	VPPLIASFVR	SKRKE	2		549.8376558	1097.659712	0.0025889	2	N	122	132
O09131	Parental	DAKTY	REYLNLYLQDSPEACDYGL	-	2	C15:+57.021	1160.033823	2318.052047	0.000451244	3	N	221	240
O09159	Exosome	AARHR	LLAEQEVLAPQVVLSLGGSSPYHSR	ATPKT	3		884.1453376	2649.412613	0.000451244	34	N	858	883
O09159	Exosome	EELWR	ASDSLEPPAADLFTGVLPNNYNPPK	YLCWD	2		1314.153547	2626.291495	0.000451244	20	N	240	265
O09159	Exosome	EELWR	ASDSLEPPAADLFTGVLPNNYNPPK	YLCWD	3		876.4382982	2626.291495	0.000451244	21	N	240	265
O09159	Exosome	NDYAR	QLAAGWGPCEVLVSNALAR	LSHYK	2	C9:+57.021	1006.523032	2011.030464	0.000451244	28	N	463	482
O09159	Exosome	NDYAR	QLAAGWGPCEVLVSNALAR	LSHYK	3	C9:+57.021	671.3512879	2011.030464	0.000622848	12	N	463	482
O09159	Exosome	NDYAR	QLAAGWGPCEVLVSNALAR	LSHYK	2	[0:-17.027,C9:+57.021	998.0095319	1994.003464	0.002884417	1	N	463	482
O09159	Exosome	TLGLR	FLQDTFGSDGLPR	VAWHI	2		726.8600449	1451.70449	0.000451244	19	N	177	190
O09159	Exosome	QTSER	FQVTLYNPLGR	KVDQM	2		654.3594837	1306.703367	0.000451244	22	N	509	520
O09159	Exosome	YNPPK	YLCWDVLCTDPPVVDNPR	SPEFN	2	C3:+57.021,C8:+57.021	1110.016691	2218.017782	0.000451244	40	N	265	283
O09159	Exosome	YKGQR	HLELEWTVGPIPVRDDWGK	EVISR	3		749.7239331	2246.148399	0.000451244	3	N	709	728
O09159	Exosome	KVRGR	HLVLLSSVSDAAAR	HRLLA	2		719.9047868	1437.793974	0.000451244	6	N	842	856
O09159	Exosome	FSGLR	QELPPQVHLLTLAR	WGPKM	3		538.9829074	1613.925322	0.000451244	3	N	894	908
O09159	Exosome	RATPK	TQFSGLRQELPPQVHLLTLAR	WGPKM	3		802.1206866	2403.33866	0.000451244	5	N	887	908
O09159	Exosome	YKGQR	HLELEWTVGPIPVR	DDWGK	3		549.307391	1644.898773	0.002296037	3	N	709	723
O09159	Exosome	PMEIR	TFLASVQWQE	HRPA-	2		604.8014673	1207.587335	0.002663018	1	N	999	1009
O09159	Parental	YNPPK	YLCWDVLCTDPPVVDNPRSPEFNAK	TLVNY	3	C3:+57.021,C8:+57.021	998.1373286	2991.388586	0.000451244	9	N	265	290
O09159	Parental	AARHR	LLAEQEVLAPQVVLSLGGSSPYHSR	ATPKT	3		884.1453376	2649.412613	0.000451244	14	N	858	883
O09159	Parental	EELWR	ASDSLEPPAADLFTGVLPNNYNPPK	YLCWD	2		1314.153547	2626.291495	0.000870037	18	N	240	265
O09159	Parental	EELWR	ASDSLEPPAADLFTGVLPNNYNPPK	YLCWD	3		876.4382982	2626.291495	0.000622848	9	N	240	265
O09159	Parental	NDYAR	QLAAGWGPCEVLVSNALAR	LSHYK	2	C9:+57.021	1006.523032	2011.030464	0.000451244	18	N	463	482
O09159	Parental	TLGLR	FLQDTFGSDGLPR	VAWHI	2		726.8600449	1451.70449	0.000451244	4	N	177	190
O09159	Parental	YNPPK	YLCWDVLCTDPPVVDNPR	SPEFN	2	C3:+57.021,C8:+57.021	1110.016691	2218.017782	0.000451244	8	N	265	283
O09159	Parental	LFQTF	TINYLQETTLAANQPLSR	ASRLK	2		1017.037258	2032.058915	0.000451244	11	N	947	965
O09159	Parental	KVRGR	HLVLLSSVSDAAAR	HRLLA	2		719.9047868	1437.793974	0.000622848	3	N	842	856
O09159	Parental	VGWLK	TVDQYYYGILSDVQHASVQYILDSVVSSLLEKPTR	RFIYV	4		997.515628	3986.031312	0.000451244	3	N	79	114

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O09159	Parental	FTINY	LQETTLAANQPLSR	ASRLK	2		771.4182583	1540.820917	0.001839721	1	N	951	965
O09172	Exosome	DCIQK	TLNEWSSQISPDLVR	EFPDV	2		872.94738	1743.87916	0.000451244	46	N	49	64
O09172	Exosome	ALLAR	ASTLHLQTGNLLNWGR	LRKKC	2		890.9768061	1779.938012	0.000823681	1	N	14	30
O09172	Exosome	ALLAR	ASTLHLQTGNLLNWGR	LRKKC	3		594.3204707	1779.938012	0.000622848	7	N	14	30
O09172	Exosome	HNDPK	ELLSEASFQEALQESIPDIEAQDWVPLWLLR	YSVIV	3		1209.286193	3624.835178	0.001463592	1	N	218	249
O09172	Exosome	RLRKK	CPSTHSEELRDCIQK	TLNEW	3	[0:-	614.9418841	1841.802252	0.000979378	1	N	34	49
O09172	Parental	DCIQK	TLNEWSSQISPDLVR	EFPDV	2		872.94738	1743.87916	0.000451244	34	N	49	64
O09172	Parental	ALLAR	ASTLHLQTGNLLNWGR	LRKKC	3		594.3204707	1779.938012	0.001871652	1	N	14	30
O09172	Parental	HNDPK	ELLSEASFQEALQESIPDIEAQDWVPLWLLR	YSVIV	3		1209.286193	3624.835178	0.000622848	5	N	218	249
O09172	Parental	HNDPK	ELLSEASFQEALQESIPDIEAQDWVPL	WLLRY	3		1019.836675	3056.486626	0.001654178	2	N	218	245
O35129	Parental	TSQNR	IYLTADNLVLNLQDESFTR	GSDSL	2		1113.07658	2224.13756	0.000451244	22	N	270	289
O35129	Parental	TSQNR	IYLTADNLVLNLQDESFTR	GSDSL	3		742.3869866	2224.13756	0.002019181	1	N	270	289
O35129	Parental	IFFNR	IGGVQQDTILAEGLHF	RIPWF	2		849.4470158	1696.878432	0.000451244	19	N	54	70
O35129	Parental	QNRIY	LTADNLVLNLQDESFTR	GSDSL	2		975.0028836	1947.990167	0.000451244	3	N	272	289
O35129	Parental	RAKDF	SLILDDVAITELSFSR	EYTAA	2		889.9808885	1777.946177	0.000637154	1	N	175	191
O35218	Exosome	DTAGR	VLELAQLLDQIWR	TKDAG	2		798.959562	1595.903524	0.00091018	1	N	242	255
O35218	Exosome	RRKQR	DEQLLTNVLETLR	GDGNV	2		772.4204667	1542.825333	0.000451244	1	N	215	228
O35218	Parental	RRKQR	DEQLLTNVLETLRGDGNVLIAVDTAGR	VLELA	3		961.5126373	2881.514512	0.000451244	1	N	215	242
O35218	Parental	DTAGR	VLELAQLLDQIWR	TKDAG	2		798.959562	1595.903524	0.000451244	2	N	242	255
O35218	Parental	QMKPR	QLIIVHGPPEASQDLAECCR	AFGGK	3	C18:+57.021,C19:+57.021	765.0405191	2292.098157	0.000998612	1	N	559	579
O35218	Parental	RRKQR	DEQLLTNVLETLR	GDGNV	2		772.4204667	1542.825333	0.000823681	1	N	215	228
O35226	Exosome	LKKEK	VNVDIINFGEEEVNTEK	LTAFV	2		974.9790741	1947.942548	0.001162105	1	N	135	152
O35226	Parental	LKKEK	VNVDIINFGEEEVNTEK	LTAFV	2		974.9790741	1947.942548	0.000451244	10	N	135	152
O35226	Parental	LKKEK	VNVDIINFGEEEVNTEKLTAFVNTLNGK	DGTGS	3		1036.535219	3106.582257	0.000451244	11	N	135	163
O35226	Parental	HSKTR	SNPENNVGLITLANDCEVLTTLTPDTGR	ILSKL	3	C16:+57.021	1005.496393	3013.465779	0.000451244	9	N	42	70
O35226	Parental	FLPTR	LQAQQDAVNIVCHSK	TRSNP	2	C12:+57.021	855.9335183	1709.851437	0.001463592	2	N	25	40
O35226	Parental	EEARR	AAAASAAEAGIATPGTEDSDDALLK	MTINQ	2		1158.564231	2315.112861	0.000451244	4	N	237	262
O35226	Parental	EEEAR	RAAAASAAEAGIATPGTEDSDDALLK	MTINQ	3		824.7457909	2471.213973	0.000637154	1	N	236	262
O35286	Exosome	PLLER	YGVIILDEAHER	TLATD	3		472.2495417	1413.725225	0.000622848	10	N	253	265
O35286	Exosome	LDAGK	FQIYFDNCPLLTIPGR	THPVE	2	C8:+57.021	977.4984941	1952.981388	0.000451244	3	N	299	315
O35286	Exosome	KRIKR	EVDDLGPEVGDIK	IIPLY	2		693.3438933	1384.672187	0.000823681	3	N	371	384
O35286	Exosome	EAKMR	FAHIDGDHLTLLNVYHAFK	QNHES	3		737.7168899	2210.12727	0.000451244	10	N	616	635
O35286	Exosome	EAKMR	FAHIDGDHLTLLNVYHAFK	QNHES	4		553.5396175	2210.12727	0.000451244	13	N	616	635
O35286	Exosome	EAHER	TLATDILMGVLK	EVVRQ	2		637.8735786	1273.731557	0.001329271	1	N	265	277
O35286	Exosome	PEILR	SNLGSVVLQLK	KLGID	2		579.3485847	1156.681569	0.001591523	1	N	504	515
O35286	Exosome	VYNPR	IRVESLLVTAISK	ASAQQ	3		476.9648538	1427.871161	0.001463592	1	N	450	463
O35286	Parental	PLLER	YGVIILDEAHER	TLATD	3		472.2495417	1413.725225	0.000622848	9	N	253	265
O35286	Parental	LDAGK	FQIYFDNCPLLTIPGR	THPVE	2	C8:+57.021	977.4984941	1952.981388	0.000451244	5	N	299	315
O35286	Parental	KRIKR	EVDDLGPEVGDIK	IIPLY	2		693.3438933	1384.672187	0.001871652	1	N	371	384
O35286	Parental	EAKMR	FAHIDGDHLTLLNVYHAFK	QNHES	3		737.7168899	2210.12727	0.001871652	1	N	616	635
O35286	Parental	EAKMR	FAHIDGDHLTLLNVYHAFK	QNHES	4		553.5396175	2210.12727	0.000698008	4	N	616	635
O35286	Parental	YLTVK	DNQVVQLHPSTVLDHKPEWVLY	NEFVL	3		873.1190114	2616.333634	0.001463592	4	N	714	736
O35326	Parental	AHRPK	LNEGVVEFASYGDLKNAIEK	LSGKE	2		1098.563305	2195.111011	0.000451244	1	N	143	163
O35326	Parental	AHRPK	LNEGVVEFASYGDLKNAIEK	LSGKE	3		732.7114703	2195.111011	0.001264573	2	N	143	163
O35326	Parental	AHRPK	LNEGVVEFASYGDLK	NAIEK	2		820.9124745	1639.809349	0.001162105	1	N	143	158
O35343	Exosome	TAALR	AVGNIVTGTDEQTQVVLNCDALSHFPALLTHPK	EKINK	4	C19:+57.021	887.2072882	3544.797953	0.000451244	2	N	306	339
O35343	Exosome	LLTVK	DAQVVQVVLDGLSNILK	MAEDQ	2		906.0178053	1810.020011	0.000451244	26	N	423	440
O35343	Exosome	LLTVK	DAQVVQVVLDGLSNILK	MAEDQ	3		604.3478035	1810.020011	0.000451244	44	N	423	440
O35343	Exosome	PLFLR	LLHSPHQNVCEQAVWALGNIIGDGPQCR	DYVIS	3	C10:+57.021,C27:+57.021	1057.185676	3168.533627	0.000451244	9	Y	164	192
O35343	Exosome	FGTQK	EAAWAISNLTISGR	KDQVA	2		744.894419	1487.773238	0.000451244	11	Y	386	400
O35343	Parental	TAALR	AVGNIVTGTDEQTQVVLNCDALSHFPALLTHPK	EKINK	4	C19:+57.021	887.2072882	3544.797953	0.000451244	8	N	306	339
O35343	Parental	LLTVK	DAQVVQVVLDGLSNILK	MAEDQ	2		906.0178053	1810.020011	0.000451244	26	N	423	440
O35343	Parental	LLTVK	DAQVVQVVLDGLSNILK	MAEDQ	3		604.3478035	1810.020011	0.000451244	34	N	423	440
O35343	Parental	PLFLR	LLHSPHQNVCEQAVWALGNIIGDGPQCR	DYVIS	3	C10:+57.021,C27:+57.021	1057.185676	3168.533627	0.000451244	6	Y	164	192
O35343	Parental	FGTQK	EAAWAISNLTISGR	KDQVA	2		744.894419	1487.773238	0.000451244	2	Y	386	400
O35343	Parental	DGDYR	VQNTSLEAIVQNASSDNQGIQLSAVQAAR	KLLSS	3		1004.850201	3011.527202	0.000451244	15	N	67	96
O35344	Exosome	PLFLR	LLHSPHQNVCEQAVWALGNIIGDGPQCR	DYVIS	3	C10:+57.021,C27:+57.021	1057.185676	3168.533627	0.000451244	9	Y	164	192
O35344	Exosome	FGTQK	EAAWAISNLTISGR	KDQVE	2		744.894419	1487.773238	0.000451244	11	Y	386	400
O35344	Exosome	LLSVK	DSQVVQVVLDGLK	NILIM	2		700.3937205	1398.771841	0.000622848	2	N	423	436
O35344	Exosome	TAALR	AVGNIVTGTDEQTQVVLNCDVLSHFPNLLSHPK	EKINK	4	C19:+57.021	901.4626541	3601.819416	0.000637154	2	N	306	339
O35344	Parental	PLFLR	LLHSPHQNVCEQAVWALGNIIGDGPQCR	DYVIS	3	C10:+57.021,C27:+57.021	1057.185676	3168.533627	0.000451244	6	Y	164	192
O35344	Parental	FGTQK	EAAWAISNLTISGR	KDQVE	2		744.894419	1487.773238	0.000451244	2	Y	386	400
O35344	Parental	LLSVK	DSQVVQVVLDGLK	NILIM	2		700.3937205	1398.771841	0.000622848	14	N	423	436
O35344	Parental	DADFK	AQNVTLEAILQNATSDNPVVQLSAVQAAR	KLLSS	3		1007.870825	3020.589074	0.000451244	2	N	67	96
O35344	Parental	GPQCR	DYVISLGVVKPLLSFINPSIPITFLR	NVTWV	3		967.9004453	2900.677936	0.002374549	1	N	192	218

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O35350	Exosome	FSEKK	AGTQELDDQIQANLPDEK	VLSEE	2		992.9770628	1983.938526	0.000451244	28	N	517	535
O35350	Exosome	FSEKK	AGTQELDDQIQANLPDEKVLSEEEIDDNFK	TLFSK	3		1135.206156	3402.595067	0.000451244	5	N	517	547
O35350	Exosome	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	2	C1:+39.994	1273.622915	2545.230229	0.001839721	2	N	48	71
O35350	Exosome	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	2	C1:+57.021	1282.136415	2562.257229	0.000451244	1	N	48	71
O35350	Exosome	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	3	C1:+57.021	855.0935431	2562.257229	0.000451244	38	N	48	71
O35350	Exosome	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	2	[0:-17.027,C1:+57.021	1273.622915	2545.230229	0.0007646	6	N	48	71
O35350	Exosome	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	3	[0:-17.027,C1:+57.021	849.4178764	2545.230229	0.000451244	8	N	48	71
O35350	Exosome	KALER	GSLLGCSINISDIRDLEAITFK	NLVRG	3	C6:+57.021	808.0934317	2421.256895	0.000451244	15	N	244	266
O35350	Exosome	AGGCR	NYPATFWVNPQFK	IRLEE	2		806.4018799	1610.78816	0.000451244	16	N	385	398
O35350	Exosome	DGATR	TDICQGALGDCWLLAAIASLTLNETILHR	VVPYG	3	C4:+57.021,C11:+57.021	1075.884892	3224.631276	0.000451244	30	N	104	133
O35350	Exosome	LPDEK	VLSEEEIDDNFK	TLFSK	2		719.3413506	1436.667101	0.000451244	22	N	535	547
O35350	Exosome	DGNGK	LGLVEFNILWNR	IRNYL	2		737.4147903	1472.813981	0.000451244	22	N	603	615
O35350	Exosome	LIITR	YSEPDLAVDFDNFVCCLVR	LETMF	2	C15:+57.021,C16:+57.021	1160.024713	2318.033826	0.000451244	23	N	661	680
O35350	Exosome	REFTK	LEICNLTPDALK	SRTLR	2	C4:+57.021	693.8687927	1385.721985	0.000735798	1	N	347	359
O35350	Exosome	KAYAK	VNGSYEALSGGCTSEAFEDFTGGVTEWYDLQK	APSDL	3	C12:+57.021	1173.184432	3516.529895	0.000451244	16	N	197	229
O35350	Exosome	SNRIR	LPPGEYIVVPSTFEPNKEGDFLLR	FFSEK	3		906.4782053	2716.411216	0.000451244	3	N	487	511
O35350	Exosome	FRFFK	LLDTDLDGVVTFDLFK	WLQLT	3		604.321143	1809.940029	0.001839721	1	N	689	705
O35350	Exosome	SRTLR	NWNTTFYEGTWR	RGSTA	2		787.8552938	1573.694988	0.000451244	19	N	364	376
O35350	Exosome	FFSEK	KAGTQELDDQIQANLPDEK	VLSEE	2		1057.024544	2112.033489	0.001943752	5	N	516	535
O35350	Exosome	FFSEK	KAGTQELDDQIQANLPDEK	VLSEE	3		705.0189629	2112.033489	0.000451244	7	N	516	535
O35350	Exosome	TKDGK	LVFVHSAQGNEFWSALLEK	AYAKV	3		725.7131455	2174.116036	0.000451244	11	N	174	193
O35350	Exosome	RDFIR	EFTKLEICNLTPDALK	SRTLR	3	C8:+57.021	631.3330114	1890.975634	0.000622848	1	N	343	359
O35350	Exosome	YDLQK	APSDLYQIILK	ALERG	2		630.8640676	1259.712535	0.000451244	4	N	229	240
O35350	Parental	FSEKK	AGTQELDDQIQANLPDEK	VLSEE	2		992.9770628	1983.938526	0.000451244	27	N	517	535
O35350	Parental	FSEKK	AGTQELDDQIQANLPDEKVLSEEEIDDNFK	TLFSK	3		1135.206156	3402.595067	0.002727428	2	N	517	547
O35350	Parental	TLRAR	CLQSGVLFQDEAFPPVSHSLGFK	ELGPH	3	C1:+57.021	855.0935431	2562.257229	0.000451244	29	N	48	71
O35350	Parental	KALER	GSLLGCSINISDIRDLEAITFK	NLVRG	3	C6:+57.021	808.0934317	2421.256895	0.000451244	2	N	244	266
O35350	Parental	AGGCR	NYPATFWVNPQFK	IRLEE	2		806.4018799	1610.78816	0.000451244	8	N	385	398
O35350	Parental	DGATR	TDICQGALGDCWLLAAIASLTLNETILHR	VVPYG	3	C4:+57.021,C11:+57.021	1075.884892	3224.631276	0.000451244	31	N	104	133
O35350	Parental	LPDEK	VLSEEEIDDNFK	TLFSK	2		719.3413506	1436.667101	0.000451244	5	N	535	547
O35350	Parental	DGNGK	LGLVEFNILWNR	IRNYL	2		737.4147903	1472.813981	0.000451244	9	N	603	615
O35350	Parental	LIITR	YSEPDLAVDFDNFVCCLVR	LETMF	2	C15:+57.021,C16:+57.021	1160.024713	2318.033826	0.000451244	12	N	661	680
O35350	Parental	KAYAK	VNGSYEALSGGCTSEAFEDFTGGVTEWYDLQK	APSDL	3	C12:+57.021	1173.184432	3516.529895	0.000451244	23	N	197	229
O35350	Parental	SRTLR	NWNTTFYEGTWR	RGSTA	2		787.8552938	1573.694988	0.000451244	4	N	364	376
O35350	Parental	FFSEK	KAGTQELDDQIQANLPDEK	VLSEE	2		1057.024544	2112.033489	0.000622848	1	N	516	535
O35350	Parental	FFSEK	KAGTQELDDQIQANLPDEK	VLSEE	3		705.0189629	2112.033489	0.001871652	1	N	516	535
O35350	Parental	TKDGK	LVFVHSAQGNEFWSALLEK	AYAKV	2		1088.065818	2174.116036	0.000451244	3	N	174	193
O35350	Parental	TKDGK	LVFVHSAQGNEFWSALLEK	AYAKV	3		725.7131455	2174.116036	0.000451244	19	N	174	193
O35350	Parental	YDLQK	APSDLYQIILK	ALERG	2		630.8640676	1259.712535	0.000823681	3	N	229	240
O35350	Parental	KALER	GSLLGCSINISDIR	DLEAI	2	C6:+57.021	752.8933305	1503.771061	0.001699387	1	N	244	258
O35350	Parental	RVVPY	GQSFQDGYAGIFHFQLWQFGEWVDVVIDDLLPTK	DGKLV	3		1319.316375	3954.925724	0.000823681	1	N	137	171
O35381	Exosome	LENLK	SLDLFNCEVTNLNAYR	ENVFK	2	C7:+57.021	964.9624728	1927.909346	0.000451244	2	N	116	132
O35381	Exosome	LENLK	SLDLFNCEVTNLNAYRENVFK	LLPQV	3	C7:+57.021	849.4166858	2545.226657	0.000823681	1	N	116	137
O35381	Exosome	SIEGK	IEGLTDEFEELEFLSTINVGLTSISNLPK	LNKLK	3		1070.222418	3207.643855	0.000451244	23	N	33	62
O35381	Parental	DVSGE	EEEDEEGYNDGEVDDEEDEEEAGEEEGSQKR	KREPD	3		1192.449767	3574.3259	0.000451244	80	N	204	235
O35381	Parental	ELRNR	TPSDVKELVLDNCK	SIEGK	2	C13:+57.021	809.411553	1616.807506	0.000622848	2	N	14	28
O35381	Parental	LENLK	SLDLFNCEVTNLNAYR	ENVFK	2	C7:+57.021	964.9624728	1927.909346	0.000451244	28	N	116	132
O35381	Parental	LENLK	SLDLFNCEVTNLNAYRENV	FKLLP	2	C7:+57.021	1136.03944	2270.06328	0.000451244	2	N	116	135
O35381	Parental	LENLK	SLDLFNCEVTNLNAYRENVFK	LLPQV	2	C7:+57.021	1273.621129	2545.226657	0.000451244	13	N	116	137
O35381	Parental	LENLK	SLDLFNCEVTNLNAYRENVFK	LLPQV	3	C7:+57.021	849.4166858	2545.226657	0.000451244	14	N	116	137
O35381	Parental	LDNCK	SIEGKIEGLTDEFEELEFLSTINVGLTSISNLPK	LNKLK	3		1241.647456	3721.918967	0.000451244	23	N	28	62
O35381	Parental	LDNCK	SIEGKIEGLTDEFEELEFLSTINVGLTSISNLPK	LNKLK	4		931.4875419	3721.918967	0.000451244	2	N	28	62
O35381	Parental	SIEGK	IEGLTDEFEELEFLSTINVGLTSISNLPK	LNKLK	3		1070.222418	3207.643855	0.000451244	90	N	33	62
O35381	Parental	SIEGK	IEGLTDEFEELEFLSTINV	GLTSI	2		1099.541704	2197.067809	0.000735798	3	N	33	52
O35381	Parental	LSENR	ISGDLEVLAEK	CPNLK	2		587.3222325	1172.628865	0.000451244	10	N	75	86
O35381	Parental	LSENR	ISGDLEVLAEKCPNLK	HLNLS	2	C12:+57.021	893.4746847	1784.933769	0.000451244	1	N	75	91
O35459	Exosome	QRLPK	VIGNQSLVNELTFSAR	KMMAD	2		874.4710222	1746.926444	0.000451244	27	N	213	229
O35459	Exosome	QEASK	RAPEEVSDHNYESIQVTSAQK	HVLHV	3		796.7195761	2387.135328	0.00091018	2	N	43	64
O35598	Exosome	TDCNR	HTQVCINGQCAGSICEK	YDLEE	3	C5:+57.021,C10:+57.021,C15:+57.021	654.6257862	1960.853959	0.000637154	4	N	558	575
O35598	Exosome	LKPGK	QCSPSQGPCCTAQCAFK	SKSEK	2	C2:+57.021,C9:+57.021,C10:+57.021,C14:+57.021	993.8994837	1985.783367	0.000451244	30	N	502	519
O35598	Exosome	SSHVK	AIDTIYQTTDFSGIR	NISFM	2		850.9286559	1699.841712	0.000451244	1	N	252	267
O35598	Exosome	QFSGR	TITLQPGSPCNDFR	GYCDV	2	C10:+57.021	803.3884123	1604.761225	0.001162105	6	N	623	637
O35598	Exosome	HVPPK	VSHITFAHEVGHNFGSPHDSGTECTPGESK	NLGQK	4	C24:+57.021	806.1143934	3220.426373	0.000451244	12	N	376	406

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O35598	Exosome	TLAER	NTCQLYIQTDHLFFK	YYGTR	3	C3:+57.021	643.3175842	1926.929353	0.002453667	1	N	220	235
O35638	Exosome	YKHDR	DIALLDLINFFIQCSGCK	GVVTA	2	C14:+57.021,C17:+57.021	1064.034352	2126.053104	0.000451244	5	N	110	128
O35638	Exosome	ELARR	FALTFGLDQLK	TREAI	2		626.8509602	1251.68632	0.001264573	2	N	954	965
O35638	Exosome	DKFNR	LLEDFLQEGEEPDEDDAYQVLSTLKR	ITAFH	3		1018.159818	3051.456054	0.000451244	14	N	667	693
O35638	Exosome	VDISR	SQLIDELADKFNR	LLEDF	3		516.9392558	1547.794368	0.000622848	2	N	654	667
O35638	Exosome	DDRTR	ITELFAVALPQLLAK	YSVDA	2		813.9956132	1625.975626	0.000998612	5	N	562	577
O35638	Parental	DKFNR	LLEDFLQEGEEPDEDDAYQVLSTLKR	ITAFH	3		1018.159818	3051.456054	0.002080925	1	N	667	693
O35639	Exosome	WVGPR	GTIKDYPGFSPSVDAEAIR	KAIRG	2		1012.010709	2022.005817	0.000451244	6	N	9	28
O35639	Exosome	KKSMK	GTGTDEDALIEILTTR	SSRQM	2		852.9366779	1703.857756	0.000451244	41	N	104	120
O35639	Exosome	KKSMK	GTGTDEDALIEILTTR	SSRQM	3		568.9603853	1703.857756	0.0007646	13	N	104	120
O35639	Exosome	NISQK	DIEDSIKGELSGHFEDLLLAIVHCAR	NTPAF	3	C24:+57.021	979.8310472	2936.469742	0.000451244	18	N	222	248
O35639	Exosome	NISQK	DIEDSIKGELSGHFEDLLLAIVHCAR	NTPAF	4	C24:+57.021	735.1252354	2936.469742	0.000451244	39	N	222	248
O35639	Exosome	HEFKK	HYGYSLYSAIQSDTSGDYR	TVLLK	2		1091.987962	2181.960324	0.000451244	51	N	293	312
O35639	Exosome	HEFKK	HYGYSLYSAIQSDTSGDYR	TVLLK	3		728.3279079	2181.960324	0.000451244	5	N	293	312
O35639	Exosome	GTDEK	TLINILTER	SNAQR	2		536.8222027	1071.628805	0.001763695	10	N	39	48
O35639	Exosome	TVYKK	SLGDDISSETSGDFR	KALLT	2		793.352978	1584.690356	0.000451244	11	N	138	153
O35639	Exosome	IMVSR	SEIDLLDIR	HEFKK	2		537.2960177	1072.576435	0.000451244	31	N	279	288
O35639	Exosome	EDSIK	GELSGHFEDLLLAIVHCAR	NTPAF	3	C17:+57.021	713.0338475	2136.078142	0.000451244	25	N	229	248
O35639	Exosome	EDSIK	GELSGHFEDLLLAIVHCAR	NTPAF	4	C17:+57.021	535.0273356	2136.078142	0.000451244	4	N	229	248
O35639	Exosome	KSLGD	DISSETSGDFRK	ALLTL	2		671.3182098	1340.62082	0.000823681	6	N	142	154
O35639	Exosome	TVYKK	SLGDDISSETSGDFRK	ALLTL	2		857.4004596	1712.785319	0.000451244	17	N	138	154
O35639	Exosome	AGENK	WGTDEDKFTEVLCLR	SFPQL	2	C13:+57.021	934.9462914	1867.876983	0.000451244	7	N	189	204
O35639	Exosome	AGENK	WGTDEDKFTEVLCLR	SFPQL	3	C13:+57.021	623.6334609	1867.876983	0.000451244	34	N	189	204
O35639	Exosome	RGTIK	DYPGFSPSVDAEAIRK	AIRGL	2		876.4341054	1750.852611	0.000823681	2	N	13	29
O35639	Exosome	IMVSR	SEIDLLDIRHEFK	KHYGY	4		404.4681294	1613.841318	0.000451244	2	N	279	292
O35639	Exosome	HQALK	GAGTDEFTLNR	IMVSR	2		590.7838058	1179.552012	0.000622848	1	N	263	274
O35639	Parental	WVGPR	GTIKDYPGFSPSVDAEAIR	KAIRG	2		1012.010709	2022.005817	0.000451244	17	N	9	28
O35639	Parental	RKAIR	GLGTDEKTLINILTER	SNAQR	2		886.9917875	1771.967975	0.000451244	4	N	32	48
O35639	Parental	RKAIR	GLGTDEKTLINILTER	SNAQR	3		591.6637917	1771.967975	0.000451244	9	N	32	48
O35639	Parental	KKSMK	GTGTDEDALIEILTTR	SSRQM	2		852.9366779	1703.857756	0.000451244	28	N	104	120
O35639	Parental	KKSMK	GTGTDEDALIEILTTR	SSRQM	3		568.9603853	1703.857756	0.000823681	14	N	104	120
O35639	Parental	NISQK	DIEDSIKGELSGHFEDLLLAIVHCAR	NTPAF	3	C24:+57.021	979.8310472	2936.469742	0.000451244	21	N	222	248
O35639	Parental	NISQK	DIEDSIKGELSGHFEDLLLAIVHCAR	NTPAF	4	C24:+57.021	735.1252354	2936.469742	0.000451244	43	N	222	248
O35639	Parental	HEFKK	HYGYSLYSAIQSDTSGDYR	TVLLK	2		1091.987962	2181.960324	0.000451244	16	N	293	312
O35639	Parental	HEFKK	HYGYSLYSAIQSDTSGDYR	TVLLK	3		728.3279079	2181.960324	0.001162105	1	N	293	312
O35639	Parental	GTDEK	TLINILTER	SNAQR	2		536.8222027	1071.628805	0.000451244	13	N	39	48
O35639	Parental	TVYKK	SLGDDISSETSGDFR	KALLT	2		793.352978	1584.690356	0.000451244	17	N	138	153
O35639	Parental	IMVSR	SEIDLLDIR	HEFKK	2		537.2960177	1072.576435	0.000451244	22	N	279	288
O35639	Parental	EDSIK	GELSGHFEDLLLAIVHCAR	NTPAF	3	C17:+57.021	713.0338475	2136.078142	0.000451244	27	N	229	248
O35639	Parental	EDSIK	GELSGHFEDLLLAIVHCAR	NTPAF	4	C17:+57.021	535.0273356	2136.078142	0.000451244	6	N	229	248
O35639	Parental	KSLGD	DISSETSGDFRK	ALLTL	2		671.3182098	1340.62082	0.000451244	11	N	142	154
O35639	Parental	TVYKK	SLGDDISSETSGDFRK	ALLTL	2		857.4004596	1712.785319	0.000451244	5	N	138	154
O35639	Parental	AGENK	WGTDEDKFTEVLCLR	SFPQL	2	C13:+57.021	934.9462914	1867.876983	0.000451244	15	N	189	204
O35639	Parental	AGENK	WGTDEDKFTEVLCLR	SFPQL	3	C13:+57.021	623.6334609	1867.876983	0.000451244	22	N	189	204
O35639	Parental	RGTIK	DYPGFSPSVDAEAIRK	AIRGL	2		876.4341054	1750.852611	0.000823681	5	N	13	29
O35639	Parental	FLAER	LHQALKGAGTDEFTLNR	IMVSR	2		935.9926532	1869.969706	0.000451244	5	N	257	274
O35639	Parental	FLAER	LHQALKGAGTDEFTLNR	IMVSR	3		624.3310355	1869.969706	0.000451244	5	N	257	274
O35639	Parental	IMVSR	SEIDLLDIRHEFK	KHYGY	4		404.4681294	1613.841318	0.000451244	3	N	279	292
O35639	Parental	HQALK	GAGTDEFTLNR	IMVSR	2		590.7838058	1179.552012	0.000451244	1	N	263	274
O35639	Parental	RGTIK	DYPGFSPSVDAEAIR	KAIRG	2		812.3866238	1622.757648	0.000622848	2	N	13	28
O35643	Exosome	PAPAR	LGAPISSGLSDLFDLTSGVGTLSGSYVAPK	AVWLP	3		970.5101223	2908.506967	0.000451244	5	N	687	717
O35643	Exosome	DIMIR	LASQANIAQVLAELKEYATEVDVDFVR	KAVRA	3		998.1929048	2991.555314	0.000451244	40	Y	344	371
O35643	Exosome	EYAER	IDNADELLESFLEGFHDESTQVQLQLLTAIVK	LFLKK	3		1205.952991	3614.835572	0.000451244	33	N	458	490
O35643	Exosome	EYAER	IDNADELLESFLEGFHDESTQVQLQLLTAIVK	LFLKK	4		904.716693	3614.835572	0.000451244	4	N	458	490
O35643	Exosome	IQFNR	NSFGLAPAAPLQVHVPLSPNQTVEISLPLNTVGSVLK	MEPLN	3		1270.038953	3807.093459	0.000451244	3	N	765	802
O35643	Exosome	DIMIR	LASQANIAQVLAELK	EYATE	2		784.9544767	1567.893353	0.000451244	33	Y	344	359
O35643	Exosome	DIMIR	LASQANIAQVLAELK	EYATE	3		523.6389178	1567.893353	0.000662267	6	Y	344	359
O35643	Exosome	KLFLK	KPTETQELVQQVLSLATQDSDNPDLR	DRGYI	3		975.8320356	2924.472707	0.000451244	15	N	494	520
O35643	Exosome	TLLKK	LAPPLVTLLSAEPELQYVALR	NINLI	2		1147.162458	2292.309317	0.000451244	12	N	283	304
O35643	Exosome	TLLKK	LAPPLVTLLSAEPELQYVALR	NINLI	3		765.1109056	2292.309317	0.000451244	47	N	283	304
O35643	Exosome	QSINK	LLTALNECTEWGQIFILDCLANYMPK	DDREA	3	C8:+57.021,C19:+57.021,M24:+15.995	1043.841553	3128.501259	0.000451244	7	N	206	232
O35643	Exosome	QSAER	CVSTLLDLIQTK	VNYVV	2	C1:+39.994	687.3709428	1372.726286	0.000851441	3	Y	390	402
O35643	Exosome	QSAER	CVSTLLDLIQTK	VNYVV	2	C1:+57.021	695.8844428	1389.753286	0.000451244	28	Y	390	402
O35643	Exosome	QSAER	CVSTLLDLIQTK	VNYVV	2	[0:-17.027,C1:+57.021	687.3709428	1372.726286	0.00091018	21	Y	390	402

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O35643	Exosome	LIQTK	VNYVVQEAIVVIK	DIFRK	2		737.4379311	1472.860262	0.000451244	8	N	402	415
O35643	Exosome	DIFRK	YPNKYESVIATLCENLDSLDEPEAR	AAMIW	3	C13:+57.021	976.1310509	2925.369753	0.000451244	7	N	420	445
O35643	Exosome	NTFVK	DCEDPNPLIR	ALAVR	2	C2:+57.021	614.7852599	1227.55492	0.000622848	2	Y	93	103
O35643	Exosome	KLFLK	KPTETQELVQQVLSLATQDSDNPDLRDR	GYIYW	3		1066.208054	3195.600761	0.001463592	4	N	494	522
O35643	Exosome	KLFLK	KPTETQELVQQVLSLATQDSDNPDLRDR	GYIYW	4		799.9079903	3195.600761	0.000870037	3	N	494	522
O35643	Exosome	VCVAK	LHDINAQLVEDQGFLDTLK	DLISD	2		1085.063473	2168.111345	0.000851441	2	N	147	166
O35643	Exosome	ATLLK	KLAPPLVTLLSAEPELQYVALR	NINLI	3		807.8092266	2420.40428	0.001162105	1	N	282	304
O35643	Exosome	LAELK	EYATEVDVDFVR	KAVRA	2		721.8440605	1441.672521	0.001329271	1	Y	359	371
O35643	Parental	PAPAR	LGAPISSGLSDLFDLTSGVGTLSGSYVAPK	AVWLP	2		1455.261284	2908.506967	0.000451244	25	N	687	717
O35643	Parental	PAPAR	LGAPISSGLSDLFDLTSGVGTLSGSYVAPK	AVWLP	3		970.5101223	2908.506967	0.000451244	20	N	687	717
O35643	Parental	DIMIR	LASQANIAQVLAELKEYATEVDVDFVR	KAVRA	3		998.1929048	2991.555314	0.000451244	39	Y	344	371
O35643	Parental	EYAER	IDNADELLESFLEGFHDESTQVQLQLLTAIVK	LFLKK	3		1205.952991	3614.835572	0.000451244	22	N	458	490
O35643	Parental	EYAER	IDNADELLESFLEGFHDESTQVQLQLLTAIVK	LFLKK	4		904.716693	3614.835572	0.001162105	3	N	458	490
O35643	Parental	IQFNR	NSFGLAPAAPLQVHVPLSPNQTVEISLPLNTVGSVLK	MEPLN	3		1270.038953	3807.093459	0.000451244	17	N	765	802
O35643	Parental	DIMIR	LASQANIAQVLAELK	EYATE	2		784.9544767	1567.893353	0.000451244	5	Y	344	359
O35643	Parental	KLFLK	KPTETQELVQQVLSLATQDSDNPDLR	DRGYI	3		975.8320356	2924.472707	0.000451244	9	N	494	520
O35643	Parental	TLLKK	LAPPLVTLLSAEPELQYVALR	NINLI	3		765.1109056	2292.309317	0.000451244	3	N	283	304
O35643	Parental	QSAER	CVSTLLDLIQTK	VNYVV	2	C1:+57.021	695.8844428	1389.753286	0.000451244	13	Y	390	402
O35643	Parental	QSAER	CVSTLLDLIQTK	VNYVV	2	[0:-17.027,C1:+57.021	687.3709428	1372.726286	0.000735798	12	Y	390	402
O35643	Parental	QSINK	LLTALNECTEWGQIFILDCLANYMPKDDR	EAQSI	3	C8:+57.021,C19:+57.021	1167.228219	3498.661257	0.001229886	2	N	206	235
O35704	Parental	VVNGK	ECVNFASFNFLGLLANPR	VKATA	2	C2:+57.021	1035.017582	2068.019565	0.000622848	1	N	98	116
O35704	Parental	PPSIR	VVVTVEQTEEELQR	AASTI	2		829.9339382	1657.852276	0.000622848	2	N	445	459
O35737	Exosome	DFQGR	STGEAFVQFASQEIAEK	ALKKH	2		921.4499525	1840.884305	0.000451244	34	Y	150	167
O35737	Exosome	GLPYR	ATENDIYNFFSPLNPVR	VHIEI	2		998.9923189	1995.969038	0.000451244	46	Y	299	316
O35737	Exosome	GLPYR	ATENDIYNFFSPLNPVR	VHIEI	3		666.3308126	1995.969038	0.000451244	28	Y	299	316
O35737	Exosome	EIVQF	FSGLEIVPNGITLPVDFQGR	STGEA	2		1080.078926	2158.142251	0.000451244	7	N	130	150
O35737	Exosome	FVRLR	GLPFGCSKEEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	3	C6:+57.021	1250.978551	3749.912254	0.001162105	1	N	116	150
O35737	Exosome	FGCSK	EEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	3		968.8434358	2903.506907	0.000451244	4	N	124	150
O35737	Parental	DFQGR	STGEAFVQFASQEIAEK	ALKKH	2		921.4499525	1840.884305	0.000451244	31	Y	150	167
O35737	Parental	GLPYR	ATENDIYNFFSPLNPVR	VHIEI	2		998.9923189	1995.969038	0.000451244	68	Y	299	316
O35737	Parental	GLPYR	ATENDIYNFFSPLNPVR	VHIEI	3		666.3308126	1995.969038	0.000451244	36	Y	299	316
O35737	Parental	EIVQF	FSGLEIVPNGITLPVDFQGR	STGEA	2		1080.078926	2158.142251	0.000451244	29	N	130	150
O35737	Parental	FVRLR	GLPFGCSKEEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	3	C6:+57.021	1250.978551	3749.912254	0.000451244	20	N	116	150
O35737	Parental	FVRLR	GLPFGCSKEEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	4	C6:+57.021	938.4858636	3749.912254	0.002374549	3	N	116	150
O35737	Parental	FGCSK	EEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	2		1452.761254	2903.506907	0.000451244	12	N	124	150
O35737	Parental	FGCSK	EEIVQFFSGLEIVPNGITLPVDFQGR	STGEA	3		968.8434358	2903.506907	0.000451244	25	N	124	150
O35737	Parental	VVKVR	GLPWSCSADEVQR	FFSDC	2	C6:+57.021	752.8463802	1503.67716	0.000451244	21	N	16	29
O35737	Parental	FIYTR	EGRPSGEAFVELESEDEVK	LALKK	2		1053.995453	2105.975305	0.000451244	24	Y	49	68
O35737	Parental	FIYTR	EGRPSGEAFVELESEDEVK	LALKK	3		702.9995684	2105.975305	0.000451244	14	Y	49	68
O35737	Parental	NMQHR	YVELFLNSTAGASGGAYEHR	YVELF	2		1071.516689	2141.017779	0.000622848	2	N	355	375
O35737	Parental	ERMRR	GAYGGGYGGYDDYNGYNDGYGFGSDRFGR	DLNYC	3		1026.417285	3076.228454	0.000451244	2	N	233	262
O35737	Parental	LNPVR	VHIEIGPDGR	VTGEA	2		546.7939765	1091.572353	0.001763695	4	Y	316	326
O35737	Parental	ERMRR	GAYGGGYGGYDDYNGYNDGYGFGSDR	FGRDL	2		1359.026532	2716.037465	0.000662267	1	N	233	259
O35737	Parental	GLPYR	ATENDIYNFFSPLNPVRV	HIEIG	2		1048.526526	2095.037452	0.000451244	5	Y	299	317
O35737	Parental	IVQFF	SGLEIVPNGITLPVDFQGR	STGEA	2		1006.544719	2011.073837	0.000451244	2	N	131	150
O35744	Exosome	KEMRK	AFEEESVEKDIPR	LLLTS	2		774.8811743	1547.746749	0.000451244	16	N	164	177
O35744	Exosome	KEMRK	AFEEESVEKDIPR	LLLTS	3		516.9233829	1547.746749	0.000451244	5	N	164	177
O35744	Exosome	QEVPY	AYQGNEWVGYDNVR	SFKLK	2		835.88204	1669.74848	0.000451244	13	N	326	340
O35744	Exosome	AASEK	LIVGFPAYGHTFILSDPSK	TGIGA	2		1031.554555	2061.09351	0.000451244	43	N	259	278
O35744	Exosome	AASEK	LIVGFPAYGHTFILSDPSK	TGIGA	3		688.03897	2061.09351	0.000451244	30	N	259	278
O35744	Exosome	YDIGK	SADLNVDSIISYWKDHGAASEK	LIVGF	3		802.7244385	2405.149916	0.000698008	1	N	237	259
O35744	Exosome	YDIGK	SADLNVDSIISYWKDHGAASEK	LIVGF	4		602.2952789	2405.149916	0.000662267	9	N	237	259
O35744	Exosome	KDIPR	LLLTSTGAGIIDVIK	SGYKI	2		757.4641459	1512.912692	0.000451244	50	N	177	192
O35744	Exosome	KDIPR	LLLTSTGAGIIDVIK	SGYKI	3		505.3120306	1512.912692	0.000451244	23	N	177	192
O35744	Exosome	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2		1036.9772	2071.9388	0.000451244	48	N	128	145
O35744	Exosome	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	3		691.6540667	2071.9388	0.000451244	24	N	128	145
O35744	Exosome	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2	Q1:-17.027	1028.4637	2054.9118	0.001162105	2	N	128	145
O35744	Exosome	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2	[0:-17.027	1028.4637	2054.9118	0.000451244	13	N	128	145
O35744	Exosome	EVCTF	LNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1190.546847	3568.61714	0.000451244	11	N	309	340
O35744	Exosome	YDIGK	SADLNVDSIISYWK	DHGAA	2		805.9071921	1609.798784	0.000451244	60	N	237	251
O35744	Exosome	NTELK	TLLAIGGWK	FGPAP	2		479.7901742	957.5647484	0.000451244	34	N	91	100
O35744	Exosome	GLLAY	YEVCTFLNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3	C4:+57.021	1456.987051	4367.937754	0.000622848	2	N	303	340
O35744	Exosome	TSTLK	GDLNIHSASCKGPY	-	2	C10:+57.021	759.8542053	1517.692811	0.001162105	2	N	384	398
O35744	Exosome	EQDLR	DYEALNGLKDK	NTELK	2		633.3227639	1264.629928	0.000451244	10	N	75	86
O35744	Exosome	LHDPK	DGYTGENSPLYK	SPYDI	2		672.3098535	1342.604107	0.000451244	11	N	218	230

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O35744	Exosome	KSGYK	IPELSQSLDYIQVMTYDLHDPK	DGYTG	3		869.100518	2604.278154	0.002453667	1	N	196	218
O35744	Exosome	KSGYK	IPELSQSLDYIQVMTYDLHDPK	DGYTG	3	M14:+15.995	874.4321846	2620.273154	0.000451244	8	N	196	218
O35744	Exosome	SDPSK	TGIGAPTISTGPPGK	YTDES	2		677.3727881	1352.729976	0.000451244	13	N	278	293
O35744	Exosome	IDVIK	SGYKIPELSQSLDYIQVMTYDLHDPK	DGYTG	4	M18:+15.995	764.8790345	3055.484938	0.000451244	4	N	192	218
O35744	Exosome	KSGYK	IPELSQSLDYIQVMTYDLHDPKDGYTGENSPLYK	SPYDI	4		983.2257252	3928.871701	0.001162105	1	N	196	230
O35744	Exosome	KSGYK	IPELSQSLDYIQVMTYDLHDPKDGYTGENSPLYK	SPYDI	4	M14:+15.995	987.2244752	3944.866701	0.002374549	1	N	196	230
O35744	Exosome	IGGWK	FGPAPFSAMVSTPQNR	QIFIQ	2		853.9201115	1705.824623	0.000662267	1	N	100	116
O35744	Exosome	AQWLK	DNNLGGAVVWPLDMDDFSGSFCHQR	HFPLT	3	C22:+57.021	946.418761	2836.232883	0.000451244	9	N	350	375
O35744	Exosome	AQWLK	DNNLGGAVVWPLDMDDFSGSFCHQR	HFPLT	3	M14:+15.995,C22:+57.021	951.7504277	2852.227883	0.000451244	9	N	350	375
O35744	Exosome	YYEVC	TFLNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1273.252211	3816.733232	0.000451244	3	N	307	340
O35744	Exosome	FCHQR	HFPLTSTLKGDLNIHSASCK	GPY-	4	C19:+57.021	557.2892552	2225.125821	0.001162105	3	N	375	395
O35744	Exosome	SEKLI	VGFPAYGHTFILSDPSK	TGIGA	2		918.4704909	1834.925382	0.000870037	2	N	261	278
O35744	Exosome	IDVIK	SGYKIPELSQSLDYIQVMTY	DLHDP	2	M18:+15.995	1176.077974	2350.140349	0.000451244	1	N	192	212
O35744	Parental	KEMRK	AFEEESVEKDIPR	LLLTS	2		774.8811743	1547.746749	0.000451244	39	N	164	177
O35744	Parental	KEMRK	AFEEESVEKDIPR	LLLTS	3		516.9233829	1547.746749	0.000662267	1	N	164	177
O35744	Parental	QEVPY	AYQGNEWVGYDNVR	SFKLK	2		835.88204	1669.74848	0.000451244	48	N	326	340
O35744	Parental	AASEK	LIVGFPAYGHTFILSDPSK	TGIGA	2		1031.554555	2061.09351	0.000451244	45	N	259	278
O35744	Parental	AASEK	LIVGFPAYGHTFILSDPSK	TGIGA	3		688.03897	2061.09351	0.000451244	38	N	259	278
O35744	Parental	YDIGK	SADLNVDSIISYWKDHGAASEK	LIVGF	2		1203.582758	2405.149916	0.000451244	10	N	237	259
O35744	Parental	YDIGK	SADLNVDSIISYWKDHGAASEK	LIVGF	3		802.7244385	2405.149916	0.000662267	9	N	237	259
O35744	Parental	YDIGK	SADLNVDSIISYWKDHGAASEK	LIVGF	4		602.2952789	2405.149916	0.000662267	10	N	237	259
O35744	Parental	KDIPR	LLLTSTGAGIIDVIK	SGYKI	2		757.4641459	1512.912692	0.000451244	101	N	177	192
O35744	Parental	KDIPR	LLLTSTGAGIIDVIK	SGYKI	3		505.3120306	1512.912692	0.000451244	15	N	177	192
O35744	Parental	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2		1036.9772	2071.9388	0.000451244	83	N	128	145
O35744	Parental	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	3		691.6540667	2071.9388	0.000451244	22	N	128	145
O35744	Parental	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2	Q1:-17.027	1028.4637	2054.9118	0.000451244	8	N	128	145
O35744	Parental	IRFLR	QYNFDGLNLDWQYPGSR	GSPPK	2	[0:-17.027	1028.4637	2054.9118	0.000451244	17	N	128	145
O35744	Parental	EVCTF	LNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1190.546847	3568.61714	0.000451244	28	N	309	340
O35744	Parental	YDIGK	SADLNVDSIISYWK	DHGAA	2		805.9071921	1609.798784	0.000451244	116	N	237	251
O35744	Parental	YDIGK	SADLNVDSIISYWK	DHGAA	3		537.6073947	1609.798784	0.002145581	1	N	237	251
O35744	Parental	NTELK	TLLAIGGWK	FGPAP	2		479.7901742	957.5647484	0.000451244	49	N	91	100
O35744	Parental	GLLAY	YEVCTFLNEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3	C4:+57.021	1456.987051	4367.937754	0.000451244	21	N	303	340
O35744	Parental	TSTLK	GDLNIHSASCKGPY	-	2	C10:+57.021	759.8542053	1517.692811	0.000451244	3	N	384	398
O35744	Parental	LHDPK	DGYTGENSPLYKSPYDIGK	SADLN	2		1052.497631	2102.979662	0.000870037	1	N	218	237
O35744	Parental	QSVIR	FLRQYNFDGLNLDWQYPGSR	GSPPK	3		830.4052631	2488.192389	0.000823681	2	N	125	145
O35744	Parental	EQDLR	DYEALNGLKDK	NTELK	2		633.3227639	1264.629928	0.000451244	13	N	75	86
O35744	Parental	LHDPK	DGYTGENSPLYK	SPYDI	2		672.3098535	1342.604107	0.000451244	50	N	218	230
O35744	Parental	KSGYK	IPELSQSLDYIQVMTYDLHDPK	DGYTG	3		869.100518	2604.278154	0.002080925	2	N	196	218
O35744	Parental	KSGYK	IPELSQSLDYIQVMTYDLHDPK	DGYTG	3	M14:+15.995	874.4321846	2620.273154	0.000637154	1	N	196	218
O35744	Parental	SDPSK	TGIGAPTISTGPPGK	YTDES	2		677.3727881	1352.729976	0.000451244	29	N	278	293
O35744	Parental	SDPSK	TGIGAPTISTGPPGKYTDESGLLAYYEVCTF	LNEGA	3	C29:+57.021	1089.192199	3264.553197	0.000451244	1	N	278	309
O35744	Parental	SDPSK	TGIGAPTISTGPPGKYTDESGLLAY	YEVCT	2		1233.624091	2465.232583	0.001943752	1	N	278	303
O35744	Parental	SFKLK	AQWLKDNNLGGAVVWPLDMDDFSGSFCHQR	HFPLT	3	C27:+57.021	1155.203438	3462.586915	0.001591523	1	N	345	375
O35744	Parental	IDVIK	SGYKIPELSQSLDYIQVMTYDLHDPK	DGYTG	4		760.8802845	3039.489938	0.001654178	3	N	192	218
O35744	Parental	QVMTY	DLHDPKDGYTGENSPLYK	SPYDI	2		1024.982148	2047.948696	0.000451244	11	N	212	230
O35744	Parental	QVMTY	DLHDPKDGYTGENSPLYK	SPYDI	3		683.6573654	2047.948696	0.000451244	4	N	212	230
O35744	Parental	KSGYK	IPELSQSLDYIQVMTYDLHDPKDGYTGENSPLYK	SPYDI	4		983.2257252	3928.871701	0.000870037	2	N	196	230
O35744	Parental	EQDLR	DYEALNGLK	DKNTE	2		511.7618107	1021.508021	0.002019181	1	N	75	84
O35744	Parental	AQWLK	DNNLGGAVVWPLDMDDFSGSFCHQR	HFPLT	3	C22:+57.021	946.418761	2836.232883	0.002981883	1	N	350	375
O35744	Parental	FLRQY	NFDGLNLDWQYPGSR	GSPPK	2		891.416247	1780.816894	0.000870037	3	N	130	145
O35744	Parental	VCTFL	NEGATEVWDAPQEVPYAYQGNEWVGYDNVR	SFKLK	3		1152.852158	3455.533075	0.000451244	2	N	310	340
O35744	Parental	APQEV	PYAYQGNEWVGYDNVR	SFKLK	2		965.9400863	1929.864573	0.000622848	3	N	324	340
O35744	Parental	GPPGK	YTDESGLLAYYEVCTF	LNEGA	2	C14:+57.021	965.9246903	1929.833781	0.000698008	1	N	293	309
O35744	Parental	GPPGK	YTDESGLLAYYEVCTFLNEGATEVWDAPQEVPY	AYQGN	3	C14:+57.021	1277.241947	3828.70244	0.001463592	1	N	293	326
O35841	Exosome	EELYR	NYGILADATEQVGQHKDAYQVILDGVK	GGTKE	3		982.5054828	2944.493048	0.000451244	3	N	9	36
O35841	Exosome	TVSGR	QQLVELVAEQADLEQAFSPSDPDCVDR	LLQCT	3	C24:+57.021	1020.480631	3058.418494	0.000451244	18	N	210	237
O35841	Exosome	KMDAK	GTLGGLFSQILQGEDIVR	ERAIK	2		952.0183367	1902.021073	0.000451244	19	N	130	148
O35841	Exosome	ENLPR	VADILTQLLQTDDSAEFNLVNNALLSIFK	MDAKG	3		1069.238403	3204.691808	0.000451244	27	N	97	126
O35841	Exosome	STKLK	TLPDEVLTKEVEELILTESK	KVLED	3		762.7495907	2285.225372	0.000451244	1	N	160	180
O35841	Exosome	RQAIK	ELPQFATGENLPR	VADIL	2		736.3811445	1470.746689	0.000823681	2	N	84	97
O35841	Exosome	VGQHK	DAYQVILDGVK	GGTKE	2		610.8302247	1219.644849	0.000451244	2	N	25	36
O35841	Parental	EELYR	NYGILADATEQVGQHKDAYQVILDGVK	GGTKE	3		982.5054828	2944.493048	0.000451244	9	N	9	36
O35841	Parental	KMDAK	GTLGGLFSQILQGEDIVRER	AIKFL	3		730.0627259	2187.164778	0.000451244	3	N	130	150
O35841	Parental	TVSGR	QQLVELVAEQADLEQAFSPSDPDCVDR	LLQCT	3	C24:+57.021	1020.480631	3058.418494	0.000451244	25	N	210	237
O35841	Parental	TVSGR	QQLVELVAEQADLEQAFSPSDPDCVDRLLQCTR	QAVPL	3	C24:+57.021,C31:+57.021	1277.615858	3829.824175	0.000451244	3	N	210	243

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O35841	Parental	KMDAK	GTLGGLFSQILQGEDIVR	ERAIK	2		952.0183367	1902.021073	0.000451244	21	N	130	148
O35841	Parental	KMDAK	GTLGGLFSQILQGEDIVR	ERAIK	3		635.0148244	1902.021073	0.000662267	3	N	130	148
O35841	Parental	ENLPR	VADILTQLLQTDDSAEFNLVNNALLSIFK	MDAKG	3		1069.238403	3204.691808	0.000451244	27	N	97	126
O35841	Parental	STKLK	TLPDEVLTKEVEELILTESK	KVLED	3		762.7495907	2285.225372	0.000451244	8	N	160	180
O35841	Parental	RQAIK	ELPQFATGENLPR	VADIL	2		736.3811445	1470.746689	0.001699387	4	N	84	97
O35855	Exosome	RSARR	LCLPDFDKQELLECIR	QLIEV	3	C2:+57.021,C14:+57.021	683.6765181	2048.006154	0.000622848	11	N	134	150
O35855	Exosome	EGRVR	EVFGSGTACQVCPVHQILYEGK	QLHIP	3	C9:+57.021,C12:+57.021	827.0632123	2478.166237	0.000451244	10	N	334	356
O35855	Exosome	EGRVR	EVFGSGTACQVCPVHQILYEGK	QLHIP	2	[0:-	1231.085419	2460.155237	0.001329271	1	N	334	356
O35855	Exosome	VGDCK	LGGNYGPTVAVQR	EAQKR	2		666.3574724	1330.699345	0.001162105	2	N	230	243
O35855	Exosome	LECIR	QLIEVDKDWVPDGNGTSLY	VRPVL	2		1075.026556	2148.037511	0.002663018	1	N	150	169
O35855	Parental	EGRVR	EVFGSGTACQVCPVHQILYEGK	QLHIP	2	C9:+57.021,C12:+57.021	1240.090919	2478.166237	0.000622848	1	N	334	356
O35855	Parental	EGRVR	EVFGSGTACQVCPVHQILYEGK	QLHIP	3	C9:+57.021,C12:+57.021	827.0632123	2478.166237	0.000451244	1	N	334	356
O35887	Parental	KIVSK	IDDDKDGFVTVDELK	GWIKF	3		570.2812359	1707.820308	0.000451244	4	N	79	94
O35887	Parental	GKLTK	EEIVDKYDLFVGSQATDFGEALVR	HDEF-	3		901.1172247	2700.328274	0.000451244	6	N	287	311
O35892	Parental	QLNNR	DATPESCSLLPQNEER	AVQLN	2	C7:+57.021	923.4180951	1844.82059	0.000451244	11	N	206	222
O35892	Parental	KRGPR	IPREENADFGGAELPVVCGNAQGF	LDKEK	2	C18:+57.021	1274.10056	2546.185521	0.000851441	3	N	374	398
O35900	Exosome	GSVVR	YVQLPADEVDTQLLQDAAR	KEALQ	2		1073.04528	2144.07496	0.000451244	32	N	68	87
O35900	Exosome	VVELK	NDLSICGTLHSVDQYLNIK	LTDIS	3	C6:+57.021	730.700534	2189.078202	0.000451244	9	N	20	39
O35900	Parental	GSVVR	YVQLPADEVDTQLLQDAAR	KEALQ	2		1073.04528	2144.07496	0.000451244	26	N	68	87
O35900	Parental	VVELK	NDLSICGTLHSVDQYLNIK	LTDIS	3	C6:+57.021	730.700534	2189.078202	0.000451244	13	N	20	39
O35904	Exosome	AGTVR	GNPNTESAAALVIYLPEVAPHPVYFPALEK	ILELG	3		1069.8962	3206.665199	0.000451244	1	N	460	490
O35904	Exosome	EMLCK	TVSSSEVNVCSEPVWK	QRLEF	2	C10:+57.021	904.4304741	1806.845348	0.000851441	1	N	356	372
O35904	Exosome	DEQRR	LCDIQPFLPVLR	LVARE	2	C2:+57.021	735.9107949	1469.80599	0.001395409	1	N	88	100
O35930	Exosome	NNKLR	ELPSGLLDGLEDLDTLYLQR	NWLRT	2		1130.58952	2259.16344	0.000451244	48	N	177	197
O35930	Exosome	NNKLR	ELPSGLLDGLEDLDTLYLQR	NWLRT	3		754.0622801	2259.16344	0.000451244	35	N	177	197
O35930	Exosome	HNNLK	SLPSLGWALPALTTLDVSFNK	LGSLS	2		1115.610059	2229.204517	0.000451244	37	N	106	127
O35930	Exosome	HNNLK	SLPSLGWALPALTTLDVSFNK	LGSLS	3		744.0759724	2229.204517	0.000451244	11	N	106	127
O35930	Exosome	GKLIK	LENLDLSHNNLK	SLPSL	2		705.3733194	1408.731039	0.001463592	2	N	94	106
O35930	Exosome	GKLIK	LENLDLSHNNLK	SLPSL	3		470.584813	1408.731039	0.000698008	10	N	94	106
O35930	Exosome	VSFNK	LGSLSPGVLDGLSQLQELYLQNNDLK	SLPPG	2		1407.748343	2813.481087	0.000451244	31	N	127	153
O35930	Exosome	VSFNK	LGSLSPGVLDGLSQLQELYLQNNDLK	SLPPG	3		938.8348289	2813.481087	0.000451244	28	N	127	153
O35930	Exosome	VASVR	CANLDNAPVYSYPGK	GCPTS	2	C1:+57.021	834.8882451	1667.76089	0.000451244	17	N	263	278
O35930	Exosome	VYLWK	QGVDVKDTTPNVASVR	CANLD	3		562.632603	1684.874409	0.000451244	7	N	247	263
O35930	Exosome	LANNK	LRELPSGLLDGLEDLDTLYLQR	NWLRT	3		843.7906719	2528.348616	0.000451244	8	N	175	197
O35930	Exosome	VTMPR	AWLLFLQGSLPTFR	SSLFL	2		824.9646474	1647.913695	0.000451244	5	N	674	688
O35930	Exosome	QTNGK	LIKLENLDLSHNNLK	SLPSL	4		441.7563325	1762.99413	0.000698008	1	N	91	106
O35930	Parental	NNKLR	ELPSGLLDGLEDLDTLYLQR	NWLRT	2		1130.58952	2259.16344	0.000451244	11	N	177	197
O35930	Parental	NNKLR	ELPSGLLDGLEDLDTLYLQR	NWLRT	3		754.0622801	2259.16344	0.000451244	4	N	177	197
O35930	Parental	HNNLK	SLPSLGWALPALTTLDVSFNK	LGSLS	2		1115.610059	2229.204517	0.000451244	7	N	106	127
O35930	Parental	VSFNK	LGSLSPGVLDGLSQLQELYLQNNDLK	SLPPG	2		1407.748343	2813.481087	0.000451244	6	N	127	153
O35930	Parental	VSFNK	LGSLSPGVLDGLSQLQELYLQNNDLK	SLPPG	3		938.8348289	2813.481087	0.000451244	1	N	127	153
O35930	Parental	VASVR	CANLDNAPVYSYPGK	GCPTS	2	C1:+57.021	834.8882451	1667.76089	0.000451244	8	N	263	278
O35930	Parental	VYLWK	QGVDVKDTTPNVASVR	CANLD	3		562.632603	1684.874409	0.002212458	1	N	247	263
O35955	Exosome	GSYSR	LPFTALGSGQGAAVALLEDR	FQPNM	2		993.5368936	1985.058187	0.000451244	32	N	160	180
O35955	Exosome	GSYSR	LPFTALGSGQGAAVALLEDR	FQPNM	3		662.6938624	1985.058187	0.000451244	9	N	160	180
O35955	Exosome	PVLTR	EVRPLTLELLEETVQAMEVE	-	2	M17:+15.995	1172.601814	2343.188027	0.000451244	7	N	253	273
O35955	Exosome	ARKTG	TTIAGLVFR	DGVIL	2		489.293081	976.5705621	0.002813207	1	N	39	48
O35955	Parental	GSYSR	LPFTALGSGQGAAVALLEDR	FQPNM	3		662.6938624	1985.058187	0.000451244	1	N	160	180
O54734	Parental	RNNAR	VIFSGSLDFFSDAFFNSAVQK	ATPGA	2		1163.573673	2325.131746	0.000622848	3	N	239	260
O54734	Parental	RNNAR	VIFSGSLDFFSDAFFNSAVQK	ATPGA	3		776.0517154	2325.131746	0.001162105	2	N	239	260
O54734	Parental	HAVGR	NTLLIAGLQAR	NNARV	2		585.3542013	1168.692803	0.002519933	2	N	224	235
O54734	Parental	FDEEK	TAVIDHHNYDVSDLGQHTLIVADTENLLK	APTIV	3		1077.881389	3230.620768	0.000662267	3	N	138	167
O54734	Parental	FDEEK	TAVIDHHNYDVSDLGQHTLIVADTENLLK	APTIV	4		808.6629921	3230.620768	0.000451244	6	N	138	167
O54774	Exosome	KLQAK	GVPVAEEVSALFAGELNPVAPK	AQKKV	2		1097.591866	2193.168132	0.000451244	6	N	588	610
O54774	Exosome	ILQQK	EQAADTEAAQEVTQLLVER	LPQFV	2		1051.024544	2100.033489	0.001162105	1	N	537	556
O54774	Exosome	RLKEK	LEDPDPGVQSAAVNVICELAR	RNPKN	2	C17:+57.021	1127.062915	2252.110231	0.000823681	4	N	191	212
O54774	Parental	KLQAK	GVPVAEEVSALFAGELNPVAPK	AQKKV	2		1097.591866	2193.168132	0.000622848	7	N	588	610
O54774	Parental	ILQQK	EQAADTEAAQEVTQLLVER	LPQFV	2		1051.024544	2100.033489	0.000451244	6	N	537	556
O54774	Parental	QMLGY	DISWAAFNIIEVMSASKFTFK	RVGYL	3		802.4123676	2404.213703	0.001264573	1	N	70	91
O54824	Exosome	SAVMK	SLLCLPSSVSCGQITCIPK	ERVSP	2	C4:+57.021,C11:+57.021,C16:+57.021	1060.530888	2119.046176	0.000451244	1	N	993	1012
O54824	Exosome	AADGR	LQEGDEILELNGESMAGLTHQDALQKF	KQAKK	4		747.3675412	2985.438965	0.002296037	1	N	257	284
O54824	Parental	APDPR	RPPEVASAIQPTPVSRDPPGPQPQASSSIR	QRISS	3		1041.550086	3121.626857	0.000451244	4	N	804	834
O54824	Parental	APDPR	RPPEVASAIQPTPVSRDPPGPQPQASSSIR	QRISS	4		781.4145141	3121.626857	0.000451244	17	N	804	834
O54824	Parental	DPLLR	LLTTQSEDTQGPGLK	MPSQR	2		794.4153813	1586.815163	0.000451244	23	N	936	951

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O54824	Parental	LSELR	EYSEGLTEPGETEDRNHCSSQAGQSVISLLSAEELEK	LIEEV	3	C18:+57.021	1360.625959	4078.854478	0.000451244	4	N	1048	1085
O54879	Exosome	PNAPK	RPPSGFFLFCSEFRPK	IKSTN	3	C10:+57.021	658.001819	1970.982057	0.000622848	3	N	94	110
O54879	Exosome	KPKGK	MSAYAFFVQTCR	EEHKK	2	M1:+15.995,C11:+57.021	748.8370128	1495.658426	0.000451244	7	N	12	24
O54890	Exosome	KITGK	YCECDDFSCVR	YKGEM	2	C2:+57.021,C4:+57.021,C9:+57.02	755.7732464	1509.530893	0.000451244	17	N	544	555
O54890	Exosome	ENLLK	DNCAPESIEFPVSEAQILEAR	PLSSK	2	C3:+57.021	1188.063112	2374.110625	0.000451244	23	N	71	92
O54890	Exosome	LCSGR	GNCECGSCVCVQPGSYGDTCEK	CPTCP	2	C3:+57.021,C5:+57.021,C8:+57.021,C10:+57.021,C20:+57.021	1262.468099	2522.920597	0.000451244	13	N	603	625
O54890	Exosome	LCSGR	GNCECGSCVCVQPGSYGDTCEK	CPTCP	3	C3:+57.021,C5:+57.021,C8:+57.021,C10:+57.021,C20:+57.021	841.9813324	2522.920597	0.000823681	1	N	603	625
O54890	Exosome	ICSQR	GECLCGQCVCHSSDFGK	ITGKY	2	C3:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	1000.889116	1999.762632	0.000451244	4	N	523	540
O54890	Exosome	ENLLK	DNCAPESIEFPVSEAQILEARPLSSK	GSGSS	3	C3:+57.021	963.1432909	2886.406473	0.0007646	11	N	71	97
O54890	Exosome	ICTTR	GVNSCQQCLAVSPVCAWCSDETLSQGSPR	CNLKE	3	C5:+57.021,C8:+57.021,C15:+57.021,C18:+57.021	1085.142399	3252.403798	0.000451244	6	N	33	62
O54890	Exosome	CGVCR	CDQGWLGSMCECSEEDYRPSQQEECSPK	EGQPI	3	C1:+57.021,M9:+15.995,C10:+57.021,C12:+57.021,C25:+57.021	1156.777374	3467.308723	0.000451244	29	N	486	514
O54890	Exosome	RCNLK	ENLLKDNCAPESIEFPVSEAQILEARPLSSK	GSGSS	4	C8:+57.021	871.9465712	3483.755085	0.000979378	4	N	66	97
O54890	Parental	KITGK	YCECDDFSCVR	YKGEM	2	C2:+57.021,C4:+57.021,C9:+57.02	755.7732464	1509.530893	0.001162105	4	N	544	555
O54890	Parental	ENLLK	DNCAPESIEFPVSEAQILEAR	PLSSK	2	C3:+57.021	1188.063112	2374.110625	0.000451244	1	N	71	92
O54890	Parental	LCSGR	GNCECGSCVCVQPGSYGDTCEK	CPTCP	2	C3:+57.021,C5:+57.021,C8:+57.021,C10:+57.021,C20:+57.021	1262.468099	2522.920597	0.000823681	2	N	603	625
O54890	Parental	ICTTR	GVNSCQQCLAVSPVCAWCSDETLSQGSPR	CNLKE	3	C5:+57.021,C8:+57.021,C15:+57.021,C18:+57.021	1085.142399	3252.403798	0.000451244	4	N	33	62
O54941	Exosome	QRNHR	LISEILSESVVPDVR	SVVTT	2		828.4648742	1654.914148	0.001162105	2	N	201	216
O54941	Parental	VDMEK	IAAEIAQAEEQAR	KRQEE	2		700.3629517	1398.710303	0.000662267	7	N	284	297
O54941	Parental	QRNHR	LISEILSESVVPDVR	SVVTT	2		828.4648742	1654.914148	0.000451244	4	N	201	216
O54950	Exosome	HDVVK	GIVSLSDILQALVLTGGEK	KP-	2		957.0518452	1912.08809	0.002813207	1	N	309	328
O54950	Exosome	HDVVK	GIVSLSDILQALVLTGGEK	KP-	3		638.3704968	1912.08809	0.000451244	4	N	309	328
O54950	Parental	HDVVK	GIVSLSDILQALVLTGGEK	KP-	2		957.0518452	1912.08809	0.000451244	6	N	309	328
O54950	Parental	HDVVK	GIVSLSDILQALVLTGGEK	KP-	3		638.3704968	1912.08809	0.000451244	7	N	309	328
O54950	Parental	IETWR	EVYLQDSFKPLVCISPNASLFDAVSSLIR	NKIHR	3	C13:+57.021	1090.235962	3267.684486	0.000622848	1	N	117	146
O54988	Exosome	EHVKR	DLNPEEFWEIIGELGDGAFGK	VYKAQ	2		1168.55822	2335.10084	0.000622848	2	N	26	47
O54988	Parental	EHVKR	DLNPEEFWEIIGELGDGAFGK	VYKAQ	2		1168.55822	2335.10084	0.000451244	26	N	26	47
O54988	Parental	AELSK	AAQSGEGDEALAPTQTLAEKPTEGPEAGGAEEEPPGGER	VEDKQ	3		1278.591509	3832.751127	0.000451244	3	N	562	601
O54988	Parental	GAEAR	ALGSEGEAAATEVDLER	KENAQ	2		859.4161096	1716.816619	0.000451244	11	N	662	679
O54988	Parental	PGGER	VEDKQPEQQPAVCEAEGQLTSTSETTR	ATLEQ	3	C13:+57.021	1006.803774	3017.387922	0.000823681	2	N	601	628
O54988	Parental	KKRPK	LENLPDTQDQQTVDVNSVSEENENNR	VTLET	3		996.454064	2986.338792	0.001463592	1	N	427	453
O54990	Exosome	NTKNK	AFSDLDGIGSVLGGR	IKDQL	2		732.3786018	1462.741604	0.000823681	2	N	226	241
O54990	Exosome	LSSVR	NSIENSLSSSDCTSDPASK	ICDSI	2	C12:+57.021	999.9317636	1997.847927	0.001162105	1	N	296	315
O55029	Exosome	KVNQK	AAESLADPTEYENLFPGLK	EAFVV	2		1033.010374	2064.005149	0.000451244	8	N	783	802
O55029	Exosome	LLGVR	SVNGLAFYDWENTELIR	RIEIQ	2		1013.997601	2025.979602	0.000451244	7	N	442	459
O55029	Exosome	YLSEK	VLAAQETHEGVTEDGIEDAFEVLGEIQEIVK	TGLWV	3		1123.563503	3367.667109	0.000451244	5	N	494	525
O55029	Exosome	VASLR	GSNNVALGYDEGSIIVK	LGREE	2		868.4472128	1734.878826	0.000451244	13	N	281	298
O55029	Exosome	DYQNK	TCVQTLEGHAQNVSCASFHPELPIIITGSEDGTVR	IWHSS	3	C2:+57.021,C15:+57.021	1275.284332	3822.829595	0.000451244	2	N	219	254
O55029	Exosome	DYQNK	TCVQTLEGHAQNVSCASFHPELPIIITGSEDGTVR	IWHSS	4	C2:+57.021,C15:+57.021	956.7151987	3822.829595	0.002519933	2	N	219	254
O55029	Parental	KVNQK	AAESLADPTEYENLFPGLK	EAFVV	2		1033.010374	2064.005149	0.000451244	20	N	783	802
O55029	Parental	KVNQK	AAESLADPTEYENLFPGLKEAFVVEEWVK	ETHAD	3		1094.547125	3280.617974	0.000451244	10	N	783	812
O55029	Parental	LLGVR	SVNGLAFYDWENTELIR	RIEIQ	2		1013.997601	2025.979602	0.000451244	29	N	442	459
O55029	Parental	YLSEK	VLAAQETHEGVTEDGIEDAFEVLGEIQEIVK	TGLWV	3		1123.563503	3367.667109	0.000451244	24	N	494	525
O55029	Parental	VASLR	GSNNVALGYDEGSIIVK	LGREE	2		868.4472128	1734.878826	0.000451244	17	N	281	298
O55029	Parental	DYQNK	TCVQTLEGHAQNVSCASFHPELPIIITGSEDGTVR	IWHSS	3	C2:+57.021,C15:+57.021	1275.284332	3822.829595	0.000451244	1	N	219	254
O55029	Parental	DYQNK	TCVQTLEGHAQNVSCASFHPELPIIITGSEDGTVR	IWHSS	4	C2:+57.021,C15:+57.021	956.7151987	3822.829595	0.000451244	8	N	219	254
O55029	Parental	FKEKK	SFKPDFGAESIYGGFLLGVR	SVNGL	2		1080.560369	2159.105137	0.000823681	1	N	422	442
O55029	Parental	FKEKK	SFKPDFGAESIYGGFLLGVR	SVNGL	3		720.7095125	2159.105137	0.001329271	2	N	422	442
O55029	Parental	LGELK	IAYQLAVEAESEQK	WKQLA	2		789.9046494	1577.793699	0.000823681	2	N	655	669
O55029	Parental	DRTIK	VWQLGSSSPNFTLEGHEK	GVNCI	3		672.6660838	2014.974851	0.000451244	3	N	168	186
O55029	Parental	EGHEK	GVNCIDYYSGGDKPYLISGADDR	LVKIW	2	C4:+57.021	1268.076751	2534.137902	0.000622848	4	N	186	209
O55029	Parental	FLQGK	LDACLELLIR	TGRLP	2	C4:+57.021	608.3422137	1214.668827	0.002374549	2	N	737	747
O55029	Parental	ALRNK	SFGSAQEFAWAHDSSEYAIR	ESNSI	3		753.6754191	2258.002857	0.001463592	1	N	386	406
O55098	Exosome	EHVRR	DLDPNDVWEIVGELGDGAFGK	VYKAK	2		1123.534745	2245.05389	0.000451244	9	N	28	49
O55098	Parental	EHVRR	DLDPNDVWEIVGELGDGAFGK	VYKAK	2		1123.534745	2245.05389	0.000451244	28	N	28	49
O55098	Parental	EHVRR	DLDPNDVWEIVGELGDGAFGK	VYKAK	3		749.3590966	2245.05389	0.000451244	6	N	28	49
O55098	Parental	VIETK	SEEELEDYIVEIEILATCDHPYIVK	LLGAY	3	C18:+57.021	1003.154974	3006.441521	0.000451244	7	N	70	95
O55106	Exosome	ETQQR	VLTLESNVDSTSSSSCQINR	VISHP	2	C16:+57.021	1099.023987	2196.032374	0.000451244	15	N	649	669
O55106	Exosome	GTDGR	IQSWSTTNPNVDPYDAYDPSVLR	GPLLG	2		1319.625154	2637.234708	0.000451244	21	N	539	562

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O55106	Exosome	AGGAK	GLGPLAEAAAAGDGAAAAGAAR	AQYSL	2		904.9666354	1807.917671	0.001329271	2	N	22	44
O55106	Exosome	APAKK	STSLDVEPIYTFR	AHKGP	2		764.3886352	1526.76167	0.000451244	9	N	500	513
O55106	Exosome	FDGIR	ALAFHPIEPVLITASEDHTLK	MWNLQ	3		768.08676	2301.23688	0.000998612	1	N	467	488
O55106	Exosome	FDGIR	ALAFHPIEPVLITASEDHTLK	MWNLQ	4		576.31702	2301.23688	0.000451244	7	N	467	488
O55106	Parental	DNESR	SAGDGTDWEKEDQCLTPEAWNVDQGVISK	LKEQY	3	C14:+57.021	1079.154695	3234.440686	0.000451244	30	N	302	331
O55106	Parental	ETQQR	VLTLESNVDSTSSSSCQINR	VISHP	2	C16:+57.021	1099.023987	2196.032374	0.000451244	5	N	649	669
O55106	Parental	GTDGR	IQSWSTTNPNVDPYDAYDPSVLR	GPLLG	2		1319.625154	2637.234708	0.000451244	11	N	539	562
O55106	Parental	AMIGK	SELTDSASVLDNFK	FLESA	2		763.3731821	1524.730764	0.000451244	1	N	221	235
O55106	Parental	DRDTK	EALKEFDFLVTSEEGDNESR	SAGDG	2		1158.037849	2314.060097	0.000451244	5	N	282	302
O55106	Parental	DRDTK	EALKEFDFLVTSEEGDNESR	SAGDG	3		772.3611658	2314.060097	0.000451244	7	N	282	302
O55106	Parental	FDGIR	ALAFHPIEPVLITASEDHTLK	MWNLQ	4		576.31702	2301.23688	0.00091018	1	N	467	488
O55131	Exosome	SGLGK	STLINSLFLTDLYSPEYPGPSHR	IKKTV	3		869.7750218	2606.301665	0.000451244	12	N	62	85
O55131	Exosome	MAQPK	NLEGYVGFANLPNQVYR	KSVKR	2		977.4950287	1952.974457	0.000451244	12	N	24	41
O55131	Parental	SGLGK	STLINSLFLTDLYSPEYPGPSHR	IKKTV	2		1304.158633	2606.301665	0.000451244	2	N	62	85
O55131	Parental	SGLGK	STLINSLFLTDLYSPEYPGPSHR	IKKTV	3		869.7750218	2606.301665	0.000451244	32	N	62	85
O55131	Parental	MAQPK	NLEGYVGFANLPNQVYR	KSVKR	2		977.4950287	1952.974457	0.000451244	6	N	24	41
O55131	Parental	EHKIK	IYEFPETDDEEENKLVK	KIKDR	2		1049.497297	2096.978993	0.002813207	1	N	220	237
O55131	Parental	KVLIK	EGGVQLLLTIVDTPGFGDAVDNSNCWQPVIDYIDSK	FEDYL	3	C25:+57.021	1312.638812	3934.893035	0.00091018	1	N	100	136
O55135	Exosome	VEVFR	QTVADQVLVGSYCVFSNQGGLVHPK	TSIED	3	C13:+57.021	901.7905232	2702.34817	0.000451244	21	N	139	164
O55135	Exosome	LVHPK	TSIEDQDELSSLLQVPLVAGTVNR	GSEVI	2		1292.677387	2583.339173	0.000451244	17	N	164	188
O55135	Exosome	LVHPK	TSIEDQDELSSLLQVPLVAGTVNR	GSEVI	3		862.1208577	2583.339173	0.000451244	14	N	164	188
O55135	Exosome	CVGNR	HGLLVPNNTTDQELQHIR	NSLPD	3		695.699899	2084.076297	0.001463592	1	N	67	85
O55135	Exosome	-MAVR	ASFENNCEVGCFAK	LTNAY	2	C7:+57.021,C11:+57.021	816.8427489	1631.669898	0.000451244	11	N	4	18
O55135	Exosome	RVEER	LSALGNVTTCNDYVALVHPDLDRETEEILADVLK	VEVFR	4	C10:+57.021	946.7336015	3782.903206	0.000451244	4	N	100	134
O55135	Parental	VEVFR	QTVADQVLVGSYCVFSNQGGLVHPK	TSIED	3	C13:+57.021	901.7905232	2702.34817	0.000451244	27	N	139	164
O55135	Parental	LVHPK	TSIEDQDELSSLLQVPLVAGTVNR	GSEVI	2		1292.677387	2583.339173	0.000451244	46	N	164	188
O55135	Parental	LVHPK	TSIEDQDELSSLLQVPLVAGTVNR	GSEVI	3		862.1208577	2583.339173	0.000451244	25	N	164	188
O55135	Parental	CVGNR	HGLLVPNNTTDQELQHIR	NSLPD	3		695.699899	2084.076297	0.000451244	1	N	67	85
O55135	Parental	-MAVR	ASFENNCEVGCFAK	LTNAY	2	C7:+57.021,C11:+57.021	816.8427489	1631.669898	0.000451244	30	N	4	18
O55135	Parental	RVEER	LSALGNVTTCNDYVALVHPDLDRETEEILADVLK	VEVFR	4	C10:+57.021	946.7336015	3782.903206	0.000823681	7	N	100	134
O55135	Parental	GCFAK	LTNAYCLVAIGGSENFYSVFEGELSDAIPVVHASIAGCR	IIGRM	3	C6:+57.021,C38:+57.021	1396.34548	4186.013039	0.0025889	1	N	18	57
O55201	Exosome	KVLPR	DLQLCSETASGVDVGGQHEWGELVQLDPR	TVGVI	3	C5:+57.021	1065.83893	3194.49339	0.001463592	1	N	514	543
O55201	Exosome	AEKIR	SLGGDVASDGDFLIFEGNR	YSRKG	2		984.9690407	1967.922481	0.000451244	1	N	344	363
O55201	Parental	KKYAK	SSVGETVYGGSDELSDDITQQQLLPGVKDPNLWTVK	CKIGE	3		1292.644885	3874.911256	0.000451244	16	N	145	181
O55201	Parental	KKYAK	SSVGETVYGGSDELSDDITQQQLLPGVKDPNLWTVK	CKIGE	4		969.7356141	3874.911256	0.000622848	1	N	145	181
O55201	Parental	KVLPR	DLQLCSETASGVDVGGQHEWGELVQLDPR	TVGVI	3	C5:+57.021	1065.83893	3194.49339	0.000622848	3	N	514	543
O55201	Parental	VRLKR	GIYKDDIAQVDYVEPSQNTISL	KMIPR	2		1234.613724	2467.211847	0.000622848	3	N	281	303
O55201	Parental	GETVY	GGSDELSDDITQQQLLPGVKDPNLWTVK	CKIGE	3		1018.519569	3052.535307	0.000823681	2	N	153	181
O55201	Parental	HDGSR	TPAQSGAWDPNNPNTPSR	AEEEY	2		955.4435244	1908.871449	0.002663018	2	N	807	825
O55201	Parental	TGKER	EHNFQPGDNVEVCEGELINLQGK	VLSVD	3	C13:+57.021	876.0786213	2625.212464	0.000451244	1	N	414	437
O55222	Exosome	AVAVR	LWLDNTENDLNQGDDHGFSPLHWACR	EGRSA	3	C25:+57.021	1037.465538	3109.373215	0.000622848	7	N	17	43
O55222	Exosome	AVAVR	LWLDNTENDLNQGDDHGFSPLHWACR	EGRSA	4	C25:+57.021	778.3511039	3109.373215	0.000451244	16	N	17	43
O55222	Exosome	EIGMK	VALEGLRPTIPPGISPHVCK	LMKIC	4	C19:+57.021	536.0533534	2140.182214	0.000451244	3	N	403	423
O55222	Exosome	HWMPY	GSLYNVLHEGTNFVVDQSQAVK	FALDM	3		802.4085618	2404.202286	0.000622848	1	N	274	296
O55222	Parental	AVAVR	LWLDNTENDLNQGDDHGFSPLHWACR	EGRSA	3	C25:+57.021	1037.465538	3109.373215	0.000451244	25	N	17	43
O55222	Parental	AVAVR	LWLDNTENDLNQGDDHGFSPLHWACR	EGRSA	4	C25:+57.021	778.3511039	3109.373215	0.000451244	17	N	17	43
O55222	Parental	YGSLY	NVLHEGTNFVVDQSQAVK	FALDM	2		993.0085003	1984.001401	0.000451244	3	N	278	296
O55222	Parental	EIGMK	VALEGLRPTIPPGISPHVCK	LMKIC	2	C19:+57.021	1071.098907	2140.182214	0.002519933	1	N	403	423
O55222	Parental	EIGMK	VALEGLRPTIPPGISPHVCK	LMKIC	4	C19:+57.021	536.0533534	2140.182214	0.000451244	6	N	403	423
O70138	Exosome	YGFPR	SVQAIDAAVSYNGK	TYFFI	2		711.8653272	1421.715054	0.000451244	45	N	372	386
O70138	Exosome	MEMPR	CGVPDSGDFLLTPGSPK	WTHTN	2	C1:+57.021	873.9222849	1745.82897	0.000451244	46	N	90	107
O70138	Exosome	MEMPR	CGVPDSGDFLLTPGSPK	WTHTN	2	[0:-17.027,C1:+57.021	865.4087849	1728.80197	0.001591523	1	N	90	107
O70138	Exosome	LFKGR	QYWALSGYDLQQGYPR	DISNY	2		972.9661041	1943.916608	0.000451244	35	N	347	363
O70138	Exosome	LFKGR	QYWALSGYDLQQGYPR	DISNY	3		648.9800027	1943.916608	0.001162105	3	N	347	363
O70138	Exosome	LFKGR	QYWALSGYDLQQGYPR	DISNY	2	Q1:-17.027	964.4526041	1926.889608	0.002453667	1	N	347	363
O70138	Exosome	LFKGR	QYWALSGYDLQQGYPR	DISNY	2	[0:-17.027	964.4526041	1926.889608	0.001763695	2	N	347	363
O70138	Exosome	SYNGK	TYFFINNQCWR	YDNQR	2	C9:+57.021	774.8565509	1547.697502	0.000451244	31	N	386	397
O70138	Exosome	QGYPR	DISNYGFPR	SVQAI	2		534.7596024	1067.503605	0.000451244	37	N	363	372
O70138	Exosome	NYAYR	EPSTYSLPQDDINGIQTIYGPSDNPIQPTGPSTPK	ACDPH	3		1243.271159	3726.790078	0.000451244	27	N	242	277
O70138	Exosome	TAIEK	AFHVWSVASPLTFTEILQGEADINIAFVSR	DHGDN	3		1106.91062	3317.708461	0.000451244	4	N	135	165
O70138	Exosome	HPQLR	TVDLNFISLFWPFLPNGLQAAYEDFDRDLVFLFK	GRQYW	3		1351.028054	4050.060761	0.002296037	1	N	311	345
O70138	Exosome	HPQLR	TVDLNFISLFWPFLPNGLQAAYEDFDRDLVFLFK	GRQYW	4		1013.52299	4050.060761	0.002080925	2	N	311	345
O70138	Exosome	GVNCR	VDAVFLQDSFFLFFSGPQYFAFNFVSHR	VTRVA	3		1111.545501	3331.613104	0.000451244	4	N	423	451
O70138	Exosome	TAIEK	AFHVWSVASPLTF	TEILQ	2		731.3804161	1460.745232	0.000870037	6	N	135	148
O70138	Parental	YGFPR	SVQAIDAAVSYNGK	TYFFI	2		711.8653272	1421.715054	0.000451244	50	N	372	386

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O70138	Parental	MEMPR	CGVPDSGDFLLTPGSPK	WTHTN	2	C1:+57.021	873.9222849	1745.82897	0.000451244	19	N	90	107
O70138	Parental	MEMPR	CGVPDSGDFLLTPGSPK	WTHTN	2	[0:-17.027,C1:+57.021	865.4087849	1728.80197	0.002884417	1	N	90	107
O70138	Parental	LFKGR	QYWALSGYDLQQGYPR	DISNY	2		972.9661041	1943.916608	0.000451244	30	N	347	363
O70138	Parental	SYNGK	TYFFINNQCWR	YDNQR	2	C9:+57.021	774.8565509	1547.697502	0.000451244	14	N	386	397
O70138	Parental	NYAYR	EPSTYSLPQDDINGIQTIYGPSDNPIQPTGPSTPK	ACDPH	3		1243.271159	3726.790078	0.000451244	14	N	242	277
O70138	Parental	TAIEK	AFHVWSVASPLTFTEILQGEADINIAFVSR	DHGDN	3		1106.91062	3317.708461	0.001943752	2	N	135	165
O70138	Parental	GVNCR	VDAVFLQDSFFLFFSGPQYFAFNFVSHR	VTRVA	3		1111.545501	3331.613104	0.000622848	1	N	423	451
O70145	Exosome	PVELR	IHPQSQPQEDTSPESDIPPPPNSSPPGR	LQLSP	3		997.8080015	2990.400604	0.000451244	82	N	300	328
O70145	Exosome	IWKQK	LFEPVVIPVGR	LFRPN	2		613.3693201	1224.72304	0.000698008	20	N	170	181
O70145	Exosome	FNGQK	GLVPCNYLEPVELR	IHPQS	2	C5:+57.021	829.9324557	1657.849311	0.000451244	25	N	286	300
O70145	Exosome	WGQVK	NYCLTLWCEHTVGDQGLIDEPIQR	ENSDA	2	C3:+57.021,C8:+57.021	1459.184067	2916.352535	0.000451244	5	N	417	441
O70145	Exosome	WGQVK	NYCLTLWCEHTVGDQGLIDEPIQR	ENSDA	3	C3:+57.021,C8:+57.021	973.1253115	2916.352535	0.000451244	42	N	417	441
O70145	Exosome	DPHSR	ICFNIGCVNTILENLQAAEQAFTK	SINRD	2	C2:+57.021,C7:+57.021	1377.683172	2753.350744	0.000451244	34	N	38	62
O70145	Exosome	DPHSR	ICFNIGCVNTILENLQAAEQAFTK	SINRD	3	C2:+57.021,C7:+57.021	918.7913812	2753.350744	0.000451244	49	N	38	62
O70145	Exosome	KKDWK	GALEAFSEVQDPHSR	ICFNI	2		821.8951474	1641.774695	0.000451244	35	N	23	38
O70145	Exosome	KKDWK	GALEAFSEVQDPHSR	ICFNI	3		548.2660316	1641.774695	0.000451244	26	N	23	38
O70145	Exosome	RICFN	IGCVNTILENLQAAEQAFTK	SINRD	2	C3:+57.021	1110.570376	2219.125152	0.000622848	1	N	42	62
O70145	Exosome	RICFN	IGCVNTILENLQAAEQAFTK	SINRD	3	C3:+57.021	740.7161841	2219.125152	0.002212458	1	N	42	62
O70145	Exosome	DYLGK	ATVVASVVHQDNFSGFAPLQPQSAEPPPRPK	TPEIF	3		1091.233986	3270.678558	0.000451244	8	N	201	232
O70145	Exosome	DYLGK	ATVVASVVHQDNFSGFAPLQPQSAEPPPRPK	TPEIF	4		818.6774395	3270.678558	0.000823681	1	N	201	232
O70145	Exosome	GLQFK	LFACEVLYNIALMHAK	KEEWK	3	C4:+57.021	631.6639273	1891.968382	0.000451244	3	N	117	133
O70145	Exosome	SRICF	NIGCVNTILENLQAAEQAFTK	SINRD	2	C4:+57.021	1167.59184	2333.16808	0.000451244	3	N	41	62
O70145	Exosome	SRICF	NIGCVNTILENLQAAEQAFTK	SINRD	3	C4:+57.021	778.7304933	2333.16808	0.000451244	3	N	41	62
O70145	Exosome	GEAHR	VLFGFVPETPEELQVMPGNIVFVLK	KGSDN	3	M16:+15.995	940.1753867	2817.50276	0.000622848	1	N	246	271
O70145	Parental	PVELR	IHPQSQPQEDTSPESDIPPPPNSSPPGR	LQLSP	3		997.8080015	2990.400604	0.000451244	102	N	300	328
O70145	Parental	IWKQK	LFEPVVIPVGR	LFRPN	2		613.3693201	1224.72304	0.000698008	22	N	170	181
O70145	Parental	FNGQK	GLVPCNYLEPVELR	IHPQS	2	C5:+57.021	829.9324557	1657.849311	0.000451244	31	N	286	300
O70145	Parental	WGQVK	NYCLTLWCEHTVGDQGLIDEPIQR	ENSDA	2	C3:+57.021,C8:+57.021	1459.184067	2916.352535	0.000451244	8	N	417	441
O70145	Parental	WGQVK	NYCLTLWCEHTVGDQGLIDEPIQR	ENSDA	3	C3:+57.021,C8:+57.021	973.1253115	2916.352535	0.000451244	42	N	417	441
O70145	Parental	DPHSR	ICFNIGCVNTILENLQAAEQAFTK	SINRD	2	C2:+57.021,C7:+57.021	1377.683172	2753.350744	0.000451244	32	N	38	62
O70145	Parental	DPHSR	ICFNIGCVNTILENLQAAEQAFTK	SINRD	3	C2:+57.021,C7:+57.021	918.7913812	2753.350744	0.000451244	38	N	38	62
O70145	Parental	KKDWK	GALEAFSEVQDPHSR	ICFNI	2		821.8951474	1641.774695	0.000451244	7	N	23	38
O70145	Parental	QVKNY	CLTLWCEHTVGDQGLIDEPIQR	ENSDA	2	C1:+39.994,C6:+57.021	1312.117439	2622.219278	0.000662267	1	N	419	441
O70145	Parental	QVKNY	CLTLWCEHTVGDQGLIDEPIQR	ENSDA	2	[0:-17.027,C1:+57.021,C6:+57.021	1312.117439	2622.219278	0.000451244	7	N	419	441
O70145	Parental	VVAIF	SYEAAQPEDLEFVEGDVILVLSHVNEEWLEGECKGK	VGIFP	4	C33:+57.021	1030.494348	4117.946193	0.00091018	1	N	465	501
O70145	Parental	VVAIF	SYEAAQPEDLEFVEGDVILVLSHVNEEWLEGECK	GKVGI	3	C33:+57.021	1311.951055	3932.829766	0.000451244	3	N	465	499
O70145	Parental	VVAIF	SYEAAQPEDLEFVEGDVILVLSHVNEEWLEGECK	GKVGI	4	C33:+57.021	984.2152415	3932.829766	0.000451244	3	N	465	499
O70145	Parental	DYLGK	ATVVASVVHQDNFSGFAPLQPQSAEPPPRPK	TPEIF	4		818.6774395	3270.678558	0.001591523	1	N	201	232
O70165	Exosome	QEKYK	LTLGQFLEGTAGDSLTK	HNNMS	2		875.9652384	1749.914877	0.000451244	4	N	241	258
O70165	Exosome	QEKYK	LTLGQFLEGTAGDSLTK	HNNMS	3		584.3127589	1749.914877	0.000698008	3	N	241	258
O70165	Exosome	DSYKR	GFGNLGTEFWLGNDYLHLLTANGNQELR	VDLQD	3		1050.520015	3148.536644	0.000451244	5	N	185	213
O70194	Exosome	FFDKR	DNSDFDLLTVSETANEPPQDEGNSFNSPR	NLAME	3		1065.804874	3194.391222	0.000451244	7	N	281	310
O70194	Exosome	LMKMR	YLEVSEPQDIECCGALEYYDK	AFDRI	2	C12:+57.021,C13:+57.021	1291.059147	2580.102693	0.000451244	16	N	183	204
O70194	Exosome	LMKMR	YLEVSEPQDIECCGALEYYDK	AFDRI	3	C12:+57.021,C13:+57.021	861.0420311	2580.102693	0.000451244	2	N	183	204
O70194	Exosome	-MAK	FMTPVIQDNPSGWGPCAVPEQFR	DMPYQ	2	M2:+15.995,C16:+57.021	1325.1152	2648.214799	0.000451244	4	N	3	26
O70194	Parental	FFDKR	DNSDFDLLTVSETANEPPQDEGNSFNSPR	NLAME	3		1065.804874	3194.391222	0.000451244	15	N	281	310
O70194	Parental	LMKMR	YLEVSEPQDIECCGALEY	YDKAF	2	C12:+57.021,C13:+57.021	1087.966529	2173.917458	0.000451244	17	N	183	201
O70194	Parental	-MAK	FMTPVIQDNPSGWGPCAVPEQFR	DMPYQ	2	M2:+15.995,C16:+57.021	1325.1152	2648.214799	0.002296037	1	N	3	26
O70251	Exosome	FGDLK	TPAGLQVLNDYLADK	SYIEG	2		809.4282917	1616.840983	0.000451244	27	N	7	22
O70251	Exosome	YLADK	SYIEGYVPSQADVAVFEAVSGPPPADLCHALR	WYNHI	3	C28:+57.021	1139.226126	3414.654977	0.000451244	35	N	22	54
O70251	Exosome	KSLGK	YGPSSVEDTTGSGAADAKDDDDIDLFGSDDEEESEEAK	KLREE	3		1322.877597	3965.609392	0.000451244	7	N	78	116
O70251	Parental	FGDLK	TPAGLQVLNDYLADK	SYIEG	2		809.4282917	1616.840983	0.000451244	27	N	7	22
O70251	Parental	YLADK	SYIEGYVPSQADVAVFEAVSGPPPADLCHALR	WYNHI	3	C28:+57.021	1139.226126	3414.654977	0.000451244	49	N	22	54
O70251	Parental	YLADK	SYIEGYVPSQADVAVFEAVSGPPPADLCHALR	WYNHI	4	C28:+57.021	854.6715441	3414.654977	0.000451244	8	N	22	54
O70251	Parental	-M	GFGDLKTPAGLQVLNDYLADK	SYIEG	3		745.7272318	2234.158295	0.000451244	7	N	1	22
O70251	Parental	AVVAK	SSILLDVKPWDDETDMTKLEECVR	SIQAD	3	C22:+57.021	960.4652655	2878.372396	0.000451244	7	N	139	163
O70251	Parental	GLQVL	NDYLADKSYIEGYVPSQADVAVFEAVSGPPPADLCHALR	WYNHI	3	C35:+57.021	1412.351553	4234.03126	0.000451244	4	N	15	54
O70252	Parental	IKDMK	YFFGENWEEQVK	CSEAA	2		788.3598777	1574.704155	0.001463592	3	N	113	125
O70252	Parental	EEMDR	NKDHPAFAPLYFPTELHR	KAALI	4		539.0291512	2152.085405	0.001162105	1	N	86	104
O70310	Exosome	LEKLK	FGIGDGNLQYYLYNWK	CPSMG	2		975.9733978	1949.931196	0.000451244	22	N	466	482
O70310	Exosome	QPVPK	LGEVVNTHGPVEPDKDNIR	QEPYT	3		697.0277927	2088.059978	0.000451244	25	N	127	146
O70310	Exosome	HKSLK	AAYSFYNVHTQTPLLDLMSDALVLAK	MKGFD	3		961.1655218	2880.473165	0.002296037	1	N	417	443
O70310	Exosome	KDNIR	QEPYTLPQGFTWDALDLGDR	GVLKE	2		1161.556012	2321.096423	0.002374549	1	N	146	166
O70310	Parental	LEKLK	FGIGDGNLQYYLYNWK	CPSMG	2		975.9733978	1949.931196	0.001162105	1	N	466	482
O70310	Parental	QPVPK	LGEVVNTHGPVEPDKDNIR	QEPYT	3		697.0277927	2088.059978	0.0007646	2	N	127	146

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O70310	Parental	KDNIR	QEPYTLPQGFTWDALDLGDR	GVLKE	2		1161.556012	2321.096423	0.000451244	3	N	146	166
O70400	Parental	AVESK	TSASGEEANSRPVVQPHPSGSLIIDKDSEVYK	MLQEK	3		1133.23438	3396.67974	0.000451244	4	N	164	196
O70400	Parental	AVESK	TSASGEEANSRPVVQPHPSGSLIIDKDSEVYK	MLQEK	4		850.177735	3396.67974	0.000451244	5	N	164	196
O70400	Parental	NLKQK	GHFFVEDQIYCEK	HARER	2	C11:+57.021	836.3775132	1670.739426	0.001943752	1	N	294	307
O70400	Parental	APSTR	VITNQYNSPTGLYSSENISNFNNAVESK	TSASG	3		1030.827062	3089.457785	0.000451244	1	N	136	164
O70435	Exosome	EYAMK	AVENSSTAIGIR	CKDGV	2		609.3283805	1216.641161	0.000622848	10	N	29	41
O70435	Exosome	KEVAK	IIYIVHDEVKDK	AFELE	2		736.4119133	1470.808227	0.000451244	10	N	196	208
O70435	Exosome	ASNFR	SNFGYNIPLK	HLADR	2		576.8065526	1151.597505	0.000698008	34	N	100	110
O70435	Exosome	EVKDK	AFELELSWVGELTK	GRHEI	2		811.4277604	1620.839921	0.000451244	20	N	208	222
O70435	Exosome	AIGIR	CKDGVVFGVEK	LVLSK	2	[0:-17.027,C1:+57.021	610.8026959	1219.589792	0.000451244	2	N	41	52
O70435	Exosome	LADAR	SLADIAREEASNFR	SNFGY	2		789.89769	1577.77978	0.000451244	4	N	86	100
O70435	Exosome	LADAR	SLADIAREEASNFR	SNFGY	3		526.9343934	1577.77978	0.000451244	17	N	86	100
O70435	Parental	ASNFR	SNFGYNIPLK	HLADR	2		576.8065526	1151.597505	0.0025889	1	N	100	110
O70435	Parental	LADAR	SLADIAREEASNFR	SNFGY	3		526.9343934	1577.77978	0.000451244	4	N	86	100
O70492	Parental	ADTRR	LITKPQNLNDAYGPPSNFLEIDVSNPQTVGVGR	GRFTT	3		1185.281553	3552.821259	0.000451244	22	N	10	43
O70492	Parental	RHVPF	RGDDGIFDDNFIEER	KQGLE	2		899.4060762	1796.796552	0.000979378	1	N	103	118
O70497	Exosome	AEKYK	LILGNFLGGGAGDSLTPHNNR	LFSTK	3		708.3717823	2122.091947	0.000451244	27	N	221	242
O70497	Exosome	TSYKR	GFGSQLGEFWLGNDNIHALTTQGTSELR	VDLSD	3		1016.83237	3047.47371	0.000451244	34	N	165	193
O70497	Parental	AEKYK	LILGNFLGGGAGDSLTPHNNR	LFSTK	3		708.3717823	2122.091947	0.000622848	4	N	221	242
O70497	Parental	TSYKR	GFGSQLGEFWLGNDNIHALTTQGTSELR	VDLSD	3		1016.83237	3047.47371	0.000451244	18	N	165	193
O70566	Parental	VHDDR	SLILSEKEVLDLFEK	MMEDM	3		588.3332715	1761.976414	0.000622848	1	N	89	104
O70566	Parental	LESLR	VSLTSHPVSWVNNFGYEGLGVLLDVLEK	LLDKK	3		1024.873395	3071.596785	0.000662267	1	N	186	214
O88307	Exosome	IPSSK	HCDGLRDCPDGSDEQHCEPFCTR	FMDFV	3	C2:+57.021,C8:+57.021,C17:+57.021,C21:+57.021	950.035642	2847.083526	0.000451244	9	N	1254	1277
O88307	Exosome	IPSSK	HCDGLRDCPDGSDEQHCEPFCTR	FMDFV	4	C2:+57.021,C8:+57.021,C17:+57.021,C21:+57.021	712.7786815	2847.083526	0.000451244	19	N	1254	1277
O88307	Exosome	SAWAK	TDLGDSPLAFEHILTR	GSSPP	2		892.96303	1783.91046	0.000451244	6	N	1824	1840
O88307	Exosome	SAWAK	TDLGDSPLAFEHILTR	GSSPP	3		595.64462	1783.91046	0.000451244	26	N	1824	1840
O88307	Exosome	FFQSR	ENQEVILEEVRDFQLR	DKYMF	2		1009.021608	2016.027615	0.002212458	3	N	287	303
O88307	Exosome	FFQSR	ENQEVILEEVRDFQLR	DKYMF	3		673.0170051	2016.027615	0.001162105	14	N	287	303
O88307	Exosome	CIPQR	WACDGDADCQDGSDEDPVSCEK	KCNGF	2	C3:+57.021,C9:+57.021,C20:+57.021	1258.449403	2514.883206	0.000451244	23	N	1215	1237
O88307	Exosome	PILSK	ESAPGLIIATGSVGK	NLASK	2		700.3937205	1398.771841	0.000451244	23	N	497	512
O88307	Exosome	QEHVK	SFSWGIDPYDQPNAIYIER	HEPFG	2		1136.039997	2270.064395	0.000451244	35	N	249	268
O88307	Exosome	QEHVK	SFSWGIDPYDQPNAIYIER	HEPFG	3		757.6959316	2270.064395	0.002080925	1	N	249	268
O88307	Exosome	STEIK	NLLLNALYTVR	VAAVT	2		645.3829588	1288.750318	0.000451244	18	N	1711	1722
O88307	Exosome	AEGLK	FSLSLENVLYYSPGGAGSDTLVR	YFANE	2		1223.118976	2444.222352	0.000451244	33	N	381	404
O88307	Exosome	AEGLK	FSLSLENVLYYSPGGAGSDTLVR	YFANE	3		815.7485841	2444.222352	0.000823681	1	N	381	404
O88307	Exosome	MSDER	NCPTTVCDADTQFR	CQESG	2	C2:+57.021,C7:+57.021	842.8563877	1683.697175	0.000451244	33	N	1110	1124
O88307	Exosome	SGQQR	SVILDSLPHPYAIAVFK	NEIYW	2		935.5278089	1869.040018	0.000451244	3	N	953	970
O88307	Exosome	SGQQR	SVILDSLPHPYAIAVFK	NEIYW	3		624.0211393	1869.040018	0.0007646	9	N	953	970
O88307	Exosome	ITFDK	GGTWEFLQAPAFTGYGEK	INCEL	2		979.9683124	1957.921025	0.000451244	25	N	446	464
O88307	Exosome	GETWK	TFVFSEKPVFVYGLLTEPGEK	STVFT	2		1194.130824	2386.246048	0.000451244	18	N	572	593
O88307	Exosome	GETWK	TFVFSEKPVFVYGLLTEPGEK	STVFT	3		796.4231493	2386.246048	0.000451244	51	N	572	593
O88307	Exosome	IAVFK	NEIYWDDWSQLSIFR	ASKHS	2		986.4659369	1970.916274	0.000622848	7	N	970	985
O88307	Exosome	PNWKR	CDGHQDCQDGQDEANCPTHSTLTCTSR	EFKCE	4	C1:+57.021,C7:+57.021,C16:+57.021,C24:+57.021	788.3055261	3149.190904	0.002296037	2	N	1490	1517
O88307	Exosome	PNWKR	CDGHQDCQDGQDEANCPTHSTLTCTSR	EFKCE	3	[0:-17.027,C1:+57.021,C7:+57.021,C16:+57.021,C24:+57.021	1045.062435	3132.163904	0.002981883	1	N	1490	1517
O88307	Exosome	AGFKK	IEVANPDGDFR	LTIVN	2		616.7994559	1231.583312	0.000451244	8	N	855	866
O88307	Exosome	FYKGK	NAGSNACVPQPCSLLCLPK	ANNSK	2	C7:+57.021,C12:+57.021,C16:+57.021	1043.49738	2084.979159	0.000451244	11	N	1014	1033
O88307	Exosome	DFGFK	MSEDLSLEVCVPDPEFSGKPYSPPVPCPVGSSYR	RTRGY	3	M1:+15.995,C10:+57.021,C27:+57.021	1266.916286	3797.725459	0.000451244	28	N	689	723
O88307	Exosome	FDYER	NCLYWSDLALDTIQR	LCLNG	2	C2:+57.021	934.4542836	1866.892967	0.000451244	23	N	799	814
O88307	Exosome	FDYER	NCLYWSDLALDTIQR	LCLNG	3	C2:+57.021	623.3054557	1866.892967	0.000823681	1	N	799	814
O88307	Exosome	CIPQR	WACDGDADCQDGSDEDPVSCEKK	CNGFH	3	C3:+57.021,C9:+57.021,C20:+57.021	882.0005231	2642.978169	0.000451244	15	N	1215	1238
O88307	Exosome	GYGEK	INCELSQGCSLHLAQR	LSQLL	2	C3:+57.021,C9:+57.021	943.4540607	1884.892521	0.000451244	18	N	464	480
O88307	Exosome	DTQFR	CQESGTCIPLSYK	CDLED	2	C1:+57.021,C7:+57.021	771.8500427	1541.684485	0.000451244	9	N	1124	1137
O88307	Exosome	LSGLR	AAVALDFDYER	NCLYW	2		635.3096565	1268.603713	0.000823681	10	N	788	799
O88307	Exosome	VLSER	CDGFLDCSDESDEKACSDELTVYK	VQNLQ	3	C1:+57.021,C7:+57.021,C16:+57.021	948.3825217	2842.124165	0.000451244	19	N	1533	1557
O88307	Exosome	LFLVR	VLIPYQGPSSDYVVVK	MIPDS	2		882.483067	1762.950534	0.000451244	11	N	1911	1927

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88307	Exosome	EPGEK	STVFTIFGSNK	ESVHS	2		600.8171173	1199.618635	0.000451244	8	N	593	604
O88307	Exosome	SALIK	WESPYDSPDQDLFYAIAVK	DLIRK	2		1122.528931	2243.042262	0.000451244	14	N	1952	1971
O88307	Exosome	SALIK	WESPYDSPDQDLFYAIAVK	DLIRK	3		748.6885541	2243.042262	0.000698008	3	N	1952	1971
O88307	Exosome	CDGLR	DCPDGSDEQHCEPFCTR	FMDFV	2	C2:+57.021,C11:+57.021,C15:+57.021	1055.388223	2108.760846	0.00091018	1	N	1260	1277
O88307	Exosome	SREFK	CEDGEACIVLSER	CDGFL	2	C1:+57.021,C7:+57.021	769.3347567	1536.653913	0.000979378	2	N	1520	1533
O88307	Exosome	HLAQR	LSQLLNLQLR	RMPIL	2		599.3698514	1196.724103	0.002374549	4	N	480	490
O88307	Exosome	KSIYR	YDLASGATEQLPLSGLR	AAVAL	2		895.9683124	1789.921025	0.000451244	8	N	771	788
O88307	Exosome	DSSIK	ITTVSLSAPDALK	IITEN	2		658.3775391	1314.739478	0.000622848	1	N	2019	2032
O88307	Exosome	LLHSK	ASNLLLGFDR	SHPNK	2		553.3041771	1104.592754	0.000451244	16	N	214	224
O88307	Exosome	MFATK	VVHLPGSQQQSSVQLWVSFGR	KPMRA	2		1170.116905	2338.21821	0.002884417	1	N	311	332
O88307	Exosome	MFATK	VVHLPGSQQQSSVQLWVSFGR	KPMRA	3		780.4138701	2338.21821	0.001763695	1	N	311	332
O88307	Exosome	TCTSR	EFKCEDGEACIVLSER	CDGFL	2	C4:+57.021,C10:+57.021	971.4377419	1940.859884	0.001162105	1	N	1517	1533
O88307	Exosome	NLASK	TNVYISSSAGAR	WREAL	2		613.3127305	1224.609861	0.000870037	1	N	517	529
O88307	Exosome	TVQAR	CLFGSQICGEPAVLLYDELSSGADAA	VIQAA	2	C1:+57.021,C8:+57.021	1372.133177	2742.250755	0.000870037	3	N	2101	2127
O88307	Parental	IPSSK	HCDGLRDCPDGSDEQHCEPFCTR	FMDFV	4	C2:+57.021,C8:+57.021,C17:+57.021,C21:+57.021	712.7786815	2847.083526	0.000451244	5	N	1254	1277
O88307	Parental	SAWAK	TDLGDSPLAFEHILTR	GSSPP	3		595.64462	1783.91046	0.000451244	16	N	1824	1840
O88307	Parental	FFQSR	ENQEVILEEVRDFQLR	DKYMF	3		673.0170051	2016.027615	0.002453667	2	N	287	303
O88307	Parental	CIPQR	WACDGDADCQDGSDEDPVSCEK	KCNGF	2	C3:+57.021,C9:+57.021,C20:+57.021	1258.449403	2514.883206	0.000451244	18	N	1215	1237
O88307	Parental	PILSK	ESAPGLIIATGSVGK	NLASK	2		700.3937205	1398.771841	0.000451244	2	N	497	512
O88307	Parental	QEHVK	SFSWGIDPYDQPNAIYIER	HEPFG	2		1136.039997	2270.064395	0.000451244	22	N	249	268
O88307	Parental	DFGFK	MSEDLSLEVCVPDPEFSGKPYSPPVPCPVGSSYRR	TRGYR	4	C10:+57.021,C27:+57.021	985.4656925	3937.83157	0.002145581	1	N	689	724
O88307	Parental	VHIGK	TSALIKWESPYDSPDQDLFYAIAVK	DLIRK	3		953.1485249	2856.422175	0.002296037	1	N	1946	1971
O88307	Parental	STEIK	NLLLNALYTVR	VAAVT	2		645.3829588	1288.750318	0.001162105	1	N	1711	1722
O88307	Parental	AEGLK	FSLSLENVLYYSPGGAGSDTLVR	YFANE	2		1223.118976	2444.222352	0.000451244	7	N	381	404
O88307	Parental	MSDER	NCPTTVCDADTQFR	CQESG	2	C2:+57.021,C7:+57.021	842.8563877	1683.697175	0.000451244	18	N	1110	1124
O88307	Parental	SGQQR	SVILDSLPHPYAIAVFK	NEIYW	3		624.0211393	1869.040018	0.001871652	1	N	953	970
O88307	Parental	ITFDK	GGTWEFLQAPAFTGYGEK	INCEL	2		979.9683124	1957.921025	0.000622848	4	N	446	464
O88307	Parental	GETWK	TFVFSEKPVFVYGLLTEPGEK	STVFT	3		796.4231493	2386.246048	0.000451244	8	N	572	593
O88307	Parental	IAVFK	NEIYWDDWSQLSIFR	ASKHS	2		986.4659369	1970.916274	0.000451244	1	N	970	985
O88307	Parental	PNWKR	CDGHQDCQDGQDEANCPTHSTLTCTSR	EFKCE	3	C1:+39.994,C7:+57.021,C16:+57.021,C24:+57.021	1045.062435	3132.163904	0.000823681	1	N	1490	1517
O88307	Parental	PNWKR	CDGHQDCQDGQDEANCPTHSTLTCTSR	EFKCE	4	C1:+57.021,C7:+57.021,C16:+57.021,C24:+57.021	788.3055261	3149.190904	0.000451244	1	N	1490	1517
O88307	Parental	FYKGK	NAGSNACVPQPCSLLCLPK	ANNSK	2	C7:+57.021,C12:+57.021,C16:+57.021	1043.49738	2084.979159	0.000622848	10	N	1014	1033
O88307	Parental	FDYER	NCLYWSDLALDTIQR	LCLNG	2	C2:+57.021	934.4542836	1866.892967	0.000451244	5	N	799	814
O88307	Parental	CIPQR	WACDGDADCQDGSDEDPVSCEKK	CNGFH	3	C3:+57.021,C9:+57.021,C20:+57.021	882.0005231	2642.978169	0.000451244	4	N	1215	1238
O88307	Parental	GYGEK	INCELSQGCSLHLAQR	LSQLL	2	C3:+57.021,C9:+57.021	943.4540607	1884.892521	0.000451244	2	N	464	480
O88307	Parental	DTQFR	CQESGTCIPLSYK	CDLED	2	C1:+57.021,C7:+57.021	771.8500427	1541.684485	0.000451244	8	N	1124	1137
O88307	Parental	VLSER	CDGFLDCSDESDEKACSDELTVYK	VQNLQ	3	C1:+57.021,C7:+57.021,C16:+57.021	948.3825217	2842.124165	0.000698008	2	N	1533	1557
O88307	Parental	SALIK	WESPYDSPDQDLFYAIAVK	DLIRK	2		1122.528931	2243.042262	0.001329271	3	N	1952	1971
O88307	Parental	LLHSK	ASNLLLGFDR	SHPNK	2		553.3041771	1104.592754	0.001352548	1	N	214	224
O88342	Exosome	DGNVR	VYSILASTLKDEGK	LLEAK	2		762.4199353	1522.824271	0.000451244	45	N	470	484
O88342	Exosome	DGNVR	VYSILASTLKDEGK	LLEAK	3		508.6158902	1522.824271	0.000451244	28	N	470	484
O88342	Exosome	RNGGK	SYIYSGSHDGHINYWDSETGENDSFSGK	GHTNQ	3		1051.443388	3151.306764	0.000451244	72	N	334	362
O88342	Exosome	RNGGK	SYIYSGSHDGHINYWDSETGENDSFSGK	GHTNQ	4		788.8344909	3151.306764	0.000735798	20	N	334	362
O88342	Exosome	LKDQK	KCFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C2:+57.021	1171.895327	3512.662581	0.000451244	44	N	436	470
O88342	Exosome	LKDQK	KCFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	4	C2:+57.021	879.1734453	3512.662581	0.000451244	22	N	436	470
O88342	Exosome	LLEAK	GPVTDVAYSHDGAFLAVCDASK	VVTVF	2	C18:+57.021	1140.533991	2279.052381	0.000451244	36	N	489	511
O88342	Exosome	LLEAK	GPVTDVAYSHDGAFLAVCDASK	VVTVF	3	C18:+57.021	760.6919271	2279.052381	0.000451244	63	N	489	511
O88342	Exosome	CDASK	VVTVFSVADGYSENNVFYGHHAK	IVCLA	2		1270.614392	2539.213185	0.000451244	12	N	511	534
O88342	Exosome	CDASK	VVTVFSVADGYSENNVFYGHHAK	IVCLA	3		847.4121949	2539.213185	0.000451244	28	N	511	534
O88342	Exosome	CDASK	VVTVFSVADGYSENNVFYGHHAK	IVCLA	4		635.8110961	2539.213185	0.000451244	32	N	511	534
O88342	Exosome	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C1:+39.994	1123.521339	3367.540618	0.000823681	6	N	437	470
O88342	Exosome	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C1:+57.021	1129.197006	3384.567618	0.000451244	70	N	437	470
O88342	Exosome	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	[0:-17.027,C1:+57.021	1123.521339	3367.540618	0.000451244	25	N	437	470
O88342	Exosome	TRPYR	LATGSDDNCAAFFEGPPFK	FKFTI	2	C9:+57.021	1022.459763	2042.903926	0.000451244	84	N	161	180
O88342	Exosome	TRPYR	LATGSDDNCAAFFEGPPFK	FKFTI	3	C9:+57.021	681.9757753	2042.903926	0.000698008	2	N	161	180
O88342	Exosome	EGREK	FGAVFLWDTGSSVGEITGHNK	VINSV	2		1111.54799	2221.080379	0.000451244	31	N	126	147
O88342	Exosome	EGREK	FGAVFLWDTGSSVGEITGHNK	VINSV	3		741.3679264	2221.080379	0.000451244	37	N	126	147

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88342	Exosome	LGESK	AHDGGIYAISWSPDSTHLLSASGDKTSK	IWDVN	3		967.8058208	2900.394062	0.000451244	10	N	231	259
O88342	Exosome	LGESK	AHDGGIYAISWSPDSTHLLSASGDKTSK	IWDVN	4		726.1063156	2900.394062	0.000622848	18	N	231	259
O88342	Exosome	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	2		1209.62476	2417.23392	0.000451244	11	N	43	65
O88342	Exosome	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	3		806.75244	2417.23392	0.000451244	19	N	43	65
O88342	Exosome	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	4		605.31628	2417.23392	0.000451244	41	N	43	65
O88342	Exosome	PDGNR	FATASADGQIFIYDGK	TGEKV	2		852.417924	1702.820248	0.000451244	28	N	203	219
O88342	Exosome	VVVAK	YAPSGFYIASGDISGK	LRIWD	2		816.8993671	1631.783134	0.000451244	25	N	65	81
O88342	Exosome	QDAHR	LHHVSSLAWLDEHTLVTTSHDASVK	EWTIT	4		696.6087598	2782.403839	0.000451244	42	N	575	600
O88342	Exosome	LGESK	AHDGGIYAISWSPDSTHLLSASGDK	TSKIW	2		1293.117496	2584.219392	0.000451244	22	N	231	256
O88342	Exosome	LGESK	AHDGGIYAISWSPDSTHLLSASGDK	TSKIW	3		862.4142641	2584.219392	0.000451244	39	N	231	256
O88342	Exosome	LGESK	AHDGGIYAISWSPDSTHLLSASGDK	TSKIW	4		647.0626481	2584.219392	0.000451244	1	N	231	256
O88342	Exosome	CLWQK	DHLLSISLSGYINYLDKNNPSKPLR	VIKGH	4		715.1361474	2856.51339	0.000451244	11	N	289	314
O88342	Exosome	DVQPK	CVAVGPGGYTVVVCIGQIVLLK	DQKKC	2	C1:+57.021,C14:+57.021	1151.636776	2301.257953	0.000451244	16	N	411	433
O88342	Exosome	DVQPK	CVAVGPGGYTVVVCIGQIVLLK	DQKKC	3	C1:+57.021,C14:+57.021	768.0937842	2301.257953	0.000451244	16	N	411	433
O88342	Exosome	DKTSK	IWDVNVNSVVSTFPMGSNVLDQQLGCLWQK	DHLLS	3	C26:+57.021	1145.567606	3433.679418	0.000451244	10	N	259	289
O88342	Exosome	VGEGR	EKFGAVFLWDTGSSVGEITGHNK	VINSV	4		620.5622839	2478.217936	0.001699387	1	N	124	147
O88342	Exosome	YEIKK	VFASLPQVER	GVSKI	2		573.3198272	1144.624054	0.001162105	3	N	7	17
O88342	Exosome	SGKLR	IWDTTQKEHLLK	YEYQP	2		756.4149873	1510.814375	0.001463592	1	N	83	95
O88342	Parental	NLTLR	DYSGQGVVKLDVQPK	CVAVG	2		816.9337412	1631.851882	0.000451244	9	N	396	411
O88342	Parental	DGNVR	VYSILASTLKDEGK	LLEAK	2		762.4199353	1522.824271	0.000451244	33	N	470	484
O88342	Parental	DGNVR	VYSILASTLKDEGK	LLEAK	3		508.6158902	1522.824271	0.000451244	14	N	470	484
O88342	Parental	RNGGK	SYIYSGSHDGHINYWDSETGENDSFSGK	GHTNQ	3		1051.443388	3151.306764	0.000622848	48	N	334	362
O88342	Parental	RNGGK	SYIYSGSHDGHINYWDSETGENDSFSGK	GHTNQ	4		788.8344909	3151.306764	0.000622848	1	N	334	362
O88342	Parental	LKDQK	KCFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C2:+57.021	1171.895327	3512.662581	0.000451244	40	N	436	470
O88342	Parental	LKDQK	KCFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	4	C2:+57.021	879.1734453	3512.662581	0.000451244	14	N	436	470
O88342	Parental	LLEAK	GPVTDVAYSHDGAFLAVCDASK	VVTVF	2	C18:+57.021	1140.533991	2279.052381	0.000451244	22	N	489	511
O88342	Parental	LLEAK	GPVTDVAYSHDGAFLAVCDASK	VVTVF	3	C18:+57.021	760.6919271	2279.052381	0.000451244	32	N	489	511
O88342	Parental	CDASK	VVTVFSVADGYSENNVFYGHHAK	IVCLA	3		847.4121949	2539.213185	0.000451244	11	N	511	534
O88342	Parental	CDASK	VVTVFSVADGYSENNVFYGHHAK	IVCLA	4		635.8110961	2539.213185	0.000451244	17	N	511	534
O88342	Parental	VNCVR	FSPDGNRFATASADGQIFIYDGK	TGEKV	2		1239.09075	2476.1659	0.000451244	9	N	196	219
O88342	Parental	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C1:+39.994	1123.521339	3367.540618	0.0007646	13	N	437	470
O88342	Parental	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	C1:+57.021	1129.197006	3384.567618	0.000451244	43	N	437	470
O88342	Parental	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVR	VYSIL	3	[0:-17.027,C1:+57.021	1123.521339	3367.540618	0.000451244	27	N	437	470
O88342	Parental	TRPYR	LATGSDDNCAAFFEGPPFK	FKFTI	2	C9:+57.021	1022.459763	2042.903926	0.000451244	64	N	161	180
O88342	Parental	EGREK	FGAVFLWDTGSSVGEITGHNK	VINSV	2		1111.54799	2221.080379	0.000451244	15	N	126	147
O88342	Parental	EGREK	FGAVFLWDTGSSVGEITGHNK	VINSV	3		741.3679264	2221.080379	0.000451244	32	N	126	147
O88342	Parental	LGESK	AHDGGIYAISWSPDSTHLLSASGDKTSK	IWDVN	3		967.8058208	2900.394062	0.000451244	8	N	231	259
O88342	Parental	LGESK	AHDGGIYAISWSPDSTHLLSASGDKTSK	IWDVN	4		726.1063156	2900.394062	0.000735798	7	N	231	259
O88342	Parental	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	2		1209.62476	2417.23392	0.000451244	8	N	43	65
O88342	Parental	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	3		806.75244	2417.23392	0.001229886	5	N	43	65
O88342	Parental	CVILR	NIDNPAIADIYTEHAHQVVVAK	YAPSG	4		605.31628	2417.23392	0.000451244	18	N	43	65
O88342	Parental	PDGNR	FATASADGQIFIYDGK	TGEKV	2		852.417924	1702.820248	0.000451244	10	N	203	219
O88342	Parental	VVVAK	YAPSGFYIASGDISGK	LRIWD	2		816.8993671	1631.783134	0.000451244	23	N	65	81
O88342	Parental	QDAHR	LHHVSSLAWLDEHTLVTTSHDASVK	EWTIT	4		696.6087598	2782.403839	0.000451244	9	N	575	600
O88342	Parental	LGESK	AHDGGIYAISWSPDSTHLLSASGDK	TSKIW	2		1293.117496	2584.219392	0.000451244	11	N	231	256
O88342	Parental	LGESK	AHDGGIYAISWSPDSTHLLSASGDK	TSKIW	3		862.4142641	2584.219392	0.000451244	24	N	231	256
O88342	Parental	DVQPK	CVAVGPGGYTVVVCIGQIVLLK	DQKKC	2	C1:+57.021,C14:+57.021	1151.636776	2301.257953	0.000451244	9	N	411	433
O88342	Parental	DVQPK	CVAVGPGGYTVVVCIGQIVLLK	DQKKC	3	C1:+57.021,C14:+57.021	768.0937842	2301.257953	0.000451244	4	N	411	433
O88342	Parental	KSYIY	SGSHDGHINYWDSETGENDSFSGK	GHTNQ	2		1313.539807	2625.064014	0.000622848	1	N	338	362
O88342	Parental	KSYIY	SGSHDGHINYWDSETGENDSFSGK	GHTNQ	3		876.0291379	2625.064014	0.000451244	3	N	338	362
O88342	Parental	QDAHR	LHHVSSLAWLDEHTLVTTSHDASVKEWTITY	-	3		1192.930632	3575.768495	0.000735798	3	N	575	606
O88342	Parental	TRPYR	LATGSDDNCAAFFEGPPFKFK	FTIGD	2	C9:+57.021	1160.041452	2318.067303	0.000622848	4	N	161	182
O88342	Parental	KDQKK	CFSIDNPGYEPEVVAVHPGGDTVAVGGTDGNVRVY	SILAS	3	C1:+57.021	1216.574254	3646.699361	0.000662267	2	N	437	472
O88342	Parental	YEIKK	VFASLPQVER	GVSKI	2		573.3198272	1144.624054	0.001264573	3	N	7	17
O88379	Parental	DADTK	DLTEALDEDADPTKSALSAVAALAAAWPQLHQGCSLK	SLDLD	4	C34:+57.021	966.7338671	3862.904268	0.001699387	1	N	504	541
O88379	Parental	QLELR	LRDFLLDIEDR	IYQGT	3		468.9214251	1403.740875	0.00091018	5	N	980	991
O88379	Parental	HKPNR	WCFYSSCAQLDQLIDALNSR	GHRES	2	C2:+57.021,C7:+57.021	1224.059618	2446.103637	0.000451244	2	N	893	913
O88379	Parental	GCSLK	SLDLDSCTLSEILR	LHILA	2	C7:+57.021	811.4090104	1620.802421	0.0025889	1	N	541	555
O88456	Exosome	GTAMR	ILGGVISAISEAAAQYNPEPPPPR	SHYSN	2		1224.150611	2446.285621	0.000637154	2	N	61	85
O88456	Exosome	GTAMR	ILGGVISAISEAAAQYNPEPPPPR	SHYSN	3		816.4363404	2446.285621	0.001162105	2	N	61	85
O88456	Exosome	FVQLA	GDDMEVSATELMNILNKVVTR	HPDLK	3	M4:+15.995,M12:+15.995	789.7231104	2366.145931	0.0025889	1	N	110	131
O88456	Exosome	MIIRR	YADESGNMDFDNFISCLVR	LDAMF	2	C16:+57.021	1126.983277	2251.950954	0.002145581	1	N	217	236
O88456	Exosome	PPPPR	SHYSNIEANESEEVR	QFRKL	2		882.3957085	1762.775817	0.000622848	1	N	85	100
O88456	Parental	GTAMR	ILGGVISAISEAAAQYNPEPPPPR	SHYSN	2		1224.150611	2446.285621	0.000451244	9	N	61	85
O88456	Parental	GTAMR	ILGGVISAISEAAAQYNPEPPPPR	SHYSN	3		816.4363404	2446.285621	0.000451244	6	N	61	85

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88487	Exosome	THSGR	EIAVGDSEGQIVIYDVGEQIAVPR	NDEWA	2		1279.161372	2556.307145	0.000451244	8	N	557	581
O88487	Exosome	THSGR	EIAVGDSEGQIVIYDVGEQIAVPR	NDEWA	3		853.1101816	2556.307145	0.000662267	2	N	557	581
O88487	Exosome	DGMGR	LDLWNLNNDTEVPTASISVEGNPALNR	VRWTH	2		1476.739038	2951.462476	0.000870037	1	N	522	549
O88487	Exosome	DGMGR	LDLWNLNNDTEVPTASISVEGNPALNR	VRWTH	3		984.8286255	2951.462476	0.001329271	1	N	522	549
O88487	Exosome	ARFGR	TLAEINANRADAEEEAATR	IPA-	3		682.3351739	2043.982122	0.000451244	1	N	590	609
O88487	Parental	THSGR	EIAVGDSEGQIVIYDVGEQIAVPR	NDEWA	2		1279.161372	2556.307145	0.000451244	9	N	557	581
O88520	Exosome	RSLAK	CSALEELNLENNNISTLPESLLSSLVK	LNSLT	3	C1:+57.021	996.5132724	2986.516417	0.000698008	3	N	305	332
O88520	Exosome	EHLPK	EIGNCTQITNLDLQHNDLLDLPDTIGNLSSLNR	LGLRY	3	C5:+57.021	1236.283251	3705.826352	0.000451244	10	N	255	288
O88520	Exosome	ENKIK	QLPAEIGELCNLITLDVAHNQLEHLPK	EIGNC	4	C10:+57.021	767.1580726	3064.60109	0.000735798	1	N	228	255
O88520	Parental	RSLAK	CSALEELNLENNNISTLPESLLSSLVK	LNSLT	3	C1:+57.021	996.5132724	2986.516417	0.000451244	1	N	305	332
O88520	Parental	EHLPK	EIGNCTQITNLDLQHNDLLDLPDTIGNLSSLNR	LGLRY	3	C5:+57.021	1236.283251	3705.826352	0.000451244	10	N	255	288
O88536	Parental	YSLER	ALSEDSGQTSDSSTSSTSPPADIELKAP	-	2		1389.644135	2777.27267	0.000451244	10	N	323	351
O88536	Parental	DFRER	FIHSLPYSLER	ALSED	3		454.5791107	1360.713932	0.000823681	3	N	312	323
O88536	Parental	YSLER	ALSEDSGQTSDSSTSSTSPPADIELK	AP-	2		1305.599196	2609.182792	0.000451244	10	N	323	349
O88544	Exosome	LSASK	LYNNITFEELGALLEIPAAK	AEKIA	2		1110.102066	2218.188533	0.000451244	36	N	314	334
O88544	Exosome	LSASK	LYNNITFEELGALLEIPAAK	AEKIA	3		740.4039776	2218.188533	0.000622848	7	N	314	334
O88544	Exosome	KIQPR	VISFEEQVASIR	QHLAS	2		689.3727881	1376.729976	0.000823681	3	N	95	107
O88544	Exosome	LVISR	QLLTDFCTHLPNLPDSTAK	EVYHF	3	C7:+57.021	724.3652628	2170.072388	0.000451244	9	N	63	82
O88544	Exosome	QILEK	AIQLSGTEQLEALK	AFVEA	2		750.9175598	1499.81952	0.000451244	6	N	32	46
O88544	Exosome	LKIAR	LYLEDDDPVQAEAYINR	ASLLQ	2		1012.484524	2022.953447	0.000451244	10	N	153	170
O88544	Exosome	PTWDK	QIQSLCFQVNNLLEK	ISQTA	2	C6:+57.021	917.4803014	1832.945003	0.000451244	4	N	372	387
O88544	Exosome	FKDER	CQQLAAYGILEK	MYLDR	2	C1:+57.021	697.3611348	1392.70667	0.000451244	2	N	254	266
O88544	Parental	LSASK	LYNNITFEELGALLEIPAAK	AEKIA	2		1110.102066	2218.188533	0.000451244	31	N	314	334
O88544	Parental	LSASK	LYNNITFEELGALLEIPAAK	AEKIA	3		740.4039776	2218.188533	0.000622848	1	N	314	334
O88544	Parental	HFETR	EALPTWDKQIQSLCFQVNNLLEK	ISQTA	3	C14:+57.021	925.4779452	2773.410436	0.00091018	1	N	364	387
O88544	Parental	LKIAR	LYLEDDDPVQAEAYINR	ASLLQ	2		1012.484524	2022.953447	0.000662267	1	N	153	170
O88544	Parental	LSASK	LYNNITFEELGALLEIPAAKAEK	IASQM	3		849.7955343	2546.363203	0.000662267	2	N	314	337
O88569	Exosome	FGDSR	GGGGNFGPGPGSNFR	GGSDG	2		689.3188785	1376.622157	0.000451244	27	N	213	228
O88569	Exosome	FGGSR	NMGGPYGGGNYGPGGSGGSGGYGGR	SRY-	2	M2:+15.995	1103.454338	2204.893076	0.000451244	7	N	325	350
O88569	Exosome	YGSGR	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	GGYGG	2		1248.02393	2494.03226	0.000451244	10	N	238	266
O88569	Exosome	SGKKR	GFGFVTFDDHDPVDK	IVLQK	2		848.3866238	1694.757648	0.000622848	3	N	153	168
O88569	Exosome	SGKKR	GFGFVTFDDHDPVDK	IVLQK	3		565.9270159	1694.757648	0.000451244	43	N	153	168
O88569	Exosome	KEQFR	KLFIGGLSFETTEESLR	NYYEQ	2		964.01272	1926.00984	0.000451244	4	N	21	38
O88569	Exosome	KEQFR	KLFIGGLSFETTEESLR	NYYEQ	3		643.01108	1926.00984	0.000451244	24	N	21	38
O88569	Exosome	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	2		1139.081665	2276.147731	0.000451244	17	N	153	173
O88569	Exosome	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	3		759.7237102	2276.147731	0.000451244	36	N	153	173
O88569	Exosome	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	4		570.0447327	2276.147731	0.000451244	3	N	153	173
O88569	Exosome	EHHLR	DYFEEYGKIDTIEIITDR	QSGKK	2		1110.539496	2219.063392	0.000622848	4	N	129	147
O88569	Exosome	EQFRK	LFIGGLSFETTEESLRNYYEQWGK	LTDCV	3		956.4682575	2866.381372	0.000622848	2	N	22	46
O88569	Exosome	VTVKK	LFVGGIKEDTEEHHLR	DYFEE	3		627.3274024	1878.958807	0.000451244	18	N	113	129
O88569	Exosome	VTVKK	LFVGGIKEDTEEHHLR	DYFEE	4		470.7475018	1878.958807	0.000870037	4	N	113	129
O88569	Exosome	EEYGK	IDTIEIITDR	QSGKK	2		594.8276821	1187.639764	0.000451244	34	N	137	147
O88569	Exosome	EQFRK	LFIGGLSFETTEESLR	NYYEQ	2		899.9652384	1797.914877	0.000451244	65	N	22	38
O88569	Exosome	YGPMK	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGR	SRY-	3	M10:+15.995	990.0857922	2967.233977	0.002981883	1	N	317	350
O88569	Exosome	FGDSR	GGGGNFGPGPGSNFRGGSDGYGSGR	GFGDG	2		1136.000258	2269.984916	0.0025889	1	N	213	238
O88569	Exosome	FGDSR	GGGGNFGPGPGSNFRGGSDGYGSGR	GFGDG	3		757.6694386	2269.984916	0.00091018	2	N	213	238
O88569	Parental	FGDSR	GGGGNFGPGPGSNFR	GGSDG	2		689.3188785	1376.622157	0.000451244	64	N	213	228
O88569	Parental	FGGSR	NMGGPYGGGNYGPGGSGGSGGYGGR	SRY-	2		1095.456838	2188.898076	0.000451244	11	N	325	350
O88569	Parental	YGSGR	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	GGYGG	2		1248.02393	2494.03226	0.000451244	103	N	238	266
O88569	Parental	YGSGR	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	GGYGG	3		832.3518866	2494.03226	0.000451244	11	N	238	266
O88569	Parental	SGKKR	GFGFVTFDDHDPVDK	IVLQK	2		848.3866238	1694.757648	0.001162105	1	N	153	168
O88569	Parental	SGKKR	GFGFVTFDDHDPVDK	IVLQK	3		565.9270159	1694.757648	0.000451244	52	N	153	168
O88569	Parental	KEQFR	KLFIGGLSFETTEESLR	NYYEQ	2		964.01272	1926.00984	0.000451244	17	N	21	38
O88569	Parental	KEQFR	KLFIGGLSFETTEESLR	NYYEQ	3		643.01108	1926.00984	0.000451244	29	N	21	38
O88569	Parental	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	2		1139.081665	2276.147731	0.000451244	38	N	153	173
O88569	Parental	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	3		759.7237102	2276.147731	0.000451244	40	N	153	173
O88569	Parental	SGKKR	GFGFVTFDDHDPVDKIVLQK	YHTIN	4		570.0447327	2276.147731	0.000451244	21	N	153	173
O88569	Parental	EHHLR	DYFEEYGKIDTIEIITDR	QSGKK	2		1110.539496	2219.063392	0.000451244	45	N	129	147
O88569	Parental	EHHLR	DYFEEYGKIDTIEIITDR	QSGKK	3		740.6955973	2219.063392	0.000451244	41	N	129	147
O88569	Parental	EQFRK	LFIGGLSFETTEESLRNYYEQWGK	LTDCV	2		1434.198486	2866.381372	0.000622848	4	N	22	46
O88569	Parental	EQFRK	LFIGGLSFETTEESLRNYYEQWGK	LTDCV	3		956.4682575	2866.381372	0.000451244	12	N	22	46
O88569	Parental	VTVKK	LFVGGIKEDTEEHHLR	DYFEE	2		940.4872037	1878.958807	0.000451244	4	N	113	129
O88569	Parental	VTVKK	LFVGGIKEDTEEHHLR	DYFEE	3		627.3274024	1878.958807	0.000451244	15	N	113	129
O88569	Parental	VTVKK	LFVGGIKEDTEEHHLR	DYFEE	4		470.7475018	1878.958807	0.000451244	8	N	113	129
O88569	Parental	EEYGK	IDTIEIITDR	QSGKK	2		594.8276821	1187.639764	0.000451244	31	N	137	147

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88569	Parental	KKRGF	GFVTFDDHDPVDKIVLQK	YHTIN	3		691.6937509	2072.057853	0.000637154	2	N	155	173
O88569	Parental	-MEK	TLETVPLER	KKREK	2		529.2985604	1056.581521	0.002453667	2	N	3	12
O88569	Parental	EQFRK	LFIGGLSFETTEESLR	NYYEQ	2		899.9652384	1797.914877	0.000451244	73	N	22	38
O88569	Parental	GFVTF	DDHDPVDKIVLQK	YHTIN	2		761.3995342	1520.783468	0.000451244	5	N	160	173
O88569	Parental	GFVTF	DDHDPVDKIVLQK	YHTIN	3		507.9356228	1520.783468	0.000451244	2	N	160	173
O88569	Parental	SGRGF	GDGYNGYGGGPGGGNFGGSPGYGGGR	GGYGG	2		1145.978991	2289.942382	0.002981883	1	N	240	266
O88569	Parental	YGSGR	GFGDGYNGYGGGPGGGNFGGSPGYGGGRG	GYGGG	2		1276.534662	2551.053724	0.001654178	1	N	238	267
O88569	Parental	FRKLF	IGGLSFETTEESLR	NYYEQ	2		769.8889993	1537.762399	0.000870037	1	N	24	38
O88593	Exosome	GHPVR	YVVISHTAGSFCNSPDSCEQQAR	NVQHY	2	C12:+57.021,C18:+57.021	1307.076528	2612.137456	0.000451244	98	N	42	65
O88593	Exosome	GHPVR	YVVISHTAGSFCNSPDSCEQQAR	NVQHY	3	C12:+57.021,C18:+57.021	871.7202854	2612.137456	0.000451244	160	N	42	65
O88593	Exosome	KRALR	AALNLLECGVSR	GFLRS	2	C8:+57.021	651.8456519	1301.675704	0.000451244	36	N	133	145
O88593	Exosome	KRALR	AALNLLECGVSR	GFLRS	3	C8:+57.021	434.8997013	1301.675704	0.000735798	1	N	133	145
O88593	Exosome	EQQAR	NVQHYHKNELGWCDVAYNFLIGEDGHVYEGR	GWNIK	4	C13:+57.021	930.6829745	3718.700698	0.000451244	7	N	65	96
O88593	Exosome	QHYHK	NELGWCDVAYNFLIGEDGHVYEGRG	WNIKG	3	C6:+57.021	957.4331757	2869.276127	0.000451244	25	N	72	97
O88593	Exosome	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	2	C6:+57.021	1407.135132	2812.254663	0.000451244	38	N	72	96
O88593	Exosome	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	3	C6:+57.021	938.4260211	2812.254663	0.000451244	72	N	72	96
O88593	Exosome	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	4	C6:+57.021	704.0714658	2812.254663	0.000823681	1	N	72	96
O88593	Exosome	VKGHR	DVQSTLSPGDQLYQVIQSWEHYRE	-	2		1439.686274	2877.356949	0.000451244	34	N	158	182
O88593	Exosome	VKGHR	DVQSTLSPGDQLYQVIQSWEHYRE	-	3		960.1267829	2877.356949	0.000451244	97	N	158	182
O88593	Exosome	VKGHR	DVQSTLSPGDQLYQVIQSWEHYR	E-	3		917.1125851	2748.314355	0.000451244	20	N	158	181
O88593	Exosome	HPVRY	VVISHTAGSFCNSPDSCEQQAR	NVQHY	3	C11:+57.021,C17:+57.021	817.3658425	2449.074128	0.000451244	5	N	43	65
O88593	Exosome	VKGHR	DVQSTLSPGDQLYQVIQSWEHY	RE-	2		1297.114422	2592.213244	0.000622848	3	N	158	180
O88593	Parental	GHPVR	YVVISHTAGSFCNSPDSCEQQAR	NVQHY	2	C12:+57.021,C18:+57.021	1307.076528	2612.137456	0.000451244	214	N	42	65
O88593	Parental	GHPVR	YVVISHTAGSFCNSPDSCEQQAR	NVQHY	3	C12:+57.021,C18:+57.021	871.7202854	2612.137456	0.000451244	343	N	42	65
O88593	Parental	ECSSR	LGHPVRYVVISHTAGSFCNSPDSCEQQAR	NVQHY	3	C18:+57.021,C24:+57.021	1091.515862	3271.524185	0.000451244	26	N	36	65
O88593	Parental	ECSSR	LGHPVRYVVISHTAGSFCNSPDSCEQQAR	NVQHY	4	C18:+57.021,C24:+57.021	818.8888463	3271.524185	0.000823681	3	N	36	65
O88593	Parental	KRALR	AALNLLECGVSR	GFLRS	2	C8:+57.021	651.8456519	1301.675704	0.000451244	100	N	133	145
O88593	Parental	KRALR	AALNLLECGVSR	GFLRS	3	C8:+57.021	434.8997013	1301.675704	0.000451244	15	N	133	145
O88593	Parental	EQQAR	NVQHYHKNELGWCDVAYNFLIGEDGHVYEGR	GWNIK	3	C13:+57.021	1240.574699	3718.700698	0.000451244	52	N	65	96
O88593	Parental	EQQAR	NVQHYHKNELGWCDVAYNFLIGEDGHVYEGR	GWNIK	4	C13:+57.021	930.6829745	3718.700698	0.000451244	41	N	65	96
O88593	Parental	QHYHK	NELGWCDVAYNFLIGEDGHVYEGRG	WNIKG	2	C6:+57.021	1435.645864	2869.276127	0.000451244	13	N	72	97
O88593	Parental	QHYHK	NELGWCDVAYNFLIGEDGHVYEGRG	WNIKG	3	C6:+57.021	957.4331757	2869.276127	0.000451244	29	N	72	97
O88593	Parental	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	2	C6:+57.021	1407.135132	2812.254663	0.000451244	61	N	72	96
O88593	Parental	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	3	C6:+57.021	938.4260211	2812.254663	0.000451244	881	N	72	96
O88593	Parental	QHYHK	NELGWCDVAYNFLIGEDGHVYEGR	GWNIK	4	C6:+57.021	704.0714658	2812.254663	0.000451244	3	N	72	96
O88593	Parental	VKGHR	DVQSTLSPGDQLYQVIQSWEHYRE	-	2		1439.686274	2877.356949	0.000451244	50	N	158	182
O88593	Parental	VKGHR	DVQSTLSPGDQLYQVIQSWEHYRE	-	3		960.1267829	2877.356949	0.000451244	401	N	158	182
O88593	Parental	VKGHR	DVQSTLSPGDQLYQVIQSWEHYRE	-	4		720.3470371	2877.356949	0.000451244	13	N	158	182
O88593	Parental	VKGHR	DVQSTLSPGDQLYQVIQSWEHYR	E-	3		917.1125851	2748.314355	0.000451244	17	N	158	181
O88593	Parental	QSTLS	PGDQLYQVIQSWEHYRE	-	2		1074.511407	2147.007214	0.000451244	10	N	165	182
O88593	Parental	QSTLS	PGDQLYQVIQSWEHYRE	-	3		716.6768714	2147.007214	0.000622848	3	N	165	182
O88593	Parental	VQSTL	SPGDQLYQVIQSWEHYRE	-	2		1118.027421	2234.039243	0.001871652	4	N	164	182
O88593	Parental	HPVRY	VVISHTAGSFCNSPDSCEQQAR	NVQHY	3	C11:+57.021,C17:+57.021	817.3658425	2449.074128	0.000451244	30	N	43	65
O88593	Parental	VKGHR	DVQSTLSPGDQLYQVIQSWEHY	RE-	2		1297.114422	2592.213244	0.000451244	23	N	158	180
O88593	Parental	VKGHR	DVQSTLSPGDQLYQVIQSWEHY	RE-	3		865.0788814	2592.213244	0.000451244	10	N	158	180
O88593	Parental	CDVAY	NFLIGEDGHVYEGR	GWNIK	2		803.3869582	1604.758316	0.000451244	16	N	82	96
O88593	Parental	HYHKN	ELGWCDVAYNFLIGEDGHVYEGR	GWNIK	3	C5:+57.021	900.4117119	2698.211736	0.000451244	12	N	73	96
O88593	Parental	QHYHK	NELGWCDVAYNFLIGEDGHVY	EGRGW	2	C6:+57.021	1236.052548	2470.089495	0.000451244	8	N	72	93
O88593	Parental	TAGSF	CNSPDSCEQQAR	NVQHY	2	C1:+57.021,C7:+57.021	726.2855982	1450.555596	0.002212458	1	N	53	65
O88593	Parental	GHRDV	QSTLSPGDQLYQVIQSWEHYRE	-	3		888.7616638	2663.261591	0.001264573	3	N	160	182
O88593	Parental	YHKNE	LGWCDVAYNFLIGEDGHVYEGR	GWNIK	3	C4:+57.021	857.3975142	2569.169143	0.000451244	1	N	74	96
O88593	Parental	GWNIK	GDHTGPIWNPMSIGITF	MGNFM	2	M11:+15.995	929.9438263	1857.872053	0.002080925	1	N	101	118
O88622	Exosome	PDMVK	IALCLPNICTQPIPLLK	QKMNH	2	C4:+57.021,C9:+57.021	982.5572662	1963.098932	0.000823681	1	N	592	609
O88622	Exosome	RELNK	AYCGFLRPGVPSENLSAVATGNWGCGAFGGDAR	LKALI	3	C3:+57.021,C25:+57.021	1138.86315	3413.56605	0.001943752	1	N	840	873
O88668	Exosome	LKISR	IWVLDYFGGPK	VVTPE	2		647.8456778	1293.675756	0.000823681	3	N	196	207
O88668	Parental	LKISR	IWVLDYFGGPK	VVTPE	2		647.8456778	1293.675756	0.001264573	6	N	196	207
O88668	Parental	PRVAR	FVTHVSDWGSLATISTIK	EVRGW	2		981.5207122	1961.025824	0.001162105	2	N	60	78
O88685	Exosome	NTQVK	VIAATNRVDILDPALLR	SGRLD	3		617.3673095	1849.078529	0.002296037	1	N	330	347
O88685	Exosome	VDAEK	LKPGDLVGVNKDSYLILETLPTEYDSR	VKAME	3		1012.53656	3034.58628	0.000451244	10	N	147	174
O88685	Exosome	FALAK	EKAPSIIFIDELDAIGTK	RFDSE	3		654.0266186	1959.056456	0.000451244	25	N	279	297
O88685	Exosome	KTSTR	QTYFLPVIGLVDAEK	LKPGD	2		846.9645101	1691.91342	0.000451244	20	N	132	147
O88685	Exosome	KTSTR	QTYFLPVIGLVDAEK	LKPGD	3		564.97894	1691.91342	0.000451244	10	N	132	147
O88685	Exosome	KTSTR	QTYFLPVIGLVDAEK	LKPGD	2	[0:-17.027	838.4510101	1674.88642	0.0007646	3	N	132	147
O88685	Exosome	IKVNK	TLPYLVSNVIELLDVDPNDQEEDGANIDLDSQR	KGKCA	3		1233.934436	3698.779908	0.000451244	16	N	87	120
O88685	Exosome	VGVNK	DSYLILETLPTEYDSR	VKAME	2		957.9707178	1913.925836	0.000451244	36	N	158	174

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88685	Parental	NTQVK	VIAATNRVDILDPALLR	SGRLD	3		617.3673095	1849.078529	0.000451244	10	N	330	347
O88685	Parental	VDAEK	LKPGDLVGVNKDSYLILETLPTEYDSR	VKAME	3		1012.53656	3034.58628	0.000451244	16	N	147	174
O88685	Parental	FALAK	EKAPSIIFIDELDAIGTK	RFDSE	2		980.5360279	1959.056456	0.000451244	7	N	279	297
O88685	Parental	FALAK	EKAPSIIFIDELDAIGTK	RFDSE	3		654.0266186	1959.056456	0.000451244	6	N	279	297
O88685	Parental	KTSTR	QTYFLPVIGLVDAEK	LKPGD	2		846.9645101	1691.91342	0.000622848	16	N	132	147
O88685	Parental	KTSTR	QTYFLPVIGLVDAEK	LKPGD	3		564.97894	1691.91342	0.000451244	4	N	132	147
O88685	Parental	IKVNK	TLPYLVSNVIELLDVDPNDQEEDGANIDLDSQR	KGKCA	3		1233.934436	3698.779908	0.000451244	13	N	87	120
O88685	Parental	IKVNK	TLPYLVSNVIELLDVDPNDQEEDGANIDLDSQR	KGKCA	4		925.7027769	3698.779908	0.001162105	1	N	87	120
O88685	Parental	VGVNK	DSYLILETLPTEYDSR	VKAME	2		957.9707178	1913.925836	0.000451244	19	N	158	174
O88685	Parental	AATNR	VDILDPALLR	SGRLD	2		562.8378528	1123.660106	0.002663018	2	N	337	347
O88712	Exosome	ALRAK	AFGFNVLFYDPYLSDGIER	ALGLQ	2		1112.042009	2222.068418	0.000451244	8	N	194	213
O88712	Exosome	NIDIK	SAGDLGIAVCNVPAASVEETADSTLCHILNLYR	RTTWL	3	C10:+57.021,C26:+57.021	1172.908314	3515.701541	0.000451244	11	N	108	141
O88712	Parental	ALRAK	AFGFNVLFYDPYLSDGIER	ALGLQ	2		1112.042009	2222.068418	0.000451244	14	N	194	213
O88712	Parental	NIDIK	SAGDLGIAVCNVPAASVEETADSTLCHILNLYR	RTTWL	3	C10:+57.021,C26:+57.021	1172.908314	3515.701541	0.000451244	15	N	108	141
O88746	Parental	NTSQR	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	LRSEL	3		1045.550981	3133.629542	0.000451244	29	N	188	219
O88746	Parental	NCGHR	FHVLVANQDFVENVLVR	TILPK	3		667.0306974	1998.068692	0.000451244	2	N	84	101
O88746	Parental	ADAFR	SSPDLTGVVAVYEDLR	RKGLE	2		860.9417633	1719.867927	0.00091018	4	N	129	145
O88746	Parental	IVHDK	VLNLIQSWADAFR	SSPDL	2		766.9151545	1531.814709	0.000451244	24	N	116	129
O88783	Exosome	VNVER	DIHSGLIGPLLICR	KGTLH	3	C13:+57.021	521.9610721	1562.859816	0.000451244	23	N	1698	1712
O88783	Exosome	TFTYK	WNILEFDEPTENDAQCLTRPYYSDVDVTR	DIASG	3	C16:+57.021	1182.875821	3545.604063	0.000451244	24	N	482	511
O88783	Exosome	VDVTR	DIASGLIGLLLICK	SRSLD	2	C13:+57.021	743.4393852	1484.86317	0.000451244	26	N	511	525
O88783	Exosome	VDVTR	DIASGLIGLLLICK	SRSLD	3	C13:+57.021	495.9621901	1484.86317	0.000451244	11	N	511	525
O88783	Exosome	RGVQR	VADIEQQAVFAVFDENKSWYIEDNINK	FCENP	3		1062.519569	3184.535307	0.001839721	1	N	536	563
O88783	Exosome	RGVQR	VADIEQQAVFAVFDENK	SWYIE	2		961.9788771	1921.942154	0.000451244	21	N	536	553
O88783	Exosome	AAQLR	QFYVAAQGILWNYHPEPTDPSLNSIPSFK	KIVYR	3		1107.219454	3318.634962	0.000451244	13	N	32	61
O88783	Exosome	KMFDK	QHVLLFAVFDESK	SRSQS	3		511.6089585	1531.803476	0.000870037	8	N	208	221
O88783	Exosome	RPTLR	LELQGCEVNGCSTPLGLEDGR	IQDKQ	2	C6:+57.021,C11:+57.021	1152.533433	2303.051267	0.001699387	1	N	2014	2035
O88783	Exosome	KEKPR	SSNSGLLGPTLYAEVGDVIK	VHFRN	2		1010.534017	2019.052433	0.000451244	11	N	78	98
O88783	Exosome	SSFKK	SWWGDYWEPSLAR	LNAQG	2		826.878769	1651.741938	0.000870037	2	N	2048	2061
O88783	Parental	VNVER	DIHSGLIGPLLICR	KGTLH	2	C13:+57.021	782.4377082	1562.859816	0.000451244	4	N	1698	1712
O88783	Parental	VNVER	DIHSGLIGPLLICR	KGTLH	3	C13:+57.021	521.9610721	1562.859816	0.000451244	30	N	1698	1712
O88783	Parental	TFTYK	WNILEFDEPTENDAQCLTRPYYSDVDVTR	DIASG	3	C16:+57.021	1182.875821	3545.604063	0.000451244	23	N	482	511
O88783	Parental	VDVTR	DIASGLIGLLLICK	SRSLD	2	C13:+57.021	743.4393852	1484.86317	0.000451244	54	N	511	525
O88783	Parental	VDVTR	DIASGLIGLLLICK	SRSLD	3	C13:+57.021	495.9621901	1484.86317	0.000451244	29	N	511	525
O88783	Parental	DDNQK	TSSPDLGQVSLSPDDNQK	TSSPD	2		944.4506808	1886.885762	0.000451244	19	N	1228	1246
O88783	Parental	RGVQR	VADIEQQAVFAVFDENKSWYIEDNINK	FCENP	3		1062.519569	3184.535307	0.000451244	4	N	536	563
O88783	Parental	RGVQR	VADIEQQAVFAVFDENK	SWYIE	2		961.9788771	1921.942154	0.000451244	4	N	536	553
O88783	Parental	AAQLR	QFYVAAQGILWNYHPEPTDPSLNSIPSFK	KIVYR	3		1107.219454	3318.634962	0.000451244	10	N	32	61
O88783	Parental	RPTLR	LELQGCEVNGCSTPLGLEDGR	IQDKQ	2	C6:+57.021,C11:+57.021	1152.533433	2303.051267	0.001162105	3	N	2014	2035
O88783	Parental	QVRFK	NLASRPYSLHAHGLSYEK	SSEGK	2		1022.024485	2042.033369	0.000823681	1	N	1621	1639
O88783	Parental	QVRFK	NLASRPYSLHAHGLSYEK	SSEGK	3		681.6855898	2042.033369	0.000451244	1	N	1621	1639
O88783	Parental	EDNQK	TSSPDLGQVPLSPDDNQK	TSSPD	2		949.4610485	1896.906497	0.000979378	2	N	1210	1228
O88842	Exosome	EKMHK	LLEVYEQLGGEEDIVNPANELIK	EGSIQ	2		1293.171406	2584.327211	0.000451244	5	N	346	369
O88842	Exosome	QCWLK	ALGTAVHGDTAGDRPGASQPQAPAGTDTP	-	3		906.1027487	2715.284846	0.001264573	1	N	704	733
O88842	Parental	KDAER	SLELISTAADHSNAAIR	KMEKM	3		590.3116409	1767.911523	0.000451244	2	N	322	339
O88842	Parental	EKMHK	LLEVYEQLGGEEDIVNPANELIK	EGSIQ	2		1293.171406	2584.327211	0.000451244	17	N	346	369
O88842	Parental	EPDPK	VTLFRPQEDVSLTQCSDPQK	LLHIA	3	C15:+57.021	783.3902481	2347.147344	0.00091018	2	N	133	153
O88842	Parental	QCWLK	ALGTAVHGDTAGDRPGASQPQAPAGTDTP	-	3		906.1027487	2715.284846	0.000451244	5	N	704	733
O88844	Exosome	LIKEK	LILPYVELDLHSYDLGIENR	DATND	3		791.4219198	2371.242359	0.000451244	20	N	29	49
O88844	Exosome	RMYQK	GQETSTNPIASIFAWSR	GLAHR	2		932.9635614	1863.911523	0.000451244	34	N	321	338
O88844	Exosome	GDQYR	ATDFVVPGPGKVEITYTPK	DGTQK	3		673.6986134	2018.07244	0.000451244	8	N	140	159
O88844	Exosome	KNIPR	LVTGWVKPIIIGR	HAYGD	3		484.6419339	1450.902402	0.001264573	7	N	119	132
O88844	Exosome	AQAMK	SEGGFIWACK	NYDGD	2	C9:+57.021	577.7688815	1153.522163	0.001943752	2	N	260	270
O88844	Exosome	SFFAK	ALEDVCIETIEAGFMTK	DLAAC	2	C6:+57.021,M15:+15.995	971.9607931	1941.905986	0.000451244	3	N	357	374
O88844	Exosome	AHRAK	LDNNTELSFFAK	ALEDV	2		699.8491458	1397.682692	0.000823681	1	N	345	357
O88844	Parental	LIKEK	LILPYVELDLHSYDLGIENR	DATND	3		791.4219198	2371.242359	0.000451244	3	N	29	49
O88844	Parental	RMYQK	GQETSTNPIASIFAWSR	GLAHR	2		932.9635614	1863.911523	0.000451244	11	N	321	338
O88844	Parental	GDQYR	ATDFVVPGPGKVEITYTPK	DGTQK	2		1010.04402	2018.07244	0.000823681	2	N	140	159
O88844	Parental	GDQYR	ATDFVVPGPGKVEITYTPK	DGTQK	3		673.6986134	2018.07244	0.000451244	4	N	140	159
O88879	Exosome	RKHPR	SLLILDDVWDPWVLK	AFDNQ	2		906.5012598	1810.98692	0.000451244	4	N	237	252
O88879	Exosome	IKECK	GSPLVVSLIGALLR	DFPNR	2		697.9406409	1393.865682	0.000823681	4	N	318	332
O88879	Exosome	DKTAK	IWSFDLLSPLHELK	GHNGC	3		566.6474133	1696.91884	0.000823681	6	N	1110	1124
O88879	Exosome	LIAGK	TGQIDYLPEAQVSCCCLSPHLEYVAFGDEDGAIK	IIELP	3	C14:+57.021,C15:+57.021,C16:+57.021	1281.583124	3841.725972	0.000622848	6	N	952	986
O88879	Exosome	HLLGR	QPFPNIVQLGLCEPETSEVYR	QAKLQ	2	C12:+57.021	1238.612772	2475.209945	0.001463592	3	N	557	578

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O88879	Exosome	INVKR	FFLSSEDPPEDVEVIVK	CCSWS	2		975.491286	1948.966972	0.000622848	1	N	785	802
O88879	Parental	RKHPR	SLLILDDVWDPWVLK	AFDNQ	2		906.5012598	1810.98692	0.000451244	13	N	237	252
O88879	Parental	DKTAK	IWSFDLLSPLHELK	GHNGC	3		566.6474133	1696.91884	0.000662267	7	N	1110	1124
O88879	Parental	LIAGK	TGQIDYLPEAQVSCCCLSPHLEYVAFGDEDGAIK	IIELP	3	C14:+57.021,C15:+57.021,C16:+57.021	1281.583124	3841.725972	0.000451244	6	N	952	986
O88879	Parental	HLLGR	QPFPNIVQLGLCEPETSEVYR	QAKLQ	2	C12:+57.021	1238.612772	2475.209945	0.000622848	5	N	557	578
O88947	Exosome	NKFQR	DTYDYDIAVLR	LKTPI	2		672.3280462	1342.640492	0.000622848	5	N	313	324
O88947	Exosome	RKLCR	LDNGDCDQFCREEQNSVVCSCASGYFLGNDGK	SCIST	3	C6:+57.021,C10:+57.021,C19:+57.021,C21:+57.021	1234.504614	3700.490441	0.000451244	28	N	130	162
O88947	Exosome	DQFCR	EEQNSVVCSCASGYFLGNDGK	SCIST	2	C8:+57.021,C10:+57.021	1160.994141	2319.972682	0.000451244	4	N	141	162
O88958	Exosome	AFEEK	IQAAGGIELFVGGIGPDGHIAFNEPGSSLVSR	TRVKT	3		1055.882953	3164.62546	0.000451244	16	N	124	156
O88958	Exosome	PGPDK	YFTLGLPTGSTPLGCYQK	LIEYY	2	C15:+57.021	1002.001067	2001.986533	0.000662267	4	N	33	51
O88958	Exosome	NNFFK	HIDIHPENTHILDGNAADLQAECDAFEEK	IQAAG	3	C23:+57.021	1101.50584	3301.494119	0.000451244	4	N	95	124
O88968	Exosome	PWMDR	LSSEQLNPSVFVGLR	LSSMQ	2		823.4495585	1644.883517	0.000451244	28	N	44	59
O88968	Exosome	WQLLR	APDTPLLQGIADYKPQDGETIELR	LVRW-	3		880.7892195	2639.344259	0.000451244	31	N	402	426
O88968	Exosome	SVTLK	VASALSPYEQTFFVFAGSSLEDVLK	LAQDG	2		1353.189599	2704.363597	0.000451244	26	N	338	363
O88968	Exosome	SVTLK	VASALSPYEQTFFVFAGSSLEDVLK	LAQDG	3		902.4623323	2704.363597	0.000451244	22	N	338	363
O88968	Exosome	EDVLK	LAQDGGGFTYGTQASLSGPYLTSVLGK	DAGDR	2		1344.679929	2687.344259	0.000451244	18	N	363	390
O88968	Exosome	EDVLK	LAQDGGGFTYGTQASLSGPYLTSVLGK	DAGDR	3		896.7892195	2687.344259	0.001943752	1	N	363	390
O88968	Exosome	SCQPK	LSGGSLALYLLALR	ANCEF	2		723.9380983	1445.860597	0.000451244	26	N	99	113
O88968	Exosome	TACIK	AGTSLLLSLQDGAFQNPLMISQLLPILNHK	TYLDL	3		1078.264118	3231.768954	0.000823681	2	N	272	302
O88968	Exosome	ILNHK	TYLDLIFPDCQASR	VMLVP	2	C10:+57.021	849.9117202	1697.80784	0.000823681	5	N	302	316
O88968	Parental	PWMDR	LSSEQLNPSVFVGLR	LSSMQ	2		823.4495585	1644.883517	0.000451244	24	N	44	59
O88968	Parental	WQLLR	APDTPLLQGIADYKPQDGETIELR	LVRW-	2		1320.679929	2639.344259	0.000451244	1	N	402	426
O88968	Parental	WQLLR	APDTPLLQGIADYKPQDGETIELR	LVRW-	3		880.7892195	2639.344259	0.000451244	13	N	402	426
O88968	Parental	SVTLK	VASALSPYEQTFFVFAGSSLEDVLK	LAQDG	2		1353.189599	2704.363597	0.000451244	31	N	338	363
O88968	Parental	SVTLK	VASALSPYEQTFFVFAGSSLEDVLK	LAQDG	3		902.4623323	2704.363597	0.000451244	29	N	338	363
O88968	Parental	EDVLK	LAQDGGGFTYGTQASLSGPYLTSVLGK	DAGDR	2		1344.679929	2687.344259	0.000451244	16	N	363	390
O88968	Parental	EDVLK	LAQDGGGFTYGTQASLSGPYLTSVLGK	DAGDR	3		896.7892195	2687.344259	0.000451244	2	N	363	390
O88968	Parental	SCQPK	LSGGSLALYLLALR	ANCEF	2		723.9380983	1445.860597	0.000451244	10	N	99	113
O88968	Parental	SCQPK	LSGGSLALYLLALR	ANCEF	3		482.9613322	1445.860597	0.000451244	1	N	99	113
O88968	Parental	TACIK	AGTSLLLSLQDGAFQNPLMISQLLPILNHK	TYLDL	3		1078.264118	3231.768954	0.000823681	1	N	272	302
O88968	Parental	ILNHK	TYLDLIFPDCQASR	VMLVP	2	C10:+57.021	849.9117202	1697.80784	0.001654178	4	N	302	316
O88968	Parental	SVLGK	DAGDREYWQLLR	APDTP	3		507.9201956	1520.737187	0.000823681	1	N	390	402
O89023	Exosome	GTSFK	NPFLITDEVVDYISGGGFSNVFPRPPYQEEAVAQFLK	SSSHL	3		1382.028782	4143.062946	0.000451244	21	N	393	430
O89023	Exosome	GTSFK	NPFLITDEVVDYISGGGFSNVFPRPPYQEEAVAQFLK	SSSHL	4		1036.773537	4143.062946	0.0007646	2	N	393	430
O89023	Exosome	KAAAR	GLTLLFASGDTGAGCWSVSGR	HKFRP	2	C15:+57.021	1056.512861	2111.010122	0.001162105	1	N	349	370
O89023	Exosome	DVAAL	SDGYWVVSNMVPIPWVSGTSASTPVFGGILSLINEHR	ILNGR	3	M10:+15.995	1330.335469	3987.983008	0.000698008	2	N	454	491
O89023	Parental	GTSFK	NPFLITDEVVDYISGGGFSNVFPRPPYQEEAVAQFLK	SSSHL	3		1382.028782	4143.062946	0.000451244	34	N	393	430
O89023	Parental	GTSFK	NPFLITDEVVDYISGGGFSNVFPRPPYQEEAVAQFLK	SSSHL	4		1036.773537	4143.062946	0.000451244	23	N	393	430
O89051	Exosome	VMPPK	NLLELLINIK	AGTYL	2		591.876978	1181.738356	0.000622848	21	N	178	188
O89051	Exosome	EENIK	IFEEDAVEFISVPVPEFADSDPANIVHDFNKK	LTAYL	3		1206.926664	3617.756593	0.002296037	1	N	120	152
O89051	Exosome	EENIK	IFEEDAVEFISVPVPEFADSDPANIVHDFNKK	LTAYL	4		905.4469483	3617.756593	0.000735798	1	N	120	152
O89051	Exosome	VITDR	IENVDNLGFFIYR	LCHDK	2		800.4124446	1598.809289	0.000823681	1	N	208	221
O89051	Parental	VMPPK	NLLELLINIK	AGTYL	2		591.876978	1181.738356	0.001162105	4	N	178	188
O89053	Exosome	YEDVR	VSQTTWDSGFCAVNPK	FMALI	2	C11:+57.021	898.9175339	1795.819468	0.000451244	117	N	29	45
O89053	Exosome	WLGGR	DAGPLLISLK	DGYVP	2		513.8138463	1025.612093	0.000451244	60	N	383	393
O89053	Exosome	MTVPR	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1058.519569	3172.535307	0.000451244	150	N	354	383
O89053	Exosome	MTVPR	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	4		794.1416268	3172.535307	0.000451244	10	N	354	383
O89053	Exosome	AVNPK	FMALICEASGGGAFLVLPLGK	TGRVD	2	C6:+57.021	1076.07097	2150.126339	0.000451244	23	N	45	66
O89053	Exosome	AVNPK	FMALICEASGGGAFLVLPLGK	TGRVD	3	C6:+57.021	717.7165798	2150.126339	0.000451244	1	N	45	66
O89053	Exosome	AVNPK	FMALICEASGGGAFLVLPLGK	TGRVD	2	M2:+15.995,C6:+57.021	1084.06847	2166.121339	0.001943752	2	N	45	66
O89053	Exosome	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C32:+57.021	1282.976765	3845.906894	0.000451244	102	N	253	287
O89053	Exosome	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	4	C32:+57.021	962.4845235	3845.906894	0.000451244	30	N	253	287
O89053	Exosome	DSSIR	YFEITSEAPF	LHYLS	2		602.282576	1202.549552	0.000622848	9	N	293	303
O89053	Exosome	DSSIR	YFEITSEAPFLHYLSMFSSK	ESQRG	2		1199.077735	2396.139869	0.000823681	3	N	293	313
O89053	Exosome	DSSIR	YFEITSEAPFLHYLSMFSSK	ESQRG	3		799.7210897	2396.139869	0.000451244	25	N	293	313
O89053	Exosome	DSSIR	YFEITSEAPFLHYLSMFSSK	ESQRG	2	M16:+15.995	1207.075235	2412.134869	0.000451244	3	N	293	313
O89053	Exosome	DSSIR	YFEITSEAPFLHYLSMFSSK	ESQRG	3	M16:+15.995	805.0527564	2412.134869	0.000451244	17	N	293	313
O89053	Exosome	SSKFR	HVFGQPAKADQCYEDVR	VSQTT	3	C12:+57.021	673.9832642	2018.926393	0.000451244	6	N	12	29
O89053	Exosome	QEDLY	PPTAGPDPALTAEEWLGGR	DAGPL	2		967.9844938	1933.953388	0.000451244	3	N	364	383
O89053	Exosome	SGVLL	PFFDPDTNIVYLCGK	GDSSI	2	C13:+57.021	893.4297458	1784.843892	0.000451244	1	N	272	287
O89053	Exosome	KLQER	LDRLEETVQAK	-	2		651.357138	1300.698676	0.000451244	2	N	450	461
O89053	Exosome	KLQER	LDRLEETVQAK	-	3		434.5740253	1300.698676	0.000451244	4	N	450	461
O89053	Exosome	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	2		1292.122247	2582.228894	0.000451244	38	N	359	383

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O89053	Exosome	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		861.7507648	2582.228894	0.000451244	35	N	359	383
O89053	Exosome	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	2	Q1:-17.027	1283.608747	2565.201894	0.000662267	2	N	359	383
O89053	Exosome	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3	Q1:-17.027	856.0750981	2565.201894	0.002374549	1	N	359	383
O89053	Exosome	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	2	[0:-17.027	1283.608747	2565.201894	0.000823681	3	N	359	383
O89053	Exosome	LEEPL	SLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C26:+57.021	1043.521768	3127.541904	0.000451244	15	N	259	287
O89053	Exosome	EPLSL	QELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	2	C24:+57.021	1464.720706	2927.425811	0.000622848	2	N	261	287
O89053	Exosome	EPLSL	QELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C24:+57.021	976.8164037	2927.425811	0.000451244	7	N	261	287
O89053	Exosome	EPLSL	QELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	2	Q1:-17.027,C24:+57.021	1456.207206	2910.398811	0.002080925	1	N	261	287
O89053	Exosome	EPLSL	QELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	Q1:-17.027,C24:+57.021	971.1407371	2910.398811	0.000662267	6	N	261	287
O89053	Exosome	SSGVL	LPFFDPDTNIVYLCGK	GDSSI	2	C14:+57.021	949.9717779	1897.927956	0.000451244	3	N	271	287
O89053	Exosome	SARRR	ATPEPSGTPSSDTVSRLEEDVR	NLNAI	2		1165.55948	2329.103359	0.001763695	1	N	416	438
O89053	Exosome	SARRR	ATPEPSGTPSSDTVSRLEEDVR	NLNAI	3		777.3755864	2329.103359	0.000870037	7	N	416	438
O89053	Exosome	TVPRK	SDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1015.821248	3044.440344	0.000451244	18	N	355	383
O89053	Exosome	VPRKS	DLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		986.8105718	2957.408316	0.00307782	1	N	356	383
O89053	Exosome	VLLPF	FDPDTNIVYLCGK	GDSSI	2	C11:+57.021	771.3691568	1540.722714	0.001839721	3	N	274	287
O89053	Exosome	EEPLS	LQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C25:+57.021	1014.511092	3040.509875	0.000451244	12	N	260	287
O89053	Exosome	KFMAL	ICEASGGGAFLVLPLGK	TGRVD	2	C2:+57.021	844.9559308	1687.896262	0.000451244	4	N	49	66
O89053	Exosome	DSSIR	YFEITSEAPFLHYL	SMFSS	2		865.4277604	1728.839921	0.000823681	4	N	293	307
O89053	Exosome	GAAVL	TLGPDVHPDTIYSVDWSR	DGALI	2		1029.500508	2056.985416	0.001162105	1	N	168	186
O89053	Exosome	DNVIL	VWDVGTGAAVLTLGPDVHPDTIYSVDWSR	DGALI	3		1042.856404	3125.545812	0.000451244	2	N	157	186
O89053	Exosome	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLC	GKGDS	3	C32:+57.021	1221.271289	3660.790467	0.000637154	1	N	253	285
O89053	Exosome	DSSIR	YFEITSEAPFLHY	LSMFS	2		808.8857283	1615.755857	0.000451244	6	N	293	306
O89053	Exosome	LWDTK	HLEEPLSLQELDTSSGVLLPF	FDPDT	2		1162.60517	2323.194741	0.002080925	1	N	253	274
O89053	Exosome	LWDTK	HLEEPLSLQELDTSSGVLLPF	FDPDT	3		775.4060468	2323.194741	0.000451244	3	N	253	274
O89053	Exosome	DTVSR	LEEDVRNLNAIVQK	LQERL	3		547.6375769	1639.889331	0.000622848	1	N	432	446
O89053	Exosome	YPPTA	GPDPALTAEEWLGGR	DAGPL	2		784.8893337	1567.763067	0.000622848	3	N	368	383
O89053	Exosome	LYPPT	AGPDPALTAEEWLGGR	DAGPL	2		820.4078906	1638.800181	0.000998612	2	N	367	383
O89053	Parental	YEDVR	VSQTTWDSGFCAVNPK	FMALI	2	C11:+57.021	898.9175339	1795.819468	0.000451244	60	N	29	45
O89053	Parental	GQPAK	ADQCYEDVRVSQTTWDSGFCAVNPK	FMALI	2	C4:+57.021,C20:+57.021	1467.145139	2932.274678	0.000451244	6	N	20	45
O89053	Parental	GQPAK	ADQCYEDVRVSQTTWDSGFCAVNPK	FMALI	3	C4:+57.021,C20:+57.021	978.4326927	2932.274678	0.000451244	14	N	20	45
O89053	Parental	WLGGR	DAGPLLISLK	DGYVP	2		513.8138463	1025.612093	0.000622848	27	N	383	393
O89053	Parental	MTVPR	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1058.519569	3172.535307	0.000451244	155	N	354	383
O89053	Parental	MTVPR	KSDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	4		794.1416268	3172.535307	0.000823681	6	N	354	383
O89053	Parental	AVNPK	FMALICEASGGGAFLVLPLGK	TGRVD	2	C6:+57.021	1076.07097	2150.126339	0.001329271	2	N	45	66
O89053	Parental	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIR	YFEIT	4	C32:+57.021	1116.308933	4461.204533	0.001162105	6	N	253	293
O89053	Parental	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	3	C32:+57.021	1282.976765	3845.906894	0.000451244	112	N	253	287
O89053	Parental	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK	GDSSI	4	C32:+57.021	962.4845235	3845.906894	0.000451244	23	N	253	287
O89053	Parental	WLGGR	DAGPLLISLKDGYVPPK	SRELR	3		595.0053777	1781.992733	0.000451244	9	N	383	400
O89053	Parental	DSSIR	YFEITSEAPF	LHYLS	2		602.282576	1202.549552	0.000622848	14	N	293	303
O89053	Parental	DSSIR	YFEITSEAPFLHYLSMFSSK	ESQRG	3		799.7210897	2396.139869	0.000451244	11	N	293	313
O89053	Parental	SSKFR	HVFGQPAKADQCYEDVR	VSQTT	4	C12:+57.021	505.7393982	2018.926393	0.001162105	1	N	12	29
O89053	Parental	QEDLY	PPTAGPDPALTAEEWLGGR	DAGPL	2		967.9844938	1933.953388	0.001839721	1	N	364	383
O89053	Parental	SGVLL	PFFDPDTNIVYLCGK	GDSSI	2	C13:+57.021	893.4297458	1784.843892	0.000451244	8	N	272	287
O89053	Parental	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	2		1292.122247	2582.228894	0.000451244	28	N	359	383
O89053	Parental	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		861.7507648	2582.228894	0.000451244	25	N	359	383
O89053	Parental	KSDLF	QEDLYPPTAGPDPALTAEEWLGGR	DAGPL	2	Q1:-17.027	1283.608747	2565.201894	0.00091018	2	N	359	383
O89053	Parental	SSGVL	LPFFDPDTNIVYLCGK	GDSSI	2	C14:+57.021	949.9717779	1897.927956	0.000823681	1	N	271	287
O89053	Parental	SARRR	ATPEPSGTPSSDTVSRLEEDVR	NLNAI	2		1165.55948	2329.103359	0.000823681	2	N	416	438
O89053	Parental	TVPRK	SDLFQEDLYPPTAGPDPALTAEEWLGGR	DAGPL	3		1015.821248	3044.440344	0.000451244	5	N	355	383
O89053	Parental	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVY	LCGKG	3		1130.233206	3387.676218	0.000451244	10	N	253	283
O89053	Parental	KSDLF	QEDLYPPTAGPDPALTAEEWLGGRDAGPLLISLK	DGYVP	3		1197.617942	3589.830427	0.000823681	1	N	359	393
O89053	Parental	QEDLY	PPTAGPDPALTAEEWLGGRDAGPLLISLK	DGYVP	3		981.5261068	2941.55492	0.000451244	1	N	364	393
O89053	Parental	VLLPF	FDPDTNIVYLCGK	GDSSI	2	C11:+57.021	771.3691568	1540.722714	0.000622848	7	N	274	287
O89053	Parental	DSSIR	YFEITSEAPFLHY	LSMFS	2		808.8857283	1615.755857	0.0025889	1	N	293	306
O89053	Parental	LWDTK	HLEEPLSLQELDTSSGVLLPF	FDPDT	3		775.4060468	2323.194741	0.000622848	1	N	253	274
O89053	Parental	LWDTK	HLEEPLSLQELDTSSGVLLPFFDPDTNIVYL	CGKGD	3		1167.927894	3500.760282	0.000979378	1	N	253	284
O89079	Exosome	LFDVK	NAFYIGSYQQCINEAQR	VKLSS	2	C11:+57.021	1031.476279	2060.936957	0.000451244	31	N	23	40
O89079	Exosome	VGGEK	LQEAYYIFQELADK	CSPTL	2		865.9359496	1729.856299	0.000451244	12	N	197	211
O89079	Exosome	VGGEK	LQEAYYIFQELADK	CSPTL	3		577.6265664	1729.856299	0.000662267	3	N	197	211
O89079	Exosome	-M	APPVPGAVSGGSGEVDELFDVK	NAFYI	2		1064.034381	2126.053161	0.000451244	7	N	1	23
O89079	Parental	LFDVK	NAFYIGSYQQCINEAQR	VKLSS	2	C11:+57.021	1031.476279	2060.936957	0.000451244	52	N	23	40
O89079	Parental	REMSR	SVDVTNTTFLLMAASIYFHDQNPDAALR	TLHQG	3		1037.513761	3109.517884	0.000451244	1	N	110	138
O89079	Parental	VGGEK	LQEAYYIFQELADK	CSPTL	2		865.9359496	1729.856299	0.000451244	10	N	197	211
O89079	Parental	-M	APPVPGAVSGGSGEVDELFDVK	NAFYI	2		1064.034381	2126.053161	0.000451244	6	N	1	23
O89079	Parental	LAQRK	YGVVLDEIKPSSAPELQAVR	MFAEY	3		724.3955936	2170.163381	0.000662267	7	N	65	85

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
O89079	Parental	YLAQR	KYGVVLDEIKPSSAPELQAVR	MFAEY	3		767.0939146	2298.258344	0.000451244	3	N	64	85
O89086	Exosome	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVKDR	ETQRS	3		1255.964001	3764.868603	0.000451244	7	N	7	41
O89086	Exosome	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVKDR	ETQRS	4		942.2249509	3764.868603	0.000451244	6	N	7	41
O89086	Exosome	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	3		1165.587983	3493.740549	0.000451244	34	N	7	39
O89086	Exosome	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	4		874.4429373	3493.740549	0.000451244	9	N	7	39
O89086	Parental	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVKDR	ETQRS	3		1255.964001	3764.868603	0.000451244	15	N	7	41
O89086	Parental	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVKDR	ETQRS	4		942.2249509	3764.868603	0.000451244	16	N	7	41
O89086	Parental	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	3		1165.587983	3493.740549	0.000451244	104	N	7	39
O89086	Parental	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	4		874.4429373	3493.740549	0.000622848	5	N	7	39
O89086	Parental	SEEGK	LFVGGLNFNTDEQALEDHFSSFGPISEVVVV	KDRET	3		1122.889662	3365.645586	0.000451244	2	N	7	38
O89086	Parental	EGKLF	VGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	3		1078.87049	3233.588071	0.000451244	10	N	9	39
O89086	Parental	EGKLF	VGGLNFNTDEQALEDHFSSFGPISEVVVVK	DRETQ	4		809.4048178	3233.588071	0.000622848	2	N	9	39
P00375	Exosome	LGKYK	LLPEYPGVLSEVQEEK	GIKYK	2		915.4807213	1828.945843	0.000622848	5	N	158	174
P00375	Exosome	LFVTR	IMQEFESDTFFPEIDLGK	YKLLP	2		1073.506611	2144.997621	0.000622848	1	N	138	156
P00405	Parental	ELPIR	MLISSEDVLHSWAVPSLGLK	TDAIP	2		1091.582987	2181.150374	0.000451244	5	N	151	171
P00405	Parental	ELPIR	MLISSEDVLHSWAVPSLGLK	TDAIP	3		728.0579247	2181.150374	0.000451244	27	N	151	171
P00405	Parental	LPIRM	LISSEDVLHSWAVPSLGLK	TDAIP	3		684.3777628	2050.109888	0.000979378	2	N	152	171
P00493	Exosome	-MPTR	SPSVVISDDEPGYDLDLFCIPNHYAEDLEK	VFIPH	3	C19:+57.021	1146.529539	3436.565218	0.000451244	39	N	4	34
P00493	Exosome	TLTGK	NVLIVEDIIDTGK	TMQTL	2		714.9013784	1427.787157	0.000451244	21	N	128	141
P00493	Exosome	EIPDK	FVVGYALDYNEYFR	DLNHV	2		878.4230094	1754.830419	0.000870037	1	N	186	200
P00493	Exosome	KGGYK	FFADLLDYIK	ALNRN	2		622.8322361	1243.648872	0.000451244	19	N	73	83
P00493	Exosome	NEYFR	DLNHVCVISETGK	AKYKA	3	C6:+57.021	491.2455372	1470.713212	0.000451244	5	N	200	213
P00493	Exosome	KRTSR	SVGYRPDFVGFEIPDKFVVGY	ALDYN	3		797.7393603	2390.194681	0.000622848	7	N	170	191
P00493	Exosome	KRTSR	SVGYRPDFVGFEIPDKFVVGYALDYNEYFR	DLNHV	4		891.4389263	3561.724505	0.001654178	1	N	170	200
P00493	Parental	-MPTR	SPSVVISDDEPGYDLDLFCIPNHYAEDLEK	VFIPH	3	C19:+57.021	1146.529539	3436.565218	0.000451244	35	N	4	34
P00493	Parental	LCVLK	GGYKFFADLLDYIK	ALNRN	3		550.6244972	1648.850091	0.001352548	4	N	69	83
P00493	Parental	TLTGK	NVLIVEDIIDTGK	TMQTL	2		714.9013784	1427.787157	0.001463592	3	N	128	141
P00493	Parental	KGGYK	FFADLLDYIK	ALNRN	2		622.8322361	1243.648872	0.000451244	3	N	73	83
P00493	Parental	-M	PTRSPSVVISDDEPGYDLDLFCIPNHYAEDLEK	VFIPH	4	C22:+57.021	948.699493	3790.766772	0.000451244	2	N	1	34
P00493	Parental	KRTSR	SVGYRPDFVGFEIPDKF	VVGYA	3		658.3321535	1971.97306	0.002884417	1	N	170	187
P00493	Parental	-MPTR	SPSVVISDDEPGYDLDLFCIPNHY	AEDLE	2	C19:+57.021	1376.626274	2751.236948	0.000451244	3	N	4	28
P01027	Exosome	GNLLR	SEETKQNEAFSLTAK	GKGRG	2		841.9157455	1681.815891	0.000451244	7	N	1320	1335
P01027	Exosome	GNLLR	SEETKQNEAFSLTAK	GKGRG	3		561.613097	1681.815891	0.000451244	16	N	1320	1335
P01027	Exosome	LQEAR	DICEGQVNSLPGSINK	AGEYI	2	C3:+57.021	865.9228163	1729.830033	0.000451244	69	N	1155	1171
P01027	Exosome	PGSVK	VYSYYNLEESCTR	FYHPE	2	C11:+57.021	842.3698852	1682.72417	0.000451244	75	N	1478	1491
P01027	Exosome	LDPEK	LGQGGVQKVDVPAADLSDQVPDTDSETR	IILQG	3		966.4761404	2896.405021	0.000451244	16	N	951	979
P01027	Exosome	GGVQK	VDVPAADLSDQVPDTDSETR	IILQG	2		1065.495817	2128.976033	0.000451244	89	N	959	979
P01027	Exosome	GGVQK	VDVPAADLSDQVPDTDSETR	IILQG	3		710.6664778	2128.976033	0.001162105	2	N	959	979
P01027	Exosome	IPSFR	LVAYYTLIGASGQR	EVVAD	2		756.4149873	1510.814375	0.000451244	18	N	530	544
P01027	Exosome	IPSFR	LVAYYTLIGASGQR	EVVAD	3		504.6125915	1510.814375	0.000451244	33	N	530	544
P01027	Exosome	FLYGK	NVDGTAFVIFGVQDGDKK	ISLAH	2		955.4868693	1908.958139	0.000451244	24	N	264	282
P01027	Exosome	FLYGK	NVDGTAFVIFGVQDGDKK	ISLAH	3		637.3271796	1908.958139	0.001229886	2	N	264	282
P01027	Exosome	KIPPK	SSVAVPYVIVPLK	IGQQE	2		686.4164673	1370.817335	0.000451244	26	N	891	904
P01027	Exosome	LGLAR	SELEEDIIPEEDIISR	SHFPQ	2		943.9656324	1885.915665	0.000451244	24	N	748	764
P01027	Exosome	ASGQR	EVVADSVWVDVKDSCIGTLVVK	GDPRD	3	C15:+57.021	806.758049	2417.250747	0.000451244	12	N	544	566
P01027	Exosome	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLKR	QVLTS	3		1118.247738	3351.719814	0.000451244	13	N	37	67
P01027	Exosome	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLKR	QVLTS	4		838.9377534	3351.719814	0.000451244	29	N	37	67
P01027	Exosome	SFEVR	VEPTETFYYIDDPNGLEVSIIAK	FLYGK	2		1307.152682	2612.289763	0.000451244	46	N	236	259
P01027	Exosome	SFEVR	VEPTETFYYIDDPNGLEVSIIAK	FLYGK	3		871.7710544	2612.289763	0.000451244	30	N	236	259
P01027	Exosome	LKAGR	QVREPGQDLVVLSLPITPEFIPSFR	LVAYY	3		946.5240375	2836.548713	0.000451244	33	N	505	530
P01027	Exosome	GRQVR	EPGQDLVVLSLPITPEFIPSFR	LVAYY	2		1227.668105	2453.32061	0.000451244	49	N	508	530
P01027	Exosome	GRQVR	EPGQDLVVLSLPITPEFIPSFR	LVAYY	3		818.7813366	2453.32061	0.000451244	45	N	508	530
P01027	Exosome	FRNAK	EADVSLTAFVLIALQEAR	DICEG	2		973.5338196	1945.052039	0.000451244	46	N	1137	1155
P01027	Exosome	FRNAK	EADVSLTAFVLIALQEAR	DICEG	3		649.3584797	1945.052039	0.000451244	11	N	1137	1155
P01027	Exosome	FRNAK	EADVSLTAFVLIALQEARDICEGQVNSLPGSINK	AGEYI	3	C21:+57.021	1219.964971	3656.871512	0.000451244	1	N	1137	1171
P01027	Exosome	TAKDR	NRWEEPDQQLYNVEATSYALLALLLLK	DFDSV	3		1064.231471	3189.671013	0.000451244	19	N	1217	1244
P01027	Exosome	IPVKR	DILSSNNQHGILPLSWNIPELVNMGQWK	IRAFY	3		1068.548917	3202.623352	0.000451244	15	N	178	206
P01027	Exosome	IPVKR	DILSSNNQHGILPLSWNIPELVNMGQWK	IRAFY	3	M24:+15.995	1073.880584	3218.618352	0.000451244	36	N	178	206
P01027	Exosome	KDRNR	WEEPDQQLYNVEATSYALLALLLLKDFDSVPPVVR	WLNEQ	3		1344.705528	4031.093184	0.000451244	4	N	1219	1254
P01027	Exosome	MRINK	TVAIHTLDPEKLGQGGVQK	VDVPA	2		996.0501681	1990.084736	0.000451244	11	N	940	959
P01027	Exosome	MRINK	TVAIHTLDPEKLGQGGVQK	VDVPA	3		664.3693788	1990.084736	0.000451244	4	N	940	959
P01027	Exosome	YIIGK	DTWVEHWPEAEECQDQKYQK	QCEEL	3	C13:+57.021	869.3803003	2605.117501	0.000451244	10	N	1624	1644
P01027	Exosome	IQTDK	TIYTPGSTVLYR	IFTVD	2		685.8698813	1369.724163	0.000451244	28	N	137	149
P01027	Exosome	LSDKK	GICVADPYEIR	VMQDF	2	C3:+57.021	646.8191028	1291.622606	0.000451244	12	N	813	824
P01027	Exosome	HSLTR	VVIEDGVGDAVLTR	KVLME	2		721.8966274	1441.777655	0.000451244	40	N	291	305

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01027	Exosome	MRINK	TVAIHTLDPEK	LGQGG	2		612.3356743	1222.655749	0.000451244	8	N	940	951
P01027	Exosome	ENCIK	AFIDCCNHITK	LREQH	2	C5:+57.021,C6:+57.021	689.8158058	1377.616012	0.000451244	5	N	722	733
P01027	Exosome	IYLEK	ISHTEEDCLTFK	VHQYF	2	C8:+57.021	740.343139	1478.670678	0.000451244	7	N	1450	1462
P01027	Exosome	IYLEK	ISHTEEDCLTFK	VHQYF	3	C8:+57.021	493.898026	1478.670678	0.000451244	5	N	1450	1462
P01027	Exosome	KGKGR	GTLSVVAVYHAK	LKSKV	2		622.8540342	1243.692468	0.00091018	4	N	1339	1351
P01027	Exosome	VRLDK	ACEPGVDYVYK	TELTN	2	C2:+57.021	650.797836	1299.580072	0.000451244	16	N	1535	1546
P01027	Exosome	WVDVK	DSCIGTLVVK	GDPRD	2	C3:+57.021	546.2921895	1090.568779	0.000451244	15	N	556	566
P01027	Exosome	LPVGK	TVVILIETPDGIPVKR	DILSS	2		875.5278089	1749.040018	0.000451244	21	N	162	178
P01027	Exosome	LPVGK	TVVILIETPDGIPVKR	DILSS	3		584.0211393	1749.040018	0.000451244	26	N	162	178
P01027	Exosome	APDTK	DLELLASGVDR	YISKY	2		594.3174815	1186.619363	0.000451244	31	N	1416	1427
P01027	Exosome	KEGHK	YVTVVANFGETVVEK	AVMVS	2		827.9384923	1653.861385	0.000451244	13	N	105	120
P01027	Exosome	TVLYR	IFTVDNNLLPVGK	TVVIL	2		715.4066309	1428.797662	0.000451244	27	N	149	162
P01027	Exosome	QLAFK	QPSSAYAAFNNRPPSTWLTAYVVK	VFSLA	3		890.1226444	2667.344533	0.000451244	15	N	1060	1084
P01027	Exosome	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLK	RQVLT	3		1066.214034	3195.618703	0.000451244	39	N	37	66
P01027	Exosome	KDRNR	WEEPDQQLYNVEATSYALLALLLLK	DFDSV	2		1460.771287	2919.526974	0.000451244	15	N	1219	1244
P01027	Exosome	KDRNR	WEEPDQQLYNVEATSYALLALLLLK	DFDSV	3		974.1834581	2919.526974	0.000451244	16	N	1219	1244
P01027	Exosome	YIIGK	DTWVEHWPEAEECQDQK	YQKQC	2	C13:+57.021	1093.958116	2185.900632	0.000451244	34	N	1624	1641
P01027	Exosome	YIIGK	DTWVEHWPEAEECQDQK	YQKQC	3	C13:+57.021	729.6413438	2185.900632	0.000451244	27	N	1624	1641
P01027	Exosome	CLTFK	VHQYFNVGLIQPGSVK	VYSYY	2		893.4864753	1784.957351	0.000451244	14	N	1462	1478
P01027	Exosome	CLTFK	VHQYFNVGLIQPGSVK	VYSYY	3		595.9935836	1784.957351	0.001699387	4	N	1462	1478
P01027	Exosome	ASGQR	EVVADSVWVDVK	DSCIG	2		673.354064	1344.692528	0.000451244	6	N	544	556
P01027	Exosome	DSETR	IILQGSPVVQMAEDAVDGER	LKHLI	2		1064.041683	2126.067767	0.000451244	8	N	979	999
P01027	Exosome	DSETR	IILQGSPVVQMAEDAVDGER	LKHLI	2	M11:+15.995	1072.039183	2142.062767	0.000451244	27	N	979	999
P01027	Exosome	AYVVK	VFSLAANLIAIDSHVLCGAVK	WLILE	2	C17:+57.021	1099.604022	2197.192444	0.000451244	16	N	1084	1105
P01027	Exosome	AYVVK	VFSLAANLIAIDSHVLCGAVK	WLILE	3	C17:+57.021	733.4052813	2197.192444	0.000451244	23	N	1084	1105
P01027	Exosome	EVEVK	AAVFNHFISDGVK	KTLKV	2		702.8676729	1403.719746	0.000451244	8	N	913	926
P01027	Exosome	EVEVK	AAVFNHFISDGVK	KTLKV	3		468.9143819	1403.719746	0.000622848	3	N	913	926
P01027	Exosome	EHAPK	QIFSAEFEVK	EYVLP	2		599.3116678	1196.607736	0.000823681	9	N	216	226
P01027	Exosome	PYEIR	VMQDFFIDLR	LPYSV	2		642.3267955	1282.637991	0.001352548	3	N	824	834
P01027	Exosome	PYEIR	VMQDFFIDLR	LPYSV	2	M2:+15.995	650.3242955	1298.632991	0.000622848	3	N	824	834
P01027	Exosome	VEAER	SGIPIVTSPYQIHFTK	TPKFF	2		894.4886837	1786.961767	0.000451244	12	N	344	360
P01027	Exosome	NIFLK	DSITTWEILAVSLSDKK	GICVA	2		953.5125528	1905.009506	0.000451244	8	N	796	813
P01027	Exosome	NIFLK	DSITTWEILAVSLSDKK	GICVA	3		636.0109685	1905.009506	0.000451244	18	N	796	813
P01027	Exosome	PGSGK	NYAGVFMDAGLAFK	TSQGL	2	M7:+15.995	760.3666917	1518.717783	0.000451244	12	N	632	646
P01027	Exosome	NLNVR	LDKACEPGVDYVYK	TELTN	2	C5:+57.021	828.9008212	1655.786042	0.000451244	17	N	1532	1546
P01027	Exosome	NLNVR	LDKACEPGVDYVYK	TELTN	3	C5:+57.021	552.9364808	1655.786042	0.000622848	5	N	1532	1546
P01027	Exosome	DIISR	SHFPQSWLWTIEELKEPEK	NGIST	3		795.4027481	2383.184844	0.000451244	13	N	764	783
P01027	Exosome	ATTFR	LLWENGNLLR	SEETK	2		614.3463763	1226.677153	0.001329271	3	N	1310	1320
P01027	Exosome	DYVYK	TELTNIELLDDFDEYTMTIQQVIK	SGSDE	2		1436.712778	2871.409956	0.000451244	11	N	1546	1570
P01027	Exosome	DYVYK	TELTNIELLDDFDEYTMTIQQVIK	SGSDE	3		958.1444521	2871.409956	0.001329271	2	N	1546	1570
P01027	Exosome	NQGAR	VGLVAVDKGVFVLNK	KNKLT	3		519.9841368	1556.929011	0.001229886	4	N	591	606
P01027	Exosome	ERSGI	PIVTSPYQIHFTK	TPKFF	2		765.9199055	1529.824211	0.0007646	1	N	347	360
P01027	Exosome	QKGKK	YLMWGLSSDLWGEKPNTSYIIGK	DTWVE	3		886.7811197	2657.319959	0.000451244	17	N	1601	1624
P01027	Exosome	EFEVK	EYVLPSFEVR	VEPTE	2		619.8249424	1237.634285	0.001763695	4	N	226	236
P01027	Exosome	GSINK	AGEYIEASYMNLQRPYTVAIAGYALALMNKLEEPYLGK	FLNTA	4		1063.543597	4250.14319	0.001162105	1	N	1171	1209
P01027	Exosome	TAKGK	GRGTLSVVAVYHAK	LKSKV	3		486.6128144	1456.815043	0.000451244	1	N	1337	1351
P01027	Exosome	NVEAT	SYALLALLLLK	DFDSV	2		609.3975462	1216.779492	0.000851441	1	N	1233	1244
P01027	Exosome	FLYGK	NVDGTAFVIFGVQDGDK	KISLA	2		891.4393878	1780.863176	0.0025889	1	N	264	281
P01027	Exosome	RQATK	TMEAHPYSTMHNSNNYLHLSVSR	MELKP	4	M2:+15.995,M10:+15.995	681.0596257	2720.207303	0.00091018	1	N	439	462
P01027	Exosome	LSVSR	MELKPGDNLNVNFHLR	TDPGH	3	M1:+15.995	638.3286663	1911.962599	0.001871652	1	N	462	478
P01027	Exosome	SEMCR	CAEENCFMQQSQEK	INLNV	2	[0:-17.027,C1:+57.021,C6:+57.021,M8:+15.995	894.3369883	1786.658377	0.001162105	1	N	1512	1526
P01027	Exosome	AFSNK	NTLIIYLEK	ISHTE	2		553.8269537	1105.638307	0.001699387	1	N	1441	1450
P01027	Parental	GLAFK	TSQGLQTEQRADLECTKPAA	RRRRS	2	C15:+57.021	1102.534522	2203.053444	0.002080925	1	N	646	666
P01027	Parental	GLAFK	TSQGLQTEQRADLECTKPAA	RRRRS	3	C15:+57.021	735.358948	2203.053444	0.000451244	10	N	646	666
P01027	Parental	GNLLR	SEETKQNEAFSLTAK	GKGRG	2		841.9157455	1681.815891	0.001329271	3	N	1320	1335
P01027	Parental	GNLLR	SEETKQNEAFSLTAK	GKGRG	3		561.613097	1681.815891	0.000451244	11	N	1320	1335
P01027	Parental	LQEAR	DICEGQVNSLPGSINK	AGEYI	2	C3:+57.021	865.9228163	1729.830033	0.000451244	37	N	1155	1171
P01027	Parental	PGSVK	VYSYYNLEESCTR	FYHPE	2	C11:+57.021	842.3698852	1682.72417	0.000451244	37	N	1478	1491
P01027	Parental	LDPEK	LGQGGVQKVDVPAADLSDQVPDTDSETR	IILQG	3		966.4761404	2896.405021	0.000451244	16	N	951	979
P01027	Parental	GGVQK	VDVPAADLSDQVPDTDSETR	IILQG	2		1065.495817	2128.976033	0.000451244	85	N	959	979
P01027	Parental	IPSFR	LVAYYTLIGASGQR	EVVAD	3		504.6125915	1510.814375	0.000622848	11	N	530	544
P01027	Parental	FLYGK	NVDGTAFVIFGVQDGDKK	ISLAH	2		955.4868693	1908.958139	0.00091018	1	N	264	282
P01027	Parental	KIPPK	SSVAVPYVIVPLK	IGQQE	2		686.4164673	1370.817335	0.000451244	7	N	891	904

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01027	Parental	LGLAR	SELEEDIIPEEDIISR	SHFPQ	2		943.9656324	1885.915665	0.000451244	23	N	748	764
P01027	Parental	KIPPK	SSVAVPYVIVPLKIGQQEVEVK	AAVFN	2		1191.686298	2381.356995	0.001264573	2	N	891	913
P01027	Parental	ASGQR	EVVADSVWVDVKDSCIGTLVVK	GDPRD	3	C15:+57.021	806.758049	2417.250747	0.000451244	7	N	544	566
P01027	Parental	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLKR	QVLTS	3		1118.247738	3351.719814	0.000735798	2	N	37	67
P01027	Parental	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLKR	QVLTS	4		838.9377534	3351.719814	0.000451244	2	N	37	67
P01027	Parental	SFEVR	VEPTETFYYIDDPNGLEVSIIAK	FLYGK	2		1307.152682	2612.289763	0.000451244	38	N	236	259
P01027	Parental	SFEVR	VEPTETFYYIDDPNGLEVSIIAK	FLYGK	3		871.7710544	2612.289763	0.000451244	19	N	236	259
P01027	Parental	LKAGR	QVREPGQDLVVLSLPITPEFIPSFR	LVAYY	3		946.5240375	2836.548713	0.000451244	16	N	505	530
P01027	Parental	LKAGR	QVREPGQDLVVLSLPITPEFIPSFR	LVAYY	3	Q1:-17.027	940.8483709	2819.521713	0.002019181	3	N	505	530
P01027	Parental	GRQVR	EPGQDLVVLSLPITPEFIPSFR	LVAYY	2		1227.668105	2453.32061	0.000451244	26	N	508	530
P01027	Parental	GRQVR	EPGQDLVVLSLPITPEFIPSFR	LVAYY	3		818.7813366	2453.32061	0.000451244	11	N	508	530
P01027	Parental	FRNAK	EADVSLTAFVLIALQEAR	DICEG	2		973.5338196	1945.052039	0.000451244	35	N	1137	1155
P01027	Parental	FRNAK	EADVSLTAFVLIALQEAR	DICEG	3		649.3584797	1945.052039	0.000451244	15	N	1137	1155
P01027	Parental	VRLDK	ACEPGVDYVYKTELTNIELLDDFDEYTMTIQQVIK	SGSDE	3	C2:+57.021	1385.334289	4152.979468	0.00307782	1	N	1535	1570
P01027	Parental	FRNAK	EADVSLTAFVLIALQEARDICEGQVNSLPGSINK	AGEYI	3	C21:+57.021	1219.964971	3656.871512	0.000451244	11	N	1137	1171
P01027	Parental	TAKDR	NRWEEPDQQLYNVEATSYALLALLLLK	DFDSV	3		1064.231471	3189.671013	0.000451244	15	N	1217	1244
P01027	Parental	LTQSK	IWDVVEKADIGCTPGSGK	NYAGV	2	C12:+57.021	966.4804984	1930.945397	0.000451244	6	N	614	632
P01027	Parental	IPVKR	DILSSNNQHGILPLSWNIPELVNMGQWK	IRAFY	3		1068.548917	3202.623352	0.000622848	11	N	178	206
P01027	Parental	IPVKR	DILSSNNQHGILPLSWNIPELVNMGQWK	IRAFY	3	M24:+15.995	1073.880584	3218.618352	0.000622848	3	N	178	206
P01027	Parental	KDRNR	WEEPDQQLYNVEATSYALLALLLLKDFDSVPPVVR	WLNEQ	3		1344.705528	4031.093184	0.001162105	5	N	1219	1254
P01027	Parental	MRINK	TVAIHTLDPEKLGQGGVQK	VDVPA	3		664.3693788	1990.084736	0.000451244	2	N	940	959
P01027	Parental	YIIGK	DTWVEHWPEAEECQDQKYQK	QCEEL	3	C13:+57.021	869.3803003	2605.117501	0.000622848	3	N	1624	1644
P01027	Parental	IQTDK	TIYTPGSTVLYR	IFTVD	2		685.8698813	1369.724163	0.000451244	10	N	137	149
P01027	Parental	LSDKK	GICVADPYEIR	VMQDF	2	C3:+57.021	646.8191028	1291.622606	0.000823681	3	N	813	824
P01027	Parental	HSLTR	VVIEDGVGDAVLTR	KVLME	2		721.8966274	1441.777655	0.000451244	44	N	291	305
P01027	Parental	VRLDK	ACEPGVDYVYK	TELTN	2	C2:+57.021	650.797836	1299.580072	0.0007646	10	N	1535	1546
P01027	Parental	LPVGK	TVVILIETPDGIPVKR	DILSS	2		875.5278089	1749.040018	0.000451244	1	N	162	178
P01027	Parental	LPVGK	TVVILIETPDGIPVKR	DILSS	3		584.0211393	1749.040018	0.000622848	5	N	162	178
P01027	Parental	APDTK	DLELLASGVDR	YISKY	2		594.3174815	1186.619363	0.000622848	7	N	1416	1427
P01027	Parental	KEGHK	YVTVVANFGETVVEK	AVMVS	2		827.9384923	1653.861385	0.000622848	8	N	105	120
P01027	Parental	TVLYR	IFTVDNNLLPVGK	TVVIL	2		715.4066309	1428.797662	0.000451244	9	N	149	162
P01027	Parental	QLAFK	QPSSAYAAFNNRPPSTWLTAYVVK	VFSLA	3		890.1226444	2667.344533	0.001763695	1	N	1060	1084
P01027	Parental	PNVLR	LESEETIVLEAHDAQGDIPVTVTVQDFLK	RQVLT	3		1066.214034	3195.618703	0.000735798	2	N	37	66
P01027	Parental	KDRNR	WEEPDQQLYNVEATSYALLALLLLK	DFDSV	2		1460.771287	2919.526974	0.000451244	1	N	1219	1244
P01027	Parental	KDRNR	WEEPDQQLYNVEATSYALLALLLLK	DFDSV	3		974.1834581	2919.526974	0.000451244	11	N	1219	1244
P01027	Parental	YIIGK	DTWVEHWPEAEECQDQK	YQKQC	2	C13:+57.021	1093.958116	2185.900632	0.000451244	12	N	1624	1641
P01027	Parental	YIIGK	DTWVEHWPEAEECQDQK	YQKQC	3	C13:+57.021	729.6413438	2185.900632	0.000451244	21	N	1624	1641
P01027	Parental	CLTFK	VHQYFNVGLIQPGSVK	VYSYY	2		893.4864753	1784.957351	0.000451244	14	N	1462	1478
P01027	Parental	ASGQR	EVVADSVWVDVK	DSCIG	2		673.354064	1344.692528	0.00091018	1	N	544	556
P01027	Parental	DSETR	IILQGSPVVQMAEDAVDGER	LKHLI	2		1064.041683	2126.067767	0.000451244	2	N	979	999
P01027	Parental	AYVVK	VFSLAANLIAIDSHVLCGAVK	WLILE	2	C17:+57.021	1099.604022	2197.192444	0.000622848	10	N	1084	1105
P01027	Parental	AYVVK	VFSLAANLIAIDSHVLCGAVK	WLILE	3	C17:+57.021	733.4052813	2197.192444	0.000823681	4	N	1084	1105
P01027	Parental	EVEVK	AAVFNHFISDGVK	KTLKV	2		702.8676729	1403.719746	0.000451244	1	N	913	926
P01027	Parental	NIFLK	DSITTWEILAVSLSDKK	GICVA	2		953.5125528	1905.009506	0.000979378	1	N	796	813
P01027	Parental	NIFLK	DSITTWEILAVSLSDKK	GICVA	3		636.0109685	1905.009506	0.000451244	8	N	796	813
P01027	Parental	HSLTR	VVIEDGVGDAVLTRK	VLMEG	3		524.2986726	1569.872618	0.00091018	1	N	291	306
P01027	Parental	ATTFR	LLWENGNLLR	SEETK	2		614.3463763	1226.677153	0.001162105	4	N	1310	1320
P01027	Parental	DYVYK	TELTNIELLDDFDEYTMTIQQVIK	SGSDE	2		1436.712778	2871.409956	0.000823681	2	N	1546	1570
P01029	Exosome	AWLHR	DSSTWLTAFVLK	ILSLA	2		684.3644317	1366.713263	0.000451244	22	N	1068	1080
P01029	Exosome	NSPEK	LQETASWLLAQQLGDGSFHDPCPVIHR	AMQGG	3	C22:+57.021	1025.842058	3074.502773	0.000451244	19	N	1095	1122
P01029	Exosome	NSPEK	LQETASWLLAQQLGDGSFHDPCPVIHR	AMQGG	4	C22:+57.021	769.6334933	3074.502773	0.000451244	18	N	1095	1122
P01029	Exosome	HGAFR	STQDTVVTLDALSAYWIASHTTEEK	ALNVT	2		1383.677584	2765.339567	0.002884417	1	N	1296	1321
P01029	Exosome	HGAFR	STQDTVVTLDALSAYWIASHTTEEK	ALNVT	3		922.7876557	2765.339567	0.000451244	27	N	1296	1321
P01029	Exosome	LQKPR	LLLFSPSVVNLGTPLSVGVQLLDAPPGQEVK	GSVFL	3		1063.271267	3186.7904	0.000451244	19	N	22	53
P01029	Exosome	KKDFK	LSSGDDFVLLSLEVPLEDVR	SCGLF	2		1102.078788	2202.141977	0.000451244	17	N	73	93
P01029	Exosome	FLGQK	ASAGLLGAHAAAITAYALTLTK	ASEDL	3		695.7287956	2084.162987	0.000451244	8	N	1178	1200
P01029	Exosome	AAPTK	SQLLATLCSGDVCQCAEGK	CPRLL	2	C8:+57.021,C13:+57.021,C15:+57.021	1048.973934	2095.932269	0.000451244	21	N	1569	1588
P01029	Exosome	PTAPR	SPTEPVPQAPALWIETTAYALLHLLLR	EGKGK	3		1000.890609	2999.648427	0.00091018	2	N	1244	1271
P01029	Exosome	NNLGR	TLEIPGSSDPNIVPDGDFSSLVR	VTASE	2		1208.106066	2414.196531	0.000451244	12	N	952	975
P01029	Exosome	VPTTR	ECVGFGASQEVVVGLVQPSSAVLYDYYSPDHK	CSVFY	3	C2:+57.021	1167.561174	3499.660122	0.000451244	7	N	1527	1559
P01029	Exosome	AFVLK	ILSLAQEQVGNSPEK	LQETA	2		806.9311986	1611.846797	0.000451244	3	N	1080	1095
P01029	Exosome	VTELR	LLVSAGSLYPAIAR	LTVQA	2		715.9224482	1429.829296	0.000451244	4	N	442	456
P01029	Exosome	SSLVR	VTASEPLETMGSEGALSPGGVASLLR	LPQGC	2	M10:+15.995	1273.144908	2544.274217	0.001162105	1	N	975	1001
P01029	Exosome	LDMSK	VFEVINSYNVGCGPGGGDDALQVFQDAGLAFSDGDR	LTQTR	3	C12:+57.021	1249.572801	3745.695004	0.000451244	6	N	621	657

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01029	Exosome	RVLKK	EIFTSTSIFQDAFTIPDISEPGTWK	ISARF	2		1415.695245	2829.37489	0.001162105	1	N	187	212
P01029	Exosome	RVLKK	EIFTSTSIFQDAFTIPDISEPGTWK	ISARF	3		944.1327634	2829.37489	0.000451244	1	N	187	212
P01029	Exosome	ISISK	DQFQAALDKINIGVR	DLEGL	3		563.3095717	1686.905315	0.002296037	1	N	314	329
P01029	Parental	AWLHR	DSSTWLTAFVLK	ILSLA	2		684.3644317	1366.713263	0.000451244	12	N	1068	1080
P01029	Parental	HGAFR	STQDTVVTLDALSAYWIASHTTEEK	ALNVT	3		922.7876557	2765.339567	0.000451244	5	N	1296	1321
P01326	Exosome	HPTQA	FVKQHLCGSHLVEALYLVCGER	GFFYT	3	C7:+57.021,C19:+57.021	872.4457681	2614.313904	0.000622848	11	N	24	46
P01326	Exosome	HLCGS	HLVEALYLVCGER	GFFYT	2	C10:+57.021	779.9062409	1557.796882	0.000451244	27	N	33	46
P01326	Exosome	HLCGS	HLVEALYLVCGER	GFFYT	3	C10:+57.021	520.2734272	1557.796882	0.000451244	42	N	33	46
P01326	Exosome	LCGSH	LVEALYLVCGER	GFFYT	2	C9:+57.021	711.3767849	1420.73797	0.000451244	29	N	34	46
P01326	Exosome	CGSHL	VEALYLVCGER	GFFYT	2	C8:+57.021	654.8347528	1307.653906	0.000451244	28	N	35	46
P01326	Exosome	SHLVE	ALYLVCGER	GFFYT	2	C6:+57.021	540.7792492	1079.542898	0.000451244	16	N	37	46
P01326	Exosome	FVKQH	LCGSHLVEALYLVCGER	GFFYT	2	C2:+57.021,C14:+57.021	988.4901118	1974.964624	0.001943752	4	N	29	46
P01326	Exosome	FVKQH	LCGSHLVEALYLVCGER	GFFYT	3	C2:+57.021,C14:+57.021	659.3293412	1974.964624	0.000451244	2	N	29	46
P01326	Exosome	RGIVD	QCCTSICSLYQLENYCN	-	2	C2:+57.021,C3:+57.021,C7:+57.021,C16:+57.021	1106.941546	2211.867491	0.000451244	16	N	93	110
P01326	Exosome	QAFVK	QHLCGSHLVEALYLVCGER	GFFYT	2	[0:-	1112.535357	2223.055113	0.000698008	1	N	27	46
P01326	Exosome	QAFVK	QHLCGSHLVEALYLVCGER	GFFYT	3	[0:-	742.0261711	2223.055113	0.000451244	3	N	27	46
P01326	Exosome	VKQHL	CGSHLVEALYLVCGER	GFFYT	2	C1:+39.994,C13:+57.021	923.4345798	1844.85356	0.000622848	2	N	30	46
P01326	Exosome	GIVDQ	CCTSICSLYQLENYCN	-	2	C1:+57.021,C2:+57.021,C6:+57.021,C15:+57.021	1042.912257	2083.808914	0.002727428	1	N	94	110
P01326	Exosome	IVDQC	CTSICSLYQLENYCN	-	2	C1:+57.021,C5:+57.021,C14:+57.021	962.897164	1923.778728	0.000622848	3	N	95	110
P01326	Parental	HPTQA	FVKQHLCGSHLVEALYLVCGER	GFFYT	3	C7:+57.021,C19:+57.021	872.4457681	2614.313904	0.001943752	1	N	24	46
P01326	Parental	LCGSH	LVEALYLVCGER	GFFYT	2	C9:+57.021	711.3767849	1420.73797	0.000451244	4	N	34	46
P01326	Parental	FVKQH	LCGSHLVEALYLVCGER	GFFYT	2	C2:+57.021,C14:+57.021	988.4901118	1974.964624	0.000451244	6	N	29	46
P01326	Parental	FVKQH	LCGSHLVEALYLVCGER	GFFYT	3	C2:+57.021,C14:+57.021	659.3293412	1974.964624	0.000622848	7	N	29	46
P01326	Parental	QAFVK	QHLCGSHLVEALYLVCGER	GFFYT	3	Q1:-17.027,C4:+57.021,C16:+57.021	742.0261711	2223.055113	0.000735798	1	N	27	46
P01326	Parental	QAFVK	QHLCGSHLVEALYLVCGER	GFFYT	3	[0:-	742.0261711	2223.055113	0.000637154	1	N	27	46
P01326	Parental	IVDQC	CTSICSLYQLENYCN	-	2	C1:+57.021,C5:+57.021,C14:+57.021	962.897164	1923.778728	0.000622848	1	N	95	110
P01639	Exosome	GTIKR	LIYATSSLDSGVPK	RFSGS	2		725.8935534	1449.771507	0.000451244	5	N	68	82
P01639	Exosome	SLTCR	ASQDIGSSLNWLQQEPDGTIKR	LIYAT	2		1222.114756	2442.213913	0.000451244	3	N	46	68
P01639	Exosome	SLTCR	ASQDIGSSLNWLQQEPDGTIKR	LIYAT	3		815.0791043	2442.213913	0.000451244	6	N	46	68
P01639	Exosome	SLTCR	ASQDIGSSLNWLQQEPDGTIK	RLIYA	2		1144.064201	2286.112802	0.00091018	2	N	46	67
P01723	Exosome	GGAIS	QAVVTQESALTTSPGETVTLTCR	SSTGA	2	Q1:-17.027,C22:+57.021	1216.602376	2431.189152	0.00307782	1	N	20	43
P01723	Exosome	GGAIS	QAVVTQESALTTSPGETVTLTCR	SSTGA	2	[0:-17.027,C22:+57.021	1216.602376	2431.189152	0.002296037	2	N	20	43
P01723	Exosome	TLTCR	SSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNR	APGVP	3		1179.24539	3534.712771	0.000622848	1	N	43	76
P01786	Exosome	QPPGK	ALEWLGFIR	NKABG	2		552.8141807	1103.612761	0.000622848	5	N	43	52
P01786	Exosome	-EVK	LVESGGGLVQPGGSLR	LSCAT	2		763.420801	1524.826002	0.000451244	9	N	3	19
P01812	Exosome	QAPGK	GLEWIGEIDPNSSTINYTPSLK	DKFII	2		1217.610984	2433.206368	0.000451244	8	N	43	65
P01812	Exosome	QAPGK	GLEWIGEIDPNSSTINYTPSLKDK	FIISR	3		893.1172247	2676.328274	0.000998612	1	N	43	67
P01837	Exosome	-	ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPK	DINVK	3	C26:+57.021	1191.25234	3570.733621	0.000451244	63	N	0	34
P01837	Exosome	DGSER	QNGVLNSWTDQDSK	DSTYS	2		796.3715051	1590.72741	0.000622848	7	N	47	61
P01837	Parental	-	ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPK	DINVK	3	C26:+57.021	1191.25234	3570.733621	0.000451244	8	N	0	34
P01868	Exosome	PPKPK	DVLTITLTPK	VTCVV	2		550.8322361	1099.648872	0.000451244	24	N	125	135
P01868	Exosome	TLTPK	VTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR	EEQFN	4	C3:+57.021	987.2299546	3944.888618	0.000451244	9	N	135	169
P01868	Exosome	LNVQK	SNWEAGNTFTCSVLHEGLHNHHTEK	SLSHS	3	C11:+57.021	969.107574	2904.299322	0.001463592	2	N	291	316
P01868	Exosome	EFKCR	VNSAAFPAPIEK	TISKT	2		622.3382169	1242.660834	0.001329271	2	N	199	211
P01868	Parental	PPKPK	DVLTITLTPK	VTCVV	2		550.8322361	1099.648872	0.001463592	1	N	125	135
P01872	Exosome	LKDGK	LVESGFTTDPVTIENK	GSTPQ	2		875.4494212	1748.883242	0.000451244	109	N	154	170
P01872	Exosome	LLSPK	SILEGSDEYLVCK	IHYGG	2	C12:+57.021	756.866447	1511.717294	0.000451244	27	N	76	89
P01872	Exosome	PRKSK	LICEATNFTPKPITVSWLK	DGKLV	2	C3:+57.021	1109.600948	2217.186296	0.000451244	35	N	132	151
P01872	Exosome	PRKSK	LICEATNFTPKPITVSWLK	DGKLV	3	C3:+57.021	740.0698987	2217.186296	0.000451244	19	N	132	151
P01872	Exosome	GGKNR	DLHVPIPAVAEMNPNVNVFVPPR	DGFSG	3		842.4498158	2524.326047	0.000451244	5	N	97	120
P01872	Exosome	GGKNR	DLHVPIPAVAEMNPNVNVFVPPR	DGFSG	2	M12:+15.995	1271.168324	2540.321047	0.002453667	1	N	97	120
P01872	Exosome	GGKNR	DLHVPIPAVAEMNPNVNVFVPPR	DGFSG	3	M12:+15.995	847.7814825	2540.321047	0.000451244	30	N	97	120
P01872	Exosome	TCLVK	GFSPADISVQWLQR	GQLLP	2		802.4155186	1602.815437	0.000451244	36	N	355	369
P01872	Exosome	TCLVK	GFSPADISVQWLQR	GQLLP	3		535.2796124	1602.815437	0.000451244	18	N	355	369
P01872	Exosome	TFSAK	GVASVCVEDWNNRK	EFVCT	2	C6:+57.021	817.3914863	1632.767373	0.000451244	24	N	286	300
P01872	Exosome	TFSAK	GVASVCVEDWNNRK	EFVCT	3	C6:+57.021	545.2635908	1632.767373	0.000451244	1	N	286	300
P01872	Exosome	TFSAK	GVASVCVEDWNNR	KEFVC	2	C6:+57.021	753.3440047	1504.672409	0.000451244	24	N	286	299
P01872	Exosome	RTGGK	YLATSQVLLSPK	SILEG	2		660.3826245	1318.749649	0.000451244	32	N	64	76
P01872	Exosome	LKDGK	LVESGFTTDPVTIENKG	STPQT	2		903.960153	1805.904706	0.000662267	1	N	154	171
P01872	Exosome	PRKSK	LICEATNFTPK	PITVS	2	C3:+57.021	647.3293033	1292.643007	0.001352548	3	N	132	143

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01872	Exosome	FYFTH	SILTVTEEEWNSGETYTCVVGHEALPHLVTER	TVDKS	4	C18:+57.021	914.9442942	3655.745977	0.000622848	5	N	396	428
P01872	Exosome	DGKLV	ESGFTTDPVTIENK	GSTPQ	2		769.3731821	1536.730764	0.001352548	1	N	156	170
P01872	Exosome	HYGGK	NRDLHVPIPAVAEMNPNVNVFVPPR	DGFSG	4	M14:+15.995	703.6240715	2810.465086	0.000622848	3	N	95	120
P01872	Exosome	PAPRK	SKLICEATNFTPKPITVSWLK	DGKLV	3	C5:+57.021	811.7788959	2432.313288	0.001162105	4	N	130	151
P01872	Exosome	PAPRK	SKLICEATNFTPKPITVSWLK	DGKLV	4	C5:+57.021	609.0861219	2432.313288	0.001763695	1	N	130	151
P01872	Exosome	RTVDK	STGKPTLYNVSLIMSDTGGTCY	-	2	C21:+57.021	1183.056442	2364.097284	0.000451244	7	N	432	454
P01872	Exosome	RTVDK	STGKPTLYNVSLIMSDTGGTCY	-	2	M14:+15.995,C21:+57.021	1191.053942	2380.092284	0.000451244	2	N	432	454
P01872	Exosome	SPQKK	FISKPNEVHKHPPAVYLLPPAR	EQLNL	3		837.4730603	2509.395781	0.000698008	2	N	317	339
P01872	Exosome	VSWLK	DGKLVESGFTTDPVTIENK	GSTPQ	2		1025.521106	2049.026612	0.000451244	4	N	151	170
P01872	Exosome	VSWLK	DGKLVESGFTTDPVTIENK	GSTPQ	3		684.0166708	2049.026612	0.000451244	3	N	151	170
P01872	Exosome	PQTYK	VISTLTISEIDWLNLNVYTCR	VDHRG	3	C20:+57.021	837.4371984	2509.288195	0.002884417	1	N	178	199
P01872	Exosome	LRESA	TVTCLVKGFSPADISVQWLQR	GQLLP	3	C4:+57.021	802.4267451	2404.256835	0.001463592	1	N	348	369
P01872	Exosome	VISTL	TISEIDWLNLNVYTCR	VDHRG	2	C15:+57.021	998.9937729	1995.971946	0.000451244	6	N	183	199
P01872	Exosome	LPQEK	YVTSAPMPEPGAPGFYFTH	SILTV	2	M7:+15.995	1042.975323	2083.935047	0.001699387	2	N	377	396
P01872	Exosome	VKGFS	PADISVQWLQR	GQLLP	2		656.8545655	1311.693531	0.000451244	1	N	358	369
P01872	Parental	LKDGK	LVESGFTTDPVTIENK	GSTPQ	2		875.4494212	1748.883242	0.000451244	2	N	154	170
P01872	Parental	PRKSK	LICEATNFTPKPITVSWLK	DGKLV	2	C3:+57.021	1109.600948	2217.186296	0.001352548	3	N	132	151
P01878	Exosome	AVQKK	AVQNSCGCYSVSSVLPGCAER	WNSGA	2	C6:+57.021,C8:+57.021,C18:+57.021	1151.006297	2299.996994	0.000451244	14	N	165	186
P01878	Exosome	GASFK	CTVTHPESGTLTGTIAK	VTVNT	3	C1:+57.021	591.6334609	1771.876983	0.000622848	1	N	194	211
P01887	Exosome	DWSFY	ILAHTEFTPTETDTYACR	VKHAS	2	C17:+57.021	1063.496877	2124.978154	0.000451244	1	N	83	101
P01887	Exosome	MSFSK	DWSFYILAHTEFTPTETDTYACR	VKHAS	3	C22:+57.021	942.090527	2823.248181	0.000451244	19	N	78	101
P01887	Exosome	SFYIL	AHTEFTPTETDTYACR	VKHAS	2	C15:+57.021	950.4128127	1898.810025	0.002981883	1	N	85	101
P01887	Parental	DWSFY	ILAHTEFTPTETDTYACR	VKHAS	2	C17:+57.021	1063.496877	2124.978154	0.000451244	27	N	83	101
P01887	Parental	DWSFY	ILAHTEFTPTETDTYACR	VKHAS	3	C17:+57.021	709.3338512	2124.978154	0.000451244	27	N	83	101
P01887	Parental	MSFSK	DWSFYILAHTEFTPTETDTYACR	VKHAS	2	C22:+57.021	1412.63189	2823.248181	0.000622848	4	N	78	101
P01887	Parental	MSFSK	DWSFYILAHTEFTPTETDTYACR	VKHAS	3	C22:+57.021	942.090527	2823.248181	0.000451244	15	N	78	101
P01900	Exosome	SHSLR	YFVTAVSRPGFGEPR	YMEVG	3		561.6270122	1681.857636	0.000451244	10	N	30	45
P01900	Exosome	AERDR	AYLEGECVEWLR	RYLKN	2	C7:+57.021	762.861499	1523.707398	0.000622848	1	N	181	193
P01900	Parental	GTFQK	WASVVVPLGK	EQKYT	2		528.3165562	1054.617512	0.00307782	1	N	267	277
P01900	Parental	SHSLR	YFVTAVSRPGFGEPR	YMEVG	3		561.6270122	1681.857636	0.001839721	1	N	30	45
P01921	Exosome	VGEYR	AVTELGRPDAEYWNSQPEILER	TRAEV	3		858.4263926	2572.255778	0.0007646	2	N	75	97
P01921	Exosome	VRWFR	NGQEETVGVSSTQLIR	NGDWT	2		859.4399191	1716.864238	0.000870037	2	N	161	177
P01942	Exosome	AAWGK	IGGHGAEYGAEALER	MFASF	2		765.3713081	1528.727016	0.000451244	118	N	17	32
P01942	Exosome	AAWGK	IGGHGAEYGAEALER	MFASF	3		510.5834721	1528.727016	0.000451244	61	N	17	32
P01942	Exosome	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	2		910.4422648	1818.86893	0.000451244	57	N	41	57
P01942	Exosome	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	3		607.2974432	1818.86893	0.000451244	64	N	41	57
P01942	Exosome	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	4		455.7250324	1818.86893	0.000451244	205	N	41	57
P01942	Exosome	ASLDK	FLASVSTVLTSK	YR-	2		626.8615249	1251.70745	0.000451244	180	N	128	140
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHKLR	VDPVN	4		777.1669732	3104.636693	0.000622848	9	N	62	93
P01942	Exosome	KGHGK	KVADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		988.856627	2963.546481	0.000451244	26	N	61	91
P01942	Exosome	KGHGK	KVADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	4		741.8944202	2963.546481	0.000451244	23	N	61	91
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	2		1418.733559	2835.451518	0.000451244	19	N	62	91
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		946.1583059	2835.451518	0.000451244	72	N	62	91
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	4		709.8706794	2835.451518	0.000451244	62	N	62	91
P01942	Exosome	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDKFLASVSTVLTSK	YR-	3	C5:+57.021	1428.766862	4283.277185	0.000451244	5	N	100	140
P01942	Exosome	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDKFLASVSTVLTSK	YR-	4	C5:+57.021	1071.827096	4283.277185	0.000451244	15	N	100	140
P01942	Exosome	PAVHA	SLDKFLASVSTVLTSK	YR-	2		848.4805243	1694.945449	0.001463592	1	N	124	140
P01942	Exosome	PAVHA	SLDKFLASVSTVLTSK	YR-	3		565.9896162	1694.945449	0.002145581	1	N	124	140
P01942	Exosome	EALER	MFASFPTTK	TYFPH	2		515.2578502	1028.5001	0.000451244	24	N	32	41
P01942	Exosome	EALER	MFASFPTTK	TYFPH	2	M1:+15.995	523.2553502	1044.4951	0.001162105	2	N	32	41
P01942	Exosome	LLVTL	ASHHPADFTPAVHASLDK	FLASV	2		950.9691781	1899.922756	0.002981883	1	N	110	128
P01942	Exosome	LLVTL	ASHHPADFTPAVHASLDK	FLASV	3		634.3153854	1899.922756	0.000451244	4	N	110	128
P01942	Exosome	LLVTL	ASHHPADFTPAVHASLDK	FLASV	4		475.988489	1899.922756	0.000451244	11	N	110	128
P01942	Exosome	LVTLA	SHHPADFTPAVHASLDK	FLASV	3		610.6363474	1828.885642	0.000662267	2	N	111	128
P01942	Exosome	LVTLA	SHHPADFTPAVHASLDK	FLASV	4		458.2292106	1828.885642	0.000622848	6	N	111	128
P01942	Exosome	AWGKI	GGHGAEYGAEALER	MFASF	2		708.829276	1415.642952	0.000451244	11	N	18	32
P01942	Exosome	HCLLV	TLASHHPADFTPAVHASLDK	FLASV	3		705.6926329	2114.054499	0.000451244	9	N	108	128
P01942	Exosome	TKTYF	PHFDVSHGSAQVK	GHGKK	2		704.8525542	1407.689508	0.000451244	3	N	44	57
P01942	Exosome	FPTTK	TYFPHFDVSHGSAQVKG	HGKKV	2		938.9529967	1875.890393	0.000451244	13	N	41	58
P01942	Exosome	FPTTK	TYFPHFDVSHGSAQVKG	HGKKV	3		626.3045978	1875.890393	0.002663018	1	N	41	58
P01942	Exosome	FPTTK	TYFPHFDVSHGSAQVKG	HGKKV	4		469.9803983	1875.890393	0.000622848	9	N	41	58
P01942	Exosome	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDK	FLASV	3	C5:+57.021	1017.534565	3049.580295	0.000451244	36	N	100	128
P01942	Exosome	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDK	FLASV	4	C5:+57.021	763.4028738	3049.580295	0.000451244	49	N	100	128
P01942	Exosome	KLLSH	CLLVTLASHHPADFTPAVHASLDK	FLASV	4	[0:-17.027,C1:+57.021	646.5813567	2582.294227	0.001395409	3	N	104	128

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P01942	Exosome	HGKKV	ADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		913.1355012	2736.383104	0.000451244	7	N	63	91
P01942	Exosome	HGKKV	ADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	4		685.1035759	2736.383104	0.000637154	6	N	63	91
P01942	Exosome	HLDDL	PGALSALSDLHAHK	LRVDP	2		708.8838543	1415.752109	0.000823681	1	N	77	91
P01942	Exosome	HLDDL	PGALSALSDLHAHK	LRVDP	3		472.9251695	1415.752109	0.000451244	20	N	77	91
P01942	Exosome	GKKVA	DALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		889.4564633	2665.34599	0.0007646	1	N	64	91
P01942	Exosome	GKKVA	DALASAAGHLDDLPGALSALSDLHAHK	LRVDP	4		667.3442975	2665.34599	0.000451244	4	N	64	91
P01942	Exosome	VADAL	ASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		789.7404229	2366.197869	0.002212458	2	N	67	91
P01942	Exosome	VADAL	ASAAGHLDDLPGALSALSDLHAHK	LRVDP	4		592.5572672	2366.197869	0.002374549	1	N	67	91
P01942	Exosome	LPGAL	SALSDLHAHK	LRVDP	2		539.7861515	1077.556703	0.002145581	3	N	81	91
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHKL	RVDPV	4		738.1416955	2948.535582	0.000622848	3	N	62	92
P01942	Exosome	ASHHP	ADFTPAVHASLDKFLASVSTVLTSK	YR-	3		869.1344386	2604.379916	0.000622848	12	N	115	140
P01942	Exosome	ASLDK	FLASVSTVLTSKY	R-	2		708.3931892	1414.770778	0.000451244	12	N	128	141
P01942	Exosome	ADALA	SAAGHLDDLPGALSALSDLHAHK	LRVDP	3		766.061385	2295.160755	0.000622848	3	N	68	91
P01942	Exosome	ADALA	SAAGHLDDLPGALSALSDLHAHK	LRVDP	4		574.7979887	2295.160755	0.00091018	1	N	68	91
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSAL	SDLHA	2		1024.537091	2047.058581	0.001162105	2	N	62	84
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSAL	SDLHA	3		683.3606604	2047.058581	0.00307782	2	N	62	84
P01942	Exosome	PVNFK	LLSHCLLVTLASHHPADFTPAVH	ASLDK	4	C5:+57.021	634.8340956	2535.305183	0.000622848	1	N	100	123
P01942	Exosome	LASAA	GHLDDLPGALSALSDLHAHK	LRVDP	2		1034.035049	2066.054499	0.001463592	1	N	71	91
P01942	Exosome	LASAA	GHLDDLPGALSALSDLHAHK	LRVDP	3		689.6926329	2066.054499	0.000451244	4	N	71	91
P01942	Exosome	LASAA	GHLDDLPGALSALSDLHAHK	LRVDP	4		517.5214247	2066.054499	0.000622848	7	N	71	91
P01942	Exosome	PVNFK	LLSHCLLVTLASHHPADFTPAVHA	SLDKF	4	C5:+57.021	652.5933741	2606.342296	0.000823681	1	N	100	124
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDLHAH	KLRVD	3		903.4599849	2707.356555	0.002519933	1	N	62	90
P01942	Exosome	KGHGK	KVADALASAAGHLDDLPGALSAL	SDLHA	2		1088.584572	2175.153544	0.002145581	1	N	61	84
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDLH	AHKLR	3		834.0946429	2499.260529	0.0025889	1	N	62	88
P01942	Exosome	DFTPA	VHASLDKFLASVSTVLTSK	YR-	3		668.3777628	2002.109888	0.001329271	1	N	121	140
P01942	Exosome	GHGKK	VADALASAAGHLDDLPGALSALSDL	HAHKL	3		788.408339	2362.201617	0.002884417	2	N	62	87
P01942	Exosome	LVTLA	SHHPADFTPAVHASLDKFLASVSTVLTSK	YR-	4		766.653433	3062.582532	0.000451244	1	N	111	140
P01942	Exosome	KGHGK	KVADALASAAGHLDDLPGALSALSDL	HAHKL	3		831.10666	2490.29658	0.0025889	1	N	61	87
P01942	Parental	AAWGK	IGGHGAEYGAEALER	MFASF	2		765.3713081	1528.727016	0.000451244	84	N	17	32
P01942	Parental	AAWGK	IGGHGAEYGAEALER	MFASF	3		510.5834721	1528.727016	0.000451244	73	N	17	32
P01942	Parental	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	2		910.4422648	1818.86893	0.000451244	3	N	41	57
P01942	Parental	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	3		607.2974432	1818.86893	0.000451244	18	N	41	57
P01942	Parental	FPTTK	TYFPHFDVSHGSAQVK	GHGKK	4		455.7250324	1818.86893	0.000451244	41	N	41	57
P01942	Parental	ASLDK	FLASVSTVLTSK	YR-	2		626.8615249	1251.70745	0.000451244	17	N	128	140
P01942	Parental	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHKLR	VDPVN	4		777.1669732	3104.636693	0.001871652	1	N	62	93
P01942	Parental	KGHGK	KVADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		988.856627	2963.546481	0.000451244	3	N	61	91
P01942	Parental	KGHGK	KVADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	4		741.8944202	2963.546481	0.000451244	6	N	61	91
P01942	Parental	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	2		1418.733559	2835.451518	0.000451244	1	N	62	91
P01942	Parental	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	3		946.1583059	2835.451518	0.000451244	29	N	62	91
P01942	Parental	GHGKK	VADALASAAGHLDDLPGALSALSDLHAHK	LRVDP	4		709.8706794	2835.451518	0.000622848	23	N	62	91
P01942	Parental	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDKFLASVSTVLTSK	YR-	4	C5:+57.021	1071.827096	4283.277185	0.000451244	5	N	100	140
P01942	Parental	PAVHA	SLDKFLASVSTVLTSK	YR-	3		565.9896162	1694.945449	0.001395409	2	N	124	140
P01942	Parental	EALER	MFASFPTTK	TYFPH	2		515.2578502	1028.5001	0.002145581	1	N	32	41
P01942	Parental	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDK	FLASV	3	C5:+57.021	1017.534565	3049.580295	0.000823681	3	N	100	128
P01942	Parental	PVNFK	LLSHCLLVTLASHHPADFTPAVHASLDK	FLASV	4	C5:+57.021	763.4028738	3049.580295	0.000451244	9	N	100	128
P01942	Parental	HLDDL	PGALSALSDLHAHK	LRVDP	3		472.9251695	1415.752109	0.000622848	1	N	77	91
P02088	Exosome	LDSLK	GTFASLSELHCDKLHVDPENFR	LLGNM	2	C11:+57.021	1286.616378	2571.217155	0.000451244	40	Y	83	105
P02088	Exosome	LDSLK	GTFASLSELHCDKLHVDPENFR	LLGNM	3	C11:+57.021	858.0801851	2571.217155	0.000451244	137	Y	83	105
P02088	Exosome	LDSLK	GTFASLSELHCDKLHVDPENFR	LLGNM	4	C11:+57.021	643.8120889	2571.217155	0.000451244	101	Y	83	105
P02088	Exosome	-M	VHLTDAEKAAVSCLWGK	VNSDE	3	C13:+57.021	628.9931006	1883.955902	0.000451244	6	N	1	18
P02088	Exosome	PWTQR	YFDSFGDLSSASAIMGNAK	VKAHG	2		990.9545453	1979.893491	0.000451244	50	N	41	60
P02088	Exosome	PWTQR	YFDSFGDLSSASAIMGNAK	VKAHG	3		660.9722969	1979.893491	0.000622848	16	N	41	60
P02088	Exosome	PWTQR	YFDSFGDLSSASAIMGNAK	VKAHG	2	M15:+15.995	998.9520453	1995.888491	0.000451244	96	N	41	60
P02088	Exosome	EALGR	LLVVYPWTQR	YFDSF	2		637.8669446	1273.718289	0.000451244	440	Y	31	41
P02088	Exosome	EALGR	LLVVYPWTQR	YFDSF	3		425.5805631	1273.718289	0.000823681	3	Y	31	41
P02088	Exosome	CLWGK	VNSDEVGGEALGR	LLVVY	2		651.818377	1301.621154	0.000451244	32	N	18	31
P02088	Exosome	CLWGK	VNSDEVGGEALGR	LLVVY	3		434.881518	1301.621154	0.000823681	5	N	18	31
P02088	Exosome	TDAEK	AAVSCLWGK	VNSDE	2	C5:+57.021	496.2554099	990.4952199	0.000451244	78	N	9	18
P02088	Exosome	HHLGK	DFTPAAQAAFQK	VVAGV	2		647.8254737	1293.635347	0.000451244	139	Y	121	133
P02088	Exosome	KAHGK	KVITAFNDGLNHLDSLK	GTFAS	2		943.0130543	1884.010509	0.000451244	2	N	66	83
P02088	Exosome	KAHGK	KVITAFNDGLNHLDSLK	GTFAS	3		629.0113029	1884.010509	0.000451244	17	N	66	83
P02088	Exosome	KAHGK	KVITAFNDGLNHLDSLK	GTFAS	4		472.0104271	1884.010509	0.000451244	1	N	66	83
P02088	Exosome	AAFQK	VVAGVATALAHK	YH-	2		568.8434695	1135.671339	0.001871652	15	Y	133	145
P02088	Exosome	VITAF	NDGLNHLDSLK	GTFAS	2		613.3127305	1224.609861	0.000451244	23	N	72	83
P02088	Exosome	VITAF	NDGLNHLDSLK	GTFAS	3		409.211087	1224.609861	0.002813207	1	N	72	83

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P02088	Exosome	LHCDK	LHVDPENFR	LLGNM	2		563.7861515	1125.556703	0.000823681	11	Y	96	105
P02088	Exosome	LDSLK	GTFASLSELHCDK	LHVDP	2	C11:+57.021	732.8433062	1463.671012	0.000451244	108	Y	83	96
P02088	Exosome	LDSLK	GTFASLSELHCDK	LHVDP	3	C11:+57.021	488.8981375	1463.671012	0.000451244	19	Y	83	96
P02088	Exosome	SLKGT	FASLSELHCDK	LHVDP	2	C9:+57.021	653.808735	1305.60187	0.000451244	6	Y	85	96
P02088	Exosome	KGTFA	SLSELHCDKLHVDPENFR	LLGNM	2	C7:+57.021	1098.529043	2195.042485	0.000451244	4	Y	87	105
P02088	Exosome	KGTFA	SLSELHCDKLHVDPENFR	LLGNM	3	C7:+57.021	732.6886284	2195.042485	0.000451244	8	Y	87	105
P02088	Exosome	KGTFA	SLSELHCDKLHVDPENFR	LLGNM	4	C7:+57.021	549.7684213	2195.042485	0.001229886	2	Y	87	105
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLKG	TFASL	2		907.4763046	1812.937009	0.000451244	18	N	67	84
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLKG	TFASL	3		605.3201364	1812.937009	0.000823681	11	N	67	84
P02088	Exosome	GKKVI	TAFNDGLNHLDSLK	GTFAS	2		772.8893337	1543.763067	0.000451244	12	N	69	83
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLK	GTFAS	2		878.9655727	1755.915545	0.000451244	72	N	67	83
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLK	GTFAS	3		586.3129818	1755.915545	0.000451244	101	N	67	83
P02088	Exosome	WTQRY	FDSFGDLSSASAIMGNAK	VKAHG	2		909.422881	1816.830162	0.000451244	6	N	42	60
P02088	Exosome	WTQRY	FDSFGDLSSASAIMGNAK	VKAHG	2	M14:+15.995	917.420381	1832.825162	0.000451244	18	N	42	60
P02088	Exosome	PENFR	LLGNMIVIVLGHHLGK	DFTPA	2		857.5139821	1713.012364	0.000622848	8	N	105	121
P02088	Exosome	PENFR	LLGNMIVIVLGHHLGK	DFTPA	3		572.0119214	1713.012364	0.000622848	5	N	105	121
P02088	Exosome	PENFR	LLGNMIVIVLGHHLGK	DFTPA	4		429.2608911	1713.012364	0.000622848	23	N	105	121
P02088	Exosome	PENFR	LLGNMIVIVLGHHLGK	DFTPA	4	M5:+15.995	433.2596411	1729.007364	0.001699387	3	N	105	121
P02088	Exosome	AAFQK	VVAGVATALAHKYH	-	2		718.9045898	1435.79358	0.000451244	18	Y	133	147
P02088	Exosome	AAFQK	VVAGVATALAHKYH	-	3		479.6056598	1435.79358	0.000451244	9	Y	133	147
P02088	Exosome	AFQKV	VAGVATALAHK	YH-	2		519.3092625	1036.602925	0.002663018	1	Y	134	145
P02088	Exosome	HHLGK	DFTPAAQAAF	QKVVA	2		519.7487033	1037.481807	0.000823681	2	Y	121	131
P02088	Exosome	HGKKV	ITAFNDGLNHLDSLK	GTFAS	2		829.4313657	1656.847131	0.000451244	4	N	68	83
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLKGTFA	SLSEL	2		1067.052908	2132.090216	0.000451244	2	N	67	87
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLKGTFA	SLSEL	3		711.7045385	2132.090216	0.000451244	5	N	67	87
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLKGTFASLSELHCDK	LHVDP	3	C27:+57.021	1068.199799	3201.575998	0.000451244	4	N	67	96
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLKGTFASLSELHCDK	LHVDP	4	C27:+57.021	801.4017995	3201.575998	0.000451244	2	N	67	96
P02088	Exosome	PENFR	LLGNMIVIVLGHHLGKDFTPAAQAAFQK	VVAGV	3		997.2201839	2988.637152	0.000451244	4	N	105	133
P02088	Exosome	PENFR	LLGNMIVIVLGHHLGKDFTPAAQAAFQK	VVAGV	4		748.1670879	2988.637152	0.001591523	2	N	105	133
P02088	Exosome	EALGR	LLVVYPWTQRY	FDSFG	2		719.3986089	1436.781618	0.001654178	8	Y	31	42
P02088	Exosome	TFASL	SELHCDKLHVDPENFR	LLGNM	3	C5:+57.021	665.9832642	1994.926393	0.001229886	1	Y	89	105
P02088	Exosome	TFASL	SELHCDKLHVDPENFR	LLGNM	4	C5:+57.021	499.7393982	1994.926393	0.001591523	1	Y	89	105
P02088	Exosome	AHGKK	VITAFNDGLNHLDSLKGTFASL	SELHC	3		778.4099027	2332.206308	0.000823681	3	N	67	89
P02088	Exosome	IVIVL	GHHLGKDFTPAAQAAFQK	VVAGV	3		641.9995087	1922.975126	0.000451244	3	Y	115	133
P02088	Exosome	PWTQR	YFDSFGDLSSAS	AIMGN	2		648.2754793	1294.535359	0.0025889	1	Y	41	53
P02088	Parental	LDSLK	GTFASLSELHCDKLHVDPENFR	LLGNM	2	C11:+57.021	1286.616378	2571.217155	0.001871652	1	Y	83	105
P02088	Parental	LDSLK	GTFASLSELHCDKLHVDPENFR	LLGNM	3	C11:+57.021	858.0801851	2571.217155	0.000451244	39	Y	83	105
P02088	Parental	LDSLK	GTFASLSELHCDKLHVDPENFR	LLGNM	4	C11:+57.021	643.8120889	2571.217155	0.000451244	15	Y	83	105
P02088	Parental	-M	VHLTDAEKAAVSCLWGK	VNSDE	2	C13:+57.021	942.9857509	1883.955902	0.000451244	7	N	1	18
P02088	Parental	-M	VHLTDAEKAAVSCLWGK	VNSDE	3	C13:+57.021	628.9931006	1883.955902	0.000451244	5	N	1	18
P02088	Parental	PWTQR	YFDSFGDLSSASAIMGNAK	VKAHG	2		990.9545453	1979.893491	0.000451244	25	N	41	60
P02088	Parental	PWTQR	YFDSFGDLSSASAIMGNAK	VKAHG	2	M15:+15.995	998.9520453	1995.888491	0.000451244	7	N	41	60
P02088	Parental	EALGR	LLVVYPWTQR	YFDSF	2		637.8669446	1273.718289	0.000451244	55	Y	31	41
P02088	Parental	CLWGK	VNSDEVGGEALGR	LLVVY	2		651.818377	1301.621154	0.000451244	18	N	18	31
P02088	Parental	TDAEK	AAVSCLWGK	VNSDE	2	C5:+57.021	496.2554099	990.4952199	0.000451244	17	N	9	18
P02088	Parental	HHLGK	DFTPAAQAAFQK	VVAGV	2		647.8254737	1293.635347	0.000451244	24	Y	121	133
P02088	Parental	KAHGK	KVITAFNDGLNHLDSLK	GTFAS	2		943.0130543	1884.010509	0.000451244	2	N	66	83
P02088	Parental	KAHGK	KVITAFNDGLNHLDSLK	GTFAS	3		629.0113029	1884.010509	0.000451244	4	N	66	83
P02088	Parental	VITAF	NDGLNHLDSLK	GTFAS	2		613.3127305	1224.609861	0.001395409	1	N	72	83
P02088	Parental	LHCDK	LHVDPENFR	LLGNM	2		563.7861515	1125.556703	0.001352548	5	Y	96	105
P02088	Parental	LDSLK	GTFASLSELHCDK	LHVDP	2	C11:+57.021	732.8433062	1463.671012	0.000451244	13	Y	83	96
P02088	Parental	LDSLK	GTFASLSELHCDK	LHVDP	3	C11:+57.021	488.8981375	1463.671012	0.001839721	2	Y	83	96
P02088	Parental	GKKVI	TAFNDGLNHLDSLK	GTFAS	2		772.8893337	1543.763067	0.000451244	1	N	69	83
P02088	Parental	AHGKK	VITAFNDGLNHLDSLK	GTFAS	2		878.9655727	1755.915545	0.000451244	9	N	67	83
P02088	Parental	AHGKK	VITAFNDGLNHLDSLK	GTFAS	3		586.3129818	1755.915545	0.000451244	16	N	67	83
P02088	Parental	WTQRY	FDSFGDLSSASAIMGNAK	VKAHG	2	M14:+15.995	917.420381	1832.825162	0.000451244	5	N	42	60
P02088	Parental	PENFR	LLGNMIVIVLGHHLGK	DFTPA	4		429.2608911	1713.012364	0.000622848	4	N	105	121
P02088	Parental	AAFQK	VVAGVATALAHKYH	-	2		718.9045898	1435.79358	0.002663018	2	Y	133	147
P02089	Exosome	LDNLK	GTFASLSELHCDKLHVDPENFR	LLGNA	2	C11:+57.021	1286.616378	2571.217155	0.000451244	40	Y	83	105
P02089	Exosome	LDNLK	GTFASLSELHCDKLHVDPENFR	LLGNA	3	C11:+57.021	858.0801851	2571.217155	0.000451244	137	Y	83	105
P02089	Exosome	LDNLK	GTFASLSELHCDKLHVDPENFR	LLGNA	4	C11:+57.021	643.8120889	2571.217155	0.000451244	101	Y	83	105
P02089	Exosome	PENFR	LLGNAIVIVLGHHLGK	DFTPA	2		827.5122961	1653.008992	0.000451244	15	N	105	121
P02089	Exosome	PENFR	LLGNAIVIVLGHHLGK	DFTPA	3		552.0107974	1653.008992	0.000451244	20	N	105	121
P02089	Exosome	PENFR	LLGNAIVIVLGHHLGK	DFTPA	4		414.2600481	1653.008992	0.000451244	66	N	105	121
P02089	Exosome	EALGR	LLVVYPWTQR	YFDSF	2		637.8669446	1273.718289	0.000451244	440	Y	31	41

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P02089	Exosome	EALGR	LLVVYPWTQR	YFDSF	3		425.5805631	1273.718289	0.000823681	3	Y	31	41
P02089	Exosome	PWTQR	YFDSFGDLSSASAIMGNPK	VKAHG	2		1003.96237	2005.909141	0.000451244	32	N	41	60
P02089	Exosome	PWTQR	YFDSFGDLSSASAIMGNPK	VKAHG	3		669.6441802	2005.909141	0.000451244	10	N	41	60
P02089	Exosome	PWTQR	YFDSFGDLSSASAIMGNPK	VKAHG	2	M15:+15.995	1011.95987	2021.904141	0.000451244	47	N	41	60
P02089	Exosome	HHLGK	DFTPAAQAAFQK	VVAGV	2		647.8254737	1293.635347	0.000451244	139	Y	121	133
P02089	Exosome	CLWAK	VNPDEVGGEALGR	LLVVY	2		656.8287447	1311.641889	0.000451244	64	N	18	31
P02089	Exosome	AAFQK	VVAGVATALAHK	YH-	2		568.8434695	1135.671339	0.001871652	15	Y	133	145
P02089	Exosome	KAHGK	KVITAFNEGLK	NLDNL	2		610.3564097	1218.697219	0.000998612	4	N	66	77
P02089	Exosome	KAHGK	KVITAFNEGLK	NLDNL	3		407.2402065	1218.697219	0.000637154	14	N	66	77
P02089	Exosome	LHCDK	LHVDPENFR	LLGNA	2		563.7861515	1125.556703	0.000823681	11	Y	96	105
P02089	Exosome	LDNLK	GTFASLSELHCDK	LHVDP	2	C11:+57.021	732.8433062	1463.671012	0.000451244	108	Y	83	96
P02089	Exosome	LDNLK	GTFASLSELHCDK	LHVDP	3	C11:+57.021	488.8981375	1463.671012	0.000451244	19	Y	83	96
P02089	Exosome	NLKGT	FASLSELHCDK	LHVDP	2	C9:+57.021	653.808735	1305.60187	0.000451244	6	Y	85	96
P02089	Exosome	TDAEK	SAVSCLWAK	VNPDE	2	C5:+57.021	511.2606923	1020.505785	0.000451244	45	N	9	18
P02089	Exosome	KGTFA	SLSELHCDKLHVDPENFR	LLGNA	2	C7:+57.021	1098.529043	2195.042485	0.000451244	4	Y	87	105
P02089	Exosome	KGTFA	SLSELHCDKLHVDPENFR	LLGNA	3	C7:+57.021	732.6886284	2195.042485	0.000451244	8	Y	87	105
P02089	Exosome	KGTFA	SLSELHCDKLHVDPENFR	LLGNA	4	C7:+57.021	549.7684213	2195.042485	0.001229886	2	Y	87	105
P02089	Exosome	AHGKK	VITAFNEGLK	NLDNL	2		546.3089281	1090.602256	0.000823681	28	N	67	77
P02089	Exosome	AAFQK	VVAGVATALAHKYH	-	2		718.9045898	1435.79358	0.000451244	18	Y	133	147
P02089	Exosome	AAFQK	VVAGVATALAHKYH	-	3		479.6056598	1435.79358	0.000451244	9	Y	133	147
P02089	Exosome	WAKVN	PDEVGGEALGR	LLVVY	2		550.2730739	1098.530548	0.002212458	2	N	20	31
P02089	Exosome	PENFR	LLGNAIVIVLGH	HLGKD	2		609.8825947	1217.749589	0.002453667	1	N	105	117
P02089	Exosome	AFQKV	VAGVATALAHK	YH-	2		519.3092625	1036.602925	0.002663018	1	Y	134	145
P02089	Exosome	HHLGK	DFTPAAQAAF	QKVVA	2		519.7487033	1037.481807	0.000823681	2	Y	121	131
P02089	Exosome	PENFR	LLGNAIVIVLGHHLGKDFTPAAQAAFQK	VVAGV	3		977.2190599	2928.63378	0.000451244	5	N	105	133
P02089	Exosome	PENFR	LLGNAIVIVLGHHLGKDFTPAAQAAFQK	VVAGV	4		733.1662449	2928.63378	0.000979378	7	N	105	133
P02089	Exosome	EALGR	LLVVYPWTQRY	FDSFG	2		719.3986089	1436.781618	0.001654178	8	Y	31	42
P02089	Exosome	TFASL	SELHCDKLHVDPENFR	LLGNA	3	C5:+57.021	665.9832642	1994.926393	0.001229886	1	Y	89	105
P02089	Exosome	TFASL	SELHCDKLHVDPENFR	LLGNA	4	C5:+57.021	499.7393982	1994.926393	0.001591523	1	Y	89	105
P02089	Exosome	IVIVL	GHHLGKDFTPAAQAAFQK	VVAGV	3		641.9995087	1922.975126	0.000451244	3	Y	115	133
P02089	Exosome	PWTQR	YFDSFGDLSSAS	AIMGN	2		648.2754793	1294.535359	0.0025889	1	Y	41	53
P02089	Exosome	WTQRY	FDSFGDLSSASAIMGNPK	VKAHG	2	M14:+15.995	930.428206	1858.840812	0.000451244	1	N	42	60
P02089	Parental	LDNLK	GTFASLSELHCDKLHVDPENFR	LLGNA	2	C11:+57.021	1286.616378	2571.217155	0.001871652	1	Y	83	105
P02089	Parental	LDNLK	GTFASLSELHCDKLHVDPENFR	LLGNA	3	C11:+57.021	858.0801851	2571.217155	0.000451244	39	Y	83	105
P02089	Parental	LDNLK	GTFASLSELHCDKLHVDPENFR	LLGNA	4	C11:+57.021	643.8120889	2571.217155	0.000451244	15	Y	83	105
P02089	Parental	PENFR	LLGNAIVIVLGHHLGK	DFTPA	3		552.0107974	1653.008992	0.000622848	2	N	105	121
P02089	Parental	PENFR	LLGNAIVIVLGHHLGK	DFTPA	4		414.2600481	1653.008992	0.000451244	27	N	105	121
P02089	Parental	EALGR	LLVVYPWTQR	YFDSF	2		637.8669446	1273.718289	0.000451244	55	Y	31	41
P02089	Parental	PWTQR	YFDSFGDLSSASAIMGNPK	VKAHG	2		1003.96237	2005.909141	0.000451244	13	N	41	60
P02089	Parental	HHLGK	DFTPAAQAAFQK	VVAGV	2		647.8254737	1293.635347	0.000451244	24	Y	121	133
P02089	Parental	CLWAK	VNPDEVGGEALGR	LLVVY	2		656.8287447	1311.641889	0.000451244	6	N	18	31
P02089	Parental	LHCDK	LHVDPENFR	LLGNA	2		563.7861515	1125.556703	0.001352548	5	Y	96	105
P02089	Parental	LDNLK	GTFASLSELHCDK	LHVDP	2	C11:+57.021	732.8433062	1463.671012	0.000451244	13	Y	83	96
P02089	Parental	LDNLK	GTFASLSELHCDK	LHVDP	3	C11:+57.021	488.8981375	1463.671012	0.001839721	2	Y	83	96
P02089	Parental	TDAEK	SAVSCLWAK	VNPDE	2	C5:+57.021	511.2606923	1020.505785	0.000622848	2	N	9	18
P02089	Parental	AHGKK	VITAFNEGLK	NLDNL	2		546.3089281	1090.602256	0.000622848	1	N	67	77
P02089	Parental	AAFQK	VVAGVATALAHKYH	-	2		718.9045898	1435.79358	0.002663018	2	Y	133	147
P02535	Exosome	EVTLR	QSVEADINGLRR	VLDEL	3		453.2447907	1356.710972	0.002019181	2	N	243	255
P02535	Exosome	QLALK	QSLEASLAETEGR	YCVQL	2		695.8445918	1389.673584	0.000451244	4	N	384	397
P02535	Exosome	MDKVR	ALEESNYELEGK	IKEWY	2		691.3282432	1380.640886	0.000451244	4	N	163	175
P03958	Parental	LKTER	VGHGYHTIEDEALYNR	LLKEN	2		937.4455358	1872.875472	0.000451244	5	N	235	251
P03958	Parental	LANSK	VDPMPWNQTEGDVTPDDVVDLVNQGLQEGEQAFGIK	VRSIL	3		1314.290226	3939.847277	0.002813207	1	N	111	147
P03958	Parental	FKNDK	ANYSLNTDDPLIFK	STLDT	2		805.9071921	1609.798784	0.001463592	1	N	287	301
P04104	Exosome	IDKVR	FLEQQNQVLQTK	WELLQ	2		738.3967946	1474.777989	0.000451244	32	N	207	219
P04104	Exosome	EINKR	TNAENEFVTIKK	DVDSA	3		465.2494303	1392.724891	0.000451244	10	N	285	297
P04104	Exosome	EINKR	TNAENEFVTIK	KDVDS	2		633.3227639	1264.629928	0.002374549	1	N	285	296
P04104	Parental	IDKVR	FLEQQNQVLQTK	WELLQ	2		738.3967946	1474.777989	0.000451244	12	N	207	219
P04202	Exosome	YLGNR	LLTPTDTPEWLSFDVTGVVR	QWLNQ	2		1123.589323	2245.163046	0.000451244	27	N	185	205
P04202	Exosome	YLGNR	LLTPTDTPEWLSFDVTGVVR	QWLNQ	3		749.3954821	2245.163046	0.000451244	9	N	185	205
P04202	Exosome	STRDR	VAGESADPEPEPEADYYAK	EVTRV	2		1019.450346	2036.885093	0.000451244	44	N	87	106
P04202	Exosome	TGVVR	QWLNQGDGIQGFR	FSAHC	2		759.8765606	1517.737521	0.000451244	7	N	205	218
P04202	Exosome	TQYSK	VLALYNQHNPGASASPCCVPQALEPLPIVYYVGR	KPKVE	3	C17:+57.021,C18:+57.021	1251.967727	3752.87978	0.000451244	22	N	338	372
P04202	Exosome	IHEPK	GYHANFCLGPCPYIWSLDTQYSK	VLALY	3	C7:+57.021,C11:+57.021	926.4212882	2776.240465	0.000451244	5	N	315	338
P04202	Exosome	LRLQR	LKSSVEQHVELYQK	YSNNS	3		563.3058272	1686.894082	0.001162105	1	N	159	173
P04202	Parental	YLGNR	LLTPTDTPEWLSFDVTGVVR	QWLNQ	2		1123.589323	2245.163046	0.000451244	20	N	185	205

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P04202	Parental	STRDR	VAGESADPEPEPEADYYAK	EVTRV	2		1019.450346	2036.885093	0.000622848	6	N	87	106
P04228	Exosome	KTVWR	LPEFGQLILFEPQGGLQNIAAEK	HNLGI	3		838.1202408	2511.337323	0.000451244	7	N	71	94
P04228	Exosome	LRNSK	SVTDGVYETSFLVNR	DHSFH	2		843.9208308	1685.826062	0.000451244	2	N	153	168
P04228	Exosome	HSFHK	LSYLTFIPSDDDIYDCKVEHWGLEEPVLK	HWEPE	3	C16:+57.021	1161.234287	3480.67946	0.002145581	1	N	174	203
P04228	Exosome	HSFHK	LSYLTFIPSDDDIYDCK	VEHWG	2	C16:+57.021	1032.977454	2063.939308	0.002212458	1	N	174	191
P04228	Parental	KTVWR	LPEFGQLILFEPQGGLQNIAAEK	HNLGI	3		838.1202408	2511.337323	0.001591523	1	N	71	94
P04919	Exosome	LLLKR	SHAEDLGNLEGVKPAVLTR	SGGAS	2		1003.537425	2005.05925	0.000451244	25	N	175	194
P04919	Exosome	LLLKR	SHAEDLGNLEGVKPAVLTR	SGGAS	3		669.3608833	2005.05925	0.000451244	35	N	175	194
P04919	Exosome	LLLKR	SHAEDLGNLEGVKPAVLTR	SGGAS	4		502.2726125	2005.05925	0.000451244	17	N	175	194
P04919	Exosome	AVLTR	SGGASEPLLPHQPSLETQLYCGQAEGGSEGPSTSGTLK	IPPDS	3	C21:+57.021	1276.606171	3826.795112	0.000451244	110	N	194	232
P04919	Exosome	AVLTR	SGGASEPLLPHQPSLETQLYCGQAEGGSEGPSTSGTLK	IPPDS	4	C21:+57.021	957.706578	3826.795112	0.000451244	25	N	194	232
P04919	Exosome	VLVGR	ANFLEKPVLGFVR	LKEAV	2		745.4304404	1488.845281	0.000451244	8	N	246	259
P04919	Exosome	VLVGR	ANFLEKPVLGFVR	LKEAV	3		497.2895603	1488.845281	0.000451244	48	N	246	259
P04919	Exosome	LGFVR	LKEAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1346.41743	4036.22889	0.000451244	25	N	259	296
P04919	Exosome	LGFVR	LKEAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	4		1010.065022	4036.22889	0.000451244	26	N	259	296
P04919	Exosome	LGFVR	LKEAVPLEDLVLPEPVGF	LLVLL	2		983.0513138	1964.087028	0.000662267	11	N	259	277
P04919	Exosome	FVRLK	EAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1266.024421	3795.049862	0.000451244	31	N	261	296
P04919	Exosome	FVRLK	EAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	4		949.7702656	3795.049862	0.000451244	8	N	261	296
P04919	Exosome	EELLR	SLESFLDCSLVLPPTDAPSEK	ALLNL	2	C8:+57.021	1153.067332	2304.119064	0.000451244	27	N	322	343
P04919	Exosome	EELLR	SLESFLDCSLVLPPTDAPSEK	ALLNL	3	C8:+57.021	769.047488	2304.119064	0.000451244	15	N	322	343
P04919	Exosome	TVMGK	ASGPGAAAQIQEVK	EQRIS	2		663.8547625	1325.693925	0.000622848	3	N	761	775
P04919	Exosome	ALLLK	RSHAEDLGNLEGVKPAVLTR	SGGAS	3		721.394587	2161.160361	0.000451244	1	N	174	194
P04919	Exosome	ALLLK	RSHAEDLGNLEGVKPAVLTR	SGGAS	4		541.2978902	2161.160361	0.000451244	19	N	174	194
P04919	Exosome	SGTLK	IPPDSETTLVLVGR	ANFLE	2		748.9201025	1495.824605	0.000451244	24	N	232	246
P04919	Exosome	APSEK	ALLNLVPVQK	ELLRR	2		547.8507632	1093.685926	0.000451244	36	N	343	353
P04919	Exosome	AVLTR	SGGASEPLLPHQPSLETQLY	CGQAE	2		1062.534548	2123.053496	0.000451244	14	N	194	214
P04919	Exosome	MMDQR	NQELQWVEAAHWIGLEENLR	EDGVW	2		1218.109277	2434.202954	0.000451244	14	N	83	103
P04919	Exosome	MMDQR	NQELQWVEAAHWIGLEENLR	EDGVW	3		812.4087847	2434.202954	0.000451244	24	N	83	103
P04919	Exosome	GVWGR	PHLSYLTFWSLLELQK	VFSKG	3		659.0282938	1974.061482	0.001395409	3	N	110	126
P04919	Exosome	KVFSK	GTFLLGLAETSLAGVANHLLDCFIYEDQIRPQDREELLR	ALLLK	4	C22:+57.021	1119.077642	4472.27937	0.000823681	8	N	130	169
P04919	Exosome	KVFSK	GTFLLGLAETSLAGVANHLLDCFIYEDQIRPQDR	EELLR	3	C22:+57.021	1278.316115	3831.924944	0.000451244	22	N	130	164
P04919	Exosome	KVFSK	GTFLLGLAETSLAGVANHLLDCFIYEDQIRPQDR	EELLR	4	C22:+57.021	958.9890361	3831.924944	0.000622848	5	N	130	164
P04919	Exosome	GKLRR	VIGDFGVPISILIMVLVDSFIK	GTYTQ	2		1188.187088	2374.358576	0.000451244	2	N	621	643
P04919	Exosome	GKLRR	VIGDFGVPISILIMVLVDSFIK	GTYTQ	3		792.4606588	2374.358576	0.000451244	2	N	621	643
P04919	Exosome	EPVGF	LLVLLGPEAPHVDYTQLGR	AAATL	2		1046.084011	2090.152422	0.000451244	3	N	277	296
P04919	Exosome	MMDQR	NQELQWVEAAHWIGLEENLREDGVWGR	PHLSY	3		1078.862552	3233.564256	0.001463592	4	N	83	110
P04919	Exosome	MMDQR	NQELQWVEAAHWIGLEENLREDGVWGR	PHLSY	4		809.3988641	3233.564256	0.002453667	1	N	83	110
P04919	Exosome	EAVPL	EDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1096.262771	3285.764913	0.000622848	1	N	266	296
P04919	Exosome	LLVLL	GPEAPHVDYTQLGR	AAATL	2		770.3816758	1538.747752	0.002212458	1	N	282	296
P04919	Exosome	LGFVR	LKEAVPLEDLVLPEPVGFLLV	LLGPE	2		1145.669585	2289.32357	0.002296037	1	N	259	280
P04919	Exosome	LGFVR	LKEAVPLEDLVLPEPVGFL	LVLLG	2		1039.593346	2077.171092	0.000622848	6	N	259	278
P04919	Exosome	LGFVR	LKEAVPLEDLVLPEPVGFLL	VLLGP	2		1096.135378	2190.255156	0.001229886	2	N	259	279
P04919	Exosome	SLETQ	LYCGQAEGGSEGPSTSGTLK	IPPDS	2	C3:+57.021	999.9575844	1997.899569	0.000451244	3	N	212	232
P04919	Exosome	AVLTR	SGGASEPLLPHQPSLETQ	LYCGQ	2		924.4608515	1846.906103	0.000451244	2	N	194	212
P04919	Exosome	FVRLK	EAVPLEDLVLPEPVGFL	LVLLG	2		919.0038323	1835.992065	0.001463592	1	N	261	278
P04919	Parental	LLLKR	SHAEDLGNLEGVKPAVLTR	SGGAS	2		1003.537425	2005.05925	0.000451244	16	N	175	194
P04919	Parental	LLLKR	SHAEDLGNLEGVKPAVLTR	SGGAS	4		502.2726125	2005.05925	0.000451244	8	N	175	194
P04919	Parental	AVLTR	SGGASEPLLPHQPSLETQLYCGQAEGGSEGPSTSGTLK	IPPDS	3	C21:+57.021	1276.606171	3826.795112	0.000451244	56	N	194	232
P04919	Parental	AVLTR	SGGASEPLLPHQPSLETQLYCGQAEGGSEGPSTSGTLK	IPPDS	4	C21:+57.021	957.706578	3826.795112	0.000451244	3	N	194	232
P04919	Parental	VLVGR	ANFLEKPVLGFVR	LKEAV	2		745.4304404	1488.845281	0.000823681	2	N	246	259
P04919	Parental	VLVGR	ANFLEKPVLGFVR	LKEAV	3		497.2895603	1488.845281	0.000451244	20	N	246	259
P04919	Parental	LGFVR	LKEAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1346.41743	4036.22889	0.000451244	3	N	259	296
P04919	Parental	LGFVR	LKEAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	4		1010.065022	4036.22889	0.000451244	11	N	259	296
P04919	Parental	LGFVR	LKEAVPLEDLVLPEPVGF	LLVLL	2		983.0513138	1964.087028	0.000622848	8	N	259	277
P04919	Parental	FVRLK	EAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	3		1266.024421	3795.049862	0.000823681	8	N	261	296
P04919	Parental	FVRLK	EAVPLEDLVLPEPVGFLLVLLGPEAPHVDYTQLGR	AAATL	4		949.7702656	3795.049862	0.000451244	1	N	261	296
P04919	Parental	EELLR	SLESFLDCSLVLPPTDAPSEK	ALLNL	2	C8:+57.021	1153.067332	2304.119064	0.000637154	9	N	322	343
P04919	Parental	SGTLK	IPPDSETTLVLVGR	ANFLE	2		748.9201025	1495.824605	0.000451244	2	N	232	246
P04919	Parental	APSEK	ALLNLVPVQK	ELLRR	2		547.8507632	1093.685926	0.000451244	9	N	343	353
P04919	Parental	MMDQR	NQELQWVEAAHWIGLEENLR	EDGVW	3		812.4087847	2434.202954	0.000698008	1	N	83	103
P04919	Parental	KVFSK	GTFLLGLAETSLAGVANHLLDCFIYEDQIRPQDREELLR	ALLLK	4	C22:+57.021	1119.077642	4472.27937	0.002813207	1	N	130	169
P04919	Parental	EPVGF	LLVLLGPEAPHVDYTQLGR	AAATL	2		1046.084011	2090.152422	0.000451244	1	N	277	296
P04919	Parental	EPVGF	LLVLLGPEAPHVDYTQLGR	AAATL	3		697.725274	2090.152422	0.001162105	1	N	277	296
P04919	Parental	MMDQR	NQELQWVEAAHWIGLEENLREDGVWGR	PHLSY	3		1078.862552	3233.564256	0.001162105	1	N	83	110
P05201	Exosome	KVEQK	IANDNSLNHEYLPILGLAEFR	SCASR	2		1200.121853	2398.228106	0.000451244	9	N	60	81

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P05201	Exosome	KVEQK	IANDNSLNHEYLPILGLAEFR	SCASR	3		800.4171688	2398.228106	0.000451244	31	N	60	81
P05201	Exosome	-M	APPSVFAQVPQAPPVLVFK	LTADF	2		996.5700081	1991.124416	0.000451244	26	N	1	20
P05201	Exosome	VMQRR	FLFPFFDSAYQGFASGDLEK	DAWAI	2		1143.541842	2285.068083	0.000451244	18	N	216	236
P05201	Exosome	VMQRR	FLFPFFDSAYQGFASGDLEK	DAWAI	3		762.6971611	2285.068083	0.000451244	12	N	216	236
P05201	Exosome	VGAYR	TDESQPWVLPVVR	KVEQK	2		763.4046196	1524.793639	0.000451244	21	N	42	55
P05201	Exosome	AQGAR	IVAATLSDPELFK	EWKGN	2		702.3931892	1402.770778	0.001162105	1	N	305	318
P05201	Exosome	GLTTK	NLDYVATSIHEAVTK	IQ-	3		554.2900657	1659.846797	0.0007646	3	N	396	411
P05201	Exosome	AQGAR	IVAATLSDPELFKEWK	GNVKT	3		616.3370159	1845.987648	0.000622848	3	N	305	321
P05201	Parental	KVEQK	IANDNSLNHEYLPILGLAEFR	SCASR	2		1200.121853	2398.228106	0.000451244	6	N	60	81
P05201	Parental	KVEQK	IANDNSLNHEYLPILGLAEFR	SCASR	3		800.4171688	2398.228106	0.000451244	27	N	60	81
P05201	Parental	-M	APPSVFAQVPQAPPVLVFK	LTADF	2		996.5700081	1991.124416	0.000823681	4	N	1	20
P05201	Parental	VMQRR	FLFPFFDSAYQGFASGDLEK	DAWAI	2		1143.541842	2285.068083	0.000451244	5	N	216	236
P05201	Parental	VGAYR	TDESQPWVLPVVR	KVEQK	2		763.4046196	1524.793639	0.000622848	9	N	42	55
P05202	Exosome	TKDGR	ISVAGVTSGNVGYLAHAIHQVTK	-	3		774.7575254	2321.249176	0.000662267	6	N	407	430
P05202	Exosome	TKDGR	ISVAGVTSGNVGYLAHAIHQVTK	-	4		581.320094	2321.249176	0.000823681	19	N	407	430
P05202	Exosome	QIAAK	NLDKEYLPIGGLAEFCK	ASAEL	2	C16:+57.021	984.0010667	1965.986533	0.000451244	37	N	90	107
P05202	Exosome	QIAAK	NLDKEYLPIGGLAEFCK	ASAEL	3	C16:+57.021	656.3366444	1965.986533	0.000451244	37	N	90	107
P05202	Exosome	LKSGR	FVTVQTISGTGALR	VGASF	2		725.4071623	1448.798725	0.002080925	1	N	125	139
P05202	Exosome	AEFCK	ASAELALGENNEVLK	SGRFV	2		779.410099	1556.804598	0.000451244	21	N	107	122
P05202	Exosome	YYDPK	TCGFDFSGALEDISK	IPEQS	2	C2:+57.021	823.8722607	1645.728921	0.000451244	29	N	185	200
P05202	Exosome	LNGAR	IAATILTSPDLR	KQWLQ	2		635.8724239	1269.729248	0.000451244	3	N	325	337
P05202	Exosome	VVKKK	NLFAFFDMAYQGFASGDGDKDAWAVR	HFIEQ	3	M8:+15.995	972.4418542	2914.302163	0.000451244	9	N	236	262
P05202	Exosome	ASARA	SSWWTHVEMGPPDPILGVTEAFKR	DTNSK	4	M9:+15.995	689.8435263	2755.342905	0.000735798	2	N	29	53
P05202	Parental	TKDGR	ISVAGVTSGNVGYLAHAIHQVTK	-	4		581.320094	2321.249176	0.000823681	25	N	407	430
P05202	Parental	QIAAK	NLDKEYLPIGGLAEFCK	ASAEL	2	C16:+57.021	984.0010667	1965.986533	0.000451244	26	N	90	107
P05202	Parental	QIAAK	NLDKEYLPIGGLAEFCK	ASAEL	3	C16:+57.021	656.3366444	1965.986533	0.000451244	35	N	90	107
P05202	Parental	LKSGR	FVTVQTISGTGALR	VGASF	2		725.4071623	1448.798725	0.000451244	20	N	125	139
P05202	Parental	AEFCK	ASAELALGENNEVLK	SGRFV	2		779.410099	1556.804598	0.000451244	19	N	107	122
P05202	Parental	YYDPK	TCGFDFSGALEDISK	IPEQS	2	C2:+57.021	823.8722607	1645.728921	0.000451244	21	N	185	200
P05202	Parental	EDISK	IPEQSVLLLHACAHNPTGVDPRPEQWK	EIASV	4	C12:+57.021	773.8992269	3091.565708	0.002884417	1	N	200	227
P06151	Exosome	LMGER	LGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	3	C8:+57.021	1204.279335	3609.814606	0.000451244	34	N	177	212
P06151	Exosome	LMGER	LGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	4	C8:+57.021	903.4614514	3609.814606	0.000451244	23	N	177	212
P06151	Exosome	SPHCK	LLIVSNPVDILTY	VAWKI	2		730.4244894	1458.833379	0.000451244	20	N	132	145
P06151	Exosome	STMIK	GLYGINEDVFLSVPCILGQNGISDVVK	VTLTP	2	C15:+57.021	1453.75234	2905.48908	0.000451244	90	N	278	305
P06151	Exosome	STMIK	GLYGINEDVFLSVPCILGQNGISDVVK	VTLTP	3	C15:+57.021	969.50416	2905.48908	0.000451244	109	N	278	305
P06151	Exosome	SPHCK	LLIVSNPVDILTYVAWK	ISGFP	2		972.5643914	1943.113183	0.000451244	107	N	132	149
P06151	Exosome	SPHCK	LLIVSNPVDILTYVAWK	ISGFP	3		648.7121943	1943.113183	0.000451244	77	N	132	149
P06151	Exosome	GVSLK	SLNPELGTDADKEQWK	EVHKQ	2		915.947577	1829.879554	0.000451244	71	N	212	228
P06151	Exosome	GVSLK	SLNPELGTDADKEQWK	EVHKQ	3		610.9676513	1829.879554	0.000622848	25	N	212	228
P06151	Exosome	FPKNR	VIGSGCNLDSAR	FRYLM	2	C6:+57.021	624.803984	1247.592368	0.000451244	2	Y	157	169
P06151	Exosome	ARLKK	SADTLWGIQK	ELQF-	2		559.7961849	1117.57677	0.000451244	57	N	318	328
P06151	Exosome	MATLK	DQLIVNLLKEEQAPQNK	ITVVG	2		990.5421759	1979.068752	0.000451244	42	N	5	22
P06151	Exosome	MATLK	DQLIVNLLKEEQAPQNK	ITVVG	3		660.697384	1979.068752	0.000451244	32	N	5	22
P06151	Exosome	SILMK	DLADELALVDVMEDK	LKGEM	2		838.4089079	1674.802216	0.000451244	6	N	42	57
P06151	Exosome	SILMK	DLADELALVDVMEDK	LKGEM	2	M12:+15.995	846.4064079	1690.797216	0.000451244	9	N	42	57
P06151	Exosome	VIKLK	GYTSWAIGLSVADLAESIMK	NLRRV	2		1056.538245	2111.06089	0.000451244	32	N	245	265
P06151	Exosome	VFLSV	PCILGQNGISDVVK	VTLTP	2	C2:+57.021	750.3982486	1498.780897	0.001162105	3	N	291	305
P06151	Exosome	KEVHK	QVVDSAYEVIK	LKGYT	2		625.8355071	1249.655414	0.000451244	51	N	232	243
P06151	Exosome	KEVHK	QVVDSAYEVIK	LKGYT	2	[0:-17.027	617.3220071	1232.628414	0.000451244	19	N	232	243
P06151	Exosome	GVHAL	SCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	3	C2:+57.021	1007.494658	3019.460574	0.000451244	6	N	183	212
P06151	Exosome	GVHAL	SCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	4	C2:+57.021	755.8729435	3019.460574	0.001463592	2	N	183	212
P06151	Exosome	CKLLI	VSNPVDILTYVAWK	ISGFP	2		802.9382953	1603.860991	0.000451244	2	N	135	149
P06151	Exosome	KEQWK	EVHKQVVDSAYEVIK	LKGYT	2		872.4679482	1742.920296	0.000451244	16	N	228	243
P06151	Exosome	KEQWK	EVHKQVVDSAYEVIK	LKGYT	3		581.9812322	1742.920296	0.001329271	3	N	228	243
P06151	Exosome	RLGVH	ALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	4	C4:+57.021	801.903238	3203.581752	0.000823681	1	N	181	212
P06151	Exosome	SPHCK	LLIVSNPVDIL	TYVAW	2		598.3689858	1194.722372	0.002296037	2	N	132	143
P06151	Exosome	SILMK	DLADELALVDVMEDKLK	GEMMD	3		639.6682144	1915.981243	0.000622848	1	N	42	59
P06151	Parental	LMGER	LGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	3	C8:+57.021	1204.279335	3609.814606	0.000451244	27	N	177	212
P06151	Parental	LMGER	LGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	SLNPE	4	C8:+57.021	903.4614514	3609.814606	0.001162105	1	N	177	212
P06151	Parental	SPHCK	LLIVSNPVDILTY	VAWKI	2		730.4244894	1458.833379	0.000451244	20	N	132	145
P06151	Parental	STMIK	GLYGINEDVFLSVPCILGQNGISDVVK	VTLTP	2	C15:+57.021	1453.75234	2905.48908	0.000451244	62	N	278	305
P06151	Parental	STMIK	GLYGINEDVFLSVPCILGQNGISDVVK	VTLTP	3	C15:+57.021	969.50416	2905.48908	0.000451244	46	N	278	305
P06151	Parental	SPHCK	LLIVSNPVDILTYVAWK	ISGFP	2		972.5643914	1943.113183	0.000451244	68	N	132	149
P06151	Parental	SPHCK	LLIVSNPVDILTYVAWK	ISGFP	3		648.7121943	1943.113183	0.000451244	31	N	132	149
P06151	Parental	STMIK	GLYGINEDVFLSVPCILGQNGISDVVKVTLTPEEEAR	LKKSA	3	C15:+57.021	1344.693028	4031.055684	0.000451244	23	N	278	315

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P06151	Parental	GVSLK	SLNPELGTDADKEQWK	EVHKQ	2		915.947577	1829.879554	0.000451244	32	N	212	228
P06151	Parental	GVSLK	SLNPELGTDADKEQWK	EVHKQ	3		610.9676513	1829.879554	0.000622848	11	N	212	228
P06151	Parental	ARLKK	SADTLWGIQK	ELQF-	2		559.7961849	1117.57677	0.002374549	1	N	318	328
P06151	Parental	MATLK	DQLIVNLLKEEQAPQNK	ITVVG	2		990.5421759	1979.068752	0.000451244	11	N	5	22
P06151	Parental	MATLK	DQLIVNLLKEEQAPQNK	ITVVG	3		660.697384	1979.068752	0.000451244	21	N	5	22
P06151	Parental	VIKLK	GYTSWAIGLSVADLAESIMK	NLRRV	2		1056.538245	2111.06089	0.000451244	5	N	245	265
P06151	Parental	KEVHK	QVVDSAYEVIK	LKGYT	2		625.8355071	1249.655414	0.000662267	7	N	232	243
P06151	Parental	NLVQR	NVNIFKFIIPNIVK	YSPHC	3		553.6717817	1657.991945	0.000451244	3	N	112	126
P06151	Parental	KEQWK	EVHKQVVDSAYEVIK	LKGYT	2		872.4679482	1742.920296	0.000637154	4	N	228	243
P06151	Parental	KLKGY	TSWAIGLSVADLAESIMKNLR	RVHPI	3	M17:+15.995	764.4075336	2290.199201	0.002374549	2	N	247	268
P06336	Exosome	SEDKR	TLTCLIQNFFPEDISVQWLGDGK	LISNS	2	C4:+57.021	1341.167912	2680.320224	0.00091018	2	N	326	349
P06336	Exosome	SEDKR	TLTCLIQNFFPEDISVQWLGDGK	LISNS	3	C4:+57.021	894.4478745	2680.320224	0.000451244	4	N	326	349
P06336	Exosome	PVVAK	DWIEGYGYQCIVDHPDFPKPIVR	SITKT	3	C10:+57.021	935.455252	2803.342356	0.000451244	11	N	275	298
P06745	Exosome	KGGPR	VWFVSNIDGTHIAK	TLASL	2		793.9204368	1585.825274	0.000451244	62	N	180	194
P06745	Exosome	KGGPR	VWFVSNIDGTHIAK	TLASL	3		529.6162246	1585.825274	0.000451244	164	N	180	194
P06745	Exosome	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	2		1423.725065	2845.43453	0.000451244	45	N	523	550
P06745	Exosome	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	3		949.4859768	2845.43453	0.000451244	137	N	523	550
P06745	Exosome	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	4		712.3664326	2845.43453	0.000451244	41	N	523	550
P06745	Exosome	KSGAR	VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	MIPCD	3		1105.881835	3314.622106	0.000451244	75	N	370	400
P06745	Exosome	KSGAR	VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	MIPCD	4		829.6633264	3314.622106	0.000451244	37	N	370	400
P06745	Exosome	NLKLR	ELFEADPERFNNFSLNLNTNHGHILVDYSK	NLVNK	3		1178.574848	3532.701144	0.000451244	17	N	27	57
P06745	Exosome	NLKLR	ELFEADPERFNNFSLNLNTNHGHILVDYSK	NLVNK	4		884.183086	3532.701144	0.000823681	3	N	27	57
P06745	Exosome	IIASK	TFTTQETITNAETAKEWFLEAAK	DPSAV	2		1315.65338	2629.29116	0.000451244	42	N	211	234
P06745	Exosome	IIASK	TFTTQETITNAETAKEWFLEAAK	DPSAV	3		877.4381868	2629.29116	0.000451244	63	N	211	234
P06745	Exosome	THIAK	TLASLSPETSLFIIASK	TFTTQ	2		889.5014568	1776.987314	0.000451244	74	N	194	211
P06745	Exosome	THIAK	TLASLSPETSLFIIASK	TFTTQ	3		593.3369045	1776.987314	0.000451244	30	N	194	211
P06745	Exosome	VDYSK	NLVNKEVMQMLVELAK	SRGVE	3		620.3430084	1858.005625	0.000451244	18	N	57	73
P06745	Exosome	GLHHK	ILLANFLAQTEALMK	GKLPE	2		838.4767309	1674.937862	0.000451244	37	N	423	438
P06745	Exosome	GLHHK	ILLANFLAQTEALMK	GKLPE	3		559.3204206	1674.937862	0.000451244	30	N	423	438
P06745	Exosome	GLHHK	ILLANFLAQTEALMK	GKLPE	2	M14:+15.995	846.4742309	1690.932862	0.000451244	5	N	423	438
P06745	Exosome	GLHHK	ILLANFLAQTEALMK	GKLPE	3	M14:+15.995	564.6520873	1690.932862	0.000451244	8	N	423	438
P06745	Exosome	GYTGK	SITDIINIGIGGSDLGPLMVTEALKPYSK	GGPRV	3		1001.542658	3001.604574	0.000451244	52	N	147	176
P06745	Exosome	GYTGK	SITDIINIGIGGSDLGPLMVTEALKPYSK	GGPRV	4		751.4089435	3001.604574	0.000451244	4	N	147	176
P06745	Exosome	GYTGK	SITDIINIGIGGSDLGPLMVTEALKPYSK	GGPRV	3	M19:+15.995	1006.874325	3017.599574	0.000451244	10	N	147	176
P06745	Exosome	LLPHK	VFEGNRPTNSIVFTK	LTPFI	2		854.955008	1707.894416	0.000451244	37	N	466	481
P06745	Exosome	LLPHK	VFEGNRPTNSIVFTK	LTPFI	3		570.3059387	1707.894416	0.000451244	18	N	466	481
P06745	Exosome	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	2		1224.109277	2446.202954	0.000451244	39	N	36	57
P06745	Exosome	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	3		816.4087847	2446.202954	0.000451244	11	N	36	57
P06745	Exosome	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	4		612.5585385	2446.202954	0.000451244	38	N	36	57
P06745	Exosome	IIASK	TFTTQETITNAETAK	EWFLE	2		828.410296	1654.804992	0.000451244	91	N	211	226
P06745	Exosome	QLAKK	IEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	2		1359.677584	2717.339567	0.000451244	22	N	524	550
P06745	Exosome	QLAKK	IEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	3		906.7876557	2717.339567	0.000451244	17	N	524	550
P06745	Exosome	AETAK	EWFLEAAKDPSAVAK	HFVAL	2		831.4308344	1660.846069	0.000451244	36	N	226	241
P06745	Exosome	AETAK	EWFLEAAKDPSAVAK	HFVAL	3		554.6231563	1660.846069	0.000451244	31	N	226	241
P06745	Exosome	SANLK	LRELFEADPER	FNNFS	2		687.8547625	1373.693925	0.002374549	1	N	25	36
P06745	Exosome	SANLK	LRELFEADPER	FNNFS	3		458.905775	1373.693925	0.001162105	13	N	25	36
P06745	Exosome	AKKIE	PELEGSSAVTSHDSSTNGLISFIK	QQRDT	3		826.07877	2475.21291	0.001463592	1	N	526	550
P06745	Exosome	RFNNF	SLNLNTNHGHILVDYSK	NLVNK	2		962.9979355	1923.980271	0.000451244	5	N	40	57
P06745	Exosome	KSGAR	VDHQTGPIVWGEPGTNGQHAF	YQLIH	2		1124.033038	2246.050476	0.002374549	2	N	370	391
P06745	Exosome	KSGAR	VDHQTGPIVWGEPGTNGQHAF	YQLIH	3		749.691292	2246.050476	0.000622848	5	N	370	391
P06745	Exosome	NLVNK	EVMQMLVELAK	SRGVE	2		645.8439644	1289.672329	0.001162105	4	N	62	73
P06745	Exosome	IVFTK	LTPFILGALIAMYEHK	IFVQG	2		909.0056556	1815.995711	0.000823681	5	N	481	497
P06745	Exosome	IVFTK	LTPFILGALIAMYEHK	IFVQG	3		606.3397037	1815.995711	0.001839721	3	N	481	497
P06745	Exosome	TPLEK	NAPVLLALLGIWYINCYGCETHALLPYDQYMHR	FAAYF	3	C16:+57.021,C19:+57.021	1322.31625	3963.925351	0.000451244	6	N	314	347
P06745	Exosome	HQGTK	MIPCDFLIPVQTQHPIRK	GLHHK	4	C4:+57.021	549.0476427	2192.159371	0.001162105	1	N	400	418
P06745	Exosome	TNTAK	VKEFGIDPQNMFEFWDWVGGR	YSLWS	3		853.0710045	2556.189613	0.002296037	1	N	252	273
P06745	Exosome	GLHHK	ILLANFLAQTEAL	MKGKL	2		708.9090065	1415.802413	0.000823681	1	N	423	436
P06745	Exosome	SAVAK	HFVALSTNTAK	VKEFG	2		594.822734	1187.629868	0.002080925	1	N	241	252
P06745	Exosome	QYMHR	FAAYFQQGDMESNGK	YITKS	2		846.8702842	1691.724968	0.000823681	4	N	347	362
P06745	Exosome	TPLEK	NAPVLLALLGIWYINCYGCETHALLPYDQY	MHRFA	3	C16:+57.021,C19:+57.021	1180.916081	3539.724842	0.002663018	1	N	314	344
P06745	Parental	KGGPR	VWFVSNIDGTHIAK	TLASL	2		793.9204368	1585.825274	0.000451244	9	N	180	194
P06745	Parental	KGGPR	VWFVSNIDGTHIAK	TLASL	3		529.6162246	1585.825274	0.000451244	29	N	180	194
P06745	Parental	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	2		1423.725065	2845.43453	0.000451244	27	N	523	550
P06745	Parental	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	3		949.4859768	2845.43453	0.000451244	50	N	523	550
P06745	Parental	KQLAK	KIEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	4		712.3664326	2845.43453	0.001162105	10	N	523	550

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P06745	Parental	KSGAR	VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	MIPCD	3		1105.881835	3314.622106	0.000451244	60	N	370	400
P06745	Parental	KSGAR	VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	MIPCD	4		829.6633264	3314.622106	0.000451244	15	N	370	400
P06745	Parental	NLKLR	ELFEADPERFNNFSLNLNTNHGHILVDYSK	NLVNK	3		1178.574848	3532.701144	0.000451244	10	N	27	57
P06745	Parental	NLKLR	ELFEADPERFNNFSLNLNTNHGHILVDYSK	NLVNK	4		884.183086	3532.701144	0.000622848	4	N	27	57
P06745	Parental	IIASK	TFTTQETITNAETAKEWFLEAAK	DPSAV	2		1315.65338	2629.29116	0.000451244	21	N	211	234
P06745	Parental	IIASK	TFTTQETITNAETAKEWFLEAAK	DPSAV	3		877.4381868	2629.29116	0.000451244	30	N	211	234
P06745	Parental	THIAK	TLASLSPETSLFIIASK	TFTTQ	2		889.5014568	1776.987314	0.000451244	22	N	194	211
P06745	Parental	THIAK	TLASLSPETSLFIIASK	TFTTQ	3		593.3369045	1776.987314	0.000451244	20	N	194	211
P06745	Parental	VDYSK	NLVNKEVMQMLVELAK	SRGVE	3		620.3430084	1858.005625	0.000451244	10	N	57	73
P06745	Parental	GLHHK	ILLANFLAQTEALMK	GKLPE	2		838.4767309	1674.937862	0.000451244	9	N	423	438
P06745	Parental	GLHHK	ILLANFLAQTEALMK	GKLPE	3		559.3204206	1674.937862	0.000451244	7	N	423	438
P06745	Parental	GYTGK	SITDIINIGIGGSDLGPLMVTEALKPYSK	GGPRV	3		1001.542658	3001.604574	0.000451244	35	N	147	176
P06745	Parental	GYTGK	SITDIINIGIGGSDLGPLMVTEALKPYSK	GGPRV	4		751.4089435	3001.604574	0.000451244	1	N	147	176
P06745	Parental	LLPHK	VFEGNRPTNSIVFTK	LTPFI	2		854.955008	1707.894416	0.000622848	14	N	466	481
P06745	Parental	LLPHK	VFEGNRPTNSIVFTK	LTPFI	3		570.3059387	1707.894416	0.002212458	1	N	466	481
P06745	Parental	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	2		1224.109277	2446.202954	0.000451244	4	N	36	57
P06745	Parental	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	3		816.4087847	2446.202954	0.000451244	3	N	36	57
P06745	Parental	ADPER	FNNFSLNLNTNHGHILVDYSK	NLVNK	4		612.5585385	2446.202954	0.000451244	2	N	36	57
P06745	Parental	IIASK	TFTTQETITNAETAK	EWFLE	2		828.410296	1654.804992	0.000451244	52	N	211	226
P06745	Parental	QLAKK	IEPELEGSSAVTSHDSSTNGLISFIK	QQRDT	3		906.7876557	2717.339567	0.001329271	1	N	524	550
P06745	Parental	AETAK	EWFLEAAKDPSAVAK	HFVAL	2		831.4308344	1660.846069	0.000451244	3	N	226	241
P06745	Parental	AETAK	EWFLEAAKDPSAVAK	HFVAL	3		554.6231563	1660.846069	0.000451244	13	N	226	241
P06745	Parental	KPYSK	GGPRVWFVSNIDGTHIAK	TLASL	4		489.2633191	1953.022076	0.001162105	3	N	176	194
P06745	Parental	RFNNF	SLNLNTNHGHILVDYSK	NLVNK	3		642.334557	1923.980271	0.000662267	1	N	40	57
P06745	Parental	KSGAR	VDHQTGPIVWGEPGTNGQHAF	YQLIH	2		1124.033038	2246.050476	0.002813207	1	N	370	391
P06745	Parental	KSGAR	VDHQTGPIVWGEPGTNGQHAF	YQLIH	3		749.691292	2246.050476	0.000451244	7	N	370	391
P06745	Parental	TPLEK	NAPVLLALLGIWY	INCYG	2		721.9244595	1441.833319	0.000622848	4	N	314	327
P06745	Parental	KSGAR	VDHQTGPIVWGEPGTNGQHAFY	QLIHQ	2		1205.564702	2409.113805	0.002727428	2	N	370	392
P06745	Parental	THIAK	TLASLSPETSLF	IIASK	2		633.3353399	1264.65508	0.002453667	1	N	194	206
P06800	Exosome	QEDSR	GVGTPEPTNSAEEPEHAANGSASPAPTQSS	-	3		959.7643499	2876.26965	0.000851441	4	N	1261	1291
P06800	Exosome	RKEPR	TVYQYQCTTWKGEELPAEPK	DLVSM	3	C7:+57.021	810.0548655	2427.141196	0.000451244	25	N	1102	1122
P06800	Exosome	VKLVK	NVINVQTDLGIPETPKPSCGDPAARK	TLVSW	3	C19:+57.021	926.4802374	2776.417312	0.000735798	5	N	363	389
P06800	Exosome	VKLVK	NVINVQTDLGIPETPKPSCGDPAAR	KTLVS	3	C19:+57.021	883.7819163	2648.322349	0.000451244	38	N	363	388
P06800	Exosome	YDYNR	VELSEINGDAGSTYINASYIDGFKEPR	KYIAA	3		982.4774813	2944.409044	0.000451244	4	N	680	707
P06800	Exosome	KLRRR	VNAFSNFFSGPIVVHCSAGVGR	TGTYI	3	C16:+57.021	774.7201515	2321.137054	0.000823681	11	N	824	846
P06800	Exosome	ADEGR	LFLAEFQSIPR	VFSKF	2		660.8696843	1319.723769	0.000451244	12	N	638	649
P06800	Exosome	LVHCR	DGSQQTGLFCALFNLLESAETEDVVDVFQVVK	SLRKA	3	C10:+57.021	1186.915505	3557.723116	0.000451244	15	N	1156	1188
P06800	Exosome	FCALF	NLLESAETEDVVDVFQVVK	SLRKA	2		1067.549864	2133.084127	0.001229886	5	N	1169	1188
P06800	Parental	GPLNK	AQEDSRGVGTPEPTNSAEEPEHAANGSASPAPTQSS	-	3		1188.530472	3562.568017	0.000451244	10	N	1255	1291
P06800	Parental	QEDSR	GVGTPEPTNSAEEPEHAANGSASPAPTQSS	-	2		1439.142625	2876.26965	0.000451244	61	N	1261	1291
P06800	Parental	QEDSR	GVGTPEPTNSAEEPEHAANGSASPAPTQSS	-	3		959.7643499	2876.26965	0.000451244	42	N	1261	1291
P06800	Parental	RKEPR	TVYQYQCTTWKGEELPAEPK	DLVSM	2	C7:+57.021	1214.578398	2427.141196	0.000451244	16	N	1102	1122
P06800	Parental	RKEPR	TVYQYQCTTWKGEELPAEPK	DLVSM	3	C7:+57.021	810.0548655	2427.141196	0.000451244	48	N	1102	1122
P06800	Parental	VKLVK	NVINVQTDLGIPETPKPSCGDPAARK	TLVSW	3	C19:+57.021	926.4802374	2776.417312	0.000451244	17	N	363	389
P06800	Parental	VKLVK	NVINVQTDLGIPETPKPSCGDPAARK	TLVSW	4	C19:+57.021	695.112128	2776.417312	0.000451244	4	N	363	389
P06800	Parental	VKLVK	NVINVQTDLGIPETPKPSCGDPAAR	KTLVS	2	C19:+57.021	1325.168974	2648.322349	0.000622848	36	N	363	388
P06800	Parental	VKLVK	NVINVQTDLGIPETPKPSCGDPAAR	KTLVS	3	C19:+57.021	883.7819163	2648.322349	0.000451244	85	N	363	388
P06800	Parental	KATGR	EVTHIQFTSWPDHGVPEDPHLLLK	LRRRV	3		932.4770873	2794.407862	0.000451244	9	N	796	820
P06800	Parental	KATGR	EVTHIQFTSWPDHGVPEDPHLLLK	LRRRV	4		699.6097655	2794.407862	0.000451244	13	N	796	820
P06800	Parental	QYQFL	YDIIASIYPAQNGQVK	KTNSQ	2		890.4679482	1778.920296	0.000823681	9	N	1207	1223
P06800	Parental	YDYNR	VELSEINGDAGSTYINASYIDGFKEPR	KYIAA	3		982.4774813	2944.409044	0.000451244	15	N	680	707
P06800	Parental	KLRRR	VNAFSNFFSGPIVVHCSAGVGR	TGTYI	2	C16:+57.021	1161.576327	2321.137054	0.000622848	5	N	824	846
P06800	Parental	KLRRR	VNAFSNFFSGPIVVHCSAGVGR	TGTYI	3	C16:+57.021	774.7201515	2321.137054	0.000451244	16	N	824	846
P06800	Parental	ADEGR	LFLAEFQSIPR	VFSKF	2		660.8696843	1319.723769	0.000451244	10	N	638	649
P06800	Parental	LKPYK	YYEVSLLAYVNGK	IQRNG	2		759.8960961	1517.776592	0.000451244	13	N	440	453
P06800	Parental	LFCAL	FNLLESAETEDVVDVFQVVK	SLRKA	2		1141.084071	2280.152541	0.000451244	14	N	1168	1188
P06800	Parental	QTGLF	CALFNLLESAETEDVVDVFQVVK	SLRKA	2	C1:+39.994	1304.646252	2607.276905	0.000622848	4	N	1165	1188
P06800	Parental	QTGLF	CALFNLLESAETEDVVDVFQVVK	SLRKA	2	C1:+57.021	1313.159752	2624.303905	0.000451244	10	N	1165	1188
P06800	Parental	QTGLF	CALFNLLESAETEDVVDVFQVVK	SLRKA	3	C1:+57.021	875.7757683	2624.303905	0.000451244	10	N	1165	1188
P06800	Parental	QTGLF	CALFNLLESAETEDVVDVFQVVK	SLRKA	2	[0:-17.027,C1:+57.021	1304.646252	2607.276905	0.002884417	1	N	1165	1188
P06800	Parental	LVHCR	DGSQQTGLFCALFNLLESAETEDVVDVFQVVK	SLRKA	3	C10:+57.021	1186.915505	3557.723116	0.000451244	26	N	1156	1188
P06800	Parental	FCALF	NLLESAETEDVVDVFQVVK	SLRKA	2		1067.549864	2133.084127	0.000451244	23	N	1169	1188
P06800	Parental	FCALF	NLLESAETEDVVDVFQVVK	SLRKA	3		712.0358424	2133.084127	0.002374549	1	N	1169	1188
P06800	Parental	DPAAR	KTLVSWPEPVSKPESASKPHGYVLCYK	NNSEK	3	C25:+57.021	1029.870954	3086.589463	0.001463592	3	N	388	415
P06800	Parental	DPAAR	KTLVSWPEPVSKPESASKPHGYVLCYK	NNSEK	4	C25:+57.021	772.6551657	3086.589463	0.000451244	11	N	388	415

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P06800	Parental	PAARK	TLVSWPEPVSKPESASKPHGYVLCYK	NNSEK	3	C24:+57.021	987.1726333	2958.4945	0.000451244	3	N	389	415
P06800	Parental	PAARK	TLVSWPEPVSKPESASKPHGYVLCYK	NNSEK	4	C24:+57.021	740.631425	2958.4945	0.0025889	3	N	389	415
P06800	Parental	RVNAF	SNFFSGPIVVHCSAGVGR	TGTYI	2	C12:+57.021	945.9678925	1889.920185	0.001871652	2	N	828	846
P06800	Parental	RVNAF	SNFFSGPIVVHCSAGVGR	TGTYI	3	C12:+57.021	630.981195	1889.920185	0.000451244	1	N	828	846
P06800	Parental	NMKKR	DPPSDPSPLEAEYQR	LPSYR	2		850.8922704	1699.768941	0.000451244	7	N	922	937
P06800	Parental	KKKNR	NSNVVPYDFNR	VPLKH	2		662.81818	1323.62076	0.002884417	2	N	960	971
P06800	Parental	EAEGK	VDVYGYVVK	LRRQR	2		521.2849217	1040.554243	0.000622848	5	N	865	874
P06800	Parental	VQNAK	CGNEDCENVLNNLEECSQIK	NISVS	2	C1:+57.021,C6:+57.021,C16:+57.021	1213.006691	2423.997782	0.000451244	11	N	232	252
P06800	Parental	KSLRK	ARPGVVCSYEQYQFLYDIIASIYPAQNGQVK	KTNSQ	3	C7:+57.021	1193.264692	3576.770675	0.000823681	3	N	1192	1223
P06800	Parental	LRKKR	SSNLDEQQELVERDDEK	QLMDV	2		1017.467059	2032.918518	0.001162105	2	N	595	612
P06800	Parental	RKEPR	TVYQYQCTTWK	GEELP	2	C7:+57.021	739.342942	1476.670284	0.001943752	2	N	1102	1113
P06800	Parental	LVKNV	INVQTDLGIPETPKPSCGDPAAR	KTLVS	3	C17:+57.021	812.7448025	2435.211007	0.000851441	2	N	365	388
P06800	Parental	KVIVM	LTELVNGDQEVCAQYWGEGK	QTYGD	2	C12:+57.021	1148.531448	2295.047296	0.000451244	5	N	1047	1067
P06800	Parental	KSLRK	ARPGVVCSYEQYQFL	YDIIA	2	C7:+57.021	908.9382693	1815.860939	0.002212458	2	N	1192	1207
P06800	Parental	VIVML	TELVNGDQEVCAQYWGEGK	QTYGD	2	C11:+57.021	1091.989416	2181.963232	0.000451244	2	N	1048	1067
P06909	Exosome	EIDYR	ECGADGWINDIPLCEVVK	CLPVT	2	C2:+57.021,C14:+57.021	1037.982317	2073.949033	0.000451244	14	N	127	145
P06909	Exosome	GPPPR	ENSEILSGSWSEQLYPEGTQATYK	CRPGY	2		1359.133009	2716.250418	0.000451244	4	N	27	51
P06909	Exosome	NCTSK	TSCPPPPQIPNTQVIETTVK	YLDGE	2	C3:+57.021	1104.072752	2206.129903	0.000622848	10	N	805	825
P06909	Exosome	RIIHR	SDDEIRYECNYGFYPVTGSTVSK	CTPTG	2	C9:+57.021	1344.100423	2686.185246	0.000823681	2	N	285	308
P06909	Exosome	RIIHR	SDDEIRYECNYGFYPVTGSTVSK	CTPTG	3	C9:+57.021	896.4028821	2686.185246	0.000451244	8	N	285	308
P06909	Exosome	CIRIK	TCSASDIHIDNGFLSESSSIYALNR	ETSYR	3	C2:+57.021	919.7647024	2756.270707	0.000451244	7	N	446	471
P06909	Exosome	LENGR	IVSGAAETDQEYYFGQVVR	FECNS	2		1066.518898	2131.022196	0.000451244	5	N	156	175
P06909	Exosome	KYSYK	CDNGFSPPSGYSWDYLR	CTAQG	2	C1:+57.021	1010.92863	2019.84166	0.000637154	4	N	356	373
P06909	Exosome	FPTCK	GQVASCAPPLEILNGEINGAK	KVEYS	2	C6:+57.021	1069.549444	2137.083287	0.001699387	1	N	623	644
P06909	Exosome	FKYGR	LYYEESLRPNFPVSIGNK	YSYKC	3		709.3692673	2125.084402	0.000451244	1	N	334	352
P07356	Exosome	RKYGK	SLYYYIQQDTKGDYQK	ALLYL	2		1006.984159	2011.952719	0.000451244	4	N	313	329
P07356	Exosome	LAKGR	RAEDGSVIDYELIDQDAR	ELYDA	2		1032.995787	2063.975974	0.000451244	35	N	178	196
P07356	Exosome	LAKGR	RAEDGSVIDYELIDQDAR	ELYDA	3		688.9997912	2063.975974	0.000451244	24	N	178	196
P07356	Exosome	AKGRR	AEDGSVIDYELIDQDAR	ELYDA	2		954.9452313	1907.874863	0.000451244	48	N	179	196
P07356	Exosome	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAERDALNIETAVK	TKGVD	3		1331.655784	3991.943953	0.000451244	8	N	10	47
P07356	Exosome	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAERDALNIETAVK	TKGVD	4		998.9937884	3991.943953	0.000451244	21	N	10	47
P07356	Exosome	ETAVK	TKGVDEVTIVNILTNR	SNVQR	2		886.4997797	1770.983959	0.000451244	18	N	47	63
P07356	Exosome	ETAVK	TKGVDEVTIVNILTNR	SNVQR	3		591.3357865	1770.983959	0.000451244	26	N	47	63
P07356	Exosome	AVKTK	GVDEVTIVNILTNR	SNVQR	2		771.9284589	1541.841318	0.000451244	33	N	49	63
P07356	Exosome	AVKTK	GVDEVTIVNILTNR	SNVQR	3		514.9549059	1541.841318	0.000451244	34	N	49	63
P07356	Exosome	KASMK	GLGTDEDSLIEIICSR	TNQEL	2	C14:+57.021	889.4357565	1776.855913	0.000451244	44	N	119	135
P07356	Exosome	KASMK	GLGTDEDSLIEIICSR	TNQEL	3	C14:+57.021	593.2931043	1776.855913	0.000451244	27	N	119	135
P07356	Exosome	PSALK	SALSGHLETVILGLLK	TPAQY	2		825.9936019	1649.971604	0.000451244	36	N	88	104
P07356	Exosome	PSALK	SALSGHLETVILGLLK	TPAQY	3		550.9983346	1649.971604	0.000451244	65	N	88	104
P07356	Exosome	ESIKK	EVKGDLENAFLNLVQCIQNKPLYFADR	LYDSM	3	C16:+57.021	1065.548651	3193.622554	0.000451244	24	N	246	273
P07356	Exosome	ESIKK	EVKGDLENAFLNLVQCIQNKPLYFADR	LYDSM	4	C16:+57.021	799.4134385	3193.622554	0.000451244	36	N	246	273
P07356	Exosome	KKEVK	GDLENAFLNLVQCIQNKPLYFADR	LYDSM	2	C13:+57.021	1419.716092	2837.416584	0.000451244	12	N	249	273
P07356	Exosome	KKEVK	GDLENAFLNLVQCIQNKPLYFADR	LYDSM	3	C13:+57.021	946.8133279	2837.416584	0.000451244	42	N	249	273
P07356	Exosome	KKEVK	GDLENAFLNLVQCIQNKPLYFADR	LYDSM	4	C13:+57.021	710.3619459	2837.416584	0.000451244	1	N	249	273
P07356	Exosome	KKEVK	GDLENAFLNLVQCIQNKPLYF	ADRLY	2	C13:+57.021	1248.633508	2495.251416	0.000451244	4	N	249	270
P07356	Exosome	KKEVK	GDLENAFLNLVQCIQNKPLYF	ADRLY	3	C13:+57.021	832.7582719	2495.251416	0.000451244	5	N	249	270
P07356	Exosome	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAER	DALNI	3		980.133826	2937.378078	0.000823681	11	N	10	37
P07356	Exosome	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAER	DALNI	4		735.3523195	2937.378078	0.001329271	9	N	10	37
P07356	Exosome	KEMYK	TDLEKDIISDTSGDFR	KLMVA	2		906.4370421	1810.858484	0.000451244	40	N	152	168
P07356	Exosome	KEMYK	TDLEKDIISDTSGDFR	KLMVA	3		604.6272947	1810.858484	0.000451244	6	N	152	168
P07356	Exosome	ESIKK	EVKGDLENAFLNLVQCIQNKPLYF	ADRLY	3	C16:+57.021	951.4935953	2851.457386	0.000451244	3	N	246	270
P07356	Exosome	LGLLK	TPAQYDASELK	ASMKG	2		611.8016643	1221.587729	0.000451244	5	N	104	115
P07356	Exosome	RKYGK	SLYYYIQQDTK	GDYQK	2		711.3515213	1420.687443	0.000451244	20	N	313	324
P07356	Exosome	SVKPY	TNFDAERDALNIETAVK	TKGVD	3		636.3222056	1905.943217	0.000622848	4	N	30	47
P07356	Exosome	LKSAL	SGHLETVILGLLK	TPAQY	2		690.4169987	1378.818397	0.001162105	2	N	91	104
P07356	Exosome	KKEVK	GDLENAFLNLVQ	CIQNK	2		666.8438635	1331.672127	0.002727428	1	N	249	261
P07356	Parental	ILTNR	SNVQRQDIAFAYQR	RTKKE	2		848.4322314	1694.848863	0.000451244	11	N	63	77
P07356	Parental	RKYGK	SLYYYIQQDTKGDYQK	ALLYL	2		1006.984159	2011.952719	0.000451244	4	N	313	329
P07356	Parental	RKYGK	SLYYYIQQDTKGDYQK	ALLYL	3		671.6587063	2011.952719	0.001162105	1	N	313	329
P07356	Parental	LAKGR	RAEDGSVIDYELIDQDAR	ELYDA	2		1032.995787	2063.975974	0.000451244	68	N	178	196
P07356	Parental	LAKGR	RAEDGSVIDYELIDQDAR	ELYDA	3		688.9997912	2063.975974	0.000451244	41	N	178	196
P07356	Parental	AKGRR	AEDGSVIDYELIDQDAR	ELYDA	2		954.9452313	1907.874863	0.000451244	37	N	179	196
P07356	Parental	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAERDALNIETAVK	TKGVD	3		1331.655784	3991.943953	0.000451244	39	N	10	47
P07356	Parental	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAERDALNIETAVK	TKGVD	4		998.9937884	3991.943953	0.000451244	33	N	10	47

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P07356	Parental	ETAVK	TKGVDEVTIVNILTNR	SNVQR	3		591.3357865	1770.983959	0.000451244	27	N	47	63
P07356	Parental	AVKTK	GVDEVTIVNILTNR	SNVQR	2		771.9284589	1541.841318	0.000451244	52	N	49	63
P07356	Parental	AVKTK	GVDEVTIVNILTNR	SNVQR	3		514.9549059	1541.841318	0.000451244	46	N	49	63
P07356	Parental	KASMK	GLGTDEDSLIEIICSR	TNQEL	2	C14:+57.021	889.4357565	1776.855913	0.000451244	51	N	119	135
P07356	Parental	KASMK	GLGTDEDSLIEIICSR	TNQEL	3	C14:+57.021	593.2931043	1776.855913	0.000451244	42	N	119	135
P07356	Parental	PSALK	SALSGHLETVILGLLK	TPAQY	2		825.9936019	1649.971604	0.000451244	26	N	88	104
P07356	Parental	PSALK	SALSGHLETVILGLLK	TPAQY	3		550.9983346	1649.971604	0.000451244	116	N	88	104
P07356	Parental	PSALK	SALSGHLETVILGLLKTPAQYDASELK	ASMKG	3		952.1907241	2853.548772	0.000451244	4	N	88	115
P07356	Parental	PSALK	SALSGHLETVILGLLKTPAQYDASELK	ASMKG	4		714.3949931	2853.548772	0.000451244	5	N	88	115
P07356	Parental	ESIKK	EVKGDLENAFLNLVQCIQNKPLYFADR	LYDSM	3	C16:+57.021	1065.548651	3193.622554	0.000451244	16	N	246	273
P07356	Parental	ESIKK	EVKGDLENAFLNLVQCIQNKPLYFADR	LYDSM	4	C16:+57.021	799.4134385	3193.622554	0.000451244	18	N	246	273
P07356	Parental	KKEVK	GDLENAFLNLVQCIQNKPLYFADR	LYDSM	3	C13:+57.021	946.8133279	2837.416584	0.000451244	28	N	249	273
P07356	Parental	KKEVK	GDLENAFLNLVQCIQNKPLYF	ADRLY	2	C13:+57.021	1248.633508	2495.251416	0.000451244	41	N	249	270
P07356	Parental	KKEVK	GDLENAFLNLVQCIQNKPLYF	ADRLY	3	C13:+57.021	832.7582719	2495.251416	0.000451244	28	N	249	270
P07356	Parental	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAER	DALNI	2		1469.696839	2937.378078	0.001162105	2	N	10	37
P07356	Parental	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAER	DALNI	3		980.133826	2937.378078	0.000451244	49	N	10	37
P07356	Parental	EILCK	LSLEGDHSTPPSAYGSVKPYTNFDAER	DALNI	4		735.3523195	2937.378078	0.000451244	33	N	10	37
P07356	Parental	KEMYK	TDLEKDIISDTSGDFR	KLMVA	2		906.4370421	1810.858484	0.000451244	22	N	152	168
P07356	Parental	KEMYK	TDLEKDIISDTSGDFR	KLMVA	3		604.6272947	1810.858484	0.000451244	19	N	152	168
P07356	Parental	RRTKK	ELPSALKSALSGHLETVILGLLK	TPAQY	3		797.1408648	2388.399195	0.000451244	2	N	81	104
P07356	Parental	ESIKK	EVKGDLENAFLNLVQCIQNKPLYF	ADRLY	2	C16:+57.021	1426.736493	2851.457386	0.000451244	7	N	246	270
P07356	Parental	ESIKK	EVKGDLENAFLNLVQCIQNKPLYF	ADRLY	3	C16:+57.021	951.4935953	2851.457386	0.000451244	16	N	246	270
P07356	Parental	IICSR	TNQELQEINRVY	KEMYK	2		753.8815086	1505.747417	0.000451244	11	N	135	147
P07356	Parental	SALKS	ALSGHLETVILGLLK	TPAQY	3		521.9876584	1562.939575	0.000451244	5	N	89	104
P07356	Parental	LGLLK	TPAQYDASELK	ASMKG	2		611.8016643	1221.587729	0.000451244	1	N	104	115
P07356	Parental	RKYGK	SLYYYIQQDTK	GDYQK	2		711.3515213	1420.687443	0.000451244	4	N	313	324
P07356	Parental	EILCK	LSLEGDHSTPPSAYGSVKPY	TNFDA	2		1053.013448	2104.011297	0.000451244	12	N	10	30
P07356	Parental	EILCK	LSLEGDHSTPPSAYGSVKPY	TNFDA	3		702.3448989	2104.011297	0.000451244	9	N	10	30
P07356	Parental	AKGRR	AEDGSVIDYELIDQDARELYDAGVK	RKGTD	2		1392.664673	2783.313746	0.000451244	1	N	179	204
P07356	Parental	AKGRR	AEDGSVIDYELIDQDARELYDAGVK	RKGTD	3		928.7790488	2783.313746	0.000735798	4	N	179	204
P07356	Parental	TKKEL	PSALKSALSGHLETVILGLLK	TPAQY	3		716.4319791	2146.272537	0.002663018	1	N	83	104
P07356	Parental	LPSAL	KSALSGHLETVILGLLK	TPAQY	3		593.6966556	1778.066567	0.000451244	9	N	87	104
P07356	Parental	ALKSA	LSGHLETVILGLLK	TPAQY	2		746.9590307	1491.902461	0.000451244	3	N	90	104
P07356	Parental	FDAER	DALNIETAVK	TKGVD	2		537.2960177	1072.576435	0.000451244	5	N	37	47
P07356	Parental	TDLEK	DIISDTSGDFRK	LMVAL	2		677.3364026	1352.657205	0.000451244	2	N	157	169
P07356	Parental	LKSAL	SGHLETVILGLLK	TPAQY	2		690.4169987	1378.818397	0.000622848	1	N	91	104
P07607	Exosome	ANGSR	DFLDSLGFSAR	QEGDL	2		614.3043741	1226.593148	0.000823681	4	N	109	120
P07607	Exosome	CGFKK	EDRTGTGTLSVFGMQAR	YSLRD	3		609.3007478	1824.878844	0.000823681	2	N	41	58
P07607	Parental	RVFWK	GVLEELLWFIK	GSTNA	2		673.8900854	1345.764571	0.002453667	1	N	76	87
P07724	Exosome	AILVR	YTQKAPQVSTPTLVEAAR	NLGRV	2		980.5290685	1959.042537	0.000451244	1	N	434	452
P07724	Exosome	DTCCK	AADKDTCFSTEGPNLVTR	CKDAL	2	C7:+57.021	991.4681193	1980.920639	0.000451244	95	N	584	602
P07724	Exosome	DTCCK	AADKDTCFSTEGPNLVTR	CKDAL	3	C7:+57.021	661.3146795	1980.920639	0.000451244	57	N	584	602
P07724	Exosome	RYTQK	APQVSTPTLVEAAR	NLGRV	2		720.3967946	1438.777989	0.000451244	81	N	438	452
P07724	Exosome	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	2	C11:+57.021	1077.014902	2152.014205	0.000451244	42	N	527	545
P07724	Exosome	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	3	C11:+57.021	718.3458683	2152.014205	0.000451244	60	N	527	545
P07724	Exosome	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	4	C11:+57.021	539.0113512	2152.014205	0.000451244	16	N	527	545
P07724	Exosome	SLVER	RPCFSALTVDETYVPK	EFKAE	2	C3:+57.021	941.9723092	1881.929018	0.000451244	14	N	508	524
P07724	Exosome	SLVER	RPCFSALTVDETYVPK	EFKAE	3	C3:+57.021	628.3174728	1881.929018	0.000451244	4	N	508	524
P07724	Exosome	LFGDK	LCAIPNLRENYGELADCCTK	QEPER	2	C2:+57.021,C17:+57.021,C18:+57.021	1199.053247	2396.090895	0.000451244	11	N	97	117
P07724	Exosome	LFGDK	LCAIPNLRENYGELADCCTK	QEPER	3	C2:+57.021,C17:+57.021,C18:+57.021	799.7047649	2396.090895	0.000451244	17	N	97	117
P07724	Exosome	SLVER	RPCFSALTVDETYVPKEFK	AETFT	3	C3:+57.021	763.0527962	2286.134989	0.000451244	9	N	508	527
P07724	Exosome	ANCDK	SLHTLFGDKLCAIPNLR	ENYGE	2	C11:+57.021	978.0304928	1954.045386	0.000622848	1	N	88	105
P07724	Exosome	ANCDK	SLHTLFGDKLCAIPNLR	ENYGE	3	C11:+57.021	652.3562619	1954.045386	0.000451244	6	N	88	105
P07724	Exosome	WAVAR	LSQTFPNADFAEITK	LATDL	2		841.425749	1680.835898	0.000451244	55	N	242	257
P07724	Exosome	DLYEK	LGEYGFQNAILVR	YTQKA	2		740.4018799	1478.78816	0.000451244	131	N	421	434
P07724	Exosome	DLYEK	LGEYGFQNAILVR	YTQKA	3		493.9371866	1478.78816	0.000622848	3	N	421	434
P07724	Exosome	KNLVK	TNCDLYEKLGEYGFQNAILVR	YTQKA	3	C3:+57.021	835.0814146	2502.220844	0.000451244	1	N	413	434
P07724	Exosome	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	2	C1:+39.994,C2:+57.021,C10:+57.021	1467.160955	2932.30631	0.001329271	1	N	383	409
P07724	Exosome	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	3	C1:+39.994,C2:+57.021,C10:+57.021	978.4432368	2932.30631	0.00091018	6	N	383	409
P07724	Exosome	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	2	C1:+57.021,C2:+57.021,C10:+57.021	1475.674455	2949.33331	0.000451244	63	N	383	409

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P07724	Exosome	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	3	C1:+57.021,C2:+57.021,C10:+57.021	984.1189035	2949.33331	0.000451244	46	N	383	409
P07724	Exosome	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	2	[0:-17.027,C1:+57.021,C2:+57.021,C10:+57.021	1467.160955	2932.30631	0.000451244	8	N	383	409
P07724	Exosome	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	3	[0:-17.027,C1:+57.021,C2:+57.021,C10:+57.021	978.4432368	2932.30631	0.000451244	23	N	383	409
P07724	Exosome	EQHFK	GLVLIAFSQYLQK	CSYDE	2		740.4326487	1478.849697	0.000451244	47	N	44	57
P07724	Exosome	EQHFK	GLVLIAFSQYLQK	CSYDE	3		493.9576992	1478.849697	0.000451244	14	N	44	57
P07724	Exosome	AEQLK	TVMDDFAQFLDTCCK	AADKD	2	C13:+57.021,C14:+57.021	925.8915822	1849.767564	0.000451244	20	N	569	584
P07724	Exosome	AEQLK	TVMDDFAQFLDTCCK	AADKD	3	C13:+57.021,C14:+57.021	617.5969881	1849.767564	0.000451244	12	N	569	584
P07724	Exosome	AEQLK	TVMDDFAQFLDTCCK	AADKD	2	M3:+15.995,C13:+57.021,C14:+57.021	933.8890822	1865.762564	0.000451244	9	N	569	584
P07724	Exosome	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	2	C1:+39.994,C2:+57.021,C12:+57.021	1403.153464	2804.291329	0.00091018	1	N	460	483
P07724	Exosome	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	3	C1:+39.994,C2:+57.021,C12:+57.021	935.7715763	2804.291329	0.000451244	7	N	460	483
P07724	Exosome	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	2	C1:+57.021,C2:+57.021,C12:+57.021	1411.666964	2821.318329	0.000451244	10	N	460	483
P07724	Exosome	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	3	C1:+57.021,C2:+57.021,C12:+57.021	941.447243	2821.318329	0.000451244	46	N	460	483
P07724	Exosome	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	2	[0:-17.027,C1:+57.021,C2:+57.021,C12:+57.021	1403.153464	2804.291329	0.000622848	3	N	460	483
P07724	Exosome	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	3	[0:-17.027,C1:+57.021,C2:+57.021,C12:+57.021	935.7715763	2804.291329	0.000451244	15	N	460	483
P07724	Exosome	YAEAK	DVFLGTFLYEYSR	RHPDY	2		805.3990029	1608.782406	0.000451244	68	N	347	360
P07724	Exosome	PEDQR	LPCVEDYLSAILNR	VCLLH	2	C3:+57.021	831.929913	1661.844226	0.000451244	63	N	469	483
P07724	Exosome	PEDQR	LPCVEDYLSAILNR	VCLLH	3	C3:+57.021	554.9558753	1661.844226	0.000451244	28	N	469	483
P07724	Exosome	EVARR	HPYFYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C23:+57.021,C24:+57.021,C32:+57.021	1472.337619	4413.989458	0.000622848	2	N	169	205
P07724	Exosome	EVARR	HPYFYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	4	C23:+57.021,C24:+57.021,C32:+57.021	1104.505164	4413.989458	0.000451244	37	N	169	205
P07724	Exosome	IPNLR	ENYGELADCCTK	QEPER	2	C9:+57.021,C10:+57.021	730.2951002	1458.5746	0.000451244	32	N	105	117
P07724	Exosome	DEHAK	LVQEVTDFAK	TCVAD	2		575.3116678	1148.607736	0.000451244	42	N	65	75
P07724	Exosome	TKVNK	ECCHGDLLECADDR	AELAK	2	C2:+57.021,C3:+57.021,C10:+57.021	875.3347308	1748.653862	0.000451244	8	N	267	281
P07724	Exosome	TKVNK	ECCHGDLLECADDR	AELAK	3	C2:+57.021,C3:+57.021,C10:+57.021	583.8924205	1748.653862	0.000451244	4	N	267	281
P07724	Exosome	YEYSR	RHPDYSVSLLLR	LAKKY	3		485.9409311	1454.799393	0.000451244	39	N	360	372
P07724	Exosome	PKEFK	AETFTFHSDICTLPEK	EKQIK	2	C11:+57.021	948.4461242	1894.876648	0.000451244	6	N	527	543
P07724	Exosome	PKEFK	AETFTFHSDICTLPEK	EKQIK	3	C11:+57.021	632.6333495	1894.876648	0.002813207	1	N	527	543
P07724	Exosome	RRHPY	FYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C20:+57.021,C21:+57.021,C29:+57.021	1339.945951	4016.814453	0.000451244	13	N	172	205
P07724	Exosome	RRHPY	FYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	4	C20:+57.021,C21:+57.021,C29:+57.021	1005.211413	4016.814453	0.000451244	5	N	172	205
P07724	Exosome	TDLTK	VNKECCHGDLLECADDR	AELAK	3	C5:+57.021,C6:+57.021,C13:+57.021	697.6278554	2089.860166	0.000451244	2	N	264	281
P07724	Exosome	TKVNK	ECCHGDLLECADDRAELAK	YMCEN	2	C2:+57.021,C3:+57.021,C10:+57.021	1131.482655	2260.94971	0.000451244	22	N	267	286
P07724	Exosome	TKVNK	ECCHGDLLECADDRAELAK	YMCEN	3	C2:+57.021,C3:+57.021,C10:+57.021	754.6577033	2260.94971	0.000451244	27	N	267	286
P07724	Exosome	DCCTK	QEPERNECFLQHK	DDNPS	3	[0:-17.027,C8:+57.021	566.5950788	1696.761836	0.001463592	2	N	117	130
P07724	Exosome	PELLY	YAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C12:+57.021,C13:+57.021,C21:+57.021	1007.780728	3020.318783	0.001162105	1	N	180	205
P07724	Exosome	PLLKK	AHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAK	DVFLG	4	C3:+57.021,M12:+15.995,C30:+57.021	1048.225455	4188.87062	0.000451244	4	N	310	347
P07724	Exosome	PLLKK	AHCLSEVEHDTMPADLPAIAADFVEDQEVCK	NYAEA	3	C3:+57.021,C30:+57.021	1166.526993	3496.55758	0.000451244	7	N	310	341
P07724	Exosome	PLLKK	AHCLSEVEHDTMPADLPAIAADFVEDQEVCK	NYAEA	4	C3:+57.021,C30:+57.021	875.1471949	3496.55758	0.000451244	9	N	310	341
P07724	Exosome	PLLKK	AHCLSEVEHDTMPADLPAIAADFVEDQEVCK	NYAEA	4	C3:+57.021,M12:+15.995,C30:+57.021	879.1459449	3512.55258	0.000451244	9	N	310	341
P07724	Parental	AILNR	VCLLHEKTPVSEHVTK	CCSGS	3	C2:+57.021	626.3368673	1875.987202	0.000451244	3	N	483	499
P07724	Parental	AILNR	VCLLHEKTPVSEHVTK	CCSGS	4	C2:+57.021	470.0046005	1875.987202	0.000451244	10	N	483	499

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P07724	Parental	AILVR	YTQKAPQVSTPTLVEAAR	NLGRV	2		980.5290685	1959.042537	0.000451244	14	N	434	452
P07724	Parental	AILVR	YTQKAPQVSTPTLVEAAR	NLGRV	3		654.021979	1959.042537	0.000451244	1	N	434	452
P07724	Parental	DTCCK	AADKDTCFSTEGPNLVTR	CKDAL	2	C7:+57.021	991.4681193	1980.920639	0.000451244	81	N	584	602
P07724	Parental	DTCCK	AADKDTCFSTEGPNLVTR	CKDAL	3	C7:+57.021	661.3146795	1980.920639	0.000451244	38	N	584	602
P07724	Parental	YAEQY	NEILTQCCAEADKESCLTPK	LDGVK	2	C7:+57.021,C8:+57.021,C16:+57.021	1184.03472	2366.053841	0.000451244	13	N	185	205
P07724	Parental	YAEQY	NEILTQCCAEADKESCLTPK	LDGVK	3	C7:+57.021,C8:+57.021,C16:+57.021	789.6924135	2366.053841	0.001162105	1	N	185	205
P07724	Parental	RYTQK	APQVSTPTLVEAAR	NLGRV	2		720.3967946	1438.777989	0.000451244	51	N	438	452
P07724	Parental	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	2	C11:+57.021	1077.014902	2152.014205	0.000451244	29	N	527	545
P07724	Parental	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	3	C11:+57.021	718.3458683	2152.014205	0.000451244	25	N	527	545
P07724	Parental	PKEFK	AETFTFHSDICTLPEKEK	QIKKQ	4	C11:+57.021	539.0113512	2152.014205	0.000451244	4	N	527	545
P07724	Parental	SLVER	RPCFSALTVDETYVPK	EFKAE	2	C3:+57.021	941.9723092	1881.929018	0.000451244	23	N	508	524
P07724	Parental	SLVER	RPCFSALTVDETYVPK	EFKAE	3	C3:+57.021	628.3174728	1881.929018	0.000451244	29	N	508	524
P07724	Parental	LFGDK	LCAIPNLRENYGELADCCTK	QEPER	3	C2:+57.021,C17:+57.021,C18:+57.021	799.7047649	2396.090895	0.000451244	2	N	97	117
P07724	Parental	QYLQK	CSYDEHAKLVQEVTDFAK	TCVAD	2	C1:+57.021	1070.504702	2138.993804	0.000451244	2	N	57	75
P07724	Parental	QYLQK	CSYDEHAKLVQEVTDFAK	TCVAD	3	C1:+57.021	714.0057346	2138.993804	0.000451244	4	N	57	75
P07724	Parental	QYLQK	CSYDEHAKLVQEVTDFAK	TCVAD	3	[0:-17.027,C1:+57.021	708.3300679	2121.966804	0.002212458	1	N	57	75
P07724	Parental	SLVER	RPCFSALTVDETYVPKEFK	AETFT	3	C3:+57.021	763.0527962	2286.134989	0.000451244	6	N	508	527
P07724	Parental	SLVER	RPCFSALTVDETYVPKEFK	AETFT	4	C3:+57.021	572.5415472	2286.134989	0.000451244	5	N	508	527
P07724	Parental	ANCDK	SLHTLFGDKLCAIPNLR	ENYGE	3	C11:+57.021	652.3562619	1954.045386	0.000451244	7	N	88	105
P07724	Parental	WAVAR	LSQTFPNADFAEITK	LATDL	2		841.425749	1680.835898	0.000451244	34	N	242	257
P07724	Parental	DLYEK	LGEYGFQNAILVR	YTQKA	2		740.4018799	1478.78816	0.000451244	822	N	421	434
P07724	Parental	DLYEK	LGEYGFQNAILVR	YTQKA	3		493.9371866	1478.78816	0.000451244	20	N	421	434
P07724	Parental	DLYEK	LGEYGFQNAILVRY	TQKAP	2		821.9335442	1641.851488	0.000451244	7	N	421	435
P07724	Parental	KNLVK	TNCDLYEKLGEYGFQNAILVR	YTQKA	2	C3:+57.021	1252.118222	2502.220844	0.000451244	13	N	413	434
P07724	Parental	KNLVK	TNCDLYEKLGEYGFQNAILVR	YTQKA	3	C3:+57.021	835.0814146	2502.220844	0.000451244	6	N	413	434
P07724	Parental	QEVCK	NYAEAKDVFLGTFLYEYSR	RHPDY	2		1143.558023	2285.100446	0.000998612	1	N	341	360
P07724	Parental	QEVCK	NYAEAKDVFLGTFLYEYSR	RHPDY	3		762.7079487	2285.100446	0.000823681	3	N	341	360
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPKNLVK	TNCDL	3	C1:+39.994,C2:+57.021,C10:+57.021	1129.87336	3386.596679	0.00091018	1	N	383	413
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPKNLVK	TNCDL	3	C1:+57.021,C2:+57.021,C10:+57.021	1135.549026	3403.623679	0.000451244	11	N	383	413
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPKNLVK	TNCDL	3	[0:-17.027,C1:+57.021,C2:+57.021,C10:+57.021	1129.87336	3386.596679	0.000451244	2	N	383	413
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	3	C1:+39.994,C2:+57.021,C10:+57.021	978.4432368	2932.30631	0.00091018	4	N	383	409
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	2	C1:+57.021,C2:+57.021,C10:+57.021	1475.674455	2949.33331	0.000451244	26	N	383	409
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	3	C1:+57.021,C2:+57.021,C10:+57.021	984.1189035	2949.33331	0.000451244	38	N	383	409
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	2	[0:-17.027,C1:+57.021,C2:+57.021,C10:+57.021	1467.160955	2932.30631	0.000698008	4	N	383	409
P07724	Parental	ATLEK	CCAEANPPACYGTVLAEFQPLVEEPK	NLVKT	3	[0:-17.027,C1:+57.021,C2:+57.021,C10:+57.021	978.4432368	2932.30631	0.000451244	14	N	383	409
P07724	Parental	EQHFK	GLVLIAFSQYLQK	CSYDE	2		740.4326487	1478.849697	0.000451244	27	N	44	57
P07724	Parental	EQHFK	GLVLIAFSQYLQK	CSYDE	3		493.9576992	1478.849697	0.000451244	7	N	44	57
P07724	Parental	AEQLK	TVMDDFAQFLDTCCK	AADKD	2	C13:+57.021,C14:+57.021	925.8915822	1849.767564	0.000451244	21	N	569	584
P07724	Parental	AEQLK	TVMDDFAQFLDTCCK	AADKD	3	C13:+57.021,C14:+57.021	617.5969881	1849.767564	0.000451244	3	N	569	584
P07724	Parental	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	2	C1:+39.994,C2:+57.021,C12:+57.021	1403.153464	2804.291329	0.000622848	1	N	460	483
P07724	Parental	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	3	C1:+39.994,C2:+57.021,C12:+57.021	935.7715763	2804.291329	0.000451244	8	N	460	483
P07724	Parental	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	2	C1:+57.021,C2:+57.021,C12:+57.021	1411.666964	2821.318329	0.000451244	9	N	460	483
P07724	Parental	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	3	C1:+57.021,C2:+57.021,C12:+57.021	941.447243	2821.318329	0.000451244	22	N	460	483
P07724	Parental	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	2	[0:-17.027,C1:+57.021,C2:+57.021,C12:+57.021	1403.153464	2804.291329	0.001162105	2	N	460	483

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P07724	Parental	RVGTK	CCTLPEDQRLPCVEDYLSAILNR	VCLLH	3	[0:-17.027,C1:+57.021,C2:+57.021,C12:+57.021	935.7715763	2804.291329	0.000451244	10	N	460	483
P07724	Parental	WAVAR	LSQTFPNADFAEITKLATDLTK	VNKEC	3		808.7606012	2423.258403	0.000451244	6	N	242	264
P07724	Parental	YAEAK	DVFLGTFLYEYSR	RHPDY	2		805.3990029	1608.782406	0.000451244	75	N	347	360
P07724	Parental	PEDQR	LPCVEDYLSAILNR	VCLLH	2	C3:+57.021	831.929913	1661.844226	0.000451244	33	N	469	483
P07724	Parental	PEDQR	LPCVEDYLSAILNR	VCLLH	3	C3:+57.021	554.9558753	1661.844226	0.000451244	53	N	469	483
P07724	Parental	EVARR	HPYFYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C23:+57.021,C24:+57.021,C32:+57.021	1472.337619	4413.989458	0.000735798	3	N	169	205
P07724	Parental	EVARR	HPYFYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	4	C23:+57.021,C24:+57.021,C32:+57.021	1104.505164	4413.989458	0.000451244	47	N	169	205
P07724	Parental	EDQRL	PCVEDYLSAILNR	VCLLH	2	C2:+57.021	775.3878809	1548.760162	0.000451244	1	N	470	483
P07724	Parental	IPNLR	ENYGELADCCTK	QEPER	2	C9:+57.021,C10:+57.021	730.2951002	1458.5746	0.000451244	34	N	105	117
P07724	Parental	DEHAK	LVQEVTDFAK	TCVAD	2		575.3116678	1148.607736	0.000451244	45	N	65	75
P07724	Parental	KCCTL	PEDQRLPCVEDYLSAILNR	VCLLH	3	C8:+57.021	763.383205	2287.126215	0.001162105	1	N	464	483
P07724	Parental	TKVNK	ECCHGDLLECADDR	AELAK	2	C2:+57.021,C3:+57.021,C10:+57.021	875.3347308	1748.653862	0.000451244	54	N	267	281
P07724	Parental	TKVNK	ECCHGDLLECADDR	AELAK	3	C2:+57.021,C3:+57.021,C10:+57.021	583.8924205	1748.653862	0.000451244	28	N	267	281
P07724	Parental	PKEFK	AETFTFHSDICTLPEK	EKQIK	2	C11:+57.021	948.4461242	1894.876648	0.000622848	1	N	527	543
P07724	Parental	PKEFK	AETFTFHSDICTLPEK	EKQIK	3	C11:+57.021	632.6333495	1894.876648	0.001591523	1	N	527	543
P07724	Parental	RRHPY	FYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C20:+57.021,C21:+57.021,C29:+57.021	1339.945951	4016.814453	0.000451244	7	N	172	205
P07724	Parental	RRHPY	FYAPELLYYAEQYNEILTQCCAEADKESCLTPK	LDGVK	4	C20:+57.021,C21:+57.021,C29:+57.021	1005.211413	4016.814453	0.000622848	1	N	172	205
P07724	Parental	TKVNK	ECCHGDLLECADDRAELAK	YMCEN	2	C2:+57.021,C3:+57.021,C10:+57.021	1131.482655	2260.94971	0.000451244	4	N	267	286
P07724	Parental	TKVNK	ECCHGDLLECADDRAELAK	YMCEN	3	C2:+57.021,C3:+57.021,C10:+57.021	754.6577033	2260.94971	0.000451244	1	N	267	286
P07724	Parental	TKVNK	ECCHGDLLECADDRAELAK	YMCEN	4	C2:+57.021,C3:+57.021,C10:+57.021	566.2452274	2260.94971	0.001329271	1	N	267	286
P07724	Parental	EKLGE	YGFQNAILVR	YTQKA	2		590.8278194	1179.640039	0.000662267	10	N	424	434
P07724	Parental	EQHFK	GLVLIAFSQY	LQKCS	2		555.8138463	1109.612093	0.002374549	1	N	44	54
P07724	Parental	DQRLP	CVEDYLSAILNR	VCLLH	2	C1:+57.021	726.861499	1451.707398	0.000451244	5	N	471	483
P07724	Parental	PELLY	YAEQYNEILTQCCAEADKESCLTPK	LDGVK	3	C12:+57.021,C13:+57.021,C21:+57.021	1007.780728	3020.318783	0.000622848	2	N	180	205
P07724	Parental	LYEKL	GEYGFQNAILVR	YTQKA	2		683.8598479	1365.704096	0.000698008	1	N	422	434
P07742	Exosome	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTKHPDYAILAAR	IAVSN	4		994.2840028	3973.104811	0.002374549	1	N	42	80
P07742	Exosome	QLLNK	QIFETIYYGALEASCELAKEYGPYETYEGSPVSK	GILQY	3	C15:+57.021	1298.27688	3891.80724	0.000622848	5	N	529	563
P07742	Exosome	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTK	HPDYA	3		956.1818943	2865.522283	0.000451244	30	N	42	70
P07742	Exosome	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	C15:+57.021	1103.540753	2205.065906	0.000451244	18	N	529	548
P07742	Exosome	QLLNK	QIFETIYYGALEASCELAK	EYGPY	3	C15:+57.021	736.0297687	2205.065906	0.000451244	12	N	529	548
P07742	Exosome	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	Q1:-17.027,C15:+57.021	1095.027253	2188.038906	0.000451244	3	N	529	548
P07742	Exosome	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	[0:-17.027,C15:+57.021	1095.027253	2188.038906	0.000451244	4	N	529	548
P07742	Exosome	NEEMK	NQIIACNGSIQSIPEIPDDLKQLYK	TVWEI	3	C6:+57.021	953.1640263	2856.468679	0.000451244	10	N	656	681
P07742	Exosome	IYTRR	VLSGEFQIVNPHLLK	DLTER	3		565.3265627	1692.956288	0.000451244	3	N	628	643
P07742	Exosome	HMLMR	VSVGIHKEDIDAAIETYNLLSEK	WFTHA	4		636.8357739	2543.311896	0.002296037	1	N	173	196
P07742	Exosome	FILMR	YPFESPEAQLLNK	QIFET	2		768.3911779	1534.766756	0.000622848	1	N	516	529
P07742	Parental	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTKHPDYAILAAR	IAVSN	3		1325.37607	3973.104811	0.002453667	1	N	42	80
P07742	Parental	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTKHPDYAILAAR	IAVSN	4		994.2840028	3973.104811	0.001591523	3	N	42	80
P07742	Parental	QLLNK	QIFETIYYGALEASCELAKEYGPYETYEGSPVSK	GILQY	3	C15:+57.021	1298.27688	3891.80724	0.000451244	16	N	529	563
P07742	Parental	QLLNK	QIFETIYYGALEASCELAKEYGPYETYEGSPVSK	GILQY	3	[0:-17.027,C15:+57.021	1292.601213	3874.78024	0.001162105	1	N	529	563
P07742	Parental	QITMK	VIQGLYSGVTTVELDTLAAETAATLTTK	HPDYA	3		956.1818943	2865.522283	0.000451244	10	N	42	70
P07742	Parental	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	C15:+57.021	1103.540753	2205.065906	0.000451244	5	N	529	548
P07742	Parental	QLLNK	QIFETIYYGALEASCELAK	EYGPY	3	C15:+57.021	736.0297687	2205.065906	0.000451244	1	N	529	548
P07742	Parental	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	Q1:-17.027,C15:+57.021	1095.027253	2188.038906	0.000451244	1	N	529	548
P07742	Parental	QLLNK	QIFETIYYGALEASCELAK	EYGPY	2	[0:-17.027,C15:+57.021	1095.027253	2188.038906	0.000451244	3	N	529	548
P07742	Parental	IYTRR	VLSGEFQIVNPHLLK	DLTER	3		565.3265627	1692.956288	0.000451244	3	N	628	643
P07759	Exosome	HEKTR	ALYQTEAFTADFQQPTEAK	NLIND	2		1080.018731	2158.021861	0.000451244	17	N	157	176
P07759	Exosome	QVVHK	AVLDVAETGTEAAAATGVIGGIR	KAILP	2		1071.574204	2141.132809	0.000451244	36	N	360	383
P07759	Exosome	QVVHK	AVLDVAETGTEAAAATGVIGGIR	KAILP	3		714.7187363	2141.132809	0.000870037	1	N	360	383
P07759	Exosome	SLYKK	LALKNPDTNIVFSPLSISAALALVSLGAK	GKTME	3		975.2342642	2922.679393	0.000823681	1	N	62	91
P07759	Exosome	KGKWK	ISFDPQDTFESEFYLDEK	RSVKV	2		1105.494754	2208.973908	0.000622848	9	N	217	235
P07759	Exosome	KLALK	NPDTNIVFSPLSISAALALVSLGAK	GKTME	2		1249.697394	2497.379187	0.000451244	2	N	66	91
P07759	Exosome	KLALK	NPDTNIVFSPLSISAALALVSLGAK	GKTME	3		833.4675291	2497.379187	0.000451244	5	N	66	91

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P07759	Exosome	MFIEK	DLQILAEFHEK	TRALY	2		671.8542312	1341.692862	0.000735798	2	N	144	155
P07759	Parental	HEKTR	ALYQTEAFTADFQQPTEAK	NLIND	2		1080.018731	2158.021861	0.000451244	18	N	157	176
P07759	Parental	QVVHK	AVLDVAETGTEAAAATGVIGGIR	KAILP	2		1071.574204	2141.132809	0.000451244	29	N	360	383
P07759	Parental	RKWRK	TLFPSQIEELNLPK	FSIAS	2		814.94886	1627.88212	0.000451244	5	N	300	314
P07759	Parental	SLYKK	LALKNPDTNIVFSPLSISAALALVSLGAK	GKTME	3		975.2342642	2922.679393	0.000823681	6	N	62	91
P07759	Parental	KGKWK	ISFDPQDTFESEFYLDEK	RSVKV	2		1105.494754	2208.973908	0.000451244	10	N	217	235
P07759	Parental	KLALK	NPDTNIVFSPLSISAALALVSLGAK	GKTME	2		1249.697394	2497.379187	0.000698008	4	N	66	91
P07759	Parental	KLALK	NPDTNIVFSPLSISAALALVSLGAK	GKTME	3		833.4675291	2497.379187	0.000622848	1	N	66	91
P07759	Parental	MFIEK	DLQILAEFHEK	TRALY	2		671.8542312	1341.692862	0.001654178	3	N	144	155
P07759	Parental	LLTTR	HFRDEELSCSVLELK	YTGNA	3	C9:+57.021	621.3089773	1860.903532	0.000622848	1	N	251	266
P07901	Exosome	GRGTK	VILHLKEDQTEYLEER	RIKEI	2		1008.026359	2014.037117	0.0007646	1	Y	185	201
P07901	Exosome	GRGTK	VILHLKEDQTEYLEER	RIKEI	3		672.3535058	2014.037117	0.000451244	3	Y	185	201
P07901	Exosome	MAAKK	HLEINPDHSIIETLR	QKAEA	2		893.9764718	1785.937344	0.001229886	1	N	633	648
P07901	Exosome	MAAKK	HLEINPDHSIIETLR	QKAEA	3		596.3202478	1785.937344	0.000451244	8	N	633	648
P07901	Exosome	PIWTR	NPDDITNEEYGEFYK	SLTND	2		917.3948429	1832.774086	0.000451244	27	N	300	315
P07901	Exosome	IGMTK	ADLINNLGTIAK	SGTKA	2		621.8567739	1241.697948	0.000451244	20	Y	100	112
P07901	Exosome	EIVKK	HSQFIGYPITLFVEKER	DKEVS	3		688.7024693	2063.084008	0.002080925	1	N	209	226
P07901	Exosome	EIVKK	HSQFIGYPITLFVEK	ERDKE	2		889.9779518	1777.940304	0.000622848	7	N	209	224
P07901	Exosome	EIVKK	HSQFIGYPITLFVEK	ERDKE	3		593.6545679	1777.940304	0.000735798	11	N	209	224
P07901	Exosome	VVSNR	LVTSPCCIVTSTYGWTANMER	IMKAQ	2	C6:+57.021,C7:+57.021,M19:+15.995	1231.56118	2461.10676	0.000451244	3	N	592	613
P07901	Exosome	DKNDK	SVKDLVILLYETALLSSGFSLEDPQTHANR	IYRMI	3		1106.252823	3315.73507	0.000451244	3	N	658	688
P07901	Exosome	DKNDK	SVKDLVILLYETALLSSGFSLEDPQTHANR	IYRMI	4		829.9415675	3315.73507	0.000451244	2	N	658	688
P07901	Exosome	DKSVK	DLVILLYETALLSSGFSLEDPQTHANR	IYRMI	3		1001.521021	3001.539664	0.000451244	19	N	661	688
P07901	Exosome	LVILL	YETALLSSGFSLEDPQTHANR	IYRMI	3		779.3771502	2335.108051	0.000451244	6	N	667	688
P07901	Exosome	EIFLR	ELISNSSDALDKIR	YESLT	2		780.9155485	1559.815497	0.000451244	18	N	46	60
P07901	Exosome	EIFLR	ELISNSSDALDKIR	YESLT	3		520.946299	1559.815497	0.002519933	1	N	46	60
P07901	Exosome	HLAVK	HFSVEGQLEFR	ALLFV	2		674.8363727	1347.657145	0.000622848	4	Y	328	339
P07901	Exosome	TVITK	HNDDEQYAWESSAGGSFTVR	TDTGE	2		1128.483575	2254.95155	0.001264573	1	Y	153	173
P07901	Exosome	EIFLR	ELISNSSDALDK	IRYES	2		646.3229609	1290.630322	0.000451244	2	N	46	58
P07901	Exosome	YRMIK	LGLGIDEDDPTVDDTSAAVTEEMPPLEGDDDTSRMEEVD	-	3	M23:+15.995,M35:+15.995	1404.265757	4209.773871	0.001591523	2	N	694	733
P07901	Parental	GRGTK	VILHLKEDQTEYLEER	RIKEI	2		1008.026359	2014.037117	0.000451244	10	Y	185	201
P07901	Parental	MAAKK	HLEINPDHSIIETLR	QKAEA	2		893.9764718	1785.937344	0.000451244	8	N	633	648
P07901	Parental	MAAKK	HLEINPDHSIIETLR	QKAEA	3		596.3202478	1785.937344	0.000451244	9	N	633	648
P07901	Parental	PIWTR	NPDDITNEEYGEFYK	SLTND	2		917.3948429	1832.774086	0.000451244	34	N	300	315
P07901	Parental	IGMTK	ADLINNLGTIAK	SGTKA	2		621.8567739	1241.697948	0.000451244	31	Y	100	112
P07901	Parental	EIVKK	HSQFIGYPITLFVEKER	DKEVS	3		688.7024693	2063.084008	0.000622848	9	N	209	226
P07901	Parental	EIVKK	HSQFIGYPITLFVEK	ERDKE	2		889.9779518	1777.940304	0.002080925	1	N	209	224
P07901	Parental	EIVKK	HSQFIGYPITLFVEK	ERDKE	3		593.6545679	1777.940304	0.00091018	12	N	209	224
P07901	Parental	VVSNR	LVTSPCCIVTSTYGWTANMER	IMKAQ	2	C6:+57.021,C7:+57.021	1223.56368	2445.11176	0.001591523	1	N	592	613
P07901	Parental	DKNDK	SVKDLVILLYETALLSSGFSLEDPQTHANR	IYRMI	3		1106.252823	3315.73507	0.000451244	8	N	658	688
P07901	Parental	DKNDK	SVKDLVILLYETALLSSGFSLEDPQTHANR	IYRMI	4		829.9415675	3315.73507	0.000451244	6	N	658	688
P07901	Parental	DKSVK	DLVILLYETALLSSGFSLEDPQTHANR	IYRMI	3		1001.521021	3001.539664	0.000451244	52	N	661	688
P07901	Parental	YMAAK	KHLEINPDHSIIETLR	QKAEA	2		958.0239533	1914.032307	0.000451244	10	N	632	648
P07901	Parental	YMAAK	KHLEINPDHSIIETLR	QKAEA	3		639.0185689	1914.032307	0.000851441	3	N	632	648
P07901	Parental	YMAAK	KHLEINPDHSIIETLR	QKAEA	4		479.5158767	1914.032307	0.001591523	1	N	632	648
P07901	Parental	LVILL	YETALLSSGFSLEDPQTHANR	IYRMI	2		1168.561825	2335.108051	0.000451244	24	N	667	688
P07901	Parental	LVILL	YETALLSSGFSLEDPQTHANR	IYRMI	3		779.3771502	2335.108051	0.000451244	28	N	667	688
P07901	Parental	RGTKV	ILHLKEDQTEYLEER	RIKEI	3		639.3307011	1914.968703	0.000451244	2	Y	186	201
P07901	Parental	EIFLR	ELISNSSDALDKIR	YESLT	2		780.9155485	1559.815497	0.000451244	18	N	46	60
P07901	Parental	HLAVK	HFSVEGQLEFR	ALLFV	2		674.8363727	1347.657145	0.000451244	1	Y	328	339
P07901	Parental	HLAVK	HFSVEGQLEFR	ALLFV	3		450.2268485	1347.657145	0.001654178	2	Y	328	339
P07901	Parental	TVITK	HNDDEQYAWESSAGGSFTVR	TDTGE	2		1128.483575	2254.95155	0.000451244	25	Y	153	173
P07901	Parental	TVITK	HNDDEQYAWESSAGGSFTVR	TDTGE	3		752.6583166	2254.95155	0.000451244	3	Y	153	173
P07901	Parental	KENQK	HIYFITGETKDQVANSAFVER	LRKHG	2		1213.111485	2424.207371	0.000451244	9	N	490	511
P07901	Parental	GEFYK	SLTNDWEEHLAVK	HFSVE	2		771.3838842	1540.752168	0.000451244	6	N	315	328
P07901	Parental	GEFYK	SLTNDWEEHLAVK	HFSVE	3		514.5918561	1540.752168	0.000451244	3	N	315	328
P07901	Parental	EELNK	TKPIWTRNPDDITNEEYGEFYK	SLTND	3		906.1016861	2715.281658	0.000451244	6	N	293	315
P07901	Parental	SKQDR	TLTIVDTGIGMTKADLINNLGTIAK	SGTKA	3		858.4793293	2572.414588	0.000823681	3	N	87	112
P07901	Parental	KIKEK	YIDQEELNKTKPIWTR	NPDDI	2		1017.536894	2033.058187	0.000451244	7	Y	284	300
P07901	Parental	KIKEK	YIDQEELNKTKPIWTR	NPDDI	3		678.6938624	2033.058187	0.000451244	5	Y	284	300
P07901	Parental	SELLR	YYTSASGDEMVSLKDYCTR	MKENQ	2	C17:+57.021	1123.490935	2244.966269	0.001591523	1	N	465	484
P07901	Parental	LDKIR	YESLTDPSKLDSGK	ELHIN	2		770.3810071	1538.746414	0.000451244	13	Y	60	74
P07901	Parental	LDKIR	YESLTDPSKLDSGK	ELHIN	3		513.9232714	1538.746414	0.002981883	1	Y	60	74
P08003	Exosome	VAKVR	EVSQPDWTPPPEVTLSLTK	DNFDD	2		1062.547124	2123.078648	0.00091018	24	N	158	177

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08003	Exosome	ILTLK	QVQEFLKDGDDVVIIGLFQGDGDPAYLQYQDAANNLR	EDYKF	3		1375.678701	4124.012702	0.000451244	27	N	287	324
P08003	Exosome	ILTLK	QVQEFLKDGDDVVIIGLFQGDGDPAYLQYQDAANNLR	EDYKF	4		1032.010975	4124.012702	0.001463592	2	N	287	324
P08003	Exosome	DLAKR	FDVSGYPTLK	IFRKG	2		563.7931109	1125.570622	0.000451244	6	N	239	249
P08003	Exosome	LEVAK	DFPEYTFAIADEEDYATEVK	DLGLS	2		1177.023876	2352.032151	0.000451244	11	N	436	456
P08003	Exosome	ATEVK	DLGLSESGEDVNAAILDESGKK	FAMEP	3		749.7049325	2246.091398	0.000451244	13	N	456	478
P08003	Exosome	MLASK	FDVSGYPTIK	ILKKG	2		563.7931109	1125.570622	0.000451244	10	N	124	134
P08003	Exosome	QEFLK	DGDDVVIIGLFQGDGDPAYLQYQDAANNLREDYK	FHHTF	3		1263.262775	3786.764926	0.000451244	2	N	294	328
P08003	Exosome	PEYEK	IASTLKDNDPPIAVAK	IDATS	3		551.6459609	1651.914483	0.000451244	9	N	96	112
P08003	Parental	VAKVR	EVSQPDWTPPPEVTLSLTK	DNFDD	2		1062.547124	2123.078648	0.000451244	23	N	158	177
P08003	Parental	ILTLK	QVQEFLKDGDDVVIIGLFQGDGDPAYLQYQDAANNLR	EDYKF	3		1375.678701	4124.012702	0.000622848	16	N	287	324
P08003	Parental	DLAKR	FDVSGYPTLK	IFRKG	2		563.7931109	1125.570622	0.000451244	2	N	239	249
P08003	Parental	LEVAK	DFPEYTFAIADEEDYATEVK	DLGLS	2		1177.023876	2352.032151	0.000622848	2	N	436	456
P08003	Parental	ATEVK	DLGLSESGEDVNAAILDESGKK	FAMEP	3		749.7049325	2246.091398	0.001329271	1	N	456	478
P08003	Parental	MLASK	FDVSGYPTIK	ILKKG	2		563.7931109	1125.570622	0.000451244	3	N	124	134
P08003	Parental	QEFLK	DGDDVVIIGLFQGDGDPAYLQYQDAANNLREDYK	FHHTF	3		1263.262775	3786.764926	0.002374549	1	N	294	328
P08003	Parental	KILKK	GQAVDYDGSRTQEEIVAK	VREVS	2		983.4797726	1964.943945	0.000979378	1	N	138	156
P08003	Parental	LSLTK	DNFDDVVNNADIILVEF	YAPWC	2		976.4683422	1950.921084	0.000823681	4	N	177	194
P08003	Parental	ATEVK	DLGLSESGEDVNAAILDESGK	KFAME	2		1060.006017	2117.996435	0.002296037	1	N	456	477
P08030	Exosome	GLDSR	GFLFGPSLAQELGVGCVLIR	KQGKL	2	C16:+57.021	1067.080183	2132.144765	0.000451244	63	N	67	87
P08030	Exosome	GLDSR	GFLFGPSLAQELGVGCVLIR	KQGKL	3	C16:+57.021	711.7227218	2132.144765	0.000451244	48	N	67	87
P08030	Exosome	KGRER	LGPIPFFSLLQYD	-	2		755.4035569	1508.791514	0.000451244	26	N	167	180
P08030	Exosome	LHQLR	AEVVECVSLVELTSLK	GRERL	2	C6:+57.021	888.476893	1774.938186	0.000451244	48	N	147	163
P08030	Exosome	LHQLR	AEVVECVSLVELTSLK	GRERL	3	C6:+57.021	592.653862	1774.938186	0.000451244	5	N	147	163
P08030	Exosome	THSGK	IDYIAGLDSR	GFLFG	2		561.7936422	1121.571684	0.000451244	12	N	57	67
P08030	Exosome	GVLFR	DISPLLKDPDSFR	ASIRL	2		751.8966274	1501.777655	0.000451244	11	N	27	40
P08030	Exosome	GVLFR	DISPLLKDPDSFR	ASIRL	3		501.6003516	1501.777655	0.000451244	5	N	27	40
P08030	Exosome	LEYGK	AELEIQKDALEPGQR	VVIVD	2		848.94738	1695.87916	0.000451244	22	N	107	122
P08030	Exosome	ARRIR	SFPDFPIPGVLF	RDISP	2		668.3533357	1334.691071	0.000451244	15	N	14	26
P08030	Exosome	GLDSR	GFLFGPSLAQELGVGCVLIRK	QGKLP	3	C16:+57.021	754.4210429	2260.239729	0.000622848	13	N	67	88
P08030	Exosome	EPGQR	VVIVDDLLATGGTMFAACDLLHQLR	AEVVE	3	C18:+57.021	910.1439094	2727.408328	0.000451244	19	N	122	147
P08030	Exosome	EPGQR	VVIVDDLLATGGTMFAACDLLHQLR	AEVVE	3	M14:+15.995,C18:+57.021	915.4755761	2743.403328	0.000451244	6	N	122	147
P08030	Exosome	ARRIR	SFPDFPIPGVLFR	DISPL	2		746.4038913	1490.792183	0.000451244	18	N	14	27
P08030	Exosome	RKQGK	LPGPTVSASYSLEYGK	AELEI	2		834.9281245	1667.840649	0.000451244	21	N	91	107
P08030	Exosome	ASHLK	STHSGKIDYIAGLDSR	GFLFG	2		860.4371794	1718.858759	0.000451244	6	N	51	67
P08030	Exosome	ASHLK	STHSGKIDYIAGLDSR	GFLFG	3		573.9607196	1718.858759	0.000451244	2	N	51	67
P08030	Exosome	RIRSF	PDFPIPGVLFR	DISPL	2		629.35367	1256.69174	0.000451244	3	N	16	27
P08030	Exosome	SLKGR	ERLGPIPFFSLLQYD	-	2		897.9754091	1793.935218	0.002212458	1	N	165	180
P08030	Exosome	GLDSR	GFLFGPSLAQELGVGCVL	IRKQG	2	C16:+57.021	932.4875951	1862.95959	0.0007646	4	N	67	85
P08030	Parental	GLDSR	GFLFGPSLAQELGVGCVLIR	KQGKL	2	C16:+57.021	1067.080183	2132.144765	0.000451244	28	N	67	87
P08030	Parental	GLDSR	GFLFGPSLAQELGVGCVLIR	KQGKL	3	C16:+57.021	711.7227218	2132.144765	0.000451244	9	N	67	87
P08030	Parental	KGRER	LGPIPFFSLLQYD	-	2		755.4035569	1508.791514	0.000451244	11	N	167	180
P08030	Parental	LHQLR	AEVVECVSLVELTSLK	GRERL	2	C6:+57.021	888.476893	1774.938186	0.000451244	7	N	147	163
P08030	Parental	LEYGK	AELEIQKDALEPGQR	VVIVD	2		848.94738	1695.87916	0.000823681	2	N	107	122
P08030	Parental	ARRIR	SFPDFPIPGVLF	RDISP	2		668.3533357	1334.691071	0.000998612	2	N	14	26
P08030	Parental	GLDSR	GFLFGPSLAQELGVGCVLIRK	QGKLP	3	C16:+57.021	754.4210429	2260.239729	0.001162105	2	N	67	88
P08032	Exosome	ENSIK	ALRDQAEVCQQQQAAPVDEAGR	EARVI	2	C9:+57.021	1220.585609	2439.155618	0.000451244	9	N	954	976
P08032	Exosome	ENSIK	ALRDQAEVCQQQQAAPVDEAGR	EARVI	3	C9:+57.021	814.0596726	2439.155618	0.000451244	30	N	954	976
P08032	Exosome	DKKCR	ALNAADPGSDLLSVQALQR	QHEVF	2		970.0163253	1938.017051	0.000451244	42	N	1202	1221
P08032	Exosome	DKKCR	ALNAADPGSDLLSVQALQR	QHEVF	3		647.0134835	1938.017051	0.000451244	9	N	1202	1221
P08032	Exosome	ATAQK	GTQLYEANQLLQFENNAEDLKR	WLEEV	2		1297.646421	2593.277242	0.000451244	25	N	677	699
P08032	Exosome	ATAQK	GTQLYEANQLLQFENNAEDLKR	WLEEV	3		865.4335472	2593.277242	0.000451244	33	N	677	699
P08032	Exosome	LQKQR	TELNEAWDTLQGLTSDRK	ESLNE	2		1039.01398	2076.012359	0.000451244	18	N	1262	1280
P08032	Exosome	LQKQR	TELNEAWDTLQGLTSDRK	ESLNE	3		693.0119197	2076.012359	0.000451244	22	N	1262	1280
P08032	Exosome	WMKEK	TALINADELPTDVASGEALLAR	HQQHK	2		1120.592594	2239.169588	0.000451244	46	N	387	409
P08032	Exosome	WMKEK	TALINADELPTDVASGEALLAR	HQQHK	3		747.3976628	2239.169588	0.000451244	26	N	387	409
P08032	Exosome	KDINK	VADELLFEELLTPEGAHIR	QELNT	2		1076.568391	2151.121181	0.000451244	16	N	1137	1156
P08032	Exosome	KDINK	VADELLFEELLTPEGAHIR	QELNT	3		718.0481938	2151.121181	0.000451244	57	N	1137	1156
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQEEK	IITLD	3		1389.649135	4165.924006	0.000451244	11	N	492	529
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQEEK	IITLD	4		1042.488802	4165.924006	0.000451244	11	N	492	529
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQEEK	IITLD	3	Q1:-17.027	1383.973469	4148.897006	0.000698008	1	N	492	529
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQEEK	IITLD	3	[0:-17.027	1383.973469	4148.897006	0.000451244	4	N	492	529
P08032	Exosome	EIKAK	QDEVNAAWDRLWSLALK	RRESL	3		672.3502071	2014.027221	0.000451244	3	N	236	253
P08032	Exosome	DPRGR	SQPAGYDYVGFTNSFFGN	-	2		985.9319269	1969.848254	0.000451244	16	N	2397	2415
P08032	Exosome	ENWIK	TIGGVISSPELAEDLTGTEILLER	HQEHH	2		1257.171406	2512.327211	0.000451244	44	N	1304	1328
P08032	Exosome	ENWIK	TIGGVISSPELAEDLTGTEILLER	HQEHH	3		838.4502038	2512.327211	0.000451244	27	N	1304	1328

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08032	Exosome	DKQIK	ALNVPSSPYTWLTVDVLGR	IWNHL	2		1044.560369	2087.105137	0.000451244	26	N	2106	2125
P08032	Exosome	DKQIK	ALNVPSSPYTWLTVDVLGR	IWNHL	3		696.7095125	2087.105137	0.000451244	12	N	2106	2125
P08032	Exosome	ATRRK	LLVDSQLLQQLYQDSDDLKTWINK	KKKLA	3		959.5067122	2875.496737	0.000451244	20	N	574	598
P08032	Exosome	ATRRK	LLVDSQLLQQLYQDSDDLKTWINK	KKKLA	4		719.8819842	2875.496737	0.000451244	2	N	574	598
P08032	Exosome	SLKTK	SNGADLTAFLTLLAK	HDTLD	2		767.9279275	1533.840255	0.000451244	60	N	1950	1965
P08032	Exosome	SLKTK	SNGADLTAFLTLLAK	HDTLD	3		512.287885	1533.840255	0.00091018	1	N	1950	1965
P08032	Exosome	LKQLR	LLWDLLLELTQEKSDVLLR	ALKFY	3		766.4425438	2296.304231	0.000451244	14	N	135	154
P08032	Exosome	VSMKK	NDVLTLLSSINKDWWK	VEADD	2		966.5154298	1931.01526	0.000622848	2	N	998	1014
P08032	Exosome	VSMKK	NDVLTLLSSINKDWWK	VEADD	3		644.6795532	1931.01526	0.000823681	4	N	998	1014
P08032	Exosome	EMLAR	EDPLKDLNDLAQELISSGTFNIDQIEEK	MNGVN	3		1058.861661	3173.561582	0.000451244	64	N	1657	1685
P08032	Exosome	FQQER	LSEIAELKDQLVAGEHSQAK	AIEEQ	2		1083.574204	2165.132809	0.000451244	4	N	1980	2000
P08032	Exosome	FQQER	LSEIAELKDQLVAGEHSQAK	AIEEQ	3		722.7187363	2165.132809	0.000451244	53	N	1980	2000
P08032	Exosome	FQQER	LSEIAELKDQLVAGEHSQAK	AIEEQ	4		542.2910022	2165.132809	0.000451244	5	N	1980	2000
P08032	Exosome	EVNGR	AEQVDGVINLGNSLIER	RVCDG	2		913.9844938	1825.953388	0.000451244	24	N	1549	1566
P08032	Exosome	EVNGR	AEQVDGVINLGNSLIER	RVCDG	3		609.6589292	1825.953388	0.000451244	12	N	1549	1566
P08032	Exosome	AHHEK	LKETYALFQFFQDLDDEEAWIEEK	LLRVS	3		1003.146961	3006.417483	0.000622848	6	N	1706	1730
P08032	Exosome	ETAER	LCESHPDATEDLQK	QRTEL	2	C2:+57.021	821.872792	1641.729984	0.000451244	1	N	1246	1260
P08032	Exosome	ETAER	LCESHPDATEDLQK	QRTEL	3	C2:+57.021	548.251128	1641.729984	0.000622848	2	N	1246	1260
P08032	Exosome	SSGPK	VLETAEEIQHR	RAEVL	2		662.8469375	1323.678275	0.000622848	1	N	15	26
P08032	Exosome	GKYQK	HESFVSEVQAK	SRVLP	2		630.815106	1259.614612	0.001162105	1	N	91	102
P08032	Exosome	IKALR	DQAEVCQQQQAAPVDEAGR	EARVI	2	C6:+57.021	1050.474464	2098.933329	0.000451244	17	N	957	976
P08032	Exosome	IKALR	DQAEVCQQQQAAPVDEAGR	EARVI	3	C6:+57.021	700.6522429	2098.933329	0.000823681	3	N	957	976
P08032	Exosome	ALKRR	ESLSNAADLQR	FKRDV	2		602.3023627	1202.589125	0.000622848	4	N	255	266
P08032	Exosome	HRNRR	EIDNTLQNINSK	RDNLE	2		694.8549595	1387.694319	0.000451244	14	N	1362	1374
P08032	Exosome	NKKKK	LADDDDYKDVQNLK	SRVQK	2		826.3946459	1650.773692	0.000451244	22	N	601	615
P08032	Exosome	NKKKK	LADDDDYKDVQNLK	SRVQK	3		551.2656972	1650.773692	0.000451244	18	N	601	615
P08032	Exosome	ERGQK	LEESYHYQVFR	RDADD	2		735.8547625	1469.693925	0.002663018	2	N	47	58
P08032	Exosome	NLLNR	HEVILADIASHEPR	IQVIT	2		793.9184255	1585.821251	0.000823681	9	N	832	846
P08032	Exosome	NLLNR	HEVILADIASHEPR	IQVIT	3		529.6148837	1585.821251	0.000823681	2	N	832	846
P08032	Exosome	VHKNR	VQDVCAQGEDILNKEETQNK	DKIST	3	C5:+57.021	773.3695127	2317.085138	0.000451244	6	N	1872	1892
P08032	Exosome	EVLHK	KFEEFQEELTAR	KGKVD	2		763.8784346	1525.741269	0.000451244	16	N	196	208
P08032	Exosome	EVLHK	KFEEFQEELTAR	KGKVD	3		509.5882231	1525.741269	0.001162105	1	N	196	208
P08032	Exosome	TLLAK	HDTLDASLQSFQQER	LSEIA	2		887.9218935	1773.828187	0.000451244	33	N	1965	1980
P08032	Exosome	LDRWK	ALKEQLLTELGK	LGDYA	3		448.2700543	1341.786763	0.000451244	11	N	1481	1493
P08032	Exosome	ALVSR	GDSGDTLAATQSLLK	KHEAL	2		738.8811743	1475.746749	0.000451244	14	N	1842	1857
P08032	Exosome	LFLSK	ASDLENWIK	TIGGV	2		538.2750853	1074.534571	0.000823681	10	N	1295	1304
P08032	Exosome	QFNWK	ADVVESWIGEK	EASLK	2		616.812032	1231.608464	0.000451244	10	Y	1932	1943
P08032	Exosome	QQICR	DSEDEEAWIQETEPSAASTHLGK	DLVAA	2		1265.564959	2529.114318	0.000451244	20	N	798	821
P08032	Exosome	QQICR	DSEDEEAWIQETEPSAASTHLGK	DLVAA	3		844.045906	2529.114318	0.000451244	16	N	798	821
P08032	Exosome	GREAR	VIALYDFEAR	SRREV	2		598.81966	1195.62372	0.000698008	10	N	979	989
P08032	Exosome	LAAWK	SQLDDVHAFQQFNWK	ADVVE	2		931.9451716	1861.874743	0.000451244	18	N	1917	1932
P08032	Exosome	LAAWK	SQLDDVHAFQQFNWK	ADVVE	3		621.6327144	1861.874743	0.000451244	7	N	1917	1932
P08032	Exosome	QIQAK	DTIGVSEETLKEFSTTYK	HFDEN	2		1024.507664	2046.999729	0.000451244	15	N	2259	2277
P08032	Exosome	QIQAK	DTIGVSEETLKEFSTTYK	HFDEN	3		683.341043	2046.999729	0.000451244	8	N	2259	2277
P08032	Exosome	LKKHK	RLEGELVAHEPAVQNVLDTAESLR	DKAAV	3		882.80023	2645.37729	0.000451244	13	N	1754	1778
P08032	Exosome	GALLK	KHEAFLVDLNAFENSIK	ALRDQ	2		988.0183367	1974.021073	0.000451244	14	N	937	954
P08032	Exosome	GALLK	KHEAFLVDLNAFENSIK	ALRDQ	3		659.0148244	1974.021073	0.000451244	23	N	937	954
P08032	Exosome	GALLK	KHEAFLVDLNAFENSIK	ALRDQ	4		494.5130683	1974.021073	0.000451244	3	N	937	954
P08032	Exosome	KKHKR	LEGELVAHEPAVQNVLDTAESLR	DKAAV	3		830.7665263	2489.276179	0.000451244	20	N	1755	1778
P08032	Exosome	SENIK	TSDDIESAFQALAEGK	AYITK	2		841.3999282	1680.784256	0.000451244	23	N	2348	2364
P08032	Exosome	AATRR	KLLVDSQLLQQLYQDSDDLK	TWINK	3		788.0887178	2361.242753	0.000451244	7	N	573	593
P08032	Exosome	LRALK	FYQYSQECEDILEWVK	EKEAI	2	C8:+57.021	1068.983071	2135.950542	0.000451244	27	N	157	173
P08032	Exosome	LQKQR	TELNEAWDTLQGLTSDR	KESLN	2		974.9664981	1947.917396	0.000451244	18	N	1262	1279
P08032	Exosome	WVKEK	EAIVTLVELGDDWER	TEVLH	2		872.9417633	1743.867927	0.000451244	18	N	175	190
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	2		1245.62208	2489.22856	0.000451244	31	N	492	515
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	3		830.7506533	2489.22856	0.000451244	22	N	492	515
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	2	Q1:-17.027	1237.10858	2472.20156	0.000451244	2	N	492	515
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	2	[0:-17.027	1237.10858	2472.20156	0.000662267	3	N	492	515
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	3	[0:-17.027	825.0749867	2472.20156	0.00091018	1	N	492	515
P08032	Exosome	ATRRK	LLVDSQLLQQLYQDSDDLK	TWINK	2		1117.581695	2233.14779	0.000451244	24	N	574	593
P08032	Exosome	ATRRK	LLVDSQLLQQLYQDSDDLK	TWINK	3		745.3903968	2233.14779	0.000451244	12	N	574	593
P08032	Exosome	DDIKR	EDPTFQALEDFGTELIDSGHR	NRREI	2		1189.05129	2376.086981	0.000451244	9	N	1338	1359
P08032	Exosome	DDIKR	EDPTFQALEDFGTELIDSGHR	NRREI	3		793.0367936	2376.086981	0.000451244	22	N	1338	1359
P08032	Exosome	IKRED	PTFQALEDFGTELIDSGHR	NRREI	3		711.6802815	2132.017445	0.000451244	6	N	1340	1359
P08032	Exosome	PQHRQ	EEPVNIPQLQQQVETLYHSLLDR	AEERR	2		1375.211928	2748.408256	0.000622848	2	N	1045	1068

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08032	Exosome	PQHRQ	EEPVNIPQLQQQVETLYHSLLDR	AEERR	3		917.1438853	2748.408256	0.000451244	6	N	1045	1068
P08032	Exosome	NTSIR	DFEFWLSEAEGLLAMKDQAR	DLTSA	3		786.0479769	2355.120531	0.001264573	2	N	1615	1635
P08032	Exosome	NTSIR	DFEFWLSEAEGLLAMKDQAR	DLTSA	3	M15:+15.995	791.3796436	2371.115531	0.000451244	21	N	1615	1635
P08032	Exosome	LKQLR	LLWDLLLELTQEK	SDVLL	2		807.4616032	1612.907606	0.000451244	25	N	135	148
P08032	Exosome	LKQLR	LLWDLLLELTQEK	SDVLL	3		538.6436688	1612.907606	0.000451244	9	N	135	148
P08032	Exosome	NTSIR	DFEFWLSEAEGLLAMK	DQARD	2	M15:+15.995	951.4536925	1900.891785	0.000823681	2	N	1615	1631
P08032	Exosome	NTSIR	DFEFWLSEAEGLLAMK	DQARD	3	M15:+15.995	634.638395	1900.891785	0.000451244	5	N	1615	1631
P08032	Exosome	GVNER	FENVQSLAAAHHEK	LKETY	2		790.8949504	1579.774301	0.000451244	1	N	1692	1706
P08032	Exosome	GVNER	FENVQSLAAAHHEK	LKETY	3		527.5992336	1579.774301	0.000622848	2	N	1692	1706
P08032	Exosome	NVATR	LIDNDHYAKEEIAAR	LQRVL	2		879.4450044	1756.874409	0.000451244	4	N	1457	1472
P08032	Exosome	NVATR	LIDNDHYAKEEIAAR	LQRVL	3		586.632603	1756.874409	0.000622848	6	N	1457	1472
P08032	Exosome	AQEGK	ISDLENVATR	LIDND	2		559.2965491	1116.577498	0.002884417	1	N	1447	1457
P08032	Exosome	ALLQK	HDDFEEAFTAQEEK	IITLD	2		848.360803	1694.706006	0.000451244	16	N	515	529
P08032	Exosome	ALLQK	HDDFEEAFTAQEEK	IITLD	3		565.909802	1694.706006	0.000622848	2	N	515	529
P08032	Exosome	SYDDR	FQSADATGQELLDGNHEASEEIREK	MTILA	3		925.4341641	2773.279092	0.000451244	7	N	423	448
P08032	Exosome	SYDDR	FQSADATGQELLDGNHEASEEIREK	MTILA	4		694.327573	2773.279092	0.000451244	4	N	423	448
P08032	Exosome	KDWWK	VEADDHQGFVPAVYVR	KLAPD	2		901.4475471	1800.879494	0.000451244	22	N	1014	1030
P08032	Exosome	KDWWK	VEADDHQGFVPAVYVR	KLAPD	3		601.3009648	1800.879494	0.000451244	3	N	1014	1030
P08032	Exosome	DVLGR	IWNHLPDIIK	EREQE	3		416.9086797	1247.702639	0.000823681	8	N	2125	2135
P08032	Exosome	WIQEK	KTENTGVELDDVWELQK	KFDEF	2		1002.500174	2002.984747	0.000451244	16	N	1099	1116
P08032	Exosome	QDYGR	DLQSVQNLLK	KHKRL	2		579.3303919	1156.645184	0.000451244	10	N	1741	1751
P08032	Exosome	EDYGK	GLADVQNLLR	KHGLL	2		549.8174517	1097.619303	0.000451244	22	N	715	725
P08032	Exosome	IQEKK	TENTGVELDDVWELQK	KFDEF	2		938.4526922	1874.889784	0.000451244	14	N	1100	1116
P08032	Exosome	DPGRK	GYVSLEDYTSFLIDKESENIK	TSDDI	3		817.4044831	2449.190049	0.000451244	12	N	2327	2348
P08032	Exosome	ENDLK	ANVQLQQYLADLHEAEAWIK	EKEPI	2		1170.603296	2339.190992	0.000451244	5	N	894	914
P08032	Exosome	ENDLK	ANVQLQQYLADLHEAEAWIK	EKEPI	3		780.7381308	2339.190992	0.000451244	19	N	894	914
P08032	Exosome	RQLQK	EHEAFLASLAGAQEDFNYLLELDK	QIKAL	2		1362.164112	2722.312624	0.000451244	10	N	2079	2103
P08032	Exosome	RQLQK	EHEAFLASLAGAQEDFNYLLELDK	QIKAL	3		908.4453414	2722.312624	0.000451244	10	N	2079	2103
P08032	Exosome	HRQEE	PVNIPQLQQQVETLYHSLLDR	AEERR	3		831.1154898	2490.323069	0.001395409	1	N	1047	1068
P08032	Exosome	LKETY	ALFQFFQDLDDEEAWIEEK	LLRVS	2		1187.050228	2372.084856	0.000451244	2	N	1711	1730
P08032	Exosome	HSQAK	AIEEQHAALLR	HWEQL	2		625.8467405	1249.677881	0.001229886	1	N	2000	2011
P08032	Exosome	QHQYR	QCLDFHLFYR	DSEQV	3	C2:+57.021	466.8926581	1397.654574	0.000451244	16	N	471	481
P08032	Exosome	KKHKR	LEGELVAHEPAVQNVLDTAESLRDK	AAVGK	3		911.8071617	2732.398085	0.000451244	15	N	1755	1780
P08032	Exosome	KKHKR	LEGELVAHEPAVQNVLDTAESLRDK	AAVGK	4		684.1073213	2732.398085	0.000451244	8	N	1755	1780
P08032	Exosome	ENRKK	MLDQCLELQLFR	GKCDQ	2	M1:+15.995,C5:+57.021	791.3921523	1580.768705	0.000451244	15	N	1387	1399
P08032	Exosome	LEWVK	EKEAIVTLVELGDDWER	TEVLH	2		1001.510541	2001.005483	0.000622848	3	N	173	190
P08032	Exosome	LEWVK	EKEAIVTLVELGDDWER	TEVLH	3		668.0096276	2001.005483	0.000451244	8	N	173	190
P08032	Exosome	EDPLK	DLNDLAQELISSGTFNIDQIEEK	MNGVN	2		1296.637927	2591.260254	0.0025889	1	N	1662	1685
P08032	Exosome	EVSMK	KNDVLTLLSSINK	DWWKV	2		722.9226452	1443.82969	0.000451244	6	N	997	1010
P08032	Exosome	EVSMK	KNDVLTLLSSINK	DWWKV	3		482.2843635	1443.82969	0.000451244	15	N	997	1010
P08032	Exosome	TYALF	QFFQDLDDEEAWIEEK	LLRVS	2		1021.455432	2040.895264	0.0025889	1	N	1714	1730
P08032	Exosome	HDDIK	REDPTFQALEDFGTELIDSGHR	NRREI	3		845.0704974	2532.188092	0.000622848	3	N	1337	1359
P08032	Exosome	KDQAR	DLTSAGNLLK	KHQLL	2		516.2907354	1030.565871	0.002019181	1	N	1635	1645
P08032	Exosome	ALLKK	HEAFLVDLNAFENSIK	ALRDQ	2		923.9708551	1845.92611	0.001162105	1	N	938	954
P08032	Exosome	ALLKK	HEAFLVDLNAFENSIK	ALRDQ	3		616.3165034	1845.92611	0.000662267	7	N	938	954
P08032	Exosome	ERGNK	MVEEGHFAAEDIASR	VESLN	3		554.5916392	1660.751518	0.000451244	17	N	856	871
P08032	Exosome	ETATK	LIDNDHYDSENIAAIR	DGLLA	3		620.303034	1857.885702	0.000622848	8	N	539	555
P08032	Exosome	SYDDR	FQSADATGQELLDGNHEASEEIR	EKMTI	2		1259.078568	2516.141536	0.002374549	1	N	423	446
P08032	Exosome	SYDDR	FQSADATGQELLDGNHEASEEIR	EKMTI	3		839.7216453	2516.141536	0.000698008	5	N	423	446
P08032	Exosome	VLHKK	FEEFQEELTAR	KGKVD	2		699.8309531	1397.646306	0.001162105	7	N	197	208
P08032	Exosome	AVAAR	LSEVANLWK	ELLEA	2		530.2958207	1058.576041	0.000451244	7	N	659	668
P08032	Exosome	NSLKR	LADEQYQLLSSAHAVEMFHR	EADDV	4	M17:+15.995	591.0383033	2360.122013	0.000451244	9	N	1168	1188
P08032	Exosome	ETATK	LIDNDHYDSENIAAIRDGLLAR	RDALR	3		828.7546207	2483.240462	0.000451244	11	N	539	561
P08032	Exosome	ETATK	LIDNDHYDSENIAAIRDGLLAR	RDALR	4		621.8179155	2483.240462	0.000823681	7	N	539	561
P08032	Exosome	RSCLR	GLNYYLPMVEEGEPEPK	FEKFL	2	M8:+15.995	990.9671641	1979.918728	0.000451244	6	N	2297	2314
P08032	Exosome	QQICR	DSEDEEAWIQETEPSAASTHLGKDLVAAK	NLLNR	3		1043.16211	3126.46293	0.000451244	10	N	798	827
P08032	Exosome	QQICR	DSEDEEAWIQETEPSAASTHLGKDLVAAK	NLLNR	4		782.6235325	3126.46293	0.001943752	2	N	798	827
P08032	Exosome	TSDRK	ESLNEAHKFFLFLSK	ASDLE	3		603.9898391	1808.946117	0.000451244	8	N	1280	1295
P08032	Exosome	IQETR	AYFLDGSLLK	ETGTL	2		563.8113036	1125.607007	0.000451244	5	N	2173	2183
P08032	Exosome	SGWMK	EKTALINADELPTDVASGEALLAR	HQQHK	3		833.1101816	2496.307145	0.000451244	5	N	385	409
P08032	Exosome	EDLKR	WLEEVEWQVTSEDYGK	GLADV	2		999.4605172	1996.905434	0.000451244	6	N	699	715
P08032	Exosome	FLIDK	ESENIKTSDDIESAFQALAEGK	AYITK	3		794.7156087	2381.123426	0.000622848	4	N	2342	2364
P08032	Exosome	LRALK	FYQYSQECEDILEWVKEK	EAIVT	3	C8:+57.021	798.7038327	2393.088098	0.000451244	6	N	157	175
P08032	Exosome	YGYHR	FLSDYDELSGWMK	EKTAL	2		795.8613965	1589.707193	0.000451244	3	N	372	385
P08032	Exosome	SRVQK	QQDFEEELAVNEIMLNNLEK	TGQEM	2		1203.578827	2405.142054	0.000451244	7	N	620	640

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08032	Exosome	SRVQK	QQDFEEELAVNEIMLNNLEK	TGQEM	2	M14:+15.995	1211.576327	2421.137054	0.000451244	7	N	620	640
P08032	Exosome	SRVQK	QQDFEEELAVNEIMLNNLEK	TGQEM	3	M14:+15.995	808.0534847	2421.137054	0.000451244	3	N	620	640
P08032	Exosome	WVKEK	EAIVTLVELGDDWERTEVLHK	KFEEF	3		818.0959838	2451.264552	0.000451244	13	N	175	196
P08032	Exosome	WVKEK	EAIVTLVELGDDWERTEVLHK	KFEEF	4		613.8239379	2451.264552	0.000451244	10	N	175	196
P08032	Exosome	RAIRR	ENDLKANVQLQQYLADLHEAEAWIK	EKEPI	3		980.5019612	2938.482484	0.000622848	3	N	889	914
P08032	Exosome	RAIRR	ENDLKANVQLQQYLADLHEAEAWIK	EKEPI	4		735.6284209	2938.482484	0.000451244	9	N	889	914
P08032	Exosome	EASLK	TKSNGADLTAFLTLLAK	HDTLD	3		588.6687656	1762.982897	0.000451244	10	N	1948	1965
P08032	Exosome	LNEIR	QLQKEHEAFLASLAGAQEDFNYLLELDK	QIKAL	3		1074.210736	3219.608807	0.000451244	5	N	2075	2103
P08032	Exosome	LNEIR	QLQKEHEAFLASLAGAQEDFNYLLELDK	QIKAL	4		805.9100016	3219.608807	0.000451244	17	N	2075	2103
P08032	Exosome	LNEIR	QLQKEHEAFLASLAGAQEDFNYLLELDK	QIKAL	3	Q1:-17.027	1068.535069	3202.581807	0.000451244	5	N	2075	2103
P08032	Exosome	LNEIR	QLQKEHEAFLASLAGAQEDFNYLLELDK	QIKAL	3	[0:-17.027	1068.535069	3202.581807	0.000451244	5	N	2075	2103
P08032	Exosome	RQLQK	EHEAFLASLAGAQEDFNYLLELDKQIK	ALNVP	3		1031.524543	3091.550229	0.000451244	10	N	2079	2106
P08032	Exosome	RQLQK	EHEAFLASLAGAQEDFNYLLELDKQIK	ALNVP	4		773.8953572	3091.550229	0.000451244	6	N	2079	2106
P08032	Exosome	KQFYR	DLEDLEEWINEMLPIACDESYKDPTNIQR	KYLKH	3	C17:+57.021	1179.545084	3535.611852	0.000451244	2	N	1505	1534
P08032	Exosome	KQFYR	DLEDLEEWINEMLPIACDESYKDPTNIQR	KYLKH	3	M12:+15.995,C17:+57.021	1184.876751	3551.606852	0.000451244	8	N	1505	1534
P08032	Exosome	ARQIK	NFEMCQEFEQNASAFLQWIQETR	AYFLD	3	M4:+15.995,C5:+57.021	974.7659663	2921.274499	0.000451244	3	N	2150	2173
P08032	Exosome	LAKTR	GVNLEESLEYLQFMENAEEEEAWLGEK	CALVS	3		1062.820697	3185.43869	0.000451244	7	N	1809	1836
P08032	Exosome	LAKTR	GVNLEESLEYLQFMENAEEEEAWLGEK	CALVS	3	M14:+15.995	1068.152363	3201.43369	0.001162105	1	N	1809	1836
P08032	Exosome	SRQQR	FNTSIRDFEFWLSEAEGLLAMK	DQARD	3	M21:+15.995	874.0971363	2619.268009	0.000823681	1	N	1609	1631
P08032	Exosome	EIREK	MTILANDWAALLELWDK	CQHQY	2		1002.019491	2002.023383	0.000451244	9	N	448	465
P08032	Exosome	EIREK	MTILANDWAALLELWDK	CQHQY	3		668.3489275	2002.023383	0.002981883	1	N	448	465
P08032	Exosome	EIREK	MTILANDWAALLELWDK	CQHQY	2	M1:+15.995	1010.016991	2018.018383	0.001763695	1	N	448	465
P08032	Exosome	RVAER	GQKLEESYHYQVFR	RDADD	2		892.4422648	1782.86893	0.000451244	2	N	44	58
P08032	Exosome	RVAER	GQKLEESYHYQVFR	RDADD	3		595.2974432	1782.86893	0.000451244	8	N	44	58
P08032	Exosome	SLLSR	FEALKEPLAIR	KKKLI	2		643.8775093	1285.739419	0.001329271	1	N	772	783
P08032	Exosome	KDINK	VADELLFEELLTPEGAHIRQELNTR	WNSLK	4		724.1323334	2892.498134	0.002019181	1	N	1137	1162
P08032	Exosome	IQQMK	LDLVSNWER	IRALA	2		566.2938094	1130.572019	0.000823681	4	N	343	352
P08032	Exosome	QIQAK	DTIGVSEETLKEFSTTY	KHFDE	2		960.4601829	1918.904766	0.000451244	3	N	2259	2276
P08032	Exosome	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQ	EEKII	3		1260.922419	3779.743856	0.002080925	1	N	492	526
P08032	Exosome	PQHRQ	EEPVNIPQLQQQVETLYHSLLDRAEER	RRRLL	4		809.4157168	3233.631667	0.00091018	2	N	1045	1072
P08032	Exosome	KMTIL	ANDWAALLELWDK	CQHQY	2		772.891345	1543.76709	0.000622848	3	N	452	465
P08032	Exosome	IKALR	DQAEVCQQQQAAPVDEAGREAR	VIALY	3	C6:+57.021	819.3791823	2455.114147	0.000451244	3	N	957	979
P08032	Exosome	GSLLK	ETGTLESQLEANK	RKQKE	2		710.3522497	1418.688899	0.000451244	1	N	2183	2196
P08032	Parental	ENSIK	ALRDQAEVCQQQQAAPVDEAGR	EARVI	2	C9:+57.021	1220.585609	2439.155618	0.000451244	2	N	954	976
P08032	Parental	ENSIK	ALRDQAEVCQQQQAAPVDEAGR	EARVI	3	C9:+57.021	814.0596726	2439.155618	0.000451244	17	N	954	976
P08032	Parental	DKKCR	ALNAADPGSDLLSVQALQR	QHEVF	2		970.0163253	1938.017051	0.000451244	14	N	1202	1221
P08032	Parental	ATAQK	GTQLYEANQLLQFENNAEDLKR	WLEEV	2		1297.646421	2593.277242	0.000451244	4	N	677	699
P08032	Parental	ATAQK	GTQLYEANQLLQFENNAEDLKR	WLEEV	3		865.4335472	2593.277242	0.000451244	13	N	677	699
P08032	Parental	LQKQR	TELNEAWDTLQGLTSDRK	ESLNE	3		693.0119197	2076.012359	0.000662267	5	N	1262	1280
P08032	Parental	WMKEK	TALINADELPTDVASGEALLAR	HQQHK	2		1120.592594	2239.169588	0.000451244	19	N	387	409
P08032	Parental	WMKEK	TALINADELPTDVASGEALLAR	HQQHK	3		747.3976628	2239.169588	0.000451244	12	N	387	409
P08032	Parental	KDINK	VADELLFEELLTPEGAHIR	QELNT	2		1076.568391	2151.121181	0.0007646	1	N	1137	1156
P08032	Parental	KDINK	VADELLFEELLTPEGAHIR	QELNT	3		718.0481938	2151.121181	0.000451244	17	N	1137	1156
P08032	Parental	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQEEK	IITLD	3		1389.649135	4165.924006	0.000451244	1	N	492	529
P08032	Parental	SWMSR	QEAFLENEDLGNSVGSVEALLQKHDDFEEAFTAQEEK	IITLD	4		1042.488802	4165.924006	0.000622848	7	N	492	529
P08032	Parental	EIKAK	QDEVNAAWDRLWSLALK	RRESL	3		672.3502071	2014.027221	0.002212458	1	N	236	253
P08032	Parental	DPRGR	SQPAGYDYVGFTNSFFGN	-	2		985.9319269	1969.848254	0.000451244	9	N	2397	2415
P08032	Parental	ENWIK	TIGGVISSPELAEDLTGTEILLER	HQEHH	2		1257.171406	2512.327211	0.000451244	21	N	1304	1328
P08032	Parental	ENWIK	TIGGVISSPELAEDLTGTEILLER	HQEHH	3		838.4502038	2512.327211	0.000451244	5	N	1304	1328
P08032	Parental	DKQIK	ALNVPSSPYTWLTVDVLGR	IWNHL	2		1044.560369	2087.105137	0.000451244	14	N	2106	2125
P08032	Parental	DKQIK	ALNVPSSPYTWLTVDVLGR	IWNHL	3		696.7095125	2087.105137	0.000451244	4	N	2106	2125
P08032	Parental	ATRRK	LLVDSQLLQQLYQDSDDLKTWINK	KKKLA	3		959.5067122	2875.496737	0.000451244	6	N	574	598
P08032	Parental	SLKTK	SNGADLTAFLTLLAK	HDTLD	2		767.9279275	1533.840255	0.000451244	4	N	1950	1965
P08032	Parental	LKQLR	LLWDLLLELTQEKSDVLLR	ALKFY	3		766.4425438	2296.304231	0.000451244	7	N	135	154
P08032	Parental	VSMKK	NDVLTLLSSINKDWWK	VEADD	3		644.6795532	1931.01526	0.001763695	2	N	998	1014
P08032	Parental	EMLAR	EDPLKDLNDLAQELISSGTFNIDQIEEK	MNGVN	3		1058.861661	3173.561582	0.000451244	20	N	1657	1685
P08032	Parental	FQQER	LSEIAELKDQLVAGEHSQAK	AIEEQ	4		542.2910022	2165.132809	0.000451244	3	N	1980	2000
P08032	Parental	EDLKR	WLEEVEWQVTSEDYGKGLADVQNLLR	KHGLL	3		1026.512526	3076.514178	0.000698008	1	N	699	725
P08032	Parental	EVNGR	AEQVDGVINLGNSLIER	RVCDG	2		913.9844938	1825.953388	0.000451244	12	N	1549	1566
P08032	Parental	AVAAR	LSEVANLWKELLEATAQK	GTQLY	3		681.709401	2042.104803	0.000823681	1	N	659	677
P08032	Parental	AHHEK	LKETYALFQFFQDLDDEEAWIEEK	LLRVS	3		1003.146961	3006.417483	0.000451244	7	N	1706	1730
P08032	Parental	IKALR	DQAEVCQQQQAAPVDEAGR	EARVI	2	C6:+57.021	1050.474464	2098.933329	0.000622848	16	N	957	976
P08032	Parental	HRNRR	EIDNTLQNINSK	RDNLE	2		694.8549595	1387.694319	0.000451244	6	N	1362	1374
P08032	Parental	NLLNR	HEVILADIASHEPR	IQVIT	2		793.9184255	1585.821251	0.002519933	1	N	832	846
P08032	Parental	NLLNR	HEVILADIASHEPR	IQVIT	3		529.6148837	1585.821251	0.000451244	4	N	832	846

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08032	Parental	TLLAK	HDTLDASLQSFQQER	LSEIA	2		887.9218935	1773.828187	0.000451244	1	N	1965	1980
P08032	Parental	QFNWK	ADVVESWIGEK	EASLK	2		616.812032	1231.608464	0.000622848	2	Y	1932	1943
P08032	Parental	QQICR	DSEDEEAWIQETEPSAASTHLGK	DLVAA	2		1265.564959	2529.114318	0.000451244	5	N	798	821
P08032	Parental	QQICR	DSEDEEAWIQETEPSAASTHLGK	DLVAA	3		844.045906	2529.114318	0.000451244	8	N	798	821
P08032	Parental	LAAWK	SQLDDVHAFQQFNWK	ADVVE	3		621.6327144	1861.874743	0.001839721	2	N	1917	1932
P08032	Parental	QIQAK	DTIGVSEETLKEFSTTYK	HFDEN	2		1024.507664	2046.999729	0.000622848	5	N	2259	2277
P08032	Parental	GALLK	KHEAFLVDLNAFENSIK	ALRDQ	2		988.0183367	1974.021073	0.000662267	1	N	937	954
P08032	Parental	GALLK	KHEAFLVDLNAFENSIK	ALRDQ	3		659.0148244	1974.021073	0.000451244	5	N	937	954
P08032	Parental	SENIK	TSDDIESAFQALAEGK	AYITK	2		841.3999282	1680.784256	0.000451244	6	N	2348	2364
P08032	Parental	LRALK	FYQYSQECEDILEWVK	EKEAI	2	C8:+57.021	1068.983071	2135.950542	0.000451244	8	N	157	173
P08032	Parental	LQKQR	TELNEAWDTLQGLTSDR	KESLN	2		974.9664981	1947.917396	0.000451244	1	N	1262	1279
P08032	Parental	WVKEK	EAIVTLVELGDDWER	TEVLH	2		872.9417633	1743.867927	0.000451244	7	N	175	190
P08032	Parental	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	2		1245.62208	2489.22856	0.000451244	13	N	492	515
P08032	Parental	SWMSR	QEAFLENEDLGNSVGSVEALLQK	HDDFE	3		830.7506533	2489.22856	0.000823681	1	N	492	515
P08032	Parental	ATRRK	LLVDSQLLQQLYQDSDDLK	TWINK	2		1117.581695	2233.14779	0.000451244	1	N	574	593
P08032	Parental	ATRRK	LLVDSQLLQQLYQDSDDLK	TWINK	3		745.3903968	2233.14779	0.000622848	6	N	574	593
P08032	Parental	DDIKR	EDPTFQALEDFGTELIDSGHR	NRREI	2		1189.05129	2376.086981	0.000451244	1	N	1338	1359
P08032	Parental	DDIKR	EDPTFQALEDFGTELIDSGHR	NRREI	3		793.0367936	2376.086981	0.000451244	2	N	1338	1359
P08032	Parental	NTSIR	DFEFWLSEAEGLLAMKDQAR	DLTSA	3	M15:+15.995	791.3796436	2371.115531	0.000622848	2	N	1615	1635
P08032	Parental	LKQLR	LLWDLLLELTQEK	SDVLL	2		807.4616032	1612.907606	0.000451244	7	N	135	148
P08032	Parental	ALLQK	HDDFEEAFTAQEEK	IITLD	2		848.360803	1694.706006	0.001229886	1	N	515	529
P08032	Parental	KDWWK	VEADDHQGFVPAVYVR	KLAPD	2		901.4475471	1800.879494	0.002080925	1	N	1014	1030
P08032	Parental	KDWWK	VEADDHQGFVPAVYVR	KLAPD	3		601.3009648	1800.879494	0.000451244	2	N	1014	1030
P08032	Parental	QDYGR	DLQSVQNLLK	KHKRL	2		579.3303919	1156.645184	0.002813207	2	N	1741	1751
P08032	Parental	EDYGK	GLADVQNLLR	KHGLL	2		549.8174517	1097.619303	0.000637154	3	N	715	725
P08032	Parental	ENDLK	ANVQLQQYLADLHEAEAWIK	EKEPI	3		780.7381308	2339.190992	0.000451244	9	N	894	914
P08032	Parental	RQLQK	EHEAFLASLAGAQEDFNYLLELDK	QIKAL	3		908.4453414	2722.312624	0.000451244	9	N	2079	2103
P08032	Parental	LKETY	ALFQFFQDLDDEEAWIEEK	LLRVS	2		1187.050228	2372.084856	0.000451244	1	N	1711	1730
P08032	Parental	QHQYR	QCLDFHLFYR	DSEQV	3	C2:+57.021	466.8926581	1397.654574	0.000662267	2	N	471	481
P08032	Parental	KDQAR	DLTSAGNLLK	KHQLL	2		516.2907354	1030.565871	0.002884417	1	N	1635	1645
P08032	Parental	ALLKK	HEAFLVDLNAFENSIK	ALRDQ	3		616.3165034	1845.92611	0.002727428	1	N	938	954
P08071	Exosome	VTEAK	NCHLAIAPNHAVVSR	TDKVE	2	C2:+57.021	829.931113	1657.846626	0.000451244	32	N	603	618
P08071	Exosome	VTEAK	NCHLAIAPNHAVVSR	TDKVE	3	C2:+57.021	553.623342	1657.846626	0.000451244	159	N	603	618
P08071	Exosome	VTEAK	NCHLAIAPNHAVVSR	TDKVE	4	C2:+57.021	415.4694565	1657.846626	0.000451244	132	N	603	618
P08071	Exosome	VTEYK	ECHLAQVPSHAVVSR	STNDK	2	C2:+57.021	845.4284031	1688.841206	0.000451244	13	N	261	276
P08071	Exosome	VTEYK	ECHLAQVPSHAVVSR	STNDK	3	C2:+57.021	563.9548687	1688.841206	0.000451244	36	N	261	276
P08071	Exosome	VTEYK	ECHLAQVPSHAVVSR	STNDK	4	C2:+57.021	423.2181016	1688.841206	0.000451244	39	N	261	276
P08071	Exosome	VTEYK	ECHLAQVPSHAVVSR	STNDK	3	[0:-18.011,C2:+57.021	557.9512021	1670.830206	0.000662267	1	N	261	276
P08071	Exosome	KPPYK	LRPVAAEVYGTK	EQPRT	2		652.3725911	1302.729582	0.001162105	2	N	91	103
P08071	Exosome	KPPYK	LRPVAAEVYGTK	EQPRT	3		435.2509941	1302.729582	0.000451244	42	N	91	103
P08071	Exosome	ASKAR	VTWCAVGSEEKR	KCDQW	2	C4:+57.021	711.346016	1420.676432	0.000451244	32	N	362	374
P08071	Exosome	ASKAR	VTWCAVGSEEKR	KCDQW	3	C4:+57.021	474.5666107	1420.676432	0.000451244	20	N	362	374
P08071	Exosome	ATTVQ	WCAVSNSEEEKCLR	WQNEM	2	C2:+57.021,C12:+57.021	884.3931374	1766.770675	0.001591523	1	N	25	39
P08071	Exosome	AGALR	CLRDNAGDVAFTR	GSTVF	2	C1:+57.021	747.8598219	1493.704044	0.000451244	7	N	215	228
P08071	Exosome	AGALR	CLRDNAGDVAFTR	GSTVF	2	[0:-17.027,C1:+57.021	739.3463219	1476.677044	0.000451244	4	N	215	228
P08071	Exosome	PGAQK	DRFPNLCSSCAGTGANK	CASSP	2	C7:+57.021,C10:+57.021	927.9147683	1853.813937	0.000451244	76	N	181	198
P08071	Exosome	PGAQK	DRFPNLCSSCAGTGANK	CASSP	3	C7:+57.021,C10:+57.021	618.9457789	1853.813937	0.000451244	70	N	181	198
P08071	Exosome	LYLTF	SYTTSIQNLNK	KQQDV	2		634.8282134	1267.640827	0.000979378	1	N	340	351
P08071	Exosome	GADPK	SNLCALCIGDEKGENK	CAPNS	2	C4:+57.021,C7:+57.021	904.4193522	1806.823104	0.000451244	307	N	516	532
P08071	Exosome	GADPK	SNLCALCIGDEKGENK	CAPNS	3	C4:+57.021,C7:+57.021	603.2821681	1806.823104	0.000451244	271	N	516	532
P08071	Exosome	TTSEK	YLGKEYVIATER	LKQCS	2		721.3884382	1440.761276	0.000451244	48	N	677	689
P08071	Exosome	TTSEK	YLGKEYVIATER	LKQCS	3		481.2615588	1440.761276	0.000451244	28	N	677	689
P08071	Exosome	ASKAR	VTWCAVGSEEK	RKCDQ	2	C4:+57.021	633.2954605	1264.575321	0.000451244	144	N	362	373
P08071	Exosome	AQKDR	FPNLCSSCAGTGANK	CASSP	2	C5:+57.021,C8:+57.021	792.3507412	1582.685882	0.000451244	63	N	183	198
P08071	Exosome	VAFTR	GSTVFEELPNKAER	DQYKL	2		788.9024411	1575.789282	0.000451244	82	N	228	242
P08071	Exosome	VAFTR	GSTVFEELPNKAER	DQYKL	3		526.2708941	1575.789282	0.000451244	29	N	228	242
P08071	Exosome	VAFLK	DSTVLQNTDGKNTEEWAR	NLKLK	2		1032.485586	2062.955573	0.000451244	178	N	562	580
P08071	Exosome	VAFLK	DSTVLQNTDGKNTEEWAR	NLKLK	3		688.6596575	2062.955573	0.000451244	89	N	562	580
P08071	Exosome	RSCKF	NEFFSQSCAPGADPK	SNLCA	2	C8:+57.021	827.8622273	1653.708855	0.000451244	146	N	501	516
P08071	Exosome	LFQSK	TKNLLFNDNTECLAK	IPGKT	2	C12:+57.021	890.9488341	1779.882068	0.000451244	121	N	653	668
P08071	Exosome	LFQSK	TKNLLFNDNTECLAK	IPGKT	3	C12:+57.021	594.3018227	1779.882068	0.000451244	128	N	653	668
P08071	Exosome	GADPK	SNLCALCIGDEK	GENKC	2	C4:+57.021,C7:+57.021	690.3183783	1378.621157	0.000451244	34	N	516	528
P08071	Exosome	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	C1:+39.994	899.3911235	1796.766647	0.000451244	5	N	198	215
P08071	Exosome	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	C1:+57.021	907.9046235	1813.793647	0.000451244	161	N	198	215
P08071	Exosome	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	[0:-17.027,C1:+57.021	899.3911235	1796.766647	0.000451244	20	N	198	215

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08071	Exosome	ANQTR	SCKFNEFFSQSCAPGADPK	SNLCA	2	C2:+57.021,C12:+57.021	1088.975023	2175.934446	0.000451244	6	N	497	516
P08071	Exosome	ANQTR	SCKFNEFFSQSCAPGADPK	SNLCA	3	C2:+57.021,C12:+57.021	726.319282	2175.934446	0.000451244	20	N	497	516
P08071	Exosome	CLAEK	AGNVAFLKDSTVLQNTDGK	NTEEW	2		989.5161581	1977.016716	0.000451244	19	N	554	573
P08071	Exosome	CLAEK	AGNVAFLKDSTVLQNTDGK	NTEEW	3		660.0133721	1977.016716	0.000451244	22	N	554	573
P08071	Exosome	YTAGK	CGLVPVLAENQK	SSKSN	2	C1:+39.994	655.8423524	1309.669105	0.0025889	1	N	422	434
P08071	Exosome	YTAGK	CGLVPVLAENQK	SSKSN	2	C1:+57.021	664.3558524	1326.696105	0.000451244	235	N	422	434
P08071	Exosome	YTAGK	CGLVPVLAENQK	SSKSN	2	[0:-17.027,C1:+57.021	655.8423524	1309.669105	0.000451244	56	N	422	434
P08071	Exosome	RDQYK	LLCPDNTWKPVTEYK	ECHLA	2	C3:+57.021	932.4694023	1862.923205	0.000451244	24	N	246	261
P08071	Exosome	RDQYK	LLCPDNTWKPVTEYK	ECHLA	3	C3:+57.021	621.9822016	1862.923205	0.000451244	12	N	246	261
P08071	Exosome	VAAVR	REDAGFTWSSLR	GKKSC	2		712.8500115	1423.684423	0.000451244	62	N	458	470
P08071	Exosome	VAAVR	REDAGFTWSSLR	GKKSC	3		475.5692743	1423.684423	0.000451244	31	N	458	470
P08071	Exosome	RDQYK	LLCPDNTWKPVTEYKECHLAQVPSHAVVSR	STNDK	3	C3:+57.021,C17:+57.021	1178.92575	3533.753851	0.000451244	22	N	246	276
P08071	Exosome	RDQYK	LLCPDNTWKPVTEYKECHLAQVPSHAVVSR	STNDK	4	C3:+57.021,C17:+57.021	884.4462627	3533.753851	0.000622848	16	N	246	276
P08071	Exosome	TRSCK	FNEFFSQSCAPGADPK	SNLCA	2	C9:+57.021	901.3964343	1800.777269	0.000451244	493	N	500	516
P08071	Exosome	TRSCK	FNEFFSQSCAPGADPK	SNLCA	3	C9:+57.021	601.2668895	1800.777269	0.000451244	33	N	500	516
P08071	Exosome	QKSSK	SNGLDCVNRPVEGYLAVAAVRR	EDAGF	3	C6:+57.021	806.089015	2415.243645	0.000823681	4	N	437	459
P08071	Exosome	KFGKK	QASGFQLFASPSGQK	DLLFK	2		776.8918764	1551.768153	0.000451244	58	N	299	314
P08071	Exosome	KFGKK	QASGFQLFASPSGQK	DLLFK	2	[0:-17.027	768.3783764	1534.741153	0.000622848	17	N	299	314
P08071	Exosome	GQRCP	GEFCLFQSK	TKNLL	2	C4:+57.021	558.263432	1114.511264	0.000451244	24	N	644	653
P08071	Exosome	QSKTK	NLLFNDNTECLAK	IPGKT	2	C10:+57.021	776.3775132	1550.739426	0.000451244	545	N	655	668
P08071	Exosome	NLKLK	DFELLCLDDTRKPVTEAK	NCHLA	2	C6:+57.021	1075.543827	2149.072054	0.000451244	35	N	585	603
P08071	Exosome	NLKLK	DFELLCLDDTRKPVTEAK	NCHLA	3	C6:+57.021	717.3651514	2149.072054	0.000451244	35	N	585	603
P08071	Exosome	NLKLK	DFELLCLDDTRKPVTEAK	NCHLA	4	C6:+57.021	538.2758135	2149.072054	0.000451244	3	N	585	603
P08071	Exosome	RNGQR	CPGEFCLFQSK	TKNLL	2	C1:+57.021,C6:+57.021	686.8049068	1371.594214	0.000451244	364	N	642	653
P08071	Exosome	RNGQR	CPGEFCLFQSK	TKNLL	2	[0:-17.027,C1:+57.021,C6:+57.021	678.2914068	1354.567214	0.000451244	68	N	642	653
P08071	Exosome	VAIMK	GDADAMSLDGGYIYTAGK	CGLVP	2		902.9070637	1803.798527	0.000451244	32	N	404	422
P08071	Exosome	DVGLY	LTFSYTTSIQNLNK	KQQDV	2		815.4282917	1628.840983	0.000823681	1	N	337	351
P08071	Exosome	AAVRR	EDAGFTWSSLR	GKKSC	2		634.7994559	1267.583312	0.000823681	50	N	459	470
P08071	Exosome	QKSSK	SNGLDCVNRPVEGYLAVAAVR	REDAG	2	C6:+57.021	1130.579067	2259.142534	0.000451244	33	N	437	458
P08071	Exosome	QKSSK	SNGLDCVNRPVEGYLAVAAVR	REDAG	3	C6:+57.021	754.0553112	2259.142534	0.000451244	743	N	437	458
P08071	Exosome	RDQYK	LLCPDNTWKPVTEY	KECHL	2	C3:+57.021	868.4219208	1734.828242	0.000451244	7	N	246	260
P08071	Exosome	ARNLK	LKDFELLCLDDTR	KPVTE	2	C8:+57.021	819.4140957	1636.812591	0.000451244	39	N	583	596
P08071	Exosome	ARNLK	LKDFELLCLDDTR	KPVTE	3	C8:+57.021	546.6119972	1636.812591	0.000451244	173	N	583	596
P08071	Exosome	PSGQK	DLLFKESAIGFVR	VPQKV	3		498.9492037	1493.824211	0.0025889	1	N	314	327
P08071	Exosome	AVVSR	STNDKEEAIWELLR	QSQEK	2		852.4341054	1702.852611	0.000451244	47	N	276	290
P08071	Exosome	AVVSR	STNDKEEAIWELLR	QSQEK	3		568.6253369	1702.852611	0.000451244	47	N	276	290
P08071	Exosome	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2		1085.071101	2168.126601	0.000622848	8	N	299	319
P08071	Exosome	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	3		723.7166671	2168.126601	0.000622848	4	N	299	319
P08071	Exosome	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2	Q1:-17.027	1076.557601	2151.099601	0.00091018	2	N	299	319
P08071	Exosome	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2	[0:-17.027	1076.557601	2151.099601	0.002080925	1	N	299	319
P08071	Exosome	KVEVL	QQVLLDQQVQFGR	NGQRC	2		779.9209682	1557.826336	0.000451244	11	N	625	638
P08071	Exosome	KVEVL	QQVLLDQQVQFGR	NGQRC	2	Q1:-17.027	771.4074682	1540.799336	0.001352548	2	N	625	638
P08071	Exosome	KVEVL	QQVLLDQQVQFGR	NGQRC	2	[0:-17.027	771.4074682	1540.799336	0.000451244	3	N	625	638
P08071	Exosome	NRASR	GRVTCISFPTTEDCIVAIMK	GDADA	2	C5:+57.021,C14:+57.021	1149.568234	2297.120868	0.000451244	8	N	384	404
P08071	Exosome	NRASR	GRVTCISFPTTEDCIVAIMK	GDADA	3	C5:+57.021,C14:+57.021	766.7147559	2297.120868	0.000622848	3	N	384	404
P08071	Exosome	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	2		1172.137503	2342.259406	0.000451244	1677	N	618	638
P08071	Exosome	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	3		781.7609355	2342.259406	0.000451244	3208	N	618	638
P08071	Exosome	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	4		586.5726516	2342.259406	0.000451244	29	N	618	638
P08071	Exosome	IATER	LKQCSSSPLLEACAFLTQ	-	2	C4:+57.021,C13:+57.021	1027.008334	2052.001069	0.000451244	163	N	689	707
P08071	Exosome	IATER	LKQCSSSPLLEACAFLTQ	-	3	C4:+57.021,C13:+57.021	685.0081563	2052.001069	0.000451244	16	N	689	707
P08071	Exosome	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	2		1361.732299	2721.448998	0.000451244	23	N	144	169
P08071	Exosome	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	3		908.1574661	2721.448998	0.000451244	148	N	144	169
P08071	Exosome	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	4		681.3700496	2721.448998	0.000622848	3	N	144	169
P08071	Exosome	TERLK	QCSSSPLLEACAFLTQ	-	2	C2:+57.021,C11:+57.021	906.4188208	1810.822042	0.000451244	153	N	691	707
P08071	Exosome	TERLK	QCSSSPLLEACAFLTQ	-	3	C2:+57.021,C11:+57.021	604.6151472	1810.822042	0.000451244	28	N	691	707
P08071	Exosome	TERLK	QCSSSPLLEACAFLTQ	-	2	Q1:-17.027,C2:+57.021,C11:+57.021	897.9053208	1793.795042	0.000451244	28	N	691	707
P08071	Exosome	TERLK	QCSSSPLLEACAFLTQ	-	2	[0:-	897.9053208	1793.795042	0.000735798	8	N	691	707
P08071	Exosome	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKF	FSKSC	3		957.1802708	2868.517412	0.000451244	14	N	144	170
P08071	Exosome	ASRGR	VTCISFPTTEDCIVAIMKGDADAMSLDGGYIYTAGK	CGLVP	3	C3:+57.021,C12:+57.021	1290.936553	3869.78626	0.000870037	3	N	386	422
P08071	Exosome	QKSSK	SNGLDCVNRPVEGY	LAVAA	2	C6:+57.021	790.3623945	1578.709189	0.000451244	18	N	437	451
P08071	Exosome	SRTDK	VEVLQQVLLDQQVQFGR	NGQRC	2		1000.052711	1998.089822	0.000451244	40	N	621	638
P08071	Exosome	SRTDK	VEVLQQVLLDQQVQFGR	NGQRC	3		667.0377405	1998.089822	0.000451244	39	N	621	638
P08071	Exosome	ASRGR	VTCISFPTTEDCIVAIMK	GDADA	2	C3:+57.021,C12:+57.021	1043.006946	2083.998293	0.000451244	48	N	386	404
P08071	Exosome	ASRGR	VTCISFPTTEDCIVAIMK	GDADA	3	C3:+57.021,C12:+57.021	695.6738976	2083.998293	0.000451244	7	N	386	404

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08071	Exosome	ASRGR	VTCISFPTTEDCIVAIMK	GDADA	2	C3:+57.021,C12:+57.021,M17:+15.995	1051.004446	2099.993293	0.000451244	10	N	386	404
P08071	Exosome	DPKSN	LCALCIGDEKGENK	CAPNS	2	C2:+57.021,C5:+57.021	803.8818741	1605.748148	0.000451244	36	N	518	532
P08071	Exosome	EKFGK	KQASGFQLFASPSGQK	DLLFK	2		840.9393579	1679.863116	0.000451244	28	N	298	314
P08071	Exosome	VAFTR	GSTVFEELPNK	AERDQ	2		610.812032	1219.608464	0.000451244	22	N	228	239
P08071	Exosome	GWKIP	IGTLRPYLNWNGPPASLEEAVSK	FFSKS	3		838.1118568	2511.31217	0.001654178	2	N	146	169
P08071	Exosome	PVTEY	KECHLAQVPSHAVVSR	STNDK	3	C3:+57.021	606.6531898	1816.936169	0.000823681	1	N	260	276
P08071	Exosome	EAKNC	HLAIAPNHAVVSR	TDKVE	3		462.2656376	1383.773513	0.001229886	1	N	605	618
P08071	Exosome	TEAKN	CHLAIAPNHAVVSR	TDKVE	3	C1:+57.021	515.6090328	1543.803698	0.000451244	6	N	604	618
P08071	Exosome	ATTVQ	WCAVSNSEEEK	CLRWQ	2	C2:+57.021	669.7854569	1337.555314	0.001395409	1	N	25	36
P08071	Exosome	KEQPR	THYYAVAVVK	NSSNF	2		575.8169203	1149.618241	0.000637154	16	N	107	117
P08071	Exosome	NEMRK	VGGPPLSCVK	KSSTR	2	C8:+57.021	507.2763424	1012.537085	0.000622848	10	N	46	56
P08071	Exosome	PKSNL	CALCIGDEKGENK	CAPNS	2	C1:+57.021,C4:+57.021	747.3398421	1492.664084	0.000451244	24	N	519	532
P08071	Exosome	SSKSN	GLDCVNRPVEGYLAVAAVR	REDAG	3	C4:+57.021	687.0303259	2058.067578	0.000451244	7	N	439	458
P08071	Exosome	NLKLK	DFELLCLDDTR	KPVTE	2	C6:+57.021	698.8245821	1395.633564	0.000451244	31	N	585	596
P08071	Exosome	AVVSR	TDKVEVLQQVLLDQQVQF	GRNGQ	2		1065.576216	2129.136832	0.000451244	1	N	618	636
P08071	Exosome	RVPQK	VDVGLYLTFSYTTSIQNLNK	KQQDV	2		1138.594606	2275.173611	0.000451244	23	N	331	351
P08071	Exosome	NSKER	YQGYTGALR	CLAEK	2		514.7621451	1027.50869	0.001871652	2	N	540	549
P08071	Exosome	KSSTR	QCIQAIVTNR	ADAMT	2	C2:+57.021	601.8194371	1201.623274	0.000622848	14	N	61	71
P08071	Exosome	KSSTR	QCIQAIVTNR	ADAMT	2	[0:-17.027,C2:+57.021	593.3059371	1184.596274	0.00307782	2	N	61	71
P08071	Exosome	IATER	LKQCSSSPLLEAC	AFLTQ	2	C4:+57.021,C13:+57.021	746.8604104	1491.705221	0.000451244	7	N	689	702
P08071	Exosome	IGTLR	PYLNWNGPPASLEEAVSK	FFSKS	2		986.4946944	1970.973789	0.000823681	2	N	151	169
P08071	Exosome	RVPQK	VDVGLYLTFSYTTSIQNLNKK	QQDVI	3		802.0973247	2403.268574	0.000451244	5	N	331	352
P08071	Exosome	LYLTF	SYTTSIQNLNKK	QQDVI	2		698.8756949	1395.73579	0.002374549	2	N	340	352
P08071	Exosome	TLRPY	LNWNGPPASLEEAVSK	FFSKS	2		856.4366481	1710.857696	0.000451244	3	N	153	169
P08071	Exosome	DADAM	SLDGGYIYTAGK	CGLVP	2		622.812032	1243.608464	0.000622848	3	N	410	422
P08071	Exosome	QYKLL	CPDNTWKPVTEYK	ECHLA	2	C1:+57.021	819.3853382	1636.755076	0.001162105	1	N	248	261
P08071	Exosome	NGQRC	PGEFCLFQSK	TKNLL	2	C5:+57.021	606.7898139	1211.564028	0.001699387	1	N	643	653
P08071	Exosome	RLKQC	SSSPLLEACAFLTQ	-	2	C9:+57.021	762.3744392	1522.733278	0.000622848	20	N	693	707
P08071	Exosome	SCKFN	EFFSQSCAPGADPK	SNLCA	2	C7:+57.021	770.8407635	1539.665927	0.002374549	1	N	502	516
P08071	Exosome	IATER	LKQCSSSPLLEACAF	LTQ-	2	C4:+57.021,C13:+57.021	855.9131743	1709.810749	0.000451244	9	N	689	704
P08071	Exosome	LKQCS	SSPLLEACAFLTQ	-	2	C8:+57.021	718.858425	1435.70125	0.002453667	1	N	694	707
P08071	Exosome	VAFLK	DSTVLQNTDGK	NTEEW	2		589.288921	1176.562242	0.001162105	7	N	562	573
P08071	Exosome	LKDST	VLQNTDGKNTEEWAR	NLKLK	2		880.9322612	1759.848922	0.000451244	6	N	565	580
P08071	Exosome	KDSTV	LQNTDGKNTEEWAR	NLKLK	2		831.3980542	1660.780508	0.000451244	10	N	566	580
P08071	Exosome	AENQK	SSKSNGLDCVNRPVEGYLAVAAVR	REDAG	3	C9:+57.021	854.7749846	2561.301554	0.0007646	2	N	434	458
P08071	Exosome	TRSCK	FNEFFSQSCAPGAD	PKSNL	2	C9:+57.021	788.8225708	1575.629542	0.002727428	1	N	500	514
P08071	Exosome	QKSSK	SNGLDCVNRPVEGYLAVA	AVRRE	2	C6:+57.021	967.4757474	1932.935895	0.000622848	4	N	437	455
P08071	Parental	VTEAK	NCHLAIAPNHAVVSR	TDKVE	2	C2:+57.021	829.931113	1657.846626	0.000451244	32	N	603	618
P08071	Parental	VTEAK	NCHLAIAPNHAVVSR	TDKVE	3	C2:+57.021	553.623342	1657.846626	0.000451244	119	N	603	618
P08071	Parental	VTEAK	NCHLAIAPNHAVVSR	TDKVE	4	C2:+57.021	415.4694565	1657.846626	0.000451244	119	N	603	618
P08071	Parental	VTEYK	ECHLAQVPSHAVVSR	STNDK	2	C2:+57.021	845.4284031	1688.841206	0.000451244	29	N	261	276
P08071	Parental	VTEYK	ECHLAQVPSHAVVSR	STNDK	3	C2:+57.021	563.9548687	1688.841206	0.000451244	56	N	261	276
P08071	Parental	VTEYK	ECHLAQVPSHAVVSR	STNDK	4	C2:+57.021	423.2181016	1688.841206	0.000451244	77	N	261	276
P08071	Parental	VTEYK	ECHLAQVPSHAVVSR	STNDK	3	[0:-18.011,C2:+57.021	557.9512021	1670.830206	0.000662267	1	N	261	276
P08071	Parental	KPPYK	LRPVAAEVYGTKEQPR	THYYA	3		605.3360094	1812.984628	0.000451244	13	N	91	107
P08071	Parental	KPPYK	LRPVAAEVYGTKEQPR	THYYA	4		454.253957	1812.984628	0.000451244	11	N	91	107
P08071	Parental	KPPYK	LRPVAAEVYGTK	EQPRT	3		435.2509941	1302.729582	0.000451244	43	N	91	103
P08071	Parental	ASKAR	VTWCAVGSEEKR	KCDQW	2	C4:+57.021	711.346016	1420.676432	0.000451244	24	N	362	374
P08071	Parental	ASKAR	VTWCAVGSEEKR	KCDQW	3	C4:+57.021	474.5666107	1420.676432	0.000451244	24	N	362	374
P08071	Parental	ATTVQ	WCAVSNSEEEKCLR	WQNEM	2	C2:+57.021,C12:+57.021	884.3931374	1766.770675	0.000451244	24	N	25	39
P08071	Parental	ATTVQ	WCAVSNSEEEKCLR	WQNEM	3	C2:+57.021,C12:+57.021	589.9313582	1766.770675	0.000451244	26	N	25	39
P08071	Parental	AGALR	CLRDNAGDVAFTR	GSTVF	2	C1:+57.021	747.8598219	1493.704044	0.000451244	22	N	215	228
P08071	Parental	AGALR	CLRDNAGDVAFTR	GSTVF	3	C1:+57.021	498.909148	1493.704044	0.000451244	35	N	215	228
P08071	Parental	AGALR	CLRDNAGDVAFTR	GSTVF	2	[0:-17.027,C1:+57.021	739.3463219	1476.677044	0.000451244	10	N	215	228
P08071	Parental	PGAQK	DRFPNLCSSCAGTGANK	CASSP	2	C7:+57.021,C10:+57.021	927.9147683	1853.813937	0.000451244	129	N	181	198
P08071	Parental	PGAQK	DRFPNLCSSCAGTGANK	CASSP	3	C7:+57.021,C10:+57.021	618.9457789	1853.813937	0.000451244	86	N	181	198
P08071	Parental	LYLTF	SYTTSIQNLNK	KQQDV	2		634.8282134	1267.640827	0.000451244	21	N	340	351
P08071	Parental	GADPK	SNLCALCIGDEKGENK	CAPNS	2	C4:+57.021,C7:+57.021	904.4193522	1806.823104	0.000451244	220	N	516	532
P08071	Parental	GADPK	SNLCALCIGDEKGENK	CAPNS	3	C4:+57.021,C7:+57.021	603.2821681	1806.823104	0.000451244	184	N	516	532
P08071	Parental	TTSEK	YLGKEYVIATER	LKQCS	2		721.3884382	1440.761276	0.000451244	25	N	677	689
P08071	Parental	TTSEK	YLGKEYVIATER	LKQCS	3		481.2615588	1440.761276	0.000451244	21	N	677	689
P08071	Parental	ASKAR	VTWCAVGSEEK	RKCDQ	2	C4:+57.021	633.2954605	1264.575321	0.000451244	89	N	362	373
P08071	Parental	AQKDR	FPNLCSSCAGTGANK	CASSP	2	C5:+57.021,C8:+57.021	792.3507412	1582.685882	0.000451244	80	N	183	198
P08071	Parental	VAFTR	GSTVFEELPNKAER	DQYKL	2		788.9024411	1575.789282	0.000451244	89	N	228	242

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08071	Parental	VAFTR	GSTVFEELPNKAER	DQYKL	3		526.2708941	1575.789282	0.000451244	41	N	228	242
P08071	Parental	VAFLK	DSTVLQNTDGKNTEEWAR	NLKLK	2		1032.485586	2062.955573	0.000451244	78	N	562	580
P08071	Parental	VAFLK	DSTVLQNTDGKNTEEWAR	NLKLK	3		688.6596575	2062.955573	0.000451244	94	N	562	580
P08071	Parental	RSCKF	NEFFSQSCAPGADPK	SNLCA	2	C8:+57.021	827.8622273	1653.708855	0.000451244	167	N	501	516
P08071	Parental	LFQSK	TKNLLFNDNTECLAK	IPGKT	2	C12:+57.021	890.9488341	1779.882068	0.000451244	61	N	653	668
P08071	Parental	LFQSK	TKNLLFNDNTECLAK	IPGKT	3	C12:+57.021	594.3018227	1779.882068	0.000451244	54	N	653	668
P08071	Parental	GADPK	SNLCALCIGDEK	GENKC	2	C4:+57.021,C7:+57.021	690.3183783	1378.621157	0.000451244	28	N	516	528
P08071	Parental	ANKCA	SSPEEPYSGYAGALR	CLRDN	2		792.3709738	1582.726348	0.000622848	6	N	200	215
P08071	Parental	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	C1:+39.994	899.3911235	1796.766647	0.000451244	8	N	198	215
P08071	Parental	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	C1:+57.021	907.9046235	1813.793647	0.000451244	141	N	198	215
P08071	Parental	TGANK	CASSPEEPYSGYAGALR	CLRDN	3	C1:+57.021	605.6056823	1813.793647	0.000451244	13	N	198	215
P08071	Parental	TGANK	CASSPEEPYSGYAGALR	CLRDN	2	[0:-17.027,C1:+57.021	899.3911235	1796.766647	0.000451244	20	N	198	215
P08071	Parental	ANQTR	SCKFNEFFSQSCAPGADPK	SNLCA	2	C2:+57.021,C12:+57.021	1088.975023	2175.934446	0.000451244	26	N	497	516
P08071	Parental	ANQTR	SCKFNEFFSQSCAPGADPK	SNLCA	3	C2:+57.021,C12:+57.021	726.319282	2175.934446	0.000451244	32	N	497	516
P08071	Parental	CLAEK	AGNVAFLKDSTVLQNTDGK	NTEEW	2		989.5161581	1977.016716	0.000451244	17	N	554	573
P08071	Parental	CLAEK	AGNVAFLKDSTVLQNTDGK	NTEEW	3		660.0133721	1977.016716	0.000451244	8	N	554	573
P08071	Parental	YTAGK	CGLVPVLAENQK	SSKSN	2	C1:+57.021	664.3558524	1326.696105	0.000451244	118	N	422	434
P08071	Parental	YTAGK	CGLVPVLAENQK	SSKSN	2	[0:-17.027,C1:+57.021	655.8423524	1309.669105	0.000451244	22	N	422	434
P08071	Parental	RDQYK	LLCPDNTWKPVTEYK	ECHLA	2	C3:+57.021	932.4694023	1862.923205	0.000451244	41	N	246	261
P08071	Parental	RDQYK	LLCPDNTWKPVTEYK	ECHLA	3	C3:+57.021	621.9822016	1862.923205	0.000451244	13	N	246	261
P08071	Parental	VAAVR	REDAGFTWSSLR	GKKSC	2		712.8500115	1423.684423	0.000451244	27	N	458	470
P08071	Parental	VAAVR	REDAGFTWSSLR	GKKSC	3		475.5692743	1423.684423	0.000823681	31	N	458	470
P08071	Parental	RDQYK	LLCPDNTWKPVTEYKECHLAQVPSHAVVSR	STNDK	3	C3:+57.021,C17:+57.021	1178.92575	3533.753851	0.000451244	44	N	246	276
P08071	Parental	RDQYK	LLCPDNTWKPVTEYKECHLAQVPSHAVVSR	STNDK	4	C3:+57.021,C17:+57.021	884.4462627	3533.753851	0.000622848	15	N	246	276
P08071	Parental	TRSCK	FNEFFSQSCAPGADPK	SNLCA	2	C9:+57.021	901.3964343	1800.777269	0.000451244	160	N	500	516
P08071	Parental	TRSCK	FNEFFSQSCAPGADPK	SNLCA	3	C9:+57.021	601.2668895	1800.777269	0.000451244	6	N	500	516
P08071	Parental	QKSSK	SNGLDCVNRPVEGYLAVAAVRR	EDAGF	3	C6:+57.021	806.089015	2415.243645	0.001329271	3	N	437	459
P08071	Parental	QKSSK	SNGLDCVNRPVEGYLAVAAVRR	EDAGF	4	C6:+57.021	604.8187112	2415.243645	0.001329271	1	N	437	459
P08071	Parental	KFGKK	QASGFQLFASPSGQK	DLLFK	2		776.8918764	1551.768153	0.000451244	54	N	299	314
P08071	Parental	KFGKK	QASGFQLFASPSGQK	DLLFK	2	[0:-17.027	768.3783764	1534.741153	0.000622848	16	N	299	314
P08071	Parental	GQRCP	GEFCLFQSK	TKNLL	2	C4:+57.021	558.263432	1114.511264	0.000622848	12	N	644	653
P08071	Parental	QSKTK	NLLFNDNTECLAK	IPGKT	2	C10:+57.021	776.3775132	1550.739426	0.000451244	85	N	655	668
P08071	Parental	NLKLK	DFELLCLDDTRKPVTEAK	NCHLA	2	C6:+57.021	1075.543827	2149.072054	0.000451244	18	N	585	603
P08071	Parental	NLKLK	DFELLCLDDTRKPVTEAK	NCHLA	3	C6:+57.021	717.3651514	2149.072054	0.000451244	31	N	585	603
P08071	Parental	RNGQR	CPGEFCLFQSK	TKNLL	2	C1:+57.021,C6:+57.021	686.8049068	1371.594214	0.000451244	146	N	642	653
P08071	Parental	RNGQR	CPGEFCLFQSK	TKNLL	2	[0:-17.027,C1:+57.021,C6:+57.021	678.2914068	1354.567214	0.000451244	27	N	642	653
P08071	Parental	QSKTK	NLLFNDNTECLAKIPGK	TTSEK	2	C10:+57.021	974.0041407	1945.992681	0.000451244	2	N	655	672
P08071	Parental	VAIMK	GDADAMSLDGGYIYTAGK	CGLVP	2		902.9070637	1803.798527	0.000451244	10	N	404	422
P08071	Parental	DVGLY	LTFSYTTSIQNLNK	KQQDV	2		815.4282917	1628.840983	0.000622848	6	N	337	351
P08071	Parental	AAVRR	EDAGFTWSSLR	GKKSC	2		634.7994559	1267.583312	0.000622848	20	N	459	470
P08071	Parental	QKSSK	SNGLDCVNRPVEGYLAVAAVR	REDAG	2	C6:+57.021	1130.579067	2259.142534	0.000451244	18	N	437	458
P08071	Parental	QKSSK	SNGLDCVNRPVEGYLAVAAVR	REDAG	3	C6:+57.021	754.0553112	2259.142534	0.000451244	335	N	437	458
P08071	Parental	RDQYK	LLCPDNTWKPVTEY	KECHL	2	C3:+57.021	868.4219208	1734.828242	0.000451244	37	N	246	260
P08071	Parental	ARNLK	LKDFELLCLDDTR	KPVTE	2	C8:+57.021	819.4140957	1636.812591	0.000451244	32	N	583	596
P08071	Parental	ARNLK	LKDFELLCLDDTR	KPVTE	3	C8:+57.021	546.6119972	1636.812591	0.000451244	135	N	583	596
P08071	Parental	PSGQK	DLLFKESAIGFVR	VPQKV	2		747.9199055	1493.824211	0.000823681	1	N	314	327
P08071	Parental	PSGQK	DLLFKESAIGFVR	VPQKV	3		498.9492037	1493.824211	0.000451244	11	N	314	327
P08071	Parental	AVVSR	STNDKEEAIWELLR	QSQEK	2		852.4341054	1702.852611	0.000451244	128	N	276	290
P08071	Parental	AVVSR	STNDKEEAIWELLR	QSQEK	3		568.6253369	1702.852611	0.000451244	322	N	276	290
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2		1085.071101	2168.126601	0.000451244	9	N	299	319
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	3		723.7166671	2168.126601	0.000451244	5	N	299	319
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2	Q1:-17.027	1076.557601	2151.099601	0.001229886	3	N	299	319
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLFK	ESAIG	2	[0:-17.027	1076.557601	2151.099601	0.001264573	2	N	299	319
P08071	Parental	KVEVL	QQVLLDQQVQFGR	NGQRC	2		779.9209682	1557.826336	0.000451244	1	N	625	638
P08071	Parental	KVEVL	QQVLLDQQVQFGR	NGQRC	2	Q1:-17.027	771.4074682	1540.799336	0.000979378	1	N	625	638
P08071	Parental	KVEVL	QQVLLDQQVQFGR	NGQRC	2	[0:-17.027	771.4074682	1540.799336	0.000451244	8	N	625	638
P08071	Parental	NRASR	GRVTCISFPTTEDCIVAIMK	GDADA	2	C5:+57.021,C14:+57.021	1149.568234	2297.120868	0.000662267	2	N	384	404
P08071	Parental	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	2		1172.137503	2342.259406	0.000451244	218	N	618	638
P08071	Parental	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	3		781.7609355	2342.259406	0.000451244	1949	N	618	638
P08071	Parental	AVVSR	TDKVEVLQQVLLDQQVQFGR	NGQRC	4		586.5726516	2342.259406	0.000451244	6	N	618	638
P08071	Parental	IATER	LKQCSSSPLLEACAFLTQ	-	2	C4:+57.021,C13:+57.021	1027.008334	2052.001069	0.000451244	133	N	689	707
P08071	Parental	IATER	LKQCSSSPLLEACAFLTQ	-	3	C4:+57.021,C13:+57.021	685.0081563	2052.001069	0.00091018	5	N	689	707
P08071	Parental	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	2		1361.732299	2721.448998	0.000451244	54	N	144	169
P08071	Parental	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	3		908.1574661	2721.448998	0.000451244	251	N	144	169
P08071	Parental	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	4		681.3700496	2721.448998	0.000451244	7	N	144	169

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLF	KESAI	2		1021.023619	2040.031638	0.000451244	5	N	299	318
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLF	KESAI	3		681.018346	2040.031638	0.000823681	4	N	299	318
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLF	KESAI	2	Q1:-17.027	1012.510119	2023.004638	0.002981883	1	N	299	318
P08071	Parental	KFGKK	QASGFQLFASPSGQKDLLF	KESAI	2	[0:-17.027	1012.510119	2023.004638	0.002981883	1	N	299	318
P08071	Parental	TERLK	QCSSSPLLEACAFLTQ	-	2	C2:+57.021,C11:+57.021	906.4188208	1810.822042	0.000451244	71	N	691	707
P08071	Parental	TERLK	QCSSSPLLEACAFLTQ	-	3	C2:+57.021,C11:+57.021	604.6151472	1810.822042	0.000451244	28	N	691	707
P08071	Parental	TERLK	QCSSSPLLEACAFLTQ	-	2	Q1:-17.027,C2:+57.021,C11:+57.021	897.9053208	1793.795042	0.000451244	23	N	691	707
P08071	Parental	TERLK	QCSSSPLLEACAFLTQ	-	2	[0:-	897.9053208	1793.795042	0.000451244	8	N	691	707
P08071	Parental	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKF	FSKSC	2		1435.266506	2868.517412	0.00091018	2	N	144	170
P08071	Parental	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKF	FSKSC	3		957.1802708	2868.517412	0.000451244	74	N	144	170
P08071	Parental	GWKIP	IGTLRPYLNWNGPPASLEEAVSKFFSK	SCVPG	4		756.1517975	3020.57599	0.002981883	1	N	146	173
P08071	Parental	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKFFSK	SCVPG	3		1077.912073	3230.712818	0.000823681	15	N	144	173
P08071	Parental	SAGWK	IPIGTLRPYLNWNGPPASLEEAVSKFFSK	SCVPG	4		808.6860045	3230.712818	0.002296037	2	N	144	173
P08071	Parental	ASRGR	VTCISFPTTEDCIVAIMKGDADAMSLDGGYIYTAGK	CGLVP	3	C3:+57.021,C12:+57.021	1290.936553	3869.78626	0.000451244	2	N	386	422
P08071	Parental	QKSSK	SNGLDCVNRPVEGY	LAVAA	2	C6:+57.021	790.3623945	1578.709189	0.000451244	35	N	437	451
P08071	Parental	DVGLY	LTFSYTTSIQNLNKK	QQDVI	2		879.4757733	1756.935947	0.000451244	6	N	337	352
P08071	Parental	SRTDK	VEVLQQVLLDQQVQFGR	NGQRC	2		1000.052711	1998.089822	0.000451244	1	N	621	638
P08071	Parental	SRTDK	VEVLQQVLLDQQVQFGR	NGQRC	3		667.0377405	1998.089822	0.000451244	5	N	621	638
P08071	Parental	ASRGR	VTCISFPTTEDCIVAIMK	GDADA	2	C3:+57.021,C12:+57.021	1043.006946	2083.998293	0.000451244	17	N	386	404
P08071	Parental	DPKSN	LCALCIGDEKGENK	CAPNS	2	C2:+57.021,C5:+57.021	803.8818741	1605.748148	0.000451244	7	N	518	532
P08071	Parental	EKFGK	KQASGFQLFASPSGQK	DLLFK	2		840.9393579	1679.863116	0.000451244	7	N	298	314
P08071	Parental	VAFTR	GSTVFEELPNK	AERDQ	2		610.812032	1219.608464	0.000451244	33	N	228	239
P08071	Parental	KTKNL	LFNDNTECLAK	IPGKT	2	C8:+57.021	662.8140174	1323.612435	0.002813207	2	N	657	668
P08071	Parental	AQKDR	FPNLCSSCAGTGANKCASSPEEPYSGYAGALR	CLRDN	3	C5:+57.021,C8:+57.021,C16:+57.021	1127.164123	3378.468969	0.00091018	1	N	183	215
P08071	Parental	GWKIP	IGTLRPYLNWNGPPASLEEAVSK	FFSKS	3		838.1118568	2511.31217	0.000451244	4	N	146	169
P08071	Parental	TGIGR	SAGWKIPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	3		1084.579094	3250.713881	0.000823681	3	N	139	169
P08071	Parental	TGIGR	SAGWKIPIGTLRPYLNWNGPPASLEEAVSK	FFSKS	4		813.6862702	3250.713881	0.002296037	1	N	139	169
P08071	Parental	GKKQA	SGFQLFASPSGQKDLLFK	ESAIG	3		657.3514366	1969.03091	0.002519933	1	N	301	319
P08071	Parental	IGFVR	VPQKVDVGLYLTF	SYTTS	2		739.9168315	1477.818063	0.000637154	6	N	327	340
P08071	Parental	LNWNG	PPASLEEAVSK	FFSKS	2		564.3013001	1126.587	0.000823681	1	N	158	169
P08071	Parental	PVTEY	KECHLAQVPSHAVVSR	STNDK	3	C3:+57.021	606.6531898	1816.936169	0.000451244	9	N	260	276
P08071	Parental	PVTEY	KECHLAQVPSHAVVSR	STNDK	4	C3:+57.021	455.2418423	1816.936169	0.000451244	39	N	260	276
P08071	Parental	TEAKN	CHLAIAPNHAVVSR	TDKVE	3	C1:+57.021	515.6090328	1543.803698	0.001352548	1	N	604	618
P08071	Parental	KEQPR	THYYAVAVVK	NSSNF	2		575.8169203	1149.618241	0.000637154	10	N	107	117
P08071	Parental	NLKLK	DFELLCLDDTR	KPVTE	2	C6:+57.021	698.8245821	1395.633564	0.000451244	8	N	585	596
P08071	Parental	KSSTR	QCIQAIVTNR	ADAMT	2	C2:+57.021	601.8194371	1201.623274	0.000451244	35	N	61	71
P08071	Parental	KSSTR	QCIQAIVTNR	ADAMT	2	[0:-17.027,C2:+57.021	593.3059371	1184.596274	0.002145581	1	N	61	71
P08071	Parental	LYLTF	SYTTSIQNLNKK	QQDVI	2		698.8756949	1395.73579	0.0007646	8	N	340	352
P08071	Parental	TLRPY	LNWNGPPASLEEAVSK	FFSKS	2		856.4366481	1710.857696	0.000451244	14	N	153	169
P08071	Parental	SCKFN	EFFSQSCAPGADPK	SNLCA	2	C7:+57.021	770.8407635	1539.665927	0.001871652	1	N	502	516
P08071	Parental	IATER	LKQCSSSPLLEACAF	LTQ-	2	C4:+57.021,C13:+57.021	855.9131743	1709.810749	0.000451244	6	N	689	704
P08071	Parental	NKAER	DQYKLLCPDNTWKPVTEY	KECHL	2	C7:+57.021	1135.543827	2269.072054	0.000451244	5	N	242	260
P08071	Parental	NKAER	DQYKLLCPDNTWKPVTEY	KECHL	3	C7:+57.021	757.3651514	2269.072054	0.002884417	1	N	242	260
P08071	Parental	IGFVR	VPQKVDVGLY	LTFSY	2		559.3167532	1116.617906	0.000622848	4	N	327	337
P08071	Parental	TGIGR	SAGWKIPIGTLRPY	LNWNG	3		520.2967149	1557.866745	0.002663018	1	N	139	153
P08071	Parental	FQSKT	KNLLFNDNTECLAK	IPGKT	2	C11:+57.021	840.4249948	1678.83439	0.000451244	2	N	654	668
P08071	Parental	GKKQA	SGFQLFASPSGQK	DLLFK	2		677.3440306	1352.672461	0.001763695	3	N	301	314
P08071	Parental	VGLYL	TFSYTTSIQNLNKK	QQDVI	2		822.9337412	1643.851882	0.002145581	1	N	338	352
P08071	Parental	RDQYK	LLCPDNTWKPV	TEYKE	2	C3:+57.021	671.8451206	1341.674641	0.002374549	1	N	246	257
P08103	Exosome	IRCWK	NRPEERPTFEYIQSVLDDFYTATESQYQQQP	-	3		1260.58737	3778.738711	0.000451244	8	N	493	524
P08103	Exosome	HYKIR	TLDSGGFYISPR	STFSS	2		656.8307561	1311.645912	0.000979378	2	N	199	211
P08103	Exosome	YISPR	STFSSLQELVLHYK	KGKDG	2		826.4386594	1650.861719	0.000698008	1	N	211	225
P08103	Exosome	YISPR	STFSSLQELVLHYK	KGKDG	3		551.2950396	1650.861719	0.000823681	2	N	211	225
P08103	Exosome	KFPIK	WTAPEAINFGSFTIK	SDVWS	2		841.4333771	1680.851154	0.002727428	1	N	420	435
P08103	Exosome	NYVAR	VNSLETEEWFFK	GISRK	2		764.8700783	1527.724557	0.000622848	1	N	133	145
P08103	Parental	IRCWK	NRPEERPTFEYIQSVLDDFYTATESQYQQQP	-	3		1260.58737	3778.738711	0.000451244	32	N	493	524
P08103	Parental	HYKIR	TLDSGGFYISPR	STFSS	2		656.8307561	1311.645912	0.001871652	2	N	199	211
P08103	Parental	YISPR	STFSSLQELVLHYK	KGKDG	3		551.2950396	1650.861719	0.000451244	10	N	211	225
P08103	Parental	KFPIK	WTAPEAINFGSFTIK	SDVWS	2		841.4333771	1680.851154	0.000823681	4	N	420	435
P08113	Exosome	AKLLR	FQSSHHSTDITSLDQYVER	MKEKQ	2		1125.525243	2249.034886	0.000451244	4	N	511	530
P08113	Exosome	AKLLR	FQSSHHSTDITSLDQYVER	MKEKQ	3		750.6860952	2249.034886	0.000451244	12	N	511	530
P08113	Exosome	EIFLR	ELISNASDALDKIR	LISLT	2		772.9180912	1543.820582	0.000622848	1	Y	102	116
P08113	Exosome	EIFLR	ELISNASDALDKIR	LISLT	3		515.6146608	1543.820582	0.001352548	1	Y	102	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08113	Exosome	LNFVK	GVVDSDDLPLNVSR	ETLQQ	2		743.3813415	1484.747083	0.000451244	8	N	434	448
P08113	Exosome	REGSR	TDDEVVQREEEAIQLDGLNASQIR	ELREK	3		910.1181759	2727.331128	0.000451244	7	N	43	67
P08113	Exosome	VVSQR	LTESPCALVASQYGWSGNMER	IMKAQ	2	C6:+57.021,M19:+15.995	1186.536251	2371.056901	0.000823681	1	N	639	660
P08113	Exosome	RLLKK	GYEVIYLTEPVDEYCIQALPEFDGKR	FQNVA	3	C15:+57.021	1035.502596	3103.484389	0.000451244	31	N	561	587
P08113	Exosome	LDKIR	LISLTDENALAGNEELTVK	IKCDK	2		1015.536756	2029.057912	0.000823681	8	N	116	135
P08113	Exosome	KNLVR	KYSQFINFPIYVWSSK	TETVE	3		669.6845271	2006.030181	0.000451244	16	N	269	285
P08113	Exosome	TLVLK	EEASDYLELDTIK	NLVRK	2		763.3675654	1524.719531	0.001943752	1	N	252	265
P08113	Exosome	GFVRA	DDEVDVDGTVEEDLGK	SREGS	2		867.8817653	1733.747931	0.002374549	1	N	21	37
P08113	Exosome	ERMLR	LSLNIDPEAQVEEEPEEEPEDTSE	DAEDS	2		1364.596319	2727.177038	0.001162105	1	N	744	768
P08113	Parental	EKSEK	FAFQAEVNR	MMKLI	2		541.2754196	1080.535239	0.000451244	22	N	75	84
P08113	Parental	AKLLR	FQSSHHSTDITSLDQYVER	MKEKQ	2		1125.525243	2249.034886	0.000451244	43	N	511	530
P08113	Parental	AKLLR	FQSSHHSTDITSLDQYVER	MKEKQ	3		750.6860952	2249.034886	0.000451244	82	N	511	530
P08113	Parental	GVGFY	SAFLVADKVIVTSK	HNNDT	2		739.4353884	1476.855177	0.000451244	8	N	200	214
P08113	Parental	CDKEK	NLLHVTDTGVGMTREELVK	NLGTI	3		704.7092955	2111.104487	0.000451244	10	N	142	161
P08113	Parental	GFVRA	DDEVDVDGTVEEDLGKSR	EGSRT	2		989.4483351	1976.88107	0.000451244	4	N	21	39
P08113	Parental	EIFLR	ELISNASDALDKIR	LISLT	2		772.9180912	1543.820582	0.000451244	36	Y	102	116
P08113	Parental	EIFLR	ELISNASDALDKIR	LISLT	3		515.6146608	1543.820582	0.000451244	10	Y	102	116
P08113	Parental	EIFLR	ELISNASDALDKIR	LISLT	3	[0:-18.011	509.6109941	1525.809582	0.000735798	1	Y	102	116
P08113	Parental	LNFVK	GVVDSDDLPLNVSR	ETLQQ	2		743.3813415	1484.747083	0.000451244	20	N	434	448
P08113	Parental	EVTFK	SILFVPTSAPR	GLFDE	2		594.3433023	1186.671005	0.000622848	8	N	384	395
P08113	Parental	REGSR	TDDEVVQREEEAIQLDGLNASQIR	ELREK	2		1364.673364	2727.331128	0.000451244	23	N	43	67
P08113	Parental	REGSR	TDDEVVQREEEAIQLDGLNASQIR	ELREK	3		910.1181759	2727.331128	0.000451244	41	N	43	67
P08113	Parental	VVSQR	LTESPCALVASQYGWSGNMER	IMKAQ	2	C6:+57.021	1178.538751	2355.061901	0.000851441	3	N	639	660
P08113	Parental	RLLKK	GYEVIYLTEPVDEYCIQALPEFDGKR	FQNVA	3	C15:+57.021	1035.502596	3103.484389	0.000451244	29	N	561	587
P08113	Parental	LVRKY	SQFINFPIYVWSSK	TETVE	2		858.4437448	1714.87189	0.000451244	30	N	271	285
P08113	Parental	LDKIR	LISLTDENALAGNEELTVK	IKCDK	2		1015.536756	2029.057912	0.000451244	101	N	116	135
P08113	Parental	ERIMK	AQAYQTGKDISTNYYASQK	KTFEI	2		1069.01398	2136.012359	0.000451244	4	N	663	682
P08113	Parental	ERIMK	AQAYQTGKDISTNYYASQK	KTFEI	3		713.0119197	2136.012359	0.000451244	10	N	663	682
P08113	Parental	KNLVR	KYSQFINFPIYVWSSK	TETVE	2		1004.022891	2006.030181	0.000451244	4	N	269	285
P08113	Parental	KNLVR	KYSQFINFPIYVWSSK	TETVE	3		669.6845271	2006.030181	0.000451244	10	N	269	285
P08113	Parental	TLVLK	EEASDYLELDTIK	NLVRK	2		763.3675654	1524.719531	0.000451244	13	N	252	265
P08113	Parental	NLVRK	YSQFINFPIYVWSSK	TETVE	2		939.9754091	1877.935218	0.000451244	3	N	270	285
P08113	Parental	EFLNK	MTEAQEDGQSTSELIGQFGVGFY	SAFLV	2		1247.558092	2493.100583	0.000451244	1	N	177	200
P08113	Parental	GFVRA	DDEVDVDGTVEEDLGK	SREGS	2		867.8817653	1733.747931	0.000451244	5	N	21	37
P08113	Parental	ERLLK	KGYEVIYLTEPVDEYCIQALPEFDGK	RFQNV	3	C16:+57.021	1026.167214	3075.478241	0.000735798	4	N	560	586
P08113	Parental	RLLKK	GYEVIYLTEPVDEYCIQALPEFDGK	RFQNV	2	C15:+57.021	1474.699439	2947.383278	0.000451244	3	N	561	586
P08226	Exosome	NLMEK	IQASVATNPIITPVAQENQ	-	2		997.5318082	1993.048016	0.000622848	5	N	292	311
P08226	Exosome	TGCLA	EGEPEVTDQLEWQSNQPWEQALNR	FWDYL	2		1442.163163	2882.310727	0.000451244	20	N	18	42
P08226	Exosome	TGCLA	EGEPEVTDQLEWQSNQPWEQALNR	FWDYL	3		961.7780422	2882.310727	0.000451244	19	N	18	42
P08226	Exosome	QGRQR	TANLGAGAAQPLR	DRAQA	2		620.344365	1238.67313	0.002453667	1	N	201	214
P08226	Exosome	KAYKK	ELEEQLGPVAEETR	ARLGK	2		800.3971886	1598.778777	0.000451244	31	N	86	100
P08226	Parental	NLMEK	IQASVATNPIITPVAQENQ	-	2		997.5318082	1993.048016	0.00091018	2	N	292	311
P08226	Parental	TGCLA	EGEPEVTDQLEWQSNQPWEQALNR	FWDYL	2		1442.163163	2882.310727	0.000451244	3	N	18	42
P08226	Parental	TGCLA	EGEPEVTDQLEWQSNQPWEQALNR	FWDYL	3		961.7780422	2882.310727	0.001329271	3	N	18	42
P08226	Parental	KAYKK	ELEEQLGPVAEETR	ARLGK	2		800.3971886	1598.778777	0.000823681	2	N	86	100
P08228	Exosome	ADEER	HVGDLGNVTAGKDGVANVSIEDR	VISLS	2		1162.085999	2322.156398	0.000451244	5	N	80	103
P08228	Exosome	ADEER	HVGDLGNVTAGKDGVANVSIEDR	VISLS	3		775.0599326	2322.156398	0.000451244	6	N	80	103
P08228	Exosome	ADEER	HVGDLGNVTAGKDGVANVSIEDR	VISLS	4		581.5468995	2322.156398	0.001763695	1	N	80	103
P08228	Exosome	-MAMK	AVCVLKGDGPVQGTIHFEQK	ASGEP	2	C3:+57.021	1092.067804	2182.120007	0.001329271	1	N	4	24
P08228	Exosome	-MAMK	AVCVLKGDGPVQGTIHFEQK	ASGEP	3	C3:+57.021	728.3811358	2182.120007	0.000451244	24	N	4	24
P08228	Exosome	SIEDR	VISLSGEHSIIGR	TMVVH	3		456.5934199	1366.75686	0.001763695	1	N	103	116
P08228	Exosome	VCVLK	GDGPVQGTIHFEQK	ASGEP	2		756.8762263	1511.736853	0.000451244	7	N	10	24
P08228	Exosome	VCVLK	GDGPVQGTIHFEQK	ASGEP	3		504.9200842	1511.736853	0.001943752	1	N	10	24
P08228	Exosome	VTAGK	DGVANVSIEDR	VISLS	2		587.7890882	1173.562576	0.002981883	1	N	92	103
P08228	Parental	ADEER	HVGDLGNVTAGKDGVANVSIEDR	VISLS	2		1162.085999	2322.156398	0.000451244	11	N	80	103
P08228	Parental	ADEER	HVGDLGNVTAGKDGVANVSIEDR	VISLS	3		775.0599326	2322.156398	0.000451244	4	N	80	103
P08228	Parental	-MAMK	AVCVLKGDGPVQGTIHFEQK	ASGEP	2	C3:+57.021	1092.067804	2182.120007	0.000451244	8	N	4	24
P08228	Parental	-MAMK	AVCVLKGDGPVQGTIHFEQK	ASGEP	3	C3:+57.021	728.3811358	2182.120007	0.000451244	22	N	4	24
P08228	Parental	SIEDR	VISLSGEHSIIGR	TMVVH	2		684.3862298	1366.75686	0.000451244	6	N	103	116
P08228	Parental	SIEDR	VISLSGEHSIIGR	TMVVH	3		456.5934199	1366.75686	0.001654178	2	N	103	116
P08228	Parental	VCVLK	GDGPVQGTIHFEQK	ASGEP	2		756.8762263	1511.736853	0.000451244	2	N	10	24
P08228	Parental	VTAGK	DGVANVSIEDR	VISLS	2		587.7890882	1173.562576	0.002884417	1	N	92	103
P08249	Exosome	GHAGK	TIIPLISQCTPK	VDFPQ	2	C9:+57.021	685.8895281	1369.763456	0.000451244	16	N	203	215
P08249	Exosome	QCTPK	VDFPQDQLATLTGR	IQEAG	2		780.9049838	1559.794368	0.000451244	25	N	215	229
P08249	Exosome	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	2		1197.127136	2392.238671	0.000451244	16	N	52	74

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08249	Exosome	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	3		798.4206903	2392.238671	0.000451244	37	N	52	74
P08249	Exosome	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	4		599.0674678	2392.238671	0.000451244	29	N	52	74
P08249	Exosome	FVQSK	ETECTYFSTPLLLGK	KGLEK	2	C4:+57.021	879.934861	1757.854122	0.000451244	29	N	281	296
P08249	Exosome	RANVK	GYLGPEQLPDCLKGCDVVVIPAGVPR	KPGMT	3	C11:+57.021,C15:+57.021	937.1509094	2808.429328	0.000451244	24	N	78	104
P08249	Exosome	QNNAK	VAVLGASGGIGQPLSLLLK	NSPLV	2		897.0489085	1792.082217	0.000451244	34	N	26	45
P08249	Exosome	QNNAK	VAVLGASGGIGQPLSLLLK	NSPLV	3		598.368539	1792.082217	0.001943752	1	N	26	45
P08249	Exosome	PDCLK	GCDVVVIPAGVPR	KPGMT	2	C2:+57.021	669.8638446	1337.712089	0.000451244	9	N	91	104
P08249	Exosome	AMNGK	EGVVECSFVQSK	ETECT	2	C6:+57.021	684.8271248	1367.63865	0.000451244	19	N	269	281
P08249	Exosome	YNPNK	IFGVTTLDIVR	ANTFV	2		617.3642347	1232.712869	0.002296037	4	N	165	176
P08249	Exosome	RANVK	GYLGPEQLPDCLK	GCDVV	2	C11:+57.021	745.3716995	1488.727799	0.000698008	10	N	78	91
P08249	Exosome	FVQSK	ETECTYFSTPLLLGKK	GLEKN	3	C4:+57.021	629.657495	1885.949085	0.001871652	3	N	281	297
P08249	Parental	GHAGK	TIIPLISQCTPK	VDFPQ	2	C9:+57.021	685.8895281	1369.763456	0.000451244	24	N	203	215
P08249	Parental	QCTPK	VDFPQDQLATLTGR	IQEAG	2		780.9049838	1559.794368	0.000451244	25	N	215	229
P08249	Parental	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	2		1197.127136	2392.238671	0.000451244	20	N	52	74
P08249	Parental	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	3		798.4206903	2392.238671	0.000451244	26	N	52	74
P08249	Parental	PLVSR	LTLYDIAHTPGVAADLSHIETR	ANVKG	4		599.0674678	2392.238671	0.000451244	24	N	52	74
P08249	Parental	FVQSK	ETECTYFSTPLLLGK	KGLEK	2	C4:+57.021	879.934861	1757.854122	0.000451244	10	N	281	296
P08249	Parental	RANVK	GYLGPEQLPDCLKGCDVVVIPAGVPR	KPGMT	2	C11:+57.021,C15:+57.021	1405.222464	2808.429328	0.000451244	14	N	78	104
P08249	Parental	RANVK	GYLGPEQLPDCLKGCDVVVIPAGVPR	KPGMT	3	C11:+57.021,C15:+57.021	937.1509094	2808.429328	0.000451244	14	N	78	104
P08249	Parental	SAQNN	AKVAVLGASGGIGQPLSLLLK	NSPLV	3		664.745898	1991.214294	0.000622848	2	N	24	45
P08249	Parental	QNNAK	VAVLGASGGIGQPLSLLLK	NSPLV	2		897.0489085	1792.082217	0.000451244	29	N	26	45
P08249	Parental	PDCLK	GCDVVVIPAGVPR	KPGMT	2	C2:+57.021	669.8638446	1337.712089	0.000451244	19	N	91	104
P08249	Parental	AMNGK	EGVVECSFVQSK	ETECT	2	C6:+57.021	684.8271248	1367.63865	0.000451244	68	N	269	281
P08249	Parental	RANVK	GYLGPEQLPDCLK	GCDVV	2	C11:+57.021	745.3716995	1488.727799	0.00091018	4	N	78	91
P08249	Parental	FVQSK	ETECTYFSTPLLLGKK	GLEKN	2	C4:+57.021	943.9823426	1885.949085	0.001463592	2	N	281	297
P08249	Parental	EVFKK	HGVYNPNKIFGVTTLDIVR	ANTFV	2		1072.087085	2142.15857	0.000451244	7	N	157	176
P08249	Parental	TRANV	KGYLGPEQLPDCLK	GCDVV	2	C12:+57.021	809.4191811	1616.822762	0.002212458	1	N	77	91
P08556	Exosome	GGVGK	SALTIQLIQNHFVDEYDPTIEDSYRK	QVVID	3		1032.516047	3094.524742	0.000637154	4	N	16	42
P08556	Exosome	GGVGK	SALTIQLIQNHFVDEYDPTIEDSYR	KQVVI	3		989.8177264	2966.429779	0.0007646	1	N	16	41
P08556	Exosome	DQYMR	TGEGFLCVFAINNSK	SFADI	2	C7:+57.021	828.9064379	1655.797276	0.001162105	1	N	73	88
P08556	Parental	GGVGK	SALTIQLIQNHFVDEYDPTIEDSYRK	QVVID	3		1032.516047	3094.524742	0.000451244	38	N	16	42
P08556	Parental	GGVGK	SALTIQLIQNHFVDEYDPTIEDSYR	KQVVI	3		989.8177264	2966.429779	0.00307782	1	N	16	41
P08556	Parental	DQYMR	TGEGFLCVFAINNSK	SFADI	2	C7:+57.021	828.9064379	1655.797276	0.001329271	1	N	73	88
P08607	Exosome	RMMVY	CKPSGEWEISVSCAK	KHCRN	2	C1:+57.021,C13:+57.021	869.4004311	1736.785262	0.000451244	6	N	102	117
P08607	Exosome	RMMVY	CKPSGEWEISVSCAK	KHCRN	2	[0:-	860.8869311	1719.758262	0.000451244	13	N	102	117
P08607	Exosome	TVVNK	TVPVWSSSPPTCEK	IICSQ	2	C12:+57.021	787.8798887	1573.744177	0.000451244	44	N	228	242
P08607	Exosome	MVYSK	ITLVTYECDK	GYRLV	2	C8:+57.021	621.3080365	1240.600473	0.000451244	4	N	321	331
P08607	Exosome	ISNGK	HSGTEDFYPYNHGISYTCDPGFR	LVGSP	2	C18:+57.021	1360.57745	2719.139299	0.000451244	14	N	191	214
P08607	Exosome	ISNGK	HSGTEDFYPYNHGISYTCDPGFR	LVGSP	3	C18:+57.021	907.3875663	2719.139299	0.000451244	40	N	191	214
P08607	Exosome	ISNGK	HSGTEDFYPYNHGISYTCDPGFR	LVGSP	4	C18:+57.021	680.7926248	2719.139299	0.000451244	15	N	191	214
P08607	Exosome	PTCEK	IICSQPNILHGVIVSGYK	ATYTH	2	C3:+57.021	999.5459757	1997.076351	0.000451244	28	N	242	260
P08607	Exosome	PTCEK	IICSQPNILHGVIVSGYK	ATYTH	3	C3:+57.021	666.6999171	1997.076351	0.000622848	6	N	242	260
P08607	Exosome	LEIYK	LTLEVELLQLQIQK	EKHTE	2		834.5012598	1666.98692	0.000451244	6	N	448	462
P08607	Exosome	LEIYK	LTLEVELLQLQIQK	EKHTE	3		556.6701065	1666.98692	0.000451244	1	N	448	462
P08607	Exosome	MVYSK	ITLVTYECDKGYR	LVGKA	2	C8:+57.021	809.4009883	1616.786377	0.000451244	9	N	321	334
P08607	Exosome	MVYSK	ITLVTYECDKGYR	LVGKA	3	C8:+57.021	539.9365922	1616.786377	0.000870037	2	N	321	334
P08607	Exosome	SCEVR	GKGVAWSNPFPECVIVK	CGPPP	2	C13:+57.021	944.4932118	1886.970824	0.000451244	8	N	163	180
P08607	Exosome	EVRGK	GVAWSNPFPECVIVK	CGPPP	2	C11:+57.021	851.9349983	1701.854397	0.000451244	19	N	165	180
P08607	Parental	TVVNK	TVPVWSSSPPTCEK	IICSQ	2	C12:+57.021	787.8798887	1573.744177	0.001943752	1	N	228	242
P08607	Parental	ISNGK	HSGTEDFYPYNHGISYTCDPGFR	LVGSP	3	C18:+57.021	907.3875663	2719.139299	0.000451244	3	N	191	214
P08752	Exosome	SGVIR	RLWADHGVQACFGR	SREYQ	3	C11:+57.021	558.2760537	1671.804761	0.00091018	2	N	129	143
P08752	Exosome	NDLER	IAQSDYIPTQQDVLR	TRVKT	2		873.955205	1745.89481	0.000451244	7	N	162	177
P08752	Exosome	ACFGR	SREYQLNDSAAYYLNDLER	IAQSD	3		774.0333835	2319.076751	0.000451244	3	N	143	162
P08752	Exosome	LFEEK	ITQSSLTICFPEYTGANKYDEAASYIQSK	FEDLN	3	C9:+57.021	1095.85922	3284.554259	0.000451244	21	N	278	307
P08752	Exosome	ICNNK	WFTDTSIILFLNKK	DLFEE	3		575.99118	1724.95014	0.002145581	5	Y	258	272
P08752	Exosome	ATDTK	NVQFVFDAVTDVIIK	NNLKD	2		854.4699596	1706.924319	0.000451244	11	Y	331	346
P08752	Exosome	ATDTK	NVQFVFDAVTDVIIK	NNLKD	3		569.9825731	1706.924319	0.000622848	2	Y	331	346
P08752	Exosome	FGRSR	EYQLNDSAAYYLNDLER	IAQSD	2		1038.979605	2075.943611	0.000451244	9	N	145	162
P08752	Exosome	RKDTK	EIYTHFTCATDTK	NVQFV	2	C8:+57.021	793.861696	1585.707792	0.000451244	2	N	318	331
P08752	Exosome	LFEEK	ITQSSLTICFPEYTGANKY	DEAAS	2	C9:+57.021	1097.030552	2192.045505	0.000451244	10	N	278	297
P08752	Exosome	ADDAR	QLFALSCAAEEQGMLPEDLSGVIR	RLWAD	2	C7:+57.021,M14:+15.995	1325.64653	2649.277459	0.000451244	3	N	105	129
P08752	Exosome	ADDAR	QLFALSCAAEEQGMLPEDLSGVIR	RLWAD	3	C7:+57.021,M14:+15.995	884.1002863	2649.277459	0.000870037	1	N	105	129
P08752	Exosome	ADDAR	QLFALSCAAEEQGMLPEDLSGVIR	RLWAD	3	[0:-	878.4246197	2632.250459	0.000451244	1	N	105	129
P08752	Parental	VKQMK	IIHEDGYSEEECRQY	RAVVY	2	C12:+57.021	964.41027	1926.80494	0.000451244	15	N	54	69
P08752	Parental	VKQMK	IIHEDGYSEEECRQY	RAVVY	3	C12:+57.021	643.2761133	1926.80494	0.0007646	2	N	54	69

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08752	Parental	SGVIR	RLWADHGVQACFGR	SREYQ	3	C11:+57.021	558.2760537	1671.804761	0.000823681	7	N	129	143
P08752	Parental	NDLER	IAQSDYIPTQQDVLR	TRVKT	2		873.955205	1745.89481	0.000451244	66	N	162	177
P08752	Parental	NDLER	IAQSDYIPTQQDVLRT	RVKTT	2		924.4790443	1846.942489	0.000451244	8	N	162	178
P08752	Parental	ACFGR	SREYQLNDSAAYYLNDLER	IAQSD	2		1160.546175	2319.076751	0.000451244	49	N	143	162
P08752	Parental	ACFGR	SREYQLNDSAAYYLNDLER	IAQSD	3		774.0333835	2319.076751	0.000451244	27	N	143	162
P08752	Parental	LFEEK	ITQSSLTICFPEYTGANKYDEAASYIQSK	FEDLN	3	C9:+57.021	1095.85922	3284.554259	0.000451244	70	N	278	307
P08752	Parental	ICNNK	WFTDTSIILFLNKK	DLFEE	2		863.48287	1724.95014	0.000451244	7	Y	258	272
P08752	Parental	ICNNK	WFTDTSIILFLNKK	DLFEE	3		575.99118	1724.95014	0.002145581	10	Y	258	272
P08752	Parental	ATDTK	NVQFVFDAVTDVIIK	NNLKD	2		854.4699596	1706.924319	0.000451244	461	Y	331	346
P08752	Parental	ATDTK	NVQFVFDAVTDVIIK	NNLKD	3		569.9825731	1706.924319	0.000451244	161	Y	331	346
P08752	Parental	FGRSR	EYQLNDSAAYYLNDLER	IAQSD	2		1038.979605	2075.943611	0.000451244	34	N	145	162
P08752	Parental	FGRSR	EYQLNDSAAYYLNDLER	IAQSD	3		692.9890036	2075.943611	0.000823681	8	N	145	162
P08752	Parental	RKDTK	EIYTHFTCATDTK	NVQFV	2	C8:+57.021	793.861696	1585.707792	0.000451244	36	N	318	331
P08752	Parental	RKDTK	EIYTHFTCATDTK	NVQFV	3	C8:+57.021	529.577064	1585.707792	0.000451244	2	N	318	331
P08752	Parental	GVIRR	LWADHGVQACFGR	SREYQ	2	C10:+57.021	758.8596249	1515.70365	0.000451244	9	N	130	143
P08752	Parental	GVIRR	LWADHGVQACFGR	SREYQ	3	C10:+57.021	506.24235	1515.70365	0.000823681	2	N	130	143
P08752	Parental	AREVK	LLLLGAGESGK	STIVK	2		529.3167532	1056.617906	0.001329271	2	Y	35	46
P08752	Parental	LFEEK	ITQSSLTICFPEYTGANKY	DEAAS	2	C9:+57.021	1097.030552	2192.045505	0.000451244	8	N	278	297
P08752	Parental	LNKRK	DTKEIYTHFTCATDTK	NVQFV	2	C11:+57.021	965.9464884	1929.877377	0.001943752	1	N	315	331
P08752	Parental	LFEEK	ITQSSLTICFPEYTGANK	YDEAA	2	C9:+57.021	1015.498888	2028.982176	0.000451244	7	N	278	296
P08752	Parental	ADDAR	QLFALSCAAEEQGMLPEDLSGVIR	RLWAD	2	C7:+57.021,M14:+15.995	1325.64653	2649.277459	0.000451244	3	N	105	129
P08752	Parental	ICNNK	WFTDTSIILFLNK	KDLFE	2		799.4353884	1596.855177	0.000451244	14	Y	258	271
P08752	Parental	RTRVK	TTGIVETHFTF	KDLHF	2		626.8145747	1251.613549	0.000622848	10	Y	181	192
P08752	Parental	HESMK	LFDSICNNK	WFTDT	2	C6:+57.021	555.7663388	1109.517078	0.000622848	4	Y	249	258
P08752	Parental	ACFGR	SREYQLNDSAAYY	LNDLE	2		790.3553237	1578.695047	0.000870037	1	N	143	156
P08752	Parental	LFEEK	ITQSSLTICFPEYTGANKYDEAASY	IQSKF	2	C9:+57.021	1415.150113	2828.284626	0.000451244	3	N	278	303
P08775	Exosome	QIAEK	INAGFGDDLNCIFNDDNAEK	LVLRI	2	C11:+57.021	1121.48978	2240.96396	0.001162105	2	N	1234	1254
P08775	Exosome	PTTPK	YSPTSPTYSPTSPVYTPTSPK	YSPTS	2		1129.547321	2257.079042	0.002519933	1	N	1887	1908
P08775	Exosome	DFSAR	TVITPDPNLSIDQVGVPR	SIAAN	2		961.023619	1920.031638	0.001229886	1	N	364	382
P08775	Parental	QIAEK	INAGFGDDLNCIFNDDNAEK	LVLRI	2	C11:+57.021	1121.48978	2240.96396	0.000622848	10	N	1234	1254
P08775	Parental	PTTPK	YSPTSPTYSPTSPVYTPTSPK	YSPTS	2		1129.547321	2257.079042	0.00091018	3	N	1887	1908
P08775	Parental	VDPVR	TTSNDIVEIFTVLGIEAVR	KALER	2		1039.062941	2076.110282	0.000637154	1	N	1356	1375
P08905	Exosome	NYNTR	ATNYNRGDQSTDYGIFQINSR	YWCND	2		1210.565431	2419.115261	0.000451244	34	N	59	80
P08905	Exosome	NYNTR	ATNYNRGDQSTDYGIFQINSR	YWCND	3		807.3795538	2419.115261	0.000451244	82	N	59	80
P08905	Exosome	TNYNR	GDQSTDYGIFQINSR	YWCND	2		850.897887	1699.780174	0.000451244	39	N	65	80
P08905	Exosome	TNYNR	GDQSTDYGIFQINSR	YWCND	3		567.6011914	1699.780174	0.000451244	7	N	65	80
P08905	Exosome	NYNTR	ATNYNRGDQSTDYGIFQIN	SRYWC	2		1088.998861	2175.982122	0.000622848	5	N	59	78
P08905	Exosome	DGKTP	RAVNACGINCSALLQDDITAAIQCAK	RVVRD	3	C6:+57.021,C10:+57.021,C24:+57.021	945.1300254	2832.366676	0.000451244	5	N	89	115
P08905	Exosome	GKTPR	AVNACGINCSALLQDDITAAIQCAKR	VVRDP	3	C5:+57.021,C9:+57.021,C23:+57.021	945.1300254	2832.366676	0.000451244	13	N	90	116
P08905	Exosome	GKTPR	AVNACGINCSALLQDDITAAIQCAK	RVVRD	2	C5:+57.021,C9:+57.021,C23:+57.021	1339.140583	2676.265565	0.000451244	111	N	90	115
P08905	Exosome	GKTPR	AVNACGINCSALLQDDITAAIQCAK	RVVRD	3	C5:+57.021,C9:+57.021,C23:+57.021	893.0963217	2676.265565	0.000451244	147	N	90	115
P08905	Exosome	RTLKR	NGMAGYYGVSLADWVCLAQHESNYNTR	ATNYN	3	C16:+57.021	1026.127758	3075.359875	0.000451244	25	N	32	59
P08905	Exosome	YGVSL	ADWVCLAQHESNYNTR	ATNYN	2	C5:+57.021	982.4396962	1962.863792	0.000451244	1	N	43	59
P08905	Exosome	AVNAC	GINCSALLQDDITAAIQCAK	RVVRD	2	C4:+57.021,C18:+57.021	1081.532705	2161.04981	0.000451244	7	N	95	115
P08905	Exosome	AVNAC	GINCSALLQDDITAAIQCAK	RVVRD	3	C4:+57.021,C18:+57.021	721.3577367	2161.04981	0.000451244	5	N	95	115
P08905	Exosome	GMAGY	YGVSLADWVCLAQHESNYNTR	ATNYN	3	C10:+57.021	828.3854971	2482.133091	0.002884417	1	N	38	59
P08905	Exosome	TNYNR	GDQSTDYGIFQIN	SRYWC	2		729.3313172	1456.647034	0.001162105	1	N	65	78
P08905	Exosome	MAGYY	GVSLADWVCLAQHESNYNTR	ATNYN	3	C9:+57.021	774.0310542	2319.069763	0.000451244	3	N	39	59
P08905	Parental	NYNTR	ATNYNRGDQSTDYGIFQINSR	YWCND	2		1210.565431	2419.115261	0.000451244	72	N	59	80
P08905	Parental	NYNTR	ATNYNRGDQSTDYGIFQINSR	YWCND	3		807.3795538	2419.115261	0.000451244	112	N	59	80
P08905	Parental	TNYNR	GDQSTDYGIFQINSR	YWCND	2		850.897887	1699.780174	0.000451244	188	N	65	80
P08905	Parental	TNYNR	GDQSTDYGIFQINSR	YWCND	3		567.6011914	1699.780174	0.000451244	18	N	65	80
P08905	Parental	NYNTR	ATNYNRGDQSTDYGIFQIN	SRYWC	2		1088.998861	2175.982122	0.000451244	14	N	59	78
P08905	Parental	DGKTP	RAVNACGINCSALLQDDITAAIQCAK	RVVRD	3	C6:+57.021,C10:+57.021,C24:+57.021	945.1300254	2832.366676	0.000451244	16	N	89	115
P08905	Parental	YYGVS	LADWVCLAQHESNYNTR	ATNYN	3	C6:+57.021	692.9904188	2075.947856	0.001352548	2	N	42	59
P08905	Parental	GKTPR	AVNACGINCSALLQDDITAAIQCAKR	VVRDP	2	C5:+57.021,C9:+57.021,C23:+57.021	1417.191138	2832.366676	0.000451244	15	N	90	116
P08905	Parental	GKTPR	AVNACGINCSALLQDDITAAIQCAKR	VVRDP	3	C5:+57.021,C9:+57.021,C23:+57.021	945.1300254	2832.366676	0.000451244	69	N	90	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P08905	Parental	GKTPR	AVNACGINCSALLQDDITAAIQCAKR	VVRDP	4	C5:+57.021,C9:+57.021,C23:+57.021	709.099469	2832.366676	0.000451244	7	N	90	116
P08905	Parental	GKTPR	AVNACGINCSALLQDDITAAIQCAK	RVVRD	2	C5:+57.021,C9:+57.021,C23:+57.021	1339.140583	2676.265565	0.000451244	277	N	90	115
P08905	Parental	GKTPR	AVNACGINCSALLQDDITAAIQCAK	RVVRD	3	C5:+57.021,C9:+57.021,C23:+57.021	893.0963217	2676.265565	0.000451244	347	N	90	115
P08905	Parental	RTLKR	NGMAGYYGVSLADWVCLAQHESNYNTR	ATNYN	3	C16:+57.021	1026.127758	3075.359875	0.000451244	22	N	32	59
P08905	Parental	YGVSL	ADWVCLAQHESNYNTR	ATNYN	2	C5:+57.021	982.4396962	1962.863792	0.000451244	20	N	43	59
P08905	Parental	YGVSL	ADWVCLAQHESNYNTR	ATNYN	3	C5:+57.021	655.2957308	1962.863792	0.000451244	12	N	43	59
P08905	Parental	AVNAC	GINCSALLQDDITAAIQCAK	RVVRD	2	C4:+57.021,C18:+57.021	1081.532705	2161.04981	0.000451244	9	N	95	115
P08905	Parental	GMAGY	YGVSLADWVCLAQHESNYNTR	ATNYN	3	C10:+57.021	828.3854971	2482.133091	0.000870037	3	N	38	59
P08905	Parental	TNYNR	GDQSTDYGIFQIN	SRYWC	2		729.3313172	1456.647034	0.000451244	3	N	65	78
P08905	Parental	MAGYY	GVSLADWVCLAQHESNYNTR	ATNYN	2	C9:+57.021	1160.542681	2319.069763	0.000451244	6	N	39	59
P08905	Parental	MAGYY	GVSLADWVCLAQHESNYNTR	ATNYN	3	C9:+57.021	774.0310542	2319.069763	0.000451244	16	N	39	59
P08905	Parental	NCSAL	LQDDITAAIQCAK	RVVRD	2	C11:+57.021	723.8667813	1445.717963	0.000823681	1	N	102	115
P08905	Parental	RATNY	NRGDQSTDYGIFQINSR	YWCND	2		985.9699064	1969.924213	0.001654178	1	N	63	80
P08905	Parental	PRAVN	ACGINCSALLQDDITAAIQCAK	RVVRD	2	C2:+57.021,C6:+57.021,C20:+57.021	1197.066355	2392.11711	0.000451244	4	N	93	115
P08905	Parental	ACGIN	CSALLQDDITAAIQCAK	RVVRD	2	C1:+57.021,C15:+57.021	939.4584774	1876.901355	0.000451244	1	N	98	115
P09055	Exosome	HLVQK	LSENNIQTIFAVTEEFQPVYK	ELKNL	2		1235.629177	2469.242753	0.000451244	16	N	325	346
P09055	Exosome	HLVQK	LSENNIQTIFAVTEEFQPVYK	ELKNL	3		824.0887178	2469.242753	0.000451244	9	N	325	346
P09055	Exosome	CTDPK	FQGPTCETCQTCLGVCAEHKECVQCR	AFNKG	4	C6:+57.021,C9:+57.021,C12:+57.021,C16:+57.021,C22:+57.021,C25:+57.021	804.5866299	3214.31532	0.000823681	5	N	624	650
P09055	Exosome	GMAEK	LRPEDITQIQPQQLLLK	LRSGE	3		678.3971573	2032.168072	0.002374549	1	N	105	122
P09055	Exosome	PFSYK	NVLSLTDRGEFFNELVGQQR	ISGNL	3		774.7332683	2321.176405	0.000451244	12	N	220	240
P09055	Exosome	KVESR	EKLPQPVQVDPVTHCK	EKDID	3	C15:+57.021	625.664984	1873.971552	0.001162105	3	N	676	692
P09055	Parental	HLVQK	LSENNIQTIFAVTEEFQPVYK	ELKNL	2		1235.629177	2469.242753	0.000451244	3	N	325	346
P09103	Exosome	EEMTK	YKPESDELTAEKITEFCHR	FLEGK	4	C17:+57.021	589.0340863	2352.105145	0.000823681	6	N	328	347
P09103	Exosome	ARVGA	DALEEEDNVLVLKK	SNFEE	2		807.9334069	1613.851214	0.001463592	4	N	19	33
P09103	Exosome	IRLAK	VDATEESDLAQQYGVR	GYPTI	2		890.9215592	1779.827518	0.000451244	85	N	83	99
P09103	Exosome	IRLAK	VDATEESDLAQQYGVR	GYPTI	3		594.2836394	1779.827518	0.001229886	1	N	83	99
P09103	Exosome	ARVGA	DALEEEDNVLVLK	KSNFE	2		743.8859253	1485.756251	0.000451244	27	N	19	32
P09103	Exosome	GFKGK	ILFIFIDSDHTDNQR	ILEFF	2		917.4606545	1832.905709	0.000451244	7	N	287	302
P09103	Exosome	GFKGK	ILFIFIDSDHTDNQR	ILEFF	3		611.9763697	1832.905709	0.000451244	19	N	287	302
P09103	Exosome	KQPVK	VLVGANFEEVAFDEK	KNVFV	2		833.9202995	1665.824999	0.000451244	32	N	372	387
P09103	Exosome	YTAGR	EADDIVNWLK	KRTGP	2		601.8067496	1201.597899	0.000451244	21	N	122	132
P09103	Exosome	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	2		1320.681941	2639.348281	0.000451244	7	N	172	197
P09103	Exosome	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3		880.7905604	2639.348281	0.000451244	54	N	172	197
P09103	Exosome	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	2	Q1:-17.027	1312.168441	2622.321281	0.000451244	9	N	172	197
P09103	Exosome	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3	Q1:-17.027	875.1148938	2622.321281	0.000451244	7	N	172	197
P09103	Exosome	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	2	[0:-17.027	1312.168441	2622.321281	0.000451244	5	N	172	197
P09103	Exosome	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3	[0:-17.027	875.1148938	2622.321281	0.000451244	5	N	172	197
P09103	Exosome	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	DVESD	3		995.8366752	2984.486626	0.000451244	35	N	134	164
P09103	Exosome	IGFFK	DVESDSAKQFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3		1157.910903	3470.709309	0.000622848	4	N	164	197
P09103	Exosome	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	3		1272.957018	3815.847653	0.000451244	53	N	134	172
P09103	Exosome	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	4		954.9697133	3815.847653	0.000451244	21	N	134	172
P09103	Exosome	GGEIK	THILLFLPK	SVSDY	2		541.342574	1080.669548	0.001871652	6	N	256	265
P09103	Exosome	LDFIK	HNQLPLVIEFTEQTAPK	IFGGE	2		983.0261617	1964.036723	0.000451244	28	N	232	249
P09103	Exosome	LDFIK	HNQLPLVIEFTEQTAPK	IFGGE	3		655.6867078	1964.036723	0.000451244	17	N	232	249
P09103	Exosome	PIWDK	LGETYKDHENIIIAK	MDSTA	2		872.4679482	1742.920296	0.000622848	2	N	411	426
P09103	Exosome	PIWDK	LGETYKDHENIIIAK	MDSTA	4		436.7378741	1742.920296	0.001591523	1	N	411	426
P09103	Exosome	GVFSK	YQLDKDGVVLFK	KFDEG	2		712.8933564	1423.771113	0.000662267	4	N	197	209
P09103	Exosome	FLEGK	IKPHLMSQEVPEDWDKQPVK	VLVGA	4	M6:+15.995	605.8129661	2419.220665	0.000622848	4	N	352	372
P09103	Parental	EEMTK	YKPESDELTAEKITEFCHR	FLEGK	2	C17:+57.021	1177.060373	2352.105145	0.001352548	6	N	328	347
P09103	Parental	EEMTK	YKPESDELTAEKITEFCHR	FLEGK	3	C17:+57.021	785.0428484	2352.105145	0.001591523	1	N	328	347
P09103	Parental	EEMTK	YKPESDELTAEKITEFCHR	FLEGK	4	C17:+57.021	589.0340863	2352.105145	0.000451244	14	N	328	347
P09103	Parental	GSEIR	LAKVDATEESDLAQQYGVR	GYPTI	2		1047.02963	2092.043659	0.000451244	14	N	80	99
P09103	Parental	GSEIR	LAKVDATEESDLAQQYGVR	GYPTI	3		698.3556865	2092.043659	0.000451244	11	N	80	99
P09103	Parental	ARVGA	DALEEEDNVLVLKK	SNFEE	2		807.9334069	1613.851214	0.000637154	8	N	19	33
P09103	Parental	IRLAK	VDATEESDLAQQYGVR	GYPTI	2		890.9215592	1779.827518	0.000451244	113	N	83	99
P09103	Parental	IRLAK	VDATEESDLAQQYGVR	GYPTI	3		594.2836394	1779.827518	0.000451244	14	N	83	99
P09103	Parental	ARVGA	DALEEEDNVLVLK	KSNFE	2		743.8859253	1485.756251	0.000451244	15	N	19	32
P09103	Parental	TASPK	EYTAGREADDIVNWLK	KRTGP	2		940.4633942	1878.911188	0.000451244	1	N	116	132
P09103	Parental	TASPK	EYTAGREADDIVNWLK	KRTGP	3		627.3115295	1878.911188	0.000451244	8	N	116	132

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P09103	Parental	GFKGK	ILFIFIDSDHTDNQR	ILEFF	2		917.4606545	1832.905709	0.000451244	19	N	287	302
P09103	Parental	GFKGK	ILFIFIDSDHTDNQR	ILEFF	3		611.9763697	1832.905709	0.000451244	21	N	287	302
P09103	Parental	KQPVK	VLVGANFEEVAFDEK	KNVFV	2		833.9202995	1665.824999	0.000451244	26	N	372	387
P09103	Parental	YTAGR	EADDIVNWLK	KRTGP	2		601.8067496	1201.597899	0.000451244	23	N	122	132
P09103	Parental	QTAPK	IFGGEIKTHILLFLPK	SVSDY	4		457.2794435	1825.086574	0.001162105	3	N	249	265
P09103	Parental	ITKEK	LLDFIKHNQLPLVIEFTEQTAPK	IFGGE	3		898.834212	2693.479236	0.000451244	3	N	226	249
P09103	Parental	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	2		1320.681941	2639.348281	0.000451244	58	N	172	197
P09103	Parental	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3		880.7905604	2639.348281	0.000451244	35	N	172	197
P09103	Parental	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	2	Q1:-17.027	1312.168441	2622.321281	0.000451244	21	N	172	197
P09103	Parental	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3	Q1:-17.027	875.1148938	2622.321281	0.000451244	8	N	172	197
P09103	Parental	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	2	[0:-17.027	1312.168441	2622.321281	0.000451244	9	N	172	197
P09103	Parental	SDSAK	QFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3	[0:-17.027	875.1148938	2622.321281	0.000451244	16	N	172	197
P09103	Parental	AATTL	SDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	3		1035.498499	3103.472098	0.000735798	7	N	142	172
P09103	Parental	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	DVESD	3		995.8366752	2984.486626	0.000451244	72	N	134	164
P09103	Parental	IGFFK	DVESDSAKQFLLAAEAIDDIPFGITSNSGVFSK	YQLDK	3		1157.910903	3470.709309	0.000451244	14	N	164	197
P09103	Parental	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	3		1272.957018	3815.847653	0.000451244	81	N	134	172
P09103	Parental	WLKKR	TGPAATTLSDTAAAESLVDSSEVTVIGFFKDVESDSAK	QFLLA	4		954.9697133	3815.847653	0.000451244	35	N	134	172
P09103	Parental	IIIAK	MDSTANEVEAVKVHSFPTLK	FFPAS	3		735.0408223	2202.099067	0.000622848	1	N	426	446
P09103	Parental	IIIAK	MDSTANEVEAVKVHSFPTLK	FFPAS	4		551.5325667	2202.099067	0.000451244	2	N	426	446
P09103	Parental	GGEIK	THILLFLPK	SVSDY	2		541.342574	1080.669548	0.002727428	1	N	256	265
P09103	Parental	LDFIK	HNQLPLVIEFTEQTAPK	IFGGE	2		983.0261617	1964.036723	0.000451244	16	N	232	249
P09103	Parental	LDFIK	HNQLPLVIEFTEQTAPK	IFGGE	3		655.6867078	1964.036723	0.000451244	38	N	232	249
P09103	Parental	PIWDK	LGETYKDHENIIIAK	MDSTA	2		872.4679482	1742.920296	0.000451244	9	N	411	426
P09103	Parental	PIWDK	LGETYKDHENIIIAK	MDSTA	3		581.9812322	1742.920296	0.000451244	3	N	411	426
P09103	Parental	GVFSK	YQLDKDGVVLFK	KFDEG	2		712.8933564	1423.771113	0.000662267	1	N	197	209
P09103	Parental	GVFSK	YQLDKDGVVLFK	KFDEG	3		475.5981709	1423.771113	0.000451244	1	N	197	209
P09103	Parental	NWLKK	RTGPAATTLSDTAAAESLVDSSEVTVIGFFK	DVESD	3		1047.870379	3140.587737	0.000451244	3	N	133	164
P09103	Parental	VLFKK	FDEGRNNFEGEITK	EKLLD	2		828.3871552	1654.75871	0.000451244	1	N	210	224
P09103	Parental	KQPVK	VLVGANFEEVAFDEKK	NVFVE	2		897.9677811	1793.919962	0.000451244	12	N	372	388
P09103	Parental	AIDDI	PFGITSNSGVFSK	YQLDK	2		670.8464061	1339.677212	0.002080925	1	N	184	197
P09103	Parental	AATTL	SDTAAAESLVDSSEVTVIGFFK	DVESD	2		1137.063335	2272.11107	0.000451244	3	N	142	164
P09405	Exosome	TLFVK	GLSEDTTEETLKESFEGSVR	ARIVT	2		1107.524574	2213.033548	0.000622848	3	N	574	594
P09405	Exosome	TLFVK	GLSEDTTEETLKESFEGSVR	ARIVT	3		738.6856495	2213.033548	0.001839721	1	N	574	594
P09405	Exosome	TGSSK	GFGFVDFNSEEDAK	AAKEA	2		781.3444246	1560.673249	0.000451244	26	N	607	621
P09405	Exosome	GTNRK	FGYVDFESAEDLEK	ALELT	2		824.8730149	1647.73043	0.000451244	17	N	350	364
P09405	Exosome	VNELK	FAISELFAK	NDLAV	2		513.2874644	1024.559329	0.000451244	20	N	326	335
P09405	Exosome	HGKPK	GYAFIEFASFEDAKEALNSCNK	MEIEG	3	C20:+57.021	837.7217749	2510.141925	0.000451244	10	N	524	546
P09405	Exosome	SGESK	TLVLSNLSYSATKETLEEVFEK	ATFIK	3		834.4394162	2500.294849	0.000451244	5	N	487	509
P09405	Exosome	GTNRK	FGYVDFESAEDLEKALELTGLK	VFGNE	3		825.4166116	2473.226435	0.000451244	8	N	350	372
P09405	Exosome	TLLAK	NLSFNITEDELKEVFEDAMEIR	LVSQD	3		881.4271822	2641.258147	0.000451244	4	N	400	422
P09405	Exosome	TLLAK	NLSFNITEDELKEVFEDAMEIR	LVSQD	3	M19:+15.995	886.7588489	2657.253147	0.000451244	4	N	400	422
P09405	Exosome	SGESK	TLVLSNLSYSATK	ETLEE	2		698.888271	1395.760942	0.000451244	33	N	487	500
P09405	Exosome	HGKPK	GYAFIEFASFEDAK	EALNS	2		797.8753606	1593.735121	0.000451244	11	N	524	538
P09405	Exosome	AKKQK	VEGSEPTTPFNLFIGNLNPNK	SVNEL	2		1144.582029	2287.148459	0.000451244	13	N	299	320
P09405	Exosome	PEAKK	QKVEGSEPTTPFNLFIGNLNPNK	SVNEL	3		848.7751332	2543.302	0.000823681	4	N	297	320
P09405	Exosome	AKAAK	EAMEDGEIDGNKVTLDWAKPK	GEGGF	3	M3:+15.995	788.0464416	2361.115925	0.000823681	1	N	624	645
P09405	Parental	TLFVK	GLSEDTTEETLKESFEGSVR	ARIVT	2		1107.524574	2213.033548	0.000451244	23	N	574	594
P09405	Parental	TLFVK	GLSEDTTEETLKESFEGSVR	ARIVT	3		738.6856495	2213.033548	0.000451244	8	N	574	594
P09405	Parental	TGSSK	GFGFVDFNSEEDAK	AAKEA	2		781.3444246	1560.673249	0.000451244	22	N	607	621
P09405	Parental	EDLEK	ALELTGLKVFGNEIK	LEKPK	3		544.6509348	1630.929405	0.002813207	1	N	364	379
P09405	Parental	GTNRK	FGYVDFESAEDLEK	ALELT	2		824.8730149	1647.73043	0.000451244	29	N	350	364
P09405	Parental	VNELK	FAISELFAK	NDLAV	2		513.2874644	1024.559329	0.001162105	12	N	326	335
P09405	Parental	HGKPK	GYAFIEFASFEDAKEALNSCNK	MEIEG	3	C20:+57.021	837.7217749	2510.141925	0.000451244	2	N	524	546
P09405	Parental	VNELK	FAISELFAKNDLAVVDVR	TGTNR	2		1004.049637	2006.083674	0.000735798	2	N	326	344
P09405	Parental	VNELK	FAISELFAKNDLAVVDVR	TGTNR	3		669.7023579	2006.083674	0.000451244	6	N	326	344
P09405	Parental	SGESK	TLVLSNLSYSATKETLEEVFEK	ATFIK	2		1251.155224	2500.294849	0.000451244	10	N	487	509
P09405	Parental	SGESK	TLVLSNLSYSATKETLEEVFEK	ATFIK	3		834.4394162	2500.294849	0.000451244	9	N	487	509
P09405	Parental	GTNRK	FGYVDFESAEDLEKALELTGLK	VFGNE	2		1237.621017	2473.226435	0.000451244	4	N	350	372
P09405	Parental	GTNRK	FGYVDFESAEDLEKALELTGLK	VFGNE	3		825.4166116	2473.226435	0.000451244	16	N	350	372
P09405	Parental	TLLAK	NLSFNITEDELKEVFEDAMEIR	LVSQD	3		881.4271822	2641.258147	0.000451244	5	N	400	422
P09405	Parental	LNPNK	SVNELKFAISELFAK	NDLAV	3		565.9825731	1694.924319	0.001871652	1	N	320	335
P09405	Parental	SGESK	TLVLSNLSYSATK	ETLEE	2		698.888271	1395.760942	0.000451244	12	N	487	500
P09405	Parental	HGKPK	GYAFIEFASFEDAK	EALNS	2		797.8753606	1593.735121	0.002212458	3	N	524	538
P09405	Parental	KGYAF	IEFASFEDAKEALNSCNK	MEIEG	2	C16:+57.021	1036.983602	2071.951604	0.000451244	2	N	528	546
P09405	Parental	TGTNR	KFGYVDFESAEDLEK	ALELT	2		888.9204965	1775.825393	0.000451244	3	N	349	364

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P09405	Parental	TGTNR	KFGYVDFESAEDLEK	ALELT	3		592.9495977	1775.825393	0.000622848	8	N	349	364
P09405	Parental	EDLEK	ALELTGLKVF	GNEIK	2		545.8294964	1089.643393	0.000451244	7	N	364	374
P09405	Parental	KTLVL	SNLSYSATKETLEEVFEK	ATFIK	2		1038.013114	2074.010628	0.000823681	1	N	491	509
P09411	Exosome	KATSR	GCITIIGGGDTATCCAK	WNTED	2	C2:+57.021,C14:+57.021,C15:+57.021	877.896967	1753.778334	0.000451244	92	N	365	382
P09411	Exosome	ASLSK	LGDVYVNDAFGTAHR	AHSSM	2		817.9002327	1633.784865	0.000451244	13	N	156	171
P09411	Exosome	ASLSK	LGDVYVNDAFGTAHR	AHSSM	3		545.6027551	1633.784865	0.000451244	67	N	156	171
P09411	Exosome	TCCAK	WNTEDKVSHVSTGGGASLELLEGK	VLPGV	2		1257.627697	2513.239793	0.000451244	24	N	382	406
P09411	Exosome	TCCAK	WNTEDKVSHVSTGGGASLELLEGK	VLPGV	3		838.7543978	2513.239793	0.000451244	36	N	382	406
P09411	Exosome	KNGVK	ITLPVDFVTADKFDENAK	TGQAT	2		1012.023285	2022.030969	0.000451244	36	N	279	297
P09411	Exosome	KNGVK	ITLPVDFVTADKFDENAK	TGQAT	3		675.0181231	2022.030969	0.000451244	12	N	279	297
P09411	Exosome	NYFAK	ALESPERPFLAILGGAK	VADKI	2		885.0019582	1767.988316	0.000451244	23	N	199	216
P09411	Exosome	NYFAK	ALESPERPFLAILGGAK	VADKI	3		590.3372388	1767.988316	0.000451244	37	N	199	216
P09411	Exosome	VLFLK	DCVGPEVENACANPAAGTVILLENLR	FHVEE	2	C2:+57.021,C11:+57.021	1391.678618	2781.341636	0.000451244	61	N	97	123
P09411	Exosome	VLFLK	DCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C2:+57.021,C11:+57.021	928.1216785	2781.341636	0.000451244	68	N	97	123
P09411	Exosome	VLFLK	DCVGPEVENACANPAAGTVILLENLR	FHVEE	4	C2:+57.021,C11:+57.021	696.3432089	2781.341636	0.000823681	2	N	97	123
P09411	Exosome	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2		1053.034321	2104.053042	0.000451244	81	N	332	350
P09411	Exosome	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	3		702.358814	2104.053042	0.000451244	36	N	332	350
P09411	Exosome	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2	Q1:-17.027	1044.520821	2087.026042	0.000451244	7	N	332	350
P09411	Exosome	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2	[0:-17.027	1044.520821	2087.026042	0.000451244	21	N	332	350
P09411	Exosome	SLLGK	DVLFLKDCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C8:+57.021,C17:+57.021	1166.597299	3496.768498	0.000451244	27	N	91	123
P09411	Exosome	SLLGK	DVLFLKDCVGPEVENACANPAAGTVILLENLR	FHVEE	4	C8:+57.021,C17:+57.021	875.1999245	3496.768498	0.000451244	9	N	91	123
P09411	Exosome	LLEGK	VLPGVDALSNV	-	2		542.3063854	1082.597171	0.001329271	17	N	406	417
P09411	Exosome	DVLFL	KDCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C3:+57.021,C12:+57.021	970.8199996	2909.436599	0.000451244	14	N	96	123
P09411	Exosome	NTEDK	VSHVSTGGGASLELLEGK	VLPGV	2		870.9604874	1739.905375	0.000451244	26	N	388	406
P09411	Exosome	NTEDK	VSHVSTGGGASLELLEGK	VLPGV	3		580.9762582	1739.905375	0.000451244	23	N	388	406
P09411	Exosome	PMPDK	YSLEPVAAELK	SLLGK	2		610.3326002	1218.6496	0.001395409	3	N	75	86
P09411	Exosome	FTFLK	VLNNMEIGTSLYDEEGAK	IVKDL	2		991.9729351	1981.93027	0.000451244	7	N	246	264
P09411	Exosome	FTFLK	VLNNMEIGTSLYDEEGAK	IVKDL	2	M5:+15.995	999.9704351	1997.92527	0.000622848	7	N	246	264
P09411	Exosome	DENAK	TGQATVASGIPAGWMGLDCGTESSKK	YAEAV	3	M15:+15.995,C19:+57.021	875.7480241	2624.220672	0.000451244	12	N	297	323
P09411	Exosome	KNGVK	ITLPVDFVTADKF	DENAK	2		733.4010143	1464.786429	0.000451244	6	N	279	292
P09411	Exosome	VLFLK	DCVGPEVENACANPAAGTVIL	LENLR	2	C2:+57.021,C11:+57.021	1079.001238	2155.986875	0.002519933	1	N	97	118
P09411	Parental	KATSR	GCITIIGGGDTATCCAK	WNTED	2	C2:+57.021,C14:+57.021,C15:+57.021	877.896967	1753.778334	0.000451244	82	N	365	382
P09411	Parental	ASLSK	LGDVYVNDAFGTAHR	AHSSM	2		817.9002327	1633.784865	0.000451244	5	N	156	171
P09411	Parental	ASLSK	LGDVYVNDAFGTAHR	AHSSM	3		545.6027551	1633.784865	0.000451244	36	N	156	171
P09411	Parental	TCCAK	WNTEDKVSHVSTGGGASLELLEGK	VLPGV	2		1257.627697	2513.239793	0.000451244	28	N	382	406
P09411	Parental	TCCAK	WNTEDKVSHVSTGGGASLELLEGK	VLPGV	3		838.7543978	2513.239793	0.000451244	28	N	382	406
P09411	Parental	KNGVK	ITLPVDFVTADKFDENAK	TGQAT	2		1012.023285	2022.030969	0.000451244	32	N	279	297
P09411	Parental	KNGVK	ITLPVDFVTADKFDENAK	TGQAT	3		675.0181231	2022.030969	0.000451244	1	N	279	297
P09411	Parental	NYFAK	ALESPERPFLAILGGAK	VADKI	2		885.0019582	1767.988316	0.000622848	3	N	199	216
P09411	Parental	NYFAK	ALESPERPFLAILGGAK	VADKI	3		590.3372388	1767.988316	0.000451244	35	N	199	216
P09411	Parental	EAVGR	AKQIVWNGPVGVFEWEAFAR	GTKSL	2		1152.60036	2303.185119	0.000451244	2	N	330	350
P09411	Parental	EAVGR	AKQIVWNGPVGVFEWEAFAR	GTKSL	3		768.736173	2303.185119	0.000451244	4	N	330	350
P09411	Parental	VLFLK	DCVGPEVENACANPAAGTVILLENLR	FHVEE	2	C2:+57.021,C11:+57.021	1391.678618	2781.341636	0.000451244	39	N	97	123
P09411	Parental	VLFLK	DCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C2:+57.021,C11:+57.021	928.1216785	2781.341636	0.000451244	47	N	97	123
P09411	Parental	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2		1053.034321	2104.053042	0.000451244	46	N	332	350
P09411	Parental	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	3		702.358814	2104.053042	0.000451244	19	N	332	350
P09411	Parental	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2	Q1:-17.027	1044.520821	2087.026042	0.000451244	6	N	332	350
P09411	Parental	VGRAK	QIVWNGPVGVFEWEAFAR	GTKSL	2	[0:-17.027	1044.520821	2087.026042	0.000451244	16	N	332	350
P09411	Parental	SLLGK	DVLFLKDCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C8:+57.021,C17:+57.021	1166.597299	3496.768498	0.000451244	7	N	91	123
P09411	Parental	SLLGK	DVLFLKDCVGPEVENACANPAAGTVILLENLR	FHVEE	4	C8:+57.021,C17:+57.021	875.1999245	3496.768498	0.000622848	6	N	91	123
P09411	Parental	LLEGK	VLPGVDALSNV	-	2		542.3063854	1082.597171	0.001352548	13	N	406	417
P09411	Parental	DVLFL	KDCVGPEVENACANPAAGTVILLENLR	FHVEE	2	C3:+57.021,C12:+57.021	1455.726099	2909.436599	0.000451244	3	N	96	123
P09411	Parental	DVLFL	KDCVGPEVENACANPAAGTVILLENLR	FHVEE	3	C3:+57.021,C12:+57.021	970.8199996	2909.436599	0.000451244	19	N	96	123
P09411	Parental	AAELK	SLLGKDVLFL	KDCVG	2		552.8373214	1103.659043	0.001463592	3	N	86	96
P09411	Parental	NTEDK	VSHVSTGGGASLELLEGK	VLPGV	2		870.9604874	1739.905375	0.000451244	7	N	388	406
P09411	Parental	NTEDK	VSHVSTGGGASLELLEGK	VLPGV	3		580.9762582	1739.905375	0.000451244	6	N	388	406
P09411	Parental	PMPDK	YSLEPVAAELK	SLLGK	2		610.3326002	1218.6496	0.001463592	3	N	75	86
P09411	Parental	SLLGK	DVLFLKDCVGPEVENACANPAAGTVIL	LENLR	2	C8:+57.021,C17:+57.021	1436.714669	2871.413738	0.000451244	6	N	91	118
P09411	Parental	FTFLK	VLNNMEIGTSLYDEEGAK	IVKDL	2		991.9729351	1981.93027	0.001463592	1	N	246	264
P09411	Parental	VLFLK	DCVGPEVENACANPAAGTVIL	LENLR	2	C2:+57.021,C11:+57.021	1079.001238	2155.986875	0.001352548	1	N	97	118
P09528	Exosome	LELHK	LATDKNDPHLCDFIETYYLSEQVK	SIKEL	2	C11:+57.021	1450.194855	2898.37411	0.000451244	13	N	120	144
P09528	Exosome	LELHK	LATDKNDPHLCDFIETYYLSEQVK	SIKEL	3	C11:+57.021	967.1325033	2898.37411	0.000451244	17	N	120	144
P09528	Exosome	LELHK	LATDKNDPHLCDFIETYYLSEQVK	SIKEL	4	C11:+57.021	725.6013275	2898.37411	0.000451244	13	N	120	144

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P09528	Exosome	LHLEK	SVNQSLLELHK	LATDK	3		423.2388656	1266.693197	0.000870037	3	N	109	120
P09528	Exosome	VTNLR	KMGAPEAGMAEYLFDK	HTLGH	3		586.6132757	1756.816427	0.002145581	1	N	157	173
P09528	Exosome	SEQVK	SIKELGDHVTNLR	KMGAP	3		494.6077291	1480.799787	0.000451244	2	N	144	157
P09581	Exosome	WHGQG	APVIEPSGPELVVEPGETVTLR	CVSNG	2		1145.120988	2288.226375	0.000451244	30	N	19	41
P09581	Exosome	WHGQG	APVIEPSGPELVVEPGETVTLR	CVSNG	3		763.749925	2288.226375	0.000622848	1	N	19	41
P09581	Exosome	HLYVK	DPAHSWNLLAQEVTVVEGQEAVLPCLITDPALK	DSVSL	3	C25:+57.021	1205.290907	3612.84932	0.000979378	6	N	102	135
P09581	Exosome	VWHGQ	GAPVIEPSGPELVVEPGETVTLR	CVSNG	2		1173.631719	2345.247839	0.000979378	1	N	18	41
P0C0S6	Exosome	DSLIK	ATIAGGGVIPHIHK	SLIGK	2		685.8993074	1369.783015	0.000451244	41	N	102	116
P0C0S6	Exosome	DSLIK	ATIAGGGVIPHIHK	SLIGK	3		457.6021383	1369.783015	0.000451244	55	N	102	116
P0C0S6	Exosome	SRSQR	AGLQFPVGR	IHRHL	2		472.7697731	943.5239462	0.000451244	1500	Y	23	32
P0C0S6	Exosome	RITPR	HLQLAIRGDEELDSLIK	ATIAG	2		975.5368936	1949.058187	0.000451244	4	N	85	102
P0C0S6	Exosome	RITPR	HLQLAIRGDEELDSLIK	ATIAG	3		650.6938624	1949.058187	0.000451244	431	N	85	102
P0C0S6	Exosome	RITPR	HLQLAIRGDEELDSLIK	ATIAG	4		488.2723468	1949.058187	0.000662267	6	N	85	102
P0C0S6	Exosome	AVYSA	AILEYLTAEVLELAGNASK	DLKVK	2		1003.04676	2004.07792	0.000451244	5	N	56	75
P0C0S6	Exosome	AVYSA	AILEYLTAEVLELAGNASK	DLKVK	3		669.0337732	2004.07792	0.000451244	26	N	56	75
P0C0S6	Exosome	TAAVY	SAAILEYLTAEVLELAGNASK	DLKVK	2		1082.081331	2162.147062	0.000451244	235	N	54	75
P0C0S6	Exosome	TAAVY	SAAILEYLTAEVLELAGNASK	DLKVK	3		721.7234873	2162.147062	0.000451244	191	N	54	75
P0C0S6	Exosome	AILEY	LTAEVLELAGNASK	DLKVK	2		708.3911779	1414.766756	0.00091018	9	N	61	75
P0C0S6	Exosome	DSLIK	ATIAGGGVIPH	IHKSL	2		496.7803378	991.5450756	0.000451244	9	N	102	113
P0C0S6	Exosome	QLAIR	GDEELDSLIK	ATIAG	2		559.7829402	1117.55028	0.000451244	45	N	92	102
P0C0S6	Exosome	TSHGR	VGATAAVYSAAILEYLTAEVLELAGNASK	DLKVK	2		1448.271651	2894.527702	0.000451244	17	N	46	75
P0C0S6	Exosome	TSHGR	VGATAAVYSAAILEYLTAEVLELAGNASK	DLKVK	3		965.8503675	2894.527702	0.000451244	39	N	46	75
P0C0S6	Exosome	TSHGR	VGATAAVYSAAILEYLTAEVLELAGNASK	DLKVK	4		724.6397256	2894.527702	0.000451244	4	N	46	75
P0C0S6	Exosome	VYSAA	ILEYLTAEVLELAGNASK	DLKVK	2		967.5282029	1933.040806	0.000451244	30	N	57	75
P0C0S6	Exosome	VYSAA	ILEYLTAEVLELAGNASK	DLKVK	3		645.3547353	1933.040806	0.000451244	34	N	57	75
P0C0S6	Exosome	YSAAI	LEYLTAEVLELAGNASK	DLKVK	2		910.9861708	1819.956742	0.000451244	18	N	58	75
P0C0S6	Exosome	SAAIL	EYLTAEVLELAGNASK	DLKVK	2		854.4441388	1706.872678	0.000451244	8	N	59	75
P0C0S6	Exosome	AAVYS	AAILEYLTAEVLELAGNASK	DLKVK	3		692.7128112	2075.115033	0.000451244	3	N	55	75
P0C0S6	Exosome	GATAA	VYSAAILEYLTAEVLELAGNASK	DLKVK	2		1213.147202	2424.278805	0.000451244	3	N	52	75
P0C0S6	Exosome	RVGAT	AAVYSAAILEYLTAEVLELAGNASK	DLKVK	2		1284.184316	2566.353032	0.000451244	1	N	50	75
P0C0S6	Parental	DSLIK	ATIAGGGVIPHIHK	SLIGK	2		685.8993074	1369.783015	0.000622848	11	N	102	116
P0C0S6	Parental	DSLIK	ATIAGGGVIPHIHK	SLIGK	3		457.6021383	1369.783015	0.000662267	17	N	102	116
P0C0S6	Parental	SRSQR	AGLQFPVGR	IHRHL	2		472.7697731	943.5239462	0.000451244	455	Y	23	32
P0C0S6	Parental	RITPR	HLQLAIRGDEELDSLIK	ATIAG	2		975.5368936	1949.058187	0.000622848	5	N	85	102
P0C0S6	Parental	RITPR	HLQLAIRGDEELDSLIK	ATIAG	3		650.6938624	1949.058187	0.000451244	39	N	85	102
P0C0S6	Parental	AVYSA	AILEYLTAEVLELAGNASK	DLKVK	3		669.0337732	2004.07792	0.00091018	2	N	56	75
P0C0S6	Parental	TAAVY	SAAILEYLTAEVLELAGNASKDLK	VKRIT	3		840.4588108	2518.353032	0.000451244	3	N	54	78
P0C0S6	Parental	TAAVY	SAAILEYLTAEVLELAGNASK	DLKVK	2		1082.081331	2162.147062	0.000451244	207	N	54	75
P0C0S6	Parental	TAAVY	SAAILEYLTAEVLELAGNASK	DLKVK	3		721.7234873	2162.147062	0.000451244	246	N	54	75
P0C0S6	Parental	AILEY	LTAEVLELAGNASK	DLKVK	2		708.3911779	1414.766756	0.000451244	42	N	61	75
P0C0S6	Parental	LEYLT	AEVLELAGNASK	DLKVK	2		601.3253065	1200.635013	0.001591523	1	N	63	75
P0C0S6	Parental	QLAIR	GDEELDSLIK	ATIAG	2		559.7829402	1117.55028	0.000451244	9	N	92	102
P0C0S6	Parental	TSHGR	VGATAAVYSAAILEYLTAEVLELAGNASK	DLKVK	3		965.8503675	2894.527702	0.001654178	1	N	46	75
P0C0S6	Parental	YSAAI	LEYLTAEVLELAGNASK	DLKVK	2		910.9861708	1819.956742	0.000451244	2	N	58	75
P0C0S6	Parental	QLAIR	GDEELDSLIKATIAGGGVIPHIHK	SLIGK	4		618.3384838	2469.322735	0.000451244	2	N	92	116
P0C0S6	Parental	ILEYL	TAEVLELAGNASK	DLKVK	2		651.8491458	1301.682692	0.001162105	1	N	62	75
P0C0S6	Parental	SLIKA	TIAGGGVIPHIHK	SLIGK	3		433.9231003	1298.745901	0.001463592	5	N	103	116
P0C0S6	Parental	QLAIR	GDEELDSLIKA	TIAGG	2		595.3014971	1188.587394	0.002374549	2	N	92	103
P0CW02	Exosome	KLKTR	QCLSFCPAGVPIRDPNIR	ERTSC	3	C2:+57.021,C6:+57.021	700.68764	2099.03952	0.000451244	6	N	72	90
P0CW02	Exosome	ERAQG	LQCYECYGVPIETSCPAVTCR	ASDGF	2	C3:+57.021,C6:+57.021,C15:+57.021,C20:+57.021	1282.057441	2562.099282	0.000451244	4	N	26	47
P0CW02	Exosome	CYECY	GVPIETSCPAVTCR	ASDGF	2	C8:+57.021,C13:+57.021	773.8713094	1545.727019	0.000451244	1	N	33	47
P0CW02	Parental	KLKTR	QCLSFCPAGVPIRDPNIR	ERTSC	3	C2:+57.021,C6:+57.021	700.68764	2099.03952	0.000451244	14	N	72	90
P0CW02	Parental	ERAQG	LQCYECYGVPIETSCPAVTCR	ASDGF	2	C3:+57.021,C6:+57.021,C15:+57.021,C20:+57.021	1282.057441	2562.099282	0.000451244	18	N	26	47
P0CW02	Parental	ERAQG	LQCYECYGVPIETSCPAVTCR	ASDGF	3	C3:+57.021,C6:+57.021,C15:+57.021,C20:+57.021	855.0408941	2562.099282	0.002212458	2	N	26	47
P0CW02	Parental	AVTCR	ASDGFCIAQNIELIEDSQRR	KLKTR	3	C6:+57.021	774.7099807	2321.106542	0.000451244	10	N	47	67
P0CW02	Parental	AVTCR	ASDGFCIAQNIELIEDSQR	RKLKT	2	C6:+57.021	1083.510516	2165.005431	0.000451244	10	N	47	66
P0CW02	Parental	AERAQ	GLQCYECYGVPIETSCPAVTCR	ASDGF	2	C4:+57.021,C7:+57.021,C16:+57.021,C21:+57.021	1310.568173	2619.120746	0.000622848	2	N	25	47
P10107	Exosome	LALAK	GDRCQDLSVNQDLADTDAR	ALYEA	2	C4:+57.021	1074.982654	2147.949707	0.000451244	20	N	185	204
P10107	Exosome	LALAK	GDRCQDLSVNQDLADTDAR	ALYEA	3	C4:+57.021	716.9910357	2147.949707	0.000451244	17	N	185	204
P10107	Exosome	RDLAK	DITSDTSGDFR	KALLA	2		607.2707283	1212.525857	0.000451244	22	N	166	177
P10107	Exosome	LAMLK	TPAQFDADELR	GAMKG	2		631.8047383	1261.593877	0.000451244	125	N	113	124

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10107	Exosome	AKGDR	CQDLSVNQDLADTDAR	ALYEA	2	C1:+57.021	910.9078945	1819.800189	0.000451244	74	N	188	204
P10107	Exosome	AKGDR	CQDLSVNQDLADTDAR	ALYEA	3	C1:+57.021	607.607863	1819.800189	0.000451244	3	N	188	204
P10107	Exosome	AKGDR	CQDLSVNQDLADTDAR	ALYEA	2	[0:-17.027,C1:+57.021	902.3943945	1802.773189	0.000622848	27	N	188	204
P10107	Exosome	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	2		972.5316112	1943.047622	0.000451244	13	N	81	98
P10107	Exosome	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	3		648.6903408	1943.047622	0.000451244	36	N	81	98
P10107	Exosome	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	4		486.7697056	1943.047622	0.000451244	41	N	81	98
P10107	Exosome	TTIVK	CATSTPAFFAEK	LYEAM	2	C1:+57.021	665.3111106	1328.606621	0.000451244	27	N	269	281
P10107	Exosome	HDMNK	ALDLELKGDIEK	CLTTI	2		672.3749965	1342.734393	0.000451244	10	N	250	262
P10107	Exosome	HDMNK	ALDLELKGDIEK	CLTTI	3		448.585931	1342.734393	0.000451244	25	N	250	262
P10107	Exosome	RQQIK	AAYLQENGKPLDEVLR	KALTG	2		908.4841296	1814.952659	0.000451244	80	N	81	97
P10107	Exosome	RQQIK	AAYLQENGKPLDEVLR	KALTG	3		605.9920198	1814.952659	0.000451244	81	N	81	97
P10107	Exosome	LKQAR	FLENQEQEYVQAVK	SYKGG	2		862.9286559	1723.841712	0.000451244	8	N	12	26
P10107	Exosome	EELKR	DLAKDITSDTSGDFR	KALLA	2		820.8922704	1639.768941	0.000451244	12	N	162	177
P10107	Exosome	EELKR	DLAKDITSDTSGDFR	KALLA	3		547.5974469	1639.768941	0.000451244	1	N	162	177
P10107	Exosome	VQAVK	SYKGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	4		681.3427605	2721.339842	0.000851441	1	N	26	53
P10107	Exosome	GDYEK	ILVALCGGN	-	2	C6:+57.021	458.7499604	915.4843208	0.000451244	6	N	337	346
P10107	Exosome	VKSYK	GGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1172.582561	2343.149522	0.002080925	2	N	29	53
P10107	Exosome	VKSYK	GGPGSAVSPYPSFNVSSDVAALHK	AIMVK	3		782.0576405	2343.149522	0.000451244	17	N	29	53
P10107	Exosome	AGERR	KGTDVNVFTTILTSR	SFPHL	2		826.4548408	1650.894082	0.000451244	3	N	213	228
P10107	Exosome	AGERR	KGTDVNVFTTILTSR	SFPHL	3		551.3058272	1650.894082	0.000451244	17	N	213	228
P10107	Exosome	FYQKK	YGISLCQAILDETKGDYEK	ILVAL	2	C6:+57.021	1102.033292	2202.050984	0.000451244	38	N	318	337
P10107	Exosome	FYQKK	YGISLCQAILDETKGDYEK	ILVAL	3	C6:+57.021	735.0247948	2202.050984	0.000451244	58	N	318	337
P10107	Exosome	FYQKK	YGISLCQAILDETK	GDYEK	2	C6:+57.021	805.9086462	1609.801692	0.000451244	24	N	318	332
P10107	Exosome	DEVLR	KALTGHLEEVVLAMLK	TPAQF	2		876.5085624	1751.001525	0.001162105	2	N	97	113
P10107	Exosome	DEVLR	KALTGHLEEVVLAMLK	TPAQF	3		584.6749749	1751.001525	0.000451244	26	N	97	113
P10107	Exosome	AIMVK	GVDEATIIDILTKR	TNAQR	2		772.4386594	1542.861719	0.000451244	41	N	58	72
P10107	Exosome	AIMVK	GVDEATIIDILTKR	TNAQR	3		515.2950396	1542.861719	0.000451244	33	N	58	72
P10107	Exosome	MVKGV	DEATIIDILTKR	TNAQR	2		694.3937205	1386.771841	0.000451244	11	N	60	72
P10107	Exosome	GERRK	GTDVNVFTTILTSR	SFPHL	2		762.4073593	1522.799119	0.000451244	38	N	214	228
P10107	Exosome	GERRK	GTDVNVFTTILTSR	SFPHL	3		508.6075062	1522.799119	0.002080925	1	N	214	228
P10107	Exosome	AIMVK	GVDEATIIDILTK	RTNAQ	2		694.3881039	1386.760608	0.000451244	61	N	58	71
P10107	Exosome	AIMVK	GVDEATIIDILTK	RTNAQ	3		463.2613359	1386.760608	0.000451244	27	N	58	71
P10107	Exosome	EVLRK	ALTGHLEEVVLAMLK	TPAQF	2		812.4610809	1622.906562	0.000451244	28	N	98	113
P10107	Exosome	EVLRK	ALTGHLEEVVLAMLK	TPAQF	3		541.9766539	1622.906562	0.000451244	44	N	98	113
P10107	Exosome	EVLRK	ALTGHLEEVVLAMLK	TPAQF	3	M13:+15.995	547.3083206	1638.901562	0.000662267	4	N	98	113
P10107	Exosome	RGAMK	GLGTDEDTLIEILTTR	SNEQI	2		873.960153	1745.904706	0.000451244	164	N	128	144
P10107	Exosome	RGAMK	GLGTDEDTLIEILTTR	SNEQI	3		582.9760354	1745.904706	0.000451244	66	N	128	144
P10107	Exosome	AMKGL	GTDEDTLIEILTTR	SNEQI	2		788.9073891	1575.799178	0.002080925	2	N	130	144
P10107	Exosome	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1236.630042	2471.244485	0.000451244	6	N	28	53
P10107	Exosome	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	3		824.7559616	2471.244485	0.000451244	13	N	28	53
P10107	Exosome	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	4		618.8189212	2471.244485	0.000451244	10	N	28	53
P10107	Exosome	KAIMV	KGVDEATIIDILTK	RTNAQ	3		505.9596569	1514.855571	0.000622848	3	N	57	71
P10107	Exosome	RDLAK	DITSDTSGDFRK	ALLAL	2		671.3182098	1340.62082	0.001162105	3	N	166	178
P10107	Exosome	MVKGV	DEATIIDILTK	RTNAQ	2		616.343165	1230.67073	0.000823681	1	N	60	71
P10107	Exosome	YGISL	CQAILDETKGDYEK	ILVAL	3	C1:+57.021	557.2631451	1668.766035	0.002519933	1	N	323	337
P10107	Parental	LALAK	GDRCQDLSVNQDLADTDAR	ALYEA	2	C4:+57.021	1074.982654	2147.949707	0.000451244	84	N	185	204
P10107	Parental	LALAK	GDRCQDLSVNQDLADTDAR	ALYEA	3	C4:+57.021	716.9910357	2147.949707	0.000451244	52	N	185	204
P10107	Parental	KQARF	LENQEQEYVQAVK	SYKGG	2		789.3944489	1576.773298	0.000451244	31	N	13	26
P10107	Parental	RDLAK	DITSDTSGDFR	KALLA	2		607.2707283	1212.525857	0.000451244	82	N	166	177
P10107	Parental	LAMLK	TPAQFDADELR	GAMKG	2		631.8047383	1261.593877	0.000451244	253	N	113	124
P10107	Parental	AKGDR	CQDLSVNQDLADTDAR	ALYEA	2	C1:+39.994	902.3943945	1802.773189	0.000998612	3	N	188	204
P10107	Parental	AKGDR	CQDLSVNQDLADTDAR	ALYEA	2	C1:+57.021	910.9078945	1819.800189	0.000451244	351	N	188	204
P10107	Parental	AKGDR	CQDLSVNQDLADTDAR	ALYEA	3	C1:+57.021	607.607863	1819.800189	0.000451244	24	N	188	204
P10107	Parental	AKGDR	CQDLSVNQDLADTDAR	ALYEA	2	[0:-17.027,C1:+57.021	902.3943945	1802.773189	0.000451244	53	N	188	204
P10107	Parental	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	2		972.5316112	1943.047622	0.000451244	67	N	81	98
P10107	Parental	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	3		648.6903408	1943.047622	0.000451244	120	N	81	98
P10107	Parental	RQQIK	AAYLQENGKPLDEVLRK	ALTGH	4		486.7697056	1943.047622	0.000451244	80	N	81	98
P10107	Parental	TTIVK	CATSTPAFFAEK	LYEAM	2	C1:+57.021	665.3111106	1328.606621	0.000451244	42	N	269	281
P10107	Parental	TTIVK	CATSTPAFFAEK	LYEAM	2	[0:-17.027,C1:+57.021	656.7976106	1311.579621	0.000622848	4	N	269	281
P10107	Parental	HDMNK	ALDLELKGDIEK	CLTTI	2		672.3749965	1342.734393	0.000451244	36	N	250	262
P10107	Parental	HDMNK	ALDLELKGDIEK	CLTTI	3		448.585931	1342.734393	0.000451244	124	N	250	262
P10107	Parental	RQQIK	AAYLQENGKPLDEVLR	KALTG	2		908.4841296	1814.952659	0.000451244	228	N	81	97
P10107	Parental	RQQIK	AAYLQENGKPLDEVLR	KALTG	3		605.9920198	1814.952659	0.000451244	187	N	81	97
P10107	Parental	LKQAR	FLENQEQEYVQAVK	SYKGG	2		862.9286559	1723.841712	0.000451244	234	N	12	26
P10107	Parental	LKQAR	FLENQEQEYVQAVK	SYKGG	3		575.6217039	1723.841712	0.000451244	12	N	12	26

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10107	Parental	EELKR	DLAKDITSDTSGDFR	KALLA	2		820.8922704	1639.768941	0.000451244	50	N	162	177
P10107	Parental	EELKR	DLAKDITSDTSGDFR	KALLA	3		547.5974469	1639.768941	0.000451244	8	N	162	177
P10107	Parental	VQAVK	SYKGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1361.677721	2721.339842	0.000451244	15	N	26	53
P10107	Parental	VQAVK	SYKGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	3		908.1210806	2721.339842	0.000451244	42	N	26	53
P10107	Parental	VQAVK	SYKGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	4		681.3427605	2721.339842	0.000451244	27	N	26	53
P10107	Parental	GDYEK	ILVALCGGN	-	2	C6:+57.021	458.7499604	915.4843208	0.000451244	40	N	337	346
P10107	Parental	VQAVK	SYKGGPGSAVSPYPSFNV	SSDVA	2		907.4419304	1812.868261	0.000622848	2	N	26	44
P10107	Parental	VKSYK	GGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1172.582561	2343.149522	0.000451244	35	N	29	53
P10107	Parental	VKSYK	GGPGSAVSPYPSFNVSSDVAALHK	AIMVK	3		782.0576405	2343.149522	0.000451244	188	N	29	53
P10107	Parental	VKSYK	GGPGSAVSPYPSFNVSSDVAALHK	AIMVK	4		586.7951804	2343.149522	0.002884417	1	N	29	53
P10107	Parental	IMVSR	SEIDMNEIKVFYQK	KYGIS	2		872.4352601	1742.85492	0.00091018	4	N	303	317
P10107	Parental	AGERR	KGTDVNVFTTILTSR	SFPHL	2		826.4548408	1650.894082	0.000451244	13	N	213	228
P10107	Parental	AGERR	KGTDVNVFTTILTSR	SFPHL	3		551.3058272	1650.894082	0.000451244	8	N	213	228
P10107	Parental	YQKKY	GISLCQAILDETKGDYEK	ILVAL	2	C5:+57.021	1020.501628	2038.987656	0.000451244	30	N	319	337
P10107	Parental	YQKKY	GISLCQAILDETKGDYEK	ILVAL	3	C5:+57.021	680.6703519	2038.987656	0.000451244	12	N	319	337
P10107	Parental	FYQKK	YGISLCQAILDETKGDYEK	ILVAL	2	C6:+57.021	1102.033292	2202.050984	0.000451244	104	N	318	337
P10107	Parental	FYQKK	YGISLCQAILDETKGDYEK	ILVAL	3	C6:+57.021	735.0247948	2202.050984	0.000451244	324	N	318	337
P10107	Parental	FYQKK	YGISLCQAILDETK	GDYEK	2	C6:+57.021	805.9086462	1609.801692	0.000451244	26	N	318	332
P10107	Parental	DEVLR	KALTGHLEEVVLAMLK	TPAQF	2		876.5085624	1751.001525	0.000451244	10	N	97	113
P10107	Parental	DEVLR	KALTGHLEEVVLAMLK	TPAQF	3		584.6749749	1751.001525	0.000451244	35	N	97	113
P10107	Parental	AIMVK	GVDEATIIDILTKR	TNAQR	2		772.4386594	1542.861719	0.000451244	115	N	58	72
P10107	Parental	AIMVK	GVDEATIIDILTKR	TNAQR	3		515.2950396	1542.861719	0.000451244	131	N	58	72
P10107	Parental	MVKGV	DEATIIDILTKR	TNAQR	2		694.3937205	1386.771841	0.000451244	15	N	60	72
P10107	Parental	MVKGV	DEATIIDILTKR	TNAQR	3		463.2650804	1386.771841	0.000451244	2	N	60	72
P10107	Parental	GERRK	GTDVNVFTTILTSR	SFPHL	2		762.4073593	1522.799119	0.000451244	59	N	214	228
P10107	Parental	GERRK	GTDVNVFTTILTSR	SFPHL	3		508.6075062	1522.799119	0.000451244	13	N	214	228
P10107	Parental	AIMVK	GVDEATIIDILTK	RTNAQ	2		694.3881039	1386.760608	0.000451244	507	N	58	71
P10107	Parental	AIMVK	GVDEATIIDILTK	RTNAQ	3		463.2613359	1386.760608	0.000451244	60	N	58	71
P10107	Parental	EVLRK	ALTGHLEEVVLAMLK	TPAQF	2		812.4610809	1622.906562	0.000451244	40	N	98	113
P10107	Parental	EVLRK	ALTGHLEEVVLAMLK	TPAQF	3		541.9766539	1622.906562	0.000451244	72	N	98	113
P10107	Parental	EVLRK	ALTGHLEEVVLAMLK	TPAQF	3	M13:+15.995	547.3083206	1638.901562	0.001329271	1	N	98	113
P10107	Parental	RGAMK	GLGTDEDTLIEILTTR	SNEQI	2		873.960153	1745.904706	0.000451244	1072	N	128	144
P10107	Parental	RGAMK	GLGTDEDTLIEILTTR	SNEQI	3		582.9760354	1745.904706	0.000451244	507	N	128	144
P10107	Parental	EVLRK	ALTGHLEEVVLAMLKTPAQFDADELR	GAMKG	3		956.5044261	2866.489878	0.000451244	3	N	98	124
P10107	Parental	EVLRK	ALTGHLEEVVLAMLKTPAQFDADELR	GAMKG	4		717.6302696	2866.489878	0.000451244	2	N	98	124
P10107	Parental	DMNKA	LDLELKGDIEK	CLTTI	2		636.8564395	1271.697279	0.000451244	15	N	251	262
P10107	Parental	DMNKA	LDLELKGDIEK	CLTTI	3		424.906893	1271.697279	0.000451244	1	N	251	262
P10107	Parental	LRKAL	TGHLEEVVLAMLK	TPAQF	2		720.4004919	1438.785384	0.000451244	3	N	100	113
P10107	Parental	AMKGL	GTDEDTLIEILTTR	SNEQI	2		788.9073891	1575.799178	0.000451244	13	N	130	144
P10107	Parental	ARFLE	NQEQEYVQAVK	SYKGG	2		668.3311202	1334.64664	0.001839721	1	N	15	26
P10107	Parental	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	2		1236.630042	2471.244485	0.000451244	9	N	28	53
P10107	Parental	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	3		824.7559616	2471.244485	0.000451244	16	N	28	53
P10107	Parental	AVKSY	KGGPGSAVSPYPSFNVSSDVAALHK	AIMVK	4		618.8189212	2471.244485	0.000451244	12	N	28	53
P10107	Parental	KAIMV	KGVDEATIIDILTK	RTNAQ	2		758.4355854	1514.855571	0.000451244	1	N	57	71
P10107	Parental	KAIMV	KGVDEATIIDILTK	RTNAQ	3		505.9596569	1514.855571	0.000622848	4	N	57	71
P10107	Parental	IMVKG	VDEATIIDILTKR	TNAQR	3		496.287885	1485.840255	0.000735798	4	N	59	72
P10107	Parental	RDLAK	DITSDTSGDFRK	ALLAL	2		671.3182098	1340.62082	0.000622848	43	N	166	178
P10107	Parental	RDLAK	DITSDTSGDFRK	ALLAL	3		447.8814065	1340.62082	0.001463592	1	N	166	178
P10107	Parental	MVKGV	DEATIIDILTK	RTNAQ	2		616.343165	1230.67073	0.000451244	8	N	60	71
P10107	Parental	YGISL	CQAILDETKGDYEK	ILVAL	2	C1:+57.021	835.3908176	1668.766035	0.000451244	20	N	323	337
P10107	Parental	YGISL	CQAILDETKGDYEK	ILVAL	3	C1:+57.021	557.2631451	1668.766035	0.000451244	29	N	323	337
P10107	Parental	LAMLK	TPAQFDADELRGAMK	GLGTD	2		825.4017515	1648.787903	0.000451244	3	N	113	128
P10107	Parental	LAMLK	TPAQFDADELRGAMK	GLGTD	3		550.6037677	1648.787903	0.000451244	5	N	113	128
P10107	Parental	GSAVS	PYPSFNVSSDVAALHK	AIMVK	2		866.4391908	1730.862782	0.000451244	2	N	37	53
P10107	Parental	AVSPY	PSFNVSSDVAALHK	AIMVK	2		736.3811445	1470.746689	0.002519933	2	N	39	53
P10107	Parental	QARFL	ENQEQEYVQAVK	SYKGG	2		732.8524168	1463.689234	0.001699387	1	N	14	26
P10107	Parental	MKGLG	TDEDTLIEILTTR	SNEQI	2		760.3966572	1518.777714	0.00091018	7	N	131	144
P10107	Parental	GISLC	QAILDETKGDYEK	ILVAL	2		755.3757248	1508.73585	0.000998612	1	N	324	337
P10107	Parental	QRQQI	KAAYLQENGKPLDEVLR	KALTG	2		972.5316112	1943.047622	0.000451244	20	N	80	97
P10107	Parental	QRQQI	KAAYLQENGKPLDEVLR	KALTG	3		648.6903408	1943.047622	0.000698008	7	N	80	97
P10107	Parental	QRQQI	KAAYLQENGKPLDEVLR	KALTG	4		486.7697056	1943.047622	0.000823681	1	N	80	97
P10107	Parental	FLKQA	RFLENQEQEYVQAVK	SYKGG	2		940.9792115	1879.942823	0.001591523	2	N	11	26
P10107	Parental	KKYGI	SLCQAILDETKGDYEK	ILVAL	2	C3:+57.021	935.4488639	1868.882128	0.000451244	3	N	321	337
P10107	Parental	KKYGI	SLCQAILDETKGDYEK	ILVAL	3	C3:+57.021	623.9685093	1868.882128	0.001654178	1	N	321	337
P10107	Parental	VFYQK	KYGISLCQAILDETK	GDYEK	3	C7:+57.021	580.3066852	1737.896656	0.000622848	2	N	317	332

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10107	Parental	VKSYK	GGPGSAVSPYPSFNVSSDVAALH	KAIMV	2		1108.535079	2215.054558	0.001839721	4	N	29	52
P10126	Exosome	MGKEK	THINIVVIGHVDSGK	STTTG	2		794.9444433	1587.873287	0.000451244	26	N	5	20
P10126	Exosome	MGKEK	THINIVVIGHVDSGK	STTTG	3		530.2988955	1587.873287	0.000451244	151	N	5	20
P10126	Exosome	QDVYK	IGGIGTVPVGR	VETGV	2		513.3092625	1024.602925	0.000451244	13	N	255	266
P10126	Exosome	NGQTR	EHALLAYTLGVK	QLIVG	2		657.8749666	1313.734333	0.000451244	48	N	134	146
P10126	Exosome	NGQTR	EHALLAYTLGVK	QLIVG	3		438.9192444	1313.734333	0.00091018	3	N	134	146
P10126	Exosome	FETSK	YYVTIIDAPGHRDFIK	NMITG	2		954.5048651	1906.99413	0.002145581	1	N	84	100
P10126	Exosome	FETSK	YYVTIIDAPGHRDFIK	NMITG	3		636.6725101	1906.99413	0.000451244	8	N	84	100
P10126	Exosome	YSQKR	YEEIVKEVSTYIK	KIGYN	3		534.2876621	1599.839586	0.000451244	7	N	166	179
P10126	Exosome	VPVGR	VETGVLKPGMVVTFAPVNVTTEVK	SVEMH	2		1258.196173	2514.376746	0.000451244	7	N	266	290
P10126	Exosome	VPVGR	VETGVLKPGMVVTFAPVNVTTEVK	SVEMH	3		839.1333819	2514.376746	0.000451244	6	N	266	290
P10126	Exosome	VPVGR	VETGVLKPGMVVTFAPVNVTTEVK	SVEMH	3	M10:+15.995	844.4650486	2530.371746	0.000451244	19	N	266	290
P10126	Exosome	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C16:+57.021	1041.555695	3121.643684	0.000451244	22	N	218	247
P10126	Exosome	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	4	C16:+57.021	781.4187209	3121.643684	0.000451244	27	N	218	247
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C15:+57.021	998.8573735	2993.54872	0.000451244	51	N	219	247
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	4	C15:+57.021	749.3949801	2993.54872	0.000451244	27	N	219	247
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLRLPLQDVYK	IGGIG	3	C15:+57.021	1317.701746	3950.081839	0.000622848	16	N	219	255
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLRLPLQDVYK	IGGIG	4	C15:+57.021	988.5282598	3950.081839	0.000451244	24	N	219	255
P10126	Exosome	FETSK	YYVTIIDAPGHR	DFIKN	2		702.8676729	1403.719746	0.000451244	38	N	84	96
P10126	Exosome	FETSK	YYVTIIDAPGHR	DFIKN	3		468.9143819	1403.719746	0.000451244	41	N	84	96
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLRLPLQDVY	KIGGI	3	C15:+57.021	1275.003425	3821.986876	0.000451244	8	N	219	254
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLRLPLQDVY	KIGGI	4	C15:+57.021	956.504519	3821.986876	0.000823681	5	N	219	254
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPL	RLPLQ	3	C15:+57.021	946.8236697	2837.447609	0.000451244	22	N	219	246
P10126	Exosome	RDFIK	NMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	3	C11:+57.021	970.48466	2908.43058	0.000451244	6	N	100	129
P10126	Exosome	RDFIK	NMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	3	M2:+15.995,C11:+57.021	975.8163267	2924.42558	0.000451244	21	N	100	129
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPL	QDVYK	3	C15:+57.021	1106.597671	3316.769613	0.000451244	4	N	219	250
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPL	QDVYK	4	C15:+57.021	830.2002031	3316.769613	0.001463592	1	N	219	250
P10126	Exosome	ETSKY	YVTIIDAPGHR	DFIKN	3		414.5599391	1240.656417	0.001654178	3	N	85	96
P10126	Exosome	QVIIL	NHPGQISAGYAPVLDCHTAHIACK	FAELK	4	C16:+57.021,C23:+57.021	655.0657078	2616.231631	0.000451244	9	N	347	371
P10126	Exosome	EAAGF	TAQVIILNHPGQISAGYAPVLDCHTAHIACK	FAELK	3	C23:+57.021,C30:+57.021	1119.239669	3354.695608	0.002145581	1	N	340	371
P10126	Exosome	EAAGF	TAQVIILNHPGQISAGYAPVLDCHTAHIACK	FAELK	4	C23:+57.021,C30:+57.021	839.6817019	3354.695608	0.001162105	5	N	340	371
P10126	Exosome	KVTRK	DGSASGTTLLEALDCILPPTRPTDK	PLRLP	3	C15:+57.021	876.7780604	2627.310781	0.000451244	5	N	219	244
P10126	Exosome	TYIKK	IGYNPDTVAFVPI	SGWNG	2		703.3722568	1404.728914	0.001395409	2	N	180	193
P10126	Exosome	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPL	RLPLQ	3	C16:+57.021	989.5219908	2965.542572	0.000662267	1	N	218	246
P10126	Exosome	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPL	RLPLQ	4	C16:+57.021	742.3934431	2965.542572	0.000698008	1	N	218	246
P10126	Exosome	TYIKK	IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK	GWKVT	3	M21:+15.995,M28:+15.995	1200.559099	3598.653898	0.000451244	5	N	180	212
P10126	Exosome	PMEAA	GFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	FAELK	3	C25:+57.021,C32:+57.021	1187.269628	3558.785485	0.000451244	1	N	338	371
P10126	Exosome	PKFLK	SGDAAIVDMVPGKPMCVESF	SDYPP	2	M9:+15.995,M15:+15.995,C16:+57.021	1071.48161	2140.94762	0.000622848	2	N	395	415
P10126	Exosome	PKFLK	SGDAAIVDMVPGKPMCVESFSDYPPLGR	FAVRD	3	M9:+15.995,M15:+15.995,C16:+57.021	1009.801829	3026.382087	0.000451244	1	N	395	423
P10126	Parental	MGKEK	THINIVVIGHVDSGK	STTTG	2		794.9444433	1587.873287	0.000451244	37	N	5	20
P10126	Parental	MGKEK	THINIVVIGHVDSGK	STTTG	3		530.2988955	1587.873287	0.000451244	328	N	5	20
P10126	Parental	QDVYK	IGGIGTVPVGR	VETGV	2		513.3092625	1024.602925	0.000451244	25	N	255	266
P10126	Parental	NGQTR	EHALLAYTLGVK	QLIVG	2		657.8749666	1313.734333	0.000451244	33	N	134	146
P10126	Parental	NGQTR	EHALLAYTLGVK	QLIVG	3		438.9192444	1313.734333	0.000662267	42	N	134	146
P10126	Parental	FETSK	YYVTIIDAPGHRDFIK	NMITG	2		954.5048651	1906.99413	0.000451244	9	N	84	100
P10126	Parental	FETSK	YYVTIIDAPGHRDFIK	NMITG	3		636.6725101	1906.99413	0.000662267	8	N	84	100
P10126	Parental	FETSK	YYVTIIDAPGHRDFIK	NMITG	4		477.7563325	1906.99413	0.000979378	1	N	84	100
P10126	Parental	YSQKR	YEEIVKEVSTYIK	KIGYN	3		534.2876621	1599.839586	0.000451244	4	N	166	179
P10126	Parental	VPVGR	VETGVLKPGMVVTFAPVNVTTEVK	SVEMH	2		1258.196173	2514.376746	0.000451244	4	N	266	290
P10126	Parental	VPVGR	VETGVLKPGMVVTFAPVNVTTEVK	SVEMH	3		839.1333819	2514.376746	0.000451244	5	N	266	290
P10126	Parental	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C16:+57.021	1041.555695	3121.643684	0.000451244	21	N	218	247
P10126	Parental	WKVTR	KDGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	4	C16:+57.021	781.4187209	3121.643684	0.000451244	31	N	218	247
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	3	C15:+57.021	998.8573735	2993.54872	0.000451244	48	N	219	247
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLR	LPLQD	4	C15:+57.021	749.3949801	2993.54872	0.000451244	21	N	219	247
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLRLPLQDVYK	IGGIG	3	C15:+57.021	1317.701746	3950.081839	0.000451244	11	N	219	255
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLRLPLQDVYK	IGGIG	4	C15:+57.021	988.5282598	3950.081839	0.000451244	21	N	219	255
P10126	Parental	FETSK	YYVTIIDAPGHR	DFIKN	2		702.8676729	1403.719746	0.000451244	29	N	84	96
P10126	Parental	FETSK	YYVTIIDAPGHR	DFIKN	3		468.9143819	1403.719746	0.000451244	43	N	84	96
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPLQDVY	KIGGI	3	C15:+57.021	1275.003425	3821.986876	0.000451244	12	N	219	254
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPLQDVY	KIGGI	4	C15:+57.021	956.504519	3821.986876	0.000451244	9	N	219	254
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPL	RLPLQ	3	C15:+57.021	946.8236697	2837.447609	0.000451244	8	N	219	246
P10126	Parental	RDFIK	NMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	2	C11:+57.021	1455.22309	2908.43058	0.000622848	2	N	100	129
P10126	Parental	RDFIK	NMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	3	C11:+57.021	970.48466	2908.43058	0.000622848	6	N	100	129

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDKPLRLPL	QDVYK	3	C15:+57.021	1106.597671	3316.769613	0.002813207	1	N	219	250
P10126	Parental	ETSKY	YVTIIDAPGHR	DFIKN	2		621.3360086	1240.656417	0.001264573	2	N	85	96
P10126	Parental	ETSKY	YVTIIDAPGHR	DFIKN	3		414.5599391	1240.656417	0.000451244	36	N	85	96
P10126	Parental	QVIIL	NHPGQISAGYAPVLDCHTAHIACK	FAELK	2	C16:+57.021,C23:+57.021	1309.123616	2616.231631	0.000823681	1	N	347	371
P10126	Parental	QVIIL	NHPGQISAGYAPVLDCHTAHIACK	FAELK	4	C16:+57.021,C23:+57.021	655.0657078	2616.231631	0.000451244	13	N	347	371
P10126	Parental	ETSKY	YVTIIDAPGHRDFIK	NMITG	2		872.9732008	1743.930802	0.000451244	3	N	85	100
P10126	Parental	ETSKY	YVTIIDAPGHRDFIK	NMITG	3		582.3180672	1743.930802	0.002519933	1	N	85	100
P10126	Parental	ETSKY	YVTIIDAPGHRDFIK	NMITG	4		436.9905004	1743.930802	0.000698008	2	N	85	100
P10126	Parental	YSQKR	YEEIVKEVSTY	IKKIG	2		680.3380796	1358.660559	0.000451244	5	N	166	177
P10126	Parental	EAAGF	TAQVIILNHPGQISAGYAPVLDCHTAHIACK	FAELK	3	C23:+57.021,C30:+57.021	1119.239669	3354.695608	0.000451244	16	N	340	371
P10126	Parental	EAAGF	TAQVIILNHPGQISAGYAPVLDCHTAHIACK	FAELK	4	C23:+57.021,C30:+57.021	839.6817019	3354.695608	0.000622848	7	N	340	371
P10126	Parental	SGTTL	LEALDCILPPTRPTDKPLRLPLQDVYK	IGGIG	3	C6:+57.021	1054.584925	3160.731376	0.001162105	5	N	228	255
P10126	Parental	APGHR	DFIKNMITGTSQADCAVLIVAAGVGEFEAGISK	NGQTR	3	C15:+57.021	1138.242788	3411.704964	0.000622848	1	N	96	129
P10126	Parental	MGKEK	THINIVVIGHVDSGKSTTTGHLIYK	CGGID	3		897.4928488	2689.455146	0.000451244	6	N	5	30
P10126	Parental	KVTRK	DGSASGTTLLEALDCILPPTRPTDK	PLRLP	3	C15:+57.021	876.7780604	2627.310781	0.000622848	7	N	219	244
P10126	Parental	SGTTL	LEALDCILPPTRPTDKPLR	LPLQD	3	C6:+57.021	735.7405526	2204.198258	0.001654178	1	N	228	247
P10518	Exosome	GVPSR	VPKDEQGSAADSEDSPTIEAVR	LLRKT	2		1151.046205	2300.07681	0.000451244	4	N	84	106
P10518	Exosome	GVPSR	VPKDEQGSAADSEDSPTIEAVR	LLRKT	3		767.7000701	2300.07681	0.000451244	22	N	84	106
P10518	Exosome	SRVPK	DEQGSAADSEDSPTIEAVR	LLRKT	2		988.9381346	1975.860669	0.000451244	29	N	87	106
P10518	Exosome	RLLRK	TFPSLLVACDVCLCPYTSHGHCGLLSENGAFLAEESR	QRLAE	4	C9:+57.021,C12:+57.021,C14:+57.021,C22:+57.021	1042.731297	4166.893989	0.000634081	2	N	110	147
P10518	Exosome	TAFRR	AGADIIITYFAPQLLK	WLKEE	2		867.4959774	1732.976355	0.000451244	26	N	309	325
P10518	Exosome	TAFRR	AGADIIITYFAPQLLK	WLKEE	3		578.6665849	1732.976355	0.000451244	13	N	309	325
P10518	Exosome	HPLLR	SWQTAASTVSASNLIYPIFVTDVPDDVQPIASLPGVAR	YGVNQ	3		1329.356899	3985.047296	0.000451244	35	N	17	55
P10518	Exosome	HPLLR	SWQTAASTVSASNLIYPIFVTDVPDDVQPIASLPGVAR	YGVNQ	4		997.2696241	3985.047296	0.000451244	24	N	17	55
P10518	Exosome	EAGLR	CVLIFGVPSR	VPKDE	2	C1:+57.021	574.3185416	1146.621483	0.000451244	14	N	74	84
P10518	Exosome	MTAFR	RAGADIIITYFAPQLLK	WLKEE	3		630.7002886	1889.077466	0.000622848	2	N	308	325
P10518	Parental	SRVPK	DEQGSAADSEDSPTIEAVR	LLRKT	2		988.9381346	1975.860669	0.000451244	4	N	87	106
P10518	Parental	HPLLR	SWQTAASTVSASNLIYPIFVTDVPDDVQPIASLPGVAR	YGVNQ	3		1329.356899	3985.047296	0.000451244	8	N	17	55
P10605	Exosome	TFDAR	EQWSNCPTIGQIR	DQGSC	2	C6:+57.021	794.8807544	1587.745909	0.000451244	9	N	87	100
P10605	Exosome	IGQIR	DQGSCGSCWAFGAVEAISDR	TCIHT	2	C5:+57.021,C8:+57.021	1086.957362	2171.899123	0.000451244	22	N	100	120
P10605	Exosome	IGQIR	DQGSCGSCWAFGAVEAISDR	TCIHT	3	C5:+57.021,C8:+57.021	724.9741743	2171.899123	0.000451244	2	N	100	120
P10605	Exosome	HTNGR	VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTKK	GLVSG	3	C13:+57.021,C14:+57.021,C18:+57.021,C22:+57.021	1374.941051	4121.799754	0.000451244	6	N	128	165
P10605	Exosome	NGVPY	WLAANSWNLDWGDNGFFK	ILRGE	2		1070.997936	2139.980271	0.000451244	10	N	293	311
P10605	Exosome	HTNGR	VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTK	KGLVS	3	C13:+57.021,C14:+57.021,C18:+57.021,C22:+57.021	1332.24273	3993.704791	0.000451244	4	N	128	164
P10605	Exosome	AEIYK	NGPVEGAFTVFSDFLTYK	SGVYK	2		996.4916204	1990.967641	0.000451244	35	N	245	263
P10605	Exosome	AEIYK	NGPVEGAFTVFSDFLTYK	SGVYK	3		664.6636802	1990.967641	0.000451244	1	N	245	263
P10605	Exosome	GHAIR	ILGWGVENGVPYWLAANSWNLDWGDNGFFK	ILRGE	3		1142.551315	3424.630545	0.002374549	1	N	281	311
P10605	Exosome	WQAGR	NFYNVDISYLK	KLCGT	2		688.3487817	1374.681963	0.000451244	2	N	45	56
P10605	Exosome	AEIYK	NGPVEGAFTVF	SDFLT	2		569.2829103	1136.550221	0.000823681	3	N	245	256
P10605	Parental	TFDAR	EQWSNCPTIGQIR	DQGSC	2	C6:+57.021	794.8807544	1587.745909	0.000451244	42	N	87	100
P10605	Parental	TFDAR	EQWSNCPTIGQIRDQGSCGSCWAFGAVEAISDR	TCIHT	3	C6:+57.021,C18:+57.021,C21:+57.021	1248.219291	3741.634472	0.000451244	8	N	87	120
P10605	Parental	IGQIR	DQGSCGSCWAFGAVEAISDR	TCIHT	2	C5:+57.021,C8:+57.021	1086.957362	2171.899123	0.000451244	37	N	100	120
P10605	Parental	IGQIR	DQGSCGSCWAFGAVEAISDR	TCIHT	3	C5:+57.021,C8:+57.021	724.9741743	2171.899123	0.000451244	19	N	100	120
P10605	Parental	HTNGR	VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTKK	GLVSG	3	C13:+57.021,C14:+57.021,C18:+57.021,C22:+57.021	1374.941051	4121.799754	0.000451244	17	N	128	165
P10605	Parental	HTNGR	VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTKK	GLVSG	4	C13:+57.021,C14:+57.021,C18:+57.021,C22:+57.021	1031.457739	4121.799754	0.000451244	2	N	128	165
P10605	Parental	NGVPY	WLAANSWNLDWGDNGFFK	ILRGE	2		1070.997936	2139.980271	0.000451244	16	N	293	311
P10605	Parental	HTNGR	VNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWSFWTK	KGLVS	3	C13:+57.021,C14:+57.021,C18:+57.021,C22:+57.021	1332.24273	3993.704791	0.000451244	42	N	128	164
P10605	Parental	AEIYK	NGPVEGAFTVFSDFLTYK	SGVYK	2		996.4916204	1990.967641	0.000451244	45	N	245	263
P10605	Parental	AEIYK	NGPVEGAFTVFSDFLTYK	SGVYK	3		664.6636802	1990.967641	0.000451244	1	N	245	263
P10605	Parental	GHAIR	ILGWGVENGVPYWLAANSWNLDWGDNGFFK	ILRGE	3		1142.551315	3424.630545	0.000451244	15	N	281	311
P10605	Parental	KLPGR	VAFGEDIDLPETFDAREQWSNCPTIGQIR	DQGSC	3	C22:+57.021	1122.20198	3363.58254	0.000735798	1	N	71	100
P10605	Parental	FKILR	GENHCGIESEIVAGIPR	TDQYW	2	C5:+57.021	919.4469899	1836.87838	0.000451244	12	N	314	331
P10605	Parental	YKEDK	HFGYTSYSVSNSVK	EIMAE	2		788.3760591	1574.736518	0.000451244	1	N	223	237
P10639	Exosome	LIESK	EAFQEALAAAGDK	LVVVD	2		660.8256707	1319.635741	0.000451244	18	N	8	21
P10639	Exosome	LIESK	EAFQEALAAAGDKLVVVDFSATWCGPCK	MIKPF	3	C24:+57.021,C27:+57.021	1014.1565	3039.446101	0.000451244	30	N	8	36
P10639	Exosome	LIESK	EAFQEALAAAGDKLVVVDFSATWCGPCK	MIKPF	4	C24:+57.021,C27:+57.021	760.8693252	3039.446101	0.000451244	1	N	8	36
P10639	Exosome	SGANK	EKLEASITEYA	-	2		627.3171472	1252.618694	0.001463592	1	N	94	105
P10639	Exosome	AAGDK	LVVVDFSATWCGPCK	MIKPF	2	C11:+57.021,C14:+57.021	869.9182597	1737.820919	0.000451244	5	N	21	36

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10639	Exosome	NVVFL	EVDVDDCQDVAADCEVK	CMPTF	2	C7:+57.021,C14:+57.021	983.9039289	1965.792258	0.000451244	4	N	55	72
P10639	Parental	LIESK	EAFQEALAAAGDK	LVVVD	2		660.8256707	1319.635741	0.000451244	70	N	8	21
P10639	Parental	DKLVV	VDFSATWCGPCK	MIKPF	2	C8:+57.021,C11:+57.021	714.3078136	1426.600027	0.000451244	7	N	24	36
P10639	Parental	LIESK	EAFQEALAAAGDKLVV	VDFSA	3		544.6266778	1630.856634	0.002453667	1	N	8	24
P10639	Parental	LIESK	EAFQEALAAAGDKLVVVDFSATWCGPCK	MIKPF	3	C24:+57.021,C27:+57.021	1014.1565	3039.446101	0.000451244	323	N	8	36
P10639	Parental	LIESK	EAFQEALAAAGDKLVVVDFSATWCGPCK	MIKPF	4	C24:+57.021,C27:+57.021	760.8693252	3039.446101	0.000451244	3	N	8	36
P10639	Parental	SGANK	EKLEASITEYA	-	2		627.3171472	1252.618694	0.000451244	7	N	94	105
P10639	Parental	AAGDK	LVVVDFSATWCGPCK	MIKPF	2	C11:+57.021,C14:+57.021	869.9182597	1737.820919	0.000451244	1	N	21	36
P10639	Parental	LIESK	EAFQEALAAAGDKLVVVDF	SATWC	2		997.0180023	1992.020405	0.000662267	6	N	8	27
P10639	Parental	LIESK	EAFQEALAAAGDKLVVVDF	SATWC	3		665.0146015	1992.020405	0.000622848	4	N	8	27
P10639	Parental	SLCDK	YSNVVFLEVDVDDCQDVAADCEVK	CMPTF	2	C14:+57.021,C21:+57.021	1395.117724	2788.219849	0.000451244	22	N	48	72
P10639	Parental	SLCDK	YSNVVFLEVDVDDCQDVAADCEVK	CMPTF	3	C14:+57.021,C21:+57.021	930.4144162	2788.219849	0.000451244	177	N	48	72
P10639	Parental	SNVVF	LEVDVDDCQDVAADCEVK	CMPTF	2	C8:+57.021,C15:+57.021	1040.445961	2078.876322	0.002453667	1	N	54	72
P10649	Exosome	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	2		1087.586386	2173.157173	0.001654178	2	N	50	69
P10649	Exosome	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	3		725.3935243	2173.157173	0.000451244	11	N	50	69
P10649	Exosome	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	4		544.2970932	2173.157173	0.000451244	22	N	50	69
P10649	Exosome	DKVTY	VDFLAYDILDQYR	MFEPK	2		815.9097348	1629.80387	0.000451244	9	N	155	168
P10649	Exosome	DKVTY	VDFLAYDILDQYR	MFEPK	3		544.2757565	1629.80387	0.002813207	1	N	155	168
P10649	Exosome	NEKFK	LGLDFPNLPYLIDGSHK	ITQSN	2		950.0046979	1897.993796	0.000698008	5	N	52	69
P10649	Exosome	NEKFK	LGLDFPNLPYLIDGSHK	ITQSN	3		633.6723986	1897.993796	0.000451244	41	N	52	69
P10649	Exosome	FAGDK	VTYVDFLAYDILDQYR	MFEPK	2		997.4994454	1992.983291	0.000451244	22	N	152	168
P10649	Exosome	FAGDK	VTYVDFLAYDILDQYR	MFEPK	3		665.3355636	1992.983291	0.000451244	29	N	152	168
P10649	Exosome	MFEPK	CLDAFPNLR	DFLAR	2	C1:+57.021	553.2768737	1104.538147	0.001871652	1	N	173	182
P10649	Exosome	MFEPK	CLDAFPNLR	DFLAR	2	[0:-17.027,C1:+57.021	544.7633737	1087.511147	0.001264573	3	N	173	182
P10649	Exosome	LNEKF	KLGLDFPNLPYLIDGSHK	ITQSN	3		676.3707197	2026.088759	0.000622848	2	N	51	69
P10649	Parental	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	2		1087.586386	2173.157173	0.000451244	5	N	50	69
P10649	Parental	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	3		725.3935243	2173.157173	0.000451244	13	N	50	69
P10649	Parental	WLNEK	FKLGLDFPNLPYLIDGSHK	ITQSN	4		544.2970932	2173.157173	0.000451244	16	N	50	69
P10649	Parental	DKVTY	VDFLAYDILDQYR	MFEPK	2		815.9097348	1629.80387	0.000451244	18	N	155	168
P10649	Parental	DKVTY	VDFLAYDILDQYR	MFEPK	3		544.2757565	1629.80387	0.000451244	11	N	155	168
P10649	Parental	NEKFK	LGLDFPNLPYLIDGSHK	ITQSN	2		950.0046979	1897.993796	0.000451244	7	N	52	69
P10649	Parental	NEKFK	LGLDFPNLPYLIDGSHK	ITQSN	3		633.6723986	1897.993796	0.000451244	27	N	52	69
P10649	Parental	FAGDK	VTYVDFLAYDILDQYR	MFEPK	2		997.4994454	1992.983291	0.000823681	1	N	152	168
P10649	Parental	MFEPK	CLDAFPNLRDFLAR	FEGLK	3	C1:+57.021	569.9597312	1706.855794	0.001352548	2	N	173	187
P10649	Parental	MFEPK	CLDAFPNLR	DFLAR	2	C1:+57.021	553.2768737	1104.538147	0.001463592	2	N	173	182
P10711	Exosome	AAALR	TGDDYVAIGADEEELGSQIEEAIYQEIR	NTDMK	3		1038.486482	3112.436047	0.000451244	10	N	153	181
P10711	Parental	AAALR	TGDDYVAIGADEEELGSQIEEAIYQEIR	NTDMK	3		1038.486482	3112.436047	0.000451244	10	N	153	181
P10711	Parental	AAALR	TGDDYVAIGADEEELGSQIEEAIY	QEIRN	2		1294.08265	2586.149701	0.000622848	3	N	153	177
P10810	Exosome	CEQVR	VFPALSTLDLSDNPELGER	GLISA	2		1037.029098	2072.042597	0.000451244	21	N	187	206
P10810	Exosome	ELGER	GLISALCPLKFPTLQVLALR	NAGME	3	C7:+57.021	737.4416669	2209.301601	0.000451244	8	N	206	226
P10810	Exosome	FGALR	VLGISGLQELTLENLEVTGTAPPPLLEATGPDLNILNLR	NVSWA	3		1361.086409	4080.235826	0.000451244	13	N	107	146
P10810	Exosome	FGALR	VLGISGLQELTLENLEVTGTAPPPLLEATGPDLNILNLR	NVSWA	4		1021.066756	4080.235826	0.001591523	1	N	107	146
P10810	Exosome	SWATR	DAWLAELQQWLKPGLK	VLSIA	2		948.5230578	1895.030516	0.000622848	1	N	153	169
P10810	Exosome	SWATR	DAWLAELQQWLKPGLK	VLSIA	3		632.6846386	1895.030516	0.000622848	7	N	153	169
P10810	Exosome	GLPAK	LSVLDLSYNR	LDRNP	2		590.3225669	1178.629534	0.001463592	1	N	292	302
P10810	Parental	CEQVR	VFPALSTLDLSDNPELGER	GLISA	2		1037.029098	2072.042597	0.000451244	32	N	187	206
P10810	Parental	ELGER	GLISALCPLKFPTLQVLALR	NAGME	3	C7:+57.021	737.4416669	2209.301601	0.000451244	14	N	206	226
P10810	Parental	FGALR	VLGISGLQELTLENLEVTGTAPPPLLEATGPDLNILNLR	NVSWA	3		1361.086409	4080.235826	0.000998612	6	N	107	146
P10810	Parental	SWATR	DAWLAELQQWLKPGLK	VLSIA	2		948.5230578	1895.030516	0.001264573	1	N	153	169
P10810	Parental	EYLLK	RVDTEADLGQFTDIIK	SLSLK	3		607.6516632	1819.93159	0.001871652	2	N	67	83
P10852	Exosome	DHLLR	LYQLLLFTLPGTPVFSYGDELGLQGALPGQPAK	APLMP	3		1168.632864	3502.875192	0.000451244	1	N	345	378
P10852	Exosome	ATKMK	EALSSWLQDGVDGFQFR	DVGKL	2		977.9688437	1953.922087	0.000451244	5	N	225	242
P10852	Exosome	GRSAR	LGASNLPAGISLPASAK	LLLST	2		783.9466516	1565.877703	0.001463592	2	N	470	487
P10852	Exosome	ETDLK	QINPTLGSQEDFKDLLQSAK	KKSIH	3		744.7222579	2231.143374	0.000451244	3	N	171	191
P10852	Exosome	ARQSR	EEDTSLKLENLSLNPYEGLLLQFPFVA	-	3		1027.201177	3078.580132	0.001943752	1	N	499	526
P10852	Parental	DHLLR	LYQLLLFTLPGTPVFSYGDELGLQGALPGQPAK	APLMP	3		1168.632864	3502.875192	0.000451244	12	N	345	378
P10852	Parental	RGKER	SLLHGDFHALSSSPDLFSYIR	HWDQN	2		1181.595471	2361.175342	0.001395409	1	N	427	448
P10852	Parental	RGKER	SLLHGDFHALSSSPDLFSYIR	HWDQN	3		788.0662475	2361.175342	0.001162105	1	N	427	448
P10852	Parental	ATKMK	EALSSWLQDGVDGFQFR	DVGKL	2		977.9688437	1953.922087	0.000451244	12	N	225	242
P10852	Parental	GRSAR	LGASNLPAGISLPASAK	LLLST	2		783.9466516	1565.877703	0.001264573	1	N	470	487
P10852	Parental	ETDLK	QINPTLGSQEDFKDLLQSAK	KKSIH	3		744.7222579	2231.143374	0.002813207	1	N	171	191
P10852	Parental	ARQSR	EEDTSLKLENLSLNPYEGLLLQFPFVA	-	3		1027.201177	3078.580132	0.000662267	1	N	499	526
P10852	Parental	SAKKK	SIHIILDLTPNYQGQNAWFLPAQADIVATK	MKEAL	3		1113.25802	3336.75066	0.002374549	1	N	193	223
P10853	Exosome	GISSK	AMGIMNSFVNDIFER	IASEA	2		872.4138052	1742.81201	0.000451244	47	N	58	73
P10853	Exosome	GISSK	AMGIMNSFVNDIFER	IASEA	3		581.9451368	1742.81201	0.000451244	5	N	58	73

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P10853	Exosome	GISSK	AMGIMNSFVNDIFER	IASEA	2	M2:+15.995	880.4113052	1758.80701	0.000451244	44	N	58	73
P10853	Exosome	GISSK	AMGIMNSFVNDIFER	IASEA	2	M2:+15.995,M5:+15.995	888.4088052	1774.80201	0.000451244	8	N	58	73
P10853	Exosome	GISSK	AMGIMNSFVNDIFER	IASEA	2	M5:+15.995	880.4113052	1758.80701	0.000451244	7	N	58	73
P10853	Exosome	RKRSR	KESYSVYVYK	VLKQV	2		633.3247752	1264.63395	0.000622848	46	N	34	44
P10853	Exosome	SSKAM	GIMNSFVNDIFER	IASEA	2		771.3750054	1540.734411	0.000451244	13	N	60	73
P10853	Exosome	ISSKA	MGIMNSFVNDIFER	IASEA	3	M1:+15.995,M4:+15.995	568.9294322	1703.764897	0.002813207	3	N	59	73
P10853	Exosome	AMGIM	NSFVNDIFER	IASEA	2		620.8019986	1239.588397	0.000698008	27	N	63	73
P10853	Exosome	KRSRK	ESYSVYVYK	VLKQV	2		569.2772936	1136.538987	0.000622848	14	N	35	44
P10853	Exosome	LKQVH	PDTGISSKAMGIMNSFVNDIFER	IASEA	3	M10:+15.995	849.0741147	2544.198944	0.001463592	1	N	50	73
P10853	Exosome	MGIMN	SFVNDIFER	IASEA	2		563.7805348	1125.54547	0.002884417	2	N	64	73
P10853	Parental	TITSR	EIQTAVRLLLPGELAK	HAVSE	2		876.0254334	1750.035267	0.00091018	4	N	93	109
P10853	Parental	TITSR	EIQTAVRLLLPGELAK	HAVSE	3		584.3528889	1750.035267	0.000451244	5	N	93	109
P10853	Parental	GISSK	AMGIMNSFVNDIFER	IASEA	2		872.4138052	1742.81201	0.000451244	16	N	58	73
P10853	Parental	SSKAM	GIMNSFVNDIFER	IASEA	2		771.3750054	1540.734411	0.001943752	1	N	60	73
P10853	Parental	AMGIM	NSFVNDIFER	IASEA	2		620.8019986	1239.588397	0.001229886	2	N	63	73
P10853	Parental	KAMGI	MNSFVNDIFER	IASEA	2		686.3222415	1370.628883	0.001352548	1	N	62	73
P11031	Exosome	WSQLK	EQISDIDDAVR	KL-	2		630.8074779	1259.599356	0.000451244	24	N	114	125
P11031	Exosome	KPGRK	GISLNMEQWSQLKEQISDIDDAVR	KL-	3		925.7926356	2774.354507	0.000451244	5	N	101	125
P11031	Exosome	KPGRK	GISLNMEQWSQLKEQISDIDDAVR	KL-	2	M6:+15.995	1396.182553	2790.349507	0.001162105	2	N	101	125
P11031	Exosome	KPGRK	GISLNMEQWSQLKEQISDIDDAVR	KL-	3	M6:+15.995	931.1243023	2790.349507	0.000451244	22	N	101	125
P11031	Exosome	SSSSR	DDNMFQIGK	MRYVS	2	M4:+15.995	542.2429711	1082.470342	0.002981883	1	N	59	68
P11031	Parental	WSQLK	EQISDIDDAVR	KL-	2		630.8074779	1259.599356	0.000622848	5	N	114	125
P11152	Exosome	KKVNR	ITGLDPAGPNFEYAEAPSR	LSPDD	2		1002.987233	2003.958867	0.000451244	8	N	178	197
P11152	Exosome	EAPSR	LSPDDADFVDVLHTFTR	GSPGR	2		974.4765016	1946.937403	0.000451244	5	N	197	214
P11152	Exosome	ALYKR	EPDSNVIVVDWLYR	AQQHY	2		852.9337412	1703.851882	0.002296037	1	N	102	116
P11247	Exosome	ISLPR	IICDNTGITTVSK	NNIFM	2	C3:+57.021	711.3691568	1420.722714	0.000451244	90	N	675	688
P11247	Exosome	AKLNR	QNQIVVDEIRER	LFEQV	2		749.9027754	1497.789951	0.000998612	2	N	533	545
P11247	Exosome	AKLNR	QNQIVVDEIRER	LFEQV	3		500.2711169	1497.789951	0.000451244	17	N	533	545
P11247	Exosome	TTVSK	NNIFMSNTYPR	DFVSC	2	M5:+15.995	686.8199086	1371.624217	0.000451244	41	N	688	699
P11247	Exosome	ALTSF	VDASGVYGSEDPLAR	KLRNL	2		768.3709738	1534.726348	0.000451244	14	N	310	325
P11247	Exosome	SVDPR	IANVFTNAFR	YGHTL	2		576.8121693	1151.608739	0.000451244	64	N	463	473
P11247	Exosome	FSFFT	GLNCETSCLQQPPCFPLK	IPPND	2	C4:+57.021,C8:+57.021,C14:+57.021	1074.997212	2147.978825	0.000451244	31	N	251	269
P11247	Exosome	SFFTG	LNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C3:+57.021,C7:+57.021,C13:+57.021	961.1313663	2880.370699	0.000622848	9	N	252	276
P11247	Exosome	FASWR	VVLEGGIDPILR	GLMAT	2		640.8827917	1279.749983	0.000451244	55	N	510	522
P11247	Exosome	FSFFT	GLNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C4:+57.021,C8:+57.021,C14:+57.021	980.1385209	2937.392163	0.001463592	1	N	251	276
P11247	Exosome	YNAWR	RFCGLPQPSTVGELGTVLK	NLELA	2	C3:+57.021	1030.054165	2058.09273	0.000451244	22	N	577	596
P11247	Exosome	YNAWR	RFCGLPQPSTVGELGTVLK	NLELA	3	C3:+57.021	687.0387099	2058.09273	0.000451244	35	N	577	596
P11247	Exosome	EQVMR	IGLDLPALNMQR	SRDHG	2		670.8719016	1339.728203	0.000637154	12	N	552	564
P11247	Exosome	NAWRR	FCGLPQPSTVGELGTVLK	NLELA	2	C2:+57.021	952.0036093	1901.991619	0.000451244	65	N	578	596
P11247	Exosome	NAWRR	FCGLPQPSTVGELGTVLK	NLELA	3	C2:+57.021	635.0050062	1901.991619	0.000451244	12	N	578	596
P11247	Exosome	FRKLR	DGDRFWWENPGVFSK	QQRQA	2		920.4266147	1838.837629	0.001839721	2	N	647	662
P11247	Exosome	FRKLR	DGDRFWWENPGVFSK	QQRQA	3		613.9536765	1838.837629	0.000451244	6	N	647	662
P11247	Exosome	NITIR	NQINALTSFVDASGVYGSEDPLARK	LRNLT	3		884.7808355	2651.319106	0.000451244	27	N	301	326
P11247	Exosome	RDGDR	FWWENPGVFSK	QQRQA	2		698.8383841	1395.661168	0.000451244	44	N	651	662
P11247	Exosome	RAFVR	WLPAEYEDGVSMPFGWTPGVNR	NGFKV	2	M12:+15.995	1262.584289	2523.152979	0.000451244	75	N	171	193
P11247	Exosome	RAFVR	WLPAEYEDGVSMPFGWTPGVNR	NGFKV	3	M12:+15.995	842.058793	2523.152979	0.000451244	49	N	171	193
P11247	Exosome	EPNGR	VGQLLACLIGTQFR	KLRDG	2	C7:+57.021	788.4377082	1574.859816	0.000451244	72	N	630	644
P11247	Exosome	EPNGR	VGQLLACLIGTQFR	KLRDG	3	C7:+57.021	525.9610721	1574.859816	0.000451244	44	N	630	644
P11247	Exosome	RTAVR	AADYLHVALDLLK	RKLQP	3		481.2736873	1440.797662	0.000451244	4	N	88	101
P11247	Exosome	NITIR	NQINALTSFVDASGVYGSEDPLAR	KLRNL	2		1262.619872	2523.224143	0.000451244	115	N	301	325
P11247	Exosome	NITIR	NQINALTSFVDASGVYGSEDPLAR	KLRNL	3		842.0825144	2523.224143	0.000451244	47	N	301	325
P11247	Exosome	SKQQR	QALASISLPR	IICDN	2		528.3145448	1054.61349	0.000451244	16	N	665	675
P11247	Exosome	SFFTG	LNCETSCLQQPPCFPLK	IPPND	2	C3:+57.021,C7:+57.021,C13:+57.021	1046.486481	2090.957361	0.000451244	42	N	252	269
P11247	Exosome	EPNGR	VGQLLACLIGTQF	RKLRD	2	C7:+57.021	710.3871526	1418.758705	0.000622848	2	N	630	643
P11247	Exosome	QINAL	TSFVDASGVYGSEDPLAR	KLRNL	2		935.9450343	1869.874469	0.000451244	12	N	307	325
P11247	Exosome	EPNGR	VGQLLACLIGTQFRK	LRDGD	2	C7:+57.021	852.4851897	1702.954779	0.000451244	7	N	630	645
P11247	Exosome	ESIKR	SLQSGSASPTELLFYFK	QPVAG	2		937.9808885	1873.946177	0.000451244	18	N	60	77
P11247	Exosome	AKLNR	QNQIVVDEIR	ERLFE	2		607.3309232	1212.646246	0.000451244	45	N	533	543
P11247	Exosome	AKLNR	QNQIVVDEIR	ERLFE	2	[0:-17.027	598.8174232	1195.619246	0.001871652	1	N	533	543
P11247	Exosome	NRSAR	IPCFLAGDMR	SSEMP	2	C3:+57.021,M9:+15.995	598.2838847	1194.552169	0.000451244	16	N	369	379
P11247	Exosome	IITYR	DYLPLVLGPAAMK	KYLPQ	2	M12:+15.995	702.3843532	1402.753106	0.001591523	3	N	434	447

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P11247	Exosome	NTYPR	DFVSCNTLPK	LNLTS	2	C5:+57.021	590.7872713	1179.558943	0.000979378	6	N	699	709
P11247	Exosome	EPATR	FSFFTGLNCETSCLQQPPCFPLK	IPPND	2	C9:+57.021,C13:+57.021,C19:+57.021	1389.639687	2777.263774	0.000622848	4	N	246	269
P11247	Exosome	EPATR	FSFFTGLNCETSCLQQPPCFPLK	IPPND	3	C9:+57.021,C13:+57.021,C19:+57.021	926.7623913	2777.263774	0.000451244	7	N	246	269
P11247	Exosome	LPAEY	EDGVSMPFGWTPGVNR	NGFKV	2	M6:+15.995	882.9047011	1763.793802	0.000451244	5	N	177	193
P11247	Exosome	RALMF	MQWGQFLDHDITLTPEPATR	FSFFT	3		786.0517214	2355.131764	0.001839721	1	N	226	246
P11247	Exosome	DPRIK	NQKDCIPFFR	SCPAC	3	C5:+57.021	442.2207747	1323.638924	0.002080925	2	N	278	288
P11247	Exosome	RTAVR	AADYLHVALDLLKR	KLQPL	3		533.307391	1596.898773	0.000451244	4	N	88	102
P11247	Exosome	RAFVR	WLPAEYEDGVSMPF	GWTPG	2	M12:+15.995	828.8667216	1655.717843	0.000451244	3	N	171	185
P11247	Exosome	ALMFM	QWGQFLDHDITLTPEPATR	FSFFT	2		1113.053439	2224.091278	0.001839721	2	N	227	246
P11247	Parental	ISLPR	IICDNTGITTVSK	NNIFM	2	C3:+57.021	711.3691568	1420.722714	0.000451244	114	N	675	688
P11247	Parental	AKLNR	QNQIVVDEIRER	LFEQV	2		749.9027754	1497.789951	0.000451244	3	N	533	545
P11247	Parental	AKLNR	QNQIVVDEIRER	LFEQV	3		500.2711169	1497.789951	0.000451244	16	N	533	545
P11247	Parental	TTVSK	NNIFMSNTYPR	DFVSC	2	M5:+15.995	686.8199086	1371.624217	0.000451244	60	N	688	699
P11247	Parental	ALTSF	VDASGVYGSEDPLAR	KLRNL	2		768.3709738	1534.726348	0.000451244	38	N	310	325
P11247	Parental	ISLPR	IICDNTGITTVSKNNIFMSNTYPR	DFVSC	2	C3:+57.021,M18:+15.995	1388.175985	2774.336371	0.000662267	5	N	675	699
P11247	Parental	ISLPR	IICDNTGITTVSKNNIFMSNTYPR	DFVSC	3	C3:+57.021,M18:+15.995	925.7865903	2774.336371	0.000451244	11	N	675	699
P11247	Parental	SVDPR	IANVFTNAFR	YGHTL	2		576.8121693	1151.608739	0.000451244	44	N	463	473
P11247	Parental	FSFFT	GLNCETSCLQQPPCFPLK	IPPND	2	C4:+57.021,C8:+57.021,C14:+57.021	1074.997212	2147.978825	0.000451244	65	N	251	269
P11247	Parental	SFFTG	LNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C3:+57.021,C7:+57.021,C13:+57.021	961.1313663	2880.370699	0.000451244	26	N	252	276
P11247	Parental	FASWR	VVLEGGIDPILR	GLMAT	2		640.8827917	1279.749983	0.000451244	63	N	510	522
P11247	Parental	FSFFT	GLNCETSCLQQPPCFPLKIPPNDPR	IKNQK	3	C4:+57.021,C8:+57.021,C14:+57.021	980.1385209	2937.392163	0.000451244	51	N	251	276
P11247	Parental	YNAWR	RFCGLPQPSTVGELGTVLK	NLELA	2	C3:+57.021	1030.054165	2058.09273	0.000451244	4	N	577	596
P11247	Parental	YNAWR	RFCGLPQPSTVGELGTVLK	NLELA	3	C3:+57.021	687.0387099	2058.09273	0.000451244	23	N	577	596
P11247	Parental	EQVMR	IGLDLPALNMQR	SRDHG	2		670.8719016	1339.728203	0.002884417	1	N	552	564
P11247	Parental	NRAFV	RWLPAEYEDGVSMPFGWTPGVNR	NGFKV	3	M13:+15.995	894.0924967	2679.25409	0.000451244	3	N	170	193
P11247	Parental	NAWRR	FCGLPQPSTVGELGTVLK	NLELA	2	C2:+57.021	952.0036093	1901.991619	0.000451244	82	N	578	596
P11247	Parental	NAWRR	FCGLPQPSTVGELGTVLK	NLELA	3	C2:+57.021	635.0050062	1901.991619	0.001264573	3	N	578	596
P11247	Parental	FRKLR	DGDRFWWENPGVFSK	QQRQA	2		920.4266147	1838.837629	0.000451244	6	N	647	662
P11247	Parental	FRKLR	DGDRFWWENPGVFSK	QQRQA	3		613.9536765	1838.837629	0.000451244	8	N	647	662
P11247	Parental	NITIR	NQINALTSFVDASGVYGSEDPLARK	LRNLT	2		1326.667353	2651.319106	0.000451244	7	N	301	326
P11247	Parental	NITIR	NQINALTSFVDASGVYGSEDPLARK	LRNLT	3		884.7808355	2651.319106	0.000451244	16	N	301	326
P11247	Parental	RDGDR	FWWENPGVFSK	QQRQA	2		698.8383841	1395.661168	0.000451244	38	N	651	662
P11247	Parental	RAFVR	WLPAEYEDGVSMPFGWTPGVNR	NGFKV	2		1254.586789	2507.157979	0.000451244	2	N	171	193
P11247	Parental	RAFVR	WLPAEYEDGVSMPFGWTPGVNR	NGFKV	2	M12:+15.995	1262.584289	2523.152979	0.000451244	56	N	171	193
P11247	Parental	RAFVR	WLPAEYEDGVSMPFGWTPGVNR	NGFKV	3	M12:+15.995	842.058793	2523.152979	0.000451244	34	N	171	193
P11247	Parental	EPNGR	VGQLLACLIGTQFR	KLRDG	2	C7:+57.021	788.4377082	1574.859816	0.000451244	61	N	630	644
P11247	Parental	EPNGR	VGQLLACLIGTQFR	KLRDG	3	C7:+57.021	525.9610721	1574.859816	0.000451244	41	N	630	644
P11247	Parental	RTAVR	AADYLHVALDLLK	RKLQP	3		481.2736873	1440.797662	0.000451244	6	N	88	101
P11247	Parental	NITIR	NQINALTSFVDASGVYGSEDPLAR	KLRNL	2		1262.619872	2523.224143	0.000451244	119	N	301	325
P11247	Parental	NITIR	NQINALTSFVDASGVYGSEDPLAR	KLRNL	3		842.0825144	2523.224143	0.000451244	27	N	301	325
P11247	Parental	SKQQR	QALASISLPR	IICDN	2		528.3145448	1054.61349	0.000622848	28	N	665	675
P11247	Parental	SFFTG	LNCETSCLQQPPCFPLK	IPPND	2	C3:+57.021,C7:+57.021,C13:+57.021	1046.486481	2090.957361	0.000451244	44	N	252	269
P11247	Parental	EPNGR	VGQLLACLIGTQF	RKLRD	2	C7:+57.021	710.3871526	1418.758705	0.000622848	19	N	630	643
P11247	Parental	QINAL	TSFVDASGVYGSEDPLAR	KLRNL	2		935.9450343	1869.874469	0.000451244	25	N	307	325
P11247	Parental	NAWRR	FCGLPQPSTVGELGTVLKNLELAR	KLMAQ	2	C2:+57.021	1300.199546	2598.383493	0.001162105	1	N	578	602
P11247	Parental	NAWRR	FCGLPQPSTVGELGTVLKNLELAR	KLMAQ	3	C2:+57.021	867.1356309	2598.383493	0.0025889	1	N	578	602
P11247	Parental	EPNGR	VGQLLACLIGTQFRK	LRDGD	2	C7:+57.021	852.4851897	1702.954779	0.000622848	1	N	630	645
P11247	Parental	ESIKR	SLQSGSASPTELLFYFK	QPVAG	2		937.9808885	1873.946177	0.001395409	4	N	60	77
P11247	Parental	NAWRR	FCGLPQPSTVGELGTVL	KNLEL	2	C2:+57.021	887.9561278	1773.896656	0.000451244	5	N	578	595
P11247	Parental	AKLNR	QNQIVVDEIR	ERLFE	2		607.3309232	1212.646246	0.000451244	22	N	533	543
P11247	Parental	LPAEY	EDGVSMPFGWTPGVNR	NGFKV	2	M6:+15.995	882.9047011	1763.793802	0.000451244	14	N	177	193
P11247	Parental	VPLAR	QVSNAIVRFPNDQLTK	DQERA	2		915.4975714	1828.979543	0.00091018	4	N	202	218
P11247	Parental	RALMF	MQWGQFLDHDITLTPEPATR	FSFFT	2		1178.573682	2355.131764	0.000451244	8	N	226	246
P11247	Parental	RALMF	MQWGQFLDHDITLTPEPATR	FSFFT	3		786.0517214	2355.131764	0.000451244	4	N	226	246
P11247	Parental	DPRIK	NQKDCIPFFR	SCPAC	2	C5:+57.021	662.8272621	1323.638924	0.001943752	1	N	278	288
P11247	Parental	RTAVR	AADYLHVALDLLKR	KLQPL	3		533.307391	1596.898773	0.000698008	2	N	88	102
P11247	Parental	RTAVR	AADYLHVALDLLKR	KLQPL	4		400.2324933	1596.898773	0.000451244	2	N	88	102
P11247	Parental	RAFVR	WLPAEYEDGVSMPF	GWTPG	2	M12:+15.995	828.8667216	1655.717843	0.001699387	2	N	171	185
P11247	Parental	ISLPR	IICDNTGITTVSKN	NIFMS	2	C3:+57.021	768.3906206	1534.765641	0.002813207	1	N	675	689

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P11247	Parental	QWGQF	LDHDITLTPEPATR	FSFFT	2		789.9102661	1577.804932	0.001463592	1	N	232	246
P11352	Exosome	LNSLK	YVRPGGGFEPNFTLFEK	CEVNG	2		979.4944974	1956.973395	0.000451244	16	N	95	112
P11352	Exosome	LNSLK	YVRPGGGFEPNFTLFEK	CEVNG	3		653.3322649	1956.973395	0.000451244	18	N	95	112
P11352	Exosome	MCAAR	LSAAAQSTVYAFSARPLTGGEPVSLGSLR	GKVLL	3		969.5177227	2905.529768	0.000451244	40	N	5	34
P11352	Exosome	SRRFR	TIDIEPDIETLLSQQSGNS	-	2		1030.505653	2058.995706	0.000451244	32	N	182	201
P11352	Exosome	SRRFR	TIDIEPDIETLLSQQSGNS	-	3		687.3397021	2058.995706	0.000451244	18	N	182	201
P11352	Exosome	RLGPR	GLVVLGFPCNQFGHQENGKNEEILNSLK	YVRPG	3	C9:+57.021	1047.864751	3140.570853	0.000451244	16	N	67	95
P11352	Exosome	RLGPR	GLVVLGFPCNQFGHQENGKNEEILNSLK	YVRPG	4	C9:+57.021	786.1505132	3140.570853	0.000451244	24	N	67	95
P11352	Exosome	WNFEK	FLVGPDGVPVR	RYSRR	2		578.3301949	1154.64479	0.00091018	4	N	164	175
P11352	Exosome	AFSAR	PLTGGEPVSLGSLR	GKVLL	2		691.8860627	1381.756525	0.000451244	2	N	20	34
P11352	Exosome	FTFLR	NALPTPSDDPTALMTDPK	YIIWS	2		942.4569208	1882.898242	0.001763695	1	N	128	146
P11352	Exosome	FTFLR	NALPTPSDDPTALMTDPK	YIIWS	2	M14:+15.995	950.4544208	1898.893242	0.000451244	1	N	128	146
P11352	Exosome	MTDPK	YIIWSPVCR	NDIAW	2	C8:+57.021	597.3107166	1192.605833	0.002080925	1	N	146	155
P11352	Exosome	QSTVY	AFSARPLTGGEPVSLGSLR	GKVLL	3		639.0185689	1914.032307	0.001162105	2	N	15	34
P11352	Parental	LNSLK	YVRPGGGFEPNFTLFEK	CEVNG	2		979.4944974	1956.973395	0.000451244	11	N	95	112
P11352	Parental	LNSLK	YVRPGGGFEPNFTLFEK	CEVNG	3		653.3322649	1956.973395	0.000451244	27	N	95	112
P11352	Parental	MCAAR	LSAAAQSTVYAFSARPLTGGEPVSLGSLR	GKVLL	2		1453.772684	2905.529768	0.002981883	1	N	5	34
P11352	Parental	MCAAR	LSAAAQSTVYAFSARPLTGGEPVSLGSLR	GKVLL	3		969.5177227	2905.529768	0.000451244	31	N	5	34
P11352	Parental	RYSRR	FRTIDIEPDIETLLSQQSGNS	-	2		1182.090416	2362.165231	0.000451244	16	N	180	201
P11352	Parental	SRRFR	TIDIEPDIETLLSQQSGNS	-	2		1030.505653	2058.995706	0.000451244	27	N	182	201
P11352	Parental	SRRFR	TIDIEPDIETLLSQQSGNS	-	3		687.3397021	2058.995706	0.000979378	9	N	182	201
P11352	Parental	RLGPR	GLVVLGFPCNQFGHQENGKNEEILNSLK	YVRPG	3	C9:+57.021	1047.864751	3140.570853	0.001699387	1	N	67	95
P11352	Parental	RLGPR	GLVVLGFPCNQFGHQENGKNEEILNSLK	YVRPG	4	C9:+57.021	786.1505132	3140.570853	0.000622848	6	N	67	95
P11352	Parental	AFSAR	PLTGGEPVSLGSLR	GKVLL	2		691.8860627	1381.756525	0.000622848	2	N	20	34
P11352	Parental	MCAAR	LSAAAQSTVYAFSAR	PLTGG	2		771.8997014	1541.783803	0.001654178	1	N	5	20
P11499	Exosome	GRGTK	VILHLKEDQTEYLEER	RVKEV	2		1008.026359	2014.037117	0.0007646	1	Y	180	196
P11499	Exosome	GRGTK	VILHLKEDQTEYLEER	RVKEV	3		672.3535058	2014.037117	0.000451244	3	Y	180	196
P11499	Exosome	EIFLR	ELISNASDALDKIR	YESLT	2		772.9180912	1543.820582	0.000622848	1	Y	41	55
P11499	Exosome	EIFLR	ELISNASDALDKIR	YESLT	3		515.6146608	1543.820582	0.001352548	1	Y	41	55
P11499	Exosome	PIWTR	NPDDITQEEYGEFYK	SLTND	2		924.4026679	1846.789736	0.000451244	41	N	291	306
P11499	Exosome	IGMTK	ADLINNLGTIAK	SGTKA	2		621.8567739	1241.697948	0.000451244	20	Y	95	107
P11499	Exosome	LVVLL	FETALLSSGFSLEDPQTHSNR	IYRMI	3		779.3771502	2335.108051	0.000451244	7	N	658	679
P11499	Exosome	YRMIK	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	MEEVD	3		1179.220242	3534.637326	0.000451244	18	N	685	719
P11499	Exosome	DKAVK	DLVVLLFETALLSSGFSLEDPQTHSNR	IYRMI	3		996.849138	2987.524014	0.000451244	19	N	652	679
P11499	Exosome	EVVKK	HSQFIGYPITLYLEK	EREKE	3		603.6580894	1807.950868	0.000823681	8	N	204	219
P11499	Exosome	YRMIK	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASRMEEVD	-	3	M35:+15.995	1385.625585	4153.853355	0.001871652	1	N	685	724
P11499	Exosome	HLAVK	HFSVEGQLEFR	ALLFI	2		674.8363727	1347.657145	0.000622848	4	Y	319	330
P11499	Exosome	GEFYK	SLTNDWEDHLAVK	HFSVE	2		764.3760591	1526.736518	0.000622848	1	N	306	319
P11499	Exosome	VVITK	HNDDEQYAWESSAGGSFTVR	ADHGE	2		1128.483575	2254.95155	0.001264573	1	Y	148	168
P11499	Exosome	TGESK	EQVANSAFVER	VRKRG	2		625.3127305	1248.609861	0.001162105	2	N	491	502
P11499	Exosome	MMAKK	HLEINPDHPIVETLR	QKAEA	3		594.9886096	1781.942429	0.000451244	2	N	624	639
P11499	Parental	YMMAK	KHLEINPDHPIVETLR	QKAEA	2		956.026496	1910.037392	0.000451244	7	N	623	639
P11499	Parental	YMMAK	KHLEINPDHPIVETLR	QKAEA	3		637.6869307	1910.037392	0.000451244	8	N	623	639
P11499	Parental	YMMAK	KHLEINPDHPIVETLR	QKAEA	4		478.517148	1910.037392	0.000451244	10	N	623	639
P11499	Parental	GRGTK	VILHLKEDQTEYLEER	RVKEV	2		1008.026359	2014.037117	0.000451244	10	Y	180	196
P11499	Parental	EIFLR	ELISNASDALDKIR	YESLT	2		772.9180912	1543.820582	0.000451244	36	Y	41	55
P11499	Parental	EIFLR	ELISNASDALDKIR	YESLT	3		515.6146608	1543.820582	0.000451244	10	Y	41	55
P11499	Parental	EIFLR	ELISNASDALDKIR	YESLT	3	[0:-18.011	509.6109941	1525.809582	0.000735798	1	Y	41	55
P11499	Parental	KETQK	SIYYITGESKEQVANSAFVER	VRKRG	2		1196.095501	2390.175402	0.000451244	15	N	481	502
P11499	Parental	KETQK	SIYYITGESKEQVANSAFVER	VRKRG	3		797.732934	2390.175402	0.000451244	12	N	481	502
P11499	Parental	PIWTR	NPDDITQEEYGEFYK	SLTND	2		924.4026679	1846.789736	0.000451244	45	N	291	306
P11499	Parental	IGMTK	ADLINNLGTIAK	SGTKA	2		621.8567739	1241.697948	0.000451244	31	Y	95	107
P11499	Parental	EVVKK	HSQFIGYPITLYLEKER	EKEIS	3		698.7059909	2093.094573	0.000451244	4	N	204	221
P11499	Parental	LVVLL	FETALLSSGFSLEDPQTHSNR	IYRMI	2		1168.561825	2335.108051	0.000451244	23	N	658	679
P11499	Parental	LVVLL	FETALLSSGFSLEDPQTHSNR	IYRMI	3		779.3771502	2335.108051	0.000451244	29	N	658	679
P11499	Parental	TISNR	LVSSPCCIVTSTYGWTANMER	IMKAQ	2	C6:+57.021,C7:+57.021	1216.555855	2431.09611	0.000823681	7	N	583	604
P11499	Parental	YRMIK	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	MEEVD	3		1179.220242	3534.637326	0.000451244	56	N	685	719
P11499	Parental	DKNDK	AVKDLVVLLFETALLSSGFSLEDPQTHSNR	IYRMI	3		1096.249302	3285.724505	0.000451244	7	N	649	679
P11499	Parental	DKNDK	AVKDLVVLLFETALLSSGFSLEDPQTHSNR	IYRMI	4		822.4389263	3285.724505	0.000451244	4	N	649	679
P11499	Parental	DKAVK	DLVVLLFETALLSSGFSLEDPQTHSNR	IYRMI	3		996.849138	2987.524014	0.000451244	75	N	652	679
P11499	Parental	EVVKK	HSQFIGYPITLYLEK	EREKE	3		603.6580894	1807.950868	0.000451244	12	N	204	219
P11499	Parental	YRMIK	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASRMEEVD	-	3		1380.293918	4137.858355	0.000451244	7	N	685	724
P11499	Parental	RGTKV	ILHLKEDQTEYLEER	RVKEV	3		639.3307011	1914.968703	0.000451244	2	Y	181	196
P11499	Parental	HLAVK	HFSVEGQLEFR	ALLFI	2		674.8363727	1347.657145	0.000451244	1	Y	319	330
P11499	Parental	HLAVK	HFSVEGQLEFR	ALLFI	3		450.2268485	1347.657145	0.001654178	2	Y	319	330

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P11499	Parental	GEFYK	SLTNDWEDHLAVK	HFSVE	2		764.3760591	1526.736518	0.000451244	2	N	306	319
P11499	Parental	GEFYK	SLTNDWEDHLAVK	HFSVE	3		509.9199727	1526.736518	0.000451244	9	N	306	319
P11499	Parental	VVITK	HNDDEQYAWESSAGGSFTVR	ADHGE	2		1128.483575	2254.95155	0.000451244	25	Y	148	168
P11499	Parental	VVITK	HNDDEQYAWESSAGGSFTVR	ADHGE	3		752.6583166	2254.95155	0.000451244	3	Y	148	168
P11499	Parental	NPQER	TLTLVDTGIGMTKADLINNLGTIAK	SGTKA	3		858.4793293	2572.414588	0.000451244	5	N	82	107
P11499	Parental	LYVRR	VFIMDSCDELIPEYLNFIR	GVVDS	2	C7:+57.021	1187.576813	2373.138026	0.000622848	4	N	359	378
P11499	Parental	YGEFY	KSLTNDWEDHLAVK	HFSVE	3		552.6182938	1654.831481	0.0007646	3	N	305	319
P11499	Parental	KIKEK	YIDQEELNKTKPIWTR	NPDDI	2		1017.536894	2033.058187	0.000451244	7	Y	275	291
P11499	Parental	KIKEK	YIDQEELNKTKPIWTR	NPDDI	3		678.6938624	2033.058187	0.000451244	5	Y	275	291
P11499	Parental	EELNK	TKPIWTRNPDDITQEEYGEFYK	SLTND	2		1365.656454	2729.297308	0.000622848	2	N	284	306
P11499	Parental	EELNK	TKPIWTRNPDDITQEEYGEFYK	SLTND	3		910.7735694	2729.297308	0.002374549	1	N	284	306
P11499	Parental	RVRKR	GFEVVYMTEPIDEYCVQQLK	EFDGK	2	C15:+57.021	1224.57701	2447.13842	0.001352548	1	N	506	526
P11499	Parental	MMAKK	HLEINPDHPIVETLR	QKAEA	2		891.9790145	1781.942429	0.000451244	7	N	624	639
P11499	Parental	MMAKK	HLEINPDHPIVETLR	QKAEA	3		594.9886096	1781.942429	0.000451244	12	N	624	639
P11499	Parental	LDKIR	YESLTDPSKLDSGK	ELKID	2		770.3810071	1538.746414	0.000451244	13	Y	55	69
P11499	Parental	LDKIR	YESLTDPSKLDSGK	ELKID	3		513.9232714	1538.746414	0.002981883	1	Y	55	69
P11499	Parental	IYRMI	KLGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	MEEVD	3		1221.918563	3662.732289	0.000451244	2	N	684	719
P11499	Parental	KETQK	SIYYITGESK	EQVAN	2		580.7958506	1159.576101	0.001591523	2	N	481	491
P11672	Exosome	QFRGR	WYVVGLAGNAVQK	KTEGS	2		702.8858657	1403.756131	0.000451244	75	N	50	63
P11672	Exosome	TRFAK	SLGLKDDNIIFSVPTDQCIDN	-	2	C18:+57.021	1182.573313	2363.131026	0.000451244	49	N	179	200
P11672	Exosome	TRFAK	SLGLKDDNIIFSVPTDQCIDN	-	3	C18:+57.021	788.7181419	2363.131026	0.000451244	19	N	179	200
P11672	Exosome	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2		1275.682275	2549.34895	0.000451244	7	N	20	43
P11672	Exosome	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	3		850.7907833	2549.34895	0.000823681	3	N	20	43
P11672	Exosome	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2	Q1:-17.027	1267.168775	2532.32195	0.000451244	46	N	20	43
P11672	Exosome	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	3	Q1:-17.027	845.1151166	2532.32195	0.000451244	45	N	20	43
P11672	Exosome	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2	[0:-17.027	1267.168775	2532.32195	0.000451244	13	N	20	43
P11672	Exosome	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	3	[0:-17.027	845.1151166	2532.32195	0.001395409	3	N	20	43
P11672	Exosome	TQNLI	PAPSLLTVPLQPDFR	SDQFR	2		825.9648444	1649.914089	0.000622848	5	N	28	43
P11672	Exosome	GNMHR	YPQVQSYNVQVATTDYNQF	AMVFF	2		1133.027087	2264.038574	0.000451244	2	N	121	140
P11672	Exosome	AQDST	QNLIPAPSLLTVPLQPDFR	SDQFR	2	Q1:-17.027	1051.586161	2101.156722	0.001329271	1	N	24	43
P11672	Parental	QFRGR	WYVVGLAGNAVQKK	TEGSF	2		766.9333472	1531.851094	0.000451244	61	N	50	64
P11672	Parental	QFRGR	WYVVGLAGNAVQKK	TEGSF	3		511.6248315	1531.851094	0.000451244	80	N	50	64
P11672	Parental	SDQFR	GRWYVVGLAGNAVQK	KTEGS	2		809.4471531	1616.878706	0.000451244	7	N	48	63
P11672	Parental	SDQFR	GRWYVVGLAGNAVQK	KTEGS	3		539.9673688	1616.878706	0.000823681	6	N	48	63
P11672	Parental	QFRGR	WYVVGLAGNAVQK	KTEGS	2		702.8858657	1403.756131	0.000451244	492	N	50	63
P11672	Parental	QFRGR	WYVVGLAGNAVQK	KTEGS	3		468.9265104	1403.756131	0.000451244	33	N	50	63
P11672	Parental	TRFAK	SLGLKDDNIIFSVPTDQCIDN	-	2	C18:+57.021	1182.573313	2363.131026	0.000451244	645	N	179	200
P11672	Parental	TRFAK	SLGLKDDNIIFSVPTDQCIDN	-	3	C18:+57.021	788.7181419	2363.131026	0.000451244	84	N	179	200
P11672	Parental	QSQAQ	DSTQNLIPAPSLLTVPLQPDFR	SDQFR	2		1211.652986	2421.290372	0.000823681	7	N	21	43
P11672	Parental	QSQAQ	DSTQNLIPAPSLLTVPLQPDFR	SDQFR	3		808.1045908	2421.290372	0.000451244	7	N	21	43
P11672	Parental	GNMHR	YPQVQSYNVQVATTDYNQFAMVFFR	KTSEN	3		1006.148642	3015.422527	0.000451244	21	N	121	146
P11672	Parental	GVLQS	QAQDSTQNLIPAPSLLTVPLQPDFR	SDQFR	3	Q1:-17.027	911.4803471	2731.417641	0.001352548	1	N	18	43
P11672	Parental	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2		1275.682275	2549.34895	0.000622848	12	N	20	43
P11672	Parental	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2	Q1:-17.027	1267.168775	2532.32195	0.000451244	531	N	20	43
P11672	Parental	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	3	Q1:-17.027	845.1151166	2532.32195	0.000451244	382	N	20	43
P11672	Parental	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	2	[0:-17.027	1267.168775	2532.32195	0.000451244	93	N	20	43
P11672	Parental	LQSQA	QDSTQNLIPAPSLLTVPLQPDFR	SDQFR	3	[0:-17.027	845.1151166	2532.32195	0.000451244	32	N	20	43
P11672	Parental	TQNLI	PAPSLLTVPLQPDFR	SDQFR	2		825.9648444	1649.914089	0.000622848	24	N	28	43
P11672	Parental	DSTQN	LIPAPSLLTVPLQPDFR	SDQFR	2		939.0489085	1876.082217	0.000451244	3	N	26	43
P11672	Parental	QDSTQ	NLIPAPSLLTVPLQPDFR	SDQFR	2		996.0703723	1990.125145	0.000451244	15	N	25	43
P11672	Parental	STQNL	IPAPSLLTVPLQPDFR	SDQFR	2		882.5068764	1762.998153	0.000451244	14	N	27	43
P11672	Parental	NLIPA	PSLLTVPLQPDFR	SDQFR	2		741.9199055	1481.824211	0.000823681	3	N	30	43
P11672	Parental	GNMHR	YPQVQSYNVQVATTDYNQF	AMVFF	2		1133.027087	2264.038574	0.000451244	26	N	121	140
P11672	Parental	KSLGL	KDDNIIFSVPTDQCIDN	-	2	C14:+57.021	997.4625026	1992.909405	0.000451244	14	N	183	200
P11672	Parental	VPSSR	AGQFTLGNMHRYPQVQSY	NVQVA	3	M9:+15.995	705.0027304	2111.984791	0.001463592	3	N	110	128
P11672	Parental	FAKSL	GLKDDNIIFSVPTDQCIDN	-	2	C16:+57.021	1082.515267	2163.014933	0.000451244	8	N	181	200
P11672	Parental	SLGLK	DDNIIFSVPTDQCIDN	-	2	C13:+57.021	933.4150211	1864.814442	0.000622848	14	N	184	200
P11672	Parental	AQDST	QNLIPAPSLLTVPLQPDFR	SDQFR	2		1060.099661	2118.183722	0.000451244	9	N	24	43
P11672	Parental	AQDST	QNLIPAPSLLTVPLQPDFR	SDQFR	3		707.0690407	2118.183722	0.000451244	4	N	24	43
P11672	Parental	QVQSY	NVQVATTDYNQFAMVFFR	KTSEN	2		1076.020554	2150.025508	0.000451244	1	N	128	146
P11680	Exosome	GRDIR	VEDCCLNAAYAFQEHDGGLCQACR	SPQWS	2	C4:+57.021,C5:+57.021,C20:+57.021,C23:+57.021	1422.582874	2843.150149	0.00091018	1	N	48	72
P11680	Exosome	GRDIR	VEDCCLNAAYAFQEHDGGLCQACR	SPQWS	3	C4:+57.021,C5:+57.021,C20:+57.021,C23:+57.021	948.7245163	2843.150149	0.000451244	60	N	48	72
P11680	Exosome	VEEKR	SCLHVPVCKDPEEK	KP-	4	C2:+57.021,C8:+57.021	425.2053869	1696.790348	0.000622848	3	N	448	462

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P11680	Exosome	PATGS	DPVLCFTQYEESSGR	CKGLL	2	C5:+57.021	894.399174	1786.782748	0.000451244	10	N	23	38
P11680	Parental	GLLGR	DIRVEDCCLNAAYAFQEHDGGLCQACR	SPQWS	4	C7:+57.021,C8:+57.021,C23:+57.021,C26:+57.021	807.8483668	3227.362267	0.000451244	5	N	45	72
P11680	Parental	GRDIR	VEDCCLNAAYAFQEHDGGLCQACR	SPQWS	3	C4:+57.021,C5:+57.021,C20:+57.021,C23:+57.021	948.7245163	2843.150149	0.000451244	32	N	48	72
P11835	Exosome	RHVLK	LTDNSNQFQTEVGK	QLISG	2		790.8817056	1579.747811	0.000451244	62	N	210	224
P11835	Exosome	VSSCR	DCIQSGPGCSWCQK	LNFTG	2	C2:+57.021,C9:+57.021,C12:+57.021	841.839452	1681.663304	0.000451244	37	N	35	49
P11835	Exosome	NMYKR	SNEFDYPSVGQLAHK	LSESN	2		846.4053479	1690.795096	0.000451244	27	N	296	311
P11835	Exosome	NMYKR	SNEFDYPSVGQLAHK	LSESN	3		564.6061653	1690.795096	0.0007646	6	N	296	311
P11835	Exosome	SSIGK	SRGDCDGVQINNPVTFQVK	VMASE	2	C5:+57.021	1067.521218	2133.026835	0.000451244	37	N	396	415
P11835	Exosome	SFVIR	ALGFTDTVTVQVRPQCECQCR	DQSRE	2	C16:+57.021,C18:+57.021,C20:+57.021	1263.088153	2524.160706	0.000735798	3	N	430	451
P11835	Exosome	SFVIR	ALGFTDTVTVQVRPQCECQCR	DQSRE	3	C16:+57.021,C18:+57.021,C20:+57.021	842.3947019	2524.160706	0.000451244	81	N	430	451
P11835	Exosome	KLSSR	VFLDHSTLPDTLK	VTYDS	3		495.9369637	1484.787491	0.000451244	23	N	367	380
P11835	Exosome	EIIPK	SAVGELSDDSSNVVQLIK	NAYYK	2		930.9816168	1859.947634	0.000451244	30	N	340	358
P11835	Exosome	EIIPK	SAVGELSDDSSNVVQLIK	NAYYK	3		620.9903445	1859.947634	0.00091018	6	N	340	358
P11835	Exosome	PCKER	DSEGCWITYTLQQK	DGRNI	2	C5:+57.021	864.8988098	1727.78202	0.000451244	23	N	667	681
P11835	Exosome	PCKER	DSEGCWITYTLQQK	DGRNI	3	C5:+57.021	576.9351399	1727.78202	0.000451244	8	N	667	681
P11835	Exosome	RNVTR	LLVFATDDGFHFAGDGK	LGAIL	2		905.4444731	1808.873346	0.000451244	33	N	258	275
P11835	Exosome	RNVTR	LLVFATDDGFHFAGDGK	LGAIL	3		603.9655821	1808.873346	0.000451244	36	N	258	275
P11835	Exosome	TESGR	IGFGSFVDKTVLPFVNTHPEK	LRNPC	3		778.0832384	2331.226315	0.000451244	15	N	166	187
P11835	Exosome	TESGR	IGFGSFVDKTVLPFVNTHPEK	LRNPC	4		583.8143788	2331.226315	0.000451244	17	N	166	187
P11835	Exosome	LNNVK	KLGGDLLQALNEITESGR	IGFGS	2		957.5187008	1913.021802	0.000451244	14	N	148	166
P11835	Exosome	LNNVK	KLGGDLLQALNEITESGR	IGFGS	3		638.6817339	1913.021802	0.000451244	14	N	148	166
P11835	Exosome	NNVKK	LGGDLLQALNEITESGR	IGFGS	2		893.4712192	1784.926838	0.000451244	47	N	149	166
P11835	Exosome	NNVKK	LGGDLLQALNEITESGR	IGFGS	3		595.9834128	1784.926838	0.000451244	5	N	149	166
P11835	Exosome	TEVGK	QLISGNLDAPEGGLDAIMQVAACPEEIGWR	NVTRL	3	C23:+57.021	1070.857157	3209.54807	0.000451244	23	N	224	254
P11835	Exosome	QLAHK	LSESNIQPIFAVTK	KMVKT	2		773.9279275	1545.840255	0.000735798	7	N	311	325
P11835	Exosome	PDTLK	VTYDSFCSNGASSIGK	SRGDC	2	C7:+57.021	846.8806171	1691.745634	0.000451244	61	N	380	396
P11835	Exosome	IGKSR	GDCDGVQINNPVTFQVK	VMASE	2	C3:+57.021	945.9546477	1889.893695	0.000451244	25	N	398	415
P11835	Exosome	CQCNR	CICDEGYQPPMCEDCPSCGSHCR	DNHTS	2	C1:+57.021,C3:+57.021,M11:+15.995,C12:+57.021,C15:+57.021,C18:+57.021,C22:+57.021	1446.006551	2889.997502	0.000735798	2	N	601	624
P11835	Exosome	CQCNR	CICDEGYQPPMCEDCPSCGSHCR	DNHTS	3	C1:+57.021,C3:+57.021,M11:+15.995,C12:+57.021,C15:+57.021,C18:+57.021,C22:+57.021	964.3403007	2889.997502	0.000451244	82	N	601	624
P11835	Exosome	TFQVK	VMASECIQEQSFVIR	ALGFT	2	M2:+15.995,C6:+57.021	906.9349126	1811.854225	0.000451244	51	N	415	430
P11835	Exosome	QKDGR	NIYNIHVEDSLECVKGPNVAA	IVGGT	2	C13:+57.021	1171.57619	2341.13678	0.000451244	19	N	684	705
P11835	Exosome	QKDGR	NIYNIHVEDSLECVKGPNVAA	IVGGT	3	C13:+57.021	781.3867266	2341.13678	0.000622848	6	N	684	705
P11835	Exosome	QKDGR	NIYNIHVEDSLECVK	GPNVA	2	C13:+57.021	916.9462914	1831.876983	0.002080925	2	N	684	699
P11835	Exosome	TESGR	IGFGSFVDK	TVLPF	2		485.2561642	968.4967284	0.001352548	2	N	166	175
P11835	Exosome	IMDPR	SIANPEFDQR	GQRKQ	2		588.7863485	1175.557097	0.0025889	1	N	83	93
P11835	Exosome	DVPNK	EIFGQYCECDNVNCER	YNSQV	2	C7:+57.021,C9:+57.021,C14:+57.021	1046.911334	2091.807068	0.000451244	15	N	528	544
P11835	Exosome	RALGF	TDTVTVQVRPQCECQCR	DQSRE	3	C12:+57.021,C14:+57.021,C16:+57.021	712.9910167	2135.94965	0.001329271	2	N	434	451
P11835	Parental	RHVLK	LTDNSNQFQTEVGK	QLISG	2		790.8817056	1579.747811	0.000451244	37	N	210	224
P11835	Parental	VSSCR	DCIQSGPGCSWCQK	LNFTG	2	C2:+57.021,C9:+57.021,C12:+57.021	841.839452	1681.663304	0.000451244	33	N	35	49
P11835	Parental	NMYKR	SNEFDYPSVGQLAHK	LSESN	2		846.4053479	1690.795096	0.000451244	12	N	296	311
P11835	Parental	NMYKR	SNEFDYPSVGQLAHK	LSESN	3		564.6061653	1690.795096	0.000451244	22	N	296	311
P11835	Parental	SSIGK	SRGDCDGVQINNPVTFQVK	VMASE	2	C5:+57.021	1067.521218	2133.026835	0.000451244	23	N	396	415
P11835	Parental	SSIGK	SRGDCDGVQINNPVTFQVK	VMASE	3	C5:+57.021	712.016745	2133.026835	0.000451244	4	N	396	415
P11835	Parental	SFVIR	ALGFTDTVTVQVRPQCECQCR	DQSRE	2	C16:+57.021,C18:+57.021,C20:+57.021	1263.088153	2524.160706	0.001329271	2	N	430	451
P11835	Parental	SFVIR	ALGFTDTVTVQVRPQCECQCR	DQSRE	3	C16:+57.021,C18:+57.021,C20:+57.021	842.3947019	2524.160706	0.000451244	36	N	430	451
P11835	Parental	KLSSR	VFLDHSTLPDTLK	VTYDS	2		743.4015456	1484.787491	0.000451244	1	N	367	380
P11835	Parental	KLSSR	VFLDHSTLPDTLK	VTYDS	3		495.9369637	1484.787491	0.000451244	8	N	367	380
P11835	Parental	KKPCK	ERDSEGCWITYTLQQK	DGRNI	2	C7:+57.021	1007.470662	2012.925724	0.000451244	3	N	665	681
P11835	Parental	EIIPK	SAVGELSDDSSNVVQLIK	NAYYK	2		930.9816168	1859.947634	0.000451244	28	N	340	358
P11835	Parental	PCKER	DSEGCWITYTLQQK	DGRNI	2	C5:+57.021	864.8988098	1727.78202	0.000451244	25	N	667	681
P11835	Parental	PCKER	DSEGCWITYTLQQK	DGRNI	3	C5:+57.021	576.9351399	1727.78202	0.000451244	2	N	667	681

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P11835	Parental	RNVTR	LLVFATDDGFHFAGDGK	LGAIL	2		905.4444731	1808.873346	0.000622848	4	N	258	275
P11835	Parental	RNVTR	LLVFATDDGFHFAGDGK	LGAIL	3		603.9655821	1808.873346	0.000451244	39	N	258	275
P11835	Parental	TESGR	IGFGSFVDKTVLPFVNTHPEK	LRNPC	3		778.0832384	2331.226315	0.000451244	11	N	166	187
P11835	Parental	TESGR	IGFGSFVDKTVLPFVNTHPEK	LRNPC	4		583.8143788	2331.226315	0.000622848	12	N	166	187
P11835	Parental	KLSSR	VFLDHSTLPDTLKVTYDSFCSNGASSIGK	SRGDC	3	C20:+57.021	1053.848655	3158.522565	0.000451244	5	N	367	396
P11835	Parental	LNNVK	KLGGDLLQALNEITESGR	IGFGS	2		957.5187008	1913.021802	0.000451244	11	N	148	166
P11835	Parental	LNNVK	KLGGDLLQALNEITESGR	IGFGS	3		638.6817339	1913.021802	0.000451244	20	N	148	166
P11835	Parental	NVKKL	GGDLLQALNEITESGR	IGFGS	2		836.9291872	1671.842774	0.000451244	7	N	150	166
P11835	Parental	NNVKK	LGGDLLQALNEITESGR	IGFGS	2		893.4712192	1784.926838	0.000451244	32	N	149	166
P11835	Parental	NNVKK	LGGDLLQALNEITESGR	IGFGS	3		595.9834128	1784.926838	0.000451244	3	N	149	166
P11835	Parental	TEVGK	QLISGNLDAPEGGLDAIMQVAACPEEIGWR	NVTRL	3	C23:+57.021	1070.857157	3209.54807	0.000451244	8	N	224	254
P11835	Parental	QLAHK	LSESNIQPIFAVTK	KMVKT	2		773.9279275	1545.840255	0.000451244	14	N	311	325
P11835	Parental	PDTLK	VTYDSFCSNGASSIGK	SRGDC	2	C7:+57.021	846.8806171	1691.745634	0.000451244	29	N	380	396
P11835	Parental	NNVKK	LGGDLLQALNEITESGRIGFGSFVDK	TVLPF	3		912.8121356	2735.413007	0.000823681	1	N	149	175
P11835	Parental	IGKSR	GDCDGVQINNPVTFQVK	VMASE	2	C3:+57.021	945.9546477	1889.893695	0.000622848	1	N	398	415
P11835	Parental	IMDPR	SIANPEFDQR	GQRKQ	2		588.7863485	1175.557097	0.00091018	4	N	83	93
P11835	Parental	DVPNK	EIFGQYCECDNVNCER	YNSQV	2	C7:+57.021,C9:+57.021,C14:+57.021	1046.911334	2091.807068	0.000451244	10	N	528	544
P11835	Parental	DTLKV	TYDSFCSNGASSIGK	SRGDC	2	C6:+57.021	797.34641	1592.67722	0.000823681	1	N	381	396
P11835	Parental	AGDGK	LGAILTPNDGR	CHLED	2		563.814909	1125.614218	0.001229886	1	N	275	286
P11835	Parental	AFRHV	LKLTDNSNQFQTEVGK	QLISG	2		911.4712192	1820.926838	0.000451244	2	N	208	224
P11835	Parental	QLAHK	LSESNIQPIFAVTKK	MVKTY	3		558.9862061	1673.935218	0.000622848	1	N	311	326
P11835	Parental	SSIGK	SRGDCDGVQINNPVTF	QVKVM	2	C5:+57.021	889.9102402	1777.80488	0.000451244	2	N	396	412
P11983	Exosome	AEFAR	SLLVIPNTLAVNAAQDSTDLVAK	LRAFH	2		1177.152819	2352.290038	0.000451244	41	N	443	466
P11983	Exosome	AEFAR	SLLVIPNTLAVNAAQDSTDLVAK	LRAFH	3		785.1044793	2352.290038	0.000451244	3	N	443	466
P11983	Exosome	HPAAK	VLCELADLQDKEVGDGTTSVVIIAAELLK	NADEL	3	C3:+57.021	1033.888339	3098.641618	0.000451244	26	N	73	102
P11983	Exosome	HPAAK	VLCELADLQDKEVGDGTTSVVIIAAELLK	NADEL	4	C3:+57.021	775.6682045	3098.641618	0.000823681	1	N	73	102
P11983	Exosome	VGLDK	MLVDDIGDVTITNDGATILK	LLEVE	2		1052.546267	2103.076935	0.000870037	1	N	43	63
P11983	Exosome	VKSLK	FATEAAITILR	IDDLI	2		603.3485847	1204.681569	0.000622848	3	N	515	526
P11983	Exosome	KEAVR	YINENLIINTDELGR	DCLIN	2		888.9604874	1775.905375	0.001463592	1	N	130	145
P11983	Exosome	ERIQK	ILATGANVILTTGGIDDMYLK	YFVEA	2	M18:+15.995	1098.085602	2194.155605	0.001654178	1	N	277	298
P11983	Parental	AEFAR	SLLVIPNTLAVNAAQDSTDLVAK	LRAFH	2		1177.152819	2352.290038	0.000451244	32	N	443	466
P11983	Parental	AEFAR	SLLVIPNTLAVNAAQDSTDLVAK	LRAFH	3		785.1044793	2352.290038	0.000451244	13	N	443	466
P11983	Parental	HPAAK	VLCELADLQDKEVGDGTTSVVIIAAELLK	NADEL	3	C3:+57.021	1033.888339	3098.641618	0.000451244	28	N	73	102
P11983	Parental	HPAAK	VLCELADLQDKEVGDGTTSVVIIAAELLK	NADEL	4	C3:+57.021	775.6682045	3098.641618	0.000823681	2	N	73	102
P11983	Parental	VGLDK	MLVDDIGDVTITNDGATILK	LLEVE	2		1052.546267	2103.076935	0.001699387	3	N	43	63
P11983	Parental	KEAVR	YINENLIINTDELGRDCLINAAK	TSMSS	2	C17:+57.021	1331.679175	2661.34275	0.000622848	5	N	130	153
P11983	Parental	SMGSR	EQLAIAEFAR	SLLVI	2		574.3094595	1146.603319	0.000451244	3	N	433	443
P12023	Exosome	CIGTK	EGILQYCQEVYPELQITNVVEANQPVTIQNWCK	RGRKQ	3	C7:+57.021,C32:+57.021	1321.980249	3962.917347	0.000451244	39	N	66	99
P12023	Exosome	VIPYR	CLVGEFVSDALLVPDKCK	FLHQE	3	C1:+57.021,C17:+57.021	684.0166518	2049.026555	0.000698008	3	N	116	134
P12023	Exosome	VIPYR	CLVGEFVSDALLVPDK	CKFLH	2	C1:+57.021	881.4585033	1760.901407	0.000451244	4	N	116	132
P12023	Parental	CIGTK	EGILQYCQEVYPELQITNVVEANQPVTIQNWCKR	GRKQC	3	C7:+57.021,C32:+57.021	1374.013953	4119.018459	0.000451244	9	N	66	100
P12023	Parental	CIGTK	EGILQYCQEVYPELQITNVVEANQPVTIQNWCKR	GRKQC	4	C7:+57.021,C32:+57.021	1030.762415	4119.018459	0.000622848	2	N	66	100
P12023	Parental	CIGTK	EGILQYCQEVYPELQITNVVEANQPVTIQNWCK	RGRKQ	3	C7:+57.021,C32:+57.021	1321.980249	3962.917347	0.000451244	32	N	66	99
P12023	Parental	VIPYR	CLVGEFVSDALLVPDKCK	FLHQE	2	[0:-	1017.007578	2031.999555	0.000622848	1	N	116	134
P12023	Parental	AMISR	WYFDVTEGK	CVPFF	2		572.7696358	1143.523672	0.001591523	1	N	306	315
P12023	Parental	VIPYR	CLVGEFVSDALLVPDK	CKFLH	2	C1:+57.021	881.4585033	1760.901407	0.000451244	7	N	116	132
P12023	Parental	HFQEK	VESLEQEAANER	QQLVE	2		687.8289417	1373.642283	0.00091018	1	N	438	450
P12023	Parental	GILQY	CQEVYPELQITNVVEANQPVTIQNWCK	RGRKQ	3	C1:+57.021,C26:+57.021	1087.528885	3259.563256	0.000622848	3	N	72	99
P12023	Parental	LSLLY	NVPAVAEEIQDEVDELLQK	EQNYS	2		1070.044945	2138.074291	0.002453667	1	N	549	568
P12246	Exosome	EYTVK	APPSIVLGQEQDNYGGGFQR	SQSFV	2		1067.022139	2132.028678	0.000451244	59	N	146	166
P12246	Exosome	LFVYR	DSPVNPNILNWQALNYEINGYVVIRPR	VWD-	3		1052.219788	3153.635965	0.002884417	1	N	194	221
P12265	Exosome	SMYPK	GYFVQDTSFDFFNYAGLHR	SVVLY	3		762.0206381	2283.038514	0.001162105	11	N	196	215
P12265	Exosome	EAALR	DFIGWVWYER	EAILP	2		685.8305591	1369.645518	0.000622848	18	N	93	103
P12265	Exosome	ADISK	LVQSGPLTTCR	ITIAI	2	C10:+57.021	616.327095	1230.63859	0.002981883	1	N	155	166
P12265	Exosome	ENWYK	THQKPIIQSEYGADAIPGIHEDPPR	MFSEE	3		923.803863	2768.388189	0.000451244	10	N	526	551
P12265	Exosome	ANSFR	TSHYPYSEEVLQLCDR	YGIVV	2	C14:+57.021	998.9573874	1995.899175	0.000451244	3	N	378	394
P12265	Exosome	ANSFR	TSHYPYSEEVLQLCDR	YGIVV	3	C14:+57.021	666.307525	1995.899175	0.002080925	1	N	378	394
P12265	Exosome	ITHTK	ALDLTRPVTFVSNAK	YDADL	2		816.4599262	1630.904252	0.001229886	2	N	467	482
P12265	Exosome	ITHTK	ALDLTRPVTFVSNAK	YDADL	3		544.6425508	1630.904252	0.000451244	9	N	467	482
P12265	Exosome	EEYQK	AVLENYHSVLDQK	RKEYV	2		758.3942519	1514.772904	0.0007646	5	N	559	572
P12265	Exosome	DIRGK	GFDWPLLVK	DFNLL	2		537.8032816	1073.590963	0.000698008	1	N	355	364
P12382	Exosome	ANIFR	NEWGSLLEELVK	EGKIS	2		708.8726209	1415.729642	0.000451244	11	N	129	141
P12382	Exosome	TREGR	LAAAYNLLQHGITNLCVIGGDGSLTGANIFR	NEWGS	3	C16:+57.021	1077.231434	3228.670901	0.000451244	2	N	98	129
P12382	Parental	ANIFR	NEWGSLLEELVK	EGKIS	2		708.8726209	1415.729642	0.001162105	5	N	129	141

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P12382	Parental	TREGR	LAAAYNLLQHGITNLCVIGGDGSLTGANIFR	NEWGS	3	C16:+57.021	1077.231434	3228.670901	0.001871652	5	N	98	129
P12787	Exosome	AGPHK	EIYPYVIQELRPTLNELGISTPEELGLDKV	-	3		1143.612017	3427.812652	0.000451244	13	N	116	146
P12787	Parental	EFDAR	WVTYFNKPDIDAWELRK	GMNTL	2		1091.060536	2180.105472	0.000451244	11	N	51	68
P12787	Parental	EFDAR	WVTYFNKPDIDAWELRK	GMNTL	3		727.7096239	2180.105472	0.000451244	11	N	51	68
P12787	Parental	EFDAR	WVTYFNKPDIDAWELRK	GMNTL	4		546.0341679	2180.105472	0.001943752	6	N	51	68
P12787	Parental	AGPHK	EIYPYVIQELRPTLNELGISTPEELGLDKV	-	3		1143.612017	3427.812652	0.000451244	57	N	116	146
P12787	Parental	WELRK	GMNTLVGYDLVPEPK	IIDAA	2		816.9192458	1631.822892	0.002519933	1	N	68	83
P12787	Parental	RWVTY	FNKPDIDAWELRK	GMNTL	4		408.7194844	1630.846737	0.001654178	1	N	55	68
P12787	Parental	ELRPT	LNELGISTPEELGLDKV	-	2		913.9914532	1825.967306	0.000451244	4	N	129	146
P12787	Parental	EFDAR	WVTYFNKPDIDAWELR	KGMNT	2		1027.013054	2052.010509	0.000451244	2	N	51	67
P12787	Parental	EFDAR	WVTYFNKPDIDAWELR	KGMNT	3		685.0113029	2052.010509	0.000823681	5	N	51	67
P12787	Parental	EIYPY	VIQELRPTLNELGISTPEELGLDKV	-	3		921.8433243	2762.506573	0.000998612	4	N	121	146
P12815	Exosome	-MAAY	SYRPGPGGGPGPAAGAALPDQSFLWNVFQR	VDKDR	3		1024.181445	3069.520935	0.000451244	30	N	4	34
P12815	Exosome	VDKDR	SGVISDNELQQALSNGTWTPFNPVTVR	SIISM	2		1465.736299	2929.456997	0.00091018	2	N	39	66
P12815	Exosome	VDKDR	SGVISDNELQQALSNGTWTPFNPVTVR	SIISM	3		977.4934657	2929.456997	0.000451244	26	N	39	66
P12815	Exosome	DRENK	AGVNFSEFTGVWK	YITDW	2		721.3596807	1440.703761	0.000451244	11	N	77	90
P12815	Exosome	TGVWK	YITDWQNVFR	TYDRD	2		671.3334659	1340.651332	0.001162105	13	N	90	100
P12815	Exosome	GFGYR	LSDQFHDILIR	KFDRQ	3		452.9143819	1355.719746	0.000451244	9	N	125	136
P12815	Parental	-MAAY	SYRPGPGGGPGPAAGAALPDQSFLWNVFQR	VDKDR	3		1024.181445	3069.520935	0.000451244	8	N	4	34
P12815	Parental	VDKDR	SGVISDNELQQALSNGTWTPFNPVTVR	SIISM	2		1465.736299	2929.456997	0.000451244	8	N	39	66
P12815	Parental	VDKDR	SGVISDNELQQALSNGTWTPFNPVTVR	SIISM	3		977.4934657	2929.456997	0.000451244	16	N	39	66
P12815	Parental	DRENK	AGVNFSEFTGVWK	YITDW	2		721.3596807	1440.703761	0.000622848	1	N	77	90
P12970	Exosome	VENKK	AQLVVIAHDVDPIELVVFLPALCR	KMGVP	2	C23:+57.021	1344.251582	2686.487564	0.001264573	1	N	151	175
P12970	Exosome	LVHRK	TCTTVAFTQVNSEDKGALAK	LVEAI	2	C2:+57.021	1071.031084	2140.046568	0.000451244	7	N	197	217
P12970	Exosome	LVHRK	TCTTVAFTQVNSEDKGALAK	LVEAI	3	C2:+57.021	714.3566559	2140.046568	0.000662267	4	N	197	217
P12970	Parental	VENKK	AQLVVIAHDVDPIELVVFLPALCR	KMGVP	2	C23:+57.021	1344.251582	2686.487564	0.000451244	4	N	151	175
P12970	Parental	VENKK	AQLVVIAHDVDPIELVVFLPALCR	KMGVP	3	C23:+57.021	896.5036546	2686.487564	0.001264573	5	N	151	175
P12970	Parental	VENKK	AQLVVIAHDVDPIELVVFLPALCR	KMGVP	4	C23:+57.021	672.629691	2686.487564	0.001839721	1	N	151	175
P12970	Parental	LVENK	KAQLVVIAHDVDPIELVVFLPALCR	KMGVP	2	C24:+57.021	1408.299063	2814.582527	0.001352548	1	N	150	175
P12970	Parental	LVENK	KAQLVVIAHDVDPIELVVFLPALCR	KMGVP	3	C24:+57.021	939.2019756	2814.582527	0.000637154	1	N	150	175
P12970	Parental	EKRPK	NFGIGQDIQPK	RDLTR	2		608.8201913	1215.624783	0.000622848	5	N	37	48
P13020	Exosome	KQFFK	NWRDPDQTDGPGLGYLSSHIANVER	VPFDA	3		933.1149887	2796.321566	0.000451244	17	N	392	417
P13020	Exosome	KQFFK	NWRDPDQTDGPGLGYLSSHIANVER	VPFDA	4		700.0881915	2796.321566	0.000451244	9	N	392	417
P13020	Exosome	MQYPR	QTQVSVLPEGGETPLFK	QFFKN	2		915.486338	1828.957076	0.000451244	37	N	371	388
P13020	Exosome	MQYPR	QTQVSVLPEGGETPLFK	QFFKN	3		610.6601587	1828.957076	0.001763695	1	N	371	388
P13020	Exosome	LKVLR	SQHVQVEEGSEPDAFWEALGGK	TAYRT	2		1200.559283	2399.102965	0.000451244	32	N	624	646
P13020	Exosome	LKVLR	SQHVQVEEGSEPDAFWEALGGK	TAYRT	3		800.7087884	2399.102965	0.000451244	6	N	624	646
P13020	Exosome	AVQHR	EVQGFESSTFSGYFK	SGLKY	2		856.8942817	1711.772963	0.000451244	44	N	145	160
P13020	Exosome	AFVLK	TPSAAYLWVGAGASEAEKTGAQELLK	VLRSQ	2		1324.682472	2647.349344	0.000451244	3	N	595	621
P13020	Exosome	AFVLK	TPSAAYLWVGAGASEAEKTGAQELLK	VLRSQ	3		883.4575813	2647.349344	0.000451244	34	N	595	621
P13020	Exosome	KQIWR	IEGSNKVPVDPATYGQFYGGDSYIILYNYR	HGGRQ	3		1133.889773	3398.64592	0.000451244	48	N	449	479
P13020	Exosome	EGSNK	VPVDPATYGQFYGGDSYIILYNYR	HGGRQ	2		1386.17174	2770.32788	0.000451244	31	N	455	479
P13020	Exosome	EGSNK	VPVDPATYGQFYGGDSYIILYNYR	HGGRQ	3		924.4504267	2770.32788	0.000451244	23	N	455	479
P13020	Exosome	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3		1425.038957	4272.093472	0.000451244	18	N	483	523
P13020	Exosome	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	4		1069.031168	4272.093472	0.000698008	4	N	483	523
P13020	Exosome	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3	[0:-17.027	1419.363291	4255.066472	0.000451244	6	N	483	523
P13020	Exosome	LQIWR	VEKFDLVPVPPNLYGDFFTGDAYVILK	TVQLR	3		1019.539353	3055.59466	0.000451244	64	N	70	97
P13020	Exosome	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNKFER	LKATQ	3	C16:+57.021,C29:+57.021	1466.327148	4395.958043	0.000451244	77	N	197	235
P13020	Exosome	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNKFER	LKATQ	4	C16:+57.021,C29:+57.021	1099.997311	4395.958043	0.000451244	45	N	197	235
P13020	Exosome	WRVEK	FDLVPVPPNLYGDFFTGDAYVILK	TVQLR	2		1350.702145	2699.388689	0.000451244	19	N	73	97
P13020	Exosome	WRVEK	FDLVPVPPNLYGDFFTGDAYVILK	TVQLR	3		900.8040298	2699.388689	0.000451244	27	N	73	97
P13020	Exosome	ITVVR	QGFEPPSFVGWFLGWDDNYWSVDPLDR	ALAEL	3		1077.161716	3228.461748	0.000451244	13	N	746	773
P13020	Exosome	AFVLK	TPSAAYLWVGAGASEAEK	TGAQE	2		904.4472128	1806.878826	0.000451244	22	N	595	613
P13020	Exosome	AFVLK	TPSAAYLWVGAGASEAEK	TGAQE	3		603.3007419	1806.878826	0.000698008	1	N	595	613
P13020	Exosome	EVMPK	SGALNSNDAFVLK	TPSAA	2		668.349313	1334.683026	0.000451244	23	N	582	595
P13020	Exosome	ASGFK	HVVPNEVVVQR	LFQVK	2		638.3625577	1274.709515	0.001943752	1	N	175	186
P13020	Exosome	QGALR	SEDCFILDHGR	DGKIF	2	C4:+57.021	674.8014413	1347.587283	0.000451244	17	N	325	336
P13020	Exosome	QGALR	SEDCFILDHGR	DGKIF	3	C4:+57.021	450.2035609	1347.587283	0.000451244	20	N	325	336
P13020	Exosome	PEFLK	AGKEPGLQIWR	VEKFD	3		418.9038172	1253.688052	0.000451244	21	N	59	70
P13020	Exosome	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNK	FERLK	3	C16:+57.021,C29:+57.021	1322.256442	3963.745925	0.000451244	38	N	197	232
P13020	Exosome	ANVER	VPFDAATLHTSTAMAAQHGMDDDGTGQK	QIWRI	3	M14:+15.995,M20:+15.995	969.0963352	2904.265606	0.000451244	7	N	417	445
P13020	Parental	KQFFK	NWRDPDQTDGPGLGYLSSHIANVER	VPFDA	4		700.0881915	2796.321566	0.000451244	26	N	392	417
P13020	Parental	MQYPR	QTQVSVLPEGGETPLFK	QFFKN	2		915.486338	1828.957076	0.000451244	42	N	371	388
P13020	Parental	MQYPR	QTQVSVLPEGGETPLFK	QFFKN	3		610.6601587	1828.957076	0.000451244	1	N	371	388
P13020	Parental	LKVLR	SQHVQVEEGSEPDAFWEALGGK	TAYRT	2		1200.559283	2399.102965	0.000451244	42	N	624	646

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P13020	Parental	LKVLR	SQHVQVEEGSEPDAFWEALGGK	TAYRT	3		800.7087884	2399.102965	0.000451244	17	N	624	646
P13020	Parental	AVQHR	EVQGFESSTFSGYFK	SGLKY	2		856.8942817	1711.772963	0.000451244	12	N	145	160
P13020	Parental	AFVLK	TPSAAYLWVGAGASEAEKTGAQELLK	VLRSQ	2		1324.682472	2647.349344	0.000451244	13	N	595	621
P13020	Parental	AFVLK	TPSAAYLWVGAGASEAEKTGAQELLK	VLRSQ	3		883.4575813	2647.349344	0.000451244	36	N	595	621
P13020	Parental	KQIWR	IEGSNKVPVDPATYGQFYGGDSYIILYNYR	HGGRQ	3		1133.889773	3398.64592	0.000451244	61	N	449	479
P13020	Parental	EGSNK	VPVDPATYGQFYGGDSYIILYNYR	HGGRQ	2		1386.17174	2770.32788	0.000451244	23	N	455	479
P13020	Parental	EGSNK	VPVDPATYGQFYGGDSYIILYNYR	HGGRQ	3		924.4504267	2770.32788	0.000451244	24	N	455	479
P13020	Parental	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3		1425.038957	4272.093472	0.000451244	51	N	483	523
P13020	Parental	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	4		1069.031168	4272.093472	0.000451244	9	N	483	523
P13020	Parental	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3	Q1:-17.027	1419.363291	4255.066472	0.00091018	3	N	483	523
P13020	Parental	RHGGR	QGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3	[0:-17.027	1419.363291	4255.066472	0.000451244	6	N	483	523
P13020	Parental	LQIWR	VEKFDLVPVPPNLYGDFFTGDAYVILK	TVQLR	3		1019.539353	3055.59466	0.000451244	60	N	70	97
P13020	Parental	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNKFER	LKATQ	3	C16:+57.021,C29:+57.021	1466.327148	4395.958043	0.000451244	73	N	197	235
P13020	Parental	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNKFER	LKATQ	4	C16:+57.021,C29:+57.021	1099.997311	4395.958043	0.000451244	41	N	197	235
P13020	Parental	WRVEK	FDLVPVPPNLYGDFFTGDAYVILK	TVQLR	2		1350.702145	2699.388689	0.000870037	8	N	73	97
P13020	Parental	WRVEK	FDLVPVPPNLYGDFFTGDAYVILK	TVQLR	3		900.8040298	2699.388689	0.000451244	32	N	73	97
P13020	Parental	ITVVR	QGFEPPSFVGWFLGWDDNYWSVDPLDR	ALAEL	3		1077.161716	3228.461748	0.000451244	29	N	746	773
P13020	Parental	AFVLK	TPSAAYLWVGAGASEAEK	TGAQE	2		904.4472128	1806.878826	0.000451244	41	N	595	613
P13020	Parental	EVMPK	SGALNSNDAFVLK	TPSAA	2		668.349313	1334.683026	0.000451244	27	N	582	595
P13020	Parental	QGALR	SEDCFILDHGR	DGKIF	2	C4:+57.021	674.8014413	1347.587283	0.000451244	10	N	325	336
P13020	Parental	QGALR	SEDCFILDHGR	DGKIF	3	C4:+57.021	450.2035609	1347.587283	0.000622848	11	N	325	336
P13020	Parental	PEFLK	AGKEPGLQIWR	VEKFD	3		418.9038172	1253.688052	0.000622848	15	N	59	70
P13020	Parental	RRVVR	ATEVPVSWDSFNNGDCFILDLGNNIYQWCGSGSNK	FERLK	3	C16:+57.021,C29:+57.021	1322.256442	3963.745925	0.000451244	25	N	197	232
P13020	Parental	NGDCF	ILDLGNNIYQWCGSGSNKFER	LKATQ	2	C12:+57.021	1236.092538	2470.169477	0.001229886	1	N	214	235
P13020	Parental	NGDCF	ILDLGNNIYQWCGSGSNKFER	LKATQ	3	C12:+57.021	824.3976256	2470.169477	0.000622848	2	N	214	235
P13020	Parental	KQIWR	IEGSNKVPVDPATY	GQFYG	2		745.3808101	1488.74602	0.000622848	2	N	449	463
P13020	Parental	LKVLR	SQHVQVEEGSEPDAF	WEALG	2		829.8687952	1657.72199	0.00091018	5	N	624	639
P13020	Parental	SAILT	AQLDEELGGTPVQSR	VVQGK	2		800.4028052	1598.79001	0.000823681	4	N	508	523
P13020	Parental	DDVML	LDTWDQVFVWVGK	DSQEE	2		796.9095378	1591.803476	0.000451244	6	N	698	711
P13020	Parental	TVQLR	NGNLQYDLHYWLGNECSQDESGAAAIF	TVQLD	3	C16:+57.021	1024.786166	3071.335099	0.001654178	5	N	102	129
P13020	Parental	DPATY	GQFYGGDSYIILYNYR	HGGRQ	2		964.96303	1927.91046	0.000622848	3	N	463	479
P13020	Parental	GSMSV	SLVADENPFAQGALR	SEDCF	2		794.4104333	1586.805267	0.000698008	1	N	310	325
P13020	Parental	GQIIY	NWQGAQSTQDEVAASAILTAQLDEELGGTPVQSR	VVQGK	3		1190.915599	3569.723396	0.000451244	18	N	489	523
P13020	Parental	PITVV	RQGFEPPSFVGWFLGWDDNYWSVDPLDR	ALAEL	3		1129.19542	3384.562859	0.000823681	1	N	745	773
P13020	Parental	KQIWR	IEGSNKVPVDPATYGQFYGGDSYIILY	NYRHG	3		989.4873177	2965.438553	0.001654178	1	N	449	476
P13020	Parental	FKNWR	DPDQTDGPGLGYLSSHIANVER	VPFDA	3		781.0405381	2340.098214	0.000823681	1	N	395	417
P13439	Exosome	YGTKR	LVEGEINPGQTCLVIEDVVTSGASVLETVEVLQK	EGLKV	3	C12:+57.021	1209.301248	3624.880345	0.000451244	11	N	107	141
P13439	Exosome	VSRPR	LLSQVADILFQTAK	NAGIS	2		773.9461203	1545.876641	0.000451244	11	N	48	62
P13439	Parental	YGTKR	LVEGEINPGQTCLVIEDVVTSGASVLETVEVLQK	EGLKV	3	C12:+57.021	1209.301248	3624.880345	0.000451244	17	N	107	141
P13439	Parental	VSRPR	LLSQVADILFQTAK	NAGIS	2		773.9461203	1545.876641	0.0025889	1	N	48	62
P13595	Exosome	AGIYK	CVVTAEDGTQSEATVNVK	IFQKL	2	C1:+57.021	954.4546776	1906.893755	0.000622848	3	N	95	113
P13595	Parental	KLMFK	NAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK	HKGRD	3	C18:+57.021	1147.253681	3438.737644	0.000823681	1	N	121	152
P13595	Parental	AGIYK	CVVTAEDGTQSEATVNVK	IFQKL	2	C1:+57.021	954.4546776	1906.893755	0.000451244	2	N	95	113
P13609	Exosome	CIEEK	GPQFDLIDESNNIGPPMNNPVLMEGPSK	DFISN	3	M17:+15.995,M23:+15.995	1014.811536	3041.411207	0.002080925	1	N	51	79
P13609	Exosome	CIEEK	GPQFDLIDESNNIGPPMNNPV	LMEGP	2	M17:+15.995	1142.531723	2283.047845	0.001352548	1	N	51	72
P13609	Parental	KPFDR	ILTEQNQDQPEDDFII	-	2		959.4579745	1916.900349	0.000622848	9	N	136	152
P13634	Exosome	PIDIK	TSEANHDSSLKPLSISYNPATAK	EIVNV	3		811.0753598	2430.20268	0.000451244	4	N	35	58
P13634	Exosome	PATAK	EIVNVGHSFHVIFDDSSNQSVLK	GGPLA	3		857.7666377	2570.276513	0.000451244	1	N	58	81
P13864	Exosome	GINGK	NLGPINQWWLSGFDGGEK	VLIGF	2		1009.492486	2016.969372	0.000451244	1	N	462	480
P13864	Exosome	APGEK	LPLFPEPLHVFAPR	ACQLS	3		544.9807267	1631.91878	0.002663018	1	N	1326	1340
P13864	Parental	DKKRR	VVDTESGAAAAVEKLEEVTAGTQLGPEEPCEQEDDNR	SLRRH	3	C30:+57.021	1315.271405	3942.790815	0.000451244	9	N	202	239
P13864	Parental	DKKRR	VVDTESGAAAAVEKLEEVTAGTQLGPEEPCEQEDDNR	SLRRH	4	C30:+57.021	986.7055036	3942.790815	0.001699387	1	N	202	239
P13864	Parental	GINGK	NLGPINQWWLSGFDGGEK	VLIGF	2		1009.492486	2016.969372	0.000451244	13	N	462	480
P13864	Parental	IYISK	IVVEFLQNNPDAVYEDLINKIETTVPPSTINVNR	FTEDS	3		1285.677861	3854.010183	0.000451244	13	N	516	550
P14069	Exosome	NFQEY	VAFLGALALIYNEALK	-	2		853.4985201	1704.98144	0.000451244	19	N	73	89
P14069	Exosome	NFQEY	VAFLGALALIYNEALK	-	3		569.3349467	1704.98144	0.000622848	20	N	73	89
P14069	Exosome	QEVNF	QEYVAFLGALALIYNEALK	-	2		1063.58077	2125.14594	0.000451244	2	N	70	89
P14069	Exosome	QEVNF	QEYVAFLGALALIYNEALK	-	3		709.3897799	2125.14594	0.000451244	2	N	70	89
P14069	Exosome	DDLDR	NKDQEVNFQEYVAFLGALALIYNEALK	-	3		1034.205033	3099.5917	0.000451244	70	N	62	89
P14069	Exosome	DDLDR	NKDQEVNFQEYVAFLGALALIYNEALK	-	4		775.9057249	3099.5917	0.001162105	2	N	62	89
P14069	Exosome	-MA	CPLDQAIGLLVAIFHK	YSGKE	3	C1:+57.021	599.0030484	1793.985745	0.000451244	25	N	2	18
P14069	Exosome	-MAC	PLDQAIGLLVAIFHK	YSGKE	2		817.9855798	1633.95556	0.000451244	34	N	3	18
P14069	Exosome	-MAC	PLDQAIGLLVAIFHK	YSGKE	3		545.6596532	1633.95556	0.000451244	11	N	3	18
P14069	Exosome	LDRNK	DQEVNFQEYVAFLGALALIYNEALK	-	2		1429.734705	2857.453809	0.000451244	41	N	64	89
P14069	Exosome	LDRNK	DQEVNFQEYVAFLGALALIYNEALK	-	3		953.492403	2857.453809	0.000451244	38	N	64	89

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P14069	Exosome	EYVAF	LGALALIYNEALK	-	2		694.9115491	1387.807498	0.000451244	29	N	76	89
P14069	Exosome	DDLDR	NKDQEVNFQEYVAFLGAL	ALIYN	2		1043.018534	2084.021467	0.002727428	2	N	62	80
P14069	Exosome	ELIQK	ELTIGSKLQDAEIAR	LMDDL	3		548.6374654	1642.888996	0.00307782	1	N	40	55
P14069	Exosome	MACPL	DQAIGLLVAIFHK	YSGKE	2		712.9171658	1423.818732	0.000451244	4	N	5	18
P14069	Exosome	EVNFQ	EYVAFLGALALIYNEALK	-	2		999.551481	1997.087362	0.000451244	7	N	71	89
P14069	Exosome	EVNFQ	EYVAFLGALALIYNEALK	-	3		666.7035873	1997.087362	0.000451244	5	N	71	89
P14069	Exosome	DDLDR	NKDQEVNFQEYVAF	LGALA	2		865.9051808	1729.794762	0.001871652	3	N	62	76
P14069	Parental	NFQEY	VAFLGALALIYNEALK	-	2		853.4985201	1704.98144	0.000622848	3	N	73	89
P14069	Parental	NFQEY	VAFLGALALIYNEALK	-	3		569.3349467	1704.98144	0.0007646	17	N	73	89
P14069	Parental	QEVNF	QEYVAFLGALALIYNEALK	-	2		1063.58077	2125.14594	0.000451244	2	N	70	89
P14069	Parental	QEVNF	QEYVAFLGALALIYNEALK	-	3		709.3897799	2125.14594	0.001162105	2	N	70	89
P14069	Parental	QEVNF	QEYVAFLGALALIYNEALK	-	2	Q1:-17.027	1055.06727	2108.11894	0.000979378	5	N	70	89
P14069	Parental	DDLDR	NKDQEVNFQEYVAFLGALALIYNEALK	-	3		1034.205033	3099.5917	0.000451244	46	N	62	89
P14069	Parental	-MA	CPLDQAIGLLVAIFHK	YSGKE	2	C1:+57.021	898.0006727	1793.985745	0.000451244	6	N	2	18
P14069	Parental	-MA	CPLDQAIGLLVAIFHK	YSGKE	3	C1:+57.021	599.0030484	1793.985745	0.000451244	47	N	2	18
P14069	Parental	-MAC	PLDQAIGLLVAIFHK	YSGKE	2		817.9855798	1633.95556	0.000451244	47	N	3	18
P14069	Parental	-MAC	PLDQAIGLLVAIFHK	YSGKE	3		545.6596532	1633.95556	0.000451244	42	N	3	18
P14069	Parental	LDRNK	DQEVNFQEYVAFLGALALIYNEALK	-	2		1429.734705	2857.453809	0.000451244	26	N	64	89
P14069	Parental	LDRNK	DQEVNFQEYVAFLGALALIYNEALK	-	3		953.492403	2857.453809	0.000451244	21	N	64	89
P14069	Parental	KKELK	ELIQKELTIGSK	LQDAE	2		679.8986387	1357.781677	0.000451244	8	N	35	47
P14069	Parental	KKELK	ELIQKELTIGSK	LQDAE	3		453.6016925	1357.781677	0.000451244	12	N	35	47
P14069	Parental	EYVAF	LGALALIYNEALK	-	2		694.9115491	1387.807498	0.000451244	17	N	76	89
P14069	Parental	ELIQK	ELTIGSKLQDAEIAR	LMDDL	3		548.6374654	1642.888996	0.000622848	3	N	40	55
P14069	Parental	MACPL	DQAIGLLVAIFHK	YSGKE	2		712.9171658	1423.818732	0.000451244	24	N	5	18
P14069	Parental	MACPL	DQAIGLLVAIFHK	YSGKE	3		475.6140439	1423.818732	0.000622848	17	N	5	18
P14069	Parental	-MAC	PLDQAIGLLVAIFHKYSGK	EGDKH	3		690.7302479	2069.167344	0.000662267	1	N	3	22
P14069	Parental	DDLDR	NKDQEVNFQEYVAF	LGALA	2		865.9051808	1729.794762	0.001654178	1	N	62	76
P14069	Parental	LDRNK	DQEVNFQEYVAF	LGALA	2		744.8362354	1487.656871	0.002374549	2	N	64	76
P14069	Parental	DDLDR	NKDQEVNFQEYVAFLGALALIY	NEALK	2		1273.152819	2544.290038	0.000451244	1	N	62	84
P14069	Parental	DDLDR	NKDQEVNFQEYVAFLGALALIY	NEALK	3		849.1044793	2544.290038	0.000622848	1	N	62	84
P14069	Parental	LDRNK	DQEVNFQEYVAFLGALALIY	NEALK	2		1152.083874	2302.152147	0.000698008	2	N	64	84
P14115	Exosome	YHLKR	NQSFCPTVNLDKLWTLVSEQTR	VNAAK	3	C5:+57.021	879.4431235	2635.305971	0.000451244	4	N	65	87
P14115	Parental	YHLKR	NQSFCPTVNLDKLWTLVSEQTR	VNAAK	2	C5:+57.021	1318.660785	2635.305971	0.001329271	1	N	65	87
P14115	Parental	YHLKR	NQSFCPTVNLDKLWTLVSEQTR	VNAAK	3	C5:+57.021	879.4431235	2635.305971	0.000451244	13	N	65	87
P14115	Parental	VNAAK	NKTGVAPIIDVVR	SGYYK	3		461.2774318	1380.808895	0.001463592	1	N	92	105
P14131	Exosome	EASKK	EIKDILIQYDR	TLLVA	3		469.2615588	1404.761276	0.000451244	7	N	106	117
P14131	Exosome	TLQYK	LLEPVLLLGK	ERFAG	2		547.8633392	1093.711078	0.000698008	3	N	50	60
P14131	Parental	EASKK	EIKDILIQYDR	TLLVA	3		469.2615588	1404.761276	0.000451244	23	N	106	117
P14148	Exosome	GMKKK	TTHFVEGGDAGNREDQINR	LIRRM	4		529.7510385	2114.972954	0.000451244	1	N	245	264
P14148	Parental	GIICM	EDLIHEIYTVGKR	FKEAN	3		524.9513843	1571.830753	0.000823681	3	N	209	222
P14148	Parental	GMKKK	TTHFVEGGDAGNREDQINR	LIRRM	3		705.9987847	2114.972954	0.001943752	2	N	245	264
P14148	Parental	GMKKK	TTHFVEGGDAGNREDQINR	LIRRM	4		529.7510385	2114.972954	0.000451244	7	N	245	264
P14152	Exosome	KKSVK	VIVVGNPANTNCLTASK	SAPSI	2	C12:+57.021	879.4646513	1756.913703	0.000451244	44	N	125	142
P14152	Exosome	DLTAK	ELTEEKETAFEFLSSA	-	2		915.9363436	1829.857087	0.000451244	10	N	318	334
P14152	Exosome	NKTWK	FVEGLPINDFSR	EKMDL	2		697.3596807	1392.703761	0.000451244	14	N	298	310
P14152	Exosome	KLQGK	EVGVYEALKDDSWLK	GEFIT	2		876.4466815	1750.877763	0.000451244	4	N	205	220
P14152	Exosome	KLQGK	EVGVYEALKDDSWLK	GEFIT	3		584.633721	1750.877763	0.000451244	16	N	205	220
P14152	Exosome	SEPIR	VLVTGAAGQIAYSLLYSIGNGSVFGK	DQPII	3		862.4711622	2584.390086	0.000622848	3	N	6	32
P14152	Exosome	ADDVK	NVIIWGNHSSTQYPDVNHAK	VKLQG	3		760.7105751	2279.108325	0.000451244	23	N	179	199
P14152	Exosome	DSWLK	GEFITTVQQR	GAAVI	2		589.8123663	1177.609133	0.000662267	1	N	220	230
P14152	Exosome	EFVSM	GVISDGNSYGVPDDLLYSFPVVIK	NKTWK	2		1277.657934	2553.300268	0.000451244	1	N	269	293
P14152	Parental	KKSVK	VIVVGNPANTNCLTASK	SAPSI	2	C12:+57.021	879.4646513	1756.913703	0.000451244	30	N	125	142
P14152	Parental	DLTAK	ELTEEKETAFEFLSSA	-	2		915.9363436	1829.857087	0.001162105	1	N	318	334
P14152	Parental	KLQGK	EVGVYEALKDDSWLK	GEFIT	3		584.633721	1750.877763	0.000698008	4	N	205	220
P14152	Parental	ADDVK	NVIIWGNHSSTQYPDVNHAK	VKLQG	2		1140.561963	2279.108325	0.000451244	2	N	179	199
P14152	Parental	ADDVK	NVIIWGNHSSTQYPDVNHAK	VKLQG	3		760.7105751	2279.108325	0.000823681	1	N	179	199
P14152	Parental	DSWLK	GEFITTVQQR	GAAVI	2		589.8123663	1177.609133	0.000622848	3	N	220	230
P14206	Exosome	DSPLR	YVDIAIPCNNK	GAHSV	2	C8:+57.021	653.8269278	1305.638256	0.001264573	5	N	155	166
P14206	Exosome	VTDPR	ADHQPLTEASYVNLPTIALCNTDSPLR	YVDIA	3	C20:+57.021	999.4979567	2995.47047	0.000451244	58	N	128	155
P14206	Exosome	RAVLK	FAAATGATPIAGR	FTPGT	2		602.3281835	1202.640767	0.001654178	4	N	89	102
P14206	Exosome	PIAGR	FTPGTFTNQIQAAFR	EPRLL	2		849.9340756	1697.852551	0.000823681	5	N	102	117
P14206	Exosome	LLAAR	AIVAIENPADVSVISSR	NTGQR	2		870.9786801	1739.94176	0.000451244	23	N	63	80
P14206	Exosome	AAAEK	AVTKEEFQGEWTAPAPEFT	AAQPE	2		1069.507999	2137.000398	0.000451244	18	N	220	239
P14206	Exosome	VTDPR	ADHQPLTEASYVNLPTIALCNTDSPLRY	VDIAI	3	C20:+57.021	1053.8524	3158.533799	0.000451244	4	N	128	156
P14206	Exosome	DHQPL	TEASYVNLPTIALCNTDSPLR	YVDIA	2	C14:+57.021	1168.083848	2334.152095	0.000451244	5	N	134	155

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P14206	Parental	DSPLR	YVDIAIPCNNK	GAHSV	2	C8:+57.021	653.8269278	1305.638256	0.000451244	11	N	155	166
P14206	Parental	VTDPR	ADHQPLTEASYVNLPTIALCNTDSPLR	YVDIA	3	C20:+57.021	999.4979567	2995.47047	0.000451244	53	N	128	155
P14206	Parental	RAVLK	FAAATGATPIAGR	FTPGT	2		602.3281835	1202.640767	0.000823681	1	N	89	102
P14206	Parental	PIAGR	FTPGTFTNQIQAAFR	EPRLL	2		849.9340756	1697.852551	0.001162105	5	N	102	117
P14206	Parental	LLAAR	AIVAIENPADVSVISSR	NTGQR	2		870.9786801	1739.94176	0.000451244	16	N	63	80
P14206	Parental	AAAEK	AVTKEEFQGEWTAPAPEFT	AAQPE	2		1069.507999	2137.000398	0.002145581	1	N	220	239
P14206	Parental	VTDPR	ADHQPLTEASYVNLPTIALCNTDSPLRY	VDIAI	3	C20:+57.021	1053.8524	3158.533799	0.000451244	11	N	128	156
P14206	Parental	IYKRK	SDGIYIINLK	RTWEK	2		568.3220355	1134.628471	0.000979378	1	N	42	52
P14211	Exosome	LPPKK	IKDPDAAKPEDWDER	AKIDD	2		892.9266445	1783.837689	0.000823681	3	N	207	222
P14211	Exosome	LPPKK	IKDPDAAKPEDWDER	AKIDD	3		595.620363	1783.837689	0.000451244	21	N	207	222
P14211	Exosome	AIYFK	EQFLDGDAWTNR	WVESK	2		726.3316516	1450.647703	0.000451244	29	N	24	36
P14211	Exosome	TYEVK	IDNSQVESGSLEDDWDFLPPKK	IKDPD	2		1260.10098	2518.186361	0.000451244	28	N	185	207
P14211	Exosome	TYEVK	IDNSQVESGSLEDDWDFLPPKK	IKDPD	3		840.4032536	2518.186361	0.000451244	53	N	185	207
P14211	Exosome	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	C1:+39.994	947.1253099	2838.35253	0.000451244	5	N	162	185
P14211	Exosome	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	4	C1:+39.994	710.5959324	2838.35253	0.000451244	6	N	162	185
P14211	Exosome	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	2	C1:+57.021	1428.697565	2855.37953	0.001839721	1	N	162	185
P14211	Exosome	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	C1:+57.021	952.8009765	2855.37953	0.000451244	27	N	162	185
P14211	Exosome	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	4	C1:+57.021	714.8526824	2855.37953	0.000451244	26	N	162	185
P14211	Exosome	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	[0:-17.027,C1:+57.021	947.1253099	2838.35253	0.000451244	20	N	162	185
P14211	Exosome	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	4	[0:-17.027,C1:+57.021	710.5959324	2838.35253	0.000451244	17	N	162	185
P14211	Exosome	NPDYK	GTWIHPEIDNPEYSPDANIY	AYDSF	2		1166.032369	2330.049139	0.002727428	2	N	286	306
P14211	Exosome	TYEVK	IDNSQVESGSLEDDWDFLPPK	KIKDP	2		1196.053499	2390.091398	0.000451244	17	N	185	206
P14211	Exosome	GLAAA	DPAIYFKEQFLDGDAWTNR	WVESK	2		1143.545447	2285.075294	0.000451244	3	N	17	36
P14211	Exosome	DANIY	AYDSFAVLGLDLWQVK	SGTIF	2		912.9806915	1823.945783	0.000451244	2	N	306	322
P14211	Exosome	LWQVK	SGTIFDNFLITNDEAYAEEFGNETWGVTK	AAEKQ	3		1090.170606	3267.488417	0.000451244	50	N	322	351
P14211	Exosome	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVK	SGTIF	3		1379.669254	4135.984362	0.000451244	40	N	286	322
P14211	Exosome	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVK	SGTIF	4		1035.00389	4135.984362	0.000662267	4	N	286	322
P14211	Exosome	DWDER	AKIDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	4		740.6048771	2958.388308	0.000451244	18	N	222	248
P14211	Exosome	PFSNK	GQTLVVQFTVK	HEQNI	2		610.3564097	1218.697219	0.000622848	16	N	87	98
P14211	Exosome	DERAK	IDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	3		920.7598771	2759.256231	0.000451244	17	N	224	248
P14211	Exosome	DPDAK	KPEDWDEEMDGEWEPPVIQNPEYK	GEWKP	3	M9:+15.995	992.7680727	2975.280818	0.000451244	15	N	248	272
P14211	Parental	LPPKK	IKDPDAAKPEDWDER	AKIDD	2		892.9266445	1783.837689	0.000451244	57	N	207	222
P14211	Parental	LPPKK	IKDPDAAKPEDWDER	AKIDD	3		595.620363	1783.837689	0.000451244	73	N	207	222
P14211	Parental	LPPKK	IKDPDAAKPEDWDER	AKIDD	4		446.9672223	1783.837689	0.000451244	24	N	207	222
P14211	Parental	PAIYF	KEQFLDGDAWTNR	WVESK	2		790.3791331	1578.742666	0.000451244	10	N	23	36
P14211	Parental	PAIYF	KEQFLDGDAWTNR	WVESK	3		527.2553554	1578.742666	0.001699387	1	N	23	36
P14211	Parental	NDEAY	AEEFGNETWGVTK	AAEKQ	2		734.3416849	1466.66777	0.000451244	36	N	338	351
P14211	Parental	AIYFK	EQFLDGDAWTNR	WVESK	2		726.3316516	1450.647703	0.000451244	33	N	24	36
P14211	Parental	DPDAK	KPEDWDEEMDGEWEPPVIQNPEYKGEWKPR	QIDNP	4	M9:+15.995	933.1760566	3728.673026	0.001162105	3	N	248	278
P14211	Parental	ALSAK	FEPFSNKGQTLVVQFTVK	HEQNI	2		1035.057462	2068.099324	0.000451244	8	N	80	98
P14211	Parental	ALSAK	FEPFSNKGQTLVVQFTVK	HEQNI	3		690.3742412	2068.099324	0.000823681	6	N	80	98
P14211	Parental	TYEVK	IDNSQVESGSLEDDWDFLPPKK	IKDPD	2		1260.10098	2518.186361	0.000451244	101	N	185	207
P14211	Parental	TYEVK	IDNSQVESGSLEDDWDFLPPKK	IKDPD	3		840.4032536	2518.186361	0.000451244	61	N	185	207
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	C1:+39.994	947.1253099	2838.35253	0.000451244	14	N	162	185
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	4	C1:+39.994	710.5959324	2838.35253	0.000451244	10	N	162	185
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	2	C1:+57.021	1428.697565	2855.37953	0.000451244	14	N	162	185
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	C1:+57.021	952.8009765	2855.37953	0.000451244	24	N	162	185
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	4	C1:+57.021	714.8526824	2855.37953	0.000451244	42	N	162	185
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	2	[0:-17.027,C1:+57.021	1420.184065	2838.35253	0.000451244	12	N	162	185
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	3	[0:-17.027,C1:+57.021	947.1253099	2838.35253	0.000451244	22	N	162	185
P14211	Parental	NKDIR	CKDDEFTHLYTLIVRPDNTYEVK	IDNSQ	4	[0:-17.027,C1:+57.021	710.5959324	2838.35253	0.000451244	30	N	162	185
P14211	Parental	DSFAV	LGLDLWQVK	SGTIF	2		536.3140135	1070.612427	0.000735798	11	N	313	322
P14211	Parental	NPDYK	GTWIHPEIDNPEYSPDANIY	AYDSF	2		1166.032369	2330.049139	0.000451244	26	N	286	306
P14211	Parental	TYEVK	IDNSQVESGSLEDDWDFLPPK	KIKDP	2		1196.053499	2390.091398	0.000451244	80	N	185	206
P14211	Parental	TYEVK	IDNSQVESGSLEDDWDFLPPK	KIKDP	3		797.7049325	2390.091398	0.001162105	3	N	185	206
P14211	Parental	GLAAA	DPAIYFKEQFLDGDAWTNR	WVESK	3		762.6995646	2285.075294	0.000451244	5	N	17	36
P14211	Parental	SGTIF	DNFLITNDEAYAEEFGNETWGVTK	AAEKQ	2		1382.125184	2762.234768	0.000451244	52	N	327	351
P14211	Parental	DLWQV	KSGTIFDNFLITNDEAYAEEFGNETWGVTK	AAEKQ	3		1132.868927	3395.58338	0.000451244	11	N	321	351
P14211	Parental	LWQVK	SGTIFDNFLITNDEAYAEEFGNETWGVTKAAEK	QMKDK	3		1223.2412	3666.700201	0.000451244	2	N	322	355
P14211	Parental	DANIY	AYDSFAVLGLDLWQVK	SGTIF	2		912.9806915	1823.945783	0.000451244	41	N	306	322
P14211	Parental	DANIY	AYDSFAVLGLDLWQVK	SGTIF	3		608.9897277	1823.945783	0.000451244	9	N	306	322
P14211	Parental	NIYAY	DSFAVLGLDLWQVK	SGTIF	2		795.9304702	1589.84534	0.000451244	26	N	308	322
P14211	Parental	LWQVK	SGTIFDNFLITNDEAYAEEFGNETWGVTK	AAEKQ	3		1090.170606	3267.488417	0.000451244	165	N	322	351
P14211	Parental	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVK	SGTIF	3		1379.669254	4135.984362	0.000451244	117	N	286	322
P14211	Parental	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQVK	SGTIF	4		1035.00389	4135.984362	0.000451244	17	N	286	322

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P14211	Parental	DWDER	AKIDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	3		987.1372361	2958.388308	0.000451244	48	N	222	248
P14211	Parental	DWDER	AKIDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	4		740.6048771	2958.388308	0.000451244	40	N	222	248
P14211	Parental	AIYFK	EQFLDGDAWTNRWVESK	HKSDF	2		1040.990308	2079.965015	0.00091018	2	N	24	41
P14211	Parental	LWQVK	SGTIFDNFLITNDEAY	AEEFG	2		910.4234034	1818.831207	0.000451244	14	N	322	338
P14211	Parental	EWKPR	QIDNPDYKGTWIHPEIDNPEYSPDANIYAYDSFAV	LGLDL	3		1353.285469	4056.833006	0.001463592	1	N	278	313
P14211	Parental	PFSNK	GQTLVVQFTVK	HEQNI	2		610.3564097	1218.697219	0.000622848	24	N	87	98
P14211	Parental	DERAK	IDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	2		1380.635916	2759.256231	0.000622848	4	N	224	248
P14211	Parental	DERAK	IDDPTDSKPEDWDKPEHIPDPDAK	KPEDW	3		920.7598771	2759.256231	0.000451244	28	N	224	248
P14211	Parental	DPDAK	KPEDWDEEMDGEWEPPVIQNPEYK	GEWKP	3	M9:+15.995	992.7680727	2975.280818	0.000451244	21	N	248	272
P14211	Parental	FTHLY	TLIVRPDNTYEVK	IDNSQ	2		774.425552	1546.835504	0.000823681	4	N	172	185
P14211	Parental	ALSAK	FEPFSNKGQTLVVQF	TVKHE	2		870.951934	1739.888268	0.002453667	2	N	80	95
P14211	Parental	AYDSF	AVLGLDLWQVK	SGTIF	2		621.3667774	1240.717955	0.001395409	3	N	311	322
P14211	Parental	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAV	LGLDL	3		1028.801965	3083.382495	0.002212458	2	N	286	313
P14211	Parental	NPDYK	GTWIHPEIDNPEYSPDANIYAYDSFAVLGLDLWQV	KSGTI	3		1336.970933	4007.889399	0.002374549	1	N	286	321
P14211	Parental	QFTVK	HEQNIDCGGGYVK	LFPSG	3	C7:+57.021	492.8897534	1475.64586	0.001329271	1	N	98	111
P14234	Exosome	ALERR	LGTGCFGDVWLGTWNCSTK	VAVKT	2	C5:+57.021,C16:+57.021	1079.987933	2157.960267	0.000451244	13	N	256	275
P14234	Exosome	SSGHR	GYVPSNYVAPVDSIQAEEWYFGK	ISRKD	2		1310.124259	2618.232917	0.000451244	16	N	113	136
P14234	Exosome	SSGHR	GYVPSNYVAPVDSIQAEEWYFGK	ISRKD	3		873.7521057	2618.232917	0.000998612	2	N	113	136
P14234	Exosome	EQAWR	LDPEERPTFEYLQSFLEDYFTSTEPQYQPGDQT	-	3		1324.265963	3969.774488	0.000622848	5	N	484	517
P14234	Exosome	RFTVK	SDVWSFGILLTELITK	GRVPY	2		911.5039994	1820.992399	0.000451244	8	N	426	442
P14234	Exosome	FGLAR	LIEDNEYNPQQGTK	FPIKW	2		824.894813	1647.774026	0.000451244	8	N	393	407
P14234	Exosome	YLQSF	LEDYFTSTEPQYQPGDQT	-	2		1059.961078	2117.906557	0.000622848	1	N	499	517
P14234	Exosome	TKGEK	FHILNNTEYDWWEAR	SLSSG	3		665.3117524	1992.911857	0.002145581	4	N	91	106
P14234	Parental	ALERR	LGTGCFGDVWLGTWNCSTK	VAVKT	2	C5:+57.021,C16:+57.021	1079.987933	2157.960267	0.000451244	29	N	256	275
P14234	Parental	SSGHR	GYVPSNYVAPVDSIQAEEWYFGK	ISRKD	2		1310.124259	2618.232917	0.000451244	37	N	113	136
P14234	Parental	SSGHR	GYVPSNYVAPVDSIQAEEWYFGK	ISRKD	3		873.7521057	2618.232917	0.000451244	18	N	113	136
P14234	Parental	EQAWR	LDPEERPTFEYLQSFLEDYFTSTEPQYQPGDQT	-	3		1324.265963	3969.774488	0.000451244	38	N	484	517
P14234	Parental	RFTVK	SDVWSFGILLTELITK	GRVPY	2		911.5039994	1820.992399	0.000451244	35	N	426	442
P14234	Parental	RFTVK	SDVWSFGILLTELITK	GRVPY	3		608.0052663	1820.992399	0.000451244	12	N	426	442
P14234	Parental	YITTR	AQFDSIQDLVR	HYMEV	2		646.3362056	1290.656811	0.000451244	6	N	201	212
P14234	Parental	FGLAR	LIEDNEYNPQQGTK	FPIKW	2		824.894813	1647.774026	0.000451244	22	N	393	407
P14234	Parental	YLQSF	LEDYFTSTEPQYQPGDQT	-	2		1059.961078	2117.906557	0.000451244	13	N	499	517
P14234	Parental	HRDLR	AANILVGEYLICK	IADFG	2	C12:+57.021	732.40026	1462.78492	0.000451244	9	N	372	385
P14234	Parental	KFPIK	WTAPEAALFGR	FTVKS	2		609.8174517	1217.619303	0.000851441	2	N	411	422
P14234	Parental	TKGEK	FHILNNTEYDWWEAR	SLSSG	2		997.4637285	1992.911857	0.000451244	8	N	91	106
P14685	Exosome	RGADK	AKPPPGGEQEPPPPAPQDVEMKEEAAAGSGSTGEGDGK	AAATE	4	M21:+15.995	929.6817031	3714.695613	0.000451244	10	N	14	52
P14685	Exosome	DIAQK	LQLDSPEDAEFIVAK	AIRDG	2		837.9334069	1673.851214	0.000451244	10	N	421	436
P14685	Exosome	TATLR	HDADGQATLLNLLLR	NYLHY	2		825.4526325	1648.889665	0.001839721	1	N	237	252
P14685	Exosome	TATLR	HDADGQATLLNLLLR	NYLHY	3		550.6376883	1648.889665	0.000451244	30	N	237	252
P14685	Exosome	YYHAR	VYEFLDKLDVVR	SFLHA	3		499.2772089	1494.808227	0.000735798	1	N	212	224
P14685	Exosome	KLVSK	SVFPEQANNNEWAR	YLYYT	2		831.3874895	1660.759379	0.000451244	11	N	269	283
P14685	Exosome	NNATR	DFLLPFLEEPMDTEADLQFRPR	TGKAA	3	M11:+15.995	899.1078124	2694.300037	0.001591523	5	N	124	146
P14685	Exosome	NLLLR	NYLHYSLYDQAEK	LVSKS	2		822.3891665	1642.762733	0.00091018	2	N	252	265
P14685	Parental	DIAQK	LQLDSPEDAEFIVAK	AIRDG	2		837.9334069	1673.851214	0.000622848	1	N	421	436
P14685	Parental	TATLR	HDADGQATLLNLLLR	NYLHY	3		550.6376883	1648.889665	0.000451244	1	N	237	252
P14685	Parental	YYHAR	VYEFLDKLDVVR	SFLHA	3		499.2772089	1494.808227	0.000451244	1	N	212	224
P14685	Parental	KLVSK	SVFPEQANNNEWAR	YLYYT	2		831.3874895	1660.759379	0.000451244	10	N	269	283
P14685	Parental	LSYSR	ISLADIAQKLQLDSPEDAEFIVAK	AIRDG	3		872.1378487	2613.390146	0.000451244	5	N	412	436
P14685	Parental	NNATR	DFLLPFLEEPMDTEADLQFRPR	TGKAA	3	M11:+15.995	899.1078124	2694.300037	0.001162105	1	N	124	146
P14733	Exosome	RSTVF	KTTIPEEEEEEEEEPIGVAVEEER	FHQQG	3		934.1018572	2799.282172	0.000451244	5	N	547	571
P14733	Exosome	ESRMR	IESLSSQLSNLQK	ESRAC	2		723.8940847	1445.772569	0.000451244	1	N	300	313
P14733	Exosome	STVFK	TTIPEEEEEEEEEPIGVAVEEER	FHQQG	2		1336.601404	2671.187208	0.000451244	33	N	548	571
P14733	Exosome	RYVLK	AGQTVTVWAANAGVTASPPTDLIWK	NQNSW	2		1277.669168	2553.322735	0.000451244	33	N	492	517
P14733	Exosome	RYVLK	AGQTVTVWAANAGVTASPPTDLIWK	NQNSW	3		852.1153784	2553.322735	0.000451244	12	N	492	517
P14733	Exosome	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	2		1272.65612	2543.29664	0.000451244	1	N	158	182
P14733	Exosome	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	3		848.7733466	2543.29664	0.000451244	37	N	158	182
P14733	Exosome	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	4		636.8319599	2543.29664	0.00091018	1	N	158	182
P14733	Exosome	LENAR	LSSEMNTSTVNSAREELMESR	MRIES	3	M5:+15.995,M18:+15.995	801.6975125	2402.069137	0.000451244	2	N	277	298
P14733	Exosome	IDKVR	SLETENSALQLQVTER	EEVRG	2		909.4661339	1816.916668	0.000451244	1	N	52	68
P14733	Exosome	STVFK	TTIPEEEEEEEEEPIGVAVEEERF	HQQGA	2		1410.135611	2818.255622	0.000823681	16	N	548	572
P14733	Parental	LTGLK	ALYETELADARR	ALDDT	2		704.3654944	1406.715389	0.002080925	1	N	80	92
P14733	Parental	LTGLK	ALYETELADARR	ALDDT	3		469.9129296	1406.715389	0.002374549	2	N	80	92
P14733	Parental	IELGK	FKAEHDQLLLNYAK	KESDL	2		845.4521012	1688.888602	0.000451244	15	N	110	124
P14733	Parental	IELGK	FKAEHDQLLLNYAK	KESDL	3		563.9706674	1688.888602	0.000451244	11	N	110	124
P14733	Parental	KHETR	LVEVDSGRQIEYEYK	LAQAL	2		914.4603202	1826.90504	0.000451244	13	N	227	242

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P14733	Parental	KHETR	LVEVDSGRQIEYEYK	LAQAL	3		609.9761468	1826.90504	0.000622848	4	N	227	242
P14733	Parental	DLENR	CQSLTEDLEFRK	NMYEE	2	C1:+57.021	763.3696882	1524.723776	0.000451244	18	N	198	210
P14733	Parental	DLENR	CQSLTEDLEFRK	NMYEE	3	C1:+57.021	509.2490588	1524.723776	0.000451244	16	N	198	210
P14733	Parental	DLENR	CQSLTEDLEFRK	NMYEE	2	[0:-17.027,C1:+57.021	754.8561882	1507.696776	0.000698008	5	N	198	210
P14733	Parental	RSTVF	KTTIPEEEEEEEEEPIGVAVEEER	FHQQG	2		1400.648886	2799.282172	0.000451244	46	N	547	571
P14733	Parental	RSTVF	KTTIPEEEEEEEEEPIGVAVEEER	FHQQG	3		934.1018572	2799.282172	0.000451244	66	N	547	571
P14733	Parental	ESRMR	IESLSSQLSNLQK	ESRAC	2		723.8940847	1445.772569	0.000451244	41	N	300	313
P14733	Parental	STVFK	TTIPEEEEEEEEEPIGVAVEEER	FHQQG	2		1336.601404	2671.187208	0.000451244	53	N	548	571
P14733	Parental	DLENR	CQSLTEDLEFR	KNMYE	2	C1:+57.021	699.3222066	1396.628813	0.000451244	16	N	198	209
P14733	Parental	DLENR	CQSLTEDLEFR	KNMYE	2	[0:-17.027,C1:+57.021	690.8087066	1379.601813	0.000622848	6	N	198	209
P14733	Parental	RYVLK	AGQTVTVWAANAGVTASPPTDLIWK	NQNSW	2		1277.669168	2553.322735	0.000451244	44	N	492	517
P14733	Parental	RYVLK	AGQTVTVWAANAGVTASPPTDLIWK	NQNSW	3		852.1153784	2553.322735	0.000451244	21	N	492	517
P14733	Parental	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	2		1272.65612	2543.29664	0.000451244	25	N	158	182
P14733	Parental	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	3		848.7733466	2543.29664	0.000451244	47	N	158	182
P14733	Parental	LGDKK	SLEGDLEDLKDQIAQLEASLSAAK	KQLAD	4		636.8319599	2543.29664	0.000622848	17	N	158	182
P14733	Parental	LTGLK	ALYETELADAR	RALDD	2		626.3149388	1250.614278	0.002453667	1	N	80	91
P14733	Parental	IDKVR	SLETENSALQLQVTEREEVR	GRELT	3		777.7315931	2330.171379	0.000451244	24	N	52	72
P14733	Parental	LMESR	MRIESLSSQLSNLQK	ESRAC	2		867.4648832	1732.914166	0.000451244	2	N	298	313
P14733	Parental	LMESR	MRIESLSSQLSNLQK	ESRAC	3		578.6458555	1732.914166	0.001463592	1	N	298	313
P14733	Parental	LENAR	LSSEMNTSTVNSAREELMESR	MRIES	3	M5:+15.995,M18:+15.995	801.6975125	2402.069137	0.000823681	1	N	277	298
P14733	Parental	DLIWK	NQNSWGTGEDVKVILK	NSQGE	2		894.4684796	1786.921359	0.00091018	4	N	517	533
P14733	Parental	IDKVR	SLETENSALQLQVTER	EEVRG	2		909.4661339	1816.916668	0.000451244	23	N	52	68
P14733	Parental	STVFK	TTIPEEEEEEEEEPIGVAVEEERFHQQGAPR	ASNKS	3		1198.555847	3592.644142	0.001162105	1	N	548	579
P14733	Parental	STVFK	TTIPEEEEEEEEEPIGVAVEEERFHQQGAPR	ASNKS	4		899.1688356	3592.644142	0.00307782	1	N	548	579
P14733	Parental	SAAKK	QLADETLLKVDLENR	CQSLT	3		586.320025	1755.936675	0.000451244	1	N	183	198
P14733	Parental	DLIWK	NQNSWGTGEDVKV	ILKNS	2		717.3369339	1432.658268	0.000622848	1	N	517	530
P14733	Parental	STVFK	TTIPEEEEEEEEEPIGVAVEEERF	HQQGA	2		1410.135611	2818.255622	0.000823681	4	N	548	572
P14733	Parental	DAQVR	LYKEELEQTYHAK	LENAR	3		551.2829111	1650.825333	0.00091018	2	N	259	272
P14733	Parental	RAGSR	ASAPATPLSPTR	LSRLQ	2		584.8201913	1167.624783	0.000662267	2	N	15	27
P14733	Parental	LGKFK	AEHDQLLLNYAK	KESDL	3		472.2495417	1413.725225	0.001162105	1	N	112	124
P14733	Parental	TVTVW	AANAGVTASPPTDLIWK	NQNSW	2		856.4548408	1710.894082	0.000451244	6	N	500	517
P14824	Exosome	YTAMK	GFGSDKESILELITSR	SNKQR	2		876.4628629	1750.910126	0.000451244	9	N	34	50
P14824	Exosome	YTAMK	GFGSDKESILELITSR	SNKQR	3		584.6445086	1750.910126	0.000451244	27	N	34	50
P14824	Exosome	VMVSR	SEIDLLNIR	REFIE	2		536.8040099	1071.59242	0.000622848	18	N	629	638
P14824	Exosome	DAYER	DLESDIIGDTSGHFQK	MLVVL	3		587.9483682	1760.821705	0.000451244	14	N	140	156
P14824	Exosome	RVELK	GTVCAANDFNPDADAK	ALRKA	2	C4:+57.021	833.3625915	1664.709583	0.000451244	25	N	354	370
P14824	Exosome	AGELK	WGTDEAQFIYILGNR	SKQHL	2		891.9446403	1781.873681	0.000451244	17	N	191	206
P14824	Exosome	AGELK	WGTDEAQFIYILGNR	SKQHL	3		594.9656935	1781.873681	0.00307782	1	N	191	206
P14824	Exosome	SLYGK	DLIEDLKYELTGK	FERLI	2		768.9119431	1535.808286	0.000451244	9	N	68	81
P14824	Exosome	SLYGK	DLIEDLKYELTGK	FERLI	3		512.9438954	1535.808286	0.000451244	6	N	68	81
P14824	Exosome	GGENR	DQAQEDAQVAAEILEIADTPSGDKTSLETR	FMTVL	3		1067.851824	3200.532072	0.000451244	17	N	516	546
P14824	Exosome	EDYHK	SLEDALSSDTSGHFR	RILIS	2		811.3767874	1620.737975	0.000451244	3	N	483	498
P14824	Exosome	RKAMK	GIGTDEATIIDIVTHR	SNAQR	2		855.955205	1709.89481	0.000451244	6	N	377	393
P14824	Exosome	RKAMK	GIGTDEATIIDIVTHR	SNAQR	3		570.9727367	1709.89481	0.000451244	14	N	377	393
P14824	Exosome	LQGTR	ENDDVVSEDLVQQDVQDLYEAGELK	WGTDE	2		1425.662328	2849.309055	0.000451244	26	N	166	191
P14824	Exosome	LQGTR	ENDDVVSEDLVQQDVQDLYEAGELK	WGTDE	3		950.777485	2849.309055	0.000451244	24	N	166	191
P14824	Exosome	SGDVK	DAFVAIVQSVK	NKPLF	2		588.8353101	1175.65502	0.000622848	6	N	587	598
P14824	Parental	YTAMK	GFGSDKESILELITSR	SNKQR	2		876.4628629	1750.910126	0.001162105	1	N	34	50
P14824	Parental	YTAMK	GFGSDKESILELITSR	SNKQR	3		584.6445086	1750.910126	0.000451244	14	N	34	50
P14824	Parental	VMVSR	SEIDLLNIR	REFIE	2		536.8040099	1071.59242	0.000662267	2	N	629	638
P14824	Parental	DAYER	DLESDIIGDTSGHFQK	MLVVL	3		587.9483682	1760.821705	0.000451244	2	N	140	156
P14824	Parental	RVELK	GTVCAANDFNPDADAK	ALRKA	2	C4:+57.021	833.3625915	1664.709583	0.000451244	10	N	354	370
P14824	Parental	AGELK	WGTDEAQFIYILGNR	SKQHL	2		891.9446403	1781.873681	0.000451244	2	N	191	206
P14824	Parental	SLYGK	DLIEDLKYELTGK	FERLI	2		768.9119431	1535.808286	0.000851441	2	N	68	81
P14824	Parental	GGENR	DQAQEDAQVAAEILEIADTPSGDKTSLETR	FMTVL	3		1067.851824	3200.532072	0.000451244	9	N	516	546
P14824	Parental	EDYHK	SLEDALSSDTSGHFR	RILIS	3		541.2537916	1620.737975	0.001699387	2	N	483	498
P14824	Parental	RKAMK	GIGTDEATIIDIVTHR	SNAQR	3		570.9727367	1709.89481	0.001943752	1	N	377	393
P14824	Parental	LQGTR	ENDDVVSEDLVQQDVQDLYEAGELK	WGTDE	2		1425.662328	2849.309055	0.000451244	18	N	166	191
P14824	Parental	LQGTR	ENDDVVSEDLVQQDVQDLYEAGELK	WGTDE	3		950.777485	2849.309055	0.000451244	16	N	166	191
P15532	Exosome	SDSVK	SAEKEISLWFQPEELVEYK	SCAQN	2		1163.086613	2324.157627	0.000451244	29	N	124	143
P15532	Exosome	SDSVK	SAEKEISLWFQPEELVEYK	SCAQN	3		775.7270089	2324.157627	0.000451244	30	N	124	143
P15532	Exosome	ANSER	TFIAIKPDGVQR	GLVGE	2		672.8858657	1343.756131	0.000622848	6	Y	6	18
P15532	Exosome	ANSER	TFIAIKPDGVQR	GLVGE	3		448.9265104	1343.756131	0.001162105	3	Y	6	18
P15532	Exosome	KSAEK	EISLWFQPEELVEYK	SCAQN	2		955.483264	1908.950928	0.000451244	42	N	128	143
P15532	Exosome	PGTIR	GDFCIQVGR	NIIHG	2	C4:+57.021	526.2533986	1050.491197	0.001162105	11	Y	105	114

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P15532	Exosome	LVGLK	FLQASEDLLKEHYTDLK	DRPFF	3		684.0217561	2049.041868	0.000698008	1	Y	39	56
P15532	Parental	SDSVK	SAEKEISLWFQPEELVEYK	SCAQN	2		1163.086613	2324.157627	0.000451244	10	N	124	143
P15532	Parental	SDSVK	SAEKEISLWFQPEELVEYK	SCAQN	3		775.7270089	2324.157627	0.000451244	12	N	124	143
P15532	Parental	ANSER	TFIAIKPDGVQR	GLVGE	3		448.9265104	1343.756131	0.001162105	3	Y	6	18
P15532	Parental	KSAEK	EISLWFQPEELVEYK	SCAQN	2		955.483264	1908.950928	0.000451244	12	N	128	143
P15532	Parental	SDSVK	SAEKEISLWFQPEELVEY	KSCAQ	2		1099.039132	2196.062664	0.000622848	4	N	124	142
P15532	Parental	PGTIR	GDFCIQVGR	NIIHG	2	C4:+57.021	526.2533986	1050.491197	0.000998612	4	Y	105	114
P15864	Exosome	MSEAA	PAAPAAAPPAEKAPAK	KKAAK	2		729.409705	1456.80381	0.000451244	3	N	5	21
P15864	Exosome	AALKK	ALAAAGYDVEKN	NSRIK	2		611.3096565	1220.603713	0.000451244	17	Y	64	76
P15864	Exosome	AALKK	ALAAAGYDVEK	NNSRI	2		554.2881927	1106.560785	0.000451244	105	Y	64	75
P15864	Exosome	AGVRR	KASGPPVSELITK	AVAAS	2		663.8855313	1325.755463	0.000451244	22	Y	33	46
P15864	Exosome	AGVRR	KASGPPVSELITK	AVAAS	3		442.9262876	1325.755463	0.000451244	54	Y	33	46
P15864	Exosome	ASKER	SGVSLAALK	KALAA	2		423.2587069	844.5018138	0.000823681	48	Y	54	63
P15864	Exosome	GVRRK	ASGPPVSELITK	AVAAS	2		599.8380498	1197.6605	0.000451244	155	Y	34	46
P15864	Exosome	-M	SEAAPAAPAAAPPAEK	APAKK	2		724.8731523	1447.730705	0.000451244	4	N	1	17
P15864	Exosome	LAALK	KALAAAGYDVEK	NNSRI	2		618.3356743	1234.655749	0.000637154	1	Y	63	75
P15864	Exosome	AALKK	ALAAAGYDVEKNNSR	IKLGL	2		789.89769	1577.77978	0.000451244	30	Y	64	79
P15864	Exosome	AALKK	ALAAAGYDVEKNNSR	IKLGL	3		526.9343934	1577.77978	0.000451244	10	Y	64	79
P15864	Exosome	RRKAS	GPPVSELITK	AVAAS	2		520.8034786	1039.591357	0.000637154	1	Y	36	46
P15864	Parental	MSEAA	PAAPAAAPPAEKAPAK	KKAAK	2		729.409705	1456.80381	0.000451244	19	N	5	21
P15864	Parental	AALKK	ALAAAGYDVEKN	NSRIK	2		611.3096565	1220.603713	0.000451244	16	Y	64	76
P15864	Parental	AALKK	ALAAAGYDVEK	NNSRI	2		554.2881927	1106.560785	0.000451244	91	Y	64	75
P15864	Parental	AGVRR	KASGPPVSELITK	AVAAS	2		663.8855313	1325.755463	0.000451244	15	Y	33	46
P15864	Parental	AGVRR	KASGPPVSELITK	AVAAS	3		442.9262876	1325.755463	0.000451244	62	Y	33	46
P15864	Parental	ASKER	SGVSLAALK	KALAA	2		423.2587069	844.5018138	0.001162105	51	Y	54	63
P15864	Parental	GVRRK	ASGPPVSELITK	AVAAS	2		599.8380498	1197.6605	0.000451244	111	Y	34	46
P15864	Parental	-M	SEAAPAAPAAAPPAEK	APAKK	2		724.8731523	1447.730705	0.000823681	2	N	1	17
P15864	Parental	AALKK	ALAAAGYDVEKNNSR	IKLGL	2		789.89769	1577.77978	0.000451244	8	Y	64	79
P16045	Exosome	LNLGK	DSNNLCLHFNPR	FNAHG	2	C6:+57.021	743.8467145	1485.677829	0.001871652	1	N	37	49
P16045	Parental	LNLGK	DSNNLCLHFNPR	FNAHG	2	C6:+57.021	743.8467145	1485.677829	0.000622848	28	N	37	49
P16045	Parental	LNLGK	DSNNLCLHFNPR	FNAHG	3	C6:+57.021	496.233743	1485.677829	0.001463592	6	N	37	49
P16045	Parental	ASDAK	SFVLNLGKDSNNLCLHFNPR	FNAHG	3	C14:+57.021	782.3991894	2344.174168	0.000451244	3	N	29	49
P16045	Parental	ASDAK	SFVLNLGKDSNNLCLHFNPR	FNAHG	4	C14:+57.021	587.0513421	2344.174168	0.001329271	5	N	29	49
P16045	Parental	HFNPR	FNAHGDANTIVCNTK	EDGTW	2	C12:+57.021	831.3889436	1660.762287	0.000451244	15	N	49	64
P16045	Parental	HFNPR	FNAHGDANTIVCNTK	EDGTW	3	C12:+57.021	554.5952291	1660.762287	0.000451244	6	N	49	64
P16045	Parental	VCNTK	EDGTWGTEHREPAFPFQPGSITEVCITFDQADLTIK	LPDGH	3	C25:+57.021	1364.981349	4091.920647	0.000451244	13	N	64	100
P16045	Parental	VCNTK	EDGTWGTEHREPAFPFQPGSITEVCITFDQADLTIK	LPDGH	4	C25:+57.021	1023.987962	4091.920647	0.000451244	5	N	64	100
P16110	Exosome	ADHFK	VAVNDAHLLQYNHR	MKNLR	2		825.4294917	1648.843383	0.000451244	12	N	224	238
P16110	Exosome	ADHFK	VAVNDAHLLQYNHR	MKNLR	3		550.6222611	1648.843383	0.000451244	47	N	224	238
P16110	Exosome	ADHFK	VAVNDAHLLQYNHR	MKNLR	4		413.2186458	1648.843383	0.000451244	58	N	224	238
P16110	Exosome	LDFRR	GNDVAFHFNPR	FNENN	3		425.2077883	1272.599965	0.001329271	2	N	165	176
P16110	Exosome	GKPFK	IQVLVEADHFK	VAVND	2		649.8593165	1297.703033	0.000451244	24	N	213	224
P16110	Exosome	GKPFK	IQVLVEADHFK	VAVND	3		433.5754777	1297.703033	0.000870037	40	N	213	224
P16110	Exosome	VLDFR	RGNDVAFHFNPR	FNENN	3		477.241492	1428.701076	0.000622848	11	N	164	176
P16110	Exosome	GKEER	QSAFPFESGKPFK	IQVLV	2		735.3753308	1468.735062	0.000451244	12	N	200	213
P16110	Exosome	GKEER	QSAFPFESGKPFK	IQVLV	3		490.5861539	1468.735062	0.000451244	29	N	200	213
P16110	Exosome	SGKPF	KIQVLVEADHFK	VAVND	3		476.2737987	1425.797996	0.002296037	2	N	212	224
P16110	Exosome	AAGPY	GVPAGPLTVPYDLPLPGGVMPR	MLITI	2	M20:+15.995	1110.098847	2218.182094	0.002663018	1	N	121	143
P16110	Parental	ADHFK	VAVNDAHLLQYNHR	MKNLR	2		825.4294917	1648.843383	0.000451244	2	N	224	238
P16110	Parental	ADHFK	VAVNDAHLLQYNHR	MKNLR	3		550.6222611	1648.843383	0.000451244	37	N	224	238
P16110	Parental	ADHFK	VAVNDAHLLQYNHR	MKNLR	4		413.2186458	1648.843383	0.000451244	37	N	224	238
P16110	Parental	LDFRR	GNDVAFHFNPR	FNENN	2		637.3077824	1272.599965	0.0007646	4	N	165	176
P16110	Parental	LDFRR	GNDVAFHFNPR	FNENN	3		425.2077883	1272.599965	0.000451244	28	N	165	176
P16110	Parental	GKPFK	IQVLVEADHFK	VAVND	2		649.8593165	1297.703033	0.000451244	5	N	213	224
P16110	Parental	GKPFK	IQVLVEADHFK	VAVND	3		433.5754777	1297.703033	0.001162105	19	N	213	224
P16110	Parental	GKEER	QSAFPFESGKPFKIQVLVEADHFK	VAVND	3		917.1503115	2748.427535	0.000979378	1	N	200	224
P16110	Parental	VLDFR	RGNDVAFHFNPR	FNENN	3		477.241492	1428.701076	0.001264573	6	N	164	176
P16110	Parental	GKEER	QSAFPFESGKPFK	IQVLV	2		735.3753308	1468.735062	0.001229886	3	N	200	213
P16110	Parental	GKEER	QSAFPFESGKPFK	IQVLV	3		490.5861539	1468.735062	0.000451244	18	N	200	213
P16110	Parental	SGKPF	KIQVLVEADHFK	VAVND	3		476.2737987	1425.797996	0.001329271	4	N	212	224
P16125	Exosome	LPKHR	VIGSGCNLDSAR	FRYLM	2	C6:+57.021	624.803984	1247.592368	0.000451244	2	Y	158	170
P16125	Exosome	SILGK	SLADELALVDVLEDK	LKGEM	2		815.4332397	1628.850879	0.000451244	2	N	43	58
P16125	Exosome	PQIVK	YSPDCTIIVVSNPVDILTYVTWK	LSGLP	2	C5:+57.021	1342.188313	2682.361026	0.000451244	3	N	127	150
P16125	Exosome	TLKEK	LIASVADDEAAVPNNK	ITVVG	2		813.9208308	1625.826062	0.001264573	1	N	7	23
P16546	Exosome	ESAFR	ALSSEGKPYVTKEELYQNLTR	EQADY	3		809.4241005	2425.248901	0.000451244	19	N	2414	2435

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P16546	Exosome	WIEEK	NQALNTDNYGHDLASVQALQR	KHEGF	2		1164.570516	2327.125432	0.000451244	18	N	1252	1273
P16546	Exosome	WIEEK	NQALNTDNYGHDLASVQALQR	KHEGF	3		776.7162774	2327.125432	0.000451244	25	N	1252	1273
P16546	Exosome	HDAFR	SSLSSAQADFNQLAELDR	QIKSF	2		976.4719476	1950.928295	0.000451244	10	N	2137	2155
P16546	Exosome	WMAAR	EAFLNTEDKGDSLDSVEALIK	KHEDF	2		1147.574067	2293.132534	0.000451244	26	N	1464	1485
P16546	Exosome	WMAAR	EAFLNTEDKGDSLDSVEALIK	KHEDF	3		765.3853114	2293.132534	0.000451244	4	N	1464	1485
P16546	Exosome	EIDAR	AGTFQAFEQFGQQLLAHGHYASPEIK	EKLDI	3		959.1441082	2874.408925	0.000451244	13	N	1391	1417
P16546	Exosome	EIDAR	AGTFQAFEQFGQQLLAHGHYASPEIK	EKLDI	4		719.6100311	2874.408925	0.000451244	21	N	1391	1417
P16546	Exosome	INGIR	GLVSSDELAKDVTGAEALLER	HQEHR	2		1087.071495	2172.127389	0.000451244	18	N	1359	1380
P16546	Exosome	INGIR	GLVSSDELAKDVTGAEALLER	HQEHR	3		725.0502631	2172.127389	0.000451244	28	N	1359	1380
P16546	Exosome	LAAAR	GQRLEESLEYQQFVANVEEEEAWINEK	MTLVA	3		1089.853388	3266.536764	0.000823681	9	N	1862	1889
P16546	Exosome	VQEEK	IAALQAFADQLIAVDHYAK	GDIAN	3		686.7059909	2057.094573	0.000451244	34	N	1500	1519
P16546	Exosome	TFAKK	ASAFNSWFENAEEDLTDPVR	CNSLE	2		1149.519626	2297.023652	0.000451244	31	N	2099	2119
P16546	Exosome	TFAKK	ASAFNSWFENAEEDLTDPVR	CNSLE	3		766.6823508	2297.023652	0.000451244	1	N	2099	2119
P16546	Exosome	WINEK	MTLVASEDYGDTLAAIQGLLK	KHEAF	2		1105.075192	2208.134784	0.000451244	5	N	1889	1910
P16546	Exosome	VTEMK	ALINADELANDVAGAEALLDR	HQEHK	2		1077.556012	2153.096423	0.000451244	3	N	381	402
P16546	Exosome	VTEMK	ALINADELANDVAGAEALLDR	HQEHK	3		718.7066078	2153.096423	0.000451244	15	N	381	402
P16546	Exosome	QQFNR	NVEDIELWLYEVEGHLASDDYGKDLTNVQNLQK	KHALL	3		1283.294076	3846.858827	0.000451244	8	N	685	718
P16546	Exosome	QQFNR	NVEDIELWLYEVEGHLASDDYGKDLTNVQNLQK	KHALL	4		962.7225067	3846.858827	0.000451244	14	N	685	718
P16546	Exosome	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3		1078.233652	3231.677555	0.000451244	34	N	2017	2047
P16546	Exosome	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	4		808.9271887	3231.677555	0.000451244	6	N	2017	2047
P16546	Exosome	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3	Q1:-17.027	1072.557985	3214.650555	0.000451244	9	N	2017	2047
P16546	Exosome	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3	[0:-17.027	1072.557985	3214.650555	0.000451244	10	N	2017	2047
P16546	Exosome	EGFER	DLAALGDKVNSLGETAQR	LIQSH	2		929.4874007	1856.959201	0.000451244	6	N	1280	1298
P16546	Exosome	TLLTK	QETFDAGLQAFQQEGIANITAL	KDQLL	2		1183.087676	2364.159752	0.000622848	1	N	2017	2039
P16546	Exosome	NLLKK	HQALQAEIAGHEPR	IKAVT	3		519.602978	1555.785534	0.001329271	1	N	825	839
P16546	Exosome	SKHQK	HQAFEAELHANADR	IRGVI	3		536.9224877	1607.744063	0.000451244	6	N	1591	1605
P16546	Exosome	QFNWK	ADVVESWIGEK	ENSLK	2		616.812032	1231.608464	0.000451244	10	Y	1984	1995
P16546	Exosome	AVKAR	LAALADQWQFLVQK	SAEKS	2		815.951737	1629.887874	0.000451244	37	N	1632	1646
P16546	Exosome	QQFSR	DVDEIEAWISEK	LQTAS	2		717.3438933	1432.672187	0.000451244	21	N	1558	1570
P16546	Exosome	NLLKK	HQLLEADISAHEDR	LKDLN	3		545.2696646	1632.785594	0.000698008	6	N	1699	1713
P16546	Exosome	LTFAK	KASAFNSWFENAEEDLTDPVR	CNSLE	2		1213.567108	2425.118615	0.000451244	1	N	2098	2119
P16546	Exosome	LTFAK	KASAFNSWFENAEEDLTDPVR	CNSLE	3		809.3806718	2425.118615	0.000451244	16	N	2098	2119
P16546	Exosome	WISEK	LQTASDESYKDPTNIQSK	HQKHQ	2		1012.992713	2023.969826	0.000451244	10	N	1570	1588
P16546	Exosome	WISEK	LQTASDESYKDPTNIQSK	HQKHQ	3		675.6644086	2023.969826	0.000451244	7	N	1570	1588
P16546	Exosome	EVLQK	KFEEFQTDLAAHEER	VNEVS	3		617.2958794	1848.864238	0.000451244	4	N	189	204
P16546	Exosome	ARGQR	LEESLEYQQFVANVEEEEAWINEK	MTLVA	2		1463.685606	2925.355611	0.000451244	6	N	1865	1889
P16546	Exosome	ARGQR	LEESLEYQQFVANVEEEEAWINEK	MTLVA	3		976.1263371	2925.355611	0.000451244	19	N	1865	1889
P16546	Exosome	KSCLR	SLGYDLPMVEEGEPDPEFEAILDTVDPNR	DGHVS	3	M8:+15.995	1088.503285	3262.486454	0.000451244	4	N	2353	2382
P16546	Exosome	DDFGR	DLASVQALLR	KHEGL	2		543.3198272	1084.624054	0.002145581	1	N	285	295
P16546	Exosome	NWMSK	QEAFLLNEDLGDSLDSVEALLK	KHEDF	2		1210.116099	2418.216598	0.000451244	11	N	485	507
P16546	Exosome	NWMSK	QEAFLLNEDLGDSLDSVEALLK	KHEDF	3		807.0799994	2418.216598	0.000451244	5	N	485	507
P16546	Exosome	SLRMK	QVEELYQSLLELGEK	RKGML	2		889.4650712	1776.914542	0.000451244	6	N	1067	1082
P16546	Exosome	FMLFR	EANELQQWITEK	EAALT	2		744.8706096	1487.725619	0.000451244	5	N	1098	1110
P16546	Exosome	DLKEK	CTELNQAWTSLGK	RADQR	2	C1:+57.021	754.3644058	1506.713212	0.000451244	3	N	1313	1326
P16546	Exosome	DDYGR	DLSSVQTLLTK	QETFD	2		602.8433321	1203.671064	0.001162105	1	N	2006	2017
P16546	Exosome	WITEK	EAALTNEEVGADLEQVEVLQK	KFDDF	2		1143.079517	2284.143433	0.000451244	3	N	1110	1131
P16546	Exosome	QRKAK	LDENSAFLQFNWK	ADVVE	2		806.3942519	1610.772904	0.000451244	12	N	1971	1984
P16546	Exosome	LDTGK	KLSDDNTIGQEEIQQR	LAQFV	3		625.3137101	1872.91773	0.001162105	2	N	1828	1844
P16546	Exosome	QQFNR	NVEDIELWLYEVEGHLASDDYGK	DLTNV	3		898.7576965	2693.249689	0.000622848	2	N	685	708
P16546	Exosome	QSHFR	KVEDLFLTFAK	KASAF	2		655.8718926	1309.728185	0.000451244	5	N	2087	2098
P16546	Exosome	QSHFR	KVEDLFLTFAK	KASAF	3		437.5838617	1309.728185	0.000735798	5	N	2087	2098
P16546	Exosome	AQSCR	QQVAPMDDETGKELVLALYDYQEK	SPREV	3	M6:+15.995	933.7851752	2798.332125	0.000451244	9	N	957	981
P16546	Exosome	NDKLR	QEFAQHANAFHQWIQETR	TYLLD	4		561.0205862	2240.051145	0.002727428	1	N	2207	2225
P16546	Exosome	DGKGR	ELPTAFDYVEFTR	SLFVN	2		794.3886352	1586.76167	0.000451244	2	N	2454	2467
P16546	Exosome	YVDGK	GRELPTAFDYVEFTR	SLFVN	3		600.9692151	1799.884245	0.001463592	5	N	2452	2467
P16546	Exosome	DTGKK	LSDDNTIGQEEIQQR	LAQFV	2		873.4191836	1744.822767	0.000451244	10	N	1829	1844
P16546	Exosome	WIQEK	LQVASDENYKDPTNLQGK	LQKHQ	3		674.0047652	2018.990895	0.000662267	1	N	63	81
P16546	Parental	FMISR	ETENVKSSEEIESAFR	ALSSE	2		927.9399489	1853.864298	0.000451244	4	N	2398	2414
P16546	Parental	FMISR	ETENVKSSEEIESAFR	ALSSE	3		618.9625659	1853.864298	0.000451244	3	N	2398	2414
P16546	Parental	ESAFR	ALSSEGKPYVTKEELYQNLTR	EQADY	2		1213.632251	2425.248901	0.000451244	4	N	2414	2435
P16546	Parental	ESAFR	ALSSEGKPYVTKEELYQNLTR	EQADY	3		809.4241005	2425.248901	0.000451244	32	N	2414	2435
P16546	Parental	WIEEK	NQALNTDNYGHDLASVQALQR	KHEGF	2		1164.570516	2327.125432	0.000451244	37	N	1252	1273
P16546	Parental	WIEEK	NQALNTDNYGHDLASVQALQR	KHEGF	3		776.7162774	2327.125432	0.000451244	41	N	1252	1273
P16546	Parental	HDAFR	SSLSSAQADFNQLAELDR	QIKSF	2		976.4719476	1950.928295	0.000451244	15	N	2137	2155
P16546	Parental	WMAAR	EAFLNTEDKGDSLDSVEALIK	KHEDF	2		1147.574067	2293.132534	0.000451244	26	N	1464	1485

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P16546	Parental	WMAAR	EAFLNTEDKGDSLDSVEALIK	KHEDF	3		765.3853114	2293.132534	0.000451244	10	N	1464	1485
P16546	Parental	EIDAR	AGTFQAFEQFGQQLLAHGHYASPEIK	EKLDI	3		959.1441082	2874.408925	0.000622848	6	N	1391	1417
P16546	Parental	EIDAR	AGTFQAFEQFGQQLLAHGHYASPEIK	EKLDI	4		719.6100311	2874.408925	0.000451244	19	N	1391	1417
P16546	Parental	INGIR	GLVSSDELAKDVTGAEALLER	HQEHR	2		1087.071495	2172.127389	0.000451244	21	N	1359	1380
P16546	Parental	INGIR	GLVSSDELAKDVTGAEALLER	HQEHR	3		725.0502631	2172.127389	0.000451244	29	N	1359	1380
P16546	Parental	LAAAR	GQRLEESLEYQQFVANVEEEEAWINEK	MTLVA	3		1089.853388	3266.536764	0.000451244	23	N	1862	1889
P16546	Parental	VQEEK	IAALQAFADQLIAVDHYAK	GDIAN	3		686.7059909	2057.094573	0.000451244	34	N	1500	1519
P16546	Parental	TFAKK	ASAFNSWFENAEEDLTDPVR	CNSLE	2		1149.519626	2297.023652	0.000451244	28	N	2099	2119
P16546	Parental	FMLFR	EANELQQWITEKEAALTNEEVGADLEQVEVLQK	KFDDF	3		1252.293964	3753.858492	0.000451244	20	N	1098	1131
P16546	Parental	WINEK	MTLVASEDYGDTLAAIQGLLK	KHEAF	2		1105.075192	2208.134784	0.000451244	20	N	1889	1910
P16546	Parental	VTEMK	ALINADELANDVAGAEALLDR	HQEHK	2		1077.556012	2153.096423	0.000451244	21	N	381	402
P16546	Parental	VTEMK	ALINADELANDVAGAEALLDR	HQEHK	3		718.7066078	2153.096423	0.000451244	12	N	381	402
P16546	Parental	QQFNR	NVEDIELWLYEVEGHLASDDYGKDLTNVQNLQK	KHALL	3		1283.294076	3846.858827	0.000451244	17	N	685	718
P16546	Parental	QQFNR	NVEDIELWLYEVEGHLASDDYGKDLTNVQNLQK	KHALL	4		962.7225067	3846.858827	0.000451244	20	N	685	718
P16546	Parental	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3		1078.233652	3231.677555	0.000451244	23	N	2017	2047
P16546	Parental	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3	Q1:-17.027	1072.557985	3214.650555	0.000451244	1	N	2017	2047
P16546	Parental	TLLTK	QETFDAGLQAFQQEGIANITALKDQLLAAK	HIQSK	3	[0:-17.027	1072.557985	3214.650555	0.001839721	1	N	2017	2047
P16546	Parental	EGFER	DLAALGDKVNSLGETAQR	LIQSH	2		929.4874007	1856.959201	0.000451244	10	N	1280	1298
P16546	Parental	TFAKK	ASAFNSWFENAEEDLTDPVRCNSLEEIK	ALREA	3	C21:+57.021	1091.166824	3270.477072	0.000622848	1	N	2099	2127
P16546	Parental	TLLTK	QETFDAGLQAFQQEGIANITAL	KDQLL	2		1183.087676	2364.159752	0.000451244	12	N	2017	2039
P16546	Parental	EKRSK	LGESQTLQQFSRDVDEIEAWISEK	LQTAS	3		936.7949218	2807.361365	0.001463592	1	N	1546	1570
P16546	Parental	NLLKK	HQALQAEIAGHEPR	IKAVT	3		519.602978	1555.785534	0.000451244	4	N	825	839
P16546	Parental	SKHQK	HQAFEAELHANADR	IRGVI	3		536.9224877	1607.744063	0.000451244	2	N	1591	1605
P16546	Parental	QFNWK	ADVVESWIGEK	ENSLK	2		616.812032	1231.608464	0.000622848	2	Y	1984	1995
P16546	Parental	AVKAR	LAALADQWQFLVQK	SAEKS	2		815.951737	1629.887874	0.000451244	18	N	1632	1646
P16546	Parental	QQFSR	DVDEIEAWISEK	LQTAS	2		717.3438933	1432.672187	0.000451244	17	N	1558	1570
P16546	Parental	NLLKK	HQLLEADISAHEDR	LKDLN	3		545.2696646	1632.785594	0.000451244	3	N	1699	1713
P16546	Parental	WISEK	LQTASDESYKDPTNIQSK	HQKHQ	2		1012.992713	2023.969826	0.000451244	10	N	1570	1588
P16546	Parental	WISEK	LQTASDESYKDPTNIQSK	HQKHQ	3		675.6644086	2023.969826	0.000451244	2	N	1570	1588
P16546	Parental	EVLQK	KFEEFQTDLAAHEER	VNEVS	2		925.4399191	1848.864238	0.000451244	2	N	189	204
P16546	Parental	EVLQK	KFEEFQTDLAAHEER	VNEVS	3		617.2958794	1848.864238	0.000451244	4	N	189	204
P16546	Parental	ARGQR	LEESLEYQQFVANVEEEEAWINEK	MTLVA	2		1463.685606	2925.355611	0.000451244	19	N	1865	1889
P16546	Parental	ARGQR	LEESLEYQQFVANVEEEEAWINEK	MTLVA	3		976.1263371	2925.355611	0.000451244	23	N	1865	1889
P16546	Parental	DDFGR	DLASVQALLR	KHEGL	2		543.3198272	1084.624054	0.001162105	2	N	285	295
P16546	Parental	NWMSK	QEAFLLNEDLGDSLDSVEALLK	KHEDF	2		1210.116099	2418.216598	0.000451244	23	N	485	507
P16546	Parental	NWMSK	QEAFLLNEDLGDSLDSVEALLK	KHEDF	3		807.0799994	2418.216598	0.000451244	2	N	485	507
P16546	Parental	NWMSK	QEAFLLNEDLGDSLDSVEALLK	KHEDF	2	Q1:-17.027	1201.602599	2401.189598	0.001763695	1	N	485	507
P16546	Parental	SLRMK	QVEELYQSLLELGEK	RKGML	2		889.4650712	1776.914542	0.000451244	12	N	1067	1082
P16546	Parental	SLRMK	QVEELYQSLLELGEK	RKGML	3		593.3126475	1776.914542	0.002296037	1	N	1067	1082
P16546	Parental	SLRMK	QVEELYQSLLELGEK	RKGML	2	[0:-17.027	880.9515712	1759.887542	0.000451244	1	N	1067	1082
P16546	Parental	FMLFR	EANELQQWITEK	EAALT	2		744.8706096	1487.725619	0.000451244	7	N	1098	1110
P16546	Parental	DLKEK	CTELNQAWTSLGK	RADQR	2	[0:-17.027,C1:+57.021	745.8509058	1489.686212	0.00307782	1	N	1313	1326
P16546	Parental	DDYGR	DLSSVQTLLTK	QETFD	2		602.8433321	1203.671064	0.000451244	11	N	2006	2017
P16546	Parental	KASAF	NSWFENAEEDLTDPVR	CNSLE	2		961.432291	1920.848982	0.000451244	30	N	2103	2119
P16546	Parental	KASAF	NSWFENAEEDLTDPVRCNSLEEIK	ALREA	3	C17:+57.021	965.7752672	2894.302401	0.000451244	2	N	2103	2127
P16546	Parental	DDYGR	DLSSVQTLLTKQETFDAGLQAFQQEGIANITAL	KDQLL	3		1184.281219	3549.820256	0.000451244	1	N	2006	2039
P16546	Parental	EKRSK	LGESQTLQQFSR	DVDEI	2		697.3576694	1392.699739	0.000451244	1	N	1546	1558
P16546	Parental	WITEK	EAALTNEEVGADLEQVEVLQK	KFDDF	2		1143.079517	2284.143433	0.000451244	31	N	1110	1131
P16546	Parental	WITEK	EAALTNEEVGADLEQVEVLQK	KFDDF	3		762.3889444	2284.143433	0.000451244	2	N	1110	1131
P16546	Parental	QRKAK	LDENSAFLQFNWK	ADVVE	2		806.3942519	1610.772904	0.000451244	11	N	1971	1984
P16546	Parental	LDTGK	KLSDDNTIGQEEIQQR	LAQFV	3		625.3137101	1872.91773	0.001229886	5	N	1828	1844
P16546	Parental	QFAAK	LIQEQHPEEELIK	TKQDE	2		803.4282917	1604.840983	0.000451244	5	N	214	227
P16546	Parental	QFAAK	LIQEQHPEEELIK	TKQDE	3		535.9547945	1604.840983	0.000622848	2	N	214	227
P16546	Parental	EDKVK	ALCAEADRLQQSHPLSASQIQVK	REELI	4	C3:+57.021	638.3331885	2549.301554	0.002663018	1	N	312	335
P16546	Parental	EDSFK	SADESGQALLAASHYASDEVREK	LSILS	4		609.2930019	2433.140808	0.000823681	2	N	418	441
P16546	Parental	DELAK	DVTGAEALLER	HQEHR	2		587.3096565	1172.603713	0.000451244	7	N	1369	1380
P16546	Parental	EDSFK	SADESGQALLAASHYASDEVR	EKLSI	3		726.3422171	2176.003251	0.000451244	6	N	418	439
P16546	Parental	AMHRR	AQLADSFHLQQFFR	DSDEL	2		854.4342427	1706.852885	0.000451244	3	N	566	580
P16546	Parental	FAKKA	SAFNSWFENAEEDLTDPVR	CNSLE	2		1114.001069	2225.986538	0.000451244	8	N	2100	2119
P16546	Parental	QQFNR	NVEDIELWLYEVEGHLASDDYGK	DLTNV	3		898.7576965	2693.249689	0.000451244	8	N	685	708
P16546	Parental	QRFHR	DADETKEWIEEK	NQALN	2		746.8442575	1491.672915	0.000451244	2	N	1240	1252
P16546	Parental	QQFFR	DSDELKSWVNEK	MKTAT	2		725.3469673	1448.678335	0.0007646	1	N	580	592
P16546	Parental	QIQVK	REELITNWEQIR	TLAAE	2		793.9184255	1585.821251	0.002813207	1	N	335	347
P16546	Parental	QSASR	ENLLEEQGSIALR	QGQID	2		736.3917092	1470.767818	0.000451244	11	N	1032	1045
P16546	Parental	QSHFR	KVEDLFLTFAK	KASAF	3		437.5838617	1309.728185	0.00091018	5	N	2087	2098

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P16546	Parental	AQSCR	QQVAPMDDETGKELVLALYDYQEK	SPREV	3	M6:+15.995	933.7851752	2798.332125	0.000451244	3	N	957	981
P16546	Parental	TNRGK	DLIGVQNLLK	KHQAL	2		556.8378528	1111.660106	0.002019181	1	N	814	824
P16546	Parental	NDKLR	QEFAQHANAFHQWIQETR	TYLLD	3		747.6915149	2240.051145	0.001871652	3	N	2207	2225
P16546	Parental	QRFNR	DVDETIGWIK	EKEQL	2		588.3013001	1174.587	0.001591523	1	N	262	272
P16546	Parental	GKVQK	HQAFEAELSANQSR	IDALE	3		529.9223763	1586.743729	0.002813207	1	N	613	627
P16546	Parental	DGKGR	ELPTAFDYVEFTR	SLFVN	2		794.3886352	1586.76167	0.000451244	3	N	2454	2467
P16546	Parental	NTGIK	DFDFWLSEVEALLASEDYGKDLASVNNLLK	KHQLL	3		1134.564956	3400.671467	0.000662267	4	N	1668	1698
P16546	Parental	TIQAR	QFQDAGHFDAENIKK	KQEAL	4		437.715936	1746.832544	0.000451244	1	N	742	757
P16546	Parental	QDLED	SLQAQQYFADANEAESWMREK	EPIVG	2	M18:+15.995	1259.569368	2517.123135	0.002212458	1	N	888	909
P16675	Exosome	SRNEA	APDQDEIDCLPGLAK	QPSFR	2	C9:+57.021	821.3933603	1640.771121	0.000622848	2	N	23	38
P16675	Exosome	CAQNK	CNFYDNKDPECVNNLLEVSR	IVGKS	3	C1:+57.021,C11:+57.021	829.3742266	2485.09928	0.000451244	16	N	240	260
P16675	Exosome	RIVGK	SGLNIYNLYAPCAGGVPGR	HRYED	2	C12:+57.021	989.9941073	1977.972615	0.000451244	17	N	264	283
P16675	Parental	SRNEA	APDQDEIDCLPGLAK	QPSFR	2	C9:+57.021	821.3933603	1640.771121	0.000451244	2	N	23	38
P16675	Parental	CAQNK	CNFYDNKDPECVNNLLEVSR	IVGKS	2	C1:+39.994,C11:+57.021	1235.04394	2468.07228	0.000451244	5	N	240	260
P16675	Parental	CAQNK	CNFYDNKDPECVNNLLEVSR	IVGKS	3	C1:+57.021,C11:+57.021	829.3742266	2485.09928	0.000451244	20	N	240	260
P16675	Parental	CAQNK	CNFYDNKDPECVNNLLEVSR	IVGKS	2	[0:-	1235.04394	2468.07228	0.001591523	3	N	240	260
P16675	Parental	ASDSK	HFHYWFVESQNDPK	NSPVV	3		611.9501549	1832.827065	0.001591523	6	N	55	69
P16675	Parental	MEVQR	RPWLVDYGESGEQVAGFVK	ECSHI	3		713.0291336	2136.064001	0.001463592	1	N	417	436
P16858	Exosome	WRDGR	GAAQNIIPASTGAAK	AVGKV	2		685.3758621	1368.736124	0.000451244	29	N	198	213
P16858	Exosome	DNSLK	IVSNASCTTNCLAPLAK	VIHDN	2	C7:+57.021,C11:+57.021	910.4557377	1818.895875	0.000451244	155	N	143	160
P16858	Exosome	DNSLK	IVSNASCTTNCLAPLAK	VIHDN	3	C7:+57.021,C11:+57.021	607.3064251	1818.895875	0.000823681	7	N	143	160
P16858	Exosome	GMAFR	VPTPNVSVVDLTCRLEKPAK	YDDIK	4	C13:+57.021	556.5600056	2222.208822	0.000451244	15	N	232	252
P16858	Exosome	GMAFR	VPTPNVSVVDLTCR	LEKPA	2	C13:+57.021	778.9089805	1555.802361	0.000451244	106	N	232	246
P16858	Exosome	GMAFR	VPTPNVSVVDLTCR	LEKPA	3	C13:+57.021	519.608587	1555.802361	0.000451244	13	N	232	246
P16858	Exosome	DNFVK	LISWYDNEYGYSNR	VVDLM	2		890.4028052	1778.79001	0.000451244	103	N	307	321
P16858	Exosome	GILGY	TEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C8:+57.021	1182.862352	3545.563655	0.000451244	54	N	274	307
P16858	Exosome	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C13:+57.021	1350.62048	4048.838039	0.000451244	1147	N	269	307
P16858	Exosome	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	4	C13:+57.021	1013.21731	4048.838039	0.000451244	34	N	269	307
P16858	Exosome	PTNIK	WGEAGAEYVVESTGVFTTMEK	AGAHL	2		1146.030981	2290.046363	0.000451244	20	N	84	105
P16858	Exosome	PTNIK	WGEAGAEYVVESTGVFTTMEK	AGAHL	3		764.3565876	2290.046363	0.000451244	5	N	84	105
P16858	Exosome	PTNIK	WGEAGAEYVVESTGVFTTMEK	AGAHL	2	M19:+15.995	1154.028481	2306.041363	0.000451244	22	N	84	105
P16858	Exosome	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	3		865.7920187	2594.352656	0.000451244	23	N	160	184
P16858	Exosome	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	4		649.5959641	2594.352656	0.000451244	28	N	160	184
P16858	Exosome	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	3	M13:+15.995	871.1236854	2610.347656	0.000451244	3	N	160	184
P16858	Exosome	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	4	M13:+15.995	653.5947141	2610.347656	0.000451244	10	N	160	184
P16858	Exosome	DNSLK	IVSNASCTTNCLAPLAKV	IHDNF	2	C7:+57.021,C11:+57.021	959.9899447	1917.964289	0.001463592	2	N	143	161
P16858	Exosome	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	2		1148.655332	2295.295064	0.000622848	10	N	64	84
P16858	Exosome	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	3		766.1061546	2295.295064	0.000451244	15	N	64	84
P16858	Exosome	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	4		574.8315659	2295.295064	0.000451244	18	N	64	84
P16858	Exosome	TGMAF	RVPTPNVSVVDLTCR	LEKPA	2	C14:+57.021	856.9595361	1711.903472	0.000451244	22	N	231	246
P16858	Exosome	TGMAF	RVPTPNVSVVDLTCR	LEKPA	3	C14:+57.021	571.6422907	1711.903472	0.000451244	42	N	231	246
P16858	Exosome	AENGK	LVINGKPITIFQER	DPTNI	2		814.4806616	1626.945723	0.000622848	11	N	64	78
P16858	Exosome	AENGK	LVINGKPITIFQER	DPTNI	3		543.3230411	1626.945723	0.000451244	43	N	64	78
P16858	Exosome	EGPLK	GILGYTEDQVVSCDFNSNSHSSTF	DAGAG	2	C13:+57.021	1332.579855	2663.14411	0.000451244	20	N	269	293
P16858	Exosome	ICSGK	VEIVAINDPF	IDLNY	2		558.8009359	1115.586272	0.000451244	10	N	25	35
P16858	Exosome	DNFVK	LISWYDNEYGYSNRV	VDLMA	2		939.9370122	1877.858424	0.002663018	1	N	307	322
P16858	Exosome	ICSGK	VEIVAINDPFIDLN	YMVYM	2		786.4199353	1570.824271	0.001352548	6	N	25	39
P16858	Exosome	FRVPT	PNVSVVDLTCR	LEKPA	2	C10:+57.021	630.3245523	1258.633505	0.000622848	3	N	235	246
P16858	Exosome	AENGK	LVINGKPITIF	QERDP	2		607.8795207	1213.743441	0.001162105	8	N	64	75
P16858	Exosome	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIAL	NDNFV	3	C13:+57.021	1111.505617	3331.49345	0.000735798	8	N	269	301
P16858	Exosome	DNFVK	LISWYDNEYGY	SNRVV	2		711.8147717	1421.613943	0.000451244	3	N	307	318
P16858	Exosome	ICSGK	VEIVAINDPFIDLNYMVYMFQYDSTHGK	FNGTV	3		1108.198674	3321.572623	0.000451244	4	N	25	53
P16858	Exosome	HSSTF	DAGAGIALNDNFVK	LISWY	2		702.8600449	1403.70449	0.001654178	1	N	293	307
P16858	Exosome	LAKVI	HDNFGIVEGLMTTVHAITATQK	TVDGP	3		795.074526	2382.200178	0.000451244	1	N	162	184
P16858	Exosome	EAGAE	YVVESTGVFTTMEK	AGAHL	2	M12:+15.995	803.887654	1605.759708	0.001591523	2	N	91	105
P16858	Exosome	NFVKL	ISWYDNEYGYSNR	VVDLM	2		833.8607732	1665.705946	0.000622848	2	N	308	321
P16858	Exosome	EGPLK	GILGYTEDQVVSCDFNSNSH	SSTFD	2	C13:+57.021	1121.48978	2240.96396	0.001763695	2	N	269	289
P16858	Exosome	KGGAK	RVIISAPSADAPMFV	MGVNH	2		787.4244983	1572.833397	0.000823681	1	N	115	130
P16858	Exosome	AFRVP	TPNVSVVDLTCR	LEKPA	2	C11:+57.021	680.8483916	1359.681183	0.000622848	3	N	234	246
P16858	Exosome	ICSGK	VEIVAINDPFIDLNYMVY	MFQYD	2	M16:+15.995	1072.535214	2143.054828	0.000451244	2	N	25	43
P16858	Parental	WRDGR	GAAQNIIPASTGAAK	AVGKV	2		685.3758621	1368.736124	0.000451244	50	N	198	213
P16858	Parental	DNSLK	IVSNASCTTNCLAPLAK	VIHDN	2	C7:+57.021,C11:+57.021	910.4557377	1818.895875	0.000451244	31	N	143	160
P16858	Parental	DNSLK	IVSNASCTTNCLAPLAK	VIHDN	3	C7:+57.021,C11:+57.021	607.3064251	1818.895875	0.001463592	2	N	143	160
P16858	Parental	GMAFR	VPTPNVSVVDLTCRLEKPAK	YDDIK	4	C13:+57.021	556.5600056	2222.208822	0.000451244	10	N	232	252
P16858	Parental	GMAFR	VPTPNVSVVDLTCR	LEKPA	2	C13:+57.021	778.9089805	1555.802361	0.000451244	56	N	232	246

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P16858	Parental	GMAFR	VPTPNVSVVDLTCR	LEKPA	3	C13:+57.021	519.608587	1555.802361	0.000622848	17	N	232	246
P16858	Parental	DNFVK	LISWYDNEYGYSNR	VVDLM	2		890.4028052	1778.79001	0.000451244	76	N	307	321
P16858	Parental	GILGY	TEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C8:+57.021	1182.862352	3545.563655	0.000451244	52	N	274	307
P16858	Parental	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	3	C13:+57.021	1350.62048	4048.838039	0.000451244	1354	N	269	307
P16858	Parental	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	LISWY	4	C13:+57.021	1013.21731	4048.838039	0.000451244	71	N	269	307
P16858	Parental	PTNIK	WGEAGAEYVVESTGVFTTMEK	AGAHL	2		1146.030981	2290.046363	0.000451244	13	N	84	105
P16858	Parental	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	2		1298.184128	2594.352656	0.000451244	4	N	160	184
P16858	Parental	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	3		865.7920187	2594.352656	0.000451244	16	N	160	184
P16858	Parental	APLAK	VIHDNFGIVEGLMTTVHAITATQK	TVDGP	4		649.5959641	2594.352656	0.000451244	34	N	160	184
P16858	Parental	DNSLK	IVSNASCTTNCLAPLAKV	IHDNF	2	C7:+57.021,C11:+57.021	959.9899447	1917.964289	0.000451244	6	N	143	161
P16858	Parental	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	2		1148.655332	2295.295064	0.000451244	8	N	64	84
P16858	Parental	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	3		766.1061546	2295.295064	0.000451244	11	N	64	84
P16858	Parental	AENGK	LVINGKPITIFQERDPTNIK	WGEAG	4		574.8315659	2295.295064	0.000451244	8	N	64	84
P16858	Parental	TGMAF	RVPTPNVSVVDLTCR	LEKPA	2	C14:+57.021	856.9595361	1711.903472	0.000451244	21	N	231	246
P16858	Parental	TGMAF	RVPTPNVSVVDLTCR	LEKPA	3	C14:+57.021	571.6422907	1711.903472	0.000451244	36	N	231	246
P16858	Parental	DNFVK	LISWYDNEYGYSNRVV	DLMAY	2		989.4712192	1976.926838	0.000698008	1	N	307	323
P16858	Parental	AENGK	LVINGKPITIFQER	DPTNI	3		543.3230411	1626.945723	0.000451244	11	N	64	78
P16858	Parental	EGPLK	GILGYTEDQVVSCDFNSNSHSSTF	DAGAG	2	C13:+57.021	1332.579855	2663.14411	0.000451244	15	N	269	293
P16858	Parental	EGPLK	GILGYTEDQVVSCDFNSNSHSSTF	DAGAG	3	C13:+57.021	888.7225032	2663.14411	0.001943752	1	N	269	293
P16858	Parental	ICSGK	VEIVAINDPF	IDLNY	2		558.8009359	1115.586272	0.000622848	12	N	25	35
P16858	Parental	ICSGK	VEIVAINDPFIDLN	YMVYM	2		786.4199353	1570.824271	0.000451244	6	N	25	39
P16858	Parental	FRVPT	PNVSVVDLTCR	LEKPA	2	C10:+57.021	630.3245523	1258.633505	0.001463592	3	N	235	246
P16858	Parental	AENGK	LVINGKPITIF	QERDP	2		607.8795207	1213.743441	0.000622848	10	N	64	75
P16858	Parental	APLAK	VIHDNFGIVEGLMTTVHAITATQKTVDGPSGK	LWRDG	4		834.9373938	3335.718375	0.000451244	2	N	160	192
P16858	Parental	EGPLK	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIAL	NDNFV	3	C13:+57.021	1111.505617	3331.49345	0.000451244	28	N	269	301
P16858	Parental	RLVTR	AAICSGKVEIVAINDPFIDLNYMVY	MFQYD	3	C4:+57.021	939.1400535	2814.396761	0.000823681	1	N	18	43
P16858	Parental	VNHEK	YDNSLKIVSNASCTTNCLAPLAK	VIHDN	2	C13:+57.021,C17:+57.021	1270.627865	2539.24013	0.000451244	3	N	137	160
P16858	Parental	KKVVK	QASEGPLKGILGYTEDQVVSCDFNSNSHSSTFDAGAGIAL	NDNFV	3	C21:+57.021	1381.646806	4141.917018	0.001329271	2	N	261	301
P16858	Parental	SLKIV	SNASCTTNCLAPLAK	VIHDN	2	C5:+57.021,C9:+57.021	804.3794986	1606.743397	0.000451244	3	N	145	160
P16858	Parental	ELNGK	LTGMAFRVPTPNVSVVDLTCR	LEKPA	3	C20:+57.021	778.4086974	2332.202692	0.002727428	1	N	225	246
P16858	Parental	RLVTR	AAICSGKVEIVAINDPFIDLNY	MVYMF	2	C4:+57.021	1211.620066	2421.224532	0.001763695	1	N	18	40
P16858	Parental	DNFVK	LISWYDNEYGY	SNRVV	2		711.8147717	1421.613943	0.000451244	2	N	307	318
P16858	Parental	NFVKL	ISWYDNEYGYSNR	VVDLM	2		833.8607732	1665.705946	0.000451244	5	N	308	321
P16858	Parental	ICSGK	VEIVAINDPFIDLNY	MVYMF	2		867.9515997	1733.887599	0.001463592	1	N	25	40
P16879	Exosome	GAIPR	AEVAELLTHSGDFLVR	ESQGK	3		586.3129818	1755.915545	0.000451244	2	N	467	483
P16879	Exosome	DNLYR	LEGDGFPSIPLLITHLLSSQQPLTK	KSGVV	3		902.1693718	2703.484715	0.000622848	1	N	514	539
P16879	Parental	MAGIL	KDILQEYLEISSLVQDDVASIHR	ELAAA	4		668.6044144	2670.386458	0.000622848	4	N	223	246
P16879	Parental	GAIPR	AEVAELLTHSGDFLVR	ESQGK	3		586.3129818	1755.915545	0.000622848	5	N	467	483
P16879	Parental	DNLYR	LEGDGFPSIPLLITHLLSSQQPLTK	KSGVV	3		902.1693718	2703.484715	0.002453667	1	N	514	539
P17047	Exosome	NSQIK	YLDFIFAVK	NEKRF	2		558.3109395	1114.606279	0.001329271	4	N	285	294
P17047	Parental	NSQIK	YLDFIFAVK	NEKRF	2		558.3109395	1114.606279	0.000451244	5	N	285	294
P17047	Parental	LSVSR	AFQINTFNLK	VQPFN	2		598.3276522	1194.639704	0.001699387	2	N	346	356
P17047	Parental	NQTNK	TITIAVPDKATHDGSSCGDDR	NSAKI	3	C17:+57.021	739.3468195	2215.017058	0.001229886	2	N	58	79
P17047	Parental	VHTVK	NPENFKVPLDVIFK	CNSVL	3		553.9755299	1658.90319	0.000451244	8	N	134	148
P17182	Exosome	CLLLK	VNQIGSVTESLQACK	LAQSN	2	C14:+57.021	817.4146271	1632.813654	0.000451244	65	N	343	358
P17182	Exosome	IFDSR	GNPTVEVDLYTAK	GLFRA	2		703.8622532	1405.708906	0.000451244	44	N	15	28
P17182	Exosome	GAWQK	FTASAGIQVVGDDLTVTNPKR	IAKAA	2		1095.082197	2188.148793	0.000451244	63	N	306	327
P17182	Exosome	GAWQK	FTASAGIQVVGDDLTVTNPKR	IAKAA	3		730.3907311	2188.148793	0.000451244	57	N	306	327
P17182	Exosome	GAWQK	FTASAGIQVVGDDLTVTNPK	RIAKA	2		1017.031641	2032.047682	0.000451244	280	N	306	326
P17182	Exosome	GAWQK	FTASAGIQVVGDDLTVTNPK	RIAKA	3		678.3570274	2032.047682	0.000451244	26	N	306	326
P17182	Exosome	KGLFR	AAVPSGASTGIYEALELR	DNDKT	2		902.9761374	1803.936675	0.000451244	55	N	32	50
P17182	Exosome	KGLFR	AAVPSGASTGIYEALELR	DNDKT	3		602.320025	1803.936675	0.000451244	14	N	32	50
P17182	Exosome	ENKSK	FGANAILGVSLAVCK	AGAVE	2	C14:+57.021	760.4189841	1518.822368	0.000451244	638	N	105	120
P17182	Exosome	ENKSK	FGANAILGVSLAVCK	AGAVE	3	C14:+57.021	507.2819227	1518.822368	0.000451244	12	N	105	120
P17182	Exosome	VPLYR	HIADLAGNPEVILPVPAFNVINGGSHAGNK	LAMQE	3		1007.868867	3020.583201	0.000451244	126	N	132	162
P17182	Exosome	VPLYR	HIADLAGNPEVILPVPAFNVINGGSHAGNK	LAMQE	4		756.1536002	3020.583201	0.000451244	70	N	132	162
P17182	Exosome	EKYGK	DATNVGDEGGFAPNILENKEALELLK	TAIAK	2		1379.201226	2756.386852	0.000451244	31	N	202	228
P17182	Exosome	EKYGK	DATNVGDEGGFAPNILENKEALELLK	TAIAK	3		919.8034173	2756.386852	0.000451244	49	N	202	228
P17182	Exosome	LADLY	KSFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		1033.489721	3097.445764	0.000451244	30	N	280	306
P17182	Exosome	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	2		1485.6832	2969.350801	0.000451244	36	N	281	306
P17182	Exosome	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		990.7914002	2969.350801	0.000451244	100	N	281	306
P17182	Exosome	MVSHR	SGETEDTFIADLVVGLCTGQIK	TGAPC	2	C17:+57.021	1177.083513	2352.151427	0.000451244	449	N	372	394
P17182	Exosome	MVSHR	SGETEDTFIADLVVGLCTGQIK	TGAPC	3	C17:+57.021	785.0582756	2352.151427	0.000451244	299	N	372	394
P17182	Exosome	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQKF	TASAG	3		1039.814205	3116.419215	0.000622848	12	N	281	307
P17182	Exosome	TAIAK	AGYTDQVVIGMDVAASEFYR	SGKYD	2		1096.520584	2191.025568	0.000451244	17	N	233	253

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P17182	Exosome	TAIAK	AGYTDQVVIGMDVAASEFYR	SGKYD	3		731.3496559	2191.025568	0.000451244	5	N	233	253
P17182	Exosome	TAIAK	AGYTDQVVIGMDVAASEFYR	SGKYD	2	M11:+15.995	1104.518084	2207.020568	0.000451244	16	N	233	253
P17182	Exosome	VPLYR	HIADLAGNPEVILPVPAFNV	INGGS	2		1043.570736	2085.125873	0.000451244	21	N	132	152
P17182	Exosome	VSIED	PFDQDDWGAWQK	FTASA	2		746.8287447	1491.641889	0.000823681	4	N	294	306
P17182	Exosome	VIKEK	YGKDATNVGDEGGFAPNILENK	EALEL	2		1155.056376	2308.097152	0.000451244	34	N	199	221
P17182	Exosome	VIKEK	YGKDATNVGDEGGFAPNILENK	EALEL	3		770.3735172	2308.097152	0.000451244	15	N	199	221
P17182	Exosome	QKFTA	SAGIQVVGDDLTVTNPK	RIAKA	2		857.4550378	1712.894476	0.000451244	10	N	309	326
P17182	Exosome	AWQKF	TASAGIQVVGDDLTVTNPK	RIAKA	2		943.497434	1884.979268	0.000451244	35	N	307	326
P17182	Exosome	EKYGK	DATNVGDEGGFAPNILENK	EALEL	2		980.9664981	1959.917396	0.000451244	183	N	202	221
P17182	Exosome	EKYGK	DATNVGDEGGFAPNILENK	EALEL	3		654.3135987	1959.917396	0.000451244	13	N	202	221
P17182	Exosome	FRAAV	PSGASTGIYEALELR	DNDKT	2		782.4048166	1562.794033	0.000823681	1	N	35	50
P17182	Exosome	DDPSR	YITPDQLADLYK	SFVQN	2		720.3749965	1438.734393	0.000451244	25	N	269	281
P17182	Exosome	YRSGK	YDLDFKSPDDPSR	YITPD	2		777.8576992	1553.699798	0.000451244	17	N	256	269
P17182	Exosome	YRSGK	YDLDFKSPDDPSR	YITPD	3		518.9077328	1553.699798	0.000451244	3	N	256	269
P17182	Exosome	PSRYI	TPDQLADLYK	SFVQN	2		582.3013001	1162.587	0.001654178	2	N	271	281
P17182	Exosome	VPLYR	HIADLAGNPEVILPVPAFNVI	NGGSH	2		1100.112768	2198.209937	0.000622848	6	N	132	153
P17182	Exosome	AAVPS	GASTGIYEALELR	DNDKT	2		690.3624204	1378.709241	0.00091018	2	N	37	50
P17182	Exosome	YPVVS	IEDPFDQDDWGAWQK	FTASA	2		925.4055449	1848.79549	0.000622848	6	N	291	306
P17182	Exosome	QNYPV	VSIEDPFDQDDWGAWQK	FTASA	2		1018.455766	2034.895932	0.000451244	18	N	289	306
P17182	Exosome	NYPVV	SIEDPFDQDDWGAWQK	FTASA	2		968.9215592	1935.827518	0.000451244	3	N	290	306
P17182	Exosome	VVSIE	DPFDQDDWGAWQK	FTASA	2		804.3422163	1606.668833	0.000451244	1	N	293	306
P17182	Exosome	AWQKF	TASAGIQVVGDDLTVTNPKR	IAKAA	2		1021.54799	2041.080379	0.000662267	9	N	307	327
P17182	Exosome	AWQKF	TASAGIQVVGDDLTVTNPKR	IAKAA	3		681.3679264	2041.080379	0.000451244	10	N	307	327
P17182	Exosome	HAGNK	LAMQEFMILPVGASSFR	EAMRI	2		948.9896801	1895.96376	0.000451244	7	N	162	179
P17182	Exosome	HAGNK	LAMQEFMILPVGASSFR	EAMRI	2	M3:+15.995	956.9871801	1911.95876	0.000451244	3	N	162	179
P17182	Exosome	HAGNK	LAMQEFMILPVGASSFR	EAMRI	2	M3:+15.995,M7:+15.995	964.9846801	1927.95376	0.000451244	4	N	162	179
P17182	Exosome	KSFVQ	NYPVVSIEDPFDQDDWGAWQK	FTASA	2		1255.069483	2508.123366	0.001352548	1	N	285	306
P17182	Exosome	AKGLF	RAAVPSGASTGIYEALELR	DNDKT	3		654.3537287	1960.037786	0.000823681	4	N	31	50
P17182	Exosome	GTENK	SKFGANAILGVSLAVCK	AGAVE	3	C16:+57.021	578.9909199	1733.94936	0.000979378	10	N	103	120
P17182	Exosome	TEDTF	IADLVVGLCTGQIK	TGAPC	2	C9:+57.021	743.9188169	1485.822034	0.000451244	2	N	380	394
P17182	Exosome	PEVIL	PVPAFNVINGGSHAGNK	LAMQE	2		839.9371496	1677.858699	0.001162105	2	N	145	162
P17182	Exosome	DDPSR	YITPDQLADLY	KSFVQ	2		656.3275149	1310.63943	0.000451244	11	N	269	280
P17182	Exosome	VQNYP	VVSIEDPFDQDDWGAWQK	FTASA	2		1067.989973	2133.964346	0.000451244	5	N	288	306
P17182	Exosome	KGLFR	AAVPSGASTGIYEALEL	RDNDK	2		824.9255819	1647.835564	0.000451244	10	N	32	49
P17182	Exosome	LYKSF	VQNYPVVSIEDPFDQDDWGAWQK	FTASA	2		1368.632979	2735.250358	0.000451244	2	N	283	306
P17182	Exosome	EKYGK	DATNVGDEGGFAPNILENKEALELL	KTAIA	2		1315.153744	2628.291889	0.001871652	1	N	202	227
P17182	Exosome	VPLYR	HIADLAGNPEVILPVPAF	NVING	2		937.0150656	1872.014531	0.000823681	3	N	132	150
P17182	Exosome	DSRGN	PTVEVDLYTAK	GLFRA	2		618.3300576	1234.644515	0.001839721	1	N	17	28
P17182	Parental	CLLLK	VNQIGSVTESLQACK	LAQSN	2	C14:+57.021	817.4146271	1632.813654	0.000451244	80	N	343	358
P17182	Parental	IFDSR	GNPTVEVDLYTAK	GLFRA	2		703.8622532	1405.708906	0.000451244	35	N	15	28
P17182	Parental	GAWQK	FTASAGIQVVGDDLTVTNPKR	IAKAA	2		1095.082197	2188.148793	0.000451244	28	N	306	327
P17182	Parental	GAWQK	FTASAGIQVVGDDLTVTNPKR	IAKAA	3		730.3907311	2188.148793	0.000451244	32	N	306	327
P17182	Parental	RIHAR	EIFDSRGNPTVEVDLYTAK	GLFRA	2		1077.53983	2153.064061	0.000451244	8	N	9	28
P17182	Parental	RIHAR	EIFDSRGNPTVEVDLYTAK	GLFRA	3		718.6958202	2153.064061	0.000451244	8	N	9	28
P17182	Parental	GAWQK	FTASAGIQVVGDDLTVTNPK	RIAKA	2		1017.031641	2032.047682	0.000451244	145	N	306	326
P17182	Parental	GAWQK	FTASAGIQVVGDDLTVTNPK	RIAKA	3		678.3570274	2032.047682	0.000698008	2	N	306	326
P17182	Parental	DLDFK	SPDDPSRYITPDQLADLYK	SFVQN	2		1097.537288	2193.058975	0.000451244	7	N	262	281
P17182	Parental	DLDFK	SPDDPSRYITPDQLADLYK	SFVQN	3		732.0274584	2193.058975	0.000451244	7	N	262	281
P17182	Parental	KGLFR	AAVPSGASTGIYEALELR	DNDKT	2		902.9761374	1803.936675	0.000451244	44	N	32	50
P17182	Parental	KGLFR	AAVPSGASTGIYEALELR	DNDKT	3		602.320025	1803.936675	0.000451244	11	N	32	50
P17182	Parental	ENKSK	FGANAILGVSLAVCK	AGAVE	2	C14:+57.021	760.4189841	1518.822368	0.000451244	347	N	105	120
P17182	Parental	ENKSK	FGANAILGVSLAVCK	AGAVE	3	C14:+57.021	507.2819227	1518.822368	0.000451244	3	N	105	120
P17182	Parental	VPLYR	HIADLAGNPEVILPVPAFNVINGGSHAGNK	LAMQE	3		1007.868867	3020.583201	0.000451244	67	N	132	162
P17182	Parental	VPLYR	HIADLAGNPEVILPVPAFNVINGGSHAGNK	LAMQE	4		756.1536002	3020.583201	0.000451244	60	N	132	162
P17182	Parental	EKYGK	DATNVGDEGGFAPNILENKEALELLK	TAIAK	2		1379.201226	2756.386852	0.000451244	36	N	202	228
P17182	Parental	EKYGK	DATNVGDEGGFAPNILENKEALELLK	TAIAK	3		919.8034173	2756.386852	0.000451244	39	N	202	228
P17182	Parental	LADLY	KSFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		1033.489721	3097.445764	0.000451244	32	N	280	306
P17182	Parental	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	2		1485.6832	2969.350801	0.000451244	24	N	281	306
P17182	Parental	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		990.7914002	2969.350801	0.000451244	49	N	281	306
P17182	Parental	MVSHR	SGETEDTFIADLVVGLCTGQIK	TGAPC	2	C17:+57.021	1177.083513	2352.151427	0.000451244	811	N	372	394
P17182	Parental	MVSHR	SGETEDTFIADLVVGLCTGQIK	TGAPC	3	C17:+57.021	785.0582756	2352.151427	0.000451244	94	N	372	394
P17182	Parental	ADLYK	SFVQNYPVVSIEDPFDQDDWGAWQKF	TASAG	3		1039.814205	3116.419215	0.000451244	11	N	281	307
P17182	Parental	ERLAK	YNQILRIEEELGSK	AKFAG	3		564.6374654	1690.888996	0.000451244	5	N	406	420
P17182	Parental	TAIAK	AGYTDQVVIGMDVAASEFYR	SGKYD	2		1096.520584	2191.025568	0.000451244	19	N	233	253
P17182	Parental	VPLYR	HIADLAGNPEVILPVPAFNV	INGGS	2		1043.570736	2085.125873	0.001352548	4	N	132	152

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P17182	Parental	VSIED	PFDQDDWGAWQK	FTASA	2		746.8287447	1491.641889	0.000622848	5	N	294	306
P17182	Parental	VIKEK	YGKDATNVGDEGGFAPNILENK	EALEL	2		1155.056376	2308.097152	0.000451244	18	N	199	221
P17182	Parental	VIKEK	YGKDATNVGDEGGFAPNILENK	EALEL	3		770.3735172	2308.097152	0.000451244	19	N	199	221
P17182	Parental	QKFTA	SAGIQVVGDDLTVTNPK	RIAKA	2		857.4550378	1712.894476	0.000451244	4	N	309	326
P17182	Parental	AWQKF	TASAGIQVVGDDLTVTNPK	RIAKA	2		943.497434	1884.979268	0.000451244	30	N	307	326
P17182	Parental	REAMR	IGAEVYHNLKNVIK	EKYGK	3		533.307391	1596.898773	0.000622848	3	N	183	197
P17182	Parental	MVSHR	SGETEDTFIADLVVGLCTGQIKTGAPCR	SERLA	3	C17:+57.021,C27:+57.021	999.1550479	2994.441744	0.000451244	6	N	372	400
P17182	Parental	AASEK	SCNCLLLKVNQIGSVTESLQACK	LAQSN	3	C2:+57.021,C4:+57.021,C22:+57.021	874.7731789	2621.296137	0.000622848	2	N	335	358
P17182	Parental	EKYGK	DATNVGDEGGFAPNILENK	EALEL	2		980.9664981	1959.917396	0.000451244	86	N	202	221
P17182	Parental	EKYGK	DATNVGDEGGFAPNILENK	EALEL	3		654.3135987	1959.917396	0.000451244	1	N	202	221
P17182	Parental	FRAAV	PSGASTGIYEALELR	DNDKT	2		782.4048166	1562.794033	0.000451244	4	N	35	50
P17182	Parental	DDPSR	YITPDQLADLYK	SFVQN	2		720.3749965	1438.734393	0.000451244	5	N	269	281
P17182	Parental	YRSGK	YDLDFKSPDDPSR	YITPD	2		777.8576992	1553.699798	0.000451244	7	N	256	269
P17182	Parental	PSRYI	TPDQLADLYK	SFVQN	2		582.3013001	1162.587	0.002019181	4	N	271	281
P17182	Parental	NYPVV	SIEDPFDQDDWGAWQK	FTASA	2		968.9215592	1935.827518	0.000451244	3	N	290	306
P17182	Parental	VVSIE	DPFDQDDWGAWQK	FTASA	2		804.3422163	1606.668833	0.001162105	2	N	293	306
P17182	Parental	AWQKF	TASAGIQVVGDDLTVTNPKR	IAKAA	2		1021.54799	2041.080379	0.000451244	8	N	307	327
P17182	Parental	AWQKF	TASAGIQVVGDDLTVTNPKR	IAKAA	3		681.3679264	2041.080379	0.000451244	5	N	307	327
P17182	Parental	HAGNK	LAMQEFMILPVGASSFR	EAMRI	3		632.9957201	1895.96376	0.001162105	2	N	162	179
P17182	Parental	DDPSR	YITPDQLADLYKSFVQNYPVVSIEDPFDQDDWGAWQK	FTASA	3		1464.366011	4390.074633	0.001591523	2	N	269	306
P17182	Parental	RLAKY	NQILRIEEELGSK	AKFAG	2		764.9206338	1527.825668	0.000662267	1	N	407	420
P17182	Parental	IFDSR	GNPTVEVDLY	TAKGL	2		553.7723754	1105.529151	0.000622848	6	N	15	25
P17182	Parental	AKGLF	RAAVPSGASTGIYEALELR	DNDKT	3		654.3537287	1960.037786	0.001463592	3	N	31	50
P17182	Parental	TEDTF	IADLVVGLCTGQIK	TGAPC	2	C9:+57.021	743.9188169	1485.822034	0.000451244	2	N	380	394
P17182	Parental	DDPSR	YITPDQLADLY	KSFVQ	2		656.3275149	1310.63943	0.000451244	6	N	269	280
P17426-2	Exosome	GDGMR	GLAVFISDIR	NCKSK	2		545.8169203	1089.618241	0.000698008	4	Y	11	21
P17426-2	Exosome	ENMVK	VGGYILGEFGNLIAGDPR	SSPPV	2		924.4866723	1846.957745	0.000451244	17	Y	498	516
P17426-2	Exosome	ENMVK	VGGYILGEFGNLIAGDPR	SSPPV	3		616.6603816	1846.957745	0.000622848	26	Y	498	516
P17426-2	Exosome	FYGNK	TSVQFQNFLPTVVHPGDLQTQLAVQTK	RVAAQ	3		999.5333728	2995.576718	0.000451244	13	N	761	788
P17426-2	Exosome	FSDGP	TAQPSLGPTPEEAFLSPGPEDIGPPIPEADELLNK	FVCKN	3		1209.609113	3625.803938	0.000451244	8	N	689	724
P17426-2	Exosome	VTKAK	LLGFGSALLDNVDPNPENFVGAGIIQTK	ALQVG	2		1450.264161	2898.512721	0.000451244	6	N	885	913
P17426-2	Exosome	VTKAK	LLGFGSALLDNVDPNPENFVGAGIIQTK	ALQVG	3		967.178707	2898.512721	0.000451244	21	N	885	913
P17426-2	Exosome	SRLSR	IVSSASTDLQDYTYYFVPAPWLSVK	LLRLL	2		1425.71598	2849.416361	0.000823681	2	N	235	260
P17426-2	Exosome	SRLSR	IVSSASTDLQDYTYYFVPAPWLSVK	LLRLL	3		950.8132536	2849.416361	0.000622848	4	N	235	260
P17426-2	Exosome	LVDVF	SDGPTAQPSLGPTPEEAFLSPGPEDIGPPIPEADELLNK	FVCKN	3		1328.320179	3981.937137	0.000622848	2	N	685	724
P17426-2	Exosome	DVFSD	GPTAQPSLGPTPEEAFLSPGPEDIGPPIPEADELLNK	FVCKN	3		1260.967188	3779.878165	0.000622848	6	N	687	724
P17426-2	Exosome	KFVCK	NSGVLFENQLLQIGVK	SEFRQ	2		879.9915905	1757.967581	0.000451244	4	N	728	744
P17426-2	Exosome	DDSRR	DTSSNDINGGVEPTPSTVSTPSPSADLLGLR	AAPPP	3		1028.837626	3083.489479	0.000851441	2	N	633	664
P17426-2	Parental	GDGMR	GLAVFISDIR	NCKSK	2		545.8169203	1089.618241	0.001162105	1	Y	11	21
P17426-2	Parental	ENMVK	VGGYILGEFGNLIAGDPR	SSPPV	3		616.6603816	1846.957745	0.000662267	3	Y	498	516
P17426-2	Parental	VTKAK	LLGFGSALLDNVDPNPENFVGAGIIQTK	ALQVG	3		967.178707	2898.512721	0.000451244	10	N	885	913
P17426-2	Parental	SRLSR	IVSSASTDLQDYTYYFVPAPWLSVK	LLRLL	2		1425.71598	2849.416361	0.001699387	1	N	235	260
P17426-2	Parental	VQTKR	VAAQVDGGAQVQQVLNIECLRDFLTPPLLSVR	FRYGG	3	C19:+57.021	1169.631486	3505.871058	0.000823681	1	N	789	821
P17426-2	Parental	LVDVF	SDGPTAQPSLGPTPEEAFLSPGPEDIGPPIPEADELLNK	FVCKN	3		1328.320179	3981.937137	0.000451244	9	N	685	724
P17426-2	Parental	HSNAK	NAILFETISLIIHYDSEPNLLVR	ACNQL	3		890.8220835	2669.44285	0.001591523	1	N	306	329
P17427	Exosome	GDGMR	GLAVFISDIR	NCKSK	2		545.8169203	1089.618241	0.000698008	4	Y	11	21
P17427	Exosome	ITKAK	IIGFGSALLEEVDPNPANFVGAGIIHTK	TTQIG	3		960.5154306	2878.522892	0.000451244	42	N	868	896
P17427	Exosome	ITKAK	IIGFGSALLEEVDPNPANFVGAGIIHTK	TTQIG	4		720.6385229	2878.522892	0.000451244	3	N	868	896
P17427	Exosome	HSNAK	NAVLFEAISLIIHHDSEPNLLVR	ACNQL	3		867.4785396	2599.412219	0.000451244	3	N	305	328
P17427	Exosome	HSNAK	NAVLFEAISLIIHHDSEPNLLVR	ACNQL	4		650.8608547	2599.412219	0.001463592	2	N	305	328
P17427	Exosome	ENLVK	VGGYILGEFGNLIAGDPR	SSPLI	2		924.4866723	1846.957745	0.000451244	17	Y	497	515
P17427	Exosome	ENLVK	VGGYILGEFGNLIAGDPR	SSPLI	3		616.6603816	1846.957745	0.000622848	26	Y	497	515
P17427	Exosome	SRLSR	IVTSASTDLQDYTYYFVPAPWLSVK	LLRLL	2		1432.723806	2863.432011	0.000451244	8	N	235	260
P17427	Exosome	SRLSR	IVTSASTDLQDYTYYFVPAPWLSVK	LLRLL	3		955.485137	2863.432011	0.000451244	8	N	235	260
P17427	Exosome	GYAAK	TVFEALQAPACHENLVK	VGGYI	2	C11:+57.021	963.9910333	1925.966467	0.000622848	1	N	480	497
P17427	Exosome	LVDVF	SDSASAVAPLAPGSEDNFAR	FVCKN	2		981.4641225	1960.912645	0.001162105	5	N	687	707
P17427	Exosome	DWTSR	VVHLLNDQHLGVVTAATSLITTLAQK	NPEEF	3		914.8557872	2741.543962	0.000451244	3	N	191	217
P17427	Exosome	DWTSR	VVHLLNDQHLGVVTAATSLITTLAQK	NPEEF	4		686.3937904	2741.543962	0.002981883	1	N	191	217
P17427	Exosome	DVFSD	SASAVAPLAPGSEDNFAR	FVCKN	2		880.4346367	1758.853673	0.000662267	4	N	689	707
P17427	Exosome	DWTSR	VVHLLNDQHLGVVTAATSLITTLAQKNPEEFK	TSVSL	4		872.4798541	3485.888217	0.002884417	1	N	191	223
P17427	Exosome	HEAVK	THIETVINALKTER	DVSVR	3		542.3059387	1623.894416	0.002212458	1	N	366	380
P17427	Parental	GDGMR	GLAVFISDIR	NCKSK	2		545.8169203	1089.618241	0.001162105	1	Y	11	21
P17427	Parental	ITKAK	IIGFGSALLEEVDPNPANFVGAGIIHTK	TTQIG	3		960.5154306	2878.522892	0.000451244	38	N	868	896
P17427	Parental	ITKAK	IIGFGSALLEEVDPNPANFVGAGIIHTK	TTQIG	4		720.6385229	2878.522892	0.001162105	2	N	868	896

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P17427	Parental	HSNAK	NAVLFEAISLIIHHDSEPNLLVR	ACNQL	3		867.4785396	2599.412219	0.000451244	3	N	305	328
P17427	Parental	HSNAK	NAVLFEAISLIIHHDSEPNLLVR	ACNQL	4		650.8608547	2599.412219	0.000622848	4	N	305	328
P17427	Parental	ENLVK	VGGYILGEFGNLIAGDPR	SSPLI	3		616.6603816	1846.957745	0.000662267	3	Y	497	515
P17427	Parental	VEYLR	LSTVASTDILATVLEEMPPFPERESSILAK	LKKKK	3		1082.239415	3243.694846	0.001654178	1	N	584	614
P17427	Parental	GYAAK	TVFEALQAPACHENLVK	VGGYI	2	C11:+57.021	963.9910333	1925.966467	0.001871652	1	N	480	497
P17427	Parental	RLYRT	SPDLVPMGDWTSR	VVHLL	3	M7:+15.995	492.8983205	1475.671562	0.001264573	2	N	178	191
P17427	Parental	LVDVF	SDSASAVAPLAPGSEDNFAR	FVCKN	2		981.4641225	1960.912645	0.000823681	2	N	687	707
P17439	Exosome	KYGLR	FWAVTAENEPTAGLFTGYPFQCLGFTPEHQR	DFISR	3	C22:+57.021	1191.22987	3570.66621	0.000451244	4	N	245	276
P17439	Exosome	VVLNR	SSEDVPLTISDPDLGFLETVSPGYSIHTYLWR	RQ-	3		1198.926664	3593.756593	0.000823681	2	N	481	513
P17439	Parental	KYGLR	FWAVTAENEPTAGLFTGYPFQCLGFTPEHQR	DFISR	3	C22:+57.021	1191.22987	3570.66621	0.000451244	16	N	245	276
P17439	Parental	VVLNR	SSEDVPLTISDPDLGFLETVSPGYSIHTYLWR	RQ-	3		1198.926664	3593.756593	0.000451244	11	N	481	513
P17563	Exosome	PCIYR	NTGTEAPDYLATVDVDPK	SPQYS	2		953.4579745	1904.900349	0.001699387	1	N	34	52
P17563	Exosome	GSIVR	GGSVQVLEDQELTCQPEPLVVK	GKRIP	2	C14:+57.021	1213.117888	2424.220175	0.000662267	2	N	357	379
P17710	Exosome	IFETK	FLSQIESDRLALLQVR	AILQQ	3		630.0270644	1887.057793	0.000622848	3	N	841	857
P17710	Exosome	LLQVR	AILQQLGLNSTCDDSILVK	TVCGV	2	C12:+57.021	1044.554195	2087.09279	0.000451244	13	N	857	876
P17710	Exosome	LYAMR	LSDEILIDILTR	FKKEM	2		700.9039211	1399.792242	0.000451244	25	N	86	98
P17710	Exosome	IVSFR	SANLVAATLGAILNR	LRDNK	3		495.2917409	1482.851823	0.000451244	7	N	437	452
P17710	Exosome	DGSEK	GDFIALDLGGSSFR	ILRVQ	2		727.8678699	1453.72014	0.001162105	2	N	133	147
P17710	Exosome	PSYVR	SIPDGTEHGDFLALDLGGTNFR	VLLVK	3		778.045512	2331.113136	0.000451244	13	N	573	595
P17710	Exosome	DGTEH	GDFLALDLGGTNFR	VLLVK	2		748.3811445	1494.746689	0.000451244	9	Y	581	595
P17710	Exosome	EILTR	LGVEPSHDDCVSVQHVCTIVSFR	SANLV	4	C10:+57.021,C17:+57.021	661.0681818	2640.241527	0.00307782	1	N	414	437
P17710	Parental	IFETK	FLSQIESDRLALLQVR	AILQQ	3		630.0270644	1887.057793	0.001943752	1	N	841	857
P17710	Parental	LLQVR	AILQQLGLNSTCDDSILVK	TVCGV	2	C12:+57.021	1044.554195	2087.09279	0.000451244	4	N	857	876
P17710	Parental	LYAMR	LSDEILIDILTR	FKKEM	2		700.9039211	1399.792242	0.000451244	20	N	86	98
P17710	Parental	IVSFR	SANLVAATLGAILNR	LRDNK	3		495.2917409	1482.851823	0.000451244	9	N	437	452
P17710	Parental	DGTEH	GDFLALDLGGTNFR	VLLVK	2		748.3811445	1494.746689	0.000451244	14	Y	581	595
P17710	Parental	YAMRL	SDEILIDILTR	FKKEM	2		644.3618891	1286.708178	0.000823681	4	N	87	98
P17710	Parental	PSYVR	SIPDGTEHGDFLALDLGGTNF	RVLLV	2		1088.513812	2175.012025	0.001162105	1	N	573	594
P17710	Parental	LTRGK	FTTSDVAAIETDKEGVQNAK	EILTR	3		708.6872132	2123.03824	0.000451244	9	N	389	409
P17710	Parental	CRQSK	IDEAVLITWTK	RFKAS	2		644.8615249	1287.70745	0.001162105	2	N	218	229
P17742	Exosome	GKTSK	KITISDCGQL	-	2	C7:+57.021	567.7950963	1133.574593	0.000451244	24	N	154	164
P17742	Exosome	NPTVF	FDITADDEPLGR	VSFEL	2		674.823128	1347.630656	0.000451244	8	N	7	19
P17742	Exosome	EPLGR	VSFELFADKVPK	TAENF	2		690.3826245	1378.749649	0.000451244	32	N	19	31
P17742	Exosome	EPLGR	VSFELFADKVPK	TAENF	3		460.5910163	1378.749649	0.000622848	27	N	19	31
P17742	Exosome	GTGGR	SIYGEKFEDENFILK	HTGPG	2		916.4597889	1830.903978	0.000451244	37	N	76	91
P17742	Exosome	GTGGR	SIYGEKFEDENFILK	HTGPG	3		611.3091259	1830.903978	0.000451244	37	N	76	91
P17742	Exosome	EPLGR	VSFELFADK	VPKTA	2		528.274554	1054.533508	0.000451244	29	N	19	28
P17742	Exosome	NFILK	HTGPGILSMANAGPNTNGSQFFICTAK	TEWLD	3	C24:+57.021	931.1149014	2790.321304	0.000451244	16	N	91	118
P17742	Exosome	NFILK	HTGPGILSMANAGPNTNGSQFFICTAK	TEWLD	3	M9:+15.995,C24:+57.021	936.4465681	2806.316304	0.000979378	3	N	91	118
P17742	Exosome	-M	VNPTVFFDITADDEPLGR	VSFEL	2		1003.497434	2004.979268	0.000451244	113	N	1	19
P17742	Exosome	-M	VNPTVFFDITADDEPLGR	VSFEL	3		669.3342227	2004.979268	0.000451244	49	N	1	19
P17742	Exosome	-MVN	PTVFFDITADDEPLGR	VSFEL	2		896.9417633	1791.867927	0.000451244	4	N	3	19
P17742	Exosome	-MV	NPTVFFDITADDEPLGR	VSFEL	2		953.963227	1905.910854	0.000622848	1	N	2	19
P17742	Exosome	IYGEK	FEDENFILK	HTGPG	2		577.7905682	1153.565536	0.000823681	19	N	82	91
P17742	Exosome	MVNPT	VFFDITADDEPLGR	VSFEL	2		797.891542	1593.767484	0.001162105	3	N	5	19
P17742	Exosome	PLGRV	SFELFADKVPK	TAENF	2		640.8484175	1279.681235	0.000451244	1	N	20	31
P17742	Parental	GKTSK	KITISDCGQL	-	2	C7:+57.021	567.7950963	1133.574593	0.000451244	30	N	154	164
P17742	Parental	NPTVF	FDITADDEPLGR	VSFEL	2		674.823128	1347.630656	0.000451244	54	N	7	19
P17742	Parental	EPLGR	VSFELFADKVPK	TAENF	2		690.3826245	1378.749649	0.000451244	26	N	19	31
P17742	Parental	EPLGR	VSFELFADKVPK	TAENF	3		460.5910163	1378.749649	0.000622848	10	N	19	31
P17742	Parental	GTGGR	SIYGEKFEDENFILK	HTGPG	2		916.4597889	1830.903978	0.000451244	39	N	76	91
P17742	Parental	GTGGR	SIYGEKFEDENFILK	HTGPG	3		611.3091259	1830.903978	0.000637154	6	N	76	91
P17742	Parental	EPLGR	VSFELFADK	VPKTA	2		528.274554	1054.533508	0.000451244	14	N	19	28
P17742	Parental	NFILK	HTGPGILSMANAGPNTNGSQFFICTAK	TEWLD	2	C24:+57.021	1396.168452	2790.321304	0.000637154	2	N	91	118
P17742	Parental	NFILK	HTGPGILSMANAGPNTNGSQFFICTAK	TEWLD	3	C24:+57.021	931.1149014	2790.321304	0.000451244	3	N	91	118
P17742	Parental	-M	VNPTVFFDITADDEPLGR	VSFEL	2		1003.497434	2004.979268	0.000451244	119	N	1	19
P17742	Parental	-M	VNPTVFFDITADDEPLGR	VSFEL	3		669.3342227	2004.979268	0.000451244	39	N	1	19
P17742	Parental	-MVN	PTVFFDITADDEPLGR	VSFEL	2		896.9417633	1791.867927	0.000451244	12	N	3	19
P17742	Parental	-M	VNPTVFFDITADDEPLGRV	SFELF	2		1053.031641	2104.047682	0.001162105	4	N	1	20
P17742	Parental	-MV	NPTVFFDITADDEPLGR	VSFEL	2		953.963227	1905.910854	0.000451244	12	N	2	19
P17742	Parental	ICTAK	TEWLDGKHVVFGK	VKEGM	2		758.4018799	1514.78816	0.000451244	8	N	118	131
P17742	Parental	IYGEK	FEDENFILK	HTGPG	2		577.7905682	1153.565536	0.000451244	18	N	82	91
P17742	Parental	FHRII	PGFMCQGGDFTR	HNGTG	2	C5:+57.021	686.7925626	1371.569525	0.00091018	1	N	57	69
P17751	Exosome	GHSER	RHVFGESDELIGQK	VSHAL	3		538.9465219	1613.816166	0.000451244	21	N	149	163
P17751	Exosome	LIGQK	VSHALAEGLGVIACIGEK	LDERE	2	C14:+57.021	912.4881264	1822.960653	0.000451244	32	N	163	181

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P17751	Exosome	LIGQK	VSHALAEGLGVIACIGEK	LDERE	3	C14:+57.021	608.6613509	1822.960653	0.000451244	23	N	163	181
P17751	Exosome	KDWSK	VVLAYEPVWAIGTGK	TATPQ	2		801.948663	1601.881726	0.000451244	35	N	210	225
P17751	Exosome	KDWSK	VVLAYEPVWAIGTGK	TATPQ	3		534.9683753	1601.881726	0.000451244	5	N	210	225
P17751	Exosome	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAKQ	-	3		1053.219231	3156.634293	0.000451244	19	N	269	299
P17751	Exosome	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAK	Q-	3		1010.533038	3028.575715	0.000451244	51	N	269	298
P17751	Exosome	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAK	Q-	4		758.1517288	3028.575715	0.000622848	2	N	269	298
P17751	Exosome	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	C1:+39.994,C7:+57.021,C22:+57.021	1182.906952	3545.697456	0.000451244	14	N	70	103
P17751	Exosome	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	C1:+57.021,C7:+57.021,C22:+57.021	1188.582619	3562.724456	0.000451244	50	N	70	103
P17751	Exosome	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	4	C1:+57.021,C7:+57.021,C22:+57.021	891.688914	3562.724456	0.001329271	1	N	70	103
P17751	Exosome	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	[0:-17.027,C1:+57.021,C7:+57.021,C22:+57.021	1182.906952	3545.697456	0.000451244	21	N	70	103
P17751	Exosome	PGMIK	DLGATWVVLGHSER	RHVFG	2		770.3998686	1538.784137	0.000451244	14	N	135	149
P17751	Exosome	PGMIK	DLGATWVVLGHSER	RHVFG	3		513.9358457	1538.784137	0.000823681	10	N	135	149
P17751	Exosome	HSERR	HVFGESDELIGQK	VSHAL	2		729.8653272	1457.715054	0.000451244	19	N	150	163
P17751	Exosome	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAY	IDFAR	3	C1:+57.021,C7:+57.021,C22:+57.021	987.8100699	2960.40681	0.000451244	2	N	70	98
P17751	Exosome	ICTLN	AANVPAGTEVVCAPPTAYIDFAR	QKLDP	2	C12:+57.021	1195.594383	2389.173165	0.002019181	1	N	80	103
P17751	Parental	GHSER	RHVFGESDELIGQK	VSHAL	3		538.9465219	1613.816166	0.000451244	15	N	149	163
P17751	Parental	LIGQK	VSHALAEGLGVIACIGEK	LDERE	2	C14:+57.021	912.4881264	1822.960653	0.000451244	21	N	163	181
P17751	Parental	LIGQK	VSHALAEGLGVIACIGEK	LDERE	3	C14:+57.021	608.6613509	1822.960653	0.000451244	22	N	163	181
P17751	Parental	KDWSK	VVLAYEPVWAIGTGK	TATPQ	2		801.948663	1601.881726	0.000451244	34	N	210	225
P17751	Parental	KDWSK	VVLAYEPVWAIGTGK	TATPQ	3		534.9683753	1601.881726	0.000451244	17	N	210	225
P17751	Parental	LIGQK	VSHALAEGLGVIACIGEKLDER	EAGIT	3	C14:+57.021	779.7462548	2336.215364	0.000451244	2	N	163	185
P17751	Parental	LIGQK	VSHALAEGLGVIACIGEKLDER	EAGIT	4	C14:+57.021	585.0616411	2336.215364	0.000451244	9	N	163	185
P17751	Parental	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAKQ	-	3		1053.219231	3156.634293	0.000451244	21	N	269	299
P17751	Parental	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAKQ	-	4		790.1663733	3156.634293	0.001162105	2	N	269	299
P17751	Parental	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAK	Q-	3		1010.533038	3028.575715	0.000451244	37	N	269	298
P17751	Parental	GATCK	ELASQPDVDGFLVGGASLKPEFVDIINAK	Q-	4		758.1517288	3028.575715	0.000451244	8	N	269	298
P17751	Parental	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	C1:+39.994,C7:+57.021,C22:+57.021	1182.906952	3545.697456	0.000451244	3	N	70	103
P17751	Parental	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	C1:+57.021,C7:+57.021,C22:+57.021	1188.582619	3562.724456	0.000451244	30	N	70	103
P17751	Parental	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	4	C1:+57.021,C7:+57.021,C22:+57.021	891.688914	3562.724456	0.001763695	1	N	70	103
P17751	Parental	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAYIDFAR	QKLDP	3	[0:-17.027,C1:+57.021,C7:+57.021,C22:+57.021	1182.906952	3545.697456	0.000622848	11	N	70	103
P17751	Parental	PGMIK	DLGATWVVLGHSERR	HVFGE	3		565.9695494	1694.885248	0.001763695	2	N	135	150
P17751	Parental	PGMIK	DLGATWVVLGHSERR	HVFGE	4		424.7291121	1694.885248	0.001763695	1	N	135	150
P17751	Parental	PGMIK	DLGATWVVLGHSER	RHVFG	2		770.3998686	1538.784137	0.000451244	17	N	135	149
P17751	Parental	PGMIK	DLGATWVVLGHSER	RHVFG	3		513.9358457	1538.784137	0.002884417	1	N	135	149
P17751	Parental	HSERR	HVFGESDELIGQK	VSHAL	2		729.8653272	1457.715054	0.000451244	11	N	150	163
P17751	Parental	HSERR	HVFGESDELIGQK	VSHAL	3		486.9128182	1457.715054	0.001352548	2	N	150	163
P17751	Parental	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAY	IDFAR	2	C1:+39.994,C7:+57.021,C22:+57.021	1472.697705	2943.37981	0.002727428	1	N	70	98
P17751	Parental	NGRKK	CLGELICTLNAANVPAGTEVVCAPPTAY	IDFAR	3	C1:+57.021,C7:+57.021,C22:+57.021	987.8100699	2960.40681	0.000870037	1	N	70	98
P17751	Parental	CTLNA	ANVPAGTEVVCAPPTAYIDFAR	QKLDP	2	C11:+57.021	1160.075826	2318.136051	0.002519933	1	N	81	103
P17918	Exosome	IITLR	AEDNADTLALVFEAPNQEK	VSDYE	2		1038.000538	2073.985476	0.000451244	7	N	91	110
P17918	Exosome	KNGVK	FSASGELGNGNIK	LSQTS	2		647.3258379	1292.636076	0.000622848	2	N	168	181
P17918	Parental	SKILK	CAGNEDIITLRAEDNADTLALVFEAPNQEK	VSDYE	3	C1:+57.021	1106.537028	3316.587685	0.000451244	3	N	80	110
P17918	Parental	ARICR	DLSHIGDAVVISCAK	NGVKF	2	C13:+57.021	792.9064379	1583.797276	0.000451244	17	N	149	164
P17918	Parental	ARICR	DLSHIGDAVVISCAK	NGVKF	3	C13:+57.021	528.9402252	1583.797276	0.000451244	6	N	149	164
P17918	Parental	IITLR	AEDNADTLALVFEAPNQEK	VSDYE	2		1038.000538	2073.985476	0.000451244	30	N	91	110
P17918	Parental	DYEMK	LMDLDVEQLGIPEQEYSCVIK	MPSGE	2	C18:+57.021	1240.108674	2478.201749	0.000622848	3	N	117	138
P17918	Parental	KNGVK	FSASGELGNGNIK	LSQTS	2		647.3258379	1292.636076	0.000451244	1	N	168	181
P18242	Exosome	LTLCK	GGCEAIVDTGTSLLVGPVEEVKELQK	AIGAV	3	C3:+57.021	910.1409988	2727.399596	0.000451244	29	N	285	311
P18242	Exosome	KELQK	AIGAVPLIQGEYMIPCEK	VSSLP	2	M13:+15.995,C16:+57.021	1003.01062	2004.005641	0.000451244	21	N	311	329
P18242	Exosome	LTLCK	GGCEAIVDTGTSLLVGPVEEVK	ELQKA	2	C3:+57.021	1115.567499	2229.119398	0.000451244	15	N	285	307
P18242	Exosome	KLGGK	NYELHPDKYILK	VSQGG	2		766.9095378	1531.803476	0.000979378	1	N	343	355
P18242	Exosome	KLVDK	NIFSFYLNRDPEGQPGGELMLGGTDSK	YYHGE	3	M20:+15.995	986.8033402	2957.386621	0.000451244	2	N	224	251

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P18242	Parental	IKVEK	QIFGEATKQPGIVFVAAK	FDGIL	2		952.5361652	1903.05673	0.000451244	9	N	174	192
P18242	Parental	IKVEK	QIFGEATKQPGIVFVAAK	FDGIL	3		635.3600435	1903.05673	0.000451244	10	N	174	192
P18242	Parental	IKVEK	QIFGEATKQPGIVFVAAK	FDGIL	2	[0:-17.027	944.0226652	1886.02973	0.001329271	1	N	174	192
P18242	Parental	LTLCK	GGCEAIVDTGTSLLVGPVEEVKELQK	AIGAV	2	C3:+57.021	1364.707598	2727.399596	0.000451244	11	N	285	311
P18242	Parental	LTLCK	GGCEAIVDTGTSLLVGPVEEVKELQK	AIGAV	3	C3:+57.021	910.1409988	2727.399596	0.000451244	47	N	285	311
P18242	Parental	KELQK	AIGAVPLIQGEYMIPCEK	VSSLP	2	C16:+57.021	995.0131204	1988.010641	0.002884417	1	N	311	329
P18242	Parental	KELQK	AIGAVPLIQGEYMIPCEK	VSSLP	2	M13:+15.995,C16:+57.021	1003.01062	2004.005641	0.000451244	15	N	311	329
P18242	Parental	SELLK	NYLDAQYYGDIGIGTPPQCFTVVFDTGSSNLWVPSIHCK	ILDIA	3	C19:+57.021,C38:+57.021	1474.028039	4419.060717	0.0025889	1	N	72	111
P18242	Parental	LTLCK	GGCEAIVDTGTSLLVGPVEEVK	ELQKA	2	C3:+57.021	1115.567499	2229.119398	0.000451244	30	N	285	307
P18242	Parental	LTLCK	GGCEAIVDTGTSLLVGPVEEVK	ELQKA	3	C3:+57.021	744.0475994	2229.119398	0.000979378	5	N	285	307
P18242	Parental	KLGGK	NYELHPDKYILK	VSQGG	2		766.9095378	1531.803476	0.001162105	7	N	343	355
P18242	Parental	IPCEK	VSSLPTVYLK	LGGKN	2		553.8269537	1105.638307	0.002212458	1	N	329	339
P18242	Parental	KLVDK	NIFSFYLNRDPEGQPGGELMLGGTDSK	YYHGE	3	M20:+15.995	986.8033402	2957.386621	0.000451244	4	N	224	251
P18242	Parental	DAQYY	GDIGIGTPPQCFTVVFDTGSSNLWVPSIHCK	ILDIA	3	C11:+57.021,C30:+57.021	1130.548168	3388.621105	0.002296037	1	N	80	111
P18242	Parental	SELLK	NYLDAQYYGDIGIGTPPQCF	TVVFD	2	C19:+57.021	1146.517809	2291.020018	0.001699387	3	N	72	92
P18337	Exosome	CHKRK	AALCYTASCQPGSCNGR	GECVE	2	C4:+57.021,C9:+57.021,C14:+57.021	936.8927473	1871.769895	0.000451244	9	N	151	168
P18337	Exosome	NTLPK	SPYYYWIGIR	KIGKM	2		659.3354773	1316.655355	0.000823681	3	N	82	92
P18572-2	Exosome	DLHTK	YIVDADDRSGEYSCIFLPEPVGR	SEINV	3	C14:+57.021	886.7553672	2657.242702	0.000451244	7	N	73	96
P18572-2	Exosome	DADDR	SGEYSCIFLPEPVGR	SEINV	2	C6:+57.021	855.9117202	1709.80784	0.000451244	11	N	81	96
P18572-2	Exosome	GQGAC	AAAGTIQTSVQEVNSK	TQLTC	2		802.4184553	1602.821311	0.000622848	2	N	20	36
P18572-2	Parental	DLHTK	YIVDADDRSGEYSCIFLPEPVGR	SEINV	3	C14:+57.021	886.7553672	2657.242702	0.001839721	2	N	73	96
P18572-2	Parental	DADDR	SGEYSCIFLPEPVGR	SEINV	2	C6:+57.021	855.9117202	1709.80784	0.000451244	10	N	81	96
P18572-2	Parental	GQGAC	AAAGTIQTSVQEVNSK	TQLTC	2		802.4184553	1602.821311	0.000622848	2	N	20	36
P18572-2	Parental	MRGGK	VLQEDTLPDLHTK	YIVDA	3		503.6038732	1507.788219	0.002145581	1	N	60	73
P18653	Exosome	GVVHR	DLKPSNILYVDESGNPECLR	ICDFG	2	C18:+57.021	1160.068198	2318.120795	0.000451244	1	N	523	543
P18653	Exosome	IGSGK	FTLSGGNWNTVSETAK	DLVSK	2		856.4184553	1710.821311	0.000622848	3	N	622	638
P18653	Exosome	DKSKR	DPSEEIEILLR	YGQHP	2		657.3515213	1312.687443	0.001871652	2	N	443	454
P18653	Parental	GVVHR	DLKPSNILYVDESGNPECLR	ICDFG	2	C18:+57.021	1160.068198	2318.120795	0.000451244	8	N	523	543
P18653	Parental	IGSGK	FTLSGGNWNTVSETAK	DLVSK	2		856.4184553	1710.821311	0.000451244	8	N	622	638
P18653	Parental	DKSKR	DPSEEIEILLR	YGQHP	2		657.3515213	1312.687443	0.000451244	1	N	443	454
P18760	Exosome	KKRKK	AVLFCLSEDKK	NIILE	2	C5:+57.021	655.3449534	1308.674307	0.000451244	18	N	34	45
P18760	Exosome	KKRKK	AVLFCLSEDKK	NIILE	3	C5:+57.021	437.2325689	1308.674307	0.000451244	4	N	34	45
P18760	Exosome	DKDCR	YALYDATYETK	ESKKE	2		669.3171472	1336.618694	0.000451244	30	N	81	92
P18760	Exosome	TLAEK	LGGSAVISLEGKPL	-	2		670.8933564	1339.771113	0.000698008	1	N	152	166
P18760	Exosome	LEEGK	EILVGDVGQTVDDPYTTFVK	MLPDK	2		1098.557689	2195.099777	0.000451244	35	N	53	73
P18760	Exosome	TKESK	KEDLVFIFWAPENAPLK	SKMIY	2		1009.043823	2016.072046	0.000451244	34	N	95	112
P18760	Exosome	TKESK	KEDLVFIFWAPENAPLK	SKMIY	3		673.0318154	2016.072046	0.000451244	42	N	95	112
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFVK	MLPDK	3		1031.53997	3091.59651	0.000451244	137	N	45	73
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFVK	MLPDK	4		773.9069276	3091.59651	0.000451244	22	N	45	73
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTF	VKMLP	2		1433.224367	2864.433133	0.000451244	28	N	45	71
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTF	VKMLP	3		955.8188445	2864.433133	0.000451244	27	N	45	71
P18760	Exosome	KESKK	EDLVFIFWAPENAPLK	SKMIY	2		944.9963416	1887.977083	0.000451244	6	N	96	112
P18760	Exosome	LTGIK	HELQANCYEEVKDR	CTLAE	3	C7:+57.021	597.6094268	1789.80488	0.000451244	19	N	132	146
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTV	DDPYT	2		1013.557492	2025.099383	0.000451244	21	N	45	64
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTV	DDPYT	3		676.0409278	2025.099383	0.000662267	1	N	45	64
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFV	KMLPD	3		988.8416491	2963.501547	0.000451244	23	N	45	72
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPYTT	FVKML	2		1359.69016	2717.364719	0.002296037	3	N	45	70
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPYTT	FVKML	3		906.7960398	2717.364719	0.002813207	1	N	45	70
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPY	TTFVK	2		1258.642481	2515.269362	0.000451244	7	N	45	68
P18760	Exosome	SEDKK	NIILEEGKEILVGDVGQTVDDPY	TTFVK	3		839.4309207	2515.269362	0.000451244	9	N	45	68
P18760	Parental	KKRKK	AVLFCLSEDKK	NIILE	2	C5:+57.021	655.3449534	1308.674307	0.000451244	13	N	34	45
P18760	Parental	DKDCR	YALYDATYETK	ESKKE	2		669.3171472	1336.618694	0.000451244	65	N	81	92
P18760	Parental	TLAEK	LGGSAVISLEGKPL	-	2		670.8933564	1339.771113	0.000451244	87	N	152	166
P18760	Parental	LEEGK	EILVGDVGQTVDDPYTTFVK	MLPDK	2		1098.557689	2195.099777	0.000451244	44	N	53	73
P18760	Parental	LEEGK	EILVGDVGQTVDDPYTTFVK	MLPDK	3		732.7077258	2195.099777	0.001763695	1	N	53	73
P18760	Parental	TKESK	KEDLVFIFWAPENAPLK	SKMIY	2		1009.043823	2016.072046	0.000451244	33	N	95	112
P18760	Parental	TKESK	KEDLVFIFWAPENAPLK	SKMIY	3		673.0318154	2016.072046	0.000451244	61	N	95	112
P18760	Parental	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFVK	MLPDK	3		1031.53997	3091.59651	0.000451244	821	N	45	73
P18760	Parental	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFVK	MLPDK	4		773.9069276	3091.59651	0.000451244	28	N	45	73
P18760	Parental	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTF	VKMLP	2		1433.224367	2864.433133	0.000451244	54	N	45	71
P18760	Parental	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTF	VKMLP	3		955.8188445	2864.433133	0.000451244	43	N	45	71
P18760	Parental	KESKK	EDLVFIFWAPENAPLK	SKMIY	2		944.9963416	1887.977083	0.000451244	25	N	96	112
P18760	Parental	LTGIK	HELQANCYEEVKDR	CTLAE	2	C7:+57.021	895.9102402	1789.80488	0.000870037	2	N	132	146
P18760	Parental	LTGIK	HELQANCYEEVKDR	CTLAE	3	C7:+57.021	597.6094268	1789.80488	0.000451244	70	N	132	146

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P18760	Parental	LTGIK	HELQANCYEEVKDR	CTLAE	4	C7:+57.021	448.4590201	1789.80488	0.000451244	2	N	132	146
P18760	Parental	SEDKK	NIILEEGKEILVGDVGQTVDDPYTTFV	KMLPD	3		988.8416491	2963.501547	0.000451244	10	N	45	72
P18760	Parental	SEDKK	NIILEEGKEILVGDVGQTVDDPY	TTFVK	2		1258.642481	2515.269362	0.000451244	17	N	45	68
P18760	Parental	SEDKK	NIILEEGKEILVGDVGQTVDDPY	TTFVK	3		839.4309207	2515.269362	0.000451244	15	N	45	68
P18760	Parental	LVGDV	GQTVDDPYTTFVK	MLPDK	2		735.8597105	1469.703821	0.00091018	4	N	60	73
P18760	Parental	LEEGK	EILVGDVGQTVDDPYTTF	VKMLP	2		984.9760001	1967.9364	0.000451244	9	N	53	71
P18760	Parental	TKESK	KEDLVFIFWAPENAPL	KSKMI	2		944.9963416	1887.977083	0.000451244	2	N	95	111
P19096	Exosome	DRATR	EACPELDYFVAFSSVSCGR	GNAGQ	2	C3:+57.021,C17:+57.021	1097.482681	2192.949762	0.000451244	21	N	2000	2019
P19096	Exosome	TNLGK	VHLTGINVNPNALFPPVEFPAPR	GTPLI	2		1250.179505	2498.343411	0.002663018	1	N	802	825
P19096	Exosome	TNLGK	VHLTGINVNPNALFPPVEFPAPR	GTPLI	3		833.788937	2498.343411	0.000622848	6	N	802	825
P19096	Exosome	LAQER	LLLPEDPLISGLLNSQALK	ACVDT	2		1017.59642	2033.17724	0.000451244	27	N	1201	1220
P19096	Exosome	LAQER	LLLPEDPLISGLLNSQALK	ACVDT	3		678.7335466	2033.17724	0.000451244	9	N	1201	1220
P19096	Exosome	EGDHR	TLLEGSGLESIINIIHSSLAEPR	VSVRE	2		1225.169	2448.322401	0.000451244	4	N	2475	2498
P19096	Exosome	EGDHR	TLLEGSGLESIINIIHSSLAEPR	VSVRE	3		817.1152669	2448.322401	0.000451244	27	N	2475	2498
P19096	Exosome	HTVLK	GHALGETLACLPSEVQPAPSLLSQEEWESLFSR	KALHL	3	C10:+57.021	1213.598399	3637.771797	0.000451244	28	N	1344	1377
P19096	Exosome	SLAAK	LSVPTYGLQCTQAAPLDSIPNLAAYYIDCIK	QVQPE	3	C10:+57.021,C29:+57.021	1152.579246	3454.714337	0.000451244	17	N	2256	2287
P19096	Exosome	LVQVR	EEEPEAVLPGAQPTLISAISK	TFCPA	2		1090.078788	2178.141977	0.001162105	4	N	1850	1871
P19096	Exosome	LLRAK	TGGTYGEDLGADYNLSQVCDGK	VSVHI	2	C19:+57.021	1160.505627	2318.995654	0.000451244	10	N	2442	2464
P19096	Exosome	PRSAR	WLSTSIPEAQWQSSLAR	TSSAE	2		980.5003111	1958.985022	0.001329271	3	N	711	728
P19096	Exosome	KTLAR	SLGLSLEETPVVFENVSFHQATILPK	TGTVA	3		952.5116861	2854.511658	0.000451244	12	N	901	927
P19096	Exosome	ECKQR	CPAGVVPACHNSEDTVTISGPQAAVNEFVEQLKQEGVFAK	EVRTG	4	C1:+57.021,C9:+57.021	1071.773245	4283.06178	0.000698008	9	N	633	673
P19096	Exosome	AIFLK	NVTFHGILLDALFEEANDSWR	EVAAL	3		816.4050403	2446.191721	0.000451244	6	N	1780	1801
P19096	Exosome	VGLKR	SFYGTALFLCR	RAIPQ	2	C10:+57.021	667.8320132	1333.648426	0.000451244	6	N	1387	1398
P19096	Exosome	FFDFK	GPSIALDTACSSSLLALQNAYQAIR	SGECP	3	C10:+57.021	874.1185284	2619.332185	0.000451244	6	N	151	176
P19096	Exosome	SQALK	ACVDTALENLSTLK	MKVAE	2	C2:+57.021	767.8929961	1533.770392	0.000451244	4	N	1220	1234
P19096	Exosome	FLCRR	AIPQEKPIFLSVEDTSFQWVDSLK	STLAT	3		926.4852485	2776.432345	0.000451244	1	N	1399	1423
P19096	Exosome	HTGGK	GVDLVLNSLAEEK	LQASV	2		693.8779033	1385.740207	0.001162105	3	N	1732	1745
P19096	Exosome	CIDGR	VIFPGTGYLCLVWK	TLARS	2	C10:+57.021	826.9473774	1651.879155	0.001591523	1	N	883	897
P19096	Exosome	AALTK	VLLSLEHGVWAPNLHFHNPNPEIPALLDGR	LQVVD	3		1119.261987	3354.762562	0.001839721	1	N	343	373
P19096	Exosome	AALTK	VLLSLEHGVWAPNLHFHNPNPEIPALLDGR	LQVVD	4		839.6984406	3354.762562	0.002296037	1	N	343	373
P19096	Exosome	YKELR	LRGYDYGPQFQGICEATLEGEQGK	LLWKD	3	C14:+57.021	906.0942714	2715.259414	0.000637154	1	N	996	1020
P19096	Exosome	TLKMK	VAEVLAGEGHLYSR	IPALL	2		750.894419	1499.773238	0.001699387	1	N	1236	1250
P19096	Exosome	YLQAR	FPQLDDTSFANSR	DTSFE	2		749.352584	1496.689568	0.000823681	2	N	1704	1717
P19096	Exosome	ELRLR	GYDYGPQFQGICEATLEGEQGK	LLWKD	2	C12:+57.021	1224.04492	2446.074239	0.000622848	1	N	998	1020
P19096	Exosome	RLSFF	FDFKGPSIALDTACSSSLLALQNAYQAIR	SGECP	3	C14:+57.021	1053.204773	3156.59092	0.001463592	1	N	147	176
P19096	Exosome	PLMKR	DHKDNLEFFLTNLGK	VHLTG	3		597.6410985	1789.899895	0.002212458	1	N	787	802
P19096	Parental	DRATR	EACPELDYFVAFSSVSCGR	GNAGQ	2	C3:+57.021,C17:+57.021	1097.482681	2192.949762	0.000451244	30	N	2000	2019
P19096	Parental	TNLGK	VHLTGINVNPNALFPPVEFPAPR	GTPLI	3		833.788937	2498.343411	0.000622848	10	N	802	825
P19096	Parental	LAQER	LLLPEDPLISGLLNSQALK	ACVDT	2		1017.59642	2033.17724	0.000451244	27	N	1201	1220
P19096	Parental	LAQER	LLLPEDPLISGLLNSQALK	ACVDT	3		678.7335466	2033.17724	0.000451244	2	N	1201	1220
P19096	Parental	EGDHR	TLLEGSGLESIINIIHSSLAEPR	VSVRE	2		1225.169	2448.322401	0.000451244	1	N	2475	2498
P19096	Parental	EGDHR	TLLEGSGLESIINIIHSSLAEPR	VSVRE	3		817.1152669	2448.322401	0.000451244	18	N	2475	2498
P19096	Parental	HTVLK	GHALGETLACLPSEVQPAPSLLSQEEWESLFSR	KALHL	3	C10:+57.021	1213.598399	3637.771797	0.000451244	14	N	1344	1377
P19096	Parental	SLAAK	LSVPTYGLQCTQAAPLDSIPNLAAYYIDCIK	QVQPE	3	C10:+57.021,C29:+57.021	1152.579246	3454.714337	0.000451244	11	N	2256	2287
P19096	Parental	LVQVR	EEEPEAVLPGAQPTLISAISK	TFCPA	2		1090.078788	2178.141977	0.000823681	2	N	1850	1871
P19096	Parental	LLRAK	TGGTYGEDLGADYNLSQVCDGK	VSVHI	2	C19:+57.021	1160.505627	2318.995654	0.000451244	11	N	2442	2464
P19096	Parental	KTLAR	SLGLSLEETPVVFENVSFHQATILPK	TGTVA	3		952.5116861	2854.511658	0.000622848	1	N	901	927
P19096	Parental	ECKQR	CPAGVVPACHNSEDTVTISGPQAAVNEFVEQLKQEGVFAK	EVRTG	4	C1:+57.021,C9:+57.021	1071.773245	4283.06178	0.000662267	12	N	633	673
P19096	Parental	AIFLK	NVTFHGILLDALFEEANDSWR	EVAAL	3		816.4050403	2446.191721	0.002019181	1	N	1780	1801
P19096	Parental	FFDFK	GPSIALDTACSSSLLALQNAYQAIR	SGECP	3	C10:+57.021	874.1185284	2619.332185	0.000662267	7	N	151	176
P19096	Parental	SQALK	ACVDTALENLSTLK	MKVAE	2	C2:+57.021	767.8929961	1533.770392	0.000622848	3	N	1220	1234
P19096	Parental	VEHSK	VLEALLPLK	SLEDR	2		498.3291322	994.6426645	0.002884417	1	N	2375	2384
P19096	Parental	FLCRR	AIPQEKPIFLSVEDTSFQWVDSLK	STLAT	3		926.4852485	2776.432345	0.000451244	2	N	1399	1423
P19096	Parental	YKELR	LRGYDYGPQFQGICEATLEGEQGK	LLWKD	3	C14:+57.021	906.0942714	2715.259414	0.000451244	1	N	996	1020
P19157	Exosome	GQLPK	FEDGDLTLYQSNAILR	HLGRS	2		927.9657697	1853.915939	0.000451244	22	N	55	71
P19157	Exosome	GQLPK	FEDGDLTLYQSNAILR	HLGRS	3		618.9797798	1853.915939	0.000451244	3	N	55	71
P19157	Exosome	DQISF	ADYNLLDLLLIHQVLAPGCLDNFPLLSAYVAR	LSARP	3	C19:+57.021	1199.976482	3596.906047	0.002080925	1	N	151	183
P19157	Exosome	-M	PPYTIVYFPVR	GRCEA	2		676.3746025	1350.733605	0.000622848	3	N	1	12
P19157	Exosome	NQGGK	AFIVGDQISF	ADYNL	2		548.7878285	1095.560057	0.000698008	2	N	141	151
P19157	Parental	GQLPK	FEDGDLTLYQSNAILR	HLGRS	2		927.9657697	1853.915939	0.000451244	3	N	55	71
P19157	Parental	NDYVK	ALPGHLKPFETLLSQNQGGK	AFIVG	2		1068.084542	2134.153485	0.00307782	1	N	121	141
P19157	Parental	DQISF	ADYNLLDLLLIHQVLAPGCLDNFPLLSAYVAR	LSARP	3	C19:+57.021	1199.976482	3596.906047	0.002374549	1	N	151	183
P19221	Exosome	ENFCR	NPDSSTTGPWCYTTDPTVR	REECS	2	C11:+57.021	1077.973766	2153.931932	0.002813207	1	N	159	178
P19221	Exosome	WGNLR	ETWTTNINEIQPSVLQVVNLPIVERPVCK	ASTRI	3	C28:+57.021	1126.269666	3375.785597	0.000823681	1	N	505	534
P19221	Parental	VMLFR	KSPQELLCGASLISDR	WVLTA	2	C8:+57.021	887.4621086	1772.908617	0.000451244	30	N	380	396

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P19221	Parental	VMLFR	KSPQELLCGASLISDR	WVLTA	3	C8:+57.021	591.9773391	1772.908617	0.000451244	26	N	380	396
P19221	Parental	MLFRK	SPQELLCGASLISDR	WVLTA	2	C7:+57.021	823.4146271	1644.813654	0.000451244	16	N	381	396
P19221	Parental	MLFRK	SPQELLCGASLISDR	WVLTA	3	C7:+57.021	549.279018	1644.813654	0.000451244	4	N	381	396
P19221	Parental	SVLQV	VNLPIVERPVCK	ASTRI	2	C11:+57.021	712.4084194	1422.801239	0.002145581	1	N	522	534
P19221	Parental	RYNWR	ENLDRDIALLK	LKKPV	3		433.9142705	1298.719411	0.001162105	2	N	453	464
P19221	Parental	PFNNR	WYQMGIVSWGEGCDR	KGKYG	2	M4:+15.995,C13:+57.021	930.3959546	1858.776309	0.000823681	3	N	578	593
P19536	Exosome	VTRSM	ASGGGVPTDEEQATGLER	EIMIA	2		887.416641	1772.817682	0.000451244	13	N	30	48
P19536	Parental	VTRSM	ASGGGVPTDEEQATGLER	EIMIA	2		887.416641	1772.817682	0.000451244	67	N	30	48
P19536	Parental	ISNKR	IVGCICEEDNCTVIWFWLHKGESQR	CPNCG	4	C4:+57.021,C6:+57.021,C11:+57.021	784.8665725	3135.43509	0.002019181	1	N	86	111
P19536	Parental	ISNKR	IVGCICEEDNCTVIWFWLHK	GESQR	3	C4:+57.021,C6:+57.021,C11:+57.021	860.4009053	2578.179316	0.000451244	13	N	86	106
P19536	Parental	AVTRS	MASGGGVPTDEEQATGLER	EIMIA	2		952.9368839	1903.858168	0.001229886	1	N	29	48
P19973	Exosome	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	3		907.739476	2720.195028	0.000451244	32	N	96	120
P19973	Exosome	VASTK	TLWETGEVQSQSASK	TPSCQ	2		825.9026381	1649.789676	0.000451244	12	N	255	270
P19973	Exosome	LISLK	SSELDEDEGFGDWSQKPEPR	QQFWG	2		1154.504173	2306.992746	0.002663018	2	N	76	96
P19973	Exosome	SHQAK	VHLEESNLSYREPDPEDAVGGSGEAEEHLIR	HQVRT	3		1145.541873	3433.602218	0.000823681	5	N	130	161
P19973	Exosome	SHQAK	VHLEESNLSYREPDPEDAVGGSGEAEEHLIR	HQVRT	4		859.4083544	3433.602218	0.000451244	11	N	130	161
P19973	Exosome	RHQVR	TPSPLALEDTVELSSPPLSPTTK	LADRT	2		1190.628842	2379.242085	0.002519933	2	N	165	188
P19973	Exosome	SNLSY	REPDPEDAVGGSGEAEEHLIR	HQVRT	3		755.024888	2262.051264	0.000851441	2	N	140	161
P19973	Exosome	NSVKK	SQPTLPISTIDER	LQQYT	2		728.8862597	1455.756919	0.00307782	1	N	208	221
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEKQTEESSHQAK	VHLEE	3		1282.907831	3845.700094	0.000451244	14	N	96	130
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEKQTEESSHQAK	VHLEE	4		962.4328236	3845.700094	0.000823681	10	N	96	130
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEKQTEESSHQAK	VHLEE	3	[0:-17.027	1277.232165	3828.673094	0.000451244	4	N	96	130
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEKQTEESSHQAK	VHLEE	4	[0:-17.027	958.1760736	3828.673094	0.000451244	7	N	96	130
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	2		1361.105314	2720.195028	0.000451244	33	N	96	120
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	3		907.739476	2720.195028	0.000451244	129	N	96	120
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	2	Q1:-17.027	1352.591814	2703.168028	0.000451244	7	N	96	120
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	2	[0:-17.027	1352.591814	2703.168028	0.000451244	9	N	96	120
P19973	Parental	KPEPR	QQFWGNEGTAEGTEPSQSERPEEK	QTEES	3	[0:-17.027	902.0638094	2703.168028	0.000823681	1	N	96	120
P19973	Parental	VASTK	TLWETGEVQSQSASK	TPSCQ	2		825.9026381	1649.789676	0.000451244	55	N	255	270
P19973	Parental	LISLK	SSELDEDEGFGDWSQKPEPR	QQFWG	2		1154.504173	2306.992746	0.000451244	40	N	76	96
P19973	Parental	LISLK	SSELDEDEGFGDWSQKPEPR	QQFWG	3		770.005382	2306.992746	0.000451244	61	N	76	96
P19973	Parental	SHQAK	VHLEESNLSYREPDPEDAVGGSGEAEEHLIR	HQVRT	3		1145.541873	3433.602218	0.000451244	73	N	130	161
P19973	Parental	SHQAK	VHLEESNLSYREPDPEDAVGGSGEAEEHLIR	HQVRT	4		859.4083544	3433.602218	0.000451244	86	N	130	161
P19973	Parental	RHQVR	TPSPLALEDTVELSSPPLSPTTK	LADRT	2		1190.628842	2379.242085	0.000451244	4	N	165	188
P19973	Parental	AIDPR	CEEQEELHAEDSEGLTTQWREDEEEAAR	EQRQR	3	C1:+39.994	1163.481826	3487.422079	0.000451244	19	N	9	38
P19973	Parental	AIDPR	CEEQEELHAEDSEGLTTQWREDEEEAAR	EQRQR	3	C1:+57.021	1169.157493	3504.449079	0.000451244	29	N	9	38
P19973	Parental	AIDPR	CEEQEELHAEDSEGLTTQWREDEEEAAR	EQRQR	4	C1:+57.021	877.1200697	3504.449079	0.000451244	15	N	9	38
P19973	Parental	AIDPR	CEEQEELHAEDSEGLTTQWREDEEEAAR	EQRQR	3	[0:-17.027,C1:+57.021	1163.481826	3487.422079	0.001871652	3	N	9	38
P19973	Parental	SNLSY	REPDPEDAVGGSGEAEEHLIR	HQVRT	3		755.024888	2262.051264	0.000451244	15	N	140	161
P19973	Parental	NLSYR	EPDPEDAVGGSGEAEEHLIR	HQVRT	2		1053.982876	2105.950153	0.001763695	1	N	141	161
P19973	Parental	NLSYR	EPDPEDAVGGSGEAEEHLIR	HQVRT	3		702.9911843	2105.950153	0.000451244	8	N	141	161
P19973	Parental	AIDPR	CEEQEELHAEDSEGLTTQWR	EEDEE	3	C1:+57.021	816.3524103	2446.033831	0.001943752	1	N	9	29
P19973	Parental	NSVKK	SQPTLPISTIDER	LQQYT	2		728.8862597	1455.756919	0.000622848	7	N	208	221
P20029	Exosome	VVEKK	TKPYIQVDIGGGQTK	TFAPE	2		802.9362839	1603.856968	0.000451244	28	N	124	139
P20029	Exosome	VVEKK	TKPYIQVDIGGGQTK	TFAPE	3		535.6267893	1603.856968	0.000451244	44	N	124	139
P20029	Exosome	GDAAK	NQLTSNPENTVFDAKR	LIGRT	2		917.4586432	1832.901686	0.000451244	16	N	82	98
P20029	Exosome	GDAAK	NQLTSNPENTVFDAKR	LIGRT	3		611.9750288	1832.901686	0.000451244	12	N	82	98
P20029	Exosome	RLIGR	TWNDPSVQQDIK	FLPFK	2		715.8496771	1429.683754	0.000451244	37	N	102	114
P20029	Exosome	PIISK	LYGSGGPPPTGEEDTSEKDEL	-	2		1089.4902	2176.9648	0.000451244	90	N	634	655
P20029	Exosome	GDAAK	NQLTSNPENTVFDAK	RLIGR	2		839.4080876	1676.800575	0.000451244	62	N	82	97
P20029	Exosome	YLGKK	VTHAVVTVPAYFNDAQR	QATKD	3		629.9957642	1886.963893	0.000451244	23	N	165	182
P20029	Exosome	VPTKK	SQIFSTASDNQPTVTIK	VYEGE	2		918.9710521	1835.926504	0.001162105	3	N	448	465
P20029	Exosome	DSDLK	KSDIDEIVLVGGSTR	IPKIQ	2		794.9311986	1587.846797	0.000451244	30	N	353	368
P20029	Exosome	DSDLK	KSDIDEIVLVGGSTR	IPKIQ	3		530.2900657	1587.846797	0.000451244	8	N	353	368
P20029	Exosome	DQGNR	ITPSYVAFTPEGER	LIGDA	2		783.8940847	1565.772569	0.000451244	36	N	61	75
P20029	Exosome	LNVMR	IINEPTAAAIAYGLDKR	EGEKN	2		908.5023224	1814.989045	0.000451244	22	N	198	215
P20029	Exosome	LNVMR	IINEPTAAAIAYGLDKR	EGEKN	3		606.0041483	1814.989045	0.000451244	23	N	198	215
P20029	Exosome	LNVMR	IINEPTAAAIAYGLDK	REGEK	2		830.4517668	1658.887934	0.000451244	32	Y	198	214
P20029	Exosome	LNVMR	IINEPTAAAIAYGLDK	REGEK	3		553.9704446	1658.887934	0.000451244	21	Y	198	214
P20029	Exosome	ETLTR	AKFEELNMDLFR	STMKP	3		504.9225491	1511.744247	0.000451244	8	N	325	337
P20029	Exosome	RPLTK	DNHLLGTFDLTGIPPAPR	GVPQI	2		967.5106788	1933.005758	0.000451244	26	N	475	493
P20029	Exosome	RPLTK	DNHLLGTFDLTGIPPAPR	GVPQI	3		645.3430525	1933.005758	0.000451244	11	N	475	493
P20029	Exosome	QHQAR	IEIESFFEGEDFSETLTR	AKFEE	2		1075.002746	2147.989892	0.000451244	75	N	307	325

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P20029	Exosome	QHQAR	IEIESFFEGEDFSETLTR	AKFEE	3		717.0044308	2147.989892	0.001943752	2	N	307	325
P20029	Exosome	GGQTK	TFAPEEISAMVLTK	MKETA	2		768.9030644	1535.790529	0.000451244	7	N	139	153
P20029	Exosome	AVEEK	IEWLESHQDADIEDFKAK	KKELE	2		1087.52418	2173.03276	0.000451244	5	N	602	620
P20029	Exosome	AVEEK	IEWLESHQDADIEDFKAK	KKELE	3		725.3520535	2173.03276	0.000451244	16	N	602	620
P20029	Exosome	AVEEK	IEWLESHQDADIEDFKAK	KKELE	4		544.2659901	2173.03276	0.000451244	4	N	602	620
P20029	Exosome	RIDTR	NELESYAYSLK	NQIGD	2		658.8225967	1315.629593	0.000451244	14	N	563	574
P20029	Exosome	KAKKK	ELEEIVQPIISK	LYGSG	2		699.3984716	1396.781343	0.000451244	19	N	622	634
P20029	Exosome	SDLKK	SDIDEIVLVGGSTR	IPKIQ	2		730.883717	1459.751834	0.000622848	13	N	354	368
P20029	Exosome	AVEEK	IEWLESHQDADIEDFK	AKKKE	2		987.9581417	1973.900683	0.000451244	17	N	602	618
P20029	Exosome	KLKER	IDTRNELESYAYSLK	NQIGD	2		901.4524952	1800.88939	0.000823681	1	N	559	574
P20029	Exosome	KLKER	IDTRNELESYAYSLK	NQIGD	3		601.3042634	1800.88939	0.000451244	11	N	559	574
P20029	Exosome	VVPTK	KSQIFSTASDNQPTVTIK	VYEGE	2		983.0185337	1964.021467	0.000451244	3	N	447	465
P20029	Exosome	RQATK	DAGTIAGLNVMR	IINEP	2		609.3195018	1216.623404	0.002663018	1	N	186	198
P20029	Exosome	KVVEK	KTKPYIQVDIGGGQTK	TFAPE	3		578.3251103	1731.951931	0.000622848	2	N	123	139
P20029	Exosome	DVSLL	TIDNGVFEVVATNGDTHLGGEDFDQR	VMEHF	2		1403.649889	2805.284178	0.000622848	4	N	236	262
P20029	Exosome	DVSLL	TIDNGVFEVVATNGDTHLGGEDFDQR	VMEHF	3		936.1025259	2805.284178	0.000451244	5	N	236	262
P20029	Exosome	REGEK	NILVFDLGGGTFDVSLL	TIDNG	2		890.4805243	1778.945449	0.000451244	2	N	219	236
P20029	Exosome	LNVMR	IINEPTAAAIAY	GLDKR	2		623.8380498	1245.6605	0.002727428	1	Y	198	210
P20029	Parental	VVEKK	TKPYIQVDIGGGQTK	TFAPE	2		802.9362839	1603.856968	0.000451244	51	N	124	139
P20029	Parental	VVEKK	TKPYIQVDIGGGQTK	TFAPE	3		535.6267893	1603.856968	0.000451244	48	N	124	139
P20029	Parental	GDAAK	NQLTSNPENTVFDAKR	LIGRT	2		917.4586432	1832.901686	0.000451244	32	N	82	98
P20029	Parental	GDAAK	NQLTSNPENTVFDAKR	LIGRT	3		611.9750288	1832.901686	0.000451244	11	N	82	98
P20029	Parental	RLIGR	TWNDPSVQQDIK	FLPFK	2		715.8496771	1429.683754	0.000451244	67	N	102	114
P20029	Parental	PIISK	LYGSGGPPPTGEEDTSEKDEL	-	2		1089.4902	2176.9648	0.000451244	119	N	634	655
P20029	Parental	GDAAK	NQLTSNPENTVFDAK	RLIGR	2		839.4080876	1676.800575	0.000451244	64	N	82	97
P20029	Parental	YLGKK	VTHAVVTVPAYFNDAQR	QATKD	2		944.4897463	1886.963893	0.000451244	46	N	165	182
P20029	Parental	YLGKK	VTHAVVTVPAYFNDAQR	QATKD	3		629.9957642	1886.963893	0.000451244	36	N	165	182
P20029	Parental	VPTKK	SQIFSTASDNQPTVTIK	VYEGE	2		918.9710521	1835.926504	0.000451244	179	N	448	465
P20029	Parental	DSDLK	KSDIDEIVLVGGSTR	IPKIQ	2		794.9311986	1587.846797	0.000451244	45	N	353	368
P20029	Parental	DSDLK	KSDIDEIVLVGGSTR	IPKIQ	3		530.2900657	1587.846797	0.000451244	19	N	353	368
P20029	Parental	DQGNR	ITPSYVAFTPEGER	LIGDA	2		783.8940847	1565.772569	0.000451244	84	N	61	75
P20029	Parental	DQGNR	ITPSYVAFTPEGER	LIGDA	3		522.9319898	1565.772569	0.000451244	2	N	61	75
P20029	Parental	LNVMR	IINEPTAAAIAYGLDKR	EGEKN	2		908.5023224	1814.989045	0.000451244	11	N	198	215
P20029	Parental	LNVMR	IINEPTAAAIAYGLDKR	EGEKN	3		606.0041483	1814.989045	0.000451244	33	N	198	215
P20029	Parental	LNVMR	IINEPTAAAIAYGLDK	REGEK	2		830.4517668	1658.887934	0.000451244	32	Y	198	214
P20029	Parental	LNVMR	IINEPTAAAIAYGLDK	REGEK	3		553.9704446	1658.887934	0.000451244	7	Y	198	214
P20029	Parental	DQGNR	ITPSYVAFTPEGERLIGDAAK	NQLTS	2		1118.086948	2234.158295	0.000622848	9	N	61	82
P20029	Parental	ETLTR	AKFEELNMDLFR	STMKP	3		504.9225491	1511.744247	0.000451244	14	N	325	337
P20029	Parental	RPLTK	DNHLLGTFDLTGIPPAPR	GVPQI	2		967.5106788	1933.005758	0.000451244	55	N	475	493
P20029	Parental	RPLTK	DNHLLGTFDLTGIPPAPR	GVPQI	3		645.3430525	1933.005758	0.000451244	23	N	475	493
P20029	Parental	QHQAR	IEIESFFEGEDFSETLTR	AKFEE	2		1075.002746	2147.989892	0.000451244	201	N	307	325
P20029	Parental	QHQAR	IEIESFFEGEDFSETLTR	AKFEE	3		717.0044308	2147.989892	0.000451244	8	N	307	325
P20029	Parental	REGEK	NILVFDLGGGTFDV	SLLTI	2		733.880446	1465.745292	0.0007646	2	N	219	233
P20029	Parental	GNRIT	PSYVAFTPEGER	LIGDA	2		676.8282134	1351.640827	0.000823681	3	N	63	75
P20029	Parental	GGQTK	TFAPEEISAMVLTK	MKETA	2		768.9030644	1535.790529	0.0007646	3	N	139	153
P20029	Parental	AVEEK	IEWLESHQDADIEDFKAK	KKELE	2		1087.52418	2173.03276	0.000451244	13	N	602	620
P20029	Parental	AVEEK	IEWLESHQDADIEDFKAK	KKELE	3		725.3520535	2173.03276	0.000451244	13	N	602	620
P20029	Parental	AVEEK	IEWLESHQDADIEDFKAK	KKELE	4		544.2659901	2173.03276	0.000451244	9	N	602	620
P20029	Parental	RIDTR	NELESYAYSLK	NQIGD	2		658.8225967	1315.629593	0.000451244	23	N	563	574
P20029	Parental	KAKKK	ELEEIVQPIISK	LYGSG	2		699.3984716	1396.781343	0.0007646	3	N	622	634
P20029	Parental	SDLKK	SDIDEIVLVGGSTR	IPKIQ	2		730.883717	1459.751834	0.000451244	26	N	354	368
P20029	Parental	AVEEK	IEWLESHQDADIEDFK	AKKKE	2		987.9581417	1973.900683	0.000451244	23	N	602	618
P20029	Parental	KLKER	IDTRNELESYAYSLK	NQIGD	2		901.4524952	1800.88939	0.000451244	1	N	559	574
P20029	Parental	KLKER	IDTRNELESYAYSLK	NQIGD	3		601.3042634	1800.88939	0.001943752	1	N	559	574
P20029	Parental	VVPTK	KSQIFSTASDNQPTVTIK	VYEGE	2		983.0185337	1964.021467	0.000451244	13	N	447	465
P20029	Parental	AYLGK	KVTHAVVTVPAYFNDAQR	QATKD	2		1008.537228	2015.058856	0.001699387	1	N	164	182
P20029	Parental	NVMRI	INEPTAAAIAYGLDKR	EGEKN	2		851.9602904	1701.904981	0.002296037	1	N	199	215
P20029	Parental	GTFDV	SLLTIDNGVFEVVATNGDTHLGGEDFDQR	VMEHF	3		1040.502578	3118.484334	0.001162105	1	N	233	262
P20029	Parental	PPAPR	GVPQIEVTFEIDVNGILR	VTAED	2		1000.047094	1998.078588	0.000451244	70	N	493	511
P20029	Parental	ETMEK	AVEEKIEWLESHQDADIEDFK	AKKKE	3		844.4032536	2530.186361	0.000735798	2	N	597	618
P20029	Parental	KVVEK	KTKPYIQVDIGGGQTK	TFAPE	3		578.3251103	1731.951931	0.00307782	1	N	123	139
P20029	Parental	LNVMR	IINEPTAAAIAY	GLDKR	2		623.8380498	1245.6605	0.002813207	1	Y	198	210
P20060	Exosome	SYELK	QVTGSGFPAILSAPWYLDLISYGQDWK	NYYKV	3		1004.843436	3011.506907	0.000451244	17	N	413	440
P20060	Exosome	ELSNK	GSYSLSHVYTPNDVR	MVLEY	2		847.9107974	1693.805995	0.000451244	19	N	236	251
P20060	Exosome	EAFRR	YYNYVFGFYK	RHHGP	2		682.3220355	1362.628471	0.000451244	14	N	79	89

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P20060	Exosome	SSLKK	NSIVWQEVFDDKVELQPGTVVEVWK	SEHYS	3		982.175074	2943.501822	0.000451244	10	N	379	404
P20060	Exosome	RMVSR	GIAAQPLYTGYCNYENKI	-	2	C12:+57.021	1037.999055	2073.982511	0.000451244	26	N	518	536
P20060	Exosome	MAFNK	FNVLHWHIVDDQSFPYQSTTFPELSNK	GSYSL	3		1083.860037	3248.556711	0.000451244	9	N	209	236
P20060	Exosome	MAFNK	FNVLHWHIVDDQSFPYQSTTFPELSNK	GSYSL	4		813.1469778	3248.556711	0.000451244	17	N	209	236
P20060	Exosome	LRGIR	VIPEFDTPGHTQSWGK	GQKNL	2		899.9420976	1797.868595	0.000451244	3	N	263	279
P20060	Parental	SYELK	QVTGSGFPAILSAPWYLDLISYGQDWK	NYYKV	3		1004.843436	3011.506907	0.000451244	19	N	413	440
P20060	Parental	ELSNK	GSYSLSHVYTPNDVR	MVLEY	2		847.9107974	1693.805995	0.000451244	13	N	236	251
P20060	Parental	EAFRR	YYNYVFGFYK	RHHGP	2		682.3220355	1362.628471	0.001463592	5	N	79	89
P20060	Parental	SSLKK	NSIVWQEVFDDKVELQPGTVVEVWK	SEHYS	3		982.175074	2943.501822	0.000451244	9	N	379	404
P20060	Parental	RMVSR	GIAAQPLYTGYCNYENKI	-	2	C12:+57.021	1037.999055	2073.982511	0.000451244	5	N	518	536
P20060	Parental	MAFNK	FNVLHWHIVDDQSFPYQSTTFPELSNK	GSYSL	3		1083.860037	3248.556711	0.000451244	8	N	209	236
P20060	Parental	MAFNK	FNVLHWHIVDDQSFPYQSTTFPELSNK	GSYSL	4		813.1469778	3248.556711	0.000451244	4	N	209	236
P20060	Parental	LRGIR	VIPEFDTPGHTQSWGK	GQKNL	2		899.9420976	1797.868595	0.000451244	1	N	263	279
P20108	Exosome	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASK	EYFEK	4	C12:+57.021	854.1676316	3412.639327	0.000662267	2	N	218	249
P20108	Exosome	KQISR	DYGVLLESAGIALR	GLFII	2		738.9069951	1475.79839	0.000451244	13	N	171	185
P20108	Exosome	GIALR	GLFIIDPNGVVK	HLSVN	2		636.3720598	1270.72852	0.000979378	14	N	185	197
P20108	Exosome	DFKGK	YLVLFFYPLDFTFVCPTEIVAFSDK	ANEFH	3	C15:+57.021	1011.178614	3030.512441	0.000622848	1	N	94	119
P20108	Parental	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASKEYFEK	VHQ-	3	C12:+57.021	1370.658206	4108.951219	0.000451244	1	N	218	254
P20108	Parental	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASKEYFEK	VHQ-	4	C12:+57.021	1028.245605	4108.951219	0.000451244	12	N	218	254
P20108	Parental	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASK	EYFEK	3	C12:+57.021	1138.554242	3412.639327	0.000451244	11	N	218	249
P20108	Parental	LRLVK	AFQFVETHGEVCPANWTPESPTIKPSPTASK	EYFEK	4	C12:+57.021	854.1676316	3412.639327	0.001943752	1	N	218	249
P20108	Parental	KQISR	DYGVLLESAGIALR	GLFII	2		738.9069951	1475.79839	0.000451244	24	N	171	185
P20108	Parental	YLVLF	FYPLDFTFVCPTEIVAFSDK	ANEFH	2	C10:+57.021	1198.579878	2395.144156	0.000979378	2	N	99	119
P20152	Exosome	FKNTR	TNEKVELQELNDR	FANYI	2		794.4028052	1586.79001	0.000451244	9	N	100	113
P20152	Exosome	SLNLR	ETNLESLPLVDTHSK	RTLLI	2		841.9339382	1681.852276	0.000451244	1	N	424	439
P20152	Exosome	SVAAK	NLQEAEEWYK	SKFAD	2		655.3071138	1308.598628	0.001229886	2	N	282	292
P20152	Exosome	NDKAR	VEVERDNLAEDIMR	LREKL	2	M13:+15.995	852.9152658	1703.814932	0.002145581	1	N	170	184
P20152	Exosome	NDKAR	VEVERDNLAEDIMR	LREKL	3	M13:+15.995	568.9461105	1703.814932	0.000451244	13	N	170	184
P20152	Exosome	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	C7:+57.021	1189.087119	2376.158637	0.000451244	28	N	321	342
P20152	Exosome	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	3	C7:+57.021	793.0606792	2376.158637	0.000451244	30	N	321	342
P20152	Exosome	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	Q1:-17.027,C7:+57.021	1180.573619	2359.131637	0.000451244	6	N	321	342
P20152	Exosome	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	[0:-17.027,C7:+57.021	1180.573619	2359.131637	0.000622848	12	N	321	342
P20152	Exosome	EQQNK	ILLAELEQLKGQGK	SRLGD	2		770.4593949	1538.90319	0.000451244	3	N	129	143
P20152	Exosome	LDLER	KVESLQEEIAFLK	KLHDE	2		767.4303031	1532.845006	0.000451244	28	N	222	235
P20152	Exosome	LDLER	KVESLQEEIAFLK	KLHDE	3		511.9561354	1532.845006	0.000451244	14	N	222	235
P20152	Exosome	EQQNK	ILLAELEQLK	GQGKS	2		585.3611607	1168.706721	0.000451244	20	N	129	139
P20152	Exosome	GEESR	ISLPLPTFSSLNLR	ETNLE	2		779.4541125	1556.892625	0.000451244	23	N	410	424
P20152	Exosome	GEESR	ISLPLPTFSSLNL	RETNL	2		701.4035569	1400.791514	0.000823681	5	N	410	423
P20152	Exosome	TLLIK	TVETRDGQVINETSQHHDDLE	-	3		808.374357	2422.099671	0.000979378	1	N	445	466
P20152	Exosome	EMLQR	EEAESTLQSFRQDVDNASLAR	LDLER	2		1183.565096	2365.114593	0.002519933	1	N	196	217
P20152	Exosome	EMLQR	EEAESTLQSFRQDVDNASLAR	LDLER	3		789.3793309	2365.114593	0.000451244	21	N	196	217
P20152	Exosome	ERQMR	EMEENFALEAANYQDTIGR	LQDEI	2		1100.99493	2199.97426	0.000451244	4	N	345	364
P20152	Exosome	ERQMR	EMEENFALEAANYQDTIGR	LQDEI	2	M2:+15.995	1108.99243	2215.96926	0.000451244	5	N	345	364
P20152	Exosome	QDSVD	FSLADAINTEFK	NTRTN	2		678.346239	1354.676878	0.000451244	35	N	85	97
P20152	Exosome	AFLKK	LHDEEIQELQAQIQEQHVQID	VDVSK	2		1272.122778	2542.229957	0.000823681	20	N	236	257
P20152	Exosome	AFLKK	LHDEEIQELQAQIQEQHVQID	VDVSK	3		848.4177857	2542.229957	0.001229886	15	N	236	257
P20152	Exosome	IAFLK	KLHDEEIQELQAQIQEQHVQID	VDVSK	3		891.1161067	2670.32492	0.002296037	3	N	235	257
P20152	Exosome	AFLKK	LHDEEIQELQAQIQEQHVQIDVD	VSKPD	3		919.7829047	2756.325314	0.001329271	2	N	236	259
P20152	Exosome	HVQID	VDVSKPDLTAALR	DVRQQ	3		462.2651918	1383.772175	0.002212458	2	N	257	270
P20152	Parental	TVETR	DGQVINETSQHHDDLE	-	2		918.9038977	1835.792195	0.000451244	85	N	450	466
P20152	Parental	TVETR	DGQVINETSQHHDDLE	-	3		612.9385318	1835.792195	0.000823681	5	N	450	466
P20152	Parental	FKNTR	TNEKVELQELNDR	FANYI	2		794.4028052	1586.79001	0.000451244	70	N	100	113
P20152	Parental	FKNTR	TNEKVELQELNDR	FANYI	3		529.9378035	1586.79001	0.000451244	80	N	100	113
P20152	Parental	WYKSK	FADLSEAANR	NNDAL	2		547.2677916	1092.519983	0.000451244	64	N	294	304
P20152	Parental	WYKSK	FADLSEAANRNNDALR	QAKQE	2		888.9353352	1775.85507	0.000451244	10	N	294	310
P20152	Parental	WYKSK	FADLSEAANRNNDALR	QAKQE	3		592.9594901	1775.85507	0.000451244	32	N	294	310
P20152	Parental	PSTSR	SLYSSSPGGAYVTR	SSAVR	2		722.8575022	1443.699404	0.000451244	67	N	50	64
P20152	Parental	SLNLR	ETNLESLPLVDTHSKR	TLLIK	2		919.9844938	1837.953388	0.000451244	47	N	424	440
P20152	Parental	SLNLR	ETNLESLPLVDTHSKR	TLLIK	3		613.6589292	1837.953388	0.000451244	46	N	424	440
P20152	Parental	SLNLR	ETNLESLPLVDTHSKR	TLLIK	4		460.4961469	1837.953388	0.000451244	49	N	424	440
P20152	Parental	SLNLR	ETNLESLPLVDTHSK	RTLLI	2		841.9339382	1681.852276	0.000451244	71	N	424	439
P20152	Parental	SLNLR	ETNLESLPLVDTHSK	RTLLI	3		561.6252255	1681.852276	0.000451244	17	N	424	439
P20152	Parental	SVAAK	NLQEAEEWYK	SKFAD	2		655.3071138	1308.598628	0.000451244	60	N	282	292
P20152	Parental	NDKAR	VEVERDNLAEDIMR	LREKL	2		844.9177658	1687.819932	0.000451244	6	N	170	184
P20152	Parental	NDKAR	VEVERDNLAEDIMR	LREKL	3		563.6144439	1687.819932	0.000823681	3	N	170	184

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P20152	Parental	NDKAR	VEVERDNLAEDIMR	LREKL	2	M13:+15.995	852.9152658	1703.814932	0.001591523	3	N	170	184
P20152	Parental	NDKAR	VEVERDNLAEDIMR	LREKL	3	M13:+15.995	568.9461105	1703.814932	0.000451244	11	N	170	184
P20152	Parental	ARHLR	EYQDLLNVK	MALDI	2		561.2960177	1120.576435	0.000637154	5	N	381	390
P20152	Parental	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	C7:+57.021	1189.087119	2376.158637	0.000451244	109	N	321	342
P20152	Parental	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	3	C7:+57.021	793.0606792	2376.158637	0.000451244	111	N	321	342
P20152	Parental	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	Q1:-17.027,C7:+57.021	1180.573619	2359.131637	0.000451244	15	N	321	342
P20152	Parental	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	3	Q1:-17.027,C7:+57.021	787.3850125	2359.131637	0.002212458	2	N	321	342
P20152	Parental	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	2	[0:-17.027,C7:+57.021	1180.573619	2359.131637	0.000451244	32	N	321	342
P20152	Parental	NEYRR	QVQSLTCEVDALKGTNESLER	QMREM	3	[0:-17.027,C7:+57.021	787.3850125	2359.131637	0.000622848	9	N	321	342
P20152	Parental	EQQNK	ILLAELEQLKGQGK	SRLGD	2		770.4593949	1538.90319	0.000451244	26	N	129	143
P20152	Parental	DLERK	VESLQEEIAFLKK	LHDEE	3		511.9561354	1532.845006	0.001162105	4	N	223	236
P20152	Parental	LDLER	KVESLQEEIAFLK	KLHDE	2		767.4303031	1532.845006	0.000451244	48	N	222	235
P20152	Parental	LDLER	KVESLQEEIAFLK	KLHDE	3		511.9561354	1532.845006	0.000451244	7	N	222	235
P20152	Parental	EQQNK	ILLAELEQLK	GQGKS	2		585.3611607	1168.706721	0.000451244	63	N	129	139
P20152	Parental	IAFLK	KLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	DVRQQ	3		1346.369979	4036.086536	0.000451244	14	N	235	270
P20152	Parental	IAFLK	KLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	DVRQQ	4		1010.029434	4036.086536	0.000451244	36	N	235	270
P20152	Parental	DLERK	VESLQEEIAFLK	KLHDE	2		703.3828215	1404.750043	0.001699387	1	N	223	235
P20152	Parental	AFLKK	LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	DVRQQ	3		1303.671657	3907.991572	0.000451244	85	N	236	270
P20152	Parental	AFLKK	LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	DVRQQ	4		978.0056931	3907.991572	0.000451244	244	N	236	270
P20152	Parental	GVRLL	QDSVDFSLADAINTEFKNTR	TNEKV	2		1136.048551	2270.081502	0.000451244	6	N	80	100
P20152	Parental	GVRLL	QDSVDFSLADAINTEFKNTR	TNEKV	2	Q1:-17.027	1127.535051	2253.054502	0.000451244	4	N	80	100
P20152	Parental	GVRLL	QDSVDFSLADAINTEFKNTR	TNEKV	2	[0:-17.027	1127.535051	2253.054502	0.002981883	1	N	80	100
P20152	Parental	VPGVR	LLQDSVDFSLADAINTEFKNTR	TNEKV	2		1249.132615	2496.24963	0.000451244	16	N	78	100
P20152	Parental	VPGVR	LLQDSVDFSLADAINTEFKNTR	TNEKV	3		833.0910099	2496.24963	0.000451244	13	N	78	100
P20152	Parental	GVRLL	QDSVDFSLADAINTEFK	NTRTN	2		950.4526922	1898.889784	0.000451244	86	N	80	97
P20152	Parental	GVRLL	QDSVDFSLADAINTEFK	NTRTN	3		633.9710614	1898.889784	0.0007646	6	N	80	97
P20152	Parental	GVRLL	QDSVDFSLADAINTEFK	NTRTN	2	Q1:-17.027	941.9391922	1881.862784	0.000451244	10	N	80	97
P20152	Parental	GVRLL	QDSVDFSLADAINTEFK	NTRTN	2	[0:-17.027	941.9391922	1881.862784	0.000451244	9	N	80	97
P20152	Parental	GEESR	ISLPLPTFSSLNLR	ETNLE	2		779.4541125	1556.892625	0.000451244	69	N	410	424
P20152	Parental	GEESR	ISLPLPTFSSLNLR	ETNLE	3		519.9720083	1556.892625	0.000622848	22	N	410	424
P20152	Parental	VPGVR	LLQDSVDFSLADAINT	EFKNT	2		861.4337711	1720.851942	0.000451244	15	N	78	94
P20152	Parental	VPGVR	LLQDSVDFSLADAINTEFK	NTRTN	2		1063.536756	2125.057912	0.000451244	750	N	78	97
P20152	Parental	VPGVR	LLQDSVDFSLADAINTEFK	NTRTN	3		709.3604375	2125.057912	0.000451244	63	N	78	97
P20152	Parental	GEESR	ISLPLPTFSSLNL	RETNL	2		701.4035569	1400.791514	0.000451244	3	N	410	423
P20152	Parental	TLLIK	TVETRDGQVINETSQHHDDLE	-	3		808.374357	2422.099671	0.000451244	7	N	445	466
P20152	Parental	EEMAR	HLREYQDLLNVK	MALDI	3		509.9479742	1526.820523	0.000823681	8	N	378	390
P20152	Parental	EMLQR	EEAESTLQSFRQDVDNASLAR	LDLER	2		1183.565096	2365.114593	0.000622848	3	N	196	217
P20152	Parental	EMLQR	EEAESTLQSFRQDVDNASLAR	LDLER	3		789.3793309	2365.114593	0.000451244	27	N	196	217
P20152	Parental	LLNVK	MALDIEIATYR	KLLEG	2		648.3373602	1294.65912	0.000622848	6	N	390	401
P20152	Parental	TTSTR	TYSLGSALRPSTSR	SLYSS	3		499.2674839	1494.779052	0.001943752	1	N	36	50
P20152	Parental	NEYRR	QVQSLTCEVDALK	GTNES	2	C7:+57.021	745.8798887	1489.744177	0.000451244	37	N	321	334
P20152	Parental	ERQMR	EMEENFALEAANYQDTIGR	LQDEI	2		1100.99493	2199.97426	0.000451244	10	N	345	364
P20152	Parental	ATYRK	LLEGEESRISLPLPTFSSLNLR	ETNLE	3		824.4555121	2470.343136	0.000451244	3	N	402	424
P20152	Parental	GEESR	ISLPLPTFSSLNLRET	NLESL	2		894.4992484	1786.982897	0.001463592	1	N	410	426
P20152	Parental	SRISL	PLPTFSSLNLR	ETNLE	2		622.8540342	1243.692468	0.000622848	9	N	413	424
P20152	Parental	EMLQR	EEAESTLQSFR	QDVDN	2		648.8074779	1295.599356	0.000451244	38	N	196	207
P20152	Parental	RLREK	LQEEMLQREEAESTLQSFR	QDVDN	3	M5:+15.995	780.7099409	2339.106423	0.000735798	7	N	188	207
P20152	Parental	DSVDF	SLADAINTEFK	NTRTN	2		604.812032	1207.608464	0.000622848	1	N	86	97
P20152	Parental	QMREM	EENFALEAANYQDTIGR	LQDEI	2		970.9533907	1939.891181	0.001329271	1	N	347	364
P20491	Exosome	EQAAA	LGEPQLCYILDAVLFLYGIVLTLLYCR	LKIQV	3	C7:+57.021,C26:+57.021	1072.57997	3214.716509	0.001943752	3	N	18	45
P20491	Parental	EQAAA	LGEPQLCYILDAVLFLYGIVLTLLYCRLK	IQVRK	3	C7:+57.021,C26:+57.021	1152.972979	3455.895536	0.001591523	3	N	18	47
P20491	Parental	EQAAA	LGEPQLCYILDAVLFLYGIVLTLLYCR	LKIQV	3	C7:+57.021,C26:+57.021	1072.57997	3214.716509	0.000823681	7	N	18	45
P20918	Exosome	DYRGK	TAVTAAGTPCQGWAAQEPHR	HSIFT	3	C10:+57.021	703.6695682	2107.985305	0.000451244	12	N	492	512
P20918	Exosome	KNYCR	NPDGDVNGPWCYTTNPR	KLYDY	2	C11:+57.021	981.9238789	1961.832158	0.000451244	10	N	532	549
P20918	Exosome	TTNPR	KLYDYCDIPLCASASSFECGKPQVEPK	KCPGR	4	C6:+57.021,C11:+57.021,C19:+57.021	791.3701507	3161.449403	0.000451244	6	N	549	576
P20918	Exosome	SLRTR	FTGQHFCGGTLIAPEWVLTAAHCLEK	SSRPE	3	C7:+57.021,C23:+57.021	981.8144088	2942.419826	0.000451244	1	N	602	628
P20918	Exosome	SLRTR	FTGQHFCGGTLIAPEWVLTAAHCLEK	SSRPE	4	C7:+57.021,C23:+57.021	736.6127566	2942.419826	0.000451244	3	N	602	628
P20918	Exosome	ENYCR	NPDGETAPWCYTTDSQLR	WEYCE	2	C10:+57.021	1055.960658	2109.905717	0.000451244	6	N	325	343
P20918	Exosome	NNRVK	STELCAGQLAGGVDSCQGDSGGPLVCFEKDK	YILQG	3	C5:+57.021,C16:+57.021,C26:+57.021	1081.484862	3241.431187	0.000662267	2	N	742	773
P20918	Exosome	NFPCK	NLEENYCRNPDGETAPWCYTTDSQLR	WEYCE	3	C7:+57.021,C18:+57.021	1063.792949	3188.355448	0.000451244	3	N	317	343
P20918	Exosome	KPGQG	DSLDGYISTQGASLFSLTK	KQLAA	2		1002.002549	2001.989498	0.000622848	1	N	19	38
P20918	Exosome	NNRVK	STELCAGQLAGGVDSCQGDSGGPLVCFEK	DKYIL	3	C5:+57.021,C16:+57.021,C26:+57.021	1000.444227	2998.309281	0.001654178	1	N	742	771

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P20918	Exosome	CDIPR	CTTPPPPPSPTYQCLK	GRGEN	2	C1:+57.021,C14:+57.021	922.4395563	1842.863513	0.002727428	2	N	261	277
P21107	Exosome	LAEKK	AADAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	11	N	78	91
P21107	Exosome	EEVAR	KLVIIEGDLER	TEERA	2		642.880249	1283.744898	0.000451244	16	Y	168	179
P21107	Exosome	EEVAR	KLVIIEGDLER	TEERA	3		428.922766	1283.744898	0.000451244	42	Y	168	179
P21107	Exosome	RAQER	LATALQKLEEAEK	AADES	3		481.9404853	1442.798056	0.000451244	2	Y	106	119
P21107	Exosome	SLNRR	IQLVEEELDRAQER	LATAL	2		864.4502868	1726.884974	0.000622848	13	Y	92	106
P21107	Exosome	AKLEK	TIDDLEDELYAQK	LKYKA	2		776.8730149	1551.73043	0.000451244	5	N	252	265
P21107	Exosome	EVARK	LVIIEGDLER	TEERA	2		578.8327674	1155.649935	0.002453667	1	Y	169	179
P21107	Parental	LAEKK	AADAEAEVASLNRR	IQLVE	2		736.8767576	1471.737915	0.000451244	4	N	78	92
P21107	Parental	LAEKK	AADAEAEVASLNRR	IQLVE	3		491.5871051	1471.737915	0.000451244	22	N	78	92
P21107	Parental	LAEKK	AADAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	40	N	78	91
P21107	Parental	EEVAR	KLVIIEGDLER	TEERA	2		642.880249	1283.744898	0.000451244	28	Y	168	179
P21107	Parental	EEVAR	KLVIIEGDLER	TEERA	3		428.922766	1283.744898	0.000451244	63	Y	168	179
P21107	Parental	RAQER	LATALQKLEEAEK	AADES	2		722.4068279	1442.798056	0.000451244	5	Y	106	119
P21107	Parental	RAQER	LATALQKLEEAEK	AADES	3		481.9404853	1442.798056	0.000823681	2	Y	106	119
P21107	Parental	SLNRR	IQLVEEELDRAQER	LATAL	2		864.4502868	1726.884974	0.000451244	29	Y	92	106
P21107	Parental	SLNRR	IQLVEEELDRAQER	LATAL	3		576.6361245	1726.884974	0.000451244	3	Y	92	106
P21107	Parental	AKLEK	TIDDLEDELYAQK	LKYKA	2		776.8730149	1551.73043	0.000451244	3	N	252	265
P21107	Parental	ASLNR	RIQLVEEELDR	AQERL	2		700.3811445	1398.746689	0.001395409	6	Y	91	102
P21107	Parental	ASLNR	RIQLVEEELDR	AQERL	3		467.2566963	1398.746689	0.001162105	3	Y	91	102
P21107	Parental	KDEEK	MELQEIQLK	EAKHI	2		566.3080714	1130.600543	0.002453667	2	Y	141	150
P21107	Parental	EVARK	LVIIEGDLER	TEERA	2		578.8327674	1155.649935	0.002813207	2	Y	169	179
P21107	Parental	SLNRR	IQLVEEELDR	AQERL	2		622.3305889	1242.645578	0.002813207	1	Y	92	102
P21107-2	Exosome	EAVKR	KIQVLQQQADDAEER	AERLQ	2		885.9531937	1769.890787	0.000451244	15	N	12	27
P21107-2	Exosome	EAVKR	KIQVLQQQADDAEER	AERLQ	3		590.9713958	1769.890787	0.000451244	27	N	12	27
P21107-2	Exosome	AVKRK	IQVLQQQADDAEER	AERLQ	2		821.9057121	1641.795824	0.000451244	45	N	13	27
P21107-2	Exosome	AVKRK	IQVLQQQADDAEERAER	LQREV	2		999.9961212	1997.976642	0.000451244	15	N	13	30
P21107-2	Exosome	AVKRK	IQVLQQQADDAEERAER	LQREV	3		667.0000141	1997.976642	0.000451244	8	N	13	30
P21107-2	Exosome	AKLEK	TIDDLEDKLK	CTKEE	2		595.3196898	1188.62378	0.001162105	8	N	215	225
P21107-2	Exosome	EEVAR	KLVIIEGDLER	TEERA	2		642.880249	1283.744898	0.000451244	16	Y	131	142
P21107-2	Exosome	EEVAR	KLVIIEGDLER	TEERA	3		428.922766	1283.744898	0.000451244	42	Y	131	142
P21107-2	Exosome	RAQER	LATALQKLEEAEK	AADES	3		481.9404853	1442.798056	0.000451244	2	Y	69	82
P21107-2	Exosome	SLNRR	IQLVEEELDRAQER	LATAL	2		864.4502868	1726.884974	0.000622848	13	Y	55	69
P21107-2	Exosome	ERRAR	EQAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	6	N	42	54
P21107-2	Exosome	EGERR	AREQAEAEVASLNR	RIQLV	2		772.3953145	1542.775029	0.000622848	1	N	40	54
P21107-2	Exosome	ERRAR	EQAEAEVASLNRR	IQLVE	3		491.5871051	1471.737915	0.00091018	3	N	42	55
P21107-2	Exosome	EVARK	LVIIEGDLER	TEERA	2		578.8327674	1155.649935	0.002453667	1	Y	132	142
P21107-2	Exosome	LCTQR	MLDQTLLDLNEM	-	2	M12:+15.995	726.3420256	1450.668451	0.002813207	1	N	236	248
P21107-2	Exosome	LCTQR	MLDQTLLDLNEM	-	2	M1:+15.995,M12:+15.995	734.3395256	1466.663451	0.001162105	6	N	236	248
P21107-2	Parental	EAVKR	KIQVLQQQADDAEER	AERLQ	2		885.9531937	1769.890787	0.000451244	58	N	12	27
P21107-2	Parental	EAVKR	KIQVLQQQADDAEER	AERLQ	3		590.9713958	1769.890787	0.000451244	55	N	12	27
P21107-2	Parental	AVKRK	IQVLQQQADDAEER	AERLQ	2		821.9057121	1641.795824	0.000451244	119	N	13	27
P21107-2	Parental	AVKRK	IQVLQQQADDAEERAER	LQREV	2		999.9961212	1997.976642	0.000451244	40	N	13	30
P21107-2	Parental	AVKRK	IQVLQQQADDAEERAER	LQREV	3		667.0000141	1997.976642	0.000451244	31	N	13	30
P21107-2	Parental	AKLEK	TIDDLEDKLK	CTKEE	2		595.3196898	1188.62378	0.000823681	8	N	215	225
P21107-2	Parental	EEVAR	KLVIIEGDLER	TEERA	2		642.880249	1283.744898	0.000451244	28	Y	131	142
P21107-2	Parental	EEVAR	KLVIIEGDLER	TEERA	3		428.922766	1283.744898	0.000451244	63	Y	131	142
P21107-2	Parental	RAQER	LATALQKLEEAEK	AADES	2		722.4068279	1442.798056	0.000451244	5	Y	69	82
P21107-2	Parental	RAQER	LATALQKLEEAEK	AADES	3		481.9404853	1442.798056	0.000823681	2	Y	69	82
P21107-2	Parental	SLNRR	IQLVEEELDRAQER	LATAL	2		864.4502868	1726.884974	0.000451244	29	Y	55	69
P21107-2	Parental	SLNRR	IQLVEEELDRAQER	LATAL	3		576.6361245	1726.884974	0.000451244	3	Y	55	69
P21107-2	Parental	ERRAR	EQAEAEVASLNR	RIQLV	2		658.826202	1315.636804	0.000451244	8	N	42	54
P21107-2	Parental	EGERR	AREQAEAEVASLNR	RIQLV	2		772.3953145	1542.775029	0.000451244	4	N	40	54
P21107-2	Parental	EGERR	AREQAEAEVASLNR	RIQLV	3		515.266143	1542.775029	0.000451244	8	N	40	54
P21107-2	Parental	ERRAR	EQAEAEVASLNRR	IQLVE	2		736.8767576	1471.737915	0.002981883	1	N	42	55
P21107-2	Parental	ERRAR	EQAEAEVASLNRR	IQLVE	3		491.5871051	1471.737915	0.00091018	5	N	42	55
P21107-2	Parental	ASLNR	RIQLVEEELDR	AQERL	2		700.3811445	1398.746689	0.001395409	6	Y	54	65
P21107-2	Parental	ASLNR	RIQLVEEELDR	AQERL	3		467.2566963	1398.746689	0.001162105	3	Y	54	65
P21107-2	Parental	KDEEK	MELQEIQLK	EAKHI	2		566.3080714	1130.600543	0.002453667	2	Y	104	113
P21107-2	Parental	EVARK	LVIIEGDLER	TEERA	2		578.8327674	1155.649935	0.002813207	2	Y	132	142
P21107-2	Parental	SLNRR	IQLVEEELDR	AQERL	2		622.3305889	1242.645578	0.002813207	1	Y	55	65
P21614	Exosome	SHLIK	LAQKVPTANLENVLPLAEDFTEILSR	CCEST	3		961.1943571	2880.559671	0.000451244	8	N	238	264
P21614	Exosome	RRDPK	GFADQFLYEYSSNYGQAPLPLLVAYTK	NYLSM	3		1019.174963	3054.501488	0.000451244	29	N	153	180
P21614	Exosome	KLAQK	VPTANLENVLPLAEDFTEILSR	CCEST	3		814.4361175	2440.284953	0.000451244	13	N	242	264

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P21614	Exosome	NQLVK	EVVSLTEECCAEGADPTCYDTR	TSELS	2	C9:+57.021,C10:+57.021,C18:+57.021	1281.524914	2561.034228	0.000451244	2	N	65	87
P21614	Parental	MAALS	HQPQEFPTYVEPTNDEICEAFR	RDPKG	2	C18:+57.021	1354.108583	2706.201565	0.000451244	12	N	127	149
P21614	Parental	MAALS	HQPQEFPTYVEPTNDEICEAFR	RDPKG	3	C18:+57.021	903.0749883	2706.201565	0.000451244	27	N	127	149
P21614	Parental	SHLIK	LAQKVPTANLENVLPLAEDFTEILSR	CCEST	3		961.1943571	2880.559671	0.000451244	3	N	238	264
P21614	Parental	RRDPK	GFADQFLYEYSSNYGQAPLPLLVAYTK	NYLSM	3		1019.174963	3054.501488	0.002374549	1	N	153	180
P21614	Parental	KLAQK	VPTANLENVLPLAEDFTEILSR	CCEST	3		814.4361175	2440.284953	0.002981883	1	N	242	264
P21614	Parental	ELSVK	SCESDAPFPVHPGTPECCTK	EGLER	3	C2:+57.021,C17:+57.021,C18:+57.021	759.318799	2274.932997	0.000637154	1	N	94	114
P21619	Exosome	SLFHR	SEAELATALSDKQGLETEVAELR	AQLAK	3		820.7541749	2459.239125	0.000637154	3	N	136	159
P21619	Parental	SLFHR	SEAELATALSDKQGLETEVAELR	AQLAK	3		820.7541749	2459.239125	0.000451244	23	N	136	159
P21619	Parental	DLENR	CQSLQEELAFSK	SVFEE	2	C1:+57.021	720.3456817	1438.675763	0.001162105	2	N	189	201
P21619	Parental	VSGIK	TLYESELADAR	RVLDE	2		634.3123961	1266.609192	0.001943752	1	N	71	82
P21619	Parental	SSGSR	LAQQTVATGVVNIDEVDPEGR	FVRLK	2		1106.066744	2210.117887	0.000451244	4	N	439	460
P21619	Parental	SVQGR	ENGEEEEEEEAEFGEEDLFHQQGDPR	TTSRG	3		1026.750546	3077.228239	0.000622848	5	N	561	587
P22366	Exosome	ASVGR	LLELLALLDREDILK	ELKSR	3		589.6929112	1766.055334	0.000622848	3	N	88	103
P22366	Exosome	DYRLK	LCVSDRDVLPGTCVWSIASELIEK	RCRRM	3	C2:+57.021,C13:+57.021	916.4631531	2746.366059	0.001162105	1	N	190	214
P22366	Parental	ASVGR	LLELLALLDREDILK	ELKSR	3		589.6929112	1766.055334	0.002212458	1	N	88	103
P22599	Exosome	PPILR	FDHPFLFIIFEEHTQSPIFVGK	VVDPT	4		662.8446733	2647.347493	0.000823681	1	N	384	406
P22599	Exosome	VEAVK	ELDQDTVFALANYILFK	GKWKK	2		1000.522921	1999.030241	0.001943752	1	N	192	209
P22599	Exosome	LGITR	IFNNGADLSGITEENAPLK	LSKAV	2		1002.008166	2002.000732	0.000451244	4	Y	328	347
P22599	Parental	PPILR	FDHPFLFIIFEEHTQSPIFVGK	VVDPT	4		662.8446733	2647.347493	0.001463592	3	N	384	406
P22599	Parental	PSFLA	EDVQETDTSQKDQSPASHEIATNLGDFAISLYR	ELVHQ	3		1222.578764	3664.712891	0.000451244	8	Y	24	57
P22599	Parental	VEAVK	ELDQDTVFALANYILFK	GKWKK	2		1000.522921	1999.030241	0.000451244	11	N	192	209
P22599	Parental	VEAVK	ELDQDTVFALANYILFK	GKWKK	3		667.3512137	1999.030241	0.000823681	1	N	192	209
P22599	Parental	GTQGK	IVEAVKELDQDTVFALANYILFK	GKWKK	3		880.4830678	2638.425803	0.001463592	1	N	186	209
P22599	Parental	LGITR	IFNNGADLSGITEENAPLK	LSKAV	2		1002.008166	2002.000732	0.000451244	15	Y	328	347
P22599	Parental	LEEAK	NHYQAEVFSVNFAESEEAKK	VINDF	3		776.3699956	2326.086587	0.000451244	9	Y	153	173
P22599	Parental	ADIHK	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	LVEKF	3		1166.937898	3497.790293	0.000451244	10	Y	112	143
P22599	Parental	ADIHK	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	LVEKF	4		875.4553733	3497.790293	0.000451244	9	Y	112	143
P22682	Parental	KLALK	NSPPYILDLLPDTYQHLR	TVLSR	2		1078.063276	2154.110951	0.002981883	1	N	76	94
P22682	Parental	INSER	KASSYQQGGGATANPVATAPSPQLSSEIER	LMSQG	3		1001.499168	3001.474104	0.000451244	15	N	840	870
P22682	Parental	RCEIK	GTEPIVVDPFDPR	GSGSL	2		721.3702454	1440.724891	0.000451244	2	N	422	435
P22682	Parental	FPDGR	NQNPDLTGLCEPTPQDHIK	VTQEQ	3	C10:+57.021	726.3482718	2176.021415	0.002453667	1	N	341	360
P22682	Parental	NSERK	ASSYQQGGGATANPVATAPSPQLSSEIER	LMSQG	2		1437.69737	2873.379141	0.000451244	1	N	841	870
P22892	Exosome	AAVPK	TFQLQLLSPSSSVVPAFNTGTITQVIK	VLNPQ	2		1438.792554	2875.569508	0.000451244	6	N	756	783
P22892	Exosome	AAVPK	TFQLQLLSPSSSVVPAFNTGTITQVIK	VLNPQ	3		959.5309692	2875.569508	0.000451244	20	N	756	783
P22892	Exosome	RGMMK	ELLYFLDSCEPEFK	ADCAS	2	C9:+57.021	895.4215864	1788.827573	0.000622848	3	N	383	397
P22892	Exosome	VQRHR	STIVDCLKDLDVSIK	RRAME	2	C6:+57.021	853.4559606	1704.896321	0.001329271	1	N	347	362
P22892	Parental	AAVPK	TFQLQLLSPSSSVVPAFNTGTITQVIK	VLNPQ	3		959.5309692	2875.569508	0.000622848	11	N	756	783
P23116	Exosome	VPEVK	DLYNWLEVEFNPLK	LCERV	2		890.4517668	1778.887934	0.000451244	27	N	388	402
P23116	Exosome	LNWVR	EQPEKEPELQQYVPQLQNNTILR	LLQQV	3		932.1510399	2793.42972	0.001463592	4	N	415	438
P23116	Exosome	IEFSR	LTSLVPFVDAFQLER	AIVDA	2		867.9754091	1733.935218	0.00091018	1	N	454	469
P23116	Exosome	NTILR	LLQQVAQIYQSIEFSR	LTSLV	2		962.0208793	1922.026159	0.000451244	24	N	438	454
P23116	Exosome	NTILR	LLQQVAQIYQSIEFSR	LTSLV	3		641.6831862	1922.026159	0.000451244	4	N	438	454
P23116	Exosome	NDMVR	FSVLQYVVPEVK	DLYNW	2		704.3982746	1406.780949	0.000451244	9	N	376	388
P23116	Exosome	DHTSR	TLSFGSDLNYATR	EDAPV	2		722.8575022	1443.699404	0.000451244	4	N	489	502
P23116	Parental	VPEVK	DLYNWLEVEFNPLK	LCERV	2		890.4517668	1778.887934	0.000451244	17	N	388	402
P23116	Parental	LNWVR	EQPEKEPELQQYVPQLQNNTILR	LLQQV	3		932.1510399	2793.42972	0.000451244	14	N	415	438
P23116	Parental	NDMVR	FSVLQYVVPEVK	DLYNW	2		704.3982746	1406.780949	0.000823681	3	N	376	388
P23249	Exosome	PFPAK	LDLQQGQDLLQGLSK	LSPST	2		828.4522982	1654.888996	0.000451244	5	N	953	968
P23249	Exosome	GKDER	EGNSPSFFNPEEAATVTSYLK	QLLAP	2		1144.540027	2287.064455	0.000451244	7	N	788	809
P23249	Exosome	PILLR	QLLPTLLQGPSIFTAPK	EVAEI	2		912.5356339	1823.055668	0.001871652	1	N	302	319
P23249	Exosome	LMDVK	ETGNPGGQLVLAGDPR	QLGPV	2		790.9055151	1579.79543	0.000622848	1	N	667	683
P23492	Exosome	TAHLK	EAQIFDYNEIPNFPQSTVQGHAGR	LVFGL	2		1359.649495	2717.28339	0.000451244	16	N	43	67
P23492	Exosome	TAHLK	EAQIFDYNEIPNFPQSTVQGHAGR	LVFGL	3		906.7689299	2717.28339	0.000451244	63	N	43	67
P23492	Exosome	HCGLR	VFGFSLITNK	VVMDY	2		563.3192958	1124.622992	0.000451244	30	N	234	244
P23492	Exosome	IMLIR	DHINLPGFCGQNPLR	GPNDE	3	C9:+57.021	579.9548687	1736.841206	0.000451244	30	N	133	148
P23492	Exosome	IMLIR	DHINLPGFCGQNPLRGPNDER	FGVRF	3	C9:+57.021	802.7174696	2405.129009	0.000451244	26	N	133	154
P23492	Exosome	GHAGR	LVFGLLNGR	CCVMM	2		494.8010733	987.5865465	0.000823681	6	N	67	76
P23492	Exosome	ETTAK	WLLQHTEYRPQVAVICGSGLGGLTAHLK	EAQIF	3	C16:+57.021	1035.55396	3103.638479	0.001162105	7	N	15	43
P23492	Exosome	ETTAK	WLLQHTEYRPQVAVICGSGLGGLTAHLK	EAQIF	4	C16:+57.021	776.9174197	3103.638479	0.000622848	22	N	15	43
P23492	Exosome	MGEQR	KLQEGTYVMLAGPNFETVAESR	LLKML	3		814.0779362	2439.210409	0.000622848	3	N	185	207
P23492	Exosome	QTLER	FVSILMESIPLPDRGS	-	2		880.9667274	1759.917855	0.000451244	8	N	273	289
P23492	Parental	TAHLK	EAQIFDYNEIPNFPQSTVQGHAGR	LVFGL	2		1359.649495	2717.28339	0.000622848	1	N	43	67

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P23492	Parental	TAHLK	EAQIFDYNEIPNFPQSTVQGHAGR	LVFGL	3		906.7689299	2717.28339	0.000451244	29	N	43	67
P23492	Parental	HCGLR	VFGFSLITNK	VVMDY	2		563.3192958	1124.622992	0.000451244	12	N	234	244
P23492	Parental	IMLIR	DHINLPGFCGQNPLRGPNDER	FGVRF	3	C9:+57.021	802.7174696	2405.129009	0.000622848	1	N	133	154
P23492	Parental	GHAGR	LVFGLLNGR	CCVMM	2		494.8010733	987.5865465	0.001943752	1	N	67	76
P23492	Parental	ETTAK	WLLQHTEYRPQVAVICGSGLGGLTAHLK	EAQIF	3	C16:+57.021	1035.55396	3103.638479	0.002813207	1	N	15	43
P23492	Parental	ETTAK	WLLQHTEYRPQVAVICGSGLGGLTAHLK	EAQIF	4	C16:+57.021	776.9174197	3103.638479	0.001763695	7	N	15	43
P23591	Exosome	RAIQK	VVADGAGLPGEEWVFVSSK	DADLT	2		973.9970699	1945.97854	0.000451244	17	N	25	44
P23591	Exosome	KQAVK	ETCTWFTDNYEQAR	K-	2	C3:+57.021	910.8811484	1819.746697	0.001463592	3	N	306	320
P23591	Exosome	HGCTF	TAVIPTNVFGPYDNFNIEDGHVLPGLIHK	VHLAK	4		795.1651706	3176.629482	0.000451244	2	N	165	194
P23591	Parental	RAIQK	VVADGAGLPGEEWVFVSSK	DADLT	2		973.9970699	1945.97854	0.000662267	5	N	25	44
P23591	Parental	RAIQK	VVADGAGLPGEEWVFVSSKDADLTDAAQTQALFQK	VQPTH	3		1221.944607	3662.81042	0.000451244	4	N	25	60
P23953	Exosome	KVLGK	YISLEGFEQPVAVFLGVPFAKPPLGSLR	FAPPQ	3		1011.227221	3030.658263	0.000451244	17	N	36	64
P23953	Exosome	ILPLK	ISEDCLYLNIYSPADLTK	SSQLP	2	C5:+57.021	1058.019653	2114.023707	0.000451244	5	N	111	129
P23953	Parental	KVLGK	YISLEGFEQPVAVFLGVPFAKPPLGSLR	FAPPQ	3		1011.227221	3030.658263	0.000451244	7	N	36	64
P23953	Parental	ILPLK	ISEDCLYLNIYSPADLTK	SSQLP	2	C5:+57.021	1058.019653	2114.023707	0.000451244	1	N	111	129
P23953	Parental	LPEGK	MNEETASLLLR	RFHSE	2	M1:+15.995	646.829942	1291.644284	0.002453667	2	N	359	370
P24063	Exosome	GAEGR	VVVLSSRPVVDVVTELSFSPEEIPVHEVECSYSAR	EEQKH	4	C30:+57.021	979.5019763	3913.976705	0.000451244	16	N	604	639
P24063	Exosome	AVGAK	DWAGGFLDLREDLQGATFVGQEPLTSDVR	GGYLG	3		1064.858585	3191.552354	0.000451244	5	N	369	398
P24063	Exosome	FLDLR	EDLQGATFVGQEPLTSDVR	GGYLG	2		1031.50853	2061.00146	0.000451244	5	N	379	398
P24063	Exosome	TYQRR	QSLFEMVSELQGDPGYPLGR	FGAAI	2	M6:+15.995	1120.039183	2238.062767	0.000451244	4	N	498	518
P24063	Exosome	VLSSR	PVVDVVTELSFSPEEIPVHEVECSYSAR	EEQKH	3	C23:+57.021	1058.848544	3173.522231	0.000735798	2	N	611	639
P24063	Exosome	AVGAK	DWAGGFLDLR	EDLQG	2		575.288527	1148.561454	0.001329271	5	N	369	379
P24063	Exosome	VQKQK	TLHIFASEPVEEFVK	ILDTF	3		582.6423279	1744.903584	0.000451244	5	N	295	310
P24063	Exosome	INGDR	LTDVAVGAPLEEQGAVYIFNGKPGGLSPQPSQR	IQGAQ	3		1132.591839	3394.752117	0.000451244	4	N	533	566
P24063	Parental	QPSQR	IQGAQVFPGIR	WFGRS	2		593.3410939	1184.666588	0.000622848	3	N	566	577
P24063	Parental	AQAGR	HFGYQVLQIEDGVVVGAPGEGDNTGGLYHCR	TSSEF	3	C30:+57.021	1115.530319	3343.567558	0.000451244	2	N	40	71
P24063	Parental	AQAGR	HFGYQVLQIEDGVVVGAPGEGDNTGGLYHCR	TSSEF	4	C30:+57.021	836.8996896	3343.567558	0.000698008	8	N	40	71
P24063	Parental	GAEGR	VVVLSSRPVVDVVTELSFSPEEIPVHEVECSYSAREEQK	HGVKL	4	C30:+57.021	1108.061658	4428.215432	0.001463592	3	N	604	643
P24063	Parental	GAEGR	VVVLSSRPVVDVVTELSFSPEEIPVHEVECSYSAR	EEQKH	3	C30:+57.021	1305.666702	3913.976705	0.000451244	1	N	604	639
P24063	Parental	GAEGR	VVVLSSRPVVDVVTELSFSPEEIPVHEVECSYSAR	EEQKH	4	C30:+57.021	979.5019763	3913.976705	0.000451244	37	N	604	639
P24063	Parental	AVGAK	DWAGGFLDLREDLQGATFVGQEPLTSDVR	GGYLG	3		1064.858585	3191.552354	0.000451244	27	N	369	398
P24063	Parental	AKAWS	YNLDTRPTQSFLAQAGR	HFGYQ	3		646.6663067	1936.97552	0.000451244	2	N	23	40
P24063	Parental	QPHSR	MPVSCEELTEGSSLLTK	TLKCN	2	C5:+57.021	940.9529254	1879.890251	0.000698008	1	N	835	852
P24063	Parental	FLDLR	EDLQGATFVGQEPLTSDVR	GGYLG	2		1031.50853	2061.00146	0.000451244	35	N	379	398
P24063	Parental	AVGAK	DWAGGFLDLR	EDLQG	2		575.288527	1148.561454	0.000735798	9	N	369	379
P24063	Parental	VQKQK	TLHIFASEPVEEFVK	ILDTF	2		873.4595919	1744.903584	0.000622848	3	N	295	310
P24063	Parental	VQKQK	TLHIFASEPVEEFVK	ILDTF	3		582.6423279	1744.903584	0.000451244	10	N	295	310
P24063	Parental	YPLGR	FGAAITALTDINGDR	LTDVA	2		767.8971587	1533.778717	0.000451244	6	N	518	533
P24063	Parental	INGDR	LTDVAVGAPLEEQGAVYIFNGKPGGLSPQPSQR	IQGAQ	3		1132.591839	3394.752117	0.000451244	17	N	533	566
P24063	Parental	LGGDR	LADVVVGAEGR	VVVLS	2		543.3016344	1084.587669	0.001871652	1	N	593	604
P24063	Parental	AGAPR	YQHVGQVLLFQAPEAGGR	WNQTQ	2		985.5162955	1969.016991	0.000451244	4	N	424	442
P24270	Exosome	GFAVK	FYTEDGNWDLVGNNTPIFFIR	DAILF	2		1259.606036	2517.196472	0.000451244	40	N	135	156
P24270	Exosome	GFAVK	FYTEDGNWDLVGNNTPIFFIR	DAILF	3		840.0732906	2517.196472	0.000451244	53	N	135	156
P24270	Exosome	EERKR	LCENIAGHLK	DAQLF	2	C2:+57.021	577.8032557	1153.590911	0.001395409	1	N	458	468
P24270	Exosome	VDVKR	FNSANEDNVTQVR	TFYTK	2		747.3531153	1492.690631	0.000451244	6	N	431	444
P24270	Exosome	SHTFK	LVNADGEAVYCK	FHYKT	2	C11:+57.021	669.8218424	1337.628085	0.000451244	25	N	221	233
P24270	Exosome	VVHAK	GAGAFGYFEVTHDITR	YSKAK	2		870.9211652	1739.82673	0.000451244	26	N	77	93
P24270	Exosome	VVHAK	GAGAFGYFEVTHDITR	YSKAK	3		580.9500434	1739.82673	0.000451244	44	N	77	93
P24270	Exosome	VMTFK	EAETFPFNPFDLTK	VWPHK	2		828.4017426	1654.787885	0.000622848	7	N	287	301
P24270	Exosome	WKEQR	ASQRPDVLTTGGGNPIGDK	LNIMT	2		941.9850251	1881.95445	0.000451244	2	N	19	38
P24270	Exosome	THRHR	LGPNYLQIPVNCPYR	ARVAN	2	C12:+57.021	902.4644543	1802.913309	0.000451244	29	N	365	380
P24270	Exosome	THRHR	LGPNYLQIPVNCPYR	ARVAN	3	C12:+57.021	601.9789029	1802.913309	0.000451244	10	N	365	380
P24270	Exosome	PEQQR	SALEHSVQCAVDVK	RFNSA	2	C9:+57.021	771.8829627	1541.750325	0.001395409	2	N	416	430
P24270	Exosome	VWDFW	SLRPESLHQVSFLFSDR	GIPDG	3		673.3538401	2017.03812	0.000451244	3	N	186	203
P24270	Exosome	IFFIR	DAILFPSFIHSQK	RNPQT	2		751.9042554	1501.792911	0.000451244	12	N	156	169
P24270	Exosome	TAGSR	GPLLVQDVVFTDEMAHFDR	ERIPE	2		1095.038944	2188.062287	0.000451244	3	N	47	66
P24270	Exosome	TAGSR	GPLLVQDVVFTDEMAHFDR	ERIPE	3		730.3618958	2188.062287	0.000451244	18	N	47	66
P24270	Exosome	IFFIR	DAILFPSFIHSQKR	NPQTH	2		829.954811	1657.894022	0.000622848	2	N	156	170
P24270	Exosome	IFFIR	DAILFPSFIHSQKR	NPQTH	3		553.6391407	1657.894022	0.000451244	5	N	156	170
P24270	Exosome	IFFIR	DAILFPSFIHSQKR	NPQTH	4		415.4813055	1657.894022	0.000451244	18	N	156	170
P24270	Exosome	TAGSR	GPLLVQDVVFTDEMAHFDRER	IPERV	3		825.4097973	2473.205992	0.000451244	4	N	47	68
P24270	Exosome	TAGSR	GPLLVQDVVFTDEMAHFDRER	IPERV	4		619.309298	2473.205992	0.000451244	16	N	47	68
P24270	Exosome	TAGSR	GPLLVQDVVFTDEMAHFDRER	IPERV	4	M14:+15.995	623.308048	2489.200992	0.001839721	1	N	47	68
P24270	Exosome	EERKR	LCENIAGHLKDAQLFIQK	KAVKN	2	C2:+57.021	1049.559614	2097.103629	0.000451244	11	N	458	476
P24270	Exosome	EERKR	LCENIAGHLKDAQLFIQK	KAVKN	3	C2:+57.021	700.042343	2097.103629	0.000451244	14	N	458	476

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P24270	Exosome	LVLNK	NPVNYFAEVEQMAFDPSNMPPGIEPSPDK	MLQGR	3		1074.158767	3219.452902	0.001871652	8	N	320	349
P24270	Exosome	HSQKR	NPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDR	GIPDG	4		1007.744685	4026.94754	0.000979378	1	N	170	203
P24270	Exosome	AVKFY	TEDGNWDLVGNNTPIFFIR	DAILF	2		1104.540165	2207.064729	0.000451244	4	N	137	156
P24270	Exosome	TAGSR	GPLLVQDVVF	TDEMA	2		543.8138463	1085.612093	0.002019181	1	N	47	57
P24270	Exosome	GFAVK	FYTEDGNWDLVGNNTPIFF	IRDAI	2		1125.013448	2248.011297	0.002519933	1	N	135	154
P24270	Parental	GFAVK	FYTEDGNWDLVGNNTPIFFIR	DAILF	2		1259.606036	2517.196472	0.000451244	12	N	135	156
P24270	Parental	VMTFK	EAETFPFNPFDLTK	VWPHK	2		828.4017426	1654.787885	0.001463592	1	N	287	301
P24270	Parental	THRHR	LGPNYLQIPVNCPYR	ARVAN	2	C12:+57.021	902.4644543	1802.913309	0.002212458	1	N	365	380
P24369	Exosome	KTVPK	TVDNFVALATGEK	GFGYK	2		682.8569709	1363.698342	0.000451244	6	N	71	84
P24369	Exosome	KVTVK	VYFDLQIGDESVGR	VVFGL	2		799.3969916	1596.778383	0.000451244	7	N	45	59
P24369	Exosome	GTGGK	SIYGERFPDENFK	LKHYG	2		801.3838842	1600.752168	0.000451244	6	N	116	129
P24369	Exosome	ANAGK	DTNGSQFFITTVK	TSWLD	2		729.3677027	1456.719805	0.000451244	7	N	145	158
P24369	Parental	KTVPK	TVDNFVALATGEK	GFGYK	2		682.8569709	1363.698342	0.000622848	2	N	71	84
P24369	Parental	KTVPK	TVDNFVALATGEKGFGYK	NSKFH	2		958.9917875	1915.967975	0.002519933	1	N	71	89
P24369	Parental	GTGGK	SIYGERFPDENFK	LKHYG	2		801.3838842	1600.752168	0.002727428	1	N	116	129
P24369	Parental	TVKVY	FDLQIGDESVGR	VVFGL	2		668.3311202	1334.64664	0.002212458	1	N	47	59
P24527	Exosome	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	2		1204.122384	2406.229169	0.000451244	14	N	288	310
P24527	Exosome	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	3		803.0841897	2406.229169	0.000451244	39	N	288	310
P24527	Exosome	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	4		602.5650922	2406.229169	0.002663018	1	N	288	310
P24527	Exosome	IADLK	DLSSHQLNEFLAQVLQK	APLPL	2		985.5212435	1969.026887	0.000451244	21	N	493	510
P24527	Exosome	IADLK	DLSSHQLNEFLAQVLQK	APLPL	3		657.3500957	1969.026887	0.000451244	31	N	493	510
P24527	Exosome	RFNQR	VPIPCYLIALVVGALESR	QIGPR	2	C5:+57.021	985.5610945	1969.106589	0.000451244	25	N	195	213
P24527	Exosome	RFNQR	VPIPCYLIALVVGALESR	QIGPR	3	C5:+57.021	657.376663	1969.106589	0.000451244	45	N	195	213
P24527	Exosome	DFARR	TLTGTAALTVQSQEENLR	SLTLD	2		966.5057904	1930.995981	0.000451244	73	N	33	51
P24527	Exosome	DFARR	TLTGTAALTVQSQEENLR	SLTLD	3		644.6731269	1930.995981	0.000451244	5	N	33	51
P24527	Exosome	GEKFR	HFHALGGWGELQNTIK	TFGES	2		904.4660742	1806.916548	0.000698008	2	N	339	355
P24527	Exosome	GEKFR	HFHALGGWGELQNTIK	TFGES	3		603.3133161	1806.916548	0.000451244	23	N	339	355
P24527	Exosome	TPSVK	LTYTAEVSVPK	ELVAL	2		604.3326002	1206.6496	0.000451244	31	N	154	165
P24527	Exosome	VPIPC	YLIALVVGALESR	QIGPR	2		702.4169987	1402.818397	0.000451244	13	N	200	213
P24527	Exosome	WVTAK	EEDLSSFSIADLKDLSSHQLNEFLAQVLQK	APLPL	3		1135.579376	3403.714728	0.000451244	10	N	480	510
P24527	Exosome	WVTAK	EEDLSSFSIADLKDLSSHQLNEFLAQVLQK	APLPL	4		851.9364821	3403.714728	0.000451244	12	N	480	510
P24527	Exosome	IPYEK	GFALLFYLEQLLGGPEVFLGFLK	AYVKK	2		1286.217234	2570.418867	0.000451244	12	N	386	409
P24527	Exosome	IPYEK	GFALLFYLEQLLGGPEVFLGFLK	AYVKK	3		857.8140891	2570.418867	0.000451244	3	N	386	409
P24527	Exosome	VVDLK	DVDPDVAYSSIPYEK	GFALL	2		849.3993969	1696.783194	0.000451244	32	N	371	386
P24527	Exosome	AYVKK	FSYQSVTTDDWK	SFLYS	2		738.8362354	1475.656871	0.000451244	15	N	414	426
P24527	Exosome	WVTAK	EEDLSSFSIADLK	DLSSH	2		727.3570007	1452.698401	0.000451244	12	N	480	493
P24527	Exosome	LVTNK	TWDHFWLNEGHTVYLER	HICGR	2		1102.021942	2202.028284	0.001699387	1	N	310	327
P24527	Exosome	LVTNK	TWDHFWLNEGHTVYLER	HICGR	3		735.017228	2202.028284	0.000451244	7	N	310	327
P24527	Exosome	LVTNK	TWDHFWLNEGHTVYLER	HICGR	4		551.514871	2202.028284	0.000622848	24	N	310	327
P24527	Exosome	CIQSK	WEEAIPLALK	MATEQ	2		585.3324032	1168.649206	0.002519933	1	N	547	557
P24527	Exosome	ALSQR	WVTAKEEDLSSFSIADLK	DLSSH	2		1020.020742	2038.025884	0.001264573	1	N	475	493
P24527	Exosome	ALSQR	WVTAKEEDLSSFSIADLK	DLSSH	3		680.3497613	2038.025884	0.000451244	17	N	475	493
P24527	Exosome	HPFTK	LVVDLKDVDPDVAYSSIPYEK	GFALL	2		1183.112828	2364.210056	0.000451244	5	N	365	386
P24527	Exosome	HPFTK	LVVDLKDVDPDVAYSSIPYEK	GFALL	3		789.0778188	2364.210056	0.000451244	20	N	365	386
P24527	Exosome	VDFAR	RTLTGTAALTVQSQEENLR	SLTLD	2		1044.556346	2087.097092	0.001162105	2	N	32	51
P24527	Exosome	VDFAR	RTLTGTAALTVQSQEENLR	SLTLD	3		696.7068307	2087.097092	0.000851441	4	N	32	51
P24527	Exosome	RPLFK	DLAAFDKSHDQAVHTYQEHK	ASMHP	3		780.7054898	2339.093069	0.000451244	6	N	573	593
P24527	Exosome	RPLFK	DLAAFDKSHDQAVHTYQEHK	ASMHP	4		585.7810673	2339.093069	0.000451244	13	N	573	593
P24527	Exosome	QIGPR	TLVWSEKEQVEK	SANEF	2		738.3911779	1474.766756	0.0007646	8	N	218	230
P24527	Exosome	AIHCR	AILPCQDTPSVK	LTYTA	2	C5:+57.021	664.8478602	1327.68012	0.001839721	1	N	142	154
P24527	Exosome	QTSGK	QHPYLFSQCQAIHCR	AILPC	3	[0:-	643.2945921	1926.860376	0.001162105	1	N	127	142
P24527	Exosome	GHIKR	MQEVYNFNAINNSEIR	FRWLR	2		971.4603292	1940.905058	0.000451244	10	N	520	536
P24527	Parental	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	2		1204.122384	2406.229169	0.000451244	8	N	288	310
P24527	Parental	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	3		803.0841897	2406.229169	0.000451244	26	N	288	310
P24527	Parental	LAGDK	SLSNVIAHEISHSWTGNLVTNK	TWDHF	4		602.5650922	2406.229169	0.000451244	6	N	288	310
P24527	Parental	IADLK	DLSSHQLNEFLAQVLQK	APLPL	2		985.5212435	1969.026887	0.000622848	3	N	493	510
P24527	Parental	IADLK	DLSSHQLNEFLAQVLQK	APLPL	3		657.3500957	1969.026887	0.000451244	18	N	493	510
P24527	Parental	RFNQR	VPIPCYLIALVVGALESR	QIGPR	2	C5:+57.021	985.5610945	1969.106589	0.000451244	17	N	195	213
P24527	Parental	RFNQR	VPIPCYLIALVVGALESR	QIGPR	3	C5:+57.021	657.376663	1969.106589	0.000451244	37	N	195	213
P24527	Parental	DFARR	TLTGTAALTVQSQEENLR	SLTLD	2		966.5057904	1930.995981	0.000451244	42	N	33	51
P24527	Parental	DFARR	TLTGTAALTVQSQEENLR	SLTLD	3		644.6731269	1930.995981	0.000451244	1	N	33	51
P24527	Parental	GEKFR	HFHALGGWGELQNTIK	TFGES	2		904.4660742	1806.916548	0.000451244	3	N	339	355
P24527	Parental	GEKFR	HFHALGGWGELQNTIK	TFGES	3		603.3133161	1806.916548	0.001591523	1	N	339	355
P24527	Parental	TPSVK	LTYTAEVSVPK	ELVAL	2		604.3326002	1206.6496	0.000698008	1	N	154	165
P24527	Parental	VPIPC	YLIALVVGALESR	QIGPR	2		702.4169987	1402.818397	0.000451244	7	N	200	213

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P24527	Parental	VPIPC	YLIALVVGALESR	QIGPR	3		468.6139324	1402.818397	0.001329271	1	N	200	213
P24527	Parental	WVTAK	EEDLSSFSIADLKDLSSHQLNEFLAQVLQK	APLPL	3		1135.579376	3403.714728	0.000451244	7	N	480	510
P24527	Parental	IPYEK	GFALLFYLEQLLGGPEVFLGFLK	AYVKK	2		1286.217234	2570.418867	0.000622848	2	N	386	409
P24527	Parental	IPYEK	GFALLFYLEQLLGGPEVFLGFLK	AYVKK	3		857.8140891	2570.418867	0.000451244	1	N	386	409
P24527	Parental	VVDLK	DVDPDVAYSSIPYEK	GFALL	2		849.3993969	1696.783194	0.000451244	8	N	371	386
P24527	Parental	AYVKK	FSYQSVTTDDWK	SFLYS	2		738.8362354	1475.656871	0.000823681	5	N	414	426
P24527	Parental	WVTAK	EEDLSSFSIADLK	DLSSH	2		727.3570007	1452.698401	0.000622848	6	N	480	493
P24527	Parental	LVTNK	TWDHFWLNEGHTVYLER	HICGR	2		1102.021942	2202.028284	0.00307782	1	N	310	327
P24527	Parental	LVTNK	TWDHFWLNEGHTVYLER	HICGR	4		551.514871	2202.028284	0.000622848	4	N	310	327
P24527	Parental	HPFTK	LVVDLKDVDPDVAYSSIPYEK	GFALL	2		1183.112828	2364.210056	0.000451244	4	N	365	386
P24527	Parental	HPFTK	LVVDLKDVDPDVAYSSIPYEK	GFALL	3		789.0778188	2364.210056	0.000451244	11	N	365	386
P24527	Parental	RPLFK	DLAAFDKSHDQAVHTY	QEHKA	2		909.4268117	1816.838023	0.001329271	2	N	573	589
P24527	Parental	RPLFK	DLAAFDKSHDQAVHTY	QEHKA	3		606.6204745	1816.838023	0.002212458	1	N	573	589
P24527	Parental	VDFAR	RTLTGTAALTVQSQEENLR	SLTLD	2		1044.556346	2087.097092	0.000622848	4	N	32	51
P24527	Parental	VDFAR	RTLTGTAALTVQSQEENLR	SLTLD	3		696.7068307	2087.097092	0.000851441	3	N	32	51
P24527	Parental	ETSPK	SSALQWLTPEQTSGKQHPYLFSQCQAIHCR	AILPC	3	C24:+57.021,C29:+57.021	1186.905238	3557.692313	0.000622848	10	N	112	142
P24527	Parental	ETSPK	SSALQWLTPEQTSGKQHPYLFSQCQAIHCR	AILPC	4	C24:+57.021,C29:+57.021	890.4308783	3557.692313	0.00307782	1	N	112	142
P24527	Parental	RPLFK	DLAAFDKSHDQAVHTYQEHK	ASMHP	3		780.7054898	2339.093069	0.001591523	3	N	573	593
P24527	Parental	RKIYR	FNQRVPIPCYLIALVVGALESR	QIGPR	3	C9:+57.021	839.1336731	2514.377619	0.000451244	2	N	191	213
P24527	Parental	QIGPR	TLVWSEKEQVEK	SANEF	2		738.3911779	1474.766756	0.001699387	1	N	218	230
P24527	Parental	AIHCR	AILPCQDTPSVK	LTYTA	2	C5:+57.021	664.8478602	1327.68012	0.001943752	1	N	142	154
P24527	Parental	QTSGK	QHPYLFSQCQAIHCR	AILPC	2	C9:+57.021,C14:+57.021	972.9514881	1943.887376	0.001352548	1	N	127	142
P24527	Parental	QTSGK	QHPYLFSQCQAIHCR	AILPC	4	C9:+57.021,C14:+57.021	486.9796441	1943.887376	0.002727428	1	N	127	142
P24547	Exosome	KFEKR	TSSAQVEGGVHSLHSYEK	RLF-	3		639.3101886	1914.907166	0.000451244	7	N	493	511
P24547	Parental	KFEKR	TSSAQVEGGVHSLHSYEK	RLF-	3		639.3101886	1914.907166	0.0007646	1	N	493	511
P24547	Parental	KFEKR	TSSAQVEGGVHSLHSYEK	RLF-	4		479.7345914	1914.907166	0.000622848	8	N	493	511
P24547	Parental	DGLTY	NDFLILPGYIDFTADQVDLTSALTK	KITLK	3		924.1448919	2769.411276	0.001162105	5	N	32	57
P24547	Parental	AAQAK	NLIDAGVDALR	VGMGS	2		578.8201913	1155.624783	0.000998612	6	N	311	322
P24549	Exosome	ANNTT	YGLAAGLFTK	DLDKA	2		520.7929139	1039.570228	0.000622848	4	N	425	435
P24549	Exosome	VKAAR	QAFQIGSPWR	TMDAS	2		595.3097938	1188.603988	0.002727428	1	N	68	78
P24549	Exosome	MFIWK	IGPALSCGNTVVVKPAEQTPLTALHLASLIK	EAGFP	3	C7:+57.021	1066.935847	3197.78414	0.001763695	1	N	179	210
P24549	Parental	ANNTT	YGLAAGLFTK	DLDKA	2		520.7929139	1039.570228	0.000451244	4	N	425	435
P25206	Exosome	MHQYR	APGEQDGDALPLGSSVDILATDDPDFTQDDQQDTR	IYEKH	3		1234.889555	3701.645265	0.000622848	4	N	508	543
P25206	Exosome	GSHIR	GDINILLIGDPSVAK	SQLLR	2		762.9357526	1523.855905	0.001591523	1	N	336	351
P25206	Parental	MHQYR	APGEQDGDALPLGSSVDILATDDPDFTQDDQQDTR	IYEKH	3		1234.889555	3701.645265	0.000451244	45	N	508	543
P25206	Parental	HVSPR	TLTSCFLSCVVCVEGIVTK	CSLVR	2	C5:+57.021,C9:+57.021,C12:+57.021	1087.038546	2172.061492	0.00091018	2	N	114	133
P25206	Parental	HVSPR	TLTSCFLSCVVCVEGIVTK	CSLVR	3	C5:+57.021,C9:+57.021,C12:+57.021	725.0282973	2172.061492	0.000451244	3	N	114	133
P25206	Parental	PTTGR	GSSGVGLTAAVTTDQETGER	RLEAG	2		968.4668622	1934.918124	0.000622848	4	N	371	391
P25206	Parental	ARMSK	TVDLQDAEEAVELVQYAYFK	KVLEK	2		1166.073703	2330.131806	0.000451244	9	N	635	655
P25206	Parental	ARMSK	TVDLQDAEEAVELVQYAYFK	KVLEK	3		777.718402	2330.131806	0.000451244	17	N	635	655
P25206	Parental	ARMSK	TVDLQDAEEAVELVQYAYFKK	VLEKE	3		820.416723	2458.226769	0.001162105	1	N	635	656
P25206	Parental	ESINR	NREEPFSSEEIQACLSR	MQDDN	2	C14:+57.021	1026.476476	2050.937351	0.000451244	2	N	778	795
P25206	Parental	ESINR	NREEPFSSEEIQACLSR	MQDDN	3	C14:+57.021	684.6535838	2050.937351	0.002663018	1	N	778	795
P25206	Parental	REAQR	DYLDFLDDEEDQGIYQNK	VRELI	2		1110.484918	2218.954235	0.000451244	18	N	17	35
P25206	Parental	KRANR	LLNNAFEELVAFQR	ALKDF	2		832.4442761	1662.872952	0.000451244	4	N	64	78
P25444	Exosome	SLPIK	ESEIIDFFLGASLKDEVLK	IMPVQ	3		718.3845831	2152.130349	0.000451244	4	N	89	108
P25444	Exosome	YTSAR	GCTATLGNFAK	ATFDA	2	C2:+57.021	570.2796134	1138.543627	0.001763695	2	N	227	238
P25444	Parental	TVFTK	SPYQEFTDHLVK	THTRV	3		488.5775469	1462.709241	0.000451244	11	N	263	275
P25444	Parental	SLPIK	ESEIIDFFLGASL	KDEVL	2		720.8670043	1439.718409	0.000622848	2	N	89	102
P25911	Exosome	CWKEK	AEERPTFDYLQSVLDDFYTATEGQYQQQP	-	3		1147.192069	3438.552808	0.000451244	10	N	483	512
P25911	Exosome	LPGQR	FQTKDPEEQGDIVVALYPYDGIHPDDLSFK	KGEKM	3		1146.224822	3435.651065	0.000451244	9	N	55	85
P25911	Exosome	LPGQR	FQTKDPEEQGDIVVALYPYDGIHPDDLSFK	KGEKM	4		859.9205664	3435.651065	0.000451244	31	N	55	85
P25911	Exosome	RFQTK	DPEEQGDIVVALYPYDGIHPDDLSFK	KGEKM	3		978.134944	2931.381432	0.000451244	24	N	59	85
P25911	Exosome	KFPIK	WTAPEAINFGCFTIK	SDVWS	2	C11:+57.021	877.9324557	1753.849311	0.000451244	10	N	408	423
P25911	Exosome	NYVAK	VNTLETEEWFFK	DITRK	2		771.8779033	1541.740207	0.000451244	8	N	120	132
P25911	Exosome	KDAER	QLLAPGNSAGAFLIR	ESETL	2		764.4362541	1526.856908	0.000451244	10	N	141	156
P25911	Exosome	KDAER	QLLAPGNSAGAFLIR	ESETL	3		509.9601027	1526.856908	0.001395409	1	N	141	156
P25911	Exosome	KDAER	QLLAPGNSAGAFLIR	ESETL	2	[0:-17.027	755.9227541	1509.829908	0.002453667	1	N	141	156
P25911	Exosome	KMCWK	EKAEERPTFDYLQSVLDDFYTATEGQYQQQP	-	3		1232.904588	3695.690364	0.000823681	1	N	481	512
P25911	Exosome	NYVAK	VNTLETEEWFFKDITR	KDAER	3		676.6744678	2027.000004	0.000622848	9	N	120	136
P25911	Exosome	NYVAK	VNTLETEEWFF	KDITR	2		707.8304217	1413.645243	0.001162105	3	N	120	131
P25911	Exosome	PGQRF	QTKDPEEQGDIVVALYPYDGIHPDDLSFK	KGEKM	3	Q1:-17.027	1091.52635	3271.555651	0.000451244	1	N	56	85
P25911	Exosome	PGQRF	QTKDPEEQGDIVVALYPYDGIHPDDLSFK	KGEKM	3	[0:-17.027	1091.52635	3271.555651	0.000735798	2	N	56	85

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P25911	Exosome	REGAK	FPIKWTAPEAINFGCFTIK	SDVWS	3	C15:+57.021	747.3909722	2239.149516	0.002453667	1	N	404	423
P25911	Exosome	RRLEK	ACISPKPQKPWDKDAWEIPR	ESIKL	3	C2:+57.021	808.0830898	2421.225869	0.001162105	4	N	224	244
P25911	Parental	CWKEK	AEERPTFDYLQSVLDDFYTATEGQYQQQP	-	3		1147.192069	3438.552808	0.000451244	29	N	483	512
P25911	Parental	KFPIK	WTAPEAINFGCFTIK	SDVWS	2	C11:+57.021	877.9324557	1753.849311	0.000451244	3	N	408	423
P25911	Parental	NYVAK	VNTLETEEWFFK	DITRK	2		771.8779033	1541.740207	0.002145581	1	N	120	132
P25911	Parental	KDAER	QLLAPGNSAGAFLIR	ESETL	2		764.4362541	1526.856908	0.001591523	1	N	141	156
P25911	Parental	KMCWK	EKAEERPTFDYLQSVLDDFYTATEGQYQQQP	-	3		1232.904588	3695.690364	0.000451244	6	N	481	512
P26039	Exosome	SDYGR	LASQAKPAAVAAENEEIGAHIK	HRVQE	3		740.0662475	2217.175342	0.000451244	36	N	1895	1917
P26039	Exosome	SDYGR	LASQAKPAAVAAENEEIGAHIK	HRVQE	4		555.3016356	2217.175342	0.000451244	16	N	1895	1917
P26039	Exosome	ASAPK	ASAGPQPLLVQSCK	AVAEQ	2	C13:+57.021	728.3851412	1454.754682	0.000451244	37	N	943	957
P26039	Exosome	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2		983.0115743	1964.007549	0.000451244	5	N	922	943
P26039	Exosome	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	3		655.6769828	1964.007549	0.000451244	7	N	922	943
P26039	Exosome	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2	Q1:-17.027	974.4980743	1946.980549	0.000451244	9	N	922	943
P26039	Exosome	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2	[0:-17.027	974.4980743	1946.980549	0.002519933	1	N	922	943
P26039	Exosome	KAAQK	AAAFEDQENETVVVK	EKMVG	2		825.4050136	1648.794427	0.000451244	44	N	2476	2491
P26039	Exosome	ISSAK	QVAASTAQLLVACK	VKADQ	2	C13:+57.021	730.4007913	1458.785983	0.000451244	32	N	2429	2443
P26039	Exosome	ISSAK	QVAASTAQLLVACK	VKADQ	2	[0:-17.027,C13:+57.021	721.8872913	1441.758983	0.001943752	1	N	2429	2443
P26039	Exosome	RLVAK	AVEGCVSASQAATEDGQLLR	GVGAA	2	C5:+57.021	1031.497408	2060.979216	0.000451244	64	N	745	765
P26039	Exosome	SAIAK	LLGEIAQGNENYAGIAAR	DVAGG	2		930.484661	1858.953722	0.000451244	5	N	1104	1122
P26039	Exosome	SQNAK	NGNLPEFGDAIATASK	ALCGF	2		802.8998984	1603.784197	0.000451244	14	N	1415	1431
P26039	Exosome	VACTK	VVAPTISSPVCQEQLVEAGR	LVAKA	2	C11:+57.021	1070.557269	2139.098938	0.000451244	47	N	721	741
P26039	Exosome	TKGTR	ALEATTEHIRQELAVFCSPEPPAK	TSTPE	3	C17:+57.021	898.7904118	2693.347835	0.000451244	19	N	2144	2168
P26039	Exosome	SRGVK	LLAALLEDEGGNGRPLLQAAK	GLAGA	2		1075.102932	2148.190264	0.000451244	30	N	592	613
P26039	Exosome	SRGVK	LLAALLEDEGGNGRPLLQAAK	GLAGA	3		717.0712214	2148.190264	0.000451244	21	N	592	613
P26039	Exosome	VQSCK	AVAEQIPLLVQGVR	GSQAQ	2		746.9464546	1491.877309	0.000451244	28	N	957	971
P26039	Exosome	VQSCK	AVAEQIPLLVQGVR	GSQAQ	3		498.3002364	1491.877309	0.000451244	4	N	957	971
P26039	Exosome	ITSMR	DKAPGQLECETAIAALNSCLR	DLDQA	2	C9:+57.021,C19:+57.021	1159.067443	2316.119287	0.000451244	27	N	1652	1673
P26039	Exosome	ITSMR	DKAPGQLECETAIAALNSCLR	DLDQA	3	C9:+57.021,C19:+57.021	773.0475623	2316.119287	0.000451244	32	N	1652	1673
P26039	Exosome	LQAAK	GLAGAVSELLR	SAQPA	2		543.3198272	1084.624054	0.000451244	14	N	613	624
P26039	Exosome	EMVTK	SNTSPEELGPLANQLTSDYGR	LASQA	2		1125.038183	2248.060766	0.000451244	25	N	1874	1895
P26039	Exosome	EAQSR	LNEAAAGLNQAATELVQASR	GTPQD	2		1014.029964	2026.044328	0.000451244	38	N	1241	1261
P26039	Exosome	EAQSR	LNEAAAGLNQAATELVQASR	GTPQD	3		676.3559094	2026.044328	0.000451244	25	N	1241	1261
P26039	Exosome	ADVVK	LGAASLGAEDPETQVVLINAVK	DVAKA	2		1098.100055	2194.18451	0.000451244	38	N	2063	2085
P26039	Exosome	ADVVK	LGAASLGAEDPETQVVLINAVK	DVAKA	3		732.4026367	2194.18451	0.000451244	8	N	2063	2085
P26039	Exosome	NSCLR	DLDQASLAAVSQQLAPR	EGISQ	2		891.9713864	1781.927173	0.000451244	31	N	1673	1690
P26039	Exosome	NSCLR	DLDQASLAAVSQQLAPR	EGISQ	3		594.9835243	1781.927173	0.000451244	31	N	1673	1690
P26039	Exosome	VAQGK	VGAIPANALDDGQWSQGLISAAR	MVAAA	2		1155.596003	2309.176405	0.000451244	39	N	2375	2398
P26039	Exosome	VAQGK	VGAIPANALDDGQWSQGLISAAR	MVAAA	3		770.7332683	2309.176405	0.000451244	35	N	2375	2398
P26039	Exosome	ADVVK	LGAASLGAEDPETQVVLINAVKDVAK	ALGDL	3		870.1451147	2607.411944	0.000622848	7	N	2063	2089
P26039	Exosome	VRQAR	ILAQATSDLVNAIKADAEGESDLENSR	KLLSA	2		1415.707404	2829.399207	0.000451244	1	N	827	854
P26039	Exosome	VRQAR	ILAQATSDLVNAIKADAEGESDLENSR	KLLSA	3		944.1408692	2829.399207	0.000451244	37	N	827	854
P26039	Exosome	EQKHK	AGFLDLKDFLPK	EYVKQ	2		682.3851672	1362.754734	0.000451244	18	N	256	268
P26039	Exosome	EQKHK	AGFLDLKDFLPK	EYVKQ	3		455.2593781	1362.754734	0.000451244	46	N	256	268
P26039	Exosome	VLKAK	SVAQRTEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	3	C22:+57.021,C32:+57.021	1198.601661	3592.781582	0.000451244	2	N	687	721
P26039	Exosome	LDQTK	TLAESALQLLYTAK	EAGGN	2		761.4303031	1520.845006	0.000451244	8	N	1766	1780
P26039	Exosome	LDQTK	TLAESALQLLYTAK	EAGGN	3		507.9561354	1520.845006	0.000451244	9	N	1766	1780
P26039	Exosome	VQGVR	GSQAQPDSPSAQLALIAASQSFLQPGGK	MVAAA	2		1377.70701	2753.398419	0.000451244	14	N	971	999
P26039	Exosome	VQGVR	GSQAQPDSPSAQLALIAASQSFLQPGGK	MVAAA	3		918.8072732	2753.398419	0.000451244	14	N	971	999
P26039	Exosome	SVAQR	TEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	3	C17:+57.021,C27:+57.021	1018.169246	3051.484337	0.000451244	42	N	692	721
P26039	Exosome	SVAQR	TEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	4	C17:+57.021,C27:+57.021	763.8788842	3051.484337	0.000451244	31	N	692	721
P26039	Exosome	ATASK	ALCGFTEAAAQAAYLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	3	C3:+57.021	1308.306167	3921.895101	0.000451244	51	N	1431	1469
P26039	Exosome	ATASK	ALCGFTEAAAQAAYLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	4	C3:+57.021	981.4815752	3921.895101	0.000451244	39	N	1431	1469
P26039	Exosome	LHYGR	ECANGYLELLDHVLLTLQKPNPDLK	QQLTG	3	C2:+57.021	965.1761548	2892.505065	0.000451244	12	N	2241	2266
P26039	Exosome	LHYGR	ECANGYLELLDHVLLTLQKPNPDLK	QQLTG	4	C2:+57.021	724.1340661	2892.505065	0.000451244	18	N	2241	2266
P26039	Exosome	GQLLR	GVGAAATAVTQALNELLQHVK	AHATG	2		1046.082	2090.148399	0.000451244	32	N	765	786
P26039	Exosome	GQLLR	GVGAAATAVTQALNELLQHVK	AHATG	3		697.7239331	2090.148399	0.000451244	36	N	765	786
P26039	Exosome	RAQCR	AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR	AAMEP	3		1152.914759	3455.720876	0.000451244	55	N	1559	1593
P26039	Exosome	RAQCR	AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR	AAMEP	4		864.9380191	3455.720876	0.000451244	26	N	1559	1593
P26039	Exosome	QLAPR	EGISQEALHTQMLTAVQEISHLIEPLASAAR	AEASQ	4		836.6888472	3342.724189	0.000451244	4	N	1690	1721
P26039	Exosome	QLAPR	EGISQEALHTQMLTAVQEISHLIEPLASAAR	AEASQ	4	M12:+15.995	840.6875972	3358.719189	0.001329271	1	N	1690	1721
P26039	Exosome	AEAMK	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1017.843941	3050.508424	0.000451244	37	N	2291	2321
P26039	Exosome	AQAAR	GVAALTSDPAVQAIVLDTASDVLDKASSLIEEAK	KASGH	3		1133.27032	3396.787559	0.000451244	17	N	1136	1170
P26039	Exosome	LRACK	EAAFHPEVAPDVR	LRALH	2		719.360212	1436.704824	0.000451244	8	N	2220	2233
P26039	Exosome	LRACK	EAAFHPEVAPDVR	LRALH	3		479.909408	1436.704824	0.000451244	14	N	2220	2233
P26039	Exosome	VAAAK	ASVPTIQDQASAMQLSQCAK	NLGTA	2	M13:+15.995,C18:+57.021	1075.514787	2149.013974	0.000451244	21	N	1005	1025

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26039	Exosome	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	3		1388.694245	4163.059336	0.000451244	23	N	634	673
P26039	Exosome	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	4		1041.772634	4163.059336	0.000451244	4	N	634	673
P26039	Exosome	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	3	M35:+15.995	1394.025912	4179.054336	0.002519933	1	N	634	673
P26039	Exosome	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	4	M35:+15.995	1045.771384	4179.054336	0.000451244	17	N	634	673
P26039	Exosome	GSQEK	LAQAAQSSVATITR	LADVV	2		708.894419	1415.773238	0.000451244	40	N	2043	2057
P26039	Exosome	ALVTK	AGALQCSPSDVYTK	KELIE	2	C6:+57.021	748.8564136	1495.697227	0.000451244	26	N	1933	1947
P26039	Exosome	MQLAK	AVASAAAALVLK	AKSVA	2		542.8403955	1083.665191	0.000823681	1	N	673	685
P26039	Exosome	RAKPK	EADESLNFEEQILEAAK	SIAAA	2		968.4632569	1934.910914	0.000451244	28	N	2333	2350
P26039	Exosome	YVQAR	DDILNGSHPVSFDK	ACEFA	2		772.3735164	1542.731433	0.000451244	28	N	220	234
P26039	Exosome	TEHIR	QELAVFCSPEPPAK	TSTPE	2	C7:+57.021	786.8902564	1571.764913	0.000451244	28	N	2154	2168
P26039	Exosome	VRQAR	ILAQATSDLVNAIK	ADAEG	2		728.9226452	1455.82969	0.000451244	29	N	827	841
P26039	Exosome	SMRDK	APGQLECETAIAALNSCLR	DLDQA	2	C7:+57.021,C17:+57.021	1037.50649	2072.997381	0.000451244	16	N	1654	1673
P26039	Exosome	MIRER	IPEALAGPPNDFGLFLSDDDPKK	GIWLE	3		819.4168344	2455.227103	0.000451244	38	N	35	58
P26039	Exosome	CRMIR	ERIPEALAGPPNDFGLFLSDDDPK	KGIWL	3		871.7664149	2612.275845	0.000451244	10	N	33	57
P26039	Exosome	AQAAR	GVAALTSDPAVQAIVLDTASDVLDK	ASSLI	2		1235.158298	2468.300997	0.000451244	8	N	1136	1161
P26039	Exosome	AQAAR	GVAALTSDPAVQAIVLDTASDVLDK	ASSLI	3		823.7747989	2468.300997	0.000451244	22	N	1136	1161
P26039	Exosome	AAEAM	KGTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1060.542262	3178.603387	0.000451244	12	N	2290	2321
P26039	Exosome	HIKHR	VQELGHGCSALVTK	AGALQ	2	C8:+57.021	749.8880481	1497.760496	0.001699387	1	N	1919	1933
P26039	Exosome	ASQAK	PAAVAAENEEIGAHIK	HRVQE	3		540.6182938	1618.831481	0.000451244	8	N	1901	1917
P26039	Exosome	SQCAK	NLGTALAELR	TAAQK	2		529.3041771	1056.592754	0.001162105	5	N	1025	1035
P26039	Exosome	VSFDK	ACEFAGFQCQIQFGPHNEQK	HKAGF	2	C2:+57.021,C9:+57.021	1198.531028	2395.046456	0.000451244	26	N	234	254
P26039	Exosome	VSFDK	ACEFAGFQCQIQFGPHNEQK	HKAGF	3	C2:+57.021,C9:+57.021	799.3566187	2395.046456	0.000451244	36	N	234	254
P26039	Exosome	LLRRK	FFYSDQNVDSRDPVQLNLLYVQAR	DDILN	3		963.1511513	2886.430054	0.000451244	35	N	196	220
P26039	Exosome	LLAAK	ALSTDPASPNLK	SQLAA	2		607.3253065	1212.635013	0.000451244	3	N	1320	1332
P26039	Exosome	NVDSR	DPVQLNLLYVQAR	DDILN	2		764.9282619	1527.840924	0.000451244	11	N	207	220
P26039	Exosome	ARSLK	TYGVSFFLVK	EKMKG	2		580.8216714	1159.627743	0.000451244	16	N	306	316
P26039	Exosome	TICAR	IGITNHDEYSLVR	ELMEE	2		758.8918764	1515.768153	0.000451244	4	N	118	131
P26039	Exosome	GPAGR	YDQATDTILTVTENIF	SSMGD	2		922.4521608	1842.888722	0.000451244	1	N	797	813
P26039	Exosome	DEKTK	EVIQEWSLTNIKR	WAASP	2		808.4442761	1614.872952	0.001763695	1	N	345	358
P26039	Exosome	QAGNR	GTQACITAASAVSGIIADLDTTIMFATAGTLNR	EGAET	3	C5:+57.021,M24:+15.995	1109.890554	3326.648263	0.000622848	2	N	1973	2006
P26039	Exosome	LDHGR	TLREQGVEEHETLLLR	RKFFY	3		641.6818453	1922.022136	0.000622848	3	N	178	194
P26039	Exosome	LDHGR	TLREQGVEEHETLLLR	RKFFY	4		481.513334	1922.022136	0.000823681	4	N	178	194
P26039	Exosome	ISAAR	MVAAATNNLCEAANAAVQGHASQEK	LISSA	3	C10:+57.021	852.7362015	2555.185205	0.000451244	7	N	2398	2423
P26039	Exosome	ISAAR	MVAAATNNLCEAANAAVQGHASQEK	LISSA	3	M1:+15.995,C10:+57.021	858.0678682	2571.180205	0.000451244	8	N	2398	2423
P26039	Exosome	LLRRK	FFYSDQNVDSRDPVQL	NLLYV	2		965.4530265	1928.890453	0.000637154	2	N	196	212
P26039	Exosome	MIRER	IPEALAGPPNDFGLFLSDDDPK	KGIWL	2		1164.57387	2327.13214	0.000451244	10	N	35	57
P26039	Exosome	MIRER	IPEALAGPPNDFGLFLSDDDPK	KGIWL	3		776.7185134	2327.13214	0.001162105	1	N	35	57
P26039	Exosome	QLGHK	VSQMAQYFEPLTLAAVGAASK	TLSHP	2		1091.564794	2181.113989	0.000823681	2	N	1730	1751
P26039	Exosome	QLGHK	VSQMAQYFEPLTLAAVGAASK	TLSHP	2	M4:+15.995	1099.562294	2197.108989	0.001591523	2	N	1730	1751
P26039	Exosome	TQFAR	ANQAIQMACQSLGEPGCTQAQVLSAATIVAK	HTSAL	3	C9:+57.021,C17:+57.021	1072.865392	3215.572776	0.002145581	1	N	1469	1500
P26039	Exosome	AAAAR	AVTDSINQLITMCTQQAPGQKECDNALR	QLETV	3	C13:+57.021,C23:+57.021	1054.837613	3161.48944	0.000735798	1	N	1340	1368
P26039	Exosome	AAAAR	AVTDSINQLITMCTQQAPGQKECDNALR	QLETV	3	M12:+15.995,C13:+57.021,C23:+57.021	1060.16928	3177.48444	0.000451244	5	N	1340	1368
P26039	Exosome	TAAQK	AQEACGPLEMDSALSVVQNLEKDLQEIK	AAARD	3	C5:+57.021	1039.181417	3114.520852	0.000451244	4	N	1040	1068
P26039	Exosome	PAIMR	SGASGPENFQVGSMPPAQQQITSGQMHR	GHMPP	3	M14:+15.995,M26:+15.995	987.1194742	2958.335023	0.000622848	1	N	454	482
P26039	Exosome	YYSVQ	TTEGEQIAQLIAGYIDIILK	KKKSK	2		1095.107349	2188.199098	0.001654178	1	N	381	401
P26039	Exosome	AAQAA	YLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	2		1331.16752	2660.319441	0.000622848	1	N	1444	1469
P26039	Exosome	GTLNR	EGAETFADHREGILK	TAKVL	3		558.2816817	1671.821645	0.0007646	1	N	2006	2021
P26039	Exosome	RKFFY	SDQNVDSRDPVQLNLLYVQAR	DDILN	3		810.7510991	2429.229897	0.00307782	1	N	199	220
P26039	Exosome	RAQCR	AATAPLLEAVDNLSAF	ASNPE	2		801.9228422	1601.830084	0.000622848	1	N	1559	1575
P26039	Exosome	CANGY	LELLDHVLLTLQKPNPDLK	QQLTG	3		733.7636173	2198.267452	0.000451244	1	N	2247	2266
P26039	Exosome	AQAAY	LVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	2		1249.635856	2497.256112	0.000998612	1	N	1445	1469
P26039	Parental	KAAQK	AAAFEDQENETVVVKEK	MVGGI	2		953.9737918	1905.931984	0.000451244	17	N	2476	2493
P26039	Parental	KAAQK	AAAFEDQENETVVVKEK	MVGGI	3		636.3184612	1905.931984	0.000637154	7	N	2476	2493
P26039	Parental	SDYGR	LASQAKPAAVAAENEEIGAHIK	HRVQE	2		1109.595471	2217.175342	0.000451244	7	N	1895	1917
P26039	Parental	SDYGR	LASQAKPAAVAAENEEIGAHIK	HRVQE	3		740.0662475	2217.175342	0.000451244	38	N	1895	1917
P26039	Parental	SDYGR	LASQAKPAAVAAENEEIGAHIK	HRVQE	4		555.3016356	2217.175342	0.000451244	13	N	1895	1917
P26039	Parental	ASAPK	ASAGPQPLLVQSCK	AVAEQ	2	C13:+57.021	728.3851412	1454.754682	0.000451244	43	N	943	957
P26039	Parental	MATAK	AVAAGNSCRQEDVIATANLSR	RAIAD	2	C8:+57.021	1102.048131	2202.080662	0.000823681	9	N	2188	2209
P26039	Parental	MATAK	AVAAGNSCRQEDVIATANLSR	RAIAD	3	C8:+57.021	735.0346872	2202.080662	0.000451244	7	N	2188	2209
P26039	Parental	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2		983.0115743	1964.007549	0.000451244	26	N	922	943
P26039	Parental	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	3		655.6769828	1964.007549	0.000451244	22	N	922	943
P26039	Parental	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2	Q1:-17.027	974.4980743	1946.980549	0.000451244	17	N	922	943
P26039	Parental	EHAAK	QAAASATQTIAAAQHAASAPK	ASAGP	2	[0:-17.027	974.4980743	1946.980549	0.002080925	10	N	922	943
P26039	Parental	KAAQK	AAAFEDQENETVVVK	EKMVG	2		825.4050136	1648.794427	0.000451244	30	N	2476	2491

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26039	Parental	ISSAK	QVAASTAQLLVACK	VKADQ	2	C13:+57.021	730.4007913	1458.785983	0.000451244	36	N	2429	2443
P26039	Parental	RLVAK	AVEGCVSASQAATEDGQLLR	GVGAA	2	C5:+57.021	1031.497408	2060.979216	0.000451244	38	N	745	765
P26039	Parental	SAIAK	LLGEIAQGNENYAGIAAR	DVAGG	2		930.484661	1858.953722	0.000451244	12	N	1104	1122
P26039	Parental	SQNAK	NGNLPEFGDAIATASK	ALCGF	2		802.8998984	1603.784197	0.000451244	14	N	1415	1431
P26039	Parental	VACTK	VVAPTISSPVCQEQLVEAGR	LVAKA	2	C11:+57.021	1070.557269	2139.098938	0.000451244	51	N	721	741
P26039	Parental	QLKPR	AKPKEADESLNFEEQILEAAK	SIAAA	2		1180.603159	2359.190718	0.000451244	9	N	2329	2350
P26039	Parental	QLKPR	AKPKEADESLNFEEQILEAAK	SIAAA	3		787.4047059	2359.190718	0.000451244	3	N	2329	2350
P26039	Parental	TKGTR	ALEATTEHIRQELAVFCSPEPPAK	TSTPE	2	C17:+57.021	1347.681718	2693.347835	0.000451244	7	N	2144	2168
P26039	Parental	TKGTR	ALEATTEHIRQELAVFCSPEPPAK	TSTPE	3	C17:+57.021	898.7904118	2693.347835	0.000451244	16	N	2144	2168
P26039	Parental	SRGVK	LLAALLEDEGGNGRPLLQAAK	GLAGA	2		1075.102932	2148.190264	0.000451244	21	N	592	613
P26039	Parental	SRGVK	LLAALLEDEGGNGRPLLQAAK	GLAGA	3		717.0712214	2148.190264	0.000451244	10	N	592	613
P26039	Parental	VQSCK	AVAEQIPLLVQGVR	GSQAQ	2		746.9464546	1491.877309	0.000451244	47	N	957	971
P26039	Parental	VQSCK	AVAEQIPLLVQGVR	GSQAQ	3		498.3002364	1491.877309	0.000451244	18	N	957	971
P26039	Parental	ITSMR	DKAPGQLECETAIAALNSCLR	DLDQA	2	C9:+57.021,C19:+57.021	1159.067443	2316.119287	0.000451244	36	N	1652	1673
P26039	Parental	ITSMR	DKAPGQLECETAIAALNSCLR	DLDQA	3	C9:+57.021,C19:+57.021	773.0475623	2316.119287	0.000451244	45	N	1652	1673
P26039	Parental	LQAAK	GLAGAVSELLR	SAQPA	2		543.3198272	1084.624054	0.000451244	31	N	613	624
P26039	Parental	EMVTK	SNTSPEELGPLANQLTSDYGR	LASQA	2		1125.038183	2248.060766	0.000451244	10	N	1874	1895
P26039	Parental	EMVTK	SNTSPEELGPLANQLTSDYGR	LASQA	3		750.3613887	2248.060766	0.001463592	1	N	1874	1895
P26039	Parental	EAQSR	LNEAAAGLNQAATELVQASR	GTPQD	2		1014.029964	2026.044328	0.000451244	57	N	1241	1261
P26039	Parental	EAQSR	LNEAAAGLNQAATELVQASR	GTPQD	3		676.3559094	2026.044328	0.000451244	8	N	1241	1261
P26039	Parental	ADVVK	LGAASLGAEDPETQVVLINAVK	DVAKA	2		1098.100055	2194.18451	0.000451244	51	N	2063	2085
P26039	Parental	ADVVK	LGAASLGAEDPETQVVLINAVK	DVAKA	3		732.4026367	2194.18451	0.000662267	3	N	2063	2085
P26039	Parental	NSCLR	DLDQASLAAVSQQLAPR	EGISQ	2		891.9713864	1781.927173	0.000451244	32	N	1673	1690
P26039	Parental	NSCLR	DLDQASLAAVSQQLAPR	EGISQ	3		594.9835243	1781.927173	0.000451244	24	N	1673	1690
P26039	Parental	VAQGK	VGAIPANALDDGQWSQGLISAAR	MVAAA	2		1155.596003	2309.176405	0.000451244	41	N	2375	2398
P26039	Parental	VAQGK	VGAIPANALDDGQWSQGLISAAR	MVAAA	3		770.7332683	2309.176405	0.000451244	36	N	2375	2398
P26039	Parental	ADVVK	LGAASLGAEDPETQVVLINAVKDVAK	ALGDL	2		1304.713772	2607.411944	0.000451244	10	N	2063	2089
P26039	Parental	ADVVK	LGAASLGAEDPETQVVLINAVKDVAK	ALGDL	3		870.1451147	2607.411944	0.000451244	10	N	2063	2089
P26039	Parental	VRQAR	ILAQATSDLVNAIKADAEGESDLENSR	KLLSA	2		1415.707404	2829.399207	0.000451244	3	N	827	854
P26039	Parental	VRQAR	ILAQATSDLVNAIKADAEGESDLENSR	KLLSA	3		944.1408692	2829.399207	0.000451244	42	N	827	854
P26039	Parental	EQKHK	AGFLDLKDFLPK	EYVKQ	2		682.3851672	1362.754734	0.001162105	6	N	256	268
P26039	Parental	EQKHK	AGFLDLKDFLPK	EYVKQ	3		455.2593781	1362.754734	0.000451244	53	N	256	268
P26039	Parental	VLKAK	SVAQRTEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	3	C22:+57.021,C32:+57.021	1198.601661	3592.781582	0.000451244	13	N	687	721
P26039	Parental	VLKAK	SVAQRTEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	4	C22:+57.021,C32:+57.021	899.2031955	3592.781582	0.000451244	7	N	687	721
P26039	Parental	LDQTK	TLAESALQLLYTAK	EAGGN	2		761.4303031	1520.845006	0.000451244	33	N	1766	1780
P26039	Parental	LDQTK	TLAESALQLLYTAK	EAGGN	3		507.9561354	1520.845006	0.000451244	22	N	1766	1780
P26039	Parental	VQGVR	GSQAQPDSPSAQLALIAASQSFLQPGGK	MVAAA	2		1377.70701	2753.398419	0.000451244	28	N	971	999
P26039	Parental	VQGVR	GSQAQPDSPSAQLALIAASQSFLQPGGK	MVAAA	3		918.8072732	2753.398419	0.000451244	8	N	971	999
P26039	Parental	SVAQR	TEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	3	C17:+57.021,C27:+57.021	1018.169246	3051.484337	0.000451244	33	N	692	721
P26039	Parental	SVAQR	TEDSGLQTQVIAAATQCALSTSQLVACTK	VVAPT	4	C17:+57.021,C27:+57.021	763.8788842	3051.484337	0.000451244	20	N	692	721
P26039	Parental	ATASK	ALCGFTEAAAQAAYLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	3	C3:+57.021	1308.306167	3921.895101	0.000451244	69	N	1431	1469
P26039	Parental	ATASK	ALCGFTEAAAQAAYLVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	4	C3:+57.021	981.4815752	3921.895101	0.000451244	50	N	1431	1469
P26039	Parental	LHYGR	ECANGYLELLDHVLLTLQKPNPDLK	QQLTG	3	C2:+57.021	965.1761548	2892.505065	0.000451244	13	N	2241	2266
P26039	Parental	LHYGR	ECANGYLELLDHVLLTLQKPNPDLK	QQLTG	4	C2:+57.021	724.1340661	2892.505065	0.000451244	50	N	2241	2266
P26039	Parental	LHYGR	ECANGYLELLDHVLLTLQKPNPDLK	QQLTG	4	[0:-18.011,C2:+57.021	719.6313161	2874.494065	0.000870037	2	N	2241	2266
P26039	Parental	GQLLR	GVGAAATAVTQALNELLQHVK	AHATG	2		1046.082	2090.148399	0.000451244	22	N	765	786
P26039	Parental	GQLLR	GVGAAATAVTQALNELLQHVK	AHATG	3		697.7239331	2090.148399	0.000451244	34	N	765	786
P26039	Parental	RAQCR	AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR	AAMEP	3		1152.914759	3455.720876	0.000451244	78	N	1559	1593
P26039	Parental	RAQCR	AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR	AAMEP	4		864.9380191	3455.720876	0.000451244	26	N	1559	1593
P26039	Parental	QLAPR	EGISQEALHTQMLTAVQEISHLIEPLASAAR	AEASQ	3		1115.249196	3342.724189	0.000451244	8	N	1690	1721
P26039	Parental	QLAPR	EGISQEALHTQMLTAVQEISHLIEPLASAAR	AEASQ	4		836.6888472	3342.724189	0.000451244	7	N	1690	1721
P26039	Parental	AEAMK	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1017.843941	3050.508424	0.000451244	86	N	2291	2321
P26039	Parental	AQAAR	GVAALTSDPAVQAIVLDTASDVLDKASSLIEEAK	KASGH	3		1133.27032	3396.787559	0.000451244	21	N	1136	1170
P26039	Parental	AQAAR	GVAALTSDPAVQAIVLDTASDVLDKASSLIEEAK	KASGH	4		850.2046898	3396.787559	0.000451244	1	N	1136	1170
P26039	Parental	VKTIK	ALDGDFTEENRAQCR	AATAP	3	C14:+57.021	594.6009313	1780.779394	0.00091018	1	N	1544	1559
P26039	Parental	LRACK	EAAFHPEVAPDVR	LRALH	2		719.360212	1436.704824	0.000451244	6	N	2220	2233
P26039	Parental	LRACK	EAAFHPEVAPDVR	LRALH	3		479.909408	1436.704824	0.000451244	20	N	2220	2233
P26039	Parental	VAAAK	ASVPTIQDQASAMQLSQCAK	NLGTA	2	C18:+57.021	1067.517287	2133.018974	0.000451244	7	N	1005	1025
P26039	Parental	VAAAK	ASVPTIQDQASAMQLSQCAK	NLGTA	2	M13:+15.995,C18:+57.021	1075.514787	2149.013974	0.000622848	2	N	1005	1025
P26039	Parental	VEDTK	VLVQNAAGSQEKLAQAAQSSVATITR	LADVV	3		881.1476297	2640.419489	0.000451244	6	N	2031	2057
P26039	Parental	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	3		1388.694245	4163.059336	0.000451244	13	N	634	673
P26039	Parental	SAEPR	QNLLQAAGNVGQASGELLQQIGESDTDPHFQDVLMQLAK	AVASA	4		1041.772634	4163.059336	0.000451244	2	N	634	673
P26039	Parental	GSQEK	LAQAAQSSVATITR	LADVV	2		708.894419	1415.773238	0.000451244	50	N	2043	2057
P26039	Parental	ALVTK	AGALQCSPSDVYTK	KELIE	2	C6:+57.021	748.8564136	1495.697227	0.000451244	52	N	1933	1947
P26039	Parental	GNSCR	QEDVIATANLSR	RAIAD	2		658.8443948	1315.67319	0.000451244	19	N	2197	2209

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26039	Parental	LLAAK	ALSTDPASPNLKSQLAAAAR	AVTDS	2		991.5374249	1981.05925	0.000451244	6	N	1320	1340
P26039	Parental	KLKQK	LHTDDELNWLDHGR	TLREQ	2		860.9060464	1719.796493	0.000451244	10	N	164	178
P26039	Parental	KLKQK	LHTDDELNWLDHGR	TLREQ	3		574.2732976	1719.796493	0.000451244	22	N	164	178
P26039	Parental	KLKQK	LHTDDELNWLDHGR	TLREQ	4		430.9569232	1719.796493	0.000622848	3	N	164	178
P26039	Parental	MQLAK	AVASAAAALVLK	AKSVA	2		542.8403955	1083.665191	0.000823681	19	N	673	685
P26039	Parental	RAKPK	EADESLNFEEQILEAAK	SIAAA	2		968.4632569	1934.910914	0.000451244	25	N	2333	2350
P26039	Parental	YVQAR	DDILNGSHPVSFDK	ACEFA	2		772.3735164	1542.731433	0.000451244	17	N	220	234
P26039	Parental	TEHIR	QELAVFCSPEPPAK	TSTPE	2	C7:+57.021	786.8902564	1571.764913	0.000451244	19	N	2154	2168
P26039	Parental	VRQAR	ILAQATSDLVNAIK	ADAEG	2		728.9226452	1455.82969	0.000451244	24	N	827	841
P26039	Parental	SMRDK	APGQLECETAIAALNSCLR	DLDQA	2	C7:+57.021,C17:+57.021	1037.50649	2072.997381	0.000451244	13	N	1654	1673
P26039	Parental	MIRER	IPEALAGPPNDFGLFLSDDDPKK	GIWLE	3		819.4168344	2455.227103	0.000451244	26	N	35	58
P26039	Parental	CRMIR	ERIPEALAGPPNDFGLFLSDDDPK	KGIWL	2		1307.145722	2612.275845	0.001943752	1	N	33	57
P26039	Parental	CRMIR	ERIPEALAGPPNDFGLFLSDDDPK	KGIWL	3		871.7664149	2612.275845	0.001352548	1	N	33	57
P26039	Parental	AQAAR	GVAALTSDPAVQAIVLDTASDVLDK	ASSLI	2		1235.158298	2468.300997	0.000451244	21	N	1136	1161
P26039	Parental	AQAAR	GVAALTSDPAVQAIVLDTASDVLDK	ASSLI	3		823.7747989	2468.300997	0.000451244	10	N	1136	1161
P26039	Parental	AAEAM	KGTEWVDPEDPTVIAENELLGAAAAIEAAAK	KLEQL	3		1060.542262	3178.603387	0.000735798	2	N	2290	2321
P26039	Parental	ASQAK	PAAVAAENEEIGAHIK	HRVQE	3		540.6182938	1618.831481	0.000622848	6	N	1901	1917
P26039	Parental	SQCAK	NLGTALAELR	TAAQK	2		529.3041771	1056.592754	0.000451244	13	N	1025	1035
P26039	Parental	VSFDK	ACEFAGFQCQIQFGPHNEQK	HKAGF	2	C2:+57.021,C9:+57.021	1198.531028	2395.046456	0.000451244	6	N	234	254
P26039	Parental	VSFDK	ACEFAGFQCQIQFGPHNEQK	HKAGF	3	C2:+57.021,C9:+57.021	799.3566187	2395.046456	0.000451244	20	N	234	254
P26039	Parental	LLRRK	FFYSDQNVDSRDPVQLNLLYVQAR	DDILN	3		963.1511513	2886.430054	0.000451244	6	N	196	220
P26039	Parental	LLAAK	ALSTDPASPNLK	SQLAA	2		607.3253065	1212.635013	0.000451244	15	N	1320	1332
P26039	Parental	TICAR	IGITNHDEYSLVR	ELMEE	2		758.8918764	1515.768153	0.000451244	8	N	118	131
P26039	Parental	GPAGR	YDQATDTILTVTENIF	SSMGD	2		922.4521608	1842.888722	0.002727428	1	N	797	813
P26039	Parental	QAGNR	GTQACITAASAVSGIIADLDTTIMFATAGTLNR	EGAET	3	C5:+57.021	1104.558888	3310.653263	0.000622848	4	N	1973	2006
P26039	Parental	LDHGR	TLREQGVEEHETLLLR	RKFFY	2		962.018868	1922.022136	0.000451244	6	N	178	194
P26039	Parental	LDHGR	TLREQGVEEHETLLLR	RKFFY	3		641.6818453	1922.022136	0.000451244	5	N	178	194
P26039	Parental	LDHGR	TLREQGVEEHETLLLR	RKFFY	4		481.513334	1922.022136	0.001162105	3	N	178	194
P26039	Parental	ISAAR	MVAAATNNLCEAANAAVQGHASQEK	LISSA	2	C10:+57.021	1278.600402	2555.185205	0.000622848	2	N	2398	2423
P26039	Parental	ISAAR	MVAAATNNLCEAANAAVQGHASQEK	LISSA	3	C10:+57.021	852.7362015	2555.185205	0.000451244	22	N	2398	2423
P26039	Parental	AAAGK	VGDDPAVWQLK	NSAKV	2		614.3225669	1226.629534	0.000622848	5	N	2104	2115
P26039	Parental	LLRRK	FFYSDQNVDSRDPVQL	NLLYV	2		965.4530265	1928.890453	0.000451244	19	N	196	212
P26039	Parental	MIRER	IPEALAGPPNDFGLFLSDDDPK	KGIWL	2		1164.57387	2327.13214	0.000451244	17	N	35	57
P26039	Parental	MIRER	IPEALAGPPNDFGLFLSDDDPK	KGIWL	3		776.7185134	2327.13214	0.000622848	1	N	35	57
P26039	Parental	QLGHK	VSQMAQYFEPLTLAAVGAASK	TLSHP	2		1091.564794	2181.113989	0.000451244	4	N	1730	1751
P26039	Parental	AEAMK	GTEWVDPEDPTVIAENELLG	AAAAI	2		1092.521303	2183.027006	0.001329271	2	N	2291	2311
P26039	Parental	AEAMK	GTEWVDPEDPTVIAENELLGAAAAIEAAAKK	LEQLK	3		1060.542262	3178.603387	0.000451244	4	N	2291	2322
P26039	Parental	RAKPK	EADESLNFEEQILEAAKSIAAATSALVK	AASAA	3		983.50867	2947.50261	0.000451244	4	N	2333	2361
P26039	Parental	ADMLR	ACKEAAFHPEVAPDVR	LRALH	3	C2:+57.021	599.6301622	1795.867087	0.000451244	3	N	2217	2233
P26039	Parental	KACEF	AGFQCQIQFGPHNEQK	HKAGF	2	C5:+57.021	944.9418747	1887.868149	0.000451244	3	N	238	254
P26039	Parental	TQFAR	ANQAIQMACQSLGEPGCTQAQVLSAATIVAK	HTSAL	3	C9:+57.021,C17:+57.021	1072.865392	3215.572776	0.000451244	3	N	1469	1500
P26039	Parental	TQFAR	ANQAIQMACQSLGEPGCTQAQVLSAATIVAK	HTSAL	3	M7:+15.995,C9:+57.021,C17:+57.021	1078.197059	3231.567776	0.001839721	1	N	1469	1500
P26039	Parental	DFGDY	QDGYYSVQTTEGEQIAQLIAGYIDIILKK	KKSKD	3		1086.570041	3256.686723	0.000451244	1	N	373	402
P26039	Parental	GAASK	TLSHPQQMALLDQTK	TLAES	2		855.9463263	1709.877053	0.001162105	3	N	1751	1766
P26039	Parental	VISAK	TMLESAGGLIQTAR	ALAVN	2		724.3828305	1446.750061	0.00091018	1	N	1604	1618
P26039	Parental	YVQAR	DDILNGSHPVSFDKACEF	AGFQC	2	C16:+57.021	1025.96267	2049.90974	0.000823681	2	N	220	238
P26039	Parental	YVQAR	DDILNGSHPVSFDKACEFAGFQCQIQFGPHNEQK	HKAGF	3	C16:+57.021,C23:+57.021	1307.59691	3919.767329	0.001352548	1	N	220	254
P26039	Parental	ALVTK	AGALQCSPSDVYTKK	ELIEC	3	C6:+57.021	542.2718634	1623.79219	0.000622848	4	N	1933	1948
P26039	Parental	KDVAK	ALGDLISATK	AAAGK	2		494.7878285	987.560057	0.000622848	13	N	2089	2099
P26039	Parental	AQAAY	LVGVSDPNSQAGQQGLVEPTQFAR	ANQAI	2		1249.635856	2497.256112	0.000823681	4	N	1445	1469
P26039	Parental	QMAQY	FEPLTLAAVGAASK	TLSHP	2		687.8855313	1373.755463	0.000823681	2	N	1737	1751
P26040	Exosome	PIDKK	APDFVFYAPR	LRINK	2		591.8012703	1181.586941	0.000451244	77	Y	263	273
P26040	Exosome	QDQIK	SQEQLAAELAEYTAK	IALLE	2		826.4128386	1650.810077	0.000451244	1	N	412	427
P26040	Exosome	QDQIK	SQEQLAAELAEYTAK	IALLE	3		551.2778258	1650.810077	0.000451244	25	N	412	427
P26040	Exosome	FLQVK	DGILSDEIYCPPETAVLLGSYAVQAK	FGDYN	2	C10:+57.021	1405.202149	2808.388697	0.000451244	40	N	107	133
P26040	Exosome	FLQVK	DGILSDEIYCPPETAVLLGSYAVQAK	FGDYN	3	C10:+57.021	937.1373658	2808.388697	0.000451244	35	N	107	133
P26040	Exosome	KFRAK	FYPEDVAEELIQDITQK	LFFLQ	2		1019.504925	2036.99425	0.000451244	31	N	83	100
P26040	Exosome	KFRAK	FYPEDVAEELIQDITQK	LFFLQ	3		680.0058832	2036.99425	0.000451244	56	N	83	100
P26040	Exosome	KLTPK	IGFPWSEIR	NISFN	2		552.7959879	1103.576376	0.000451244	26	Y	237	246
P26040	Exosome	ERVQR	QLLTLSNELSQAR	DENKR	2		736.9075264	1471.799453	0.000451244	12	N	529	542
P26040	Exosome	ERVQR	QLLTLSNELSQAR	DENKR	2	[0:-17.027	728.3940264	1454.772453	0.000451244	15	N	529	542
P26040	Exosome	TIGLR	EVWYFGLQYVDNK	GFPTW	2		830.9044524	1659.793305	0.000451244	15	N	40	53
P26040	Exosome	QFKFR	AKFYPEDVAEELIQDITQK	LFFLQ	2		1119.070963	2236.126327	0.000451244	16	N	81	100
P26040	Exosome	QFKFR	AKFYPEDVAEELIQDITQK	LFFLQ	3		746.3832422	2236.126327	0.000451244	5	N	81	100

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26040	Exosome	PINVR	VTTMDAELEFAIQPNTTGK	QLFDQ	2		1033.509685	2065.003769	0.000451244	10	Y	8	27
P26040	Parental	PIDKK	APDFVFYAPR	LRINK	2		591.8012703	1181.586941	0.000451244	29	Y	263	273
P26040	Parental	QDQIK	SQEQLAAELAEYTAK	IALLE	2		826.4128386	1650.810077	0.001871652	1	N	412	427
P26040	Parental	QDQIK	SQEQLAAELAEYTAK	IALLE	3		551.2778258	1650.810077	0.000451244	6	N	412	427
P26040	Parental	EELER	QAQDQIKSQEQLAAELAEYTAK	IALLE	2		1232.122247	2462.228894	0.000451244	12	N	405	427
P26040	Parental	EELER	QAQDQIKSQEQLAAELAEYTAK	IALLE	3		821.7507648	2462.228894	0.000451244	15	N	405	427
P26040	Parental	FLQVK	DGILSDEIYCPPETAVLLGSYAVQAK	FGDYN	2	C10:+57.021	1405.202149	2808.388697	0.000451244	32	N	107	133
P26040	Parental	FLQVK	DGILSDEIYCPPETAVLLGSYAVQAK	FGDYN	3	C10:+57.021	937.1373658	2808.388697	0.000451244	27	N	107	133
P26040	Parental	KFRAK	FYPEDVAEELIQDITQK	LFFLQ	2		1019.504925	2036.99425	0.000451244	12	N	83	100
P26040	Parental	KFRAK	FYPEDVAEELIQDITQK	LFFLQ	3		680.0058832	2036.99425	0.000451244	33	N	83	100
P26040	Parental	KPIDK	KAPDFVFYAPR	LRINK	3		437.5684345	1309.681904	0.002374549	3	Y	262	273
P26040	Parental	KLTPK	IGFPWSEIR	NISFN	2		552.7959879	1103.576376	0.000823681	4	Y	237	246
P26040	Parental	ERVQR	QLLTLSNELSQAR	DENKR	2		736.9075264	1471.799453	0.000451244	14	N	529	542
P26040	Parental	QFKFR	AKFYPEDVAEELIQDITQK	LFFLQ	2		1119.070963	2236.126327	0.000451244	4	N	81	100
P26040	Parental	QFKFR	AKFYPEDVAEELIQDITQK	LFFLQ	3		746.3832422	2236.126327	0.000451244	9	N	81	100
P26040	Parental	RVTTM	DAELEFAIQPNTTGK	QLFDQ	2		817.4075563	1632.799513	0.000622848	7	Y	12	27
P26041	Exosome	KEVHK	SGYLAGDKLLPQR	VLEQH	2		709.3940549	1416.77251	0.000662267	1	N	143	156
P26041	Exosome	PIDKK	APDFVFYAPR	LRINK	2		591.8012703	1181.586941	0.000451244	77	Y	263	273
P26041	Exosome	TIGLR	EVWFFGLQYQDTK	AFSTW	2		830.9044524	1659.793305	0.000451244	40	N	40	53
P26041	Exosome	TIGLR	EVWFFGLQYQDTK	AFSTW	3		554.272235	1659.793305	0.000451244	5	N	40	53
P26041	Exosome	LFKFR	AKFYPEDVSEELIQDITQR	LFFLQ	2		1141.071495	2280.127389	0.000451244	31	N	81	100
P26041	Exosome	LFKFR	AKFYPEDVSEELIQDITQR	LFFLQ	3		761.0502631	2280.127389	0.000451244	52	N	81	100
P26041	Exosome	IKNKK	GSELWLGVDALGLNIYEQNDRLTPK	IGFPW	2		1401.227578	2800.439556	0.000451244	4	N	212	237
P26041	Exosome	IKNKK	GSELWLGVDALGLNIYEQNDRLTPK	IGFPW	3		934.487652	2800.439556	0.000451244	9	N	212	237
P26041	Exosome	IKNKK	GSELWLGVDALGLNIYEQNDR	LTPKI	2		1181.587843	2361.160086	0.000451244	58	N	212	233
P26041	Exosome	IKNKK	GSELWLGVDALGLNIYEQNDR	LTPKI	3		788.0611621	2361.160086	0.000451244	18	N	212	233
P26041	Exosome	KFRAK	FYPEDVSEELIQDITQR	LFFLQ	2		1041.505456	2080.995312	0.000451244	53	N	83	100
P26041	Exosome	KFRAK	FYPEDVSEELIQDITQR	LFFLQ	3		694.6729041	2080.995312	0.000451244	90	N	83	100
P26041	Exosome	FLQVK	EGILNDDIYCPPETAVLLASYAVQSK	YGDFN	2	C10:+57.021	1433.712881	2865.410161	0.000451244	90	N	107	133
P26041	Exosome	FLQVK	EGILNDDIYCPPETAVLLASYAVQSK	YGDFN	3	C10:+57.021	956.1445204	2865.410161	0.000451244	132	N	107	133
P26041	Exosome	RLTPK	IGFPWSEIR	NISFN	2		552.7959879	1103.576376	0.000451244	26	Y	237	246
P26041	Exosome	QKHLK	ALTSELANAR	DESKK	2		523.2859843	1044.556369	0.001162105	13	N	523	533
P26041	Exosome	LAKER	QEAEEAKEALLQASR	DQKKT	2		836.9291872	1671.842774	0.000451244	18	N	393	408
P26041	Exosome	LAKER	QEAEEAKEALLQASR	DQKKT	3		558.2887248	1671.842774	0.000451244	7	N	393	408
P26041	Exosome	SIKNK	KGSELWLGVDALGLNIYEQNDR	LTPKI	2		1245.635325	2489.255049	0.000451244	8	N	211	233
P26041	Exosome	SIKNK	KGSELWLGVDALGLNIYEQNDR	LTPKI	3		830.7594831	2489.255049	0.001699387	1	N	211	233
P26041	Exosome	RAELK	TAMSTPHVAEPAENEHDEQDENGAE	ASAEL	3	M3:+15.995	908.7041315	2723.088995	0.001654178	2	N	464	489
P26041	Exosome	RAELK	TAMSTPHVAEPAENEHDEQDENGAEASAELR	ADAMA	3	M3:+15.995	1117.815473	3350.423019	0.000451244	20	N	464	495
P26041	Exosome	RAELK	TAMSTPHVAEPAENEHDEQDENGAEASAELR	ADAMA	4	M3:+15.995	838.6135548	3350.423019	0.000622848	28	N	464	495
P26041	Exosome	QKHLK	ALTSELANARDESK	KTAND	2		752.8842483	1503.752897	0.000451244	1	N	523	537
P26041	Exosome	QKHLK	ALTSELANARDESK	KTAND	3		502.2587655	1503.752897	0.000662267	3	N	523	537
P26041	Exosome	LEYLK	IAQDLEMYGVNYFSIK	NKKGS	2		945.9694671	1889.923334	0.000451244	20	N	193	209
P26041	Exosome	TISVR	VTTMDAELEFAIQPNTTGK	QLFDQ	2		1033.509685	2065.003769	0.000451244	10	Y	8	27
P26041	Exosome	RGMLR	EDAVLEYLK	IAQDL	2		540.2851187	1078.554637	0.000622848	4	N	184	193
P26041	Exosome	KTIGL	REVWFFGLQYQDTK	AFSTW	3		606.3059387	1815.894416	0.00091018	1	N	39	53
P26041	Exosome	HEEHR	GMLREDAVLEYLK	IAQDL	3		512.9417207	1535.801762	0.000451244	1	N	180	193
P26041	Exosome	DDIYC	PPETAVLLASYAVQSK	YGDFN	2		837.4595919	1672.903584	0.002145581	1	N	117	133
P26041	Parental	KEVHK	SGYLAGDKLLPQR	VLEQH	2		709.3940549	1416.77251	0.000451244	8	N	143	156
P26041	Parental	KEVHK	SGYLAGDKLLPQR	VLEQH	3		473.2653032	1416.77251	0.000622848	8	N	143	156
P26041	Parental	PIDKK	APDFVFYAPR	LRINK	2		591.8012703	1181.586941	0.000451244	29	Y	263	273
P26041	Parental	TIGLR	EVWFFGLQYQDTK	AFSTW	2		830.9044524	1659.793305	0.000451244	15	N	40	53
P26041	Parental	LFKFR	AKFYPEDVSEELIQDITQR	LFFLQ	2		1141.071495	2280.127389	0.000451244	46	N	81	100
P26041	Parental	LFKFR	AKFYPEDVSEELIQDITQR	LFFLQ	3		761.0502631	2280.127389	0.000451244	20	N	81	100
P26041	Parental	IKNKK	GSELWLGVDALGLNIYEQNDRLTPK	IGFPW	2		1401.227578	2800.439556	0.000451244	9	N	212	237
P26041	Parental	IKNKK	GSELWLGVDALGLNIYEQNDRLTPK	IGFPW	3		934.487652	2800.439556	0.000451244	8	N	212	237
P26041	Parental	IKNKK	GSELWLGVDALGLNIYEQNDR	LTPKI	2		1181.587843	2361.160086	0.000451244	27	N	212	233
P26041	Parental	IKNKK	GSELWLGVDALGLNIYEQNDR	LTPKI	3		788.0611621	2361.160086	0.000451244	4	N	212	233
P26041	Parental	KFRAK	FYPEDVSEELIQDITQR	LFFLQ	2		1041.505456	2080.995312	0.000451244	24	N	83	100
P26041	Parental	KFRAK	FYPEDVSEELIQDITQR	LFFLQ	3		694.6729041	2080.995312	0.000451244	45	N	83	100
P26041	Parental	FLQVK	EGILNDDIYCPPETAVLLASYAVQSK	YGDFN	2	C10:+57.021	1433.712881	2865.410161	0.000451244	59	N	107	133
P26041	Parental	FLQVK	EGILNDDIYCPPETAVLLASYAVQSK	YGDFN	3	C10:+57.021	956.1445204	2865.410161	0.000451244	46	N	107	133
P26041	Parental	KPIDK	KAPDFVFYAPR	LRINK	3		437.5684345	1309.681904	0.002374549	3	Y	262	273
P26041	Parental	RLTPK	IGFPWSEIR	NISFN	2		552.7959879	1103.576376	0.000823681	4	Y	237	246
P26041	Parental	LAKER	QEAEEAKEALLQASR	DQKKT	3		558.2887248	1671.842774	0.000698008	3	N	393	408
P26041	Parental	SIKNK	KGSELWLGVDALGLNIYEQNDR	LTPKI	2		1245.635325	2489.255049	0.000870037	1	N	211	233

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26041	Parental	RVTTM	DAELEFAIQPNTTGK	QLFDQ	2		817.4075563	1632.799513	0.000622848	7	Y	12	27
P26041	Parental	RGMLR	EDAVLEYLK	IAQDL	2		540.2851187	1078.554637	0.000622848	2	N	184	193
P26043	Exosome	PIDKK	APDFVFYAPR	LRINK	2		591.8012703	1181.586941	0.000451244	77	Y	263	273
P26043	Exosome	FLQVK	EAILNDEIYCPPETAVLLASYAVQAK	YGDYN	2	C10:+57.021	1439.731073	2877.446547	0.000451244	26	N	107	133
P26043	Exosome	FLQVK	EAILNDEIYCPPETAVLLASYAVQAK	YGDYN	3	C10:+57.021	960.1566489	2877.446547	0.000451244	21	N	107	133
P26043	Exosome	KLTPK	IGFPWSEIR	NISFN	2		552.7959879	1103.576376	0.000451244	26	Y	237	246
P26043	Exosome	KFRAK	FFPEDVSEELIQEITQR	LFFLQ	2		1040.515824	2079.016048	0.000451244	15	N	83	100
P26043	Exosome	KFRAK	FFPEDVSEELIQEITQR	LFFLQ	3		694.0131492	2079.016048	0.000451244	88	N	83	100
P26043	Exosome	ADQMK	NQEQLAAELAEFTAK	IALLE	2		831.9208308	1661.826062	0.000451244	12	N	412	427
P26043	Exosome	ADQMK	NQEQLAAELAEFTAK	IALLE	3		554.9498206	1661.826062	0.000451244	18	N	412	427
P26043	Exosome	TVGLR	EVWFFGLQYVDSK	GYSTW	2		809.4015456	1616.787491	0.000451244	12	N	40	53
P26043	Exosome	ERVKK	QLQALSSELAQAR	DETKK	2		707.886594	1413.757588	0.000451244	4	N	526	539
P26043	Exosome	ERVKK	QLQALSSELAQAR	DETKK	2	[0:-17.027	699.373094	1396.730588	0.000451244	3	N	526	539
P26043	Exosome	IKNKK	GTELWLGVDALGLNIYEHDDKLTPK	IGFPW	3		933.1522693	2796.433408	0.001162105	1	N	212	237
P26043	Exosome	IKNKK	GTELWLGVDALGLNIYEHDDKLTPK	IGFPW	4		700.116152	2796.433408	0.000823681	1	N	212	237
P26043	Exosome	PINVR	VTTMDAELEFAIQPNTTGK	QLFDQ	2		1033.509685	2065.003769	0.000451244	10	Y	8	27
P26043	Exosome	QFKFR	AKFFPEDVSEELIQEITQR	LFFLQ	3		760.3905082	2278.148125	0.000622848	7	N	81	100
P26043	Exosome	AVQAK	YGDYNKEIHKPGYLANDR	LLPQR	4		539.0162408	2152.033763	0.001264573	5	N	133	151
P26043	Parental	PIDKK	APDFVFYAPR	LRINK	2		591.8012703	1181.586941	0.000451244	29	Y	263	273
P26043	Parental	FLQVK	EAILNDEIYCPPETAVLLASYAVQAK	YGDYN	2	C10:+57.021	1439.731073	2877.446547	0.000451244	5	N	107	133
P26043	Parental	FLQVK	EAILNDEIYCPPETAVLLASYAVQAK	YGDYN	3	C10:+57.021	960.1566489	2877.446547	0.000451244	21	N	107	133
P26043	Parental	KPIDK	KAPDFVFYAPR	LRINK	3		437.5684345	1309.681904	0.002374549	3	Y	262	273
P26043	Parental	KLTPK	IGFPWSEIR	NISFN	2		552.7959879	1103.576376	0.000823681	4	Y	237	246
P26043	Parental	KFRAK	FFPEDVSEELIQEITQR	LFFLQ	3		694.0131492	2079.016048	0.000451244	4	N	83	100
P26043	Parental	IKNKK	GTELWLGVDALGLNIYEHDDKLTPK	IGFPW	4		700.116152	2796.433408	0.000451244	1	N	212	237
P26043	Parental	RVTTM	DAELEFAIQPNTTGK	QLFDQ	2		817.4075563	1632.799513	0.000622848	7	Y	12	27
P26350	Exosome	EGGEE	EEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1003.717348	3008.128644	0.002296037	1	N	63	90
P26350	Exosome	EEEEE	GGEEEEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1127.760053	3380.256758	0.001162105	1	N	59	90
P26350	Parental	EGGEE	EEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1003.717348	3008.128644	0.000451244	60	N	63	90
P26350	Parental	EEGGE	EEEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1046.731546	3137.171237	0.000451244	46	N	62	90
P26350	Parental	EEEEE	GGEEEEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1127.760053	3380.256758	0.000451244	119	N	59	90
P26350	Parental	EEEEE	GGEEEEEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	3		1075.726349	3224.155647	0.000451244	53	N	59	89
P26350	Parental	EGGEE	EEEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	2		1427.021566	2852.027533	0.000451244	29	N	63	89
P26350	Parental	EGGEE	EEEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	3		951.6836442	2852.027533	0.000451244	34	N	63	89
P26350	Parental	LKEKK	EVVEEAENGRDAPANGNAQNEENGEQEADNEVDEEEEE	GGEEE	3		1396.564964	4186.671492	0.000451244	28	N	21	59
P26350	Parental	DEEEE	EGGEEEEEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		1170.77425	3509.299351	0.000451244	10	N	58	90
P26350	Parental	EEGGE	EEEEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	3		994.6978419	2981.070126	0.000451244	19	N	62	89
P26350	Parental	LKEKK	EVVEEAENGRDAPANGNAQNEENGEQE	ADNEV	2		1450.114596	2898.213591	0.000979378	1	N	21	48
P26350	Parental	LKEKK	EVVEEAENGRDAPANGNAQNEENGEQE	ADNEV	3		967.0789972	2898.213591	0.001352548	3	N	21	48
P26350	Parental	GGEEE	EEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	2		1362.50027	2722.984939	0.000451244	9	N	64	89
P26350	Parental	GGEEE	EEEEEGDGEEEDGDEDEEAEAPTGK	RVAED	3		908.6694465	2722.984939	0.000451244	5	N	64	89
P26350	Parental	GGEEE	EEEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		960.7031502	2879.086051	0.000451244	30	N	64	90
P26350	Parental	GEEEE	EEEEGDGEEEDGDEDEEAEAPTGKR	VAEDD	3		917.6889525	2750.043457	0.000451244	12	N	65	90
P26350	Parental	GEEEE	EEEEGDGEEEDGDEDEEAEAPTGK	RVAED	2		1297.978973	2593.942346	0.000451244	16	N	65	89
P26369	Exosome	YGLVK	SIEIPRPVDGVEVPGCGK	IFVEF	3	C16:+57.021	637.0001438	1907.977031	0.000451244	4	N	413	431
P26369	Exosome	PGCGK	IFVEFTSVFDCQK	AMQGL	2	C11:+57.021	810.392632	1618.769664	0.000451244	9	N	431	444
P26369	Exosome	DSAHK	LFIGGLPNYLNDDQVKELLTSFGPLK	AFNLV	3		964.5238146	2890.548044	0.000451244	25	N	260	286
P26369	Exosome	NAQMR	LGGLTQAPGNPVLAVQINQDKNFAFLEFR	SVDET	3		1053.231805	3156.672016	0.000622848	11	N	174	203
P26369	Exosome	NAQMR	LGGLTQAPGNPVLAVQINQDK	NFAFL	2		1067.087282	2132.158964	0.000637154	2	N	174	195
P26369	Parental	YGLVK	SIEIPRPVDGVEVPGCGK	IFVEF	2	C16:+57.021	954.9963156	1907.977031	0.000451244	7	N	413	431
P26369	Parental	YGLVK	SIEIPRPVDGVEVPGCGK	IFVEF	3	C16:+57.021	637.0001438	1907.977031	0.000451244	24	N	413	431
P26369	Parental	PGCGK	IFVEFTSVFDCQK	AMQGL	2	C11:+57.021	810.392632	1618.769664	0.000451244	13	N	431	444
P26369	Parental	DSAHK	LFIGGLPNYLNDDQVKELLTSFGPLK	AFNLV	2		1446.281822	2890.548044	0.000451244	2	N	260	286
P26369	Parental	DSAHK	LFIGGLPNYLNDDQVKELLTSFGPLK	AFNLV	3		964.5238146	2890.548044	0.000451244	27	N	260	286
P26369	Parental	NAQMR	LGGLTQAPGNPVLAVQINQDKNFAFLEFR	SVDET	3		1053.231805	3156.672016	0.000622848	19	N	174	203
P26369	Parental	NAQMR	LGGLTQAPGNPVLAVQINQDK	NFAFL	2		1067.087282	2132.158964	0.000451244	12	N	174	195
P26443	Exosome	RVKAK	IIAEGANGPTTPEADKIFLER	NIMVI	2		1121.589855	2241.164109	0.000451244	17	N	399	420
P26443	Exosome	RVKAK	IIAEGANGPTTPEADKIFLER	NIMVI	3		748.062503	2241.164109	0.000451244	37	N	399	420
P26443	Exosome	FPKAK	VYEGSILEADCDILIPAASEK	QLTKS	2	C11:+57.021	1147.067332	2292.119064	0.000451244	39	N	365	386
P26443	Exosome	FPKAK	VYEGSILEADCDILIPAASEK	QLTKS	3	C11:+57.021	765.047488	2292.119064	0.000451244	12	N	365	386
P26443	Exosome	RFGAK	CVGVGESDGSIWNPDGIDPK	ELEDF	2	C1:+39.994	1042.965184	2083.914768	0.001264573	1	N	326	346
P26443	Exosome	RFGAK	CVGVGESDGSIWNPDGIDPK	ELEDF	2	C1:+57.021	1051.478684	2100.941768	0.000451244	38	N	326	346
P26443	Exosome	RFGAK	CVGVGESDGSIWNPDGIDPK	ELEDF	2	[0:-17.027,C1:+57.021	1042.965184	2083.914768	0.002519933	1	N	326	346
P26443	Exosome	ARRHY	SEAAADREDDPNFFK	MVEGF	2		856.3820698	1710.74854	0.000451244	15	N	53	68
P26443	Exosome	RKFGK	HGGTIPVVPTAEFQDR	ISGAS	2		862.4422648	1722.86893	0.000451244	10	N	480	496

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P26443	Exosome	FPIRR	DDGSWEVIEGYR	AQHSQ	2		713.3182098	1424.62082	0.000451244	4	N	124	136
P26443	Exosome	KGGIR	YSTDVSVDEVK	ALASL	2		621.2989544	1240.582309	0.000451244	1	N	151	162
P26443	Exosome	GIDPK	ELEDFKLQHGSILGFPK	AKVYE	3		653.3514366	1957.03091	0.000451244	5	N	346	363
P26443	Exosome	ELAKK	GFIGPGIDVPAPDMSTGER	EMSWI	2	M14:+15.995	966.4625802	1930.90956	0.000451244	10	N	212	231
P26443	Parental	RVKAK	IIAEGANGPTTPEADKIFLER	NIMVI	2		1121.589855	2241.164109	0.000451244	4	N	399	420
P26443	Parental	RVKAK	IIAEGANGPTTPEADKIFLER	NIMVI	3		748.062503	2241.164109	0.000451244	25	N	399	420
P26443	Parental	FPKAK	VYEGSILEADCDILIPAASEK	QLTKS	2	C11:+57.021	1147.067332	2292.119064	0.000451244	41	N	365	386
P26443	Parental	RFGAK	CVGVGESDGSIWNPDGIDPK	ELEDF	2	C1:+57.021	1051.478684	2100.941768	0.000451244	19	N	326	346
P26443	Parental	ARRHY	SEAAADREDDPNFFK	MVEGF	2		856.3820698	1710.74854	0.000451244	8	N	53	68
P26443	Parental	RKFGK	HGGTIPVVPTAEFQDR	ISGAS	2		862.4422648	1722.86893	0.001352548	1	N	480	496
P26443	Parental	MELAK	KGFIGPGIDVPAPDMSTGER	EMSWI	4		511.7601809	2043.009524	0.002727428	1	N	211	231
P26450	Exosome	HRDGK	YGFSDPLTFNSVVELINHYR	NESLA	3		791.0626144	2370.164443	0.000451244	11	N	389	409
P26450	Exosome	LTVNK	GSLVALGFSDGQEARPEDIGWLNGYNETTGER	GDFPG	3		1146.878596	3437.612388	0.000451244	8	N	34	66
P26450	Exosome	PGSSK	TEADTEQQALPLPDLAEQFAPPDVAPPLLIK	LLEAI	3		1109.917329	3326.728587	0.000451244	8	N	103	134
P26450	Exosome	LLNAR	VLSEIFSPVLFR	FPAAS	2		703.9062668	1405.796934	0.000622848	3	N	262	274
P26450	Parental	LTVNK	GSLVALGFSDGQEARPEDIGWLNGYNETTGER	GDFPG	3		1146.878596	3437.612388	0.000451244	14	N	34	66
P26450	Parental	PGSSK	TEADTEQQALPLPDLAEQFAPPDVAPPLLIK	LLEAI	3		1109.917329	3326.728587	0.000451244	21	N	103	134
P26516	Exosome	TPTSK	TFEHVTSEIGAEEAEEVGVEHLLR	DIKDT	4		671.0823092	2680.298037	0.001162105	5	N	153	177
P26516	Exosome	DVKPK	DLGLPTEAYISVEEVHDDGTPTSK	TFEHV	2		1287.116827	2572.218055	0.000451244	6	N	129	153
P26516	Exosome	LAVQK	VVVHPLVLLSVVDHFNR	IGKVG	3		648.3795495	1942.115248	0.000451244	3	N	8	25
P26516	Exosome	LAVQK	VVVHPLVLLSVVDHFNR	IGKVG	4		486.5366121	1942.115248	0.000451244	27	N	8	25
P26516	Exosome	VASGK	LPINHQIIYQLQDVFNLLPDASLQEFVK	AFYLK	3		1099.262883	3294.765248	0.000451244	17	N	219	247
P26516	Exosome	GNQKR	VVGVLLGSWQK	KVLDV	2		593.35367	1184.69174	0.001463592	5	N	34	45
P26516	Exosome	ELMKR	YCPNSVLVIIDVKPK	DLGLP	3	C2:+57.021	582.3274206	1743.958862	0.000451244	2	N	114	129
P26516	Parental	TPTSK	TFEHVTSEIGAEEAEEVGVEHLLR	DIKDT	4		671.0823092	2680.298037	0.000451244	6	N	153	177
P26516	Parental	DVKPK	DLGLPTEAYISVEEVHDDGTPTSK	TFEHV	2		1287.116827	2572.218055	0.000451244	6	N	129	153
P26516	Parental	DVKPK	DLGLPTEAYISVEEVHDDGTPTSK	TFEHV	3		858.4138183	2572.218055	0.001763695	1	N	129	153
P26516	Parental	LAVQK	VVVHPLVLLSVVDHFNR	IGKVG	3		648.3795495	1942.115248	0.000451244	4	N	8	25
P26516	Parental	LAVQK	VVVHPLVLLSVVDHFNR	IGKVG	4		486.5366121	1942.115248	0.000451244	31	N	8	25
P26516	Parental	VASGK	LPINHQIIYQLQDVFNLLPDASLQEFVK	AFYLK	3		1099.262883	3294.765248	0.000622848	6	N	219	247
P26516	Parental	HQIIY	QLQDVFNLLPDASLQEFVK	AFYLK	2		1102.584041	2203.152482	0.001329271	1	N	228	247
P26638	Exosome	KMKKK	EAVGDDESVPENVLNFDDLTADALAALK	VSQIK	2		1466.209445	2930.40329	0.000451244	4	N	71	99
P26638	Exosome	KMKKK	EAVGDDESVPENVLNFDDLTADALAALK	VSQIK	3		977.8088966	2930.40329	0.000622848	7	N	71	99
P26638	Exosome	GYFLK	GPLVFLEQALIQYALR	TLGSR	2		916.027976	1830.040352	0.000451244	3	N	197	213
P26638	Exosome	GYFLK	GPLVFLEQALIQYALR	TLGSR	3		611.0212507	1830.040352	0.001654178	2	N	197	213
P26638	Exosome	SGAFR	ELVSCSNCTDYQAR	RLRIR	2	C5:+57.021,C8:+57.021	851.86167	1701.70774	0.000451244	8	N	390	404
P26638	Exosome	HAASK	KLDLEAWFPGSGAFR	ELVSC	3		565.2952625	1692.862388	0.001162105	3	N	375	390
P26638	Exosome	EKMKK	KEAVGDDESVPENVLNFDDLTADALAALK	VSQIK	3		1020.507218	3058.498253	0.000451244	2	N	70	99
P26638	Parental	KMKKK	EAVGDDESVPENVLNFDDLTADALAALK	VSQIK	2		1466.209445	2930.40329	0.000870037	4	N	71	99
P26638	Parental	KMKKK	EAVGDDESVPENVLNFDDLTADALAALK	VSQIK	3		977.8088966	2930.40329	0.000451244	10	N	71	99
P26645	Exosome	GATAE	GAKDEAAAAAGGEGAAAPGEQAGGAGAEGAAGGEPR	EAEAA	3		1003.129915	3006.366344	0.001654178	1	N	183	219
P26645	Exosome	AADKE	AAEAEPAEPSSPAAEAEGASASSTSSPK	AEDGA	2		1294.086256	2586.156911	0.002727428	1	N	102	130
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	2		1392.696779	2783.377959	0.000451244	32	N	7	31
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	3		928.8004529	2783.377959	0.000451244	85	N	7	31
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	4		696.8522897	2783.377959	0.000622848	22	N	7	31
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	2		1328.649298	2655.282996	0.000451244	5	N	7	30
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	3		886.1021319	2655.282996	0.000451244	14	N	7	30
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	4		664.8285489	2655.282996	0.000622848	3	N	7	30
P27005	Exosome	KNDFK	KMVTTECPQFVQNINIENLFR	ELDIN	3	C7:+57.021	861.1019331	2580.282399	0.000451244	14	N	35	56
P27005	Exosome	KMVTT	ECPQFVQNINIENLFR	ELDIN	2	C2:+57.021	1010.99939	2019.983179	0.000698008	6	N	40	56
P27005	Exosome	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	2	C6:+57.021	1227.101518	2452.187436	0.000451244	110	N	36	56
P27005	Exosome	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	3	C6:+57.021	818.4036121	2452.187436	0.000451244	60	N	36	56
P27005	Exosome	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	2	M1:+15.995,C6:+57.021	1235.099018	2468.182436	0.000451244	67	N	36	56
P27005	Exosome	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	3	M1:+15.995,C6:+57.021	823.7352787	2468.182436	0.000451244	37	N	36	56
P27005	Exosome	DFKKM	VTTECPQFVQNINIENLFR	ELDIN	2	C5:+57.021	1161.581275	2321.14695	0.000451244	19	N	37	56
P27005	Exosome	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2		1213.101938	2424.188276	0.000451244	159	N	56	77
P27005	Exosome	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	3		809.0705587	2424.188276	0.000451244	21	N	56	77
P27005	Exosome	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2	M18:+15.995	1221.099438	2440.183276	0.000451244	98	N	56	77
P27005	Exosome	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	3	M18:+15.995	814.4022254	2440.183276	0.000451244	26	N	56	77
P27005	Exosome	SELEK	ALSNLIDVYHNY	SNIQG	2		711.357138	1420.698676	0.000870037	5	N	7	19
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQGN	HHALY	2		1017.998133	2033.980665	0.001329271	4	N	7	25
P27005	Exosome	LEKAL	SNLIDVYHNYSNIQGNHHALYK	NDFKK	3		867.4267269	2599.256781	0.000622848	6	N	9	31
P27005	Exosome	-M	PSELEKALSNLIDVYHNYSNIQGNHHALYK	NDFKK	4		867.6895412	3466.726965	0.000451244	3	N	1	31
P27005	Exosome	SELEK	ALSNLIDVYHNYSNIQ	GNHHA	2		932.4659369	1862.916274	0.000451244	1	N	7	23
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALYKNDFK	KMVTT	3		1096.878202	3287.611206	0.000451244	17	N	7	35

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALYKNDFK	KMVTT	4		822.9106016	3287.611206	0.002145581	1	N	7	35
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	2		1392.696779	2783.377959	0.000451244	93	N	7	31
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	3		928.8004529	2783.377959	0.000451244	297	N	7	31
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALYK	NDFKK	4		696.8522897	2783.377959	0.000622848	46	N	7	31
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	2		1328.649298	2655.282996	0.000451244	107	N	7	30
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	3		886.1021319	2655.282996	0.000451244	364	N	7	30
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALY	KNDFK	4		664.8285489	2655.282996	0.000622848	75	N	7	30
P27005	Parental	KNDFK	KMVTTECPQFVQNINIENLFR	ELDIN	2	C7:+57.021	1291.149	2580.282399	0.000451244	14	N	35	56
P27005	Parental	KNDFK	KMVTTECPQFVQNINIENLFR	ELDIN	3	C7:+57.021	861.1019331	2580.282399	0.000451244	27	N	35	56
P27005	Parental	KNDFK	KMVTTECPQFVQNINIENLFR	ELDIN	3	M2:+15.995,C7:+57.021	866.4335998	2596.277399	0.002019181	1	N	35	56
P27005	Parental	FKKMV	TTECPQFVQNINIENLFR	ELDIN	2	C4:+57.021	1112.047068	2222.078536	0.000451244	19	N	38	56
P27005	Parental	FKKMV	TTECPQFVQNINIENLFR	ELDIN	3	C4:+57.021	741.7006455	2222.078536	0.000451244	5	N	38	56
P27005	Parental	KKMVT	TECPQFVQNINIENLFR	ELDIN	2	C3:+57.021	1061.523229	2121.030858	0.000451244	38	N	39	56
P27005	Parental	KKMVT	TECPQFVQNINIENLFR	ELDIN	3	C3:+57.021	708.0180859	2121.030858	0.000451244	19	N	39	56
P27005	Parental	KMVTT	ECPQFVQNINIENLFR	ELDIN	2	C2:+57.021	1010.99939	2019.983179	0.000451244	5	N	40	56
P27005	Parental	KMVTT	ECPQFVQNINIENLFR	ELDIN	2	E1:-18.011,C2:+57.021	1001.99389	2001.972179	0.000823681	7	N	40	56
P27005	Parental	KMVTT	ECPQFVQNINIENLFR	ELDIN	2	[0:-18.011,C2:+57.021	1001.99389	2001.972179	0.000823681	5	N	40	56
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	2	C6:+57.021	1227.101518	2452.187436	0.000451244	807	N	36	56
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	3	C6:+57.021	818.4036121	2452.187436	0.000451244	437	N	36	56
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	2	M1:+15.995,C6:+57.021	1235.099018	2468.182436	0.000451244	106	N	36	56
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLFR	ELDIN	3	M1:+15.995,C6:+57.021	823.7352787	2468.182436	0.000451244	49	N	36	56
P27005	Parental	DFKKM	VTTECPQFVQNINIENLFR	ELDIN	2	C5:+57.021	1161.581275	2321.14695	0.000451244	38	N	37	56
P27005	Parental	DFKKM	VTTECPQFVQNINIENLFR	ELDIN	3	C5:+57.021	774.7234501	2321.14695	0.000451244	26	N	37	56
P27005	Parental	ENLFR	ELDINSDNAINFEEF	LAMVI	2		885.3973856	1768.779171	0.000451244	71	N	56	71
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLF	RELDI	2	C6:+57.021	1149.050963	2296.086325	0.000451244	40	N	36	55
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLF	RELDI	3	C6:+57.021	766.3699084	2296.086325	0.000451244	8	N	36	55
P27005	Parental	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2		1213.101938	2424.188276	0.000451244	867	N	56	77
P27005	Parental	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	3		809.0705587	2424.188276	0.000451244	620	N	56	77
P27005	Parental	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2	E1:-18.011	1204.096438	2406.177276	0.000451244	4	N	56	77
P27005	Parental	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2	M18:+15.995	1221.099438	2440.183276	0.000451244	64	N	56	77
P27005	Parental	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	3	M18:+15.995	814.4022254	2440.183276	0.000451244	11	N	56	77
P27005	Parental	ENLFR	ELDINSDNAINFEEFLAMVIK	VGVAS	2	[0:-18.011	1204.096438	2406.177276	0.000451244	2	N	56	77
P27005	Parental	NAINF	EEFLAMVIK	VGVAS	2		540.2944327	1078.573265	0.001162105	16	N	68	77
P27005	Parental	ECPQF	VQNINIENLFR	ELDIN	2		680.3731224	1358.730645	0.000451244	23	N	45	56
P27005	Parental	ENLFR	ELDINSDNAINF	EEFLA	2		682.8205853	1363.625571	0.000451244	30	N	56	68
P27005	Parental	SELEK	ALSNLIDVYHNY	SNIQG	2		711.357138	1420.698676	0.000451244	9	N	7	19
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGN	HHALY	2		1017.998133	2033.980665	0.000451244	7	N	7	25
P27005	Parental	VTTEC	PQFVQNINIENLFR	ELDIN	2		866.4630002	1730.9104	0.000451244	24	N	42	56
P27005	Parental	VTTEC	PQFVQNINIENLFR	ELDIN	3		577.9779335	1730.9104	0.000451244	5	N	42	56
P27005	Parental	LEKAL	SNLIDVYHNYSNIQGNHHALYK	NDFKK	2		1300.63619	2599.256781	0.000451244	4	N	9	31
P27005	Parental	LEKAL	SNLIDVYHNYSNIQGNHHALYK	NDFKK	3		867.4267269	2599.256781	0.000451244	27	N	9	31
P27005	Parental	LEKAL	SNLIDVYHNYSNIQGNHHALYK	NDFKK	4		650.8219952	2599.256781	0.001699387	2	N	9	31
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHH	ALYKN	2		1155.057044	2308.098489	0.000451244	10	N	7	27
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHH	ALYKN	3		770.373963	2308.098489	0.000451244	18	N	7	27
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHH	ALYKN	4		578.0324222	2308.098489	0.000622848	11	N	7	27
P27005	Parental	-M	PSELEKALSNLIDVYHNYSNIQGNHHALYK	NDFKK	4		867.6895412	3466.726965	0.000622848	3	N	1	31
P27005	Parental	ENLFR	ELDINSDNAINFEEFL	AMVIK	2		941.9394176	1881.863235	0.000451244	9	N	56	72
P27005	Parental	KALSN	LIDVYHNYSNIQGNHHALYK	NDFKK	3		800.4017416	2398.181825	0.000451244	14	N	11	31
P27005	Parental	MVTTE	CPQFVQNINIENLFR	ELDIN	2	C1:+57.021	946.478093	1890.940586	0.000451244	17	N	41	56
P27005	Parental	CPQFV	QNINIENLFR	ELDIN	2		630.8389154	1259.662231	0.000451244	3	N	46	56
P27005	Parental	SDNAI	NFEEFLAMVIK	VGVAS	2		670.8501035	1339.684607	0.002145581	1	N	66	77
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLFRE	LDINS	3	C6:+57.021	861.4178098	2581.230029	0.001763695	3	N	36	57
P27005	Parental	KNDFK	KMVTTECPQFVQNINIENLF	RELDI	2	C7:+57.021	1213.098444	2424.181288	0.000662267	1	N	35	55
P27005	Parental	NDFKK	MVTTECPQFVQNINIENLFRELDINSDNAINF	EEFLA	3	C6:+57.021	1266.941949	3797.802447	0.002981883	1	N	36	68
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHAL	YKNDF	2		1247.117633	2492.219667	0.000637154	3	N	7	29
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHAL	YKNDF	3		831.747689	2492.219667	0.000622848	9	N	7	29
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHAL	YKNDF	4		624.0627167	2492.219667	0.001699387	2	N	7	29
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHA	LYKND	3		794.0530009	2379.135603	0.001839721	1	N	7	28
P27005	Parental	LIDVY	HNYSNIQGNHHALYK	NDFKK	3		599.2928036	1794.855011	0.000823681	2	N	16	31
P27005	Parental	SELEK	ALSNLIDVYHNYSNIQGNHHALYKN	DFKKM	3		966.8147621	2897.420886	0.000662267	4	N	7	32
P27005	Parental	SELEK	ALSNLIDVYHNYSN	IQGNH	2		811.894616	1621.773632	0.000637154	7	N	7	21
P27005	Parental	TECPQ	FVQNINIENLFR	ELDIN	2		753.9073294	1505.799059	0.000735798	3	N	44	56
P27005	Parental	LSNLI	DVYHNYSNIQGNHHALYK	NDFKK	3		725.0123655	2172.013697	0.000451244	3	N	13	31
P27005	Parental	SELEK	ALSNLIDVYHN	YSNIQ	2		629.8254737	1257.635347	0.001463592	1	N	7	18
P27005	Parental	EKALS	NLIDVYHNYSNIQGNHHALYK	NDFKK	3		838.4160508	2512.224752	0.000823681	3	N	10	31

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27005	Parental	ALSNL	IDVYHNYSNIQGNHHALYK	NDFKK	3		762.7070535	2285.097761	0.000622848	2	N	12	31
P27601	Exosome	GESVK	YFLDNLDKLGVPDYIPSQQDILLAR	RPTKG	3		969.5153192	2905.522557	0.000451244	2	N	175	200
P27601	Exosome	RQTNR	LTESLNIFETIVNNR	VFSNV	2		881.9708551	1761.92611	0.000451244	3	N	264	279
P27601	Parental	GESVK	YFLDNLDKLGVPDYIPSQQDILLAR	RPTKG	3		969.5153192	2905.522557	0.001463592	4	N	175	200
P27601	Parental	LPAIR	ALWEDSGIQNAYDR	RREFQ	2		819.3818728	1636.748146	0.001352548	2	N	150	164
P27601	Parental	RQTNR	LTESLNIFETIVNNR	VFSNV	2		881.9708551	1761.92611	0.000451244	1	N	264	279
P27612	Exosome	NIEGK	AQCLSVISTILEVVQDLEATFR	LLVAL	3	C3:+57.021	831.44072	2491.29876	0.000735798	1	N	721	743
P27612	Exosome	VLLEK	ILSLICNNSSEKPTAQQLQILWK	AINWP	3	C6:+57.021	895.4865522	2683.436257	0.000451244	10	N	578	601
P27612	Exosome	EATFR	LLVALGTLISDDSNAIQLAK	SLGVD	2		1028.088959	2054.162318	0.000451244	21	N	743	763
P27612	Exosome	AQTIR	LPAQSIWCCCVLENGDIVVGASDGIIR	VFTES	3	C8:+57.021,C9:+57.021,C10:+57.021	1001.489331	3001.444592	0.000451244	11	N	268	295
P27612	Exosome	QILWK	AINWPEDIVFPALDILR	LSIKH	2		991.5414476	1981.067295	0.000451244	18	N	601	618
P27612	Exosome	YFPKK	EALTFDQANPTQILGK	LKELN	2		873.4575805	1744.899561	0.000451244	8	N	538	554
P27612	Exosome	EDCVR	GLAILSETEFLSCANDASIRR	WQITG	3	C13:+57.021	775.0622429	2322.163329	0.000451244	5	N	195	216
P27612	Exosome	TIDSK	TGDLGDINAEQLPGR	EHLSE	2		778.3896978	1554.763796	0.001162105	1	N	325	340
P27612	Exosome	EDCVR	GLAILSETEFLSCANDASIR	RWQIT	2	C13:+57.021	1084.038909	2166.062218	0.000451244	2	N	195	215
P27612	Exosome	GPSYK	LPYNVSDDPWLVAYNFLQK	NDLNP	2		1141.578758	2281.141917	0.000622848	2	N	417	436
P27612	Exosome	TGGGR	YVPGTSGPSNTVQTADPFTGAGR	YMPGS	2		1140.548718	2279.081836	0.002519933	2	N	476	499
P27612	Exosome	ELDVR	GLVCCLYPPGAFVSVSR	DRTTR	2	C4:+57.021,C5:+57.021	941.4711908	1880.926782	0.001162105	3	N	22	39
P27612	Parental	QILWK	AINWPEDIVFPALDILR	LSIKH	2		991.5414476	1981.067295	0.001463592	1	N	601	618
P27659	Exosome	LDWAR	ERLEQQVPVNQVFGQDEMIDVIGVTK	GKGYK	3	M18:+15.995	996.5101568	2986.50707	0.00091018	1	N	198	224
P27659	Parental	DLSDK	SINPLGGFVHY	GEVTN	2		602.3120021	1202.608404	0.002212458	2	N	312	323
P27659	Parental	GKLIK	NNASTDYDLSDKSINPLGGFVHY	GEVTN	2		1264.090947	2526.166294	0.000451244	10	N	300	323
P27659	Parental	GKLIK	NNASTDYDLSDKSINPLGGFVHY	GEVTN	3		843.0632313	2526.166294	0.002374549	2	N	300	323
P27661	Exosome	RIIPR	HLQLAIRNDEELNK	LLGGV	2		846.9555393	1691.895479	0.000451244	159	Y	82	96
P27661	Exosome	RIIPR	HLQLAIRNDEELNK	LLGGV	3		564.9729596	1691.895479	0.000451244	991	Y	82	96
P27661	Exosome	RIIPR	HLQLAIRNDEELNK	LLGGV	4		423.9816697	1691.895479	0.000451244	66	Y	82	96
P27661	Exosome	SRSSR	AGLQFPVGR	VHRLL	2		472.7697731	943.5239462	0.000451244	1500	Y	21	30
P27661	Exosome	LEYLT	AEILELAGNAAR	DNKKT	2		614.3387483	1226.661897	0.000451244	66	Y	60	72
P27661	Exosome	LEYLT	AEILELAGNAAR	DNKKT	3		409.8950988	1226.661897	0.001463592	3	Y	60	72
P27661	Exosome	VLEYL	TAEILELAGNAAR	DNKKT	2		664.8625875	1327.709575	0.000451244	73	Y	59	72
P27661	Exosome	AVLEY	LTAEILELAGNAAR	DNKKT	2		721.4046196	1440.793639	0.000451244	693	Y	58	72
P27661	Exosome	AVLEY	LTAEILELAGNAAR	DNKKT	3		481.2723464	1440.793639	0.000451244	322	Y	58	72
P27661	Exosome	KLLGG	VTIAQGGVLPNIQAV	LLPKK	2		740.4306374	1478.845675	0.000451244	735	Y	100	115
P27661	Exosome	KLLGG	VTIAQGGVLPNIQAV	LLPKK	3		493.9563583	1478.845675	0.000451244	21	Y	100	115
P27661	Exosome	GVTIA	QGGVLPNIQAVLLPK	KSSAT	2		773.9699298	1545.92426	0.000451244	2	Y	104	119
P27661	Exosome	GVTIA	QGGVLPNIQAVLLPK	KSSAT	2	[0:-17.027	765.4564298	1528.89726	0.001943752	3	Y	104	119
P27661	Exosome	GGVTI	AQGGVLPNIQAVLLPK	KSSAT	2		809.4884867	1616.961373	0.000451244	33	Y	103	119
P27661	Exosome	LGGVT	IAQGGVLPNIQAVLLPK	KSSAT	2		866.0305187	1730.045437	0.000451244	24	Y	102	119
P27661	Exosome	LLGGV	TIAQGGVLPNIQAVLLPK	KSSAT	2		916.554358	1831.093116	0.000451244	20	Y	101	119
P27661	Exosome	LLGGV	TIAQGGVLPNIQAVLLPK	KSSAT	3		611.372172	1831.093116	0.000622848	2	Y	101	119
P27661	Exosome	KLLGG	VTIAQGGVLPNIQAVLLPK	KSSAT	2		966.088565	1930.16153	0.000451244	1015	Y	100	119
P27661	Exosome	KLLGG	VTIAQGGVLPNIQAVLLPK	KSSAT	3		644.3949767	1930.16153	0.000451244	301	Y	100	119
P27661	Exosome	QGGVL	PNIQAVLLPK	KSSAT	2		546.8429381	1091.670276	0.000451244	57	Y	109	119
P27661	Exosome	NKLLG	GVTIAQGGVLPNIQAVLLPK	KSSAT	2		994.5992969	1987.182994	0.000451244	143	N	99	119
P27661	Exosome	NKLLG	GVTIAQGGVLPNIQAVLLPK	KSSAT	3		663.4021313	1987.182994	0.000451244	73	N	99	119
P27661	Exosome	EELNK	LLGGVTIAQGGVLPNIQAV	LLPKK	2		910.5361652	1819.05673	0.000451244	110	N	96	115
P27661	Exosome	EELNK	LLGGVTIAQGGVLPNIQAV	LLPKK	3		607.3600435	1819.05673	0.000451244	22	N	96	115
P27661	Exosome	LAAVL	EYLTAEILELAGNAAR	DNKKT	2		867.4575805	1732.899561	0.000451244	127	Y	56	72
P27661	Exosome	LAAVL	EYLTAEILELAGNAAR	DNKKT	3		578.640987	1732.899561	0.000451244	83	Y	56	72
P27661	Exosome	LAAVL	EYLTAEILELAGNAAR	DNKKT	2	E1:-18.011	858.4520805	1714.888561	0.000451244	13	Y	56	72
P27661	Exosome	LAAVL	EYLTAEILELAGNAAR	DNKKT	3	E1:-18.011	572.6373203	1714.888561	0.000451244	14	Y	56	72
P27661	Exosome	LAAVL	EYLTAEILELAGNAAR	DNKKT	2	[0:-18.011	858.4520805	1714.888561	0.000998612	4	Y	56	72
P27661	Exosome	LAAVL	EYLTAEILELAGNAAR	DNKKT	3	[0:-18.011	572.6373203	1714.888561	0.001329271	6	Y	56	72
P27661	Exosome	EELNK	LLGGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1136.194093	2270.372586	0.000451244	88	N	96	119
P27661	Exosome	EELNK	LLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		757.7986619	2270.372586	0.000451244	51	N	96	119
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAV	LLPKK	2		1331.724671	2661.433742	0.000451244	220	N	89	115
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAV	LLPKK	3		888.1523808	2661.433742	0.000451244	109	N	89	115
P27661	Exosome	YLAAV	LEYLTAEILELAGNAAR	DNKKT	2		923.9996126	1845.983625	0.000451244	1105	Y	55	72
P27661	Exosome	YLAAV	LEYLTAEILELAGNAAR	DNKKT	3		616.335675	1845.983625	0.000451244	1302	Y	55	72
P27661	Exosome	HYAER	VGAGAPVYLAAVLEY	LTAEI	2		746.9064638	1491.797328	0.000451244	92	N	43	58
P27661	Exosome	HYAER	VGAGAPVYLAAVLEY	LTAEI	3		498.2735759	1491.797328	0.001943752	1	N	43	58
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		1038.590999	3112.749598	0.000451244	154	N	89	119
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	4		779.1951994	3112.749598	0.000451244	32	N	89	119
P27661	Exosome	VYLAA	VLEYLTAEILELAGNAAR	DNKKT	2		973.5338196	1945.052039	0.000451244	625	Y	54	72

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27661	Exosome	VYLAA	VLEYLTAEILELAGNAAR	DNKKT	3		649.3584797	1945.052039	0.000451244	910	Y	54	72
P27661	Exosome	YLTAE	ILELAGNAAR	DNKKT	2		514.2988947	1026.582189	0.000622848	2	Y	62	72
P27661	Exosome	PVYLA	AVLEYLTAEILELAGNAAR	DNKKT	2		1009.052376	2016.089153	0.000451244	342	Y	53	72
P27661	Exosome	PVYLA	AVLEYLTAEILELAGNAAR	DNKKT	3		673.0375177	2016.089153	0.000451244	299	Y	53	72
P27661	Exosome	APVYL	AAVLEYLTAEILELAGNAAR	DNKKT	2		1044.570933	2087.126267	0.000451244	349	Y	52	72
P27661	Exosome	APVYL	AAVLEYLTAEILELAGNAAR	DNKKT	3		696.7165556	2087.126267	0.000451244	563	Y	52	72
P27661	Exosome	GAPVY	LAAVLEYLTAEILELAGNAAR	DNKKT	2		1101.112965	2200.210331	0.000451244	205	N	51	72
P27661	Exosome	GAPVY	LAAVLEYLTAEILELAGNAAR	DNKKT	3		734.4112436	2200.210331	0.000451244	250	N	51	72
P27661	Exosome	AGAPV	YLAAVLEYLTAEILELAGNAAR	DNKKT	2		1182.64463	2363.27366	0.000451244	22	N	50	72
P27661	Exosome	AGAPV	YLAAVLEYLTAEILELAGNAAR	DNKKT	3		788.7656865	2363.27366	0.000451244	16	N	50	72
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAARDNK	KTRII	3		1091.589547	3271.745241	0.000451244	14	N	43	75
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAARDNK	KTRII	4		818.9441101	3271.745241	0.000998612	1	N	43	75
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1458.298003	2914.580407	0.000451244	404	N	43	72
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		972.5346022	2914.580407	0.000451244	777	N	43	72
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	4		729.6529017	2914.580407	0.000451244	315	N	43	72
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGN	AARDN	2		1309.210334	2616.405068	0.000451244	29	N	43	69
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGN	AARDN	3		873.1428226	2616.405068	0.000451244	33	N	43	69
P27661	Exosome	LNKLL	GGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1023.110029	2044.204458	0.000451244	17	N	98	119
P27661	Exosome	LNKLL	GGVTIAQGGVLPNIQAVLLPK	KSSAT	3		682.4092859	2044.204458	0.000622848	8	N	98	119
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYL	TAEIL	2		803.4484958	1604.881392	0.000451244	19	N	43	59
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLT	AEILE	2		853.9723351	1705.92907	0.000451244	28	N	43	60
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLT	AEILE	3		569.6508234	1705.92907	0.000451244	23	N	43	60
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEIL	ELAGN	2		1067.096253	2132.176905	0.000870037	7	N	43	64
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEIL	ELAGN	3		711.7334351	2132.176905	0.000451244	17	N	43	64
P27661	Exosome	AQGGV	LPNIQAVLLPK	KSSAT	2		603.3849702	1204.75434	0.001162105	1	Y	108	119
P27661	Exosome	EYLTA	EILELAGNAAR	DNKKT	2		578.8201913	1155.624783	0.000451244	37	Y	61	72
P27661	Exosome	AAVLE	YLTAEILELAGNAAR	DNKKT	2		802.9362839	1603.856968	0.000451244	70	Y	57	72
P27661	Exosome	EELNK	LLGGVTIAQGGVLPNIQ	AVLLP	2		825.4834013	1648.951203	0.000451244	14	N	96	113
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPN	IQAVL	2		1126.100586	2250.185573	0.000451244	23	N	89	111
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPN	IQAVL	3		751.0696576	2250.185573	0.000451244	10	N	89	111
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTA	EILEL	2		889.490892	1776.966184	0.000451244	17	N	43	61
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTA	EILEL	3		593.3298614	1776.966184	0.000451244	16	N	43	61
P27661	Exosome	ERVGA	GAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1344.734508	2687.453415	0.000823681	2	N	46	72
P27661	Exosome	ERVGA	GAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		896.825605	2687.453415	0.000451244	6	N	46	72
P27661	Exosome	AERVG	AGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1380.253064	2758.490529	0.000451244	7	N	45	72
P27661	Exosome	AERVG	AGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		920.504643	2758.490529	0.000451244	16	N	45	72
P27661	Exosome	VGAGA	PVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1280.705219	2559.394838	0.000451244	37	N	48	72
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILEL	AGNAA	2		1188.159581	2374.303563	0.000451244	15	N	43	66
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILEL	AGNAA	3		792.4423209	2374.303563	0.000451244	26	N	43	66
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAA	RDNKK	2		1380.247448	2758.479296	0.000451244	17	N	43	71
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAA	RDNKK	3		920.5008985	2758.479296	0.000451244	27	N	43	71
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELA	GNAAR	2		1223.678138	2445.340677	0.001162105	11	N	43	67
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELA	GNAAR	3		816.1213589	2445.340677	0.000622848	10	N	43	67
P27661	Exosome	YAERV	GAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		939.5117976	2815.511993	0.000451244	8	N	44	72
P27661	Exosome	EELNK	LLGGVTIAQGGVLPN	IQAVL	2		704.9120805	1407.808561	0.000662267	11	N	96	111
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQ	AVLLP	2		1246.671907	2491.328214	0.000451244	38	N	89	113
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQ	AVLLP	3		831.4505382	2491.328214	0.000451244	18	N	89	113
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAE	ILELA	3		636.3440591	1906.008777	0.000451244	3	N	43	62
P27661	Exosome	RVGAG	APVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		877.8184505	2630.431951	0.000662267	2	N	47	72
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNA	ARDNK	2		1344.728891	2687.442182	0.002374549	1	N	43	70
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNA	ARDNK	3		896.8218606	2687.442182	0.000451244	6	N	43	70
P27661	Exosome	GHYAE	RVGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		1024.568306	3070.681518	0.001871652	1	N	42	72
P27661	Exosome	QLAIR	NDEELNKLLGGV	TIAQG	2		650.8413208	1299.667042	0.000451244	3	N	89	101
P27661	Exosome	QLAIR	NDEELNKLLGGV	TIAQG	3		434.2301472	1299.667042	0.000451244	5	N	89	101
P27661	Exosome	HYAER	VGAGAPVYLAAV	LEYLT	2		544.3114708	1086.607342	0.002453667	1	N	43	55
P27661	Exosome	KLLGG	VTIAQGGVLPN	IQAVL	2		534.8065526	1067.597505	0.001329271	2	Y	100	111
P27661	Exosome	KLLGG	VTIAQGGVLPNIQA	VLLPK	2		690.8964304	1379.777261	0.000451244	189	Y	100	114
P27661	Exosome	VTIAQ	GGVLPNIQAVLLPK	KSSAT	2		709.9406409	1417.865682	0.001943752	1	Y	105	119
P27661	Exosome	HYAER	VGAGAPVYLAAVL	EYLTA	2		600.8535029	1199.691406	0.001943752	1	N	43	56
P27661	Exosome	EELNK	LLGGVTIAQGGVLPNIQA	VLLPK	2		861.0019582	1719.988316	0.000622848	18	N	96	114
P27661	Exosome	EELNK	LLGGVTIAQGGVLPNIQA	VLLPK	3		574.3372388	1719.988316	0.001871652	1	N	96	114
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQA	VLLPK	2		1282.190464	2562.365328	0.000451244	38	N	89	114
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQA	VLLPK	3		855.1295761	2562.365328	0.000451244	21	N	89	114
P27661	Exosome	KLLGG	VTIAQGGVLPNIQ	AVLLP	2		655.3778735	1308.740147	0.000622848	27	Y	100	113
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILE	LAGNA	3		754.7476329	2261.219499	0.001591523	1	N	43	65

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27661	Exosome	QLAIR	NDEELNKLLGGVTIAQ	GGVLP	2		857.4550378	1712.894476	0.0007646	2	N	89	105
P27661	Exosome	HYAER	VGAGAPVYLAAVLEYLTAEILELAG	NAARD	3		835.1285135	2502.36214	0.000451244	1	N	43	68
P27661	Exosome	KLLGG	VTIAQGGVLPNIQAVLL	PKKSS	2		853.5147015	1705.013803	0.001699387	1	Y	100	117
P27661	Parental	RIIPR	HLQLAIRNDEELNK	LLGGV	2		846.9555393	1691.895479	0.000451244	25	Y	82	96
P27661	Parental	RIIPR	HLQLAIRNDEELNK	LLGGV	3		564.9729596	1691.895479	0.000451244	98	Y	82	96
P27661	Parental	RIIPR	HLQLAIRNDEELNK	LLGGV	4		423.9816697	1691.895479	0.000451244	5	Y	82	96
P27661	Parental	SRSSR	AGLQFPVGR	VHRLL	2		472.7697731	943.5239462	0.000451244	455	Y	21	30
P27661	Parental	LEYLT	AEILELAGNAAR	DNKKT	2		614.3387483	1226.661897	0.000451244	149	Y	60	72
P27661	Parental	LEYLT	AEILELAGNAAR	DNKKT	3		409.8950988	1226.661897	0.000662267	10	Y	60	72
P27661	Parental	VLEYL	TAEILELAGNAAR	DNKKT	2		664.8625875	1327.709575	0.000451244	59	Y	59	72
P27661	Parental	AVLEY	LTAEILELAGNAAR	DNKKT	2		721.4046196	1440.793639	0.000451244	1756	Y	58	72
P27661	Parental	AVLEY	LTAEILELAGNAAR	DNKKT	3		481.2723464	1440.793639	0.000451244	1299	Y	58	72
P27661	Parental	KLLGG	VTIAQGGVLPNIQAVLLPKK	SSATV	2		1030.136047	2058.256493	0.000451244	1	Y	100	120
P27661	Parental	KLLGG	VTIAQGGVLPNIQAVLLPKK	SSATV	3		687.0932977	2058.256493	0.000451244	9	Y	100	120
P27661	Parental	KLLGG	VTIAQGGVLPNIQAV	LLPKK	2		740.4306374	1478.845675	0.000451244	213	Y	100	115
P27661	Parental	KLLGG	VTIAQGGVLPNIQAV	LLPKK	3		493.9563583	1478.845675	0.001329271	3	Y	100	115
P27661	Parental	GVTIA	QGGVLPNIQAVLLPK	KSSAT	2		773.9699298	1545.92426	0.000451244	60	Y	104	119
P27661	Parental	GVTIA	QGGVLPNIQAVLLPK	KSSAT	3		516.3158865	1545.92426	0.000451244	10	Y	104	119
P27661	Parental	GVTIA	QGGVLPNIQAVLLPK	KSSAT	2	[0:-17.027	765.4564298	1528.89726	0.00091018	14	Y	104	119
P27661	Parental	GGVTI	AQGGVLPNIQAVLLPK	KSSAT	2		809.4884867	1616.961373	0.000451244	325	Y	103	119
P27661	Parental	GGVTI	AQGGVLPNIQAVLLPK	KSSAT	3		539.9949245	1616.961373	0.000451244	19	Y	103	119
P27661	Parental	LGGVT	IAQGGVLPNIQAVLLPK	KSSAT	2		866.0305187	1730.045437	0.000451244	62	Y	102	119
P27661	Parental	LGGVT	IAQGGVLPNIQAVLLPK	KSSAT	3		577.6896125	1730.045437	0.000451244	21	Y	102	119
P27661	Parental	LLGGV	TIAQGGVLPNIQAVLLPK	KSSAT	2		916.554358	1831.093116	0.000451244	480	Y	101	119
P27661	Parental	LLGGV	TIAQGGVLPNIQAVLLPK	KSSAT	3		611.372172	1831.093116	0.000451244	56	Y	101	119
P27661	Parental	KLLGG	VTIAQGGVLPNIQAVLLPK	KSSAT	2		966.088565	1930.16153	0.000451244	1497	Y	100	119
P27661	Parental	KLLGG	VTIAQGGVLPNIQAVLLPK	KSSAT	3		644.3949767	1930.16153	0.000451244	991	Y	100	119
P27661	Parental	KLLGG	VTIAQGGVLPNIQAVLLPK	KSSAT	4		483.5481825	1930.16153	0.001162105	1	Y	100	119
P27661	Parental	EELNK	LLGGVTIAQGGVLPNIQAVLLPKK	SSATV	3		800.496983	2398.467549	0.002374549	1	N	96	120
P27661	Parental	QGGVL	PNIQAVLLPK	KSSAT	2		546.8429381	1091.670276	0.000451244	135	Y	109	119
P27661	Parental	NKLLG	GVTIAQGGVLPNIQAVLLPK	KSSAT	2		994.5992969	1987.182994	0.000451244	619	N	99	119
P27661	Parental	NKLLG	GVTIAQGGVLPNIQAVLLPK	KSSAT	3		663.4021313	1987.182994	0.000451244	154	N	99	119
P27661	Parental	EELNK	LLGGVTIAQGGVLPNIQAV	LLPKK	2		910.5361652	1819.05673	0.000451244	61	N	96	115
P27661	Parental	EELNK	LLGGVTIAQGGVLPNIQAV	LLPKK	3		607.3600435	1819.05673	0.000622848	5	N	96	115
P27661	Parental	LAAVL	EYLTAEILELAGNAAR	DNKKT	2		867.4575805	1732.899561	0.000451244	60	Y	56	72
P27661	Parental	LAAVL	EYLTAEILELAGNAAR	DNKKT	3		578.640987	1732.899561	0.000451244	106	Y	56	72
P27661	Parental	LAAVL	EYLTAEILELAGNAAR	DNKKT	3	E1:-18.011	572.6373203	1714.888561	0.000451244	29	Y	56	72
P27661	Parental	LAAVL	EYLTAEILELAGNAAR	DNKKT	3	[0:-18.011	572.6373203	1714.888561	0.000870037	6	Y	56	72
P27661	Parental	EELNK	LLGGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1136.194093	2270.372586	0.000451244	173	N	96	119
P27661	Parental	EELNK	LLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		757.7986619	2270.372586	0.000451244	77	N	96	119
P27661	Parental	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAV	LLPKK	2		1331.724671	2661.433742	0.000451244	33	N	89	115
P27661	Parental	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAV	LLPKK	3		888.1523808	2661.433742	0.000451244	23	N	89	115
P27661	Parental	YLAAV	LEYLTAEILELAGNAAR	DNKKT	2		923.9996126	1845.983625	0.000451244	127	Y	55	72
P27661	Parental	YLAAV	LEYLTAEILELAGNAAR	DNKKT	3		616.335675	1845.983625	0.000451244	230	Y	55	72
P27661	Parental	HYAER	VGAGAPVYLAAVLEY	LTAEI	2		746.9064638	1491.797328	0.000451244	60	N	43	58
P27661	Parental	HYAER	VGAGAPVYLAAVLEY	LTAEI	3		498.2735759	1491.797328	0.000451244	2	N	43	58
P27661	Parental	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		1038.590999	3112.749598	0.000451244	141	N	89	119
P27661	Parental	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	4		779.1951994	3112.749598	0.000451244	18	N	89	119
P27661	Parental	VYLAA	VLEYLTAEILELAGNAAR	DNKKT	2		973.5338196	1945.052039	0.000451244	63	Y	54	72
P27661	Parental	VYLAA	VLEYLTAEILELAGNAAR	DNKKT	3		649.3584797	1945.052039	0.000451244	120	Y	54	72
P27661	Parental	YLTAE	ILELAGNAAR	DNKKT	2		514.2988947	1026.582189	0.000622848	1	Y	62	72
P27661	Parental	PVYLA	AVLEYLTAEILELAGNAAR	DNKKT	2		1009.052376	2016.089153	0.000451244	52	Y	53	72
P27661	Parental	PVYLA	AVLEYLTAEILELAGNAAR	DNKKT	3		673.0375177	2016.089153	0.000451244	71	Y	53	72
P27661	Parental	APVYL	AAVLEYLTAEILELAGNAAR	DNKKT	2		1044.570933	2087.126267	0.000451244	817	Y	52	72
P27661	Parental	APVYL	AAVLEYLTAEILELAGNAAR	DNKKT	3		696.7165556	2087.126267	0.000451244	954	Y	52	72
P27661	Parental	GAPVY	LAAVLEYLTAEILELAGNAAR	DNKKT	2		1101.112965	2200.210331	0.000451244	354	N	51	72
P27661	Parental	GAPVY	LAAVLEYLTAEILELAGNAAR	DNKKT	3		734.4112436	2200.210331	0.000451244	605	N	51	72
P27661	Parental	AGAPV	YLAAVLEYLTAEILELAGNAAR	DNKKT	2		1182.64463	2363.27366	0.001162105	1	N	50	72
P27661	Parental	AGAPV	YLAAVLEYLTAEILELAGNAAR	DNKKT	3		788.7656865	2363.27366	0.000451244	3	N	50	72
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAARDNK	KTRII	3		1091.589547	3271.745241	0.0007646	1	N	43	75
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	2		1458.298003	2914.580407	0.000451244	42	N	43	72
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	3		972.5346022	2914.580407	0.000451244	298	N	43	72
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEILELAGNAAR	DNKKT	4		729.6529017	2914.580407	0.000451244	62	N	43	72
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEILELAGN	AARDN	2		1309.210334	2616.405068	0.000451244	6	N	43	69
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEILELAGN	AARDN	3		873.1428226	2616.405068	0.000451244	3	N	43	69

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27661	Parental	LAIRN	DEELNKLLGGVTIAQGGVLPNIQAVLLPK	KSSAT	3		1000.57669	2998.70667	0.000451244	10	N	90	119
P27661	Parental	LNKLL	GGVTIAQGGVLPNIQAVLLPK	KSSAT	2		1023.110029	2044.204458	0.000622848	12	N	98	119
P27661	Parental	HYAER	VGAGAPVYLAAVLEYL	TAEIL	2		803.4484958	1604.881392	0.001699387	1	N	43	59
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLT	AEILE	2		853.9723351	1705.92907	0.000451244	18	N	43	60
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLT	AEILE	3		569.6508234	1705.92907	0.000451244	6	N	43	60
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEIL	ELAGN	2		1067.096253	2132.176905	0.000823681	1	N	43	64
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEIL	ELAGN	3		711.7334351	2132.176905	0.000662267	1	N	43	64
P27661	Parental	AQGGV	LPNIQAVLLPK	KSSAT	2		603.3849702	1204.75434	0.000823681	10	Y	108	119
P27661	Parental	EYLTA	EILELAGNAAR	DNKKT	2		578.8201913	1155.624783	0.000451244	6	Y	61	72
P27661	Parental	AAVLE	YLTAEILELAGNAAR	DNKKT	2		802.9362839	1603.856968	0.001395409	1	Y	57	72
P27661	Parental	QLAIR	NDEELNKLLGGVTIAQGGVLPN	IQAVL	2		1126.100586	2250.185573	0.000622848	11	N	89	111
P27661	Parental	HYAER	VGAGAPVYLAAVLEYLTAEILEL	AGNAA	3		792.4423209	2374.303563	0.002212458	1	N	43	66
P27661	Parental	EELNK	LLGGVTIAQGGVLPN	IQAVL	2		704.9120805	1407.808561	0.00091018	4	N	96	111
P27661	Parental	QLAIR	NDEELNKLLGGV	TIAQG	2		650.8413208	1299.667042	0.000451244	4	N	89	101
P27661	Parental	KLLGG	VTIAQGGVLPN	IQAVL	2		534.8065526	1067.597505	0.002453667	3	Y	100	111
P27661	Parental	KLLGG	VTIAQGGVLPNIQA	VLLPK	2		690.8964304	1379.777261	0.000451244	19	Y	100	114
P27661	Parental	VTIAQ	GGVLPNIQAVLLPK	KSSAT	2		709.9406409	1417.865682	0.001162105	1	Y	105	119
P27661	Parental	EELNK	LLGGVTIAQGGVLPNIQA	VLLPK	2		861.0019582	1719.988316	0.00091018	3	N	96	114
P27661	Parental	QLAIR	NDEELNKLLGGVTIAQGGVLPNIQA	VLLPK	2		1282.190464	2562.365328	0.000622848	6	N	89	114
P27773	Exosome	YPTLK	IFRDGEEAGAYDGPR	TADGI	2		826.8873223	1651.759045	0.000451244	29	N	104	119
P27773	Exosome	YPTLK	IFRDGEEAGAYDGPR	TADGI	3		551.5941482	1651.759045	0.000451244	20	N	104	119
P27773	Exosome	NTCNK	YGVSGYPTLK	IFRDG	2		542.7878285	1083.560057	0.000451244	36	N	94	104
P27773	Exosome	IVIAK	MDATANDVPSPYEVK	GFPTI	2		818.8803176	1635.745035	0.000451244	12	N	433	448
P27773	Exosome	VGFFR	DLFSDGHSEFLK	AASNL	2		697.8334957	1393.651391	0.000451244	2	N	161	173
P27773	Exosome	RLAAA	SDVLELTDENFESR	VSDTG	2		827.3842782	1652.752956	0.000451244	31	N	24	38
P27773	Exosome	EEFKK	FISDKDASVVGFFR	DLFSD	2		794.4124446	1586.809289	0.000451244	22	N	147	161
P27773	Exosome	EEFKK	FISDKDASVVGFFR	DLFSD	3		529.9442298	1586.809289	0.000451244	9	N	147	161
P27773	Exosome	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1360.201029	2718.386458	0.000451244	24	N	304	329
P27773	Exosome	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	3		907.1366193	2718.386458	0.000662267	2	N	304	329
P27773	Exosome	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	4		680.6044144	2718.386458	0.001395409	3	N	304	329
P27773	Exosome	GKIKK	FIQDSIFGLCPHMTEDNKDLIQGK	DLLTA	3	C10:+57.021	936.123174	2805.346122	0.000451244	3	N	234	258
P27773	Exosome	GKIKK	FIQDSIFGLCPHMTEDNKDLIQGK	DLLTA	4	C10:+57.021	702.3443305	2805.346122	0.000451244	8	N	234	258
P27773	Exosome	LIQGK	DLLTAYYDVDYEK	NAKGS	2		804.3779331	1606.740266	0.000451244	47	N	258	271
P27773	Exosome	VASRK	TFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1296.153547	2590.291495	0.000451244	42	N	305	329
P27773	Exosome	VASRK	TFSHELSDFGLESTTGEVPVVAIR	TAKGE	3		864.4382982	2590.291495	0.000451244	38	N	305	329
P27773	Exosome	YEGGR	ELNDFISYLQR	EATNP	2		699.357138	1396.698676	0.000451244	25	N	471	482
P27773	Exosome	SRDGK	ALEQFLQEYFDGNLKR	YLKSE	2		986.0026866	1969.989773	0.000451244	30	N	347	363
P27773	Exosome	SRDGK	ALEQFLQEYFDGNLKR	YLKSE	3		657.6710577	1969.989773	0.000451244	54	N	347	363
P27773	Exosome	SRDGK	ALEQFLQEYFDGNLK	RYLKS	2		907.952131	1813.888662	0.000451244	19	N	347	362
P27773	Exosome	SRDGK	ALEQFLQEYFDGNLK	RYLKS	3		605.637354	1813.888662	0.000451244	24	N	347	362
P27773	Exosome	PYEVK	GFPTIYFSPANK	KLTPK	2		671.346042	1340.676484	0.002453667	3	N	448	460
P27773	Exosome	SYLQR	EATNPPIIQEEKPK	KKKKA	2		797.4282917	1592.840983	0.000622848	4	N	482	496
P27773	Exosome	SYLQR	EATNPPIIQEEKPK	KKKKA	3		531.9547945	1592.840983	0.000622848	1	N	482	496
P27773	Exosome	RDNYR	FAHTNIESLVK	EYDDN	2		629.8436665	1257.671733	0.000662267	1	N	183	194
P27773	Exosome	RDNYR	FAHTNIESLVK	EYDDN	3		420.231711	1257.671733	0.00091018	16	N	183	194
P27773	Exosome	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	2		1151.577278	2301.138957	0.000823681	2	N	194	214
P27773	Exosome	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	3		768.054119	2301.138957	0.000451244	21	N	194	214
P27773	Exosome	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	4		576.2925392	2301.138957	0.000622848	2	N	194	214
P27773	Exosome	ESLVK	EYDDNGEGITIFRPLHLANKFEDK	TVAYT	3		941.1317568	2820.37187	0.000451244	25	N	194	218
P27773	Exosome	ESLVK	EYDDNGEGITIFRPLHLANKFEDK	TVAYT	4		706.1007676	2820.37187	0.000451244	18	N	194	218
P27773	Exosome	ELGEK	LSKDPNIVIAK	MDATA	3		399.9120898	1196.712869	0.000622848	1	N	422	433
P27773	Exosome	GHCKR	LAPEYEAAATR	LKGIV	2		596.3043741	1190.593148	0.002453667	1	N	62	73
P27773	Exosome	FISDK	DASVVGFFR	DLFSD	2		499.2592382	996.5028764	0.001871652	6	N	152	161
P27773	Exosome	KRYLK	SEPIPESNEGPVK	VVVAE	2		691.8440605	1381.672521	0.000451244	3	N	366	379
P27773	Exosome	GNLKR	YLKSEPIPESNEGPVK	VVVAE	2		893.9652384	1785.914877	0.001162105	3	N	363	379
P27773	Parental	YPTLK	IFRDGEEAGAYDGPR	TADGI	2		826.8873223	1651.759045	0.000451244	43	N	104	119
P27773	Parental	YPTLK	IFRDGEEAGAYDGPR	TADGI	3		551.5941482	1651.759045	0.000451244	45	N	104	119
P27773	Parental	VPLAK	VDCTANTNTCNKYGVSGYPTLK	IFRDG	2	C3:+57.021,C10:+57.021	1232.06764	2462.119681	0.000451244	9	N	82	104
P27773	Parental	VPLAK	VDCTANTNTCNKYGVSGYPTLK	IFRDG	3	C3:+57.021,C10:+57.021	821.7143603	2462.119681	0.000451244	16	N	82	104
P27773	Parental	NTCNK	YGVSGYPTLK	IFRDG	2		542.7878285	1083.560057	0.000451244	24	N	94	104
P27773	Parental	IVIAK	MDATANDVPSPYEVK	GFPTI	2		818.8803176	1635.745035	0.000451244	5	N	433	448
P27773	Parental	VGFFR	DLFSDGHSEFLK	AASNL	2		697.8334957	1393.651391	0.000451244	5	N	161	173
P27773	Parental	VGFFR	DLFSDGHSEFLK	AASNL	3		465.5582638	1393.651391	0.00091018	3	N	161	173
P27773	Parental	RLAAA	SDVLELTDENFESR	VSDTG	2		827.3842782	1652.752956	0.000451244	41	N	24	38
P27773	Parental	EEFKK	FISDKDASVVGFFR	DLFSD	2		794.4124446	1586.809289	0.000451244	21	N	147	161

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27773	Parental	EEFKK	FISDKDASVVGFFR	DLFSD	3		529.9442298	1586.809289	0.000622848	5	N	147	161
P27773	Parental	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1360.201029	2718.386458	0.000451244	27	N	304	329
P27773	Parental	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	3		907.1366193	2718.386458	0.000451244	27	N	304	329
P27773	Parental	AVASR	KTFSHELSDFGLESTTGEVPVVAIR	TAKGE	4		680.6044144	2718.386458	0.000622848	2	N	304	329
P27773	Parental	GKIKK	FIQDSIFGLCPHMTEDNKDLIQGK	DLLTA	3	C10:+57.021	936.123174	2805.346122	0.000451244	1	N	234	258
P27773	Parental	GKIKK	FIQDSIFGLCPHMTEDNKDLIQGK	DLLTA	4	C10:+57.021	702.3443305	2805.346122	0.000451244	1	N	234	258
P27773	Parental	LIQGK	DLLTAYYDVDYEK	NAKGS	2		804.3779331	1606.740266	0.000451244	37	N	258	271
P27773	Parental	VASRK	TFSHELSDFGLESTTGEVPVVAIR	TAKGE	2		1296.153547	2590.291495	0.000451244	44	N	305	329
P27773	Parental	VASRK	TFSHELSDFGLESTTGEVPVVAIR	TAKGE	3		864.4382982	2590.291495	0.000451244	54	N	305	329
P27773	Parental	YEGGR	ELNDFISYLQR	EATNP	2		699.357138	1396.698676	0.000451244	20	N	471	482
P27773	Parental	SRDGK	ALEQFLQEYFDGNLKR	YLKSE	2		986.0026866	1969.989773	0.000451244	30	N	347	363
P27773	Parental	SRDGK	ALEQFLQEYFDGNLKR	YLKSE	3		657.6710577	1969.989773	0.000451244	55	N	347	363
P27773	Parental	SRDGK	ALEQFLQEYFDGNLK	RYLKS	2		907.952131	1813.888662	0.000451244	24	N	347	362
P27773	Parental	SRDGK	ALEQFLQEYFDGNLK	RYLKS	3		605.637354	1813.888662	0.000451244	22	N	347	362
P27773	Parental	PYEVK	GFPTIYFSPANKK	LTPKK	2		735.3935235	1468.771447	0.001654178	3	N	448	461
P27773	Parental	PYEVK	GFPTIYFSPANK	KLTPK	2		671.346042	1340.676484	0.001839721	2	N	448	460
P27773	Parental	SYLQR	EATNPPIIQEEKPK	KKKKA	2		797.4282917	1592.840983	0.000451244	14	N	482	496
P27773	Parental	SYLQR	EATNPPIIQEEKPK	KKKKA	3		531.9547945	1592.840983	0.000451244	11	N	482	496
P27773	Parental	RDNYR	FAHTNIESLVK	EYDDN	2		629.8436665	1257.671733	0.000451244	7	N	183	194
P27773	Parental	RDNYR	FAHTNIESLVK	EYDDN	3		420.231711	1257.671733	0.000451244	10	N	183	194
P27773	Parental	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	2		1151.577278	2301.138957	0.000451244	4	N	194	214
P27773	Parental	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	3		768.054119	2301.138957	0.000451244	13	N	194	214
P27773	Parental	ESLVK	EYDDNGEGITIFRPLHLANK	FEDKT	4		576.2925392	2301.138957	0.000451244	7	N	194	214
P27773	Parental	ESLVK	EYDDNGEGITIFRPLHLANKFEDK	TVAYT	3		941.1317568	2820.37187	0.000451244	28	N	194	218
P27773	Parental	ESLVK	EYDDNGEGITIFRPLHLANKFEDK	TVAYT	4		706.1007676	2820.37187	0.000622848	9	N	194	218
P27773	Parental	ELGEK	LSKDPNIVIAK	MDATA	3		399.9120898	1196.712869	0.002296037	1	N	422	433
P27773	Parental	KRYLK	SEPIPESNEGPVK	VVVAE	2		691.8440605	1381.672521	0.000622848	15	N	366	379
P27773	Parental	VVGFF	RDLFSDGHSEFLK	AASNL	3		517.5919675	1549.752503	0.000622848	8	N	160	173
P27773	Parental	GNLKR	YLKSEPIPESNEGPVK	VVVAE	2		893.9652384	1785.914877	0.002374549	1	N	363	379
P27773	Parental	ASRKT	FSHELSDFGLESTTGEVPVVAIR	TAKGE	3		830.7557387	2489.243816	0.000451244	7	N	306	329
P27773	Parental	EEFKK	FISDKDASVVGFF	RDLFS	2		716.3618891	1430.708178	0.001329271	2	N	147	160
P27773	Parental	GKIKK	FIQDSIFGLCPH	MTEDN	2	C10:+57.021	717.3480274	1432.680455	0.001871652	1	N	234	246
P27784	Exosome	IPCKR	FIYYFPTSGGCIKPGIIF	ISRRG	2	C11:+57.021	1040.534545	2079.053491	0.001329271	2	N	62	80
P27784	Exosome	KEDRR	YNPPIIHQGFQDTSSDCCFSYATQIPCK	RFIYY	3	C17:+57.021,C18:+57.021,C27:+57.021	1112.158309	3333.451528	0.000451244	1	N	33	61
P27784	Parental	IPCKR	FIYYFPTSGGCIKPGIIF	ISRRG	2	C11:+57.021	1040.534545	2079.053491	0.000451244	3	N	62	80
P27870	Exosome	KKAFR	GLLELVEFYQQNSLKDCFK	SLDTT	3	C17:+57.021	777.7282012	2330.161204	0.000451244	4	N	736	755
P27870	Exosome	FGLKR	SELFEAFDLFDVQDFGK	VIYTL	2		1003.97326	2005.930921	0.000451244	12	N	90	107
P27870	Exosome	QDFGK	VIYTLSALSWTPIAQNK	GIMPF	2		953.028173	1904.040746	0.001264573	4	N	107	124
P27870	Exosome	AQALR	DGVLLCQLLNNLLPQAINLR	EVNLR	2	C6:+57.021	1139.141303	2276.267006	0.002019181	1	N	38	58
P27870	Exosome	AQALR	DGVLLCQLLNNLLPQAINLR	EVNLR	3	C6:+57.021	759.7634687	2276.267006	0.000622848	7	N	38	58
P27870	Exosome	WWEGR	NTATNEVGWFPCNR	VHPYV	2	C12:+57.021	833.3758362	1664.736072	0.000451244	8	N	640	654
P27870	Exosome	EIYGR	IGWFPSNYVEEDYSEYC	-	2	C17:+57.021	1079.441236	2156.866872	0.001162105	3	N	828	845
P27870	Exosome	NETLR	QITNFQLSIENLDQSLANYGRPK	IDGEL	3		883.7930754	2648.355826	0.000451244	10	N	381	404
P27870	Exosome	NETLR	QITNFQLSIENLDQSLANYGRPK	IDGEL	3	[0:-17.027	878.1174088	2631.328826	0.00091018	1	N	381	404
P27870	Exosome	LKELK	DALAGPGATTLYQVFIK	YKERF	2		882.9806915	1763.945783	0.000870037	1	N	255	272
P27870	Exosome	KKAFR	GLLELVEFYQQNSLK	DCFKS	2		890.9781488	1779.940698	0.000451244	4	N	736	751
P27870	Parental	KKAFR	GLLELVEFYQQNSLKDCFK	SLDTT	3	C17:+57.021	777.7282012	2330.161204	0.000622848	8	N	736	755
P27870	Parental	FGLKR	SELFEAFDLFDVQDFGK	VIYTL	2		1003.97326	2005.930921	0.000451244	28	N	90	107
P27870	Parental	KFGLK	RSELFEAFDLFDVQDFGK	VIYTL	3		721.685144	2162.032032	0.002145581	1	N	89	107
P27870	Parental	AQALR	DGVLLCQLLNNLLPQAINLR	EVNLR	2	C6:+57.021	1139.141303	2276.267006	0.000451244	9	N	38	58
P27870	Parental	AQALR	DGVLLCQLLNNLLPQAINLR	EVNLR	3	C6:+57.021	759.7634687	2276.267006	0.000622848	5	N	38	58
P27870	Parental	WWEGR	NTATNEVGWFPCNR	VHPYV	2	C12:+57.021	833.3758362	1664.736072	0.000451244	18	N	640	654
P27870	Parental	EIYGR	IGWFPSNYVEEDYSEYC	-	2	C17:+57.021	1079.441236	2156.866872	0.000451244	3	N	828	845
P27870	Parental	NETLR	QITNFQLSIENLDQSLANYGRPK	IDGEL	2		1325.185713	2648.355826	0.000451244	1	N	381	404
P27870	Parental	NETLR	QITNFQLSIENLDQSLANYGRPK	IDGEL	3		883.7930754	2648.355826	0.000823681	11	N	381	404
P27870	Parental	KKAFR	GLLELVEFYQQNSLK	DCFKS	2		890.9781488	1779.940698	0.001763695	1	N	736	751
P27931	Exosome	NIELR	VKGTTTEPIPVIISPLETIPASLGSR	LIVPC	3		892.8447767	2675.51093	0.000451244	15	N	239	265
P27931	Exosome	ELRVK	GTTTEPIPVIISPLETIPASLGSR	LIVPC	2		1225.181576	2448.347553	0.000451244	17	N	241	265
P27931	Exosome	ELRVK	GTTTEPIPVIISPLETIPASLGSR	LIVPC	3		817.123651	2448.347553	0.002453667	1	N	241	265
P27931	Exosome	RMWVK	GNILWILPAVQQDSGTYICTFR	NASHC	2	C19:+57.021	1276.652232	2551.288864	0.000451244	15	N	101	123
P27931	Exosome	RMWVK	GNILWILPAVQQDSGTYICTFR	NASHC	3	C19:+57.021	851.4374213	2551.288864	0.000451244	13	N	101	123
P27931	Exosome	PVVLR	CPLAPHSDISSSSHSFLTWSK	LDSSQ	3	C1:+57.021	782.0394383	2343.094915	0.000451244	7	N	63	84
P27931	Exosome	LKVFK	NTEASLPHVSYLQISALSTTGLLVCPDLKEFISSNADGK	IQWYK	4	C25:+57.021	1044.785094	4175.109176	0.000451244	2	N	139	178
P27931	Parental	NIELR	VKGTTTEPIPVIISPLETIPASLGSR	LIVPC	3		892.8447767	2675.51093	0.002519933	1	N	239	265

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P27931	Parental	RMWVK	GNILWILPAVQQDSGTYICTFR	NASHC	2	C19:+57.021	1276.652232	2551.288864	0.000451244	9	N	101	123
P27931	Parental	RMWVK	GNILWILPAVQQDSGTYICTFR	NASHC	3	C19:+57.021	851.4374213	2551.288864	0.000451244	3	N	101	123
P28063	Exosome	AVDSR	ATAGSYISSLR	MNKVI	2		563.2990917	1124.582583	0.000637154	8	N	91	102
P28063	Exosome	CGWDK	KGPGLYYVDDNGTR	LSGQM	2		777.8815086	1553.747417	0.000451244	3	N	178	192
P28063	Exosome	CGWDK	KGPGLYYVDDNGTR	LSGQM	3		518.9236058	1553.747417	0.000823681	2	N	178	192
P28063	Exosome	DGWVK	VESSDVSDLLYK	YGEAA	2		677.8409865	1353.666373	0.000451244	30	N	258	270
P28063	Exosome	DSGYR	QDLSPEEAYDLGRR	AIAYA	2		824.9004297	1647.785259	0.002145581	1	N	216	230
P28063	Exosome	MYHMK	EDGWVKVESSDVSDLLYK	YGEAA	2		1035.007832	2068.000063	0.0007646	3	N	252	270
P28076	Exosome	LAMNR	DGSSGGVIYLVTITAAGVDHR	VILGD	3		696.6960431	2087.064729	0.000451244	3	N	185	206
P28076	Exosome	NISYK	YREDLLAHLIVAGWDQR	EGGQV	3		685.6977183	2054.069755	0.000451244	30	N	109	126
P28076	Exosome	NISYK	YREDLLAHLIVAGWDQR	EGGQV	4		514.5252387	2054.069755	0.000451244	9	N	109	126
P28076	Parental	LAMNR	DGSSGGVIYLVTITAAGVDHR	VILGD	3		696.6960431	2087.064729	0.000451244	3	N	185	206
P28271	Exosome	VGMFR	DFNDTSQDPDFTQVVELDLK	TVVPC	2		1163.540224	2325.064849	0.000451244	3	N	344	364
P28271	Exosome	LQPPK	SIVDAYVLLNLGDSVTTDHISPAGNIAR	NSPAA	3		971.1773661	2910.508698	0.000622848	3	N	660	688
P28293	Exosome	MCANR	FQFYNSQTQICVGNPR	ERKSA	2	C11:+57.021	979.9628071	1957.910014	0.000451244	55	N	175	191
P28293	Exosome	MCANR	FQFYNSQTQICVGNPR	ERKSA	3	C11:+57.021	653.6444714	1957.910014	0.000979378	1	N	175	191
P28293	Exosome	PRERK	SAFRGDSGGPLVCSNVAQGIVSY	GSNNG	2	C13:+57.021	1171.065989	2340.116379	0.002813207	1	N	194	217
P28293	Exosome	PRERK	SAFRGDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C13:+57.021	1208.921876	3623.742229	0.000451244	27	N	194	230
P28293	Exosome	PYMAF	LLIQSPEGLSACGGFLVR	EDFVL	2	C12:+57.021	959.0170511	1916.018502	0.000451244	20	N	37	55
P28293	Exosome	PYMAF	LLIQSPEGLSACGGFLVR	EDFVL	3	C12:+57.021	639.680634	1916.018502	0.000451244	7	N	37	55
P28293	Exosome	HSYPY	MAFLLIQSPEGLSACGGFLVR	EDFVL	2	C15:+57.021	1133.590058	2265.164516	0.000451244	3	N	34	55
P28293	Exosome	QASKK	LQPGDLCTVAGWGR	VSQSR	2	C7:+57.021	765.3803902	1528.74518	0.000451244	13	N	135	149
P28293	Exosome	PQASK	KLQPGDLCTVAGWGR	VSQSR	2	C8:+57.021	829.4278718	1656.840144	0.000451244	9	N	134	149
P28293	Exosome	PQASK	KLQPGDLCTVAGWGR	VSQSR	3	C8:+57.021	553.2878479	1656.840144	0.000451244	12	N	134	149
P28293	Exosome	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C9:+57.021	1055.175654	3162.503561	0.000451244	16	N	198	230
P28293	Exosome	ITVLR	AIRHPDYNPQNIR	NDIML	3		531.9468562	1592.817169	0.000451244	3	N	93	106
P28293	Exosome	PQNIR	NDIMLLQLR	RRARR	2		558.3162308	1114.616862	0.000998612	2	N	106	115
P28293	Exosome	LVCSN	VAQGIVSYGSNNGNPPAVFTK	IQSFM	2		1060.542707	2119.069815	0.001162105	1	N	209	230
P28293	Parental	VSQSR	GTNVLQEVQLR	VQMDQ	2		628.8520228	1255.688446	0.000451244	17	N	154	165
P28293	Parental	MCANR	FQFYNSQTQICVGNPR	ERKSA	2	C11:+57.021	979.9628071	1957.910014	0.000451244	52	N	175	191
P28293	Parental	MCANR	FQFYNSQTQICVGNPR	ERKSA	3	C11:+57.021	653.6444714	1957.910014	0.0007646	1	N	175	191
P28293	Parental	PRERK	SAFRGDSGGPLVCSNVAQGIVSY	GSNNG	2	C13:+57.021	1171.065989	2340.116379	0.000451244	6	N	194	217
P28293	Parental	PRERK	SAFRGDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C13:+57.021	1208.921876	3623.742229	0.000451244	19	N	194	230
P28293	Parental	PYMAF	LLIQSPEGLSACGGFLVR	EDFVL	2	C12:+57.021	959.0170511	1916.018502	0.000451244	47	N	37	55
P28293	Parental	PYMAF	LLIQSPEGLSACGGFLVR	EDFVL	3	C12:+57.021	639.680634	1916.018502	0.000451244	23	N	37	55
P28293	Parental	HSYPY	MAFLLIQSPEGLSACGGFLVR	EDFVL	2	C15:+57.021	1133.590058	2265.164516	0.000451244	12	N	34	55
P28293	Parental	HSYPY	MAFLLIQSPEGLSACGGFLVR	EDFVL	3	C15:+57.021	756.0626386	2265.164516	0.000451244	15	N	34	55
P28293	Parental	EVQLR	VQMDQMCANRFQFYNSQTQICVGNPR	ERKSA	3	M3:+15.995,M6:+15.995,C7:+57.021,C21:+57.021	1075.476079	3223.404836	0.001839721	8	N	165	191
P28293	Parental	QASKK	LQPGDLCTVAGWGR	VSQSR	2	C7:+57.021	765.3803902	1528.74518	0.000451244	10	N	135	149
P28293	Parental	PQASK	KLQPGDLCTVAGWGR	VSQSR	2	C8:+57.021	829.4278718	1656.840144	0.000451244	8	N	134	149
P28293	Parental	PQASK	KLQPGDLCTVAGWGR	VSQSR	3	C8:+57.021	553.2878479	1656.840144	0.000451244	15	N	134	149
P28293	Parental	KSAFR	GDSGGPLVCSNVAQGIVSY	GSNNG	2	C9:+57.021	940.4466555	1878.877711	0.000451244	22	N	198	217
P28293	Parental	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVFTK	IQSFM	3	C9:+57.021	1055.175654	3162.503561	0.000622848	5	N	198	230
P28293	Parental	PRERK	SAFRGDSGGPLVCSNVAQGIVSYGSNNGNPPAVF	TKIQS	3	C13:+57.021	1132.540996	3394.599587	0.000451244	7	N	194	228
P28293	Parental	SKKLQ	PGDLCTVAGWGR	VSQSR	2	C5:+57.021	644.8090694	1287.602539	0.001463592	1	N	137	149
P28293	Parental	MAFLL	IQSPEGLSACGGFLVR	EDFVL	2	C10:+57.021	845.932987	1689.850374	0.000451244	20	N	39	55
P28293	Parental	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVF	TKIQS	2	C9:+57.021	1467.68826	2933.360919	0.000451244	7	N	198	228
P28293	Parental	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVF	TKIQS	3	C9:+57.021	978.7947731	2933.360919	0.000735798	3	N	198	228
P28293	Parental	SYPYM	AFLLIQSPEGLSACGGFLVR	EDFVL	2	C14:+57.021	1068.069815	2134.12403	0.000451244	7	N	35	55
P28293	Parental	KSAFR	GDSGGPLVCSNVAQGIVSYGSNNGNPPAVFT	KIQSF	3	C9:+57.021	1012.477333	3034.408598	0.001264573	1	N	198	229
P28293	Parental	ITVLR	AIRHPDYNPQNIR	NDIML	3		531.9468562	1592.817169	0.001463592	2	N	93	106
P28293	Parental	RFQFY	NSQTQICVGNPR	ERKSA	2	C7:+57.021	687.33344	1372.65128	0.000622848	4	N	179	191
P28352	Exosome	WIKKK	GLDWVKEEAPDILCLQETK	CSENK	2	C14:+57.021	1122.564759	2243.113919	0.000451244	4	N	78	97
P28352	Exosome	WIKKK	GLDWVKEEAPDILCLQETK	CSENK	3	C14:+57.021	748.7124396	2243.113919	0.000451244	24	N	78	97
P28352	Exosome	DLASR	KPLVLCGDLNVAHEEIDLR	NPKGN	3	C6:+57.021	731.0565407	2190.146222	0.000451244	5	N	201	220
P28352	Exosome	TPQER	QGFGELLQAVPLADSFR	HLYPN	2		924.4866723	1846.957745	0.000451244	31	N	236	253
P28352	Exosome	TPQER	QGFGELLQAVPLADSFR	HLYPN	2	Q1:-17.027	915.9731723	1829.930745	0.000622848	2	N	236	253
P28352	Exosome	TPQER	QGFGELLQAVPLADSFR	HLYPN	2	[0:-17.027	915.9731723	1829.930745	0.000451244	3	N	236	253
P28352	Exosome	NVGWR	LDYFLLSHSLLPALCDSK	IRSKA	2	C15:+57.021	1046.543099	2091.070597	0.000451244	4	N	280	298
P28352	Exosome	NVGWR	LDYFLLSHSLLPALCDSK	IRSKA	3	C15:+57.021	698.0313325	2091.070597	0.000451244	12	N	280	298
P28352	Exosome	KKTEK	EAAGEGPVLYEDPPDQK	TSPSG	2		907.9263102	1813.83702	0.000451244	31	N	34	51
P28352	Exosome	DLASR	KPLVLCGDLNVAHEEIDLRNPK	GNKKN	4	C6:+57.021	633.3420192	2529.336877	0.000451244	1	N	201	223
P28352	Parental	WIKKK	GLDWVKEEAPDILCLQETK	CSENK	2	C14:+57.021	1122.564759	2243.113919	0.000451244	8	N	78	97
P28352	Parental	WIKKK	GLDWVKEEAPDILCLQETK	CSENK	3	C14:+57.021	748.7124396	2243.113919	0.000451244	2	N	78	97

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P28352	Parental	KKTEK	EAAGEGPVLYEDPPDQK	TSPSG	2		907.9263102	1813.83702	0.000451244	9	N	34	51
P28474	Exosome	APLDK	VCLLGCGISTGYGAAVNTAK	VEPGS	2	C2:+57.021,C6:+57.021	1006.500677	2010.985753	0.000451244	25	N	168	188
P28474	Exosome	VTKLK	AGDTVIPLYIPQCGECK	FCLNP	2	C13:+57.021,C16:+57.021	960.9633956	1919.911191	0.000451244	13	N	84	101
P28474	Exosome	DKFAK	AKEFGASECISPQDFSK	SIQEV	2	C9:+57.021	950.941206	1899.866812	0.001943752	1	N	231	248
P28474	Exosome	DKFAK	AKEFGASECISPQDFSK	SIQEV	3	C9:+57.021	634.2967373	1899.866812	0.000451244	11	N	231	248
P28474	Exosome	FAKAK	EFGASECISPQDFSK	SIQEV	2	C7:+57.021	851.3751675	1700.734735	0.000451244	14	N	233	248
P28474	Exosome	VIRCK	AAVAWEAGKPLSIEEIEVAPPK	AHEVR	2		1153.126073	2304.236546	0.000451244	2	N	9	31
P28474	Exosome	VIRCK	AAVAWEAGKPLSIEEIEVAPPK	AHEVR	3		769.0866486	2304.236546	0.000451244	12	N	9	31
P28474	Exosome	ISVAK	IDPSAPLDKVCLLGCGISTGYGAAVNTAK	VEPGS	3	C11:+57.021,C15:+57.021	983.500267	2947.477401	0.000451244	5	N	159	188
P28474	Parental	APLDK	VCLLGCGISTGYGAAVNTAK	VEPGS	2	C2:+57.021,C6:+57.021	1006.500677	2010.985753	0.000451244	4	N	168	188
P28474	Parental	DKFAK	AKEFGASECISPQDFSK	SIQEV	2	C9:+57.021	950.941206	1899.866812	0.000823681	2	N	231	248
P28650	Exosome	RTGLR	ICDLLSDFDEFSAR	FKNLA	2	C2:+57.021	844.3855352	1686.75547	0.000451244	47	N	181	195
P28650	Exosome	AYTTR	VGIGAFPTEQINEIGDLLQNR	GHEWG	2		1142.600754	2283.185907	0.000451244	25	N	304	325
P28650	Exosome	AYTTR	VGIGAFPTEQINEIGDLLQNR	GHEWG	3		762.069769	2283.185907	0.000451244	58	N	304	325
P28650	Exosome	IINTK	AVSFIGNGVVIHLPGLFEEAEKNEK	KGLKD	3		899.813588	2696.417364	0.000451244	19	N	93	118
P28650	Exosome	IINTK	AVSFIGNGVVIHLPGLFEEAEKNEK	KGLKD	4		675.112141	2696.417364	0.000622848	5	N	93	118
P28650	Exosome	EGKGK	VVDLLATDADIVSR	CQGGN	2		743.9097348	1485.80387	0.000451244	35	N	48	62
P28650	Exosome	VVDGK	EYDFHLLPSGIINTK	AVSFI	2		873.9572164	1745.898833	0.000622848	2	N	78	93
P28650	Exosome	IISDR	AHLVFDFHQAVDGLQEVQR	QAQEG	2		1105.061599	2208.107597	0.000451244	3	N	133	152
P28650	Exosome	IISDR	AHLVFDFHQAVDGLQEVQR	QAQEG	3		737.0436657	2208.107597	0.000451244	20	N	133	152
P28650	Exosome	EILQK	VEVEYETLPGWK	ADTTG	2		725.3671714	1448.718743	0.000451244	11	N	398	410
P28650	Exosome	LNGKR	IPYFPANQEILQKVEVEYETLPGWK	ADTTG	3		997.8554529	2990.542959	0.000451244	3	N	385	410
P28650	Exosome	ATGSR	VTVVLGAQWGDEGKGK	VVDLL	2		822.4417334	1642.867867	0.000451244	5	Y	32	48
P28650	Exosome	ATGSR	VTVVLGAQWGDEGKGK	VVDLL	3		548.6304223	1642.867867	0.0007646	2	Y	32	48
P28650	Exosome	LALTK	LDILDVLSEIK	VGISY	2		629.3691828	1256.722766	0.002296037	1	N	363	374
P28650	Parental	RTGLR	ICDLLSDFDEFSAR	FKNLA	2	C2:+57.021	844.3855352	1686.75547	0.000451244	5	N	181	195
P28650	Parental	AYTTR	VGIGAFPTEQINEIGDLLQNR	GHEWG	2		1142.600754	2283.185907	0.000451244	6	N	304	325
P28650	Parental	AYTTR	VGIGAFPTEQINEIGDLLQNR	GHEWG	3		762.069769	2283.185907	0.000451244	3	N	304	325
P28650	Parental	IINTK	AVSFIGNGVVIHLPGLFEEAEKNEK	KGLKD	4		675.112141	2696.417364	0.002374549	1	N	93	118
P28650	Parental	EGKGK	VVDLLATDADIVSR	CQGGN	2		743.9097348	1485.80387	0.000622848	2	N	48	62
P28656	Exosome	ALQER	LDGLVDTPTGYIESLPK	VVKRR	2		909.4807213	1816.945843	0.000451244	29	N	55	72
P28656	Exosome	LFDKR	FEIINAIYEPTEEECEWKPDEEDEVSEELKEK	AKIED	3	C15:+57.021	1319.598347	3955.771642	0.000451244	11	N	117	149
P28656	Exosome	LFDKR	FEIINAIYEPTEEECEWKPDEEDEVSEELKEK	AKIED	4	C15:+57.021	989.9507105	3955.771642	0.000451244	27	N	117	149
P28656	Exosome	KEDPK	GIPEFWLTVFK	NVDLL	2		668.8691529	1335.722706	0.000451244	15	N	165	176
P28656	Parental	ALQER	LDGLVDTPTGYIESLPK	VVKRR	2		909.4807213	1816.945843	0.000451244	28	N	55	72
P28656	Parental	LFDKR	FEIINAIYEPTEEECEWKPDEEDEVSEELKEK	AKIED	3	C15:+57.021	1319.598347	3955.771642	0.000451244	38	N	117	149
P28656	Parental	LFDKR	FEIINAIYEPTEEECEWKPDEEDEVSEELKEK	AKIED	4	C15:+57.021	989.9507105	3955.771642	0.000451244	17	N	117	149
P28656	Parental	KEDPK	GIPEFWLTVFK	NVDLL	2		668.8691529	1335.722706	0.000451244	4	N	165	176
P28656	Parental	QPMSF	VLEFHFEPNDYFTNEVLTK	TYRMR	3		781.3833536	2341.126661	0.000451244	12	N	212	231
P28658	Exosome	FRCLR	NACIECSVNQNSIR	NLDTI	2	C3:+57.021,C6:+57.021	832.8776544	1663.739709	0.000451244	10	N	89	103
P28658	Exosome	EAHQK	HPASEWPFLIISDHFLK	SPELV	3		679.6917932	2036.051979	0.000622848	3	N	209	226
P28658	Exosome	SNQER	ITLLDIVIAK	LVGEE	2		549.8607966	1097.705993	0.002884417	1	N	243	253
P28658	Parental	FRCLR	NACIECSVNQNSIR	NLDTI	2	C3:+57.021,C6:+57.021	832.8776544	1663.739709	0.000451244	12	N	89	103
P28658	Parental	EAHQK	HPASEWPFLIISDHFLK	SPELV	3		679.6917932	2036.051979	0.001591523	6	N	209	226
P28658	Parental	VYAVR	NLTEDNSQNQDVIAK	MEEQG	2		844.9084518	1687.801304	0.000622848	3	N	423	438
P28665	Exosome	QSGRK	NLFDELVLDKDLFQCVSFIIPR	LSSSD	3	C15:+57.021	894.4721316	2680.392995	0.000451244	11	N	71	93
P28665	Exosome	VPSSR	LSEDQEDCILYSSWLAEK	HTNLV	2	C8:+57.021	1093.501825	2184.98805	0.000451244	27	N	626	644
P28665	Exosome	AVLVK	NKESVVFVQTDKPVYKPGQSVK	FRVVS	3		826.4519905	2476.332572	0.000451244	5	N	123	145
P28665	Exosome	AVLVK	NKESVVFVQTDKPVYKPGQSVK	FRVVS	4		620.0909429	2476.332572	0.000451244	18	N	123	145
P28665	Exosome	ASQTR	LQVTASPQSLCGLR	AVDQS	2	C11:+57.021	765.4091477	1528.802695	0.000451244	6	N	576	590
P28665	Exosome	MWLTK	QQNSNGGFSSTQDTVVALDALSK	YGAVT	2		1184.075297	2366.134994	0.000451244	9	N	1242	1265
P28665	Exosome	MHLEK	QLSAFAIWVQTVPLTCNNPK	GHNSF	2	C16:+57.021	1144.099104	2286.182608	0.000451244	21	N	1338	1358
P28665	Exosome	MHLEK	QLSAFAIWVQTVPLTCNNPK	GHNSF	3	C16:+57.021	763.0686692	2286.182608	0.002663018	2	N	1338	1358
P28665	Exosome	MHLEK	QLSAFAIWVQTVPLTCNNPK	GHNSF	2	[0:-17.027,C16:+57.021	1135.585604	2269.155608	0.001162105	1	N	1338	1358
P28665	Exosome	FVKVR	LVDIKGDPIPNEK	VFIKA	3		479.9369637	1436.787491	0.001264573	1	N	360	373
P28665	Exosome	FIIPR	LSSSDEEDFLYVDIK	GPTHE	2		880.4177867	1758.819973	0.000622848	1	N	93	108
P28665	Exosome	QNGER	EGNTWLTAFVLK	SFAQA	2		689.8724239	1377.729248	0.000451244	10	N	1037	1049
P28665	Exosome	DTVVK	VLIVEPEGIKQEHTFSSLFCASDAEISEK	MSLVL	3	C20:+57.021	1088.543232	3262.606295	0.000622848	2	N	903	932
P28665	Exosome	DTVVK	VLIVEPEGIKQEHTFSSLFCASDAEISEK	MSLVL	4	C20:+57.021	816.6593738	3262.606295	0.002663018	1	N	903	932
P28665	Exosome	SRSQK	TTLVTIQSTGSFSQK	FQVEN	2		799.425749	1596.835898	0.000451244	12	N	1276	1291
P28665	Exosome	LCGLR	AVDQSVLLLKPESELSPSWIYNLPGMQQNK	FVPSS	3		1128.922309	3383.743527	0.000698008	3	N	590	620
P28665	Exosome	FIIPR	LSSSDEEDFLYVDIKGPTHEFSK	RKAVL	4		661.5674976	2642.23879	0.000451244	5	N	93	116
P28665	Exosome	FAQAR	AFIFIDESHITHAFTWLSQK	QKDNG	3		797.7431047	2390.205914	0.000622848	5	N	1055	1075
P28665	Exosome	LVKNK	ESVVFVQTDKPVYKPGQSVK	FRVVS	3		745.7393603	2234.194681	0.001229886	1	N	125	145
P28665	Exosome	VSMDK	MLRPLNELLPLAYIEDPKK	NRIMQ	4	M1:+15.995	568.0716148	2268.255259	0.001591523	2	N	153	172

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P28665	Parental	QSGRK	NLFDELVLDKDLFQCVSFIIPR	LSSSD	3	C15:+57.021	894.4721316	2680.392995	0.000451244	9	N	71	93
P28665	Parental	VPSSR	LSEDQEDCILYSSWLAEK	HTNLV	2	C8:+57.021	1093.501825	2184.98805	0.000451244	7	N	626	644
P28665	Parental	MHLEK	QLSAFAIWVQTVPLTCNNPK	GHNSF	2	C16:+57.021	1144.099104	2286.182608	0.001839721	1	N	1338	1358
P28665	Parental	DTVVK	VLIVEPEGIKQEHTFSSLFCASDAEISEK	MSLVL	3	C20:+57.021	1088.543232	3262.606295	0.000735798	1	N	903	932
P28667	Exosome	KRNRK	EGGGDSSASSPTEEEQEQGEMSACSDEGTAQEGK	AAATP	3	M21:+15.995,C24:+57.021	1159.781792	3476.321976	0.000622848	1	N	110	144
P28667	Parental	DLTPK	GEGESPPVNGTDEAAGATGDAIEPAPPSQEAEAKGEVAPK	ETPKK	3		1277.600004	3829.776613	0.000451244	29	N	43	83
P28667	Parental	DLTPK	GEGESPPVNGTDEAAGATGDAIEPAPPSQEAEAKGEVAPK	ETPKK	4		958.4519533	3829.776613	0.000622848	1	N	43	83
P28667	Parental	SAASK	EGDTEEEAGPQAAEPSTPSGPESGPTPASAEQNE	-	3		1118.47363	3352.397489	0.000622848	6	N	166	200
P28667	Parental	DLTPK	GEGESPPVNGTDEAAGATGDAIEPAPPSQEAEAK	GEVAP	3		1083.827567	3248.459301	0.000823681	1	N	43	77
P28798	Exosome	CPFAK	AVCCEDHIHCCPAGFQCHTEK	GTCEM	3	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021	872.6814401	2615.02092	0.000451244	16	N	309	330
P28798	Exosome	CPFAK	AVCCEDHIHCCPAGFQCHTEK	GTCEM	4	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021	654.7630301	2615.02092	0.000451244	26	N	309	330
P28798	Exosome	LQIGD	IGCDQHTSCPVGQTCCPSLK	GSWAC	3	C3:+57.021,C9:+57.021,C15:+57.021,C16:+57.021	768.9990292	2303.973688	0.000451244	28	N	439	459
P28798	Exosome	CPDAK	TQCPDDSTCCELPTGK	YGCCP	2	C3:+57.021,C9:+57.021,C10:+57.021	934.8764285	1867.737257	0.000451244	56	N	211	227
P28798	Exosome	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	C1:+57.021,M3:+15.995,C7:+57.021,C13:+57.021,C14:+57.021	970.3406533	1938.665707	0.000451244	63	N	281	296
P28798	Exosome	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	[0:-17.027,C1:+57.021,M3:+15.995,C7:+57.021,C13:+57.021,C14:+57.021	961.8271533	1921.638707	0.000451244	6	N	281	296
P28798	Exosome	PLQIG	DIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C4:+57.021,C10:+57.021,C16:+57.021,C17:+57.021	807.3413436	2419.000631	0.000451244	5	N	438	459
P28798	Exosome	CPSLK	GSWACCQLPHAVCCEDR	QHCCP	2	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021	1053.423657	2104.831715	0.000451244	10	N	459	476
P28798	Exosome	CPSLK	GSWACCQLPHAVCCEDR	QHCCP	3	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021	702.6183716	2104.831715	0.000451244	8	N	459	476
P28798	Exosome	YTCCR	LNTGAWGCCPFAK	AVCCE	2	C8:+57.021,C9:+57.021	741.3369054	1480.658211	0.000451244	15	N	296	309
P28798	Exosome	LPTGK	YGCCPMPNAICCSDHLHCCPQDTVCDLIQSK	CLSKN	3	C3:+57.021,C4:+57.021,M6:+15.995,C11:+57.021,C12:+57.021,C18:+57.021,C19:+57.021,C25:+57.021	1271.510349	3811.507648	0.000622848	3	N	227	258
P28798	Exosome	LPTGK	YGCCPMPNAICCSDHLHCCPQDTVCDLIQSK	CLSKN	4	C3:+57.021,C4:+57.021,M6:+15.995,C11:+57.021,C12:+57.021,C18:+57.021,C19:+57.021,C25:+57.021	953.8847121	3811.507648	0.000451244	10	N	227	258
P28798	Exosome	NTCCK	LNSGDWGCCPIPEAVCCSDNQHCCPQGFTCLAQGYCQK	GDTMV	4	C8:+57.021,C9:+57.021,C16:+57.021,C17:+57.021,C23:+57.021,C24:+57.021,C30:+57.021,C36:+57.021	1134.453884	4533.784337	0.000451244	32	N	378	416
P28798	Exosome	KIPAR	QTTPLQIGDIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C12:+57.021,C18:+57.021,C24:+57.021,C25:+57.021	1086.8263	3257.455499	0.000622848	9	N	430	459
P28798	Parental	CPFAK	AVCCEDHIHCCPAGFQCHTEK	GTCEM	3	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021	872.6814401	2615.02092	0.000451244	63	N	309	330
P28798	Parental	CPFAK	AVCCEDHIHCCPAGFQCHTEK	GTCEM	4	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021	654.7630301	2615.02092	0.000451244	61	N	309	330
P28798	Parental	CPFAK	AVCCEDHIHCCPAGFQCHTEKGTCEM	GILQV	3	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021,C24:+57.021,M26:+15.995	1070.740576	3209.198327	0.000823681	5	N	309	335
P28798	Parental	CPFAK	AVCCEDHIHCCPAGFQCHTEKGTCEM	GILQV	4	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021,C24:+57.021,M26:+15.995	803.3073819	3209.198327	0.001654178	5	N	309	335
P28798	Parental	GYPVK	EVKCDMEVSCPEGYTCCR	LNTGA	2	C4:+57.021,M6:+15.995,C10:+57.021,C16:+57.021,C17:+57.021	1148.443638	2294.871677	0.000451244	10	N	278	296
P28798	Parental	GYPVK	EVKCDMEVSCPEGYTCCR	LNTGA	3	C4:+57.021,M6:+15.995,C10:+57.021,C16:+57.021,C17:+57.021	765.9650256	2294.871677	0.000451244	2	N	278	296
P28798	Parental	LQIGD	IGCDQHTSCPVGQTCCPSLK	GSWAC	2	C3:+57.021,C9:+57.021,C15:+57.021,C16:+57.021	1152.994644	2303.973688	0.000451244	24	N	439	459
P28798	Parental	LQIGD	IGCDQHTSCPVGQTCCPSLK	GSWAC	3	C3:+57.021,C9:+57.021,C15:+57.021,C16:+57.021	768.9990292	2303.973688	0.000451244	52	N	439	459
P28798	Parental	CPDAK	TQCPDDSTCCELPTGK	YGCCP	2	C3:+57.021,C9:+57.021,C10:+57.021	934.8764285	1867.737257	0.000451244	142	N	211	227
P28798	Parental	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	C1:+39.994,M3:+15.995,C7:+57.021,C13:+57.021,C14:+57.021	961.8271533	1921.638707	0.001699387	1	N	281	296
P28798	Parental	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	C1:+57.021,C7:+57.021,C13:+57.021,C14:+57.021	962.3431533	1922.670707	0.000622848	5	N	281	296

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P28798	Parental	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	C1:+57.021,M3:+15.995,C7:+57.021,C13:+57.021,C14:+57.021	970.3406533	1938.665707	0.000451244	142	N	281	296
P28798	Parental	VKEVK	CDMEVSCPEGYTCCR	LNTGA	2	[0:-17.027,C1:+57.021,M3:+15.995,C7:+57.021,C13:+57.021,C14:+57.021	961.8271533	1921.638707	0.000451244	31	N	281	296
P28798	Parental	PLQIG	DIGCDQHTSCPVGQTCCPSLK	GSWAC	2	C4:+57.021,C10:+57.021,C16:+57.021,C17:+57.021	1210.508115	2419.000631	0.000451244	18	N	438	459
P28798	Parental	PLQIG	DIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C4:+57.021,C10:+57.021,C16:+57.021,C17:+57.021	807.3413436	2419.000631	0.000451244	32	N	438	459
P28798	Parental	CPSLK	GSWACCQLPHAVCCEDRQHCCPAGYTCNVK	ARTCE	3	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021,C20:+57.021,C21:+57.021,C27:+57.021	1227.830605	3680.468415	0.000451244	4	N	459	489
P28798	Parental	CPSLK	GSWACCQLPHAVCCEDRQHCCPAGYTCNVK	ARTCE	4	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021,C20:+57.021,C21:+57.021,C27:+57.021	921.1249037	3680.468415	0.000451244	8	N	459	489
P28798	Parental	CPSLK	GSWACCQLPHAVCCEDR	QHCCP	2	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021	1053.423657	2104.831715	0.000451244	65	N	459	476
P28798	Parental	CPSLK	GSWACCQLPHAVCCEDR	QHCCP	3	C5:+57.021,C6:+57.021,C13:+57.021,C14:+57.021	702.6183716	2104.831715	0.000451244	43	N	459	476
P28798	Parental	YTCCR	LNTGAWGCCPFAK	AVCCE	2	C8:+57.021,C9:+57.021	741.3369054	1480.658211	0.000451244	41	N	296	309
P28798	Parental	LPTGK	YGCCPMPNAICCSDHLHCCPQDTVCDLIQSK	CLSKN	3	C3:+57.021,C4:+57.021,M6:+15.995,C11:+57.021,C12:+57.021,C18:+57.021,C19:+57.021,C25:+57.021	1271.510349	3811.507648	0.000451244	29	N	227	258
P28798	Parental	LPTGK	YGCCPMPNAICCSDHLHCCPQDTVCDLIQSK	CLSKN	4	C3:+57.021,C4:+57.021,M6:+15.995,C11:+57.021,C12:+57.021,C18:+57.021,C19:+57.021,C25:+57.021	953.8847121	3811.507648	0.000451244	36	N	227	258
P28798	Parental	NTCCK	LNSGDWGCCPIPEAVCCSDNQHCCPQGFTCLAQGYCQK	GDTMV	4	C8:+57.021,C9:+57.021,C16:+57.021,C17:+57.021,C23:+57.021,C24:+57.021,C30:+57.021,C36:+57.021	1134.453884	4533.784337	0.000451244	42	N	378	416
P28798	Parental	EKIPA	RQTTPLQIGDIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C13:+57.021,C19:+57.021,C25:+57.021,C26:+57.021	1138.860003	3413.55661	0.000451244	7	N	429	459
P28798	Parental	EKIPA	RQTTPLQIGDIGCDQHTSCPVGQTCCPSLK	GSWAC	4	C13:+57.021,C19:+57.021,C25:+57.021,C26:+57.021	854.3969526	3413.55661	0.000451244	1	N	429	459
P28798	Parental	KIPAR	QTTPLQIGDIGCDQHTSCPVGQTCCPSLK	GSWAC	3	C12:+57.021,C18:+57.021,C24:+57.021,C25:+57.021	1086.8263	3257.455499	0.000451244	20	N	430	459
P28798	Parental	QIGDI	GCDQHTSCPVGQTCCPSLK	GSWAC	3	C2:+57.021,C8:+57.021,C14:+57.021,C15:+57.021	731.3043412	2190.889624	0.000451244	22	N	440	459
P28798	Parental	IGDIG	CDQHTSCPVGQTCCPSLK	GSWAC	3	C1:+57.021,C7:+57.021,C13:+57.021,C14:+57.021	712.2971866	2133.86816	0.000451244	12	N	441	459
P28798	Parental	QTCCK	DSAGVWACCPYLK	GVCCR	2	C8:+57.021,C9:+57.021	763.8420206	1525.668441	0.000451244	17	N	531	544
P28798	Parental	YPVKE	VKCDMEVSCPEGYTCCR	LNTGA	3	C3:+57.021,M5:+15.995,C9:+57.021,C15:+57.021,C16:+57.021	722.9508279	2165.829084	0.001463592	1	N	279	296
P28798	Parental	CPMPN	AICCSDHLHCCPQDTVCDLIQSK	CLSKN	2	C3:+57.021,C4:+57.021,C10:+57.021,C11:+57.021,C17:+57.021	1409.097072	2816.178544	0.000451244	2	N	235	258
P28798	Parental	CCEDR	VHCCPHGASCDLVHTR	CVSPT	3	C3:+57.021,C4:+57.021,C10:+57.021	635.9470826	1904.817848	0.001699387	1	N	160	176
P28798	Parental	CCEDR	VHCCPHGASCDLVHTR	CVSPT	4	C3:+57.021,C4:+57.021,C10:+57.021	477.2122619	1904.817848	0.000622848	3	N	160	176
P28798	Parental	QKTNR	AVSLPFSVVCPDAK	TQCPD	2	C10:+57.021	745.3898923	1488.764185	0.002663018	1	N	197	211
P28867	Exosome	APFLR	ISFNSYELGSLQVEDEASQPFCAVK	MKEAL	2	C22:+57.021	1409.66593	2817.316261	0.000451244	9	N	6	31
P28867	Exosome	GINQK	LLAEALNQVTQR	SSRKL	2		678.3862298	1354.75686	0.000451244	10	N	285	297
P28867	Exosome	FELYR	ATFYAAEIICGLQFLHSK	GIIYR	3	C10:+57.021	690.356039	2068.044717	0.000451244	21	N	447	465
P28867	Exosome	IHYIK	NHEFIATFFGQPTFCSVCK	EFVWG	2	C15:+57.021,C18:+57.021	1145.524683	2289.033766	0.001162105	3	N	157	176
P28867	Exosome	IHYIK	NHEFIATFFGQPTFCSVCK	EFVWG	3	C15:+57.021,C18:+57.021	764.0190553	2289.033766	0.000451244	14	N	157	176
P28867	Exosome	HPFFK	TINWSLLEK	RKVEP	2		552.3089281	1102.602256	0.000823681	12	N	602	611
P28867	Exosome	FGEGR	ASTFCGTPDYIAPEILQGLK	YSFSV	2	C5:+57.021	1091.048745	2180.08189	0.001162105	6	N	502	522
P28867	Exosome	KNNGK	AEFWLDLQPQAK	VLMCV	2		723.3753308	1444.735062	0.000451244	3	N	101	113
P28867	Exosome	QPQAK	VLMCVQYFLEDGDCK	QSMRS	2	C4:+57.021,C14:+57.021	938.9176	1875.8196	0.002663018	1	N	113	128
P28867	Exosome	KPKVK	SPSDYSNFDPEFLNEKPQLSF	SDKNL	2		1231.063867	2460.112133	0.001871652	1	N	623	644
P28867	Exosome	KPKVK	SPSDYSNFDPEFLNEKPQLSFSDK	NLIDS	3		931.0964893	2790.266068	0.000451244	2	N	623	647
P28867	Parental	APFLR	ISFNSYELGSLQVEDEASQPFCAVK	MKEAL	2	C22:+57.021	1409.66593	2817.316261	0.000451244	5	N	6	31
P28867	Parental	GINQK	LLAEALNQVTQR	SSRKL	2		678.3862298	1354.75686	0.000451244	2	N	285	297
P28867	Parental	FELYR	ATFYAAEIICGLQFLHSK	GIIYR	3	C10:+57.021	690.356039	2068.044717	0.00307782	1	N	447	465
P28867	Parental	IHYIK	NHEFIATFFGQPTFCSVCK	EFVWG	3	C15:+57.021,C18:+57.021	764.0190553	2289.033766	0.000451244	11	N	157	176
P28867	Parental	HPFFK	TINWSLLEK	RKVEP	2		552.3089281	1102.602256	0.001162105	7	N	602	611

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P28867	Parental	IVLMR	AAEDPVSEVTVGVSVLAER	CKKNN	2		964.5027164	1926.989833	0.000851441	2	N	75	94
P28867	Parental	RISFN	SYELGSLQVEDEASQPFCAVK	MKEAL	2	C18:+57.021	1179.052213	2356.088826	0.000451244	1	N	10	31
P29341	Exosome	MITRR	SLGYAYVNFQQPADAER	ALDTM	2		964.9610187	1927.906437	0.000451244	38	N	50	67
P29341	Exosome	SGKSK	GFGFVSFER	HEDAQ	2		523.2592382	1044.502876	0.000451244	3	N	231	240
P29341	Exosome	SIDNK	ALYDTFSAFGNILSCK	VVCDE	2	C15:+57.021	903.9404777	1805.865355	0.000451244	28	N	113	129
P29341	Exosome	SIDNK	ALYDTFSAFGNILSCK	VVCDE	3	C15:+57.021	602.9629185	1805.865355	0.001591523	2	N	113	129
P29341	Exosome	ENGSK	GYGFVHFETQEAAER	AIEKM	2		870.9029724	1739.790345	0.000451244	7	N	138	153
P29341	Exosome	MLYEK	FSPAGPILSIR	VCRDM	2		579.3380199	1156.66044	0.000451244	14	N	30	41
P29341	Exosome	GGRSK	GFGFVCFSSPEEATK	AVTEM	2	C6:+57.021	831.877346	1661.739092	0.000451244	24	N	333	348
P29341	Exosome	DERLR	KEFSPFGTITSAK	VMMEG	3		471.5860424	1411.734727	0.001699387	3	N	311	324
P29341	Parental	MITRR	SLGYAYVNFQQPADAER	ALDTM	2		964.9610187	1927.906437	0.000451244	9	N	50	67
P29341	Parental	SGKSK	GFGFVSFER	HEDAQ	2		523.2592382	1044.502876	0.000451244	18	N	231	240
P29341	Parental	SIDNK	ALYDTFSAFGNILSCK	VVCDE	2	C15:+57.021	903.9404777	1805.865355	0.000451244	15	N	113	129
P29341	Parental	SIDNK	ALYDTFSAFGNILSCK	VVCDE	3	C15:+57.021	602.9629185	1805.865355	0.002296037	1	N	113	129
P29341	Parental	ENGSK	GYGFVHFETQEAAER	AIEKM	3		580.9379149	1739.790345	0.000451244	25	N	138	153
P29341	Parental	MLYEK	FSPAGPILSIR	VCRDM	2		579.3380199	1156.66044	0.000637154	6	N	30	41
P29341	Parental	MASVR	AVPNPVINPYQPAPPSGYF	MAAIP	2		1014.51543	2027.01526	0.0007646	5	N	390	409
P29341	Parental	DERLR	KEFSPFGTITSAK	VMMEG	3		471.5860424	1411.734727	0.000451244	1	N	311	324
P29341	Parental	PESLR	SKVDEAVAVLQAHQAK	EAAQK	3		565.3130933	1692.91588	0.000823681	1	N	604	620
P29351	Exosome	RWFHR	DLSGPDAETLLK	GRGVP	2		629.8304217	1257.645243	0.000451244	15	N	7	19
P29351	Exosome	EYKLR	TLQISPLDNGDLVR	EIWHY	2		770.9206338	1539.825668	0.000451244	18	N	393	407
P29351	Exosome	EDTAK	AGFWEEFESLQKQEVK	NLHQR	2		977.9814198	1953.94724	0.000451244	5	N	241	257
P29351	Exosome	EDTAK	AGFWEEFESLQKQEVK	NLHQR	3		652.3235465	1953.94724	0.000451244	11	N	241	257
P29351	Exosome	CEGGR	YTVGGSETFDSLTDLVEHFKK	TGIEE	2		1187.084602	2372.153604	0.000451244	2	N	175	196
P29351	Exosome	CEGGR	YTVGGSETFDSLTDLVEHFKK	TGIEE	3		791.725668	2372.153604	0.000451244	20	N	175	196
P29351	Exosome	CEGGR	YTVGGSETFDSLTDLVEHFKK	TGIEE	4		594.046201	2372.153604	0.000451244	38	N	175	196
P29351	Exosome	EDTAK	AGFWEEFESLQK	QEVKN	2		735.8491458	1469.682692	0.000451244	33	N	241	253
P29351	Exosome	EDTAK	AGFWEEFESLQK	QEVKN	3		490.9020305	1469.682692	0.0025889	1	N	241	253
P29351	Exosome	TFLVR	ESLSQPGDFVLSVLNDQPK	AGPGS	2		1037.029098	2072.042597	0.000451244	46	N	136	155
P29351	Exosome	TFLVR	ESLSQPGDFVLSVLNDQPK	AGPGS	3		691.6886656	2072.042597	0.000451244	35	N	136	155
P29351	Exosome	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSFLDQINQR	QESLP	3		1256.613414	3766.816843	0.000451244	16	N	407	439
P29351	Exosome	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSFLDQINQR	QESLP	4		942.7120106	3766.816843	0.000622848	11	N	407	439
P29351	Exosome	VGTQR	VYGLYSVTNSR	EHDTA	2		629.8254737	1257.635347	0.000451244	15	N	372	383
P29351	Exosome	VTHIR	IQNSGDFYDLYGGEKFATLTELVEYYTQQQGILQDR	DGTII	3		1401.678478	4202.012033	0.000979378	1	N	53	89
P29351	Exosome	IIHLK	YPLNCSDPTSER	WYHGH	2	C5:+57.021	719.8172884	1437.618977	0.000451244	33	N	97	109
P29351	Exosome	CEGGR	YTVGGSETFDSLTDLVEHFK	KTGIE	3		749.0273469	2244.058641	0.000451244	37	N	175	195
P29351	Exosome	YGGEK	FATLTELVEYYTQQQGILQDR	DGTII	2		1258.637533	2515.259466	0.000451244	28	N	68	89
P29351	Exosome	YGGEK	FATLTELVEYYTQQQGILQDR	DGTII	3		839.427622	2515.259466	0.000451244	39	N	68	89
P29351	Exosome	SISTK	GLDCDIDIQK	TIQMV	2	C4:+57.021	588.7821859	1175.548772	0.000451244	11	N	476	486
P29351	Exosome	VTHIR	IQNSGDFYDLYGGEK	FATLT	2		853.3893635	1704.763127	0.000451244	25	N	53	68
P29351	Exosome	PTSER	WYHGHISGGQAESLLQAK	GEPWT	2		991.4981027	1980.980605	0.000451244	13	N	109	127
P29351	Exosome	PTSER	WYHGHISGGQAESLLQAK	GEPWT	3		661.3346685	1980.980605	0.000451244	18	N	109	127
P29351	Exosome	PTSER	WYHGHISGGQAESLLQAK	GEPWT	4		496.2529514	1980.980605	0.002813207	2	N	109	127
P29351	Exosome	YGGEK	FATLTELVEYYTQQQGILQDRDGTIIHLK	YPLNC	3		1131.92834	3392.761619	0.000451244	8	N	68	97
P29351	Exosome	YGGEK	FATLTELVEYYTQQQGILQDRDGTIIHLK	YPLNC	4		849.1982047	3392.761619	0.000451244	15	N	68	97
P29351	Exosome	IQSQK	GQESEYGNITYPPAVR	SAHAK	2		890.9291872	1779.842774	0.000451244	22	N	530	546
P29351	Exosome	QINQR	QESLPHAGPIIVHCSAGIGR	TGTII	2	C14:+57.021	1050.044663	2098.073726	0.000451244	4	N	439	459
P29351	Exosome	QINQR	QESLPHAGPIIVHCSAGIGR	TGTII	4	C14:+57.021	525.5262314	2098.073726	0.000823681	3	N	439	459
P29351	Exosome	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSF	LDQIN	2		1450.688089	2899.360577	0.000622848	1	N	407	432
P29351	Exosome	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSF	LDQIN	3		967.4613258	2899.360577	0.002981883	1	N	407	432
P29351	Exosome	ILQGR	DSNIPGSDYINANYVK	NQLLG	2		885.421195	1768.82679	0.000451244	17	N	292	308
P29351	Exosome	KGRNK	CVPYWPEVGTQR	VYGLY	2	[0:-17.027,C1:+57.021	737.8428838	1473.670168	0.000451244	7	N	360	372
P29351	Exosome	GEKFA	TLTELVEYYTQQQGILQDR	DGTII	2		1149.584769	2297.153938	0.00091018	2	N	70	89
P29351	Parental	RWFHR	DLSGPDAETLLK	GRGVP	2		629.8304217	1257.645243	0.000451244	7	N	7	19
P29351	Parental	EYKLR	TLQISPLDNGDLVR	EIWHY	2		770.9206338	1539.825668	0.000823681	17	N	393	407
P29351	Parental	EDTAK	AGFWEEFESLQKQEVK	NLHQR	2		977.9814198	1953.94724	0.000451244	10	N	241	257
P29351	Parental	EDTAK	AGFWEEFESLQKQEVK	NLHQR	3		652.3235465	1953.94724	0.000451244	8	N	241	257
P29351	Parental	CEGGR	YTVGGSETFDSLTDLVEHFKK	TGIEE	3		791.725668	2372.153604	0.000870037	2	N	175	196
P29351	Parental	CEGGR	YTVGGSETFDSLTDLVEHFKK	TGIEE	4		594.046201	2372.153604	0.000451244	31	N	175	196
P29351	Parental	EDTAK	AGFWEEFESLQK	QEVKN	2		735.8491458	1469.682692	0.000451244	19	N	241	253
P29351	Parental	EDTAK	AGFWEEFESLQK	QEVKN	3		490.9020305	1469.682692	0.002145581	2	N	241	253
P29351	Parental	TFLVR	ESLSQPGDFVLSVLNDQPK	AGPGS	2		1037.029098	2072.042597	0.000451244	32	N	136	155
P29351	Parental	TFLVR	ESLSQPGDFVLSVLNDQPK	AGPGS	3		691.6886656	2072.042597	0.000451244	21	N	136	155
P29351	Parental	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSFLDQINQR	QESLP	3		1256.613414	3766.816843	0.000622848	6	N	407	439
P29351	Parental	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSFLDQINQR	QESLP	4		942.7120106	3766.816843	0.000622848	15	N	407	439

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P29351	Parental	VGTQR	VYGLYSVTNSR	EHDTA	2		629.8254737	1257.635347	0.000451244	7	N	372	383
P29351	Parental	VTHIR	IQNSGDFYDLYGGEKFATLTELVEYYTQQQGILQDR	DGTII	3		1401.678478	4202.012033	0.000451244	4	N	53	89
P29351	Parental	IIHLK	YPLNCSDPTSER	WYHGH	2	C5:+57.021	719.8172884	1437.618977	0.000451244	27	N	97	109
P29351	Parental	CEGGR	YTVGGSETFDSLTDLVEHFK	KTGIE	3		749.0273469	2244.058641	0.000451244	2	N	175	195
P29351	Parental	YGGEK	FATLTELVEYYTQQQGILQDR	DGTII	2		1258.637533	2515.259466	0.000451244	21	N	68	89
P29351	Parental	YGGEK	FATLTELVEYYTQQQGILQDR	DGTII	3		839.427622	2515.259466	0.000451244	21	N	68	89
P29351	Parental	SISTK	GLDCDIDIQK	TIQMV	2	C4:+57.021	588.7821859	1175.548772	0.000451244	3	N	476	486
P29351	Parental	VTHIR	IQNSGDFYDLYGGEK	FATLT	2		853.3893635	1704.763127	0.000451244	15	N	53	68
P29351	Parental	PTSER	WYHGHISGGQAESLLQAK	GEPWT	2		991.4981027	1980.980605	0.000451244	4	N	109	127
P29351	Parental	PTSER	WYHGHISGGQAESLLQAK	GEPWT	3		661.3346685	1980.980605	0.000622848	4	N	109	127
P29351	Parental	YGGEK	FATLTELVEYYTQQQGILQDRDGTIIHLK	YPLNC	3		1131.92834	3392.761619	0.001352548	1	N	68	97
P29351	Parental	YGGEK	FATLTELVEYYTQQQGILQDRDGTIIHLK	YPLNC	4		849.1982047	3392.761619	0.000622848	4	N	68	97
P29351	Parental	IQSQK	GQESEYGNITYPPAVR	SAHAK	2		890.9291872	1779.842774	0.000451244	31	N	530	546
P29351	Parental	QINQR	QESLPHAGPIIVHCSAGIGR	TGTII	2	C14:+57.021	1050.044663	2098.073726	0.000451244	3	N	439	459
P29351	Parental	QINQR	QESLPHAGPIIVHCSAGIGR	TGTII	3	C14:+57.021	700.3657086	2098.073726	0.000622848	4	N	439	459
P29351	Parental	QINQR	QESLPHAGPIIVHCSAGIGR	TGTII	4	C14:+57.021	525.5262314	2098.073726	0.001871652	2	N	439	459
P29351	Parental	GDLVR	EIWHYQYLSWPDHGVPSEPGGVLSF	LDQIN	2		1450.688089	2899.360577	0.000622848	2	N	407	432
P29351	Parental	ILQGR	DSNIPGSDYINANYVK	NQLLG	2		885.421195	1768.82679	0.000998612	4	N	292	308
P29391	Exosome	TSQIR	QNYSTEVEAAVNR	LVNLH	2		740.8554908	1479.695382	0.000451244	26	N	6	19
P29391	Exosome	LAMEK	NLNQALLDLHALGSAR	TDPHL	2		853.4713566	1704.927113	0.000451244	17	N	105	121
P29391	Exosome	LAMEK	NLNQALLDLHALGSAR	TDPHL	3		569.3168377	1704.927113	0.000451244	9	N	105	121
P29391	Exosome	TNLRR	VAGPQPAQTGAPQGSLGEYLFER	LTLKH	2		1187.095835	2372.176071	0.000451244	23	N	154	177
P29391	Exosome	TNLRR	VAGPQPAQTGAPQGSLGEYLFER	LTLKH	3		791.7331569	2372.176071	0.000451244	19	N	154	177
P29391	Exosome	DRGGR	ALFQDVQKPSQDEWGK	TQEAM	2		938.4659369	1874.916274	0.000451244	10	N	76	92
P29391	Exosome	DRGGR	ALFQDVQKPSQDEWGK	TQEAM	3		625.9798913	1874.916274	0.000451244	7	N	76	92
P29391	Exosome	TYLSL	GFFFDRDDVALEGVGHFFR	ELAEE	3		744.3609947	2230.059584	0.000823681	3	N	34	53
P29391	Exosome	TYLSL	GFFFDRDDVALEGVGHFFR	ELAEE	4		558.522696	2230.059584	0.000622848	4	N	34	53
P29391	Exosome	NLHLR	ASYTYLSLGFFFDRDDVALEGVGHFFR	ELAEE	3		1043.842206	3128.503219	0.002663018	1	N	26	53
P29391	Exosome	TNLRR	VAGPQPAQTGAPQGSLGEYL	FERLT	2		970.9897762	1939.963952	0.002374549	2	N	154	174
P29416	Exosome	WGALR	GLETFSQLVWK	SAEGT	2		654.353867	1306.692134	0.000451244	22	N	137	148
P29416	Exosome	KDMYK	VEPLAFHGTPEQK	ALVIG	2		726.8782376	1451.740875	0.001654178	1	N	435	448
P29416	Exosome	CELVR	RGIQAQPISVGYCEQEFEQT	-	2	C13:+57.021	1170.550172	2339.084744	0.000451244	3	N	508	528
P29416	Exosome	ELVRR	GIQAQPISVGYCEQEFEQT	-	2	C12:+57.021	1092.499616	2182.983633	0.000451244	18	N	509	528
P29416	Exosome	FTDFK	QLESFYIQTLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		1252.289603	3753.845408	0.000622848	2	N	348	379
P29416	Exosome	RAGFR	ALLSAPWYLNR	VKYGP	2		652.3620264	1302.708453	0.00307782	1	N	412	423
P29416	Exosome	TYHRR	YTLYPNNFQFR	YHVSS	2		731.8598479	1461.704096	0.002884417	1	N	36	47
P29416	Exosome	FRRYR	NLLFGSGSWPRPS	FSNKQ	2		709.3652974	1416.714995	0.0025889	1	N	69	82
P29416	Exosome	PELTR	KGSFNPVTHIYTAQDVK	EVIEY	3		635.6675361	1903.979208	0.000451244	2	N	223	240
P29416	Exosome	NFQFR	YHVSSAAQAGCVVLDEAFRR	YRNLL	3	C11:+57.021	746.0361396	2235.085019	0.001591523	1	N	47	67
P29416	Exosome	SFYIQ	TLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		916.1257202	2745.353761	0.000622848	3	N	356	379
P29416	Parental	WGALR	GLETFSQLVWK	SAEGT	2		654.353867	1306.692134	0.000451244	2	N	137	148
P29416	Parental	CELVR	RGIQAQPISVGYCEQEFEQT	-	2	C13:+57.021	1170.550172	2339.084744	0.000451244	4	N	508	528
P29416	Parental	FTDFK	QLESFYIQTLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		1252.289603	3753.845408	0.000451244	3	N	348	379
P29416	Parental	MAYNK	FNVFHWHLVDDSSFPYESFTFPELTR	KGSFN	3		1073.173845	3216.498134	0.000622848	4	N	197	223
P29416	Parental	MAYNK	FNVFHWHLVDDSSFPYESFTFPELTR	KGSFN	4		805.1323334	3216.498134	0.001943752	2	N	197	223
P29416	Parental	LESFY	IQTLLDIVSDYDKGYVVWQEVFDNK	VKVRP	3		996.5066008	2986.496402	0.002981883	1	N	354	379
P29452	Exosome	RAKRK	QFINSVSIGTINGLLDELLEKR	VLNQE	3		820.4555121	2458.343136	0.000622848	3	N	11	33
P29452	Exosome	RHPVR	GSLFIESLIK	HMKEY	2		553.8269537	1105.638307	0.001162105	5	N	343	353
P29452	Parental	RAKRK	QFINSVSIGTINGLLDELLEKR	VLNQE	3		820.4555121	2458.343136	0.000451244	6	N	11	33
P29621	Exosome	KLALK	NPDTNIVFSPLSISAALAIVSLGAK	GNTLE	2		1249.697394	2497.379187	0.000451244	12	N	65	90
P29621	Exosome	KLALK	NPDTNIVFSPLSISAALAIVSLGAK	GNTLE	3		833.4675291	2497.379187	0.000451244	12	N	65	90
P29621	Exosome	SLYKK	LALKNPDTNIVFSPLSISAALAIVSLGAK	GNTLE	3		975.2342642	2922.679393	0.000451244	4	N	61	90
P29621	Parental	KLALK	NPDTNIVFSPLSISAALAIVSLGAK	GNTLE	2		1249.697394	2497.379187	0.000451244	11	N	65	90
P29621	Parental	KLALK	NPDTNIVFSPLSISAALAIVSLGAK	GNTLE	3		833.4675291	2497.379187	0.000451244	15	N	65	90
P29621	Parental	SLYKK	LALKNPDTNIVFSPLSISAALAIVSLGAK	GNTLE	3		975.2342642	2922.679393	0.000451244	13	N	61	90
P29699	Exosome	VEISR	AQNVPLPVSTLVEFVIAATDCTAK	EVTDP	2	C21:+57.021	1272.67283	2543.33006	0.000451244	35	N	187	211
P29699	Exosome	VEISR	AQNVPLPVSTLVEFVIAATDCTAK	EVTDP	3	C21:+57.021	848.7844867	2543.33006	0.000451244	34	N	187	211
P29699	Exosome	GLGFR	ELACDDPEAEQVALLAVDYLNNHLLQGFK	QVLNQ	3	C4:+57.021	1095.875093	3284.601878	0.000451244	31	N	28	57
P29699	Exosome	NCSVR	QLTEHAVEGDCDFHILK	QDGQF	2	C11:+57.021	1006.48103	2010.946459	0.002212458	1	N	103	120
P29699	Exosome	NCSVR	QLTEHAVEGDCDFHILK	QDGQF	3	C11:+57.021	671.3232865	2010.946459	0.00091018	1	N	103	120
P29699	Exosome	YHDLR	HAFSPVASVESASGETLHSPK	VGQPG	3		713.3557979	2137.043994	0.000451244	4	N	301	322
P29699	Parental	VEISR	AQNVPLPVSTLVEFVIAATDCTAK	EVTDP	2	C21:+57.021	1272.67283	2543.33006	0.000451244	27	N	187	211
P29699	Parental	VEISR	AQNVPLPVSTLVEFVIAATDCTAK	EVTDP	3	C21:+57.021	848.7844867	2543.33006	0.000451244	28	N	187	211
P29699	Parental	GLGFR	ELACDDPEAEQVALLAVDYLNNHLLQGFK	QVLNQ	3	C4:+57.021	1095.875093	3284.601878	0.000451244	35	N	28	57
P29699	Parental	VEISR	AQNVPLPVSTLVEFVIAATDCTAKEVTDPAK	CNLLA	3	C21:+57.021	1095.574643	3283.70053	0.000823681	1	N	187	218

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P29699	Parental	NCSVR	QLTEHAVEGDCDFHILK	QDGQF	2	C11:+57.021	1006.48103	2010.946459	0.000451244	1	N	103	120
P29699	Parental	NCSVR	QLTEHAVEGDCDFHILK	QDGQF	3	C11:+57.021	671.3232865	2010.946459	0.000637154	1	N	103	120
P29699	Parental	YHDLR	HAFSPVASVESASGETLHSPK	VGQPG	3		713.3557979	2137.043994	0.000637154	3	N	301	322
P29758	Exosome	PLGCR	IAIAALEVLEEENLAENADK	MGAIL	2		1078.060596	2154.105591	0.000451244	15	N	331	351
P29758	Exosome	TLTSR	AFYNNVLGEYEEYITK	LFNYN	2		976.9679781	1951.920356	0.000451244	11	N	113	129
P29758	Exosome	KVCLR	LRDNGLLAKPTHGDIIR	LAPPL	4		473.0238689	1888.064275	0.001463592	2	N	396	413
P29758	Exosome	DVEGR	QYFDFLSAYGAVSQGHCHPK	IIDAM	4	C17:+57.021	578.7696926	2311.047571	0.00091018	2	N	76	96
P29758	Exosome	ELCTR	HQVLFIADEIQTGLAR	TGRWL	3		604.3323764	1809.973729	0.000451244	4	N	255	271
P29758	Parental	PLGCR	IAIAALEVLEEENLAENADK	MGAIL	2		1078.060596	2154.105591	0.000451244	22	N	331	351
P29758	Parental	TLTSR	AFYNNVLGEYEEYITK	LFNYN	2		976.9679781	1951.920356	0.001162105	4	N	113	129
P29788	Exosome	PGYPK	LIQDVWGIEGPIDAAFTR	INCQG	2		1001.026162	2000.036723	0.000451244	36	N	193	211
P29788	Exosome	PGYPK	LIQDVWGIEGPIDAAFTR	INCQG	3		667.6867078	2000.036723	0.000622848	3	N	193	211
P29788	Parental	PKLIQ	DVWGIEGPIDAAFTR	INCQG	2		823.9128088	1645.810018	0.000451244	30	N	196	211
P29788	Parental	PKLIQ	DVWGIEGPIDAAFTR	INCQG	3		549.6111392	1645.810018	0.000870037	1	N	196	211
P29788	Parental	PGYPK	LIQDVWGIEGPIDAAFTR	INCQG	2		1001.026162	2000.036723	0.000451244	11	N	193	211
P29788	Parental	LIQDV	WGIEGPIDAAFTR	INCQG	2		716.8651302	1431.71466	0.001162105	2	N	198	211
P30355	Parental	-	MDQEAVGNVVLLALVTLISVVQNAFFAHKVEHESK	AHNGR	4		959.7663576	3835.03423	0.002453667	1	N	0	35
P30355	Parental	FVRQK	YFVGYLGER	TQSTP	2		552.2801706	1102.544741	0.002663018	1	N	96	105
P30355	Parental	-	MDQEAVGNVVLLALVTLISVVQNAFFAHK	VEHES	3		1042.906042	3125.694726	0.001264573	3	N	0	29
P30355	Parental	-	MDQEAVGNVVLLALVTLISVVQNAFFAHK	VEHES	4		782.4314816	3125.694726	0.002374549	2	N	0	29
P30416	Exosome	LFDQR	ELCFEVGEGESLDLPCGLEEAIQR	MEKGE	3	C3:+57.021,C16:+57.021	917.4266562	2749.256568	0.000622848	1	N	186	210
P30416	Exosome	VATMK	VGEVCHITCKPEYAYGAAGSPPK	IPPNA	3	C5:+57.021,C9:+57.021	831.0632123	2490.166237	0.000622848	9	N	98	121
P30416	Exosome	MIGDR	VFVHYTGWLLDGTK	FDSSL	3		545.9563583	1634.845675	0.000451244	2	N	52	66
P30416	Parental	LFDQR	ELCFEVGEGESLDLPCGLEEAIQR	MEKGE	2	C3:+57.021,C16:+57.021	1375.636084	2749.256568	0.000451244	8	N	186	210
P30416	Parental	LFDQR	ELCFEVGEGESLDLPCGLEEAIQR	MEKGE	3	C3:+57.021,C16:+57.021	917.4266562	2749.256568	0.000451244	3	N	186	210
P30416	Parental	VATMK	VGEVCHITCKPEYAYGAAGSPPK	IPPNA	3	C5:+57.021,C9:+57.021	831.0632123	2490.166237	0.000451244	2	N	98	121
P30416	Parental	MIGDR	VFVHYTGWLLDGTK	FDSSL	3		545.9563583	1634.845675	0.000735798	4	N	52	66
P30681	Exosome	RPKIK	IEHPGLSIGDTAK	KLGEM	2		669.357138	1336.698676	0.00091018	2	N	114	127
P30681	Exosome	RPKIK	IEHPGLSIGDTAK	KLGEM	3		446.5740253	1336.698676	0.000451244	31	N	114	127
P30681	Exosome	ENRPK	IKIEHPGLSIGDTAK	KLGEM	2		789.9466516	1577.877703	0.000451244	62	N	112	127
P30681	Exosome	ENRPK	IKIEHPGLSIGDTAK	KLGEM	3		526.9670344	1577.877703	0.000451244	93	N	112	127
P30681	Exosome	TGSKK	KNEPEDEEEEEEEEEEEDDEEEEEDEE	-	3		1133.728084	3398.160851	0.001763695	9	N	183	210
P30681	Exosome	PNAPK	RPPSAFFLFCSENRPK	IKIEH	3	C10:+57.021	651.6652069	1951.972221	0.000451244	2	N	96	112
P30681	Exosome	EEHKK	KHPDSSVNFAEFSK	KCSER	2		796.8893337	1591.763067	0.000451244	12	N	29	43
P30681	Exosome	EEHKK	KHPDSSVNFAEFSK	KCSER	3		531.5954891	1591.763067	0.000451244	32	N	29	43
P30681	Exosome	KPRGK	MSSYAFFVQTCR	EEHKK	2	C11:+57.021	748.8369701	1495.65834	0.000451244	6	Y	12	24
P30681	Exosome	KPRGK	MSSYAFFVQTCR	EEHKK	2	M1:+15.995,C11:+57.021	756.8344701	1511.65334	0.000451244	16	Y	12	24
P30681	Exosome	EHKKK	HPDSSVNFAEFSK	KCSER	2		732.8418521	1463.668104	0.000451244	4	N	30	43
P30681	Exosome	EHKKK	HPDSSVNFAEFSKK	CSERW	3		531.5954891	1591.763067	0.000622848	3	N	30	44
P30681	Exosome	PPSAF	FLFCSENRPK	IKIEH	2	C4:+57.021	649.3218126	1296.628025	0.001162105	1	N	102	112
P30681	Parental	RPKIK	IEHPGLSIGDTAK	KLGEM	3		446.5740253	1336.698676	0.000451244	25	N	114	127
P30681	Parental	ENRPK	IKIEHPGLSIGDTAK	KLGEM	2		789.9466516	1577.877703	0.000451244	63	N	112	127
P30681	Parental	ENRPK	IKIEHPGLSIGDTAK	KLGEM	3		526.9670344	1577.877703	0.000451244	92	N	112	127
P30681	Parental	TGSKK	KNEPEDEEEEEEEEEEEDDEEEEEDEE	-	3		1133.728084	3398.160851	0.000451244	77	N	183	210
P30681	Parental	PNAPK	RPPSAFFLFCSENRPK	IKIEH	3	C10:+57.021	651.6652069	1951.972221	0.000451244	1	N	96	112
P31230	Parental	RLEQK	GAEADQIIEYLKQQVALLK	EKAIL	3		710.7322057	2129.173217	0.000451244	2	N	14	33
P31230	Parental	IVTAK	KHPDADSLYVEEVDVGEAAPR	TVVSG	3		766.3735172	2296.097152	0.002519933	1	N	164	185
P31230	Parental	QVRVR	LSTPLQTNCTASESVVQSPSVATTASPATKEQIK	AGEEK	3	C9:+57.021	1177.933448	3530.776943	0.001943752	1	N	81	115
P31725	Exosome	SQMER	SITTIIDTFHQYSRK	EGHPD	2		905.4788473	1808.942095	0.000451244	11	N	11	26
P31725	Exosome	SQMER	SITTIIDTFHQYSRK	EGHPD	3		603.9884982	1808.942095	0.000451244	16	N	11	26
P31725	Exosome	SQMER	SITTIIDTFHQYSRK	EGHPD	4		453.2433236	1808.942095	0.000823681	15	N	11	26
P31725	Exosome	SQMER	SITTIIDTFHQYSR	KEGHP	2		841.4313657	1680.847131	0.000451244	147	N	11	25
P31725	Exosome	SQMER	SITTIIDTFHQYSR	KEGHP	3		561.2901771	1680.847131	0.000451244	669	N	11	25
P31725	Exosome	MERSI	TTIIDTFHQYSR	KEGHP	2		741.3733194	1480.731039	0.000451244	16	N	13	25
P31725	Exosome	ERSIT	TIIDTFHQYSR	KEGHP	2		690.8494801	1379.68336	0.000451244	27	N	14	25
P31725	Exosome	SQMER	SITTIIDTFHQY	SRKEG	2		719.8647959	1437.713992	0.000451244	30	N	11	23
P31725	Exosome	MLMAK	LIFACHEKLHENNPR	GHGHS	2	C5:+57.021	939.4758847	1876.936169	0.000451244	2	N	86	101
P31725	Exosome	MLMAK	LIFACHEKLHENNPR	GHGHS	3	C5:+57.021	626.6531898	1876.936169	0.000451244	3	N	86	101
P31725	Exosome	MAKLI	FACHEKLHENNPR	GHGHS	3	C3:+57.021	551.2638137	1650.768041	0.002212458	1	N	88	101
P31725	Exosome	SITTI	IDTFHQYSR	KEGHP	2		583.7836088	1165.551618	0.0025889	2	N	16	25
P31725	Parental	SQMER	SITTIIDTFHQYSRK	EGHPD	2		905.4788473	1808.942095	0.000451244	32	N	11	26
P31725	Parental	SQMER	SITTIIDTFHQYSRK	EGHPD	3		603.9884982	1808.942095	0.000451244	45	N	11	26
P31725	Parental	SQMER	SITTIIDTFHQYSRK	EGHPD	4		453.2433236	1808.942095	0.000451244	63	N	11	26
P31725	Parental	SQMER	SITTIIDTFHQYSR	KEGHP	2		841.4313657	1680.847131	0.000451244	731	N	11	25
P31725	Parental	SQMER	SITTIIDTFHQYSR	KEGHP	3		561.2901771	1680.847131	0.000451244	2328	N	11	25

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P31725	Parental	MERSI	TTIIDTFHQYSR	KEGHP	2		741.3733194	1480.731039	0.000451244	57	N	13	25
P31725	Parental	MERSI	TTIIDTFHQYSR	KEGHP	3		494.584813	1480.731039	0.000451244	29	N	13	25
P31725	Parental	ERSIT	TIIDTFHQYSR	KEGHP	2		690.8494801	1379.68336	0.000451244	29	N	14	25
P31725	Parental	SQMER	SITTIIDTFHQY	SRKEG	2		719.8647959	1437.713992	0.000451244	50	N	11	23
P31725	Parental	SQMER	SITTIIDTFHQY	SRKEG	3		480.2457973	1437.713992	0.000451244	9	N	11	23
P31725	Parental	SQMER	SITTIIDTF	HQYSR	2		505.7743868	1009.533174	0.000622848	13	N	11	20
P31725	Parental	KKEFR	QMVEAQLATFMKK	EKRNE	2		762.8998023	1523.784005	0.000451244	3	N	39	52
P31725	Parental	KKEFR	QMVEAQLATFMKK	EKRNE	3		508.9358016	1523.784005	0.000451244	5	N	39	52
P31725	Parental	MLMAK	LIFACHEKLHENNPR	GHGHS	3	C5:+57.021	626.6531898	1876.936169	0.000451244	7	N	86	101
P31725	Parental	MLMAK	LIFACHEKLHENNPR	GHGHS	4	C5:+57.021	470.2418423	1876.936169	0.000622848	5	N	86	101
P31725	Parental	MAKLI	FACHEKLHENNPR	GHGHS	3	C3:+57.021	551.2638137	1650.768041	0.000451244	6	N	88	101
P31725	Parental	SITTI	IDTFHQYSR	KEGHP	2		583.7836088	1165.551618	0.001763695	5	N	16	25
P31725	Parental	MERSI	TTIIDTFHQYSRK	EGHPD	2		805.420801	1608.826002	0.000451244	4	N	13	26
P31725	Parental	ERSIT	TIIDTFHQYSRK	EGHPD	2		754.8969617	1507.778323	0.000451244	3	N	14	26
P31725	Parental	RSITT	IIDTFHQYSR	KEGHP	2		640.3256409	1278.635682	0.000622848	16	N	15	25
P31725	Parental	KKEKR	NEALINDIMEDLDTNQDNQLSF	EECMM	2		1276.577013	2551.138425	0.000451244	9	N	55	77
P31725	Parental	KKEKR	NEALINDIMEDLDTNQDNQLSFEECMML	MAKLI	3	C25:+57.021	1115.814078	3344.418833	0.000823681	3	N	55	83
P31725	Parental	KKEKR	NEALINDIMEDLDTNQDNQLSFEECMM	LMAKL	3	C25:+57.021,M26:+15.995	1083.451056	3247.329769	0.002296037	1	N	55	82
P31725	Parental	KKEFR	QMVEAQLATFMK	KEKRN	2		698.8523208	1395.689042	0.000622848	1	N	39	51
P31725	Parental	QMERS	ITTIIDTFHQYSR	KEGHP	3		532.279501	1593.815103	0.000622848	5	N	12	25
P31750	Exosome	GATMK	TFCGTPEYLAPEVLEDNDYGR	AVDWW	2	C3:+57.021	1223.547295	2445.07899	0.000451244	24	N	307	328
P31750	Exosome	IMQHR	FFANIVWQDVYEK	KLSPP	2		829.9148201	1657.81404	0.001162105	1	N	406	419
P31750	Parental	GATMK	TFCGTPEYLAPEVLEDNDYGR	AVDWW	2	C3:+57.021	1223.547295	2445.07899	0.000451244	17	N	307	328
P31750	Parental	IMQHR	FFANIVWQDVYEK	KLSPP	2		829.9148201	1657.81404	0.001943752	1	N	406	419
P31786	Exosome	YSHFK	QATVGDVNTDRPGLLDLK	GKAKW	3		638.0098505	1911.006152	0.000451244	7	N	33	51
P31786	Parental	YSHFK	QATVGDVNTDRPGLLDLK	GKAKW	2		956.5108758	1911.006152	0.000451244	15	N	33	51
P31786	Parental	YSHFK	QATVGDVNTDRPGLLDLK	GKAKW	3		638.0098505	1911.006152	0.000451244	22	N	33	51
P31786	Parental	YSHFK	QATVGDVNTDRPGLLDLK	GKAKW	2	[0:-17.027	947.9973758	1893.979152	0.000735798	2	N	33	51
P31786	Parental	YSHFK	QATVGDVNTDRPGLLDLKGK	AKWDS	2		1049.069089	2096.122578	0.000451244	7	N	33	53
P31786	Parental	YSHFK	QATVGDVNTDRPGLLDLKGK	AKWDS	3		699.7153262	2096.122578	0.000451244	6	N	33	53
P31786	Parental	YSHFK	QATVGDVNTDRPGLLDLKGK	AKWDS	4		525.0384446	2096.122578	0.000451244	9	N	33	53
P31809	Exosome	NTTVK	ELDSVTLTCLSNDIGANIQWLFNSQSLQLTER	MTLSQ	3	C9:+57.021	1222.609075	3664.803826	0.000451244	2	N	337	369
P31809	Parental	NTTVK	ELDSVTLTCLSNDIGANIQWLFNSQSLQLTER	MTLSQ	3	C9:+57.021	1222.609075	3664.803826	0.000451244	5	N	337	369
P31809	Parental	DPIKR	EDAGEYQCEISNPVSVR	RSNSI	2	C8:+57.021	976.936652	1951.857704	0.000451244	4	N	386	403
P31938	Exosome	EPPPK	LPSGVFSLEFQDFVNK	CLIKN	2		913.9703238	1825.925048	0.000451244	14	N	324	340
P31938	Exosome	-MPK	KKPTPIQLNPAPDGSAVNGTSSAETNLEALQK	KLEEL	3		1092.907716	3275.699747	0.000451244	11	N	3	35
P31938	Exosome	-MPK	KKPTPIQLNPAPDGSAVNGTSSAETNLEALQK	KLEEL	4		819.9327367	3275.699747	0.001871652	1	N	3	35
P31938	Parental	EPPPK	LPSGVFSLEFQDFVNK	CLIKN	2		913.9703238	1825.925048	0.00091018	1	N	324	340
P31938	Parental	-MPK	KKPTPIQLNPAPDGSAVNGTSSAETNLEALQK	KLEEL	3		1092.907716	3275.699747	0.000451244	3	N	3	35
P32020	Exosome	EEVMK	SKPVFDFLTILQCCPTSDGAAAAILSSEEFVQQYGLQSK	AVEIV	3	C13:+57.021,C14:+57.021	1436.039945	4305.096434	0.002145581	1	N	211	250
P32020	Exosome	EEVMK	SKPVFDFLTILQCCPTSDGAAAAILSSEEFVQQYGLQSK	AVEIV	4	C13:+57.021,C14:+57.021	1077.281909	4305.096434	0.002981883	1	N	211	250
P32020	Parental	EAGQK	ALEDAQIPYSAVEQACVGYVYGDSTSGQR	AIYHS	3	C16:+57.021	1045.484264	3133.429393	0.000451244	13	N	45	74
P32020	Parental	EEVMK	SKPVFDFLTILQCCPTSDGAAAAILSSEEFVQQYGLQSK	AVEIV	3	C13:+57.021,C14:+57.021	1436.039945	4305.096434	0.000451244	46	N	211	250
P32020	Parental	EEVMK	SKPVFDFLTILQCCPTSDGAAAAILSSEEFVQQYGLQSK	AVEIV	4	C13:+57.021,C14:+57.021	1077.281909	4305.096434	0.000451244	27	N	211	250
P32020	Parental	AQIPY	SAVEQACVGYVYGDSTSGQR	AIYHS	2	C7:+57.021	1067.479215	2132.942831	0.000451244	11	N	54	74
P32020	Parental	KSKPV	FDFLTILQCCPTSDGAAAAILSSEEFVQQYGLQSK	AVEIV	3	C9:+57.021,C10:+57.021	1298.957222	3893.848265	0.0025889	1	N	215	250
P32020	Parental	GPGGK	EATWVVDVK	NGKGS	2		523.7800035	1045.544407	0.002080925	4	N	470	479
P32067	Exosome	NRLNR	LTTDFNVIVQALSK	SKAKL	2		774.9357526	1547.855905	0.000451244	10	N	60	74
P32067	Exosome	HKTFK	GSIFAVFDSIQSAK	KFVEI	2		735.3858955	1468.756191	0.000451244	9	N	151	165
P32067	Parental	ALEAK	ICHQIEYYFGDFNLPR	DKFLK	3	C2:+57.021	691.3283718	2070.961716	0.000622848	4	N	16	32
P32067	Parental	GCLLK	FSGDLDDQTCREDLHFLFSNHGEIK	WVDFA	3	C10:+57.021	994.1228898	2979.345269	0.001162105	3	N	234	259
P32067	Parental	NRLNR	LTTDFNVIVQALSK	SKAKL	2		774.9357526	1547.855905	0.000451244	8	N	60	74
P32921	Exosome	GELKK	TLIDVLQPLIAEHQAR	RKAVT	3		606.3480264	1816.020679	0.000451244	27	N	436	452
P32921	Exosome	DCIGK	ISFPAVQAAPSFSNSFPK	IFRDR	2		947.9890478	1893.962496	0.000451244	16	N	281	299
P32921	Exosome	SDATK	ASEDFVDPWTVR	TSSAK	2		711.3389453	1420.662291	0.000451244	5	N	83	95
P32921	Exosome	FNQVK	GIFGFTDSDCIGK	ISFPA	2	C10:+57.021	708.8271248	1415.63865	0.000451244	7	N	268	281
P32921	Exosome	IFRDR	TDIQCLIPCAIDQDPYFR	MTRDV	2	C5:+57.021,C9:+57.021	1113.021973	2224.028346	0.000451244	10	N	304	322
P32921	Exosome	IFRDR	TDIQCLIPCAIDQDPYFR	MTRDV	3	C5:+57.021,C9:+57.021	742.3505821	2224.028346	0.000622848	3	N	304	322
P32921	Exosome	PKIFR	DRTDIQCLIPCAIDQDPYFR	MTRDV	2	C7:+57.021,C11:+57.021	1248.586	2495.156401	0.002080925	1	N	302	322
P32921	Exosome	PKIFR	DRTDIQCLIPCAIDQDPYFR	MTRDV	3	C7:+57.021,C11:+57.021	832.7266002	2495.156401	0.000451244	4	N	302	322
P32921	Exosome	KYLWK	DLTLEQAYSYTVENAKDIIACGFDINK	TFIFS	3	C21:+57.021	1031.169506	3090.485117	0.000451244	6	N	208	235
P32921	Exosome	TSSAK	GIDYDKLIVQFGSSK	IDKEL	3		557.2985612	1668.872284	0.000451244	2	N	100	115
P32921	Exosome	KYLWK	DLTLEQAYSYTVENAK	DIIAC	2		922.9497853	1843.883971	0.00091018	1	N	208	224
P32921	Parental	GELKK	TLIDVLQPLIAEHQAR	RKAVT	3		606.3480264	1816.020679	0.000451244	7	N	436	452
P34022	Exosome	AGSDR	AWVWNTHADFADECPKPELLAIR	FLNAE	3	C14:+57.021	913.7834801	2738.32704	0.000451244	5	N	118	141

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P34022	Exosome	AGSDR	AWVWNTHADFADECPKPELLAIR	FLNAE	4	C14:+57.021	685.5895601	2738.32704	0.001229886	3	N	118	141
P34022	Exosome	DTSTE	NADESNHDPQFEPIVSLPEQEIK	TLEED	3		879.4211958	2635.240187	0.000451244	11	N	16	39
P34022	Exosome	EQEIK	TLEEDEEELFK	MRAKL	2		691.3226265	1380.629653	0.002453667	1	N	39	50
P34022	Parental	MAAAK	DSHEDHDTSTENADESNHDPQFEPIVSLPEQEIK	TLEED	3		1297.235614	3888.683441	0.000451244	33	N	5	39
P34022	Parental	AGSDR	AWVWNTHADFADECPKPELLAIR	FLNAE	2	C14:+57.021	1370.17132	2738.32704	0.000451244	2	N	118	141
P34022	Parental	AGSDR	AWVWNTHADFADECPKPELLAIR	FLNAE	3	C14:+57.021	913.7834801	2738.32704	0.000451244	33	N	118	141
P34022	Parental	AGSDR	AWVWNTHADFADECPKPELLAIR	FLNAE	4	C14:+57.021	685.5895601	2738.32704	0.000451244	5	N	118	141
P34022	Parental	AKLFR	FASENDLPEWKER	GTGDV	2		810.886791	1619.757982	0.002981883	2	N	57	70
P34022	Parental	AKLFR	FASENDLPEWK	ERGTG	2		668.3149388	1334.614278	0.002453667	1	N	57	68
P34022	Parental	EQEIK	TLEEDEEELFK	MRAKL	2		691.3226265	1380.629653	0.000451244	1	N	39	50
P34152	Exosome	ALRTL	LATVDETIPALPASTHR	EIEMA	3		597.9920198	1790.952659	0.002080925	1	N	1002	1019
P34152	Exosome	QVKSD	YMQEIADQVDQEIALK	LGCLE	3	M2:+15.995	637.312459	1908.913977	0.002019181	1	N	154	170
P34884	Exosome	TNVPR	ASVPEGFLSELTQQLAQATGK	PAQYI	2		1088.068755	2174.12191	0.000451244	22	N	12	33
P34884	Exosome	TNVPR	ASVPEGFLSELTQQLAQATGK	PAQYI	3		725.7151033	2174.12191	0.001162105	2	N	12	33
P34884	Exosome	TNVPR	ASVPEGFLSELTQQLAQATGKPAQY	IAVHV	3		878.7856979	2633.333694	0.000451244	12	N	12	37
P34884	Exosome	QLMTF	SGTNDPCALCSLHSIGK	IGGAQ	3	C7:+57.021,C10:+57.021	606.2822795	1815.823439	0.001943752	1	N	50	67
P34884	Exosome	RNYSK	LLCGLLSDR	LHISP	2	C3:+57.021	523.7870743	1045.558549	0.002145581	2	N	78	87
P34884	Parental	TNVPR	ASVPEGFLSELTQQLAQATGK	PAQYI	2		1088.068755	2174.12191	0.000451244	11	N	12	33
P34884	Parental	TNVPR	ASVPEGFLSELTQQLAQATGKPAQY	IAVHV	2		1317.674647	2633.333694	0.000451244	6	N	12	37
P35123	Exosome	TQVGR	FAPQFSGYQQQDSQELLAFILDGLHEDLNR	VKKKP	3		1160.567582	3478.679346	0.000622848	2	N	381	411
P35123	Exosome	EAWNK	LLNWYGCVEGQQPIVR	KVVEH	2	C7:+57.021	966.4937431	1930.971886	0.001591523	2	N	103	119
P35123	Exosome	EQLSK	LDNTIQDAGLYQGQVLVIEPQNEDGTWPR	QSLQS	3		1090.541144	3268.600033	0.000622848	1	N	197	226
P35123	Parental	TQVGR	FAPQFSGYQQQDSQELLAFILDGLHEDLNRVK	KKPYL	4		927.4684807	3705.842723	0.000451244	4	N	381	413
P35123	Parental	TQVGR	FAPQFSGYQQQDSQELLAFILDGLHEDLNR	VKKKP	3		1160.567582	3478.679346	0.000451244	16	N	381	411
P35123	Parental	DSETR	SLYFDEQESEACEK	HLSMS	2	C12:+57.021	867.86209	1733.70858	0.000451244	9	N	746	760
P35123	Parental	EQLSK	LDNTIQDAGLYQGQVLVIEPQNEDGTWPR	QSLQS	3		1090.541144	3268.600033	0.000870037	2	N	197	226
P35123	Parental	PRHKR	LFTFSLVNSCGTADINSLATDGK	LLKLN	2	C10:+57.021	1216.094412	2430.173225	0.000622848	4	N	704	727
P35173	Parental	EAVEY	KSQVVAGQNLFIK	IDVGN	2		716.4200727	1430.824545	0.000451244	3	N	49	62
P35173	Parental	EAVEY	KSQVVAGQNLFIK	IDVGN	3		477.9493151	1430.824545	0.000662267	15	N	49	62
P35173	Parental	MIADK	VRPLLEEQTNEKYEK	FEAVE	2		938.4946944	1874.973789	0.000823681	4	N	28	43
P35173	Parental	MIADK	VRPLLEEQTNEKYEK	FEAVE	3		625.9990629	1874.973789	0.000451244	22	N	28	43
P35173	Parental	MIADK	VRPLLEEQTNEKYEK	FEAVE	4		469.7512472	1874.973789	0.001162105	13	N	28	43
P35173	Parental	MKVFR	GLSGEDDLKLK	GYQTN	2		587.819857	1173.624114	0.00091018	1	N	77	88
P35174-2	Exosome	AIEYK	VQVVQGLNYFIK	MNVGR	2		704.4038913	1406.792183	0.000451244	31	N	50	62
P35174-2	Exosome	-MTEY	TIEIIGGLSEARPATSEIQEIADK	VRPLL	2		1271.17448	2540.33336	0.000451244	8	N	4	28
P35174-2	Exosome	-MTEY	TIEIIGGLSEARPATSEIQEIADK	VRPLL	3		847.7855865	2540.33336	0.000451244	21	N	4	28
P35174-2	Exosome	MNVGR	GCYLHINVLSGISSENDLELTGYQTNK	AKNDE	3	C2:+57.021	1009.1576	3024.4494	0.000451244	36	N	67	94
P35174-2	Exosome	TIEII	GGLSEARPATSEIQEIADKVR	PLLEE	3		743.0612735	2226.160421	0.001352548	2	N	9	30
P35174-2	Exosome	TIEII	GGLSEARPATSEIQEIADK	VRPLL	2		986.5032477	1970.990895	0.00091018	1	N	9	28
P35174-2	Exosome	KAIEY	KVQVVQGLNYFIK	MNVGR	3		512.6368486	1534.887146	0.001699387	1	N	49	62
P35174-2	Exosome	MTEYT	IEIIGGLSEARPATSEIQEIADK	VRPLL	3		814.103027	2439.285681	0.000622848	5	N	5	28
P35174-2	Parental	AIEYK	VQVVQGLNYFIK	MNVGR	2		704.4038913	1406.792183	0.000451244	73	N	50	62
P35174-2	Parental	-MTEY	TIEIIGGLSEARPATSEIQEIADK	VRPLL	2		1271.17448	2540.33336	0.000451244	42	N	4	28
P35174-2	Parental	-MTEY	TIEIIGGLSEARPATSEIQEIADK	VRPLL	3		847.7855865	2540.33336	0.000451244	46	N	4	28
P35174-2	Parental	MNVGR	GCYLHINVLSGISSENDLELTGYQTNK	AKNDE	3	C2:+57.021	1009.1576	3024.4494	0.000451244	1528	N	67	94
P35174-2	Parental	TIEII	GGLSEARPATSEIQEIADKVR	PLLEE	2		1114.08801	2226.160421	0.001352548	3	N	9	30
P35174-2	Parental	TIEII	GGLSEARPATSEIQEIADKVR	PLLEE	3		743.0612735	2226.160421	0.001162105	14	N	9	30
P35174-2	Parental	TIEII	GGLSEARPATSEIQEIADK	VRPLL	2		986.5032477	1970.990895	0.000451244	16	N	9	28
P35174-2	Parental	TIEII	GGLSEARPATSEIQEIADK	VRPLL	3		658.0047652	1970.990895	0.000451244	15	N	9	28
P35174-2	Parental	KAIEY	KVQVVQGLNYFIK	MNVGR	2		768.4513728	1534.887146	0.000451244	24	N	49	62
P35174-2	Parental	KAIEY	KVQVVQGLNYFIK	MNVGR	3		512.6368486	1534.887146	0.000823681	24	N	49	62
P35174-2	Parental	GCYLH	INVLSGISSENDLELTGYQTNK	AKNDE	2		1198.103523	2394.191446	0.000451244	29	N	72	94
P35174-2	Parental	GCYLH	INVLSGISSENDLELTGYQTNK	AKNDE	3		799.0716154	2394.191446	0.000622848	4	N	72	94
P35174-2	Parental	-MTEY	TIEIIGGLSEARPATSEIQEIADKVRPLLEEK	TNEKY	3		1169.309109	3504.903926	0.000451244	14	N	4	36
P35174-2	Parental	LSEAR	PATSEIQEIADKVRPLLEEK	TNEKY	4		567.313206	2265.221624	0.000451244	4	N	16	36
P35174-2	Parental	IEIIG	GLSEARPATSEIQEIADK	VRPLL	2		957.9925159	1913.969432	0.002296037	2	N	10	28
P35174-2	Parental	YQTNK	AKNDELTYF	-	2		550.7670931	1099.518586	0.00307782	1	N	94	103
P35174-2	Parental	YLHIN	VLSGISSENDLELTGYQTNK	AKNDE	2		1084.540027	2167.064455	0.000451244	2	N	74	94
P35235	Exosome	MTSRR	WFHPNITGVEAENLLLTR	GVDGS	3		704.0413736	2109.100721	0.000823681	3	N	5	23
P35235	Exosome	SKPKK	SYIATQGCLQNTVNDFWR	MVFQE	2	C8:+57.021	1087.010486	2172.005371	0.001329271	2	N	325	343
P35235	Exosome	TDKVK	QGFWEEFETLQQQECK	LLYSR	2	C15:+57.021	1043.96267	2085.90974	0.0025889	1	N	244	260
P35276	Exosome	EDGRR	LADDLGFEFFEASAK	ENINV	2		830.3991999	1658.7828	0.000622848	5	N	152	167
P35276	Exosome	SFLFR	YADDSFTPAFVSTVGIDFK	VKTVY	2		1040.499642	2078.983685	0.000451244	1	N	41	60
P35276	Exosome	RHDKR	IKLQIWDTAGQER	YRTIT	3		519.9514958	1556.831087	0.000735798	1	Y	70	83
P35276	Parental	DKRIK	LQIWDTAGQER	YRTIT	2		658.8338301	1315.65206	0.001591523	2	Y	72	83

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P35276	Parental	EDGRR	LADDLGFEFFEASAK	ENINV	2		830.3991999	1658.7828	0.000451244	6	N	152	167
P35276	Parental	SFLFR	YADDSFTPAFVSTVGIDFK	VKTVY	2		1040.499642	2078.983685	0.000451244	13	N	41	60
P35278	Exosome	PMYYR	GAQAAIVVYDITNTDTFAR	AKNWV	2		1013.516158	2025.016716	0.000451244	26	N	92	111
P35278	Exosome	PMYYR	GAQAAIVVYDITNTDTFAR	AKNWV	3		676.0133721	2025.016716	0.001162105	2	N	92	111
P35278	Parental	PMYYR	GAQAAIVVYDITNTDTFAR	AKNWV	2		1013.516158	2025.016716	0.000451244	42	N	92	111
P35278	Parental	KELQR	QASPNIVIALAGNK	ADLAS	2		698.4018799	1394.78816	0.000662267	1	N	121	135
P35282	Exosome	AKQNK	GIEELFLDLCKR	MIETA	3	C10:+57.021	498.2661612	1491.775084	0.000451244	13	N	165	177
P35282	Parental	AKQNK	GIEELFLDLCKR	MIETA	3	C10:+57.021	498.2661612	1491.775084	0.000451244	10	N	165	177
P35282	Parental	PIYYR	DSNGAILVYDVTDEDSFQK	VKNWV	2		1058.490003	2114.964406	0.000451244	17	N	88	107
P35343	Exosome	RNPVK	VNLSTLVCYEDVGNNTSR	LRVVL	2	C8:+57.021	1020.986676	2039.957752	0.000451244	4	N	187	205
P35343	Exosome	EFLAK	EGRPSFVSSSSANTSTTL	-	2		914.4401161	1826.864632	0.0007646	6	N	341	359
P35343	Parental	EFLAK	EGRPSFVSSSSANTSTTL	-	2		914.4401161	1826.864632	0.000823681	2	N	341	359
P35441	Exosome	GVQYK	NNEEWTVDSCTECHCQNSVTICKK	VSCPI	3	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	1000.417641	2998.229522	0.000451244	100	N	326	350
P35441	Exosome	GVQYK	NNEEWTVDSCTECHCQNSVTICKK	VSCPI	4	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	750.5651804	2998.229522	0.000451244	61	N	326	350
P35441	Exosome	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	2	C1:+57.021,C10:+57.021,C13:+57.021	974.9265901	1947.83758	0.000451244	30	N	607	623
P35441	Exosome	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	3	C1:+57.021,C10:+57.021,C13:+57.021	650.2869934	1947.83758	0.000451244	51	N	607	623
P35441	Exosome	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	2	[0:-17.027,C1:+57.021,C10:+57.021,C13:+57.021	966.4130901	1930.81058	0.000451244	53	N	607	623
P35441	Exosome	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	3	[0:-17.027,C1:+57.021,C10:+57.021,C13:+57.021	644.6113267	1930.81058	0.001871652	1	N	607	623
P35441	Exosome	LQNVR	FVFGTTPEDILR	NKGCS	2		697.8698813	1393.724163	0.000451244	53	N	216	228
P35441	Exosome	VSNGK	AGTLDLSLSLPGKQQVVSVEEALLATGQWK	SITLF	3		1046.906876	3137.697228	0.000451244	7	N	124	154
P35441	Exosome	VARLR	VAKGDVNDNFQGVLQNVR	FVFGT	2		987.0141169	1972.012634	0.000451244	15	N	198	216
P35441	Exosome	VARLR	VAKGDVNDNFQGVLQNVR	FVFGT	3		658.3453446	1972.012634	0.000451244	15	N	198	216
P35441	Exosome	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDF	SGTFF	2	C8:+57.021	1336.613166	2671.210733	0.000622848	14	N	984	1008
P35441	Exosome	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDF	SGTFF	3	C8:+57.021	891.4113776	2671.210733	0.00091018	4	N	984	1008
P35441	Exosome	QRRSR	LCNNPTPQFGGKDCVGDVTENQVCNK	QDCPI	2	C2:+57.021,C14:+57.021,C24:+57.021	1476.157492	2950.299384	0.000451244	20	N	517	543
P35441	Exosome	QRRSR	LCNNPTPQFGGKDCVGDVTENQVCNK	QDCPI	3	C2:+57.021,C14:+57.021,C24:+57.021	984.4409282	2950.299384	0.000451244	94	N	517	543
P35441	Exosome	SPAFR	IENANLIPAVPDDKFQDLLDAVWADK	GFIFL	2		1455.748343	2909.481087	0.000451244	14	N	60	86
P35441	Exosome	SPAFR	IENANLIPAVPDDKFQDLLDAVWADK	GFIFL	3		970.8348289	2909.481087	0.000451244	68	N	60	86
P35441	Exosome	SPAFR	IENANLIPAVPDDKFQDLLDAVWADK	GFIFL	4		728.3780716	2909.481087	0.001871652	2	N	60	86
P35441	Exosome	GIQCK	DVDECKEVPDACFNHNGEHR	CKNTD	2	C5:+57.021,C12:+57.021	1214.505739	2426.995877	0.000451244	11	N	587	607
P35441	Exosome	GIQCK	DVDECKEVPDACFNHNGEHR	CKNTD	3	C5:+57.021,C12:+57.021	810.0064257	2426.995877	0.000451244	78	N	587	607
P35441	Exosome	GIQCK	DVDECKEVPDACFNHNGEHR	CKNTD	4	C5:+57.021,C12:+57.021	607.7567693	2426.995877	0.000451244	31	N	587	607
P35441	Exosome	DGSWK	CGACPPGYSGNGIQCK	DVDEC	2	C1:+57.021,C4:+57.021,C15:+57.021	863.3605516	1724.705503	0.000451244	27	N	571	587
P35441	Exosome	DGSWK	CGACPPGYSGNGIQCK	DVDEC	2	[0:-17.027,C1:+57.021,C4:+57.021,C15:+57.021	854.8470516	1707.678503	0.000870037	4	N	571	587
P35441	Exosome	QFGGK	DCVGDVTENQVCNK	QDCPI	2	C2:+57.021,C12:+57.021	819.3483955	1636.681191	0.000451244	46	N	529	543
P35441	Exosome	QRRSR	LCNNPTPQFGGK	DCVGD	2	C2:+57.021	666.8221768	1331.628754	0.000451244	9	N	517	529
P35441	Exosome	GEHLR	NALWHTGNTPGQVR	TLWHD	2		775.8952847	1549.774969	0.000451244	44	N	1077	1091
P35441	Exosome	GEHLR	NALWHTGNTPGQVR	TLWHD	3		517.5994565	1549.774969	0.000979378	5	N	1077	1091
P35441	Exosome	PLDPK	GTSQNDPNWVVR	HQGKE	2		686.8343614	1371.653123	0.000451244	48	N	968	980
P35441	Exosome	ILNER	DNCQYVYNVDQR	DTDMD	2	C3:+57.021	787.3389193	1572.662239	0.000451244	100	N	810	822
P35441	Exosome	EHRCK	NTDPGYNCLPCPPR	FTGSQ	2	C8:+57.021,C11:+57.021	830.8640157	1659.712431	0.000451244	192	N	609	623
P35441	Exosome	GVQYK	NNEEWTVDSCTECHCQNSVTICK	KVSCP	2	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	1436.075079	2870.134558	0.000451244	36	N	326	349
P35441	Exosome	GVQYK	NNEEWTVDSCTECHCQNSVTICK	KVSCP	3	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	957.7193195	2870.134558	0.000451244	144	N	326	349
P35441	Exosome	TGQWK	SITLFVQEDR	AQLYI	2		604.3200242	1206.624448	0.000451244	20	N	154	164
P35441	Exosome	LKGLR	TIVTTLQDSIR	KVTEE	2		623.8542312	1245.692862	0.000451244	144	N	288	299
P35441	Exosome	VSNGK	AGTLDLSLSLPGK	QQVVS	2		636.3644317	1270.713263	0.000451244	24	N	124	137
P35441	Exosome	INTER	DDDYAGFVFGYQSSSR	FYVVM	2		907.3873522	1812.759104	0.000451244	16	N	1018	1034
P35441	Exosome	SLPGK	QQVVSVEEALLATGQWK	SITLF	2		943.5050621	1884.994524	0.000451244	54	N	137	154
P35441	Exosome	SLPGK	QQVVSVEEALLATGQWK	SITLF	3		629.3393081	1884.994524	0.000451244	43	N	137	154
P35441	Exosome	SLPGK	QQVVSVEEALLATGQWK	SITLF	2	Q1:-17.027	934.9915621	1867.967524	0.000451244	11	N	137	154

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P35441	Exosome	SLPGK	QQVVSVEEALLATGQWK	SITLF	2	[0:-17.027	934.9915621	1867.967524	0.000451244	16	N	137	154
P35441	Exosome	YIGHK	TKDLQAICGLSCDELSSMVLELK	GLRTI	3	C8:+57.021,C12:+57.021	870.7658446	2609.274134	0.000451244	11	N	262	285
P35441	Exosome	YIGHK	TKDLQAICGLSCDELSSMVLELK	GLRTI	3	C8:+57.021,C12:+57.021,M18:+15.995	876.0975113	2625.269134	0.000451244	5	N	262	285
P35441	Exosome	HMCGS	NRIPESGGDNGVFDIFELIGGAR	RGPGR	2		1217.112017	2432.208434	0.000451244	12	N	18	41
P35441	Exosome	HMCGS	NRIPESGGDNGVFDIFELIGGAR	RGPGR	3		811.7439445	2432.208434	0.000451244	80	N	18	41
P35441	Exosome	CGSNR	IPESGGDNGVFDIFELIGGAR	RGPGR	2		1082.039997	2162.064395	0.000451244	59	N	20	41
P35441	Exosome	CGSNR	IPESGGDNGVFDIFELIGGAR	RGPGR	3		721.6959316	2162.064395	0.000451244	21	N	20	41
P35441	Exosome	ITRIR	LCNSPSPQMNGKPCEGEAR	ETKAC	3	C2:+57.021,C14:+57.021	711.3156549	2130.923565	0.000851441	1	N	460	479
P35441	Exosome	VSELK	RPPLCFHNGVQYK	NNEEW	3	C5:+57.021	539.2772831	1614.808449	0.000451244	36	N	313	326
P35441	Exosome	VSELK	RPPLCFHNGVQYK	NNEEW	4	C5:+57.021	404.7099124	1614.808449	0.000451244	9	N	313	326
P35441	Exosome	RRLVK	GQDLSSPAFR	IENAN	2		539.2703343	1076.525069	0.000823681	4	N	50	60
P35441	Exosome	NKNAK	CNYLGHYSDPMYR	CECKP	2	C1:+57.021	838.3535157	1674.691431	0.000451244	3	N	662	675
P35441	Exosome	NKNAK	CNYLGHYSDPMYR	CECKP	2	C1:+57.021,M11:+15.995	846.3510157	1690.686431	0.000451244	24	N	662	675
P35441	Exosome	NKNAK	CNYLGHYSDPMYR	CECKP	3	C1:+57.021,M11:+15.995	564.5699438	1690.686431	0.000451244	5	N	662	675
P35441	Exosome	NKNAK	CNYLGHYSDPMYR	CECKP	2	[0:-17.027,C1:+57.021	829.8400157	1657.664431	0.000451244	5	N	662	675
P35441	Exosome	NKNAK	CNYLGHYSDPMYR	CECKP	2	[0:-	837.8375157	1673.659431	0.000451244	15	N	662	675
P35441	Exosome	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	3	C1:+39.994,C4:+57.021,C24:+57.021	1373.220263	4116.637388	0.000451244	16	N	773	810
P35441	Exosome	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	4	C1:+39.994,C4:+57.021,C24:+57.021	1030.167147	4116.637388	0.000823681	2	N	773	810
P35441	Exosome	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	3	C1:+57.021,C4:+57.021,C24:+57.021	1378.895929	4133.664388	0.000451244	86	N	773	810
P35441	Exosome	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	4	C1:+57.021,C4:+57.021,C24:+57.021	1034.423897	4133.664388	0.000451244	69	N	773	810
P35441	Exosome	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	3	[0:-17.027,C1:+57.021,C4:+57.021,C24:+57.021	1373.220263	4116.637388	0.000622848	15	N	773	810
P35441	Exosome	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	4	[0:-17.027,C1:+57.021,C4:+57.021,C24:+57.021	1030.167147	4116.637388	0.001839721	2	N	773	810
P35441	Exosome	LAVER	KDNTGQIFSVVSNGK	AGTLD	2		797.4157156	1592.815831	0.000622848	1	N	109	124
P35441	Exosome	LAVER	KDNTGQIFSVVSNGK	AGTLD	3		531.9464104	1592.815831	0.000451244	20	N	109	124
P35441	Exosome	AVERK	DNTGQIFSVVSNGK	AGTLD	2		733.3682341	1464.720868	0.001162105	5	N	110	124
P35441	Exosome	VVMWK	QVTQSYWDTNPTR	AQGYS	2		798.3765904	1594.737581	0.000451244	89	N	1041	1054
P35441	Exosome	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTER	DDDYA	3	C8:+57.021	1275.596835	3823.767106	0.000622848	7	N	984	1018
P35441	Exosome	DNCPY	NHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	3	C18:+57.021	1109.147151	3324.418053	0.000451244	37	N	779	810
P35441	Exosome	DNCPY	NHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	4	C18:+57.021	832.1123133	3324.418053	0.000451244	24	N	779	810
P35441	Exosome	ADTDK	NGEGDACAVDIDGDGILNER	DNCQY	2	C7:+57.021	1045.45848	2088.90136	0.000451244	17	N	790	810
P35441	Exosome	DGDGR	GDACKDDFDHDNVPDIDDICPENFDISETDFR	RFQMI	3	C4:+57.021,C20:+57.021	1262.85315	3785.536051	0.000451244	20	N	926	958
P35441	Exosome	DGDGR	GDACKDDFDHDNVPDIDDICPENFDISETDFR	RFQMI	4	C4:+57.021,C20:+57.021	947.3918128	3785.536051	0.000451244	4	N	926	958
P35441	Exosome	GDACK	DDFDHDNVPDIDDICPENFDISETDFR	RFQMI	3	C15:+57.021	1085.782927	3254.325382	0.000451244	16	N	931	958
P35441	Exosome	CKNTD	PGYNCLPCPPR	FTGSQ	2	C5:+57.021,C8:+57.021	665.8052411	1329.594882	0.001352548	4	N	612	623
P35441	Exosome	KACKK	DACPINGGWGPWSPWDICSVTCGGGVQR	RSRLC	3	C3:+57.021,C18:+57.021,C22:+57.021	1030.45328	3088.336439	0.000622848	8	N	486	514
P35441	Exosome	TEENR	ELVSELKRPPLCFHNGVQYK	NNEEW	3	C12:+57.021	805.4268565	2413.25717	0.000451244	10	N	306	326
P35441	Exosome	TEENR	ELVSELKRPPLCFHNGVQYK	NNEEW	4	C12:+57.021	604.3220924	2413.25717	0.000451244	10	N	306	326
P35441	Exosome	IPDDR	DNCPFHYNPAQYDYDRDDVGDR	CDNCP	3	C3:+57.021	911.3740969	2731.098891	0.000451244	6	N	751	773
P35441	Exosome	IPDDR	DNCPFHYNPAQYDYDRDDVGDR	CDNCP	4	C3:+57.021	683.7825227	2731.098891	0.000451244	4	N	751	773
P35441	Exosome	SGTFF	INTERDDDYAGFVFGYQSSSR	FYVVM	2		1214.046539	2426.077479	0.000451244	4	N	1013	1034
P35441	Exosome	SGTFF	INTERDDDYAGFVFGYQSSSR	FYVVM	3		809.700293	2426.077479	0.000451244	2	N	1013	1034
P35441	Exosome	ADTDK	NGEGDACAVDIDGDGILNERDNCQYVYNVDQR	DTDMD	3	C7:+57.021,C23:+57.021	1215.52548	3643.553039	0.000451244	5	N	790	822
P35441	Exosome	VQEDR	AQLYIDCDKMESAELDVPIQSIFTR	DLASV	3	C7:+57.021	981.481027	2941.419681	0.000451244	13	N	164	189
P35441	Exosome	VQEDR	AQLYIDCDKMESAELDVPIQSIFTR	DLASV	3	C7:+57.021,M10:+15.995	986.8126937	2957.414681	0.000698008	5	N	164	189
P35441	Exosome	GDACK	DDFDHDNVPDIDDICPENFDISETDFRR	FQMIP	3	C15:+57.021	1137.816631	3410.426493	0.000451244	7	N	931	959
P35441	Exosome	GDACK	DDFDHDNVPDIDDICPENFDISETDFRR	FQMIP	4	C15:+57.021	853.6144232	3410.426493	0.000451244	6	N	931	959
P35441	Exosome	GHKTK	DLQAICGLSCDELSSMVLELK	GLRTI	2	C6:+57.021,C10:+57.021	1191.073546	2380.131492	0.000451244	5	N	264	285
P35441	Exosome	GHKTK	DLQAICGLSCDELSSMVLELK	GLRTI	3	C6:+57.021,C10:+57.021	794.384964	2380.131492	0.000451244	11	N	264	285
P35441	Exosome	GHKTK	DLQAICGLSCDELSSMVLELK	GLRTI	2	C6:+57.021,C10:+57.021,M16:+15.995	1199.071046	2396.126492	0.000823681	8	N	264	285
P35441	Exosome	LRVAK	GDVNDNFQGVLQNVR	FVFGT	2		837.9138715	1673.812143	0.000451244	6	N	201	216
P35441	Exosome	LRVAK	GDVNDNFQGVLQNVR	FVFGT	3		558.945181	1673.812143	0.000451244	2	N	201	216
P35441	Exosome	IDCDK	MESAELDVPIQSIFTR	DLASV	2		918.4645489	1834.913498	0.000622848	6	N	173	189
P35441	Exosome	AVERK	DNTGQIFSVVSNGKAGTLDLSLSLPGK	QQVVS	3		906.8156572	2717.423572	0.0025889	1	N	110	137
P35441	Exosome	MCGSN	RIPESGGDNGVFDIFELIGGAR	RGPGR	3		773.7296353	2318.165506	0.000451244	2	N	19	41

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P35441	Exosome	DACAV	DIDGDGILNERDNCQYVYNVDQR	DTDMD	3	C14:+57.021	924.4160733	2770.22482	0.001463592	1	N	799	822
P35441	Exosome	LKGLR	TIVTTLQDSIRK	VTEEN	2		687.9017127	1373.787825	0.000870037	1	N	288	300
P35441	Parental	GVQYK	NNEEWTVDSCTECHCQNSVTICKK	VSCPI	3	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	1000.417641	2998.229522	0.000451244	15	N	326	350
P35441	Parental	GVQYK	NNEEWTVDSCTECHCQNSVTICKK	VSCPI	4	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	750.5651804	2998.229522	0.001463592	1	N	326	350
P35441	Parental	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	2	C1:+57.021,C10:+57.021,C13:+57.021	974.9265901	1947.83758	0.000451244	1	N	607	623
P35441	Parental	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	3	C1:+57.021,C10:+57.021,C13:+57.021	650.2869934	1947.83758	0.000451244	5	N	607	623
P35441	Parental	NGEHR	CKNTDPGYNCLPCPPR	FTGSQ	2	[0:-17.027,C1:+57.021,C10:+57.021,C13:+57.021	966.4130901	1930.81058	0.000451244	11	N	607	623
P35441	Parental	LQNVR	FVFGTTPEDILR	NKGCS	2		697.8698813	1393.724163	0.000451244	20	N	216	228
P35441	Parental	VSNGK	AGTLDLSLSLPGKQQVVSVEEALLATGQWK	SITLF	3		1046.906876	3137.697228	0.000451244	8	N	124	154
P35441	Parental	VARLR	VAKGDVNDNFQGVLQNVR	FVFGT	2		987.0141169	1972.012634	0.000451244	8	N	198	216
P35441	Parental	VARLR	VAKGDVNDNFQGVLQNVR	FVFGT	3		658.3453446	1972.012634	0.000451244	9	N	198	216
P35441	Parental	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDF	SGTFF	2	C8:+57.021	1336.613166	2671.210733	0.000451244	6	N	984	1008
P35441	Parental	RHQGK	ELVQTVNCDPGLAVGYDEFNAVDF	SGTFF	3	C8:+57.021	891.4113776	2671.210733	0.001871652	3	N	984	1008
P35441	Parental	QRRSR	LCNNPTPQFGGKDCVGDVTENQVCNK	QDCPI	3	C2:+57.021,C14:+57.021,C24:+57.021	984.4409282	2950.299384	0.000451244	11	N	517	543
P35441	Parental	SPAFR	IENANLIPAVPDDKFQDLLDAVWADK	GFIFL	3		970.8348289	2909.481087	0.000451244	27	N	60	86
P35441	Parental	GIQCK	DVDECKEVPDACFNHNGEHR	CKNTD	3	C5:+57.021,C12:+57.021	810.0064257	2426.995877	0.000662267	4	N	587	607
P35441	Parental	DGSWK	CGACPPGYSGNGIQCK	DVDEC	2	C1:+57.021,C4:+57.021,C15:+57.021	863.3605516	1724.705503	0.000698008	2	N	571	587
P35441	Parental	QFGGK	DCVGDVTENQVCNK	QDCPI	2	C2:+57.021,C12:+57.021	819.3483955	1636.681191	0.000451244	11	N	529	543
P35441	Parental	GEHLR	NALWHTGNTPGQVR	TLWHD	2		775.8952847	1549.774969	0.000451244	6	N	1077	1091
P35441	Parental	GEHLR	NALWHTGNTPGQVR	TLWHD	3		517.5994565	1549.774969	0.001839721	2	N	1077	1091
P35441	Parental	ILNER	DNCQYVYNVDQR	DTDMD	2	C3:+57.021	787.3389193	1572.662239	0.001871652	1	N	810	822
P35441	Parental	EHRCK	NTDPGYNCLPCPPR	FTGSQ	2	C8:+57.021,C11:+57.021	830.8640157	1659.712431	0.000451244	19	N	609	623
P35441	Parental	GVQYK	NNEEWTVDSCTECHCQNSVTICK	KVSCP	3	C10:+57.021,C13:+57.021,C15:+57.021,C22:+57.021	957.7193195	2870.134558	0.000622848	3	N	326	349
P35441	Parental	LKGLR	TIVTTLQDSIR	KVTEE	2		623.8542312	1245.692862	0.000451244	1	N	288	299
P35441	Parental	SLPGK	QQVVSVEEALLATGQWK	SITLF	2		943.5050621	1884.994524	0.000451244	10	N	137	154
P35441	Parental	SLPGK	QQVVSVEEALLATGQWK	SITLF	3		629.3393081	1884.994524	0.001162105	1	N	137	154
P35441	Parental	YIGHK	TKDLQAICGLSCDELSSMVLELK	GLRTI	3	C8:+57.021,C12:+57.021	870.7658446	2609.274134	0.001162105	2	N	262	285
P35441	Parental	HMCGS	NRIPESGGDNGVFDIFELIGGAR	RGPGR	2		1217.112017	2432.208434	0.000451244	3	N	18	41
P35441	Parental	HMCGS	NRIPESGGDNGVFDIFELIGGAR	RGPGR	3		811.7439445	2432.208434	0.000451244	6	N	18	41
P35441	Parental	CGSNR	IPESGGDNGVFDIFELIGGAR	RGPGR	2		1082.039997	2162.064395	0.000451244	1	N	20	41
P35441	Parental	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	3	C1:+57.021,C4:+57.021,C24:+57.021	1378.895929	4133.664388	0.000451244	2	N	773	810
P35441	Parental	DVGDR	CDNCPYNHNPDQADTDKNGEGDACAVDIDGDGILNER	DNCQY	4	C1:+57.021,C4:+57.021,C24:+57.021	1034.423897	4133.664388	0.000851441	6	N	773	810
P35441	Parental	VVMWK	QVTQSYWDTNPTR	AQGYS	2		798.3765904	1594.737581	0.000451244	15	N	1041	1054
P35461	Exosome	SHRSK	VKSNLCLPICPTTLDNTEITGNAVNVK	TYCCK	3	C6:+57.021,C10:+57.021	991.1793049	2970.514515	0.001162105	3	N	45	72
P35461	Exosome	RSKVK	SNLCLPICPTTLDNTEITGNAVNVK	TYCCK	2	C4:+57.021,C8:+57.021	1372.683369	2743.351138	0.000451244	37	N	47	72
P35461	Exosome	RSKVK	SNLCLPICPTTLDNTEITGNAVNVK	TYCCK	3	C4:+57.021,C8:+57.021	915.4581792	2743.351138	0.000451244	37	N	47	72
P35461	Parental	SHRSK	VKSNLCLPICPTTLDNTEITGNAVNVK	TYCCK	3	C6:+57.021,C10:+57.021	991.1793049	2970.514515	0.000451244	9	N	45	72
P35461	Parental	RSKVK	SNLCLPICPTTLDNTEITGNAVNVK	TYCCK	2	C4:+57.021,C8:+57.021	1372.683369	2743.351138	0.000451244	40	N	47	72
P35461	Parental	RSKVK	SNLCLPICPTTLDNTEITGNAVNVK	TYCCK	3	C4:+57.021,C8:+57.021	915.4581792	2743.351138	0.000451244	20	N	47	72
P35461	Parental	PICPT	TLDNTEITGNAVNVK	TYCCK	2		794.9130058	1587.810412	0.000735798	3	N	57	72
P35486	Exosome	VEVRK	EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR	GANQW	3		1278.267526	3831.779179	0.000451244	9	N	344	378
P35486	Exosome	QKIIR	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	AHGFT	3	C3:+57.021,C6:+57.021,C12:+57.021,C13:+57.021	1178.860003	3533.55661	0.002296037	1	N	88	119
P35486	Parental	VEVRK	EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR	GANQW	3		1278.267526	3831.779179	0.000451244	33	N	344	378
P35486	Parental	CDLHR	LEEGPPVTTVLTR	EDGLK	2		706.3937205	1410.771841	0.000870037	1	N	45	58
P35505	Exosome	NPKPR	IGVAIGDQILDLSVIK	HLFTG	2		827.4934347	1652.971269	0.000451244	42	N	31	47
P35505	Exosome	DWSAR	DIQQWEYVPLGPFLGK	SFGTT	2		945.493966	1888.972332	0.000451244	38	N	237	253
P35505	Exosome	QGQTR	TFLLDGDEVIITGHCQGDGYR	VGFGQ	2	C15:+57.021	1183.557997	2365.100394	0.000451244	19	N	381	402
P35505	Exosome	QGQTR	TFLLDGDEVIITGHCQGDGYR	VGFGQ	3	C15:+57.021	789.3745981	2365.100394	0.000451244	8	N	381	402
P35505	Exosome	WKEAR	ASLQNLLSASQAR	LRDDK	2		679.8734866	1357.731373	0.002019181	1	N	82	95
P35505	Exosome	GIMFR	GKENALLPNWLHLPVGYHGR	ASSIV	4		568.5596129	2270.207252	0.000451244	8	N	142	162
P35505	Parental	NPKPR	IGVAIGDQILDLSVIK	HLFTG	2		827.4934347	1652.971269	0.000451244	10	N	31	47
P35505	Parental	DWSAR	DIQQWEYVPLGPFLGK	SFGTT	2		945.493966	1888.972332	0.000451244	16	N	237	253
P35505	Parental	QGQTR	TFLLDGDEVIITGHCQGDGYR	VGFGQ	2	C15:+57.021	1183.557997	2365.100394	0.001654178	2	N	381	402

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P35505	Parental	WKEAR	ASLQNLLSASQAR	LRDDK	2		679.8734866	1357.731373	0.001591523	1	N	82	95
P35550	Parental	YGEKR	VSISEGDDKIEYR	AWNPF	3		504.2514995	1509.731099	0.001229886	2	N	128	141
P35550	Parental	PFRSK	LAAAILGGVDQIHIKPGAK	VLYLG	3		624.7075547	1871.099264	0.002663018	1	N	149	168
P35550	Parental	PFRSK	LAAAILGGVDQIHIKPGAK	VLYLG	4		468.782616	1871.099264	0.000451244	11	N	149	168
P35550	Parental	EPYER	DHAVVVGVYRPPPK	VKN-	3		511.9565811	1532.846343	0.001264573	7	N	310	324
P35550	Parental	KPGAK	VLYLGAASGTTVSHVSDIVGPDGLVY	AVEFS	2		1295.674116	2589.332631	0.002212458	3	N	168	194
P35550	Parental	VISIK	ANCIDSTASAEAVFASEVK	KMQQE	2	C3:+57.021	985.4625026	1968.909405	0.000451244	2	N	271	290
P35564	Exosome	IWKPR	KIPNPDFFEDLEPFK	MTPFS	3		612.6458495	1834.914148	0.000622848	5	N	401	416
P35564	Exosome	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSKSK	SDAST	4		792.8462583	3167.353833	0.001871652	3	N	20	48
P35564	Exosome	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSK	SKSDA	3		985.0834139	2952.226842	0.000451244	7	N	20	46
P35564	Exosome	VNPSR	EIEDPEDRKPEDWDERPK	IADPD	3		761.6895054	2282.045116	0.001329271	1	N	275	293
P35564	Exosome	VNPSR	EIEDPEDRKPEDWDERPK	IADPD	4		571.519079	2282.045116	0.000698008	3	N	275	293
P35564	Exosome	IANPK	CESAPGCGVWQRPMIDNPNYK	GKWKP	3	C1:+57.021,C7:+57.021,M14:+15.995	832.3684473	2494.081942	0.000451244	5	N	360	381
P35564	Parental	PPSPK	VTYKAPVPTGEVYFADSFDR	GSLSG	3		754.7079487	2261.100446	0.000451244	5	N	58	78
P35564	Parental	IWKPR	KIPNPDFFEDLEPFK	MTPFS	2		918.4648742	1834.914148	0.000451244	11	N	401	416
P35564	Parental	IWKPR	KIPNPDFFEDLEPFK	MTPFS	3		612.6458495	1834.914148	0.000451244	54	N	401	416
P35564	Parental	AISAK	LNKPFLFDTKPLIVQYEVNFQNGIECGGAYVK	LLSKT	3	C26:+57.021	1234.639759	3700.895876	0.000451244	22	N	135	167
P35564	Parental	AISAK	LNKPFLFDTKPLIVQYEVNFQNGIECGGAYVK	LLSKT	4	C26:+57.021	926.231769	3700.895876	0.000662267	3	N	135	167
P35564	Parental	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSKSK	SDAST	3		1056.792411	3167.353833	0.000451244	19	N	20	48
P35564	Parental	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSKSK	SDAST	4		792.8462583	3167.353833	0.000622848	19	N	20	48
P35564	Parental	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSK	SKSDA	2		1477.121221	2952.226842	0.000451244	2	N	20	46
P35564	Parental	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSK	SKSDA	3		985.0834139	2952.226842	0.000451244	38	N	20	46
P35564	Parental	AAVEA	HDGHDDDAIDIEDDLDDVIEEVEDSK	SKSDA	4		739.0645104	2952.226842	0.000851441	2	N	20	46
P35564	Parental	KLLSK	TAELSLDQFHDKTPY	TIMFG	3		588.9533421	1763.836626	0.001591523	2	N	171	186
P35564	Parental	KVTYK	APVPTGEVYFADSFDRGSLSGWILSK	AKKDD	3		933.804981	2798.391543	0.000451244	7	N	62	88
P35564	Parental	KPLIV	QYEVNFQNGIECGGAYVK	LLSKT	2	C12:+57.021	1038.478487	2074.941374	0.0007646	9	N	149	167
P35564	Parental	DSFDR	GSLSGWILSK	AKKDD	2		524.2958207	1046.576041	0.000662267	9	N	78	88
P35564	Parental	KVTYK	APVPTGEVYFADSFDR	GSLSG	2		885.9208308	1769.826062	0.000451244	5	N	62	78
P35564	Parental	KTHLY	TLILNPDNSFEILVDQSVVNSGNLLNDMTPPVNPSR	EIEDP	3		1308.333877	3921.978232	0.00091018	4	N	239	275
P35564	Parental	VNPSR	EIEDPEDRKPEDWDERPK	IADPD	3		761.6895054	2282.045116	0.000823681	9	N	275	293
P35564	Parental	VNPSR	EIEDPEDRKPEDWDERPK	IADPD	4		571.519079	2282.045116	0.001162105	5	N	275	293
P35564	Parental	KLLSK	TAELSLDQFHDK	TPYTI	2		702.3442276	1402.672855	0.000823681	2	N	171	183
P35564	Parental	IANPK	CESAPGCGVWQRPMIDNPNYK	GKWKP	3	C1:+57.021,C7:+57.021,M14:+15.995	832.3684473	2494.081942	0.000851441	1	N	360	381
P35585	Exosome	PISVK	FEIPYFTTSGIQVR	YLKII	2		829.4333771	1656.851154	0.000451244	19	N	379	393
P35585	Exosome	LMSYR	LNTHVKPLIWIESVIEK	HSHSR	3		673.7266149	2018.156445	0.000662267	5	N	268	285
P35700	Exosome	GISFR	GLFIIDDKGILR	QITIN	3		453.9385275	1358.792183	0.000662267	5	N	128	140
P35700	Exosome	QFTDK	HGEVCPAGWKPGSDTIKPDVNK	SKEYF	3	C5:+57.021	798.0623544	2391.163663	0.000622848	10	N	168	190
P35700	Exosome	QFTDK	HGEVCPAGWKPGSDTIKPDVNK	SKEYF	4	C5:+57.021	598.7987158	2391.163663	0.000451244	44	N	168	190
P35700	Exosome	EYKGK	YVVFFFYPLDFTFVCPTEIIAFSDR	ADEFK	3	C15:+57.021	1031.842113	3092.502939	0.000451244	12	N	37	62
P35700	Exosome	KGILR	QITINDLPVGR	SVDEI	2	[0:-17.027	604.835616	1207.655632	0.00307782	1	N	140	151
P35700	Exosome	DEFKK	LNCQVIGASVDSHFCHLAWINTPK	KQGGL	3	C3:+57.021,C15:+57.021	923.1198322	2766.336097	0.000451244	4	N	68	92
P35700	Exosome	DEFKK	LNCQVIGASVDSHFCHLAWINTPK	KQGGL	4	C3:+57.021,C15:+57.021	692.5918241	2766.336097	0.000622848	8	N	68	92
P35700	Exosome	YVVFF	FYPLDFTFVCPTEIIAFSDR	ADEFK	2	C10:+57.021	1219.590777	2437.165955	0.000451244	8	N	42	62
P35700	Exosome	ADEFK	KLNCQVIGASVDSHFCHLAWINTPK	KQGGL	4	C4:+57.021,C16:+57.021	724.6155649	2894.43106	0.001591523	2	N	67	92
P35700	Parental	GISFR	GLFIIDDKGILR	QITIN	3		453.9385275	1358.792183	0.000622848	9	N	128	140
P35700	Parental	DEIIR	LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVNK	SKEYF	3	C15:+57.021	1190.600074	3568.776823	0.001463592	2	N	158	190
P35700	Parental	DEIIR	LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVNK	SKEYF	4	C15:+57.021	893.2020058	3568.776823	0.000823681	6	N	158	190
P35700	Parental	QFTDK	HGEVCPAGWKPGSDTIKPDVNK	SKEYF	2	C5:+57.021	1196.589632	2391.163663	0.002145581	1	N	168	190
P35700	Parental	QFTDK	HGEVCPAGWKPGSDTIKPDVNK	SKEYF	3	C5:+57.021	798.0623544	2391.163663	0.000662267	3	N	168	190
P35700	Parental	QFTDK	HGEVCPAGWKPGSDTIKPDVNK	SKEYF	4	C5:+57.021	598.7987158	2391.163663	0.000451244	26	N	168	190
P35700	Parental	KGILR	QITINDLPVGR	SVDEI	2		613.349116	1224.682632	0.002374549	1	N	140	151
P35700	Parental	KGILR	QITINDLPVGR	SVDEI	2	[0:-17.027	604.835616	1207.655632	0.000851441	1	N	140	151
P35700	Parental	DEFKK	LNCQVIGASVDSHFCHLAWINTPK	KQGGL	4	C3:+57.021,C15:+57.021	692.5918241	2766.336097	0.000451244	6	N	68	92
P35700	Parental	YVVFF	FYPLDFTFVCPTEIIAFSDR	ADEFK	2	C10:+57.021	1219.590777	2437.165955	0.000451244	17	N	42	62
P35821	Exosome	ADQLR	FSYLAVIEGAK	FIMGD	2		599.3298606	1196.644121	0.000622848	7	N	268	279
P35821	Exosome	LFKVR	ESGSLSLEHGPIVVHCSAGIGR	SGTFC	3	C16:+57.021	754.7150661	2261.121798	0.000451244	3	N	199	221
P35821	Parental	LFKVR	ESGSLSLEHGPIVVHCSAGIGR	SGTFC	3	C16:+57.021	754.7150661	2261.121798	0.000451244	2	N	199	221
P35831	Exosome	KKCER	YWPLYGEDPITFAPFK	ISCEN	2		972.483067	1942.950534	0.000451244	6	N	145	161
P35831	Parental	SVVDR	TSKPQELSAGALKVDDVSQNSCADCSAAHSHR	AAESS	4	C22:+57.021,C25:+57.021	857.3997751	3425.567901	0.002374549	1	N	473	505
P35831	Parental	VTRNK	TSISTASATVSPASSAESACTR	RVLPM	2	C20:+57.021	1071.502887	2140.990175	0.000451244	8	N	621	643
P35831	Parental	KKCER	YWPLYGEDPITFAPFK	ISCEN	2		972.483067	1942.950534	0.001162105	1	N	145	161
P35979	Exosome	SGTIK	EILGTAQSVGCNVDGR	HPHDI	2	C11:+57.021	838.4073333	1674.799067	0.000451244	25	N	130	146
P35979	Exosome	SGTIK	EILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS	-	3	C11:+57.021,C32:+57.021	1235.240903	3702.699309	0.001871652	1	N	130	165

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P35979	Exosome	TIQNR	QAQIEVVPSASALIIK	ALKEP	2		833.9910592	1665.966518	0.000451244	17	N	67	83
P35979	Exosome	QKNIK	HSGNITFDEIVNIAR	QMRHR	3		562.6255598	1684.853279	0.000451244	12	N	99	114
P35979	Exosome	VVYLR	CTGGEVGATSALAPK	IGPLG	2	C1:+57.021	709.8511312	1417.686662	0.000451244	14	N	16	31
P35979	Exosome	NVDGR	HPHDIIDDINSGAVECPAS	-	2	C16:+57.021	1023.963201	2045.910802	0.00091018	4	N	146	165
P35979	Parental	SGTIK	EILGTAQSVGCNVDGR	HPHDI	2	C11:+57.021	838.4073333	1674.799067	0.000451244	67	N	130	146
P35979	Parental	SGTIK	EILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS	-	3	C11:+57.021,C32:+57.021	1235.240903	3702.699309	0.000451244	11	N	130	165
P35979	Parental	TIQNR	QAQIEVVPSASALIIK	ALKEP	2		833.9910592	1665.966518	0.000451244	10	N	67	83
P35979	Parental	RSLAR	ELSGTIKEILGTAQSVGCNVDGR	HPHDI	2	C18:+57.021	1202.610761	2403.205922	0.000451244	7	N	123	146
P35979	Parental	RSLAR	ELSGTIKEILGTAQSVGCNVDGR	HPHDI	3	C18:+57.021	802.0764407	2403.205922	0.000451244	2	N	123	146
P35979	Parental	VVYLR	CTGGEVGATSALAPK	IGPLG	2	C1:+57.021	709.8511312	1417.686662	0.000451244	15	N	16	31
P35979	Parental	NVDGR	HPHDIIDDINSGAVECPAS	-	2	C16:+57.021	1023.963201	2045.910802	0.000622848	21	N	146	165
P35979	Parental	NVDGR	HPHDIIDDINSGAVECPAS	-	3	C16:+57.021	682.9780674	2045.910802	0.001329271	5	N	146	165
P35991	Exosome	IDVEK	ITCVETVIPEKNPPPER	QIPRR	3	C3:+57.021	660.347432	1978.018896	0.001871652	1	N	60	77
P35991	Exosome	SIIER	FPYPFQVVYDEGPLYVFSPTEELR	KRWIH	2		1446.710698	2891.405796	0.000451244	3	N	97	121
P35991	Exosome	SIIER	FPYPFQVVYDEGPLYVFSPTEELR	KRWIH	3		964.8097321	2891.405796	0.000451244	1	N	97	121
P35991	Exosome	FQVVY	DEGPLYVFSPTEELR	KRWIH	2		876.4284887	1750.841377	0.002519933	1	N	106	121
P36371	Parental	VRNPR	VLILDEATSALDAQCEQALQNWR	SQGDR	2	C15:+57.021	1322.6557	2643.2958	0.000451244	21	N	625	648
P36371	Parental	VRNPR	VLILDEATSALDAQCEQALQNWR	SQGDR	3	C15:+57.021	882.1063999	2643.2958	0.000451244	38	N	625	648
P36371	Parental	NGSGK	STVAALLQNLYQPTGGQLLLDGEPLTEYDHHYLHR	QVVLV	4		991.5068659	3961.996264	0.000823681	1	N	508	543
P36993	Exosome	FVKSR	LEVSDDLENVCNWVVDTCLHK	GSRDN	3	C11:+57.021,C18:+57.021	849.0616486	2544.161546	0.000451244	2	N	261	282
P36993	Exosome	CVDGK	GPTEQLVSPEPEVYEIVR	AEEDE	2		1021.526192	2041.036783	0.000851441	1	N	213	231
P36993	Exosome	CEFVK	SRLEVSDDLENVCNWVVDTCLHK	GSRDN	3	C13:+57.021,C20:+57.021	930.1060284	2787.294685	0.002145581	1	N	259	282
P37040	Parental	KKTGR	NIIVFYGSQTGTAEEFANR	LSKDA	2		1059.019065	2116.02253	0.000451244	2	N	78	97
P37040	Parental	TNPPR	TNVLYELAQYASEPSEQEHLHK	MASSS	3		862.7543978	2585.239793	0.000451244	14	N	382	404
P37040	Parental	TNPPR	TNVLYELAQYASEPSEQEHLHK	MASSS	4		647.3177483	2585.239793	0.000451244	28	N	382	404
P37040	Parental	LGAQR	IFELGLGDDDGNLEEDFITWR	EQFWP	2		1227.577141	2453.138682	0.000451244	25	N	199	220
P37040	Parental	LGAQR	IFELGLGDDDGNLEEDFITWR	EQFWP	3		818.7206941	2453.138682	0.000622848	7	N	199	220
P37040	Parental	EHLWK	LIHEGGAHIYVCGDAR	NMAKD	4	C12:+57.021	442.7207427	1766.851771	0.001229886	4	N	618	634
P37040	Parental	PFDAK	NPFLAAVTTNR	KLNQG	2		602.3281835	1202.640767	0.000662267	2	N	279	290
P37913	Exosome	RPYVR	IDGAVAPDHWLDPSIVWEVK	CADLS	3		749.7201886	2246.137166	0.001162105	1	N	823	843
P37913	Exosome	SGRLR	LGLAEQSVLAALAQAVSLTPPGQEFPTVVVDAGK	GKTAE	3		1126.284123	3375.82897	0.002981883	1	N	449	483
P37913	Parental	RPYVR	IDGAVAPDHWLDPSIVWEVK	CADLS	3		749.7201886	2246.137166	0.000851441	6	N	823	843
P37913	Parental	LKLKK	DYLDGVGDTLDLVVIGAYLGR	GKRAG	2		1112.578955	2223.142311	0.000451244	12	N	745	766
P37913	Parental	SGRLR	LGLAEQSVLAALAQAVSLTPPGQEFPTVVVDAGK	GKTAE	3		1126.284123	3375.82897	0.000451244	2	N	449	483
P37913	Parental	SLDTK	DTEQIAEFLEQSVK	DSCEG	2		818.9073891	1635.799178	0.002019181	2	N	700	714
P38060	Exosome	AAGAK	EVSVFGAVSELFTR	KNANC	2		770.9044524	1539.793305	0.000451244	11	N	122	136
P38060	Exosome	AAGAK	EVSVFGAVSELFTRK	NANCS	3		556.970556	1667.888268	0.000870037	5	N	122	137
P38060	Exosome	VNLQK	LLEAGDFICQALNR	KTSSK	3	C9:+57.021	540.61222	1618.81326	0.001162105	1	N	298	312
P38060	Exosome	SISVR	GYVSCALGCPYEGK	VSPAK	2	C5:+57.021,C9:+57.021	780.8447603	1559.673921	0.000451244	3	N	165	179
P38060	Parental	AAGAK	EVSVFGAVSELFTR	KNANC	2		770.9044524	1539.793305	0.000622848	11	N	122	136
P38647	Exosome	IPTKK	SQVFSTAADGQTQVEIK	VCQGE	2		904.955402	1807.895204	0.000622848	3	N	468	485
P38647	Exosome	MKLTR	AQFEGIVTDLIKR	TIAPC	3		497.2844749	1488.830025	0.000451244	10	N	348	361
P38647	Exosome	VFEVK	STNGDTFLGGEDFDQALLR	HIVKE	2		1028.485055	2054.95451	0.000451244	4	N	265	284
P38647	Exosome	MKLTR	AQFEGIVTDLIK	RTIAP	2		667.3722568	1332.728914	0.002145581	1	N	348	360
P38647	Exosome	DVTPL	SLGIETLGGVFTK	LINRN	2		661.3722568	1320.728914	0.001329271	2	N	443	456
P38647	Parental	IPTKK	SQVFSTAADGQTQVEIK	VCQGE	2		904.955402	1807.895204	0.000451244	27	N	468	485
P38647	Parental	MKLTR	AQFEGIVTDLIKR	TIAPC	3		497.2844749	1488.830025	0.000451244	25	N	348	361
P38647	Parental	VFEVK	STNGDTFLGGEDFDQALLR	HIVKE	2		1028.485055	2054.95451	0.000451244	27	N	265	284
P38647	Parental	AEGAR	TTPSVVAFTADGER	LVGMP	2		725.8627845	1449.709969	0.000451244	12	N	85	99
P38647	Parental	AGDNK	LLGQFTLIGIPPAPR	GVPQI	2		796.9802975	1591.944995	0.000451244	1	N	498	513
P38647	Parental	MPAKR	QAVTNPNNTFYATK	RLIGR	2		784.8893337	1567.763067	0.000823681	1	N	107	121
P38647	Parental	DVTPL	SLGIETLGGVFTK	LINRN	2		661.3722568	1320.728914	0.002663018	1	N	443	456
P39039	Exosome	AEENK	AIQEVATGIAFLGITDEATEGQFMYVTGGR	LTYSN	3	M24:+15.995	1054.520721	3160.538764	0.000451244	4	N	163	193
P39039	Exosome	YSNWK	KDEPNNHGSGEDCVIILDNGLWNDISCQASFK	AVCEF	3	C13:+57.021,C27:+57.021	1211.551077	3631.629832	0.000451244	2	N	200	232
P39039	Exosome	YSNWK	KDEPNNHGSGEDCVIILDNGLWNDISCQASFK	AVCEF	4	C13:+57.021,C27:+57.021	908.9152581	3631.629832	0.000451244	9	N	200	232
P39039	Exosome	FSKVK	SLCTELQGTVAIPR	NAEEN	3	C3:+57.021	515.608587	1543.802361	0.000823681	1	N	143	157
P39054	Exosome	EPCLK	CVDLVIQELISTVR	QCTSK	2	C1:+39.994	814.4398881	1626.864176	0.00307782	1	N	426	440
P39054	Exosome	EPCLK	CVDLVIQELISTVR	QCTSK	2	C1:+57.021	822.9533881	1643.891176	0.000451244	12	N	426	440
P39054	Exosome	EPCLK	CVDLVIQELISTVR	QCTSK	3	C1:+57.021	548.9715254	1643.891176	0.000451244	2	N	426	440
P39054	Exosome	EPCLK	CVDLVIQELISTVR	QCTSK	2	[0:-17.027,C1:+57.021	814.4398881	1626.864176	0.000451244	4	N	426	440
P39054	Exosome	PLVNK	LQDAFSSIGQSCHLDLPQIAVVGGQSAGK	SSVLE	3	C12:+57.021	995.1699515	2982.486454	0.000451244	16	N	15	44
P39054	Exosome	DFEKR	IEGSGDQVDTLELSGGAR	INRIF	2		902.4401161	1802.864632	0.000622848	1	N	343	361
P39054	Exosome	YKDLR	QIELACDSQEDVDSWK	ASFLR	2	C6:+57.021	961.9257529	1921.835906	0.000451244	11	N	601	617
P39054	Exosome	PGITK	VPVGDQPPDIEYQIK	DMILQ	2		849.4413991	1696.867198	0.000451244	4	N	142	157
P39054	Exosome	VETIR	NLVDSYVAIINK	SIRDL	2		674.8777063	1347.739813	0.000451244	11	N	657	669

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P39054	Exosome	PINLR	VYSPHVLNLTLIDLPGITK	VPVGD	3		698.4055414	2092.193224	0.000622848	9	N	123	142
P39054	Exosome	YHALK	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	RPVSS	3		1376.689377	4127.04473	0.000451244	15	N	730	769
P39054	Exosome	IHGVR	TGLFTPDLAFEAIVKK	QVVKL	3		583.9982231	1748.971269	0.000735798	5	N	399	415
P39054	Exosome	IHGVR	TGLFTPDLAFEAIVK	KQVVK	2		811.4459531	1620.876306	0.000622848	6	N	399	414
P39054	Exosome	ASFLR	AGVYPEKDQAENEDGAQENTFSMDPQLER	QVETI	3	M23:+15.995	1095.481543	3283.421228	0.000622848	4	N	622	651
P39054	Exosome	QSAGK	SSVLENFVGR	DFLPR	2		554.2938094	1106.572019	0.001943752	1	N	44	54
P39054	Parental	QSAGK	SSVLENFVGRDFLPR	GSGIV	3		579.3095717	1734.905315	0.000451244	6	N	44	59
P39054	Parental	EPCLK	CVDLVIQELISTVR	QCTSK	2	C1:+39.994	814.4398881	1626.864176	0.000451244	4	N	426	440
P39054	Parental	EPCLK	CVDLVIQELISTVR	QCTSK	2	C1:+57.021	822.9533881	1643.891176	0.000451244	14	N	426	440
P39054	Parental	EPCLK	CVDLVIQELISTVR	QCTSK	3	C1:+57.021	548.9715254	1643.891176	0.000451244	5	N	426	440
P39054	Parental	EPCLK	CVDLVIQELISTVR	QCTSK	2	[0:-17.027,C1:+57.021	814.4398881	1626.864176	0.000451244	7	N	426	440
P39054	Parental	PLVNK	LQDAFSSIGQSCHLDLPQIAVVGGQSAGK	SSVLE	3	C12:+57.021	995.1699515	2982.486454	0.000451244	37	N	15	44
P39054	Parental	DFEKR	IEGSGDQVDTLELSGGAR	INRIF	2		902.4401161	1802.864632	0.000622848	3	N	343	361
P39054	Parental	YKDLR	QIELACDSQEDVDSWK	ASFLR	2	C6:+57.021	961.9257529	1921.835906	0.000451244	20	N	601	617
P39054	Parental	PGITK	VPVGDQPPDIEYQIK	DMILQ	2		849.4413991	1696.867198	0.001329271	8	N	142	157
P39054	Parental	PINLR	VYSPHVLNLTLIDLPGITK	VPVGD	3		698.4055414	2092.193224	0.000662267	4	N	123	142
P39054	Parental	YHALK	EALNIIGDISTSTVSTPVPPPVDDTWLQNTSGHSPTPQR	RPVSS	3		1376.689377	4127.04473	0.001591523	1	N	730	769
P39054	Parental	IHGVR	TGLFTPDLAFEAIVKK	QVVKL	3		583.9982231	1748.971269	0.000451244	3	N	399	415
P39054	Parental	IHGVR	TGLFTPDLAFEAIVK	KQVVK	2		811.4459531	1620.876306	0.001763695	1	N	399	414
P39654	Exosome	WGNWK	DGTILNVAATSISDLPVDQR	FREDK	2		1043.04528	2084.07496	0.000451244	26	N	146	166
P39654	Exosome	WGNWK	DGTILNVAATSISDLPVDQR	FREDK	3		695.6994532	2084.07496	0.000451244	2	N	146	166
P39654	Exosome	EIRNK	SLDIPYEYLRPSLVENSVAI	-	2		1139.602431	2277.189261	0.000451244	11	N	643	663
P39654	Exosome	WISVK	GPGDQGSEYTFPCYR	WVQGT	2	C13:+57.021	867.3651341	1732.714668	0.000451244	14	N	84	99
P39654	Exosome	LDLLK	QAGAFLTYSSLCPPDDLAER	GLLDI	2	C12:+57.021	1106.023259	2210.030918	0.000451244	13	N	431	451
P39654	Exosome	VYRIR	VSTGDSVYAGSNNEVYLWLIGQHGEASLGK	LFRPC	3		1051.183068	3150.525805	0.000451244	11	N	7	37
P39654	Exosome	FPCYR	WVQGTSILNLPEGTGCTVVEDSQGLFR	NHREE	3	C16:+57.021	988.4908021	2962.449006	0.000451244	25	N	99	126
P39654	Exosome	LVMLK	LQPDGQLLPIAIQLELPK	TGSTP	2		993.5858552	1985.15611	0.000451244	11	N	305	323
P39654	Exosome	LVMLK	LQPDGQLLPIAIQLELPK	TGSTP	3		662.7265034	1985.15611	0.000451244	6	N	305	323
P39654	Exosome	DLYYK	TDQAVQDDYELQSWCQEITEIGLQGAQDR	GFPTS	3	C15:+57.021	1132.848043	3395.520728	0.000451244	16	N	485	514
P39654	Exosome	EAEFK	VDVSEYLGPLLFVR	VQKWH	2		803.9461203	1605.876641	0.000451244	4	N	50	64
P39654	Exosome	EELKK	GTLFEADFFLLDGIK	ANVIL	2		843.4434105	1684.871221	0.000451244	7	N	271	286
P39654	Exosome	VTCWK	SLDDFNYVFK	SGHTK	2		624.3013001	1246.587	0.000735798	5	N	199	209
P39654	Exosome	DLAER	GLLDIDTCFYAK	DALQL	2	C8:+57.021	708.3476931	1414.679786	0.000451244	5	N	451	463
P39654	Exosome	KCWVR	SSDLQLHELQAHLLR	GHLVA	3		587.3203593	1758.937678	0.000451244	1	N	349	364
P39654	Parental	WGNWK	DGTILNVAATSISDLPVDQR	FREDK	2		1043.04528	2084.07496	0.000451244	16	N	146	166
P39654	Parental	WGNWK	DGTILNVAATSISDLPVDQR	FREDK	3		695.6994532	2084.07496	0.000451244	6	N	146	166
P39654	Parental	EIRNK	SLDIPYEYLRPSLVENSVAI	-	2		1139.602431	2277.189261	0.000451244	6	N	643	663
P39654	Parental	WISVK	GPGDQGSEYTFPCYR	WVQGT	2	C13:+57.021	867.3651341	1732.714668	0.000451244	9	N	84	99
P39654	Parental	LDLLK	QAGAFLTYSSLCPPDDLAER	GLLDI	2	C12:+57.021	1106.023259	2210.030918	0.000451244	17	N	431	451
P39654	Parental	VYRIR	VSTGDSVYAGSNNEVYLWLIGQHGEASLGK	LFRPC	3		1051.183068	3150.525805	0.000451244	10	N	7	37
P39654	Parental	FPCYR	WVQGTSILNLPEGTGCTVVEDSQGLFR	NHREE	3	C16:+57.021	988.4908021	2962.449006	0.000451244	11	N	99	126
P39654	Parental	LVMLK	LQPDGQLLPIAIQLELPK	TGSTP	2		993.5858552	1985.15611	0.000451244	6	N	305	323
P39654	Parental	LVMLK	LQPDGQLLPIAIQLELPK	TGSTP	3		662.7265034	1985.15611	0.001463592	1	N	305	323
P39654	Parental	DLYYK	TDQAVQDDYELQSWCQEITEIGLQGAQDR	GFPTS	3	C15:+57.021	1132.848043	3395.520728	0.000451244	14	N	485	514
P39654	Parental	EAEFK	VDVSEYLGPLLFVR	VQKWH	2		803.9461203	1605.876641	0.000622848	3	N	50	64
P39654	Parental	EAEFK	VDVSEYLGPLLFVR	VQKWH	3		536.3000135	1605.876641	0.002884417	1	N	50	64
P39654	Parental	EELKK	GTLFEADFFLLDGIK	ANVIL	2		843.4434105	1684.871221	0.000451244	4	N	271	286
P39654	Parental	DLAER	GLLDIDTCFYAK	DALQL	2	C8:+57.021	708.3476931	1414.679786	0.000451244	3	N	451	463
P39654	Parental	KCWVR	SSDLQLHELQAHLLR	GHLVA	4		440.7422195	1758.937678	0.000451244	1	N	349	364
P39655	Exosome	DPRTK	AVLSQFQADLDNLEKEITAR	NEQLD	2		1131.092761	2260.169923	0.000451244	15	N	621	641
P39655	Exosome	DPRTK	AVLSQFQADLDNLEKEITAR	NEQLD	3		754.3977742	2260.169923	0.000451244	9	N	621	641
P39655	Exosome	FPCYR	WVQGEGILSLPEGTAR	LAGDN	2		856.9524653	1711.889331	0.000451244	26	N	98	114
P39655	Exosome	ALYAR	DALQLWEVTAR	YVKGM	2		651.3465733	1300.677547	0.000735798	3	N	462	473
P39655	Exosome	DPRTK	AVLSQFQADLDNLEK	EITAR	2		845.9364809	1689.857362	0.000451244	3	N	621	636
P39655	Exosome	NTRSR	TQLISDGGIFDQVVSTGGGGHVQLLTR	AVAQL	3		919.1511513	2754.430054	0.000451244	6	N	404	431
P39655	Exosome	EKELK	NGSLFEADFILLDGIPANVIR	GEPQY	2		1137.61059	2273.20558	0.000451244	5	N	269	290
P39655	Exosome	EKELK	NGSLFEADFILLDGIPANVIR	GEPQY	3		758.7429933	2273.20558	0.000451244	12	N	269	290
P39655	Exosome	LRPAR	GKEEEFDFDVPEDLGPLQFVK	LHKQH	2		1219.59226	2437.16892	0.000451244	18	N	43	64
P39655	Exosome	LRPAR	GKEEEFDFDVPEDLGPLQFVK	LHKQH	3		813.3974399	2437.16892	0.000451244	21	N	43	64
P39655	Exosome	EITAR	NEQLDLPYEYLKPSR	IENSI	2		932.9761374	1863.936675	0.000451244	9	N	641	656
P39655	Exosome	EITAR	NEQLDLPYEYLKPSR	IENSI	3		622.320025	1863.936675	0.000451244	10	N	641	656
P39655	Exosome	QLLTR	AVAQLTYHSLCPPDDLANR	GLLRI	2	C11:+57.021	1071.026136	2140.036672	0.000451244	5	N	431	450
P39655	Exosome	YTLLR	SWNHLEDFDQIFWGQK	SALAE	3		683.9871573	2048.938072	0.000451244	10	N	195	211
P39655	Exosome	RYRVR	VVTGAWLFSGSLNLVR	LWLVG	2		859.9835685	1717.951537	0.001943752	1	N	7	23
P39655	Exosome	RYRVR	VVTGAWLFSGSLNLVR	LWLVG	3		573.6583123	1717.951537	0.000823681	2	N	7	23

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P39655	Exosome	VKLHK	QHTVVDDAWFCNLITVQGPGTSAEAVFPCYR	WVQGE	3	C11:+57.021,C29:+57.021	1180.222344	3537.643632	0.000451244	12	N	67	98
P39655	Exosome	VKLHK	QHTVVDDAWFCNLITVQGPGTSAEAVFPCYR	WVQGE	3	[0:-17.027,C11:+57.021,C29:+57.021	1174.546677	3520.616632	0.002663018	1	N	67	98
P39655	Parental	DPRTK	AVLSQFQADLDNLEKEITAR	NEQLD	2		1131.092761	2260.169923	0.000451244	5	N	621	641
P39655	Parental	DPRTK	AVLSQFQADLDNLEKEITAR	NEQLD	3		754.3977742	2260.169923	0.000451244	5	N	621	641
P39655	Parental	FPCYR	WVQGEGILSLPEGTAR	LAGDN	2		856.9524653	1711.889331	0.000451244	4	N	98	114
P39655	Parental	ALYAR	DALQLWEVTAR	YVKGM	2		651.3465733	1300.677547	0.001264573	2	N	462	473
P39655	Parental	EKELK	NGSLFEADFILLDGIPANVIR	GEPQY	2		1137.61059	2273.20558	0.000451244	5	N	269	290
P39655	Parental	LRPAR	GKEEEFDFDVPEDLGPLQFVK	LHKQH	2		1219.59226	2437.16892	0.000451244	9	N	43	64
P39655	Parental	LRPAR	GKEEEFDFDVPEDLGPLQFVK	LHKQH	3		813.3974399	2437.16892	0.000451244	11	N	43	64
P39655	Parental	YTLLR	SWNHLEDFDQIFWGQK	SALAE	2		1025.476836	2048.938072	0.002296037	2	N	195	211
P39655	Parental	YTLLR	SWNHLEDFDQIFWGQK	SALAE	3		683.9871573	2048.938072	0.000823681	2	N	195	211
P40124	Exosome	AYLSK	NSLDCEIVSAK	SSEMN	2	C5:+57.021	618.3007428	1234.585886	0.000451244	29	N	421	432
P40124	Exosome	DSASR	SALFAQINQGESITHALK	HVSDD	2		964.5159611	1927.016322	0.000451244	26	N	253	271
P40124	Exosome	DSASR	SALFAQINQGESITHALK	HVSDD	3		643.3465741	1927.016322	0.000451244	33	N	253	271
P40124	Exosome	GKKWR	VENQENVSNLVIDDTELK	QVAYI	2		1030.013645	2058.011691	0.000451244	86	N	329	347
P40124	Exosome	GKKWR	VENQENVSNLVIDDTELK	QVAYI	3		687.0116969	2058.011691	0.000451244	9	N	329	347
P40124	Exosome	GKKWR	VENQENVSNLVIDDTELKQVAYIYK	CVNTT	3		975.5016269	2923.481481	0.000451244	22	N	329	354
P40124	Exosome	YVQAF	DSLLANPVAEYLK	MSKEI	2		716.888271	1431.760942	0.000451244	10	N	46	59
P40124	Exosome	GAVPY	VQAFDSLLANPVAEYLK	MSKEI	2		939.5045308	1876.993462	0.000451244	33	N	42	59
P40124	Exosome	GAVPY	VQAFDSLLANPVAEYLK	MSKEI	3		626.6722872	1876.993462	0.000451244	6	N	42	59
P40124	Exosome	NRGSK	FFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	3		1028.894353	3083.65966	0.000451244	28	N	125	154
P40124	Exosome	NRGSK	FFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	4		771.922715	3083.65966	0.000451244	26	N	125	154
P40124	Exosome	DSPSK	GAVPYVQAFDSLLANPVAEYLK	MSKEI	2		1183.126073	2364.236546	0.000451244	102	N	37	59
P40124	Exosome	DSPSK	GAVPYVQAFDSLLANPVAEYLK	MSKEI	3		789.0866486	2364.236546	0.000451244	53	N	37	59
P40124	Exosome	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITFR	EKNRG	3	C9:+57.021	1271.00717	3809.998109	0.000451244	13	N	83	118
P40124	Exosome	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITFR	EKNRG	4	C9:+57.021	953.5073273	3809.998109	0.000451244	2	N	83	118
P40124	Exosome	PAGNK	LSDLLAPISEQIQEVITFR	EKNRG	2		1086.599691	2171.183782	0.000451244	83	N	99	118
P40124	Exosome	PAGNK	LSDLLAPISEQIQEVITFR	EKNRG	3		724.7357273	2171.183782	0.000451244	34	N	99	118
P40124	Exosome	DNCKK	LGLVFDDVVGIVEIINSR	DVKVQ	2		979.5520123	1957.088425	0.000451244	86	N	376	394
P40124	Exosome	DNCKK	LGLVFDDVVGIVEIINSR	DVKVQ	3		653.3706082	1957.088425	0.000451244	150	N	376	394
P40124	Exosome	IVSAK	SSEMNVLIPTEGGDFNEFPVPEQFK	TLWNG	2		1406.163255	2810.310911	0.001654178	2	N	432	457
P40124	Exosome	IVSAK	SSEMNVLIPTEGGDFNEFPVPEQFK	TLWNG	2	M4:+15.995	1414.160755	2826.305911	0.001352548	1	N	432	457
P40124	Exosome	VDNCK	KLGLVFDDVVGIVEIINSR	DVKVQ	2		1043.599494	2085.183388	0.000451244	13	N	375	394
P40124	Exosome	VDNCK	KLGLVFDDVVGIVEIINSR	DVKVQ	3		696.0689293	2085.183388	0.000451244	25	N	375	394
P40124	Exosome	PAGNK	LSDLLAPISEQIQEVITF	REKNR	2		1008.549135	2015.082671	0.000451244	8	N	99	117
P40124	Exosome	VDWVR	AYLSIWTELQAYIK	EFHTT	2		849.9592277	1697.902855	0.000451244	41	N	183	197
P40124	Exosome	SGPVR	SGPKPFSAPKPQTSPSPKPATK	KEPAL	4		559.5592786	2234.205914	0.000451244	3	N	293	315
P40124	Exosome	LKLER	ALLATASQCQQPAGNK	LSDLL	2	C9:+57.021	829.4202437	1656.824887	0.000451244	18	N	83	99
P40124	Exosome	AYIYK	CVNTTLQIK	GKINS	2	C1:+57.021	538.7923566	1075.569113	0.001162105	2	N	354	363
P40124	Exosome	KPATK	KEPALLELEGK	KWRVE	2		613.8536999	1225.6918	0.000622848	11	N	315	326
P40124	Exosome	KPATK	KEPALLELEGK	KWRVE	3		409.5717332	1225.6918	0.000451244	27	N	315	326
P40124	Exosome	NRGSK	FFNHLSAVSESIQALGWVALAAK	PGPFV	2		1230.158239	2458.300877	0.000451244	18	N	125	148
P40124	Exosome	NRGSK	FFNHLSAVSESIQALGWVALAAK	PGPFV	3		820.4414258	2458.300877	0.000451244	31	N	125	148
P40124	Exosome	RAVGR	LEAVSHTSDMHCGYGDSPSK	GAVPY	3	C12:+57.021	726.6461008	2176.914903	0.000823681	5	N	17	37
P40124	Exosome	QAYIK	EFHTTGLAWSK	TGPVA	3		426.2160609	1275.624783	0.001699387	1	N	197	208
P40124	Exosome	LEGKK	WRVENQENVSNLVIDDTELK	QVAYI	3		801.0718383	2400.192115	0.000451244	27	N	327	347
P40124	Exosome	AGNKL	SDLLAPISEQIQEVITFR	EKNRG	2		1030.057659	2058.099718	0.000451244	9	N	100	118
P40124	Exosome	LSDLL	APISEQIQEVITFR	EKNRG	2		815.944109	1629.872618	0.000451244	1	N	104	118
P40124	Exosome	SKGAV	PYVQAFDSLLANPVAEYLK	MSKEI	2		1069.562577	2137.109554	0.000451244	5	N	40	59
P40124	Exosome	SKGAV	PYVQAFDSLLANPVAEYLK	MSKEI	3		713.3776514	2137.109554	0.001329271	1	N	40	59
P40124	Exosome	ERLER	AVGRLEAVSHTSDMHCGYGDSPSK	GAVPY	4	M14:+15.995,C16:+57.021	645.0423013	2576.138005	0.000451244	1	N	13	37
P40124	Exosome	QVMGK	VPTISINKTDGCHAYLSK	NSLDC	3	C12:+57.021	668.6791817	2003.014145	0.000451244	6	N	403	421
P40124	Exosome	PATKK	EPALLELEGK	KWRVE	2		549.8062183	1097.596837	0.002981883	1	N	316	326
P40124	Exosome	FFNHL	SAVSESIQALGWVALAAKPGPFVK	EMNDA	3		809.4534428	2425.336929	0.000622848	5	N	130	154
P40124	Exosome	VPYVQ	AFDSLLANPVAEYLK	MSKEI	2		825.9410349	1649.86647	0.001229886	4	N	44	59
P40124	Parental	AYLSK	NSLDCEIVSAK	SSEMN	2	C5:+57.021	618.3007428	1234.585886	0.000451244	30	N	421	432
P40124	Parental	DSASR	SALFAQINQGESITHALK	HVSDD	2		964.5159611	1927.016322	0.000451244	36	N	253	271
P40124	Parental	DSASR	SALFAQINQGESITHALK	HVSDD	3		643.3465741	1927.016322	0.000451244	43	N	253	271
P40124	Parental	GKKWR	VENQENVSNLVIDDTELK	QVAYI	2		1030.013645	2058.011691	0.000451244	119	N	329	347
P40124	Parental	GKKWR	VENQENVSNLVIDDTELK	QVAYI	3		687.0116969	2058.011691	0.000451244	4	N	329	347
P40124	Parental	GKKWR	VENQENVSNLVIDDTELKQVAY	IYKCV	2		1260.627362	2519.239125	0.000451244	9	N	329	351
P40124	Parental	GKKWR	VENQENVSNLVIDDTELKQVAYIYK	CVNTT	3		975.5016269	2923.481481	0.000451244	12	N	329	354
P40124	Parental	YVQAF	DSLLANPVAEYLK	MSKEI	2		716.888271	1431.760942	0.000451244	18	N	46	59
P40124	Parental	LGLVF	DDVVGIVEIINSR	DVKVQ	2		714.8888023	1427.762005	0.000451244	23	N	381	394

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P40124	Parental	LGLVF	DDVVGIVEIINSR	DVKVQ	3		476.9284682	1427.762005	0.000451244	14	N	381	394
P40124	Parental	GAVPY	VQAFDSLLANPVAEYLK	MSKEI	2		939.5045308	1876.993462	0.000451244	45	N	42	59
P40124	Parental	GAVPY	VQAFDSLLANPVAEYLK	MSKEI	3		626.6722872	1876.993462	0.000451244	7	N	42	59
P40124	Parental	WVRAY	LSIWTELQAYIK	EFHTT	2		732.9090065	1463.802413	0.000451244	15	N	185	197
P40124	Parental	NRGSK	FFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	3		1028.894353	3083.65966	0.000451244	28	N	125	154
P40124	Parental	NRGSK	FFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	4		771.922715	3083.65966	0.000451244	31	N	125	154
P40124	Parental	DSPSK	GAVPYVQAFDSLLANPVAEYLK	MSKEI	2		1183.126073	2364.236546	0.000451244	93	N	37	59
P40124	Parental	DSPSK	GAVPYVQAFDSLLANPVAEYLK	MSKEI	3		789.0866486	2364.236546	0.000451244	31	N	37	59
P40124	Parental	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITFR	EKNRG	3	C9:+57.021	1271.00717	3809.998109	0.000451244	12	N	83	118
P40124	Parental	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITFR	EKNRG	4	C9:+57.021	953.5073273	3809.998109	0.000451244	7	N	83	118
P40124	Parental	PAGNK	LSDLLAPISEQIQEVITFR	EKNRG	2		1086.599691	2171.183782	0.000451244	60	N	99	118
P40124	Parental	PAGNK	LSDLLAPISEQIQEVITFR	EKNRG	3		724.7357273	2171.183782	0.000451244	14	N	99	118
P40124	Parental	DNCKK	LGLVFDDVVGIVEIINSR	DVKVQ	2		979.5520123	1957.088425	0.000451244	78	N	376	394
P40124	Parental	DNCKK	LGLVFDDVVGIVEIINSR	DVKVQ	3		653.3706082	1957.088425	0.000451244	123	N	376	394
P40124	Parental	LKLER	ALLATASQCQQPAGNKLSDLLAPISEQIQEVITF	REKNR	3	C9:+57.021	1218.973466	3653.896998	0.000451244	11	N	83	117
P40124	Parental	IVSAK	SSEMNVLIPTEGGDFNEFPVPEQFK	TLWNG	2		1406.163255	2810.310911	0.000451244	4	N	432	457
P40124	Parental	VDNCK	KLGLVFDDVVGIVEIINSR	DVKVQ	2		1043.599494	2085.183388	0.000823681	1	N	375	394
P40124	Parental	VDNCK	KLGLVFDDVVGIVEIINSR	DVKVQ	3		696.0689293	2085.183388	0.000451244	21	N	375	394
P40124	Parental	PAGNK	LSDLLAPISEQIQEVITFREK	NRGSK	3		810.448246	2428.321338	0.000622848	3	N	99	120
P40124	Parental	RGSKF	FNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	2		1469.303423	2936.591246	0.0025889	1	N	126	154
P40124	Parental	RGSKF	FNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	3		979.8715487	2936.591246	0.000451244	8	N	126	154
P40124	Parental	RGSKF	FNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	4		735.1556115	2936.591246	0.000451244	17	N	126	154
P40124	Parental	PAGNK	LSDLLAPISEQIQEVITF	REKNR	2		1008.549135	2015.082671	0.000451244	34	N	99	117
P40124	Parental	PAGNK	LSDLLAPISEQIQEVITF	REKNR	3		672.7020235	2015.082671	0.000823681	7	N	99	117
P40124	Parental	VDWVR	AYLSIWTELQAYIK	EFHTT	2		849.9592277	1697.902855	0.000451244	7	N	183	197
P40124	Parental	LKLER	ALLATASQCQQPAGNK	LSDLL	2	C9:+57.021	829.4202437	1656.824887	0.000451244	62	N	83	99
P40124	Parental	KPATK	KEPALLELEGK	KWRVE	3		409.5717332	1225.6918	0.000622848	19	N	315	326
P40124	Parental	NRGSK	FFNHLSAVSESIQALGWVALAAK	PGPFV	2		1230.158239	2458.300877	0.000451244	6	N	125	148
P40124	Parental	NRGSK	FFNHLSAVSESIQALGWVALAAK	PGPFV	3		820.4414258	2458.300877	0.000451244	7	N	125	148
P40124	Parental	QAYIK	EFHTTGLAWSK	TGPVA	2		638.8201913	1275.624783	0.000451244	5	N	197	208
P40124	Parental	LEGKK	WRVENQENVSNLVIDDTELK	QVAYI	3		801.0718383	2400.192115	0.000451244	9	N	327	347
P40124	Parental	AGNKL	SDLLAPISEQIQEVITFR	EKNRG	2		1030.057659	2058.099718	0.000451244	6	N	100	118
P40124	Parental	ERLER	AVGRLEAVSHTSDMHCGYGDSPSK	GAVPY	4	C16:+57.021	641.0435513	2560.143005	0.000451244	6	N	13	37
P40124	Parental	QVMGK	VPTISINKTDGCHAYLSK	NSLDC	2	C12:+57.021	1002.514873	2003.014145	0.000451244	5	N	403	421
P40124	Parental	QVMGK	VPTISINKTDGCHAYLSK	NSLDC	3	C12:+57.021	668.6791817	2003.014145	0.000451244	5	N	403	421
P40124	Parental	LKLER	ALLATASQCQQPAGNKL	SDLLA	2	C9:+57.021	885.9622758	1769.908952	0.000451244	14	N	83	100
P40124	Parental	GKKWR	VENQENVSNLVIDDTELKQVAYIY	KCVNT	2		1398.701059	2795.386517	0.000451244	4	N	329	353
P40124	Parental	REKNR	GSKFFNHLSAVSESIQALGWVALAAKPGPFVK	EMNDA	4		839.9598289	3355.808116	0.001162105	2	N	122	154
P40124	Parental	DNCKK	LGLVFDDVVGIVEIINSRDVK	VQVMG	3		767.4340483	2299.278745	0.001162105	1	N	376	397
P40124	Parental	GDVQK	HAEMVHTGLKLER	ALLAT	3		507.6054429	1519.792929	0.001871652	2	N	70	83
P40124	Parental	PATKK	EPALLELEGK	KWRVE	2		549.8062183	1097.596837	0.001591523	3	N	316	326
P40124	Parental	NVLIP	TEGGDFNEFPVPEQFK	TLWNG	2		920.9235705	1839.831541	0.00091018	1	N	441	457
P40142	Exosome	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	2		1097.074706	2192.133812	0.000451244	6	N	186	205
P40142	Exosome	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	3		731.7190706	2192.133812	0.000823681	8	N	186	205
P40142	Exosome	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	4		549.041253	2192.133812	0.000451244	21	N	186	205
P40142	Exosome	FDINR	LGQSDPAPLQHQVDIYQK	RCEAF	2		1019.02415	2036.032701	0.000451244	86	N	186	204
P40142	Exosome	FDINR	LGQSDPAPLQHQVDIYQK	RCEAF	3		679.6853669	2036.032701	0.000451244	50	N	186	204
P40142	Exosome	ICFIR	TSRPENAIIYSNNEDFQVGQAK	VVLKS	2		1241.104389	2480.193177	0.000451244	120	N	471	493
P40142	Exosome	ICFIR	TSRPENAIIYSNNEDFQVGQAK	VVLKS	3		827.7388591	2480.193177	0.000451244	170	N	471	493
P40142	Exosome	DIYQK	RCEAFGWHTIIVDGHSVEELCK	AFGQA	3	C2:+57.021,C21:+57.021	881.7531493	2642.236048	0.000451244	3	N	204	226
P40142	Exosome	DIYQK	RCEAFGWHTIIVDGHSVEELCK	AFGQA	4	C2:+57.021,C21:+57.021	661.566812	2642.236048	0.000451244	42	N	204	226
P40142	Exosome	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	2	C1:+39.994,C20:+57.021	1235.561768	2469.107937	0.000451244	5	N	205	226
P40142	Exosome	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	3	C1:+39.994,C20:+57.021	824.043779	2469.107937	0.000451244	3	N	205	226
P40142	Exosome	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	2	C1:+57.021,C20:+57.021	1244.075268	2486.134937	0.000451244	43	N	205	226
P40142	Exosome	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	3	C1:+57.021,C20:+57.021	829.7194456	2486.134937	0.000451244	54	N	205	226
P40142	Exosome	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	4	C1:+57.021,C20:+57.021	622.5415342	2486.134937	0.000451244	65	N	205	226
P40142	Exosome	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	2	[0:-	1235.561768	2469.107937	0.000451244	27	N	205	226
P40142	Exosome	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	3	[0:-	824.043779	2469.107937	0.000451244	22	N	205	226
P40142	Exosome	QSKKK	ILATPPQEDAPSVDIANIR	MPTPP	2		1010.539633	2019.063667	0.000451244	233	N	283	302
P40142	Exosome	QSKKK	ILATPPQEDAPSVDIANIR	MPTPP	3		674.0290222	2019.063667	0.000451244	67	N	283	302
P40142	Exosome	GCATR	DRTVPFCSTFAAFFTR	AFDQI	2	C7:+57.021	961.9648185	1921.914037	0.000451244	7	N	379	395
P40142	Exosome	GCATR	DRTVPFCSTFAAFFTR	AFDQI	3	C7:+57.021	641.6458123	1921.914037	0.000451244	25	N	379	395
P40142	Exosome	EAMAF	AGIYKLDNLVAIFDINR	LGQSD	3		645.6953147	1934.062544	0.000451244	11	N	169	186
P40142	Exosome	RDRTV	PFCSTFAAFFTR	AFDQI	2	C3:+57.021	726.342745	1450.66989	0.000451244	37	N	383	395
P40142	Exosome	ATRDR	TVPFCSTFAAFFTR	AFDQI	2	C5:+57.021	826.4007913	1650.785983	0.000451244	54	N	381	395

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P40142	Exosome	ATRDR	TVPFCSTFAAFFTR	AFDQI	3	C5:+57.021	551.2697942	1650.785983	0.000451244	39	N	381	395
P40142	Exosome	APILY	AVWAEAGFLPEAELLNLR	KISSD	2		1000.036529	1998.057459	0.000451244	45	N	83	101
P40142	Exosome	APILY	AVWAEAGFLPEAELLNLR	KISSD	3		667.0269529	1998.057459	0.000451244	25	N	83	101
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	2		1475.303423	2948.591246	0.000451244	7	N	75	102
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	3		983.8715487	2948.591246	0.000451244	43	N	75	102
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	4		738.1556115	2948.591246	0.000451244	54	N	75	102
P40142	Exosome	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	2		1005.00457	2007.993539	0.000451244	21	N	264	281
P40142	Exosome	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	3		670.3389797	2007.993539	0.000451244	39	N	264	281
P40142	Exosome	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	2	M2:+15.995	1013.00207	2023.988539	0.000451244	25	N	264	281
P40142	Exosome	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	3	M2:+15.995	675.6706464	2023.988539	0.000451244	53	N	264	281
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	2		1411.255941	2820.496283	0.000451244	35	N	75	101
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	3		941.1732277	2820.496283	0.000451244	54	N	75	101
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	4		706.1318707	2820.496283	0.000451244	32	N	75	101
P40142	Exosome	AELLK	MFGIDKDAIVQAVK	GLVTK	2		767.9190488	1533.822498	0.000451244	17	N	603	617
P40142	Exosome	AELLK	MFGIDKDAIVQAVK	GLVTK	3		512.2819659	1533.822498	0.000451244	51	N	603	617
P40142	Exosome	AELLK	MFGIDKDAIVQAVK	GLVTK	2	M1:+15.995	775.9165488	1549.817498	0.000451244	10	N	603	617
P40142	Exosome	AELLK	MFGIDKDAIVQAVK	GLVTK	3	M1:+15.995	517.6136325	1549.817498	0.000451244	18	N	603	617
P40142	Exosome	AGIYK	LDNLVAIFDINR	LGQSD	2		701.8886053	1401.761611	0.000451244	103	N	174	186
P40142	Exosome	AGIYK	LDNLVAIFDINR	LGQSD	3		468.2616702	1401.761611	0.000622848	27	N	174	186
P40142	Exosome	ATKGR	ILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	3		1063.542374	3187.603721	0.000451244	603	N	555	586
P40142	Exosome	ATKGR	ILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	4		797.9087303	3187.603721	0.000451244	28	N	555	586
P40142	Exosome	APILY	AVWAEAGFLPEAELLNLRK	ISSDL	2		1064.084011	2126.152422	0.000823681	1	N	83	102
P40142	Exosome	APILY	AVWAEAGFLPEAELLNLRK	ISSDL	3		709.725274	2126.152422	0.000451244	11	N	83	102
P40142	Exosome	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	2		988.5341539	1975.052708	0.000451244	14	N	246	264
P40142	Exosome	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	3		659.3587026	1975.052708	0.000451244	24	N	246	264
P40142	Exosome	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	4		494.7709769	1975.052708	0.000622848	28	N	246	264
P40142	Exosome	LLNLR	KISSDLDGHPVPK	QAFTD	3		464.9214251	1391.740875	0.000451244	1	N	101	114
P40142	Exosome	LNLRK	ISSDLDGHPVPK	QAFTD	2		632.8307561	1263.645912	0.000622848	2	N	102	114
P40142	Exosome	LNLRK	ISSDLDGHPVPK	QAFTD	3		422.223104	1263.645912	0.000823681	4	N	102	114
P40142	Exosome	LAMFR	SVPMSTVFYPSDGVATEK	AVELA	2		957.961839	1913.908078	0.001352548	2	N	438	456
P40142	Exosome	LAMFR	SVPMSTVFYPSDGVATEK	AVELA	2	M4:+15.995	965.959339	1929.903078	0.000451244	79	N	438	456
P40142	Exosome	QVTVI	GAGVTLHEALAAAESLKK	DKISI	2		883.4944974	1764.973395	0.001395409	1	N	506	524
P40142	Exosome	QVTVI	GAGVTLHEALAAAESLKK	DKISI	3		589.3322649	1764.973395	0.000662267	5	N	506	524
P40142	Exosome	KVVLK	SKDDQVTVIGAGVTLHEALAAAESLK	KDKIS	2		1312.201029	2622.386458	0.00307782	1	N	497	523
P40142	Exosome	KVVLK	SKDDQVTVIGAGVTLHEALAAAESLK	KDKIS	3		875.1366193	2622.386458	0.000451244	28	N	497	523
P40142	Exosome	KVVLK	SKDDQVTVIGAGVTLHEALAAAESLK	KDKIS	4		656.6044144	2622.386458	0.000451244	20	N	497	523
P40142	Exosome	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021	1266.596797	2531.177994	0.000451244	18	N	114	140
P40142	Exosome	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	3	C19:+57.021	844.7337979	2531.177994	0.000451244	4	N	114	140
P40142	Exosome	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021,M21:+15.995	1274.594297	2547.172994	0.000451244	17	N	114	140
P40142	Exosome	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	3	C19:+57.021,M21:+15.995	850.0654646	2547.172994	0.000451244	1	N	114	140
P40142	Exosome	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	2	Q1:-17.027,C19:+57.021	1258.083297	2514.150994	0.001162105	1	N	114	140
P40142	Exosome	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	2	[0:-17.027,C19:+57.021,M21:+15.995	1266.080797	2530.145994	0.002296037	1	N	114	140
P40142	Exosome	VLKSK	DDQVTVIGAGVTLHEALAAAESLKK	DKISI	3		846.1259431	2535.354429	0.000451244	19	N	499	524
P40142	Exosome	VLKSK	DDQVTVIGAGVTLHEALAAAESLKK	DKISI	4		634.8464073	2535.354429	0.000622848	5	N	499	524
P40142	Exosome	KKILA	TPPQEDAPSVDIANIR	MPTPP	2		861.9370122	1721.858424	0.000662267	3	N	286	302
P40142	Exosome	KISIR	VLDPFTIKPLDR	KLILD	2		707.4091736	1412.802747	0.000451244	21	N	530	542
P40142	Exosome	KISIR	VLDPFTIKPLDR	KLILD	3		471.9420491	1412.802747	0.000451244	17	N	530	542
P40142	Exosome	RTVPF	CSTFAAFFTR	AFDQI	2	C1:+57.021	604.2821561	1206.548712	0.000622848	13	N	385	395
P40142	Exosome	VQSKK	KILATPPQEDAPSVDIANIR	MPTPP	2		1074.587115	2147.15863	0.000451244	14	N	282	302
P40142	Exosome	KILAT	PPQEDAPSVDIANIR	MPTPP	2		811.413173	1620.810746	0.000823681	2	N	287	302
P40142	Exosome	DQVTV	IGAGVTLHEALAAAESLKK	DKISI	3		627.0269529	1878.057459	0.001395409	1	N	505	524
P40142	Exosome	IFDIN	RLGQSDPAPLQHQVDIYQK	RCEAF	3		731.7190706	2192.133812	0.000451244	11	N	185	204
P40142	Exosome	MFRSV	PMSTVFYPSDGVATEK	AVELA	2	M2:+15.995	872.9091178	1743.802636	0.001329271	1	N	440	456
P40142	Exosome	LSKGH	AAPILYAVWAEAGFLPEAELLNLR	KISSD	3		876.4797691	2626.415907	0.001463592	1	N	77	101
P40142	Exosome	FAGIY	KLDNLVAIFDINR	LGQSD	3		510.9599913	1529.856574	0.000823681	5	N	173	186
P40142	Exosome	KGRGI	TGIEDKEAWHGKPLPK	NMAEQ	3		602.65686	1804.94718	0.000451244	3	N	248	264
P40142	Exosome	TVIGA	GVTLHEALAAAESLKK	DKISI	3		546.6460724	1636.914817	0.000451244	3	N	508	524
P40142	Exosome	PILYA	VWAEAGFLPEAELLNLR	KISSD	2		964.5179725	1927.020345	0.000662267	4	N	84	101
P40142	Exosome	VWEAM	AFAGIYKLDNLVAIFDINR	LGQSD	3		718.3971573	2152.168072	0.002519933	1	N	167	186
P40142	Exosome	RFVLS	KGHAAPILYAVWAEAGFLPEAELLNLR	KISSD	4		738.1556115	2948.591246	0.000823681	1	N	74	101
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELL	NLRKI	2		1219.64189	2437.26818	0.000823681	3	N	75	98
P40142	Exosome	LSKGH	AAPILYAVWAEAGFLPEAELLNLRK	ISSDL	3		919.1780901	2754.51087	0.000451244	3	N	77	102
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNL	RKISS	2		1333.205386	2664.395172	0.001463592	2	N	75	100
P40142	Exosome	FVLSK	GHAAPILYAVWAEAGFLPEAELLNL	RKISS	3		889.1395239	2664.395172	0.002727428	1	N	75	100

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P40142	Exosome	QSKKK	ILATPPQEDAPSVDIAN	IRMPT	2		875.9470456	1749.878491	0.001943752	2	N	283	300
P40142	Exosome	GIYKL	DNLVAIFDINR	LGQSD	2		645.3465733	1288.677547	0.000451244	1	N	175	186
P40142	Exosome	IGEAV	SAAVVGEPGVTVTR	LAVSQ	2		671.8704126	1341.725225	0.002663018	2	N	572	586
P40142	Exosome	LYAVW	AEAGFLPEAELLNLR	KISSD	2		821.944109	1641.872618	0.000698008	5	N	86	101
P40142	Exosome	ANRLR	ISSIQATTAAGSGHPTSC	CSAAE	2	C18:+57.021	873.410073	1744.804546	0.000823681	1	N	23	41
P40142	Exosome	DLAMF	RSVPMSTVFYPSDGVATEK	AVELA	3	M5:+15.995	696.3425297	2086.004189	0.001229886	1	N	437	456
P40142	Exosome	RILTV	EDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	3		921.4476335	2761.3195	0.002080925	1	N	559	586
P40142	Parental	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	2		1097.074706	2192.133812	0.000451244	7	N	186	205
P40142	Parental	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	3		731.7190706	2192.133812	0.000451244	8	N	186	205
P40142	Parental	FDINR	LGQSDPAPLQHQVDIYQKR	CEAFG	4		549.041253	2192.133812	0.000451244	11	N	186	205
P40142	Parental	FDINR	LGQSDPAPLQHQVDIYQK	RCEAF	2		1019.02415	2036.032701	0.000451244	52	N	186	204
P40142	Parental	FDINR	LGQSDPAPLQHQVDIYQK	RCEAF	3		679.6853669	2036.032701	0.000451244	34	N	186	204
P40142	Parental	ICFIR	TSRPENAIIYSNNEDFQVGQAK	VVLKS	2		1241.104389	2480.193177	0.000451244	53	N	471	493
P40142	Parental	ICFIR	TSRPENAIIYSNNEDFQVGQAK	VVLKS	3		827.7388591	2480.193177	0.000451244	63	N	471	493
P40142	Parental	DIYQK	RCEAFGWHTIIVDGHSVEELCK	AFGQA	3	C2:+57.021,C21:+57.021	881.7531493	2642.236048	0.000451244	9	N	204	226
P40142	Parental	DIYQK	RCEAFGWHTIIVDGHSVEELCK	AFGQA	4	C2:+57.021,C21:+57.021	661.566812	2642.236048	0.000451244	15	N	204	226
P40142	Parental	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	3	C1:+39.994,C20:+57.021	824.043779	2469.107937	0.000451244	5	N	205	226
P40142	Parental	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	2	C1:+57.021,C20:+57.021	1244.075268	2486.134937	0.001162105	1	N	205	226
P40142	Parental	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	3	C1:+57.021,C20:+57.021	829.7194456	2486.134937	0.000451244	28	N	205	226
P40142	Parental	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	4	C1:+57.021,C20:+57.021	622.5415342	2486.134937	0.000451244	27	N	205	226
P40142	Parental	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	2	[0:-	1235.561768	2469.107937	0.000451244	8	N	205	226
P40142	Parental	IYQKR	CEAFGWHTIIVDGHSVEELCK	AFGQA	3	[0:-	824.043779	2469.107937	0.000451244	17	N	205	226
P40142	Parental	QSKKK	ILATPPQEDAPSVDIANIR	MPTPP	2		1010.539633	2019.063667	0.000451244	136	N	283	302
P40142	Parental	QSKKK	ILATPPQEDAPSVDIANIR	MPTPP	3		674.0290222	2019.063667	0.000451244	39	N	283	302
P40142	Parental	ARATK	GRILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	3		1134.583232	3400.726296	0.000451244	4	N	553	586
P40142	Parental	GCATR	DRTVPFCSTFAAFFTR	AFDQI	3	C7:+57.021	641.6458123	1921.914037	0.000451244	13	N	379	395
P40142	Parental	EAMAF	AGIYKLDNLVAIFDINR	LGQSD	2		968.0390721	1934.062544	0.000451244	10	N	169	186
P40142	Parental	EAMAF	AGIYKLDNLVAIFDINR	LGQSD	3		645.6953147	1934.062544	0.000451244	16	N	169	186
P40142	Parental	RDRTV	PFCSTFAAFFTR	AFDQI	2	C3:+57.021	726.342745	1450.66989	0.000451244	30	N	383	395
P40142	Parental	ATRDR	TVPFCSTFAAFFTR	AFDQI	2	C5:+57.021	826.4007913	1650.785983	0.000823681	4	N	381	395
P40142	Parental	ATRDR	TVPFCSTFAAFFTR	AFDQI	3	C5:+57.021	551.2697942	1650.785983	0.000451244	22	N	381	395
P40142	Parental	APILY	AVWAEAGFLPEAELLNLR	KISSD	2		1000.036529	1998.057459	0.000451244	45	N	83	101
P40142	Parental	APILY	AVWAEAGFLPEAELLNLR	KISSD	3		667.0269529	1998.057459	0.000451244	34	N	83	101
P40142	Parental	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	2		1475.303423	2948.591246	0.000622848	1	N	75	102
P40142	Parental	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	3		983.8715487	2948.591246	0.000451244	11	N	75	102
P40142	Parental	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLRK	ISSDL	4		738.1556115	2948.591246	0.000451244	33	N	75	102
P40142	Parental	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	2		1005.00457	2007.993539	0.000451244	13	N	264	281
P40142	Parental	KPLPK	NMAEQIIQEIYSQVQSK	KKILA	3		670.3389797	2007.993539	0.000451244	9	N	264	281
P40142	Parental	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	2		1411.255941	2820.496283	0.000823681	1	N	75	101
P40142	Parental	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	3		941.1732277	2820.496283	0.000451244	26	N	75	101
P40142	Parental	FVLSK	GHAAPILYAVWAEAGFLPEAELLNLR	KISSD	4		706.1318707	2820.496283	0.000451244	4	N	75	101
P40142	Parental	AELLK	MFGIDKDAIVQAVK	GLVTK	2		767.9190488	1533.822498	0.000451244	4	N	603	617
P40142	Parental	AELLK	MFGIDKDAIVQAVK	GLVTK	3		512.2819659	1533.822498	0.000451244	4	N	603	617
P40142	Parental	AGIYK	LDNLVAIFDINR	LGQSD	2		701.8886053	1401.761611	0.000451244	47	N	174	186
P40142	Parental	AGIYK	LDNLVAIFDINR	LGQSD	3		468.2616702	1401.761611	0.000622848	4	N	174	186
P40142	Parental	ATKGR	ILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	3		1063.542374	3187.603721	0.000451244	96	N	555	586
P40142	Parental	ATKGR	ILTVEDHYYEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	4		797.9087303	3187.603721	0.000451244	8	N	555	586
P40142	Parental	APILY	AVWAEAGFLPEAELLNLRK	ISSDL	2		1064.084011	2126.152422	0.000451244	7	N	83	102
P40142	Parental	APILY	AVWAEAGFLPEAELLNLRK	ISSDL	3		709.725274	2126.152422	0.000451244	10	N	83	102
P40142	Parental	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	2		988.5341539	1975.052708	0.000622848	3	N	246	264
P40142	Parental	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	3		659.3587026	1975.052708	0.000622848	3	N	246	264
P40142	Parental	TFKGR	GITGIEDKEAWHGKPLPK	NMAEQ	4		494.7709769	1975.052708	0.000622848	4	N	246	264
P40142	Parental	KVVLK	SKDDQVTVIGAGVTLHEALAAAESLK	KDKIS	3		875.1366193	2622.386458	0.000622848	2	N	497	523
P40142	Parental	KVVLK	SKDDQVTVIGAGVTLHEALAAAESLK	KDKIS	4		656.6044144	2622.386458	0.000870037	3	N	497	523
P40142	Parental	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021	1266.596797	2531.177994	0.000451244	2	N	114	140
P40142	Parental	HPVPK	QAFTDVATGSLGQGLGAACGMAYTGK	YFDKA	3	C19:+57.021	844.7337979	2531.177994	0.001463592	1	N	114	140
P40142	Parental	KKILA	TPPQEDAPSVDIANIR	MPTPP	2		861.9370122	1721.858424	0.001162105	1	N	286	302
P40142	Parental	KISIR	VLDPFTIKPLDR	KLILD	2		707.4091736	1412.802747	0.001871652	1	N	530	542
P40142	Parental	VQSKK	KILATPPQEDAPSVDIANIR	MPTPP	2		1074.587115	2147.15863	0.000451244	4	N	282	302
P40142	Parental	FAGIY	KLDNLVAIFDINR	LGQSD	3		510.9599913	1529.856574	0.000451244	14	N	173	186
P40142	Parental	AGVTL	HEALAAAESLKK	DKISI	3		423.2388656	1266.693197	0.000622848	5	N	512	524
P40142	Parental	VEDHY	YEGGIGEAVSAAVVGEPGVTVTR	LAVSQ	2		1109.571662	2217.127723	0.000451244	5	N	563	586
P40142	Parental	EAGFL	PEAELLNLR	KISSD	2		527.7987276	1053.581855	0.002981883	1	N	92	101
P40142	Parental	KVVLK	SKDDQVTVIGAGVTL	HEALA	2		751.9071921	1501.798784	0.002981883	1	N	497	512
P40223	Parental	FQLYR	ITVAPLYPGIVGPPVNVYTFAGER	APPHA	2		1265.689372	2529.363143	0.000823681	1	N	504	528

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P40223	Parental	FQLYR	ITVAPLYPGIVGPPVNVYTFAGER	APPHA	3		844.1288478	2529.363143	0.002813207	1	N	504	528
P40223	Parental	SFRSR	ADCQYQGDTIPDCVAK	KRQNN	2	C3:+57.021,C13:+57.021	920.8957099	1839.77582	0.002145581	1	N	165	181
P40240	Exosome	RETLK	AIHMALDCCGIAGPLEQFISDTCPK	KQLLE	2	M4:+15.995,C8:+57.021,C9:+57.021,C23:+57.021	1410.644687	2819.273773	0.000451244	22	N	142	167
P40240	Exosome	RETLK	AIHMALDCCGIAGPLEQFISDTCPK	KQLLE	3	M4:+15.995,C8:+57.021,C9:+57.021,C23:+57.021	940.7657245	2819.273773	0.000451244	66	N	142	167
P40240	Exosome	DEVIK	ELQEFYKDTYQK	LRSKD	2		796.3860925	1590.756585	0.000451244	8	N	117	129
P40240	Exosome	RETLK	AIHMALDCCGIAGPLEQFISDTCPKK	QLLES	3	M4:+15.995,C8:+57.021,C9:+57.021,C23:+57.021	983.4640455	2947.368736	0.001162105	3	N	142	168
P40240	Exosome	RETLK	AIHMALDCCGIAGPLEQFISDTCPKK	QLLES	4	M4:+15.995,C8:+57.021,C9:+57.021,C23:+57.021	737.8499841	2947.368736	0.000451244	10	N	142	168
P40240	Exosome	CCGIA	GPLEQFISDTCPK	KQLLE	2	C11:+57.021	746.3613318	1490.707064	0.000451244	1	N	154	167
P41216	Parental	FEQVK	GIAVHPELFSIDNGLLTPTLK	AKRPE	3		745.7514888	2234.231066	0.000622848	5	N	655	676
P41216	Parental	WISYK	EVAELAECIGSGLIQK	GFKPC	3	C8:+57.021	572.96644	1715.87592	0.001871652	1	N	125	141
P41241	Exosome	MTQLR	HSNLVQLLGVIVEEK	GGLYI	3		559.9898391	1676.946117	0.000451244	27	N	244	259
P41241	Exosome	LFLVR	ESTNYPGDYTLCVSCEGK	VEHYR	2	C12:+57.021,C15:+57.021	1040.435396	2078.855192	0.000451244	11	N	107	125
P41241	Exosome	EQAER	LLYPPETGLFLVR	ESTNY	2		759.4404738	1516.865348	0.000451244	6	N	94	107
P41241	Exosome	YEVMK	NCWHLDAATRPTFLQLR	EQLEH	4	C2:+57.021	525.5209491	2098.052596	0.001763695	4	N	420	437
P41241	Exosome	LPFCK	GDVLTIVAVTKDPNWYK	AKNKV	3		640.3478035	1918.020011	0.000451244	3	N	32	49
P41241	Exosome	ERLLY	PPETGLFLVR	ESTNY	2		564.8247454	1127.633891	0.002813207	1	N	97	107
P41241	Parental	LFLVR	ESTNYPGDYTLCVSCEGK	VEHYR	2	C12:+57.021,C15:+57.021	1040.435396	2078.855192	0.000622848	3	N	107	125
P41245	Exosome	RRDGR	LWCATTSNFDTDKK	WGFCP	2	C3:+57.021	843.8935275	1685.771455	0.000451244	84	N	370	384
P41245	Exosome	RRDGR	LWCATTSNFDTDKK	WGFCP	3	C3:+57.021	562.9316183	1685.771455	0.000451244	36	N	370	384
P41245	Exosome	FLNHR	GSPLQGPFLTAR	TWPAL	2		622.3438336	1242.672067	0.000451244	68	N	564	576
P41245	Exosome	LMLQK	QLSLPQTGELDSQTLK	AIRTP	2		879.4681452	1756.92069	0.000451244	59	N	77	93
P41245	Exosome	LMLQK	QLSLPQTGELDSQTLK	AIRTP	2	[0:-17.027	870.9546452	1739.89369	0.000622848	18	N	77	93
P41245	Exosome	SDGYR	WCATTANYDQDKLYGFCPTR	VDATV	2	C2:+57.021,C17:+57.021	1234.043968	2466.072337	0.000451244	53	N	312	332
P41245	Exosome	SDGYR	WCATTANYDQDKLYGFCPTR	VDATV	3	C2:+57.021,C17:+57.021	823.0319122	2466.072337	0.000451244	85	N	312	332
P41245	Exosome	QSVIR	VDKEFSGVPWNSHDIFQYQDK	AYFCH	2		1270.098575	2538.18155	0.000451244	27	N	667	688
P41245	Exosome	QSVIR	VDKEFSGVPWNSHDIFQYQDK	AYFCH	3		847.0683167	2538.18155	0.000451244	39	N	667	688
P41245	Exosome	RSLDK	LGLGPEVTHVSGLLPR	RLGKA	2		822.9757434	1643.935887	0.000451244	12	N	621	637
P41245	Exosome	RSLDK	LGLGPEVTHVSGLLPR	RLGKA	3		548.986429	1643.935887	0.000451244	79	N	621	637
P41245	Exosome	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	2		1044.594743	2087.173886	0.000451244	30	N	617	637
P41245	Exosome	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	3		696.7324286	2087.173886	0.000451244	59	N	617	637
P41245	Exosome	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	4		522.8012714	2087.173886	0.000451244	47	N	617	637
P41245	Exosome	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	2	C13:+57.021	1277.613107	2553.210613	0.000451244	44	N	275	297
P41245	Exosome	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	3	C13:+57.021	852.0780045	2553.210613	0.000451244	42	N	275	297
P41245	Exosome	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	4	C13:+57.021	639.3104533	2553.210613	0.000451244	30	N	275	297
P41245	Exosome	TARTW	PALPATLDSAFEDPQTKR	VFFFS	2		979.0054263	1955.995253	0.000451244	8	N	578	596
P41245	Exosome	TARTW	PALPATLDSAFEDPQTKR	VFFFS	3		653.0062175	1955.995253	0.000662267	1	N	578	596
P41245	Exosome	FLTAR	TWPALPATLDSAFEDPQTKR	VFFFS	2		1122.568922	2243.122244	0.000451244	20	N	576	596
P41245	Exosome	FLTAR	TWPALPATLDSAFEDPQTKR	VFFFS	3		748.7152147	2243.122244	0.001463592	1	N	576	596
P41245	Exosome	WSLGK	GVVIPTYYGNSNGAPCHFPFTFEGR	SYSAC	2	C16:+57.021	1394.153127	2786.290655	0.000451244	29	N	214	239
P41245	Exosome	WSLGK	GVVIPTYYGNSNGAPCHFPFTFEGR	SYSAC	3	C16:+57.021	929.7713516	2786.290655	0.000622848	33	N	214	239
P41245	Exosome	PFDGK	DGLLAHAFPPGAGVQGDAHFDDDELWSLGK	GVVIP	3		1045.832258	3134.473375	0.000451244	100	N	184	214
P41245	Exosome	PFDGK	DGLLAHAFPPGAGVQGDAHFDDDELWSLGK	GVVIP	4		784.6261439	3134.473375	0.000451244	134	N	184	214
P41245	Exosome	DAFAR	AFAVWGEVAPLTFTR	VYGPE	2		832.943912	1663.872224	0.000451244	97	N	143	158
P41245	Exosome	DAFAR	AFAVWGEVAPLTFTR	VYGPE	3		555.6318746	1663.872224	0.000451244	33	N	143	158
P41245	Exosome	FCPTR	VDATVVGGNSAGELCVFPFVFLGK	QYSSC	2	C15:+57.021	1242.135883	2482.256167	0.000451244	167	N	332	356
P41245	Exosome	FCPTR	VDATVVGGNSAGELCVFPFVFLGK	QYSSC	3	C15:+57.021	828.4265222	2482.256167	0.000451244	92	N	332	356
P41245	Exosome	FLTAR	TWPALPATLDSAFEDPQTK	RVFFF	2		1044.518366	2087.021133	0.000451244	26	N	576	595
P41245	Exosome	FLTAR	TWPALPATLDSAFEDPQTK	RVFFF	3		696.681511	2087.021133	0.000451244	3	N	576	595
P41245	Exosome	SDGYR	WCATTANYDQDK	LYGFC	2	C2:+57.021	736.8094634	1471.603327	0.000823681	2	N	312	324
P41245	Exosome	TTDGR	NDGTPWCSTTADYDKDGK	FGFCP	2	C7:+57.021	1015.923742	2029.831883	0.000451244	57	N	249	267
P41245	Exosome	LTFTR	VYGPEADIVIQFGVAEHGDGYPFDGK	DGLLA	3		927.4454528	2779.312958	0.000451244	131	N	158	184
P41245	Exosome	IRVDK	EFSGVPWNSHDIFQYQDK	AYFCH	2		1099.003415	2195.99123	0.000622848	13	N	670	688
P41245	Exosome	IRVDK	EFSGVPWNSHDIFQYQDK	AYFCH	3		733.0048766	2195.99123	0.001162105	6	N	670	688
P41245	Exosome	FPLNK	DDIDGIQYLYGR	GSKPD	2		714.3442276	1426.672855	0.000451244	13	N	433	445
P41245	Exosome	VVGGN	SAGELCVFPFVFLGK	QYSSC	2	C6:+57.021	835.934467	1669.853334	0.000451244	7	N	341	356
P41245	Exosome	TTDGR	NDGTPWCSTTADYDK	DGKFG	2	C7:+57.021	865.8520566	1729.688513	0.000823681	1	N	249	264
P41245	Exosome	FCPTR	VDATVVGGNSAGELCVFPF	VFLGK	2	C15:+57.021	969.9672238	1937.918848	0.000451244	11	N	332	351
P41245	Exosome	DAFAR	AFAVWGEVAPLTF	TRVYG	2		704.3695171	1406.723434	0.000622848	9	N	143	156
P41245	Exosome	RRDGR	LWCATTSNFDTDK	KWGFC	2	C3:+57.021	779.8460459	1557.676492	0.000451244	7	N	370	383
P41245	Exosome	FCPTR	VDATVVGGNSAGELCVFPFVF	LGKQY	2	C15:+57.021	1093.035638	2184.055676	0.000823681	2	N	332	353
P41245	Exosome	DTDKK	WGFCPDQGYSLF	LVAAH	2	C4:+57.021	738.8165601	1475.61752	0.000637154	3	N	384	396

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P41245	Exosome	RVDAT	VVGGNSAGELCVFPFVFLGK	QYSSC	2	C11:+57.021	1049.045809	2096.076017	0.000451244	7	N	336	356
P41245	Parental	RRDGR	LWCATTSNFDTDKK	WGFCP	2	C3:+57.021	843.8935275	1685.771455	0.000451244	46	N	370	384
P41245	Parental	RRDGR	LWCATTSNFDTDKK	WGFCP	3	C3:+57.021	562.9316183	1685.771455	0.000451244	36	N	370	384
P41245	Parental	FLNHR	GSPLQGPFLTAR	TWPAL	2		622.3438336	1242.672067	0.000451244	33	N	564	576
P41245	Parental	LMLQK	QLSLPQTGELDSQTLK	AIRTP	2		879.4681452	1756.92069	0.000451244	38	N	77	93
P41245	Parental	LMLQK	QLSLPQTGELDSQTLK	AIRTP	2	[0:-17.027	870.9546452	1739.89369	0.000451244	17	N	77	93
P41245	Parental	SDGYR	WCATTANYDQDKLYGFCPTR	VDATV	2	C2:+57.021,C17:+57.021	1234.043968	2466.072337	0.000451244	58	N	312	332
P41245	Parental	SDGYR	WCATTANYDQDKLYGFCPTR	VDATV	3	C2:+57.021,C17:+57.021	823.0319122	2466.072337	0.000451244	29	N	312	332
P41245	Parental	QSVIR	VDKEFSGVPWNSHDIFQYQDK	AYFCH	2		1270.098575	2538.18155	0.000451244	18	N	667	688
P41245	Parental	QSVIR	VDKEFSGVPWNSHDIFQYQDK	AYFCH	3		847.0683167	2538.18155	0.000451244	39	N	667	688
P41245	Parental	RSLDK	LGLGPEVTHVSGLLPR	RLGKA	2		822.9757434	1643.935887	0.000451244	11	N	621	637
P41245	Parental	RSLDK	LGLGPEVTHVSGLLPR	RLGKA	3		548.986429	1643.935887	0.000451244	98	N	621	637
P41245	Parental	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	2		1044.594743	2087.173886	0.000451244	35	N	617	637
P41245	Parental	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	3		696.7324286	2087.173886	0.000451244	26	N	617	637
P41245	Parental	VLGPR	SLDKLGLGPEVTHVSGLLPR	RLGKA	4		522.8012714	2087.173886	0.000451244	41	N	617	637
P41245	Parental	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	2	C13:+57.021	1277.613107	2553.210613	0.000451244	53	N	275	297
P41245	Parental	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	3	C13:+57.021	852.0780045	2553.210613	0.000451244	41	N	275	297
P41245	Parental	CPSER	LYTEHGNGEGKPCVFPFIFEGR	SYSAC	4	C13:+57.021	639.3104533	2553.210613	0.000451244	21	N	275	297
P41245	Parental	TARTW	PALPATLDSAFEDPQTKR	VFFFS	2		979.0054263	1955.995253	0.000451244	2	N	578	596
P41245	Parental	TARTW	PALPATLDSAFEDPQTKR	VFFFS	3		653.0062175	1955.995253	0.000451244	5	N	578	596
P41245	Parental	FLTAR	TWPALPATLDSAFEDPQTKR	VFFFS	2		1122.568922	2243.122244	0.000451244	21	N	576	596
P41245	Parental	WSLGK	GVVIPTYYGNSNGAPCHFPFTFEGR	SYSAC	2	C16:+57.021	1394.153127	2786.290655	0.000451244	39	N	214	239
P41245	Parental	WSLGK	GVVIPTYYGNSNGAPCHFPFTFEGR	SYSAC	3	C16:+57.021	929.7713516	2786.290655	0.000451244	27	N	214	239
P41245	Parental	PFDGK	DGLLAHAFPPGAGVQGDAHFDDDELWSLGK	GVVIP	3		1045.832258	3134.473375	0.000451244	72	N	184	214
P41245	Parental	PFDGK	DGLLAHAFPPGAGVQGDAHFDDDELWSLGK	GVVIP	4		784.6261439	3134.473375	0.000451244	105	N	184	214
P41245	Parental	DAFAR	AFAVWGEVAPLTFTR	VYGPE	2		832.943912	1663.872224	0.000451244	82	N	143	158
P41245	Parental	DAFAR	AFAVWGEVAPLTFTR	VYGPE	3		555.6318746	1663.872224	0.000451244	26	N	143	158
P41245	Parental	FCPTR	VDATVVGGNSAGELCVFPFVFLGK	QYSSC	2	C15:+57.021	1242.135883	2482.256167	0.000451244	184	N	332	356
P41245	Parental	FCPTR	VDATVVGGNSAGELCVFPFVFLGK	QYSSC	3	C15:+57.021	828.4265222	2482.256167	0.000451244	49	N	332	356
P41245	Parental	FLTAR	TWPALPATLDSAFEDPQTK	RVFFF	2		1044.518366	2087.021133	0.000451244	19	N	576	595
P41245	Parental	FLTAR	TWPALPATLDSAFEDPQTK	RVFFF	3		696.681511	2087.021133	0.000451244	10	N	576	595
P41245	Parental	YDQDK	LYGFCPTRVDATVVGGNSAGELCVFPFVFLGK	QYSSC	3	C5:+57.021,C23:+57.021	1159.916192	3476.725176	0.000451244	3	N	324	356
P41245	Parental	DLPRD	MIDDAFARAFAVWGEVAPLTFTR	VYGPE	3		862.1059376	2583.294413	0.002727428	1	N	135	158
P41245	Parental	IRTPR	CGVPDVGRFQTFK	GLKWD	3	C1:+57.021	504.2542556	1509.739367	0.001162105	1	N	99	112
P41245	Parental	SDGYR	WCATTANYDQDK	LYGFC	2	C2:+57.021	736.8094634	1471.603327	0.000622848	8	N	312	324
P41245	Parental	TTDGR	NDGTPWCSTTADYDKDGK	FGFCP	2	C7:+57.021	1015.923742	2029.831883	0.000451244	18	N	249	267
P41245	Parental	LTFTR	VYGPEADIVIQFGVAEHGDGYPFDGK	DGLLA	3		927.4454528	2779.312958	0.000451244	183	N	158	184
P41245	Parental	IRVDK	EFSGVPWNSHDIFQYQDK	AYFCH	2		1099.003415	2195.99123	0.000622848	5	N	670	688
P41245	Parental	IRVDK	EFSGVPWNSHDIFQYQDK	AYFCH	3		733.0048766	2195.99123	0.001463592	3	N	670	688
P41245	Parental	FPLNK	DDIDGIQYLYGR	GSKPD	2		714.3442276	1426.672855	0.000451244	6	N	433	445
P41245	Parental	FCPTR	VDATVVGGNSAGELCVFPF	VFLGK	2	C15:+57.021	969.9672238	1937.918848	0.000451244	12	N	332	351
P41245	Parental	RRDGR	LWCATTSNFDTDK	KWGFC	2	C3:+57.021	779.8460459	1557.676492	0.000451244	4	N	370	383
P41245	Parental	NVDVF	DAIAEIQGALHFFK	DGWYW	3		520.6125915	1558.814375	0.001264573	1	N	539	553
P41245	Parental	WSLGK	GVVIPTYYGNSNGAPCHFPF	TFEGR	2	C16:+57.021	1099.012497	2196.009394	0.00307782	1	N	214	234
P41245	Parental	TARTW	PALPATLDSAFEDPQTK	RVFFF	2		900.9548707	1799.894141	0.000451244	4	N	578	595
P41245	Parental	DTDKK	WGFCPDQGYSLF	LVAAH	2	C4:+57.021	738.8165601	1475.61752	0.000979378	7	N	384	396
P41245	Parental	YPLYS	YLEGFPLNKDDIDGIQYLYGR	GSKPD	3		830.4169459	2488.227438	0.002519933	1	N	424	445
P41245	Parental	KGVVI	PTYYGNSNGAPCHFPFTFEGR	SYSAC	3	C12:+57.021	807.0238996	2418.048299	0.001329271	1	N	218	239
P42208	Exosome	TRLLK	ASIPFSVVGSNQLIEAK	GKKVR	2		880.4835983	1758.951597	0.000451244	12	N	232	249
P42208	Exosome	GVKLR	LTVVDTPGYGDAINCR	DCFKT	2	C15:+57.021	875.9253589	1749.835118	0.000451244	7	N	96	112
P42208	Exosome	SGLGK	STLINSLFLTDLYPER	IIPGA	2		941.5019881	1880.988376	0.000451244	3	N	50	66
P42208	Parental	TRLLK	ASIPFSVVGSNQLIEAK	GKKVR	2		880.4835983	1758.951597	0.002374549	1	N	232	249
P42208	Parental	SGLGK	STLINSLFLTDLYPER	IIPGA	2		941.5019881	1880.988376	0.000451244	6	N	50	66
P42208	Parental	-MSK	QQPTQFINPETPGYVGFANLPNQVHR	KSVKK	3		984.8304122	2951.467836	0.001839721	1	N	3	29
P42227	Exosome	DWKRR	QQIACIGGPPNICLDRLENWITSLAESQLQTR	QQIKK	3	C5:+57.021,C13:+57.021	1227.954257	3680.839372	0.001943752	1	N	246	278
P42227	Exosome	WEESR	LLQTAATAAQQGGQANHPTAAVVTEK	QQMLE	3		859.4529417	2575.335425	0.000451244	44	N	114	140
P42227	Exosome	TLAEK	LLGPGVNYSGCQITWAK	FCKEN	2	C11:+57.021	932.475019	1862.934438	0.000735798	5	N	531	548
P42227	Exosome	PMELR	QFLAPWIESQDWAYAASK	ESHAT	2		1056.015794	2110.015988	0.000451244	3	N	31	49
P42227	Exosome	EAFGK	YCRPESQEHPEADPGSAAPYLK	TKFIC	3	C2:+57.021	834.7170239	2501.127672	0.002813207	1	N	685	707
P42227	Exosome	EQKMK	VVENLQDDFDFNYK	TLKSQ	2		873.4050136	1744.794427	0.000451244	3	N	163	177
P42227	Parental	DWKRR	QQIACIGGPPNICLDRLENWITSLAESQLQTR	QQIKK	3	C5:+57.021,C13:+57.021	1227.954257	3680.839372	0.000451244	9	N	246	278
P42227	Parental	DWKRR	QQIACIGGPPNICLDRLENWITSLAESQLQTR	QQIKK	3	[0:-	1222.278591	3663.812372	0.000851441	2	N	246	278
P42227	Parental	WEESR	LLQTAATAAQQGGQANHPTAAVVTEK	QQMLE	3		859.4529417	2575.335425	0.000451244	19	N	114	140
P42227	Parental	TLAEK	LLGPGVNYSGCQITWAK	FCKEN	2	C11:+57.021	932.475019	1862.934438	0.001395409	1	N	531	548
P42227	Parental	PMELR	QFLAPWIESQDWAYAASK	ESHAT	2		1056.015794	2110.015988	0.001763695	3	N	31	49

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P42227	Parental	DQMRR	SIVSELAGLLSAMEYVQK	TLTDE	3		646.6804543	1937.017963	0.000451244	1	N	215	233
P42227	Parental	EAFGK	YCRPESQEHPEADPGSAAPYLK	TKFIC	3	C2:+57.021	834.7170239	2501.127672	0.000451244	3	N	685	707
P42227	Parental	EQKMK	VVENLQDDFDFNYK	TLKSQ	2		873.4050136	1744.794427	0.002145581	1	N	163	177
P42227	Parental	GNGGR	ANCDASLIVTEELHLITFETEVYHQGLK	IDLET	4	C3:+57.021	808.4068162	3229.596065	0.000451244	7	N	423	451
P42227	Parental	TNNPK	NVNFFTKPPIGTWDQVAEVLSWQFSSTTK	RGLSI	3		1109.894859	3326.661176	0.00091018	1	N	488	517
P42232	Exosome	QESLR	IQAQFAQLGQLNPQER	MSRET	2		920.9873708	1839.959142	0.001352548	1	N	181	197
P42232	Exosome	SLADR	LGDLNYLIYVFPDRPKDEVYSK	YYTPV	4		661.847413	2643.358452	0.001162105	2	N	659	681
P42232	Exosome	QENIK	ATQLLEGLVQELQK	KAEHQ	3		523.966923	1568.877369	0.000622848	2	N	56	70
P42232	Parental	SLADR	LGDLNYLIYVFPDRPKDEVYSK	YYTPV	4		661.847413	2643.358452	0.002519933	1	N	659	681
P42567	Exosome	ISSLK	AEITSQESQISSYEEELLK	AREEL	2		1092.531868	2183.048136	0.000451244	4	N	430	449
P42567	Exosome	EELSR	LQQETAQLEESVESGK	AQLEP	2		888.4370421	1774.858484	0.000451244	1	N	456	472
P42567	Parental	LQAQK	QQVQELLGELDEQKAQLEEQLQEVR	KKCAE	3		994.1794353	2979.514906	0.000451244	5	N	391	416
P42567	Parental	SSLQK	NITGSSPVADFSAIKELDTLNNEIVDLQR	EKNNV	3		1053.877645	3158.609535	0.000451244	13	N	318	347
P42567	Parental	EVRKK	CAEEAQLISSLKAEITSQESQISSYEEELLK	AREEL	3	C1:+39.994	1166.234642	3495.680526	0.000823681	3	N	418	449
P42567	Parental	EVRKK	CAEEAQLISSLKAEITSQESQISSYEEELLK	AREEL	3	[0:-17.027,C1:+57.021	1166.234642	3495.680526	0.002080925	1	N	418	449
P42567	Parental	ISSLK	AEITSQESQISSYEEELLK	AREEL	2		1092.531868	2183.048136	0.000451244	20	N	430	449
P42567	Parental	VPPPR	FHDSSSPLLTSGPSVAELPWAVK	SEDKA	3		809.0853077	2424.232523	0.001229886	1	N	102	125
P42567	Parental	QRLAR	LNQQEQEDLELAIALSK	SEISE	2		971.5105414	1941.005483	0.000637154	2	N	874	891
P42567	Parental	EELSR	LQQETAQLEESVESGK	AQLEP	2		888.4370421	1774.858484	0.000451244	1	N	456	472
P42567	Parental	GNTGR	VLALDAAAFLK	KSGLP	2		566.342771	1130.669942	0.001591523	2	N	33	44
P42567	Parental	EDKAK	YDAIFDSLSPVDGFLSGDK	VKPVL	2		1023.489275	2044.962949	0.001162105	3	N	131	150
P42669	Exosome	DALAK	LIDDYGVEEEPAELPEGTSLTVDNKR	FFFDV	3		963.805375	2888.392725	0.000451244	35	N	203	229
P42669	Exosome	QTVNR	GPGLGSTQGQTIALPAQGLIEFR	DALAK	2		1156.124396	2310.233192	0.000451244	14	N	175	198
P42669	Exosome	AVEFR	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	RALKS	3		1090.849978	3269.526533	0.001943752	1	N	110	139
P42669	Parental	DALAK	LIDDYGVEEEPAELPEGTSLTVDNKR	FFFDV	3		963.805375	2888.392725	0.000451244	17	N	203	229
P42669	Parental	QREKR	AACEQLHQQQQQQQEETTAATLLLQGEEEGEED	-	3	C3:+57.021	1257.22954	3768.66522	0.000622848	3	N	288	321
P42932	Exosome	FVLVF	AGALLELAEELLR	IGLSV	2		699.4040883	1396.792577	0.00091018	3	N	107	120
P42932	Exosome	YAIKK	FAEAFEAIPR	ALAEN	2		575.7987276	1149.581855	0.000823681	4	N	440	450
P42932	Exosome	TFLAK	LIAQACVSIFPDSGNFNVDNIR	VCKIL	2	C6:+57.021	1225.610564	2449.205528	0.000451244	26	N	181	203
P42932	Exosome	TFLAK	LIAQACVSIFPDSGNFNVDNIR	VCKIL	3	C6:+57.021	817.4096427	2449.205528	0.000451244	4	N	181	203
P42932	Exosome	IELAK	QITSYGETCPGLEQYAIKK	FAEAF	3	C9:+57.021	729.3651514	2185.072054	0.000451244	6	N	421	440
P42932	Exosome	IELAK	QITSYGETCPGLEQYAIK	KFAEA	2	C9:+57.021	1029.496345	2056.977091	0.000451244	6	N	421	439
P42932	Exosome	NRLEK	LFVTNDAATILR	ELEVQ	2		667.3778735	1332.740147	0.000451244	16	N	62	74
P42932	Parental	FVLVF	AGALLELAEELLR	IGLSV	2		699.4040883	1396.792577	0.000451244	14	N	107	120
P42932	Parental	YAIKK	FAEAFEAIPR	ALAEN	2		575.7987276	1149.581855	0.000451244	5	N	440	450
P42932	Parental	TFLAK	LIAQACVSIFPDSGNFNVDNIR	VCKIL	2	C6:+57.021	1225.610564	2449.205528	0.000451244	29	N	181	203
P42932	Parental	TFLAK	LIAQACVSIFPDSGNFNVDNIR	VCKIL	3	C6:+57.021	817.4096427	2449.205528	0.000622848	1	N	181	203
P42932	Parental	IELAK	QITSYGETCPGLEQYAIKK	FAEAF	2	C9:+57.021	1093.543827	2185.072054	0.000451244	6	N	421	440
P42932	Parental	IELAK	QITSYGETCPGLEQYAIKK	FAEAF	3	C9:+57.021	729.3651514	2185.072054	0.000451244	7	N	421	440
P42932	Parental	IELAK	QITSYGETCPGLEQYAIK	KFAEA	2	C9:+57.021	1029.496345	2056.977091	0.000451244	27	N	421	439
P42932	Parental	NRLEK	LFVTNDAATILR	ELEVQ	2		667.3778735	1332.740147	0.000662267	17	N	62	74
P42932	Parental	QEGNK	NVGLDIEAEVPAVK	DMLEA	2		727.3990029	1452.782406	0.000870037	2	N	476	490
P43024	Exosome	HLRIR	TKPFPWGDGNHTLF	HNPHV	3		539.6005745	1615.778323	0.002981883	1	N	82	96
P43024	Parental	NHTLF	HNPHVNPLPTGYEDE	-	2		859.8926047	1717.769609	0.000622848	10	N	96	111
P43024	Parental	HLRIR	TKPFPWGDGNHTLF	HNPHV	3		539.6005745	1615.778323	0.000851441	13	N	82	96
P43274	Exosome	-M	SETAPAAPAAPAPAEKTPVK	KKARK	3		635.3428296	1903.005089	0.001763695	6	N	1	21
P43274	Exosome	AALKK	ALAAAGYDVEKN	NSRIK	2		611.3096565	1220.603713	0.000451244	17	Y	64	76
P43274	Exosome	GGAKR	KTSGPPVSELITK	AVAAS	2		678.8908137	1355.766027	0.000451244	12	N	33	46
P43274	Exosome	GGAKR	KTSGPPVSELITK	AVAAS	3		452.9298091	1355.766027	0.000451244	56	N	33	46
P43274	Exosome	AALKK	ALAAAGYDVEK	NNSRI	2		554.2881927	1106.560785	0.000451244	105	Y	64	75
P43274	Exosome	ASKER	SGVSLAALK	KALAA	2		423.2587069	844.5018138	0.000823681	48	Y	54	63
P43274	Exosome	GAKRK	TSGPPVSELITK	AVAAS	2		614.8433321	1227.671064	0.000451244	107	N	34	46
P43274	Exosome	LAALK	KALAAAGYDVEK	NNSRI	2		618.3356743	1234.655749	0.000637154	1	Y	63	75
P43274	Exosome	AALKK	ALAAAGYDVEKNNSR	IKLGL	2		789.89769	1577.77978	0.000451244	30	Y	64	79
P43274	Exosome	AALKK	ALAAAGYDVEKNNSR	IKLGL	3		526.9343934	1577.77978	0.000451244	10	Y	64	79
P43274	Exosome	-M	SETAPAAPAAPAPAEK	TPVKK	2		739.8784346	1477.741269	0.000451244	10	N	1	17
P43274	Exosome	KRKTS	GPPVSELITK	AVAAS	2		520.8034786	1039.591357	0.000637154	1	Y	36	46
P43274	Parental	-M	SETAPAAPAAPAPAEKTPVK	KKARK	2		952.5103444	1903.005089	0.000823681	6	N	1	21
P43274	Parental	-M	SETAPAAPAAPAPAEKTPVK	KKARK	3		635.3428296	1903.005089	0.000451244	6	N	1	21
P43274	Parental	AALKK	ALAAAGYDVEKN	NSRIK	2		611.3096565	1220.603713	0.000451244	16	Y	64	76
P43274	Parental	GGAKR	KTSGPPVSELITK	AVAAS	2		678.8908137	1355.766027	0.001162105	1	N	33	46
P43274	Parental	GGAKR	KTSGPPVSELITK	AVAAS	3		452.9298091	1355.766027	0.000451244	7	N	33	46
P43274	Parental	AALKK	ALAAAGYDVEK	NNSRI	2		554.2881927	1106.560785	0.000451244	91	Y	64	75
P43274	Parental	ASKER	SGVSLAALK	KALAA	2		423.2587069	844.5018138	0.001162105	51	Y	54	63
P43274	Parental	GAKRK	TSGPPVSELITK	AVAAS	2		614.8433321	1227.671064	0.000451244	119	N	34	46

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P43274	Parental	MSETA	PAAPAAPAPAEKTPVK	KKARK	2		758.4306374	1514.845675	0.000451244	4	N	5	21
P43274	Parental	AALKK	ALAAAGYDVEKNNSR	IKLGL	2		789.89769	1577.77978	0.000451244	8	Y	64	79
P43274	Parental	-M	SETAPAAPAAPAPAEK	TPVKK	2		739.8784346	1477.741269	0.000451244	31	N	1	17
P43275	Exosome	AALKK	SLAAAGYDVEK	NNSRI	2		562.28565	1122.5557	0.000451244	11	N	66	77
P43275	Exosome	SSKER	SGVSLAALK	KSLAA	2		423.2587069	844.5018138	0.000823681	48	Y	56	65
P43275	Exosome	AAAPR	KKPAGPSVSELIVQAVSSSK	ERSGV	2		1006.573476	2011.131352	0.000451244	16	N	34	54
P43275	Exosome	AAAPR	KKPAGPSVSELIVQAVSSSK	ERSGV	3		671.3849174	2011.131352	0.000451244	17	N	34	54
P43275	Exosome	AAAPR	KKPAGPSVSELIVQAVSSSK	ERSGV	4		503.790638	2011.131352	0.002080925	1	N	34	54
P43275	Exosome	AALKK	SLAAAGYDVEKNNSR	IKLGL	2		797.8951474	1593.774695	0.000451244	6	N	66	81
P43275	Exosome	-MSE	TAPVAQAASTATEKPAAAK	KTKKP	2		892.481587	1782.947574	0.000451244	1	N	3	22
P43275	Exosome	AAPRK	KPAGPSVSELIVQAVSSSK	ERSGV	2		942.5259945	1883.036389	0.001591523	2	N	35	54
P43275	Exosome	AAPRK	KPAGPSVSELIVQAVSSSK	ERSGV	3		628.6865964	1883.036389	0.002519933	1	N	35	54
P43275	Parental	AALKK	SLAAAGYDVEK	NNSRI	2		562.28565	1122.5557	0.000451244	33	N	66	77
P43275	Parental	SSKER	SGVSLAALK	KSLAA	2		423.2587069	844.5018138	0.001162105	51	Y	56	65
P43275	Parental	AAAPR	KKPAGPSVSELIVQAVSSSK	ERSGV	2		1006.573476	2011.131352	0.000451244	9	N	34	54
P43275	Parental	AAAPR	KKPAGPSVSELIVQAVSSSK	ERSGV	3		671.3849174	2011.131352	0.000451244	27	N	34	54
P43275	Parental	AALKK	SLAAAGYDVEKNNSR	IKLGL	2		797.8951474	1593.774695	0.000451244	2	N	66	81
P43275	Parental	MSETA	PVAQAASTATEKPAAAKK	TKKPA	2		870.4866723	1738.957745	0.000451244	7	N	5	23
P43275	Parental	MSETA	PVAQAASTATEKPAAAK	KTKKP	2		806.4391908	1610.862782	0.001699387	1	N	5	22
P43275	Parental	AALKK	SLAAAGYDVEKN	NSRIK	2		619.3071138	1236.598628	0.000451244	3	N	66	78
P43276	Exosome	GAAKR	KATGPPVSELITK	AVSAS	2		670.8933564	1339.771113	0.000451244	39	N	33	46
P43276	Exosome	GAAKR	KATGPPVSELITK	AVSAS	3		447.5981709	1339.771113	0.000451244	44	N	33	46
P43276	Exosome	AAKRK	ATGPPVSELITK	AVSAS	2		606.8458748	1211.67615	0.000451244	36	N	34	46
P43276	Exosome	-M	SETAPAETAAPAPVEK	SPAKK	2		784.8942817	1567.772963	0.000451244	10	N	1	17
P43276	Exosome	PALKK	ALAAGGYDVEK	NNSRI	2		547.2803676	1092.545135	0.000451244	3	N	64	75
P43276	Exosome	KRKAT	GPPVSELITK	AVSAS	2		520.8034786	1039.591357	0.000637154	1	Y	36	46
P43276	Parental	GAAKR	KATGPPVSELITK	AVSAS	2		670.8933564	1339.771113	0.000451244	30	N	33	46
P43276	Parental	GAAKR	KATGPPVSELITK	AVSAS	3		447.5981709	1339.771113	0.000451244	55	N	33	46
P43276	Parental	AAKRK	ATGPPVSELITK	AVSAS	2		606.8458748	1211.67615	0.000451244	63	N	34	46
P43276	Parental	-M	SETAPAETAAPAPVEK	SPAKK	2		784.8942817	1567.772963	0.000451244	32	N	1	17
P43276	Parental	PALKK	ALAAGGYDVEK	NNSRI	2		547.2803676	1092.545135	0.000451244	20	N	64	75
P43276	Parental	MSETA	PAETAAPAPVEK	SPAKK	2		590.8145747	1179.613549	0.002727428	2	N	5	17
P43277	Exosome	-M	SETAPAAPAAPAPVEK	TPVKK	2		753.8940847	1505.772569	0.000451244	47	N	1	17
P43277	Exosome	AALKK	ALAAAGYDVEKN	NSRIK	2		611.3096565	1220.603713	0.000451244	17	Y	65	77
P43277	Exosome	AALKK	ALAAAGYDVEK	NNSRI	2		554.2881927	1106.560785	0.000451244	105	Y	65	76
P43277	Exosome	AAGKR	KASGPPVSELITK	AVAAS	2		663.8855313	1325.755463	0.000451244	22	Y	34	47
P43277	Exosome	AAGKR	KASGPPVSELITK	AVAAS	3		442.9262876	1325.755463	0.000451244	54	Y	34	47
P43277	Exosome	ASKER	SGVSLAALK	KALAA	2		423.2587069	844.5018138	0.000823681	48	Y	55	64
P43277	Exosome	AGKRK	ASGPPVSELITK	AVAAS	2		599.8380498	1197.6605	0.000451244	155	Y	35	47
P43277	Exosome	LAALK	KALAAAGYDVEK	NNSRI	2		618.3356743	1234.655749	0.000637154	1	Y	64	76
P43277	Exosome	AALKK	ALAAAGYDVEKNNSR	IKLGL	2		789.89769	1577.77978	0.000451244	30	Y	65	80
P43277	Exosome	AALKK	ALAAAGYDVEKNNSR	IKLGL	3		526.9343934	1577.77978	0.000451244	10	Y	65	80
P43277	Exosome	MSETA	PAAPAAPAPVEK	TPVKK	2		559.8143777	1117.613155	0.000451244	1	N	5	17
P43277	Exosome	-MSE	TAPAAPAAPAPVEK	TPVKK	2		645.8567739	1289.697948	0.000451244	12	N	3	17
P43277	Exosome	KRKAS	GPPVSELITK	AVAAS	2		520.8034786	1039.591357	0.000637154	1	Y	37	47
P43277	Parental	-M	SETAPAAPAAPAPVEKTPVK	KKAKK	2		966.5259945	1931.036389	0.000451244	6	N	1	21
P43277	Parental	-M	SETAPAAPAAPAPVEKTPVK	KKAKK	3		644.6865964	1931.036389	0.000451244	3	N	1	21
P43277	Parental	-M	SETAPAAPAAPAPVEK	TPVKK	2		753.8940847	1505.772569	0.000451244	74	N	1	17
P43277	Parental	AALKK	ALAAAGYDVEKN	NSRIK	2		611.3096565	1220.603713	0.000451244	16	Y	65	77
P43277	Parental	AALKK	ALAAAGYDVEK	NNSRI	2		554.2881927	1106.560785	0.000451244	91	Y	65	76
P43277	Parental	AAGKR	KASGPPVSELITK	AVAAS	2		663.8855313	1325.755463	0.000451244	15	Y	34	47
P43277	Parental	AAGKR	KASGPPVSELITK	AVAAS	3		442.9262876	1325.755463	0.000451244	62	Y	34	47
P43277	Parental	ASKER	SGVSLAALK	KALAA	2		423.2587069	844.5018138	0.001162105	51	Y	55	64
P43277	Parental	AGKRK	ASGPPVSELITK	AVAAS	2		599.8380498	1197.6605	0.000451244	111	Y	35	47
P43277	Parental	AALKK	ALAAAGYDVEKNNSR	IKLGL	2		789.89769	1577.77978	0.000451244	8	Y	65	80
P43430	Exosome	LKLER	KAQLNSAVDTIALPK	SKDWV	2		784.9544767	1567.893353	0.000451244	9	N	115	130
P43430	Exosome	LKLER	KAQLNSAVDTIALPK	SKDWV	3		523.6389178	1567.893353	0.000451244	3	N	115	130
P43430	Parental	LKLER	KAQLNSAVDTIALPK	SKDWV	2		784.9544767	1567.893353	0.000451244	5	N	115	130
P43430	Parental	IALPK	SKDWVKPGQVCTVAGWGK	LANCT	2	C11:+57.021	1002.0123	2002.009	0.000451244	2	N	130	148
P45376	Exosome	YCHSK	GIVVTAYSPLGSPDRPWAKPEDPSLLEDPR	IKAIA	3		1088.23013	3261.66699	0.000451244	30	N	203	233
P45376	Exosome	YCHSK	GIVVTAYSPLGSPDRPWAKPEDPSLLEDPR	IKAIA	4		816.4245475	3261.66699	0.000622848	9	N	203	233
P45376	Exosome	KPGLK	YKPAVNQIECHPYLTQEK	LIEYC	3	C10:+57.021	740.0372576	2217.088373	0.000451244	8	N	177	195
P45376	Exosome	EGLVK	TIGVSNFNPLQIER	ILNKP	2		794.428626	1586.841652	0.000451244	5	N	155	169
P45376	Exosome	DLGYR	HIDCAQVYQNEKEVGVALQEK	LKEQV	3	C4:+57.021	820.0729191	2457.195357	0.000451244	9	N	41	62
P45376	Parental	DLGYR	HIDCAQVYQNEKEVGVAL	QEKLK	2	C4:+57.021	1037.007412	2071.999223	0.001699387	1	N	41	59

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P45878	Parental	GYGER	GAPPKIPGGATLVFEVELLK	IERRS	3		679.3983868	2035.17176	0.000622848	4	N	113	133
P45878	Parental	HYTGK	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	GWDQG	3		1018.508781	3052.502944	0.000451244	8	N	57	85
P45878	Parental	GAPPK	IPGGATLVFEVELLK	IERRS	2		793.4641459	1584.912692	0.001699387	3	N	118	133
P45878	Parental	HYTGK	LEDGTEFDSSLPQNQPFVF	SLGTG	2		1085.502913	2168.990227	0.000451244	3	N	57	76
P45878	Parental	LHMHY	TGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK	GWDQG	3		1113.896817	3338.66705	0.001943752	1	N	54	85
P46061	Exosome	DYFPK	ALAPLLLAFVTKPNGALETCSFAR	HNLLQ	3	C20:+57.021	854.1370832	2559.38785	0.000451244	2	N	555	579
P46061	Parental	DYFPK	ALAPLLLAFVTKPNGALETCSFAR	HNLLQ	3	C20:+57.021	854.1370832	2559.38785	0.000451244	15	N	555	579
P46061	Parental	TPSRK	ILDPNSGEPAPVLSSPTPTDLSTFLSFPSPEK	LLRLG	3		1114.233206	3339.676218	0.000451244	29	N	415	447
P46061	Parental	MFTGR	LRSEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVR	GFEAL	3		1335.383336	4003.126609	0.000622848	3	N	91	130
P46061	Parental	MFTGR	LRSEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVR	GFEAL	4		1001.789452	4003.126609	0.002080925	1	N	91	130
P46061	Parental	TGRLR	SEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVR	GFEAL	3		1245.654945	3733.941434	0.000451244	3	N	93	130
P46414	Parental	KRANR	TEENVSDGSPNAGTVEQTPK	KPGLR	2		1030.474884	2058.934169	0.000451244	8	N	169	189
P46414	Parental	SQNKR	ANRTEENVSDGSPNAGTVEQTPK	KPGLR	3		801.0462403	2400.115321	0.000451244	7	N	166	189
P46460	Exosome	PIGPR	FSNLVLQALLVLLK	KAPPQ	2		786.0006986	1569.985797	0.001463592	2	N	617	631
P46460	Parental	LPQRK	WAGLSIGQDIEVALYSFDKAK	QCIGT	3		771.0709985	2310.189595	0.000451244	3	N	68	89
P46460	Parental	PIGPR	FSNLVLQALLVLLK	KAPPQ	2		786.0006986	1569.985797	0.000451244	4	N	617	631
P46460	Parental	PIGPR	FSNLVLQALLVLLK	KAPPQ	3		524.3363991	1569.985797	0.002374549	1	N	617	631
P46460	Parental	AVETK	NFSGAELEGLVR	AAQST	2		646.3362056	1290.656811	0.001352548	2	N	434	446
P46467	Exosome	AQEDK	AGNYEEALQLYQHAVQYFLHVVK	YEAQG	4		680.8517583	2719.375833	0.000735798	13	N	23	46
P46467	Exosome	RTPWR	GILLFGPPGTGK	SYLAK	2		578.8403955	1155.665191	0.00091018	5	N	168	180
P46467	Exosome	QELGR	KTDGYSGADISIIVR	DALMQ	3		532.2865441	1593.836232	0.001352548	1	N	331	346
P46467	Exosome	SYLAK	AVATEANNSTFFSISSSDLVSK	WLGES	2		1138.058584	2274.101568	0.000451244	9	N	185	207
P46467	Exosome	AQEDK	AGNYEEALQLYQHAVQY	FLHVV	2		998.9741261	1995.932652	0.00091018	2	N	23	40
P46467	Exosome	WDMLR	SLSSTKPTVNEQDLLK	LKKFT	2		880.4759703	1758.936341	0.001162105	1	N	416	432
P46467	Exosome	WDMLR	SLSSTKPTVNEQDLLK	LKKFT	3		587.3199135	1758.936341	0.001839721	1	N	416	432
P46467	Exosome	PEKKK	LQNQLQGAIVIERPNVK	WSDVA	3		640.7062138	1919.095241	0.001264573	2	N	115	132
P46467	Exosome	FQLAR	ENKPSIIFIDEIDSLCGSR	SENES	3	C16:+57.021	731.7004226	2192.077868	0.000622848	2	N	224	243
P46467	Parental	AQEDK	AGNYEEALQLYQHAVQY	FLHVV	2		998.9741261	1995.932652	0.002296037	1	N	23	40
P46471	Exosome	ARTKK	ACLIFFDEIDAIGGAR	FDDGA	2	C2:+57.021	884.4406449	1766.86569	0.000451244	13	N	268	284
P46471	Exosome	DKPIR	ALDEGDIALLK	TYGQS	2		579.3247752	1156.63395	0.000662267	7	N	23	34
P46471	Exosome	LTGIK	ESDTGLAPPALWDLAADKQTLQSEQPLQVAR	CTKII	3		1116.907716	3347.699747	0.000451244	23	N	66	97
P46471	Exosome	LHPER	FVNLGIEPPKGVLLFGPPGTGK	TLCAR	3		746.4284575	2236.261973	0.000662267	1	N	200	222
P46471	Exosome	SRQIK	QVEDDIQQLLK	KINEL	2		664.8569709	1327.698342	0.000451244	2	N	46	57
P46471	Parental	ARTKK	ACLIFFDEIDAIGGAR	FDDGA	2	C2:+57.021	884.4406449	1766.86569	0.000622848	4	N	268	284
P46471	Parental	DKPIR	ALDEGDIALLK	TYGQS	2		579.3247752	1156.63395	0.000451244	6	N	23	34
P46471	Parental	LTGIK	ESDTGLAPPALWDLAADKQTLQSEQPLQVAR	CTKII	3		1116.907716	3347.699747	0.000451244	14	N	66	97
P46471	Parental	LHPER	FVNLGIEPPKGVLLFGPPGTGK	TLCAR	3		746.4284575	2236.261973	0.000451244	5	N	200	222
P46638	Exosome	AFAEK	NNLSFIETSALDSTNVEEAFKNILTEIYR	IVSQK	3		1111.228455	3330.661964	0.000735798	3	N	145	174
P46638	Exosome	AFAEK	NNLSFIETSALDSTNVEEAFK	NILTE	2		1165.063867	2328.112133	0.000451244	36	N	145	166
P46638	Exosome	AFAEK	NNLSFIETSALDSTNVEEAFK	NILTE	3		777.0451777	2328.112133	0.000451244	4	N	145	166
P46638	Exosome	SAYYR	GAVGALLVYDIAK	HLTYE	2		645.3773421	1288.739084	0.000451244	19	Y	82	95
P46638	Parental	AFAEK	NNLSFIETSALDSTNVEEAFKNILTEIYR	IVSQK	3		1111.228455	3330.661964	0.000451244	25	N	145	174
P46638	Parental	GKTIK	AQIWDTAGQER	YRAIT	2		637.8103549	1273.60511	0.000451244	21	Y	61	72
P46638	Parental	AFAEK	NNLSFIETSALDSTNVEEAFK	NILTE	2		1165.063867	2328.112133	0.000451244	34	N	145	166
P46638	Parental	AFAEK	NNLSFIETSALDSTNVEEAFK	NILTE	3		777.0451777	2328.112133	0.000451244	5	N	145	166
P46638	Parental	SAYYR	GAVGALLVYDIAK	HLTYE	2		645.3773421	1288.739084	0.000451244	14	Y	82	95
P46638	Parental	AFAEK	NNLSFIETSALDSTNVEEAF	KNILT	2		1101.016385	2200.01717	0.001162105	1	N	145	165
P46664	Exosome	ANQYK	SIYPTLEIDIEGELQQLK	GYMER	2		1045.057325	2088.099049	0.000451244	20	N	203	221
P46664	Exosome	AYTTR	VGIGAFPTEQDNEIGELLQTR	GREFG	2		1144.082394	2286.149187	0.000622848	1	N	303	324
P46664	Exosome	AYTTR	VGIGAFPTEQDNEIGELLQTR	GREFG	3		763.0575291	2286.149187	0.000451244	11	N	303	324
P46664	Exosome	GRKRR	CGWLDLVSLK	YAHMI	2	C1:+57.021	595.8158317	1189.616063	0.000622848	6	N	337	347
P46664	Exosome	SGGNR	VTVVLGAQWGDEGKGK	VVDLL	2		822.4417334	1642.867867	0.000451244	5	Y	29	45
P46664	Exosome	SGGNR	VTVVLGAQWGDEGKGK	VVDLL	3		548.6304223	1642.867867	0.0007646	2	Y	29	45
P46664	Exosome	KPMVK	DGVYFLYEALHGPPK	KILVE	3		569.291518	1704.851154	0.000823681	1	N	232	247
P46664	Parental	ANQYK	SIYPTLEIDIEGELQQLK	GYMER	2		1045.057325	2088.099049	0.000451244	7	N	203	221
P46664	Parental	AYTTR	VGIGAFPTEQDNEIGELLQTR	GREFG	2		1144.082394	2286.149187	0.000451244	8	N	303	324
P46664	Parental	AYTTR	VGIGAFPTEQDNEIGELLQTR	GREFG	3		763.0575291	2286.149187	0.000451244	7	N	303	324
P46935	Parental	NRLTR	DDFLGQVDVPLYPLPTENPR	MERPY	2		1143.07658	2284.13756	0.000622848	8	N	158	178
P46935	Parental	ELDLR	FIIDEELFGQTHQHELK	TGGSE	3		695.3536172	2083.037452	0.001395409	1	N	686	703
P47738	Exosome	PFDSR	TEQGPQVDETQFK	KILGY	2		753.8576992	1505.699798	0.000451244	41	N	357	370
P47738	Exosome	SGSGR	ELGEYGLQAYTEVK	TVTVK	2		800.3991999	1598.7828	0.000451244	34	N	494	508
P47738	Exosome	VKAAR	AAFQLGSPWR	RMDAS	2		566.7990619	1131.582524	0.000622848	21	N	86	96
P47738	Exosome	LSRLL	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	3	C19:+57.021	1259.932775	3776.774926	0.000451244	38	N	19	53
P47738	Exosome	LSRLL	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	4	C19:+57.021	945.2015314	3776.774926	0.00091018	7	N	19	53
P47738	Exosome	EGVDK	VAFTGSTEVGHLIQVAAGSSNLKR	VTLEL	3		814.7753561	2441.302668	0.000451244	26	N	259	283

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P47738	Exosome	EGVDK	VAFTGSTEVGHLIQVAAGSSNLKR	VTLEL	4		611.3334671	2441.302668	0.000451244	7	N	259	283
P47738	Exosome	CAGSR	TFVQENVYDEFVER	SVARA	2		887.9182882	1773.820976	0.000451244	30	N	326	340
P47738	Exosome	CAGSR	TFVQENVYDEFVER	SVARA	3		592.2814588	1773.820976	0.001264573	1	N	326	340
P47738	Exosome	KYHGK	TIPIDGDFFSYTR	HEPVG	2		766.3755278	1530.735456	0.000451244	9	N	161	174
P47738	Exosome	ANLIK	EAGFPPGVVNIVPGFGPTAGAAIASHEGVDK	VAFTG	3		987.8422063	2960.503219	0.000451244	88	N	228	259
P47738	Exosome	VVVMK	VAEQTPLTALYVANLIK	EAGFP	2		922.5305486	1843.045497	0.000451244	57	N	211	228
P47738	Exosome	VVVMK	VAEQTPLTALYVANLIK	EAGFP	3		615.356299	1843.045497	0.000451244	37	N	211	228
P47738	Exosome	AVFTK	DLDKANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C21:+57.021	1299.624837	3895.851111	0.000451244	60	N	453	488
P47738	Exosome	AVFTK	DLDKANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	4	C21:+57.021	974.9705776	3895.851111	0.000451244	19	N	453	488
P47738	Exosome	ANDSK	YGLAAAVFTK	DLDKA	2		520.7929139	1039.570228	0.000451244	33	N	443	453
P47738	Exosome	IERDR	TYLAALETLDNGKPYVISY	LVDLD	2		1066.052042	2130.088484	0.002663018	1	N	118	137
P47738	Exosome	AVSRK	TFPTVNPSTGEVICQVAEGNKEDVDK	AVKAA	3	C14:+57.021	945.455646	2833.343538	0.000622848	6	N	54	80
P47738	Exosome	KDLDK	ANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C17:+57.021	1142.547199	3424.618197	0.000622848	32	N	457	488
P47738	Exosome	QPEVF	CNQIFINNEWHDAVSR	KTFPT	2	C1:+39.994	993.4498384	1984.884077	0.001871652	2	N	37	53
P47738	Exosome	QPEVF	CNQIFINNEWHDAVSR	KTFPT	2	C1:+57.021	1001.963338	2001.911077	0.001395409	1	N	37	53
P47738	Exosome	QPEVF	CNQIFINNEWHDAVSR	KTFPT	3	C1:+57.021	668.3114923	2001.911077	0.001654178	1	N	37	53
P47738	Exosome	EGVDK	VAFTGSTEVGHLIQVAAGSSNLK	RVTLE	2		1143.608579	2285.201557	0.000451244	11	N	259	282
P47738	Exosome	EGVDK	VAFTGSTEVGHLIQVAAGSSNLK	RVTLE	3		762.7416524	2285.201557	0.000451244	24	N	259	282
P47738	Exosome	SRKTF	PTVNPSTGEVICQVAEGNKEDVDK	AVKAA	3	C12:+57.021	862.7502818	2585.227445	0.001329271	2	N	56	80
P47738	Exosome	AGTVW	INCYDVFGAQSPFGGYK	MSGSG	2	C3:+57.021	961.941009	1921.866418	0.000451244	8	N	471	488
P47738	Exosome	AAADR	GYFIQPTVFGDVK	DGMTI	2		735.8855313	1469.755463	0.000451244	15	N	396	409
P47738	Exosome	IERDR	TYLAALETLDNGKPYVISYLVDLDMVLK	CLRYY	3		1053.23008	3156.66684	0.00091018	1	N	118	146
P47738	Exosome	SRLLS	AAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	4	C18:+57.021	923.4435243	3689.742897	0.002813207	1	N	20	53
P47738	Exosome	TVWIN	CYDVFGAQSPFGGYK	MSGSG	2	C1:+57.021	848.3775132	1694.739426	0.002019181	1	N	473	488
P47738	Exosome	RAKSR	VVGNPFDSR	TEQGP	2		495.75432	989.49304	0.002296037	1	N	348	357
P47738	Exosome	AAADR	GYFIQPTVF	GDVKD	2		536.2796393	1070.543679	0.00307782	1	N	396	405
P47738	Exosome	AVFTK	DLDKANYLSQALQAGTVW	INCYD	2		997.0054263	1991.995253	0.000451244	4	N	453	471
P47738	Parental	PFDSR	TEQGPQVDETQFK	KILGY	2		753.8576992	1505.699798	0.000451244	34	N	357	370
P47738	Parental	SGSGR	ELGEYGLQAYTEVK	TVTVK	2		800.3991999	1598.7828	0.000451244	28	N	494	508
P47738	Parental	VKAAR	AAFQLGSPWR	RMDAS	2		566.7990619	1131.582524	0.000451244	15	N	86	96
P47738	Parental	LSRLL	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSRK	TFPTV	3	C19:+57.021	1302.631096	3904.869889	0.002519933	1	N	19	54
P47738	Parental	LSRLL	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	3	C19:+57.021	1259.932775	3776.774926	0.000451244	41	N	19	53
P47738	Parental	LSRLL	SAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	4	C19:+57.021	945.2015314	3776.774926	0.000451244	20	N	19	53
P47738	Parental	EGVDK	VAFTGSTEVGHLIQVAAGSSNLKR	VTLEL	3		814.7753561	2441.302668	0.000451244	27	N	259	283
P47738	Parental	EGVDK	VAFTGSTEVGHLIQVAAGSSNLKR	VTLEL	4		611.3334671	2441.302668	0.000979378	2	N	259	283
P47738	Parental	QEGAK	LLCGGGAAADRGYFIQPTVFGDVK	DGMTI	3	C3:+57.021	838.0936545	2511.257564	0.0007646	5	N	385	409
P47738	Parental	CAGSR	TFVQENVYDEFVER	SVARA	2		887.9182882	1773.820976	0.000451244	12	N	326	340
P47738	Parental	KYHGK	TIPIDGDFFSYTR	HEPVG	2		766.3755278	1530.735456	0.000451244	7	N	161	174
P47738	Parental	ANLIK	EAGFPPGVVNIVPGFGPTAGAAIASHEGVDK	VAFTG	3		987.8422063	2960.503219	0.000451244	71	N	228	259
P47738	Parental	VVVMK	VAEQTPLTALYVANLIK	EAGFP	2		922.5305486	1843.045497	0.000451244	44	N	211	228
P47738	Parental	VVVMK	VAEQTPLTALYVANLIK	EAGFP	3		615.356299	1843.045497	0.000451244	34	N	211	228
P47738	Parental	AVFTK	DLDKANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C21:+57.021	1299.624837	3895.851111	0.000451244	65	N	453	488
P47738	Parental	AVFTK	DLDKANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	4	C21:+57.021	974.9705776	3895.851111	0.000451244	12	N	453	488
P47738	Parental	ANDSK	YGLAAAVFTK	DLDKA	2		520.7929139	1039.570228	0.000451244	36	N	443	453
P47738	Parental	HGKTI	PIDGDFFSYTR	HEPVG	2		659.3096565	1316.603713	0.000622848	5	N	163	174
P47738	Parental	IERDR	TYLAALETLDNGKPYVISY	LVDLD	2		1066.052042	2130.088484	0.000451244	10	N	118	137
P47738	Parental	AVSRK	TFPTVNPSTGEVICQVAEGNKEDVDK	AVKAA	3	C14:+57.021	945.455646	2833.343538	0.000451244	11	N	54	80
P47738	Parental	RLSRL	LSAAATSAVPAPNHQPEVFCNQIFINNEWHDAVSR	KTFPT	4	C20:+57.021	973.4725475	3889.85899	0.000823681	1	N	18	53
P47738	Parental	KDLDK	ANYLSQALQAGTVWINCYDVFGAQSPFGGYK	MSGSG	3	C17:+57.021	1142.547199	3424.618197	0.000622848	28	N	457	488
P47738	Parental	QPEVF	CNQIFINNEWHDAVSR	KTFPT	2	C1:+39.994	993.4498384	1984.884077	0.002019181	6	N	37	53
P47738	Parental	QPEVF	CNQIFINNEWHDAVSR	KTFPT	2	[0:-17.027,C1:+57.021	993.4498384	1984.884077	0.0025889	2	N	37	53
P47738	Parental	EGVDK	VAFTGSTEVGHLIQVAAGSSNLK	RVTLE	2		1143.608579	2285.201557	0.00091018	1	N	259	282
P47738	Parental	EGVDK	VAFTGSTEVGHLIQVAAGSSNLK	RVTLE	3		762.7416524	2285.201557	0.000451244	3	N	259	282
P47738	Parental	FSYTR	HEPVGVCGQIIPWNFPLLMQAWK	LGPAL	3	C7:+57.021	907.4665467	2719.37624	0.000823681	1	N	174	197
P47738	Parental	EVVGR	ANDSKYGLAAAVFTK	DLDKA	2		778.409902	1554.804204	0.001162105	1	N	438	453
P47738	Parental	AGTVW	INCYDVFGAQSPFGGYK	MSGSG	2	C3:+57.021	961.941009	1921.866418	0.000622848	6	N	471	488
P47738	Parental	KEAGF	PPGVVNIVPGFGPTAGAAIASHEGVDK	VAFTG	3		853.1190114	2556.333634	0.001352548	1	N	232	259
P47740	Parental	MVQER	EKEILAAIAADLSK	SELNA	3		491.284252	1470.829356	0.000451244	16	N	37	51
P47740	Parental	ENTAK	ILAELLPQYLDQDLYAIVNGGIPETTELLK	QRFDH	3		1114.941475	3341.801024	0.000451244	20	N	145	175
P47754	Exosome	RIAAK	FIIHAPPGEFNEVFNDVR	LLLNN	2		1051.029236	2100.042871	0.00091018	12	N	19	37
P47754	Exosome	RIAAK	FIIHAPPGEFNEVFNDVR	LLLNN	3		701.0220905	2100.042871	0.000451244	33	N	19	37
P47754	Exosome	DNLLR	EGAAHAFAQYNLDQFTPVKIEGYEDQVLITEHGDLGNGK	FLDPK	4		1069.521707	4274.055629	0.000451244	3	N	47	86
P47754	Exosome	TVYGK	KVDGQQTIIACIESHQFQAK	NFWNG	3	C11:+57.021	767.7270832	2300.157849	0.000451244	4	N	146	166
P47754	Exosome	FNDVR	LLLNNDNLLR	EGAAH	2		599.3516587	1196.687717	0.000979378	12	Y	37	47
P47754	Exosome	RSEWK	FTVTPSTTQVVGILK	IQVHY	2		795.9592277	1589.902855	0.000451244	21	N	178	193

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P47754	Exosome	VGILK	IQVHYYEDGNVQLVSHK	DIQDS	2		1015.011043	2028.006486	0.000451244	7	Y	193	210
P47754	Exosome	LVSHK	DIQDSLTVSNEVQTAK	EFIKI	2		874.4395848	1746.86357	0.000451244	15	N	210	226
P47754	Exosome	ETALR	AYVKEHYPNGVCTVYGK	KVDGQ	3	C12:+57.021	662.3247388	1983.950816	0.000622848	1	N	129	146
P47754	Parental	RIAAK	FIIHAPPGEFNEVFNDVR	LLLNN	2		1051.029236	2100.042871	0.000451244	21	N	19	37
P47754	Parental	RIAAK	FIIHAPPGEFNEVFNDVR	LLLNN	3		701.0220905	2100.042871	0.000451244	29	N	19	37
P47754	Parental	DNLLR	EGAAHAFAQYNLDQFTPVKIEGYEDQVLITEHGDLGNGK	FLDPK	4		1069.521707	4274.055629	0.000451244	26	N	47	86
P47754	Parental	TVYGK	KVDGQQTIIACIESHQFQAK	NFWNG	3	C11:+57.021	767.7270832	2300.157849	0.000451244	19	N	146	166
P47754	Parental	FNDVR	LLLNNDNLLR	EGAAH	2		599.3516587	1196.687717	0.001162105	13	Y	37	47
P47754	Parental	DHLRK	EATDPRPYEAENAIESWR	TSVET	3		711.9999027	2132.976308	0.002374549	2	N	103	121
P47754	Parental	RSEWK	FTVTPSTTQVVGILK	IQVHY	2		795.9592277	1589.902855	0.000451244	19	N	178	193
P47754	Parental	VGILK	IQVHYYEDGNVQLVSHK	DIQDS	2		1015.011043	2028.006486	0.000451244	2	Y	193	210
P47754	Parental	LVSHK	DIQDSLTVSNEVQTAK	EFIKI	2		874.4395848	1746.86357	0.000451244	4	N	210	226
P47754	Parental	DNLLR	EGAAHAFAQYNLDQFTPVK	IEGYE	2		1054.016325	2106.017051	0.000451244	3	N	47	66
P47757	Exosome	SARLR	KLEVEANNAFDQYR	DLYFE	2		848.9186225	1695.821645	0.000451244	51	N	94	108
P47757	Exosome	SARLR	KLEVEANNAFDQYR	DLYFE	3		566.2816817	1695.821645	0.000451244	4	N	94	108
P47757	Exosome	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLK	IARDK	2	C13:+57.021	1392.223081	2782.430562	0.000451244	7	N	23	48
P47757	Exosome	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLK	IARDK	3	C13:+57.021	928.4846541	2782.430562	0.000451244	43	N	23	48
P47757	Exosome	LIDLV	PSLCEDLLSSVDQPLK	IARDK	2	C4:+57.021	900.9563248	1799.89705	0.000451244	3	N	32	48
P47757	Exosome	SKKIK	GCWDSIHVVEVQEK	SSGRT	2	C2:+57.021	843.4015197	1684.787439	0.000451244	24	N	145	159
P47757	Exosome	SKKIK	GCWDSIHVVEVQEK	SSGRT	3	C2:+57.021	562.6036131	1684.787439	0.000451244	24	N	145	159
P47757	Exosome	ENKIR	STLNEIYFGK	TKDIV	2		586.3038428	1170.592086	0.000451244	7	N	225	235
P47757	Exosome	ARLRK	LEVEANNAFDQYR	DLYFE	2		784.8711409	1567.726682	0.000451244	17	N	95	108
P47757	Exosome	KVVGK	DYLLCDYNR	DGDSY	2	C5:+57.021	616.274528	1230.533456	0.002296037	4	N	57	66
P47757	Exosome	GDSYR	SPWSNKYDPPLEDGAMPSAR	LRKLE	3	M16:+15.995	745.3448218	2233.011066	0.000451244	22	N	72	92
P47757	Exosome	KVVGK	DYLLCDYNRDGDSYR	SPWSN	2	C5:+57.021	962.9104372	1923.805274	0.000451244	7	N	57	72
P47757	Parental	SARLR	KLEVEANNAFDQYR	DLYFE	2		848.9186225	1695.821645	0.000451244	47	N	94	108
P47757	Parental	SARLR	KLEVEANNAFDQYR	DLYFE	3		566.2816817	1695.821645	0.000451244	7	N	94	108
P47757	Parental	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLKIAR	DKVVG	3	C13:+57.021	1041.892084	3122.652851	0.000823681	7	N	23	51
P47757	Parental	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLK	IARDK	2	C13:+57.021	1392.223081	2782.430562	0.000451244	24	N	23	48
P47757	Parental	QQIEK	NLSDLIDLVPSLCEDLLSSVDQPLK	IARDK	3	C13:+57.021	928.4846541	2782.430562	0.000451244	57	N	23	48
P47757	Parental	LIDLV	PSLCEDLLSSVDQPLK	IARDK	2	C4:+57.021	900.9563248	1799.89705	0.000451244	16	N	32	48
P47757	Parental	SKKIK	GCWDSIHVVEVQEK	SSGRT	2	C2:+57.021	843.4015197	1684.787439	0.000451244	23	N	145	159
P47757	Parental	SKKIK	GCWDSIHVVEVQEK	SSGRT	3	C2:+57.021	562.6036131	1684.787439	0.000451244	16	N	145	159
P47757	Parental	ENKIR	STLNEIYFGK	TKDIV	2		586.3038428	1170.592086	0.000451244	11	N	225	235
P47757	Parental	ARLRK	LEVEANNAFDQYR	DLYFE	2		784.8711409	1567.726682	0.000451244	13	N	95	108
P47757	Parental	KVVGK	DYLLCDYNR	DGDSY	2	C5:+57.021	616.274528	1230.533456	0.001463592	6	N	57	66
P47757	Parental	GDSYR	SPWSNKYDPPLEDGAMPSAR	LRKLE	3	M16:+15.995	745.3448218	2233.011066	0.000451244	1	N	72	92
P47757	Parental	DGSKK	IKGCWDSIHVVEVQEK	SSGRT	2	C4:+57.021	963.9910333	1925.966467	0.000451244	4	N	143	159
P47757	Parental	FDQYR	DLYFEGGVSSVYLWDLDHGFAGVILIK	KAGDG	3		1005.183569	3012.527308	0.000637154	20	N	108	135
P47757	Parental	VSSVY	LWDLDHGFAGVILIK	KAGDG	3		566.3194081	1695.934824	0.000451244	5	N	120	135
P47791	Exosome	VESHK	LGGTCVNVGCVPK	KVMWN	2	C5:+57.021,C10:+57.021	680.8392809	1359.662962	0.000451244	18	N	75	88
P47791	Exosome	LNLNK	VGIQTDEKGHILVDEFQNTNVK	GVYAV	2		1242.640607	2483.265614	0.000451244	10	N	324	346
P47791	Exosome	LNLNK	VGIQTDEKGHILVDEFQNTNVK	GVYAV	3		828.7630047	2483.265614	0.000451244	39	N	324	346
P47791	Exosome	MGATK	ADFDNTVAIHPTSSEELVTLR	-	2		1158.079851	2314.144102	0.000451244	28	N	479	500
P47791	Exosome	MGATK	ADFDNTVAIHPTSSEELVTLR	-	3		772.3891673	2314.144102	0.000451244	31	N	479	500
P47791	Exosome	DKVLR	NFDSLISSNCTEELENAGVEVLK	FTQVK	2	C10:+57.021	1284.610624	2567.205647	0.000451244	41	N	246	269
P47791	Exosome	DKVLR	NFDSLISSNCTEELENAGVEVLK	FTQVK	3	C10:+57.021	856.7430158	2567.205647	0.000451244	34	N	246	269
P47791	Exosome	DLPSR	SVIVGAGYIAVEIAGILSALGSK	TSLMI	2		1094.633534	2187.251467	0.000451244	42	N	211	234
P47791	Exosome	DLPSR	SVIVGAGYIAVEIAGILSALGSK	TSLMI	3		730.0916225	2187.251467	0.000451244	52	N	211	234
P47791	Exosome	AYVSR	LNTIYQNNLTK	SHIEI	2		661.3596807	1320.703761	0.000622848	18	N	131	142
P47791	Exosome	QTDEK	GHILVDEFQNTNVK	GVYAV	2		807.4182583	1612.820917	0.000451244	14	N	332	346
P47791	Exosome	NNLTK	SHIEIIHGYATFADGPRPTVEVNGK	KFTAP	3		903.4650702	2707.371811	0.000451244	13	N	142	167
P47791	Exosome	NNLTK	SHIEIIHGYATFADGPRPTVEVNGK	KFTAP	4		677.8507527	2707.371811	0.001162105	2	N	142	167
P47791	Exosome	KEVKK	TSSGLELQVVTSVPGR	KPTTT	2		815.4444731	1628.873346	0.000451244	21	N	278	294
P47791	Exosome	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	3		1055.203581	3162.587343	0.000451244	50	N	383	412
P47791	Exosome	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	4		791.6546357	3162.587343	0.000451244	49	N	383	412
P47791	Exosome	FTAPH	ILIATGGVPTVPHESQIPGASLGITSDGFFQLEDLPSR	SVIVG	3		1307.353377	3919.036732	0.000451244	9	N	173	211
P47791	Exosome	DVCGK	ALLTPVAIAAGR	KLAHR	2		576.8591195	1151.702639	0.000451244	27	N	357	369
P47791	Exosome	LFECK	QDSKLDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	3		1207.941085	3620.799855	0.000451244	18	N	379	412
P47791	Exosome	LFECK	QDSKLDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	4		906.2077638	3620.799855	0.000451244	30	N	379	412
P47791	Exosome	LFECK	QDSKLDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	4	Q1:-17.027	901.9510138	3603.772855	0.000823681	3	N	379	412
P47791	Exosome	LFECK	QDSKLDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	4	[0:-17.027	901.9510138	3603.772855	0.000823681	5	N	379	412
P47791	Exosome	VKEVK	KTSSGLELQVVTSVPGR	KPTTT	2		879.4919547	1756.968309	0.000451244	20	N	277	294
P47791	Exosome	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHKYGK	DNVKI	4		878.6995746	3510.767098	0.000451244	3	N	383	415
P47791	Exosome	MGATK	ADFDNTVAIHPTSSEEL	VTLR-	2		923.429217	1844.842834	0.000622848	5	N	479	496

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P47791	Parental	VESHK	LGGTCVNVGCVPK	KVMWN	2	C5:+57.021,C10:+57.021	680.8392809	1359.662962	0.000451244	11	N	75	88
P47791	Parental	LNLNK	VGIQTDEKGHILVDEFQNTNVK	GVYAV	2		1242.640607	2483.265614	0.000451244	8	N	324	346
P47791	Parental	LNLNK	VGIQTDEKGHILVDEFQNTNVK	GVYAV	3		828.7630047	2483.265614	0.000451244	17	N	324	346
P47791	Parental	MGATK	ADFDNTVAIHPTSSEELVTLR	-	2		1158.079851	2314.144102	0.000451244	36	N	479	500
P47791	Parental	MGATK	ADFDNTVAIHPTSSEELVTLR	-	3		772.3891673	2314.144102	0.000451244	38	N	479	500
P47791	Parental	DKVLR	NFDSLISSNCTEELENAGVEVLK	FTQVK	2	C10:+57.021	1284.610624	2567.205647	0.000451244	34	N	246	269
P47791	Parental	DKVLR	NFDSLISSNCTEELENAGVEVLK	FTQVK	3	C10:+57.021	856.7430158	2567.205647	0.000451244	18	N	246	269
P47791	Parental	DLPSR	SVIVGAGYIAVEIAGILSALGSK	TSLMI	2		1094.633534	2187.251467	0.000451244	24	N	211	234
P47791	Parental	DLPSR	SVIVGAGYIAVEIAGILSALGSK	TSLMI	3		730.0916225	2187.251467	0.000451244	29	N	211	234
P47791	Parental	ELGAR	AAVVESHKLGGTCVNVGCVPK	KVMWN	3	C13:+57.021,C18:+57.021	728.0419715	2181.102514	0.000451244	4	N	67	88
P47791	Parental	DKVLR	NFDSLISSNCTEELENAGVEVLKFTQVK	EVKKT	3	C10:+57.021	1057.855698	3170.543695	0.000870037	3	N	246	274
P47791	Parental	KEVKK	TSSGLELQVVTSVPGR	KPTTT	2		815.4444731	1628.873346	0.000451244	4	N	278	294
P47791	Parental	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	3		1055.203581	3162.587343	0.000622848	3	N	383	412
P47791	Parental	KQDSK	LDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	4		791.6546357	3162.587343	0.000451244	15	N	383	412
P47791	Parental	DVCGK	ALLTPVAIAAGR	KLAHR	2		576.8591195	1151.702639	0.002453667	1	N	357	369
P47791	Parental	LFECK	QDSKLDYDNIPTVVFSHPPIGTVGLTEDEAVHK	YGKDN	4		906.2077638	3620.799855	0.001162105	2	N	379	412
P47809	Exosome	SGNIK	LCDFGISGQLVDSIAK	TRDAG	2	C2:+57.021	861.9404777	1721.865355	0.000451244	7	N	242	258
P47809	Exosome	DKFYK	YVYSVLDDVIPEEILGK	ITLAT	2		976.5173038	1951.019008	0.001763695	3	N	188	205
P47809	Exosome	GYDVR	SDVWSLGITLYELATGR	FPYPK	3		627.6637917	1879.967975	0.000735798	2	N	285	302
P47809	Exosome	DVVMR	SSDCPYIVQFYGALFR	EGDCW	2	C4:+57.021	961.9592018	1921.902804	0.002884417	1	N	152	168
P47809	Parental	SGNIK	LCDFGISGQLVDSIAK	TRDAG	2	C2:+57.021	861.9404777	1721.865355	0.001162105	2	N	242	258
P47811	Exosome	VKCQK	LTDDHVQFLIYQILR	GLKYI	3		625.3443934	1873.00978	0.000451244	23	N	121	136
P47811	Exosome	LKHMK	HENVIGLLDVFTPAR	SLEEF	3		560.9743005	1679.899501	0.000451244	24	N	79	94
P47811	Exosome	EVPER	YQNLSPVGSGAYGSVCAAFDTK	TGHRV	2	C16:+57.021	1146.533991	2291.052381	0.000451244	17	N	23	45
P47811	Exosome	AQMPK	MNFANVFIGANPLAVDLLEK	MLVLD	2		1088.577705	2175.13981	0.000451244	13	N	267	287
P47811	Exosome	AQMPK	MNFANVFIGANPLAVDLLEK	MLVLD	2	M1:+15.995	1096.575205	2191.13481	0.000451244	7	N	267	287
P47811	Exosome	DSDKR	ITAAQALAHAYFAQYHDPDDEPVADPYDQSFESR	DLLID	3		1280.247237	3837.71831	0.000451244	3	N	296	330
P47811	Exosome	DSDKR	ITAAQALAHAYFAQYHDPDDEPVADPYDQSFESR	DLLID	4		960.4373776	3837.71831	0.000451244	7	N	296	330
P47811	Exosome	DIIHR	DLKPSNLAVNEDCELK	ILDFG	2	C13:+57.021	922.9568561	1843.898112	0.000451244	7	N	149	165
P47811	Parental	VKCQK	LTDDHVQFLIYQILR	GLKYI	3		625.3443934	1873.00978	0.000451244	29	N	121	136
P47811	Parental	AQMPK	MNFANVFIGANPLAVDLLEK	MLVLD	2		1088.577705	2175.13981	0.000451244	11	N	267	287
P47811	Parental	DSDKR	ITAAQALAHAYFAQYHDPDDEPVADPYDQSFESR	DLLID	3		1280.247237	3837.71831	0.001654178	1	N	296	330
P47811	Parental	DSDKR	ITAAQALAHAYFAQYHDPDDEPVADPYDQSFESR	DLLID	4		960.4373776	3837.71831	0.000451244	4	N	296	330
P47811	Parental	DIIHR	DLKPSNLAVNEDCELK	ILDFG	2	C13:+57.021	922.9568561	1843.898112	0.000451244	8	N	149	165
P47811	Parental	LAHAY	FAQYHDPDDEPVADPYDQSFESR	DLLID	2		1364.575858	2727.136116	0.000622848	1	N	307	330
P47811	Parental	LAHAY	FAQYHDPDDEPVADPYDQSFESR	DLLID	3		910.0531721	2727.136116	0.000451244	5	N	307	330
P47911	Exosome	VVFLK	QLDSGLLLVTGPLVINR	VPLRR	2		904.5361652	1807.05673	0.000451244	16	N	174	191
P47911	Exosome	VVFLK	QLDSGLLLVTGPLVINR	VPLRR	3		603.3600435	1807.05673	0.000451244	2	N	174	191
P47911	Exosome	VRRLR	SSITPGTVLIILTGR	HRGKR	2		764.4593949	1526.90319	0.000451244	13	N	149	164
P47911	Exosome	VRRLR	SSITPGTVLIILTGR	HRGKR	3		509.9755299	1526.90319	0.000622848	12	N	149	164
P47911	Parental	VVFLK	QLDSGLLLVTGPLVINR	VPLRR	2		904.5361652	1807.05673	0.000823681	2	N	174	191
P47911	Parental	KADQK	AVDLQILPK	IKAVP	2		498.808564	995.6015279	0.001839721	1	N	259	268
P47941	Exosome	CAYDK	TALALEVGDIVK	VTRMN	2		614.8615249	1227.70745	0.001591523	1	N	253	265
P47941	Exosome	LEYVR	TLYDFPGNDAEDLPFK	KGELL	2		921.4337711	1840.851942	0.001162105	2	N	129	145
P47941	Parental	MFLVR	DSSTCPGDYVLSVSENSR	VSHYI	2	C5:+57.021	986.9315666	1971.847533	0.000451244	8	N	39	57
P47941	Parental	EPAPR	YPSPPVGSVSAPNLPTAEENLEYVR	TLYDF	2		1343.672104	2685.328608	0.000451244	3	N	104	129
P47941	Parental	NRRFK	IGDQEFDHLPALLEFYK	IHYLD	3		679.01108	2034.00984	0.001162105	1	N	72	89
P47955	Exosome	LACIY	SALILHDDEVTVTEDKINALIK	AAGVS	3		813.1115225	2436.311167	0.000451244	5	N	11	33
P47955	Exosome	NALIK	AAGVSVEPFWPGLFAK	ALANV	2		838.4462875	1674.876975	0.000451244	29	N	33	49
P47955	Exosome	KVEAK	KEESEESEDDMGFGLFD	-	2	M11:+15.995	990.3891405	1978.762681	0.000451244	8	N	97	114
P47955	Parental	LACIY	SALILHDDEVTVTEDKINALIK	AAGVS	2		1219.163384	2436.311167	0.000451244	19	N	11	33
P47955	Parental	LACIY	SALILHDDEVTVTEDKINALIK	AAGVS	3		813.1115225	2436.311167	0.000451244	37	N	11	33
P47955	Parental	LACIY	SALILHDDEVTVTEDKINALIK	AAGVS	4		610.0855919	2436.311167	0.000451244	8	N	11	33
P47955	Parental	NALIK	AAGVSVEPFWPGLFAK	ALANV	2		838.4462875	1674.876975	0.000451244	33	N	33	49
P47955	Parental	ALANV	NIGSLICNVGAGGPAPAAGAAPAGGAAPSTAAAPAEEK	KVEAK	3	C7:+57.021	1105.553013	3313.635638	0.000622848	7	N	54	92
P47955	Parental	AKALA	NVNIGSLICNVGAGGPAPAAGAAPAGGAAPSTAAAPAEEK	KVEAK	3	C9:+57.021	1176.590127	3526.74698	0.000622848	11	N	52	92
P47955	Parental	LICNV	GAGGPAPAAGAAPAGGAAPSTAAAPAEEK	KVEAK	2		1172.580549	2343.145499	0.000622848	2	N	63	92
P47955	Parental	LACIY	SALILHDDEVTVTEDK	INALI	2		892.9497853	1783.883971	0.000622848	2	N	11	27
P47962	Exosome	KYGVK	VGLTNYAAAYCTGLLLAR	RLLNR	2	C11:+57.021	964.009226	1926.002852	0.000451244	17	N	89	107
P47962	Exosome	RVTNR	DIICQIAYAR	IEGDM	2	C4:+57.021	611.8163631	1221.617126	0.000823681	5	N	58	68
P47962	Exosome	FGMDK	IYEGQVEVNGGEYNVESIDGQPGAFTCYLDAGLAR	TTTGN	3	C27:+57.021	1264.58834	3790.74162	0.000662267	5	N	117	152
P47962	Exosome	RMIVR	VTNRDIICQIAYAR	IEGDM	3	C8:+57.021	564.9668858	1691.877257	0.000735798	1	N	54	68
P47962	Exosome	IAYAR	IEGDMIVCAAYAHELPK	YGVKV	3	M5:+15.995,C8:+57.021	644.9783801	1931.91174	0.000823681	3	N	68	85
P47962	Parental	KYGVK	VGLTNYAAAYCTGLLLAR	RLLNR	2	C11:+57.021	964.009226	1926.002852	0.000451244	15	N	89	107
P47962	Parental	FGMDK	IYEGQVEVNGGEYNVESIDGQPGAFTCY	LDAGL	3	C27:+57.021	1032.457715	3094.349746	0.002080925	2	N	117	145

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P47968	Exosome	MAVNK	AGPVVTDNGNFILDWK	FDRVH	2		873.4470158	1744.878432	0.000451244	7	N	238	254
P47968	Exosome	RIAER	VKQENLDLICIPTSFQAR	QLILQ	2	C10:+57.021	1066.562354	2131.109108	0.000451244	1	N	111	129
P47968	Exosome	RIAER	VKQENLDLICIPTSFQAR	QLILQ	3	C10:+57.021	711.3775027	2131.109108	0.000451244	6	N	111	129
P47968	Parental	MAVNK	AGPVVTDNGNFILDWK	FDRVH	2		873.4470158	1744.878432	0.000451244	5	N	238	254
P47968	Parental	RIAER	VKQENLDLICIPTSFQAR	QLILQ	2	C10:+57.021	1066.562354	2131.109108	0.000451244	1	N	111	129
P48024	Exosome	GDQRK	NICQFLIEIGLAKDDQLK	VHGF-	3	C3:+57.021	706.7140034	2117.11861	0.000823681	2	N	91	109
P48024	Exosome	AFKKK	FACNGTVIEHPEYGEVIQLQGDQR	KNICQ	3	C3:+57.021	920.7734208	2759.296862	0.000823681	2	N	66	90
P48024	Parental	GDQRK	NICQFLIEIGLAKDDQLK	VHGF-	3	C3:+57.021	706.7140034	2117.11861	0.000735798	1	N	91	109
P48024	Parental	AFKKK	FACNGTVIEHPEYGEVIQLQGDQR	KNICQ	3	C3:+57.021	920.7734208	2759.296862	0.000451244	22	N	66	90
P48024	Parental	AFKKK	FACNGTVIEHPEYGEVIQLQGDQRK	NICQF	3	C3:+57.021	963.4717419	2887.391826	0.0025889	1	N	66	91
P48024	Parental	AFKKK	FACNGTVIEHPEYGEVIQLQGDQRK	NICQF	4	C3:+57.021	722.8557564	2887.391826	0.001162105	1	N	66	91
P48025	Exosome	VYLDR	SLLTLEDNELGSGNFGTVK	KGYYQ	2		997.5079988	1993.000398	0.000451244	22	N	361	380
P48025	Exosome	REYVK	QTWNLQGQALEQAIISQKPQLEK	LIATT	3		884.4770873	2650.407862	0.000451244	15	N	132	155
P48025	Exosome	REYVK	QTWNLQGQALEQAIISQKPQLEK	LIATT	3	[0:-17.027	878.8014206	2633.380862	0.002145581	3	N	132	155
P48025	Exosome	IPEGK	KFDTLWQLVEHY	SYKPD	2		789.9017127	1577.787825	0.001699387	1	N	231	243
P48025	Parental	VYLDR	SLLTLEDNELGSGNFGTVK	KGYYQ	2		997.5079988	1993.000398	0.000451244	12	N	361	380
P48036	Exosome	AGELK	WGTDEEKFITIFGTR	SVSHL	2		900.4522982	1798.888996	0.000451244	6	N	184	199
P48036	Exosome	AGELK	WGTDEEKFITIFGTR	SVSHL	3		600.6374654	1798.888996	0.000451244	22	N	184	199
P48036	Exosome	IIASR	TPEELSAIKQVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	3		1295.260989	3882.759566	0.000451244	19	N	115	149
P48036	Exosome	-MATR	GTVTDFPGFDGR	ADAEV	2		634.7994559	1267.583312	0.000451244	27	N	4	16
P48036	Exosome	RKAMK	GLGTDEDSILNLLTSR	SNAQR	2		852.4446701	1702.87374	0.000451244	10	N	27	43
P48036	Exosome	RKAMK	GLGTDEDSILNLLTSR	SNAQR	3		568.6323801	1702.87374	0.001463592	3	N	27	43
P48036	Exosome	LSAIK	QVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	2		1458.128652	2914.241704	0.000451244	41	N	124	149
P48036	Exosome	LSAIK	QVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	3		972.4217012	2914.241704	0.000451244	21	N	124	149
P48036	Exosome	ETIDR	ETSGNLEQLLLAVVK	SIRSI	2		807.4595919	1612.903584	0.000451244	20	N	225	240
P48036	Exosome	TLFGR	DLVDDLKSELTGK	FEKLI	2		716.880643	1431.745686	0.000451244	9	N	61	74
P48036	Exosome	TLFGR	DLVDDLKSELTGK	FEKLI	3		478.256362	1431.745686	0.000451244	6	N	61	74
P48036	Exosome	VVVSR	SEIDLFNIR	KEFRK	2		553.7961849	1105.57677	0.000823681	6	N	274	283
P48036	Exosome	YMTIS	GFQIEETIDRETSGNLEQLLLAVVK	SIRSI	3		934.8348289	2801.481087	0.002296037	1	N	215	240
P48036	Parental	AGELK	WGTDEEKFITIFGTR	SVSHL	3		600.6374654	1798.888996	0.000451244	24	N	184	199
P48036	Parental	IIASR	TPEELSAIKQVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	3		1295.260989	3882.759566	0.000451244	13	N	115	149
P48036	Parental	-MATR	GTVTDFPGFDGR	ADAEV	2		634.7994559	1267.583312	0.000451244	15	N	4	16
P48036	Parental	-MATR	GTVTDFPGFDGRADAEVLR	KAMKG	2		1011.998133	2021.980665	0.00091018	3	N	4	23
P48036	Parental	-MATR	GTVTDFPGFDGRADAEVLR	KAMKG	3		675.001355	2021.980665	0.001839721	1	N	4	23
P48036	Parental	RKAMK	GLGTDEDSILNLLTSR	SNAQR	2		852.4446701	1702.87374	0.000451244	16	N	27	43
P48036	Parental	LSAIK	QVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	2		1458.128652	2914.241704	0.000451244	31	N	124	149
P48036	Parental	LSAIK	QVYEEEYGSNLEDDVVGDTSGYYQR	MLVVL	3		972.4217012	2914.241704	0.000451244	7	N	124	149
P48036	Parental	ETIDR	ETSGNLEQLLLAVVK	SIRSI	2		807.4595919	1612.903584	0.000451244	18	N	225	240
P48036	Parental	TLFGR	DLVDDLKSELTGK	FEKLI	2		716.880643	1431.745686	0.000451244	10	N	61	74
P48036	Parental	TLFGR	DLVDDLKSELTGK	FEKLI	3		478.256362	1431.745686	0.000870037	8	N	61	74
P48036	Parental	VVVSR	SEIDLFNIR	KEFRK	2		553.7961849	1105.57677	0.002374549	4	N	274	283
P48193	Exosome	NMHCK	VSLLDDTVYECVVEK	HAKGQ	2	C11:+57.021	884.9376007	1767.859601	0.000451244	16	N	214	229
P48193	Exosome	SFFIK	IRPGEQEHYESTIGFK	LPSYR	3		630.9835243	1889.927173	0.000451244	2	N	451	467
P48193	Exosome	TFNVK	FYPPDPAQLTEDITR	YYLCL	2		881.9364809	1761.857362	0.000698008	3	N	288	303
P48193	Exosome	ESTDR	SPRPTSAPAIAQSQVTEGPGAPIKK	TPKEA	3		830.1226444	2487.344533	0.000451244	10	N	555	580
P48193	Exosome	ESTDR	SPRPTSAPAIAQSQVTEGPGAPIKK	TPKEA	4		622.8439333	2487.344533	0.000451244	6	N	555	580
P48193	Exosome	KVEEK	RGEEPAEPAEPEPTEAWK	VEKTH	2		1011.974323	2021.933046	0.000451244	10	N	591	609
P48193	Exosome	KVEEK	RGEEPAEPAEPEPTEAWK	VEKTH	3		674.9854821	2021.933046	0.000451244	12	N	591	609
P48193	Exosome	HSPFR	TLNINGQVPTGDGPPLVK	TQTVT	2		910.4997797	1818.983959	0.000870037	4	N	709	727
P48193	Exosome	RKKKR	ERLDGENIYIR	HSNLM	3		459.909408	1376.704824	0.001463592	1	N	645	656
P48193	Exosome	VEEKR	GEEPAEPAEPEPTEAWK	VEKTH	2		933.9237675	1865.831935	0.000637154	1	N	592	609
P48193	Exosome	ANAVK	SEIPTKDVPIVHTETK	TITYE	4		449.247069	1792.957076	0.00307782	1	N	741	757
P48193	Exosome	RIEKR	IVITGDADIDHDQVLVQAIK	EAKEQ	2		1082.086948	2162.158295	0.001329271	1	N	813	833
P48193	Parental	NMHCK	VSLLDDTVYECVVEK	HAKGQ	2	C11:+57.021	884.9376007	1767.859601	0.000451244	4	N	214	229
P48193	Parental	ESTDR	SPRPTSAPAIAQSQVTEGPGAPIKK	TPKEA	3		830.1226444	2487.344533	0.000451244	1	N	555	580
P48193	Parental	ESTDR	SPRPTSAPAIAQSQVTEGPGAPIKK	TPKEA	4		622.8439333	2487.344533	0.000622848	1	N	555	580
P48758	Exosome	PKATK	SPEEGAETPVYLALLPPDAEGPHGQFVQDK	KVEPW	3		1064.523091	3190.545872	0.000451244	10	N	242	272
P48758	Exosome	EDTKK	GVHAEEGWPNSAYGVTK	IGVTV	2		901.4293544	1800.843109	0.002663018	1	N	181	198
P48999	Exosome	QMVQR	AVQDLTYSSLCFPEAIK	ARGMD	2	C11:+57.021	971.4852494	1940.954899	0.000622848	3	N	439	456
P48999	Exosome	PPTAK	GVVTIEQIVDTLPDR	GRSCW	2		827.9546737	1653.893747	0.001763695	1	N	580	595
P48999	Parental	QMVQR	AVQDLTYSSLCFPEAIK	ARGMD	2	C11:+57.021	971.4852494	1940.954899	0.000451244	18	N	439	456
P48999	Parental	PPTAK	GVVTIEQIVDTLPDRGR	SCWHL	3		623.3465741	1867.016322	0.000451244	14	N	580	597
P48999	Parental	KDLPR	DIQFDSEKGVDFVLNYSK	AMENL	3		702.0131492	2103.016048	0.000451244	4	N	166	184
P48999	Parental	IRFRK	NLEAIVSVIAER	NKNKK	2		657.3753308	1312.735062	0.000451244	29	N	640	652
P48999	Parental	IRFRK	NLEAIVSVIAER	NKNKK	3		438.5861539	1312.735062	0.001871652	1	N	640	652

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P48999	Parental	NLANK	IVPIAIQLNQTPGESNPIFLPTDSKYDWLLAK	IWVRS	3		1194.647173	3580.91812	0.000451244	16	N	320	352
P48999	Parental	NKNKK	LPYYYLSPDRIPNSVAI	-	2		991.0256304	1980.035661	0.001591523	3	N	657	674
P48999	Parental	PPTAK	GVVTIEQIVDTLPDR	GRSCW	2		827.9546737	1653.893747	0.000451244	15	N	580	595
P48999	Parental	PPTAK	GVVTIEQIVDTLPDR	GRSCW	3		552.3057158	1653.893747	0.000823681	5	N	580	595
P48999	Parental	HLLDK	AFYNDFER	GAVDS	2		531.2385028	1060.461406	0.001943752	2	N	40	48
P48999	Parental	FDSEK	GVDFVLNYSK	AMENL	2		571.2985604	1140.581521	0.00091018	1	N	174	184
P48999	Parental	NDFER	GAVDSYDVTVDEELGEIYLVK	IEKRK	2		1157.570993	2313.126386	0.000451244	5	N	48	69
P48999	Parental	NLANK	IVPIAIQLNQTPGESNPIFLPTDSK	YDWLL	2		1346.731965	2691.44833	0.000451244	4	N	320	345
P48999	Parental	NLANK	IVPIAIQLNQTPGESNPIFLPTDSK	YDWLL	3		898.1572433	2691.44833	0.000622848	3	N	320	345
P48999	Parental	FYFYR	DDGLLVWEAIQSF	TMEVV	2		746.8700783	1491.724557	0.001229886	1	N	472	485
P49138	Exosome	FGFAK	ETTSHNSLTTPCYTPYYVAPEVLGPEK	YDKSC	3	C12:+57.021	1018.818584	3053.432353	0.000451244	8	N	198	225
P49138	Exosome	KTRIR	MGQYEFPNPEWSEVSEEVK	MLIRN	2		1143.007506	2283.999412	0.001264573	1	N	266	285
P49222	Exosome	VRAVK	EGELQLDPAVPELFAAVNASCVVWK	CCEDG	3	C21:+57.021	914.7987959	2741.372988	0.000451244	9	N	372	397
P49222	Exosome	NQVMR	LSTNLSFSCFEQTPPENSFLR	VTAMA	2	C9:+57.021	1237.586755	2473.157909	0.000637154	4	N	542	563
P49222	Exosome	TGQGR	AVYETQAWVSAAVACTVLR	CLGIP	2	C15:+57.021	1048.035972	2094.056344	0.002663018	1	N	261	280
P49222	Exosome	ALKKK	SVLPISQTQAAQEGALLYK	RRGSV	2		1009.052376	2016.089153	0.000451244	4	N	225	244
P49222	Parental	VRAVK	EGELQLDPAVPELFAAVNASCVVWK	CCEDG	3	C21:+57.021	914.7987959	2741.372988	0.000662267	4	N	372	397
P49290	Exosome	ISLSR	IVCDNTGITTVSR	DIFRA	2	C3:+57.021	718.3644058	1434.713212	0.000451244	9	N	674	687
P49290	Exosome	LRLYK	TPDNIDIWVGAIAEPLLPGAR	VGPLL	2		1109.597483	2217.179365	0.000451244	14	N	608	629
P49290	Exosome	LPGAR	VGPLLACLFENQFR	RARDG	2	C7:+57.021	832.4351655	1662.854731	0.000451244	4	N	629	643
P49290	Parental	ISLSR	IVCDNTGITTVSR	DIFRA	2	C3:+57.021	718.3644058	1434.713212	0.000451244	7	N	674	687
P49290	Parental	LRLYK	TPDNIDIWVGAIAEPLLPGAR	VGPLL	2		1109.597483	2217.179365	0.000451244	14	N	608	629
P49312	Exosome	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	2		940.4872037	1878.958807	0.000622848	1	N	106	122
P49312	Exosome	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	3		627.3274024	1878.958807	0.000451244	21	N	106	122
P49312	Exosome	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	4		470.7475018	1878.958807	0.000870037	3	N	106	122
P49312	Exosome	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	2		1141.079123	2280.142645	0.000451244	2	N	146	166
P49312	Exosome	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	3		761.0553484	2280.142645	0.000451244	43	N	146	166
P49312	Exosome	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	4		571.0434613	2280.142645	0.000451244	8	N	146	166
P49312	Exosome	EQLRK	LFIGGLSFETTDESLR	SHFEQ	2		892.9574134	1783.899227	0.000451244	34	N	15	31
P49312	Exosome	PEQLR	KLFIGGLSFETTDESLR	SHFEQ	2		957.0048949	1911.99419	0.000451244	18	N	14	31
P49312	Parental	NFGGR	SSGPYGGGGQYFAKPR	NQGGY	2		814.8949504	1627.774301	0.000622848	5	N	284	300
P49312	Parental	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	2		940.4872037	1878.958807	0.000451244	13	N	106	122
P49312	Parental	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	3		627.3274024	1878.958807	0.000451244	24	N	106	122
P49312	Parental	LTVKK	IFVGGIKEDTEEHHLR	DYFEQ	4		470.7475018	1878.958807	0.000451244	7	N	106	122
P49312	Parental	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	2		1141.079123	2280.142645	0.000451244	1	N	146	166
P49312	Parental	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	3		761.0553484	2280.142645	0.000451244	25	N	146	166
P49312	Parental	SGKKR	GFAFVTFDDHDSVDKIVIQK	YHTVN	4		571.0434613	2280.142645	0.000451244	15	N	146	166
P49312	Parental	EQLRK	LFIGGLSFETTDESLR	SHFEQ	2		892.9574134	1783.899227	0.000451244	47	N	15	31
P49312	Parental	PEQLR	KLFIGGLSFETTDESLR	SHFEQ	2		957.0048949	1911.99419	0.000451244	27	N	14	31
P49312	Parental	PEQLR	KLFIGGLSFETTDESLR	SHFEQ	3		638.3391966	1911.99419	0.000622848	2	N	14	31
P49710	Exosome	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEKEQR	WGAKT	4		951.9336621	3803.703448	0.000823681	2	N	3	37
P49710	Exosome	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEK	EQRWG	3		1131.174855	3390.501166	0.000451244	7	N	3	34
P49710	Parental	DRMDK	SAVGHEYVADVEKHSSQTDAAR	GFGGK	3		786.3759208	2356.104362	0.000451244	9	N	96	118
P49710	Parental	DRMDK	SAVGHEYVADVEKHSSQTDAAR	GFGGK	4		590.0338906	2356.104362	0.000451244	12	N	96	118
P49710	Parental	AQLPK	KISSEVWPPAESHLPPESQPVR	SRREY	2		1235.64041	2469.26522	0.000451244	4	N	296	318
P49710	Parental	AQLPK	KISSEVWPPAESHLPPESQPVR	SRREY	3		824.0962067	2469.26522	0.000451244	77	N	296	318
P49710	Parental	AQLPK	KISSEVWPPAESHLPPESQPVR	SRREY	4		618.324105	2469.26522	0.001162105	8	N	296	318
P49710	Parental	QLPKK	ISSEVWPPAESHLPPESQPVR	SRREY	3		781.3978857	2341.170257	0.000451244	3	N	297	318
P49710	Parental	VKMSR	EVQQPSMPVEEPAAPAQLPK	KISSE	2		1073.546602	2145.077603	0.000451244	16	N	276	296
P49710	Parental	VKMSR	EVQQPSMPVEEPAAPAQLPK	KISSE	2	M7:+15.995	1081.544102	2161.072603	0.000451244	12	N	276	296
P49710	Parental	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEKEQR	WGAKT	3		1268.908949	3803.703448	0.000451244	61	N	3	37
P49710	Parental	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEKEQR	WGAKT	4		951.9336621	3803.703448	0.000451244	51	N	3	37
P49710	Parental	-MWK	SVVGHDVSVSVETQGDDWDTDPDFVNDISEK	EQRWG	3		1131.174855	3390.501166	0.000451244	33	N	3	34
P49710	Parental	DRADK	SAVGFDYKGEVEK	HASQK	2		714.8544282	1427.693256	0.000451244	12	N	133	146
P49710	Parental	DRADK	SAVGFDYKGEVEK	HASQK	3		476.9055521	1427.693256	0.000662267	1	N	133	146
P49710	Parental	RGQCR	GHFGLFPANYVK	LL-	2		675.3542013	1348.692803	0.000622848	3	N	472	484
P49710	Parental	SLPTR	QSPLQNHLEDNEEPPALPPR	TPEGL	3		761.0456235	2280.11347	0.000451244	5	N	331	351
P49710	Parental	DRMDK	SAVGHEYVADVEK	HSSQT	2		702.3442276	1402.672855	0.000451244	1	N	96	109
P49710	Parental	DRMDK	SAVGHEYVADVEK	HSSQT	3		468.5654184	1402.672855	0.002663018	1	N	96	109
P49710	Parental	ALPPR	TPEGLQVVEEPVYEAAPELEPEPEPDYEPEPE	TEPDY	3		1203.217838	3606.630115	0.002813207	2	N	351	383
P49717	Parental	SLGQK	LVIWGTDVNVATCK	ENFQR	2	C13:+57.021	788.4138987	1574.812197	0.000622848	2	N	148	162
P49717	Parental	QLNAR	TSVLAAANPIESQWNPK	KTTIE	2		913.4763046	1824.937009	0.000451244	4	N	609	626
P49718	Exosome	MDMKK	AIACLLFGGSR	KRLPD	2	C4:+57.021	582.8136234	1163.611647	0.001264573	2	N	350	361
P49718	Exosome	EEFRR	LAALPNIYELISK	SISPS	2		722.9246565	1443.833713	0.002453667	1	N	323	336
P49718	Parental	TLNSR	CSVLAAANSVFGR	WDETK	2	C1:+57.021	676.3432764	1350.670953	0.001591523	2	N	480	493

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P49722	Exosome	SPSGK	LVQIEYALAAVAGGAPSVGIK	AANGV	2		1014.080937	2026.146274	0.000451244	44	N	18	39
P49722	Exosome	SPSGK	LVQIEYALAAVAGGAPSVGIK	AANGV	3		676.3898913	2026.146274	0.000451244	42	N	18	39
P49722	Exosome	FLEKR	YNEDLELEDAIHTAILTLK	ESFEG	2		1101.070963	2200.126327	0.000451244	28	N	177	196
P49722	Exosome	FLEKR	YNEDLELEDAIHTAILTLK	ESFEG	3		734.3832422	2200.126327	0.000451244	46	N	177	196
P49722	Exosome	HRARK	LAQQYYLVYQEPIPTAQLVQR	VASVM	2		1261.176628	2520.337657	0.000637154	35	N	92	113
P49722	Exosome	HRARK	LAQQYYLVYQEPIPTAQLVQR	VASVM	3		841.1203523	2520.337657	0.000622848	25	N	92	113
P49722	Exosome	TFLEK	RYNEDLELEDAIHTAILTLK	ESFEG	3		786.4169459	2356.227438	0.000451244	42	N	176	196
P49722	Exosome	TFLEK	RYNEDLELEDAIHTAILTLK	ESFEG	4		590.0646594	2356.227438	0.000451244	12	N	176	196
P49722	Exosome	-MAER	GYSFSLTTFSPSGK	LVQIE	2		739.8622532	1477.708906	0.000451244	22	N	4	18
P49722	Exosome	LAQQY	YLVYQEPIPTAQLVQR	VASVM	2		959.5257975	1917.035995	0.000451244	10	N	97	113
P49722	Exosome	VHRAR	KLAQQYYLVYQEPIPTAQLVQR	VASVM	2		1325.22411	2648.43262	0.001264573	11	N	91	113
P49722	Exosome	FLEKR	YNEDLELEDAIHTAILTL	KESFE	2		1037.023482	2072.031363	0.000451244	1	N	177	195
P49722	Parental	SPSGK	LVQIEYALAAVAGGAPSVGIK	AANGV	2		1014.080937	2026.146274	0.000451244	22	N	18	39
P49722	Parental	SPSGK	LVQIEYALAAVAGGAPSVGIK	AANGV	3		676.3898913	2026.146274	0.000451244	11	N	18	39
P49722	Parental	FLEKR	YNEDLELEDAIHTAILTLK	ESFEG	3		734.3832422	2200.126327	0.000451244	38	N	177	196
P49722	Parental	TFLEK	RYNEDLELEDAIHTAILTLK	ESFEG	3		786.4169459	2356.227438	0.000451244	5	N	176	196
P49722	Parental	LAQQY	YLVYQEPIPTAQLVQR	VASVM	2		959.5257975	1917.035995	0.000823681	1	N	97	113
P49722	Parental	FLEKR	YNEDLELEDAIHTAILTL	KESFE	2		1037.023482	2072.031363	0.000870037	3	N	177	195
P49722	Parental	GVRPF	GVSLLICGWNEGRPYLFQSDPSGAYFAWK	ATAMG	3	C7:+57.021	1106.873246	3317.596339	0.000451244	2	N	130	159
P49813	Exosome	NKVLK	TLNVESNFISGAGILR	LVEAL	2		845.9602904	1689.904981	0.000451244	8	N	255	271
P49813	Exosome	LEKYR	DLDEDEILGALTEEELR	TLENE	2		980.4738216	1958.932043	0.002813207	1	N	11	28
P49813	Exosome	RELEK	YRDLDEDEILGALTEEELR	TLENE	2		1140.056042	2278.096483	0.001162105	1	N	9	28
P50247	Exosome	LSGIR	GISEETTTGVHNLYK	MMSNG	2		824.9130058	1647.810412	0.000451244	29	N	151	166
P50247	Exosome	LSGIR	GISEETTTGVHNLYK	MMSNG	3		550.2779372	1647.810412	0.000451244	6	N	151	166
P50247	Exosome	HFLPK	KLDEAVAEAHLGK	LNVKL	3		460.9214251	1379.740875	0.000451244	6	N	388	401
P50247	Exosome	VFAWK	GETDEEYLWCIEQTLHFK	DGPLN	2	C10:+57.021	1149.523092	2297.030583	0.000451244	5	N	103	121
P50247	Exosome	VFAWK	GETDEEYLWCIEQTLHFK	DGPLN	3	C10:+57.021	766.6846611	2297.030583	0.000451244	15	N	103	121
P50247	Exosome	GAEVR	WSSCNIFSTQDHAAAAIAK	AGIPV	2	C4:+57.021	1039.491929	2076.968258	0.000622848	1	N	75	94
P50247	Exosome	GAEVR	WSSCNIFSTQDHAAAAIAK	AGIPV	3	C4:+57.021	693.3305525	2076.968258	0.000622848	5	N	75	94
P50247	Exosome	KLPYK	VADIGLAAWGR	KALDI	2		564.8121693	1127.608739	0.000451244	3	N	8	19
P50247	Exosome	NGILK	VPAINVNDSVTK	SKFDN	2		628.8464061	1255.677212	0.000451244	3	N	174	186
P50247	Parental	LSGIR	GISEETTTGVHNLYK	MMSNG	2		824.9130058	1647.810412	0.000451244	6	N	151	166
P50247	Parental	VFAWK	GETDEEYLWCIEQTLHFK	DGPLN	3	C10:+57.021	766.6846611	2297.030583	0.000637154	3	N	103	121
P50247	Parental	GAEVR	WSSCNIFSTQDHAAAAIAK	AGIPV	3	C4:+57.021	693.3305525	2076.968258	0.001699387	1	N	75	94
P50396	Exosome	AAQGK	YIAIASTTVETAEPEKEVEPALELLEPIDQK	FVAIS	3		1142.931304	3425.770512	0.000451244	64	N	348	379
P50396	Exosome	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	2		1071.057462	2140.099324	0.000451244	63	Y	221	240
P50396	Exosome	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	3		714.3742412	2140.099324	0.000451244	29	Y	221	240
P50396	Exosome	RDVYR	KFDLGQDVIDFTGHALALYR	TDDYL	3		760.399338	2278.174614	0.000451244	38	N	173	193
P50396	Exosome	RDVYR	KFDLGQDVIDFTGHALALYR	TDDYL	4		570.5514535	2278.174614	0.000451244	22	N	173	193
P50396	Exosome	LALYR	TDDYLDQPCLETINR	IKLYS	2	C9:+57.021	926.9230133	1851.830427	0.000451244	18	N	193	208
P50396	Exosome	LHMDR	NPYYGGESSSITPLEELYK	RFQIL	2		1074.013114	2146.010628	0.000451244	34	N	35	54
P50396	Exosome	RRFRK	FLVFVANFDENDPK	TFEGV	2		827.9097348	1653.80387	0.000451244	10	N	142	156
P50396	Exosome	SHPIK	NTNDANSCQIIIPQNQVNR	KSDIY	2	C8:+57.021	1100.032481	2198.049362	0.000622848	20	Y	309	328
P50396	Exosome	YGKSP	YLYPLYGLGELPQGFAR	LSAIY	2		979.0150656	1956.014531	0.000451244	3	Y	223	240
P50396	Exosome	ARYGK	SPYLYPLYGLGELPQGF	ARLSA	2		957.4883494	1912.961099	0.000622848	3	Y	221	238
P50396	Exosome	LHMDR	NPYYGGESSSITPLEELYKR	FQILE	2		1152.06367	2302.111739	0.000622848	2	N	35	55
P50396	Exosome	LHMDR	NPYYGGESSSITPLEELYKR	FQILE	3		768.3783797	2302.111739	0.000451244	7	N	35	55
P50396	Exosome	MGRGR	DWNVDLIPK	FLMAN	2		550.293278	1098.570956	0.000823681	11	Y	70	79
P50396	Exosome	VARCK	QLICDPSYIPDR	VQKAG	2	C4:+57.021	738.861499	1475.707398	0.001871652	3	N	278	290
P50396	Exosome	SHPIK	NTNDANSCQIIIPQNQVNRK	SDIYV	3	C8:+57.021	776.3892416	2326.144325	0.000451244	5	Y	309	329
P50396	Exosome	DVYRK	FDLGQDVIDFTGHALALYR	TDDYL	3		717.701017	2150.079651	0.000451244	5	N	174	193
P50396	Parental	AAQGK	YIAIASTTVETAEPEKEVEPALELLEPIDQK	FVAIS	3		1142.931304	3425.770512	0.000451244	37	N	348	379
P50396	Parental	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	2		1071.057462	2140.099324	0.000451244	37	Y	221	240
P50396	Parental	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	3		714.3742412	2140.099324	0.000451244	11	Y	221	240
P50396	Parental	RDVYR	KFDLGQDVIDFTGHALALYR	TDDYL	3		760.399338	2278.174614	0.000451244	15	N	173	193
P50396	Parental	RDVYR	KFDLGQDVIDFTGHALALYR	TDDYL	4		570.5514535	2278.174614	0.000451244	14	N	173	193
P50396	Parental	ESLAR	YGKSPYLYPLYGLGELPQGFAR	LSAIY	2		1245.14734	2488.279079	0.000451244	1	Y	218	240
P50396	Parental	ESLAR	YGKSPYLYPLYGLGELPQGFAR	LSAIY	3		830.4341598	2488.279079	0.000823681	4	Y	218	240
P50396	Parental	LHMDR	NPYYGGESSSITPLEELYK	RFQIL	2		1074.013114	2146.010628	0.000622848	4	N	35	54
P50396	Parental	SHPIK	NTNDANSCQIIIPQNQVNR	KSDIY	2	C8:+57.021	1100.032481	2198.049362	0.000622848	8	Y	309	328
P50396	Parental	SHPIK	NTNDANSCQIIIPQNQVNRK	SDIYV	3	C8:+57.021	776.3892416	2326.144325	0.001352548	1	Y	309	329
P50429	Exosome	ARASG	ATQPPHVVFVLADDLGWNDLGFHGSVIR	TPHLD	4		765.8982342	3059.561737	0.000451244	7	N	41	69
P50429	Exosome	GPPTK	TLWLFDINQDPEER	HDVSR	2		888.4341054	1774.852611	0.000451244	7	N	471	485
P50429	Exosome	HPSPR	VELLHNIDQDFFDGLPCPG	KNMTP	2	C17:+57.021	1093.51507	2185.014539	0.001463592	3	N	389	408
P50429	Parental	ARASG	ATQPPHVVFVLADDLGWNDLGFHGSVIR	TPHLD	3		1020.861712	3059.561737	0.000451244	18	N	41	69

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P50429	Parental	ARASG	ATQPPHVVFVLADDLGWNDLGFHGSVIR	TPHLD	4		765.8982342	3059.561737	0.000451244	30	N	41	69
P50429	Parental	GPPTK	TLWLFDINQDPEER	HDVSR	2		888.4341054	1774.852611	0.000451244	16	N	471	485
P50429	Parental	GPPTK	TLWLFDINQDPEER	HDVSR	3		592.6253369	1774.852611	0.001329271	1	N	471	485
P50429	Parental	HDVSR	EHPHIVQNLLSR	LQYYH	3		481.6007974	1441.778992	0.000622848	1	N	490	502
P50429	Parental	EGGIR	GTGFVASPLLK	QKGVK	2		545.3192958	1088.622992	0.002080925	1	N	328	339
P50431	Exosome	LCQKR	ALQAYHLDPQCWGVNVQPYSGSPANFAVYTALVEPHGR	IMGLD	4	C11:+57.021	1054.01458	4212.027118	0.002145581	1	N	93	131
P50431	Exosome	NFASR	AVLEALGSCLNNK	YSEGY	2	C9:+57.021	694.8640416	1387.712483	0.000622848	7	N	53	66
P50431	Exosome	LANCR	ALSDALTELGYK	IVTGG	2		640.8407895	1279.665979	0.000451244	4	N	330	342
P50431	Exosome	SMPYK	VYPETGYINYDQLEENASLFHPK	LIIAG	3		909.7699364	2726.286409	0.002212458	1	N	167	190
P50431	Parental	NFASR	AVLEALGSCLNNK	YSEGY	2	C9:+57.021	694.8640416	1387.712483	0.001839721	1	N	53	66
P50446	Exosome	MDNNR	SLDLDSIIAEVK	AQYED	2		651.8617219	1301.707844	0.000451244	31	N	315	327
P50446	Exosome	LMNVK	LALDVEIATYR	KLLEG	2		632.3513243	1262.687049	0.001591523	2	N	444	455
P50446	Parental	MDNNR	SLDLDSIIAEVK	AQYED	2		651.8617219	1301.707844	0.000451244	1	N	315	327
P50516	Exosome	SKNLR	VGSHITGGDIYGIVNENSLIK	HKIML	2		1093.576747	2185.137894	0.000451244	28	N	142	163
P50516	Exosome	SKNLR	VGSHITGGDIYGIVNENSLIK	HKIML	3		729.3870981	2185.137894	0.000451244	28	N	142	163
P50516	Exosome	LTGQR	VLDALFPCVQGGTTAIPGAFGCGK	TVISQ	2	C8:+57.021,C22:+57.021	1218.606204	2435.196809	0.000451244	7	N	232	256
P50516	Exosome	LTGQR	VLDALFPCVQGGTTAIPGAFGCGK	TVISQ	3	C8:+57.021,C22:+57.021	812.7400696	2435.196809	0.000451244	11	N	232	256
P50516	Exosome	PLRTK	AKEILQEEEDLAEIVQLVGK	ASLAE	2		1127.612995	2253.210391	0.000451244	6	N	478	498
P50516	Exosome	PLRTK	AKEILQEEEDLAEIVQLVGK	ASLAE	3		752.0779302	2253.210391	0.000451244	18	N	478	498
P50516	Exosome	RTKAK	EILQEEEDLAEIVQLVGK	ASLAE	2		1028.046957	2054.078314	0.001654178	1	N	480	498
P50516	Exosome	RTKAK	EILQEEEDLAEIVQLVGK	ASLAE	3		685.7005712	2054.078314	0.000451244	33	N	480	498
P50516	Exosome	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDKK	LAQRK	3		1272.99519	3815.96217	0.000451244	40	N	400	438
P50516	Exosome	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDK	KLAQR	3		1230.296869	3687.867206	0.000451244	18	N	400	437
P50516	Exosome	PVAAR	EASIYTGITLSEYFR	DMGYH	2		875.4388564	1748.862113	0.000451244	3	N	323	338
P50516	Exosome	QSLSK	YSNSDVIIYVGCGER	GNEMS	2	C12:+57.021	866.4042593	1730.792919	0.000451244	20	N	265	280
P50516	Exosome	YELVR	VGHSELVGEIIR	LEGDM	2		654.8676729	1307.719746	0.000622848	4	N	44	56
P50516	Exosome	LEVAK	LIKDDFLQQNGYTPYDR	FCPFY	2		1043.516158	2085.016716	0.000451244	7	N	513	530
P50516	Exosome	LEVAK	LIKDDFLQQNGYTPYDR	FCPFY	3		696.0133721	2085.016716	0.000451244	19	N	513	530
P50516	Exosome	PPRNR	GSVTYIAPPGNYDASDVVLELEFEGVKEK	FSMVQ	3		1042.855958	3125.544475	0.002374549	2	N	173	202
P50516	Exosome	SKYMR	ALDEYYDKHFTEFVPLR	TKAKE	3		715.0218676	2142.042203	0.000451244	3	N	459	476
P50516	Exosome	DGEAK	IKADYAQLLEDMQNAFR	SLED-	3		676.0074529	2024.998959	0.001463592	1	N	596	613
P50516	Exosome	EISGR	LAEMPADSGYPAYLGAR	LASFY	2	M4:+15.995	899.428009	1796.840418	0.001264573	2	N	364	381
P50516	Parental	SKNLR	VGSHITGGDIYGIVNENSLIK	HKIML	2		1093.576747	2185.137894	0.000451244	23	N	142	163
P50516	Parental	SKNLR	VGSHITGGDIYGIVNENSLIK	HKIML	3		729.3870981	2185.137894	0.000451244	22	N	142	163
P50516	Parental	LTGQR	VLDALFPCVQGGTTAIPGAFGCGK	TVISQ	2	C8:+57.021,C22:+57.021	1218.606204	2435.196809	0.000451244	28	N	232	256
P50516	Parental	LTGQR	VLDALFPCVQGGTTAIPGAFGCGK	TVISQ	3	C8:+57.021,C22:+57.021	812.7400696	2435.196809	0.001463592	4	N	232	256
P50516	Parental	PLRTK	AKEILQEEEDLAEIVQLVGK	ASLAE	2		1127.612995	2253.210391	0.000451244	11	N	478	498
P50516	Parental	PLRTK	AKEILQEEEDLAEIVQLVGK	ASLAE	3		752.0779302	2253.210391	0.000451244	13	N	478	498
P50516	Parental	RTKAK	EILQEEEDLAEIVQLVGK	ASLAE	2		1028.046957	2054.078314	0.000451244	13	N	480	498
P50516	Parental	RTKAK	EILQEEEDLAEIVQLVGK	ASLAE	3		685.7005712	2054.078314	0.000451244	31	N	480	498
P50516	Parental	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDKK	LAQRK	3		1272.99519	3815.96217	0.000451244	30	N	400	438
P50516	Parental	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDKK	LAQRK	4		954.9983424	3815.96217	0.000823681	6	N	400	438
P50516	Parental	GNPER	EGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDK	KLAQR	3		1230.296869	3687.867206	0.000451244	15	N	400	437
P50516	Parental	PVAAR	EASIYTGITLSEYFR	DMGYH	2		875.4388564	1748.862113	0.000662267	5	N	323	338
P50516	Parental	QSLSK	YSNSDVIIYVGCGER	GNEMS	2	C12:+57.021	866.4042593	1730.792919	0.000451244	11	N	265	280
P50516	Parental	LEVAK	LIKDDFLQQNGYTPYDR	FCPFY	2		1043.516158	2085.016716	0.000451244	16	N	513	530
P50516	Parental	LEVAK	LIKDDFLQQNGYTPYDR	FCPFY	3		696.0133721	2085.016716	0.000451244	3	N	513	530
P50516	Parental	PPRNR	GSVTYIAPPGNYDASDVVLELEFEGVKEK	FSMVQ	3		1042.855958	3125.544475	0.000451244	3	N	173	202
P50516	Parental	SKYMR	ALDEYYDKHFTEFVPLR	TKAKE	2		1072.028901	2142.042203	0.000451244	2	N	459	476
P50518	Exosome	IATKK	DVDVQIDQEAYLPEEIAGGVEIYNGDRK	IKVSN	3		1045.8426	3134.504401	0.000451244	5	N	161	189
P50518	Exosome	KDTTR	YQVLLDGLVLQGLYQLLEPR	MIVRC	2		1165.660083	2329.304566	0.000451244	6	N	111	131
P50518	Exosome	KDTTR	YQVLLDGLVLQGLYQLLEPR	MIVRC	3		777.4426552	2329.304566	0.000451244	6	N	111	131
P50518	Exosome	LKVLR	ARDDLITDLLNEAK	QRLSK	2		793.9233735	1585.831147	0.000451244	17	N	85	99
P50518	Exosome	LKVLR	ARDDLITDLLNEAK	QRLSK	3		529.6181823	1585.831147	0.000451244	21	N	85	99
P50518	Exosome	VLRAR	DDLITDLLNEAK	QRLSK	2		680.354261	1358.692922	0.000823681	1	N	87	99
P50518	Parental	IATKK	DVDVQIDQEAYLPEEIAGGVEIYNGDRK	IKVSN	3		1045.8426	3134.504401	0.000451244	11	N	161	189
P50518	Parental	KDTTR	YQVLLDGLVLQGLYQLLEPR	MIVRC	2		1165.660083	2329.304566	0.000451244	1	N	111	131
P50518	Parental	KDTTR	YQVLLDGLVLQGLYQLLEPR	MIVRC	3		777.4426552	2329.304566	0.001763695	1	N	111	131
P50518	Parental	DTTRY	QVLLDGLVLQGLYQLLEPR	MIVRC	2		1084.128419	2166.241237	0.000451244	4	N	112	131
P50518	Parental	DTTRY	QVLLDGLVLQGLYQLLEPR	MIVRC	3		723.0882124	2166.241237	0.000451244	6	N	112	131
P50518	Parental	DTTRY	QVLLDGLVLQGLYQLLEPR	MIVRC	2	Q1:-17.027	1075.614919	2149.214237	0.000451244	3	N	112	131
P50518	Parental	LKVLR	ARDDLITDLLNEAK	QRLSK	2		793.9233735	1585.831147	0.000451244	11	N	85	99
P50518	Parental	LKVLR	ARDDLITDLLNEAK	QRLSK	3		529.6181823	1585.831147	0.000451244	17	N	85	99
P50518	Parental	RYQVL	LDGLVLQGLYQLLEPR	MIVRC	2		914.0228907	1826.030181	0.002727428	1	N	115	131
P50518	Parental	RYQVL	LDGLVLQGLYQLLEPR	MIVRC	3		609.6845271	1826.030181	0.000622848	4	N	115	131

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P50543	Exosome	TQLSK	TEFLSFMNTELAAFTK	NQKDP	2		925.4561925	1848.896785	0.000451244	6	N	31	47
P50543	Exosome	TETER	CIESLIAVFQK	YSGKD	2	C1:+39.994	645.8418211	1289.668042	0.000451244	3	N	7	18
P50543	Exosome	TETER	CIESLIAVFQK	YSGKD	2	C1:+57.021	654.3553211	1306.695042	0.000451244	50	N	7	18
P50543	Exosome	TETER	CIESLIAVFQK	YSGKD	2	[0:-17.027,C1:+57.021	645.8418211	1289.668042	0.000451244	45	N	7	18
P50543	Exosome	DRMMK	KLDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C6:+57.021,C26:+57.021	1370.341958	4108.002474	0.000451244	18	N	60	96
P50543	Exosome	DRMMK	KLDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	4	C6:+57.021,C26:+57.021	1028.008419	4108.002474	0.000451244	39	N	60	96
P50543	Exosome	RMMKK	LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C5:+57.021,C25:+57.021	1327.643637	3979.907511	0.000451244	17	N	61	96
P50543	Exosome	DRMMK	KLDLNCDGQLDFQEF	LNLIG	2	C6:+57.021	921.4226491	1840.829698	0.0007646	2	N	60	75
P50543	Parental	-M	PTETERCIESLIAVFQK	YSGKD	2	C7:+57.021	1011.02253	2020.029461	0.000451244	3	N	1	18
P50543	Parental	-M	PTETERCIESLIAVFQK	YSGKD	3	C7:+57.021	674.3509536	2020.029461	0.000451244	11	N	1	18
P50543	Parental	TQLSK	TEFLSFMNTELAAFTK	NQKDP	2		925.4561925	1848.896785	0.000451244	43	N	31	47
P50543	Parental	TQLSK	TEFLSFMNTELAAFTK	NQKDP	3		617.3067283	1848.896785	0.000451244	7	N	31	47
P50543	Parental	TETER	CIESLIAVFQK	YSGKD	2	C1:+57.021	654.3553211	1306.695042	0.000451244	577	N	7	18
P50543	Parental	TETER	CIESLIAVFQK	YSGKD	3	C1:+57.021	436.5728141	1306.695042	0.000451244	33	N	7	18
P50543	Parental	TETER	CIESLIAVFQK	YSGKD	2	[0:-17.027,C1:+57.021	645.8418211	1289.668042	0.000451244	404	N	7	18
P50543	Parental	DRMMK	KLDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C6:+57.021,C26:+57.021	1370.341958	4108.002474	0.000451244	129	N	60	96
P50543	Parental	DRMMK	KLDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	4	C6:+57.021,C26:+57.021	1028.008419	4108.002474	0.000451244	875	N	60	96
P50543	Parental	FLNLI	GGLAIACHDSFIQTSQK	RI-	2	C7:+57.021	916.9519081	1831.888216	0.000451244	18	N	79	96
P50543	Parental	RMMKK	LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQKR	I-	4	C5:+57.021,C25:+57.021	1035.009956	4136.008622	0.000451244	8	N	61	97
P50543	Parental	KLDLN	CDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C1:+57.021,C21:+57.021	1175.897637	3524.669512	0.000451244	1	N	65	96
P50543	Parental	RMMKK	LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C5:+57.021,C25:+57.021	1327.643637	3979.907511	0.000451244	87	N	61	96
P50543	Parental	RMMKK	LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQTSQK	RI-	4	C5:+57.021,C25:+57.021	995.9846777	3979.907511	0.000451244	38	N	61	96
P50543	Parental	DRMMK	KLDLNCDGQLDFQEF	LNLIG	2	C6:+57.021	921.4226491	1840.829698	0.000451244	23	N	60	75
P50543	Parental	LNLIG	GLAIACHDSFIQTSQK	RI-	2	C6:+57.021	888.4411762	1774.866752	0.000622848	4	N	80	96
P50543	Parental	KYSGK	DGNNTQLSKTEFLSFMNTELAAFTK	NQKDP	3		936.4572529	2806.348359	0.000870037	2	N	22	47
P50543	Parental	DFQEF	LNLIGGLAIACHDSFIQTSQK	RI-	2	C11:+57.021	1143.599468	2285.183336	0.000451244	11	N	75	96
P50543	Parental	DFQEF	LNLIGGLAIACHDSFIQTSQK	RI-	3	C11:+57.021	762.7355786	2285.183336	0.000622848	3	N	75	96
P50543	Parental	GQLDF	QEFLNLIGGLAIACHDSFIQTSQK	RI-	3	C14:+57.021	897.4587736	2689.352921	0.000451244	4	N	72	96
P50543	Parental	PTETE	RCIESLIAVFQK	YSGKD	3	C2:+57.021	488.6065178	1462.796153	0.001395409	1	N	6	18
P50543	Parental	EFLNL	IGGLAIACHDSFIQTSQK	RI-	2	C8:+57.021	973.4939401	1944.97228	0.000451244	5	N	78	96
P50543	Parental	DRMMK	KLDLNCDGQLDFQEFLNLIGGLAIAC	HDSFI	3	C6:+57.021,C26:+57.021	979.821229	2936.440287	0.00307782	1	N	60	86
P50543	Parental	RMMKK	LDLNCDGQLDFQEF	LNLIG	2	C5:+57.021	857.3751675	1712.734735	0.002019181	1	N	61	75
P50544	Exosome	KYLPR	VASGQALAAFCLTEPSSGSDVASIR	SSAIP	2	C11:+57.021	1247.616043	2493.216487	0.000451244	4	N	205	230
P50544	Exosome	LQGLK	ELGAFGLQVPSELGGLGLSNTQYAR	LAEIV	2		1289.169532	2576.323463	0.000451244	3	N	138	163
P50544	Exosome	LQGLK	ELGAFGLQVPSELGGLGLSNTQYAR	LAEIV	3		859.7822878	2576.323463	0.002019181	1	N	138	163
P50544	Exosome	LNGSK	IWISNGGLADIFTVFAK	TPIKD	2		926.5043338	1850.993068	0.000823681	3	N	248	265
P50544	Parental	RLYAR	EATQAVLDKPETLSSDASTR	EKPAR	3		707.0224845	2118.044053	0.000823681	1	N	43	63
P50544	Parental	LQGLK	ELGAFGLQVPSELGGLGLSNTQYAR	LAEIV	2		1289.169532	2576.323463	0.000451244	2	N	138	163
P50580	Exosome	EAALR	LVKPGNQNTQVTEAWNK	VAHSF	3		643.0064404	1925.995921	0.000451244	17	N	155	172
P50580	Exosome	KEMKK	GIAFPTSISVNNCVCHFSPLK	SDQDY	2	C13:+57.021,C15:+57.021	1174.57999	2347.144379	0.000451244	19	N	72	93
P50580	Exosome	NRVLR	SLVEASSSGVSVLSLCEK	GDAMI	2	C16:+57.021	926.472339	1850.929078	0.000451244	17	N	33	51
P50580	Exosome	VECAK	HELLQPFNVLYEK	EGEFV	2		815.4359198	1628.85624	0.000451244	7	N	298	311
P50580	Exosome	VECAK	HELLQPFNVLYEK	EGEFV	3		543.9598798	1628.85624	0.000870037	8	N	298	311
P50580	Exosome	VECAK	HELLQPFNVLYEKEGEFVAQFK	FTVLL	3		889.1273954	2664.358786	0.000451244	13	N	298	320
P50580	Exosome	VECAK	HELLQPFNVLYEKEGEFVAQFK	FTVLL	4		667.0974966	2664.358786	0.000451244	14	N	298	320
P50580	Exosome	KKASK	TVENATSGETLEENGAGD	-	2		897.3877462	1792.759892	0.001329271	3	N	376	394
P50580	Exosome	EKEMK	KGIAFPTSISVNNCVCHFSPLK	SDQDY	4	C14:+57.021,C16:+57.021	619.8176356	2475.239342	0.001699387	1	N	71	93
P50580	Parental	VECAK	HELLQPFNVLYEKEGEFVAQF	KFTVL	3		846.4290744	2536.263823	0.000979378	1	N	298	319
P50580	Parental	EAALR	LVKPGNQNTQVTEAWNK	VAHSF	2		964.0057606	1925.995921	0.000451244	13	N	155	172
P50580	Parental	EAALR	LVKPGNQNTQVTEAWNK	VAHSF	3		643.0064404	1925.995921	0.0007646	5	N	155	172
P50580	Parental	KEMKK	GIAFPTSISVNNCVCHFSPLK	SDQDY	2	C13:+57.021,C15:+57.021	1174.57999	2347.144379	0.002374549	1	N	72	93
P50580	Parental	KEMKK	GIAFPTSISVNNCVCHFSPLK	SDQDY	3	C13:+57.021,C15:+57.021	783.3892597	2347.144379	0.001871652	2	N	72	93
P50580	Parental	NRVLR	SLVEASSSGVSVLSLCEK	GDAMI	2	C16:+57.021	926.472339	1850.929078	0.000451244	13	N	33	51
P50580	Parental	VECAK	HELLQPFNVLYEK	EGEFV	3		543.9598798	1628.85624	0.0007646	1	N	298	311
P50580	Parental	KKASK	TVENATSGETLEENGAGD	-	2		897.3877462	1792.759892	0.002453667	1	N	376	394
P50580	Parental	EKEMK	KGIAFPTSISVNNCVCHFSPLK	SDQDY	2	C14:+57.021,C16:+57.021	1238.627471	2475.239342	0.002145581	1	N	71	93
P50580	Parental	GDLVK	IDLGVHVDGFIANVAHTFVIGVAQGTQVTGR	KADVI	4		798.6799821	3190.688729	0.002981883	1	N	107	138
P50637	Parental	PPAAR	LLYPYLAWLAFATVLNYYVWRDNSGR	RGGSR	3		1055.550587	3163.62836	0.000451244	1	N	135	161
P50637	Parental	PPAAR	LLYPYLAWLAFATVLNYYVWR	DNSGR	2		1318.209743	2634.403886	0.00307782	1	N	135	156
P51125	Exosome	PLLPK	ESQEQLAPLSDDFLLDALSQDFSSPANISSLEFEDAK	LSAAI	3		1352.974848	4055.901145	0.000451244	7	N	575	612
P51125	Exosome	EETSK	SLSESELIGELSADFDR	STYQD	2		934.4501495	1866.884699	0.0025889	1	N	441	458
P51125	Exosome	ESKTK	FQDVPSAGGESVAGGGTVATALDK	VVGKK	2		1117.550926	2233.086253	0.000451244	14	N	180	204
P51125	Exosome	KEKKR	KVEEEVINDQALQALSDSLGTR	QPDPP	3		805.7507648	2414.228894	0.000451244	16	N	359	381
P51125	Parental	LASLK	GVVPEDAVETLAGSLGTR	EADPE	2		885.9657697	1769.915939	0.000662267	2	N	504	522
P51125	Parental	LASLK	GVVPEDAVETLAGSLGTR	EADPE	3		590.9797798	1769.915939	0.00091018	1	N	504	522

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P51125	Parental	PLLPK	ESQEQLAPLSDDFLLDALSQDFSSPANISSLEFEDAK	LSAAI	3		1352.974848	4055.901145	0.000451244	41	N	575	612
P51125	Parental	PLLPK	ESQEQLAPLSDDFLLDALSQDFSSPANISSLEFEDAK	LSAAI	4		1014.983086	4055.901145	0.000622848	2	N	575	612
P51125	Parental	ESKTK	FQDVPSAGGESVAGGGTVATALDKVVGK	KKEQK	3		873.1209692	2616.339508	0.000451244	3	N	180	208
P51125	Parental	EETSK	SLSESELIGELSADFDR	STYQD	2		934.4501495	1866.884699	0.000451244	20	N	441	458
P51125	Parental	EETSK	SLSESELIGELSADFDR	STYQD	3		623.3026997	1866.884699	0.001463592	1	N	441	458
P51125	Parental	ESKTK	FQDVPSAGGESVAGGGTVATALDK	VVGKK	2		1117.550926	2233.086253	0.000451244	2	N	180	204
P51125	Parental	KEKKR	KVEEEVINDQALQALSDSLGTR	QPDPP	2		1208.122247	2414.228894	0.000451244	5	N	359	381
P51125	Parental	KEKKR	KVEEEVINDQALQALSDSLGTR	QPDPP	3		805.7507648	2414.228894	0.000451244	12	N	359	381
P51125	Parental	ERQEK	CGEDEDTVPAEYR	LKPAK	2	C1:+57.021	770.8149427	1539.614285	0.000451244	6	N	407	420
P51125	Parental	FEDAK	LSAAISEVVSQTPAPSTHAAAPLPGTEQK	DKELD	3		953.5018497	2857.482149	0.000451244	15	N	612	641
P51125	Parental	QLAPL	SDDFLLDALSQDFSSPANISSLEFEDAK	LSAAI	3		1021.144056	3060.408769	0.000451244	8	N	584	612
P51125	Parental	SKTKF	QDVPSAGGESVAGGGTVATALDK	VVGKK	2		1044.016719	2086.017839	0.000823681	3	N	181	204
P51150	Exosome	ETSAK	EAINVEQAFQTIAR	NALKQ	2		795.4182583	1588.820917	0.000451244	16	N	157	171
P51150	Exosome	ETSAK	EAINVEQAFQTIAR	NALKQ	3		530.6147722	1588.820917	0.000622848	2	N	157	171
P51150	Exosome	VAFYR	GADCCVLVFDVTAPNTFK	TLDSW	2	C4:+57.021,C5:+57.021	1007.474127	2012.932655	0.000451244	9	N	79	97
P51150	Exosome	PNTFK	TLDSWRDEFLIQASPR	DPENF	2		967.492486	1932.969372	0.000870037	6	N	97	113
P51150	Exosome	PNTFK	TLDSWRDEFLIQASPR	DPENF	3		645.330924	1932.969372	0.000451244	26	N	97	113
P51150	Exosome	QASPR	DPENFPFVVLGNK	IDLEN	2		738.3806131	1474.745626	0.000451244	4	N	113	126
P51150	Exosome	AGQER	FQSLGVAFYR	GADCC	2		594.3145448	1186.61349	0.001871652	1	N	69	79
P51150	Exosome	QTIAR	NALKQETEVELYNEFPEP	IKLDK	2		1075.518563	2149.021527	0.000622848	3	N	171	189
P51150	Exosome	SNQYK	ATIGADFLTK	EVMVD	2		518.7878285	1035.560057	0.000823681	3	N	38	48
P51150	Parental	QASPR	DPENFPFVVLGNKIDLENR	QVATK	2		1108.571465	2215.127329	0.001229886	2	N	113	132
P51150	Parental	QASPR	DPENFPFVVLGNKIDLENR	QVATK	3		739.3835765	2215.127329	0.000451244	8	N	113	132
P51150	Parental	ETSAK	EAINVEQAFQTIAR	NALKQ	2		795.4182583	1588.820917	0.000451244	18	N	157	171
P51150	Parental	ETSAK	EAINVEQAFQTIAR	NALKQ	3		530.6147722	1588.820917	0.000622848	5	N	157	171
P51150	Parental	VAFYR	GADCCVLVFDVTAPNTFK	TLDSW	2	C4:+57.021,C5:+57.021	1007.474127	2012.932655	0.000451244	3	N	79	97
P51150	Parental	PNTFK	TLDSWRDEFLIQASPR	DPENF	2		967.492486	1932.969372	0.000622848	7	N	97	113
P51150	Parental	PNTFK	TLDSWRDEFLIQASPR	DPENF	3		645.330924	1932.969372	0.000451244	24	N	97	113
P51150	Parental	QASPR	DPENFPFVVLGNK	IDLEN	2		738.3806131	1474.745626	0.000451244	16	N	113	126
P51150	Parental	GVAFY	RGADCCVLVFDVTAPNTFK	TLDSW	2	C5:+57.021,C6:+57.021	1085.524683	2169.033766	0.002080925	1	N	78	97
P51174	Exosome	RESVR	KFFQEEVIPHHTEWEK	AGEVS	3		695.3465741	2083.016322	0.000451244	1	N	65	81
P51174	Exosome	RESVR	KFFQEEVIPHHTEWEK	AGEVS	4		521.7618806	2083.016322	0.000451244	3	N	65	81
P51174	Exosome	EKAGK	QGLLGINIAEK	HGGIG	2		578.3407596	1154.665919	0.000622848	7	N	95	106
P51174	Exosome	KMGMK	AQDTAELFFEDVR	LPANA	2		770.8680669	1539.720534	0.000451244	15	N	254	267
P51174	Exosome	KMGMK	AQDTAELFFEDVRLPANALLGEENK	GFYYL	3		930.8035287	2789.387186	0.000451244	14	N	254	279
P51174	Exosome	NIAEK	HGGIGGDLLSTAVTWEEQAYSNCTGPGFSLH	SDIVM	3	C23:+57.021	1087.835409	3260.482826	0.002374549	1	N	106	137
P51174	Exosome	ESVRK	FFQEEVIPHHTEWEK	AGEVS	3		652.648253	1954.921359	0.002080925	1	N	66	81
P51174	Exosome	NIAEK	HGGIGGDLLSTAVTWEEQAY	SNCTG	2		1052.503248	2102.990895	0.000451244	6	N	106	126
P51174	Exosome	MTAGK	CIGAIAMTEPGAGSDLQGVR	TNAKR	2	C1:+57.021,M7:+15.995	1009.985665	2017.95573	0.000622848	4	N	165	185
P51174	Parental	RESVR	KFFQEEVIPHHTEWEK	AGEVS	3		695.3465741	2083.016322	0.001162105	2	N	65	81
P51174	Parental	RESVR	KFFQEEVIPHHTEWEK	AGEVS	4		521.7618806	2083.016322	0.000451244	4	N	65	81
P51174	Parental	EKAGK	QGLLGINIAEK	HGGIG	2		578.3407596	1154.665919	0.000998612	3	N	95	106
P51174	Parental	NIAEK	HGGIGGDLLSTAVTWEEQAYSNCTGPGFSLH	SDIVM	3	C23:+57.021	1087.835409	3260.482826	0.000622848	3	N	106	137
P51174	Parental	ESVRK	FFQEEVIPHHTEWEK	AGEVS	2		978.4684796	1954.921359	0.002884417	1	N	66	81
P51174	Parental	NIAEK	HGGIGGDLLSTAVTWEEQAY	SNCTG	2		1052.503248	2102.990895	0.000622848	2	N	106	126
P51410	Exosome	GTLRR	DFNHINVELSLLGK	KKKRL	3		533.6232677	1597.846403	0.000451244	6	N	36	50
P51410	Exosome	-MK	TILSNQTVDIPENVEITLK	GRTVI	2		1064.081331	2126.147062	0.000451244	15	N	2	21
P51410	Exosome	RYKMR	SVYAHFPINVVIQENGSLVEIR	NFLGE	2		1242.666428	2483.317256	0.000662267	1	N	93	115
P51410	Exosome	RYKMR	SVYAHFPINVVIQENGSLVEIR	NFLGE	3		828.7802186	2483.317256	0.000622848	2	N	93	115
P51410	Exosome	SQAQK	DELILEGNDIELVSNSAALIQQATTVK	NKDIR	3		962.1770318	2883.507695	0.000451244	1	N	141	168
P51410	Parental	GTLRR	DFNHINVELSLLGK	KKKRL	3		533.6232677	1597.846403	0.000451244	8	N	36	50
P51410	Parental	-MK	TILSNQTVDIPENVEITLK	GRTVI	2		1064.081331	2126.147062	0.000451244	15	N	2	21
P51410	Parental	RVRMR	TGVACSVSQAQKDELILEGNDIELVSNSAALIQQATTVK	NKDIR	3	C5:+57.021	1367.705885	4100.094254	0.000451244	17	N	129	168
P51410	Parental	RVRMR	TGVACSVSQAQKDELILEGNDIELVSNSAALIQQATTVK	NKDIR	4	C5:+57.021	1026.031364	4100.094254	0.001943752	1	N	129	168
P51410	Parental	DIRKF	LDGIYVSEKGTVQQADE	-	2		926.4526922	1850.889784	0.000451244	2	N	175	192
P51410	Parental	MRSVY	AHFPINVVIQENGSLVEIR	NFLGE	2		1068.084542	2134.153485	0.000451244	5	N	96	115
P51410	Parental	TGVAC	SVSQAQKDELILEGNDIELVSNSAALIQQATTVK	NKDIR	3		1204.970933	3611.889399	0.000451244	11	N	134	168
P51410	Parental	RYKMR	SVYAHFPINVVIQENGSLVEIR	NFLGE	2		1242.666428	2483.317256	0.000451244	3	N	93	115
P51410	Parental	RYKMR	SVYAHFPINVVIQENGSLVEIR	NFLGE	3		828.7802186	2483.317256	0.000451244	5	N	93	115
P51410	Parental	-MK	TILSNQTVDIPENVEITL	KGRTV	2		1000.033849	1998.052099	0.002145581	2	N	2	20
P51410	Parental	SQAQK	DELILEGNDIELVSNSAALIQQATTVK	NKDIR	3		962.1770318	2883.507695	0.000451244	1	N	141	168
P51437	Exosome	GKAER	QLPEQCAFKEQGVVK	QCMGA	2	C6:+57.021	880.9539194	1759.892239	0.000662267	1	N	88	103
P51437	Exosome	GKAER	QLPEQCAFKEQGVVK	QCMGA	2	[0:-17.027,C6:+57.021	872.4404194	1742.865239	0.000622848	6	N	88	103
P51437	Exosome	DTNLY	RLLDLDPEPQGDEDPDTPK	SVRFR	2		1075.516552	2149.017504	0.000451244	3	N	53	72
P51437	Exosome	DTNLY	RLLDLDPEPQGDEDPDTPK	SVRFR	3		717.3469681	2149.017504	0.000451244	5	N	53	72

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P51437	Exosome	TNLYR	LLDLDPEPQGDEDPDTPK	SVRFR	2		997.4659966	1992.916393	0.000451244	90	N	54	72
P51437	Exosome	DAVLR	AVDDFNQQSLDTNLYR	LLDLD	2		949.9481083	1897.880617	0.000451244	75	N	38	54
P51437	Exosome	DAVLR	AVDDFNQQSLDTNLYR	LLDLD	3		633.6346722	1897.880617	0.000451244	3	N	38	54
P51437	Exosome	CMGAV	TLNPAADSFDISCNEPGAQPFR	FKKIS	2	C13:+57.021	1204.053079	2406.090558	0.001329271	1	N	109	131
P51437	Exosome	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	C2:+57.021,C19:+57.021	1018.456733	3052.346798	0.000698008	5	N	103	131
P51437	Exosome	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	C2:+57.021,M3:+15.995,C19:+57.021	1023.788399	3068.341798	0.000451244	35	N	103	131
P51437	Exosome	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	Q1:-17.027,C2:+57.021,M3:+15.995,C19:+57.021	1018.112733	3051.314798	0.000870037	1	N	103	131
P51437	Exosome	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	[0:-17.027,C2:+57.021,M3:+15.995,C19:+57.021	1018.112733	3051.314798	0.000451244	11	N	103	131
P51437	Exosome	DAVLR	AVDDFNQQSLDTNLY	RLLDL	2		871.8975527	1741.779505	0.000451244	6	N	38	53
P51437	Exosome	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQP	FRFKK	2	C2:+57.021,M3:+15.995,C19:+57.021	1383.593937	2765.172273	0.000451244	18	N	103	129
P51437	Exosome	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQP	FRFKK	3	C2:+57.021,M3:+15.995,C19:+57.021	922.7318911	2765.172273	0.001871652	1	N	103	129
P51437	Parental	LYRLL	DLDPEPQGDEDPDTPK	SVRFR	2		884.3819325	1766.748265	0.000451244	20	N	56	72
P51437	Parental	GKAER	QLPEQCAFKEQGVVK	QCMGA	2	C6:+57.021	880.9539194	1759.892239	0.000451244	25	N	88	103
P51437	Parental	GKAER	QLPEQCAFKEQGVVK	QCMGA	3	C6:+57.021	587.6385463	1759.892239	0.000451244	4	N	88	103
P51437	Parental	GKAER	QLPEQCAFKEQGVVK	QCMGA	2	[0:-17.027,C6:+57.021	872.4404194	1742.865239	0.000451244	29	N	88	103
P51437	Parental	DTNLY	RLLDLDPEPQGDEDPDTPK	SVRFR	2		1075.516552	2149.017504	0.000451244	147	N	53	72
P51437	Parental	DTNLY	RLLDLDPEPQGDEDPDTPK	SVRFR	3		717.3469681	2149.017504	0.000451244	87	N	53	72
P51437	Parental	TNLYR	LLDLDPEPQGDEDPDTPKSVR	FRVKE	2		1168.566773	2335.117947	0.000451244	28	N	54	75
P51437	Parental	TNLYR	LLDLDPEPQGDEDPDTPKSVR	FRVKE	3		779.3804489	2335.117947	0.000451244	22	N	54	75
P51437	Parental	TNLYR	LLDLDPEPQGDEDPDTPK	SVRFR	2		997.4659966	1992.916393	0.000451244	203	N	54	72
P51437	Parental	TNLYR	LLDLDPEPQGDEDPDTPK	SVRFR	3		665.3132644	1992.916393	0.000451244	15	N	54	72
P51437	Parental	DAVLR	AVDDFNQQSLDTNLYR	LLDLD	2		949.9481083	1897.880617	0.000451244	329	N	38	54
P51437	Parental	DAVLR	AVDDFNQQSLDTNLYR	LLDLD	3		633.6346722	1897.880617	0.000451244	32	N	38	54
P51437	Parental	TNLYR	LLDLDPEPQGDEDPDTPKSV	RFRVK	2		1090.516218	2179.016836	0.000451244	19	N	54	74
P51437	Parental	CMGAV	TLNPAADSFDISCNEPGAQPFR	FKKIS	2	C13:+57.021	1204.053079	2406.090558	0.000451244	20	N	109	131
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	C2:+57.021,C19:+57.021	1018.456733	3052.346798	0.000451244	16	N	103	131
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	C2:+57.021,M3:+15.995,C19:+57.021	1023.788399	3068.341798	0.000451244	39	N	103	131
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	Q1:-17.027,C2:+57.021,M3:+15.995,C19:+57.021	1018.112733	3051.314798	0.000451244	3	N	103	131
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	[0:-	1012.781066	3035.319798	0.000451244	2	N	103	131
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPFR	FKKIS	3	[0:-17.027,C2:+57.021,M3:+15.995,C19:+57.021	1018.112733	3051.314798	0.000451244	14	N	103	131
P51437	Parental	DAVLR	AVDDFNQQSLDTNLY	RLLDL	2		871.8975527	1741.779505	0.000451244	50	N	38	53
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPF	RFKKI	2	C2:+57.021,C19:+57.021	1449.130644	2896.245687	0.000622848	4	N	103	130
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPF	RFKKI	3	C2:+57.021,C19:+57.021	966.4230291	2896.245687	0.002663018	1	N	103	130
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPF	RFKKI	2	C2:+57.021,M3:+15.995,C19:+57.021	1457.128144	2912.240687	0.000451244	23	N	103	130
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQPF	RFKKI	3	C2:+57.021,M3:+15.995,C19:+57.021	971.7546958	2912.240687	0.000451244	7	N	103	130
P51437	Parental	TLNPA	ADSFDISCNEPGAQPFR	FKKIS	2	C8:+57.021	955.9208049	1909.82601	0.000451244	10	N	114	131
P51437	Parental	QGVVK	QCMGAVTLNPAADSFDISCNEPGAQP	FRFKK	2	C2:+57.021,M3:+15.995,C19:+57.021	1383.593937	2765.172273	0.001654178	1	N	103	129
P51437	Parental	TNLYR	LLDLDPEPQGDEDPDTPKS	VRFRV	2		1040.982011	2079.948422	0.000622848	2	N	54	73
P51437	Parental	VLRAV	DDFNQQSLDTNLYR	LLDLD	2		864.8953444	1727.775089	0.002019181	1	N	40	54
P51437	Parental	GAVTL	NPAADSFDISCNEPGAQPFR	FKKIS	2	C11:+57.021	1096.987208	2191.958815	0.002080925	1	N	111	131
P51437	Parental	GKAER	QLPEQCAFK	EQGVV	2	C6:+57.021	560.7767065	1119.537813	0.002813207	1	N	88	97
P51807	Exosome	YQHSK	VNQWTTNVLEQTLSQLTK	LGRPF	2		1052.05819	2102.10078	0.000622848	9	N	38	56
P51807	Exosome	YQHSK	VNQWTTNVLEQTLSQLTK	LGRPF	3		701.7080601	2102.10078	0.000823681	2	N	38	56
P51807	Exosome	SSIVK	EAIESAIGGNAYQHSK	VNQWT	2		837.9082548	1673.80091	0.001943752	1	N	22	38
P51807	Exosome	SSIVK	EAIESAIGGNAYQHSK	VNQWT	3		558.9414365	1673.80091	0.000451244	1	N	22	38
P51807	Parental	YQHSK	VNQWTTNVLEQTLSQLTK	LGRPF	2		1052.05819	2102.10078	0.000622848	8	N	38	56
P51807	Parental	YQHSK	VNQWTTNVLEQTLSQLTK	LGRPF	3		701.7080601	2102.10078	0.000622848	5	N	38	56
P51859	Exosome	PNKRK	GFSEGLWEIENNPTVK	ASGYQ	2		910.4472128	1818.878826	0.000451244	15	N	80	96
P51859	Exosome	PKRPK	ESGDHEEEDKEIAALEGERPLPVEVEK	NSTPS	4		759.3681666	3033.441466	0.001162105	2	N	170	197
P51859	Exosome	STANK	YQVFFFGTHETAFLGPK	DLFPY	2		994.9994156	1987.983231	0.0025889	1	N	44	61

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P51859	Exosome	STANK	YQVFFFGTHETAFLGPK	DLFPY	3		663.668877	1987.983231	0.000870037	3	N	44	61
P51859	Parental	EAAVK	STANKYQVFFFGTHETAFLGPK	DLFPY	3		830.7537809	2489.237943	0.002296037	1	N	39	61
P51859	Parental	EAAVK	STANKYQVFFFGTHETAFLGPK	DLFPY	4		623.3172857	2489.237943	0.000451244	4	N	39	61
P51859	Parental	VEVEK	NSTPSEPDSGQGPPAEEEEGEEEAAKEEAEAQGVR	DHESL	3		1214.193415	3639.556844	0.000451244	50	N	197	232
P51859	Parental	PNKRK	GFSEGLWEIENNPTVK	ASGYQ	2		910.4472128	1818.878826	0.000451244	5	N	80	96
P51859	Parental	PKRPK	ESGDHEEEDKEIAALEGERPLPVEVEK	NSTPS	3		1012.154955	3033.441466	0.000823681	6	N	170	197
P51863	Exosome	EQECR	NIVWIAECIAQR	HRAKI	2	C8:+57.021	736.8878511	1471.760102	0.000451244	7	N	327	339
P51863	Exosome	EQECR	NIVWIAECIAQR	HRAKI	3	C8:+57.021	491.5945007	1471.760102	0.000622848	1	N	327	339
P51863	Exosome	VRGLK	AGVLSQADYLNLVQCETLEDLK	LHLQS	2	C15:+57.021	1240.12317	2478.23074	0.000451244	6	N	24	46
P51863	Parental	PHCGR	LYPEGLAQLAR	ADDYE	2		615.8462091	1229.676818	0.000451244	1	N	246	257
P51863	Parental	EQECR	NIVWIAECIAQR	HRAKI	2	C8:+57.021	736.8878511	1471.760102	0.000451244	5	N	327	339
P51863	Parental	EQECR	NIVWIAECIAQR	HRAKI	3	C8:+57.021	491.5945007	1471.760102	0.000451244	29	N	327	339
P51863	Parental	AQLAR	ADDYEQVKNVADYYPEYK	LLFEG	2		1105.500371	2208.985141	0.000451244	4	N	257	275
P51863	Parental	AQLAR	ADDYEQVKNVADYYPEYK	LLFEG	3		737.3361805	2208.985141	0.000451244	1	N	257	275
P51863	Parental	EADRR	AFIITINSFGTELSKEDR	AKLFP	2		1021.034184	2040.052767	0.000622848	2	N	219	237
P51863	Parental	LEDLK	LHLQSTDYGNFLANEASPLTV	SVIDD	2		1145.571662	2289.127723	0.000451244	6	N	46	67
P51863	Parental	VRGLK	AGVLSQADYLNLVQCETLEDLK	LHLQS	2	C15:+57.021	1240.12317	2478.23074	0.000451244	30	N	24	46
P51863	Parental	VRGLK	AGVLSQADYLNLVQCETLEDLK	LHLQS	3	C15:+57.021	827.0847133	2478.23074	0.000451244	14	N	24	46
P51863	Parental	YPEYK	LLFEGAGSNPGDK	TLEDR	2		652.8282134	1303.640827	0.001329271	1	N	275	288
P51863	Parental	YPEYK	LLFEGAGSNPGDKTLEDR	FFEHE	2		959.9794085	1917.943217	0.000451244	2	N	275	293
P51863	Parental	EADRR	AFIITINSFGTELSK	EDRAK	2		820.94886	1639.88212	0.001162105	4	N	219	234
P51863	Parental	LEDLK	LHLQSTDYGNFLANEASPLTVSVIDDK	LKEKM	3		983.1614932	2946.461079	0.000451244	5	N	46	73
P51881	Exosome	VSFAK	DFLAGGVAAAISK	TAVAP	2		610.3382169	1218.660834	0.002080925	1	N	10	23
P51881	Exosome	TQFWR	YFAGNLASGGAAGATSLCFVYPLDFAR	TRLAA	2	C18:+57.021	1398.676435	2795.337271	0.000451244	5	N	111	138
P51881	Exosome	TQFWR	YFAGNLASGGAAGATSLCFVYPLDFAR	TRLAA	3	C18:+57.021	932.7868902	2795.337271	0.0025889	1	N	111	138
P51881	Parental	VSFAK	DFLAGGVAAAISK	TAVAP	2		610.3382169	1218.660834	0.000451244	17	N	10	23
P51881	Parental	ANVIR	YFPTQALNFAFK	DKYKQ	2		723.8749666	1445.734333	0.00307782	1	N	80	92
P51881	Parental	TQFWR	YFAGNLASGGAAGATSLCFVYPLDFAR	TRLAA	2	C18:+57.021	1398.676435	2795.337271	0.000451244	36	N	111	138
P51881	Parental	TQFWR	YFAGNLASGGAAGATSLCFVYPLDFAR	TRLAA	3	C18:+57.021	932.7868902	2795.337271	0.000451244	11	N	111	138
P51881	Parental	DCVVR	IPKEQGVLSFWR	GNLAN	3		487.2739102	1458.798331	0.001591523	1	N	60	72
P52480	Exosome	PITAR	NTGIICTIGPASR	SVEML	2	C6:+57.021	680.3563838	1358.697168	0.000451244	64	N	43	56
P52480	Exosome	EASFK	CCSGAIIVLTK	SGRSA	2	C1:+57.021,C2:+57.021	611.3201927	1220.624785	0.000622848	43	N	422	433
P52480	Exosome	EHMCR	LDIDSAPITAR	NTGII	2		586.3200242	1170.624448	0.000451244	51	N	32	43
P52480	Exosome	QVKEK	GADFLVTEVENGGSLGSKK	GVNLP	2		954.489609	1906.963618	0.000451244	7	N	188	207
P52480	Exosome	QVKEK	GADFLVTEVENGGSLGSKK	GVNLP	3		636.6623393	1906.963618	0.000451244	21	N	188	207
P52480	Exosome	SLQVK	EKGADFLVTEVENGGSLGSK	KGVNL	2		1019.010906	2036.006211	0.000451244	40	N	186	206
P52480	Exosome	SLQVK	EKGADFLVTEVENGGSLGSK	KGVNL	3		679.6765371	2036.006211	0.000451244	23	N	186	206
P52480	Exosome	QVKEK	GADFLVTEVENGGSLGSK	KGVNL	2		890.4421274	1778.868655	0.000451244	95	N	188	206
P52480	Exosome	HLIAR	EAEAAIYHLQLFEELRR	LAPIT	2		1044.547793	2087.079985	0.000735798	1	N	383	400
P52480	Exosome	HLIAR	EAEAAIYHLQLFEELRR	LAPIT	3		696.7011284	2087.079985	0.000451244	41	N	383	400
P52480	Exosome	HLIAR	EAEAAIYHLQLFEELRR	LAPIT	4		522.7777963	2087.079985	0.000451244	32	N	383	400
P52480	Exosome	EVGSK	IYVDDGLISLQVK	EKGAD	2		731.9117461	1461.807892	0.000451244	59	N	173	186
P52480	Exosome	EVGSK	IYVDDGLISLQVK	EKGAD	3		488.2770974	1461.807892	0.000451244	3	N	173	186
P52480	Exosome	FEELR	RLAPITSDPTEAAAVGAVEASFK	CCSGA	2		1151.108411	2300.201223	0.000451244	21	N	399	422
P52480	Exosome	FEELR	RLAPITSDPTEAAAVGAVEASFK	CCSGA	3		767.741541	2300.201223	0.000451244	31	N	399	422
P52480	Exosome	AYMEK	CDENILWLDYK	NICKV	2	C1:+57.021	734.8427749	1467.66995	0.000451244	41	N	151	162
P52480	Exosome	AYMEK	CDENILWLDYK	NICKV	2	[0:-17.027,C1:+57.021	726.3292749	1450.64295	0.000451244	17	N	151	162
P52480	Exosome	IMVAR	GDLGIEIPAEKVFLAQK	MMIGR	3		610.0125323	1827.014197	0.002981883	1	N	294	311
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	3		1015.868421	3044.581863	0.000451244	32	N	92	120
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	4		762.1532659	3044.581863	0.000451244	31	N	92	120
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	3	[0:-18.011	1009.864754	3026.570863	0.000823681	3	N	92	120
P52480	Exosome	IKNVR	EATESFASDPILYRPVAV	ALDTK	2		983.0023522	1963.989104	0.000451244	42	N	92	110
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVALDTK	GPEIR	2		1247.147734	2492.279867	0.000451244	24	N	92	115
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVALDTK	GPEIR	3		831.7677558	2492.279867	0.000451244	44	N	92	115
P52480	Exosome	HLIAR	EAEAAIYHLQLFEELR	RLAPI	2		966.497237	1930.978874	0.000451244	15	N	383	399
P52480	Exosome	HLIAR	EAEAAIYHLQLFEELR	RLAPI	3		644.6674247	1930.978874	0.000451244	32	N	383	399
P52480	Exosome	PVLCK	DAVLNAWAEDVDLR	VNLAM	2		793.894616	1585.773632	0.000451244	90	N	475	489
P52480	Exosome	PVLCK	DAVLNAWAEDVDLR	VNLAM	3		529.5990107	1585.773632	0.000451244	7	N	475	489
P52480	Exosome	EELRR	LAPITSDPTEAAAVGAVEASFK	CCSGA	2		1073.057856	2144.100112	0.000451244	92	N	400	422
P52480	Exosome	EELRR	LAPITSDPTEAAAVGAVEASFK	CCSGA	3		715.7078372	2144.100112	0.000451244	57	N	400	422
P52480	Exosome	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	3	C16:+57.021	1165.55235	3493.63365	0.000451244	24	N	342	376
P52480	Exosome	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	4	C16:+57.021	874.4162125	3493.63365	0.000823681	2	N	342	376
P52480	Exosome	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	3	C16:+57.021,M18:+15.995	1170.884017	3509.62865	0.000451244	16	N	342	376
P52480	Exosome	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	4	C16:+57.021,M18:+15.995	878.4149625	3509.62865	0.001162105	1	N	342	376
P52480	Exosome	AHLYR	GIFPVLCKDAVLNAWAEDVDLR	VNLAM	3	C7:+57.021	834.4337882	2500.277965	0.000451244	7	N	467	489

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P52480	Exosome	IQDLK	FGVEQDVDMVFASFIR	KAADV	2		930.4539841	1858.892368	0.000451244	12	N	230	246
P52480	Exosome	IQDLK	FGVEQDVDMVFASFIR	KAADV	3		620.6385894	1858.892368	0.000451244	28	N	230	246
P52480	Exosome	IQDLK	FGVEQDVDMVFASFIR	KAADV	2	M9:+15.995	938.4514841	1874.887368	0.000451244	21	N	230	246
P52480	Exosome	IQDLK	FGVEQDVDMVFASFIR	KAADV	3	M9:+15.995	625.9702561	1874.887368	0.000451244	22	N	230	246
P52480	Exosome	MNVAR	LNFSHGTHEYHAETIK	NVREA	2		942.4559035	1882.896207	0.001591523	4	N	73	89
P52480	Exosome	MNVAR	LNFSHGTHEYHAETIK	NVREA	3		628.639869	1882.896207	0.000451244	48	N	73	89
P52480	Exosome	MNVAR	LNFSHGTHEYHAETIK	NVREA	4		471.7318517	1882.896207	0.000451244	39	N	73	89
P52480	Exosome	LGSKK	GVNLPGAAVDLPAVSEKDIQDLK	FGVEQ	2		1175.137169	2348.258738	0.000451244	43	N	207	230
P52480	Exosome	LGSKK	GVNLPGAAVDLPAVSEKDIQDLK	FGVEQ	3		783.7607126	2348.258738	0.000451244	5	N	207	230
P52480	Exosome	SLGSK	KGVNLPGAAVDLPAVSEK	DIQDL	2		882.9968729	1763.978146	0.000451244	34	N	206	224
P52480	Exosome	SLGSK	KGVNLPGAAVDLPAVSEK	DIQDL	3		589.0005153	1763.978146	0.000451244	13	N	206	224
P52480	Exosome	IMVAR	GDLGIEIPAEKV	FLAQK	2		620.8433321	1239.671064	0.001162105	4	N	294	306
P52480	Exosome	IMVAR	GDLGIEIPAEK	VFLAQ	2		571.3091251	1140.60265	0.000451244	72	N	294	305
P52480	Exosome	RGFFK	KGDVVIVLTGWRPGSGFTN	TMRVV	2		1002.039603	2002.063607	0.000451244	6	N	504	523
P52480	Exosome	RGFFK	KGDVVIVLTGWRPGSGFTN	TMRVV	3		668.3623356	2002.063607	0.000622848	7	N	504	523
P52480	Exosome	LGSKK	GVNLPGAAVDLPAVSEK	DIQDL	2		818.9493913	1635.883183	0.000451244	14	N	207	224
P52480	Exosome	GETAK	GDYPLEAVR	MQHLI	2		510.2619779	1018.508356	0.001871652	5	N	367	376
P52480	Exosome	GSKIY	VDDGLISLQVK	EKGAD	2		593.8380498	1185.6605	0.000622848	7	N	175	186
P52480	Exosome	SKKGV	NLPGAAVDLPAVSEKDIQDLK	FGVEQ	2		1097.09223	2192.16886	0.000451244	8	N	209	230
P52480	Exosome	EVGSK	IYVDDGLISLQV	KEKGA	2		667.8642646	1333.712929	0.001162105	4	N	173	185
P52480	Exosome	PRPTR	AEGSDVANAVLDGADCIMLSGETAK	GDYPL	2	C16:+57.021	1247.575727	2493.135854	0.000451244	13	N	342	367
P52480	Exosome	PRPTR	AEGSDVANAVLDGADCIMLSGETAK	GDYPL	3	C16:+57.021	832.0530848	2493.135854	0.000451244	12	N	342	367
P52480	Exosome	PRPTR	AEGSDVANAVLDGADCIMLSGETAK	GDYPL	2	C16:+57.021,M18:+15.995	1255.573227	2509.130854	0.000451244	14	N	342	367
P52480	Exosome	GATLK	ITLDNAYMEKCDENILWLDYK	NICKV	3	M8:+15.995,C11:+57.021	888.4175039	2662.229112	0.000662267	3	N	141	162
P52480	Exosome	RGFFK	KGDVVIVLTGWRPGSGFTNTMR	VVPVP	4		598.5710206	2390.252882	0.002374549	1	N	504	526
P52480	Exosome	RGFFK	KGDVVIVLTGWRPGSGFTNTMR	VVPVP	4	M21:+15.995	602.5697706	2406.247882	0.002145581	1	N	504	526
P52480	Exosome	HEGVR	RFDEILEASDGIMVAR	GDLGI	3		607.9774937	1820.909081	0.000451244	17	N	278	294
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVA	LDTKG	2		1018.520909	2035.026218	0.000451244	21	N	92	111
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVAL	DTKGP	2		1075.062941	2148.110282	0.000451244	7	N	92	112
P52480	Exosome	SLQVK	EKGADFLVTEVENGGSLG	SKKGV	2		911.4474098	1820.87922	0.001162105	1	N	186	204
P52480	Exosome	GRCNR	AGKPVICATQMLESMIK	KPRPT	3	C7:+57.021	626.3283277	1875.961583	0.000622848	3	N	319	336
P52480	Exosome	KGADF	LVTEVENGGSLGSK	KGVNL	2		695.3651601	1388.71472	0.000823681	6	N	192	206
P52480	Exosome	GATLK	ITLDNAYMEK	CDENI	2	M8:+15.995	607.292661	1212.569722	0.000451244	3	N	141	151
P52480	Exosome	KGVNL	PGAAVDLPAVSEKDIQDLK	FGVEQ	2		983.5287342	1965.041868	0.000622848	2	N	211	230
P52480	Exosome	IKNVR	EATESFASDPILYRPVAVALDT	KGPEI	2		1183.100252	2364.184904	0.000451244	3	N	92	114
P52480	Exosome	IKNVR	EATESFASDPILYRPVA	VALDT	2		933.4681452	1864.92069	0.000735798	1	N	92	109
P52480	Exosome	RGFFK	KGDVVIVLTGWRPGSGF	TNTMR	2		894.4943004	1786.973001	0.001871652	1	N	504	521
P52480	Exosome	RGFFK	KGDVVIVLTGWRPGSGF	TNTMR	3		596.6654669	1786.973001	0.000851441	6	N	504	521
P52480	Parental	PITAR	NTGIICTIGPASR	SVEML	2	C6:+57.021	680.3563838	1358.697168	0.000451244	67	N	43	56
P52480	Parental	EASFK	CCSGAIIVLTK	SGRSA	2	C1:+57.021,C2:+57.021	611.3201927	1220.624785	0.000622848	20	N	422	433
P52480	Parental	EHMCR	LDIDSAPITAR	NTGII	2		586.3200242	1170.624448	0.000451244	66	N	32	43
P52480	Parental	QVKEK	GADFLVTEVENGGSLGSKK	GVNLP	2		954.489609	1906.963618	0.000451244	9	N	188	207
P52480	Parental	QVKEK	GADFLVTEVENGGSLGSKK	GVNLP	3		636.6623393	1906.963618	0.000451244	18	N	188	207
P52480	Parental	EVGSK	IYVDDGLISLQVKEK	GADFL	3		573.9896162	1718.945449	0.000735798	4	N	173	188
P52480	Parental	SLQVK	EKGADFLVTEVENGGSLGSK	KGVNL	2		1019.010906	2036.006211	0.000451244	32	N	186	206
P52480	Parental	SLQVK	EKGADFLVTEVENGGSLGSK	KGVNL	3		679.6765371	2036.006211	0.000451244	14	N	186	206
P52480	Parental	QVKEK	GADFLVTEVENGGSLGSK	KGVNL	2		890.4421274	1778.868655	0.000451244	61	N	188	206
P52480	Parental	HLIAR	EAEAAIYHLQLFEELRR	LAPIT	3		696.7011284	2087.079985	0.000451244	9	N	383	400
P52480	Parental	HLIAR	EAEAAIYHLQLFEELRR	LAPIT	4		522.7777963	2087.079985	0.000451244	8	N	383	400
P52480	Parental	AYMEK	CDENILWLDYKNICK	VVEVG	2	C1:+57.021,C14:+57.021	992.4688451	1982.92209	0.000451244	7	N	151	166
P52480	Parental	AYMEK	CDENILWLDYKNICK	VVEVG	3	C1:+57.021,C14:+57.021	661.9818301	1982.92209	0.000637154	1	N	151	166
P52480	Parental	AYMEK	CDENILWLDYKNICK	VVEVG	2	[0:-	983.9553451	1965.89509	0.001699387	4	N	151	166
P52480	Parental	EVGSK	IYVDDGLISLQVK	EKGAD	2		731.9117461	1461.807892	0.000451244	69	N	173	186
P52480	Parental	FEELR	RLAPITSDPTEAAAVGAVEASFK	CCSGA	2		1151.108411	2300.201223	0.000451244	8	N	399	422
P52480	Parental	FEELR	RLAPITSDPTEAAAVGAVEASFK	CCSGA	3		767.741541	2300.201223	0.000622848	5	N	399	422
P52480	Parental	AYMEK	CDENILWLDYK	NICKV	2	C1:+57.021	734.8427749	1467.66995	0.000451244	18	N	151	162
P52480	Parental	AYMEK	CDENILWLDYK	NICKV	2	[0:-17.027,C1:+57.021	726.3292749	1450.64295	0.000451244	8	N	151	162
P52480	Parental	IMVAR	GDLGIEIPAEKVFLAQK	MMIGR	2		914.5148985	1827.014197	0.000451244	2	N	294	311
P52480	Parental	IMVAR	GDLGIEIPAEKVFLAQK	MMIGR	3		610.0125323	1827.014197	0.000451244	7	N	294	311
P52480	Parental	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	3		1015.868421	3044.581863	0.000451244	46	N	92	120
P52480	Parental	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	4		762.1532659	3044.581863	0.000451244	40	N	92	120
P52480	Parental	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	3	E1:-18.011	1009.864754	3026.570863	0.000451244	3	N	92	120
P52480	Parental	IKNVR	EATESFASDPILYRPVAVALDTKGPEIR	TGLIK	3	[0:-18.011	1009.864754	3026.570863	0.000622848	1	N	92	120
P52480	Parental	IKNVR	EATESFASDPILYRPVAV	ALDTK	2		983.0023522	1963.989104	0.000451244	34	N	92	110
P52480	Parental	IKNVR	EATESFASDPILYRPVAVALDTK	GPEIR	2		1247.147734	2492.279867	0.000451244	23	N	92	115

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P52480	Parental	IKNVR	EATESFASDPILYRPVAVALDTK	GPEIR	3		831.7677558	2492.279867	0.000451244	50	N	92	115
P52480	Parental	HLIAR	EAEAAIYHLQLFEELR	RLAPI	3		644.6674247	1930.978874	0.001763695	1	N	383	399
P52480	Parental	PVLCK	DAVLNAWAEDVDLR	VNLAM	2		793.894616	1585.773632	0.000451244	37	N	475	489
P52480	Parental	PVLCK	DAVLNAWAEDVDLR	VNLAM	3		529.5990107	1585.773632	0.000451244	14	N	475	489
P52480	Parental	EELRR	LAPITSDPTEAAAVGAVEASFK	CCSGA	2		1073.057856	2144.100112	0.000451244	85	N	400	422
P52480	Parental	EELRR	LAPITSDPTEAAAVGAVEASFK	CCSGA	3		715.7078372	2144.100112	0.000451244	34	N	400	422
P52480	Parental	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	3	C16:+57.021	1165.55235	3493.63365	0.000451244	36	N	342	376
P52480	Parental	PRPTR	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	MQHLI	4	C16:+57.021	874.4162125	3493.63365	0.000451244	9	N	342	376
P52480	Parental	AHLYR	GIFPVLCKDAVLNAWAEDVDLR	VNLAM	2	C7:+57.021	1251.146782	2500.277965	0.002663018	1	N	467	489
P52480	Parental	AHLYR	GIFPVLCKDAVLNAWAEDVDLR	VNLAM	3	C7:+57.021	834.4337882	2500.277965	0.000451244	7	N	467	489
P52480	Parental	IQDLK	FGVEQDVDMVFASFIRK	AADVH	3		663.3369105	1986.987331	0.000823681	7	N	230	247
P52480	Parental	IQDLK	FGVEQDVDMVFASFIR	KAADV	2		930.4539841	1858.892368	0.000451244	11	N	230	246
P52480	Parental	IQDLK	FGVEQDVDMVFASFIR	KAADV	3		620.6385894	1858.892368	0.000451244	17	N	230	246
P52480	Parental	MNVAR	LNFSHGTHEYHAETIK	NVREA	3		628.639869	1882.896207	0.000451244	40	N	73	89
P52480	Parental	MNVAR	LNFSHGTHEYHAETIK	NVREA	4		471.7318517	1882.896207	0.000451244	31	N	73	89
P52480	Parental	LGSKK	GVNLPGAAVDLPAVSEKDIQDLK	FGVEQ	2		1175.137169	2348.258738	0.000451244	22	N	207	230
P52480	Parental	LGSKK	GVNLPGAAVDLPAVSEKDIQDLK	FGVEQ	3		783.7607126	2348.258738	0.001463592	2	N	207	230
P52480	Parental	MNVAR	LNFSHGTHEYHAETIKNVR	EATES	3		751.7106866	2252.10866	0.000451244	3	N	73	92
P52480	Parental	MNVAR	LNFSHGTHEYHAETIKNVR	EATES	4		564.0349649	2252.10866	0.000451244	12	N	73	92
P52480	Parental	SLGSK	KGVNLPGAAVDLPAVSEK	DIQDL	2		882.9968729	1763.978146	0.000451244	28	N	206	224
P52480	Parental	SLGSK	KGVNLPGAAVDLPAVSEK	DIQDL	3		589.0005153	1763.978146	0.000451244	17	N	206	224
P52480	Parental	IMVAR	GDLGIEIPAEKV	FLAQK	2		620.8433321	1239.671064	0.001871652	1	N	294	306
P52480	Parental	IMVAR	GDLGIEIPAEK	VFLAQ	2		571.3091251	1140.60265	0.000451244	15	N	294	305
P52480	Parental	RGFFK	KGDVVIVLTGWRPGSGFTN	TMRVV	2		1002.039603	2002.063607	0.000823681	1	N	504	523
P52480	Parental	RGFFK	KGDVVIVLTGWRPGSGFTN	TMRVV	3		668.3623356	2002.063607	0.001162105	1	N	504	523
P52480	Parental	LGSKK	GVNLPGAAVDLPAVSEK	DIQDL	2		818.9493913	1635.883183	0.000451244	8	N	207	224
P52480	Parental	GETAK	GDYPLEAVR	MQHLI	2		510.2619779	1018.508356	0.001943752	4	N	367	376
P52480	Parental	PRPTR	AEGSDVANAVLDGADCIMLSGETAK	GDYPL	2	C16:+57.021	1247.575727	2493.135854	0.000451244	9	N	342	367
P52480	Parental	EELRR	LAPITSDPTEAAAVGAVEASF	KCCSG	2		1009.010374	2016.005149	0.000451244	10	N	400	421
P52480	Parental	EELRR	LAPITSDPTEAAAVGAVEASF	KCCSG	3		673.0095162	2016.005149	0.002813207	1	N	400	421
P52480	Parental	GATLK	ITLDNAYMEKCDENILWLDYK	NICKV	2	C11:+57.021	1324.124856	2646.234112	0.002296037	1	N	141	162
P52480	Parental	GATLK	ITLDNAYMEKCDENILWLDYK	NICKV	3	C11:+57.021	883.0858373	2646.234112	0.000870037	2	N	141	162
P52480	Parental	LRRLA	PITSDPTEAAAVGAVEASFK	CCSGA	2		980.9972669	1959.978934	0.001162105	1	N	402	422
P52480	Parental	FPVLC	KDAVLNAWAEDVDLR	VNLAM	2		857.9420976	1713.868595	0.000451244	1	N	474	489
P52480	Parental	FPVLC	KDAVLNAWAEDVDLR	VNLAM	3		572.2973317	1713.868595	0.000451244	11	N	474	489
P52480	Parental	ATESF	ASDPILYRPVAVALDTK	GPEIR	3		610.344282	1828.009446	0.001162105	2	N	98	115
P52503	Parental	RFVDR	QKEVNENFAIDLIAQQPVNEVEHR	IIACD	3		940.8145392	2819.420218	0.000451244	7	N	51	75
P52503	Parental	RFVDR	QKEVNENFAIDLIAQQPVNEVEHR	IIACD	4		705.8628544	2819.420218	0.000622848	3	N	51	75
P52503	Parental	RFVDR	QKEVNENFAIDLIAQQPVNEVEHR	IIACD	3	Q1:-17.027	935.1388725	2802.393218	0.0025889	1	N	51	75
P52503	Parental	RFVDR	QKEVNENFAIDLIAQQPVNEVEHR	IIACD	3	[0:-17.027	935.1388725	2802.393218	0.000451244	3	N	51	75
P52503	Parental	VDRQK	EVNENFAIDLIAQQPVNEVEHR	IIACD	3		855.4300256	2563.266677	0.000451244	12	N	53	75
P52624	Exosome	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGKR	VIRNT	4	C24:+57.021	990.2744308	3957.066523	0.000451244	7	N	139	176
P52624	Exosome	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGK	RVIRN	3	C24:+57.021	1267.996271	3800.965412	0.000451244	31	N	139	175
P52624	Exosome	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGK	RVIRN	4	C24:+57.021	951.249153	3800.965412	0.000451244	18	N	139	175
P52624	Exosome	NTFIK	YVAAELGLDHPGKEYPNICAGTDR	YAMYK	3	C19:+57.021	882.7591116	2645.253935	0.000451244	19	N	71	95
P52624	Exosome	NTFIK	YVAAELGLDHPGKEYPNICAGTDR	YAMYK	4	C19:+57.021	662.3212837	2645.253935	0.002080925	1	N	71	95
P52624	Exosome	TLLDR	LQGDQINTPHDVLVEYQQRPQR	LVGHF	3		878.7848028	2633.331008	0.000622848	7	N	276	298
P52624	Exosome	TLLDR	LQGDQINTPHDVLVEYQQRPQR	LVGHF	4		659.3405521	2633.331008	0.001162105	8	N	276	298
P52624	Exosome	EGQGR	LDGALCSYTEKDK	QSYLR	3	C6:+57.021	500.573431	1498.696893	0.000451244	4	N	220	233
P52624	Exosome	ACGLK	AAVVCVTLLDR	LQGDQ	2	C5:+57.021	608.8398382	1215.664076	0.000622848	1	N	265	276
P52624	Parental	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGKR	VIRNT	4	C24:+57.021	990.2744308	3957.066523	0.000451244	5	N	139	176
P52624	Parental	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGK	RVIRN	3	C24:+57.021	1267.996271	3800.965412	0.000451244	29	N	139	175
P52624	Parental	ITIIR	IGTSGGIGLEPGSVVITQQAVNECFKPEFEQIVLGK	RVIRN	4	C24:+57.021	951.249153	3800.965412	0.000451244	2	N	139	175
P52624	Parental	TLLDR	LQGDQINTPHDVLVEYQQRPQR	LVGHF	3		878.7848028	2633.331008	0.000622848	2	N	276	298
P52633	Exosome	GLQER	CESLVEIYSQLQQEIGAASGELEPK	TRASL	3	C1:+57.021	926.7886251	2777.342475	0.000622848	4	N	227	252
P52633	Parental	QDLTK	LLLENQGEAGGSLGSQPLLQPSPYGQSGISLSHLDLR	TNPSW	3		1278.001226	3830.980279	0.000451244	20	N	795	832
P52633	Parental	GLQER	CESLVEIYSQLQQEIGAASGELEPK	TRASL	3	C1:+57.021	926.7886251	2777.342475	0.002884417	1	N	227	252
P52633	Parental	GFISK	QYVTSLLLNEPDGTFLLR	FSDSE	2		1040.060202	2078.104803	0.001591523	1	N	544	562
P53994	Exosome	GKQIK	LQIWDTAGQESFR	SITRS	2		775.8840513	1549.752503	0.001329271	1	N	56	69
P53994	Exosome	DITRR	DTFNHLTTWLEDAR	QHSNS	2		859.9107974	1717.805995	0.001329271	1	N	91	105
P53994	Exosome	DITRR	DTFNHLTTWLEDAR	QHSNS	3		573.6097983	1717.805995	0.000451244	7	N	91	105
P53994	Parental	ETSAK	TASNVEEAFINTAKEIYEK	IQEGV	3		719.6957087	2156.063726	0.001229886	3	N	151	170
P53994	Parental	ETSAK	TASNVEEAFINTAK	EIYEK	2		747.8758919	1493.736184	0.000823681	14	N	151	165
P53994	Parental	GKQIK	LQIWDTAGQESFR	SITRS	2		775.8840513	1549.752503	0.000451244	7	N	56	69
P53994	Parental	TGVGK	SCLLLQFTDKR	FQPVH	3	C2:+57.021	460.9153513	1379.722654	0.001229886	4	N	19	30

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P53996-2	Parental	RSRGR	GFQFVSSSLPDICYR	CGESG	2	C13:+57.021	888.4249948	1774.83439	0.000451244	7	N	34	49
P53996-2	Parental	DICYR	CGESGHLAKDCDLQEDACYNCGR	GGHIA	3	C1:+39.994,C11:+57.021,C18:+57.021,C21:+57.021	900.017438	2697.028914	0.000979378	1	N	49	72
P53996-2	Parental	DICYR	CGESGHLAKDCDLQEDACYNCGR	GGHIA	3	C1:+57.021,C11:+57.021,C18:+57.021,C21:+57.021	905.6931047	2714.055914	0.000451244	11	N	49	72
P53996-2	Parental	DICYR	CGESGHLAKDCDLQEDACYNCGR	GGHIA	4	C1:+57.021,C11:+57.021,C18:+57.021,C21:+57.021	679.5217785	2714.055914	0.000451244	1	N	49	72
P53996-2	Parental	DICYR	CGESGHLAKDCDLQEDACYNCGR	GGHIA	3	[0:-17.027,C1:+57.021,C11:+57.021,C18:+57.021,C21:+57.021	900.017438	2697.028914	0.000622848	2	N	49	72
P53996-2	Parental	GHLAK	DCDLQEDACYNCGR	GGHIA	2	C2:+57.021,C9:+57.021,C12:+57.021	888.3243631	1774.633126	0.000451244	3	N	58	72
P54071	Exosome	DVQLK	YFDLGLPNRDQTNDQVTIDSALATQK	YSVAV	3		975.1531091	2922.435927	0.000451244	16	N	80	106
P54071	Exosome	LSNVK	LNEHFLNTTDFLDTIK	SNLDR	2		960.9892448	1919.96289	0.000451244	1	N	426	442
P54071	Exosome	LSNVK	LNEHFLNTTDFLDTIK	SNLDR	3		640.9954299	1919.96289	0.000451244	44	N	426	442
P54071	Exosome	AYDGR	FKDIFQEIFDK	HYKTD	3		477.2507712	1428.728914	0.000622848	6	N	261	272
P54071	Exosome	REHQK	GRPTSTNPIASIFAWTR	GLEHR	3		625.667759	1873.979877	0.000451244	18	N	360	377
P54071	Exosome	GLPNR	DQTNDQVTIDSALATQK	YSVAV	2		924.4532235	1846.890847	0.000451244	12	N	89	106
P54071	Exosome	FIKEK	LILPHVDVQLK	YFDLG	3		425.5997347	1273.775804	0.000998612	1	N	69	80
P54071	Exosome	SVAVK	CATITPDEARVEEFK	LKKMW	3	C1:+57.021	589.2860612	1764.834784	0.000622848	5	N	112	127
P54071	Exosome	DVQLK	YFDLGLPNR	DQTND	2		547.7856202	1093.55564	0.001229886	1	N	80	89
P54071	Exosome	GAMTK	DLAGCIHGLSNVK	LNEHF	2	C5:+57.021	692.3563838	1382.697168	0.000823681	1	N	413	426
P54071	Exosome	GAMTK	DLAGCIHGLSNVK	LNEHF	3	C5:+57.021	461.9068558	1382.697168	0.000735798	1	N	413	426
P54071	Parental	DVQLK	YFDLGLPNRDQTNDQVTIDSALATQK	YSVAV	3		975.1531091	2922.435927	0.000451244	12	N	80	106
P54071	Parental	LSNVK	LNEHFLNTTDFLDTIK	SNLDR	3		640.9954299	1919.96289	0.000451244	25	N	426	442
P54071	Parental	AYDGR	FKDIFQEIFDK	HYKTD	3		477.2507712	1428.728914	0.001329271	1	N	261	272
P54071	Parental	REHQK	GRPTSTNPIASIFAWTR	GLEHR	3		625.667759	1873.979877	0.001162105	8	N	360	377
P54071	Parental	GLPNR	DQTNDQVTIDSALATQK	YSVAV	2		924.4532235	1846.890847	0.000622848	1	N	89	106
P54103	Parental	KSEAK	DNFFQVFSPVFER	NSRWS	2		816.3967946	1630.777989	0.000451244	9	N	175	188
P54103	Parental	PDKRK	AAGEPIKEGDNDYFTCITK	AYEML	2	C16:+57.021	1064.99671	2127.977819	0.000662267	1	N	124	143
P54103	Parental	APSER	FEGPCIDSTPWTTEEQK	LLEQA	2	C5:+57.021	1012.949228	2023.882856	0.000851441	1	N	543	560
P54310	Exosome	PVTLK	VVEDLPHGFLSLAALCR	ETRQA	3	C16:+57.021	633.0052291	1895.992287	0.001591523	2	N	717	734
P54310	Exosome	CFYGR	CLGFQFTPAIRPF	LQTLS	2	C1:+57.021	777.4005943	1552.785589	0.0025889	1	N	167	180
P54310	Exosome	FAGVR	EQALGLEPTLGQLLGVAHHFDLDTETPANGYR	SLVHT	4		866.4381863	3461.721545	0.001395409	1	N	41	73
P54728	Exosome	FQQMR	QIIQQNPSLLPALLQQIGR	ENPQL	2		1065.623835	2129.232069	0.000637154	6	N	289	308
P54728	Parental	FQQMR	QIIQQNPSLLPALLQQIGR	ENPQL	2		1065.623835	2129.232069	0.000451244	18	N	289	308
P54728	Parental	FQQMR	QIIQQNPSLLPALLQQIGR	ENPQL	3		710.7518231	2129.232069	0.000451244	14	N	289	308
P54728	Parental	FACEK	NENLAANFLLQQNFDED	-	2		997.958673	1993.901746	0.001162105	3	N	399	416
P54775	Exosome	SRYKK	LQQELEFLEVQEEYIKDEQK	NLKKE	3		846.7590374	2537.253712	0.000451244	26	N	46	66
P54775	Exosome	ILVEK	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	YKKLQ	3		1224.620012	3670.836635	0.000451244	36	N	10	43
P54775	Exosome	FRLAK	ENAPAIIFIDEIDAIATK	RFDAQ	2		972.5203778	1943.025156	0.000622848	7	N	255	273
P54775	Exosome	FRLAK	ENAPAIIFIDEIDAIATK	RFDAQ	3		648.6828519	1943.025156	0.000451244	10	N	255	273
P54775	Exosome	EEVKR	IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	ILSTI	3		1185.289937	3552.846411	0.000451244	49	N	81	114
P54775	Exosome	EEVKR	IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	ILSTI	4		889.2194028	3552.846411	0.000451244	2	N	81	114
P54775	Exosome	KNLKK	EFLHAQEEVKR	IQSIP	3		462.5777698	1384.709909	0.001162105	1	N	70	81
P54775	Exosome	TGLSF	LGPEPEDLEDLYSR	YKKLQ	2		816.891739	1631.767878	0.002080925	2	N	29	43
P54775	Exosome	FRLAK	ENAPAIIFIDEIDAIATKR	FDAQT	3		700.7165556	2099.126267	0.000451244	3	N	255	274
P54775	Exosome	KQEVR	EAVELPLTHFELYK	QIGID	3		563.6351733	1687.88212	0.001654178	1	N	178	192
P54775	Parental	SRYKK	LQQELEFLEVQEEYIKDEQK	NLKKE	2		1269.634656	2537.253712	0.002080925	3	N	46	66
P54775	Parental	SRYKK	LQQELEFLEVQEEYIKDEQK	NLKKE	3		846.7590374	2537.253712	0.000451244	31	N	46	66
P54775	Parental	ILVEK	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	YKKLQ	3		1224.620012	3670.836635	0.000451244	36	N	10	43
P54775	Parental	ILVEK	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	YKKLQ	4		918.7169587	3670.836635	0.002080925	1	N	10	43
P54775	Parental	RDVFR	LAKENAPAIIFIDEIDAIATK	RFDAQ	3		752.7548989	2255.241297	0.000451244	8	N	252	273
P54775	Parental	FRLAK	ENAPAIIFIDEIDAIATK	RFDAQ	2		972.5203778	1943.025156	0.000451244	15	N	255	273
P54775	Parental	FRLAK	ENAPAIIFIDEIDAIATK	RFDAQ	3		648.6828519	1943.025156	0.000698008	7	N	255	273
P54775	Parental	EEVKR	IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	ILSTI	3		1185.289937	3552.846411	0.000451244	44	N	81	114
P54775	Parental	EEVKR	IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	ILSTI	4		889.2194028	3552.846411	0.000451244	3	N	81	114
P54818	Exosome	LQRVR	IIASDNLWEPISSSLLLDQELWK	VVDVI	2		1335.705416	2669.395232	0.000451244	6	N	222	245
P54818	Exosome	LQRVR	IIASDNLWEPISSSLLLDQELWK	VVDVI	3		890.8062105	2669.395232	0.000451244	4	N	222	245
P54818	Parental	LQRVR	IIASDNLWEPISSSLLLDQELWK	VVDVI	3		890.8062105	2669.395232	0.001763695	1	N	222	245
P54818	Parental	MSGKK	LWSSEDFSTINSNVGAGCWSR	ILNQN	2	C18:+57.021	1187.032146	2372.048693	0.000451244	1	N	269	290
P54822	Exosome	SANRR	ICLAEAFLTADTILNTLQNISEGLVVYPK	VIERR	3	C2:+57.021	1069.572463	3205.693988	0.000451244	13	N	338	367
P54822	Exosome	LIILR	NAFDLLLPK	LARVI	2		515.8007389	1029.585878	0.000451244	20	N	125	134
P54822	Exosome	HCCPK	AAGIIHLGATSCYVGDNTDLIILR	NAFDL	3	C12:+57.021	848.4480974	2542.320892	0.002981883	1	N	101	125
P54822	Exosome	IERIR	ADAYFSPIHSQLEHLLDPSSFTGR	APQQV	3		896.7737923	2687.297977	0.001654178	1	N	428	452

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P54822	Exosome	QTYTR	KVDIEVLSVLASLGASVHK	ICTDI	3		655.718008	1964.130624	0.001699387	1	N	245	264
P54822	Parental	SANRR	ICLAEAFLTADTILNTLQNISEGLVVYPK	VIERR	3	C2:+57.021	1069.572463	3205.693988	0.000451244	10	N	338	367
P54822	Parental	LIILR	NAFDLLLPK	LARVI	2		515.8007389	1029.585878	0.001395409	1	N	125	134
P54822	Parental	QTYTR	KVDIEVLSVLASLGASVHK	ICTDI	3		655.718008	1964.130624	0.002080925	2	N	245	264
P54823	Exosome	RGPVK	ASAGPGGGGTQPQPQLNQLK	NTSTI	2		953.4930173	1904.970435	0.000870037	6	N	26	46
P54823	Exosome	LPKNR	QILLYSATFPLSVQK	FMNSH	2		854.4881524	1706.960705	0.000451244	20	N	271	286
P54823	Exosome	RFNLK	SIEEQLGTEIKPIPSNIDK	SLYVA	2		1056.065681	2110.115762	0.000451244	4	N	447	466
P54823	Exosome	NGTGK	SGAYLIPLLER	LDLKK	2		616.3564097	1230.697219	0.001839721	1	N	146	157
P54823	Parental	RGPVK	ASAGPGGGGTQPQPQLNQLK	NTSTI	2		953.4930173	1904.970435	0.000451244	21	N	26	46
P54823	Parental	RFNLK	SIEEQLGTEIKPIPSNIDK	SLYVA	2		1056.065681	2110.115762	0.000451244	21	N	447	466
P54823	Parental	RFNLK	SIEEQLGTEIKPIPSNIDK	SLYVA	3		704.3797206	2110.115762	0.000451244	6	N	447	466
P54823	Parental	SNIDK	SLYVAEYHSEPAEDEKP	-	2		982.4501495	1962.884699	0.000823681	2	N	466	483
P54923	Exosome	YLELR	GILDGNSAPVFPQPFGVK	ERDQF	2		921.9915905	1841.967581	0.000622848	3	N	239	257
P54923	Exosome	EEAGR	ALYSLGSKEDPVLDP	-	2		802.41485	1602.8141	0.002296037	1	N	347	362
P55264	Exosome	AENNR	VFTLNLSAPFISQFFK	EALMD	2		930.009252	1858.002904	0.000451244	16	N	207	223
P55264	Exosome	TAFPV	LDQNQEEIIDTNGAGDAFVGGFLSQLVSDKPLTECIR	AGHYA	3	C35:+57.021	1350.663908	4048.968325	0.000451244	6	N	300	337
P55264	Exosome	ILKRK	AADAHVDAHYYEQNEQPTGTCAACITGGNR	SLVAN	3	C21:+57.021,C24:+57.021	1093.13912	3276.393959	0.000451244	9	N	118	148
P55264	Exosome	ILKRK	AADAHVDAHYYEQNEQPTGTCAACITGGNR	SLVAN	4	C21:+57.021,C24:+57.021	820.1062897	3276.393959	0.000451244	6	N	118	148
P55264	Exosome	QNSMK	VAQWLIQEPHK	AATFF	3		450.2511055	1347.729917	0.001654178	6	N	87	98
P55264	Exosome	TGGNR	SLVANLAAANCYK	KEKHL	2	C11:+57.021	697.8587593	1393.701919	0.000451244	4	N	148	161
P55264	Exosome	QEPHK	AATFFGCIGIDKFGEILK	RKAAD	3	C7:+57.021	663.0171347	1986.028004	0.000823681	1	N	98	116
P55264	Exosome	EILKR	KAADAHVDAHYYEQNEQPTGTCAACITGGNR	SLVAN	4	C22:+57.021,C25:+57.021	852.1300305	3404.488922	0.001654178	1	N	117	148
P55772	Parental	QKLAK	DIQVSSGGVLKDPCFNPGYEK	VVNVS	3	C14:+57.021	770.7075772	2309.099332	0.001162105	2	N	267	288
P55772	Parental	YLLGR	FTQEQSWLSLISDSQK	QETFG	2		948.9710521	1895.926504	0.000451244	10	N	188	204
P55772	Parental	FQGAK	IITGQEEGAYGWITINYLLGR	FTQEQ	2		1184.121322	2366.227044	0.000451244	1	N	167	188
P55937	Parental	GSLAR	LPDQQDTAQDASVEVNR	GFKEE	2		943.4484725	1884.881345	0.000451244	4	N	36	53
P55937	Parental	MLEAK	NASLASSNNDLQVAEEQYQR	LMAKV	2		1119.025607	2236.035614	0.000451244	1	N	490	510
P56391	Exosome	QNQTK	NCWQNYLDFHR	CEKAM	3	C2:+57.021	518.2302215	1551.667264	0.001329271	1	N	28	39
P56391	Exosome	RRVYK	SLCPVSWVSAWDDR	IAEGT	2	C3:+57.021	839.3884123	1676.761225	0.000451244	4	N	62	76
P56391	Parental	IKNYK	TAPFDSRFPNQNQTK	NCWQN	2		875.9295215	1749.843443	0.001463592	1	N	13	28
P56391	Parental	QNQTK	NCWQNYLDFHR	CEKAM	2	C2:+57.021	776.8414322	1551.667264	0.001463592	2	N	28	39
P56391	Parental	QNQTK	NCWQNYLDFHR	CEKAM	3	C2:+57.021	518.2302215	1551.667264	0.000451244	19	N	28	39
P56391	Parental	RRVYK	SLCPVSWVSAWDDR	IAEGT	2	C3:+57.021	839.3884123	1676.761225	0.000451244	26	N	62	76
P56391	Parental	AWDDR	IAEGTFPGKI	-	2		516.7903712	1031.565142	0.000823681	7	N	76	86
P56391	Parental	AMTAK	GGDVSVCEWYR	RVYKS	2	C7:+57.021	664.2907094	1326.565819	0.000622848	1	N	47	58
P56391	Parental	RRVYK	SLCPVSWVSAWDDRIAEGTFPGK	I-	3	C3:+57.021	860.0850476	2577.231743	0.000622848	1	N	62	85
P56395	Parental	YDLTK	FLEEHPGGEEVLREQAGGDATENFEDVGHSTDAR	ELSKT	4		925.4207218	3697.651687	0.0007646	1	N	39	73
P56395	Parental	EEVLR	EQAGGDATENFEDVGHSTDAR	ELSKT	2		1103.468122	2204.920644	0.001839721	1	N	52	73
P56399	Exosome	DKLEK	IFQNAPTDPTQDFSTQVAK	LGHGL	2		1054.518898	2107.022196	0.000451244	26	N	360	379
P56399	Exosome	DMNQR	IGEWELIQESGVPLKPLFGPGYTGIR	NLGNS	3		952.8485212	2855.522163	0.000451244	32	N	303	329
P56399	Exosome	YTGIR	NLGNSCYLNSVVQVLFSIPDFQR	KYVDK	2	C6:+57.021	1335.671153	2669.326706	0.000451244	5	N	329	352
P56399	Exosome	YTGIR	NLGNSCYLNSVVQVLFSIPDFQR	KYVDK	3	C6:+57.021	890.7833687	2669.326706	0.000451244	14	N	329	352
P56399	Exosome	PELVR	AQVPFSSCLEAYGAPEQVDDFWSTALQAK	SVAVK	3	C8:+57.021	1072.504888	3214.491265	0.000451244	29	N	524	553
P56399	Exosome	IQIKK	FTFGLDWVPK	KLDVS	2		605.3192958	1208.622992	0.000451244	9	N	575	585
P56399	Exosome	VKTTR	FASFPDYLVIQIK	KFTFG	2		770.9246565	1539.833713	0.001329271	1	N	561	574
P56399	Exosome	ISQLR	GTGLQPGEEELPDIAPPLVTPDEPK	GSLGF	2		1300.161038	2598.306476	0.000451244	11	N	603	628
P56399	Exosome	KCDMR	ENLWLNLTDGSILCGR	RYFDG	2	C14:+57.021	930.9675581	1859.919516	0.000451244	16	N	205	221
P56399	Exosome	ISEGR	SAAESISESVPVGPK	VRDGP	2		729.3782675	1456.740935	0.000622848	4	N	778	793
P56399	Exosome	AQVPF	SSCLEAYGAPEQVDDFWSTALQAK	SVAVK	2	C3:+57.021	1337.110791	2672.205982	0.002453667	1	N	529	553
P56399	Exosome	AQVPF	SSCLEAYGAPEQVDDFWSTALQAK	SVAVK	3	C3:+57.021	891.7431272	2672.205982	0.000451244	5	N	529	553
P56399	Exosome	TQVAK	LGHGLLSGEYSKPALESGDGEQVPEQK	EVQDG	3		942.4704381	2824.387914	0.000622848	5	N	379	406
P56399	Exosome	FSTNR	QQDAQEFFLHLINMVER	NCRSS	3		706.6866023	2117.036407	0.000979378	2	N	432	449
P56399	Exosome	-MAE	LSEEALLSVLPTIR	VPKAG	2		770.9514027	1539.887205	0.001943752	1	N	3	17
P56399	Exosome	IVRDR	VTSAVEALLSADSASR	KQEVQ	2		788.9130058	1575.810412	0.000622848	3	N	146	162
P56399	Exosome	PDIVR	DRVTSAVEALLSADSASR	KQEVQ	3		616.6539553	1846.938466	0.000451244	1	N	144	162
P56399	Exosome	DEDVK	IVILPDYLEIAR	DGLGG	2		707.9193742	1413.823148	0.001329271	3	N	121	133
P56399	Exosome	LEIAR	DGLGGLPDIVR	DRVTS	2		556.3094595	1110.603319	0.001463592	2	N	133	144
P56399	Parental	DKLEK	IFQNAPTDPTQDFSTQVAK	LGHGL	2		1054.518898	2107.022196	0.000451244	32	N	360	379
P56399	Parental	DMNQR	IGEWELIQESGVPLKPLFGPGYTGIR	NLGNS	2		1428.768882	2855.522163	0.000998612	1	N	303	329
P56399	Parental	DMNQR	IGEWELIQESGVPLKPLFGPGYTGIR	NLGNS	3		952.8485212	2855.522163	0.000451244	49	N	303	329
P56399	Parental	YTGIR	NLGNSCYLNSVVQVLFSIPDFQRK	YVDKL	3	C6:+57.021	933.4816897	2797.421669	0.000451244	5	N	329	353
P56399	Parental	YTGIR	NLGNSCYLNSVVQVLFSIPDFQR	KYVDK	2	C6:+57.021	1335.671153	2669.326706	0.000451244	22	N	329	352
P56399	Parental	YTGIR	NLGNSCYLNSVVQVLFSIPDFQR	KYVDK	3	C6:+57.021	890.7833687	2669.326706	0.000451244	31	N	329	352
P56399	Parental	PELVR	AQVPFSSCLEAYGAPEQVDDFWSTALQAK	SVAVK	3	C8:+57.021	1072.504888	3214.491265	0.000451244	19	N	524	553
P56399	Parental	IQIKK	FTFGLDWVPK	KLDVS	2		605.3192958	1208.622992	0.001463592	3	N	575	585

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P56399	Parental	VKTTR	FASFPDYLVIQIK	KFTFG	2		770.9246565	1539.833713	0.000622848	4	N	561	574
P56399	Parental	ISQLR	GTGLQPGEEELPDIAPPLVTPDEPK	GSLGF	2		1300.161038	2598.306476	0.000451244	10	N	603	628
P56399	Parental	KCDMR	ENLWLNLTDGSILCGR	RYFDG	2	C14:+57.021	930.9675581	1859.919516	0.000451244	5	N	205	221
P56399	Parental	TQVAK	LGHGLLSGEYSKPALESGDGEQVPEQKEVQDGIAPR	MFKAL	3		1264.301453	3789.880959	0.000451244	5	N	379	415
P56399	Parental	TQVAK	LGHGLLSGEYSKPALESGDGEQVPEQKEVQDGIAPR	MFKAL	4		948.4780398	3789.880959	0.000451244	1	N	379	415
P56399	Parental	ISEGR	SAAESISESVPVGPK	VRDGP	2		729.3782675	1456.740935	0.000637154	3	N	778	793
P56399	Parental	AQVPF	SSCLEAYGAPEQVDDFWSTALQAK	SVAVK	2	C3:+57.021	1337.110791	2672.205982	0.002080925	1	N	529	553
P56399	Parental	TQVAK	LGHGLLSGEYSKPALESGDGEQVPEQK	EVQDG	3		942.4704381	2824.387914	0.000622848	12	N	379	406
P56399	Parental	DEDVK	IVILPDYLEIAR	DGLGG	2		707.9193742	1413.823148	0.001591523	2	N	121	133
P56480	Exosome	AKGGK	IGLFGGAGVGK	TVLIM	2		488.285256	974.554912	0.000823681	2	N	201	212
P56480	Exosome	GRDSR	LVLEVAQHLGESTVR	TIAMD	2		825.962833	1649.910066	0.000735798	1	N	94	109
P56480	Exosome	GRDSR	LVLEVAQHLGESTVR	TIAMD	3		550.977822	1649.910066	0.000451244	4	N	94	109
P56480	Exosome	VRGQK	VLDSGAPIKIPVGPETLGR	IMNVI	2		960.0521795	1918.088759	0.000823681	3	N	124	143
P56480	Exosome	VRGQK	VLDSGAPIKIPVGPETLGR	IMNVI	3		640.3707197	1918.088759	0.000451244	1	N	124	143
P56480	Exosome	DNIFR	FTQAGSEVSALLGR	IPSAV	2		718.3811445	1434.746689	0.000451244	8	N	310	324
P56480	Exosome	TVLSR	AIAELGIYPAVDPLDSTSR	IMDPN	2		994.5209092	1987.026218	0.000451244	33	N	387	406
P56480	Exosome	GARAR	VALTGLTVAEYFR	DQEGQ	2		720.3988059	1438.782012	0.000451244	24	N	281	294
P56480	Exosome	ITTTK	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1281.665732	3841.973797	0.000451244	16	N	350	387
P56480	Exosome	ITTTK	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	4		961.5012492	3841.973797	0.000451244	17	N	350	387
P56480	Exosome	TTTKK	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1238.967411	3713.878834	0.000451244	23	N	351	387
P56480	Exosome	AGVGK	TVLIMELINNVAK	AHGGY	2		729.423967	1456.832334	0.000451244	6	N	212	225
P56480	Exosome	KETIK	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	ADKLA	3		1117.552105	3349.632914	0.002374549	2	N	489	519
P56480	Exosome	KETIK	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	ADKLA	3	M20:+15.995	1122.883771	3365.627914	0.000622848	1	N	489	519
P56480	Exosome	AEYFR	DQEGQDVLLFIDNIFR	FTQAG	2		961.4868693	1920.958139	0.000451244	34	N	294	310
P56480	Exosome	AEYFR	DQEGQDVLLFIDNIFR	FTQAG	3		641.3271796	1920.958139	0.000451244	12	N	294	310
P56480	Exosome	RKIQR	FLSQPFQVAEVF	TGHMG	2		706.3669744	1410.718349	0.000823681	6	N	462	474
P56480	Parental	NNVAK	AHGGYSVFAGVGER	TREGN	2		703.8447291	1405.673858	0.000451244	2	N	225	239
P56480	Parental	NNVAK	AHGGYSVFAGVGER	TREGN	3		469.5657527	1405.673858	0.000451244	50	N	225	239
P56480	Parental	AKGGK	IGLFGGAGVGK	TVLIM	2		488.285256	974.554912	0.000622848	15	N	201	212
P56480	Parental	GRDSR	LVLEVAQHLGESTVR	TIAMD	2		825.962833	1649.910066	0.000451244	27	N	94	109
P56480	Parental	GRDSR	LVLEVAQHLGESTVR	TIAMD	3		550.977822	1649.910066	0.000451244	32	N	94	109
P56480	Parental	VTGIK	VVDLLAPYAK	GGKIG	2		544.8216714	1087.627743	0.000451244	30	N	188	198
P56480	Parental	VRGQK	VLDSGAPIKIPVGPETLGR	IMNVI	2		960.0521795	1918.088759	0.000451244	34	N	124	143
P56480	Parental	VRGQK	VLDSGAPIKIPVGPETLGR	IMNVI	3		640.3707197	1918.088759	0.000451244	50	N	124	143
P56480	Parental	DNIFR	FTQAGSEVSALLGR	IPSAV	2		718.3811445	1434.746689	0.000451244	29	N	310	324
P56480	Parental	TVLSR	AIAELGIYPAVDPLDSTSR	IMDPN	2		994.5209092	1987.026218	0.000451244	67	N	387	406
P56480	Parental	TVLSR	AIAELGIYPAVDPLDSTSR	IMDPN	3		663.3498728	1987.026218	0.000451244	11	N	387	406
P56480	Parental	GARAR	VALTGLTVAEYFR	DQEGQ	2		720.3988059	1438.782012	0.000451244	20	N	281	294
P56480	Parental	ITTTK	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1281.665732	3841.973797	0.000451244	53	N	350	387
P56480	Parental	ITTTK	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	4		961.5012492	3841.973797	0.000451244	29	N	350	387
P56480	Parental	TTTKK	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	AIAEL	3		1238.967411	3713.878834	0.000451244	52	N	351	387
P56480	Parental	AGVGK	TVLIMELINNVAK	AHGGY	2		729.423967	1456.832334	0.000451244	18	N	212	225
P56480	Parental	KETIK	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	ADKLA	3		1117.552105	3349.632914	0.000451244	13	N	489	519
P56480	Parental	LQDYK	SLQDIIAILGMDELSEEDKLTVSR	ARKIQ	3		892.465637	2674.373511	0.000451244	8	N	432	456
P56480	Parental	TATGR	IVAVIGAVVDVQFDEGLPPILNALEVQGR	DSRLV	3		1011.232923	3030.67537	0.000451244	213	N	62	91
P56480	Parental	AEYFR	DQEGQDVLLFIDNIFR	FTQAG	2		961.4868693	1920.958139	0.000451244	36	N	294	310
P56480	Parental	AEYFR	DQEGQDVLLFIDNIFR	FTQAG	3		641.3271796	1920.958139	0.000451244	24	N	294	310
P56480	Parental	GARAR	VALTGLTVAEYFRDQEGQDVLLFIDNIFR	FTQAG	3		1114.917663	3341.72959	0.000451244	28	N	281	310
P56480	Parental	GARAR	VALTGLTVAEYFRDQEGQDVLLFIDNIFR	FTQAG	4		836.4401976	3341.72959	0.00307782	1	N	281	310
P56480	Parental	PIKTK	QFAPIHAEAPEFIEMSVEQEILVTGIKVVDLLAPYAK	GGKIG	4		1024.79886	4095.164242	0.000451244	9	N	161	198
P56480	Parental	PIKTK	QFAPIHAEAPEFIEMSVEQEILVTGIK	VVDLL	3		1009.523486	3025.547059	0.0007646	7	N	161	188
P56480	Parental	RKIQR	FLSQPFQVAEVF	TGHMG	2		706.3669744	1410.718349	0.000451244	10	N	462	474
P56480	Parental	RKIQR	FLSQPFQVAEVFTGHMGK	LVPLK	3		675.0089053	2022.003316	0.002019181	1	N	462	480
P56480	Parental	ITTTK	KGSITSVQAIYVPADDLTDPAPATTF	AHLDA	2		1339.682138	2677.348675	0.001463592	3	N	350	376
P56480	Parental	ARARV	ALTGLTVAEYFR	DQEGQ	2		670.8645989	1339.713598	0.000451244	7	N	282	294
P56546	Parental	NVDIK	AAGELGIAVCNIPSAAVEETADSTVCHILNLYR	RNTWL	3	C10:+57.021,C26:+57.021	1172.248559	3513.722276	0.000451244	8	N	114	147
P56546	Parental	NCVNK	EFFVTSAPWSVIDQQAIHPELNGATYR	YPPGI	3		1026.177478	3075.509033	0.000451244	7	N	359	386
P56565	Exosome	KKELK	DLLQTELSGFLDVQKDADAVDK	VMKEL	3		807.4117491	2419.211847	0.000451244	6	N	35	57
P56565	Exosome	KLSKK	ELKDLLQTELSGFLDVQK	DADAV	3		692.7128112	2075.115033	0.000451244	9	N	32	50
P56565	Parental	KKELK	DLLQTELSGFLDVQKDADAVDK	VMKEL	3		807.4117491	2419.211847	0.000451244	13	N	35	57
P56565	Parental	KLSKK	ELKDLLQTELSGFLDVQK	DADAV	2		1038.565317	2075.115033	0.002884417	1	N	32	50
P56565	Parental	KLSKK	ELKDLLQTELSGFLDVQK	DADAV	3		692.7128112	2075.115033	0.000451244	10	N	32	50
P56565	Parental	KKELK	DLLQTELSGFLDVQK	DADAV	2		853.4545065	1704.893413	0.000451244	4	N	35	50
P56565	Parental	KKELK	DLLQTELSGFLDVQK	DADAV	3		569.3056043	1704.893413	0.000451244	4	N	35	50
P56812	Parental	EAEMR	NSILAQVLDQSAR	ARLSN	2		707.886594	1413.757588	0.000451244	18	N	40	53

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P56812	Parental	QLSGK	VSEQGLIEILEK	VSQQT	2		679.3828215	1356.750043	0.000451244	2	N	86	98
P56959	Exosome	RETGK	LKGEATVSFDDPPSAK	AAIDW	2		831.4232064	1660.830813	0.000637154	2	N	325	341
P56959	Exosome	RETGK	LKGEATVSFDDPPSAK	AAIDW	3		554.6180709	1660.830813	0.001264573	1	N	325	341
P56959	Exosome	PPSAK	AAIDWFDGKEFSGNPIK	VSFAT	2		947.9708551	1893.92611	0.000451244	13	N	341	358
P56959	Exosome	PPSAK	AAIDWFDGKEFSGNPIK	VSFAT	3		632.3165034	1893.92611	0.000451244	20	N	341	358
P56959	Exosome	FGGPR	DQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	4		1032.972313	4127.858052	0.000451244	2	N	262	299
P56959	Exosome	DQGSR	HDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	3		1195.880443	3584.617928	0.000451244	27	N	267	299
P56959	Parental	RETGK	LKGEATVSFDDPPSAK	AAIDW	2		831.4232064	1660.830813	0.000451244	32	N	325	341
P56959	Parental	RETGK	LKGEATVSFDDPPSAK	AAIDW	3		554.6180709	1660.830813	0.000451244	4	N	325	341
P56959	Parental	PPSAK	AAIDWFDGKEFSGNPIK	VSFAT	2		947.9708551	1893.92611	0.000451244	5	N	341	358
P56959	Parental	PPSAK	AAIDWFDGKEFSGNPIK	VSFAT	3		632.3165034	1893.92611	0.000451244	5	N	341	358
P56959	Parental	FGGPR	DQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	3		1376.960484	4127.858052	0.000451244	12	N	262	299
P56959	Parental	FGGPR	DQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	4		1032.972313	4127.858052	0.000451244	8	N	262	299
P56959	Parental	DQGSR	HDSEQDNSDNNTIFVQGLGENVTIESVADYFK	QIGII	3		1195.880443	3584.617928	0.000451244	26	N	267	299
P56959	Parental	NNTIF	VQGLGENVTIESVADYFK	QIGII	2		984.9998096	1967.984019	0.000451244	31	N	281	299
P56959	Parental	PPSAK	AAIDWFDGKEF	SGNPI	2		649.8067496	1297.597899	0.001654178	4	Y	341	352
P56959	Parental	TGKLK	GEATVSFDDPPSAK	AAIDW	2		710.8336927	1419.651785	0.001763695	1	Y	327	341
P57716	Exosome	RLDSR	SFFWNVAPGAESAVASFVTQLAAAEALHK	APDVT	3		1007.182451	3018.523954	0.000823681	3	N	284	313
P57716	Exosome	VRLAR	ALSPAFELSQWSSTEYSTWAESR	WKDIQ	2		1317.111879	2632.208159	0.001839721	1	N	628	651
P57716	Parental	RLDSR	SFFWNVAPGAESAVASFVTQLAAAEALHKAPDVTTLSR	NVMFV	4		990.7632376	3959.02175	0.000823681	5	N	284	322
P57716	Parental	RLDSR	SFFWNVAPGAESAVASFVTQLAAAEALHK	APDVT	3		1007.182451	3018.523954	0.000698008	1	N	284	313
P57716	Parental	KFPVR	LENIDSFVELGQVALR	TSLDL	2		901.9865052	1801.95741	0.000451244	2	N	354	370
P57746	Exosome	IRAKK	DNVAGVTLPVFEHYHEGTDSYELTGLAR	GGEQL	3		1030.832147	3089.473041	0.000451244	4	N	98	126
P57746	Parental	IRAKK	DNVAGVTLPVFEHYHEGTDSYELTGLAR	GGEQL	3		1030.832147	3089.473041	0.000451244	10	N	98	126
P57746	Parental	LAEAK	FTAGDFSTTVIQNVNK	AQVKI	2		871.4419304	1740.868261	0.000622848	1	N	73	89
P57759	Exosome	EELQK	SLNILTAFR	KKEAE	2		517.8038129	1033.592026	0.000622848	21	N	244	253
P57759	Parental	EELQK	SLNILTAFR	KKEAE	2		517.8038129	1033.592026	0.000451244	35	N	244	253
P57759	Parental	GLHTK	GALPLDTVTF	YKVIP	2		517.282379	1032.549158	0.001329271	1	N	38	48
P57759	Parental	YKLDK	ESYPVFYLFR	DGDLE	2		660.8353101	1319.65502	0.002019181	2	N	114	124
P57780	Exosome	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	2		1102.014314	2202.013028	0.000451244	8	N	772	792
P57780	Exosome	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	3		735.0121426	2202.013028	0.000451244	53	N	772	792
P57780	Exosome	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	4		551.511057	2202.013028	0.000451244	14	N	772	792
P57780	Exosome	EELRR	ELPPDQAEYCIAR	MAPYQ	2	C10:+57.021	781.3696882	1560.723776	0.000451244	37	Y	870	883
P57780	Exosome	EKTEK	QLETIDQLHLEYAKR	AAPFN	3		619.6675361	1855.979208	0.000451244	3	N	522	537
P57780	Exosome	EKTEK	QLETIDQLHLEYAKR	AAPFN	4		465.0026021	1855.979208	0.002374549	1	N	522	537
P57780	Exosome	YCIAR	MAPYQGPDAAPGALDYK	SFSTA	2		882.9172345	1763.818869	0.000451244	11	N	883	900
P57780	Exosome	SNHIK	LSGSNPYTTVTPQIINSK	WEKVQ	2		960.5078018	1919.000004	0.000451244	77	N	605	623
P57780	Exosome	YDKLR	KDDPVTNLNNAFEVAEK	YLDIP	2		952.4739589	1902.932318	0.000451244	8	N	217	234
P57780	Exosome	YDKLR	KDDPVTNLNNAFEVAEK	YLDIP	3		635.3185726	1902.932318	0.000451244	19	N	217	234
P57780	Exosome	KVQEK	CQLEINFNTLQTK	LRLSN	2	C1:+39.994	796.3929379	1590.770276	0.000451244	5	Y	351	364
P57780	Exosome	KVQEK	CQLEINFNTLQTK	LRLSN	2	C1:+57.021	804.9064379	1607.797276	0.000451244	45	Y	351	364
P57780	Exosome	KVQEK	CQLEINFNTLQTK	LRLSN	2	[0:-17.027,C1:+57.021	796.3929379	1590.770276	0.000451244	4	Y	351	364
P57780	Exosome	DFMSR	ETTDTDTADQVIASFK	VLAGD	2		871.410493	1740.805386	0.000451244	24	N	838	854
P57780	Exosome	EDYER	LASDLLEWIR	RTIPW	2		608.3407596	1214.665919	0.000622848	20	Y	301	311
P57780	Exosome	TIILR	FAIQDISVEETSAKEGLLLWCQR	KTAPY	3	C21:+57.021	898.4586621	2692.352586	0.000451244	18	Y	153	176
P57780	Exosome	KQYER	SIVDYKPSLDLLEQQHQLIQEALIFDNK	HTNYT	3		1099.917552	3296.729256	0.000451244	32	N	696	724
P57780	Exosome	KQYER	SIVDYKPSLDLLEQQHQLIQEALIFDNK	HTNYT	4		825.190114	3296.729256	0.000451244	4	N	696	724
P57780	Exosome	RDGLK	LMLLLEVISGER	LPKPE	2		686.897585	1371.77957	0.000451244	28	Y	84	96
P57780	Exosome	TTIAR	TINEVENQILTR	DAKGI	2		715.3864268	1428.757254	0.000451244	49	Y	746	758
P57780	Exosome	EQAEK	GYEEWLLNEIR	RLERL	2		711.357138	1420.698676	0.000451244	18	Y	396	407
P57780	Exosome	AHQDR	VEQIAAIAQELNELDYYDSHNVNTR	CQKIC	3		969.137459	2904.388977	0.000451244	46	N	470	495
P57780	Exosome	AHQDR	VEQIAAIAQELNELDYYDSHNVNTR	CQKIC	4		727.1050443	2904.388977	0.000451244	2	N	470	495
P57780	Exosome	MEHIR	VGWEQLLTTIAR	TINEV	2		693.891148	1385.766696	0.000451244	85	Y	734	746
P57780	Exosome	MEHIR	VGWEQLLTTIAR	TINEV	3		462.930032	1385.766696	0.000870037	3	Y	734	746
P57780	Exosome	LDIPK	MLDAEDIVNTARPDEK	AIMTY	3		606.2968919	1815.867276	0.000637154	7	N	240	256
P57780	Exosome	SKGVK	LVSIGAEEIVDGNAK	MTLGM	2		757.9071921	1513.798784	0.000698008	1	N	126	141
P57780	Exosome	TRCQK	ICDQWDNLGSLTHSR	REALE	3	C2:+57.021	601.2814216	1800.820865	0.000451244	14	N	498	513
P57780	Exosome	EKTEK	QLETIDQLHLEYAK	RAAPF	2		850.9468486	1699.878097	0.000451244	22	N	522	536
P57780	Exosome	EKTEK	QLETIDQLHLEYAK	RAAPF	3		567.6338324	1699.878097	0.000451244	23	N	522	536
P57780	Exosome	EKTEK	QLETIDQLHLEYAK	RAAPF	2	[0:-17.027	842.4333486	1682.851097	0.000451244	8	N	522	536
P57780	Exosome	TIILR	FAIQDISVEETSAK	EGLLL	2		769.3913749	1536.76715	0.000823681	33	Y	153	167
P57780	Exosome	HISWK	DGLAFNALIHR	HRPEL	2		613.8361757	1225.656751	0.000451244	16	N	194	205
P57780	Exosome	HISWK	DGLAFNALIHR	HRPEL	3		409.5600505	1225.656751	0.002663018	1	N	194	205
P57780	Exosome	IASFK	VLAGDKNFITAEELR	RELPP	2		838.4548408	1674.894082	0.000451244	10	N	854	869
P57780	Exosome	SHLRK	AGTQIENIDEDFRDGLK	LMLLL	2		960.9690407	1919.922481	0.000451244	9	N	67	84

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P57780	Exosome	SHLRK	AGTQIENIDEDFRDGLK	LMLLL	3		640.9819605	1919.922481	0.000622848	2	N	67	84
P57780	Exosome	EHLRR	QFASQANMVGPWIQTK	MEEIG	2		903.4543185	1804.893037	0.000622848	1	N	653	669
P57780	Exosome	EHLRR	QFASQANMVGPWIQTK	MEEIG	2	M8:+15.995	911.4518185	1820.888037	0.000451244	17	N	653	669
P57780	Exosome	ETSAK	EGLLLWCQR	KTAPY	2	C7:+57.021	587.8057984	1173.595997	0.000870037	10	Y	167	176
P57780	Exosome	DKLRK	DDPVTNLNNAFEVAEK	YLDIP	2		888.4264774	1774.837355	0.00091018	2	N	218	234
P57780	Exosome	PEEFK	ACLISLGYDVENDRQGDAEFNR	IMSVV	3	C2:+57.021	848.0594497	2541.154949	0.000451244	12	N	792	814
P57780	Exosome	PEEFK	ACLISLGYDVENDR	QGDAE	2	C2:+57.021	812.8857024	1623.755805	0.001654178	1	N	792	806
P57780	Exosome	KQQRK	TFTAWCNSHLR	KAGTQ	2	C6:+57.021	696.8277935	1391.639987	0.000634081	2	Y	55	66
P57780	Exosome	EQAEK	GYEEWLLNEIRR	LERLD	3		526.6077291	1576.799787	0.000451244	11	Y	396	408
P57780	Exosome	EDYER	LASDLLEWIRR	TIPWL	3		457.9301435	1370.76703	0.001654178	6	Y	301	312
P57780	Exosome	PSEGR	MVSDINNGWQHLEQAEKGYEEWLLNEIR	RLERL	4	M1:+15.995	855.1602095	3416.609638	0.001264573	1	N	379	407
P57780	Exosome	RPDEK	AIMTYVSSFYHAFSGAQK	AETAA	3		669.9931438	2006.956031	0.002453667	1	Y	256	274
P57780	Exosome	MFIVH	TIEEIEGLISAHDQFK	STLPD	2		915.4681452	1828.92069	0.000451244	4	N	559	575
P57780	Exosome	MFIVH	TIEEIEGLISAHDQFK	STLPD	3		610.6480302	1828.92069	0.000451244	3	N	559	575
P57780	Exosome	MLKQR	DYETATLSDIK	ALIRK	2		628.3067794	1254.597959	0.000451244	6	N	440	451
P57780	Parental	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	2		1102.014314	2202.013028	0.000451244	6	N	772	792
P57780	Parental	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	3		735.0121426	2202.013028	0.000451244	34	N	772	792
P57780	Parental	MQEFR	ASFNHFDKDHGGALGPEEFK	ACLIS	4		551.511057	2202.013028	0.000451244	17	N	772	792
P57780	Parental	EELRR	ELPPDQAEYCIAR	MAPYQ	2	C10:+57.021	781.3696882	1560.723776	0.000451244	39	Y	870	883
P57780	Parental	EKTEK	QLETIDQLHLEYAKR	AAPFN	3		619.6675361	1855.979208	0.000622848	3	N	522	537
P57780	Parental	EKTEK	QLETIDQLHLEYAKR	AAPFN	4		465.0026021	1855.979208	0.0007646	3	N	522	537
P57780	Parental	EKTEK	QLETIDQLHLEYAKR	AAPFN	3	[0:-17.027	613.9918695	1838.952208	0.000735798	1	N	522	537
P57780	Parental	YCIAR	MAPYQGPDAAPGALDYK	SFSTA	2		882.9172345	1763.818869	0.000451244	12	N	883	900
P57780	Parental	SNHIK	LSGSNPYTTVTPQIINSK	WEKVQ	2		960.5078018	1919.000004	0.000451244	60	N	605	623
P57780	Parental	YDKLR	KDDPVTNLNNAFEVAEK	YLDIP	2		952.4739589	1902.932318	0.000451244	17	N	217	234
P57780	Parental	YDKLR	KDDPVTNLNNAFEVAEK	YLDIP	3		635.3185726	1902.932318	0.000451244	11	N	217	234
P57780	Parental	KVQEK	CQLEINFNTLQTK	LRLSN	2	C1:+57.021	804.9064379	1607.797276	0.000451244	35	Y	351	364
P57780	Parental	KVQEK	CQLEINFNTLQTK	LRLSN	2	[0:-17.027,C1:+57.021	796.3929379	1590.770276	0.001943752	1	Y	351	364
P57780	Parental	DFMSR	ETTDTDTADQVIASFK	VLAGD	2		871.410493	1740.805386	0.000451244	28	N	838	854
P57780	Parental	EDYER	LASDLLEWIR	RTIPW	2		608.3407596	1214.665919	0.000823681	17	Y	301	311
P57780	Parental	TIILR	FAIQDISVEETSAKEGLLLWCQR	KTAPY	3	C21:+57.021	898.4586621	2692.352586	0.000451244	19	Y	153	176
P57780	Parental	KQYER	SIVDYKPSLDLLEQQHQLIQEALIFDNK	HTNYT	3		1099.917552	3296.729256	0.000451244	34	N	696	724
P57780	Parental	KQYER	SIVDYKPSLDLLEQQHQLIQEALIFDNK	HTNYT	4		825.190114	3296.729256	0.000451244	7	N	696	724
P57780	Parental	RDGLK	LMLLLEVISGER	LPKPE	2		686.897585	1371.77957	0.000451244	9	Y	84	96
P57780	Parental	TTIAR	TINEVENQILTR	DAKGI	2		715.3864268	1428.757254	0.000451244	20	Y	746	758
P57780	Parental	EQAEK	GYEEWLLNEIR	RLERL	2		711.357138	1420.698676	0.000451244	22	Y	396	407
P57780	Parental	EQAEK	GYEEWLLNEIR	RLERL	3		474.5740253	1420.698676	0.001591523	2	Y	396	407
P57780	Parental	AHQDR	VEQIAAIAQELNELDYYDSHNVNTR	CQKIC	2		1453.202289	2904.388977	0.002884417	1	N	470	495
P57780	Parental	AHQDR	VEQIAAIAQELNELDYYDSHNVNTR	CQKIC	3		969.137459	2904.388977	0.000451244	30	N	470	495
P57780	Parental	AHQDR	VEQIAAIAQELNELDYYDSHNVNTR	CQKIC	4		727.1050443	2904.388977	0.000451244	2	N	470	495
P57780	Parental	MEHIR	VGWEQLLTTIAR	TINEV	2		693.891148	1385.766696	0.000451244	35	Y	734	746
P57780	Parental	MEHIR	VGWEQLLTTIAR	TINEV	3		462.930032	1385.766696	0.002080925	5	Y	734	746
P57780	Parental	LDIPK	MLDAEDIVNTARPDEK	AIMTY	3		606.2968919	1815.867276	0.001763695	2	N	240	256
P57780	Parental	SKGVK	LVSIGAEEIVDGNAK	MTLGM	2		757.9071921	1513.798784	0.000451244	25	N	126	141
P57780	Parental	TRCQK	ICDQWDNLGSLTHSR	REALE	2	C2:+57.021	901.4182324	1800.820865	0.000451244	3	N	498	513
P57780	Parental	TRCQK	ICDQWDNLGSLTHSR	REALE	3	C2:+57.021	601.2814216	1800.820865	0.000451244	5	N	498	513
P57780	Parental	EKTEK	QLETIDQLHLEYAK	RAAPF	2		850.9468486	1699.878097	0.000451244	12	N	522	536
P57780	Parental	EKTEK	QLETIDQLHLEYAK	RAAPF	3		567.6338324	1699.878097	0.000451244	21	N	522	536
P57780	Parental	EKTEK	QLETIDQLHLEYAK	RAAPF	2	[0:-17.027	842.4333486	1682.851097	0.000451244	5	N	522	536
P57780	Parental	TIILR	FAIQDISVEETSAK	EGLLL	2		769.3913749	1536.76715	0.00091018	7	Y	153	167
P57780	Parental	HISWK	DGLAFNALIHR	HRPEL	2		613.8361757	1225.656751	0.000998612	3	N	194	205
P57780	Parental	HISWK	DGLAFNALIHR	HRPEL	3		409.5600505	1225.656751	0.00307782	1	N	194	205
P57780	Parental	IASFK	VLAGDKNFITAEELR	RELPP	2		838.4548408	1674.894082	0.000451244	8	N	854	869
P57780	Parental	SHLRK	AGTQIENIDEDFRDGLK	LMLLL	2		960.9690407	1919.922481	0.000637154	1	N	67	84
P57780	Parental	ETSAK	EGLLLWCQR	KTAPY	2	C7:+57.021	587.8057984	1173.595997	0.000979378	5	Y	167	176
P57780	Parental	PEEFK	ACLISLGYDVENDRQGDAEFNR	IMSVV	2	C2:+57.021	1271.585275	2541.154949	0.000451244	8	N	792	814
P57780	Parental	PEEFK	ACLISLGYDVENDRQGDAEFNR	IMSVV	3	C2:+57.021	848.0594497	2541.154949	0.000451244	16	N	792	814
P57780	Parental	PEEFK	ACLISLGYDVENDR	QGDAE	2	C2:+57.021	812.8857024	1623.755805	0.000451244	5	N	792	806
P57780	Parental	KQQRK	TFTAWCNSHLR	KAGTQ	2	C6:+57.021	696.8277935	1391.639987	0.002080925	2	Y	55	66
P57780	Parental	EQAEK	GYEEWLLNEIRR	LERLD	3		526.6077291	1576.799787	0.000451244	10	Y	396	408
P57780	Parental	KALIR	KHEAFESDLAAHQDR	VEQIA	4		439.2122891	1752.817957	0.000622848	6	Y	455	470
P57780	Parental	PPDQA	EYCIARMAPYQGPDAAPGALDYK	SFSTA	3	C3:+57.021,M7:+15.995	858.3985552	2572.172266	0.00307782	1	N	877	900
P57780	Parental	TAPYK	NVNVQNFHISWK	DGLAF	2		743.3840215	1484.752443	0.001699387	1	N	182	194
P57784	Exosome	NRICR	IGEGLDQALPCLTELILTNNSLVELGDLDPLASLK	SLTYL	3	C11:+57.021	1245.664298	3733.969495	0.000451244	22	N	78	113
P57784	Exosome	ELDLR	GYKIPVIENLGATLDQFDAIDFSDNEIR	KLDGF	3		1051.863336	3152.566607	0.000622848	3	N	27	55

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P57784	Exosome	-MVK	LTAELIEQAAQYTNAVR	DRELD	2		946.0001439	1889.984688	0.000451244	9	N	3	20
P57784	Exosome	-M	VKLTAELIEQAAQYTNAVR	DRELD	3		706.7238216	2117.148065	0.001699387	1	N	1	20
P57784	Exosome	LASLK	SLTYLSILR	NPVTN	2		533.3192958	1064.622992	0.001839721	2	N	113	122
P57784	Parental	NRICR	IGEGLDQALPCLTELILTNNSLVELGDLDPLASLK	SLTYL	3	C11:+57.021	1245.664298	3733.969495	0.000451244	26	N	78	113
P57784	Parental	NRICR	IGEGLDQALPCLTELILTNNSLVELGDLDPLASLK	SLTYL	4	C11:+57.021	934.5001736	3733.969495	0.000451244	7	N	78	113
P57784	Parental	ELDLR	GYKIPVIENLGATLDQFDAIDFSDNEIR	KLDGF	3		1051.863336	3152.566607	0.000451244	3	N	27	55
P57784	Parental	-MVK	LTAELIEQAAQYTNAVR	DRELD	2		946.0001439	1889.984688	0.000451244	10	N	3	20
P57784	Parental	-M	VKLTAELIEQAAQYTNAVR	DRELD	2		1059.581832	2117.148065	0.001162105	2	N	1	20
P57784	Parental	-M	VKLTAELIEQAAQYTNAVR	DRELD	3		706.7238216	2117.148065	0.000622848	3	N	1	20
P57784	Parental	YKIPV	IENLGATLDQFDAIDFSDNEIR	KLDGF	2		1248.598605	2495.18161	0.000451244	4	N	33	55
P57784	Parental	ARRSK	TFNPGAGLPTDK	KKGGP	2		609.3121991	1216.608798	0.000823681	2	N	179	191
P57784	Parental	VEAIK	NAIANASTLAEVER	LKGLL	2		729.8815086	1457.747417	0.001329271	1	N	205	219
P57784	Parental	PGRER	RSGPSDEGEEEIEDDTVTNGS	-	2		1111.962535	2221.90947	0.000622848	3	N	234	255
P57784	Parental	LRGYK	IPVIENLGATLDQFDAIDFSDNEIR	KLDGF	2		1403.201226	2804.386852	0.000823681	1	N	30	55
P57784	Parental	LRGYK	IPVIENLGATLDQFDAIDFSDNEIR	KLDGF	3		935.8034173	2804.386852	0.002981883	1	N	30	55
P58058	Exosome	RQEIR	HGDSISITTSCYPLPSICVCDPVSDWFESLAQCLHWNVR	KKQAH	4	C11:+57.021,C18:+57.021,C20:+57.021,C33:+57.021	1152.52769	4606.079558	0.000823681	3	N	387	426
P58058	Exosome	YVEKK	VLEDPAIVSDENFGPVK	KKFCT	2		914.9705208	1827.925442	0.000451244	23	N	142	159
P58058	Exosome	PICPH	SLSFRPIVVPAGVELK	IMLSP	3		571.3422127	1711.003238	0.000870037	3	N	347	363
P58058	Exosome	SITTS	CYPLPSICVCDPVSDWFESLAQCLHWNVR	KKQAH	3	C1:+57.021,C8:+57.021,C10:+57.021,C23:+57.021	1203.545356	3607.612669	0.002727428	1	N	397	426
P58058	Exosome	PRDKK	TAIHNGLSENGLDTEGGK	QAMQY	3		604.9627888	1811.864967	0.000451244	1	N	253	271
P58058	Parental	RQEIR	HGDSISITTSCYPLPSICVCDPVSDWFESLAQCLHWNVR	KKQAH	4	C11:+57.021,C18:+57.021,C20:+57.021,C33:+57.021	1152.52769	4606.079558	0.00091018	6	N	387	426
P58058	Parental	YVEKK	VLEDPAIVSDENFGPVK	KKFCT	2		914.9705208	1827.925442	0.000451244	14	N	142	159
P58252	Exosome	VVSYR	ETVSEESNVLCLSK	SPNKH	2	C11:+57.021	797.8853681	1593.755136	0.000451244	48	N	580	594
P58252	Exosome	KARAR	YLAEKYEWDVAEAR	KIWCF	2		871.9233735	1741.831147	0.000451244	21	N	633	647
P58252	Exosome	KARAR	YLAEKYEWDVAEAR	KIWCF	3		581.6181823	1741.831147	0.001352548	4	N	633	647
P58252	Exosome	PTARR	CLYASVLTAQPR	LMEPI	2	C1:+57.021	689.861302	1377.707004	0.000451244	3	N	727	739
P58252	Exosome	PTARR	CLYASVLTAQPR	LMEPI	2	[0:-17.027,C1:+57.021	681.347802	1360.680004	0.000451244	10	N	727	739
P58252	Exosome	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	2		1072.043071	2142.070543	0.000451244	2	N	605	625
P58252	Exosome	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	3		715.0313143	2142.070543	0.000451244	36	N	605	625
P58252	Exosome	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	4		536.5254357	2142.070543	0.000451244	40	N	605	625
P58252	Exosome	MFVVK	AYLPVNESFGFTADLR	SNTGG	2		900.4522982	1798.888996	0.000451244	57	N	785	801
P58252	Exosome	MFVVK	AYLPVNESFGFTADLR	SNTGG	3		600.6374654	1798.888996	0.000451244	27	N	785	801
P58252	Exosome	VAEAR	KIWCFGPDGTGPNILTDITK	GVQYL	2	C4:+57.021	1117.070012	2232.124424	0.000451244	27	N	647	667
P58252	Exosome	VAEAR	KIWCFGPDGTGPNILTDITK	GVQYL	3	C4:+57.021	745.0492747	2232.124424	0.000451244	34	N	647	667
P58252	Exosome	TADLR	SNTGGQAFPQCVFDHWQILPGDPFDNSSRPSQVVAETR	KRKGL	3	C11:+57.021	1415.666646	4243.976539	0.000451244	43	N	801	839
P58252	Exosome	TADLR	SNTGGQAFPQCVFDHWQILPGDPFDNSSRPSQVVAETR	KRKGL	4	C11:+57.021	1062.001935	4243.976539	0.000451244	115	N	801	839
P58252	Exosome	KKLPR	TFCQLILDPIFK	VFDAI	2	C3:+57.021	747.9051782	1493.794756	0.000451244	73	N	287	299
P58252	Exosome	KKLPR	TFCQLILDPIFK	VFDAI	3	C3:+57.021	498.9393855	1493.794756	0.000698008	3	N	287	299
P58252	Exosome	AEARK	IWCFGPDGTGPNILTDITK	GVQYL	2	C3:+57.021	1053.02253	2104.029461	0.000451244	32	N	648	667
P58252	Exosome	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	2		1177.113497	2352.211394	0.000451244	33	N	667	688
P58252	Exosome	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	3		785.0782645	2352.211394	0.000451244	43	N	667	688
P58252	Exosome	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	4		589.0606484	2352.211394	0.000622848	2	N	667	688
P58252	Exosome	NKMDR	ALLELQLEPEELYQTFQR	IVENV	2		1110.581498	2219.147396	0.000451244	46	N	162	180
P58252	Exosome	NKMDR	ALLELQLEPEELYQTFQR	IVENV	3		740.7235988	2219.147396	0.000451244	30	N	162	180
P58252	Exosome	LMMGR	YVEPIEDVPCGNIVGLVGVDQFLVK	TGTIT	2	C10:+57.021	1380.220144	2758.424689	0.000451244	52	N	456	481
P58252	Exosome	LMMGR	YVEPIEDVPCGNIVGLVGVDQFLVK	TGTIT	3	C10:+57.021	920.4826963	2758.424689	0.000451244	71	N	456	481
P58252	Exosome	RKGLK	EGIPALDNFLDKL	-	2		722.888271	1443.760942	0.000451244	40	N	845	858
P58252	Exosome	IKQSK	DGSGFLINLIDSPGHVDFSSEVTAALR	VTDGA	2		1409.206843	2816.398085	0.000451244	17	N	93	120
P58252	Exosome	IKQSK	DGSGFLINLIDSPGHVDFSSEVTAALR	VTDGA	3		939.8071617	2816.398085	0.000451244	112	N	93	120
P58252	Exosome	CITIK	STAISLFYELSENDLNFIK	QSKDG	2		1102.560231	2203.104863	0.000451244	64	N	71	90
P58252	Exosome	CITIK	STAISLFYELSENDLNFIK	QSKDG	3		735.3760876	2203.104863	0.000451244	24	N	71	90
P58252	Exosome	-M	VNFTVDQIR	AIMDK	2		546.2963521	1090.577104	0.000451244	2	N	1	10
P58252	Exosome	TAQPR	LMEPIYLVEIQCPEQVVGGIYGVLNR	KRGHV	3	C12:+57.021	997.1894073	2988.544822	0.000451244	21	N	739	765
P58252	Exosome	TAQPR	LMEPIYLVEIQCPEQVVGGIYGVLNR	KRGHV	3	M2:+15.995,C12:+57.021	1002.521074	3004.539822	0.002374549	1	N	739	765
P58252	Exosome	VDHGK	STLTDSLVCK	AGIIA	2	C9:+57.021	562.2871041	1122.558608	0.000451244	7	N	32	42
P58252	Exosome	TAALR	VTDGALVVVDCVSGVCVQTETVLR	QAIAE	2	C11:+57.021,C16:+57.021	1288.656623	2575.297645	0.000451244	29	N	120	144
P58252	Exosome	TAALR	VTDGALVVVDCVSGVCVQTETVLR	QAIAE	3	C11:+57.021,C16:+57.021	859.4403484	2575.297645	0.000823681	4	N	120	144
P58252	Exosome	VPCGN	IVGLVGVDQFLVK	TGTIT	2		693.9219169	1385.828234	0.001162105	1	N	468	481
P58252	Exosome	AISLF	YELSENDLNFIK	QSKDG	2		742.8675356	1483.719471	0.000451244	8	N	78	90
P58252	Exosome	KGVQY	LNEIKDSVVAGFQWATK	EGALC	3		636.0076698	1904.99961	0.000451244	7	N	671	688
P58252	Exosome	LMMGR	YVEPIEDVPCGNIVGLVGVDQF	LVKTG	2	C10:+57.021	1210.096424	2418.177248	0.001943752	1	N	456	478
P58252	Exosome	IKQSK	DGSGFLINLIDSPGHVDF	SSEVT	2		951.9657697	1901.915939	0.0007646	3	N	93	111

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P58252	Exosome	AVMRR	WLPAGDALLQMITIHLPSPVTAQK	YRCEL	3		867.4810045	2599.419614	0.000622848	6	N	342	366
P58252	Exosome	EICLK	DLEEDHACIPIKK	SDPVV	3	C8:+57.021	523.2647089	1566.770727	0.000637154	4	N	559	572
P58252	Exosome	DPIFK	VFDAIMNFR	KEETA	2		556.7820238	1111.548448	0.002145581	1	N	299	308
P58252	Exosome	VTAQK	YRCELLYEGPPDDEAAMGIK	SCDPK	3	C3:+57.021,M17:+15.995	781.6929681	2342.055504	0.001162105	2	N	366	386
P58252	Exosome	AQKYR	CELLYEGPPDDEAAMGIK	SCDPK	2	C1:+57.021	1004.455832	2006.896064	0.001264573	1	N	368	386
P58252	Exosome	AQKYR	CELLYEGPPDDEAAMGIK	SCDPK	2	C1:+57.021,M15:+15.995	1012.453332	2022.891064	0.001162105	6	N	368	386
P58252	Exosome	IPTAR	RCLYASVLTAQPR	LMEPI	3	C2:+57.021	512.2771717	1533.808115	0.00091018	2	N	726	739
P58252	Exosome	KAVMR	RWLPAGDALLQMITIHLPSPVTAQK	YRCEL	4		689.8879812	2755.520725	0.000451244	1	N	341	366
P58252	Exosome	EPIYL	VEIQCPEQVVGGIYGVLNR	KRGHV	2	C5:+57.021	1065.554529	2129.093458	0.000823681	1	N	746	765
P58252	Parental	VVSYR	ETVSEESNVLCLSK	SPNKH	2	C11:+57.021	797.8853681	1593.755136	0.000451244	16	N	580	594
P58252	Parental	KARAR	YLAEKYEWDVAEAR	KIWCF	2		871.9233735	1741.831147	0.000451244	22	N	633	647
P58252	Parental	KARAR	YLAEKYEWDVAEAR	KIWCF	3		581.6181823	1741.831147	0.000662267	3	N	633	647
P58252	Parental	PTARR	CLYASVLTAQPR	LMEPI	2	C1:+57.021	689.861302	1377.707004	0.000451244	23	N	727	739
P58252	Parental	PTARR	CLYASVLTAQPR	LMEPI	2	[0:-17.027,C1:+57.021	681.347802	1360.680004	0.000451244	5	N	727	739
P58252	Parental	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	2		1072.043071	2142.070543	0.000451244	17	N	605	625
P58252	Parental	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	3		715.0313143	2142.070543	0.000451244	13	N	605	625
P58252	Parental	RLYMK	ARPFPDGLAEDIDKGEVSAR	QELKA	4		536.5254357	2142.070543	0.000451244	34	N	605	625
P58252	Parental	MFVVK	AYLPVNESFGFTADLR	SNTGG	2		900.4522982	1798.888996	0.000451244	57	N	785	801
P58252	Parental	MFVVK	AYLPVNESFGFTADLR	SNTGG	3		600.6374654	1798.888996	0.000451244	6	N	785	801
P58252	Parental	VAEAR	KIWCFGPDGTGPNILTDITK	GVQYL	2	C4:+57.021	1117.070012	2232.124424	0.000451244	28	N	647	667
P58252	Parental	VAEAR	KIWCFGPDGTGPNILTDITK	GVQYL	3	C4:+57.021	745.0492747	2232.124424	0.000451244	44	N	647	667
P58252	Parental	TADLR	SNTGGQAFPQCVFDHWQILPGDPFDNSSRPSQVVAETR	KRKGL	3	C11:+57.021	1415.666646	4243.976539	0.000451244	51	N	801	839
P58252	Parental	TADLR	SNTGGQAFPQCVFDHWQILPGDPFDNSSRPSQVVAETR	KRKGL	4	C11:+57.021	1062.001935	4243.976539	0.000451244	85	N	801	839
P58252	Parental	KKLPR	TFCQLILDPIFK	VFDAI	2	C3:+57.021	747.9051782	1493.794756	0.000451244	34	N	287	299
P58252	Parental	KKLPR	TFCQLILDPIFK	VFDAI	3	C3:+57.021	498.9393855	1493.794756	0.001463592	1	N	287	299
P58252	Parental	AEARK	IWCFGPDGTGPNILTDITK	GVQYL	2	C3:+57.021	1053.02253	2104.029461	0.000451244	34	N	648	667
P58252	Parental	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	2		1177.113497	2352.211394	0.000451244	17	N	667	688
P58252	Parental	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	3		785.0782645	2352.211394	0.000451244	11	N	667	688
P58252	Parental	TDITK	GVQYLNEIKDSVVAGFQWATK	EGALC	4		589.0606484	2352.211394	0.000451244	6	N	667	688
P58252	Parental	NKMDR	ALLELQLEPEELYQTFQR	IVENV	2		1110.581498	2219.147396	0.000451244	36	N	162	180
P58252	Parental	NKMDR	ALLELQLEPEELYQTFQR	IVENV	3		740.7235988	2219.147396	0.000451244	22	N	162	180
P58252	Parental	LMMGR	YVEPIEDVPCGNIVGLVGVDQFLVK	TGTIT	2	C10:+57.021	1380.220144	2758.424689	0.000451244	42	N	456	481
P58252	Parental	LMMGR	YVEPIEDVPCGNIVGLVGVDQFLVK	TGTIT	3	C10:+57.021	920.4826963	2758.424689	0.000451244	50	N	456	481
P58252	Parental	RKGLK	EGIPALDNFLDKL	-	2		722.888271	1443.760942	0.000451244	25	N	845	858
P58252	Parental	IKQSK	DGSGFLINLIDSPGHVDFSSEVTAALR	VTDGA	2		1409.206843	2816.398085	0.000451244	23	N	93	120
P58252	Parental	IKQSK	DGSGFLINLIDSPGHVDFSSEVTAALR	VTDGA	3		939.8071617	2816.398085	0.000451244	127	N	93	120
P58252	Parental	CITIK	STAISLFYELSENDLNFIK	QSKDG	2		1102.560231	2203.104863	0.000451244	41	N	71	90
P58252	Parental	CITIK	STAISLFYELSENDLNFIK	QSKDG	3		735.3760876	2203.104863	0.000451244	14	N	71	90
P58252	Parental	CITIK	STAISLFYELSENDLNFIKQSK	DGSGF	2		1274.153016	2546.290432	0.001352548	1	N	71	93
P58252	Parental	CITIK	STAISLFYELSENDLNFIKQSK	DGSGF	3		849.7712773	2546.290432	0.000451244	9	N	71	93
P58252	Parental	-M	VNFTVDQIR	AIMDK	2		546.2963521	1090.577104	0.001591523	1	N	1	10
P58252	Parental	VKAYL	PVNESFGFTADLR	SNTGG	2		726.8600449	1451.70449	0.000451244	4	N	788	801
P58252	Parental	TAQPR	LMEPIYLVEIQCPEQVVGGIYGVLNR	KRGHV	3	C12:+57.021	997.1894073	2988.544822	0.000451244	12	N	739	765
P58252	Parental	TAALR	VTDGALVVVDCVSGVCVQTETVLR	QAIAE	2	C11:+57.021,C16:+57.021	1288.656623	2575.297645	0.000451244	52	N	120	144
P58252	Parental	TAALR	VTDGALVVVDCVSGVCVQTETVLR	QAIAE	3	C11:+57.021,C16:+57.021	859.4403484	2575.297645	0.001162105	1	N	120	144
P58252	Parental	PVVSY	RETVSEESNVLCLSK	SPNKH	2	C12:+57.021	875.9359237	1749.856247	0.000451244	8	N	579	594
P58252	Parental	AISLF	YELSENDLNFIK	QSKDG	2		742.8675356	1483.719471	0.000622848	1	N	78	90
P58252	Parental	KGVQY	LNEIKDSVVAGFQWATK	EGALC	2		953.5076048	1904.99961	0.000451244	14	N	671	688
P58252	Parental	LMMGR	YVEPIEDVPCGNIVGLVGVDQF	LVKTG	2	C10:+57.021	1210.096424	2418.177248	0.000622848	12	N	456	478
P58252	Parental	MYVAK	FAAKGEGQLSAAER	AKKVE	3		478.9165626	1433.726288	0.000451244	8	N	235	249
P58252	Parental	IKQSK	DGSGFLINLIDSPGHVDF	SSEVT	2		951.9657697	1901.915939	0.000622848	3	N	93	111
P58252	Parental	YLAEK	YEWDVAEAR	KIWCF	2		569.7623421	1137.509084	0.001763695	4	N	638	647
P58252	Parental	EPIYL	VEIQCPEQVVGGIYGVLNR	KRGHV	2	C5:+57.021	1065.554529	2129.093458	0.000451244	3	N	746	765
P58252	Parental	LKEGI	PALDNFLDKL	-	2		573.3142105	1144.612821	0.000979378	4	N	848	858
P58252	Parental	LPRTF	CQLILDPIFK	VFDAI	2	C1:+57.021	623.8471319	1245.678664	0.00091018	1	N	289	299
P58389	Exosome	TWYAK	LDQEAENLVATVVPTHLAAAVPEVAVYLK	EAVGN	3		1020.892567	3059.6543	0.000451244	35	N	111	140
P58389	Exosome	GKWKR	SQAYADYIGFILTLNEGVK	GKKLT	2		1051.544384	2101.073169	0.000451244	1	N	41	60
P58389	Exosome	GNSTR	IDYGTGHEAAFAAFLCCLCK	IGVLR	3	C16:+57.021,C17:+57.021,C19:+57.021	768.6797796	2303.015939	0.001329271	3	N	148	168
P58389	Exosome	DTLDR	WIDETPPVDQPSR	FGNKA	2		770.3760591	1538.736518	0.000622848	3	N	86	99
P58389	Exosome	EAIEK	LVALLDTLDR	WIDET	2		564.8353101	1127.65502	0.002453667	2	N	76	86
P58389	Parental	TWYAK	LDQEAENLVATVVPTHLAAAVPEVAVYLK	EAVGN	3		1020.892567	3059.6543	0.000451244	25	N	111	140
P58389	Parental	EAIEK	LVALLDTLDRWIDETPPVDQPSR	FGNKA	3		883.8014595	2648.380978	0.000451244	8	N	76	99
P58389	Parental	GKWKR	SQAYADYIGFILTLNEGVK	GKKLT	2		1051.544384	2101.073169	0.001352548	2	N	41	60
P58389	Parental	DTLDR	WIDETPPVDQPSR	FGNKA	2		770.3760591	1538.736518	0.000622848	4	N	86	99

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P58389	Parental	EAIEK	LVALLDTLDR	WIDET	2		564.8353101	1127.65502	0.002296037	1	N	76	86
P58742	Parental	AVLMK	GNPQVQDGNPVILLFR	TRNSP	2		883.9815571	1765.947514	0.000451244	1	N	416	432
P58742	Parental	HLSLR	SEDLIAEFAQVTNWSSCCLR	VFAWH	2	C17:+57.021,C18:+57.021	1193.543801	2385.072002	0.000870037	1	N	135	155
P58742	Parental	LFRTR	NSPVFELLPCGIIQGEPGAQAQLITFHPSFNK	GALLS	3	C10:+57.021	1170.601415	3508.780846	0.000451244	12	N	434	466
P59108	Exosome	EEAAR	DIVQFVPFR	EFRNA	2		560.811638	1119.607676	0.000451244	25	Y	500	509
P59108	Exosome	ETLAK	AVLAELPQQVVQYFK	HKNLP	2		866.9857768	1731.955954	0.000451244	13	N	521	536
P59108	Exosome	FDQDK	SSAQLDEHDFLGQFSCSLGTIVSSK	KITRP	3	C16:+57.021	905.0976816	2712.269645	0.001699387	1	N	100	125
P59108	Parental	EEAAR	DIVQFVPFR	EFRNA	2		560.811638	1119.607676	0.000698008	12	Y	500	509
P59108	Parental	ETLAK	AVLAELPQQVVQYFK	HKNLP	2		866.9857768	1731.955954	0.000451244	8	N	521	536
P59108	Parental	DVTSK	SDPFCVLFIEDNGR	WMEFD	2	C5:+57.021	834.8882451	1667.76089	0.000451244	3	N	43	57
P59108	Parental	PPDWK	VSHEFAINFNPTNPFCSGVDGIAQAYSACLPHIR	FYGPT	3	C16:+57.021,C29:+57.021	1263.935086	3788.781857	0.000451244	1	N	372	406
P59108	Parental	PPDWK	VSHEFAINFNPTNPFCSGVDGIAQAYSACLPHIR	FYGPT	4	C16:+57.021,C29:+57.021	948.2032642	3788.781857	0.000622848	4	N	372	406
P59108	Parental	FDQDK	SSAQLDEHDFLGQFSCSLGTIVSSK	KITRP	3	C16:+57.021	905.0976816	2712.269645	0.000979378	2	N	100	125
P59325	Exosome	TVEER	VNILFDFVK	KKKEE	2		547.816389	1093.617178	0.000451244	10	N	237	246
P59325	Parental	TVEER	VNILFDFVK	KKKEE	2		547.816389	1093.617178	0.001943752	3	N	237	246
P59325	Parental	GFIKK	FVLCPECENPETDLHVNPK	KQTIG	2	C4:+57.021,C7:+57.021	1149.530162	2297.044725	0.000823681	2	N	95	114
P59325	Parental	GFIKK	FVLCPECENPETDLHVNPK	KQTIG	3	C4:+57.021,C7:+57.021	766.6893749	2297.044725	0.001264573	4	N	95	114
P59708	Exosome	TPETR	GTAYVVYEDIFDAK	NACDH	2		795.888468	1589.761336	0.001763695	1	N	57	71
P59708	Parental	IFDAK	NACDHLSGFNVCNR	YLVVL	2	C3:+57.021,C12:+57.021	832.3568892	1662.698178	0.000698008	4	N	71	85
P59708	Parental	TPETR	GTAYVVYEDIFDAK	NACDH	2		795.888468	1589.761336	0.001463592	2	N	57	71
P59999	Exosome	VRSSK	ELLLQPVTISR	NEKEK	2		634.8827917	1267.749983	0.001162105	25	N	44	55
P59999	Exosome	LSAVR	ATLQAALCLENFSSQVVER	HNKPE	2	C8:+57.021	1068.541619	2135.067637	0.000451244	146	N	13	32
P59999	Parental	VRSSK	ELLLQPVTISR	NEKEK	2		634.8827917	1267.749983	0.001162105	5	N	44	55
P59999	Parental	LSAVR	ATLQAALCLENFSSQVVER	HNKPE	2	C8:+57.021	1068.541619	2135.067637	0.000451244	24	N	13	32
P59999	Parental	LSAVR	ATLQAALCLENFSSQVVER	HNKPE	3	C8:+57.021	712.6970125	2135.067637	0.000451244	13	N	13	32
P60122	Exosome	TYLHR	ALESSIAPIVIFASNR	GNCVI	3		563.3179557	1686.930467	0.000451244	21	N	317	333
P60122	Exosome	IIKIR	AQTEGINISEEALNHLGEIGTK	TTLRY	3		775.3963219	2323.165566	0.001763695	3	N	378	400
P60122	Exosome	NCVIR	GTEDITSPHGIPLDLLDR	VMIIR	2		975.0028836	1947.990167	0.000823681	1	N	339	357
P60122	Exosome	NCVIR	GTEDITSPHGIPLDLLDR	VMIIR	3		650.3378557	1947.990167	0.000451244	2	N	339	357
P60122	Exosome	KTTLR	YSVQLLTPANLLAK	INGKD	2		765.948663	1529.881726	0.000823681	6	N	404	418
P60122	Exosome	PGTGK	TALALAIAQELGSK	VPFCP	2		693.4040883	1384.792577	0.000451244	21	N	76	90
P60122	Exosome	KVVNK	YIDQGVAELVPGVLF	VDEVH	2		810.4381281	1618.860656	0.000622848	2	N	285	300
P60122	Parental	TYLHR	ALESSIAPIVIFASNR	GNCVI	3		563.3179557	1686.930467	0.000451244	23	N	317	333
P60122	Parental	KRQGR	CDTYATEFDLEAEEYVPLPK	GDVHK	2	C1:+57.021	1195.541147	2389.066694	0.000451244	15	N	205	225
P60122	Parental	NCVIR	GTEDITSPHGIPLDLLDR	VMIIR	2		975.0028836	1947.990167	0.000823681	2	N	339	357
P60122	Parental	NCVIR	GTEDITSPHGIPLDLLDR	VMIIR	3		650.3378557	1947.990167	0.000451244	4	N	339	357
P60122	Parental	KTTLR	YSVQLLTPANLLAK	INGKD	2		765.948663	1529.881726	0.002212458	1	N	404	418
P60122	Parental	PGTGK	TALALAIAQELGSK	VPFCP	2		693.4040883	1384.792577	0.000451244	18	N	76	90
P60229	Exosome	YRYAK	FQYECGNYSGAAEYLYFFR	VLVPA	2	C5:+57.021	1193.017976	2384.020353	0.000451244	9	N	136	155
P60229	Exosome	HFLDR	HLVFPLLEFLSVK	EIYNE	3		514.641711	1540.901733	0.001162105	3	N	16	29
P60229	Parental	YRYAK	FQYECGNYSGAAEYLYFFR	VLVPA	2	C5:+57.021	1193.017976	2384.020353	0.000451244	12	N	136	155
P60229	Parental	EDLTR	LKETIDNNSVSSPLQSLQQR	TWLIH	2		1129.093293	2256.170985	0.001162105	1	N	191	211
P60229	Parental	QKKLR	ECESVLVNDFFLVACLEDFIENAR	LFIFE	3	C2:+57.021,C15:+57.021	963.7861844	2888.335153	0.000451244	4	N	313	337
P60229	Parental	HFLDR	HLVFPLLEFLSVK	EIYNE	3		514.641711	1540.901733	0.001839721	2	N	16	29
P60229	Parental	GAQKK	LRECESVLVNDFFLVACLEDFIENAR	LFIFE	3	C4:+57.021,C17:+57.021	1053.514576	3157.520328	0.000622848	7	N	311	337
P60335	Exosome	NSTER	AITIAGVPQSVTECVK	QICLV	2	C14:+57.021	836.9508454	1671.886091	0.000451244	5	N	144	160
P60335	Exosome	NCPER	IITLTGPTNAIFK	AFAMI	2		694.9115491	1387.807498	0.000451244	10	N	57	70
P60335	Exosome	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	2		1089.100389	2176.185179	0.000451244	14	N	325	346
P60335	Exosome	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	3		726.4028596	2176.185179	0.000451244	11	N	325	346
P60335	Exosome	SPEVK	GYWASLDASTQTTHELTIPNNLIGCIIGR	QGANI	3	C25:+57.021	1067.871794	3200.591982	0.001763695	1	N	268	297
P60335	Exosome	IKEIR	ESTGAQVQVAGDMLPNSTER	AITIA	2	M13:+15.995	1053.492597	2104.969595	0.000451244	17	Y	124	144
P60335	Parental	NSTER	AITIAGVPQSVTECVK	QICLV	2	C14:+57.021	836.9508454	1671.886091	0.000451244	28	N	144	160
P60335	Parental	GGQDR	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	LNQVA	4	C1:+39.994	982.9669166	3927.836466	0.000451244	4	N	200	237
P60335	Parental	GGQDR	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	LNQVA	3	C1:+57.021	1315.962289	3944.863466	0.000451244	17	N	200	237
P60335	Parental	GGQDR	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	LNQVA	4	C1:+57.021	987.2236666	3944.863466	0.000451244	29	N	200	237
P60335	Parental	GGQDR	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	LNQVA	3	[0:-17.027,C1:+57.021	1310.286622	3927.836466	0.000735798	4	N	200	237
P60335	Parental	GGQDR	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	LNQVA	4	[0:-17.027,C1:+57.021	982.9669166	3927.836466	0.000451244	10	N	200	237
P60335	Parental	NCPER	IITLTGPTNAIFK	AFAMI	2		694.9115491	1387.807498	0.000622848	16	N	57	70
P60335	Parental	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	2		1089.100389	2176.185179	0.000451244	32	N	325	346
P60335	Parental	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	3		726.4028596	2176.185179	0.000451244	22	N	325	346
P60335	Parental	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	2	Q1:-17.027	1080.586889	2159.158179	0.001654178	3	N	325	346
P60335	Parental	GSSGR	QVTITGSAASISLAQYLINAR	LSSEK	2	[0:-17.027	1080.586889	2159.158179	0.000662267	6	N	325	346
P60335	Parental	SPEVK	GYWASLDASTQTTHELTIPNNLIGCIIGR	QGANI	3	C25:+57.021	1067.871794	3200.591982	0.000451244	17	N	268	297
P60335	Parental	PVTLR	LVVPATQCGSLIGK	GGCKI	2	C8:+57.021	721.9057095	1441.795819	0.000823681	1	N	101	115
P60670	Exosome	SVGLK	AFGAPNVVEDEIDQYLSK	QDGKI	2		997.9894418	1993.963284	0.000451244	14	N	98	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P60670	Exosome	PLGIR	AEVAAIYEPPQIGTQNSLELLEDPKAEVVDEIAAK	LGLRK	3		1250.982838	3749.925115	0.000823681	5	N	267	302
P60670	Exosome	TTFPK	DPVYTFSISQNPFPIENR	DVLGE	2		1062.523983	2123.032366	0.000622848	2	N	458	476
P60670	Exosome	QTWKK	SEQWATIEQLCSTVGVQLPGLHEFGAVGGSAR	AATSA	3	C11:+57.021	1128.893258	3383.656374	0.002727428	2	N	545	577
P60670	Parental	SVGLK	AFGAPNVVEDEIDQYLSK	QDGKI	2		997.9894418	1993.963284	0.000451244	4	N	98	116
P60670	Parental	PLGIR	AEVAAIYEPPQIGTQNSLELLEDPKAEVVDEIAAK	LGLRK	3		1250.982838	3749.925115	0.000979378	3	N	267	302
P60670	Parental	QTWKK	SEQWATIEQLCSTVGVQLPGLHEFGAVGGSAR	AATSA	3	C11:+57.021	1128.893258	3383.656374	0.000451244	4	N	545	577
P60670	Parental	PIENR	DVLGETQDFHSLATYLSQNTSSVF	LDTIS	2		1330.130269	2658.244938	0.002884417	1	N	476	500
P60710	Exosome	MWISK	QEYDESGPSIVHR	KCF-	2		758.8554908	1515.695382	0.000451244	64	N	359	372
P60710	Exosome	MWISK	QEYDESGPSIVHR	KCF-	3		506.2395939	1515.695382	0.000451244	119	N	359	372
P60710	Exosome	MWISK	QEYDESGPSIVHR	KCF-	2	Q1:-17.027	750.3419908	1498.668382	0.00091018	40	N	359	372
P60710	Exosome	MWISK	QEYDESGPSIVHR	KCF-	3	Q1:-17.027	500.5639272	1498.668382	0.00307782	1	N	359	372
P60710	Exosome	MWISK	QEYDESGPSIVHR	KCF-	2	[0:-17.027	750.3419908	1498.668382	0.000451244	41	N	359	372
P60710	Exosome	MWISK	QEYDESGPSIVHR	KCF-	3	[0:-17.027	500.5639272	1498.668382	0.000662267	15	N	359	372
P60710	Exosome	ILTER	GYSFTTTAER	EIVRD	2		566.7676244	1131.519649	0.000451244	189	N	196	206
P60710	Exosome	DDMEK	IWHHTFYNELR	VAPEE	2		758.3787391	1514.741878	0.000451244	140	Y	84	95
P60710	Exosome	DDMEK	IWHHTFYNELR	VAPEE	3		505.9217594	1514.741878	0.000451244	697	Y	84	95
P60710	Exosome	DRMQK	EITALAPSTMK	IKIIA	2		581.3133538	1160.611108	0.000451244	62	Y	315	326
P60710	Exosome	DRMQK	EITALAPSTMK	IKIIA	2	M10:+15.995	589.3108538	1176.606108	0.000451244	21	Y	315	326
P60710	Exosome	ILTER	GYSFTTTAEREIVR	DIKEK	2		815.4157156	1628.815831	0.000662267	11	N	196	210
P60710	Exosome	ILTER	GYSFTTTAEREIVR	DIKEK	3		543.9464104	1628.815831	0.000662267	15	N	196	210
P60710	Exosome	YNELR	VAPEEHPVLLTEAPLNPK	ANREK	2		977.5363622	1953.057124	0.000451244	144	N	95	113
P60710	Exosome	YNELR	VAPEEHPVLLTEAPLNPK	ANREK	3		652.0268415	1953.057124	0.000451244	176	N	95	113
P60710	Exosome	ELRVA	PEEHPVLLTEAPLNPK	ANREK	2		892.4835983	1782.951597	0.000451244	115	N	97	113
P60710	Exosome	ELRVA	PEEHPVLLTEAPLNPK	ANREK	3		595.3249989	1782.951597	0.000451244	57	N	97	113
P60710	Exosome	SSLEK	SYELPDGQVITIGNER	FRCPE	2		895.9501196	1789.884639	0.000451244	1549	Y	238	254
P60710	Exosome	SSLEK	SYELPDGQVITIGNER	FRCPE	3		597.6360131	1789.884639	0.000451244	140	Y	238	254
P60710	Exosome	HAILR	LDLAGRDLTDYLMK	ILTER	3		541.9523969	1622.833791	0.000622848	2	Y	177	191
P60710	Exosome	HAILR	LDLAGRDLTDYLMK	ILTER	3	M13:+15.995	547.2840636	1638.828791	0.000451244	3	Y	177	191
P60710	Exosome	EKSYE	LPDGQVITIGNER	FRCPE	2		706.3811445	1410.746689	0.000823681	17	Y	241	254
P60710	Exosome	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	2		1108.039141	2214.062681	0.000451244	128	N	291	312
P60710	Exosome	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	3		739.0286938	2214.062681	0.000451244	19	N	291	312
P60710	Exosome	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	2	M14:+15.995	1116.036641	2230.057681	0.000451244	252	N	291	312
P60710	Exosome	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	3	M14:+15.995	744.3603605	2230.057681	0.000451244	47	N	291	312
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		1061.876811	3182.607033	0.000451244	52	Y	147	177
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	4		796.6595584	3182.607033	0.000451244	35	Y	147	177
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3	M6:+15.995	1067.208478	3198.602033	0.000451244	106	Y	147	177
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	4	M6:+15.995	800.6583084	3198.602033	0.000451244	70	Y	147	177
P60710	Exosome	TPAMY	VAIQAVLSLYASGR	TTGIV	2		724.41753	1446.81946	0.000451244	459	Y	133	147
P60710	Exosome	TPAMY	VAIQAVLSLYASGR	TTGIV	3		483.2809533	1446.81946	0.000451244	9	Y	133	147
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTF	NSIMK	3	C3:+57.021,C18:+57.021	987.7840097	2960.328629	0.000451244	22	N	254	279
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTF	NSIMK	3	C3:+57.021,M15:+15.995,C18:+57.021	993.1156764	2976.323629	0.000451244	39	N	254	279
P60710	Exosome	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	2	C4:+57.021	1404.159624	2806.303648	0.000451244	16	N	213	238
P60710	Exosome	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	3	C4:+57.021	936.4423494	2806.303648	0.000451244	32	N	213	238
P60710	Exosome	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	2	C4:+57.021,M14:+15.995	1412.157124	2822.298648	0.000451244	12	N	213	238
P60710	Exosome	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	3	C4:+57.021,M14:+15.995	941.774016	2822.298648	0.000451244	23	N	213	238
P60710	Exosome	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	2	C2:+57.021	1275.590846	2549.166092	0.000451244	980	N	215	238
P60710	Exosome	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	3	C2:+57.021	850.7298306	2549.166092	0.000451244	290	N	215	238
P60710	Exosome	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	2	C2:+57.021,M12:+15.995	1283.588346	2565.161092	0.000451244	906	N	215	238
P60710	Exosome	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	3	C2:+57.021,M12:+15.995	856.0614973	2565.161092	0.000451244	581	N	215	238
P60710	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	KCF-	3		1367.346117	4099.014951	0.001699387	2	N	336	372
P60710	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	KCF-	4		1025.761538	4099.014951	0.000451244	4	N	336	372
P60710	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	KCF-	4	M19:+15.995	1029.760288	4115.009951	0.000622848	1	N	336	372
P60710	Exosome	PPERK	YSVWIGGSILASLSTF	QQMWI	2		850.94886	1699.88212	0.000451244	183	Y	336	352
P60710	Exosome	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3		1085.208517	3252.60215	0.000451244	16	N	118	147
P60710	Exosome	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M14:+15.995	1090.540183	3268.59715	0.000823681	2	N	118	147
P60710	Exosome	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M1:+15.995	1090.540183	3268.59715	0.000622848	2	N	118	147
P60710	Exosome	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M1:+15.995,M14:+15.995	1095.87185	3284.59215	0.001591523	2	N	118	147
P60710	Exosome	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M1:+15.995,M5:+15.995	1095.87185	3284.59215	0.000823681	3	N	118	147
P60710	Exosome	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M1:+15.995,M5:+15.995,M14:+15.995	1101.203517	3300.58715	0.002019181	1	N	118	147
P60710	Exosome	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M5:+15.995	1090.540183	3268.59715	0.002453667	2	N	118	147
P60710	Exosome	NELRV	APEEHPVLLTEAPLNPK	ANREK	2		928.0021552	1853.98871	0.000451244	5	N	96	113
P60710	Exosome	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	2		1172.086622	2342.157645	0.000451244	16	N	290	312
P60710	Exosome	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	3		781.7270149	2342.157645	0.000451244	2	N	290	312

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P60710	Exosome	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	2	M15:+15.995	1180.084122	2358.152645	0.000451244	43	N	290	312
P60710	Exosome	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	3	M15:+15.995	787.0586815	2358.152645	0.000451244	39	N	290	312
P60710	Exosome	QQMWI	SKQEYDESGPSIVHR	KCF-	3		577.9485911	1730.822373	0.001654178	1	N	357	372
P60710	Exosome	FYNEL	RVAPEEHPVLLTEAPLNPK	ANREK	2		1055.586918	2109.158236	0.000451244	7	N	94	113
P60710	Exosome	FYNEL	RVAPEEHPVLLTEAPLNPK	ANREK	3		704.0605452	2109.158236	0.000451244	43	N	94	113
P60710	Exosome	YNELR	VAPEEHPVLL	TEAPL	2		552.3089281	1102.602256	0.000823681	14	N	95	105
P60710	Exosome	RKDLY	ANTVLSGGTTMYPGIADR	MQKEI	2		912.4519728	1822.888346	0.000451244	12	N	294	312
P60710	Exosome	RKDLY	ANTVLSGGTTMYPGIADR	MQKEI	2	M11:+15.995	920.4494728	1838.883346	0.000451244	42	N	294	312
P60710	Exosome	LEKSY	ELPDGQVITIGNER	FRCPE	2		770.9024411	1539.789282	0.000451244	9	Y	240	254
P60710	Exosome	VTHTV	PIYEGYALPHAILR	LDLAG	2		806.9464546	1611.877309	0.000451244	5	Y	163	177
P60710	Exosome	VTHTV	PIYEGYALPHAILR	LDLAG	3		538.3002364	1611.877309	0.000451244	26	Y	163	177
P60710	Exosome	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	2		1291.156424	2580.297249	0.000451244	3	Y	153	177
P60710	Exosome	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		861.1068829	2580.297249	0.000451244	38	Y	153	177
P60710	Exosome	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	4		646.0821122	2580.297249	0.000451244	12	Y	153	177
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	2		1365.65814	2729.30068	0.002884417	1	Y	147	173
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	3		910.7746934	2729.30068	0.000451244	40	Y	147	173
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	2	M6:+15.995	1373.65564	2745.29568	0.001395409	4	Y	147	173
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	3	M6:+15.995	916.1063601	2745.29568	0.000451244	2	Y	147	173
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+39.994,M13:+15.995,C16:+57.021,M27:+15.995	1082.813324	3245.416573	0.00091018	5	N	256	284
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,C16:+57.021	1077.825658	3230.453573	0.000451244	13	N	256	284
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,C16:+57.021,M27:+15.995	1083.157324	3246.448573	0.002519933	3	N	256	284
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,M13:+15.995,C16:+57.021	1083.157324	3246.448573	0.000451244	3	N	256	284
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,M13:+15.995,C16:+57.021,M27:+15.995	1088.488991	3262.443573	0.000451244	40	N	256	284
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	4	C1:+57.021,M13:+15.995,C16:+57.021,M27:+15.995	816.6186932	3262.443573	0.000823681	1	N	256	284
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	[0:-	1072.149991	3213.426573	0.000735798	1	N	256	284
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	2	C1:+39.994,M13:+15.995,C16:+57.021	1329.071352	2656.127104	0.001162105	5	N	256	279
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	3	C1:+39.994,M13:+15.995,C16:+57.021	886.3835013	2656.127104	0.002884417	1	N	256	279
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	2	C1:+57.021,C16:+57.021	1329.587352	2657.159104	0.000622848	8	N	256	279
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	2	C1:+57.021,M13:+15.995,C16:+57.021	1337.584852	2673.154104	0.000451244	25	N	256	279
P60710	Exosome	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	3	C1:+57.021,M13:+15.995,C16:+57.021	892.059168	2673.154104	0.000451244	14	N	256	279
P60710	Exosome	GMGQK	DSYVGDEAQSK	RGILT	2		599.7652787	1197.514957	0.000451244	79	Y	50	61
P60710	Exosome	WISKQ	EYDESGPSIVHR	KCF-	2		694.826202	1387.636804	0.000451244	6	N	360	372
P60710	Exosome	GIVMD	SGDGVTHTVPIYEGYALPHAILR	LDLAG	4		617.3253764	2465.270306	0.002145581	1	Y	154	177
P60710	Exosome	SSSLE	KSYELPDGQVITIGNER	FRCPE	2		959.9976012	1917.979602	0.000451244	31	Y	237	254
P60710	Exosome	SSSLE	KSYELPDGQVITIGNER	FRCPE	3		640.3343341	1917.979602	0.000451244	14	Y	237	254
P60710	Exosome	KLCYV	ALDFEQEMATAASSSSLEK	SYELP	2		1007.96785	2013.920099	0.000451244	5	N	219	238
P60710	Exosome	KLCYV	ALDFEQEMATAASSSSLEK	SYELP	2	M8:+15.995	1015.96535	2029.915099	0.000451244	36	N	219	238
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGY	ALPHA	2		1156.541713	2311.067826	0.000622848	6	Y	147	169
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGY	ALPHA	2	M6:+15.995	1164.539213	2327.062826	0.000451244	16	Y	147	169
P60710	Exosome	PAMYV	AIQAVLSLYASGR	TTGIV	2		674.883323	1347.751046	0.000451244	6	Y	134	147
P60710	Exosome	SSLEK	SYELPDGQVITI	GNERF	2		667.8460718	1333.676544	0.000451244	16	Y	238	250
P60710	Exosome	EKLCY	VALDFEQEMATAASSSSLEK	SYELP	2		1057.502057	2112.988513	0.000451244	4	N	218	238
P60710	Exosome	EKLCY	VALDFEQEMATAASSSSLEK	SYELP	2	M9:+15.995	1065.499557	2128.983513	0.000451244	18	N	218	238
P60710	Exosome	FQQMW	ISKQEYDESGPSIVHR	KCF-	3		615.6432791	1843.906437	0.000451244	8	N	356	372
P60710	Exosome	FQQMW	ISKQEYDESGPSIVHR	KCF-	4		461.9844093	1843.906437	0.000451244	3	N	356	372
P60710	Exosome	YNELR	VAPEEHPVLLTEAPLN	PKANR	2		864.9624987	1727.909397	0.001162105	6	N	95	111
P60710	Exosome	MFETF	NTPAMYVAIQAVLSLYASGR	TTGIV	2		1063.059679	2124.103758	0.001943752	1	Y	127	147
P60710	Exosome	MFETF	NTPAMYVAIQAVLSLYASGR	TTGIV	3		709.0423861	2124.103758	0.000451244	16	Y	127	147
P60710	Exosome	MFETF	NTPAMYVAIQAVLSLYASGR	TTGIV	2	M5:+15.995	1071.057179	2140.098758	0.000622848	1	Y	127	147
P60710	Exosome	MWISK	QEYDESGPSIVHRK	CF-	2	[0:-17.027	814.3894724	1626.763345	0.000622848	17	N	359	373
P60710	Exosome	MWISK	QEYDESGPSIVHRK	CF-	3	[0:-17.027	543.2622483	1626.763345	0.001943752	3	N	359	373
P60710	Exosome	SSSSL	EKSYELPDGQVITIGNER	FRCPE	2	[0:-18.011	1015.513398	2029.011196	0.001839721	6	Y	236	254
P60710	Exosome	GMGQK	DSYVGDEAQSKR	GILTL	2		677.8158343	1353.616069	0.0007646	84	Y	50	62
P60710	Exosome	GMGQK	DSYVGDEAQSKR	GILTL	3		452.2131562	1353.616069	0.000698008	28	Y	50	62
P60710	Exosome	KSYEL	PDGQVITIGNER	FRCPE	2		649.8391124	1297.662625	0.000451244	13	Y	242	254
P60710	Exosome	PPERK	YSVWIGGSILA	SLSTF	2		583.3167532	1164.617906	0.001591523	4	Y	336	347

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P60710	Exosome	RVAPE	EHPVLLTEAPLNPK	ANREK	2		779.4359198	1556.85624	0.000979378	2	N	99	113
P60710	Exosome	SLSTF	QQMWISKQEYDESGPSIVHR	KCF-	3	M3:+15.995	812.0539305	2433.138391	0.000451244	4	N	352	372
P60710	Exosome	DDAPR	AVFPSIVGRPR	HQGVM	3		400.2405408	1197.698222	0.001264573	25	Y	28	39
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C3:+57.021,C18:+57.021	1178.882166	3533.623098	0.001329271	1	N	254	284
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	4	C3:+57.021,C18:+57.021	884.4135745	3533.623098	0.000451244	9	N	254	284
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	4	C3:+57.021,C18:+57.021,M29:+15.995	888.4123245	3549.618098	0.000451244	12	N	254	284
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	4	C3:+57.021,M15:+15.995,C18:+57.021	888.4123245	3549.618098	0.000451244	5	N	254	284
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C3:+57.021,M15:+15.995,C18:+57.021,M29:+15.995	1189.545499	3565.613098	0.000451244	12	N	254	284
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	4	C3:+57.021,M15:+15.995,C18:+57.021,M29:+15.995	892.4110745	3565.613098	0.000451244	20	N	254	284
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAIL	RLDLA	3		1009.843107	3026.505922	0.000451244	4	Y	147	176
P60710	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAIL	RLDLA	3	M6:+15.995	1015.174774	3042.500922	0.000451244	10	Y	147	176
P60710	Exosome	APPER	KYSVWIGGSILASLSTF	QQMWI	2		914.9963416	1827.977083	0.000451244	165	Y	335	352
P60710	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2		1301.672865	2601.33013	0.000622848	7	Y	336	359
P60710	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2	M19:+15.995	1309.670365	2617.32513	0.002145581	4	Y	336	359
P60710	Exosome	SGMCK	AGFAGDDAPR	AVFPS	2		488.7283022	975.4410044	0.000451244	39	Y	18	28
P60710	Exosome	DGVTH	TVPIYEGYALPHAILR	LDLAG	2		907.0045009	1811.993402	0.000451244	10	Y	161	177
P60710	Exosome	DGVTH	TVPIYEGYALPHAILR	LDLAG	3		605.0056006	1811.993402	0.000823681	1	Y	161	177
P60710	Exosome	CYVAL	DFEQEMATAASSSSLEK	SYELP	2		915.9072607	1829.798921	0.000451244	3	N	221	238
P60710	Exosome	CYVAL	DFEQEMATAASSSSLEK	SYELP	2	M6:+15.995	923.9047607	1845.793921	0.000451244	8	N	221	238
P60710	Exosome	SSLEK	SYELPDGQVITIGNERFR	CPEAL	2		1047.534882	2093.054164	0.002453667	2	Y	238	256
P60710	Exosome	YVAIQ	AVLSLYASGR	TTGIV	2		518.7934452	1035.57129	0.000622848	1	Y	137	147
P60710	Exosome	DLYAN	TVLSGGTTMYPGIADR	MQKEI	2		819.9119521	1637.808304	0.00307782	1	N	296	312
P60710	Exosome	DLYAN	TVLSGGTTMYPGIADR	MQKEI	2	M9:+15.995	827.9094521	1653.803304	0.001162105	1	N	296	312
P60710	Exosome	EEHPV	LLTEAPLNPK	ANREK	2		548.3245782	1094.633556	0.000823681	6	Y	103	113
P60710	Exosome	HTVPI	YEGYALPHAILR	LDLAG	3		468.2546271	1401.740481	0.000823681	1	Y	165	177
P60710	Exosome	ILTLK	YPIEHGIVTNWDDMEK	IWHHT	2		973.9518056	1945.888011	0.001162105	1	N	68	84
P60710	Exosome	ILTLK	YPIEHGIVTNWDDMEK	IWHHT	2	M14:+15.995	981.9493056	1961.883011	0.001329271	1	N	68	84
P60710	Exosome	ILTLK	YPIEHGIVTNWDDMEK	IWHHT	3	M14:+15.995	654.9688037	1961.883011	0.000698008	4	N	68	84
P60710	Exosome	DLAGR	DLTDYLMK	ILTER	2		499.7473153	997.4790306	0.002145581	1	Y	183	191
P60710	Exosome	LRVAP	EEHPVLLTEAPLNPK	ANREK	2		843.9572164	1685.898833	0.000451244	4	N	98	113
P60710	Exosome	MTQIM	FETFNTPAMYVAIQAVLSLYASGR	TTGIV	2		1325.173229	2648.330858	0.000662267	1	N	123	147
P60710	Exosome	MTQIM	FETFNTPAMYVAIQAVLSLYASGR	TTGIV	3		883.7847527	2648.330858	0.000622848	6	N	123	147
P60710	Exosome	SSLEK	SYELPDGQVITIGN	ERFRC	2		753.3782675	1504.740935	0.000622848	1	Y	238	252
P60710	Exosome	LCYVA	LDFEQEMATAASSSSLEK	SYELP	2	M7:+15.995	980.4467928	1958.877986	0.001839721	1	N	220	238
P60710	Exosome	SLEKS	YELPDGQVITIGNER	FRCPE	2		852.4341054	1702.852611	0.001162105	1	Y	239	254
P60710	Exosome	SSLEK	SYELPDGQVITIGNERF	RCPEA	2		969.4843266	1936.953053	0.000451244	3	Y	238	255
P60710	Exosome	PPERK	YSVWIGGSILASLSTFQ	QMWIS	2		914.9781488	1827.940698	0.000451244	2	Y	336	353
P60710	Exosome	IRKDL	YANTVLSGGTTMYPGIADR	MQKEI	2	M12:+15.995	1001.981137	2001.946674	0.000823681	1	N	293	312
P60710	Exosome	PPERK	YSVWIGGSIL	ASLST	2		547.7981962	1093.580792	0.002981883	1	Y	336	346
P60710	Exosome	YVALD	FEQEMATAASSSSLEK	SYELP	2	M5:+15.995	866.3912892	1730.766978	0.000979378	1	N	222	238
P60710	Exosome	MDSGD	GVTHTVPIYEGYALPHAILR	LDLAG	4		552.5552675	2206.18987	0.00091018	1	Y	157	177
P60710	Exosome	LYANT	VLSGGTTMYPGIADR	MQKEI	2	M8:+15.995	777.3856128	1552.755626	0.00307782	1	Y	297	312
P60710	Exosome	IGNER	FRCPEALFQPSFLGMESCGIHETTFN	SIMKC	3	C3:+57.021,M15:+15.995,C18:+57.021	1031.129986	3090.366557	0.000451244	1	N	254	280
P60710	Parental	MWISK	QEYDESGPSIVHR	KCF-	2		758.8554908	1515.695382	0.000451244	71	N	359	372
P60710	Parental	MWISK	QEYDESGPSIVHR	KCF-	3		506.2395939	1515.695382	0.000451244	137	N	359	372
P60710	Parental	MWISK	QEYDESGPSIVHR	KCF-	2	Q1:-17.027	750.3419908	1498.668382	0.001329271	9	N	359	372
P60710	Parental	MWISK	QEYDESGPSIVHR	KCF-	2	[0:-17.027	750.3419908	1498.668382	0.001229886	20	N	359	372
P60710	Parental	MWISK	QEYDESGPSIVHR	KCF-	3	[0:-17.027	500.5639272	1498.668382	0.001463592	4	N	359	372
P60710	Parental	ILTER	GYSFTTTAER	EIVRD	2		566.7676244	1131.519649	0.000451244	124	N	196	206
P60710	Parental	DDMEK	IWHHTFYNELR	VAPEE	2		758.3787391	1514.741878	0.000451244	73	Y	84	95
P60710	Parental	DDMEK	IWHHTFYNELR	VAPEE	3		505.9217594	1514.741878	0.000451244	211	Y	84	95
P60710	Parental	DRMQK	EITALAPSTMK	IKIIA	2		581.3133538	1160.611108	0.000451244	9	Y	315	326
P60710	Parental	ILTER	GYSFTTTAEREIVR	DIKEK	2		815.4157156	1628.815831	0.000622848	8	N	196	210
P60710	Parental	ILTER	GYSFTTTAEREIVR	DIKEK	3		543.9464104	1628.815831	0.000451244	25	N	196	210
P60710	Parental	YNELR	VAPEEHPVLLTEAPLNPK	ANREK	2		977.5363622	1953.057124	0.000451244	136	N	95	113
P60710	Parental	YNELR	VAPEEHPVLLTEAPLNPK	ANREK	3		652.0268415	1953.057124	0.000451244	143	N	95	113
P60710	Parental	ELRVA	PEEHPVLLTEAPLNPK	ANREK	2		892.4835983	1782.951597	0.000451244	73	N	97	113
P60710	Parental	ELRVA	PEEHPVLLTEAPLNPK	ANREK	3		595.3249989	1782.951597	0.000451244	52	N	97	113
P60710	Parental	SSLEK	SYELPDGQVITIGNER	FRCPE	2		895.9501196	1789.884639	0.000451244	1486	Y	238	254
P60710	Parental	SSLEK	SYELPDGQVITIGNER	FRCPE	3		597.6360131	1789.884639	0.000451244	118	Y	238	254

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P60710	Parental	HAILR	LDLAGRDLTDYLMK	ILTER	2		812.4246953	1622.833791	0.000451244	6	Y	177	191
P60710	Parental	HAILR	LDLAGRDLTDYLMK	ILTER	3		541.9523969	1622.833791	0.000451244	6	Y	177	191
P60710	Parental	HAILR	LDLAGRDLTDYLMK	ILTER	3	M13:+15.995	547.2840636	1638.828791	0.002080925	1	Y	177	191
P60710	Parental	EKSYE	LPDGQVITIGNER	FRCPE	2		706.3811445	1410.746689	0.000451244	27	Y	241	254
P60710	Parental	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	2		1108.039141	2214.062681	0.000451244	81	N	291	312
P60710	Parental	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	3		739.0286938	2214.062681	0.000451244	11	N	291	312
P60710	Parental	VDIRK	DLYANTVLSGGTTMYPGIADR	MQKEI	2	M14:+15.995	1116.036641	2230.057681	0.000451244	23	N	291	312
P60710	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		1061.876811	3182.607033	0.000451244	9	Y	147	177
P60710	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	4		796.6595584	3182.607033	0.000451244	15	Y	147	177
P60710	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3	M6:+15.995	1067.208478	3198.602033	0.000451244	9	Y	147	177
P60710	Parental	TPAMY	VAIQAVLSLYASGR	TTGIV	2		724.41753	1446.81946	0.000451244	976	Y	133	147
P60710	Parental	TPAMY	VAIQAVLSLYASGR	TTGIV	3		483.2809533	1446.81946	0.000451244	14	Y	133	147
P60710	Parental	IGNER	FRCPEALFQPSFLGMESCGIHETTF	NSIMK	3	C3:+57.021,C18:+57.021	987.7840097	2960.328629	0.000451244	10	N	254	279
P60710	Parental	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	2	C4:+57.021	1404.159624	2806.303648	0.000451244	5	N	213	238
P60710	Parental	VRDIK	EKLCYVALDFEQEMATAASSSSLEK	SYELP	3	C4:+57.021	936.4423494	2806.303648	0.000451244	34	N	213	238
P60710	Parental	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	2	C2:+57.021	1275.590846	2549.166092	0.000451244	423	N	215	238
P60710	Parental	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	3	C2:+57.021	850.7298306	2549.166092	0.000451244	83	N	215	238
P60710	Parental	DIKEK	LCYVALDFEQEMATAASSSSLEK	SYELP	2	C2:+57.021,M12:+15.995	1283.588346	2565.161092	0.000451244	8	N	215	238
P60710	Parental	DIKEK	LCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNER	FRCPE	3	C2:+57.021	1441.354524	4321.040171	0.000451244	25	N	215	254
P60710	Parental	DIKEK	LCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNER	FRCPE	4	C2:+57.021	1081.267843	4321.040171	0.000622848	8	N	215	254
P60710	Parental	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	KCF-	3		1367.346117	4099.014951	0.000823681	2	N	336	372
P60710	Parental	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	KCF-	4		1025.761538	4099.014951	0.000662267	4	N	336	372
P60710	Parental	PPERK	YSVWIGGSILASLSTF	QQMWI	2		850.94886	1699.88212	0.000451244	562	Y	336	352
P60710	Parental	ANREK	MTQIMFETFNTPAMYVAIQAVLSLYASGR	TTGIV	3		1085.208517	3252.60215	0.000451244	21	N	118	147
P60710	Parental	NELRV	APEEHPVLLTEAPLNPK	ANREK	2		928.0021552	1853.98871	0.000451244	7	N	96	113
P60710	Parental	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	2		1172.086622	2342.157645	0.000451244	6	N	290	312
P60710	Parental	DVDIR	KDLYANTVLSGGTTMYPGIADR	MQKEI	3		781.7270149	2342.157645	0.0007646	6	N	290	312
P60710	Parental	DYLMK	ILTERGYSFTTTAER	EIVRD	2		872.94738	1743.87916	0.000451244	5	N	191	206
P60710	Parental	DYLMK	ILTERGYSFTTTAER	EIVRD	3		582.3008533	1743.87916	0.001162105	1	N	191	206
P60710	Parental	YNELR	VAPEEHPVLLTEAPLNPKANR	EKMTQ	3		765.7538923	2294.238277	0.000451244	3	N	95	116
P60710	Parental	LEKSY	ELPDGQVITIGNER	FRCPE	2		770.9024411	1539.789282	0.000698008	3	Y	240	254
P60710	Parental	VTHTV	PIYEGYALPHAILR	LDLAG	2		806.9464546	1611.877309	0.002212458	2	Y	163	177
P60710	Parental	VTHTV	PIYEGYALPHAILR	LDLAG	3		538.3002364	1611.877309	0.000451244	13	Y	163	177
P60710	Parental	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		861.1068829	2580.297249	0.001943752	1	Y	153	177
P60710	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	3		910.7746934	2729.30068	0.000998612	7	Y	147	173
P60710	Parental	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,C16:+57.021	1077.825658	3230.453573	0.000451244	5	N	256	284
P60710	Parental	NERFR	CPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C1:+57.021,M13:+15.995,C16:+57.021,M27:+15.995	1088.488991	3262.443573	0.001463592	1	N	256	284
P60710	Parental	NERFR	CPEALFQPSFLGMESCGIHETTF	NSIMK	2	C1:+57.021,C16:+57.021	1329.587352	2657.159104	0.000451244	5	N	256	279
P60710	Parental	GMGQK	DSYVGDEAQSK	RGILT	2		599.7652787	1197.514957	0.000451244	28	Y	50	61
P60710	Parental	FQQMW	ISKQEYDESGPSIVHR	KCF-	3		615.6432791	1843.906437	0.000451244	8	N	356	372
P60710	Parental	FQQMW	ISKQEYDESGPSIVHR	KCF-	4		461.9844093	1843.906437	0.000451244	5	N	356	372
P60710	Parental	YNELR	VAPEEHPVLLTEAPLN	PKANR	2		864.9624987	1727.909397	0.002813207	1	N	95	111
P60710	Parental	MFETF	NTPAMYVAIQAVLSLYASGR	TTGIV	3		709.0423861	2124.103758	0.001329271	1	Y	127	147
P60710	Parental	MWISK	QEYDESGPSIVHRK	CF-	3		548.9379149	1643.790345	0.000622848	15	N	359	373
P60710	Parental	MWISK	QEYDESGPSIVHRK	CF-	2	[0:-17.027	814.3894724	1626.763345	0.000823681	18	N	359	373
P60710	Parental	MWISK	QEYDESGPSIVHRK	CF-	3	[0:-17.027	543.2622483	1626.763345	0.001591523	6	N	359	373
P60710	Parental	GMGQK	DSYVGDEAQSKR	GILTL	2		677.8158343	1353.616069	0.0007646	27	Y	50	62
P60710	Parental	GMGQK	DSYVGDEAQSKR	GILTL	3		452.2131562	1353.616069	0.000622848	25	Y	50	62
P60710	Parental	KSYEL	PDGQVITIGNER	FRCPE	2		649.8391124	1297.662625	0.000451244	27	Y	242	254
P60710	Parental	SLSTF	QQMWISKQEYDESGPSIVHR	KCF-	2		1209.579496	2417.143391	0.000451244	4	N	352	372
P60710	Parental	SLSTF	QQMWISKQEYDESGPSIVHR	KCF-	3		806.7222638	2417.143391	0.000451244	2	N	352	372
P60710	Parental	DDAPR	AVFPSIVGRPR	HQGVM	3		400.2405408	1197.698222	0.001162105	38	Y	28	39
P60710	Parental	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	3	C3:+57.021,C18:+57.021	1178.882166	3533.623098	0.000451244	4	N	254	284
P60710	Parental	IGNER	FRCPEALFQPSFLGMESCGIHETTFNSIMK	CDVDI	4	C3:+57.021,C18:+57.021	884.4135745	3533.623098	0.000622848	1	N	254	284
P60710	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAIL	RLDLA	3		1009.843107	3026.505922	0.000451244	5	Y	147	176
P60710	Parental	DLAGR	DLTDYLMKILTER	GYSFT	3		537.6206472	1609.838542	0.000823681	2	Y	183	196
P60710	Parental	APPER	KYSVWIGGSILASLSTF	QQMWI	2		914.9963416	1827.977083	0.000451244	160	Y	335	352
P60710	Parental	GIADR	MQKEITALAPSTMK	IKIIA	2		774.9103671	1547.805134	0.000622848	3	Y	312	326
P60710	Parental	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2		1301.672865	2601.33013	0.000622848	2	Y	336	359
P60710	Parental	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	3		868.1178433	2601.33013	0.000622848	1	Y	336	359
P60710	Parental	SGMCK	AGFAGDDAPR	AVFPS	2		488.7283022	975.4410044	0.000622848	19	Y	18	28
P60766	Exosome	HHCPK	TPFLLVGTQIDLRDDPSTIEK	LAKNK	2		1179.631719	2357.247839	0.000451244	27	N	107	128
P60766	Exosome	HHCPK	TPFLLVGTQIDLRDDPSTIEK	LAKNK	3		786.7570796	2357.247839	0.000451244	53	N	107	128
P60766	Exosome	QKGLK	NVFDEAILAALEPPEPK	KSRRC	2		926.9887135	1851.961827	0.000451244	48	N	166	183

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P60766	Exosome	QKGLK	NVFDEAILAALEPPEPK	KSRRC	3		618.328409	1851.961827	0.000451244	80	N	166	183
P60766	Exosome	ALTQK	GLKNVFDEAILAALEPPEPK	KSRRC	3		717.7285727	2150.162318	0.001162105	3	N	163	183
P60766	Exosome	EDYDR	LRPLSYPQTDVFLVCF	SVVSP	2	C15:+57.021	978.0086947	1954.001789	0.000979378	3	N	66	82
P60766	Exosome	EDYDR	LRPLSYPQTDVFLVCFSVVSPSSFENVK	EKWVP	3	C15:+57.021	1072.553402	3214.636807	0.000451244	17	N	66	94
P60766	Exosome	GAVGK	TCLLISYTTNKFPSEYVPTVF	DNYAV	2	C2:+57.021	1240.624817	2479.234034	0.000451244	3	N	16	37
P60766	Exosome	HHCPK	TPFLLVGTQIDLR	DDPST	2		736.9277305	1471.839861	0.000451244	5	N	107	120
P60766	Exosome	EDYDR	LRPLSYPQTDVF	LVCFS	2		718.3831558	1434.750712	0.000622848	9	Y	66	78
P60766	Exosome	AVTVM	IGGEPYTLGLFDTAGQEDYDR	LRPLS	2		1159.035109	2316.054618	0.000451244	6	N	45	66
P60766	Exosome	GAVGK	TCLLISYTTNK	FPSEY	2	C2:+57.021	657.3424107	1312.669221	0.000622848	4	N	16	27
P60766	Exosome	QTDVF	LVCFSVVSPSSFENVK	EKWVP	2	C3:+57.021	899.9561278	1797.896656	0.000451244	4	N	78	94
P60766	Parental	HHCPK	TPFLLVGTQIDLRDDPSTIEK	LAKNK	2		1179.631719	2357.247839	0.000451244	19	N	107	128
P60766	Parental	HHCPK	TPFLLVGTQIDLRDDPSTIEK	LAKNK	3		786.7570796	2357.247839	0.000451244	36	N	107	128
P60766	Parental	EDYDR	LRPLSYPQTDVFLVCFSVVSPSSFENVKEK	WVPEI	3	C15:+57.021	1158.265921	3471.774364	0.001943752	2	N	66	96
P60766	Parental	EDYDR	LRPLSYPQTDVFLVCFSVVSPSSFENVKEK	WVPEI	4	C15:+57.021	868.9513909	3471.774364	0.000451244	7	N	66	96
P60766	Parental	QKGLK	NVFDEAILAALEPPEPK	KSRRC	2		926.9887135	1851.961827	0.000451244	21	N	166	183
P60766	Parental	QKGLK	NVFDEAILAALEPPEPK	KSRRC	3		618.328409	1851.961827	0.000451244	45	N	166	183
P60766	Parental	ALTQK	GLKNVFDEAILAALEPPEPK	KSRRC	2		1076.088959	2150.162318	0.000451244	2	N	163	183
P60766	Parental	ALTQK	GLKNVFDEAILAALEPPEPK	KSRRC	3		717.7285727	2150.162318	0.000622848	5	N	163	183
P60766	Parental	EDYDR	LRPLSYPQTDVFLVCF	SVVSP	2	C15:+57.021	978.0086947	1954.001789	0.000979378	4	N	66	82
P60766	Parental	EDYDR	LRPLSYPQTDVFLVCFSVVSPSSFENVK	EKWVP	3	C15:+57.021	1072.553402	3214.636807	0.000451244	18	N	66	94
P60766	Parental	GAVGK	TCLLISYTTNKFPSEYVPTVF	DNYAV	2	C2:+57.021	1240.624817	2479.234034	0.001591523	1	N	16	37
P60766	Parental	HHCPK	TPFLLVGTQIDLR	DDPST	2		736.9277305	1471.839861	0.000823681	6	N	107	120
P60766	Parental	EDYDR	LRPLSYPQTDVF	LVCFS	2		718.3831558	1434.750712	0.001264573	9	Y	66	78
P60766	Parental	PKTPF	LLVGTQIDLRDDPSTIEK	LAKNK	2		1007.047291	2012.078982	0.001162105	1	N	110	128
P60766	Parental	QTDVF	LVCFSVVSPSSFENVK	EKWVP	2	C3:+57.021	899.9561278	1797.896656	0.000622848	5	N	78	94
P60843	Exosome	ESLLR	GIYAYGFEKPSAIQQR	AILPC	2		914.4735649	1826.93153	0.000451244	5	Y	45	61
P60843	Exosome	ESLLR	GIYAYGFEKPSAIQQR	AILPC	3		609.9849766	1826.93153	0.000451244	45	Y	45	61
P60843	Exosome	SGTGK	TATFAISILQQIELDLK	ATQAL	2		952.5411133	1903.066627	0.000451244	25	N	82	99
P60843	Exosome	SGTGK	TATFAISILQQIELDLK	ATQAL	3		635.3633422	1903.066627	0.000451244	2	N	82	99
P60843	Exosome	LPCIK	GYDVIAQAQSGTGK	TATFA	2		697.8496771	1393.683754	0.000451244	20	N	68	82
P60843	Exosome	EMLSR	GFKDQIYDIFQK	LNSNT	2		751.3884382	1500.761276	0.000451244	4	N	190	202
P60843	Exosome	EMLSR	GFKDQIYDIFQK	LNSNT	3		501.2615588	1500.761276	0.000451244	26	N	190	202
P60843	Exosome	REEWK	LDTLCDLYETLTITQAVIFINTR	RKVDW	2	C5:+57.021	1357.209777	2712.403953	0.000451244	2	N	259	282
P60843	Exosome	REEWK	LDTLCDLYETLTITQAVIFINTR	RKVDW	3	C5:+57.021	905.1424511	2712.403953	0.000823681	3	N	259	282
P60843	Exosome	DLLAR	GIDVQQVSLVINYDLPTNR	ENYIH	2		1072.571465	2143.127329	0.000451244	17	N	334	353
P60843	Exosome	LEGIR	QFYINVEREEWK	LDTLC	2		820.9075264	1639.799453	0.001162105	1	N	247	259
P60843	Exosome	SGSSR	VLITTDLLAR	GIDVQ	2		557.8456778	1113.675756	0.001162105	7	N	324	334
P60843	Exosome	KTATF	AISILQQIELDLK	ATQAL	2		742.4406708	1482.865742	0.000451244	2	N	86	99
P60843	Exosome	PKYIK	MFVLDEADEMLSR	GFKDQ	2		778.360707	1554.705814	0.000823681	2	N	177	190
P60843	Exosome	DIFQK	LNSNTQVVLLSATMPSDVLEVTK	KFMRD	2		1230.157245	2458.298889	0.000823681	1	N	202	225
P60843	Exosome	DIFQK	LNSNTQVVLLSATMPSDVLEVTK	KFMRD	2	M14:+15.995	1238.154745	2474.293889	0.002080925	1	N	202	225
P60843	Exosome	KRTLR	DIETFYNTSIEEMPLNVADLI	-	2		1214.085954	2426.156307	0.000823681	1	N	385	406
P60843	Exosome	ELDLK	ATQALVLAPTR	ELAQQ	2		570.8409268	1139.666254	0.000698008	3	N	99	110
P60843	Exosome	LRGIY	AYGFEKPSAIQQR	AILPC	2		747.8891367	1493.762673	0.001763695	1	Y	48	61
P60843	Exosome	SGTGK	TATFAISILQQIELDLKATQALVLAPTR	ELAQQ	3		1009.248573	3024.72232	0.000451244	3	N	82	110
P60843	Exosome	EEDKR	TLRDIETFYNTSIEEMPLNVADLI	-	2		1399.202381	2796.389161	0.000451244	1	N	382	406
P60843	Parental	ESLLR	GIYAYGFEKPSAIQQR	AILPC	2		914.4735649	1826.93153	0.000451244	15	Y	45	61
P60843	Parental	ESLLR	GIYAYGFEKPSAIQQR	AILPC	3		609.9849766	1826.93153	0.000451244	37	Y	45	61
P60843	Parental	DLLAR	GIDVQQVSLVINYDLPTNRENYIHR	IGRGG	3		986.181222	2955.520266	0.000451244	10	N	334	359
P60843	Parental	DLLAR	GIDVQQVSLVINYDLPTNRENYIHR	IGRGG	4		739.8878665	2955.520266	0.000451244	2	N	334	359
P60843	Parental	SGTGK	TATFAISILQQIELDLK	ATQAL	2		952.5411133	1903.066627	0.000451244	6	N	82	99
P60843	Parental	LPCIK	GYDVIAQAQSGTGK	TATFA	2		697.8496771	1393.683754	0.000451244	31	N	68	82
P60843	Parental	EMLSR	GFKDQIYDIFQK	LNSNT	3		501.2615588	1500.761276	0.000451244	8	N	190	202
P60843	Parental	REEWK	LDTLCDLYETLTITQAVIFINTR	RKVDW	2	C5:+57.021	1357.209777	2712.403953	0.000451244	5	N	259	282
P60843	Parental	REEWK	LDTLCDLYETLTITQAVIFINTR	RKVDW	3	C5:+57.021	905.1424511	2712.403953	0.000451244	8	N	259	282
P60843	Parental	DLLAR	GIDVQQVSLVINYDLPTNR	ENYIH	2		1072.571465	2143.127329	0.000451244	13	N	334	353
P60843	Parental	REEWK	LDTLCDLYETLTITQAVIF	INTRR	2	C5:+57.021	1115.071886	2228.128172	0.001329271	3	N	259	278
P60843	Parental	KTATF	AISILQQIELDLK	ATQAL	2		742.4406708	1482.865742	0.000451244	7	N	86	99
P60867	Exosome	RIHKR	LIDLHSPSEIVK	QITSI	3		450.9262876	1349.755463	0.000451244	2	N	87	99
P60867	Parental	RIHKR	LIDLHSPSEIVK	QITSI	2		675.8855313	1349.755463	0.000823681	1	N	87	99
P60867	Parental	RIHKR	LIDLHSPSEIVK	QITSI	3		450.9262876	1349.755463	0.001763695	1	N	87	99
P60867	Parental	KDTGK	TPVEPEVAIHR	IRITL	3		416.5634606	1246.666982	0.001699387	1	N	8	19
P60898	Parental	IYVNK	ITHEVDELTQIIADVSQDPTLPR	TEDHP	3		864.1173362	2589.328608	0.000451244	14	N	57	80
P60898	Parental	LYACR	NCDYQQEADNSCIYVNK	ITHEV	2	C2:+57.021,C12:+57.021	1060.936095	2119.856589	0.000451244	21	N	40	57
P61022	Exosome	PLGDR	IINAFFSEGEDQVNFR	GFMRT	2		943.4581118	1884.900624	0.000451244	1	N	65	81

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P61022	Exosome	SIADR	TIQEADQDGDSAISFTEFVK	VLEKV	2		1101.016385	2200.01717	0.000622848	4	N	158	178
P61022	Parental	PLGDR	IINAFFSEGEDQVNFR	GFMRT	2		943.4581118	1884.900624	0.000451244	8	N	65	81
P61022	Parental	SIADR	TIQEADQDGDSAISFTEFVK	VLEKV	2		1101.016385	2200.01717	0.000451244	14	N	158	178
P61079	Exosome	LTISK	VLLSICSLLCDPNPDDPLVPEIAR	IYKTD	2	C6:+57.021,C10:+57.021	1353.695748	2705.375896	0.000451244	26	N	101	125
P61079	Exosome	LTISK	VLLSICSLLCDPNPDDPLVPEIAR	IYKTD	3	C6:+57.021,C10:+57.021	902.7997652	2705.375896	0.000451244	8	N	101	125
P61079	Exosome	AFTTR	IYHPNINSNGSICLDILR	SQWSP	3	C13:+57.021	700.3619641	2098.062492	0.000823681	3	N	72	90
P61079	Parental	LTISK	VLLSICSLLCDPNPDDPLVPEIAR	IYKTD	2	C6:+57.021,C10:+57.021	1353.695748	2705.375896	0.000451244	26	N	101	125
P61079	Parental	LTISK	VLLSICSLLCDPNPDDPLVPEIAR	IYKTD	3	C6:+57.021,C10:+57.021	902.7997652	2705.375896	0.000451244	30	N	101	125
P61079	Parental	AFTTR	IYHPNINSNGSICLDILR	SQWSP	2	C13:+57.021	1050.039046	2098.062492	0.000451244	8	N	72	90
P61079	Parental	AFTTR	IYHPNINSNGSICLDILR	SQWSP	3	C13:+57.021	700.3619641	2098.062492	0.001591523	1	N	72	90
P61087	Exosome	AMTLR	TVLLSLQALLAAAEPDDPQDAVVANQYK	QNPEM	3		985.1892717	2952.544415	0.000451244	3	N	107	135
P61087	Parental	AMTLR	TVLLSLQALLAAAEPDDPQDAVVANQYK	QNPEM	3		985.1892717	2952.544415	0.000451244	4	N	107	135
P61087	Parental	RFITK	IWHPNISSVTGAICLDILK	DQWAA	3	C14:+57.021	713.05436	2136.13968	0.000979378	2	N	78	97
P61089	Exosome	ALQIR	TVLLSIQALLSAPNPDDPLANDVAEQWK	TNEAQ	3		1006.864788	3017.570964	0.000451244	16	N	102	130
P61089	Exosome	ESNAR	YFHVVIAGPQDSPFEGGTFK	LELFL	2		1098.542176	2195.068752	0.000451244	2	N	33	53
P61089	Exosome	ESNAR	YFHVVIAGPQDSPFEGGTFK	LELFL	3		732.697384	2195.068752	0.000451244	22	N	33	53
P61089	Parental	KETQR	LLAEPVPGIKAEPDESNAR	YFHVV	2		1003.531808	2005.048016	0.000622848	2	N	14	33
P61089	Parental	KETQR	LLAEPVPGIKAEPDESNAR	YFHVV	3		669.3571388	2005.048016	0.000451244	7	N	14	33
P61089	Parental	ALQIR	TVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQAIETAR	AWTRL	3		1401.72431	4202.14953	0.00091018	5	N	102	141
P61089	Parental	ALQIR	TVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQAIETAR	AWTRL	4		1051.545182	4202.14953	0.000622848	7	N	102	141
P61089	Parental	ALQIR	TVLLSIQALLSAPNPDDPLANDVAEQWK	TNEAQ	3		1006.864788	3017.570964	0.000451244	28	N	102	130
P61089	Parental	ESNAR	YFHVVIAGPQDSPFEGGTFK	LELFL	2		1098.542176	2195.068752	0.000451244	4	N	33	53
P61089	Parental	ESNAR	YFHVVIAGPQDSPFEGGTFK	LELFL	3		732.697384	2195.068752	0.000451244	12	N	33	53
P61089	Parental	ESNAR	YFHVVIAGPQDSPFEGGTF	KLELF	2		1034.494694	2066.973789	0.001329271	3	N	33	52
P61161	Exosome	MIKEK	LCYVGYNIEQEQK	LALET	2	C2:+57.021	822.3906206	1642.765641	0.000451244	88	N	219	232
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	3	C1:+39.994	852.1058556	2553.294167	0.0025889	1	N	19	42
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	2	C1:+57.021	1286.168383	2570.321167	0.002374549	1	N	19	42
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	3	C1:+57.021	857.7815223	2570.321167	0.000451244	32	N	19	42
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	4	C1:+57.021	643.5880917	2570.321167	0.000451244	30	N	19	42
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	3	[0:-17.027,C1:+57.021	852.1058556	2553.294167	0.001264573	29	N	19	42
P61161	Exosome	EQEQK	LALETTVLVESYTLPDGR	IIKVG	2		989.0311097	1976.046619	0.000451244	69	N	232	250
P61161	Exosome	EQEQK	LALETTVLVESYTLPDGR	IIKVG	3		659.6900065	1976.046619	0.000451244	22	N	232	250
P61161	Exosome	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		1313.349856	3937.026167	0.000451244	184	N	258	294
P61161	Exosome	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	4		985.2643417	3937.026167	0.000451244	28	N	258	294
P61161	Exosome	LLLLR	GYAFNHSADFETVR	MIKEK	2		807.3713081	1612.727016	0.000451244	59	N	200	214
P61161	Exosome	LLLLR	GYAFNHSADFETVR	MIKEK	3		538.5834721	1612.727016	0.000451244	26	N	200	214
P61161	Exosome	DSQGR	KVVVCDNGTGFVK	CGYAG	2	C5:+57.021	711.8744094	1421.733219	0.000451244	7	N	6	19
P61161	Exosome	DSQGR	KVVVCDNGTGFVK	CGYAG	3	C5:+57.021	474.9188729	1421.733219	0.000451244	10	N	6	19
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	C1:+39.994	1037.993882	2073.972164	0.000622848	5	N	19	38
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	3	C1:+39.994	692.3318546	2073.972164	0.002080925	1	N	19	38
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	C1:+57.021	1046.507382	2090.999164	0.000451244	26	N	19	38
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	3	C1:+57.021	698.0075212	2090.999164	0.000451244	29	N	19	38
P61161	Exosome	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	[0:-17.027,C1:+57.021	1037.993882	2073.972164	0.000451244	20	N	19	38
P61161	Exosome	LFQPH	LINVEGVGVAELLFNTIQAADIDTR	SEFYK	2		1336.219222	2670.422843	0.000451244	20	N	269	294
P61161	Exosome	LFQPH	LINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		891.1487478	2670.422843	0.000451244	17	N	269	294
P61161	Exosome	SQGRK	VVVCDNGTGFVK	CGYAG	2	C4:+57.021	647.8269278	1293.638256	0.000451244	4	N	7	19
P61161	Exosome	VRMIK	EKLCYVGYNIEQEQK	LALET	2	C4:+57.021	950.9593988	1899.903198	0.000451244	29	N	217	232
P61161	Exosome	VRMIK	EKLCYVGYNIEQEQK	LALET	3	C4:+57.021	634.3088659	1899.903198	0.000451244	12	N	217	232
P61161	Exosome	SEFYK	HIVLSGGSTMYPGLPSR	LEREL	2	M10:+15.995	894.4596435	1786.903687	0.000451244	21	N	299	316
P61161	Exosome	SEFYK	HIVLSGGSTMYPGLPSR	LEREL	3	M10:+15.995	596.6423623	1786.903687	0.001329271	1	N	299	316
P61161	Exosome	VGGER	FEAPEALFQPHLINVEGVGVAELL	FNTIQ	2		1296.689569	2591.363537	0.000451244	5	N	258	282
P61161	Exosome	VGGER	FEAPEALFQPHLINVEGVGVAELL	FNTIQ	3		864.7956458	2591.363537	0.001329271	3	N	258	282
P61161	Exosome	WDDMK	HLWDYTFGPEK	LNIDT	2		696.8332987	1391.650997	0.000622848	15	N	86	97
P61161	Exosome	VAELL	FNTIQAADIDTR	SEFYK	2		682.8443948	1363.67319	0.000451244	2	N	282	294
P61161	Exosome	APEAL	FQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		1060.89497	3179.661511	0.000622848	7	N	265	294
P61161	Exosome	RSTTK	VGNIEIKDLMVGDEASELR	SMLEV	3		696.6934226	2087.056868	0.002519933	1	N	46	65
P61161	Exosome	HICPV	YEGFSLPHLTR	RLDIA	3		440.5634606	1318.666982	0.001591523	1	N	169	180
P61161	Exosome	GVGVA	ELLFNTIQAADIDTR	SEFYK	2		860.4497555	1718.883911	0.000622848	4	N	279	294
P61161	Exosome	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAA	DIDTR	3		1113.254276	3336.739427	0.001763695	1	N	258	289
P61161	Parental	MIKEK	LCYVGYNIEQEQK	LALET	2	C2:+57.021	822.3906206	1642.765641	0.000451244	45	N	219	232
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	2	C1:+57.021	1286.168383	2570.321167	0.001871652	2	N	19	42
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	3	C1:+57.021	857.7815223	2570.321167	0.000451244	31	N	19	42
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	4	C1:+57.021	643.5880917	2570.321167	0.000823681	16	N	19	42
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGRPIIR	STTKV	3	[0:-17.027,C1:+57.021	852.1058556	2553.294167	0.000823681	25	N	19	42
P61161	Parental	EQEQK	LALETTVLVESYTLPDGR	IIKVG	2		989.0311097	1976.046619	0.000451244	26	N	232	250

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P61161	Parental	EQEQK	LALETTVLVESYTLPDGR	IIKVG	3		659.6900065	1976.046619	0.000637154	1	N	232	250
P61161	Parental	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		1313.349856	3937.026167	0.000451244	57	N	258	294
P61161	Parental	VGGER	FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	4		985.2643417	3937.026167	0.000451244	20	N	258	294
P61161	Parental	LLLLR	GYAFNHSADFETVR	MIKEK	2		807.3713081	1612.727016	0.000451244	11	N	200	214
P61161	Parental	LLLLR	GYAFNHSADFETVR	MIKEK	3		538.5834721	1612.727016	0.000451244	7	N	200	214
P61161	Parental	WDDMK	HLWDYTFGPEKLNIDTR	NCKIL	2		1053.026693	2104.037786	0.000622848	1	N	86	103
P61161	Parental	WDDMK	HLWDYTFGPEKLNIDTR	NCKIL	3		702.3537287	2104.037786	0.000823681	3	N	86	103
P61161	Parental	WDDMK	HLWDYTFGPEKLNIDTR	NCKIL	4		527.0172465	2104.037786	0.000451244	3	N	86	103
P61161	Parental	MIKEK	LCYVGYNIEQEQKLALETTVLVESYTLPDGR	IIKVG	3	C2:+57.021	1201.275034	3600.801701	0.000823681	3	N	219	250
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	C1:+39.994	1037.993882	2073.972164	0.00091018	3	N	19	38
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	C1:+57.021	1046.507382	2090.999164	0.001229886	1	N	19	38
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	3	C1:+57.021	698.0075212	2090.999164	0.000622848	7	N	19	38
P61161	Parental	TGFVK	CGYAGSNFPEHIFPALVGR	PIIRS	2	[0:-17.027,C1:+57.021	1037.993882	2073.972164	0.000451244	5	N	19	38
P61161	Parental	LFQPH	LINVEGVGVAELLFNTIQAADIDTR	SEFYK	2		1336.219222	2670.422843	0.000451244	5	N	269	294
P61161	Parental	LFQPH	LINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		891.1487478	2670.422843	0.000451244	6	N	269	294
P61161	Parental	VRMIK	EKLCYVGYNIEQEQK	LALET	2	C4:+57.021	950.9593988	1899.903198	0.000451244	4	N	217	232
P61161	Parental	VGGER	FEAPEALFQPHLINVEGVGVAELL	FNTIQ	2		1296.689569	2591.363537	0.000698008	5	N	258	282
P61161	Parental	VLTLY	AQGLLTGVVVDSGDGVTHICPVYEGFSLPHLTR	RLDIA	3	C20:+57.021	1165.596441	3493.765924	0.000451244	7	N	147	180
P61161	Parental	VLTLY	AQGLLTGVVVDSGDGVTHICPVYEGFSLPHLTR	RLDIA	4	C20:+57.021	874.449281	3493.765924	0.000451244	8	N	147	180
P61161	Parental	GRIIK	VGGERFEAPEALFQPHLINVEGVGVAELL	FNTIQ	3		1030.880661	3089.618583	0.000823681	1	N	253	282
P61161	Parental	VAELL	FNTIQAADIDTR	SEFYK	2		682.8443948	1363.67319	0.000998612	2	N	282	294
P61161	Parental	APEAL	FQPHLINVEGVGVAELLFNTIQAADIDTR	SEFYK	3		1060.89497	3179.661511	0.000451244	8	N	265	294
P61164	Exosome	MDLRR	TLFSNIVLSGGSTLFK	GFGDR	2		842.4699596	1682.924319	0.000451244	28	N	292	308
P61164	Exosome	MDLRR	TLFSNIVLSGGSTLFK	GFGDR	3		561.9825731	1682.924319	0.000451244	16	N	292	308
P61164	Exosome	APQER	LYSTWIGGSILASLDTFKK	MWVSK	3		700.7178965	2099.13029	0.000979378	19	N	336	355
P61164	Exosome	LETEK	AQYYLPDGSTIEIGPSR	FRAPE	2		933.9657697	1865.915939	0.000451244	22	N	238	255
P61164	Exosome	APQER	LYSTWIGGSILASLDTFK	KMWVS	2		986.5254632	1971.035326	0.002453667	1	N	336	354
P61164	Exosome	AIKER	ACYLSINPQKDETLETEK	AQYYL	2	C2:+57.021	1070.017642	2138.019684	0.000622848	2	N	220	238
P61164	Exosome	YVYSK	DQLQTFSEEHPVLLTEAPLNPR	KNRER	2		1267.648432	2533.281264	0.000451244	6	N	96	118
P61164	Exosome	YVYSK	DQLQTFSEEHPVLLTEAPLNPR	KNRER	3		845.4348881	2533.281264	0.000451244	24	N	96	118
P61164	Exosome	PSRFR	APELLFRPDLIGEESEGIHEVLVFAIQK	SDMDL	4		788.1780123	3148.680849	0.000823681	2	N	257	285
P61164	Parental	MDLRR	TLFSNIVLSGGSTLFK	GFGDR	2		842.4699596	1682.924319	0.000451244	19	N	292	308
P61164	Parental	IGPSR	FRAPELLFRPDLIGEESEGIHEVLVFAIQK	SDMDL	4		863.9703936	3451.850374	0.001463592	2	N	255	285
P61164	Parental	APQER	LYSTWIGGSILASLDTFKK	MWVSK	3		700.7178965	2099.13029	0.001352548	4	N	336	355
P61164	Parental	LETEK	AQYYLPDGSTIEIGPSR	FRAPE	2		933.9657697	1865.915939	0.000451244	22	N	238	255
P61164	Parental	YVYSK	DQLQTFSEEHPVLLTEAPLNPR	KNRER	2		1267.648432	2533.281264	0.001763695	3	N	96	118
P61164	Parental	YVYSK	DQLQTFSEEHPVLLTEAPLNPR	KNRER	3		845.4348881	2533.281264	0.001943752	1	N	96	118
P61164	Parental	QLQTF	SEEHPVLLTEAPLNPR	KNRER	2		901.4763046	1800.937009	0.000622848	6	N	102	118
P61202	Exosome	PFISK	ELNIDVADVESLLVQCILDNTIHGR	IDQVN	3	C16:+57.021	946.1555308	2835.443193	0.000698008	4	N	376	401
P61202	Exosome	RGGAR	YTALDKWTNQLNSLNQAVVSK	LA-	3		798.4206903	2392.238671	0.000823681	1	N	420	441
P61202	Parental	PFISK	ELNIDVADVESLLVQCILDNTIHGR	IDQVN	3	C16:+57.021	946.1555308	2835.443193	0.000451244	14	N	376	401
P61205	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	2		1219.596534	2437.177468	0.000451244	1	Y	79	99
P61205	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	3		813.4002892	2437.177468	0.000451244	76	Y	79	99
P61205	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	4		610.3021669	2437.177468	0.000451244	7	Y	79	99
P61205	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	2		1162.125739	2322.235877	0.000451244	32	Y	38	59
P61205	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	3		775.0864257	2322.235877	0.000451244	20	Y	38	59
P61205	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEY	KNISF	2		1098.078257	2194.140914	0.000451244	5	Y	38	58
P61205	Exosome	SLRHR	NWYIQATCATSGDGLYEGLDWLANQLK	NKK-	3	C8:+57.021	1029.82244	3086.443921	0.000451244	3	N	151	178
P61205	Exosome	EELMR	MLAEDELRDAVLLVFANK	QDLPN	2		1024.04878	2046.08196	0.000451244	13	Y	109	127
P61205	Exosome	EELMR	MLAEDELRDAVLLVFANK	QDLPN	3		683.0351201	2046.08196	0.000451244	44	Y	109	127
P61205	Exosome	EELMR	MLAEDELRDAVLLVFANK	QDLPN	3	M1:+15.995	688.3667867	2062.07696	0.000451244	9	Y	109	127
P61205	Exosome	TVEYK	NISFTVWDVGGQDK	IRPLW	2		783.3838842	1564.752168	0.000451244	11	Y	59	73
P61205	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NISFT	2		1282.715252	2563.414904	0.000662267	1	Y	36	59
P61205	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NISFT	3		855.4794348	2563.414904	0.000451244	17	Y	36	59
P61205	Exosome	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.000823681	1	Y	38	51
P61205	Exosome	EDELR	DAVLLVFANK	QDLPN	2		545.3192958	1088.622992	0.000451244	3	Y	117	127
P61205	Exosome	VFANK	QDLPNAMNAAEITDKLGLHSLR	HRNWY	4		602.5659352	2406.232541	0.000451244	3	Y	127	149
P61205	Exosome	VFANK	QDLPNAMNAAEITDK	LGLHS	2	M7:+15.995	823.8887167	1645.761833	0.000823681	2	Y	127	142
P61205	Exosome	RPLWR	HYFQNTQGLIFVVDSNDR	ERVNE	3		718.3523878	2152.033763	0.000622848	1	Y	79	97
P61205	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	2		1219.596534	2437.177468	0.001463592	1	Y	79	99
P61205	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	3		813.4002892	2437.177468	0.000451244	23	Y	79	99
P61205	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	4		610.3021669	2437.177468	0.001943752	2	Y	79	99
P61205	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	2		1162.125739	2322.235877	0.000451244	26	Y	38	59
P61205	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	3		775.0864257	2322.235877	0.000451244	19	Y	38	59
P61205	Parental	LYKLK	LGEIVTTIPTIGFNVETVEY	KNISF	2		1098.078257	2194.140914	0.000451244	17	Y	38	58

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P61205	Parental	SLRHR	NWYIQATCATSGDGLYEGLDWLANQLK	NKK-	3	C8:+57.021	1029.82244	3086.443921	0.000451244	8	N	151	178
P61205	Parental	EELMR	MLAEDELRDAVLLVFANK	QDLPN	3		683.0351201	2046.08196	0.000451244	20	Y	109	127
P61205	Parental	TVEYK	NISFTVWDVGGQDK	IRPLW	2		783.3838842	1564.752168	0.000451244	5	Y	59	73
P61205	Parental	LHSLR	HRNWYIQATCATSGDGLYEGLDWLANQLK	NKK-	3	C10:+57.021	1127.542448	3379.603944	0.000823681	2	N	149	178
P61205	Parental	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.00307782	1	Y	38	51
P61205	Parental	EDELR	DAVLLVFANK	QDLPN	2		545.3192958	1088.622992	0.000451244	19	Y	117	127
P61219	Parental	LDDLE	NAEEEGQENVEILPSGERPQANQKR	ITTPY	3		941.4608246	2821.359074	0.000698008	3	N	26	51
P61219	Parental	LDDLE	NAEEEGQENVEILPSGERPQANQK	RITTP	3		889.4271209	2665.257963	0.001395409	2	N	26	50
P61222	Exosome	GELQR	VALALCLGKPADVYLIDEPSAYLDSEQR	LMAAR	3	C6:+57.021	1036.197396	3105.568787	0.000451244	7	N	469	497
P61222	Exosome	PNLGK	YDDPPDWQEILTYFR	GSELQ	2		979.4524952	1956.88939	0.000622848	9	N	133	148
P61222	Exosome	KDETK	TQAIVCQQLDLTHLK	ERNVE	2	C6:+57.021	884.475019	1766.934438	0.000451244	2	N	195	210
P61222	Exosome	KDETK	TQAIVCQQLDLTHLK	ERNVE	3	C6:+57.021	589.985946	1766.934438	0.00091018	2	N	195	210
P61222	Exosome	ICIKK	CPFGALSIVNLPSNLEK	ETTHR	2	C1:+57.021	929.9905019	1857.965404	0.000451244	1	N	64	81
P61222	Exosome	HLKER	NVEDLSGGELQR	FACAV	2		658.826202	1315.636804	0.001943752	1	N	212	224
P61222	Exosome	FKLHR	LPIPRPGEVLGLVGTNGIGK	STALK	3		663.0619976	1986.162593	0.000637154	1	N	96	116
P61222	Parental	GELQR	VALALCLGKPADVYLIDEPSAYLDSEQR	LMAAR	3	C6:+57.021	1036.197396	3105.568787	0.000451244	3	N	469	497
P61222	Parental	GELQR	VALALCLGKPADVYLIDEPSAY	LDSEQ	2	C6:+57.021	1189.619535	2377.22347	0.000451244	1	N	469	491
P61222	Parental	ICIKK	CPFGALSIVNLPSNLEK	ETTHR	2	C1:+57.021	929.9905019	1857.965404	0.000622848	2	N	64	81
P61290	Exosome	VAELR	TVESEAASYLDQISR	YYITR	2		834.9079204	1667.800241	0.000451244	2	N	166	181
P61290	Exosome	VAELR	TVESEAASYLDQISR	YYITR	3		556.9412136	1667.800241	0.002374549	1	N	166	181
P61290	Parental	SFRER	ITSEAEDLVANFFPK	KLLEL	3		560.954683	1679.840649	0.002296037	1	N	21	36
P61290	Parental	LLIPR	IEDGNNFGVSIQEETVAELRTVESEAASYLDQISR	YYITR	3		1290.627894	3868.860283	0.000998612	1	N	146	181
P61327	Exosome	VQDLK	CLVFSLIGLHFK	IKPI-	3	C1:+57.021	478.6043371	1432.789611	0.000451244	6	N	130	142
P61327	Exosome	PEGLR	VFYYLVQDLK	CLVFS	2		644.3533357	1286.691071	0.001943752	1	N	120	130
P61327	Exosome	EELKR	IIDDSEITKEDDALWPPPDR	VGRQE	2		1163.066409	2324.117218	0.000451244	1	N	62	82
P61327	Exosome	GHKGK	FGHEFLEFEFRPDGK	LRYAN	4		464.4762201	1853.873681	0.001943752	1	N	16	31
P61327	Parental	EELKR	IIDDSEITKEDDALWPPPDR	VGRQE	2		1163.066409	2324.117218	0.000698008	2	N	62	82
P61750	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	IQEGA	2		1219.596534	2437.177468	0.000451244	1	Y	79	99
P61750	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	IQEGA	3		813.4002892	2437.177468	0.000451244	76	Y	79	99
P61750	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	IQEGA	4		610.3021669	2437.177468	0.000451244	7	Y	79	99
P61750	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	2		1162.125739	2322.235877	0.000451244	32	Y	38	59
P61750	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	3		775.0864257	2322.235877	0.000451244	20	Y	38	59
P61750	Exosome	SLRNR	TWYVQATCATQGTGLYEGLDWLSNELSKR	-	3	C8:+57.021	1116.538592	3346.592376	0.000451244	3	N	151	180
P61750	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEY	KNICF	2		1098.078257	2194.140914	0.000451244	5	Y	38	58
P61750	Exosome	TVEYK	NICFTVWDVGGQDK	IRPLW	2	C3:+57.021	819.8829627	1637.750325	0.000451244	29	Y	59	73
P61750	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NICFT	2		1282.715252	2563.414904	0.000662267	1	Y	36	59
P61750	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NICFT	3		855.4794348	2563.414904	0.000451244	17	Y	36	59
P61750	Exosome	SLRNR	TWYVQATCATQGTGLYEGLDWLSNELSK	R-	3	C8:+57.021	1064.504888	3190.491265	0.000451244	11	N	151	179
P61750	Exosome	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.000823681	1	Y	38	51
P61750	Exosome	RPLWR	HYFQNTQGLIFVVDSNDR	ERIQE	3		718.3523878	2152.033763	0.000622848	1	Y	79	97
P61750	Exosome	AVLQK	MLLEDELQDAVLLLFANK	QDLPN	2		1038.058814	2074.102027	0.000451244	1	N	109	127
P61750	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	IQEGA	2		1219.596534	2437.177468	0.001463592	1	Y	79	99
P61750	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	IQEGA	3		813.4002892	2437.177468	0.000451244	23	Y	79	99
P61750	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	IQEGA	4		610.3021669	2437.177468	0.001943752	2	Y	79	99
P61750	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	2		1162.125739	2322.235877	0.000451244	26	Y	38	59
P61750	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	3		775.0864257	2322.235877	0.000451244	19	Y	38	59
P61750	Parental	SLRNR	TWYVQATCATQGTGLYEGLDWLSNELSKR	-	3	C8:+57.021	1116.538592	3346.592376	0.000451244	11	N	151	180
P61750	Parental	LYKLK	LGEIVTTIPTIGFNVETVEY	KNICF	2		1098.078257	2194.140914	0.000451244	17	Y	38	58
P61750	Parental	TVEYK	NICFTVWDVGGQDK	IRPLW	2	C3:+57.021	819.8829627	1637.750325	0.000451244	1	Y	59	73
P61750	Parental	SLRNR	TWYVQATCATQGTGLYEGLDWLSNELSK	R-	3	C8:+57.021	1064.504888	3190.491265	0.000451244	6	N	151	179
P61750	Parental	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.00307782	1	Y	38	51
P61750	Parental	AVLQK	MLLEDELQDAVLLLFANK	QDLPN	2		1038.058814	2074.102027	0.002981883	1	N	109	127
P61924	Parental	LYTVK	AILILDNDGDRLFAK	YYDDT	2		837.4652086	1672.914817	0.000622848	1	N	14	29
P61924	Parental	QVVHR	VALRGEDVPLTEQTVSQVLQSAK	EQIKW	3		823.4505382	2467.328214	0.000662267	7	N	145	168
P61924	Parental	NVEKR	ALLENMEGLFLAVDEIVDGGVILESDPQQVVHR	VALRG	3		1202.622699	3604.844698	0.002080925	2	N	112	145
P61924	Parental	RVALR	GEDVPLTEQTVSQVLQSAK	EQIKW	2		1015.026556	2028.037511	0.000451244	3	N	149	168
P61961	Exosome	TAVLK	FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK	HGSEL	3		1192.630182	3574.867147	0.000451244	6	N	34	69
P61961	Parental	TAVLK	FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK	HGSEL	3		1192.630182	3574.867147	0.000451244	27	N	34	69
P61961	Parental	AVLKF	AAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK	HGSEL	3		1143.607378	3427.798733	0.00091018	3	N	35	69
P61961	Parental	AAEEF	KVPAATSAIITNDGIGINPAQTAGNVFLK	HGSEL	3		961.1981016	2880.570905	0.000451244	1	N	40	69
P61965	Exosome	SPNGK	YILAATLDNTLK	LWDYS	2		668.3800818	1334.744564	0.000451244	3	N	227	239
P61965	Exosome	ISGHK	LGISDVAWSSDSNLLVSASDDKTLK	IWDVS	3		874.4488629	2620.323189	0.002212458	2	N	87	112
P61965	Exosome	DGLCR	IWDTASGQCLK	TLIDD	2	C9:+57.021	639.8112777	1277.606955	0.001654178	2	N	196	207
P61965	Parental	VTGGK	WIVSGSEDNLVYIWNLQTK	EIVQK	2		1133.081665	2264.147731	0.000622848	5	N	272	291
P61979	Exosome	VECIK	IILDLISESPIKGR	AQPYD	3		518.6474133	1552.91884	0.00091018	3	N	207	221

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P61979	Exosome	YAGGR	GSYGDLGGPIITTQVTIPK	DLAGS	2		959.020545	1916.02549	0.000451244	30	N	377	396
P61979	Exosome	VECIK	IILDLISESPIK	GRAQP	2		670.9059325	1339.796265	0.000451244	39	N	207	219
P61979	Exosome	GSEDR	IITITGTQDQIQNAQYLLQNSVK	QYSGK	2		1295.198289	2588.380978	0.000451244	30	N	433	456
P61979	Exosome	GASIK	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	QYSGK	3		1277.320513	3828.93814	0.000451244	20	N	422	456
P61979	Exosome	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	3	C29:+57.021	1352.34915	4054.024049	0.000451244	44	N	103	139
P61979	Exosome	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	4	C29:+57.021	1014.513812	4054.024049	0.000451244	16	N	103	139
P61979	Exosome	PIKGR	AQPYDPNFYDETYDYGGF	TMMFD	2		1081.437239	2160.858878	0.000622848	7	N	221	239
P61979	Exosome	SGPER	ILSISADIETIGEILK	KIIPT	2		857.9960072	1713.976414	0.000451244	5	N	86	102
P61979	Exosome	SGPER	ILSISADIETIGEILKK	IIPTL	2		922.0434888	1842.071378	0.000451244	1	N	86	103
P61979	Exosome	SGPER	ILSISADIETIGEILKK	IIPTL	3		615.0315925	1842.071378	0.000451244	3	N	86	103
P61979	Exosome	IKALR	TDYNASVSVPDSSGPER	ILSIS	2		890.9033664	1779.791133	0.000451244	10	N	69	86
P61979	Exosome	EILKK	IIPTLEEGLQLPSPTAT	SQLPL	2		890.491089	1778.966578	0.000979378	1	N	103	120
P61979	Parental	QTTIK	LFQECCPHSTDRVVLIGGKPDR	VVECI	2	C5:+57.021,C6:+57.021	1292.641641	2583.267682	0.000735798	2	N	179	201
P61979	Parental	QTTIK	LFQECCPHSTDRVVLIGGKPDR	VVECI	3	C5:+57.021,C6:+57.021	862.0970275	2583.267682	0.000451244	11	N	179	201
P61979	Parental	DCELR	LLIHQSLAGGIIGVK	GAKIK	2		759.9724724	1517.929345	0.000662267	6	N	148	163
P61979	Parental	DCELR	LLIHQSLAGGIIGVK	GAKIK	3		506.9842483	1517.929345	0.000451244	20	N	148	163
P61979	Parental	VECIK	IILDLISESPIKGR	AQPYD	2		777.4672199	1552.91884	0.000451244	7	N	207	221
P61979	Parental	VECIK	IILDLISESPIKGR	AQPYD	3		518.6474133	1552.91884	0.000451244	15	N	207	221
P61979	Parental	YAGGR	GSYGDLGGPIITTQVTIPK	DLAGS	2		959.020545	1916.02549	0.000451244	66	N	377	396
P61979	Parental	VECIK	IILDLISESPIK	GRAQP	2		670.9059325	1339.796265	0.000451244	41	N	207	219
P61979	Parental	GSEDR	IITITGTQDQIQNAQYLLQNSVK	QYSGK	2		1295.198289	2588.380978	0.000451244	45	N	433	456
P61979	Parental	GSEDR	IITITGTQDQIQNAQYLLQNSVK	QYSGK	3		863.8014595	2588.380978	0.000451244	27	N	433	456
P61979	Parental	YAGGR	GSYGDLGGPIITTQVTIPKDLAGSIIGK	GGQRI	2		1386.263629	2770.511658	0.000823681	1	N	377	405
P61979	Parental	YAGGR	GSYGDLGGPIITTQVTIPKDLAGSIIGK	GGQRI	3		924.5116861	2770.511658	0.000451244	6	N	377	405
P61979	Parental	GASIK	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	QYSGK	3		1277.320513	3828.93814	0.000451244	44	N	422	456
P61979	Parental	GASIK	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	QYSGK	4		958.242335	3828.93814	0.00307782	1	N	422	456
P61979	Parental	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	3	C29:+57.021	1352.34915	4054.024049	0.000451244	59	N	103	139
P61979	Parental	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	4	C29:+57.021	1014.513812	4054.024049	0.000451244	33	N	103	139
P61979	Parental	EGLQL	PSPTATSQLPLESDAVECLNYQHYK	GSDFD	3	C18:+57.021	950.1204862	2847.338059	0.001229886	1	N	114	139
P61979	Parental	PIKGR	AQPYDPNFYDETYDYGGF	TMMFD	2		1081.437239	2160.858878	0.000451244	33	N	221	239
P61979	Parental	SGPER	ILSISADIETIGEILK	KIIPT	2		857.9960072	1713.976414	0.000451244	23	N	86	102
P61979	Parental	GKNIK	ALRTDYNASVSVPDSSGPER	ILSIS	2		1061.014511	2120.013422	0.000451244	11	N	66	86
P61979	Parental	GKNIK	ALRTDYNASVSVPDSSGPER	ILSIS	3		707.6789406	2120.013422	0.000622848	2	N	66	86
P61979	Parental	SGPER	ILSISADIETIGEILKK	IIPTL	3		615.0315925	1842.071378	0.000451244	37	N	86	103
P61979	Parental	IKALR	TDYNASVSVPDSSGPER	ILSIS	2		890.9033664	1779.791133	0.000451244	29	N	69	86
P61979	Parental	IKQIR	HESGASIKIDEPLEGSEDR	IITIT	2		1034.993244	2067.970888	0.000451244	7	N	414	433
P61979	Parental	IKQIR	HESGASIKIDEPLEGSEDR	IITIT	3		690.3314295	2067.970888	0.000451244	1	N	414	433
P61979	Parental	SEWQM	AYEPQGGSGYDYSYAGGR	GSYGD	2		949.4035336	1896.791467	0.000451244	11	N	359	377
P61979	Parental	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYKG	SDFDC	3	C29:+57.021	1371.356304	4111.045513	0.000622848	5	N	103	140
P61979	Parental	EILKK	IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYKG	SDFDC	4	C29:+57.021	1028.769178	4111.045513	0.002813207	1	N	103	140
P61979	Parental	GEILK	KIIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	3	C30:+57.021	1395.047471	4182.119013	0.000979378	1	N	102	139
P61979	Parental	GEILK	KIIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	GSDFD	4	C30:+57.021	1046.537553	4182.119013	0.000622848	7	N	102	139
P61982	Exosome	AAAMK	NVTELNEPLSNEER	NLLSV	2		822.3977199	1642.77984	0.000451244	43	N	28	42
P61982	Exosome	THPIR	LGLALNYSVFYYEIQNAPEQACHLAK	TAFDD	3	C22:+57.021	1004.836021	3011.484663	0.000451244	34	N	172	198
P61982	Exosome	THPIR	LGLALNYSVFYYEIQNAPEQACHLAK	TAFDD	4	C22:+57.021	753.8789659	3011.484663	0.000622848	1	N	172	198
P61982	Exosome	EKIEK	ELEAVCQDVLSLLDNYLIK	NCSET	2	C6:+57.021	1118.082785	2234.14997	0.000451244	34	N	91	110
P61982	Exosome	EKIEK	ELEAVCQDVLSLLDNYLIK	NCSET	3	C6:+57.021	745.7244567	2234.14997	0.000451244	23	N	91	110
P61982	Exosome	CHLAK	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1101.210184	3300.607153	0.000451244	22	N	198	227
P61982	Exosome	CHLAK	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1106.541851	3316.602153	0.000451244	10	N	198	227
P61982	Exosome	CHLAK	TAFDDAIAELDTLNEDSYK	DSTLI	2		1065.989836	2129.964072	0.000451244	31	N	198	217
P61982	Exosome	CHLAK	TAFDDAIAELDTLNEDSYK	DSTLI	3		710.9958239	2129.964072	0.002727428	1	N	198	217
P61982	Exosome	AYREK	IEKELEAVCQDVLSLLDNYLIK	NCSET	3	C9:+57.021	869.1316635	2604.371591	0.000451244	7	N	88	110
P61982	Exosome	MQLLR	DNLTLWTSDQQDDDGGEGNN	-	2		1097.444312	2192.873025	0.000451244	4	N	227	247
P61982	Parental	AAAMK	NVTELNEPLSNEER	NLLSV	2		822.3977199	1642.77984	0.000451244	84	N	28	42
P61982	Parental	AAAMK	NVTELNEPLSNEERNLLSVAYK	NVVGA	3		844.7700479	2531.286744	0.001162105	5	N	28	50
P61982	Parental	THPIR	LGLALNYSVFYYEIQNAPEQACHLAK	TAFDD	3	C22:+57.021	1004.836021	3011.484663	0.000451244	41	N	172	198
P61982	Parental	EKIEK	ELEAVCQDVLSLLDNYLIK	NCSET	2	C6:+57.021	1118.082785	2234.14997	0.000451244	37	N	91	110
P61982	Parental	EKIEK	ELEAVCQDVLSLLDNYLIK	NCSET	3	C6:+57.021	745.7244567	2234.14997	0.000451244	31	N	91	110
P61982	Parental	CHLAK	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1101.210184	3300.607153	0.000451244	29	N	198	227
P61982	Parental	CHLAK	TAFDDAIAELDTLNEDSYK	DSTLI	2		1065.989836	2129.964072	0.000451244	22	N	198	217
P61982	Parental	AYREK	IEKELEAVCQDVLSLLDNYLIK	NCSET	3	C9:+57.021	869.1316635	2604.371591	0.000451244	3	N	88	110
P61982	Parental	IMQLL	RDNLTLWTSDQQDDDGGEGNN	-	2		1175.494868	2348.974136	0.000451244	16	N	226	247
P61982	Parental	EKIEK	ELEAVCQDVLSLLDNYLIKNCSETQYESK	VFYLK	3	C6:+57.021,C21:+57.021	1154.553425	3460.636875	0.000451244	3	N	91	120
P61982	Parental	NYSVF	YYEIQNAPEQACHLAK	TAFDD	2	C12:+57.021	967.9571904	1933.898781	0.000979378	2	N	182	198
P61982	Parental	THPIR	LGLALNYSVF	YYEIQ	2		548.8060213	1095.596443	0.001943752	1	N	172	182

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P61982	Parental	MQLLR	DNLTLWTSDQQDDDGGEGNN	-	2		1097.444312	2192.873025	0.000622848	13	N	227	247
P62082	Exosome	RPRSR	TLTAVHDAILEDLVFPSEIVGKR	IRVKL	3		841.7992788	2522.374436	0.001162105	1	N	120	143
P62082	Exosome	RPRSR	TLTAVHDAILEDLVFPSEIVGKR	IRVKL	4		631.6014091	2522.374436	0.000735798	4	N	120	143
P62082	Exosome	GGGRK	AIIIFVPVPQLK	SFQKI	2		669.4319204	1336.848241	0.000451244	19	N	58	70
P62082	Exosome	RPRSR	TLTAVHDAILEDLVFPSEIVGK	RIRVK	3		789.7655751	2366.273325	0.000451244	13	N	120	142
P62082	Exosome	SSSAK	IVKPNGEKPDEFESGISQALLELEMNSDLK	AQLRE	3	M25:+15.995	1116.229496	3345.665087	0.001591523	1	N	7	37
P62082	Exosome	SSSAK	IVKPNGEKPDEFESGISQALLELEMNSDLK	AQLRE	4	M25:+15.995	837.4240719	3345.665087	0.00091018	4	N	7	37
P62082	Parental	RPRSR	TLTAVHDAILEDLVFPSEIVGKR	IRVKL	2		1262.195018	2522.374436	0.002453667	1	N	120	143
P62082	Parental	RPRSR	TLTAVHDAILEDLVFPSEIVGKR	IRVKL	3		841.7992788	2522.374436	0.000451244	10	N	120	143
P62082	Parental	RPRSR	TLTAVHDAILEDLVFPSEIVGKR	IRVKL	4		631.6014091	2522.374436	0.000451244	27	N	120	143
P62082	Parental	GGGRK	AIIIFVPVPQLK	SFQKI	2		669.4319204	1336.848241	0.000451244	27	N	58	70
P62082	Parental	LTAVH	DAILEDLVFPSEIVGKR	IRVKL	3		634.3513251	1900.030575	0.0007646	8	N	126	143
P62082	Parental	GVYKK	LTGKDVNFEFPEFQL	-	2		892.4492242	1782.882848	0.000451244	10	N	179	194
P62082	Parental	RPRSR	TLTAVHDAILEDLVFPSEIVGK	RIRVK	2		1184.144463	2366.273325	0.000451244	10	N	120	142
P62082	Parental	RPRSR	TLTAVHDAILEDLVFPSEIVGK	RIRVK	3		789.7655751	2366.273325	0.000451244	24	N	120	142
P62082	Parental	RSRTL	TAVHDAILEDLVFPSEIVGKR	IRVKL	4		578.0684734	2308.242694	0.000451244	6	N	122	143
P62082	Parental	SSSAK	IVKPNGEKPDEFESGISQALLELEMNSDLK	AQLRE	3	M25:+15.995	1116.229496	3345.665087	0.000451244	4	N	7	37
P62082	Parental	KLTGK	DVNFEFPEFQL	-	2		692.8251394	1383.634679	0.001463592	9	N	183	194
P62082	Parental	RSRTL	TAVHDAILEDLVFPSEIVGK	RIRVK	3		718.3883275	2152.141583	0.000662267	2	N	122	142
P62082	Parental	LTAVH	DAILEDLVFPSEIVGK	RIRVK	2		872.9725321	1743.929464	0.00307782	1	N	126	142
P62137	Exosome	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	2	C5:+57.021,C8:+57.021	1057.500342	2112.985084	0.000451244	18	Y	150	168
P62137	Exosome	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	3	C5:+57.021,C8:+57.021	705.3361615	2112.985084	0.000451244	25	Y	150	168
P62137	Exosome	DLICR	AHQVVEDGYEFFAK	RQLVT	2		820.3917092	1638.767818	0.000451244	14	Y	246	260
P62137	Exosome	DLICR	AHQVVEDGYEFFAK	RQLVT	3		547.2637395	1638.767818	0.001871652	4	Y	246	260
P62137	Exosome	VDRGK	QSLETICLLLAYK	IRYPE	2	C7:+57.021	776.4264748	1550.83735	0.000451244	17	Y	98	111
P62137	Exosome	VDRGK	QSLETICLLLAYK	IRYPE	2	Q1:-17.027,C7:+57.021	767.9129748	1533.81035	0.001229886	1	Y	98	111
P62137	Exosome	VDRGK	QSLETICLLLAYK	IRYPE	2	[0:-17.027,C7:+57.021	767.9129748	1533.81035	0.000870037	6	Y	98	111
P62137	Exosome	CLKSR	EIFLSQPILLELEAPLK	ICGDI	2		977.0695066	1952.123413	0.000451244	34	Y	43	60
P62137	Exosome	CLKSR	EIFLSQPILLELEAPLK	ICGDI	3		651.7156044	1952.123413	0.000662267	5	Y	43	60
P62137	Exosome	GLCLK	SREIFLSQPILLELEAPLK	ICGDI	2		1098.636076	2195.256553	0.001763695	1	Y	41	60
P62137	Exosome	GLCLK	SREIFLSQPILLELEAPLK	ICGDI	3		732.7599843	2195.256553	0.000451244	40	Y	41	60
P62137	Exosome	YDLLR	LFEYGGFPPESNYLFLGDYVDR	GKQSL	2		1299.613527	2597.211453	0.000451244	30	N	74	96
P62137	Exosome	YDLLR	LFEYGGFPPESNYLFLGDYVDR	GKQSL	3		866.7449511	2597.211453	0.000451244	28	N	74	96
P62137	Exosome	LLAYK	IRYPENFFLLR	GNHEC	3		489.942272	1466.803416	0.000451244	21	N	111	122
P62137	Exosome	EAPLK	ICGDIHGQYYDLLR	LFEYG	2	C2:+57.021	861.9173369	1721.819074	0.000451244	5	N	60	74
P62137	Exosome	EAPLK	ICGDIHGQYYDLLR	LFEYG	3	C2:+57.021	574.9474913	1721.819074	0.000451244	12	N	60	74
P62137	Exosome	LWKTF	TDCFNCLPIAAIVDEK	IFCCH	2	C3:+57.021,C6:+57.021	933.442296	1864.868992	0.001591523	1	Y	152	168
P62137	Exosome	SRPGK	NVQLTENEIR	GLCLK	2		608.3205555	1214.625511	0.001329271	3	N	26	36
P62137	Exosome	DYVDR	GKQSLETICLLLAYK	IRYPE	3	C9:+57.021	579.6590588	1735.953777	0.000622848	2	Y	96	111
P62137	Exosome	REIFL	SQPILLELEAPLK	ICGDI	2		725.9299389	1449.844278	0.000451244	2	Y	47	60
P62137	Parental	DLICR	AHQVVEDGYEFFAKR	QLVTL	2		898.4422648	1794.86893	0.000451244	1	Y	246	261
P62137	Parental	DLICR	AHQVVEDGYEFFAKR	QLVTL	3		599.2974432	1794.86893	0.00091018	1	Y	246	261
P62137	Parental	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	2	C5:+57.021,C8:+57.021	1057.500342	2112.985084	0.000451244	14	Y	150	168
P62137	Parental	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	3	C5:+57.021,C8:+57.021	705.3361615	2112.985084	0.000662267	13	Y	150	168
P62137	Parental	DLICR	AHQVVEDGYEFFAK	RQLVT	2		820.3917092	1638.767818	0.000451244	22	Y	246	260
P62137	Parental	DLICR	AHQVVEDGYEFFAK	RQLVT	3		547.2637395	1638.767818	0.001229886	1	Y	246	260
P62137	Parental	VDRGK	QSLETICLLLAYK	IRYPE	2	C7:+57.021	776.4264748	1550.83735	0.000662267	2	Y	98	111
P62137	Parental	CLKSR	EIFLSQPILLELEAPLK	ICGDI	2		977.0695066	1952.123413	0.000451244	22	Y	43	60
P62137	Parental	CLKSR	EIFLSQPILLELEAPLK	ICGDI	3		651.7156044	1952.123413	0.000451244	4	Y	43	60
P62137	Parental	GLCLK	SREIFLSQPILLELEAPLK	ICGDI	3		732.7599843	2195.256553	0.000451244	6	Y	41	60
P62137	Parental	YDLLR	LFEYGGFPPESNYLFLGDYVDR	GKQSL	2		1299.613527	2597.211453	0.000451244	20	N	74	96
P62137	Parental	YDLLR	LFEYGGFPPESNYLFLGDYVDR	GKQSL	3		866.7449511	2597.211453	0.000451244	7	N	74	96
P62137	Parental	LLAYK	IRYPENFFLLR	GNHEC	3		489.942272	1466.803416	0.000662267	5	N	111	122
P62137	Parental	EAPLK	ICGDIHGQYYDLLR	LFEYG	3	C2:+57.021	574.9474913	1721.819074	0.000451244	10	N	60	74
P62137	Parental	EVVAK	FLHKHDLDLICR	AHQVV	3	C11:+57.021	522.9455335	1565.8132	0.002981883	1	N	234	246
P62137	Parental	LWKTF	TDCFNCLPIAAIVDEK	IFCCH	2	C3:+57.021,C6:+57.021	933.442296	1864.868992	0.000823681	2	Y	152	168
P62137	Parental	SRPGK	NVQLTENEIR	GLCLK	2		608.3205555	1214.625511	0.002296037	1	N	26	36
P62141	Exosome	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	2	C5:+57.021,C8:+57.021	1057.500342	2112.985084	0.000451244	18	Y	149	167
P62141	Exosome	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	3	C5:+57.021,C8:+57.021	705.3361615	2112.985084	0.000451244	25	Y	149	167
P62141	Exosome	DLICR	AHQVVEDGYEFFAK	RQLVT	2		820.3917092	1638.767818	0.000451244	14	Y	245	259
P62141	Exosome	DLICR	AHQVVEDGYEFFAK	RQLVT	3		547.2637395	1638.767818	0.001871652	4	Y	245	259
P62141	Exosome	VDRGK	QSLETICLLLAYK	IKYPE	2	C7:+57.021	776.4264748	1550.83735	0.000451244	17	Y	97	110
P62141	Exosome	VDRGK	QSLETICLLLAYK	IKYPE	2	Q1:-17.027,C7:+57.021	767.9129748	1533.81035	0.001229886	1	Y	97	110
P62141	Exosome	VDRGK	QSLETICLLLAYK	IKYPE	2	[0:-17.027,C7:+57.021	767.9129748	1533.81035	0.000870037	6	Y	97	110
P62141	Exosome	CIKSR	EIFLSQPILLELEAPLK	ICGDI	2		977.0695066	1952.123413	0.000451244	34	Y	42	59

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62141	Exosome	CIKSR	EIFLSQPILLELEAPLK	ICGDI	3		651.7156044	1952.123413	0.000662267	5	Y	42	59
P62141	Exosome	TDLLR	LFEYGGFPPEANYLFLGDYVDR	GKQSL	2		1291.616069	2581.216539	0.000451244	29	N	73	95
P62141	Exosome	TDLLR	LFEYGGFPPEANYLFLGDYVDR	GKQSL	3		861.4133129	2581.216539	0.000451244	32	N	73	95
P62141	Exosome	GLCIK	SREIFLSQPILLELEAPLK	ICGDI	2		1098.636076	2195.256553	0.001763695	1	Y	40	59
P62141	Exosome	GLCIK	SREIFLSQPILLELEAPLK	ICGDI	3		732.7599843	2195.256553	0.000451244	40	Y	40	59
P62141	Exosome	LLAYK	IKYPENFFLLR	GNHEC	3		480.6068893	1438.797268	0.000451244	29	N	110	121
P62141	Exosome	LWKTF	TDCFNCLPIAAIVDEK	IFCCH	2	C3:+57.021,C6:+57.021	933.442296	1864.868992	0.001591523	1	Y	151	167
P62141	Exosome	DVVSK	FLNRHDLDLICR	AHQVV	3	C11:+57.021	524.6089213	1570.803364	0.002212458	1	N	233	245
P62141	Exosome	EAPLK	ICGDIHGQYTDLLR	LFEYG	2	C2:+57.021	830.9095119	1659.803424	0.001871652	1	N	59	73
P62141	Exosome	DYVDR	GKQSLETICLLLAYK	IKYPE	3	C9:+57.021	579.6590588	1735.953777	0.000622848	2	Y	95	110
P62141	Exosome	REIFL	SQPILLELEAPLK	ICGDI	2		725.9299389	1449.844278	0.000451244	2	Y	46	59
P62141	Parental	DLICR	AHQVVEDGYEFFAKR	QLVTL	2		898.4422648	1794.86893	0.000451244	1	Y	245	260
P62141	Parental	DLICR	AHQVVEDGYEFFAKR	QLVTL	3		599.2974432	1794.86893	0.00091018	1	Y	245	260
P62141	Parental	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	2	C5:+57.021,C8:+57.021	1057.500342	2112.985084	0.000451244	14	Y	149	167
P62141	Parental	IKLWK	TFTDCFNCLPIAAIVDEK	IFCCH	3	C5:+57.021,C8:+57.021	705.3361615	2112.985084	0.000662267	13	Y	149	167
P62141	Parental	DLICR	AHQVVEDGYEFFAK	RQLVT	2		820.3917092	1638.767818	0.000451244	22	Y	245	259
P62141	Parental	DLICR	AHQVVEDGYEFFAK	RQLVT	3		547.2637395	1638.767818	0.001229886	1	Y	245	259
P62141	Parental	VDRGK	QSLETICLLLAYK	IKYPE	2	C7:+57.021	776.4264748	1550.83735	0.000662267	2	Y	97	110
P62141	Parental	CIKSR	EIFLSQPILLELEAPLK	ICGDI	2		977.0695066	1952.123413	0.000451244	22	Y	42	59
P62141	Parental	CIKSR	EIFLSQPILLELEAPLK	ICGDI	3		651.7156044	1952.123413	0.000451244	4	Y	42	59
P62141	Parental	TDLLR	LFEYGGFPPEANYLFLGDYVDR	GKQSL	2		1291.616069	2581.216539	0.000451244	9	N	73	95
P62141	Parental	TDLLR	LFEYGGFPPEANYLFLGDYVDR	GKQSL	3		861.4133129	2581.216539	0.002453667	2	N	73	95
P62141	Parental	GLCIK	SREIFLSQPILLELEAPLK	ICGDI	3		732.7599843	2195.256553	0.000451244	6	Y	40	59
P62141	Parental	LLAYK	IKYPENFFLLR	GNHEC	3		480.6068893	1438.797268	0.000823681	5	N	110	121
P62141	Parental	LWKTF	TDCFNCLPIAAIVDEK	IFCCH	2	C3:+57.021,C6:+57.021	933.442296	1864.868992	0.000823681	2	Y	151	167
P62192	Exosome	MATNR	IETLDPALIRPGR	IDRKI	3		484.2845863	1449.830359	0.001463592	2	N	333	346
P62192	Exosome	REIQR	TMLELLNQLDGFDSR	GDVKV	2		876.4357914	1750.855983	0.000622848	1	N	307	322
P62192	Parental	MATNR	IETLDPALIRPGR	IDRKI	3		484.2845863	1449.830359	0.000823681	3	N	333	346
P62192	Parental	MKVEK	APQETYADIGGLDNQIQEIK	ESVEL	2		1102.048019	2202.080439	0.000451244	20	N	178	198
P62196	Exosome	NAKVR	LLREELQLLQEQGSYVGEVVR	AMDKK	2		1229.669168	2457.322735	0.000735798	1	N	57	78
P62196	Exosome	NAKVR	LLREELQLLQEQGSYVGEVVR	AMDKK	3		820.1153784	2457.322735	0.000451244	22	N	57	78
P62196	Exosome	VRLLR	EELQLLQEQGSYVGEVVR	AMDKK	2		1038.534548	2075.053496	0.000622848	2	N	60	78
P62196	Exosome	IKEIK	EVIELPVKHPELFEALGIAQPK	GVLLY	3		819.7970981	2456.367894	0.000823681	4	N	162	184
P62196	Exosome	HPEGK	FVVDVDKNIDINDVTPNCR	VALRN	2	C18:+57.021	1117.049808	2232.084016	0.002981883	1	N	94	113
P62196	Exosome	HPEGK	FVVDVDKNIDINDVTPNCR	VALRN	3	C18:+57.021	745.0358053	2232.084016	0.000451244	13	N	94	113
P62196	Parental	NAKVR	LLREELQLLQEQGSYVGEVVR	AMDKK	3		820.1153784	2457.322735	0.000451244	6	N	57	78
P62196	Parental	YYLSK	IEELQLIVNDK	SQNLR	2		657.3697141	1312.723828	0.000451244	2	N	27	38
P62204	Exosome	REAFR	VFDKDGNGYISAAELR	HVMTN	2		877.9395549	1753.86351	0.000451244	117	N	91	107
P62204	Exosome	REAFR	VFDKDGNGYISAAELR	HVMTN	3		585.6289699	1753.86351	0.000451244	5	N	91	107
P62204	Exosome	IAEFK	EAFSLFDKDGDGTITTK	ELGTV	2		922.9497853	1843.883971	0.000451244	88	N	14	31
P62204	Exosome	IAEFK	EAFSLFDKDGDGTITTK	ELGTV	3		615.6357902	1843.883971	0.000451244	122	N	14	31
P62204	Exosome	IAEFK	EAFSLFDKDGDGTITTK	ELGTV	2	[0:-18.011	913.9442853	1825.872971	0.000451244	3	N	14	31
P62204	Exosome	ARKMK	DTDSEEEIREAFR	VFDKD	2		798.8609702	1595.70634	0.000662267	3	N	78	91
P62204	Exosome	ARKMK	DTDSEEEIREAFR	VFDKD	3		532.9099135	1595.70634	0.002212458	2	N	78	91
P62204	Exosome	DEMIR	EADIDGDGQVNYEEFVQMMTAK	-	2	M18:+15.995,M19:+15.995	1261.539128	2521.062655	0.000451244	6	N	127	149
P62204	Parental	REAFR	VFDKDGNGYISAAELR	HVMTN	2		877.9395549	1753.86351	0.000451244	116	N	91	107
P62204	Parental	REAFR	VFDKDGNGYISAAELR	HVMTN	3		585.6289699	1753.86351	0.000451244	58	N	91	107
P62204	Parental	IAEFK	EAFSLFDKDGDGTITTK	ELGTV	2		922.9497853	1843.883971	0.000451244	64	N	14	31
P62204	Parental	IAEFK	EAFSLFDKDGDGTITTK	ELGTV	3		615.6357902	1843.883971	0.000451244	69	N	14	31
P62204	Parental	ARKMK	DTDSEEEIREAFR	VFDKD	2		798.8609702	1595.70634	0.000998612	3	N	78	91
P62204	Parental	ARKMK	DTDSEEEIREAFR	VFDKD	3		532.9099135	1595.70634	0.00091018	2	N	78	91
P62204	Parental	REAFR	VFDKDGNGYISAAEL	RHVMT	2		799.8889993	1597.762399	0.000637154	2	N	91	106
P62242	Exosome	KKNAK	ISSLLEEQFQQGK	LLACI	2		753.8940847	1505.772569	0.000451244	8	N	157	170
P62242	Exosome	TRKTR	IIDVVYNASNNELVR	TKTLV	2		859.9577477	1717.899895	0.000451244	1	N	77	92
P62242	Parental	KKNAK	ISSLLEEQFQQGK	LLACI	2		753.8940847	1505.772569	0.000451244	21	N	157	170
P62242	Parental	KYRAL	RLDVGNFSWGSECCTR	KTRII	2	C13:+57.021,C14:+57.021	972.4280429	1942.840486	0.000451244	1	N	58	74
P62242	Parental	KYRAL	RLDVGNFSWGSECCTR	KTRII	3	C13:+57.021,C14:+57.021	648.6212952	1942.840486	0.001871652	2	N	58	74
P62242	Parental	GQCGR	ADGYVLEGKELEFY	LRKIK	2		816.8937504	1631.771901	0.000622848	7	N	184	198
P62242	Parental	TRKTR	IIDVVYNASNNELVR	TKTLV	2		859.9577477	1717.899895	0.001591523	1	N	77	92
P62259	Exosome	ETELK	LICCDILDVLDKHLIPAANTGESK	VFYYK	2	C3:+57.021,C4:+57.021	1348.193372	2694.371145	0.000698008	2	N	94	118
P62259	Exosome	ETELK	LICCDILDVLDKHLIPAANTGESK	VFYYK	3	C3:+57.021,C4:+57.021	899.1315149	2694.371145	0.000451244	30	N	94	118
P62259	Exosome	ETELK	LICCDILDVLDKHLIPAANTGESK	VFYYK	4	C3:+57.021,C4:+57.021	674.6005862	2694.371145	0.000451244	29	N	94	118
P62259	Exosome	CRLAK	AAFDDAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1086.874913	3257.601339	0.000451244	25	N	196	225
P62259	Exosome	CRLAK	AAFDDAIAELDTLSEESYKDSTLIMQLLR	DNLTL	4		815.4081348	3257.601339	0.000451244	2	N	196	225
P62259	Exosome	CRLAK	AAFDDAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1092.20658	3273.596339	0.000451244	2	N	196	225

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62259	Exosome	CRLAK	AAFDDAIAELDTLSEESYK	DSTLI	2		1044.486929	2086.958258	0.000451244	44	N	196	215
P62259	Exosome	CRLAK	AAFDDAIAELDTLSEESYK	DSTLI	3		696.6605527	2086.958258	0.000451244	14	N	196	215
P62259	Exosome	ETELK	LICCDILDVLDK	HLIPA	2	C3:+57.021,C4:+57.021	738.8755291	1475.735458	0.000451244	30	N	94	106
P62259	Exosome	MQLLR	DNLTLWTSDMQGDGEEQNKEALQDVEDENQ	-	3	M10:+15.995	1156.494177	3466.45913	0.000451244	19	N	225	255
P62259	Exosome	CRLAK	AAFDDAIAELDTLSEESY	KDSTL	2		980.4394474	1958.863295	0.001162105	1	N	196	214
P62259	Exosome	GNDRK	EAAENSLVAYK	AASDI	2		597.8042069	1193.592814	0.001264573	1	N	142	153
P62259	Exosome	LVAYK	AASDIAMTELPPTHPIR	LGLAL	2	M7:+15.995	918.4702082	1834.924816	0.000622848	1	N	153	170
P62259	Exosome	LVAYK	AASDIAMTELPPTHPIR	LGLAL	3	M7:+15.995	612.6494055	1834.924816	0.000451244	6	N	153	170
P62259	Exosome	THPIR	LGLALNFSVF	YYEIL	2		540.808564	1079.601528	0.002453667	1	Y	170	180
P62259	Parental	ETELK	LICCDILDVLDKHLIPAANTGESK	VFYYK	3	C3:+57.021,C4:+57.021	899.1315149	2694.371145	0.000451244	24	N	94	118
P62259	Parental	ETELK	LICCDILDVLDKHLIPAANTGESK	VFYYK	4	C3:+57.021,C4:+57.021	674.6005862	2694.371145	0.000451244	20	N	94	118
P62259	Parental	CRLAK	AAFDDAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1086.874913	3257.601339	0.000451244	35	N	196	225
P62259	Parental	CRLAK	AAFDDAIAELDTLSEESYKDSTLIMQLLR	DNLTL	4		815.4081348	3257.601339	0.001162105	2	N	196	225
P62259	Parental	CRLAK	AAFDDAIAELDTLSEESYK	DSTLI	2		1044.486929	2086.958258	0.000451244	34	N	196	215
P62259	Parental	CRLAK	AAFDDAIAELDTLSEESYK	DSTLI	3		696.6605527	2086.958258	0.000451244	18	N	196	215
P62259	Parental	ETELK	LICCDILDVLDK	HLIPA	2	C3:+57.021,C4:+57.021	738.8755291	1475.735458	0.000451244	23	N	94	106
P62259	Parental	THPIR	LGLALNFSVFY	YEILN	2		622.3402283	1242.664857	0.001352548	2	Y	170	181
P62259	Parental	CRLAK	AAFDDAIAELDTLSEESY	KDSTL	2		980.4394474	1958.863295	0.000451244	15	N	196	214
P62259	Parental	GDYHR	YLAEFATGNDRK	EAAEN	2		692.8469375	1383.678275	0.000451244	6	N	130	142
P62259	Parental	GDYHR	YLAEFATGNDRK	EAAEN	3		462.2338916	1383.678275	0.001264573	1	N	130	142
P62259	Parental	GNDRK	EAAENSLVAYK	AASDI	2		597.8042069	1193.592814	0.000451244	14	N	142	153
P62259	Parental	FSVFY	YEILNSPDR	ACRLA	2		553.7779921	1105.540384	0.001463592	1	N	181	190
P62259	Parental	ELKLI	CCDILDVLDK	HLIPA	2	C1:+57.021,C2:+57.021	625.791465	1249.56733	0.000622848	1	N	96	106
P62264	Exosome	KGKEK	KEEQVISLGPQVAEGENVFGVCHIFASF	NDTFV	3	C22:+57.021	1031.178336	3090.511607	0.001264573	1	N	9	37
P62264	Parental	IFASF	NDTFVHVTDLSGKETICR	VTGGM	2	C17:+57.021	1046.510319	2091.005037	0.000451244	10	N	37	55
P62264	Parental	IFASF	NDTFVHVTDLSGKETICR	VTGGM	3	C17:+57.021	698.009479	2091.005037	0.000451244	22	N	37	55
P62264	Parental	KGKEK	KEEQVISLGPQVAEGENVFGVCHIFASF	NDTFV	3	C22:+57.021	1031.178336	3090.511607	0.000451244	16	N	9	37
P62264	Parental	KGKEK	KEEQVISLGPQVAEGENVFGVCHIF	ASFND	2	C22:+57.021	1393.694825	2785.37405	0.000823681	1	N	9	34
P62264	Parental	GKEKK	EEQVISLGPQVAEGENVFGVCHIFASF	NDTFV	3	C21:+57.021	988.4800145	2962.416643	0.000662267	8	N	10	37
P62264	Parental	IFASF	NDTFVHVTDLSGK	ETICR	2		716.8575022	1431.699404	0.000451244	5	N	37	50
P62264	Parental	GKEKK	EEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGK	ETICR	4	C21:+57.021	1095.034172	4376.105488	0.002296037	1	N	10	50
P62264	Parental	MKIGR	IEDVTPIPSDSTR	RKGGR	2		715.3626174	1428.709635	0.001352548	1	N	128	141
P62267	Exosome	KNGKK	ITAFVPNDGCLNFIEENDEVLVAGFGR	KGHAV	3	C10:+57.021	999.4871691	2995.438107	0.000451244	10	N	80	107
P62267	Exosome	IKNGK	KITAFVPNDGCLNFIEENDEVLVAGFGR	KGHAV	3	C11:+57.021	1042.18549	3123.53307	0.000451244	1	N	79	107
P62267	Parental	GCLNF	IEENDEVLVAGFGR	KGHAV	2		774.3891665	1546.762733	0.000451244	10	N	93	107
P62267	Parental	KNGKK	ITAFVPNDGCLNFIEENDEVLVAGFGR	KGHAV	3	C10:+57.021	999.4871691	2995.438107	0.000451244	23	N	80	107
P62267	Parental	IKNGK	KITAFVPNDGCLNFIEENDEVLVAGFGR	KGHAV	3	C11:+57.021	1042.18549	3123.53307	0.000451244	9	N	79	107
P62281	Exosome	SPCFR	DVQIGDIVTVGECRPLSK	TVRFN	2	C13:+57.021	993.5201549	1985.02471	0.000451244	2	N	118	136
P62281	Exosome	SPCFR	DVQIGDIVTVGECRPLSK	TVRFN	3	C13:+57.021	662.6827033	1985.02471	0.000622848	4	N	118	136
P62281	Exosome	YIDKK	CPFTGNVSIR	GRILS	2	C1:+57.021	575.7876056	1149.559611	0.001654178	1	N	59	69
P62281	Parental	SPCFR	DVQIGDIVTVGECRPLSK	TVRFN	2	C13:+57.021	993.5201549	1985.02471	0.000451244	17	N	118	136
P62281	Parental	SPCFR	DVQIGDIVTVGECRPLSK	TVRFN	3	C13:+57.021	662.6827033	1985.02471	0.000451244	6	N	118	136
P62281	Parental	LSPCF	RDVQIGDIVTVGECRPLSK	TVRFN	2	C14:+57.021	1071.57071	2141.125821	0.002080925	1	N	117	136
P62281	Parental	LSPCF	RDVQIGDIVTVGECRPLSK	TVRFN	3	C14:+57.021	714.716407	2141.125821	0.000451244	9	N	117	136
P62281	Parental	LSPCF	RDVQIGDIVTVGECRPLSK	TVRFN	4	C14:+57.021	536.2892552	2141.125821	0.000451244	1	N	117	136
P62315	Exosome	KMTLK	NREPVQLETLSIR	GNNIR	2		777.9340756	1553.852551	0.000823681	3	N	48	61
P62315	Exosome	KMTLK	NREPVQLETLSIR	GNNIR	3		518.9586504	1553.852551	0.001329271	3	N	48	61
P62315	Exosome	RFLMK	LSHETVTIELK	NGTQV	3		423.9070045	1268.697613	0.000451244	4	N	9	20
P62315	Exosome	GNNIR	YFILPDSLPLDTLLVDVEPK	VKSKK	2		1144.12775	2286.2399	0.000451244	37	N	66	86
P62315	Exosome	GNNIR	YFILPDSLPLDTLLVDVEPK	VKSKK	3		763.0877666	2286.2399	0.000451244	30	N	66	86
P62315	Exosome	RYFIL	PDSLPLDTLLVDVEPK	VKSKK	2		875.9778145	1749.940029	0.000622848	2	N	70	86
P62315	Exosome	NNIRY	FILPDSLPLDTLLVDVEPK	VKSKK	2		1062.596086	2123.176571	0.000622848	1	N	67	86
P62315	Exosome	NIRYF	ILPDSLPLDTLLVDVEPK	VKSKK	2		989.0618786	1976.108157	0.00091018	4	N	68	86
P62315	Parental	KMTLK	NREPVQLETLSIR	GNNIR	3		518.9586504	1553.852551	0.002374549	1	N	48	61
P62315	Parental	RFLMK	LSHETVTIELK	NGTQV	3		423.9070045	1268.697613	0.002145581	1	N	9	20
P62315	Parental	GNNIR	YFILPDSLPLDTLL	VDVEP	2		810.4507042	1618.885808	0.000451244	6	N	66	80
P62315	Parental	GNNIR	YFILPDSLPL	DTLLV	2		589.3293292	1176.643058	0.002813207	1	N	66	76
P62317	Exosome	ELQKR	EEEEFNTGPLSVLTQSVK	NNTQV	2		1004.000007	2005.984413	0.000451244	38	N	19	37
P62317	Exosome	EELQK	REEEEFNTGPLSVLTQSVK	NNTQV	2		1082.050562	2162.085524	0.000451244	6	N	18	37
P62317	Exosome	EELQK	REEEEFNTGPLSVLTQSVK	NNTQV	3		721.7029748	2162.085524	0.000451244	24	N	18	37
P62317	Parental	ELQKR	EEEEFNTGPLSVLTQSVK	NNTQV	2		1004.000007	2005.984413	0.000451244	23	N	19	37
P62317	Parental	EELQK	REEEEFNTGPLSVLTQSVK	NNTQV	2		1082.050562	2162.085524	0.000451244	2	N	18	37
P62317	Parental	EELQK	REEEEFNTGPLSVLTQSVK	NNTQV	3		721.7029748	2162.085524	0.000451244	9	N	18	37
P62320	Exosome	GVPIK	VLHEAEGHIVTCETNTGEVYR	GKLIE	2	C12:+57.021	1207.574178	2413.132757	0.000451244	39	N	8	29
P62320	Exosome	GVPIK	VLHEAEGHIVTCETNTGEVYR	GKLIE	3	C12:+57.021	805.3853857	2413.132757	0.000451244	92	N	8	29

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62320	Exosome	GVPIK	VLHEAEGHIVTCETNTGEVYR	GKLIE	4	C12:+57.021	604.2909892	2413.132757	0.000451244	11	N	8	29
P62320	Exosome	YRDGR	VAQLEQVYIR	GSKIR	2		609.8462091	1217.676818	0.001654178	9	N	54	64
P62320	Parental	GVPIK	VLHEAEGHIVTCETNTGEVYRGK	LIEAE	3	C12:+57.021	867.0908613	2598.249184	0.000451244	3	N	8	31
P62320	Parental	GVPIK	VLHEAEGHIVTCETNTGEVYRGK	LIEAE	4	C12:+57.021	650.570096	2598.249184	0.001763695	3	N	8	31
P62320	Parental	GVPIK	VLHEAEGHIVTCETNTGEVYR	GKLIE	2	C12:+57.021	1207.574178	2413.132757	0.000451244	44	N	8	29
P62320	Parental	GVPIK	VLHEAEGHIVTCETNTGEVYR	GKLIE	3	C12:+57.021	805.3853857	2413.132757	0.000451244	97	N	8	29
P62320	Parental	GVPIK	VLHEAEGHIVTCETNTGEVY	RGKLI	2	C12:+57.021	1129.523623	2257.031646	0.000622848	11	N	8	28
P62320	Parental	VPIKV	LHEAEGHIVTCETNTGEVYR	GKLIE	3	C11:+57.021	772.362581	2314.064343	0.000451244	3	N	9	29
P62331	Exosome	RIRDR	NWYVQPSCATSGDGLYEGLTWLTSNYKS	-	3	C8:+57.021	1066.489238	3196.444315	0.000622848	10	N	147	175
P62331	Exosome	LYKLK	LGQSVTTIPTVGFNVETVTYK	NVKFN	2		1127.602431	2253.189261	0.000870037	4	N	34	55
P62331	Exosome	RIRDR	NWYVQPSCATSGDGLYEGLTWLTSNYK	S-	3	C8:+57.021	1037.478562	3109.412286	0.000622848	8	N	147	174
P62331	Exosome	DREMR	DAIILIFANK	QDLPD	2		559.3349459	1116.654292	0.000622848	7	N	113	123
P62331	Exosome	RPLWR	HYYTGTQGLIFVVDCADRDR	IDEAR	3	C15:+57.021	796.0467043	2385.116713	0.000451244	3	N	75	95
P62331	Parental	RIRDR	NWYVQPSCATSGDGLYEGLTWLTSNYKS	-	3	C8:+57.021	1066.489238	3196.444315	0.000451244	9	N	147	175
P62331	Parental	RIRDR	NWYVQPSCATSGDGLYEGLTWLTSNYK	S-	3	C8:+57.021	1037.478562	3109.412286	0.000451244	11	N	147	174
P62334	Exosome	ENDLK	ALQSVGQIVGEVLK	QLTEE	2		720.9251879	1439.834776	0.000451244	24	N	48	62
P62334	Exosome	IRELR	EVIELPLTNPELFQR	VGIIP	2		899.4914234	1796.967247	0.000451244	10	N	146	161
P62334	Exosome	ENDLK	ALQSVGQIVGEVL	KQLTE	2		656.8777063	1311.739813	0.002519933	1	N	48	61
P62334	Parental	ENDLK	ALQSVGQIVGEVLK	QLTEE	2		720.9251879	1439.834776	0.000451244	10	N	48	62
P62334	Parental	IRELR	EVIELPLTNPELFQR	VGIIP	2		899.4914234	1796.967247	0.000451244	6	N	146	161
P62334	Parental	CNFLK	VVSSSIVDKYIGESAR	LIREM	3		570.640987	1708.899561	0.001654178	2	N	197	213
P62482	Exosome	AIAER	LGCTLPQLAIAWCLR	NEGVS	2	C3:+57.021,C13:+57.021	886.4709938	1770.926388	0.000622848	10	N	298	313
P62482	Exosome	QVLPK	LSSSIVHEIDSILGNKPYSK	KDYRS	3		729.7272318	2186.158295	0.001162105	1	N	342	362
P62482	Exosome	AWCLR	NEGVSSVLLGASNAEQLMENIGAIQVLPK	LSSSI	3	M18:+15.995	999.8574451	2996.548935	0.000622848	2	N	313	342
P62492	Exosome	AFAEK	NGLSFIETSALDSTNVEAAFQTILTEIYR	IVSQK	3		1068.542262	3202.603387	0.000451244	20	N	145	174
P62492	Exosome	SAYYR	GAVGALLVYDIAK	HLTYE	2		645.3773421	1288.739084	0.000451244	19	Y	82	95
P62492	Parental	AFAEK	NGLSFIETSALDSTNVEAAFQTILTEIYR	IVSQK	3		1068.542262	3202.603387	0.000451244	37	N	145	174
P62492	Parental	TDEAR	AFAEKNGLSFIETSALDSTNVEAAFQTILTEIYR	IVSQK	3		1250.635662	3748.883585	0.002296037	2	N	140	174
P62492	Parental	GKTIK	AQIWDTAGQER	YRAIT	2		637.8103549	1273.60511	0.000451244	21	Y	61	72
P62492	Parental	SAYYR	GAVGALLVYDIAK	HLTYE	2		645.3773421	1288.739084	0.000451244	14	Y	82	95
P62702	Exosome	TGPHK	LRECLPLIIFLR	NRLKY	3	C4:+57.021	514.9781745	1541.911124	0.001463592	7	N	37	49
P62702	Exosome	DPLIK	VNDTIQIDLETGKITDFIK	FDTGN	3		721.7234873	2162.147062	0.001654178	1	N	155	174
P62702	Exosome	PHKLR	ECLPLIIFLR	NRLKY	2	C2:+57.021	637.3707742	1272.725948	0.002663018	1	N	39	49
P62702	Parental	DPLIK	VNDTIQIDLETGK	ITDFI	2		723.3782675	1444.740935	0.000451244	5	N	155	168
P62715	Exosome	GISPR	GAGYTFGQDISETFNHANGLTLVSR	AHQLV	3		885.7652968	2654.272491	0.000451244	25	N	214	239
P62715	Exosome	WCHDR	NVVTIFSAPNYCYR	CGNQA	2	C12:+57.021	852.4144301	1702.81326	0.000451244	20	N	254	268
P62715	Exosome	DDTLK	YSFLQFDPAPR	RGEPH	2		670.8358414	1339.656083	0.000451244	1	N	283	294
P62715	Exosome	ANVWK	YFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIR	ALDRL	4	C21:+57.021	1056.534813	4222.108054	0.001871652	4	N	144	181
P62715	Exosome	NHESR	QITQVYGFYDECLR	KYGNA	2	C12:+57.021	896.4224521	1790.829304	0.000451244	7	N	121	135
P62715	Exosome	KAFTK	ELDQWVEQLNECK	QLNEN	2	C12:+57.021	845.8909848	1689.76637	0.000451244	5	N	8	21
P62715	Exosome	NHESR	QITQVYGFYDECLRK	YGNAN	3	C12:+57.021	640.6492224	1918.924267	0.002080925	1	N	121	136
P62715	Parental	GISPR	GAGYTFGQDISETFNHANGLTLVSR	AHQLV	3		885.7652968	2654.272491	0.000451244	16	N	214	239
P62715	Parental	WCHDR	NVVTIFSAPNYCYR	CGNQA	2	C12:+57.021	852.4144301	1702.81326	0.000451244	12	N	254	268
P62715	Parental	VWKYF	TDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIR	ALDRL	4	C19:+57.021	979.0018778	3911.976311	0.002080925	1	N	146	181
P62715	Parental	DDTLK	YSFLQFDPAPR	RGEPH	2		670.8358414	1339.656083	0.000622848	6	N	283	294
P62715	Parental	ANVWK	YFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIR	ALDRL	4	C21:+57.021	1056.534813	4222.108054	0.001871652	3	N	144	181
P62715	Parental	NHESR	QITQVYGFYDECLR	KYGNA	2	C12:+57.021	896.4224521	1790.829304	0.000451244	5	N	121	135
P62715	Parental	KAFTK	ELDQWVEQLNECK	QLNEN	2	C12:+57.021	845.8909848	1689.76637	0.000870037	2	N	8	21
P62746	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2		1004.966498	2007.917396	0.000451244	25	Y	51	68
P62746	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	3		670.3135987	2007.917396	0.002813207	2	Y	51	68
P62746	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	Q1:-17.027	996.4529981	1990.890396	0.000622848	3	Y	51	68
P62746	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	[0:-17.027	996.4529981	1990.890396	0.000823681	4	Y	51	68
P62746	Exosome	IVFSK	DEFPEVYVPTVFENYVADIEVDGK	QVELA	2		1387.658328	2773.301056	0.000451244	11	N	27	51
P62746	Exosome	IVFSK	DEFPEVYVPTVFENYVADIEVDGK	QVELA	3		925.4414855	2773.301056	0.000451244	19	N	27	51
P62746	Exosome	GACGK	TCLLIVFSK	DEFPE	2	C2:+57.021	540.8100181	1079.604436	0.0007646	23	Y	18	27
P62746	Parental	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2		1004.966498	2007.917396	0.000451244	33	Y	51	68
P62746	Parental	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	Q1:-17.027	996.4529981	1990.890396	0.000622848	3	Y	51	68
P62746	Parental	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	[0:-17.027	996.4529981	1990.890396	0.000823681	7	Y	51	68
P62746	Parental	VPTVF	ENYVADIEVDGKQVELALWDTAGQEDYDR	LRPLS	3		1114.520186	3340.537158	0.000451244	3	Y	39	68
P62746	Parental	IVFSK	DEFPEVYVPTVFENYVADIEVDGK	QVELA	2		1387.658328	2773.301056	0.000451244	9	N	27	51
P62746	Parental	IVFSK	DEFPEVYVPTVFENYVADIEVDGK	QVELA	3		925.4414855	2773.301056	0.000451244	19	N	27	51
P62746	Parental	GACGK	TCLLIVFSKDEFPEVYVPTVFENYVADIEVDGK	QVELA	3	C2:+57.021	1279.306111	3834.894932	0.000451244	3	N	18	51
P62746	Parental	GACGK	TCLLIVFSK	DEFPE	2	C2:+57.021	540.8100181	1079.604436	0.000823681	10	Y	18	27
P62751	Parental	KAYVR	LAPDYDALDVANKIGII	-	2		900.9912562	1799.966912	0.000637154	4	N	139	156
P62751	Parental	KAYVR	LAPDYDALDVANKIGII	-	3		600.9967708	1799.966912	0.000637154	2	N	139	156

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62751	Parental	KKAYV	RLAPDYDALDVANK	IGII-	2		780.9049838	1559.794368	0.000451244	14	N	138	152
P62751	Parental	KAYVR	LAPDYDALDVANK	IGII-	2		702.8544282	1403.693256	0.000622848	10	N	139	152
P62754	Exosome	FYEKR	MATEVAADALGEEWKGY	VVRIS	2	M1:+15.995	928.9227565	1855.829913	0.00091018	2	N	31	48
P62754	Parental	EKRMA	TEVAADALGEEWKGYVVR	ISGGN	3		665.0062175	1991.995253	0.000662267	1	N	33	51
P62754	Parental	FYEKR	MATEVAADALGEEWKGY	VVRIS	2		920.9252565	1839.834913	0.000451244	6	N	31	48
P62754	Parental	-MK	LNISFPATGCQK	LIEVD	2	C10:+57.021	668.3402024	1334.664805	0.000451244	15	N	2	14
P62754	Parental	-	MKLNISFPATGCQK	LIEVD	2	C12:+57.021	797.9079268	1593.800254	0.0007646	4	N	0	14
P62754	Parental	-	MKLNISFPATGCQK	LIEVD	3	C12:+57.021	532.2745512	1593.800254	0.00091018	2	N	0	14
P62754	Parental	EKRMA	TEVAADALGEEWK	GYVVR	2		709.8440605	1417.672521	0.002145581	1	N	33	46
P62754	Parental	KKGEK	DIPGLTDTTVPR	RLGPK	2		642.8438635	1283.672127	0.002080925	1	N	119	131
P62774	Exosome	DKTVK	GPDGLTALEATDNQAIK	ALLQ-	2		857.4368451	1712.85809	0.000622848	9	N	97	114
P62774	Exosome	LEGGR	KPLHYAADCGQLEILEFLLLK	GADIN	3	C9:+57.021	824.4507792	2470.328938	0.000451244	6	N	36	57
P62774	Parental	FLLLK	GADINAPDKHHITPLLSAVYEGHVSCVK	LLLSK	3	C26:+57.021	1010.182191	3027.523174	0.000451244	17	N	57	85
P62774	Parental	FLLLK	GADINAPDKHHITPLLSAVYEGHVSCVK	LLLSK	4	C26:+57.021	757.8885936	3027.523174	0.000451244	21	N	57	85
P62774	Parental	DKTVK	GPDGLTALEATDNQAIK	ALLQ-	2		857.4368451	1712.85809	0.000451244	27	N	97	114
P62774	Parental	EDVNR	TLEGGRKPLHYAADCGQLEILEFLLLK	GADIN	3	C15:+57.021	1028.890237	3083.647312	0.000451244	5	N	30	57
P62774	Parental	LEGGR	KPLHYAADCGQLEILEFLLLK	GADIN	3	C9:+57.021	824.4507792	2470.328938	0.000451244	25	N	36	57
P62774	Parental	LEGGR	KPLHYAADCGQLEILEFLLLK	GADIN	4	C9:+57.021	618.5900344	2470.328938	0.000998612	3	N	36	57
P62806	Exosome	RKVLR	DNIQGITKPAIR	RLARR	2		663.3809475	1324.746295	0.000451244	210	N	24	36
P62806	Exosome	RKVLR	DNIQGITKPAIR	RLARR	3		442.5898983	1324.746295	0.000451244	116	N	24	36
P62806	Exosome	KRKTV	TAMDVVYALKR	QGRTL	2		633.8478951	1265.68019	0.000451244	7	N	82	93
P62806	Exosome	KRKTV	TAMDVVYALKR	QGRTL	2	M3:+15.995	641.8453951	1281.67519	0.000637154	3	N	82	93
P62806	Exosome	GGVKR	ISGLIYEETRGVLK	VFLEN	2		789.4490272	1576.882454	0.000451244	25	N	46	60
P62806	Exosome	GGVKR	ISGLIYEETRGVLK	VFLEN	3		526.6352848	1576.882454	0.000451244	54	N	46	60
P62806	Exosome	VLKVF	LENVIRDAVTYTEHAK	RKTVT	2		929.9870365	1857.958473	0.000451244	4	N	62	78
P62806	Exosome	VLKVF	LENVIRDAVTYTEHAK	RKTVT	3		620.327291	1857.958473	0.000451244	12	N	62	78
P62806	Exosome	RGVLK	VFLENVIR	DAVTY	2		495.293081	988.5705621	0.000451244	1505	N	60	68
P62806	Exosome	HAKRK	TVTAMDVVYALKR	QGRTL	2		733.9059414	1465.796283	0.000451244	27	N	80	93
P62806	Exosome	HAKRK	TVTAMDVVYALKR	QGRTL	3		489.6065609	1465.796283	0.000451244	43	N	80	93
P62806	Exosome	HAKRK	TVTAMDVVYALKR	QGRTL	2	M5:+15.995	741.9034414	1481.791283	0.000451244	99	N	80	93
P62806	Exosome	HAKRK	TVTAMDVVYALKR	QGRTL	3	M5:+15.995	494.9382276	1481.791283	0.000451244	108	N	80	93
P62806	Exosome	GVLKV	FLENVIRDAVTYTEHAK	RKTVT	2		1003.521243	2005.026887	0.000622848	4	N	61	78
P62806	Exosome	GVLKV	FLENVIRDAVTYTEHAK	RKTVT	3		669.3500957	2005.026887	0.000823681	1	N	61	78
P62806	Exosome	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	2		1053.055451	2104.095301	0.000451244	34	N	60	78
P62806	Exosome	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	3		702.3729003	2104.095301	0.000451244	197	N	60	78
P62806	Exosome	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	4		527.0316253	2104.095301	0.000451244	34	N	60	78
P62806	Exosome	RGVLK	VFLENVIRDAVTY	TEHAK	2		769.9148201	1537.81404	0.001264573	3	N	60	73
P62806	Exosome	GGVKR	ISGLIYEETR	GVLKV	2		590.8145747	1179.613549	0.000451244	883	N	46	56
P62806	Exosome	YEETR	GVLKVFLENVIR	DAVTY	2		693.9275335	1385.839467	0.000622848	9	N	56	68
P62806	Exosome	YEETR	GVLKVFLENVIR	DAVTY	3		462.954289	1385.839467	0.000451244	19	N	56	68
P62806	Exosome	ENVIR	DAVTYTEHAK	RKTVT	2		567.7754495	1133.535299	0.000451244	104	N	68	78
P62806	Exosome	HRKVL	RDNIQGITKPAIR	RLARR	2		741.431503	1480.847406	0.000662267	8	N	23	36
P62806	Exosome	HRKVL	RDNIQGITKPAIR	RLARR	3		494.623602	1480.847406	0.000451244	36	N	23	36
P62806	Exosome	RGGVK	RISGLIYEETR	GVLKV	2		668.8651302	1335.71466	0.000451244	27	N	45	56
P62806	Exosome	RGGVK	RISGLIYEETR	GVLKV	3		446.2460202	1335.71466	0.000451244	10	N	45	56
P62806	Exosome	GGVKR	ISGLIYEETRG	VLKVF	2		619.3253065	1236.635013	0.000451244	20	N	46	57
P62806	Exosome	EHAKR	KTVTAMDVVYALK	RQGRT	2		719.9028674	1437.790135	0.000451244	2	N	79	92
P62806	Exosome	EHAKR	KTVTAMDVVYALK	RQGRT	3		480.2711783	1437.790135	0.000451244	23	N	79	92
P62806	Exosome	EHAKR	KTVTAMDVVYALK	RQGRT	2	M6:+15.995	727.9003674	1453.785135	0.000451244	38	N	79	92
P62806	Exosome	EHAKR	KTVTAMDVVYALK	RQGRT	3	M6:+15.995	485.6028449	1453.785135	0.000451244	23	N	79	92
P62806	Exosome	HAKRK	TVTAMDVVYALK	RQGRT	2		655.8553858	1309.695172	0.000451244	24	N	80	92
P62806	Exosome	HAKRK	TVTAMDVVYALK	RQGRT	3		437.5728572	1309.695172	0.000451244	13	N	80	92
P62806	Exosome	HAKRK	TVTAMDVVYALK	RQGRT	2	M5:+15.995	663.8528858	1325.690172	0.000451244	243	N	80	92
P62806	Exosome	HAKRK	TVTAMDVVYALK	RQGRT	3	M5:+15.995	442.9045239	1325.690172	0.000451244	8	N	80	92
P62806	Exosome	RKTVT	AMDVVYALK	RQGRT	2	M2:+15.995	513.2710003	1024.526401	0.002981883	1	N	83	92
P62806	Exosome	RGVLK	VFLENVIRDAVTYTEH	AKRKT	2		953.489412	1904.963224	0.000622848	8	N	60	76
P62806	Exosome	RGVLK	VFLENVIRDAVTYTEH	AKRKT	3		635.9955413	1904.963224	0.000451244	28	N	60	76
P62806	Exosome	RHRKV	LRDNIQGITKPAIR	RLARR	3		532.3182901	1593.93147	0.001463592	2	N	22	36
P62806	Exosome	KRKTV	TAMDVVYALK	RQGRT	2		555.7973395	1109.579079	0.002374549	1	N	82	92
P62806	Exosome	KRHRK	VLRDNIQGITKPAIR	RLARR	2		847.5077421	1692.999884	0.000998612	1	N	21	36
P62806	Exosome	LKVFL	ENVIRDAVTYTEHAK	RKTVT	2		873.4450044	1744.874409	0.000851441	1	N	63	78
P62806	Parental	RKVLR	DNIQGITKPAIR	RLARR	2		663.3809475	1324.746295	0.000451244	99	N	24	36
P62806	Parental	RKVLR	DNIQGITKPAIR	RLARR	3		442.5898983	1324.746295	0.000451244	73	N	24	36
P62806	Parental	KRKTV	TAMDVVYALKR	QGRTL	2		633.8478951	1265.68019	0.000451244	3	N	82	93
P62806	Parental	GGVKR	ISGLIYEETRGVLK	VFLEN	2		789.4490272	1576.882454	0.000451244	11	N	46	60

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62806	Parental	VLKVF	LENVIRDAVTYTEHAK	RKTVT	2		929.9870365	1857.958473	0.001943752	1	N	62	78
P62806	Parental	VLKVF	LENVIRDAVTYTEHAK	RKTVT	4		465.4974182	1857.958473	0.000870037	1	N	62	78
P62806	Parental	RGVLK	VFLENVIR	DAVTY	2		495.293081	988.5705621	0.000451244	797	N	60	68
P62806	Parental	HAKRK	TVTAMDVVYALKR	QGRTL	2		733.9059414	1465.796283	0.000637154	3	N	80	93
P62806	Parental	HAKRK	TVTAMDVVYALKR	QGRTL	3		489.6065609	1465.796283	0.000451244	13	N	80	93
P62806	Parental	HAKRK	TVTAMDVVYALKR	QGRTL	2	M5:+15.995	741.9034414	1481.791283	0.000451244	1	N	80	93
P62806	Parental	HAKRK	TVTAMDVVYALKR	QGRTL	3	M5:+15.995	494.9382276	1481.791283	0.001264573	5	N	80	93
P62806	Parental	GVLKV	FLENVIRDAVTYTEHAK	RKTVT	3		669.3500957	2005.026887	0.000622848	4	N	61	78
P62806	Parental	GVLKV	FLENVIRDAVTYTEHAK	RKTVT	4		502.2645217	2005.026887	0.000622848	3	N	61	78
P62806	Parental	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	2		1053.055451	2104.095301	0.000451244	10	N	60	78
P62806	Parental	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	3		702.3729003	2104.095301	0.000451244	48	N	60	78
P62806	Parental	RGVLK	VFLENVIRDAVTYTEHAK	RKTVT	4		527.0316253	2104.095301	0.000451244	20	N	60	78
P62806	Parental	RGVLK	VFLENVIRDAVTY	TEHAK	2		769.9148201	1537.81404	0.000622848	3	N	60	73
P62806	Parental	RGVLK	VFLENVIRDAVTY	TEHAK	3		513.6124801	1537.81404	0.001463592	2	N	60	73
P62806	Parental	GGVKR	ISGLIYEETR	GVLKV	2		590.8145747	1179.613549	0.000451244	68	N	46	56
P62806	Parental	YEETR	GVLKVFLENVIR	DAVTY	3		462.954289	1385.839467	0.000451244	1	N	56	68
P62806	Parental	HRKVL	RDNIQGITKPAIR	RLARR	2		741.431503	1480.847406	0.000662267	1	N	23	36
P62806	Parental	HRKVL	RDNIQGITKPAIR	RLARR	3		494.623602	1480.847406	0.000451244	30	N	23	36
P62806	Parental	HAKRK	TVTAMDVVYALK	RQGRT	2		655.8553858	1309.695172	0.002080925	1	N	80	92
P62814	Exosome	RLTYK	TVSGVNGPLVILDHVK	FPRYA	3		549.9863175	1646.935553	0.000637154	4	N	48	64
P62814	Exosome	ARGQK	IPIFSAAGLPHNEIAAQICR	QAGLV	2	C19:+57.021	1089.578339	2177.141077	0.000451244	30	N	188	208
P62814	Exosome	ARGQK	IPIFSAAGLPHNEIAAQICR	QAGLV	3	C19:+57.021	726.7214924	2177.141077	0.000451244	36	N	188	208
P62814	Exosome	PYENR	TVYETLDIGWQLLR	IFPKE	2		853.959759	1705.903918	0.000451244	35	N	471	485
P62814	Exosome	PYENR	TVYETLDIGWQLLR	IFPKE	3		569.6424394	1705.903918	0.001699387	1	N	471	485
P62814	Exosome	VQAMK	AVVGEEALTSDDLLYLEFLQKFEK	NFITQ	3		919.8131422	2756.416027	0.000451244	15	N	436	460
P62814	Exosome	VSGSK	AVVQVFEGTSGIDAK	KTSCE	2		760.9019097	1519.788219	0.000451244	27	N	93	108
P62814	Exosome	IITPR	LALTTAEFLAYQCEK	HVLVI	2	C13:+57.021	879.4428532	1756.870106	0.000451244	32	N	276	291
P62814	Exosome	IITPR	LALTTAEFLAYQCEK	HVLVI	3	C13:+57.021	586.6311688	1756.870106	0.000451244	8	N	276	291
P62814	Exosome	VQAMK	AVVGEEALTSDDLLYLEFLQK	FEKNF	2		1177.112828	2352.210056	0.000451244	32	N	436	457
P62814	Exosome	VQAMK	AVVGEEALTSDDLLYLEFLQK	FEKNF	3		785.0778188	2352.210056	0.000735798	5	N	436	457
P62814	Exosome	VKFPR	YAEIVHLTLPDGTKR	SGQVL	3		571.6497054	1711.925716	0.00091018	1	N	67	82
P62814	Exosome	QLHNR	QIYPPINVLPSLSR	LMKSA	2		798.959562	1595.903524	0.001162105	4	N	386	400
P62814	Exosome	GIDAK	KTSCEFTGDILR	TPVSE	3	C4:+57.021	476.2383826	1425.691748	0.001352548	3	N	108	120
P62814	Parental	RLTYK	TVSGVNGPLVILDHVK	FPRYA	3		549.9863175	1646.935553	0.002453667	1	N	48	64
P62814	Parental	ARGQK	IPIFSAAGLPHNEIAAQICR	QAGLV	2	C19:+57.021	1089.578339	2177.141077	0.000451244	6	N	188	208
P62814	Parental	ARGQK	IPIFSAAGLPHNEIAAQICR	QAGLV	3	C19:+57.021	726.7214924	2177.141077	0.000451244	23	N	188	208
P62814	Parental	RLTYK	TVSGVNGPLVILDHVKFPR	YAEIV	4		512.7972604	2047.157842	0.000622848	5	N	48	67
P62814	Parental	PYENR	TVYETLDIGWQLLR	IFPKE	2		853.959759	1705.903918	0.000451244	6	N	471	485
P62814	Parental	PYENR	TVYETLDIGWQLLR	IFPKE	3		569.6424394	1705.903918	0.000451244	5	N	471	485
P62814	Parental	VQAMK	AVVGEEALTSDDLLYLEFLQKFEK	NFITQ	3		919.8131422	2756.416027	0.000451244	6	N	436	460
P62814	Parental	VSGSK	AVVQVFEGTSGIDAK	KTSCE	2		760.9019097	1519.788219	0.000451244	15	N	93	108
P62814	Parental	IITPR	LALTTAEFLAYQCEK	HVLVI	3	C13:+57.021	586.6311688	1756.870106	0.001352548	1	N	276	291
P62814	Parental	VQAMK	AVVGEEALTSDDLLYLEFLQK	FEKNF	2		1177.112828	2352.210056	0.000451244	12	N	436	457
P62814	Parental	VKFPR	YAEIVHLTLPDGTKR	SGQVL	4		428.989229	1711.925716	0.001329271	1	N	67	82
P62814	Parental	QLHNR	QIYPPINVLPSLSR	LMKSA	2		798.959562	1595.903524	0.001699387	2	N	386	400
P62814	Parental	VQAMK	AVVGEEALTSDDLLY	LEFLQ	2		797.8964901	1593.77738	0.001162105	2	N	436	451
P62814	Parental	QKFEK	NFITQGPYENR	TVYET	2		669.826005	1337.63641	0.001395409	1	N	460	471
P62827	Exosome	DISAK	SNYNFEKPFLWLAR	KLIGD	2		892.9600934	1783.904587	0.000451244	27	N	152	166
P62827	Exosome	DISAK	SNYNFEKPFLWLAR	KLIGD	3		595.6426622	1783.904587	0.000451244	64	N	152	166
P62827	Exosome	FHTNR	GPIKFNVWDTAGQEK	FGGLR	2		845.4339084	1688.852217	0.000451244	7	N	56	71
P62827	Exosome	FHTNR	GPIKFNVWDTAGQEK	FGGLR	3		563.9585389	1688.852217	0.000823681	8	N	56	71
P62827	Exosome	RGPIK	FNVWDTAGQEK	FGGLR	2		647.8072809	1293.598962	0.000451244	34	N	60	71
P62827	Exosome	RDLVR	VCENIPIVLCGNK	VDIKD	2	C2:+57.021,C10:+57.021	758.3865953	1514.757591	0.000451244	16	N	110	123
P62827	Exosome	EFEKK	YVATLGVEVHPLVFHTNR	GPIKF	2		1026.555421	2051.095241	0.000451244	23	N	38	56
P62827	Exosome	EFEKK	YVATLGVEVHPLVFHTNR	GPIKF	3		684.7062138	2051.095241	0.000451244	39	N	38	56
P62827	Exosome	EFEKK	YVATLGVEVHPLVFHTNR	GPIKF	4		513.7816103	2051.095241	0.000451244	35	N	38	56
P62827	Exosome	FHRKK	NLQYYDISAK	SNYNF	2		607.8067496	1213.597899	0.000451244	14	N	142	152
P62827	Exosome	RDLVR	VCENIPIVLCGNKVDIK	DRKVK	2	C2:+57.021,C10:+57.021	986.0237875	1970.031975	0.000451244	22	N	110	127
P62827	Exosome	RDLVR	VCENIPIVLCGNKVDIK	DRKVK	3	C2:+57.021,C10:+57.021	657.685125	1970.031975	0.000451244	26	N	110	127
P62827	Exosome	GEFEK	KYVATLGVEVHPLVFHTNR	GPIKF	2		1090.602902	2179.190204	0.000622848	1	N	37	56
P62827	Exosome	GEFEK	KYVATLGVEVHPLVFHTNR	GPIKF	3		727.4045348	2179.190204	0.000451244	10	N	37	56
P62827	Exosome	GEFEK	KYVATLGVEVHPLVFHTNR	GPIKF	4		545.8053511	2179.190204	0.000451244	12	N	37	56
P62827	Exosome	AAQYE	HDLEVAQTTALPDEDDDL	-	2		998.9532533	1995.890907	0.001763695	6	N	198	216
P62827	Exosome	PPEVV	MDPALAAQYEHDLEVAQTTALPDEDDDL	-	3		1029.464802	3085.371005	0.000451244	29	N	188	216
P62827	Exosome	PPEVV	MDPALAAQYEHDLEVAQTTALPDEDDDL	-	3	M1:+15.995	1034.796468	3101.366005	0.002080925	3	N	188	216

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62827	Exosome	LWLAR	KLIGDPNLEFVAMPALAPPEVV	MDPAL	2		1160.63522	2319.254839	0.000451244	5	N	166	188
P62827	Exosome	LWLAR	KLIGDPNLEFVAMPALAPPEVV	MDPAL	2	M13:+15.995	1168.63272	2335.249839	0.000622848	8	N	166	188
P62827	Exosome	LAAQY	EHDLEVAQTTALPDEDDDL	-	2		1063.47455	2124.9335	0.000451244	6	N	197	216
P62827	Exosome	VMDPA	LAAQYEHDLEVAQTTALPDEDDDL	-	2		1336.614649	2671.213698	0.001839721	1	N	192	216
P62827	Exosome	DISAK	SNYNFEKPFLW	LARKL	2		722.8489488	1443.682298	0.000451244	7	N	152	163
P62827	Exosome	PALAA	QYEHDLEVAQTTALPDEDDDL	-	2		1209.035503	2416.055406	0.000451244	2	N	195	216
P62827	Exosome	WLARK	LIGDPNLEFVAMPALAPPEVV	MDPAL	2		1096.587738	2191.159876	0.001162105	1	N	167	188
P62827	Exosome	WLARK	LIGDPNLEFVAMPALAPPEVV	MDPAL	2	M12:+15.995	1104.585238	2207.154876	0.000622848	2	N	167	188
P62827	Parental	DISAK	SNYNFEKPFLWLAR	KLIGD	2		892.9600934	1783.904587	0.000622848	1	N	152	166
P62827	Parental	DISAK	SNYNFEKPFLWLAR	KLIGD	3		595.6426622	1783.904587	0.000451244	32	N	152	166
P62827	Parental	FHTNR	GPIKFNVWDTAGQEK	FGGLR	2		845.4339084	1688.852217	0.000451244	5	N	56	71
P62827	Parental	RGPIK	FNVWDTAGQEK	FGGLR	2		647.8072809	1293.598962	0.000451244	7	N	60	71
P62827	Parental	EFEKK	YVATLGVEVHPLVFHTNR	GPIKF	4		513.7816103	2051.095241	0.000451244	8	N	38	56
P62830	Exosome	SGAKF	RISLGLPVGAVINCADNTGAK	NLYII	3	C14:+57.021	709.3847688	2125.130906	0.000823681	1	N	14	35
P62830	Exosome	GAKFR	ISLGLPVGAVINCADNTGAK	NLYII	2	C13:+57.021	985.5226976	1969.029795	0.000451244	9	N	15	35
P62830	Parental	SGAKF	RISLGLPVGAVINCADNTGAK	NLYII	2	C14:+57.021	1063.573253	2125.130906	0.000451244	7	N	14	35
P62830	Parental	SGAKF	RISLGLPVGAVINCADNTGAK	NLYII	3	C14:+57.021	709.3847688	2125.130906	0.000451244	17	N	14	35
P62830	Parental	GAKFR	ISLGLPVGAVINCADNTGAK	NLYII	2	C13:+57.021	985.5226976	1969.029795	0.000451244	11	N	15	35
P62830	Parental	GVFLY	FEDNAGVIVNNK	GEMKG	2		660.3336629	1318.651726	0.000451244	17	N	97	109
P62835	Exosome	FALVY	SITAQSTFNDLQDLR	EQILR	2		854.9291872	1707.842774	0.000451244	6	N	82	97
P62835	Exosome	ESSAK	SKINVNEIFYDLVR	QINRK	2		855.4652086	1708.914817	0.000451244	1	N	149	163
P62835	Exosome	ESSAK	SKINVNEIFYDLVR	QINRK	3		570.6460724	1708.914817	0.000451244	25	N	149	163
P62835	Exosome	GGVGK	SALTVQFVQGIFVEK	YDPTI	2		833.4646772	1664.913754	0.000451244	29	N	16	31
P62835	Exosome	FALVY	SITAQSTFNDLQDLREQILR	VKDTE	3		783.4121949	2347.213185	0.000622848	1	N	82	102
P62835	Exosome	DLYMK	NGQGFALVYSITAQSTFNDLQDLREQILR	VKDTE	3		1099.900784	3296.678952	0.000451244	19	N	73	102
P62835	Exosome	SAKSK	INVNEIFYDLVR	QINRK	2		747.9017127	1493.787825	0.000451244	36	N	151	163
P62835	Exosome	MREYK	LVVLGSGGVGK	SALTV	2		493.3061884	984.5967769	0.001591523	3	N	5	16
P62835	Exosome	DLYMK	NGQGFALVYSITAQSTFNDLQDLR	EQILR	2		1329.662071	2657.308542	0.000662267	1	N	73	97
P62835	Exosome	DLYMK	NGQGFALVYSITAQSTFNDLQDLR	EQILR	3		886.7773139	2657.308542	0.000823681	1	N	73	97
P62835	Parental	FALVY	SITAQSTFNDLQDLR	EQILR	2		854.9291872	1707.842774	0.000451244	16	N	82	97
P62835	Parental	ESSAK	SKINVNEIFYDLVR	QINRK	3		570.6460724	1708.914817	0.000451244	11	N	149	163
P62835	Parental	GGVGK	SALTVQFVQGIFVEK	YDPTI	2		833.4646772	1664.913754	0.000451244	31	N	16	31
P62835	Parental	GGVGK	SALTVQFVQGIFVEK	YDPTI	3		555.9790515	1664.913754	0.000823681	1	N	16	31
P62835	Parental	FALVY	SITAQSTFNDLQDLREQILR	VKDTE	3		783.4121949	2347.213185	0.000451244	5	N	82	102
P62835	Parental	DLYMK	NGQGFALVYSITAQSTFNDLQDLREQILR	VKDTE	3		1099.900784	3296.678952	0.000451244	21	N	73	102
P62835	Parental	QNLAR	QWCNCAFLESSAK	SKINV	2	C3:+57.021,C5:+57.021	800.8478343	1599.680069	0.000451244	9	N	136	149
P62835	Parental	SAKSK	INVNEIFYDLVR	QINRK	2		747.9017127	1493.787825	0.000451244	13	N	151	163
P62835	Parental	GGVGK	SALTVQFVQGIFVEKYDPTIEDSYR	KQVEV	3		969.1593125	2904.454537	0.000451244	5	N	16	41
P62835	Parental	MREYK	LVVLGSGGVGK	SALTV	2		493.3061884	984.5967769	0.001352548	1	N	5	16
P62835	Parental	DLYMK	NGQGFALVYSITAQSTFNDLQDLR	EQILR	3		886.7773139	2657.308542	0.002981883	1	N	73	97
P62858	Exosome	KGPVR	EGDVLTLLESER	EARRL	2		680.8518855	1359.688171	0.000451244	2	N	51	63
P62858	Parental	IRNVK	GPVREGDVLTLLESER	EARRL	3		590.6517746	1768.931924	0.002296037	1	N	47	63
P62858	Parental	KGPVR	EGDVLTLLESER	EARRL	2		680.8518855	1359.688171	0.000451244	15	N	51	63
P62858	Parental	KGPVR	EGDVLTLLESEREAR	RLR-	3		572.9641297	1715.868989	0.000823681	2	N	51	66
P62869	Parental	GLAFR	ADDTFEALRIEPFSSPPELPDVMKPQDSGGSANEQAVQ	-	3		1358.308056	4071.900769	0.001699387	1	N	80	118
P62869	Parental	LDDGK	TLGECGFTSQTARPQAPATVGLAFR	ADDTF	3	C5:+57.021	879.446868	2635.317204	0.000451244	7	N	55	80
P62874	Exosome	IRDAR	KACADATLSQITNNIDPVGR	IQMRT	2	C3:+57.021	1072.54215	2143.0687	0.000451244	1	N	22	42
P62874	Exosome	RDARK	ACADATLSQITNNIDPVGR	IQMRT	2	C2:+57.021	1008.494668	2014.973737	0.000451244	13	N	23	42
P62874	Exosome	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	C14:+57.021,C31:+57.021	1174.509101	3520.503903	0.000451244	48	N	219	251
P62874	Exosome	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	Q1:-17.027,C14:+57.021,C31:+57.021	1168.833434	3503.476903	0.000451244	1	N	219	251
P62874	Exosome	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	[0:-17.027,C14:+57.021,C31:+57.021	1168.833434	3503.476903	0.000451244	3	N	219	251
P62874	Exosome	SKSGR	LLLAGYDDFNCNVWDALKADR	AGVLA	3	C11:+57.021	823.7341263	2468.178979	0.000622848	7	N	283	304
P62874	Exosome	GHDNR	VSCLGVTDDGMAVATGSWDSFLK	IWN-	2	C3:+57.021,M11:+15.995	1216.559391	2431.103183	0.000451244	13	Y	314	337
P62874	Exosome	SKSGR	LLLAGYDDFNCNVWDALK	ADRAG	2	C11:+57.021	1064.014705	2126.013811	0.000451244	20	N	283	301
P62874	Exosome	SQDGK	LIIWDSYTTNK	VHAIP	2		677.3566067	1352.697613	0.000451244	1	Y	78	89
P62874	Parental	IRDAR	KACADATLSQITNNIDPVGR	IQMRT	2	C3:+57.021	1072.54215	2143.0687	0.000451244	8	N	22	42
P62874	Parental	IRDAR	KACADATLSQITNNIDPVGR	IQMRT	3	C3:+57.021	715.3640333	2143.0687	0.002981883	1	N	22	42
P62874	Parental	RDARK	ACADATLSQITNNIDPVGR	IQMRT	2	C2:+57.021	1008.494668	2014.973737	0.000451244	6	N	23	42
P62874	Parental	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	C14:+57.021,C31:+57.021	1174.509101	3520.503903	0.000451244	45	N	219	251
P62874	Parental	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	Q1:-17.027,C14:+57.021,C31:+57.021	1168.833434	3503.476903	0.000451244	1	N	219	251
P62874	Parental	EGMCR	QTFTGHESDINAICFFPNGNAFATGSDDATCR	LFDLR	3	[0:-17.027,C14:+57.021,C31:+57.021	1168.833434	3503.476903	0.000823681	4	N	219	251

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62874	Parental	SKSGR	LLLAGYDDFNCNVWDALKADR	AGVLA	2	C11:+57.021	1235.097289	2468.178979	0.000451244	5	N	283	304
P62874	Parental	SKSGR	LLLAGYDDFNCNVWDALKADR	AGVLA	3	C11:+57.021	823.7341263	2468.178979	0.000451244	13	N	283	304
P62874	Parental	GHDNR	VSCLGVTDDGMAVATGSWDSFLK	IWN-	2	C3:+57.021	1208.561891	2415.108183	0.000451244	5	Y	314	337
P62874	Parental	SKSGR	LLLAGYDDFNCNVWDALK	ADRAG	2	C11:+57.021	1064.014705	2126.013811	0.000451244	14	N	283	301
P62874	Parental	SQDGK	LIIWDSYTTNK	VHAIP	2		677.3566067	1352.697613	0.000451244	10	Y	78	89
P62880	Exosome	IRDAR	KACGDSTLTQITAGLDPVGR	IQMRT	2	C3:+57.021	1030.525969	2059.036337	0.000451244	1	N	22	42
P62880	Exosome	IRDAR	KACGDSTLTQITAGLDPVGR	IQMRT	3	C3:+57.021	687.3532457	2059.036337	0.000451244	6	N	22	42
P62880	Exosome	DSMCR	QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	3	C31:+57.021	1170.528644	3508.562533	0.000451244	41	N	219	251
P62880	Exosome	LFDLR	ADQELLMYSHDNIICGITSVAFSR	SGRLL	3	C15:+57.021	914.1075239	2739.299172	0.000451244	2	N	256	280
P62880	Exosome	LFDLR	ADQELLMYSHDNIICGITSVAFSR	SGRLL	3	M7:+15.995,C15:+57.021	919.4391906	2755.294172	0.000451244	5	N	256	280
P62880	Exosome	VRVSR	ELPGHTGYLSCCR	FLDDN	2	C11:+57.021,C12:+57.021	775.3480015	1548.680403	0.000823681	1	N	137	150
P62880	Exosome	VRVSR	ELPGHTGYLSCCR	FLDDN	3	C11:+57.021,C12:+57.021	517.234601	1548.680403	0.000451244	2	N	137	150
P62880	Exosome	APDGR	TFVSGACDASIK	LWDVR	2	C7:+57.021	628.3032855	1254.590971	0.000451244	5	N	197	209
P62880	Exosome	RDARK	ACGDSTLTQITAGLDPVGR	IQMRT	2	C2:+57.021	966.478487	1930.941374	0.000451244	9	N	23	42
P62880	Exosome	RDARK	ACGDSTLTQITAGLDPVGR	IQMRT	3	C2:+57.021	644.6549247	1930.941374	0.00091018	1	N	23	42
P62880	Exosome	GHDNR	VSCLGVTDDGMAVATGSWDSFLK	IWN-	2	C3:+57.021,M11:+15.995	1216.559391	2431.103183	0.000451244	13	Y	314	337
P62880	Exosome	SQDGK	LIIWDSYTTNK	VHAIP	2		677.3566067	1352.697613	0.000451244	1	Y	78	89
P62880	Exosome	LSCCR	FLDDNQIITSSGDTTCALWDIETGQQTVGF	AGHSG	3	C16:+57.021	1111.514001	3331.518602	0.001352548	2	N	150	180
P62880	Exosome	CRQTF	IGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	3	C28:+57.021	1045.137088	3132.387863	0.000622848	1	N	222	251
P62880	Parental	IRDAR	KACGDSTLTQITAGLDPVGR	IQMRT	2	C3:+57.021	1030.525969	2059.036337	0.000451244	33	N	22	42
P62880	Parental	IRDAR	KACGDSTLTQITAGLDPVGR	IQMRT	3	C3:+57.021	687.3532457	2059.036337	0.000451244	21	N	22	42
P62880	Parental	DSMCR	QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	3	C31:+57.021	1170.528644	3508.562533	0.000451244	90	N	219	251
P62880	Parental	DSMCR	QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	4	C31:+57.021	878.1484332	3508.562533	0.000823681	1	N	219	251
P62880	Parental	DSMCR	QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	3	Q1:-17.027,C31:+57.021	1164.852978	3491.535533	0.000451244	10	N	219	251
P62880	Parental	DSMCR	QTFIGHESDINAVAFFPNGYAFTTGSDDATCR	LFDLR	3	[0:-17.027,C31:+57.021	1164.852978	3491.535533	0.000451244	9	N	219	251
P62880	Parental	LFDLR	ADQELLMYSHDNIICGITSVAFSR	SGRLL	3	C15:+57.021	914.1075239	2739.299172	0.000451244	3	N	256	280
P62880	Parental	VRVSR	ELPGHTGYLSCCR	FLDDN	2	C11:+57.021,C12:+57.021	775.3480015	1548.680403	0.000451244	3	N	137	150
P62880	Parental	VRVSR	ELPGHTGYLSCCR	FLDDN	3	C11:+57.021,C12:+57.021	517.234601	1548.680403	0.000451244	32	N	137	150
P62880	Parental	APDGR	TFVSGACDASIK	LWDVR	2	C7:+57.021	628.3032855	1254.590971	0.000451244	16	N	197	209
P62880	Parental	RDARK	ACGDSTLTQITAGLDPVGR	IQMRT	2	C2:+57.021	966.478487	1930.941374	0.000451244	12	N	23	42
P62880	Parental	DARKA	CGDSTLTQITAGLDPVGR	IQMRT	2	C1:+57.021	930.9599301	1859.90426	0.000451244	3	N	24	42
P62880	Parental	GHDNR	VSCLGVTDDGMAVATGSWDSFLK	IWN-	2	C3:+57.021	1208.561891	2415.108183	0.000451244	5	Y	314	337
P62880	Parental	APDGR	TFVSGACDASIKLWDVR	DSMCR	2	C7:+57.021	962.9832082	1923.950816	0.000735798	2	N	197	214
P62880	Parental	SRSGR	LLLAGYDDFNCNIWDAMKGDR	AGVLA	3	C11:+57.021	829.7196002	2486.135401	0.000451244	1	N	283	304
P62880	Parental	AIPLR	SSWVMTCAYAPSGNFVACGGLDNICSIYSLK	TREGN	3	C7:+57.021,C18:+57.021,C25:+57.021	1143.51885	3427.533151	0.001162105	2	N	96	127
P62880	Parental	SQDGK	LIIWDSYTTNK	VHAIP	2		677.3566067	1352.697613	0.000451244	10	Y	78	89
P62880	Parental	SRSGR	LLLAGYDDFNCNIWDAMK	GDRAG	2	C11:+57.021	1080.000741	2157.985883	0.001352548	1	N	283	301
P62880	Parental	WVMTC	AYAPSGNFVACGGLDNICSIYSLK	TREGN	2	C11:+57.021,C18:+57.021	1289.109308	2576.203017	0.000622848	1	N	103	127
P62889	Exosome	GKYYR	VCTLAIIDPGDSDIIR	SMPEQ	2	C2:+57.021	879.4590346	1756.902469	0.000451244	27	N	90	106
P62889	Exosome	QGKAK	LVILANNCPALR	KSEIE	2	C8:+57.021	677.3874869	1352.759374	0.000451244	7	N	44	56
P62889	Parental	GKYYR	VCTLAIIDPGDSDIIR	SMPEQ	2	C2:+57.021	879.4590346	1756.902469	0.000451244	22	N	90	106
P62889	Parental	GKYYR	VCTLAIIDPGDSDIIR	SMPEQ	3	C2:+57.021	586.6419564	1756.902469	0.001654178	2	N	90	106
P62889	Parental	QGKAK	LVILANNCPALR	KSEIE	2	C8:+57.021	677.3874869	1352.759374	0.000451244	6	N	44	56
P62889	Parental	AMLAK	TGVHHYSGNNIELGTACGK	YYRVC	3	C17:+57.021	672.3185354	2013.932206	0.000823681	10	N	68	87
P62908	Exosome	EFLTR	ELAEDGYSGVEVR	VTPTR	2		712.3391423	1422.662685	0.000451244	11	N	27	40
P62908	Exosome	SKKRK	FVADGIFKAELNEFLTR	ELAED	3		657.3514366	1969.03091	0.000451244	3	N	10	27
P62908	Exosome	KVATR	GLCAIAQAESLR	YKLLG	2	C3:+57.021	644.8378268	1287.660054	0.000451244	12	N	94	106
P62908	Exosome	KIGPK	KPLPDHVSIVEPKDEILPTTPISEQK	GGKPE	3		970.866129	2909.574987	0.000698008	1	N	201	227
P62908	Exosome	KIGPK	KPLPDHVSIVEPK	DEILP	3		486.9492037	1457.824211	0.000622848	7	N	201	214
P62908	Exosome	VVQKR	FGFPEGSVELY	AEKVA	2		622.7958506	1243.576101	0.000998612	3	N	76	87
P62908	Exosome	ISEQK	GGKPEPPAMPQPVPTA	-	2	M9:+15.995	795.4038056	1588.792011	0.002884417	2	N	227	243
P62908	Parental	EFLTR	ELAEDGYSGVEVR	VTPTR	2		712.3391423	1422.662685	0.000451244	36	N	27	40
P62908	Parental	SKKRK	FVADGIFKAELNEFLTR	ELAED	3		657.3514366	1969.03091	0.000451244	4	N	10	27
P62908	Parental	KVATR	GLCAIAQAESLR	YKLLG	2	C3:+57.021	644.8378268	1287.660054	0.000451244	7	N	94	106
P62908	Parental	KIGPK	KPLPDHVSIVEPKDEILPTTPISEQK	GGKPE	3		970.866129	2909.574987	0.000451244	2	N	201	227
P62908	Parental	KIGPK	KPLPDHVSIVEPK	DEILP	3		486.9492037	1457.824211	0.000451244	21	N	201	214
P62908	Parental	IVEPK	DEILPTTPISEQK	GGKPE	2		735.888468	1469.761336	0.000735798	1	N	214	227
P62908	Parental	VVQKR	FGFPEGSVELY	AEKVA	2		622.7958506	1243.576101	0.002296037	1	N	76	87
P62960	Exosome	RKYLR	SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	YAADR	3		1158.229183	3471.664149	0.000662267	10	N	99	135
P62960	Exosome	RGPPR	NYQQNYQNSESGEKNEGSESAPEGQAQQR	RPYRR	3		1086.470777	3256.38893	0.001162105	2	N	154	183
P62960	Exosome	RPYAR	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	QNMYR	4	M14:+15.995	810.6371672	3238.517469	0.000451244	19	N	202	232
P62960	Exosome	VEGEK	GAEAANVTGPGGVPVQGSK	YAADR	2		848.4371794	1694.858759	0.000451244	20	N	116	135
P62960	Exosome	RKYLR	SVGDGETVEFDVVEGEK	GAEAA	2		898.4157753	1794.815951	0.000451244	8	N	99	116
P62960	Parental	RKYLR	SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	YAADR	3		1158.229183	3471.664149	0.000451244	10	N	99	135

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P62960	Parental	RGPPR	NYQQNYQNSESGEKNEGSESAPEGQAQQR	RPYRR	3		1086.470777	3256.38893	0.000451244	3	N	154	183
P62960	Parental	RPYAR	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	QNMYR	4		806.6384172	3222.522469	0.000622848	3	N	202	232
P62960	Parental	RPYAR	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	QNMYR	4	M14:+15.995	810.6371672	3238.517469	0.000451244	8	N	202	232
P62960	Parental	ETVEF	DVVEGEKGAEAANVTGPGGVPVQGSK	YAADR	3		818.0825144	2451.224143	0.000622848	1	N	109	135
P62960	Parental	VEGEK	GAEAANVTGPGGVPVQGSKY	AADRN	2		929.9688437	1857.922087	0.000451244	20	N	116	136
P62960	Parental	VEGEK	GAEAANVTGPGGVPVQGSK	YAADR	2		848.4371794	1694.858759	0.000451244	25	N	116	135
P62960	Parental	RKYLR	SVGDGETVEFDVVEGEK	GAEAA	2		898.4157753	1794.815951	0.000451244	15	N	99	116
P62962	Exosome	AVPGK	TFVSITPAEVGVLVGKDR	SSFFV	2		944.5310799	1887.04656	0.000451244	9	N	38	56
P62962	Exosome	AVPGK	TFVSITPAEVGVLVGKDR	SSFFV	3		630.0233199	1887.04656	0.000979378	4	N	38	56
P62962	Exosome	VGKDR	SSFFVNGLTLGGQK	CSVIR	2		727.8860627	1453.756525	0.000451244	61	N	56	70
P62962	Exosome	AVPGK	TFVSITPAEVGVLVGK	DRSSF	2		808.9670527	1615.918505	0.000451244	44	N	38	54
P62962	Exosome	AVPGK	TFVSITPAEVGVLVGK	DRSSF	3		539.6473018	1615.918505	0.000451244	5	N	38	54
P62962	Exosome	IVGYK	DSPSVWAAVPGK	TFVSI	2		607.3147418	1212.613884	0.000451244	4	N	26	38
P62962	Exosome	CSVIR	DSLLQDGEFTMDLR	TKSTG	2		820.3857671	1638.755934	0.000451244	17	N	75	89
P62962	Parental	AVPGK	TFVSITPAEVGVLVGKDR	SSFFV	2		944.5310799	1887.04656	0.000451244	20	N	38	56
P62962	Parental	AVPGK	TFVSITPAEVGVLVGKDR	SSFFV	3		630.0233199	1887.04656	0.000451244	34	N	38	56
P62962	Parental	VGKDR	SSFFVNGLTLGGQK	CSVIR	2		727.8860627	1453.756525	0.000451244	80	N	56	70
P62962	Parental	LGGQK	CSVIRDSLLQDGEFTMDLR	TKSTG	3	C1:+57.021	752.3650459	2254.071738	0.000451244	5	N	70	89
P62962	Parental	AVPGK	TFVSITPAEVGVLVGK	DRSSF	2		808.9670527	1615.918505	0.000451244	71	N	38	54
P62962	Parental	AVPGK	TFVSITPAEVGVLVGK	DRSSF	3		539.6473018	1615.918505	0.000451244	18	N	38	54
P62962	Parental	IVGYK	DSPSVWAAVPGK	TFVSI	2		607.3147418	1212.613884	0.001463592	4	N	26	38
P62962	Parental	GWNAY	IDSLMADGTCQDAAIVGYKDSPSVWAAVPGK	TFVSI	3	C10:+57.021	1074.853412	3221.536836	0.000622848	3	N	7	38
P62962	Parental	CSVIR	DSLLQDGEFTMDLR	TKSTG	2		820.3857671	1638.755934	0.000451244	8	N	75	89
P62962	Parental	AIVGY	KDSPSVWAAVPGK	TFVSI	2		671.3622234	1340.708847	0.00091018	6	N	25	38
P62962	Parental	VLVGK	DRSSFFVNGLTLGGQK	CSVIR	2		863.4500898	1724.88458	0.00307782	1	N	54	70
P62962	Parental	PGKTF	VSITPAEVGVLVGKDR	SSFFV	2		820.4730336	1638.930467	0.000451244	1	N	40	56
P62962	Parental	PGKTF	VSITPAEVGVLVGK	DRSSF	2		684.9090065	1367.802413	0.000823681	1	N	40	54
P62983	Exosome	TLTGK	TITLEVEPSDTIENVK	AKIQD	2		894.4678109	1786.920022	0.000451244	30	N	11	27
P62983	Parental	HYCGK	CCLTYCFNKPEDK	-	2	C1:+57.021,C2:+57.021,C6:+57.02	867.8676782	1733.719756	0.000451244	33	N	143	156
P62983	Parental	HYCGK	CCLTYCFNKPEDK	-	3	C1:+57.021,C2:+57.021,C6:+57.02	578.9143854	1733.719756	0.000451244	13	N	143	156
P62983	Parental	HYCGK	CCLTYCFNKPEDK	-	2	[0:-17.027,C1:+57.021,C2:+57.021,C6:+57.021	859.3541782	1716.692756	0.000451244	6	N	143	156
P62983	Parental	TLTGK	TITLEVEPSDTIENVKAK	IQDKE	2		994.0338494	1986.052099	0.000451244	11	N	11	29
P62983	Parental	TLTGK	TITLEVEPSDTIENVKAK	IQDKE	3		663.0251663	1986.052099	0.000451244	5	N	11	29
P62983	Parental	TLTGK	TITLEVEPSDTIENVK	AKIQD	2		894.4678109	1786.920022	0.000451244	67	N	11	27
P62983	Parental	LEDGR	TLSDYNIQKESTL	HLVLR	2		756.3835498	1510.7515	0.000698008	7	N	54	67
P62983	Parental	NVKAK	IQDKEGIPPDQQR	LIFAG	3		508.5991221	1522.773966	0.001162105	4	N	29	42
P62996	Exosome	EVFSK	YGPIADVSIVYDQQSR	RSRGF	2		905.9526623	1809.889725	0.000451244	40	N	140	156
P62996	Exosome	HVGNR	ANPDPNCCLGVFGLSLYTTER	DLREV	2	C7:+57.021,C8:+57.021	1192.554169	2383.092738	0.001162105	1	N	111	132
P62996	Exosome	SRRSR	GFAFVYFENVDDAK	EAKER	2		811.3808101	1620.74602	0.000451244	6	N	159	173
P62996	Exosome	SRRSR	GFAFVYFENVDDAKEAK	ERANG	2		975.4681452	1948.92069	0.000698008	1	N	159	176
P62996	Parental	EVFSK	YGPIADVSIVYDQQSR	RSRGF	2		905.9526623	1809.889725	0.000451244	46	N	140	156
P62996	Parental	HVGNR	ANPDPNCCLGVFGLSLYTTER	DLREV	2	C7:+57.021,C8:+57.021	1192.554169	2383.092738	0.000451244	29	N	111	132
P62996	Parental	HVGNR	ANPDPNCCLGVFGLSLYTTER	DLREV	3	C7:+57.021,C8:+57.021	795.3720459	2383.092738	0.000451244	20	N	111	132
P62996	Parental	EVFSK	YGPIADVSIVYDQQSRR	SRGFA	3		656.3380786	1965.990836	0.000979378	1	N	140	157
P62996	Parental	SRRSR	GFAFVYFENVDDAK	EAKER	2		811.3808101	1620.74602	0.000622848	9	N	159	173
P63001	Exosome	EDYDR	LRPLSYPQTDVFLICF	SLVSP	2	C15:+57.021	985.0165197	1968.017439	0.000451244	8	Y	66	82
P63001	Exosome	DGKPV	NLGLWDTAGQEDYDR	LRPLS	2		876.8953444	1751.775089	0.000451244	20	Y	51	66
P63001	Exosome	IGAVK	YLECSALTQR	GLKTV	2	C4:+57.021	620.8034527	1239.591305	0.000451244	35	Y	153	163
P63001	Exosome	MVDGK	PVNLGLWDTAGQEDYDR	LRPLS	2		974.9559333	1947.896267	0.000451244	14	Y	49	66
P63001	Exosome	GAVGK	TCLLISYTTNAFPGEYIPTVFDNY	SANVM	2	C2:+57.021	1400.165035	2798.31447	0.000451244	11	Y	16	40
P63001	Exosome	GAVGK	TCLLISYTTNAFPGEYIPTVFDNY	SANVM	3	C2:+57.021	933.7792899	2798.31447	0.0025889	1	Y	16	40
P63001	Exosome	GAVGK	TCLLISYTTNAFPGEYIPT	VFDNY	2	C2:+57.021	1081.030021	2160.044442	0.000823681	8	Y	16	35
P63001	Exosome	GAVGK	TCLLISYTTNAFPGEYIPTVF	DNYSA	2	C2:+57.021	1204.098435	2406.18127	0.000622848	21	Y	16	37
P63001	Exosome	EDYDR	LRPLSYPQTDVF	LICFS	2		718.3831558	1434.750712	0.000622848	9	Y	66	78
P63001	Exosome	EDYDR	LRPLSYPQTDVFLIC	FSLVS	2	C15:+57.021	911.4823127	1820.949025	0.001162105	3	Y	66	81
P63001	Exosome	EDYDR	LRPLSYPQTDVFLICFS	LVSPA	2	C15:+57.021	1028.532534	2055.049468	0.000622848	2	Y	66	83
P63001	Exosome	YPEVR	HHCPNTPIILVGTK	LDLRD	3	C3:+57.021	529.6209384	1585.839415	0.000823681	2	N	102	116
P63001	Exosome	QTDVF	LICFSLVSPASFENVR	AKWYP	2	C3:+57.021	919.9773945	1837.939189	0.001763695	1	N	78	94
P63001	Parental	EDYDR	LRPLSYPQTDVFLICF	SLVSP	2	C15:+57.021	985.0165197	1968.017439	0.000979378	17	Y	66	82
P63001	Parental	EDYDR	LRPLSYPQTDVFLICFSLVSPASFENVR	AKWYP	3	C15:+57.021	1085.900914	3254.679341	0.000451244	6	N	66	94
P63001	Parental	DGKPV	NLGLWDTAGQEDYDR	LRPLS	2		876.8953444	1751.775089	0.000451244	5	Y	51	66
P63001	Parental	IGAVK	YLECSALTQR	GLKTV	2	C4:+57.021	620.8034527	1239.591305	0.000451244	22	Y	153	163
P63001	Parental	MVDGK	PVNLGLWDTAGQEDYDR	LRPLS	2		974.9559333	1947.896267	0.000823681	1	Y	49	66

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63001	Parental	GAVGK	TCLLISYTTNAFPGEYIPTVFDNY	SANVM	2	C2:+57.021	1400.165035	2798.31447	0.002212458	2	Y	16	40
P63001	Parental	GAVGK	TCLLISYTTNAFPGEYIPT	VFDNY	2	C2:+57.021	1081.030021	2160.044442	0.001943752	1	Y	16	35
P63001	Parental	GAVGK	TCLLISYTTNAFPGEYIPTVF	DNYSA	2	C2:+57.021	1204.098435	2406.18127	0.000622848	4	Y	16	37
P63001	Parental	EDYDR	LRPLSYPQTDVF	LICFS	2		718.3831558	1434.750712	0.001264573	9	Y	66	78
P63005	Exosome	DMTIK	LWDFQGFECIR	TMHGH	2	C9:+57.021	735.8456519	1469.675704	0.000451244	25	N	175	186
P63005	Exosome	LDFHK	TAPYVVTGSVDQTVK	VWECR	2		782.9150171	1563.814434	0.000451244	27	N	390	405
P63005	Exosome	KAELR	EHEHVVECISWAPESSYSSISEATGSETK	KSGKP	3	C8:+57.021	1079.482701	3235.424702	0.000451244	8	N	273	302
P63005	Exosome	DATIK	VWDYETGDFER	TLKGH	2		708.8074779	1415.599356	0.002663018	1	N	133	144
P63005	Exosome	REWVR	MVRPNQDGTLIASCSNDQTVR	VWVVA	3	C14:+57.021	788.0464874	2361.116062	0.000451244	6	N	238	259
P63005	Exosome	ERTLK	GHTDSVQDISFDHSGK	LLASC	3		577.2645792	1728.770338	0.00091018	2	N	147	163
P63005	Parental	DMTIK	LWDFQGFECIR	TMHGH	2	C9:+57.021	735.8456519	1469.675704	0.000451244	8	N	175	186
P63005	Parental	LDFHK	TAPYVVTGSVDQTVK	VWECR	2		782.9150171	1563.814434	0.000451244	15	N	390	405
P63005	Parental	DATIK	VWDYETGDFER	TLKGH	2		708.8074779	1415.599356	0.001871652	1	N	133	144
P63017	Exosome	IFEVK	STAGDTHLGGEDFDNR	MVNHF	2		846.366951	1690.718302	0.000451244	15	N	220	236
P63017	Exosome	IFEVK	STAGDTHLGGEDFDNR	MVNHF	3		564.5805674	1690.718302	0.000451244	3	N	220	236
P63017	Exosome	AKLDK	SQIHDIVLVGGSTR	IPKIQ	2		741.4076936	1480.799787	0.000451244	68	N	328	342
P63017	Exosome	AKLDK	SQIHDIVLVGGSTR	IPKIQ	3		494.6077291	1480.799787	0.000451244	31	N	328	342
P63017	Exosome	LRDAK	LDKSQIHDIVLVGGSTR	IPKIQ	2		919.5106788	1837.005758	0.000451244	37	N	325	342
P63017	Exosome	LRDAK	LDKSQIHDIVLVGGSTR	IPKIQ	3		613.3430525	1837.005758	0.000451244	23	N	325	342
P63017	Exosome	DQGNR	TTPSYVAFTDTER	LIGDA	2		744.3547923	1486.693985	0.000451244	63	N	36	49
P63017	Exosome	LNVLR	IINEPTAAAIAYGLDKK	VGAER	2		894.4992484	1786.982897	0.000451244	27	N	171	188
P63017	Exosome	LNVLR	IINEPTAAAIAYGLDKK	VGAER	3		596.6687656	1786.982897	0.002981883	1	N	171	188
P63017	Exosome	AYLGK	TVTNAVVTVPAYFNDSQR	QATKD	2		991.5030507	1980.990501	0.000451244	79	N	137	155
P63017	Exosome	AYLGK	TVTNAVVTVPAYFNDSQR	QATKD	3		661.3379672	1980.990501	0.000451244	25	N	137	155
P63017	Exosome	LNVLR	IINEPTAAAIAYGLDK	KVGAE	2		830.4517668	1658.887934	0.000451244	32	Y	171	187
P63017	Exosome	LNVLR	IINEPTAAAIAYGLDK	KVGAE	3		553.9704446	1658.887934	0.000451244	21	Y	171	187
P63017	Exosome	VLIKR	NTTIPTKQTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3		1177.253552	3528.737255	0.000451244	6	N	416	447
P63017	Exosome	KGETK	SFYPEEVSSMVLTK	MKEIA	2		808.897979	1615.780358	0.000451244	13	N	112	126
P63017	Exosome	KGETK	SFYPEEVSSMVLTK	MKEIA	2	M10:+15.995	816.895479	1631.775358	0.002212458	1	N	112	126
P63017	Exosome	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2		1387.66755	2773.3195	0.000451244	60	N	423	447
P63017	Exosome	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3		925.4476335	2773.3195	0.000451244	46	N	423	447
P63017	Exosome	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2	Q1:-17.027	1379.15405	2756.2925	0.000451244	13	N	423	447
P63017	Exosome	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3	Q1:-17.027	919.7719668	2756.2925	0.000451244	2	N	423	447
P63017	Exosome	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2	[0:-17.027	1379.15405	2756.2925	0.000451244	10	N	423	447
P63017	Exosome	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3	[0:-17.027	919.7719668	2756.2925	0.000451244	5	N	423	447
P63017	Exosome	KELNK	SINPDEAVAYGAAVQAAILSGDK	SENVQ	2		1130.576944	2259.138288	0.000451244	35	N	361	384
P63017	Exosome	KELNK	SINPDEAVAYGAAVQAAILSGDK	SENVQ	3		754.0538961	2259.138288	0.000451244	29	N	361	384
P63017	Exosome	GGGTF	DVSILTIEDGIFEVK	STAGD	2		839.4514325	1676.887265	0.000451244	3	N	205	220
P63017	Exosome	ERAKR	TLSSSTQASIEIDSLYEGIDFYTSITR	ARFEE	3		999.8245467	2996.45024	0.000451244	12	N	272	299
P63017	Exosome	VGAER	NVLIFDLGGGTFDVSILTIEDGIFEVK	STAGD	2		1456.27112	2910.52664	0.000451244	8	N	193	220
P63017	Exosome	VGAER	NVLIFDLGGGTFDVSILTIEDGIFEVK	STAGD	3		971.1833466	2910.52664	0.000451244	16	N	193	220
P63017	Exosome	TSITR	ARFEELNADLFR	GTLDP	2		740.8813116	1479.747023	0.000451244	16	N	299	311
P63017	Exosome	TSITR	ARFEELNADLFR	GTLDP	3		494.2568078	1479.747023	0.000451244	2	N	299	311
P63017	Exosome	PKIQK	LLQDFFNGKELNK	SINPD	2		783.4202697	1564.824939	0.000662267	6	N	348	361
P63017	Exosome	PKIQK	LLQDFFNGKELNK	SINPD	3		522.6161131	1564.824939	0.0025889	1	N	348	361
P63017	Exosome	TFTTY	SDNQPGVLIQVYEGER	AMTKD	2		902.4477441	1802.879888	0.000451244	13	N	431	447
P63017	Exosome	RQATK	DAGTIAGLNVLR	IINEP	2		600.3412909	1198.666982	0.001463592	16	N	159	171
P63017	Exosome	KELNK	SINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPL	SLGIE	3		1304.016431	3909.025892	0.002019181	2	N	361	399
P63017	Exosome	LSGDK	SENVQDLLLLDVTPLSLGIETAGGVMTVLIK	RNTTI	3		1080.267194	3237.778181	0.000451244	13	N	384	415
P63017	Exosome	EDKQK	ILDKCNEIISWLDK	NQTAE	2	C5:+57.021	873.9586705	1745.901741	0.000451244	10	N	569	583
P63017	Exosome	EDKQK	ILDKCNEIISWLDK	NQTAE	3	C5:+57.021	582.975047	1745.901741	0.000451244	28	N	569	583
P63017	Exosome	-MSK	GPAVGIDLGTTYSCVGVFQHGK	VEIIA	2	C14:+57.021	1132.062718	2262.109837	0.000451244	13	N	3	25
P63017	Exosome	-MSK	GPAVGIDLGTTYSCVGVFQHGK	VEIIA	3	C14:+57.021	755.0444122	2262.109837	0.000451244	20	N	3	25
P63017	Exosome	KILDK	CNEIISWLDK	NQTAE	2	C1:+57.021	639.3136532	1276.611706	0.000622848	10	N	573	583
P63017	Exosome	KILDK	CNEIISWLDK	NQTAE	2	[0:-17.027,C1:+57.021	630.8001532	1259.584706	0.002727428	1	N	573	583
P63017	Exosome	GDAAK	NQVAMNPTNTVFDAK	RLIGR	2	M5:+15.995	833.3992515	1664.782903	0.000451244	47	N	56	71
P63017	Exosome	PKIQK	LLQDFFNGK	ELNKS	2		541.2879957	1080.560391	0.000451244	31	N	348	357
P63017	Exosome	QTQTF	TTYSDNQPGVLIQVYEGER	AMTKD	2		1085.027087	2168.038574	0.000451244	1	N	428	447
P63017	Exosome	PPAPR	GVPQIEVTFDIDANGILNVSAVDK	STGKE	2		1257.658466	2513.301331	0.000622848	10	N	469	493
P63017	Exosome	GNRTT	PSYVAFTDTER	LIGDA	2		643.3071138	1284.598628	0.000622848	1	N	38	49
P63017	Exosome	ITRAR	FEELNADLFR	GTLDP	2		627.3121991	1252.608798	0.000735798	4	N	301	311
P63017	Exosome	VGAER	NVLIFDLGGGTF	DVSIL	2		626.8327674	1251.649935	0.000451244	4	N	193	205
P63017	Exosome	QSDMK	HWPFMVVNDAGRPK	VQVEY	3	M5:+15.995	557.2809878	1668.819563	0.000451244	10	N	88	102
P63017	Exosome	LSGDK	SENVQDLLLLDVTPLSLGIETAGGVMTVLIKR	NTTIP	3		1132.300898	3393.879293	0.000622848	1	N	384	416
P63017	Exosome	KVSSK	NSLESYAFNMK	ATVED	2	M10:+15.995	660.3010174	1318.586435	0.000451244	11	N	539	550

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63017	Exosome	DVSIL	TIEDGIFEVK	STAGD	2		575.8036756	1149.591751	0.001162105	1	N	210	220
P63017	Exosome	TIPTK	QTQTFTTYSDNQPGVLIQ	VYEGE	2		1020.997798	2039.979996	0.000622848	2	N	423	441
P63017	Exosome	VGAER	NVLIFDLGGGTFDVSIL	TIEDG	2		890.4805243	1778.945449	0.0007646	3	N	193	210
P63017	Exosome	KELNK	SINPDEAVAYGAAVQAA	ILSGD	2		823.9051808	1645.794762	0.002727428	1	N	361	378
P63017	Exosome	EAVAY	GAAVQAAILSGDK	SENVQ	2		600.8332987	1199.650997	0.000851441	1	N	371	384
P63017	Exosome	EHQQK	ELEKVCNPIITK	LYQSA	3	C6:+57.021	481.9344115	1442.779835	0.001162105	1	N	597	609
P63017	Exosome	LNVLR	IINEPTAAAIAY	GLDKK	2		623.8380498	1245.6605	0.002727428	1	Y	171	183
P63017	Parental	IFEVK	STAGDTHLGGEDFDNR	MVNHF	2		846.366951	1690.718302	0.000451244	62	N	220	236
P63017	Parental	IFEVK	STAGDTHLGGEDFDNR	MVNHF	3		564.5805674	1690.718302	0.000451244	52	N	220	236
P63017	Parental	AKLDK	SQIHDIVLVGGSTR	IPKIQ	2		741.4076936	1480.799787	0.000451244	31	N	328	342
P63017	Parental	AKLDK	SQIHDIVLVGGSTR	IPKIQ	3		494.6077291	1480.799787	0.000451244	42	N	328	342
P63017	Parental	LRDAK	LDKSQIHDIVLVGGSTR	IPKIQ	2		919.5106788	1837.005758	0.000451244	27	N	325	342
P63017	Parental	LRDAK	LDKSQIHDIVLVGGSTR	IPKIQ	3		613.3430525	1837.005758	0.000451244	13	N	325	342
P63017	Parental	NDSQR	QATKDAGTIAGLNVLR	IINEP	2		814.4604575	1626.905315	0.000451244	9	N	155	171
P63017	Parental	NDSQR	QATKDAGTIAGLNVLR	IINEP	3		543.3095717	1626.905315	0.000451244	9	N	155	171
P63017	Parental	NDSQR	QATKDAGTIAGLNVLR	IINEP	2	[0:-17.027	805.9469575	1609.878315	0.001229886	6	N	155	171
P63017	Parental	DQGNR	TTPSYVAFTDTER	LIGDA	2		744.3547923	1486.693985	0.000451244	64	N	36	49
P63017	Parental	LNVLR	IINEPTAAAIAYGLDKK	VGAER	2		894.4992484	1786.982897	0.000451244	23	N	171	188
P63017	Parental	LNVLR	IINEPTAAAIAYGLDKK	VGAER	3		596.6687656	1786.982897	0.000451244	3	N	171	188
P63017	Parental	AYLGK	TVTNAVVTVPAYFNDSQR	QATKD	2		991.5030507	1980.990501	0.000451244	98	N	137	155
P63017	Parental	AYLGK	TVTNAVVTVPAYFNDSQR	QATKD	3		661.3379672	1980.990501	0.000451244	27	N	137	155
P63017	Parental	LNVLR	IINEPTAAAIAYGLDK	KVGAE	2		830.4517668	1658.887934	0.000451244	32	Y	171	187
P63017	Parental	LNVLR	IINEPTAAAIAYGLDK	KVGAE	3		553.9704446	1658.887934	0.000451244	7	Y	171	187
P63017	Parental	VLIKR	NTTIPTKQTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3		1177.253552	3528.737255	0.000451244	8	N	416	447
P63017	Parental	KGETK	SFYPEEVSSMVLTK	MKEIA	2		808.897979	1615.780358	0.000823681	6	N	112	126
P63017	Parental	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2		1387.66755	2773.3195	0.000451244	72	N	423	447
P63017	Parental	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3		925.4476335	2773.3195	0.000451244	44	N	423	447
P63017	Parental	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2	Q1:-17.027	1379.15405	2756.2925	0.000451244	8	N	423	447
P63017	Parental	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3	Q1:-17.027	919.7719668	2756.2925	0.001329271	1	N	423	447
P63017	Parental	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	2	[0:-17.027	1379.15405	2756.2925	0.000451244	17	N	423	447
P63017	Parental	TIPTK	QTQTFTTYSDNQPGVLIQVYEGER	AMTKD	3	[0:-17.027	919.7719668	2756.2925	0.001352548	1	N	423	447
P63017	Parental	RQATK	DAGTIAGLNVLRI	INEPT	2		656.883323	1311.751046	0.001699387	1	N	159	172
P63017	Parental	KELNK	SINPDEAVAYGAAVQAAILSGDK	SENVQ	2		1130.576944	2259.138288	0.000451244	45	N	361	384
P63017	Parental	KELNK	SINPDEAVAYGAAVQAAILSGDK	SENVQ	3		754.0538961	2259.138288	0.000451244	18	N	361	384
P63017	Parental	GGGTF	DVSILTIEDGIFEVK	STAGD	2		839.4514325	1676.887265	0.000451244	19	N	205	220
P63017	Parental	GGGTF	DVSILTIEDGIFEVK	STAGD	3		559.9702217	1676.887265	0.000622848	1	N	205	220
P63017	Parental	ERAKR	TLSSSTQASIEIDSLYEGIDFY	TSITR	2		1220.07664	2438.137679	0.000451244	60	N	272	294
P63017	Parental	ERAKR	TLSSSTQASIEIDSLYEGIDFYTSITR	ARFEE	3		999.8245467	2996.45024	0.000451244	17	N	272	299
P63017	Parental	VGAER	NVLIFDLGGGTFDVSILTIEDGIFEVK	STAGD	2		1456.27112	2910.52664	0.000451244	11	N	193	220
P63017	Parental	VGAER	NVLIFDLGGGTFDVSILTIEDGIFEVK	STAGD	3		971.1833466	2910.52664	0.000451244	146	N	193	220
P63017	Parental	TSITR	ARFEELNADLFR	GTLDP	2		740.8813116	1479.747023	0.000451244	12	N	299	311
P63017	Parental	TSITR	ARFEELNADLFR	GTLDP	3		494.2568078	1479.747023	0.000451244	7	N	299	311
P63017	Parental	PKIQK	LLQDFFNGKELNK	SINPD	2		783.4202697	1564.824939	0.000451244	5	N	348	361
P63017	Parental	PKIQK	LLQDFFNGKELNK	SINPD	3		522.6161131	1564.824939	0.002884417	1	N	348	361
P63017	Parental	TFTTY	SDNQPGVLIQVYEGER	AMTKD	2		902.4477441	1802.879888	0.000451244	23	N	431	447
P63017	Parental	RQATK	DAGTIAGLNVLR	IINEP	2		600.3412909	1198.666982	0.001871652	4	N	159	171
P63017	Parental	KELNK	SINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPL	SLGIE	3		1304.016431	3909.025892	0.000622848	10	N	361	399
P63017	Parental	EDKQK	ILDKCNEIISWLDK	NQTAE	2	C5:+57.021	873.9586705	1745.901741	0.000451244	9	N	569	583
P63017	Parental	EDKQK	ILDKCNEIISWLDK	NQTAE	3	C5:+57.021	582.975047	1745.901741	0.000451244	18	N	569	583
P63017	Parental	-MSK	GPAVGIDLGTTYSCVGVFQHGK	VEIIA	2	C14:+57.021	1132.062718	2262.109837	0.000451244	6	N	3	25
P63017	Parental	-MSK	GPAVGIDLGTTYSCVGVFQHGK	VEIIA	3	C14:+57.021	755.0444122	2262.109837	0.000451244	16	N	3	25
P63017	Parental	KILDK	CNEIISWLDK	NQTAE	2	C1:+57.021	639.3136532	1276.611706	0.000870037	3	N	573	583
P63017	Parental	GDAAK	NQVAMNPTNTVFDAK	RLIGR	2	M5:+15.995	833.3992515	1664.782903	0.000451244	8	N	56	71
P63017	Parental	PKIQK	LLQDFFNGK	ELNKS	2		541.2879957	1080.560391	0.000451244	9	N	348	357
P63017	Parental	QTQTF	TTYSDNQPGVLIQVYEGER	AMTKD	2		1085.027087	2168.038574	0.002145581	1	N	428	447
P63017	Parental	PPAPR	GVPQIEVTFDIDANGILNVSAVDK	STGKE	2		1257.658466	2513.301331	0.000451244	74	N	469	493
P63017	Parental	PPAPR	GVPQIEVTFDIDANGILNVSAVDK	STGKE	3		838.7749103	2513.301331	0.000998612	4	N	469	493
P63017	Parental	GNRTT	PSYVAFTDTER	LIGDA	2		643.3071138	1284.598628	0.000451244	7	N	38	49
P63017	Parental	LGTTY	SCVGVFQHGKVEIIANDQGNR	TTPSY	2	C2:+57.021	1164.579598	2327.143596	0.000451244	6	N	15	36
P63017	Parental	LGTTY	SCVGVFQHGKVEIIANDQGNR	TTPSY	3	C2:+57.021	776.7223321	2327.143596	0.000451244	3	N	15	36
P63017	Parental	AYLGK	TVTNAVVTVPAYF	NDSQR	2		691.3722568	1380.728914	0.001162105	2	N	137	150
P63017	Parental	VGAER	NVLIFDLGGGTF	DVSIL	2		626.8327674	1251.649935	0.000998612	3	N	193	205
P63017	Parental	EAVAY	GAAVQAAILSGDK	SENVQ	2		600.8332987	1199.650997	0.000451244	4	N	371	384
P63017	Parental	LNVLR	IINEPTAAAIAY	GLDKK	2		623.8380498	1245.6605	0.002813207	1	Y	171	183
P63017	Parental	NVLIF	DLGGGTFDVSILTIEDGIFEVK	STAGD	2		1163.097178	2324.178756	0.000451244	7	N	198	220

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63017	Parental	TSITR	ARFEELNADLF	RGTLD	2		662.8307561	1323.645912	0.002813207	1	N	299	310
P63017	Parental	-MSK	GPAVGIDLGTTY	SCVGV	2		582.3013001	1162.587	0.002453667	1	N	3	15
P63024	Parental	ERDQK	LSELDDRADALQAGASQFETSAAK	LKRKY	3		832.0739075	2493.198322	0.000451244	3	N	46	70
P63024	Parental	ELDDR	ADALQAGASQFETSAAK	LKRKY	2		833.4080876	1664.800575	0.000823681	1	N	53	70
P63028	Exosome	MIIYR	DLISHDELFSDIYK	IREIA	2		847.9177568	1693.819914	0.000451244	6	N	5	19
P63028	Exosome	MIIYR	DLISHDELFSDIYK	IREIA	3		565.6144379	1693.819914	0.000622848	22	N	5	19
P63028	Exosome	-MIIY	RDLISHDELFSDIYK	IREIA	3		617.6481416	1849.921025	0.000451244	5	N	4	19
P63028	Parental	MIIYR	DLISHDELFSDIYK	IREIA	2		847.9177568	1693.819914	0.000622848	2	N	5	19
P63028	Parental	MIIYR	DLISHDELFSDIYK	IREIA	3		565.6144379	1693.819914	0.000622848	18	N	5	19
P63028	Parental	SDIYK	IREIADGLCLEVEGK	MVSRT	2	C9:+57.021	851.4459272	1700.876254	0.000451244	7	N	19	34
P63028	Parental	SDIYK	IREIADGLCLEVEGK	MVSRT	3	C9:+57.021	567.9665515	1700.876254	0.000451244	6	N	19	34
P63028	Parental	-MIIY	RDLISHDELFSDIYK	IREIA	3		617.6481416	1849.921025	0.000451244	5	N	4	19
P63028	Parental	QKPER	VKPFMTGAAEQIK	HILAN	3		473.927523	1418.759169	0.001839721	1	N	110	123
P63038	Parental	GAKLV	QDVANNTNEEAGDGTTTATVLAR	SIAKE	2		1174.552186	2347.088772	0.000451244	13	N	98	121
P63038	Parental	CALLR	CIPALDSLKPANEDQK	IGIEI	2	C1:+57.021	899.9541164	1797.892633	0.000451244	10	N	446	462
P63038	Parental	NIGAK	LVQDVANNTNEEAGDGTTTATVLAR	SIAKE	2		1280.628425	2559.24125	0.000451244	63	N	96	121
P63038	Parental	NIGAK	LVQDVANNTNEEAGDGTTTATVLAR	SIAKE	3		854.0882167	2559.24125	0.000451244	7	N	96	121
P63038	Parental	GPKGR	TVIIEQSWGSPK	VTKDG	2		672.8620562	1343.708512	0.000451244	6	N	60	72
P63038	Parental	HIEKR	IQEITEQLDITTSEYEKEK	LNERL	2		1149.0739	2296.1322	0.000451244	6	N	370	389
P63038	Parental	HIEKR	IQEITEQLDITTSEYEKEK	LNERL	3		766.3852	2296.1322	0.001162105	3	N	370	389
P63038	Parental	LSEKK	ISSVQSIVPALEIANAHR	KPLVI	3		635.6904523	1904.047957	0.000451244	2	N	250	268
P63038	Parental	LNATR	AAVEEGIVLGGGCALLR	CIPAL	2	C13:+57.021	842.9564621	1683.897324	0.000451244	11	N	429	446
P63038	Parental	LNATR	AAVEEGIVLGGGCALLR	CIPAL	3	C13:+57.021	562.3069081	1683.897324	0.000451244	5	N	429	446
P63038	Parental	SKGQK	CEFQDAYVLLSEK	KISSV	2	C1:+57.021	801.3797216	1600.743843	0.000451244	13	N	236	249
P63038	Parental	SKGQK	CEFQDAYVLLSEK	KISSV	3	C1:+57.021	534.589081	1600.743843	0.001352548	1	N	236	249
P63038	Parental	SKGQK	CEFQDAYVLLSEK	KISSV	2	[0:-17.027,C1:+57.021	792.8662216	1583.716843	0.000451244	5	N	236	249
P63038	Parental	ANAHR	KPLVIIAEDVDGEALSTLVLNR	LKVGL	2		1183.171012	2364.326423	0.000622848	2	N	268	290
P63038	Parental	ANAHR	KPLVIIAEDVDGEALSTLVLNR	LKVGL	3		789.1166078	2364.326423	0.001162105	1	N	268	290
P63038	Parental	KVVRT	ALLDAAGVASLLTTAEAVVTEIPKEEK	DPGMG	3		913.8395799	2738.49534	0.000451244	14	N	527	554
P63038	Parental	MTIAK	NAGVEGSLIVEK	ILQSS	2		608.3331316	1214.650663	0.000823681	5	N	481	493
P63038	Parental	SKGQK	CEFQDAYVLLSEKK	ISSVQ	2	[0:-17.027,C1:+57.021	856.9137031	1711.811806	0.000451244	2	N	236	250
P63038	Parental	MKFDR	GYISPYFINTSK	GQKCE	2		695.3566067	1388.697613	0.002212458	2	N	221	233
P63038	Parental	TKVVR	TALLDAAGVASLLTTAEAVVTEIPKEEK	DPGMG	3		947.5221394	2839.543018	0.000451244	18	N	526	554
P63038	Parental	KVVRT	ALLDAAGVASLLTTAEAVVTEIPK	EEKDP	2		1177.165395	2352.31519	0.001329271	1	N	527	551
P63038	Parental	PVEIR	RGVMLAVDAVIAELK	KQSKP	3	M4:+15.995	534.308432	1599.901896	0.000662267	1	N	141	156
P63038	Parental	NIGAK	LVQDVANNTNEEAGDGTTTATVL	ARSIA	2		1167.059313	2332.103025	0.000823681	3	N	96	119
P63038	Parental	LLSEK	KISSVQSIVPALEIANAHR	KPLVI	4		509.04353	2032.14292	0.002212458	1	N	249	268
P63073	Exosome	KQQRR	SDLDRFWLETLLCLIGESFDDYSDDVCGAVVNVR	AKGDK	3	C13:+57.021,C27:+57.021	1326.955881	3977.844242	0.000622848	5	N	123	157
P63073	Exosome	SDLDR	FWLETLLCLIGESFDDYSDDVCGAVVNVR	AKGDK	3	C8:+57.021,C22:+57.021	1131.532184	3391.573152	0.000622848	1	N	128	157
P63073	Exosome	AKGDK	IAIWTTECENR	DAVTH	2	C8:+57.021	696.8327415	1391.649883	0.000451244	12	N	162	173
P63073	Parental	KQQRR	SDLDRFWLETLLCLIGESFDDYSDDVCGAVVNVR	AKGDK	3	C13:+57.021,C27:+57.021	1326.955881	3977.844242	0.001463592	2	N	123	157
P63085	Exosome	IFPGK	HYLDQLNHILGILGSPSQEDLNCIINLK	ARNYL	3	C23:+57.021	1073.227689	3216.659668	0.000451244	2	N	229	257
P63085	Exosome	IFPGK	HYLDQLNHILGILGSPSQEDLNCIINLK	ARNYL	4	C23:+57.021	805.172717	3216.659668	0.000451244	6	N	229	257
P63085	Exosome	LPKEK	LKELIFEETAR	FQPGY	3		450.2544042	1347.739813	0.000622848	11	N	340	351
P63085	Exosome	NVLHR	DLKPSNLLLNTTCDLK	ICDFG	2	C13:+57.021	922.9932416	1843.970883	0.000451244	2	N	146	162
P63085	Exosome	NVLHR	DLKPSNLLLNTTCDLK	ICDFG	3	C13:+57.021	615.6647611	1843.970883	0.000451244	8	N	146	162
P63085	Exosome	FGLAR	VADPDHDHTGFLTEYVATR	WYRAP	3		715.3401478	2142.997043	0.000451244	6	N	170	189
P63085	Exosome	NPHKR	IEVEQALAHPY	LEQYY	2		635.3278492	1268.640098	0.000870037	5	N	299	310
P63085	Exosome	KGYTK	SIDIWSVGCILAEMLSNRPIFPGK	HYLDQ	3	C9:+57.021	901.8051166	2702.39195	0.000735798	2	Y	205	229
P63085	Parental	PGKHY	LDQLNHILGILGSPSQEDLNCIINLK	ARNYL	3	C21:+57.021	973.1869425	2916.537427	0.000451244	3	N	231	257
P63085	Parental	LPKEK	LKELIFEETAR	FQPGY	3		450.2544042	1347.739813	0.002727428	2	N	340	351
P63094	Exosome	ACYER	SNEYQLIDCAQYFLDKIDVIK	QADYV	3	C9:+57.021	859.0968418	2574.267125	0.000451244	9	N	165	186
P63094	Exosome	PEFAR	YTTPEDATPEPGEDPR	VTRAK	2		887.8924674	1773.769335	0.000451244	8	N	317	333
P63094	Parental	ACYER	SNEYQLIDCAQYFLDKIDVIK	QADYV	3	C9:+57.021	859.0968418	2574.267125	0.000451244	6	N	165	186
P63094	Parental	PEFAR	YTTPEDATPEPGEDPR	VTRAK	2		887.8924674	1773.769335	0.000451244	11	N	317	333
P63094	Parental	RATHR	LLLLGAGESGK	STIVK	2		529.3167532	1056.617906	0.001329271	2	Y	42	53
P63101	Exosome	SLLEK	FLIPNASQPESK	VFYLK	2		665.8542312	1329.692862	0.00091018	5	N	103	115
P63101	Exosome	IMQLL	RDNLTLWTSDTQGDEAEAGEGGEN	-	2		1283.052747	2564.089894	0.000451244	8	N	221	245
P63101	Exosome	GDDKK	GIVDQSQQAYQEAFEISKK	EMQPT	2		1085.04528	2168.07496	0.000451244	22	N	139	158
P63101	Exosome	GDDKK	GIVDQSQQAYQEAFEISKK	EMQPT	3		723.6994532	2168.07496	0.000451244	20	N	139	158
P63101	Exosome	GDDKK	GIVDQSQQAYQEAFEISK	KEMQP	2		1020.997798	2039.979996	0.000451244	48	N	139	157
P63101	Exosome	GDDKK	GIVDQSQQAYQEAFEISK	KEMQP	3		681.0011321	2039.979996	0.000451244	23	N	139	157
P63101	Exosome	MQLLR	DNLTLWTSDTQGDEAEAGEGGEN	-	2		1205.002192	2407.988783	0.000451244	32	N	222	245
P63101	Exosome	MQLLR	DNLTLWTSDTQGDEAEAGEGGEN	-	3		803.6707277	2407.988783	0.00307782	1	N	222	245
P63101	Exosome	ETELR	DICNDVLSLLEK	FLIPN	2	C3:+57.021	709.8637073	1417.711815	0.000451244	56	N	91	103

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63101	Exosome	EYREK	IETELRDICNDVLSLLEK	FLIPN	2	C9:+57.021	1080.564759	2159.113919	0.000451244	24	N	85	103
P63101	Exosome	EYREK	IETELRDICNDVLSLLEK	FLIPN	3	C9:+57.021	720.7124396	2159.113919	0.000451244	38	N	85	103
P63101	Exosome	CSLAK	TAFDEAIAELDTLSEESYK	DSTLI	2		1066.500036	2130.984473	0.000451244	47	N	193	212
P63101	Exosome	CSLAK	TAFDEAIAELDTLSEESYK	DSTLI	3		711.3359576	2130.984473	0.000451244	38	N	193	212
P63101	Exosome	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	2		1159.109891	2316.204183	0.000451244	40	Y	167	187
P63101	Exosome	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	3		773.075861	2316.204183	0.000451244	22	Y	167	187
P63101	Exosome	CSLAK	TAFDEAIAELDTLSEESY	KDSTL	2		1002.452555	2002.88951	0.000451244	10	N	193	211
P63101	Exosome	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1101.550318	3301.627554	0.000451244	27	N	193	222
P63101	Exosome	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	4		826.4146885	3301.627554	0.000451244	5	N	193	222
P63101	Exosome	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1106.881985	3317.622554	0.000451244	20	N	193	222
P63101	Exosome	AACMK	SVTEQGAELSNEER	NLLSV	2		774.8609702	1547.70634	0.000451244	49	N	27	41
P63101	Exosome	AGDDK	KGIVDQSQQAYQEAFEISK	KEMQP	2		1085.04528	2168.07496	0.000451244	9	N	138	157
P63101	Exosome	AGDDK	KGIVDQSQQAYQEAFEISK	KEMQP	3		723.6994532	2168.07496	0.000451244	11	N	138	157
P63101	Exosome	THPIR	LGLALNFSVF	YYEIL	2		540.808564	1079.601528	0.002453667	1	Y	167	177
P63101	Parental	SLLEK	FLIPNASQPESK	VFYLK	2		665.8542312	1329.692862	0.000451244	20	N	103	115
P63101	Parental	IMQLL	RDNLTLWTSDTQGDEAEAGEGGEN	-	2		1283.052747	2564.089894	0.000451244	69	N	221	245
P63101	Parental	IMQLL	RDNLTLWTSDTQGDEAEAGEGGEN	-	3		855.7044314	2564.089894	0.000451244	6	N	221	245
P63101	Parental	GDDKK	GIVDQSQQAYQEAFEISKK	EMQPT	2		1085.04528	2168.07496	0.000451244	21	N	139	158
P63101	Parental	GDDKK	GIVDQSQQAYQEAFEISKK	EMQPT	3		723.6994532	2168.07496	0.000451244	5	N	139	158
P63101	Parental	AACMK	SVTEQGAELSNEERNLLSVAYK	NVVGA	2		1219.114422	2436.213244	0.000451244	13	N	27	49
P63101	Parental	AACMK	SVTEQGAELSNEERNLLSVAYK	NVVGA	3		813.0788814	2436.213244	0.000451244	6	N	27	49
P63101	Parental	GDDKK	GIVDQSQQAYQEAFEISK	KEMQP	2		1020.997798	2039.979996	0.000451244	55	N	139	157
P63101	Parental	GDDKK	GIVDQSQQAYQEAFEISK	KEMQP	3		681.0011321	2039.979996	0.001162105	3	N	139	157
P63101	Parental	MQLLR	DNLTLWTSDTQGDEAEAGEGGEN	-	2		1205.002192	2407.988783	0.000451244	58	N	222	245
P63101	Parental	ETELR	DICNDVLSLLEK	FLIPN	2	C3:+57.021	709.8637073	1417.711815	0.000451244	65	N	91	103
P63101	Parental	ETELR	DICNDVLSLLEK	FLIPN	3	C3:+57.021	473.5784049	1417.711815	0.000451244	5	N	91	103
P63101	Parental	EYREK	IETELRDICNDVLSLLEK	FLIPN	2	C9:+57.021	1080.564759	2159.113919	0.000451244	27	N	85	103
P63101	Parental	EYREK	IETELRDICNDVLSLLEK	FLIPN	3	C9:+57.021	720.7124396	2159.113919	0.000451244	33	N	85	103
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESYK	DSTLI	2		1066.500036	2130.984473	0.000451244	49	N	193	212
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESYK	DSTLI	3		711.3359576	2130.984473	0.000451244	34	N	193	212
P63101	Parental	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	2		1159.109891	2316.204183	0.000622848	12	Y	167	187
P63101	Parental	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	3		773.075861	2316.204183	0.000451244	5	Y	167	187
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESY	KDSTL	2		1002.452555	2002.88951	0.000451244	34	N	193	211
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3		1101.550318	3301.627554	0.000451244	16	N	193	222
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	4		826.4146885	3301.627554	0.000451244	6	N	193	222
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1106.881985	3317.622554	0.000451244	11	N	193	222
P63101	Parental	AACMK	SVTEQGAELSNEER	NLLSV	2		774.8609702	1547.70634	0.000451244	89	N	27	41
P63101	Parental	AGDDK	KGIVDQSQQAYQEAFEISK	KEMQP	2		1085.04528	2168.07496	0.000451244	6	N	138	157
P63101	Parental	AGDDK	KGIVDQSQQAYQEAFEISK	KEMQP	3		723.6994532	2168.07496	0.000451244	1	N	138	157
P63101	Parental	THPIR	LGLALNFSVFY	YEILN	2		622.3402283	1242.664857	0.001352548	2	Y	167	178
P63101	Parental	FSVFY	YEILNSPEKACSLAK	TAFDE	2	C11:+57.021	861.9404777	1721.865355	0.000451244	3	Y	178	193
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESYKDSTL	IMQLL	2		1274.595394	2547.175187	0.000451244	5	N	193	216
P63101	Parental	CSLAK	TAFDEAIAELDTLSEESYKDSTLIMQLL	RDNLT	3		1049.516614	3145.526443	0.002453667	2	N	193	221
P63101	Parental	ETELR	DICNDVLSLLEKFLIPNASQPESK	VFYLK	3	C3:+57.021	910.805839	2729.394117	0.001352548	1	N	91	115
P63139	Parental	AKDAK	ECVQECVSEFISFITSEASER	CHQEK	2	C2:+57.021,C6:+57.021	1254.056938	2506.098277	0.000451244	7	N	83	104
P63139	Parental	AKDAK	ECVQECVSEFISFITSEASER	CHQEK	3	C2:+57.021,C6:+57.021	836.3738922	2506.098277	0.000451244	21	N	83	104
P63139	Parental	GKIAK	DAKECVQECVSEFISFITSEASER	CHQEK	3	C5:+57.021,C9:+57.021	941.0935656	2820.257297	0.000823681	1	N	80	104
P63147	Exosome	ILQNR	WSPTYDVSSILTSIQSLLDEPNPNSPANSQAAQLYQENKR	EYEKR	4		1116.300913	4461.17245	0.001943752	1	N	95	135
P63147	Parental	ILQNR	WSPTYDVSSILTSIQSLLDEPNPNSPANSQAAQLYQENKR	EYEKR	4		1116.300913	4461.17245	0.000451244	15	N	95	135
P63147	Parental	ILQNR	WSPTYDVSSILTSIQSLLDEPNPNSPANSQAAQLY	QENKR	3		1269.618559	3805.832278	0.002296037	1	N	95	130
P63158	Exosome	EYRPK	IKGEHPGLSIGDVAK	KLGEM	2		760.9257192	1519.835838	0.000451244	22	N	112	127
P63158	Exosome	EYRPK	IKGEHPGLSIGDVAK	KLGEM	3		507.6197461	1519.835838	0.000451244	40	N	112	127
P63158	Exosome	EEHKK	KHPDASVNFSEFSK	KCSER	2		796.8893337	1591.763067	0.000451244	5	N	29	43
P63158	Exosome	EEHKK	KHPDASVNFSEFSK	KCSER	3		531.5954891	1591.763067	0.000451244	21	N	29	43
P63158	Exosome	KPRGK	MSSYAFFVQTCR	EEHKK	2	C11:+57.021	748.8369701	1495.65834	0.000451244	6	Y	12	24
P63158	Exosome	KPRGK	MSSYAFFVQTCR	EEHKK	2	M1:+15.995,C11:+57.021	756.8344701	1511.65334	0.000451244	16	Y	12	24
P63158	Exosome	DVAKK	LGEMWNNTAADDKQPYEK	KAAKL	2	M4:+15.995	1063.478959	2124.942317	0.000451244	1	N	128	146
P63158	Exosome	DVAKK	LGEMWNNTAADDKQPYEK	KAAKL	3	M4:+15.995	709.3219057	2124.942317	0.001162105	2	N	128	146
P63158	Exosome	EHKKK	HPDASVNFSEFSK	KCSER	2		732.8418521	1463.668104	0.001329271	1	N	30	43
P63158	Exosome	PNAPK	RPPSAFFLFCSEYRPK	IKGEH	3	C10:+57.021	668.0053406	2000.992622	0.000451244	2	N	96	112
P63158	Parental	EYRPK	IKGEHPGLSIGDVAK	KLGEM	2		760.9257192	1519.835838	0.000451244	21	N	112	127
P63158	Parental	EYRPK	IKGEHPGLSIGDVAK	KLGEM	3		507.6197461	1519.835838	0.000451244	40	N	112	127
P63242	Exosome	HGHAK	VHLVGIDIFTGK	KYEDI	2		649.8775093	1297.739419	0.000451244	14	N	55	67
P63242	Exosome	HGHAK	VHLVGIDIFTGK	KYEDI	3		433.5876062	1297.739419	0.000451244	28	N	55	67
P63242	Exosome	VPNIK	RNDFQLIGIQDGYLSLLQDSGEVR	EDLRL	3		912.8037516	2735.387855	0.000451244	40	N	85	109

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P63242	Exosome	PNIKR	NDFQLIGIQDGYLSLLQDSGEVREDLR	LPEGD	3		1031.854952	3092.541455	0.000451244	10	N	86	113
P63242	Exosome	PNIKR	NDFQLIGIQDGYLSLLQDSGEVR	EDLRL	2		1290.651172	2579.286744	0.000451244	43	N	86	109
P63242	Exosome	PNIKR	NDFQLIGIQDGYLSLLQDSGEVR	EDLRL	3		860.7700479	2579.286744	0.000451244	45	N	86	109
P63242	Exosome	IFTGK	KYEDICPSTHNMDVPNIK	RNDFQ	3	C6:+57.021,M12:+15.995	726.3386367	2175.99251	0.001162105	5	N	67	85
P63242	Parental	HGHAK	VHLVGIDIFTGK	KYEDI	2		649.8775093	1297.739419	0.000451244	9	N	55	67
P63242	Parental	HGHAK	VHLVGIDIFTGK	KYEDI	3		433.5876062	1297.739419	0.000622848	36	N	55	67
P63242	Parental	VPNIK	RNDFQLIGIQDGYLSLLQDSGEVR	EDLRL	2		1368.701727	2735.387855	0.000451244	10	N	85	109
P63242	Parental	VPNIK	RNDFQLIGIQDGYLSLLQDSGEVR	EDLRL	3		912.8037516	2735.387855	0.000451244	46	N	85	109
P63242	Parental	PNIKR	NDFQLIGIQDGYLSLLQDSGEVREDLR	LPEGD	3		1031.854952	3092.541455	0.000451244	20	N	86	113
P63242	Parental	PNIKR	NDFQLIGIQDGYLSLLQDSGEVR	EDLRL	2		1290.651172	2579.286744	0.000451244	64	N	86	109
P63242	Parental	PNIKR	NDFQLIGIQDGYLSLLQDSGEVR	EDLRL	3		860.7700479	2579.286744	0.000451244	45	N	86	109
P63242	Parental	SGEVR	EDLRLPEGDLGK	EIEQK	3		447.9056636	1340.693591	0.001699387	1	N	109	121
P63242	Parental	EIEQK	YDCGEEILITVLSAMTEEAAVAIK	AMAK-	2	C3:+57.021	1313.653446	2625.291292	0.0007646	1	N	126	150
P63276	Exosome	KEMLK	LLDFGSLSNLQVTQPTVGMNFK	TPRGA	2	M19:+15.995	1213.12579	2424.23598	0.000451244	2	N	107	129
P63276	Parental	ERERR	DNYVPEVSALDQEIIEVDPDTK	EMLKL	2		1245.100646	2488.185692	0.000451244	41	N	81	103
P63276	Parental	ERERR	DNYVPEVSALDQEIIEVDPDTK	EMLKL	3		830.4030307	2488.185692	0.000622848	7	N	81	103
P63276	Parental	KEMLK	LLDFGSLSNLQVTQPTVGMNFK	TPRGA	2		1205.12829	2408.24098	0.000451244	8	N	107	129
P63276	Parental	KEMLK	LLDFGSLSNLQVTQPTVGMNFK	TPRGA	2	M19:+15.995	1213.12579	2424.23598	0.000451244	2	N	107	129
P63276	Parental	KEMLK	LLDFGSLSNLQVTQPT	VGMNF	2		866.959956	1731.904312	0.000451244	4	N	107	123
P63276	Parental	HTNKR	VCEEIAIIPSKK	LRNKI	3	C2:+57.021	462.927257	1385.758371	0.000451244	5	N	33	45
P63276	Parental	ERERR	DNYVPEVSALDQEIIEVDPDTKEMLK	LLDFG	3		997.4903995	2989.447798	0.001162105	2	N	81	107
P63276	Parental	EERER	RDNYVPEVSALDQEIIEVDPDTK	EMLKL	3		882.4367344	2644.286803	0.000451244	10	N	80	103
P63280	Exosome	AITIK	QILLGIQELLNEPNIQDPAQAEAYTIYCQNR	VEYEK	3	C28:+57.021	1205.942277	3614.803432	0.000451244	24	N	110	141
P63280	Exosome	AITIK	QILLGIQELLNEPNIQDPAQAEAYTIYCQNR	VEYEK	3	[0:-17.027,C28:+57.021	1200.266611	3597.776432	0.001591523	1	N	110	141
P63280	Parental	AITIK	QILLGIQELLNEPNIQDPAQAEAYTIYCQNR	VEYEK	3	C28:+57.021	1205.942277	3614.803432	0.000451244	17	N	110	141
P63280	Parental	AITIK	QILLGIQELLNEPNIQDPAQAEAY	TIYCQ	2		1340.695579	2679.375559	0.000451244	17	N	110	134
P63280	Parental	AITIK	QILLGIQELLNEPNIQDPAQAEAY	TIYCQ	3		894.1329862	2679.375559	0.001943752	3	N	110	134
P63280	Parental	AITIK	QILLGIQELLNEPNIQDPAQAEAY	TIYCQ	2	Q1:-17.027	1332.182079	2662.348559	0.00091018	2	N	110	134
P63280	Parental	AITIK	QILLGIQELLNEPNIQDPAQAEAY	TIYCQ	2	[0:-17.027	1332.182079	2662.348559	0.0025889	1	N	110	134
P63280	Parental	AITIK	QILLGIQELLNEPNIQDPAQAEAYTIY	CQNRV	3		1019.864677	3056.57063	0.000698008	3	N	110	137
P63321	Parental	SYRKK	VVLDGEEVQIDILDTAGQEDYAAIRDNYFR	SGEGF	3		1143.227114	3426.657942	0.000451244	6	N	54	84
P63321	Parental	VEEAK	NRADQWNVNYVETSAK	TRANV	2		947.9562677	1893.896935	0.000451244	1	N	143	159
P63325	Exosome	PKKNR	IAIYELLFK	EGVMV	2		555.3344146	1108.653229	0.000698008	16	N	8	17
P63325	Exosome	QFAWR	HFYWYLTNEGIQYLR	DYLHL	3		668.3323764	2001.973729	0.000637154	4	N	65	80
P63325	Exosome	IQYLR	DYLHLPPEIVPATLR	RSRPE	3		578.6582009	1732.951203	0.001943752	1	N	80	95
P63325	Parental	IQYLR	DYLHLPPEIVPATLR	RSRPE	3		578.6582009	1732.951203	0.002727428	1	N	80	95
P63328	Exosome	RMYRK	SQTTGFPSLITIFSAPNYLDVYNNK	AAVLK	3		930.8048696	2789.391209	0.000451244	12	N	293	318
P63328	Exosome	HNTVR	GCSYFYSYPAVCDFLQHNNLLSILR	AHEAQ	3	C2:+57.021,C12:+57.021	1013.149569	3036.425306	0.000451244	5	N	254	279
P63328	Exosome	YRMYR	KSQTTGFPSLITIFSAPNYLDVYNNK	AAVLK	3		973.5031906	2917.486172	0.00091018	1	N	292	318
P63328	Parental	RMYRK	SQTTGFPSLITIFSAPNYLDVYNNK	AAVLK	2		1395.703404	2789.391209	0.00091018	1	N	293	318
P67778	Exosome	EGDSK	AAELIANSLATAGDGLIELR	KLEAA	2		999.5474583	1997.079317	0.000451244	19	N	219	239
P67778	Exosome	EGDSK	AAELIANSLATAGDGLIELR	KLEAA	3		666.7009055	1997.079317	0.000451244	2	N	219	239
P67778	Exosome	LSRSR	NITYLPAGQSVLLQLPQ	-	2		928.020348	1854.025096	0.000451244	8	N	255	272
P67778	Parental	LIELR	KLEAAEDIAYQLSR	SRNIT	2		803.9259162	1605.836232	0.000451244	23	N	239	253
P67778	Parental	LIELR	KLEAAEDIAYQLSR	SRNIT	3		536.2865441	1605.836232	0.000451244	12	N	239	253
P67778	Parental	SQLPR	IYTSIGEDYDERVLPSITTEILK	SVVAR	3		885.7974921	2654.369076	0.000451244	10	N	105	128
P67778	Parental	EGDSK	AAELIANSLATAGDGLIELR	KLEAA	2		999.5474583	1997.079317	0.000451244	58	N	219	239
P67778	Parental	EGDSK	AAELIANSLATAGDGLIELR	KLEAA	3		666.7009055	1997.079317	0.000451244	30	N	219	239
P67778	Parental	FDRFR	GVQDIVVGEGTHFLIPWVQKPIIFDCR	SRPRN	3	C26:+57.021	1041.886827	3122.637082	0.000451244	33	N	43	70
P67778	Parental	FDRFR	GVQDIVVGEGTHFLIPWVQKPIIFDCR	SRPRN	4	C26:+57.021	781.6670705	3122.637082	0.001162105	13	N	43	70
P67778	Parental	EQQKK	AAIISAEGDSKAAELIANSLATAGDGLIELR	KLEAA	3		1014.210736	3039.608807	0.000451244	14	N	208	239
P67778	Parental	RAATF	GLILDDVSLTHLTFGKEFTEAVEAK	QVAQQ	2		1367.22143	2732.42726	0.000451244	1	N	161	186
P67778	Parental	RAATF	GLILDDVSLTHLTFGKEFTEAVEAK	QVAQQ	4		684.114615	2732.42726	0.000451244	1	N	161	186
P67778	Parental	ESIGK	FGLALAVAGGVVNSALYNVDAGHR	AVIFD	3		791.089275	2370.244425	0.000622848	13	N	11	35
P67778	Parental	YQLSR	SRNITYLPAGQSVLLQLPQ	-	2		1049.586918	2097.158236	0.000451244	9	N	253	272
P67778	Parental	LSRSR	NITYLPAGQSVLLQLPQ	-	2		928.020348	1854.025096	0.000451244	23	N	255	272
P67778	Parental	SQLPR	IYTSIGEDYDER	VLPSI	2		730.8311501	1459.6467	0.000451244	23	N	105	117
P67778	Parental	RAATF	GLILDDVSLTHLTFGK	EFTEA	2		864.9806915	1727.945783	0.000637154	1	N	161	177
P67778	Parental	RAATF	GLILDDVSLTHLTFGK	EFTEA	3		576.9897277	1727.945783	0.001264573	6	N	161	177
P67778	Parental	RSRPR	NVPVITGSKDLQNVNITLR	ILFRP	2		1041.089825	2080.164049	0.0025889	1	N	74	93
P67778	Parental	ITGSK	DLQNVNITLR	ILFRP	2		593.3334659	1184.651332	0.000622848	10	N	83	93
P67778	Parental	DLTER	AATFGLILDDVSLTHLTFGK	EFTEA	3		707.0531677	2118.136103	0.001943752	1	N	157	177
P67778	Parental	SVVAR	FDAGELITQR	ELVSR	2		575.2990917	1148.582583	0.001162105	5	N	133	143
P67778	Parental	RSRNI	TYLPAGQSVLLQLPQ	-	2		814.4568522	1626.898104	0.002813207	2	N	257	272
P67871	Exosome	FCGLR	GNEFFCEVDEDYIQDKFNLTGLNEQVPHYR	QALDM	3	C6:+57.021	1226.226854	3675.657162	0.001839721	1	N	17	47

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P67871	Parental	FCGLR	GNEFFCEVDEDYIQDKFNLTGLNEQVPHYR	QALDM	3	C6:+57.021	1226.226854	3675.657162	0.000451244	8	N	17	47
P67871	Parental	FCGLR	GNEFFCEVDEDYIQDK	FNLTG	2	C6:+57.021	1004.417761	2006.819921	0.000451244	1	N	17	33
P67984	Parental	KVNGK	AGNLGGGVVTIER	SKSKI	2		621.8441978	1241.672796	0.000451244	7	N	52	65
P67984	Parental	QVLKF	TLDCTHPVEDGIMDAANFEQFLQER	IKVNG	3	C4:+57.021	979.4448644	2935.311193	0.000979378	1	N	21	46
P67984	Parental	ESYEL	RYFQINQDEEEEEDED	-	2		1044.419775	2086.823949	0.000451244	8	N	112	128
P67984	Parental	SYELR	YFQINQDEEEEEDED	-	2		966.3692191	1930.722838	0.000622848	3	N	113	128
P68033	Exosome	DDMEK	IWHHTFYNELR	VAPEE	2		758.3787391	1514.741878	0.000451244	140	Y	86	97
P68033	Exosome	DDMEK	IWHHTFYNELR	VAPEE	3		505.9217594	1514.741878	0.000451244	697	Y	86	97
P68033	Exosome	DRMQK	EITALAPSTMK	IKIIA	2		581.3133538	1160.611108	0.000451244	62	Y	317	328
P68033	Exosome	DRMQK	EITALAPSTMK	IKIIA	2	M10:+15.995	589.3108538	1176.606108	0.000451244	21	Y	317	328
P68033	Exosome	YNELR	VAPEEHPTLLTEAPLNPK	ANREK	2		978.5259945	1955.036389	0.000451244	15	N	97	115
P68033	Exosome	YNELR	VAPEEHPTLLTEAPLNPK	ANREK	3		652.6865964	1955.036389	0.000870037	7	N	97	115
P68033	Exosome	SSLEK	SYELPDGQVITIGNER	FRCPE	2		895.9501196	1789.884639	0.000451244	1549	Y	240	256
P68033	Exosome	SSLEK	SYELPDGQVITIGNER	FRCPE	3		597.6360131	1789.884639	0.000451244	140	Y	240	256
P68033	Exosome	HAIMR	LDLAGRDLTDYLMK	ILTER	3		541.9523969	1622.833791	0.000622848	2	Y	179	193
P68033	Exosome	HAIMR	LDLAGRDLTDYLMK	ILTER	3	M13:+15.995	547.2840636	1638.828791	0.000451244	3	Y	179	193
P68033	Exosome	EKSYE	LPDGQVITIGNER	FRCPE	2		706.3811445	1410.746689	0.000823681	17	Y	243	256
P68033	Exosome	VPAMY	VAIQAVLSLYASGR	TTGIV	2		724.41753	1446.81946	0.000451244	459	Y	135	149
P68033	Exosome	VPAMY	VAIQAVLSLYASGR	TTGIV	3		483.2809533	1446.81946	0.000451244	9	Y	135	149
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	3		1153.21946	3456.63498	0.001162105	4	N	70	97
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	4		865.1665449	3456.63498	0.000622848	4	N	70	97
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	3	M14:+15.995	1158.551127	3472.62998	0.001162105	3	N	70	97
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	4	M14:+15.995	869.1652949	3472.62998	0.000823681	4	N	70	97
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	3		982.4625612	2944.364284	0.001871652	1	N	70	93
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	4		737.0988709	2944.364284	0.000823681	5	N	70	93
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	3	M14:+15.995	987.7942279	2960.359284	0.002019181	1	N	70	93
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	4	M14:+15.995	741.0976209	2960.359284	0.000451244	2	N	70	93
P68033	Exosome	DIKEK	LCYVALDFENEMATAASSSSLEK	SYELP	2	C2:+57.021,M12:+15.995	1276.580521	2551.145442	0.000451244	29	N	217	240
P68033	Exosome	DIKEK	LCYVALDFENEMATAASSSSLEK	SYELP	3	C2:+57.021,M12:+15.995	851.3896139	2551.145442	0.000451244	20	N	217	240
P68033	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHR	KCF-	3	M19:+15.995	1367.346146	4099.015037	0.000622848	2	N	338	374
P68033	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHR	KCF-	4	M19:+15.995	1025.761559	4099.015037	0.000451244	5	N	338	374
P68033	Exosome	PPERK	YSVWIGGSILASLSTF	QQMWI	2		850.94886	1699.88212	0.000451244	183	Y	338	354
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEK	IWHHT	2		980.9596307	1959.903661	0.000451244	31	N	70	86
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEK	IWHHT	3		654.3090204	1959.903661	0.000451244	73	N	70	86
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEK	IWHHT	2	M14:+15.995	988.9571307	1975.898661	0.000451244	36	N	70	86
P68033	Exosome	ILTLK	YPIEHGIITNWDDMEK	IWHHT	3	M14:+15.995	659.6406871	1975.898661	0.000451244	37	N	70	86
P68033	Exosome	VRDIK	EKLCYVALDFENEMATAASSSSLEK	SYELP	3	C4:+57.021,M14:+15.995	937.1021327	2808.282998	0.000451244	9	N	215	240
P68033	Exosome	ELRVA	PEEHPTLLTEAPLNPK	ANREK	2		893.4732306	1784.930861	0.000451244	3	N	99	115
P68033	Exosome	ELRVA	PEEHPTLLTEAPLNPK	ANREK	3		595.9847537	1784.930861	0.002145581	1	N	99	115
P68033	Exosome	LEKSY	ELPDGQVITIGNER	FRCPE	2		770.9024411	1539.789282	0.000451244	9	Y	242	256
P68033	Exosome	GMGQK	DSYVGDEAQSK	RGILT	2		599.7652787	1197.514957	0.000451244	79	Y	52	63
P68033	Exosome	SSSLE	KSYELPDGQVITIGNER	FRCPE	2		959.9976012	1917.979602	0.000451244	31	Y	239	256
P68033	Exosome	SSSLE	KSYELPDGQVITIGNER	FRCPE	3		640.3343341	1917.979602	0.000451244	14	Y	239	256
P68033	Exosome	PAMYV	AIQAVLSLYASGR	TTGIV	2		674.883323	1347.751046	0.000451244	6	Y	136	149
P68033	Exosome	SSLEK	SYELPDGQVITI	GNERF	2		667.8460718	1333.676544	0.000451244	16	Y	240	252
P68033	Exosome	SSSSL	EKSYELPDGQVITIGNER	FRCPE	2	[0:-18.011	1015.513398	2029.011196	0.001839721	6	Y	238	256
P68033	Exosome	GMGQK	DSYVGDEAQSKR	GILTL	2		677.8158343	1353.616069	0.0007646	84	Y	52	64
P68033	Exosome	GMGQK	DSYVGDEAQSKR	GILTL	3		452.2131562	1353.616069	0.000698008	28	Y	52	64
P68033	Exosome	KSYEL	PDGQVITIGNER	FRCPE	2		649.8391124	1297.662625	0.000451244	13	Y	244	256
P68033	Exosome	PPERK	YSVWIGGSILA	SLSTF	2		583.3167532	1164.617906	0.001591523	4	Y	338	349
P68033	Exosome	DDAPR	AVFPSIVGRPR	HQGVM	3		400.2405408	1197.698222	0.001264573	25	Y	30	41
P68033	Exosome	APPER	KYSVWIGGSILASLSTF	QQMWI	2		914.9963416	1827.977083	0.000451244	165	Y	337	354
P68033	Exosome	NELRV	APEEHPTLLTEAPLNPK	ANREK	2		928.9917875	1855.967975	0.000698008	1	N	98	115
P68033	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2		1301.672865	2601.33013	0.000622848	7	Y	338	361
P68033	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2	M19:+15.995	1309.670365	2617.32513	0.002145581	4	Y	338	361
P68033	Exosome	SGLVK	AGFAGDDAPR	AVFPS	2		488.7283022	975.4410044	0.000451244	39	Y	20	30
P68033	Exosome	SSLEK	SYELPDGQVITIGNERFR	CPETL	2		1047.534882	2093.054164	0.002453667	2	Y	240	258
P68033	Exosome	IDIRK	DLYANNVLSGGTTMYPGIADR	MQKEI	2		1114.536765	2227.05793	0.001352548	2	N	293	314
P68033	Exosome	IDIRK	DLYANNVLSGGTTMYPGIADR	MQKEI	2	M14:+15.995	1122.534265	2243.05293	0.000451244	10	N	293	314
P68033	Exosome	YVAIQ	AVLSLYASGR	TTGIV	2		518.7934452	1035.57129	0.000622848	1	Y	139	149
P68033	Exosome	EEHPT	LLTEAPLNPK	ANREK	2		548.3245782	1094.633556	0.000823681	6	Y	105	115
P68033	Exosome	DLAGR	DLTDYLMK	ILTER	2		499.7473153	997.4790306	0.002145581	1	Y	185	193
P68033	Exosome	GILTL	KYPIEHGIITNWDDMEK	IWHHT	3	M15:+15.995	702.3390082	2103.993624	0.000823681	3	N	69	86
P68033	Exosome	SSLEK	SYELPDGQVITIGN	ERFRC	2		753.3782675	1504.740935	0.000622848	1	Y	240	254
P68033	Exosome	SLEKS	YELPDGQVITIGNER	FRCPE	2		852.4341054	1702.852611	0.001162105	1	Y	241	256

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68033	Exosome	SSLEK	SYELPDGQVITIGNERF	RCPET	2		969.4843266	1936.953053	0.000451244	3	Y	240	257
P68033	Exosome	PPERK	YSVWIGGSILASLSTFQ	QMWIS	2		914.9781488	1827.940698	0.000451244	2	Y	338	355
P68033	Exosome	PPERK	YSVWIGGSIL	ASLST	2		547.7981962	1093.580792	0.002981883	1	Y	338	348
P68033	Exosome	MTQIM	FETFNVPAMYVAIQAVLSLYASGR	TTGIV	2		1324.183597	2646.351594	0.001699387	1	N	125	149
P68033	Exosome	MWISK	QEYDEAGPSIVHRK	CF-	2		814.9055151	1627.79543	0.002663018	1	N	361	375
P68033	Exosome	LYANN	VLSGGTTMYPGIADR	MQKEI	2	M8:+15.995	777.3856128	1552.755626	0.00307782	1	Y	299	314
P68033	Parental	DDMEK	IWHHTFYNELR	VAPEE	2		758.3787391	1514.741878	0.000451244	73	Y	86	97
P68033	Parental	DDMEK	IWHHTFYNELR	VAPEE	3		505.9217594	1514.741878	0.000451244	211	Y	86	97
P68033	Parental	DRMQK	EITALAPSTMK	IKIIA	2		581.3133538	1160.611108	0.000451244	9	Y	317	328
P68033	Parental	YNELR	VAPEEHPTLLTEAPLNPK	ANREK	2		978.5259945	1955.036389	0.000451244	19	N	97	115
P68033	Parental	YNELR	VAPEEHPTLLTEAPLNPK	ANREK	3		652.6865964	1955.036389	0.002145581	3	N	97	115
P68033	Parental	SSLEK	SYELPDGQVITIGNER	FRCPE	2		895.9501196	1789.884639	0.000451244	1486	Y	240	256
P68033	Parental	SSLEK	SYELPDGQVITIGNER	FRCPE	3		597.6360131	1789.884639	0.000451244	118	Y	240	256
P68033	Parental	HAIMR	LDLAGRDLTDYLMK	ILTER	2		812.4246953	1622.833791	0.000451244	6	Y	179	193
P68033	Parental	HAIMR	LDLAGRDLTDYLMK	ILTER	3		541.9523969	1622.833791	0.000451244	6	Y	179	193
P68033	Parental	HAIMR	LDLAGRDLTDYLMK	ILTER	3	M13:+15.995	547.2840636	1638.828791	0.002080925	1	Y	179	193
P68033	Parental	EKSYE	LPDGQVITIGNER	FRCPE	2		706.3811445	1410.746689	0.000451244	27	Y	243	256
P68033	Parental	VPAMY	VAIQAVLSLYASGR	TTGIV	2		724.41753	1446.81946	0.000451244	976	Y	135	149
P68033	Parental	VPAMY	VAIQAVLSLYASGR	TTGIV	3		483.2809533	1446.81946	0.000451244	14	Y	135	149
P68033	Parental	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	3		1153.21946	3456.63498	0.000451244	9	N	70	97
P68033	Parental	ILTLK	YPIEHGIITNWDDMEKIWHHTFYNELR	VAPEE	4		865.1665449	3456.63498	0.000622848	9	N	70	97
P68033	Parental	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	2		1473.189942	2944.364284	0.000622848	1	N	70	93
P68033	Parental	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	3		982.4625612	2944.364284	0.000622848	2	N	70	93
P68033	Parental	ILTLK	YPIEHGIITNWDDMEKIWHHTFY	NELRV	4		737.0988709	2944.364284	0.001162105	3	N	70	93
P68033	Parental	DIKEK	LCYVALDFENEMATAASSSSLEK	SYELP	2	C2:+57.021,M12:+15.995	1276.580521	2551.145442	0.000451244	8	N	217	240
P68033	Parental	DIKEK	LCYVALDFENEMATAASSSSLEK	SYELP	3	C2:+57.021,M12:+15.995	851.3896139	2551.145442	0.000622848	2	N	217	240
P68033	Parental	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHR	KCF-	3	M19:+15.995	1367.346146	4099.015037	0.000451244	2	N	338	374
P68033	Parental	PPERK	YSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHR	KCF-	4	M19:+15.995	1025.761559	4099.015037	0.000622848	6	N	338	374
P68033	Parental	PPERK	YSVWIGGSILASLSTF	QQMWI	2		850.94886	1699.88212	0.000451244	562	Y	338	354
P68033	Parental	ILTLK	YPIEHGIITNWDDMEK	IWHHT	2		980.9596307	1959.903661	0.000451244	26	N	70	86
P68033	Parental	ILTLK	YPIEHGIITNWDDMEK	IWHHT	3		654.3090204	1959.903661	0.000451244	24	N	70	86
P68033	Parental	DIKEK	LCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNER	FRCPE	3	C2:+57.021,M12:+15.995	1442.014307	4323.019521	0.000823681	2	N	217	256
P68033	Parental	DIKEK	LCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNER	FRCPE	4	C2:+57.021,M12:+15.995	1081.76268	4323.019521	0.001463592	2	N	217	256
P68033	Parental	VRDIK	EKLCYVALDFENEMATAASSSSLEK	SYELP	2	C4:+57.021,M14:+15.995	1405.149299	2808.282998	0.000823681	3	N	215	240
P68033	Parental	VRDIK	EKLCYVALDFENEMATAASSSSLEK	SYELP	3	C4:+57.021,M14:+15.995	937.1021327	2808.282998	0.000637154	3	N	215	240
P68033	Parental	ELRVA	PEEHPTLLTEAPLNPK	ANREK	2		893.4732306	1784.930861	0.000451244	10	N	99	115
P68033	Parental	LEKSY	ELPDGQVITIGNER	FRCPE	2		770.9024411	1539.789282	0.000698008	3	Y	242	256
P68033	Parental	GMGQK	DSYVGDEAQSK	RGILT	2		599.7652787	1197.514957	0.000451244	28	Y	52	63
P68033	Parental	GMGQK	DSYVGDEAQSKR	GILTL	2		677.8158343	1353.616069	0.0007646	27	Y	52	64
P68033	Parental	GMGQK	DSYVGDEAQSKR	GILTL	3		452.2131562	1353.616069	0.000622848	25	Y	52	64
P68033	Parental	KSYEL	PDGQVITIGNER	FRCPE	2		649.8391124	1297.662625	0.000451244	27	Y	244	256
P68033	Parental	DDAPR	AVFPSIVGRPR	HQGVM	3		400.2405408	1197.698222	0.001162105	38	Y	30	41
P68033	Parental	AQSKR	GILTLKYPIEHGIITNWDDMEK	IWHHT	3		862.7811197	2585.319959	0.000451244	7	N	64	86
P68033	Parental	DLAGR	DLTDYLMKILTER	GYSFV	3		537.6206472	1609.838542	0.000823681	2	Y	185	198
P68033	Parental	APPER	KYSVWIGGSILASLSTF	QQMWI	2		914.9963416	1827.977083	0.000451244	160	Y	337	354
P68033	Parental	GIADR	MQKEITALAPSTMK	IKIIA	2		774.9103671	1547.805134	0.000622848	3	Y	314	328
P68033	Parental	NELRV	APEEHPTLLTEAPLNPK	ANREK	2		928.9917875	1855.967975	0.000622848	4	N	98	115
P68033	Parental	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2		1301.672865	2601.33013	0.000622848	2	Y	338	361
P68033	Parental	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	3		868.1178433	2601.33013	0.000622848	1	Y	338	361
P68033	Parental	SGLVK	AGFAGDDAPR	AVFPS	2		488.7283022	975.4410044	0.000622848	19	Y	20	30
P68037	Exosome	KPATK	TDQVIQSLIALVNDPQPEHPLRADLAEEYSK	DRKKF	3		1163.934042	3488.778726	0.002519933	1	N	100	131
P68037	Exosome	KPATK	TDQVIQSLIALVNDPQPEHPLRADLAEEYSK	DRKKF	4		873.2024814	3488.778726	0.000451244	5	N	100	131
P68037	Exosome	KGAFR	IEINFPAEYPFKPPK	ITFKT	3		597.3228182	1788.945055	0.000622848	5	N	52	67
P68037	Exosome	KPATK	TDQVIQSLIALVNDPQPEHPLR	ADLAE	3		828.447128	2482.317984	0.000451244	10	N	100	122
P68037	Exosome	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDK	GAFRI	3		951.4875406	2851.439222	0.000451244	2	N	23	48
P68037	Exosome	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDKGAFR	IEINF	3		1095.230241	3282.667324	0.000451244	11	N	23	52
P68037	Parental	KPATK	TDQVIQSLIALVNDPQPEHPLRADLAEEYSK	DRKKF	4		873.2024814	3488.778726	0.000735798	4	N	100	131
P68037	Parental	KPATK	TDQVIQSLIALVNDPQPEHPLR	ADLAE	2		1242.166792	2482.317984	0.00091018	1	N	100	122
P68037	Parental	KPATK	TDQVIQSLIALVNDPQPEHPLR	ADLAE	3		828.447128	2482.317984	0.000451244	25	N	100	122
P68037	Parental	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDK	GAFRI	2		1426.727411	2851.439222	0.000451244	7	N	23	48
P68037	Parental	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDK	GAFRI	3		951.4875406	2851.439222	0.000451244	13	N	23	48
P68037	Parental	MKNFR	NIQVDEANLLTWQGLIVPDNPPYDKGAFR	IEINF	3		1095.230241	3282.667324	0.000451244	12	N	23	52
P68040	Exosome	VSCVR	FSPNSSNPIIVSCGWDK	LVKVW	2	C13:+57.021	954.4517409	1906.887882	0.000451244	52	N	155	172
P68040	Exosome	STSSK	AEPPQCTSLAWSADGQTLFAGYTDNLVR	VWQVT	3	C6:+57.021	1023.485828	3067.434084	0.000451244	44	N	280	308
P68040	Exosome	VGHTK	DVLSVAFSSDNR	QIVSG	2		655.3232952	1308.63099	0.000451244	31	N	106	118

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68040	Exosome	DLEGK	IIVDELKQEVISTSSK	AEPPQ	2		895.0018209	1787.988042	0.000451244	18	N	264	280
P68040	Exosome	DLEGK	IIVDELKQEVISTSSK	AEPPQ	3		597.0038139	1787.988042	0.000451244	12	N	264	280
P68040	Exosome	LGVCK	YTVQDESHSEWVSCVR	FSPNS	2	C14:+57.021	991.4393618	1980.863124	0.000451244	21	N	139	155
P68040	Exosome	LGVCK	YTVQDESHSEWVSCVR	FSPNS	3	C14:+57.021	661.2955079	1980.863124	0.000451244	24	N	139	155
P68040	Exosome	LNEGK	HLYTLDGGDIINALCFSPNR	YWLCA	2	C15:+57.021	1138.560343	2275.105086	0.000451244	30	N	225	245
P68040	Exosome	LNEGK	HLYTLDGGDIINALCFSPNR	YWLCA	3	C15:+57.021	759.3761618	2275.105086	0.000451244	39	N	225	245
P68040	Exosome	NCKLK	TNHIGHTGYLNTVTVSPDGSLCASGGK	DGQAM	2	C22:+57.021	1372.159138	2742.302676	0.000451244	5	N	185	212
P68040	Exosome	NCKLK	TNHIGHTGYLNTVTVSPDGSLCASGGK	DGQAM	3	C22:+57.021	915.1086921	2742.302676	0.000451244	19	N	185	212
P68040	Exosome	NCKLK	TNHIGHTGYLNTVTVSPDGSLCASGGK	DGQAM	4	C22:+57.021	686.583469	2742.302676	0.001839721	6	N	185	212
P68040	Exosome	FSPNR	YWLCAATGPSIK	IWDLE	2	C4:+57.021	683.8451206	1365.674641	0.000451244	10	N	245	257
P68040	Exosome	GVCKY	TVQDESHSEWVSCVR	FSPNS	2	C13:+57.021	909.9076975	1817.799795	0.000622848	1	N	140	155
P68040	Exosome	GKHLY	TLDGGDIINALCFSPNR	YWLCA	2	C12:+57.021	931.9571904	1861.898781	0.000451244	10	N	228	245
P68040	Exosome	DGTLR	LWDLTTGTTTR	RFVGH	2		632.8307561	1263.645912	0.000823681	5	N	88	99
P68040	Exosome	RGTLK	GHNGWVTQIATTPQFPDMILSASR	DKTII	3		876.439868	2626.296204	0.001264573	2	N	12	36
P68040	Exosome	LNEGK	HLYTLDGGDIINALCFSPNRY	WLCAA	3	C15:+57.021	813.7306047	2438.168414	0.000622848	4	N	225	246
P68040	Exosome	STSSK	AEPPQCTSLAWSADGQTLF	AGYTD	2	C6:+57.021	1039.97832	2077.94104	0.002080925	1	N	280	299
P68040	Exosome	IIMWK	LTRDETNYGIPQR	ALRGH	2		781.9002327	1561.784865	0.000622848	1	N	44	57
P68040	Exosome	GHTGY	LNTVTVSPDGSLCASGGK	DGQAM	2	C13:+57.021	881.9359237	1761.856247	0.00091018	1	N	194	212
P68040	Parental	VSCVR	FSPNSSNPIIVSCGWDK	LVKVW	2	C13:+57.021	954.4517409	1906.887882	0.000451244	32	N	155	172
P68040	Parental	STSSK	AEPPQCTSLAWSADGQTLFAGYTDNLVR	VWQVT	3	C6:+57.021	1023.485828	3067.434084	0.000451244	24	N	280	308
P68040	Parental	VGHTK	DVLSVAFSSDNR	QIVSG	2		655.3232952	1308.63099	0.000451244	17	N	106	118
P68040	Parental	DLEGK	IIVDELKQEVISTSSK	AEPPQ	2		895.0018209	1787.988042	0.000451244	4	N	264	280
P68040	Parental	DLEGK	IIVDELKQEVISTSSK	AEPPQ	3		597.0038139	1787.988042	0.000451244	3	N	264	280
P68040	Parental	LGVCK	YTVQDESHSEWVSCVR	FSPNS	2	C14:+57.021	991.4393618	1980.863124	0.000451244	15	N	139	155
P68040	Parental	LGVCK	YTVQDESHSEWVSCVR	FSPNS	3	C14:+57.021	661.2955079	1980.863124	0.001264573	2	N	139	155
P68040	Parental	LNEGK	HLYTLDGGDIINALCFSPNR	YWLCA	2	C15:+57.021	1138.560343	2275.105086	0.000451244	25	N	225	245
P68040	Parental	LNEGK	HLYTLDGGDIINALCFSPNR	YWLCA	3	C15:+57.021	759.3761618	2275.105086	0.000451244	27	N	225	245
P68040	Parental	NCKLK	TNHIGHTGYLNTVTVSPDGSLCASGGK	DGQAM	2	C22:+57.021	1372.159138	2742.302676	0.000451244	2	N	185	212
P68040	Parental	NCKLK	TNHIGHTGYLNTVTVSPDGSLCASGGK	DGQAM	3	C22:+57.021	915.1086921	2742.302676	0.000451244	10	N	185	212
P68040	Parental	FSPNR	YWLCAATGPSIK	IWDLE	2	C4:+57.021	683.8451206	1365.674641	0.000451244	10	N	245	257
P68040	Parental	GVCKY	TVQDESHSEWVSCVR	FSPNS	2	C13:+57.021	909.9076975	1817.799795	0.000451244	1	N	140	155
P68040	Parental	DGTLR	LWDLTTGTTTR	RFVGH	2		632.8307561	1263.645912	0.001763695	3	N	88	99
P68254	Exosome	GDDRK	QTIENSQGAYQEAFDISKK	EMQPT	2		1079.027087	2156.038574	0.000662267	1	N	139	158
P68254	Exosome	GDDRK	QTIENSQGAYQEAFDISKK	EMQPT	3		719.6873247	2156.038574	0.000451244	15	N	139	158
P68254	Exosome	FSVFY	YEILNNPELACTLAK	TAFDE	2	C11:+57.021	874.9483027	1747.881005	0.000451244	6	N	178	193
P68254	Exosome	ESELR	SICTTVLELLDKYLIANATNPESK	VFYLK	2	C3:+57.021	1347.207234	2692.398868	0.000451244	4	N	91	115
P68254	Exosome	ESELR	SICTTVLELLDKYLIANATNPESK	VFYLK	3	C3:+57.021	898.4740893	2692.398868	0.000451244	34	N	91	115
P68254	Exosome	ESELR	SICTTVLELLDKYLIANATNPESK	VFYLK	4	C3:+57.021	674.107517	2692.398868	0.001591523	1	N	91	115
P68254	Exosome	THPIR	LGLALNFSVFYYEILNNPELACTLAK	TAFDE	3	C22:+57.021	991.8529007	2972.535302	0.000823681	3	N	167	193
P68254	Exosome	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1105.882068	3314.622803	0.000451244	27	N	193	222
P68254	Exosome	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1111.213734	3330.617803	0.000622848	5	N	193	222
P68254	Exosome	ATCMK	AVTEQGAELSNEER	NLLSV	2		766.8635129	1531.711426	0.001162105	3	N	27	41
P68254	Exosome	ELLDK	YLIANATNPESK	VFYLK	2		660.8438635	1319.672127	0.000451244	9	N	103	115
P68254	Exosome	ESELR	SICTTVLELLDK	YLIAN	2	C3:+57.021	696.3764506	1390.737301	0.000451244	31	N	91	103
P68254	Exosome	CTLAK	TAFDEAIAELDTLNEDSYK	DSTLI	2		1072.997661	2143.979722	0.000451244	17	N	193	212
P68254	Exosome	CTLAK	TAFDEAIAELDTLNEDSYK	DSTLI	3		715.6677073	2143.979722	0.001162105	2	N	193	212
P68254	Exosome	THPIR	LGLALNFSVF	YYEIL	2		540.808564	1079.601528	0.002453667	1	Y	167	177
P68254	Parental	GDDRK	QTIENSQGAYQEAFDISKK	EMQPT	3		719.6873247	2156.038574	0.000451244	24	N	139	158
P68254	Parental	FSVFY	YEILNNPELACTLAK	TAFDE	2	C11:+57.021	874.9483027	1747.881005	0.000451244	31	N	178	193
P68254	Parental	ESELR	SICTTVLELLDKYLIANATNPESK	VFYLK	3	C3:+57.021	898.4740893	2692.398868	0.000451244	29	N	91	115
P68254	Parental	ESELR	SICTTVLELLDKYLIANATNPESK	VFYLK	4	C3:+57.021	674.107517	2692.398868	0.000979378	6	N	91	115
P68254	Parental	THPIR	LGLALNFSVFYYEILNNPELACTLAK	TAFDE	3	C22:+57.021	991.8529007	2972.535302	0.000622848	3	N	167	193
P68254	Parental	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1105.882068	3314.622803	0.000451244	35	N	193	222
P68254	Parental	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1111.213734	3330.617803	0.000451244	7	N	193	222
P68254	Parental	ATCMK	AVTEQGAELSNEER	NLLSV	2		766.8635129	1531.711426	0.001162105	1	N	27	41
P68254	Parental	ESELR	SICTTVLELLDK	YLIAN	2	C3:+57.021	696.3764506	1390.737301	0.000451244	1	N	91	103
P68254	Parental	CTLAK	TAFDEAIAELDTLNEDSYK	DSTLI	2		1072.997661	2143.979722	0.000451244	20	N	193	212
P68254	Parental	CTLAK	TAFDEAIAELDTLNEDSYK	DSTLI	3		715.6677073	2143.979722	0.000622848	4	N	193	212
P68254	Parental	THPIR	LGLALNFSVFY	YEILN	2		622.3402283	1242.664857	0.001352548	2	Y	167	178
P68254	Parental	CTLAK	TAFDEAIAELDTLNEDSYKDSTLIMQLL	RDNLT	3		1053.848364	3158.521692	0.002296037	2	N	193	221
P68254	Parental	MQLLR	DNLTLWTSDSAGEECDAAEGAEN	-	2	C15:+57.021	1227.995821	2453.976041	0.000823681	4	N	222	245
P68254	Parental	IMQLL	RDNLTLWTSDSAGEECDAAEGAEN	-	2	C16:+57.021	1306.046376	2610.077152	0.000451244	5	N	221	245
P68368	Exosome	DICRR	NLDIERPTYTNLNR	LISQI	2		859.9451716	1717.874743	0.000451244	15	Y	215	229
P68368	Exosome	DICRR	NLDIERPTYTNLNR	LISQI	3		573.6327144	1717.874743	0.000451244	5	Y	215	229
P68368	Exosome	DVVPK	DVNAAIAAIK	TKRSI	2		493.2879957	984.5603914	0.000823681	6	N	326	336

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68368	Exosome	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2		1208.106734	2414.197869	0.000451244	4	Y	84	105
P68368	Exosome	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3		805.7404229	2414.197869	0.000451244	34	Y	84	105
P68368	Exosome	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	4		604.5572672	2414.197869	0.000451244	3	Y	84	105
P68368	Exosome	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	Q1:-17.027	800.0647563	2397.170869	0.000451244	5	Y	84	105
P68368	Exosome	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	[0:-17.027	800.0647563	2397.170869	0.000622848	17	Y	84	105
P68368	Exosome	PTGFK	VGINYQPPTVVPGGDLAK	VQRAV	2		912.9968729	1823.978146	0.000451244	11	Y	352	370
P68368	Exosome	VPYPR	IHFPLATYAPVISAEK	AYHEQ	2		878.9857768	1755.955954	0.000451244	5	Y	264	280
P68368	Exosome	VPYPR	IHFPLATYAPVISAEK	AYHEQ	3		586.3264512	1755.955954	0.000451244	29	Y	264	280
P68368	Exosome	ISAEK	AYHEQLSVAEITNACFEPANQMVK	CDPRH	3	C15:+57.021,M22:+15.995	922.7673072	2765.278522	0.000622848	5	Y	280	304
P68368	Exosome	IKTKR	SIQFVDWCPTGFK	VGINY	2	C8:+57.021	792.8796917	1583.743783	0.000451244	27	N	339	352
P68368	Exosome	MPSDK	TIGGGDDSFTTFFCETGAGK	HVPRA	2	C14:+57.021	1034.452135	2066.88867	0.000451244	31	N	40	60
P68368	Exosome	KHVPR	AVFVDLEPTVIDEIR	NGPYR	2		858.4648742	1714.914148	0.000451244	35	N	64	79
P68368	Exosome	KHVPR	AVFVDLEPTVIDEIR	NGPYR	3		572.6458495	1714.914148	0.000451244	17	N	64	79
P68368	Exosome	TNLNR	LISQIVSSITASLR	FDGAL	2		744.4437448	1486.87189	0.000451244	67	N	229	243
P68368	Exosome	TNLNR	LISQIVSSITASLR	FDGAL	3		496.6317632	1486.87189	0.000451244	17	N	229	243
P68368	Exosome	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	2		1205.108411	2408.201223	0.000451244	72	Y	243	264
P68368	Exosome	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	3		803.741541	2408.201223	0.000451244	22	Y	243	264
P68368	Exosome	GKKSK	LEFSIYPAPQVSTAVVEPY	NSILT	2		1055.54131	2109.067021	0.000451244	18	Y	166	185
P68368	Exosome	DYGKK	SKLEFSIYPAPQVSTAVVEPY	NSILT	2		1163.104806	2324.194012	0.000451244	18	Y	164	185
P68368	Exosome	DYGKK	SKLEFSIYPAPQVSTAVVEPY	NSILT	3		775.7391374	2324.194012	0.00091018	1	Y	164	185
P68368	Exosome	AKVQR	AVCMLSNTTAIAEAWAR	LDHKF	2	C3:+57.021	932.9561367	1863.896673	0.000662267	2	Y	373	390
P68368	Exosome	YTIGK	EIIDPVLDR	IRKLS	2		535.2985604	1068.581521	0.000735798	7	N	112	121
P68368	Exosome	NGPYR	QLFHPEQLITGK	EDAAN	2	[0:-17.027	697.377648	1392.739696	0.000662267	2	Y	84	96
P68368	Parental	DICRR	NLDIERPTYTNLNR	LISQI	2		859.9451716	1717.874743	0.000622848	18	Y	215	229
P68368	Parental	DICRR	NLDIERPTYTNLNR	LISQI	3		573.6327144	1717.874743	0.000823681	3	Y	215	229
P68368	Parental	DVVPK	DVNAAIAAIK	TKRSI	2		493.2879957	984.5603914	0.00091018	4	N	326	336
P68368	Parental	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2		1208.106734	2414.197869	0.000451244	42	Y	84	105
P68368	Parental	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3		805.7404229	2414.197869	0.000451244	42	Y	84	105
P68368	Parental	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	4		604.5572672	2414.197869	0.000451244	7	Y	84	105
P68368	Parental	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2	Q1:-17.027	1199.593234	2397.170869	0.000451244	8	Y	84	105
P68368	Parental	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	Q1:-17.027	800.0647563	2397.170869	0.000662267	6	Y	84	105
P68368	Parental	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2	[0:-17.027	1199.593234	2397.170869	0.000622848	10	Y	84	105
P68368	Parental	NGPYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	[0:-17.027	800.0647563	2397.170869	0.000622848	29	Y	84	105
P68368	Parental	PTGFK	VGINYQPPTVVPGGDLAK	VQRAV	2		912.9968729	1823.978146	0.000451244	103	Y	352	370
P68368	Parental	AIKTK	RSIQFVDWCPTGFK	VGINY	3	C9:+57.021	580.9560982	1739.844895	0.000451244	21	N	338	352
P68368	Parental	VPYPR	IHFPLATYAPVISAEK	AYHEQ	2		878.9857768	1755.955954	0.000451244	2	Y	264	280
P68368	Parental	VPYPR	IHFPLATYAPVISAEK	AYHEQ	3		586.3264512	1755.955954	0.000451244	48	Y	264	280
P68368	Parental	ISAEK	AYHEQLSVAEITNACFEPANQMVK	CDPRH	3	C15:+57.021	917.4356406	2749.283522	0.002019181	1	Y	280	304
P68368	Parental	IKTKR	SIQFVDWCPTGFK	VGINY	2	C8:+57.021	792.8796917	1583.743783	0.000451244	34	N	339	352
P68368	Parental	MPSDK	TIGGGDDSFTTFFCETGAGK	HVPRA	2	C14:+57.021	1034.452135	2066.88867	0.000451244	43	N	40	60
P68368	Parental	KHVPR	AVFVDLEPTVIDEIRNGPYR	QLFHP	2		1152.105672	2302.195743	0.000451244	2	N	64	84
P68368	Parental	KHVPR	AVFVDLEPTVIDEIRNGPYR	QLFHP	3		768.4063812	2302.195743	0.000451244	5	N	64	84
P68368	Parental	KHVPR	AVFVDLEPTVIDEIR	NGPYR	2		858.4648742	1714.914148	0.000451244	48	N	64	79
P68368	Parental	KHVPR	AVFVDLEPTVIDEIR	NGPYR	3		572.6458495	1714.914148	0.000451244	29	N	64	79
P68368	Parental	IKTKR	SIQFVDWCPTGFKVGINYQPPTVVPGGDLAK	VQRAV	3	C8:+57.021	1130.91159	3389.711369	0.000451244	18	N	339	370
P68368	Parental	TNLNR	LISQIVSSITASLR	FDGAL	2		744.4437448	1486.87189	0.000451244	111	N	229	243
P68368	Parental	TNLNR	LISQIVSSITASLR	FDGAL	3		496.6317632	1486.87189	0.000451244	33	N	229	243
P68368	Parental	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	2		1205.108411	2408.201223	0.000451244	157	Y	243	264
P68368	Parental	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	3		803.741541	2408.201223	0.000451244	31	Y	243	264
P68368	Parental	KHVPR	AVFVDLEPTVIDEIRNGPY	RQLFH	2		1074.055116	2146.094632	0.000451244	10	N	64	83
P68368	Parental	KHVPR	AVFVDLEPTVIDEIRNGPY	RQLFH	3		716.3726774	2146.094632	0.000451244	7	N	64	83
P68368	Parental	GKKSK	LEFSIYPAPQVSTAVVEPY	NSILT	2		1055.54131	2109.067021	0.000451244	38	Y	166	185
P68368	Parental	NNYAR	GHYTIGKEIIDPVLDR	IRKLS	2		913.4944974	1824.973395	0.000451244	3	N	105	121
P68368	Parental	NNYAR	GHYTIGKEIIDPVLDR	IRKLS	3		609.3322649	1824.973395	0.000451244	9	N	105	121
P68368	Parental	DYGKK	SKLEFSIYPAPQVSTAVVEPY	NSILT	2		1163.104806	2324.194012	0.000451244	38	Y	164	185
P68368	Parental	DRIRK	LSDQCTGLQGFLVFHSFGGGTGSGFTSLLMER	LSVDY	3	C5:+57.021	1136.211711	3405.611733	0.000622848	6	N	124	156
P68368	Parental	AKVQR	AVCMLSNTTAIAEAWAR	LDHKF	2	C3:+57.021	932.9561367	1863.896673	0.000451244	4	Y	373	390
P68368	Parental	YTIGK	EIIDPVLDR	IRKLS	2		535.2985604	1068.581521	0.000735798	25	N	112	121
P68368	Parental	MAALE	KDYEEVGIDSYEDEDEGEE	-	2		1125.44057	2248.86554	0.000451244	1	N	429	448
P68368	Parental	LDRIR	KLSDQCTGLQGFLVFHSFGGGTGSGFTSLL	MERLS	3	C6:+57.021	1040.181969	3117.522506	0.000451244	3	N	123	153
P68368	Parental	AVCML	SNTTAIAEAWAR	LDHKF	2		645.826005	1289.63641	0.000451244	2	Y	378	390
P68368	Parental	NGPYR	QLFHPEQLITGK	EDAAN	2		705.891148	1409.766696	0.001871652	1	Y	84	96
P68368	Parental	NGPYR	QLFHPEQLITGK	EDAAN	3		470.930032	1409.766696	0.00091018	3	Y	84	96
P68368	Parental	NGPYR	QLFHPEQLITGK	EDAAN	2	[0:-17.027	697.377648	1392.739696	0.000451244	7	Y	84	96
P68368	Parental	GALNV	DLTEFQTNLVPYPR	IHFPL	2		846.9337412	1691.851882	0.000451244	1	Y	250	264

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68368	Parental	TNLNR	LISQIVSSITA	SLRFD	2		566.3351429	1130.654686	0.000622848	5	N	229	240
P68369	Exosome	DICRR	NLDIERPTYTNLNR	LIGQI	2		859.9451716	1717.874743	0.000451244	15	Y	215	229
P68369	Exosome	DICRR	NLDIERPTYTNLNR	LIGQI	3		573.6327144	1717.874743	0.000451244	5	Y	215	229
P68369	Exosome	DVVPK	DVNAAIATIK	TKRTI	2		508.293278	1014.570956	0.001943752	1	N	326	336
P68369	Exosome	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2		1208.106734	2414.197869	0.000451244	4	Y	84	105
P68369	Exosome	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3		805.7404229	2414.197869	0.000451244	34	Y	84	105
P68369	Exosome	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	4		604.5572672	2414.197869	0.000451244	3	Y	84	105
P68369	Exosome	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	Q1:-17.027	800.0647563	2397.170869	0.000451244	5	Y	84	105
P68369	Exosome	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	[0:-17.027	800.0647563	2397.170869	0.000622848	17	Y	84	105
P68369	Exosome	PTGFK	VGINYQPPTVVPGGDLAK	VQRAV	2		912.9968729	1823.978146	0.000451244	11	Y	352	370
P68369	Exosome	VPYPR	IHFPLATYAPVISAEK	AYHEQ	2		878.9857768	1755.955954	0.000451244	5	Y	264	280
P68369	Exosome	VPYPR	IHFPLATYAPVISAEK	AYHEQ	3		586.3264512	1755.955954	0.000451244	29	Y	264	280
P68369	Exosome	ISAEK	AYHEQLSVAEITNACFEPANQMVK	CDPRH	3	C15:+57.021,M22:+15.995	922.7673072	2765.278522	0.000622848	5	Y	280	304
P68369	Exosome	MPSDK	TIGGGDDSFNTFFSETGAGK	HVPRA	2		1004.450681	2006.885762	0.000451244	39	N	40	60
P68369	Exosome	IKTKR	TIQFVDWCPTGFK	VGINY	2	C8:+57.021	799.8875168	1597.759434	0.000451244	8	N	339	352
P68369	Exosome	KHVPR	AVFVDLEPTVIDEVR	TGTYR	2		851.4570492	1700.898498	0.000451244	32	N	64	79
P68369	Exosome	TNLNR	LIGQIVSSITASLR	FDGAL	2		729.4384624	1456.861325	0.000451244	20	N	229	243
P68369	Exosome	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	2		1205.108411	2408.201223	0.000451244	72	Y	243	264
P68369	Exosome	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	3		803.741541	2408.201223	0.000451244	22	Y	243	264
P68369	Exosome	GKKSK	LEFSIYPAPQVSTAVVEPY	NSILT	2		1055.54131	2109.067021	0.000451244	18	Y	166	185
P68369	Exosome	NNYAR	GHYTIGKEIIDLVLDR	IRKLA	3		614.6760316	1841.004695	0.000451244	1	N	105	121
P68369	Exosome	DYGKK	SKLEFSIYPAPQVSTAVVEPY	NSILT	2		1163.104806	2324.194012	0.000451244	18	Y	164	185
P68369	Exosome	DYGKK	SKLEFSIYPAPQVSTAVVEPY	NSILT	3		775.7391374	2324.194012	0.00091018	1	Y	164	185
P68369	Exosome	YTIGK	EIIDLVLDR	IRKLA	2		543.3142105	1084.612821	0.00091018	14	N	112	121
P68369	Exosome	AKVQR	AVCMLSNTTAIAEAWAR	LDHKF	2	C3:+57.021	932.9561367	1863.896673	0.000662267	2	Y	373	390
P68369	Exosome	TGTYR	QLFHPEQLITGK	EDAAN	2	[0:-17.027	697.377648	1392.739696	0.000662267	2	Y	84	96
P68369	Parental	DICRR	NLDIERPTYTNLNR	LIGQI	2		859.9451716	1717.874743	0.000622848	18	Y	215	229
P68369	Parental	DICRR	NLDIERPTYTNLNR	LIGQI	3		573.6327144	1717.874743	0.000823681	3	Y	215	229
P68369	Parental	DVVPK	DVNAAIATIK	TKRTI	2		508.293278	1014.570956	0.000451244	52	N	326	336
P68369	Parental	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2		1208.106734	2414.197869	0.000451244	42	Y	84	105
P68369	Parental	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3		805.7404229	2414.197869	0.000451244	42	Y	84	105
P68369	Parental	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	4		604.5572672	2414.197869	0.000451244	7	Y	84	105
P68369	Parental	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2	Q1:-17.027	1199.593234	2397.170869	0.000451244	8	Y	84	105
P68369	Parental	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	Q1:-17.027	800.0647563	2397.170869	0.000662267	6	Y	84	105
P68369	Parental	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	2	[0:-17.027	1199.593234	2397.170869	0.000622848	10	Y	84	105
P68369	Parental	TGTYR	QLFHPEQLITGKEDAANNYAR	GHYTI	3	[0:-17.027	800.0647563	2397.170869	0.000622848	29	Y	84	105
P68369	Parental	PTGFK	VGINYQPPTVVPGGDLAK	VQRAV	2		912.9968729	1823.978146	0.000451244	103	Y	352	370
P68369	Parental	VPYPR	IHFPLATYAPVISAEK	AYHEQ	2		878.9857768	1755.955954	0.000451244	2	Y	264	280
P68369	Parental	VPYPR	IHFPLATYAPVISAEK	AYHEQ	3		586.3264512	1755.955954	0.000451244	48	Y	264	280
P68369	Parental	ISAEK	AYHEQLSVAEITNACFEPANQMVK	CDPRH	3	C15:+57.021	917.4356406	2749.283522	0.002019181	1	Y	280	304
P68369	Parental	MPSDK	TIGGGDDSFNTFFSETGAGK	HVPRA	2		1004.450681	2006.885762	0.000451244	65	N	40	60
P68369	Parental	IKTKR	TIQFVDWCPTGFK	VGINY	2	C8:+57.021	799.8875168	1597.759434	0.000451244	23	N	339	352
P68369	Parental	KHVPR	AVFVDLEPTVIDEVR	TGTYR	2		851.4570492	1700.898498	0.000451244	75	N	64	79
P68369	Parental	KHVPR	AVFVDLEPTVIDEVR	TGTYR	3		567.9739661	1700.898498	0.000451244	37	N	64	79
P68369	Parental	KHVPR	AVFVDLEPTVIDEVRTGTY	RQLFH	2		1062.547124	2123.078648	0.001654178	2	N	64	83
P68369	Parental	KHVPR	AVFVDLEPTVIDEVRTGTY	RQLFH	3		708.7006826	2123.078648	0.000451244	1	N	64	83
P68369	Parental	TNLNR	LIGQIVSSITASLR	FDGAL	2		729.4384624	1456.861325	0.000451244	27	N	229	243
P68369	Parental	TNLNR	LIGQIVSSITASLR	FDGAL	3		486.6282416	1456.861325	0.000451244	6	N	229	243
P68369	Parental	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	2		1205.108411	2408.201223	0.000451244	157	Y	243	264
P68369	Parental	TASLR	FDGALNVDLTEFQTNLVPYPR	IHFPL	3		803.741541	2408.201223	0.000451244	31	Y	243	264
P68369	Parental	GKKSK	LEFSIYPAPQVSTAVVEPY	NSILT	2		1055.54131	2109.067021	0.000451244	38	Y	166	185
P68369	Parental	NNYAR	GHYTIGKEIIDLVLDR	IRKLA	2		921.5101474	1841.004695	0.000451244	2	N	105	121
P68369	Parental	NNYAR	GHYTIGKEIIDLVLDR	IRKLA	3		614.6760316	1841.004695	0.000451244	10	N	105	121
P68369	Parental	DYGKK	SKLEFSIYPAPQVSTAVVEPY	NSILT	2		1163.104806	2324.194012	0.000451244	38	Y	164	185
P68369	Parental	YTIGK	EIIDLVLDR	IRKLA	2		543.3142105	1084.612821	0.0007646	28	N	112	121
P68369	Parental	AKVQR	AVCMLSNTTAIAEAWAR	LDHKF	2	C3:+57.021	932.9561367	1863.896673	0.000451244	4	Y	373	390
P68369	Parental	AVCML	SNTTAIAEAWAR	LDHKF	2		645.826005	1289.63641	0.000451244	2	Y	378	390
P68369	Parental	MPSDK	TIGGGDDSFNTFFSETGAGKHVPR	AVFVD	3		833.0634542	2496.166963	0.001264573	1	N	40	64
P68369	Parental	IKTKR	TIQFVDWCPTGFKVGINYQPPTVVPGGDLAK	VQRAV	3	C8:+57.021	1135.583473	3403.727019	0.000622848	3	N	339	370
P68369	Parental	TGTYR	QLFHPEQLITGK	EDAAN	2		705.891148	1409.766696	0.001871652	1	Y	84	96
P68369	Parental	TGTYR	QLFHPEQLITGK	EDAAN	3		470.930032	1409.766696	0.00091018	3	Y	84	96
P68369	Parental	TGTYR	QLFHPEQLITGK	EDAAN	2	[0:-17.027	697.377648	1392.739696	0.000451244	7	Y	84	96
P68369	Parental	GALNV	DLTEFQTNLVPYPR	IHFPL	2		846.9337412	1691.851882	0.000451244	1	Y	250	264
P68369	Parental	AALEK	DYEEVGVDSVEGEGEEEGEEY	-	2		1174.956584	2347.897568	0.000451244	2	N	430	451
P68369	Parental	DRIRK	LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER	LSVDY	3	C5:+57.021	1130.880073	3389.616818	0.000622848	5	N	124	156

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68369	Parental	LDRIR	KLADQCTGLQGFLVFHSFGGGTGSGFTSLL	MERLS	3	C6:+57.021	1034.85033	3101.527591	0.001591523	4	N	123	153
P68369	Parental	DRIRK	LADQCTGLQGFLVFHSFGGGTGSGFTSLL	MERLS	3	C5:+57.021	992.1520093	2973.432628	0.001162105	1	N	124	153
P68372	Exosome	-MR	EIVHLQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	3	Y	2	19
P68372	Exosome	-MR	EIVHLQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	21	Y	2	19
P68372	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000662267	3	Y	81	103
P68372	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	9	Y	81	103
P68372	Exosome	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		1039.479773	3115.41592	0.000451244	41	Y	19	46
P68372	Exosome	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	4		779.8617801	3115.41592	0.000451244	14	Y	19	46
P68372	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	2		1044.04254	2086.06948	0.000451244	4	Y	103	122
P68372	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	3		696.3642934	2086.06948	0.000451244	41	Y	103	122
P68372	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	4		522.5251701	2086.06948	0.000451244	6	Y	103	122
P68372	Exosome	NVQNK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	24	Y	336	350
P68372	Exosome	NVQNK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	1	Y	336	350
P68372	Exosome	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021	1104.516428	3310.525885	0.000451244	17	Y	122	154
P68372	Exosome	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021,M25:+15.995	1109.848095	3326.520885	0.000451244	8	Y	122	154
P68372	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	2		979.9950585	1957.974517	0.000451244	26	Y	103	121
P68372	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	3		653.6659724	1957.974517	0.000451244	38	Y	103	121
P68372	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	17	Y	77	103
P68372	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	66	Y	77	103
P68372	Exosome	-	MREIVHLQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000622848	1	Y	0	19
P68372	Exosome	-	MREIVHLQAGQCGNQIGAK	FWEVI	3	M1:+15.995,C12:+57.021	709.3583655	2125.051697	0.000451244	2	Y	0	19
P68372	Exosome	LQLER	INVYYNEATGGK	YVPRA	2		664.8282134	1327.640827	0.000451244	11	N	46	58
P68372	Exosome	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		990.4569687	2968.347506	0.000451244	10	Y	20	46
P68372	Exosome	PRHGR	YLTVAAVFR	GRMSM	2		520.3009061	1038.586212	0.000622848	18	Y	309	318
P68372	Exosome	PRGLK	MSATFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.000451244	8	Y	362	380
P68372	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.001162105	2	Y	216	241
P68372	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	M17:+15.995,C23:+57.021	908.7829573	2723.325472	0.001699387	1	Y	216	241
P68372	Exosome	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	28	Y	183	213
P68372	Exosome	PRGLK	MSATFIGNSTAIQELFK	RISEQ	2		929.4749166	1856.934233	0.000622848	2	Y	362	379
P68372	Exosome	KYVPR	AVLVDLEPGTMDSVR	SGPFG	2	M11:+15.995	809.4118276	1616.808055	0.000698008	4	Y	62	77
P68372	Exosome	SQQYR	ALTVPELTQQMFDAK	NMMAA	2		846.4378027	1690.860005	0.00091018	1	Y	282	297
P68372	Exosome	-M	REIVHLQAGQCGNQIGAK	FWEVI	3	C11:+57.021	660.3465369	1978.016211	0.002981883	1	Y	1	19
P68372	Parental	-MR	EIVHLQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	41	Y	2	19
P68372	Parental	-MR	EIVHLQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	28	Y	2	19
P68372	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000451244	30	Y	81	103
P68372	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	20	Y	81	103
P68372	Parental	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		1039.479773	3115.41592	0.000451244	80	Y	19	46
P68372	Parental	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	4		779.8617801	3115.41592	0.000451244	30	Y	19	46
P68372	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	2		1044.04254	2086.06948	0.000451244	30	Y	103	122
P68372	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	3		696.3642934	2086.06948	0.000451244	68	Y	103	122
P68372	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	4		522.5251701	2086.06948	0.000451244	45	Y	103	122
P68372	Parental	NVQNK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	38	Y	336	350
P68372	Parental	NVQNK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	19	Y	336	350
P68372	Parental	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021	1104.516428	3310.525885	0.000451244	27	Y	122	154
P68372	Parental	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021,M25:+15.995	1109.848095	3326.520885	0.000451244	16	Y	122	154
P68372	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	2		979.9950585	1957.974517	0.000451244	36	Y	103	121
P68372	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	3		653.6659724	1957.974517	0.000451244	49	Y	103	121
P68372	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	50	Y	77	103
P68372	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	220	Y	77	103
P68372	Parental	VPSPK	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	4	C27:+57.021,C37:+57.021	1149.032553	4592.099013	0.001162105	8	Y	174	213
P68372	Parental	-	MREIVHLQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000622848	5	Y	0	19
P68372	Parental	LQLER	INVYYNEATGGK	YVPRA	2		664.8282134	1327.640827	0.000451244	31	N	46	58
P68372	Parental	LQLER	INVYYNEATGGKYVPR	AVLVD	2		922.4710222	1842.926444	0.000451244	10	N	46	62
P68372	Parental	LQLER	INVYYNEATGGKYVPR	AVLVD	3		615.3166148	1842.926444	0.000823681	2	N	46	62
P68372	Parental	EYPDR	IMNTFSVVPSPK	VSDTV	2		660.355553	1318.695506	0.001763695	2	Y	162	174
P68372	Parental	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		990.4569687	2968.347506	0.000451244	33	Y	20	46
P68372	Parental	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLER	INVYY	4		743.0946766	2968.347506	0.00091018	1	Y	20	46
P68372	Parental	PRHGR	YLTVAAVFR	GRMSM	2		520.3009061	1038.586212	0.000622848	23	Y	309	318
P68372	Parental	PRGLK	MSATFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.000622848	7	Y	362	380
P68372	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.000451244	22	Y	216	241
P68372	Parental	EPYNA	TLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C16:+57.021,C26:+57.021	1140.190598	3417.548394	0.000823681	4	Y	185	213
P68372	Parental	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	125	Y	183	213
P68372	Parental	PRGLK	MSATFIGNSTAIQELFK	RISEQ	2		929.4749166	1856.934233	0.000451244	4	Y	362	379

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68372	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	KLAVN	4	C23:+57.021	955.7347788	3818.907915	0.001654178	2	Y	216	251
P68372	Parental	TTCLR	FPGQLNADLRK	LAVNM	3		420.2354554	1257.682966	0.001162105	3	Y	241	252
P68372	Parental	TTCLR	FPGQLNADLR	KLAVN	2		565.8018016	1129.588003	0.000451244	5	Y	241	251
P68372	Parental	GNNWA	KGHYTEGAELVDSVLDVVR	KEAES	2		1044.04254	2086.06948	0.000451244	3	Y	102	121
P68372	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAKG	HYTEG	3		952.4603192	2854.357558	0.000823681	4	Y	77	104
P68372	Parental	QIGAK	FWEVISDEHGIDPTGTY	HGDSD	2		983.4474098	1964.87922	0.000823681	1	Y	19	36
P68372	Parental	LVSEY	QQYQDATAEEEGEFEEEAEEEVA	-	2		1330.536261	2659.056922	0.000622848	1	N	422	445
P68404-2	Parental	DGWFK	LLSQEEGEYFNVPVPPEGSEGNEELR	QKFER	2		1459.68868	2917.361759	0.001463592	1	N	276	302
P68404-2	Parental	GVTTK	TFCGTPDYIAPEIIAYQPYGK	SVDWW	2	C3:+57.021	1202.58041	2403.145219	0.000451244	7	N	499	520
P68404-2	Parental	QEVIR	NIDQSEFEGFSFVNSEFLKPEVK	S-	2		1345.65338	2689.29116	0.000622848	1	N	649	672
P68404-2	Parental	QEVIR	NIDQSEFEGFSFVNSEFLKPEVK	S-	3		897.4381868	2689.29116	0.000451244	11	N	649	672
P68433	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	2		668.349313	1334.683026	0.000451244	87	Y	73	84
P68433	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	3		445.902142	1334.683026	0.000451244	127	Y	73	84
P68433	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	2	[0:-18.011	659.343813	1316.672026	0.002212458	1	Y	73	84
P68433	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	24	Y	73	84
P68433	Exosome	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	205	Y	102	116
P68433	Exosome	ACEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	51	Y	100	116
P68433	Exosome	ACEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	68	Y	100	116
P68433	Exosome	EACEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	28	Y	99	116
P68433	Exosome	EACEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002080925	1	Y	99	116
P68433	Exosome	KTDLR	FQSSAVMALQEACEAY	LVGLF	2	M7:+15.995,C13:+57.021	910.8954531	1819.775306	0.000451244	25	N	84	100
P68433	Exosome	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	2	C4:+57.021,C18:+57.021	1326.625323	2651.235045	0.000451244	23	N	93	116
P68433	Exosome	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C4:+57.021,C18:+57.021	884.752815	2651.235045	0.000451244	69	N	93	116
P68433	Exosome	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	2	Q1:-17.027,C4:+57.021,C18:+57.021	1318.111823	2634.208045	0.000735798	14	N	93	116
P68433	Exosome	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	Q1:-17.027,C4:+57.021,C18:+57.021	879.0771483	2634.208045	0.000451244	18	N	93	116
P68433	Exosome	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	[0:-	879.0771483	2634.208045	0.000735798	4	N	93	116
P68433	Exosome	SSAVM	ALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C6:+57.021,C20:+57.021	946.126541	2835.356223	0.000451244	24	N	91	116
P68433	Exosome	SSAVM	ALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	C6:+57.021,C20:+57.021	709.8468557	2835.356223	0.000662267	2	N	91	116
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C13:+57.021,C27:+57.021	936.4563991	3741.794396	0.0025889	1	N	84	117
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAKR	VTIMP	4	M7:+15.995,C13:+57.021,C27:+57.021	940.4551491	3757.789396	0.000451244	26	N	84	117
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C13:+57.021,C27:+57.021	1196.238895	3585.693285	0.000451244	248	N	84	116
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	C13:+57.021,C27:+57.021	897.4311213	3585.693285	0.000451244	84	N	84	116
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	M7:+15.995,C13:+57.021,C27:+57.021	1201.570562	3601.688285	0.000451244	712	N	84	116
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	M7:+15.995,C13:+57.021,C27:+57.021	901.4298713	3601.688285	0.000451244	224	N	84	116
P68433	Exosome	CEAYL	VGLFEDTNLCAIHAK	RVTIM	2	C10:+57.021	844.4275375	1686.839475	0.000451244	56	Y	101	116
P68433	Exosome	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	56	Y	104	116
P68433	Exosome	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	68	Y	103	116
P68433	Exosome	MALQE	ACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C2:+57.021,C16:+57.021	799.0524247	2394.133874	0.000622848	5	N	95	116
P68433	Exosome	VMALQ	EACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C3:+57.021,C17:+57.021	842.0666225	2523.176467	0.000451244	5	N	94	116
P68433	Exosome	VMALQ	EACEAYLVGLFEDTNLCAIHAK	RVTIM	3	E1:-	836.0629558	2505.165467	0.000622848	5	N	94	116
P68433	Exosome	FKTDL	RFQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	M8:+15.995,C14:+57.021,C28:+57.021	940.4551491	3757.789396	0.000451244	10	N	83	116
P68433	Exosome	DLRFQ	SSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	M5:+15.995,C11:+57.021,C25:+57.021	1109.861565	3326.561294	0.000451244	17	N	86	116
P68433	Exosome	ALQEA	CEAYLVGLFEDTNLCAIHAK	RVTIM	2	C1:+57.021,C15:+57.021	1162.55618	2323.09676	0.000662267	2	N	96	116
P68433	Exosome	ALQEA	CEAYLVGLFEDTNLCAIHAK	RVTIM	3	C1:+57.021,C15:+57.021	775.3733868	2323.09676	0.000451244	9	N	96	116
P68433	Exosome	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.001699387	2	Y	105	116
P68433	Exosome	TDLRF	QSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	C12:+57.021,C26:+57.021	860.6640178	3438.624871	0.000622848	1	N	85	116
P68433	Exosome	TDLRF	QSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	M6:+15.995,C12:+57.021,C26:+57.021	1152.547757	3454.619871	0.000451244	9	N	85	116
P68433	Exosome	LQEAC	EAYLVGLFEDTNLCAIHAK	RVTIM	2	C14:+57.021	1082.541087	2163.066575	0.000451244	10	Y	97	116
P68433	Exosome	LQEAC	EAYLVGLFEDTNLCAIHAK	RVTIM	2	E1:-18.011,C14:+57.021	1073.535587	2145.055575	0.001871652	3	Y	97	116
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIH	AKRVT	3	C13:+57.021,C27:+57.021	1129.861536	3386.561208	0.000451244	6	N	84	114
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIH	AKRVT	3	M7:+15.995,C13:+57.021,C27:+57.021	1135.193203	3402.556208	0.000451244	10	N	84	114
P68433	Exosome	SAVMA	LQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C5:+57.021,C19:+57.021	922.447503	2764.319109	0.000451244	12	N	92	116
P68433	Exosome	QSSAV	MALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C7:+57.021,C21:+57.021	989.8067029	2966.396709	0.000451244	4	N	90	116
P68433	Exosome	QSSAV	MALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	M1:+15.995,C7:+57.021,C21:+57.021	995.1383696	2982.391709	0.000451244	7	N	90	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68433	Exosome	QSSAV	MALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	M1:+15.995,C7:+57.021,C21:+57.021	746.6057272	2982.391709	0.00091018	1	N	90	116
P68433	Exosome	RFQSS	AVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C9:+57.021,C23:+57.021	1046.508546	3136.502237	0.000451244	3	N	88	116
P68433	Exosome	RFQSS	AVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	M3:+15.995,C9:+57.021,C23:+57.021	1051.840212	3152.497237	0.000451244	27	N	88	116
P68433	Exosome	RFQSS	AVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	M3:+15.995,C9:+57.021,C23:+57.021	789.1321092	3152.497237	0.000451244	3	N	88	116
P68433	Exosome	QEACE	AYLVGLFEDTNLCAIHAK	RVTIM	2	C13:+57.021	1018.019791	2034.023981	0.000451244	5	Y	98	116
P68433	Exosome	AQDFK	TDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	C17:+57.021,C31:+57.021	1018.746071	4070.953082	0.002374549	1	N	80	116
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHA	KRVTI	3	M7:+15.995,C13:+57.021,C27:+57.021	1158.872241	3473.593322	0.002145581	1	N	84	115
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLC	AIHAK	3	M7:+15.995,C13:+57.021,C27:+57.021	1028.133173	3081.376118	0.002080925	1	N	84	111
P68433	Exosome	KTDLR	FQSSAVMALQEACEAYLV	GLFED	2	M7:+15.995,C13:+57.021	1016.971692	2031.927784	0.002374549	1	N	84	102
P68433	Parental	QRLVR	EIAQDFKTDLR	FQSSA	2		668.349313	1334.683026	0.000451244	20	Y	73	84
P68433	Parental	QRLVR	EIAQDFKTDLR	FQSSA	3		445.902142	1334.683026	0.000451244	88	Y	73	84
P68433	Parental	QRLVR	EIAQDFKTDLR	FQSSA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	2	Y	73	84
P68433	Parental	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	49	Y	102	116
P68433	Parental	ACEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	188	Y	100	116
P68433	Parental	ACEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	307	Y	100	116
P68433	Parental	EACEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	7	Y	99	116
P68433	Parental	EACEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002727428	1	Y	99	116
P68433	Parental	KTDLR	FQSSAVMALQEACEAY	LVGLF	2	C13:+57.021	902.8979531	1803.780306	0.000451244	2	N	84	100
P68433	Parental	KTDLR	FQSSAVMALQEACEAY	LVGLF	2	M7:+15.995,C13:+57.021	910.8954531	1819.775306	0.000451244	13	N	84	100
P68433	Parental	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	2	C4:+57.021,C18:+57.021	1326.625323	2651.235045	0.000451244	36	N	93	116
P68433	Parental	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C4:+57.021,C18:+57.021	884.752815	2651.235045	0.000451244	79	N	93	116
P68433	Parental	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	2	Q1:-17.027,C4:+57.021,C18:+57.021	1318.111823	2634.208045	0.000735798	25	N	93	116
P68433	Parental	AVMAL	QEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	Q1:-17.027,C4:+57.021,C18:+57.021	879.0771483	2634.208045	0.000735798	22	N	93	116
P68433	Parental	SSAVM	ALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C6:+57.021,C20:+57.021	946.126541	2835.356223	0.000451244	25	N	91	116
P68433	Parental	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C13:+57.021,C27:+57.021	936.4563991	3741.794396	0.000622848	3	N	84	117
P68433	Parental	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAKR	VTIMP	4	M7:+15.995,C13:+57.021,C27:+57.021	940.4551491	3757.789396	0.001329271	2	N	84	117
P68433	Parental	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C13:+57.021,C27:+57.021	1196.238895	3585.693285	0.000451244	49	N	84	116
P68433	Parental	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	C13:+57.021,C27:+57.021	897.4311213	3585.693285	0.000451244	13	N	84	116
P68433	Parental	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	M7:+15.995,C13:+57.021,C27:+57.021	1201.570562	3601.688285	0.000451244	42	N	84	116
P68433	Parental	KTDLR	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	M7:+15.995,C13:+57.021,C27:+57.021	901.4298713	3601.688285	0.000451244	31	N	84	116
P68433	Parental	ACEAY	LVGLFEDTNLCAIHAKR	VTIMP	2	C11:+57.021	979.0201251	1956.02465	0.001871652	2	Y	100	117
P68433	Parental	ACEAY	LVGLFEDTNLCAIHAKR	VTIMP	4	C11:+57.021	490.0139625	1956.02465	0.000451244	6	Y	100	117
P68433	Parental	CEAYL	VGLFEDTNLCAIHAK	RVTIM	3	C10:+57.021	563.287625	1686.839475	0.000998612	3	Y	101	116
P68433	Parental	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	2	Y	104	116
P68433	Parental	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	5	Y	103	116
P68433	Parental	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.000451244	1	Y	105	116
P68433	Parental	TDLRF	QSSAVMALQEACEAYLVGLFEDTNLCAIHAK	RVTIM	4	Q1:-17.027,M6:+15.995,C12:+57.021,C26:+57.021	860.4060178	3437.592871	0.001264573	1	N	85	116
P68433	Parental	SAVMA	LQEACEAYLVGLFEDTNLCAIHAK	RVTIM	3	C5:+57.021,C19:+57.021	922.447503	2764.319109	0.000451244	9	N	92	116
P68510	Exosome	ASAMK	AVTELNEPLSNEDRNLLSVAYK	NVVGA	2		1238.14044	2474.26528	0.000637154	12	N	28	50
P68510	Exosome	ASAMK	AVTELNEPLSNEDRNLLSVAYK	NVVGA	3		825.7628933	2474.26528	0.000451244	15	N	28	50
P68510	Exosome	SGEKK	NSVVEASEAAYKEAFEISK	EHMQP	2		1036.513281	2071.010962	0.000451244	29	N	143	162
P68510	Exosome	SGEKK	NSVVEASEAAYKEAFEISK	EHMQP	3		691.3447874	2071.010962	0.000622848	5	N	143	162
P68510	Exosome	THPIR	LGLALNFSVFYYEIQNAPEQACLLAK	QAFDD	3	C22:+57.021	991.512767	2971.514901	0.000451244	16	N	172	198
P68510	Exosome	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1110.213817	3327.618052	0.000451244	12	N	198	227
P68510	Exosome	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1115.545484	3343.613052	0.000451244	4	N	198	227
P68510	Exosome	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	Q1:-17.027	1104.538151	3310.591052	0.000698008	1	N	198	227
P68510	Exosome	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	[0:-17.027	1104.538151	3310.591052	0.000698008	2	N	198	227
P68510	Exosome	FSVFY	YEIQNAPEQACLLAK	QAFDD	2	C11:+57.021	874.4381022	1746.860604	0.000622848	1	N	183	198
P68510	Exosome	ASAMK	AVTELNEPLSNEDR	NLLSV	2		793.886988	1585.758376	0.000451244	49	N	28	42
P68510	Exosome	EKIEK	ELETVCNDVLALLDK	FLIKN	2	C6:+57.021	866.4455929	1730.875586	0.000451244	29	N	91	106
P68510	Exosome	AYREK	IEKELETVCNDVLALLDK	FLIKN	2	C9:+57.021	1051.556403	2101.097206	0.000451244	8	N	88	106
P68510	Exosome	AYREK	IEKELETVCNDVLALLDK	FLIKN	3	C9:+57.021	701.3735354	2101.097206	0.000451244	18	N	88	106
P68510	Exosome	EKIEK	ELETVCNDVLALLDKFLIK	NCNDF	2	C6:+57.021	1117.111346	2232.207091	0.000451244	1	N	91	110

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P68510	Exosome	EKIEK	ELETVCNDVLALLDKFLIK	NCNDF	3	C6:+57.021	745.0768304	2232.207091	0.000451244	15	N	91	110
P68510	Exosome	IMQLL	RDNLTLWTSDQQDEEAGEGN	-	2		1139.496879	2276.978159	0.00091018	1	N	226	246
P68510	Exosome	SGEKK	NSVVEASEAAYK	EAFEI	2		634.3123961	1266.609192	0.000451244	2	N	143	155
P68510	Exosome	THPIR	LGLALNFSVF	YYEIQ	2		540.808564	1079.601528	0.002453667	1	Y	172	182
P68510	Exosome	MQLLR	DNLTLWTSDQQDEEAGEGN	-	2		1061.446324	2120.877048	0.000823681	1	N	227	246
P68510	Parental	ASAMK	AVTELNEPLSNEDRNLLSVAYK	NVVGA	2		1238.14044	2474.26528	0.000451244	4	N	28	50
P68510	Parental	ASAMK	AVTELNEPLSNEDRNLLSVAYK	NVVGA	3		825.7628933	2474.26528	0.000451244	11	N	28	50
P68510	Parental	SGEKK	NSVVEASEAAYKEAFEISK	EHMQP	2		1036.513281	2071.010962	0.000451244	14	N	143	162
P68510	Parental	SGEKK	NSVVEASEAAYKEAFEISK	EHMQP	3		691.3447874	2071.010962	0.001763695	1	N	143	162
P68510	Parental	THPIR	LGLALNFSVFYYEIQNAPEQACLLAK	QAFDD	3	C22:+57.021	991.512767	2971.514901	0.000451244	16	N	172	198
P68510	Parental	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3		1110.213817	3327.618052	0.000451244	14	N	198	227
P68510	Parental	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	Q1:-17.027	1104.538151	3310.591052	0.000451244	2	N	198	227
P68510	Parental	CLLAK	QAFDDAIAELDTLNEDSYKDSTLIMQLLR	DNLTL	3	[0:-17.027	1104.538151	3310.591052	0.000451244	7	N	198	227
P68510	Parental	FSVFY	YEIQNAPEQACLLAK	QAFDD	2	C11:+57.021	874.4381022	1746.860604	0.000451244	12	N	183	198
P68510	Parental	ASAMK	AVTELNEPLSNEDR	NLLSV	2		793.886988	1585.758376	0.000451244	53	N	28	42
P68510	Parental	EKIEK	ELETVCNDVLALLDK	FLIKN	2	C6:+57.021	866.4455929	1730.875586	0.000451244	15	N	91	106
P68510	Parental	AYREK	IEKELETVCNDVLALLDK	FLIKN	2	C9:+57.021	1051.556403	2101.097206	0.000662267	6	N	88	106
P68510	Parental	AYREK	IEKELETVCNDVLALLDK	FLIKN	3	C9:+57.021	701.3735354	2101.097206	0.000451244	9	N	88	106
P68510	Parental	EKIEK	ELETVCNDVLALLDKFLIK	NCNDF	2	C6:+57.021	1117.111346	2232.207091	0.000451244	6	N	91	110
P68510	Parental	EKIEK	ELETVCNDVLALLDKFLIK	NCNDF	3	C6:+57.021	745.0768304	2232.207091	0.001871652	5	N	91	110
P68510	Parental	THPIR	LGLALNFSVFY	YEIQN	2		622.3402283	1242.664857	0.001352548	2	Y	172	183
P68510	Parental	IMQLL	RDNLTLWTSDQQDEEAGEGN	-	2		1139.496879	2276.978159	0.000451244	13	N	226	246
P68510	Parental	SGEKK	NSVVEASEAAYK	EAFEI	2		634.3123961	1266.609192	0.000451244	1	N	143	155
P68510	Parental	CLLAK	QAFDDAIAELDTLNEDSYK	DSTLI	2		1079.495285	2156.974971	0.000823681	1	N	198	217
P70158	Exosome	DLQPK	SLYALVQQFATK	DSKQF	2		684.880249	1367.744898	0.000451244	1	N	383	395
P70158	Parental	APADR	APAVGQFWHVTDLHLDPTYHITDDR	TKVCA	3		968.807496	2903.399088	0.001699387	1	N	30	55
P70158	Parental	APADR	APAVGQFWHVTDLHLDPTYHITDDR	TKVCA	4		726.857572	2903.399088	0.000451244	6	N	30	55
P70158	Parental	DLQPK	SLYALVQQFATK	DSKQF	2		684.880249	1367.744898	0.000451244	8	N	383	395
P70168	Exosome	KFLER	AAVENLPTFLVELSR	VLANP	2		829.959759	1657.903918	0.000451244	23	N	27	42
P70168	Exosome	KFLER	AAVENLPTFLVELSR	VLANP	3		553.6424394	1657.903918	0.000451244	21	N	27	42
P70168	Exosome	KFYAK	GALQYLVPILTQTLTKQDENDDDDDWNPCK	AAGVC	3	C29:+57.021	1169.219476	3504.635029	0.000622848	4	N	316	346
P70168	Exosome	KFYAK	GALQYLVPILTQTLTKQDENDDDDDWNPCK	AAGVC	4	C29:+57.021	877.1665573	3504.635029	0.000622848	7	N	316	346
P70168	Exosome	KFYAK	GALQYLVPILTQTLTK	QDEND	2		880.0223594	1758.029119	0.000451244	18	N	316	332
P70168	Exosome	KFYAK	GALQYLVPILTQTLTK	QDEND	3		587.0175062	1758.029119	0.000451244	29	N	316	332
P70168	Exosome	GDLCR	ALQSNILPFCDEVMQLLLENLGNENVHR	SVKPQ	3	C10:+57.021	1089.548434	3265.621903	0.000451244	8	N	679	707
P70168	Exosome	WTVGR	ICELLPEAAINDVYLAPLLQCLIEGLSAEPR	VASNV	3	C2:+57.021,C21:+57.021	1160.942296	3479.803487	0.000451244	28	N	434	465
P70168	Exosome	SNNVK	LAATNALLNSLEFTK	ANFDK	2		803.4464845	1604.877369	0.000451244	30	N	191	206
P70168	Exosome	LIVQK	LLETTDRPDGHQNNLR	SSAYE	3		626.9859278	1877.934383	0.001162105	3	N	509	525
P70168	Exosome	GEFKK	YLEVVLNTLQQASQAQVDK	SDFDM	2		1074.071298	2146.126995	0.000451244	24	N	730	749
P70168	Exosome	TEHMK	ESTLEAIGYICQDIDPEQLQDK	SNEIL	2	C11:+57.021	1283.105174	2564.194748	0.000451244	36	N	147	169
P70168	Exosome	TEHMK	ESTLEAIGYICQDIDPEQLQDK	SNEIL	3	C11:+57.021	855.7393828	2564.194748	0.000451244	11	N	147	169
P70168	Exosome	ENVHR	SVKPQILSVFGDIALAIGGEFK	KYLEV	3		763.7671389	2288.278017	0.000451244	2	N	707	729
P70168	Exosome	GIGLK	NYAEYQVCLAAVGLVGDLCR	ALQSN	2	C8:+57.021,C19:+57.021	1136.048522	2270.081445	0.000451244	7	N	659	679
P70168	Exosome	GIGLK	NYAEYQVCLAAVGLVGDLCR	ALQSN	3	C8:+57.021,C19:+57.021	757.7016149	2270.081445	0.000451244	16	N	659	679
P70168	Exosome	STSDR	IQFNDLQSLLCATLQNVLR	KVQHQ	2	C11:+57.021	1123.602011	2245.188421	0.000451244	13	N	574	593
P70168	Exosome	STSDR	IQFNDLQSLLCATLQNVLR	KVQHQ	3	C11:+57.021	749.4039404	2245.188421	0.000451244	16	N	574	593
P70168	Exosome	LNELR	ESCLEAYTGIVQGLK	GDQEN	2	C3:+57.021	834.4193781	1666.823156	0.001329271	3	N	762	777
P70168	Exosome	QTLTK	QDENDDDDDWNPCK	AAGVC	2	C13:+57.021	883.3160352	1764.61647	0.001162105	4	N	332	346
P70168	Exosome	ENVHR	SVKPQILSVFGDIALAIGGEFKK	YLEVV	3		806.4654599	2416.37298	0.000823681	2	N	707	730
P70168	Exosome	ENVHR	SVKPQILSVFGDIALAIGGEFKK	YLEVV	4		605.1010449	2416.37298	0.000451244	12	N	707	730
P70168	Exosome	WTVGR	ICELLPEAAINDVYLAPLLQ	CLIEG	2	C2:+57.021	1128.103521	2254.191441	0.001763695	1	N	434	454
P70168	Exosome	GEFKK	YLEVVLNTLQQASQAQVDKSDFDMVDYLNELR	ESCLE	3	M24:+15.995	1254.284552	3759.830256	0.000622848	1	N	730	762
P70168	Exosome	DRIQF	NDLQSLLCATLQNVLR	KVQHQ	3	C8:+57.021	620.0002552	1856.977366	0.000451244	2	N	577	593
P70168	Parental	TILEK	TVSPDRLELEAAQK	FLERA	2		778.9180912	1555.820582	0.002663018	1	N	9	23
P70168	Parental	KFLER	AAVENLPTFLVELSR	VLANP	2		829.959759	1657.903918	0.000451244	30	N	27	42
P70168	Parental	KFLER	AAVENLPTFLVELSR	VLANP	3		553.6424394	1657.903918	0.000451244	10	N	27	42
P70168	Parental	KFYAK	GALQYLVPILTQTLTKQDENDDDDDWNPCK	AAGVC	3	C29:+57.021	1169.219476	3504.635029	0.000451244	5	N	316	346
P70168	Parental	KFYAK	GALQYLVPILTQTLTKQDENDDDDDWNPCK	AAGVC	4	C29:+57.021	877.1665573	3504.635029	0.000451244	2	N	316	346
P70168	Parental	KFYAK	GALQYLVPILTQTLTK	QDEND	2		880.0223594	1758.029119	0.001839721	2	N	316	332
P70168	Parental	KFYAK	GALQYLVPILTQTLTK	QDEND	3		587.0175062	1758.029119	0.000451244	26	N	316	332
P70168	Parental	GDLCR	ALQSNILPFCDEVMQLLLENLGNENVHR	SVKPQ	3	C10:+57.021	1089.548434	3265.621903	0.000451244	2	N	679	707
P70168	Parental	WTVGR	ICELLPEAAINDVYLAPLLQCLIEGLSAEPR	VASNV	3	C2:+57.021,C21:+57.021	1160.942296	3479.803487	0.000451244	33	N	434	465
P70168	Parental	SNNVK	LAATNALLNSLEFTK	ANFDK	2		803.4464845	1604.877369	0.000451244	26	N	191	206
P70168	Parental	GEFKK	YLEVVLNTLQQASQAQVDK	SDFDM	2		1074.071298	2146.126995	0.000451244	22	N	730	749
P70168	Parental	TEHMK	ESTLEAIGYICQDIDPEQLQDK	SNEIL	2	C11:+57.021	1283.105174	2564.194748	0.000451244	22	N	147	169

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P70168	Parental	TEHMK	ESTLEAIGYICQDIDPEQLQDK	SNEIL	3	C11:+57.021	855.7393828	2564.194748	0.000451244	4	N	147	169
P70168	Parental	GIGLK	NYAEYQVCLAAVGLVGDLCR	ALQSN	3	C8:+57.021,C19:+57.021	757.7016149	2270.081445	0.00307782	1	N	659	679
P70168	Parental	STSDR	IQFNDLQSLLCATLQNVLR	KVQHQ	2	C11:+57.021	1123.602011	2245.188421	0.000451244	13	N	574	593
P70168	Parental	STSDR	IQFNDLQSLLCATLQNVLR	KVQHQ	3	C11:+57.021	749.4039404	2245.188421	0.000451244	20	N	574	593
P70168	Parental	LNELR	ESCLEAYTGIVQGLK	GDQEN	2	C3:+57.021	834.4193781	1666.823156	0.001395409	2	N	762	777
P70168	Parental	FILSF	IDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLK	LVEAR	3	C17:+57.021,C26:+57.021	1218.590873	3652.749219	0.000622848	2	N	800	835
P70168	Parental	FILSF	IDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLK	LVEAR	4	C17:+57.021,C26:+57.021	914.1951048	3652.749219	0.000451244	7	N	800	835
P70168	Parental	SAEPR	VASNVCWAFSSLAEAAYEAADVADDQEEPATY	CLSSS	3	C6:+57.021	1150.837032	3449.487696	0.00091018	1	N	465	497
P70168	Parental	FILSF	IDHIAGDEDHTDGVVACAAGLIGDLCTAFGK	DVLKL	3	C17:+57.021,C26:+57.021	1066.832745	3197.474835	0.000451244	8	N	800	831
P70168	Parental	QTLTK	QDENDDDDDWNPCK	AAGVC	2	C13:+57.021	883.3160352	1764.61647	0.000451244	10	N	332	346
P70168	Parental	ENVHR	SVKPQILSVFGDIALAIGGEFKK	YLEVV	4		605.1010449	2416.37298	0.000451244	7	N	707	730
P70195	Exosome	KNCSK	IHFISPNIYCCGAGTAADTDMTTQLISSNLELHSLTTGR	LPRVV	4	C10:+57.021,C11:+57.021	1067.26235	4265.018202	0.0007646	5	N	76	115
P70195	Exosome	KNCSK	IHFISPNIYCCGAGTAADTDMTTQLISSNLELHSLTTGR	LPRVV	4	C10:+57.021,C11:+57.021,M21:+15.995	1071.2611	4281.013202	0.000451244	28	N	76	115
P70195	Exosome	QMLFR	YQGYIGAALVLGGVDVTGPHLYSIYPHGSTDK	LPYVT	3		1116.902013	3347.68264	0.000451244	11	N	132	164
P70195	Exosome	QMLFR	YQGYIGAALVLGGVDVTGPHLYSIYPHGSTDK	LPYVT	4		837.9284601	3347.68264	0.000451244	8	N	132	164
P70195	Exosome	EEEAK	KLVSEAIAAGIFNDLGSGSNIDLCVISK	SKLDF	3	C24:+57.021	964.5113146	2890.510544	0.000451244	4	N	195	223
P70195	Exosome	VLTEK	VTPLEIEVLEETVQTMDTS	-	3		712.0210935	2133.03988	0.002663018	1	N	258	277
P70195	Exosome	VLTEK	VTPLEIEVLEETVQTMDTS	-	2	M16:+15.995	1075.52524	2149.03488	0.000451244	47	N	258	277
P70195	Exosome	VLTEK	VTPLEIEVLEETVQTMDTS	-	3	M16:+15.995	717.3527601	2149.03488	0.000451244	9	N	258	277
P70195	Exosome	EEAKK	LVSEAIAAGIFNDLGSGSNIDLCVISK	SKLDF	2	C23:+57.021	1382.21559	2762.415581	0.000451244	22	N	196	223
P70195	Exosome	EEAKK	LVSEAIAAGIFNDLGSGSNIDLCVISK	SKLDF	3	C23:+57.021	921.8129936	2762.415581	0.000451244	14	N	196	223
P70195	Exosome	EEAKK	LVSEAIAAGIFNDLGSGSNIDLCVISK	SKLDF	4	C23:+57.021	691.6116952	2762.415581	0.000451244	2	N	196	223
P70195	Exosome	FISPN	IYCCGAGTAADTDMTTQLISSNLELHSLTTGR	LPRVV	3	C3:+57.021,C4:+57.021,M14:+15.995	1158.537809	3472.590028	0.001591523	1	N	83	115
P70195	Exosome	ISKSK	LDFLRPFSVPNK	KGTRL	3		478.2702772	1431.787431	0.001463592	1	N	225	237
P70195	Exosome	ARKTG	TTIAGVVYKDGIVLGADTR	ATEGM	2		975.0392691	1948.062938	0.000451244	2	N	43	62
P70268	Exosome	QSEPR	SWSLLEQLGLAGADLAAPGVQQQLELERER	LKREI	3		1093.244551	3276.710252	0.000451244	5	N	11	41
P70268	Exosome	STVLK	LDNTVVGQTAWKPCGPNAWDQSFTLELER	ARELE	3	C14:+57.021	1111.538704	3331.592711	0.000451244	12	N	399	428
P70268	Exosome	QSEPR	SWSLLEQLGLAGADLAAPGVQQQLELER	ERLKR	3		998.1966492	2991.566548	0.000451244	6	N	11	39
P70268	Exosome	QPFFR	SLGWDVLLAR	RLPPP	2		565.3223699	1128.62914	0.000851441	1	N	879	889
P70268	Exosome	KIVYR	DLKLDNLLLDTEGYVK	IADFG	3		617.0038139	1847.988042	0.000451244	2	N	743	759
P70268	Exosome	VVGCK	NLPETIPWSPPPSVGASGTPESR	TPFLS	2		1188.595668	2375.175736	0.001699387	2	N	337	360
P70268	Parental	QSEPR	SWSLLEQLGLAGADLAAPGVQQQLELERER	LKREI	3		1093.244551	3276.710252	0.000451244	16	N	11	41
P70268	Parental	STVLK	LDNTVVGQTAWKPCGPNAWDQSFTLELER	ARELE	3	C14:+57.021	1111.538704	3331.592711	0.000451244	9	N	399	428
P70268	Parental	QSEPR	SWSLLEQLGLAGADLAAPGVQQQLELER	ERLKR	3		998.1966492	2991.566548	0.000451244	15	N	11	39
P70268	Parental	QPFFR	SLGWDVLLAR	RLPPP	2		565.3223699	1128.62914	0.000622848	5	N	879	889
P70268	Parental	KIVYR	DLKLDNLLLDTEGYVK	IADFG	3		617.0038139	1847.988042	0.001654178	1	N	743	759
P70268	Parental	MQLRR	ALQALQAGELESQAAPDEAQGDPELGAVELR	IEELR	3		1059.528904	3175.563313	0.000451244	1	N	186	217
P70268	Parental	RLLRR	LIPSAVATGTFSPNASPGAEIR	HTGDI	2		1078.571465	2155.127329	0.000451244	3	N	524	546
P70290	Exosome	HKQDK	IAILDIEPQTLK	TVRTA	2		677.4035569	1352.791514	0.000451244	28	N	374	386
P70290	Exosome	LKTVR	TAELSPFIVFIAPTDQGTQTEALQQLQK	DSEAI	3		1025.540193	3073.597179	0.000451244	37	N	389	417
P70290	Exosome	EAGLK	FVTGDIIQIINKDDSNWWQGR	VEGSS	3		835.756073	2504.244819	0.000451244	19	N	185	206
P70290	Exosome	EGSSK	ESAGLIPSPELQEWR	VASVA	2		856.4366481	1710.857696	0.000622848	4	N	212	227
P70290	Exosome	EAGLK	FVTGDIIQIINK	DDSNW	2		680.8958991	1359.776198	0.000979378	1	N	185	197
P70290	Exosome	AGLKF	VTGDIIQIINKDDSNWWQGR	VEGSS	3		786.7332683	2357.176405	0.001763695	1	N	186	206
P70290	Exosome	PFIVF	IAPTDQGTQTEALQQLQK	DSEAI	2		985.5136155	1969.011631	0.000451244	2	N	399	417
P70290	Parental	HKQDK	IAILDIEPQTLK	TVRTA	2		677.4035569	1352.791514	0.000622848	2	N	374	386
P70290	Parental	LKTVR	TAELSPFIVFIAPTDQGTQTEALQQLQK	DSEAI	3		1025.540193	3073.597179	0.000451244	34	N	389	417
P70290	Parental	LKTVR	TAELSPFIVFIAPTDQGTQTEALQQLQKDSEAIR	SQYAH	3		1249.314811	3744.921033	0.000451244	10	N	389	423
P70290	Parental	EAGLK	FVTGDIIQIINKDDSNWWQGR	VEGSS	3		835.756073	2504.244819	0.000451244	3	N	185	206
P70290	Parental	LQEWR	VASVAHSAPSEAPSCSPFGK	KKKCK	2	C15:+57.021	993.4732047	1984.930809	0.001162105	1	N	227	247
P70290	Parental	AGLKF	VTGDIIQIINKDDSNWWQGR	VEGSS	3		786.7332683	2357.176405	0.000662267	1	N	186	206
P70290	Parental	ETLKK	LQEAFDQACSSPQWVPVSWVY	-	2	C9:+57.021	1249.078565	2496.141531	0.000451244	2	N	445	466
P70296	Exosome	VVNMK	GNDISSGTVLSDYVGSGPPSGTGLHR	YVWLV	2		1265.612578	2529.209556	0.000451244	1	N	93	119
P70296	Exosome	TGLHR	YVWLVYEQEQPLSCDEPILSNK	SGDNR	2	C14:+57.021	1355.657377	2709.299154	0.000451244	37	N	119	141
P70296	Exosome	TGLHR	YVWLVYEQEQPLSCDEPILSNK	SGDNR	3	C14:+57.021	904.107518	2709.299154	0.000451244	23	N	119	141
P70296	Exosome	LDPGK	LYTLVLTDPDAPSR	KDPKF	2		780.9175598	1559.81952	0.000451244	7	N	62	76
P70296	Parental	VVNMK	GNDISSGTVLSDYVGSGPPSGTGLHR	YVWLV	2		1265.612578	2529.209556	0.000698008	4	N	93	119
P70296	Parental	VVNMK	GNDISSGTVLSDYVGSGPPSGTGLHR	YVWLV	3		844.077652	2529.209556	0.000451244	3	N	93	119
P70296	Parental	TGLHR	YVWLVYEQEQPLSCDEPILSNK	SGDNR	2	C14:+57.021	1355.657377	2709.299154	0.000451244	35	N	119	141
P70296	Parental	TGLHR	YVWLVYEQEQPLSCDEPILSNK	SGDNR	3	C14:+57.021	904.107518	2709.299154	0.000451244	22	N	119	141
P70296	Parental	TFRKK	YNLGAPVAGTCYQAEWDDYVPKLYEQLSGK	-	3	C11:+57.021	1145.878614	3434.612443	0.000823681	3	N	157	187
P70296	Parental	QHALR	VDYAGVTVDELGK	VLTPT	2		683.3489787	1364.682357	0.000451244	16	N	26	39
P70296	Parental	SGTVL	SDYVGSGPPSGTGLHR	YVWLV	2		793.88204	1585.74848	0.002727428	2	N	103	119

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P70315	Exosome	SLFSR	AGISEAQLTDAETSKLIYDFIEDQGGLEAVR	QEMRR	3		1113.891731	3338.651794	0.000451244	2	N	275	306
P70315	Exosome	PSGFK	HVSHVGWDPQNGFDVNNLDPDLR	SLFSR	4		658.5643522	2630.226209	0.001699387	1	N	247	270
P70315	Exosome	SLFSR	AGISEAQLTDAETSK	LIYDF	2		760.8760889	1519.736578	0.000451244	2	N	275	290
P70315	Parental	SLFSR	AGISEAQLTDAETSKLIYDFIEDQGGLEAVR	QEMRR	3		1113.891731	3338.651794	0.000451244	5	N	275	306
P70315	Parental	RPGGR	GGPAVQQNIPSNLLQDHENQR	LFELL	2		1158.078508	2314.141417	0.000637154	1	N	15	36
P70315	Parental	RPGGR	GGPAVQQNIPSNLLQDHENQR	LFELL	3		772.3882722	2314.141417	0.000622848	5	N	15	36
P70315	Parental	PPPCR	GGGGGGGGGGGGGGGGGGGGQPLRPPVVGSNK	GRSGP	3		773.3835211	2317.127163	0.001162105	4	N	323	353
P70315	Parental	AETSK	LIYDFIEDQGGLEAVR	QEMRR	2		919.4706879	1836.925776	0.000451244	2	N	290	306
P70315	Parental	SGGPL	SLGLVTVDIQNPDITSSR	YRGLP	2		958.0107086	1914.005817	0.000823681	1	N	195	213
P70333	Exosome	DFQGR	STGEAFVQFASQEIAEK	ALKKH	2		921.4499525	1840.884305	0.000451244	34	Y	150	167
P70333	Parental	ERMRR	GAYGGGYGGYDDYGGYNDGYGFGSDRFGR	DLNYC	3		1007.41013	3019.20699	0.000451244	2	N	233	262
P70333	Parental	DFQGR	STGEAFVQFASQEIAEK	ALKKH	2		921.4499525	1840.884305	0.000451244	31	Y	150	167
P70333	Parental	FIYTR	EGRPSGEAFVELESEDEVK	LALKK	2		1053.995453	2105.975305	0.000451244	24	Y	49	68
P70333	Parental	FIYTR	EGRPSGEAFVELESEDEVK	LALKK	3		702.9995684	2105.975305	0.000451244	14	Y	49	68
P70333	Parental	LNPMR	VHIEIGPDGR	VTGEA	2		546.7939765	1091.572353	0.001763695	4	Y	316	326
P70333	Parental	ERMRR	GAYGGGYGGYDDYGGYNDGYGFGSDR	FGRDL	2		1330.5158	2659.016001	0.002374549	1	N	233	259
P70335	Exosome	LRDPK	SEVNSDCLLDGLDALVYDLDFPALRK	NKNID	3	C7:+57.021	980.155308	2937.442524	0.000451244	6	N	22	48
P70335	Exosome	LEAKR	LLEFELAQLTK	QYRGN	2		652.877175	1303.73875	0.002884417	1	N	819	830
P70335	Exosome	WETLR	DTVAPVVPDLSSDIDTSNFDDLEEDKGDEETFPIPK	AFVGN	3		1317.279938	3948.816413	0.000622848	6	N	349	385
P70335	Parental	LRDPK	SEVNSDCLLDGLDALVYDLDFPALRK	NKNID	3	C7:+57.021	980.155308	2937.442524	0.000451244	20	N	22	48
P70335	Parental	WETLR	DTVAPVVPDLSSDIDTSNFDDLEEDKGDEETFPIPK	AFVGN	3		1317.279938	3948.816413	0.000622848	10	N	349	385
P70349	Exosome	FEDDR	CLAFHDISPQAPTHFLVIPK	KHISQ	3	C1:+57.021	764.4053928	2290.192778	0.000451244	3	N	37	57
P70349	Exosome	FEDDR	CLAFHDISPQAPTHFLVIPK	KHISQ	4	C1:+57.021	573.5559946	2290.192778	0.000451244	4	N	37	57
P70349	Parental	DEIAK	AQVAQPGGDTIFGK	IIRKE	2		694.8625875	1387.709575	0.000451244	23	N	7	21
P70349	Parental	EIPAK	IIFEDDRCLAFHDISPQAPTHFLVIPK	KHISQ	4	C8:+57.021	795.6645278	3178.626911	0.000823681	2	N	30	57
P70349	Parental	FEDDR	CLAFHDISPQAPTHFLVIPK	KHISQ	3	C1:+57.021	764.4053928	2290.192778	0.000451244	4	N	37	57
P70349	Parental	FEDDR	CLAFHDISPQAPTHFLVIPK	KHISQ	4	C1:+57.021	573.5559946	2290.192778	0.000451244	4	N	37	57
P70349	Parental	FEDDR	CLAFHDISPQAPTHFLVIPK	KHISQ	3	[0:-17.027,C1:+57.021	758.7297261	2273.165778	0.000698008	2	N	37	57
P70372	Exosome	RFDKR	SEAEEAITSFNGHKPPGSSEPITVK	FAANP	3		871.4333243	2611.276573	0.000622848	4	N	157	182
P70372	Parental	RFDKR	SEAEEAITSFNGHKPPGSSEPITVK	FAANP	3		871.4333243	2611.276573	0.000451244	11	N	157	182
P70372	Parental	QEELR	SLFSSIGEVESAK	LIRDK	2		677.3489787	1352.682357	0.000622848	3	N	37	50
P70388	Parental	YKKQK	ETELNGVAVQLNECEKHR	EKINK	3	C14:+57.021	709.3483833	2125.02175	0.002813207	1	N	976	994
P70388	Parental	HIRAR	DSLIQSLATHLELDGFER	GPFSE	3		682.0168937	2043.027281	0.000622848	1	N	367	385
P70398	Exosome	DLLAK	LAWDFSPEQLDHLFDCFK	ASWTN	3	C16:+57.021	756.6862248	2267.035275	0.000451244	1	N	455	473
P70398	Parental	AGVAK	LEGDNVNPESQLIQQNEQSESEKAGSTK	YRLVG	3		1020.485364	3058.432693	0.000451244	5	N	1834	1862
P70398	Parental	RTGQR	AQENYEGGEEVSPPQTK	GSVKC	2		931.9242988	1861.832998	0.000451244	8	N	2535	2552
P70398	Parental	DLLAK	LAWDFSPEQLDHLFDCFK	ASWTN	3	C16:+57.021	756.6862248	2267.035275	0.002145581	3	N	455	473
P70398	Parental	PVNLR	EQHDALEFFNSLVDSLDEALK	ALGHP	3		807.3925774	2419.154332	0.001395409	3	N	1681	1702
P70398	Parental	DLKRK	WTWAVEWLGDELER	RPYTG	2		895.4313657	1788.847131	0.000451244	1	N	2414	2428
P70398	Parental	LKQIR	EICSLFGEAPQNLSQSQR	SPHVF	2	C3:+57.021	1032.494668	2062.973737	0.000451244	1	N	574	592
P70441	Exosome	DSPKR	QVSTEPSSTSSSSSDPILDLNISLAVAK	ERAHQ	2		1417.219813	2832.424025	0.000451244	7	N	300	328
P70441	Exosome	DSPKR	QVSTEPSSTSSSSSDPILDLNISLAVAK	ERAHQ	3		945.1491418	2832.424025	0.001162105	3	N	300	328
P70441	Exosome	LAGDR	LVEVNGENVEKETHQQVVSR	IRAAL	3		765.3965448	2293.166234	0.000451244	20	N	58	78
P70441	Exosome	LAGDR	LVEVNGENVEKETHQQVVSR	IRAAL	4		574.2993586	2293.166234	0.000823681	3	N	58	78
P70441	Exosome	LNAVR	LLVVDPETDER	LKKLG	2		643.3358713	1284.656143	0.000998612	3	N	87	98
P70441	Exosome	RPQEK	SEQAEPPAAADTHEAGDQNEAEKSHLR	ELRPR	4		722.8320169	2887.296868	0.002884417	1	N	116	143
P70441	Parental	LNAVR	LLVVDPETDERLK	KLGVS	2		763.9253849	1525.83517	0.001162105	3	N	87	100
P70441	Parental	GQFIR	AVDPDSPAEASGLR	AQDRI	2		692.8393094	1383.663019	0.000451244	22	N	175	189
P70441	Parental	DSPKR	QVSTEPSSTSSSSSDPILDLNISLAVAK	ERAHQ	2		1417.219813	2832.424025	0.000451244	6	N	300	328
P70441	Parental	DSPKR	QVSTEPSSTSSSSSDPILDLNISLAVAK	ERAHQ	3		945.1491418	2832.424025	0.00091018	3	N	300	328
P70441	Parental	LAGDR	LVEVNGENVEKETHQQVVSR	IRAAL	2		1147.590917	2293.166234	0.000451244	4	N	58	78
P70441	Parental	LAGDR	LVEVNGENVEKETHQQVVSR	IRAAL	3		765.3965448	2293.166234	0.000451244	17	N	58	78
P70441	Parental	LNAVR	LLVVDPETDER	LKKLG	2		643.3358713	1284.656143	0.001329271	1	N	87	98
P70441	Parental	RPQEK	SEQAEPPAAADTHEAGDQNEAEKSHLR	ELRPR	4		722.8320169	2887.296868	0.002374549	1	N	116	143
P70441	Parental	FKKCK	VIPSQEHLDGPLPEPFSNGEIQK	ESSRE	3		844.4312551	2530.270365	0.001763695	1	N	238	261
P70444	Exosome	PSLLR	DVFHTTVNFINQNLFSYVR	NLVRN	3		772.0592043	2313.154213	0.001352548	2	N	168	187
P70444	Parental	PSLLR	DVFHTTVNFINQNLFSYVR	NLVRN	2		1157.584906	2313.154213	0.000735798	6	N	168	187
P70444	Parental	PSLLR	DVFHTTVNFINQNLFSYVR	NLVRN	3		772.0592043	2313.154213	0.000451244	11	N	168	187
P70444	Parental	GLGAE	HITDLLVFGFLQSSGCTR	QELEV	2	C16:+57.021	1026.022865	2050.03013	0.000451244	4	N	14	32
P70444	Parental	GLGAE	HITDLLVFGFLQSSGCTR	QELEV	3	C16:+57.021	684.3511765	2050.03013	0.001871652	3	N	14	32
P70444	Parental	EVLGR	ELPVQAYWEADLEDELQTDGSQASR	SFNQG	2		1425.657379	2849.299159	0.000451244	2	N	40	65
P70460	Exosome	LPRMK	SSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	2	C16:+57.021	1320.054398	2638.093196	0.000451244	9	N	316	341
P70460	Exosome	LPRMK	SSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	3	C16:+57.021	880.3721988	2638.093196	0.000451244	59	N	316	341
P70460	Exosome	TTLPR	MKSSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	3	M1:+15.995,C18:+57.021	972.0823485	2913.223645	0.000451244	3	N	314	341
P70460	Exosome	TTLPR	MKSSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	4	M1:+15.995,C18:+57.021	729.3137113	2913.223645	0.0025889	1	N	314	341

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P70460	Exosome	IRGVK	YNQATPIFHQWR	DARQV	3		520.928914	1559.763342	0.002981883	1	N	71	83
P70460	Exosome	PRMKS	SSSVTTSEAHPSTPCSSDDSDLER	VKQEL	3	C15:+57.021	851.3615227	2551.061168	0.0025889	1	N	317	341
P70460	Parental	LPRMK	SSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	2	C16:+57.021	1320.054398	2638.093196	0.000451244	23	N	316	341
P70460	Parental	LPRMK	SSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	3	C16:+57.021	880.3721988	2638.093196	0.000451244	120	N	316	341
P70460	Parental	QAFSR	VQIYHNPTANSFR	VVGRK	2		773.8922107	1545.768821	0.001763695	1	N	35	48
P70460	Parental	TTLPR	MKSSSSVTTSEAHPSTPCSSDDSDLER	VKQEL	3	C18:+57.021	966.7506818	2897.228645	0.000622848	4	N	314	341
P70460	Parental	IRGVK	YNQATPIFHQWR	DARQV	3		520.928914	1559.763342	0.000698008	5	N	71	83
P70670	Exosome	FGEAK	IEDLSQQAQLAAAEK	FKVQG	2		807.9208308	1613.826062	0.000451244	35	N	2099	2114
P70670	Exosome	PDVYK	SPASDTYIVFGEAK	IEDLS	2		742.8675356	1483.719471	0.000451244	3	N	2085	2099
P70670	Exosome	FGEAK	IEDLSQQAQLAAAEKF	KVQGE	2		881.4550378	1760.894476	0.000451244	1	N	2099	2115
P70670	Exosome	SDSDE	SVPELEEQDSTQTATQQAQLAAAAEIDEEPVSK	AKQSR	3		1171.89587	3512.664209	0.002727428	1	N	2005	2038
P70670	Parental	FGEAK	IEDLSQQAQLAAAEK	FKVQG	2		807.9208308	1613.826062	0.000451244	68	N	2099	2114
P70670	Parental	PDVYK	SPASDTYIVFGEAK	IEDLS	2		742.8675356	1483.719471	0.000451244	13	N	2085	2099
P70670	Parental	PDVYK	SPASDTYIVFGEAKIEDLSQQAQLAAAEK	FKVQG	3		1027.519458	3079.534973	0.002145581	1	N	2085	2114
P70670	Parental	IRKSK	NILFVITKPDVY	KSPAS	2		711.4060996	1420.796599	0.000451244	9	N	2072	2084
P70670	Parental	IRKSK	NILFVITKPDVYK	SPASD	2		775.4535812	1548.891562	0.000451244	4	N	2072	2085
P70670	Parental	TYIVF	GEAKIEDLSQQAQLAAAEK	FKVQG	2		1000.518898	1999.022196	0.002663018	1	N	2095	2114
P70677	Exosome	MACQK	IPVEADFLYAYSTAPGYYSWR	NSKDG	2		1235.09223	2468.16886	0.000451244	25	N	186	207
P70677	Exosome	MACQK	IPVEADFLYAYSTAPGYYSWR	NSKDG	3		823.7307533	2468.16886	0.001591523	6	N	186	207
P70677	Exosome	DHSKR	SSFVCVILSHGDEGVIYGTNGPVELKK	LTSFF	3	C5:+57.021	969.1640263	2904.468679	0.001329271	3	N	111	138
P70677	Exosome	DSSYK	MDYPEMGICIIINNK	NFHKS	3	M1:+15.995,C9:+57.021	609.6214282	1825.840885	0.001763695	1	N	38	53
P70677	Parental	MACQK	IPVEADFLYAYSTAPGYYSWR	NSKDG	2		1235.09223	2468.16886	0.000451244	15	N	186	207
P70697	Exosome	FSTCR	SPEACCELTLQPLR	RFPLD	2	C5:+57.021,C6:+57.021	837.4029738	1672.790348	0.000451244	8	N	60	74
P70697	Exosome	RDLER	LRDPAAAASELGYVFQAITLTR	QRLAG	3		788.4292973	2362.264492	0.000451244	8	N	120	142
P70697	Exosome	ERVGK	AVTLQGNLDPCALYASEEEIGR	LVQQM	2	C11:+57.021	1203.584212	2405.152824	0.000451244	7	N	297	319
P70697	Exosome	ERVGK	AVTLQGNLDPCALYASEEEIGR	LVQQM	3	C11:+57.021	802.7254079	2405.152824	0.002884417	1	N	297	319
P70698	Exosome	SSIYR	VPLLLEEQGVVDYFLR	RLDLP	2		945.5227235	1889.029847	0.000451244	4	N	252	268
P70698	Exosome	SSIYR	VPLLLEEQGVVDYFLR	RLDLP	3		630.6844157	1889.029847	0.000451244	9	N	252	268
P70698	Exosome	-MK	YILVTGGVISGIGK	GVIAS	2		688.9115491	1375.807498	0.000451244	3	N	2	16
P70698	Parental	SSIYR	VPLLLEEQGVVDYFLR	RLDLP	2		945.5227235	1889.029847	0.000622848	1	N	252	268
P70698	Parental	KLEIK	YIDSTDLEPSTLQEEPVRY	HEAWQ	2		1128.03986	2254.06412	0.000823681	3	N	335	354
P70699	Exosome	RAHVR	GDTVARPLFLEFPEDPSTWSVDR	QLLWG	3		878.7665263	2633.276179	0.000451244	3	N	719	742
P70699	Parental	PPSSR	FDCAPDKGISQEQCEAR	GCCYV	3	C3:+57.021,C14:+57.021	670.9598652	2009.856195	0.000451244	2	N	89	106
P70699	Parental	NVHLR	EGYIIPLQGPSLTTTESR	KQPMA	2		981.5130841	1961.010568	0.001329271	1	N	820	838
P80313	Exosome	EIIPR	QLCDNAGFDATNILNK	LRARH	2	C3:+57.021	897.4282658	1792.840932	0.000451244	19	N	447	463
P80313	Exosome	VILLK	EGTDSSQGIPQLVSNISACQVIAEAVR	TTLGP	2	C19:+57.021	1415.206285	2828.396971	0.000698008	2	N	10	37
P80313	Exosome	VILLK	EGTDSSQGIPQLVSNISACQVIAEAVR	TTLGP	3	C19:+57.021	943.8067902	2828.396971	0.000451244	7	N	10	37
P80313	Exosome	NAEIR	VHTVEDYQAIVDAEWNILYDKLEK	IHQSG	3		964.4874291	2890.438887	0.000451244	3	N	256	280
P80313	Exosome	NAEIR	VHTVEDYQAIVDAEWNILYDKLEK	IHQSG	4		723.6175218	2890.438887	0.00091018	2	N	256	280
P80313	Exosome	VDIAK	SQDAEVGDGTTSVTLLAAEFLK	QVKPY	2		1126.568785	2251.121969	0.000451244	35	N	84	106
P80313	Exosome	VDIAK	SQDAEVGDGTTSVTLLAAEFLK	QVKPY	3		751.3817898	2251.121969	0.000451244	8	N	84	106
P80313	Exosome	PAMVR	INALTAASEAACLIVSVDETIKNPR	STVDP	3	C12:+57.021	886.1377001	2655.3897	0.000451244	40	N	499	524
P80313	Exosome	PAMVR	INALTAASEAACLIVSVDETIKNPR	STVDP	4	C12:+57.021	664.8552251	2655.3897	0.000451244	2	N	499	524
P80313	Exosome	PAMVR	INALTAASEAACLIVSVDETIK	NPRST	3	C12:+57.021	763.7387659	2288.192898	0.000451244	13	N	499	521
P80313	Exosome	PVILL	KEGTDSSQGIPQLVSNISACQVIAEAVR	TTLGP	3	C20:+57.021	986.5051113	2956.491934	0.002813207	1	N	9	37
P80313	Exosome	KLRAR	HAQGGMWYGVDINNENIADNFQAFVWEPAMVR	INALT	3	M6:+15.995,M30:+15.995	1237.896885	3710.667256	0.002296037	1	N	467	499
P80313	Parental	EIIPR	QLCDNAGFDATNILNK	LRARH	2	C3:+57.021	897.4282658	1792.840932	0.000451244	21	N	447	463
P80313	Parental	VILLK	EGTDSSQGIPQLVSNISACQVIAEAVR	TTLGP	2	C19:+57.021	1415.206285	2828.396971	0.000451244	16	N	10	37
P80313	Parental	VILLK	EGTDSSQGIPQLVSNISACQVIAEAVR	TTLGP	3	C19:+57.021	943.8067902	2828.396971	0.000451244	17	N	10	37
P80313	Parental	NAEIR	VHTVEDYQAIVDAEWNILYDKLEK	IHQSG	3		964.4874291	2890.438887	0.000451244	8	N	256	280
P80313	Parental	NAEIR	VHTVEDYQAIVDAEWNILYDKLEK	IHQSG	4		723.6175218	2890.438887	0.000451244	16	N	256	280
P80313	Parental	VDIAK	SQDAEVGDGTTSVTLLAAEFLK	QVKPY	2		1126.568785	2251.121969	0.000451244	33	N	84	106
P80313	Parental	VDIAK	SQDAEVGDGTTSVTLLAAEFLK	QVKPY	3		751.3817898	2251.121969	0.000451244	16	N	84	106
P80313	Parental	PAMVR	INALTAASEAACLIVSVDETIKNPR	STVDP	2	C12:+57.021	1328.70265	2655.3897	0.00307782	1	N	499	524
P80313	Parental	PAMVR	INALTAASEAACLIVSVDETIKNPR	STVDP	3	C12:+57.021	886.1377001	2655.3897	0.000451244	41	N	499	524
P80313	Parental	PAMVR	INALTAASEAACLIVSVDETIKNPR	STVDP	4	C12:+57.021	664.8552251	2655.3897	0.000451244	3	N	499	524
P80313	Parental	PAMVR	INALTAASEAACLIVSVDETIK	NPRST	3	C12:+57.021	763.7387659	2288.192898	0.000451244	7	N	499	521
P80314	Exosome	VDMSR	VQDDEVGDGTTSVTVLAAELLR	EAESL	2		1144.584966	2287.154332	0.000451244	43	N	89	111
P80314	Exosome	VDMSR	VQDDEVGDGTTSVTVLAAELLR	EAESL	3		763.3925774	2287.154332	0.000451244	24	N	89	111
P80314	Exosome	HVIKK	LGGSLADSYLDEGFLLDKK	IGVNQ	2		1021.028567	2040.041534	0.000451244	1	N	204	223
P80314	Exosome	HVIKK	LGGSLADSYLDEGFLLDKK	IGVNQ	3		681.0216447	2040.041534	0.000451244	7	N	204	223
P80314	Exosome	AETAR	LSSFIGAIAIGDLVK	STLGP	2		752.4432135	1502.870827	0.000451244	32	N	25	40
P80314	Exosome	AGVER	LALVTGGEIASTFDHPELVK	LGSCK	2		1049.065484	2096.115368	0.000451244	10	N	322	342
P80314	Exosome	AGVER	LALVTGGEIASTFDHPELVK	LGSCK	3		699.7129226	2096.115368	0.000451244	17	N	322	342
P80314	Exosome	FQVKR	QVLLSAAEAAEVILR	VDNII	2		791.9623017	1581.909003	0.000451244	14	N	501	516

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P80314	Exosome	FQVKR	QVLLSAAEAAEVILR	VDNII	3		528.3108011	1581.909003	0.001395409	2	N	501	516
P80314	Exosome	TKAAR	EALLSSAVDHGSDEAR	FWQDL	2		828.8953444	1655.775089	0.000451244	13	N	138	154
P80314	Exosome	TKAAR	EALLSSAVDHGSDEAR	FWQDL	3		552.9328296	1655.775089	0.002453667	1	N	138	154
P80314	Exosome	TIVLR	GATQQILDEAER	SLHDA	2		665.8340271	1329.652454	0.0007646	1	N	376	388
P80314	Exosome	AKALR	MLPTIIADNAGYDSADLVAQLR	AAHSE	2		1174.102272	2346.188945	0.000451244	8	N	444	466
P80314	Exosome	HVIKK	LGGSLADSYLDEGFLLDK	KIGVN	2		956.9810855	1911.946571	0.000451244	5	N	204	222
P80314	Exosome	CFINR	QLIYNYPEQLFGAAGVMAIEHADFAGVER	LALVT	3	M17:+15.995	1075.86119	3224.560169	0.001162105	1	N	293	322
P80314	Parental	VDMSR	VQDDEVGDGTTSVTVLAAELLR	EAESL	2		1144.584966	2287.154332	0.000451244	38	N	89	111
P80314	Parental	VDMSR	VQDDEVGDGTTSVTVLAAELLR	EAESL	3		763.3925774	2287.154332	0.000451244	24	N	89	111
P80314	Parental	FQVKR	QVLLSAAEAAEVILRVDNIIK	AAPRK	3		755.7779265	2264.310379	0.000451244	9	N	501	522
P80314	Parental	HVIKK	LGGSLADSYLDEGFLLDKK	IGVNQ	2		1021.028567	2040.041534	0.000451244	6	N	204	223
P80314	Parental	HVIKK	LGGSLADSYLDEGFLLDKK	IGVNQ	3		681.0216447	2040.041534	0.000451244	8	N	204	223
P80314	Parental	AETAR	LSSFIGAIAIGDLVK	STLGP	2		752.4432135	1502.870827	0.000451244	26	N	25	40
P80314	Parental	AETAR	LSSFIGAIAIGDLVK	STLGP	3		501.9647423	1502.870827	0.000622848	8	N	25	40
P80314	Parental	AGVER	LALVTGGEIASTFDHPELVK	LGSCK	2		1049.065484	2096.115368	0.000451244	4	N	322	342
P80314	Parental	FQVKR	QVLLSAAEAAEVILR	VDNII	2		791.9623017	1581.909003	0.000735798	3	N	501	516
P80314	Parental	TKAAR	EALLSSAVDHGSDEAR	FWQDL	2		828.8953444	1655.775089	0.000451244	17	N	138	154
P80314	Parental	TKAAR	EALLSSAVDHGSDEAR	FWQDL	3		552.9328296	1655.775089	0.001162105	1	N	138	154
P80314	Parental	DEAER	SLHDALCVLAQTVKDPR	TVYGG	4	C7:+57.021	481.5087787	1922.003915	0.001329271	1	N	388	405
P80314	Parental	TIVLR	GATQQILDEAER	SLHDA	2		665.8340271	1329.652454	0.001871652	1	N	376	388
P80315	Exosome	VELSK	AQDIEAGDGTTSVVIIAGSLLDSCTK	LLQKG	2	C24:+57.021	1311.152656	2620.289711	0.000451244	3	N	96	122
P80315	Exosome	VELSK	AQDIEAGDGTTSVVIIAGSLLDSCTK	LLQKG	3	C24:+57.021	874.4377038	2620.289711	0.000451244	4	N	96	122
P80315	Exosome	LVKKR	ALIAGGGAPEIELALR	LTEYS	2		775.9491943	1549.882789	0.000451244	3	N	419	435
P80315	Exosome	KSILR	DALSDLALHFLNK	MKIMV	2		728.8938877	1455.772175	0.000451244	32	N	306	319
P80315	Exosome	KSILR	DALSDLALHFLNK	MKIMV	3		486.2651918	1455.772175	0.000622848	2	N	306	319
P80315	Exosome	VEKAK	IGLIQFCLSAPK	TDMDN	2	C7:+57.021	673.8789634	1345.742327	0.000451244	14	N	245	257
P80315	Exosome	KIVKK	LGGTIDDCELVEGLVLTQK	VANSG	2	C8:+57.021	1030.532928	2059.050256	0.000451244	12	N	213	232
P80315	Exosome	KIVKK	LGGTIDDCELVEGLVLTQK	VANSG	3	C8:+57.021	687.3578853	2059.050256	0.002019181	1	N	213	232
P80315	Exosome	NAVMK	VIDPATATSVDLR	DIKIV	2		679.3702454	1356.724891	0.001162105	2	N	193	206
P80315	Parental	VELSK	AQDIEAGDGTTSVVIIAGSLLDSCTK	LLQKG	2	C24:+57.021	1311.152656	2620.289711	0.000451244	19	N	96	122
P80315	Parental	VELSK	AQDIEAGDGTTSVVIIAGSLLDSCTK	LLQKG	3	C24:+57.021	874.4377038	2620.289711	0.000451244	26	N	96	122
P80315	Parental	LVKKR	ALIAGGGAPEIELALR	LTEYS	2		775.9491943	1549.882789	0.000622848	8	N	419	435
P80315	Parental	KSILR	DALSDLALHFLNK	MKIMV	2		728.8938877	1455.772175	0.000451244	16	N	306	319
P80315	Parental	KSILR	DALSDLALHFLNK	MKIMV	3		486.2651918	1455.772175	0.001264573	1	N	306	319
P80315	Parental	VEKAK	IGLIQFCLSAPK	TDMDN	2	C7:+57.021	673.8789634	1345.742327	0.000823681	4	N	245	257
P80315	Parental	KIVKK	LGGTIDDCELVEGLVLTQK	VANSG	2	C8:+57.021	1030.532928	2059.050256	0.000451244	10	N	213	232
P80315	Parental	KIVKK	LGGTIDDCELVEGLVLTQK	VANSG	3	C8:+57.021	687.3578853	2059.050256	0.000823681	2	N	213	232
P80315	Parental	KLLQK	GIHPTIISESFQK	ALEKG	3		486.2651918	1455.772175	0.000451244	4	N	126	139
P80315	Parental	LLIQK	SILRDALSDLALHFLNK	MKIMV	3		642.6989477	1925.073443	0.001839721	2	N	302	319
P80315	Parental	LLIQK	SILRDALSDLALHFLNK	MKIMV	4		482.2761608	1925.073443	0.000823681	2	N	302	319
P80316	Exosome	LTSEK	LGFAGVVQEISFGTTK	DKMLV	2		827.4464845	1652.877369	0.000451244	24	N	352	368
P80316	Exosome	IKQIK	ETGANLAICQWGFDDEANHLLLQNGLPAVR	WVGGP	3	C9:+57.021	1108.214331	3321.619594	0.000451244	27	N	293	323
P80316	Exosome	LPAVR	WVGGPEIELIAIATGGR	IVPRF	2		869.9784831	1737.941366	0.000451244	7	N	323	340
P80316	Exosome	LPAVR	WVGGPEIELIAIATGGR	IVPRF	3		580.3215887	1737.941366	0.000451244	2	N	323	340
P80316	Exosome	VELSK	SQDDEIGDGTTGVVVLAGALLEEAEQLLDR	GIHPI	3		1038.521527	3112.541181	0.000451244	32	N	96	126
P80316	Exosome	VVDAK	IAILTCPFEPPKPK	TKHKL	3	C6:+57.021	537.6377065	1609.88972	0.001871652	3	N	247	261
P80316	Exosome	KISDK	VLVDINNPEPLIQTAK	TTLGS	2		882.4992484	1762.982897	0.000451244	13	N	154	170
P80316	Exosome	ARQVK	ESNPALGIDCLHK	GSNDM	3	C10:+57.021	485.2420156	1452.702647	0.000451244	7	N	483	496
P80316	Exosome	GVVVL	AGALLEEAEQLLDR	GIHPI	2		764.4048166	1526.794033	0.000451244	5	N	112	126
P80316	Exosome	IRDNR	VVYGGGAAEISCALAVSQEADKCPTLEQYAMR	AFADA	3	C12:+57.021,C23:+57.021,M31:+15.995	1154.211145	3459.610035	0.002519933	1	N	417	449
P80316	Parental	LTSEK	LGFAGVVQEISFGTTK	DKMLV	2		827.4464845	1652.877369	0.000451244	20	N	352	368
P80316	Parental	IKQIK	ETGANLAICQWGFDDEANHLLLQNGLPAVR	WVGGP	3	C9:+57.021	1108.214331	3321.619594	0.000451244	39	N	293	323
P80316	Parental	LPAVR	WVGGPEIELIAIATGGR	IVPRF	2		869.9784831	1737.941366	0.000451244	16	N	323	340
P80316	Parental	LPAVR	WVGGPEIELIAIATGGR	IVPRF	3		580.3215887	1737.941366	0.000451244	5	N	323	340
P80316	Parental	VELSK	SQDDEIGDGTTGVVVLAGALLEEAEQLLDR	GIHPI	3		1038.521527	3112.541181	0.000451244	43	N	96	126
P80316	Parental	VVDAK	IAILTCPFEPPKPK	TKHKL	3	C6:+57.021	537.6377065	1609.88972	0.000622848	6	N	247	261
P80316	Parental	KISDK	VLVDINNPEPLIQTAK	TTLGS	2		882.4992484	1762.982897	0.000451244	12	N	154	170
P80316	Parental	EEMIK	QIKETGANLAICQWGFDDEANHLLLQNGLPAVR	WVGGP	3	C12:+57.021	1231.293533	3690.857199	0.000451244	4	N	290	323
P80316	Parental	EEMIK	QIKETGANLAICQWGFDDEANHLLLQNGLPAVR	WVGGP	4	C12:+57.021	923.7220997	3690.857199	0.001162105	4	N	290	323
P80316	Parental	VELSK	SQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIR	IADGY	4		947.4936899	3785.943559	0.000662267	2	N	96	132
P80316	Parental	ARQVK	ESNPALGIDCLHK	GSNDM	3	C10:+57.021	485.2420156	1452.702647	0.002727428	2	N	483	496
P80317	Exosome	LIIPK	VLAQNSGFDLQETLVK	VQAEH	2		881.4732306	1760.930861	0.000451244	16	N	449	465
P80317	Exosome	SLIAK	VATAQDDITGDGTTSNVLIIGELLK	QADLY	2		1272.674313	2543.333025	0.000451244	20	N	79	104
P80317	Exosome	SLIAK	VATAQDDITGDGTTSNVLIIGELLK	QADLY	3		848.7854751	2543.333025	0.000870037	1	N	79	104

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P80317	Exosome	LRAVK	NAIDDGCVVPGAGAVEVALAEALIK	YKPSV	2	C7:+57.021	1226.64153	2451.26746	0.000451244	10	N	399	424
P80317	Exosome	LRAVK	NAIDDGCVVPGAGAVEVALAEALIK	YKPSV	3	C7:+57.021	818.0969532	2451.26746	0.000451244	25	N	399	424
P80317	Exosome	SLRTK	VHAELADVLTEAVVDSILAIR	KKDEP	2		1117.623697	2233.231795	0.000451244	1	N	159	180
P80317	Exosome	SLRTK	VHAELADVLTEAVVDSILAIR	KKDEP	3		745.4183982	2233.231795	0.000451244	19	N	159	180
P80317	Exosome	RTSLR	TKVHAELADVLTEAVVDSILAIR	KKDEP	3		821.7992788	2462.374436	0.000451244	7	N	157	180
P80317	Exosome	SVKGR	AQLGVQAFADALLIIPK	VLAQN	2		884.5225265	1767.029453	0.000451244	14	N	432	449
P80317	Exosome	IAKVA	TAQDDITGDGTTSNVLIIGELLK	QADLY	2		1187.621549	2373.227497	0.000451244	1	N	81	104
P80317	Exosome	VINQK	GIDPFSLDALAK	EGIVA	2		623.8380498	1245.6605	0.000622848	7	N	295	307
P80317	Parental	LIIPK	VLAQNSGFDLQETLVK	VQAEH	2		881.4732306	1760.930861	0.000451244	26	N	449	465
P80317	Parental	SLIAK	VATAQDDITGDGTTSNVLIIGELLK	QADLY	2		1272.674313	2543.333025	0.000451244	41	N	79	104
P80317	Parental	SLIAK	VATAQDDITGDGTTSNVLIIGELLK	QADLY	3		848.7854751	2543.333025	0.000451244	14	N	79	104
P80317	Parental	LRAVK	NAIDDGCVVPGAGAVEVALAEALIK	YKPSV	2	C7:+57.021	1226.64153	2451.26746	0.000451244	9	N	399	424
P80317	Parental	LRAVK	NAIDDGCVVPGAGAVEVALAEALIK	YKPSV	3	C7:+57.021	818.0969532	2451.26746	0.000451244	11	N	399	424
P80317	Parental	SLRTK	VHAELADVLTEAVVDSILAIR	KKDEP	2		1117.623697	2233.231795	0.000451244	15	N	159	180
P80317	Parental	SLRTK	VHAELADVLTEAVVDSILAIR	KKDEP	3		745.4183982	2233.231795	0.000451244	31	N	159	180
P80317	Parental	SLRTK	VHAELADVLTEAVVDSILAIR	KKDEP	4		559.3157487	2233.231795	0.000451244	3	N	159	180
P80317	Parental	RTSLR	TKVHAELADVLTEAVVDSILAIR	KKDEP	2		1232.195018	2462.374436	0.000979378	2	N	157	180
P80317	Parental	RTSLR	TKVHAELADVLTEAVVDSILAIR	KKDEP	3		821.7992788	2462.374436	0.000451244	1	N	157	180
P80317	Parental	RTSLR	TKVHAELADVLTEAVVDSILAIR	KKDEP	4		616.6014091	2462.374436	0.000662267	6	N	157	180
P80317	Parental	SVKGR	AQLGVQAFADALLIIPK	VLAQN	2		884.5225265	1767.029453	0.002145581	1	N	432	449
P80317	Parental	SLIAK	VATAQDDITGDGTTSNVLIIGELLKQADLYISEGLHPR	IITEG	4		1006.777813	4023.080053	0.000451244	3	N	79	117
P80317	Parental	IAKVA	TAQDDITGDGTTSNVLIIGELLK	QADLY	2		1187.621549	2373.227497	0.000451244	9	N	81	104
P80317	Parental	IAKVA	TAQDDITGDGTTSNVLIIGELLK	QADLY	3		792.0836324	2373.227497	0.000451244	1	N	81	104
P80318	Exosome	LQTYK	TAVETAVLLLR	IDDIV	2		593.3642347	1184.712869	0.001352548	4	N	507	518
P80318	Exosome	KVISR	WSSLACNIALDAVK	TVQFE	2	C6:+57.021	774.3982486	1546.780897	0.000451244	9	N	167	181
P80318	Exosome	MQVCR	NVLLDPQLVPGGGASEMAVAHALTEK	SKAMT	3		873.1271785	2616.358136	0.001699387	1	N	399	425
P80318	Exosome	EVIPR	TLIQNCGASTIR	LLTSL	2	C6:+57.021	667.3485587	1332.681517	0.001162105	4	N	449	461
P80318	Exosome	LVDMK	ELGIWEPLAVK	LQTYK	2		627.8587852	1253.70197	0.002019181	1	N	491	502
P80318	Exosome	LEIKK	IGDEYFTFITDCKDPK	ACTIL	3	C12:+57.021	650.3051214	1947.891964	0.000622848	1	N	354	370
P80318	Parental	QWPYR	AVAQALEVIPR	TLIQN	2		583.8487518	1165.681904	0.000451244	2	N	438	449
P80318	Parental	KVISR	WSSLACNIALDAVK	TVQFE	2	C6:+57.021	774.3982486	1546.780897	0.000451244	7	N	167	181
P80318	Parental	EVIPR	TLIQNCGASTIR	LLTSL	2	C6:+57.021	667.3485587	1332.681517	0.000698008	5	N	449	461
P80318	Parental	ACGAR	IVSRPEELREDDVGTGAGLLEIK	KIGDE	3		832.7821764	2495.323129	0.000622848	1	N	330	353
P81117	Exosome	KTFFK	LHDVNNDGFLDEQELEALFTR	ELEKV	3		825.7315931	2474.171379	0.000451244	16	N	251	272
P81117	Parental	KTFFK	LHDVNNDGFLDEQELEALFTR	ELEKV	2		1238.09349	2474.171379	0.001162105	1	N	251	272
P81117	Parental	KTFFK	LHDVNNDGFLDEQELEALFTR	ELEKV	3		825.7315931	2474.171379	0.000451244	30	N	251	272
P81117	Parental	KTFFK	LHDVNNDGFLDEQELEALFTRELEK	VYNPQ	3		992.1529977	2973.435593	0.002145581	1	N	251	276
P81117	Parental	HLLLK	QFEHLNHQNPNTFESR	DLDML	3		666.6457941	1996.913982	0.000451244	1	N	137	153
P81117	Parental	IRSGR	LSQELDLVSHK	VRTRL	3		423.5668708	1267.677212	0.001264573	1	N	87	98
P81117	Parental	KDQLK	EVWEETDGLDPNDFDPK	TFFKL	2		1003.437239	2004.858878	0.001329271	3	N	230	247
P81117	Parental	HPGSK	DQLKEVWEETDGLDPNDFDPK	TFFKL	2		1245.569513	2489.123426	0.002145581	1	N	226	247
P81117	Parental	HPGSK	DQLKEVWEETDGLDPNDFDPK	TFFKL	3		830.7156087	2489.123426	0.001591523	2	N	226	247
P81117	Parental	DEYLK	QVIEVLETDPHFR	EKLQK	3		528.279501	1581.815103	0.000451244	12	N	59	72
P82198	Exosome	RPQER	GDELADSALEIFK	QASAY	2		704.354261	1406.692922	0.000451244	26	N	642	655
P82198	Exosome	PDSAK	TLLELAGESDVSTAIDILK	QAGLD	2		994.54405	1987.0725	0.000451244	121	N	377	396
P82198	Exosome	PDSAK	TLLELAGESDVSTAIDILK	QAGLD	3		663.3653	1987.0725	0.000622848	13	N	377	396
P82198	Exosome	TINGK	AVISNKDILATNGVIHFIDELLIPDSAK	TLLEL	3		1002.889045	3005.643735	0.000451244	10	N	349	377
P82198	Exosome	TINGK	AVISNKDILATNGVIHFIDELLIPDSAK	TLLEL	4		752.4187338	3005.643735	0.000451244	12	N	349	377
P82198	Exosome	KICGK	STVISYECCPGYEK	VPGEK	2	C8:+57.021,C9:+57.021	846.8658897	1691.716179	0.000451244	56	N	76	90
P82198	Exosome	TNILK	YHIGDEILVSGGIGALVR	LKSLQ	2		935.015597	1868.015594	0.000451244	2	N	570	588
P82198	Exosome	TNILK	YHIGDEILVSGGIGALVR	LKSLQ	3		623.6796646	1868.015594	0.000451244	33	N	570	588
P82198	Exosome	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEK	IPAET	3		1012.184298	3033.529493	0.000451244	34	N	257	287
P82198	Exosome	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEK	IPAET	4		759.3901734	3033.529493	0.000451244	1	N	257	287
P82198	Exosome	HLIDK	VISTITNNIQQIIEIEDTFETLR	AAVAA	2		1345.716512	2689.417424	0.000451244	37	N	234	257
P82198	Exosome	HLIDK	VISTITNNIQQIIEIEDTFETLR	AAVAA	3		897.4802745	2689.417424	0.000451244	29	N	234	257
P82198	Exosome	VFVYR	NSLCIENSCIAAHDKR	GRFGT	2	C4:+57.021,C9:+57.021	944.4436929	1886.871786	0.000451244	7	N	469	485
P82198	Exosome	VFVYR	NSLCIENSCIAAHDKR	GRFGT	3	C4:+57.021,C9:+57.021	629.965062	1886.871786	0.000451244	6	N	469	485
P82198	Exosome	VFVYR	NSLCIENSCIAAHDKR	GRFGT	4	C4:+57.021,C9:+57.021	472.7257465	1886.871786	0.00091018	2	N	469	485
P82198	Exosome	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEKIPAETLNR	ILGDP	3		1310.348403	3928.02181	0.000451244	39	N	257	295
P82198	Exosome	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEKIPAETLNR	ILGDP	4		983.0132525	3928.02181	0.000823681	4	N	257	295
P82198	Exosome	VISNK	DILATNGVIHFIDELLIPDSAK	TLLEL	2		1197.649912	2393.284224	0.000451244	15	N	355	377
P82198	Exosome	VISNK	DILATNGVIHFIDELLIPDSAK	TLLEL	3		798.7692081	2393.284224	0.000451244	46	N	355	377
P82198	Exosome	HLSGK	EQLTFLAPLNSVFK	DGVPR	2		803.9461203	1605.876641	0.001329271	13	N	407	421
P82198	Exosome	KGDNR	FSMLVAAIQSAGLMEILNR	EGVYT	3	M3:+15.995,M14:+15.995	699.3680506	2095.080752	0.000451244	17	N	514	533
P82198	Exosome	QLASK	YLYSGQTLDTLGGK	KLRVF	2		758.3886352	1514.76167	0.002145581	1	N	447	461

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P82198	Exosome	ETLNR	ILGDPEALRDLLNNHILK	SAMCA	3		682.0570236	2043.147671	0.000979378	5	N	295	313
P82198	Exosome	ETLNR	ILGDPEALRDLLNNHILK	SAMCA	4		511.7947177	2043.147671	0.000451244	12	N	295	313
P82198	Exosome	QLASK	YLYSGQTLDTLGGKK	LRVFV	2		822.4361168	1642.856634	0.000451244	6	N	447	462
P82198	Exosome	IDILK	QAGLDTHLSGKEQLTFLAPLNSVFK	DGVPR	3		905.4891044	2713.443913	0.000451244	5	N	396	421
P82198	Exosome	IDILK	QAGLDTHLSGKEQLTFLAPLNSVFK	DGVPR	4		679.3687783	2713.443913	0.002884417	1	N	396	421
P82198	Exosome	KICGK	STVISYECCPGYEKVPGEK	GCPAA	2	C8:+57.021,C9:+57.021	1102.005989	2201.996378	0.000451244	7	N	76	95
P82198	Exosome	KICGK	STVISYECCPGYEKVPGEK	GCPAA	3	C8:+57.021,C9:+57.021	735.0065925	2201.996378	0.000451244	5	N	76	95
P82198	Parental	RPQER	GDELADSALEIFK	QASAY	2		704.354261	1406.692922	0.000451244	28	N	642	655
P82198	Parental	PDSAK	TLLELAGESDVSTAIDILK	QAGLD	2		994.54405	1987.0725	0.000451244	46	N	377	396
P82198	Parental	TINGK	AVISNKDILATNGVIHFIDELLIPDSAK	TLLEL	3		1002.889045	3005.643735	0.000451244	2	N	349	377
P82198	Parental	TINGK	AVISNKDILATNGVIHFIDELLIPDSAK	TLLEL	4		752.4187338	3005.643735	0.000451244	4	N	349	377
P82198	Parental	KICGK	STVISYECCPGYEK	VPGEK	2	C8:+57.021,C9:+57.021	846.8658897	1691.716179	0.000451244	11	N	76	90
P82198	Parental	TNILK	YHIGDEILVSGGIGALVR	LKSLQ	3		623.6796646	1868.015594	0.00091018	1	N	570	588
P82198	Parental	FETLR	AAVAASGLNTVLEGDGQFTLLAPTNEAFEK	IPAET	3		1012.184298	3033.529493	0.000451244	15	N	257	287
P82198	Parental	HLIDK	VISTITNNIQQIIEIEDTFETLR	AAVAA	2		1345.716512	2689.417424	0.000451244	27	N	234	257
P82198	Parental	HLIDK	VISTITNNIQQIIEIEDTFETLR	AAVAA	3		897.4802745	2689.417424	0.000451244	24	N	234	257
P82198	Parental	VISNK	DILATNGVIHFIDELLIPDSAK	TLLEL	3		798.7692081	2393.284224	0.000451244	18	N	355	377
P82198	Parental	ETLNR	ILGDPEALRDLLNNHILK	SAMCA	4		511.7947177	2043.147671	0.000735798	5	N	295	313
P83870	Exosome	SYQGR	CVICGGPGVSDAYYCK	ECTIQ	2	C1:+57.021,C4:+57.021,C15:+57.021	903.3862351	1804.75687	0.000451244	14	N	57	73
P83870	Parental	SYQGR	CVICGGPGVSDAYYCKECTIQEK	DRDGC	3	C1:+57.021,C4:+57.021,C15:+57.021,C18:+57.021	898.7269752	2693.157526	0.00091018	3	N	57	80
P83870	Parental	SYQGR	CVICGGPGVSDAYYCK	ECTIQ	2	C1:+57.021,C4:+57.021,C15:+57.021	903.3862351	1804.75687	0.000451244	30	N	57	73
P83870	Parental	CTLVR	ICDECNYGSYQGR	CVICG	2	C2:+57.021,C5:+57.021	811.3221807	1620.628761	0.001162105	3	N	44	57
P83917	Exosome	EYLLK	WKGFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	3	C19:+57.021	1247.561791	3739.661972	0.000451244	2	N	41	72
P83917	Exosome	LLKWK	GFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	3	C17:+57.021	1142.837032	3425.487696	0.000451244	11	N	43	72
P83917	Parental	KQNKK	KVEEVLEEEEEEYVVEK	VLDRR	2		1055.010237	2108.004874	0.000451244	23	N	8	25
P83917	Parental	KQNKK	KVEEVLEEEEEEYVVEK	VLDRR	3		703.6760913	2108.004874	0.00091018	3	N	8	25
P83917	Parental	EYLLK	WKGFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	3	C19:+57.021	1247.561791	3739.661972	0.000451244	37	N	41	72
P83917	Parental	EYLLK	WKGFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	4	C19:+57.021	935.9232931	3739.661972	0.000622848	1	N	41	72
P83917	Parental	LLKWK	GFSDEDNTWEPEENLDCPDLIAEFLQSQK	TAHET	3	C17:+57.021	1142.837032	3425.487696	0.000451244	23	N	43	72
P83917	Parental	EANVK	CPQVVISFYEER	LTWHS	2	C1:+57.021	763.869324	1525.723048	0.000979378	3	N	155	167
P84078	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	2		1219.596534	2437.177468	0.000451244	1	Y	79	99
P84078	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	3		813.4002892	2437.177468	0.000451244	76	Y	79	99
P84078	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	4		610.3021669	2437.177468	0.000451244	7	Y	79	99
P84078	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	2		1162.125739	2322.235877	0.000451244	32	Y	38	59
P84078	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	3		775.0864257	2322.235877	0.000451244	20	Y	38	59
P84078	Exosome	LHSLR	HRNWYIQATCATSGDGLYEGLDWLSNQLR	NQK-	3	C10:+57.021	1142.209469	3423.605007	0.000451244	6	N	149	178
P84078	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEY	KNISF	2		1098.078257	2194.140914	0.000451244	5	Y	38	58
P84078	Exosome	SLRHR	NWYIQATCATSGDGLYEGLDWLSNQLR	NQK-	3	C8:+57.021	1044.489461	3130.444984	0.000451244	42	N	151	178
P84078	Exosome	EELMR	MLAEDELRDAVLLVFANK	QDLPN	2		1024.04878	2046.08196	0.000451244	13	Y	109	127
P84078	Exosome	EELMR	MLAEDELRDAVLLVFANK	QDLPN	3		683.0351201	2046.08196	0.000451244	44	Y	109	127
P84078	Exosome	EELMR	MLAEDELRDAVLLVFANK	QDLPN	3	M1:+15.995	688.3667867	2062.07696	0.000451244	9	Y	109	127
P84078	Exosome	TVEYK	NISFTVWDVGGQDK	IRPLW	2		783.3838842	1564.752168	0.000451244	11	Y	59	73
P84078	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NISFT	2		1282.715252	2563.414904	0.000662267	1	Y	36	59
P84078	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NISFT	3		855.4794348	2563.414904	0.000451244	17	Y	36	59
P84078	Exosome	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.000823681	1	Y	38	51
P84078	Exosome	EDELR	DAVLLVFANK	QDLPN	2		545.3192958	1088.622992	0.000451244	3	Y	117	127
P84078	Exosome	YIQAT	CATSGDGLYEGLDWLSNQLR	NQK-	2	C1:+57.021	1128.02379	2254.03198	0.000451244	9	N	158	178
P84078	Exosome	VFANK	QDLPNAMNAAEITDKLGLHSLR	HRNWY	4		602.5659352	2406.232541	0.000451244	3	Y	127	149
P84078	Exosome	HRNWY	IQATCATSGDGLYEGLDWLSNQLR	NQK-	2	C5:+57.021	1334.637507	2667.259414	0.000823681	4	N	154	178
P84078	Exosome	VFANK	QDLPNAMNAAEITDK	LGLHS	2	M7:+15.995	823.8887167	1645.761833	0.000823681	2	Y	127	142
P84078	Exosome	RPLWR	HYFQNTQGLIFVVDSNDR	ERVNE	3		718.3523878	2152.033763	0.000622848	1	Y	79	97
P84078	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	2		1219.596534	2437.177468	0.001463592	1	Y	79	99
P84078	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	3		813.4002892	2437.177468	0.000451244	23	Y	79	99
P84078	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VNEAR	4		610.3021669	2437.177468	0.001943752	2	Y	79	99
P84078	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	2		1162.125739	2322.235877	0.000451244	26	Y	38	59
P84078	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NISFT	3		775.0864257	2322.235877	0.000451244	19	Y	38	59
P84078	Parental	LHSLR	HRNWYIQATCATSGDGLYEGLDWLSNQLR	NQK-	3	C10:+57.021	1142.209469	3423.605007	0.000451244	19	N	149	178
P84078	Parental	LYKLK	LGEIVTTIPTIGFNVETVEY	KNISF	2		1098.078257	2194.140914	0.000451244	17	Y	38	58
P84078	Parental	SLRHR	NWYIQATCATSGDGLYEGLDWLSNQLR	NQK-	3	C8:+57.021	1044.489461	3130.444984	0.000451244	28	N	151	178
P84078	Parental	EELMR	MLAEDELRDAVLLVFANK	QDLPN	3		683.0351201	2046.08196	0.000451244	20	Y	109	127
P84078	Parental	TVEYK	NISFTVWDVGGQDK	IRPLW	2		783.3838842	1564.752168	0.000451244	5	Y	59	73
P84078	Parental	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.00307782	1	Y	38	51

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P84078	Parental	EDELR	DAVLLVFANK	QDLPN	2		545.3192958	1088.622992	0.000451244	19	Y	117	127
P84084	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VQESA	2		1219.596534	2437.177468	0.000451244	1	Y	79	99
P84084	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VQESA	3		813.4002892	2437.177468	0.000451244	76	Y	79	99
P84084	Exosome	RPLWR	HYFQNTQGLIFVVDSNDRER	VQESA	4		610.3021669	2437.177468	0.000451244	7	Y	79	99
P84084	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	2		1162.125739	2322.235877	0.000451244	32	Y	38	59
P84084	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	3		775.0864257	2322.235877	0.000451244	20	Y	38	59
P84084	Exosome	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSKR	-	3	C8:+57.021	1119.538704	3355.592711	0.001352548	1	N	151	180
P84084	Exosome	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSKR	-	4	C8:+57.021	839.9059776	3355.592711	0.000823681	2	N	151	180
P84084	Exosome	LYKLK	LGEIVTTIPTIGFNVETVEY	KNICF	2		1098.078257	2194.140914	0.000451244	5	Y	38	58
P84084	Exosome	TVEYK	NICFTVWDVGGQDK	IRPLW	2	C3:+57.021	819.8829627	1637.750325	0.000451244	29	Y	59	73
P84084	Exosome	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSK	R-	3	C8:+57.021	1067.505	3199.491599	0.000451244	45	N	151	179
P84084	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NICFT	2		1282.715252	2563.414904	0.000662267	1	Y	36	59
P84084	Exosome	TILYK	LKLGEIVTTIPTIGFNVETVEYK	NICFT	3		855.4794348	2563.414904	0.000451244	17	Y	36	59
P84084	Exosome	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.000823681	1	Y	38	51
P84084	Exosome	EDELR	DAVLLVFANK	QDMPN	2		545.3192958	1088.622992	0.000451244	3	Y	117	127
P84084	Exosome	DELQK	MLQEDELRDAVLLVFANK	QDMPN	3		702.0422747	2103.103424	0.000451244	6	N	109	127
P84084	Exosome	DELQK	MLQEDELRDAVLLVFANK	QDMPN	3	M1:+15.995	707.3739413	2119.098424	0.000451244	7	N	109	127
P84084	Exosome	RPLWR	HYFQNTQGLIFVVDSNDR	ERVQE	3		718.3523878	2152.033763	0.000622848	1	Y	79	97
P84084	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VQESA	2		1219.596534	2437.177468	0.001463592	1	Y	79	99
P84084	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VQESA	3		813.4002892	2437.177468	0.000451244	23	Y	79	99
P84084	Parental	RPLWR	HYFQNTQGLIFVVDSNDRER	VQESA	4		610.3021669	2437.177468	0.001943752	2	Y	79	99
P84084	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	2		1162.125739	2322.235877	0.000451244	26	Y	38	59
P84084	Parental	LYKLK	LGEIVTTIPTIGFNVETVEYK	NICFT	3		775.0864257	2322.235877	0.000451244	19	Y	38	59
P84084	Parental	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSKR	-	3	C8:+57.021	1119.538704	3355.592711	0.001839721	3	N	151	180
P84084	Parental	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSKR	-	4	C8:+57.021	839.9059776	3355.592711	0.000451244	9	N	151	180
P84084	Parental	LYKLK	LGEIVTTIPTIGFNVETVEY	KNICF	2		1098.078257	2194.140914	0.000451244	17	Y	38	58
P84084	Parental	TVEYK	NICFTVWDVGGQDK	IRPLW	2	C3:+57.021	819.8829627	1637.750325	0.000451244	1	Y	59	73
P84084	Parental	HLRSR	TWYVQATCATQGTGLYDGLDWLSHELSK	R-	3	C8:+57.021	1067.505	3199.491599	0.000451244	24	N	151	179
P84084	Parental	LYKLK	LGEIVTTIPTIGF	NVETV	2		680.8902824	1359.764965	0.00307782	1	Y	38	51
P84084	Parental	EDELR	DAVLLVFANK	QDMPN	2		545.3192958	1088.622992	0.000451244	19	Y	117	127
P84089	Exosome	EHLKR	MNPNSPSITYDISQLFDFIDDLADLSCLVYR	ADTQT	3	M1:+15.995,C27:+57.021	1213.572891	3637.695273	0.002727428	1	N	42	73
P84089	Exosome	CLVYR	ADTQTYQPYNKDWIK	EKIYV	3		624.3043749	1869.889725	0.002019181	2	N	73	88
P84089	Parental	EHLKR	MNPNSPSITYDISQLFDFIDDLADLSCLVYR	ADTQT	3	C27:+57.021	1208.241224	3621.700273	0.000622848	3	N	42	73
P84089	Parental	DISQL	FDFIDDLADLSCLVYR	ADTQT	2	C12:+57.021	981.4695993	1960.923599	0.000451244	2	N	57	73
P84089	Parental	DISQL	FDFIDDLADLSCLVYR	ADTQT	3	C12:+57.021	654.6489996	1960.923599	0.000451244	3	N	57	73
P84089	Parental	CLVYR	ADTQTYQPYNKDWIK	EKIYV	2		935.9526623	1869.889725	0.000451244	8	N	73	88
P84089	Parental	CLVYR	ADTQTYQPYNKDWIK	EKIYV	3		624.3043749	1869.889725	0.000637154	13	N	73	88
P84091	Exosome	EENIK	NNFVLIYELLDEILDFGYPQNSETGALK	TFITQ	3		1072.543603	3214.60741	0.000622848	1	N	102	130
P84091	Exosome	SKSGK	QSIAIDDCTFHQCVR	LSKFD	3	C8:+57.021,C13:+57.021	617.282391	1848.823773	0.001229886	8	N	238	253
P84091	Exosome	KIEVR	IPTPLNTSGVQVICMK	GKAKY	2	C14:+57.021,M15:+15.995	887.4658486	1772.916097	0.000451244	2	N	323	339
P84091	Parental	EENIK	NNFVLIYELLDEILDFGYPQNSETGALK	TFITQ	3		1072.543603	3214.60741	0.000451244	1	N	102	130
P84091	Parental	SKSGK	QSIAIDDCTFHQCVR	LSKFD	3	C8:+57.021,C13:+57.021	617.282391	1848.823773	0.002884417	1	N	238	253
P84091	Parental	FVLIY	ELLDEILDFGYPQNSETGALK	TFITQ	2		1176.584435	2351.15327	0.000451244	4	N	109	130
P84096	Exosome	DTLRR	LKEQGQAPITPQQGQALAK	QIHAV	2		1003.555618	2005.095635	0.000451244	7	N	128	147
P84096	Exosome	DTLRR	LKEQGQAPITPQQGQALAK	QIHAV	3		669.3730118	2005.095635	0.000451244	18	N	128	147
P84096	Exosome	IHAVR	YLECSALQQDGVKEVFAEAVR	AVLNP	2	C4:+57.021	1206.597122	2411.178645	0.000451244	10	N	153	174
P84096	Exosome	IHAVR	YLECSALQQDGVKEVFAEAVR	AVLNP	3	C4:+57.021	804.7340149	2411.178645	0.000451244	27	N	153	174
P84096	Exosome	AVDGR	TVNLNLWDTAGQEEYDR	LRTLS	2		1012.471948	2022.928295	0.000451244	63	N	49	66
P84096	Exosome	NAFPK	EYIPTVFDNYSAQSAVDGR	TVNLN	2		1066.500705	2130.98581	0.000451244	33	N	30	49
P84096	Exosome	NAFPK	EYIPTVFDNYSAQSAVDGR	TVNLN	3		711.3364034	2130.98581	0.000451244	4	N	30	49
P84096	Exosome	AVDGR	TVNLNLWDTAGQEEYDRLR	TLSYP	3		765.0456235	2292.11347	0.000451244	22	N	49	68
P84096	Exosome	GAVGK	TCLLICYTTNAFPK	EYIPT	2	C2:+57.021,C6:+57.021	851.4206352	1700.82567	0.000451244	31	N	16	30
P84096	Exosome	LRRLK	EQGQAPITPQQGQALAK	QIHAV	2		882.9661041	1763.916608	0.000451244	16	N	130	147
P84096	Exosome	IHAVR	YLECSALQQDGVK	EVFAE	2	C4:+57.021	755.8642386	1509.712877	0.000451244	32	N	153	166
P84096	Exosome	YDRLR	TLSYPQTNVFVICFSIASPPSYENVR	HKWHP	3	C13:+57.021	997.1640263	2988.468679	0.000823681	6	N	68	94
P84096	Exosome	HAVRY	LECSALQQDGVKEVFAEAVR	AVLNP	2	C3:+57.021	1125.065458	2248.115316	0.000622848	1	N	154	174
P84096	Exosome	HAVRY	LECSALQQDGVKEVFAEAVR	AVLNP	3	C3:+57.021	750.379572	2248.115316	0.000451244	2	N	154	174
P84096	Parental	DTLRR	LKEQGQAPITPQQGQALAK	QIHAV	2		1003.555618	2005.095635	0.000451244	7	N	128	147
P84096	Parental	DTLRR	LKEQGQAPITPQQGQALAK	QIHAV	3		669.3730118	2005.095635	0.000451244	8	N	128	147
P84096	Parental	IHAVR	YLECSALQQDGVKEVFAEAVR	AVLNP	2	C4:+57.021	1206.597122	2411.178645	0.001699387	2	N	153	174
P84096	Parental	IHAVR	YLECSALQQDGVKEVFAEAVR	AVLNP	3	C4:+57.021	804.7340149	2411.178645	0.000451244	12	N	153	174
P84096	Parental	AVDGR	TVNLNLWDTAGQEEYDR	LRTLS	2		1012.471948	2022.928295	0.000451244	28	N	49	66
P84096	Parental	NAFPK	EYIPTVFDNYSAQSAVDGR	TVNLN	2		1066.500705	2130.98581	0.000451244	31	N	30	49
P84096	Parental	AVDGR	TVNLNLWDTAGQEEYDRLR	TLSYP	2		1147.064535	2292.11347	0.000823681	5	N	49	68
P84096	Parental	AVDGR	TVNLNLWDTAGQEEYDRLR	TLSYP	3		765.0456235	2292.11347	0.000451244	15	N	49	68

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P84096	Parental	GAVGK	TCLLICYTTNAFPK	EYIPT	2	C2:+57.021,C6:+57.021	851.4206352	1700.82567	0.000451244	13	N	16	30
P84096	Parental	GAVGK	TCLLICYTTNAFPKEYIPTVFDNYSAQSAVDGR	TVNLN	3	C2:+57.021,C6:+57.021	1272.274773	3813.80092	0.000451244	6	N	16	49
P84096	Parental	LRRLK	EQGQAPITPQQGQALAK	QIHAV	2		882.9661041	1763.916608	0.000622848	7	N	130	147
P84099	Exosome	CGKKK	VWLDPNETNEIANANSR	QQIRK	2		971.9668324	1941.918065	0.000451244	11	N	21	38
P84099	Parental	CGKKK	VWLDPNETNEIANANSR	QQIRK	2		971.9668324	1941.918065	0.000451244	21	N	21	38
P84099	Parental	GKKKV	WLDPNETNEIANANSR	QQIRK	2		922.4326254	1842.849651	0.000451244	1	N	22	38
P84104	Exosome	PLDCK	VYVGNLGNNGNKTELER	AFGYY	2		938.9797428	1875.943886	0.001395409	1	N	11	28
P84104	Exosome	PLDCK	VYVGNLGNNGNKTELER	AFGYY	3		626.3224285	1875.943886	0.000637154	4	N	11	28
P84104	Exosome	VWVAR	NPPGFAFVEFEDPRDAADAVR	ELDGR	2		1160.553803	2319.092007	0.000637154	4	N	43	64
P84104	Exosome	VWVAR	NPPGFAFVEFEDPRDAADAVR	ELDGR	3		774.0384689	2319.092007	0.000451244	26	N	43	64
P84104	Exosome	TELER	AFGYYGPLR	SVWVA	2		522.2696059	1042.523612	0.00307782	1	N	28	37
P84104	Parental	PLDCK	VYVGNLGNNGNKTELER	AFGYY	2		938.9797428	1875.943886	0.000451244	33	N	11	28
P84104	Parental	PLDCK	VYVGNLGNNGNKTELER	AFGYY	3		626.3224285	1875.943886	0.000451244	15	N	11	28
P84104	Parental	VWVAR	NPPGFAFVEFEDPRDAADAVR	ELDGR	2		1160.553803	2319.092007	0.000451244	20	N	43	64
P84104	Parental	VWVAR	NPPGFAFVEFEDPRDAADAVR	ELDGR	3		774.0384689	2319.092007	0.000451244	27	N	43	64
P84104	Parental	TELER	AFGYYGPLR	SVWVA	2		522.2696059	1042.523612	0.001839721	3	N	28	37
P84104	Parental	VWVAR	NPPGFAFVEFEDPR	DAADA	2		811.3864268	1620.757254	0.000451244	2	Y	43	57
P84104	Parental	VWVAR	NPPGFAFVEFEDPR	DAADA	3		541.2602179	1620.757254	0.002296037	2	Y	43	57
P84228	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	2		668.349313	1334.683026	0.000451244	87	Y	73	84
P84228	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	3		445.902142	1334.683026	0.000451244	127	Y	73	84
P84228	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	2	[0:-18.011	659.343813	1316.672026	0.002212458	1	Y	73	84
P84228	Exosome	QRLVR	EIAQDFKTDLR	FQSSA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	24	Y	73	84
P84228	Exosome	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	205	Y	102	116
P84228	Exosome	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	51	Y	100	116
P84228	Exosome	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	68	Y	100	116
P84228	Exosome	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	28	Y	99	116
P84228	Exosome	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002080925	1	Y	99	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAY	LVGLF	2	M7:+15.995	874.3963745	1746.777149	0.000451244	54	N	84	100
P84228	Exosome	KTDLR	FQSSAVMALQEASEAY	LVGLF	3	M7:+15.995	583.2668497	1746.777149	0.001329271	2	N	84	100
P84228	Exosome	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C18:+57.021	1290.126244	2578.236888	0.000451244	34	Y	93	116
P84228	Exosome	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C18:+57.021	860.420096	2578.236888	0.000451244	79	Y	93	116
P84228	Exosome	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C18:+57.021	645.567022	2578.236888	0.000451244	3	Y	93	116
P84228	Exosome	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	Q1:-17.027,C18:+57.021	1281.612744	2561.209888	0.000451244	16	Y	93	116
P84228	Exosome	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	Q1:-17.027,C18:+57.021	854.7444293	2561.209888	0.000451244	30	Y	93	116
P84228	Exosome	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	[0:-17.027,C18:+57.021	1281.612744	2561.209888	0.001699387	1	Y	93	116
P84228	Exosome	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	[0:-17.027,C18:+57.021	854.7444293	2561.209888	0.001763695	1	Y	93	116
P84228	Exosome	SSAVM	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C20:+57.021	1382.186833	2762.358066	0.000451244	23	Y	91	116
P84228	Exosome	SSAVM	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C20:+57.021	921.7938219	2762.358066	0.000451244	32	Y	91	116
P84228	Exosome	SSAVM	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C20:+57.021	691.5973165	2762.358066	0.000451244	13	Y	91	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	C27:+57.021	1223.93988	3668.796239	0.000451244	1	N	84	117
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C27:+57.021	918.2068598	3668.796239	0.000451244	28	N	84	117
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	M7:+15.995,C27:+57.021	1229.271546	3684.791239	0.000451244	26	N	84	117
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	M7:+15.995,C27:+57.021	922.2056098	3684.791239	0.000451244	45	N	84	117
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1171.906176	3512.695128	0.000451244	248	N	84	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C27:+57.021	879.181582	3512.695128	0.000451244	84	N	84	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M7:+15.995,C27:+57.021	1177.237843	3528.690128	0.000451244	1310	N	84	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M7:+15.995,C27:+57.021	883.180332	3528.690128	0.000451244	435	N	84	116
P84228	Exosome	AQDFK	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C31:+57.021	1000.496531	3997.954925	0.000622848	1	N	80	116
P84228	Exosome	AQDFK	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M11:+15.995,C31:+57.021	1004.495281	4013.949925	0.000451244	36	N	80	116
P84228	Exosome	TDLRF	QSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M6:+15.995,C26:+57.021	1128.215038	3381.621714	0.000451244	13	N	85	116
P84228	Exosome	TDLRF	QSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M6:+15.995,C26:+57.021	846.4132285	3381.621714	0.002080925	1	N	85	116
P84228	Exosome	SEAYL	VGLFEDTNLCAIHAK	RVTIM	2	C10:+57.021	844.4275375	1686.839475	0.000451244	56	Y	101	116
P84228	Exosome	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	56	Y	104	116
P84228	Exosome	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	68	Y	103	116
P84228	Exosome	VMALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C17:+57.021	1226.096955	2450.17831	0.000451244	4	Y	94	116
P84228	Exosome	VMALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C17:+57.021	817.7339034	2450.17831	0.000451244	7	Y	94	116
P84228	Exosome	VMALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	2	E1:-18.011,C17:+57.021	1217.091455	2432.16731	0.000451244	8	Y	94	116
P84228	Exosome	VMALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	3	E1:-18.011,C17:+57.021	811.7302367	2432.16731	0.0007646	1	Y	94	116
P84228	Exosome	RFQSS	AVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C23:+57.021	1022.175826	3063.504079	0.000451244	4	N	88	116
P84228	Exosome	RFQSS	AVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C23:+57.021	766.8838199	3063.504079	0.001329271	2	N	88	116
P84228	Exosome	RFQSS	AVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M3:+15.995,C23:+57.021	1027.507493	3079.499079	0.000451244	52	N	88	116
P84228	Exosome	RFQSS	AVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M3:+15.995,C23:+57.021	770.8825699	3079.499079	0.000451244	8	N	88	116
P84228	Exosome	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.001699387	2	Y	105	116
P84228	Exosome	LRFQS	SAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M4:+15.995,C24:+57.021	1056.518169	3166.531108	0.000451244	11	N	87	116
P84228	Exosome	DLRFQ	SSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C25:+57.021	1080.197179	3237.568136	0.000662267	1	N	86	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P84228	Exosome	DLRFQ	SSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M5:+15.995,C25:+57.021	1085.528845	3253.563136	0.000451244	6	N	86	116
P84228	Exosome	DLRFQ	SSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M5:+15.995,C25:+57.021	814.3985841	3253.563136	0.000451244	11	N	86	116
P84228	Exosome	ALQEA	SEAYLVGLFEDTNLCAIHAK	RVTIM	2	C15:+57.021	1126.057102	2250.098603	0.000451244	18	Y	96	116
P84228	Exosome	ALQEA	SEAYLVGLFEDTNLCAIHAK	RVTIM	3	C15:+57.021	751.0406677	2250.098603	0.000451244	26	Y	96	116
P84228	Exosome	LQEAS	EAYLVGLFEDTNLCAIHAK	RVTIM	2	C14:+57.021	1082.541087	2163.066575	0.000451244	10	Y	97	116
P84228	Exosome	LQEAS	EAYLVGLFEDTNLCAIHAK	RVTIM	2	E1:-18.011,C14:+57.021	1073.535587	2145.055575	0.001871652	3	Y	97	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIH	AKRVT	3	M7:+15.995,C27:+57.021	1110.860484	3329.558051	0.000451244	21	N	84	114
P84228	Exosome	MALQE	ASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C16:+57.021	1161.575659	2321.135717	0.000451244	2	Y	95	116
P84228	Exosome	MALQE	ASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C16:+57.021	774.7197057	2321.135717	0.000451244	15	Y	95	116
P84228	Exosome	QSSAV	MALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C21:+57.021	965.4739839	2893.398552	0.000451244	9	N	90	116
P84228	Exosome	QSSAV	MALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M1:+15.995,C21:+57.021	970.8056505	2909.393552	0.000451244	18	N	90	116
P84228	Exosome	QSSAV	MALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M1:+15.995,C21:+57.021	728.3561879	2909.393552	0.002981883	1	N	90	116
P84228	Exosome	SAVMA	LQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C19:+57.021	898.114784	2691.320952	0.000451244	1	Y	92	116
P84228	Exosome	FKTDL	RFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M8:+15.995,C28:+57.021	922.2056098	3684.791239	0.000451244	22	N	83	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLF	EDTNL	2	M7:+15.995	1139.059585	2276.103569	0.000637154	9	N	84	105
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLF	EDTNL	3	M7:+15.995	759.7089897	2276.103569	0.000451244	6	N	84	105
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLC	AIHAK	3	M7:+15.995,C27:+57.021	1003.800454	3008.377961	0.000451244	6	N	84	111
P84228	Exosome	QEASE	AYLVGLFEDTNLCAIHAK	RVTIM	2	C13:+57.021	1018.019791	2034.023981	0.000451244	5	Y	98	116
P84228	Exosome	DFKTD	LRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C29:+57.021	1261.634568	3781.880303	0.000622848	1	N	82	116
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLV	GLFED	2	M7:+15.995	980.4726136	1958.929627	0.001871652	5	N	84	102
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAI	HAKRV	3	M7:+15.995,C27:+57.021	1065.17418	3192.499139	0.001699387	1	N	84	113
P84228	Exosome	KTDLR	FQSSAVMALQEASEAYLVGL	FEDTN	2	M7:+15.995	1065.525378	2129.035155	0.001943752	1	N	84	104
P84228	Exosome	RFQSS	AVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	M3:+15.995,C23:+57.021	809.9078477	3235.600191	0.00091018	4	N	88	117
P84228	Parental	QRLVR	EIAQDFKTDLR	FQSSA	2		668.349313	1334.683026	0.000451244	20	Y	73	84
P84228	Parental	QRLVR	EIAQDFKTDLR	FQSSA	3		445.902142	1334.683026	0.000451244	88	Y	73	84
P84228	Parental	QRLVR	EIAQDFKTDLR	FQSSA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	2	Y	73	84
P84228	Parental	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	49	Y	102	116
P84228	Parental	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	188	Y	100	116
P84228	Parental	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	307	Y	100	116
P84228	Parental	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	7	Y	99	116
P84228	Parental	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002727428	1	Y	99	116
P84228	Parental	KTDLR	FQSSAVMALQEASEAY	LVGLF	2		866.3988745	1730.782149	0.000451244	5	N	84	100
P84228	Parental	KTDLR	FQSSAVMALQEASEAY	LVGLF	3		577.935183	1730.782149	0.001329271	2	N	84	100
P84228	Parental	KTDLR	FQSSAVMALQEASEAY	LVGLF	2	M7:+15.995	874.3963745	1746.777149	0.000451244	26	N	84	100
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C18:+57.021	1290.126244	2578.236888	0.000451244	47	Y	93	116
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C18:+57.021	860.420096	2578.236888	0.000451244	48	Y	93	116
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C18:+57.021	645.567022	2578.236888	0.000622848	5	Y	93	116
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	Q1:-17.027,C18:+57.021	1281.612744	2561.209888	0.000451244	40	Y	93	116
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	Q1:-17.027,C18:+57.021	854.7444293	2561.209888	0.000451244	28	Y	93	116
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	[0:-17.027,C18:+57.021	1281.612744	2561.209888	0.001654178	4	Y	93	116
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	[0:-17.027,C18:+57.021	854.7444293	2561.209888	0.001871652	2	Y	93	116
P84228	Parental	SSAVM	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C20:+57.021	1382.186833	2762.358066	0.000451244	4	Y	91	116
P84228	Parental	SSAVM	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C20:+57.021	921.7938219	2762.358066	0.000451244	33	Y	91	116
P84228	Parental	SSAVM	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C20:+57.021	691.5973165	2762.358066	0.000451244	4	Y	91	116
P84228	Parental	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	C27:+57.021	1223.93988	3668.796239	0.000637154	1	N	84	117
P84228	Parental	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C27:+57.021	918.2068598	3668.796239	0.000451244	10	N	84	117
P84228	Parental	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	M7:+15.995,C27:+57.021	922.2056098	3684.791239	0.000451244	8	N	84	117
P84228	Parental	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1171.906176	3512.695128	0.000451244	53	N	84	116
P84228	Parental	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C27:+57.021	879.181582	3512.695128	0.000451244	40	N	84	116
P84228	Parental	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	M7:+15.995,C27:+57.021	1177.237843	3528.690128	0.000451244	97	N	84	116
P84228	Parental	KTDLR	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	M7:+15.995,C27:+57.021	883.180332	3528.690128	0.000451244	46	N	84	116
P84228	Parental	AQDFK	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C31:+57.021	1000.496531	3997.954925	0.000451244	2	N	80	116
P84228	Parental	TDLRF	QSSAVMALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C26:+57.021	1122.883371	3365.626714	0.000622848	1	N	85	116
P84228	Parental	ASEAY	LVGLFEDTNLCAIHAKR	VTIMP	2	C11:+57.021	979.0201251	1956.02465	0.001871652	2	Y	100	117
P84228	Parental	ASEAY	LVGLFEDTNLCAIHAKR	VTIMP	4	C11:+57.021	490.0139625	1956.02465	0.000451244	6	Y	100	117
P84228	Parental	SEAYL	VGLFEDTNLCAIHAK	RVTIM	3	C10:+57.021	563.287625	1686.839475	0.000998612	3	Y	101	116
P84228	Parental	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	2	Y	104	116
P84228	Parental	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	5	Y	103	116
P84228	Parental	AVMAL	QEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	[0:-17.027,C18:+57.021	906.778133	2717.310999	0.002453667	1	Y	93	117
P84228	Parental	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.000451244	1	Y	105	116
P84244	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	2		668.349313	1334.683026	0.000451244	87	Y	73	84
P84244	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	3		445.902142	1334.683026	0.000451244	127	Y	73	84
P84244	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	2	[0:-18.011	659.343813	1316.672026	0.002212458	1	Y	73	84
P84244	Exosome	QRLVR	EIAQDFKTDLR	FQSAA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	24	Y	73	84
P84244	Exosome	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	205	Y	102	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P84244	Exosome	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	51	Y	100	116
P84244	Exosome	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	68	Y	100	116
P84244	Exosome	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	28	Y	99	116
P84244	Exosome	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002080925	1	Y	99	116
P84244	Exosome	KTDLR	FQSAAIGALQEASEAY	LVGLF	2		828.3997312	1654.783862	0.000451244	24	N	84	100
P84244	Exosome	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C18:+57.021	1290.126244	2578.236888	0.000451244	34	Y	93	116
P84244	Exosome	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C18:+57.021	860.420096	2578.236888	0.000451244	79	Y	93	116
P84244	Exosome	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C18:+57.021	645.567022	2578.236888	0.000451244	3	Y	93	116
P84244	Exosome	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	Q1:-17.027,C18:+57.021	1281.612744	2561.209888	0.000451244	16	Y	93	116
P84244	Exosome	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	Q1:-17.027,C18:+57.021	854.7444293	2561.209888	0.000451244	30	Y	93	116
P84244	Exosome	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	[0:-17.027,C18:+57.021	1281.612744	2561.209888	0.001699387	1	Y	93	116
P84244	Exosome	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	[0:-17.027,C18:+57.021	854.7444293	2561.209888	0.001763695	1	Y	93	116
P84244	Exosome	SAAIG	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C20:+57.021	1382.186833	2762.358066	0.000451244	23	Y	91	116
P84244	Exosome	SAAIG	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C20:+57.021	921.7938219	2762.358066	0.000451244	32	Y	91	116
P84244	Exosome	SAAIG	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C20:+57.021	691.5973165	2762.358066	0.000451244	13	Y	91	116
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	C27:+57.021	1198.607118	3592.797953	0.000451244	14	N	84	117
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C27:+57.021	899.2072882	3592.797953	0.000451244	30	N	84	117
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1146.573414	3436.696841	0.000451244	656	N	84	116
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C27:+57.021	860.1820104	3436.696841	0.000451244	88	N	84	116
P84244	Exosome	SEAYL	VGLFEDTNLCAIHAK	RVTIM	2	C10:+57.021	844.4275375	1686.839475	0.000451244	56	Y	101	116
P84244	Exosome	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	56	Y	104	116
P84244	Exosome	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	68	Y	103	116
P84244	Exosome	IGALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C17:+57.021	1226.096955	2450.17831	0.000451244	4	Y	94	116
P84244	Exosome	IGALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C17:+57.021	817.7339034	2450.17831	0.000451244	7	Y	94	116
P84244	Exosome	IGALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	2	E1:-18.011,C17:+57.021	1217.091455	2432.16731	0.000451244	8	Y	94	116
P84244	Exosome	IGALQ	EASEAYLVGLFEDTNLCAIHAK	RVTIM	3	E1:-18.011,C17:+57.021	811.7302367	2432.16731	0.0007646	1	Y	94	116
P84244	Exosome	FKTDL	RFQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C28:+57.021	1198.607118	3592.797953	0.000451244	6	N	83	116
P84244	Exosome	FKTDL	RFQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C28:+57.021	899.2072882	3592.797953	0.000451244	29	N	83	116
P84244	Exosome	RFQSA	AIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C23:+57.021	1002.174703	3003.500708	0.000451244	10	N	88	116
P84244	Exosome	RFQSA	AIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C23:+57.021	751.8829769	3003.500708	0.001162105	2	N	88	116
P84244	Exosome	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.001699387	2	Y	105	116
P84244	Exosome	ALQEA	SEAYLVGLFEDTNLCAIHAK	RVTIM	2	C15:+57.021	1126.057102	2250.098603	0.000451244	18	Y	96	116
P84244	Exosome	ALQEA	SEAYLVGLFEDTNLCAIHAK	RVTIM	3	C15:+57.021	751.0406677	2250.098603	0.000451244	26	Y	96	116
P84244	Exosome	LQEAS	EAYLVGLFEDTNLCAIHAK	RVTIM	2	C14:+57.021	1082.541087	2163.066575	0.000451244	10	Y	97	116
P84244	Exosome	LQEAS	EAYLVGLFEDTNLCAIHAK	RVTIM	2	E1:-18.011,C14:+57.021	1073.535587	2145.055575	0.001871652	3	Y	97	116
P84244	Exosome	GALQE	ASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C16:+57.021	1161.575659	2321.135717	0.000451244	2	Y	95	116
P84244	Exosome	GALQE	ASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C16:+57.021	774.7197057	2321.135717	0.000451244	15	Y	95	116
P84244	Exosome	QSAAI	GALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C21:+57.021	940.8009765	2819.37953	0.000451244	2	N	90	116
P84244	Exosome	AAIGA	LQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C19:+57.021	898.114784	2691.320952	0.000451244	1	Y	92	116
P84244	Exosome	DLRFQ	SAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C25:+57.021	1054.864417	3161.56985	0.000451244	8	N	86	116
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIH	AKRVT	3	C27:+57.021	1080.196055	3237.564764	0.000823681	2	N	84	114
P84244	Exosome	FQSAA	IGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C22:+57.021	978.4956646	2932.463594	0.000622848	4	N	89	116
P84244	Exosome	QEASE	AYLVGLFEDTNLCAIHAK	RVTIM	2	C13:+57.021	1018.019791	2034.023981	0.000451244	5	Y	98	116
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLF	EDTNL	2		1093.062941	2184.110282	0.000823681	3	N	84	105
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNL	CAIHA	2		1379.185044	2756.354489	0.001871652	2	N	84	110
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNL	CAIHA	3		919.7926297	2756.354489	0.002727428	1	N	84	110
P84244	Exosome	TDLRF	QSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C26:+57.021	1097.550609	3289.628427	0.001943752	1	N	85	116
P84244	Exosome	KTDLR	FQSAAIGALQEASEAYLV	GLFED	2		934.4759703	1866.936341	0.000451244	4	N	84	102
P84244	Parental	QRLVR	EIAQDFKTDLR	FQSAA	2		668.349313	1334.683026	0.000451244	20	Y	73	84
P84244	Parental	QRLVR	EIAQDFKTDLR	FQSAA	3		445.902142	1334.683026	0.000451244	88	Y	73	84
P84244	Parental	QRLVR	EIAQDFKTDLR	FQSAA	3	[0:-18.011	439.8984753	1316.672026	0.000451244	2	Y	73	84
P84244	Parental	EAYLV	GLFEDTNLCAIHAK	RVTIM	2	C9:+57.021	794.8933305	1587.771061	0.000451244	49	Y	102	116
P84244	Parental	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	2	C11:+57.021	900.9695695	1799.923539	0.000451244	188	Y	100	116
P84244	Parental	ASEAY	LVGLFEDTNLCAIHAK	RVTIM	3	C11:+57.021	600.982313	1799.923539	0.000451244	307	Y	100	116
P84244	Parental	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	2	C12:+57.021	982.5012338	1962.986868	0.000451244	7	Y	99	116
P84244	Parental	EASEA	YLVGLFEDTNLCAIHAK	RVTIM	3	C12:+57.021	655.3367559	1962.986868	0.002727428	1	Y	99	116
P84244	Parental	KTDLR	FQSAAIGALQEASEAY	LVGLF	2		828.3997312	1654.783862	0.000451244	25	N	84	100
P84244	Parental	KTDLR	FQSAAIGALQEASEAY	LVGLF	3		552.6024208	1654.783862	0.00091018	1	N	84	100
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C18:+57.021	1290.126244	2578.236888	0.000451244	47	Y	93	116
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C18:+57.021	860.420096	2578.236888	0.000451244	48	Y	93	116
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C18:+57.021	645.567022	2578.236888	0.000622848	5	Y	93	116
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	Q1:-17.027,C18:+57.021	1281.612744	2561.209888	0.000451244	40	Y	93	116
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	Q1:-17.027,C18:+57.021	854.7444293	2561.209888	0.000451244	28	Y	93	116
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	[0:-17.027,C18:+57.021	1281.612744	2561.209888	0.001654178	4	Y	93	116
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	[0:-17.027,C18:+57.021	854.7444293	2561.209888	0.001871652	2	Y	93	116

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P84244	Parental	SAAIG	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	2	C20:+57.021	1382.186833	2762.358066	0.000451244	4	Y	91	116
P84244	Parental	SAAIG	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C20:+57.021	921.7938219	2762.358066	0.000451244	33	Y	91	116
P84244	Parental	SAAIG	ALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C20:+57.021	691.5973165	2762.358066	0.000451244	4	Y	91	116
P84244	Parental	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	C27:+57.021	1198.607118	3592.797953	0.000662267	2	N	84	117
P84244	Parental	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAKR	VTIMP	4	C27:+57.021	899.2072882	3592.797953	0.000451244	11	N	84	117
P84244	Parental	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	3	C27:+57.021	1146.573414	3436.696841	0.000451244	130	N	84	116
P84244	Parental	KTDLR	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C27:+57.021	860.1820104	3436.696841	0.000451244	29	N	84	116
P84244	Parental	AQDFK	TDLRFQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C31:+57.021	981.4969596	3921.956638	0.000622848	2	N	80	116
P84244	Parental	ASEAY	LVGLFEDTNLCAIHAKR	VTIMP	2	C11:+57.021	979.0201251	1956.02465	0.001871652	2	Y	100	117
P84244	Parental	ASEAY	LVGLFEDTNLCAIHAKR	VTIMP	4	C11:+57.021	490.0139625	1956.02465	0.000451244	6	Y	100	117
P84244	Parental	SEAYL	VGLFEDTNLCAIHAK	RVTIM	3	C10:+57.021	563.287625	1686.839475	0.000998612	3	Y	101	116
P84244	Parental	YLVGL	FEDTNLCAIHAK	RVTIM	2	C7:+57.021	709.8405665	1417.665533	0.000451244	2	Y	104	116
P84244	Parental	AYLVG	LFEDTNLCAIHAK	RVTIM	2	C8:+57.021	766.3825986	1530.749597	0.000451244	5	Y	103	116
P84244	Parental	QDFKT	DLRFQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	RVTIM	4	C30:+57.021	956.23504	3820.90896	0.0025889	1	N	81	116
P84244	Parental	AIGAL	QEASEAYLVGLFEDTNLCAIHAKR	VTIMP	3	[0:-17.027,C18:+57.021	906.778133	2717.310999	0.002453667	1	Y	93	117
P84244	Parental	LVGLF	EDTNLCAIHAK	RVTIM	2	C6:+57.021	636.3063595	1270.597119	0.000451244	1	Y	105	116
P84244	Parental	KTDLR	FQSAAIGALQEASEAYLV	GLFED	2		934.4759703	1866.936341	0.000451244	3	N	84	102
P85094	Exosome	ELDGR	SQLQSVLLCGIETQACILNTALDLLHR	GLQVH	3	C9:+57.021,C16:+57.021	1022.874216	3065.599247	0.000622848	2	N	98	125
P85094	Exosome	LKVAR	LLDVPILLTEQYPEGLGPTVPELGAQGIRPVSK	TCFSM	3		1167.319057	3498.93377	0.000451244	12	N	49	82
P85094	Parental	ELDGR	SQLQSVLLCGIETQACILNTALDLLHR	GLQVH	3	C9:+57.021,C16:+57.021	1022.874216	3065.599247	0.000451244	10	N	98	125
P85094	Parental	LKVAR	LLDVPILLTEQYPEGLGPTVPELGAQGIRPVSK	TCFSM	3		1167.319057	3498.93377	0.000622848	5	N	49	82
P97302	Parental	LCTDK	DGALALPSLCPKYR	KFQKA	3	C10:+57.021	520.9453106	1559.812532	0.002884417	1	N	214	228
P97302	Parental	QILAK	YSASDCPLSFLISEK	GKSTP	2	C6:+57.021	858.9113859	1715.807172	0.001329271	1	N	643	658
P97302	Parental	DEVCR	CVEFLSVHNIEESCFQFLK	FKFLD	3	C1:+57.021,C14:+57.021	796.0452701	2385.11241	0.001654178	1	N	108	127
P97310	Exosome	PIGGR	YDPSLTFSENVDLTEPIISR	FDVLC	2		1148.571327	2295.127055	0.000451244	8	N	636	656
P97310	Exosome	EDIKR	GLALALFGGEPK	NPGGK	2		586.8378528	1171.660106	0.000622848	2	N	493	505
P97310	Exosome	MDKAR	QINIHNLSAFYDSDLFK	FNKFS	3		675.6745793	2024.000338	0.002145581	1	N	870	887
P97310	Exosome	LSFRR	DNNDLLLFILK	QLVAE	2		659.3747995	1316.733999	0.000823681	2	N	826	837
P97310	Parental	DGMER	DYRPIPELDVYEAEGLALDDEDVEELTASQR	EAAER	3		1184.22896	3549.663481	0.000451244	17	N	79	110
P97310	Parental	PIGGR	YDPSLTFSENVDLTEPIISR	FDVLC	2		1148.571327	2295.127055	0.000451244	2	N	636	656
P97311	Exosome	EKCQK	LFLDFLEEFQGSDGEIK	YLQFA	2		993.9889105	1985.962221	0.000451244	2	N	28	45
P97311	Exosome	IRPER	NTLVVSFADLEQFNQQLSTTIQEEFYR	VYPYL	3		1074.198607	3219.572421	0.002145581	1	N	58	85
P97311	Parental	EKCQK	LFLDFLEEFQGSDGEIK	YLQFA	2		993.9889105	1985.962221	0.000451244	29	N	28	45
P97311	Parental	EKCQK	LFLDFLEEFQGSDGEIK	YLQFA	3		662.995207	1985.962221	0.002884417	1	N	28	45
P97311	Parental	IRPER	NTLVVSFADLEQFNQQLSTTIQEEFYR	VYPYL	3		1074.198607	3219.572421	0.000451244	7	N	58	85
P97311	Parental	GQVVR	THPVHPELVSGTFLCLDCQTVIKDVEQQFK	YTQPN	4	C15:+57.021,C18:+57.021	882.1933708	3524.742283	0.000451244	4	N	143	173
P97311	Parental	LVVSF	ADLEQFNQQLSTTIQEEFYR	VYPYL	2		1230.58804	2459.16048	0.000451244	12	N	65	85
P97311	Parental	RFDLF	FILVDECNEVTDYAIAR	RIVDL	2	C7:+57.021	1014.491063	2026.966526	0.000998612	2	N	533	550
P97311	Parental	QAGLK	GSSEGSESYEEDPYLVVNPNYLLED	-	2		1403.117221	2804.218843	0.000622848	3	N	796	821
P97311	Parental	EKCQK	LFLDFLEEFQGSDGEIKY	LQFAE	2		1075.520575	2149.02555	0.000823681	3	N	28	46
P97315	Exosome	AKCGK	GLESTTLADKDGEIYCK	GCYAK	2	C16:+57.021	950.4541463	1898.892693	0.000451244	4	N	151	168
P97315	Exosome	AKCGK	GLESTTLADKDGEIYCK	GCYAK	3	C16:+57.021	633.9720308	1898.892693	0.000622848	2	N	151	168
P97315	Exosome	MVCKK	NLDSTTVAVHGEEIYCK	SCYGK	2	C16:+57.021	968.4597629	1934.903926	0.000451244	2	N	42	59
P97315	Parental	AKCGK	GLESTTLADKDGEIYCK	GCYAK	2	C16:+57.021	950.4541463	1898.892693	0.000451244	25	N	151	168
P97315	Parental	AKCGK	GLESTTLADKDGEIYCK	GCYAK	3	C16:+57.021	633.9720308	1898.892693	0.000451244	10	N	151	168
P97315	Parental	MVCKK	NLDSTTVAVHGEEIYCK	SCYGK	2	C16:+57.021	968.4597629	1934.903926	0.000451244	16	N	42	59
P97315	Parental	MVCKK	NLDSTTVAVHGEEIYCK	SCYGK	3	C16:+57.021	645.9757753	1934.903926	0.000622848	1	N	42	59
P97315	Parental	GVCQK	TVYFAEEVQCEGNSFHK	SCFLC	2	C10:+57.021	1022.957387	2043.899175	0.000451244	5	N	15	32
P97315	Parental	GVCQK	TVYFAEEVQCEGNSFHK	SCFLC	3	C10:+57.021	682.307525	2043.899175	0.000451244	3	N	15	32
P97315	Parental	NFGPK	GFGFGQGAGALVHSE	-	2		717.344562	1432.673524	0.001943752	1	N	178	193
P97315	Parental	KYGPK	GYGYGQGAGTLSTDKGESLG	IKHEE	2		959.4453984	1916.875197	0.002374549	1	N	69	89
P97315	Parental	KYGPK	GYGYGQGAGTLSTDKGESLGIK	HEEAP	2		1080.034912	2158.054224	0.001352548	1	N	69	91
P97351	Exosome	GLKGR	VFEVSLADLQNDEVAFRK	FKLIT	3		694.0290222	2079.063667	0.000451244	8	N	65	83
P97351	Exosome	GLKGR	VFEVSLADLQNDEVAFR	KFKLI	2		976.4921517	1950.968703	0.000451244	6	N	65	82
P97351	Exosome	KGRVF	EVSLADLQNDEVAFR	KFKLI	2		853.4237377	1704.831875	0.000451244	1	N	67	82
P97351	Exosome	KDIEK	ACQSIYPLHDVFVR	KVKML	3	C2:+57.021	568.9560982	1703.844895	0.002212458	2	N	199	213
P97351	Parental	GLKGR	VFEVSLADLQNDEVAFRK	FKLIT	3		694.0290222	2079.063667	0.000451244	8	N	65	83
P97351	Parental	GLKGR	VFEVSLADLQNDEVAFR	KFKLI	2		976.4921517	1950.968703	0.000451244	19	N	65	82
P97351	Parental	KGRVF	EVSLADLQNDEVAFR	KFKLI	2		853.4237377	1704.831875	0.000637154	3	N	67	82
P97355	Exosome	KYMRR	TCGDVLDNLRGDCYQVLIEDCIPVLK	MYAKE	3	C2:+57.021,C13:+57.021,C21:+57.021	1022.496262	3064.465387	0.000451244	8	N	235	261
P97355	Exosome	TADGR	LVEYDIDEVVYDEDSPYQNIK	ILHSK	2		1273.595197	2545.174793	0.000451244	4	N	130	151
P97355	Exosome	KQDGK	YFTQGNCVNLTEALSLYEEQLGR	LYCPV	2	C7:+57.021	1353.147708	2704.279815	0.000451244	2	N	311	334
P97355	Parental	KYMRR	TCGDVLDNLRGDCYQVLIEDCIPVLK	MYAKE	3	C2:+57.021,C13:+57.021,C21:+57.021	1022.496262	3064.465387	0.001395409	2	N	235	261

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P97363	Parental	AAHTK	EILDTALKEIDEVGDLLQLK	YSRHR	3		752.4180639	2254.230792	0.000451244	14	N	516	536
P97363	Parental	YSRHR	LVPLLDRPFDETTYEETED	-	2		1141.539693	2281.063786	0.000622848	1	N	541	560
P97364	Exosome	WSAGR	SFSNYRPFEPQTLGFSPSWR	LTSFS	3		801.7225922	2402.144377	0.000622848	2	N	33	53
P97364	Exosome	AKQQK	NEVSFVIHNLPIIAK	MAAIS	3		565.3265627	1692.956288	0.000870037	1	N	337	352
P97369	Exosome	ALMRR	EFQREDIALSYQDAEGDLVR	LLSDE	2		1177.567108	2353.118615	0.000451244	13	N	276	296
P97369	Exosome	ALMRR	EFQREDIALSYQDAEGDLVR	LLSDE	3		785.3806718	2353.118615	0.000451244	9	N	276	296
P97369	Exosome	ELSFK	AGDVIFLLSK	INKDW	2		531.8138463	1061.612093	0.000451244	33	N	192	202
P97369	Exosome	EDTGK	TIKDIAVEEDLSSTPLFK	DLLAL	2		1003.538768	2005.061935	0.000451244	15	N	250	268
P97369	Exosome	EDTGK	TIKDIAVEEDLSSTPLFK	DLLAL	3		669.3617784	2005.061935	0.000451244	22	N	250	268
P97369	Exosome	FLLSK	INKDWLEGTSQGATGIFPGSFVK	ILKDF	2		1226.629511	2451.243422	0.000451244	21	N	202	225
P97369	Exosome	FLLSK	INKDWLEGTSQGATGIFPGSFVK	ILKDF	3		818.0889407	2451.243422	0.000451244	21	N	202	225
P97369	Exosome	AQQLR	SESDFEQLPDDVAVSANIADIEEKR	GFTSH	3		926.4424367	2776.30391	0.000451244	5	N	8	33
P97369	Exosome	GKTIK	DIAVEEDLSSTPLFK	DLLAL	2		832.4254147	1662.835229	0.000451244	11	N	253	268
P97369	Exosome	AQQLR	SESDFEQLPDDVAVSANIADIEEK	RGFTS	2		1311.109199	2620.202799	0.000451244	23	N	8	32
P97369	Exosome	AQQLR	SESDFEQLPDDVAVSANIADIEEK	RGFTS	3		874.408733	2620.202799	0.001463592	3	N	8	32
P97369	Exosome	GSFVK	ILKDFPEDEDTTNWLR	CYFYE	2		996.489609	1990.963618	0.00091018	2	N	225	241
P97369	Exosome	GSFVK	ILKDFPEDEDTTNWLR	CYFYE	3		664.6623393	1990.963618	0.000451244	3	N	225	241
P97369	Exosome	DPDVR	IFFYQSAYDAEQVPQALR	RLRPR	2		1073.534351	2145.053102	0.000451244	45	N	130	148
P97369	Exosome	DPDVR	IFFYQSAYDAEQVPQALR	RLRPR	3		716.0255006	2145.053102	0.001229886	2	N	130	148
P97369	Exosome	EDTGK	TIKDIAVEEDLSSTPLF	KDLLA	2		939.491286	1876.966972	0.000451244	5	N	250	267
P97369	Exosome	REFQR	EDIALSYQDAEGDLVR	LLSDE	2		897.4317597	1792.847919	0.000451244	3	N	280	296
P97369	Exosome	NAYMK	NLLSLPVCVL	MDPDV	2	C8:+57.021	564.328575	1126.64155	0.001591523	3	N	114	124
P97369	Exosome	NAYMK	NLLSLPVCVLMDPDVR	IFFYQ	2	C8:+57.021	920.9869056	1839.958211	0.000622848	7	N	114	130
P97369	Exosome	MDPDV	RIFFYQSAYDAEQVPQALR	RLRPR	3		768.0592043	2301.154213	0.001463592	1	N	129	148
P97369	Exosome	SKINK	DWLEGTSQGATGIFPGSFVK	ILKDF	2		1049.018534	2096.021467	0.000451244	5	N	205	225
P97369	Exosome	DPDVR	IFFYQSAYDAEQVPQALRR	LRPRT	3		768.0592043	2301.154213	0.000998612	2	N	130	149
P97369	Parental	ALMRR	EFQREDIALSYQDAEGDLVR	LLSDE	2		1177.567108	2353.118615	0.000451244	29	N	276	296
P97369	Parental	ALMRR	EFQREDIALSYQDAEGDLVR	LLSDE	3		785.3806718	2353.118615	0.000451244	6	N	276	296
P97369	Parental	ELSFK	AGDVIFLLSK	INKDW	2		531.8138463	1061.612093	0.000698008	22	N	192	202
P97369	Parental	EDTGK	TIKDIAVEEDLSSTPLFK	DLLAL	2		1003.538768	2005.061935	0.000451244	11	N	250	268
P97369	Parental	EDTGK	TIKDIAVEEDLSSTPLFK	DLLAL	3		669.3617784	2005.061935	0.000451244	14	N	250	268
P97369	Parental	FLLSK	INKDWLEGTSQGATGIFPGSFVK	ILKDF	2		1226.629511	2451.243422	0.000451244	47	N	202	225
P97369	Parental	FLLSK	INKDWLEGTSQGATGIFPGSFVK	ILKDF	3		818.0889407	2451.243422	0.000451244	25	N	202	225
P97369	Parental	AQQLR	SESDFEQLPDDVAVSANIADIEEKR	GFTSH	2		1389.159755	2776.30391	0.000451244	10	N	8	33
P97369	Parental	AQQLR	SESDFEQLPDDVAVSANIADIEEKR	GFTSH	3		926.4424367	2776.30391	0.000451244	21	N	8	33
P97369	Parental	GKTIK	DIAVEEDLSSTPLFK	DLLAL	2		832.4254147	1662.835229	0.000451244	26	N	253	268
P97369	Parental	GKTIK	DIAVEEDLSSTPLFK	DLLAL	3		555.2862098	1662.835229	0.001162105	4	N	253	268
P97369	Parental	AQQLR	SESDFEQLPDDVAVSANIADIEEK	RGFTS	2		1311.109199	2620.202799	0.000451244	39	N	8	32
P97369	Parental	AQQLR	SESDFEQLPDDVAVSANIADIEEK	RGFTS	3		874.408733	2620.202799	0.000451244	35	N	8	32
P97369	Parental	GKTIK	DIAVEEDLSSTPLFKDLLALMR	REFQR	3		826.1054919	2475.293076	0.001463592	2	N	253	275
P97369	Parental	GSFVK	ILKDFPEDEDTTNWLR	CYFYE	2		996.489609	1990.963618	0.000451244	12	N	225	241
P97369	Parental	GSFVK	ILKDFPEDEDTTNWLR	CYFYE	3		664.6623393	1990.963618	0.000451244	7	N	225	241
P97369	Parental	DPDVR	IFFYQSAYDAEQVPQALR	RLRPR	2		1073.534351	2145.053102	0.000451244	9	N	130	148
P97369	Parental	EDTGK	TIKDIAVEEDLSSTPLF	KDLLA	2		939.491286	1876.966972	0.000451244	15	N	250	267
P97369	Parental	RIFFY	QSAYDAEQVPQALRR	LRPRT	3		577.9644641	1730.869992	0.000735798	1	N	134	149
P97369	Parental	REFQR	EDIALSYQDAEGDLVR	LLSDE	2		897.4317597	1792.847919	0.000451244	4	N	280	296
P97369	Parental	NAYMK	NLLSLPVCVL	MDPDV	2	C8:+57.021	564.328575	1126.64155	0.000823681	16	N	114	124
P97369	Parental	RIFFY	QSAYDAEQVPQALR	RLRPR	2		788.3922405	1574.768881	0.001162105	2	N	134	148
P97370	Exosome	VKMNR	IIDLIPDGYPQISCLPK	EENAT	2	C14:+57.021	971.5216349	1941.02767	0.001871652	1	N	177	194
P97370	Parental	LAEWK	LFIYNPSSGEFLGR	TSKSW	2		800.4124446	1598.809289	0.000622848	2	N	17	31
P97370	Parental	VKMNR	IIDLIPDGYPQISCLPK	EENAT	2	C14:+57.021	971.5216349	1941.02767	0.0025889	2	N	177	194
P97371	Exosome	VGDYR	QLVHELDEAEYQEIR	LMVME	2		936.4608515	1870.906103	0.000451244	10	N	198	213
P97371	Exosome	VGDYR	QLVHELDEAEYQEIR	LMVME	3		624.6431677	1870.906103	0.000451244	2	N	198	213
P97371	Exosome	VGDYR	QLVHELDEAEYQEIR	LMVME	2	[0:-17.027	927.9473515	1853.879103	0.000698008	5	N	198	213
P97371	Exosome	VMEIR	NAYAVLYDIILK	NFEKL	2		698.3982746	1394.780949	0.000451244	29	N	220	232
P97371	Exosome	VLLQR	LKPEIKDVTEQLNLVTTWLQLQIPR	IEDGN	4		744.6791852	2974.685541	0.001352548	2	N	116	141
P97371	Exosome	KPEIK	DVTEQLNLVTTWLQLQIPR	IEDGN	2		1134.123865	2266.232129	0.000451244	26	N	122	141
P97371	Exosome	KPEIK	DVTEQLNLVTTWLQLQIPR	IEDGN	3		756.4185097	2266.232129	0.000451244	17	N	122	141
P97371	Exosome	LQIPR	IEDGNNFGVAVQEK	VFELM	2		760.3735164	1518.731433	0.000451244	3	N	141	155
P97371	Parental	VGDYR	QLVHELDEAEYQEIR	LMVME	2		936.4608515	1870.906103	0.000451244	25	N	198	213
P97371	Parental	VGDYR	QLVHELDEAEYQEIR	LMVME	3		624.6431677	1870.906103	0.000451244	9	N	198	213
P97371	Parental	VGDYR	QLVHELDEAEYQEIR	LMVME	2	Q1:-17.027	927.9473515	1853.879103	0.001699387	1	N	198	213
P97371	Parental	VGDYR	QLVHELDEAEYQEIR	LMVME	2	[0:-17.027	927.9473515	1853.879103	0.001264573	2	N	198	213
P97371	Parental	VMEIR	NAYAVLYDIILK	NFEKL	2		698.3982746	1394.780949	0.000451244	19	N	220	232
P97371	Parental	VLLQR	LKPEIKDVTEQLNLVTTWLQLQIPR	IEDGN	3		992.5696469	2974.685541	0.001162105	10	N	116	141

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P97371	Parental	VLLQR	LKPEIKDVTEQLNLVTTWLQLQIPR	IEDGN	4		744.6791852	2974.685541	0.000622848	6	N	116	141
P97371	Parental	KPEIK	DVTEQLNLVTTWLQLQIPR	IEDGN	2		1134.123865	2266.232129	0.000451244	38	N	122	141
P97371	Parental	KPEIK	DVTEQLNLVTTWLQLQIPR	IEDGN	3		756.4185097	2266.232129	0.000451244	20	N	122	141
P97371	Parental	DLCSK	TENLLGSYFPK	KISEL	2		634.8302247	1267.644849	0.000451244	3	N	24	35
P97372	Exosome	VLDLR	AFYAELYHIISSNLEK	IVNPK	2		949.4888807	1896.962161	0.000622848	1	N	210	226
P97372	Exosome	VLDLR	AFYAELYHIISSNLEK	IVNPK	3		633.3285205	1896.962161	0.000451244	23	N	210	226
P97372	Exosome	VDVFR	QNLFQEADDFLCTFLPR	KIISL	2	C12:+57.021	1057.504505	2112.99341	0.000451244	11	N	21	38
P97372	Exosome	VDVFR	QNLFQEADDFLCTFLPR	KIISL	3	C12:+57.021	705.3389366	2112.99341	0.000451244	11	N	21	38
P97372	Exosome	PGNEK	LLALLALVKPEVWTLK	EKCIL	2		904.0769376	1806.138275	0.001463592	1	N	99	115
P97372	Exosome	PGNEK	LLALLALVKPEVWTLK	EKCIL	3		603.0538918	1806.138275	0.001162105	17	N	99	115
P97372	Exosome	HLIPK	IEDGNDFGVAIQEK	VLERV	2		767.8733493	1533.731099	0.000622848	8	N	131	145
P97372	Exosome	TFLPR	KIISLSQLLQEDSLNVADLSSLR	APLDI	2		1271.70849	2541.40138	0.000451244	1	N	38	61
P97372	Exosome	TFLPR	KIISLSQLLQEDSLNVADLSSLR	APLDI	3		848.1415932	2541.40138	0.000451244	21	N	38	61
P97372	Exosome	FLPRK	IISLSQLLQEDSLNVADLSSLR	APLDI	2		1207.661008	2413.306416	0.000451244	7	N	39	61
P97372	Exosome	FLPRK	IISLSQLLQEDSLNVADLSSLR	APLDI	3		805.4432721	2413.306416	0.000823681	3	N	39	61
P97372	Exosome	TLKEK	CILVITWIQHLIPK	IEDGN	3	C1:+57.021	578.6763841	1733.005752	0.002727428	1	N	117	131
P97372	Parental	VLDLR	AFYAELYHIISSNLEK	IVNPK	2		949.4888807	1896.962161	0.000622848	7	N	210	226
P97372	Parental	VLDLR	AFYAELYHIISSNLEK	IVNPK	3		633.3285205	1896.962161	0.000451244	25	N	210	226
P97372	Parental	VDVFR	QNLFQEADDFLCTFLPR	KIISL	2	C12:+57.021	1057.504505	2112.99341	0.000451244	16	N	21	38
P97372	Parental	VDVFR	QNLFQEADDFLCTFLPR	KIISL	3	C12:+57.021	705.3389366	2112.99341	0.000622848	14	N	21	38
P97372	Parental	VDVFR	QNLFQEADDFLCTFLPR	KIISL	2	[0:-17.027,C12:+57.021	1048.991005	2095.96641	0.000998612	1	N	21	38
P97372	Parental	PGNEK	LLALLALVKPEVWTLK	EKCIL	3		603.0538918	1806.138275	0.000451244	17	N	99	115
P97372	Parental	TFLPR	KIISLSQLLQEDSLNVADLSSLR	APLDI	2		1271.70849	2541.40138	0.000451244	6	N	38	61
P97372	Parental	TFLPR	KIISLSQLLQEDSLNVADLSSLR	APLDI	3		848.1415932	2541.40138	0.000451244	11	N	38	61
P97372	Parental	FLPRK	IISLSQLLQEDSLNVADLSSLR	APLDI	2		1207.661008	2413.306416	0.000451244	4	N	39	61
P97372	Parental	FLPRK	IISLSQLLQEDSLNVADLSSLR	APLDI	3		805.4432721	2413.306416	0.001352548	1	N	39	61
P97372	Parental	QVDVF	RQNLFQEADDFLCTFLPR	KIISL	3	C13:+57.021	757.3726403	2269.094521	0.001591523	1	N	20	38
P97372	Parental	TLKEK	CILVITWIQHLIPK	IEDGN	3	C1:+57.021	578.6763841	1733.005752	0.000823681	6	N	117	131
P97372	Parental	KIISL	SQLLQEDSLNVADLSSLR	APLDI	2		994.5188978	1987.022196	0.000451244	4	N	43	61
P97376	Parental	GAPHR	EVDEGPSPPEQFTAVKL	SDSRI	2		921.960153	1841.904706	0.001463592	2	N	85	102
P97376	Parental	GAPHR	EVDEGPSPPEQFTAVK	LSDSR	2		865.418121	1728.820642	0.000622848	7	N	85	101
P97384	Exosome	RMYGK	SLYHDITGDTSGDYRK	ILLKI	2		914.4295514	1826.843503	0.000451244	18	N	477	493
P97384	Exosome	RMYGK	SLYHDITGDTSGDYRK	ILLKI	3		609.9556342	1826.843503	0.000451244	26	N	477	493
P97384	Exosome	RMYGK	SLYHDITGDTSGDYRK	ILLKI	4		457.7186757	1826.843503	0.000451244	3	N	477	493
P97384	Exosome	IMVSR	SELDLLDIR	AEYKR	2		537.2960177	1072.576435	0.000451244	45	N	459	468
P97384	Exosome	QFGNR	GTITAASGFDPLRDAEVLR	KAMKG	2		995.0241503	1988.032701	0.000451244	22	N	189	208
P97384	Exosome	QFGNR	GTITAASGFDPLRDAEVLR	KAMKG	3		663.6853669	1988.032701	0.000451244	20	N	189	208
P97384	Exosome	RKAMK	GFGTDEQAIIDCLGSR	SNKQR	2	C12:+57.021	869.9071662	1737.798732	0.000451244	29	N	212	228
P97384	Exosome	RKAMK	GFGTDEQAIIDCLGSR	SNKQR	3	C12:+57.021	580.2740441	1737.798732	0.000451244	1	N	212	228
P97384	Exosome	LALMK	TPVLFDVYEIK	EAIKG	2		662.3639004	1322.712201	0.000451244	29	N	269	280
P97384	Exosome	LALMK	TPVLFDVYEIKEAIK	GAGTD	3		588.9981117	1763.970935	0.000451244	6	N	269	284
P97384	Exosome	VYEIK	EAIKGAGTDEACLIEIFASR	SNEHI	2	C12:+57.021	1076.041452	2150.067303	0.000451244	5	N	280	300
P97384	Exosome	VYEIK	EAIKGAGTDEACLIEIFASR	SNEHI	3	C12:+57.021	717.696901	2150.067303	0.000451244	18	N	280	300
P97384	Exosome	KEAIK	GAGTDEACLIEIFASR	SNEHI	2	C8:+57.021	855.4120844	1708.808569	0.000451244	35	N	284	300
P97384	Exosome	KEAIK	GAGTDEACLIEIFASR	SNEHI	3	C8:+57.021	570.6106563	1708.808569	0.000451244	2	N	284	300
P97384	Exosome	SLVQR	DVQELYAAGENR	LGTDE	2		682.826202	1363.636804	0.000451244	17	N	357	369
P97384	Exosome	CSRSR	AHLVAVFNEYQR	MTGRD	2		723.878572	1445.741544	0.000451244	3	N	386	398
P97384	Exosome	CSRSR	AHLVAVFNEYQR	MTGRD	3		482.921648	1445.741544	0.000451244	27	N	386	398
P97384	Exosome	AGENR	LGTDESKFNAILCSR	SRAHL	2	C13:+57.021	855.9279016	1709.840203	0.000451244	2	N	369	384
P97384	Exosome	AGENR	LGTDESKFNAILCSR	SRAHL	3	C13:+57.021	570.9545344	1709.840203	0.000451244	3	N	369	384
P97384	Exosome	RMYGK	SLYHDITGDTSGDYR	KILLK	2		850.3820698	1698.74854	0.000451244	20	N	477	492
P97384	Exosome	QFGNR	GTITAASGFDPLR	DAEVL	2		653.3440306	1304.672461	0.000451244	3	N	189	202
P97384	Exosome	KDLIK	DLKSELSGNFEK	TILAL	3		456.2336688	1365.677606	0.000622848	1	N	250	262
P97384	Parental	RMYGK	SLYHDITGDTSGDYRK	ILLKI	2		914.4295514	1826.843503	0.000451244	4	N	477	493
P97384	Parental	RMYGK	SLYHDITGDTSGDYRK	ILLKI	3		609.9556342	1826.843503	0.001162105	4	N	477	493
P97384	Parental	IMVSR	SELDLLDIR	AEYKR	2		537.2960177	1072.576435	0.000451244	37	N	459	468
P97384	Parental	QFGNR	GTITAASGFDPLRDAEVLR	KAMKG	2		995.0241503	1988.032701	0.000451244	7	N	189	208
P97384	Parental	QFGNR	GTITAASGFDPLRDAEVLR	KAMKG	3		663.6853669	1988.032701	0.000451244	4	N	189	208
P97384	Parental	RKAMK	GFGTDEQAIIDCLGSR	SNKQR	2	C12:+57.021	869.9071662	1737.798732	0.000451244	16	N	212	228
P97384	Parental	RKAMK	GFGTDEQAIIDCLGSR	SNKQR	3	C12:+57.021	580.2740441	1737.798732	0.000451244	1	N	212	228
P97384	Parental	LALMK	TPVLFDVYEIK	EAIKG	2		662.3639004	1322.712201	0.000451244	24	N	269	280
P97384	Parental	LALMK	TPVLFDVYEIKEAIK	GAGTD	3		588.9981117	1763.970935	0.000451244	13	N	269	284
P97384	Parental	VYEIK	EAIKGAGTDEACLIEIFASR	SNEHI	2	C12:+57.021	1076.041452	2150.067303	0.000451244	4	N	280	300
P97384	Parental	VYEIK	EAIKGAGTDEACLIEIFASR	SNEHI	3	C12:+57.021	717.696901	2150.067303	0.000622848	8	N	280	300
P97384	Parental	KEAIK	GAGTDEACLIEIFASR	SNEHI	2	C8:+57.021	855.4120844	1708.808569	0.000451244	29	N	284	300

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P97384	Parental	KEAIK	GAGTDEACLIEIFASR	SNEHI	3	C8:+57.021	570.6106563	1708.808569	0.000451244	5	N	284	300
P97384	Parental	TEFQK	TLEEAIRSDTSGHFQR	LLISL	3		616.3067784	1845.896935	0.001264573	2	N	318	334
P97384	Parental	SLVQR	DVQELYAAGENR	LGTDE	2		682.826202	1363.636804	0.000451244	19	N	357	369
P97384	Parental	CSRSR	AHLVAVFNEYQR	MTGRD	2		723.878572	1445.741544	0.001871652	3	N	386	398
P97384	Parental	CSRSR	AHLVAVFNEYQR	MTGRD	3		482.921648	1445.741544	0.000451244	4	N	386	398
P97384	Parental	AGENR	LGTDESKFNAILCSR	SRAHL	2	C13:+57.021	855.9279016	1709.840203	0.000451244	1	N	369	384
P97384	Parental	AGENR	LGTDESKFNAILCSR	SRAHL	3	C13:+57.021	570.9545344	1709.840203	0.002019181	1	N	369	384
P97425	Exosome	ACNPR	TPQDSPMYPVVPVHLDGTF	-	2		1050.509488	2099.003375	0.000823681	4	Y	137	156
P97425	Exosome	ACNPR	TPQDSPMYPVVPVHLDGTF	-	2	M7:+15.995	1058.506988	2114.998375	0.000451244	20	Y	137	156
P97425	Exosome	ACNPR	TPQDSPMYPVVPVHLDGTF	-	3	M7:+15.995	706.0072585	2114.998375	0.000823681	9	Y	137	156
P97425	Exosome	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDNISR	NCHNS	3	C17:+57.021,C24:+57.021	1055.833079	3164.475838	0.000451244	38	N	62	92
P97425	Exosome	LHTSF	ANAVGVCGNPSGLCSDNISR	NCHNS	2	C7:+57.021,C14:+57.021	1024.467896	2046.920193	0.000451244	3	N	72	92
P97425	Exosome	YQPRR	SLEYYTVACNPR	TPQDS	2	C9:+57.021	736.8458489	1471.676098	0.000451244	13	N	125	137
P97425	Parental	ACNPR	TPQDSPMYPVVPVHLDGTF	-	2	M7:+15.995	1058.506988	2114.998375	0.00091018	2	Y	137	156
P97425	Parental	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDNISR	NCHNS	3	C17:+57.021,C24:+57.021	1055.833079	3164.475838	0.000451244	9	N	62	92
P97425	Parental	LHTSF	ANAVGVCGNPSGLCSDNISR	NCHNS	2	C7:+57.021,C14:+57.021	1024.467896	2046.920193	0.000823681	1	N	72	92
P97425	Parental	YQPRR	SLEYYTVACNPR	TPQDS	2	C9:+57.021	736.8458489	1471.676098	0.000451244	8	N	125	137
P97426	Exosome	YQSRR	SLEYYTVACDPR	TPQDS	2	C9:+57.021	737.3378567	1472.660113	0.000451244	40	N	124	136
P97426	Exosome	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDKR	SQNCH	3	C17:+57.021,C24:+57.021	993.811727	2978.411781	0.000451244	16	N	62	90
P97426	Exosome	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDKR	SQNCH	4	C17:+57.021,C24:+57.021	745.6107452	2978.411781	0.000451244	33	N	62	90
P97426	Exosome	ACDPR	TPQDSPMYPVVPVHLDGTF	-	2		1050.509488	2099.003375	0.000823681	4	Y	136	155
P97426	Exosome	ACDPR	TPQDSPMYPVVPVHLDGTF	-	2	M7:+15.995	1058.506988	2114.998375	0.000451244	20	Y	136	155
P97426	Exosome	ACDPR	TPQDSPMYPVVPVHLDGTF	-	3	M7:+15.995	706.0072585	2114.998375	0.000823681	9	Y	136	155
P97426	Exosome	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDK	RSQNC	3	C17:+57.021,C24:+57.021	941.7780232	2822.31067	0.000622848	1	N	62	89
P97426	Exosome	NSSSR	VHITVCNITSR	ATNYT	3	C6:+57.021	433.8998127	1298.676038	0.001943752	2	N	100	111
P97426	Parental	YQSRR	SLEYYTVACDPR	TPQDS	2	C9:+57.021	737.3378567	1472.660113	0.000451244	24	N	124	136
P97426	Parental	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDKR	SQNCH	3	C17:+57.021,C24:+57.021	993.811727	2978.411781	0.000735798	3	N	62	90
P97426	Parental	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDKR	SQNCH	4	C17:+57.021,C24:+57.021	745.6107452	2978.411781	0.000451244	10	N	62	90
P97426	Parental	ACDPR	TPQDSPMYPVVPVHLDGTF	-	2	M7:+15.995	1058.506988	2114.998375	0.00091018	2	Y	136	155
P97426	Parental	LHTSF	ANAVGVCGNPSGLCSDKR	SQNCH	2	C7:+57.021,C14:+57.021	931.4358679	1860.856136	0.002374549	1	N	72	90
P97426	Parental	RRTCK	GLNTFLHTSFANAVGVCGNPSGLCSDK	RSQNC	3	C17:+57.021,C24:+57.021	941.7780232	2822.31067	0.000451244	1	N	62	89
P97429	Exosome	GGTVK	AASGFNATEDAQTLR	KAMKG	2		776.3740478	1550.732496	0.000451244	1	N	9	24
P97429	Exosome	EQSIK	SETSGSFEDALLAIVK	CMRSK	2		833.9308642	1665.846128	0.000451244	9	N	225	241
P97429	Exosome	RKAMK	GLGTDEDAIIGILAYR	NTAQR	2		838.9468486	1675.878097	0.000451244	3	N	28	44
P97429	Exosome	RKAMK	GLGTDEDAIIGILAYR	NTAQR	3		559.6338324	1675.878097	0.000451244	2	N	28	44
P97429	Exosome	RRAMK	GAGTDEGCLIEILASR	TPEEI	2	C8:+57.021	831.4120844	1660.808569	0.000622848	3	N	100	116
P97429	Parental	GGTVK	AASGFNATEDAQTLR	KAMKG	2		776.3740478	1550.732496	0.000622848	1	N	9	24
P97450	Exosome	YKSKR	QASGGPVDIGPEYQQDLDRELYK	LKQMY	3		860.086036	2577.234708	0.000451244	11	N	54	77
P97450	Parental	FPTFK	FDDPKFEVIDKPQS	-	2		832.9124745	1663.809349	0.000451244	11	N	94	108
P97450	Parental	FPTFK	FDDPKFEVIDKPQS	-	3		555.6109163	1663.809349	0.000451244	12	N	94	108
P97450	Parental	YKSKR	QASGGPVDIGPEYQQDLDRELYK	LKQMY	2		1289.625154	2577.234708	0.000451244	24	N	54	77
P97450	Parental	YKSKR	QASGGPVDIGPEYQQDLDRELYK	LKQMY	3		860.086036	2577.234708	0.000451244	50	N	54	77
P97450	Parental	YKSKR	QASGGPVDIGPEYQQDLDRELYK	LKQMY	2	Q1:-17.027	1281.111654	2560.207708	0.000451244	6	N	54	77
P97450	Parental	YKSKR	QASGGPVDIGPEYQQDLDRELYK	LKQMY	2	[0:-17.027	1281.111654	2560.207708	0.000451244	9	N	54	77
P97450	Parental	YKSKR	QASGGPVDIGPEYQQDLDRELY	KLKQM	2		1225.577672	2449.139745	0.000451244	8	N	54	76
P97450	Parental	YKSKR	QASGGPVDIGPEYQQDLDR	ELYKL	2		1022.982679	2043.949759	0.000451244	14	N	54	73
P97484	Exosome	SRTLR	QGAAASPLSQAGEAPEEPSVYATLAAARPEAVPK	DMEQ-	3		1112.235832	3333.684097	0.001162105	1	N	803	837
P97484	Exosome	EGPQK	LSWTQDSQYNYSTR	KYHAL	2		874.897887	1747.780174	0.000451244	4	N	162	176
P97484	Exosome	YSYDR	NRPYVWSPPSESVELLVSGNLQKPTIK	AEPGS	3		1013.549023	3037.623669	0.001162105	1	N	202	229
P97484	Parental	SRTLR	QGAAASPLSQAGEAPEEPSVYATLAAARPEAVPK	DMEQ-	3		1112.235832	3333.684097	0.000451244	10	N	803	837
P97492	Parental	QGEGR	GSSLSIHSLPSGPSSPFSTEEQPVASWAQSFER	LLQDP	3		1163.890613	3488.64844	0.000451244	2	N	37	70
P97492	Parental	STGNR	QTCDIEGLVELLNR	VQSSG	2	C3:+57.021	830.4224521	1658.829304	0.000451244	6	N	495	509
P97492	Parental	SRPGK	YCCVYLPDGTASLALAR	PGLTI	2	C2:+57.021,C3:+57.021	965.4635627	1928.911525	0.000451244	8	N	303	320
P97492	Parental	GNEQK	ALVLDQDCTVLADQEVR	LENRI	2	C8:+57.021	972.9886876	1943.961775	0.000979378	1	N	353	370
P97493	Parental	TRVCL	TTFNVQDGPDFQDRVVNSETPVVVDFHAQWCGPCK	ILGPR	4	C31:+57.021,C34:+57.021	1013.219377	4048.846308	0.000979378	2	N	59	94
P97493	Parental	TRVCL	TTFNVQDGPDFQDR	VVNSE	2		820.3715051	1638.72741	0.000451244	4	N	59	73
P97496	Exosome	MNIEK	TLVQNNCLTRPNIYLIPDIDLK	LANKL	3	C7:+57.021	871.8075142	2612.399143	0.000451244	1	N	156	178
P97496	Parental	APTNK	TLAGLVVQLLQFQEDAFGK	HVTNP	2		1039.070569	2076.125539	0.000451244	4	N	74	93
P97496	Parental	MNIEK	TLVQNNCLTRPNIYLIPDIDLK	LANKL	3	C7:+57.021	871.8075142	2612.399143	0.000451244	2	N	156	178
P97797	Exosome	VGQSR	LLIYSFTGEHFPR	VTNVS	3		527.2809533	1578.81946	0.001763695	3	N	76	89
P97797	Parental	VHLSR	AQPAPKPEPSFSEYASVQVQR	K-	3		772.7260023	2315.154607	0.000823681	5	N	491	512
P97797	Parental	DFSIR	ISNVTPEDAGTYYCVK	FQKGP	2	C14:+57.021	908.9250246	1815.834449	0.001943752	2	N	107	123
P97797	Parental	DVHSK	VICEVAHITLDRSPLR	GIANL	3	C3:+57.021	627.0124951	1878.014085	0.000637154	1	N	226	242
P97797	Parental	VGQSR	LLIYSFTGEHFPR	VTNVS	3		527.2809533	1578.81946	0.002374549	1	N	76	89
P97797	Parental	DVHSK	VICEVAHITLDR	SPLRG	2	C3:+57.021	713.3798589	1424.744118	0.002663018	1	N	226	238

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P97797	Parental	DVHSK	VICEVAHITLDR	SPLRG	3	C3:+57.021	475.9225059	1424.744118	0.0007646	1	N	226	238
P97807	Exosome	AAMPR	IYELAAGGTAVGTGLNTR	IGFAE	2		882.4684796	1762.921359	0.000451244	36	N	265	283
P97807	Exosome	GSTLK	ETAIELGYLTAEQFDEWVKPK	DMLGP	2		1234.123727	2466.231854	0.000451244	16	N	480	501
P97807	Exosome	GSTLK	ETAIELGYLTAEQFDEWVKPK	DMLGP	3		823.0850848	2466.231854	0.000451244	37	N	480	501
P97807	Exosome	GILKR	AAAEVNQEYGLDPK	IASAI	2		752.8680669	1503.720534	0.000451244	22	N	98	112
P97807	Parental	AAMPR	IYELAAGGTAVGTGLNTR	IGFAE	2		882.4684796	1762.921359	0.000451244	47	N	265	283
P97807	Parental	GSTLK	ETAIELGYLTAEQFDEWVKPK	DMLGP	3		823.0850848	2466.231854	0.000451244	14	N	480	501
P97807	Parental	KTAHK	NGSTLKETAIELGYLTAEQFDEWVKPK	DMLGP	3		1023.192793	3066.55498	0.00091018	2	N	474	501
P97807	Parental	KTAHK	NGSTLKETAIELGYLTAEQFDEWVKPK	DMLGP	4		767.646545	3066.55498	0.000823681	3	N	474	501
P97807	Parental	GILKR	AAAEVNQEYGLDPK	IASAI	2		752.8680669	1503.720534	0.000662267	5	N	98	112
P97807	Parental	ASVSF	TDNCVVGIQANTER	INKLM	2	C4:+57.021	788.8731263	1575.730653	0.000637154	1	N	427	441
P97814	Parental	NELVY	ASIEVQATQGNLNSSAQDYR	ALYDY	2		1076.517418	2151.019236	0.000451244	14	N	344	364
P97814	Parental	YEEVR	LTLEGCDVEGDINGFIQSK	STGRE	2	C6:+57.021	1048.004535	2093.993469	0.000451244	32	N	253	272
P97814	Parental	HGSPK	TTPSAPAASTETLTPTPER	NELVY	2		964.4845236	1926.953447	0.000451244	3	N	320	339
P97821	Exosome	LIAGK	YAQDFGVVEESCFPYTAK	DSPCK	2	C12:+57.021	1055.975246	2109.934892	0.000451244	46	N	308	326
P97821	Exosome	HTGLS	DPFNPFELTNHAVLLVGYGRDPVTGIEYWIIK	NSWGS	4		919.2323132	3672.898053	0.001591523	2	N	393	425
P97821	Exosome	FRIRR	GTDECAIESIAVAAIPIPK	L-	2	C5:+57.021	978.0116314	1954.007663	0.000451244	6	N	442	461
P97821	Exosome	VGYGR	DPVTGIEYWIIK	NSWGS	2		717.3879069	1432.760214	0.000451244	6	N	413	425
P97821	Exosome	SWDWR	NVQGVNYVSPVR	NQESC	2		666.3574724	1330.699345	0.000622848	1	N	237	249
P97821	Parental	LIAGK	YAQDFGVVEESCFPYTAK	DSPCK	2	C12:+57.021	1055.975246	2109.934892	0.000451244	47	N	308	326
P97821	Parental	FRIRR	GTDECAIESIAVAAIPIPKL	-	2	C5:+57.021	1034.553663	2067.091727	0.000451244	7	N	442	462
P97821	Parental	FRIRR	GTDECAIESIAVAAIPIPKL	-	3	C5:+57.021	690.0383756	2067.091727	0.001329271	4	N	442	462
P97821	Parental	HTGLS	DPFNPFELTNHAVLLVGYGRDPVTGIEYWIIK	NSWGS	3		1225.307151	3672.898053	0.000823681	2	N	393	425
P97821	Parental	HTGLS	DPFNPFELTNHAVLLVGYGRDPVTGIEYWIIK	NSWGS	4		919.2323132	3672.898053	0.000451244	9	N	393	425
P97821	Parental	FRIRR	GTDECAIESIAVAAIPIPK	L-	2	C5:+57.021	978.0116314	1954.007663	0.000622848	1	N	442	461
P97821	Parental	VGYGR	DPVTGIEYWIIK	NSWGS	2		717.3879069	1432.760214	0.000451244	4	N	413	425
P97821	Parental	SWDWR	NVQGVNYVSPVR	NQESC	2		666.3574724	1330.699345	0.000451244	1	N	237	249
P97822	Exosome	LSGNK	IKDLSTVEALQNLK	NLKSL	2		786.4543095	1570.893019	0.002981883	1	N	99	113
P97822	Exosome	LKNLK	SLDLFNCEITNLEDYR	ESIFE	2	C7:+57.021	1001.465045	2000.914491	0.000622848	1	N	116	132
P97822	Exosome	GNKIK	DLSTVEALQNLK	NLKSL	2		665.8647959	1329.713992	0.001699387	1	N	101	113
P97822	Parental	LNKLR	KLELSDNIISGGLEVLAEK	CPNLT	2		1014.565317	2027.115033	0.000451244	13	N	67	86
P97822	Parental	LNKLR	KLELSDNIISGGLEVLAEK	CPNLT	3		676.7128112	2027.115033	0.000451244	11	N	67	86
P97822	Parental	LSGNK	IKDLSTVEALQNLK	NLKSL	2		786.4543095	1570.893019	0.000451244	15	N	99	113
P97822	Parental	LSGNK	IKDLSTVEALQNLK	NLKSL	3		524.6388063	1570.893019	0.001162105	4	N	99	113
P97822	Parental	LKNLK	SLDLFNCEITNLEDYR	ESIFE	2	C7:+57.021	1001.465045	2000.914491	0.000451244	6	N	116	132
P97822	Parental	GNKIK	DLSTVEALQNLK	NLKSL	2		665.8647959	1329.713992	0.000451244	8	N	101	113
P97822	Parental	LEDYR	ESIFELLQQITY	LDGFD	2		742.3881039	1482.760608	0.000823681	7	N	132	144
P97822	Parental	LKNLK	SLDLFNCEITNLEDYRESIFELLQQITY	LDGFD	3	C7:+57.021	1156.229313	3465.664538	0.002813207	1	N	116	144
P97822	Parental	VLAEK	CPNLTYLNLSGNK	IKDLS	2	C1:+57.021	747.3747735	1492.733947	0.002212458	1	N	86	99
P97823	Exosome	TTQQK	LAGVTALSCWLPLR	ASFSQ	2	C9:+57.021	778.9348013	1555.854003	0.000451244	27	N	135	149
P97823	Exosome	IPSNR	IILGGFSQGGALSLYTALTTQQK	LAGVT	2		1184.150079	2366.284559	0.000451244	21	N	112	135
P97823	Exosome	IPSNR	IILGGFSQGGALSLYTALTTQQK	LAGVT	3		789.7693195	2366.284559	0.000622848	11	N	112	135
P97823	Exosome	VERLK	ALINPANVTFK	IYEGM	2		594.3433023	1186.671005	0.002727428	1	N	190	201
P97823	Exosome	AAVIF	LHGLGDTGHGWAEAFAGIK	SPHIK	3		646.3275139	1935.959142	0.000451244	6	N	26	45
P97823	Exosome	VPAAR	KATAAVIFLHGLGDTGHGWAEAFAGIK	SPHIK	3		913.4858057	2737.434017	0.002884417	1	N	18	45
P97823	Exosome	VPAAR	KATAAVIFLHGLGDTGHGWAEAFAGIK	SPHIK	4		685.3663042	2737.434017	0.000451244	6	N	18	45
P97823	Exosome	NSANR	DISVLQCHGDCDPLVPLMFGSLTVER	LKALI	3	C7:+57.021,C11:+57.021	986.8103359	2957.407608	0.000451244	8	N	162	188
P97823	Exosome	NSANR	DISVLQCHGDCDPLVPLMFGSLTVER	LKALI	3	C7:+57.021,C11:+57.021,M18:+15.995	992.1420026	2973.402608	0.000451244	1	N	162	188
P97823	Exosome	WLPLR	ASFSQGPINSANR	DISVL	2		674.8343614	1347.653123	0.000451244	4	N	149	162
P97823	Exosome	PAARK	ATAAVIFLHGLGDTGHGWAEAFAGIK	SPHIK	3		870.7874846	2609.339054	0.00091018	1	N	19	45
P97823	Exosome	IPSNR	IILGGFSQGGALSLY	TALTT	2		748.4119133	1494.808227	0.001395409	1	N	112	127
P97823	Parental	TTQQK	LAGVTALSCWLPLR	ASFSQ	2	C9:+57.021	778.9348013	1555.854003	0.000451244	11	N	135	149
P97823	Parental	IPSNR	IILGGFSQGGALSLYTALTTQQK	LAGVT	2		1184.150079	2366.284559	0.000451244	3	N	112	135
P97823	Parental	VERLK	ALINPANVTFK	IYEGM	2		594.3433023	1186.671005	0.00091018	2	N	190	201
P97855	Exosome	NSGGK	LPNFGFVVFDDSEPVQK	VLSNR	2		969.486338	1936.957076	0.000451244	9	N	374	391
P97855	Exosome	RFYGK	NSSYAHGGLDSNGKPADAVYGQK	EIHRK	3		779.3687662	2335.082899	0.001329271	4	N	36	59
P97855	Exosome	RFYGK	NSSYAHGGLDSNGKPADAVYGQK	EIHRK	4		584.7785246	2335.082899	0.001395409	1	N	36	59
P97855	Parental	VVELR	INSGGKLPNFGFVVFDDSEPVQK	VLSNR	2		1247.634793	2493.253987	0.000823681	1	N	368	391
P97855	Parental	VVELR	INSGGKLPNFGFVVFDDSEPVQK	VLSNR	3		832.0924623	2493.253987	0.000451244	6	N	368	391
P97855	Parental	DDVQK	STSPAPADVAPAQEDLR	TFSWA	2		862.9266445	1723.837689	0.000451244	8	N	228	245
P97855	Parental	NSGGK	LPNFGFVVFDDSEPVQK	VLSNR	2		969.486338	1936.957076	0.000451244	18	N	374	391
P97855	Parental	RFYGK	NSSYAHGGLDSNGKPADAVYGQK	EIHRK	3		779.3687662	2335.082899	0.001463592	3	N	36	59
P97855	Parental	RFYGK	NSSYAHGGLDSNGKPADAVYGQK	EIHRK	4		584.7785246	2335.082899	0.001699387	1	N	36	59
P97855	Parental	NSGGK	LPNFGFVVFDDSEPVQKV	LSNRP	2		1019.020545	2036.02549	0.001162105	3	N	374	392

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P97855	Parental	KSELK	DFFQNFGNVVELR	INSGG	2		792.894419	1583.773238	0.000451244	3	N	355	368
P97864	Exosome	RNPGK	GSWFVQALCSILNEHGK	DLEIM	3	C9:+57.021	649.3248503	1944.951151	0.000451244	4	N	237	254
P97864	Exosome	QDLLR	KASEEDHSNSACFACVLLSHGEEDLIYGK	DGVTP	4	C12:+57.021,C15:+57.021	817.373966	3265.464664	0.000622848	5	N	124	153
P97864	Parental	IQACR	GTELDDGIQADSGPINDIDANPR	NKIPV	2		1192.054561	2382.093523	0.000451244	6	N	187	210
P97864	Parental	DANPR	NKIPVEADFLFAYSTVPGYYSWR	NPGKG	3		908.4555121	2722.343136	0.001463592	1	N	210	233
P97872	Parental	MAKKR	IAVIGAGASGLTCIK	CCLEE	2	C13:+57.021	715.9057095	1429.795819	0.000622848	1	N	5	20
P97872	Parental	LTCIK	CCLEEGLEPVCFER	SGDIG	2	C1:+57.021,C2:+57.021,C11:+57.021	899.3836924	1796.751785	0.000451244	6	N	20	34
P97872	Parental	KPKHR	ALSQHPTVNDDLPNR	IIAGL	3		559.6170643	1675.827793	0.002080925	2	N	277	292
P98083	Exosome	PVNQR	ACHILECPEGLAQDVISTIGQAFELR	FKQYL	3	C2:+57.021,C7:+57.021	976.4847283	2926.430785	0.000451244	7	N	285	311
P98083	Parental	PVNQR	ACHILECPEGLAQDVISTIGQAFELR	FKQYL	3	C2:+57.021,C7:+57.021	976.4847283	2926.430785	0.000451244	21	N	285	311
P98083	Parental	PVNQR	ACHILECPEGLAQDVISTIGQAF	ELRFK	2	C2:+57.021,C7:+57.021	1265.109308	2528.203017	0.000451244	1	N	285	308
P98083	Parental	PCPGR	ELFDDPSYVNIQNLDK	ARQAG	2		955.4630599	1908.91052	0.000451244	14	N	415	431
P99024	Exosome	-M	REIVHIQAGQCGNQIGAK	FWEVI	3	C11:+57.021	660.3465369	1978.016211	0.000637154	2	Y	1	19
P99024	Exosome	-	MREIVHIQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000622848	4	Y	0	19
P99024	Exosome	-	MREIVHIQAGQCGNQIGAK	FWEVI	3	M1:+15.995,C12:+57.021	709.3583655	2125.051697	0.001229886	2	Y	0	19
P99024	Exosome	-MR	EIVHIQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	7	Y	2	19
P99024	Exosome	-MR	EIVHIQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	6	Y	2	19
P99024	Exosome	LQLDR	ISVYYNEATGGK	YVPRA	2		651.3227639	1300.629928	0.000451244	19	N	46	58
P99024	Exosome	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	3		985.7850854	2954.331856	0.000451244	5	N	20	46
P99024	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000662267	3	Y	81	103
P99024	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	9	Y	81	103
P99024	Exosome	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	3		1034.80789	3101.40027	0.000451244	9	N	19	46
P99024	Exosome	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	4		776.3578675	3101.40027	0.000451244	10	N	19	46
P99024	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	2		1044.04254	2086.06948	0.000451244	4	Y	103	122
P99024	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	3		696.3642934	2086.06948	0.000451244	41	Y	103	122
P99024	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	4		522.5251701	2086.06948	0.000451244	6	Y	103	122
P99024	Exosome	NVQNK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	24	Y	336	350
P99024	Exosome	NVQNK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	1	Y	336	350
P99024	Exosome	SQQYR	ALTVPELTQQVFDAK	NMMAA	2		830.4517668	1658.887934	0.000451244	19	N	282	297
P99024	Exosome	SQQYR	ALTVPELTQQVFDAK	NMMAA	3		553.9704446	1658.887934	0.000451244	9	N	282	297
P99024	Exosome	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021	1104.516428	3310.525885	0.000451244	17	Y	122	154
P99024	Exosome	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021,M25:+15.995	1109.848095	3326.520885	0.000451244	8	Y	122	154
P99024	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	2		979.9950585	1957.974517	0.000451244	26	Y	103	121
P99024	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	3		653.6659724	1957.974517	0.000451244	38	Y	103	121
P99024	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	17	Y	77	103
P99024	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	66	Y	77	103
P99024	Exosome	PRHGR	YLTVAAVFR	GRMSM	2		520.3009061	1038.586212	0.000622848	18	Y	309	318
P99024	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.001162105	2	Y	216	241
P99024	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	M17:+15.995,C23:+57.021	908.7829573	2723.325472	0.001699387	1	Y	216	241
P99024	Exosome	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	28	Y	183	213
P99024	Parental	-M	REIVHIQAGQCGNQIGAK	FWEVI	3	C11:+57.021	660.3465369	1978.016211	0.002453667	1	Y	1	19
P99024	Parental	-	MREIVHIQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000451244	2	Y	0	19
P99024	Parental	-MR	EIVHIQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	30	Y	2	19
P99024	Parental	-MR	EIVHIQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	33	Y	2	19
P99024	Parental	LQLDR	ISVYYNEATGGK	YVPRA	2		651.3227639	1300.629928	0.000451244	49	N	46	58
P99024	Parental	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	3		985.7850854	2954.331856	0.000451244	54	N	20	46
P99024	Parental	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	4		739.590764	2954.331856	0.001943752	1	N	20	46
P99024	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000451244	30	Y	81	103
P99024	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	20	Y	81	103
P99024	Parental	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	3		1034.80789	3101.40027	0.000451244	45	N	19	46
P99024	Parental	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLDR	ISVYY	4		776.3578675	3101.40027	0.000451244	26	N	19	46
P99024	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	2		1044.04254	2086.06948	0.000451244	30	Y	103	122
P99024	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	3		696.3642934	2086.06948	0.000451244	68	Y	103	122
P99024	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	EAESC	4		522.5251701	2086.06948	0.000451244	45	Y	103	122
P99024	Parental	NVQNK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	38	Y	336	350
P99024	Parental	NVQNK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	19	Y	336	350
P99024	Parental	SQQYR	ALTVPELTQQVFDAK	NMMAA	2		830.4517668	1658.887934	0.000451244	59	N	282	297
P99024	Parental	SQQYR	ALTVPELTQQVFDAK	NMMAA	3		553.9704446	1658.887934	0.000451244	30	N	282	297
P99024	Parental	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021	1104.516428	3310.525885	0.000451244	27	Y	122	154
P99024	Parental	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	C5:+57.021,C7:+57.021,M25:+15.995	1109.848095	3326.520885	0.000451244	16	Y	122	154
P99024	Parental	PRGLK	MAVTFIGNSTAIQELFKR	ISEQF	3		676.0317099	2025.07173	0.000451244	11	N	362	380
P99024	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	2		979.9950585	1957.974517	0.000451244	36	Y	103	121

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P99024	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KEAES	3		653.6659724	1957.974517	0.000451244	49	Y	103	121
P99024	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	50	Y	77	103
P99024	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	220	Y	77	103
P99024	Parental	VPSPK	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	4	C27:+57.021,C37:+57.021	1149.032553	4592.099013	0.001162105	8	Y	174	213
P99024	Parental	LQLDR	ISVYYNEATGGKYVPR	AILVD	3		606.3129818	1815.915545	0.001871652	1	N	46	62
P99024	Parental	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLDRISVYYNEATGGK	YVPRA	4		1097.012709	4384.019638	0.000870037	1	N	19	58
P99024	Parental	EYPDR	IMNTFSVVPSPK	VSDTV	2		660.355553	1318.695506	0.001763695	2	Y	162	174
P99024	Parental	PRHGR	YLTVAAVFR	GRMSM	2		520.3009061	1038.586212	0.000622848	23	Y	309	318
P99024	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.000451244	22	Y	216	241
P99024	Parental	EPYNA	TLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C16:+57.021,C26:+57.021	1140.190598	3417.548394	0.000823681	4	Y	185	213
P99024	Parental	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	125	Y	183	213
P99024	Parental	RALTV	PELTQQVFDAK	NMMAA	2		638.3331316	1274.650663	0.001654178	1	N	286	297
P99024	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	KLAVN	4	C23:+57.021	955.7347788	3818.907915	0.001654178	2	Y	216	251
P99024	Parental	TTCLR	FPGQLNADLRK	LAVNM	3		420.2354554	1257.682966	0.001162105	3	Y	241	252
P99024	Parental	TTCLR	FPGQLNADLR	KLAVN	2		565.8018016	1129.588003	0.000451244	5	Y	241	251
P99024	Parental	GNNWA	KGHYTEGAELVDSVLDVVR	KEAES	2		1044.04254	2086.06948	0.000451244	3	Y	102	121
P99024	Parental	PRGLK	MAVTFIGNSTAIQELFK	RISEQ	2		935.4931093	1868.970619	0.000451244	8	N	362	379
P99024	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAKG	HYTEG	3		952.4603192	2854.357558	0.000823681	4	Y	77	104
P99024	Parental	KYVPR	AILVDLEPGTMDSVR	SGPFG	2		808.4221527	1614.828705	0.000662267	1	Y	62	77
P99024	Parental	QIGAK	FWEVISDEHGIDPTGTY	HGDSD	2		983.4474098	1964.87922	0.000823681	1	Y	19	36
P99026	Exosome	VLGVK	FDGGVVIAADMLGSYGSLAR	FRNIS	2		1000.00183	1997.98806	0.000451244	13	N	60	80
P99026	Exosome	TVTEK	GVEIEGPLSAQTNWDIAH	MISGF	2		968.9741261	1935.932652	0.002374549	1	N	240	258
P99026	Exosome	QPLLR	EVLEKQPVLSQTEAR	ELVER	3		576.3165034	1725.92611	0.000451244	2	N	196	211
P99026	Exosome	SRIMR	VNDSTMLGASGDYADFQYLK	QVLGQ	2		1098.002224	2193.988848	0.000622848	9	N	89	109
P99026	Exosome	TVTEK	GVEIEGPLSAQTNWDIAHMISGFE	-	2		1301.118651	2600.221702	0.000451244	5	N	240	264
P99026	Exosome	TVTEK	GVEIEGPLSAQTNWDIAHMISGFE	-	2	M19:+15.995	1309.116151	2616.216702	0.000622848	2	N	240	264
P99026	Exosome	YVDML	GVAYEAPSLATGYGAYLAQPLLR	EVLEK	2		1191.129147	2380.242694	0.000451244	6	N	173	196
P99026	Parental	QPLLR	EVLEKQPVLSQTEAR	ELVER	2		863.9708551	1725.92611	0.000451244	6	N	196	211
P99027	Exosome	KDIKK	ILDSVGIEADDDRLNK	VISEL	2		886.955402	1771.895204	0.000451244	10	N	25	41
P99027	Exosome	ELNGK	NIEDVIAQGVGK	LASVP	2		621.8385811	1241.661562	0.000451244	29	N	49	61
P99027	Exosome	DRLNK	VISELNGKNIEDVIAQGVGK	LASVP	3		695.0518268	2082.132081	0.002374549	1	N	41	61
P99027	Exosome	-MR	YVASYLLAALGGNSSPSAK	DIKKI	2		934.9917875	1867.967975	0.000451244	40	N	2	21
P99027	Exosome	-MR	YVASYLLAALGGNSSPSAK	DIKKI	3		623.6637917	1867.967975	0.000451244	32	N	2	21
P99027	Exosome	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	2		1387.720117	2773.424634	0.000622848	20	N	61	94
P99027	Exosome	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	3		925.4826781	2773.424634	0.000451244	44	N	61	94
P99027	Exosome	KKDEK	KEESEESDDDMGFGLFD	-	2	M11:+15.995	983.3813155	1964.747031	0.000622848	2	N	98	115
P99027	Parental	KDIKK	ILDSVGIEADDDRLNK	VISEL	2		886.955402	1771.895204	0.000451244	22	N	25	41
P99027	Parental	KDIKK	ILDSVGIEADDDRLNK	VISEL	3		591.6395347	1771.895204	0.000451244	29	N	25	41
P99027	Parental	ELNGK	NIEDVIAQGVGK	LASVP	2		621.8385811	1241.661562	0.000451244	32	N	49	61
P99027	Parental	DRLNK	VISELNGKNIEDVIAQGVGK	LASVP	2		1042.07384	2082.132081	0.000451244	23	N	41	61
P99027	Parental	DRLNK	VISELNGKNIEDVIAQGVGK	LASVP	3		695.0518268	2082.132081	0.000451244	15	N	41	61
P99027	Parental	-MR	YVASYLLAALGGNSSPSAKDIK	KILDS	3		742.3991151	2224.173945	0.000870037	1	N	2	24
P99027	Parental	-MR	YVASYLLAALGGNSSPSAK	DIKKI	2		934.9917875	1867.967975	0.000451244	65	N	2	21
P99027	Parental	-MR	YVASYLLAALGGNSSPSAK	DIKKI	3		623.6637917	1867.967975	0.000451244	45	N	2	21
P99027	Parental	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	2		1387.720117	2773.424634	0.000451244	51	N	61	94
P99027	Parental	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	3		925.4826781	2773.424634	0.000451244	48	N	61	94
P99027	Parental	MRYVA	SYLLAALGGNSSPSAK	DIKKI	2		768.4073593	1534.799119	0.000451244	5	N	5	21
P99027	Parental	ASVPA	GGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	2		1118.564368	2235.113136	0.00307782	1	N	67	94
P99027	Parental	VGKLA	SVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	KDEKK	2		1295.659528	2589.303456	0.001463592	1	N	63	94
P99027	Parental	QGVGK	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKK	DEKKE	3		968.1809991	2901.519597	0.00091018	2	N	61	95
P99028	Exosome	RVSSR	SQTEEDCTEELFDFLHAR	DHCVA	3	C7:+57.021	742.9921537	2225.953061	0.000451244	2	N	58	76
P99028	Parental	RVSSR	SQTEEDCTEELFDFLHAR	DHCVA	2	C7:+57.021	1113.984331	2225.953061	0.000451244	21	N	58	76
P99028	Parental	RVSSR	SQTEEDCTEELFDFLHAR	DHCVA	3	C7:+57.021	742.9921537	2225.953061	0.000451244	36	N	58	76
P99028	Parental	MLTGS	GDPKEEEEEELVDPLTTVR	EHCEQ	2		1093.029492	2184.043385	0.000451244	18	N	13	32
P99028	Parental	MLTGS	GDPKEEEEEELVDPLTTVR	EHCEQ	3		729.0222616	2184.043385	0.001329271	3	N	13	32
P99029	Exosome	PGCSK	THLPGFVEQAGALK	AKGAQ	2		734.4018799	1466.78816	0.001839721	2	N	98	112
P99029	Exosome	PGCSK	THLPGFVEQAGALK	AKGAQ	3		489.9371866	1466.78816	0.000451244	25	N	98	112
P99029	Exosome	EGKVR	LLADPTGAFGK	ATDLL	2		545.3011031	1088.586606	0.000451244	11	N	144	155
P99029	Exosome	LFKGK	KGVLFGVPGAFTPGCSK	THLPG	2	C15:+57.021	861.4560979	1720.896596	0.000451244	5	N	81	98
P99029	Exosome	LFKGK	KGVLFGVPGAFTPGCSK	THLPG	3	C15:+57.021	574.6399986	1720.896596	0.002296037	1	N	81	98
P99029	Exosome	GAFGK	ATDLLLDDSLVSLFGNR	RLKRF	2		924.9892448	1847.96289	0.000451244	31	N	155	172
P99029	Exosome	NGIVK	ALNVEPDGTGLTCSLAPNILSQL	-	2	C13:+57.021	1192.112605	2382.20961	0.000451244	22	N	187	210
P99029	Exosome	NGIVK	ALNVEPDGTGLTCSLAPNILSQL	-	3	C13:+57.021	795.0776701	2382.20961	0.000622848	3	N	187	210
P99029	Exosome	GAFGK	ATDLLLDDSLVSLFGNRR	LKRFS	2		1003.0398	2004.064001	0.000451244	7	N	155	173
P99029	Exosome	GAFGK	ATDLLLDDSLVSLFGNRR	LKRFS	3		669.0291336	2004.064001	0.000451244	31	N	155	173

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
P99029	Exosome	MAPIK	VGDAIPSVEVFEGEPGKK	VNLAE	2		929.4837953	1856.951991	0.001162105	2	N	53	71
P99029	Exosome	MAPIK	VGDAIPSVEVFEGEPGK	KVNLA	2		865.4363138	1728.857028	0.000451244	9	N	53	70
P99029	Parental	PGCSK	THLPGFVEQAGALKAK	GAQVV	2		833.9679184	1665.920237	0.001943752	1	N	98	114
P99029	Parental	PGCSK	THLPGFVEQAGALKAK	GAQVV	3		556.3145456	1665.920237	0.000451244	11	N	98	114
P99029	Parental	PGCSK	THLPGFVEQAGALK	AKGAQ	2		734.4018799	1466.78816	0.000622848	2	N	98	112
P99029	Parental	PGCSK	THLPGFVEQAGALK	AKGAQ	3		489.9371866	1466.78816	0.000451244	77	N	98	112
P99029	Parental	EGKVR	LLADPTGAFGK	ATDLL	2		545.3011031	1088.586606	0.000451244	28	N	144	155
P99029	Parental	LFKGK	KGVLFGVPGAFTPGCSK	THLPG	2	C15:+57.021	861.4560979	1720.896596	0.000451244	11	N	81	98
P99029	Parental	LFKGK	KGVLFGVPGAFTPGCSK	THLPG	3	C15:+57.021	574.6399986	1720.896596	0.001395409	8	N	81	98
P99029	Parental	SAVTM	APIKVGDAIPSVEVFEGEPGK	KVNLA	2		1070.070766	2138.125933	0.000451244	12	N	49	70
P99029	Parental	ALKAK	GAQVVACLSVNDVFVIEEWGR	AHQAE	2	C7:+57.021	1174.5891	2347.1626	0.000451244	74	N	114	135
P99029	Parental	GAFGK	ATDLLLDDSLVSLFGNR	RLKRF	2		924.9892448	1847.96289	0.000451244	42	N	155	172
P99029	Parental	GAFGK	ATDLLLDDSLVSLFGNR	RLKRF	3		616.9954299	1847.96289	0.000451244	24	N	155	172
P99029	Parental	NGIVK	ALNVEPDGTGLTCSLAPNILSQL	-	2	C13:+57.021	1192.112605	2382.20961	0.000451244	47	N	187	210
P99029	Parental	NGIVK	ALNVEPDGTGLTCSLAPNILSQL	-	3	C13:+57.021	795.0776701	2382.20961	0.000451244	12	N	187	210
P99029	Parental	GAFGK	ATDLLLDDSLVSLFGNRR	LKRFS	2		1003.0398	2004.064001	0.000451244	14	N	155	173
P99029	Parental	GAFGK	ATDLLLDDSLVSLFGNRR	LKRFS	3		669.0291336	2004.064001	0.000451244	28	N	155	173
P99029	Parental	GAFGK	ATDLLLDDSLVSLF	GNRRL	2		761.4064936	1520.797387	0.000662267	5	N	155	169
P99029	Parental	MAPIK	VGDAIPSVEVFEGEPGKK	VNLAE	2		929.4837953	1856.951991	0.000451244	17	N	53	71
P99029	Parental	MAPIK	VGDAIPSVEVFEGEPGK	KVNLA	2		865.4363138	1728.857028	0.000622848	16	N	53	70
P99029	Parental	GEPGK	KVNLAELFK	GKKGV	2		531.3218385	1060.628077	0.001591523	1	N	70	79
P99029	Parental	FKGKK	GVLFGVPGAFTPGCSK	THLPG	2	C14:+57.021	797.4086164	1592.801633	0.000451244	10	N	82	98
P99029	Parental	EGKVR	LLADPTGAFGKATDLLLDDSLVSLFGNR	RLKRF	3		973.854112	2918.538936	0.001839721	1	N	144	172
Q00519	Exosome	MSQTK	DQTIAPSSSLFNPEDFKPLDPTQEPIFPPELLR	LKDTP	3		1246.968752	3737.882857	0.000451244	72	N	187	220
Q00519	Exosome	MSQTK	DQTIAPSSSLFNPEDFKPLDPTQEPIFPPELLR	LKDTP	4		935.4785141	3737.882857	0.000451244	19	N	187	220
Q00519	Exosome	PGYRR	TLLSPEEILVSIVIPYSR	KGEFF	2		1015.083145	2028.150691	0.000451244	16	N	397	415
Q00519	Exosome	PGYRR	TLLSPEEILVSIVIPYSR	KGEFF	3		677.0580302	2028.150691	0.000451244	54	N	397	415
Q00519	Exosome	PEKIR	NACVDQFTTLCATGTPENCK	SWSVR	2	C3:+57.021,C11:+57.021,C19:+57.021	1143.992855	2285.970111	0.000451244	60	N	1309	1329
Q00519	Exosome	YTLLR	NKPEPTVEEIENAFQGNLCR	CTGYR	2	C19:+57.021	1173.063447	2344.111293	0.000451244	31	N	131	151
Q00519	Exosome	YTLLR	NKPEPTVEEIENAFQGNLCR	CTGYR	3	C19:+57.021	782.3782311	2344.111293	0.000451244	28	N	131	151
Q00519	Exosome	IPTSK	IHITETSTNTVPNTSPTAASASADLNGQAIYEACQTILK	RLEPF	3	C34:+57.021	1363.674585	4088.000354	0.000451244	74	N	1063	1102
Q00519	Exosome	IPTSK	IHITETSTNTVPNTSPTAASASADLNGQAIYEACQTILK	RLEPF	4	C34:+57.021	1023.007888	4088.000354	0.002453667	1	N	1063	1102
Q00519	Exosome	GKETR	STLISTAVALAAYK	TGRPV	2		704.9064638	1407.797328	0.000451244	36	N	807	821
Q00519	Exosome	GKETR	STLISTAVALAAYK	TGRPV	3		470.2735759	1407.797328	0.000451244	6	N	807	821
Q00519	Exosome	KVVEK	NADPETTLLVYLR	RKLGL	2		752.9044524	1503.793305	0.000451244	39	N	21	34
Q00519	Exosome	KVVEK	NADPETTLLVYLR	RKLGL	3		502.272235	1503.793305	0.002981883	1	N	21	34
Q00519	Exosome	GMCGK	LDPTFASATLLFQK	DPPAN	2		776.4250207	1550.834441	0.000451244	25	N	540	554
Q00519	Exosome	GMCGK	LDPTFASATLLFQK	DPPAN	3		517.9526138	1550.834441	0.000451244	11	N	540	554
Q00519	Exosome	GMCGK	LDPTFASATLLFQKDPPANVQLFQEVPK	GQSEE	3		1038.889045	3113.643735	0.000451244	35	N	540	568
Q00519	Exosome	ARGVK	ITYEDLPAIITIQDAIK	NNSFY	2		959.0331211	1916.050642	0.000451244	38	N	689	706
Q00519	Exosome	ARGVK	ITYEDLPAIITIQDAIK	NNSFY	3		639.6913474	1916.050642	0.000451244	30	N	689	706
Q00519	Exosome	TGFYK	TPNLGYSFETNSGNPFHYFSYGVACSEVEIDCLTGDHK	NLRTD	3	C25:+57.021,C32:+57.021	1438.300487	4311.878061	0.0007646	3	N	1137	1175
Q00519	Exosome	TGFYK	TPNLGYSFETNSGNPFHYFSYGVACSEVEIDCLTGDHK	NLRTD	4	C25:+57.021,C32:+57.021	1078.977315	4311.878061	0.000451244	26	N	1137	1175
Q00519	Exosome	TSEAK	KVPGFVCFLTSEDVPGSNITGIFNDETVFAK	DEVTC	3	C7:+57.021	1130.230877	3387.66923	0.000451244	26	N	629	660
Q00519	Exosome	IYASK	AVGEPPLFLASSIFFAIK	DAIRA	2		954.0380094	1906.060419	0.000451244	25	N	1260	1278
Q00519	Exosome	IYASK	AVGEPPLFLASSIFFAIK	DAIRA	3		636.361273	1906.060419	0.002727428	1	N	1260	1278
Q00519	Exosome	KAVGE	PPLFLASSIFFAIK	DAIRA	2		775.953217	1549.890834	0.001162105	2	N	1264	1278
Q00519	Exosome	PSTYK	IPAFGSIPIEFR	VSLLR	2		673.8775093	1345.739419	0.000451244	28	N	1231	1243
Q00519	Exosome	FEGER	VTWIQVSTMEELLDLK	AQHPD	2		953.0060496	1903.996499	0.000451244	4	N	235	251
Q00519	Exosome	PGYRR	TLLSPEEILVSIVIPY	SRKGE	2		893.5165755	1785.017551	0.000637154	2	N	397	413
Q00519	Exosome	LLFQK	DPPANVQLFQEVPK	GQSEE	2		791.417727	1580.819854	0.000698008	8	N	554	568
Q00519	Exosome	FTLPR	CWDECIASSQYQAR	KMEVE	2	C1:+57.021,C5:+57.021	887.3696622	1772.723724	0.000451244	22	N	969	983
Q00519	Exosome	FTLPR	CWDECIASSQYQAR	KMEVE	2	[0:-17.027,C1:+57.021,C5:+57.021	878.8561622	1755.696724	0.000451244	8	N	969	983
Q00519	Exosome	VGFMK	TGTIVALEVAHFSNGGNSEDLSR	SIMER	2		1187.585832	2373.156064	0.000451244	16	N	855	878
Q00519	Exosome	VGFMK	TGTIVALEVAHFSNGGNSEDLSR	SIMER	3		792.0598212	2373.156064	0.000451244	10	N	855	878
Q00519	Exosome	-MTR	TTVDELVFFVNGK	KVVEK	2		734.888271	1467.760942	0.000451244	12	N	3	16
Q00519	Exosome	KQLSK	SWNEELLQDVCAGLAEELHLAPDAPGGMVEFR	RTLTL	3	C11:+57.021	1185.22943	3552.664891	0.000451244	3	N	478	510
Q00519	Exosome	TVFAK	DEVTCVGHIIGAVVADTPEHAHR	AARGV	4	C5:+57.021	621.5582599	2482.20184	0.000451244	7	N	660	683
Q00519	Exosome	GNLCR	CTGYRPILQGFR	TFAKD	3	C1:+57.021	489.9227288	1466.744786	0.001699387	9	N	151	163
Q00519	Exosome	DSNAK	QLFQLDSPATPEK	IRNAC	2		737.3833528	1472.751106	0.000451244	21	N	1294	1307
Q00519	Exosome	IPTSK	IHITETSTNTVPNTSPTAASASADLNGQAIYEACQTILKR	LEPFK	4	C34:+57.021	1062.033166	4244.101465	0.000451244	9	N	1063	1103
Q00519	Exosome	AACPL	SLVESVLADAIATLPEQR	TEVFR	3		638.0182346	1911.031304	0.000662267	2	N	307	325
Q00519	Parental	MSQTK	DQTIAPSSSLFNPEDFKPLDPTQEPIFPPELLR	LKDTP	3		1246.968752	3737.882857	0.000451244	44	N	187	220
Q00519	Parental	MSQTK	DQTIAPSSSLFNPEDFKPLDPTQEPIFPPELLR	LKDTP	4		935.4785141	3737.882857	0.002296037	1	N	187	220

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q00519	Parental	PGYRR	TLLSPEEILVSIVIPYSR	KGEFF	2		1015.083145	2028.150691	0.000451244	7	N	397	415
Q00519	Parental	PGYRR	TLLSPEEILVSIVIPYSR	KGEFF	3		677.0580302	2028.150691	0.000451244	22	N	397	415
Q00519	Parental	PEKIR	NACVDQFTTLCATGTPENCK	SWSVR	2	C3:+57.021,C11:+57.021,C19:+57.021	1143.992855	2285.970111	0.000451244	5	N	1309	1329
Q00519	Parental	IPTSK	IHITETSTNTVPNTSPTAASASADLNGQAIYEACQTILK	RLEPF	3	C34:+57.021	1363.674585	4088.000354	0.000451244	9	N	1063	1102
Q00519	Parental	GMCGK	LDPTFASATLLFQK	DPPAN	2		776.4250207	1550.834441	0.000451244	5	N	540	554
Q00519	Parental	GMCGK	LDPTFASATLLFQK	DPPAN	3		517.9526138	1550.834441	0.000622848	1	N	540	554
Q00519	Parental	GMCGK	LDPTFASATLLFQKDPPANVQLFQEVPK	GQSEE	3		1038.889045	3113.643735	0.000451244	8	N	540	568
Q00519	Parental	ARGVK	ITYEDLPAIITIQDAIK	NNSFY	2		959.0331211	1916.050642	0.000823681	3	N	689	706
Q00519	Parental	ARGVK	ITYEDLPAIITIQDAIK	NNSFY	3		639.6913474	1916.050642	0.000451244	9	N	689	706
Q00519	Parental	TGFYK	TPNLGYSFETNSGNPFHYFSYGVACSEVEIDCLTGDHK	NLRTD	4	C25:+57.021,C32:+57.021	1078.977315	4311.878061	0.000451244	7	N	1137	1175
Q00519	Parental	TSEAK	KVPGFVCFLTSEDVPGSNITGIFNDETVFAK	DEVTC	3	C7:+57.021	1130.230877	3387.66923	0.000622848	2	N	629	660
Q00519	Parental	IYASK	AVGEPPLFLASSIFFAIK	DAIRA	2		954.0380094	1906.060419	0.001329271	2	N	1260	1278
Q00519	Parental	ARGVK	ITYEDLPAIITIQDAIKNNSFYGPEVK	IEKGD	3		1018.201289	3051.580466	0.000622848	3	N	689	716
Q00519	Parental	VGFMK	TGTIVALEVAHFSNGGNSEDLSR	SIMER	3		792.0598212	2373.156064	0.000698008	1	N	855	878
Q00612	Exosome	HKIDR	EKPQPIPYVYGSR	GPTEA	2		767.4071623	1532.798725	0.000451244	22	N	474	487
Q00612	Exosome	HKIDR	EKPQPIPYVYGSR	GPTEA	3		511.9407082	1532.798725	0.000662267	14	N	474	487
Q00612	Exosome	EFFAR	NSYVAGQYDDAASYK	HLNSH	2		826.3658884	1650.716177	0.000451244	73	N	104	119
Q00612	Exosome	IWWLF	RDGLLPEDTFIVGYAR	SRLTV	3		607.9884982	1820.942095	0.000451244	10	N	56	72
Q00612	Exosome	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	3		917.4551224	2749.341967	0.000451244	18	Y	175	198
Q00612	Exosome	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	4		688.3432918	2749.341967	0.000451244	7	Y	175	198
Q00612	Exosome	GTEGR	GGYFDEFGIIR	DVMQN	2		637.3147418	1272.613884	0.000451244	33	Y	246	257
Q00612	Exosome	WWLFR	DGLLPEDTFIVGYAR	SRLTV	2		833.4282917	1664.840983	0.000451244	42	N	57	72
Q00612	Exosome	WWLFR	DGLLPEDTFIVGYAR	SRLTV	3		555.9547945	1664.840983	0.000451244	25	N	57	72
Q00612	Exosome	PIWNR	DNIACVILTFKEPFGTEGR	GGYFD	2	C5:+57.021	1084.046537	2166.077474	0.000451244	40	Y	227	246
Q00612	Exosome	PIWNR	DNIACVILTFKEPFGTEGR	GGYFD	3	C5:+57.021	723.0336246	2166.077474	0.000451244	52	Y	227	246
Q00612	Exosome	DLAKK	KIYPTIWWLFR	DGLLP	3		508.2910126	1521.849638	0.001162105	7	Y	46	57
Q00612	Exosome	LAKKK	IYPTIWWLFR	DGLLP	2		697.8851373	1393.754675	0.000451244	37	Y	47	57
Q00612	Exosome	MQANR	LFYLALPPTVYEAVTK	NIQET	2		913.0114603	1824.007321	0.000451244	23	Y	136	152
Q00612	Exosome	MQANR	LFYLALPPTVYEAVTK	NIQET	3		609.0102402	1824.007321	0.000451244	26	Y	136	152
Q00612	Exosome	EAVTK	NIQETCMSQTGWNR	IIVEK	2	C6:+57.021,M7:+15.995	870.8753863	1739.735173	0.000451244	5	N	152	166
Q00612	Exosome	RLQFR	DVAGDIFHQQCK	RNELV	2	C11:+57.021	709.330366	1416.645132	0.000451244	12	N	374	386
Q00612	Exosome	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	2		973.4904747	1944.965349	0.000451244	39	Y	175	192
Q00612	Exosome	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	3		649.3295831	1944.965349	0.000451244	18	Y	175	192
Q00612	Exosome	PIWNR	DNIACVILTFK	EPFGT	2	C5:+57.021	647.3474961	1292.679392	0.000451244	5	Y	227	238
Q00612	Exosome	KMMTK	KPGMFFNPEESELDLTYGNR	YKNVK	2		1172.549873	2343.084145	0.001763695	1	N	407	427
Q00612	Exosome	KMMTK	KPGMFFNPEESELDLTYGNR	YKNVK	2	M4:+15.995	1180.547373	2359.079145	0.000451244	18	N	407	427
Q00612	Exosome	KMMTK	KPGMFFNPEESELDLTYGNR	YKNVK	3	M4:+15.995	787.3675151	2359.079145	0.000451244	23	N	407	427
Q00612	Exosome	RDGLL	PEDTFIVGYAR	SRLTV	2		634.3200242	1266.624448	0.001463592	1	N	61	72
Q00612	Exosome	FRDGL	LPEDTFIVGYAR	SRLTV	2		690.8620562	1379.708512	0.001162105	3	N	60	72
Q00612	Exosome	ELMKR	VGFQYEGTYK	WVNPH	2		596.2881927	1190.560785	0.000622848	8	N	498	508
Q00612	Exosome	PIWNR	DNIACVILTF	KEPFG	2	C5:+57.021	583.3000145	1164.584429	0.000622848	9	Y	227	237
Q00612	Exosome	TFAAA	VLYVENERWDGVPFILR	CGKAL	3		702.3779857	2104.110557	0.000823681	3	N	340	357
Q00612	Exosome	TATFA	AAVLYVENERWDGVPFILR	CGKAL	3		749.7360616	2246.184785	0.000622848	2	N	338	357
Q00612	Exosome	TTATF	AAAVLYVENERWDGVPFILR	CGKAL	3		773.4150995	2317.221899	0.000451244	12	N	337	357
Q00612	Exosome	ATFAA	AVLYVENERWDGVPFILR	CGKAL	3		726.0570236	2175.147671	0.000451244	1	N	339	357
Q00612	Exosome	VKVLK	CISEVETDNVVLGQYVGNPNGEGE	AANGY	2	C1:+57.021	1290.08223	2578.148861	0.000451244	3	N	293	317
Q00612	Exosome	KPFGR	DLQSSNQLSNHISSLF	REDQI	2		895.4399191	1788.864238	0.000451244	6	Y	175	191
Q00612	Exosome	EFFAR	NSYVAGQYDDAASY	KHLNS	2		762.3184068	1522.621214	0.002813207	1	N	104	118
Q00612	Exosome	VENER	WDGVPFILR	CGKAL	2		551.8063556	1101.597111	0.000735798	2	Y	348	357
Q00612	Exosome	WWLFR	DGLLPEDTFIVGY	ARSRL	2		719.8591792	1437.702758	0.001943752	1	N	57	70
Q00612	Parental	HKIDR	EKPQPIPYVYGSR	GPTEA	2		767.4071623	1532.798725	0.000451244	13	N	474	487
Q00612	Parental	HKIDR	EKPQPIPYVYGSR	GPTEA	3		511.9407082	1532.798725	0.00091018	8	N	474	487
Q00612	Parental	EFFAR	NSYVAGQYDDAASYK	HLNSH	2		826.3658884	1650.716177	0.000451244	80	N	104	119
Q00612	Parental	KAEVR	LQFRDVAGDIFHQQCK	RNELV	3	C15:+57.021	654.6602329	1960.957299	0.000451244	3	N	370	386
Q00612	Parental	KAEVR	LQFRDVAGDIFHQQCK	RNELV	4	C15:+57.021	491.2471247	1960.957299	0.000451244	5	N	370	386
Q00612	Parental	IWWLF	RDGLLPEDTFIVGYAR	SRLTV	2		911.4788473	1820.942095	0.000451244	14	N	56	72
Q00612	Parental	IWWLF	RDGLLPEDTFIVGYAR	SRLTV	3		607.9884982	1820.942095	0.000451244	15	N	56	72
Q00612	Parental	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	3		917.4551224	2749.341967	0.000451244	14	Y	175	198
Q00612	Parental	KPFGR	DLQSSNQLSNHISSLFREDQIYR	IDHYL	4		688.3432918	2749.341967	0.001463592	2	Y	175	198
Q00612	Parental	GTEGR	GGYFDEFGIIR	DVMQN	2		637.3147418	1272.613884	0.000451244	15	Y	246	257
Q00612	Parental	WWLFR	DGLLPEDTFIVGYAR	SRLTV	2		833.4282917	1664.840983	0.000451244	33	N	57	72
Q00612	Parental	WWLFR	DGLLPEDTFIVGYAR	SRLTV	3		555.9547945	1664.840983	0.000451244	17	N	57	72
Q00612	Parental	PIWNR	DNIACVILTFKEPFGTEGR	GGYFD	2	C5:+57.021	1084.046537	2166.077474	0.000451244	19	Y	227	246
Q00612	Parental	PIWNR	DNIACVILTFKEPFGTEGR	GGYFD	3	C5:+57.021	723.0336246	2166.077474	0.000451244	37	Y	227	246

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q00612	Parental	DLAKK	KIYPTIWWLFR	DGLLP	3		508.2910126	1521.849638	0.001162105	12	Y	46	57
Q00612	Parental	LAKKK	IYPTIWWLFR	DGLLP	2		697.8851373	1393.754675	0.000451244	26	Y	47	57
Q00612	Parental	EPFFK	ATPEERPKLEEFFAR	NSYVA	3		607.3166148	1818.926444	0.001463592	1	N	89	104
Q00612	Parental	MQANR	LFYLALPPTVYEAVTK	NIQET	2		913.0114603	1824.007321	0.000622848	9	Y	136	152
Q00612	Parental	MQANR	LFYLALPPTVYEAVTK	NIQET	3		609.0102402	1824.007321	0.001229886	8	Y	136	152
Q00612	Parental	LAKKK	IYPTIWWLFRDGLLPEDTFIVGYAR	SRLTV	3		1014.536166	3040.585098	0.002212458	2	N	47	72
Q00612	Parental	EAVTK	NIQETCMSQTGWNR	IIVEK	2	C6:+57.021	862.8778863	1723.740173	0.000451244	10	N	152	166
Q00612	Parental	RLQFR	DVAGDIFHQQCK	RNELV	2	C11:+57.021	709.330366	1416.645132	0.000698008	29	N	374	386
Q00612	Parental	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	2		973.4904747	1944.965349	0.000451244	21	Y	175	192
Q00612	Parental	KPFGR	DLQSSNQLSNHISSLFR	EDQIY	3		649.3295831	1944.965349	0.000451244	14	Y	175	192
Q00612	Parental	PIWNR	DNIACVILTFK	EPFGT	2	C5:+57.021	647.3474961	1292.679392	0.000451244	6	Y	227	238
Q00612	Parental	RDGLL	PEDTFIVGYAR	SRLTV	2		634.3200242	1266.624448	0.002080925	1	N	61	72
Q00612	Parental	FRDGL	LPEDTFIVGYAR	SRLTV	2		690.8620562	1379.708512	0.00307782	1	N	60	72
Q00612	Parental	ELMKR	VGFQYEGTYK	WVNPH	2		596.2881927	1190.560785	0.00307782	1	N	498	508
Q00612	Parental	PIWNR	DNIACVILTF	KEPFG	2	C5:+57.021	583.3000145	1164.584429	0.000451244	4	Y	227	237
Q00612	Parental	FYLAL	PPTVYEAVTK	NIQET	2		552.8009359	1103.586272	0.001162105	2	Y	142	152
Q00612	Parental	ANRLF	YLALPPTVYEAVTK	NIQET	2		782.9352213	1563.854843	0.002019181	1	Y	138	152
Q00612	Parental	KPFGR	DLQSSNQLSNHISSLF	REDQI	2		895.4399191	1788.864238	0.000823681	5	Y	175	191
Q00623	Exosome	KDSGR	DYVSQFESSSLGQQLNLNLLENWDTLGSTVSQLQER	LGPLT	3		1367.001732	4097.981796	0.000451244	12	N	50	86
Q00623	Exosome	GPLTR	DFWDNLEKETDWVR	QEMNK	3		618.2887248	1851.842774	0.000451244	3	N	92	106
Q00623	Parental	VDAVK	DSGRDYVSQFESSSLGQQLNLNLLENWDTLGSTVSQLQER	LGPLT	4		1129.298636	4513.163342	0.000823681	7	N	46	86
Q00623	Parental	KDSGR	DYVSQFESSSLGQQLNLNLLENWDTLGSTVSQLQER	LGPLT	3		1367.001732	4097.981796	0.000451244	14	N	50	86
Q00623	Parental	GPLTR	DFWDNLEKETDWVR	QEMNK	3		618.2887248	1851.842774	0.001871652	5	N	92	106
Q00623	Parental	EVKQK	VQPYLDEFQK	KWKED	2		633.8223997	1265.629199	0.001463592	2	N	119	129
Q00896	Exosome	LGITR	IFNNGADLSGITEENAPLK	LSQAV	2		1002.008166	2002.000732	0.000451244	4	Y	328	347
Q00896	Exosome	VEAVK	KLDQDTVFALANYILFK	GKWKK	3		667.035337	1998.082611	0.000451244	2	N	192	209
Q00896	Exosome	PPILR	FDHPFLFIIFEEHTQSPLFVGK	VVDPT	4		662.8446733	2647.347493	0.000823681	1	N	384	406
Q00896	Parental	PSFLA	EDVQETDTSQKDQSPASHEIATNLGDFAISLYR	ELVHQ	3		1222.578764	3664.712891	0.000451244	8	Y	24	57
Q00896	Parental	LGITR	IFNNGADLSGITEENAPLK	LSQAV	2		1002.008166	2002.000732	0.000451244	15	Y	328	347
Q00896	Parental	VEAVK	KLDQDTVFALANYILFK	GKWKK	3		667.035337	1998.082611	0.001352548	1	N	192	209
Q00896	Parental	LEEAK	NHYQAEVFSVNFAESEEAKK	VINDF	3		776.3699956	2326.086587	0.000451244	9	Y	153	173
Q00896	Parental	ADIHK	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	LVEKF	3		1166.937898	3497.790293	0.000451244	10	Y	112	143
Q00896	Parental	ADIHK	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	LVEKF	4		875.4553733	3497.790293	0.000451244	9	Y	112	143
Q00PI9	Exosome	HVLCK	NCVVELNFGQKEEPFFPPPEEFVFIHAVPVEER	VRTAV	4	C2:+57.021	983.2360456	3928.912983	0.000451244	13	N	404	437
Q00PI9	Parental	EMDPK	SRDLLVQQASQCLSK	LVQIA	2	C12:+57.021	866.9544507	1731.893301	0.000451244	9	N	504	519
Q00PI9	Parental	EMDPK	SRDLLVQQASQCLSK	LVQIA	3	C12:+57.021	578.3055672	1731.893301	0.000451244	5	N	504	519
Q00PI9	Parental	HVLCK	NCVVELNFGQKEEPFFPPPEEFVFIHAVPVEER	VRTAV	3	C2:+57.021	1310.645461	3928.912983	0.000451244	20	N	404	437
Q00PI9	Parental	HVLCK	NCVVELNFGQKEEPFFPPPEEFVFIHAVPVEER	VRTAV	4	C2:+57.021	983.2360456	3928.912983	0.000451244	35	N	404	437
Q00PI9	Parental	DPKSR	DLLVQQASQCLSK	LVQIA	2	C10:+57.021	745.3878809	1488.760162	0.000451244	6	N	506	519
Q00PI9	Parental	ISKDR	YGGQPLFSEKFPTLWSGAR	STYGV	3		714.3658572	2140.074172	0.000451244	2	N	261	280
Q00PI9	Parental	HVLCK	NCVVELNFGQK	EEPFF	2	C2:+57.021	654.3245523	1306.633505	0.0007646	1	N	404	415
Q00PI9	Parental	NFGQK	EEPFFPPPEEFVFIHAVPVEER	VRTAV	3		881.1044793	2640.290038	0.000451244	4	N	415	437
Q00PI9	Parental	GRGLK	AENGQFEEFGQTFGENDVIGCFANFETEEVELSFSK	NGEDL	3	C21:+57.021	1369.269224	4104.784273	0.000622848	4	N	340	376
Q00PI9	Parental	SRSKR	NFILDQCNVYNSGQR	RKLLL	2	C7:+57.021	914.4260574	1826.836515	0.000451244	4	N	529	544
Q00PI9	Parental	TFSRK	VVVVVPNEEDWKR	RLELR	3		523.6197461	1567.835838	0.000451244	6	N	556	569
Q01102	Exosome	GFVLK	GNDAIQCADSGQWTAPAPFCEALQCPEFPVPSK	AQVNC	3	C7:+57.021,C20:+57.021,C25:+57.021	1216.877983	3647.610548	0.000451244	18	N	361	394
Q01102	Exosome	NSTYK	STCQFMCDEGFYLSGPER	LDCSP	2	C3:+57.021,M6:+15.995,C7:+57.02	1100.442742	2198.869883	0.000451244	8	N	471	489
Q01102	Exosome	VGTNK	TLTEEAENWADNEPNNKK	NNQDC	3		701.6595461	2101.955238	0.000451244	3	N	108	126
Q01102	Parental	GFVLK	GNDAIQCADSGQWTAPAPFCEALQCPEFPVPSK	AQVNC	3	C7:+57.021,C20:+57.021,C25:+57.021	1216.877983	3647.610548	0.000451244	12	N	361	394
Q01102	Parental	SGPER	LDCSPSGHWTGTPPTCEAIK	CPGIF	3	C3:+57.021,C16:+57.021	738.6702033	2212.98721	0.000662267	5	N	489	509
Q01320	Exosome	PGLYK	IFDEILVNAADNK	QRDPK	2		731.3833528	1460.751106	0.000622848	2	Y	82	95
Q01320	Exosome	LLRHR	FLEEFITPIVK	VSKNK	2		668.3820932	1334.748586	0.0025889	2	Y	567	578
Q01320	Exosome	EKFIK	AAIGCGIVESILNWVK	FKAQI	2	C5:+57.021	865.4692053	1728.922811	0.000451244	1	N	399	415
Q01320	Parental	KIRKK	IKSENVEGTPAEDGAEPGSLR	QRIEK	3		719.3542341	2155.039302	0.000622848	18	N	1236	1257
Q01320	Parental	RKKIK	SENVEGTPAEDGAEPGSLR	QRIEK	2		957.9379376	1913.860275	0.000451244	21	N	1238	1257
Q01320	Parental	EKFIK	AAIGCGIVESILNWVKF	KAQIQ	2	C5:+57.021	939.0034123	1875.991225	0.000622848	3	N	399	416
Q01320	Parental	SKKAK	GEEQDFPVDLEDTIAPR	AKSDR	2		965.955599	1929.895598	0.000622848	4	N	1488	1505
Q01320	Parental	PGLYK	IFDEILVNAADNK	QRDPK	2		731.3833528	1460.751106	0.000451244	7	Y	82	95
Q01339	Exosome	AIAGR	ICPKPDDLPFATVVPLK	TSYDP	3	C2:+57.021	637.3537469	1909.037841	0.000451244	14	N	21	38
Q01339	Exosome	LYKDK	ATFGCHETYKLDGPEEAECTK	TGTWS	3	C5:+57.021,C19:+57.021	815.0230824	2442.045847	0.000451244	6	N	229	250
Q01339	Exosome	RCVPR	VCPFAGILENGIVR	YTSFE	3	C2:+57.021	515.6136724	1543.817617	0.001654178	1	N	82	96
Q01339	Exosome	GGMRR	FTCPLTGMWPINTLR	CVPRV	2	C3:+57.021,M8:+15.995	911.9529084	1821.890217	0.002727428	1	N	63	78
Q01339	Exosome	TSSSK	CTEEGKWSPDIPACAR	ITCPP	3	C1:+57.021,C14:+57.021	626.2822795	1875.823439	0.000823681	1	N	123	139

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q01339	Exosome	VVPLK	TSYDPGEQIVYSCKPGYVSR	GGMRR	3	C13:+57.021	769.3638105	2305.068031	0.002145581	1	N	38	58
Q01514	Exosome	LIKSK	SSPDQSDVDNSANFVGFFPIFVWTLR	DFSLD	3		982.4755235	2944.403171	0.000451244	20	N	155	181
Q01514	Exosome	QEALR	ILSAITQPVVVVAIVGLYR	TGKSY	2		1006.119865	2010.22413	0.000698008	1	N	29	48
Q01514	Exosome	QEALR	ILSAITQPVVVVAIVGLYR	TGKSY	3		671.0825101	2010.22413	0.000662267	3	N	29	48
Q01514	Parental	LIKSK	SSPDQSDVDNSANFVGFFPIFVWTLR	DFSLD	3		982.4755235	2944.403171	0.000622848	4	N	155	181
Q01853	Exosome	GKKRR	EAVCIVLSDDTCSDEKIR	MNRVV	2	C4:+57.021,C12:+57.021	1055.493246	2108.970891	0.000451244	31	N	65	83
Q01853	Exosome	GKKRR	EAVCIVLSDDTCSDEKIR	MNRVV	3	C4:+57.021,C12:+57.021	703.998097	2108.970891	0.002145581	2	N	65	83
Q01853	Exosome	TLLAK	AIANECQANFISIK	GPELL	2	C6:+57.021	789.9011555	1577.786711	0.000451244	68	N	529	543
Q01853	Exosome	NLRVR	LGDVISIQPCPDVK	YGKRI	2	C10:+57.021	770.9059065	1539.796213	0.000451244	66	N	95	109
Q01853	Exosome	RNNLR	VRLGDVISIQPCPDVK	YGKRI	2	C12:+57.021	898.4906691	1794.965738	0.000451244	7	N	93	109
Q01853	Exosome	RNNLR	VRLGDVISIQPCPDVK	YGKRI	3	C12:+57.021	599.3297127	1794.965738	0.000451244	3	N	93	109
Q01853	Exosome	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	2		1106.586583	2211.157567	0.000451244	34	N	487	505
Q01853	Exosome	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	3		738.0603223	2211.157567	0.000451244	33	N	487	505
Q01853	Exosome	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	4		553.7971917	2211.157567	0.000451244	39	N	487	505
Q01853	Exosome	NRPNR	LIVDEAINEDNSVVSLSQPK	MDELQ	2		1085.566045	2169.11649	0.000451244	66	N	25	45
Q01853	Exosome	NRPNR	LIVDEAINEDNSVVSLSQPK	MDELQ	3		724.04663	2169.11649	0.000451244	47	N	25	45
Q01853	Exosome	SPVAK	DVDLEFLAK	MTNGF	2		525.2798363	1048.544073	0.000451244	33	N	668	677
Q01853	Exosome	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	2		1159.639879	2317.264158	0.000451244	11	N	365	386
Q01853	Exosome	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	3		773.4291858	2317.264158	0.000451244	24	N	365	386
Q01853	Exosome	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	4		580.3238394	2317.264158	0.000662267	21	N	365	386
Q01853	Exosome	LSQPK	MDELQLFRGDTVLLK	GKKRR	3		593.3226013	1776.944404	0.001162105	1	N	45	60
Q01853	Exosome	PSALR	ETVVEVPQVTWEDIGGLEDVKR	ELQEL	2		1249.642815	2497.270031	0.000451244	30	N	465	487
Q01853	Exosome	PSALR	ETVVEVPQVTWEDIGGLEDVKR	ELQEL	3		833.4311436	2497.270031	0.000451244	43	N	465	487
Q01853	Exosome	PSALR	ETVVEVPQVTWEDIGGLEDVKR	ELQEL	4		625.3253077	2497.270031	0.000451244	4	N	465	487
Q01853	Exosome	LRPGR	LDQLIYIPLPDEK	SRVAI	2		778.9326786	1555.849757	0.000823681	16	N	638	651
Q01853	Exosome	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	KKMDL	3	C26:+57.021	1224.935963	3671.784488	0.000451244	52	N	389	424
Q01853	Exosome	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	KKMDL	4	C26:+57.021	918.9539219	3671.784488	0.000998612	5	N	389	424
Q01853	Exosome	EVERR	IVSQLLTLMDGLK	QRAHV	2		715.9185175	1429.821435	0.000451244	35	N	323	336
Q01853	Exosome	EVERR	IVSQLLTLMDGLK	QRAHV	3		477.614945	1429.821435	0.0025889	1	N	323	336
Q01853	Exosome	EEAEK	NAPAIIFIDELDAIAPKR	EKTHG	2		984.0521795	1966.088759	0.000451244	17	N	295	313
Q01853	Exosome	EEAEK	NAPAIIFIDELDAIAPKR	EKTHG	3		656.3707197	1966.088759	0.000451244	19	N	295	313
Q01853	Exosome	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	C5:+57.021	962.4799671	1922.944334	0.000451244	60	N	567	584
Q01853	Exosome	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	3	C5:+57.021	641.9892447	1922.944334	0.000451244	57	N	567	584
Q01853	Exosome	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	Q1:-17.027,C5:+57.021	953.9664671	1905.917334	0.000622848	22	N	567	584
Q01853	Exosome	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	[0:-17.027,C5:+57.021	953.9664671	1905.917334	0.0007646	7	N	567	584
Q01853	Exosome	TLIAR	AVANETGAFFFLINGPEIMSK	LAGES	2		1128.572619	2255.129639	0.000451244	25	N	256	277
Q01853	Exosome	TLIAR	AVANETGAFFFLINGPEIMSK	LAGES	3		752.7176796	2255.129639	0.000451244	3	N	256	277
Q01853	Exosome	SNLRK	AFEEAEKNAPAIIFIDELDAIAPK	REKTH	2		1308.184316	2614.353032	0.000451244	4	N	288	312
Q01853	Exosome	SNLRK	AFEEAEKNAPAIIFIDELDAIAPK	REKTH	3		872.4588108	2614.353032	0.000451244	29	N	288	312
Q01853	Exosome	EEAEK	NAPAIIFIDELDAIAPK	REKTH	2		906.0016239	1809.987648	0.000451244	96	N	295	312
Q01853	Exosome	EEAEK	NAPAIIFIDELDAIAPK	REKTH	3		604.3370159	1809.987648	0.000451244	79	N	295	312
Q01853	Exosome	EPIKR	EDEEESLNEVGYDDIGGCRK	QLAQI	2	C18:+57.021	1157.492717	2312.969834	0.000451244	14	N	191	211
Q01853	Exosome	EPIKR	EDEEESLNEVGYDDIGGCRK	QLAQI	3	C18:+57.021	771.9977445	2312.969834	0.000451244	21	N	191	211
Q01853	Exosome	VKPPR	GILLYGPPGTGK	TLIAR	2		586.8378528	1171.660106	0.000451244	11	N	239	251
Q01853	Exosome	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIRK	KMDLI	3	C26:+57.021	1267.634284	3799.879451	0.000451244	1	N	389	425
Q01853	Exosome	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIRK	KMDLI	4	C26:+57.021	950.9776627	3799.879451	0.000451244	7	N	389	425
Q01853	Exosome	KYGKR	IHVLPIDDTVEGITGNLFEVY	LKPYF	2		1172.607713	2343.199826	0.000451244	8	N	113	134
Q01853	Exosome	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIR	KGDIF	3		1331.05097	3990.12951	0.000451244	7	N	113	147
Q01853	Exosome	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIR	KGDIF	4		998.5401774	3990.12951	0.000451244	28	N	113	147
Q01853	Exosome	MDDFR	WALSQSNPSALR	ETVVE	2		665.3496473	1328.683695	0.000662267	28	N	453	465
Q01853	Exosome	EDVKR	ELQELVQYPVEHPDK	FLKFG	2		912.4628629	1822.910126	0.000451244	15	N	487	502
Q01853	Exosome	EDVKR	ELQELVQYPVEHPDK	FLKFG	3		608.6445086	1822.910126	0.000451244	35	N	487	502
Q01853	Exosome	GKKRR	EAVCIVLSDDTCSDEK	IRMNR	2	C4:+57.021,C12:+57.021	920.9006579	1839.785716	0.000451244	37	N	65	81
Q01853	Exosome	RERER	QTNPSAMEVEEDDPVPEIR	RDHFE	2		1078.494763	2154.973926	0.000451244	5	N	713	732
Q01853	Exosome	RERER	QTNPSAMEVEEDDPVPEIR	RDHFE	2	M7:+15.995	1086.492263	2170.968926	0.000451244	28	N	713	732
Q01853	Exosome	AVEFK	VVETDPSPYCIVAPDTVIHCEGEPIKR	EDEEE	3	C10:+57.021,C20:+57.021	1027.83906	3080.493779	0.000451244	38	N	164	191
Q01853	Exosome	AVEFK	VVETDPSPYCIVAPDTVIHCEGEPIKR	EDEEE	4	C10:+57.021,C20:+57.021	771.1312448	3080.493779	0.000451244	28	N	164	191
Q01853	Exosome	MSTKK	NVFIIGATNRPDIIDPAILRPGR	LDQLI	3		840.1471243	2517.417973	0.000451244	25	N	615	638
Q01853	Exosome	MSTKK	NVFIIGATNRPDIIDPAILRPGR	LDQLI	4		630.3622932	2517.417973	0.001162105	3	N	615	638
Q01853	Exosome	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPY	FLEAY	3		949.1727819	2844.494946	0.000622848	4	N	113	138
Q01853	Exosome	EFLAK	MTNGFSGADLTEICQR	ACKLA	2	C14:+57.021	900.4064766	1798.797353	0.000451244	8	N	677	693
Q01853	Exosome	EFLAK	MTNGFSGADLTEICQR	ACKLA	2	M1:+15.995,C14:+57.021	908.4039766	1814.792353	0.000451244	32	N	677	693
Q01853	Exosome	EPIKR	EDEEESLNEVGYDDIGGCR	KQLAQ	2	C18:+57.021	1093.445235	2184.87487	0.000451244	32	N	191	210
Q01853	Exosome	PSALR	ETVVEVPQVTWEDIGGLEDVK	RELQE	2		1171.59226	2341.16892	0.000451244	6	N	465	486
Q01853	Exosome	RRFGR	FDREVDIGIPDATGR	LEILQ	2		830.9186225	1659.821645	0.000451244	7	N	362	377

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q01853	Exosome	QAAPC	VLFFDELDSIAK	ARGGN	2		698.8720896	1395.728579	0.000662267	8	N	572	584
Q01853	Exosome	AVEFK	VVETDPSPYCIVAPDTVIHCEGEPIK	REDEE	3	C10:+57.021,C20:+57.021	975.8053561	2924.392668	0.000662267	2	N	164	190
Q01853	Exosome	AEKNA	PAIIFIDELDAIAPK	REKTH	2		813.4616032	1624.907606	0.000451244	11	N	297	312
Q01853	Exosome	DNDIR	KYEMFAQTLQQSR	GFGSF	2	M4:+15.995	823.4043369	1644.793074	0.000622848	14	N	753	766
Q01853	Exosome	DNDIR	KYEMFAQTLQQSR	GFGSF	3	M4:+15.995	549.2721579	1644.793074	0.001943752	3	N	753	766
Q01853	Exosome	RERER	QTNPSAMEVEEDDPVPEIRR	DHFEE	3	M7:+15.995	776.6978124	2327.070037	0.000451244	22	N	713	733
Q01853	Exosome	GMSTK	KNVFIIGATNRPDIIDPAILRPGR	LDQLI	3		882.8454453	2645.512936	0.00091018	8	N	614	638
Q01853	Exosome	GMSTK	KNVFIIGATNRPDIIDPAILRPGR	LDQLI	4		662.386034	2645.512936	0.000451244	5	N	614	638
Q01853	Exosome	FISIK	GPELLTMWFGESEANVR	EIFDK	2	M7:+15.995	976.4651229	1950.914646	0.000451244	11	N	543	560
Q01853	Exosome	DATGR	LEILQIHTK	NMKLA	2		547.8325704	1093.649541	0.002519933	1	N	377	386
Q01853	Exosome	ARQAA	PCVLFFDELDSIAK	ARGGN	2	C2:+57.021	827.4135644	1652.811529	0.001162105	1	N	570	584
Q01853	Exosome	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIRK	GDIFL	4		1030.563918	4118.224473	0.000622848	1	N	113	148
Q01853	Exosome	GLKQR	AHVIVMAATNRPNSIDPALRR	FGRFD	3		768.0907333	2301.2488	0.000823681	4	N	338	359
Q01853	Exosome	GEVER	RIVSQLLTLMDGLK	QRAHV	2		793.9690731	1585.922546	0.000622848	2	N	322	336
Q01853	Exosome	GEVER	RIVSQLLTLMDGLK	QRAHV	3		529.6486487	1585.922546	0.000622848	6	N	322	336
Q01853	Exosome	IRRER	ERQTNPSAMEVEEDDPVPEIR	RDHFE	3	M9:+15.995	819.7120101	2456.11263	0.000451244	5	N	711	732
Q01853	Exosome	LRETV	VEVPQVTWEDIGGLEDVKR	ELQEL	2		1085.063473	2168.111345	0.000451244	6	N	468	487
Q01853	Exosome	LRETV	VEVPQVTWEDIGGLEDVKR	ELQEL	3		723.7115817	2168.111345	0.000451244	1	N	468	487
Q01853	Exosome	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQ	AIRKK	3	C26:+57.021	1111.528533	3331.562198	0.001943752	2	N	389	421
Q01853	Exosome	MTPSK	GVLFYGPPGCGK	TLLAK	2	C10:+57.021	626.3134562	1250.611312	0.000451244	2	N	512	524
Q01853	Exosome	FGSFR	FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG	-	3		1074.112367	3219.3137	0.002453667	1	N	772	806
Q01853	Exosome	GRFDR	EVDIGIPDATGR	LEILQ	2		621.8203883	1241.625177	0.002519933	1	N	365	377
Q01853	Parental	GKKRR	EAVCIVLSDDTCSDEKIR	MNRVV	2	C4:+57.021,C12:+57.021	1055.493246	2108.970891	0.000451244	4	N	65	83
Q01853	Parental	TLLAK	AIANECQANFISIK	GPELL	2	C6:+57.021	789.9011555	1577.786711	0.000451244	28	N	529	543
Q01853	Parental	NLRVR	LGDVISIQPCPDVK	YGKRI	2	C10:+57.021	770.9059065	1539.796213	0.000451244	28	N	95	109
Q01853	Parental	RNNLR	VRLGDVISIQPCPDVK	YGKRI	2	C12:+57.021	898.4906691	1794.965738	0.000698008	1	N	93	109
Q01853	Parental	RNNLR	VRLGDVISIQPCPDVK	YGKRI	3	C12:+57.021	599.3297127	1794.965738	0.000451244	6	N	93	109
Q01853	Parental	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	2		1106.586583	2211.157567	0.000451244	13	N	487	505
Q01853	Parental	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	3		738.0603223	2211.157567	0.000451244	25	N	487	505
Q01853	Parental	EDVKR	ELQELVQYPVEHPDKFLK	FGMTP	4		553.7971917	2211.157567	0.000451244	28	N	487	505
Q01853	Parental	NRPNR	LIVDEAINEDNSVVSLSQPK	MDELQ	2		1085.566045	2169.11649	0.000451244	90	N	25	45
Q01853	Parental	NRPNR	LIVDEAINEDNSVVSLSQPK	MDELQ	3		724.04663	2169.11649	0.000451244	27	N	25	45
Q01853	Parental	SPVAK	DVDLEFLAK	MTNGF	2		525.2798363	1048.544073	0.000451244	36	N	668	677
Q01853	Parental	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	2		1159.639879	2317.264158	0.000451244	9	N	365	386
Q01853	Parental	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	3		773.4291858	2317.264158	0.000451244	22	N	365	386
Q01853	Parental	GRFDR	EVDIGIPDATGRLEILQIHTK	NMKLA	4		580.3238394	2317.264158	0.001329271	7	N	365	386
Q01853	Parental	LQQSR	GFGSFRFPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG	-	3		1291.216665	3870.626595	0.000451244	12	N	766	806
Q01853	Parental	LSQPK	MDELQLFRGDTVLLK	GKKRR	3		593.3226013	1776.944404	0.001654178	1	N	45	60
Q01853	Parental	PSALR	ETVVEVPQVTWEDIGGLEDVKR	ELQEL	2		1249.642815	2497.270031	0.000451244	35	N	465	487
Q01853	Parental	PSALR	ETVVEVPQVTWEDIGGLEDVKR	ELQEL	3		833.4311436	2497.270031	0.000451244	26	N	465	487
Q01853	Parental	LRPGR	LDQLIYIPLPDEK	SRVAI	2		778.9326786	1555.849757	0.000998612	13	N	638	651
Q01853	Parental	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	KKMDL	3	C26:+57.021	1224.935963	3671.784488	0.000451244	32	N	389	424
Q01853	Parental	EVERR	IVSQLLTLMDGLK	QRAHV	2		715.9185175	1429.821435	0.000451244	2	N	323	336
Q01853	Parental	EEAEK	NAPAIIFIDELDAIAPKR	EKTHG	2		984.0521795	1966.088759	0.000451244	6	N	295	313
Q01853	Parental	EEAEK	NAPAIIFIDELDAIAPKR	EKTHG	3		656.3707197	1966.088759	0.000870037	2	N	295	313
Q01853	Parental	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	C5:+57.021	962.4799671	1922.944334	0.000451244	29	N	567	584
Q01853	Parental	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	3	C5:+57.021	641.9892447	1922.944334	0.000451244	30	N	567	584
Q01853	Parental	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	Q1:-17.027,C5:+57.021	953.9664671	1905.917334	0.000662267	9	N	567	584
Q01853	Parental	FDKAR	QAAPCVLFFDELDSIAK	ARGGN	2	[0:-17.027,C5:+57.021	953.9664671	1905.917334	0.000662267	7	N	567	584
Q01853	Parental	TLIAR	AVANETGAFFFLINGPEIMSK	LAGES	2		1128.572619	2255.129639	0.000451244	2	N	256	277
Q01853	Parental	SNLRK	AFEEAEKNAPAIIFIDELDAIAPK	REKTH	3		872.4588108	2614.353032	0.000451244	5	N	288	312
Q01853	Parental	EEAEK	NAPAIIFIDELDAIAPK	REKTH	2		906.0016239	1809.987648	0.000451244	44	N	295	312
Q01853	Parental	EEAEK	NAPAIIFIDELDAIAPK	REKTH	3		604.3370159	1809.987648	0.000451244	28	N	295	312
Q01853	Parental	EPIKR	EDEEESLNEVGYDDIGGCRK	QLAQI	2	C18:+57.021	1157.492717	2312.969834	0.000823681	1	N	191	211
Q01853	Parental	EPIKR	EDEEESLNEVGYDDIGGCRK	QLAQI	3	C18:+57.021	771.9977445	2312.969834	0.000451244	6	N	191	211
Q01853	Parental	VKPPR	GILLYGPPGTGK	TLIAR	2		586.8378528	1171.660106	0.002019181	3	N	239	251
Q01853	Parental	TKNMK	LADDVDLEQVANETHGHVGADLAALCSEAALQAIRK	KMDLI	4	C26:+57.021	950.9776627	3799.879451	0.000622848	5	N	389	425
Q01853	Parental	KYGKR	IHVLPIDDTVEGITGNLFEVY	LKPYF	2		1172.607713	2343.199826	0.000451244	19	N	113	134
Q01853	Parental	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIR	KGDIF	4		998.5401774	3990.12951	0.000451244	10	N	113	147
Q01853	Parental	EDVKR	ELQELVQYPVEHPDK	FLKFG	2		912.4628629	1822.910126	0.000451244	2	N	487	502
Q01853	Parental	EDVKR	ELQELVQYPVEHPDK	FLKFG	3		608.6445086	1822.910126	0.000451244	21	N	487	502
Q01853	Parental	GKKRR	EAVCIVLSDDTCSDEK	IRMNR	2	C4:+57.021,C12:+57.021	920.9006579	1839.785716	0.0025889	1	N	65	81
Q01853	Parental	MSTKK	NVFIIGATNRPDIIDPAILRPGR	LDQLI	3		840.1471243	2517.417973	0.000451244	6	N	615	638
Q01853	Parental	KYGKR	IHVLPIDDTVEGITGNLFEVYLKPY	FLEAY	3		949.1727819	2844.494946	0.001395409	1	N	113	138
Q01853	Parental	EFLAK	MTNGFSGADLTEICQR	ACKLA	2	C14:+57.021	900.4064766	1798.797353	0.001264573	1	N	677	693

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q01853	Parental	EPIKR	EDEEESLNEVGYDDIGGCR	KQLAQ	2	C18:+57.021	1093.445235	2184.87487	0.000451244	3	N	191	210
Q01853	Parental	NLRVR	LGDVISIQPCPDVKY	GKRIH	2	C10:+57.021	852.4375708	1702.859542	0.001329271	2	N	95	110
Q01853	Parental	KYGKR	IHVLPIDDTVEGITGNLF	EVYLK	2		977.020545	1952.02549	0.000823681	3	N	113	131
Q02053	Exosome	SMVTK	DNPGVVTCLDEAR	HGFET	2	C8:+57.021	723.338388	1444.661176	0.000451244	11	N	226	239
Q02053	Exosome	KSGVK	IHVSDQELQSANASVDDSRLEELK	ATLPS	3		895.1110213	2682.309664	0.000451244	41	N	806	830
Q02053	Exosome	ERTLR	LAGTQPLEVLEAVQR	SLVLQ	2		812.4573835	1622.899167	0.000451244	29	N	678	693
Q02053	Exosome	ERTLR	LAGTQPLEVLEAVQR	SLVLQ	3		541.974189	1622.899167	0.000451244	47	N	678	693
Q02053	Exosome	PPRPR	NEEDATELVGLAQAVNAR	SPPSV	2		950.4744903	1898.933381	0.000451244	39	N	350	368
Q02053	Exosome	PPRPR	NEEDATELVGLAQAVNAR	SPPSV	3		633.9855935	1898.933381	0.000451244	30	N	350	368
Q02053	Exosome	GSQDR	AAVASLLQSVQVPEFTPK	SGVKI	2		943.0256304	1884.035661	0.000451244	42	N	784	802
Q02053	Exosome	GSQDR	AAVASLLQSVQVPEFTPK	SGVKI	3		629.0196869	1884.035661	0.000451244	19	N	784	802
Q02053	Exosome	PMEIK	VLGPYTFSICDTSNFSDYIR	GGIVS	2	C10:+57.021	1178.052016	2354.088432	0.000451244	55	N	268	288
Q02053	Exosome	PDTER	IYDDDFFQNLDGVANALDNIDAR	MYMDR	2		1307.606961	2613.198322	0.000451244	46	N	558	581
Q02053	Exosome	PDTER	IYDDDFFQNLDGVANALDNIDAR	MYMDR	3		872.0739075	2613.198322	0.000451244	38	N	558	581
Q02053	Exosome	LDSYK	NGFLNLALPFFGFSEPLAAPR	HQYYN	2		1139.605111	2277.194621	0.000451244	24	N	923	944
Q02053	Exosome	LDSYK	NGFLNLALPFFGFSEPLAAPR	HQYYN	3		760.0726737	2277.194621	0.000451244	14	N	923	944
Q02053	Exosome	LIAGK	IIPAIATTTAAVVGLVCLELYK	VVQGH	2	C17:+57.021	1158.666288	2315.316976	0.000451244	31	N	889	911
Q02053	Exosome	LIAGK	IIPAIATTTAAVVGLVCLELYK	VVQGH	3	C17:+57.021	772.7801253	2315.316976	0.000451244	29	N	889	911
Q02053	Exosome	PVTAY	TGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		987.1978787	2958.570236	0.000451244	11	N	147	174
Q02053	Exosome	VSQPR	LAELNSYVPVTAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		1460.77249	4379.294069	0.000451244	30	N	134	174
Q02053	Exosome	VSQPR	LAELNSYVPVTAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	4		1095.831317	4379.294069	0.000451244	8	N	134	174
Q02053	Exosome	LGGVK	AVTLHDQGTTQWADLSSQFYLR	EEDIG	2		1269.125124	2536.234648	0.000451244	3	N	97	119
Q02053	Exosome	LGGVK	AVTLHDQGTTQWADLSSQFYLR	EEDIG	3		846.4193494	2536.234648	0.000451244	26	N	97	119
Q02053	Exosome	LSKQK	YFLVGAGAIGCELLK	NFAMI	2	C11:+57.021	805.934467	1609.853334	0.000451244	56	N	470	485
Q02053	Exosome	ASNLR	AENYDISPADR	HKSKL	2		625.7865455	1249.557491	0.000451244	7	N	869	880
Q02053	Exosome	TERIY	DDDFFQNLDGVANALDNIDAR	MYMDR	2		1169.533265	2337.05093	0.000451244	8	N	560	581
Q02053	Exosome	TERIY	DDDFFQNLDGVANALDNIDAR	MYMDR	3		780.0247766	2337.05093	0.000451244	3	N	560	581
Q02053	Exosome	SYVPV	TAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		1098.913919	3293.718357	0.000451244	9	N	144	174
Q02053	Exosome	GRHVR	ALVLELCCNDESGEDVEVPYVR	YTIR-	2	C7:+57.021,C8:+57.021	1283.593688	2565.171776	0.000451244	10	N	1032	1054
Q02053	Exosome	ICTLK	NFPNAIEHTLQWAR	DEFEG	2		848.9318672	1695.848134	0.000451244	14	N	635	649
Q02053	Exosome	RAAVA	SLLQSVQVPEFTPK	SGVKI	2		786.9357526	1571.855905	0.00307782	2	N	788	802
Q02053	Exosome	CNNIR	QLLHNFPPDQLTSSGAPFWSGPK	RCPHP	2		1262.635128	2523.254655	0.000823681	1	N	723	746
Q02053	Exosome	CNNIR	QLLHNFPPDQLTSSGAPFWSGPK	RCPHP	3		842.0926851	2523.254655	0.000451244	27	N	723	746
Q02053	Exosome	LGGVK	AVTLHDQGTTQWADLSSQFYLREEDIGK	NRAEV	3		1070.190223	3207.547269	0.000451244	17	N	97	125
Q02053	Exosome	LGGVK	AVTLHDQGTTQWADLSSQFYLREEDIGK	NRAEV	4		802.8946172	3207.547269	0.000451244	14	N	97	125
Q02053	Exosome	EGLFK	QPAENVNQYLTDSK	FVERT	2		803.8895307	1605.763461	0.000451244	22	N	657	671
Q02053	Exosome	NGMAK	NGSEADIDESLYSR	QLYVL	2		778.3476956	1554.679791	0.000451244	11	N	43	57
Q02053	Exosome	MQWLY	FDALECLPEDKEALTEEK	CLPRQ	2	C6:+57.021	1069.0042	2135.992801	0.000451244	4	N	425	443
Q02053	Exosome	LQWAR	DEFEGLFKQPAENVNQYLTDSK	FVERT	2		1286.614255	2571.21291	0.000622848	4	N	649	671
Q02053	Exosome	LQWAR	DEFEGLFKQPAENVNQYLTDSK	FVERT	3		858.07877	2571.21291	0.000451244	23	N	649	671
Q02053	Exosome	PMEIK	VLGPYTFSICDTSNF	SDYIR	2	C10:+57.021	860.8982785	1719.780957	0.000451244	6	N	268	283
Q02053	Exosome	EKLSK	QKYFLVGAGAIGCELLK	NFAMI	2	C13:+57.021	934.0112374	1866.006875	0.000451244	7	N	468	485
Q02053	Exosome	EKLSK	QKYFLVGAGAIGCELLK	NFAMI	3	C13:+57.021	623.0100916	1866.006875	0.000451244	22	N	468	485
Q02053	Exosome	EKLSK	QKYFLVGAGAIGCELLK	NFAMI	2	Q1:-17.027,C13:+57.021	925.4977374	1848.979875	0.002981883	1	N	468	485
Q02053	Exosome	EKLSK	QKYFLVGAGAIGCELLK	NFAMI	2	[0:-17.027,C13:+57.021	925.4977374	1848.979875	0.001229886	4	N	468	485
Q02053	Exosome	TLGTK	GNVQVVIPFLTESYSSSQDPPEK	SIPIC	3		841.0872655	2520.238396	0.000735798	9	N	604	627
Q02053	Exosome	PRQNR	YDGQVAVFGSDFQEK	LSKQK	2		845.3919062	1688.768212	0.000451244	5	N	450	465
Q02053	Exosome	HVRAL	VLELCCNDESGEDVEVPYVR	YTIR-	2	C5:+57.021,C6:+57.021	1191.533099	2381.050598	0.000622848	6	N	1034	1054
Q02053	Exosome	VSQPR	LAELNSYVPVTAY	TGPLV	2		720.3749965	1438.734393	0.002884417	1	N	134	147
Q02053	Exosome	LEELK	ATLPSPDKLPGFK	MYPID	3		457.5946493	1369.760548	0.000998612	1	N	830	843
Q02053	Exosome	KISFK	SLPASLVEPDFVMTDFAK	YSRPA	2		983.9956819	1965.975764	0.0007646	3	N	304	322
Q02053	Exosome	DLIRK	LAYVAAGDLAPINAFIGGLAAQEVMK	ACSGK	3	M25:+15.995	873.8004312	2618.377894	0.000451244	1	N	385	411
Q02053	Exosome	SNLNR	QFLFRPWDVTK	LKSDT	2		718.8884083	1435.761217	0.000622848	1	N	515	526
Q02053	Exosome	EAVQR	SLVLQRPQTWGDCVTW	ACHHW	2	C13:+57.021	973.4833754	1944.951151	0.002519933	1	N	693	709
Q02053	Parental	SMVTK	DNPGVVTCLDEAR	HGFET	2	C8:+57.021	723.338388	1444.661176	0.000451244	12	N	226	239
Q02053	Parental	KSGVK	IHVSDQELQSANASVDDSRLEELK	ATLPS	2		1342.162632	2682.309664	0.001463592	1	N	806	830
Q02053	Parental	KSGVK	IHVSDQELQSANASVDDSRLEELK	ATLPS	3		895.1110213	2682.309664	0.000451244	26	N	806	830
Q02053	Parental	ERTLR	LAGTQPLEVLEAVQR	SLVLQ	2		812.4573835	1622.899167	0.000451244	13	N	678	693
Q02053	Parental	ERTLR	LAGTQPLEVLEAVQR	SLVLQ	3		541.974189	1622.899167	0.000451244	35	N	678	693
Q02053	Parental	PPRPR	NEEDATELVGLAQAVNAR	SPPSV	2		950.4744903	1898.933381	0.000451244	36	N	350	368
Q02053	Parental	PPRPR	NEEDATELVGLAQAVNAR	SPPSV	3		633.9855935	1898.933381	0.000451244	5	N	350	368
Q02053	Parental	GSQDR	AAVASLLQSVQVPEFTPK	SGVKI	2		943.0256304	1884.035661	0.000451244	25	N	784	802
Q02053	Parental	GSQDR	AAVASLLQSVQVPEFTPK	SGVKI	3		629.0196869	1884.035661	0.000451244	9	N	784	802
Q02053	Parental	PMEIK	VLGPYTFSICDTSNFSDYIR	GGIVS	2	C10:+57.021	1178.052016	2354.088432	0.000451244	35	N	268	288
Q02053	Parental	SHQNR	VGPDTERIYDDDFFQNLDGVANALDNIDAR	MYMDR	3		1123.527563	3367.55929	0.000451244	11	N	551	581

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q02053	Parental	PDTER	IYDDDFFQNLDGVANALDNIDAR	MYMDR	2		1307.606961	2613.198322	0.000451244	38	N	558	581
Q02053	Parental	PDTER	IYDDDFFQNLDGVANALDNIDAR	MYMDR	3		872.0739075	2613.198322	0.000451244	20	N	558	581
Q02053	Parental	LDSYK	NGFLNLALPFFGFSEPLAAPR	HQYYN	2		1139.605111	2277.194621	0.000451244	16	N	923	944
Q02053	Parental	LDSYK	NGFLNLALPFFGFSEPLAAPR	HQYYN	3		760.0726737	2277.194621	0.000451244	3	N	923	944
Q02053	Parental	LIAGK	IIPAIATTTAAVVGLVCLELYK	VVQGH	2	C17:+57.021	1158.666288	2315.316976	0.000451244	14	N	889	911
Q02053	Parental	LIAGK	IIPAIATTTAAVVGLVCLELYK	VVQGH	3	C17:+57.021	772.7801253	2315.316976	0.000622848	12	N	889	911
Q02053	Parental	PVTAY	TGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		987.1978787	2958.570236	0.000451244	14	N	147	174
Q02053	Parental	VSQPR	LAELNSYVPVTAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	3		1460.77249	4379.294069	0.000451244	32	N	134	174
Q02053	Parental	VSQPR	LAELNSYVPVTAYTGPLVEDFLSSFQVVVLTNSPLEAQLR	VGEFC	4		1095.831317	4379.294069	0.000451244	11	N	134	174
Q02053	Parental	KCLPR	QNRYDGQVAVFGSDFQEK	LSKQK	2		1044.493214	2086.970829	0.000451244	6	N	447	465
Q02053	Parental	KCLPR	QNRYDGQVAVFGSDFQEK	LSKQK	3		696.6647429	2086.970829	0.000622848	1	N	447	465
Q02053	Parental	KCLPR	QNRYDGQVAVFGSDFQEK	LSKQK	2	[0:-17.027	1035.979714	2069.943829	0.000451244	1	N	447	465
Q02053	Parental	LGGVK	AVTLHDQGTTQWADLSSQFYLR	EEDIG	2		1269.125124	2536.234648	0.000451244	2	N	97	119
Q02053	Parental	LGGVK	AVTLHDQGTTQWADLSSQFYLR	EEDIG	3		846.4193494	2536.234648	0.000451244	6	N	97	119
Q02053	Parental	LSKQK	YFLVGAGAIGCELLK	NFAMI	2	C11:+57.021	805.934467	1609.853334	0.000451244	40	N	470	485
Q02053	Parental	TERIY	DDDFFQNLDGVANALDNIDAR	MYMDR	2		1169.533265	2337.05093	0.000451244	10	N	560	581
Q02053	Parental	LGGVK	AVTLHDQGTTQWADLSSQFYLREEDIGK	NRAEV	3		1070.190223	3207.547269	0.000622848	2	N	97	125
Q02053	Parental	LGGVK	AVTLHDQGTTQWADLSSQFYLREEDIGK	NRAEV	4		802.8946172	3207.547269	0.000451244	7	N	97	125
Q02053	Parental	EGLFK	QPAENVNQYLTDSK	FVERT	2		803.8895307	1605.763461	0.00091018	7	N	657	671
Q02053	Parental	NGMAK	NGSEADIDESLYSR	QLYVL	2		778.3476956	1554.679791	0.000451244	2	N	43	57
Q02053	Parental	MQWLY	FDALECLPEDKEALTEEK	CLPRQ	2	C6:+57.021	1069.0042	2135.992801	0.000451244	3	N	425	443
Q02053	Parental	LQWAR	DEFEGLFKQPAENVNQYLTDSK	FVERT	2		1286.614255	2571.21291	0.000451244	2	N	649	671
Q02053	Parental	LQWAR	DEFEGLFKQPAENVNQYLTDSK	FVERT	3		858.07877	2571.21291	0.000451244	7	N	649	671
Q02053	Parental	PMEIK	VLGPYTFSICDTSNF	SDYIR	2	C10:+57.021	860.8982785	1719.780957	0.000451244	7	N	268	283
Q02053	Parental	LELYK	VVQGHQQLDSYKNGFLNLALPFFGFSEPLAAPR	HQYYN	3		1220.970762	3659.888885	0.001463592	1	N	911	944
Q02053	Parental	LELYK	VVQGHQQLDSYKNGFLNLALPFFGFSEPLAAPR	HQYYN	4		915.9800213	3659.888885	0.002374549	1	N	911	944
Q02053	Parental	PRQNR	YDGQVAVFGSDFQEK	LSKQK	2		845.3919062	1688.768212	0.000451244	1	N	450	465
Q02357	Exosome	GLASR	IIALGPTGAQFLSPVIVEIPHFASHGR	GDREL	3		943.1926222	2826.554467	0.000451244	7	N	970	997
Q02357	Exosome	GLASR	IIALGPTGAQFLSPVIVEIPHFASHGR	GDREL	4		707.6464167	2826.554467	0.000451244	24	N	970	997
Q02357	Exosome	VIMSR	LCQDYDTIGPEGGSLR	SKLVP	2	C2:+57.021	890.9124485	1779.809297	0.000637154	6	N	1064	1080
Q02357	Exosome	YGKVR	LAELLLEHDAHPNAAGK	NGLTP	3		600.3202478	1797.937344	0.000451244	24	N	546	563
Q02357	Exosome	SLRSK	LVPLVQATFPENAVTK	KVKLA	2		863.9910592	1725.966518	0.000451244	7	N	1082	1098
Q02357	Exosome	NAKTK	LGYSPLHQAAQQGHTDIVTLLLK	NGASP	3		835.1276183	2502.359455	0.000451244	9	N	728	751
Q02357	Exosome	NAKTK	LGYSPLHQAAQQGHTDIVTLLLK	NGASP	4		626.5976637	2502.359455	0.000451244	7	N	728	751
Q02357	Exosome	TTSLR	LLCSVIGGTDQAQWEDITGTTK	LIYAN	2	C3:+57.021	1197.086587	2392.157575	0.000451244	32	N	1167	1189
Q02357	Exosome	TLLLK	NGASPNEVSSNGTTPLAIAK	RLGYI	2		964.4901403	1926.964681	0.000451244	15	N	751	771
Q02357	Exosome	TKKVK	LALQAQPVPDELVTK	LLGNQ	2		811.4621346	1620.908669	0.000451244	6	N	1101	1116
Q02357	Exosome	AELAR	ELQFSVEDINR	IRVEN	2		675.3389453	1348.662291	0.000451244	10	N	1419	1430
Q02357	Exosome	NLGNK	SGLTPLHLVSQEGHVPVADVLIK	HGVTV	3		803.7887141	2408.342742	0.000451244	14	N	662	685
Q02357	Exosome	NLGNK	SGLTPLHLVSQEGHVPVADVLIK	HGVTV	4		603.0934856	2408.342742	0.000451244	7	N	662	685
Q02357	Exosome	DVLSK	TGFTPLHIAAHYENLNVAQLLLNR	GASVN	3		902.4894387	2704.444916	0.000622848	5	N	200	224
Q02357	Exosome	AIAKR	LGYISVTDVLK	VVTDE	2		604.350793	1206.685986	0.000622848	9	N	772	783
Q02357	Exosome	TDVLK	VVTDETSVVLVSDK	HRMSY	2		745.9015754	1489.787551	0.000451244	6	N	783	797
Q02357	Exosome	INRIR	VENPNSLLDQSTALLTLWVDR	EGENA	2		1192.626968	2383.238337	0.000451244	1	N	1432	1453
Q02357	Exosome	DFVPK	LDQVVESPAIPR	IPCVT	2		662.3675057	1322.719411	0.001229886	2	N	845	857
Q02357	Exosome	NDDTR	TAAVLLQNDPNPDVLSK	TGFTP	2		897.9839625	1793.952325	0.000451244	7	N	183	200
Q02357	Exosome	EDINR	IRVENPNSLLDQSTALLTLWVDR	EGENA	3		885.1489706	2652.423512	0.000451244	9	N	1430	1453
Q02357	Exosome	KRVCR	IITTDFPLYFVIMSR	LCQDY	2		908.4898383	1814.964077	0.002019181	1	N	1049	1064
Q02357	Exosome	DMQVW	SAGLTPSLVTAEDSSLECSKAEDSDAIPEWK	LEGAH	3	C18:+57.021	1098.517411	3292.528833	0.001463592	3	N	1565	1596
Q02357	Exosome	HTAAR	EGHVDTALALLEK	EASQA	2		698.3780705	1394.740541	0.000823681	4	N	508	521
Q02357	Exosome	INRIR	VENPNSLLDQSTALLTLWVDREGENAK	MENLY	3		1004.847797	3011.519991	0.000451244	4	N	1432	1459
Q02357	Exosome	PAIPR	IPCVTPETVVIR	SEDQE	2	C3:+57.021	692.3871526	1382.758705	0.002212458	1	N	857	869
Q02357	Parental	GLASR	IIALGPTGAQFLSPVIVEIPHFASHGR	GDREL	4		707.6464167	2826.554467	0.000622848	10	N	970	997
Q02357	Parental	VIMSR	LCQDYDTIGPEGGSLR	SKLVP	2	C2:+57.021	890.9124485	1779.809297	0.000622848	3	N	1064	1080
Q02357	Parental	YGKVR	LAELLLEHDAHPNAAGK	NGLTP	3		600.3202478	1797.937344	0.000451244	1	N	546	563
Q02357	Parental	SLRSK	LVPLVQATFPENAVTK	KVKLA	2		863.9910592	1725.966518	0.001162105	1	N	1082	1098
Q02357	Parental	TTSLR	LLCSVIGGTDQAQWEDITGTTK	LIYAN	2	C3:+57.021	1197.086587	2392.157575	0.000451244	8	N	1167	1189
Q02357	Parental	TLLLK	NGASPNEVSSNGTTPLAIAK	RLGYI	2		964.4901403	1926.964681	0.0025889	1	N	751	771
Q02357	Parental	DFVPK	LDQVVESPAIPR	IPCVT	3		441.9142705	1322.719411	0.0025889	1	N	845	857
Q02819	Exosome	TFEAR	DLELLIQTATR	DLAQY	2		636.8620562	1271.708512	0.000451244	4	N	151	162
Q02819	Exosome	LYYHR	YLQEVINVLETDGHFR	EKLQA	3		644.9991744	1931.974123	0.000451244	5	N	52	68
Q02819	Exosome	TNQDR	LVTLEEFLASTQR	KEFGD	2		753.9122775	1505.808955	0.001162105	2	N	309	322
Q02819	Exosome	RFNPK	TFFILHDINSDGVLDEQELEALFTK	ELEKV	3		965.4873177	2893.438553	0.002080925	1	N	245	270
Q02819	Parental	LYYHR	YLQEVINVLETDGHFREK	LQAAN	4		548.2857199	2189.111679	0.000451244	3	N	52	70
Q02819	Parental	TFEAR	DLELLIQTATR	DLAQY	2		636.8620562	1271.708512	0.000451244	19	N	151	162

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q02819	Parental	LYYHR	YLQEVINVLETDGHFR	EKLQA	2		966.9948615	1931.974123	0.000622848	1	N	52	68
Q02819	Parental	LYYHR	YLQEVINVLETDGHFR	EKLQA	3		644.9991744	1931.974123	0.000451244	24	N	52	68
Q02819	Parental	TNQDR	LVTLEEFLASTQR	KEFGD	2		753.9122775	1505.808955	0.000622848	13	N	309	322
Q02819	Parental	TNQDR	LVTLEEFLASTQR	KEFGD	3		502.9441183	1505.808955	0.000622848	15	N	309	322
Q02819	Parental	RFNPK	TFFILHDINSDGVLDEQELEALFTKELEK	VYDPK	3		1131.908722	3392.702767	0.000823681	9	N	245	274
Q02819	Parental	RFNPK	TFFILHDINSDGVLDEQELEALFTKELEK	VYDPK	4		849.1834917	3392.702767	0.000622848	4	N	245	274
Q02819	Parental	RFNPK	TFFILHDINSDGVLDEQELEALFTK	ELEKV	3		965.4873177	2893.438553	0.000451244	15	N	245	270
Q02819	Parental	TNQDR	LVTLEEFLASTQRK	EFGDT	3		545.6424394	1633.903918	0.002212458	1	N	309	323
Q02819	Parental	QTATR	DLAQYDAAHHEEFKR	YEMLK	3		610.6242189	1828.849257	0.000622848	3	N	162	177
Q02819	Parental	QTATR	DLAQYDAAHHEEFKR	YEMLK	4		458.2201142	1828.849257	0.001352548	1	N	162	177
Q02819	Parental	QAQLK	EVWEELDGLDPNRFNPK	TFFIL	2		1029.500508	2056.985416	0.000451244	9	N	228	245
Q03265	Exosome	RDNGK	HALIIYDDLSK	QAVAY	2		644.3513243	1286.687049	0.002981883	1	N	305	316
Q03265	Exosome	DVVKR	TGAIVDVPVGEELLGR	VVDAL	2		812.9493913	1623.883183	0.000451244	8	N	133	149
Q03265	Exosome	SKITK	FENAFLSHVISQHQSLLGNIR	SDGKI	3		804.092908	2409.255324	0.000451244	12	N	506	527
Q03265	Exosome	EVAAF	AQFGSDLDAATQQLLSR	GVRLT	2		910.9610187	1819.906437	0.000451244	3	N	446	463
Q03265	Exosome	ELAQY	REVAAFAQFGSDLDAATQQLLSR	GVRLT	3		832.0948658	2493.261197	0.001162105	1	N	440	463
Q03265	Exosome	LAQYR	EVAAFAQFGSDLDAATQQLLSR	GVRLT	2		1169.587843	2337.160086	0.000451244	20	N	441	463
Q03265	Exosome	LAQYR	EVAAFAQFGSDLDAATQQLLSR	GVRLT	3		780.0611621	2337.160086	0.000451244	4	N	441	463
Q03265	Exosome	QSDAK	LKEIVTNFLAGFEP	-	2		789.4328457	1576.850091	0.002813207	1	N	539	553
Q03265	Exosome	DAKLK	EIVTNFLAGFEP	-	2		668.8433321	1335.671064	0.002519933	1	N	541	553
Q03265	Parental	RDNGK	HALIIYDDLSK	QAVAY	2		644.3513243	1286.687049	0.000451244	19	N	305	316
Q03265	Parental	ILEER	ILGADTSVDLEETGR	VLSIG	2		788.3971886	1574.778777	0.000451244	63	N	58	73
Q03265	Parental	RQTGK	TSIAIDTIINQK	RFNDG	2		658.8751636	1315.734727	0.000451244	25	N	218	230
Q03265	Parental	VVKRT	GAIVDVPVGEELLGR	VVDAL	2		762.425552	1522.835504	0.000622848	6	N	134	149
Q03265	Parental	DVVKR	TGAIVDVPVGEELLGR	VVDAL	2		812.9493913	1623.883183	0.000451244	33	N	133	149
Q03265	Parental	SKITK	FENAFLSHVISQHQSLLGNIR	SDGKI	3		804.092908	2409.255324	0.000451244	34	N	506	527
Q03265	Parental	SKITK	FENAFLSHVISQHQSLLGNIR	SDGKI	4		603.321631	2409.255324	0.000451244	29	N	506	527
Q03265	Parental	EVAAF	AQFGSDLDAATQQLLSR	GVRLT	2		910.9610187	1819.906437	0.000451244	26	N	446	463
Q03265	Parental	EVAAF	AQFGSDLDAATQQLLSR	GVRLT	3		607.6432791	1819.906437	0.000451244	5	N	446	463
Q03265	Parental	ELAQY	REVAAFAQFGSDLDAATQQLLSR	GVRLT	3		832.0948658	2493.261197	0.000451244	17	N	440	463
Q03265	Parental	LAQYR	EVAAFAQFGSDLDAATQQLLSR	GVRLT	2		1169.587843	2337.160086	0.000451244	36	N	441	463
Q03265	Parental	LAQYR	EVAAFAQFGSDLDAATQQLLSR	GVRLT	3		780.0611621	2337.160086	0.000451244	34	N	441	463
Q03265	Parental	AGTMK	LELAQYREVAAFAQFGSDLDAATQQLLSR	GVRLT	3		1071.218113	3210.630939	0.000451244	3	N	434	463
Q03265	Parental	RQTGK	TSIAIDTIINQKR	FNDGT	2		736.9257192	1471.835838	0.000637154	1	N	218	231
Q03265	Parental	RPPGR	EAYPGDVFYLHSR	LLERA	2		777.3733194	1552.731039	0.000622848	6	N	334	347
Q03265	Parental	RPPGR	EAYPGDVFYLHSR	LLERA	3		518.584813	1552.731039	0.001463592	3	N	334	347
Q03265	Parental	ELLGR	VVDALGNAIDGKGPIGSK	TRRRV	3		570.9848652	1709.931196	0.002145581	1	N	149	167
Q03265	Parental	QSDAK	LKEIVTNFLAGFEP	-	2		789.4328457	1576.850091	0.000451244	5	N	539	553
Q03265	Parental	ILEER	ILGADTSVDLEETGRVLSIGDGIAR	VHGLR	3		853.1209692	2556.339508	0.000622848	3	N	58	83
Q03265	Parental	ERAAK	MNDSFGGGSLTALPVIETQAGDVSAYIPTNVISITDGQIF	LETEL	3		1367.012581	4098.014342	0.002145581	2	N	354	394
Q03265	Parental	QTGIK	AVDSLVPIGR	GQREL	2		513.8012703	1025.586941	0.000979378	5	N	194	204
Q03265	Parental	EETGR	VLSIGDGIAR	VHGLR	2		500.7934452	999.5712904	0.000823681	6	N	73	83
Q03265	Parental	ELLGR	VVDALGNAIDGK	GPIGS	2		586.3200242	1170.624448	0.000451244	2	N	149	161
Q03265	Parental	KITKF	ENAFLSHVISQHQSLLGNIR	SDGKI	3		755.0701034	2262.18691	0.000451244	6	N	507	527
Q04750	Exosome	CCSLR	VEHINLHPELDGQEYVVEFDFPGKDSIR	YYNKV	3		1094.874235	3281.599304	0.000451244	37	N	510	538
Q04750	Exosome	CCSLR	VEHINLHPELDGQEYVVEFDFPGKDSIR	YYNKV	4		821.4076261	3281.599304	0.000451244	25	N	510	538
Q04750	Exosome	KLALR	AGNEKEEGETADTVGCCSLR	VEHIN	2	C16:+57.021,C17:+57.021	1091.970666	2181.925732	0.000451244	17	N	490	510
Q04750	Exosome	KLALR	AGNEKEEGETADTVGCCSLR	VEHIN	3	C16:+57.021,C17:+57.021	728.3163773	2181.925732	0.000451244	37	N	490	510
Q04750	Exosome	CCSLR	VEHINLHPELDGQEYVVEFDFPGK	DSIRY	2		1406.185379	2810.355158	0.002727428	1	N	510	534
Q04750	Exosome	CCSLR	VEHINLHPELDGQEYVVEFDFPGK	DSIRY	3		937.7928525	2810.355158	0.000451244	14	N	510	534
Q04750	Exosome	CCSLR	VEHINLHPELDGQEYVVEFDFPGK	DSIRY	4		703.5965894	2810.355158	0.000622848	4	N	510	534
Q04750	Exosome	AKVFR	TYNASITLQQQLK	ELTAP	2		754.409902	1506.804204	0.000451244	21	N	592	605
Q04750	Exosome	FLEHK	GPVFAPPYEPLPESVK	FYYDG	2		863.956685	1725.89777	0.000451244	15	N	225	241
Q04750	Exosome	RHDNK	VTWLVSWTENIQGSIK	YIMLN	2		930.9968729	1859.978146	0.001591523	3	N	411	427
Q04750	Exosome	QQQLK	ELTAPDENVPAK	ILSYN	2		642.3280462	1282.640492	0.000451244	7	N	605	617
Q04750	Exosome	EQKWK	WWEEERYPEGIK	WKFLE	2		811.3864268	1620.757254	0.000622848	1	N	206	218
Q04750	Parental	CCSLR	VEHINLHPELDGQEYVVEFDFPGKDSIR	YYNKV	3		1094.874235	3281.599304	0.000451244	13	N	510	538
Q04750	Parental	CCSLR	VEHINLHPELDGQEYVVEFDFPGKDSIR	YYNKV	4		821.4076261	3281.599304	0.000451244	8	N	510	538
Q04750	Parental	KLALR	AGNEKEEGETADTVGCCSLR	VEHIN	2	C16:+57.021,C17:+57.021	1091.970666	2181.925732	0.000451244	19	N	490	510
Q04750	Parental	KLALR	AGNEKEEGETADTVGCCSLR	VEHIN	3	C16:+57.021,C17:+57.021	728.3163773	2181.925732	0.000451244	41	N	490	510
Q04750	Parental	NHRER	IANFKIEPPGLFR	GRGNH	3		501.2895603	1500.845281	0.001395409	1	N	351	364
Q04750	Parental	CCSLR	VEHINLHPELDGQEYVVEFDFPGK	DSIRY	3		937.7928525	2810.355158	0.000451244	4	N	510	534
Q04750	Parental	FLEHK	GPVFAPPYEPLPESVK	FYYDG	2		863.956685	1725.89777	0.000451244	6	N	225	241
Q04750	Parental	QQQLK	ELTAPDENVPAK	ILSYN	2		642.3280462	1282.640492	0.000998612	1	N	605	617
Q04998	Parental	IIVRS	SPTPGSEGHGSAPDCPSCALATLPK	DGPNS	3	C15:+57.021,C18:+57.021	832.0496315	2493.125494	0.000451244	11	N	20	45

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q04998	Parental	SLDVR	IACEQCQESGASLVLLGK	KKKKE	2	C3:+57.021,C6:+57.021	981.9848593	1961.954119	0.000451244	4	N	241	259
Q05144	Exosome	EDYDR	LRPLSYPQTDVFLICFSLVSPASYENVR	AKWFP	3	C15:+57.021	1091.232552	3270.674255	0.000451244	10	N	66	94
Q05144	Exosome	KLKEK	KLAPITYPQGLALAK	DIDSV	2		792.4801303	1582.944661	0.000823681	12	N	132	147
Q05144	Exosome	KLKEK	KLAPITYPQGLALAK	DIDSV	3		528.6560202	1582.944661	0.000451244	21	N	132	147
Q05144	Exosome	EDYDR	LRPLSYPQTDVFLICF	SLVSP	2	C15:+57.021	985.0165197	1968.017439	0.000451244	8	Y	66	82
Q05144	Exosome	LKEKK	LAPITYPQGLALAK	DIDSV	2		728.4326487	1454.849697	0.000451244	43	N	133	147
Q05144	Exosome	DSKPV	NLGLWDTAGQEDYDR	LRPLS	2		876.8953444	1751.775089	0.000451244	20	Y	51	66
Q05144	Exosome	FPEVR	HHCPSTPIILVGTK	LDLRD	2	C3:+57.021	780.4220581	1558.828516	0.000451244	19	N	102	116
Q05144	Exosome	FPEVR	HHCPSTPIILVGTK	LDLRD	3	C3:+57.021	520.6173054	1558.828516	0.000451244	31	N	102	116
Q05144	Exosome	IDSVK	YLECSALTQR	GLKTV	2	C4:+57.021	620.8034527	1239.591305	0.000451244	35	Y	153	163
Q05144	Exosome	MVDSK	PVNLGLWDTAGQEDYDR	LRPLS	2		974.9559333	1947.896267	0.000451244	14	Y	49	66
Q05144	Exosome	GAVGK	TCLLISYTTNAFPGEYIPTVFDNY	SANVM	2	C2:+57.021	1400.165035	2798.31447	0.000451244	11	Y	16	40
Q05144	Exosome	GAVGK	TCLLISYTTNAFPGEYIPTVFDNY	SANVM	3	C2:+57.021	933.7792899	2798.31447	0.0025889	1	Y	16	40
Q05144	Exosome	GAVGK	TCLLISYTTNAFPGEYIPT	VFDNY	2	C2:+57.021	1081.030021	2160.044442	0.000823681	8	Y	16	35
Q05144	Exosome	GAVGK	TCLLISYTTNAFPGEYIPTVF	DNYSA	2	C2:+57.021	1204.098435	2406.18127	0.000622848	21	Y	16	37
Q05144	Exosome	EDYDR	LRPLSYPQTDVF	LICFS	2		718.3831558	1434.750712	0.000622848	9	Y	66	78
Q05144	Exosome	FLICF	SLVSPASYENVR	AKWFP	2		661.3414879	1320.667376	0.0007646	3	N	82	94
Q05144	Exosome	EDYDR	LRPLSYPQTDVFLIC	FSLVS	2	C15:+57.021	911.4823127	1820.949025	0.001162105	3	Y	66	81
Q05144	Exosome	SANVM	VDSKPVNLGLWDTAGQEDYDR	LRPLS	2		1189.567108	2377.118615	0.000451244	2	N	45	66
Q05144	Exosome	SANVM	VDSKPVNLGLWDTAGQEDYDR	LRPLS	3		793.3806718	2377.118615	0.000451244	15	N	45	66
Q05144	Exosome	EDYDR	LRPLSYPQTDVFLICFS	LVSPA	2	C15:+57.021	1028.532534	2055.049468	0.000622848	2	Y	66	83
Q05144	Exosome	VFDNY	SANVMVDSKPVNLGLWDTAGQEDYDR	LRPLS	3	M5:+15.995	966.1193284	2895.334585	0.000451244	9	N	40	66
Q05144	Exosome	QTDVF	LICFSLVSPASYENVR	AKWFP	2	C3:+57.021	927.9748519	1853.934104	0.000451244	12	N	78	94
Q05144	Exosome	ANVMV	DSKPVNLGLWDTAGQEDYDR	LRPLS	3		760.3578671	2278.050201	0.000698008	3	N	46	66
Q05144	Exosome	IPTVF	DNYSANVMVDSKPVNLGLWDTAGQEDYDR	LRPLS	3	M8:+15.995	1096.830395	3287.467784	0.000451244	3	N	37	66
Q05144	Parental	EDYDR	LRPLSYPQTDVFLICFSLVSPASYENVR	AKWFP	3	C15:+57.021	1091.232552	3270.674255	0.000451244	39	N	66	94
Q05144	Parental	KLKEK	KLAPITYPQGLALAK	DIDSV	2		792.4801303	1582.944661	0.001871652	1	N	132	147
Q05144	Parental	KLKEK	KLAPITYPQGLALAK	DIDSV	3		528.6560202	1582.944661	0.000735798	3	N	132	147
Q05144	Parental	EDYDR	LRPLSYPQTDVFLICF	SLVSP	2	C15:+57.021	985.0165197	1968.017439	0.000979378	17	Y	66	82
Q05144	Parental	LKEKK	LAPITYPQGLALAK	DIDSV	2		728.4326487	1454.849697	0.000451244	12	N	133	147
Q05144	Parental	DSKPV	NLGLWDTAGQEDYDR	LRPLS	2		876.8953444	1751.775089	0.000451244	5	Y	51	66
Q05144	Parental	FPEVR	HHCPSTPIILVGTK	LDLRD	2	C3:+57.021	780.4220581	1558.828516	0.001162105	1	N	102	116
Q05144	Parental	FPEVR	HHCPSTPIILVGTK	LDLRD	3	C3:+57.021	520.6173054	1558.828516	0.001329271	11	N	102	116
Q05144	Parental	IDSVK	YLECSALTQR	GLKTV	2	C4:+57.021	620.8034527	1239.591305	0.000451244	22	Y	153	163
Q05144	Parental	MVDSK	PVNLGLWDTAGQEDYDR	LRPLS	2		974.9559333	1947.896267	0.000823681	1	Y	49	66
Q05144	Parental	GAVGK	TCLLISYTTNAFPGEYIPTVFDNY	SANVM	2	C2:+57.021	1400.165035	2798.31447	0.002212458	2	Y	16	40
Q05144	Parental	GAVGK	TCLLISYTTNAFPGEYIPT	VFDNY	2	C2:+57.021	1081.030021	2160.044442	0.001943752	1	Y	16	35
Q05144	Parental	GAVGK	TCLLISYTTNAFPGEYIPTVF	DNYSA	2	C2:+57.021	1204.098435	2406.18127	0.000622848	4	Y	16	37
Q05144	Parental	EDYDR	LRPLSYPQTDVF	LICFS	2		718.3831558	1434.750712	0.001264573	9	Y	66	78
Q05144	Parental	FLICF	SLVSPASYENVR	AKWFP	2		661.3414879	1320.667376	0.000622848	3	N	82	94
Q06890	Exosome	GMVLG	EQEVSDNELQELSTQGSR	YINKE	2		1024.972509	2047.929417	0.000622848	23	N	21	39
Q06890	Exosome	GQCEK	CQEILSVDCSTNNPAQANLR	QELND	2	C1:+57.021,C9:+57.021	1145.531225	2289.04685	0.000451244	14	N	303	323
Q06890	Exosome	QVAER	LTEQYKELLQSFQSK	MLNTS	3		614.6601587	1840.957076	0.000851441	3	N	335	350
Q06890	Exosome	EVVVK	LFDSDPITVVLPEEVSKDNPK	FMDTV	2		1171.610453	2341.205305	0.000451244	12	N	407	428
Q06890	Exosome	EVVVK	LFDSDPITVVLPEEVSKDNPK	FMDTV	3		781.4095684	2341.205305	0.000451244	3	N	407	428
Q06890	Exosome	DSFAR	ASGIIDTLFQDR	FFARE	2		668.349313	1334.683026	0.000698008	10	N	181	193
Q06890	Parental	GMVLG	EQEVSDNELQELSTQGSR	YINKE	2		1024.972509	2047.929417	0.000451244	11	N	21	39
Q06890	Parental	GQCEK	CQEILSVDCSTNNPAQANLR	QELND	2	C1:+57.021,C9:+57.021	1145.531225	2289.04685	0.000451244	3	N	303	323
Q07076	Exosome	RKAMK	GFGTDEQAIVDVVSNR	SNDQR	2		853.9213622	1705.827124	0.000451244	14	N	174	190
Q07076	Exosome	RKAMK	GFGTDEQAIVDVVSNR	SNDQR	3		569.6168414	1705.827124	0.001463592	3	N	174	190
Q07076	Exosome	ESGLK	TILQCALNRPAFFAER	LYYSM	2	C5:+57.021	954.0017353	1905.987871	0.00307782	1	N	383	399
Q07076	Exosome	ESGLK	TILQCALNRPAFFAER	LYYSM	3	C5:+57.021	636.3370902	1905.987871	0.000451244	25	N	383	399
Q07076	Exosome	IVVTR	SEIDLVQIK	QMFTQ	2		522.8009359	1043.586272	0.000451244	14	N	421	430
Q07076	Exosome	GTQER	VLIEILCTR	TNQEI	2	C7:+57.021	558.8261995	1115.636799	0.002080925	16	N	253	262
Q07076	Exosome	SSVSR	EFSGYVESGLK	TILQC	2		608.2987574	1214.581915	0.001943752	3	N	372	383
Q07076	Exosome	AGEGR	LGTDESCFNMILATR	SFPQL	2	C7:+57.021	864.408488	1726.801376	0.000637154	1	N	331	346
Q07076	Exosome	ESGLK	TILQCALNRPAFF	AERLY	2	C5:+57.021	775.9113262	1549.807052	0.001463592	2	N	383	396
Q07076	Parental	RKAMK	GFGTDEQAIVDVVSNR	SNDQR	2		853.9213622	1705.827124	0.000451244	22	N	174	190
Q07076	Parental	IVVTR	SEIDLVQIK	QMFTQ	2		522.8009359	1043.586272	0.000451244	2	N	421	430
Q07076	Parental	SSVSR	EFSGYVESGLK	TILQC	2		608.2987574	1214.581915	0.001162105	2	N	372	383
Q07797	Exosome	FYRGR	WGTVCDNLWNLLDAHVVCR	ALGYE	3	C5:+57.021,C18:+57.021	776.7054708	2327.093012	0.000451244	42	N	44	63
Q07797	Exosome	LDLLK	AVDQWSTETIASHEDIER	LVEQV	2		1043.987962	2085.960324	0.000451244	21	N	323	341
Q07797	Exosome	LDLLK	AVDQWSTETIASHEDIER	LVEQV	3		696.3279079	2085.960324	0.000451244	24	N	323	341
Q07797	Exosome	KCLHK	LASAYGATELQDYCGR	LFATL	2	C14:+57.021	887.9071662	1773.798732	0.000451244	26	N	229	245
Q07797	Exosome	ALLPK	SELAVSSELDLLK	AVDQW	2		702.3855612	1402.755522	0.000823681	7	N	310	323

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q07797	Exosome	DYCGR	LFATLLPQDPTFHTPLDLYAYAR	ATGDS	2		1332.197561	2662.379522	0.000451244	7	N	245	268
Q07797	Exosome	DYCGR	LFATLLPQDPTFHTPLDLYAYAR	ATGDS	3		888.4676406	2662.379522	0.000451244	18	N	245	268
Q07797	Exosome	TNSSK	TPSLFPCASGAFSSFR	VVIRP	2	C7:+57.021	866.4118874	1730.808175	0.000451244	16	N	546	562
Q07797	Exosome	TYKPR	LYTSSTWSSLVMASTWR	AQRYE	2	M12:+15.995	996.4807729	1990.945946	0.001162105	2	N	407	424
Q07797	Exosome	GYENR	VLILCGGYSVVDVTSFEGSK	APIPT	2	C5:+57.021	1065.543296	2129.070991	0.000823681	5	N	513	533
Q07797	Exosome	GSVAR	YNSYQSFQTPQHPSFLFK	DKQIS	3		740.3572503	2218.048351	0.000451244	8	N	446	464
Q07797	Exosome	TLILR	TNPEAQALWQVVGSSVIMR	VDAEC	3		696.030369	2085.067707	0.001162105	1	N	177	196
Q07797	Parental	FYRGR	WGTVCDNLWNLLDAHVVCR	ALGYE	3	C5:+57.021,C18:+57.021	776.7054708	2327.093012	0.000451244	14	N	44	63
Q07797	Parental	DYCGR	LFATLLPQDPTFHTPLDLYAYAR	ATGDS	2		1332.197561	2662.379522	0.001162105	2	N	245	268
Q07797	Parental	DYCGR	LFATLLPQDPTFHTPLDLYAYAR	ATGDS	3		888.4676406	2662.379522	0.002019181	1	N	245	268
Q08093	Exosome	EAELR	SWIEGLTGLSIGPDFQK	GLKDG	2		924.4810556	1846.946511	0.000451244	23	N	35	52
Q08093	Parental	IYDPK	YCPQGSAADGAPAGDGQGEAPEYLAYCQEEAGY	-	3	C2:+57.021,C27:+57.021	1151.470201	3451.387202	0.000451244	29	N	272	305
Q08093	Parental	EAELR	SWIEGLTGLSIGPDFQK	GLKDG	2		924.4810556	1846.946511	0.000451244	38	N	35	52
Q08093	Parental	EAELR	SWIEGLTGLSIGPDFQK	GLKDG	3		616.6566371	1846.946511	0.000451244	3	N	35	52
Q08761	Exosome	SVVAR	LEAVSLCSDQQSQLK	CNVNR	2	C7:+57.021	853.4251918	1704.834784	0.000451244	10	N	560	575
Q08761	Exosome	LVDSR	SGTSQDIVVFVENSVVAR	LEAVS	2		953.9976012	1905.979602	0.000979378	1	N	542	560
Q08761	Exosome	LVDSR	SGTSQDIVVFVENSVVAR	LEAVS	3		636.3343341	1905.979602	0.000622848	5	N	542	560
Q08761	Exosome	AQDQK	SCEGIPVCLSLDLDKNYELLYLAEQFAGVVLYLK	FRLPD	3	C2:+57.021,C8:+57.021	1311.673875	3931.998224	0.001871652	2	N	280	314
Q08943	Exosome	PVHIR	FDEISFVNFAR	GTTTT	2		672.8332987	1343.650997	0.000451244	4	N	370	381
Q08943	Exosome	NVLSK	ADVIQATGDAICIFR	ELQCL	2	C12:+57.021	825.4197124	1648.823825	0.000451244	6	N	188	203
Q08943	Exosome	WGTVK	FGGQLLSFDIGDQPVFEIPLSNVSQCTTGK	NEVTL	3	C26:+57.021	1085.539822	3253.596065	0.000451244	9	N	113	143
Q08943	Exosome	LMEVR	FYVPPTQEDGVDPVEAFAQNVLSK	ADVIQ	2		1325.655923	2649.296246	0.000622848	1	N	164	188
Q08943	Parental	PVHIR	FDEISFVNFAR	GTTTT	2		672.8332987	1343.650997	0.000451244	12	N	370	381
Q08943	Parental	NVLSK	ADVIQATGDAICIFR	ELQCL	2	C12:+57.021	825.4197124	1648.823825	0.000451244	9	N	188	203
Q08943	Parental	WGTVK	FGGQLLSFDIGDQPVFEIPLSNVSQCTTGK	NEVTL	3	C26:+57.021	1085.539822	3253.596065	0.000451244	31	N	113	143
Q08943	Parental	ASREK	IKSDHPGISITDLSK	KAGEI	3		537.6303109	1609.867533	0.000622848	3	N	564	579
Q08943	Parental	SKTGK	VDNIQAGELTEGIWR	RVALG	2		850.9342726	1699.852945	0.000622848	2	N	39	54
Q09014	Exosome	YLVPK	DGKNNVADITGPIILQTYR	AIADY	2		1044.558357	2087.101115	0.000451244	18	N	143	162
Q09014	Exosome	YLVPK	DGKNNVADITGPIILQTYR	AIADY	3		696.7081716	2087.101115	0.000451244	6	N	143	162
Q09014	Exosome	VPASY	LEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	2		1437.664339	2873.313078	0.000451244	15	N	209	235
Q09014	Exosome	VPASY	LEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		958.7788259	2873.313078	0.000451244	10	N	209	235
Q09014	Exosome	PKDGK	NNVADITGPIILQTYR	AIADY	2		894.4866723	1786.957745	0.000451244	10	N	146	162
Q09014	Exosome	EVIHK	LLDGWWVVR	KGDIT	2		572.3196302	1142.62366	0.000622848	17	N	258	267
Q09014	Exosome	QMKTK	RGWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1264.264005	3789.768615	0.000451244	53	N	201	235
Q09014	Exosome	MKTKR	GWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1212.230301	3633.667503	0.000451244	44	N	202	235
Q09014	Exosome	PSTPR	VKPQPAVPPRPSSDLILHR	CTEST	4		527.5593472	2106.206189	0.000451244	3	N	358	377
Q09014	Exosome	PKDGK	NNVADITGPIILQTY	RAIAD	2		816.4361168	1630.856634	0.000451244	12	N	146	161
Q09014	Exosome	ADYEK	SSGTEMTVATGDVVDVVEK	SESGW	2	M6:+15.995	970.4624429	1938.909286	0.000451244	4	N	169	188
Q09014	Exosome	QMKTK	RGWVPASYLEPLDSPDEAEDPDPNYAGEPY	VTIKA	3		1117.165632	3348.473495	0.002663018	2	N	201	231
Q09014	Parental	YLVPK	DGKNNVADITGPIILQTYR	AIADY	2		1044.558357	2087.101115	0.000451244	28	N	143	162
Q09014	Parental	YLVPK	DGKNNVADITGPIILQTYR	AIADY	3		696.7081716	2087.101115	0.000622848	3	N	143	162
Q09014	Parental	VPASY	LEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	2		1437.664339	2873.313078	0.000451244	25	N	209	235
Q09014	Parental	VPASY	LEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		958.7788259	2873.313078	0.000451244	1	N	209	235
Q09014	Parental	PKDGK	NNVADITGPIILQTYR	AIADY	2		894.4866723	1786.957745	0.000451244	2	N	146	162
Q09014	Parental	EVIHK	LLDGWWVVR	KGDIT	2		572.3196302	1142.62366	0.000622848	23	N	258	267
Q09014	Parental	QMKTK	RGWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1264.264005	3789.768615	0.000451244	52	N	201	235
Q09014	Parental	MKTKR	GWVPASYLEPLDSPDEAEDPDPNYAGEPYVTIK	AYAAV	3		1212.230301	3633.667503	0.000451244	44	N	202	235
Q09014	Parental	PDDLK	LPTDSQAKKPETYLVPK	DGKNN	3		639.0232085	1914.046225	0.000451244	4	N	126	143
Q09014	Parental	PSTPR	VKPQPAVPPRPSSDLILHR	CTEST	4		527.5593472	2106.206189	0.000698008	2	N	358	377
Q09014	Parental	YLVPK	DGKNNVADITGPIILQTY	RAIAD	2		966.5078018	1931.000004	0.000451244	1	N	143	161
Q09014	Parental	VKISR	CPHLLDFFK	VRPDD	2	[0:-17.027,C1:+57.021	580.283942	1158.552284	0.002727428	1	N	110	119
Q09014	Parental	PKDGK	NNVADITGPIILQTY	RAIAD	2		816.4361168	1630.856634	0.000823681	2	N	146	161
Q09014	Parental	QMKTK	RGWVPASYLEPLDSPDEAEDPDPNYAGEPY	VTIKA	3		1117.165632	3348.473495	0.000451244	1	N	201	231
Q09200	Exosome	LARSR	SLADQLLIAPANSPLQYPLQGVEVQPLR	SILVP	3		1010.89279	3029.654969	0.000451244	9	N	130	158
Q09200	Exosome	QGPPR	LDLLDLAPEPR	YAHIP	2		626.3513243	1250.687049	0.002727428	1	N	48	59
Q09200	Parental	LARSR	SLADQLLIAPANSPLQYPLQGVEVQPLR	SILVP	3		1010.89279	3029.654969	0.000451244	2	N	130	158
Q09PK2	Exosome	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	2		1260.145663	2518.275725	0.000622848	8	N	96	118
Q09PK2	Exosome	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	3		840.4330417	2518.275725	0.000451244	28	N	96	118
Q09PK2	Exosome	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	4		630.5767313	2518.275725	0.000451244	31	N	96	118
Q09PK2	Exosome	GAEMK	ILGVWDTEISLGK	TKLKA	2		715.8986387	1429.781677	0.000451244	32	N	250	263
Q09PK2	Exosome	LRFLK	ESLKGDALDVYNGLSSQAQGDFSFVK	QALLR	2		1388.177751	2774.339902	0.000451244	36	N	138	164
Q09PK2	Exosome	LRFLK	ESLKGDALDVYNGLSSQAQGDFSFVK	QALLR	3		925.7877672	2774.339902	0.000451244	42	N	138	164
Q09PK2	Exosome	LGKTK	LKAEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		1245.971267	3734.890402	0.000451244	1	N	265	299
Q09PK2	Exosome	LGKTK	LKAEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	4		934.7304004	3734.890402	0.000451244	35	N	265	299
Q09PK2	Exosome	QALLR	AFGAPGEAFSEPEEILFANSMGK	GYYLK	2		1200.065356	2398.115111	0.000451244	6	N	169	192

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q09PK2	Exosome	QALLR	AFGAPGEAFSEPEEILFANSMGK	GYYLK	3		800.3795037	2398.115111	0.000451244	3	N	169	192
Q09PK2	Exosome	QALLR	AFGAPGEAFSEPEEILFANSMGK	GYYLK	2	M21:+15.995	1208.062856	2414.110111	0.000451244	40	N	169	192
Q09PK2	Exosome	QALLR	AFGAPGEAFSEPEEILFANSMGK	GYYLK	3	M21:+15.995	805.7111703	2414.110111	0.000451244	36	N	169	192
Q09PK2	Exosome	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPFNNVVK	VANGA	3		1323.013244	3966.016331	0.000451244	34	N	206	242
Q09PK2	Exosome	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPFNNVVK	VANGA	4		992.5118826	3966.016331	0.000451244	45	N	206	242
Q09PK2	Exosome	GKKFR	LLPVGSSLEDEFDLELIEEEEGSSAPEGSH	-	3		1072.165297	3213.472492	0.000451244	42	N	309	339
Q09PK2	Exosome	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPF	NNVVK	3		1138.240695	3411.698684	0.001871652	2	N	206	237
Q09PK2	Exosome	KTKLK	AEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		1165.578258	3493.711374	0.000451244	4	N	267	299
Q09PK2	Exosome	KTKLK	AEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	4		874.4356436	3493.711374	0.000451244	19	N	267	299
Q09PK2	Exosome	KESLK	GDALDVYNGLSSQAQGDFSFVK	QALLR	2		1159.550926	2317.086253	0.000451244	21	N	142	164
Q09PK2	Exosome	LWLHR	FEVIDDLNHWDHATK	LRFLK	2		920.4371794	1838.858759	0.000451244	12	N	118	133
Q09PK2	Exosome	LWLHR	FEVIDDLNHWDHATK	LRFLK	3		613.9607196	1838.858759	0.001162105	7	N	118	133
Q09PK2	Exosome	LWLHR	FEVIDDLNHWDHATK	LRFLK	4		460.7224897	1838.858759	0.000622848	11	N	118	133
Q09PK2	Exosome	SKEGR	REHAFVPEPFTGTNLAPSLWLHR	FEVID	3		892.4667455	2674.376836	0.000637154	3	N	95	118
Q09PK2	Exosome	SKEGR	REHAFVPEPFTGTNLAPSLWLHR	FEVID	4		669.6020091	2674.376836	0.000451244	14	N	95	118
Q09PK2	Exosome	EFLVA	NASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		955.4656871	2863.373661	0.002884417	1	N	273	299
Q09PK2	Exosome	AFVPE	PFTGTNLAPSLWLHR	FEVID	3		570.6427737	1708.904921	0.000451244	1	N	103	118
Q09PK2	Parental	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	2		1260.145663	2518.275725	0.000451244	13	N	96	118
Q09PK2	Parental	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	3		840.4330417	2518.275725	0.000451244	26	N	96	118
Q09PK2	Parental	KEGRR	EHAFVPEPFTGTNLAPSLWLHR	FEVID	4		630.5767313	2518.275725	0.000451244	32	N	96	118
Q09PK2	Parental	GAEMK	ILGVWDTEISLGK	TKLKA	2		715.8986387	1429.781677	0.000451244	43	N	250	263
Q09PK2	Parental	LRFLK	ESLKGDALDVYNGLSSQAQGDFSFVK	QALLR	2		1388.177751	2774.339902	0.000451244	44	N	138	164
Q09PK2	Parental	LRFLK	ESLKGDALDVYNGLSSQAQGDFSFVK	QALLR	3		925.7877672	2774.339902	0.000451244	48	N	138	164
Q09PK2	Parental	LGKTK	LKAEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		1245.971267	3734.890402	0.000451244	19	N	265	299
Q09PK2	Parental	LGKTK	LKAEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	4		934.7304004	3734.890402	0.000451244	593	N	265	299
Q09PK2	Parental	QALLR	AFGAPGEAFSEPEEILFANSMGK	GYYLK	2		1200.065356	2398.115111	0.000451244	16	N	169	192
Q09PK2	Parental	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPFNNVVK	VANGA	3		1323.013244	3966.016331	0.000451244	70	N	206	242
Q09PK2	Parental	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPFNNVVK	VANGA	4		992.5118826	3966.016331	0.000451244	147	N	206	242
Q09PK2	Parental	LKGKK	FRLLPVGSSLEDEFDLELIEEEEGSSAPEGSH	-	3		1173.221806	3516.642017	0.000451244	17	N	307	339
Q09PK2	Parental	GKKFR	LLPVGSSLEDEFDLELIEEEEGSSAPEGSH	-	3		1072.165297	3213.472492	0.000451244	145	N	309	339
Q09PK2	Parental	HVPVR	FLVDSGAQVSVVHPALWEEVTDGDLDTLRPF	NNVVK	3		1138.240695	3411.698684	0.000451244	11	N	206	237
Q09PK2	Parental	KTKLK	AEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	3		1165.578258	3493.711374	0.000451244	15	N	267	299
Q09PK2	Parental	KTKLK	AEFLVANASAEEAIIGTDVLQDHNAVLDFEHR	TCTLK	4		874.4356436	3493.711374	0.000451244	30	N	267	299
Q09PK2	Parental	KESLK	GDALDVYNGLSSQAQGDFSFVK	QALLR	2		1159.550926	2317.086253	0.000451244	12	N	142	164
Q09PK2	Parental	KESLK	GDALDVYNGLSSQAQGDFSFVK	QALLR	3		773.3698842	2317.086253	0.000451244	2	N	142	164
Q09PK2	Parental	LWLHR	FEVIDDLNHWDHATK	LRFLK	2		920.4371794	1838.858759	0.000451244	20	N	118	133
Q09PK2	Parental	LWLHR	FEVIDDLNHWDHATK	LRFLK	3		613.9607196	1838.858759	0.000451244	8	N	118	133
Q09PK2	Parental	LWLHR	FEVIDDLNHWDHATK	LRFLK	4		460.7224897	1838.858759	0.000451244	22	N	118	133
Q09PK2	Parental	SKEGR	REHAFVPEPFTGTNLAPSLWLHR	FEVID	3		892.4667455	2674.376836	0.000622848	2	N	95	118
Q09PK2	Parental	SKEGR	REHAFVPEPFTGTNLAPSLWLHR	FEVID	4		669.6020091	2674.376836	0.000451244	10	N	95	118
Q09PK2	Parental	QALLR	AFGAPGEAFSEPEEILF	ANSMG	2		905.9308642	1809.846128	0.001463592	4	N	169	186
Q09PK2	Parental	VPEPF	TGTNLAPSLWLHR	FEVID	3		489.2690477	1464.783743	0.000622848	4	N	105	118
Q11011	Exosome	ELIQK	VLTFALSEEVRPQDTVSVIGGVAGGSK	HGRKA	2		1358.729954	2715.444307	0.000451244	3	N	795	822
Q11011	Exosome	ELIQK	VLTFALSEEVRPQDTVSVIGGVAGGSK	HGRKA	3		906.1559024	2715.444307	0.000451244	34	N	795	822
Q11011	Exosome	ADYTR	AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	GASVI	3		1237.927393	3710.758778	0.000451244	29	N	407	441
Q11011	Exosome	ADYTR	AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	GASVI	4		928.6974946	3710.758778	0.000451244	22	N	407	441
Q11011	Exosome	PSAER	TIQQCCENILLNAAWLK	RDADS	2	C5:+57.021,C6:+57.021	1038.024319	2074.033038	0.000451244	32	N	883	900
Q11011	Exosome	PSAER	TIQQCCENILLNAAWLK	RDADS	3	C5:+57.021,C6:+57.021	692.3521459	2074.033038	0.000451244	29	N	883	900
Q11011	Exosome	PPVDR	LGLQNDLFSLAR	AGIIS	2		673.8754979	1345.735396	0.000451244	35	N	616	628
Q11011	Exosome	RPFER	LPAEVSPINYSLCLKPDLLDFTFEGK	LEAAA	3	C13:+57.021	989.5125441	2965.514232	0.000451244	19	N	54	80
Q11011	Exosome	NVIDR	KPYPDDENLVEVK	FARTP	2		773.3939175	1544.772235	0.000451244	6	N	222	235
Q11011	Exosome	NEDEK	VTLSFPSTLQTGTGTLK	IDFVG	2		875.9834312	1749.951262	0.000823681	4	N	129	146
Q11011	Exosome	LPFYK	DYFNVPYPLPK	IDLIA	2		676.8484175	1351.681235	0.000451244	15	N	294	305
Q11011	Exosome	TGTLK	IDFVGELNDK	MKGFY	2		575.293475	1148.57135	0.000451244	13	N	146	156
Q11011	Exosome	DQWVK	LNLGTVGFYR	TQYSS	2		570.3145448	1138.61349	0.000451244	6	N	581	591
Q11011	Exosome	AGEVR	YAAVTQFEATDARR	AFPCW	3		533.6027551	1597.784865	0.001229886	2	N	173	187
Q11011	Exosome	NRIER	VLGATLSPELIQK	VLTFA	2		684.9090065	1367.802413	0.000451244	15	N	782	795
Q11011	Exosome	PIGER	LGWDPKPGEGHLDALLR	GLVLG	2		937.5001141	1872.984628	0.000622848	5	N	690	707
Q11011	Exosome	PIGER	LGWDPKPGEGHLDALLR	GLVLG	4		469.253957	1872.984628	0.000451244	18	N	690	707
Q11011	Exosome	EPAIK	ATFDISLVVPK	DRVAL	2		595.3455106	1188.675421	0.000622848	8	N	198	209
Q11011	Exosome	KFQQK	NAATEDLWESLESASGKPIAAVMNTWTK	QMGFP	3		1007.494367	3019.4597	0.000451244	9	N	472	500
Q11011	Exosome	PSAER	TIQQCCENILLNAAWLKR	DADSI	3	C5:+57.021,C6:+57.021	744.3858496	2230.134149	0.002519933	2	N	883	901
Q11011	Exosome	AGEVR	YAAVTQFEATDAR	RAFPC	2		721.8496771	1441.683754	0.001654178	1	N	173	186
Q11011	Exosome	KAAWK	FIKDNWEELHNR	YQGGF	4		400.9526465	1599.779386	0.000451244	1	N	830	842
Q11011	Exosome	SADLR	SPVYLTVLK	HGDGA	2		510.3109395	1018.606279	0.000622848	4	N	745	754

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q11011	Parental	ELIQK	VLTFALSEEVRPQDTVSVIGGVAGGSK	HGRKA	3		906.1559024	2715.444307	0.000451244	8	N	795	822
Q11011	Parental	ADYTR	AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	GASVI	3		1237.927393	3710.758778	0.000451244	26	N	407	441
Q11011	Parental	ADYTR	AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	GASVI	4		928.6974946	3710.758778	0.001352548	3	N	407	441
Q11011	Parental	PSAER	TIQQCCENILLNAAWLK	RDADS	2	C5:+57.021,C6:+57.021	1038.024319	2074.033038	0.000451244	2	N	883	900
Q11011	Parental	PSAER	TIQQCCENILLNAAWLK	RDADS	3	C5:+57.021,C6:+57.021	692.3521459	2074.033038	0.001463592	4	N	883	900
Q11011	Parental	PPVDR	LGLQNDLFSLAR	AGIIS	2		673.8754979	1345.735396	0.000451244	5	N	616	628
Q11011	Parental	NRIER	VLGATLSPELIQK	VLTFA	2		684.9090065	1367.802413	0.001329271	3	N	782	795
Q11011	Parental	PIGER	LGWDPKPGEGHLDALLR	GLVLG	2		937.5001141	1872.984628	0.001839721	1	N	690	707
Q11011	Parental	PIGER	LGWDPKPGEGHLDALLR	GLVLG	4		469.253957	1872.984628	0.002884417	1	N	690	707
Q11011	Parental	KFQQK	NAATEDLWESLESASGKPIAAVMNTWTK	QMGFP	3		1007.494367	3019.4597	0.001943752	1	N	472	500
Q11011	Parental	VKFAR	TPVMSTYLVAFVVGEYDFVETR	SKDGV	3	M4:+15.995	847.0862372	2538.235312	0.002374549	1	N	238	260
Q11136	Exosome	YFKEK	YAVDDVQYTDEIASVLTSR	NPSVL	2		1073.02147	2144.027341	0.000451244	20	N	120	139
Q11136	Exosome	NETLK	VPLALFALNR	QRLCE	2		557.3431053	1112.670611	0.002145581	2	N	17	27
Q11136	Exosome	RGGMR	HTSYTCICCSGENAAVLHYGHAGAPNDR	TIKDG	4	C6:+57.021,C8:+57.021,C9:+57.02	780.3384449	3117.32258	0.001943752	1	N	237	265
Q11136	Parental	YFKEK	YAVDDVQYTDEIASVLTSR	NPSVL	2		1073.02147	2144.027341	0.000451244	5	N	120	139
Q1HFZ0	Exosome	ALLEK	SEGALELADVSAELPGLK	WMPGV	2		899.9758031	1797.936006	0.000662267	1	N	338	356
Q1HFZ0	Parental	KDLAK	GSVVLKYEPDSANPDTLQCPIVLCGWR	GKASI	3	C19:+57.021,C24:+57.021	1025.507533	3073.499199	0.00307782	1	N	653	680
Q1HFZ0	Parental	SVVLK	YEPDSANPDTLQCPIVLCGWR	GKASI	2	C13:+57.021,C18:+57.021	1246.072726	2490.129851	0.000451244	3	N	659	680
Q1HFZ0	Parental	SKKMK	LFGFKEDPFVFIPEDDPLFPPIEK	FYALD	3		946.1548397	2835.441119	0.00307782	1	N	510	534
Q1HFZ0	Parental	ALLEK	SEGALELADVSAELPGLK	WMPGV	2		899.9758031	1797.936006	0.00091018	1	N	338	356
Q1HFZ0	Parental	ARGRR	FQQPPQPEGEEDASDGGR	KRGQA	2		972.4224547	1942.829309	0.000622848	4	N	9	27
Q20BD0	Exosome	DPVKK	IFVGGLNPEATEEK	IREYF	2		752.3886352	1502.76167	0.000622848	7	N	160	174
Q20BD0	Exosome	ATEEK	IREYFGQFGEIEAIELPIDPK	LNKRR	3		822.0973247	2463.268574	0.000451244	25	N	174	195
Q20BD0	Exosome	KIREY	FGQFGEIEAIELPIDPK	LNKRR	2		951.9965386	1901.977477	0.000823681	4	N	178	195
Q20BD0	Exosome	EEKIR	EYFGQFGEIEAIELPIDPK	LNKRR	2		1098.049499	2194.083399	0.000451244	29	N	176	195
Q20BD0	Exosome	EEKIR	EYFGQFGEIEAIELPIDPK	LNKRR	3		732.368933	2194.083399	0.000622848	4	N	176	195
Q20BD0	Parental	DYSPY	GYYGYGPGYDYSQGSTNYGK	SQRRG	2		1098.961413	2195.907225	0.000451244	25	N	298	318
Q20BD0	Parental	DPVKK	IFVGGLNPEATEEK	IREYF	2		752.3886352	1502.76167	0.000451244	39	N	160	174
Q20BD0	Parental	ATEEK	IREYFGQFGEIEAIELPIDPK	LNKRR	3		822.0973247	2463.268574	0.000451244	21	N	174	195
Q20BD0	Parental	KIREY	FGQFGEIEAIELPIDPK	LNKRR	2		951.9965386	1901.977477	0.000451244	45	N	178	195
Q20BD0	Parental	KIREY	FGQFGEIEAIELPIDPK	LNKRR	3		635.0002924	1901.977477	0.001162105	4	N	178	195
Q20BD0	Parental	EEKIR	EYFGQFGEIEAIELPIDPK	LNKRR	2		1098.049499	2194.083399	0.000451244	49	N	176	195
Q20BD0	Parental	DYFTK	FGEVVDCTIK	MDPNT	2	C7:+57.021	584.2896468	1166.563694	0.000451244	25	Y	97	107
Q20BD0	Parental	DPVKK	IFVGGLNPEATEEKIR	EYFGQ	2		886.9812228	1771.946846	0.000637154	2	N	160	176
Q20BD0	Parental	DPVKK	IFVGGLNPEATEEKIR	EYFGQ	3		591.6567485	1771.946846	0.000870037	2	N	160	176
Q2NL51	Exosome	RDSGK	VTTVVATVGQGPER	SQEVA	2		707.3889695	1412.762339	0.000451244	8	N	99	113
Q2NL51	Exosome	FKSSK	TPPEAIALCSSLLEYTPSSR	LSPLE	2	C9:+57.021	1096.549109	2191.082619	0.000451244	6	N	372	392
Q2NL51	Exosome	GVCHR	DIKPQNLLVDPDTAVLK	LCDFG	3		627.0232085	1878.046225	0.000870037	3	N	243	260
Q2NL51	Parental	DELRR	LGAQLPNDRPLPPLFNFSPGELSIQPSLNAILIPPHLR	SPAGP	4		1036.328813	4141.284054	0.000451244	6	N	409	447
Q2VLH6	Exosome	PTSIK	ALGWANSSAGSGYIWMDK	VSCTG	2		957.4466904	1912.877781	0.000979378	1	N	98	116
Q2VLH6	Exosome	EIWHK	GSWGTVCDDSWDLNDAK	VVCKQ	2	C7:+57.021	963.402445	1924.78929	0.000451244	2	N	948	965
Q2VLH6	Exosome	VQCPK	GVDTLWQCPSSPWK	QRQAS	2	C8:+57.021	830.8933305	1659.771061	0.002374549	1	N	897	911
Q2VLH6	Exosome	VKALK	EAAFGPGTGPIWLNEIK	CRGNE	2		900.4704909	1798.925382	0.000451244	4	N	981	998
Q2VLH6	Exosome	RLEVR	FQGEWGTVCDDNWDLR	DASVV	2	C9:+57.021	999.4262544	1996.836909	0.000451244	2	N	281	297
Q2YFS3	Parental	NQPES	CSGVQGGSIDIPFSFYFPWK	LAKDP	2	C1:+57.021	1146.54363	2291.07166	0.002374549	1	N	47	67
Q2YFS3	Parental	RSNRK	NGFGVNQPESCSGVQGGSIDIPFSFYFPWK	LAKDP	3	C11:+57.021	1107.848878	3320.523234	0.000823681	1	N	37	67
Q2YFS3	Parental	NNIVY	ASISLSSPTSPGTAPNLPVHGNPQEETVYSIVK	AK-	3		1126.579488	3376.715063	0.001943752	1	N	267	300
Q3TBD2	Exosome	LVRGY	RSPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1151.590164	3451.747091	0.000451244	15	N	90	124
Q3TBD2	Exosome	VRGYR	SPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1099.55646	3295.64598	0.000451244	21	N	91	124
Q3TBD2	Exosome	HQVHK	SWPISISDTEVGLDTSSGDLK	KFDRT	2		1104.03986	2206.06412	0.000823681	3	N	617	638
Q3TBD2	Exosome	KLQGR	LQLFGQDFSQAALSTPDGVPFIVK	KCVCE	2		1289.681744	2577.347887	0.000451244	9	N	752	776
Q3TBD2	Exosome	KLQGR	LQLFGQDFSQAALSTPDGVPFIVKK	CVCEI	3		902.8220835	2705.44285	0.000451244	2	N	752	777
Q3TBD2	Parental	LVRGY	RSPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1151.590164	3451.747091	0.000451244	35	N	90	124
Q3TBD2	Parental	WTLVR	GYRSPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1224.951761	3671.831884	0.000451244	5	N	88	124
Q3TBD2	Parental	KLQGR	LQLFGQDFSQAALSTPDGVPF	IVKKC	2		1119.558023	2237.100446	0.001352548	4	N	752	773
Q3TBD2	Parental	VRGYR	SPLSAASPAELPTEGAFPDGVEDISTLLADVAR	FAEGL	3		1099.55646	3295.64598	0.000451244	25	N	91	124
Q3TBD2	Parental	VRGYR	SPLSAASPAELPTEGAFPDGVEDISTLLADVARF	AEGLE	3		1148.579265	3442.714394	0.000451244	4	N	91	125
Q3TBD2	Parental	EGLEK	LKECVLQDDLLEAR	RPLAH	2	C4:+57.021	851.4459272	1700.876254	0.000622848	5	N	131	145
Q3TBD2	Parental	EGLEK	LKECVLQDDLLEAR	RPLAH	3	C4:+57.021	567.9665515	1700.876254	0.001329271	3	N	131	145
Q3TBD2	Parental	HQVHK	SWPISISDTEVGLDTSSGDLK	KFDRT	2		1104.03986	2206.06412	0.000451244	25	N	617	638
Q3TBD2	Parental	CESSK	LYDPGQQYASHVR	QLQRG	3		511.9201956	1532.737187	0.002519933	1	N	531	544
Q3TBD2	Parental	KLQGR	LQLFGQDFSQAALSTPDGVPFIVK	KCVCE	2		1289.681744	2577.347887	0.000451244	3	N	752	776
Q3TBD2	Parental	QVISR	YPLLNTVETLTAAGTLIAK	VKAFH	2		995.0674952	1988.11939	0.000698008	4	N	166	185
Q3TBD2	Parental	QVISR	YPLLNTVETLTAAGTLIAK	VKAFH	3		663.7142635	1988.11939	0.00307782	1	N	166	185
Q3TDN2	Parental	ANFPR	RVLPCVPSEEWPNPPTLQEAGLSHTEVLFVQDLTDE	-	3	C5:+57.021	1368.340766	4101.998897	0.002145581	1	N	409	445

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3TDN2	Parental	DEFCR	NALCAPEVISLINSR	MLFWA	2	C4:+57.021	828.940812	1655.866024	0.001329271	2	N	190	205
Q3TGF2	Parental	LEKQK	LQEEQENAPEFVK	VKGNL	2		780.8811743	1559.746749	0.000451244	21	N	100	113
Q3TGF2	Parental	LELEK	QKLQEEQENAPEFVK	VKGNL	2		908.9579447	1815.900289	0.000662267	8	N	98	113
Q3THE2	Exosome	MFGEK	LNGTDPEDVIR	NAFAC	2		614.8125633	1227.609527	0.000451244	52	Y	93	104
Q3THE2	Exosome	PIDKK	GNFNYIEFTR	ILKHG	2		630.8045413	1259.593483	0.000451244	20	Y	151	161
Q3THE2	Exosome	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	3		811.3815729	2431.121319	0.001463592	1	Y	124	144
Q3THE2	Exosome	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	3	M6:+15.995	816.7132396	2447.116319	0.000451244	12	Y	124	144
Q3THE2	Exosome	EDVIR	NAFACFDEEATGTIQEDYLR	ELLTT	2	C5:+57.021	1175.518538	2349.021475	0.000451244	92	N	104	124
Q3THE2	Exosome	EDVIR	NAFACFDEEATGTIQEDYLR	ELLTT	3	C5:+57.021	784.0149584	2349.021475	0.000451244	7	N	104	124
Q3THE2	Exosome	TMGDR	FTDEEVDELYR	EAPID	2		708.3204182	1414.625236	0.000451244	24	Y	133	144
Q3THE2	Exosome	PQRAT	SNVFAMFDQSQIQEFK	EAFNM	2	M6:+15.995	967.9518483	1933.888097	0.000451244	6	Y	19	35
Q3THE2	Exosome	KRPQR	ATSNVFAMFDQSQIQEFK	EAFNM	2	M8:+15.995	1053.994245	2105.972889	0.000451244	21	Y	17	35
Q3THE2	Exosome	KRPQR	ATSNVFAMFDQSQIQEF	KEAFN	2	M8:+15.995	989.9467629	1977.877926	0.000451244	13	Y	17	34
Q3THE2	Exosome	IDQNR	DGFIDKEDLHDMLASLGK	NPTDA	3		668.6634633	2002.96699	0.000451244	6	Y	45	63
Q3THE2	Parental	MFGEK	LNGTDPEDVIR	NAFAC	2		614.8125633	1227.609527	0.000451244	58	Y	93	104
Q3THE2	Parental	PIDKK	GNFNYIEFTR	ILKHG	2		630.8045413	1259.593483	0.000451244	36	Y	151	161
Q3THE2	Parental	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	2		1216.568459	2431.121319	0.000622848	4	Y	124	144
Q3THE2	Parental	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	3		811.3815729	2431.121319	0.000451244	8	Y	124	144
Q3THE2	Parental	EDVIR	NAFACFDEEATGTIQEDYLR	ELLTT	2	C5:+57.021	1175.518538	2349.021475	0.000451244	820	N	104	124
Q3THE2	Parental	EDVIR	NAFACFDEEATGTIQEDYLR	ELLTT	3	C5:+57.021	784.0149584	2349.021475	0.000451244	26	N	104	124
Q3THE2	Parental	TMGDR	FTDEEVDELYR	EAPID	2		708.3204182	1414.625236	0.000451244	58	Y	133	144
Q3THE2	Parental	MFGEK	LNGTDPEDVIRNAFACFDEEATGTIQEDYLR	ELLTT	3	C16:+57.021	1187.214614	3558.620442	0.000451244	2	N	93	124
Q3THE2	Parental	FLTMF	GEKLNGTDPEDVIR	NAFAC	2		771.8920734	1541.768547	0.000451244	4	Y	90	104
Q3THE2	Parental	LLTTM	GDRFTDEEVDELYR	EAPID	2		872.3951772	1742.774754	0.002813207	1	Y	130	144
Q3THE2	Parental	VIRNA	FACFDEEATGTIQEDYLR	ELLTT	2	C3:+57.021	1082.978517	2163.941434	0.000451244	2	N	106	124
Q3THE2	Parental	IDQNR	DGFIDKEDLHDMLASLGK	NPTDA	3		668.6634633	2002.96699	0.000451244	8	Y	45	63
Q3THK3	Parental	NTAYY	IFTQCADGAFEAFPVQNWYNFTPLAR	HRTLT	3	C5:+57.021	1021.820483	3062.438048	0.000451244	6	N	125	151
Q3THK3	Parental	ENTAY	YIFTQCADGAFEAFPVQNWYNFTPLAR	HRTLT	3	C6:+57.021	1076.174925	3225.501376	0.002296037	2	N	124	151
Q3THK7	Exosome	KVILK	NFLYDIAGCSGNFTVQNR	ELECI	2	C9:+57.021	1038.484104	2074.952607	0.000451244	17	N	204	222
Q3THK7	Exosome	HNINR	VVYIFGPPVKEPPTDVTPTFLTTGVLSTLR	QADFE	3		1082.267634	3243.779501	0.000451244	22	N	559	589
Q3THK7	Exosome	QGDCR	SYSYVCGISSKDEPDWESLIFLAR	LIPRM	3	C6:+57.021	941.4499438	2821.326431	0.000451244	11	N	524	548
Q3THK7	Exosome	DRRVR	ELFVQSEIFPLETPAFAIK	EQGFR	2		1090.088428	2178.161255	0.000451244	15	N	46	65
Q3THK7	Exosome	EQGFR	AIIISGGPNSVYAEDAPWFDPAIFTIGKPILGICY	GMQMM	3	C34:+57.021	1255.979781	3764.915943	0.002374549	1	N	70	105
Q3THK7	Exosome	GISSK	DEPDWESLIFLAR	LIPRM	2		795.8940847	1589.772569	0.000451244	4	N	535	548
Q3THK7	Exosome	GLAIR	VICAEEPYICKDFPETNNILK	IVADF	3	C3:+57.021,C10:+57.021	851.7505229	2552.228169	0.000622848	1	N	446	467
Q3THK7	Parental	KVILK	NFLYDIAGCSGNFTVQNR	ELECI	2	C9:+57.021	1038.484104	2074.952607	0.000451244	6	N	204	222
Q3THK7	Parental	HNINR	VVYIFGPPVKEPPTDVTPTFLTTGVLSTLR	QADFE	3		1082.267634	3243.779501	0.000451244	9	N	559	589
Q3THK7	Parental	QGDCR	SYSYVCGISSKDEPDWESLIFLAR	LIPRM	3	C6:+57.021	941.4499438	2821.326431	0.000451244	6	N	524	548
Q3THK7	Parental	DRRVR	ELFVQSEIFPLETPAFAIK	EQGFR	2		1090.088428	2178.161255	0.000451244	10	N	46	65
Q3THK7	Parental	EQGFR	AIIISGGPNSVYAEDAPWFDPAIFTIGKPILGICY	GMQMM	3	C34:+57.021	1255.979781	3764.915943	0.00307782	1	N	70	105
Q3TIU4	Exosome	DSFIR	TVSYNILADTYAQTEFSR	TVLYP	2		1040.005623	2077.995647	0.001264573	3	N	295	313
Q3TIU4	Exosome	QEVDR	AVFSDSLVPALEAFGLEGVFR	IKQHE	2		1112.586583	2223.157567	0.000451244	1	N	353	374
Q3TIU4	Parental	QEVDR	AVFSDSLVPALEAFGLEGVFR	IKQHE	2		1112.586583	2223.157567	0.00091018	1	N	353	374
Q3TIX9	Exosome	LNNIK	ANDYANAVLQALSNVPPLR	NYFLE	3		676.0292451	2025.064335	0.000823681	2	N	230	249
Q3TIX9	Exosome	QAVHK	NTTYDLIANIVHDGKPSEGSYR	IHVLH	3		817.4035879	2449.187364	0.000698008	4	N	492	514
Q3TIX9	Exosome	AKLSR	AYDGTTYLPGIVGLNNIK	ANDYA	2		955.0074376	1907.999275	0.000451244	1	N	212	230
Q3TIX9	Parental	LNNIK	ANDYANAVLQALSNVPPLR	NYFLE	2		1013.539968	2025.064335	0.001264573	1	N	230	249
Q3TIX9	Parental	LNNIK	ANDYANAVLQALSNVPPLR	NYFLE	3		676.0292451	2025.064335	0.00091018	1	N	230	249
Q3TIX9	Parental	AKLSR	AYDGTTYLPGIVGLNNIK	ANDYA	2		955.0074376	1907.999275	0.000851441	3	N	212	230
Q3TIX9	Parental	LHTLK	FYCLPDNYEIIDSSLEDITYVLKPTFTK	QQIAN	3	C3:+57.021	1128.891749	3383.651848	0.001329271	2	N	170	198
Q3TJD7	Parental	TPGGK	AAQAGVAVGDWVLNIDGENAGSLTHIEAQNK	IRACG	3		1050.193967	3147.558502	0.001463592	3	N	38	69
Q3TJD7	Parental	SQVPR	TEAPAPASTIPQESWPGPTTPSPTSRPPWAVDPAFAER	YAPDK	3		1333.989098	3998.943894	0.002212458	1	N	195	233
Q3TKT4	Exosome	TNHKV	LLFCQMTSLMTIMEDYFAYR	GFKYL	2	C4:+57.021,M6:+15.995,M13:+15.995	1283.080635	2564.145669	0.00307782	1	N	1099	1119
Q3TKT4	Parental	KKDKR	LAYLLQQTDEYVANLTELVR	QHKAA	3		784.753558	2351.237274	0.000451244	3	N	549	569
Q3TKT4	Parental	EVDAR	HIIENAKQDVDDEYGVSQALAR	GLQSY	3		824.4107425	2470.208828	0.000622848	1	N	704	726
Q3TLH4	Parental	LKNRK	VKDAQQVEPEGQEKPSPAVVR	STDPE	4		573.5557302	2290.191721	0.001943752	2	N	2079	2100
Q3TLH4	Parental	DQDEK	QLGQDESTAITSEQNDILK	VVEKR	2		1045.516552	2089.017504	0.000622848	1	N	197	216
Q3TRM8	Exosome	HPGER	ASVCPHEGVPRPSGSLELECLQQFK	VTRTQ	3	C4:+57.021,C20:+57.021	942.4620351	2824.362705	0.000823681	2	N	14	39
Q3TRM8	Exosome	HPGER	ASVCPHEGVPRPSGSLELECLQQFK	VTRTQ	4	C4:+57.021,C20:+57.021	707.0984763	2824.362705	0.000622848	7	N	14	39
Q3TRM8	Exosome	TKGFR	CSGVEGQDVVQLLR	DAIQR	2	C1:+57.021	780.3962373	1558.776875	0.000451244	11	N	187	201
Q3TRM8	Exosome	NQGLK	LGFNFSFPCHQTGLDR	STLIS	2	C9:+57.021	948.4467929	1894.877986	0.000622848	3	N	160	176
Q3TRM8	Exosome	NQGLK	LGFNFSFPCHQTGLDR	STLIS	3	C9:+57.021	632.6337952	1894.877986	0.000451244	32	N	160	176
Q3TRM8	Exosome	LNWTK	GFNASGCEGQDVVYLLR	EAIRR	2	C7:+57.021	942.9493654	1883.883131	0.000451244	45	N	626	643
Q3TRM8	Exosome	VLLVR	VAEGSVQIINQVYSIPECR	AQGSG	2	C18:+57.021	1081.549444	2161.083287	0.000451244	36	N	552	571

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3TRM8	Exosome	TGTAR	VHTILQDLGLSPR	ASDAE	2		724.9151545	1447.814709	0.000451244	33	N	362	375
Q3TRM8	Exosome	TGTAR	VHTILQDLGLSPR	ASDAE	3		483.612703	1447.814709	0.000451244	24	N	362	375
Q3TRM8	Exosome	PTYVR	ATPDGSERGDFLALDLGGTNFR	VLLVR	3		770.3772617	2308.108385	0.000451244	14	N	525	547
Q3TRM8	Exosome	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	C1:+39.994	983.4668312	1964.918062	0.000451244	14	N	143	160
Q3TRM8	Exosome	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	C1:+57.021	991.9803312	1981.945062	0.000451244	30	N	143	160
Q3TRM8	Exosome	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	[0:-17.027,C1:+57.021	983.4668312	1964.918062	0.000451244	7	N	143	160
Q3TRM8	Exosome	PTYVR	STPHGTEQGDFLVLELGATGASLR	VLWVT	2		1228.624957	2455.234314	0.000451244	16	N	78	102
Q3TRM8	Exosome	PTYVR	STPHGTEQGDFLVLELGATGASLR	VLWVT	3		819.419238	2455.234314	0.000451244	13	N	78	102
Q3TRM8	Exosome	GSGQK	LFDHIVDCIVDFQKR	QGLSG	3	C8:+57.021	635.6614624	1903.960987	0.000451244	24	N	578	593
Q3TRM8	Exosome	GSGQK	LFDHIVDCIVDFQKR	QGLSG	4	C8:+57.021	476.9980468	1903.960987	0.000622848	2	N	578	593
Q3TRM8	Exosome	AVCTR	AAQLCAAALAAVLSR	LQHSR	2	C5:+57.021	743.4142331	1484.812866	0.000451244	33	N	392	407
Q3TRM8	Exosome	AVCTR	AAQLCAAALAAVLSR	LQHSR	3	C5:+57.021	495.945422	1484.812866	0.000451244	27	N	392	407
Q3TRM8	Exosome	SFPCK	QLGLDQGILLNWTK	GFNAS	2		799.9491943	1597.882789	0.000451244	24	N	612	626
Q3TRM8	Exosome	SFPCK	QLGLDQGILLNWTK	GFNAS	2	Q1:-17.027	791.4356943	1580.855789	0.000622848	2	N	612	626
Q3TRM8	Exosome	SFPCK	QLGLDQGILLNWTK	GFNAS	2	[0:-17.027	791.4356943	1580.855789	0.000451244	17	N	612	626
Q3TRM8	Exosome	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	2	C18:+57.021	1036.019791	2070.023981	0.000451244	34	N	593	612
Q3TRM8	Exosome	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	3	C18:+57.021	691.0157938	2070.023981	0.000451244	24	N	593	612
Q3TRM8	Exosome	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	2	Q1:-17.027,C18:+57.021	1027.506291	2052.996981	0.002212458	5	N	593	612
Q3TRM8	Exosome	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	2	[0:-17.027,C18:+57.021	1027.506291	2052.996981	0.000451244	4	N	593	612
Q3TRM8	Exosome	RVEPR	SREFVIPQEVILGAGQQLFDFAAR	CLSEF	2		1346.216816	2690.418033	0.000979378	1	N	119	143
Q3TRM8	Exosome	RVEPR	SREFVIPQEVILGAGQQLFDFAAR	CLSEF	3		897.8138109	2690.418033	0.000451244	28	N	119	143
Q3TRM8	Exosome	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDRESLTPGAQR	FEKMI	3	C2:+57.021	1401.999068	4202.973805	0.000451244	29	N	265	303
Q3TRM8	Exosome	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDRESLTPGAQR	FEKMI	4	C2:+57.021	1051.751251	4202.973805	0.000622848	1	N	265	303
Q3TRM8	Exosome	EPRSR	EFVIPQEVILGAGQQLFDFAAR	CLSEF	2		1224.650246	2447.284893	0.000451244	45	N	121	143
Q3TRM8	Exosome	EPRSR	EFVIPQEVILGAGQQLFDFAAR	CLSEF	3		816.769431	2447.284893	0.000451244	46	N	121	143
Q3TRM8	Exosome	TLSTR	FDTSVDQASINPGK	QRFEK	2		739.8602419	1477.704884	0.000451244	42	N	729	743
Q3TRM8	Exosome	AVSRR	AAQLCGAGVAAVVEK	IRENR	2	C5:+57.021	722.3851412	1442.754682	0.000451244	10	N	834	849
Q3TRM8	Exosome	GSGQK	LFDHIVDCIVDFQK	RQGLS	2	C8:+57.021	874.937738	1747.859876	0.000451244	32	N	578	592
Q3TRM8	Exosome	GSGQK	LFDHIVDCIVDFQK	RQGLS	3	C8:+57.021	583.6277587	1747.859876	0.000451244	37	N	578	592
Q3TRM8	Exosome	LQHSR	EQQTLQVAVATGGR	VFERH	2		729.3895008	1456.763402	0.000451244	36	N	412	426
Q3TRM8	Exosome	DGSGK	GAALVTAVACR	LTQMA	2	C10:+57.021	544.7979733	1087.580347	0.000622848	4	N	904	915
Q3TRM8	Exosome	GEIVR	HILLHLTNLGVLFR	GQKTQ	3		549.3353925	1644.982777	0.000451244	4	N	760	774
Q3TRM8	Exosome	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDR	ESLTP	3	C2:+57.021	1088.839937	3263.49641	0.000451244	10	N	265	294
Q3TRM8	Exosome	ATVRK	LAPQCTVTFLQSEDGSGK	GAALV	2	C5:+57.021	969.467588	1936.919576	0.000451244	11	N	886	904
Q3TRM8	Exosome	GASLR	VLWVTLTGTK	ECRVE	2		559.3349459	1116.654292	0.000451244	13	N	102	112
Q3TRM8	Exosome	DGSER	GDFLALDLGGTNFR	VLLVR	2		748.3811445	1494.746689	0.000451244	9	Y	533	547
Q3TRM8	Exosome	SATVR	KLAPQCTVTFLQSEDGSGK	GAALV	2	C6:+57.021	1033.51507	2065.014539	0.000451244	12	N	885	904
Q3TRM8	Exosome	QRFEK	MIGGLYLGELVR	LVLVH	2		660.8713702	1319.72714	0.000451244	11	N	306	318
Q3TRM8	Exosome	IFKTK	FLSEIESDSLALR	QVRAI	2		740.3886352	1478.76167	0.000451244	13	N	790	803
Q3TRM8	Exosome	FKVTR	TQLQQIQASLLCSMEQALK	GQDSP	2	C12:+57.021	1095.56678	2189.11796	0.000622848	5	N	42	61
Q3TRM8	Exosome	RDIFK	TKFLSEIESDSLALR	QVRAI	3		570.3092374	1707.904312	0.000451244	2	N	788	803
Q3TRM8	Exosome	DFQKR	QGLSGQSLPLGFTF	SFPCK	2		726.3806131	1450.745626	0.002981883	1	N	593	607
Q3TRM8	Parental	HPGER	ASVCPHEGVPRPSGSLELECLQQFK	VTRTQ	3	C4:+57.021,C20:+57.021	942.4620351	2824.362705	0.000451244	3	N	14	39
Q3TRM8	Parental	HPGER	ASVCPHEGVPRPSGSLELECLQQFK	VTRTQ	4	C4:+57.021,C20:+57.021	707.0984763	2824.362705	0.000622848	9	N	14	39
Q3TRM8	Parental	TKGFR	CSGVEGQDVVQLLR	DAIQR	2	C1:+57.021	780.3962373	1558.776875	0.000451244	12	N	187	201
Q3TRM8	Parental	TKGFR	CSGVEGQDVVQLLR	DAIQR	2	[0:-17.027,C1:+57.021	771.8827373	1541.749875	0.000451244	1	N	187	201
Q3TRM8	Parental	NQGLK	LGFNFSFPCHQTGLDR	STLIS	2	C9:+57.021	948.4467929	1894.877986	0.000622848	2	N	160	176
Q3TRM8	Parental	NQGLK	LGFNFSFPCHQTGLDR	STLIS	3	C9:+57.021	632.6337952	1894.877986	0.000451244	32	N	160	176
Q3TRM8	Parental	LNWTK	GFNASGCEGQDVVYLLR	EAIRR	2	C7:+57.021	942.9493654	1883.883131	0.000451244	40	N	626	643
Q3TRM8	Parental	VLLVR	VAEGSVQIINQVYSIPECR	AQGSG	2	C18:+57.021	1081.549444	2161.083287	0.000451244	71	N	552	571
Q3TRM8	Parental	TGTAR	VHTILQDLGLSPR	ASDAE	2		724.9151545	1447.814709	0.000451244	4	N	362	375
Q3TRM8	Parental	TGTAR	VHTILQDLGLSPR	ASDAE	3		483.612703	1447.814709	0.000451244	22	N	362	375
Q3TRM8	Parental	PTYVR	ATPDGSERGDFLALDLGGTNFR	VLLVR	2		1155.061993	2308.108385	0.000870037	2	N	525	547
Q3TRM8	Parental	PTYVR	ATPDGSERGDFLALDLGGTNFR	VLLVR	3		770.3772617	2308.108385	0.000451244	9	N	525	547
Q3TRM8	Parental	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	C1:+39.994	983.4668312	1964.918062	0.000451244	5	N	143	160
Q3TRM8	Parental	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	C1:+57.021	991.9803312	1981.945062	0.000451244	29	N	143	160
Q3TRM8	Parental	DFAAR	CLSEFLDAYPVENQGLK	LGFNF	2	[0:-17.027,C1:+57.021	983.4668312	1964.918062	0.000451244	4	N	143	160
Q3TRM8	Parental	PTYVR	STPHGTEQGDFLVLELGATGASLR	VLWVT	2		1228.624957	2455.234314	0.000451244	17	N	78	102
Q3TRM8	Parental	PTYVR	STPHGTEQGDFLVLELGATGASLR	VLWVT	3		819.419238	2455.234314	0.000451244	26	N	78	102
Q3TRM8	Parental	GSGQK	LFDHIVDCIVDFQKR	QGLSG	3	C8:+57.021	635.6614624	1903.960987	0.000451244	11	N	578	593
Q3TRM8	Parental	GSGQK	LFDHIVDCIVDFQKR	QGLSG	4	C8:+57.021	476.9980468	1903.960987	0.000451244	17	N	578	593
Q3TRM8	Parental	AVCTR	AAQLCAAALAAVLSR	LQHSR	2	C5:+57.021	743.4142331	1484.812866	0.000451244	22	N	392	407
Q3TRM8	Parental	AVCTR	AAQLCAAALAAVLSR	LQHSR	3	C5:+57.021	495.945422	1484.812866	0.000451244	21	N	392	407
Q3TRM8	Parental	SFPCK	QLGLDQGILLNWTK	GFNAS	2		799.9491943	1597.882789	0.000451244	17	N	612	626
Q3TRM8	Parental	SFPCK	QLGLDQGILLNWTK	GFNAS	2	Q1:-17.027	791.4356943	1580.855789	0.001329271	1	N	612	626

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3TRM8	Parental	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	2	C18:+57.021	1036.019791	2070.023981	0.000451244	27	N	593	612
Q3TRM8	Parental	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	3	C18:+57.021	691.0157938	2070.023981	0.000823681	6	N	593	612
Q3TRM8	Parental	DFQKR	QGLSGQSLPLGFTFSFPCK	QLGLD	2	[0:-17.027,C18:+57.021	1027.506291	2052.996981	0.001352548	2	N	593	612
Q3TRM8	Parental	FKVTR	TQLQQIQASLLCSMEQALKGQDSPAPSVR	MLPTY	3	C12:+57.021	1062.208189	3183.601168	0.000823681	1	N	42	71
Q3TRM8	Parental	RVEPR	SREFVIPQEVILGAGQQLFDFAAR	CLSEF	2		1346.216816	2690.418033	0.000622848	3	N	119	143
Q3TRM8	Parental	RVEPR	SREFVIPQEVILGAGQQLFDFAAR	CLSEF	3		897.8138109	2690.418033	0.000451244	35	N	119	143
Q3TRM8	Parental	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDRESLTPGAQR	FEKMI	3	C2:+57.021	1401.999068	4202.973805	0.000451244	33	N	265	303
Q3TRM8	Parental	EPRSR	EFVIPQEVILGAGQQLFDFAAR	CLSEF	2		1224.650246	2447.284893	0.000451244	34	N	121	143
Q3TRM8	Parental	EPRSR	EFVIPQEVILGAGQQLFDFAAR	CLSEF	3		816.769431	2447.284893	0.000451244	28	N	121	143
Q3TRM8	Parental	TLSTR	FDTSVDQASINPGK	QRFEK	2		739.8602419	1477.704884	0.000451244	9	N	729	743
Q3TRM8	Parental	AVSRR	AAQLCGAGVAAVVEK	IRENR	2	C5:+57.021	722.3851412	1442.754682	0.000451244	8	N	834	849
Q3TRM8	Parental	GSGQK	LFDHIVDCIVDFQK	RQGLS	2	C8:+57.021	874.937738	1747.859876	0.000637154	2	N	578	592
Q3TRM8	Parental	GSGQK	LFDHIVDCIVDFQK	RQGLS	3	C8:+57.021	583.6277587	1747.859876	0.000451244	24	N	578	592
Q3TRM8	Parental	LQHSR	EQQTLQVAVATGGR	VFERH	2		729.3895008	1456.763402	0.000622848	3	N	412	426
Q3TRM8	Parental	GEIVR	HILLHLTNLGVLFR	GQKTQ	3		549.3353925	1644.982777	0.000451244	2	N	760	774
Q3TRM8	Parental	EDRGR	TCVSIEWGSFYDEDALGPVLTTFDSALDR	ESLTP	3	C2:+57.021	1088.839937	3263.49641	0.000451244	7	N	265	294
Q3TRM8	Parental	DGSER	GDFLALDLGGTNFR	VLLVR	2		748.3811445	1494.746689	0.000451244	14	Y	533	547
Q3TRM8	Parental	SATVR	KLAPQCTVTFLQSEDGSGK	GAALV	2	C6:+57.021	1033.51507	2065.014539	0.000451244	6	N	885	904
Q3TVI8	Exosome	HDRLR	FRDFVDALEDSLEEVALK	QTGDD	3		699.3569159	2095.047348	0.000870037	1	N	651	669
Q3TVI8	Parental	HDRLR	FRDFVDALEDSLEEVALK	QTGDD	3		699.3569159	2095.047348	0.000451244	1	N	651	669
Q3TVI8	Parental	HSWGK	DNSPDALSSWEELLR	RKYRP	2		866.41337	1730.81114	0.000823681	2	N	560	575
Q3TVI8	Parental	EVALK	QTGDDDEVDDFEDFVFGHFF	GDKAL	2		1190.979999	2379.944399	0.00091018	1	N	669	689
Q3TW96	Exosome	APEAR	AALLAELASLEADALR	EHCQR	2		813.9572164	1625.898833	0.000451244	17	N	31	47
Q3TW96	Exosome	APEAR	AALLAELASLEADALR	EHCQR	3		542.9740776	1625.898833	0.000451244	30	N	31	47
Q3TW96	Exosome	NILVR	LADPVFIGFCVLQGADCGAK	VVEKA	2	C10:+57.021,C17:+57.021	1069.524152	2137.032703	0.000451244	31	N	261	281
Q3TW96	Exosome	IKMEK	FVFDVFQFAK	NFVAF	2		624.3271209	1246.638642	0.000451244	8	N	383	393
Q3TW96	Exosome	DMKQR	GVEFVHVYCVDNILVR	LADPV	3	C9:+57.021	640.3333458	1917.976637	0.000451244	7	N	245	261
Q3TW96	Exosome	QVVEY	SEISPEIAGQLGADGGLLYNAGNICNHFFTR	GFLDV	3	C25:+57.021	1107.870453	3320.58796	0.001264573	1	N	307	338
Q3TW96	Parental	APEAR	AALLAELASLEADALR	EHCQR	2		813.9572164	1625.898833	0.002519933	2	N	31	47
Q3TW96	Parental	APEAR	AALLAELASLEADALR	EHCQR	3		542.9740776	1625.898833	0.000451244	22	N	31	47
Q3TW96	Parental	GPTIK	FFKEHDFFHLDPTNVVLFEQR	MLPAV	4		667.0859262	2664.312505	0.000823681	1	N	179	200
Q3TW96	Parental	APEAR	AALLAELASLEADALREHCQR	AAAAG	4	C19:+57.021	585.0553531	2336.190212	0.000998612	1	N	31	52
Q3TW96	Parental	IKMEK	FVFDVFQFAK	NFVAF	2		624.3271209	1246.638642	0.001463592	2	N	383	393
Q3TXS7	Exosome	FILFR	TPEQCPSVVSLLSESYNPHVR	YGAAM	3	C5:+57.021	800.3938812	2398.158243	0.000451244	16	N	628	649
Q3TXS7	Exosome	TYLPK	DTSPGSAYQEGGGLYALGLIHANHGGDIIDYLLNQLK	NASND	4		968.4884075	3869.92243	0.000451244	5	N	429	466
Q3TXS7	Exosome	FALHK	LNAVVNDFWAEISESVDKIEVLYEDEGFR	SRQFA	3		1129.552938	3385.635415	0.000451244	4	N	26	55
Q3TXS7	Exosome	DHYTK	QCVENADLPEGEKKPIDQR	LEGIV	3	C2:+57.021	742.6991931	2225.074179	0.000823681	1	N	110	129
Q3TXS7	Exosome	DHYTK	QCVENADLPEGEKKPIDQR	LEGIV	4	C2:+57.021	557.2763448	2225.074179	0.000622848	11	N	110	129
Q3TXS7	Exosome	DHYTK	QCVENADLPEGEKKPIDQR	LEGIV	3	[0:-17.027,C2:+57.021	737.0235265	2208.047179	0.002296037	1	N	110	129
Q3TXS7	Exosome	DDVRR	AAVESLGFILFR	TPEQC	2		661.8775093	1321.739419	0.000451244	5	N	616	628
Q3TXS7	Exosome	AHGPK	IEEEEQEPEPPEPFEYIDD	-	2		1167.495148	2332.974696	0.001591523	1	N	934	953
Q3TXS7	Exosome	IQNLR	TVGTPIASVPGSTNTGTVPGSEKDSDPMETEEK	TASAV	3	M28:+15.995	1112.188025	3333.540675	0.001264573	3	N	269	302
Q3TXS7	Exosome	KAIRR	LLHVAVSDVNDDVRR	AAVES	3		569.9765926	1706.906378	0.000622848	1	N	601	616
Q3TXS7	Exosome	-MI	TSAAGIISLLDEEEPQLK	EFALH	2		957.5074674	1912.999335	0.000823681	2	N	2	20
Q3TXS7	Parental	FILFR	TPEQCPSVVSLLSESYNPHVR	YGAAM	3	C5:+57.021	800.3938812	2398.158243	0.000451244	16	N	628	649
Q3TXS7	Parental	TYLPK	DTSPGSAYQEGGGLYALGLIHANHGGDIIDYLLNQLK	NASND	3		1290.981943	3869.92243	0.002296037	1	N	429	466
Q3TXS7	Parental	TYLPK	DTSPGSAYQEGGGLYALGLIHANHGGDIIDYLLNQLK	NASND	4		968.4884075	3869.92243	0.000451244	8	N	429	466
Q3TXS7	Parental	FALHK	LNAVVNDFWAEISESVDKIEVLYEDEGFR	SRQFA	3		1129.552938	3385.635415	0.000451244	16	N	26	55
Q3TXS7	Parental	DDVRR	AAVESLGFILFR	TPEQC	2		661.8775093	1321.739419	0.000451244	3	N	616	628
Q3TXS7	Parental	-	MITSAAGIISLLDEEEPQLKEFALHK	LNAVV	4		721.6352863	2882.509945	0.000451244	2	N	0	26
Q3TXS7	Parental	AHGPK	IEEEEQEPEPPEPFEYIDD	-	2		1167.495148	2332.974696	0.000622848	12	N	934	953
Q3TXS7	Parental	IIILK	DTSEDVEELVEPVAAHGPK	IEEEE	2		1011.487263	2020.958927	0.000622848	6	N	915	934
Q3TZZ7	Parental	HIAAK	EPTPSIASDISLPIATQELR	QRLRQ	2		1069.57113	2137.126661	0.000662267	2	N	674	694
Q3TZZ7	Parental	EELAK	GWTQWYDLTEDGTRPQVIT	-	2		1133.542904	2265.070209	0.000451244	4	N	826	845
Q3U0V1	Exosome	EYYKK	IGQQPQQPGAPPQQDYTK	AWEEY	2		990.9928502	1979.9701	0.000451244	14	N	629	647
Q3U0V1	Exosome	GENVK	AINQQTGAFVEISR	QLPPN	2		767.4051509	1532.794702	0.000622848	2	N	449	463
Q3U0V1	Exosome	EHAAR	IINDLLQSLR	SGPPG	2		592.8540342	1183.692468	0.000823681	6	N	385	395
Q3U0V1	Exosome	DSGCK	VQISPDSGGLPER	SVSLT	2		677.8522198	1353.68884	0.001591523	4	N	178	191
Q3U0V1	Exosome	EYYKK	QAQVATGGGPGAPPGSQPDYSAAWAEYYR	QQAAY	3		984.7902822	2951.347447	0.001162105	2	N	655	684
Q3U0V1	Parental	EYYKK	IGQQPQQPGAPPQQDYTK	AWEEY	2		990.9928502	1979.9701	0.000451244	35	N	629	647
Q3U0V1	Parental	EYGSR	VGGGIDVPVPR	HSVGV	2		533.3067198	1064.59784	0.000622848	6	N	321	332
Q3U0V1	Parental	GENVK	AINQQTGAFVEISR	QLPPN	2		767.4051509	1532.794702	0.000451244	42	N	449	463
Q3U0V1	Parental	QIAAK	IGGDAATTVNNNTPDFGFGGQKR	QLEDG	2		1169.065067	2336.114533	0.000451244	10	N	88	111
Q3U0V1	Parental	QIAAK	IGGDAATTVNNNTPDFGFGGQKR	QLEDG	3		779.7126443	2336.114533	0.000451244	15	N	88	111
Q3U0V1	Parental	EHAAR	IINDLLQSLR	SGPPG	2		592.8540342	1183.692468	0.000622848	31	N	385	395

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3U0V1	Parental	EQINK	IQQDSGCKVQISPDSGGLPER	SVSLT	2	C7:+57.021	1136.055622	2270.095643	0.000851441	1	N	170	191
Q3U0V1	Parental	EQINK	IQQDSGCKVQISPDSGGLPER	SVSLT	3	C7:+57.021	757.7063477	2270.095643	0.000451244	1	N	170	191
Q3U0V1	Parental	DSGCK	VQISPDSGGLPER	SVSLT	2		677.8522198	1353.68884	0.000451244	8	N	178	191
Q3U0V1	Parental	PDSKK	LASQGDSIGSQLGPIHPPPR	TSMTE	2		1014.037592	2026.059584	0.000823681	1	N	123	143
Q3U0V1	Parental	PDSKK	LASQGDSIGSQLGPIHPPPR	TSMTE	3		676.3609947	2026.059584	0.000451244	2	N	123	143
Q3U0V1	Parental	RAGVK	MILIQDGSQNTNVDKPLR	IIGDP	3		681.3620073	2041.062622	0.001162105	1	N	267	285
Q3U0V1	Parental	EYYKK	QAQVATGGGPGAPPGSQPDYSAAWAEYYR	QQAAY	2		1476.681523	2951.347447	0.000823681	3	N	655	684
Q3U0V1	Parental	EYYKK	QAQVATGGGPGAPPGSQPDYSAAWAEYYR	QQAAY	3		984.7902822	2951.347447	0.0007646	14	N	655	684
Q3U0V1	Parental	EEYYK	KIGQQPQQPGAPPQQDYT	KAWEE	2		990.9928502	1979.9701	0.000823681	1	N	628	646
Q3U0V1	Parental	QIAAK	IGGDAATTVNNNTPDFGFGGQK	RQLED	2		1091.014511	2180.013422	0.000451244	23	N	88	110
Q3U0V1	Parental	GAGDR	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	KDAFA	2		1164.047739	2326.079879	0.000622848	4	N	40	71
Q3U0V1	Parental	GAGDR	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	KDAFA	3		776.3677596	2326.079879	0.001162105	3	N	40	71
Q3U0V1	Parental	QPDSK	KLASQGDSIGSQLGPIHPPPR	TSMTE	3		719.0593158	2154.154547	0.000979378	2	N	122	143
Q3U0V1	Parental	EEYYK	KIGQQPQQPGAPPQQDYTK	AWEEY	3		703.6961545	2108.065063	0.000451244	5	N	628	647
Q3U0V1	Parental	GAGDR	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIRK	DAFAD	3		819.0660807	2454.174842	0.000823681	12	N	40	72
Q3U0V1	Parental	WAAYY	SHYYQQPPGPVPGPAPAPAAPPAQGEPPQPPPTGQSDYTK	AWEEY	3		1358.992731	4073.954793	0.000451244	6	N	581	621
Q3U0V2	Exosome	DELCK	LTCDCTGQGGAIQVASAGSK	FPVSS	2	C3:+57.021,C5:+57.021	990.9593729	1979.903146	0.000622848	3	N	161	181
Q3U0V2	Exosome	YEYER	DGLYEQAFQLLR	RFMQA	2		726.8782376	1451.740875	0.000622848	3	N	256	268
Q3U0V2	Parental	ATLQR	LVEALEENELTSLAEDLLGQAEPDGGLA	-	2		1448.719645	2895.423691	0.000451244	11	N	282	310
Q3U0V2	Parental	ATLQR	LVEALEENELTSLAEDLLGQAEPDGGLA	-	3		966.1490303	2895.423691	0.000451244	12	N	282	310
Q3U0V2	Parental	VAIYK	ALQTALSESGDSSDVLQILK	IHCSD	2		1038.047488	2074.079376	0.000451244	3	N	43	63
Q3U0V2	Parental	DELCK	LTCDCTGQGGAIQVASAGSK	FPVSS	2	C3:+57.021,C5:+57.021	990.9593729	1979.903146	0.000622848	1	N	161	181
Q3U141	Parental	SLKTR	IQEDTGILETDQELLQEAGLVLLPDKPATQCISDSK	TNEGL	3	C31:+57.021	1323.340431	3966.997894	0.000451244	2	N	339	375
Q3U141	Parental	CCGLR	EGAVLTLLSDIASALR	YLHEN	2		814.9650414	1627.914483	0.000451244	2	N	118	134
Q3U1F9	Parental	PVPVK	LLDENANLPQEGGGQAEEQAAEGTGGHSK	RFSSL	3		969.7837445	2906.327833	0.000451244	30	N	260	289
Q3U1F9	Parental	HHVPK	ESDYESIGDLQQCR	DVTRL	2	C13:+57.021	850.3653311	1698.715062	0.000451244	1	N	410	424
Q3U1J4	Exosome	VLSSR	IEVQDSSGGTTALRPSASTQALSSSVSSSK	LFSSS	3		980.1586999	2937.4527	0.000451244	34	N	739	769
Q3U1J4	Exosome	FHTER	KTEPATGFIDGDLIESFLDISRPK	MQEVV	3		883.797715	2648.369745	0.000451244	41	N	1080	1104
Q3U1J4	Exosome	FHTER	KTEPATGFIDGDLIESFLDISRPK	MQEVV	4		663.1002363	2648.369745	0.000451244	11	N	1080	1104
Q3U1J4	Exosome	KGESK	DLLFILTAK	YNACI	2		517.3187645	1032.621929	0.002145581	2	N	74	83
Q3U1J4	Exosome	LWPLR	SDPGRETDDTLVLSFVGQTR	VLMLN	3		731.6981123	2192.070937	0.000451244	11	N	414	434
Q3U1J4	Exosome	YESPR	KICYQEVSQCFGVLSSR	IEVQD	2	C3:+57.021,C10:+57.021	1030.998301	2059.981002	0.000451244	1	N	722	739
Q3U1J4	Exosome	NVQDR	IGRPSETGIIGIIDPECR	MIGLR	3	C17:+57.021	661.6828147	1982.025044	0.000622848	9	N	111	129
Q3U1J4	Exosome	VIDVK	FLYGCQAPTICFVYQDPQGR	HVKTY	2	C5:+57.021,C11:+57.021	1210.561797	2419.107994	0.000451244	15	N	168	188
Q3U1J4	Exosome	GDLMR	SVLLLAYKPMEGNFEEIAR	DFNPN	3	M10:+15.995	732.7177081	2195.129724	0.001654178	4	N	928	947
Q3U1J4	Exosome	DISAR	ILKLPSFELLHK	EMLGG	3		479.9663061	1436.875518	0.002019181	1	N	567	579
Q3U1J4	Parental	VLSSR	IEVQDSSGGTTALRPSASTQALSSSVSSSK	LFSSS	3		980.1586999	2937.4527	0.000451244	45	N	739	769
Q3U1J4	Parental	FHTER	KTEPATGFIDGDLIESFLDISRPK	MQEVV	3		883.797715	2648.369745	0.000451244	6	N	1080	1104
Q3U1J4	Parental	FHTER	KTEPATGFIDGDLIESFLDISRPK	MQEVV	4		663.1002363	2648.369745	0.000451244	10	N	1080	1104
Q3U1J4	Parental	SGMKR	EATADDLIKVVEELTR	IH-	2		901.4812526	1800.946905	0.000622848	1	N	1122	1138
Q3U1J4	Parental	SGMKR	EATADDLIKVVEELTR	IH-	3		601.3234351	1800.946905	0.000451244	10	N	1122	1138
Q3U1J4	Parental	YESPR	KICYQEVSQCFGVLSSR	IEVQD	2	C3:+57.021,C10:+57.021	1030.998301	2059.981002	0.000451244	1	N	722	739
Q3U1J4	Parental	NVQDR	IGRPSETGIIGIIDPECR	MIGLR	3	C17:+57.021	661.6828147	1982.025044	0.002663018	1	N	111	129
Q3U1J4	Parental	VDLER	QGQGQLVTCSGAFK	EGSLR	2	C9:+57.021	740.864573	1479.713546	0.001352548	1	N	369	383
Q3U1J4	Parental	VIDVK	FLYGCQAPTICFVYQDPQGR	HVKTY	2	C5:+57.021,C11:+57.021	1210.561797	2419.107994	0.000451244	3	N	168	188
Q3U1Z5	Parental	LEEQR	ATFHTPEAPPNLAPAPPR	LLEDK	2		942.492289	1882.968978	0.000451244	22	N	80	98
Q3U1Z5	Parental	LEEQR	ATFHTPEAPPNLAPAPPR	LLEDK	3		628.664126	1882.968978	0.001395409	3	N	80	98
Q3U1Z5	Parental	PAPPR	LLEDKEQLYSTILSHQCQR	IEAQR	2	C17:+57.021	1181.097289	2360.178979	0.000451244	12	N	98	117
Q3U1Z5	Parental	PAPPR	LLEDKEQLYSTILSHQCQR	IEAQR	3	C17:+57.021	787.7341263	2360.178979	0.000451244	29	N	98	117
Q3U1Z5	Parental	PAPPR	LLEDKEQLYSTILSHQCQR	IEAQR	4	C17:+57.021	591.0525447	2360.178979	0.000451244	9	N	98	117
Q3U1Z5	Parental	HQCQR	IEAQRSDPPLPPGGQELLELLR	VQGGG	3		847.8065448	2540.396234	0.000451244	4	N	117	140
Q3U1Z5	Parental	IEAQR	SDPPLPPGGQELLELLLR	VQGGG	2		972.5441873	1943.072775	0.000451244	22	N	122	140
Q3U1Z5	Parental	ALGPR	SGSLLSLQTELLLDLVAEAQSR	RLEEQ	3		781.7642342	2342.269303	0.000451244	2	N	52	74
Q3U1Z5	Parental	SDPPL	PPGGQELLELLLR	VQGGG	2		717.9199055	1433.824211	0.001943752	2	N	127	140
Q3U2G2	Exosome	PISLR	WNSPAEEGLSDCEVFPK	NHAAP	2	C12:+57.021	982.9386633	1963.861727	0.000451244	12	N	405	422
Q3U2G2	Exosome	LTFYR	KEPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1143.901679	3428.681637	0.000451244	21	N	436	466
Q3U2G2	Exosome	TFYRK	EPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1101.203358	3300.586674	0.000451244	30	N	437	466
Q3U2G2	Exosome	VEAEK	SNLAYDIVQLPTGLTGIK	VTYME	2		952.0309127	1902.046225	0.000451244	30	N	84	102
Q3U2G2	Exosome	VAVAR	AGGIETIANEYSDR	CTPAC	2		748.3553237	1494.695047	0.000451244	7	N	19	33
Q3U2G2	Exosome	EAVTR	GCALQCAILSPAFK	VREFS	2	C2:+57.021,C6:+57.021	768.389138	1534.762676	0.000451244	6	N	374	388
Q3U2G2	Exosome	KGKLK	VLATAFDTTLGGR	KFDEV	2		661.3596807	1320.703761	0.001463592	4	N	221	234
Q3U2G2	Exosome	KAKVK	TSTVDLPIESQLLWQLDR	EMLGL	2		1057.560566	2113.105531	0.000451244	19	N	575	593
Q3U2G2	Exosome	KAKVK	TSTVDLPIESQLLWQLDR	EMLGL	3		705.3763105	2113.105531	0.001264573	1	N	575	593
Q3U2G2	Exosome	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDK	KLPEM	3		1110.149815	3327.426044	0.000451244	19	N	800	834
Q3U2G2	Exosome	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDK	KLPEM	4		832.864311	3327.426044	0.000451244	25	N	800	834

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3U2G2	Exosome	ISSFK	NKEDQYEHLDAADVTK	VEKST	3		625.9626774	1874.864632	0.000622848	5	N	719	735
Q3U2G2	Exosome	TFTLK	LEDTENWLYEDGEDQPK	QVYVD	2		1040.953253	2079.890907	0.000451244	43	N	653	670
Q3U2G2	Exosome	SKLKK	EDIYAVEIVGGATR	IPAVK	2		746.8862597	1491.756919	0.000451244	1	N	332	346
Q3U2G2	Exosome	TLGGR	KFDEVLVNHFCEEFGK	KYKLD	3	C11:+57.021	666.652744	1996.934832	0.000451244	1	N	234	250
Q3U2G2	Exosome	KFFGK	ELSTTLNADEAVTR	GCALQ	2		760.3840812	1518.752562	0.000451244	9	N	360	374
Q3U2G2	Exosome	KEEEK	MQVDQEEPHTEEQQQQPQTPAENKAESEEMETSQAGSK	DKKTD	4	M1:+15.995,M30:+15.995	1087.220508	4344.850833	0.002663018	1	N	521	559
Q3U2G2	Exosome	ESVLK	KPVVDCVVSVPSFYTDAERR	SVMDA	3	C6:+57.021	775.3953335	2323.1626	0.002296037	1	N	134	154
Q3U2G2	Parental	PISLR	WNSPAEEGLSDCEVFPK	NHAAP	2	C12:+57.021	982.9386633	1963.861727	0.000451244	6	N	405	422
Q3U2G2	Parental	LTFYR	KEPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1143.901679	3428.681637	0.000451244	15	N	436	466
Q3U2G2	Parental	TFYRK	EPFTLEAYYSSPQDLPYPDPAIAQFSVQK	VTPQS	3		1101.203358	3300.586674	0.000451244	37	N	437	466
Q3U2G2	Parental	VEAEK	SNLAYDIVQLPTGLTGIK	VTYME	2		952.0309127	1902.046225	0.000451244	25	N	84	102
Q3U2G2	Parental	VAVAR	AGGIETIANEYSDR	CTPAC	2		748.3553237	1494.695047	0.000451244	8	N	19	33
Q3U2G2	Parental	EAVTR	GCALQCAILSPAFK	VREFS	2	C2:+57.021,C6:+57.021	768.389138	1534.762676	0.000451244	8	N	374	388
Q3U2G2	Parental	HGRAF	SDPFVEAEKSNLAYDIVQLPTGLTGIK	VTYME	2		1453.263826	2904.512052	0.001162105	1	N	75	102
Q3U2G2	Parental	HGRAF	SDPFVEAEKSNLAYDIVQLPTGLTGIK	VTYME	3		969.1784841	2904.512052	0.000451244	5	N	75	102
Q3U2G2	Parental	RFHGR	AFSDPFVEAEKSNLAYDIVQLPTGLTGIK	VTYME	3		1041.880327	3122.61758	0.001871652	2	N	73	102
Q3U2G2	Parental	KGKLK	VLATAFDTTLGGR	KFDEV	2		661.3596807	1320.703761	0.002884417	1	N	221	234
Q3U2G2	Parental	KAKVK	TSTVDLPIESQLLWQLDR	EMLGL	2		1057.560566	2113.105531	0.000451244	22	N	575	593
Q3U2G2	Parental	KAKVK	TSTVDLPIESQLLWQLDR	EMLGL	3		705.3763105	2113.105531	0.000622848	2	N	575	593
Q3U2G2	Parental	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDK	KLPEM	3		1110.149815	3327.426044	0.000451244	25	N	800	834
Q3U2G2	Parental	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDK	KLPEM	4		832.864311	3327.426044	0.000451244	19	N	800	834
Q3U2G2	Parental	TFTLK	LEDTENWLYEDGEDQPK	QVYVD	2		1040.953253	2079.890907	0.000451244	14	N	653	670
Q3U2G2	Parental	AFKVR	EFSITDVVPYPISLR	WNSPA	2		868.4674169	1734.919234	0.000637154	3	N	390	405
Q3U2G2	Parental	EIEAK	IKELTSICSPIISKPKPK	VEPPK	2	C8:+57.021	1020.100584	2038.185568	0.001329271	1	N	773	791
Q3U2G2	Parental	KEEPK	HAEQNGPVDGQGDNPGSQAAEHGADTAVPSDGDKK	LPEMD	4		864.8880518	3455.521007	0.000451244	1	N	800	835
Q3U5Q7	Exosome	PDTRR	DLLQLLGSCQEAARPQLAEFQADSQGLLWQR	LWELQ	3	C9:+57.021	1181.267095	3540.777886	0.000451244	21	N	144	175
Q3U5Q7	Exosome	MARPR	RFTVELPDCSLTHFVLGDATDHR	DARLA	4	C9:+57.021	672.3319171	2685.296468	0.000451244	3	N	35	58
Q3U5Q7	Exosome	ARPRR	FTVELPDCSLTHFVLGDATDHR	DARLA	3	C8:+57.021	844.0729191	2529.195357	0.000622848	1	N	36	58
Q3U5Q7	Exosome	SESLK	AVLLQSPPPCISQWR	KIFDD	2	C10:+57.021	876.466997	1750.918394	0.000870037	2	N	277	292
Q3U5V8	Parental	ESLYR	VIQDIQDENQLLLIDVR	RLGRQ	2		1012.555283	2023.094967	0.001591523	1	N	46	63
Q3U5V8	Parental	QELSR	SYDQQFPDGDNDFDAPREDIVFETDHILESLY	RVIQD	3		1264.227619	3789.659458	0.001463592	1	N	13	45
Q3U5V8	Parental	-MKDR	LAELQELSR	SYDQQ	2		529.7961849	1057.57677	0.0025889	1	N	4	13
Q3U7R1	Exosome	LRLER	LTPRPTAAELEEVLQVNSLIQTQK	SSELA	3		893.4961475	2677.465042	0.000451244	14	N	754	778
Q3U7R1	Exosome	QVHLR	LEWLSLLPDAEKLDQVLQWNR	GITSR	3		856.1275069	2565.359121	0.000451244	16	N	435	456
Q3U7R1	Exosome	LGRYK	VSLTTVLNSGFLDEWLTLEDVPSGR	LHLRL	2		1374.708687	2747.401774	0.000451244	3	N	722	747
Q3U7R1	Exosome	LGRYK	VSLTTVLNSGFLDEWLTLEDVPSGR	LHLRL	3		916.8083912	2747.401774	0.000451244	3	N	722	747
Q3U7R1	Exosome	SHKTK	TVSQSSAPVWEESASFLIR	KPHAE	2		1047.529266	2093.042931	0.000451244	17	N	822	841
Q3U7R1	Exosome	KDDSR	ALTLGALTLPLAR	LLTAS	2		655.414259	1308.812918	0.000451244	11	N	540	553
Q3U7R1	Exosome	IQTQK	SSELAAALLSVFLER	AEDLP	2		803.4464845	1604.877369	0.000451244	21	N	778	793
Q3U7R1	Exosome	IQTQK	SSELAAALLSVFLER	AEDLP	3		535.966923	1604.877369	0.000451244	1	N	778	793
Q3U7R1	Exosome	VLPNR	LLVPLVPDLQDVAQLR	SPLPR	2		895.0332584	1788.050917	0.000622848	2	N	297	313
Q3U7R1	Exosome	VLPNR	LLVPLVPDLQDVAQLR	SPLPR	3		597.0247723	1788.050917	0.000451244	2	N	297	313
Q3U7R1	Parental	LRLER	LTPRPTAAELEEVLQVNSLIQTQK	SSELA	3		893.4961475	2677.465042	0.000451244	26	N	754	778
Q3U7R1	Parental	QVHLR	LEWLSLLPDAEKLDQVLQWNR	GITSR	3		856.1275069	2565.359121	0.000451244	25	N	435	456
Q3U7R1	Parental	IQTQK	SSELAAALLSVFLERAEDLPLR	KGTKP	3		800.7764741	2399.306022	0.000451244	7	N	778	800
Q3U7R1	Parental	LGRYK	VSLTTVLNSGFLDEWLTLEDVPSGR	LHLRL	2		1374.708687	2747.401774	0.000451244	12	N	722	747
Q3U7R1	Parental	SHKTK	TVSQSSAPVWEESASFLIR	KPHAE	2		1047.529266	2093.042931	0.000451244	28	N	822	841
Q3U7R1	Parental	SHKTK	TVSQSSAPVWEESASFLIR	KPHAE	3		698.688777	2093.042931	0.002453667	2	N	822	841
Q3U7R1	Parental	KDDSR	ALTLGALTLPLAR	LLTAS	2		655.414259	1308.812918	0.000451244	13	N	540	553
Q3U7R1	Parental	EFNER	FEWDLPLDGTLR	RKLDV	2		731.3727881	1460.729976	0.000451244	9	N	1028	1040
Q3U7R1	Parental	PQKKR	TLNPEFNERFEWDLPLDGTLR	RKLDV	3		854.7594831	2561.255049	0.002080925	2	N	1019	1040
Q3U7R1	Parental	IQTQK	SSELAAALLSVFLER	AEDLP	2		803.4464845	1604.877369	0.000451244	14	N	778	793
Q3U7R1	Parental	IQTQK	SSELAAALLSVFLER	AEDLP	3		535.966923	1604.877369	0.000451244	15	N	778	793
Q3U7R1	Parental	TRESK	ATYSTNSPVWEEAFRF	FLQDP	2		952.9448373	1903.874075	0.002453667	3	N	505	521
Q3U7R1	Parental	VLPNR	LLVPLVPDLQDVAQLR	SPLPR	2		895.0332584	1788.050917	0.000451244	8	N	297	313
Q3U7R1	Parental	VLPNR	LLVPLVPDLQDVAQLR	SPLPR	3		597.0247723	1788.050917	0.000451244	19	N	297	313
Q3U7R1	Parental	LDVGK	VLQAGVLDNWYPLQGGQGQVHLR	LEWLS	2		1274.675119	2547.334637	0.000451244	6	N	412	435
Q3U7R1	Parental	LDVGK	VLQAGVLDNWYPLQGGQGQVHLR	LEWLS	3		850.1193457	2547.334637	0.001162105	3	N	412	435
Q3U7R1	Parental	EVRHR	LTHGDSPSEAPVGPLGQVK	LTVWY	2		944.9923189	1887.969038	0.000451244	3	N	945	964
Q3U7R1	Parental	YMSHR	ELPAWVSFPDVEK	AEWLN	2		758.888271	1515.760942	0.001591523	1	N	115	128
Q3U7R1	Parental	LPLAR	LLTASELTLDQWFQLSSSGPNSR	LYMKL	2		1275.645889	2549.276179	0.000823681	2	N	553	576
Q3U7R1	Parental	QYMEK	LLAETVAPAVR	GANPH	2		570.3433023	1138.671005	0.001763695	2	N	149	160
Q3U7R1	Parental	IQTQK	SSELAAALLSVF	LERAE	2		604.3326002	1206.6496	0.001871652	5	N	778	790
Q3U9G9	Exosome	LRAPR	EELSPASSGNAVYDFFIGR	ELNPR	2		1029.992516	2057.969432	0.000823681	1	N	364	383
Q3U9G9	Parental	GEVVR	GRWPGSSLYYEVEILSHDNK	SQLYT	3		784.054119	2349.138957	0.000451244	7	N	13	33

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3U9G9	Parental	GEVVR	GRWPGSSLYYEVEILSHDNK	SQLYT	4		588.2925392	2349.138957	0.000451244	8	N	13	33
Q3U9G9	Parental	ILQVK	LTPLVLKPFGNSVSVY	NGEPE	2		867.4959774	1732.976355	0.000451244	1	N	126	142
Q3U9G9	Parental	TPQRK	DLEFGGVPGAVLIMLGLPACVLLLLLQCR	QKDPG	3	C20:+57.021,C28:+57.021	1046.581317	3136.72055	0.000823681	13	N	216	245
Q3U9G9	Parental	LRAPR	EELSPASSGNAVYDFFIGR	ELNPR	2		1029.992516	2057.969432	0.000451244	7	N	364	383
Q3U9G9	Parental	REEVK	AKEIESEEQNLVTK	GPAPL	2		809.4206637	1616.825727	0.000622848	6	N	186	200
Q3U9G9	Parental	REEVK	AKEIESEEQNLVTK	GPAPL	3		539.9497091	1616.825727	0.000451244	5	N	186	200
Q3U9G9	Parental	EVKAK	EIESEEQNLVTK	GPAPL	2		709.8546252	1417.69365	0.000451244	17	N	188	200
Q3U9G9	Parental	GSSLY	YEVEILSHDNK	SQLYT	2		673.8334957	1345.651391	0.000451244	35	N	22	33
Q3U9G9	Parental	GSSLY	YEVEILSHDNK	SQLYT	3		449.5582638	1345.651391	0.000451244	4	N	22	33
Q3U9G9	Parental	NLVTK	GPAPLGTFQVTTPQR	KDLEF	2		785.4233437	1568.831087	0.000451244	8	N	200	215
Q3U9G9	Parental	VVRGR	WPGSSLYYEVEILSHDNK	SQLYT	3		713.0132606	2136.016382	0.000451244	8	N	15	33
Q3U9G9	Parental	TSTGK	SLLVSGWWGFVR	HPNYL	2		703.883126	1405.750652	0.000622848	3	N	543	555
Q3UDE2	Exosome	KDYMK	LSQESPQVLLNQFPCENLLTVK	DCLAS	2	C15:+57.021	1279.170454	2556.325309	0.000451244	7	N	341	363
Q3UDE2	Exosome	KDYMK	LSQESPQVLLNQFPCENLLTVK	DCLAS	3	C15:+57.021	853.1162363	2556.325309	0.000451244	7	N	341	363
Q3UDE2	Exosome	PQFEK	QYPEFPWSDVQAEIFK	AFTEL	2		992.478513	1982.941426	0.000622848	3	N	532	548
Q3UDE2	Parental	KDYMK	LSQESPQVLLNQFPCENLLTVKDCLASIAR	RAGGP	3	C15:+57.021,C24:+57.021	1148.593778	3442.757933	0.002080925	1	N	341	371
Q3UEB3	Parental	RAFNR	IYVASVHQDLSDDDIKSVFEAFGK	IKSCT	4		671.5872274	2682.317709	0.000451244	3	N	232	256
Q3UEB3	Parental	AIMCR	VYVGSIYYELGEDTIR	QAFAP	2		938.9705208	1875.925442	0.000451244	9	N	135	151
Q3UEB3	Parental	STGTK	LGLPPLTPEQQEALQK	AKKYA	2		881.4914234	1760.967247	0.001943752	1	N	58	74
Q3UEB3	Parental	GRNIK	VGRPSNIGQAQPIIDQLAEEAR	AFNRI	3		788.0878227	2361.240068	0.000451244	2	N	206	228
Q3UHD6	Exosome	RAGEK	ELILTVLSVPPHEADNLDPSDDSLGQSFYDYTEK	QAVPI	3		1269.94282	3806.80506	0.000451244	12	N	124	158
Q3UHD6	Exosome	RLPGK	WPFSLSEQQLDAR	RRGLE	2		788.8918764	1575.768153	0.000662267	2	N	220	233
Q3UHD6	Exosome	VRVKK	NSTTDQVYQAIAAK	VGMDS	2		755.3813415	1508.747083	0.000662267	1	N	291	305
Q3UHD6	Parental	RAGEK	ELILTVLSVPPHEADNLDPSDDSLGQSFYDYTEK	QAVPI	3		1269.94282	3806.80506	0.000451244	14	N	124	158
Q3UI43	Parental	SVGSR	SEGEGEAATADGGAASVPGAGPKPWQVPASASEVQIR	TPRVN	3		1178.908555	3533.702266	0.000451244	45	N	52	89
Q3UI43	Parental	TSDPR	ELCSCLYDLETASCSTFNLEGLFSLIQQK	TELPV	3	C3:+57.021,C5:+57.021,C14:+57.021	1142.868313	3425.58154	0.000451244	8	N	168	197
Q3UJB0	Exosome	LQGKR	GIEKPPFELPDFIK	RTGIQ	3		543.9682639	1628.881392	0.000870037	2	N	498	512
Q3UJB0	Parental	ELQAR	LAEIGAPIQGSREELVER	LQTYT	2		984.0319754	1966.048351	0.000622848	2	N	35	53
Q3UJB0	Parental	ELQAR	LAEIGAPIQGSREELVER	LQTYT	3		656.3572503	1966.048351	0.001352548	2	N	35	53
Q3UJB0	Parental	LQGKR	GIEKPPFELPDFIK	RTGIQ	3		543.9682639	1628.881392	0.000451244	10	N	498	512
Q3UJB0	Parental	KDSGR	SRGSDPPAADVEIEYVTEEPEIYEPNFIFF	KRIFE	3		1154.208949	3459.603447	0.00091018	7	N	339	369
Q3UJB0	Parental	ETDTR	SSLGQSASETEEDTVSISKK	EKNRK	2		1042.006017	2081.996435	0.000451244	3	N	284	304
Q3UJB0	Parental	ELQAR	LAEIGAPIQGSR	EELVE	2		606.3412909	1210.666982	0.001229886	2	N	35	47
Q3UJB0	Parental	PPPLR	VGEPVALSEEER	LKLAQ	2		657.8309531	1313.646306	0.000662267	1	N	134	146
Q3UJB0	Parental	SGRSR	GSDPPAADVEIEYVTEEPEIYEPNFIFF	KRIFE	3		1073.164569	3216.470307	0.000823681	1	N	341	369
Q3UJB9	Exosome	RTLLK	GFTGSVADLAFAHLNSPQLACLDEAGNLFVWR	LALVK	3	C21:+57.021	1159.573748	3475.697844	0.000998612	2	N	173	205
Q3UJB9	Exosome	NLQEK	QVICLSGDDSSTCIGILAK	EVEIV	2	C4:+57.021,C13:+57.021	1019.003249	2035.990898	0.0007646	1	N	77	96
Q3UJB9	Parental	PCVSR	SLEPVAGQLSNSVATK	LTAVE	2		800.9311986	1599.846797	0.000622848	10	N	1062	1078
Q3UJB9	Parental	EGQQR	GGQLQEQLTQQLSQALSSAVAGR	LERSV	2		1185.622749	2369.229897	0.000622848	7	N	1020	1043
Q3UJB9	Parental	AVGSR	LTEHQVAEPPEDWPALIWQQQR	ELAEL	3		891.1141489	2670.319047	0.000451244	2	N	942	964
Q3UJB9	Parental	GDGDR	HSTPSLLEAALTQEVATPDSQVWPTAPDITR	ETCST	3		1111.232199	3330.673198	0.000451244	4	N	809	840
Q3UJB9	Parental	SPRPR	QGPELGSQLGLDGGPGDGDR	HSTPS	2		962.953922	1923.892244	0.001162105	1	N	789	809
Q3UJB9	Parental	ELLQR	LCAQLEGLQSTVTDHVER	ALETR	3	C2:+57.021	686.009479	2055.005037	0.00091018	2	N	979	997
Q3UKJ7	Exosome	LSFSK	DSSQILSASFDQTIR	IHGLK	2		834.4159126	1666.816225	0.000451244	5	N	317	332
Q3UKJ7	Exosome	SSGKR	EGGDFVCCALSPR	GEWIY	2	C7:+57.021,C8:+57.021	734.3214523	1466.627305	0.000451244	1	N	440	453
Q3UKJ7	Parental	VECAR	FSPDGQYLVTGSVDGFIEVWNFTTGK	IRKDL	2		1432.693037	2863.370473	0.000451244	1	N	221	247
Q3ULJ0	Exosome	LPGHK	LPENVVAVPNLSEAVQDADLLVFVIPHQFIHK	ICDEI	4		888.7374971	3550.918788	0.000823681	4	N	70	102
Q3ULJ0	Exosome	ARTGK	TIEELEKELLNGQK	LQGPQ	3		548.633721	1642.877763	0.000622848	9	N	284	298
Q3ULJ0	Exosome	KIFCK	GQVSTATFLESCGVADLITTCYGGR	NRRVA	2	C12:+57.021,C21:+57.021	1332.125687	2662.235773	0.000451244	11	N	246	271
Q3ULJ0	Exosome	KIFCK	GQVSTATFLESCGVADLITTCYGGR	NRRVA	3	C12:+57.021,C21:+57.021	888.4197245	2662.235773	0.000451244	4	N	246	271
Q3ULJ0	Exosome	LNGQK	LQGPQTSAEVYR	ILRQK	2		674.8469375	1347.678275	0.002663018	1	N	298	310
Q3ULJ0	Parental	LPGHK	LPENVVAVPNLSEAVQDADLLVFVIPHQFIHK	ICDEI	3		1184.647396	3550.918788	0.002884417	1	N	70	102
Q3ULJ0	Parental	LPGHK	LPENVVAVPNLSEAVQDADLLVFVIPHQFIHK	ICDEI	4		888.7374971	3550.918788	0.000451244	19	N	70	102
Q3ULJ0	Parental	LPGHK	LPENVVAVPNLSEAVQDADLLVFVIPHQF	IHKIC	3		1058.568083	3172.680849	0.000451244	7	N	70	99
Q3ULJ0	Parental	ITLIK	GIDEGPDGLKLISDIIR	EKMGI	3		604.335675	1809.983625	0.001839721	1	N	122	139
Q3ULJ0	Parental	KIFCK	GQVSTATFLESCGVADLITTCYGGR	NRRVA	2	C12:+57.021,C21:+57.021	1332.125687	2662.235773	0.000451244	1	N	246	271
Q3ULJ0	Parental	STATF	LESCGVADLITTCYGGR	NRRVA	2	C4:+57.021,C13:+57.021	936.4350022	1870.854404	0.000451244	2	N	254	271
Q3ULJ0	Parental	TPNFR	ITVVDDADTVELCGALK	NIVAV	2	C13:+57.021	909.9616071	1817.907614	0.001943752	2	N	189	206
Q3UM45	Exosome	SNRIR	AIENIDTLTNLESLFLGK	NKITK	2		996.0389348	1990.06227	0.000451244	21	N	200	218
Q3UM45	Exosome	NKITK	LQNLDALTNLTVLSVQSNR	LAKIE	2		1050.076914	2098.138229	0.000451244	18	N	223	242
Q3UM45	Exosome	LVNLR	ELYLSNNGIEVIEGLENNNK	LTMLD	2		1131.566576	2261.117553	0.000622848	5	N	256	276
Q3UM45	Exosome	QNLIK	CIENLEELQSLR	ELDLY	2	C1:+57.021	752.3775132	1502.739426	0.001463592	1	N	112	124
Q3UM45	Exosome	QNLIK	CIENLEELQSLR	ELDLY	2	[0:-17.027,C1:+57.021	743.8640132	1485.712426	0.001352548	2	N	112	124
Q3UM45	Exosome	NRLAK	IEGLQSLVNLR	ELYLS	2		621.3647661	1240.713932	0.000998612	2	N	245	256

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3UM45	Parental	SNRIR	AIENIDTLTNLESLFLGK	NKITK	2		996.0389348	1990.06227	0.000451244	26	N	200	218
Q3UM45	Parental	NKITK	LQNLDALTNLTVLSVQSNR	LAKIE	2		1050.076914	2098.138229	0.000451244	13	N	223	242
Q3UM45	Parental	LVNLR	ELYLSNNGIEVIEGLENNNK	LTMLD	2		1131.566576	2261.117553	0.000451244	8	N	256	276
Q3UND0	Exosome	SSPQR	SQPIDDEIYEELPEEEEDTASVK	MDEQG	2		1333.098497	2664.181395	0.000451244	20	N	251	274
Q3UND0	Exosome	IKDVK	SVYLQEFQDKGDAEDGDEYDDPFAGPADTISLASER	YDKDD	3		1317.584131	3949.728994	0.000451244	12	N	56	92
Q3UND0	Exosome	LASER	YDKDDDGPSDGNQFPPIAAQDLPFVIK	AGYLE	3		988.1422101	2961.40323	0.000451244	31	N	92	119
Q3UND0	Exosome	TSGDK	STDYANFYQGLWDCTGALSDELSFK	RGDVI	2	C14:+57.021	1444.639912	2887.264225	0.000451244	13	N	293	318
Q3UND0	Exosome	TSGDK	STDYANFYQGLWDCTGALSDELSFK	RGDVI	3	C14:+57.021	963.4292083	2887.264225	0.000451244	11	N	293	318
Q3UND0	Exosome	-M	PNPSCTSSPGPLPEEIR	NLLAD	2	C5:+57.021	919.4413732	1836.867146	0.001763695	2	N	1	18
Q3UND0	Exosome	PEEIR	NLLADVETFVADTLKGENLSK	KAKEK	3		759.7377965	2276.189989	0.000637154	2	N	18	39
Q3UND0	Exosome	PEEIR	NLLADVETFVADTLK	GENLS	2		824.9437746	1647.871949	0.000451244	1	N	18	33
Q3UND0	Exosome	AASPK	DAEEWVQQLK	FILQD	2		623.3096565	1244.603713	0.002080925	1	N	205	215
Q3UND0	Exosome	EKRRK	DHSFLGFEWQK	RWCAL	3		465.2232155	1392.646246	0.001352548	3	N	128	139
Q3UND0	Parental	SSPQR	SQPIDDEIYEELPEEEEDTASVK	MDEQG	2		1333.098497	2664.181395	0.000451244	50	N	251	274
Q3UND0	Parental	VQQLK	FILQDLGSDVIPEDDEERGELYDDVDHPAAVSSPQR	SQPID	3		1342.966687	4025.876662	0.000451244	46	N	215	251
Q3UND0	Parental	VQQLK	FILQDLGSDVIPEDDEERGELYDDVDHPAAVSSPQR	SQPID	4		1007.476965	4025.876662	0.000451244	9	N	215	251
Q3UND0	Parental	IKDVK	SVYLQEFQDKGDAEDGDEYDDPFAGPADTISLASER	YDKDD	3		1317.584131	3949.728994	0.000451244	49	N	56	92
Q3UND0	Parental	LASER	YDKDDDGPSDGNQFPPIAAQDLPFVIK	AGYLE	3		988.1422101	2961.40323	0.000451244	69	N	92	119
Q3UND0	Parental	GKGSR	DSVHHTSGDKSTDYANFYQGLWDCTGALSDELSFK	RGDVI	3	C24:+57.021	1317.918637	3950.732512	0.002663018	1	N	283	318
Q3UND0	Parental	GKGSR	DSVHHTSGDKSTDYANFYQGLWDCTGALSDELSFK	RGDVI	4	C24:+57.021	988.6909279	3950.732512	0.000451244	2	N	283	318
Q3UND0	Parental	TSGDK	STDYANFYQGLWDCTGALSDELSFK	RGDVI	2	C14:+57.021	1444.639912	2887.264225	0.000451244	31	N	293	318
Q3UND0	Parental	TSGDK	STDYANFYQGLWDCTGALSDELSFK	RGDVI	3	C14:+57.021	963.4292083	2887.264225	0.000451244	22	N	293	318
Q3UND0	Parental	-M	PNPSCTSSPGPLPEEIR	NLLAD	2	C5:+57.021	919.4413732	1836.867146	0.000451244	6	N	1	18
Q3UND0	Parental	PEEIR	NLLADVETFVADTLKGENLSK	KAKEK	2		1139.102795	2276.189989	0.000451244	4	N	18	39
Q3UND0	Parental	PEEIR	NLLADVETFVADTLKGENLSK	KAKEK	3		759.7377965	2276.189989	0.000622848	2	N	18	39
Q3UND0	Parental	EKRRK	DHSFLGFEWQKR	WCALS	3		517.2569192	1548.747358	0.001162105	3	N	128	140
Q3UND0	Parental	PEEIR	NLLADVETFVADTLK	GENLS	2		824.9437746	1647.871949	0.000451244	12	N	18	33
Q3UND0	Parental	DKQQK	GEFAIDGYDVR	MNNTL	2		621.2940064	1240.572413	0.000451244	5	N	161	172
Q3UND0	Parental	APDKR	IYQFTAASPKDAEEWVQQLK	FILQD	2		1176.59768	2351.179759	0.000451244	3	N	195	215
Q3UND0	Parental	QQLKF	ILQDLGSDVIPEDDEERGELYDDVDHPAAVSSPQR	SQPID	3		1293.943883	3878.808248	0.000451244	8	N	216	251
Q3UND0	Parental	QQLKF	ILQDLGSDVIPEDDEERGELYDDVDHPAAVSSPQR	SQPID	4		970.709862	3878.808248	0.000870037	3	N	216	251
Q3UND0	Parental	KDGKK	DCCFEICAPDKR	IYQFT	2	C2:+57.021,C3:+57.021,C7:+57.02	785.8258133	1569.636027	0.000451244	7	N	183	195
Q3UND0	Parental	KDGKK	DCCFEICAPDKR	IYQFT	3	C2:+57.021,C3:+57.021,C7:+57.02	524.2198089	1569.636027	0.000451244	1	N	183	195
Q3UND0	Parental	AASPK	DAEEWVQQLK	FILQD	2		623.3096565	1244.603713	0.001699387	3	N	205	215
Q3UND0	Parental	TSGDK	STDYANFYQGLWDCTGALSDELSFKR	GDVIY	3	C14:+57.021	1015.462912	3043.365336	0.000451244	4	N	293	319
Q3UND0	Parental	EKRRK	DHSFLGFEWQK	RWCAL	2		697.3309232	1392.646246	0.000451244	2	N	128	139
Q3UND0	Parental	EKRRK	DHSFLGFEWQK	RWCAL	3		465.2232155	1392.646246	0.002374549	2	N	128	139
Q3UND0	Parental	VKSVY	LQEFQDKGDAEDGDEYDDPFAGPADTISLASER	YDKDD	3		1201.196208	3600.565223	0.000451244	12	N	59	92
Q3UP87	Exosome	GLNFR	SVQVVLGAHDLR	RQERT	2		647.3678401	1292.72008	0.000451244	20	N	77	89
Q3UP87	Exosome	GLNFR	SVQVVLGAHDLR	RQERT	3		431.9144934	1292.72008	0.002080925	2	N	77	89
Q3UP87	Exosome	MCRRR	VNVCTLVPR	RQAGI	2	C4:+57.021	529.2950665	1056.574533	0.000451244	21	N	183	192
Q3UP87	Exosome	TLVPR	RQAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C6:+57.021,C16:+57.021	1017.502893	3049.48528	0.000451244	40	N	192	220
Q3UP87	Exosome	AGICF	GDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C9:+57.021	1109.549975	2217.08435	0.000451244	17	N	199	220
Q3UP87	Exosome	AGICF	GDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C9:+57.021	740.0359167	2217.08435	0.000622848	3	N	199	220
Q3UP87	Exosome	DSFIR	GGCGSGLYPDAFAPVAEF	ADWIN	2	C3:+57.021	907.9066349	1813.79767	0.001839721	2	N	220	238
Q3UP87	Exosome	AFAPV	AEFADWINSIIR	SHNDH	2		717.8729553	1433.730311	0.000823681	2	N	235	247
Q3UP87	Exosome	RRQAG	ICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C2:+57.021,C12:+57.021	1319.641307	2637.267014	0.000451244	9	N	196	220
Q3UP87	Exosome	RRQAG	ICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C2:+57.021,C12:+57.021	880.0968046	2637.267014	0.000451244	13	N	196	220
Q3UP87	Exosome	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C5:+57.021,C15:+57.021	1447.699885	2893.384169	0.000451244	44	N	193	220
Q3UP87	Exosome	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C5:+57.021,C15:+57.021	965.4691897	2893.384169	0.000451244	50	N	193	220
Q3UP87	Exosome	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	Q1:-17.027,C5:+57.021,C15:+57.021	1439.186385	2876.357169	0.000451244	5	N	193	220
Q3UP87	Exosome	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	Q1:-17.027,C5:+57.021,C15:+57.021	959.793523	2876.357169	0.000451244	6	N	193	220
Q3UP87	Exosome	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	[0:-	1439.186385	2876.357169	0.000451244	4	N	193	220
Q3UP87	Exosome	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	[0:-	959.793523	2876.357169	0.000451244	10	N	193	220
Q3UP87	Exosome	PRRQA	GICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C3:+57.021,C13:+57.021	1348.152039	2694.288478	0.000451244	38	N	195	220
Q3UP87	Exosome	PRRQA	GICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C3:+57.021,C13:+57.021	899.1039592	2694.288478	0.000451244	38	N	195	220
Q3UP87	Exosome	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIR	SHNDH	2	C3:+57.021	1442.19245	2882.369299	0.000451244	32	N	220	247
Q3UP87	Exosome	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIR	SHNDH	3	C3:+57.021	961.7975664	2882.369299	0.000451244	28	N	220	247
Q3UP87	Exosome	PVAEF	ADWINSIIR	SHNDH	2		544.2988947	1086.582189	0.001654178	2	N	238	247
Q3UP87	Exosome	SLQRR	GGHFCGATLIAR	NFVMS	2	C5:+57.021	630.3196042	1258.623608	0.002212458	1	N	49	61
Q3UP87	Exosome	FSVQR	IFENGFDPSQLL	NDIVI	2		690.346239	1378.676878	0.001699387	2	N	102	114
Q3UP87	Exosome	GLNFR	SVQVVLGAHDLRR	QERTR	3		483.9481971	1448.821191	0.002145581	1	N	77	90
Q3UP87	Parental	GLNFR	SVQVVLGAHDLR	RQERT	2		647.3678401	1292.72008	0.000451244	27	N	77	89

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3UP87	Parental	GLNFR	SVQVVLGAHDLR	RQERT	3		431.9144934	1292.72008	0.000823681	12	N	77	89
Q3UP87	Parental	MCRRR	VNVCTLVPR	RQAGI	2	C4:+57.021	529.2950665	1056.574533	0.000622848	23	N	183	192
Q3UP87	Parental	TLVPR	RQAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C6:+57.021,C16:+57.021	1017.502893	3049.48528	0.000451244	35	N	192	220
Q3UP87	Parental	AGICF	GDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C9:+57.021	1109.549975	2217.08435	0.000451244	102	N	199	220
Q3UP87	Parental	AGICF	GDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C9:+57.021	740.0359167	2217.08435	0.000451244	36	N	199	220
Q3UP87	Parental	DSFIR	GGCGSGLYPDAFAPVAEF	ADWIN	2	C3:+57.021	907.9066349	1813.79767	0.000622848	35	N	220	238
Q3UP87	Parental	AFAPV	AEFADWINSIIR	SHNDH	2		717.8729553	1433.730311	0.000451244	21	N	235	247
Q3UP87	Parental	AFAPV	AEFADWINSIIR	SHNDH	3		478.9179035	1433.730311	0.000979378	1	N	235	247
Q3UP87	Parental	RRQAG	ICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C2:+57.021,C12:+57.021	1319.641307	2637.267014	0.000451244	24	N	196	220
Q3UP87	Parental	RRQAG	ICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C2:+57.021,C12:+57.021	880.0968046	2637.267014	0.000451244	16	N	196	220
Q3UP87	Parental	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C5:+57.021,C15:+57.021	1447.699885	2893.384169	0.000451244	51	N	193	220
Q3UP87	Parental	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C5:+57.021,C15:+57.021	965.4691897	2893.384169	0.000451244	38	N	193	220
Q3UP87	Parental	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	Q1:-17.027,C5:+57.021,C15:+57.021	1439.186385	2876.357169	0.000451244	3	N	193	220
Q3UP87	Parental	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	Q1:-17.027,C5:+57.021,C15:+57.021	959.793523	2876.357169	0.000451244	13	N	193	220
Q3UP87	Parental	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	[0:-	1439.186385	2876.357169	0.000451244	5	N	193	220
Q3UP87	Parental	LVPRR	QAGICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	[0:-	959.793523	2876.357169	0.001463592	3	N	193	220
Q3UP87	Parental	PRRQA	GICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	2	C3:+57.021,C13:+57.021	1348.152039	2694.288478	0.000451244	118	N	195	220
Q3UP87	Parental	PRRQA	GICFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C3:+57.021,C13:+57.021	899.1039592	2694.288478	0.000451244	158	N	195	220
Q3UP87	Parental	GGPLV	CNNLVQGIDSFIR	GGCGS	2	C1:+57.021	768.3856726	1534.755745	0.000451244	13	N	207	220
Q3UP87	Parental	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIR	SHNDH	2	C3:+57.021	1442.19245	2882.369299	0.000451244	30	N	220	247
Q3UP87	Parental	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIR	SHNDH	3	C3:+57.021	961.7975664	2882.369299	0.000451244	34	N	220	247
Q3UP87	Parental	IRGGC	GSGLYPDAFAPVAEFADWINSIIR	SHNDH	2		1305.155893	2608.296186	0.000451244	9	N	223	247
Q3UP87	Parental	IRGGC	GSGLYPDAFAPVAEFADWINSIIR	SHNDH	3		870.439862	2608.296186	0.001463592	1	N	223	247
Q3UP87	Parental	GGCGS	GLYPDAFAPVAEFADWINSIIR	SHNDH	2		1233.129147	2464.242694	0.000451244	4	N	225	247
Q3UP87	Parental	PVAEF	ADWINSIIR	SHNDH	2		544.2988947	1086.582189	0.000979378	11	N	238	247
Q3UP87	Parental	RQAGI	CFGDSGGPLVCNNLVQGIDSFIR	GGCGS	3	C1:+57.021,C11:+57.021	842.4021166	2524.18295	0.001395409	2	N	197	220
Q3UP87	Parental	SLQRR	GGHFCGATLIAR	NFVMS	2	C5:+57.021	630.3196042	1258.623608	0.001395409	2	N	49	61
Q3UP87	Parental	SATIN	ANVQVAQLPAQGQGVGDR	TPCLA	2		904.4746276	1806.933655	0.000451244	14	N	129	147
Q3UP87	Parental	FSVQR	IFENGFDPSQLL	NDIVI	2		690.346239	1378.676878	0.001591523	5	N	102	114
Q3UP87	Parental	DSFIR	GGCGSGLYPDAFAPVAEFADWINSIIRS	HNDHL	3	C3:+57.021	990.8082426	2969.401328	0.000451244	2	N	220	248
Q3UP87	Parental	TLIAR	NFVMSAAHCVNGLNFR	SVQVV	2	C9:+57.021	918.9355386	1835.855477	0.000451244	2	N	61	77
Q3UP87	Parental	ATINA	NVQVAQLPAQGQGVGDR	TPCLA	2		868.9560707	1735.896541	0.000451244	6	N	130	147
Q3UP87	Parental	GPLVC	NNLVQGIDSFIR	GGCGS	2		688.3705798	1374.72556	0.002813207	1	N	208	220
Q3UP87	Parental	SGGPL	VCNNLVQGIDSFIR	GGCGS	2	C2:+57.021	817.9198796	1633.824159	0.000823681	6	N	206	220
Q3UPH1	Exosome	VAAVR	DAFQEVFGLAVVVGEAGQSNIAPQPVGYAAGLK	GAQER	3		1101.573897	3301.69829	0.001463592	1	N	272	305
Q3UPH1	Exosome	VHGIR	LEAFTQATPVPLEFVQQAQSLTPQDYNLR	WSGLL	3		1102.233652	3303.677555	0.002374549	1	N	357	386
Q3UPH1	Parental	VAAVR	DAFQEVFGLAVVVGEAGQSNIAPQPVGYAAGLK	GAQER	3		1101.573897	3301.69829	0.000451244	22	N	272	305
Q3UPH1	Parental	VHGIR	LEAFTQATPVPLEFVQQAQSLTPQDYNLR	WSGLL	3		1102.233652	3303.677555	0.000451244	29	N	357	386
Q3UPH1	Parental	DYNLR	WSGLLVTVGEVLEK	SLLNV	2		765.4328457	1528.850091	0.001871652	1	N	386	400
Q3UPH1	Parental	AIHEK	QTAVSVENFIAELLPDKWFDIGCLVVEDPVHGIR	LEAFT	4	C23:+57.021	967.500508	3865.970832	0.000622848	2	N	323	357
Q3UPL0	Exosome	GKDAK	ILCSNPNTGEVLYELPTNTQWCFDIQWCPR	NPAVL	3	C3:+57.021,C22:+57.021,C28:+57.021	1237.905873	3710.694218	0.000451244	2	N	284	314
Q3UPL0	Exosome	SFGGK	LVTFESVAVPLQQGAEQQR	RQPVF	2		1050.558357	2099.101115	0.000823681	1	N	403	422
Q3UPL0	Exosome	ACWTK	AQDGSSPLSLQDLIEK	VVILR	2		850.9392206	1699.862841	0.000622848	2	N	706	722
Q3UPL0	Parental	LKNWR	EALAAVLTYAKPDEFSALCDLLGTR	LEREG	3	C19:+57.021	908.8023174	2723.383552	0.000698008	1	N	649	674
Q3UPL0	Parental	GKDAK	ILCSNPNTGEVLYELPTNTQWCFDIQWCPR	NPAVL	3	C3:+57.021,C22:+57.021,C28:+57.021	1237.905873	3710.694218	0.000823681	1	N	284	314
Q3UQ44	Exosome	SAKLK	NSCISEEERDAYEELLTQAEIQSNISTVNR	MAAVD	3	C3:+57.021	1166.881523	3497.62117	0.000451244	3	N	273	303
Q3UQ44	Exosome	KNVSK	VLWLDEIQQAINEANVDENR	AKQWV	2		1185.09075	2368.1659	0.000451244	2	N	514	534
Q3UQ44	Exosome	LLYYR	YMNPAIVAPDGFDIIDMTAGGQINSNQR	RNLGS	3		1003.480064	3007.416791	0.002374549	1	N	1107	1135
Q3UQ44	Parental	PAFSK	IGGILANELSVDEAALHAAVIAINEAIEK	GVAKQ	3		982.2050333	2943.5917	0.000451244	25	N	198	227
Q3UQ44	Parental	SAKLK	NSCISEEERDAYEELLTQAEIQSNISTVNR	MAAVD	3	C3:+57.021	1166.881523	3497.62117	0.000451244	18	N	273	303
Q3UQ44	Parental	PAFSK	IGGILANELSVDEAALHAAVIAINEAIEKGVAK	QTIIT	4		825.7112136	3298.813655	0.000622848	2	N	198	231
Q3UQ44	Parental	KNVSK	VLWLDEIQQAINEANVDENR	AKQWV	2		1185.09075	2368.1659	0.000451244	21	N	514	534
Q3UQ44	Parental	KNVSK	VLWLDEIQQAINEANVDENR	AKQWV	3		790.3964333	2368.1659	0.002519933	1	N	514	534
Q3UQ44	Parental	IITLR	NPNAVLTCVDDSLSQEYQK	ELWEA	2	C8:+57.021	1091.010348	2180.005097	0.000451244	4	N	238	257
Q3UQ44	Parental	YLLLK	LFKTALEEEIK	SKVDQ	2		660.8746323	1319.733665	0.001329271	2	N	937	948
Q3UQ44	Parental	KVTDK	VLGSIISSLDLLPYGLR	YIAKV	2		908.5330912	1815.050582	0.002981883	1	N	1057	1074
Q3UQ44	Parental	VEVYK	AWVNQLETQTGEASKLPYDVTTEQALTYPEVK	NKLEA	3		1203.937341	3608.788622	0.000451244	1	N	1009	1041
Q3UQ44	Parental	LCLSK	ESWLTGEEIEDIVEEVTSDYIR	EKLWS	2		1306.61666	2611.217721	0.000662267	2	N	631	653
Q3UQ44	Parental	LCLSK	ESWLTGEEIEDIVEEVTSDYIR	EKLWS	3		871.4137069	2611.217721	0.00307782	1	N	631	653
Q3UW53	Exosome	LPEGR	GSTSQSTSGGLTENTSCPGPIEEPFEAQEPAEK	VLPAI	3	C17:+57.021	1141.511096	3421.509888	0.002663018	1	N	785	818
Q3UW53	Exosome	EREVR	EKEAQPLEAEAPGVDLGILPEGR	GSTSQ	3		806.7557387	2417.243816	0.000451244	3	N	762	785

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3UW53	Exosome	VLLPK	AFPVYLWQPYLR	HGYFC	2		776.9197085	1551.823817	0.000451244	12	N	159	171
Q3UW53	Exosome	HDYMK	QTTFEAQAFLEAVQFFR	QEKGH	2		1017.010512	2032.005423	0.000451244	6	N	203	220
Q3UW53	Exosome	HDYMK	QTTFEAQAFLEAVQFFR	QEKGH	3		678.3429411	2032.005423	0.000451244	6	N	203	220
Q3UW53	Exosome	EVREK	EAQPLEAEAPGVDLGILPEGR	GSTSQ	2		1081.06093	2160.10626	0.001463592	2	N	764	785
Q3UW53	Exosome	TIRKK	IFQEALIQITLPTVQK	ALAST	2		921.5409163	1841.066233	0.000451244	14	N	493	509
Q3UW53	Exosome	FSEVR	ALFEKEVDELSQSFHATQDSAQLK	EGLQQ	3		907.7842456	2720.329337	0.000451244	19	N	365	389
Q3UW53	Exosome	ALFEK	EVDELSQSFHATQDSAQLK	EGLQQ	2		1067.008894	2132.002189	0.000451244	2	N	370	389
Q3UW53	Exosome	ALFEK	EVDELSQSFHATQDSAQLK	EGLQQ	3		711.6751962	2132.002189	0.000451244	8	N	370	389
Q3UW53	Exosome	PAGGK	VLTSEEEYSLLSDKHFPDPTASSEK	NSQPF	3		937.1191825	2808.334148	0.000451244	1	N	124	149
Q3UW53	Exosome	PAGGK	VLTSEEEYSLLSDKHFPDPTASSEK	NSQPF	4		703.0913369	2808.334148	0.000451244	1	N	124	149
Q3UW53	Exosome	SQFLK	TKPPLEPGTVLYEAELSQFAEDIRK	WKDRY	4		708.6266182	2830.475273	0.000451244	4	N	60	85
Q3UW53	Exosome	PAGGK	VLTSEEEYSLLSDK	HFPDP	2		806.9017724	1611.787945	0.000451244	2	N	124	138
Q3UW53	Parental	LPEGR	GSTSQSTSGGLTENTSCPGPIEEPFEAQEPAEK	VLPAI	3	C17:+57.021	1141.511096	3421.509888	0.000451244	39	N	785	818
Q3UW53	Parental	EREVR	EKEAQPLEAEAPGVDLGILPEGR	GSTSQ	2		1209.629708	2417.243816	0.000451244	4	N	762	785
Q3UW53	Parental	EREVR	EKEAQPLEAEAPGVDLGILPEGR	GSTSQ	3		806.7557387	2417.243816	0.000451244	34	N	762	785
Q3UW53	Parental	VLLPK	AFPVYLWQPYLR	HGYFC	2		776.9197085	1551.823817	0.000451244	12	N	159	171
Q3UW53	Parental	HDYMK	QTTFEAQAFLEAVQFFR	QEKGH	2		1017.010512	2032.005423	0.000662267	1	N	203	220
Q3UW53	Parental	EVREK	EAQPLEAEAPGVDLGILPEGR	GSTSQ	2		1081.06093	2160.10626	0.000451244	29	N	764	785
Q3UW53	Parental	TIRKK	IFQEALIQITLPTVQK	ALAST	2		921.5409163	1841.066233	0.000870037	3	N	493	509
Q3UW53	Parental	FSEVR	ALFEKEVDELSQSFHATQDSAQLK	EGLQQ	3		907.7842456	2720.329337	0.000451244	8	N	365	389
Q3UW53	Parental	ALFEK	EVDELSQSFHATQDSAQLK	EGLQQ	2		1067.008894	2132.002189	0.000451244	13	N	370	389
Q3UW53	Parental	ALFEK	EVDELSQSFHATQDSAQLK	EGLQQ	3		711.6751962	2132.002189	0.00091018	3	N	370	389
Q3UW53	Parental	CNHVR	SEVEQQRDLTSQFLK	TKPPL	2		904.4633942	1806.911188	0.000870037	1	N	45	60
Q3UW53	Parental	KELKK	LLTVTVSVESAPVVENDIHNGTPVPQENIKEEESK	IHPEA	4		951.2407979	3800.931992	0.000451244	1	N	705	740
Q3UYV9	Exosome	KVGEK	SACSLESNLEGLAGVLEADLPNYK	SKILR	2	C3:+57.021	1275.623534	2549.231468	0.000451244	14	N	41	65
Q3UYV9	Exosome	KVGEK	SACSLESNLEGLAGVLEADLPNYK	SKILR	3	C3:+57.021	850.7516227	2549.231468	0.000451244	3	N	41	65
Q3UYV9	Exosome	LLPEK	LTIYTTLVGLLNAR	NYNFG	3		516.6438917	1546.908275	0.00307782	1	N	82	96
Q3UYV9	Exosome	RDFTR	LFVWEILHSTIR	KMNKH	3		505.2895603	1512.845281	0.002374549	1	N	634	646
Q3UYV9	Exosome	EKCMR	LSYHQHILDIVPPTFSALCPANPTCIYK	YGDES	3	C19:+57.021,C25:+57.021	1085.882711	3254.624734	0.001654178	1	N	458	486
Q3UYV9	Exosome	NFQFR	WSWEDWSDCLTQDLESPKPK	FVREV	3	C9:+57.021	836.3780082	2506.110625	0.000870037	1	N	427	447
Q3UYV9	Exosome	DKMIR	TQIVDCAAVANWIFSSELSR	DFTRL	2	C6:+57.021	1134.060176	2266.104751	0.000451244	1	N	610	630
Q3UYV9	Parental	KVGEK	SACSLESNLEGLAGVLEADLPNYK	SKILR	2	C3:+57.021	1275.623534	2549.231468	0.000451244	25	N	41	65
Q3UYV9	Parental	KVGEK	SACSLESNLEGLAGVLEADLPNYK	SKILR	3	C3:+57.021	850.7516227	2549.231468	0.000622848	2	N	41	65
Q3UYV9	Parental	LLPEK	LTIYTTLVGLLNAR	NYNFG	3		516.6438917	1546.908275	0.001699387	2	N	82	96
Q3UZ39	Exosome	KSDSR	ASNSPEQSSCLEGLDSEVPGPTEDLKTDLGK	GSFEP	3	C10:+57.021	1087.508915	3259.503346	0.000451244	16	N	344	375
Q3UZ39	Exosome	LAGAK	CEQQVQSQDQENTSDLKNSEQIESHK	VTNKS	4	C1:+57.021	773.0986746	3088.363498	0.000451244	3	N	310	336
Q3UZ39	Exosome	CTDSR	GTGGNQREDEVQAGDTTVEDQVGTVASGPAK	QSKGT	3		1025.148864	3072.423191	0.000451244	9	N	401	432
Q3UZ39	Parental	KSDSR	ASNSPEQSSCLEGLDSEVPGPTEDLKTDLGK	GSFEP	3	C10:+57.021	1087.508915	3259.503346	0.000451244	57	N	344	375
Q3UZ39	Parental	TDLGK	GSFEPCPDYILGQTAEIDKVTCTDSR	GTGGN	3	C6:+57.021,C22:+57.021	987.1200033	2958.33661	0.000451244	21	N	375	401
Q3UZ39	Parental	EMLEK	HGIILNSEIATNGETSDTVNDVGYQAPTK	ITKEE	3		1015.498945	3043.473435	0.000451244	5	N	194	223
Q3UZ39	Parental	LAGAK	CEQQVQSQDQENTSDLKNSEQIESHK	VTNKS	3	C1:+57.021	1030.462299	3088.363498	0.000451244	6	N	310	336
Q3UZ39	Parental	LAGAK	CEQQVQSQDQENTSDLKNSEQIESHK	VTNKS	4	C1:+57.021	773.0986746	3088.363498	0.000451244	6	N	310	336
Q3UZ39	Parental	CTDSR	GTGGNQREDEVQAGDTTVEDQVGTVASGPAK	QSKGT	3		1025.148864	3072.423191	0.000451244	31	N	401	432
Q3UZ39	Parental	HPGEK	AENQRPAEDSALSPGPLAGAK	CEQQV	2		1040.027421	2078.039243	0.000451244	10	N	289	310
Q3UZ39	Parental	HPGEK	AENQRPAEDSALSPGPLAGAK	CEQQV	3		693.6875476	2078.039243	0.001463592	1	N	289	310
Q3UZ39	Parental	GSSGK	QNKVEEDGPTEGPTDILDQNSPQCEDR	EISPV	3	C24:+57.021	1024.455033	3070.3417	0.000451244	18	N	628	655
Q3UZ39	Parental	TDLGK	GSFEPCPDYILGQTAEIDK	VTCTD	2	C6:+57.021	1070.499085	2138.98257	0.000451244	5	N	375	394
Q3UZ39	Parental	GGNQR	EDEVQAGDTTVEDQVGTVASGPAK	QSKGT	2		1202.062052	2402.108504	0.001264573	1	N	408	432
Q3UZ39	Parental	GKQNK	VEEDGPTEGPTDILDQNSPQCEDREISPVGEK	GPQCD	3	C21:+57.021	1180.869172	3539.584116	0.000451244	7	N	631	663
Q3UZ39	Parental	GKQNK	VEEDGPTEGPTDILDQNSPQCEDR	EISPV	2	C21:+57.021	1351.080416	2700.145232	0.002145581	1	N	631	655
Q3UZA1	Exosome	EPDTK	QKEEAPLEPSCSPGADHAAGEITSEIQNEK	AVSMD	4	C11:+57.021	806.37725	3221.4778	0.000851441	1	N	368	398
Q3UZA1	Exosome	NAGEK	VGQNPDTASQGHPEVQAPSQTGSPEAENGCGSPR	EETTP	3	C30:+57.021	1149.513945	3445.518436	0.000451244	6	N	265	299
Q3UZA1	Exosome	SPGIR	SHPSEAEEVPVSFDQPPEGTHLPSYNK	VRTRG	3		993.4654642	2977.372993	0.001229886	1	N	131	158
Q3UZA1	Parental	FRDYR	AVEPSQENGAREENGDDVFASK	SKDPG	2		1175.033629	2348.051658	0.000698008	1	N	188	210
Q3UZA1	Parental	FRDYR	AVEPSQENGAREENGDDVFASK	SKDPG	3		783.691686	2348.051658	0.000622848	8	N	188	210
Q3UZA1	Parental	EPDTK	QKEEAPLEPSCSPGADHAAGEITSEIQNEK	AVSMD	3	C11:+57.021	1074.833733	3221.4778	0.000451244	34	N	368	398
Q3UZA1	Parental	EPDTK	QKEEAPLEPSCSPGADHAAGEITSEIQNEK	AVSMD	4	C11:+57.021	806.37725	3221.4778	0.000451244	26	N	368	398
Q3UZA1	Parental	EPDTK	QKEEAPLEPSCSPGADHAAGEITSEIQNEK	AVSMD	3	Q1:-17.027,C11:+57.021	1069.158067	3204.4508	0.000823681	1	N	368	398
Q3UZA1	Parental	EPDTK	QKEEAPLEPSCSPGADHAAGEITSEIQNEK	AVSMD	3	[0:-17.027,C11:+57.021	1069.158067	3204.4508	0.000622848	9	N	368	398
Q3UZA1	Parental	PLIEK	LQANLAFDPAALLPGASPK	SPGLK	2		947.5257975	1893.035995	0.000451244	54	N	88	107
Q3UZA1	Parental	NAGEK	VGQNPDTASQGHPEVQAPSQTGSPEAENGCGSPR	EETTP	3	C30:+57.021	1149.513945	3445.518436	0.000451244	66	N	265	299
Q3UZA1	Parental	SPGIR	SHPSEAEEVPVSFDQPPEGTHLPSYNK	VRTRG	3		993.4654642	2977.372993	0.000451244	6	N	131	158
Q3UZZ4	Exosome	QHPER	TLYWVAPLNTDAR	ALEYY	2		760.3993372	1518.783074	0.000451244	32	N	277	290
Q3UZZ4	Exosome	DYRIR	YGQGGGTVAFNNNLYVNWYNGGNIAK	INLTT	2		1396.165312	2790.315024	0.000622848	17	N	316	342
Q3UZZ4	Exosome	DYRIR	YGQGGGTVAFNNNLYVNWYNGGNIAK	INLTT	3		931.112808	2790.315024	0.000622848	9	N	316	342

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3UZZ4	Exosome	LEYYR	LYDSLDNLLIYSHFR	DYRIR	2		934.9812228	1867.946846	0.000451244	18	N	296	311
Q3UZZ4	Exosome	LEYYR	LYDSLDNLLIYSHFR	DYRIR	3		623.6567485	1867.946846	0.000451244	40	N	296	311
Q3UZZ4	Exosome	PFDQK	LYVYNDGYLLNYDLVFLQTPR	QPV-	2		1290.163187	2578.310773	0.000451244	57	N	481	502
Q3UZZ4	Exosome	PFDQK	LYVYNDGYLLNYDLVFLQTPR	QPV-	3		860.4447245	2578.310773	0.000451244	38	N	481	502
Q3UZZ4	Exosome	KMQER	IQSINYHPFDQK	LYVYN	2		745.3758621	1488.736124	0.000451244	19	N	469	481
Q3UZZ4	Exosome	KMQER	IQSINYHPFDQK	LYVYN	3		497.2531747	1488.736124	0.000735798	11	N	469	481
Q3UZZ4	Exosome	TLNTK	TEEIFYYYDTNTER	EGNLG	2		922.4052106	1842.794821	0.000451244	43	N	441	455
Q3UZZ4	Exosome	EVMEK	DSISYTELDFELIK	LEVKE	2		836.9199652	1671.82433	0.000451244	10	N	138	152
Q3UZZ4	Exosome	DRVER	LEYTAHILSQK	FEREF	2		651.8567739	1301.697948	0.000451244	31	N	93	104
Q3UZZ4	Exosome	LLVEK	LESLDQNNVLSIR	RQILA	2		750.9049838	1499.794368	0.000451244	24	N	192	205
Q3UZZ4	Exosome	AYNNR	FSYANVNWQDIDLAVDEQALWAIYATEASTGNIVISK	LNDTT	3		1372.67993	4115.01639	0.000870037	9	N	364	401
Q3UZZ4	Exosome	KLYVY	NDGYLLNYDLVFLQTPR	QPV-	2		1021.023619	2040.031638	0.000451244	15	N	485	502
Q3UZZ4	Exosome	KLYVY	NDGYLLNYDLVFLQTPR	QPV-	3		681.018346	2040.031638	0.000451244	3	N	485	502
Q3UZZ4	Exosome	FSKVK	EYVQLISVYEK	RLLNL	2		685.8642646	1369.712929	0.000735798	2	N	113	124
Q3UZZ4	Exosome	REFSK	VKEYVQLISVYEK	RLLNL	2		799.4459531	1596.876306	0.000451244	3	N	111	124
Q3UZZ4	Parental	QHPER	TLYWVAPLNTDAR	ALEYY	2		760.3993372	1518.783074	0.000451244	28	N	277	290
Q3UZZ4	Parental	LEYYR	LYDSLDNLLIYSHFRDYR	IRYGQ	3		768.3872095	2302.138229	0.000451244	3	N	296	314
Q3UZZ4	Parental	LEYYR	LYDSLDNLLIYSHFRDYR	IRYGQ	4		576.5423571	2302.138229	0.000451244	4	N	296	314
Q3UZZ4	Parental	DYRIR	YGQGGGTVAFNNNLYVNWYNGGNIAK	INLTT	2		1396.165312	2790.315024	0.000451244	22	N	316	342
Q3UZZ4	Parental	LEYYR	LYDSLDNLLIYSHFR	DYRIR	2		934.9812228	1867.946846	0.000451244	7	N	296	311
Q3UZZ4	Parental	LEYYR	LYDSLDNLLIYSHFR	DYRIR	3		623.6567485	1867.946846	0.000451244	39	N	296	311
Q3UZZ4	Parental	PFDQK	LYVYNDGYLLNYDLVFLQTPR	QPV-	2		1290.163187	2578.310773	0.000451244	47	N	481	502
Q3UZZ4	Parental	PFDQK	LYVYNDGYLLNYDLVFLQTPR	QPV-	3		860.4447245	2578.310773	0.000451244	22	N	481	502
Q3UZZ4	Parental	KMQER	IQSINYHPFDQK	LYVYN	2		745.3758621	1488.736124	0.000451244	5	N	469	481
Q3UZZ4	Parental	KMQER	IQSINYHPFDQK	LYVYN	3		497.2531747	1488.736124	0.002663018	1	N	469	481
Q3UZZ4	Parental	TLNTK	TEEIFYYYDTNTER	EGNLG	2		922.4052106	1842.794821	0.000451244	43	N	441	455
Q3UZZ4	Parental	EVMEK	DSISYTELDFELIK	LEVKE	2		836.9199652	1671.82433	0.000451244	3	N	138	152
Q3UZZ4	Parental	DRVER	LEYTAHILSQK	FEREF	2		651.8567739	1301.697948	0.0007646	1	N	93	104
Q3UZZ4	Parental	LLVEK	LESLDQNNVLSIR	RQILA	2		750.9049838	1499.794368	0.000451244	14	N	192	205
Q3UZZ4	Parental	AYNNR	FSYANVNWQDIDLAVDEQALWAIYATEASTGNIVISK	LNDTT	3		1372.67993	4115.01639	0.000870037	22	N	364	401
Q3UZZ4	Parental	KLYVY	NDGYLLNYDLVFLQTPR	QPV-	2		1021.023619	2040.031638	0.000451244	24	N	485	502
Q3UZZ4	Parental	KLYVY	NDGYLLNYDLVFLQTPR	QPV-	3		681.018346	2040.031638	0.001699387	1	N	485	502
Q3UZZ4	Parental	REFSK	VKEYVQLISVYEK	RLLNL	2		799.4459531	1596.876306	0.000451244	8	N	111	124
Q3UZZ4	Parental	EVEIR	NMTLLVEKLESLDQNNVLSIR	RQILA	2	M2:+15.995	1223.155079	2444.294558	0.002019181	1	N	184	205
Q3V0K9	Exosome	NEGNA	TLTLALVWQLMR	RYTLK	2		722.9213945	1443.827189	0.000451244	28	Y	490	502
Q3V0K9	Exosome	NEGNA	TLTLALVWQLMR	RYTLK	3		482.2835297	1443.827189	0.000451244	4	Y	490	502
Q3V0K9	Exosome	SFKDK	SISTSLPVLDLIDAIAPNAVR	QEMIK	2		1083.112965	2164.210331	0.000451244	11	N	546	567
Q3V0K9	Exosome	INKKK	LTPFTVSENLNLALNSASAIGCTVVNIGAQDLK	EGKPH	3	C22:+57.021	1144.268102	3429.780906	0.002727428	1	N	186	219
Q3V0K9	Exosome	EELMK	LSPEELLLR	WVNYH	2		535.3167532	1068.617906	0.001463592	2	Y	265	274
Q3V0K9	Parental	NEGNA	TLTLALVWQLMR	RYTLK	2		722.9213945	1443.827189	0.000451244	3	Y	490	502
Q3V0K9	Parental	NEGNA	TLTLALVWQLMR	RYTLK	3		482.2835297	1443.827189	0.000451244	3	Y	490	502
Q3V0K9	Parental	SFKDK	SISTSLPVLDLIDAIAPNAVR	QEMIK	2		1083.112965	2164.210331	0.000451244	3	N	546	567
Q3V0K9	Parental	EELMK	LSPEELLLR	WVNYH	2		535.3167532	1068.617906	0.001264573	2	Y	265	274
Q3V1G4	Exosome	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	2	C1:+57.021	1057.513058	2113.010516	0.000451244	4	N	489	508
Q3V1G4	Exosome	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	3	C1:+57.021	705.3446388	2113.010516	0.000451244	11	N	489	508
Q3V1G4	Exosome	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	2	[0:-17.027,C1:+57.021	1048.999558	2095.983516	0.000622848	7	N	489	508
Q3V1G4	Exosome	QGASR	KEDFYTVETITSGSSCK	CACVA	2	C16:+57.021	976.4516036	1950.887607	0.000451244	18	N	98	115
Q3V1G4	Exosome	GSSCK	CACVAPPSAVNPCEGDFR	LQKLR	2	C1:+57.021,C3:+57.021,C13:+57.021	1003.92933	2005.84306	0.000451244	18	N	115	133
Q3V1G4	Exosome	EYEER	FLQEETVSQQINSIELLR	TQPLV	2		1074.071298	2146.126995	0.000451244	1	N	245	263
Q3V1G4	Exosome	SRDLK	LSTIIDLLEGAFYGLDLLK	LHSVT	2		1047.590803	2093.166006	0.000451244	20	N	146	165
Q3V1G4	Exosome	SRDLK	LSTIIDLLEGAFYGLDLLK	LHSVT	3		698.7298021	2093.166006	0.000451244	6	N	146	165
Q3V1G4	Exosome	QIVPR	LLFENEYSYTTQIDYNPK	DRLLY	2		1119.534214	2237.052827	0.000870037	3	N	707	725
Q3V1G4	Parental	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	2	C1:+57.021	1057.513058	2113.010516	0.000451244	28	N	489	508
Q3V1G4	Parental	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	3	C1:+57.021	705.3446388	2113.010516	0.000451244	7	N	489	508
Q3V1G4	Parental	NVIGR	CKDTLSTITGPTTQNTYGR	NEGAW	2	[0:-17.027,C1:+57.021	1048.999558	2095.983516	0.000451244	10	N	489	508
Q3V1G4	Parental	QGASR	KEDFYTVETITSGSSCK	CACVA	2	C16:+57.021	976.4516036	1950.887607	0.000451244	34	N	98	115
Q3V1G4	Parental	QGASR	KEDFYTVETITSGSSCK	CACVA	3	C16:+57.021	651.3036691	1950.887607	0.000451244	3	N	98	115
Q3V1G4	Parental	GSSCK	CACVAPPSAVNPCEGDFR	LQKLR	2	C1:+57.021,C3:+57.021,C13:+57.021	1003.92933	2005.84306	0.000451244	44	N	115	133
Q3V1G4	Parental	EYEER	FLQEETVSQQINSIELLR	TQPLV	2		1074.071298	2146.126995	0.000451244	20	N	245	263
Q3V1G4	Parental	TGLRR	NFYGNCFVICGVLYAVDSYNQR	NANIS	2	C6:+57.021,C10:+57.021	1330.1071	2658.1986	0.000451244	5	N	666	688
Q3V1G4	Parental	SRDLK	LSTIIDLLEGAFY	GLDLL	2		727.8930221	1453.770444	0.000451244	14	N	146	159
Q3V1G4	Parental	SRDLK	LSTIIDLLEGAFYGLDLLK	LHSVT	2		1047.590803	2093.166006	0.000451244	28	N	146	165
Q3V1G4	Parental	SRDLK	LSTIIDLLEGAFYGLDLLK	LHSVT	3		698.7298021	2093.166006	0.000451244	10	N	146	165

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q3V1G4	Parental	GSSCK	CACVAPPSAVNPCEGDFRLQK	LREAD	3	C1:+57.021,C3:+57.021,C13:+57.021	792.7013548	2375.080664	0.002663018	1	N	115	136
Q3V1G4	Parental	QIVPR	LLFENEYSYTTQIDYNPK	DRLLY	2		1119.534214	2237.052827	0.002145581	1	N	707	725
Q3V1G4	Parental	SALQR	DAAAAYAHPEYEER	FLQEE	2		796.8529482	1591.690296	0.000451244	5	N	231	245
Q3V1G4	Parental	AKDDR	IYVTNYYYGNTLVEFR	NLENF	2		1007.999613	2013.983625	0.002145581	2	N	523	539
Q3V1L4	Exosome	TGKLK	IGTYTGPLQHGIVYSGGSSDTICDLLGAK	GKDIL	3	C23:+57.021	994.162574	2979.464322	0.000451244	31	N	313	342
Q3V1L4	Exosome	GNLLK	VDAYGNLLVCAHGFNFIR	GPETR	3	C10:+57.021	689.3477664	2065.019899	0.000735798	10	N	111	129
Q3V1L4	Exosome	LLGAK	GKDILYIGDHIFGDILK	SKKRQ	3		639.6880487	1916.040746	0.000451244	28	N	342	359
Q3V1L4	Exosome	LLGAK	GKDILYIGDHIFGDILK	SKKRQ	4		480.0179865	1916.040746	0.000451244	2	N	342	359
Q3V1L4	Exosome	LTVER	LVSIGYPQELLSFAYDSTFPTR	GLVFD	2		1252.639544	2503.263489	0.000451244	28	N	76	98
Q3V1L4	Exosome	LTVER	LVSIGYPQELLSFAYDSTFPTR	GLVFD	3		835.4289629	2503.263489	0.000451244	16	N	76	98
Q3V1L4	Exosome	DDTER	FYILNTLFNLPETYLLACLVDFFTNCPR	YTSCD	3	C18:+57.021,C26:+57.021	1152.245538	3453.713215	0.000451244	8	N	149	177
Q3V1L4	Exosome	AELYK	HLDSSSNERPDISSIQR	RIKKV	3		647.6527258	1939.934777	0.000451244	8	N	404	421
Q3V1L4	Exosome	RQGWR	TFLVIPELAQELHVWTDK	SSLFE	2		1070.078394	2138.141189	0.002145581	1	N	367	385
Q3V1L4	Exosome	RQGWR	TFLVIPELAQELHVWTDK	SSLFE	3		713.7215295	2138.141189	0.002145581	2	N	367	385
Q3V1L4	Exosome	VWTDK	SSLFEELQSLDIFLAELYK	HLDSS	2		1123.086082	2244.156564	0.000451244	6	N	385	404
Q3V1L4	Exosome	LAVYK	SPEYESLGFELTVER	LVSIG	2		878.425946	1754.836292	0.000451244	7	N	61	76
Q3V1L4	Exosome	SQVMR	YADLYAASFINLLYYPFSYLFR	AAHVL	2		1355.683755	2709.35191	0.000823681	2	N	456	478
Q3V1L4	Exosome	TFPTR	GLVFDTLYGNLLK	VDAYG	2		726.9090065	1451.802413	0.000451244	2	N	98	111
Q3V1L4	Exosome	PWQSY	FDLILVDAR	KPLFF	2		531.3036458	1060.591692	0.000823681	6	N	282	291
Q3V1L4	Parental	LLGAK	GKDILYIGDHIFGDILK	SKKRQ	3		639.6880487	1916.040746	0.00307782	1	N	342	359
Q3V1L4	Parental	LTVER	LVSIGYPQELLSFAYDSTFPTR	GLVFD	2		1252.639544	2503.263489	0.000451244	17	N	76	98
Q3V1L4	Parental	RQGWR	TFLVIPELAQELHVWTDK	SSLFE	3		713.7215295	2138.141189	0.002813207	1	N	367	385
Q3V1L4	Parental	VWTDK	SSLFEELQSLDIFLAELYK	HLDSS	2		1123.086082	2244.156564	0.000451244	1	N	385	404
Q3V1L4	Parental	LPETY	LLACLVDFFTNCPR	YTSCD	2	C4:+57.021,C12:+57.021	863.4262519	1724.836904	0.000451244	6	N	163	177
Q3V3R1	Exosome	FLSGK	LSGGSPGVPVDKLIAEESVSLLAAALR	IQNMV	3		883.8327596	2648.474879	0.000622848	3	N	298	325
Q3V3R1	Exosome	VPVDK	LIAEESVSLLAAALR	IQNMV	2		778.4568522	1554.898104	0.000622848	4	N	310	325
Q3V3R1	Exosome	KGVPR	DFTLPISDVR	ASIGA	2		581.8092923	1161.602985	0.00091018	3	N	924	934
Q3V3R1	Exosome	VPLKK	EYTEENIQLVADGCCNLQK	QIQIA	2	C14:+57.021,C15:+57.021	1142.514709	2283.013819	0.001699387	1	N	763	782
Q3V3R1	Exosome	QNLAK	EAGLDITHICLPPDSGEDEIIDEILK	INEDP	3	C10:+57.021	964.8113184	2891.410555	0.001943752	1	N	119	145
Q3V3R1	Parental	FLSGK	LSGGSPGVPVDKLIAEESVSLLAAALR	IQNMV	3		883.8327596	2648.474879	0.000451244	9	N	298	325
Q3V3R1	Parental	CNLQK	QIQIAQLFGVPVVVALNVFK	TDTRA	3		728.4370644	2182.287793	0.002145581	1	N	782	802
Q3V3R1	Parental	QNLAK	EAGLDITHICLPPDSGEDEIIDEILKINEDPR	VHGLT	4	C10:+57.021	904.9480395	3615.760958	0.000622848	1	N	119	151
Q3V3R1	Parental	VPVDK	LIAEESVSLLAAALR	IQNMV	2		778.4568522	1554.898104	0.000823681	1	N	310	325
Q497J0	Parental	AVEYK	TQAVAGENIFIK	MDVGH	2		645.8567739	1289.697948	0.000451244	26	N	44	56
Q497J0	Parental	FIHIK	VFNGPTGKDNYELHGYQTDK	TKDDE	2		1142.037986	2282.060372	0.001352548	1	N	68	88
Q497J0	Parental	EAVEY	KTQAVAGENIFIK	MDVGH	2		709.9042554	1417.792911	0.000451244	26	N	43	56
Q497J0	Parental	EAVEY	KTQAVAGENIFIK	MDVGH	3		473.605437	1417.792911	0.000451244	25	N	43	56
Q497J0	Parental	GPTGK	DNYELHGYQTDK	TKDDE	2		741.8289417	1481.642283	0.000451244	4	N	76	88
Q4KML4	Exosome	FQDDR	CANLFEALVGTLK	AAKRR	2	C1:+39.994	709.8711099	1417.72662	0.001162105	3	N	38	51
Q4KML4	Exosome	FQDDR	CANLFEALVGTLK	AAKRR	2	C1:+57.021	718.3846099	1434.75362	0.000451244	7	N	38	51
Q4KML4	Exosome	FQDDR	CANLFEALVGTLK	AAKRR	2	[0:-17.027,C1:+57.021	709.8711099	1417.72662	0.000451244	1	N	38	51
Q4KML4	Parental	FQDDR	CANLFEALVGTLK	AAKRR	2	C1:+39.994	709.8711099	1417.72662	0.000637154	4	N	38	51
Q4KML4	Parental	FQDDR	CANLFEALVGTLK	AAKRR	2	C1:+57.021	718.3846099	1434.75362	0.000451244	31	N	38	51
Q4KML4	Parental	FQDDR	CANLFEALVGTLK	AAKRR	3	C1:+57.021	479.2590066	1434.75362	0.000451244	6	N	38	51
Q4KML4	Parental	FQDDR	CANLFEALVGTLK	AAKRR	2	[0:-17.027,C1:+57.021	709.8711099	1417.72662	0.000451244	10	N	38	51
Q4KML4	Parental	KLSVK	FGVLFQDDRCANLFEALVGTLK	AAKRR	3	C10:+57.021	838.4337882	2512.277965	0.000451244	2	N	29	51
Q4KML4	Parental	KIVTY	AGELLLQGVHDDVDIVLLQD	-	2		1081.57113	2161.126661	0.00307782	2	N	61	81
Q4LDD4	Exosome	RLPCK	AGLSLQQAQEGWFALTGSELR	AVFPE	2		1131.579821	2261.144042	0.000451244	2	N	873	894
Q4LDD4	Exosome	EFSRR	WCVLSDGVLSYYENER	AVTPN	2	C2:+57.021	995.4544806	1988.893361	0.002453667	1	N	774	790
Q4LDD4	Parental	RLPCK	AGLSLQQAQEGWFALTGSELR	AVFPE	2		1131.579821	2261.144042	0.000451244	3	N	873	894
Q4QRL3	Parental	KAVLR	GQELGDRLEHLQEELEQAALER	QKFLQ	3		855.096935	2562.267405	0.000451244	5	N	885	907
Q4QRL3	Parental	KAVLR	GQELGDRLEHLQEELEQAALER	QKFLQ	4		641.5746513	2562.267405	0.002212458	2	N	885	907
Q4QRL3	Parental	GPRLR	AQVEAAEQQVQALESQVR	CHLEE	2		992.5088644	1983.002129	0.001699387	1	N	841	859
Q4QRL3	Parental	ELKAR	ALQLEEELIQLR	QYPVD	2		727.9148201	1453.81404	0.00091018	1	N	949	961
Q4QRL3	Parental	GLESK	LGPQKPQQTSEGVPDAWSR	EEPTP	2		1041.024682	2080.033763	0.002519933	1	N	697	716
Q4QRL3	Parental	DAWSR	EEPTPGETLVSAIPEEQALRDEVAQLR	REVAG	3		993.1758023	2976.504007	0.000451244	14	N	716	743
Q4QRL3	Parental	EVEEK	AEQLLDSQAEVQGLEAEIR	RLRQE	2		1050.034912	2098.054224	0.000451244	3	N	282	301
Q4QRL3	Parental	HGGPR	LGADGAGSTESLGGPLETELPEGR	EADGT	2		1157.064398	2312.113196	0.001463592	1	N	1342	1366
Q501J6	Exosome	PYLER	GDGPICLVLAPTR	ELAQQ	2	C6:+57.021	684.869127	1367.722654	0.000451244	6	Y	162	175
Q501J6	Exosome	RELIK	VLEEANQAINPK	LMQLV	2		663.357138	1324.698676	0.000451244	16	N	456	468
Q501J6	Exosome	TGSGK	TLAYLLPAIVHINHQPYLER	GDGPI	3		787.7746278	2360.300483	0.001162105	1	N	142	162
Q501J6	Parental	FRSGK	APILIATDVASR	GLDVE	2		613.8593165	1225.703033	0.000823681	10	Y	389	401
Q501J6	Parental	PYLER	GDGPICLVLAPTR	ELAQQ	2	C6:+57.021	684.869127	1367.722654	0.001264573	12	Y	162	175
Q52KI8	Exosome	HKKEK	AVTIATPATAAPAAVSAATTTSAQEEPAAAPEPR	KETES	3		1064.212916	3189.615349	0.000979378	2	N	876	910

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q52KI8	Parental	HKKEK	AVTIATPATAAPAAVSAATTTSAQEEPAAAPEPR	KETES	3		1064.212916	3189.615349	0.000451244	54	N	876	910
Q52KI8	Parental	APEPR	KETESEAEDDNLDDLER	HLREK	2		1004.435425	2006.855249	0.002212458	1	N	910	927
Q569Z6	Exosome	KSSSK	DSRPSQAAGDNQGDEAKEQTFSGGTSQDIK	GSESS	3		1042.140368	3123.397704	0.001463592	1	N	185	215
Q569Z6	Exosome	KSSSK	DSRPSQAAGDNQGDEAKEQTFSGGTSQDIK	GSESS	4		781.857226	3123.397704	0.000451244	6	N	185	215
Q569Z6	Parental	KSSSK	DSRPSQAAGDNQGDEAKEQTFSGGTSQDIK	GSESS	3		1042.140368	3123.397704	0.000451244	26	N	185	215
Q569Z6	Parental	KSSSK	DSRPSQAAGDNQGDEAKEQTFSGGTSQDIK	GSESS	4		781.857226	3123.397704	0.000451244	21	N	185	215
Q569Z6	Parental	SPVGK	SPPATGSAYGSSQKEESAASGGAAYSK	RYLEE	3		849.3934172	2545.156852	0.000622848	15	N	319	346
Q571E4	Exosome	LGISK	NTFVFFTSDNGAALISAPNEGGSNGPFLCGK	QTTFE	3	C29:+57.021	1063.836749	3188.486848	0.000451244	12	N	277	308
Q571E4	Exosome	TQHAR	QSPFFLYWAIDATHAPVYASR	QFLGT	3		814.0748544	2439.201163	0.000451244	15	N	220	241
Q571E4	Exosome	TQHAR	QSPFFLYWAIDATHAPVYASR	QFLGT	2	[0:-17.027	1212.094882	2422.174163	0.0025889	2	N	220	241
Q571E4	Exosome	DSVGK	ILSLLQNLGISK	NTFVF	2		649.9062668	1297.796934	0.000451244	20	N	265	277
Q571E4	Exosome	FHPLK	HGFDEWFGSPNCHFGPYDNK	AKPNI	3	C12:+57.021	804.3363662	2409.985699	0.001162105	1	N	150	170
Q571E4	Parental	LGISK	NTFVFFTSDNGAALISAPNEGGSNGPFLCGK	QTTFE	3	C29:+57.021	1063.836749	3188.486848	0.000451244	28	N	277	308
Q571E4	Parental	TQHAR	QSPFFLYWAIDATHAPVYASR	QFLGT	2		1220.608382	2439.201163	0.001839721	1	N	220	241
Q571E4	Parental	TQHAR	QSPFFLYWAIDATHAPVYASR	QFLGT	3		814.0748544	2439.201163	0.000451244	16	N	220	241
Q571E4	Parental	TQHAR	QSPFFLYWAIDATHAPVYASR	QFLGT	2	Q1:-17.027	1212.094882	2422.174163	0.002212458	1	N	220	241
Q571E4	Parental	DSVGK	ILSLLQNLGISK	NTFVF	2		649.9062668	1297.796934	0.000451244	12	N	265	277
Q571E4	Parental	GDAVR	EIDDSVGKILSLLQNLGISK	NTFVF	2		1071.604973	2141.194347	0.000451244	1	N	257	277
Q571E4	Parental	GDAVR	EIDDSVGKILSLLQNLGISK	NTFVF	3		714.7392488	2141.194347	0.000451244	5	N	257	277
Q571E4	Parental	FHPLK	HGFDEWFGSPNCHFGPYDNK	AKPNI	3	C12:+57.021	804.3363662	2409.985699	0.000662267	3	N	150	170
Q571I9	Exosome	QKHQR	LLWTLESLVTGR	AVREV	2		694.4013486	1386.787097	0.000451244	31	N	117	129
Q571I9	Exosome	SPRAR	AGLLWALAAALER	RKPVL	2		677.8962334	1353.776867	0.000451244	38	N	588	601
Q571I9	Exosome	SPRAR	AGLLWALAAALER	RKPVL	3		452.2667556	1353.776867	0.000451244	18	N	588	601
Q571I9	Exosome	KPEHR	NPAPCQDPITGENLASCLQAEAEDIAAAVEAAK	IAFKA	3	C5:+57.021,C17:+57.021	1142.204907	3423.591321	0.000451244	14	N	54	87
Q571I9	Exosome	AKDIR	GAVEAAHQAAPGWGAQSPR	ARAGL	2		930.9591447	1859.902689	0.000451244	3	N	567	586
Q571I9	Exosome	AKDIR	GAVEAAHQAAPGWGAQSPR	ARAGL	3		620.9753631	1859.902689	0.000823681	10	N	567	586
Q571I9	Exosome	VWSER	LGQALELGYGLQVGTVWINAHGLR	DPAVP	3		855.8032461	2564.386338	0.000451244	5	N	434	458
Q571I9	Exosome	TWGTR	VQDQGQTLQVTGLR	GPVLR	2		771.9158828	1541.816166	0.000451244	29	N	637	651
Q571I9	Exosome	QPSTR	EIFTTLEYGPVPESHACALAWLDTHNR	LLGHH	3	C17:+57.021	1043.169951	3126.486454	0.000451244	13	N	11	38
Q571I9	Parental	QKHQR	LLWTLESLVTGR	AVREV	2		694.4013486	1386.787097	0.000451244	22	N	117	129
Q571I9	Parental	SPRAR	AGLLWALAAALER	RKPVL	2		677.8962334	1353.776867	0.000451244	24	N	588	601
Q571I9	Parental	SPRAR	AGLLWALAAALER	RKPVL	3		452.2667556	1353.776867	0.000451244	7	N	588	601
Q571I9	Parental	KPEHR	NPAPCQDPITGENLASCLQAEAEDIAAAVEAAK	IAFKA	3	C5:+57.021,C17:+57.021	1142.204907	3423.591321	0.000451244	32	N	54	87
Q571I9	Parental	TWGTR	VQDQGQTLQVTGLR	GPVLR	2		771.9158828	1541.816166	0.000451244	1	N	637	651
Q5EG47	Exosome	TLFKK	ICDGIFYTPQYLNPSVISLLK	HMLQV	2	C2:+57.021	1221.143177	2440.270754	0.000451244	12	N	236	257
Q5EG47	Exosome	TLFKK	ICDGIFYTPQYLNPSVISLLK	HMLQV	3	C2:+57.021	814.4313847	2440.270754	0.001264573	1	N	236	257
Q5EG47	Parental	TLFKK	ICDGIFYTPQYLNPSVISLLK	HMLQV	2	C2:+57.021	1221.143177	2440.270754	0.000451244	19	N	236	257
Q5EG47	Parental	TLFKK	ICDGIFYTPQYLNPSVISLLK	HMLQV	3	C2:+57.021	814.4313847	2440.270754	0.000451244	7	N	236	257
Q5EG47	Parental	EVCEK	FECSEEEVLSCLYNR	NHQDP	2	C3:+57.021,C11:+57.021	967.9166423	1933.817685	0.000622848	1	N	310	325
Q5FWK3	Exosome	KTFLR	ELPEPLLTFDLYPHVVGFLNIDESQR	VEVTQ	3		1014.525995	3040.554586	0.000451244	17	N	323	349
Q5FWK3	Exosome	NTFTK	FLLDHQGELFPSTDAQGV	-	2		987.4843266	1972.953053	0.001699387	1	N	421	439
Q5FWK3	Parental	KTFLR	ELPEPLLTFDLYPHVVGFLNIDESQR	VEVTQ	3		1014.525995	3040.554586	0.000451244	33	N	323	349
Q5FWK3	Parental	NTFTK	FLLDHQGELFPSTDAQGV	-	2		987.4843266	1972.953053	0.000451244	9	N	421	439
Q5FWK3	Parental	DESQR	VEVTQQVLQTLPEENYQVLHFLTAFLVQISAHCDQNK	MTNTN	4	C33:+57.021	1085.806361	4339.194243	0.000823681	4	N	349	386
Q5FWK3	Parental	DESQR	VEVTQQVLQTLPEENYQVLHFLTAF	LVQIS	3		982.8469574	2945.517472	0.001162105	2	N	349	374
Q5RKN9	Exosome	RIAAK	FITHAPPGEFNEVFNDVR	LLLNN	2		1045.011043	2088.006486	0.000735798	5	N	19	37
Q5RKN9	Exosome	RIAAK	FITHAPPGEFNEVFNDVR	LLLNN	3		697.009962	2088.006486	0.000451244	30	N	19	37
Q5RKN9	Exosome	TVYAK	TIDGQQTIIACIESHQFQPK	NFWNG	2	C11:+57.021	1157.578733	2313.141865	0.000451244	31	N	146	166
Q5RKN9	Exosome	TVYAK	TIDGQQTIIACIESHQFQPK	NFWNG	3	C11:+57.021	772.0550884	2313.141865	0.000451244	21	N	146	166
Q5RKN9	Exosome	FNDVR	LLLNNDNLLR	EGAAH	2		599.3516587	1196.687717	0.000979378	12	Y	37	47
Q5RKN9	Exosome	DSALR	AYVKDHYSNGFCTVYAK	TIDGQ	3	C12:+57.021	674.9844937	2021.930081	0.000451244	18	N	129	146
Q5RKN9	Exosome	DHLRK	EASDPQPEDVDGGLK	SWRES	2		778.8578962	1555.700192	0.000451244	38	N	103	118
Q5RKN9	Exosome	LVSHK	DVQDSVTVSNEIQTTK	EFIKI	2		882.4370421	1762.858484	0.000451244	34	N	210	226
Q5RKN9	Exosome	RSEWK	FTITPPSAQVVGVLK	IQVHY	2		778.956488	1555.897376	0.000451244	29	N	178	193
Q5RKN9	Exosome	RAYVK	DHYSNGFCTVYAK	TIDGQ	2	C8:+57.021	781.3409307	1560.666261	0.000451244	11	N	133	146
Q5RKN9	Exosome	VGVLK	IQVHYYEDGNVQLVSHK	DVQDS	2		1015.011043	2028.006486	0.000451244	7	Y	193	210
Q5RKN9	Exosome	FTPVK	IEGYDDQVLITEHGDLGNSR	FLDPR	2		1116.032901	2230.050201	0.0025889	1	N	66	86
Q5RKN9	Parental	DHLRK	EASDPQPEDVDGGLKSWR	ESCDS	2		993.4641225	1984.912645	0.000451244	10	N	103	121
Q5RKN9	Parental	DHLRK	EASDPQPEDVDGGLKSWR	ESCDS	3		662.6453484	1984.912645	0.000451244	6	N	103	121
Q5RKN9	Parental	RIAAK	FITHAPPGEFNEVFNDVR	LLLNN	2		1045.011043	2088.006486	0.000451244	14	N	19	37
Q5RKN9	Parental	RIAAK	FITHAPPGEFNEVFNDVR	LLLNN	3		697.009962	2088.006486	0.000451244	15	N	19	37
Q5RKN9	Parental	TVYAK	TIDGQQTIIACIESHQFQPK	NFWNG	2	C11:+57.021	1157.578733	2313.141865	0.000451244	32	N	146	166
Q5RKN9	Parental	TVYAK	TIDGQQTIIACIESHQFQPK	NFWNG	3	C11:+57.021	772.0550884	2313.141865	0.000451244	17	N	146	166
Q5RKN9	Parental	FNDVR	LLLNNDNLLR	EGAAH	2		599.3516587	1196.687717	0.001162105	13	Y	37	47
Q5RKN9	Parental	DSALR	AYVKDHYSNGFCTVYAK	TIDGQ	2	C12:+57.021	1011.972841	2021.930081	0.000622848	7	N	129	146

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q5RKN9	Parental	DSALR	AYVKDHYSNGFCTVYAK	TIDGQ	3	C12:+57.021	674.9844937	2021.930081	0.000451244	3	N	129	146
Q5RKN9	Parental	DHLRK	EASDPQPEDVDGGLK	SWRES	2		778.8578962	1555.700192	0.000451244	32	N	103	118
Q5RKN9	Parental	LVSHK	DVQDSVTVSNEIQTTK	EFIKI	2		882.4370421	1762.858484	0.000451244	12	N	210	226
Q5RKN9	Parental	RSEWK	FTITPPSAQVVGVLK	IQVHY	2		778.956488	1555.897376	0.000451244	16	N	178	193
Q5RKN9	Parental	RSEWK	FTITPPSAQVVGVLK	IQVHY	3		519.6402587	1555.897376	0.000622848	1	N	178	193
Q5RKN9	Parental	RAYVK	DHYSNGFCTVYAK	TIDGQ	2	C8:+57.021	781.3409307	1560.666261	0.000451244	9	N	133	146
Q5RKN9	Parental	VGVLK	IQVHYYEDGNVQLVSHK	DVQDS	2		1015.011043	2028.006486	0.000451244	2	Y	193	210
Q5RKN9	Parental	FTPVK	IEGYDDQVLITEHGDLGNSR	FLDPR	2		1116.032901	2230.050201	0.0007646	8	N	66	86
Q5RKN9	Parental	FTPVK	IEGYDDQVLITEHGDLGNSR	FLDPR	3		744.3578671	2230.050201	0.000622848	2	N	66	86
Q5SFM8	Parental	WHKPK	VPSISTETEEEEVKEEETETSDLFLHDDDDEDEDEYESR	SWRR-	4		1155.732854	4618.900215	0.000823681	4	N	1017	1056
Q5SFM8	Parental	SWLAK	LLEPICDADPSALANYVVALVK	KDKPE	2	C6:+57.021	1186.132809	2370.250019	0.000451244	12	N	15	37
Q5SFM8	Parental	SWLAK	LLEPICDADPSALANYVVALVKK	DKPEK	3	C6:+57.021	833.7894606	2498.344982	0.000451244	2	N	15	38
Q5SQX6	Exosome	VRKKK	NVLISVLQAIR	KTICD	2		613.3855015	1224.755403	0.001654178	6	N	503	514
Q5SQX6	Exosome	LGQQR	RFDLFDFCYHLLK	VQRQD	3	C8:+57.021	591.9645937	1772.870381	0.001264573	1	N	1171	1184
Q5SQX6	Exosome	DRIRK	YQILNNEVFAILNK	YMKSV	2		839.9623017	1677.909003	0.001162105	2	N	1209	1223
Q5SQX6	Parental	VRKKK	NVLISVLQAIR	KTICD	2		613.3855015	1224.755403	0.002080925	2	N	503	514
Q5SQX6	Parental	RLEAK	YAPLHLVPLIER	LGTPQ	3		474.2824057	1419.823817	0.002145581	2	Y	1052	1064
Q5SSL4	Exosome	KIMGK	GQIQLDPQTVESK	NWHTD	2		721.8784346	1441.741269	0.000622848	2	N	593	606
Q5SSL4	Exosome	MKPLK	ATATTSQPVLTIQQIETIFYK	IQDIY	2		1177.136638	2352.257675	0.0025889	1	N	121	142
Q5SUA5	Exosome	EQPHR	GILAVLDEACSTAGPITDR	IFLQT	2	C10:+57.021	979.9965126	1957.977425	0.000451244	2	N	468	487
Q5SUA5	Exosome	PLYGR	DLVWPTPPAVLQPFQDTCR	VLFSR	2	C18:+57.021	1120.562354	2239.109108	0.000637154	2	N	776	795
Q5SUA5	Parental	RGARR	LISVEPRPEQPEPDFQSSR	STFTL	3		737.7067192	2210.096758	0.000451244	5	N	995	1014
Q5SUA5	Parental	DFQIK	HYAGDVTYSVEGFIDKNR	DSLFQ	3		691.001355	2069.980665	0.001329271	2	N	524	542
Q5SUA5	Parental	FEKGR	IYTYIGEVLVSVNPYQELPLYGPEAIAK	YQGRE	3		1047.225434	3138.652903	0.001162105	2	N	43	71
Q5SUA5	Parental	RIYTY	IGEVLVSVNPYQELPLYGPEAIAK	YQGRE	2		1300.205052	2598.394503	0.000451244	14	N	47	71
Q5SUA5	Parental	EQPHR	GILAVLDEACSTAGPITDR	IFLQT	2	C10:+57.021	979.9965126	1957.977425	0.000451244	11	N	468	487
Q5SUA5	Parental	KYQGR	ELYERPPHLYAVANAAYK	AMKRR	3		702.3658572	2104.074172	0.000451244	1	N	75	93
Q5SUA5	Parental	NGPQK	GGLEVADEALVGYVAK	LTATP	2		795.9228422	1589.830084	0.002374549	1	N	303	319
Q5SUH6	Exosome	MWKVR	ELVDKATNVVMNYSEIESK	VREAT	4		543.0245745	2168.067098	0.000451244	1	N	8	27
Q5SUH6	Parental	TVQPK	QDAFANFANFSK	-	2		680.3205555	1358.625511	0.000622848	6	N	629	641
Q5SUH6	Parental	ANPSK	TIDLGAAAHYTGDKASPDQNASTHTPQSSAKPSVPSSK	SSGDL	3		1274.956345	3821.845636	0.000823681	1	N	283	321
Q5SUH6	Parental	ANPSK	TIDLGAAAHYTGDKASPDQNASTHTPQSSAKPSVPSSK	SSGDL	4		956.4692091	3821.845636	0.000451244	8	N	283	321
Q5SUH6	Parental	IYDLR	SLENYHFVDEHGKDQGINIR	QKVKE	3		791.0528895	2370.135268	0.000451244	2	N	109	129
Q5SUH6	Parental	VPSSK	SSGDLVDLFDGSSQSAGGSADLFGGF	ADFGS	2		1247.05677	2492.09794	0.0025889	1	N	321	347
Q5SUR0	Exosome	PGQHR	LGGTALAQCFSQLGEHPPDLDLPENLVR	AFHIT	3	C9:+57.021	1016.513718	3046.517755	0.000451244	44	N	861	889
Q5SUR0	Exosome	EVGPR	LNFSTPASTNIVSVCQAAGLR	AVDRV	2	C15:+57.021	1103.568168	2205.120736	0.000451244	26	N	93	114
Q5SUR0	Exosome	LDTFR	GVAFVGGFSYADVLGSAK	GWAAA	2		872.9493913	1743.883183	0.000451244	15	N	1108	1126
Q5SUR0	Exosome	KAAAR	LAVSEALTNLVFALVTDLR	DVKCS	2		1023.086219	2044.156839	0.000451244	19	N	740	759
Q5SUR0	Exosome	KAAAR	LAVSEALTNLVFALVTDLR	DVKCS	3		682.3934129	2044.156839	0.000451244	4	N	740	759
Q5SUR0	Exosome	KIEAK	GLVPLHWADDDGNPTEQYPLNPNGSPGGIAGICSQDGR	HLALM	3	C33:+57.021	1325.617293	3973.828478	0.000451244	50	N	1251	1289
Q5SUR0	Exosome	SMAAR	VGTETVQAPGSLVISAYAVCPDITATVTPDLK	HPGGK	3	C20:+57.021	1091.902648	3272.684545	0.000451244	23	N	810	842
Q5SUR0	Exosome	IYTSR	FQLGDPTLNALEIWGAEYQESNALLLRPSDR	DFLSR	3		1172.930632	3515.768495	0.000662267	4	N	541	572
Q5SUR0	Exosome	VGELR	ALWEETSFQLDLLQAEPR	CVIEE	2		1073.544916	2145.074231	0.000451244	5	N	1007	1025
Q5SUR0	Exosome	CPLVR	DDVAQEPWLVPGSNDLLLEVGPR	LNFST	2		1260.142983	2518.270365	0.000451244	19	N	70	93
Q5SUR0	Exosome	CPLVR	DDVAQEPWLVPGSNDLLLEVGPR	LNFST	3		840.4312551	2518.270365	0.000451244	21	N	70	93
Q5SUR0	Exosome	QELQR	NPSTVEVFDLAQSNSEHSR	HWFFK	2		1058.998861	2115.982122	0.000451244	4	N	212	231
Q5SUR0	Exosome	QELQR	NPSTVEVFDLAQSNSEHSR	HWFFK	3		706.3351739	2115.982122	0.000451244	1	N	212	231
Q5SUR0	Exosome	DYGNK	FGEPVLAGFAR	SLGLQ	2		582.3145448	1162.61349	0.000451244	5	N	395	406
Q5SUR0	Exosome	LGSAK	GWAAAVTFNPQAR	EELGR	2		694.8576395	1387.699679	0.000823681	4	N	1126	1139
Q5SUR0	Exosome	PALEK	ANQELGLALDSWDLDFYTK	RFQEL	2		1100.034381	2198.053161	0.000451244	16	N	186	205
Q5SUR0	Exosome	GLKER	TGPSYYLPPTFPVASVPCKPGGPVPR	VAILR	3	C18:+57.021	914.475876	2740.404228	0.001463592	3	N	1037	1063
Q5SUR0	Exosome	SMAAR	VGTETVQAPGSLVISAYAVCPDITATVTPDLKHPGGK	GHLLY	4	C20:+57.021	938.241328	3748.934112	0.000451244	11	N	810	847
Q5SUR0	Exosome	PAPLK	GSIDILAEGRPALEK	ANQEL	2		784.9362839	1567.856968	0.000622848	2	N	171	186
Q5SUR0	Exosome	PAPLK	GSIDILAEGRPALEK	ANQEL	3		523.6267893	1567.856968	0.001943752	1	N	171	186
Q5SUR0	Exosome	CLVGK	TGQGDAPLTPPTPVDLDLDWVLGK	MPQKE	3		835.7677558	2504.279867	0.000451244	3	N	610	634
Q5SUR0	Exosome	NRVIR	ACVEAPGGNPICSLHDQGAGGNGNVLK	ELSDP	3	C2:+57.021,C12:+57.021	898.0906012	2691.248404	0.000622848	9	N	500	527
Q5SUR0	Exosome	KAAAR	LAVSEALTNLVFALVTDLRDVK	CSGNW	3		796.456853	2386.347159	0.000451244	3	N	740	762
Q5SUR0	Exosome	IYTSR	FQLGDPTLNALEIWGAEYQESNALLLRPSDRDFLSR	ASARE	4		1034.528064	4134.081056	0.001871652	2	N	541	577
Q5SUR0	Exosome	GKKVK	FLRPEDSTRPSCFQQQQGLR	HVVFT	3	C12:+57.021	817.4050031	2449.191609	0.001699387	1	N	282	302
Q5SUR0	Exosome	QCTGR	GAHVVAGTAGYCFGNLHIPDYNLPWEDPSFQYPGNFAR	PLEVA	4	C12:+57.021	1060.246205	4236.953619	0.000622848	4	N	339	377
Q5SUR0	Parental	PGQHR	LGGTALAQCFSQLGEHPPDLDLPENLVR	AFHIT	3	C9:+57.021	1016.513718	3046.517755	0.000451244	44	N	861	889
Q5SUR0	Parental	EVGPR	LNFSTPASTNIVSVCQAAGLR	AVDRV	2	C15:+57.021	1103.568168	2205.120736	0.000451244	3	N	93	114
Q5SUR0	Parental	KAAAR	LAVSEALTNLVFALVTDLR	DVKCS	2		1023.086219	2044.156839	0.000451244	2	N	740	759
Q5SUR0	Parental	KAAAR	LAVSEALTNLVFALVTDLR	DVKCS	3		682.3934129	2044.156839	0.000451244	6	N	740	759
Q5SUR0	Parental	KIEAK	GLVPLHWADDDGNPTEQYPLNPNGSPGGIAGICSQDGR	HLALM	3	C33:+57.021	1325.617293	3973.828478	0.000451244	5	N	1251	1289

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q5SUR0	Parental	SMAAR	VGTETVQAPGSLVISAYAVCPDITATVTPDLK	HPGGK	3	C20:+57.021	1091.902648	3272.684545	0.000823681	3	N	810	842
Q5SUR0	Parental	CPLVR	DDVAQEPWLVPGSNDLLLEVGPR	LNFST	2		1260.142983	2518.270365	0.001162105	1	N	70	93
Q5SUR0	Parental	QELQR	NPSTVEVFDLAQSNSEHSR	HWFFK	2		1058.998861	2115.982122	0.000451244	1	N	212	231
Q5SUR0	Parental	PALEK	ANQELGLALDSWDLDFYTK	RFQEL	2		1100.034381	2198.053161	0.001229886	1	N	186	205
Q5SUR0	Parental	CLVGK	TGQGDAPLTPPTPVDLDLDWVLGK	MPQKE	2		1253.147734	2504.279867	0.001162105	3	N	610	634
Q5SUR0	Parental	NRVIR	ACVEAPGGNPICSLHDQGAGGNGNVLK	ELSDP	3	C2:+57.021,C12:+57.021	898.0906012	2691.248404	0.001395409	1	N	500	527
Q5SUR0	Parental	KAAAR	LAVSEALTNLVFALVTDLRDVK	CSGNW	3		796.456853	2386.347159	0.001264573	1	N	740	762
Q5SUR0	Parental	QCTGR	GAHVVAGTAGYCFGNLHIPDYNLPWEDPSFQYPGNFAR	PLEVA	4	C12:+57.021	1060.246205	4236.953619	0.000698008	2	N	339	377
Q5SVD0	Exosome	GGGER	APVAGTLEPDAAVTPIVPNPASLTHSLAAICSPR	LCPLS	3	C31:+57.021	1131.933054	3392.775761	0.000622848	2	N	52	86
Q5SVD0	Exosome	ICSPR	LCPLSFGEGVEFDPLPPK	EIKYT	2	C2:+57.021	1001.503442	2000.991284	0.001763695	4	N	86	104
Q5SVD0	Parental	-MVGR	LSLQDVPELVDTK	KKGDG	2		728.8988357	1455.782071	0.001162105	8	N	4	17
Q5SVD0	Parental	GGGER	APVAGTLEPDAAVTPIVPNPASLTHSLAAICSPR	LCPLS	3	C31:+57.021	1131.933054	3392.775761	0.000451244	42	N	52	86
Q5SVD0	Parental	ICSPR	LCPLSFGEGVEFDPLPPK	EIKYT	2	C2:+57.021	1001.503442	2000.991284	0.000451244	14	N	86	104
Q5XJF6	Exosome	TPRPK	FSVCVLGDQQHCDEAK	AVDIP	2	C4:+57.021,C12:+57.021	946.9169766	1891.818353	0.000451244	36	N	62	78
Q5XJF6	Exosome	TPRPK	FSVCVLGDQQHCDEAK	AVDIP	3	C4:+57.021,C12:+57.021	631.6139178	1891.818353	0.000451244	10	N	62	78
Q5XJF6	Exosome	KKLAK	KYDAFLASESLIK	QIPRI	2		742.9039211	1483.792242	0.000451244	10	N	105	118
Q5XJF6	Parental	TPRPK	FSVCVLGDQQHCDEAK	AVDIP	2	C4:+57.021,C12:+57.021	946.9169766	1891.818353	0.000451244	12	N	62	78
Q5XJF6	Parental	TPRPK	FSVCVLGDQQHCDEAK	AVDIP	3	C4:+57.021,C12:+57.021	631.6139178	1891.818353	0.000823681	2	N	62	78
Q5XJY5	Exosome	LITTK	NSNILEDLETLR	LFSRV	2		708.8706096	1415.725619	0.000451244	1	N	72	84
Q5XJY5	Exosome	NVDKK	LFTAESLIGLK	NPEKS	2		596.3533357	1190.691071	0.001763695	3	N	336	347
Q5XJY5	Parental	LITTK	NSNILEDLETLR	LFSRV	2		708.8706096	1415.725619	0.000451244	27	N	72	84
Q5XJY5	Parental	NVDKK	LFTAESLIGLKNPEK	SFPVN	3		553.9825731	1658.924319	0.002663018	1	N	336	351
Q5XJY5	Parental	DAKNK	SGSLEFSIPGQPNDFFPVQVSFISK	KNYCN	2		1364.18739	2726.35918	0.000451244	3	N	450	475
Q5XJY5	Parental	DAKNK	SGSLEFSIPGQPNDFFPVQVSFISK	KNYCN	3		909.7941934	2726.35918	0.000451244	3	N	450	475
Q60597	Exosome	ILHIK	HWLDSPWPGFFTLDGQPR	SMTCP	3		719.3503185	2155.027556	0.000451244	4	N	582	600
Q60597	Parental	ILHIK	HWLDSPWPGFFTLDGQPR	SMTCP	3		719.3503185	2155.027556	0.000451244	5	N	582	600
Q60597	Parental	DIFFR	NTNAGAPPGTAYQSPLSLSR	SSLAT	2		1001.503582	2000.991564	0.001463592	3	N	81	101
Q60597	Parental	TELQR	FLDTAFDLDAFKK	FS-	3		510.9333307	1529.776592	0.001654178	2	N	1008	1021
Q60605-2	Exosome	GDVMR	ALGQNPTNAEVLK	VLGNP	2		677.8704126	1353.725225	0.000451244	54	N	37	50
Q60605-2	Exosome	QTVAK	NKDQGTYEDYVEGLR	VFDKE	2		893.9162768	1785.816954	0.000451244	52	N	79	94
Q60605-2	Exosome	QTVAK	NKDQGTYEDYVEGLR	VFDKE	3		596.2801179	1785.816954	0.000451244	41	N	79	94
Q60605-2	Exosome	EMNVK	VLDFEHFLPMLQTVAK	NKDQG	2		944.5060197	1886.996439	0.002727428	1	N	63	79
Q60605-2	Exosome	EMNVK	VLDFEHFLPMLQTVAK	NKDQG	3		630.0066132	1886.996439	0.000451244	22	N	63	79
Q60605-2	Exosome	TLGEK	MTEEEVEMLVAGHEDSNGCINYEELVR	MVLNG	3	M1:+15.995,C19:+57.021	1057.130534	3168.368202	0.000451244	30	N	119	146
Q60605-2	Exosome	TLGEK	MTEEEVEMLVAGHEDSNGCINYEELVR	MVLNG	3	M8:+15.995,C19:+57.021	1057.130534	3168.368202	0.000451244	24	N	119	146
Q60605-2	Exosome	VEGLR	VFDKEGNGTVMGAEIR	HVLVT	3	M11:+15.995	580.2863557	1737.835667	0.000451244	11	N	94	110
Q60605-2	Exosome	TAEFK	EAFQLFDR	TGDGK	2		513.2566955	1024.497791	0.002519933	4	N	13	21
Q60605-2	Exosome	TGDGK	ILYSQCGDVMR	ALGQN	2	C6:+57.021	671.3184132	1340.621226	0.000451244	2	N	26	37
Q60605-2	Exosome	VAKNK	DQGTYEDYVEGLR	VFDKE	2		772.8473315	1543.679063	0.000451244	1	N	81	94
Q60605-2	Parental	GDVMR	ALGQNPTNAEVLK	VLGNP	2		677.8704126	1353.725225	0.000451244	85	N	37	50
Q60605-2	Parental	QTVAK	NKDQGTYEDYVEGLR	VFDKE	2		893.9162768	1785.816954	0.000451244	79	N	79	94
Q60605-2	Parental	QTVAK	NKDQGTYEDYVEGLR	VFDKE	3		596.2801179	1785.816954	0.000451244	60	N	79	94
Q60605-2	Parental	GDVMR	ALGQNPTNAEVLKV	LGNPK	2		727.4046196	1452.793639	0.000451244	34	N	37	51
Q60605-2	Parental	EMNVK	VLDFEHFLPMLQTVAK	NKDQG	2		944.5060197	1886.996439	0.001352548	1	N	63	79
Q60605-2	Parental	EMNVK	VLDFEHFLPMLQTVAK	NKDQG	3		630.0066132	1886.996439	0.000451244	30	N	63	79
Q60605-2	Parental	TLGEK	MTEEEVEMLVAGHEDSNGCINYEELVR	MVLNG	3	M1:+15.995,C19:+57.021	1057.130534	3168.368202	0.000451244	17	N	119	146
Q60605-2	Parental	TLGEK	MTEEEVEMLVAGHEDSNGCINYEELVR	MVLNG	3	M8:+15.995,C19:+57.021	1057.130534	3168.368202	0.000451244	18	N	119	146
Q60605-2	Parental	VEGLR	VFDKEGNGTVMGAEIR	HVLVT	2		861.9281335	1721.840667	0.000451244	8	N	94	110
Q60605-2	Parental	VEGLR	VFDKEGNGTVMGAEIR	HVLVT	3		574.954689	1721.840667	0.000622848	2	N	94	110
Q60605-2	Parental	TGDGK	ILYSQCGDVMR	ALGQN	2	C6:+57.021	671.3184132	1340.621226	0.002813207	1	N	26	37
Q60605-2	Parental	VAKNK	DQGTYEDYVEGLR	VFDKE	2		772.8473315	1543.679063	0.000451244	18	N	81	94
Q60631	Exosome	QIFLR	DIEQMPQQPTYVQALFDFDPQEDGELGFR	RGDFI	3	M5:+15.995	1143.858062	3428.550786	0.000451244	2	N	149	178
Q60631	Exosome	GDILK	VLNEECDQNWYK	AELNG	2	C6:+57.021	799.3514954	1596.687391	0.000451244	30	N	26	38
Q60631	Exosome	AFLIR	ESESAPGDFSLSVK	FGNDV	2		726.8468001	1451.678	0.002374549	2	N	86	100
Q60631	Exosome	YVQAL	FDFDPQEDGELGFR	RGDFI	2		836.3684311	1670.721262	0.000979378	1	N	164	178
Q60631	Parental	QIFLR	DIEQMPQQPTYVQALFDFDPQEDGELGFR	RGDFI	3		1138.526395	3412.555786	0.000451244	2	N	149	178
Q60631	Parental	LWVVK	FNSLNELVDYHR	STSVS	2		753.8709439	1505.726288	0.001943752	1	N	124	136
Q60631	Parental	LWVVK	FNSLNELVDYHR	STSVS	3		502.9165626	1505.726288	0.000851441	8	N	124	136
Q60631	Parental	GDILK	VLNEECDQNWYK	AELNG	2	C6:+57.021	799.3514954	1596.687391	0.000451244	26	N	26	38
Q60631	Parental	AFLIR	ESESAPGDFSLSVK	FGNDV	2		726.8468001	1451.678	0.000823681	1	N	86	100
Q60634	Parental	EVNIK	TAEAQLAYELQGAR	EQQKI	2		760.8893337	1519.763067	0.000451244	13	N	233	247
Q60634	Parental	SEVNR	LLAELPASVHALTGVDLSKIPLIK	NATGA	3		833.5039147	2497.488344	0.000622848	3	N	397	421
Q60634	Parental	SEVNR	LLAELPASVHALTGVDLSKIPLIK	NATGA	4		625.379886	2497.488344	0.002145581	1	N	397	421
Q60634	Parental	EGHLR	SILGTLTVEQIYQDRDQFAK	LVREV	3		775.741541	2324.201223	0.0025889	1	N	112	132
Q60634	Parental	VQRKK	QIAVEAQEILR	TDKEL	2		635.3622234	1268.708847	0.000622848	2	N	266	277

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q60634	Parental	SEVNR	LLAELPASVHALTGVDLSK	IPLIK	2		967.5520123	1933.088425	0.000451244	6	N	397	416
Q60634	Parental	SEVNR	LLAELPASVHALTGVDLSK	IPLIK	3		645.3706082	1933.088425	0.0007646	9	N	397	416
Q60634	Parental	GEKVK	QVLLAQAEAEK	IRKIG	2		600.3356743	1198.655749	0.000851441	3	N	307	318
Q60648	Exosome	PAVIK	SLTIQPDPIVVPGDVVVSLEGK	TSVPL	2		1131.633731	2261.251861	0.000451244	14	N	49	71
Q60648	Parental	PAVIK	SLTIQPDPIVVPGDVVVSLEGK	TSVPL	2		1131.633731	2261.251861	0.000451244	32	N	49	71
Q60648	Parental	PAVIK	SLTIQPDPIVVPGDVVVSLEGK	TSVPL	3		754.7584205	2261.251861	0.0007646	11	N	49	71
Q60648	Parental	KRLSQ	LGGFSWDNCDEGKDPAVIK	SLTIQ	3	C9:+57.021	703.3303296	2106.967589	0.001329271	1	N	30	49
Q60648	Parental	RLSQL	GGFSWDNCDEGKDPAVIK	SLTIQ	2	C8:+57.021	997.9495624	1993.883525	0.001463592	2	N	31	49
Q60664	Parental	TNCLK	LLESLTPLCEEDNQAQEIVK	KLEKS	2	C9:+57.021	1165.083513	2328.151427	0.000451244	28	N	239	259
Q60664	Parental	LDVTR	GCQCPLPTEDSILGQELLDCTR	MNEDQ	2	C2:+57.021,C4:+57.021,C20:+57.021	1281.585109	2561.154617	0.002453667	1	N	21	43
Q60668	Exosome	DYTGY	NNYYGYGDYSNQQSGYGK	VSRRG	2		1039.43028	2076.844959	0.000451244	2	N	323	341
Q60668	Exosome	DYFSK	FGEVVDCTLKLDPITGR	SRGFG	3	C7:+57.021	640.6683941	1918.981782	0.000451244	11	N	119	136
Q60668	Exosome	GAMVA	AAAQGPAAAAGSGSGGGGSAAGGTEGGSAEAEGAK	IDASK	3		915.7489227	2744.223368	0.00307782	1	N	32	67
Q60668	Parental	DYTGY	NNYYGYGDYSNQQSGYGK	VSRRG	2		1039.43028	2076.844959	0.000451244	30	N	323	341
Q60668	Parental	DYFSK	FGEVVDCTLK	LDPIT	2	C7:+57.021	584.2896468	1166.563694	0.000451244	16	N	119	129
Q60668	Parental	EPVKK	IFVGGLSPDTPEEKIR	EYFGG	2		879.4757733	1756.935947	0.000451244	1	N	183	199
Q60668	Parental	EPVKK	IFVGGLSPDTPEEKIR	EYFGG	3		586.6531155	1756.935947	0.000451244	2	N	183	199
Q60668	Parental	DYFSK	FGEVVDCTLKLDPITGR	SRGFG	2	C7:+57.021	960.4986911	1918.981782	0.000451244	4	N	119	136
Q60668	Parental	DYFSK	FGEVVDCTLKLDPITGR	SRGFG	3	C7:+57.021	640.6683941	1918.981782	0.000451244	12	N	119	136
Q60668	Parental	EPVKK	IFVGGLSPDTPEEK	IREYF	2		744.8831857	1487.750771	0.000451244	36	N	183	197
Q60675	Exosome	FRTTR	PTGVLLGVSSQK	MDGMG	2		593.346042	1184.676484	0.001395409	1	N	2968	2980
Q60675	Exosome	STAYK	EVYLEPSEEHIEEVSLK	EEAFT	3		677.3375214	2028.989164	0.002663018	1	N	635	652
Q60676	Exosome	PDVTK	AFLEENQLDYIIR	SHEVK	2		812.4230094	1622.830419	0.000622848	4	N	412	425
Q60676	Exosome	ENAIK	FYSQAIELNPGNAIYYGNR	SLAYL	2		1095.534882	2189.054164	0.000451244	12	N	49	68
Q60692	Exosome	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK	EMCYR	3		1352.683675	4055.027624	0.000451244	41	N	78	117
Q60692	Exosome	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK	EMCYR	4		1014.764706	4055.027624	0.000451244	51	N	78	117
Q60692	Exosome	YIANR	VTDKLTPIHDHIFCCR	SGSAA	2	C14:+57.021,C15:+57.021	1006.495729	2010.975857	0.000451244	1	N	62	78
Q60692	Exosome	YIANR	VTDKLTPIHDHIFCCR	SGSAA	3	C14:+57.021,C15:+57.021	671.3330857	2010.975857	0.000451244	28	N	62	78
Q60692	Exosome	GGVIR	LAAIQESGVER	QVLLG	2		586.8176487	1171.619697	0.000622848	8	N	208	219
Q60692	Exosome	SGVER	QVLLGDQIPK	FTIAT	2		555.8300277	1109.644455	0.000451244	5	N	219	229
Q60692	Exosome	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLF	KEMCY	3		1309.985353	3926.93266	0.000451244	4	N	78	116
Q60692	Parental	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK	EMCYR	4		1014.764706	4055.027624	0.000451244	16	N	78	117
Q60692	Parental	YIANR	VTDKLTPIHDHIFCCR	SGSAA	2	C14:+57.021,C15:+57.021	1006.495729	2010.975857	0.000451244	2	N	62	78
Q60692	Parental	YIANR	VTDKLTPIHDHIFCCR	SGSAA	3	C14:+57.021,C15:+57.021	671.3330857	2010.975857	0.000451244	6	N	62	78
Q60692	Parental	SGVER	QVLLGDQIPK	FTIAT	2		555.8300277	1109.644455	0.002813207	1	N	219	229
Q60692	Parental	IFCCR	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLF	KEMCY	3		1309.985353	3926.93266	0.002374549	1	N	78	116
Q60737	Exosome	VRIAK	VLGTEDLYDYIDKYNIELDPR	FNDIL	3		848.7555158	2543.243147	0.000451244	18	N	247	268
Q60737	Exosome	THRPR	EYWDYESHVVEWGNQDDYQLVR	KLGRG	3		944.0846951	2829.230685	0.00091018	1	N	21	43
Q60737	Parental	VRIAK	VLGTEDLYDYIDKYNIELDPR	FNDIL	3		848.7555158	2543.243147	0.000451244	13	N	247	268
Q60737	Parental	THRPR	EYWDYESHVVEWGNQDDYQLVR	KLGRG	3		944.0846951	2829.230685	0.000451244	10	N	21	43
Q60737	Parental	DPVSR	TPALVFEHVNNTDFK	QLYQT	3		577.9620605	1730.862782	0.00091018	4	N	107	122
Q60739	Exosome	HSNER	YDLLVTPQQGNSEPVVQDLAQLVEEATGVPLPFQK	LIFKG	3		1274.998711	3821.972734	0.001162105	1	N	164	199
Q60739	Parental	HSNER	YDLLVTPQQGNSEPVVQDLAQLVEEATGVPLPFQK	LIFKG	3		1274.998711	3821.972734	0.000451244	13	N	164	199
Q60739	Parental	KVQVF	LAECDTVEQYICQETER	LQSTN	2	C4:+57.021,C12:+57.021	1072.467228	2142.918855	0.0007646	4	N	328	345
Q60767	Exosome	KEKMR	LVSITDPYQQAFLAVQATLR	NSSFW	2		1117.613133	2233.210665	0.000451244	25	N	1138	1158
Q60767	Exosome	FRPLK	FLNWDPGTPVAPVIGGSSCAR	MDTES	2	C19:+57.021	1101.044329	2200.073057	0.000622848	9	N	298	319
Q60767	Exosome	EDIAR	LVWLGLNQLYSAR	GWEWS	2		766.9333472	1531.851094	0.000451244	21	N	274	287
Q60767	Exosome	SDVWK	KGGSEENLCAQPYHEIYTR	DGNSY	3	C9:+57.021	751.3519048	2251.032314	0.000451244	2	N	141	160
Q60767	Exosome	KCFLK	VNSGPVTFSQASGICHSYGGTLPSVLSR	GEQDF	3	C15:+57.021	960.1436252	2877.407476	0.000451244	2	N	966	994
Q60767	Exosome	WSDGR	AFDYVPWQSLQSPGDCVVLYPK	GIWRR	2	C16:+57.021	1285.125516	2568.235431	0.001162105	2	N	1473	1495
Q60767	Parental	KEKMR	LVSITDPYQQAFLAVQATLR	NSSFW	2		1117.613133	2233.210665	0.000451244	18	N	1138	1158
Q60767	Parental	FRPLK	FLNWDPGTPVAPVIGGSSCAR	MDTES	2	C19:+57.021	1101.044329	2200.073057	0.001162105	2	N	298	319
Q60767	Parental	EDIAR	LVWLGLNQLYSAR	GWEWS	2		766.9333472	1531.851094	0.000451244	2	N	274	287
Q60767	Parental	ILSWK	EAYVSCQNQGADLLSIHSAAELAYITGK	EDIAR	3	C6:+57.021	1003.825962	3008.454486	0.001699387	1	N	241	269
Q60790	Parental	ACGSK	SVYDGPEQEEYSTFVIDDPQETYK	TLKQV	2		1420.127589	2838.239578	0.000451244	16	N	754	778
Q60790	Parental	ASNLK	FGDEFLGELRLPLK	ILRHS	3		545.3036466	1632.88754	0.001591523	1	N	237	251
Q60790	Parental	WLCCR	ASSDTAAGCTPCTGGLPANIQLDIDGDRETER	IYSLF	3	C9:+57.021,C12:+57.021	1116.840628	3347.498484	0.000622848	2	N	700	732
Q60864	Exosome	KEQER	LAYINPDLALEEK	NKGNE	2		744.9013784	1487.787157	0.000451244	10	N	351	364
Q60864	Exosome	EKGNK	ALSAGNIDDALQCYSEAIKLDPQNHVLYSNR	SAAYA	4	C13:+57.021	869.6786292	3474.683317	0.000622848	2	N	13	44
Q60864	Exosome	EKGNK	ALSAGNIDDALQCYSEAIK	LDPQN	2	C13:+57.021	1019.991427	2037.967255	0.000451244	33	N	13	32
Q60864	Exosome	EEAKR	TYEEGLKHEANNLQLK	EGLQN	3		629.6589292	1885.953388	0.000451244	16	N	93	109
Q60864	Exosome	DPTYR	ELIEQLQNKPSDLGTK	LQDPR	2		906.9892448	1811.96289	0.000451244	8	N	153	169
Q60864	Exosome	DPTYR	ELIEQLQNKPSDLGTK	LQDPR	3		604.9954299	1811.96289	0.000451244	9	N	153	169
Q60864	Parental	DVYQK	ALDLDSSCKEAADGYQR	CMMAQ	2	C8:+57.021	949.9313696	1897.847139	0.000451244	12	N	453	470

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q60864	Parental	DVYQK	ALDLDSSCKEAADGYQR	CMMAQ	3	C8:+57.021	633.6235131	1897.847139	0.000451244	6	N	453	470
Q60864	Parental	KEQER	LAYINPDLALEEK	NKGNE	2		744.9013784	1487.787157	0.000622848	12	N	351	364
Q60864	Parental	EKGNK	ALSAGNIDDALQCYSEAIKLDPQNHVLYSNR	SAAYA	3	C13:+57.021	1159.235572	3474.683317	0.000451244	10	N	13	44
Q60864	Parental	EKGNK	ALSAGNIDDALQCYSEAIKLDPQNHVLYSNR	SAAYA	4	C13:+57.021	869.6786292	3474.683317	0.000451244	1	N	13	44
Q60864	Parental	ACYTK	LLEFQLALKDCEECIQLEPTFIK	GYTRK	3	C11:+57.021,C14:+57.021	946.4871872	2836.438162	0.001591523	2	N	406	429
Q60864	Parental	EKGNK	ALSAGNIDDALQCYSEAIK	LDPQN	2	C13:+57.021	1019.991427	2037.967255	0.000451244	7	N	13	32
Q60864	Parental	EEAKR	TYEEGLKHEANNLQLK	EGLQN	2		943.9844938	1885.953388	0.000451244	2	N	93	109
Q60864	Parental	EEAKR	TYEEGLKHEANNLQLK	EGLQN	3		629.6589292	1885.953388	0.000451244	7	N	93	109
Q60864	Parental	DPTYR	ELIEQLQNKPSDLGTK	LQDPR	2		906.9892448	1811.96289	0.000451244	7	N	153	169
Q60864	Parental	DPTYR	ELIEQLQNKPSDLGTK	LQDPR	3		604.9954299	1811.96289	0.000451244	5	N	153	169
Q60864	Parental	ALQCY	SEAIKLDPQNHVLYSNR	SAAYA	2		992.5164925	1983.017385	0.001463592	1	N	27	44
Q60864	Parental	ALQCY	SEAIKLDPQNHVLYSNR	SAAYA	3		662.013595	1983.017385	0.000622848	1	N	27	44
Q60864	Parental	DPRTR	SLLSDPTYRELIEQLQNKPSDLGTK	LQDPR	3		949.1701001	2844.4869	0.002981883	1	N	144	169
Q60864	Parental	EKGNK	ALSAGNIDDALQCY	SEAIK	2	C13:+57.021	755.8460459	1509.676492	0.002374549	2	N	13	27
Q60865	Exosome	DMSLR	LNEQYEHASIHLWDLLEGK	EKPVC	4		574.5410858	2294.133143	0.001264573	3	N	200	219
Q60865	Exosome	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	2		1233.636667	2465.257735	0.000451244	12	N	167	189
Q60865	Exosome	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	3		822.7603783	2465.257735	0.000451244	1	N	167	189
Q60865	Exosome	DAVSK	YQEVTNNLEFAK	ELQRS	2		728.3598777	1454.704155	0.002727428	1	N	96	108
Q60865	Parental	NKGER	LNQDQLDAVSKYQEVTNNLEFAK	ELQRS	3		889.780724	2666.318772	0.000823681	3	N	85	108
Q60865	Parental	DMSLR	LNEQYEHASIHLWDLLEGK	EKPVC	2		1148.074372	2294.133143	0.001229886	1	N	200	219
Q60865	Parental	DMSLR	LNEQYEHASIHLWDLLEGK	EKPVC	3		765.7188477	2294.133143	0.000451244	3	N	200	219
Q60865	Parental	DMSLR	LNEQYEHASIHLWDLLEGK	EKPVC	4		574.5410858	2294.133143	0.000451244	8	N	200	219
Q60865	Parental	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	2		1233.636667	2465.257735	0.000451244	41	N	167	189
Q60865	Parental	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	3		822.7603783	2465.257735	0.000451244	12	N	167	189
Q60865	Parental	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	2	Q1:-17.027	1225.123167	2448.230735	0.000451244	2	N	167	189
Q60865	Parental	RTDLK	QGLSGVPILSEEELSLLDEFYK	LVDPE	2	[0:-17.027	1225.123167	2448.230735	0.000451244	9	N	167	189
Q60865	Parental	NKGER	LNQDQLDAVSKY	QEVTN	2		697.3520527	1392.688505	0.002663018	1	N	85	97
Q60865	Parental	VVGTY	HGSQDQPHQVPGNHQQPPQQNTGFPR	SSQPY	4		729.8467986	2915.355995	0.000622848	1	N	571	597
Q60865	Parental	QKRLK	TVLELQYVLDKLGDDDVR	TDLKQ	3		697.7043157	2090.089547	0.001162105	1	N	145	163
Q60875	Exosome	VLINR	ILQNSHGVEEEYQDLASALGLVK	ELLSN	3		838.4347766	2512.28093	0.000451244	1	N	401	424
Q60875	Parental	GNQLR	SPQEEVLQPLINLYGLLHGLQAVVVQQER	LMEAL	3		1090.933536	3269.777209	0.000451244	23	N	731	760
Q60875	Parental	GNQLR	SPQEEVLQPLINLYGLLHGLQAVVVQQER	LMEAL	4		818.4521023	3269.777209	0.000451244	2	N	731	760
Q60875	Parental	EEIRR	QLAALGQNEPLPAEAPWAR	RPLDP	2		1016.534685	2031.05377	0.000451244	4	N	857	876
Q60875	Parental	KEVMK	KQDVIYELIQTELHHVR	TLKIM	4		531.0422586	2120.137835	0.000622848	2	N	236	253
Q60875	Parental	EVMKK	QDVIYELIQTELHHVR	TLKIM	4		499.0185179	1992.042871	0.000451244	2	N	237	253
Q60902	Parental	PPSER	GTPIPDSSSTLASGEFTGVKELDDISQEIAQLQR	EKYSL	3		1197.267638	3588.779514	0.000622848	4	N	362	396
Q60902	Parental	LEAHR	SLEQYDQVPDGVSGTSLPDLATLNEGILLAER	GGFGA	3		1134.242653	3399.704558	0.000451244	23	N	557	589
Q60902	Parental	SELNR	LQQEETQLEQSIQAGR	AQLET	2		929.4692079	1856.922816	0.000451244	4	N	505	521
Q60902	Parental	FTGVK	ELDDISQEIAQLQR	EKYSL	2		829.4237377	1656.831875	0.000451244	1	N	382	396
Q60930	Exosome	TFTEK	WNTDNTLGTEIAIEDQICQGLK	LTFDT	2	C18:+57.021	1260.108051	2518.200502	0.000451244	1	N	86	108
Q60930	Parental	SISAK	VNNSSLIGVGYTQTLRPGVK	LTLSA	2		1052.082	2102.148399	0.000451244	7	N	248	268
Q60930	Parental	SISAK	VNNSSLIGVGYTQTLRPGVK	LTLSA	3		701.7239331	2102.148399	0.00307782	1	N	248	268
Q60930	Parental	TFTEK	WNTDNTLGTEIAIEDQICQGLK	LTFDT	2	C18:+57.021	1260.108051	2518.200502	0.000451244	21	N	86	108
Q60930	Parental	DVKTK	SCSGVEFSTSGSSNTDTGKVSGTLETK	YKWCE	3	C2:+57.021	908.4156275	2722.223482	0.001162105	2	N	46	73
Q60930	Parental	DVKTK	SCSGVEFSTSGSSNTDTGK	VSGTL	2	C2:+57.021	954.4000993	1906.784599	0.000451244	3	N	46	65
Q60930	Parental	SIYQK	VCEDFDTSVNLAWTSGTNCTR	FGIAA	2	C2:+57.021,C19:+57.021	1217.025973	2432.036345	0.000622848	3	N	209	230
Q60931	Exosome	RPGVK	LTLSALIDGK	NFNAG	2		515.8113036	1029.607007	0.002453667	1	N	256	266
Q60931	Parental	RPGVK	LTLSALIDGK	NFNAG	2		515.8113036	1029.607007	0.001264573	6	N	256	266
Q60931	Parental	TFTQK	WNTDNTLGTEISWENKLAEGLK	LTLDT	2		1260.12479	2518.23398	0.001654178	1	N	74	96
Q60932	Parental	CFSAK	VNNSSLIGLGYTQTLKPGIK	LTLSA	2		1052.094576	2102.173551	0.000622848	2	N	249	269
Q60932	Parental	CFSAK	VNNSSLIGLGYTQTLKPGIK	LTLSA	3		701.7323171	2102.173551	0.000622848	13	N	249	269
Q60932	Parental	GIAAK	YQVDPDACFSAK	VNNSS	2	C8:+57.021	700.8114747	1399.607349	0.000870037	1	N	237	249
Q60932	Parental	TGYKR	EHINLGCDVDFDIAGPSIR	GALVL	2	C7:+57.021	1064.510319	2127.005037	0.001162105	1	N	133	152
Q60932	Parental	TFTEK	WNTDNTLGTEITVEDQLAR	GLKLT	2		1088.529994	2175.044388	0.000451244	36	N	87	106
Q60932	Parental	KPGIK	LTLSALLDGK	NVNAG	2		515.8113036	1029.607007	0.000622848	7	N	269	279
Q60953	Exosome	DRYQR	DYQEIAGQLSCLEAVLQR	IRTSG	2	C11:+57.021	1047.020519	2092.025438	0.002212458	1	N	311	329
Q60953	Parental	DRYQR	DYQEIAGQLSCLEAVLQR	IRTSG	2	C11:+57.021	1047.020519	2092.025438	0.000451244	18	N	311	329
Q60953	Parental	QLLTR	GFEEFKLCLQDFISCITQR	INAAV	3	C8:+57.021,C15:+57.021	797.7207865	2390.13896	0.000823681	2	N	378	397
Q60953	Parental	FEEFK	LCLQDFISCITQR	INAAV	3	C2:+57.021,C9:+57.021	551.9413061	1652.800518	0.000451244	4	N	384	397
Q60953	Parental	CTRCK	GLADFWCFECEQLICSK	CFEAH	2	C7:+57.021,C10:+57.021,C15:+57.021	1081.970663	2161.925727	0.000451244	9	N	138	155
Q60953	Parental	VPEKK	ILLPNNNHVTSDTGETEER	VVVIS	2		1070.019793	2138.023987	0.002453667	1	N	546	565
Q60953	Parental	AKCPK	LLPCLHTLCSGCLEAPGLQCPICK	APGQA	3	C4:+57.021,C9:+57.021,C12:+57.021,C20:+57.021,C23:+57.021	933.1154743	2796.323023	0.000451244	4	N	73	97
Q60953	Parental	CPICK	APGQADANGEALDNVFFESLQR	RLAVF	2		1175.05945	2348.1033	0.001162105	1	N	97	119

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q60960	Exosome	SPALR	AVGNIVTGDDIQTQVILNCSALQSLLHLLSSPK	ESIKK	3	C19:+57.021	1168.962901	3503.865304	0.001352548	1	N	318	351
Q60960	Exosome	STMCR	DYVLNCNILPPLLQLFSK	QNRLT	2	C6:+57.021	1074.082391	2146.149182	0.001699387	2	N	204	222
Q60960	Parental	SPALR	AVGNIVTGDDIQTQVILNCSALQSLLHLLSSPK	ESIKK	3	C19:+57.021	1168.962901	3503.865304	0.000622848	14	N	318	351
Q60960	Parental	VMDAK	IVQVALNGLENILR	LGEQE	2		776.4650116	1550.914423	0.000451244	10	N	438	452
Q60960	Parental	STMCR	DYVLNCNILPPLLQLFSK	QNRLT	2	C6:+57.021	1074.082391	2146.149182	0.000823681	1	N	204	222
Q60963	Exosome	RTGEK	YPLIVFSHGLGAFR	TIYSA	3		526.2931933	1575.85618	0.000451244	18	N	142	156
Q60963	Exosome	MITIK	GSVHQNFDDFTFVTGK	IIGNK	2		899.9239048	1797.83221	0.000451244	2	N	346	362
Q60963	Exosome	MITIK	GSVHQNFDDFTFVTGK	IIGNK	3		600.2852032	1797.83221	0.000451244	4	N	346	362
Q60963	Exosome	ELYSR	TLQPLLFINSAK	FQTPK	2		672.8984417	1343.781283	0.000451244	1	N	308	320
Q60963	Exosome	EHRDR	SASATYFFEDQVAAK	VENRS	2		817.8889993	1633.762399	0.000451244	1	N	181	196
Q60972	Exosome	IIATK	TPSSDVLVFDYTKHPSKPDPSGECNPDLR	LRGHQ	3	C24:+57.021	1086.850947	3257.529442	0.001264573	1	N	143	172
Q60972	Exosome	IIATK	TPSSDVLVFDYTKHPSKPDPSGECNPDLR	LRGHQ	4	C24:+57.021	815.3901604	3257.529442	0.000451244	5	N	143	172
Q60972	Exosome	WDLSK	IGEEQSPEDAEDGPPELLFIHGGHTAK	ISDFS	3		958.4583096	2872.351529	0.000451244	19	N	349	376
Q60972	Exosome	WDLSK	IGEEQSPEDAEDGPPELLFIHGGHTAK	ISDFS	4		719.0956822	2872.351529	0.000451244	26	N	349	376
Q60972	Exosome	RGHQK	EGYGLSWNPNLSGHLLSASDDHTICLWDISAVPK	EGKVV	3	C25:+57.021	1251.605665	3751.793596	0.000451244	12	N	178	212
Q60972	Exosome	RGHQK	EGYGLSWNPNLSGHLLSASDDHTICLWDISAVPK	EGKVV	4	C25:+57.021	938.9561989	3751.793596	0.000451244	7	N	178	212
Q60972	Exosome	VVDAK	TIFTGHTAVVEDVSWHLLHESLFGSVADDQK	LMIWD	4		860.4300956	3437.689182	0.000823681	5	N	220	251
Q60972	Exosome	IIATK	TPSSDVLVFDYTK	HPSKP	2		736.3699111	1470.724222	0.001463592	1	Y	143	156
Q60972	Exosome	GHTAK	ISDFSWNPNEPWVICSV	SEDNI	2	C15:+57.021	1025.472673	2048.929747	0.000451244	12	Y	376	393
Q60972	Parental	IIATK	TPSSDVLVFDYTKHPSKPDPSGECNPDLR	LRGHQ	3	C24:+57.021	1086.850947	3257.529442	0.000451244	21	N	143	172
Q60972	Parental	IIATK	TPSSDVLVFDYTKHPSKPDPSGECNPDLR	LRGHQ	4	C24:+57.021	815.3901604	3257.529442	0.000451244	11	N	143	172
Q60972	Parental	WDLSK	IGEEQSPEDAEDGPPELLFIHGGHTAK	ISDFS	3		958.4583096	2872.351529	0.000451244	32	N	349	376
Q60972	Parental	WDLSK	IGEEQSPEDAEDGPPELLFIHGGHTAK	ISDFS	4		719.0956822	2872.351529	0.000451244	12	N	349	376
Q60972	Parental	RGHQK	EGYGLSWNPNLSGHLLSASDDHTICLWDISAVPK	EGKVV	3	C25:+57.021	1251.605665	3751.793596	0.000451244	33	N	178	212
Q60972	Parental	RGHQK	EGYGLSWNPNLSGHLLSASDDHTICLWDISAVPK	EGKVV	4	C25:+57.021	938.9561989	3751.793596	0.000451244	22	N	178	212
Q60972	Parental	VVDAK	TIFTGHTAVVEDVSWHLLHESLFGSVADDQK	LMIWD	3		1146.904194	3437.689182	0.001264573	3	N	220	251
Q60972	Parental	VVDAK	TIFTGHTAVVEDVSWHLLHESLFGSVADDQK	LMIWD	4		860.4300956	3437.689182	0.000451244	7	N	220	251
Q60972	Parental	IIATK	TPSSDVLVFDYTK	HPSKP	2		736.3699111	1470.724222	0.001699387	1	Y	143	156
Q60973	Exosome	IIATK	TPSSDVLVFDYTKHPAKPDPSGECNPDLR	LRGHQ	3	C24:+57.021	1081.519309	3241.534527	0.001162105	1	N	142	171
Q60973	Exosome	IIATK	TPSSDVLVFDYTKHPAKPDPSGECNPDLR	LRGHQ	4	C24:+57.021	811.3914317	3241.534527	0.000451244	9	N	142	171
Q60973	Exosome	WDLSK	IGEEQSAEDAEDGPPELLFIHGGHTAK	ISDFS	3		949.7864263	2846.335879	0.000451244	4	N	348	375
Q60973	Exosome	WDLSK	IGEEQSAEDAEDGPPELLFIHGGHTAK	ISDFS	4		712.5917697	2846.335879	0.001329271	1	N	348	375
Q60973	Exosome	IVDAK	AIFTGHSAVVEDVAWHLLHESLFGSVADDQK	LMIWD	3		1126.897151	3377.668053	0.000451244	2	N	219	250
Q60973	Exosome	IVDAK	AIFTGHSAVVEDVAWHLLHESLFGSVADDQK	LMIWD	4		845.4248132	3377.668053	0.000451244	7	N	219	250
Q60973	Exosome	IIATK	TPSSDVLVFDYTK	HPAKP	2		736.3699111	1470.724222	0.001463592	1	Y	142	155
Q60973	Exosome	IWDTR	SNTTSKPSHLVDAHTAEVNCLSFNPYSEFILATGSADK	TVALW	3	C20:+57.021	1370.323775	4107.947924	0.001763695	2	N	257	295
Q60973	Exosome	GHTAK	ISDFSWNPNEPWVICSV	SEDNI	2	C15:+57.021	1025.472673	2048.929747	0.000451244	12	Y	375	392
Q60973	Exosome	LVVAR	VHIPNDDAQFDASHCDSDKGEFGGFGSVTGK	IECEI	3	C15:+57.021	1098.818306	3293.431518	0.000622848	1	N	82	113
Q60973	Exosome	LVVAR	VHIPNDDAQFDASHCDSDKGEFGGFGSVTGK	IECEI	4	C15:+57.021	824.3656796	3293.431518	0.000451244	9	N	82	113
Q60973	Exosome	KPEGK	DYALHWLVLGTHTSDEQNHLVVAR	VHIPN	4		694.3562022	2773.393609	0.000451244	10	N	58	82
Q60973	Parental	IIATK	TPSSDVLVFDYTKHPAKPDPSGECNPDLR	LRGHQ	3	C24:+57.021	1081.519309	3241.534527	0.000622848	1	N	142	171
Q60973	Parental	IIATK	TPSSDVLVFDYTKHPAKPDPSGECNPDLR	LRGHQ	4	C24:+57.021	811.3914317	3241.534527	0.000451244	6	N	142	171
Q60973	Parental	WDLSK	IGEEQSAEDAEDGPPELLFIHGGHTAK	ISDFS	3		949.7864263	2846.335879	0.000451244	20	N	348	375
Q60973	Parental	IVDAK	AIFTGHSAVVEDVAWHLLHESLFGSVADDQK	LMIWD	4		845.4248132	3377.668053	0.000451244	7	N	219	250
Q60973	Parental	IIATK	TPSSDVLVFDYTK	HPAKP	2		736.3699111	1470.724222	0.001699387	1	Y	142	155
Q60973	Parental	LVVAR	VHIPNDDAQFDASHCDSDKGEFGGFGSVTGK	IECEI	3	C15:+57.021	1098.818306	3293.431518	0.000823681	1	N	82	113
Q60973	Parental	LVVAR	VHIPNDDAQFDASHCDSDKGEFGGFGSVTGK	IECEI	4	C15:+57.021	824.3656796	3293.431518	0.000979378	2	N	82	113
Q60973	Parental	KPEGK	DYALHWLVLGTHTSDEQNHLVVAR	VHIPN	4		694.3562022	2773.393609	0.001763695	3	N	58	82
Q60973	Parental	RGHQK	EGYGLSWNSNLSGHLLSASDDHTVCLWDINAGPK	EGKIV	3	C25:+57.021	1238.58152	3712.721159	0.0025889	1	N	177	211
Q60973	Parental	RGHQK	EGYGLSWNSNLSGHLLSASDDHTVCLWDINAGPK	EGKIV	4	C25:+57.021	929.1880897	3712.721159	0.000622848	1	N	177	211
Q61024	Exosome	MTDRR	IGCLLSGGLDSSLVAASLLK	QLKEA	2	C3:+57.021	987.5509237	1973.086247	0.000451244	10	N	252	272
Q61024	Exosome	MTDRR	IGCLLSGGLDSSLVAASLLK	QLKEA	3	C3:+57.021	658.7032158	1973.086247	0.000823681	1	N	252	272
Q61024	Exosome	VEMVK	YHHCTDEPLHAIYDSVEK	LFPGF	3	C4:+57.021	738.6692339	2212.984302	0.001162105	2	N	203	221
Q61024	Parental	MTDRR	IGCLLSGGLDSSLVAASLLK	QLKEA	2	C3:+57.021	987.5509237	1973.086247	0.000451244	8	N	252	272
Q61029	Exosome	GTESR	SSTPLPTVSSSAENTR	QNGSN	2		817.4055449	1632.79549	0.000451244	17	Y	156	172
Q61029	Exosome	DQLVR	YGVNPGPIVGTTR	KLYEK	2		665.8598479	1329.704096	0.000451244	5	Y	125	138
Q61029	Exosome	GANSK	GPPDFSSDEEREPTPVLGSGASVGR	GRGAV	3		848.4056571	2542.193571	0.000451244	5	Y	60	85
Q61029	Exosome	TDKPR	LEDKDDLDVTELSNEELLDQLVR	YGVNP	3		901.1191825	2700.334148	0.000451244	30	Y	102	125
Q61029	Exosome	SQHFR	IDGAVISESTPIAETIK	ASSNE	2		872.4728963	1742.930193	0.002519933	2	N	268	285
Q61029	Exosome	-M	PEFLEDPSVLTK	DKLKS	2		687.8617219	1373.707844	0.000451244	4	Y	1	13
Q61029	Exosome	KDKLK	SELVANNVTLPAGEQR	KDVYV	2		849.4450044	1696.874409	0.000823681	3	Y	17	33
Q61029	Exosome	GEQRK	DVYVQLYLQHLTAR	NRPPL	3		573.6461838	1717.915151	0.001839721	3	Y	34	48
Q61029	Parental	GTESR	SSTPLPTVSSSAENTR	QNGSN	2		817.4055449	1632.79549	0.000451244	63	Y	156	172
Q61029	Parental	DQLVR	YGVNPGPIVGTTR	KLYEK	2		665.8598479	1329.704096	0.000451244	27	Y	125	138
Q61029	Parental	GANSK	GPPDFSSDEEREPTPVLGSGASVGR	GRGAV	2		1272.104586	2542.193571	0.000698008	6	Y	60	85

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61029	Parental	GANSK	GPPDFSSDEEREPTPVLGSGASVGR	GRGAV	3		848.4056571	2542.193571	0.000451244	74	Y	60	85
Q61029	Parental	HNQSY	SQAGVTETEWTSGSSTGGPLQALTR	ESTRG	2		1261.112411	2520.209222	0.000451244	40	N	222	247
Q61029	Parental	TDKPR	LEDKDDLDVTELSNEELLDQLVR	YGVNP	2		1351.174874	2700.334148	0.000451244	24	Y	102	125
Q61029	Parental	TDKPR	LEDKDDLDVTELSNEELLDQLVR	YGVNP	3		901.1191825	2700.334148	0.000451244	23	Y	102	125
Q61029	Parental	SQHFR	IDGAVISESTPIAETIK	ASSNE	2		872.4728963	1742.930193	0.000637154	18	N	268	285
Q61029	Parental	-M	PEFLEDPSVLTK	DKLKS	2		687.8617219	1373.707844	0.000451244	23	Y	1	13
Q61029	Parental	KDKLK	SELVANNVTLPAGEQRK	DVYVQ	2		913.492486	1824.969372	0.000451244	7	Y	17	34
Q61029	Parental	KDKLK	SELVANNVTLPAGEQR	KDVYV	2		849.4450044	1696.874409	0.000451244	53	Y	17	33
Q61029	Parental	-M	PEFLEDPSVLTKDK	LKSEL	3		539.95105	1616.82975	0.001329271	1	Y	1	15
Q61029	Parental	TLKQR	RTEHNQSYSQAGVTETEWTSGSSTGGPLQALTR	ESTRG	3		1179.559926	3535.656379	0.000622848	4	N	214	247
Q61029	Parental	LKQRR	TEHNQSYSQAGVTETEWTSGSSTGGPLQALTR	ESTRG	3		1127.526223	3379.555268	0.000823681	3	N	215	247
Q61029	Parental	TSQHF	RIDGAVISESTPIAETIK	ASSNE	2		950.5234518	1899.031304	0.000451244	9	N	267	285
Q61029	Parental	LTKDK	LKSELVANNVTLPAGEQR	KDVYV	2		970.0345181	1938.053436	0.000451244	13	Y	15	33
Q61029	Parental	LTKDK	LKSELVANNVTLPAGEQR	KDVYV	3		647.025612	1938.053436	0.000622848	1	Y	15	33
Q61029	Parental	RRPIK	GAAGRPLELSDFR	MEESF	3		463.5814028	1387.720808	0.000979378	1	N	367	380
Q61033	Exosome	GTESR	SSTPLPTVSSSAENTR	QNGSN	2		817.4055449	1632.79549	0.000451244	17	Y	156	172
Q61033	Exosome	DQLVR	YGVNPGPIVGTTR	KLYEK	2		665.8598479	1329.704096	0.000451244	5	Y	125	138
Q61033	Exosome	GANSK	GPPDFSSDEEREPTPVLGSGASVGR	GRGAV	3		848.4056571	2542.193571	0.000451244	5	Y	60	85
Q61033	Exosome	AFVAK	SLQADISQAAQIINSDPSDAQQALR	ILNRT	2		1320.665342	2639.315084	0.00307782	1	N	590	615
Q61033	Exosome	TDKPR	LEDKDDLDVTELSNEELLDQLVR	YGVNP	3		901.1191825	2700.334148	0.000451244	30	Y	102	125
Q61033	Exosome	AQAIR	DYVNSLLVQGGVGSLPGTSDSVPTLDVENICKR	LSQSS	3	C31:+57.021	1163.922883	3488.745248	0.000451244	10	N	376	409
Q61033	Exosome	-M	PEFLEDPSVLTK	DKLKS	2		687.8617219	1373.707844	0.000451244	4	Y	1	13
Q61033	Exosome	KDKLK	SELVANNVTLPAGEQR	KDVYV	2		849.4450044	1696.874409	0.000823681	3	Y	17	33
Q61033	Exosome	GEQRK	DVYVQLYLQHLTAR	NRPPL	3		573.6461838	1717.915151	0.001839721	3	Y	34	48
Q61033	Parental	GTESR	SSTPLPTVSSSAENTR	QNGSN	2		817.4055449	1632.79549	0.000451244	63	Y	156	172
Q61033	Parental	DQLVR	YGVNPGPIVGTTR	KLYEK	2		665.8598479	1329.704096	0.000451244	27	Y	125	138
Q61033	Parental	GANSK	GPPDFSSDEEREPTPVLGSGASVGR	GRGAV	2		1272.104586	2542.193571	0.000698008	6	Y	60	85
Q61033	Parental	GANSK	GPPDFSSDEEREPTPVLGSGASVGR	GRGAV	3		848.4056571	2542.193571	0.000451244	74	Y	60	85
Q61033	Parental	AFVAK	SLQADISQAAQIINSDPSDAQQALR	ILNRT	2		1320.665342	2639.315084	0.000451244	10	N	590	615
Q61033	Parental	AFVAK	SLQADISQAAQIINSDPSDAQQALR	ILNRT	3		880.7794946	2639.315084	0.000823681	2	N	590	615
Q61033	Parental	TDKPR	LEDKDDLDVTELSNEELLDQLVR	YGVNP	2		1351.174874	2700.334148	0.000451244	24	Y	102	125
Q61033	Parental	TDKPR	LEDKDDLDVTELSNEELLDQLVR	YGVNP	3		901.1191825	2700.334148	0.000451244	23	Y	102	125
Q61033	Parental	AQAIR	DYVNSLLVQGGVGSLPGTSDSVPTLDVENICKR	LSQSS	3	C31:+57.021	1163.922883	3488.745248	0.000451244	47	N	376	409
Q61033	Parental	-M	PEFLEDPSVLTK	DKLKS	2		687.8617219	1373.707844	0.000451244	23	Y	1	13
Q61033	Parental	KDKLK	SELVANNVTLPAGEQRK	DVYVQ	2		913.492486	1824.969372	0.000451244	7	Y	17	34
Q61033	Parental	KDKLK	SELVANNVTLPAGEQR	KDVYV	2		849.4450044	1696.874409	0.000451244	53	Y	17	33
Q61033	Parental	-M	PEFLEDPSVLTKDK	LKSEL	3		539.95105	1616.82975	0.001329271	1	Y	1	15
Q61033	Parental	IEAAR	ILSVPKVDDEILGFISEATPR	AATQA	3		767.0901701	2298.24711	0.000451244	7	N	528	549
Q61033	Parental	DCVPF	SELASTPSGAFFQGISFPEISTRPPLGR	TELQA	3		983.8422063	2948.503219	0.002296037	1	N	205	233
Q61033	Parental	EATPR	AATQASSTESCDKHLDLALCR	SYEAA	3	C11:+57.021,C20:+57.021	778.6988216	2333.073065	0.000622848	4	N	549	570
Q61033	Parental	LTKDK	LKSELVANNVTLPAGEQR	KDVYV	2		970.0345181	1938.053436	0.000451244	13	Y	15	33
Q61033	Parental	LTKDK	LKSELVANNVTLPAGEQR	KDVYV	3		647.025612	1938.053436	0.000622848	1	Y	15	33
Q61033	Parental	LSVPK	VDDEILGFISEATPR	AATQA	2		831.4232064	1660.830813	0.000451244	2	N	534	549
Q61033	Parental	LSVPK	VDDEILGFISEATPR	AATQA	3		554.6180709	1660.830813	0.000451244	13	N	534	549
Q61033	Parental	AQAIR	DYVNSLLVQGGVGSLPGTSDSVPTLDVENICK	RLSQS	3	C31:+57.021	1111.889179	3332.644137	0.000451244	4	N	376	408
Q61035	Exosome	KKNPK	LLNQLQYCEEAGIPLVAIIGEQELKDGVIK	LRSVA	3	C8:+57.021	1118.606055	3352.794765	0.000451244	46	N	447	477
Q61035	Exosome	EVADR	IGDYVQQHGGVSLVEQLLQDPK	LSQNK	2		1212.132418	2422.249236	0.0007646	3	N	266	288
Q61035	Exosome	EVADR	IGDYVQQHGGVSLVEQLLQDPK	LSQNK	3		808.4242119	2422.249236	0.000451244	33	N	266	288
Q61035	Exosome	KKNPK	LLNQLQYCEEAGIPLVAIIGEQELK	DGVIK	2	C8:+57.021	1421.257258	2840.498917	0.000451244	17	N	447	472
Q61035	Exosome	KKNPK	LLNQLQYCEEAGIPLVAIIGEQELK	DGVIK	3	C8:+57.021	947.8407722	2840.498917	0.000451244	26	N	447	472
Q61035	Exosome	LSLAR	GLDYYTGVIYEAVLLQMPTQAGEEPLGVGSIAAGGR	YDGLV	3	M17:+15.995	1237.957888	3710.850263	0.000451244	23	N	326	362
Q61035	Exosome	LGDLK	LLFEYLILFGIDDK	ISFDL	2		849.9718038	1697.928008	0.000622848	3	N	303	317
Q61035	Exosome	GIDDK	ISFDLSLAR	GLDYY	2		511.2879957	1020.560391	0.001654178	6	N	317	326
Q61035	Exosome	LLSLR	YDLTVPFAR	YLAMN	2		541.2879957	1080.560391	0.000451244	12	N	128	137
Q61035	Exosome	LLEER	LKLVSELWDAGIK	AELLY	3		491.2893374	1470.844612	0.002981883	1	N	424	437
Q61035	Exosome	RCFKR	HGAEVIDTPVFELK	ETLTG	3		518.9441183	1553.808955	0.000451244	2	N	86	100
Q61035	Parental	KKNPK	LLNQLQYCEEAGIPLVAIIGEQELKDGVIK	LRSVA	3	C8:+57.021	1118.606055	3352.794765	0.000451244	21	N	447	477
Q61035	Parental	EVADR	IGDYVQQHGGVSLVEQLLQDPK	LSQNK	3		808.4242119	2422.249236	0.000451244	9	N	266	288
Q61074	Exosome	GKLQK	ALQDAFLAIDAK	LTTEE	2		638.3513243	1274.687049	0.000823681	1	N	92	104
Q61074	Parental	PPHTK	SGIGTGDEPGPQGLNGEAGPEDPSRETPSQENGPTAK	GHTGF	3		1211.889889	3632.646268	0.000451244	66	N	172	209
Q61074	Parental	GPTAK	GHTGFSSNSEHGTEAGQISEPGTATGEAGPSCSSASDK	LPRVA	4	C32:+57.021	923.8968009	3691.556004	0.000451244	3	N	209	247
Q61074	Parental	PPHTK	SGIGTGDEPGPQGLNGEAGPEDPSR	ETPSQ	2		1197.544361	2393.073122	0.00091018	2	N	172	197
Q61081	Exosome	ERKKR	LGPGGLDPVEVYESLPEELQK	CFDVK	2		1135.084071	2268.152541	0.000451244	10	N	287	308
Q61081	Exosome	ERKKR	LGPGGLDPVEVYESLPEELQK	CFDVK	3		757.0586471	2268.152541	0.000637154	9	N	287	308
Q61081	Exosome	VPNSK	SGEAKEGEEAGPGDPLLEAVPK	AGNEK	3		727.3626182	2179.064455	0.000662267	4	N	348	370

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61081	Exosome	QRKLK	ELEVAESDGQVELER	LRAEA	2		851.9106601	1701.80572	0.000622848	4	N	69	84
Q61081	Parental	ERKKR	LGPGGLDPVEVYESLPEELQK	CFDVK	2		1135.084071	2268.152541	0.000451244	40	N	287	308
Q61081	Parental	ERKKR	LGPGGLDPVEVYESLPEELQK	CFDVK	3		757.0586471	2268.152541	0.000823681	17	N	287	308
Q61081	Parental	VPNSK	SGEAKEGEEAGPGDPLLEAVPK	AGNEK	2		1090.540027	2179.064455	0.000451244	16	N	348	370
Q61081	Parental	VPNSK	SGEAKEGEEAGPGDPLLEAVPK	AGNEK	3		727.3626182	2179.064455	0.000451244	12	N	348	370
Q61081	Parental	QRKLK	ELEVAESDGQVELER	LRAEA	2		851.9106601	1701.80572	0.000451244	14	N	69	84
Q61081	Parental	ECQRK	LKELEVAESDGQVELER	LRAEA	2		972.5001737	1942.984747	0.001699387	1	N	67	84
Q61093	Exosome	ERIVR	GQTAESLEEHNLDICADKIEEWGK	IKECP	3	C15:+57.021	924.764591	2771.270373	0.000451244	1	N	229	253
Q61093	Exosome	GISDR	YSIALSDIGDNENEEYLNFAR	EKIKN	2		1217.064398	2432.113196	0.000451244	8	N	136	157
Q61093	Exosome	SIHIR	IVGDWTEGLFNACGCDKQEFQDAWK	LPKIA	3	C13:+57.021,C15:+57.021	992.10955	2973.30525	0.000451244	7	N	356	381
Q61093	Exosome	PKVSK	LEWHPFTLTSAPEEDFFSIHIR	IVGDW	4		668.8345713	2671.307085	0.000622848	3	N	334	356
Q61093	Exosome	DNEFK	TIASEHPNTTIGVFLCGPEALAETLSK	QSISN	2	C16:+57.021	1428.726322	2855.437045	0.000698008	2	N	521	548
Q61093	Exosome	DNEFK	TIASEHPNTTIGVFLCGPEALAETLSK	QSISN	3	C16:+57.021	952.8201482	2855.437045	0.000451244	18	N	521	548
Q61093	Exosome	YSIAL	SDIGDNENEEYLNFAR	EKIKN	2		943.4140983	1884.812597	0.000451244	1	N	141	157
Q61093	Exosome	DNEFK	TIASEHPNTTIGVFLCGPEAL	AETLS	2	C16:+57.021	1114.057102	2226.098603	0.002981883	1	N	521	542
Q61093	Exosome	SIHIR	IVGDWTEGLFNACGCDKQEF	QDAWK	2	C13:+57.021,C15:+57.021	1173.51197	2345.008339	0.000451244	5	N	356	376
Q61093	Parental	NFLSY	NIYLTGWDESQANHFAVHHDEEKDVITGLK	QKTLY	3		1156.227448	3465.658945	0.000451244	24	N	476	506
Q61093	Parental	ERIVR	GQTAESLEEHNLDICADKIEEWGK	IKECP	3	C15:+57.021	924.764591	2771.270373	0.000451244	11	N	229	253
Q61093	Parental	CVNAR	VGISDRYSIALSDIGDNENEEYLNFAR	EKIKN	3		1020.82354	3059.44722	0.000451244	11	N	130	157
Q61093	Parental	GISDR	YSIALSDIGDNENEEYLNFAR	EKIKN	2		1217.064398	2432.113196	0.000451244	39	N	136	157
Q61093	Parental	SIHIR	IVGDWTEGLFNACGCDKQEFQDAWK	LPKIA	3	C13:+57.021,C15:+57.021	992.10955	2973.30525	0.000451244	26	N	356	381
Q61093	Parental	EFKTI	ASEHPNTTIGVFLCGPEALAETLSK	QSISN	3	C14:+57.021	881.4429006	2641.305302	0.000451244	15	N	523	548
Q61093	Parental	PKVSK	LEWHPFTLTSAPEEDFFSIHIR	IVGDW	3		891.443495	2671.307085	0.000451244	2	N	334	356
Q61093	Parental	PKVSK	LEWHPFTLTSAPEEDFFSIHIR	IVGDW	4		668.8345713	2671.307085	0.000451244	21	N	334	356
Q61093	Parental	DNEFK	TIASEHPNTTIGVFLCGPEALAETLSK	QSISN	2	C16:+57.021	1428.726322	2855.437045	0.000451244	38	N	521	548
Q61093	Parental	DNEFK	TIASEHPNTTIGVFLCGPEALAETLSK	QSISN	3	C16:+57.021	952.8201482	2855.437045	0.000451244	86	N	521	548
Q61093	Parental	DNEFK	TIASEHPNTTIGVFLCGPEALAETLSK	QSISN	4	C16:+57.021	714.8670611	2855.437045	0.000622848	2	N	521	548
Q61093	Parental	QMQER	NNANFLSYNIYLTGWDESQANHFAVHHDEEKDVITGLK	QKTLY	4		1098.275969	4389.072676	0.000622848	6	N	468	506
Q61093	Parental	SYNIY	LTGWDESQANHFAVHHDEEKDVITGLK	QKTLY	3		1026.164008	3075.468624	0.000451244	10	N	479	506
Q61093	Parental	SYNIY	LTGWDESQANHFAVHHDEEKDVITGLK	QKTLY	4		769.8749561	3075.468624	0.000823681	1	N	479	506
Q61093	Parental	ESGPR	GVHFIFNKENF	-	2		676.3438336	1350.672067	0.002374549	1	N	559	570
Q61093	Parental	GLKQK	TLYGRPNWDNEFK	TIASE	2		820.3973259	1638.779052	0.000451244	3	N	508	521
Q61093	Parental	TTIGV	FLCGPEALAETLSK	QSISN	2	C3:+57.021	768.392632	1534.769664	0.000637154	2	N	534	548
Q61093	Parental	SIHIR	IVGDWTEGLFNACGCDK	QEFQD	2	C13:+57.021,C15:+57.021	971.4271772	1940.838754	0.000451244	6	N	356	373
Q61093	Parental	FKTIA	SEHPNTTIGVFLCGPEALAETLSK	QSISN	3	C13:+57.021	857.7638627	2570.268188	0.000823681	3	N	524	548
Q61093	Parental	NFLSY	NIYLTGWDESQANHFAVHHDEEK	DVITG	3		914.084918	2739.231354	0.001162105	1	N	476	499
Q61093	Parental	YSIAL	SDIGDNENEEYLNFAR	EKIKN	2		943.4140983	1884.812597	0.000622848	1	N	141	157
Q61093	Parental	QMQER	NNANFLSYNIYLTGWDESQANHFAVHHDEEK	DVITG	3		1221.889495	3662.645086	0.000979378	1	N	468	499
Q61096	Exosome	LQLSR	FPGSHFCGGTLIHPR	FVLTA	2	C7:+57.021	841.9149315	1681.814263	0.000451244	1	N	51	66
Q61096	Exosome	LQLSR	FPGSHFCGGTLIHPR	FVLTA	3	C7:+57.021	561.6125544	1681.814263	0.000451244	4	N	51	66
Q61096	Exosome	LQLSR	FPGSHFCGGTLIHPR	FVLTA	4	C7:+57.021	421.4613658	1681.814263	0.000451244	21	N	51	66
Q61096	Exosome	ASLGK	EVAVASLPQQDQTLSQGTQCLAMGWGR	LGTQA	3	C20:+57.021	977.8081371	2930.401011	0.000451244	3	N	134	161
Q61096	Exosome	TLVPR	RAAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	4	C6:+57.021,C16:+57.021	765.3894878	3057.526751	0.000451244	14	N	195	224
Q61096	Exosome	SFVIR	ECASLQFPDFFAR	VSMYV	2	C2:+57.021	794.3669485	1586.718297	0.000451244	35	N	224	237
Q61096	Exosome	DFFAR	VSMYVDWIQNVLR	GAEP-	2	M3:+15.995	819.9196228	1637.823646	0.000451244	38	N	237	250
Q61096	Exosome	RRAAG	ICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C2:+57.021,C12:+57.021	901.7844495	2702.329948	0.000451244	26	N	199	224
Q61096	Exosome	PRRAA	GICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C3:+57.021,C13:+57.021	1380.683506	2759.351412	0.001329271	3	N	198	224
Q61096	Exosome	PRRAA	GICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C3:+57.021,C13:+57.021	920.7916041	2759.351412	0.000451244	51	N	198	224
Q61096	Exosome	LVPRR	AAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C5:+57.021,C15:+57.021	968.14968	2901.42564	0.000451244	57	N	196	224
Q61096	Exosome	LTAAH	CLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C1:+39.994	1059.53615	3175.585049	0.000451244	2	N	73	101
Q61096	Exosome	LTAAH	CLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C1:+57.021	1065.211816	3192.612049	0.000823681	1	N	73	101
Q61096	Exosome	LIHPR	FVLTAAHCLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C8:+57.021	1311.679053	3932.013759	0.000451244	15	N	66	101
Q61096	Exosome	LIHPR	FVLTAAHCLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	4	C8:+57.021	984.0112398	3932.013759	0.000451244	31	N	66	101
Q61096	Exosome	TFLCR	EHNVCTLVPR	RAAGI	2	C5:+57.021	612.811612	1223.607624	0.0025889	1	N	185	195
Q61096	Parental	LQLSR	FPGSHFCGGTLIHPR	FVLTA	2	C7:+57.021	841.9149315	1681.814263	0.000451244	6	N	51	66
Q61096	Parental	LQLSR	FPGSHFCGGTLIHPR	FVLTA	3	C7:+57.021	561.6125544	1681.814263	0.000451244	26	N	51	66
Q61096	Parental	LQLSR	FPGSHFCGGTLIHPR	FVLTA	4	C7:+57.021	421.4613658	1681.814263	0.000451244	49	N	51	66
Q61096	Parental	EVAVA	SLPQQDQTLSQGTQCLAMGWGR	LGTQA	2	C15:+57.021	1231.581481	2461.147362	0.000451244	7	N	139	161
Q61096	Parental	LQLNR	TASLGKEVAVASLPQQDQTLSQGTQCLAMGWGR	LGTQA	3	C26:+57.021	1163.580574	3487.718323	0.000451244	17	N	128	161
Q61096	Parental	ASLGK	EVAVASLPQQDQTLSQGTQCLAMGWGR	LGTQA	2	C20:+57.021	1466.208306	2930.401011	0.000451244	20	N	134	161
Q61096	Parental	ASLGK	EVAVASLPQQDQTLSQGTQCLAMGWGR	LGTQA	3	C20:+57.021	977.8081371	2930.401011	0.000451244	20	N	134	161
Q61096	Parental	IRECA	SLQFPDFFAR	VSMYV	2		614.3120021	1226.608404	0.001352548	4	N	227	237
Q61096	Parental	TLVPR	RAAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C6:+57.021,C16:+57.021	1020.183384	3057.526751	0.000451244	11	N	195	224
Q61096	Parental	TLVPR	RAAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	4	C6:+57.021,C16:+57.021	765.3894878	3057.526751	0.000451244	37	N	195	224
Q61096	Parental	SFVIR	ECASLQFPDFFAR	VSMYV	2	C2:+57.021	794.3669485	1586.718297	0.000451244	39	N	224	237

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61096	Parental	SFVIR	ECASLQFPDFFAR	VSMYV	3	C2:+57.021	529.913899	1586.718297	0.001352548	9	N	224	237
Q61096	Parental	DFFAR	VSMYVDWIQNVLR	GAEP-	2		811.9221228	1621.828646	0.000451244	7	N	237	250
Q61096	Parental	DFFAR	VSMYVDWIQNVLR	GAEP-	2	M3:+15.995	819.9196228	1637.823646	0.000451244	30	N	237	250
Q61096	Parental	RRAAG	ICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C2:+57.021,C12:+57.021	1352.172774	2702.329948	0.000451244	2	N	199	224
Q61096	Parental	RRAAG	ICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C2:+57.021,C12:+57.021	901.7844495	2702.329948	0.000451244	61	N	199	224
Q61096	Parental	PRRAA	GICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C3:+57.021,C13:+57.021	1380.683506	2759.351412	0.000451244	56	N	198	224
Q61096	Parental	PRRAA	GICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C3:+57.021,C13:+57.021	920.7916041	2759.351412	0.000451244	332	N	198	224
Q61096	Parental	LVPRR	AAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C5:+57.021,C15:+57.021	1451.72062	2901.42564	0.000451244	11	N	196	224
Q61096	Parental	LVPRR	AAGICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C5:+57.021,C15:+57.021	968.14968	2901.42564	0.000451244	73	N	196	224
Q61096	Parental	VPRRA	AGICFGDSGGPLICNGILHGVDSFVIR	ECASL	2	C4:+57.021,C14:+57.021	1416.202063	2830.388526	0.000451244	8	N	197	224
Q61096	Parental	VPRRA	AGICFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C4:+57.021,C14:+57.021	944.470642	2830.388526	0.000451244	72	N	197	224
Q61096	Parental	DFFAR	VSMYVDWIQNVLRG	AEP-	3	M3:+15.995	565.9561698	1694.845109	0.001763695	3	N	237	251
Q61096	Parental	LTAAH	CLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C1:+39.994	1059.53615	3175.585049	0.000451244	11	N	73	101
Q61096	Parental	LTAAH	CLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C1:+57.021	1065.211816	3192.612049	0.000451244	33	N	73	101
Q61096	Parental	LTAAH	CLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	4	C1:+57.021	799.1608123	3192.612049	0.000823681	3	N	73	101
Q61096	Parental	LIHPR	FVLTAAHCLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C8:+57.021	1311.679053	3932.013759	0.000451244	39	N	66	101
Q61096	Parental	LIHPR	FVLTAAHCLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	4	C8:+57.021	984.0112398	3932.013759	0.000451244	75	N	66	101
Q61096	Parental	RAAGI	CFGDSGGPLICNGILHGVDSFVIR	ECASL	3	C1:+57.021,C11:+57.021	864.0897615	2589.245884	0.000451244	8	N	200	224
Q61096	Parental	TFLCR	EHNVCTLVPR	RAAGI	2	C5:+57.021	612.811612	1223.607624	0.002813207	1	N	185	195
Q61096	Parental	AGICF	GDSGGPLICNGILHGVDSFVIR	ECASL	2	C9:+57.021	1142.081442	2282.147285	0.000451244	12	N	202	224
Q61096	Parental	AGICF	GDSGGPLICNGILHGVDSFVIR	ECASL	3	C9:+57.021	761.7235616	2282.147285	0.000451244	17	N	202	224
Q61096	Parental	AAHCL	QDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3		974.1737331	2919.497799	0.000451244	17	N	75	101
Q61096	Parental	RECAS	LQFPDFFAR	VSMYV	2		570.7959879	1139.576376	0.0025889	1	N	228	237
Q61096	Parental	GHEAR	PHSRPYVASLQLSR	FPGSH	3		537.6307566	1609.86887	0.002663018	2	N	37	51
Q61096	Parental	LVTVV	LGAHDLLSSEPEQQK	FTISQ	2		826.4184553	1650.821311	0.000451244	6	N	86	101
Q61096	Parental	QLVTV	VLGAHDLLSSEPEQQK	FTISQ	2		875.9526623	1749.889725	0.000451244	3	N	85	101
Q61096	Parental	QLVTV	VLGAHDLLSSEPEQQK	FTISQ	3		584.3043749	1749.889725	0.000451244	2	N	85	101
Q61096	Parental	SWQLV	TVVLGAHDLLSSEPEQQK	FTISQ	2		976.0107086	1950.005817	0.000735798	1	N	83	101
Q61096	Parental	SWQLV	TVVLGAHDLLSSEPEQQK	FTISQ	3		651.0097391	1950.005817	0.000451244	1	N	83	101
Q61096	Parental	ASLGK	EVAVASLPQQDQTLSQGTQCL	AMGWG	2	C20:+57.021	1137.05783	2272.10006	0.000451244	4	N	134	155
Q61096	Parental	RPHSR	PYVASLQLSR	FPGSH	2		567.3198272	1132.624054	0.00091018	4	N	41	51
Q61096	Parental	GGPLI	CNGILHGVDSFVIR	ECASL	2	C1:+57.021	793.9093149	1585.80303	0.002296037	1	N	210	224
Q61096	Parental	VLTAA	HCLQDISWQLVTVVLGAHDLLSSEPEQQK	FTISQ	3	C2:+57.021	1110.89812	3329.670961	0.002813207	1	N	72	101
Q61103	Exosome	RARKR	IIEPDDFLDDLDDEDYEEDTPK	RRGKG	2		1321.064123	2640.112646	0.000823681	2	N	156	178
Q61103	Parental	KINKK	TGQPEELVSCSDCGR	SGHPS	2	C10:+57.021,C13:+57.021	847.8591274	1693.702655	0.000451244	4	N	285	300
Q61103	Parental	RARKR	IIEPDDFLDDLDDEDYEEDTPK	RRGKG	2		1321.064123	2640.112646	0.000451244	23	N	156	178
Q61103	Parental	APDPR	VDDDSLGEFPVSNSR	ARKRI	2		818.8766203	1635.737641	0.002519933	1	N	137	152
Q61147	Exosome	GTFSK	TIDKPAWLGFLGPVIK	AEVED	3		585.6788249	1754.013075	0.000637154	19	N	82	98
Q61147	Exosome	HVAPK	ETFTYEWTVPK	EMGPT	2		700.8407895	1399.665979	0.002374549	1	N	507	518
Q61147	Exosome	DDNIR	MFTTAPDQVDKEDEDFQESNK	MHSMN	3	M1:+15.995	830.6925041	2489.054112	0.000451244	12	N	593	614
Q61147	Exosome	AHGVK	TESSTVVPTLPGEVR	TYTWQ	2		786.417924	1570.820248	0.000451244	9	N	835	850
Q61147	Exosome	LNHLK	AGLQAFFQVR	DCNKP	2		568.814712	1135.613824	0.000622848	9	N	344	354
Q61147	Exosome	VDAPK	DIASGLIGPLILCK	KGSLY	2	C13:+57.021	735.4237351	1468.83187	0.000451244	14	N	186	200
Q61147	Exosome	VDAPK	DIASGLIGPLILCK	KGSLY	3	C13:+57.021	490.6184234	1468.83187	0.000451244	1	N	186	200
Q61147	Exosome	VDRVK	DLYSGLIGPLIVCR	KSYVK	2	C13:+57.021	788.4320915	1574.848583	0.000451244	17	N	882	896
Q61147	Exosome	TDFQR	ADDKVLPGQQYVYVLHANEPSPGEGDSNCVTR	IYHSH	3	C29:+57.021	1172.555082	3514.641846	0.000698008	2	N	144	176
Q61147	Exosome	NQCQR	QFEDFTVYLGER	TYYVA	2		752.3598777	1502.704155	0.002296037	1	N	715	727
Q61147	Exosome	DGRQK	DVDKEFYLFPTVFDENESLLLDDNIR	MFTTA	3		1049.512192	3145.513175	0.000622848	12	N	567	593
Q61147	Exosome	GPVIK	AEVEDKVYVHLK	NLASR	3		477.2615588	1428.761276	0.000451244	1	N	98	110
Q61152	Parental	TTALR	RVPADQNSSGPDAYEEVTDGAQTGGLGFNLR	IGRPK	3		1074.508503	3220.50211	0.000451244	29	N	405	436
Q61152	Parental	GPGPR	APTSTDTPIYSQVAPR	AQRPV	2		852.4341054	1702.852611	0.000451244	20	N	371	387
Q61166	Exosome	FGKLR	NIELICQENEGENDPVLQR	IVDIL	2	C6:+57.021	1135.539804	2269.064009	0.000451244	22	N	222	241
Q61166	Exosome	DKLVK	GKFQDNFEFVQWFK	KFFDA	3		607.2987841	1818.872952	0.000823681	4	N	98	112
Q61166	Exosome	LVKGK	FQDNFEFVQWFK	KFFDA	2		817.8860627	1633.756525	0.001162105	3	N	100	112
Q61166	Parental	FGKLR	NIELICQENEGENDPVLQR	IVDIL	2	C6:+57.021	1135.539804	2269.064009	0.000451244	45	N	222	241
Q61166	Parental	FGKLR	NIELICQENEGENDPVLQR	IVDIL	3	C6:+57.021	757.3624696	2269.064009	0.000870037	2	N	222	241
Q61166	Parental	PVAAR	QGQETAVAPSLVAPALSKPK	KPLGS	2		996.5603687	1991.105137	0.000451244	9	N	130	150
Q61166	Parental	LVKGK	FQDNFEFVQWFK	KFFDA	2		817.8860627	1633.756525	0.000622848	2	N	100	112
Q61166	Parental	QWFKK	FFDANYDGKEYDPVAAR	QGQET	2		989.4530265	1976.890453	0.002019181	1	N	113	130
Q61166	Parental	PVLQR	IVDILYATDEGFVIPDEGGPQEEQEEY	-	3		1019.13679	3054.386971	0.000622848	3	N	241	268
Q61171	Exosome	ADVTK	SLSQNYGVLKNDEGIAYR	GLFII	3		676.3451217	2026.011965	0.000451244	3	N	109	127
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSK	HN-	4	C15:+57.021	1111.527717	4442.079667	0.000451244	30	N	157	196
Q61171	Exosome	AQIGK	SAPDFTATAVVDGAFKEIK	LSDYR	2		984.0101773	1966.004755	0.000451244	17	N	10	29
Q61171	Exosome	AEDFR	KLGCEVLGVSVDSQFTHLAWINTPR	KEGGL	3	C4:+57.021	943.1572061	2826.448218	0.000451244	9	N	66	91
Q61171	Exosome	AEDFR	KLGCEVLGVSVDSQFTHLAWINTPR	KEGGL	4	C4:+57.021	707.6198546	2826.448218	0.000451244	13	N	66	91

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61171	Exosome	EDFRK	LGCEVLGVSVDSQFTHLAWINTPR	KEGGL	2	C3:+57.021	1350.184428	2698.353255	0.000979378	1	N	67	91
Q61171	Exosome	EDFRK	LGCEVLGVSVDSQFTHLAWINTPR	KEGGL	3	C3:+57.021	900.458885	2698.353255	0.000451244	144	N	67	91
Q61171	Exosome	YVVLF	FYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C10:+57.021	1013.14111	3036.399931	0.000622848	5	N	41	66
Q61171	Exosome	DYRGK	YVVLFFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C15:+57.021	1220.258655	3657.752565	0.000451244	18	N	36	66
Q61171	Exosome	ADVTK	SLSQNYGVLK	NDEGI	2		554.8040099	1107.59242	0.000451244	6	N	109	119
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSK	EYFSK	4	C15:+57.021	947.9523849	3787.77834	0.002080925	1	N	157	191
Q61171	Exosome	INTPR	KEGGLGPLNIPLLADVTK	SLSQN	2		918.0359981	1834.056396	0.000451244	16	N	91	109
Q61171	Exosome	INTPR	KEGGLGPLNIPLLADVTK	SLSQN	3		612.3599321	1834.056396	0.000451244	35	N	91	109
Q61171	Exosome	NTPRK	EGGLGPLNIPLLADVTK	SLSQN	2		853.9885165	1705.961433	0.000451244	20	N	92	109
Q61171	Exosome	YVVLF	FYPLDFTFVCPTEIIAFSDHAEDFRK	LGCEV	4	C10:+57.021	792.1315235	3164.494894	0.000622848	5	N	41	67
Q61171	Exosome	KGVLR	QITVNDLPVGR	SVDEA	2		606.3412909	1210.666982	0.000451244	20	N	139	150
Q61171	Exosome	AQIGK	SAPDFTATAVVDGAFK	EIKLS	2		798.8993671	1595.783134	0.000451244	6	N	10	26
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYF	SKHN-	3	C15:+57.021	1409.992025	4226.952675	0.000451244	9	N	157	194
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYF	SKHN-	4	C15:+57.021	1057.745969	4226.952675	0.000451244	6	N	157	194
Q61171	Exosome	DYRGK	YVVLFFYPLDFTFVCPTEIIAFSDHAEDFRK	LGCEV	3	C15:+57.021	1262.956976	3785.847529	0.001591523	2	N	36	67
Q61171	Exosome	DYRGK	YVVLFFYPLDFTFVCPTEIIAFSDHAEDFRK	LGCEV	4	C15:+57.021	947.4696821	3785.847529	0.000823681	3	N	36	67
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDS	KEYFS	3	C15:+57.021	1220.902259	3659.683376	0.000451244	1	N	157	190
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDS	KEYFS	4	C15:+57.021	915.9286441	3659.683376	0.000823681	1	N	157	190
Q61171	Exosome	LSDYR	GKYVVLFFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C17:+57.021	1281.964131	3842.868992	0.000451244	5	N	34	66
Q61171	Exosome	LSDYR	GKYVVLFFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	4	C17:+57.021	961.7250481	3842.868992	0.001162105	2	N	34	66
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEY	FSKHN	3	C15:+57.021	1360.96922	4079.884261	0.000451244	5	N	157	193
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEY	FSKHN	4	C15:+57.021	1020.978865	4079.884261	0.001654178	3	N	157	193
Q61171	Exosome	KYVVL	FFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C11:+57.021	1062.163915	3183.468345	0.001162105	1	N	40	66
Q61171	Exosome	DEALR	LVQAFQYTDEHGEVCPA	GWKPG	2	C15:+57.021	982.4466555	1962.877711	0.002981883	1	N	157	174
Q61171	Exosome	FFYPL	DFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C6:+57.021	839.7182533	2516.13136	0.001839721	1	N	45	66
Q61171	Parental	ADVTK	SLSQNYGVLKNDEGIAYR	GLFII	2		1014.013783	2026.011965	0.001162105	3	N	109	127
Q61171	Parental	ADVTK	SLSQNYGVLKNDEGIAYR	GLFII	3		676.3451217	2026.011965	0.000451244	5	N	109	127
Q61171	Parental	DEALR	LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSK	HN-	4	C15:+57.021	1111.527717	4442.079667	0.000451244	26	N	157	196
Q61171	Parental	AQIGK	SAPDFTATAVVDGAFKEIK	LSDYR	2		984.0101773	1966.004755	0.000451244	3	N	10	29
Q61171	Parental	AEDFR	KLGCEVLGVSVDSQFTHLAWINTPR	KEGGL	3	C4:+57.021	943.1572061	2826.448218	0.000622848	1	N	66	91
Q61171	Parental	AEDFR	KLGCEVLGVSVDSQFTHLAWINTPR	KEGGL	4	C4:+57.021	707.6198546	2826.448218	0.000998612	2	N	66	91
Q61171	Parental	EDFRK	LGCEVLGVSVDSQFTHLAWINTPR	KEGGL	3	C3:+57.021	900.458885	2698.353255	0.000451244	29	N	67	91
Q61171	Parental	YVVLF	FYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C10:+57.021	1013.14111	3036.399931	0.000823681	4	N	41	66
Q61171	Parental	DYRGK	YVVLFFYPLDFTFVCPTEIIAFSDHAEDFR	KLGCE	3	C15:+57.021	1220.258655	3657.752565	0.002145581	2	N	36	66
Q61171	Parental	NTPRK	EGGLGPLNIPLLADVTK	SLSQN	2		853.9885165	1705.961433	0.000622848	5	N	92	109
Q61171	Parental	KGVLR	QITVNDLPVGR	SVDEA	2		606.3412909	1210.666982	0.001591523	1	N	139	150
Q61171	Parental	AQIGK	SAPDFTATAVVDGAFK	EIKLS	2		798.8993671	1595.783134	0.000451244	4	N	10	26
Q61176	Exosome	EYDVR	DHGDLAFVDVPNDSSFQIVK	NPRSV	2		1102.037455	2202.059309	0.000451244	6	N	48	68
Q61176	Exosome	EYDVR	DHGDLAFVDVPNDSSFQIVK	NPRSV	3		735.0275698	2202.059309	0.001329271	1	N	48	68
Q61176	Exosome	AEEVK	STVNTAVALTLACFGTQR	EGNHK	2	C13:+57.021	955.4939401	1908.97228	0.000451244	4	N	290	308
Q61176	Exosome	AEEVK	STVNTAVALTLACFGTQR	EGNHK	3	C13:+57.021	637.3318934	1908.97228	0.000622848	3	N	290	308
Q61176	Exosome	LGRKK	RPIHLSFDVDGLDPAFTPATGTPVLGGLSYR	EGLYI	4		818.179815	3268.68806	0.001699387	1	N	224	255
Q61176	Exosome	LKELK	GKFPDVPGFSWVTPCISAK	DIVYI	3	C15:+57.021	698.356039	2092.044717	0.000451244	3	N	153	172
Q61176	Exosome	RPIHL	SFDVDGLDPAFTPATGTPVLGGLSYR	EGLYI	2		1327.161372	2652.307145	0.000451244	1	N	229	255
Q61176	Parental	EYDVR	DHGDLAFVDVPNDSSFQIVK	NPRSV	2		1102.037455	2202.059309	0.000451244	2	N	48	68
Q61176	Parental	AEEVK	STVNTAVALTLACFGTQR	EGNHK	2	C13:+57.021	955.4939401	1908.97228	0.000451244	3	N	290	308
Q61176	Parental	SSKPK	SLEIIGAPFSK	GQPRG	2		581.3298606	1160.644121	0.000823681	2	N	6	17
Q61176	Parental	SGHAR	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVSFLLK	ELKGK	4	C6:+57.021	1021.275968	4081.072671	0.001591523	1	N	113	150
Q61176	Parental	RSVGK	ANEELAGVVAEVQK	NGRVS	2		728.8862597	1455.756919	0.000698008	2	N	75	89
Q61191	Exosome	LAFMR	VYCGPSPSCLVQSSSLSNAHIDYTTKPAIIFR	IAARN	4	C3:+57.021,C9:+57.021	892.9448242	3567.748097	0.000823681	3	N	1960	1992
Q61191	Exosome	MSGCR	LGDLWTLDIETLTWNKPSLSGVAPLPR	SLHSA	3		998.2101186	2991.606956	0.000451244	19	N	228	255
Q61191	Exosome	APVKK	ENQWFDVGVIK	GTSVM	2		667.8411238	1333.666648	0.000622848	2	N	1818	1829
Q61191	Parental	LAFMR	VYCGPSPSCLVQSSSLSNAHIDYTTKPAIIFR	IAARN	4	C3:+57.021,C9:+57.021	892.9448242	3567.748097	0.001162105	3	N	1960	1992
Q61191	Parental	MSGCR	LGDLWTLDIETLTWNKPSLSGVAPLPR	SLHSA	3		998.2101186	2991.606956	0.000451244	15	N	228	255
Q61191	Parental	LIVVF	GGGNEGIVDELHVYNTATNQWFIPAVR	GDIPP	3		986.4900556	2956.446767	0.000451244	8	N	48	75
Q61206	Exosome	YEIWR	ELFSPLHALNFGIGGDTTR	HVLWR	3		682.3537287	2044.037786	0.000451244	12	N	60	79
Q61206	Parental	NIKPK	VIVVWVGTNNHENTAEEVAGGIEAIVQLINTR	QPQAK	3		1149.27451	3444.80013	0.002080925	1	N	96	128
Q61206	Parental	YEIWR	ELFSPLHALNFGIGGDTTR	HVLWR	2		1023.026693	2044.037786	0.000451244	1	N	60	79
Q61206	Parental	YEIWR	ELFSPLHALNFGIGGDTTR	HVLWR	3		682.3537287	2044.037786	0.000451244	7	N	60	79
Q61207	Exosome	HYLEK	TCEWIHDSSLSASCK	EVVDS	3	C2:+57.021,C14:+57.021	594.2593634	1779.75469	0.000622848	2	N	92	107
Q61207	Exosome	DPYQK	QCDDFVAEYEPLLLEILVEVMDPGFVCSK	IGVCP	3	C2:+57.021,M21:+15.995,C27:+57.021	1144.541609	3430.601427	0.000823681	3	N	482	511
Q61207	Exosome	AALEK	GCSFLPDPYQK	QCDDF	2	C2:+57.021	656.3058282	1310.596056	0.000622848	3	N	471	482
Q61207	Exosome	SASCK	EVVDSYLPVILDMIK	GEMSN	2		867.4738539	1732.932108	0.000823681	4	N	107	122
Q61207	Exosome	SASCK	EVVDSYLPVILDMIK	GEMSN	2	M13:+15.995	875.4713539	1748.927108	0.000451244	24	N	107	122

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61207	Exosome	SASCK	EVVDSYLPVILDMIK	GEMSN	3	M13:+15.995	583.9835026	1748.927108	0.000451244	9	N	107	122
Q61207	Exosome	SASCK	EVVDSYLPVILDMIKGEMSNPGEVCSALNLCQS	LQEYL	3	M13:+15.995,M18:+15.995,C25:+57.021,C31:+57.021	1233.913806	3698.718017	0.001943752	2	N	107	140
Q61207	Parental	HYLEK	TCEWIHDSSLSASCK	EVVDS	3	C2:+57.021,C14:+57.021	594.2593634	1779.75469	0.000451244	29	N	92	107
Q61207	Parental	DQQPK	EICVLAGFCNE	VKRVP	2	C3:+57.021,C9:+57.021	656.2890895	1310.562579	0.000823681	11	N	264	275
Q61207	Parental	DQQPK	EICVLAGFCNEV	KRVPM	2	C3:+57.021,C9:+57.021	705.8232965	1409.630993	0.000698008	10	N	264	276
Q61207	Parental	CDICK	TVVTEAGNLLK	DNATQ	2		572.8327674	1143.649935	0.000451244	7	N	67	78
Q61207	Parental	DPYQK	QCDDFVAEYEPLLLEILVEVMDPGFVCSK	IGVCP	3	C2:+57.021,C27:+57.021	1139.209942	3414.606427	0.000451244	9	N	482	511
Q61207	Parental	DPYQK	QCDDFVAEYEPLLLEILVEVMDPGFVCSK	IGVCP	3	C2:+57.021,M21:+15.995,C27:+57.021	1144.541609	3430.601427	0.001162105	2	N	482	511
Q61207	Parental	HYLEK	TCEWIHDSSLSASCKEVVDSYLPVILDMIK	GEMSN	3	C2:+57.021,C14:+57.021	1165.899879	3494.676238	0.001839721	1	N	92	122
Q61207	Parental	AALEK	GCSFLPDPYQK	QCDDF	2	C2:+57.021	656.3058282	1310.596056	0.001264573	14	N	471	482
Q61207	Parental	SASCK	EVVDSYLPVILDMIK	GEMSN	2		867.4738539	1732.932108	0.001329271	2	N	107	122
Q61207	Parental	SASCK	EVVDSYLPVILDMIK	GEMSN	3		578.6518359	1732.932108	0.000451244	2	N	107	122
Q61207	Parental	SASCK	EVVDSYLPVILDMIK	GEMSN	2	M13:+15.995	875.4713539	1748.927108	0.000451244	13	N	107	122
Q61207	Parental	SASCK	EVVDSYLPVILDMIK	GEMSN	3	M13:+15.995	583.9835026	1748.927108	0.001839721	1	N	107	122
Q61210-5	Exosome	DVQRR	FIQEVVQSQQAAVSR	QLEDF	2		845.4500898	1688.88458	0.000451244	6	N	135	150
Q61210-5	Exosome	RLMKR	RQESGYLIEEIGDVLLAR	FDGAE	3		687.7045385	2060.090216	0.001229886	4	N	539	557
Q61210-5	Exosome	HVAER	LLSHLEETQHTISTDEEK	SAAVV	3		704.0153299	2109.02259	0.000451244	2	N	194	212
Q61210-5	Exosome	EEFCR	LRPLLSQLGGTLSPNLAAPER	SAQTG	3		735.0906159	2202.248448	0.000823681	1	N	951	972
Q61210-5	Exosome	VLSLK	QILLSTEEDSGAGPPR	DGDGV	2		835.4237377	1668.831875	0.000451244	3	N	893	909
Q61210-5	Exosome	QRLTK	YPLLLQSIGQNTEESTER	GKVEL	2		1039.52418	2077.03276	0.000451244	3	N	625	643
Q61210-5	Exosome	PKEAK	KAFLDFYHSFLEK	TAVLR	3		548.9527252	1643.834776	0.000451244	1	N	91	104
Q61210-5	Exosome	TDSVD	SREPGVDTPQEPGDTPPQGPTSLEPLAPPESTEDNGETER	RWKRL	3		1405.314704	4212.920712	0.001463592	1	N	332	372
Q61210-5	Exosome	LMKRR	QESGYLIEEIGDVLLAR	FDGAE	2		953.0023522	1903.989104	0.000451244	1	N	540	557
Q61210-5	Exosome	LMKRR	QESGYLIEEIGDVLLAR	FDGAE	3		635.6708348	1903.989104	0.002212458	1	N	540	557
Q61210-5	Parental	VLSLK	QILLSTEEDSGAGPPRDGDGVPGGR	APGPV	3		827.4057686	2479.193906	0.000451244	7	N	893	918
Q61210-5	Parental	DVQRR	FIQEVVQSQQAAVSR	QLEDF	2		845.4500898	1688.88458	0.000451244	24	N	135	150
Q61210-5	Parental	RLMKR	RQESGYLIEEIGDVLLAR	FDGAE	3		687.7045385	2060.090216	0.001162105	3	N	539	557
Q61210-5	Parental	PGPPR	SGLVSIIIGAEDEDFENELEANSEDQNSQFQSLEQVKR	RPAHL	3		1423.342482	4267.004047	0.000451244	30	N	14	52
Q61210-5	Parental	PGPPR	SGLVSIIIGAEDEDFENELEANSEDQNSQFQSLEQVKR	RPAHL	4		1067.758812	4267.004047	0.000451244	4	N	14	52
Q61210-5	Parental	PGPPR	SGLVSIIIGAEDEDFENELEANSEDQNSQFQSLEQVK	RRPAH	3		1371.308779	4110.902936	0.000451244	35	N	14	51
Q61210-5	Parental	HVAER	LLSHLEETQHTISTDEEK	SAAVV	2		1055.519095	2109.02259	0.000622848	4	N	194	212
Q61210-5	Parental	HVAER	LLSHLEETQHTISTDEEK	SAAVV	3		704.0153299	2109.02259	0.000451244	26	N	194	212
Q61210-5	Parental	EEFCR	LRPLLSQLGGTLSPNLAAPER	SAQTG	3		735.0906159	2202.248448	0.002374549	1	N	951	972
Q61210-5	Parental	ARTER	LLNDLLPFCRPGPEGQLAATALQK	VLSLK	2	C9:+57.021	1311.707539	2621.399477	0.002663018	1	N	864	888
Q61210-5	Parental	ARTER	LLNDLLPFCRPGPEGQLAATALQK	VLSLK	3	C9:+57.021	874.8076257	2621.399477	0.001395409	2	N	864	888
Q61210-5	Parental	VLSLK	QILLSTEEDSGAGPPR	DGDGV	2		835.4237377	1668.831875	0.000451244	7	N	893	909
Q61210-5	Parental	QRLTK	YPLLLQSIGQNTEESTER	GKVEL	2		1039.52418	2077.03276	0.000451244	8	N	625	643
Q61210-5	Parental	VPGGR	APGPVHTQEIEENLLSLEVAIR	QLEEL	3		805.7679786	2414.280536	0.001839721	1	N	918	940
Q61210-5	Parental	PKEAK	KAFLDFYHSFLEK	TAVLR	3		548.9527252	1643.834776	0.000735798	2	N	91	104
Q61210-5	Parental	EVAIR	QLEELEEEFCR	LRPLL	2	C10:+57.021	741.3327713	1480.649943	0.001162105	3	N	940	951
Q61233	Exosome	AGCTK	ITNFSTDIKDSK	AYYHL	2		684.8544282	1367.693256	0.000451244	14	N	285	297
Q61233	Exosome	AGCTK	ITNFSTDIKDSK	AYYHL	3		456.9055521	1367.693256	0.001463592	10	N	285	297
Q61233	Exosome	GGNMK	KLENCNYAVDLGK	NQAKF	2	C5:+57.021	762.3800559	1522.744512	0.000451244	24	N	455	468
Q61233	Exosome	GGNMK	KLENCNYAVDLGK	NQAKF	3	C5:+57.021	508.5893039	1522.744512	0.000451244	22	N	455	468
Q61233	Exosome	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEK	YAFVN	2	C4:+57.021	1385.609341	2769.203081	0.000451244	20	N	97	123
Q61233	Exosome	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEK	YAFVN	3	C4:+57.021	924.0754938	2769.203081	0.000451244	103	N	97	123
Q61233	Exosome	RLGCR	QFVTATDVVR	GNPKL	2		568.3094595	1134.603319	0.000451244	34	N	347	357
Q61233	Exosome	RLGCR	QFVTATDVVR	GNPKL	2	[0:-17.027	559.7959595	1117.576319	0.000451244	16	N	347	357
Q61233	Exosome	IKDSK	AYYHLLEQVAPK	GDEEG	2		716.3856985	1430.755797	0.000451244	32	N	297	309
Q61233	Exosome	IVLCK	MINLSVPDTIDER	TINKK	2		751.8801206	1501.744641	0.000451244	11	N	165	178
Q61233	Exosome	WQLMR	RYTLNILEDIGGGQK	VNDDI	2		838.9524653	1675.889331	0.000451244	28	N	500	515
Q61233	Exosome	WQLMR	RYTLNILEDIGGGQK	VNDDI	3		559.6375769	1675.889331	0.000451244	34	N	500	515
Q61233	Exosome	KIGAR	VYALPEDLVEVNPK	MVMTV	2		793.4277604	1584.839921	0.000451244	40	N	596	610
Q61233	Exosome	KIGAR	VYALPEDLVEVNPK	MVMTV	3		529.2877736	1584.839921	0.000451244	10	N	596	610
Q61233	Exosome	KNQAK	FSLVGIAGQDLNEGNR	TLTLA	2		845.431897	1688.848194	0.000451244	79	N	472	488
Q61233	Exosome	KNQAK	FSLVGIAGQDLNEGNR	TLTLA	3		563.957198	1688.848194	0.000451244	22	N	472	488
Q61233	Exosome	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVNWINK	ALEND	3	C4:+57.021	1302.602649	3904.784547	0.000451244	57	N	97	132
Q61233	Exosome	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVNWINK	ALEND	4	C4:+57.021	977.2039368	3904.784547	0.000451244	80	N	97	132
Q61233	Exosome	MMELR	EAFAKVDTDGNGYISCNELNDLFK	AACLP	2	C16:+57.021	1360.629348	2719.243096	0.000451244	1	N	15	39
Q61233	Exosome	MMELR	EAFAKVDTDGNGYISCNELNDLFK	AACLP	3	C16:+57.021	907.4221652	2719.243096	0.000451244	11	N	15	39
Q61233	Exosome	QLMRR	YTLNILEDIGGGQK	VNDDI	2		760.9019097	1519.788219	0.000451244	27	N	501	515
Q61233	Exosome	EAFAK	VDTDGNGYISCNELNDLFK	AACLP	2	C11:+57.021	1087.489249	2172.962898	0.000451244	144	N	20	39
Q61233	Exosome	EAFAK	VDTDGNGYISCNELNDLFK	AACLP	3	C11:+57.021	725.3287658	2172.962898	0.001591523	1	N	20	39

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61233	Exosome	DPDCR	HVIPMNPNTDDLFNAVGDGIVLCK	MINLS	2	C23:+57.021	1320.151739	2638.287879	0.000622848	13	N	141	165
Q61233	Exosome	DPDCR	HVIPMNPNTDDLFNAVGDGIVLCK	MINLS	3	C23:+57.021	880.4370929	2638.287879	0.000451244	38	N	141	165
Q61233	Exosome	DPDCR	HVIPMNPNTDDLFNAVGDGIVLCK	MINLS	3	M5:+15.995,C23:+57.021	885.7687596	2654.282879	0.000637154	8	N	141	165
Q61233	Exosome	IKDSK	AYYHLLEQVAPKGDEEGIPAVVIDMSGLR	EKDDI	3		1057.545061	3169.611784	0.000451244	25	N	297	326
Q61233	Exosome	IKDSK	AYYHLLEQVAPKGDEEGIPAVVIDMSGLR	EKDDI	4		793.4107461	3169.611784	0.000451244	18	N	297	326
Q61233	Exosome	GGGQK	VNDDIIVNWVNTTLK	EAQKS	2		872.4679482	1742.920296	0.000451244	79	N	515	530
Q61233	Exosome	GGGQK	VNDDIIVNWVNTTLK	EAQKS	3		581.9812322	1742.920296	0.000451244	35	N	515	530
Q61233	Exosome	GGGQK	VNDDIIVNWVNTTLKEAQK	SSSIA	3		734.0589814	2199.153544	0.000451244	11	N	515	534
Q61233	Exosome	RGNPK	LNLAFIANLFNKYPALHKPENQDIDWGALEGETR	EERTF	3		1300.00279	3896.984971	0.000451244	13	N	361	395
Q61233	Exosome	RGNPK	LNLAFIANLFNKYPALHKPENQDIDWGALEGETR	EERTF	4		975.2540427	3896.984971	0.000451244	21	N	361	395
Q61233	Exosome	RGNPK	LNLAFIANLFNK	YPALH	2		689.3986089	1376.781618	0.000451244	77	N	361	373
Q61233	Exosome	RGNPK	LNLAFIANLFNK	YPALH	3		459.9350059	1376.781618	0.000451244	9	N	361	373
Q61233	Exosome	GVNPR	VNHLYSDLSDALVIFQLYEK	IKVPV	2		1184.115705	2366.21581	0.000451244	45	N	412	432
Q61233	Exosome	GVNPR	VNHLYSDLSDALVIFQLYEK	IKVPV	3		789.7464034	2366.21581	0.000451244	111	N	412	432
Q61233	Exosome	AEDLK	EGKPYLVLGLLWQVIK	IGLFA	2		928.5563694	1855.097139	0.000451244	19	N	217	233
Q61233	Exosome	AEDLK	EGKPYLVLGLLWQVIK	IGLFA	3		619.3735129	1855.097139	0.000451244	72	N	217	233
Q61233	Exosome	NEGNR	TLTLALVWQLMR	RYTLN	2		722.9213945	1443.827189	0.000451244	28	Y	488	500
Q61233	Exosome	NEGNR	TLTLALVWQLMR	RYTLN	3		482.2835297	1443.827189	0.000451244	4	Y	488	500
Q61233	Exosome	QLMRR	YTLNILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		1082.573785	3244.697956	0.000451244	77	N	501	530
Q61233	Exosome	INKKK	LTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C22:+57.021	1174.947251	3521.818354	0.000451244	59	N	184	217
Q61233	Exosome	INKKK	LTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	4	C22:+57.021	881.4623884	3521.818354	0.000451244	46	N	184	217
Q61233	Exosome	PKIST	SLPVLDLIDAIQPGSINYDLLK	TENLD	2		1199.167938	2396.320275	0.000451244	4	N	548	570
Q61233	Exosome	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLK	TENLD	2		1349.749823	2697.484047	0.000451244	126	N	545	570
Q61233	Exosome	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLK	TENLD	3		900.1691489	2697.484047	0.000451244	172	N	545	570
Q61233	Exosome	IDAIQ	PGSINYDLLK	TENLD	2		560.3063854	1118.597171	0.000451244	6	N	560	570
Q61233	Exosome	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLKTENLDDEEK	LNNAK	3		1257.986249	3770.935346	0.002727428	1	N	545	579
Q61233	Exosome	TINKK	KLTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C23:+57.021	1217.645572	3649.913317	0.000451244	31	N	183	217
Q61233	Exosome	TINKK	KLTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	4	C23:+57.021	913.4861292	3649.913317	0.000451244	35	N	183	217
Q61233	Exosome	YDLLK	TENLDDEEKLNNAK	YAISM	2		816.8897277	1631.763855	0.000622848	1	N	570	584
Q61233	Exosome	ELLLR	WANYHLENAGCTK	ITNFS	2	C11:+57.021	782.3543724	1562.693145	0.000451244	3	N	272	285
Q61233	Exosome	ELLLR	WANYHLENAGCTK	ITNFS	3	C11:+57.021	521.9055149	1562.693145	0.000451244	8	N	272	285
Q61233	Exosome	NLFNK	YPALHKPENQDIDWGALEGETREER	TFRNW	3		985.1412035	2952.40021	0.000451244	53	N	373	398
Q61233	Exosome	NLFNK	YPALHKPENQDIDWGALEGETREER	TFRNW	4		739.1078526	2952.40021	0.000451244	67	N	373	398
Q61233	Exosome	NLFNK	YPALHKPENQDIDWGALEGETR	EERTF	2		1270.114756	2538.213913	0.000451244	16	N	373	395
Q61233	Exosome	NLFNK	YPALHKPENQDIDWGALEGETR	EERTF	3		847.0791043	2538.213913	0.000451244	42	N	373	395
Q61233	Exosome	SEEEK	YAFVNWINK	ALEND	2		577.8038129	1153.592026	0.000451244	21	N	123	132
Q61233	Exosome	WQVIK	IGLFADIELSR	NEALI	2		617.346042	1232.676484	0.001162105	10	N	233	244
Q61233	Exosome	KLTPF	TIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C18:+57.021	1022.196278	3063.565433	0.000451244	45	N	188	217
Q61233	Exosome	KLTPF	TIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	4	C18:+57.021	766.8991583	3063.565433	0.000451244	21	N	188	217
Q61233	Exosome	AGCTK	ITNFSTDIK	DSKAY	2		519.7774608	1037.539322	0.001162105	3	N	285	294
Q61233	Exosome	GNMKK	LENCNYAVDLGK	NQAKF	2	C4:+57.021	698.3325743	1394.649549	0.000451244	24	N	456	468
Q61233	Exosome	QVAPK	GDEEGIPAVVIDMSGLR	EKDDI	2		879.4410737	1756.866547	0.000451244	16	N	309	326
Q61233	Exosome	WQVIK	IGLFADIELSRNEALIALLR	EGESL	3		743.099	2226.2736	0.000823681	2	N	233	253
Q61233	Exosome	IELSR	NEALIALLR	EGESL	2		506.811638	1011.607676	0.000451244	11	N	244	253
Q61233	Exosome	NDLFK	AACLPLPGYR	VREIT	2	C3:+57.021	559.2950665	1116.574533	0.000451244	7	N	39	49
Q61233	Exosome	ISTSL	PVLDLIDAIQPGSINYDLLK	TENLD	2		1099.109891	2196.204183	0.000451244	3	N	550	570
Q61233	Exosome	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKY	AFVNW	3	C4:+57.021	978.4299367	2932.26641	0.000451244	7	N	97	124
Q61233	Exosome	VNHLY	SDLSDALVIFQLYEK	IKVPV	2		870.956882	1739.898164	0.000451244	2	N	417	432
Q61233	Exosome	VNHLY	SDLSDALVIFQLYEK	IKVPV	3		580.9738547	1739.898164	0.000451244	4	N	417	432
Q61233	Exosome	RYTLN	ILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		918.8277857	2753.459957	0.000451244	15	N	505	530
Q61233	Exosome	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVN	WINKA	3	C4:+57.021	1122.168893	3363.483279	0.000662267	3	N	97	128
Q61233	Exosome	EDLMK	LSPEELLLR	WANYH	2		535.3167532	1068.617906	0.001463592	2	Y	263	272
Q61233	Exosome	PFTIQ	ENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C15:+57.021	908.1328376	2721.375113	0.000451244	5	N	191	217
Q61233	Exosome	INKKK	LTPFTIQENLNLALNSASAIGCHVV	NIGAE	2	C22:+57.021	1341.69991	2681.384221	0.000870037	1	N	184	209
Q61233	Exosome	GVNPR	VNHLYSDLSDALVIFQ	LYEKI	2		917.4732306	1832.930861	0.000451244	4	N	412	428
Q61233	Exosome	GYRVR	EITENLMATGDLDQDGKISFDEFIK	VFHGL	3		943.7886683	2828.342605	0.002019181	1	N	51	76
Q61233	Parental	AGCTK	ITNFSTDIKDSK	AYYHL	2		684.8544282	1367.693256	0.000451244	7	N	285	297
Q61233	Parental	AGCTK	ITNFSTDIKDSK	AYYHL	3		456.9055521	1367.693256	0.001871652	1	N	285	297
Q61233	Parental	GGNMK	KLENCNYAVDLGK	NQAKF	2	C5:+57.021	762.3800559	1522.744512	0.000451244	40	N	455	468
Q61233	Parental	GGNMK	KLENCNYAVDLGK	NQAKF	3	C5:+57.021	508.5893039	1522.744512	0.000622848	8	N	455	468
Q61233	Parental	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEK	YAFVN	2	C4:+57.021	1385.609341	2769.203081	0.000451244	12	N	97	123
Q61233	Parental	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEK	YAFVN	3	C4:+57.021	924.0754938	2769.203081	0.000451244	94	N	97	123
Q61233	Parental	RLGCR	QFVTATDVVR	GNPKL	2		568.3094595	1134.603319	0.000451244	37	N	347	357
Q61233	Parental	RLGCR	QFVTATDVVR	GNPKL	2	[0:-17.027	559.7959595	1117.576319	0.000637154	2	N	347	357
Q61233	Parental	IKDSK	AYYHLLEQVAPK	GDEEG	2		716.3856985	1430.755797	0.000451244	16	N	297	309

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61233	Parental	IKDSK	AYYHLLEQVAPK	GDEEG	3		477.926399	1430.755797	0.000451244	19	N	297	309
Q61233	Parental	IVLCK	MINLSVPDTIDER	TINKK	2		751.8801206	1501.744641	0.000622848	6	N	165	178
Q61233	Parental	WQLMR	RYTLNILEDIGGGQK	VNDDI	2		838.9524653	1675.889331	0.000622848	10	N	500	515
Q61233	Parental	WQLMR	RYTLNILEDIGGGQK	VNDDI	3		559.6375769	1675.889331	0.000451244	23	N	500	515
Q61233	Parental	KIGAR	VYALPEDLVEVNPK	MVMTV	2		793.4277604	1584.839921	0.000451244	39	N	596	610
Q61233	Parental	KIGAR	VYALPEDLVEVNPK	MVMTV	3		529.2877736	1584.839921	0.000622848	2	N	596	610
Q61233	Parental	KNQAK	FSLVGIAGQDLNEGNR	TLTLA	2		845.431897	1688.848194	0.000451244	57	N	472	488
Q61233	Parental	KNQAK	FSLVGIAGQDLNEGNR	TLTLA	3		563.957198	1688.848194	0.000451244	10	N	472	488
Q61233	Parental	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVNWINK	ALEND	3	C4:+57.021	1302.602649	3904.784547	0.000451244	73	N	97	132
Q61233	Parental	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAFVNWINK	ALEND	4	C4:+57.021	977.2039368	3904.784547	0.000451244	94	N	97	132
Q61233	Parental	MMELR	EAFAKVDTDGNGYISCNELNDLFK	AACLP	2	C16:+57.021	1360.629348	2719.243096	0.000451244	14	N	15	39
Q61233	Parental	MMELR	EAFAKVDTDGNGYISCNELNDLFK	AACLP	3	C16:+57.021	907.4221652	2719.243096	0.000451244	17	N	15	39
Q61233	Parental	QLMRR	YTLNILEDIGGGQK	VNDDI	2		760.9019097	1519.788219	0.000451244	17	N	501	515
Q61233	Parental	EAFAK	VDTDGNGYISCNELNDLFK	AACLP	2	C11:+57.021	1087.489249	2172.962898	0.000451244	147	N	20	39
Q61233	Parental	EAFAK	VDTDGNGYISCNELNDLFK	AACLP	3	C11:+57.021	725.3287658	2172.962898	0.000451244	9	N	20	39
Q61233	Parental	DPDCR	HVIPMNPNTDDLFNAVGDGIVLCK	MINLS	2	C23:+57.021	1320.151739	2638.287879	0.000451244	9	N	141	165
Q61233	Parental	DPDCR	HVIPMNPNTDDLFNAVGDGIVLCK	MINLS	3	C23:+57.021	880.4370929	2638.287879	0.000451244	11	N	141	165
Q61233	Parental	IKDSK	AYYHLLEQVAPKGDEEGIPAVVIDMSGLR	EKDDI	3		1057.545061	3169.611784	0.000451244	11	N	297	326
Q61233	Parental	IKDSK	AYYHLLEQVAPKGDEEGIPAVVIDMSGLR	EKDDI	4		793.4107461	3169.611784	0.000451244	9	N	297	326
Q61233	Parental	GGGQK	VNDDIIVNWVNTTLK	EAQKS	2		872.4679482	1742.920296	0.000451244	59	N	515	530
Q61233	Parental	GGGQK	VNDDIIVNWVNTTLK	EAQKS	3		581.9812322	1742.920296	0.000451244	30	N	515	530
Q61233	Parental	GGGQK	VNDDIIVNWVNTTLKEAQK	SSSIA	2		1100.584572	2199.153544	0.000451244	6	N	515	534
Q61233	Parental	GGGQK	VNDDIIVNWVNTTLKEAQK	SSSIA	3		734.0589814	2199.153544	0.000451244	9	N	515	534
Q61233	Parental	RGNPK	LNLAFIANLFNKYPALHKPENQDIDWGALEGETR	EERTF	3		1300.00279	3896.984971	0.000451244	19	N	361	395
Q61233	Parental	RGNPK	LNLAFIANLFNKYPALHKPENQDIDWGALEGETR	EERTF	4		975.2540427	3896.984971	0.000451244	18	N	361	395
Q61233	Parental	RGNPK	LNLAFIANLFNK	YPALH	2		689.3986089	1376.781618	0.000451244	76	N	361	373
Q61233	Parental	RGNPK	LNLAFIANLFNK	YPALH	3		459.9350059	1376.781618	0.000451244	13	N	361	373
Q61233	Parental	GVNPR	VNHLYSDLSDALVIFQLYEK	IKVPV	2		1184.115705	2366.21581	0.000451244	36	N	412	432
Q61233	Parental	GVNPR	VNHLYSDLSDALVIFQLYEK	IKVPV	3		789.7464034	2366.21581	0.000451244	106	N	412	432
Q61233	Parental	AEDLK	EGKPYLVLGLLWQVIK	IGLFA	2		928.5563694	1855.097139	0.000451244	14	N	217	233
Q61233	Parental	AEDLK	EGKPYLVLGLLWQVIK	IGLFA	3		619.3735129	1855.097139	0.000451244	42	N	217	233
Q61233	Parental	LMRRY	TLNILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		1028.219342	3081.634627	0.000451244	42	N	502	530
Q61233	Parental	NEGNR	TLTLALVWQLMR	RYTLN	2		722.9213945	1443.827189	0.000451244	3	Y	488	500
Q61233	Parental	NEGNR	TLTLALVWQLMR	RYTLN	3		482.2835297	1443.827189	0.000451244	3	Y	488	500
Q61233	Parental	QLMRR	YTLNILEDIGGGQKVNDDIIVNWVNTTLK	EAQKS	3		1082.573785	3244.697956	0.000451244	48	N	501	530
Q61233	Parental	INKKK	LTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C22:+57.021	1174.947251	3521.818354	0.000451244	46	N	184	217
Q61233	Parental	INKKK	LTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	4	C22:+57.021	881.4623884	3521.818354	0.000451244	21	N	184	217
Q61233	Parental	PKIST	SLPVLDLIDAIQPGSINYDLLK	TENLD	2		1199.167938	2396.320275	0.000451244	22	N	548	570
Q61233	Parental	PKIST	SLPVLDLIDAIQPGSINYDLLK	TENLD	3		799.7812252	2396.320275	0.000451244	12	N	548	570
Q61233	Parental	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLK	TENLD	2		1349.749823	2697.484047	0.000451244	63	N	545	570
Q61233	Parental	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLK	TENLD	3		900.1691489	2697.484047	0.000451244	272	N	545	570
Q61233	Parental	IDAIQ	PGSINYDLLK	TENLD	2		560.3063854	1118.597171	0.000451244	5	N	560	570
Q61233	Parental	FKDPK	ISTSLPVLDLIDAIQPGSINYDLLKTENLDDEEK	LNNAK	3		1257.986249	3770.935346	0.000823681	7	N	545	579
Q61233	Parental	TSLPV	LDLIDAIQPGSINYDLLK	TENLD	2		1001.049302	2000.083005	0.000451244	7	N	552	570
Q61233	Parental	TINKK	KLTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C23:+57.021	1217.645572	3649.913317	0.000451244	16	N	183	217
Q61233	Parental	TINKK	KLTPFTIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	4	C23:+57.021	913.4861292	3649.913317	0.000451244	28	N	183	217
Q61233	Parental	ELLLR	WANYHLENAGCTK	ITNFS	2	C11:+57.021	782.3543724	1562.693145	0.000451244	6	N	272	285
Q61233	Parental	ELLLR	WANYHLENAGCTK	ITNFS	3	C11:+57.021	521.9055149	1562.693145	0.000622848	4	N	272	285
Q61233	Parental	NLFNK	YPALHKPENQDIDWGALEGETREER	TFRNW	3		985.1412035	2952.40021	0.000451244	38	N	373	398
Q61233	Parental	NLFNK	YPALHKPENQDIDWGALEGETREER	TFRNW	4		739.1078526	2952.40021	0.000451244	23	N	373	398
Q61233	Parental	NLFNK	YPALHKPENQDIDWGALEGETR	EERTF	2		1270.114756	2538.213913	0.000451244	8	N	373	395
Q61233	Parental	NLFNK	YPALHKPENQDIDWGALEGETR	EERTF	3		847.0791043	2538.213913	0.000451244	21	N	373	395
Q61233	Parental	SEEEK	YAFVNWINK	ALEND	2		577.8038129	1153.592026	0.000451244	10	N	123	132
Q61233	Parental	WQVIK	IGLFADIELSR	NEALI	2		617.346042	1232.676484	0.001943752	2	N	233	244
Q61233	Parental	KLTPF	TIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	3	C18:+57.021	1022.196278	3063.565433	0.000451244	53	N	188	217
Q61233	Parental	KLTPF	TIQENLNLALNSASAIGCHVVNIGAEDLK	EGKPY	4	C18:+57.021	766.8991583	3063.565433	0.000451244	5	N	188	217
Q61233	Parental	AGCTK	ITNFSTDIK	DSKAY	2		519.7774608	1037.539322	0.002212458	2	N	285	294
Q61233	Parental	GNMKK	LENCNYAVDLGK	NQAKF	2	C4:+57.021	698.3325743	1394.649549	0.000451244	6	N	456	468
Q61233	Parental	WQVIK	IGLFADIELSRNEALIALLR	EGESL	3		743.099	2226.2736	0.000451244	2	N	233	253
Q61233	Parental	IELSR	NEALIALLR	EGESL	2		506.811638	1011.607676	0.000451244	11	N	244	253
Q61233	Parental	NDLFK	AACLPLPGYR	VREIT	2	C3:+57.021	559.2950665	1116.574533	0.002813207	1	N	39	49
Q61233	Parental	ISTSL	PVLDLIDAIQPGSINYDLLK	TENLD	2		1099.109891	2196.204183	0.000451244	1	N	550	570
Q61233	Parental	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKY	AFVNW	3	C4:+57.021	978.4299367	2932.26641	0.000637154	3	N	97	124
Q61233	Parental	LMRRY	TLNILEDIGGGQK	VNDDI	2		679.3702454	1356.724891	0.000451244	9	N	502	515
Q61233	Parental	VNHLY	SDLSDALVIFQLYEK	IKVPV	2		870.956882	1739.898164	0.000451244	12	N	417	432

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61233	Parental	VNHLY	SDLSDALVIFQLYEK	IKVPV	3		580.9738547	1739.898164	0.000451244	9	N	417	432
Q61233	Parental	NWINK	ALENDPDCRHVIPMNPNTDDLFNAVGDGIVLCK	MINLS	3	C8:+57.021,C32:+57.021	1237.251975	3708.732524	0.001162105	1	N	132	165
Q61233	Parental	GNMKK	LENCNYAVDLGKNQAK	FSLVG	2	C4:+57.021	918.9493654	1835.883131	0.000451244	1	N	456	472
Q61233	Parental	GNMKK	LENCNYAVDLGKNQAK	FSLVG	3	C4:+57.021	612.9688436	1835.883131	0.000622848	1	N	456	472
Q61233	Parental	AINKK	EGICAIGGTSEQSSVGTQHSY	SEEEK	2	C4:+57.021	1084.481955	2166.94831	0.000622848	7	N	97	118
Q61233	Parental	EDLMK	LSPEELLLR	WANYH	2		535.3167532	1068.617906	0.001264573	2	Y	263	272
Q61233	Parental	NQAKF	SLVGIAGQDLNEGNR	TLTLA	2		771.89769	1541.77978	0.000622848	2	N	473	488
Q61233	Parental	AINKK	EGICAIGGTSEQSSVGTQHSYSEEEKYAF	VNWIN	3	C4:+57.021	1051.131779	3150.371938	0.001162105	3	N	97	126
Q61362	Exosome	PTFGK	SFTLASSENQLGAPISGEGLPGR	FTKEA	2		1144.580018	2287.144436	0.000451244	47	N	272	295
Q61362	Exosome	PTFGK	SFTLASSENQLGAPISGEGLPGR	FTKEA	3		763.3892787	2287.144436	0.000451244	31	N	272	295
Q61362	Exosome	APFLR	SYGFDGLDLAWLYPR	LRDKQ	2		886.9362839	1771.856968	0.000451244	21	N	137	152
Q61362	Exosome	APFLR	SYGFDGLDLAWLYPR	LRDKQ	3		591.6267893	1771.856968	0.001763695	1	N	137	152
Q61362	Exosome	GRFTK	EAGTLAYYEICDFLK	GAEVH	2	C11:+57.021	896.927036	1791.838472	0.000451244	18	N	298	313
Q61362	Exosome	GRFTK	EAGTLAYYEICDFLK	GAEVH	3	C11:+57.021	598.2872906	1791.838472	0.000451244	8	N	298	313
Q61362	Exosome	TCQPK	EFFPLTNAIKDALA	-	2		775.4171957	1548.818791	0.000451244	4	N	375	389
Q61362	Exosome	CSAYK	LVCYFTSWSQYR	EGVGS	2	C3:+57.021	805.3773162	1608.739032	0.000451244	17	N	31	43
Q61362	Exosome	TCQPK	EFFPLTNAIK	DALA-	2		590.3245782	1178.633556	0.002212458	5	N	375	385
Q61362	Exosome	PGREK	LLLSAALSAGK	VAIDT	2		522.3271209	1042.638642	0.001763695	1	N	180	191
Q61362	Parental	PTFGK	SFTLASSENQLGAPISGEGLPGRFTK	EAGTL	3		888.792964	2663.355492	0.000451244	2	N	272	298
Q61362	Parental	PTFGK	SFTLASSENQLGAPISGEGLPGR	FTKEA	2		1144.580018	2287.144436	0.000451244	45	N	272	295
Q61362	Parental	PTFGK	SFTLASSENQLGAPISGEGLPGR	FTKEA	3		763.3892787	2287.144436	0.000451244	12	N	272	295
Q61362	Parental	GRFTK	EAGTLAYYEICDFLKGAEVHR	LSNEK	3	C11:+57.021	814.7304933	2441.16808	0.000451244	3	N	298	319
Q61362	Parental	APFLR	SYGFDGLDLAWLYPR	LRDKQ	2		886.9362839	1771.856968	0.000451244	26	N	137	152
Q61362	Parental	APFLR	SYGFDGLDLAWLYPR	LRDKQ	3		591.6267893	1771.856968	0.001654178	1	N	137	152
Q61362	Parental	GRFTK	EAGTLAYYEICDFLK	GAEVH	2	C11:+57.021	896.927036	1791.838472	0.000451244	14	N	298	313
Q61362	Parental	TCQPK	EFFPLTNAIKDALA	-	2		775.4171957	1548.818791	0.002727428	1	N	375	389
Q61362	Parental	CSAYK	LVCYFTSWSQYR	EGVGS	2	C3:+57.021	805.3773162	1608.739032	0.000451244	2	N	31	43
Q61362	Parental	PFATK	GNQWVGYEDKESVK	NKVGF	2		819.8920734	1637.768547	0.000451244	1	N	330	344
Q61362	Parental	TCQPK	EFFPLTNAIK	DALA-	2		590.3245782	1178.633556	0.001352548	3	N	375	385
Q61508	Exosome	NMTIR	CCELPYPEQACCGEEEKLAFIENLCGPR	RNSWK	3	C1:+39.994,C2:+57.021,C11:+57.021,C12:+57.021,C25:+57.021	1138.151491	3411.431073	0.000622848	3	N	467	495
Q61508	Exosome	NMTIR	CCELPYPEQACCGEEEKLAFIENLCGPR	RNSWK	3	C1:+57.021,C2:+57.021,C11:+57.021,C12:+57.021,C25:+57.021	1143.827158	3428.458073	0.000451244	29	N	467	495
Q61508	Exosome	NMTIR	CCELPYPEQACCGEEEKLAFIENLCGPR	RNSWK	3	[0:-17.027,C1:+57.021,C2:+57.021,C11:+57.021,C12:+57.021,C25:+57.02	1138.151491	3411.431073	0.000451244	6	N	467	495
Q61508	Exosome	CLPER	QHVIYGPWNLPQTGYSHLSR	QGETL	3		785.0665818	2352.176345	0.000823681	1	N	204	224
Q61508	Exosome	SHLSR	QGETLNVLETGYSR	CCRCR	2		783.8920734	1565.768547	0.000451244	7	N	224	238
Q61508	Exosome	TNYLR	NVALVAGDTGNATGLGEQGPTR	GTDAN	2		1049.530328	2097.045056	0.000451244	5	N	524	546
Q61508	Exosome	TCTWK	AWEGTLDGYCER	ELAIK	2	C10:+57.021	728.812006	1455.608412	0.000622848	6	N	379	391
Q61508	Exosome	HIEQK	EIDPPAQPQEEIVQK	EVKPH	2		860.9417633	1719.867927	0.000622848	3	N	132	147
Q61508	Parental	NMTIR	CCELPYPEQACCGEEEKLAFIENLCGPR	RNSWK	3	C1:+57.021,C2:+57.021,C11:+57.021,C12:+57.021,C25:+57.021	1143.827158	3428.458073	0.002813207	1	N	467	495
Q61508	Parental	HIEQK	EIDPPAQPQEEIVQK	EVKPH	2		860.9417633	1719.867927	0.001162105	1	N	132	147
Q61508	Parental	NMTIR	CCELPYPEQACCGEEEK	LAFIE	2	C1:+57.021,C2:+57.021,C11:+57.021,C12:+57.021	1079.912454	2157.809308	0.001162105	1	N	467	484
Q61543	Exosome	YRIDR	ALNEACESVIQTACK	HIRSG	2	C6:+57.021,C14:+57.021	847.3978884	1692.780177	0.000451244	14	N	497	512
Q61543	Exosome	DCEHR	LLELQYFISR	DWKLD	2		641.3642347	1280.712869	0.000735798	4	N	541	551
Q61543	Exosome	WCSEK	TETGQELECLQDHLDDLAVECR	DIVGN	3	C9:+57.021,C21:+57.021	877.7271057	2630.157917	0.000451244	5	N	646	668
Q61543	Exosome	ALDYR	LDPQLQLHCSDEIANLCAEEAAAQEQTGQVEECLK	VNLLK	3	C9:+57.021,C17:+57.021,C33:+57.021	1333.278652	3996.812556	0.000451244	10	N	996	1031
Q61543	Exosome	LKESK	ADIFVDPVLHTACALDIK	HHCAA	3	C13:+57.021	666.6840442	1997.028733	0.001699387	3	N	1054	1072
Q61543	Exosome	REVCK	STISEIKECAEEPVGK	GYMVS	3	C9:+57.021	592.9613547	1775.860664	0.001395409	1	N	177	193
Q61543	Parental	YRIDR	ALNEACESVIQTACK	HIRSG	2	C6:+57.021,C14:+57.021	847.3978884	1692.780177	0.000451244	9	N	497	512
Q61543	Parental	DCEHR	LLELQYFISR	DWKLD	2		641.3642347	1280.712869	0.000979378	1	N	541	551
Q61543	Parental	WCSEK	TETGQELECLQDHLDDLAVECR	DIVGN	3	C9:+57.021,C21:+57.021	877.7271057	2630.157917	0.001162105	2	N	646	668
Q61543	Parental	ALDYR	LDPQLQLHCSDEIANLCAEEAAAQEQTGQVEECLK	VNLLK	3	C9:+57.021,C17:+57.021,C33:+57.021	1333.278652	3996.812556	0.000451244	7	N	996	1031
Q61545	Exosome	NVQHR	AGDWQCPNPGCGNQNFAWR	TECNQ	2	C6:+57.021,C11:+57.021	1117.965855	2233.91611	0.000823681	4	N	517	536
Q61545	Exosome	NSAIY	VQGLNDNVTLDDLADFFK	QCGVV	2		1012.502716	2022.989833	0.000451244	1	N	363	381
Q61545	Exosome	PPTAK	AAVEWFDGKDFQGSK	LKVSL	2		842.9024411	1683.789282	0.000451244	2	N	423	438
Q61545	Parental	NVQHR	AGDWQCPNPGCGNQNFAWR	TECNQ	2	C6:+57.021,C11:+57.021	1117.965855	2233.91611	0.000451244	27	N	517	536
Q61545	Parental	NSAIY	VQGLNDNVTLDDLADFFK	QCGVV	2		1012.502716	2022.989833	0.000451244	29	N	363	381
Q61545	Parental	PPTAK	AAVEWFDGKDFQGSK	LKVSL	2		842.9024411	1683.789282	0.000451244	1	N	423	438
Q61545	Parental	TGKPK	GDATVSYEDPPTAK	AAVEW	2		725.8389751	1449.66235	0.000622848	8	N	409	423

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61550	Exosome	RALAK	TGAESISLLELCR	NTNRK	2	C12:+57.021	724.8746064	1447.733613	0.000451244	6	N	577	590
Q61550	Exosome	LVLKK	QQAIELTQEEPYSDIIATPGPR	FHII-	2		1228.61934	2455.223081	0.000451244	5	N	609	631
Q61550	Parental	RALAK	TGAESISLLELCR	NTNRK	2	C12:+57.021	724.8746064	1447.733613	0.000451244	9	N	577	590
Q61550	Parental	DEFLK	EFENPEVPREEQQPQQQQPQPQR	DVIDE	3		949.4537815	2845.337944	0.000451244	12	N	418	441
Q61550	Parental	LVLKK	QQAIELTQEEPYSDIIATPGPR	FHII-	2		1228.61934	2455.223081	0.000451244	1	N	609	631
Q61550	Parental	PEENR	EAAYNAITLPEEFHDFDQPLPDLDDIDVAQQFSLNQSR	VEEIT	3		1454.687813	4361.040039	0.001162105	2	N	101	139
Q61578	Exosome	GESTR	AVPTGDVEDLPCGLLLSSVGYK	SRPID	2	C12:+57.021	1145.585692	2289.155784	0.000823681	4	N	344	366
Q61578	Exosome	LEDLK	AGLLPSGPRPGYVAIQALLSNR	GVRPV	3		750.7626107	2249.264432	0.001395409	1	N	429	451
Q61598	Exosome	LALYR	TDDYLDQPCCETINR	IKLYS	2	C9:+57.021,C10:+57.021	950.396074	1898.776548	0.000451244	73	N	193	208
Q61598	Exosome	LFVPK	DLGTDSQIFISR	AYDAT	2		676.3467703	1350.677941	0.000451244	26	N	390	402
Q61598	Exosome	PIEQK	FVSISDLFVPK	DLGTD	2		626.3533357	1250.691071	0.000451244	37	N	379	390
Q61598	Exosome	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	2		1148.092564	2294.169529	0.001162105	1	N	173	193
Q61598	Exosome	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	3		765.7309762	2294.169529	0.000451244	52	N	173	193
Q61598	Exosome	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	4		574.5501822	2294.169529	0.000451244	24	N	173	193
Q61598	Exosome	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	2		1071.057462	2140.099324	0.000451244	63	Y	221	240
Q61598	Exosome	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	3		714.3742412	2140.099324	0.000451244	29	Y	221	240
Q61598	Exosome	DVYKK	FDLGQDVIDFTGHSLALYR	TDDYL	2		1084.045083	2166.074566	0.000451244	31	N	174	193
Q61598	Exosome	DVYKK	FDLGQDVIDFTGHSLALYR	TDDYL	3		723.0326552	2166.074566	0.000451244	37	N	174	193
Q61598	Exosome	GQVIR	VICILSHPIKNTNDANSCQIIIPQNQVNR	KSDIY	3	C3:+57.021,C18:+57.021	1120.582095	3358.722885	0.000698008	3	N	299	328
Q61598	Exosome	GQVIR	VICILSHPIKNTNDANSCQIIIPQNQVNR	KSDIY	4	C3:+57.021,C18:+57.021	840.6885213	3358.722885	0.000698008	5	N	299	328
Q61598	Exosome	GKIYK	VPSTEAEALASSLMGLFEK	RRFRK	2		990.5038711	1978.992142	0.000823681	1	N	118	137
Q61598	Exosome	GKIYK	VPSTEAEALASSLMGLFEK	RRFRK	3		660.6718474	1978.992142	0.000451244	28	N	118	137
Q61598	Exosome	SHPIK	NTNDANSCQIIIPQNQVNR	KSDIY	2	C8:+57.021	1100.032481	2198.049362	0.000622848	20	Y	309	328
Q61598	Exosome	KEPEK	EIRPALELLEPIEQK	FVSIS	2		889.5070734	1776.998547	0.001463592	1	N	364	379
Q61598	Exosome	KEPEK	EIRPALELLEPIEQK	FVSIS	3		593.340649	1776.998547	0.000451244	27	N	364	379
Q61598	Exosome	YGKSP	YLYPLYGLGELPQGFAR	LSAIY	2		979.0150656	1956.014531	0.000451244	3	Y	223	240
Q61598	Exosome	IFISR	AYDATTHFETTCDDIKDIYK	RMTGS	3	C12:+57.021	803.030497	2406.068091	0.000451244	18	N	402	422
Q61598	Exosome	RRFRK	FLVYVANFDEKDPR	TFEGV	2		856.9362839	1711.856968	0.000622848	8	N	142	156
Q61598	Exosome	RRFRK	FLVYVANFDEKDPR	TFEGV	3		571.6267893	1711.856968	0.000451244	20	N	142	156
Q61598	Exosome	ARYGK	SPYLYPLYGLGELPQGF	ARLSA	2		957.4883494	1912.961099	0.000622848	3	Y	221	238
Q61598	Exosome	MGRGR	DWNVDLIPK	FLMAN	2		550.293278	1098.570956	0.000823681	11	Y	70	79
Q61598	Exosome	IARCK	QLICDPSYVK	DRVEK	2	C4:+57.021	611.8107464	1221.605893	0.000870037	5	N	278	288
Q61598	Exosome	QGFAR	LSAIYGGTYMLNKPIEEIIVQNGK	VVGVK	3		884.4758077	2650.404023	0.000451244	2	N	240	264
Q61598	Exosome	YKGGK	IYKVPSTEAEALASSLMGLFEK	RRFRK	3		795.4192993	2383.234498	0.000451244	17	N	115	137
Q61598	Exosome	GQLVK	MLLFTEVTR	YMDFK	2		555.3053317	1108.595063	0.001839721	2	N	89	98
Q61598	Exosome	SHPIK	NTNDANSCQIIIPQNQVNRK	SDIYV	3	C8:+57.021	776.3892416	2326.144325	0.000451244	5	Y	309	329
Q61598	Exosome	EKEIR	PALELLEPIEQK	FVSIS	2		690.3931892	1378.770778	0.000451244	6	N	367	379
Q61598	Parental	LALYR	TDDYLDQPCCETINR	IKLYS	2	C9:+57.021,C10:+57.021	950.396074	1898.776548	0.000451244	40	N	193	208
Q61598	Parental	LFVPK	DLGTDSQIFISR	AYDAT	2		676.3467703	1350.677941	0.000451244	3	N	390	402
Q61598	Parental	PIEQK	FVSISDLFVPK	DLGTD	2		626.3533357	1250.691071	0.000451244	25	N	379	390
Q61598	Parental	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	2		1148.092564	2294.169529	0.000451244	7	N	173	193
Q61598	Parental	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	3		765.7309762	2294.169529	0.000451244	34	N	173	193
Q61598	Parental	RDVYK	KFDLGQDVIDFTGHSLALYR	TDDYL	4		574.5501822	2294.169529	0.000451244	31	N	173	193
Q61598	Parental	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	2		1071.057462	2140.099324	0.000451244	37	Y	221	240
Q61598	Parental	ARYGK	SPYLYPLYGLGELPQGFAR	LSAIY	3		714.3742412	2140.099324	0.000451244	11	Y	221	240
Q61598	Parental	DVYKK	FDLGQDVIDFTGHSLALYR	TDDYL	2		1084.045083	2166.074566	0.000451244	15	N	174	193
Q61598	Parental	DVYKK	FDLGQDVIDFTGHSLALYR	TDDYL	3		723.0326552	2166.074566	0.000451244	27	N	174	193
Q61598	Parental	PIEQK	FVSISDLFVPKDLGTDSQIFISR	AYDAT	2		1292.687026	2583.358452	0.002212458	1	N	379	402
Q61598	Parental	PIEQK	FVSISDLFVPKDLGTDSQIFISR	AYDAT	3		862.127284	2583.358452	0.000451244	7	N	379	402
Q61598	Parental	ESLAR	YGKSPYLYPLYGLGELPQGFAR	LSAIY	2		1245.14734	2488.279079	0.000451244	1	Y	218	240
Q61598	Parental	ESLAR	YGKSPYLYPLYGLGELPQGFAR	LSAIY	3		830.4341598	2488.279079	0.000823681	4	Y	218	240
Q61598	Parental	GQVIR	VICILSHPIKNTNDANSCQIIIPQNQVNR	KSDIY	3	C3:+57.021,C18:+57.021	1120.582095	3358.722885	0.000451244	2	N	299	328
Q61598	Parental	GQVIR	VICILSHPIKNTNDANSCQIIIPQNQVNR	KSDIY	4	C3:+57.021,C18:+57.021	840.6885213	3358.722885	0.002296037	1	N	299	328
Q61598	Parental	SHPIK	NTNDANSCQIIIPQNQVNR	KSDIY	2	C8:+57.021	1100.032481	2198.049362	0.000622848	8	Y	309	328
Q61598	Parental	KEPEK	EIRPALELLEPIEQK	FVSIS	3		593.340649	1776.998547	0.001943752	1	N	364	379
Q61598	Parental	SLALY	RTDDYLDQPCCETINR	IKLYS	2	C10:+57.021,C11:+57.021	1028.44663	2054.877659	0.000451244	13	N	192	208
Q61598	Parental	SLALY	RTDDYLDQPCCETINR	IKLYS	3	C10:+57.021,C11:+57.021	685.9670197	2054.877659	0.000451244	7	N	192	208
Q61598	Parental	SHPIK	NTNDANSCQIIIPQNQVNRK	SDIYV	3	C8:+57.021	776.3892416	2326.144325	0.001352548	1	Y	309	329
Q61599	Exosome	-MTEK	DAQPQLEEADDDLDSKLNYKPPPQK	SLKEL	3		952.1300816	2853.366845	0.000622848	11	N	4	29
Q61599	Exosome	MRVDK	ATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		982.1411534	2943.40006	0.000451244	6	N	137	163
Q61599	Exosome	MRVDK	ATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3	M4:+15.995	987.47282	2959.39506	0.000451244	40	N	137	163
Q61599	Exosome	TKYKK	TLLGDVPVVADPTVPNVTVTR	LSLVC	2		1082.10514	2162.194681	0.000451244	43	N	49	70
Q61599	Exosome	TKYKK	TLLGDVPVVADPTVPNVTVTR	LSLVC	3		721.7393603	2162.194681	0.000451244	31	N	49	70
Q61599	Exosome	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	2		1305.119507	2608.223415	0.0007646	1	N	174	195
Q61599	Exosome	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	3		870.415605	2608.223415	0.000451244	23	N	174	195

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61599	Exosome	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	4		653.0636537	2608.223415	0.000451244	22	N	174	195
Q61599	Exosome	TKYKK	TLLGDVPVVADPTVPNVTVTRL	SLVCD	2		1138.647172	2275.278745	0.000451244	10	N	49	71
Q61599	Exosome	VTVTR	LSLVCDSAPGPITMDLTGDLEALKK	DTFVL	3	C5:+57.021	882.124292	2643.349476	0.000451244	33	N	70	95
Q61599	Exosome	-MTEK	DAQPQLEEADDDLDSK	LNYKP	2		894.8926644	1787.769729	0.000451244	5	N	4	20
Q61599	Exosome	RTGMR	VDKATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	4	M7:+15.995	826.4041451	3301.58538	0.001264573	1	N	134	163
Q61599	Exosome	YKKTL	LGDVPVVADPTVPNVTVTR	LSLVC	2		975.0392691	1948.062938	0.000451244	38	N	51	70
Q61599	Parental	EALKK	DTFVLKEGIEYR	VKINF	2		735.3858955	1468.756191	0.000622848	3	N	95	107
Q61599	Parental	EALKK	DTFVLKEGIEYR	VKINF	3		490.593197	1468.756191	0.000451244	4	N	95	107
Q61599	Parental	-MTEK	DAQPQLEEADDDLDSKLNYKPPPQK	SLKEL	2		1427.691222	2853.366845	0.000451244	5	N	4	29
Q61599	Parental	-MTEK	DAQPQLEEADDDLDSKLNYKPPPQK	SLKEL	3		952.1300816	2853.366845	0.000451244	19	N	4	29
Q61599	Parental	KATFM	VGSYGPRPEEYEFLTPVEEAPK	GMLAR	2		1247.610984	2493.206368	0.000451244	15	N	141	163
Q61599	Parental	KATFM	VGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		832.0765893	2493.206368	0.000451244	15	N	141	163
Q61599	Parental	MRVDK	ATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		982.1411534	2943.40006	0.000451244	17	N	137	163
Q61599	Parental	MRVDK	ATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3	M4:+15.995	987.47282	2959.39506	0.000451244	7	N	137	163
Q61599	Parental	TKYKK	TLLGDVPVVADPTVPNVTVTR	LSLVC	2		1082.10514	2162.194681	0.000451244	305	N	49	70
Q61599	Parental	TKYKK	TLLGDVPVVADPTVPNVTVTR	LSLVC	3		721.7393603	2162.194681	0.000451244	27	N	49	70
Q61599	Parental	PVVAD	PTVPNVTVTR	LSLVC	2		542.3120021	1082.608404	0.0025889	1	N	60	70
Q61599	Parental	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	2		1305.119507	2608.223415	0.000451244	43	N	174	195
Q61599	Parental	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	3		870.415605	2608.223415	0.000451244	47	N	174	195
Q61599	Parental	TYHNK	SFFTDDDKQDHLTWEWNLAIK	KDWTE	4		653.0636537	2608.223415	0.000451244	38	N	174	195
Q61599	Parental	TKYKK	TLLGDVPVVADPTVPNVTVTRL	SLVCD	2		1138.647172	2275.278745	0.000451244	21	N	49	71
Q61599	Parental	TKYKK	TLLGDVPVVADPTVPNVTVTRL	SLVCD	3		759.4340483	2275.278745	0.000451244	6	N	49	71
Q61599	Parental	VTVTR	LSLVCDSAPGPITMDLTGDLEALKK	DTFVL	2	C5:+57.021	1322.682538	2643.349476	0.000451244	7	N	70	95
Q61599	Parental	VTVTR	LSLVCDSAPGPITMDLTGDLEALKK	DTFVL	3	C5:+57.021	882.124292	2643.349476	0.000451244	34	N	70	95
Q61599	Parental	LTKYK	KTLLGDVPVVADPTVPNVTVTR	LSLVC	2		1146.152622	2290.289644	0.000451244	24	N	48	70
Q61599	Parental	LTKYK	KTLLGDVPVVADPTVPNVTVTR	LSLVC	3		764.4376813	2290.289644	0.000622848	1	N	48	70
Q61599	Parental	KYKKT	LLGDVPVVADPTVPNVTVTR	LSLVC	2		1031.581301	2061.147002	0.000823681	2	N	50	70
Q61599	Parental	-MTEK	DAQPQLEEADDDLDSK	LNYKP	2		894.8926644	1787.769729	0.000451244	24	N	4	20
Q61599	Parental	EALKK	DTFVLKEGIEY	RVKIN	2		657.3353399	1312.65508	0.000735798	4	N	95	106
Q61599	Parental	RTGMR	VDKATFMVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		1096.204593	3285.59038	0.000451244	7	N	134	163
Q61599	Parental	KTLLG	DVPVVADPTVPNVTVTR	LSLVC	2		889.9865052	1777.95741	0.000823681	2	N	53	70
Q61599	Parental	DKATF	MVGSYGPRPEEYEFLTPVEEAPK	GMLAR	3		875.7567512	2624.246854	0.002884417	1	N	140	163
Q61635	Exosome	WSLVK	DNSIIAQATSAAEAFCAVK	GGPES	2	C16:+57.021	983.9808625	1965.946125	0.000451244	18	N	360	379
Q61635	Exosome	TNLIK	TGVTEPCIFLISNLDLGAFDFPK	LEETL	2	C7:+57.021	1277.648824	2553.282047	0.000451244	14	N	224	247
Q61635	Exosome	TNLIK	TGVTEPCIFLISNLDLGAFDFPK	LEETL	3	C7:+57.021	852.1018157	2553.282047	0.002019181	1	N	224	247
Q61635	Exosome	KGELK	CLDFWSLVK	DNSII	2	C1:+57.021	584.2972748	1166.57895	0.001463592	12	N	351	360
Q61635	Exosome	IQIQK	AISAAENAILEVAVIGQSGTGK	SSFIN	2		1050.071298	2098.126995	0.000870037	1	N	65	87
Q61635	Exosome	IQIQK	AISAAENAILEVAVIGQSGTGK	SSFIN	3		700.3834651	2098.126995	0.002519933	1	N	65	87
Q61635	Exosome	TNLIK	TGVTEPCIFLISNLDLGAFDFPKLEETLLK	ELPGH	3	C7:+57.021	1127.595156	3379.762068	0.000451244	10	N	224	254
Q61635	Exosome	ISSSR	FSLNDALLAQK	IKDAG	2		610.3382169	1218.660834	0.0025889	1	N	164	175
Q61635	Exosome	SAFLK	GASENSFQQLAK	EFLPQ	2		640.3180128	1278.620426	0.001591523	2	N	10	22
Q61635	Exosome	QQLAK	EFLPQYSALISK	AGGML	2		698.3800818	1394.744564	0.000662267	2	N	22	34
Q61635	Exosome	EPCIF	LISNLDLGAFDFPKLEETLLK	ELPGH	3		792.7740706	2375.298812	0.001162105	1	N	233	254
Q61635	Exosome	LKDYR	SYFGLDDQSIKEIAEK	LGAPL	3		614.9760354	1841.904706	0.001264573	1	N	322	338
Q61635	Parental	WSLVK	DNSIIAQATSAAEAFCAVK	GGPES	2	C16:+57.021	983.9808625	1965.946125	0.000451244	1	N	360	379
Q61635	Parental	KGELK	CLDFWSLVK	DNSII	2	C1:+57.021	584.2972748	1166.57895	0.002663018	1	N	351	360
Q61635	Parental	TNLIK	TGVTEPCIFLISNLDLGAFDFPKLEETLLK	ELPGH	3	C7:+57.021	1127.595156	3379.762068	0.001162105	2	N	224	254
Q61635	Parental	VYYRR	TQFLNIVVDDAKHLLR	KIETV	4		471.2696071	1881.047228	0.000451244	4	N	396	412
Q61646	Exosome	RQFYR	LRAEGDGVYTLNDEK	QWVNT	2		840.4159126	1678.816225	0.000451244	61	N	57	72
Q61646	Exosome	RQFYR	LRAEGDGVYTLNDEK	QWVNT	3		560.6132084	1678.816225	0.000451244	61	N	57	72
Q61646	Exosome	IAPGR	VGYVSGWGR	NANFR	2		490.7515803	979.4875607	0.000451244	62	N	218	227
Q61646	Exosome	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	2	C14:+57.021,C18:+57.021	1250.619843	2499.224086	0.000451244	23	N	72	94
Q61646	Exosome	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	3	C14:+57.021,C18:+57.021	834.0824954	2499.224086	0.000451244	107	N	72	94
Q61646	Exosome	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	4	C14:+57.021,C18:+57.021	625.8138216	2499.224086	0.000451244	59	N	72	94
Q61646	Exosome	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	3	Q1:-17.027,C14:+57.021,C18:+57.021	828.4068288	2482.197086	0.001591523	9	N	72	94
Q61646	Exosome	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	2	[0:-17.027,C14:+57.021,C18:+57.021	1242.106343	2482.197086	0.002374549	1	N	72	94
Q61646	Exosome	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	3	[0:-17.027,C14:+57.021,C18:+57.021	828.4068288	2482.197086	0.000622848	20	N	72	94
Q61646	Exosome	LSFDK	SCAVAEYGVYVR	ATDLK	2	C2:+57.021	687.3298346	1372.644069	0.000451244	106	N	320	332
Q61646	Exosome	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	C15:+57.021	1172.873424	3515.596871	0.000451244	7	N	18	49
Q61646	Exosome	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	4	C15:+57.021	879.9070176	3515.596871	0.000698008	6	N	18	49
Q61646	Exosome	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	M8:+15.995,C15:+57.021	1178.20509	3531.591871	0.000451244	83	N	18	49
Q61646	Exosome	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	4	M8:+15.995,C15:+57.021	883.9057676	3531.591871	0.000451244	40	N	18	49

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61646	Exosome	KMISR	HGLTTGATLISDQWLLTTAK	NLFLN	2		1064.076383	2126.137166	0.000451244	88	N	123	143
Q61646	Exosome	KMISR	HGLTTGATLISDQWLLTTAK	NLFLN	3		709.7201886	2126.137166	0.000451244	292	N	123	143
Q61646	Exosome	TASAK	DITPTLTLYVGKNQLVEIEK	VVLHP	2		1137.633731	2273.251861	0.000451244	1	N	156	176
Q61646	Exosome	AGLTK	YQEDTCYGDAGSAFAIHDMEEDTWYAAGILSFDK	SCAVA	3	C6:+57.021	1292.882424	3875.623873	0.000451244	16	N	286	320
Q61646	Exosome	AGLTK	YQEDTCYGDAGSAFAIHDMEEDTWYAAGILSFDK	SCAVA	3	C6:+57.021,M19:+15.995	1298.214091	3891.618873	0.000451244	343	N	286	320
Q61646	Exosome	TDRLK	YVMLPVADQDK	CVVHY	2	M3:+15.995	647.8215857	1293.627571	0.000451244	60	N	238	249
Q61646	Exosome	FYRLR	AEGDGVYTLNDEK	QWVNT	2		705.823325	1409.63105	0.000451244	24	N	59	72
Q61646	Exosome	TASAK	DITPTLTLYVGK	NQLVE	2		660.8746323	1319.733665	0.000451244	32	N	156	168
Q61646	Exosome	QLFAV	ELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	M7:+15.995,C14:+57.021	1145.182286	3432.523457	0.000451244	15	N	19	49
Q61646	Exosome	QLFAV	ELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	4	M7:+15.995,C14:+57.021	859.1386641	3432.523457	0.000870037	6	N	19	49
Q61646	Exosome	GVYVR	ATDLKDWVQETMAK	N-	3		545.9402684	1634.797405	0.000451244	10	N	332	346
Q61646	Exosome	GVYVR	ATDLKDWVQETMAK	N-	2	M12:+15.995	826.4040026	1650.792405	0.000451244	7	N	332	346
Q61646	Exosome	SAKDI	TPTLTLYVGK	NQLVE	2		546.8191287	1091.622657	0.000451244	1	N	158	168
Q61646	Exosome	FYRLR	AEGDGVYTLNDEKQWVNTVAGEK	LPECE	2		1262.104054	2522.192509	0.000451244	8	N	59	82
Q61646	Exosome	LVTER	VMPICLPSKDYIAPGR	VGYVS	2	C5:+57.021	908.9763408	1815.937082	0.000451244	4	N	202	218
Q61646	Parental	RQFYR	LRAEGDGVYTLNDEK	QWVNT	2		840.4159126	1678.816225	0.000451244	87	N	57	72
Q61646	Parental	RQFYR	LRAEGDGVYTLNDEK	QWVNT	3		560.6132084	1678.816225	0.000451244	44	N	57	72
Q61646	Parental	IAPGR	VGYVSGWGR	NANFR	2		490.7515803	979.4875607	0.000451244	79	N	218	227
Q61646	Parental	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	2	C14:+57.021,C18:+57.021	1250.619843	2499.224086	0.000451244	20	N	72	94
Q61646	Parental	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	3	C14:+57.021,C18:+57.021	834.0824954	2499.224086	0.000451244	87	N	72	94
Q61646	Parental	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	4	C14:+57.021,C18:+57.021	625.8138216	2499.224086	0.000451244	66	N	72	94
Q61646	Parental	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	3	Q1:-17.027,C14:+57.021,C18:+57.021	828.4068288	2482.197086	0.001229886	6	N	72	94
Q61646	Parental	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	3	[0:-17.027,C14:+57.021,C18:+57.021	828.4068288	2482.197086	0.001162105	6	N	72	94
Q61646	Parental	LNDEK	QWVNTVAGEKLPECEAVCGKPK	HPVDQ	4	[0:-17.027,C14:+57.021,C18:+57.021	621.5570716	2482.197086	0.000823681	1	N	72	94
Q61646	Parental	LSFDK	SCAVAEYGVYVR	ATDLK	2	C2:+57.021	687.3298346	1372.644069	0.000451244	82	N	320	332
Q61646	Parental	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	C15:+57.021	1172.873424	3515.596871	0.000698008	7	N	18	49
Q61646	Parental	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	4	C15:+57.021	879.9070176	3515.596871	0.000823681	1	N	18	49
Q61646	Parental	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	3	M8:+15.995,C15:+57.021	1178.20509	3531.591871	0.000451244	46	N	18	49
Q61646	Parental	GQLFA	VELGNDAMDFEDDSCPKPPEIANGYVEHLVR	YRCRQ	4	M8:+15.995,C15:+57.021	883.9057676	3531.591871	0.000451244	14	N	18	49
Q61646	Parental	KMISR	HGLTTGATLISDQWLLTTAK	NLFLN	2		1064.076383	2126.137166	0.000451244	113	N	123	143
Q61646	Parental	KMISR	HGLTTGATLISDQWLLTTAK	NLFLN	3		709.7201886	2126.137166	0.000451244	248	N	123	143
Q61646	Parental	TASAK	DITPTLTLYVGKNQLVEIEK	VVLHP	2		1137.633731	2273.251861	0.000451244	8	N	156	176
Q61646	Parental	TASAK	DITPTLTLYVGKNQLVEIEK	VVLHP	3		758.7584205	2273.251861	0.001463592	1	N	156	176
Q61646	Parental	AGLTK	YQEDTCYGDAGSAFAIHDMEEDTWYAAGILSFDK	SCAVA	3	C6:+57.021	1292.882424	3875.623873	0.000451244	20	N	286	320
Q61646	Parental	AGLTK	YQEDTCYGDAGSAFAIHDMEEDTWYAAGILSFDK	SCAVA	3	C6:+57.021,M19:+15.995	1298.214091	3891.618873	0.000451244	59	N	286	320
Q61646	Parental	TDRLK	YVMLPVADQDK	CVVHY	2		639.8240857	1277.632571	0.000622848	3	N	238	249
Q61646	Parental	FYRLR	AEGDGVYTLNDEK	QWVNT	2		705.823325	1409.63105	0.000451244	40	N	59	72
Q61646	Parental	TASAK	DITPTLTLYVGK	NQLVE	2		660.8746323	1319.733665	0.000451244	20	N	156	168
Q61646	Parental	GVYVR	ATDLKDWVQETMAK	N-	2		818.4065026	1634.797405	0.000870037	1	N	332	346
Q61646	Parental	GVYVR	ATDLKDWVQETMAK	N-	3		545.9402684	1634.797405	0.000451244	2	N	332	346
Q61646	Parental	FYRLR	AEGDGVYTLNDEKQWVNTVAGEK	LPECE	2		1262.104054	2522.192509	0.000451244	3	N	59	82
Q61646	Parental	LNDEK	QWVNTVAGEKLPECEAVCGK	PKHPV	2	C14:+57.021,C18:+57.021	1138.04598	2274.076359	0.000451244	1	N	72	92
Q61646	Parental	KMISR	HGLTTGATLISDQWLLT	TAKNL	2		913.9865052	1825.95741	0.000735798	2	N	123	140
Q61655	Exosome	AMLSR	VEPADRYPQCLCLSPTYELALQTGK	VIEQM	3	C10:+57.021,C12:+57.021	970.4774623	2908.408987	0.000451244	11	N	154	179
Q61655	Exosome	ERGQK	VSEQIVIGTPGTVLDWCSK	LKFID	2	C17:+57.021	1045.035638	2088.055676	0.000451244	10	N	207	226
Q61655	Parental	NKLIR	SNLVDNTNQVEVLQRDPSSPLYSVK	SFEEL	3		934.8143163	2801.419549	0.000451244	7	N	66	91
Q61655	Parental	AMLSR	VEPADRYPQCLCLSPTYELALQTGK	VIEQM	3	C10:+57.021,C12:+57.021	970.4774623	2908.408987	0.000662267	1	N	154	179
Q61655	Parental	ERGQK	VSEQIVIGTPGTVLDWCSK	LKFID	2	C17:+57.021	1045.035638	2088.055676	0.000451244	5	N	207	226
Q61655	Parental	NKLIR	SNLVDNTNQVEVLQR	DPSSP	2		864.9479113	1727.880223	0.000451244	3	N	66	81
Q61656	Exosome	LAPTR	ELAQQVQQVAAEYCR	ACRLK	2	C14:+57.021	896.936258	1791.856916	0.000451244	5	N	177	192
Q61656	Exosome	LAPTR	ELAQQVQQVAAEYCR	ACRLK	3	C14:+57.021	598.2934387	1791.856916	0.000451244	1	N	177	192
Q61656	Exosome	PFLER	GDGPICLVLAPTR	ELAQQ	2	C6:+57.021	684.869127	1367.722654	0.000451244	6	Y	164	177
Q61656	Exosome	ATPGR	LIDFLECGK	TNLRR	2	C7:+57.021	547.7814576	1093.547315	0.000637154	4	N	227	236
Q61656	Exosome	TGSGK	TLSYLLPAIVHINHQPFLER	GDGPI	4		591.0829208	2360.300483	0.001699387	3	N	144	164
Q61656	Exosome	PNNIK	QVSDLISVLR	EANQA	2	[0:-17.027	556.8194346	1111.623269	0.001763695	2	N	451	461
Q61656	Exosome	ARSTK	TGTAYTFFTPNNIK	QVSDL	2		787.8966274	1573.777655	0.002453667	1	N	437	451
Q61656	Exosome	PKFEK	NFYQEHPDLAR	RTAQE	2		695.3314546	1388.647309	0.000622848	1	N	56	67
Q61656	Exosome	TNLRR	TTYLVLDEADR	MLDMG	2		648.3280462	1294.640492	0.002296037	2	N	241	252
Q61656	Parental	LAPTR	ELAQQVQQVAAEYCR	ACRLK	2	C14:+57.021	896.936258	1791.856916	0.000451244	37	N	177	192
Q61656	Parental	EDVKF	VINYDYPNSSEDYIHR	IGRTA	2		992.9559333	1983.896267	0.000451244	24	N	412	428
Q61656	Parental	EDVKF	VINYDYPNSSEDYIHR	IGRTA	3		662.3065556	1983.896267	0.000451244	11	N	412	428
Q61656	Parental	DVASR	GLDVEDVKFVINYDYPNSSEDYIHR	IGRTA	3		996.4739597	2986.398479	0.000451244	2	N	403	428

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61656	Parental	FKHGK	APILIATDVASR	GLDVE	2		613.8593165	1225.703033	0.000823681	10	Y	391	403
Q61656	Parental	PFLER	GDGPICLVLAPTR	ELAQQ	2	C6:+57.021	684.869127	1367.722654	0.001264573	12	Y	164	177
Q61656	Parental	ATPGR	LIDFLECGK	TNLRR	2	C7:+57.021	547.7814576	1093.547315	0.000451244	7	N	227	236
Q61656	Parental	TGSGK	TLSYLLPAIVHINHQPFLER	GDGPI	4		591.0829208	2360.300483	0.002727428	1	N	144	164
Q61656	Parental	QNGVY	SAANYTNGSFGSNFVSAGIQTSFR	TGNPT	2		1242.083456	2482.151313	0.000622848	2	N	535	559
Q61687	Parental	KVLVF	SQSLISLDLIEDFLELASR	EKTED	2		1075.073506	2148.131412	0.000451244	6	N	2023	2042
Q61687	Parental	PMLPK	DTILAELLQIHK	EHIVG	3		465.2736873	1392.797662	0.001943752	1	N	2216	2228
Q61704	Exosome	AIGGK	FPLYNLGFGNNLNYNFLETLALENHGLAR	RIYED	3		1108.898715	3323.672744	0.000451244	4	N	419	448
Q61704	Exosome	LDQQR	SCPTCTDSLLNGDFTIVYDVNR	ESPGN	2	C2:+57.021,C5:+57.021	1274.078205	2546.14081	0.000451244	1	N	234	256
Q61704	Parental	AIGGK	FPLYNLGFGNNLNYNFLETLALENHGLAR	RIYED	3		1108.898715	3323.672744	0.000451244	8	N	419	448
Q61704	Parental	LDQQR	SCPTCTDSLLNGDFTIVYDVNR	ESPGN	2	C2:+57.021,C5:+57.021	1274.078205	2546.14081	0.001162105	1	N	234	256
Q61739	Exosome	MDLDR	NSYPDLAVGSLSDSVTIFR	SRPVI	2		1021.015991	2040.016382	0.000451244	11	N	444	463
Q61739	Exosome	GISVK	NIGDINQDGYPDIAVGAPYDDLGK	VFIYH	2		1260.598605	2519.18161	0.001591523	1	N	382	406
Q61739	Exosome	SSRRR	VNSLPEVLPILNSNEAK	TVQTD	2		919.0074376	1835.999275	0.000662267	1	N	596	613
Q61739	Exosome	AHEAK	LIATFPDTLTYSAYR	ELRAF	2		866.4517668	1730.887934	0.002884417	1	N	699	714
Q61739	Parental	MDLDR	NSYPDLAVGSLSDSVTIFR	SRPVI	2		1021.015991	2040.016382	0.000622848	1	N	444	463
Q61739	Parental	ATFTK	DFHYIVFGAPGTYNWK	GIVRV	2		957.962833	1913.910066	0.001329271	1	N	198	214
Q61749	Exosome	HSLVR	AGVPTSYLLIPAASYVLPEVSK	VLLGA	2		1138.133367	2274.251133	0.00091018	5	N	379	401
Q61749	Exosome	KFCER	VQTDAFVSNELDDPDDLQCK	RGDQV	2	C19:+57.021	1155.015828	2308.016055	0.001871652	1	N	447	467
Q61749	Parental	LKQAR	KGEQGGVPPQACPSTAGETTSGVK	RVPEH	3	C12:+57.021	781.7133909	2342.116773	0.000622848	6	N	118	142
Q61753	Exosome	PPRDR	ALVDHENVISCPHLGASTK	EAQSR	3	C11:+57.021	683.3462026	2047.015208	0.002080925	2	N	270	289
Q61753	Exosome	QVVGR	AGTGVDNVDLEAATR	KGILV	2		744.8685982	1487.721596	0.000451244	7	N	75	90
Q61753	Exosome	GALLR	ALQSGQCAGAALDVFTEEPPRDR	ALVDH	3	C7:+57.021	830.0680566	2487.18077	0.000451244	14	N	247	270
Q61753	Exosome	QVVEK	QNLSKEELIAELQDCEGLIVR	SATKV	3	C15:+57.021	819.7603411	2456.257623	0.000451244	6	N	33	54
Q61753	Exosome	GTSLK	NAGTCLSPAVIVGLLR	EASKQ	2	C5:+57.021	820.9615475	1639.907495	0.000451244	15	N	364	380
Q61753	Exosome	AGSPK	GTIQVVTQGTSLK	NAGTC	2		666.3806131	1330.745626	0.000451244	2	N	351	364
Q61753	Exosome	PCCRK	ILQDGGLQVVEK	QNLSK	2		649.8698813	1297.724163	0.001264573	1	N	21	33
Q61753	Parental	PPRDR	ALVDHENVISCPHLGASTK	EAQSR	2	C11:+57.021	1024.515404	2047.015208	0.000451244	6	N	270	289
Q61753	Parental	PPRDR	ALVDHENVISCPHLGASTK	EAQSR	3	C11:+57.021	683.3462026	2047.015208	0.000622848	5	N	270	289
Q61753	Parental	PPRDR	ALVDHENVISCPHLGASTK	EAQSR	4	C11:+57.021	512.7616019	2047.015208	0.002296037	2	N	270	289
Q61753	Parental	VNCAR	GGIVDEGALLR	ALQSG	2		550.3094595	1098.603319	0.000870037	2	N	236	247
Q61753	Parental	QVVGR	AGTGVDNVDLEAATR	KGILV	2		744.8685982	1487.721596	0.000451244	16	N	75	90
Q61753	Parental	GALLR	ALQSGQCAGAALDVFTEEPPRDR	ALVDH	3	C7:+57.021	830.0680566	2487.18077	0.000451244	4	N	247	270
Q61753	Parental	QVVEK	QNLSKEELIAELQDCEGLIVR	SATKV	3	C15:+57.021	819.7603411	2456.257623	0.000451244	7	N	33	54
Q61753	Parental	EIWPL	CDFITVHTPLLPSTTGLLNDSTFAQCK	KGVRV	3	C1:+39.994,C26:+57.021	1007.156239	3018.445316	0.001395409	1	N	199	226
Q61753	Parental	EIWPL	CDFITVHTPLLPSTTGLLNDSTFAQCK	KGVRV	3	C1:+57.021,C26:+57.021	1012.831905	3035.472316	0.000451244	17	N	199	226
Q61753	Parental	SFGMK	TVGYDPIISPEVAASFGVQQLPLEEIWPL	CDFIT	3		1056.888822	3167.643067	0.001162105	7	N	170	199
Q61753	Parental	GTSLK	NAGTCLSPAVIVGLLR	EASKQ	2	C5:+57.021	820.9615475	1639.907495	0.000451244	3	N	364	380
Q61753	Parental	AGSPK	GTIQVVTQGTSLK	NAGTC	2		666.3806131	1330.745626	0.000622848	1	N	351	364
Q61768	Exosome	EQKKR	QLEESVDSLGEELVQLR	AQEKV	2		972.5001737	1942.984747	0.000451244	13	N	658	675
Q61768	Exosome	KNINK	SLSALGNVISALAEGSTYVPYR	DSKMT	2		1134.59768	2267.179759	0.000451244	6	N	256	278
Q61768	Exosome	KNINK	SLSALGNVISALAEGSTYVPYR	DSKMT	3		756.7343864	2267.179759	0.001699387	1	N	256	278
Q61768	Exosome	AQKQK	ISFLENNLEQLTK	VHKQL	2		774.9175598	1547.81952	0.000451244	1	N	831	844
Q61768	Exosome	NKTLR	NTIQWLENELNR	WRNGE	2		765.3895008	1528.763402	0.002813207	1	N	355	367
Q61768	Exosome	GGNCR	TTIVICCSPSSYNESETK	STLLF	2	C6:+57.021,C7:+57.021	1038.466696	2074.917793	0.000823681	1	N	295	313
Q61768	Parental	KNINK	SLSALGNVISALAEGSTYVPYRDSK	MTRIL	3		866.7856979	2597.333694	0.000451244	6	N	256	281
Q61768	Parental	EQKKR	QLEESVDSLGEELVQLR	AQEKV	2		972.5001737	1942.984747	0.000451244	14	N	658	675
Q61768	Parental	EQKKR	QLEESVDSLGEELVQLR	AQEKV	3		648.6693825	1942.984747	0.000622848	2	N	658	675
Q61768	Parental	EQKKR	QLEESVDSLGEELVQLR	AQEKV	2	Q1:-17.027	963.9866737	1925.957747	0.000622848	1	N	658	675
Q61768	Parental	YAFDR	VFQSSTSQEQVYNDCAK	KIVKD	2	C15:+57.021	995.944477	1989.873354	0.000451244	21	N	50	67
Q61768	Parental	KNINK	SLSALGNVISALAEGSTYVPYR	DSKMT	2		1134.59768	2267.179759	0.000451244	17	N	256	278
Q61768	Parental	KNINK	SLSALGNVISALAEGSTYVPYR	DSKMT	3		756.7343864	2267.179759	0.000451244	5	N	256	278
Q61768	Parental	AKLYK	QLDDKDEEINQQSQLVEK	LKTQM	2		1080.027284	2158.038968	0.000823681	1	N	430	448
Q61768	Parental	KNINK	SLSALGNVISALAEGSTYVPY	RDSKM	2		1056.547124	2111.078648	0.000451244	5	N	256	277
Q61792	Exosome	AHYPK	QSFTMVADTPENLR	LKQQS	2	M5:+15.995	812.885977	1623.756354	0.000823681	3	N	59	73
Q61792	Parental	FEKNK	GKGFSVVADTPELQR	IKKTQ	2		802.4260834	1602.836567	0.000451244	5	N	94	109
Q61792	Parental	FEKNK	GKGFSVVADTPELQR	IKKTQ	3		535.2866556	1602.836567	0.000451244	7	N	94	109
Q61792	Parental	KNKGK	GFSVVADTPELQR	IKKTQ	2		709.8678699	1417.72014	0.000451244	13	N	96	109
Q61792	Parental	AHYPK	QSFTMVADTPENLR	LKQQS	2		804.888477	1607.761354	0.000451244	1	N	59	73
Q61792	Parental	AHYPK	QSFTMVADTPENLR	LKQQS	2	M5:+15.995	812.885977	1623.756354	0.002145581	1	N	59	73
Q61792	Parental	QRIKK	TQDQISNIKYHEEFEK	SRMGP	2		1004.984691	2007.953782	0.000451244	4	N	112	128
Q61805	Exosome	EMIQK	SVTSDLQPYLQTLPVTAEIDNVLGIDYSLVAAPQAK	AQVLD	3		1277.342367	3829.0037	0.000451244	32	N	203	239
Q61805	Parental	DLQPY	LQTLPVTAEIDNVLGIDYSLVAAPQAK	AQVLD	2		1420.276737	2838.537873	0.000637154	2	N	212	239
Q61805	Parental	DLQPY	LQTLPVTAEIDNVLGIDYSLVAAPQAK	AQVLD	3		947.1870911	2838.537873	0.000698008	6	N	212	239
Q61805	Parental	EMIQK	SVTSDLQPYLQTLPVTAEIDNVLGIDYSLVAAPQAK	AQVLD	3		1277.342367	3829.0037	0.000451244	40	N	203	239

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61805	Parental	KAVGR	GQYEFHSLEIQNCELR	GSSLK	2	C13:+57.021	1011.970829	2021.926058	0.000451244	7	N	73	89
Q61838	Exosome	LKFTK	VNTNYRPGLPFSGQVLLVDEK	GKPIP	2		1173.626771	2345.237943	0.002296037	1	N	353	374
Q61838	Exosome	LKFTK	VNTNYRPGLPFSGQVLLVDEK	GKPIP	3		782.7537809	2345.237943	0.000451244	9	N	353	374
Q61838	Exosome	HLKVK	AAPLSLCALTAVDQSVLLLKPEAK	LSPQS	3	C7:+57.021	836.8087437	2507.402831	0.000451244	18	N	587	611
Q61838	Exosome	VADGK	APFALQVNTLPLNFDK	AGDHR	2		894.4886837	1786.961767	0.000451244	23	N	1357	1373
Q61838	Exosome	PNIQR	TEVNTNHVLIYIEK	LTNQT	2		836.9493913	1671.883183	0.000451244	16	N	1426	1440
Q61838	Exosome	HVYTK	ALLAYAFALAGNK	AKRSE	2		661.8775093	1321.739419	0.000451244	3	N	1159	1172
Q61838	Exosome	TFGNH	GGGNTPGNTWLTAFVLK	AFAQA	2		866.955008	1731.894416	0.000451244	8	N	1043	1060
Q61838	Exosome	KWISK	QQNSHGGFSSTQDTVVALQALSK	YGAAT	2		1202.099106	2402.182613	0.000451244	6	N	1258	1281
Q61838	Exosome	KWISK	QQNSHGGFSSTQDTVVALQALSK	YGAAT	3		801.7353376	2402.182613	0.000451244	12	N	1258	1281
Q61838	Exosome	PKRNR	IFQWQNIHLAGGLHQLSFPLSVEPALGIYK	VVVQK	3		1126.278867	3375.813201	0.002374549	5	N	172	202
Q61838	Exosome	CIQIR	VDLEISPDFLAVPVGGHENSHCICGNER	KTVSW	3	C22:+57.021,C24:+57.021	1041.15393	3120.43839	0.000451244	9	N	837	865
Q61838	Exosome	VYTPK	HSLGDNDAHSIFQSVGINIFTNSK	IHKPR	2		1301.138763	2600.261926	0.000622848	4	N	658	682
Q61838	Exosome	RETVR	KYFPETWIWDLVPLDVSGDGELAVK	VPDTI	3		959.8290152	2876.463646	0.000451244	3	N	744	769
Q61838	Exosome	IHKPR	FCQEFQHYPAMGGVAPQALAVAASGPGSSFR	AMGVP	3	C2:+57.021,M11:+15.995	1085.51012	3253.506959	0.000451244	4	N	687	718
Q61838	Exosome	LLPGK	TVQGAFFGVPVYK	DHENC	2		706.8827917	1411.749983	0.000451244	5	N	624	637
Q61838	Exosome	KPEAK	LSPQSIYNLLPGK	TVQGA	2		715.4066309	1428.797662	0.002813207	1	N	611	624
Q61838	Exosome	HSAVR	NALFCLETAWASISQSQESHVYTK	ALLAY	3	C5:+57.021	924.1099215	2769.306365	0.000451244	12	N	1135	1159
Q61838	Exosome	LLPGK	TVQGAFFGVPVYKDHENCISGEDITHNGIVYTPK	HSLGD	4	C18:+57.021	948.9640239	3791.824896	0.001943752	2	N	624	658
Q61838	Exosome	EVEAK	IKEEGTGIELTGIGSCEIANALSK	LKFTK	2	C16:+57.021	1245.641727	2489.267854	0.001264573	3	N	324	348
Q61838	Exosome	IQIIK	AESPVFVQTDKPIYKPGQIVK	FRVVS	3		782.1024101	2343.28383	0.002663018	1	N	122	143
Q61838	Exosome	YSRYR	STCHNQNSMSICEEFSQQADDKGCFR	QVVKT	4	C3:+57.021,M9:+15.995,C12:+57.021,C24:+57.021	788.819678	3151.247512	0.000622848	1	N	274	300
Q61838	Exosome	NYVTK	GSGSGCVYLQTSLK	YNILP	2	C6:+57.021	728.8589563	1455.702313	0.000622848	1	N	1333	1347
Q61838	Exosome	VPVYK	DHENCISGEDITHNGIVYTPK	HSLGD	3	C5:+57.021	800.3696241	2398.085472	0.000622848	1	N	637	658
Q61878	Exosome	CKRFR	WVDGSSWNFAYWAAGQPCPGGGR	CVTLC	2	C18:+57.021	1263.556123	2525.096646	0.000451244	23	N	174	197
Q61878	Exosome	CKRFR	WVDGSSWNFAYWAAGQPCPGGGR	CVTLC	3	C18:+57.021	842.706682	2525.096646	0.000622848	2	N	174	197
Q61878	Exosome	QSAVR	GINQGQVWIGGR	IKGWG	2		642.8445321	1283.673464	0.000823681	2	N	151	163
Q61878	Exosome	RRCYR	GTLASIHSFSVNFGIQSAVR	GINQG	3		697.7047614	2090.090884	0.000622848	1	N	131	151
Q61878	Parental	SIHSF	SVNFGIQSAVR	GINQG	2		589.3203585	1176.625117	0.000451244	6	N	140	151
Q61878	Parental	PGGGR	CVTLCTQGGHWR	LSHCV	2	C1:+57.021,C5:+57.021	737.8376039	1473.659608	0.000622848	11	N	197	209
Q61878	Parental	PGGGR	CVTLCTQGGHWR	LSHCV	3	C1:+57.021,C5:+57.021	492.2276693	1473.659608	0.000451244	9	N	197	209
Q61878	Parental	PGGGR	CVTLCTQGGHWR	LSHCV	2	[0:-17.027,C1:+57.021,C5:+57.021	729.3241039	1456.632608	0.000698008	7	N	197	209
Q61878	Parental	CKRFR	WVDGSSWNFAYWAAGQPCPGGGR	CVTLC	2	C18:+57.021	1263.556123	2525.096646	0.000451244	36	N	174	197
Q61878	Parental	CKRFR	WVDGSSWNFAYWAAGQPCPGGGR	CVTLC	3	C18:+57.021	842.706682	2525.096646	0.000451244	13	N	174	197
Q61878	Parental	QSAVR	GINQGQVWIGGR	IKGWG	2		642.8445321	1283.673464	0.000451244	6	N	151	163
Q61878	Parental	DGSSW	NFAYWAAGQPCPGGGR	CVTLC	2	C11:+57.021	854.8863711	1707.757142	0.000451244	12	N	181	197
Q61878	Parental	SSWNF	AYWAAGQPCPGGGR	CVTLC	2	C9:+57.021	724.3307003	1446.645801	0.000622848	1	N	183	197
Q61881	Exosome	GENTR	IAQPGDHVSVTGIFLPVLR	TGFQQ	3		673.7182308	2018.131293	0.002663018	1	N	263	282
Q61881	Exosome	RCISR	GFTPAQFQAALDEYEELNVWQVNTSR	TRITF	3		1005.149588	3012.425363	0.000698008	1	N	687	713
Q61881	Exosome	QVALY	VDLDDIAEDDPELVDSICENAK	RYSRL	2	C18:+57.021	1238.05789	2474.100179	0.000451244	1	N	49	71
Q61881	Exosome	VKMTK	SDDDVSGAGELSSEELK	QIAEE	2		869.3872148	1736.75883	0.000823681	3	N	308	325
Q61881	Exosome	KRYSR	LFGDVVQELLPEYK	EKEVV	2		825.4434105	1648.871221	0.001654178	2	N	75	89
Q61881	Exosome	YNPRR	SLEQNVQLPAALLSR	FDLLW	2		819.962833	1637.910066	0.002727428	1	N	499	514
Q61881	Parental	GENTR	IAQPGDHVSVTGIFLPVLR	TGFQQ	3		673.7182308	2018.131293	0.000451244	8	N	263	282
Q61881	Parental	RCISR	GFTPAQFQAALDEYEELNVWQVNTSR	TRITF	3		1005.149588	3012.425363	0.000451244	8	N	687	713
Q61881	Parental	QVALY	VDLDDIAEDDPELVDSICENAK	RYSRL	2	C18:+57.021	1238.05789	2474.100179	0.000451244	13	N	49	71
Q61881	Parental	QVALY	VDLDDIAEDDPELVDSICENAK	RYSRL	3	C18:+57.021	825.7078597	2474.100179	0.001162105	1	N	49	71
Q61881	Parental	VKMTK	SDDDVSGAGELSSEELK	QIAEE	2		869.3872148	1736.75883	0.000451244	10	N	308	325
Q61881	Parental	KRYSR	LFGDVVQELLPEYK	EKEVV	2		825.4434105	1648.871221	0.000451244	1	N	75	89
Q61881	Parental	ALLSR	FDLLWLIQDRPDRDNDLR	LAQHI	4		575.8005314	2299.170926	0.00307782	1	N	514	532
Q61881	Parental	ALLSR	FDLLWLIQDRPDR	DNDLR	3		562.9707789	1685.888937	0.001329271	1	N	514	527
Q61937	Exosome	KNCFR	MTDQEAIQDLWQWR	KSL-	2		910.425758	1818.835916	0.000451244	13	N	275	289
Q61937	Exosome	LATLK	MSVQPTVSLGGFEITPPVVLR	LKCGS	2		1114.111912	2226.208224	0.000451244	33	N	80	101
Q61937	Exosome	LATLK	MSVQPTVSLGGFEITPPVVLR	LKCGS	3		743.0772078	2226.208224	0.000622848	7	N	80	101
Q61937	Exosome	LATLK	MSVQPTVSLGGFEITPPVVLR	LKCGS	3	M1:+15.995	748.4088745	2242.203224	0.002296037	1	N	80	101
Q61937	Exosome	QLSLR	TVSLGAGAKDELHIVEAEAMNYEGSPIK	VTLAT	3	M20:+15.995	982.4907622	2944.448887	0.000451244	37	N	45	73
Q61937	Exosome	QLSLR	TVSLGAGAKDELHIVEAEAMNYEGSPIK	VTLAT	4	M20:+15.995	737.1200217	2944.448887	0.000451244	3	N	45	73
Q61937	Parental	KNCFR	MTDQEAIQDLWQWRK	SL-	3		649.9847597	1946.930879	0.002019181	1	N	275	290
Q61937	Parental	ATLKM	SVQPTVSLGGFEITPPVVLR	LKCGS	2		1048.591669	2095.167738	0.000451244	16	N	81	101
Q61937	Parental	ATLKM	SVQPTVSLGGFEITPPVVLR	LKCGS	3		699.3970459	2095.167738	0.000622848	3	N	81	101
Q61937	Parental	KNCFR	MTDQEAIQDLWQWR	KSL-	2		910.425758	1818.835916	0.000451244	24	N	275	289
Q61937	Parental	KNCFR	MTDQEAIQDLWQWR	KSL-	3		607.2864387	1818.835916	0.001162105	2	N	275	289
Q61937	Parental	LATLK	MSVQPTVSLGGFEITPPVVLR	LKCGS	2		1114.111912	2226.208224	0.000451244	38	N	80	101
Q61937	Parental	LATLK	MSVQPTVSLGGFEITPPVVLR	LKCGS	3		743.0772078	2226.208224	0.000622848	2	N	80	101

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q61937	Parental	LATLK	MSVQPTVSLGGFEITPPVVL	RLKCG	2		1036.061356	2070.107112	0.000451244	16	N	80	100
Q61937	Parental	QKKVK	LDEDDEDDDEDDEDDEDDDDDDFDEEETEEKVPVK	KSVRD	3		1393.165867	4176.4742	0.001329271	1	N	157	192
Q61990	Exosome	GSTDR	QVTITGSAASISLAQYLINVR	LSSET	2		1103.116039	2204.216479	0.001162105	1	N	330	351
Q61990	Exosome	SPEVK	GYWAGLDASAQTTSHELTIPNDLIGCIIGR	QGAKI	3	C26:+57.021	1077.203432	3228.586897	0.000451244	2	N	272	302
Q61990	Exosome	NSTER	AITIAGIPQSIIECVK	QICVV	2	C14:+57.021	856.9846883	1711.953777	0.000451244	10	N	144	160
Q61990	Exosome	IKEIR	ESTGAQVQVAGDMLPNSTER	AITIA	2	M13:+15.995	1053.492597	2104.969595	0.000451244	17	Y	124	144
Q61990	Exosome	NCPER	IITLAGPTNAIFK	AFAMI	2		679.9062668	1357.796934	0.000622848	4	N	57	70
Q61990	Exosome	PVTLR	LVVPASQCGSLIGK	GGCKI	2	C8:+57.021	714.8978845	1427.780169	0.00307782	1	N	101	115
Q61990	Parental	GAQIK	IANPVEGSTDRQVTITGSAASISLAQYLINVR	LSSET	3		1115.598994	3343.773581	0.000823681	5	N	319	351
Q61990	Parental	GSTDR	QVTITGSAASISLAQYLINVR	LSSET	2		1103.116039	2204.216479	0.000451244	19	N	330	351
Q61990	Parental	GSTDR	QVTITGSAASISLAQYLINVR	LSSET	3		735.7466263	2204.216479	0.000637154	1	N	330	351
Q61990	Parental	SPEVK	GYWAGLDASAQTTSHELTIPNDLIGCIIGR	QGAKI	3	C26:+57.021	1077.203432	3228.586897	0.000451244	40	N	272	302
Q61990	Parental	NSTER	AITIAGIPQSIIECVK	QICVV	2	C14:+57.021	856.9846883	1711.953777	0.000451244	11	N	144	160
Q62059	Exosome	QAAWR	NGFDQCDYGWLSDASVR	HPVTV	2	C6:+57.021	995.4237118	1988.831824	0.000451244	5	N	288	305
Q62059	Exosome	FNTFR	CLCLPSYVGALCEQDTETCDYGWHK	FQGQC	3	C1:+57.021,C3:+57.021,C12:+57.021,C19:+57.021	1021.430999	3061.269596	0.000451244	6	N	3112	3137
Q62059	Exosome	TYGFR	SPQETYDVYCYVDHLDGDVFHITAPSK	FTFEE	4	C10:+57.021	789.8622414	3155.417766	0.002296037	1	N	233	260
Q62059	Exosome	PTEAR	DVEEMTTLTRLETDV	TKSDK	3		584.6176311	1750.829493	0.001591523	1	N	759	774
Q62086	Parental	LTQLK	VLQLGTLVDNLSIDPSSGDIWVGCHPNGQR	LFVYH	3	C24:+57.021	1083.210698	3246.608695	0.000451244	16	N	259	289
Q62086	Parental	SPDKK	YVYVADILAHEIHVLEK	QPNMN	4		503.777265	2011.07786	0.000451244	3	N	232	249
Q62167	Exosome	QMLAR	DFLDEYIFLAVGR	VGSTS	2		779.4015456	1556.787491	0.000622848	3	N	394	407
Q62167	Exosome	INITK	DLLDLLVEAK	QEVPS	2		564.8296934	1127.643787	0.000451244	10	N	554	564
Q62167	Exosome	EIDKR	SFLLDLLNATGK	DSLTL	2		646.3669744	1290.718349	0.000451244	9	N	428	440
Q62167	Exosome	ISNVK	HVINFDLPSDIEEYVHR	IGRTG	3		695.0134835	2082.017051	0.000451244	11	N	511	528
Q62167	Exosome	GRTGR	VGNLGLATSFFNER	NINIT	2		762.894419	1523.773238	0.002884417	1	N	534	548
Q62167	Exosome	TGSGK	TAAFLLPILSQIYADGPGEALR	AMKEN	2		1158.634065	2315.25253	0.000451244	8	N	230	252
Q62167	Exosome	TGSGK	TAAFLLPILSQIYADGPGEALR	AMKEN	3		772.7586434	2315.25253	0.000451244	7	N	230	252
Q62167	Exosome	KTAAF	LLPILSQIYADGPGEALR	AMKEN	2		963.5389049	1925.06221	0.000662267	3	N	234	252
Q62167	Exosome	SYRSR	VRPCVVYGGAEIGQQIR	DLERG	3	C4:+57.021	634.6723614	1900.993684	0.002296037	1	N	294	311
Q62167	Parental	FFNER	NINITKDLLDLLVEAK	QEVPS	2		906.5280059	1811.040412	0.000451244	2	N	548	564
Q62167	Parental	FFNER	NINITKDLLDLLVEAK	QEVPS	3		604.6879373	1811.040412	0.000451244	8	N	548	564
Q62167	Parental	QMLAR	DFLDEYIFLAVGR	VGSTS	2		779.4015456	1556.787491	0.000622848	16	N	394	407
Q62167	Parental	INITK	DLLDLLVEAK	QEVPS	2		564.8296934	1127.643787	0.000662267	20	N	554	564
Q62167	Parental	EIDKR	SFLLDLLNATGK	DSLTL	2		646.3669744	1290.718349	0.000451244	15	N	428	440
Q62167	Parental	ISNVK	HVINFDLPSDIEEYVHR	IGRTG	3		695.0134835	2082.017051	0.000451244	9	N	511	528
Q62167	Parental	PPSER	LEQELFSGGNTGINFEKYDDIPVEATGNNCPPHIESF	SDVEM	3	C30:+57.021	1380.30438	4137.889741	0.000451244	4	N	145	182
Q62167	Parental	PPSER	LEQELFSGGNTGINFEK	YDDIP	2		941.963227	1881.910854	0.000451244	12	N	145	162
Q62167	Parental	GRTGR	VGNLGLATSFFNER	NINIT	2		762.894419	1523.773238	0.001162105	2	N	534	548
Q62167	Parental	PPSER	LEQELFSGGNTGINFEKY	DDIPV	2		1023.494891	2044.974183	0.000622848	1	N	145	163
Q62178	Exosome	SEPVR	NLQLAPAQGAVFAGFSGGIWR	VPRAN	2		1080.571602	2159.127604	0.000451244	20	N	470	491
Q62178	Exosome	FFQQK	GLRDFDTLLLSDDGNTLYVGAR	EAVLA	3		804.4120834	2410.21285	0.000451244	7	N	59	81
Q62178	Exosome	GSLHK	AVVPQDSSAYLVEEIQLSPDSEPVR	NLQLA	2		1364.687951	2727.360303	0.000451244	6	N	445	470
Q62178	Exosome	GSLHK	AVVPQDSSAYLVEEIQLSPDSEPVR	NLQLA	3		910.1279009	2727.360303	0.000451244	14	N	445	470
Q62178	Exosome	YVGAR	EAVLALNIQNPGIPR	LKNMI	2		802.9600934	1603.904587	0.000451244	19	N	81	96
Q62178	Exosome	TTFLK	AQLLCAQPGQLPFNIIR	HAVLL	2	C5:+57.021	970.0330355	1938.050471	0.000451244	18	N	288	305
Q62178	Exosome	VGGTR	SSAVCAFSLTDIER	VFKGK	2	C5:+57.021	778.3749705	1554.734341	0.000451244	7	N	334	348
Q62178	Parental	SEPVR	NLQLAPAQGAVFAGFSGGIWR	VPRAN	2		1080.571602	2159.127604	0.000451244	13	N	470	491
Q62178	Parental	FFQQK	GLRDFDTLLLSDDGNTLYVGAR	EAVLA	3		804.4120834	2410.21285	0.000451244	1	N	59	81
Q62178	Parental	GSLHK	AVVPQDSSAYLVEEIQLSPDSEPVR	NLQLA	2		1364.687951	2727.360303	0.002019181	2	N	445	470
Q62178	Parental	GSLHK	AVVPQDSSAYLVEEIQLSPDSEPVR	NLQLA	3		910.1279009	2727.360303	0.001162105	1	N	445	470
Q62178	Parental	YVGAR	EAVLALNIQNPGIPR	LKNMI	2		802.9600934	1603.904587	0.002519933	1	N	81	96
Q62178	Parental	TTFLK	AQLLCAQPGQLPFNIIR	HAVLL	2	C5:+57.021	970.0330355	1938.050471	0.000451244	10	N	288	305
Q62186	Parental	TYEVR	FFDEESYSLLR	KAQRN	2		703.3358713	1404.656143	0.000698008	3	N	104	115
Q62186	Parental	RKAQR	NNEDVSIIPPLFTVSVDHR	GTWNG	2		1076.555815	2151.096029	0.002884417	1	N	119	138
Q62186	Parental	RKAQR	NNEDVSIIPPLFTVSVDHR	GTWNG	3		718.0398098	2151.096029	0.000451244	9	N	119	138
Q62186	Parental	SVDHR	GTWNGPWVSTEVLAAVIGIVIYYLAFSAK	SHIQA	3		1042.562381	3124.663743	0.000823681	7	N	138	167
Q62193	Exosome	KSRVR	AQHIVPCTISQLLSATLTDEVFR	IGDVE	3	C7:+57.021	867.1235024	2598.347107	0.000451244	13	N	42	65
Q62193	Exosome	PMDVR	QWVDTDDASGENAVVPPETYVK	VAGHL	2		1210.566773	2419.117947	0.00307782	1	N	105	127
Q62193	Parental	KSRVR	AQHIVPCTISQLLSATLTDEVFR	IGDVE	3	C7:+57.021	867.1235024	2598.347107	0.000451244	12	N	42	65
Q62193	Parental	PMDVR	QWVDTDDASGENAVVPPETYVK	VAGHL	3	[0:-17.027	801.7047823	2402.090947	0.0025889	1	N	105	127
Q62219	Parental	PYCRR	DFLQLFAPR	CQGCQ	2		553.8038129	1105.592026	0.001395409	3	N	336	345
Q62219	Parental	LFAPR	CQGCQGPILDNYISALSALWHPDCFVCR	ECLAP	3	C1:+57.021,C4:+57.021,C24:+57.021,C27:+57.021	1113.171742	3336.491825	0.000451244	4	N	345	373
Q62261	Exosome	LDILK	IVSSNDVGHDEYSTQSLVK	KHKDV	2		1039.505987	2076.996375	0.000451244	4	N	765	784
Q62261	Exosome	LDILK	IVSSNDVGHDEYSTQSLVK	KHKDV	3		693.3399249	2076.996375	0.002080925	2	N	765	784

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q62261	Exosome	SALER	LTTLELLEVR	RQQEE	2		593.8562425	1185.696885	0.001162105	8	N	2078	2088
Q62261	Exosome	LADLK	QLWGLLIEETEKR	HRRLE	3		538.9670344	1613.877703	0.000622848	8	N	1571	1584
Q62261	Exosome	DKLKK	SNAHYNLQNAFNLAEQHLGLTK	LLDPE	3		828.4195723	2482.235317	0.000622848	7	N	227	249
Q62261	Exosome	DKLKK	SNAHYNLQNAFNLAEQHLGLTK	LLDPE	4		621.5666292	2482.235317	0.000451244	7	N	227	249
Q62261	Exosome	SMLKK	HQILEQAVEDYAETVHQLSK	TSRAL	3		780.0611621	2337.160086	0.000451244	29	N	1633	1653
Q62261	Exosome	FQLNR	EVDDLEQWIAER	EVVAG	2		751.8602419	1501.704884	0.000451244	10	N	1705	1717
Q62261	Exosome	SENQR	LVSQDNFGFDLPAVEAATK	KHEAI	2		1011.513084	2021.010568	0.000451244	27	N	443	462
Q62261	Exosome	RDLQK	FLQDCQELSLWINEK	MLTAQ	2	C5:+57.021	961.9697665	1921.923933	0.000451244	5	N	1279	1294
Q62261	Exosome	QQFLR	DLDDFQSWLSR	TQTAI	2		691.3232952	1380.63099	0.000451244	21	N	1069	1080
Q62261	Exosome	HQFSR	DASVAEAWLLGQEPYLSSR	EIGQS	2		1046.52144	2091.027281	0.000451244	18	N	2024	2043
Q62261	Exosome	HQFSR	DASVAEAWLLGQEPYLSSR	EIGQS	3		698.0168937	2091.027281	0.000622848	2	N	2024	2043
Q62261	Exosome	IAEWK	DGLNEAWADLLELIDTR	TQILA	2		972.489609	1942.963618	0.000451244	31	N	1780	1797
Q62261	Exosome	IAEWK	DGLNEAWADLLELIDTR	TQILA	3		648.6623393	1942.963618	0.000451244	8	N	1780	1797
Q62261	Exosome	SDLQK	EAEKLESEHPDQAQAILSR	LAEIS	2		1076.037986	2150.060372	0.000622848	1	N	1017	1036
Q62261	Exosome	SDLQK	EAEKLESEHPDQAQAILSR	LAEIS	3		717.6945907	2150.060372	0.000451244	19	N	1017	1036
Q62261	Exosome	DIFER	SQNIITDSSSLNAEAIR	QRLAD	2		909.9637584	1817.911917	0.000451244	22	N	1547	1564
Q62261	Exosome	LNNRK	FANSLVGVQQQLQAFNTYR	TVEKP	2		1092.563974	2183.112348	0.000451244	28	N	329	348
Q62261	Exosome	DPNTK	VSEEAESQQWDTSKGDQVSQNGLPAEQGSPR	MAGTM	3		1115.514094	3343.518882	0.000622848	12	N	2108	2139
Q62261	Exosome	DNVIR	LWEYLLELLR	ARRQR	2		674.3877099	1346.75982	0.000451244	20	N	508	518
Q62261	Exosome	KFTEK	GNLEVLLFTIQSK	MRANN	2		731.4197383	1460.823877	0.000451244	14	N	359	372
Q62261	Exosome	ASAQK	FATDGEGYKPCDPQVIR	DRVAH	2	C11:+57.021	976.9624728	1951.909346	0.000451244	4	N	593	610
Q62261	Exosome	ASAQK	FATDGEGYKPCDPQVIR	DRVAH	3	C11:+57.021	651.6442485	1951.909346	0.000451244	4	N	593	610
Q62261	Exosome	IIYIR	EQWANLEQLSAIR	KKRLE	2		779.4051509	1556.794702	0.000451244	18	N	723	736
Q62261	Exosome	TVQTK	FMELLEPLSERK	HNLLA	2	M2:+15.995	754.3954492	1506.775298	0.002519933	1	N	1466	1478
Q62261	Exosome	VKKHK	DVAEEITNYRPTIDTLHEQASALPQAHAESPDVK	GRLAG	3		1249.28217	3744.82311	0.001839721	1	N	787	821
Q62261	Exosome	KMIEK	YESLASDLLEWIEQTIIILNNRK	FANSL	3		921.1643978	2760.469794	0.00091018	2	N	306	329
Q62261	Exosome	VDRKK	DALLSALSIQNYHLECNETK	SWIRE	2	C16:+57.021	1160.068198	2318.120795	0.000622848	2	N	948	968
Q62261	Exosome	HQFNR	DVEDEILWVGER	MPLAT	2		730.357335	1458.69907	0.000622848	1	N	1492	1504
Q62261	Exosome	EAATK	KHEAIETDIAAYEER	VQAVV	2		887.9344696	1773.853339	0.000451244	1	N	462	477
Q62261	Exosome	EAATK	KHEAIETDIAAYEER	VQAVV	3		592.2922464	1773.853339	0.000998612	1	N	462	477
Q62261	Exosome	KKSAK	DALLLWCQMK	TAGYP	2	C7:+57.021,M9:+15.995	647.3204673	1292.625335	0.002080925	1	Y	176	186
Q62261	Parental	LDILK	IVSSNDVGHDEYSTQSLVK	KHKDV	2		1039.505987	2076.996375	0.000451244	11	N	765	784
Q62261	Parental	SALER	LTTLELLEVR	RQQEE	2		593.8562425	1185.696885	0.001162105	17	N	2078	2088
Q62261	Parental	LADLK	QLWGLLIEETEKR	HRRLE	2		807.9466516	1613.877703	0.002453667	1	N	1571	1584
Q62261	Parental	LADLK	QLWGLLIEETEKR	HRRLE	3		538.9670344	1613.877703	0.000451244	19	N	1571	1584
Q62261	Parental	DKLKK	SNAHYNLQNAFNLAEQHLGLTK	LLDPE	3		828.4195723	2482.235317	0.000622848	11	N	227	249
Q62261	Parental	DKLKK	SNAHYNLQNAFNLAEQHLGLTK	LLDPE	4		621.5666292	2482.235317	0.000451244	12	N	227	249
Q62261	Parental	SMLKK	HQILEQAVEDYAETVHQLSK	TSRAL	3		780.0611621	2337.160086	0.000451244	32	N	1633	1653
Q62261	Parental	SMLKK	HQILEQAVEDYAETVHQLSK	TSRAL	4		585.2978216	2337.160086	0.001871652	3	N	1633	1653
Q62261	Parental	FQLNR	EVDDLEQWIAER	EVVAG	2		751.8602419	1501.704884	0.000451244	7	N	1705	1717
Q62261	Parental	SENQR	LVSQDNFGFDLPAVEAATK	KHEAI	2		1011.513084	2021.010568	0.000451244	30	N	443	462
Q62261	Parental	RDLQK	FLQDCQELSLWINEK	MLTAQ	2	C5:+57.021	961.9697665	1921.923933	0.000622848	10	N	1279	1294
Q62261	Parental	QQFLR	DLDDFQSWLSR	TQTAI	2		691.3232952	1380.63099	0.000451244	12	N	1069	1080
Q62261	Parental	HQFSR	DASVAEAWLLGQEPYLSSR	EIGQS	2		1046.52144	2091.027281	0.000451244	33	N	2024	2043
Q62261	Parental	HQFSR	DASVAEAWLLGQEPYLSSR	EIGQS	3		698.0168937	2091.027281	0.000451244	29	N	2024	2043
Q62261	Parental	DERHR	LFQLNREVDDLEQWIAER	EVVAG	3		758.7224807	2273.144042	0.0025889	1	N	1699	1717
Q62261	Parental	IAEWK	DGLNEAWADLLELIDTR	TQILA	2		972.489609	1942.963618	0.000451244	30	N	1780	1797
Q62261	Parental	IAEWK	DGLNEAWADLLELIDTR	TQILA	3		648.6623393	1942.963618	0.000451244	13	N	1780	1797
Q62261	Parental	SDLQK	EAEKLESEHPDQAQAILSR	LAEIS	2		1076.037986	2150.060372	0.000451244	3	N	1017	1036
Q62261	Parental	SDLQK	EAEKLESEHPDQAQAILSR	LAEIS	3		717.6945907	2150.060372	0.000451244	36	N	1017	1036
Q62261	Parental	EVRKK	EIEELQSQAQALSQEGK	STDEV	2		944.4688736	1886.922147	0.000451244	16	N	1434	1451
Q62261	Parental	DIFER	SQNIITDSSSLNAEAIR	QRLAD	2		909.9637584	1817.911917	0.000451244	17	N	1547	1564
Q62261	Parental	LNNRK	FANSLVGVQQQLQAFNTYR	TVEKP	2		1092.563974	2183.112348	0.000451244	32	N	329	348
Q62261	Parental	DRKAK	SALPAQSAATLPAR	TLETP	2		677.3784048	1352.74121	0.000451244	1	N	2176	2190
Q62261	Parental	DPNTK	VSEEAESQQWDTSKGDQVSQNGLPAEQGSPR	MAGTM	3		1115.514094	3343.518882	0.000451244	65	N	2108	2139
Q62261	Parental	PASSR	AQTLPTSVVTITSESSPGKR	EKDKE	2		1030.055648	2058.095695	0.000451244	9	N	2324	2344
Q62261	Parental	RVSCR	ITDLYTDLRDGR	MLIKL	3		479.9164512	1436.725954	0.001699387	1	N	74	86
Q62261	Parental	DNVIR	LWEYLLELLR	ARRQR	2		674.3877099	1346.75982	0.000823681	16	N	508	518
Q62261	Parental	ASAQK	FATDGEGYKPCDPQVIRDR	VAHME	4	C11:+57.021	556.76715	2223.0374	0.0007646	3	N	593	612
Q62261	Parental	KFTEK	GNLEVLLFTIQSK	MRANN	2		731.4197383	1460.823877	0.000622848	7	N	359	372
Q62261	Parental	ASAQK	FATDGEGYKPCDPQVIR	DRVAH	2	C11:+57.021	976.9624728	1951.909346	0.001264573	1	N	593	610
Q62261	Parental	ASAQK	FATDGEGYKPCDPQVIR	DRVAH	3	C11:+57.021	651.6442485	1951.909346	0.000622848	1	N	593	610
Q62261	Parental	IIYIR	EQWANLEQLSAIR	KKRLE	2		779.4051509	1556.794702	0.000451244	19	N	723	736
Q62261	Parental	KMIEK	YESLASDLLEWIEQTIIILNNRK	FANSL	3		921.1643978	2760.469794	0.000451244	2	N	306	329
Q62261	Parental	VDRKK	DALLSALSIQNYHLECNETK	SWIRE	2	C16:+57.021	1160.068198	2318.120795	0.000451244	10	N	948	968

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q62261	Parental	VDRKK	DALLSALSIQNYHLECNETK	SWIRE	3	C16:+57.021	773.7147318	2318.120795	0.002813207	1	N	948	968
Q62261	Parental	IRKKR	LEEASLLHQFQADADDIDAWMLDILK	IVSSN	3		1000.827346	2999.458638	0.000622848	1	N	739	765
Q62261	Parental	TEAEK	LLTQHENIKNEIDNYEEDYQK	MRDMG	3		879.4211958	2635.240187	0.000451244	13	N	1099	1120
Q62261	Parental	HQFNR	DVEDEILWVGER	MPLAT	2		730.357335	1458.69907	0.000451244	9	N	1492	1504
Q62261	Parental	EAATK	KHEAIETDIAAYEER	VQAVV	2		887.9344696	1773.853339	0.000622848	1	N	462	477
Q62261	Parental	FLRQR	LQALDTGWNELHK	MWENR	3		508.9322127	1523.773238	0.000451244	3	N	1143	1156
Q62318	Exosome	AEGPR	LASPSGSTSSGLEVVAPEVTSAPVSGPGILDDSATICR	VCQKP	3	C37:+57.021	1228.947645	3683.819536	0.000451244	6	N	591	629
Q62318	Exosome	VSLER	LDLDLTSDSQPPVFK	VFPGS	2		837.9334069	1673.851214	0.001162105	1	N	492	507
Q62318	Parental	RLQEK	LSPPYSSPQEFAQDVGR	MFKQF	2		939.4555692	1876.895538	0.000451244	14	N	750	767
Q62318	Parental	AEGPR	LASPSGSTSSGLEVVAPEVTSAPVSGPGILDDSATICR	VCQKP	3	C37:+57.021	1228.947645	3683.819536	0.000451244	27	N	591	629
Q62318	Parental	TLTCR	DCQLNAHKDHQYQFLEDAVR	NQRKL	3	C2:+57.021	829.7208798	2486.139239	0.0007646	8	N	231	251
Q62318	Parental	TLTCR	DCQLNAHKDHQYQFLEDAVR	NQRKL	4	C2:+57.021	622.5426098	2486.139239	0.00091018	1	N	231	251
Q62318	Parental	RDGER	TVYCNVHKHEPLVLFCESCDTLTCR	DCQLN	3	C4:+57.021,C16:+57.021,C19:+57.021,C24:+57.021	1046.813554	3137.417263	0.002884417	1	N	206	231
Q62318	Parental	RKVPR	VSLERLDLDLTSDSQPPVFK	VFPGS	3		753.7342749	2258.179425	0.001943752	1	N	487	507
Q62318	Parental	FGDTK	FSAVLVEPPPLNLPSAGLSSQELSGPGDGP	-	3		978.1699886	2931.486566	0.001229886	2	N	804	834
Q62318	Parental	PPVFK	VFPGSTTEDYNLIVIER	GAAAA	2		977.0023522	1951.989104	0.000451244	3	N	507	524
Q62318	Parental	VSLER	LDLDLTSDSQPPVFK	VFPGS	2		837.9334069	1673.851214	0.000451244	16	N	492	507
Q62318	Parental	AGGEK	RPAASSAAAASAAASSPAGGGGEAQELLEHCGVCR	ERLRP	3	C31:+57.021,C34:+57.021	1108.853202	3323.536206	0.000451244	5	N	35	70
Q62318	Parental	AGGEK	RPAASSAAAASAAASSPAGGGGEAQELLEHCGVCR	ERLRP	4	C31:+57.021,C34:+57.021	831.8918516	3323.536206	0.000451244	15	N	35	70
Q62318	Parental	KQFNK	LTEDKADVQSIIGLQR	FFETR	2		893.489412	1784.963224	0.000870037	2	N	774	790
Q62318	Parental	KQFNK	LTEDKADVQSIIGLQR	FFETR	3		595.9955413	1784.963224	0.000451244	2	N	774	790
Q62348	Exosome	GDYSR	PLHISTFINELDSGFR	LLNLK	3		615.9884982	1844.942095	0.000451244	18	N	166	182
Q62348	Exosome	EQTAR	EILTLLQGVHQGTGFQDIPK	RCLKA	3		732.0675884	2193.179365	0.000622848	3	N	36	56
Q62348	Exosome	SELSR	LSVNSVTAGDYSRPLHISTFINELDSGFR	LLNLK	3		1065.874346	3194.599639	0.000451244	9	N	153	182
Q62348	Exosome	SELSR	LSVNSVTAGDYSRPLHISTFINELDSGFR	LLNLK	4		799.6577097	3194.599639	0.000451244	5	N	153	182
Q62348	Exosome	TLVTR	EAVTEILGIEPDREK	GFHLD	2		849.9495883	1697.883577	0.000698008	7	N	116	131
Q62348	Exosome	TLVTR	EAVTEILGIEPDREK	GFHLD	3		566.9689922	1697.883577	0.000451244	4	N	116	131
Q62348	Exosome	KYDVK	KVEEVVYDLSIR	GFNKE	3		483.9369637	1448.787491	0.000451244	2	N	203	215
Q62376	Exosome	LPHEK	HHNQPYCGIAPYIR	EFEDP	3	C7:+57.021	575.9478256	1724.820077	0.001352548	1	N	32	46
Q62376	Exosome	LFAPR	DPIPYLPPLEK	LPHEK	2		641.358618	1280.701636	0.002019181	3	N	16	27
Q62376	Parental	RDEAR	GGGGSGQDNGLEGLGSDGR	DMYME	2		845.3753074	1688.735015	0.000622848	22	N	403	422
Q62376	Parental	LFAPR	DPIPYLPPLEK	LPHEK	2		641.358618	1280.701636	0.000998612	3	N	16	27
Q62383	Parental	KKLKR	IKEDGDEEGEGEEAEDEEQR	GPELK	3		764.9794498	2291.914949	0.001943752	1	N	491	511
Q62383	Parental	ENPER	LKDLDLDAFAEELER	QGYGD	3		592.9725138	1775.894141	0.001943752	1	N	1098	1113
Q62393	Exosome	EELRR	ELTKVEEEIQTLSQVLAAK	EKHLA	2		1065.089156	2128.162712	0.000451244	5	N	80	99
Q62393	Exosome	EELRR	ELTKVEEEIQTLSQVLAAK	EKHLA	3		710.3953707	2128.162712	0.000451244	16	N	80	99
Q62393	Exosome	VGLLK	TEPVAEEGEDAVTMLSAPEALTEEEQEELRR	ELTKV	3	M14:+15.995	1158.874217	3473.599252	0.000622848	5	N	49	80
Q62393	Parental	QAGQK	ASAAFSSVGSVITK	KLEDV	2		662.8595135	1323.703427	0.000451244	22	N	148	162
Q62393	Parental	EELRR	ELTKVEEEIQTLSQVLAAK	EKHLA	2		1065.089156	2128.162712	0.000451244	26	N	80	99
Q62393	Parental	EELRR	ELTKVEEEIQTLSQVLAAK	EKHLA	3		710.3953707	2128.162712	0.000451244	20	N	80	99
Q62418	Exosome	YSFHK	ESTSFQDVGPQAPVGSVYQK	TNAIS	2		1062.516355	2123.01711	0.000451244	17	N	144	164
Q62418	Exosome	VVTEK	SPTDWALFTYEGNSNDIR	VAGTG	2		1043.479773	2084.943945	0.000451244	18	N	23	41
Q62418	Exosome	SNDIR	VAGTGEGGLEELVEELNSGK	VMYAF	2		994.4950884	1986.974577	0.000451244	19	N	41	61
Q62418	Exosome	SGLPK	FVLINWTGEGVNDVRK	GACAN	3		616.3323764	1845.973729	0.001871652	1	N	78	94
Q62418	Exosome	SGLPK	FVLINWTGEGVNDVR	KGACA	2		859.947183	1717.878766	0.000451244	4	N	78	93
Q62418	Parental	EKVAK	ASGANYSFHKESTSFQDVGPQAPVGSVYQK	TNAIS	3		1062.842935	3185.505404	0.000451244	15	N	134	164
Q62418	Parental	EKVAK	ASGANYSFHKESTSFQDVGPQAPVGSVYQK	TNAIS	4		797.384151	3185.505404	0.000451244	4	N	134	164
Q62418	Parental	YSFHK	ESTSFQDVGPQAPVGSVYQK	TNAIS	2		1062.516355	2123.01711	0.000451244	66	N	144	164
Q62418	Parental	VVTEK	SPTDWALFTYEGNSNDIR	VAGTG	2		1043.479773	2084.943945	0.000451244	33	N	23	41
Q62418	Parental	SNDIR	VAGTGEGGLEELVEELNSGK	VMYAF	2		994.4950884	1986.974577	0.000451244	37	N	41	61
Q62418	Parental	SNDIR	VAGTGEGGLEELVEELNSGK	VMYAF	3		663.3326589	1986.974577	0.002374549	4	N	41	61
Q62418	Parental	GLCAR	ALYDYQAADDTEISFDPENLITGIEVIDEGWWR	GYGPD	3		1282.267526	3843.779179	0.000451244	21	N	383	416
Q62418	Parental	SGLPK	FVLINWTGEGVNDVRK	GACAN	3		616.3323764	1845.973729	0.002813207	1	N	78	94
Q62418	Parental	EAYVR	VVTEKSPTDWALFTYEGNSNDIR	VAGTG	2		1321.640804	2641.266008	0.001162105	1	N	18	41
Q62418	Parental	SGLPK	FVLINWTGEGVNDVR	KGACA	2		859.947183	1717.878766	0.000451244	3	N	78	93
Q62418	Parental	PFLQK	QLTQPETSYGREPTAPVSR	PAAGV	3		706.3594309	2116.054893	0.001654178	3	N	296	315
Q62419	Exosome	LDYHR	QAVQILEELADKLK	RRVRE	3		533.3106897	1596.908669	0.000451244	5	N	227	241
Q62419	Exosome	QPSCK	ALYDFEPENDGELGFR	EGDLI	2		936.4264774	1870.837355	0.000823681	2	N	312	328
Q62419	Parental	LDYHR	QAVQILEELADKLK	RRVRE	3		533.3106897	1596.908669	0.000451244	15	N	227	241
Q62419	Parental	QPSCK	ALYDFEPENDGELGFR	EGDLI	2		936.4264774	1870.837355	0.001162105	3	N	312	328
Q62422	Exosome	NQQNK	LGDTALHAAAWK	GYADI	2		627.3360086	1252.656417	0.000823681	1	N	138	150
Q62422	Exosome	NQQNK	LGDTALHAAAWK	GYADI	3		418.5599391	1252.656417	0.001943752	3	N	138	150
Q62422	Exosome	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAKR	GNLSW	3		941.8144277	2822.419883	0.001162105	1	N	57	83
Q62422	Exosome	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAKR	GNLSW	4		706.6127708	2822.419883	0.000451244	23	N	57	83

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q62422	Exosome	AAAWK	GYADIVQLLLAK	GARTD	2		652.3851672	1302.754734	0.000451244	30	N	150	162
Q62422	Exosome	HGGHK	DIVEVLFTQPNVELNQQNK	LGDTA	2		1114.582029	2227.148459	0.000451244	36	N	119	138
Q62422	Exosome	HGGHK	DIVEVLFTQPNVELNQQNK	LGDTA	3		743.3906196	2227.148459	0.000451244	17	N	119	138
Q62422	Exosome	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAK	RGNLS	2		1334.167186	2666.318772	0.000637154	5	N	57	82
Q62422	Exosome	AWKGY	ADIVQLLLAK	GARTD	2		542.342771	1082.669942	0.001763695	2	N	152	162
Q62422	Parental	NQQNK	LGDTALHAAAWK	GYADI	2		627.3360086	1252.656417	0.000451244	9	N	138	150
Q62422	Parental	NQQNK	LGDTALHAAAWK	GYADI	3		418.5599391	1252.656417	0.000622848	8	N	138	150
Q62422	Parental	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAKR	GNLSW	2		1412.217742	2822.419883	0.000823681	2	N	57	83
Q62422	Parental	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAKR	GNLSW	4		706.6127708	2822.419883	0.000451244	21	N	57	83
Q62422	Parental	NGLDK	AGSTALYWACHGGHKDIVEVLFTQPNVELNQQNK	LGDTA	3	C10:+57.021	1275.632326	3823.873577	0.000451244	13	N	104	138
Q62422	Parental	AAAWK	GYADIVQLLLAK	GARTD	2		652.3851672	1302.754734	0.000451244	25	N	150	162
Q62422	Parental	AAAWK	GYADIVQLLLAK	GARTD	3		435.2593781	1302.754734	0.000451244	3	N	150	162
Q62422	Parental	NQQNK	LGDTALHAAAWKGYADIVQLLLAK	GARTD	3		846.8079972	2537.400592	0.000823681	2	N	138	162
Q62422	Parental	HGGHK	DIVEVLFTQPNVELNQQNK	LGDTA	2		1114.582029	2227.148459	0.000451244	26	N	119	138
Q62422	Parental	HGGHK	DIVEVLFTQPNVELNQQNK	LGDTA	3		743.3906196	2227.148459	0.000451244	20	N	119	138
Q62422	Parental	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAK	RGNLS	2		1334.167186	2666.318772	0.000451244	10	N	57	82
Q62422	Parental	TCKGR	TGLIPSNYVAEQAESIDNPLHEAAK	RGNLS	3		889.780724	2666.318772	0.000451244	2	N	57	82
Q62422	Parental	AWKGY	ADIVQLLLAK	GARTD	2		542.342771	1082.669942	0.001162105	5	N	152	162
Q62431	Parental	LPSPK	LPVTPLGLAASTNGSSITPAPK	IKKEE	2		1046.586583	2091.157567	0.000451244	7	N	379	401
Q62431	Parental	TVPGR	LPVSLAGHPVVAAQAAAVQAAAAQAAVAAQAAALEQLR	EKLES	3		1192.332582	3573.974346	0.000451244	6	N	417	455
Q62448	Parental	QLCLR	LAEDAPNFDGPAAEGQPGQK	QSTTF	2		1006.471948	2010.928295	0.000451244	8	N	138	158
Q62448	Parental	QFAAR	AIISELVSISELAQPLESGTHFPLFLLCLQQLAK	LQDRE	3	C28:+57.021	1256.021869	3765.042206	0.001839721	1	N	648	682
Q62448	Parental	QFAAR	AIISELVSISELAQPLESGTHFPLFLLCLQQLAK	LQDRE	4	C28:+57.021	942.2683515	3765.042206	0.001229886	1	N	648	682
Q62465	Exosome	YDKVK	LQSRPAVPPAPGPGQLTLR	VRACG	3		652.3782086	1954.111226	0.000451244	13	N	76	95
Q62465	Exosome	LQANR	AVCGFHLGYLDGEVELVNSVVTR	LVALY	3	C3:+57.021	845.4288143	2533.263043	0.000622848	4	N	334	357
Q62465	Exosome	MAMAR	TWWNQFSVTALQLLQANR	AVCGF	2		1088.569059	2175.122519	0.000451244	23	N	316	334
Q62465	Exosome	MAMAR	TWWNQFSVTALQLLQANR	AVCGF	3		726.0486396	2175.122519	0.002212458	2	N	316	334
Q62465	Exosome	HIKPR	IDSVWPFEK	VADAM	2		560.7878285	1119.560057	0.001329271	3	N	370	379
Q62465	Exosome	LQLCR	TVENVTVFGTASASK	HEVLK	2		755.891542	1509.767484	0.000451244	10	N	223	238
Q62465	Exosome	APPLR	CLVLTGFGGYDK	VKLQS	2	C1:+57.021	665.3293033	1328.643007	0.002884417	1	N	62	74
Q62465	Exosome	APPLR	CLVLTGFGGYDK	VKLQS	2	[0:-17.027,C1:+57.021	656.8158033	1311.616007	0.000823681	4	N	62	74
Q62465	Parental	YDKVK	LQSRPAVPPAPGPGQLTLR	VRACG	3		652.3782086	1954.111226	0.000451244	10	N	76	95
Q62465	Parental	LQANR	AVCGFHLGYLDGEVELVNSVVTR	LVALY	3	C3:+57.021	845.4288143	2533.263043	0.000451244	7	N	334	357
Q62465	Parental	MAMAR	TWWNQFSVTALQLLQANR	AVCGF	2		1088.569059	2175.122519	0.000451244	1	N	316	334
Q62465	Parental	MAMAR	TWWNQFSVTALQLLQANR	AVCGF	3		726.0486396	2175.122519	0.000998612	6	N	316	334
Q62465	Parental	HIKPR	IDSVWPFEK	VADAM	2		560.7878285	1119.560057	0.002663018	4	N	370	379
Q62465	Parental	APPLR	CLVLTGFGGYDKVK	LQSRP	3	C1:+57.021	519.6099279	1555.806384	0.000451244	4	N	62	76
Q62465	Parental	LQLCR	TVENVTVFGTASASK	HEVLK	2		755.891542	1509.767484	0.000451244	3	N	223	238
Q62465	Parental	APPLR	CLVLTGFGGYDK	VKLQS	2	C1:+57.021	665.3293033	1328.643007	0.002663018	1	N	62	74
Q62465	Parental	APPLR	CLVLTGFGGYDK	VKLQS	2	[0:-17.027,C1:+57.021	656.8158033	1311.616007	0.002813207	1	N	62	74
Q62469	Exosome	TPTER	YFFNVADEAALLEK	AGTLG	2		815.4121103	1628.808621	0.001463592	4	N	336	350
Q62469	Exosome	LHLTR	STNINFYEISSDENAPSVIK	SVEDI	2		1114.540027	2227.064455	0.001763695	1	N	939	959
Q62469	Exosome	PLDLR	VDISLENPGTSPALEAYSETVK	VFSIP	2		1160.581892	2319.148184	0.001352548	1	N	754	776
Q62469	Parental	LPGAK	IFSGPSSEQFGYSVQQLTNPQGNWLLVGSPWSGFPENR	MGDVY	3		1404.347285	4210.018456	0.000451244	5	N	35	73
Q62523	Exosome	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	C1:+39.994,C4:+57.021,C17:+57.021,C26:+57.021	1039.776907	3116.307321	0.000451244	3	N	528	555
Q62523	Exosome	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	[0:-17.027,C1:+57.021,C4:+57.021,C17:+57.021,C26:+57.021	1039.776907	3116.307321	0.000451244	13	N	528	555
Q62523	Exosome	RATGK	AYHPQCFTCVVCACPLEGTSFIVDQANQPHCVPDYHK	QYAPR	4	C6:+57.021,C9:+57.021,C12:+57.021,C14:+57.021,C31:+57.021	1102.239011	4404.924843	0.000451244	8	N	453	490
Q62523	Exosome	QYAPR	CSVCSEPIMPEPGRDETVR	VVALD	3	C1:+57.021,C4:+57.021,M9:+15.99	745.6663818	2233.975745	0.000622848	4	N	495	514
Q62523	Exosome	GQQFY	SLEGAPYCEGCYTDTLEK	CNTCG	2	C8:+57.021,C11:+57.021	1046.945597	2091.875594	0.001699387	2	N	417	435
Q62523	Parental	APKPK	VNPFRPGDSEPPVAAGAQR	AQMGR	2		983.0010095	1963.986419	0.000451244	21	N	35	54
Q62523	Parental	APKPK	VNPFRPGDSEPPVAAGAQR	AQMGR	3		655.6699397	1963.986419	0.000451244	5	N	35	54
Q62523	Parental	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	C1:+39.994,C4:+57.021,C17:+57.021,C26:+57.021	1039.776907	3116.307321	0.000451244	16	N	528	555
Q62523	Parental	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	C1:+57.021,C4:+57.021,C17:+57.021,C26:+57.021	1045.452574	3133.334321	0.000451244	9	N	528	555
Q62523	Parental	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	4	C1:+57.021,C4:+57.021,C17:+57.021,C26:+57.021	784.3413803	3133.334321	0.000451244	7	N	528	555
Q62523	Parental	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	[0:-17.027,C1:+57.021,C4:+57.021,C17:+57.021,C26:+57.021	1039.776907	3116.307321	0.000451244	35	N	528	555

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q62523	Parental	RATGK	AYHPQCFTCVVCACPLEGTSFIVDQANQPHCVPDYHK	QYAPR	3	C6:+57.021,C9:+57.021,C12:+57.021,C14:+57.021,C31:+57.021	1469.316081	4404.924843	0.000451244	19	N	453	490
Q62523	Parental	RATGK	AYHPQCFTCVVCACPLEGTSFIVDQANQPHCVPDYHK	QYAPR	4	C6:+57.021,C9:+57.021,C12:+57.021,C14:+57.021,C31:+57.021	1102.239011	4404.924843	0.000451244	17	N	453	490
Q62523	Parental	MKCYK	CEDCGKPLSIEADDNGCFPLDGHVLCRK	CHSAR	4	C1:+57.021,C4:+57.021,C17:+57.021,C26:+57.021	816.3651211	3261.429284	0.001162105	1	N	528	556
Q62523	Parental	NFHMK	CYKCEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	3	C1:+57.021,C4:+57.021,C7:+57.021,C20:+57.021,C29:+57.021	1195.848733	3584.522799	0.000451244	5	N	525	555
Q62523	Parental	NFHMK	CYKCEDCGKPLSIEADDNGCFPLDGHVLCR	KCHSA	4	C1:+57.021,C4:+57.021,C7:+57.021,C20:+57.021,C29:+57.021	897.1384996	3584.522799	0.001162105	1	N	525	555
Q62523	Parental	QYAPR	CSVCSEPIMPEPGRDETVR	VVALD	3	C1:+57.021,C4:+57.021	740.3347151	2217.980745	0.000622848	3	N	495	514
Q62523	Parental	RATGK	AYHPQCFTCVVCACPLEGTSFIVDQANQPH	CVPDY	3	C6:+57.021,C9:+57.021,C12:+57.021,C14:+57.021	1169.517578	3505.529333	0.000622848	5	N	453	483
Q62523	Parental	GQQFY	SLEGAPYCEGCYTDTLEK	CNTCG	2	C8:+57.021,C11:+57.021	1046.945597	2091.875594	0.000622848	4	N	417	435
Q62523	Parental	PVVSK	FSPGAPSGPGPQPNQK	MVPPD	2		783.3895008	1564.763402	0.000451244	13	N	270	286
Q62523	Parental	HITCF	TCHQCQQQLQGQQFYSLEGAPYCEGCYTDTLEK	CNTCG	3	C2:+57.021,C5:+57.021,C23:+57.021,C26:+57.021	1343.237756	4026.689869	0.000823681	2	N	402	435
Q63810	Exosome	PLVQR	VIDIFDTDGNGEVDFKEFIEGVSQFSVK	GDKEQ	3		1045.512192	3133.513175	0.000451244	44	N	57	85
Q63810	Exosome	DGDGR	ISFEEFCAVVGGLDIHKK	MVVDV	4	C7:+57.021	513.0177079	2048.039632	0.000451244	21	N	147	165
Q63810	Exosome	DGDGR	ISFEEFCAVVGGLDIHK	KMVVD	3	C7:+57.021	640.9893561	1919.944668	0.001871652	1	N	147	164
Q63810	Parental	PLVQR	VIDIFDTDGNGEVDFKEFIEGVSQFSVK	GDKEQ	3		1045.512192	3133.513175	0.000451244	35	N	57	85
Q63810	Parental	DGDGR	ISFEEFCAVVGGLDIHKK	MVVDV	4	C7:+57.021	513.0177079	2048.039632	0.000622848	3	N	147	165
Q63844	Exosome	NVLHR	DLKPSNLLINTTCDLK	ICDFG	2	C13:+57.021	922.9932416	1843.970883	0.000451244	6	N	166	182
Q63844	Exosome	NVLHR	DLKPSNLLINTTCDLK	ICDFG	3	C13:+57.021	615.6647611	1843.970883	0.000451244	10	N	166	182
Q63844	Exosome	YKLLK	SQQLSNDHICYFLYQILR	GLKYI	2	C10:+57.021	1149.57071	2297.125821	0.000451244	1	N	135	153
Q63844	Exosome	YKLLK	SQQLSNDHICYFLYQILR	GLKYI	3	C10:+57.021	766.716407	2297.125821	0.000451244	13	N	135	153
Q63844	Exosome	LPKER	LKELIFQETAR	FQPGA	3		449.926399	1346.755797	0.000662267	3	N	360	371
Q63844	Exosome	FGLAR	IADPEHDHTGFLTEYVATR	WYRAP	3		724.6839145	2171.028344	0.000451244	3	N	190	209
Q63844	Exosome	LAHPY	LEQYYDPTDEPVAEEPFTFDMELDDLPKER	LKELI	3	M21:+15.995	1216.54733	3646.618591	0.000870037	6	N	330	360
Q63844	Exosome	NPNKR	ITVEEALAHPY	LEQYY	2		621.8223997	1241.629199	0.000823681	5	N	319	330
Q63844	Exosome	LAHPY	LEQYYDPTDEPVAEEPFTFDMELDDLPK	ERLKE	3	M21:+15.995	1121.499429	3361.474887	0.000622848	2	N	330	358
Q63844	Exosome	KGYTK	SIDIWSVGCILAEMLSNRPIFPGK	HYLDQ	3	C9:+57.021	901.8051166	2702.39195	0.000735798	2	Y	225	249
Q63844	Exosome	NPNKR	ITVEEALAHPYLEQYYDPTDEPVAEEPFTF	DMELD	3		1171.880721	3512.618762	0.001352548	1	N	319	349
Q64012	Parental	LTQIK	SNIDALLGRLEQIAEEQK	ANPDG	3		676.3642934	2026.06948	0.000451244	1	N	198	216
Q64012	Parental	SSSSR	LPAPQEDTASEAGTPQGEVQTR	DDGDE	2		1141.548915	2281.08223	0.000451244	27	N	260	282
Q640N3	Exosome	PQVLR	SCAEFVQEYGVVDGIYR	LSGVS	2	C2:+57.021	996.4623056	1990.909011	0.000451244	2	N	38	55
Q640N3	Exosome	NMHAR	NLAIVWAPNLLR	SKDIE	2		690.4120506	1378.808501	0.000622848	2	N	167	179
Q64152	Exosome	FNNPK	VQASLAANTFTITGHAETK	QLTEM	2		980.5108758	1959.006152	0.000451244	5	N	120	139
Q64152	Exosome	FNNPK	VQASLAANTFTITGHAETK	QLTEM	3		654.0098505	1959.006152	0.000698008	7	N	120	139
Q64152	Parental	FNNPK	VQASLAANTFTITGHAETK	QLTEM	2		980.5108758	1959.006152	0.000451244	31	N	120	139
Q64152	Parental	FNNPK	VQASLAANTFTITGHAETK	QLTEM	3		654.0098505	1959.006152	0.000451244	12	N	120	139
Q64152	Parental	SVDGK	APLATGEDDDDEVPDLVENFDEASKNEAN	-	3		1040.453618	3118.337455	0.000622848	18	N	175	204
Q64277	Exosome	AYPTR	GFFADFEIPYLQK	DKVTR	2		787.8986387	1573.781677	0.000637154	7	N	196	209
Q64277	Parental	AYPTR	GFFADFEIPYLQK	DKVTR	2		787.8986387	1573.781677	0.000451244	13	N	196	209
Q64277	Parental	ENTRR	LVALCDVLYGK	VGDFL	2	C5:+57.021	625.8445892	1249.673578	0.00307782	1	N	118	129
Q64277	Parental	WEAFK	GVLDKDPCSVLPSDYDLFINLSR	HPIPR	3	C8:+57.021	875.1076294	2622.299488	0.000870037	1	N	68	91
Q64324	Exosome	SSLIR	NLEQLGGTVTNSAGSGTSSR	LERRE	2		968.4724789	1934.929358	0.000451244	30	N	439	459
Q64324	Exosome	DRLDR	KLWPFVSDPAPVPSSQAAVSAR	FGHWH	3		770.7467378	2309.216813	0.000451244	3	N	493	515
Q64324	Exosome	DINKR	REPIPSLEAIYLLSPTEK	SVQAL	3		686.0495347	2055.125204	0.0007646	8	N	64	82
Q64324	Exosome	SPTEK	SVQALIADFQGTPTFTYK	AAHIF	2		994.01272	1986.00984	0.000451244	12	N	82	100
Q64324	Exosome	VKTLK	EIHLAFLPYEAQVFSLDAPHSTYNLYCPFR	AGERG	3	C27:+57.021	1200.254016	3597.738647	0.000622848	2	N	131	161
Q64324	Exosome	VKTLK	EIHLAFLPYEAQVFSLDAPHSTYNLYCPFR	AGERG	4	C27:+57.021	900.4424617	3597.738647	0.000622848	3	N	131	161
Q64324	Exosome	SSCCK	MSDILAEGITIVEDINKR	REPIP	3		673.0265131	2016.056139	0.000451244	6	N	46	64
Q64324	Exosome	GERGR	QLDALAQQIATLCATLQEYPSIR	YRKGP	3	C13:+57.021	868.4551406	2602.342022	0.000451244	6	N	167	190
Q64324	Exosome	TFTYK	AAHIFFTDTCPEPLFSELGR	SRLAK	2	C10:+57.021	1154.557269	2307.098938	0.000451244	3	N	100	120
Q64324	Exosome	SIRYR	KGPEDTAQLAHAVLAK	LNAFK	3		550.3059387	1647.894416	0.002813207	2	N	192	208
Q64324	Exosome	INKRR	EPIPSLEAIYLLSPTEK	SVQAL	2		950.5198465	1899.024093	0.000622848	7	N	65	82
Q64324	Parental	SSLIR	NLEQLGGTVTNSAGSGTSSR	LERRE	2		968.4724789	1934.929358	0.000451244	24	N	439	459
Q64324	Parental	DRLDR	KLWPFVSDPAPVPSSQAAVSAR	FGHWH	2		1155.616207	2309.216813	0.001162105	2	N	493	515
Q64324	Parental	DRLDR	KLWPFVSDPAPVPSSQAAVSAR	FGHWH	3		770.7467378	2309.216813	0.000451244	5	N	493	515
Q64324	Parental	DINKR	REPIPSLEAIYLLSPTEK	SVQAL	2		1028.570402	2055.125204	0.0007646	4	N	64	82
Q64324	Parental	SPTEK	SVQALIADFQGTPTFTYK	AAHIF	2		994.01272	1986.00984	0.000451244	26	N	82	100
Q64324	Parental	AKAVK	TLKEIHLAFLPYEAQVFSLDAPHSTYNLYCPFR	AGERG	4	C30:+57.021	985.9991381	3939.965352	0.000451244	6	N	128	161
Q64324	Parental	VKTLK	EIHLAFLPYEAQVFSLDAPHSTYNLYCPFR	AGERG	4	C27:+57.021	900.4424617	3597.738647	0.000622848	6	N	131	161
Q64324	Parental	SSCCK	MSDILAEGITIVEDINKR	REPIP	3		673.0265131	2016.056139	0.000451244	8	N	46	64

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q64324	Parental	GERGR	QLDALAQQIATLCATLQEYPSIR	YRKGP	2	C13:+57.021	1302.178811	2602.342022	0.000451244	10	N	167	190
Q64324	Parental	GERGR	QLDALAQQIATLCATLQEYPSIR	YRKGP	3	C13:+57.021	868.4551406	2602.342022	0.000451244	12	N	167	190
Q64324	Parental	GERGR	QLDALAQQIATLCATLQEYPSIR	YRKGP	3	[0:-17.027,C13:+57.021	862.7794739	2585.315022	0.000451244	8	N	167	190
Q64324	Parental	TFTYK	AAHIFFTDTCPEPLFSELGR	SRLAK	2	C10:+57.021	1154.557269	2307.098938	0.000451244	1	N	100	120
Q64324	Parental	TFTYK	AAHIFFTDTCPEPLFSELGR	SRLAK	3	C10:+57.021	770.0407792	2307.098938	0.000979378	2	N	100	120
Q64324	Parental	SIRYR	KGPEDTAQLAHAVLAK	LNAFK	3		550.3059387	1647.894416	0.000622848	2	N	192	208
Q64324	Parental	SPTEK	SVQALIADFQGTPTFTY	KAAHI	2		929.9652384	1857.914877	0.000622848	2	N	82	99
Q64324	Parental	INKRR	EPIPSLEAIYLLSPTEK	SVQAL	2		950.5198465	1899.024093	0.000451244	2	N	65	82
Q64433	Exosome	YGGTK	VVLDDKDYFLFR	DSDIL	3		510.6053255	1528.792577	0.002884417	1	N	80	92
Q64433	Parental	KSQGK	VLQATVVAVGSGGK	GKSGE	2		643.3778735	1284.740147	0.000451244	29	N	40	54
Q64433	Parental	YGGTK	VVLDDKDYFLFR	DSDIL	2		765.4040883	1528.792577	0.000451244	3	N	80	92
Q64433	Parental	YGGTK	VVLDDKDYFLFR	DSDIL	3		510.6053255	1528.792577	0.000451244	22	N	80	92
Q64433	Parental	GGTKV	VLDDKDYFLFR	DSDIL	3		477.5825208	1429.724163	0.002374549	1	N	81	92
Q64433	Parental	YGGTK	VVLDDKDYFLF	RDSDI	2		687.3535327	1372.691465	0.001699387	2	N	80	91
Q64442	Exosome	CKIGR	YNLTPTIFFCATPPDDGNLCR	FYKHN	2	C10:+57.021,C20:+57.021	1236.569819	2471.124038	0.000622848	21	N	110	131
Q64442	Exosome	CKIGR	YNLTPTIFFCATPPDDGNLCR	FYKHN	3	C10:+57.021,C20:+57.021	824.7158126	2471.124038	0.000823681	1	N	110	131
Q64442	Exosome	PGDIR	LENYPIPELGPNDVLLK	MHSVG	2		962.5254632	1923.035326	0.000451244	12	N	21	38
Q64442	Exosome	DFCYK	LPDSVTFEEGALIEPLSVGIYACR	RGSVS	2	C23:+57.021	1318.667745	2635.319889	0.000451244	1	N	142	166
Q64442	Parental	CKIGR	YNLTPTIFFCATPPDDGNLCR	FYKHN	2	C10:+57.021,C20:+57.021	1236.569819	2471.124038	0.001591523	4	N	110	131
Q64455	Exosome	HGPIK	AYAVILTTGEAAQPSADVLK	YTYED	2		1009.544384	2017.073169	0.000662267	8	N	749	769
Q64455	Exosome	SYTVK	ILTQVGDGTTSLVPGWNLFCTEPEPVTSFHCEVVPK	EPALV	3	C20:+57.021,C31:+57.021	1338.992266	4013.953399	0.000451244	25	N	597	633
Q64455	Exosome	GQVLC	AGAAPNPIFDIEAVVSPTSVLLTWK	HNDSG	3		866.1394125	2595.394838	0.002019181	1	N	35	60
Q64455	Parental	HGPIK	AYAVILTTGEAAQPSADVLK	YTYED	2		1009.544384	2017.073169	0.000451244	10	N	749	769
Q64455	Parental	SYTVK	ILTQVGDGTTSLVPGWNLFCTEPEPVTSFHCEVVPK	EPALV	3	C20:+57.021,C31:+57.021	1338.992266	4013.953399	0.000451244	32	N	597	633
Q64455	Parental	SHPLR	QFHFTSWPDHGVPDTTDLLINFR	YLVRD	4		686.5875617	2742.319047	0.001352548	1	N	1097	1120
Q64511	Exosome	SSLAR	LLFPAVDDNLLK	FLYDD	2		679.3904495	1356.765299	0.000823681	4	N	824	836
Q64511	Exosome	PGLYK	IFDEILVNAADNK	QRDKN	2		731.3833528	1460.751106	0.000622848	2	Y	92	105
Q64511	Exosome	SKKPK	KTSFDQDSDVDIFPSDFTSEPPALPR	TGRAR	3		971.1264485	2910.355946	0.000451244	3	N	1560	1586
Q64511	Exosome	LLKHG	FLEEFITPIVK	ASKNK	2		668.3820932	1334.748586	0.0025889	2	Y	577	588
Q64511	Parental	PSLLK	HGFLEEFITPIVK	ASKNK	3		510.617454	1528.828962	0.000870037	6	N	575	588
Q64511	Parental	SSLAR	LLFPAVDDNLLK	FLYDD	2		679.3904495	1356.765299	0.000870037	1	N	824	836
Q64511	Parental	PGLYK	IFDEILVNAADNK	QRDKN	2		731.3833528	1460.751106	0.000451244	7	Y	92	105
Q64511	Parental	ELKVK	ASPITNDGEDEFVPSDGLDKDEYAFSSGK	SKATP	3		1030.795316	3089.362547	0.001264573	2	N	1385	1414
Q64514	Exosome	DGKPK	IIDIIDTTGSGDVNTATEVEPK	DGEII	2		1144.579349	2287.143099	0.000451244	38	N	63	85
Q64514	Exosome	PRGLR	EGLHYTEVCGYDIASPNAGPLFR	VPITA	3	C9:+57.021	856.0729191	2565.195357	0.000451244	6	N	605	628
Q64514	Exosome	QWMTK	LDSTDIYNELKETYPAYLPLYVAR	LHQLD	3		949.8204082	2846.437825	0.000451244	27	N	1048	1072
Q64514	Exosome	TWSSR	GPSADGALGVSISAPGGAIASVPNWTLR	GTQLM	2		1311.188256	2620.360912	0.000735798	6	N	412	440
Q64514	Exosome	ERMKR	LNEIVDAANAVISHIDQTALAVYIAMK	TDPRP	3	M26:+15.995	967.1798595	2898.516178	0.000622848	3	N	1085	1112
Q64514	Exosome	VINHK	CDLVNYSYGEATHWPNSGR	ICEVI	2	C1:+57.021	1113.487375	2224.959149	0.00091018	2	N	321	340
Q64514	Exosome	VGNNR	GIYLRDPVQVAAPSDHGVGIEPVFPENTENSEK	ISFQL	3		1188.925546	3563.753239	0.000451244	3	N	531	564
Q64514	Exosome	VGNNR	GIYLRDPVQVAAPSDHGVGIEPVFPENTENSEK	ISFQL	4		891.9461098	3563.753239	0.000451244	16	N	531	564
Q64514	Exosome	SQANK	LIKEELQSQVELLNSFEK	KYSDP	2		1074.083874	2146.152147	0.001162105	2	N	168	186
Q64514	Exosome	SQANK	LIKEELQSQVELLNSFEK	KYSDP	3		716.3918491	2146.152147	0.002813207	1	N	168	186
Q64514	Exosome	SLPEK	GTLIEAFPVLGGK	AIEFC	2		651.3773421	1300.739084	0.000451244	2	N	715	728
Q64514	Exosome	SFEKK	YSDPGPVYDCLVWHDGETWR	ACVDS	3	C10:+57.021	818.0273098	2451.058529	0.002374549	1	N	187	207
Q64514	Parental	DGKPK	IIDIIDTTGSGDVNTATEVEPKDGEIIGLSGR	VLKIP	3		1095.895253	3284.662358	0.000451244	8	N	63	95
Q64514	Parental	DGKPK	IIDIIDTTGSGDVNTATEVEPK	DGEII	2		1144.579349	2287.143099	0.000451244	20	N	63	85
Q64514	Parental	PRGLR	EGLHYTEVCGYDIASPNAGPLFR	VPITA	3	C9:+57.021	856.0729191	2565.195357	0.000451244	5	N	605	628
Q64514	Parental	QWMTK	LDSTDIYNELKETYPAYLPLYVAR	LHQLD	3		949.8204082	2846.437825	0.000637154	9	N	1048	1072
Q64514	Parental	ERMKR	LNEIVDAANAVISHIDQTALAVYIAMK	TDPRP	3		961.8481928	2882.521178	0.001699387	1	N	1085	1112
Q64514	Parental	GIYLR	DPVQVAAPSDHGVGIEPVFPENTENSEK	ISFQL	3		988.1408692	2961.399207	0.000622848	1	N	536	564
Q64516	Exosome	EKLAK	EVGTSYGCYFVPAFSGLYAPYWEPSAR	GIICG	3	C8:+57.021	1025.47286	3073.39518	0.000851441	4	N	356	383
Q64516	Exosome	QEFPR	EGWVEQDPKEILQSVYECIEK	TCEKL	3	C18:+57.021	860.4163515	2578.225654	0.000451244	1	N	49	70
Q64521	Parental	DVRAK	CVINASGPFTDSVR	KMDDK	2	C1:+57.021	761.8698553	1521.724111	0.000451244	12	N	284	298
Q64521	Parental	AGPSR	TVGLFLQGGKDWSPTLYIR	LVQDY	3		717.725274	2150.152422	0.0007646	4	N	463	482
Q64521	Parental	LMTLK	NTPEFDILVIGGGATGCGCALDAVTR	GLKTA	2	C17:+57.021,C19:+57.021	1332.641504	2663.267408	0.000451244	16	N	65	91
Q64521	Parental	LMTLK	NTPEFDILVIGGGATGCGCALDAVTR	GLKTA	3	C17:+57.021,C19:+57.021	888.7636026	2663.267408	0.000451244	14	N	65	91
Q64521	Parental	VVGVR	LVSEFPYIEAEVK	YGIKE	2		762.4037539	1522.791908	0.000451244	5	N	525	538
Q64521	Parental	GYKSR	TEQLTDSTEISLLPSDIDR	YKKRF	2		1067.032035	2132.04847	0.000451244	17	N	608	627
Q64521	Parental	SRRTR	LAFLNVQAAEEALPR	IVELM	2		821.4521012	1640.888602	0.000622848	10	N	557	572
Q64521	Parental	PMLQK	DKLVGAIVYYDGQHNDAR	MNLAI	3		678.6733498	2032.996649	0.001654178	1	N	209	227
Q64521	Parental	TLYIR	LVQDYGLESEVAQHLAK	TYGDK	3		633.9990629	1898.973789	0.002374549	1	N	482	499
Q64523	Exosome	RIIPR	HLQLAIRNDEELNK	LLGKV	2		846.9555393	1691.895479	0.000451244	159	Y	82	96
Q64523	Exosome	RIIPR	HLQLAIRNDEELNK	LLGKV	3		564.9729596	1691.895479	0.000451244	991	Y	82	96
Q64523	Exosome	RIIPR	HLQLAIRNDEELNK	LLGKV	4		423.9816697	1691.895479	0.000451244	66	Y	82	96

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q64523	Exosome	QLAIR	NDEELNKLLGK	VTIAQ	2		636.8438635	1271.672127	0.000451244	174	N	89	100
Q64523	Exosome	QLAIR	NDEELNKLLGK	VTIAQ	3		424.898509	1271.672127	0.000451244	240	N	89	100
Q64523	Exosome	SRSSR	AGLQFPVGR	VHRLL	2		472.7697731	943.5239462	0.000451244	1500	Y	21	30
Q64523	Exosome	LEYLT	AEILELAGNAAR	DNKKT	2		614.3387483	1226.661897	0.000451244	66	Y	60	72
Q64523	Exosome	LEYLT	AEILELAGNAAR	DNKKT	3		409.8950988	1226.661897	0.001463592	3	Y	60	72
Q64523	Exosome	VLEYL	TAEILELAGNAAR	DNKKT	2		664.8625875	1327.709575	0.000451244	73	Y	59	72
Q64523	Exosome	AVLEY	LTAEILELAGNAAR	DNKKT	2		721.4046196	1440.793639	0.000451244	693	Y	58	72
Q64523	Exosome	AVLEY	LTAEILELAGNAAR	DNKKT	3		481.2723464	1440.793639	0.000451244	322	Y	58	72
Q64523	Exosome	KLLGK	VTIAQGGVLPNIQAV	LLPKK	2		740.4306374	1478.845675	0.000451244	735	Y	100	115
Q64523	Exosome	KLLGK	VTIAQGGVLPNIQAV	LLPKK	3		493.9563583	1478.845675	0.000451244	21	Y	100	115
Q64523	Exosome	KVTIA	QGGVLPNIQAVLLPK	KTESH	2		773.9699298	1545.92426	0.000451244	2	Y	104	119
Q64523	Exosome	KVTIA	QGGVLPNIQAVLLPK	KTESH	2	[0:-17.027	765.4564298	1528.89726	0.001943752	3	Y	104	119
Q64523	Exosome	GKVTI	AQGGVLPNIQAVLLPK	KTESH	2		809.4884867	1616.961373	0.000451244	33	Y	103	119
Q64523	Exosome	LGKVT	IAQGGVLPNIQAVLLPK	KTESH	2		866.0305187	1730.045437	0.000451244	24	Y	102	119
Q64523	Exosome	LLGKV	TIAQGGVLPNIQAVLLPK	KTESH	2		916.554358	1831.093116	0.000451244	20	Y	101	119
Q64523	Exosome	LLGKV	TIAQGGVLPNIQAVLLPK	KTESH	3		611.372172	1831.093116	0.000622848	2	Y	101	119
Q64523	Exosome	KLLGK	VTIAQGGVLPNIQAVLLPK	KTESH	2		966.088565	1930.16153	0.000451244	1015	Y	100	119
Q64523	Exosome	KLLGK	VTIAQGGVLPNIQAVLLPK	KTESH	3		644.3949767	1930.16153	0.000451244	301	Y	100	119
Q64523	Exosome	QGGVL	PNIQAVLLPK	KTESH	2		546.8429381	1091.670276	0.000451244	57	Y	109	119
Q64523	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKT	2		867.4575805	1732.899561	0.000451244	127	Y	56	72
Q64523	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKT	3		578.640987	1732.899561	0.000451244	83	Y	56	72
Q64523	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKT	2	E1:-18.011	858.4520805	1714.888561	0.000451244	13	Y	56	72
Q64523	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKT	3	E1:-18.011	572.6373203	1714.888561	0.000451244	14	Y	56	72
Q64523	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKT	2	[0:-18.011	858.4520805	1714.888561	0.000998612	4	Y	56	72
Q64523	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKT	3	[0:-18.011	572.6373203	1714.888561	0.001329271	6	Y	56	72
Q64523	Exosome	YMAAV	LEYLTAEILELAGNAAR	DNKKT	2		923.9996126	1845.983625	0.000451244	1105	Y	55	72
Q64523	Exosome	YMAAV	LEYLTAEILELAGNAAR	DNKKT	3		616.335675	1845.983625	0.000451244	1302	Y	55	72
Q64523	Exosome	VYMAA	VLEYLTAEILELAGNAAR	DNKKT	2		973.5338196	1945.052039	0.000451244	625	Y	54	72
Q64523	Exosome	VYMAA	VLEYLTAEILELAGNAAR	DNKKT	3		649.3584797	1945.052039	0.000451244	910	Y	54	72
Q64523	Exosome	YLTAE	ILELAGNAAR	DNKKT	2		514.2988947	1026.582189	0.000622848	2	Y	62	72
Q64523	Exosome	PVYMA	AVLEYLTAEILELAGNAAR	DNKKT	2		1009.052376	2016.089153	0.000451244	342	Y	53	72
Q64523	Exosome	PVYMA	AVLEYLTAEILELAGNAAR	DNKKT	3		673.0375177	2016.089153	0.000451244	299	Y	53	72
Q64523	Exosome	APVYM	AAVLEYLTAEILELAGNAAR	DNKKT	2		1044.570933	2087.126267	0.000451244	349	Y	52	72
Q64523	Exosome	APVYM	AAVLEYLTAEILELAGNAAR	DNKKT	3		696.7165556	2087.126267	0.000451244	563	Y	52	72
Q64523	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	2		1110.091176	2218.166753	0.000451244	78	Y	51	72
Q64523	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	3		740.3967175	2218.166753	0.000451244	63	Y	51	72
Q64523	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	2	M1:+15.995	1118.088676	2234.161753	0.000451244	21	Y	51	72
Q64523	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	3	M1:+15.995	745.7283842	2234.161753	0.000451244	39	Y	51	72
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	2		1467.276214	2932.536828	0.000451244	135	N	43	72
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	3		978.5200762	2932.536828	0.000451244	215	N	43	72
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	4		734.1420071	2932.536828	0.000451244	56	N	43	72
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	2	M9:+15.995	1475.273714	2948.531828	0.000451244	32	N	43	72
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	3	M9:+15.995	983.8517428	2948.531828	0.000451244	184	N	43	72
Q64523	Exosome	AQGGV	LPNIQAVLLPK	KTESH	2		603.3849702	1204.75434	0.001162105	1	Y	108	119
Q64523	Exosome	EYLTA	EILELAGNAAR	DNKKT	2		578.8201913	1155.624783	0.000451244	37	Y	61	72
Q64523	Exosome	AAVLE	YLTAEILELAGNAAR	DNKKT	2		802.9362839	1603.856968	0.000451244	70	Y	57	72
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEILELAGN	AARDN	2		1318.188545	2634.36149	0.000622848	4	N	43	69
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEILELAGN	AARDN	3		879.1282965	2634.36149	0.000451244	17	N	43	69
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEY	LTAEI	2		755.8846746	1509.753749	0.000622848	22	N	43	58
Q64523	Exosome	VGAGA	PVYMAAVLEYLTAEILELAGNAAR	DNKKT	2		1289.68343	2577.351259	0.000451244	2	Y	48	72
Q64523	Exosome	KLLGK	VTIAQGGVLPN	IQAVL	2		534.8065526	1067.597505	0.001329271	2	Y	100	111
Q64523	Exosome	KLLGK	VTIAQGGVLPNIQA	VLLPK	2		690.8964304	1379.777261	0.000451244	189	Y	100	114
Q64523	Exosome	VTIAQ	GGVLPNIQAVLLPK	KTESH	2		709.9406409	1417.865682	0.001943752	1	Y	105	119
Q64523	Exosome	KLLGK	VTIAQGGVLPNIQ	AVLLP	2		655.3778735	1308.740147	0.000622848	27	Y	100	113
Q64523	Exosome	RLLRK	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	3		1208.622922	3622.845367	0.002813207	1	N	37	72
Q64523	Exosome	RLLRK	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	4		906.7191417	3622.845367	0.00091018	1	N	37	72
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTA	EILEL	2		898.4691029	1794.922606	0.002296037	1	N	43	61
Q64523	Exosome	NYAER	VGAGAPVYMAAVLEYLTAEIL	ELAGN	2		1076.074464	2150.133327	0.002884417	1	N	43	64
Q64523	Exosome	KLLGK	VTIAQGGVLPNIQAVLL	PKKTE	2		853.5147015	1705.013803	0.001699387	1	Y	100	117
Q64523	Parental	RIIPR	HLQLAIRNDEELNK	LLGKV	2		846.9555393	1691.895479	0.000451244	25	Y	82	96
Q64523	Parental	RIIPR	HLQLAIRNDEELNK	LLGKV	3		564.9729596	1691.895479	0.000451244	98	Y	82	96
Q64523	Parental	RIIPR	HLQLAIRNDEELNK	LLGKV	4		423.9816697	1691.895479	0.000451244	5	Y	82	96
Q64523	Parental	QLAIR	NDEELNKLLGK	VTIAQ	2		636.8438635	1271.672127	0.000451244	95	N	89	100
Q64523	Parental	QLAIR	NDEELNKLLGK	VTIAQ	3		424.898509	1271.672127	0.000451244	74	N	89	100
Q64523	Parental	SRSSR	AGLQFPVGR	VHRLL	2		472.7697731	943.5239462	0.000451244	455	Y	21	30

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q64523	Parental	LEYLT	AEILELAGNAAR	DNKKT	2		614.3387483	1226.661897	0.000451244	149	Y	60	72
Q64523	Parental	LEYLT	AEILELAGNAAR	DNKKT	3		409.8950988	1226.661897	0.000662267	10	Y	60	72
Q64523	Parental	VLEYL	TAEILELAGNAAR	DNKKT	2		664.8625875	1327.709575	0.000451244	59	Y	59	72
Q64523	Parental	AVLEY	LTAEILELAGNAAR	DNKKT	2		721.4046196	1440.793639	0.000451244	1756	Y	58	72
Q64523	Parental	AVLEY	LTAEILELAGNAAR	DNKKT	3		481.2723464	1440.793639	0.000451244	1299	Y	58	72
Q64523	Parental	KLLGK	VTIAQGGVLPNIQAVLLPKK	TESHK	2		1030.136047	2058.256493	0.000451244	1	Y	100	120
Q64523	Parental	KLLGK	VTIAQGGVLPNIQAVLLPKK	TESHK	3		687.0932977	2058.256493	0.000451244	9	Y	100	120
Q64523	Parental	KLLGK	VTIAQGGVLPNIQAV	LLPKK	2		740.4306374	1478.845675	0.000451244	213	Y	100	115
Q64523	Parental	KLLGK	VTIAQGGVLPNIQAV	LLPKK	3		493.9563583	1478.845675	0.001329271	3	Y	100	115
Q64523	Parental	KVTIA	QGGVLPNIQAVLLPK	KTESH	2		773.9699298	1545.92426	0.000451244	60	Y	104	119
Q64523	Parental	KVTIA	QGGVLPNIQAVLLPK	KTESH	3		516.3158865	1545.92426	0.000451244	10	Y	104	119
Q64523	Parental	KVTIA	QGGVLPNIQAVLLPK	KTESH	2	[0:-17.027	765.4564298	1528.89726	0.00091018	14	Y	104	119
Q64523	Parental	GKVTI	AQGGVLPNIQAVLLPK	KTESH	2		809.4884867	1616.961373	0.000451244	325	Y	103	119
Q64523	Parental	GKVTI	AQGGVLPNIQAVLLPK	KTESH	3		539.9949245	1616.961373	0.000451244	19	Y	103	119
Q64523	Parental	LGKVT	IAQGGVLPNIQAVLLPK	KTESH	2		866.0305187	1730.045437	0.000451244	62	Y	102	119
Q64523	Parental	LGKVT	IAQGGVLPNIQAVLLPK	KTESH	3		577.6896125	1730.045437	0.000451244	21	Y	102	119
Q64523	Parental	LLGKV	TIAQGGVLPNIQAVLLPK	KTESH	2		916.554358	1831.093116	0.000451244	480	Y	101	119
Q64523	Parental	LLGKV	TIAQGGVLPNIQAVLLPK	KTESH	3		611.372172	1831.093116	0.000451244	56	Y	101	119
Q64523	Parental	KLLGK	VTIAQGGVLPNIQAVLLPK	KTESH	2		966.088565	1930.16153	0.000451244	1497	Y	100	119
Q64523	Parental	KLLGK	VTIAQGGVLPNIQAVLLPK	KTESH	3		644.3949767	1930.16153	0.000451244	991	Y	100	119
Q64523	Parental	KLLGK	VTIAQGGVLPNIQAVLLPK	KTESH	4		483.5481825	1930.16153	0.001162105	1	Y	100	119
Q64523	Parental	QGGVL	PNIQAVLLPK	KTESH	2		546.8429381	1091.670276	0.000451244	135	Y	109	119
Q64523	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKT	2		867.4575805	1732.899561	0.000451244	60	Y	56	72
Q64523	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKT	3		578.640987	1732.899561	0.000451244	106	Y	56	72
Q64523	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKT	3	E1:-18.011	572.6373203	1714.888561	0.000451244	29	Y	56	72
Q64523	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKT	3	[0:-18.011	572.6373203	1714.888561	0.000870037	6	Y	56	72
Q64523	Parental	YMAAV	LEYLTAEILELAGNAAR	DNKKT	2		923.9996126	1845.983625	0.000451244	127	Y	55	72
Q64523	Parental	YMAAV	LEYLTAEILELAGNAAR	DNKKT	3		616.335675	1845.983625	0.000451244	230	Y	55	72
Q64523	Parental	VYMAA	VLEYLTAEILELAGNAAR	DNKKT	2		973.5338196	1945.052039	0.000451244	63	Y	54	72
Q64523	Parental	VYMAA	VLEYLTAEILELAGNAAR	DNKKT	3		649.3584797	1945.052039	0.000451244	120	Y	54	72
Q64523	Parental	YLTAE	ILELAGNAAR	DNKKT	2		514.2988947	1026.582189	0.000622848	1	Y	62	72
Q64523	Parental	PVYMA	AVLEYLTAEILELAGNAAR	DNKKT	2		1009.052376	2016.089153	0.000451244	52	Y	53	72
Q64523	Parental	PVYMA	AVLEYLTAEILELAGNAAR	DNKKT	3		673.0375177	2016.089153	0.000451244	71	Y	53	72
Q64523	Parental	APVYM	AAVLEYLTAEILELAGNAAR	DNKKT	2		1044.570933	2087.126267	0.000451244	817	Y	52	72
Q64523	Parental	APVYM	AAVLEYLTAEILELAGNAAR	DNKKT	3		696.7165556	2087.126267	0.000451244	954	Y	52	72
Q64523	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	2		1110.091176	2218.166753	0.000451244	93	Y	51	72
Q64523	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	3		740.3967175	2218.166753	0.000451244	96	Y	51	72
Q64523	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	2	M1:+15.995	1118.088676	2234.161753	0.000451244	29	Y	51	72
Q64523	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKT	3	M1:+15.995	745.7283842	2234.161753	0.000451244	43	Y	51	72
Q64523	Parental	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	2		1467.276214	2932.536828	0.000451244	5	N	43	72
Q64523	Parental	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	3		978.5200762	2932.536828	0.000451244	28	N	43	72
Q64523	Parental	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	4		734.1420071	2932.536828	0.000451244	6	N	43	72
Q64523	Parental	NYAER	VGAGAPVYMAAVLEYLTAEILELAGNAAR	DNKKT	3	M9:+15.995	983.8517428	2948.531828	0.000451244	2	N	43	72
Q64523	Parental	AQGGV	LPNIQAVLLPK	KTESH	2		603.3849702	1204.75434	0.000823681	10	Y	108	119
Q64523	Parental	EYLTA	EILELAGNAAR	DNKKT	2		578.8201913	1155.624783	0.000451244	6	Y	61	72
Q64523	Parental	AAVLE	YLTAEILELAGNAAR	DNKKT	2		802.9362839	1603.856968	0.001395409	1	Y	57	72
Q64523	Parental	KLLGK	VTIAQGGVLPN	IQAVL	2		534.8065526	1067.597505	0.002453667	3	Y	100	111
Q64523	Parental	KLLGK	VTIAQGGVLPNIQA	VLLPK	2		690.8964304	1379.777261	0.000451244	19	Y	100	114
Q64523	Parental	VTIAQ	GGVLPNIQAVLLPK	KTESH	2		709.9406409	1417.865682	0.001162105	1	Y	105	119
Q64674	Exosome	EGWFR	ETCSLWPGQALSLQVEQLLHHR	RSRYQ	4	C3:+57.021	651.3357311	2601.311725	0.000622848	9	N	22	44
Q64674	Exosome	YQLMK	TALKEDGILCCQGECQWLHLDLIK	EMRHF	3	C10:+57.021,C11:+57.021,C15:+57.021	967.4750216	2899.401665	0.000451244	11	N	194	218
Q64674	Exosome	YQLMK	TALKEDGILCCQGECQWLHLDLIK	EMRHF	4	C10:+57.021,C11:+57.021,C15:+57.021	725.8582162	2899.401665	0.000451244	2	N	194	218
Q64674	Exosome	PNPRK	VLIIGGGDGGVLR	EVVKH	2		613.3673087	1224.719017	0.000735798	1	N	96	109
Q64674	Exosome	REVVK	HPSVESVVQCEIDEDVIEVSKK	FLPGM	3	C10:+57.021	842.7516227	2525.231468	0.000451244	5	N	113	135
Q64674	Exosome	HPNPR	KVLIIGGGDGGVLR	EVVKH	3		451.9457935	1352.813981	0.000451244	7	N	95	109
Q64674	Parental	YQLMK	TALKEDGILCCQGECQWLHLDLIK	EMRHF	4	C10:+57.021,C11:+57.021,C15:+57.021	725.8582162	2899.401665	0.000451244	7	N	194	218
Q64727	Exosome	IDGSR	GILSGTSDLLLTFDEAEVR	KIIRV	2		1018.531474	2035.047348	0.000451244	25	N	113	132
Q64727	Exosome	IDGSR	GILSGTSDLLLTFDEAEVR	KIIRV	3		679.3569159	2035.047348	0.000451244	19	N	113	132
Q64727	Exosome	EVDGK	AIPDLTAPVAAVQAAVSNLVR	VGKET	2		1038.594743	2075.173886	0.000451244	51	N	35	56
Q64727	Exosome	EVDGK	AIPDLTAPVAAVQAAVSNLVR	VGKET	3		692.7324286	2075.173886	0.000451244	44	N	35	56
Q64727	Exosome	LEQLR	LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK	AGEVI	3		1342.684793	4025.030978	0.00307782	1	N	853	889
Q64727	Exosome	LEQLR	LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK	AGEVI	4		1007.265544	4025.030978	0.000451244	23	N	853	889

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q64727	Exosome	LNQAK	GWLRDPNASPGDAGEQAIR	QILDE	2		1005.493549	2008.971497	0.000451244	8	N	281	300
Q64727	Exosome	LNQAK	GWLRDPNASPGDAGEQAIR	QILDE	3		670.6649658	2008.971497	0.000451244	40	N	281	300
Q64727	Exosome	DLLAK	CDRVDQLTAQLADLAAR	GEGES	2	C1:+39.994	949.9731464	1897.930693	0.000451244	13	N	544	561
Q64727	Exosome	DLLAK	CDRVDQLTAQLADLAAR	GEGES	3	C1:+39.994	633.6513643	1897.930693	0.000451244	19	N	544	561
Q64727	Exosome	DLLAK	CDRVDQLTAQLADLAAR	GEGES	2	C1:+57.021	958.4866464	1914.957693	0.000451244	1	N	544	561
Q64727	Exosome	DLLAK	CDRVDQLTAQLADLAAR	GEGES	3	C1:+57.021	639.3270309	1914.957693	0.000451244	30	N	544	561
Q64727	Exosome	DLLAK	CDRVDQLTAQLADLAAR	GEGES	2	[0:-17.027,C1:+57.021	949.9731464	1897.930693	0.001162105	2	N	544	561
Q64727	Exosome	DGKAI	PDLTAPVAAVQAAVSNLVR	VGKET	3		631.3587026	1891.052708	0.000451244	12	N	37	56
Q64727	Exosome	VMDAK	AVAGNISDPGLQK	SFLDS	2		635.3440306	1268.672461	0.000451244	2	N	802	815
Q64727	Exosome	VAMQK	AQQVSQGLDVLTAK	VENAA	2		729.4020769	1456.788554	0.000451244	59	N	352	366
Q64727	Exosome	NEIIR	VLQLTSWDEDAWASK	DTEAM	2		874.9286559	1747.841712	0.000451244	27	N	246	261
Q64727	Exosome	IDGSR	GILSGTSDLLLTFDEAEVRK	IIRVC	2		1082.578955	2163.142311	0.000451244	27	N	113	133
Q64727	Exosome	IDGSR	GILSGTSDLLLTFDEAEVRK	IIRVC	3		722.055237	2163.142311	0.000451244	13	N	113	133
Q64727	Exosome	IRVCK	GILEYLTVAEVVETMEDLVTYTK	NLGPG	2		1308.672393	2615.329186	0.000451244	8	N	139	162
Q64727	Exosome	IRVCK	GILEYLTVAEVVETMEDLVTYTK	NLGPG	3		872.7841955	2615.329186	0.002374549	1	N	139	162
Q64727	Exosome	VRVGK	ETVQTTEDQILKR	DMPPA	2		780.9155485	1559.815497	0.000451244	12	N	59	72
Q64727	Exosome	VRVGK	ETVQTTEDQILKR	DMPPA	3		520.946299	1559.815497	0.000662267	1	N	59	72
Q64727	Exosome	AKCDR	VDQLTAQLADLAAR	GEGES	2		742.9075264	1483.799453	0.000451244	7	N	547	561
Q64727	Exosome	EQAIR	QILDEAGKVGELCAGK	ERREI	2	C13:+57.021	844.4381022	1686.860604	0.000451244	15	N	300	316
Q64727	Exosome	EQAIR	QILDEAGKVGELCAGK	ERREI	3	C13:+57.021	563.2946681	1686.860604	0.000451244	8	N	300	316
Q64727	Exosome	EQAQR	WIDNPTVDDR	GVGQA	2		615.7916309	1229.567662	0.000451244	23	N	502	512
Q64727	Exosome	TTPIK	LLAVAATAPPDAPNREEVFDER	AANFE	3		794.4085618	2380.202286	0.000451244	7	N	607	629
Q64727	Exosome	SPQAR	ALASQLQDSLK	DLKAQ	2		587.3278492	1172.640098	0.002374549	1	N	570	581
Q64727	Exosome	SPQAR	ALASQLQDSLKDLK	AQMQE	3		510.6231563	1528.846069	0.000451244	10	N	570	584
Q64727	Exosome	VFHTR	TIESILEPVAQQISHLVIMHEEGEVDGK	AIPDL	3		1034.532822	3100.575065	0.000451244	4	N	7	35
Q64727	Exosome	VFHTR	TIESILEPVAQQISHLVIMHEEGEVDGK	AIPDL	4		776.1515662	3100.575065	0.000662267	5	N	7	35
Q64727	Exosome	VFHTR	TIESILEPVAQQISHLVIMHEEGEVDGK	AIPDL	3	M19:+15.995	1039.864488	3116.570065	0.000622848	1	N	7	35
Q64727	Exosome	QSIAK	KIDAAQNWLADPNGGPEGEEQIR	GALAE	3		836.7424922	2507.204076	0.000451244	1	N	386	409
Q64727	Exosome	MNTVK	ELLPVLISAMK	IFVTT	2		607.3653894	1212.715179	0.002296037	3	N	199	210
Q64727	Exosome	NACTK	LVQAAQMLQSDPYSVPAR	DYLID	2		987.5098221	1973.004044	0.002813207	1	N	87	105
Q64727	Exosome	NACTK	LVQAAQMLQSDPYSVPAR	DYLID	2	M7:+15.995	995.5073221	1988.999044	0.000823681	1	N	87	105
Q64727	Exosome	VAKVR	EAFQPQEPDFPPPPPDLEQLR	LTDEL	2		1224.098044	2446.180487	0.002813207	2	N	832	853
Q64727	Parental	IDGSR	GILSGTSDLLLTFDEAEVR	KIIRV	2		1018.531474	2035.047348	0.000451244	16	N	113	132
Q64727	Parental	EVDGK	AIPDLTAPVAAVQAAVSNLVR	VGKET	2		1038.594743	2075.173886	0.000451244	22	N	35	56
Q64727	Parental	EVDGK	AIPDLTAPVAAVQAAVSNLVR	VGKET	3		692.7324286	2075.173886	0.000451244	12	N	35	56
Q64727	Parental	LEQLR	LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK	AGEVI	3		1342.684793	4025.030978	0.000622848	5	N	853	889
Q64727	Parental	LEQLR	LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK	AGEVI	4		1007.265544	4025.030978	0.000622848	9	N	853	889
Q64727	Parental	EQAQR	WIDNPTVDDRGVGQAAIR	GLVAE	2		992.0062919	1981.996984	0.000451244	5	N	502	520
Q64727	Parental	EQAQR	WIDNPTVDDRGVGQAAIR	GLVAE	3		661.6734613	1981.996984	0.000451244	2	N	502	520
Q64727	Parental	LNQAK	GWLRDPNASPGDAGEQAIR	QILDE	2		1005.493549	2008.971497	0.000698008	2	N	281	300
Q64727	Parental	LNQAK	GWLRDPNASPGDAGEQAIR	QILDE	3		670.6649658	2008.971497	0.000451244	9	N	281	300
Q64727	Parental	DLLAK	CDRVDQLTAQLADLAAR	GEGES	2	C1:+57.021	958.4866464	1914.957693	0.000451244	4	N	544	561
Q64727	Parental	VAMQK	AQQVSQGLDVLTAK	VENAA	2		729.4020769	1456.788554	0.000451244	9	N	352	366
Q64727	Parental	NEIIR	VLQLTSWDEDAWASK	DTEAM	2		874.9286559	1747.841712	0.000451244	17	N	246	261
Q64727	Parental	IDGSR	GILSGTSDLLLTFDEAEVRK	IIRVC	2		1082.578955	2163.142311	0.000451244	8	N	113	133
Q64727	Parental	EQAIR	QILDEAGKVGELCAGK	ERREI	2	C13:+57.021	844.4381022	1686.860604	0.001162105	1	N	300	316
Q64727	Parental	SPQAR	ALASQLQDSLKDLK	AQMQE	3		510.6231563	1528.846069	0.001943752	1	N	570	584
Q64727	Parental	DKRIR	TNLLQVCERIPTISTQLK	ILSTV	2	C7:+57.021	1057.585829	2113.156058	0.001329271	1	N	978	996
Q64727	Parental	DKRIR	TNLLQVCERIPTISTQLK	ILSTV	3	C7:+57.021	705.3931528	2113.156058	0.001943752	1	N	978	996
Q64727	Parental	NACTK	LVQAAQMLQSDPYSVPARDYLIDGSR	GILSG	3		965.1557969	2892.443991	0.000451244	2	N	87	113
Q64727	Parental	VFHTR	TIESILEPVAQQISHLVIMHEEGEVDGK	AIPDL	3		1034.532822	3100.575065	0.001162105	1	N	7	35
Q64737	Exosome	TAQWR	AFTNPEDACSFITSANFPALVVK	ASGLA	2	C9:+57.021	1250.115148	2498.214696	0.000451244	13	N	125	148
Q64737	Exosome	GAYTK	GVEITGFPEAQALGLQVFHAGTALK	DGKVV	3		852.1275069	2553.359121	0.001763695	1	N	350	375
Q64737	Exosome	EFNCR	FGDPECQVILPLLK	SDLYE	2	C6:+57.021	814.9397494	1627.863899	0.000451244	5	N	292	306
Q64737	Exosome	CKDEK	IELVVVGPEAPLAAGIVGDLTSAGVR	CFGPT	3		835.1430455	2502.405737	0.002374549	1	N	66	92
Q64737	Parental	TAQWR	AFTNPEDACSFITSANFPALVVK	ASGLA	2	C9:+57.021	1250.115148	2498.214696	0.000451244	14	N	125	148
Q64737	Parental	GAYTK	GVEITGFPEAQALGLQVFHAGTALK	DGKVV	3		852.1275069	2553.359121	0.001763695	1	N	350	375
Q64737	Parental	EFNCR	FGDPECQVILPLLK	SDLYE	2	C6:+57.021	814.9397494	1627.863899	0.001943752	4	N	292	306
Q64737	Parental	GAYTK	GVEITGFPEAQALGLQVFHAGTALKDGK	VVTSG	4		714.3834227	2853.502491	0.001229886	1	N	350	378
Q65Z40	Parental	DLKNR	IGGLENLNETFEEDIIQSVLRPSNCR	TYCRA	3	C25:+57.021	1001.833228	3002.476284	0.000451244	9	N	276	302
Q65Z40	Parental	VQHVK	HFNDVVEFGENQEFTDDIEYLLSGLK	STQPL	3		1020.149253	3057.42436	0.000622848	3	N	649	675
Q65Z40	Parental	DHSLR	LAGQVHAVQALVQLFLER	ERAAQ	3		664.7183423	1991.131627	0.000870037	2	N	1035	1053
Q65Z40	Parental	VTTVR	EYLPEGDFSIMTEMLK	KFLSF	2	[0:-18.011,M14:+15.995	950.9393436	1899.863087	0.001229886	1	N	1154	1170
Q66JX5	Exosome	LKDLK	LVGEKIGSLGLGTGEDEDYADDFNSASHR	SEKSE	3		1018.14305	3051.405749	0.002080925	1	N	318	347
Q66JX5	Parental	GLEGR	ENLAQDLGIIEAEGTVGGPLLLEVIRR	CQQKE	3		959.2016231	2874.581469	0.00091018	1	N	107	134

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q66JX5	Parental	GLEGR	ENLAQDLGIIEAEGTVGGPLLLEVIR	RCQQK	3		907.1679194	2718.480358	0.000451244	3	N	107	133
Q68FD5	Exosome	ELFAR	KFNALFAQGNYSEAAK	VAANA	2		879.9446403	1757.873681	0.000451244	8	N	366	382
Q68FD5	Exosome	ELFAR	KFNALFAQGNYSEAAK	VAANA	3		586.9656935	1757.873681	0.000451244	5	N	366	382
Q68FD5	Exosome	SNFGR	LASTLVHLGEYQAAVDGAR	KANST	2		986.018868	1970.022136	0.000451244	3	N	1226	1245
Q68FD5	Exosome	SNFGR	LASTLVHLGEYQAAVDGAR	KANST	3		657.6818453	1970.022136	0.000451244	15	N	1226	1245
Q68FD5	Exosome	AKTNR	LAELEEFINGPNNAHIQQVGDR	CYDEK	2		1232.614924	2463.214247	0.000451244	9	N	1182	1204
Q68FD5	Exosome	AKTNR	LAELEEFINGPNNAHIQQVGDR	CYDEK	3		822.0792157	2463.214247	0.000451244	27	N	1182	1204
Q68FD5	Exosome	IYMNR	ISGETIFVTAPHEATAGIIGVNR	KGQVL	2		1177.129678	2352.243756	0.000451244	7	N	297	320
Q68FD5	Exosome	IYMNR	ISGETIFVTAPHEATAGIIGVNR	KGQVL	3		785.0890521	2352.243756	0.000451244	14	N	297	320
Q68FD5	Exosome	YQALR	TSIDAYDNFDNISLAQR	LEKHE	2		971.9612157	1941.906831	0.000451244	35	N	1481	1498
Q68FD5	Exosome	DAKQK	WLLLTGISAQQNR	VVGAM	2		750.420604	1498.825608	0.000451244	3	N	163	176
Q68FD5	Exosome	VAYER	GQCDLELINVCNENSLFK	SLSRY	2	C3:+57.021,C11:+57.021	1077.00378	2151.991961	0.000451244	40	N	923	941
Q68FD5	Exosome	VAYER	GQCDLELINVCNENSLFK	SLSRY	3	C3:+57.021,C11:+57.021	718.3384536	2151.991961	0.001763695	2	N	923	941
Q68FD5	Exosome	EKRNR	LKLLLPWLEAR	IHEGC	3		451.2873796	1350.838739	0.001162105	6	N	854	865
Q68FD5	Exosome	GDLVK	SVDPTLALSVYLR	ANVPN	2		717.4040883	1432.792577	0.000451244	18	N	468	481
Q68FD5	Exosome	VLYAK	KVGYTPDWIFLLR	NVMRI	3		536.6368486	1606.887146	0.000451244	23	N	506	519
Q68FD5	Exosome	NHNNK	SVNESLNNLFITEEDYQALR	TSIDA	2		1178.077308	2354.139017	0.000451244	36	N	1461	1481
Q68FD5	Exosome	NHNNK	SVNESLNNLFITEEDYQALR	TSIDA	3		785.7208055	2354.139017	0.000451244	18	N	1461	1481
Q68FD5	Exosome	SNPYR	RPLIDQVVQTALSETQDPEEVSVTVK	AFMTA	2		1441.261815	2880.50803	0.000451244	3	N	967	993
Q68FD5	Exosome	SNPYR	RPLIDQVVQTALSETQDPEEVSVTVK	AFMTA	3		961.1771432	2880.50803	0.000451244	18	N	967	993
Q68FD5	Exosome	FAIFR	KFDVNTSAVQVLIEHIGNLDR	AYEFA	3		790.0926851	2367.254655	0.000451244	23	N	1073	1094
Q68FD5	Exosome	FAIFR	KFDVNTSAVQVLIEHIGNLDR	AYEFA	4		592.8214639	2367.254655	0.000451244	24	N	1073	1094
Q68FD5	Exosome	LYAKK	VGYTPDWIFLLR	NVMRI	2		740.4038913	1478.792183	0.000451244	9	N	507	519
Q68FD5	Exosome	IGVNR	KGQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C8:+57.021	1142.276709	3423.806726	0.000451244	15	N	320	350
Q68FD5	Exosome	QEEKR	ECFGACLFTCYDLLRPDVVLETAWR	HNIMD	3	C2:+57.021,C6:+57.021,C10:+57.021	1031.15406	3090.438779	0.000451244	20	N	1563	1588
Q68FD5	Exosome	EYINR	LDNYDAPDIANIAISNELFEEAFAIFR	KFDVN	3		1024.50526	3070.49238	0.000451244	14	N	1046	1073
Q68FD5	Exosome	GLLQR	ALEHFTDLYDIKR	AVVHT	4		405.9654883	1619.830753	0.001329271	1	N	625	638
Q68FD5	Exosome	GVNRK	GQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C7:+57.021	1099.578388	3295.711763	0.000451244	8	N	321	350
Q68FD5	Exosome	RVMEY	INRLDNYDAPDIANIAISNELFEEAFAIFR	KFDVN	3		1152.247961	3453.720482	0.000823681	2	N	1043	1073
Q68FD5	Exosome	QAGGK	LHIIEVGTPPTGNQPFPK	KAVDV	3		649.0234314	1944.046894	0.000451244	4	N	227	245
Q68FD5	Exosome	NVPNK	VIQCFAETGQVQK	IVLYA	2	C4:+57.021	754.3825986	1506.749597	0.000451244	45	N	487	500
Q68FD5	Exosome	LKEAK	LTDQLPLIIVCDR	FDFVH	2	C11:+57.021	778.4295488	1554.843498	0.000451244	3	N	767	780
Q68FD5	Exosome	FSEHR	NLQNLLILTAIK	ADRTR	2		677.4273664	1352.839133	0.000451244	30	N	1022	1034
Q68FD5	Exosome	RKKAR	ESYVETELIFALAK	TNRLA	2		806.9275932	1611.839586	0.000451244	5	N	1165	1179
Q68FD5	Exosome	QVASK	YHEQLSTQSLIELFESFK	SFEGL	3		733.7043157	2198.089547	0.000622848	8	N	688	706
Q68FD5	Exosome	DTIRR	FQSVPAQPGQTSPLLQYFGILLDQGQLNK	YESLE	3		1063.231582	3186.671347	0.000451244	27	N	400	429
Q68FD5	Exosome	ASESK	DTELAEELLQWFLQEEKR	ECFGA	3		759.7186248	2276.132475	0.000451244	5	N	1545	1563
Q68FD5	Exosome	FESFK	SFEGLFYFLGSIVNFSQDPDVHFK	YIQAA	3		931.7906719	2792.348616	0.001162105	2	N	706	730
Q68FD5	Exosome	ASESK	DTELAEELLQWFLQEEK	RECFG	2		1061.023482	2120.031363	0.000451244	16	N	1545	1562
Q68FD5	Exosome	ASESK	DTELAEELLQWFLQEEK	RECFG	3		707.6849211	2120.031363	0.002212458	1	N	1545	1562
Q68FD5	Exosome	IVCDR	FDFVHDLVLYLYR	NNLQK	3		567.300125	1698.876975	0.000823681	5	N	780	793
Q68FD5	Exosome	SVTVK	AFMTADLPNELIELLEK	IVLDN	2	M3:+15.995	982.0088319	1962.002064	0.000451244	7	N	993	1010
Q68FD5	Exosome	DSYIK	ADDPSSYMEVVQAANASGNWEELVK	YLQMA	2	M8:+15.995	1363.616712	2725.217824	0.000451244	17	N	1130	1155
Q68FD5	Exosome	DSYIK	ADDPSSYMEVVQAANASGNWEELVK	YLQMA	3	M8:+15.995	909.4137413	2725.217824	0.000451244	5	N	1130	1155
Q68FD5	Exosome	VNPSR	LPVVIGGLLDVDCSEDVIK	NLILV	3	C13:+57.021	681.0347426	2040.080828	0.000662267	5	N	811	830
Q68FD5	Exosome	GLLQR	ALEHFTDLYDIK	RAVVH	3		488.9176806	1463.729642	0.000622848	2	N	625	637
Q68FD5	Exosome	NIIPY	ITNVLQNPDLALR	MAVRN	2		733.9204368	1465.825274	0.002727428	1	N	337	350
Q68FD5	Exosome	EFAER	CNEPAVWSQLAK	AQLQK	2	C1:+57.021	701.8431092	1401.670618	0.0007646	3	N	1101	1113
Q68FD5	Exosome	EFAER	CNEPAVWSQLAK	AQLQK	2	[0:-17.027,C1:+57.021	693.3296092	1384.643618	0.001763695	1	N	1101	1113
Q68FD5	Exosome	PDTIR	RFQSVPAQPGQTSPLLQYFGILLDQGQLNK	YESLE	3		1115.265286	3342.772458	0.001699387	1	N	399	429
Q68FD5	Exosome	RNRLK	LLLPWLEAR	IHEGC	2		555.8376558	1109.659712	0.000735798	2	N	856	865
Q68FD5	Exosome	IYVQK	VNPSRLPVVIGGLLDVDCSEDVIK	NLILV	3	C18:+57.021	865.4671576	2593.378073	0.000451244	5	N	806	830
Q68FD5	Exosome	SVDRK	VSQPIEGHAASFAQFK	MEGNA	3		572.9621719	1715.863116	0.001654178	1	N	189	205
Q68FD5	Exosome	DPSSY	MEVVQAANASGNWEELVK	YLQMA	2	M1:+15.995	995.9811371	1989.946674	0.000451244	1	N	1137	1155
Q68FD5	Parental	ELFAR	KFNALFAQGNYSEAAK	VAANA	2		879.9446403	1757.873681	0.000451244	15	N	366	382
Q68FD5	Parental	SNFGR	LASTLVHLGEYQAAVDGAR	KANST	2		986.018868	1970.022136	0.000451244	13	N	1226	1245
Q68FD5	Parental	SNFGR	LASTLVHLGEYQAAVDGAR	KANST	3		657.6818453	1970.022136	0.000451244	12	N	1226	1245
Q68FD5	Parental	AKTNR	LAELEEFINGPNNAHIQQVGDR	CYDEK	2		1232.614924	2463.214247	0.000451244	26	N	1182	1204
Q68FD5	Parental	AKTNR	LAELEEFINGPNNAHIQQVGDR	CYDEK	3		822.0792157	2463.214247	0.000451244	33	N	1182	1204
Q68FD5	Parental	IYMNR	ISGETIFVTAPHEATAGIIGVNR	KGQVL	2		1177.129678	2352.243756	0.000451244	27	N	297	320
Q68FD5	Parental	IYMNR	ISGETIFVTAPHEATAGIIGVNR	KGQVL	3		785.0890521	2352.243756	0.000451244	18	N	297	320
Q68FD5	Parental	YQALR	TSIDAYDNFDNISLAQR	LEKHE	2		971.9612157	1941.906831	0.000451244	32	N	1481	1498
Q68FD5	Parental	DAKQK	WLLLTGISAQQNR	VVGAM	2		750.420604	1498.825608	0.000451244	13	N	163	176
Q68FD5	Parental	VAYER	GQCDLELINVCNENSLFK	SLSRY	2	C3:+57.021,C11:+57.021	1077.00378	2151.991961	0.000451244	39	N	923	941

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q68FD5	Parental	VAYER	GQCDLELINVCNENSLFK	SLSRY	3	C3:+57.021,C11:+57.021	718.3384536	2151.991961	0.000622848	6	N	923	941
Q68FD5	Parental	EKRNR	LKLLLPWLEAR	IHEGC	3		451.2873796	1350.838739	0.001162105	12	N	854	865
Q68FD5	Parental	GDLVK	SVDPTLALSVYLR	ANVPN	2		717.4040883	1432.792577	0.000451244	16	N	468	481
Q68FD5	Parental	VLYAK	KVGYTPDWIFLLR	NVMRI	3		536.6368486	1606.887146	0.000451244	25	N	506	519
Q68FD5	Parental	NHNNK	SVNESLNNLFITEEDYQALR	TSIDA	2		1178.077308	2354.139017	0.000451244	46	N	1461	1481
Q68FD5	Parental	NHNNK	SVNESLNNLFITEEDYQALR	TSIDA	3		785.7208055	2354.139017	0.000451244	22	N	1461	1481
Q68FD5	Parental	SNPYR	RPLIDQVVQTALSETQDPEEVSVTVK	AFMTA	2		1441.261815	2880.50803	0.000451244	3	N	967	993
Q68FD5	Parental	SNPYR	RPLIDQVVQTALSETQDPEEVSVTVK	AFMTA	3		961.1771432	2880.50803	0.000451244	32	N	967	993
Q68FD5	Parental	FAIFR	KFDVNTSAVQVLIEHIGNLDR	AYEFA	2		1184.635128	2367.254655	0.000451244	3	N	1073	1094
Q68FD5	Parental	FAIFR	KFDVNTSAVQVLIEHIGNLDR	AYEFA	3		790.0926851	2367.254655	0.000451244	41	N	1073	1094
Q68FD5	Parental	FAIFR	KFDVNTSAVQVLIEHIGNLDR	AYEFA	4		592.8214639	2367.254655	0.000451244	46	N	1073	1094
Q68FD5	Parental	LYAKK	VGYTPDWIFLLR	NVMRI	2		740.4038913	1478.792183	0.000451244	5	N	507	519
Q68FD5	Parental	YDIKR	AVVHTHLLNPEWLVNYFGSLSVEDSLECLR	AMLSA	3	C28:+57.021	1166.589287	3496.74446	0.000823681	7	N	638	668
Q68FD5	Parental	YDIKR	AVVHTHLLNPEWLVNYFGSLSVEDSLECLR	AMLSA	4	C28:+57.021	875.1939151	3496.74446	0.000622848	6	N	638	668
Q68FD5	Parental	IGVNR	KGQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C8:+57.021	1142.276709	3423.806726	0.000451244	18	N	320	350
Q68FD5	Parental	QEEKR	ECFGACLFTCYDLLRPDVVLETAWR	HNIMD	3	C2:+57.021,C6:+57.021,C10:+57.021	1031.15406	3090.438779	0.000451244	27	N	1563	1588
Q68FD5	Parental	EYINR	LDNYDAPDIANIAISNELFEEAFAIFR	KFDVN	3		1024.50526	3070.49238	0.000451244	28	N	1046	1073
Q68FD5	Parental	GLLQR	ALEHFTDLYDIKR	AVVHT	3		540.9513843	1619.830753	0.000451244	19	N	625	638
Q68FD5	Parental	GLLQR	ALEHFTDLYDIKR	AVVHT	4		405.9654883	1619.830753	0.000451244	17	N	625	638
Q68FD5	Parental	YDAAK	LLYNNVSNFGR	LASTL	2		648.8389154	1295.662231	0.000622848	9	N	1215	1226
Q68FD5	Parental	GVNRK	GQVLSVCVEEENIIPYITNVLQNPDLALR	MAVRN	3	C7:+57.021	1099.578388	3295.711763	0.000451244	10	N	321	350
Q68FD5	Parental	RVMEY	INRLDNYDAPDIANIAISNELFEEAFAIFR	KFDVN	3		1152.247961	3453.720482	0.000451244	18	N	1043	1073
Q68FD5	Parental	SVYLR	ANVPNKVIQCFAETGQVQK	IVLYA	2	C10:+57.021	1066.052154	2130.088707	0.000451244	6	N	481	500
Q68FD5	Parental	SVYLR	ANVPNKVIQCFAETGQVQK	IVLYA	3	C10:+57.021	711.037369	2130.088707	0.000451244	3	N	481	500
Q68FD5	Parental	QAGGK	LHIIEVGTPPTGNQPFPK	KAVDV	2		973.0312471	1944.046894	0.000451244	23	N	227	245
Q68FD5	Parental	QAGGK	LHIIEVGTPPTGNQPFPK	KAVDV	3		649.0234314	1944.046894	0.000451244	7	N	227	245
Q68FD5	Parental	NVPNK	VIQCFAETGQVQK	IVLYA	2	C4:+57.021	754.3825986	1506.749597	0.000451244	48	N	487	500
Q68FD5	Parental	LKEAK	LTDQLPLIIVCDR	FDFVH	2	C11:+57.021	778.4295488	1554.843498	0.000698008	3	N	767	780
Q68FD5	Parental	FSEHR	NLQNLLILTAIK	ADRTR	2		677.4273664	1352.839133	0.000451244	16	N	1022	1034
Q68FD5	Parental	RKKAR	ESYVETELIFALAK	TNRLA	2		806.9275932	1611.839586	0.000870037	2	N	1165	1179
Q68FD5	Parental	QVASK	YHEQLSTQSLIELFESFK	SFEGL	3		733.7043157	2198.089547	0.000451244	15	N	688	706
Q68FD5	Parental	DTIRR	FQSVPAQPGQTSPLLQYFGILLDQGQLNK	YESLE	3		1063.231582	3186.671347	0.000451244	25	N	400	429
Q68FD5	Parental	ASESK	DTELAEELLQWFLQEEKR	ECFGA	3		759.7186248	2276.132475	0.000622848	9	N	1545	1563
Q68FD5	Parental	FESFK	SFEGLFYFLGSIVNFSQDPDVHFK	YIQAA	3		931.7906719	2792.348616	0.000451244	15	N	706	730
Q68FD5	Parental	ASESK	DTELAEELLQWFLQEEK	RECFG	2		1061.023482	2120.031363	0.000451244	21	N	1545	1562
Q68FD5	Parental	ASESK	DTELAEELLQWFLQEEK	RECFG	3		707.6849211	2120.031363	0.000622848	1	N	1545	1562
Q68FD5	Parental	IVCDR	FDFVHDLVLYLYR	NNLQK	3		567.300125	1698.876975	0.000823681	13	N	780	793
Q68FD5	Parental	VNPSR	LPVVIGGLLDVDCSEDVIK	NLILV	2	C13:+57.021	1021.048214	2040.080828	0.000451244	14	N	811	830
Q68FD5	Parental	VNPSR	LPVVIGGLLDVDCSEDVIK	NLILV	3	C13:+57.021	681.0347426	2040.080828	0.000451244	5	N	811	830
Q68FD5	Parental	GLLQR	ALEHFTDLYDIK	RAVVH	3		488.9176806	1463.729642	0.000451244	12	N	625	637
Q68FD5	Parental	NIIPY	ITNVLQNPDLALR	MAVRN	2		733.9204368	1465.825274	0.000622848	8	N	337	350
Q68FD5	Parental	VNPSR	LPVVIGGLLDVDCSEDVIKNLILVVR	GQFST	3	C13:+57.021	950.2124289	2847.613887	0.000451244	2	N	811	837
Q68FD5	Parental	YSVDR	KVSQPIEGHAASFAQFK	MEGNA	3		615.660493	1843.958079	0.0007646	2	N	188	205
Q68FD5	Parental	ELLEK	IVLDNSVFSEHR	NLQNL	2		708.3680371	1414.720474	0.000451244	3	N	1010	1022
Q68FD5	Parental	EFAER	CNEPAVWSQLAK	AQLQK	2	C1:+57.021	701.8431092	1401.670618	0.000823681	3	N	1101	1113
Q68FD5	Parental	AIFRK	FDVNTSAVQVLIEHIGNLDR	AYEFA	3		747.3943641	2239.159692	0.00091018	2	N	1074	1094
Q68FD5	Parental	PDTIR	RFQSVPAQPGQTSPLLQYFGILLDQGQLNK	YESLE	3		1115.265286	3342.772458	0.000622848	17	N	399	429
Q68FD5	Parental	IYVQK	VNPSRLPVVIGGLLDVDCSEDVIK	NLILV	3	C18:+57.021	865.4671576	2593.378073	0.000451244	3	N	806	830
Q68FD5	Parental	RMAVR	NNLAGAEELFAR	KFNAL	2		652.8338301	1303.65206	0.000451244	4	N	354	366
Q68FD5	Parental	FLITK	YGYIHLYDLETGTCIY	MNRIS	2	C14:+57.021	990.9563248	1979.89705	0.002374549	1	N	278	294
Q68FD5	Parental	LFARK	FNALFAQGNYSEAAK	VAANA	2		815.8971587	1629.778717	0.000698008	1	N	367	382
Q68FL6	Exosome	LTRPK	VPVLQLDSGNYLFSASAICR	YFFLL	2	C19:+57.021	1105.567636	2209.119673	0.000451244	5	N	47	67
Q68FL6	Exosome	-MR	LFVSEGSPGSLPVLAAAAR	ARGRA	2		921.5101474	1841.004695	0.000451244	1	N	2	21
Q68FL6	Exosome	QFMAK	DNVPFHGLVFPCSVLGAEDNYTLVK	HIIAT	3	C12:+57.021	931.1305455	2790.368237	0.001463592	1	N	556	581
Q68FL6	Exosome	RARGR	AELLISTVGPEECVVPFLTRPK	VPVLQ	3	C13:+57.021	819.1140557	2454.318767	0.001264573	1	N	25	47
Q68FL6	Parental	LTRPK	VPVLQLDSGNYLFSASAICR	YFFLL	2	C19:+57.021	1105.567636	2209.119673	0.000451244	1	N	47	67
Q68FL6	Parental	-MR	LFVSEGSPGSLPVLAAAAR	ARGRA	2		921.5101474	1841.004695	0.002145581	1	N	2	21
Q68FL6	Parental	QFMAK	DNVPFHGLVFPCSVLGAEDNYTLVK	HIIAT	3	C12:+57.021	931.1305455	2790.368237	0.000451244	11	N	556	581
Q68FL6	Parental	RARGR	AELLISTVGPEECVVPFLTRPK	VPVLQ	3	C13:+57.021	819.1140557	2454.318767	0.000451244	1	N	25	47
Q68FL6	Parental	DLLIK	NNSELLNNLGNFINR	AGMFV	2		866.4427961	1730.869992	0.002453667	1	N	643	658
Q69ZK0	Exosome	PSSIR	TLVDNIQQYVEDGKNQLLLALLK	CTDTE	3		876.825605	2627.453415	0.000451244	1	N	1281	1304
Q69ZK0	Exosome	ATAVK	IDQLIRPINALDELYR	LMKTF	3		648.030586	1941.068358	0.000637154	3	N	1519	1535
Q69ZK0	Exosome	FVHPK	AGAAGSLGAGLIPVSSELCYR	LGACQ	2	C19:+57.021	1025.025604	2048.035609	0.000451244	3	N	1544	1565
Q69ZK0	Parental	PSSIR	TLVDNIQQYVEDGKNQLLLALLK	CTDTE	3		876.825605	2627.453415	0.000451244	8	N	1281	1304

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q69ZK0	Parental	ATAVK	IDQLIRPINALDELYR	LMKTF	3		648.030586	1941.068358	0.000823681	2	N	1519	1535
Q69ZK0	Parental	APSWK	CSPAVDEDSQGQGLNDSSYGSASGAPSQQDR	GLSFL	3	C1:+57.021	1057.445197	3169.312191	0.000622848	2	N	1020	1051
Q69ZK0	Parental	VLFTK	ALESVEGPPPPGNQAAEELQQEINAQSLEK	VQQYY	3		1058.525271	3172.552414	0.002453667	1	N	1461	1491
Q69ZK0	Parental	LGGRK	TTDIPLEGYLLSPIQR	ICKYP	2		908.4967057	1814.977811	0.000451244	1	N	177	193
Q69ZK0	Parental	QAGRK	IYSINEDLVFLRPFSEVETILNQFFCSR	RPLRL	3	C26:+57.021	1146.24675	3435.716849	0.000823681	1	N	662	690
Q6A026	Exosome	TAAKR	DLALVNDQLLGFVR	ERTLD	2		786.9413693	1571.867139	0.000823681	2	N	389	403
Q6A026	Exosome	IFSNK	EVQLAQIFEPLSR	SLNAD	2		765.4202697	1528.824939	0.000451244	1	N	749	762
Q6A026	Parental	KPYVR	SAGTETGSNINANSELSPSAGSR	SREQS	2		1104.012697	2206.009793	0.000451244	9	N	1157	1180
Q6A026	Parental	NKDVR	LLVACCLADIFR	IYAPE	2	C5:+57.021,C6:+57.021	725.8809488	1449.746298	0.000451244	6	N	86	98
Q6A026	Parental	KTNEK	LYTVCDVALCVINSK	SALCN	3	C5:+57.021,C10:+57.021	585.6322496	1753.873349	0.000622848	5	N	1073	1088
Q6A026	Parental	SAGSR	SREQSSEASETGVSENEENPVR	IISVT	3		807.6973883	2420.068765	0.002145581	1	N	1180	1202
Q6A026	Parental	IFSNK	EVQLAQIFEPLSR	SLNAD	2		765.4202697	1528.824939	0.001162105	1	N	749	762
Q6A068	Parental	SEVAR	QTAEESGITNSASSTLLSEYNVTNNSIALR	TPRTP	3		1057.520297	3169.537492	0.000622848	9	N	321	351
Q6A068	Parental	MGLMK	QLNDLWDQIEQAHLELR	TFEEL	3		707.6961545	2120.065063	0.000823681	3	N	733	750
Q6A068	Parental	LKRKK	ESDLPSAILQTSGVSEFTK	KRSKL	2		1005.007832	2008.000063	0.000451244	5	N	271	290
Q6A068	Parental	REHLR	LGLLGLPAPK	NDFEI	2		489.8214744	977.6273487	0.001699387	1	N	477	487
Q6A068	Parental	ELEER	EIDDTYIEDAADVDAR	KQAIR	2		905.9030321	1809.790464	0.001162105	2	N	505	521
Q6A068	Parental	KAVQK	DLPRPSEVNETILRPLNVEPPLTDLQK	SEELI	4		771.6743655	3082.666262	0.000451244	8	N	543	570
Q6A4J8	Exosome	VMCDR	AGFIQDTSLILYEEVKPNLTER	IQDYD	3		846.1151555	2535.322066	0.000451244	16	N	724	746
Q6A4J8	Exosome	IRESK	LSEVLQAVTDHDIPQQLVER	LQEEK	3		764.0732906	2289.196472	0.000451244	25	N	524	544
Q6A4J8	Exosome	DVVSR	CTKEEAIEHNYGGHDDDLSVR	HCTNA	3	C1:+57.021	815.6963999	2444.0658	0.001943752	2	N	488	509
Q6A4J8	Exosome	DVVSR	CTKEEAIEHNYGGHDDDLSVR	HCTNA	4	C1:+57.021	612.0242499	2444.0658	0.000823681	2	N	488	509
Q6A4J8	Exosome	AHFHK	EVFGTFGIPFLLR	IHQGE	2		748.4195413	1494.823483	0.001591523	1	N	998	1011
Q6A4J8	Exosome	DQNIK	INDRFEFPEQLPLDEFLQK	TDPKD	2		1189.605505	2377.195409	0.001699387	1	N	421	440
Q6A4J8	Exosome	DQNIK	INDRFEFPEQLPLDEFLQK	TDPKD	3		793.4062697	2377.195409	0.000451244	14	N	421	440
Q6A4J8	Exosome	IKGKK	NIFESFVDYVAVEQLDGDNKYDAGEHGLQEAEK	GVKFL	4		933.185757	3728.711828	0.000622848	1	N	359	392
Q6A4J8	Exosome	VSLDK	ALDELMDGDIIVFQKDDPENDNSELPTAK	EYFRD	3	M6:+15.995	1083.510439	3247.507918	0.000662267	2	N	756	785
Q6A4J8	Parental	VMCDR	AGFIQDTSLILYEEVKPNLTER	IQDYD	3		846.1151555	2535.322066	0.000451244	18	N	724	746
Q6A4J8	Parental	IRESK	LSEVLQAVTDHDIPQQLVER	LQEEK	3		764.0732906	2289.196472	0.000451244	4	N	524	544
Q6A4J8	Parental	DQNIK	INDRFEFPEQLPLDEFLQK	TDPKD	3		793.4062697	2377.195409	0.000451244	10	N	421	440
Q6A4J8	Parental	IKGKK	NIFESFVDYVAVEQLDGDNKYDAGEHGLQEAEK	GVKFL	3		1243.911743	3728.711828	0.000451244	3	N	359	392
Q6A4J8	Parental	PWTIF	LETVDPELAASGATLPK	FDKDH	2		856.4597889	1710.903978	0.000451244	1	N	662	679
Q6BCL1	Parental	EIYEL	YDAVEATDDSSISPR	GRDEM	2		813.3686281	1624.721656	0.000451244	5	N	516	531
Q6BCL1	Parental	PRKPK	LPGSVSECSLPSASAGSSPQCPLSPGLIVPGIPR	WRSED	3	C8:+57.021,C21:+57.021	1125.574495	3373.700084	0.000451244	6	N	401	435
Q6BCL1	Parental	KCGSR	ELDSHSPQPDISTFPK	NNENF	2		899.4368451	1796.85809	0.000451244	5	N	246	262
Q6BCL1	Parental	SEQPK	KSSQSELSAVSLKPLQLQFADLPR	KPPQP	4		661.3687783	2641.443913	0.00091018	1	N	50	74
Q6BCL1	Parental	GELSK	RPPQLETPQEPSAPPAQK	LLKPE	2		986.018868	1970.022136	0.001162105	1	N	150	168
Q6BCL1	Parental	GELSK	RPPQLETPQEPSAPPAQK	LLKPE	3		657.6818453	1970.022136	0.000451244	10	N	150	168
Q6BCL1	Parental	NLQAK	FQTSQPELGELFR	KTPKP	2		776.3942519	1550.772904	0.00091018	4	N	13	26
Q6BCL1	Parental	GYVPR	TALLPLETEVYDDVSF	GDPLD	2		906.4516295	1810.887659	0.000622848	3	N	648	664
Q6BCL1	Parental	QTPPR	KPESCNPQSHSPLPDFNAFPK	KHPQL	3	C5:+57.021	799.7149546	2396.121464	0.000451244	14	N	296	317
Q6BCL1	Parental	GFSRK	SQPQSESIEVSQTSPSK	CGSRE	2		909.9399489	1817.864298	0.000823681	4	N	225	242
Q6DFW4	Parental	KSEVK	TYDPSGDSTLPTCSK	KRKIE	2	C13:+57.021	814.8593503	1627.703101	0.000451244	27	N	426	441
Q6DFW4	Parental	IMRCR	EWYGWHFPELGK	IISDN	3		516.9143819	1547.719746	0.000823681	1	N	184	196
Q6DFZ1	Parental	ISLCK	FTALSSESIENLPSVFGSNPK	AHIAA	2		1112.560763	2223.105925	0.000823681	1	N	983	1004
Q6DFZ1	Parental	MTLPI	ILNPALIEATSPVPLLATPRPTDPIPTSEVN	-	3		1079.597931	3235.770393	0.002374549	1	N	1830	1861
Q6DFZ1	Parental	FSNLK	EVLNSVTELSEIEPNVFLRPFLEVIR	SEDTT	3		1014.889045	3041.643735	0.000622848	4	N	47	73
Q6DTY7	Exosome	SQMKR	TIQTAEALSVPYEQWK	VLNEI	2		932.478513	1862.941426	0.001699387	2	N	306	322
Q6DTY7	Exosome	SDVRK	FLSEEGGHVAVFDATNTTR	ERRAM	3		684.3329932	2049.97558	0.002727428	1	N	116	135
Q6DTY7	Exosome	VKTYK	SFEFFLPDNEEGLK	IRKQC	2		836.3991999	1670.7828	0.001162105	2	N	87	101
Q6DTY7	Parental	QAVMR	CLLAYFLDKAAEELPYLK	CPLHT	3	C1:+57.021	719.7152329	2156.122299	0.000451244	6	N	396	414
Q6DTY7	Parental	SQMKR	TIQTAEALSVPYEQWK	VLNEI	2		932.478513	1862.941426	0.000823681	4	N	306	322
Q6DTY7	Parental	DFMRR	IECYENSYESLDEDLDRDLSYIK	IMDVG	3	C3:+57.021	957.0958949	2868.264285	0.000979378	2	N	194	217
Q6DTY7	Parental	QNGYK	TFFVESICVDPEVVAANIVQVK	LGSPD	3	C8:+57.021	822.0982941	2463.271482	0.000622848	1	N	151	173
Q6GQT9	Parental	SVSGK	VSCLDTCGDLLVTLQSLSR	QGEKR	2	C3:+57.021,C7:+57.021	1069.035081	2136.054561	0.000451244	4	N	500	519
Q6GQT9	Parental	PPLLR	DGENYVVLLDTTLPR	SQYDY	2		852.944306	1703.873012	0.000622848	1	N	1097	1112
Q6GQT9	Parental	RSCHR	FEQAFYTYDTSSPSILTLTAIR	HHVLG	2		1262.634459	2523.253318	0.000451244	4	N	635	657
Q6GQT9	Parental	YAVSK	EDGSFSFYSLPSGGYTVVPFYR	GERIT	2		1238.07932	2474.143039	0.000451244	9	N	266	288
Q6GQT9	Parental	SFEIK	AEDDQPLPGVLLSLSGGVFR	SNLLT	2		1035.547458	2069.079317	0.000451244	4	N	875	895
Q6IRU2	Exosome	AVKRK	IQALQQQADDAEDRAQGLQR	ELDGE	2		1127.562691	2253.109782	0.000451244	12	N	13	33
Q6IRU2	Exosome	AVKRK	IQALQQQADDAEDRAQGLQR	ELDGE	3		752.044394	2253.109782	0.000451244	15	N	13	33
Q6IRU2	Exosome	VSELK	CGDLEEELKNVTNNLK	SLEAA	2	C1:+57.021	938.4597629	1874.903926	0.000451244	5	N	153	169
Q6IRU2	Exosome	VSELK	CGDLEEELKNVTNNLK	SLEAA	3	C1:+57.021	625.9757753	1874.903926	0.000451244	29	N	153	169
Q6IRU2	Exosome	VSELK	CGDLEEELKNVTNNLK	SLEAA	2	[0:-17.027,C1:+57.021	929.9462629	1857.876926	0.000451244	8	N	153	169
Q6IRU2	Exosome	LAQAK	EENVGLHQTLDQTLNELNCI	-	2	C19:+57.021	1170.560737	2339.105874	0.000451244	29	N	228	248

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6IRU2	Exosome	ALNRR	IQLLEEELDRAQEQLATALQNLEEAEK	AADES	3		1042.20565	3123.59355	0.000451244	25	N	55	82
Q6IRU2	Exosome	EELDR	AQEQLATALQNLEEAEKAADESER	GMKVI	3		882.0952598	2643.262379	0.000451244	34	N	65	89
Q6IRU2	Exosome	DLEEK	LAQAKEENVGLHQTLDQTLNELNCI	-	3	C24:+57.021	951.1470354	2850.417706	0.000451244	5	N	223	248
Q6IRU2	Exosome	AVKRK	IQALQQQADDAEDR	AQGLQ	2		800.882237	1599.748874	0.000451244	14	N	13	27
Q6IRU2	Exosome	EELDR	AQEQLATALQNLEEAEK	AADES	2		943.4792413	1884.942883	0.000451244	1	N	65	82
Q6IRU2	Exosome	EELDR	AQEQLATALQNLEEAEK	AADES	3		629.3220942	1884.942883	0.000451244	2	N	65	82
Q6IRU2	Exosome	EAVKR	KIQALQQQADDAEDR	AQGLQ	3		576.9557457	1727.843837	0.000451244	2	N	12	27
Q6IRU2	Parental	AVKRK	IQALQQQADDAEDRAQGLQR	ELDGE	2		1127.562691	2253.109782	0.000451244	8	N	13	33
Q6IRU2	Parental	AVKRK	IQALQQQADDAEDRAQGLQR	ELDGE	3		752.044394	2253.109782	0.000451244	19	N	13	33
Q6IRU2	Parental	VSELK	CGDLEEELKNVTNNLK	SLEAA	2	C1:+57.021	938.4597629	1874.903926	0.000622848	1	N	153	169
Q6IRU2	Parental	VSELK	CGDLEEELKNVTNNLK	SLEAA	3	C1:+57.021	625.9757753	1874.903926	0.000451244	25	N	153	169
Q6IRU2	Parental	VSELK	CGDLEEELKNVTNNLK	SLEAA	2	[0:-17.027,C1:+57.021	929.9462629	1857.876926	0.000451244	4	N	153	169
Q6IRU2	Parental	LAQAK	EENVGLHQTLDQTLNELNCI	-	2	C19:+57.021	1170.560737	2339.105874	0.000451244	29	N	228	248
Q6IRU2	Parental	LAQAK	EENVGLHQTLDQTLNELNCI	-	3	C19:+57.021	780.7097578	2339.105874	0.000451244	5	N	228	248
Q6IRU2	Parental	ALNRR	IQLLEEELDRAQEQLATALQNLEEAEK	AADES	3		1042.20565	3123.59355	0.000451244	29	N	55	82
Q6IRU2	Parental	ALNRR	IQLLEEELDRAQEQLATALQNLEEAEK	AADES	4		781.9061876	3123.59355	0.002296037	1	N	55	82
Q6IRU2	Parental	EELDR	AQEQLATALQNLEEAEKAADESER	GMKVI	3		882.0952598	2643.262379	0.000451244	17	N	65	89
Q6IRU2	Parental	DLEEK	LAQAKEENVGLHQTLDQTLNELNCI	-	2	C24:+57.021	1426.216653	2850.417706	0.000451244	7	N	223	248
Q6IRU2	Parental	DLEEK	LAQAKEENVGLHQTLDQTLNELNCI	-	3	C24:+57.021	951.1470354	2850.417706	0.000451244	8	N	223	248
Q6IRU2	Parental	AVKRK	IQALQQQADDAEDR	AQGLQ	2		800.882237	1599.748874	0.000451244	15	N	13	27
Q6IRU2	Parental	EELDR	AQEQLATALQNLEEAEK	AADES	2		943.4792413	1884.942883	0.000451244	12	N	65	82
Q6IRU2	Parental	EAVKR	KIQALQQQADDAEDR	AQGLQ	3		576.9557457	1727.843837	0.0025889	1	N	12	27
Q6NSR8	Exosome	KQGFK	DNLHAVFCLAENAVGPNATRPDDIHLLYSGK	TVEIN	4	C8:+57.021	852.6758895	3406.672358	0.001591523	2	N	303	334
Q6NSR8	Exosome	HAGER	ATGFGVALLLALFGR	ASEDP	2		753.4460905	1504.876581	0.001763695	1	N	474	489
Q6NSR8	Exosome	PGMKR	DCGGAAAVLGAFR	AAIKQ	2	C2:+57.021	632.8090694	1263.602539	0.002884417	1	N	282	295
Q6NSR8	Exosome	YGVGK	AALHPPALAILSHTPDGATQTIAWVGK	GIVYD	4		684.8767705	2735.475882	0.001329271	1	N	233	260
Q6NVF9	Exosome	SAISR	AVSDASAGDYGSAIETLVTAISLIK	QSKVS	2		1226.645024	2451.274448	0.000451244	26	N	431	456
Q6NVF9	Exosome	SAISR	AVSDASAGDYGSAIETLVTAISLIK	QSKVS	3		818.0992825	2451.274448	0.000451244	2	N	431	456
Q6NVF9	Parental	SAISR	AVSDASAGDYGSAIETLVTAISLIK	QSKVS	2		1226.645024	2451.274448	0.000451244	37	N	431	456
Q6NVF9	Parental	SAISR	AVSDASAGDYGSAIETLVTAISLIK	QSKVS	3		818.0992825	2451.274448	0.000451244	26	N	431	456
Q6NVF9	Parental	RIALY	IGNLTWWTTDEDLTEAVHSLGVNDILEIK	FFENR	3		1094.889662	3281.645586	0.000622848	4	N	84	113
Q6NZB0	Exosome	NQIER	LTRPGSSYFNLNPFEVLQIDPEVTDEEIK	KRFRQ	3		1117.565067	3349.671801	0.000451244	12	N	45	74
Q6NZB0	Parental	NQIER	LTRPGSSYFNLNPFEVLQIDPEVTDEEIK	KRFRQ	3		1117.565067	3349.671801	0.000451244	35	N	45	74
Q6NZB0	Parental	KQLKK	EGKPTNVEEDDPELFK	QAVYK	2		923.9394176	1845.863235	0.000622848	1	N	143	159
Q6NZB0	Parental	KKRFR	QLSILVHPDKNQDDADR	AQKAF	4		491.7517785	1962.975914	0.000851441	2	N	78	95
Q6NZC7	Exosome	MHNPK	VIVQFQPSSVPDEWGTTQDGQTRPR	VVKRG	3		943.4707725	2827.388917	0.000823681	2	N	393	418
Q6NZC7	Parental	MHNPK	VIVQFQPSSVPDEWGTTQDGQTRPR	VVKRG	3		943.4707725	2827.388917	0.000451244	13	N	393	418
Q6NZC7	Parental	NFKGK	VSVAGHSLGSLILFDILSNQR	DMCVS	3		742.7467378	2225.216813	0.00091018	2	N	572	593
Q6NZJ6	Exosome	RPMGK	ATSLLLEILGLLCK	SMGPK	2	C13:+57.021	772.4603176	1542.905035	0.001839721	1	N	1371	1385
Q6NZJ6	Exosome	RPMGK	ATSLLLEILGLLCK	SMGPK	3	C13:+57.021	515.3094784	1542.905035	0.000451244	9	N	1371	1385
Q6NZJ6	Exosome	LNDMK	EAVQCVQELASPSLLFIFVR	LGIES	3	C5:+57.021	769.4123245	2305.213573	0.000451244	2	N	1260	1280
Q6NZJ6	Exosome	GSNQR	VFDWIDANLNEQQIASNTLVR	ALMTT	2		1223.622217	2445.228835	0.001162105	1	N	1459	1480
Q6NZJ6	Parental	RPMGK	ATSLLLEILGLLCK	SMGPK	2	C13:+57.021	772.4603176	1542.905035	0.000451244	9	N	1371	1385
Q6NZJ6	Parental	RPMGK	ATSLLLEILGLLCK	SMGPK	3	C13:+57.021	515.3094784	1542.905035	0.000451244	19	N	1371	1385
Q6NZJ6	Parental	EERLK	GVIDLIFEK	AISEP	2		517.3005718	1032.585544	0.000735798	4	N	799	808
Q6NZJ6	Parental	RLLQK	YLCDEQKELQALYALQALVVTLEQPANLLR	MFFDA	3	C3:+57.021	1168.292359	3501.853677	0.001591523	1	N	1513	1543
Q6NZJ6	Parental	GSNQR	VFDWIDANLNEQQIASNTLVR	ALMTT	2		1223.622217	2445.228835	0.000451244	6	N	1459	1480
Q6NZJ6	Parental	MSGAR	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	SQGAA	3		1171.592567	3511.754302	0.000451244	4	N	208	242
Q6P069-2	Exosome	LNGWR	QHFISFDSDRSGTVDPQELQK	ALTTM	3		812.0598212	2433.156064	0.000451244	13	N	91	112
Q6P069-2	Exosome	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	2	C1:+39.994,C19:+57.021	1128.032647	2254.049694	0.000451244	6	N	41	61
Q6P069-2	Exosome	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	3	C1:+39.994,C19:+57.021	752.3576979	2254.049694	0.000698008	5	N	41	61
Q6P069-2	Exosome	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	2	C1:+57.021,C19:+57.021	1136.546147	2271.076694	0.000451244	47	N	41	61
Q6P069-2	Exosome	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	3	C1:+57.021,C19:+57.021	758.0333645	2271.076694	0.000451244	21	N	41	61
Q6P069-2	Exosome	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	2	[0:-	1128.032647	2254.049694	0.000451244	26	N	41	61
Q6P069-2	Exosome	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	3	[0:-	752.3576979	2254.049694	0.000451244	21	N	41	61
Q6P069-2	Exosome	LNGWR	QHFISFDSDR	SGTVD	2		626.291798	1250.567996	0.00091018	4	N	91	101
Q6P069-2	Exosome	LNGWR	QHFISFDSDR	SGTVD	2	[0:-17.027	617.778298	1233.540996	0.001352548	1	N	91	101
Q6P069-2	Exosome	FNEFK	ELWAVLNGWR	QHFIS	2		622.3332689	1242.650938	0.000698008	16	N	81	91
Q6P069-2	Exosome	AFPGQ	TQDPLYGYFAAVAGQDGQIDADELQR	CLTQS	2		1421.170457	2840.325314	0.000622848	1	N	15	41
Q6P069-2	Exosome	LYGYF	AAVAGQDGQIDADELQR	CLTQS	2		878.9271759	1755.838752	0.000622848	8	N	24	41
Q6P069-2	Exosome	STSGK	ITFDDYIACCVK	LRALT	2	C9:+57.021,C10:+57.021	752.844229	1503.672858	0.000451244	14	N	138	150
Q6P069-2	Exosome	SFRRR	DSGQQGVVNFSYDDFIQCVMTV	-	2	C18:+57.021	1255.054431	2508.093261	0.000451244	4	N	161	183
Q6P069-2	Exosome	-MQYG	GAPGGPAFPGQTQDPLYGYFAAVAGQDGQIDADELQR	CLTQS	3		1259.93136	3776.77068	0.001162105	8	N	4	41
Q6P069-2	Exosome	PLYGY	FAAVAGQDGQIDADELQR	CLTQS	2		952.4613829	1902.907166	0.000451244	5	N	23	41
Q6P069-2	Exosome	DELQR	CLTQSGIAGGYKPF	NLETC	2	C1:+57.021	749.8718667	1497.728133	0.000622848	2	N	41	55

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6P069-2	Exosome	GTMGF	NEFKELWAVLNGWR	QHFIS	3		587.9744119	1760.899836	0.000451244	1	N	77	91
Q6P069-2	Exosome	-MQY	GGAPGGPAFPGQTQDPLYGYFAAVAGQDGQIDADELQR	CLTQS	3		1278.938515	3833.792144	0.001591523	2	N	3	41
Q6P069-2	Exosome	QYGGA	PGGPAFPGQTQDPLYGYFAAVAGQDGQIDADELQR	CLTQS	3		1217.245168	3648.712103	0.002019181	1	N	6	41
Q6P069-2	Parental	LNGWR	QHFISFDSDRSGTVDPQELQK	ALTTM	2		1217.585832	2433.156064	0.000451244	8	N	91	112
Q6P069-2	Parental	LNGWR	QHFISFDSDRSGTVDPQELQK	ALTTM	3		812.0598212	2433.156064	0.000451244	14	N	91	112
Q6P069-2	Parental	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	2	C1:+39.994,C19:+57.021	1128.032647	2254.049694	0.000451244	4	N	41	61
Q6P069-2	Parental	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	3	C1:+39.994,C19:+57.021	752.3576979	2254.049694	0.000735798	2	N	41	61
Q6P069-2	Parental	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	2	C1:+57.021,C19:+57.021	1136.546147	2271.076694	0.000451244	46	N	41	61
Q6P069-2	Parental	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	3	C1:+57.021,C19:+57.021	758.0333645	2271.076694	0.000451244	37	N	41	61
Q6P069-2	Parental	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	2	[0:-	1128.032647	2254.049694	0.000451244	23	N	41	61
Q6P069-2	Parental	DELQR	CLTQSGIAGGYKPFNLETCR	LMVSM	3	[0:-	752.3576979	2254.049694	0.000823681	4	N	41	61
Q6P069-2	Parental	LNGWR	QHFISFDSDR	SGTVD	2	[0:-17.027	617.778298	1233.540996	0.002212458	3	N	91	101
Q6P069-2	Parental	AFPGQ	TQDPLYGYFAAVAGQDGQIDADELQR	CLTQS	2		1421.170457	2840.325314	0.000698008	3	N	15	41
Q6P069-2	Parental	LYGYF	AAVAGQDGQIDADELQR	CLTQS	2		878.9271759	1755.838752	0.000823681	2	N	24	41
Q6P069-2	Parental	STSGK	ITFDDYIACCVK	LRALT	2	C9:+57.021,C10:+57.021	752.844229	1503.672858	0.000451244	8	N	138	150
Q6P069-2	Parental	-M	QYGGAPGGPAFPGQTQDPLYGYFAAVAGQDGQIDADELQR	CLTQS	3		1375.97915	4124.91405	0.002981883	1	N	1	41
Q6P1B1	Exosome	EEFRR	QQADFVDLSFPTISSTGPNGAIIHYAPVPETNR	TLSLD	3		1181.590387	3541.74776	0.000451244	24	N	371	404
Q6P1B1	Exosome	NFNNR	GSLTFEPLTLVPIQTK	MIDVN	2		872.4987171	1742.981834	0.000451244	20	N	554	570
Q6P1B1	Exosome	KMGLK	DTPTQEDWLVSVLPEGSR	VGVDP	2		1014.997798	2027.979996	0.000823681	2	N	98	116
Q6P1B1	Exosome	RQAMR	NSEYVAEPIQAYIIPSGDAHQSEYIAPCDCR	RAFVS	3	C28:+57.021,C30:+57.021	1185.205019	3552.591656	0.000451244	16	N	18	49
Q6P1B1	Exosome	RAHIK	DAVALCELFNWLEQEVPK	GGVTE	2	C6:+57.021	1081.035638	2160.055676	0.000451244	17	N	336	354
Q6P1B1	Exosome	DSFAR	SALWDSGLDYLHGTGHGVGSFLNVHEGPCGISYK	TFSDE	4	C29:+57.021	908.4326253	3629.699301	0.000451244	5	N	473	507
Q6P1B1	Exosome	RQAMR	NSEYVAEPIQAYIIPSGDAHQSEYIAPCDCRR	AFVSG	3	C28:+57.021,C30:+57.021	1237.238722	3708.692767	0.000823681	3	N	18	50
Q6P1B1	Exosome	RQAMR	NSEYVAEPIQAYIIPSGDAHQSEYIAPCDCRR	AFVSG	4	C28:+57.021,C30:+57.021	928.1809917	3708.692767	0.001264573	2	N	18	50
Q6P1B1	Exosome	PETNR	TLSLDEVYLIDSGAQYK	DGTTD	2		957.9889105	1913.962221	0.000451244	9	N	404	421
Q6P1B1	Exosome	KMAER	SIAWFVVTALDEIAWLFNLR	GSDVE	3		788.7637287	2363.267786	0.000451244	1	N	192	212
Q6P1B1	Exosome	PEGSR	VGVDPLIIPTDYWK	KMAKV	2		808.4406708	1614.865742	0.002519933	1	N	116	130
Q6P1B1	Parental	EEFRR	QQADFVDLSFPTISSTGPNGAIIHYAPVPETNR	TLSLD	3		1181.590387	3541.74776	0.000451244	14	N	371	404
Q6P1B1	Parental	NFNNR	GSLTFEPLTLVPIQTK	MIDVN	2		872.4987171	1742.981834	0.000622848	5	N	554	570
Q6P1B1	Parental	RQAMR	NSEYVAEPIQAYIIPSGDAHQSEYIAPCDCR	RAFVS	3	C28:+57.021,C30:+57.021	1185.205019	3552.591656	0.000451244	12	N	18	49
Q6P1B1	Parental	RAHIK	DAVALCELFNWLEQEVPK	GGVTE	2	C6:+57.021	1081.035638	2160.055676	0.000451244	7	N	336	354
Q6P1B1	Parental	DSFAR	SALWDSGLDYLHGTGHGVGSFLNVHEGPCGISYK	TFSDE	3	C29:+57.021	1210.907567	3629.699301	0.000735798	2	N	473	507
Q6P1B1	Parental	DSFAR	SALWDSGLDYLHGTGHGVGSFLNVHEGPCGISYK	TFSDE	4	C29:+57.021	908.4326253	3629.699301	0.000451244	9	N	473	507
Q6P1B1	Parental	KMAER	SIAWFVVTALDEIAWLFNLR	GSDVE	3		788.7637287	2363.267786	0.002145581	1	N	192	212
Q6P1F6	Exosome	DPSNR	SFFSEIISSISDVK	FSHSG	2		779.9041181	1557.792636	0.000451244	5	N	278	292
Q6P1F6	Exosome	QSHSR	GEYNVYSTFQSHEPEFDYLK	SLEIE	3		818.3697728	2452.085918	0.000622848	3	N	68	88
Q6P1F6	Parental	DPSNR	SFFSEIISSISDVK	FSHSG	2		779.9041181	1557.792636	0.000451244	4	N	278	292
Q6P1F6	Parental	FSQVK	GAVDDDVAEADIISTVEFNHSGELLATGDK	GGRVV	3		1030.158477	3087.452031	0.000622848	1	N	18	48
Q6P1F6	Parental	ADDLR	INLWHLEITDR	SFNIV	3		470.5898983	1408.746295	0.002981883	1	N	199	210
Q6P2B1	Exosome	TLVEK	YSNDVTSLPFLLEILTVLPEEVHSR	SLRIG	3		957.8433243	2870.506573	0.000622848	4	N	132	157
Q6P2B1	Exosome	VTLLR	SQVVIPILQWAIASTTLDHR	DANSS	3		750.0869829	2247.237549	0.002374549	3	N	769	789
Q6P2B1	Exosome	GELQR	SVHAWEISDQLLQIR	QDVES	3		598.9886096	1793.942429	0.001463592	1	N	39	54
Q6P2B1	Parental	TLVEK	YSNDVTSLPFLLEILTVLPEEVHSR	SLRIG	3		957.8433243	2870.506573	0.000451244	8	N	132	157
Q6P4S8	Exosome	QGRTR	AGTQVPVLGPEDDLAGIFLQIFPLSPDPR	WQSSS	3		1021.545278	3061.612435	0.000451244	2	N	1340	1369
Q6P4S8	Exosome	TEAMR	LGPASGLLVDWLETLDPEVVCSCPDLQWK	LLFSR	3	C21:+57.021,C23:+57.021	1099.877403	3296.608809	0.000622848	1	N	1613	1642
Q6P4T2	Exosome	SKLYR	AALETDENLLLCAPTGAGK	TNVAL	2	C12:+57.021	972.4910631	1942.966526	0.000451244	16	N	490	509
Q6P4T2	Exosome	RKQTR	LTAIDILTTCAADIQR	QRFLH	3	C10:+57.021	592.3174728	1773.929018	0.000451244	15	N	1570	1586
Q6P4T2	Exosome	TKETR	ETYEVLLSFIQAALGDQPR	DILCG	2		1075.560566	2149.105531	0.000451244	1	N	110	129
Q6P4T2	Exosome	TKETR	ETYEVLLSFIQAALGDQPR	DILCG	3		717.3763105	2149.105531	0.001395409	1	N	110	129
Q6P4T2	Exosome	QEDVR	LIGLSATLPNYEDVATFLR	VDPAK	2		1047.068027	2092.120453	0.000451244	16	N	647	666
Q6P4T2	Exosome	EDEER	NALLQLTDSQIADVAR	FCNRY	2		864.4684796	1726.921359	0.000823681	2	N	1993	2009
Q6P4T2	Exosome	TELGR	IASHYYITNDTVQTYNQLLKPTLSEIELFR	VFSLS	4		893.4679494	3569.840598	0.0007646	13	N	986	1016
Q6P4T2	Exosome	LLKAK	YAQDEHLITFFVPVFEPLPPQYFIR	VVSDR	3		1022.864171	3065.569114	0.000451244	8	N	1244	1269
Q6P4T2	Exosome	VDPAK	GLFYFDNSFRPVPLEQTYVGITEK	KAIKR	3		940.8134765	2819.41703	0.000451244	16	N	671	695
Q6P4T2	Exosome	KTKVR	GLIEIISNAAEYENIPIR	HHEDN	2		1008.044551	2014.073503	0.000451244	6	N	1843	1861
Q6P4T2	Exosome	KTKVR	GLIEIISNAAEYENIPIR	HHEDN	3		672.3656343	2014.073503	0.000451244	3	N	1843	1861
Q6P4T2	Exosome	QTQVF	NTVYNSDDNVFVGAPTGSGK	TICAE	2		1021.47723	2040.93886	0.002145581	1	N	1336	1356
Q6P4T2	Exosome	FPFER	LYDLNHNEIGELIR	MPKMG	3		566.9656935	1697.873681	0.000451244	1	N	1152	1166
Q6P4T2	Exosome	GISHR	HLSDHLSELVEQTLSDLEQSK	CISIE	4		602.8044738	2407.186695	0.001463592	1	N	1779	1800
Q6P4T2	Exosome	TQLVR	LIVLDEIHLLHDDRGPVLEALVAR	AIRNI	3		902.848744	2705.522832	0.002212458	1	N	610	634
Q6P4T2	Exosome	KDSIR	SGGPVVVLVQLEREEEVTGPVIAPLFPQK	REEGW	3		1029.908328	3086.701585	0.00091018	1	N	2030	2059
Q6P4T2	Parental	SKLYR	AALETDENLLLCAPTGAGK	TNVAL	2	C12:+57.021	972.4910631	1942.966526	0.000451244	17	N	490	509
Q6P4T2	Parental	RKQTR	LTAIDILTTCAADIQR	QRFLH	3	C10:+57.021	592.3174728	1773.929018	0.000451244	6	N	1570	1586
Q6P4T2	Parental	LEILK	TASDDRECENQLVLLLGFNTFDFIK	VLRQH	3	C8:+57.021	982.483536	2944.427208	0.000451244	10	N	294	319
Q6P4T2	Parental	TKETR	ETYEVLLSFIQAALGDQPR	DILCG	2		1075.560566	2149.105531	0.000451244	33	N	110	129

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6P4T2	Parental	TKETR	ETYEVLLSFIQAALGDQPR	DILCG	3		717.3763105	2149.105531	0.000451244	24	N	110	129
Q6P4T2	Parental	QEDVR	LIGLSATLPNYEDVATFLR	VDPAK	2		1047.068027	2092.120453	0.000451244	11	N	647	666
Q6P4T2	Parental	LLKAK	YAQDEHLITFFVPVFEPLPPQYFIR	VVSDR	3		1022.864171	3065.569114	0.001162105	3	N	1244	1269
Q6P4T2	Parental	VDPAK	GLFYFDNSFRPVPLEQTYVGITEK	KAIKR	3		940.8134765	2819.41703	0.000451244	1	N	671	695
Q6P4T2	Parental	KTKVR	GLIEIISNAAEYENIPIR	HHEDN	2		1008.044551	2014.073503	0.000451244	2	N	1843	1861
Q6P4T2	Parental	KTKVR	GLIEIISNAAEYENIPIR	HHEDN	3		672.3656343	2014.073503	0.000451244	1	N	1843	1861
Q6P4T2	Parental	GDQPR	DILCGAADEVLAVLK	NEKLR	2	C4:+57.021	793.926839	1585.838078	0.000451244	3	N	129	144
Q6P4T2	Parental	GDQPR	DILCGAADEVLAVLK	NEKLR	3	C4:+57.021	529.6204926	1585.838078	0.000451244	2	N	129	144
Q6P4T2	Parental	QTQVF	NTVYNSDDNVFVGAPTGSGK	TICAE	2		1021.47723	2040.93886	0.002080925	3	N	1336	1356
Q6P4T2	Parental	FPFER	LYDLNHNEIGELIR	MPKMG	3		566.9656935	1697.873681	0.000622848	1	N	1152	1166
Q6P4T2	Parental	GISHR	HLSDHLSELVEQTLSDLEQSK	CISIE	3		803.403365	2407.186695	0.000979378	1	N	1779	1800
Q6P542	Exosome	VESLK	AANAAENDFSVSQAEVSSR	QAMLE	2		976.9513793	1951.887159	0.001654178	1	N	267	286
Q6P542	Exosome	EYTVR	FTFPDPPPLSPPVLGLHGVTFGYEGQKPLFK	NLDFG	4		846.4528424	3381.780169	0.002519933	1	N	603	634
Q6P542	Parental	VESLK	AANAAENDFSVSQAEVSSR	QAMLE	2		976.9513793	1951.887159	0.000451244	22	N	267	286
Q6P542	Parental	PKGPK	QQPPEPEWIGDGEGTSPADK	VVKKG	2		1069.487795	2136.959989	0.00091018	1	N	6	26
Q6P542	Parental	GQKAR	VVFAELACREPDVLILDEPTNNLDIESIDALGEAINDYK	GAVIV	3	C8:+57.021	1458.728467	4373.162	0.000823681	3	N	742	781
Q6P542	Parental	SHDAR	LITETNCQLWVVEEQGVSQIDGDFDDYKR	EVLEA	3	C7:+57.021	1153.212433	3456.6139	0.000451244	4	N	792	821
Q6P5E4	Exosome	EGLHR	LGIEGLSLHNILK	LNIQP	2		703.9224482	1405.829296	0.000451244	17	N	426	439
Q6P5E4	Exosome	EGLHR	LGIEGLSLHNILK	LNIQP	3		469.6175655	1405.829296	0.000451244	35	N	426	439
Q6P5E4	Exosome	DDIYR	IYSHDGTDSPPDANDVVVILNNFK	SKIIK	3		877.4298027	2629.266008	0.000451244	23	N	1177	1201
Q6P5E4	Exosome	VAVLR	AYNYVAQEVDGYHAFQTLTQIYNK	VRTGE	2		1418.683003	2835.350407	0.000451244	3	N	553	577
Q6P5E4	Exosome	VAVLR	AYNYVAQEVDGYHAFQTLTQIYNK	VRTGE	3		946.1246022	2835.350407	0.000451244	18	N	553	577
Q6P5E4	Exosome	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	C3:+57.021	953.5162885	2857.525466	0.000451244	6	N	156	181
Q6P5E4	Exosome	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	4	C3:+57.021	715.3891664	2857.525466	0.000451244	25	N	156	181
Q6P5E4	Exosome	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	Q1:-17.027,C3:+57.021	947.8406219	2840.498466	0.000622848	8	N	156	181
Q6P5E4	Exosome	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	[0:-17.027,C3:+57.021	947.8406219	2840.498466	0.001162105	8	N	156	181
Q6P5E4	Exosome	ISNGR	IIGPLEDNELFNQDDFHLLENIILK	TSGQK	3		984.8504789	2951.528037	0.000451244	18	N	898	923
Q6P5E4	Exosome	QVPIK	SLPQEWLWCETWCDDASK	KRAKT	2	C9:+57.021,C13:+57.021	1155.993413	2309.971225	0.000451244	18	N	1466	1484
Q6P5E4	Exosome	QVPIK	SLPQEWLWCETWCDDASK	KRAKT	3	C9:+57.021,C13:+57.021	770.9982085	2309.971225	0.001699387	1	N	1466	1484
Q6P5E4	Exosome	HNILK	LNIQPSETDYAVDIR	SPAIS	2		867.4393878	1732.863176	0.000451244	24	N	439	454
Q6P5E4	Exosome	LTAKR	EYLDLTASNNFYVDDFAR	FSALD	2		1076.995256	2151.974911	0.000451244	16	N	704	722
Q6P5E4	Exosome	KSFYR	YVLEPEISFTADSSFAK	GPIAK	2		952.4703536	1902.925107	0.000451244	21	N	1038	1055
Q6P5E4	Exosome	LKELR	DFNLDGAPYGYTPFCDSR	REMDG	2	C15:+57.021	1047.94702	2093.878439	0.000451244	28	N	1371	1389
Q6P5E4	Exosome	IWGYK	ILFLDVLFPLVVDK	FLFVD	2		815.9950819	1629.974564	0.000698008	7	N	1339	1353
Q6P5E4	Exosome	AVDIR	SPAISWVNNLEVDSR	YNSWP	2		843.9264475	1685.837295	0.000451244	18	N	454	469
Q6P5E4	Exosome	KLKPK	EGETYYDVVAVVDPVTR	EAQRL	2		956.4708849	1910.92617	0.000451244	9	N	981	998
Q6P5E4	Exosome	KLKPK	EGETYYDVVAVVDPVTR	EAQRL	3		637.9831899	1910.92617	0.001699387	3	N	981	998
Q6P5E4	Exosome	SKEIY	DDSFIRPVTFWIVGDFDSPSGR	QLLYD	3		838.4085618	2512.202286	0.000735798	5	N	753	775
Q6P5E4	Exosome	SLTTK	WFSAPLLLEASEFLAEDSQEK	FWSFV	2		1205.594803	2409.174005	0.000451244	4	N	54	75
Q6P5E4	Exosome	SLTTK	WFSAPLLLEASEFLAEDSQEK	FWSFV	3		804.0658017	2409.174005	0.000622848	3	N	54	75
Q6P5E4	Exosome	LVVDK	FLFVDADQIVR	TDLKE	2		661.8593165	1321.703033	0.002884417	1	N	1353	1364
Q6P5E4	Exosome	REAQR	LAPLLLVLTQLINMNLR	VFMNC	2		968.0953364	1934.175073	0.000622848	1	N	1002	1019
Q6P5E4	Exosome	REAQR	LAPLLLVLTQLINMNLR	VFMNC	3		645.7328242	1934.175073	0.000451244	3	N	1002	1019
Q6P5E4	Exosome	NYVFR	HYISNPSKEPVYLSGYGVELAIK	STEYK	3		855.4518791	2563.332237	0.000451244	2	N	228	251
Q6P5E4	Exosome	FQEEK	ELGTLHTEETQEGSQKHEEL	-	3		765.6965485	2294.066245	0.000451244	2	N	1531	1551
Q6P5E4	Exosome	ISNGR	IIGPLEDNELFNQDDFHLL	ENIIL	2		1121.55548	2241.095361	0.002813207	1	N	898	917
Q6P5E4	Exosome	FINGL	HIDLDTQDIFSLFDTLR	NEARV	3		683.6816224	2048.021467	0.002212458	1	N	398	415
Q6P5E4	Exosome	QKYFK	GTIGLQPGDSALFINGLHIDLDTQDIFSLFDTLR	NEARV	3		1234.972497	3701.89409	0.000451244	1	N	381	415
Q6P5E4	Exosome	EAAVR	IVPEWQDYDQEIK	QLQTL	2		831.9046494	1661.793699	0.002019181	1	N	1508	1521
Q6P5E4	Exosome	YNKVR	TGETVKVEHVVSVLEK	KYPYV	3		585.3285205	1752.962161	0.001463592	1	N	579	595
Q6P5E4	Parental	EGLHR	LGIEGLSLHNILK	LNIQP	3		469.6175655	1405.829296	0.000451244	20	N	426	439
Q6P5E4	Parental	DDIYR	IYSHDGTDSPPDANDVVVILNNFK	SKIIK	3		877.4298027	2629.266008	0.000451244	5	N	1177	1201
Q6P5E4	Parental	VAVLR	AYNYVAQEVDGYHAFQTLTQIYNK	VRTGE	3		946.1246022	2835.350407	0.000451244	16	N	553	577
Q6P5E4	Parental	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	C3:+57.021	953.5162885	2857.525466	0.000622848	6	N	156	181
Q6P5E4	Parental	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	4	C3:+57.021	715.3891664	2857.525466	0.000451244	22	N	156	181
Q6P5E4	Parental	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	Q1:-17.027,C3:+57.021	947.8406219	2840.498466	0.000622848	8	N	156	181
Q6P5E4	Parental	SVHGK	QTCDLDTLESLLLTAADRPKPLLFK	GDHRY	3	[0:-17.027,C3:+57.021	947.8406219	2840.498466	0.001162105	5	N	156	181
Q6P5E4	Parental	ISNGR	IIGPLEDNELFNQDDFHLLENIILK	TSGQK	3		984.8504789	2951.528037	0.000451244	28	N	898	923
Q6P5E4	Parental	QVPIK	SLPQEWLWCETWCDDASK	KRAKT	2	C9:+57.021,C13:+57.021	1155.993413	2309.971225	0.000451244	16	N	1466	1484
Q6P5E4	Parental	HNILK	LNIQPSETDYAVDIR	SPAIS	2		867.4393878	1732.863176	0.000451244	9	N	439	454
Q6P5E4	Parental	LTAKR	EYLDLTASNNFYVDDFAR	FSALD	2		1076.995256	2151.974911	0.000622848	5	N	704	722
Q6P5E4	Parental	KSFYR	YVLEPEISFTADSSFAK	GPIAK	2		952.4703536	1902.925107	0.000622848	11	N	1038	1055
Q6P5E4	Parental	LKELR	DFNLDGAPYGYTPFCDSR	REMDG	2	C15:+57.021	1047.94702	2093.878439	0.000622848	10	N	1371	1389
Q6P5E4	Parental	IWGYK	ILFLDVLFPLVVDK	FLFVD	2		815.9950819	1629.974564	0.000622848	3	N	1339	1353
Q6P5E4	Parental	SLTTK	WFSAPLLLEASEFLAEDSQEK	FWSFV	2		1205.594803	2409.174005	0.000451244	9	N	54	75

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6P5E4	Parental	IQQLR	VEEDVASDLVMKVDALLSAQPK	GEARI	3		786.4143254	2356.219576	0.002519933	1	N	937	959
Q6P5F9	Exosome	MVILK	LLSEEVFDFSSGQITQVK	AKHLK	2		1014.020742	2026.025884	0.000451244	42	N	172	190
Q6P5F9	Exosome	MVILK	LLSEEVFDFSSGQITQVK	AKHLK	3		676.3497613	2026.025884	0.000451244	17	N	172	190
Q6P5F9	Exosome	DFSQK	LDINLLDNVVNCLYHGEGAQQR	MAQEV	2	C12:+57.021	1271.129652	2540.243705	0.000451244	1	N	22	44
Q6P5F9	Exosome	DFSQK	LDINLLDNVVNCLYHGEGAQQR	MAQEV	3	C12:+57.021	847.7557015	2540.243705	0.000451244	33	N	22	44
Q6P5F9	Exosome	NMNTK	YYGLQILENVIK	TRWKI	2		726.9090065	1451.802413	0.000451244	36	N	76	88
Q6P5F9	Exosome	DAQVK	LFVTGLFSLNQDIPAFK	EHLRD	2		955.5252662	1909.034932	0.000451244	22	N	995	1012
Q6P5F9	Exosome	NTNIR	LAYSNGKDDEQNFIQNLSLFLCTFLK	EHGQL	3	C22:+57.021	1026.846586	3077.516358	0.000451244	11	N	305	331
Q6P5F9	Exosome	LVQIK	EFAGEDTSDLFLEER	ETALR	2		879.3973856	1756.779171	0.000451244	15	N	1023	1038
Q6P5F9	Exosome	EDEKR	FLVTVIKDLLGLCEQK	RGKDN	2	C13:+57.021	938.5345453	1875.053491	0.001162105	1	N	515	531
Q6P5F9	Exosome	EDEKR	FLVTVIKDLLGLCEQK	RGKDN	3	C13:+57.021	626.0256302	1875.053491	0.000451244	5	N	515	531
Q6P5F9	Exosome	PAQFK	LVLDSIIWAFK	HTMRN	2		652.884803	1303.754006	0.001229886	1	N	872	883
Q6P5F9	Parental	MVILK	LLSEEVFDFSSGQITQVK	AKHLK	2		1014.020742	2026.025884	0.000451244	29	N	172	190
Q6P5F9	Parental	MVILK	LLSEEVFDFSSGQITQVK	AKHLK	3		676.3497613	2026.025884	0.002296037	1	N	172	190
Q6P5F9	Parental	DHAAR	QLLDFSQKLDINLLDNVVNCLYHGEGAQQR	MAQEV	3	C20:+57.021	1167.591579	3499.751337	0.000451244	5	N	14	44
Q6P5F9	Parental	DHAAR	QLLDFSQKLDINLLDNVVNCLYHGEGAQQR	MAQEV	4	C20:+57.021	875.9456342	3499.751337	0.000451244	9	N	14	44
Q6P5F9	Parental	DHAAR	QLLDFSQKLDINLLDNVVNCLYHGEGAQQR	MAQEV	3	[0:-17.027,C20:+57.021	1161.915912	3482.724337	0.000451244	1	N	14	44
Q6P5F9	Parental	DFSQK	LDINLLDNVVNCLYHGEGAQQR	MAQEV	3	C12:+57.021	847.7557015	2540.243705	0.000451244	17	N	22	44
Q6P5F9	Parental	NMNTK	YYGLQILENVIK	TRWKI	2		726.9090065	1451.802413	0.000451244	14	N	76	88
Q6P5F9	Parental	DAQVK	LFVTGLFSLNQDIPAFK	EHLRD	2		955.5252662	1909.034932	0.000622848	3	N	995	1012
Q6P5F9	Parental	NTNIR	LAYSNGKDDEQNFIQNLSLFLCTFLK	EHGQL	3	C22:+57.021	1026.846586	3077.516358	0.000823681	3	N	305	331
Q6P5F9	Parental	EDEKR	FLVTVIKDLLGLCEQK	RGKDN	3	C13:+57.021	626.0256302	1875.053491	0.002374549	1	N	515	531
Q6P8X1	Exosome	KNMVK	SADGVIVSGVKDVDDFFEHER	TFLLE	4		581.0320879	2320.097152	0.000823681	2	N	193	214
Q6P8X1	Exosome	AAFRK	NLVELAELELK	HAKGN	2		635.8668073	1269.718015	0.000451244	15	N	375	386
Q6P8X1	Exosome	DDYNR	IGSSLYALGTQDSTDICK	FFLKV	2	C17:+57.021	964.9674208	1927.919242	0.000451244	10	N	247	265
Q6P8X1	Exosome	LKHAK	GNLQLLQNCLAVLNGDT	-	2	C9:+57.021	921.9728405	1841.930081	0.000622848	1	N	389	406
Q6P8X1	Parental	KNMVK	SADGVIVSGVKDVDDFFEHER	TFLLE	3		774.3735172	2320.097152	0.000451244	3	N	193	214
Q6P8X1	Parental	KNMVK	SADGVIVSGVKDVDDFFEHER	TFLLE	4		581.0320879	2320.097152	0.000622848	11	N	193	214
Q6P8X1	Parental	AAFRK	NLVELAELELK	HAKGN	2		635.8668073	1269.718015	0.000451244	9	N	375	386
Q6P8X1	Parental	DDYNR	IGSSLYALGTQDSTDICKF	FLKVS	2	C17:+57.021	1038.501628	2074.987656	0.000451244	11	N	247	266
Q6P9Q4	Exosome	VVTVR	VQYLEDTDPFACANFPEPR	RAPTC	2	C12:+57.021	1135.015434	2268.015267	0.000451244	12	N	19	38
Q6P9Q4	Exosome	TRCAK	VDFEQLTENLGQLECR	SQAAE	2	C15:+57.021	975.9652125	1949.914825	0.001352548	1	N	921	937
Q6P9Q4	Parental	VVTVR	VQYLEDTDPFACANFPEPR	RAPTC	2	C12:+57.021	1135.015434	2268.015267	0.000870037	2	N	19	38
Q6P9Q6	Parental	LKKAR	VSTDQAAAEQLTLAQAELQSQWEAK	CEQLL	2		1358.675375	2715.33515	0.000451244	5	N	781	806
Q6P9Q6	Parental	SVSSR	DSAAPSPIPASDSLSADPVVTPLPLPLKPGEPGLR	SKSNS	3		1154.622916	3460.845349	0.000622848	13	N	304	339
Q6P9Q6	Parental	AHQQK	LALLQDECLALQAQIAAFTEQK	EHMQR	3	C8:+57.021	825.4371984	2473.288195	0.000698008	2	N	835	857
Q6P9Q6	Parental	EKSSR	IEEQNDKISDLIER	NQRYV	3		567.9604967	1700.85809	0.00307782	1	N	585	599
Q6PAV2	Exosome	MKSLK	LVIQSTGGGESYLPVSHTCFNLLDLPK	YTEKE	3	C19:+57.021	982.5077931	2944.499979	0.001871652	1	N	1006	1033
Q6PAV2	Exosome	PRNIK	SLSDIQIVQVACGYYHSLALSK	ASEVF	3	C12:+57.021	818.0899101	2451.24633	0.000637154	6	N	132	154
Q6PAV2	Exosome	FCVKR	IFSGGDQSFSHYSSPQNCGPPDDFR	CSDPS	3	C18:+57.021	934.7335137	2801.177141	0.001943752	1	N	366	391
Q6PAV2	Exosome	NRQNR	QEFVDAYVDYIFNK	SVASL	2		875.9202995	1749.824999	0.000823681	1	N	893	907
Q6PCP5	Parental	QVPER	IVVTGNNEDISFSRPADLDLIQSTPFKPLALK	TPPRV	3		1166.966794	3497.876983	0.001871652	1	N	56	88
Q6PCP5	Parental	QVPER	IVVTGNNEDISFSRPADLDLIQSTPFKPLALK	TPPRV	4		875.4770458	3497.876983	0.001763695	1	N	56	88
Q6PCP5	Parental	KTPPR	VLTLSERPLDFLDLERPLPTPQSEESR	AVGRL	4		785.1679103	3136.640441	0.001264573	2	N	92	119
Q6PD03	Exosome	KEIKR	ATLNELVEYVSTNR	GVIVE	2		804.9155485	1607.815497	0.000870037	1	N	98	112
Q6PD03	Exosome	KEIKR	ATLNELVEYVSTNR	GVIVE	3		536.946299	1607.815497	0.001162105	2	N	98	112
Q6PD03	Exosome	LPQLK	DATSNEQQELFCQK	LQQCC	2	C12:+57.021	849.3756989	1696.735798	0.000451244	6	N	60	74
Q6PD03	Exosome	YIDQK	FVQQLLELFDSEDPRER	DFLKT	3		707.69241	2120.05383	0.000451244	2	N	187	204
Q6PD03	Exosome	KEVMF	LGEIEEILDVIEPTQFK	KIEEP	2		987.0280357	1972.040471	0.002727428	1	N	329	346
Q6PD03	Parental	KEIKR	ATLNELVEYVSTNR	GVIVE	2		804.9155485	1607.815497	0.000622848	3	N	98	112
Q6PD03	Parental	KEIKR	ATLNELVEYVSTNR	GVIVE	3		536.946299	1607.815497	0.000451244	5	N	98	112
Q6PDG5	Exosome	TKVER	DIGEGNLSTAAAAALAAAAVK	AKHLA	2		943.0054263	1883.995253	0.000451244	13	N	851	872
Q6PDG5	Exosome	TKVER	DIGEGNLSTAAAAALAAAAVK	AKHLA	3		629.0062175	1883.995253	0.000451244	9	N	851	872
Q6PDG5	Exosome	MTIEK	SLVQNNCLSRPNIFLCPEIEPK	LLGKL	3	C7:+57.021,C16:+57.021	876.7808165	2627.319049	0.000451244	3	N	129	151
Q6PDG5	Exosome	PPTNK	SLSSLVVQLLQFQEEVFGK	HVSNA	2		1076.088959	2150.162318	0.000637154	2	N	47	66
Q6PDG5	Exosome	LHFLR	LPIEDPYLEDSEASLGPLAYQPIPF	SQSGN	2		1387.694714	2773.373827	0.001395409	1	N	641	666
Q6PDG5	Parental	TKVER	DIGEGNLSTAAAAALAAAAVK	AKHLA	2		943.0054263	1883.995253	0.000451244	25	N	851	872
Q6PDG5	Parental	TKVER	DIGEGNLSTAAAAALAAAAVK	AKHLA	3		629.0062175	1883.995253	0.000451244	17	N	851	872
Q6PDG5	Parental	PVMKR	DKQVLLHWGYYPDSYDTWIPASEIEASVEDAPTPEKPR	KVHAK	4		1101.534549	4402.106996	0.000622848	1	N	197	235
Q6PDG5	Parental	MTIEK	SLVQNNCLSRPNIFLCPEIEPK	LLGKL	3	C7:+57.021,C16:+57.021	876.7808165	2627.319049	0.001591523	1	N	129	151
Q6PDG5	Parental	PPTNK	SLSSLVVQLLQFQEEVFGK	HVSNA	2		1076.088959	2150.162318	0.000451244	2	N	47	66
Q6PDG5	Parental	LHFLR	LPIEDPYLEDSEASLGPLAYQPIPF	SQSGN	2		1387.694714	2773.373827	0.001162105	2	N	641	666
Q6PDG5	Parental	LHFLR	LPIEDPYLEDSEASLGPLAYQPIPF	SQSGN	3		925.4657425	2773.373827	0.000451244	3	N	641	666
Q6PDI5	Exosome	EEIIR	SATETIGSFLDSTSPLLAIAACTALGEIGR	NGPLP	3	C22:+57.021	1008.185267	3021.532402	0.000451244	7	N	787	817
Q6PDI5	Exosome	LGIVK	FIEAEQVPELEAVLHLVIASSDTR	HSVAT	3		889.4732314	2665.396294	0.000622848	1	N	244	268

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6PDI5	Exosome	YSSVR	TEALSVVELLLK	KLEEA	2		657.8981074	1313.780615	0.0007646	3	N	1779	1791
Q6PDI5	Exosome	PAGAK	VNDVVPWVLDVILNK	HIISP	2		861.9936019	1721.971604	0.001395409	2	N	929	944
Q6PDI5	Exosome	PAGAK	VNDVVPWVLDVILNK	HIISP	3		574.9983346	1721.971604	0.000451244	3	N	929	944
Q6PDI5	Exosome	KMKER	AIQTLGYFPVGDGVFPHQK	LLLQG	3		692.030586	2073.068358	0.002884417	1	N	855	874
Q6PDI5	Exosome	HLFTK	DIALVQQLFEALCKEEPETR	LAIQE	3	C13:+57.021	797.0741486	2388.199046	0.000451244	2	N	431	451
Q6PDI5	Parental	EEIIR	SATETIGSFLDSTSPLLAIAACTALGEIGR	NGPLP	3	C22:+57.021	1008.185267	3021.532402	0.000451244	11	N	787	817
Q6PDI5	Parental	LGIVK	FIEAEQVPELEAVLHLVIASSDTR	HSVAT	3		889.4732314	2665.396294	0.000637154	2	N	244	268
Q6PDI5	Parental	PHAPK	LIPALLESLSVLEPQVLNYLSLR	ATEQE	2		1290.754712	2579.493823	0.001943752	1	N	1290	1313
Q6PDI5	Parental	PHAPK	LIPALLESLSVLEPQVLNYLSLR	ATEQE	3		860.8390744	2579.493823	0.000622848	6	N	1290	1313
Q6PDI5	Parental	YSSVR	TEALSVVELLLK	KLEEA	2		657.8981074	1313.780615	0.00091018	3	N	1779	1791
Q6PDI5	Parental	PAGAK	VNDVVPWVLDVILNK	HIISP	3		574.9983346	1721.971604	0.000451244	10	N	929	944
Q6PDI5	Parental	YAAKR	VIGDNPWTPEQLEQCK	LGIVK	2	C15:+57.021	957.4570233	1912.898447	0.00091018	1	N	223	239
Q6PDI5	Parental	LSTYK	ELCSLASDLSQPDLVYK	FMNLA	2	C3:+57.021	969.4801641	1936.944728	0.001654178	1	N	1062	1079
Q6PDI5	Parental	NEKER	ELQLESLLGAFESLGK	AWPRN	3		578.6493711	1732.924713	0.000451244	1	N	1680	1696
Q6PDM2	Exosome	LKNRR	GGPPFAFVEFEDPRDAEDAVYGR	DGYDY	2		1271.088207	2540.160815	0.000998612	6	N	51	74
Q6PDM2	Exosome	LKNRR	GGPPFAFVEFEDPRDAEDAVYGR	DGYDY	3		847.7280715	2540.160815	0.000451244	27	N	51	74
Q6PDM2	Exosome	ADVYR	DGTGVVEFVR	KEDMT	2		539.7805348	1077.54547	0.000823681	2	N	154	164
Q6PDM2	Parental	KDHMR	EAGDVCYADVYR	DGTGV	2	C6:+57.021	709.3065565	1416.597513	0.000451244	20	N	142	154
Q6PDM2	Parental	KDHMR	EAGDVCYADVYRDGTGVVEFVR	KEDMT	2	C6:+57.021	1239.074011	2476.132423	0.001162105	4	N	142	164
Q6PDM2	Parental	KDHMR	EAGDVCYADVYRDGTGVVEFVR	KEDMT	3	C6:+57.021	826.3852742	2476.132423	0.000451244	7	N	142	164
Q6PDM2	Parental	LKNRR	GGPPFAFVEFEDPRDAEDAVYGR	DGYDY	2		1271.088207	2540.160815	0.000451244	17	N	51	74
Q6PDM2	Parental	LKNRR	GGPPFAFVEFEDPRDAEDAVYGR	DGYDY	3		847.7280715	2540.160815	0.000451244	33	N	51	74
Q6PDM2	Parental	ADVYR	DGTGVVEFVR	KEDMT	2		539.7805348	1077.54547	0.000451244	25	N	154	164
Q6PDM2	Parental	GDVCY	ADVYRDGTGVVEFVR	KEDMT	2		841.9289902	1681.84238	0.000451244	2	N	149	164
Q6PDM2	Parental	PPDIR	TKDIEDVFYK	YGAIR	2		629.3222325	1256.628865	0.000823681	6	N	28	38
Q6PDM2	Parental	NNDCR	IYVGNLPPDIR	TKDIE	2		628.8540342	1255.692468	0.001463592	1	N	17	28
Q6PDQ2	Exosome	CRVCK	DGGELLCCDTCPSSYHIHCLNPPLPEIPNGEWLCPR	CTCPA	4	C7:+57.021,C8:+57.021,C11:+57.021,C19:+57.021,C34:+57.021	1066.725736	4262.871745	0.000735798	1	N	449	485
Q6PDQ2	Parental	ALNTR	FAEVECLAESHQHLSK	ESMAG	3	C6:+57.021	628.9688436	1883.883131	0.000451244	4	N	1824	1840
Q6PDQ2	Parental	EGHSK	GPFLVSAPLSTIINWER	EFEMW	2		950.5205152	1899.02543	0.000622848	14	N	768	785
Q6PDQ2	Parental	SLFMR	HLCEPGADGAETFADGVPR	EGLSR	2	C3:+57.021	999.9526364	1997.889673	0.000451244	7	N	1458	1477
Q6PDQ2	Parental	ARRFK	LLEQALVIEEQLR	RAAYL	2		777.4490272	1552.882454	0.001352548	3	N	1790	1803
Q6PDQ2	Parental	CRVCK	DGGELLCCDTCPSSYHIHCLNPPLPEIPNGEWLCPR	CTCPA	3	C7:+57.021,C8:+57.021,C11:+57.021,C19:+57.021,C34:+57.021	1421.965048	4262.871745	0.001329271	2	N	449	485
Q6PDQ2	Parental	CRVCK	DGGELLCCDTCPSSYHIHCLNPPLPEIPNGEWLCPR	CTCPA	4	C7:+57.021,C8:+57.021,C11:+57.021,C19:+57.021,C34:+57.021	1066.725736	4262.871745	0.001352548	1	N	449	485
Q6PDQ2	Parental	PLLAR	VGGNIEVLGFNAR	QRKAF	2		673.3652974	1344.714995	0.001162105	2	N	1399	1412
Q6PE01	Exosome	VKRPR	HELLLGAAGAGPGAGPQQATPGALLQAGPPR	CSSLQ	3		958.518057	2872.530771	0.000451244	5	N	21	52
Q6PE01	Exosome	ELLLG	AAGAGPGAGPQQATPGALLQAGPPR	CSSLQ	2		1106.085605	2210.15561	0.001699387	3	N	27	52
Q6PE01	Exosome	LAVTF	NDTSDQIISGGIDNDIKVWDLR	QNKLT	3		825.4106311	2473.208493	0.000622848	1	N	202	224
Q6PE01	Exosome	DIRKK	AAVQTFQNTYQVLAVTFNDTSDQIISGGIDNDIK	VWDLR	3		1229.611516	3685.811148	0.000451244	1	N	185	219
Q6PE01	Parental	VKRPR	HELLLGAAGAGPGAGPQQATPGALLQAGPPR	CSSLQ	3		958.518057	2872.530771	0.000451244	8	N	21	52
Q6PEB6	Exosome	NLMSK	DNLIVPILEEEVQNSVSGESEA	-	2		1186.079714	2370.143827	0.000451244	20	N	203	225
Q6PEB6	Exosome	NLMSK	DNLIVPILEEEVQNSVSGESEA	-	3		791.0557424	2370.143827	0.001329271	1	N	203	225
Q6PEB6	Exosome	SNIDK	ILEPPEGQDEGVWKYEHLR	QFCLE	4		574.5410858	2294.133143	0.002374549	1	N	56	75
Q6PEB6	Exosome	YFHHR	QIFDEYENETFLCHR	FTKFV	3	C13:+57.021	667.63212	1999.87296	0.000451244	2	N	175	190
Q6PEB6	Parental	NLMSK	DNLIVPILEEEVQNSVSGESEA	-	2		1186.079714	2370.143827	0.000451244	29	N	203	225
Q6PFD9	Parental	APPER	SSLIQDWETSGLVYLDYIR	VIEML	2		1129.57113	2257.126661	0.000451244	3	N	1678	1697
Q6PFD9	Parental	LLQSK	FASGTFLSPSASVQECR	TPRTS	2	C16:+57.021	922.4360908	1842.856582	0.000451244	12	N	1051	1068
Q6PFD9	Parental	SGDHR	LALLLSQLVGSQSVR	ELLTM	2		792.478119	1582.940638	0.001463592	2	N	1356	1371
Q6PFD9	Parental	WGHLK	ELDGQLDEPSEYIQTLER	RRAFS	2		1068.011103	2134.006605	0.002212458	2	N	1283	1301
Q6PFD9	Parental	NGERF	SFLSKPVDENNQQDGEDDSLVSR	FYTNP	3		860.4005718	2578.178315	0.000622848	1	N	634	657
Q6PFR5	Parental	EVFSR	YGPLSGVNVVYDQR	TGRSR	2		783.8997014	1565.783803	0.000451244	6	N	139	153
Q6PFR5	Parental	HTGSR	ANPDPNTCLGVFGLSLYTTER	DLREV	2	C8:+57.021	1163.062915	2324.110231	0.000451244	16	N	110	131
Q6PFR5	Parental	HTGSR	ANPDPNTCLGVFGLSLYTTER	DLREV	3	C8:+57.021	775.7112102	2324.110231	0.000451244	2	N	110	131
Q6PGG2	Parental	SVLKR	FLQELTDPVVPFHLYDAFISLAK	TLHAD	3		888.4760246	2662.404674	0.000823681	4	N	624	647
Q6PGG2	Parental	ASSWR	DLSPEGPAPLTEEELDLR	LIRTK	2		990.9921815	1979.968763	0.002519933	2	N	72	90
Q6PGG2	Parental	DAVSR	TTCCADPEPEESEEHL	-	2	C3:+57.021,C4:+57.021	952.3697219	1902.723844	0.001943752	3	N	955	971
Q6PGG2	Parental	EGRKR	YSDIFQSLDNLEISLGNVTFDPLAGDPVRR	EDLEP	3		1117.900561	3350.678283	0.000979378	2	N	17	47
Q6PHU5	Exosome	INVIK	FSTDEGQCWQSYVFTQEPIYFTGLASEPGAR	SMNIS	3	C8:+57.021	1191.208912	3570.603335	0.000451244	29	N	546	577
Q6PHU5	Exosome	DILER	NCEEDDYTTWLAHSTDPGDYKDGCILGYK	EQFLR	3	C2:+57.021,C24:+57.021	1141.818941	3422.433424	0.000451244	2	N	608	637
Q6PHU5	Exosome	NGSCK	ADLGALELWR	TSDLG	2		572.3120021	1142.608404	0.000735798	7	N	276	286
Q6PHU5	Exosome	SFITR	QWVSYTVDFKDILER	NCEED	3		633.6602701	1897.95741	0.001162105	3	N	593	608
Q6PHU5	Parental	DILER	NCEEDDYTTWLAHSTDPGDYKDGCILGY	KEQFL	3	C2:+57.021,C24:+57.021	1099.12062	3294.338461	0.000451244	13	N	608	636
Q6PHU5	Parental	INVIK	FSTDEGQCWQSYVFTQEPIYFTGLASEPGAR	SMNIS	3	C8:+57.021	1191.208912	3570.603335	0.000451244	33	N	546	577

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6PHU5	Parental	GRWRR	GAPAEDQDCGRLPDFIAK	LTNNT	2	C9:+57.021	980.4653796	1958.915159	0.000622848	1	N	75	93
Q6PHU5	Parental	NGSCK	ADLGALELWR	TSDLG	2		572.3120021	1142.608404	0.001329271	1	N	276	286
Q6PHZ2	Exosome	YQQIK	AGAYDFPSPEWDTVTPEAK	DLINK	2		1040.979074	2079.942548	0.000451244	10	N	227	246
Q6PHZ2	Exosome	QEIIK	VTEQLIEAINNGDFEAYTK	ICDPG	2		1078.031838	2154.048076	0.000622848	1	N	352	371
Q6PHZ2	Parental	YQQIK	AGAYDFPSPEWDTVTPEAK	DLINK	2		1040.979074	2079.942548	0.000451244	37	N	227	246
Q6PHZ2	Parental	QEIIK	VTEQLIEAINNGDFEAYTK	ICDPG	2		1078.031838	2154.048076	0.000823681	5	N	352	371
Q6SJQ7	Parental	THVPR	TGLEEETTEYSSIR	RPLPA	2		807.8788286	1613.742057	0.000451244	15	N	315	329
Q6SJQ7	Parental	APFPR	EEVSYAALTLAGLGQEPTYGNTGCPITHVPR	TGLEE	3	C24:+57.021	1101.210475	3300.608026	0.000451244	12	N	284	315
Q6SJQ7	Parental	APFPR	EEVSYAALTLAGLGQEPTYGNTGCPITHVPR	TGLEE	4	C24:+57.021	826.1598066	3300.608026	0.001699387	1	N	284	315
Q6SJQ7	Parental	EVSYA	ALTLAGLGQEPTYGNTGCPITHVPR	TGLEE	3	C18:+57.021	875.1151183	2622.321955	0.00307782	1	N	290	315
Q6URW6	Exosome	EKKQR	KFDQLLAEEK	AAVLR	2		610.8302247	1219.644849	0.000823681	9	Y	1472	1482
Q6URW6	Exosome	LIYTY	SGLFCVVINPYK	QLPIY	2	C5:+57.021	698.8685957	1395.721591	0.001264573	2	Y	133	145
Q6URW6	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	2		863.9784831	1725.941366	0.000451244	29	Y	240	256
Q6URW6	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	3		576.3215887	1725.941366	0.000451244	18	Y	240	256
Q6URW6	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	2	Q1:-17.027	855.4649831	1708.914366	0.000698008	1	Y	240	256
Q6URW6	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	2	[0:-17.027	855.4649831	1708.914366	0.000451244	22	Y	240	256
Q6URW6	Exosome	KAQTK	EQADFALEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	16	N	437	449
Q6URW6	Exosome	MLQDR	EDQSILCTGESGAGK	TENTK	2	C7:+57.021	776.3516924	1550.687785	0.000451244	7	Y	185	200
Q6URW6	Exosome	DLIER	PANPPGLLALLDEECWFPK	ATDKS	2	C15:+57.021	1084.048548	2166.081496	0.000451244	1	N	547	566
Q6URW6	Parental	EKKQR	KFDQLLAEEK	AAVLR	2		610.8302247	1219.644849	0.000698008	42	Y	1472	1482
Q6URW6	Parental	LIYTY	SGLFCVVINPYK	QLPIY	2	C5:+57.021	698.8685957	1395.721591	0.000451244	3	Y	133	145
Q6URW6	Parental	GELER	QLLQANPILEAFGNAK	TVKND	2		863.9784831	1725.941366	0.000451244	37	Y	240	256
Q6URW6	Parental	GELER	QLLQANPILEAFGNAK	TVKND	3		576.3215887	1725.941366	0.000451244	27	Y	240	256
Q6URW6	Parental	GELER	QLLQANPILEAFGNAK	TVKND	2	Q1:-17.027	855.4649831	1708.914366	0.000451244	6	Y	240	256
Q6URW6	Parental	GELER	QLLQANPILEAFGNAK	TVKND	2	[0:-17.027	855.4649831	1708.914366	0.000451244	15	Y	240	256
Q6URW6	Parental	DYVQK	AQTKEQADFALEALAK	ATYER	2		867.4575805	1732.899561	0.000451244	3	N	433	449
Q6URW6	Parental	DYVQK	AQTKEQADFALEALAK	ATYER	3		578.640987	1732.899561	0.000451244	2	N	433	449
Q6URW6	Parental	KAQTK	EQADFALEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	8	N	437	449
Q6URW6	Parental	MLQDR	EDQSILCTGESGAGK	TENTK	2	C7:+57.021	776.3516924	1550.687785	0.000451244	22	Y	185	200
Q6URW6	Parental	KKQRK	FDQLLAEEK	AAVLR	2		546.7827432	1091.549886	0.00091018	11	Y	1473	1482
Q6URW6	Parental	MLQDR	EDQSILCTGESGAGKTENTK	KVIQY	3	C7:+57.021	708.9956753	2123.963626	0.000451244	5	Y	185	205
Q6WVG3	Exosome	SRLQR	EAEYFELPELVR	RLGAP	2		747.8779033	1493.740207	0.000451244	26	N	115	127
Q6WVG3	Exosome	ELVRR	LGAPQQPGPGPPPPHSR	RGVHK	3		563.9660279	1688.874684	0.000451244	1	N	128	145
Q6WVG3	Exosome	TSLAK	EVFGDTLNESRDPDRPPER	YTSRY	3		743.6897282	2228.045785	0.000662267	9	N	248	267
Q6WVG3	Exosome	RGVHK	EGSLGDELLPLGYAEPEPQEGASAGAPSPTLELASR	SPSGG	3		1203.592122	3607.752965	0.000451244	3	N	150	186
Q6WVG3	Exosome	YVTRR	CTVVSVPDSLLWR	MFTQQ	2	C1:+57.021	766.4007913	1530.785983	0.000622848	16	N	49	62
Q6WVG3	Exosome	LDYLR	DLQLVLPDYFPER	SRLQR	2		802.9201025	1603.824605	0.002145581	2	N	97	110
Q6WVG3	Parental	SRLQR	EAEYFELPELVRR	LGAPQ	3		550.9549059	1649.841318	0.002453667	3	N	115	128
Q6WVG3	Parental	GFFFR	YILDYLRDLQLVLPDYFPER	SRLQR	3		847.7849696	2540.331509	0.000451244	3	N	90	110
Q6WVG3	Parental	SRLQR	EAEYFELPELVR	RLGAP	2		747.8779033	1493.740207	0.000451244	23	N	115	127
Q6WVG3	Parental	RGVHK	EGSLGDELLPLGYAEPEPQEGASAGAPSPTLELASR	SPSGG	3		1203.592122	3607.752965	0.000451244	9	N	150	186
Q6WVG3	Parental	LPLGY	AEPEPQEGASAGAPSPTLELASR	SPSGG	2		1133.053833	2264.092066	0.002145581	2	N	163	186
Q6WVG3	Parental	YVTRR	CTVVSVPDSLLWR	MFTQQ	2	C1:+57.021	766.4007913	1530.785983	0.000979378	1	N	49	62
Q6ZPJ3	Exosome	EDGAK	LYDVCPHVSDSGLFFDDSYGFYPGQVLIGPAK	IFSSV	3	C5:+57.021	1188.566148	3562.675043	0.000622848	6	N	234	266
Q6ZPJ3	Exosome	VVDKR	VQSCPDPAVYGVVQSGDHVGR	TCMVK	3	C4:+57.021	743.0238996	2226.048299	0.000979378	1	N	589	610
Q6ZPJ3	Parental	DIVIR	IGNTEDGALPKEDEPSVGQVAR	VDVSS	3		761.3806718	2281.118615	0.001654178	1	N	656	678
Q6ZQ38	Exosome	SEEVK	SAASYALGSISVGNLPEYLPFVLQEITSQPK	RQYLL	3		1093.910286	3278.707458	0.000451244	18	N	873	904
Q6ZQ38	Exosome	EENVK	ADVFHAYLSLLK	QTRPV	3		459.5911278	1375.749983	0.000637154	6	N	391	403
Q6ZQ38	Exosome	ECLGK	LTLIDPETLLPR	LKGYL	2		690.9090065	1379.802413	0.000823681	20	N	957	969
Q6ZQ38	Exosome	QRALK	LGTLSALDILIK	NYSDS	2		628.8953677	1255.775135	0.000622848	6	N	667	679
Q6ZQ38	Exosome	GSPLK	IDLRPVLGEGVPILASFLR	KNQRA	3		689.0776476	2064.209543	0.000622848	12	N	641	660
Q6ZQ38	Exosome	SSLSK	ISGSILNELIGLVR	SPLLQ	2		742.4462875	1482.876975	0.000451244	18	N	729	743
Q6ZQ38	Exosome	RACPK	EGPAVVGQFIQDVK	NSRST	2		743.8991701	1485.78274	0.000451244	10	N	812	826
Q6ZQ38	Exosome	DMLSR	QGGLLVNFHPSILTCLLPQLTSPR	LAVRK	3	C15:+57.021	887.8233872	2660.446762	0.000622848	8	N	164	188
Q6ZQ38	Parental	SEEVK	SAASYALGSISVGNLPEYLPFVLQEITSQPK	RQYLL	3		1093.910286	3278.707458	0.000451244	8	N	873	904
Q6ZQ38	Parental	EENVK	ADVFHAYLSLLK	QTRPV	3		459.5911278	1375.749983	0.000637154	2	N	391	403
Q6ZQ38	Parental	GSPLK	IDLRPVLGEGVPILASFLR	KNQRA	3		689.0776476	2064.209543	0.002519933	1	N	641	660
Q6ZQ38	Parental	SSLSK	ISGSILNELIGLVR	SPLLQ	2		742.4462875	1482.876975	0.000451244	11	N	729	743
Q6ZQ38	Parental	DMLSR	QGGLLVNFHPSILTCLLPQLTSPR	LAVRK	3	C15:+57.021	887.8233872	2660.446762	0.000622848	2	N	164	188
Q6ZQ38	Parental	PSLIR	DLLDSVLPHLYNETK	VRKEL	3		586.3092374	1755.904312	0.000622848	4	N	1042	1057
Q6ZQ38	Parental	PLVVK	FCNVDDDELREYCIQAFESFVR	RCPKE	3	C2:+57.021,C13:+57.021	938.0831123	2811.225937	0.001699387	1	N	262	284
Q6ZQA0	Exosome	CPASR	TTCVQAGLVGYLLETLNTGTALGAR	CQEQL	2	C3:+57.021	1290.178811	2578.342022	0.002080925	1	N	485	510
Q6ZQA0	Exosome	PKVQK	LLSGPWVSDSGVSAQALAVAPDGK	LLFSG	2		1163.108411	2324.201223	0.000451244	5	N	2436	2460
Q6ZQA0	Parental	CPASR	TTCVQAGLVGYLLETLNTGTALGAR	CQEQL	2	C3:+57.021	1290.178811	2578.342022	0.000823681	3	N	485	510
Q6ZQA0	Parental	AGRTY	NDLSQYPVFPWVLQDYVSPVLDLSNPAVFR	DLSKP	3		1160.26143	3477.760891	0.000823681	3	N	2078	2108

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6ZQA0	Parental	TIAGR	TYNDLSQYPVFPWVLQDYVSPVLDLSNPAVFR	DLSKP	3		1248.298433	3741.871898	0.000451244	7	N	2076	2108
Q6ZQA0	Parental	PKVQK	LLSGPWVSDSGVSAQALAVAPDGK	LLFSG	2		1163.108411	2324.201223	0.000451244	8	N	2436	2460
Q6ZQA0	Parental	LNQLK	AFFAEVVSEAVPLVLALVPHR	QSHSF	3		755.4320905	2263.272872	0.000451244	8	N	2361	2382
Q6ZQA0	Parental	LLMLR	NFLQNHTVNQESLVQCQGPAIIGALLR	KVPSS	3	C16:+57.021	1007.529703	3019.565708	0.002019181	1	N	957	984
Q6ZQA0	Parental	RQRIR	LHDCGLQGLVASLSEESISPQLCQGLYK	LFVGT	3	C4:+57.021,C23:+57.021	1034.846214	3101.515243	0.000451244	7	N	1197	1225
Q6ZQA0	Parental	AALSR	ALTTSSSETEHASTAVAASER	CSWLV	3		702.6702223	2104.987267	0.002663018	1	N	1627	1648
Q6ZQA0	Parental	ALGAR	CQEQLLALLQALGR	VSLRP	2	C1:+57.021	806.9458974	1611.876195	0.001352548	2	N	510	524
Q6ZQI3	Parental	LPILR	STPEDQILYQTER	YNEET	2		790.3840812	1578.752562	0.000451244	24	N	89	102
Q6ZQI3	Parental	YQTER	YNEETFGYEVPVKEEGDYVLVLK	FAEVY	3		907.4500924	2719.326877	0.000451244	21	N	102	125
Q6ZQK5	Exosome	SPRFR	AALEEVEGDVAELELKLDK	LVKLC	3		691.0322094	2070.073228	0.000622848	1	N	18	37
Q6ZQK5	Parental	LFLKR	GANQHATDEEGKDPLSIAVEAANADIVTLLR	LARMN	4		805.4131741	3217.621497	0.000823681	5	N	688	719
Q6ZQK5	Parental	SALQR	VQCIPGNTSCCDCGLADPR	WASIN	2	C3:+57.021,C10:+57.021,C11:+57.021,C13:+57.021	1090.452612	2178.889624	0.000451244	5	N	404	423
Q6ZQK5	Parental	SPRFR	AALEEVEGDVAELELKLDK	LVKLC	3		691.0322094	2070.073228	0.002813207	1	N	18	37
Q6ZWM4	Exosome	ESHER	VFSSSQGVEQVVLGLYIVR	GDNVA	2		1040.576019	2079.136438	0.000451244	1	N	44	63
Q6ZWM4	Exosome	ESHER	VFSSSQGVEQVVLGLYIVR	GDNVA	3		694.0532792	2079.136438	0.000451244	3	N	44	63
Q6ZWM4	Exosome	VGTLK	GFDQTINLILDESHER	VFSSS	3		629.6468007	1885.917002	0.000451244	24	N	28	44
Q6ZWM4	Exosome	LYIVR	GDNVAVIGEIDEETDSALDLGNIR	AEPLN	2		1258.112076	2514.208553	0.001699387	1	N	63	87
Q6ZWM4	Parental	ESHER	VFSSSQGVEQVVLGLYIVR	GDNVA	2		1040.576019	2079.136438	0.000451244	17	N	44	63
Q6ZWM4	Parental	ESHER	VFSSSQGVEQVVLGLYIVR	GDNVA	3		694.0532792	2079.136438	0.000451244	3	N	44	63
Q6ZWM4	Parental	LYIVR	GDNVAVIGEIDEETDSALDLGNIRAEPLNSVAH	-	3		1145.229295	3432.664484	0.002519933	1	N	63	96
Q6ZWM4	Parental	VGTLK	GFDQTINLILDESHER	VFSSS	3		629.6468007	1885.917002	0.000451244	4	N	28	44
Q6ZWM4	Parental	LYIVR	GDNVAVIGEIDEETDSALDLGNIR	AEPLN	2		1258.112076	2514.208553	0.000451244	7	N	63	87
Q6ZWQ0	Exosome	LDELR	QSSLTMDGGDVPLLEDMASGIVELFQK	KNNVT	3	M6:+15.995	966.1372205	2895.388261	0.000451244	1	N	5216	5243
Q6ZWQ0	Exosome	EEIER	EAIILETLQEDLPEISK	TNAAP	2		971.025493	1940.035386	0.002296037	1	N	3471	3488
Q6ZWQ0	Exosome	KTKER	QYGLLSGFQDQLVMAEASLNTSLAEVESLK	IGSLD	4		811.1634022	3240.622409	0.002019181	1	N	2507	2537
Q6ZWQ0	Parental	EIEYK	VASLLETCKDQGLGDCGTTQQEAEALSWK	LKTVK	3	C8:+57.021,C16:+57.021	1065.836155	3194.485065	0.000451244	3	N	4278	4307
Q6ZWQ0	Parental	VSMEK	LLLDCQDIENQLALK	SKALD	2	C5:+57.021	893.4746847	1784.933769	0.000451244	1	N	5193	5208
Q6ZWQ0	Parental	KFLQK	AQDLTSLLEELK	SQGNY	2		680.3724538	1358.729308	0.002981883	1	N	2181	2193
Q6ZWQ0	Parental	APSPR	LSQTDEGATPPIEAALLDFPR	EQGAF	2		1121.074037	2240.132475	0.001763695	1	N	4186	4207
Q6ZWQ0	Parental	LPLEK	ECSLLCASDLPLCTVAVQDLHPVEIDGVYQNLR	DIRDS	3	C2:+57.021,C6:+57.021,C13:+57.021	1262.283009	3783.825627	0.000451244	15	N	1228	1261
Q6ZWQ0	Parental	EEIER	EAIILETLQEDLPEISK	TNAAP	2		971.025493	1940.035386	0.000622848	4	N	3471	3488
Q6ZWQ0	Parental	HEHLK	QEQQEVGDKPSAGASECTVAER	DASER	3	C17:+57.021	792.6962884	2375.065465	0.000823681	1	N	4062	4084
Q6ZWQ9	Exosome	MFGEK	LNGTDPEDVIR	NAFAC	2		614.8125633	1227.609527	0.000451244	52	Y	93	104
Q6ZWQ9	Exosome	PIDKK	GNFNYIEFTR	ILKHG	2		630.8045413	1259.593483	0.000451244	20	Y	151	161
Q6ZWQ9	Exosome	NAFAC	FDEEAIGTIQEDYLR	ELLTT	2		899.9288529	1797.842106	0.002884417	1	N	109	124
Q6ZWQ9	Exosome	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	3		811.3815729	2431.121319	0.001463592	1	Y	124	144
Q6ZWQ9	Exosome	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	3	M6:+15.995	816.7132396	2447.116319	0.000451244	12	Y	124	144
Q6ZWQ9	Exosome	EDVIR	NAFACFDEEAIGTIQEDYLR	ELLTT	2	C5:+57.021	1181.53673	2361.057861	0.000451244	45	N	104	124
Q6ZWQ9	Exosome	EDVIR	NAFACFDEEAIGTIQEDYLR	ELLTT	3	C5:+57.021	788.0270869	2361.057861	0.000451244	24	N	104	124
Q6ZWQ9	Exosome	TMGDR	FTDEEVDELYR	EAPID	2		708.3204182	1414.625236	0.000451244	24	Y	133	144
Q6ZWQ9	Exosome	PQRAT	SNVFAMFDQSQIQEFK	EAFNM	2	M6:+15.995	967.9518483	1933.888097	0.000451244	6	Y	19	35
Q6ZWQ9	Exosome	KRPQR	ATSNVFAMFDQSQIQEFK	EAFNM	2	M8:+15.995	1053.994245	2105.972889	0.000451244	21	Y	17	35
Q6ZWQ9	Exosome	KRPQR	ATSNVFAMFDQSQIQEF	KEAFN	2	M8:+15.995	989.9467629	1977.877926	0.000451244	13	Y	17	34
Q6ZWQ9	Exosome	RNAFA	CFDEEAIGTIQEDYLR	ELLTT	2	C1:+57.021	979.9439457	1957.872291	0.000622848	4	N	108	124
Q6ZWQ9	Parental	MFGEK	LNGTDPEDVIR	NAFAC	2		614.8125633	1227.609527	0.000451244	58	Y	93	104
Q6ZWQ9	Parental	PIDKK	GNFNYIEFTR	ILKHG	2		630.8045413	1259.593483	0.000451244	36	Y	151	161
Q6ZWQ9	Parental	NAFAC	FDEEAIGTIQEDYLR	ELLTT	2		899.9288529	1797.842106	0.000451244	17	N	109	124
Q6ZWQ9	Parental	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	2		1216.568459	2431.121319	0.000622848	4	Y	124	144
Q6ZWQ9	Parental	EDYLR	ELLTTMGDRFTDEEVDELYR	EAPID	3		811.3815729	2431.121319	0.000451244	8	Y	124	144
Q6ZWQ9	Parental	EDVIR	NAFACFDEEAIGTIQEDYLR	ELLTT	2	C5:+57.021	1181.53673	2361.057861	0.000451244	230	N	104	124
Q6ZWQ9	Parental	EDVIR	NAFACFDEEAIGTIQEDYLR	ELLTT	3	C5:+57.021	788.0270869	2361.057861	0.000451244	47	N	104	124
Q6ZWQ9	Parental	TMGDR	FTDEEVDELYR	EAPID	2		708.3204182	1414.625236	0.000451244	58	Y	133	144
Q6ZWQ9	Parental	FLTMF	GEKLNGTDPEDVIR	NAFAC	2		771.8920734	1541.768547	0.000451244	4	Y	90	104
Q6ZWQ9	Parental	LLTTM	GDRFTDEEVDELYR	EAPID	2		872.3951772	1742.774754	0.002813207	1	Y	130	144
Q6ZWQ9	Parental	VIRNA	FACFDEEAIGTIQEDYLR	ELLTT	2	C3:+57.021	1088.99671	2175.977819	0.000451244	7	N	106	124
Q6ZWR6	Exosome	KAAAR	ESSNLTGDSQILEAR	LHNLQ	2		810.3977199	1618.77984	0.001943752	2	N	2428	2443
Q6ZWR6	Exosome	QALCK	QQAVLQAGVVDYETFAK	SLEAL	2		933.9839625	1865.952325	0.000451244	5	N	7345	7362
Q6ZWR6	Exosome	EVSER	TAAFPSSSGVLYTVAKEELK	KFEAF	3		700.0409278	2097.099383	0.002981883	1	N	8023	8043
Q6ZWR6	Exosome	SQYDK	ALQDLVDLLDTGQEK	MTGDQ	2		829.4363138	1656.857028	0.000451244	12	N	6596	6611
Q6ZWR6	Exosome	EVNMR	WNNLLEEIAEQLHSSK	ALLQL	3		637.6589292	1909.953388	0.000451244	10	N	7222	7238
Q6ZWR6	Exosome	GLKEK	FSLLDHFQSIVSEAEDHTGALQQLAAK	SRELY	4		739.6271496	2954.477398	0.000451244	3	N	2767	2794
Q6ZWR6	Exosome	MDKNK	NLFSQAFPEDSDNRDVIEDTLGCLLGR	LSLLD	3	C23:+57.021	1027.824621	3080.450463	0.000451244	25	N	6440	6467
Q6ZWR6	Exosome	EKFTK	AKELISADLEHTLAELQELDGDVQEALR	TRQAT	4		777.4035464	3105.582986	0.001463592	1	N	4952	4980

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6ZWR6	Exosome	AILAR	KEYTSLIELTTQSLGDLEDQFLK	MRKMP	3		891.1291303	2670.363991	0.000451244	4	N	4671	4694
Q6ZWR6	Exosome	FTKAK	ELISADLEHTLAELQELDGDVQEALR	TRQAT	3		969.8247696	2906.450909	0.000451244	5	N	4954	4980
Q6ZWR6	Exosome	LSRFR	LLTGSSEAVQVQVDNLQNLHDELEKQEGGLQK	FGSIT	4		880.7041169	3518.785268	0.000622848	4	N	7160	7192
Q6ZWR6	Exosome	QELSR	QLEVIENSIPSVGLVEESEDRLVER	TNLYQ	3		947.1614932	2838.461079	0.000451244	17	N	6706	6731
Q6ZWR6	Exosome	QASLK	TYQNEVTGLCAQGR	ELMKG	2	C10:+57.021	798.875669	1595.735738	0.000622848	2	N	4502	4516
Q6ZWR6	Exosome	DDGKR	LLMSVSCSELESQLNQLGEHWLSNTNK	VSKEL	3	M3:+15.995,C7:+57.021	1045.16954	3132.48522	0.000622848	3	N	6758	6785
Q6ZWR6	Exosome	DSLGK	INEILSVLEQEAQSSTLFK	QKHQE	2		1075.073506	2148.131412	0.000451244	2	N	833	852
Q6ZWR6	Exosome	EKLRK	WLAEVSHLPLSGLGNIPVPLQQVR	MLFDE	3		875.1626629	2622.464589	0.001591523	1	N	7580	7604
Q6ZWR6	Exosome	LLGDR	NSVENALKDCQELEDLIK	AKEKE	3	C10:+57.021	706.6846611	2117.030583	0.000622848	3	N	7057	7075
Q6ZWR6	Exosome	SNKEG	QQAIQDQLEMLK	KAWAE	2	M10:+15.995	730.8748809	1459.734162	0.002884417	2	N	2697	2709
Q6ZWR6	Exosome	KDGIK	LLALLEVLSGQK	LPCEQ	2		642.4008173	1282.786035	0.000451244	6	N	62	74
Q6ZWR6	Exosome	DRMKK	EYIDVTTTLFGFATEAHR	KLSEP	3		691.0097391	2070.005817	0.000823681	1	N	711	729
Q6ZWR6	Parental	KAAAR	ESSNLTGDSQILEAR	LHNLQ	2		810.3977199	1618.77984	0.000451244	16	N	2428	2443
Q6ZWR6	Parental	EIEQK	VVALSQLSVHNENLLLEGK	AHTKE	2		1032.078926	2062.142251	0.000451244	3	N	6145	6164
Q6ZWR6	Parental	EIEQK	VVALSQLSVHNENLLLEGK	AHTKE	3		688.3885504	2062.142251	0.001463592	5	N	6145	6164
Q6ZWR6	Parental	CLLGR	LSLLDSVVDQR	CHQMK	2		622.8464061	1243.677212	0.000451244	8	N	6467	6478
Q6ZWR6	Parental	QALCK	QQAVLQAGVVDYETFAK	SLEAL	2		933.9839625	1865.952325	0.000451244	21	N	7345	7362
Q6ZWR6	Parental	EVSER	TAAFPSSSGVLYTVAKEELK	KFEAF	3		700.0409278	2097.099383	0.000451244	6	N	8023	8043
Q6ZWR6	Parental	SAKQK	LLQNILEQEQEQVLYSSPNR	LLSGV	2		1201.12205	2400.2285	0.000451244	12	N	6314	6334
Q6ZWR6	Parental	SAKQK	LLQNILEQEQEQVLYSSPNR	LLSGV	3		801.0839668	2400.2285	0.000451244	20	N	6314	6334
Q6ZWR6	Parental	DVEER	LFVATAPLPEETEACLFNQEALAK	DIKEM	2	C15:+57.021	1331.67557	2661.335539	0.000451244	19	N	6403	6427
Q6ZWR6	Parental	DVEER	LFVATAPLPEETEACLFNQEALAK	DIKEM	3	C15:+57.021	888.1196465	2661.335539	0.000451244	11	N	6403	6427
Q6ZWR6	Parental	SQYDK	ALQDLVDLLDTGQEK	MTGDQ	2		829.4363138	1656.857028	0.000451244	32	N	6596	6611
Q6ZWR6	Parental	SQYDK	ALQDLVDLLDTGQEK	MTGDQ	3		553.2934758	1656.857028	0.000451244	7	N	6596	6611
Q6ZWR6	Parental	EVNMR	WNNLLEEIAEQLHSSK	ALLQL	2		955.9844938	1909.953388	0.001395409	1	N	7222	7238
Q6ZWR6	Parental	EVNMR	WNNLLEEIAEQLHSSK	ALLQL	3		637.6589292	1909.953388	0.000451244	31	N	7222	7238
Q6ZWR6	Parental	GLKEK	FSLLDHFQSIVSEAEDHTGALQQLAAK	SRELY	4		739.6271496	2954.477398	0.000451244	19	N	2767	2794
Q6ZWR6	Parental	MDKNK	NLFSQAFPEDSDNRDVIEDTLGCLLGR	LSLLD	3	C23:+57.021	1027.824621	3080.450463	0.000451244	31	N	6440	6467
Q6ZWR6	Parental	EKFTK	AKELISADLEHTLAELQELDGDVQEALR	TRQAT	4		777.4035464	3105.582986	0.0007646	2	N	4952	4980
Q6ZWR6	Parental	AILAR	KEYTSLIELTTQSLGDLEDQFLK	MRKMP	3		891.1291303	2670.363991	0.000451244	11	N	4671	4694
Q6ZWR6	Parental	FTKAK	ELISADLEHTLAELQELDGDVQEALR	TRQAT	3		969.8247696	2906.450909	0.000451244	22	N	4954	4980
Q6ZWR6	Parental	LSRFR	LLTGSSEAVQVQVDNLQNLHDELEKQEGGLQK	FGSIT	4		880.7041169	3518.785268	0.000451244	8	N	7160	7192
Q6ZWR6	Parental	VEAGK	QLLLSADSGAEAALQAELTDIQEKWK	AASMH	3		943.4945837	2827.460351	0.000622848	2	N	7632	7658
Q6ZWR6	Parental	QELSR	QLEVIENSIPSVGLVEESEDRLVER	TNLYQ	3		947.1614932	2838.461079	0.000451244	26	N	6706	6731
Q6ZWR6	Parental	QELSR	QLEVIENSIPSVGLVEESEDRLVER	TNLYQ	3	[0:-17.027	941.4858265	2821.434079	0.001463592	1	N	6706	6731
Q6ZWR6	Parental	ISQIK	VTIQEIESKIDSIVGLEEEAQSFAQFVTTGESAR	IKAKL	3		1237.958693	3710.852679	0.000451244	2	N	1485	1519
Q6ZWR6	Parental	LLEEK	LSDQLEEQRQEQALQR	YRCEA	3		657.6683759	1969.981728	0.000451244	12	N	6080	6096
Q6ZWR6	Parental	QASLK	TYQNEVTGLCAQGR	ELMKG	2	C10:+57.021	798.875669	1595.735738	0.000451244	9	N	4502	4516
Q6ZWR6	Parental	KGYMK	LLGECSGSIDSVR	RLEHK	2	C5:+57.021	696.8433062	1391.671012	0.000451244	5	N	8378	8391
Q6ZWR6	Parental	RTHQR	QSSLQQQKEFEQELAEQK	SLLRS	3		726.6944793	2177.060038	0.002145581	1	N	6236	6254
Q6ZWR6	Parental	ETFAK	SLEALEVWMVEAEGILQGQDPTHSSDLSTIQER	MEELK	3		1223.59699	3667.76757	0.001162105	2	N	7362	7395
Q6ZWR6	Parental	EMFSR	QQILHSIIVDGQNLLEQGQVDDREEF	SLKLT	3		1008.507663	3022.49959	0.000979378	1	N	7510	7536
Q6ZWR6	Parental	EMFSR	QQILHSIIVDGQNLLEQGQVDDREEF	SLKLT	3	Q1:-17.027	1002.831997	3005.47259	0.002296037	1	N	7510	7536
Q6ZWR6	Parental	RVGEK	IQMLEGLLESWSEYENSVQSLK	AWFAN	2		1292.136509	2582.257418	0.000451244	1	N	7016	7038
Q6ZWR6	Parental	TQVER	FVKDITAWLINVEESLTR	CAQTE	3		712.0568008	2133.147002	0.000637154	1	N	2309	2327
Q6ZWR6	Parental	HLEQK	LYDGVSATSTWLNDVEER	LFVAT	2		1027.98743	2053.959261	0.000451244	8	N	6385	6403
Q6ZWR6	Parental	EKLKK	DYQEEIAVAQENK	IQLQE	2		768.8629815	1535.710363	0.000451244	15	N	7823	7836
Q6ZWR6	Parental	LNHNK	IEQIIAQGEQLIEK	SEPLD	2		806.4517668	1610.887934	0.000451244	14	N	8165	8179
Q6ZWR6	Parental	LNHNK	IEQIIAQGEQLIEK	SEPLD	3		537.9704446	1610.887934	0.002727428	1	N	8165	8179
Q6ZWR6	Parental	NAFLK	ACDELTDILPEQEQQGLQEAVR	KLHKQ	2	C2:+57.021	1271.608415	2541.201231	0.000637154	3	N	980	1002
Q6ZWR6	Parental	ITTAK	CFDLPQNLSEVSSSLQK	IQEFL	2	C1:+57.021	976.475413	1950.935226	0.000698008	1	N	3087	3104
Q6ZWR6	Parental	ERSGR	DTPASVDSIPLEWDHDYDLSR	DLESA	2		1216.056573	2430.097546	0.001943752	2	N	8276	8297
Q6ZWR6	Parental	ERSGR	DTPASVDSIPLEWDHDYDLSR	DLESA	3		811.0403152	2430.097546	0.000622848	3	N	8276	8297
Q6ZWR6	Parental	RDIEK	HSTGVASVLNLCEVLLHDCDACATDAECDSIQQATR	NLDRR	3	C12:+57.021,C19:+57.021,C22:+57.021,C28:+57.021	1339.599465	4015.774996	0.000451244	10	N	7941	7977
Q6ZWR6	Parental	RDIEK	HSTGVASVLNLCEVLLHDCDACATDAECDSIQQATR	NLDRR	4	C12:+57.021,C19:+57.021,C22:+57.021,C28:+57.021	1004.951549	4015.774996	0.000451244	10	N	7941	7977
Q6ZWR6	Parental	WILEK	ENELSSLEASASAADVQISQIK	VTIQE	2		1145.574598	2289.133597	0.001463592	1	N	1463	1485
Q6ZWR6	Parental	EGELR	NLQVALEQAQTILTSPEVGR	RSLKE	2		1084.090022	2166.164443	0.000451244	2	N	5640	5660
Q6ZWR6	Parental	DDGKR	LLMSVSCSELESQLNQLGEHWLSNTNK	VSKEL	3	M3:+15.995,C7:+57.021	1045.16954	3132.48522	0.001162105	2	N	6758	6785
Q6ZWR6	Parental	PLQSK	VDDCFQLFEEASQVVER	RKLAL	2	C4:+57.021	1035.975777	2069.935954	0.000451244	12	N	1843	1860
Q6ZWR6	Parental	SNWDR	YGDTVASLQAWLEDAEK	MLSQS	2		948.4552348	1894.89487	0.001839721	1	N	617	634
Q6ZWR6	Parental	QTQDK	TSVTSLLDGLSQAFGEASSQSGGTDR	QSIHL	2		1286.112608	2570.209616	0.000451244	19	N	6351	6377
Q6ZWR6	Parental	QTQDK	TSVTSLLDGLSQAFGEASSQSGGTDR	QSIHL	3		857.7443385	2570.209616	0.000451244	17	N	6351	6377
Q6ZWR6	Parental	LEQIK	FFEEELQCLEETESSLSSYSDWYGSTHK	NFKNV	3	C8:+57.021	1130.154361	3387.439683	0.000451244	7	N	3696	3724

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q6ZWR6	Parental	DSLGK	INEILSVLEQEAQSSTLFK	QKHQE	2		1075.073506	2148.131412	0.000451244	9	N	833	852
Q6ZWR6	Parental	EIESK	IDSIVGLEEEAQSFAQFVTTGESAR	IKAKL	2		1342.656651	2683.297702	0.000451244	10	N	1494	1519
Q6ZWR6	Parental	EIESK	IDSIVGLEEEAQSFAQFVTTGESAR	IKAKL	3		895.4403674	2683.297702	0.000451244	6	N	1494	1519
Q6ZWR6	Parental	ERFVK	DITAWLINVEESLTR	CAQTE	2		880.4654056	1758.915211	0.000451244	5	N	2312	2327
Q6ZWR6	Parental	ERFVK	DITAWLINVEESLTR	CAQTE	3		587.3128704	1758.915211	0.000622848	1	N	2312	2327
Q6ZWR6	Parental	TWLER	CEAIASSPEKDISADR	GKVES	3	C1:+57.021	583.6092039	1747.804212	0.000451244	4	N	1671	1687
Q6ZWR6	Parental	AHLPK	QIVSSIQEQITK	ANEEF	2		687.3858955	1372.756191	0.00091018	1	N	2477	2489
Q6ZWR6	Parental	KELTK	NPETPTELQFIEADLR	QKLEH	2		936.9710521	1871.926504	0.000451244	5	N	2264	2280
Q6ZWR6	Parental	EEAHR	EIEDKPVATSNIQELQAQISLHEE	LAQKI	3		907.7912887	2720.350466	0.001264573	1	N	5768	5792
Q6ZWR6	Parental	EKLRK	WLAEVSHLPLSGLGNIPVPLQQVR	MLFDE	3		875.1626629	2622.464589	0.000451244	14	N	7580	7604
Q6ZWR6	Parental	ISADR	GKVESELQLIQALQNEVVSQASLYSNLLQLK	EALFS	3		1148.298433	3441.871898	0.000451244	3	N	1687	1718
Q6ZWR6	Parental	ILARK	EYTSLIELTTQSLGDLEDQFLK	MRKMP	2		1272.142314	2542.269028	0.000451244	1	N	4672	4694
Q6ZWR6	Parental	KNTAK	DIQQTEQLIEQR	LVQAQ	2		750.886791	1499.757982	0.000451244	3	N	4107	4119
Q6ZWR6	Parental	LLGDR	NSVENALKDCQELEDLIK	AKEKE	3	C10:+57.021	706.6846611	2117.030583	0.000622848	4	N	7057	7075
Q6ZWR6	Parental	KDIRK	ELQSQQNSITSTQEELNSLCR	KHHSV	2	C20:+57.021	1233.082565	2464.149529	0.001329271	2	N	2345	2366
Q6ZWR6	Parental	LQRYR	CEADELDHWLLNTK	ATLDV	3	C1:+57.021	581.9387729	1742.792919	0.000622848	1	N	6098	6112
Q6ZWR6	Parental	QLTSR	YQALLLQVLEQIK	FFEEE	2		779.9643131	1557.913026	0.000451244	6	N	3683	3696
Q6ZWR6	Parental	NDLLK	GLETVKDSLFILR	ELGEQ	3		497.6246086	1489.850426	0.002884417	1	N	7294	7307
Q6ZWR6	Parental	KGGCR	STQLLTSYQSLLR	VTKEK	2		755.417727	1508.819854	0.000823681	1	N	2595	2608
Q6ZWR6	Parental	EQKNK	YLGLYTVLPSEISLQLAEVALDLK	IHDQI	3		883.4986064	2647.472419	0.000451244	3	N	5382	5406
Q6ZWR6	Parental	LIEQR	LVQAQNLTQGWEEIK	SLKAE	2		878.9655727	1755.915545	0.002145581	1	N	4119	4134
Q6ZWR6	Parental	QSALR	IPEDVVASLPLCHAALR	LQEEA	3	C12:+57.021	621.0052291	1859.992287	0.001871652	1	N	5695	5712
Q6ZWR6	Parental	GQMLK	FSSLAPDLDRLNELGYR	LPLND	3		656.0063289	1964.995587	0.002663018	1	N	7405	7422
Q6ZWR6	Parental	ISADR	GKVESELQLIQALQNEVVSQASLY	SNLLQ	2		1323.703404	2645.391209	0.000662267	2	N	1687	1711
Q6ZWR6	Parental	KHWTR	YQSEAAALNHWLQCAK	DRLAF	3	C14:+57.021	630.6373168	1888.88855	0.002080925	1	N	6802	6818
Q6ZWV3	Exosome	RKKAK	VDEFPLCGHMVSDEYEQLSSEALEAAR	ICANK	3	C7:+57.021,M10:+15.995	1033.462501	3097.364102	0.000451244	6	N	42	69
Q6ZWV3	Exosome	LGRKK	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	ICANK	3	C9:+57.021,M12:+15.995	1099.83986	3296.496179	0.000823681	1	N	40	69
Q6ZWX6	Exosome	AVKIR	ADIEVACYGYEGIDAVK	EALRA	2	C7:+57.021	936.938132	1871.860664	0.000451244	15	N	192	209
Q6ZWX6	Exosome	YDAFK	HAVSDPSILDSLDLNEDEREVLINNINR	RLTPQ	4		798.4053491	3189.590196	0.000622848	6	N	154	182
Q6ZWX6	Parental	YSILR	HVAEVLEYTKDEQLESLFQR	TAWVF	2		1217.616601	2433.217601	0.000735798	1	N	113	133
Q6ZWX6	Parental	YSILR	HVAEVLEYTKDEQLESLFQR	TAWVF	3		812.0803338	2433.217601	0.000451244	5	N	113	133
Q6ZWX6	Parental	YSILR	HVAEVLEYTKDEQLESLFQR	TAWVF	4		609.3122003	2433.217601	0.000870037	4	N	113	133
Q6ZWX6	Parental	AVKIR	ADIEVACYGYEGIDAVK	EALRA	2	C7:+57.021	936.938132	1871.860664	0.000451244	22	N	192	209
Q6ZWX6	Parental	YDAFK	HAVSDPSILDSLDLNEDEREVLINNINR	RLTPQ	3		1064.204532	3189.590196	0.000662267	8	N	154	182
Q6ZWX6	Parental	YDAFK	HAVSDPSILDSLDLNEDEREVLINNINR	RLTPQ	4		798.4053491	3189.590196	0.000451244	4	N	154	182
Q6ZWZ6	Parental	PMYVK	LVEALCAEHQINLIK	VDDNK	2	C6:+57.021	875.9799372	1749.944274	0.000451244	14	N	63	78
Q6ZWZ6	Parental	KDYGK	ESQAKDVIEEYFK	CKK-	2		793.3913749	1584.76715	0.000451244	4	N	116	129
Q6ZWZ6	Parental	KDYGK	ESQAKDVIEEYFK	CKK-	3		529.2635166	1584.76715	0.000622848	2	N	116	129
Q6ZWZ6	Parental	DDNKK	LGEWVGLCK	IDREG	2	C8:+57.021	531.2763424	1060.537085	0.000451244	12	N	84	93
Q6ZWZ6	Parental	ALDKR	QAHLCVLASNCDEPMYVK	LVEAL	2	C5:+57.021,C11:+57.021	1067.989619	2133.963639	0.001763695	1	N	45	63
Q6ZWZ6	Parental	-	MAEEGIAAGGVMDVNTALQE	VLKTA	4		502.2361102	2004.913241	0.002080925	1	N	0	20
Q76MZ3	Exosome	KSLQK	IGPILDNSTLQSEVKPILEK	LTQDQ	2		1097.620623	2193.225647	0.000451244	20	N	546	566
Q76MZ3	Exosome	KSLQK	IGPILDNSTLQSEVKPILEK	LTQDQ	3		732.0830156	2193.225647	0.001162105	2	N	546	566
Q76MZ3	Exosome	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	2	C9:+57.021	971.5252403	1941.034881	0.000451244	37	Y	381	398
Q76MZ3	Exosome	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	3	C9:+57.021	648.0194268	1941.034881	0.000451244	16	Y	381	398
Q76MZ3	Exosome	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	3		756.4185097	2266.232129	0.000451244	10	Y	398	418
Q76MZ3	Exosome	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	2	Q1:-17.027	1125.610365	2249.205129	0.000451244	2	Y	398	418
Q76MZ3	Exosome	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	2	[0:-17.027	1125.610365	2249.205129	0.000998612	1	Y	398	418
Q76MZ3	Exosome	PILGK	DNTIEHLLPLFLAQLKDECPEVR	LNIIS	3	C19:+57.021	917.4779452	2749.410436	0.000451244	49	N	358	381
Q76MZ3	Exosome	PILGK	DNTIEHLLPLFLAQLKDECPEVR	LNIIS	4	C19:+57.021	688.3604089	2749.410436	0.000451244	39	N	358	381
Q76MZ3	Exosome	DVDVK	YFAQEALTVLSLA	-	2		713.3853642	1424.755128	0.000451244	16	N	576	589
Q76MZ3	Exosome	PILGK	DNTIEHLLPLFLAQLK	DECPE	3		622.3564105	1864.045831	0.000451244	25	N	358	374
Q76MZ3	Exosome	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	3		642.3583683	1924.051705	0.000451244	7	Y	398	416
Q76MZ3	Exosome	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2	Q1:-17.027	954.5201524	1907.024705	0.002080925	1	Y	398	416
Q76MZ3	Exosome	WFTSR	TSACGLFSVCYPR	VSSAV	2	C4:+57.021,C10:+57.021	759.3474701	1516.67934	0.000451244	2	Y	144	157
Q76MZ3	Exosome	VESLR	AISHEHSPSDLEAHFVPLVK	RLAGG	3		738.3836879	2212.127664	0.001229886	2	N	113	133
Q76MZ3	Exosome	NSIKK	LSTIALALGVER	TRSEL	2		621.8749666	1241.734333	0.000622848	3	Y	34	46
Q76MZ3	Exosome	NQHVK	SALASVIMGLSPILGK	DNTIE	2		778.958174	1555.900748	0.000451244	9	N	342	358
Q76MZ3	Exosome	VLLAL	AEQLGTFTTLVGGPEYVHCLLPPLESLATVEETVVR	DKAVE	3	C19:+57.021	1309.347081	3925.017842	0.000451244	4	N	69	105
Q76MZ3	Exosome	MTTLF	CINVLSEVCGQDITTK	HMLPT	2	C1:+57.021,C9:+57.021	918.9452028	1835.874806	0.000451244	1	N	503	519
Q76MZ3	Parental	KSLQK	IGPILDNSTLQSEVKPILEK	LTQDQ	2		1097.620623	2193.225647	0.000451244	13	N	546	566
Q76MZ3	Parental	KSLQK	IGPILDNSTLQSEVKPILEK	LTQDQ	3		732.0830156	2193.225647	0.000823681	13	N	546	566
Q76MZ3	Parental	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	2	C9:+57.021	971.5252403	1941.034881	0.000451244	32	Y	381	398
Q76MZ3	Parental	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	3	C9:+57.021	648.0194268	1941.034881	0.000451244	12	Y	381	398
Q76MZ3	Parental	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	3		756.4185097	2266.232129	0.000451244	26	Y	398	418

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q76MZ3	Parental	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	2	[0:-17.027	1125.610365	2249.205129	0.000622848	1	Y	398	418
Q76MZ3	Parental	PILGK	DNTIEHLLPLFLAQLKDECPEVR	LNIIS	3	C19:+57.021	917.4779452	2749.410436	0.000451244	33	N	358	381
Q76MZ3	Parental	PILGK	DNTIEHLLPLFLAQLKDECPEVR	LNIIS	4	C19:+57.021	688.3604089	2749.410436	0.000451244	31	N	358	381
Q76MZ3	Parental	DVDVK	YFAQEALTVLSLA	-	2		713.3853642	1424.755128	0.002145581	3	N	576	589
Q76MZ3	Parental	PILGK	DNTIEHLLPLFLAQLK	DECPE	3		622.3564105	1864.045831	0.000451244	17	N	358	374
Q76MZ3	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2		963.0336524	1924.051705	0.000451244	15	Y	398	416
Q76MZ3	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	3		642.3583683	1924.051705	0.000451244	20	Y	398	416
Q76MZ3	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2	Q1:-17.027	954.5201524	1907.024705	0.00307782	1	Y	398	416
Q76MZ3	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2	[0:-17.027	954.5201524	1907.024705	0.000451244	2	Y	398	416
Q76MZ3	Parental	VESLR	AISHEHSPSDLEAHFVPLVK	RLAGG	3		738.3836879	2212.127664	0.000851441	4	N	113	133
Q76MZ3	Parental	VESLR	AISHEHSPSDLEAHFVPLVK	RLAGG	4		554.039716	2212.127664	0.000451244	13	N	113	133
Q76MZ3	Parental	GEFAK	VLELDNVKSEIIPMFSNLASDEQDSVR	LLAVE	3		1016.845177	3047.51213	0.002727428	1	N	194	221
Q76MZ3	Parental	NSIKK	LSTIALALGVER	TRSEL	2		621.8749666	1241.734333	0.002296037	1	Y	34	46
Q76MZ3	Parental	SHKVK	EFCENLSADCR	ENVIM	2	C3:+57.021,C10:+57.021	700.78216	1399.54872	0.001162105	1	N	307	318
Q76MZ3	Parental	QLGTF	TTLVGGPEYVHCLLPPLESLATVEETVVR	DKAVE	3	C12:+57.021	1060.560446	3178.657937	0.000451244	4	N	76	105
Q78PY7	Exosome	LIGKK	VNVTVDYIRPASPATETVPAFSER	TCATV	3		873.7858094	2618.334028	0.000451244	17	N	414	438
Q78PY7	Exosome	AFSTR	VLPAQATEYAFAFIQVPQDEDARTDAVDSVVR	DIQNT	3		1174.590275	3520.747426	0.002727428	1	N	787	819
Q78PY7	Exosome	AFSTR	VLPAQATEYAFAFIQVPQDEDARTDAVDSVVR	DIQNT	4		881.1946564	3520.747426	0.000451244	10	N	787	819
Q78PY7	Exosome	EEKER	SASYKPVFVTEITDDLHFYVQDVETGTQLEK	LMENM	3		1187.25467	3558.740609	0.000622848	1	N	678	709
Q78PY7	Exosome	LYLPK	ETCLITFLLAGIECPR	GARNL	3	C3:+57.021,C14:+57.021	631.6586873	1891.952662	0.000451244	29	N	546	562
Q78PY7	Exosome	IYLGK	DTNGENIAESLVAEGLATR	REGMR	2		980.485055	1958.95451	0.000451244	29	N	116	135
Q78PY7	Exosome	IYLGK	DTNGENIAESLVAEGLATR	REGMR	3		653.9926367	1958.95451	0.00091018	1	N	116	135
Q78PY7	Exosome	AFSER	TCATVTIGGINIAEALVSK	GLATV	2	C2:+57.021	959.5196236	1917.023647	0.001463592	2	N	438	457
Q78PY7	Exosome	AFSTR	VLPAQATEYAFAFIQVPQDEDAR	TDAVD	2		1290.142983	2578.270365	0.000451244	10	N	787	810
Q78PY7	Exosome	AFSTR	VLPAQATEYAFAFIQVPQDEDAR	TDAVD	3		860.4312551	2578.270365	0.000451244	9	N	787	810
Q78PY7	Exosome	PTFRR	ETDGSETPEPFAAEAK	FFTES	2		839.8762859	1677.736972	0.000622848	9	N	233	249
Q78PY7	Exosome	DSVVR	DIQNTQCLLNVEHLSASCPHVTLQFADSK	GDVGL	3	C7:+57.021,C18:+57.021	1109.203061	3324.585782	0.000451244	4	N	819	848
Q78PY7	Exosome	IYLGK	DTNGENIAESLVAEGLATRR	EGMRA	3		706.0263404	2115.055621	0.000622848	7	N	116	136
Q78PY7	Exosome	RLLQR	DVQIILESCHNQNLLGTILHPNGNITELLLK	EGFAR	3	C9:+57.021	1170.631375	3508.870724	0.001162105	1	N	259	290
Q78PY7	Exosome	EGFAR	CVDWSIAVYTR	GAEKL	2	C1:+57.021	685.3323773	1368.649155	0.002080925	1	N	295	306
Q78PY7	Exosome	KPVFV	TEITDDLHFYVQDVETGTQLEK	LMENM	3		861.0821801	2580.22314	0.000451244	7	N	687	709
Q78PY7	Exosome	DSVVR	DIQNTQCLLNVEHLSASCPHVTLQF	ADSKG	3	C7:+57.021,C18:+57.021	975.4727113	2923.394734	0.00091018	4	N	819	844
Q78PY7	Exosome	AFSTR	VLPAQATEYAFAFIQVPQDEDARTDAVD	SVVRD	3		1027.500286	3079.477458	0.001943752	1	N	787	815
Q78PY7	Exosome	NLARR	AAATQPDGKDTPDEPWAFPAR	EFLRK	3		747.6910691	2240.049807	0.000451244	5	N	62	83
Q78PY7	Parental	LIGKK	VNVTVDYIRPASPATETVPAFSER	TCATV	3		873.7858094	2618.334028	0.000451244	3	N	414	438
Q78PY7	Parental	AFSTR	VLPAQATEYAFAFIQVPQDEDARTDAVDSVVR	DIQNT	3		1174.590275	3520.747426	0.000451244	33	N	787	819
Q78PY7	Parental	AFSTR	VLPAQATEYAFAFIQVPQDEDARTDAVDSVVR	DIQNT	4		881.1946564	3520.747426	0.00091018	5	N	787	819
Q78PY7	Parental	EEKER	SASYKPVFVTEITDDLHFYVQDVETGTQLEK	LMENM	3		1187.25467	3558.740609	0.000451244	17	N	678	709
Q78PY7	Parental	EEKER	SASYKPVFVTEITDDLHFYVQDVETGTQLEK	LMENM	4		890.6929522	3558.740609	0.000823681	5	N	678	709
Q78PY7	Parental	LYLPK	ETCLITFLLAGIECPR	GARNL	2	C3:+57.021,C14:+57.021	946.984131	1891.952662	0.000451244	2	N	546	562
Q78PY7	Parental	LYLPK	ETCLITFLLAGIECPR	GARNL	3	C3:+57.021,C14:+57.021	631.6586873	1891.952662	0.000451244	28	N	546	562
Q78PY7	Parental	IYLGK	DTNGENIAESLVAEGLATR	REGMR	2		980.485055	1958.95451	0.000451244	6	N	116	135
Q78PY7	Parental	AFSTR	VLPAQATEYAFAFIQVPQDEDAR	TDAVD	2		1290.142983	2578.270365	0.000451244	16	N	787	810
Q78PY7	Parental	AFSTR	VLPAQATEYAFAFIQVPQDEDAR	TDAVD	3		860.4312551	2578.270365	0.000622848	5	N	787	810
Q78PY7	Parental	PTFRR	ETDGSETPEPFAAEAK	FFTES	2		839.8762859	1677.736972	0.000622848	7	N	233	249
Q78PY7	Parental	DSVVR	DIQNTQCLLNVEHLSASCPHVTLQFADSK	GDVGL	3	C7:+57.021,C18:+57.021	1109.203061	3324.585782	0.000451244	15	N	819	848
Q78PY7	Parental	DSVVR	DIQNTQCLLNVEHLSASCPHVTLQFADSK	GDVGL	4	C7:+57.021,C18:+57.021	832.1542456	3324.585782	0.001162105	1	N	819	848
Q78PY7	Parental	DSVVR	DIQNTQCLLNVEHLSASCPHVTLQFADSKGDVGLGLVK	EGLVM	4	C7:+57.021,C18:+57.021	1041.777059	4163.077036	0.001352548	2	N	819	857
Q78PY7	Parental	IENPR	HFVDSHHQKPVNAIIEHVR	DGSVV	4		566.5520535	2262.177014	0.000451244	3	N	184	203
Q78PY7	Parental	IYLGK	DTNGENIAESLVAEGLATRR	EGMRA	3		706.0263404	2115.055621	0.002145581	1	N	116	136
Q78PY7	Parental	RLLQR	DVQIILESCHNQNLLGTILHPNGNITELLLK	EGFAR	3	C9:+57.021	1170.631375	3508.870724	0.000451244	3	N	259	290
Q78PY7	Parental	MENMR	NDISSHPPVEGSYAPR	RGEFC	2		863.4137043	1724.811809	0.002374549	2	N	715	731
Q78PY7	Parental	PRGAR	NLPGLVQEGEPFSEEATLFTK	ELVLQ	2		1153.581695	2305.14779	0.000451244	5	N	565	586
Q78PY7	Parental	NLARR	AAATQPDGKDTPDEPWAFPAR	EFLRK	3		747.6910691	2240.049807	0.002519933	1	N	62	83
Q78PY7	Parental	DDDQR	SSHYDELLAAEAR	AIKNG	2		731.352584	1460.689568	0.000451244	1	N	472	485
Q78ZA7	Exosome	TYKMK	SEPDKADPFSFEGPEIVDCDGCTIDWK	KGKNV	3	C19:+57.021,C22:+57.021	1038.783168	3113.326105	0.000451244	12	N	228	255
Q78ZA7	Exosome	ELNPK	GIPEFWFTIFR	NVDML	2		706.8722269	1411.728854	0.000451244	8	N	157	168
Q78ZA7	Exosome	RTITK	QVPNESFFNFFSPLK	ASGDG	2		900.951934	1799.888268	0.001591523	4	N	282	297
Q78ZA7	Parental	KADPF	SFEGPEIVDCDGCTIDWK	KGKNV	2	C10:+57.021,C13:+57.021	1064.453589	2126.891578	0.000451244	2	N	237	255
Q7M6Y3	Exosome	TAASR	ATTLSNAVSSLASTGLSLTK	VDERE	2		961.5261915	1921.036783	0.000451244	7	N	298	318
Q7M6Y3	Exosome	SEFLK	VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGK	KIKDS	4		943.7409651	3770.93266	0.000451244	8	N	252	288
Q7M6Y3	Exosome	VGIDR	GDIPDLSQAPSSLLDALEQHLASLEGK	KIKDS	3		935.4824552	2803.423966	0.000451244	1	N	261	288
Q7M6Y3	Parental	VFGNK	STNVAVDSGGFDELGGLLKPTVASQNQSLPVAK	LPPNK	3		1100.575966	3298.704498	0.000698008	2	N	496	529
Q7M6Y3	Parental	TAASR	ATTLSNAVSSLASTGLSLTK	VDERE	2		961.5261915	1921.036783	0.000451244	8	N	298	318
Q7M6Y3	Parental	SEFLK	VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGK	KIKDS	3		1257.985353	3770.93266	0.001463592	3	N	252	288

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q7M6Y3	Parental	SEFLK	VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGK	KIKDS	4		943.7409651	3770.93266	0.000451244	13	N	252	288
Q7M6Y3	Parental	LPPNK	LVSDDLDSSLANLVGNLGIGNGTTK	NDVSW	2		1237.14318	2472.270759	0.000451244	13	N	534	559
Q7M6Y3	Parental	LPPNK	LVSDDLDSSLANLVGNLGIGNGTTK	NDVSW	3		825.0980531	2472.270759	0.000698008	6	N	534	559
Q7M6Y3	Parental	WGDPF	SATLDAVEDAIPSLNPFLTK	SSGDV	2		1051.554949	2101.094298	0.000451244	1	N	422	442
Q7TMB8	Exosome	ERIRK	FQILNDEIITILDK	YLKSG	2		837.9697924	1673.923985	0.000637154	1	N	1210	1224
Q7TMB8	Exosome	IKKKK	NVIQSVLQAIR	KTVCD	2		620.8727583	1239.729917	0.001763695	1	N	504	515
Q7TMB8	Parental	RLESK	YAPLHLVPLIER	LGTPQ	3		474.2824057	1419.823817	0.002145581	2	Y	1053	1065
Q7TMK9	Exosome	VLFVR	NLANTVTEEILEK	SFSQF	2		737.3939175	1472.772235	0.000451244	12	N	343	356
Q7TMK9	Exosome	GKIPR	DLFEDELVPLFEK	AGPIW	2		797.4064936	1592.797387	0.000451244	16	N	171	184
Q7TMK9	Exosome	DLDER	AIEALKEFNEDGALAVLQQFK	DSDLS	3		778.7500364	2333.226709	0.000451244	5	N	60	81
Q7TMK9	Parental	VLFVR	NLANTVTEEILEK	SFSQF	2		737.3939175	1472.772235	0.000451244	20	N	343	356
Q7TMK9	Parental	GKIPR	DLFEDELVPLFEK	AGPIW	2		797.4064936	1592.797387	0.000451244	24	N	171	184
Q7TMK9	Parental	ALLER	TGYTLDVTTGQR	KYGGP	2		656.3311202	1310.64664	0.000979378	2	Y	130	142
Q7TMK9	Parental	DLDER	AIEALKEFNEDGALAVLQQF	KDSDL	2		1103.573673	2205.131746	0.000451244	10	N	60	80
Q7TMK9	Parental	DLDER	AIEALKEFNEDGALAVLQQFK	DSDLS	2		1167.621155	2333.226709	0.000451244	12	N	60	81
Q7TMK9	Parental	DLDER	AIEALKEFNEDGALAVLQQFK	DSDLS	3		778.7500364	2333.226709	0.000451244	10	N	60	81
Q7TMK9	Parental	GLPQK	VAEKLDEIYVAGLVAHSDLDER	AIEAL	2		1221.629708	2441.243816	0.000451244	1	N	38	60
Q7TMK9	Parental	GLPQK	VAEKLDEIYVAGLVAHSDLDER	AIEAL	4		611.318754	2441.243816	0.000622848	3	N	38	60
Q7TMK9	Parental	KVAEK	LDEIYVAGLVAHSDLDER	AIEAL	3		672.3413773	2014.000732	0.002884417	1	N	42	60
Q7TMK9	Parental	TGQRK	YGGPPPDSVYSGQQPSVGTEIFVGK	IPRDL	2		1283.627165	2565.238731	0.001839721	1	N	143	168
Q7TMY8	Exosome	FVNQK	GLLPLVTILGLPNLPIDFPTSAACQAVAGVCK	SILTL	3	C24:+57.021,C31:+57.021	1102.605066	3304.791799	0.0025889	1	N	797	829
Q7TMY8	Parental	FVNQK	GLLPLVTILGLPNLPIDFPTSAACQAVAGVCK	SILTL	3	C24:+57.021,C31:+57.021	1102.605066	3304.791799	0.000622848	1	N	797	829
Q7TMY8	Parental	HIIAR	SDDELLDDFFHDQSTATSQAGTLSSIPTALTR	WTEEC	3		1147.2099	3438.6063	0.000451244	7	N	2618	2650
Q7TMY8	Parental	LILQR	LLGPSAAADILQLSSSLPLQSR	GRARL	3		746.4220312	2236.242694	0.000870037	1	N	2579	2601
Q7TNC4	Exosome	VSKKR	LAETQEEISAEVAAK	AERVH	2		794.9073891	1587.799178	0.000451244	3	N	107	122
Q7TNC4	Parental	VSKKR	LAETQEEISAEVAAK	AERVH	2		794.9073891	1587.799178	0.000451244	8	N	107	122
Q7TNC4	Parental	DRVCK	SHLLNCCPHDVLSGTR	MDLGE	2	C6:+57.021,C7:+57.021	933.4409533	1864.866307	0.000451244	5	N	37	53
Q7TNC4	Parental	DRVCK	SHLLNCCPHDVLSGTR	MDLGE	3	C6:+57.021,C7:+57.021	622.6299022	1864.866307	0.000451244	3	N	37	53
Q7TNC4	Parental	AKAER	VHELNEEIGKLLAK	VEQLG	3		531.6389178	1591.893353	0.001871652	2	N	125	139
Q7TNC4	Parental	KLLAK	VEQLGAEGNVEESQK	VMDEV	2		808.8922704	1615.768941	0.000451244	8	N	139	154
Q7TNG5	Exosome	VVDSK	CSNEAVLVATFHPTDPSLLITCGK	SHIYF	2	C1:+39.994,C22:+57.021	1307.13784	2612.260081	0.001395409	2	N	202	226
Q7TNG5	Exosome	VVDSK	CSNEAVLVATFHPTDPSLLITCGK	SHIYF	2	C1:+57.021,C22:+57.021	1315.65134	2629.287081	0.001329271	1	N	202	226
Q7TNG5	Exosome	VVDSK	CSNEAVLVATFHPTDPSLLITCGK	SHIYF	3	C1:+57.021,C22:+57.021	877.4368269	2629.287081	0.000451244	33	N	202	226
Q7TNG5	Exosome	SDYSK	VQEVEVPEDFGPVR	TVAEG	2		800.4048166	1598.794033	0.001162105	5	N	327	341
Q7TNG5	Exosome	PPHVR	VWDSVSLSTLHVLGLGVFDR	AVCCV	2		1100.5922	2199.1688	0.000870037	3	N	140	160
Q7TNG5	Exosome	PPHVR	VWDSVSLSTLHVLGLGVFDR	AVCCV	3		734.0640668	2199.1688	0.000451244	3	N	140	160
Q7TNG5	Exosome	VAFSK	SNGGNLLCAVDESNDHVLSVWDWAK	ESKVV	3	C8:+57.021	929.4331757	2785.276127	0.000451244	22	N	169	194
Q7TNG5	Exosome	DDFGK	VHLFSYPCCQPR	ALSHK	2	C8:+57.021,C9:+57.021	782.3634546	1562.711309	0.001162105	2	N	596	608
Q7TNG5	Parental	VVDSK	CSNEAVLVATFHPTDPSLLITCGK	SHIYF	3	C1:+57.021,C22:+57.021	877.4368269	2629.287081	0.000451244	3	N	202	226
Q7TNG5	Parental	ADTVR	NVEWATATCVLGFGVFGIWPEGADGTDINAVAR	SHDGK	3	C9:+57.021	1165.233392	3492.676775	0.000622848	2	N	548	581
Q7TNG5	Parental	KGGNR	ITQEVQGAHDGGVFALCALR	DGTLV	3	C17:+57.021	714.6972353	2141.068306	0.001229886	1	N	284	304
Q7TNG5	Parental	PPHVR	VWDSVSLSTLHVLGLGVFDR	AVCCV	3		734.0640668	2199.1688	0.000622848	3	N	140	160
Q7TNG5	Parental	EDPAR	SAGFHPSGSVLAVGTVTGR	WLLLD	2		900.4740963	1798.932593	0.00091018	1	N	422	441
Q7TNG5	Parental	VAFSK	SNGGNLLCAVDESNDHVLSVWDWAK	ESKVV	3	C8:+57.021	929.4331757	2785.276127	0.000451244	4	N	169	194
Q7TNP2	Exosome	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	2	C9:+57.021	971.5252403	1941.034881	0.000451244	37	Y	393	410
Q7TNP2	Exosome	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	3	C9:+57.021	648.0194268	1941.034881	0.000451244	16	Y	393	410
Q7TNP2	Exosome	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	3		756.4185097	2266.232129	0.000451244	10	Y	410	430
Q7TNP2	Exosome	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	2	Q1:-17.027	1125.610365	2249.205129	0.000451244	2	Y	410	430
Q7TNP2	Exosome	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	2	[0:-17.027	1125.610365	2249.205129	0.000998612	1	Y	410	430
Q7TNP2	Exosome	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	3		642.3583683	1924.051705	0.000451244	7	Y	410	428
Q7TNP2	Exosome	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2	Q1:-17.027	954.5201524	1907.024705	0.002080925	1	Y	410	428
Q7TNP2	Exosome	GSGPG	AAGGDGDDSLYPIAVLIDELR	NEDVQ	2		1080.545113	2159.074625	0.000823681	6	N	12	33
Q7TNP2	Exosome	GSGPG	AAGGDGDDSLYPIAVLIDELR	NEDVQ	3		720.6993417	2159.074625	0.000451244	6	N	12	33
Q7TNP2	Exosome	WFTSR	TSACGLFSVCYPR	ASNAV	2	C4:+57.021,C10:+57.021	759.3474701	1516.67934	0.000451244	2	Y	156	169
Q7TNP2	Exosome	NSIKK	LSTIALALGVER	TRTEL	2		621.8749666	1241.734333	0.000622848	3	Y	46	58
Q7TNP2	Parental	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	2	C9:+57.021	971.5252403	1941.034881	0.000451244	32	Y	393	410
Q7TNP2	Parental	CPEVR	LNIISNLDCVNEVIGIR	QLSQS	3	C9:+57.021	648.0194268	1941.034881	0.000451244	12	Y	393	410
Q7TNP2	Parental	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	3		756.4185097	2266.232129	0.000451244	26	Y	410	430
Q7TNP2	Parental	VIGIR	QLSQSLLPAIVELAEDAKWR	VRLAI	2	[0:-17.027	1125.610365	2249.205129	0.000622848	1	Y	410	430
Q7TNP2	Parental	AVGPK	IALSDLIPAFQSLLRDCEAEVR	AAAAH	3	C17:+57.021	839.4444644	2515.309993	0.000662267	2	N	289	311
Q7TNP2	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2		963.0336524	1924.051705	0.000451244	15	Y	410	428
Q7TNP2	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	3		642.3583683	1924.051705	0.000451244	20	Y	410	428
Q7TNP2	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2	Q1:-17.027	954.5201524	1907.024705	0.00307782	1	Y	410	428
Q7TNP2	Parental	VIGIR	QLSQSLLPAIVELAEDAK	WRVRL	2	[0:-17.027	954.5201524	1907.024705	0.000451244	2	Y	410	428
Q7TNP2	Parental	GSGPG	AAGGDGDDSLYPIAVLIDELR	NEDVQ	2		1080.545113	2159.074625	0.00091018	6	N	12	33

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q7TNP2	Parental	GSGPG	AAGGDGDDSLYPIAVLIDELR	NEDVQ	3		720.6993417	2159.074625	0.000622848	5	N	12	33
Q7TNP2	Parental	GSGPG	AAGGDGDDSLYPIAVLIDELRNEDVQLR	LNSIK	3		1005.507552	3013.499256	0.000662267	1	N	12	40
Q7TNP2	Parental	NSIKK	LSTIALALGVER	TRTEL	2		621.8749666	1241.734333	0.002296037	1	Y	46	58
Q7TNV0	Parental	SSLKK	NVGQFSGFPFEK	GSTQY	2		678.8332987	1355.650997	0.000451244	11	N	129	141
Q7TNV0	Parental	KQICK	EVYENYPAYDLTER	KDFIK	2		881.4024709	1760.789342	0.000451244	44	N	353	367
Q7TNV0	Parental	NAMLK	SICEVLDLER	SGVNS	2	C3:+57.021	617.3111106	1232.606621	0.000451244	6	N	162	172
Q7TPD0	Exosome	SSSSK	LAQLTLEQILEHLDNLR	LNLAN	3		673.7131455	2018.116036	0.000451244	1	N	913	930
Q7TPD0	Parental	SSSSK	LAQLTLEQILEHLDNLR	LNLAN	3		673.7131455	2018.116036	0.000451244	22	N	913	930
Q7TPD0	Parental	KAHFR	GEVLPEEVTEESLEESVGKPLYLIFR	NLCQM	3		988.1818943	2961.522283	0.001699387	2	N	630	656
Q7TPD0	Parental	ELLWK	DIIHNPQALSPQFTGILQLLQSR	TSRKF	3		863.8102893	2588.407468	0.001463592	3	N	271	294
Q7TPR4	Exosome	DELRR	ELPPDQAEYCIAR	MAPYA	2	C10:+57.021	781.3696882	1560.723776	0.000451244	37	Y	850	863
Q7TPR4	Exosome	MASFK	ILAGDKNYITEDELR	RELPP	2		875.4550378	1748.894476	0.000451244	36	N	834	849
Q7TPR4	Exosome	MASFK	ILAGDKNYITEDELR	RELPP	3		583.9726252	1748.894476	0.000451244	21	N	834	849
Q7TPR4	Exosome	KVQEK	CQLEINFNTLQTK	LRLSN	2	C1:+39.994	796.3929379	1590.770276	0.000451244	5	Y	331	344
Q7TPR4	Exosome	KVQEK	CQLEINFNTLQTK	LRLSN	2	C1:+57.021	804.9064379	1607.797276	0.000451244	45	Y	331	344
Q7TPR4	Exosome	KVQEK	CQLEINFNTLQTK	LRLSN	2	[0:-17.027,C1:+57.021	796.3929379	1590.770276	0.000451244	4	Y	331	344
Q7TPR4	Exosome	ARCQK	ICDQWDNLGALTQK	RREAL	2	C2:+57.021	831.4015197	1660.787439	0.000451244	29	N	478	492
Q7TPR4	Exosome	SHLRK	AGTQIENIEEDFRDGLK	LMLLL	2		967.9768658	1933.938132	0.000451244	27	N	47	64
Q7TPR4	Exosome	SHLRK	AGTQIENIEEDFRDGLK	LMLLL	3		645.6538438	1933.938132	0.000451244	22	N	47	64
Q7TPR4	Exosome	ERLRK	QFGAQANVIGPWIQTK	MEEIG	2		879.4708252	1756.92605	0.000451244	31	N	633	649
Q7TPR4	Exosome	PEEFK	ACLISLGYDIGNDPQGEAEFAR	IMSIV	2	C2:+57.021	1198.563279	2395.110959	0.000451244	17	N	772	794
Q7TPR4	Exosome	PEEFK	ACLISLGYDIGNDPQGEAEFAR	IMSIV	3	C2:+57.021	799.3781196	2395.110959	0.000451244	33	N	772	794
Q7TPR4	Exosome	NYKPK	IDQLECDHQLIQEALIFDNK	HTNYN	2	C6:+57.021	1221.602405	2441.189209	0.000451244	35	N	684	704
Q7TPR4	Exosome	NYKPK	IDQLECDHQLIQEALIFDNK	HTNYN	3	C6:+57.021	814.7375364	2441.189209	0.000451244	35	N	684	704
Q7TPR4	Exosome	ERTEK	LLETIDQLYLEYAKR	AAPFN	2		934.5123558	1867.009112	0.000451244	11	N	502	517
Q7TPR4	Exosome	ERTEK	LLETIDQLYLEYAKR	AAPFN	3		623.3441705	1867.009112	0.000735798	18	N	502	517
Q7TPR4	Exosome	EDYEK	LASDLLEWIR	RTIPW	2		608.3407596	1214.665919	0.000622848	20	Y	281	291
Q7TPR4	Exosome	TIILR	FAIQDISVEETSAKEGLLLWCQR	KTAPY	3	C21:+57.021	898.4586621	2692.352586	0.000451244	18	Y	133	156
Q7TPR4	Exosome	ERTEK	LLETIDQLYLEYAK	RAAPF	2		856.4618002	1710.908	0.000451244	39	N	502	516
Q7TPR4	Exosome	ERTEK	LLETIDQLYLEYAK	RAAPF	3		571.3104668	1710.908	0.000451244	21	N	502	516
Q7TPR4	Exosome	RDGLK	LMLLLEVISGER	LAKPE	2		686.897585	1371.77957	0.000451244	28	Y	64	76
Q7TPR4	Exosome	PSEGR	MVSDINNAWGCLEQAEKGYEEWLLNEIR	RLERL	3	C11:+57.021	1123.195949	3366.564448	0.000451244	15	N	359	387
Q7TPR4	Exosome	PSEGR	MVSDINNAWGCLEQAEKGYEEWLLNEIR	RLERL	3	M1:+15.995,C11:+57.021	1128.527616	3382.559448	0.000451244	31	N	359	387
Q7TPR4	Exosome	TTIAR	TINEVENQILTR	DAKGI	2		715.3864268	1428.757254	0.000451244	49	Y	726	738
Q7TPR4	Exosome	EQAEK	GYEEWLLNEIR	RLERL	2		711.357138	1420.698676	0.000451244	18	Y	376	387
Q7TPR4	Exosome	MEHIR	VGWEQLLTTIAR	TINEV	2		693.891148	1385.766696	0.000451244	85	Y	714	726
Q7TPR4	Exosome	MEHIR	VGWEQLLTTIAR	TINEV	3		462.930032	1385.766696	0.000870037	3	Y	714	726
Q7TPR4	Exosome	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	2		1146.027953	2290.040305	0.000451244	3	N	752	772
Q7TPR4	Exosome	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	3		764.3545685	2290.040305	0.000451244	27	N	752	772
Q7TPR4	Exosome	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	4		573.5178763	2290.040305	0.001463592	8	N	752	772
Q7TPR4	Exosome	EAMLR	QKDYETATLSEIK	ALLKK	2		763.3913749	1524.76715	0.000451244	4	N	418	431
Q7TPR4	Exosome	EAMLR	QKDYETATLSEIK	ALLKK	2	[0:-17.027	754.8778749	1507.74015	0.000451244	22	N	418	431
Q7TPR4	Exosome	YGKLR	KDDPLTNLNTAFDVAER	FLDIP	2		959.9794085	1917.943217	0.000451244	31	N	197	214
Q7TPR4	Exosome	YGKLR	KDDPLTNLNTAFDVAER	FLDIP	3		640.3222056	1917.943217	0.000451244	26	N	197	214
Q7TPR4	Exosome	ADKER	LAILGIHNEVSK	IVQTY	2		647.3804161	1292.745232	0.000451244	29	N	565	577
Q7TPR4	Exosome	ADKER	LAILGIHNEVSK	IVQTY	3		431.9228774	1292.745232	0.000979378	10	N	565	577
Q7TPR4	Exosome	EEIGR	ISIEMHGTLEDQLSHLR	QYEKS	3	M5:+15.995	665.6708693	1993.989208	0.000451244	6	N	655	672
Q7TPR4	Exosome	TIILR	FAIQDISVEETSAK	EGLLL	2		769.3913749	1536.76715	0.000823681	33	Y	133	147
Q7TPR4	Exosome	PSEGR	MVSDINNAWGCLEQAEK	GYEEW	2	C11:+57.021	982.945966	1963.876332	0.000451244	20	N	359	376
Q7TPR4	Exosome	PSEGR	MVSDINNAWGCLEQAEK	GYEEW	2	M1:+15.995,C11:+57.021	990.943466	1979.871332	0.000451244	20	N	359	376
Q7TPR4	Exosome	GKLRK	DDPLTNLNTAFDVAER	FLDIP	2		895.9319269	1789.848254	0.000451244	27	N	198	214
Q7TPR4	Exosome	AHQDR	VEQIAAIAQELNELDYYDSPSVNAR	CQKIC	2		1404.688483	2807.361365	0.000451244	39	N	450	475
Q7TPR4	Exosome	AHQDR	VEQIAAIAQELNELDYYDSPSVNAR	CQKIC	3		936.7949218	2807.361365	0.000451244	7	N	450	475
Q7TPR4	Exosome	MDHYD	SQQTNDYMQPEEDWDRDLLLDPAWEK	QQRKT	3	M8:+15.995	1080.147724	3237.419772	0.000451244	21	N	5	31
Q7TPR4	Exosome	VDPNR	LGVVTFQAFIDFMSR	ETADT	2		865.9508803	1729.886161	0.002884417	1	N	803	818
Q7TPR4	Exosome	SHLRK	AGTQIENIEEDFR	DGLKL	2		761.3631487	1520.710697	0.002453667	1	N	47	60
Q7TPR4	Exosome	HISWK	DGLGFCALIHR	HRPEL	2	C6:+57.021	629.8219798	1257.62836	0.000451244	22	N	174	185
Q7TPR4	Exosome	HISWK	DGLGFCALIHR	HRPEL	3	C6:+57.021	420.2172532	1257.62836	0.000451244	14	N	174	185
Q7TPR4	Exosome	TAPYK	NVNIQNFHISWK	DGLGF	2		750.3918465	1498.768093	0.000451244	8	N	162	174
Q7TPR4	Exosome	TAPYK	NVNIQNFHISWK	DGLGF	3		500.5971643	1498.768093	0.00307782	1	N	162	174
Q7TPR4	Exosome	ETSAK	EGLLLWCQR	KTAPY	2	C7:+57.021	587.8057984	1173.595997	0.000870037	10	Y	147	156
Q7TPR4	Exosome	NERLR	KQFGAQANVIGPWIQTK	MEEIG	2		943.5183068	1885.021014	0.000662267	2	N	632	649
Q7TPR4	Exosome	NRICK	VLAVNQENEQLMEDYEK	LASDL	2		1026.483667	2050.951734	0.000451244	3	N	264	281
Q7TPR4	Exosome	NRICK	VLAVNQENEQLMEDYEK	LASDL	2	M12:+15.995	1034.481167	2066.946734	0.000622848	3	N	264	281
Q7TPR4	Exosome	NRICK	VLAVNQENEQLMEDYEKLASDLLEWIR	RTIPW	3	M12:+15.995	1088.875164	3263.602093	0.000451244	11	N	264	291

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q7TPR4	Exosome	LDIPK	MLDAEDIVGTARPDEK	AIMTY	2		880.430706	1758.845812	0.000823681	1	N	220	236
Q7TPR4	Exosome	LDIPK	MLDAEDIVGTARPDEK	AIMTY	3		587.2897373	1758.845812	0.000451244	8	N	220	236
Q7TPR4	Exosome	KQQRK	TFTAWCNSHLR	KAGTQ	2	C6:+57.021	696.8277935	1391.639987	0.000634081	2	Y	35	46
Q7TPR4	Exosome	EQAEK	GYEEWLLNEIRR	LERLD	3		526.6077291	1576.799787	0.000451244	11	Y	376	388
Q7TPR4	Exosome	SKGVK	LVSIGAEEIVDGNVK	MTLGM	2		771.9228422	1541.830084	0.000451244	11	N	106	121
Q7TPR4	Exosome	EDYEK	LASDLLEWIRR	TIPWL	3		457.9301435	1370.76703	0.001654178	6	Y	281	292
Q7TPR4	Exosome	ALLKK	HEAFESDLAAHQDRVEQIAAIAQELNELDYYDSPSVNAR	CQKIC	3		1472.365733	4414.073799	0.002296037	2	N	436	475
Q7TPR4	Exosome	ALLKK	HEAFESDLAAHQDRVEQIAAIAQELNELDYYDSPSVNAR	CQKIC	4		1104.52625	4414.073799	0.000622848	2	N	436	475
Q7TPR4	Exosome	RPDEK	AIMTYVSSFYHAFSGAQK	AETAA	3		669.9931438	2006.956031	0.002453667	1	Y	236	254
Q7TPR4	Exosome	TFIVH	TIEEIQGLTTAHEQFK	ATLPD	2		922.9735948	1843.93159	0.000451244	3	N	539	555
Q7TPR4	Exosome	NEVSK	IVQTYHVNMAGTNPYTTITPQEINGK	WDHVR	3	M9:+15.995	969.4838305	2905.428092	0.001162105	2	N	577	603
Q7TPR4	Parental	DELRR	ELPPDQAEYCIAR	MAPYA	2	C10:+57.021	781.3696882	1560.723776	0.000451244	39	Y	850	863
Q7TPR4	Parental	MASFK	ILAGDKNYITEDELR	RELPP	2		875.4550378	1748.894476	0.000451244	40	N	834	849
Q7TPR4	Parental	MASFK	ILAGDKNYITEDELR	RELPP	3		583.9726252	1748.894476	0.000451244	29	N	834	849
Q7TPR4	Parental	KVQEK	CQLEINFNTLQTK	LRLSN	2	C1:+57.021	804.9064379	1607.797276	0.000451244	35	Y	331	344
Q7TPR4	Parental	KVQEK	CQLEINFNTLQTK	LRLSN	2	[0:-17.027,C1:+57.021	796.3929379	1590.770276	0.001943752	1	Y	331	344
Q7TPR4	Parental	ARCQK	ICDQWDNLGALTQK	RREAL	2	C2:+57.021	831.4015197	1660.787439	0.000451244	28	N	478	492
Q7TPR4	Parental	SHLRK	AGTQIENIEEDFRDGLK	LMLLL	2		967.9768658	1933.938132	0.000451244	20	N	47	64
Q7TPR4	Parental	SHLRK	AGTQIENIEEDFRDGLK	LMLLL	3		645.6538438	1933.938132	0.000451244	16	N	47	64
Q7TPR4	Parental	ERLRK	QFGAQANVIGPWIQTK	MEEIG	2		879.4708252	1756.92605	0.000451244	7	N	633	649
Q7TPR4	Parental	ERLRK	QFGAQANVIGPWIQTK	MEEIG	3		586.6498168	1756.92605	0.002145581	1	N	633	649
Q7TPR4	Parental	PEEFK	ACLISLGYDIGNDPQGEAEFAR	IMSIV	2	C2:+57.021	1198.563279	2395.110959	0.000451244	15	N	772	794
Q7TPR4	Parental	PEEFK	ACLISLGYDIGNDPQGEAEFAR	IMSIV	3	C2:+57.021	799.3781196	2395.110959	0.000451244	4	N	772	794
Q7TPR4	Parental	NYKPK	IDQLECDHQLIQEALIFDNK	HTNYN	2	C6:+57.021	1221.602405	2441.189209	0.000451244	49	N	684	704
Q7TPR4	Parental	NYKPK	IDQLECDHQLIQEALIFDNK	HTNYN	3	C6:+57.021	814.7375364	2441.189209	0.000451244	38	N	684	704
Q7TPR4	Parental	ERTEK	LLETIDQLYLEYAKR	AAPFN	2		934.5123558	1867.009112	0.00091018	6	N	502	517
Q7TPR4	Parental	ERTEK	LLETIDQLYLEYAKR	AAPFN	3		623.3441705	1867.009112	0.000735798	15	N	502	517
Q7TPR4	Parental	EDYEK	LASDLLEWIR	RTIPW	2		608.3407596	1214.665919	0.000823681	17	Y	281	291
Q7TPR4	Parental	TIILR	FAIQDISVEETSAKEGLLLWCQR	KTAPY	3	C21:+57.021	898.4586621	2692.352586	0.000451244	19	Y	133	156
Q7TPR4	Parental	ERTEK	LLETIDQLYLEYAK	RAAPF	2		856.4618002	1710.908	0.000451244	35	N	502	516
Q7TPR4	Parental	ERTEK	LLETIDQLYLEYAK	RAAPF	3		571.3104668	1710.908	0.000451244	21	N	502	516
Q7TPR4	Parental	EALER	TEKLLETIDQLYLEYAK	RAAPF	3		690.7055451	2069.093235	0.001162105	2	N	499	516
Q7TPR4	Parental	RDGLK	LMLLLEVISGER	LAKPE	2		686.897585	1371.77957	0.000451244	9	Y	64	76
Q7TPR4	Parental	PSEGR	MVSDINNAWGCLEQAEKGYEEWLLNEIR	RLERL	3	C11:+57.021	1123.195949	3366.564448	0.000451244	11	N	359	387
Q7TPR4	Parental	PSEGR	MVSDINNAWGCLEQAEKGYEEWLLNEIR	RLERL	3	M1:+15.995,C11:+57.021	1128.527616	3382.559448	0.000451244	6	N	359	387
Q7TPR4	Parental	TTIAR	TINEVENQILTR	DAKGI	2		715.3864268	1428.757254	0.000451244	20	Y	726	738
Q7TPR4	Parental	EQAEK	GYEEWLLNEIR	RLERL	2		711.357138	1420.698676	0.000451244	22	Y	376	387
Q7TPR4	Parental	EQAEK	GYEEWLLNEIR	RLERL	3		474.5740253	1420.698676	0.001591523	2	Y	376	387
Q7TPR4	Parental	MEHIR	VGWEQLLTTIAR	TINEV	2		693.891148	1385.766696	0.000451244	35	Y	714	726
Q7TPR4	Parental	MEHIR	VGWEQLLTTIAR	TINEV	3		462.930032	1385.766696	0.002080925	5	Y	714	726
Q7TPR4	Parental	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	2		1146.027953	2290.040305	0.000662267	1	N	752	772
Q7TPR4	Parental	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	3		764.3545685	2290.040305	0.000451244	13	N	752	772
Q7TPR4	Parental	MNEFR	ASFNHFDRDHSGTLGPEEFK	ACLIS	4		573.5178763	2290.040305	0.001699387	2	N	752	772
Q7TPR4	Parental	EAMLR	QKDYETATLSEIK	ALLKK	2		763.3913749	1524.76715	0.000451244	10	N	418	431
Q7TPR4	Parental	EAMLR	QKDYETATLSEIK	ALLKK	2	[0:-17.027	754.8778749	1507.74015	0.000451244	11	N	418	431
Q7TPR4	Parental	YGKLR	KDDPLTNLNTAFDVAER	FLDIP	2		959.9794085	1917.943217	0.000451244	27	N	197	214
Q7TPR4	Parental	YGKLR	KDDPLTNLNTAFDVAER	FLDIP	3		640.3222056	1917.943217	0.000451244	17	N	197	214
Q7TPR4	Parental	ADKER	LAILGIHNEVSK	IVQTY	2		647.3804161	1292.745232	0.000451244	8	N	565	577
Q7TPR4	Parental	ADKER	LAILGIHNEVSK	IVQTY	3		431.9228774	1292.745232	0.000698008	2	N	565	577
Q7TPR4	Parental	TIILR	FAIQDISVEETSAK	EGLLL	2		769.3913749	1536.76715	0.00091018	7	Y	133	147
Q7TPR4	Parental	PSEGR	MVSDINNAWGCLEQAEK	GYEEW	2	C11:+57.021	982.945966	1963.876332	0.000823681	2	N	359	376
Q7TPR4	Parental	PSEGR	MVSDINNAWGCLEQAEK	GYEEW	2	M1:+15.995,C11:+57.021	990.943466	1979.871332	0.000451244	7	N	359	376
Q7TPR4	Parental	GKLRK	DDPLTNLNTAFDVAER	FLDIP	2		895.9319269	1789.848254	0.000451244	4	N	198	214
Q7TPR4	Parental	AHQDR	VEQIAAIAQELNELDYYDSPSVNAR	CQKIC	2		1404.688483	2807.361365	0.000451244	25	N	450	475
Q7TPR4	Parental	HISWK	DGLGFCALIHR	HRPEL	2	C6:+57.021	629.8219798	1257.62836	0.000451244	14	N	174	185
Q7TPR4	Parental	HISWK	DGLGFCALIHR	HRPEL	3	C6:+57.021	420.2172532	1257.62836	0.000622848	5	N	174	185
Q7TPR4	Parental	TAPYK	NVNIQNFHISWK	DGLGF	2		750.3918465	1498.768093	0.000662267	7	N	162	174
Q7TPR4	Parental	TAPYK	NVNIQNFHISWK	DGLGF	3		500.5971643	1498.768093	0.000622848	2	N	162	174
Q7TPR4	Parental	ETSAK	EGLLLWCQR	KTAPY	2	C7:+57.021	587.8057984	1173.595997	0.000979378	5	Y	147	156
Q7TPR4	Parental	NERLR	KQFGAQANVIGPWIQTK	MEEIG	2		943.5183068	1885.021014	0.000451244	7	N	632	649
Q7TPR4	Parental	LDIPK	MLDAEDIVGTARPDEK	AIMTY	3		587.2897373	1758.845812	0.001591523	1	N	220	236
Q7TPR4	Parental	KQQRK	TFTAWCNSHLR	KAGTQ	2	C6:+57.021	696.8277935	1391.639987	0.002080925	2	Y	35	46
Q7TPR4	Parental	EQAEK	GYEEWLLNEIRR	LERLD	3		526.6077291	1576.799787	0.000451244	10	Y	376	388
Q7TPR4	Parental	MLRQK	DYETATLSEIK	ALLKK	2		635.3146045	1268.613609	0.00307782	1	N	420	431
Q7TPR4	Parental	KALLK	KHEAFESDLAAHQDR	VEQIA	4		439.2122891	1752.817957	0.000622848	6	Y	435	450

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q7TPR4	Parental	SKGVK	LVSIGAEEIVDGNVK	MTLGM	2		771.9228422	1541.830084	0.000979378	1	N	106	121
Q7TPR4	Parental	ALLKK	HEAFESDLAAHQDRVEQIAAIAQELNELDYYDSPSVNAR	CQKIC	4		1104.52625	4414.073799	0.001264573	1	N	436	475
Q7TPR4	Parental	GKLRK	DDPLTNLNTAFDVAERF	LDIPK	2		969.4661339	1936.916668	0.000823681	2	N	198	215
Q7TPV4	Exosome	LEHSR	EFLDFFWDIAKPDQETR	LRATE	3		719.6816224	2156.021467	0.000451244	2	N	31	48
Q7TPV4	Exosome	LGVGR	EAARPCYSLALAQLLQSFEDIPLCDILDQIQEK	YSLQA	3	C6:+57.021,C24:+57.021	1283.313228	3846.916285	0.002145581	1	N	83	116
Q7TPV4	Exosome	TTPEK	NAASQQDAVTEGAMPAATGKDQPPSTGK	KKRKR	3	M14:+15.995	915.4317949	2743.271985	0.001463592	1	N	1194	1222
Q7TPV4	Exosome	ARELR	VCFEDPEWEQLITQLLGK	ATQTL	2	C2:+57.021	1103.048745	2204.08189	0.000823681	3	N	1041	1059
Q7TPV4	Exosome	ARELR	VCFEDPEWEQLITQLLGK	ATQTL	3	C2:+57.021	735.7017635	2204.08189	0.001329271	2	N	1041	1059
Q7TPV4	Exosome	WRVTR	FLNAEALQSYVAWLR	DMFLQ	2		890.9732008	1779.930802	0.000451244	5	N	394	409
Q7TPV4	Exosome	DFQIR	ALDLIEVLVTK	QPEHP	2		607.3742681	1212.732936	0.001395409	4	N	826	837
Q7TPV4	Exosome	LRSPK	YLELFLLAK	QRVPT	2		555.3344146	1108.653229	0.002145581	1	N	211	220
Q7TPV4	Exosome	RPSLF	ANLFGVLALFQSGR	LVKDK	2		746.9176972	1491.819794	0.000451244	2	N	132	146
Q7TPV4	Exosome	LHIFK	SPAESCDVLGDIQTCIK	KSMEQ	2	C6:+57.021,C15:+57.021	946.9401174	1891.864635	0.000451244	1	N	606	623
Q7TPV4	Parental	LEHSR	EFLDFFWDIAKPDQETR	LRATE	3		719.6816224	2156.021467	0.001871652	2	N	31	48
Q7TPV4	Parental	LGVGR	EAARPCYSLALAQLLQSFEDIPLCDILDQIQEK	YSLQA	3	C6:+57.021,C24:+57.021	1283.313228	3846.916285	0.000451244	11	N	83	116
Q7TPV4	Parental	ARELR	VCFEDPEWEQLITQLLGK	ATQTL	2	C2:+57.021	1103.048745	2204.08189	0.000451244	14	N	1041	1059
Q7TPV4	Parental	ARELR	VCFEDPEWEQLITQLLGK	ATQTL	3	C2:+57.021	735.7017635	2204.08189	0.002727428	1	N	1041	1059
Q7TPV4	Parental	WRVTR	FLNAEALQSYVAWLR	DMFLQ	2		890.9732008	1779.930802	0.000451244	7	N	394	409
Q7TPV4	Parental	DFQIR	ALDLIEVLVTK	QPEHP	2		607.3742681	1212.732936	0.002145581	1	N	826	837
Q7TPV4	Parental	GEHQK	ELSILELLNTLLR	TVNHE	2		763.9617704	1525.907941	0.000451244	5	N	1078	1091
Q7TQI3	Exosome	NCFYR	AFGFSHLEALLDDSKELQR	FKAVS	3		726.0398098	2175.096029	0.000451244	29	N	94	113
Q7TQI3	Exosome	NCFYR	AFGFSHLEALLDDSKELQR	FKAVS	4		544.7818073	2175.096029	0.000622848	6	N	94	113
Q7TQI3	Exosome	AQQDR	IQQEIAVQNPLVSER	LELSV	2		862.4710222	1722.926444	0.000451244	24	N	36	51
Q7TQI3	Exosome	EQVEK	QTSVADLLASFNDQSTSDYLVVYLR	LLTSG	3		935.8034173	2804.386852	0.000451244	2	N	151	176
Q7TQI3	Exosome	NCFYR	AFGFSHLEALLDDSK	ELQRF	3		550.6110278	1648.809683	0.000451244	4	N	94	109
Q7TQI3	Parental	NCFYR	AFGFSHLEALLDDSKELQR	FKAVS	3		726.0398098	2175.096029	0.000451244	15	N	94	113
Q7TQI3	Parental	NCFYR	AFGFSHLEALLDDSKELQR	FKAVS	4		544.7818073	2175.096029	0.000451244	4	N	94	113
Q7TSI3	Exosome	EERLR	YKYPSVACEILTSDVPQINDALGADESLLNR	LYGFL	3	C8:+57.021	1151.240212	3450.697235	0.000451244	12	N	74	105
Q7TSI3	Exosome	SLLNR	LYGFLQSGDSLNPLLASFFSK	VMGIL	2		1152.599691	2303.183782	0.000451244	12	N	105	126
Q7TSI3	Exosome	SLLNR	LYGFLQSGDSLNPLLASFFSK	VMGIL	3		768.7357273	2303.183782	0.000622848	1	N	105	126
Q7TSI3	Parental	-MFWK	FDLHTSSHLDTLLEKEDLSLPELLDEEDVLQECK	VVNRK	4	C33:+57.021	1003.49154	4009.93496	0.002884417	1	N	4	38
Q7TSI3	Parental	LHGMR	SAPSSLDSATRDPSTSVPDFK	AHQSP	3		722.3506011	2164.028403	0.000851441	2	N	792	813
Q7TSI3	Parental	EERLR	YKYPSVACEILTSDVPQINDALGADESLLNR	LYGFL	3	C8:+57.021	1151.240212	3450.697235	0.000451244	21	N	74	105
Q7TSI3	Parental	SLLNR	LYGFLQSGDSLNPLLASFFSK	VMGIL	2		1152.599691	2303.183782	0.000451244	6	N	105	126
Q7TSI3	Parental	MTSAF	IDHFGFNDEEFGEQEESVNAPFDK	TANIT	3		934.0723437	2799.193631	0.001162105	7	N	565	589
Q7TSS2	Parental	GDPVR	IHCNITESYPAVPPIWSVESDDPNLAAVLER	LVDIK	3	C3:+57.021	1164.908685	3491.702655	0.000451244	7	N	103	134
Q7TSS2	Parental	HERFR	IASACLDELSCEFLLAGAGGAGAGAAPGPHLPSR	GSVPG	3	C5:+57.021,C11:+57.021	1098.539784	3292.595953	0.000451244	12	N	60	94
Q7TSV4	Exosome	EHLKK	ELDELVGAIEEHFFQPQK	YNLQP	2		1065.031641	2128.047682	0.000451244	10	N	594	612
Q7TSV4	Exosome	EHLKK	ELDELVGAIEEHFFQPQK	YNLQP	3		710.3570274	2128.047682	0.000451244	30	N	594	612
Q7TSV4	Exosome	RRFAR	LAATAFITQGVPVYLFSDITPTPFVPYTVSHLK	LCAGI	3		1198.648514	3592.922142	0.000451244	13	N	130	163
Q7TSV4	Exosome	RRFAR	LAATAFITQGVPVYLFSDITPTPFVPYTVSHLK	LCAGI	4		899.2383356	3592.922142	0.000451244	8	N	130	163
Q7TSV4	Exosome	EPKIK	YYAELCAPPGNSDPEHLKK	ELDEL	3	C6:+57.021	730.3496127	2188.025438	0.000451244	20	N	575	594
Q7TSV4	Exosome	AIALK	EGFHFEETLTGFK	WMGNR	2		771.3677027	1540.719805	0.002374549	1	N	398	411
Q7TSV4	Exosome	AQWLR	WDQNPLTSESVK	QLIAG	2		702.3442276	1402.672855	0.000622848	6	N	32	44
Q7TSV4	Parental	EHLKK	ELDELVGAIEEHFFQPQK	YNLQP	2		1065.031641	2128.047682	0.000451244	5	N	594	612
Q7TSV4	Parental	EHLKK	ELDELVGAIEEHFFQPQK	YNLQP	3		710.3570274	2128.047682	0.000451244	15	N	594	612
Q7TSV4	Parental	EPKIK	YYAELCAPPGNSDPEHLKK	ELDEL	3	C6:+57.021	730.3496127	2188.025438	0.000662267	2	N	575	594
Q7TSV4	Parental	AQWLR	WDQNPLTSESVK	QLIAG	2		702.3442276	1402.672855	0.001763695	3	N	32	44
Q7TSV4	Parental	SGEWR	VFSGNELGALLGWWLFTSWK	EKNQD	2		1156.099661	2310.183722	0.000451244	2	N	348	368
Q80T06	Exosome	ENIQK	SLAGSSGPGASSGPGGDHSELIVR	ITSLE	3		732.3616116	2194.061435	0.000451244	24	N	59	83
Q80T06	Exosome	ELIVR	ITSLEVENQNLR	GVVQD	2		708.3786018	1414.741604	0.000451244	15	N	83	95
Q80T06	Exosome	NQNLR	GVVQDLQQAISK	LEARL	2		643.3596807	1284.703761	0.000451244	12	N	95	107
Q80T06	Exosome	NQNLR	GVVQDLQQAISKLEAR	LSSLE	3		585.6640146	1753.968644	0.001162105	1	N	95	111
Q80T06	Parental	ENIQK	SLAGSSGPGASSGPGGDHSELIVR	ITSLE	2		1098.038517	2194.061435	0.000451244	23	N	59	83
Q80T06	Parental	ENIQK	SLAGSSGPGASSGPGGDHSELIVR	ITSLE	3		732.3616116	2194.061435	0.000451244	27	N	59	83
Q80T06	Parental	ELIVR	ITSLEVENQNLR	GVVQD	2		708.3786018	1414.741604	0.000451244	26	N	83	95
Q80T06	Parental	NQNLR	GVVQDLQQAISK	LEARL	2		643.3596807	1284.703761	0.000451244	13	N	95	107
Q80T06	Parental	NQNLR	GVVQDLQQAISKLEAR	LSSLE	2		877.9921219	1753.968644	0.000451244	10	N	95	111
Q80T06	Parental	NQNLR	GVVQDLQQAISKLEAR	LSSLE	3		585.6640146	1753.968644	0.000451244	10	N	95	111
Q80T06	Parental	ETCVR	SIQLDGLVWGASK	LVPVG	2		687.3753308	1372.735062	0.000451244	12	N	219	232
Q80T06	Parental	EITKF	EEHVQSVDIAAFNKI	-	3		567.2936987	1698.857696	0.001352548	1	N	266	281
Q80TH2	Exosome	TQLER	LDLGSNEFTEVPEVLEQLSGLR	EFWMD	2		1223.129541	2444.243482	0.000451244	6	N	188	210
Q80TH2	Parental	QSLHK	LSLPDNDLTTLPASIANLINLR	ELDVS	2		1182.660811	2363.306022	0.000451244	1	N	73	95
Q80TH2	Parental	QSLHK	LSLPDNDLTTLPASIANLINLR	ELDVS	3		788.7764741	2363.306022	0.001162105	2	N	73	95
Q80TH2	Parental	TQLER	LDLGSNEFTEVPEVLEQLSGLR	EFWMD	2		1223.129541	2444.243482	0.000451244	16	N	188	210

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q80TP3	Parental	ELFGR	VFMEDVGAEPGSILTELGGFEVKESK	FRREM	4	M3:+15.995	696.847203	2783.357612	0.000451244	1	N	2192	2218
Q80TP3	Parental	TGRDR	GSGLLGSQPQPVIPASVIPEELISQAQVVLQGK	SRSVI	3		1113.956118	3338.844955	0.002981883	1	N	167	200
Q80TP3	Parental	IRTGR	DRGSGLLGSQPQPVIPASVIPEELISQAQVVLQGK	SRSVI	3		1204.332136	3609.973009	0.002080925	1	N	165	200
Q80TY0	Parental	IGTCK	ALYTFEGQNEGTISVVEGETLSVIEEDKGDGWTR	IRRNE	3		1243.930914	3728.769343	0.000451244	14	N	555	589
Q80TY0	Parental	ESEHK	VLAPDFDDEFDDEEPLPAIGTCK	ALYTF	2	C22:+57.021	1297.08645	2592.1573	0.000451244	23	N	532	555
Q80U16-5	Parental	TESLF	LESSVAEALLQESDEASELKPVELDTFEGNITK	QLVKR	3		1197.932032	3590.772697	0.000451244	23	N	502	535
Q80U16-5	Parental	GVATR	SGTESLFLESSVAEALLQESDEASELKPVELDTFEGNITK	QLVKR	3		1438.374789	4312.100968	0.000451244	32	N	495	535
Q80U16-5	Parental	GVATR	SGTESLFLESSVAEALLQESDEASELKPVELDTFEGNITK	QLVKR	4		1079.033042	4312.100968	0.002519933	2	N	495	535
Q80U16-5	Parental	SEAGR	SFLDGSLEDAFNGLFLALDPHKK	QYKEF	4		634.3291217	2533.285287	0.000451244	29	N	567	590
Q80U16-5	Parental	TPTFK	DQSFFSNLPDDIFESGK	AAEEK	2		973.4448671	1944.874134	0.000451244	9	N	382	399
Q80U16-5	Parental	EVNGK	QSWDGAETVFLPLIVGFISIK	VTELK	2		1160.633534	2319.251467	0.001763695	1	N	273	294
Q80U93	Exosome	SLIKT	LELISTEGERQPK	SSGSF	2		750.4073593	1498.799119	0.000451244	1	N	416	429
Q80U93	Parental	TPPSK	LGELLFPSSLAGETLGSFSGLR	VGQAE	2		1126.102598	2250.189595	0.000451244	12	N	1328	1350
Q80U93	Parental	SLIKT	LELISTEGERQPK	SSGSF	2		750.4073593	1498.799119	0.0025889	1	N	416	429
Q80U93	Parental	NSGAK	TFGGFGSSSFGEQKPAGTFSSGGGSVASQGFGFSTPNK	TGGFG	3		1221.233039	3660.675717	0.000735798	2	N	1923	1961
Q80UM3	Exosome	QHYDK	IGQPSIALEYINTAIESTPTLIELFLVK	AKIYK	3		1025.241084	3072.699853	0.000870037	3	N	386	414
Q80UM3	Exosome	EEFRK	TQQTSPDKVDYEYSELLLYQNQVLR	EAGLY	3		1010.840531	3029.498193	0.000622848	4	N	176	201
Q80UM3	Exosome	KITLR	SYVDLLKLEDVLR	QHPFY	3		521.6316518	1561.871555	0.000622848	4	N	536	549
Q80UM3	Parental	QHYDK	IGQPSIALEYINTAIESTPTLIELF	LVKAK	2		1367.234006	2732.452412	0.000451244	3	N	386	411
Q80UP5	Exosome	YVQMK	WEFTSWVPLVSR	ICPND	2		753.891148	1505.766696	0.000451244	3	N	127	139
Q80UP5	Exosome	DTSSR	FPLHLLVWNNDYEQLEK	ELRDQ	3		720.0376291	2157.089487	0.002374549	1	N	10	27
Q80UP5	Parental	LESSR	SQDLSGPASNGGVSHTHSYEAQYER	AIQES	3		893.0678156	2676.180047	0.000451244	2	N	499	524
Q80UR4	Exosome	KLDTR	VVLSEHVYPVSLPAASLR	ISSKK	3		646.3671981	1936.078194	0.000823681	5	N	140	158
Q80UR4	Exosome	PYHLR	EVAVPIVENNDCEQK	YQTNS	2	C12:+57.021	872.4148241	1742.814048	0.000622848	2	N	186	201
Q80UR4	Exosome	ISSKK	TCWVAGWGVIENYMPLPPPYHLR	EVAVP	3	C2:+57.021,M14:+15.995	924.7860849	2771.334855	0.001943752	1	N	163	186
Q80UR4	Parental	KLDTR	VVLSEHVYPVSLPAASLR	ISSKK	2		969.0468971	1936.078194	0.002884417	1	N	140	158
Q80UR4	Parental	PYHLR	EVAVPIVENNDCEQK	YQTNS	2	C12:+57.021	872.4148241	1742.814048	0.001162105	1	N	186	201
Q80UR4	Parental	ISSKK	TCWVAGWGVIENYMPLPPPYHLR	EVAVP	3	C2:+57.021,M14:+15.995	924.7860849	2771.334855	0.002981883	1	N	163	186
Q80VD1	Exosome	SQLDK	NSEICQEVQAVCDALGVPK	SDTSD	2	C5:+57.021,C12:+57.021	1059.00378	2115.991961	0.000823681	3	N	142	161
Q80VD1	Exosome	LGVPK	SDTSDIPLLLSQVESK	VKDIL	2		866.4547035	1730.893807	0.000823681	3	N	161	177
Q80VD1	Parental	QALSK	AAEGGLSSPEFSELCIWLGSQIK	SLCNL	2	C15:+57.021	1240.112605	2478.20961	0.000451244	27	N	37	60
Q80VD1	Parental	QALSK	AAEGGLSSPEFSELCIWLGSQIK	SLCNL	3	C15:+57.021	827.0776701	2478.20961	0.001463592	1	N	37	60
Q80VD1	Parental	GSQIK	SLCNLEESITSAGRDDLESFQLEISGFLK	EMACP	3	C3:+57.021	1086.866374	3257.575723	0.000451244	27	N	60	89
Q80VD1	Parental	SQLDK	NSEICQEVQAVCDALGVPK	SDTSD	2	C5:+57.021,C12:+57.021	1059.00378	2115.991961	0.00307782	1	N	142	161
Q80VP1	Parental	PPGSK	ASNPFLPSGAPPTGPSVTNPFQPAPPATLTLNQLR	LSPVP	3		1185.958522	3554.852165	0.000622848	4	N	498	533
Q80VP1	Parental	FDRLR	TALPTSGSSTGELELLAGEVPAR	SPGAF	2		1128.590052	2255.164503	0.000451244	9	N	410	433
Q80VQ0	Exosome	NAITR	FYGDNPQTSPNLGR	IINQK	2		783.3713081	1564.727016	0.000622848	3	N	270	284
Q80VQ0	Parental	AAAAK	HLTPITLELGGKNPCYVDDNCDPQIVANR	VAWFR	3	C15:+57.021,C21:+57.021	1103.871423	3308.590868	0.001162105	1	N	202	231
Q80VQ0	Parental	NAITR	FYGDNPQTSPNLGR	IINQK	2		783.3713081	1564.727016	0.000451244	11	N	270	284
Q80VQ0	Parental	ELGGK	NPCYVDDNCDPQIVANR	VAWFR	2	C3:+57.021,C9:+57.021	1025.441347	2048.867095	0.000451244	1	N	214	231
Q80VQ0	Parental	EVLPR	YLDQSCFTVVLGGR	QETGQ	2	C6:+57.021	807.9011555	1613.786711	0.000451244	5	N	156	170
Q80WJ7	Parental	NWSDR	SIFSGIGSTAEPVSQSTTSDYQWDVSR	NQPYI	2		1453.178479	2904.341358	0.000622848	2	N	340	367
Q80WJ7	Parental	NWSDR	SIFSGIGSTAEPVSQSTTSDYQWDVSR	NQPYI	3		969.1215861	2904.341358	0.000662267	3	N	340	367
Q80WJ7	Parental	RNQPY	IDDEWSGLNGLSSADPSSDWNAPAEEWGNWVDEDRASLLK	SQEPI	3		1478.00246	4430.983981	0.000451244	1	N	371	411
Q80WQ2	Exosome	LLSHR	LQCVPNPELLQTEDCLK	AAPKS	2	C3:+57.021,C15:+57.021	1029.005792	2055.995984	0.001162105	1	N	716	733
Q80WQ2	Exosome	RNQLK	DLQTPESQNLFCCLYR	SWCHN	2	C12:+57.021,C13:+57.021	1022.466834	2042.918067	0.001871652	1	N	607	623
Q80WQ2	Parental	LLSHR	LQCVPNPELLQTEDCLK	AAPKS	2	C3:+57.021,C15:+57.021	1029.005792	2055.995984	0.000823681	1	N	716	733
Q80WQ2	Parental	EVVLK	DLEVLAEIASSPAGQTDDPGAPDGPDLR	VNHSE	3		936.117953	2805.330459	0.002453667	1	N	461	489
Q80X41	Exosome	HGDIK	ASNLLLSHKNPDQVYLVDYGLAYR	YCPDG	3		917.1489706	2748.423512	0.000451244	4	N	179	203
Q80X41	Exosome	RKEWK	LGLPIGQGGFGCIYLADTNSSKPVGSDAPCVVK	VEPSD	3	C12:+57.021,C30:+57.021	1126.56734	3376.67862	0.000451244	26	N	38	71
Q80X41	Exosome	FGCIY	LADTNSSKPVGSDAPCVVK	VEPSD	3	C16:+57.021	648.9950584	1943.961775	0.000451244	4	N	52	71
Q80X41	Exosome	RKEWK	LGLPIGQGGFGCIY	LADTN	2	C12:+57.021	726.3715025	1450.727405	0.001591523	1	N	38	52
Q80X41	Exosome	MESVK	LLEYTEKPLYQNLR	DILLQ	3		593.9933607	1778.956682	0.000451244	2	N	307	321
Q80X41	Exosome	QLSLR	ILDILEYIHEHEYVHGDIK	ASNLL	3		779.4027481	2335.184844	0.000622848	1	N	160	179
Q80X41	Exosome	QLSLR	ILDILEYIHEHEYVHGDIK	ASNLL	4		584.8040111	2335.184844	0.000622848	1	N	160	179
Q80X41	Exosome	EDPKR	CHDGTLEFTSIDAHK	GVAPS	3	C1:+57.021	577.5986392	1729.772518	0.000451244	4	N	219	234
Q80X41	Parental	HGDIK	ASNLLLSHKNPDQVYLVDYGLAYR	YCPDG	3		917.1489706	2748.423512	0.002212458	1	N	179	203
Q80X41	Parental	RKEWK	LGLPIGQGGFGCIYLADTNSSKPVGSDAPCVVK	VEPSD	3	C12:+57.021,C30:+57.021	1126.56734	3376.67862	0.000451244	8	N	38	71
Q80X41	Parental	FGCIY	LADTNSSKPVGSDAPCVVK	VEPSD	2	C16:+57.021	972.9886876	1943.961775	0.000451244	11	N	52	71
Q80X41	Parental	FGCIY	LADTNSSKPVGSDAPCVVK	VEPSD	3	C16:+57.021	648.9950584	1943.961775	0.000451244	12	N	52	71
Q80X41	Parental	RKEWK	LGLPIGQGGFGCIY	LADTN	2	C12:+57.021	726.3715025	1450.727405	0.002453667	1	N	38	52
Q80X50	Parental	TAGQR	IDLAVLLGK	TPSSM	2		471.3056571	940.5957142	0.002663018	2	N	301	310
Q80X50	Parental	PGAWR	TATEEWGTEDWNEDLSETK	IFTAS	2		1120.977457	2239.939314	0.000451244	7	N	258	277
Q80X50	Parental	MLQTR	FPLDYYSIPFPTPTTPLTGR	DGSLA	2		1142.088959	2282.162318	0.002884417	1	N	849	869
Q80X90	Exosome	SDGLR	LIALLEVLSQK	RMHHK	2		613.8900854	1225.764571	0.000451244	38	Y	49	60

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q80X90	Exosome	SDGLR	LIALLEVLSQK	RMHHK	3		409.5959902	1225.764571	0.002019181	1	Y	49	60
Q80X90	Exosome	DGTCK	VSYFPTVPGVYIVSTK	FADEH	2		878.9801601	1755.94472	0.0007646	2	N	2058	2074
Q80X90	Exosome	CSQVK	LGSAADFLLDISETDLSTLTASIK	APSGR	2		1241.152682	2480.289763	0.000662267	2	N	1919	1943
Q80X90	Exosome	VTGQR	LVSPGSANETSSILVESVTR	SSTET	2		1023.53983	2045.064061	0.000823681	1	N	2475	2495
Q80X90	Parental	KCDAR	VLSDDEEDVDFDIIHNANDTFTVK	YVPPA	3		917.7597657	2750.255897	0.000451244	10	N	786	810
Q80X90	Parental	SDGLR	LIALLEVLSQK	RMHHK	2		613.8900854	1225.764571	0.000451244	43	Y	49	60
Q80X90	Parental	SDGLR	LIALLEVLSQK	RMHHK	3		409.5959902	1225.764571	0.000622848	5	Y	49	60
Q80X90	Parental	DAIPK	SPFGVQIGEACNPNACR	ASGRG	2	C11:+57.021,C16:+57.021	938.925136	1875.834672	0.002296037	1	N	439	456
Q80X90	Parental	DGTCK	VSYFPTVPGVYIVSTK	FADEH	2		878.9801601	1755.94472	0.001352548	1	N	2058	2074
Q80X90	Parental	LVKQK	GFLDGVYSFEYYPSTPGK	YSVAV	2		1013.975803	2025.936006	0.00091018	2	N	504	522
Q80X90	Parental	WQDGK	ALGALVDSCAPGLCPDWESWDPR	KPVDN	2	C9:+57.021,C14:+57.021	1286.583458	2571.151315	0.000451244	3	N	169	192
Q80X90	Parental	CRDNK	DGSCSAEYIPFAPGDYDVNITYGGVHIPGSPFR	VPSKD	3	C4:+57.021	1186.880906	3557.619319	0.000451244	7	N	1379	1412
Q80X90	Parental	CSQVK	LGSAADFLLDISETDLSTLTASIK	APSGR	2		1241.152682	2480.289763	0.000451244	5	N	1919	1943
Q80X90	Parental	VTGQR	LVSPGSANETSSILVESVTR	SSTET	2		1023.53983	2045.064061	0.000451244	1	N	2475	2495
Q80X90	Parental	YDASK	VTASGPGLSAYGVPASLPVEFAIDAR	DAGEG	2		1273.169	2544.322401	0.000823681	2	N	1519	1545
Q80X90	Parental	IVDTR	DAGYGGISLAVEGPSKVDIQTEDLEDGTCK	VSYFP	3	C29:+57.021	1042.159446	3123.454939	0.002080925	1	N	2028	2058
Q80X90	Parental	LEHGK	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	AEVSI	3	C8:+57.021,C11:+57.021	982.4672916	2944.378475	0.002212458	1	N	1147	1177
Q80XU3	Parental	VRNRK	VVDYSQFQESDDADEDYGRDSGPPAK	KIRSS	3		964.0815675	2889.221303	0.000451244	1	N	9	35
Q80XU3	Parental	PVRNR	KVVDYSQFQESDDADEDYGR	DSGPP	3		789.3405418	2364.998225	0.000823681	1	N	8	28
Q80Y14	Parental	LHGVR	DYAAYNVLDDPELR	QGIKD	2		827.3919062	1652.768212	0.000451244	19	N	79	93
Q80Y14	Parental	VVFLK	GTPEQPQCGFSNAVVQILR	LHGVR	2	C8:+57.021	1051.028678	2100.041757	0.000451244	24	N	55	74
Q80ZJ2	Exosome	AAGEK	TVFTEQPTWVIDPIDGTTNFVHR	FPFVA	2		1337.169532	2672.323463	0.000451244	4	N	78	101
Q80ZJ2	Exosome	AAGEK	TVFTEQPTWVIDPIDGTTNFVHR	FPFVA	3		891.7822878	2672.323463	0.000451244	31	N	78	101
Q80ZJ2	Exosome	MSSIK	EKYPCHSFIGEESVAAGEK	TVFTE	3	C5:+57.021	713.3338512	2136.978154	0.001654178	2	N	59	78
Q80ZJ2	Exosome	DVMIK	SSPADLVTVTDQKVEK	MLMSS	2		858.9548707	1715.894141	0.002019181	1	N	36	52
Q80ZJ2	Exosome	EDITK	SLLVTELGSSR	KPETL	2		581.3278492	1160.640098	0.001699387	5	N	156	167
Q80ZJ2	Parental	AAGEK	TVFTEQPTWVIDPIDGTTNFVHR	FPFVA	2		1337.169532	2672.323463	0.000823681	1	N	78	101
Q80ZJ2	Parental	AAGEK	TVFTEQPTWVIDPIDGTTNFVHR	FPFVA	3		891.7822878	2672.323463	0.000451244	12	N	78	101
Q80ZJ2	Parental	MSSIK	EKYPCHSFIGEESVAAGEK	TVFTE	2	C5:+57.021	1069.496877	2136.978154	0.000823681	1	N	59	78
Q80ZJ2	Parental	MSSIK	EKYPCHSFIGEESVAAGEK	TVFTE	3	C5:+57.021	713.3338512	2136.978154	0.001352548	1	N	59	78
Q80ZJ2	Parental	DVMIK	SSPADLVTVTDQKVEK	MLMSS	2		858.9548707	1715.894141	0.000451244	1	N	36	52
Q80ZX0	Exosome	PTGGR	VSVFQTQLPSLGAGLLQSR	EDPNQ	2		1001.060536	2000.105472	0.00091018	2	N	790	809
Q80ZX0	Exosome	LSDAR	DALVNAVVDPLSAYSSAVASVPR	STLTA	2		1151.108411	2300.201223	0.000451244	4	N	1022	1045
Q80ZX0	Exosome	LSDAR	DALVNAVVDPLSAYSSAVASVPR	STLTA	3		767.741541	2300.201223	0.000451244	2	N	1022	1045
Q810A7	Exosome	PPFEK	NFYNEHEEITNLTPQQLIDLR	HKLNL	3		863.0982759	2586.271428	0.000870037	2	N	215	236
Q810A7	Parental	MHQIR	KSEYTQPTPIQCQGVPVALSGR	DMIGI	3	C12:+57.021	806.081526	2415.221178	0.002663018	1	N	269	291
Q810A7	Parental	PPFEK	NFYNEHEEITNLTPQQLIDLR	HKLNL	3		863.0982759	2586.271428	0.000823681	6	N	215	236
Q810B6	Exosome	HTACR	HGLANLTAELLQQGANPNLQTEEALPVPK	ESPVL	3		1022.87932	3065.614561	0.000451244	23	N	500	529
Q810B6	Exosome	RSGVR	LGVNNNQGVNIFNYQVATK	QLLFR	2		1047.042874	2092.070149	0.001162105	2	N	1069	1088
Q810B6	Parental	HTACR	HGLANLTAELLQQGANPNLQTEEALPVPK	ESPVL	3		1022.87932	3065.614561	0.000451244	22	N	500	529
Q810B6	Parental	RSGVR	LGVNNNQGVNIFNYQVATK	QLLFR	2		1047.042874	2092.070149	0.001162105	1	N	1069	1088
Q810B6	Parental	LNNIR	ALLTECTVDAEAFNLR	GQSPL	2	C6:+57.021	911.9541164	1821.892633	0.000622848	2	N	989	1005
Q810B6	Parental	SPKKY	SADVMSEMAQIAEALLQAGANPNMQDSKGR	TPLHL	4		784.1237546	3132.463819	0.000662267	1	N	338	368
Q810B6	Parental	RQDSK	SALFLLEHQADINVR	TQDGE	3		575.981455	1724.920965	0.002019181	1	N	636	651
Q8BFQ8	Parental	VVLDR	HLVTGQNANSTVPAVQNLLFLCGSR	K-	3	C22:+57.021	899.4697841	2695.385952	0.00091018	1	N	194	219
Q8BFQ8	Parental	IDGAR	YHALLIPSCPGALTDLASSGSLAR	ILQHF	3	C9:+57.021	824.0971761	2469.268128	0.000451244	5	N	85	109
Q8BFR5	Exosome	PVPTR	DLDKPFLLPVESVYSIPGR	GTVVT	3		715.7250511	2144.151753	0.000637154	3	N	252	271
Q8BFR5	Exosome	KSVQK	LLDAVDTYIPVPTR	DLDKP	2		786.9357526	1571.855905	0.00091018	4	N	238	252
Q8BFR5	Parental	PVPTR	DLDKPFLLPVESVYSIPGR	GTVVT	3		715.7250511	2144.151753	0.000622848	10	N	252	271
Q8BFR5	Parental	KSVQK	LLDAVDTYIPVPTR	DLDKP	2		786.9357526	1571.855905	0.000662267	7	N	238	252
Q8BFR5	Parental	ELEIR	ELLTEFGYKGEETPVIVGSALCALEQR	DPELG	3	C22:+57.021	1003.846474	3008.516023	0.000451244	14	N	200	227
Q8BFY6	Exosome	DCFIK	VCTQLQVLTEAFR	EKDTA	2	C2:+57.021	782.9115232	1563.807446	0.000451244	17	N	236	249
Q8BFY6	Exosome	TKSGR	IDVAGFSALWK	FLQQW	2		603.8300277	1205.644455	0.000622848	3	N	161	172
Q8BFY6	Parental	DCFIK	VCTQLQVLTEAFR	EKDTA	2	C2:+57.021	782.9115232	1563.807446	0.000451244	6	N	236	249
Q8BFY6	Parental	TKSGR	IDVAGFSALWK	FLQQW	2		603.8300277	1205.644455	0.000698008	6	N	161	172
Q8BFY9	Exosome	DLLPK	LCSLLDSEDYNTCEGAFGALQK	ICEDS	2	C2:+57.021,C13:+57.021	1246.059481	2490.103362	0.000451244	13	N	140	162
Q8BFY9	Exosome	DLLPK	LCSLLDSEDYNTCEGAFGALQK	ICEDS	3	C2:+57.021,C13:+57.021	831.042254	2490.103362	0.000823681	1	N	140	162
Q8BFY9	Exosome	TVQQK	LEQLNQYPDFNNYLIFVLTK	LKSED	2		1236.64463	2471.27366	0.000451244	7	N	44	64
Q8BFY9	Exosome	TVQQK	LEQLNQYPDFNNYLIFVLTK	LKSED	3		824.7656865	2471.27366	0.000451244	19	N	44	64
Q8BFY9	Exosome	YMLQR	TQDQDENVALEACEFWLTLAEQPICK	DVLVR	3	C13:+57.021,C25:+57.021	1036.814691	3107.420674	0.000451244	32	N	272	298
Q8BFY9	Exosome	TDFIK	SECLNNIGDSSPLIR	ATVGI	2	C3:+57.021	837.9097089	1673.803818	0.000451244	3	N	100	115
Q8BFY9	Exosome	IILLK	GDVEEDETIPDSEQDIRPR	FHRSR	3		734.005382	2198.992746	0.002145581	1	N	327	346
Q8BFY9	Exosome	MIVAL	DLLSGLAEGLGGNIEQLVAR	SNILT	3		675.7045385	2024.090216	0.000451244	1	N	653	673
Q8BFY9	Exosome	VNGMK	YSDIDIILLK	GDVEE	2		596.8453435	1191.675087	0.002080925	2	N	317	327
Q8BFY9	Exosome	MPEVR	QSSFALLGDLTK	ACFQH	2		640.3487817	1278.681963	0.002519933	1	N	692	704

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BFY9	Parental	DLLPK	LCSLLDSEDYNTCEGAFGALQK	ICEDS	2	C2:+57.021,C13:+57.021	1246.059481	2490.103362	0.000451244	27	N	140	162
Q8BFY9	Parental	SPLIR	ATVGILITTIASKGELQNWPDLLPK	LCSLL	3		893.5096169	2677.505451	0.000451244	8	N	115	140
Q8BFY9	Parental	TVQQK	LEQLNQYPDFNNYLIFVLTK	LKSED	2		1236.64463	2471.27366	0.000451244	11	N	44	64
Q8BFY9	Parental	TVQQK	LEQLNQYPDFNNYLIFVLTK	LKSED	3		824.7656865	2471.27366	0.000451244	21	N	44	64
Q8BFY9	Parental	YMLQR	TQDQDENVALEACEFWLTLAEQPICKDVLVR	HLPKL	3	C13:+57.021,C25:+57.021	1230.931007	3689.76962	0.000451244	10	N	272	303
Q8BFY9	Parental	TTIQR	TVQQKLEQLNQYPDFNNYLIFVLTK	LKSED	3		1019.541757	3055.601871	0.00307782	1	N	39	64
Q8BFY9	Parental	YMLQR	TQDQDENVALEACEFWLTLAEQPICK	DVLVR	3	C13:+57.021,C25:+57.021	1036.814691	3107.420674	0.000451244	18	N	272	298
Q8BFY9	Parental	TDFIK	SECLNNIGDSSPLIR	ATVGI	2	C3:+57.021	837.9097089	1673.803818	0.000637154	2	N	100	115
Q8BFY9	Parental	FHRSR	TVAQQHEEDGIEEEDDDDDEIDDDDTISDWNLR	KCSAA	3		1292.858649	3875.552546	0.001871652	4	N	351	384
Q8BFY9	Parental	IILLK	GDVEEDETIPDSEQDIRPR	FHRSR	3		734.005382	2198.992746	0.000823681	1	N	327	346
Q8BFY9	Parental	DSNKR	VQEAACSAFATLEEEACTELVPYLAYILDTLVFAFSK	YQHKN	3	C6:+57.021,C17:+57.021	1390.682987	4169.025561	0.000451244	4	N	503	540
Q8BFY9	Parental	FHRSR	TVAQQHEEDGIEEEDDDDDEIDDDDTISDWNLRK	CSAAA	4		1001.919677	4003.647509	0.000451244	1	N	351	385
Q8BFZ3	Exosome	YNELR	VAPDEHPILLTEAPLNPK	INREK	2		977.5363622	1953.057124	0.000451244	63	N	96	114
Q8BFZ3	Exosome	YNELR	VAPDEHPILLTEAPLNPK	INREK	3		652.0268415	1953.057124	0.000451244	292	N	96	114
Q8BFZ3	Exosome	ELRVA	PDEHPILLTEAPLNPK	INREK	2		892.4835983	1782.951597	0.000451244	27	N	98	114
Q8BFZ3	Exosome	ELRVA	PDEHPILLTEAPLNPK	INREK	3		595.3249989	1782.951597	0.000451244	47	N	98	114
Q8BFZ3	Exosome	SSLER	SYELPDGQVITIGNER	FRCPE	2		895.9501196	1789.884639	0.000451244	1549	Y	239	255
Q8BFZ3	Exosome	SSLER	SYELPDGQVITIGNER	FRCPE	3		597.6360131	1789.884639	0.000451244	140	Y	239	255
Q8BFZ3	Exosome	HAILR	LDLAGRDLTDYLMK	ILTER	3		541.9523969	1622.833791	0.000622848	2	Y	178	192
Q8BFZ3	Exosome	HAILR	LDLAGRDLTDYLMK	ILTER	3	M13:+15.995	547.2840636	1638.828791	0.000451244	3	Y	178	192
Q8BFZ3	Exosome	ERSYE	LPDGQVITIGNER	FRCPE	2		706.3811445	1410.746689	0.000823681	17	Y	242	255
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		1061.876811	3182.607033	0.000451244	52	Y	148	178
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	4		796.6595584	3182.607033	0.000451244	35	Y	148	178
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3	M6:+15.995	1067.208478	3198.602033	0.000451244	106	Y	148	178
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	4	M6:+15.995	800.6583084	3198.602033	0.000451244	70	Y	148	178
Q8BFZ3	Exosome	TPAMY	VAIQAVLSLYASGR	TTGIV	2		724.41753	1446.81946	0.000451244	459	Y	134	148
Q8BFZ3	Exosome	TPAMY	VAIQAVLSLYASGR	TTGIV	3		483.2809533	1446.81946	0.000451244	9	Y	134	148
Q8BFZ3	Exosome	PPERK	YSVWIGGSILASLSTF	QQMWI	2		850.94886	1699.88212	0.000451244	183	Y	337	353
Q8BFZ3	Exosome	NELRV	APDEHPILLTEAPLNPK	INREK	2		928.0021552	1853.98871	0.000451244	10	N	97	114
Q8BFZ3	Exosome	LERSY	ELPDGQVITIGNER	FRCPE	2		770.9024411	1539.789282	0.000451244	9	Y	241	255
Q8BFZ3	Exosome	VTHTV	PIYEGYALPHAILR	LDLAG	2		806.9464546	1611.877309	0.000451244	5	Y	164	178
Q8BFZ3	Exosome	VTHTV	PIYEGYALPHAILR	LDLAG	3		538.3002364	1611.877309	0.000451244	26	Y	164	178
Q8BFZ3	Exosome	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	2		1291.156424	2580.297249	0.000451244	3	Y	154	178
Q8BFZ3	Exosome	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		861.1068829	2580.297249	0.000451244	38	Y	154	178
Q8BFZ3	Exosome	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	4		646.0821122	2580.297249	0.000451244	12	Y	154	178
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	2		1365.65814	2729.30068	0.002884417	1	Y	148	174
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	3		910.7746934	2729.30068	0.000451244	40	Y	148	174
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	2	M6:+15.995	1373.65564	2745.29568	0.001395409	4	Y	148	174
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	3	M6:+15.995	916.1063601	2745.29568	0.000451244	2	Y	148	174
Q8BFZ3	Exosome	GIVMD	SGDGVTHTVPIYEGYALPHAILR	LDLAG	4		617.3253764	2465.270306	0.002145581	1	Y	155	178
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGY	ALPHA	2		1156.541713	2311.067826	0.000622848	6	Y	148	170
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGY	ALPHA	2	M6:+15.995	1164.539213	2327.062826	0.000451244	16	Y	148	170
Q8BFZ3	Exosome	PAMYV	AIQAVLSLYASGR	TTGIV	2		674.883323	1347.751046	0.000451244	6	Y	135	148
Q8BFZ3	Exosome	SSLER	SYELPDGQVITI	GNERF	2		667.8460718	1333.676544	0.000451244	16	Y	239	251
Q8BFZ3	Exosome	MFEAF	NTPAMYVAIQAVLSLYASGR	TTGIV	2		1063.059679	2124.103758	0.001943752	1	Y	128	148
Q8BFZ3	Exosome	MFEAF	NTPAMYVAIQAVLSLYASGR	TTGIV	3		709.0423861	2124.103758	0.000451244	16	Y	128	148
Q8BFZ3	Exosome	MFEAF	NTPAMYVAIQAVLSLYASGR	TTGIV	2	M5:+15.995	1071.057179	2140.098758	0.000622848	1	Y	128	148
Q8BFZ3	Exosome	INREK	MTQIMFEAFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M5:+15.995,M14:+15.995	1085.868328	3254.581585	0.001162105	2	N	119	148
Q8BFZ3	Exosome	RSYEL	PDGQVITIGNER	FRCPE	2		649.8391124	1297.662625	0.000451244	13	Y	243	255
Q8BFZ3	Exosome	DVKEK	LCYVALDFEQEMVTAAASSSLER	SYELP	3	C2:+57.021	864.0773418	2589.208625	0.000451244	4	N	216	239
Q8BFZ3	Exosome	PPERK	YSVWIGGSILA	SLSTF	2		583.3167532	1164.617906	0.001591523	4	Y	337	348
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAIL	RLDLA	3		1009.843107	3026.505922	0.000451244	4	Y	148	177
Q8BFZ3	Exosome	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAIL	RLDLA	3	M6:+15.995	1015.174774	3042.500922	0.000451244	10	Y	148	177
Q8BFZ3	Exosome	APPER	KYSVWIGGSILASLSTF	QQMWI	2		914.9963416	1827.977083	0.000451244	165	Y	336	353
Q8BFZ3	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2		1301.672865	2601.33013	0.000622848	7	Y	337	360
Q8BFZ3	Exosome	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2	M19:+15.995	1309.670365	2617.32513	0.002145581	4	Y	337	360
Q8BFZ3	Exosome	DGVTH	TVPIYEGYALPHAILR	LDLAG	2		907.0045009	1811.993402	0.000451244	10	Y	162	178
Q8BFZ3	Exosome	DGVTH	TVPIYEGYALPHAILR	LDLAG	3		605.0056006	1811.993402	0.000823681	1	Y	162	178
Q8BFZ3	Exosome	SSLER	SYELPDGQVITIGNERFR	CPEAI	2		1047.534882	2093.054164	0.002453667	2	Y	239	257
Q8BFZ3	Exosome	YVAIQ	AVLSLYASGR	TTGIV	2		518.7934452	1035.57129	0.000622848	1	Y	138	148
Q8BFZ3	Exosome	DEHPI	LLTEAPLNPK	INREK	2		548.3245782	1094.633556	0.000823681	6	Y	104	114
Q8BFZ3	Exosome	HTVPI	YEGYALPHAILR	LDLAG	3		468.2546271	1401.740481	0.000823681	1	Y	166	178
Q8BFZ3	Exosome	DLAGR	DLTDYLMK	ILTER	2		499.7473153	997.4790306	0.002145581	1	Y	184	192
Q8BFZ3	Exosome	SSLER	SYELPDGQVITIGN	ERFRC	2		753.3782675	1504.740935	0.000622848	1	Y	239	253
Q8BFZ3	Exosome	SLERS	YELPDGQVITIGNER	FRCPE	2		852.4341054	1702.852611	0.001162105	1	Y	240	255

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BFZ3	Exosome	SSLER	SYELPDGQVITIGNERF	RCPEA	2		969.4843266	1936.953053	0.000451244	3	Y	239	256
Q8BFZ3	Exosome	PPERK	YSVWIGGSILASLSTFQ	QMWIS	2		914.9781488	1827.940698	0.000451244	2	Y	337	354
Q8BFZ3	Exosome	PPERK	YSVWIGGSIL	ASLST	2		547.7981962	1093.580792	0.002981883	1	Y	337	347
Q8BFZ3	Exosome	MDSGD	GVTHTVPIYEGYALPHAILR	LDLAG	4		552.5552675	2206.18987	0.00091018	1	Y	158	178
Q8BFZ3	Exosome	PKINR	EKMTQIMFEAFNTPAMYVAIQAVLSLYASGR	TTGIV	3	M3:+15.995,M16:+15.995	1171.580847	3511.719142	0.001943752	1	N	117	148
Q8BFZ3	Parental	YNELR	VAPDEHPILLTEAPLNPK	INREK	2		977.5363622	1953.057124	0.000451244	57	N	96	114
Q8BFZ3	Parental	YNELR	VAPDEHPILLTEAPLNPK	INREK	3		652.0268415	1953.057124	0.000451244	183	N	96	114
Q8BFZ3	Parental	ELRVA	PDEHPILLTEAPLNPK	INREK	2		892.4835983	1782.951597	0.000451244	13	N	98	114
Q8BFZ3	Parental	ELRVA	PDEHPILLTEAPLNPK	INREK	3		595.3249989	1782.951597	0.000451244	14	N	98	114
Q8BFZ3	Parental	SSLER	SYELPDGQVITIGNER	FRCPE	2		895.9501196	1789.884639	0.000451244	1486	Y	239	255
Q8BFZ3	Parental	SSLER	SYELPDGQVITIGNER	FRCPE	3		597.6360131	1789.884639	0.000451244	118	Y	239	255
Q8BFZ3	Parental	HAILR	LDLAGRDLTDYLMK	ILTER	2		812.4246953	1622.833791	0.000451244	6	Y	178	192
Q8BFZ3	Parental	HAILR	LDLAGRDLTDYLMK	ILTER	3		541.9523969	1622.833791	0.000451244	6	Y	178	192
Q8BFZ3	Parental	HAILR	LDLAGRDLTDYLMK	ILTER	3	M13:+15.995	547.2840636	1638.828791	0.002080925	1	Y	178	192
Q8BFZ3	Parental	ERSYE	LPDGQVITIGNER	FRCPE	2		706.3811445	1410.746689	0.000451244	27	Y	242	255
Q8BFZ3	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		1061.876811	3182.607033	0.000451244	9	Y	148	178
Q8BFZ3	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	4		796.6595584	3182.607033	0.000451244	15	Y	148	178
Q8BFZ3	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	LDLAG	3	M6:+15.995	1067.208478	3198.602033	0.000451244	9	Y	148	178
Q8BFZ3	Parental	TPAMY	VAIQAVLSLYASGR	TTGIV	2		724.41753	1446.81946	0.000451244	976	Y	134	148
Q8BFZ3	Parental	TPAMY	VAIQAVLSLYASGR	TTGIV	3		483.2809533	1446.81946	0.000451244	14	Y	134	148
Q8BFZ3	Parental	PPERK	YSVWIGGSILASLSTF	QQMWI	2		850.94886	1699.88212	0.000451244	562	Y	337	353
Q8BFZ3	Parental	NELRV	APDEHPILLTEAPLNPK	INREK	2		928.0021552	1853.98871	0.000451244	3	N	97	114
Q8BFZ3	Parental	NELRV	APDEHPILLTEAPLNPK	INREK	3		619.0040368	1853.98871	0.000451244	1	N	97	114
Q8BFZ3	Parental	LERSY	ELPDGQVITIGNER	FRCPE	2		770.9024411	1539.789282	0.000698008	3	Y	241	255
Q8BFZ3	Parental	VTHTV	PIYEGYALPHAILR	LDLAG	2		806.9464546	1611.877309	0.002212458	2	Y	164	178
Q8BFZ3	Parental	VTHTV	PIYEGYALPHAILR	LDLAG	3		538.3002364	1611.877309	0.000451244	13	Y	164	178
Q8BFZ3	Parental	TGIVM	DSGDGVTHTVPIYEGYALPHAILR	LDLAG	3		861.1068829	2580.297249	0.001943752	1	Y	154	178
Q8BFZ3	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	AILRL	3		910.7746934	2729.30068	0.000998612	7	Y	148	174
Q8BFZ3	Parental	MFEAF	NTPAMYVAIQAVLSLYASGR	TTGIV	3		709.0423861	2124.103758	0.001329271	1	Y	128	148
Q8BFZ3	Parental	RSYEL	PDGQVITIGNER	FRCPE	2		649.8391124	1297.662625	0.000451244	27	Y	243	255
Q8BFZ3	Parental	YASGR	TTGIVMDSGDGVTHTVPIYEGYALPHAIL	RLDLA	3		1009.843107	3026.505922	0.000451244	5	Y	148	177
Q8BFZ3	Parental	DLAGR	DLTDYLMKILTER	GYNFT	3		537.6206472	1609.838542	0.000823681	2	Y	184	197
Q8BFZ3	Parental	APPER	KYSVWIGGSILASLSTF	QQMWI	2		914.9963416	1827.977083	0.000451244	160	Y	336	353
Q8BFZ3	Parental	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	2		1301.672865	2601.33013	0.000622848	2	Y	337	360
Q8BFZ3	Parental	PPERK	YSVWIGGSILASLSTFQQMWISK	QEYDE	3		868.1178433	2601.33013	0.000622848	1	Y	337	360
Q8BFZ3	Parental	VDIRK	DLFANTVLSGGSTMYPGIADR	MQKEI	2		1093.033858	2184.052117	0.002519933	1	N	292	313
Q8BG05	Exosome	SFGGR	SSGSPYGGGYGSGGGSGGYGSR	RF-	2		955.8991467	1909.782693	0.000622848	7	N	355	377
Q8BG05	Exosome	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	2		1141.079123	2280.142645	0.000451244	3	N	167	187
Q8BG05	Exosome	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	3		761.0553484	2280.142645	0.000451244	19	N	167	187
Q8BG05	Exosome	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	4		571.0434613	2280.142645	0.000451244	6	N	167	187
Q8BG05	Exosome	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	2		1221.103326	2440.191052	0.000451244	5	N	36	57
Q8BG05	Exosome	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	3		814.4048174	2440.191052	0.000451244	15	N	36	57
Q8BG05	Exosome	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	4		611.055563	2440.191052	0.000451244	24	N	36	57
Q8BG05	Exosome	EQLRK	LFIGGLSFETTDDSLR	EHFEK	2		885.9495883	1769.883577	0.000451244	13	N	36	52
Q8BG05	Exosome	LTVKK	IFVGGIKEDTEEYNLR	DYFEK	2		941.9814198	1881.94724	0.000451244	4	N	127	143
Q8BG05	Exosome	LTVKK	IFVGGIKEDTEEYNLR	DYFEK	3		628.3235465	1881.94724	0.000451244	7	N	127	143
Q8BG05	Exosome	SGKKR	GFAFVTFDDHDTVDK	IVVQK	3		571.9305375	1712.768212	0.000622848	12	N	167	182
Q8BG05	Exosome	PEQLR	KLFIGGLSFETTDDSLR	EHFEK	3		633.6673133	1897.97854	0.0007646	2	N	35	52
Q8BG05	Parental	SFGGR	SSGSPYGGGYGSGGGSGGYGSR	RF-	2		955.8991467	1909.782693	0.000451244	18	N	355	377
Q8BG05	Parental	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	2		1141.079123	2280.142645	0.000451244	11	N	167	187
Q8BG05	Parental	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	3		761.0553484	2280.142645	0.000451244	26	N	167	187
Q8BG05	Parental	SGKKR	GFAFVTFDDHDTVDKIVVQK	YHTIN	4		571.0434613	2280.142645	0.000451244	5	N	167	187
Q8BG05	Parental	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	2		1221.103326	2440.191052	0.000451244	35	N	36	57
Q8BG05	Parental	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	3		814.4048174	2440.191052	0.000451244	17	N	36	57
Q8BG05	Parental	EQLRK	LFIGGLSFETTDDSLREHFEK	WGTLT	4		611.055563	2440.191052	0.000451244	40	N	36	57
Q8BG05	Parental	EQLRK	LFIGGLSFETTDDSLR	EHFEK	2		885.9495883	1769.883577	0.000451244	23	N	36	52
Q8BG05	Parental	LTVKK	IFVGGIKEDTEEYNLR	DYFEK	2		941.9814198	1881.94724	0.000451244	3	N	127	143
Q8BG05	Parental	LTVKK	IFVGGIKEDTEEYNLR	DYFEK	3		628.3235465	1881.94724	0.000451244	3	N	127	143
Q8BG05	Parental	SGKKR	GFAFVTFDDHDTVDK	IVVQK	3		571.9305375	1712.768212	0.0007646	4	N	167	182
Q8BG05	Parental	LTVKK	IFVGGIKEDTEEY	NLRDY	2		750.3673684	1498.719137	0.000451244	14	N	127	140
Q8BG05	Parental	PEQLR	KLFIGGLSFETTDDSLR	EHFEK	2		949.9970699	1897.97854	0.000451244	6	N	35	52
Q8BG05	Parental	PEQLR	KLFIGGLSFETTDDSLR	EHFEK	3		633.6673133	1897.97854	0.000698008	1	N	35	52
Q8BG32	Exosome	THLAK	LYDNLLEQNLIR	VIEPF	2		752.4124446	1502.809289	0.000451244	6	N	325	337
Q8BG32	Exosome	LTDYR	AELRDDPIISTHLAK	LYDNL	3		560.3094602	1677.904981	0.000823681	10	N	310	325
Q8BG32	Exosome	EKDWK	TAYSYFYEAFEGYDSIDSPK	AITSL	2		1177.013311	2352.011022	0.000451244	1	N	226	246

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BG32	Exosome	AVQVK	EQSILELGSLLAK	TGQAA	2		700.9039211	1399.792242	0.000451244	3	N	46	59
Q8BG32	Parental	SIVKR	DIQENDEEAVQVKEQSILELGSLLAK	TGQAA	3		966.8367866	2897.48696	0.000451244	2	N	33	59
Q8BG32	Parental	EKDWK	TAYSYFYEAFEGYDSIDSPK	AITSL	2		1177.013311	2352.011022	0.000979378	1	N	226	246
Q8BG32	Parental	AVQVK	EQSILELGSLLAK	TGQAA	2		700.9039211	1399.792242	0.001352548	5	N	46	59
Q8BG32	Parental	VEFQR	AQSLLSTDREASIDILHSIVK	RDIQE	3		766.0889407	2295.243422	0.000451244	6	N	11	32
Q8BGD9	Exosome	SRLPK	SPPYTAFLGNLPYDVTEDSIKDFFR	GLNIS	3		964.8083912	2891.401774	0.000451244	28	N	92	117
Q8BGD9	Exosome	PDRLK	GFGYAEFEDLDSLLSALSLNEESLGNRR	IRVDV	3		1034.83919	3101.494171	0.000451244	23	N	137	165
Q8BGD9	Parental	SRLPK	SPPYTAFLGNLPYDVTEDSIKDFFR	GLNIS	3		964.8083912	2891.401774	0.000451244	24	N	92	117
Q8BGD9	Parental	PDRLK	GFGYAEFEDLDSLLSALSLNEESLGNRR	IRVDV	3		1034.83919	3101.494171	0.000451244	26	N	137	165
Q8BGD9	Parental	GPSRK	DGNKVDVVGATQGQAGSCSR	GPGDG	3	C18:+57.021	669.3170831	2004.927849	0.001463592	2	N	525	545
Q8BGD9	Parental	PDRLK	GFGYAEFEDLDSLLSALSLNEESLGNR	RIRVD	2		1473.70433	2945.393059	0.000451244	1	N	137	164
Q8BGD9	Parental	PDRLK	GFGYAEFEDLDSLLSALSLNEESLGNR	RIRVD	3		982.8054865	2945.393059	0.000451244	5	N	137	164
Q8BGD9	Parental	KGFGY	AEFEDLDSLLSALSLNEESLGNRR	IRVDV	3		893.4476335	2677.3195	0.00091018	2	N	141	165
Q8BGE6	Exosome	YDTLR	FAEFEDFPETSEPVWILGR	KYSIF	2		1135.044748	2268.073897	0.000451244	14	N	12	31
Q8BGE6	Exosome	LIPLR	LGLTDINEAYVETLK	HCFMM	2		839.949057	1677.882514	0.00091018	1	N	229	244
Q8BGE6	Parental	YDTLR	FAEFEDFPETSEPVWILGR	KYSIF	2		1135.044748	2268.073897	0.000451244	7	N	12	31
Q8BGG7	Exosome	CMQAR	LVGEALLESNTVIDHVYCSPSLR	CVQTA	3	C18:+57.021	858.1077408	2571.299823	0.000451244	1	N	439	462
Q8BGG7	Parental	CMQAR	LVGEALLESNTVIDHVYCSPSLR	CVQTA	3	C18:+57.021	858.1077408	2571.299823	0.001162105	2	N	439	462
Q8BGG7	Parental	STGGR	SVQAACDWLFSHVGDPFLDDPLPR	EYVLY	3	C6:+57.021	914.7712401	2741.29032	0.000451244	4	N	53	77
Q8BGJ5	Exosome	VIHVR	KLPSDVTEGEVISLGLPFGK	VTNLL	3		696.0530563	2085.135769	0.000451244	10	N	63	83
Q8BGJ5	Exosome	KPGSK	NFQNIFPPSATLHLSNIPPSVSEDDLK	SLFSS	3		994.1737331	2979.497799	0.000451244	5	N	442	469
Q8BGJ5	Exosome	AAASR	IAIPGLAGAGNSVLLVSNLNPER	VTPQS	2		1138.142589	2274.269577	0.000451244	21	N	323	346
Q8BGJ5	Exosome	AAASR	IAIPGLAGAGNSVLLVSNLNPER	VTPQS	3		759.0976591	2274.269577	0.000451244	19	N	323	346
Q8BGJ5	Exosome	LNPER	VTPQSLFILFGVYGDVQR	VKILF	2		1020.052179	2038.088759	0.000451244	6	N	346	364
Q8BGJ5	Exosome	LNPER	VTPQSLFILFGVYGDVQR	VKILF	3		680.3707197	2038.088759	0.000451244	24	N	346	364
Q8BGJ5	Exosome	LNPER	VTPQSLFILFGVY	GDVQR	2		742.4139247	1482.812249	0.000823681	1	N	346	359
Q8BGJ5	Exosome	ITFTK	NNQFQALLQYADPVSAQHAK	LSLDG	2		1122.064338	2242.113076	0.000451244	10	N	217	237
Q8BGJ5	Exosome	ITFTK	NNQFQALLQYADPVSAQHAK	LSLDG	3		748.3788255	2242.113076	0.000451244	20	N	217	237
Q8BGJ5	Exosome	AQHAK	LSLDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	949.448444	1896.881288	0.000451244	25	N	237	253
Q8BGJ5	Exosome	SPVLR	IIVENLFYPVTLDVLHQIFSK	FGTVL	2		1244.696665	2487.377731	0.000823681	1	N	184	205
Q8BGJ5	Exosome	SPVLR	IIVENLFYPVTLDVLHQIFSK	FGTVL	3		830.1337103	2487.377731	0.000637154	11	N	184	205
Q8BGJ5	Parental	VQLPR	EGQEDQGLTKDYGSSPLHR	FKKPG	3		706.3351739	2115.982122	0.000451244	6	N	416	435
Q8BGJ5	Parental	VIHVR	KLPSDVTEGEVISLGLPFGK	VTNLL	2		1043.575684	2085.135769	0.000451244	13	N	63	83
Q8BGJ5	Parental	VIHVR	KLPSDVTEGEVISLGLPFGK	VTNLL	3		696.0530563	2085.135769	0.000451244	18	N	63	83
Q8BGJ5	Parental	KPGSK	NFQNIFPPSATLHLSNIPPSVSEDDLK	SLFSS	3		994.1737331	2979.497799	0.001699387	5	N	442	469
Q8BGJ5	Parental	AAASR	IAIPGLAGAGNSVLLVSNLNPER	VTPQS	2		1138.142589	2274.269577	0.000451244	28	N	323	346
Q8BGJ5	Parental	AAASR	IAIPGLAGAGNSVLLVSNLNPER	VTPQS	3		759.0976591	2274.269577	0.000451244	23	N	323	346
Q8BGJ5	Parental	LNPER	VTPQSLFILFGVYGDVQR	VKILF	3		680.3707197	2038.088759	0.000451244	7	N	346	364
Q8BGJ5	Parental	LNPER	VTPQSLFILFGVY	GDVQR	2		742.4139247	1482.812249	0.001699387	4	N	346	359
Q8BGJ5	Parental	ITFTK	NNQFQALLQYADPVSAQHAK	LSLDG	2		1122.064338	2242.113076	0.000451244	24	N	217	237
Q8BGJ5	Parental	ITFTK	NNQFQALLQYADPVSAQHAK	LSLDG	3		748.3788255	2242.113076	0.000451244	26	N	217	237
Q8BGJ5	Parental	AQHAK	LSLDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	949.448444	1896.881288	0.000451244	11	N	237	253
Q8BGJ5	Parental	SPVLR	IIVENLFYPVTLDVLHQIFSK	FGTVL	3		830.1337103	2487.377731	0.000622848	16	N	184	205
Q8BGQ7	Exosome	QATGK	NVGCLQEALQLATSFAQLR	LGDVK	2	C4:+57.021	1060.052154	2118.088707	0.000451244	13	N	943	962
Q8BGQ7	Exosome	QATGK	NVGCLQEALQLATSFAQLR	LGDVK	3	C4:+57.021	707.037369	2118.088707	0.000451244	30	N	943	962
Q8BGQ7	Exosome	IPVER	LYVTYFGGDEAAGLEPDLECR	QIWQN	2	C20:+57.021	1188.046931	2374.078262	0.000451244	12	N	132	153
Q8BGQ7	Exosome	VVLDK	TCFYAEQGGQIYDEGYLVK	VDDSS	2	C2:+57.021	1121.01236	2240.009119	0.000451244	3	N	531	550
Q8BGQ7	Exosome	KDVQR	EIADLGEALATAVIPQWQK	DEQRE	2		1027.052376	2052.089153	0.000451244	9	N	793	812
Q8BGQ7	Exosome	KDVQR	EIADLGEALATAVIPQWQK	DEQRE	3		685.0375177	2052.089153	0.000451244	8	N	793	812
Q8BGQ7	Exosome	ELACK	MALELLTQEFGIPVER	LYVTY	2		923.4931093	1844.970619	0.000823681	5	N	116	132
Q8BGQ7	Exosome	NEAGK	ITCLCQVPQNAANR	GLKAS	2	C3:+57.021,C5:+57.021	822.9009326	1643.786265	0.000451244	7	N	898	912
Q8BGQ7	Exosome	RIGGR	DAAHLVNQDDPNVLEIWNLVFIQYNR	ESDGV	3		1032.856627	3095.546481	0.000622848	1	N	198	224
Q8BGQ7	Exosome	DLECR	QIWQNLGLDEAR	ILPGN	2		721.8734866	1441.731373	0.000451244	3	N	153	165
Q8BGQ7	Exosome	NAQVR	GGYVLHIGTIYGNLK	VGDQV	3		535.6318746	1603.872224	0.000451244	1	N	569	584
Q8BGQ7	Exosome	ADHAR	TITVALADGGRPDNTGR	GYVLR	2		857.4480785	1712.880557	0.002212458	1	N	303	320
Q8BGQ7	Parental	QATGK	NVGCLQEALQLATSFAQLR	LGDVK	2	C4:+57.021	1060.052154	2118.088707	0.000451244	10	N	943	962
Q8BGQ7	Parental	QATGK	NVGCLQEALQLATSFAQLR	LGDVK	3	C4:+57.021	707.037369	2118.088707	0.000451244	22	N	943	962
Q8BGQ7	Parental	IPVER	LYVTYFGGDEAAGLEPDLECR	QIWQN	2	C20:+57.021	1188.046931	2374.078262	0.000451244	21	N	132	153
Q8BGQ7	Parental	VVLDK	TCFYAEQGGQIYDEGYLVK	VDDSS	2	C2:+57.021	1121.01236	2240.009119	0.000451244	6	N	531	550
Q8BGQ7	Parental	KDVQR	EIADLGEALATAVIPQWQK	DEQRE	2		1027.052376	2052.089153	0.000622848	13	N	793	812
Q8BGQ7	Parental	PDPVR	VVSIGVPVSELLDDPCGPAGSLTSVEFCGGTHLR	NSSHA	3	C16:+57.021,C28:+57.021	1175.916809	3524.727027	0.000622848	2	N	695	729
Q8BGQ7	Parental	ELACK	MALELLTQEFGIPVER	LYVTY	2		923.4931093	1844.970619	0.001162105	2	N	116	132
Q8BGQ7	Parental	TAWLL	YDTYGFPVDLTGLIAEEK	GLVVD	2		1016.002018	2029.988436	0.000451244	5	N	414	432
Q8BGQ7	Parental	NEAGK	ITCLCQVPQNAANR	GLKAS	2	C3:+57.021,C5:+57.021	822.9009326	1643.786265	0.000451244	1	N	898	912
Q8BGQ7	Parental	RIGGR	DAAHLVNQDDPNVLEIWNLVFIQYNR	ESDGV	3		1032.856627	3095.546481	0.000622848	5	N	198	224

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BGQ7	Parental	DLECR	QIWQNLGLDEAR	ILPGN	2		721.8734866	1441.731373	0.001839721	2	N	153	165
Q8BGQ7	Parental	DDSPK	YNYQSDSSGSYVFECTVATVLALR	REKMF	2	C15:+57.021	1365.639715	2729.263831	0.000451244	1	N	486	510
Q8BGQ7	Parental	DDSPK	YNYQSDSSGSYVFECTVATVLALR	REKMF	3	C15:+57.021	910.7624103	2729.263831	0.001943752	1	N	486	510
Q8BGT7	Parental	LKLKK	DLQEVIELTKDLLSTQPSETLASSDSFASTQPTHSWK	VGDKC	4		1023.259453	4089.006613	0.000451244	5	N	37	74
Q8BGT7	Parental	LASYK	AQLQQVEAALSGNGENEDLLK	LKKDL	2		1114.064201	2226.112802	0.000451244	11	N	13	34
Q8BGT7	Parental	IELTK	DLLSTQPSETLASSDSFASTQPTHSWK	VGDKC	3		974.4653528	2920.372658	0.000662267	9	N	47	74
Q8BH04	Exosome	RIMTR	LGTPVLQALGDGDFIK	CLHSV	2		822.4543095	1642.893019	0.000451244	8	N	193	209
Q8BH04	Exosome	QDLPK	EVLAELEALEGR	VQKM-	2		664.8569709	1327.698342	0.000451244	6	N	624	636
Q8BH04	Exosome	GRRPK	GVPLVYEAFNWR	HGVFV	2		725.8780406	1449.740481	0.000451244	3	N	457	469
Q8BH04	Exosome	GLVPK	EGALDLSGLSAVDTSQLFSIPK	DFWEQ	2		1124.58952	2247.16344	0.000451244	3	N	578	600
Q8BH04	Exosome	GLVPK	EGALDLSGLSAVDTSQLF	SIPKD	2		911.9576104	1821.899621	0.000823681	2	N	578	596
Q8BH04	Exosome	GDFIK	CLHSVGQPLTGHGDPVGQWPCNPEK	TLIGH	3	C1:+57.021,C21:+57.021	924.0992082	2769.274225	0.001871652	3	N	209	234
Q8BH04	Exosome	WICRR	LEGEDSAQETPIGLVPK	EGALD	2		891.960153	1781.904706	0.000622848	2	N	561	578
Q8BH04	Exosome	DFVAR	SAHLCQPEGIHICDGTEAENTAILALLEEQGLIR	KLPKY	3	C5:+57.021,C13:+57.021	1253.620944	3757.839431	0.000451244	1	N	50	84
Q8BH04	Parental	VRDIR	GYLTEQVNQDLPKEVLAELEALEGR	VQKM-	3		938.8227004	2813.444701	0.001162105	4	N	611	636
Q8BH04	Parental	GLVPK	EGALDLSGLSAVDTSQLFSIPKDFWEQEVR	DIRGY	3		1113.224933	3336.6514	0.000451244	7	N	578	608
Q8BH04	Parental	GLVPK	EGALDLSGLSAVDTSQLFSIPK	DFWEQ	2		1124.58952	2247.16344	0.0025889	1	N	578	600
Q8BH43	Exosome	GSLSK	YAEDIFGEICTQASAFASR	VNSLA	2	C10:+57.021	1068.489052	2134.962504	0.000451244	13	N	45	64
Q8BH43	Exosome	RHLCR	QTLPSDTSELECR	TNITL	2	C12:+57.021	768.3542351	1534.69287	0.000451244	4	N	15	28
Q8BH43	Exosome	RVQVK	VTQLDPKEEEVSLQGINTR	KAFRS	3		719.3784911	2155.112073	0.000451244	10	N	78	97
Q8BH43	Parental	GSLSK	YAEDIFGEICTQASAFASR	VNSLA	2	C10:+57.021	1068.489052	2134.962504	0.000451244	10	N	45	64
Q8BH43	Parental	GSLSK	YAEDIFGEICTQASAFASR	VNSLA	3	C10:+57.021	712.6619678	2134.962504	0.000451244	1	N	45	64
Q8BH43	Parental	RHLCR	QTLPSDTSELECR	TNITL	2	C12:+57.021	768.3542351	1534.69287	0.000451244	10	N	15	28
Q8BH43	Parental	EQEKR	DVVGNDVATILSR	RIAVE	2		679.8678699	1357.72014	0.002727428	1	N	461	474
Q8BH59	Parental	TTGPR	VSALNVLQDLGLFGLYK	GAKAC	3		617.3527775	1849.034932	0.000451244	5	N	465	482
Q8BH59	Parental	QSAIR	YGQVTPLEIDILYQLADLYNASGR	LTLAD	2		1356.698122	2711.380644	0.000451244	6	N	259	283
Q8BH59	Parental	QSAIR	YGQVTPLEIDILYQLADLYNASGR	LTLAD	3		904.801348	2711.380644	0.000823681	2	N	259	283
Q8BH59	Parental	AGTRK	DIEVTKEEFAQSAIR	YGQVT	2		868.4472128	1734.878826	0.001839721	1	N	244	259
Q8BH61	Exosome	DRSVR	LSVQSSPECIVGK	FRMYV	2	C9:+57.021	702.3638745	1402.712149	0.000451244	20	N	144	157
Q8BH61	Exosome	KEFKK	ESFEETLDPFSSK	KKEVL	2		758.346633	1514.677666	0.000451244	13	N	571	584
Q8BH61	Exosome	ETPVR	YGQCWVFAGVFNTFLR	CLGIP	2	C4:+57.021	982.9777289	1963.939858	0.000451244	20	N	311	327
Q8BH61	Exosome	ETPVR	YGQCWVFAGVFNTFLR	CLGIP	3	C4:+57.021	655.6544192	1963.939858	0.0025889	2	N	311	327
Q8BH61	Exosome	GVNLK	DYLNVTAVHLFK	ERWDS	2		710.3856985	1418.755797	0.000451244	12	N	43	55
Q8BH61	Exosome	GVNLK	DYLNVTAVHLFK	ERWDS	3		473.926399	1418.755797	0.001329271	1	N	43	55
Q8BH61	Exosome	YITAK	QDGTHVVEAVDATHIGK	LIVTK	2		888.9479113	1775.880223	0.000823681	1	N	446	463
Q8BH61	Exosome	YITAK	QDGTHVVEAVDATHIGK	LIVTK	3		592.9678742	1775.880223	0.000451244	18	N	446	463
Q8BH61	Exosome	YITAK	QDGTHVVEAVDATHIGK	LIVTK	3	[0:-17.027	587.2922075	1758.853223	0.002296037	2	N	446	463
Q8BH61	Exosome	GLVPR	GVNLKDYLNVTAVHLFK	ERWDS	3		644.3636765	1930.06763	0.000451244	7	N	38	55
Q8BH61	Exosome	GLVPR	GVNLKDYLNVTAVHLFK	ERWDS	4		483.5247074	1930.06763	0.000451244	8	N	38	55
Q8BH61	Exosome	VGKFR	MYVAVWTPYGILR	TRRDP	2		784.9188518	1567.822104	0.000622848	8	N	159	172
Q8BH61	Exosome	EVLVR	AGEYMSHLLEQGFLHFFVTAR	INESR	4		614.057746	2452.199784	0.002519933	1	N	591	612
Q8BH61	Exosome	QEEER	LALETALMYGAK	KTLNT	2	M8:+15.995	648.8476035	1295.679607	0.001229886	2	N	492	504
Q8BH61	Exosome	FGGRR	AVPPNNSNAAEVDLPTEELQGLVPR	GVNLK	2		1315.675178	2629.334756	0.002727428	1	N	13	38
Q8BH61	Exosome	FGGRR	AVPPNNSNAAEVDLPTEELQGLVPR	GVNLK	3		877.4527188	2629.334756	0.000451244	2	N	13	38
Q8BH61	Exosome	TFGGR	RAVPPNNSNAAEVDLPTEELQGLVPR	GVNLK	3		929.4864225	2785.435868	0.0025889	1	N	12	38
Q8BH61	Exosome	SDSLR	HVYGELDLQIQR	RPTM-	2		735.8891367	1469.762673	0.000451244	3	N	716	728
Q8BH61	Exosome	GVNLK	DYLNVTAVHLF	KERWD	2		646.3382169	1290.660834	0.000451244	6	N	43	54
Q8BH61	Parental	KEFKK	ESFEETLDPFSSK	KKEVL	2		758.346633	1514.677666	0.000622848	3	N	571	584
Q8BH61	Parental	YITAK	QDGTHVVEAVDATHIGK	LIVTK	3		592.9678742	1775.880223	0.001699387	1	N	446	463
Q8BH61	Parental	GVNLK	DYLNVTAVHLF	KERWD	2		646.3382169	1290.660834	0.000622848	3	N	43	54
Q8BH69	Exosome	IDKPR	IIEVAPQVATQNVNPTPGATS	-	2		1054.055648	2106.095695	0.000451244	9	N	371	392
Q8BH69	Exosome	AKQQR	NEVSFVIHNLPVLAK	MAAVS	2		840.478119	1678.940638	0.000451244	5	N	283	298
Q8BH69	Exosome	AKQQR	NEVSFVIHNLPVLAK	MAAVS	3		560.6546793	1678.940638	0.000622848	2	N	283	298
Q8BH69	Parental	IDKPR	IIEVAPQVATQNVNPTPGATS	-	2		1054.055648	2106.095695	0.000451244	2	N	371	392
Q8BH74	Exosome	LYRDR	IQSSLEEENMFAIAGINASEKMVVETLFQR	DSLVR	4	M10:+15.995,M22:+15.995	854.923832	3415.664128	0.001463592	1	N	230	260
Q8BH74	Parental	SAHKR	VLIQANQEDNFGTATPR	SQIIP	2		937.4742933	1872.932987	0.000622848	2	N	31	48
Q8BH74	Parental	SGNLK	QLLPVCDTWEDTVWAYFR	VMVDS	2	C6:+57.021	1150.046537	2298.077474	0.000622848	4	N	437	455
Q8BH74	Parental	EDRLK	IDVIDWLVFDPAQR	AEALR	2		843.9466516	1685.877703	0.001329271	6	N	672	686
Q8BH74	Parental	DSLVR	QSQLVVDWLESIAKDEIGEFSDNIEFYAK	SVYWE	3		1125.221189	3372.640166	0.000622848	1	N	265	294
Q8BH78	Exosome	APKRR	GSGSVVVDLLYWR	DIKKT	2		725.8886053	1449.761611	0.001699387	1	N	163	176
Q8BH78	Parental	PPAFK	YQFVTEPEDEEDEEDEEEEEDDEDLEELEVLER	KPAAG	3		1368.552668	4102.634604	0.000451244	21	N	25	58
Q8BH78	Parental	EVLER	KPAAGLSAAPVPPAAAPLLDFSSDSVPPAPR	GPLPA	3		989.8699849	2966.586555	0.000823681	2	N	58	89
Q8BH95	Exosome	LNRPK	ALNALCNGLIEELNQALETFEQDPAVGAIVLTGGDK	AFAAG	3	C6:+57.021	1261.975535	3782.903206	0.000451244	7	N	56	92
Q8BH95	Exosome	ELRRF	ASGANFQYIITEK	KGKNS	2		721.3702454	1440.724891	0.001162105	1	N	27	40
Q8BH95	Parental	LNRPK	ALNALCNGLIEELNQALETFEQDPAVGAIVLTGGDK	AFAAG	3	C6:+57.021	1261.975535	3782.903206	0.000451244	22	N	56	92

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BH95	Parental	YAGEK	AQFGQPEILLGTIPGAGGTQR	LTRAV	2		1056.06635	2110.117099	0.000451244	13	N	157	178
Q8BHD7	Exosome	PNQAR	AQAALQAVSAVQSGNLSLPGATANEGTLLPGQSPVLR	IIIEN	3		1196.311624	3585.911471	0.000451244	17	N	117	154
Q8BHD7	Exosome	MSSPY	AGAAGFAPAIAFPQAAGLSVPAVPGALGPLTLTSSAVSGR	MAIPG	3		1206.993455	3617.956965	0.001329271	2	N	276	316
Q8BHD7	Exosome	AQYAK	MALDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	950.4291975	1898.842795	0.000451244	3	N	207	223
Q8BHD7	Exosome	ITFTK	NNQFQALLQYADPVNAQYAK	MALDG	2		1148.571996	2295.128392	0.000451244	10	N	187	207
Q8BHD7	Parental	PNQAR	AQAALQAVSAVQSGNLSLPGATANEGTLLPGQSPVLR	IIIEN	3		1196.311624	3585.911471	0.000451244	36	N	117	154
Q8BHD7	Parental	PNQAR	AQAALQAVSAVQSGNLSLPGATANEGTLLPGQSPVLR	IIIEN	4		897.4856678	3585.911471	0.000451244	4	N	117	154
Q8BHD7	Parental	MSSPY	AGAAGFAPAIAFPQAAGLSVPAVPGALGPLTLTSSAVSGR	MAIPG	3		1206.993455	3617.956965	0.001654178	5	N	276	316
Q8BHD7	Parental	AQYAK	MALDGQNIYNACCTLR	IDFSK	2	C12:+57.021,C13:+57.021	950.4291975	1898.842795	0.000823681	2	N	207	223
Q8BHD7	Parental	VLHLR	KIPCDVTEAEVISLGLPFGK	VTNLL	2	C4:+57.021	1087.082588	2172.149576	0.001943752	1	N	35	55
Q8BHD7	Parental	ITFTK	NNQFQALLQYADPVNAQYAK	MALDG	2		1148.571996	2295.128392	0.000451244	28	N	187	207
Q8BHD7	Parental	ITFTK	NNQFQALLQYADPVNAQYAK	MALDG	3		766.0505974	2295.128392	0.000451244	10	N	187	207
Q8BHD7	Parental	SPVLR	IIIENLFYPVTLEVLHQIFSK	FGTVL	3		839.477477	2515.409031	0.000823681	3	N	154	175
Q8BHG1	Exosome	QLYPR	QDFLTGDQLLFEYKPEVIAEALNQLVPQK	ANLVL	3		1116.257686	3345.749657	0.000451244	19	N	588	617
Q8BHG1	Exosome	YRYIK	LQNGLQALLISDLSNVEGK	TGNAT	2		1006.555283	2011.094967	0.000451244	24	N	114	133
Q8BHG1	Exosome	YRYIK	LQNGLQALLISDLSNVEGK	TGNAT	3		671.3727889	2011.094967	0.000451244	25	N	114	133
Q8BHG1	Exosome	PLIQK	SAANVVLFDIFVNILTHNLAEPAYEADVAQLEYK	LVAGE	3		1259.984514	3776.930141	0.000451244	6	N	728	762
Q8BHG1	Exosome	SFEEK	IENLTEDAFNTQVTALIK	LKECE	2		1010.534017	2019.052433	0.000451244	5	N	1016	1034
Q8BHG1	Exosome	ITDIR	AFTATLSLFPYHK	IVK-	3		499.2701657	1494.787097	0.000451244	5	N	1145	1158
Q8BHG1	Exosome	RNKAK	STCSCPDLQPNGQDLGESGR	LARLG	2	C3:+57.021,C5:+57.021	1089.463008	2176.910416	0.000451244	24	N	56	76
Q8BHG1	Exosome	TELWK	SNFDLNPDLHLPAENK	YIATD	3		608.6361245	1822.884974	0.000451244	13	N	656	672
Q8BHG1	Exosome	TVDKK	IEEFLSSFEEKIENLTEDAFNTQVTALIK	LKECE	3		1120.236727	3357.686782	0.000451244	6	N	1005	1034
Q8BHG1	Exosome	LCKVR	ALNKGDANSEVTVYYQSGTR	SLREY	3		725.0227074	2172.044722	0.000451244	3	N	920	940
Q8BHG1	Exosome	DLKEK	WFGTQYSIEDIENSWTELWK	SNFDL	2		1266.590052	2531.164503	0.000823681	4	N	636	656
Q8BHG1	Exosome	EEEGR	SFSNVGDPEIIK	SPSDP	2		653.3384139	1304.661228	0.001591523	2	N	90	102
Q8BHG1	Parental	QLYPR	QDFLTGDQLLFEYKPEVIAEALNQLVPQK	ANLVL	3		1116.257686	3345.749657	0.000451244	13	N	588	617
Q8BHG1	Parental	YRYIK	LQNGLQALLISDLSNVEGK	TGNAT	2		1006.555283	2011.094967	0.000451244	2	N	114	133
Q8BHG1	Parental	RNKAK	STCSCPDLQPNGQDLGESGR	LARLG	2	C3:+57.021,C5:+57.021	1089.463008	2176.910416	0.000451244	16	N	56	76
Q8BHG1	Parental	DLKEK	WFGTQYSIEDIENSWTELWK	SNFDL	2		1266.590052	2531.164503	0.000823681	5	N	636	656
Q8BHJ5	Exosome	AVVLR	GHESEVFICAWNPVSDLLASGSGDSTAR	IWNLS	3	C9:+57.021	988.1264114	2961.355834	0.000451244	14	N	166	194
Q8BHJ5	Exosome	DSTAR	IWNLSENSTSGPTQLVLR	HCIRE	2		1008.031975	2014.048351	0.000451244	5	N	194	212
Q8BHJ5	Parental	AVVLR	GHESEVFICAWNPVSDLLASGSGDSTAR	IWNLS	3	C9:+57.021	988.1264114	2961.355834	0.000451244	26	N	166	194
Q8BHJ5	Parental	DSTAR	IWNLSENSTSGPTQLVLR	HCIRE	2		1008.031975	2014.048351	0.000451244	20	N	194	212
Q8BHN3	Exosome	LSPYR	ALLDTLQLGPDALTVHLIHEVTK	VLLVL	3		833.1395239	2496.395172	0.000698008	2	N	61	84
Q8BHN3	Exosome	LSPYR	ALLDTLQLGPDALTVHLIHEVTK	VLLVL	4		625.106593	2496.395172	0.000451244	24	N	61	84
Q8BHN3	Exosome	FDVFR	QYASLTGTQALPPLFSLGYHQSR	WNYRD	3		845.7717231	2534.291769	0.000451244	16	N	377	400
Q8BHN3	Exosome	HEVTK	VLLVLELQGLQK	NMTRI	2		676.9297419	1351.843884	0.000451244	15	N	84	96
Q8BHN3	Exosome	QRAPR	VPQESKDPAEGNGAQPEATPGDGDKPEETQEK	AEKDE	4		834.6346286	3334.507314	0.000622848	3	N	185	217
Q8BHN3	Exosome	HSFHR	DLGIFWLNAAETWVDISSNTAGK	TLFGK	2		1254.624426	2507.233251	0.000451244	8	N	309	332
Q8BHN3	Exosome	HSFHR	DLGIFWLNAAETWVDISSNTAGK	TLFGK	3		836.7522171	2507.233251	0.000698008	2	N	309	332
Q8BHN3	Exosome	YVKTR	DGSDYEGWCWPGSASYPDFTNPR	MRAWW	2	C9:+57.021	1332.540533	2663.065465	0.000451244	11	N	493	516
Q8BHN3	Exosome	FLLRR	FSFSGSTLVSSSADPK	GHLET	2		808.8942817	1615.772963	0.000622848	4	N	864	880
Q8BHN3	Exosome	QSYQK	HHGPQTLYLPVTLSSIPVFQR	GGTIV	3		797.4380157	2389.290647	0.001329271	1	N	784	805
Q8BHN3	Exosome	GLYVK	TRDGSDYEGWCWPGSASYPDFTNPR	MRAWW	3	C11:+57.021	974.4125517	2920.214255	0.002453667	1	N	491	516
Q8BHN3	Exosome	LIHPV	SDAGAHGVQVYLPGQEEVWYDIQSYQK	HHGPQ	3		1023.153109	3066.435927	0.002813207	1	N	757	784
Q8BHN3	Parental	LSPYR	ALLDTLQLGPDALTVHLIHEVTK	VLLVL	4		625.106593	2496.395172	0.000451244	25	N	61	84
Q8BHN3	Parental	PRRPR	YRVPDVLVADPPTAR	LSVSG	3		556.9743005	1667.899501	0.000622848	1	N	112	127
Q8BHN3	Parental	FDVFR	QYASLTGTQALPPLFSLGYHQSR	WNYRD	3		845.7717231	2534.291769	0.000451244	10	N	377	400
Q8BHN3	Parental	HEVTK	VLLVLELQGLQK	NMTRI	2		676.9297419	1351.843884	0.000451244	7	N	84	96
Q8BHN3	Parental	QRAPR	VPQESKDPAEGNGAQPEATPGDGDKPEETQEK	AEKDE	3		1112.510238	3334.507314	0.001162105	2	N	185	217
Q8BHN3	Parental	QRAPR	VPQESKDPAEGNGAQPEATPGDGDKPEETQEK	AEKDE	4		834.6346286	3334.507314	0.000451244	22	N	185	217
Q8BHN3	Parental	HSFHR	DLGIFWLNAAETWVDISSNTAGK	TLFGK	2		1254.624426	2507.233251	0.000451244	9	N	309	332
Q8BHN3	Parental	HSFHR	DLGIFWLNAAETWVDISSNTAGK	TLFGK	3		836.7522171	2507.233251	0.000451244	6	N	309	332
Q8BHN3	Parental	YVKTR	DGSDYEGWCWPGSASYPDFTNPR	MRAWW	2	C9:+57.021	1332.540533	2663.065465	0.000451244	6	N	493	516
Q8BHN3	Parental	SPESR	LSFQHDPETSVLILR	KPGVS	3		585.653227	1753.936281	0.000451244	9	N	914	929
Q8BHN3	Parental	TLFGK	MLDYLQGSGETPQTDIR	WMSES	2		962.4599948	1922.90439	0.000622848	1	N	337	354
Q8BIJ6	Exosome	DPKRR	SCQTALAEILDVLVR	AFAPI	3	C2:+57.021	563.3067966	1686.89699	0.000451244	6	N	817	832
Q8BIJ6	Exosome	RNTLR	FLLGNLTGFNPETDSVPVK	NMYVI	2		1024.539102	2047.062604	0.000451244	7	N	731	750
Q8BIJ6	Parental	DPKRR	SCQTALAEILDVLVR	AFAPI	3	C2:+57.021	563.3067966	1686.89699	0.000451244	6	N	817	832
Q8BIQ5	Parental	DRSLR	SVFVGNIPYEATEEQLKDIFSEVGPVVSFR	LVYDR	3		1119.573674	3355.697622	0.000451244	12	N	16	46
Q8BIQ5	Parental	KEELK	SLGTGAPVIESPYGESISPEDAPESISK	AVASL	2		1409.187981	2816.360362	0.000451244	5	N	102	130
Q8BIQ5	Parental	DRSLR	SVFVGNIPYEATEEQLKDIFSEVGPVVSF	RLVYD	3		1067.53997	3199.59651	0.000451244	11	N	16	45
Q8BIQ5	Parental	ESISK	AVASLPPEQMFELMK	QMKLC	2		845.9312995	1689.846999	0.001763695	1	N	130	145
Q8BIW1	Exosome	VSRKK	LLPVLQEALSAYLDSAK	MASGQ	2		916.0147313	1830.013863	0.002212458	1	N	350	367
Q8BIW1	Parental	VSRKK	LLPVLQEALSAYLDSAK	MASGQ	2		916.0147313	1830.013863	0.000451244	2	N	350	367

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BIW1	Parental	FYLTK	TSEAEDIFIPVLNIK	RSELP	2		844.9594247	1687.903249	0.001699387	1	N	44	59
Q8BJ71	Exosome	QVKQR	ILHTLLASGEDALDFTQESEPSYIGDVNPPGR	SSLDS	3		1147.898997	3440.673592	0.000451244	3	N	143	175
Q8BJ71	Exosome	HISQR	LESLSAATTFEPLEPVKDTDIQGFLK	NEKDN	3		950.4993347	2848.474604	0.000451244	3	N	77	103
Q8BJ71	Parental	QVKQR	ILHTLLASGEDALDFTQESEPSYIGDVNPPGR	SSLDS	3		1147.898997	3440.673592	0.000451244	38	N	143	175
Q8BJ71	Parental	HISQR	LESLSAATTFEPLEPVKDTDIQGFLK	NEKDN	3		950.4993347	2848.474604	0.000451244	21	N	77	103
Q8BJ71	Parental	YLWLK	LNQVCFDDDGTSSPQDR	LTLSQ	2	C5:+57.021	977.4160837	1952.816567	0.000451244	22	N	417	434
Q8BJS4	Exosome	SQSPR	VILQPDVHPGNCWAFQGPQGFAVVR	LSARI	3	C12:+57.021	931.4748694	2791.401208	0.000451244	9	N	603	628
Q8BJS4	Exosome	KELGR	LEAQLASLRQELAALTLK	QNSVA	3		656.721641	1967.141523	0.000451244	4	N	427	445
Q8BJS4	Exosome	TYETK	TALLSLFGIPLWYHSQSPR	VILQP	3		729.3972688	2185.168406	0.000451244	4	N	584	603
Q8BJS4	Exosome	ALTLK	QNSVADEVGLLPQK	IQAAR	2		749.3995342	1496.783468	0.000451244	1	N	445	459
Q8BJS4	Parental	SSNMK	HLSPAPQLGPSSDSHTSYY	SESVV	2		1022.47449	2042.933381	0.000622848	25	N	52	71
Q8BJS4	Parental	SSNMK	HLSPAPQLGPSSDSHTSYY	SESVV	3		681.9855935	2042.933381	0.000823681	12	N	52	71
Q8BJS4	Parental	TAESK	ASEDFFGSSSGYSSEDDLAGYTDSDQHSSGSR	LRSAA	3		1116.782686	3347.324658	0.000451244	15	N	133	165
Q8BJS4	Parental	SQSPR	VILQPDVHPGNCWAFQGPQGFAVVR	LSARI	3	C12:+57.021	931.4748694	2791.401208	0.000451244	29	N	603	628
Q8BJS4	Parental	KELGR	LEAQLASLRQELAALTLK	QNSVA	3		656.721641	1967.141523	0.000451244	5	N	427	445
Q8BJS4	Parental	TYETK	TALLSLFGIPLWYHSQSPR	VILQP	3		729.3972688	2185.168406	0.000622848	17	N	584	603
Q8BJS4	Parental	SSNMK	HLSPAPQLGPSSDSHTSYYSESVVR	ESYIG	3		901.1004566	2700.27797	0.002519933	2	N	52	77
Q8BJS4	Parental	ALTLK	QNSVADEVGLLPQK	IQAAR	2		749.3995342	1496.783468	0.002663018	1	N	445	459
Q8BJS4	Parental	EDLRR	DTVAHIQEELATLR	AEHHQ	3		532.6182938	1594.831481	0.000451244	5	N	363	377
Q8BJS4	Parental	TAESK	ASEDFFGSSSGYSSEDDLAGY	TDSDQ	2		1095.935258	2189.854915	0.001871652	1	N	133	154
Q8BJS4	Parental	VSLAR	SALLDDHLHSEPYWSGDLR	GRRRR	3		737.6875476	2210.039243	0.002212458	1	N	91	110
Q8BJU0	Parental	DNRKR	LAYAIIQFLHGQLR	HGGLS	3		548.319631	1641.935493	0.000735798	2	N	6	20
Q8BJU0	Parental	HLYGK	AIELNPANAVYFCNR	AAAYS	2	C13:+57.021	876.4306115	1750.845623	0.000451244	2	N	117	132
Q8BJW6	Exosome	AKTIK	YQAVPSEVPSEEPK	VATAY	2		780.3835498	1558.7515	0.002212458	1	N	427	441
Q8BJW6	Exosome	TEVDK	TGASYYGEQTLHYIATNGESAVVQLPK	NGPIY	3		966.4825666	2896.4243	0.000451244	1	N	245	272
Q8BJW6	Parental	NQLEK	IQKETALLQELEDLELGV	-	2		1021.057325	2040.099049	0.001943752	1	N	563	581
Q8BJY1	Exosome	THHGR	QYLAQEGVIDQISNIIVGADSDPFSGFYLPGFVK	FFGNL	3		1229.958076	3686.850828	0.000451244	15	N	241	275
Q8BJY1	Exosome	SQIGR	IVENSEAVTEILNNAELLK	QIVYC	2		1050.065681	2098.115762	0.000451244	25	N	109	128
Q8BJY1	Exosome	SQIGR	IVENSEAVTEILNNAELLK	QIVYC	3		700.3797206	2098.115762	0.001162105	3	N	109	128
Q8BJY1	Exosome	YLRLR	AYLSEGPYYVKPVATTAVEGAD	-	2		1151.068421	2300.121241	0.000451244	1	N	482	504
Q8BJY1	Exosome	LEELR	ALQSVVQAVPLHELR	EQAAE	3		553.990062	1658.946786	0.000622848	2	N	23	38
Q8BJY1	Parental	THHGR	QYLAQEGVIDQISNIIVGADSDPFSGFYLPGFVK	FFGNL	3		1229.958076	3686.850828	0.000451244	21	N	241	275
Q8BJY1	Parental	SQIGR	IVENSEAVTEILNNAELLK	QIVYC	2		1050.065681	2098.115762	0.000451244	16	N	109	128
Q8BJY1	Parental	SQIGR	IVENSEAVTEILNNAELLK	QIVYC	3		700.3797206	2098.115762	0.001943752	1	N	109	128
Q8BJY1	Parental	YLRLR	AYLSEGPYYVKPVATTAVEGAD	-	2		1151.068421	2300.121241	0.000451244	8	N	482	504
Q8BK64	Exosome	EELYR	VFTTQELVQAFTHAPAALEADR	GGKFH	3		805.748807	2414.223021	0.000451244	29	N	224	246
Q8BK64	Parental	IPTCK	ITLKETFLTSPEELYR	VFTTQ	3		647.3512137	1939.030241	0.001162105	1	N	208	224
Q8BK64	Parental	EELYR	VFTTQELVQAFTHAPAALEADR	GGKFH	3		805.748807	2414.223021	0.000451244	10	N	224	246
Q8BK67	Exosome	VEAPR	LIEALSHEAIVLAACGR	NHTLA	2	C15:+57.021	911.9961186	1821.976637	0.000451244	18	N	192	209
Q8BK67	Exosome	VEAPR	LIEALSHEAIVLAACGR	NHTLA	3	C15:+57.021	608.3333458	1821.976637	0.000622848	20	N	192	209
Q8BK67	Exosome	ATAGK	AAGAAAIITEPEHTK	ERVKL	2		740.3942519	1478.772904	0.002519933	3	N	75	90
Q8BK67	Exosome	DSQKR	VFSWGFGGYGR	LGHAE	2		616.7965192	1231.577438	0.000451244	22	N	348	359
Q8BK67	Exosome	GVRVR	TVVSGSCAAHSLLITTEGK	LWSWG	2	C7:+57.021	965.9990553	1929.982511	0.000451244	17	N	149	168
Q8BK67	Exosome	GVRVR	TVVSGSCAAHSLLITTEGK	LWSWG	3	C7:+57.021	644.3353035	1929.982511	0.000622848	5	N	149	168
Q8BK67	Exosome	ARAQR	IEYDCELVPR	RVAIF	2	C5:+57.021	647.3111106	1292.606621	0.000622848	12	N	298	308
Q8BK67	Exosome	AACGR	NHTLALTDTGSVFAFGENK	MGQLG	3		674.6696054	2020.985416	0.000622848	4	N	209	228
Q8BK67	Exosome	LACGK	SSIIVAADESTISWGPSPTFGELGYGDHKPK	SSTAA	3		1082.87049	3245.588071	0.001162105	5	N	437	468
Q8BK67	Exosome	NVVVR	DVACGANHTLVLDSQKR	VFSWG	3	C4:+57.021	628.651626	1882.931478	0.000451244	10	N	331	348
Q8BK67	Exosome	LMDCK	GNLYSFGCPEYGQLGHNSDGK	FIARA	2	C8:+57.021	1150.505764	2298.995929	0.000451244	10	N	270	291
Q8BK67	Exosome	LMDCK	GNLYSFGCPEYGQLGHNSDGK	FIARA	3	C8:+57.021	767.3397763	2298.995929	0.000622848	2	N	270	291
Q8BK67	Exosome	ATAGK	AAGAAAIITEPEHTKER	VKLEG	3		588.9800027	1763.916608	0.000451244	2	N	75	92
Q8BK67	Parental	VEAPR	LIEALSHEAIVLAACGR	NHTLA	2	C15:+57.021	911.9961186	1821.976637	0.000451244	1	N	192	209
Q8BK67	Parental	VEAPR	LIEALSHEAIVLAACGR	NHTLA	3	C15:+57.021	608.3333458	1821.976637	0.00091018	3	N	192	209
Q8BK67	Parental	GVRVR	TVVSGSCAAHSLLITTEGK	LWSWG	2	C7:+57.021	965.9990553	1929.982511	0.001162105	2	N	149	168
Q8BK67	Parental	LMDCK	GNLYSFGCPEYGQLGHNSDGK	FIARA	3	C8:+57.021	767.3397763	2298.995929	0.002981883	1	N	270	291
Q8BKC5	Exosome	ANVVR	QVQTSGGLWTECIAQLSPEQQAAIQELLNSA	-	3	C12:+57.021	1124.224673	3369.65062	0.000451244	24	N	1066	1097
Q8BKC5	Exosome	VLLRR	LLSSAFDEVYPALPSDVQTAIK	SELLM	2		1182.62082	2363.226041	0.000451244	35	N	68	90
Q8BKC5	Exosome	VLLRR	LLSSAFDEVYPALPSDVQTAIK	SELLM	3		788.7498136	2363.226041	0.000451244	3	N	68	90
Q8BKC5	Exosome	QKGTK	LVLEQVVTSIASVADTAEEK	FVPYY	2		1051.565514	2101.115427	0.000451244	22	N	506	526
Q8BKC5	Exosome	QKGTK	LVLEQVVTSIASVADTAEEK	FVPYY	3		701.3796092	2101.115427	0.000451244	39	N	506	526
Q8BKC5	Exosome	APEAK	TKENVNATENCISAVGK	IMKFK	2	C11:+57.021	917.9521051	1833.88861	0.000451244	2	N	961	978
Q8BKC5	Exosome	APEAK	TKENVNATENCISAVGK	IMKFK	3	C11:+57.021	612.3040034	1833.88861	0.000451244	14	N	961	978
Q8BKC5	Exosome	LRQVK	RQDEDYDEQVEESLQDEDDNDVYILTK	VSDIL	3		1101.815216	3302.422247	0.000451244	26	N	814	841
Q8BKC5	Exosome	PWPDR	QWGLCIFDDIVEHCSPASFK	YAEYF	3	C5:+57.021,C14:+57.021	803.7051364	2408.092009	0.000451244	3	N	881	901
Q8BKC5	Exosome	AELAR	NLIDEDGNNQWPEGLK	FLFDS	2		921.4373764	1840.859153	0.000451244	20	N	118	134

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BKC5	Exosome	YILTK	VSDILHSIFSSYK	EKVLP	3		499.2650804	1494.771841	0.000451244	5	N	841	854
Q8BKC5	Exosome	LLRGK	TIECISLIGLAVGK	EKFMQ	2	C4:+57.021	737.4211924	1472.826785	0.000451244	17	N	556	570
Q8BKC5	Exosome	VALFK	HFADLLPGFLQAVNDSCYQNDDSVLK	SLVEI	3	C17:+57.021	989.471519	2965.391157	0.000451244	15	N	212	238
Q8BKC5	Exosome	TLSAR	ATAAFILANEHNVALFK	HFADL	3		610.6689885	1828.983565	0.000735798	9	N	195	212
Q8BKC5	Exosome	NVVRK	QAEETYENIPGR	SKITF	2		703.8314844	1405.647369	0.000451244	1	N	27	39
Q8BKC5	Exosome	NNMQR	QLALEVIVTLSETAAAMLR	KHTSL	2	[0:-17.027	1006.558755	2011.10191	0.002019181	1	N	276	295
Q8BKC5	Parental	ANVVR	QVQTSGGLWTECIAQLSPEQQAAIQELLNSA	-	3	C12:+57.021	1124.224673	3369.65062	0.000451244	19	N	1066	1097
Q8BKC5	Parental	ANVVR	QVQTSGGLWTECIAQLSPEQQAAIQELLNSA	-	3	Q1:-17.027,C12:+57.021	1118.549007	3352.62362	0.000451244	3	N	1066	1097
Q8BKC5	Parental	VLLRR	LLSSAFDEVYPALPSDVQTAIK	SELLM	2		1182.62082	2363.226041	0.000698008	1	N	68	90
Q8BKC5	Parental	QKGTK	LVLEQVVTSIASVADTAEEK	FVPYY	3		701.3796092	2101.115427	0.002663018	1	N	506	526
Q8BKC5	Parental	APEAK	TKENVNATENCISAVGK	IMKFK	3	C11:+57.021	612.3040034	1833.88861	0.000622848	1	N	961	978
Q8BKC5	Parental	LRQVK	RQDEDYDEQVEESLQDEDDNDVYILTK	VSDIL	3		1101.815216	3302.422247	0.000979378	3	N	814	841
Q8BL97	Exosome	DSETK	VYVGNLGTGAGKGELER	AFSYY	2		860.4553722	1718.895144	0.000451244	8	N	41	58
Q8BL97	Exosome	DSETK	VYVGNLGTGAGKGELER	AFSYY	3		573.9728481	1718.895144	0.001591523	1	N	41	58
Q8BL97	Exosome	VWIAR	NPPGFAFVEFEDPRDAEDAVR	GLDGK	2		1189.556543	2377.097486	0.001162105	5	N	73	94
Q8BL97	Exosome	VWIAR	NPPGFAFVEFEDPRDAEDAVR	GLDGK	3		793.3736287	2377.097486	0.000451244	33	N	73	94
Q8BL97	Parental	DSETK	VYVGNLGTGAGKGELER	AFSYY	2		860.4553722	1718.895144	0.000451244	19	N	41	58
Q8BL97	Parental	DSETK	VYVGNLGTGAGKGELER	AFSYY	3		573.9728481	1718.895144	0.001352548	3	N	41	58
Q8BL97	Parental	VWIAR	NPPGFAFVEFEDPRDAEDAVR	GLDGK	2		1189.556543	2377.097486	0.000451244	15	N	73	94
Q8BL97	Parental	VWIAR	NPPGFAFVEFEDPRDAEDAVR	GLDGK	3		793.3736287	2377.097486	0.000451244	28	N	73	94
Q8BL97	Parental	GELER	AFSYYGPLR	TVWIA	2		537.2748883	1072.534177	0.000451244	8	N	58	67
Q8BL97	Parental	VWIAR	NPPGFAFVEFEDPR	DAEDA	2		811.3864268	1620.757254	0.000451244	2	Y	73	87
Q8BL97	Parental	VWIAR	NPPGFAFVEFEDPR	DAEDA	3		541.2602179	1620.757254	0.002296037	2	Y	73	87
Q8BMA6	Exosome	QMRLR	SGGTEGLLAEKLEALITQTR	AKQAA	3		696.3834651	2086.126995	0.000451244	2	N	265	285
Q8BMA6	Exosome	GGASK	NSLKDLPDVQELITQVR	SEKCS	3		656.697384	1967.068752	0.002663018	1	N	503	520
Q8BMA6	Parental	IDKVR	IFLLGLADNEAAIVQAESEETKER	LFESM	3		882.7927411	2645.354823	0.000451244	13	N	310	334
Q8BMA6	Parental	SAGSK	ANKEFGDSLSLEILQIIK	ESQQQ	3		673.3776514	2017.109554	0.001162105	4	N	48	66
Q8BMA6	Parental	QMRLR	SGGTEGLLAEKLEALITQTR	AKQAA	3		696.3834651	2086.126995	0.001162105	4	N	265	285
Q8BMA6	Parental	KNSLK	DLPDVQELITQVR	SEKCS	2		763.4151843	1524.814769	0.002453667	1	N	507	520
Q8BMD8	Parental	WNEWR	DYFLFNPVTDIEEIIR	FWKHS	2		992.5072704	1982.998941	0.000451244	1	N	148	164
Q8BMD8	Parental	RALDR	NGDGVVDIGELQQGLQSLGIPLGQDAEEK	IFTTG	3		993.8355572	2978.483272	0.000451244	12	N	33	62
Q8BMJ2	Exosome	DKLKR	EIELYGCPPDFPEEEEEEEESSAKPGDIVVR	DKAKG	3	C7:+57.021	1193.538652	3577.592555	0.000451244	15	N	108	139
Q8BMJ2	Exosome	IPKEK	LDQLKQEFEFWYPVDLR	ASGKD	3		742.713034	2225.115702	0.000823681	1	N	656	673
Q8BMJ2	Parental	DKLKR	EIELYGCPPDFPEEEEEEEESSAKPGDIVVR	DKAKG	3	C7:+57.021	1193.538652	3577.592555	0.000451244	39	N	108	139
Q8BMJ2	Parental	GLGTR	LPWDEQWLIESLSDSTIY	MAFYT	2		1098.031307	2194.047013	0.002080925	3	N	584	602
Q8BMJ2	Parental	DIVKF	SEAEHWLDYFPPLAVQDLK	TIGLK	3		753.3763105	2257.105531	0.000451244	1	N	176	195
Q8BMJ3	Parental	PEHAK	INETDTFGPGDDDEIQFDDIGDDDEDIDDI	-	3		1120.118741	3357.332823	0.000451244	12	N	114	144
Q8BMJ3	Parental	KLRKK	VWINTSDIILVGLR	DYQDN	2		799.9673871	1597.919174	0.002884417	1	N	68	82
Q8BMK4	Exosome	LKELK	QSLGELPGTVESLQEQVLSLLSQDQAQAEGLPPQDFLDR	LSSLD	3		1412.715592	4235.123375	0.000979378	2	N	466	505
Q8BMK4	Parental	GVEQK	VQSLQATFGTFESLLR	NSQHK	2		898.9812228	1795.946846	0.000451244	20	N	140	156
Q8BMK4	Parental	LKELK	QSLGELPGTVESLQEQVLSLLSQDQAQAEGLPPQDFLDR	LSSLD	3		1412.715592	4235.123375	0.000451244	33	N	466	505
Q8BMK4	Parental	LKELK	QSLGELPGTVESLQEQVLSLLSQDQAQAEGLPPQDFLDR	LSSLD	4		1059.788644	4235.123375	0.000622848	10	N	466	505
Q8BMK4	Parental	LKELK	QSLGELPGTVESLQEQVLSLLSQDQAQAEGLPPQDFLDR	LSSLD	3	Q1:-17.027	1407.039925	4218.096375	0.001463592	1	N	466	505
Q8BMK4	Parental	LKELK	QSLGELPGTVESLQEQVLSLLSQDQAQAEGLPPQDFLDR	LSSLD	3	[0:-17.027	1407.039925	4218.096375	0.001264573	3	N	466	505
Q8BMK4	Parental	YTEVR	ELVSLKQEQQAFK	QAADS	2		774.425552	1546.835504	0.00091018	4	N	306	319
Q8BMK4	Parental	EVLQK	LQNEILKDLSDGIHVVK	DARER	4		481.0248059	1920.068024	0.000451244	1	N	185	202
Q8BMK4	Parental	ASTVR	SLGETQLALSSDLK	ELKQS	2		731.3939175	1460.772235	0.000451244	12	N	449	463
Q8BMK4	Parental	VASAR	HTESLESLLSK	SQEYE	2		622.3305889	1242.645578	0.000662267	1	N	409	420
Q8BMK4	Parental	ELKQS	LGELPGTVESLQEQVLSLLSQDQAQAEGLPPQDFLDR	LSSLD	3		1341.018723	4020.032769	0.000823681	1	N	468	505
Q8BMK4	Parental	LESAK	GLLDDLRNDLDR	LFLKV	3		472.2482008	1413.721202	0.000979378	4	N	551	563
Q8BML9	Parental	FQFER	LGYFSVDPDSHQGQIVFNR	TVTLK	3		727.0242711	2178.049413	0.000451244	2	N	745	764
Q8BML9	Parental	STQLR	EAATQAHQILGSTIDKATGVLL	YDLVS	2		1119.110954	2236.206308	0.001839721	1	N	34	56
Q8BMS1	Exosome	GVDPK	KLDALTTGFGFPVGAATLADEVGVDVAQHVAEDLGK	AFGER	3		1204.625097	3610.851891	0.000622848	5	N	569	605
Q8BMS1	Exosome	GVDPK	KLDALTTGFGFPVGAATLADEVGVDVAQHVAEDLGK	AFGER	4		903.7207727	3610.851891	0.000451244	5	N	569	605
Q8BMS1	Exosome	TKDRK	TVLGVPEVLLGILPGAGGTQR	LPKMV	2		1024.099661	2046.183722	0.001591523	3	N	166	187
Q8BMS1	Parental	IDAVK	AGLEQGSDAGYLAESQK	FGELA	2		862.4108273	1722.806055	0.000451244	36	N	309	326
Q8BMS1	Parental	DRKTV	LGVPEVLLGILPGAGGTQR	LPKMV	2		924.0416148	1846.06763	0.000451244	15	N	168	187
Q8BMS1	Parental	DRKTV	LGVPEVLLGILPGAGGTQR	LPKMV	3		616.3636765	1846.06763	0.000451244	9	N	168	187
Q8BMS1	Parental	GVDPK	KLDALTTGFGFPVGAATLADEVGVDVAQHVAEDLGK	AFGER	3		1204.625097	3610.851891	0.000451244	31	N	569	605
Q8BMS1	Parental	GVDPK	KLDALTTGFGFPVGAATLADEVGVDVAQHVAEDLGK	AFGER	4		903.7207727	3610.851891	0.000451244	27	N	569	605
Q8BMS1	Parental	RVITR	FVNEAVLCLQEGILATPAEGDIGAVFGLGFPPCLGGPFR	FVDLY	3	C8:+57.021,C33:+57.021	1363.692151	4088.053053	0.002453667	1	N	680	719
Q8BMS1	Parental	SPEER	TIEYLEEVAVNFAK	GLADR	2		813.4252177	1624.834835	0.000622848	2	N	235	249
Q8BMS1	Parental	RTIEY	LEEVAVNFAK	GLADR	2		560.3063854	1118.597171	0.002981883	1	N	239	249
Q8BMS1	Parental	TKDRK	TVLGVPEVLLGILPGAGGTQR	LPKMV	2		1024.099661	2046.183722	0.000451244	7	N	166	187
Q8BMS1	Parental	IDAVK	AGLEQGSDAGYLAESQKFGELALTK	ESKAL	2		1292.151005	2582.286409	0.001871652	1	N	309	334

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BMS1	Parental	IDAVK	AGLEQGSDAGYLAESQKFGELALTK	ESKAL	3		861.7699364	2582.286409	0.000451244	10	N	309	334
Q8BMS1	Parental	HKVLK	EVESVTPEHCIFASNTSALPINQIAAVSK	RPEKV	3	C10:+57.021	1038.192533	3111.5542	0.001229886	1	N	460	489
Q8BMS1	Parental	IDAVK	AGLEQGSDAGYLAESQKF	GELAL	2		935.9450343	1869.874469	0.000451244	4	N	309	327
Q8BND5	Exosome	MHQVR	SPSNAILWLWTSHNR	VNARL	2		891.4582492	1780.900898	0.000451244	3	N	471	486
Q8BND5	Exosome	MHQVR	SPSNAILWLWTSHNR	VNARL	3		594.6414328	1780.900898	0.000451244	11	N	471	486
Q8BND5	Exosome	QWPPR	ELCSACHNELNGQVPLWDLGATLNFLK	AHFSP	3	C3:+57.021,C6:+57.021	1033.839283	3098.494448	0.000451244	56	N	509	536
Q8BND5	Exosome	LNFLK	AHFSPANIVIDSSASR	HTGRR	2		836.4266147	1670.837629	0.000451244	6	N	536	552
Q8BND5	Exosome	LQAMR	SYVQFFFGCR	DCADH	2	C9:+57.021	655.8032557	1309.590911	0.000451244	14	N	443	453
Q8BND5	Exosome	VLTEK	VNWVGCQGSEPHFR	GFPCS	2	C6:+57.021	836.8863711	1671.757142	0.002981883	1	N	390	404
Q8BND5	Exosome	DLVNK	FGVTDFPSCYLLLR	NGSVS	2	C9:+57.021	844.4295488	1686.843498	0.000823681	7	N	231	245
Q8BND5	Exosome	ANDVK	DWRPALNLAVLDCAEETNSAVCR	EFNIA	3	C13:+57.021,C22:+57.021	887.4235804	2659.247341	0.000451244	9	N	91	114
Q8BND5	Exosome	SYLGR	EVTLDLSQYHAVAVR	RVLNT	2		850.9524653	1699.889331	0.002145581	3	N	204	219
Q8BND5	Exosome	SAVCR	EFNIAGFPTVR	FFQAF	2		625.8305591	1249.645518	0.002296037	2	N	114	125
Q8BND5	Exosome	ADRSK	IYMADLESALHYILR	VEVGK	3		603.3190797	1806.933839	0.000451244	1	N	301	316
Q8BND5	Parental	MHQVR	SPSNAILWLWTSHNR	VNARL	3		594.6414328	1780.900898	0.000451244	15	N	471	486
Q8BND5	Parental	QWPPR	ELCSACHNELNGQVPLWDLGATLNFLK	AHFSP	3	C3:+57.021,C6:+57.021	1033.839283	3098.494448	0.000451244	45	N	509	536
Q8BND5	Parental	LNFLK	AHFSPANIVIDSSASR	HTGRR	2		836.4266147	1670.837629	0.000451244	7	N	536	552
Q8BND5	Parental	LNFLK	AHFSPANIVIDSSASR	HTGRR	3		557.9536765	1670.837629	0.000622848	7	N	536	552
Q8BND5	Parental	LQAMR	SYVQFFFGCR	DCADH	2	C9:+57.021	655.8032557	1309.590911	0.000451244	4	N	443	453
Q8BND5	Parental	DLVNK	FGVTDFPSCYLLLR	NGSVS	2	C9:+57.021	844.4295488	1686.843498	0.000451244	2	N	231	245
Q8BND5	Parental	ANDVK	DWRPALNLAVLDCAEETNSAVCR	EFNIA	3	C13:+57.021,C22:+57.021	887.4235804	2659.247341	0.000451244	11	N	91	114
Q8BND5	Parental	FTRNK	ADYLALVFEREDSYLGR	EVTLD	3		673.0062175	2015.995253	0.001839721	1	N	187	204
Q8BP47	Exosome	HFFDR	GYCEVTTPTLVQTQVEGGATLFK	LDYFG	2	C3:+57.021	1250.125713	2498.235825	0.000451244	18	N	274	297
Q8BP47	Exosome	EGYKR	EGIDPAPYYWYTDQR	KYGTC	2		937.4237377	1872.831875	0.000451244	12	N	502	517
Q8BP47	Exosome	DRVLK	SPVASIVYELNPNFKPPK	RPFRR	2		1000.54673	1999.07786	0.00091018	4	N	378	396
Q8BP47	Exosome	TDQRK	YGTCPHGGYGLGLER	FLSWI	2	C4:+57.021	818.8807544	1635.745909	0.001264573	1	N	518	533
Q8BP47	Exosome	HDVKK	EDGTFYEFGDDIPEAPER	LMTDT	2		1043.947971	2085.880342	0.000622848	3	N	418	436
Q8BP47	Parental	EGYKR	EGIDPAPYYWYTDQR	KYGTC	2		937.4237377	1872.831875	0.000622848	6	N	502	517
Q8BP47	Parental	EEAKK	IIIKNDPSLPEPACVK	ISALE	2	C14:+57.021	897.4954201	1792.97524	0.000451244	7	N	111	127
Q8BP47	Parental	GGSMR	SWDSEEILEGYKR	EGIDP	3		537.9270159	1610.757648	0.000622848	4	N	489	502
Q8BP47	Parental	HFFDR	GYCEVTTPTLVQTQVEGGATLF	KLDYF	2	C3:+57.021	1186.078231	2370.140862	0.000451244	15	N	274	296
Q8BP47	Parental	TDQRK	YGTCPHGGYGLGLER	FLSWI	2	C4:+57.021	818.8807544	1635.745909	0.000662267	1	N	518	533
Q8BP47	Parental	SSQLY	LETCLPALGDVFCIAQSYR	AEQSR	2	C4:+57.021,C13:+57.021	1107.040166	2212.064732	0.000451244	8	N	314	333
Q8BP47	Parental	PFLTF	EDLLNRLEDLVCDVVDR	VLKSP	3	C12:+57.021	691.6812509	2072.020353	0.000622848	2	N	358	375
Q8BP47	Parental	HDVKK	EDGTFYEFGDDIPEAPER	LMTDT	2		1043.947971	2085.880342	0.000622848	3	N	418	436
Q8BP47	Parental	EHDVK	KEDGTFYEFGDDIPEAPER	LMTDT	2		1107.995453	2213.975305	0.0025889	2	N	417	436
Q8BP47	Parental	SRTRR	HLAEFTHVEAECPFLTFEDLLNRLEDLVCDVVDR	VLKSP	4	C12:+57.021,C29:+57.021	1026.247869	4100.960275	0.000451244	2	N	341	375
Q8BP56	Exosome	GEEVK	QADVVLLGYPVPFPLTPDIR	RKNLE	2		1105.615144	2209.214688	0.000451244	4	N	497	517
Q8BP56	Exosome	EVTAR	AEPWAPLLEAELWPSLAHLPLTPGQK	VSFPH	3		955.5168829	2863.527249	0.000823681	8	N	649	675
Q8BPU7	Exosome	EIKLR	LLDLENIQIPDAPPPIPK	EPSNY	2		992.0622129	1982.108826	0.000662267	13	N	697	715
Q8BPU7	Exosome	SPNHK	VLHYGDLEESPQGEVPHDSLQDKLPVADIK	AVVTG	4		832.9233747	3327.662299	0.000451244	5	N	584	614
Q8BPU7	Exosome	DLYQK	VAQEITIGQLIPHLQGTDQEIQTYTIAVINALFLK	APDER	3		1293.714246	3878.119339	0.001162105	1	N	218	253
Q8BPU7	Parental	EIKLR	LLDLENIQIPDAPPPIPK	EPSNY	2		992.0622129	1982.108826	0.000451244	19	N	697	715
Q8BPU7	Parental	SPNHK	VLHYGDLEESPQGEVPHDSLQDKLPVADIK	AVVTG	3		1110.228566	3327.662299	0.000451244	1	N	584	614
Q8BPU7	Parental	SPNHK	VLHYGDLEESPQGEVPHDSLQDKLPVADIK	AVVTG	4		832.9233747	3327.662299	0.000451244	10	N	584	614
Q8BPU7	Parental	DLYQK	VAQEITIGQLIPHLQGTDQEIQTYTIAVINALFLKAPDER	RQEMA	4		1112.602766	4446.379864	0.002813207	1	N	218	258
Q8BPU7	Parental	EIKLR	LLDLENIQIPDAPPPIPKEPSNYDFVYDCN	-	3	C29:+57.021	1162.897675	3485.669624	0.000451244	1	N	697	727
Q8BPU7	Parental	DLYQK	VAQEITIGQLIPHLQGTDQEIQTYTIAVINALFLK	APDER	3		1293.714246	3878.119339	0.000451244	9	N	218	253
Q8BPU7	Parental	DLYQK	VAQEITIGQLIPHLQGTDQEIQTYTIAVINALFLK	APDER	4		970.5376348	3878.119339	0.000979378	3	N	218	253
Q8BQ30	Parental	RRRAK	LGLPPGEGSPVPGNAEAGPPDPDESAVLLEAIGPVHQNR	FIQQE	3		1285.317215	3852.928244	0.0007646	4	N	50	89
Q8BQ30	Parental	SRPLR	AQQNLCSGPSPLPPEHSGTEGSR	QQEEE	3	C6:+57.021	802.7086398	2405.102519	0.000451244	3	N	371	394
Q8BQ46	Exosome	FGGHR	DYGPRPDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFK	QIGII	3		1402.960261	4205.857383	0.000451244	20	N	214	253
Q8BQ46	Parental	PPSAK	AAIDWFDGKEFHGNIIK	VSFAT	3		654.3358979	1959.984294	0.000451244	1	N	295	312
Q8BQ46	Parental	PPSAK	AAIDWFDGKEFHGNIIK	VSFAT	4		491.0038734	1959.984294	0.000823681	1	N	295	312
Q8BQ46	Parental	FGGHR	DYGPRPDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFK	QIGII	3		1402.960261	4205.857383	0.000451244	44	N	214	253
Q8BQ46	Parental	PPSAK	AAIDWFDGKEF	HGNII	2		649.8067496	1297.597899	0.001654178	4	Y	295	306
Q8BQ46	Parental	TGKPK	GEATVSFDDPPSAK	AAIDW	2		710.8336927	1419.651785	0.001763695	1	Y	281	295
Q8BQ47	Parental	TGKEK	ISDGQEEADDEEEEEEEEITK	TSGNP	2		1226.996438	2451.977275	0.000451244	11	N	212	233
Q8BQ47	Parental	QKGVK	VDLGIPLELWDEPSVEVTFLK	KQCET	2		1200.141389	2398.267177	0.0025889	1	N	138	159
Q8BRF7	Exosome	LRDAR	NSLFTGDPLGTGQFSFQRPLLVLVDR	NIDLA	3		959.8472917	2876.518475	0.000451244	10	N	234	260
Q8BRF7	Exosome	CQDLR	NQLYESYYLNFISAISR	SKLED	2		1041.021076	2080.026553	0.000451244	2	N	104	121
Q8BRF7	Exosome	EQYKK	ALTDAGCNLSPLQYIK	QWKAF	2	C7:+57.021	882.4537523	1762.891905	0.000451244	4	N	475	491
Q8BRF7	Exosome	SAISR	SKLEDIANAALAASAVTQVAK	VFDQY	3		691.0518268	2070.132081	0.000622848	3	N	121	142
Q8BRF7	Parental	LRDAR	NSLFTGDPLGTGQFSFQRPLLVLVDR	NIDLA	3		959.8472917	2876.518475	0.000451244	3	N	234	260
Q8BRF7	Parental	WQKHK	GSPFPEVAESVQQELESYR	AQEDE	2		1076.513812	2151.012025	0.000451244	1	N	327	346

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BRF7	Parental	CQDLR	NQLYESYYLNFISAISR	SKLED	2		1041.021076	2080.026553	0.000451244	5	N	104	121
Q8BRF7	Parental	EQYKK	ALTDAGCNLSPLQYIK	QWKAF	2	C7:+57.021	882.4537523	1762.891905	0.002727428	1	N	475	491
Q8BRN9	Parental	ATAQK	LASEDAALVDDDEESDTPAQAPLAK	KPAQT	2		1286.101374	2570.187149	0.000451244	3	N	469	494
Q8BRN9	Parental	EVKVR	LREPLSSQDVQTVTENWLVLEPR	GL-	3		903.8122471	2708.413341	0.001591523	1	N	823	846
Q8BT60	Exosome	KPAGK	GSITISAEEIKDNR	VVLFE	2		766.8998984	1531.784197	0.000451244	7	N	125	139
Q8BT60	Exosome	LPQIR	LYGPTNFSPIINHVAR	FAAAA	3		600.3253332	1797.9526	0.000451244	16	N	390	406
Q8BT60	Exosome	EVAIR	DIVQFVPFR	QFQNA	2		560.811638	1119.607676	0.000451244	25	Y	484	493
Q8BT60	Exosome	GGSLR	APSGEVAIRDIVQFVPFR	QFQNA	3		667.7025808	2000.084342	0.000451244	22	N	475	493
Q8BT60	Exosome	DIDNK	TIELSDDDFLGECEVTLGQIVSSK	KLTRP	2	C13:+57.021	1328.139214	2654.262828	0.000451244	35	N	85	109
Q8BT60	Exosome	DIDNK	TIELSDDDFLGECEVTLGQIVSSK	KLTRP	3	C13:+57.021	885.762076	2654.262828	0.000451244	21	N	85	109
Q8BT60	Exosome	QNAPK	EALAQCVLAEIPQQVVGY	FNTYK	2	C6:+57.021	994.5117985	1987.007997	0.000870037	2	N	500	518
Q8BT60	Exosome	QNAPK	EALAQCVLAEIPQQVVGY	FNTYK	3	C6:+57.021	663.343799	1987.007997	0.000622848	5	N	500	518
Q8BT60	Exosome	QNAPK	EALAQCVLAEIPQQVVGYFNTYK	LLPPK	2	C6:+57.021	1321.170454	2640.325309	0.000451244	24	N	500	523
Q8BT60	Exosome	QNAPK	EALAQCVLAEIPQQVVGYFNTYK	LLPPK	3	C6:+57.021	881.1162363	2640.325309	0.000451244	29	N	500	523
Q8BT60	Exosome	NHVAR	FAAAATQQQTASQYFVLLIITDGVITDLDETR	QAIVN	3		1167.270543	3498.788228	0.000451244	20	N	406	438
Q8BT60	Exosome	DVTSK	SDPLCVLFLNTSGHQWYEVER	TERIK	2	C5:+57.021	1275.608021	2549.200443	0.000823681	4	N	26	47
Q8BT60	Exosome	DVTSK	SDPLCVLFLNTSGHQWYEVER	TERIK	3	C5:+57.021	850.7412809	2549.200443	0.000451244	37	N	26	47
Q8BT60	Exosome	QCVTK	VELNVSCNNLLDADVTSK	SDPLC	2	C7:+57.021	995.9914273	1989.967255	0.000451244	8	N	8	26
Q8BT60	Exosome	KTIEL	SDDDFLGECEVTLGQIVSSK	KLTRP	2	C9:+57.021	1100.010014	2198.004428	0.001839721	2	N	89	109
Q8BT60	Exosome	KEASR	SSPVEYECINEK	KRQKK	2	C8:+57.021	727.8273218	1453.639044	0.000451244	11	N	241	253
Q8BT60	Parental	KPAGK	GSITISAEEIKDNR	VVLFE	2		766.8998984	1531.784197	0.000451244	31	N	125	139
Q8BT60	Parental	KPAGK	GSITISAEEIKDNR	VVLFE	3		511.6025323	1531.784197	0.000451244	2	N	125	139
Q8BT60	Parental	LPQIR	LYGPTNFSPIINHVAR	FAAAA	2		899.9840998	1797.9526	0.000451244	24	N	390	406
Q8BT60	Parental	LPQIR	LYGPTNFSPIINHVAR	FAAAA	3		600.3253332	1797.9526	0.000622848	12	N	390	406
Q8BT60	Parental	EVAIR	DIVQFVPFR	QFQNA	2		560.811638	1119.607676	0.000698008	12	Y	484	493
Q8BT60	Parental	GGSLR	APSGEVAIRDIVQFVPFR	QFQNA	3		667.7025808	2000.084342	0.000451244	19	N	475	493
Q8BT60	Parental	DIDNK	TIELSDDDFLGECEVTLGQIVSSK	KLTRP	2	C13:+57.021	1328.139214	2654.262828	0.000451244	40	N	85	109
Q8BT60	Parental	DIDNK	TIELSDDDFLGECEVTLGQIVSSK	KLTRP	3	C13:+57.021	885.762076	2654.262828	0.000451244	25	N	85	109
Q8BT60	Parental	QNAPK	EALAQCVLAEIPQQVVGY	FNTYK	2	C6:+57.021	994.5117985	1987.007997	0.000451244	4	N	500	518
Q8BT60	Parental	QNAPK	EALAQCVLAEIPQQVVGY	FNTYK	3	C6:+57.021	663.343799	1987.007997	0.000451244	13	N	500	518
Q8BT60	Parental	VQKLK	FGIYDIDNKTIELSDDDFLGECEVTLGQIVSSK	KLTRP	3	C22:+57.021	1240.933113	3719.77594	0.000451244	4	N	76	109
Q8BT60	Parental	QNAPK	EALAQCVLAEIPQQVVGYFNTYK	LLPPK	2	C6:+57.021	1321.170454	2640.325309	0.000451244	44	N	500	523
Q8BT60	Parental	QNAPK	EALAQCVLAEIPQQVVGYFNTYK	LLPPK	3	C6:+57.021	881.1162363	2640.325309	0.000451244	37	N	500	523
Q8BT60	Parental	NHVAR	FAAAATQQQTASQYFVLLIITDGVITDLDETR	QAIVN	3		1167.270543	3498.788228	0.000451244	40	N	406	438
Q8BT60	Parental	DVTSK	SDPLCVLFLNTSGHQWYEVER	TERIK	2	C5:+57.021	1275.608021	2549.200443	0.000451244	12	N	26	47
Q8BT60	Parental	DVTSK	SDPLCVLFLNTSGHQWYEVER	TERIK	3	C5:+57.021	850.7412809	2549.200443	0.000451244	26	N	26	47
Q8BT60	Parental	PKFSK	TFVIDYYFEVVQK	LKFGI	2		825.9248535	1649.834107	0.0007646	5	N	61	74
Q8BT60	Parental	QCVTK	VELNVSCNNLLDADVTSKSDPLCVLFLNTSGHQWYEVER	TERIK	4	C7:+57.021,C23:+57.021	1131.297084	4521.157137	0.001162105	1	N	8	47
Q8BT60	Parental	QCVTK	VELNVSCNNLLDADVTSK	SDPLC	2	C7:+57.021	995.9914273	1989.967255	0.000451244	10	N	8	26
Q8BT60	Parental	VQKLK	FGIYDIDNK	TIELS	2		542.7696358	1083.523672	0.000622848	15	Y	76	85
Q8BT60	Parental	EVVQK	LKFGIYDIDNK	TIELS	3		442.5753663	1324.702699	0.001264573	1	N	74	85
Q8BT60	Parental	VLAEI	PQQVVGYFNTYK	LLPPK	2		722.3675057	1442.719411	0.002813207	1	N	511	523
Q8BT60	Parental	KTIEL	SDDDFLGECEVTLGQIVSSK	KLTRP	2	C9:+57.021	1100.010014	2198.004428	0.000451244	14	N	89	109
Q8BT60	Parental	KEASR	SSPVEYECINEK	KRQKK	2	C8:+57.021	727.8273218	1453.639044	0.000451244	1	N	241	253
Q8BT60	Parental	DKTIK	VECYDYDNDGSHDLIGTF	QTTMT	2	C3:+57.021	1060.431399	2118.847199	0.0025889	1	N	211	229
Q8BT60	Parental	GDMDK	TIKVECYDYDNDGSHDLIGTF	QTTMT	2	C6:+57.021	1231.544752	2461.073905	0.002453667	1	N	208	229
Q8BTE6	Exosome	PLQLL	GTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C3:+57.021,C7:+57.021,C13:+57.021,C19:+57.021,C24:+57.021,C28:+57.021	1210.480338	3628.417613	0.002884417	2	N	32	63
Q8BTE6	Exosome	AELCR	GDWDCGPEEQCVSIGCSHICTTN	-	2	C5:+57.021,C11:+57.021,C16:+57.021,C20:+57.021	1341.519408	2681.023217	0.000451244	20	N	40	63
Q8BTE6	Exosome	AELCR	GDWDCGPEEQCVSIGCSHICTTN	-	3	C5:+57.021,C11:+57.021,C16:+57.021,C20:+57.021	894.6822056	2681.023217	0.000451244	2	N	40	63
Q8BTE6	Exosome	RPLQL	LGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C4:+57.021,C8:+57.021,C14:+57.021,C20:+57.021,C25:+57.021,C29:+57.021	1248.175026	3741.501677	0.000451244	8	N	31	63
Q8BTE6	Exosome	VRPLQ	LLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C5:+57.021,C9:+57.021,C15:+57.021,C21:+57.021,C26:+57.021,C30:+57.021	1285.869714	3854.585741	0.000451244	2	N	30	63
Q8BTE6	Parental	PLQLL	GTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C3:+57.021,C7:+57.021,C13:+57.021,C19:+57.021,C24:+57.021,C28:+57.021	1210.480338	3628.417613	0.000451244	6	N	32	63
Q8BTE6	Parental	AELCR	GDWDCGPEEQCVSIGCSHICTTN	-	2	C5:+57.021,C11:+57.021,C16:+57.021,C20:+57.021	1341.519408	2681.023217	0.000451244	156	N	40	63

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTE6	Parental	AELCR	GDWDCGPEEQCVSIGCSHICTTN	-	3	C5:+57.021,C11:+57.021,C16:+57.021,C20:+57.021	894.6822056	2681.023217	0.000451244	41	N	40	63
Q8BTE6	Parental	QELQA	AVRPLQLLGTCAELCR	GDWDC	2	C11:+57.021,C15:+57.021	928.9953644	1855.975129	0.000451244	13	N	24	40
Q8BTE6	Parental	QELQA	AVRPLQLLGTCAELCR	GDWDC	3	C11:+57.021,C15:+57.021	619.6661762	1855.975129	0.000451244	65	N	24	40
Q8BTE6	Parental	RPLQL	LGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C4:+57.021,C8:+57.021,C14:+57.021,C20:+57.021,C25:+57.021,C29:+57.021	1248.175026	3741.501677	0.000451244	30	N	31	63
Q8BTE6	Parental	VRPLQ	LLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C5:+57.021,C9:+57.021,C15:+57.021,C21:+57.021,C26:+57.021,C30:+57.021	1285.869714	3854.585741	0.000451244	21	N	30	63
Q8BTE6	Parental	AAVRP	LQLLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C7:+57.021,C11:+57.021,C17:+57.021,C23:+57.021,C28:+57.021,C32:+57.021	1366.250594	4095.728383	0.000451244	32	N	28	63
Q8BTE6	Parental	QLLGT	CAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C1:+57.021,C5:+57.021,C11:+57.021,C17:+57.021,C22:+57.021,C26:+57.021	1157.790624	3470.348471	0.001763695	1	N	34	63
Q8BTE6	Parental	LQAAV	RPLQLLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	3	C9:+57.021,C13:+57.021,C19:+57.021,C25:+57.021,C30:+57.021,C34:+57.021	1450.635219	4348.882258	0.002981883	1	N	26	63
Q8BTE6	Parental	LQAAV	RPLQLLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	4	C9:+57.021,C13:+57.021,C19:+57.021,C25:+57.021,C30:+57.021,C34:+57.021	1088.228364	4348.882258	0.002663018	3	N	26	63
Q8BTE6	Parental	QELQA	AVRPLQLLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	4	C11:+57.021,C15:+57.021,C21:+57.021,C27:+57.021,C32:+57.021,C36:+57.021	1130.754746	4518.987786	0.0007646	6	N	24	63
Q8BTE6	Parental	ELQAA	VRPLQLLGTCAELCRGDWDCGPEEQCVSIGCSHICTTN	-	4	C10:+57.021,C14:+57.021,C20:+57.021,C26:+57.021,C31:+57.021,C35:+57.021	1112.995468	4447.950672	0.002212458	1	N	25	63
Q8BTE6	Parental	AAVRP	LQLLGTCAELCR	GDWDC	2	C7:+57.021,C11:+57.021	717.3656629	1432.715726	0.000451244	13	N	28	40
Q8BTE6	Parental	LQAAV	RPLQLLGTCAELCR	GDWDC	3	C9:+57.021,C13:+57.021	562.9643336	1685.869601	0.000622848	1	N	26	40
Q8BTE6	Parental	VRPLQ	LLGTCAELCR	GDWDC	2	C5:+57.021,C9:+57.021	596.7943421	1191.573084	0.000823681	4	N	30	40
Q8BTI8	Parental	ARTPA	ALAALSLTGSGTPPTAANYPSSSR	TPQAP	2		1145.587843	2289.160086	0.000870037	1	N	2256	2280
Q8BTI8	Parental	ELKER	LGLIQEDVASSCIPR	DKFSP	2	C12:+57.021	829.4328198	1656.85004	0.000451244	5	N	1132	1147
Q8BTI8	Parental	PQKSR	DSPTGSSGSFHLCPGVTPSSIVPGESCFSASFVQQK	GHTQT	3	C13:+57.021,C27:+57.021	1247.910383	3740.707748	0.002813207	1	N	991	1027
Q8BTM8	Exosome	PSRVR	VHGPGIQSGTTNKPNKFTVETR	GAGTG	3		790.0843011	2367.229503	0.000823681	1	N	1359	1381
Q8BTM8	Exosome	PSRVR	VHGPGIQSGTTNKPNKFTVETR	GAGTG	4		592.8151758	2367.229503	0.000451244	14	N	1359	1381
Q8BTM8	Exosome	PGLNR	TGVELGKPTHFTVNAK	TAGKG	2		849.962833	1697.910066	0.000451244	5	N	884	900
Q8BTM8	Exosome	PGLNR	TGVELGKPTHFTVNAK	TAGKG	3		566.977822	1697.910066	0.000451244	26	N	884	900
Q8BTM8	Exosome	PGLNR	TGVELGKPTHFTVNAK	TAGKG	4		425.4853165	1697.910066	0.000451244	43	N	884	900
Q8BTM8	Exosome	KAPLR	VQVQDNEGCSVEATVK	DNGNG	2	C9:+57.021	881.9177309	1761.819862	0.000451244	72	N	708	724
Q8BTM8	Exosome	MPSGK	VAQPSITDNKDGTVTVR	YSPSE	2		900.9766688	1799.937738	0.000451244	17	N	1814	1831
Q8BTM8	Exosome	MPSGK	VAQPSITDNKDGTVTVR	YSPSE	3		600.9870458	1799.937738	0.000451244	11	N	1814	1831
Q8BTM8	Exosome	PSKVK	AFGPGLQGGNAGSPAR	FTIDT	2		728.8687356	1455.721871	0.000451244	50	N	1071	1087
Q8BTM8	Exosome	GDASK	VTAQGPGLEPSGNIANK	TTYFE	2		826.9342726	1651.852945	0.000451244	67	N	383	400
Q8BTM8	Exosome	QGVFR	EATTEFSVDAR	ALTQT	2		613.288921	1224.562242	0.000451244	10	N	1272	1283
Q8BTM8	Exosome	PGLEK	TGVAVNKPAEFTVDAK	HAGKA	2		823.9415663	1645.867533	0.000451244	50	N	684	700
Q8BTM8	Exosome	PGLEK	TGVAVNKPAEFTVDAK	HAGKA	3		549.6303109	1645.867533	0.000451244	26	N	684	700
Q8BTM8	Exosome	VHGPR	TPCEEILVK	HMGSR	2	C3:+57.021	544.7867399	1087.55788	0.002212458	1	N	2598	2607
Q8BTM8	Exosome	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	2		1142.054167	2282.092735	0.001162105	1	N	916	936
Q8BTM8	Exosome	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	3		761.7053783	2282.092735	0.000451244	2	N	916	936
Q8BTM8	Exosome	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	4		571.5309837	2282.092735	0.000451244	16	N	916	936
Q8BTM8	Exosome	SILVK	YNDQHIPGSPFTAR	VTGDD	2		801.8871253	1601.758651	0.001763695	1	N	1937	1951
Q8BTM8	Exosome	SILVK	YNDQHIPGSPFTAR	VTGDD	3		534.9273502	1601.758651	0.000451244	41	N	1937	1951
Q8BTM8	Exosome	VPIPR	SPYTVTVGQACNPAACR	AIGRG	2	C11:+57.021,C16:+57.021	926.4275115	1850.839423	0.000451244	74	N	467	484
Q8BTM8	Exosome	VPIPR	SPYTVTVGQACNPAACR	AIGRG	3	C11:+57.021,C16:+57.021	617.9542744	1850.839423	0.002080925	1	N	467	484
Q8BTM8	Exosome	PGMVR	ANLPQSFQVDTSK	AGVAP	2		717.8653272	1433.715054	0.000451244	31	N	1464	1477
Q8BTM8	Exosome	TVETR	GAGTGGLGLAVEGPSEAK	MSCMD	2		785.9077234	1569.799847	0.000451244	68	N	1381	1399
Q8BTM8	Exosome	KVASK	IVSPSGAAVPCKVEPGLGADNSVVR	FVPRE	2	C11:+57.021	1240.152596	2478.289592	0.002080925	2	N	1007	1032
Q8BTM8	Exosome	KVASK	IVSPSGAAVPCKVEPGLGADNSVVR	FVPRE	3	C11:+57.021	827.1043307	2478.289592	0.000451244	73	N	1007	1032
Q8BTM8	Exosome	KAPLR	VQVQDNEGCSVEATVKDNGNGTYSCSYVPR	KPVKH	3	C9:+57.021,C25:+57.021	1111.829952	3332.466455	0.000451244	48	N	708	738
Q8BTM8	Exosome	VTGPR	LVSNHSLHETSSVFVDSLTK	VATVP	2		1100.566379	2199.117159	0.000451244	29	N	2520	2540
Q8BTM8	Exosome	VTGPR	LVSNHSLHETSSVFVDSLTK	VATVP	3		734.0468529	2199.117159	0.000451244	64	N	2520	2540
Q8BTM8	Exosome	HVKAR	VANPSGNLTDTYVQDCGDGTYK	VEYTP	2	C16:+57.021	1188.026727	2374.037854	0.000451244	11	N	1296	1318
Q8BTM8	Exosome	TVETR	SAGQGEVLVYVEDPAGHQEEAK	VTANN	2		1157.053833	2312.092066	0.000451244	30	N	309	331
Q8BTM8	Exosome	TVETR	SAGQGEVLVYVEDPAGHQEEAK	VTANN	3		771.7051554	2312.092066	0.000451244	25	N	309	331

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Exosome	SFEDR	KDGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C5:+57.021	1193.565488	2385.115376	0.000451244	3	N	2288	2310
Q8BTM8	Exosome	TYTVK	YIPVQQGPVGVNVTYGGDHIPK	SPFSV	2		1169.613664	2337.211728	0.000451244	44	N	936	958
Q8BTM8	Exosome	TYTVK	YIPVQQGPVGVNVTYGGDHIPK	SPFSV	3		780.078376	2337.211728	0.000451244	18	N	936	958
Q8BTM8	Exosome	TVKYI	PVQQGPVGVNVTYGGDHIPK	SPFSV	3		688.0292451	2061.064335	0.000622848	4	N	938	958
Q8BTM8	Exosome	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	2	C11:+57.021	1383.655897	2765.296194	0.000451244	1	N	2367	2391
Q8BTM8	Exosome	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	3	C11:+57.021	922.7731979	2765.296194	0.000451244	34	N	2367	2391
Q8BTM8	Exosome	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	4	C11:+57.021	692.3318485	2765.296194	0.000451244	18	N	2367	2391
Q8BTM8	Exosome	CVSKR	IANLQTDLSDGLR	LIALL	2		708.3786018	1414.741604	0.000451244	20	N	63	76
Q8BTM8	Exosome	TIDAK	DAGEGLLAVQITDPEGKPK	KTHIQ	3		646.6779894	1937.010568	0.000451244	4	N	1573	1592
Q8BTM8	Exosome	VSVKF	NEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1160.564368	2319.113136	0.000451244	15	N	2311	2333
Q8BTM8	Exosome	VSVKF	NEEHIPDSPFVVPVASPSGDAR	RLTVS	3		774.045512	2319.113136	0.000451244	4	N	2311	2333
Q8BTM8	Exosome	KTGLK	AHEPTYFTVDCTEAGQGDVSIGIK	CAPGV	2	C11:+57.021	1298.105508	2594.195417	0.000451244	8	N	785	809
Q8BTM8	Exosome	KTGLK	AHEPTYFTVDCTEAGQGDVSIGIK	CAPGV	3	C11:+57.021	865.7396057	2594.195417	0.000451244	46	N	785	809
Q8BTM8	Exosome	FEDRK	DGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C4:+57.021	1129.518006	2257.020412	0.000451244	16	N	2289	2310
Q8BTM8	Exosome	FEDRK	DGSCGVAYVVQEPGDYEVSVK	FNEEH	3	C4:+57.021	753.3479375	2257.020412	0.001943752	1	N	2289	2310
Q8BTM8	Exosome	NDKNR	TFSVWYVPEVTGTHK	VTVLF	2		875.944109	1749.872618	0.000662267	8	N	340	355
Q8BTM8	Exosome	NDKNR	TFSVWYVPEVTGTHK	VTVLF	3		584.2986726	1749.872618	0.000451244	13	N	340	355
Q8BTM8	Exosome	DHIPK	SPFSVGVSPSLDLSK	IKVSG	2		760.4042853	1518.792971	0.000451244	29	N	958	973
Q8BTM8	Exosome	EVSVK	FNEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1234.098575	2466.18155	0.000451244	27	N	2310	2333
Q8BTM8	Exosome	EVSVK	FNEEHIPDSPFVVPVASPSGDAR	RLTVS	3		823.0683167	2466.18155	0.000451244	46	N	2310	2333
Q8BTM8	Exosome	VQGPK	GLVEPVDVVDNADGTQTVNYVPSR	EGSYS	2		1272.632979	2543.250358	0.000451244	48	N	1491	1515
Q8BTM8	Exosome	VQGPK	GLVEPVDVVDNADGTQTVNYVPSR	EGSYS	3		848.7579194	2543.250358	0.000451244	24	N	1491	1515
Q8BTM8	Exosome	GDARR	LTVSSLQESGLKVNQPASFAVSLNGAK	GAIDA	3		915.8314187	2744.470856	0.000451244	3	N	2334	2361
Q8BTM8	Exosome	YVPSR	EGSYSISVLYGEEEVPR	SPFKV	2		957.4605172	1912.905434	0.000451244	46	N	1515	1532
Q8BTM8	Exosome	YVPSR	EGSYSISVLYGEEEVPR	SPFKV	3		638.6429448	1912.905434	0.000698008	1	N	1515	1532
Q8BTM8	Exosome	VICVR	FGGEHVPNSPFQVTALAGDQPTVQTPLR	SQQLA	3		988.5057056	2962.493717	0.000451244	21	N	1725	1753
Q8BTM8	Exosome	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	2	C14:+57.021	1382.174257	2762.332914	0.000451244	28	N	1246	1272
Q8BTM8	Exosome	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C14:+57.021	921.7854379	2762.332914	0.000451244	29	N	1246	1272
Q8BTM8	Exosome	SDGLR	LIALLEVLSQKK	MHRKH	2		677.9375669	1353.859534	0.001162105	3	N	76	88
Q8BTM8	Exosome	SDGLR	LIALLEVLSQKK	MHRKH	3		452.2943113	1353.859534	0.00091018	3	N	76	88
Q8BTM8	Exosome	WQSGR	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	EAMQQ	3	C9:+57.021,C14:+57.021	1081.504851	3241.491154	0.000451244	72	N	196	226
Q8BTM8	Exosome	WQSGR	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	EAMQQ	4	C9:+57.021,C14:+57.021	811.3805884	3241.491154	0.000451244	11	N	196	226
Q8BTM8	Exosome	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C26:+57.021	1345.662062	4033.962786	0.000451244	42	N	1234	1272
Q8BTM8	Exosome	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	4	C26:+57.021	1009.498497	4033.962786	0.000451244	12	N	1234	1272
Q8BTM8	Exosome	NSVVR	FVPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1329.014362	3984.019685	0.000451244	39	N	1032	1069
Q8BTM8	Exosome	NSVVR	FVPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	4		997.0127211	3984.019685	0.000451244	23	N	1032	1069
Q8BTM8	Exosome	DGTYK	VEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C35:+57.021	1428.318467	4281.932	0.000451244	23	N	1318	1357
Q8BTM8	Exosome	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	2	C1:+57.021	1023.004338	2043.993075	0.000451244	35	N	809	828
Q8BTM8	Exosome	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	2	[0:-17.027,C1:+57.021	1014.490838	2026.966075	0.000622848	1	N	809	828
Q8BTM8	Exosome	SIGIK	CAPGVVGPTEADIDFDIIRNDNDTFTVK	YTPCG	3	C1:+57.021	1027.161122	3078.459965	0.000451244	22	N	809	837
Q8BTM8	Exosome	FEDRK	DGSCGVAYVVQEPGDYEVSVKF	NEEHI	2	C4:+57.021	1203.052213	2404.088826	0.000451244	15	N	2289	2311
Q8BTM8	Exosome	SCDVR	YWPQEAGEYAVHVLCNSEDIR	LSPFM	2	C15:+57.021	1268.582004	2535.148407	0.000451244	40	N	634	655
Q8BTM8	Exosome	SCDVR	YWPQEAGEYAVHVLCNSEDIR	LSPFM	3	C15:+57.021	846.057269	2535.148407	0.000451244	30	N	634	655
Q8BTM8	Exosome	DVRYW	PQEAGEYAVHVLCNSEDIR	LSPFM	3	C13:+57.021	729.6763885	2186.005765	0.000451244	9	N	636	655
Q8BTM8	Exosome	RFVPR	EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1162.584127	3484.728981	0.000451244	48	N	1036	1069
Q8BTM8	Exosome	RFVPR	EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	4		872.1900454	3484.728981	0.000662267	18	N	1036	1069
Q8BTM8	Exosome	SDGLR	LIALLEVLSQK	KMHRK	2		613.8900854	1225.764571	0.000451244	38	Y	76	87
Q8BTM8	Exosome	SDGLR	LIALLEVLSQK	KMHRK	3		409.5959902	1225.764571	0.002019181	1	Y	76	87
Q8BTM8	Exosome	EERVK	QKDLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1256.284963	3765.83149	0.000451244	29	N	529	563
Q8BTM8	Exosome	GIVGK	SADFVVEAIGDDVGTLGFSVEGPSQAK	IECDD	2		1348.159027	2694.302453	0.000451244	61	N	593	620
Q8BTM8	Exosome	GIVGK	SADFVVEAIGDDVGTLGFSVEGPSQAK	IECDD	3		899.1086178	2694.302453	0.000451244	32	N	593	620
Q8BTM8	Exosome	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK	RLRNG	3	C33:+57.021	1254.999681	3761.975643	0.000451244	19	N	1964	2000
Q8BTM8	Exosome	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK	RLRNG	4	C33:+57.021	941.5017106	3761.975643	0.000451244	23	N	1964	2000
Q8BTM8	Exosome	RVKQK	DLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1170.90045	3509.677949	0.000451244	38	N	531	563
Q8BTM8	Exosome	GDAVR	DVDIIDHHDNTYTVK	YIPVQ	3		595.620363	1783.837689	0.000451244	21	N	921	936
Q8BTM8	Exosome	GIWTR	EAGAGGLAIAVEGPSKAEISFEDR	KDGSC	2		1187.598408	2373.181216	0.002453667	3	N	2264	2288
Q8BTM8	Exosome	GIWTR	EAGAGGLAIAVEGPSKAEISFEDR	KDGSC	3		792.0682052	2373.181216	0.000451244	5	N	2264	2288
Q8BTM8	Exosome	TGTHK	VTVLFAGQHIAK	SPFEV	3		428.5877176	1282.739753	0.000823681	7	N	355	367
Q8BTM8	Exosome	TLVVK	WGDEHIPGSPYR	IMVP-	3		471.8902364	1412.647309	0.000451244	20	N	2631	2643
Q8BTM8	Exosome	QHIAK	SPFEVYVDKSQGDASK	VTAQG	2		878.9235705	1755.831541	0.000851441	1	N	367	383
Q8BTM8	Exosome	SSHSR	CGQSAAVASPGGSIDSR	DAEMP	2	C1:+57.021	810.3760332	1618.736466	0.000870037	1	N	7	24
Q8BTM8	Exosome	EGPSK	AEISCTDNQDGTCSVSYLPVLPGDYSILVK	YNDQH	3	C5:+57.021,C13:+57.021	1101.191827	3300.552082	0.000451244	31	N	1907	1937
Q8BTM8	Exosome	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGR	EEPCL	2		1447.280008	2892.544415	0.000451244	34	N	1964	1993
Q8BTM8	Exosome	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGR	EEPCL	3		965.1892717	2892.544415	0.000451244	34	N	1964	1993
Q8BTM8	Exosome	DSLTK	VATVPQHATSGPGPADVSK	VVAKG	2		909.9713864	1817.927173	0.000823681	3	N	2540	2559

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Exosome	DSLTK	VATVPQHATSGPGPADVSK	VVAKG	3		606.9835243	1817.927173	0.000451244	20	N	2540	2559
Q8BTM8	Exosome	PKKAR	AYGPGIEPTGNMVK	KRAEF	2	M12:+15.995	725.356324	1448.697048	0.000451244	3	N	285	299
Q8BTM8	Exosome	EATVK	DNGNGTYSCSYVPR	KPVKH	2	C9:+57.021	795.3363767	1588.657153	0.000451244	7	N	724	738
Q8BTM8	Exosome	GIWTR	EAGAGGLAIAVEGPSK	AEISF	2		713.8809773	1425.746355	0.000451244	34	N	2264	2280
Q8BTM8	Exosome	ESGLK	VNQPASFAVSLNGAK	GAIDA	2		751.9022441	1501.788888	0.000451244	8	N	2346	2361
Q8BTM8	Exosome	CMDNK	DGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFK	VPVHD	3	C4:+57.021	1193.884317	3578.62955	0.000451244	29	N	1406	1439
Q8BTM8	Exosome	AVPCK	VEPGLGADNSVVR	FVPRE	2		656.8469375	1311.678275	0.000451244	10	N	1019	1032
Q8BTM8	Exosome	TVNTK	DAGEGGLSLAIEGPSK	AEISC	2		750.8811743	1499.746749	0.000451244	12	N	1891	1907
Q8BTM8	Exosome	KVASK	IVSPSGAAVPCK	VEPGL	2	C11:+57.021	593.3187386	1184.621877	0.000451244	1	N	1007	1019
Q8BTM8	Exosome	EPTYF	TVDCTEAGQGDVSIGIK	CAPGV	2	C4:+57.021	875.4201064	1748.824613	0.000451244	1	N	792	809
Q8BTM8	Exosome	AGKGK	LDVQFSGLAK	GDAVR	2		539.3011031	1076.586606	0.000451244	6	N	906	916
Q8BTM8	Exosome	HVKAR	VANPSGNLTDTYVQDCGDGTY	KVEYT	2	C16:+57.021	1123.979245	2245.94289	0.001871652	4	N	1296	1317
Q8BTM8	Exosome	GDARR	LTVSSLQESGLK	VNQPA	2		631.354064	1260.692528	0.000451244	5	N	2334	2346
Q8BTM8	Exosome	IPGTY	TVTITWGGQNIGR	SPFEV	2		701.8760293	1401.736459	0.000823681	2	N	550	563
Q8BTM8	Exosome	KTAGK	GKLDVQFSGLAK	GDAVR	3		421.5754777	1261.703033	0.002453667	1	N	904	916
Q8BTM8	Exosome	SGDAR	RLTVSSLQESGLK	VNQPA	2		709.4046196	1416.793639	0.002374549	1	N	2333	2346
Q8BTM8	Exosome	TVTIK	YGGQPVPNFPSK	LQVEP	2		645.8280164	1289.640433	0.00307782	1	N	1234	1246
Q8BTM8	Exosome	RFIPR	ENGIYLIDVK	FNGTH	2		582.3194928	1162.623386	0.000622848	8	N	2395	2405
Q8BTM8	Exosome	GDGTY	KVEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C36:+57.021	1471.016788	4410.026963	0.001943752	4	N	1317	1357
Q8BTM8	Exosome	PRSPY	TVTVGQACNPAACR	AIGRG	2	C8:+57.021,C13:+57.021	752.853451	1503.691302	0.001839721	1	N	470	484
Q8BTM8	Exosome	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVF	REATT	3	C26:+57.021	1293.628358	3877.861675	0.000451244	8	N	1234	1271
Q8BTM8	Exosome	TFTVK	YTPCGAGSYTIMVLFADQATPTSPIR	VKVEP	2	C4:+57.021	1409.183237	2816.350873	0.000451244	6	N	837	863
Q8BTM8	Exosome	TFTVK	YTPCGAGSYTIMVLFADQATPTSPIR	VKVEP	3	C4:+57.021	939.7914243	2816.350873	0.000735798	4	N	837	863
Q8BTM8	Exosome	SPSGK	THEAEIVEGENHTYCIR	FVPAE	3	C15:+57.021	686.6500622	2056.926787	0.001329271	1	N	2184	2201
Q8BTM8	Exosome	TIEIC	SEAGLPAEVYIQDHGDGTHTITYIPLCPGAYTVTIK	YGGQP	3	C27:+57.021	1296.643897	3886.908291	0.000451244	4	N	1198	1234
Q8BTM8	Exosome	TIEIC	SEAGLPAEVYIQDHGDGTHTITYIPLCPGAYTVTIK	YGGQP	4	C27:+57.021	972.7348728	3886.908291	0.0025889	1	N	1198	1234
Q8BTM8	Exosome	WIQNK	LPQLPITNFSR	DWQSG	2		643.3673087	1284.719017	0.002519933	1	N	179	190
Q8BTM8	Exosome	GIVGK	SADFVVEAIGDDVGTL	GFSVE	2		804.3941145	1606.772629	0.001329271	1	N	593	609
Q8BTM8	Parental	PSRVR	VHGPGIQSGTTNKPNKFTVETR	GAGTG	3		790.0843011	2367.229503	0.000451244	34	N	1359	1381
Q8BTM8	Parental	PSRVR	VHGPGIQSGTTNKPNKFTVETR	GAGTG	4		592.8151758	2367.229503	0.000451244	48	N	1359	1381
Q8BTM8	Parental	PGLNR	TGVELGKPTHFTVNAK	TAGKG	2		849.962833	1697.910066	0.000451244	20	N	884	900
Q8BTM8	Parental	PGLNR	TGVELGKPTHFTVNAK	TAGKG	3		566.977822	1697.910066	0.000451244	37	N	884	900
Q8BTM8	Parental	PGLNR	TGVELGKPTHFTVNAK	TAGKG	4		425.4853165	1697.910066	0.000451244	64	N	884	900
Q8BTM8	Parental	KAPLR	VQVQDNEGCSVEATVK	DNGNG	2	C9:+57.021	881.9177309	1761.819862	0.000451244	124	N	708	724
Q8BTM8	Parental	MPSGK	VAQPSITDNKDGTVTVR	YSPSE	2		900.9766688	1799.937738	0.000451244	30	N	1814	1831
Q8BTM8	Parental	MPSGK	VAQPSITDNKDGTVTVR	YSPSE	3		600.9870458	1799.937738	0.000451244	31	N	1814	1831
Q8BTM8	Parental	PSKVK	AFGPGLQGGNAGSPAR	FTIDT	2		728.8687356	1455.721871	0.000451244	82	N	1071	1087
Q8BTM8	Parental	GDASK	VTAQGPGLEPSGNIANK	TTYFE	2		826.9342726	1651.852945	0.000451244	116	N	383	400
Q8BTM8	Parental	QGVFR	EATTEFSVDAR	ALTQT	2		613.288921	1224.562242	0.000451244	64	N	1272	1283
Q8BTM8	Parental	PGLEK	TGVAVNKPAEFTVDAK	HAGKA	2		823.9415663	1645.867533	0.000451244	58	N	684	700
Q8BTM8	Parental	PGLEK	TGVAVNKPAEFTVDAK	HAGKA	3		549.6303109	1645.867533	0.000451244	50	N	684	700
Q8BTM8	Parental	VHGPR	TPCEEILVK	HMGSR	2	C3:+57.021	544.7867399	1087.55788	0.000823681	31	N	2598	2607
Q8BTM8	Parental	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	2		1142.054167	2282.092735	0.000451244	17	N	916	936
Q8BTM8	Parental	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	3		761.7053783	2282.092735	0.000451244	10	N	916	936
Q8BTM8	Parental	SGLAK	GDAVRDVDIIDHHDNTYTVK	YIPVQ	4		571.5309837	2282.092735	0.000451244	14	N	916	936
Q8BTM8	Parental	SILVK	YNDQHIPGSPFTAR	VTGDD	2		801.8871253	1601.758651	0.000451244	8	N	1937	1951
Q8BTM8	Parental	SILVK	YNDQHIPGSPFTAR	VTGDD	3		534.9273502	1601.758651	0.000451244	40	N	1937	1951
Q8BTM8	Parental	EGKPK	KTHIQDNHDGTYTVAYVPDVPGR	YTILI	3		861.7582537	2582.251361	0.000451244	24	N	1592	1615
Q8BTM8	Parental	VPIPR	SPYTVTVGQACNPAACR	AIGRG	2	C11:+57.021,C16:+57.021	926.4275115	1850.839423	0.000451244	51	N	467	484
Q8BTM8	Parental	VPIPR	SPYTVTVGQACNPAACR	AIGRG	3	C11:+57.021,C16:+57.021	617.9542744	1850.839423	0.000451244	3	N	467	484
Q8BTM8	Parental	LISIK	YGGPYHIGGSPFK	AKVTG	2		690.3412909	1378.666982	0.000451244	3	N	2500	2513
Q8BTM8	Parental	LISIK	YGGPYHIGGSPFK	AKVTG	3		460.5634606	1378.666982	0.000451244	39	N	2500	2513
Q8BTM8	Parental	PGMVR	ANLPQSFQVDTSK	AGVAP	2		717.8653272	1433.715054	0.000451244	56	N	1464	1477
Q8BTM8	Parental	TVETR	GAGTGGLGLAVEGPSEAK	MSCMD	2		785.9077234	1569.799847	0.000451244	92	N	1381	1399
Q8BTM8	Parental	KVASK	IVSPSGAAVPCKVEPGLGADNSVVR	FVPRE	2	C11:+57.021	1240.152596	2478.289592	0.000451244	42	N	1007	1032
Q8BTM8	Parental	KVASK	IVSPSGAAVPCKVEPGLGADNSVVR	FVPRE	3	C11:+57.021	827.1043307	2478.289592	0.000451244	131	N	1007	1032
Q8BTM8	Parental	KAPLR	VQVQDNEGCSVEATVKDNGNGTYSCSYVPR	KPVKH	3	C9:+57.021,C25:+57.021	1111.829952	3332.466455	0.000451244	65	N	708	738
Q8BTM8	Parental	VTGPR	LVSNHSLHETSSVFVDSLTK	VATVP	2		1100.566379	2199.117159	0.000451244	48	N	2520	2540
Q8BTM8	Parental	VTGPR	LVSNHSLHETSSVFVDSLTK	VATVP	3		734.0468529	2199.117159	0.000451244	37	N	2520	2540
Q8BTM8	Parental	VTGPR	LVSNHSLHETSSVFVDSLTK	VATVP	4		550.7870897	2199.117159	0.002212458	1	N	2520	2540
Q8BTM8	Parental	HVKAR	VANPSGNLTDTYVQDCGDGTYK	VEYTP	2	C16:+57.021	1188.026727	2374.037854	0.000451244	54	N	1296	1318
Q8BTM8	Parental	TVETR	SAGQGEVLVYVEDPAGHQEEAK	VTANN	2		1157.053833	2312.092066	0.000451244	10	N	309	331
Q8BTM8	Parental	TVETR	SAGQGEVLVYVEDPAGHQEEAK	VTANN	3		771.7051554	2312.092066	0.000451244	18	N	309	331
Q8BTM8	Parental	SFEDR	KDGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C5:+57.021	1193.565488	2385.115376	0.000451244	23	N	2288	2310
Q8BTM8	Parental	SFEDR	KDGSCGVAYVVQEPGDYEVSVK	FNEEH	3	C5:+57.021	796.0462585	2385.115376	0.000451244	25	N	2288	2310

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Parental	TYTVK	YIPVQQGPVGVNVTYGGDHIPK	SPFSV	2		1169.613664	2337.211728	0.000451244	49	N	936	958
Q8BTM8	Parental	TYTVK	YIPVQQGPVGVNVTYGGDHIPK	SPFSV	3		780.078376	2337.211728	0.000622848	8	N	936	958
Q8BTM8	Parental	TVKYI	PVQQGPVGVNVTYGGDHIPK	SPFSV	3		688.0292451	2061.064335	0.000451244	25	N	938	958
Q8BTM8	Parental	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	2	C11:+57.021	1383.655897	2765.296194	0.000451244	9	N	2367	2391
Q8BTM8	Parental	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	3	C11:+57.021	922.7731979	2765.296194	0.000451244	40	N	2367	2391
Q8BTM8	Parental	AIDAK	VHSPSGALEECYVTEIDQDKYAVR	FIPRE	4	C11:+57.021	692.3318485	2765.296194	0.000451244	73	N	2367	2391
Q8BTM8	Parental	CVSKR	IANLQTDLSDGLR	LIALL	2		708.3786018	1414.741604	0.000451244	31	N	63	76
Q8BTM8	Parental	PGMVR	ANLPQSFQVDTSKAGVAPLQVK	VQGPK	2		1149.626771	2297.237943	0.000451244	14	N	1464	1486
Q8BTM8	Parental	PGMVR	ANLPQSFQVDTSKAGVAPLQVK	VQGPK	3		766.7537809	2297.237943	0.001395409	2	N	1464	1486
Q8BTM8	Parental	TIDAK	DAGEGLLAVQITDPEGKPK	KTHIQ	2		969.5130841	1937.010568	0.000451244	61	N	1573	1592
Q8BTM8	Parental	TIDAK	DAGEGLLAVQITDPEGKPK	KTHIQ	3		646.6779894	1937.010568	0.000451244	35	N	1573	1592
Q8BTM8	Parental	EVSVK	FNEEHIPDSPFVVPVASPSGDARR	LTVSS	3		875.1020204	2622.282661	0.000451244	6	N	2310	2334
Q8BTM8	Parental	VSVKF	NEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1160.564368	2319.113136	0.000451244	32	N	2311	2333
Q8BTM8	Parental	VSVKF	NEEHIPDSPFVVPVASPSGDAR	RLTVS	3		774.045512	2319.113136	0.000451244	18	N	2311	2333
Q8BTM8	Parental	KTGLK	AHEPTYFTVDCTEAGQGDVSIGIK	CAPGV	2	C11:+57.021	1298.105508	2594.195417	0.001352548	1	N	785	809
Q8BTM8	Parental	KTGLK	AHEPTYFTVDCTEAGQGDVSIGIK	CAPGV	3	C11:+57.021	865.7396057	2594.195417	0.000451244	42	N	785	809
Q8BTM8	Parental	FEDRK	DGSCGVAYVVQEPGDYEVSVK	FNEEH	2	C4:+57.021	1129.518006	2257.020412	0.000451244	84	N	2289	2310
Q8BTM8	Parental	FEDRK	DGSCGVAYVVQEPGDYEVSVK	FNEEH	3	C4:+57.021	753.3479375	2257.020412	0.000451244	4	N	2289	2310
Q8BTM8	Parental	NDKNR	TFSVWYVPEVTGTHK	VTVLF	2		875.944109	1749.872618	0.000662267	11	N	340	355
Q8BTM8	Parental	NDKNR	TFSVWYVPEVTGTHK	VTVLF	3		584.2986726	1749.872618	0.000622848	23	N	340	355
Q8BTM8	Parental	DHIPK	SPFSVGVSPSLDLSK	IKVSG	2		760.4042853	1518.792971	0.000451244	33	N	958	973
Q8BTM8	Parental	DHIPK	SPFSVGVSPSLDLSKIK	VSGLG	3		587.6651326	1759.971998	0.001463592	1	N	958	975
Q8BTM8	Parental	EVSVK	FNEEHIPDSPFVVPVASPSGDAR	RLTVS	2		1234.098575	2466.18155	0.000451244	41	N	2310	2333
Q8BTM8	Parental	EVSVK	FNEEHIPDSPFVVPVASPSGDAR	RLTVS	3		823.0683167	2466.18155	0.000451244	55	N	2310	2333
Q8BTM8	Parental	VQGPK	GLVEPVDVVDNADGTQTVNYVPSR	EGSYS	2		1272.632979	2543.250358	0.000451244	160	N	1491	1515
Q8BTM8	Parental	VQGPK	GLVEPVDVVDNADGTQTVNYVPSR	EGSYS	3		848.7579194	2543.250358	0.000451244	43	N	1491	1515
Q8BTM8	Parental	GDARR	LTVSSLQESGLKVNQPASFAVSLNGAK	GAIDA	3		915.8314187	2744.470856	0.001264573	3	N	2334	2361
Q8BTM8	Parental	YVPSR	EGSYSISVLYGEEEVPR	SPFKV	2		957.4605172	1912.905434	0.000451244	119	N	1515	1532
Q8BTM8	Parental	YVPSR	EGSYSISVLYGEEEVPR	SPFKV	3		638.6429448	1912.905434	0.000451244	6	N	1515	1532
Q8BTM8	Parental	YVPSR	EGSYSISVLYGEEEVPRSPFK	VKVLP	2		1187.084602	2372.153604	0.000451244	21	N	1515	1536
Q8BTM8	Parental	YVPSR	EGSYSISVLYGEEEVPRSPFK	VKVLP	3		791.725668	2372.153604	0.000451244	15	N	1515	1536
Q8BTM8	Parental	VICVR	FGGEHVPNSPFQVTALAGDQPTVQTPLR	SQQLA	3		988.5057056	2962.493717	0.000451244	31	N	1725	1753
Q8BTM8	Parental	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	2	C14:+57.021	1382.174257	2762.332914	0.000451244	70	N	1246	1272
Q8BTM8	Parental	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C14:+57.021	921.7854379	2762.332914	0.000451244	85	N	1246	1272
Q8BTM8	Parental	SDGLR	LIALLEVLSQKK	MHRKH	2		677.9375669	1353.859534	0.000451244	2	N	76	88
Q8BTM8	Parental	TYTVK	YIPVQQGPVGVNVTYGGDHIPKSPFSVGVSPSLDLSK	IKVSG	3		1280.339179	3837.994138	0.000451244	14	N	936	973
Q8BTM8	Parental	TYTVK	YIPVQQGPVGVNVTYGGDHIPKSPFSVGVSPSLDLSK	IKVSG	4		960.5063346	3837.994138	0.000451244	4	N	936	973
Q8BTM8	Parental	IIDTR	DAGYGGLSLSIEGPSKVDINTEDLEDGTCR	VTYCP	3	C29:+57.021	1056.826467	3167.456002	0.000451244	35	N	2073	2103
Q8BTM8	Parental	WQSGR	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	EAMQQ	3	C9:+57.021,C14:+57.021	1081.504851	3241.491154	0.000451244	86	N	196	226
Q8BTM8	Parental	WQSGR	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	EAMQQ	4	C9:+57.021,C14:+57.021	811.3805884	3241.491154	0.000451244	19	N	196	226
Q8BTM8	Parental	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C26:+57.021	1345.662062	4033.962786	0.000451244	56	N	1234	1272
Q8BTM8	Parental	TVTIK	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	4	C26:+57.021	1009.498497	4033.962786	0.000451244	9	N	1234	1272
Q8BTM8	Parental	NSVVR	FVPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1329.014362	3984.019685	0.000451244	52	N	1032	1069
Q8BTM8	Parental	NSVVR	FVPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	4		997.0127211	3984.019685	0.000451244	37	N	1032	1069
Q8BTM8	Parental	TYDGV	PVPGSPFPLEAVAPTKPSK	VKAFG	2		960.0359981	1918.056396	0.002080925	1	N	1050	1069
Q8BTM8	Parental	DGTYK	VEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C35:+57.021	1428.318467	4281.932	0.000451244	38	N	1318	1357
Q8BTM8	Parental	DGTYK	VEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	4	C35:+57.021	1071.4908	4281.932	0.000451244	21	N	1318	1357
Q8BTM8	Parental	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	2	C1:+39.994	1014.490838	2026.966075	0.000451244	7	N	809	828
Q8BTM8	Parental	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	2	C1:+57.021	1023.004338	2043.993075	0.000451244	27	N	809	828
Q8BTM8	Parental	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	3	C1:+57.021	682.3388251	2043.993075	0.001463592	1	N	809	828
Q8BTM8	Parental	SIGIK	CAPGVVGPTEADIDFDIIR	NDNDT	2	[0:-17.027,C1:+57.021	1014.490838	2026.966075	0.000451244	7	N	809	828
Q8BTM8	Parental	ASKVK	ASGPGLNTTGVPASLPVEFTIDAK	DAGEG	2		1171.616069	2341.216539	0.000451244	26	N	1549	1573
Q8BTM8	Parental	ASKVK	ASGPGLNTTGVPASLPVEFTIDAK	DAGEG	3		781.4133129	2341.216539	0.002080925	1	N	1549	1573
Q8BTM8	Parental	SIGIK	CAPGVVGPTEADIDFDIIRNDNDTFTVK	YTPCG	3	C1:+57.021	1027.161122	3078.459965	0.000451244	34	N	809	837
Q8BTM8	Parental	FEDRK	DGSCGVAYVVQEPGDYEVSVKF	NEEHI	2	C4:+57.021	1203.052213	2404.088826	0.000451244	20	N	2289	2311
Q8BTM8	Parental	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFREATTEFSVDAR	ALTQT	3	C14:+57.021	1323.969332	3968.884596	0.000451244	10	N	1246	1283
Q8BTM8	Parental	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVFREATTEFSVDAR	ALTQT	4	C14:+57.021	993.2289489	3968.884596	0.002663018	1	N	1246	1283
Q8BTM8	Parental	SCDVR	YWPQEAGEYAVHVLCNSEDIR	LSPFM	2	C15:+57.021	1268.582004	2535.148407	0.000451244	37	N	634	655
Q8BTM8	Parental	SCDVR	YWPQEAGEYAVHVLCNSEDIR	LSPFM	3	C15:+57.021	846.057269	2535.148407	0.000451244	24	N	634	655
Q8BTM8	Parental	DVRYW	PQEAGEYAVHVLCNSEDIR	LSPFM	3	C13:+57.021	729.6763885	2186.005765	0.000451244	36	N	636	655
Q8BTM8	Parental	RFVPR	EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	3		1162.584127	3484.728981	0.000451244	114	N	1036	1069
Q8BTM8	Parental	RFVPR	EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	VKAFG	4		872.1900454	3484.728981	0.000662267	11	N	1036	1069
Q8BTM8	Parental	SDGLR	LIALLEVLSQK	KMHRK	2		613.8900854	1225.764571	0.000451244	43	Y	76	87
Q8BTM8	Parental	SDGLR	LIALLEVLSQK	KMHRK	3		409.5959902	1225.764571	0.000622848	5	Y	76	87
Q8BTM8	Parental	EERVK	QKDLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1256.284963	3765.83149	0.000451244	29	N	529	563

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Parental	AQLEC	LDNGDGTCSVSYVPTEPGDYNINILFADTHIPGSPFK	AHVAP	3	C8:+57.021	1337.630316	4009.867549	0.000451244	2	N	1114	1151
Q8BTM8	Parental	GIVGK	SADFVVEAIGDDVGTLGFSVEGPSQAK	IECDD	2		1348.159027	2694.302453	0.000451244	212	N	593	620
Q8BTM8	Parental	GIVGK	SADFVVEAIGDDVGTLGFSVEGPSQAK	IECDD	3		899.1086178	2694.302453	0.000451244	366	N	593	620
Q8BTM8	Parental	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK	RLRNG	3	C33:+57.021	1254.999681	3761.975643	0.000451244	35	N	1964	2000
Q8BTM8	Parental	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK	RLRNG	4	C33:+57.021	941.5017106	3761.975643	0.000451244	24	N	1964	2000
Q8BTM8	Parental	RVKQK	DLGDGVYGFEYYPTIPGTYTVTITWGGQNIGR	SPFEV	3		1170.90045	3509.677949	0.000451244	43	N	531	563
Q8BTM8	Parental	GDAVR	DVDIIDHHDNTYTVK	YIPVQ	2		892.9266445	1783.837689	0.000451244	29	N	921	936
Q8BTM8	Parental	GDAVR	DVDIIDHHDNTYTVK	YIPVQ	3		595.620363	1783.837689	0.000451244	37	N	921	936
Q8BTM8	Parental	NQKVR	AWGPGLEGGIVGK	SADFV	2		620.8383841	1239.661168	0.000451244	27	N	580	593
Q8BTM8	Parental	VHVKK	NGQHVASSPIPVVISQSEIGDASR	VRVSG	3		816.7546207	2447.240462	0.000451244	20	N	2025	2049
Q8BTM8	Parental	GIWTR	EAGAGGLAIAVEGPSKAEISFEDR	KDGSC	2		1187.598408	2373.181216	0.000451244	5	N	2264	2288
Q8BTM8	Parental	GIWTR	EAGAGGLAIAVEGPSKAEISFEDR	KDGSC	3		792.0682052	2373.181216	0.000451244	13	N	2264	2288
Q8BTM8	Parental	DSLTK	VATVPQHATSGPGPADVSKV	VAKGL	3		640.0063289	1916.995587	0.001871652	1	N	2540	2560
Q8BTM8	Parental	ASKVK	AEGPGLNRTGVELGKPTHFTVNAK	TAGKG	4		624.0861918	2492.313567	0.001162105	1	N	876	900
Q8BTM8	Parental	TGTHK	VTVLFAGQHIAK	SPFEV	2		642.3776765	1282.739753	0.000451244	10	N	355	367
Q8BTM8	Parental	TGTHK	VTVLFAGQHIAK	SPFEV	3		428.5877176	1282.739753	0.000622848	8	N	355	367
Q8BTM8	Parental	TLVVK	WGDEHIPGSPYR	IMVP-	3		471.8902364	1412.647309	0.000735798	14	N	2631	2643
Q8BTM8	Parental	QHIAK	SPFEVYVDKSQGDASK	VTAQG	2		878.9235705	1755.831541	0.000451244	5	N	367	383
Q8BTM8	Parental	QHIAK	SPFEVYVDKSQGDASK	VTAQG	3		586.2849803	1755.831541	0.000662267	2	N	367	383
Q8BTM8	Parental	SSHSR	CGQSAAVASPGGSIDSR	DAEMP	2	C1:+57.021	810.3760332	1618.736466	0.000634081	4	N	7	24
Q8BTM8	Parental	SSHSR	CGQSAAVASPGGSIDSR	DAEMP	2	[0:-17.027,C1:+57.021	801.8625332	1601.709466	0.002145581	1	N	7	24
Q8BTM8	Parental	IINIK	FADQHVPGSPFSVK	VTGEG	3		505.9250581	1514.751774	0.001329271	1	N	2119	2133
Q8BTM8	Parental	KAPLR	VQVQDNEGCSVEATVKDNGNGTY	SCSYV	2	C9:+57.021	1242.551097	2483.086595	0.000451244	8	N	708	731
Q8BTM8	Parental	TIDAK	DAGEGLLAVQITDPEGKPKK	THIQD	3		689.3763105	2065.105531	0.001839721	1	N	1573	1593
Q8BTM8	Parental	EGPSK	AEISCTDNQDGTCSVSYLPVLPGDYSILVK	YNDQH	3	C5:+57.021,C13:+57.021	1101.191827	3300.552082	0.000451244	26	N	1907	1937
Q8BTM8	Parental	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGR	EEPCL	2		1447.280008	2892.544415	0.000451244	31	N	1964	1993
Q8BTM8	Parental	MSHLK	VGSAADIPINISETDLSLLTATVVPPSGR	EEPCL	3		965.1892717	2892.544415	0.000451244	29	N	1964	1993
Q8BTM8	Parental	DSLTK	VATVPQHATSGPGPADVSK	VVAKG	2		909.9713864	1817.927173	0.000451244	22	N	2540	2559
Q8BTM8	Parental	DSLTK	VATVPQHATSGPGPADVSK	VVAKG	3		606.9835243	1817.927173	0.000451244	46	N	2540	2559
Q8BTM8	Parental	EATVK	DNGNGTYSCSYVPR	KPVKH	2	C9:+57.021	795.3363767	1588.657153	0.000451244	11	N	724	738
Q8BTM8	Parental	GIWTR	EAGAGGLAIAVEGPSK	AEISF	2		713.8809773	1425.746355	0.000451244	41	N	2264	2280
Q8BTM8	Parental	ESGLK	VNQPASFAVSLNGAK	GAIDA	2		751.9022441	1501.788888	0.000451244	31	N	2346	2361
Q8BTM8	Parental	CMDNK	DGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFK	VPVHD	3	C4:+57.021	1193.884317	3578.62955	0.000451244	29	N	1406	1439
Q8BTM8	Parental	AVPCK	VEPGLGADNSVVR	FVPRE	2		656.8469375	1311.678275	0.000451244	21	N	1019	1032
Q8BTM8	Parental	TVNTK	DAGEGGLSLAIEGPSK	AEISC	2		750.8811743	1499.746749	0.000451244	20	N	1891	1907
Q8BTM8	Parental	KVASK	IVSPSGAAVPCK	VEPGL	2	C11:+57.021	593.3187386	1184.621877	0.001229886	2	N	1007	1019
Q8BTM8	Parental	EPTYF	TVDCTEAGQGDVSIGIK	CAPGV	2	C4:+57.021	875.4201064	1748.824613	0.000451244	9	N	792	809
Q8BTM8	Parental	AGKGK	LDVQFSGLAK	GDAVR	2		539.3011031	1076.586606	0.000451244	4	N	906	916
Q8BTM8	Parental	GDARR	LTVSSLQESGLK	VNQPA	2		631.354064	1260.692528	0.000451244	1	N	2334	2346
Q8BTM8	Parental	KNRTF	SVWYVPEVTGTHK	VTVLF	2		751.8860627	1501.756525	0.002813207	1	N	342	355
Q8BTM8	Parental	IPGTY	TVTITWGGQNIGR	SPFEV	2		701.8760293	1401.736459	0.000823681	6	N	550	563
Q8BTM8	Parental	ASRVR	VSGQGLHEGHTFEPAEFIIDTR	DAGYG	2		1220.598742	2439.181884	0.000622848	4	N	2051	2073
Q8BTM8	Parental	ASRVR	VSGQGLHEGHTFEPAEFIIDTR	DAGYG	3		814.0684281	2439.181884	0.000451244	3	N	2051	2073
Q8BTM8	Parental	AEVGV	PAEFGIWTR	EAGAG	2		538.7803378	1075.545076	0.000451244	2	N	2255	2264
Q8BTM8	Parental	VTIKY	GGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	EATTE	3	C25:+57.021	1291.307619	3870.899458	0.000698008	1	N	1235	1272
Q8BTM8	Parental	SIGIK	CAPGVVGPTEADIDFDIIRNDNDTF	TVKYT	2	C1:+57.021	1376.132255	2750.248909	0.000622848	10	N	809	834
Q8BTM8	Parental	SIGIK	CAPGVVGPTEADIDFDIIRNDNDTF	TVKYT	3	C1:+57.021	917.7574364	2750.248909	0.000451244	9	N	809	834
Q8BTM8	Parental	VYVDK	SQGDASKVTAQGPGLEPSGNIANK	TTYFE	2		1163.585832	2325.156064	0.000451244	4	N	376	400
Q8BTM8	Parental	VYVDK	SQGDASKVTAQGPGLEPSGNIANK	TTYFE	3		776.0598212	2325.156064	0.000451244	3	N	376	400
Q8BTM8	Parental	TILIK	YGGDEIPFSPYR	VRAVP	2		700.8282134	1399.640827	0.001463592	4	N	1621	1633
Q8BTM8	Parental	SGLAK	GDAVRDVDIIDHHDNTY	TVKYI	2		977.9486396	1953.881679	0.002212458	1	N	916	933
Q8BTM8	Parental	EAGTY	SLNVTYGGHQVPGSPFKVPVHDVTDASK	VKCSG	3		979.5020726	2935.482818	0.000823681	1	N	1422	1450
Q8BTM8	Parental	EYTPY	EEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C29:+57.021	1177.539098	3529.593893	0.000451244	15	N	1324	1357
Q8BTM8	Parental	CVSKR	IANLQTDLSDGLRLIALLEVLSQK	KMHRK	3		875.1730048	2622.495614	0.000622848	3	N	63	87
Q8BTM8	Parental	GIVGK	SADFVVEAIGDDVGTLGF	SVEGP	2		906.4390534	1810.862507	0.002296037	1	N	593	611
Q8BTM8	Parental	KTAGK	GKLDVQFSGLAK	GDAVR	3		421.5754777	1261.703033	0.000698008	5	N	904	916
Q8BTM8	Parental	DGVPV	PGSPFPLEAVAPTKPSK	VKAFG	2		861.9754091	1721.935218	0.002981883	1	N	1052	1069
Q8BTM8	Parental	SGDAR	RLTVSSLQESGLK	VNQPA	2		709.4046196	1416.793639	0.000451244	4	N	2333	2346
Q8BTM8	Parental	TVTIK	YGGQPVPNFPSK	LQVEP	2		645.8280164	1289.640433	0.001463592	7	N	1234	1246
Q8BTM8	Parental	QHIAK	SPFEVYVDK	SQGDA	2		542.2720113	1082.528423	0.000451244	9	N	367	376
Q8BTM8	Parental	RFIPR	ENGIYLIDVK	FNGTH	2		582.3194928	1162.623386	0.000622848	8	N	2395	2405
Q8BTM8	Parental	DGTCR	VTYCPTEPGNYIINIK	FADQH	2	C4:+57.021	941.4746847	1880.933769	0.000451244	10	N	2103	2119
Q8BTM8	Parental	GDGTY	KVEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	3	C36:+57.021	1471.016788	4410.026963	0.000451244	4	N	1317	1357
Q8BTM8	Parental	GDGTY	KVEYTPYEEGVHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	VRVHG	4	C36:+57.021	1103.514541	4410.026963	0.000823681	2	N	1317	1357
Q8BTM8	Parental	WQSGR	ALGALVDSCAPGLCPDWDSWDASKPV	NNARE	2	C9:+57.021,C14:+57.021	1394.141337	2786.267074	0.000622848	1	N	196	222

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BTM8	Parental	SCDVR	YWPQEAGEYAVHVLCNSEDI	RLSPF	2	C15:+57.021	1190.531448	2379.047296	0.000451244	8	N	634	654
Q8BTM8	Parental	PRSPY	TVTVGQACNPAACR	AIGRG	2	C8:+57.021,C13:+57.021	752.853451	1503.691302	0.000451244	29	N	470	484
Q8BTM8	Parental	GLGDK	VDVGKDQEFTVK	SKGAG	2		682.8569709	1363.698342	0.000823681	1	N	982	994
Q8BTM8	Parental	VTGPR	LVSNHSLHETSSVF	VDSLT	2		778.8893337	1555.763067	0.000451244	2	N	2520	2534
Q8BTM8	Parental	IPRSP	YTVTVGQACNPAACR	AIGRG	2	C9:+57.021,C14:+57.021	834.3851153	1666.754631	0.000451244	1	N	469	484
Q8BTM8	Parental	LIDVK	FNGTHIPGSPFK	IRVGE	2		651.3360086	1300.656417	0.000622848	1	N	2405	2417
Q8BTM8	Parental	LIDVK	FNGTHIPGSPFK	IRVGE	3		434.5599391	1300.656417	0.000451244	9	N	2405	2417
Q8BTM8	Parental	KYIPV	QQGPVGVNVTYGGDHIPK	SPFSV	3		622.6555191	1864.943157	0.001352548	1	N	940	958
Q8BTM8	Parental	SPFQV	TALAGDQPTVQTPLR	SQQLA	2		784.4260834	1566.836567	0.001463592	2	N	1738	1753
Q8BTM8	Parental	AIDAK	VHSPSGALEECYVTEIDQDK	YAVRF	2	C11:+57.021	1139.020913	2276.026226	0.000451244	1	N	2367	2387
Q8BTM8	Parental	AIDAK	VHSPSGALEECYVTEIDQDK	YAVRF	3	C11:+57.021	759.6832087	2276.026226	0.000622848	1	N	2367	2387
Q8BTM8	Parental	VDVTY	DGSPVPSSPFQVPVTEGCDPSR	VRVHG	2	C18:+57.021	1158.034355	2314.05311	0.001871652	4	N	1335	1357
Q8BTM8	Parental	VEVTY	DGVPVPGSPFPLEAVAPTKPSK	VKAFG	2		1095.594409	2189.173217	0.000451244	6	N	1047	1069
Q8BTM8	Parental	PLQFY	VDYVNCGHITAYGPGLTHGVVNKPATFTVNTK	DAGEG	4	C6:+57.021	858.4361736	3429.713495	0.002374549	4	N	1859	1891
Q8BTM8	Parental	TYTVK	YIPVQQGPVGVNVTY	GGDHI	2		817.4333771	1632.851154	0.000451244	4	N	936	951
Q8BTM8	Parental	GDAVR	DVDIIDHHDNTY	TVKYI	2		728.8211167	1455.626633	0.000823681	1	N	921	933
Q8BTM8	Parental	NFPSK	LQVEPAVDTSGVQCYGPGIEGQGVF	REATT	2	C14:+57.021	1304.123701	2606.231803	0.000451244	1	N	1246	1271
Q8BTM8	Parental	RVKQK	DLGDGVYGFEYYPTIPGTY	TVTIT	2		1063.983825	2125.95205	0.002663018	1	N	531	550
Q8BTM8	Parental	NSVVR	FVPREEGPYEVEVTY	DGVPV	2		907.4363138	1812.857028	0.0025889	1	N	1032	1047
Q8BTS4	Parental	PAQIK	QLLQNPPAGVDPIIWEQAK	VDNPD	2		1059.073643	2116.131687	0.000823681	2	N	297	316
Q8BTS4	Parental	EEQLR	VQLDTIQGELNAPTQFK	GRLNE	2		951.5025194	1900.989439	0.000851441	2	N	414	431
Q8BTZ7	Exosome	DPSAR	IGQNCSIGPNVSLGPGVVVEDGVCIR	RCTVL	2	C5:+57.021,C24:+57.021	1348.678421	2695.341242	0.000451244	4	N	261	287
Q8BTZ7	Exosome	DPSAR	IGQNCSIGPNVSLGPGVVVEDGVCIR	RCTVL	3	C5:+57.021,C24:+57.021	899.4548805	2695.341242	0.001699387	2	N	261	287
Q8BTZ7	Exosome	DPSAR	IGQNCSIGPNVSLGPGVVVEDGVCIRR	CTVLR	3	C5:+57.021,C24:+57.021	951.4885842	2851.442353	0.000451244	4	N	261	288
Q8BTZ7	Exosome	KHPER	LYSGPGIVGNVLVDPSAR	IGQNC	2		907.4944974	1812.973395	0.000451244	1	N	243	261
Q8BTZ7	Exosome	DAHIR	SHSWLESCIVGWR	CRVGQ	3	C8:+57.021	539.5931598	1615.756079	0.000622848	8	N	298	311
Q8BTZ7	Exosome	IGQPK	DFLTGMCLFLQSLR	QKHPE	2	C7:+57.021	850.9288593	1699.842119	0.000622848	2	N	223	237
Q8BTZ7	Parental	DPSAR	IGQNCSIGPNVSLGPGVVVEDGVCIRR	CTVLR	3	C5:+57.021,C24:+57.021	951.4885842	2851.442353	0.000823681	3	N	261	288
Q8BTZ7	Parental	KHPER	LYSGPGIVGNVLVDPSAR	IGQNC	2		907.4944974	1812.973395	0.001654178	1	N	243	261
Q8BU30	Exosome	NIIQK	DSVPVCPVDASGCFTEEVTHFVGQYVK	DADKN	3	C6:+57.021,C13:+57.021	1009.800494	3026.378081	0.000662267	4	N	344	371
Q8BU30	Exosome	NIIQK	DSVPVCPVDASGCFTEEVTHF	VGQYV	2	C6:+57.021,C13:+57.021	1177.00926	2352.00292	0.002981883	1	N	344	365
Q8BU30	Parental	ISRNR	YWGTPIPLWVSEDLEEVVCIGSVAELEELSGTK	ISDLH	3	C19:+57.021	1235.946694	3704.816682	0.001654178	2	N	461	494
Q8BU30	Parental	VKNAK	LSVFHGETEIQNQTDLLSLSGR	TLCVT	3		815.419238	2443.234314	0.000451244	2	N	1128	1150
Q8BU30	Parental	-M	VQQVPENISFPAEEEK	ILEFW	2		922.4577775	1842.899955	0.001943752	2	N	1	17
Q8BUK6	Parental	NKMLK	LNQEDSDNEKIALLQSLLDDANLR	KNELE	3		909.7985548	2726.372264	0.000622848	6	N	478	502
Q8BUK6	Parental	ISELR	QQNDELTTLADEAQSLKDEIDVLR	HSSDK	3		915.4581982	2743.351195	0.000451244	12	N	283	307
Q8BUK6	Parental	KKILK	GILDYNHEILGQQINDFTLPDVNLIGEHSDAAELGR	MLQLI	4		994.9978681	3975.960272	0.001162105	3	N	81	117
Q8BUK6	Parental	SDNEK	IALLQSLLDDANLR	KNELE	2		777.9466516	1553.877703	0.001463592	3	N	488	502
Q8BUM3	Exosome	GPLLR	LVAEVETPETAANSGPIVVHCSAGIGR	TGCFI	3	C21:+57.021	912.1328376	2733.375113	0.000451244	9	N	269	296
Q8BUM3	Exosome	EGKEK	CVHYWPTEEEAYGPFQIR	IQDMK	2	[0:-17.027,C1:+57.021	1133.007186	2263.998772	0.000622848	1	N	203	221
Q8BUM3	Exosome	EEFLK	IPSNFVNPEDLDIPGHASK	DRYKT	3		684.0133721	2049.016716	0.000451244	1	N	103	122
Q8BV13	Exosome	MRNLR	ELEDLIIEAVYTDIIQGK	LDQRN	3		688.0371833	2061.08815	0.000823681	4	N	126	144
Q8BV13	Exosome	NNIVK	TLHEWCDGCEAVLLGIEQQVLR	ANQYK	2	C6:+57.021,C9:+57.021	1313.641307	2625.267014	0.001463592	1	N	172	194
Q8BVE3	Exosome	FLLEK	LGESVQDLSSFDEYSSELK	SGRLE	2		1066.997661	2131.979722	0.000451244	32	N	341	360
Q8BVE3	Exosome	KILTK	LLEVSDDPQVLAVAAHDVGEYVR	HYPRG	3		832.4312551	2494.270365	0.000451244	11	N	396	419
Q8BVE3	Parental	FLLEK	LGESVQDLSSFDEYSSELK	SGRLE	2		1066.997661	2131.979722	0.000451244	30	N	341	360
Q8BVE3	Parental	KILTK	LLEVSDDPQVLAVAAHDVGEYVR	HYPRG	3		832.4312551	2494.270365	0.000451244	11	N	396	419
Q8BVG4	Exosome	RMDPK	ICPADPAFFSFINNSDLWVANIETGEER	RLTFC	3	C2:+57.021	1071.505	3211.491599	0.000451244	20	N	191	219
Q8BVG4	Exosome	RPQQR	LQLVLLPPALFIPAVESEAQR	QAAAR	2		1152.670451	2303.325301	0.001699387	1	N	374	395
Q8BVG4	Exosome	RPQQR	LQLVLLPPALFIPAVESEAQR	QAAAR	3		768.7829004	2303.325301	0.000451244	21	N	374	395
Q8BVG4	Parental	RMDPK	ICPADPAFFSFINNSDLWVANIETGEER	RLTFC	3	C2:+57.021	1071.505	3211.491599	0.000451244	4	N	191	219
Q8BVG4	Parental	RPQQR	LQLVLLPPALFIPAVESEAQR	QAAAR	3		768.7829004	2303.325301	0.002981883	1	N	374	395
Q8BWT1	Exosome	LSVQK	ALDLDPSKTNVSGGAIALGHPLGGSGSR	ITAHL	3		883.1319797	2646.372539	0.001162105	2	N	332	360
Q8BWT1	Exosome	HVGLR	VGVPTETGALTLNR	LCGSG	2		714.3967946	1426.777989	0.0025889	1	N	76	90
Q8BWT1	Exosome	SVFKK	DGTVTAGNASGVSDGAGAVIIASEDAVK	KHNFT	2		1266.625351	2531.235102	0.000451244	14	N	241	269
Q8BWT1	Exosome	SVFKK	DGTVTAGNASGVSDGAGAVIIASEDAVK	KHNFT	3		844.752834	2531.235102	0.002374549	1	N	241	269
Q8BWT1	Exosome	LTLNR	LCGSGFQSIVSGCQEICSK	DAEVV	2	C2:+57.021,C13:+57.021,C17:+57.021	1058.976477	2115.937354	0.000451244	15	N	90	109
Q8BWT1	Exosome	SVFKK	DGTVTAGNASGVSDGAGAVIIASEDAVKK	HNFTP	3		887.451155	2659.330065	0.000622848	4	N	241	270
Q8BWT1	Exosome	VAAKR	TPFGAYGGLLK	DFSAT	2		562.3114708	1122.607342	0.002663018	1	N	14	25
Q8BWT1	Exosome	GLDLK	LEDTLWAGLTDQHVK	LPMGM	3		575.9655821	1724.873346	0.000451244	3	N	143	158
Q8BWT1	Exosome	GGLLK	DFSATDLTEFAAR	AALSA	2		722.3416849	1442.66777	0.000451244	3	N	25	38
Q8BWT1	Parental	LSVQK	ALDLDPSKTNVSGGAIALGHPLGGSGSR	ITAHL	3		883.1319797	2646.372539	0.000451244	4	N	332	360
Q8BWT1	Parental	LSVQK	ALDLDPSKTNVSGGAIALGHPLGGSGSR	ITAHL	4		662.6009348	2646.372539	0.001162105	1	N	332	360
Q8BWT1	Parental	HVGLR	VGVPTETGALTLNR	LCGSG	2		714.3967946	1426.777989	0.001264573	2	N	76	90

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8BWT1	Parental	SVFKK	DGTVTAGNASGVSDGAGAVIIASEDAVK	KHNFT	2		1266.625351	2531.235102	0.000451244	9	N	241	269
Q8BWT1	Parental	LTLNR	LCGSGFQSIVSGCQEICSK	DAEVV	2	C2:+57.021,C13:+57.021,C17:+57.021	1058.976477	2115.937354	0.000451244	23	N	90	109
Q8BWY3	Exosome	SKVLK	LVDISYGGENGFNQAIELSTEVLSNVK	FIQEK	2		1448.73289	2895.45018	0.000451244	12	N	252	279
Q8BWY3	Exosome	SKVLK	LVDISYGGENGFNQAIELSTEVLSNVK	FIQEK	3		966.1578601	2895.45018	0.000823681	3	N	252	279
Q8BWY3	Exosome	GKEKK	VNIDFEPFKPINTSLYLCDNK	FHTEA	3	C18:+57.021	843.0897986	2526.245996	0.000451244	7	N	109	130
Q8BWY3	Exosome	NNYKK	FGATLEIVTDKSQEGSQFVK	GFGGI	3		728.7114703	2183.111011	0.000823681	4	N	384	404
Q8BWY3	Parental	SKVLK	LVDISYGGENGFNQAIELSTEVLSNVK	FIQEK	2		1448.73289	2895.45018	0.000451244	4	N	252	279
Q8BWY3	Parental	SKVLK	LVDISYGGENGFNQAIELSTEVLSNVK	FIQEK	3		966.1578601	2895.45018	0.000451244	7	N	252	279
Q8BWY3	Parental	GKEKK	VNIDFEPFKPINTSLYLCDNK	FHTEA	3	C18:+57.021	843.0897986	2526.245996	0.000622848	1	N	109	130
Q8BX94	Exosome	EWRTR	WFSPGNNPYTGAPDWLYAGHYFER	NFSDC	3		949.0984988	2844.272097	0.000451244	1	N	451	475
Q8BX94	Exosome	SQWER	TGKPFNPLLGETYELIR	EDLGF	3		650.0233199	1947.04656	0.000451244	1	N	147	164
Q8BX94	Exosome	IMYGK	WTECLWGIDPASYESFK	KQEKR	2	C4:+57.021	1044.972506	2087.929412	0.001943752	1	N	301	318
Q8BX94	Parental	EWRTR	WFSPGNNPYTGAPDWLYAGHYFER	NFSDC	3		949.0984988	2844.272097	0.001591523	1	N	451	475
Q8BXK9	Exosome	GSQRK	FLDGDELTLADCNLLPK	LHVVK	2	C12:+57.021	967.4827067	1932.949813	0.000451244	2	N	174	191
Q8BXK9	Exosome	GSQRK	FLDGDELTLADCNLLPK	LHVVK	3	C12:+57.021	645.3244045	1932.949813	0.001699387	1	N	174	191
Q8BXK9	Exosome	KGSQR	KFLDGDELTLADCNLLPK	LHVVK	2	C13:+57.021	1031.530188	2061.044777	0.000451244	1	N	173	191
Q8BXK9	Parental	GSQRK	FLDGDELTLADCNLLPK	LHVVK	2	C12:+57.021	967.4827067	1932.949813	0.000622848	2	N	174	191
Q8BXK9	Parental	KGSQR	KFLDGDELTLADCNLLPK	LHVVK	2	C13:+57.021	1031.530188	2061.044777	0.001871652	1	N	173	191
Q8BY71	Exosome	ETVHR	YYISFPTVLDITAEDPSR	SYLKL	2		1044.020742	2086.025884	0.000451244	5	N	259	277
Q8BY71	Exosome	EYSSK	VDENFDCVEADDVEGK	IRQII	2	C7:+57.021	920.8810111	1839.746422	0.000622848	2	N	91	107
Q8BY71	Parental	ETVHR	YYISFPTVLDITAEDPSR	SYLKL	2		1044.020742	2086.025884	0.000451244	5	N	259	277
Q8BY71	Parental	EYSSK	VDENFDCVEADDVEGK	IRQII	2	C7:+57.021	920.8810111	1839.746422	0.000823681	5	N	91	107
Q8BY71	Parental	SLLEK	ETNFKPFGTLLHTYTVPSQTGGETFTFQIHK	ADMTC	4		882.447017	3525.756868	0.002981883	1	N	129	160
Q8BYA0	Exosome	EQRNR	LCDLLGVPRPQLVPKPIPGS	-	3	C2:+57.021	719.4138883	2155.218265	0.000622848	1	N	1176	1196
Q8BYA0	Exosome	PTMDR	ILQIAESYLVVSDK	ARDAA	2		789.4434105	1576.871221	0.000622848	1	N	188	202
Q8BYA0	Exosome	WAFAR	AYEPQELTPFVTAISSALVIAAVFDR	NVNCR	3		936.8326482	2807.474545	0.000622848	1	N	478	504
Q8BYA0	Parental	KSDQK	LLSDSLTSDGDEDYDVPEGVETVIEQLLVGLK	DKDTV	3		1150.242207	3447.70322	0.000622848	1	N	340	372
Q8BYC6	Parental	MESLR	MGFGNLVTLDFPKEDYR	-	3		667.9966653	2000.966596	0.002519933	1	N	881	898
Q8BYC6	Parental	MDLIR	LQHQTELENQLEYNK	RRERE	2		943.9663011	1885.917002	0.000823681	1	N	676	691
Q8BYC6	Parental	LAERK	PPLFNMNAMSALYHIAQNDSPTLQSR	EWTDS	3	M6:+15.995	978.1414107	2931.400832	0.002981883	1	N	218	244
Q8BYI6	Exosome	EIKKR	ATSGGEWPQILVFPEGTCTNR	SCLIT	2	C18:+57.021	1160.555257	2319.094915	0.000451244	2	N	205	226
Q8BYI6	Parental	EIKKR	ATSGGEWPQILVFPEGTCTNR	SCLIT	2	C18:+57.021	1160.555257	2319.094915	0.000622848	7	N	205	226
Q8BYI6	Parental	TVKGK	VASPLEAPIFVVAPHSTFFDGIACVVAGLPSLVSR	NENAQ	3	C24:+57.021	1208.648366	3622.921697	0.001463592	1	N	131	166
Q8BYW1	Exosome	ILVEK	CAEFILEHGVSEEGIFRLPGQDNLVK	QLRDA	3	[0:-17.027,C1:+57.021	980.8237423	2939.447827	0.000823681	1	N	183	209
Q8BYW1	Parental	ILVEK	CAEFILEHGVSEEGIFRLPGQDNLVK	QLRDA	3	C1:+39.994	980.8237423	2939.447827	0.000451244	2	N	183	209
Q8BYW1	Parental	ILVEK	CAEFILEHGVSEEGIFRLPGQDNLVK	QLRDA	3	[0:-17.027,C1:+57.021	980.8237423	2939.447827	0.000451244	7	N	183	209
Q8BYW1	Parental	PPLSR	TDSFSNTASSPDATSPTGPLPSDQHQEDSGKAPR	ENPGD	4		872.1481688	3484.561475	0.000622848	1	N	393	427
Q8BYW1	Parental	EKRNR	VLEEEVKEFVK	SMEKP	3		450.2506597	1347.728579	0.000979378	1	N	626	637
Q8BYW1	Parental	GSTVK	EIATNPEEAGKFVFEVIPASSDQNR	IGQDS	2		1374.677918	2747.340236	0.000851441	1	N	98	123
Q8BYW1	Parental	APVPR	SSVGWDATEDPPLSR	TDSFS	2		808.8817056	1615.747811	0.001871652	2	N	378	393
Q8BYW1	Parental	EEAGK	FVFEVIPASSDQNR	IGQDS	2		804.9049838	1607.794368	0.000622848	1	N	109	123
Q8BZA9	Exosome	GAYMR	SLFGYFLSDLR	CSLPG	2		659.346042	1316.676484	0.000451244	7	N	203	214
Q8BZA9	Exosome	QVKMR	GKDFFDFICQLILGK	AGQRE	3	C9:+57.021	600.9836539	1799.927562	0.000979378	2	N	131	146
Q8BZA9	Exosome	KAGQR	ESVLPGAPGSGLESSLAEVFPVGK	HGSLG	2		1164.11062	2326.20564	0.001943752	1	N	150	174
Q8C079	Parental	RNQRK	DSEGYSESPDLEFEYADTD	KWAAE	3		723.6154488	2167.822946	0.0025889	1	N	57	76
Q8C079	Parental	YITAK	NSISVLDYPHCVVNELPELTAESLEAGDNNQFCWR	NLFSC	3	C11:+57.021,C33:+57.021	1359.630168	4075.867103	0.000622848	4	N	628	663
Q8C079	Parental	RRYDR	THSNPDFLPVDNCLQSVLGQR	VDLPE	3	C13:+57.021	799.7257423	2396.153827	0.000622848	3	N	785	806
Q8C0C7	Exosome	VGAVK	SLQALGEVIEAELR	STKCW	2		764.4230094	1526.830419	0.000451244	17	N	42	56
Q8C0C7	Exosome	VGAVK	SLQALGEVIEAELR	STKCW	3		509.9512729	1526.830419	0.000451244	9	N	42	56
Q8C0C7	Parental	VGAVK	SLQALGEVIEAELR	STKCW	2		764.4230094	1526.830419	0.000451244	10	N	42	56
Q8C0C7	Parental	VGAVK	SLQALGEVIEAELR	STKCW	3		509.9512729	1526.830419	0.000451244	13	N	42	56
Q8C0C7	Parental	ELLLR	RLEVADGGLDSAELATQLGVEHQAVVGAVK	SLQAL	3		1011.539075	3031.593825	0.002296037	1	N	12	42
Q8C0D5	Exosome	EIRKR	TSGLASPQLVFSHWEVIPSDPFWVPTTEEEYLHFGEK	ADSEN	4		1065.770994	4259.052776	0.002981883	1	N	1050	1087
Q8C0D5	Exosome	MFIIK	AVLPVAESFGFADEIR	KRTSG	2		860.9493913	1719.883183	0.001162105	1	N	1032	1048
Q8C0D5	Parental	RHAEK	LAAAQGQTSQGPTQDGGALETSPHEDEPRGDEPDVASVSR	QPVSQ	4		1015.97385	4059.8642	0.001162105	2	N	452	492
Q8C0E2	Exosome	GKKEK	YFLFYDGETVSGK	VSLSL	2		763.3646287	1524.713657	0.000451244	6	N	36	49
Q8C0E2	Exosome	VSLVK	DLARPGEITQSQAFDFEFTHVEKPYESYTGQNVK	LRYFL	4		983.725315	3930.87006	0.002019181	1	N	91	125
Q8C0G2	Exosome	LPTIK	NDASQQTNCGVAVLDKDIIQLSEYLK	EALHR	3	C9:+57.021	974.8223288	2921.443587	0.000698008	2	N	177	203
Q8C0G2	Parental	LPTIK	NDASQQTNCGVAVLDKDIIQLSEYLK	EALHR	3	C9:+57.021	974.8223288	2921.443587	0.000451244	5	N	177	203
Q8C0G2	Parental	ELQTK	LESLQGDGEQQSSETQDLQDQLKK	SEEEK	3		902.102303	2703.283509	0.000451244	13	N	378	402
Q8C0I1	Exosome	PEYQK	YGSVAFPNFEQGVACLR	EIAKQ	2	C15:+57.021	957.9622758	1913.908952	0.000451244	3	N	376	393
Q8C0I1	Exosome	KTTSK	TSINPSEAPPSIVNEDFLQELK	EARIS	2		1214.616266	2427.216933	0.000823681	2	N	134	156
Q8C0I1	Parental	PEYQK	YGSVAFPNFEQGVACLR	EIAKQ	2	C15:+57.021	957.9622758	1913.908952	0.000451244	13	N	376	393
Q8C0I1	Parental	ECKAR	RAASAAGASPAATPAAPESGTIPK	KRQEV	3		717.378714	2149.112742	0.000451244	9	N	48	72

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8C0I1	Parental	SQMNR	ILWVDENNLTAHVEAGITGQDLER	QLKES	3		898.4563518	2692.345656	0.000823681	3	N	252	276
Q8C0I1	Parental	KTTSK	TSINPSEAPPSIVNEDFLQELK	EARIS	2		1214.616266	2427.216933	0.001654178	3	N	134	156
Q8C0I1	Parental	CKARR	AASAAGASPAATPAAPESGTIPK	KRQEV	2		997.5136155	1993.011631	0.000451244	21	N	49	72
Q8C0I1	Parental	GMFER	IPDIVVWPTCHDDVVK	IVNLA	3	C10:+57.021	631.6577179	1891.949754	0.000451244	2	N	191	207
Q8C0I1	Parental	IAYIR	DLGLEYYVIGESFETSAPWDR	VIDLC	2		1224.074234	2446.132869	0.000451244	13	N	502	523
Q8C0I1	Parental	LPTLR	DWIQNTLGVSLEHK	TTSKT	3		547.2866556	1638.836567	0.002663018	2	N	116	130
Q8C0I1	Parental	ERQLK	ESGYCTGHEPDSLEFSTVGGWISTR	ASGMK	2	C5:+57.021	1386.614229	2771.212858	0.000823681	1	N	279	304
Q8C0L0	Parental	GLSGR	FFVTTLPAFFHAK	DGIFR	3		509.2787727	1524.812918	0.002981883	1	N	98	111
Q8C0L0	Parental	RAVVK	EGSVSPKEDGAHPADTQDVVEDALR	QRKSQ	3		874.7479715	2621.220515	0.000451244	9	N	299	324
Q8C0L0	Parental	AAAAA	EGLEQAALPAEESR	VQPMT	2		750.3709738	1498.726348	0.001763695	1	N	20	34
Q8C0L0	Parental	SVSPK	EDGAHPADTQDVVEDALR	QRKSQ	2		969.4459298	1936.87626	0.000451244	9	N	306	324
Q8C147	Exosome	KTLQK	QTFESETLECSEPDTQTGPR	HPLNV	2	C10:+57.021	1156.503084	2310.990569	0.000451244	6	N	160	180
Q8C147	Exosome	VCSGR	YFTESGLVGLLEQAAELFSTGGLYETVNEVYK	LVIPI	3		1176.587649	3526.739546	0.001162105	1	N	1722	1754
Q8C147	Exosome	EISHR	LEGFYGQCFGAEFVEVIKDSTPVDK	TKLDP	3	C8:+57.021	945.7900775	2834.346832	0.000451244	1	N	1829	1854
Q8C147	Exosome	SCQQK	QGASGESLLGYSWLPILLNER	LQTGS	2		1152.105672	2302.195743	0.000451244	1	N	658	679
Q8C147	Parental	KTLQK	QTFESETLECSEPDTQTGPR	HPLNV	2	C10:+57.021	1156.503084	2310.990569	0.000451244	41	N	160	180
Q8C147	Parental	VCSGR	YFTESGLVGLLEQAAELFSTGGLYETVNEVYK	LVIPI	3		1176.587649	3526.739546	0.000451244	3	N	1722	1754
Q8C147	Parental	KERKK	ISENFHCDLNSDQFK	GFLRA	3	C7:+57.021	618.6093153	1852.804546	0.001352548	1	N	299	314
Q8C147	Parental	RFSDR	FKDDITTIVNVVTSEIAALLVKPQK	ESEQA	3		914.8604268	2741.55788	0.000451244	5	N	1016	1041
Q8C147	Parental	RFSDR	FKDDITTIVNVVTSEIAALLVKPQK	ESEQA	4		686.3972701	2741.55788	0.001162105	2	N	1016	1041
Q8C147	Parental	EISHR	LEGFYGQCFGAEFVEVIKDSTPVDK	TKLDP	3	C8:+57.021	945.7900775	2834.346832	0.000851441	2	N	1829	1854
Q8C147	Parental	SCQQK	QGASGESLLGYSWLPILLNER	LQTGS	2		1152.105672	2302.195743	0.000451244	4	N	658	679
Q8C147	Parental	EVKVK	IAALYLPLVGIILDALPQLYDFTDAR	SGRSR	3		958.8725553	2873.594266	0.001699387	1	N	1211	1237
Q8C147	Parental	SGRSR	ASGSYEEQDVANGINQNVALAIAGNHFNLK	TSGAM	3		1048.850201	3143.527202	0.000451244	1	N	1242	1272
Q8C166	Exosome	AAQQR	SASQYFVLLLLTDGAVTDVEATCK	AVVDA	2	C23:+57.021	1301.159752	2600.303905	0.000662267	1	N	408	432
Q8C166	Exosome	DIGSK	SDPLCVLLQDVGGAWAELCR	TERVR	2	C5:+57.021,C19:+57.021	1130.048522	2258.081445	0.000451244	32	N	25	45
Q8C166	Exosome	DIGSK	SDPLCVLLQDVGGAWAELCR	TERVR	3	C5:+57.021,C19:+57.021	753.7016149	2258.081445	0.000451244	3	N	25	45
Q8C166	Exosome	DFLGK	SDPFLEFFR	QGDGK	2		579.285453	1156.555306	0.002981883	1	N	156	165
Q8C166	Exosome	PIQVR	CSDYDSDGSHDLIGTFHTTLAQLQAVPAEFECVHPEK	QQRKK	4	C1:+39.994,C32:+57.021	1040.217924	4156.840497	0.000451244	1	N	210	247
Q8C166	Exosome	PIQVR	CSDYDSDGSHDLIGTFHTTLAQLQAVPAEFECVHPEK	QQRKK	4	C1:+57.021,C32:+57.021	1044.474674	4173.867497	0.001162105	1	N	210	247
Q8C166	Exosome	LPQVR	LYGPTNFAPIINHVAR	FAAQA	3		594.993695	1781.957685	0.000622848	3	N	383	399
Q8C166	Parental	AAQQR	SASQYFVLLLLTDGAVTDVEATCK	AVVDA	2	C23:+57.021	1301.159752	2600.303905	0.000451244	6	N	408	432
Q8C166	Parental	DIGSK	SDPLCVLLQDVGGAWAELCR	TERVR	2	C5:+57.021,C19:+57.021	1130.048522	2258.081445	0.000451244	38	N	25	45
Q8C166	Parental	DIGSK	SDPLCVLLQDVGGAWAELCR	TERVR	3	C5:+57.021,C19:+57.021	753.7016149	2258.081445	0.000451244	34	N	25	45
Q8C166	Parental	PTWKR	FSVSLQHFCGGDLSTPIQVR	CSDYD	3	C9:+57.021	750.0445236	2247.110171	0.001162105	4	N	190	210
Q8C166	Parental	NLDKK	DFLGKSDPFLEFFR	QGDGK	3		573.291518	1716.851154	0.00091018	2	N	151	165
Q8C166	Parental	VQKLR	FGIYDIDNK	TPELG	2		542.7696358	1083.523672	0.000622848	15	Y	74	83
Q8C166	Parental	QNAPR	ETLAQTVLAEVPTQMVSYFR	AQGWA	2		1142.088634	2282.161667	0.001162105	1	N	493	513
Q8C166	Parental	LIGTF	HTTLAQLQAVPAEFECVHPEK	QQRKK	3	C16:+57.021	802.4024881	2404.184064	0.001352548	1	N	226	247
Q8C166	Parental	DFLGK	SDPFLEFFR	QGDGK	2		579.285453	1156.555306	0.001395409	4	N	156	165
Q8C166	Parental	PIQVR	CSDYDSDGSHDLIGTFHTTLAQLQAVPAEFECVHPEK	QQRKK	4	C1:+39.994,C32:+57.021	1040.217924	4156.840497	0.000622848	2	N	210	247
Q8C1A5	Exosome	CVYDR	VGAQNFEDVSYESTLK	ALADV	2		893.9288529	1785.842106	0.000451244	4	N	50	66
Q8C1A5	Exosome	LPFTR	EELGGLPEDFLSSLEK	AEDGK	2		881.9414289	1761.867258	0.002080925	2	N	193	209
Q8C1A5	Exosome	IDFNK	NLNEDTTFLPFTREELGGLPEDFLSSLEK	AEDGK	3		1104.549305	3310.624516	0.000451244	5	N	180	209
Q8C1A5	Exosome	IVLAK	VDQVLHTQTDADPAEEYAR	LCQEI	3		720.0069458	2156.997437	0.000451244	2	N	559	578
Q8C1A5	Exosome	NIKKR	LSLLCIDFNK	NLNED	2	C5:+57.021	611.8289391	1221.642278	0.001871652	2	N	170	180
Q8C1B7	Exosome	QLVNK	STSQGFCFNILCVGETGIGK	STLMD	2	C7:+57.021,C12:+57.021	1088.014148	2174.012696	0.000451244	21	N	34	54
Q8C1B7	Exosome	FQKKK	AAAQLLQSQAQQSGAQQTK	KDKDK	2		979.0090316	1956.002463	0.000451244	8	N	399	418
Q8C1B7	Exosome	NEELR	NLSLSGHVGFDSLPDQLVNK	STSQG	2		1070.555815	2139.096029	0.000451244	3	N	14	34
Q8C1B7	Parental	QLVNK	STSQGFCFNILCVGETGIGK	STLMD	2	C7:+57.021,C12:+57.021	1088.014148	2174.012696	0.000451244	8	N	34	54
Q8C1B7	Parental	FQKKK	AAAQLLQSQAQQSGAQQTK	KDKDK	2		979.0090316	1956.002463	0.000451244	23	N	399	418
Q8C1B7	Parental	NEELR	NLSLSGHVGFDSLPDQLVNK	STSQG	2		1070.555815	2139.096029	0.0007646	1	N	14	34
Q8C2Q3	Parental	AAPYR	TQSSASLAASYAAQQHPQAAASYR	GQPGS	2		1233.094355	2464.173111	0.000451244	3	N	517	541
Q8C2Q3	Parental	AAPYR	TQSSASLAASYAAQQHPQAAASYR	GQPGS	3		822.3988369	2464.173111	0.000451244	18	N	517	541
Q8C2Q3	Parental	RSPPR	ASYVAPLTAQPATYR	AQPSV	2		804.9231765	1607.830753	0.000451244	2	N	223	238
Q8C2Q3	Parental	GTGGF	SATFDYQQAFGNSTGGFDGQAR	QPTPP	2		1163.0125	2324.009399	0.000451244	10	N	181	203
Q8C3J5	Exosome	GDDVR	NAPGQYIQCFTVQPVLDEHPR	FKNKP	3	C9:+57.021	823.7378708	2468.190212	0.000451244	1	N	1398	1419
Q8C3J5	Exosome	HRQLK	ETLYETIIGYFDK	GKMWE	2		796.3986686	1590.781737	0.000451244	1	N	1276	1289
Q8C3J5	Exosome	LSHLK	DLIAWQIPFLGAGIK	IHEKR	2		821.4723053	1640.929011	0.002296037	2	N	1569	1584
Q8C3J5	Exosome	LIKHK	LSQGIFPTSFIHLK	EVTVE	3		529.9684868	1586.88206	0.000451244	6	N	53	67
Q8C3J5	Parental	VEKRR	NIENIIPAEIPLAQEVTTTLWEWGSIWK	QLYVA	3		1084.571605	3250.691414	0.000698008	12	N	75	103
Q8C3J5	Parental	GDDVR	NAPGQYIQCFTVQPVLDEHPR	FKNKP	3	C9:+57.021	823.7378708	2468.190212	0.000451244	8	N	1398	1419
Q8C3J5	Parental	HRQLK	ETLYETIIGYFDK	GKMWE	2		796.3986686	1590.781737	0.001654178	1	N	1276	1289
Q8C3J5	Parental	LSHLK	DLIAWQIPFLGAGIK	IHEKR	2		821.4723053	1640.929011	0.002727428	1	N	1569	1584

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8C3J5	Parental	LIKHK	LSQGIFPTSFIHLK	EVTVE	3		529.9684868	1586.88206	0.001591523	4	N	53	67
Q8C3J5	Parental	MKILR	TKPDYFAVGYYGQGFPSFLR	NKVFI	2		1157.071101	2312.126601	0.00307782	1	N	1336	1356
Q8C4Y3	Exosome	VEVKR	QIWQDNQALFGDEVSPLLKQYILEK	ESALF	3		992.5224737	2974.544021	0.001839721	1	N	147	172
Q8C4Y3	Exosome	ETLPR	DSPDLLLLLR	LLALG	2		577.8431351	1153.67067	0.001162105	1	N	333	343
Q8C570	Exosome	RTKLK	TSEQLDQPIAACCFNHNGNIFAYASSYDWSK	GHEFY	3	C12:+57.021,C13:+57.021	1198.861363	3593.56069	0.000451244	12	N	309	340
Q8C570	Exosome	ANDVR	CWEVQDSGQTIPK	AQQMH	2	C1:+57.021	774.3618631	1546.708126	0.001162105	2	N	67	80
Q8C570	Exosome	FKCHR	SNGTNTSAPQDIYAVNGIAFHPVHGTLATVGSDGR	FSFWD	4		881.9348051	3523.70802	0.001352548	1	N	261	296
Q8C5P5	Exosome	RISTY	STIAIPNIESIAELPLDYK	FTRFS	2		1044.067692	2086.119784	0.000451244	7	N	412	431
Q8C5P5	Exosome	QFLVK	EKGYDEGLLTLTPEDWDFCCK	GLALD	3	C19:+57.021,C20:+57.021	859.3823877	2575.123763	0.000451244	5	N	43	64
Q8C5P5	Exosome	CCSGK	CYFYDNYFDLPGALLCAR	VVDSL	2	C1:+57.021,C16:+57.021	1129.505959	2256.996318	0.000622848	6	N	133	151
Q8C5P5	Exosome	LVKEK	GYDEGLLTLTPEDWDFCCK	GLALD	2	C17:+57.021,C18:+57.021	1160.000903	2317.986207	0.000622848	2	N	45	64
Q8C5P5	Parental	RISTY	STIAIPNIESIAELPLDYK	FTRFS	2		1044.067692	2086.119784	0.000451244	11	N	412	431
Q8C6G8	Exosome	TGGQR	GQFYQCDLDGNLLDSWEGVR	VQCLW	2	C6:+57.021	1186.534522	2371.053444	0.000451244	1	N	447	467
Q8C6G8	Exosome	LLQQK	YLEYLEDGKVLEALQVLR	CELTP	3		717.7285727	2150.162318	0.000823681	1	N	199	217
Q8C6G8	Parental	TGGQR	GQFYQCDLDGNLLDSWEGVR	VQCLW	2	C6:+57.021	1186.534522	2371.053444	0.000451244	16	N	447	467
Q8C6G8	Parental	YHNTK	LDNNLDSVSLLIDHVCSR	RQFPC	3	C16:+57.021	690.6813624	2069.020687	0.000451244	8	N	302	320
Q8C708	Exosome	GLQPR	VTLEQISAFWK	REGRT	2		661.3616921	1320.707784	0.000451244	13	N	205	216
Q8C708	Exosome	DPSQR	APTLVWRPGGELWIEPTSSAR	ERSED	3		775.0784874	2322.212062	0.000622848	7	N	69	90
Q8C708	Parental	GLQPR	VTLEQISAFWK	REGRT	2		661.3616921	1320.707784	0.001654178	1	N	205	216
Q8CAQ8	Parental	TAYAR	LRGIEQAVQSHAVAEEEAR	KAHQL	3		698.3631754	2092.066126	0.000622848	7	N	544	563
Q8CAQ8	Parental	TAYAR	LRGIEQAVQSHAVAEEEAR	KAHQL	4		524.0243315	2092.066126	0.000622848	1	N	544	563
Q8CAQ8	Parental	DALNR	TSSVTLQTITAQNAAVQAVK	AHSNI	2		1016.05819	2030.10078	0.000451244	12	N	229	249
Q8CAQ8	Parental	VEAIR	VNCSDNEFTQALTAAIPPESLTR	GVYSE	2	C3:+57.021	1267.613501	2533.211401	0.001591523	3	N	599	622
Q8CAQ8	Parental	DLAGK	LSTDDLNSLIAHAHR	RIDQL	4		416.4699321	1661.848528	0.00091018	4	N	394	409
Q8CAQ8	Parental	YARLR	GIEQAVQSHAVAEEEAR	KAHQL	2		912.4482755	1822.880951	0.002374549	2	N	546	563
Q8CAQ8	Parental	DDFRK	ELDSITPDITPGWK	GMSIS	2		786.4017426	1570.787885	0.001591523	4	N	370	384
Q8CB87	Exosome	HRTLR	LCWSPPPSPSSTSAPQTPR	IVRQI	2	C2:+57.021	1026.994304	2051.973009	0.002813207	1	N	139	158
Q8CB87	Parental	DARPK	GSFLWSLPGALTAESGTVEAAF	RDQLA	2		1106.052573	2210.089547	0.000451244	5	N	229	251
Q8CB87	Parental	AEGQR	ELEAQLLHLSSTQQEANRENLQLR	EAERD	3		940.8253268	2819.45258	0.000622848	2	N	26	50
Q8CB87	Parental	ESHAK	GFQEAPGQVLSLDSLPTHLPQSLEEQLRPEEGNLGER	GQQDP	3		1357.685967	4070.0345	0.000451244	1	N	359	396
Q8CB87	Parental	ESHAK	GFQEAPGQVLSLDSLPTHLPQSLEEQLRPEEGNLGER	GQQDP	4		1018.516425	4070.0345	0.000622848	5	N	359	396
Q8CB87	Parental	DARPK	GSFLWSLPGALTAESGTVEAAFR	DQLAF	2		1184.103129	2366.190658	0.000451244	4	N	229	252
Q8CB87	Parental	LVDNK	TFALQLWDTAGQER	YHSLT	2		818.4104333	1634.805267	0.000622848	1	N	584	598
Q8CB87	Parental	ISISK	ISALQFSQEPASDPDPGPR	GSPEV	2		1006.49014	2010.964681	0.000451244	1	N	167	186
Q8CBW3	Exosome	LEETK	AYTTQSLASVAYQINALANNVLQLLDIQASQLR	RMESS	3		1197.644603	3589.910409	0.001591523	2	N	51	84
Q8CBW3	Exosome	QNLTR	VADYCENNYIQATDK	RKALE	2	C5:+57.021	902.3966313	1802.777663	0.000451244	3	N	28	43
Q8CBW3	Parental	LEETK	AYTTQSLASVAYQINALANNVLQLLDIQASQLR	RMESS	3		1197.644603	3589.910409	0.000622848	2	N	51	84
Q8CBW3	Parental	QNLTR	VADYCENNYIQATDK	RKALE	2	C5:+57.021	902.3966313	1802.777663	0.000451244	2	N	28	43
Q8CBW3	Parental	QNLTR	VADYCENNYIQATDKR	KALEE	3	C5:+57.021	653.9673912	1958.878774	0.001591523	1	N	28	44
Q8CBW3	Parental	AVVQY	SDPYADGDPAWAPK	NYIEK	2		745.3338599	1488.65212	0.00307782	1	N	404	418
Q8CBY8	Exosome	LRYMK	ESQVLLTLTNPVENLTHVTLLECDEGDPDNINSTAK	VVVPP	3	C23:+57.021	1327.319919	3978.936357	0.002212458	1	N	328	364
Q8CBY8	Parental	LRYMK	ESQVLLTLTNPVENLTHVTLLECDEGDPDNINSTAK	VVVPP	3	C23:+57.021	1327.319919	3978.936357	0.00091018	6	N	328	364
Q8CBY8	Parental	QKEVK	IEPAQAVAEVEPLPEDYYTRPVNLTEVTTL	QQRLL	3		1119.908722	3356.702767	0.000451244	10	N	222	252
Q8CC86	Exosome	KAAFR	FLGPDGSLLLDLLQLAEEPPPKAGQELR	VWPRG	3		1006.217162	3015.628085	0.000698008	1	N	425	453
Q8CC86	Exosome	KAAFR	FLGPDGSLLLDLLQLAEEPPPKAGQELR	VWPRG	4		754.9148213	3015.628085	0.002727428	1	N	425	453
Q8CC86	Exosome	AFRLR	DADVQFLASVLPPDTDPAFFEHLR	ALDCS	3		900.7821764	2699.323129	0.000451244	17	N	73	97
Q8CC86	Exosome	KAAFR	FLGPDGSLLLDLLQLAEEPPPK	AGQEL	2		1181.649381	2361.283162	0.000451244	4	N	425	447
Q8CC86	Exosome	KAAFR	FLGPDGSLLLDLLQLAEEPPPK	AGQEL	3		788.1021872	2361.283162	0.000451244	14	N	425	447
Q8CC86	Exosome	WRAGR	ACEAAEFELFFR	HCPFG	2	C2:+57.021	745.342942	1488.670284	0.000622848	4	N	34	46
Q8CC86	Exosome	YSVRR	SGLPNFLAVALALGELGYR	AVGVR	2		981.0468971	1960.078194	0.000451244	5	N	294	313
Q8CC86	Exosome	YSVRR	SGLPNFLAVALALGELGYR	AVGVR	3		654.3671981	1960.078194	0.000451244	6	N	294	313
Q8CC86	Exosome	RLAQK	GSEVNVIGIGTSVVTCPK	QPSMG	2	C16:+57.021	908.9775915	1815.939583	0.000451244	4	N	369	387
Q8CC86	Parental	KAAFR	FLGPDGSLLLDLLQLAEEPPPKAGQELR	VWPRG	3		1006.217162	3015.628085	0.000451244	7	N	425	453
Q8CC86	Parental	KAAFR	FLGPDGSLLLDLLQLAEEPPPKAGQELR	VWPRG	4		754.9148213	3015.628085	0.002374549	1	N	425	453
Q8CC86	Parental	KAAFR	FLGPDGSLLLDLLQLAEEPPPK	AGQEL	3		788.1021872	2361.283162	0.000451244	1	N	425	447
Q8CC86	Parental	YSVRR	SGLPNFLAVALALGELGYR	AVGVR	2		981.0468971	1960.078194	0.000451244	2	N	294	313
Q8CCF0	Exosome	APEYR	VIVDANNLTVEIENELNIIHK	FIRDK	3		797.436229	2389.285287	0.001264573	1	N	91	112
Q8CCF0	Parental	APEYR	VIVDANNLTVEIENELNIIHK	FIRDK	3		797.436229	2389.285287	0.000451244	4	N	91	112
Q8CCF0	Parental	TIRDR	SSGTASSVAFTPLQGLEIVNPQAAEK	KVAEA	2		1301.672104	2601.328608	0.001162105	4	N	444	470
Q8CCJ3	Parental	SELCK	AYDLPGDFLTQALTQR	LGRII	2		904.96303	1807.91046	0.002212458	1	N	144	160
Q8CCJ3	Parental	DCLRK	HIQDAPEEFISELAEYLIKPLNK	MYLEV	3		899.8098435	2696.406131	0.000451244	3	N	488	511
Q8CCK0	Exosome	IEYLA	AEILELAGNAAR	DNKKA	2		614.3387483	1226.661897	0.000451244	66	Y	57	69
Q8CCK0	Exosome	IEYLA	AEILELAGNAAR	DNKKA	3		409.8950988	1226.661897	0.001463592	3	Y	57	69
Q8CCK0	Exosome	RIAPR	HILLAVANDEELNQLLK	GVTIA	2		967.0418118	1932.068024	0.000451244	50	Y	79	96
Q8CCK0	Exosome	RIAPR	HILLAVANDEELNQLLK	GVTIA	3		645.0304745	1932.068024	0.000451244	67	Y	79	96

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CCK0	Exosome	YLAAE	ILELAGNAAR	DNKKA	2		514.2988947	1026.582189	0.000622848	2	Y	59	69
Q8CCK0	Exosome	GAPVY	MAAVIEYLAAEILELAGNAAR	DNKKA	2		1095.085894	2188.156188	0.0007646	1	N	48	69
Q8CCK0	Exosome	GAPVY	MAAVIEYLAAEILELAGNAAR	DNKKA	3		730.393196	2188.156188	0.000735798	11	N	48	69
Q8CCK0	Exosome	EYLAA	EILELAGNAAR	DNKKA	2		578.8201913	1155.624783	0.000451244	37	Y	58	69
Q8CCK0	Exosome	TFKYR	ISVGAPVYMAAVIEYLAAEILELAGNAAR	DNKKA	3		992.5357262	2974.583779	0.000451244	2	N	40	69
Q8CCK0	Exosome	TFKYR	ISVGAPVYMAAVIEYLAAEILELAGNAAR	DNKKA	3	M9:+15.995	997.8673929	2990.578779	0.000451244	22	N	40	69
Q8CCK0	Exosome	PVYMA	AVIEYLAAEILELAGNAAR	DNKKA	4		497.5274471	1986.078588	0.002212458	2	N	50	69
Q8CCK0	Parental	IEYLA	AEILELAGNAAR	DNKKA	2		614.3387483	1226.661897	0.000451244	149	Y	57	69
Q8CCK0	Parental	IEYLA	AEILELAGNAAR	DNKKA	3		409.8950988	1226.661897	0.000662267	10	Y	57	69
Q8CCK0	Parental	RIAPR	HILLAVANDEELNQLLK	GVTIA	2		967.0418118	1932.068024	0.000451244	16	Y	79	96
Q8CCK0	Parental	RIAPR	HILLAVANDEELNQLLK	GVTIA	3		645.0304745	1932.068024	0.000451244	10	Y	79	96
Q8CCK0	Parental	YLAAE	ILELAGNAAR	DNKKA	2		514.2988947	1026.582189	0.000622848	1	Y	59	69
Q8CCK0	Parental	GAPVY	MAAVIEYLAAEILELAGNAAR	DNKKA	2		1095.085894	2188.156188	0.000451244	5	N	48	69
Q8CCK0	Parental	GAPVY	MAAVIEYLAAEILELAGNAAR	DNKKA	3		730.393196	2188.156188	0.000735798	19	N	48	69
Q8CCK0	Parental	EYLAA	EILELAGNAAR	DNKKA	2		578.8201913	1155.624783	0.000451244	6	Y	58	69
Q8CCK0	Parental	HILLA	VANDEELNQLLK	GVTIA	2		693.3677027	1384.719805	0.000622848	1	Y	84	96
Q8CCK0	Parental	RHILL	AVANDEELNQLLK	GVTIA	2		728.8862597	1455.756919	0.001463592	1	Y	83	96
Q8CCS6	Parental	EADAR	SIYVGNVDYGATAEELEAHFHGCGSVNR	VTILC	3	C23:+57.021	1018.133677	3051.377632	0.000451244	6	N	168	196
Q8CCS6	Parental	EADAR	SIYVGNVDYGATAEELEAHFHGCGSVNR	VTILC	4	C23:+57.021	763.852208	3051.377632	0.001162105	2	N	168	196
Q8CCS6	Parental	AGEGD	PGGAGDYGNGLESEELEPGELLPEPEPEEEPPRPR	APPGA	3		1248.250535	3741.728206	0.000622848	2	N	39	74
Q8CD10	Parental	FKTVK	TNETEYQDPTVKEPGVNTTLQVR	FFGKR	3		873.7685955	2618.282387	0.000823681	1	N	211	234
Q8CD10	Parental	DTVFK	IFDLDGDECLSHGEFLGVLK	NRMHR	3	C9:+57.021	755.3686729	2263.082619	0.000622848	1	N	369	389
Q8CDN6	Exosome	RNKVR	IDQYQGADAVGLEEK	IKQHL	2		818.3971886	1634.778777	0.000451244	14	N	87	102
Q8CDN6	Exosome	LRYVK	FQNVNSVTLFVQSNQGEEETTR	ISYFT	2		1264.107128	2526.198657	0.000451244	16	N	237	259
Q8CDN6	Exosome	FFRNK	VRIDQYQGADAVGLEEK	IKQHL	2		945.9819511	1889.948302	0.000622848	4	N	85	102
Q8CDN6	Exosome	EEAER	SEPTQALELTEDDIKEDGIVPLR	YVKFQ	3		856.7733466	2567.29664	0.000451244	13	N	211	234
Q8CDN6	Exosome	-M	VGVKPVGSDPDFQPELSGAGSR	LAVVK	3		733.7067192	2198.096758	0.000823681	8	N	1	23
Q8CDN6	Exosome	PFINK	AGCECLNESDEHGFDNCLRK	DMSFL	4	C3:+57.021,C5:+57.021,C17:+57.021	603.500859	2409.972236	0.001591523	1	N	132	152
Q8CDN6	Exosome	PFINK	AGCECLNESDEHGFDNCLR	KDMSF	3	C3:+57.021,C5:+57.021,C17:+57.021	761.6335577	2281.877273	0.000698008	4	N	132	151
Q8CDN6	Exosome	-MV	GVKPVGSDPDFQPELSGAGSR	LAVVK	3		700.6839145	2099.028344	0.002663018	1	N	2	23
Q8CDN6	Parental	RNKVR	IDQYQGADAVGLEEK	IKQHL	2		818.3971886	1634.778777	0.000451244	32	N	87	102
Q8CDN6	Parental	LRYVK	FQNVNSVTLFVQSNQGEEETTR	ISYFT	2		1264.107128	2526.198657	0.000451244	8	N	237	259
Q8CDN6	Parental	FFRNK	VRIDQYQGADAVGLEEK	IKQHL	2		945.9819511	1889.948302	0.000451244	4	N	85	102
Q8CDN6	Parental	EEAER	SEPTQALELTEDDIKEDGIVPLR	YVKFQ	3		856.7733466	2567.29664	0.000622848	9	N	211	234
Q8CDN6	Parental	-M	VGVKPVGSDPDFQPELSGAGSR	LAVVK	2		1100.056179	2198.096758	0.000451244	6	N	1	23
Q8CDN6	Parental	-M	VGVKPVGSDPDFQPELSGAGSR	LAVVK	3		733.7067192	2198.096758	0.002145581	3	N	1	23
Q8CDN6	Parental	PFINK	AGCECLNESDEHGFDNCLRK	DMSFL	4	C3:+57.021,C5:+57.021,C17:+57.021	603.500859	2409.972236	0.000451244	1	N	132	152
Q8CDN6	Parental	PFINK	AGCECLNESDEHGFDNCLR	KDMSF	3	C3:+57.021,C5:+57.021,C17:+57.021	761.6335577	2281.877273	0.001229886	2	N	132	151
Q8CEC0	Parental	LNKGR	AYTASLGETAVAFDFGPLVTVSK	NIFEQ	2		1172.607713	2343.199826	0.000451244	2	N	230	253
Q8CEC0	Parental	IFEQK	DRDVVAYPLYILYENGETFLTYVSLLHSPGNIGK	LLGPL	4		965.0008851	3855.97234	0.000451244	4	N	259	293
Q8CEC0	Parental	ELALK	LASGEDDPFASDFSCPIK	LHRDP	2	C15:+57.021	978.4384962	1954.861392	0.000451244	8	N	377	395
Q8CEC6	Exosome	INMLK	LGYFPGQCEWIYCPGDAISSVAASEK	STGKI	2	C8:+57.021,C13:+57.021	1453.162269	2904.308938	0.000698008	3	N	172	198
Q8CEC6	Exosome	INMLK	LGYFPGQCEWIYCPGDAISSVAASEK	STGKI	3	C8:+57.021,C13:+57.021	969.1107795	2904.308938	0.000451244	6	N	172	198
Q8CEC6	Parental	EGSEK	TELSEREPALAVAGSEENDDENEER	WVGPL	3		930.4168388	2788.227116	0.001591523	1	N	24	49
Q8CEC6	Parental	INMLK	LGYFPGQCEWIYCPGDAISSVAASEK	STGKI	3	C8:+57.021,C13:+57.021	969.1107795	2904.308938	0.000622848	1	N	172	198
Q8CFI7	Exosome	MSVQR	IVEDAPPIDLQAEAQHASGEVEEPPR	YLLKF	3		933.1266714	2796.356614	0.001763695	1	N	57	83
Q8CFI7	Exosome	PIMLR	STYCLLNGLTDRDLCELNECPLDPGGYFIINGSEK	VLIAQ	3	C4:+57.021,C15:+57.021,C20:+57.021	1345.292121	4032.852964	0.002981883	1	N	157	192
Q8CFI7	Parental	MSVQR	IVEDAPPIDLQAEAQHASGEVEEPPR	YLLKF	3		933.1266714	2796.356614	0.000451244	7	N	57	83
Q8CFQ3	Exosome	YPTEK	IIWDENIVPTEYYSGEGCLALPK	LNLQF	2	C18:+57.021	1334.15447	2666.29334	0.001871652	1	N	431	454
Q8CFQ3	Exosome	MSRVK	NSGTACPDAAPDAAQVATFFPFHEYFANAPQPIFK	GRSYE	3	C6:+57.021	1266.594989	3796.761567	0.000662267	1	N	952	987
Q8CFV9	Exosome	GRGSK	QLGIPTANFPEQVVDNLPADVSTGIYYGWASVGSGDVHK	MVVSI	3		1368.011791	4101.011973	0.000451244	3	N	21	60
Q8CFV9	Exosome	LRPEK	NFDSLESLISAIQGDIEEAKK	QLDLP	3		769.7291896	2306.164169	0.001395409	1	N	107	128
Q8CFX1	Exosome	YRPVR	EQDAYSTLLSHIFHCR	KESFI	4	C15:+57.021	494.9879447	1975.920579	0.000451244	1	N	451	467
Q8CFX1	Exosome	GQVRR	ELQKPDGFQSLTPTFAGVLVHIDNLR	WEGVP	4		724.64006	2894.52904	0.001264573	1	N	319	345
Q8CFX1	Exosome	YRQLK	TVEDYQTLNKDIETQVQQDGLWEAGR	IFYFS	3		1012.82354	3035.44722	0.001329271	1	N	109	135
Q8CG03	Exosome	KIQNK	LTDLETLALLIAALSHDLDHR	GVNNS	3		777.4291858	2329.264158	0.000451244	5	N	627	648
Q8CG03	Exosome	KIQNK	LTDLETLALLIAALSHDLDHR	GVNNS	4		583.3238394	2329.264158	0.000451244	26	N	627	648
Q8CG03	Exosome	AQTLK	ITDFSFSDFELSDLETALCTIR	MFTDL	2	C19:+57.021	1290.612635	2579.20967	0.000451244	22	N	545	567
Q8CG03	Exosome	AQTLK	ITDFSFSDFELSDLETALCTIR	MFTDL	3	C19:+57.021	860.7443567	2579.20967	0.000451244	1	N	545	567
Q8CG03	Exosome	KEGIR	AHTESCSCSLQQSPHADNTTPGAPAR	KISAS	3	C6:+57.021,C8:+57.021	927.40877	2779.20291	0.001591523	1	N	63	89

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CG03	Exosome	PIQQR	IAELVAAEFFDQGDR	ERKEL	2		840.9155485	1679.815497	0.000622848	6	N	767	782
Q8CG03	Exosome	MQVQK	CTIFIVDEDCPDSFSR	VFHME	2	C1:+57.021,C10:+57.021	980.9244674	1959.833335	0.000451244	4	N	356	372
Q8CG03	Exosome	EEETR	ELQALSAAVVPSAQTLK	ITDFS	2		863.4914234	1724.967247	0.000451244	9	N	528	545
Q8CG03	Exosome	PIQQR	IAELVAAEFFDQGDRER	KELNM	2		983.4874007	1964.959201	0.000870037	1	N	767	784
Q8CG03	Exosome	PIQQR	IAELVAAEFFDQGDRER	KELNM	3		655.9942004	1964.959201	0.000622848	8	N	767	784
Q8CG03	Exosome	LENKR	NQVLLDLASLIFEEQQSLEVILKK	IAATI	3		924.192065	2769.552795	0.000870037	2	N	319	343
Q8CG03	Exosome	FLISR	LFDVAEGSTLEEASNNCIR	LEWNK	2	C17:+57.021	1062.997241	2123.978882	0.000451244	5	N	193	212
Q8CG03	Parental	KIQNK	LTDLETLALLIAALSHDLDHR	GVNNS	4		583.3238394	2329.264158	0.000451244	7	N	627	648
Q8CG03	Parental	AQTLK	ITDFSFSDFELSDLETALCTIR	MFTDL	2	C19:+57.021	1290.612635	2579.20967	0.000823681	3	N	545	567
Q8CG19	Exosome	TPDHR	HCQDIDECQQGNLCMNGQCR	NTDGS	3	C2:+57.021,C8:+57.021,C14:+57.021,M15:+15.995,C19:+57.021	846.9926374	2537.954512	0.001162105	2	N	1067	1087
Q8CG19	Exosome	CPRGK	GLVPAGESSYDTGGENYKDADECLLFGEEICK	NGYCL	3	C23:+57.021,C31:+57.021	1175.188923	3522.543368	0.000451244	18	N	1396	1428
Q8CG19	Exosome	TEGFR	GWNGQCLDVDECLQPK	VCTNG	2	C6:+57.021,C12:+57.021	959.9248017	1917.834003	0.000451244	6	N	1022	1038
Q8CG19	Exosome	ASEKR	CVQPTESNEQIEETDVYQDLCWEHLSEEYVCSRPLVGK	QTTYT	4	C1:+57.021,C21:+57.021,C31:+57.021	1157.52308	4626.061119	0.000451244	11	N	1496	1534
Q8CG19	Exosome	EEICK	NGYCLNTQPGYECYCK	QGTYY	2	C4:+57.021,C13:+57.021,C15:+57.021	1013.908063	2025.800526	0.000451244	10	N	1428	1444
Q8CG19	Parental	ASEKR	CVQPTESNEQIEETDVYQDLCWEHLSEEYVCSRPLVGK	QTTYT	4	C1:+57.021,C21:+57.021,C31:+57.021	1157.52308	4626.061119	0.000823681	2	N	1496	1534
Q8CG19	Parental	EGSYK	CLCLPGYIPSDKPNYCTPLNSALNLDKESDLE	-	3	C1:+57.021,C3:+57.021,C16:+57.021	1232.912582	3695.714345	0.000735798	5	N	1680	1712
Q8CG29	Exosome	GLYAR	LFDFLVEAINR	AMQKP	2		668.8671416	1335.718683	0.000451244	7	N	360	371
Q8CG29	Exosome	VQHVK	DIILQSNPLLEAFGNAK	TVRNN	2		922.0021552	1841.98871	0.000451244	11	N	141	158
Q8CG29	Exosome	VQHVK	DIILQSNPLLEAFGNAK	TVRNN	3		615.0040368	1841.98871	0.000451244	2	N	141	158
Q8CG29	Exosome	GNYAR	VESVDLLAFPAYLLGIDSGR	LQEKL	2		1068.073309	2134.131018	0.000451244	28	N	296	316
Q8CG29	Exosome	GNYAR	VESVDLLAFPAYLLGIDSGR	LQEKL	3		712.384806	2134.131018	0.000451244	2	N	296	316
Q8CG29	Exosome	EIFQK	NGFEQFCINFVNEK	LQQIF	2	C7:+57.021	873.4015197	1744.787439	0.000622848	2	N	395	409
Q8CG29	Parental	NSINR	NFVGDYLGLEERPELR	QFLAK	2		953.9870365	1905.958473	0.000622848	6	N	737	753
Q8CG29	Parental	NSINR	NFVGDYLGLEERPELR	QFLAK	3		636.327291	1905.958473	0.001162105	3	N	737	753
Q8CG29	Parental	GLYAR	LFDFLVEAINR	AMQKP	2		668.8671416	1335.718683	0.000451244	34	N	360	371
Q8CG29	Parental	VQHVK	DIILQSNPLLEAFGNAK	TVRNN	2		922.0021552	1841.98871	0.000451244	40	N	141	158
Q8CG29	Parental	VQHVK	DIILQSNPLLEAFGNAK	TVRNN	3		615.0040368	1841.98871	0.000451244	10	N	141	158
Q8CG29	Parental	GNYAR	VESVDLLAFPAYLLGIDSGRLQEK	LTSRK	3		878.4782053	2632.411216	0.000451244	8	N	296	320
Q8CG29	Parental	GNYAR	VESVDLLAFPAYLLGIDSGR	LQEKL	2		1068.073309	2134.131018	0.000451244	24	N	296	316
Q8CG29	Parental	GNYAR	VESVDLLAFPAYLLGIDSGR	LQEKL	3		712.384806	2134.131018	0.000451244	17	N	296	316
Q8CG29	Parental	ELTLK	AEQEEYVQEGIR	WTPIE	2		725.8445918	1449.673584	0.000451244	9	N	420	432
Q8CG29	Parental	YFNNK	IVCDLIENK	LSPPG	2	C3:+57.021	552.2921895	1102.568779	0.001699387	1	N	442	451
Q8CG29	Parental	EIFQK	NGFEQFCINFVNEK	LQQIF	2	C7:+57.021	873.4015197	1744.787439	0.000451244	1	N	395	409
Q8CG29	Parental	HYAGK	VSYDVSGFCER	NRDVL	2	C9:+57.021	659.7905423	1317.565485	0.001463592	1	N	508	519
Q8CG29	Parental	SRRPR	ARPPSEHSTEFLNVPDQGVAGMQRK	RSIGQ	4	M22:+15.995	692.595511	2766.350844	0.001871652	1	N	996	1021
Q8CG29	Parental	SLSTR	QDDFFILQEEAADSF	LESIF	2		887.8944787	1773.773357	0.002884417	1	N	827	842
Q8CG29	Parental	GPRCR	ALYQYIGQDVDELSFNVNEVIEILIEDSSGWWK	GRLHG	3		1291.63555	3871.883251	0.0025889	1	N	1047	1080
Q8CGC7	Exosome	EYKEK	TGQEYKPGNPSAAAVQTVSTK	SSSNT	3		712.0312028	2133.070209	0.000451244	21	N	794	815
Q8CGC7	Exosome	SSAPK	ERPAPAVSSTCATAEDSSVLYSR	VAVQG	3	C11:+57.021	818.724067	2453.148801	0.000451244	7	N	733	756
Q8CGC7	Exosome	QLQRR	GFFICDQPYEPVSPYSCR	EAPCI	2	C5:+57.021,C17:+57.021	1111.487766	2220.959932	0.001162105	5	N	675	693
Q8CGC7	Exosome	ELYAR	VYEELLAIPVVR	GRKTE	2		700.9115491	1399.807498	0.000451244	9	N	1195	1207
Q8CGC7	Exosome	AKLEK	VLEDIQLNLFTR	ASEDL	2		730.9095378	1459.803476	0.001162105	4	N	1403	1415
Q8CGC7	Exosome	TEKEK	FAGGDYTTTIEAFISASGR	AIQGA	2		982.4739589	1962.932318	0.000451244	5	N	1215	1234
Q8CGC7	Exosome	AEIKK	LGVENCYFPIFVSQAALEK	EKNHI	3	C6:+57.021	729.0384871	2184.092061	0.000451244	3	N	1070	1089
Q8CGC7	Exosome	LDAGK	VAQIPFCGEIDCEDWIK	KMTAR	2	C7:+57.021,C12:+57.021	1040.47941	2078.94322	0.001591523	1	N	1441	1458
Q8CGC7	Exosome	LSKRK	LTWFVNEGLVDGWDDPRFPTVR	GVLRR	3		873.7717231	2618.291769	0.001162105	1	N	437	459
Q8CGC7	Parental	EYKEK	TGQEYKPGNPSAAAVQTVSTK	SSSNT	2		1067.542904	2133.070209	0.001463592	2	N	794	815
Q8CGC7	Parental	EYKEK	TGQEYKPGNPSAAAVQTVSTK	SSSNT	3		712.0312028	2133.070209	0.000451244	36	N	794	815
Q8CGC7	Parental	SSAPK	ERPAPAVSSTCATAEDSSVLYSR	VAVQG	3	C11:+57.021	818.724067	2453.148801	0.000451244	9	N	733	756
Q8CGC7	Parental	SSAPK	ERPAPAVSSTCATAEDSSVLY	SRVAV	2	C11:+57.021	1106.015631	2210.015661	0.000451244	6	N	733	754
Q8CGC7	Parental	LKAEK	ASKDQVDSAVQELLQLK	AQYKS	2		936.5078018	1871.000004	0.000451244	4	N	922	939
Q8CGC7	Parental	LKAEK	ASKDQVDSAVQELLQLK	AQYKS	3		624.6744678	1871.000004	0.000451244	3	N	922	939
Q8CGC7	Parental	QPHPR	TGNKYNVYPTYDFACPIVDSIEGVTHALR	TTEYH	3	C15:+57.021	1100.871683	3299.591648	0.000451244	1	N	366	395
Q8CGC7	Parental	QPHPR	TGNKYNVYPTYDFACPIVDSIEGVTHALR	TTEYH	4	C15:+57.021	825.905712	3299.591648	0.000451244	3	N	366	395
Q8CGC7	Parental	EYKEK	TGKDYVPGQPPASQNSHSNPVSNAQPAGAEKPEAK	VLFDR	4		890.4361749	3557.7135	0.001162105	1	N	867	902
Q8CGC7	Parental	AKLEK	VLEDIQLNLFTR	ASEDL	2		730.9095378	1459.803476	0.000451244	3	N	1403	1415
Q8CGC7	Parental	TEKEK	FAGGDYTTTIEAFISASGR	AIQGA	2		982.4739589	1962.932318	0.000451244	1	N	1215	1234
Q8CGC7	Parental	AEIKK	LGVENCYFPIFVSQAALEK	EKNHI	3	C6:+57.021	729.0384871	2184.092061	0.000823681	1	N	1070	1089
Q8CGC7	Parental	RTGNK	YNVYPTYDFACPIVDSIEGVTHALR	TTEYH	3	C11:+57.021	967.4693383	2899.384615	0.000823681	4	N	370	395
Q8CGC7	Parental	QLQRR	GFFICDQPYEPVSPY	SCREA	2	C5:+57.021	909.9061035	1817.796607	0.001699387	1	N	675	690

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CGC7	Parental	FLRTR	EFLWQEGHSAFATFEEAADEVLQILELYAR	VYEEL	3		1171.572333	3511.693599	0.000451244	1	N	1165	1195
Q8CGP4	Exosome	RITPR	HLQLAIRNDEELNK	LLGRV	2		846.9555393	1691.895479	0.000451244	159	Y	82	96
Q8CGP4	Exosome	RITPR	HLQLAIRNDEELNK	LLGRV	3		564.9729596	1691.895479	0.000451244	991	Y	82	96
Q8CGP4	Exosome	RITPR	HLQLAIRNDEELNK	LLGRV	4		423.9816697	1691.895479	0.000451244	66	Y	82	96
Q8CGP4	Exosome	SRSSR	AGLQFPVGR	VHRLL	2		472.7697731	943.5239462	0.000451244	1500	Y	21	30
Q8CGP4	Exosome	QLAIR	NDEELNKLLGR	VTIAQ	2		650.8469375	1299.678275	0.000451244	82	N	89	100
Q8CGP4	Exosome	QLAIR	NDEELNKLLGR	VTIAQ	3		434.2338916	1299.678275	0.000451244	1253	N	89	100
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPNIQAV	LLPKK	2		740.4306374	1478.845675	0.000451244	735	Y	100	115
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPNIQAV	LLPKK	3		493.9563583	1478.845675	0.000451244	21	Y	100	115
Q8CGP4	Exosome	RVTIA	QGGVLPNIQAVLLPK	KTESH	2		773.9699298	1545.92426	0.000451244	2	Y	104	119
Q8CGP4	Exosome	RVTIA	QGGVLPNIQAVLLPK	KTESH	2	[0:-17.027	765.4564298	1528.89726	0.001943752	3	Y	104	119
Q8CGP4	Exosome	GRVTI	AQGGVLPNIQAVLLPK	KTESH	2		809.4884867	1616.961373	0.000451244	33	Y	103	119
Q8CGP4	Exosome	LGRVT	IAQGGVLPNIQAVLLPK	KTESH	2		866.0305187	1730.045437	0.000451244	24	Y	102	119
Q8CGP4	Exosome	LLGRV	TIAQGGVLPNIQAVLLPK	KTESH	2		916.554358	1831.093116	0.000451244	20	Y	101	119
Q8CGP4	Exosome	LLGRV	TIAQGGVLPNIQAVLLPK	KTESH	3		611.372172	1831.093116	0.000622848	2	Y	101	119
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPNIQAVLLPK	KTESH	2		966.088565	1930.16153	0.000451244	1015	Y	100	119
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPNIQAVLLPK	KTESH	3		644.3949767	1930.16153	0.000451244	301	Y	100	119
Q8CGP4	Exosome	QGGVL	PNIQAVLLPK	KTESH	2		546.8429381	1091.670276	0.000451244	57	Y	109	119
Q8CGP4	Exosome	APVYL	AAVLEYLTAEVLELAGNAAR	DNKKT	2		1037.563108	2073.110617	0.000451244	54	N	52	72
Q8CGP4	Exosome	APVYL	AAVLEYLTAEVLELAGNAAR	DNKKT	3		692.0446723	2073.110617	0.000451244	75	N	52	72
Q8CGP4	Exosome	PVYLA	AVLEYLTAEVLELAGNAAR	DNKKT	2		1002.044551	2002.073503	0.000451244	101	N	53	72
Q8CGP4	Exosome	PVYLA	AVLEYLTAEVLELAGNAAR	DNKKT	3		668.3656343	2002.073503	0.000451244	76	N	53	72
Q8CGP4	Exosome	NYAQR	IGAGAPVYLAAVLEYLTAEVLELAGNAAR	DNKKT	3		972.5346022	2914.580407	0.000451244	32	N	43	72
Q8CGP4	Exosome	AQGGV	LPNIQAVLLPK	KTESH	2		603.3849702	1204.75434	0.001162105	1	Y	108	119
Q8CGP4	Exosome	QRIGA	GAPVYLAAVLEYLTAEVLELAGNAAR	DNKKT	3		892.1537217	2673.437765	0.000637154	1	N	46	72
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPN	IQAVL	2		534.8065526	1067.597505	0.001329271	2	Y	100	111
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPNIQA	VLLPK	2		690.8964304	1379.777261	0.000451244	189	Y	100	114
Q8CGP4	Exosome	VTIAQ	GGVLPNIQAVLLPK	KTESH	2		709.9406409	1417.865682	0.001943752	1	Y	105	119
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPNIQ	AVLLP	2		655.3778735	1308.740147	0.000622848	27	Y	100	113
Q8CGP4	Exosome	KLLGR	VTIAQGGVLPNIQAVLL	PKKTE	2		853.5147015	1705.013803	0.001699387	1	Y	100	117
Q8CGP4	Parental	RITPR	HLQLAIRNDEELNK	LLGRV	2		846.9555393	1691.895479	0.000451244	25	Y	82	96
Q8CGP4	Parental	RITPR	HLQLAIRNDEELNK	LLGRV	3		564.9729596	1691.895479	0.000451244	98	Y	82	96
Q8CGP4	Parental	RITPR	HLQLAIRNDEELNK	LLGRV	4		423.9816697	1691.895479	0.000451244	5	Y	82	96
Q8CGP4	Parental	SRSSR	AGLQFPVGR	VHRLL	2		472.7697731	943.5239462	0.000451244	455	Y	21	30
Q8CGP4	Parental	QLAIR	NDEELNKLLGR	VTIAQ	2		650.8469375	1299.678275	0.000451244	46	N	89	100
Q8CGP4	Parental	QLAIR	NDEELNKLLGR	VTIAQ	3		434.2338916	1299.678275	0.000451244	400	N	89	100
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQAVLLPKK	TESHK	2		1030.136047	2058.256493	0.000451244	1	Y	100	120
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQAVLLPKK	TESHK	3		687.0932977	2058.256493	0.000451244	9	Y	100	120
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQAV	LLPKK	2		740.4306374	1478.845675	0.000451244	213	Y	100	115
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQAV	LLPKK	3		493.9563583	1478.845675	0.001329271	3	Y	100	115
Q8CGP4	Parental	RVTIA	QGGVLPNIQAVLLPK	KTESH	2		773.9699298	1545.92426	0.000451244	60	Y	104	119
Q8CGP4	Parental	RVTIA	QGGVLPNIQAVLLPK	KTESH	3		516.3158865	1545.92426	0.000451244	10	Y	104	119
Q8CGP4	Parental	RVTIA	QGGVLPNIQAVLLPK	KTESH	2	[0:-17.027	765.4564298	1528.89726	0.00091018	14	Y	104	119
Q8CGP4	Parental	GRVTI	AQGGVLPNIQAVLLPK	KTESH	2		809.4884867	1616.961373	0.000451244	325	Y	103	119
Q8CGP4	Parental	GRVTI	AQGGVLPNIQAVLLPK	KTESH	3		539.9949245	1616.961373	0.000451244	19	Y	103	119
Q8CGP4	Parental	LGRVT	IAQGGVLPNIQAVLLPK	KTESH	2		866.0305187	1730.045437	0.000451244	62	Y	102	119
Q8CGP4	Parental	LGRVT	IAQGGVLPNIQAVLLPK	KTESH	3		577.6896125	1730.045437	0.000451244	21	Y	102	119
Q8CGP4	Parental	LLGRV	TIAQGGVLPNIQAVLLPK	KTESH	2		916.554358	1831.093116	0.000451244	480	Y	101	119
Q8CGP4	Parental	LLGRV	TIAQGGVLPNIQAVLLPK	KTESH	3		611.372172	1831.093116	0.000451244	56	Y	101	119
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQAVLLPK	KTESH	2		966.088565	1930.16153	0.000451244	1497	Y	100	119
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQAVLLPK	KTESH	3		644.3949767	1930.16153	0.000451244	991	Y	100	119
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQAVLLPK	KTESH	4		483.5481825	1930.16153	0.001162105	1	Y	100	119
Q8CGP4	Parental	QGGVL	PNIQAVLLPK	KTESH	2		546.8429381	1091.670276	0.000451244	135	Y	109	119
Q8CGP4	Parental	APVYL	AAVLEYLTAEVLELAGNAAR	DNKKT	2		1037.563108	2073.110617	0.000451244	25	N	52	72
Q8CGP4	Parental	APVYL	AAVLEYLTAEVLELAGNAAR	DNKKT	3		692.0446723	2073.110617	0.000451244	24	N	52	72
Q8CGP4	Parental	PVYLA	AVLEYLTAEVLELAGNAAR	DNKKT	2		1002.044551	2002.073503	0.000451244	31	N	53	72
Q8CGP4	Parental	PVYLA	AVLEYLTAEVLELAGNAAR	DNKKT	3		668.3656343	2002.073503	0.000451244	22	N	53	72
Q8CGP4	Parental	NYAQR	IGAGAPVYLAAVLEYLTAEVLELAGNAAR	DNKKT	3		972.5346022	2914.580407	0.000451244	26	N	43	72
Q8CGP4	Parental	GAPVY	LAAVLEYLTAEVLELAGNAAR	DNKKT	3		729.7393603	2186.194681	0.000622848	3	N	51	72
Q8CGP4	Parental	AQGGV	LPNIQAVLLPK	KTESH	2		603.3849702	1204.75434	0.000823681	10	Y	108	119
Q8CGP4	Parental	KLLGR	VTIAQGGVLPN	IQAVL	2		534.8065526	1067.597505	0.002453667	3	Y	100	111
Q8CGP4	Parental	KLLGR	VTIAQGGVLPNIQA	VLLPK	2		690.8964304	1379.777261	0.000451244	19	Y	100	114
Q8CGP4	Parental	VTIAQ	GGVLPNIQAVLLPK	KTESH	2		709.9406409	1417.865682	0.001162105	1	Y	105	119
Q8CH18	Parental	WNAQR	IQTLPNQNQSQTQPLLK	TPTAV	2		976.0345181	1950.053436	0.000451244	8	N	201	218
Q8CH18	Parental	DLYHK	SCALAEDPQDLR	DGFQH	2	C2:+57.021	687.8198311	1373.624062	0.00091018	2	N	460	472

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CHC4	Parental	RAPSR	TPGPPSSQGSPVDTQPAAQKDSSQTLEPK	RPPPP	3		979.1480237	2934.420671	0.000622848	1	N	1074	1103
Q8CHC4	Parental	RAPSR	TPGPPSSQGSPVDTQPAAQK	DSSQT	2		975.4823153	1948.949031	0.000451244	3	N	1074	1094
Q8CHG3	Parental	LKQLR	ASILEENEEEDVVKLIQAVGESLVK	VKEEE	3		914.4872062	2740.438219	0.000451244	6	N	758	783
Q8CHG3	Parental	ENKIK	CLQEDSAVQCEELR	TLVRD	2	C1:+57.021,C10:+57.021	868.8826025	1735.749605	0.001943752	1	N	807	821
Q8CHK3	Parental	FFRYR	TYLDWLEQPFPEAVPSLRPLLR	RAWPA	3		880.8115187	2639.411156	0.000735798	3	N	171	193
Q8CHK3	Parental	AAKAR	AGGGPTLQCPPPSSPEIAASLEYDYETIR	NIDCY	3	C9:+57.021	1026.157489	3075.449066	0.000451244	5	N	271	300
Q8CHP8	Exosome	AERAK	LLLAEVDTLLFDCDGVLWR	GETAV	2	C13:+57.021	1124.588038	2247.160475	0.002019181	1	N	22	41
Q8CHP8	Exosome	TCSLK	TILTLTGVSSLEDVK	SNQES	2		788.4461501	1574.8767	0.001162105	8	N	275	290
Q8CHP8	Exosome	GKPSR	FIFDCVSQEYGINPER	TVMVG	2	C5:+57.021	987.4570233	1972.898447	0.000451244	17	N	238	254
Q8CHP8	Exosome	EKLRR	LGFGGPVGPEAGLEVFGTAYCSALYLR	QRLAG	2	C21:+57.021	1401.202286	2800.388972	0.000451244	11	N	83	110
Q8CHP8	Exosome	EKLRR	LGFGGPVGPEAGLEVFGTAYCSALYLR	QRLAG	3	C21:+57.021	934.4707907	2800.388972	0.000451244	19	N	83	110
Q8CHP8	Parental	AERAK	LLLAEVDTLLFDCDGVLWR	GETAV	2	C13:+57.021	1124.588038	2247.160475	0.000451244	1	N	22	41
Q8CHP8	Parental	AERAK	LLLAEVDTLLFDCDGVLWR	GETAV	3	C13:+57.021	750.0612917	2247.160475	0.0007646	3	N	22	41
Q8CHP8	Parental	TCSLK	TILTLTGVSSLEDVK	SNQES	2		788.4461501	1574.8767	0.000622848	1	N	275	290
Q8CHP8	Parental	GKPSR	FIFDCVSQEYGINPER	TVMVG	2	C5:+57.021	987.4570233	1972.898447	0.000451244	15	N	238	254
Q8CHP8	Parental	AEKLR	RLGFGGPVGPEAGLEVFGTAY	CSALY	2		1047.536894	2093.058187	0.001264573	3	N	82	103
Q8CI94	Exosome	ENISR	VLYPNDNFFEGK	ELRLK	2		721.8516885	1441.687777	0.000451244	21	Y	278	290
Q8CI94	Exosome	GGLGR	LAACFLDSMATLGLAAYGYGIR	YEFGI	2	C4:+57.021	1167.584973	2333.154345	0.000451244	23	Y	139	161
Q8CI94	Exosome	GGLGR	LAACFLDSMATLGLAAYGYGIR	YEFGI	3	C4:+57.021	778.725915	2333.154345	0.000451244	32	Y	139	161
Q8CI94	Exosome	GGLGR	LAACFLDSMATLGLAAYGYGIR	YEFGI	2	C4:+57.021,M9:+15.995	1175.582473	2349.149345	0.001162105	1	Y	139	161
Q8CI94	Exosome	ITPRR	WLLLCNPGLAEIIVER	IGEGF	2	C5:+57.021	948.5245119	1895.033424	0.000823681	1	N	491	507
Q8CI94	Exosome	IIVER	IGEGFLTDLSQLKK	LLSLV	3		516.9597684	1547.855905	0.000451244	7	N	507	521
Q8CI94	Exosome	SQLKK	LLSLVDDEAFIRDVAK	VKQEN	3		602.0004038	1802.977811	0.001839721	1	N	521	537
Q8CI94	Exosome	TEYAR	EIWGVEPSDLQIPPPNLPKD	-	2		1122.581498	2243.147396	0.002884417	1	N	823	843
Q8CI94	Exosome	PNDFK	LKDFNVGDYIEAVLDR	NLAEN	3		622.9919083	1865.952325	0.000451244	9	N	254	270
Q8CI94	Exosome	GKELR	LKQEYFVVAATL	QDIIR	2		691.3904495	1380.765299	0.002813207	1	Y	293	305
Q8CI94	Parental	ENISR	VLYPNDNFFEGK	ELRLK	2		721.8516885	1441.687777	0.001871652	1	Y	278	290
Q8CI94	Parental	ITPRR	WLLLCNPGLAEIIVER	IGEGF	2	C5:+57.021	948.5245119	1895.033424	0.002981883	1	N	491	507
Q8CI94	Parental	ENISR	VLYPNDNFFEGKELR	LKQEY	3		614.3129818	1839.915545	0.000637154	3	Y	278	293
Q8CI94	Parental	IIVER	IGEGFLTDLSQLKK	LLSLV	3		516.9597684	1547.855905	0.000451244	3	N	507	521
Q8CI95	Parental	GWQYR	FFVLNNEAGLLEYFVNEQSR	NQKPR	3		797.066136	2388.175008	0.000451244	3	N	83	103
Q8CI95	Parental	NQKPR	GTLQLAGAVISPSDEDSHTFTVNAASGEQYK	LRATD	3		1065.181505	3192.521114	0.001329271	2	N	108	139
Q8CI95	Parental	WRMPK	SEVASGVSSSSSTPAITDHAPLPEEAPTQSVSDCYTVR	FVAEQ	3	C34:+57.021	1307.27649	3918.806071	0.000637154	1	N	470	508
Q8CIE6	Exosome	EITKK	IQVPNCDEIFYAGTGNLLLR	DADSI	2	C6:+57.021	1147.086193	2292.156787	0.000451244	11	N	447	467
Q8CIE6	Exosome	EITKK	IQVPNCDEIFYAGTGNLLLR	DADSI	3	C6:+57.021	765.0600623	2292.156787	0.000622848	2	N	447	467
Q8CIE6	Exosome	VEKFR	SILLSVPLLVVDNKQEIAEAQQLITICR	EYIVG	3	C27:+57.021	1055.263852	3162.768156	0.000823681	8	N	1030	1058
Q8CIE6	Exosome	ETAMR	LLHDQVGVIQFGPY	KQLFL	2		793.4228124	1584.830025	0.000451244	1	N	941	955
Q8CIE6	Exosome	KNFDK	LSFLYLITGNLEK	LRKMM	2		755.9299389	1509.844278	0.001463592	1	N	702	715
Q8CIE6	Exosome	YQRTK	NFDKLSFLYLITGNLEK	LRKMM	3		672.3669752	2014.077526	0.001839721	1	N	698	715
Q8CIE6	Exosome	GEDAE	LQLDEDGFVEAPEGLGEDVLGK	GQEEG	2		1165.574067	2329.132534	0.00091018	1	N	850	872
Q8CIE6	Exosome	TFARR	LLELGPKPEVAQQTR	KILSA	3		560.3215887	1677.941366	0.000622848	3	N	1127	1142
Q8CIE6	Exosome	GQICR	VTTVTEIGKDVIGLR	ISPLQ	3		534.3143227	1599.919568	0.002019181	2	N	1202	1217
Q8CIE6	Exosome	HGIIR	TLDLPIYVTR	VKGNN	2		595.8431351	1189.67067	0.001763695	1	N	562	572
Q8CIE6	Exosome	VRNAK	LVGQSIIAYLQK	KGYPE	2		666.8984417	1331.781283	0.000451244	3	N	619	631
Q8CIE6	Exosome	EDAEL	QLDEDGFVEAPEGLGEDVLGK	GQEEG	2	Q1:-17.027	1100.518535	2199.02147	0.000823681	1	N	851	872
Q8CIE6	Exosome	EDAEL	QLDEDGFVEAPEGLGEDVLGK	GQEEG	2	[0:-17.027	1100.518535	2199.02147	0.002145581	1	N	851	872
Q8CIE6	Parental	EITKK	IQVPNCDEIFYAGTGNLLLR	DADSI	2	C6:+57.021	1147.086193	2292.156787	0.000451244	18	N	447	467
Q8CIE6	Parental	VEKFR	SILLSVPLLVVDNKQEIAEAQQLITICR	EYIVG	3	C27:+57.021	1055.263852	3162.768156	0.000735798	5	N	1030	1058
Q8CIE6	Parental	KPVEK	CPLSGACYSPEFK	GQICR	2	C1:+57.021,C7:+57.021	758.3340284	1514.652457	0.000451244	5	N	1184	1197
Q8CIE6	Parental	ETAMR	LLHDQVGVIQFGPY	KQLFL	2		793.4228124	1584.830025	0.000637154	5	N	941	955
Q8CIE6	Parental	KNFDK	LSFLYLITGNLEK	LRKMM	2		755.9299389	1509.844278	0.000451244	9	N	702	715
Q8CIE6	Parental	LLCTR	ASNLENSTYDLYTIPK	DADSQ	2		914.952328	1827.889056	0.000634081	3	N	382	398
Q8CIE6	Parental	DVLGK	GQEEGGGWDVEEDLELPPELDVPSGVSGSAEDGFFVPPTK	GTSPT	3		1391.31012	4170.906959	0.00091018	2	N	872	912
Q8CIE6	Parental	YQRTK	NFDKLSFLYLITGNLEK	LRKMM	3		672.3669752	2014.077526	0.002145581	3	N	698	715
Q8CIE6	Parental	VRNAK	LVGQSIIAYLQK	KGYPE	2		666.8984417	1331.781283	0.001162105	1	N	619	631
Q8CIH5	Exosome	GKNQK	AFVFILEPK	KQGDP	2		532.3134822	1062.611364	0.000451244	28	N	870	879
Q8CIH5	Exosome	IADAK	LSFGDDIEQAVEEEPVQDTPPTELHFGEK	WFHKK	3		1086.177649	3255.509546	0.000451244	38	N	502	531
Q8CIH5	Exosome	DEFKK	DSSVFILGNTDRPDASAVYLQDFQR	FLLHE	2		1407.688817	2813.362034	0.000451244	7	N	223	248
Q8CIH5	Exosome	DEFKK	DSSVFILGNTDRPDASAVYLQDFQR	FLLHE	3		938.7951447	2813.362034	0.000451244	35	N	223	248
Q8CIH5	Exosome	PTQEK	VTFEIYDPNLAFLR	FVVYE	2		849.4490272	1696.882454	0.000451244	4	N	1119	1133
Q8CIH5	Exosome	SNKFK	TTVVNDNGLSPVWAPTQEK	VTFEI	2		1028.52144	2055.027281	0.000451244	42	N	1100	1119
Q8CIH5	Exosome	VQAIR	DHAFVTSSFPVILSIEEHCSVEQQR	HMAKV	3	C19:+57.021	972.4716304	2914.391491	0.000451244	6	N	390	415
Q8CIH5	Exosome	VQAIR	DHAFVTSSFPVILSIEEHCSVEQQR	HMAKV	4	C19:+57.021	729.6056728	2914.391491	0.000451244	8	N	390	415
Q8CIH5	Exosome	PKLGR	SIACPFVEVEICGAEYDSNK	FKTTV	2	C4:+57.021,C12:+57.021	1144.514178	2287.012756	0.002080925	1	N	1078	1098
Q8CIH5	Exosome	GSLCK	GILDLNTYNVVK	APQGK	2		674.8777063	1347.739813	0.000451244	22	N	850	862

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8CIH5	Exosome	RAGCR	CIELDCWDGPDGKPIIYHGWTR	TTKIK	4	C1:+57.021,C6:+57.021	672.8140872	2687.225149	0.000451244	23	N	354	376
Q8CIH5	Exosome	QDFQR	FLLHEQQELWAQDLNK	VRERM	2		1006.515961	2011.016322	0.000451244	10	N	248	264
Q8CIH5	Exosome	QDFQR	FLLHEQQELWAQDLNK	VRERM	3		671.3465741	2011.016322	0.000735798	1	N	248	264
Q8CIH5	Exosome	TFLVR	ESETFPNDYTLSFWR	SGRVQ	2		946.42902	1890.84244	0.000451244	13	N	564	579
Q8CIH5	Exosome	KYWER	NQSIAIELSDLVVYCKPTSK	TKDHL	2	C15:+57.021	1133.093684	2264.171768	0.001352548	1	N	922	942
Q8CIH5	Exosome	NGVMK	YYLTDNLTFNSIYALIQHYR	EAHLR	3		836.7573025	2507.248507	0.000998612	3	N	598	618
Q8CIH5	Exosome	EPFLF	VDEFLTYLFSR	ENSIW	2		695.3566067	1388.697613	0.000451244	4	N	286	297
Q8CIH5	Exosome	GTSAY	FESLVELVSYYEK	HALYR	2		803.4064936	1604.797387	0.002374549	1	N	709	722
Q8CIH5	Exosome	DALVK	EFNVNENQLQLYQEK	CNRRL	2		948.4608515	1894.906103	0.002212458	1	N	1233	1248
Q8CIH5	Exosome	DYGTR	IQQYFPSNYVEDISAGDAEEMEKQIIEDNPLGSLCK	GILDL	3	M21:+15.995,C35:+57.021	1382.977193	4145.908179	0.000451244	11	N	814	850
Q8CIH5	Exosome	FLKDK	LVEIGAQKDELSFEQFHLFYK	KLMFD	3		847.7728411	2540.295123	0.00091018	1	N	186	207
Q8CIH5	Exosome	EFELR	LTDPVPNPNPHESKPWYYDSLSR	GEAED	4		678.8322942	2711.297977	0.00307782	1	N	630	653
Q8CIH5	Exosome	RQLRR	RQEELNNQLFLYDTHQNLR	GANRD	3		811.0758056	2430.204017	0.002813207	1	N	1205	1224
Q8CIH5	Exosome	LAFLR	FVVYEEDMFSDPNFLAHATYPIK	GIKSG	3		911.7688797	2732.283239	0.001943752	1	N	1133	1156
Q8CIH5	Exosome	FATDR	VEELFEWFQSIR	EITWK	2		791.8991701	1581.78274	0.002212458	1	N	892	904
Q8CIH5	Parental	GKNQK	AFVFILEPK	KQGDP	2		532.3134822	1062.611364	0.000451244	19	N	870	879
Q8CIH5	Parental	IADAK	LSFGDDIEQAVEEEPVQDTPPTELHFGEK	WFHKK	3		1086.177649	3255.509546	0.000451244	53	N	502	531
Q8CIH5	Parental	IADAK	LSFGDDIEQAVEEEPVQDTPPTELHFGEK	WFHKK	4		814.8851865	3255.509546	0.000451244	1	N	502	531
Q8CIH5	Parental	SNKFK	TTVVNDNGLSPVWAPTQEKVTFEIYDPNLAFLR	FVVYE	3		1245.640858	3733.899175	0.000451244	9	N	1100	1133
Q8CIH5	Parental	DEFKK	DSSVFILGNTDRPDASAVYLQDFQR	FLLHE	3		938.7951447	2813.362034	0.000451244	25	N	223	248
Q8CIH5	Parental	SNKFK	TTVVNDNGLSPVWAPTQEK	VTFEI	2		1028.52144	2055.027281	0.000451244	17	N	1100	1119
Q8CIH5	Parental	VQAIR	DHAFVTSSFPVILSIEEHCSVEQQR	HMAKV	3	C19:+57.021	972.4716304	2914.391491	0.000979378	1	N	390	415
Q8CIH5	Parental	VQAIR	DHAFVTSSFPVILSIEEHCSVEQQR	HMAKV	4	C19:+57.021	729.6056728	2914.391491	0.000622848	1	N	390	415
Q8CIH5	Parental	RAGCR	CIELDCWDGPDGKPIIYHGWTR	TTKIK	4	C1:+57.021,C6:+57.021	672.8140872	2687.225149	0.000622848	2	N	354	376
Q8CIH5	Parental	QDFQR	FLLHEQQELWAQDLNK	VRERM	2		1006.515961	2011.016322	0.000451244	2	N	248	264
Q8CIH5	Parental	NGVMK	YYLTDNLTFNSIYALIQHYR	EAHLR	3		836.7573025	2507.248507	0.000451244	8	N	598	618
Q8CIH5	Parental	EPFLF	VDEFLTYLFSR	ENSIW	2		695.3566067	1388.697613	0.000622848	9	N	286	297
Q8CIH5	Parental	GTSAY	FESLVELVSYYEK	HALYR	2		803.4064936	1604.797387	0.001264573	1	N	709	722
Q8CIM3	Exosome	PPRPK	AVNVAFLGCPGFAEVLQTFR	TCRGM	2	C9:+57.021	1098.567439	2195.119279	0.000622848	4	N	291	311
Q8CIM3	Exosome	IIPGR	VITDPEQLQTCNVDWLK	TVRGC	2	C11:+57.021	1030.012163	2058.008725	0.000451244	4	N	91	108
Q8CIM3	Exosome	YPVQR	LPFSTVSEEDLAAFECIIPGR	VITDP	2	C16:+57.021	1176.083316	2350.151033	0.000451244	3	N	70	91
Q8CIN4	Exosome	ALNTK	GSETSAVVTEEDDDDEDAAPPVIAPRPDHTK	SIYTR	3		1088.49945	3262.474951	0.001162105	3	N	160	191
Q8CIN4	Exosome	ENPLR	ALYLIATNGTPELQNPEK	LSPIF	2		986.5234518	1971.031304	0.000451244	46	N	450	468
Q8CIN4	Exosome	EGSVK	LTDFGFCAQITPEQSKR	STMVG	2	C7:+57.021	999.4913974	1996.967195	0.000622848	3	N	383	400
Q8CIN4	Exosome	EGSVK	LTDFGFCAQITPEQSKR	STMVG	3	C7:+57.021	666.6635316	1996.967195	0.000735798	3	N	383	400
Q8CIN4	Exosome	AAVCR	ECLQALEFLHANQVIHR	DIKSD	3	C2:+57.021	693.358554	2077.052262	0.001162105	8	N	350	367
Q8CIN4	Exosome	AAVCR	ECLQALEFLHANQVIHR	DIKSD	4	C2:+57.021	520.2708655	2077.052262	0.000451244	9	N	350	367
Q8CIN4	Exosome	TRYEK	IGQGASGTVFTATDVALGQEVAIK	QINLQ	2		1167.121519	2332.227438	0.000451244	12	N	254	278
Q8CIN4	Exosome	EGSVK	LTDFGFCAQITPEQSK	RSTMV	2	C7:+57.021	921.4408419	1840.866084	0.00307782	1	N	383	399
Q8CIN4	Parental	ALNTK	GSETSAVVTEEDDDDEDAAPPVIAPRPDHTK	SIYTR	3		1088.49945	3262.474951	0.000451244	68	N	160	191
Q8CIN4	Parental	ALNTK	GSETSAVVTEEDDDDEDAAPPVIAPRPDHTK	SIYTR	4		816.6265379	3262.474951	0.000451244	13	N	160	191
Q8CIN4	Parental	ENPLR	ALYLIATNGTPELQNPEK	LSPIF	2		986.5234518	1971.031304	0.000451244	30	N	450	468
Q8CIN4	Parental	SIYTR	SVIDPIPAPVGDSNVDSGAK	SSDKQ	2		969.4948914	1936.974183	0.000451244	20	N	196	216
Q8CIN4	Parental	SGTVF	TATDVALGQEVAIK	QINLQ	2		708.3911779	1414.766756	0.000870037	8	N	264	278
Q8CIN4	Parental	EGSVK	LTDFGFCAQITPEQSKR	STMVG	2	C7:+57.021	999.4913974	1996.967195	0.000451244	5	N	383	400
Q8CIN4	Parental	AAVCR	ECLQALEFLHANQVIHR	DIKSD	4	C2:+57.021	520.2708655	2077.052262	0.000622848	6	N	350	367
Q8CIN4	Parental	TVKQK	YLSFTPPEKDGFPSGTPALNTK	GSETS	2		1184.097512	2366.179425	0.000698008	7	N	138	160
Q8CIN4	Parental	TVKQK	YLSFTPPEKDGFPSGTPALNTK	GSETS	3		789.7342749	2366.179425	0.001943752	3	N	138	160
Q8CIS0	Parental	KSPIS	MKQASEFQALMR	TVKGH	2	M11:+15.995	728.3583443	1454.701089	0.001654178	1	N	515	527
Q8CIS0	Parental	MYKHR	MNTVMLQLEEVERER	DQAFH	3	M1:+15.995,M5:+15.995	636.9772222	1907.908267	0.001162105	2	N	364	379
Q8CJG0	Exosome	IIFYR	DGVSEGQFQQVLHHELLAIR	EACIK	4		569.8005314	2275.170926	0.001162105	3	N	669	689
Q8CJG0	Exosome	WDDNR	FSSDELQILTYQLCHTYVR	CTRSV	3	C14:+57.021	791.7233387	2372.146616	0.000451244	10	N	774	793
Q8CJG0	Exosome	TAFYK	AQPVIEFVCEVLDFK	SIEEQ	2	C9:+57.021	897.461046	1792.906492	0.002453667	1	N	227	242
Q8CJG0	Exosome	TAFYK	AQPVIEFVCEVLDFK	SIEEQ	3	C9:+57.021	598.6432973	1792.906492	0.000451244	3	N	227	242
Q8CJG0	Exosome	GQEQK	HTYLPLEVCNIVAGQR	CIKKL	3	C9:+57.021	623.993212	1868.956236	0.000451244	4	N	336	352
Q8JZQ9	Exosome	EPEVR	AKPAAQSEEETATSPAASPTPQSAER	SPSQE	3		871.4198549	2611.236165	0.000451244	12	N	61	87
Q8JZQ9	Exosome	QSAER	SPSQEPSAPGKAEAVGEQAR	GHPSA	3		665.9963811	1994.965743	0.001264573	1	N	87	107
Q8JZQ9	Exosome	DRTPK	GTQGVVTNFEIFR	MREKQ	2		734.3836872	1466.751774	0.000451244	8	N	524	537
Q8JZQ9	Exosome	WWSHK	VDNAYWLWTFQGR	LLQKN	2		828.4024112	1654.789222	0.000451244	10	N	665	678
Q8JZQ9	Exosome	GDVLK	DRPQEADGIDSVIVVDNVPQVGPDRLEK	LKNVI	3		1020.858585	3059.552354	0.000451244	12	N	163	191
Q8JZQ9	Exosome	SPCER	YLVTFSPLMDTQDDPQAIIIWDILTGHK	KRGFH	3	M9:+15.995	1082.885112	3245.631937	0.000451244	8	N	375	403
Q8JZQ9	Exosome	DGKTK	GYIFLEYASPAHAVDAVK	NADGY	2		976.0021552	1949.98871	0.002663018	1	N	219	237
Q8JZQ9	Exosome	ISGIK	DFSWSPGGNIIAFWVPEDKDIPAR	VTLMQ	3		906.4506496	2716.328549	0.000451244	10	N	457	481
Q8JZQ9	Exosome	GDVLK	DRPQEADGIDSVIVVDNVPQVGPDR	LEKLK	3		897.4513779	2689.330734	0.00091018	1	N	163	188
Q8JZQ9	Exosome	EIRVR	NLFNVVDCK	LHWQK	2	C8:+57.021	554.7767065	1107.537813	0.002374549	1	N	496	505

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8JZQ9	Exosome	KMFDK	QQANTIFWSPQGQFVVLAGLR	SMNGA	2		1180.629648	2359.243697	0.001871652	1	N	597	618
Q8JZQ9	Parental	AEPAR	QQPASESPPTDEAAGSGGSEVGQTEDAEEDAEAGPEPEVR	AKPAA	3		1337.576364	4009.705693	0.000451244	42	N	21	61
Q8JZQ9	Parental	EPEVR	AKPAAQSEEETATSPAASPTPQSAER	SPSQE	2		1306.625882	2611.236165	0.000451244	1	N	61	87
Q8JZQ9	Parental	EPEVR	AKPAAQSEEETATSPAASPTPQSAER	SPSQE	3		871.4198549	2611.236165	0.000451244	39	N	61	87
Q8JZQ9	Parental	KQIQR	FSHQGVQLIDFSPCER	YLVTF	2	C14:+57.021	960.4573576	1918.899115	0.001463592	1	N	359	375
Q8JZQ9	Parental	QSAER	SPSQEPSAPGKAEAVGEQAR	GHPSA	3		665.9963811	1994.965743	0.000451244	5	N	87	107
Q8JZQ9	Parental	DRTPK	GTQGVVTNFEIFR	MREKQ	2		734.3836872	1466.751774	0.000451244	2	N	524	537
Q8JZQ9	Parental	GDVLK	DRPQEADGIDSVIVVDNVPQVGPDRLEK	LKNVI	3		1020.858585	3059.552354	0.000451244	19	N	163	191
Q8JZQ9	Parental	DGKTK	GYIFLEYASPAHAVDAVK	NADGY	2		976.0021552	1949.98871	0.000662267	1	N	219	237
Q8JZQ9	Parental	GDVLK	DRPQEADGIDSVIVVDNVPQVGPDR	LEKLK	3		897.4513779	2689.330734	0.000451244	4	N	163	188
Q8JZQ9	Parental	ESGDR	TSIFWNDVKDPVSIEER	ARWTE	2		1018.010709	2034.005817	0.000451244	2	N	304	321
Q8JZQ9	Parental	ESGDR	TSIFWNDVKDPVSIEER	ARWTE	3		679.0097391	2034.005817	0.000451244	10	N	304	321
Q8JZQ9	Parental	KMFDK	QQANTIFWSPQGQFVVLAGLR	SMNGA	2		1180.629648	2359.243697	0.00091018	1	N	597	618
Q8JZQ9	Parental	SKFGK	IINDYYPEEDGKTK	GYIFL	2		842.9073891	1683.799178	0.001162105	2	N	205	219
Q8JZV7	Exosome	VRGGR	ILDPEKLFFEER	RVADE	3		512.6088471	1534.803141	0.001463592	3	N	37	49
Q8JZV7	Exosome	EAYLR	SFEANAFHDVLATYGPLDNVCIVTLAPELDR	SHEVI	3	C21:+57.021	1149.90153	3446.681191	0.00091018	1	N	161	192
Q8JZV7	Parental	LGNGR	HTLGQQEVEVDGLIAYIAGTK	TLGGS	3		748.062503	2241.164109	0.000622848	2	N	305	326
Q8K0C9	Exosome	RSVAK	IYLGQLECFSLGNLDAK	RDWGH	2	C8:+57.021	970.9932416	1939.970883	0.000451244	8	N	229	246
Q8K0C9	Exosome	EGNMK	LHYGDLTDSTCLVK	IINEV	2	C11:+57.021	811.3984456	1620.781291	0.000451244	2	N	81	95
Q8K0C9	Exosome	QSHVK	ISFDLAEYTADVDGVGTLR	LLDAI	2		1021.507999	2041.000398	0.000451244	4	N	115	134
Q8K0C9	Exosome	GKLRK	VALITGITGQDGSYLAEFLLEK	GYEVH	2		1169.631188	2337.246776	0.000622848	2	N	24	46
Q8K0E8	Exosome	MEYCR	TPCTVSCNIPVVSGK	ECEEI	2	C3:+57.021,C7:+57.021	809.9000669	1617.784534	0.000451244	73	N	214	229
Q8K0E8	Exosome	MEYCR	TPCTVSCNIPVVSGKECEEIIR	KGGET	2	C3:+57.021,C7:+57.021,C17:+57.021	1274.613669	2547.211738	0.000451244	9	N	214	236
Q8K0E8	Exosome	MEYCR	TPCTVSCNIPVVSGKECEEIIR	KGGET	3	C3:+57.021,C7:+57.021,C17:+57.021	850.0783795	2547.211738	0.000451244	40	N	214	236
Q8K0E8	Exosome	QAQVK	ENENVINEYSSILEDQR	LYIDE	2		1026.47997	2050.944339	0.000451244	29	N	153	170
Q8K0E8	Exosome	QAQVK	ENENVINEYSSILEDQR	LYIDE	3		684.6559131	2050.944339	0.000451244	6	N	153	170
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLK	DMWKK	3		1024.863224	3071.566273	0.000451244	49	N	114	142
Q8K0E8	Exosome	LEDQR	LYIDETVNDNIPLNLR	VLRSI	2		951.5025194	1900.989439	0.000451244	41	N	170	186
Q8K0E8	Exosome	LEDQR	LYIDETVNDNIPLNLR	VLRSI	3		634.6709463	1900.989439	0.000451244	8	N	170	186
Q8K0E8	Exosome	SKIQK	LESDISAQMEYCR	TPCTV	2	M9:+15.995,C12:+57.021	809.3481387	1616.680677	0.000451244	24	N	201	214
Q8K0E8	Exosome	EDAKK	YCGLPGEYWLGNDK	ISQLT	2	C2:+57.021	836.3775132	1670.739426	0.000451244	14	N	304	318
Q8K0E8	Exosome	GDKVK	AHYGGFTVQNEASK	YQVSV	2		754.8605762	1507.705552	0.000451244	6	N	343	357
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTF	QYLTL	2		1107.032566	2212.049533	0.000451244	10	N	114	135
Q8K0E8	Exosome	YCDMK	TENGGWTVIQNR	QDGSV	2		687.8421864	1373.668773	0.000451244	10	N	263	275
Q8K0E8	Exosome	NEDAK	KYCGLPGEYWLGNDK	ISQLT	2	C3:+57.021	900.4249948	1798.83439	0.000451244	5	N	303	318
Q8K0E8	Exosome	NEDAK	KYCGLPGEYWLGNDK	ISQLT	3	C3:+57.021	600.6192632	1798.83439	0.000979378	6	N	303	318
Q8K0E8	Exosome	KKVER	RPPDAGGCLHADTDMGVLCPTGCTLQQTLLNQERPIK	SSIAE	4	C8:+57.021,C19:+57.021,C23:+57.021	1030.751409	4118.974434	0.000451244	9	N	77	114
Q8K0E8	Exosome	KKVER	RPPDAGGCLHADTDMGVLCPTGCTLQQTLLNQERPIK	SSIAE	4	C8:+57.021,M15:+15.995,C19:+57.021,C23:+57.021	1034.750159	4134.969434	0.000451244	6	N	77	114
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTFQY	LTLLK	2		1252.59352	2503.171439	0.000451244	5	N	114	137
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTFQYL	TLLKD	2		1309.135552	2616.255503	0.000451244	5	N	114	138
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLL	KDMWK	2		1472.743455	2943.47131	0.000451244	8	N	114	141
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLL	KDMWK	3		982.1649033	2943.47131	0.001162105	2	N	114	141
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLT	LLKDM	2		1359.659391	2717.303182	0.000622848	3	N	114	139
Q8K0E8	Exosome	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLKDMWK	KKQAQ	3	M30:+15.995	1216.942126	3647.802978	0.000451244	12	N	114	146
Q8K0E8	Exosome	DLRSK	IQKLESDISAQMEYCR	TPCTV	2	M12:+15.995,C15:+57.021	993.9669411	1985.918282	0.000451244	7	N	198	214
Q8K0E8	Exosome	DLRSK	IQKLESDISAQMEYCR	TPCTV	3	M12:+15.995,C15:+57.021	662.9805608	1985.918282	0.001352548	1	N	198	214
Q8K0E8	Exosome	PVDRR	KEEPPSLRPAPPPISGGGYR	ARPAK	3		702.3766448	2104.106534	0.000823681	3	N	42	62
Q8K0E8	Exosome	EDAKK	YCGLPGEYWLGNDKISQLTR	MGPTE	3	C2:+57.021	790.7234501	2369.14695	0.002981883	1	N	304	324
Q8K0E8	Exosome	DQRLY	IDETVNDNIPLNLR	VLRSI	2		813.428823	1624.842046	0.001871652	1	N	172	186
Q8K0E8	Parental	MEYCR	TPCTVSCNIPVVSGK	ECEEI	2	C3:+57.021,C7:+57.021	809.9000669	1617.784534	0.000451244	28	N	214	229
Q8K0E8	Parental	MEYCR	TPCTVSCNIPVVSGKECEEIIR	KGGET	2	C3:+57.021,C7:+57.021,C17:+57.021	1274.613669	2547.211738	0.000451244	9	N	214	236
Q8K0E8	Parental	MEYCR	TPCTVSCNIPVVSGKECEEIIR	KGGET	3	C3:+57.021,C7:+57.021,C17:+57.021	850.0783795	2547.211738	0.000451244	22	N	214	236
Q8K0E8	Parental	QAQVK	ENENVINEYSSILEDQR	LYIDE	2		1026.47997	2050.944339	0.000451244	22	N	153	170
Q8K0E8	Parental	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLK	DMWKK	3		1024.863224	3071.566273	0.000451244	28	N	114	142
Q8K0E8	Parental	QAQVK	ENENVINEYSSILEDQRLYIDETVNDNIPLNLR	VLRSI	3		1312.315539	3933.923218	0.000451244	13	N	153	186
Q8K0E8	Parental	LEDQR	LYIDETVNDNIPLNLR	VLRSI	2		951.5025194	1900.989439	0.000451244	24	N	170	186
Q8K0E8	Parental	YCDMK	TENGGWTVIQNR	QDGSV	2		687.8421864	1373.668773	0.001395409	2	N	263	275
Q8K0E8	Parental	KKVER	RPPDAGGCLHADTDMGVLCPTGCTLQQTLLNQERPIK	SSIAE	4	C8:+57.021,C19:+57.021,C23:+57.021	1030.751409	4118.974434	0.000451244	2	N	77	114

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8K0E8	Parental	ERPIK	SSIAELNNNIQSVSDTSSVTFQYLTLLKDMWK	KKQAQ	3		1211.610459	3631.807978	0.000451244	5	N	114	146
Q8K0E8	Parental	PVDRR	KEEPPSLRPAPPPISGGGYR	ARPAK	3		702.3766448	2104.106534	0.001839721	1	N	42	62
Q8K0E8	Parental	EDAKK	YCGLPGEYWLGNDKISQLTR	MGPTE	2	C2:+57.021	1185.581275	2369.14695	0.000451244	5	N	304	324
Q8K0E8	Parental	EDAKK	YCGLPGEYWLGNDKISQLTR	MGPTE	3	C2:+57.021	790.7234501	2369.14695	0.000735798	2	N	304	324
Q8K0E8	Parental	GDKVK	AHYGGFTVQNEASKYQVSVNK	YKGTA	2		1164.074903	2326.134206	0.000998612	1	N	343	364
Q8K0E8	Parental	GDKVK	AHYGGFTVQNEASKYQVSVNK	YKGTA	4		582.5413515	2326.134206	0.001162105	2	N	343	364
Q8K0E8	Parental	EEIIR	KGGETSEMYLIQPDTSIKPYR	VYCDM	3		805.0743032	2412.199509	0.001871652	1	N	236	257
Q8K0E8	Parental	MWKKK	QAQVKENENVINEYSSILEDQR	LYIDE	2		1303.638793	2605.261985	0.000451244	5	N	148	170
Q8K0E8	Parental	MWKKK	QAQVKENENVINEYSSILEDQR	LYIDE	3		869.4284618	2605.261985	0.000451244	5	N	148	170
Q8K124	Exosome	PAGER	ALTPDSASSGANPESQEDAETPAKEDSDVK	SLPNS	3		1016.125613	3045.353439	0.000451244	7	N	230	260
Q8K124	Parental	SEKLK	VSWENPSPEKPSAPESAQLSSSETPEATPR	ESKKP	3		1065.841259	3194.500378	0.000451244	29	N	272	302
Q8K124	Parental	KQTEK	LLNQVLGSEPPPVCAESLLSQAVEQLR	QATQV	3	C14:+57.021	983.190464	2946.547992	0.000451244	19	N	430	457
Q8K124	Parental	PAGER	ALTPDSASSGANPESQEDAETPAKEDSDVK	SLPNS	3		1016.125613	3045.353439	0.000451244	11	N	230	260
Q8K124	Parental	LQEMR	DLGELNQETPGLVQK	RKELV	2		820.9286559	1639.841712	0.000451244	27	N	467	482
Q8K124	Parental	DGLSR	LDLDVPDSGPPVFAPLSDISEDQPQEPPR	ALMPP	3		1044.179212	3129.514237	0.000451244	18	N	173	202
Q8K124	Parental	TLSEK	LKVSWENPSPEKPSAPESAQLSSSETPEATPR	ESKKP	3		1146.234269	3435.679406	0.002080925	1	N	270	302
Q8K183	Exosome	VYRDK	VVPVADIITPNQFEAELLSGR	KIHSQ	2		1134.615872	2267.216145	0.000622848	4	N	139	160
Q8K183	Exosome	LPVYR	DKVVPVADIITPNQFEAELLSGR	KIHSQ	3		837.7871503	2510.338051	0.001871652	1	N	137	160
Q8K1B8	Exosome	QLTPR	ILEAHQNVAQLSLTEAQLR	FIQAW	2		1067.584906	2133.154213	0.000451244	31	N	521	540
Q8K1B8	Exosome	QLTPR	ILEAHQNVAQLSLTEAQLR	FIQAW	3		712.0592043	2133.154213	0.000451244	15	N	521	540
Q8K1B8	Exosome	YHINK	LTLSGDVGELASGDLGLDDLDAALNNLEVK	LKGSA	3		1009.850984	3026.529553	0.000451244	29	N	303	333
Q8K1B8	Exosome	SWELR	VFVGEEDPEAQSVTLR	VTGES	2		888.4446701	1774.87374	0.000451244	87	N	19	35
Q8K1B8	Exosome	LSLQR	AGGSNGGSGNKPQGPEAPAEGLNPYGLVAPR	FQRKF	3		973.8168313	2918.427094	0.000451244	66	N	477	508
Q8K1B8	Exosome	HDLTK	VVLAGGVAPTLFR	GMPAH	2		650.3933265	1298.771053	0.000451244	20	N	166	179
Q8K1B8	Exosome	LSYYK	SQDEAPGDPTQQLNLK	GCEVV	2		870.9241018	1739.832604	0.000451244	56	N	385	401
Q8K1B8	Exosome	MAGMK	TASGDYIDSSWELR	VFVGE	2		800.3684311	1598.721262	0.000451244	24	N	5	19
Q8K1B8	Exosome	VLRLR	ASFSKPLFQTVAAICR	LLSIR	2	C15:+57.021	898.4801044	1794.944609	0.000451244	26	N	113	129
Q8K1B8	Exosome	VLRLR	ASFSKPLFQTVAAICR	LLSIR	3	C15:+57.021	599.3226696	1794.944609	0.000451244	29	N	113	129
Q8K1B8	Exosome	SVTLR	VTGESHIGGVLLK	IVEEI	2		655.3778735	1308.740147	0.000451244	11	N	35	48
Q8K1B8	Exosome	VLWLR	FKYYSFFDLDPK	TDPVR	3		523.9261761	1568.755128	0.002019181	7	N	250	262
Q8K1B8	Exosome	STRER	ARGEELDEDLFLQLTGGHEAF	-	2		1174.064201	2346.112802	0.000622848	12	N	644	665
Q8K1B8	Exosome	STRER	ARGEELDEDLFLQLTGGHEAF	-	3		783.0454006	2346.112802	0.001162105	1	N	644	665
Q8K1B8	Exosome	ASKGR	TMADSSYASEVQAILAFLSLQR	AGGSN	2		1201.107555	2400.199509	0.000451244	8	N	455	477
Q8K1B8	Exosome	ASKGR	TMADSSYASEVQAILAFLSLQR	AGGSN	2	M2:+15.995	1209.105055	2416.194509	0.000451244	4	N	455	477
Q8K1B8	Exosome	ASKGR	TMADSSYASEVQAILAFLSLQR	AGGSN	3	M2:+15.995	806.4059698	2416.194509	0.000823681	1	N	455	477
Q8K1B8	Exosome	KFCIK	LLVPSPEGMSEIYLR	CQDEQ	2		852.4559955	1702.896391	0.002663018	2	N	419	434
Q8K1B8	Exosome	EAQLR	FIQAWQSLPDFGISYVMVR	FKGSR	2		1129.077872	2256.140144	0.000451244	3	N	540	559
Q8K1B8	Exosome	QLNLK	GCEVVPDVNVSGQK	FCIKL	2	C2:+57.021	744.3618631	1486.708126	0.000451244	12	N	401	415
Q8K1B8	Exosome	WLRFK	YYSFFDLDPK	TDPVR	2		647.8036756	1293.591751	0.000451244	9	N	252	262
Q8K1B8	Exosome	RERAR	GEELDEDLFLQLTGGHEAF	-	2		1060.495088	2118.974577	0.000622848	9	N	646	665
Q8K1B8	Exosome	LLLQR	LPRPSSLPDKTQLHSR	WLDSS	3		611.3432754	1831.006426	0.000622848	2	N	212	228
Q8K1B8	Exosome	LLLQR	LPRPSSLPDKTQLHSR	WLDSS	4		458.7594066	1831.006426	0.000451244	7	N	212	228
Q8K1B8	Exosome	EKKKK	EKEPEEEVHDLTK	VVLAG	3		528.2585427	1581.752228	0.000451244	6	N	153	166
Q8K1B8	Exosome	YHINK	LTLSGDVGELASGDLGLDDLD	AALNN	2		1038.005486	2073.995372	0.000451244	5	N	303	324
Q8K1B8	Exosome	NRLIR	IDLAVGDVVK	TWRFS	2		514.8034786	1027.591357	0.000662267	2	N	578	588
Q8K1B8	Parental	QLTPR	ILEAHQNVAQLSLTEAQLR	FIQAW	2		1067.584906	2133.154213	0.000451244	6	N	521	540
Q8K1B8	Parental	QLTPR	ILEAHQNVAQLSLTEAQLR	FIQAW	3		712.0592043	2133.154213	0.001162105	3	N	521	540
Q8K1B8	Parental	YHINK	LTLSGDVGELASGDLGLDDLDAALNNLEVK	LKGSA	3		1009.850984	3026.529553	0.000451244	25	N	303	333
Q8K1B8	Parental	SWELR	VFVGEEDPEAQSVTLR	VTGES	2		888.4446701	1774.87374	0.000451244	47	N	19	35
Q8K1B8	Parental	LSYYK	SQDEAPGDPTQQLNLKGCEVVPDVNVSGQK	FCIKL	3	C18:+57.021	1070.517857	3208.53017	0.000451244	9	N	385	415
Q8K1B8	Parental	LSLQR	AGGSNGGSGNKPQGPEAPAEGLNPYGLVAPR	FQRKF	3		973.8168313	2918.427094	0.000451244	10	N	477	508
Q8K1B8	Parental	HDLTK	VVLAGGVAPTLFR	GMPAH	2		650.3933265	1298.771053	0.000622848	1	N	166	179
Q8K1B8	Parental	LSYYK	SQDEAPGDPTQQLNLK	GCEVV	2		870.9241018	1739.832604	0.000451244	12	N	385	401
Q8K1B8	Parental	VLWLR	FKYYSFFDLDPK	TDPVR	3		523.9261761	1568.755128	0.001654178	1	N	250	262
Q8K1B8	Parental	VAIEF	DEHINVAFSCVSASCR	IVHEY	2	C10:+57.021,C15:+57.021	926.4093188	1850.803038	0.000622848	2	N	611	627
Q8K1B8	Parental	STRER	ARGEELDEDLFLQLTGGHEAF	-	2		1174.064201	2346.112802	0.000698008	2	N	644	665
Q8K1B8	Parental	STRER	ARGEELDEDLFLQLTGGHEAF	-	3		783.0454006	2346.112802	0.000451244	4	N	644	665
Q8K1B8	Parental	NKLTL	SGDVGELASGDLGLDDLDAALNNLEVK	LKGSA	3		900.7790488	2699.313746	0.000451244	2	N	306	333
Q8K1B8	Parental	HDLTK	VVLAGGVAPTLF	RGMPA	2		572.342771	1142.669942	0.001162105	2	N	166	178
Q8K1B8	Parental	ASKGR	TMADSSYASEVQAILAFLSLQR	AGGSN	2		1201.107555	2400.199509	0.000451244	3	N	455	477
Q8K1B8	Parental	KFCIK	LLVPSPEGMSEIYLR	CQDEQ	2		852.4559955	1702.896391	0.0025889	1	N	419	434
Q8K1B8	Parental	RERAR	GEELDEDLFLQLTGGHEAF	-	2		1060.495088	2118.974577	0.000451244	5	N	646	665
Q8K1M6	Exosome	ELKTR	INVLAAQYQSLLNSYGEPVDDKSATLLQLITK	FATEY	3		1169.298321	3504.871564	0.000451244	20	N	313	345
Q8K1M6	Exosome	ETFGR	TLESVDPLGGLNTIDILTAIR	NATGP	2		1106.115705	2210.21581	0.000451244	16	N	382	403
Q8K1M6	Exosome	LRFPK	LHDAIVEVVTCLLR	KRLPV	3	C11:+57.021	546.6399986	1636.896596	0.00091018	3	N	465	479

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8K1M6	Exosome	QLITK	FATEYCNTIEGTAK	YIETS	2	C6:+57.021	802.8669783	1603.718357	0.000451244	2	N	345	359
Q8K1M6	Parental	ELKTR	INVLAAQYQSLLNSYGEPVDDKSATLLQLITK	FATEY	3		1169.298321	3504.871564	0.000451244	2	N	313	345
Q8K1M6	Parental	ETFGR	TLESVDPLGGLNTIDILTAIR	NATGP	2		1106.115705	2210.21581	0.000451244	14	N	382	403
Q8K1M6	Parental	PVINK	LQDVFNTVGADIIQLPQIVVVGTQSSGK	SSVLE	3		976.2015117	2925.581135	0.000451244	6	N	10	38
Q8K1M6	Parental	LRFPK	LHDAIVEVVTCLLR	KRLPV	3	C11:+57.021	546.6399986	1636.896596	0.001763695	1	N	465	479
Q8K1T1	Parental	LSLPR	SPLQASHAQVLDLSK	NGLQV	2		797.4339084	1592.852217	0.000823681	2	N	59	74
Q8K1T1	Parental	LSLPR	SPLQASHAQVLDLSK	NGLQV	3		531.9585389	1592.852217	0.0007646	3	N	59	74
Q8K1T1	Parental	YMNYR	SVDQDSQPVYCNLESLGR	-	2	C11:+57.021	1033.976309	2065.937017	0.000451244	19	N	279	297
Q8K1T1	Parental	DLELK	ADCSCGLASWYALR	QNCSG	2	C3:+57.021,C5:+57.021	815.3611089	1628.706618	0.000451244	7	N	117	131
Q8K1X4	Exosome	SRIVR	NALLQQTQPLDSSGEQTVTTLYTNWYLESLLR	QASSG	3		1228.292006	3681.852619	0.002212458	1	N	767	799
Q8K1X4	Exosome	RTAVK	ELETVLNDEPGLLGPK	ALFAF	2		862.4597889	1722.903978	0.000451244	4	N	349	365
Q8K1X4	Exosome	LAGVK	AYISFIQSLAQFLGADASR	IVRNA	2		1029.536894	2057.058187	0.000451244	2	N	745	764
Q8K1X4	Parental	SRIVR	NALLQQTQPLDSSGEQTVTTLYTNWYLESLLR	QASSG	3		1228.292006	3681.852619	0.000451244	10	N	767	799
Q8K1X4	Parental	RTAVK	ELETVLNDEPGLLGPK	ALFAF	2		862.4597889	1722.903978	0.001699387	1	N	349	365
Q8K1X4	Parental	LAGVK	AYISFIQSLAQFLGADASR	IVRNA	2		1029.536894	2057.058187	0.000451244	3	N	745	764
Q8K1X4	Parental	GVKAY	ISFIQSLAQFLGADASR	IVRNA	3		608.6603816	1822.957745	0.002453667	1	N	747	764
Q8K1X4	Parental	DTDIK	VTLSVFELACAAGVSCDIDPALVAAIANLK	ADNSS	3	C10:+57.021,C16:+57.021	1030.206972	3087.597516	0.001699387	1	N	954	984
Q8K274	Exosome	PIKVV	DAPGGGSMLVMEHLDMR	YLSSH	2	M8:+15.995,M16:+15.995	924.4084799	1846.80136	0.002145581	1	N	77	94
Q8K274	Exosome	EQAER	QYVDQFGFDVVTCCGYLPQVNDWQK	NWVEF	3	C13:+57.021,C14:+57.021	1022.797083	3065.36785	0.001162105	1	N	137	162
Q8K296	Exosome	NEKYK	LCGSYPQELIVPAWITDKELESVAGFR	SWKRI	3	C2:+57.021	1026.858714	3077.552743	0.000451244	3	N	186	213
Q8K296	Exosome	APLAK	ESSMAAEGPVVLYQEPQLDDATLR	SHQGP	3	[0:-18.011,M4:+15.995	873.0869319	2616.237396	0.002145581	1	N	725	749
Q8K296	Exosome	ETENK	ASEQPAGFDTLQK	YPTPN	2		696.3442276	1390.672855	0.000662267	1	N	935	948
Q8K296	Parental	NEKYK	LCGSYPQELIVPAWITDKELESVAGFR	SWKRI	3	C2:+57.021	1026.858714	3077.552743	0.000451244	18	N	186	213
Q8K296	Parental	SVLHR	TSSPGNTLSLLQAPCALPLDK	CRQGI	2	C15:+57.021	1092.072752	2182.129903	0.000823681	5	N	898	919
Q8K296	Parental	PVDAK	VGLGISQSSSLLPSQVPFETR	GPHIN	2		1101.592397	2201.169194	0.000823681	2	N	815	836
Q8K2B3	Exosome	HGANR	LGANSLLDLVVFGR	ACALS	2		737.425355	1472.83511	0.000451244	11	N	451	465
Q8K2B3	Exosome	VVFGR	ACALSIAESCRPGDKVPSIK	ANAGE	3	C2:+57.021,C10:+57.021	720.3699767	2158.08653	0.002884417	1	N	465	485
Q8K2B3	Exosome	AMVTR	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	GEGGI	3	C5:+57.021,C23:+57.021,C29:+57.021	1122.861716	3365.561747	0.000451244	12	N	282	312
Q8K2B3	Exosome	GAGLR	AAFGLSEAGFNTACLTK	LFPTR	2	C14:+57.021	879.4302771	1756.844954	0.000451244	2	N	75	92
Q8K2B3	Exosome	KASAK	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	AAFGL	3		977.161716	2928.461748	0.00091018	2	N	46	75
Q8K2B3	Parental	HGANR	LGANSLLDLVVFGR	ACALS	2		737.425355	1472.83511	0.000451244	9	N	451	465
Q8K2B3	Parental	VVFGR	ACALSIAESCRPGDKVPSIK	ANAGE	3	C2:+57.021,C10:+57.021	720.3699767	2158.08653	0.002080925	1	N	465	485
Q8K2B3	Parental	AMVTR	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	GEGGI	3	C5:+57.021,C23:+57.021,C29:+57.021	1122.861716	3365.561747	0.000451244	19	N	282	312
Q8K2H4	Exosome	SLNHK	LDSHAELLDATQHTLQQQIQTLVK	EGLRG	3		910.8194017	2729.434805	0.000451244	2	N	90	114
Q8K2H4	Exosome	ADSER	LLQLWVSAVQSSIASAFSQAHLENSPR	GPGQV	3		980.5178342	2938.530102	0.002453667	1	N	346	373
Q8K2H4	Parental	EFVLR	LVEAQATYFQQGHEELNR	LAQYR	3		711.684026	2132.028678	0.000979378	1	N	194	212
Q8K2K6	Parental	DNFPK	SSSADFGTFSTSQSHQTASTVSK	VSTNK	3		783.3599364	2347.056409	0.000451244	4	N	290	313
Q8K2K6	Parental	VSTNK	AGLQTADKYAALANLDNIFSAGQGGDQGSGFGTTGK	APVGS	3		1167.901401	3500.680803	0.000451244	11	N	318	354
Q8K2T1	Exosome	MTSVR	LPCYFENLLSYFLPQK	AADGK	2	C3:+57.021	1016.516353	2031.017105	0.000451244	4	N	161	177
Q8K2T1	Exosome	MTSVR	LPCYFENLLSYFLPQK	AADGK	3	C3:+57.021	678.0135017	2031.017105	0.000823681	5	N	161	177
Q8K2T1	Exosome	RLNPK	AQTLDQWLEQHKGDFAQL	-	3		710.0206381	2127.038514	0.001654178	1	N	291	309
Q8K2Z4	Exosome	SICEK	ELLDGNQVLAAFVPLLLK	VCNNP	2		977.0751233	1952.134647	0.000451244	4	N	992	1010
Q8K2Z4	Parental	SICEK	ELLDGNQVLAAFVPLLLK	VCNNP	2		977.0751233	1952.134647	0.000451244	10	N	992	1010
Q8K2Z4	Parental	VLVCK	NAIQLLASFLANNPFSCK	LSDID	3	C17:+57.021	670.0159053	2007.024316	0.000823681	5	N	422	440
Q8K310	Exosome	GKNLR	YQLLQLVEPFGVISNHLILNK	INEAF	3		813.4655714	2437.373314	0.000622848	7	N	412	433
Q8K310	Parental	PDEYR	IGPYQPNVPVGIDYVIPK	TGFYC	2		985.0438231	1968.072046	0.000451244	17	N	779	797
Q8K310	Parental	GKNLR	YQLLQLVEPFGVISNHLILNK	INEAF	3		813.4655714	2437.373314	0.001162105	10	N	412	433
Q8K310	Parental	GFYCK	LCSLFYTNEEVAK	NTHCS	2	C2:+57.021	787.3822642	1572.748928	0.001463592	1	N	803	816
Q8K310	Parental	SSQHR	GDTDQASNILASFGLSAR	DLDEL	2		911.950651	1821.885702	0.000451244	10	N	102	120
Q8K352	Exosome	ELLER	IGLEEHTSTLLLNGYQTLEDFK	ELRET	3		841.099394	2520.274782	0.001943752	3	N	263	285
Q8K352	Exosome	CGRAR	VHTDFTPSPYDHDSLK	LQKGD	3		620.2922464	1857.853339	0.000622848	3	N	179	195
Q8K352	Exosome	ELLER	IGLEEHTSTLLLNGYQTLEDFKELR	ETHLN	4		730.6334376	2918.50255	0.000979378	3	N	263	288
Q8K352	Parental	LGSFK	FIYVDVLPEEAVGPVRPSR	RQSKG	3		715.0569122	2142.147337	0.001463592	1	N	225	244
Q8K352	Parental	VDIPR	DSGCFEGSESGRDEAELAGTEEQLQGLSLSGAP	-	3	C4:+57.021	1128.499079	3382.473837	0.000622848	5	N	347	380
Q8K352	Parental	CGRAR	VHTDFTPSPYDHDSLK	LQKGD	3		620.2922464	1857.853339	0.000451244	11	N	179	195
Q8K352	Parental	ELLER	IGLEEHTSTLLLNGYQTLEDFKELR	ETHLN	3		973.8419834	2918.50255	0.000451244	14	N	263	288
Q8K352	Parental	ELLER	IGLEEHTSTLLLNGYQTLEDFKELR	ETHLN	4		730.6334376	2918.50255	0.000451244	27	N	263	288
Q8K352	Parental	LKLQK	GDVIQIVEKPPVGTWLGLLNGK	LGSFK	3		778.4462883	2332.315465	0.000851441	2	N	198	220
Q8K352	Parental	CGRAR	VHTDFTPSPYDHDSLKLQK	GDVIQ	3		743.371448	2227.090944	0.002884417	1	N	179	198
Q8K352	Parental	VVSEK	EFNLDDNIPEDDSGVLTPEDSGK	SGKKL	2		1253.559342	2505.103085	0.000451244	2	N	44	67
Q8K352	Parental	QHRAK	LLTAAELLLDYDTGSEEAEEGAESSQEPVAHTVSEPK	VDIPR	3		1305.955565	3914.843296	0.000451244	1	N	305	342
Q8K352	Parental	QHRAK	LLTAAELLLDYDTGSEEAEEGAESSQEPVAHTVSEPK	VDIPR	4		979.718624	3914.843296	0.000622848	4	N	305	342
Q8K354	Exosome	DQGSR	TVEEGAETPVYLALLPPDATEPHGQLVR	DKVVQ	3		1001.521021	3001.539664	0.000451244	5	N	242	270

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8K354	Exosome	DFLRK	EYGGLNVLVNNAGIAFR	MDDPT	2		903.9790145	1805.942429	0.000451244	7	N	79	96
Q8K354	Exosome	KPHGR	VVNISSLQGLK	ALENC	2		579.3485847	1156.681569	0.002374549	1	N	134	145
Q8K354	Exosome	EARGR	AAVQQLQAEGLSPR	FHQLD	2		734.3998686	1466.784137	0.000451244	4	N	44	58
Q8K354	Parental	DQGSR	TVEEGAETPVYLALLPPDATEPHGQLVR	DKVVQ	3		1001.521021	3001.539664	0.000451244	1	N	242	270
Q8K3K8	Parental	LRAEK	ADLLGIVSELQLK	LNSGG	2		699.9142888	1397.812978	0.000451244	6	N	164	177
Q8K3K8	Parental	EKVDK	MLLQELSEKLELAEQALASK	QLQMD	3		748.7438944	2243.208283	0.0025889	1	N	423	443
Q8K411	Exosome	MVYFR	AFSSLNTLPEDLRPIVPLFCSVLTK	LGCGI	3	C20:+57.021	939.8458575	2816.514173	0.001943752	1	N	599	624
Q8K411	Exosome	HLQNK	LLPDHTYSVVSGGDPLCIPELTWEQLK	QFHAT	3	C17:+57.021	1023.18672	3066.536759	0.000451244	13	N	224	251
Q8K411	Exosome	TQNPK	DFQNLLSVYLDATFFPCLR	ELDFW	2	C17:+57.021	1160.077837	2318.140074	0.000451244	2	N	154	173
Q8K411	Exosome	KVGEK	IHGFTVNQVTPVPELFLTAVK	LSHDN	3		770.7672503	2309.278351	0.001654178	1	N	45	66
Q8K411	Exosome	SPFYK	ALIESGLGTDFSPDVGYNGYTR	EAYFS	2		1166.558751	2331.101903	0.000451244	12	N	363	385
Q8K411	Parental	MVYFR	AFSSLNTLPEDLRPIVPLFCSVLTK	LGCGI	3	C20:+57.021	939.8458575	2816.514173	0.001871652	1	N	599	624
Q8K426	Exosome	EKKVK	ELLANRDDCPSTVTK	TFSCT	2	C9:+57.021	859.9228163	1717.830033	0.000451244	23	N	42	57
Q8K426	Exosome	EKKVK	ELLANRDDCPSTVTK	TFSCT	3	C9:+57.021	573.6178108	1717.830033	0.000451244	20	N	42	57
Q8K426	Exosome	STVTK	TFSCTSITASGR	LASCP	2	C4:+57.021	644.3038168	1286.592034	0.000451244	37	N	57	69
Q8K426	Exosome	VPVNT	EGTLESIVEKK	VKELL	2		616.8407895	1231.665979	0.002813207	1	N	29	40
Q8K426	Exosome	VPVNT	EGTLESIVEKK	VKELL	3		411.5631263	1231.665979	0.000451244	11	N	29	40
Q8K426	Exosome	SWDIR	DGNTCHCQCSTMDWATAR	CCQLA	3	C5:+57.021,C7:+57.021,C9:+57.02	724.2768287	2169.807086	0.000451244	1	N	94	112
Q8K426	Parental	EKKVK	ELLANRDDCPSTVTK	TFSCT	2	C9:+57.021	859.9228163	1717.830033	0.000451244	103	N	42	57
Q8K426	Parental	EKKVK	ELLANRDDCPSTVTK	TFSCT	3	C9:+57.021	573.6178108	1717.830033	0.000451244	86	N	42	57
Q8K426	Parental	EKKVK	ELLANRDDCPSTVTK	TFSCT	2	[0:-18.011,C9:+57.021	850.9173163	1699.819033	0.000451244	8	N	42	57
Q8K426	Parental	STVTK	TFSCTSITASGR	LASCP	2	C4:+57.021	644.3038168	1286.592034	0.000451244	36	N	57	69
Q8K426	Parental	VPVNT	EGTLESIVEKK	VKELL	2		616.8407895	1231.665979	0.000622848	13	N	29	40
Q8K426	Parental	VPVNT	EGTLESIVEKK	VKELL	3		411.5631263	1231.665979	0.000823681	12	N	29	40
Q8K426	Parental	VPVNT	EGTLESIVEK	KVKEL	2		552.7933079	1103.571016	0.000823681	14	N	29	39
Q8K426	Parental	SWDIR	DGNTCHCQCSTMDWATAR	CCQLA	2	C5:+57.021,C7:+57.021,C9:+57.02	1085.911343	2169.807086	0.000451244	3	N	94	112
Q8K426	Parental	SWDIR	DGNTCHCQCSTMDWATAR	CCQLA	3	C5:+57.021,C7:+57.021,C9:+57.02	724.2768287	2169.807086	0.001699387	1	N	94	112
Q8K426	Parental	TVTGC	ACGYGCGSWDIR	DGNTC	2	C2:+57.021,C6:+57.021	701.2874125	1400.559225	0.000451244	7	N	82	94
Q8K482	Exosome	VLFNK	VLVNDGDVYNPNTGIFTAPYDGR	YLITA	2		1249.103857	2496.192115	0.000451244	57	N	949	972
Q8K482	Exosome	VLFNK	VLVNDGDVYNPNTGIFTAPYDGR	YLITA	3		833.0718383	2496.192115	0.000823681	3	N	949	972
Q8K482	Exosome	ISGLK	NSVQQFYSHVFQISTDLQDLVK	FQPSA	2		1298.656257	2595.296914	0.000451244	8	N	758	780
Q8K482	Exosome	ISGLK	NSVQQFYSHVFQISTDLQDLVK	FQPSA	3		866.1067714	2595.296914	0.000451244	23	N	758	780
Q8K482	Exosome	LDTCK	ESAHGVQSGVSAIEGR	VFQLE	2		792.3927718	1582.769944	0.001591523	4	N	688	704
Q8K482	Exosome	LDTCK	ESAHGVQSGVSAIEGR	VFQLE	3		528.5977812	1582.769944	0.001943752	3	N	688	704
Q8K482	Exosome	TCEYK	LVGLQQQCDDYGSSYLGVIELIGEK	EASLK	2	C8:+57.021	1392.691948	2783.368296	0.000451244	15	N	352	377
Q8K482	Exosome	TCEYK	LVGLQQQCDDYGSSYLGVIELIGEK	EASLK	3	C8:+57.021	928.7972321	2783.368296	0.000451244	13	N	352	377
Q8K482	Exosome	IADLR	AQLQDPVAQPSCCNGQK	SSDFG	2	C12:+57.021,C13:+57.021	950.9357007	1899.855801	0.000451244	19	N	389	406
Q8K482	Exosome	IVHLK	AGDGVNVVVTGGR	LAHTD	2		600.8207227	1199.625845	0.000979378	2	N	1036	1049
Q8K482	Exosome	NVTEK	NAEEHCFYIEETLR	GTING	2	C6:+57.021	905.9071662	1809.798732	0.000451244	10	N	467	481
Q8K482	Exosome	NVTEK	NAEEHCFYIEETLR	GTING	3	C6:+57.021	604.2740441	1809.798732	0.002212458	2	N	467	481
Q8K482	Exosome	EGQLK	QLQEAAQGPTVTMTTNELYQAYVDSK	IDALR	3	M13:+15.995	968.131234	2901.370302	0.000451244	4	N	300	326
Q8K482	Exosome	RGLPR	GVDGQMGQGPIHSSEGYAGAPGYPK	SPPVT	3	M6:+15.995	826.0453236	2475.112571	0.000637154	4	N	887	912
Q8K482	Exosome	AIEGR	VFQLEQTCR	RLDTI	2	C8:+57.021	590.792888	1179.570176	0.000823681	4	N	704	713
Q8K482	Exosome	MKDIK	SELAEVKDTLK	TKSDK	2		616.8407895	1231.665979	0.000698008	1	N	268	279
Q8K482	Parental	VLFNK	VLVNDGDVYNPNTGIFTAPYDGR	YLITA	2		1249.103857	2496.192115	0.000451244	45	N	949	972
Q8K482	Parental	ISGLK	NSVQQFYSHVFQISTDLQDLVK	FQPSA	3		866.1067714	2595.296914	0.000451244	22	N	758	780
Q8K482	Parental	TCEYK	LVGLQQQCDDYGSSYLGVIELIGEK	EASLK	2	C8:+57.021	1392.691948	2783.368296	0.000622848	3	N	352	377
Q8K482	Parental	TCEYK	LVGLQQQCDDYGSSYLGVIELIGEK	EASLK	3	C8:+57.021	928.7972321	2783.368296	0.000451244	4	N	352	377
Q8K482	Parental	IADLR	AQLQDPVAQPSCCNGQK	SSDFG	2	C12:+57.021,C13:+57.021	950.9357007	1899.855801	0.001839721	2	N	389	406
Q8K482	Parental	NVTEK	NAEEHCFYIEETLR	GTING	2	C6:+57.021	905.9071662	1809.798732	0.000622848	1	N	467	481
Q8K4I3	Exosome	GSVEK	YCLEPQTEADCIDNINDFLK	GCATL	2	C2:+57.021,C11:+57.021	1229.548749	2457.081898	0.000451244	15	N	55	75
Q8K4I3	Parental	GSVEK	YCLEPQTEADCIDNINDFLK	GCATL	2	C2:+57.021,C11:+57.021	1229.548749	2457.081898	0.000451244	30	N	55	75
Q8K4I3	Parental	RPCGR	SSSLSAATSSQTNPQVAVPSTAPEQHSEEK	AEMTE	3		1019.153726	3054.437778	0.000451244	3	N	121	151
Q8K4I3	Parental	RKDSV	PQVLLPEEEKLIIEETR	SNGQT	3		679.3811729	2035.120119	0.002981883	1	N	680	697
Q8K4I3	Parental	APLTK	NYYTVVLQNILDTEKEYAK	ELQSL	3		768.7306419	2303.168526	0.001162105	2	N	238	257
Q8K4I3	Parental	NDFLK	GCATLQVEVFEPDDLYSGANFSK	VLNTL	2	C2:+57.021	1274.089327	2546.163054	0.000451244	14	N	75	98
Q8K4L3	Exosome	KDFWK	LLGGQTSYQSAGDPKEDELYETAIIETNCVYR	LTDDK	3	C29:+57.021	1207.573919	3619.698358	0.000451244	18	N	1491	1523
Q8K4L3	Exosome	HSIPR	SPVELEEDFDVIFDPYAPK	LTSSV	2		1105.53114	2209.046679	0.000451244	2	N	1277	1296
Q8K4L3	Exosome	FQLAK	HLWNGTFDYENCDINPLDPGECNPLIPR	KGQGR	3	C12:+57.021,C22:+57.021	1119.508373	3355.501718	0.000698008	6	N	1580	1608
Q8K4L3	Parental	KTESK	NALTVAAEDSGVQTR	GAFEE	2		766.3896978	1530.763796	0.000451244	25	N	910	925
Q8K4L3	Parental	KDFWK	LLGGQTSYQSAGDPKEDELYETAIIETNCVYR	LTDDK	3	C29:+57.021	1207.573919	3619.698358	0.000451244	37	N	1491	1523
Q8K4L3	Parental	HSIPR	SPVELEEDFDVIFDPYAPK	LTSSV	2		1105.53114	2209.046679	0.000451244	25	N	1277	1296
Q8K4L3	Parental	RMNAR	YQTQPVTLGEVEQVQSGK	LISFS	2		996.0081659	1990.000732	0.000451244	3	N	808	826
Q8K4L3	Parental	KFSLK	EFGETTSEQTEVAAR	KASVQ	2		827.8819026	1653.748205	0.000451244	8	N	1013	1028
Q8K4L3	Parental	ANEGR	ESAEPGEPDSSTLSLAEK	LALFN	2		923.9317896	1845.847979	0.001329271	3	N	759	777

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8K4L3	Parental	GVQTR	GAFEEEEEPSYPILGR	VREGD	2		911.9288529	1821.842106	0.000451244	7	N	925	941
Q8K4L3	Parental	FQLAK	HLWNGTFDYENCDINPLDPGECNPLIPR	KGQGR	3	C12:+57.021,C22:+57.021	1119.508373	3355.501718	0.000451244	3	N	1580	1608
Q8K4Z3	Exosome	KGDVR	EPFHSILSVLSGLTVPIASIDIPSGWDVEK	GNPSG	3		1069.571493	3205.69108	0.000823681	2	N	191	221
Q8K4Z3	Exosome	TSMSK	SPPTVLVICGPGNNGGDGLVCAR	HLKLF	2	C9:+57.021,C21:+57.021	1155.570153	2309.124706	0.000451244	5	N	100	123
Q8K4Z3	Exosome	ARHLK	LFGYQPTIYYPK	RPNKP	2		745.3904495	1488.765299	0.002080925	2	N	126	138
Q8K4Z3	Exosome	ALEKK	YQLNLPSYPDTECVYR	LQ-	2	C13:+57.021	1009.470131	2016.924661	0.000979378	2	N	264	280
Q8K4Z3	Parental	TSMSK	SPPTVLVICGPGNNGGDGLVCAR	HLKLF	2	C9:+57.021,C21:+57.021	1155.570153	2309.124706	0.001763695	1	N	100	123
Q8K4Z5	Exosome	TIVPK	EPPPEFEFIADPPSISAFDLDVVK	LTAQF	3		887.1112996	2658.310499	0.000622848	3	N	144	168
Q8K4Z5	Parental	KTEWK	LNGQGLVFTLPLTDQVSVIK	VKIHE	2		1071.612601	2141.209603	0.00091018	3	N	719	739
Q8K4Z5	Parental	QLPQK	VQAQVIQETIVPKEPPPEFEFIADPPSISAFDLDVVK	LTAQF	3		1365.052705	4092.134714	0.001943752	2	N	131	168
Q8K4Z5	Parental	DRSIR	EKQSDDEVYAPGLDIESSLK	QLAER	2		1112.037317	2222.059035	0.001162105	3	N	445	465
Q8K4Z5	Parental	SIREK	QSDDEVYAPGLDIESSLK	QLAER	2		983.4685392	1964.921478	0.000622848	7	N	447	465
Q8K4Z5	Parental	TIVPK	EPPPEFEFIADPPSISAFDLDVVK	LTAQF	2		1330.163049	2658.310499	0.001264573	1	N	144	168
Q8K4Z5	Parental	TIVPK	EPPPEFEFIADPPSISAFDLDVVK	LTAQF	3		887.1112996	2658.310499	0.000622848	2	N	144	168
Q8K4Z5	Parental	QLPQK	VQAQVIQETIVPK	EPPPE	2		726.9251879	1451.834776	0.000451244	6	N	131	144
Q8K4Z5	Parental	INNPK	FNFLNPNDPYHAYYR	HKVSE	3		644.3010762	1929.879829	0.00307782	1	N	80	95
Q8K558	Exosome	GQGSA	DSHPEVLQAPVGSSILVQCHYR	LQDVR	3	C19:+57.021	831.4169087	2491.227326	0.000451244	14	N	20	42
Q8K558	Exosome	VRALK	VWCQFLQEGCHPLVTSAVDR	RAPGN	3	C3:+57.021,C10:+57.021	801.3843973	2401.129792	0.000637154	7	N	50	70
Q8K558	Exosome	GDKGK	IASCEPVQDPPNSQTPPSK	-	2	C4:+57.021	1026.489052	2050.962504	0.000823681	3	N	298	317
Q8K558	Exosome	QTLHR	VSLLVLPPVPGPR	EGEEA	2		672.4246267	1342.833653	0.000622848	5	N	118	131
Q8K558	Parental	GQGSA	DSHPEVLQAPVGSSILVQCHYR	LQDVR	2	C19:+57.021	1246.621463	2491.227326	0.000451244	5	N	20	42
Q8K558	Parental	GQGSA	DSHPEVLQAPVGSSILVQCHYR	LQDVR	3	C19:+57.021	831.4169087	2491.227326	0.000451244	7	N	20	42
Q8K558	Parental	VRALK	VWCQFLQEGCHPLVTSAVDR	RAPGN	3	C3:+57.021,C10:+57.021	801.3843973	2401.129792	0.001162105	2	N	50	70
Q8K558	Parental	GDKGK	IASCEPVQDPPNSQTPPSK	-	2	C4:+57.021	1026.489052	2050.962504	0.000622848	2	N	298	317
Q8K558	Parental	QTLHR	VSLLVLPPVPGPR	EGEEA	2		672.4246267	1342.833653	0.0007646	4	N	118	131
Q8QZT1	Exosome	KPLAR	IAAFADAAVDPIDFPLAPAYAVPK	VLKYA	2		1222.149548	2442.283496	0.000451244	9	N	308	332
Q8QZT1	Exosome	RIAAF	ADAAVDPIDFPLAPAYAVPK	VLKYA	2		1021.036195	2040.05679	0.001463592	1	N	312	332
Q8QZT1	Exosome	QAPTR	QATLGAGLPISTPCTTVNK	VCASG	2	C14:+57.021	965.009423	1928.003246	0.000451244	10	N	102	121
Q8QZT1	Exosome	VPKLK	TVFQKENGTITAANASTLNDGAAALVLMTAEAAQR	LNVKP	3	M28:+15.995	1188.937486	3563.789059	0.001871652	1	N	265	300
Q8QZT1	Parental	KPLAR	IAAFADAAVDPIDFPLAPAYAVPK	VLKYA	2		1222.149548	2442.283496	0.000451244	12	N	308	332
Q8QZT1	Parental	KPLAR	IAAFADAAVDPIDFPLAPAYAVPK	VLKYA	3		815.1022987	2442.283496	0.002884417	1	N	308	332
Q8QZT1	Parental	RIAAF	ADAAVDPIDFPLAPAYAVPK	VLKYA	2		1021.036195	2040.05679	0.000451244	8	N	312	332
Q8QZT1	Parental	MNISR	QEQDTYALSSYTR	SKEAW	2		781.360606	1560.705612	0.000451244	2	N	205	218
Q8QZT1	Parental	LARIA	AFADAAVDPIDFPLAPAYAVPK	VLKYA	2		1130.088959	2258.162318	0.001264573	1	N	310	332
Q8QZT1	Parental	QAPTR	QATLGAGLPISTPCTTVNK	VCASG	2	C14:+57.021	965.009423	1928.003246	0.00091018	7	N	102	121
Q8QZW8	Exosome	KLFFR	ELPQPLVPALLLPDFR	DALEL	2		909.5303516	1817.045103	0.000451244	4	N	362	378
Q8QZW8	Parental	KLFFR	ELPQPLVPALLLPDFRDALELSEPEQCLSK	IQKLI	3	C27:+57.021	1139.937693	3416.789679	0.000451244	10	N	362	392
Q8QZW8	Parental	ETLTR	DSSALQPQEWLDPQGLPSLSQSVPWLAL	SEQPG	3		1021.521021	3061.539664	0.000622848	4	N	9	37
Q8QZW8	Parental	KLFFR	ELPQPLVPALLLPDFR	DALEL	2		909.5303516	1817.045103	0.000451244	15	N	362	378
Q8QZW8	Parental	GQEGK	LDLDSAEWDDIHVVTGALK	LFFRE	3		699.6886656	2096.042597	0.000637154	3	N	339	358
Q8QZW8	Parental	LPDFR	DALELSEPEQCLSK	IQKLI	2	C11:+57.021	809.8853681	1617.755136	0.000622848	2	N	378	392
Q8QZY1	Exosome	LQQLK	VFSDEVQQQAQLSTIR	SFLKL	2		924.9766688	1847.937738	0.000451244	39	N	445	461
Q8QZY1	Exosome	LRMQK	GDPQVYEELFSYACPK	FLSPV	2	C14:+57.021	951.9328497	1901.850099	0.000451244	14	N	403	419
Q8QZY1	Exosome	MPVAK	LAGFLDLTEQEFR	IQLLV	2		769.8966274	1537.777655	0.000823681	3	N	474	487
Q8QZY1	Exosome	RSNPK	VWNVHSVLNVLHSLVDK	SNINR	2		980.0446888	1958.073778	0.001591523	1	N	220	237
Q8QZY1	Exosome	RSNPK	VWNVHSVLNVLHSLVDK	SNINR	3		653.6990592	1958.073778	0.000451244	17	N	220	237
Q8QZY1	Exosome	RSNPK	VWNVHSVLNVLHSLVDK	SNINR	4		490.5262444	1958.073778	0.000451244	15	N	220	237
Q8QZY1	Exosome	ERFFK	NTPWPEAEAIAPQVGNDAVFLILYK	ELYYR	3		919.4818383	2755.422115	0.000451244	21	N	108	133
Q8QZY1	Exosome	SNINR	QLEVYTSGGDPESVAGEYGR	HSLYK	2		1057.487795	2112.959989	0.000451244	27	N	242	262
Q8QZY1	Exosome	VGLLR	LHSLLGDYYQAIK	VLENI	3		507.6089585	1519.803476	0.001229886	1	N	279	292
Q8QZY1	Exosome	LAYER	QYEQQTYQVIPEVIK	NFIQY	2		933.486338	1864.957076	0.001654178	1	N	38	53
Q8QZY1	Parental	LQQLK	VFSDEVQQQAQLSTIR	SFLKL	2		924.9766688	1847.937738	0.000451244	28	N	445	461
Q8QZY1	Parental	LRMQK	GDPQVYEELFSYACPK	FLSPV	2	C14:+57.021	951.9328497	1901.850099	0.000451244	13	N	403	419
Q8QZY1	Parental	MPVAK	LAGFLDLTEQEFR	IQLLV	2		769.8966274	1537.777655	0.000979378	1	N	474	487
Q8QZY1	Parental	RSNPK	VWNVHSVLNVLHSLVDK	SNINR	3		653.6990592	1958.073778	0.000622848	9	N	220	237
Q8QZY1	Parental	RSNPK	VWNVHSVLNVLHSLVDK	SNINR	4		490.5262444	1958.073778	0.000451244	11	N	220	237
Q8QZY1	Parental	ERFFK	NTPWPEAEAIAPQVGNDAVFLILYK	ELYYR	3		919.4818383	2755.422115	0.000451244	10	N	108	133
Q8QZY1	Parental	SNINR	QLEVYTSGGDPESVAGEYGR	HSLYK	2		1057.487795	2112.959989	0.001463592	1	N	242	262
Q8QZY1	Parental	LAYER	QYEQQTYQVIPEVIK	NFIQY	2		933.486338	1864.957076	0.001329271	2	N	38	53
Q8QZY6	Exosome	ESNIK	SYRDDIDLQNLIDSLQK	ANQCC	2		1018.518898	2035.022196	0.000451244	16	N	132	149
Q8QZY6	Exosome	ESNIK	SYRDDIDLQNLIDSLQK	ANQCC	3		679.3485319	2035.022196	0.000451244	29	N	132	149
Q8QZY6	Exosome	YSREK	CGVPFSCCVPDPAQK	VVNTQ	2	C1:+57.021,C7:+57.021,C8:+57.02	861.3756704	1720.735741	0.000451244	8	N	179	194
Q8QZY9	Exosome	PISER	NQDATVYVGGLDEK	VSEPL	2		754.8655242	1507.715448	0.000823681	14	N	9	23
Q8QZY9	Exosome	MPKDR	VTGQHQGYGFVEFLSEEDADYAIK	IMNMI	3		901.7578079	2702.250024	0.000451244	5	N	48	72
Q8QZY9	Parental	PISER	NQDATVYVGGLDEK	VSEPL	2		754.8655242	1507.715448	0.000451244	12	N	9	23

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8QZY9	Parental	MPKDR	VTGQHQGYGFVEFLSEEDADYAIK	IMNMI	3		901.7578079	2702.250024	0.000451244	20	N	48	72
Q8QZY9	Parental	EIDEK	LLYDTFSAFGVILQTPK	IMRDP	2		957.025099	1912.034598	0.001654178	1	N	114	131
Q8QZY9	Parental	SAHNK	NLDVGANIFIGNLDPEIDEK	LLYDT	2		1093.552938	2185.090275	0.000451244	4	N	94	114
Q8R010	Exosome	SALGR	SPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQR	WLKSC	3		1246.315145	3735.922036	0.000451244	8	N	265	301
Q8R010	Exosome	DGLSK	MIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGK	DYGAL	3	M1:+15.995	1289.317921	3864.930364	0.000451244	3	N	78	114
Q8R010	Exosome	NVHSK	TTSPATDAGHVQETSEPSLQALESR	QDDIL	3		871.4198549	2611.236165	0.000637154	2	N	33	58
Q8R010	Parental	SALGR	SPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQR	WLKSC	3		1246.315145	3735.922036	0.000451244	33	N	265	301
Q8R010	Parental	SALGR	SPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQR	WLKSC	4		934.988309	3735.922036	0.000622848	3	N	265	301
Q8R016	Exosome	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLR	RATVQ	2	C23:+57.021	1420.224281	2838.432962	0.002519933	1	N	17	42
Q8R016	Exosome	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLR	RATVQ	3	C23:+57.021	947.1521207	2838.432962	0.000451244	33	N	17	42
Q8R016	Exosome	EEIFR	VVCICLGNPPETFTWEYR	DKDKN	2	C3:+57.021,C5:+57.021	1121.027059	2240.038517	0.000451244	56	N	218	236
Q8R016	Exosome	DKVER	CYFFLNAFVDTAQK	KEPED	2	C1:+39.994	853.897856	1705.780112	0.000870037	3	N	110	124
Q8R016	Exosome	DKVER	CYFFLNAFVDTAQK	KEPED	2	C1:+57.021	862.411356	1722.807112	0.000451244	15	N	110	124
Q8R016	Exosome	DKVER	CYFFLNAFVDTAQK	KEPED	3	C1:+57.021	575.2768374	1722.807112	0.000637154	4	N	110	124
Q8R016	Exosome	DKVER	CYFFLNAFVDTAQK	KEPED	2	[0:-17.027,C1:+57.021	853.897856	1705.780112	0.000451244	16	N	110	124
Q8R016	Exosome	ICLRR	ATVQGAQHVFQHVVPQEGKPVTNQK	SSGRC	3		909.8162144	2726.425243	0.000451244	15	N	43	68
Q8R016	Exosome	ICLRR	ATVQGAQHVFQHVVPQEGKPVTNQK	SSGRC	4		682.6141108	2726.425243	0.000451244	5	N	43	68
Q8R016	Exosome	VGGRK	TLYNNQPIDFLK	KMVAA	2		733.3884382	1464.761276	0.000662267	1	N	297	309
Q8R016	Exosome	KNYHK	IGPITPLQFYK	EHVKP	2		638.8691529	1275.722706	0.000662267	11	N	244	255
Q8R016	Exosome	AASIK	DGEAVWFGCDVGK	HFNGK	2	C9:+57.021	720.3169242	1438.618248	0.000451244	5	N	317	330
Q8R016	Exosome	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLRR	ATVQG	3	C23:+57.021	999.1858244	2994.534073	0.000451244	4	N	17	43
Q8R016	Exosome	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLRR	ATVQG	4	C23:+57.021	749.6413183	2994.534073	0.000451244	12	N	17	43
Q8R016	Exosome	DICLR	RATVQGAQHVFQHVVPQEGKPVTNQK	SSGRC	4		721.6393886	2882.526354	0.000451244	14	N	42	68
Q8R016	Exosome	VVDKK	HVPEEVLAVLEQEPIVLPAWDPMGALA	E-	3		975.1811719	2922.520116	0.000622848	1	N	427	454
Q8R016	Exosome	DKVER	CYFFLNAFVDTAQKK	EPEDG	3	C1:+57.021	617.9751584	1850.902075	0.000451244	1	N	110	125
Q8R016	Parental	ALIQK	LNSDPQFVLAQNVGTTHDLLDICLR	RATVQ	3	C23:+57.021	947.1521207	2838.432962	0.000451244	14	N	17	42
Q8R016	Parental	ICLRR	ATVQGAQHVFQHVVPQEGKPVTNQK	SSGRC	4		682.6141108	2726.425243	0.000451244	1	N	43	68
Q8R050	Exosome	KIRLK	GIEEEEILPGFILCDLNNLCHSGR	TFDAQ	3	C14:+57.021,C20:+57.021	929.1145239	2784.320172	0.000451244	9	N	504	528
Q8R050	Exosome	GANLK	EQSDFCPWYIGLPFIPYLDNLPNFNR	SVDGP	3	C6:+57.021	1072.515059	3214.521777	0.000622848	5	N	407	433
Q8R050	Exosome	GANLK	EQSDFCPWYIGLPFIPY	LDNLP	2	C6:+57.021	1066.495617	2130.975634	0.001162105	1	N	407	424
Q8R050	Parental	AAFSR	QLNVNAKPFVPNVHAAEFVPSFLR	GPAQP	3		898.8225292	2693.444188	0.000823681	3	N	67	91
Q8R050	Parental	AAFSR	QLNVNAKPFVPNVHAAEFVPSFLR	GPAQP	4		674.3688469	2693.444188	0.001943752	3	N	67	91
Q8R050	Parental	AAFSR	QLNVNAKPFVPNVHAAEFVPSFLR	GPAQP	3	Q1:-17.027	893.1468626	2676.417188	0.000823681	1	N	67	91
Q8R050	Parental	NLKIR	LKGIEEEEILPGFILCDLNNLCHSGR	TFDAQ	4	C16:+57.021,C22:+57.021	757.3825997	3025.499199	0.000451244	4	N	502	528
Q8R050	Parental	KIRLK	GIEEEEILPGFILCDLNNLCHSGR	TFDAQ	3	C14:+57.021,C20:+57.021	929.1145239	2784.320172	0.000451244	8	N	504	528
Q8R050	Parental	GANLK	EQSDFCPWYIGLPFIPYLDNLPNFNR	SVDGP	3	C6:+57.021	1072.515059	3214.521777	0.000622848	6	N	407	433
Q8R050	Parental	GANLK	EQSDFCPWYIGLPFIPY	LDNLP	2	C6:+57.021	1066.495617	2130.975634	0.000823681	7	N	407	424
Q8R081	Exosome	LNVFK	NDQDTWDYTNPNLSGQGDPGSNPNKR	QRQPP	3		964.0928009	2889.255003	0.000451244	35	N	274	300
Q8R081	Exosome	MNCDR	VFNVFCLYGNVEK	VKFMK	2	C6:+57.021	794.8953418	1587.775084	0.000451244	21	N	395	408
Q8R081	Exosome	VVHIR	GLIDGVVEADLVEALQEFGPISYVVVMPK	KRQAL	3		1029.882792	3086.624975	0.000451244	4	N	104	133
Q8R081	Exosome	VVHIR	GLIDGVVEADLVEALQEFGPISYVVVMPK	KRQAL	3	M27:+15.995	1035.214458	3102.619975	0.000451244	7	N	104	133
Q8R081	Exosome	VVHIR	GLIDGVVEADLVEALQEFGPISY	VVVMP	2		1217.62356	2433.23152	0.001463592	1	N	104	127
Q8R081	Exosome	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	C13:+57.021	1463.369496	4387.085087	0.000451244	13	N	135	175
Q8R081	Exosome	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	4	C13:+57.021	1097.779072	4387.085087	0.000451244	11	N	135	175
Q8R081	Exosome	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	Q1:-17.027,C13:+57.021	1457.693829	4370.058087	0.000622848	3	N	135	175
Q8R081	Exosome	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	[0:-17.027,C13:+57.021	1457.693829	4370.058087	0.001162105	2	N	135	175
Q8R081	Exosome	SDDSR	SVNSVLLFTILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C26:+57.021,C29:+57.021	1290.005847	3866.994141	0.000451244	9	N	186	220
Q8R081	Exosome	SDDSR	SVNSVLLFTILNPIYSITTDVLYTICNPCGPVQR	IVIFR	4	C26:+57.021,C29:+57.021	967.7563353	3866.994141	0.002813207	1	N	186	220
Q8R081	Exosome	SVLLF	TILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C18:+57.021,C21:+57.021	1003.512395	3007.513786	0.000451244	1	N	194	220
Q8R081	Exosome	AQRAK	ASLNGADIYSGCCTLK	IEYAK	2	C12:+57.021,C13:+57.021	865.3978884	1728.780177	0.000451244	6	N	245	261
Q8R081	Exosome	SDDSR	SVNSVLLFTILNPIYSITTDVLY	TICNP	2		1293.209803	2584.404005	0.001463592	1	N	186	209
Q8R081	Parental	LNVFK	NDQDTWDYTNPNLSGQGDPGSNPNKR	QRQPP	2		1445.635301	2889.255003	0.002145581	1	N	274	300
Q8R081	Parental	LNVFK	NDQDTWDYTNPNLSGQGDPGSNPNKR	QRQPP	3		964.0928009	2889.255003	0.000451244	95	N	274	300
Q8R081	Parental	MNCDR	VFNVFCLYGNVEK	VKFMK	2	C6:+57.021	794.8953418	1587.775084	0.000451244	22	N	395	408
Q8R081	Parental	AAKNR	IQHPSNVLHFFNAPLEVTEENFFEICDELGVK	RPTSV	3	C26:+57.021	1258.282411	3771.823833	0.000451244	4	N	492	524
Q8R081	Parental	AAKNR	IQHPSNVLHFFNAPLEVTEENFFEICDELGVK	RPTSV	4	C26:+57.021	943.9637583	3771.823833	0.000451244	3	N	492	524
Q8R081	Parental	VVHIR	GLIDGVVEADLVEALQEFGPISYVVVMPK	KRQAL	3		1029.882792	3086.624975	0.000451244	9	N	104	133
Q8R081	Parental	VVHIR	GLIDGVVEADLVEALQEFGPISY	VVVMP	2		1217.62356	2433.23152	0.000823681	28	N	104	127
Q8R081	Parental	VVHIR	GLIDGVVEADLVEALQEFGPISY	VVVMP	3		812.0849733	2433.23152	0.000823681	16	N	104	127
Q8R081	Parental	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	C13:+57.021	1463.369496	4387.085087	0.000451244	39	N	135	175
Q8R081	Parental	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	4	C13:+57.021	1097.779072	4387.085087	0.000451244	26	N	135	175
Q8R081	Parental	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	Q1:-17.027,C13:+57.021	1457.693829	4370.058087	0.002374549	1	N	135	175
Q8R081	Parental	MPKKR	QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	ISRPG	3	[0:-17.027,C13:+57.021	1457.693829	4370.058087	0.000637154	3	N	135	175
Q8R081	Parental	SDDSR	SVNSVLLFTILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C26:+57.021,C29:+57.021	1290.005847	3866.994141	0.000622848	6	N	186	220
Q8R081	Parental	SVLLF	TILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C18:+57.021,C21:+57.021	1003.512395	3007.513786	0.000451244	14	N	194	220

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R081	Parental	NSVLL	FTILNPIYSITTDVLYTICNPCGPVQR	IVIFR	3	C19:+57.021,C22:+57.021	1052.5352	3154.5822	0.000451244	5	N	193	220
Q8R081	Parental	AQRAK	ASLNGADIYSGCCTLK	IEYAK	2	C12:+57.021,C13:+57.021	865.3978884	1728.780177	0.000451244	12	N	245	261
Q8R081	Parental	MNCDR	VFNVFCLYGNVEKV	KFMKS	2	C6:+57.021	844.4295488	1686.843498	0.000451244	4	N	395	409
Q8R0G9	Exosome	NHHSR	LPDLVNSAILLALNKR	ECEVP	3		584.0248837	1749.051251	0.001839721	1	N	658	674
Q8R0G9	Parental	LPQEK	IVFDTQGDGILGAGSCAGVPILFSR	NSGLV	2	C16:+57.021	1275.654972	2549.294343	0.001162105	7	N	440	465
Q8R0G9	Parental	SVTPR	ENVSLLAEDLEESLTSSVGGR	GSESM	2		1103.048216	2204.080833	0.000622848	3	N	475	496
Q8R0G9	Parental	YLQKR	SELLSPLLTLGQYPWAASLAEK	YCDFD	2		1194.147005	2386.278411	0.000451244	6	N	842	864
Q8R0G9	Parental	EDKMK	AHCLLVDFLHQVGLFR	RLSSY	3	C3:+57.021	642.3456971	1924.013691	0.002212458	1	N	605	621
Q8R0G9	Parental	NHHSR	LPDLVNSAILLALNKR	ECEVP	3		584.0248837	1749.051251	0.001763695	1	N	658	674
Q8R0G9	Parental	QKLIK	DGIQLSEYLPEVTDLLR	AEQLG	2		981.0154596	1960.015319	0.000451244	4	N	1109	1126
Q8R0G9	Parental	EKMCR	FLTAVQGGSFILSSVGSQLVR	LIPES	3		722.7359501	2165.18445	0.002663018	1	N	209	230
Q8R0H9	Parental	NPLNK	ELNWASINSFCEQLNEDFEGPPLATR	LLAHK	3	C11:+57.021	1013.138428	3036.391885	0.000622848	3	N	23	49
Q8R0H9	Parental	PTLFR	LASDTEDNDEALAEILQANDNLTQVINLYK	QLVRG	3		1111.883124	3332.625973	0.000451244	42	N	264	294
Q8R0H9	Parental	RPTLF	RLASDTEDNDEALAEILQANDNLTQVINLYK	QLVRG	3		1163.916828	3488.727084	0.000451244	1	N	263	294
Q8R0J7	Exosome	NMAEK	FLDGELPLDSFIDVYQSK	RKLAH	2		1043.523118	2085.030635	0.000451244	9	N	127	145
Q8R0J7	Exosome	LASNR	SLAEGNLLYQPQLDAQK	ARLTQ	2		944.4946944	1886.973789	0.001162105	2	N	53	70
Q8R0T6	Exosome	RSAVR	LAITVLDIGAGNVFK	GPKLL	2		765.948663	1529.881726	0.000451244	12	N	147	162
Q8R0T6	Parental	RSAVR	LAITVLDIGAGNVFKGPK	LLEDK	2		907.0332584	1812.050917	0.000451244	4	N	147	165
Q8R0T6	Parental	RSAVR	LAITVLDIGAGNVFK	GPKLL	2		765.948663	1529.881726	0.000451244	30	N	147	162
Q8R0T6	Parental	QCFTK	CGQSEHSPCDVGNLQR	YWLNY	2	C1:+39.994,C9:+57.021	913.8807	1825.7458	0.002453667	3	N	52	68
Q8R0T6	Parental	QCFTK	CGQSEHSPCDVGNLQR	YWLNY	2	[0:-17.027,C1:+57.021,C9:+57.021	913.8807	1825.7458	0.001871652	4	N	52	68
Q8R146	Exosome	LSGGK	CELLSDESLAVCSPR	LSPDQ	2	C1:+57.021,C12:+57.021	868.4031708	1734.790742	0.000451244	23	N	291	306
Q8R146	Exosome	-MER	QVLLSEPQEAAALYR	GLSRQ	2		844.4548408	1686.894082	0.000451244	5	N	3	18
Q8R146	Exosome	RGLSR	QPSLSAACLGPEVTTQYGGLYR	TVHTE	2	C8:+57.021	1184.584015	2367.15243	0.000451244	26	N	22	44
Q8R146	Exosome	RGLSR	QPSLSAACLGPEVTTQYGGLYR	TVHTE	2	[0:-17.027,C8:+57.021	1176.070515	2350.12543	0.002374549	2	N	22	44
Q8R146	Exosome	HQDVK	DVQFAVQQVLQEEHFDAR	RVALM	2		1080.029964	2158.044328	0.000451244	7	N	561	579
Q8R146	Exosome	HQDVK	DVQFAVQQVLQEEHFDAR	RVALM	3		720.3559094	2158.044328	0.000451244	22	N	561	579
Q8R146	Exosome	HWGIR	VLHPPPDQENVQYADLDFEAILLQPSNSPDK	SQVPM	3		1163.911126	3488.709977	0.000451244	7	N	466	497
Q8R146	Exosome	HWGIR	VLHPPPDQENVQYADLDFEAILLQPSNSPDK	SQVPM	4		873.1852943	3488.709977	0.001329271	3	N	466	497
Q8R146	Exosome	PPAGK	EQSVSWVSLEEAEPIPDIHWGIR	VLHPP	2		1339.166989	2676.318378	0.000823681	2	N	443	466
Q8R146	Exosome	PPAGK	EQSVSWVSLEEAEPIPDIHWGIR	VLHPP	3		893.113926	2676.318378	0.000451244	43	N	443	466
Q8R146	Exosome	DIVPR	QLGESFSGIYCSLLPLGCWSADSQR	VVFDS	2	C11:+57.021,C18:+57.021	1416.160061	2830.304522	0.000451244	30	N	350	375
Q8R146	Exosome	DIVPR	QLGESFSGIYCSLLPLGCWSADSQR	VVFDS	3	C11:+57.021,C18:+57.021	944.4426406	2830.304522	0.000451244	35	N	350	375
Q8R146	Exosome	LVNYR	GSTGFGQDSILSLPGNVGHQDVK	DVQFA	2		1157.077643	2312.139685	0.000698008	4	N	538	561
Q8R146	Exosome	LVNYR	GSTGFGQDSILSLPGNVGHQDVK	DVQFA	3		771.7210284	2312.139685	0.000622848	1	N	538	561
Q8R146	Exosome	VQRSR	QDLFAVDTQTGSVTSLTAGGSAGSWK	LLTID	2		1292.630436	2583.245273	0.000823681	2	N	385	411
Q8R146	Exosome	HQDVK	DVQFAVQQVLQEEHFDARR	VALMG	3		772.3896131	2314.145439	0.000451244	2	N	561	580
Q8R146	Exosome	CTNRR	SALYYVDLSGGK	CELLS	2		636.8276821	1271.639764	0.000451244	1	N	279	291
Q8R146	Exosome	DWYTK	VTSLVVDIVPR	QLGES	2		599.3642347	1196.712869	0.001591523	2	N	339	350
Q8R146	Exosome	CTNRR	SALYYVDLSGGKCELLSDESLAVCSPR	LSPDQ	3	C13:+57.021,C24:+57.021	997.1477819	2988.419946	0.000622848	1	N	279	306
Q8R146	Parental	PPAGK	EQSVSWVSLEEAEPIPDIHWGIR	VLHPP	3		893.113926	2676.318378	0.000451244	6	N	443	466
Q8R146	Parental	DIVPR	QLGESFSGIYCSLLPLGCWSADSQR	VVFDS	3	C11:+57.021,C18:+57.021	944.4426406	2830.304522	0.002080925	3	N	350	375
Q8R180	Exosome	SASYK	YSEEANRIEECEQAER	LGAVD	3	C11:+57.021	671.6256938	2011.853681	0.001162105	2	N	119	135
Q8R180	Exosome	EQAER	LGAVDESLSEETQK	AVLQW	2		753.3706394	1504.725679	0.000451244	10	N	135	149
Q8R180	Exosome	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	C1:+39.994,C3:+57.021,C12:+57.021,C14:+57.021	1088.111955	3261.312466	0.001162105	1	N	34	60
Q8R180	Exosome	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	C1:+57.021,C3:+57.021,C12:+57.021,C14:+57.021	1093.787622	3278.339466	0.000451244	30	N	34	60
Q8R180	Exosome	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	[0:-17.027,C1:+57.021,C3:+57.021,C12:+57.021,C14:+57.021	1088.111955	3261.312466	0.000451244	3	N	34	60
Q8R180	Exosome	QCGRR	DCAVKPCHSDEVPDGIK	SASYK	3	C2:+57.021,C7:+57.021	642.9612061	1925.860218	0.000823681	3	N	97	114
Q8R180	Exosome	LQWTK	HDDSSDSFCEIDDIQSPDAEYVDLLLNPER	YTGYK	3	C9:+57.021	1165.511096	3493.509888	0.000451244	13	N	156	186
Q8R180	Exosome	DAENK	ALLLEILHEIK	SFPLH	2		646.4033599	1290.79112	0.001395409	4	N	337	348
Q8R180	Exosome	DAENK	ALLLEILHEIK	SFPLH	3		431.2715066	1290.79112	0.000823681	6	N	337	348
Q8R180	Exosome	FQLTR	QEIVSLFNAFGR	ISTSV	2		690.8676729	1379.719746	0.000622848	1	N	433	445
Q8R180	Exosome	PDAWR	IWSVIYEENCFKPQTIQRPLASGR	GKSKE	3	C10:+57.021	964.8327225	2891.474767	0.002519933	2	N	197	221
Q8R180	Parental	SASYK	YSEEANRIEECEQAER	LGAVD	2	C11:+57.021	1006.934641	2011.853681	0.000622848	5	N	119	135
Q8R180	Parental	SASYK	YSEEANRIEECEQAER	LGAVD	3	C11:+57.021	671.6256938	2011.853681	0.000622848	8	N	119	135
Q8R180	Parental	EQAER	LGAVDESLSEETQK	AVLQW	2		753.3706394	1504.725679	0.000451244	13	N	135	149
Q8R180	Parental	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	C1:+39.994,C3:+57.021,C12:+57.021,C14:+57.021	1088.111955	3261.312466	0.000451244	1	N	34	60
Q8R180	Parental	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	C1:+57.021,C3:+57.021,C12:+57.021,C14:+57.021	1093.787622	3278.339466	0.000451244	37	N	34	60

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R180	Parental	TAAQR	CFCQVSGYLDDCTCDVETIDKFNNYR	LFPRL	3	[0:-17.027,C1:+57.021,C3:+57.021,C12:+57.021,C14:+57.021	1088.111955	3261.312466	0.000451244	1	N	34	60
Q8R180	Parental	QCGRR	DCAVKPCHSDEVPDGIK	SASYK	3	C2:+57.021,C7:+57.021	642.9612061	1925.860218	0.001871652	2	N	97	114
Q8R180	Parental	LQWTK	HDDSSDSFCEIDDIQSPDAEYVDLLLNPER	YTGYK	3	C9:+57.021	1165.511096	3493.509888	0.000451244	24	N	156	186
Q8R180	Parental	DAENK	ALLLEILHEIK	SFPLH	3		431.2715066	1290.79112	0.001699387	2	N	337	348
Q8R1B4	Exosome	VVMHR	TEPTAQQNLALQLAEK	LGSLV	2		877.9683124	1753.921025	0.000451244	14	N	844	860
Q8R1B4	Exosome	RFYIR	ILADLEDYLNELWEDKEGK	KKMNK	3		765.0465186	2292.116156	0.000622848	1	N	108	127
Q8R1B4	Exosome	KMNGK	VWDLFPEADKVR	TMLVR	3		492.2616702	1473.761611	0.000451244	8	N	762	774
Q8R1B4	Exosome	SGRAK	ELLGQGLLLR	SLQER	2		556.345845	1110.67609	0.001699387	1	N	641	651
Q8R1B4	Parental	VVMHR	TEPTAQQNLALQLAEK	LGSLV	2		877.9683124	1753.921025	0.000451244	7	N	844	860
Q8R1B4	Parental	RDVTK	CLEEFELLGK	AYGKA	2	[0:-17.027,C1:+57.021	610.7970792	1219.578558	0.001591523	7	N	78	88
Q8R1B4	Parental	RFYIR	ILADLEDYLNELWEDKEGK	KKMNK	2		1147.065878	2292.116156	0.00091018	2	N	108	127
Q8R1B4	Parental	RFYIR	ILADLEDYLNELWEDKEGK	KKMNK	3		765.0465186	2292.116156	0.001162105	4	N	108	127
Q8R1B4	Parental	KMNGK	VWDLFPEADKVR	TMLVR	3		492.2616702	1473.761611	0.000451244	3	N	762	774
Q8R1B4	Parental	QSSGR	AKELLGQGLLLR	SLQER	3		437.6105223	1309.808167	0.0025889	1	N	639	651
Q8R1B4	Parental	DRKSK	RLDEEEEDNEGGEWER	VRGGV	2		996.4148266	1990.814053	0.001162105	2	N	285	301
Q8R1G6	Parental	LQLDR	SQTASPGQTNGEGSLEVLATR	FQGSL	2		1052.019793	2102.023987	0.000451244	12	N	82	103
Q8R1G6	Parental	SSSFR	LLQEALEAEERGGTPAFVPSSLSSQASLPTSR	ALATP	3		1110.239354	3327.694662	0.000451244	6	N	240	272
Q8R1G6	Parental	IQEGR	YRHPGCYTCADCGLNLK	MRGHF	3	C6:+57.021,C9:+57.021,C12:+57.021	695.6415477	2083.901243	0.000698008	2	N	301	318
Q8R1G6	Parental	EAEER	GGTPAFVPSSLSSQASLPTSR	ALATP	2		1024.02689	2046.03818	0.002453667	1	N	251	272
Q8R1G6	Parental	AADLR	PGDIIVAINGQSAENMLHAEAQSK	IRQSA	3		831.7521116	2492.232935	0.001654178	1	N	44	68
Q8R1Q8	Exosome	LASTY	ASGPLANELASGSGGPAAGDDEDGQNLWSCILSEVSTR	SRSKL	3	C30:+57.021	1263.582025	3787.722675	0.000451244	3	N	21	59
Q8R1Q8	Exosome	QKLIR	DFQEYVEPGEDFPASPQR	RTTGA	2		1055.97178	2109.927961	0.0007646	3	N	192	210
Q8R1Q8	Exosome	SPQRR	TTGAQEDRGDSVVLPLGADTLTHNLGLPVLVVCTK	CDAIS	3	C33:+57.021	1216.308849	3645.903146	0.000451244	1	N	211	246
Q8R1Q8	Parental	DPNMK	AGATSEGVLANFFNSLLSK	KTGSP	2		963.5025194	1924.989439	0.000451244	3	N	435	454
Q8R1Q8	Parental	LASTY	ASGPLANELASGSGGPAAGDDEDGQNLWSCILSEVSTR	SRSKL	3	C30:+57.021	1263.582025	3787.722675	0.000451244	2	N	21	59
Q8R1Q8	Parental	KGLLK	FSLDALSLR	DTLVM	2		511.2879957	1020.560391	0.002374549	2	N	133	142
Q8R1Q8	Parental	SLLSK	KTGSPGGPGVGGSPGGGAAGASPSLPPSAK	KSGQK	3		820.7546207	2459.240462	0.002519933	2	N	454	484
Q8R1Q8	Parental	QKLIR	DFQEYVEPGEDFPASPQR	RTTGA	2		1055.97178	2109.927961	0.000451244	4	N	192	210
Q8R1Q8	Parental	SPQRR	TTGAQEDRGDSVVLPLGADTLTHNLGLPVLVVCTK	CDAIS	3	C33:+57.021	1216.308849	3645.903146	0.002145581	1	N	211	246
Q8R1Q8	Parental	DDQTR	CNVWILDGDLYHK	GLLKF	3	C1:+57.021	544.9331821	1631.776146	0.001463592	2	N	116	129
Q8R2S8	Exosome	VTCPR	GATHCYKGDIALQGGGLTTR	VSIQG	3	C5:+57.021	692.6815853	2075.021356	0.000622848	8	N	725	745
Q8R2S8	Exosome	DVSER	CSPPSETTELSCYR	GVMFE	2	C1:+57.021,C12:+57.021	843.858596	1685.701592	0.000451244	19	N	579	593
Q8R2S8	Exosome	VTEHR	TGPGLSVTSYTR	VCRKK	2		619.822931	1237.630262	0.000451244	8	N	468	480
Q8R2S8	Exosome	THCYK	GDIALQGGGLTTR	VSIQG	2		629.8416551	1257.66771	0.000451244	10	N	732	745
Q8R2S8	Exosome	LTRHR	TGPGISIVSYVHVCR	DRDFC	2	C14:+57.021	822.9302473	1643.844895	0.000451244	4	N	279	294
Q8R2S8	Exosome	LTRHR	TGPGISIVSYVHVCR	DRDFC	3	C14:+57.021	548.9560982	1643.844895	0.000451244	23	N	279	294
Q8R2S8	Exosome	PGSLR	CPLCLSNDSCENAPEQVCPVGSTHCYDGVLR	LRGDG	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1198.843759	3593.507877	0.000451244	33	N	133	164
Q8R2S8	Exosome	TLRCR	HCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	3	C2:+57.021,C8:+57.021,C16:+57.021,C23:+57.021	1118.177332	3351.508597	0.000451244	47	N	323	354
Q8R2S8	Exosome	TLRCR	HCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	4	C2:+57.021,C8:+57.021,C16:+57.021,C23:+57.021	838.8849493	3351.508597	0.000451244	15	N	323	354
Q8R2S8	Exosome	FLGSK	GCSSPGAQDNIGVSIFSR	LPGML	2	C2:+57.021	926.4366222	1850.857644	0.000451244	16	N	643	661
Q8R2S8	Exosome	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLRG	GGIIS	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1281.221118	3840.639954	0.000451244	12	N	510	544
Q8R2S8	Exosome	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C1:+39.994,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1256.538297	3766.59149	0.000451244	17	N	510	543
Q8R2S8	Exosome	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1262.213963	3783.61849	0.000451244	102	N	510	543
Q8R2S8	Exosome	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	4	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	946.9124225	3783.61849	0.000451244	26	N	510	543
Q8R2S8	Exosome	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	[V.-17.027,C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.02	1256.538297	3766.59149	0.000622848	26	N	510	543
Q8R2S8	Exosome	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	4	[J.-17.027,C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.02	942.6556725	3766.59149	0.00091018	2	N	510	543
Q8R2S8	Exosome	HGTLK	TIQDISKLPLQWTAGQK	ICNVG	2		964.0365294	1926.057459	0.000451244	11	N	408	425
Q8R2S8	Exosome	HGTLK	TIQDISKLPLQWTAGQK	ICNVG	3		643.0269529	1926.057459	0.000451244	6	N	408	425
Q8R2S8	Exosome	VNSTK	ILEELPTPTVPGSLR	CPLCL	2		811.4621346	1620.908669	0.000451244	14	N	118	133
Q8R2S8	Exosome	VHVCR	DRDFCNDLSTTDPLWTPPPDTELGTLR	CRHCL	3	C5:+57.021	1044.82451	3131.450129	0.000451244	54	N	294	321
Q8R2S8	Exosome	VCRKK	DFCNDLSTTAPLWAPPPVTAPGTTR	CPLCF	2	C3:+57.021	1343.152793	2684.289986	0.001591523	5	N	485	510

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R2S8	Exosome	VCRKK	DFCNDLSTTAPLWAPPPVTAPGTTR	CPLCF	3	C3:+57.021	895.7711287	2684.289986	0.000451244	21	N	485	510
Q8R2S8	Exosome	GAGEK	TCEVSEGCQDLIMLLYNGPK	VNLVI	2	C2:+57.021,C8:+57.021	1164.039506	2326.063412	0.000622848	2	N	48	68
Q8R2S8	Exosome	GAGEK	TCEVSEGCQDLIMLLYNGPK	VNLVI	3	C2:+57.021,C8:+57.021	776.3622708	2326.063412	0.000451244	18	N	48	68
Q8R2S8	Exosome	EEPVK	WTAPGSQVCAPDEICQETLLLIDVGQK	SAFLG	3	C9:+57.021,C15:+57.021	1010.163543	3027.46723	0.000451244	33	N	609	636
Q8R2S8	Exosome	PVDVR	EDCGLQLDALK	CQHGT	2	C3:+57.021	631.3085679	1260.601536	0.002519933	1	N	390	401
Q8R2S8	Exosome	VIWLR	TGPGLSVVSYTR	VCRHG	2		618.8332987	1235.650997	0.000451244	20	N	91	103
Q8R2S8	Exosome	SERCS	PPSETTELSCYR	GVMFE	2	C10:+57.021	720.327489	1438.639378	0.000451244	4	N	581	593
Q8R2S8	Exosome	CPLCF	SEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C5:+57.021,C13:+57.021,C20:+57.021	1036.458759	3106.352877	0.000622848	7	N	515	543
Q8R2S8	Parental	VTCPR	GATHCYKGDIALQGGGLTTR	VSIQG	2	C5:+57.021	1038.518478	2075.021356	0.000451244	14	N	725	745
Q8R2S8	Parental	VTCPR	GATHCYKGDIALQGGGLTTR	VSIQG	3	C5:+57.021	692.6815853	2075.021356	0.000451244	16	N	725	745
Q8R2S8	Parental	DVSER	CSPPSETTELSCYR	GVMFE	2	C1:+39.994,C12:+57.021	835.345096	1668.674592	0.000451244	1	N	579	593
Q8R2S8	Parental	DVSER	CSPPSETTELSCYR	GVMFE	2	C1:+57.021,C12:+57.021	843.858596	1685.701592	0.000451244	57	N	579	593
Q8R2S8	Parental	DVSER	CSPPSETTELSCYR	GVMFE	2	[0:-	835.345096	1668.674592	0.000622848	5	N	579	593
Q8R2S8	Parental	VTEHR	TGPGLSVTSYTR	VCRKK	2		619.822931	1237.630262	0.000451244	15	N	468	480
Q8R2S8	Parental	THCYK	GDIALQGGGLTTR	VSIQG	2		629.8416551	1257.66771	0.000622848	14	N	732	745
Q8R2S8	Parental	LTRHR	TGPGISIVSYVHVCR	DRDFC	2	C14:+57.021	822.9302473	1643.844895	0.000451244	15	N	279	294
Q8R2S8	Parental	LTRHR	TGPGISIVSYVHVCR	DRDFC	3	C14:+57.021	548.9560982	1643.844895	0.000451244	48	N	279	294
Q8R2S8	Parental	PGSLR	CPLCLSNDSCENAPEQVCPVGSTHCYDGVLR	LRGDG	3	C1:+39.994,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1193.168092	3576.480877	0.00091018	1	N	133	164
Q8R2S8	Parental	PGSLR	CPLCLSNDSCENAPEQVCPVGSTHCYDGVLR	LRGDG	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1198.843759	3593.507877	0.000451244	48	N	133	164
Q8R2S8	Parental	PGSLR	CPLCLSNDSCENAPEQVCPVGSTHCYDGVLR	LRGDG	3	[0:-17.027,C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1193.168092	3576.480877	0.00091018	1	N	133	164
Q8R2S8	Parental	TLRCR	HCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	3	C2:+57.021,C8:+57.021,C16:+57.021,C23:+57.021	1118.177332	3351.508597	0.000451244	101	N	323	354
Q8R2S8	Parental	TLRCR	HCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	4	C2:+57.021,C8:+57.021,C16:+57.021,C23:+57.021	838.8849493	3351.508597	0.000451244	17	N	323	354
Q8R2S8	Parental	FLGSK	GCSSPGAQDNIGVSIFSR	LPGML	2	C2:+57.021	926.4366222	1850.857644	0.000451244	45	N	643	661
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLRG	GGIIS	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1281.221118	3840.639954	0.000451244	24	N	510	544
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C1:+39.994,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1256.538297	3766.59149	0.000451244	6	N	510	543
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	4	C1:+39.994,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	942.6556725	3766.59149	0.000698008	1	N	510	543
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1262.213963	3783.61849	0.000451244	188	N	510	543
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	4	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	946.9124225	3783.61849	0.000451244	44	N	510	543
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	[0:-17.027,C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1256.538297	3766.59149	0.000622848	14	N	510	543
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	4	[0:-17.027,C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	942.6556725	3766.59149	0.00091018	5	N	510	543
Q8R2S8	Parental	HGTLK	TIQDISKLPLQWTAGQK	ICNVG	2		964.0365294	1926.057459	0.000451244	20	N	408	425
Q8R2S8	Parental	HGTLK	TIQDISKLPLQWTAGQK	ICNVG	3		643.0269529	1926.057459	0.000451244	19	N	408	425
Q8R2S8	Parental	VNSTK	ILEELPTPTVPGSLR	CPLCL	2		811.4621346	1620.908669	0.000451244	15	N	118	133
Q8R2S8	Parental	PGSLR	CPLCLSNDSCENAPEQVCPVGSTHCYDGVLRL	RGDGI	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1236.538447	3706.591941	0.00307782	1	N	133	165
Q8R2S8	Parental	VHVCR	DRDFCNDLSTTDPLWTPPPDTELGTLR	CRHCL	3	C5:+57.021	1044.82451	3131.450129	0.000451244	80	N	294	321
Q8R2S8	Parental	VHVCR	DRDFCNDLSTTDPLWTPPPDTELGTLR	CRHCL	4	C5:+57.021	783.8703321	3131.450129	0.000735798	3	N	294	321
Q8R2S8	Parental	VCRKK	DFCNDLSTTAPLWAPPPVTAPGTTR	CPLCF	2	C3:+57.021	1343.152793	2684.289986	0.000451244	35	N	485	510
Q8R2S8	Parental	VCRKK	DFCNDLSTTAPLWAPPPVTAPGTTR	CPLCF	3	C3:+57.021	895.7711287	2684.289986	0.000451244	29	N	485	510
Q8R2S8	Parental	TAGQK	ICNVGEGCQDTLMLIENGEQVNLVLTK	GCTTA	3	C2:+57.021,C8:+57.021	1016.499939	3046.476416	0.000451244	4	N	425	452
Q8R2S8	Parental	GAGEK	TCEVSEGCQDLIMLLYNGPK	VNLVI	2	C2:+57.021,C8:+57.021	1164.039506	2326.063412	0.000451244	17	N	48	68
Q8R2S8	Parental	GAGEK	TCEVSEGCQDLIMLLYNGPK	VNLVI	3	C2:+57.021,C8:+57.021	776.3622708	2326.063412	0.000451244	22	N	48	68
Q8R2S8	Parental	EEPVK	WTAPGSQVCAPDEICQETLLLIDVGQK	SAFLG	3	C9:+57.021,C15:+57.021	1010.163543	3027.46723	0.000451244	25	N	609	636
Q8R2S8	Parental	LGTLR	CRHCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1223.554431	3667.639894	0.000451244	5	N	321	354
Q8R2S8	Parental	LGTLR	CRHCLSTGSCVSASELVCPAGSTHCYSGVLSLR	GGGVI	4	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	917.9177735	3667.639894	0.000451244	5	N	321	354
Q8R2S8	Parental	LVIIK	GCTEVEDQEPKVI	WLRTG	2	C2:+57.021	752.3537038	1502.691808	0.002981883	1	N	75	88
Q8R2S8	Parental	PVDVR	EDCGLQLDALK	CQHGT	2	C3:+57.021	631.3085679	1260.601536	0.000451244	20	N	390	401

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R2S8	Parental	AQAVR	NVAELPLRWWGAGEK	TCEVS	2		863.4577178	1724.899836	0.001654178	2	N	33	48
Q8R2S8	Parental	VIWLR	TGPGLSVVSYTR	VCRHG	2		618.8332987	1235.650997	0.000451244	17	N	91	103
Q8R2S8	Parental	SERCS	PPSETTELSCYR	GVMFE	2	C10:+57.021	720.327489	1438.639378	0.000451244	21	N	581	593
Q8R2S8	Parental	QDISK	LPLQWTAGQK	ICNVG	2		571.3223699	1140.62914	0.000451244	8	N	415	425
Q8R2S8	Parental	MSENC	DLIGPQALDCNSGSLETVR	NVSDL	2	C10:+57.021	1023.002326	2043.989053	0.000451244	6	N	203	222
Q8R2S8	Parental	PGTTR	CPLCFSEQACENAPEQVCPAGSTHCYSGVL	SLRGG	3	C1:+57.021,C4:+57.021,C10:+57.021,C18:+57.021,C25:+57.021	1143.474895	3427.401286	0.001654178	1	N	510	540
Q8R2S8	Parental	CPLCF	SEQACENAPEQVCPAGSTHCYSGVLSLR	GGGII	3	C5:+57.021,C13:+57.021,C20:+57.021	1036.458759	3106.352877	0.000451244	7	N	515	543
Q8R2S8	Parental	LGDSK	TIGIFSAEESSNYR	HEDDV	2		787.3787988	1572.741998	0.000622848	2	N	764	778
Q8R2S8	Parental	TLRCR	HCLSTGSCVSASELVCPAGSTHCYSGVLSLRG	GGVIS	3	C2:+57.021,C8:+57.021,C16:+57.021,C23:+57.021	1137.184487	3408.530061	0.000823681	2	N	323	355
Q8R2S8	Parental	VCRDR	DFCNDLSTTDPLWTPPPDTELGTLR	CRHCL	2	C3:+57.021	1431.168837	2860.322074	0.001871652	2	N	296	321
Q8R2Y8	Parental	EPGSR	TVLGIGPGPVELIDEVTGHLK	LY-	3		715.4040891	2143.188867	0.000451244	5	N	158	179
Q8R2Y8	Parental	KVVVK	APDEDTLIQLLTHAK	TLGLT	3		555.6338324	1663.878097	0.000451244	2	N	121	136
Q8R307	Parental	QFIGR	AVEDTEAQGFAGLFAAYTDHPPPFR	EFPSN	3		903.0982759	2706.271428	0.0025889	1	N	234	259
Q8R307	Parental	KPTER	TQATLLTTWLTELYLSR	LGALQ	2		1005.54947	2009.083339	0.001352548	1	N	485	502
Q8R326	Parental	ALTVK	NLSPVVSNELLEQAFSQFGPVEK	AVVVV	2		1266.653183	2531.290766	0.000451244	1	N	160	183
Q8R326	Parental	ALTVK	NLSPVVSNELLEQAFSQFGPVEK	AVVVV	3		844.7713888	2531.290766	0.000451244	6	N	160	183
Q8R326	Parental	NMNNR	GTIPGPPMGPGPAMGPEGAANMGTPMIPDNGAVHNDR	FPQGP	4	M14:+15.995	900.1645412	3596.626965	0.002296037	1	N	429	466
Q8R3G1	Exosome	RKNSR	VTFSEDDEIINPEDVDPSVGRF	RNMVQ	2		1240.577338	2479.139076	0.000451244	8	N	200	222
Q8R3G1	Exosome	RKNSR	VTFSEDDEIINPEDVDPSVGR	FRNMV	2		1167.043131	2332.070662	0.000622848	1	N	200	221
Q8R3G1	Parental	RKNSR	VTFSEDDEIINPEDVDPSVGRF	RNMVQ	2		1240.577338	2479.139076	0.000451244	10	N	200	222
Q8R460	Exosome	RETPD	FGEVFDLDQQVWIFR	NQALV	2		949.9759404	1897.936281	0.002145581	1	N	18	33
Q8R460	Parental	HISGR	ETPDFGEVFDLDQQVWIFR	NQALV	2		1171.06093	2340.10626	0.000451244	11	N	14	33
Q8R460	Parental	FYHTR	TGGTSTFESVAFPGHYIASSK	TGNPI	2		1072.518898	2143.022196	0.000451244	5	N	118	139
Q8R460	Parental	FYHTR	TGGTSTFESVAFPGHYIASSK	TGNPI	3		715.3485319	2143.022196	0.000622848	8	N	118	139
Q8R4R6	Parental	VMEMR	SPLLAGGSPPQPVVPAHKDK	SGAPP	3		665.7061023	1994.094907	0.002374549	1	N	65	85
Q8R4R6	Parental	APPVR	SIYDDISSPGLGSTPLTSR	RQANI	2		983.4923487	1964.969097	0.000451244	16	N	92	111
Q8R550	Exosome	SNFIK	ELSGESDELGISQDEQLSK	SRPEG	2		1032.484918	2062.954235	0.000451244	8	N	153	172
Q8R550	Exosome	DLSDR	SNDIDLEGFDSVISSTEK	LSHPT	2		978.4581715	1954.900743	0.001871652	1	N	501	519
Q8R550	Parental	SNFIK	ELSGESDELGISQDEQLSK	SRPEG	2		1032.484918	2062.954235	0.000451244	15	N	153	172
Q8R550	Parental	ELELK	VGDIIEVVGEVEEGWWEGVLNGK	TGMFP	2		1257.132084	2512.248567	0.000451244	26	N	120	143
Q8R550	Parental	ELELK	VGDIIEVVGEVEEGWWEGVLNGK	TGMFP	3		838.423989	2512.248567	0.000451244	8	N	120	143
Q8R550	Parental	KDYCK	VIFPYEAQNDDELTIK	EGDIV	2		947.9758031	1893.936006	0.000622848	1	N	317	333
Q8R550	Parental	RRRRR	CQVAFSYLPQNDDELELK	VGDII	2	C1:+57.021	1085.01236	2168.009119	0.000451244	9	N	102	120
Q8R574	Parental	DVGGR	IAIIVDDIIDDVDSFLAAAETLKER	GAYKI	3		915.8239298	2744.448389	0.000451244	4	N	263	288
Q8R574	Parental	DVGGR	IAIIVDDIIDDVDSFLAAAETLK	ERGAY	2		1230.660143	2459.304685	0.002080925	1	N	263	286
Q8R5A3	Exosome	RQLAR	DVLDNLFEK	THCDC	2		546.7827432	1091.549886	0.000637154	9	N	204	213
Q8R5A3	Exosome	LQIER	VFEDHENVVEVLSDWTR	DTENK	3		692.0012436	2072.980331	0.000451244	31	N	235	252
Q8R5A3	Exosome	NLFEK	THCDCNVDWCLYEIYPELQIER	VFEDH	2	C3:+57.021,C5:+57.021,C10:+57.021	1457.135497	2912.255394	0.001654178	2	N	213	235
Q8R5A3	Exosome	NLFEK	THCDCNVDWCLYEIYPELQIER	VFEDH	3	C3:+57.021,C5:+57.021,C10:+57.021	971.7595981	2912.255394	0.000451244	12	N	213	235
Q8R5A3	Parental	RQLAR	DVLDNLFEK	THCDC	2		546.7827432	1091.549886	0.000735798	2	N	204	213
Q8R5A3	Parental	LQIER	VFEDHENVVEVLSDWTR	DTENK	2		1037.497965	2072.980331	0.000451244	10	N	235	252
Q8R5A3	Parental	LQIER	VFEDHENVVEVLSDWTR	DTENK	3		692.0012436	2072.980331	0.000451244	31	N	235	252
Q8R5A3	Parental	NLFEK	THCDCNVDWCLYEIYPELQIER	VFEDH	2	C3:+57.021,C5:+57.021,C10:+57.021	1457.135497	2912.255394	0.000451244	9	N	213	235
Q8R5A3	Parental	NLFEK	THCDCNVDWCLYEIYPELQIER	VFEDH	3	C3:+57.021,C5:+57.021,C10:+57.021	971.7595981	2912.255394	0.000451244	23	N	213	235
Q8R5H1	Exosome	NHLKR	NDSIIVDIFHGLFK	STLVC	3		539.9598798	1616.85624	0.002663018	4	N	429	443
Q8R5H1	Exosome	TQVGR	FAPQFSGYQQQDCQELLAFLLDGLHEDLNR	IRKKP	3	C13:+57.021	1184.900301	3551.677503	0.000451244	4	N	368	398
Q8R5H1	Exosome	ENHLK	RNDSIIVDIFHGLFK	STLVC	3		591.9935836	1772.957351	0.000451244	1	N	428	443
Q8R5H1	Parental	NHLKR	NDSIIVDIFHGLFK	STLVC	3		539.9598798	1616.85624	0.000451244	12	N	429	443
Q8R5H1	Parental	TQVGR	FAPQFSGYQQQDCQELLAFLLDGLHEDLNRIR	KKPYI	4	C13:+57.021	956.2234696	3820.862678	0.002374549	1	N	368	400
Q8R5H1	Parental	TQVGR	FAPQFSGYQQQDCQELLAFLLDGLHEDLNR	IRKKP	3	C13:+57.021	1184.900301	3551.677503	0.000451244	30	N	368	398
Q8R5H1	Parental	ENHLK	RNDSIIVDIFHGLFK	STLVC	3		591.9935836	1772.957351	0.000870037	1	N	428	443
Q8R5L1	Exosome	SQGQK	AEEQEPELTSTPNFVVEVTK	TDGKK	2		1124.05551	2246.09542	0.000451244	32	N	152	172
Q8R5L1	Exosome	TDGKK	TLVLDCHYPEDEIGHEDEAESDIFSIK	EVSFQ	3	C6:+57.021	1054.480408	3160.417825	0.000451244	72	N	177	204
Q8R5L1	Exosome	TDGKK	TLVLDCHYPEDEIGHEDEAESDIFSIK	EVSFQ	4	C6:+57.021	791.1122564	3160.417825	0.001763695	1	N	177	204
Q8R5L1	Exosome	FLADR	GVDNTFADELVELSTALEHQEYITFLEDLK	SFVKN	3		1147.231754	3438.671861	0.000451244	29	N	243	273
Q8R5L1	Exosome	FLADR	GVDNTFADELVELSTALEHQEYITF	LEDLK	2		1421.177416	2840.339233	0.000622848	1	N	243	268
Q8R5L1	Exosome	TEGDK	AFVEFLTDEIKEEK	KIQKH	2		849.4357824	1696.855965	0.000823681	5	N	78	92
Q8R5L1	Exosome	TEGDK	AFVEFLTDEIKEEK	KIQKH	3		566.6264549	1696.855965	0.000451244	9	N	78	92

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8R5L1	Exosome	IFSIK	EVSFQATGDSEWR	DTNYT	2		756.3422163	1510.668833	0.001162105	2	N	204	217
Q8R5L1	Exosome	FLADR	GVDNTFADELVELSTALEHQEY	ITFLE	2		1240.577338	2479.139076	0.001871652	3	N	243	265
Q8R5L1	Parental	SQGQK	AEEQEPELTSTPNFVVEVTK	TDGKK	2		1124.05551	2246.09542	0.000451244	26	N	152	172
Q8R5L1	Parental	TDGKK	TLVLDCHYPEDEIGHEDEAESDIFSIK	EVSFQ	3	C6:+57.021	1054.480408	3160.417825	0.000451244	84	N	177	204
Q8R5L1	Parental	FLADR	GVDNTFADELVELSTALEHQEYITFLEDLKSFVK	NQ-	3		1300.98636	3899.93568	0.000622848	3	N	243	277
Q8R5L1	Parental	FLADR	GVDNTFADELVELSTALEHQEYITFLEDLK	SFVKN	3		1147.231754	3438.671861	0.000451244	22	N	243	273
Q8R5L1	Parental	FLADR	GVDNTFADELVELSTALEHQEYITF	LEDLK	2		1421.177416	2840.339233	0.000735798	5	N	243	268
Q8R5L1	Parental	TEGDK	AFVEFLTDEIKEEK	KIQKH	2		849.4357824	1696.855965	0.000451244	5	N	78	92
Q8R5L1	Parental	TEGDK	AFVEFLTDEIKEEK	KIQKH	3		566.6264549	1696.855965	0.000622848	1	N	78	92
Q8R5L1	Parental	IFSIK	EVSFQATGDSEWR	DTNYT	2		756.3422163	1510.668833	0.000451244	9	N	204	217
Q8R5L1	Parental	FLADR	GVDNTFADELVELSTALEHQEY	ITFLE	2		1240.577338	2479.139076	0.000451244	14	N	243	265
Q8VBT6	Parental	QALTK	QLEEGQKGQEETSGAPDLSPER	VLSLK	2		1193.062387	2384.109173	0.000622848	2	N	465	487
Q8VBT6	Parental	QALTK	QLEEGQKGQEETSGAPDLSPER	VLSLK	3		795.7108577	2384.109173	0.000451244	39	N	465	487
Q8VBT6	Parental	QALTK	QLEEGQKGQEETSGAPDLSPER	VLSLK	2	Q1:-17.027	1184.548887	2367.082173	0.001943752	1	N	465	487
Q8VBT6	Parental	QALTK	QLEEGQKGQEETSGAPDLSPER	VLSLK	2	[0:-17.027	1184.548887	2367.082173	0.002884417	2	N	465	487
Q8VBT6	Parental	AMLSR	EAWTVSDREGADSLGVQGTEYGSDPGDNFPGTTGR	VWVLE	3		1210.20733	3627.598589	0.000451244	29	N	271	306
Q8VBT6	Parental	SREKR	NSWATEPTLVLDTEAKDEPDWEDSPEVSTEELFVGER	SEAAQ	3		1407.648912	4219.923337	0.000451244	4	N	396	433
Q8VBT6	Parental	PTVER	QTQAAEELGEVTEGKVVGEEAQEVLEGLR	SGQSE	3		1033.521638	3097.541515	0.000451244	9	N	39	68
Q8VBT6	Parental	PTVER	QTQAAEELGEVTEGKVVGEEAQEVLEGLR	SGQSE	3	Q1:-17.027	1027.845972	3080.514515	0.000870037	2	N	39	68
Q8VBT6	Parental	PTVER	QTQAAEELGEVTEGKVVGEEAQEVLEGLR	SGQSE	3	[0:-17.027	1027.845972	3080.514515	0.000451244	1	N	39	68
Q8VBT6	Parental	HQALR	GALDSFSAFVSYLVGDTVPTVER	QTQAA	2		1215.613527	2429.211453	0.000451244	27	N	16	39
Q8VBT6	Parental	HQALR	GALDSFSAFVSYLVGDTVPTVER	QTQAA	3		810.7449511	2429.211453	0.000451244	20	N	16	39
Q8VBT6	Parental	VLSLK	EYPGPVGFAGPELEAWGNWSR	GVDRR	2		1160.045614	2318.075628	0.000451244	26	N	492	513
Q8VBT6	Parental	IVGIR	AVDTEEGPKWEAGLAPETELGK	AWCSE	2		1164.074234	2326.132869	0.000622848	3	N	644	666
Q8VBT6	Parental	LSPER	VLSLKEYPGPVGFAGPELEAWGNWSR	GVDRR	3		953.820854	2858.439162	0.000451244	4	N	487	513
Q8VBT6	Parental	SFSAF	VSYLVGDTVPTVER	QTQAA	2		767.9097348	1533.80387	0.00091018	7	N	25	39
Q8VBT6	Parental	GEAGR	GTELEETTEKQSGQEVGLVGSAEK	VSGYD	3		836.0772062	2505.208219	0.000451244	4	N	678	702
Q8VBT6	Parental	GERAR	AQGTQCPGAESEDQAMLSR	EAWTV	2	C6:+57.021	1018.444319	2034.873038	0.001591523	1	N	252	271
Q8VBT6	Parental	SQEVK	ADAEAGKEQTATEQAVEIR	AEGGQ	3		672.9997912	2015.975974	0.000451244	4	N	524	543
Q8VBT6	Parental	THRDR	SSNTAQEIWEHGEEEASSGEPLR	TCEQK	2		1272.0682	2542.1208	0.000451244	7	N	142	165
Q8VBT6	Parental	THRDR	SSNTAQEIWEHGEEEASSGEPLR	TCEQK	3		848.3814001	2542.1208	0.000451244	16	N	142	165
Q8VBT6	Parental	VTEGK	VVGEEAQEVLEGLR	SGQSE	2		764.4048166	1526.794033	0.000451244	16	N	54	68
Q8VBT6	Parental	EETRR	CQEGSLAGEQTWGWR	ADSSA	2	C1:+57.021	882.8918504	1763.768101	0.000451244	2	N	83	98
Q8VBT6	Parental	EETRR	CQEGSLAGEQTWGWR	ADSSA	2	[0:-17.027,C1:+57.021	874.3783504	1746.741101	0.001699387	1	N	83	98
Q8VBT9	Exosome	RHTVK	VTPSTVLLQVLEDTCR	RQDFN	2	C15:+57.021	915.9854166	1829.955233	0.000451244	7	N	25	41
Q8VBT9	Exosome	GEFSR	GDLNHEGDANTSGTGLEGGPKPTDAQTK	QSTSE	4		692.575114	2766.269256	0.000823681	1	N	218	246
Q8VBT9	Parental	AFCSR	QTLWELLSHFAQTR	ERLQQ	3		577.3060501	1728.89475	0.000735798	6	N	111	125
Q8VBV7	Exosome	ATRRR	AFALVSQAYTSIIADDFAAFVGLPVEEAVK	GVLEQ	3		1048.216939	3141.627417	0.000662267	10	N	116	146
Q8VBV7	Exosome	VSLNR	FIPLSEPAPVPPIPNEQQLAR	LTDYV	2		1157.134232	2312.252864	0.000637154	20	N	178	199
Q8VBV7	Exosome	VSQAY	TSIIADDFAAFVGLPVEEAVK	GVLEQ	2		1096.578424	2191.141248	0.000823681	4	N	125	146
Q8VBV7	Exosome	PPAIK	SANSELGGIWSVGQR	IWQRD	2		780.8924077	1559.769215	0.000451244	1	N	65	80
Q8VBV7	Exosome	EEAVK	GVLEQGWQADSTTR	MVLPR	2		774.3765904	1546.737581	0.000622848	9	N	146	160
Q8VBV7	Parental	ATRRR	AFALVSQAYTSIIADDFAAFVGLPVEEAVK	GVLEQ	3		1048.216939	3141.627417	0.002453667	1	N	116	146
Q8VBV7	Parental	VSLNR	FIPLSEPAPVPPIPNEQQLAR	LTDYV	2		1157.134232	2312.252864	0.000451244	8	N	178	199
Q8VBV7	Parental	VSQAY	TSIIADDFAAFVGLPVEEAVK	GVLEQ	2		1096.578424	2191.141248	0.000451244	12	N	125	146
Q8VBW6	Exosome	TEILK	NLVLPGIGSFTIIDGNLVSGEDAGNNFFLQK	SSIGK	3		1083.89838	3248.671741	0.000451244	10	N	47	78
Q8VBW6	Exosome	STLLR	LADVLWNSQIPLLICR	TYGLV	2	C15:+57.021	956.0299615	1910.044323	0.002727428	1	N	138	154
Q8VBW6	Exosome	NHVAK	LLQSVGQAPESISEK	ELKLL	2		793.425749	1584.835898	0.000451244	4	N	363	378
Q8VBW6	Parental	TEILK	NLVLPGIGSFTIIDGNLVSGEDAGNNFFLQK	SSIGK	3		1083.89838	3248.671741	0.000451244	5	N	47	78
Q8VC03	Exosome	GRDRR	LVQWGPGLVALQEAEIPEHFGAVR	AIAEG	3		872.8031347	2615.386004	0.000451244	8	N	538	562
Q8VC03	Exosome	DTETR	EIVSDVTDGNEQLSVVR	YSPDG	2		930.4714162	1858.927232	0.000451244	1	N	671	688
Q8VC30	Exosome	RKRIR	AAPTEPPEAPEATAAGGVTSKQMALVLDR	ICTTL	4	M23:+15.995	724.3701053	2893.449221	0.001162105	1	N	351	380
Q8VC30	Exosome	LVLDR	ICTTLIGLEEHLNALDR	AAGDG	3	C2:+57.021	656.6791817	1967.014145	0.000451244	7	N	380	397
Q8VC30	Exosome	AGAGR	ASYISSAQLDQPDPGAVAAAAIFR	AILEV	2		1210.116768	2418.217936	0.000451244	1	N	543	567
Q8VC88	Exosome	EELQR	CLTQSGISGTYAPFSLETCR	IMIAM	2	C1:+39.994,C19:+57.021	1116.008837	2230.002075	0.001162105	4	N	78	98
Q8VC88	Exosome	EELQR	CLTQSGISGTYAPFSLETCR	IMIAM	2	C1:+57.021,C19:+57.021	1124.522337	2247.029075	0.000451244	7	N	78	98
Q8VC88	Exosome	EELQR	CLTQSGISGTYAPFSLETCR	IMIAM	2	[0:-	1116.008837	2230.002075	0.000451244	15	N	78	98
Q8VC88	Exosome	SKNGR	IFFDDYVACCVK	LRALT	2	C9:+57.021,C10:+57.021	768.8467717	1535.677943	0.000451244	16	N	175	187
Q8VC88	Exosome	FNEFK	ELWAALNAWK	QNFMT	2		601.3223699	1200.62914	0.000451244	18	N	118	128
Q8VC88	Exosome	MWTYF	TAVAGQDGEVDAEELQR	CLTQS	2		894.424466	1786.833332	0.000451244	13	N	61	78
Q8VC88	Exosome	SMWTY	FTAVAGQDGEVDAEELQR	CLTQS	2		967.958673	1933.901746	0.000622848	3	N	60	78
Q8VC88	Exosome	DYTGK	MGFNEFKELWAALNAWK	QNFMT	3		685.6772671	2054.008401	0.000451244	9	N	111	128
Q8VC88	Exosome	WTYFT	AVAGQDGEVDAEELQR	CLTQS	2		843.9006267	1685.785653	0.000851441	3	N	62	78
Q8VC88	Parental	EELQR	CLTQSGISGTYAPFSLETCR	IMIAM	2	[0:-	1116.008837	2230.002075	0.0007646	3	N	78	98
Q8VC88	Parental	SKNGR	IFFDDYVACCVK	LRALT	2	C9:+57.021,C10:+57.021	768.8467717	1535.677943	0.000451244	1	N	175	187

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VC88	Parental	FNEFK	ELWAALNAWK	QNFMT	2		601.3223699	1200.62914	0.000451244	10	N	118	128
Q8VC88	Parental	MWTYF	TAVAGQDGEVDAEELQR	CLTQS	2		894.424466	1786.833332	0.000451244	21	N	61	78
Q8VC88	Parental	SMWTY	FTAVAGQDGEVDAEELQR	CLTQS	2		967.958673	1933.901746	0.000451244	6	N	60	78
Q8VCI0	Exosome	AASQS	DPTGVHCATAYWSPESK	KVEIK	2	C7:+57.021	953.4257231	1904.835846	0.000451244	15	N	36	53
Q8VCI0	Exosome	AASQS	DPTGVHCATAYWSPESK	KVEIK	3	C7:+57.021	635.9530821	1904.835846	0.000451244	4	N	36	53
Q8VCI0	Exosome	DPFWR	HTGYVVTQLDGLYLGAQKR	ASEEK	3		707.0485282	2118.122184	0.000451244	3	N	161	180
Q8VCI0	Exosome	KGTLY	IVEQIPTYVEYSDQTNVLR	KGYWA	2		1134.081862	2266.148125	0.000451244	2	N	376	395
Q8VCI0	Exosome	VTINR	SLDKGTLYIVEQIPTYVEYSDQTNVLR	KGYWA	3		1048.875353	3143.602659	0.000451244	38	N	368	395
Q8VCI0	Exosome	TICCR	EDLNGASPSPGGCYDTK	VADIF	2	C13:+57.021	884.3784385	1766.741277	0.000451244	17	N	477	494
Q8VCI0	Exosome	CYDTK	VADIFLASQYK	AYAIS	2		627.8405925	1253.665585	0.001162105	4	N	494	505
Q8VCI0	Exosome	ASQYK	AYAISGPTVQDGLPPFNWNR	FNETL	2		1102.050699	2202.085799	0.000451244	12	N	505	525
Q8VCI0	Exosome	RSLDK	GTLYIVEQIPTYVEYSDQTNVLR	KGYWA	2		1351.19013	2700.36466	0.000451244	11	N	372	395
Q8VCI0	Exosome	RSLDK	GTLYIVEQIPTYVEYSDQTNVLR	KGYWA	3		901.1293532	2700.36466	0.000451244	18	N	372	395
Q8VCI0	Exosome	NDSIK	TTGWGILEIR	AGYGS	2		573.3198272	1144.624054	0.000451244	11	N	76	86
Q8VCI0	Exosome	LLVHK	LGLDYSYDLAPR	AKIFR	2		691.8516885	1381.687777	0.001763695	1	N	422	434
Q8VCI0	Exosome	DPFWR	HTGYVVTQLDGLYLGAQK	RASEE	2		982.0183367	1962.021073	0.000451244	12	N	161	179
Q8VCI0	Exosome	DPFWR	HTGYVVTQLDGLYLGAQK	RASEE	3		655.0148244	1962.021073	0.000451244	12	N	161	179
Q8VCI0	Parental	AASQS	DPTGVHCATAYWSPESK	KVEIK	2	C7:+57.021	953.4257231	1904.835846	0.000451244	13	N	36	53
Q8VCI0	Parental	AASQS	DPTGVHCATAYWSPESK	KVEIK	3	C7:+57.021	635.9530821	1904.835846	0.001329271	1	N	36	53
Q8VCI0	Parental	DPFWR	HTGYVVTQLDGLYLGAQKR	ASEEK	3		707.0485282	2118.122184	0.000451244	4	N	161	180
Q8VCI0	Parental	KGTLY	IVEQIPTYVEYSDQTNVLR	KGYWA	2		1134.081862	2266.148125	0.000451244	20	N	376	395
Q8VCI0	Parental	VTINR	SLDKGTLYIVEQIPTYVEYSDQTNVLR	KGYWA	3		1048.875353	3143.602659	0.000451244	12	N	368	395
Q8VCI0	Parental	TICCR	EDLNGASPSPGGCYDTK	VADIF	2	C13:+57.021	884.3784385	1766.741277	0.000451244	71	N	477	494
Q8VCI0	Parental	CYDTK	VADIFLASQYK	AYAIS	2		627.8405925	1253.665585	0.001329271	3	N	494	505
Q8VCI0	Parental	ASQYK	AYAISGPTVQDGLPPFNWNR	FNETL	2		1102.050699	2202.085799	0.000451244	23	N	505	525
Q8VCI0	Parental	NDSIK	TTGWGILEIR	AGYGS	2		573.3198272	1144.624054	0.000451244	1	N	76	86
Q8VCI5	Parental	ASQEK	FFQELFDSELASQATAEFEK	AMKEL	2		1169.050228	2336.084856	0.000451244	8	N	69	89
Q8VCI5	Parental	SVMVK	ICEQFEAETPTDSEATQR	ARFEA	2	C2:+57.021	1056.463231	2110.910862	0.000451244	5	N	227	245
Q8VCM7	Exosome	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	2	C7:+57.021	1221.59184	2441.16808	0.000451244	64	N	200	221
Q8VCM7	Exosome	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	3	C7:+57.021	814.7304933	2441.16808	0.000451244	15	N	200	221
Q8VCM7	Exosome	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	2	Q1:-17.027,C7:+57.021	1213.07834	2424.14108	0.000451244	3	N	200	221
Q8VCM7	Exosome	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	2	[0:-17.027,C7:+57.021	1213.07834	2424.14108	0.000451244	8	N	200	221
Q8VCM7	Exosome	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLR	TLEDI	3	C5:+57.021,C9:+57.021	1029.455275	3085.342424	0.000451244	67	N	39	66
Q8VCM7	Exosome	GTYSK	SSTTNGFDDGIIWATWK	SRWYS	2		949.9501196	1897.884639	0.000451244	64	N	381	398
Q8VCM7	Exosome	GTYSK	SSTTNGFDDGIIWATWK	SRWYS	3		633.6360131	1897.884639	0.000823681	5	N	381	398
Q8VCM7	Exosome	NLKQK	VAQLEAQCQEPCKDSVQIHDTTGK	DCQEI	2	C8:+57.021,C12:+57.021	1371.644775	2741.27395	0.000451244	4	N	152	176
Q8VCM7	Exosome	NLKQK	VAQLEAQCQEPCKDSVQIHDTTGK	DCQEI	3	C8:+57.021,C12:+57.021	914.7657833	2741.27395	0.000451244	43	N	152	176
Q8VCM7	Exosome	NLKQK	VAQLEAQCQEPCKDSVQIHDTTGK	DCQEI	4	C8:+57.021,C12:+57.021	686.3262875	2741.27395	0.000451244	16	N	152	176
Q8VCM7	Exosome	YVATR	DNCCILDER	FGSFC	2	C3:+57.021,C4:+57.021	597.7475888	1193.479578	0.000451244	26	N	30	39
Q8VCM7	Exosome	EEIVK	YEALLLTHETSIR	YLQEI	2		773.417727	1544.819854	0.000451244	14	N	120	133
Q8VCM7	Exosome	EEIVK	YEALLLTHETSIR	YLQEI	3		515.9477513	1544.819854	0.000451244	5	N	120	133
Q8VCM7	Exosome	WIQYK	EGFGHLSPTGTTEFWLGNEK	IHLIS	2		1104.024347	2206.033095	0.000451244	36	N	237	257
Q8VCM7	Exosome	WIQYK	EGFGHLSPTGTTEFWLGNEK	IHLIS	3		736.3521649	2206.033095	0.000451244	34	N	237	257
Q8VCM7	Exosome	WIQYK	EGFGHLSPTGTTEFWLGNEK	IHLIS	3	E1:-18.011	730.3484982	2188.022095	0.000451244	1	N	237	257
Q8VCM7	Exosome	QEPCK	DSVQIHDTTGKDCQEIANK	GAKES	3	C13:+57.021	720.3396649	2157.995595	0.001699387	1	N	165	184
Q8VCM7	Exosome	ETSIR	YLQEIYNSNNQK	ITNLK	2		757.3682341	1512.720868	0.000451244	24	N	133	145
Q8VCM7	Exosome	NKGAK	ESGLYFIRPLK	AKQQF	2		661.8775093	1321.739419	0.000451244	13	N	187	198
Q8VCM7	Exosome	KELIK	AIQVYYNPDQPPKPGMIDSATQK	SKKMV	2	M16:+15.995	1289.136886	2576.258172	0.000451244	10	N	87	110
Q8VCM7	Exosome	KELIK	AIQVYYNPDQPPKPGMIDSATQK	SKKMV	3	M16:+15.995	859.7605241	2576.258172	0.000451244	13	N	87	110
Q8VCM7	Exosome	DWNGR	TSTADYAMFR	VGPES	2	M8:+15.995	589.761528	1177.507456	0.001229886	2	N	281	291
Q8VCM7	Exosome	IRPLK	AKQQFLVYCEIDGSGNGWTVLQK	RIDGS	2	C9:+57.021	1321.157878	2640.300157	0.000451244	2	N	198	221
Q8VCM7	Exosome	IRPLK	AKQQFLVYCEIDGSGNGWTVLQK	RIDGS	3	C9:+57.021	881.1078523	2640.300157	0.000622848	7	N	198	221
Q8VCM7	Exosome	QKSKK	MVEEIVKYEALLLTHETSIR	YLQEI	3		792.0949271	2373.261381	0.000451244	12	N	113	133
Q8VCM7	Exosome	QFLVY	CEIDGSGNGWTVLQK	RIDGS	2	C1:+57.021	832.3911519	1662.766704	0.000451244	6	N	206	221
Q8VCM7	Exosome	SDKYR	LTYAYFIGGDAGDAFDGYDFGDDPSDK	FFTSH	2		1446.612106	2891.208613	0.000451244	6	N	300	327
Q8VCM7	Exosome	SDKYR	LTYAYFIGGDAGDAFDGYDFGDDPSDK	FFTSH	3		964.7440042	2891.208613	0.000451244	4	N	300	327
Q8VCM7	Exosome	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLRTLEDILFR	AENRT	3	C5:+57.021,C9:+57.021	1358.634919	4072.881356	0.000451244	6	N	39	74
Q8VCM7	Exosome	SDKYR	LTYAYFIGGDAGDAFDGYDFGDDPSDKFFTSH	NGMQF	3		1171.169153	3510.48406	0.000451244	2	N	300	332
Q8VCM7	Exosome	NWIQY	KEGFGHLSPTGTTEFWLGNEK	IHLIS	3		779.0504859	2334.128058	0.000823681	1	N	236	257
Q8VCM7	Exosome	NWIQY	KEGFGHLSPTGTTEFWLGNEK	IHLIS	4		584.5398145	2334.128058	0.002519933	1	N	236	257
Q8VCM7	Exosome	PLKAK	QQFLVYCEIDGSGNGWTVLQKR	IDGSL	3	C7:+57.021	866.764197	2597.269191	0.001763695	1	N	200	222
Q8VCM7	Exosome	ILDER	FGSFCPTTCGIADFLSSY	QTDVD	2	C5:+57.021,C9:+57.021	1015.437211	2028.858821	0.002212458	1	N	39	57
Q8VCM7	Parental	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	2	C7:+57.021	1221.59184	2441.16808	0.000451244	23	N	200	221
Q8VCM7	Parental	PLKAK	QQFLVYCEIDGSGNGWTVLQK	RIDGS	2	[0:-17.027,C7:+57.021	1213.07834	2424.14108	0.00091018	1	N	200	221
Q8VCM7	Parental	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLR	TLEDI	3	C5:+57.021,C9:+57.021	1029.455275	3085.342424	0.000451244	29	N	39	66

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VCM7	Parental	GTYSK	SSTTNGFDDGIIWATWK	SRWYS	2		949.9501196	1897.884639	0.000451244	21	N	381	398
Q8VCM7	Parental	GTYSK	SSTTNGFDDGIIWATWK	SRWYS	3		633.6360131	1897.884639	0.000451244	3	N	381	398
Q8VCM7	Parental	NLKQK	VAQLEAQCQEPCKDSVQIHDTTGK	DCQEI	3	C8:+57.021,C12:+57.021	914.7657833	2741.27395	0.000451244	14	N	152	176
Q8VCM7	Parental	NLKQK	VAQLEAQCQEPCKDSVQIHDTTGK	DCQEI	4	C8:+57.021,C12:+57.021	686.3262875	2741.27395	0.002374549	1	N	152	176
Q8VCM7	Parental	YVATR	DNCCILDER	FGSFC	2	C3:+57.021,C4:+57.021	597.7475888	1193.479578	0.000622848	6	N	30	39
Q8VCM7	Parental	WIQYK	EGFGHLSPTGTTEFWLGNEK	IHLIS	2		1104.024347	2206.033095	0.000451244	5	N	237	257
Q8VCM7	Parental	WIQYK	EGFGHLSPTGTTEFWLGNEK	IHLIS	3		736.3521649	2206.033095	0.000451244	10	N	237	257
Q8VCM7	Parental	KELIK	AIQVYYNPDQPPKPGMIDSATQK	SKKMV	2		1281.139386	2560.263172	0.000622848	4	N	87	110
Q8VCM7	Parental	KELIK	AIQVYYNPDQPPKPGMIDSATQK	SKKMV	3		854.4288575	2560.263172	0.001839721	2	N	87	110
Q8VCM7	Parental	QKSKK	MVEEIVKYEALLLTHETSIR	YLQEI	3		792.0949271	2373.261381	0.000451244	6	N	113	133
Q8VCM7	Parental	QKSKK	MVEEIVKYEALLLTHETSIR	YLQEI	4		594.3231454	2373.261381	0.000451244	4	N	113	133
Q8VCM7	Parental	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLRTLEDILFR	AENRT	3	C5:+57.021,C9:+57.021	1358.634919	4072.881356	0.000823681	2	N	39	74
Q8VCM7	Parental	ILDER	FGSFCPTTCGIADFLSSYQTDVDNDLRTLEDILFR	AENRT	4	C5:+57.021,C9:+57.021	1019.228139	4072.881356	0.001162105	2	N	39	74
Q8VCM7	Parental	NWIQY	KEGFGHLSPTGTTEFWLGNEK	IHLIS	2		1168.071829	2334.128058	0.000451244	7	N	236	257
Q8VCM7	Parental	NWIQY	KEGFGHLSPTGTTEFWLGNEK	IHLIS	3		779.0504859	2334.128058	0.000622848	4	N	236	257
Q8VCM7	Parental	PLKAK	QQFLVYCEIDGSGNGWTVLQKR	IDGSL	3	C7:+57.021	866.764197	2597.269191	0.000823681	1	N	200	222
Q8VCM7	Parental	ETSIR	YLQEIYNSNNQKITNLK	QKVAQ	2		1042.045083	2082.074566	0.001162105	1	N	133	150
Q8VCN9	Exosome	ARGCK	VLCGPVTTSVFLEDCRDCVLAVACQQLR	VHTTK	3	C3:+57.021,C15:+57.021,C18:+57.021,C24:+57.021	1089.531047	3265.569741	0.000451244	1	N	229	257
Q8VCN9	Exosome	QVTSR	AIVEDCSGIQFAPYTWSYPGIDKDFQDSGLDR	SKNNW	3	C6:+57.021	1217.563355	3649.666664	0.000451244	7	N	273	305
Q8VCT3	Exosome	RTLAK	DTFAATASQLHSNVVNYVQQILAPKDS	-	3		973.161716	2916.461748	0.000735798	8	N	623	650
Q8VCT3	Exosome	LNKLR	VKIEPGVDPDDTYNETPYEK	GYCFV	2		1155.045142	2308.074685	0.000451244	2	N	396	416
Q8VCT3	Exosome	LNKLR	VKIEPGVDPDDTYNETPYEK	GYCFV	3		770.3660283	2308.074685	0.000451244	20	N	396	416
Q8VCT3	Exosome	YAQRR	ISTILFGAAYTCLEAATGR	ALLRQ	2	C12:+57.021	1008.017248	2014.018896	0.000451244	20	N	357	376
Q8VCT3	Exosome	YAQRR	ISTILFGAAYTCLEAATGR	ALLRQ	3	C12:+57.021	672.347432	2014.018896	0.002374549	1	N	357	376
Q8VCT3	Exosome	GPRSR	VWAEPCLIEAAKEEYSGVIEEFLATGEK	LFGPY	3	C6:+57.021	1056.853406	3167.536818	0.000451244	43	N	248	276
Q8VCT3	Exosome	GPRSR	VWAEPCLIEAAKEEYSGVIEEFLATGEK	LFGPY	4	C6:+57.021	792.8920046	3167.536818	0.000451244	5	N	248	276
Q8VCT3	Exosome	ISTWK	TYQLVYFLDK	ILQKS	2		645.342968	1288.670336	0.000451244	16	N	531	541
Q8VCT3	Exosome	VDEFK	FQSILAEDFLEFYLEYFPELK	KKGVD	2		1321.159778	2640.303957	0.000451244	4	N	446	467
Q8VCT3	Exosome	TPYEK	GYCFVSYLAHLVGDQDQFDK	FLKAY	3	C3:+57.021	788.0321722	2361.073117	0.000451244	22	N	416	436
Q8VCT3	Exosome	SAAAR	RPLHSAQAVDVASASSFR	AFEIL	3		633.6664181	1897.975854	0.000451244	9	N	14	32
Q8VCT3	Exosome	ASELR	LDSHSCLEVTAATLR	RGQPG	2	C6:+57.021	836.9200766	1671.824553	0.000451244	7	N	79	94
Q8VCT3	Exosome	ATLRR	GQPGDQQAPAEPVPFHTQPFSHYGQALCVAFR	QPCGA	3	C28:+57.021	1179.897114	3536.667941	0.002813207	1	N	95	127
Q8VCT3	Exosome	ATLRR	GQPGDQQAPAEPVPFHTQPFSHYGQALCVAFR	QPCGA	4	C28:+57.021	885.1747853	3536.667941	0.000622848	4	N	95	127
Q8VCT3	Exosome	KLRVK	IEPGVDPDDTYNETPYEK	GYCFV	2		1041.463454	2080.911308	0.000451244	11	N	398	416
Q8VCT3	Exosome	AVLNR	AFFPCFDTPAVK	CTYSA	2	C5:+57.021	700.339671	1398.663742	0.000451244	8	N	176	188
Q8VCT3	Exosome	RTLAK	DTFAATASQLHSNVVNYVQQILAPK	DS-	3		905.8087255	2714.402777	0.001162105	1	N	623	648
Q8VCT3	Exosome	ELKKK	GVDSIPGFEFDR	WLNTP	2		669.8203883	1337.625177	0.002019181	1	N	469	481
Q8VCT3	Exosome	TPYEK	GYCFVSYLAHLVGDQDQFDKFLK	AYVDE	3	C3:+57.021	917.447986	2749.320558	0.000451244	2	N	416	439
Q8VCT3	Exosome	ELTYR	VGEGPGVCWLAPEQTAGK	KKPFV	2	C8:+57.021	928.4542836	1854.892967	0.000451244	1	N	143	161
Q8VCT3	Parental	RTLAK	DTFAATASQLHSNVVNYVQQILAPKDS	-	3		973.161716	2916.461748	0.000735798	4	N	623	650
Q8VCT3	Parental	LNKLR	VKIEPGVDPDDTYNETPYEK	GYCFV	2		1155.045142	2308.074685	0.000451244	9	N	396	416
Q8VCT3	Parental	LNKLR	VKIEPGVDPDDTYNETPYEK	GYCFV	3		770.3660283	2308.074685	0.000451244	15	N	396	416
Q8VCT3	Parental	GPRSR	VWAEPCLIEAAKEEYSGVIEEFLATGEK	LFGPY	3	C6:+57.021	1056.853406	3167.536818	0.000451244	16	N	248	276
Q8VCT3	Parental	VDEFK	FQSILAEDFLEFYLEYFPELK	KKGVD	2		1321.159778	2640.303957	0.000451244	3	N	446	467
Q8VCT3	Parental	TPYEK	GYCFVSYLAHLVGDQDQFDK	FLKAY	3	C3:+57.021	788.0321722	2361.073117	0.000698008	5	N	416	436
Q8VCT3	Parental	SAAAR	RPLHSAQAVDVASASSFR	AFEIL	3		633.6664181	1897.975854	0.000823681	6	N	14	32
Q8VCT3	Parental	RTLAK	DTFAATASQLHSNVVNYVQQILAPK	DS-	3		905.8087255	2714.402777	0.001654178	1	N	623	648
Q8VD04	Parental	QEIVR	LSKECVGSPDPDLEPGEAN	-	2	C5:+57.021	1007.457417	2012.899235	0.001463592	4	N	787	806
Q8VD04	Parental	AIPAR	SLSSSPQAQPPRPAELSDEEVAELFQR	LAETQ	3		990.1602637	2967.457391	0.001329271	1	N	652	679
Q8VD04	Parental	RANSR	LLEQLQEIGQEKEQLTQDLQEAR	KSAEK	3		913.8106833	2738.40865	0.000451244	9	N	365	388
Q8VD58	Parental	DLEVK	LFESSEHINDTSNLK	TDNVE	2		867.421195	1732.82679	0.000451244	13	N	291	306
Q8VD58	Parental	WKPSK	STLLADDLEVK	LFESS	2		602.3275149	1202.63943	0.000622848	1	N	280	291
Q8VDD5	Exosome	KQLKR	QLEEAEEEAQRANASR	RKLQR	3		610.9579264	1829.850379	0.000451244	4	N	1877	1893
Q8VDD5	Exosome	LEKAK	QTLENERGELANEVK	ALLQG	2		865.4399191	1728.864238	0.000451244	18	N	1219	1234
Q8VDD5	Exosome	LEKAK	QTLENERGELANEVK	ALLQG	3		577.2958794	1728.864238	0.000451244	5	N	1219	1234
Q8VDD5	Exosome	EKKQK	KFDQLLAEEK	TISAK	2		610.8302247	1219.644849	0.000823681	9	Y	1444	1454
Q8VDD5	Exosome	ERAKR	QAQQERDELADEIANSSGK	GALAL	2		1044.993776	2087.971951	0.000451244	35	N	1697	1716
Q8VDD5	Exosome	ERAKR	QAQQERDELADEIANSSGK	GALAL	3		696.9984503	2087.971951	0.000451244	22	N	1697	1716
Q8VDD5	Exosome	ERAKR	QAQQERDELADEIANSSGK	GALAL	2	Q1:-17.027	1036.480276	2070.944951	0.00307782	1	N	1697	1716
Q8VDD5	Exosome	ERAKR	QAQQERDELADEIANSSGK	GALAL	2	[0:-17.027	1036.480276	2070.944951	0.001162105	14	N	1697	1716
Q8VDD5	Exosome	ALEAK	IAQLEEQLDNETKER	QAASK	2		908.4583088	1814.901018	0.000451244	18	N	1815	1830
Q8VDD5	Exosome	ALEAK	IAQLEEQLDNETKER	QAASK	3		605.9748059	1814.901018	0.000451244	14	N	1815	1830
Q8VDD5	Exosome	ALEAK	IAQLEEQLDNETK	ERQAA	2		765.8864567	1529.757313	0.000451244	47	N	1815	1828
Q8VDD5	Exosome	FQEFR	QRYEILTPNSIPK	GFMDG	3		520.2916295	1557.851488	0.000451244	6	N	718	731

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDD5	Exosome	EMRQK	HSQAVEELADQLEQTKR	VKATL	2		991.5010394	1980.986479	0.000451244	5	N	1193	1210
Q8VDD5	Exosome	EMRQK	HSQAVEELADQLEQTKR	VKATL	3		661.3366263	1980.986479	0.000451244	36	N	1193	1210
Q8VDD5	Exosome	EFRQR	YEILTPNSIPK	GFMDG	2		637.8536999	1273.6918	0.000622848	7	N	720	731
Q8VDD5	Exosome	NDRLK	KANLQIDQINTDLNLER	SHAQK	2		999.5348822	1997.054164	0.000451244	17	N	1753	1770
Q8VDD5	Exosome	NDRLK	KANLQIDQINTDLNLER	SHAQK	3		666.6925215	1997.054164	0.000451244	21	N	1753	1770
Q8VDD5	Exosome	KKAGK	LDPHLVLDQLR	CNGVL	2		659.8780406	1317.740481	0.000451244	4	N	682	693
Q8VDD5	Exosome	KKAGK	LDPHLVLDQLR	CNGVL	3		440.2546271	1317.740481	0.000451244	20	N	682	693
Q8VDD5	Exosome	TAAQK	VSHLLGINVTDFTR	GILTP	2		786.4311687	1570.846737	0.000451244	17	N	373	387
Q8VDD5	Exosome	TAAQK	VSHLLGINVTDFTR	GILTP	3		524.6233791	1570.846737	0.000451244	58	N	373	387
Q8VDD5	Exosome	MGLLR	VISGVLQLGNIAFKK	ERNTD	2		793.9855798	1585.95556	0.000451244	18	N	341	356
Q8VDD5	Exosome	DRLKK	ANLQIDQINTDLNLER	SHAQK	2		935.4874007	1868.959201	0.000451244	41	N	1754	1770
Q8VDD5	Exosome	RLEAR	IAQLEEELEEEQGNTELINDR	LKKAN	2		1236.590977	2471.166354	0.000451244	60	N	1730	1751
Q8VDD5	Exosome	RLEAR	IAQLEEELEEEQGNTELINDR	LKKAN	3		824.7299179	2471.166354	0.000451244	23	N	1730	1751
Q8VDD5	Exosome	LYVDK	NFINNPLAQADWAAK	KLVWV	2		836.9262505	1671.836901	0.000451244	21	N	14	29
Q8VDD5	Exosome	LIYTY	SGLFCVVINPYK	NLPIY	2	C5:+57.021	698.8685957	1395.721591	0.001264573	2	Y	113	125
Q8VDD5	Exosome	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	2		1167.032241	2332.048882	0.000451244	26	N	940	959
Q8VDD5	Exosome	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	3		778.3574273	2332.048882	0.002813207	1	N	940	959
Q8VDD5	Exosome	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	2	M1:+15.995	1175.029741	2348.043882	0.000451244	12	N	940	959
Q8VDD5	Exosome	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	3	M1:+15.995	783.689094	2348.043882	0.000451244	3	N	940	959
Q8VDD5	Exosome	QAADK	YLYVDKNFINNPLAQADWAAK	KLVWV	3		818.7537809	2453.237943	0.000622848	5	N	8	29
Q8VDD5	Exosome	DKVTK	LQVELDSVTGLLSQSDSK	SSKLT	2		960.0025492	1917.989498	0.000451244	43	N	1277	1295
Q8VDD5	Exosome	DKVTK	LQVELDSVTGLLSQSDSK	SSKLT	3		640.3376328	1917.989498	0.000451244	13	N	1277	1295
Q8VDD5	Exosome	MGLLR	VISGVLQLGNIAFK	KERNT	2		729.9380983	1457.860597	0.000451244	44	N	341	355
Q8VDD5	Exosome	MGLLR	VISGVLQLGNIAFK	KERNT	3		486.9613322	1457.860597	0.000622848	9	N	341	355
Q8VDD5	Exosome	KTKTR	LQQELDDLLVDLDHQR	QSVSN	2		975.5005081	1948.985416	0.000451244	32	N	1417	1433
Q8VDD5	Exosome	KTKTR	LQQELDDLLVDLDHQR	QSVSN	3		650.6696054	1948.985416	0.000451244	31	N	1417	1433
Q8VDD5	Exosome	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	2		998.5205152	1995.02543	0.000637154	2	N	272	289
Q8VDD5	Exosome	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	3		666.0162768	1995.02543	0.000451244	21	N	272	289
Q8VDD5	Exosome	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	4		499.7641576	1995.02543	0.000451244	22	N	272	289
Q8VDD5	Exosome	LKKIR	ELETQISELQEDLESER	ASRNK	2		1024.48746	2046.959321	0.000451244	17	N	1107	1124
Q8VDD5	Exosome	LKKIR	ELETQISELQEDLESER	ASRNK	3		683.3275736	2046.959321	0.002080925	1	N	1107	1124
Q8VDD5	Exosome	LMAEK	LQLQEQLQAETELCAEAEELR	ARLTA	2	C14:+57.021	1251.113334	2500.211067	0.000451244	36	N	882	903
Q8VDD5	Exosome	LMAEK	LQLQEQLQAETELCAEAEELR	ARLTA	3	C14:+57.021	834.411489	2500.211067	0.000998612	1	N	882	903
Q8VDD5	Exosome	SKSSK	LTKDFSALESQLQDTQELLQEENR	QKLSL	3		945.8055979	2834.393394	0.000451244	10	N	1298	1322
Q8VDD5	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	2		863.9784831	1725.941366	0.000451244	29	Y	209	225
Q8VDD5	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	3		576.3215887	1725.941366	0.000451244	18	Y	209	225
Q8VDD5	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	2	Q1:-17.027	855.4649831	1708.914366	0.000698008	1	Y	209	225
Q8VDD5	Exosome	GELER	QLLQANPILEAFGNAK	TVKND	2	[0:-17.027	855.4649831	1708.914366	0.000451244	22	Y	209	225
Q8VDD5	Exosome	LEKTK	TRLQQELDDLLVDLDHQR	QSVSN	3		736.3858686	2206.134206	0.000451244	22	N	1415	1433
Q8VDD5	Exosome	LEKTK	TRLQQELDDLLVDLDHQR	QSVSN	4		552.5413515	2206.134206	0.000451244	28	N	1415	1433
Q8VDD5	Exosome	SKLTK	DFSALESQLQDTQELLQEENRQK	LSLST	2		1375.167914	2748.320229	0.000451244	10	N	1301	1324
Q8VDD5	Exosome	SKLTK	DFSALESQLQDTQELLQEENRQK	LSLST	3		917.1145429	2748.320229	0.000451244	27	N	1301	1324
Q8VDD5	Exosome	EKTRR	KLEGDSTDLSDQIAELQAQIAELK	MQLAK	3		872.4523845	2614.333754	0.000451244	40	N	1051	1075
Q8VDD5	Exosome	SKLTK	DFSALESQLQDTQELLQEENR	QKLSL	2		1247.091144	2492.166688	0.000451244	52	N	1301	1322
Q8VDD5	Exosome	SKLTK	DFSALESQLQDTQELLQEENR	QKLSL	3		831.7300293	2492.166688	0.000451244	30	N	1301	1322
Q8VDD5	Exosome	GKFIR	INFDVNGYIVGANIETYLLEK	SRAIR	2		1193.120988	2384.226375	0.000451244	3	N	240	261
Q8VDD5	Exosome	GKFIR	INFDVNGYIVGANIETYLLEK	SRAIR	3		795.749925	2384.226375	0.000622848	4	N	240	261
Q8VDD5	Exosome	NFIDF	GLDLQPCIDLIEKPAGPPGILALLDEECWFPK	ATDKS	3	C7:+57.021,C28:+57.021	1202.286062	3603.834787	0.001699387	1	N	504	536
Q8VDD5	Exosome	EKQKR	DLGEELEALKTELEDTLDSTAAQQELR	SKREQ	3		1006.498611	3016.472432	0.000451244	59	N	1135	1162
Q8VDD5	Exosome	EKQKR	DLGEELEALKTELEDTLDSTAAQQELR	SKREQ	4		755.125908	3016.472432	0.001699387	1	N	1135	1162
Q8VDD5	Exosome	DLEAR	VEEEEERCQYLQAEK	KKMQQ	3	C8:+57.021	647.295285	1938.862455	0.000622848	3	N	923	938
Q8VDD5	Exosome	MALKK	IRELETQISELQEDLESER	ASRNK	2		1159.080048	2316.144496	0.000451244	17	N	1105	1124
Q8VDD5	Exosome	MALKK	IRELETQISELQEDLESER	ASRNK	3		773.0559653	2316.144496	0.000451244	30	N	1105	1124
Q8VDD5	Exosome	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	2		1009.535506	2017.055411	0.000451244	4	N	617	637
Q8VDD5	Exosome	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	2	M10:+15.995	1017.533006	2033.050411	0.000451244	35	N	617	637
Q8VDD5	Exosome	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	3	M10:+15.995	678.6912704	2033.050411	0.000451244	17	N	617	637
Q8VDD5	Exosome	EKSKR	ALEQQVEEMKTQLEELEDELQATEDAK	LRLEV	3		1049.834895	3146.481284	0.001699387	1	N	1528	1555
Q8VDD5	Exosome	EKSKR	ALEQQVEEMKTQLEELEDELQATEDAK	LRLEV	3	M9:+15.995	1055.166561	3162.476284	0.000451244	27	N	1528	1555
Q8VDD5	Exosome	DLQPC	IDLIEKPAGPPGILALLDEECWFPK	ATDKS	3	C21:+57.021	941.1667081	2820.476724	0.000451244	3	N	511	536
Q8VDD5	Exosome	ENTKK	VIQYLAHVASSHK	SKKDQ	3		484.9372981	1451.788494	0.000451244	11	N	186	199
Q8VDD5	Exosome	RLTAK	KQELEEICHDLEAR	VEEEE	2	C8:+57.021	885.4282658	1768.840932	0.000451244	30	N	909	923
Q8VDD5	Exosome	RLTAK	KQELEEICHDLEAR	VEEEE	3	C8:+57.021	590.6214439	1768.840932	0.000451244	1	N	909	923
Q8VDD5	Exosome	EMRQK	HSQAVEELADQLEQTK	RVKAT	3		609.3029225	1824.885368	0.000451244	1	N	1193	1209
Q8VDD5	Exosome	NHEKK	AGKLDPHLVLDQLR	CNGVL	3		525.6391407	1573.894022	0.000451244	3	N	679	693
Q8VDD5	Exosome	EHKRK	KVEAQLQELQVK	FSEGE	3		471.6089585	1411.803476	0.001943752	2	N	1248	1260

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDD5	Exosome	MMQDR	EDQSILCTGESGAGK	TENTK	2	C7:+57.021	776.3516924	1550.687785	0.000451244	7	Y	165	180
Q8VDD5	Exosome	KVFFR	AGVLAHLEEER	DLKIT	2		612.3230982	1222.630596	0.000451244	7	N	764	775
Q8VDD5	Exosome	LLEDR	VAEFTTNLMEEEEK	SKSLA	2	M9:+15.995	843.3829328	1684.750266	0.000451244	30	N	1000	1014
Q8VDD5	Exosome	GEHLK	TDLLLEPYNK	YRFLS	2		603.3247752	1204.63395	0.000451244	16	N	289	299
Q8VDD5	Exosome	INPYK	NLPIYSEEIVEMYK	GKKRH	2	M12:+15.995	872.429686	1742.843772	0.000451244	26	N	125	139
Q8VDD5	Exosome	VEEMK	TQLEELEDELQATEDAK	LRLEV	2		981.4634539	1960.911308	0.000451244	14	N	1538	1555
Q8VDD5	Exosome	VEEMK	TQLEELEDELQATEDAK	LRLEV	3		654.6449026	1960.911308	0.000451244	5	N	1538	1555
Q8VDD5	Exosome	LLEDR	VAEFTTNLMEEEEKSK	SLAKL	2	M9:+15.995	950.9464286	1899.877257	0.000451244	21	N	1000	1016
Q8VDD5	Exosome	LLEDR	VAEFTTNLMEEEEKSK	SLAKL	3	M9:+15.995	634.3002191	1899.877257	0.000451244	8	N	1000	1016
Q8VDD5	Exosome	KVTKL	QVELDSVTGLLSQSDSK	SSKLT	2		903.4605172	1804.905434	0.000451244	7	N	1278	1295
Q8VDD5	Exosome	EKLQL	QEQLQAETELCAEAEELR	ARLTA	2	C11:+57.021	1073.999981	2145.984361	0.001395409	1	N	885	903
Q8VDD5	Exosome	EKLQL	QEQLQAETELCAEAEELR	ARLTA	2	[0:-17.027,C11:+57.021	1065.486481	2128.957361	0.000451244	4	N	885	903
Q8VDD5	Exosome	DLIEK	PAGPPGILALLDEECWFPK	ATDKS	2	C15:+57.021	1055.537816	2109.060033	0.000451244	4	N	517	536
Q8VDD5	Exosome	ERDLK	ITDVIIGFQACCR	GYLAR	2	C11:+57.021,C12:+57.021	776.8842198	1551.75284	0.000451244	6	N	778	791
Q8VDD5	Exosome	DKYLY	VDKNFINNPLAQADWAAK	KLVWV	2		1008.021411	2014.027221	0.000451244	9	N	11	29
Q8VDD5	Exosome	DKYLY	VDKNFINNPLAQADWAAK	KLVWV	3		672.3502071	2014.027221	0.000735798	2	N	11	29
Q8VDD5	Exosome	EWLMK	NMDPLNDNIATLLHQSSDKFVSELWK	DVDRI	3	M2:+15.995	1011.16639	3030.47577	0.000662267	6	N	587	613
Q8VDD5	Exosome	EWLMK	NMDPLNDNIATLLHQSSDKFVSELWK	DVDRI	4	M2:+15.995	758.6267425	3030.47577	0.000451244	17	N	587	613
Q8VDD5	Exosome	KAQTK	EQADFAIEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	9	N	407	419
Q8VDD5	Exosome	EKQKR	DLGEELEALKTELEDTLD	STAAQ	2		1016.994587	2031.973574	0.000622848	8	N	1135	1153
Q8VDD5	Exosome	DMKKK	MEDGVGCLETAEEAK	RRLQK	2	C7:+57.021	819.8532112	1637.690822	0.000622848	5	N	1372	1387
Q8VDD5	Exosome	DFSAL	ESQLQDTQELLQEENR	QKLSL	2		980.4668622	1958.918124	0.000823681	1	N	1306	1322
Q8VDD5	Exosome	ADKYL	YVDKNFINNPLAQADWAAK	KLVWV	3		726.70465	2177.09055	0.002212458	1	N	10	29
Q8VDD5	Exosome	AADKY	LYVDKNFINNPLAQADWAAK	KLVWV	3		764.399338	2290.174614	0.002981883	1	N	9	29
Q8VDD5	Exosome	KVFFR	AGVLAHLEEERDLK	ITDVI	3		527.2866556	1578.836567	0.002453667	1	N	764	778
Q8VDD5	Parental	KQLKR	QLEEAEEEAQRANASR	RKLQR	3		610.9579264	1829.850379	0.000451244	16	N	1877	1893
Q8VDD5	Parental	LEKAK	QTLENERGELANEVK	ALLQG	2		865.4399191	1728.864238	0.000451244	37	N	1219	1234
Q8VDD5	Parental	LEKAK	QTLENERGELANEVK	ALLQG	3		577.2958794	1728.864238	0.000451244	34	N	1219	1234
Q8VDD5	Parental	EKKQK	KFDQLLAEEK	TISAK	2		610.8302247	1219.644849	0.000698008	42	Y	1444	1454
Q8VDD5	Parental	ERAKR	QAQQERDELADEIANSSGK	GALAL	2		1044.993776	2087.971951	0.000451244	79	N	1697	1716
Q8VDD5	Parental	ERAKR	QAQQERDELADEIANSSGK	GALAL	3		696.9984503	2087.971951	0.000451244	64	N	1697	1716
Q8VDD5	Parental	ERAKR	QAQQERDELADEIANSSGK	GALAL	2	Q1:-17.027	1036.480276	2070.944951	0.002663018	1	N	1697	1716
Q8VDD5	Parental	ERAKR	QAQQERDELADEIANSSGK	GALAL	2	[0:-17.027	1036.480276	2070.944951	0.001162105	31	N	1697	1716
Q8VDD5	Parental	ALEAK	IAQLEEQLDNETKER	QAASK	2		908.4583088	1814.901018	0.000451244	35	N	1815	1830
Q8VDD5	Parental	ALEAK	IAQLEEQLDNETKER	QAASK	3		605.9748059	1814.901018	0.000451244	40	N	1815	1830
Q8VDD5	Parental	ALEAK	IAQLEEQLDNETK	ERQAA	2		765.8864567	1529.757313	0.000451244	76	N	1815	1828
Q8VDD5	Parental	FQEFR	QRYEILTPNSIPK	GFMDG	3		520.2916295	1557.851488	0.000451244	5	N	718	731
Q8VDD5	Parental	EMRQK	HSQAVEELADQLEQTKR	VKATL	2		991.5010394	1980.986479	0.000451244	52	N	1193	1210
Q8VDD5	Parental	EMRQK	HSQAVEELADQLEQTKR	VKATL	3		661.3366263	1980.986479	0.000451244	72	N	1193	1210
Q8VDD5	Parental	EMRQK	HSQAVEELADQLEQTKR	VKATL	4		496.2544197	1980.986479	0.000451244	29	N	1193	1210
Q8VDD5	Parental	DYVQK	AQTKEQADFAIEALAK	ATYER	2		867.4575805	1732.899561	0.000451244	6	N	403	419
Q8VDD5	Parental	DYVQK	AQTKEQADFAIEALAK	ATYER	3		578.640987	1732.899561	0.001871652	1	N	403	419
Q8VDD5	Parental	EFRQR	YEILTPNSIPK	GFMDG	2		637.8536999	1273.6918	0.000451244	25	N	720	731
Q8VDD5	Parental	NDRLK	KANLQIDQINTDLNLER	SHAQK	2		999.5348822	1997.054164	0.000451244	21	N	1753	1770
Q8VDD5	Parental	NDRLK	KANLQIDQINTDLNLER	SHAQK	3		666.6925215	1997.054164	0.000451244	30	N	1753	1770
Q8VDD5	Parental	QLKDK	ADFCIIHY	AGKVD	2	C4:+57.021	519.7395927	1037.463585	0.001352548	5	N	565	573
Q8VDD5	Parental	KKAGK	LDPHLVLDQLR	CNGVL	2		659.8780406	1317.740481	0.000451244	14	N	682	693
Q8VDD5	Parental	KKAGK	LDPHLVLDQLR	CNGVL	3		440.2546271	1317.740481	0.000451244	64	N	682	693
Q8VDD5	Parental	TAAQK	VSHLLGINVTDFTR	GILTP	2		786.4311687	1570.846737	0.000451244	23	N	373	387
Q8VDD5	Parental	TAAQK	VSHLLGINVTDFTR	GILTP	3		524.6233791	1570.846737	0.000451244	79	N	373	387
Q8VDD5	Parental	MGLLR	VISGVLQLGNIAFKK	ERNTD	2		793.9855798	1585.95556	0.000451244	8	N	341	356
Q8VDD5	Parental	DRLKK	ANLQIDQINTDLNLER	SHAQK	2		935.4874007	1868.959201	0.000451244	130	N	1754	1770
Q8VDD5	Parental	DRLKK	ANLQIDQINTDLNLER	SHAQK	3		623.9942004	1868.959201	0.000698008	6	N	1754	1770
Q8VDD5	Parental	RLEAR	IAQLEEELEEEQGNTELINDRLK	KANLQ	2		1357.18049	2712.345381	0.000451244	6	N	1730	1753
Q8VDD5	Parental	RLEAR	IAQLEEELEEEQGNTELINDRLK	KANLQ	3		905.122927	2712.345381	0.000451244	5	N	1730	1753
Q8VDD5	Parental	RLEAR	IAQLEEELEEEQGNTELINDR	LKKAN	2		1236.590977	2471.166354	0.000451244	205	N	1730	1751
Q8VDD5	Parental	RLEAR	IAQLEEELEEEQGNTELINDR	LKKAN	3		824.7299179	2471.166354	0.000451244	18	N	1730	1751
Q8VDD5	Parental	LYVDK	NFINNPLAQADWAAK	KLVWV	2		836.9262505	1671.836901	0.000451244	33	N	14	29
Q8VDD5	Parental	LIYTY	SGLFCVVINPYK	NLPIY	2	C5:+57.021	698.8685957	1395.721591	0.000451244	3	Y	113	125
Q8VDD5	Parental	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	2		1167.032241	2332.048882	0.000451244	32	N	940	959
Q8VDD5	Parental	AEKKK	MQQNIQELEEQLEEEESAR	QKLQL	3		778.3574273	2332.048882	0.000451244	3	N	940	959
Q8VDD5	Parental	LMAEK	LQLQEQLQAETELCAEAEELRAR	LTAKK	3	C14:+57.021	910.1242307	2727.349292	0.000451244	20	N	882	905
Q8VDD5	Parental	QAADK	YLYVDKNFINNPLAQADWAAK	KLVWV	2		1227.626771	2453.237943	0.000451244	20	N	8	29
Q8VDD5	Parental	QAADK	YLYVDKNFINNPLAQADWAAK	KLVWV	3		818.7537809	2453.237943	0.000451244	19	N	8	29
Q8VDD5	Parental	DKVTK	LQVELDSVTGLLSQSDSK	SSKLT	2		960.0025492	1917.989498	0.000451244	168	N	1277	1295

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDD5	Parental	DKVTK	LQVELDSVTGLLSQSDSK	SSKLT	3		640.3376328	1917.989498	0.000451244	14	N	1277	1295
Q8VDD5	Parental	MGLLR	VISGVLQLGNIAFK	KERNT	2		729.9380983	1457.860597	0.000451244	37	N	341	355
Q8VDD5	Parental	MGLLR	VISGVLQLGNIAFK	KERNT	3		486.9613322	1457.860597	0.000451244	8	N	341	355
Q8VDD5	Parental	KTKTR	LQQELDDLLVDLDHQR	QSVSN	2		975.5005081	1948.985416	0.000451244	54	N	1417	1433
Q8VDD5	Parental	KTKTR	LQQELDDLLVDLDHQR	QSVSN	3		650.6696054	1948.985416	0.000451244	51	N	1417	1433
Q8VDD5	Parental	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	2		998.5205152	1995.02543	0.000622848	1	N	272	289
Q8VDD5	Parental	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	3		666.0162768	1995.02543	0.001264573	5	N	272	289
Q8VDD5	Parental	AKEER	TFHIFYYLLSGAGEHLK	TDLLL	4		499.7641576	1995.02543	0.000451244	26	N	272	289
Q8VDD5	Parental	LKKIR	ELETQISELQEDLESER	ASRNK	2		1024.48746	2046.959321	0.000451244	32	N	1107	1124
Q8VDD5	Parental	LKKIR	ELETQISELQEDLESER	ASRNK	3		683.3275736	2046.959321	0.000451244	8	N	1107	1124
Q8VDD5	Parental	LMAEK	LQLQEQLQAETELCAEAEELR	ARLTA	2	C14:+57.021	1251.113334	2500.211067	0.000451244	326	N	882	903
Q8VDD5	Parental	LMAEK	LQLQEQLQAETELCAEAEELR	ARLTA	3	C14:+57.021	834.411489	2500.211067	0.000451244	52	N	882	903
Q8VDD5	Parental	SKSSK	LTKDFSALESQLQDTQELLQEENR	QKLSL	2		1418.204497	2834.393394	0.000451244	7	N	1298	1322
Q8VDD5	Parental	SKSSK	LTKDFSALESQLQDTQELLQEENR	QKLSL	3		945.8055979	2834.393394	0.000451244	11	N	1298	1322
Q8VDD5	Parental	GELER	QLLQANPILEAFGNAK	TVKND	2		863.9784831	1725.941366	0.000451244	37	Y	209	225
Q8VDD5	Parental	GELER	QLLQANPILEAFGNAK	TVKND	3		576.3215887	1725.941366	0.000451244	27	Y	209	225
Q8VDD5	Parental	GELER	QLLQANPILEAFGNAK	TVKND	2	Q1:-17.027	855.4649831	1708.914366	0.000451244	6	Y	209	225
Q8VDD5	Parental	GELER	QLLQANPILEAFGNAK	TVKND	2	[0:-17.027	855.4649831	1708.914366	0.000451244	15	Y	209	225
Q8VDD5	Parental	LEKTK	TRLQQELDDLLVDLDHQR	QSVSN	2		1104.074903	2206.134206	0.000451244	3	N	1415	1433
Q8VDD5	Parental	LEKTK	TRLQQELDDLLVDLDHQR	QSVSN	3		736.3858686	2206.134206	0.000451244	39	N	1415	1433
Q8VDD5	Parental	LEKTK	TRLQQELDDLLVDLDHQR	QSVSN	4		552.5413515	2206.134206	0.000451244	46	N	1415	1433
Q8VDD5	Parental	SKLTK	DFSALESQLQDTQELLQEENRQK	LSLST	2		1375.167914	2748.320229	0.000451244	22	N	1301	1324
Q8VDD5	Parental	SKLTK	DFSALESQLQDTQELLQEENRQK	LSLST	3		917.1145429	2748.320229	0.000451244	25	N	1301	1324
Q8VDD5	Parental	EKTRR	KLEGDSTDLSDQIAELQAQIAELK	MQLAK	2		1308.174677	2614.333754	0.000451244	9	N	1051	1075
Q8VDD5	Parental	EKTRR	KLEGDSTDLSDQIAELQAQIAELK	MQLAK	3		872.4523845	2614.333754	0.000451244	55	N	1051	1075
Q8VDD5	Parental	SKLTK	DFSALESQLQDTQELLQEENR	QKLSL	2		1247.091144	2492.166688	0.000451244	141	N	1301	1322
Q8VDD5	Parental	SKLTK	DFSALESQLQDTQELLQEENR	QKLSL	3		831.7300293	2492.166688	0.000451244	47	N	1301	1322
Q8VDD5	Parental	GKFIR	INFDVNGYIVGANIETYLLEK	SRAIR	2		1193.120988	2384.226375	0.000451244	40	N	240	261
Q8VDD5	Parental	GKFIR	INFDVNGYIVGANIETYLLEK	SRAIR	3		795.749925	2384.226375	0.000451244	4	N	240	261
Q8VDD5	Parental	NFIDF	GLDLQPCIDLIEKPAGPPGILALLDEECWFPK	ATDKS	3	C7:+57.021,C28:+57.021	1202.286062	3603.834787	0.000451244	10	N	504	536
Q8VDD5	Parental	EKQKR	DLGEELEALKTELEDTLDSTAAQQELR	SKREQ	3		1006.498611	3016.472432	0.000451244	242	N	1135	1162
Q8VDD5	Parental	EKQKR	DLGEELEALKTELEDTLDSTAAQQELR	SKREQ	4		755.125908	3016.472432	0.000451244	26	N	1135	1162
Q8VDD5	Parental	DLEAR	VEEEEERCQYLQAEK	KKMQQ	2	C8:+57.021	970.4390275	1938.862455	0.00091018	1	N	923	938
Q8VDD5	Parental	DLEAR	VEEEEERCQYLQAEK	KKMQQ	3	C8:+57.021	647.295285	1938.862455	0.000451244	1	N	923	938
Q8VDD5	Parental	RRLQK	DLEGLSQRLEEK	VAAYD	2		708.8706096	1415.725619	0.000622848	6	N	1392	1404
Q8VDD5	Parental	MALKK	IRELETQISELQEDLESER	ASRNK	2		1159.080048	2316.144496	0.000451244	22	N	1105	1124
Q8VDD5	Parental	MALKK	IRELETQISELQEDLESER	ASRNK	3		773.0559653	2316.144496	0.000451244	16	N	1105	1124
Q8VDD5	Parental	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	2		1009.535506	2017.055411	0.000451244	6	N	617	637
Q8VDD5	Parental	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	3		673.3596037	2017.055411	0.002019181	1	N	617	637
Q8VDD5	Parental	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	2	M10:+15.995	1017.533006	2033.050411	0.000451244	12	N	617	637
Q8VDD5	Parental	KDVDR	IIGLDQVAGMSETALPGAFK	TRKGM	3	M10:+15.995	678.6912704	2033.050411	0.000451244	1	N	617	637
Q8VDD5	Parental	EKSKR	ALEQQVEEMKTQLEELEDELQATEDAK	LRLEV	3		1049.834895	3146.481284	0.000451244	12	N	1528	1555
Q8VDD5	Parental	DLQPC	IDLIEKPAGPPGILALLDEECWFPK	ATDKS	3	C21:+57.021	941.1667081	2820.476724	0.000451244	5	N	511	536
Q8VDD5	Parental	ENTKK	VIQYLAHVASSHK	SKKDQ	3		484.9372981	1451.788494	0.0007646	5	N	186	199
Q8VDD5	Parental	RLTAK	KQELEEICHDLEAR	VEEEE	2	C8:+57.021	885.4282658	1768.840932	0.000451244	25	N	909	923
Q8VDD5	Parental	RLTAK	KQELEEICHDLEAR	VEEEE	3	C8:+57.021	590.6214439	1768.840932	0.000451244	5	N	909	923
Q8VDD5	Parental	RLTAK	KQELEEICHDLEAR	VEEEE	4	C8:+57.021	443.2180329	1768.840932	0.0025889	3	N	909	923
Q8VDD5	Parental	EMRQK	HSQAVEELADQLEQTK	RVKAT	2		913.4504838	1824.885368	0.000451244	5	N	1193	1209
Q8VDD5	Parental	EMRQK	HSQAVEELADQLEQTK	RVKAT	3		609.3029225	1824.885368	0.000451244	19	N	1193	1209
Q8VDD5	Parental	NHEKK	AGKLDPHLVLDQLR	CNGVL	2		787.954811	1573.894022	0.000451244	6	N	679	693
Q8VDD5	Parental	EHKRK	KVEAQLQELQVK	FSEGE	2		706.9095378	1411.803476	0.000451244	11	N	1248	1260
Q8VDD5	Parental	EHKRK	KVEAQLQELQVK	FSEGE	3		471.6089585	1411.803476	0.000451244	21	N	1248	1260
Q8VDD5	Parental	MMQDR	EDQSILCTGESGAGK	TENTK	2	C7:+57.021	776.3516924	1550.687785	0.000451244	22	Y	165	180
Q8VDD5	Parental	LLEDR	VAEFTTNLMEEEEK	SKSLA	2	M9:+15.995	843.3829328	1684.750266	0.000662267	9	N	1000	1014
Q8VDD5	Parental	GEHLK	TDLLLEPYNK	YRFLS	2		603.3247752	1204.63395	0.000451244	22	N	289	299
Q8VDD5	Parental	INPYK	NLPIYSEEIVEMYK	GKKRH	2	M12:+15.995	872.429686	1742.843772	0.000451244	6	N	125	139
Q8VDD5	Parental	VEEMK	TQLEELEDELQATEDAK	LRLEV	2		981.4634539	1960.911308	0.000451244	24	N	1538	1555
Q8VDD5	Parental	VEEMK	TQLEELEDELQATEDAK	LRLEV	3		654.6449026	1960.911308	0.000823681	2	N	1538	1555
Q8VDD5	Parental	KVTKL	QVELDSVTGLLSQSDSK	SSKLT	2		903.4605172	1804.905434	0.000451244	1	N	1278	1295
Q8VDD5	Parental	DLIEK	PAGPPGILALLDEECWFPK	ATDKS	2	C15:+57.021	1055.537816	2109.060033	0.000622848	4	N	517	536
Q8VDD5	Parental	DKYLY	VDKNFINNPLAQADWAAK	KLVWV	2		1008.021411	2014.027221	0.000451244	11	N	11	29
Q8VDD5	Parental	DKYLY	VDKNFINNPLAQADWAAK	KLVWV	3		672.3502071	2014.027221	0.000979378	7	N	11	29
Q8VDD5	Parental	KAQTK	EQADFAIEALAK	ATYER	2		653.3384139	1304.661228	0.000451244	11	N	407	419
Q8VDD5	Parental	QLEEE	LEEEQGNTELINDR	LKKAN	2		830.3951772	1658.774754	0.000451244	1	N	1737	1751
Q8VDD5	Parental	EAKLK	KLEEDQIIMEDQNCK	LAKEK	2	C14:+57.021	946.9403493	1891.865099	0.000451244	7	N	974	989

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDD5	Parental	RKLQR	ELEDATETADAMNR	EVSSL	2		783.3415566	1564.667513	0.000451244	10	N	1898	1912
Q8VDD5	Parental	VLMIK	ALELDSNLYR	IGQSK	2		597.3121991	1192.608798	0.000451244	8	N	745	755
Q8VDD5	Parental	EKKLK	SMEAEMIQLQEELAAAER	AKRQA	2		1024.98552	2047.95544	0.000622848	1	N	1676	1694
Q8VDD5	Parental	LEEER	DLKITDVIIGF	QACCR	2		617.358618	1232.701636	0.000622848	2	N	775	786
Q8VDD5	Parental	EEYQR	EGIEWNFIDFGLDLQPCIDLIEKPAGPPGILAL	LDEEC	3	C17:+57.021	1217.632381	3649.873743	0.000451244	6	N	494	527
Q8VDD5	Parental	KKQKK	FDQLLAEEK	TISAK	2		546.7827432	1091.549886	0.00091018	11	Y	1445	1454
Q8VDD5	Parental	IQEMR	QKHSQAVEELADQLEQTK	RVKAT	2		1041.527254	2081.038908	0.000451244	3	N	1191	1209
Q8VDD5	Parental	IQEMR	QKHSQAVEELADQLEQTK	RVKAT	3		694.6874361	2081.038908	0.001463592	1	N	1191	1209
Q8VDD5	Parental	SILKK	TLEDEAKTHEAQIQEMR	QKHSQ	2		1014.986908	2027.958216	0.000622848	1	N	1174	1191
Q8VDD5	Parental	VPSSK	NGFEPASLKEEVGEEAIVELVENGK	KVKVN	3		896.4523845	2686.333754	0.000451244	4	N	38	63
Q8VDD5	Parental	LSLAR	ALEEAMEQKAELER	LNKQF	2		823.9068667	1645.798133	0.001264573	1	N	1483	1497
Q8VDD5	Parental	RTEKK	LKDVLLQVEDER	RNAEQ	2		728.9044524	1455.793305	0.000823681	1	N	1843	1855
Q8VDD5	Parental	LEALK	TELEDTLDSTAAQQELR	SKREQ	2		960.4637882	1918.911976	0.000451244	20	N	1145	1162
Q8VDD5	Parental	SSKLT	KDFSALESQLQDTQELLQEENR	QKLSL	3		874.4283504	2620.261651	0.000451244	6	N	1300	1322
Q8VDD5	Parental	DMKKK	MEDGVGCLETAEEAKR	RLQKD	3	C7:+57.021	598.9384445	1793.791934	0.001162105	1	N	1372	1388
Q8VDD5	Parental	DMKKK	MEDGVGCLETAEEAK	RRLQK	2	C7:+57.021	819.8532112	1637.690822	0.000451244	1	N	1372	1387
Q8VDD5	Parental	QLKDK	ADFCIIHYAGK	VDYKA	2	C4:+57.021	647.8163631	1293.617126	0.000451244	1	N	565	576
Q8VDD5	Parental	RLKKA	NLQIDQINTDLNLER	SHAQK	2		899.9688437	1797.922087	0.000451244	1	N	1755	1770
Q8VDD5	Parental	LEKTK	TRLQQELDDLLVDLDHQ	RQSVS	2		1026.024347	2050.033095	0.00307782	1	N	1415	1432
Q8VDD5	Parental	MMQDR	EDQSILCTGESGAGKTENTK	KVIQY	3	C7:+57.021	708.9956753	2123.963626	0.000451244	5	Y	165	185
Q8VDD5	Parental	MQLAK	KEEELQAALAR	VEEEA	3		419.8986204	1256.672461	0.002519933	1	N	1080	1091
Q8VDD5	Parental	AADKY	LYVDKNFINNPLAQADWAAK	KLVWV	3		764.399338	2290.174614	0.0007646	1	N	9	29
Q8VDD5	Parental	GKFIR	INFDVNGYIVGANIETY	LLEKS	2		951.4681452	1900.92069	0.001162105	1	N	240	257
Q8VDD5	Parental	KTRRK	LEGDSTDLSDQIAELQAQIAELK	MQLAK	2		1244.127195	2486.23879	0.001162105	1	N	1052	1075
Q8VDJ3	Parental	PLPEK	AACLESAQEPAGAWSNK	IRPIK	2	C3:+57.021	895.4126157	1788.809631	0.000451244	30	N	50	67
Q8VDJ3	Parental	CEAAK	EALEALVPVTIEVEVPFDLHR	YIIGQ	3		792.7656865	2375.27366	0.002080925	1	N	964	985
Q8VDJ3	Parental	PQQIK	VATLNSEEENDPPTYK	DAFPP	2		903.9237675	1805.831935	0.000451244	1	N	25	41
Q8VDK1	Exosome	QEAAR	LGACLAFLPEAFDFIAR	NPAET	2	C4:+57.021	955.9955873	1909.975575	0.000451244	7	N	72	89
Q8VDK1	Exosome	ELSLK	LAQAGAEILTYPSAFGSVTGPAHWEVLLR	ARAIE	3		1018.873618	3053.597454	0.000451244	8	N	210	239
Q8VDK1	Exosome	DFIAR	NPAETLLLSEPLNGDLLGQYSQLAR	ECGIW	3		904.8121356	2711.413007	0.000451244	4	N	89	114
Q8VDK1	Exosome	LLRAR	AIESQCYVIAAAQCGR	HHETR	2	C6:+57.021,C14:+57.021	898.9246047	1795.833609	0.000451244	10	N	241	257
Q8VDL4	Exosome	AAAER	FFSDKETFHDIAQAASEFPGAQHYVGGNAALIGQR	FAANT	4		945.711005	3778.81282	0.000451244	13	N	131	166
Q8VDL4	Exosome	KDPVR	TVGLGDAISAEGLFYSEARPD	-	2		1084.529463	2167.043325	0.000451244	19	N	475	496
Q8VDL4	Exosome	AAGAR	VAGTQACATETIDTNR	VSLRA	2	C7:+57.021	854.402248	1706.788896	0.000451244	10	N	408	424
Q8VDL4	Parental	IDTNR	VSLRAPQEFTTSHLESGSR	IVLNP	3		701.3595424	2101.055227	0.000451244	3	N	424	443
Q8VDL4	Parental	ESGSR	IVLNPDKPVVEWHR	EGITF	4		426.2418553	1700.936221	0.001162105	1	N	443	457
Q8VDL4	Parental	WSSLR	LGPAPVPVGPLSPESR	LAAAW	2		786.9413693	1571.867139	0.00091018	10	N	40	56
Q8VDL4	Parental	VEWHR	EGITFHFTPVLVCKDPVR	TVGLG	2	C13:+57.021	1058.056708	2114.097815	0.000451244	10	N	457	475
Q8VDL4	Parental	VEWHR	EGITFHFTPVLVCKDPVR	TVGLG	3	C13:+57.021	705.7070717	2114.097815	0.000451244	28	N	457	475
Q8VDL4	Parental	VEWHR	EGITFHFTPVLVCKDPVR	TVGLG	4	C13:+57.021	529.5322538	2114.097815	0.000451244	20	N	457	475
Q8VDL4	Parental	AAAER	FFSDKETFHDIAQAASEFPGAQHYVGGNAALIGQR	FAANT	3		1260.612073	3778.81282	0.000451244	29	N	131	166
Q8VDL4	Parental	AAAER	FFSDKETFHDIAQAASEFPGAQHYVGGNAALIGQR	FAANT	4		945.711005	3778.81282	0.000451244	30	N	131	166
Q8VDL4	Parental	KDPVR	TVGLGDAISAEGLFYSEARPD	-	2		1084.529463	2167.043325	0.000451244	24	N	475	496
Q8VDL4	Parental	KDPVR	TVGLGDAISAEGLFYSEARPD	-	3		723.355575	2167.043325	0.001162105	2	N	475	496
Q8VDL4	Parental	LQRKR	LLEVVTAISDIPTGIPVHLELASMTNR	ELMSS	3		963.8638429	2888.568129	0.000662267	3	N	277	304
Q8VDL4	Parental	MALWR	GSACAGFLALAVGCVFLLEPELPGTALR	SLWSS	2	C4:+57.021,C14:+57.021	1445.253764	2888.491929	0.00307782	1	N	5	33
Q8VDL4	Parental	MALWR	GSACAGFLALAVGCVFLLEPELPGTALR	SLWSS	3	C4:+57.021,C14:+57.021	963.8384429	2888.491929	0.000451244	13	N	5	33
Q8VDL4	Parental	AAGAR	VAGTQACATETIDTNR	VSLRA	2	C7:+57.021	854.402248	1706.788896	0.000451244	84	N	408	424
Q8VDL4	Parental	ILHSR	SDLEEAFLYFMGK	GAAAE	2		775.3663147	1548.717029	0.001162105	2	N	112	125
Q8VDL4	Parental	NTDLK	VLLCGPIGPK	LHELL	2	C4:+57.021	527.3101852	1052.60477	0.000662267	8	N	174	184
Q8VDL4	Parental	SPESR	LAAAWDALIAQPARR	WRRVA	3		541.6428851	1621.905255	0.002212458	1	N	56	71
Q8VDL4	Parental	PVRTV	GLGDAISAEGLFYSEARPD	-	2		984.4714162	1966.927232	0.000451244	2	N	477	496
Q8VDL4	Parental	ISGVK	LLQALGLSPGSGK	DHAIL	2		620.8671416	1239.718683	0.001352548	1	N	91	104
Q8VDL4	Parental	RVSLR	APQEFTTSHLESGSR	IVLNP	2		823.8926047	1645.769609	0.001943752	2	N	428	443
Q8VDL4	Parental	RVSLR	APQEFTTSHLESGSR	IVLNP	3		549.5976698	1645.769609	0.001264573	2	N	428	443
Q8VDL4	Parental	FFSDK	ETFHDIAQAASEFPGAQHYVGGNAALIGQR	FAANT	3		1052.515152	3154.522057	0.000451244	1	N	136	166
Q8VDL4	Parental	SDLTR	IHFHTLVYHILATVDGHWANQLAAVAAGAR	VAGTQ	3		1084.911289	3251.710467	0.002080925	1	N	378	408
Q8VDL4	Parental	SDLTR	IHFHTLVYHILATVDGHWANQLAAVAAGAR	VAGTQ	4		813.9354167	3251.710467	0.002519933	1	N	378	408
Q8VDM4	Exosome	SEPFR	SFANTLVDVCAYAGSGNVLK	VQQLL	2	C10:+57.021	1043.517612	2085.019624	0.000451244	30	N	588	608
Q8VDM4	Exosome	AHGER	AELATEEFLPVTPILEGFVILR	KNPNY	2		1229.186131	2456.356661	0.000451244	19	N	879	901
Q8VDM4	Exosome	AHGER	AELATEEFLPVTPILEGFVILR	KNPNY	3		819.7933537	2456.356661	0.000451244	32	N	879	901
Q8VDM4	Exosome	PTLRR	AVPLALALISVSNPR	LNILD	2		760.9621047	1519.908609	0.000451244	26	N	688	703
Q8VDM4	Exosome	PTLRR	AVPLALALISVSNPR	LNILD	3		507.6440031	1519.908609	0.000451244	25	N	688	703
Q8VDM4	Exosome	CLKYR	LVGSQEELASWGHEYVR	HLAGE	2		980.4821183	1958.948637	0.000451244	3	N	143	160
Q8VDM4	Exosome	CLKYR	LVGSQEELASWGHEYVR	HLAGE	3		653.9906789	1958.948637	0.000451244	4	N	143	160

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDM4	Exosome	AHGER	AELATEEFLPVTPILEGFVILRK	NPNYD	3		862.4916747	2584.451624	0.001463592	2	N	879	902
Q8VDM4	Exosome	NAYAK	VCLYLTSCVNYVPEPENSALLR	CALGV	2	C2:+57.021,C8:+57.021	1299.140608	2596.265617	0.000451244	25	N	228	250
Q8VDM4	Exosome	NHLGK	GEAIEAILAALEVVSEPFR	SFANT	2		1007.546927	2013.078254	0.000451244	21	N	569	588
Q8VDM4	Exosome	NHLGK	GEAIEAILAALEVVSEPFR	SFANT	3		672.0338846	2013.078254	0.000451244	10	N	569	588
Q8VDM4	Exosome	AGKPK	TITGFQTHTTPVLLAHGER	AELAT	2		1040.053242	2078.090884	0.000662267	1	N	860	879
Q8VDM4	Exosome	AGKPK	TITGFQTHTTPVLLAHGER	AELAT	3		693.7047614	2078.090884	0.000823681	1	N	860	879
Q8VDM4	Exosome	DTYAR	WLPLGLGLNHLGK	GEAIE	3		473.2825171	1416.824151	0.002884417	1	N	556	569
Q8VDM4	Exosome	VDSAR	MNLASSFVNGFVNAAFGQDK	LLTDD	2		1059.010186	2116.004772	0.000451244	3	N	369	389
Q8VDM4	Parental	SEPFR	SFANTLVDVCAYAGSGNVLK	VQQLL	2	C10:+57.021	1043.517612	2085.019624	0.000451244	16	N	588	608
Q8VDM4	Parental	AHGER	AELATEEFLPVTPILEGFVILR	KNPNY	2		1229.186131	2456.356661	0.000451244	25	N	879	901
Q8VDM4	Parental	AHGER	AELATEEFLPVTPILEGFVILR	KNPNY	3		819.7933537	2456.356661	0.000451244	29	N	879	901
Q8VDM4	Parental	PTLRR	AVPLALALISVSNPR	LNILD	2		760.9621047	1519.908609	0.000622848	9	N	688	703
Q8VDM4	Parental	PTLRR	AVPLALALISVSNPR	LNILD	3		507.6440031	1519.908609	0.000622848	17	N	688	703
Q8VDM4	Parental	CLKYR	LVGSQEELASWGHEYVR	HLAGE	2		980.4821183	1958.948637	0.000451244	4	N	143	160
Q8VDM4	Parental	AHGER	AELATEEFLPVTPILEGFVILRK	NPNYD	3		862.4916747	2584.451624	0.000870037	5	N	879	902
Q8VDM4	Parental	NAYAK	VCLYLTSCVNYVPEPENSALLR	CALGV	2	C2:+57.021,C8:+57.021	1299.140608	2596.265617	0.000451244	17	N	228	250
Q8VDM4	Parental	NHLGK	GEAIEAILAALEVVSEPFR	SFANT	2		1007.546927	2013.078254	0.000451244	10	N	569	588
Q8VDM4	Parental	NHLGK	GEAIEAILAALEVVSEPFR	SFANT	3		672.0338846	2013.078254	0.000451244	9	N	569	588
Q8VDM4	Parental	DTYAR	WLPLGLGLNHLGK	GEAIE	3		473.2825171	1416.824151	0.001463592	2	N	556	569
Q8VDM4	Parental	VDSAR	MNLASSFVNGFVNAAFGQDK	LLTDD	2		1059.010186	2116.004772	0.001763695	2	N	369	389
Q8VDM4	Parental	KVCLY	LTSCVNYVPEPENSALLR	CALGV	2	C4:+57.021	1031.517612	2061.019624	0.001162105	2	N	232	250
Q8VDM4	Parental	EDYIK	SGALLACGIVNSGVR	NECDP	2	C7:+57.021	737.3960403	1472.776481	0.000823681	6	N	441	456
Q8VDM6	Exosome	PHVVR	IGWSLDSCSTQLGEEPFSYGYGGTGKK	STNSR	3	C8:+57.021	975.4521244	2923.332973	0.000451244	14	N	284	311
Q8VDM6	Exosome	DRRGR	SPQPPAEEDEDDFDDTLVAIDTYNCDLHFK	VARDR	3	C25:+57.021	1166.172192	3495.493175	0.000451244	3	N	194	224
Q8VDM6	Exosome	STNSR	FENYGDKFAENDVIGCFADFECGNDVELSFTK	NGKWM	3	C16:+57.021,C22:+57.021	1246.539955	3736.596466	0.000451244	8	N	316	348
Q8VDM6	Exosome	VARDR	SSGYPLTIEGFAYLWSGAR	ASYGV	2		1038.015794	2074.015988	0.000451244	4	N	229	248
Q8VDM6	Exosome	NFGQR	AEPYCSVLPGFTFIQHLPLSER	IRGTI	3	C5:+57.021	854.4337882	2560.277965	0.000451244	2	N	387	409
Q8VDM6	Exosome	ARKKR	NYILDQTNVYGSAQR	RKMRP	2		871.4293544	1740.843109	0.000451244	29	N	501	516
Q8VDM6	Exosome	NYAGR	WDVLIQQATQCLNR	LIQIA	2	C11:+57.021	872.943886	1743.872172	0.000451244	8	N	477	491
Q8VDM6	Exosome	PHVVR	IGWSLDSCSTQLGEEPFSYGYGGTGK	KSTNS	2	C8:+57.021	1398.626805	2795.23801	0.0007646	8	N	284	310
Q8VDM6	Exosome	FRIQK	EALGGQALYPHVLVK	NCAVE	3		532.303758	1593.887874	0.000451244	5	N	361	376
Q8VDM6	Exosome	NFGQR	AEPYCSVLPGFTFIQHLPL	SERIR	2	C5:+57.021	1095.058916	2188.102232	0.000622848	4	N	387	406
Q8VDM6	Exosome	REDRR	GRSPQPPAEEDEDDFDDTLVAIDTYNCDLHFK	VARDR	3	C27:+57.021	1237.21305	3708.61575	0.001871652	1	N	192	224
Q8VDM6	Exosome	PHVVR	IGWSLDSCSTQLGEEPF	SYGYG	2	C8:+57.021	963.4332138	1924.850828	0.001264573	1	N	284	301
Q8VDM6	Parental	PHVVR	IGWSLDSCSTQLGEEPFSYGYGGTGKK	STNSR	3	C8:+57.021	975.4521244	2923.332973	0.000451244	23	N	284	311
Q8VDM6	Parental	DRRGR	SPQPPAEEDEDDFDDTLVAIDTYNCDLHFK	VARDR	3	C25:+57.021	1166.172192	3495.493175	0.000451244	14	N	194	224
Q8VDM6	Parental	STNSR	FENYGDKFAENDVIGCFADFECGNDVELSFTK	NGKWM	3	C16:+57.021,C22:+57.021	1246.539955	3736.596466	0.000451244	10	N	316	348
Q8VDM6	Parental	VARDR	SSGYPLTIEGFAYLWSGAR	ASYGV	2		1038.015794	2074.015988	0.000451244	14	N	229	248
Q8VDM6	Parental	ARKKR	NYILDQTNVYGSAQR	RKMRP	2		871.4293544	1740.843109	0.000451244	10	N	501	516
Q8VDM6	Parental	NYAGR	WDVLIQQATQCLNR	LIQIA	2	C11:+57.021	872.943886	1743.872172	0.000451244	5	N	477	491
Q8VDM6	Parental	GFQRK	AIVICPTDEDLKDR	TVKRT	3	C5:+57.021	548.9472684	1643.818405	0.001395409	5	N	528	542
Q8VDM6	Parental	PHVVR	IGWSLDSCSTQLGEEPFSYGYGGTGK	KSTNS	2	C8:+57.021	1398.626805	2795.23801	0.000451244	7	N	284	310
Q8VDM6	Parental	DNITR	QNQFYETPVIKQENESSYDR	RPLDM	3		825.7194646	2474.134994	0.001943752	1	N	106	126
Q8VDM6	Parental	FRIQK	EALGGQALYPHVLVK	NCAVE	3		532.303758	1593.887874	0.000662267	2	N	361	376
Q8VDM6	Parental	NFGQR	AEPYCSVLPGFTFIQHLPL	SERIR	2	C5:+57.021	1095.058916	2188.102232	0.000823681	3	N	387	406
Q8VDM6	Parental	EISVK	HLPSTEPDPHVVR	IGWSL	3		495.2604408	1482.757922	0.001699387	1	N	271	284
Q8VDM6	Parental	GNYNR	APQQQPPPQQPPPPQPPPQQPPPPPSYSPAR	NPPGA	3		1110.234097	3327.678892	0.001162105	6	N	693	724
Q8VDN2	Exosome	KAIAK	GVGIISEGNETVEDIAAR	LNIPV	2		915.4661339	1828.916668	0.000451244	4	N	629	647
Q8VDN2	Exosome	LLHGK	EQPLDEELKDAFQNAYLELGGLGER	VLGFC	3		945.4668051	2833.377015	0.000451244	8	N	526	551
Q8VDN2	Exosome	NCLVK	NLEAVETLGSTSTICSDK	TGTLT	2	C15:+57.021	962.9623355	1923.909071	0.000451244	4	N	359	377
Q8VDN2	Parental	KAIAK	GVGIISEGNETVEDIAAR	LNIPV	2		915.4661339	1828.916668	0.000451244	19	N	629	647
Q8VDN2	Parental	LLHGK	EQPLDEELKDAFQNAYLELGGLGER	VLGFC	3		945.4668051	2833.377015	0.000451244	12	N	526	551
Q8VDN2	Parental	NCLVK	NLEAVETLGSTSTICSDKTGTLTQNR	MTVAH	3	C15:+57.021	932.7945503	2795.360251	0.000451244	2	N	359	385
Q8VDN2	Parental	VAHMW	FDNQIHEADTTENQSGVSFDK	TSATW	2		1191.52818	2381.040759	0.000451244	1	N	392	413
Q8VDN2	Parental	VAHMW	FDNQIHEADTTENQSGVSFDK	TSATW	3		794.688053	2381.040759	0.000851441	2	N	392	413
Q8VDN2	Parental	EGCQR	QGAIVAVTGDGVNDSPALK	KADIG	2		906.4790443	1810.942489	0.000823681	3	N	707	726
Q8VDP3	Exosome	KHGAR	LLLGLVGDCLVEPFWPLGTGVAR	GFLAA	2	C9:+57.021	1241.680261	2481.344922	0.000451244	27	N	385	408
Q8VDP3	Exosome	KHGAR	LLLGLVGDCLVEPFWPLGTGVAR	GFLAA	3	C9:+57.021	828.122774	2481.344922	0.000451244	22	N	385	408
Q8VDP3	Exosome	FVNGR	TVEETQVPEISGVAR	IYNQK	2		807.9208308	1613.826062	0.000637154	5	N	248	263
Q8VDP3	Exosome	GSGWR	AQLQPNPPAQLASYEFDVLISAAGGK	FVPEG	2		1343.198289	2684.380978	0.001329271	1	N	195	221
Q8VDP3	Parental	KHGAR	LLLGLVGDCLVEPFWPLGTGVAR	GFLAA	2	C9:+57.021	1241.680261	2481.344922	0.000451244	13	N	385	408
Q8VDP3	Parental	KHGAR	LLLGLVGDCLVEPFWPLGTGVAR	GFLAA	3	C9:+57.021	828.122774	2481.344922	0.000451244	5	N	385	408
Q8VDP3	Parental	GSGWR	AQLQPNPPAQLASYEFDVLISAAGGK	FVPEG	3		895.8014595	2684.380978	0.002145581	1	N	195	221
Q8VDP3	Parental	HSAFK	NTSHSSGLVSQPSGTPSAILF	LGKLQ	2		1044.024347	2086.033095	0.0025889	1	N	611	632
Q8VDP4	Exosome	HHPSR	IQVSSEKEAAPDTGAEPSPEDSDPTYSSK	VLLLS	3		1008.126954	3021.357462	0.000451244	7	N	280	309

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VDP4	Exosome	FLLGR	KEEEAVLVGGEWSPSLDGLDPQADPQVLVR	TAIRC	3		1078.549528	3232.625185	0.000451244	22	N	352	382
Q8VDP4	Exosome	TYSSK	VLLLSSPGLEEFYR	CCMLF	2		811.9435776	1621.871555	0.002374549	1	N	309	323
Q8VDP4	Exosome	LQYSR	AEVLDDGLPEDVLFGNLDLLPPSGK	STKPG	3		875.1220872	2622.342862	0.001591523	2	N	762	787
Q8VDP4	Exosome	LCQQK	ATEAAPQPHEASGEAEATEQAPDVSEQADTSK	QNTET	3		1084.819072	3251.433815	0.000451244	11	N	446	478
Q8VDP4	Parental	HHPSR	IQVSSEKEAAPDTGAEPSPEDSDPTYSSK	VLLLS	3		1008.126954	3021.357462	0.000451244	31	N	280	309
Q8VDP4	Parental	FLLGR	KEEEAVLVGGEWSPSLDGLDPQADPQVLVR	TAIRC	3		1078.549528	3232.625185	0.000451244	52	N	352	382
Q8VDP4	Parental	TYSSK	VLLLSSPGLEEFYR	CCMLF	2		811.9435776	1621.871555	0.000622848	8	N	309	323
Q8VDP4	Parental	LQYSR	AEVLDDGLPEDVLFGNLDLLPPSGK	STKPG	2		1312.179231	2622.342862	0.000698008	4	N	762	787
Q8VDP4	Parental	LQYSR	AEVLDDGLPEDVLFGNLDLLPPSGK	STKPG	3		875.1220872	2622.342862	0.001943752	4	N	762	787
Q8VDP4	Parental	LPGGR	NFSGAASTSLLGPPPGLLTPPVATDLSQNAR	HLQSG	3		1017.203804	3048.588011	0.00091018	3	N	16	47
Q8VDP4	Parental	LCQQK	ATEAAPQPHEASGEAEATEQAPDVSEQADTSK	QNTET	3		1084.819072	3251.433815	0.000451244	34	N	446	478
Q8VDP4	Parental	VSSEK	EAAPDTGAEPSPEDSDPTYSSK	VLLLS	2		1125.980196	2249.944793	0.000451244	16	N	287	309
Q8VDP4	Parental	ALGQK	QGILGAQPQLIFQPHR	IPPLF	3		601.6728444	1801.995133	0.000851441	1	N	138	154
Q8VDP4	Parental	PTEHK	GLVPHNGSLINVGSLLQRAEQQD	SGRLY	2		1223.146391	2444.277182	0.001352548	1	N	799	822
Q8VDQ8	Exosome	KKAYR	DVAWLGDCDQGCLALADLLGWK	KELED	2	C8:+57.021,C12:+57.021	1238.585469	2475.155338	0.000622848	4	N	316	338
Q8VDQ8	Exosome	DLVRR	EHANIDAQSGSQAPNPSTTISPGK	SPPPA	3		803.0548473	2406.141142	0.000451244	6	N	347	371
Q8VDQ8	Parental	DLVRR	EHANIDAQSGSQAPNPSTTISPGKSPPPAK	EAART	4		746.8736848	2983.463539	0.001591523	2	N	347	377
Q8VDQ8	Parental	KKAYR	DVAWLGDCDQGCLALADLLGWK	KELED	2	C8:+57.021,C12:+57.021	1238.585469	2475.155338	0.000451244	8	N	316	338
Q8VDQ8	Parental	KKAYR	DVAWLGDCDQGCLALADLLGWK	KELED	3	C8:+57.021,C12:+57.021	826.0595793	2475.155338	0.000823681	2	N	316	338
Q8VDQ8	Parental	DLVRR	EHANIDAQSGSQAPNPSTTISPGK	SPPPA	3		803.0548473	2406.141142	0.000979378	2	N	347	371
Q8VDW0	Exosome	DFQRR	ILVATNLFGR	GMDIE	2		552.3327376	1102.649875	0.001654178	5	Y	338	348
Q8VDW0	Exosome	MPSVK	VSVFFGGLSIK	KDEDV	2		577.3349459	1152.654292	0.000851441	9	N	143	154
Q8VDW0	Exosome	RFGTK	GLAVTFVSDENDAK	ILNDV	2		733.3626174	1464.709635	0.000451244	6	N	383	397
Q8VDW0	Exosome	KKDVK	GSYVSIHSSGFR	DFLLK	2		648.8207227	1295.625845	0.001763695	1	Y	35	47
Q8VDW0	Exosome	-MAE	QDVENELLDYDEDEEPQAPQESTPAPPKK	DVKGS	3		1104.507835	3310.500104	0.002727428	1	N	3	32
Q8VDW0	Exosome	-MAE	QDVENELLDYDEDEEPQAPQESTPAPPKK	DVKGS	3	[0:-17.027	1098.832168	3293.473104	0.001229886	1	N	3	32
Q8VDW0	Parental	ENDAK	ILNDVQDRFEVNVAELPEEIDISTYIEQSR	-	3		1178.925324	3533.752571	0.000451244	4	N	397	427
Q8VDW0	Parental	SEKNR	KLFDLLDVLEFNQVVIFVK	SVQRC	3		760.4403631	2278.297689	0.001699387	1	Y	275	294
Q8VDW0	Parental	EKNRK	LFDLLDVLEFNQVVIFVK	SVQRC	2		1076.109163	2150.202726	0.000451244	6	Y	276	294
Q8VDW0	Parental	KKDVK	GSYVSIHSSGFRDFLLKPELLR	AIVDC	4		631.0950226	2520.34889	0.002296037	3	Y	35	57
Q8VDW0	Parental	DFQRR	ILVATNLFGR	GMDIE	2		552.3327376	1102.649875	0.001395409	3	Y	338	348
Q8VDW0	Parental	MPSVK	VSVFFGGLSIK	KDEDV	2		577.3349459	1152.654292	0.000823681	2	N	143	154
Q8VDW0	Parental	RFGTK	GLAVTFVSDENDAK	ILNDV	2		733.3626174	1464.709635	0.000870037	2	N	383	397
Q8VDW0	Parental	ENDAK	ILNDVQDRFEVNVAELPEEIDISTY	IEQSR	3		974.4858653	2920.434196	0.002212458	4	N	397	422
Q8VE11	Exosome	DGWDR	TSQVCSLGSLLLDSYYR	TMKGF	2	C5:+57.021	981.4857807	1960.955961	0.000451244	8	N	342	359
Q8VE11	Exosome	SKSQR	LTVLEPNTASFNFK	FWRNM	2		790.9201025	1579.824605	0.000622848	3	N	479	493
Q8VE37	Exosome	ELQEK	VVQVSAGDSHTAALTEDGR	VFLWG	2		956.9721147	1911.928629	0.002453667	1	N	120	139
Q8VE37	Exosome	KVSHR	SHNTEPGLVLTLGQGDVGQLGLGESVLER	KKPAL	3		992.5197919	2974.535976	0.000451244	16	N	28	57
Q8VE37	Exosome	PGLVL	TLGQGDVGQLGLGESVLER	KKPAL	2		964.5083331	1927.001066	0.000451244	2	N	38	57
Q8VE37	Exosome	FAISR	EGHVYGFGLSNYHQLGTPGTGSCFIPQNLTSFK	NSTKS	4	C23:+57.021	904.1850844	3612.709137	0.000622848	2	N	257	290
Q8VE37	Parental	ELQEK	VVQVSAGDSHTAALTEDGR	VFLWG	2		956.9721147	1911.928629	0.000451244	3	N	120	139
Q8VE37	Parental	ELQEK	VVQVSAGDSHTAALTEDGR	VFLWG	3		638.3173432	1911.928629	0.000451244	33	N	120	139
Q8VE37	Parental	KVSHR	SHNTEPGLVLTLGQGDVGQLGLGESVLER	KKPAL	3		992.5197919	2974.535976	0.000451244	2	N	28	57
Q8VE37	Parental	PGLVL	TLGQGDVGQLGLGESVLER	KKPAL	2		964.5083331	1927.001066	0.000451244	24	N	38	57
Q8VE47	Exosome	HFMNR	ISNGGLEEGQPVDLVLSCVDNFEAR	MAINT	2	C18:+57.021	1359.655897	2717.296194	0.000451244	2	N	161	186
Q8VE47	Exosome	HFMNR	ISNGGLEEGQPVDLVLSCVDNFEAR	MAINT	3	C18:+57.021	906.7731979	2717.296194	0.000451244	4	N	161	186
Q8VE47	Parental	HFMNR	ISNGGLEEGQPVDLVLSCVDNFEAR	MAINT	3	C18:+57.021	906.7731979	2717.296194	0.000622848	1	N	161	186
Q8VE47	Parental	EYKKR	AAALPTQEAEPQEEAEVVHEDNEWGIELVSEVSEEELK	NSSGP	3		1411.999834	4232.976101	0.000451244	4	N	316	354
Q8VEE0	Exosome	VHWLR	TQFPTLDIEVDGGVGPDTVQK	CAEAG	2		1108.55822	2215.10084	0.000451244	12	N	164	185
Q8VEE0	Exosome	ASGCK	IGPSILNSDLANLGAECLR	MLDSG	2	C17:+57.021	1007.025604	2012.035609	0.000451244	20	N	6	25
Q8VEE0	Parental	VHWLR	TQFPTLDIEVDGGVGPDTVQK	CAEAG	2		1108.55822	2215.10084	0.000451244	6	N	164	185
Q8VEE0	Parental	ASGCK	IGPSILNSDLANLGAECLR	MLDSG	2	C17:+57.021	1007.025604	2012.035609	0.000451244	19	N	6	25
Q8VEE0	Parental	ASGCK	IGPSILNSDLANLGAECLR	MLDSG	3	C17:+57.021	671.6863363	2012.035609	0.000662267	2	N	6	25
Q8VEE4	Exosome	LHEAK	SENLGQGDKADYFSTVAAVVFLR	KENCM	3		829.7558501	2486.24415	0.000451244	3	N	458	481
Q8VEE4	Exosome	SGEIR	ATAFNEQVDKFFPLIEVNK	VYYFS	3		737.388439	2209.141917	0.000451244	1	N	243	262
Q8VEE4	Parental	STAAK	AYGASKPFGKPAGTGLLQPSGGTQSK	VVPIA	3		835.7752447	2504.302334	0.002519933	1	N	166	192
Q8VEE4	Parental	LHEAK	SENLGQGDKADYFSTVAAVVFLR	KENCM	3		829.7558501	2486.24415	0.000979378	2	N	458	481
Q8VEH3	Exosome	SISCK	EKDNIDITLQWLIQHSK	SRRS-	3		694.3729003	2080.095301	0.000451244	7	N	165	182
Q8VEH3	Exosome	IEASK	NELHNLLDKPQLQGIPVLVLGNKR	DLAGA	4		677.8952289	2707.549716	0.000622848	2	N	108	132
Q8VEH3	Parental	SISCK	EKDNIDITLQWLIQHSK	SRRS-	3		694.3729003	2080.095301	0.000451244	9	N	165	182
Q8VEH3	Parental	SISCK	EKDNIDITLQWLIQHSK	SRRS-	4		521.0316253	2080.095301	0.000451244	10	N	165	182
Q8VEK3	Exosome	ARKKR	NFILDQTNVSAAAQR	RKMCL	2		824.4266147	1646.837629	0.000451244	20	N	551	566
Q8VEK3	Exosome	VITCF	ANFETDEVELSYAK	NGQDL	2		808.3784645	1614.741329	0.00091018	1	N	385	399
Q8VEK3	Exosome	FKISK	EVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	3	C14:+57.021,C17:+57.021	1033.176229	3096.505287	0.000451244	12	N	412	438
Q8VEK3	Exosome	FKISK	EVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	4	C14:+57.021,C17:+57.021	775.1341218	3096.505287	0.000451244	14	N	412	438

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VEK3	Exosome	NFGQK	EKPYFPIPEDCTFIQNVPLEDR	VRGPK	2	C11:+57.021	1354.157544	2706.299488	0.000622848	3	N	438	460
Q8VEK3	Exosome	NFGQK	EKPYFPIPEDCTFIQNVPLEDR	VRGPK	3	C11:+57.021	903.1076294	2706.299488	0.000451244	42	N	438	460
Q8VEK3	Exosome	LKGIK	TCNCETEDYGEKFDENDVITCFANFETDEVELSYAK	NGQDL	3	C2:+57.021,C4:+57.021,C21:+57.021	1448.268147	4341.781041	0.000451244	13	N	363	399
Q8VEK3	Exosome	DLMDR	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	SGAGL	3	M15:+15.995	999.4762863	2995.405459	0.0007646	2	N	37	68
Q8VEK3	Exosome	VLKMK	GNFTLPEVAECFDEITY	VELQK	2	C11:+57.021	1002.948697	2003.881793	0.00091018	1	N	613	630
Q8VEK3	Exosome	YSRAK	SPQPPVEEEDEHFDDTVVCLDTYNCDLHFK	ISRDR	4	C19:+57.021,C25:+57.021	909.6451791	3634.549516	0.000451244	12	N	246	276
Q8VEK3	Exosome	EGEDE	LGDEEEGAGDENGHGEQQSQPPAAAAQQQPSQQR	GAGKE	3		1182.190562	3543.548285	0.000451244	6	N	138	172
Q8VEK3	Exosome	VLKMK	GNFTLPEVAECFDEITYVELQKEEAQK	LLEQY	3	C11:+57.021	1063.176549	3186.506247	0.001943752	2	N	613	640
Q8VEK3	Exosome	NFGQK	EKPYFPIPEDCTFIQNVPL	EDRVR	2	C11:+57.021	1154.07222	2306.128841	0.000851441	1	N	438	457
Q8VEK3	Parental	EDHGR	GYFEYIEENKYSR	AKSPQ	2		849.3944489	1696.773298	0.000451244	11	N	231	244
Q8VEK3	Parental	EDHGR	GYFEYIEENKYSR	AKSPQ	3		566.5988992	1696.773298	0.00091018	3	N	231	244
Q8VEK3	Parental	ARKKR	NFILDQTNVSAAAQR	RKMCL	2		824.4266147	1646.837629	0.000451244	34	N	551	566
Q8VEK3	Parental	VITCF	ANFETDEVELSYAK	NGQDL	2		808.3784645	1614.741329	0.000451244	39	N	385	399
Q8VEK3	Parental	GVAFK	ISKEVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	3	C17:+57.021,C20:+57.021	1142.579914	3424.716343	0.000451244	4	N	409	438
Q8VEK3	Parental	FKISK	EVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	3	C14:+57.021,C17:+57.021	1033.176229	3096.505287	0.000451244	43	N	412	438
Q8VEK3	Parental	FKISK	EVLADRPLFPHVLCHNCAVEFNFGQK	EKPYF	4	C14:+57.021,C17:+57.021	775.1341218	3096.505287	0.000451244	26	N	412	438
Q8VEK3	Parental	EAAGK	SSGPTSLFAVTVAPPGAR	QGQQQ	2		857.9602904	1713.904981	0.000451244	21	N	181	199
Q8VEK3	Parental	NFGQK	EKPYFPIPEDCTFIQNVPLEDRVR	GPKGP	3	C11:+57.021	988.1641378	2961.469013	0.000451244	11	N	438	462
Q8VEK3	Parental	NFGQK	EKPYFPIPEDCTFIQNVPLEDRVR	GPKGP	4	C11:+57.021	741.3750533	2961.469013	0.00091018	2	N	438	462
Q8VEK3	Parental	NFGQK	EKPYFPIPEDCTFIQNVPLEDR	VRGPK	2	C11:+57.021	1354.157544	2706.299488	0.000451244	41	N	438	460
Q8VEK3	Parental	NFGQK	EKPYFPIPEDCTFIQNVPLEDR	VRGPK	3	C11:+57.021	903.1076294	2706.299488	0.000451244	46	N	438	460
Q8VEK3	Parental	LKGIK	TCNCETEDYGEKFDENDVITCFANFETDEVELSYAK	NGQDL	3	C2:+57.021,C4:+57.021,C21:+57.021	1448.268147	4341.781041	0.000451244	41	N	363	399
Q8VEK3	Parental	LKGIK	TCNCETEDYGEKFDENDVITCFANFETDEVELSYAK	NGQDL	4	C2:+57.021,C4:+57.021,C21:+57.021	1086.45306	4341.781041	0.000870037	3	N	363	399
Q8VEK3	Parental	DLMDR	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	SGAGL	3		994.1446196	2979.410459	0.000451244	8	N	37	68
Q8VEK3	Parental	DLMDR	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	SGAGL	3	M15:+15.995	999.4762863	2995.405459	0.0007646	2	N	37	68
Q8VEK3	Parental	VLKMK	GNFTLPEVAECFDEITY	VELQK	2	C11:+57.021	1002.948697	2003.881793	0.000451244	24	N	613	630
Q8VEK3	Parental	YSRAK	SPQPPVEEEDEHFDDTVVCLDTYNCDLHFK	ISRDR	4	C19:+57.021,C25:+57.021	909.6451791	3634.549516	0.002296037	1	N	246	276
Q8VEK3	Parental	EGEDE	LGDEEEGAGDENGHGEQQSQPPAAAAQQQPSQQR	GAGKE	3		1182.190562	3543.548285	0.000451244	50	N	138	172
Q8VEK3	Parental	QGFQE	GEDELGDEEEGAGDENGHGEQQSQPPAAAAQQQPSQQR	GAGKE	3		1325.568426	3973.681878	0.000451244	4	N	134	172
Q8VEK3	Parental	LKGIK	TCNCETEDYGEKFDENDVITCF	ANFET	2	C2:+57.021,C4:+57.021,C21:+57.021	1373.532936	2745.050272	0.000823681	9	N	363	385
Q8VEK3	Parental	RTQKK	AEVEGKDLPEHAVLK	MKGNF	4		409.4746831	1633.867533	0.002727428	1	N	596	611
Q8VEK3	Parental	FQEGE	DELGDEEEGAGDENGHGEQQSQPPAAAAQQQPSQQR	GAGKE	3		1263.547074	3787.617821	0.000451244	4	N	136	172
Q8VEK3	Parental	HGRGY	FEYIEENKYSR	AKSPQ	2		739.3520527	1476.688505	0.000735798	1	N	233	244
Q8VEK3	Parental	NFGQK	EKPYFPIPEDCTF	IQNVP	2	C11:+57.021	821.8768147	1641.738029	0.002981883	1	N	438	451
Q8VEM8	Exosome	FGSMK	YYALCGFGGVLSCGLTHTAVVPLDLVK	CRMQV	3	C5:+57.021,C13:+57.021	970.8348099	2909.48103	0.000451244	1	N	58	85
Q8VEM8	Parental	FGSMK	YYALCGFGGVLSCGLTHTAVVPLDLVK	CRMQV	3	C5:+57.021,C13:+57.021	970.8348099	2909.48103	0.000451244	25	N	58	85
Q8VEM8	Parental	YEVFK	ALYSNILGEENTYLWR	TSLYL	2		971.489412	1940.963224	0.000622848	4	N	140	156
Q8VH51	Exosome	NVYVK	CPSIAAAIAAVNALHGR	WFAGK	3	C1:+57.021	564.6388806	1690.893242	0.000662267	1	N	477	494
Q8VH51	Parental	NVYVK	CPSIAAAIAAVNALHGR	WFAGK	3	C1:+57.021	564.6388806	1690.893242	0.000451244	29	N	477	494
Q8VH51	Parental	HVTER	TDASSASSFLDSDELERTGIDLGTTGR	LQLMA	3		934.4410958	2800.299887	0.000622848	9	N	329	356
Q8VH51	Parental	RIRPR	DLEEFFSTVGK	VRDVR	2		636.3118648	1270.60813	0.000451244	3	N	167	178
Q8VH51	Parental	KGIAY	VEFVDVSSVPLAIGLTGQR	VLGVP	2		994.0470941	1986.078588	0.000451244	26	N	198	217
Q8VH51	Parental	HVTER	TDASSASSFLDSDELER	TGIDL	2		915.4059389	1828.796278	0.000451244	18	N	329	346
Q8VHM5	Exosome	VLFVR	NLATTVTEEILEK	SFSEF	2		730.8962931	1459.776986	0.000451244	9	N	346	359
Q8VHM5	Exosome	DLDER	AIDALREFNEEGALSVLQQFK	ESDLS	3		793.4170573	2377.227772	0.000823681	1	N	63	84
Q8VHM5	Parental	ALLER	TGYTLDVTTGQR	KYGGP	2		656.3311202	1310.64664	0.000979378	2	Y	133	145
Q8VHM5	Parental	VLFVR	NLATTVTEEILEK	SFSEF	2		730.8962931	1459.776986	0.000451244	8	N	346	359
Q8VHM5	Parental	GKIPR	DLYEDELVPLFEK	AGPIW	2		805.4039509	1608.792302	0.001229886	3	N	174	187
Q8VHX6	Exosome	SDGLR	LIALLEVLSQK	RMYRK	2		613.8900854	1225.764571	0.000451244	38	Y	70	81
Q8VHX6	Exosome	SDGLR	LIALLEVLSQK	RMYRK	3		409.5959902	1225.764571	0.002019181	1	Y	70	81
Q8VHX6	Exosome	GQVGK	SADFVVEAIGTEVGTLGFSIEGPSQAKIECDDK	GDGSC	3	C30:+57.021	1157.22786	3468.660181	0.001162105	3	N	589	622
Q8VHX6	Exosome	GQVGK	SADFVVEAIGTEVGTL	GFSIE	2		804.4123073	1606.809015	0.001463592	3	N	589	605
Q8VHX6	Parental	SDGLR	LIALLEVLSQK	RMYRK	2		613.8900854	1225.764571	0.000451244	43	Y	70	81
Q8VHX6	Parental	SDGLR	LIALLEVLSQK	RMYRK	3		409.5959902	1225.764571	0.000622848	5	Y	70	81
Q8VHX6	Parental	GQVGK	SADFVVEAIGTEVGTLGFSIEGPSQAKIECDDK	GDGSC	3	C30:+57.021	1157.22786	3468.660181	0.000823681	1	N	589	622
Q8VI36	Exosome	TAMGK	TWHPEHFVCTHCQEEIGSR	NFFER	3	C9:+57.021,C12:+57.021	804.020118	2409.036954	0.000451244	5	N	375	394
Q8VI36	Exosome	GGCAR	AILENYISALNTLWHPECFVCR	ECFTP	2	C18:+57.021,C21:+57.021	1353.662042	2705.308485	0.000451244	3	N	481	503
Q8VI36	Exosome	GGCAR	AILENYISALNTLWHPECFVCR	ECFTP	3	C18:+57.021,C21:+57.021	902.7772949	2705.308485	0.000451244	26	N	481	503
Q8VI36	Exosome	KQLNK	GTFKEQNDKPYCQSCFVK	LFC-	3	C12:+57.021,C15:+57.021	746.0104484	2235.007945	0.000979378	2	N	570	588
Q8VI36	Parental	TAMGK	TWHPEHFVCTHCQEEIGSR	NFFER	2	C9:+57.021,C12:+57.021	1205.526277	2409.036954	0.000451244	4	N	375	394
Q8VI36	Parental	TAMGK	TWHPEHFVCTHCQEEIGSR	NFFER	3	C9:+57.021,C12:+57.021	804.020118	2409.036954	0.000451244	9	N	375	394

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q8VI36	Parental	TAMGK	TWHPEHFVCTHCQEEIGSR	NFFER	4	C9:+57.021,C12:+57.021	603.2670385	2409.036954	0.000451244	12	N	375	394
Q8VI36	Parental	LFSPR	CYYCNGPILDKVVTALDR	TWHPE	2	C1:+57.021,C4:+57.021	1079.027059	2156.038517	0.000622848	1	N	416	434
Q8VI36	Parental	LFSPR	CYYCNGPILDKVVTALDR	TWHPE	3	C1:+57.021,C4:+57.021	719.6873057	2156.038517	0.000622848	1	N	416	434
Q8VI36	Parental	LFSPR	CYYCNGPILDKVVTALDR	TWHPE	2	[0:-17.027,C1:+57.021,C4:+57.021	1070.513559	2139.011517	0.000451244	8	N	416	434
Q8VI36	Parental	GGCAR	AILENYISALNTLWHPECFVCR	ECFTP	2	C18:+57.021,C21:+57.021	1353.662042	2705.308485	0.000451244	11	N	481	503
Q8VI36	Parental	GGCAR	AILENYISALNTLWHPECFVCR	ECFTP	3	C18:+57.021,C21:+57.021	902.7772949	2705.308485	0.000451244	27	N	481	503
Q8VI36	Parental	KQLNK	GTFKEQNDKPYCQSCFVK	LFC-	3	C12:+57.021,C15:+57.021	746.0104484	2235.007945	0.000451244	7	N	570	588
Q8VI36	Parental	TALDR	TWHPEHFFCAQCGAFFGPEGFHEKDGK	AYCRK	3	C9:+57.021,C12:+57.021	1075.136322	3222.385566	0.000451244	4	N	434	461
Q8VI36	Parental	TALDR	TWHPEHFFCAQCGAFFGPEGFHEKDGK	AYCRK	4	C9:+57.021,C12:+57.021	806.6041915	3222.385566	0.000622848	7	N	434	461
Q8VI36	Parental	NFFER	DGQPYCEKDYHSLFSPR	CYYCN	2	C6:+57.021	1049.968286	2097.920973	0.000451244	6	N	399	416
Q8VI36	Parental	NFFER	DGQPYCEKDYHSLFSPR	CYYCN	3	C6:+57.021	700.314791	2097.920973	0.002145581	1	N	399	416
Q8VI36	Parental	PSGSR	YAHQQPPSPLPVYSSSAK	NSSAS	2		978.9948615	1955.974123	0.002981883	1	N	75	93
Q8VI36	Parental	RNGGR	GLEDVRPSVESLLDELESSVPSPVPAITVNQGEMSSPQR	VTSSQ	3		1383.693911	4148.058333	0.001763695	1	N	208	247
Q8VI36	Parental	TALDR	TWHPEHFFCAQCGAFFGPEGFHEK	DGKAY	4	C9:+57.021,C12:+57.021	731.568349	2922.242196	0.000622848	4	N	434	458
Q8VI36	Parental	LFSPR	CYYCNGPILDK	VVTAL	2	C1:+57.021,C4:+57.021	701.8101891	1401.604778	0.000451244	3	N	416	427
Q8VI93	Exosome	GTAWR	WDVLAQEAESSFSQQCFK	QASGV	2	C16:+57.021	1080.489052	2158.962504	0.000451244	7	N	310	328
Q8VI93	Exosome	ILQFR	LASADGEHWIDVSLVPAFDVLGQPR	SGVKP	3		898.1296876	2691.365663	0.001329271	2	N	131	156
Q8VI93	Exosome	ALQGR	SDADLVVFLSCFR	QFSEQ	2	C11:+57.021	764.877149	1527.738698	0.000451244	3	N	865	878
Q8VI93	Exosome	QQCFK	QASGVLVQPWEGPGLPR	AGILD	2		895.9815571	1789.947514	0.000451244	2	N	328	345
Q8VI93	Exosome	RPDPR	VYTDLIHSCSNAGEFSTCFTELQR	DFITS	3	C9:+57.021,C18:+57.021	945.7621503	2834.263051	0.001871652	1	N	959	983
Q8VI93	Exosome	LKRPR	PVILDPADPTWDVGNGTAWR	WDVLA	2		1090.542707	2179.069815	0.002080925	1	N	290	310
Q8VIJ6	Exosome	TQRCR	LFVGNLPADITEDEFKR	LFAKY	3		655.3428296	1963.005089	0.000451244	6	N	290	307
Q8VIJ6	Exosome	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3	C1:+57.021	1199.60656	3595.796281	0.000451244	16	N	422	454
Q8VIJ6	Exosome	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3	[0:-17.027,C1:+57.021	1193.930894	3578.769281	0.000451244	2	N	422	454
Q8VIJ6	Exosome	NLSPY	VSNELLEEAFSQFGPIER	AVVIV	2		1033.015991	2064.016382	0.000451244	4	N	373	391
Q8VIJ6	Exosome	ALSVR	NLSPYVSNELLEEAFSQFGPIER	AVVIV	2		1320.153547	2638.291495	0.000451244	2	N	368	391
Q8VIJ6	Exosome	ALSVR	NLSPYVSNELLEEAFSQFGPIER	AVVIV	3		880.4382982	2638.291495	0.000451244	18	N	368	391
Q8VIJ6	Exosome	TTTPR	PVIVEPLEQLDDEDGLPEK	LAQKN	2		1068.041871	2134.068143	0.001591523	1	N	435	454
Q8VIJ6	Parental	TQRCR	LFVGNLPADITEDEFKR	LFAKY	2		982.5103444	1963.005089	0.000622848	1	N	290	307
Q8VIJ6	Parental	TQRCR	LFVGNLPADITEDEFKR	LFAKY	3		655.3428296	1963.005089	0.000451244	9	N	290	307
Q8VIJ6	Parental	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEKLAQK	NPMYQ	3	C1:+39.994	1340.689133	4019.044	0.000451244	7	N	422	458
Q8VIJ6	Parental	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEKLAQK	NPMYQ	4	C1:+57.021	1010.02555	4036.071	0.000735798	4	N	422	458
Q8VIJ6	Parental	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEKLAQK	NPMYQ	3	[0:-17.027,C1:+57.021	1340.689133	4019.044	0.000622848	5	N	422	458
Q8VIJ6	Parental	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3	C1:+39.994	1193.930894	3578.769281	0.000451244	8	N	422	454
Q8VIJ6	Parental	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3	C1:+57.021	1199.60656	3595.796281	0.000451244	38	N	422	454
Q8VIJ6	Parental	KAFER	CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3	[0:-17.027,C1:+57.021	1193.930894	3578.769281	0.000451244	13	N	422	454
Q8VIJ6	Parental	NLSPY	VSNELLEEAFSQFGPIER	AVVIV	2		1033.015991	2064.016382	0.000451244	24	N	373	391
Q8VIJ6	Parental	ALSVR	NLSPYVSNELLEEAFSQFGPIER	AVVIV	2		1320.153547	2638.291495	0.000451244	36	N	368	391
Q8VIJ6	Parental	ALSVR	NLSPYVSNELLEEAFSQFGPIER	AVVIV	3		880.4382982	2638.291495	0.000451244	22	N	368	391
Q8VIJ6	Parental	AALSV	RNLSPYVSNELLEEAFSQFGPIER	AVVIV	3		932.4720019	2794.392606	0.000451244	5	N	367	391
Q8VIJ6	Parental	TTTPR	PVIVEPLEQLDDEDGLPEK	LAQKN	2		1068.041871	2134.068143	0.000451244	21	N	435	454
Q8VIJ6	Parental	TPRPV	IVEPLEQLDDEDGLPEK	LAQKN	2		969.9812825	1937.946965	0.000451244	6	N	437	454
Q8VIJ6	Parental	SEGVF	LLTTTPRPVIVEPLEQLDDEDGLPEK	LAQKN	3		973.1855273	2916.533182	0.000451244	9	N	428	454
Q8VIJ6	Parental	TQRCR	LFVGNLPADITEDEFK	RLFAK	2		904.4597889	1806.903978	0.000622848	7	N	290	306
Q91UZ5	Exosome	ASGAK	CVLTHSPTWIIDPIDGTCNFVHR	FPTVA	3	C1:+39.994,C18:+57.021	907.7686491	2720.282547	0.000451244	4	N	91	114
Q91UZ5	Exosome	ASGAK	CVLTHSPTWIIDPIDGTCNFVHR	FPTVA	3	[0:-	907.7686491	2720.282547	0.001229886	3	N	91	114
Q91UZ5	Exosome	RVSTK	TSAADLVTETDHRVEDLIVSELR	KRFPS	3		857.1088407	2568.303122	0.000451244	1	N	49	72
Q91UZ5	Exosome	RVSTK	TSAADLVTETDHRVEDLIVSELR	KRFPS	4		643.0835805	2568.303122	0.001763695	1	N	49	72
Q91UZ5	Parental	ASGAK	CVLTHSPTWIIDPIDGTCNFVHR	FPTVA	3	[0:-	907.7686491	2720.282547	0.001463592	1	N	91	114
Q91UZ5	Parental	RVSTK	TSAADLVTETDHRVEDLIVSELR	KRFPS	3		857.1088407	2568.303122	0.000622848	3	N	49	72
Q91UZ5	Parental	RVSTK	TSAADLVTETDHRVEDLIVSELR	KRFPS	4		643.0835805	2568.303122	0.001229886	3	N	49	72
Q91V12	Exosome	KNVDK	VLEVPPIVYLR	QEQEE	2		649.3980776	1296.780555	0.001264573	4	N	173	184
Q91V12	Exosome	KLTNK	ATLWYVPLSLK	NVDKV	2		645.876978	1289.738356	0.000622848	9	N	158	169
Q91V41	Exosome	EAAKK	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	3		1050.857467	3149.549	0.000451244	11	N	171	201
Q91V41	Exosome	EAAKK	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	4		788.39505	3149.549	0.000451244	13	N	171	201
Q91V41	Exosome	LEAAK	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	4		820.4187908	3277.643963	0.000451244	6	N	170	201
Q91V41	Exosome	LTDAR	NLTNPNTVIILIGNK	ADLEA	2		812.4755763	1622.935553	0.000451244	13	N	110	125
Q91V41	Exosome	YEEAK	QFAEENGLLFLEASAK	TGENV	2		883.952131	1765.888662	0.000451244	6	N	140	156
Q91V41	Exosome	EASAK	TGENVEDAFLEAAKK	IYQNI	3		541.2743042	1620.799513	0.000451244	8	N	156	171
Q91V41	Exosome	VSGQK	IKLQIWDTAGQER	FRAVT	3		519.9514958	1556.831087	0.000735798	1	Y	59	72
Q91V41	Parental	EAAKK	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	3		1050.857467	3149.549	0.000451244	15	N	171	201
Q91V41	Parental	EAAKK	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	4		788.39505	3149.549	0.000622848	8	N	171	201
Q91V41	Parental	LEAAK	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	LTSEP	4		820.4187908	3277.643963	0.0025889	1	N	170	201
Q91V41	Parental	LTDAR	NLTNPNTVIILIGNK	ADLEA	2		812.4755763	1622.935553	0.000451244	4	N	110	125
Q91V41	Parental	GQKIK	LQIWDTAGQER	FRAVT	2		658.8338301	1315.65206	0.001591523	2	Y	61	72

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91V41	Parental	EASAK	TGENVEDAFLEAAKK	IYQNI	3		541.2743042	1620.799513	0.000451244	6	N	156	171
Q91V55	Exosome	KLFGK	WSTDDVQINDISLQDYIAVK	EKYAK	2		1162.076777	2322.137954	0.000451244	11	N	22	42
Q91V55	Exosome	FRNIK	TIAECLADELINAAK	GSSNS	2	C5:+57.021	816.4193781	1630.823156	0.000451244	9	N	167	182
Q91V55	Exosome	FRNIK	TIAECLADELINAAK	GSSNS	3	C5:+57.021	544.6155187	1630.823156	0.000451244	2	N	167	182
Q91V55	Exosome	SPLRR	VNQAIWLLCTGAR	EAAFR	2	C9:+57.021	751.4011257	1500.786651	0.000451244	2	N	146	159
Q91V55	Parental	KLFGK	WSTDDVQINDISLQDYIAVK	EKYAK	2		1162.076777	2322.137954	0.000451244	20	N	22	42
Q91V55	Parental	FRNIK	TIAECLADELINAAK	GSSNS	2	C5:+57.021	816.4193781	1630.823156	0.000451244	37	N	167	182
Q91V55	Parental	FRNIK	TIAECLADELINAAK	GSSNS	3	C5:+57.021	544.6155187	1630.823156	0.000451244	29	N	167	182
Q91V55	Parental	IIHLL	TGENPLQVLVNAIINSGPR	EDSTR	2		996.5477926	1991.079985	0.000451244	20	N	103	122
Q91V55	Parental	IIHLL	TGENPLQVLVNAIINSGPR	EDSTR	3		664.7011284	1991.079985	0.000451244	22	N	103	122
Q91V55	Parental	IIHLL	TGENPLQVLVNAIINSGPREDSTR	IGRAG	3		860.7845799	2579.33034	0.000823681	1	N	103	127
Q91V55	Parental	KLFGK	WSTDDVQINDISL	QDYIA	2		753.3600747	1504.704549	0.0025889	1	N	22	35
Q91V92	Exosome	VDMLR	NCGSFTREEADEYVDIGALNGIFVLGR	SMGFI	3	C2:+57.021	1001.482307	3001.42352	0.000451244	10	N	1028	1055
Q91V92	Exosome	VFVPR	SFDELGEIIQSVYEDLVAK	GAIVP	2		1078.044414	2154.073228	0.000451244	29	N	778	797
Q91V92	Exosome	VFVPR	SFDELGEIIQSVYEDLVAK	GAIVP	3		719.0322094	2154.073228	0.000451244	17	N	778	797
Q91V92	Exosome	KRRGK	LGLVGVNLSLDGVK	SWLKP	2		692.414456	1382.813312	0.000451244	22	N	68	82
Q91V92	Exosome	YAQIR	TIAIIAEGIPEALTR	KLIKK	2		784.4568522	1566.898104	0.000451244	31	N	582	597
Q91V92	Exosome	KGFLK	NFLIEPFVPHSQAEEFYVCIYATR	EGDYV	3	C19:+57.021	977.4779452	2929.410436	0.000823681	2	N	103	127
Q91V92	Exosome	GSFTR	EEADEYVDIGALNGIFVLGR	SMGFI	2		1090.547655	2179.079711	0.000451244	33	N	1035	1055
Q91V92	Exosome	GSFTR	EEADEYVDIGALNGIFVLGR	SMGFI	3		727.3677035	2179.079711	0.000735798	1	N	1035	1055
Q91V92	Exosome	ARAGK	DLVSSLTSGLLTIGDR	FGGAL	2		823.952131	1645.888662	0.000451244	37	N	908	924
Q91V92	Exosome	ARAGK	DLVSSLTSGLLTIGDR	FGGAL	3		549.637354	1645.888662	0.000451244	20	N	908	924
Q91V92	Exosome	KDFVK	QHFPATPLLDYALEVEK	ITTSK	3		657.6794418	1970.014925	0.000451244	30	N	985	1002
Q91V92	Exosome	PEDKK	EVLASFISGLFNFYEDLYFTYLEINPLVVTK	DGVYI	3		1215.63253	3643.874189	0.000451244	6	N	178	209
Q91V92	Exosome	ADAMK	KHPEVDVLINFASLR	SAYDS	3		579.9935836	1736.957351	0.000451244	6	N	551	566
Q91V92	Exosome	NIISR	TTDGVYEGVAIGGDRYPGSTF	MDHVL	2		1081.505987	2160.996375	0.000451244	9	N	666	687
Q91V92	Exosome	FKYAR	VTPDTDWAHLLQDHPWLLSQSLVVKPDQLIK	RRGKL	3		1198.310784	3591.908952	0.001329271	1	N	33	64
Q91V92	Exosome	FKYAR	VTPDTDWAHLLQDHPWLLSQSLVVKPDQLIK	RRGKL	4		898.985038	3591.908952	0.000823681	5	N	33	64
Q91V92	Exosome	KADQK	GVTIIGPATVGGIKPGCFK	IGNTG	2	C17:+57.021	936.5245119	1871.033424	0.000622848	3	N	606	625
Q91V92	Exosome	ASVVY	SDTICDLGGVNELANYGEYSGAPSEQQTYDYAK	TILSL	3	C5:+57.021	1205.862017	3614.562652	0.000451244	4	N	288	321
Q91V92	Exosome	CATMF	SSEVQFGHAGACANQASETAVAK	NQALK	3	C12:+57.021	774.0259689	2319.054507	0.000622848	5	N	742	765
Q91V92	Exosome	PPFGR	EAYPEEAYIADLDAK	SGASL	2		849.3993969	1696.783194	0.000735798	3	N	244	259
Q91V92	Exosome	IICAR	AGKDLVSSLTSGLLTIGDR	FGGAL	2		952.0289014	1902.042203	0.000451244	4	N	905	924
Q91V92	Exosome	IICAR	AGKDLVSSLTSGLLTIGDR	FGGAL	3		635.0218676	1902.042203	0.000451244	10	N	905	924
Q91V92	Exosome	LVVTK	DGVYILDLAAK	VDATA	2		589.3273179	1176.639036	0.000823681	7	N	209	220
Q91V92	Exosome	DYICK	VKWGDIEFPPPFGR	EAYPE	3		548.9564697	1643.846009	0.001699387	1	N	230	244
Q91V92	Parental	VDMLR	NCGSFTREEADEYVDIGALNGIFVLGR	SMGFI	3	C2:+57.021	1001.482307	3001.42352	0.000451244	14	N	1028	1055
Q91V92	Parental	VFVPR	SFDELGEIIQSVYEDLVAK	GAIVP	2		1078.044414	2154.073228	0.000451244	31	N	778	797
Q91V92	Parental	VFVPR	SFDELGEIIQSVYEDLVAK	GAIVP	3		719.0322094	2154.073228	0.000451244	22	N	778	797
Q91V92	Parental	YAQIR	TIAIIAEGIPEALTR	KLIKK	2		784.4568522	1566.898104	0.000735798	2	N	582	597
Q91V92	Parental	GSFTR	EEADEYVDIGALNGIFVLGR	SMGFI	2		1090.547655	2179.079711	0.000451244	18	N	1035	1055
Q91V92	Parental	ARAGK	DLVSSLTSGLLTIGDR	FGGAL	2		823.952131	1645.888662	0.000451244	8	N	908	924
Q91V92	Parental	ARAGK	DLVSSLTSGLLTIGDR	FGGAL	3		549.637354	1645.888662	0.000451244	6	N	908	924
Q91V92	Parental	KDFVK	QHFPATPLLDYALEVEK	ITTSK	3		657.6794418	1970.014925	0.000451244	10	N	985	1002
Q91V92	Parental	PEDKK	EVLASFISGLFNFYEDLYFTYLEINPLVVTK	DGVYI	3		1215.63253	3643.874189	0.000451244	4	N	178	209
Q91V92	Parental	NIISR	TTDGVYEGVAIGGDRYPGSTF	MDHVL	2		1081.505987	2160.996375	0.000451244	14	N	666	687
Q91V92	Parental	ASVVY	SDTICDLGGVNELANYGEYSGAPSEQQTYDYAK	TILSL	3	C5:+57.021	1205.862017	3614.562652	0.000451244	16	N	288	321
Q91V92	Parental	CATMF	SSEVQFGHAGACANQASETAVAK	NQALK	2	C12:+57.021	1160.535053	2319.054507	0.000451244	3	N	742	765
Q91V92	Parental	CATMF	SSEVQFGHAGACANQASETAVAK	NQALK	3	C12:+57.021	774.0259689	2319.054507	0.000451244	12	N	742	765
Q91VC3	Exosome	EDLLR	GIYAYGFEKPSAIQQR	AIKQI	2		914.4735649	1826.93153	0.000451244	5	Y	51	67
Q91VC3	Exosome	EDLLR	GIYAYGFEKPSAIQQR	AIKQI	3		609.9849766	1826.93153	0.000451244	45	Y	51	67
Q91VC3	Exosome	DVWAR	GLDVPQVSLIINYDLPNNR	ELYIH	2		1070.574007	2139.132415	0.000451244	26	N	339	358
Q91VC3	Exosome	REEWK	FDTLCDLYDTLTITQAVIFCNTK	RKVDW	2	C5:+57.021,C20:+57.021	1376.664113	2751.312627	0.000451244	6	N	264	287
Q91VC3	Exosome	REEWK	FDTLCDLYDTLTITQAVIFCNTK	RKVDW	3	C5:+57.021,C20:+57.021	918.1120089	2751.312627	0.000451244	5	N	264	287
Q91VC3	Exosome	LRGIY	AYGFEKPSAIQQR	AIKQI	2		747.8891367	1493.762673	0.001763695	1	Y	54	67
Q91VC3	Exosome	GEDIR	KLDYGQHVVAGTPGR	VFDMI	3		533.2868785	1596.837235	0.001463592	2	N	151	166
Q91VC3	Exosome	EDIRK	LDYGQHVVAGTPGR	VFDMI	3		490.5885574	1468.742272	0.000823681	1	N	152	166
Q91VC3	Parental	EDLLR	GIYAYGFEKPSAIQQR	AIKQI	2		914.4735649	1826.93153	0.000451244	15	Y	51	67
Q91VC3	Parental	EDLLR	GIYAYGFEKPSAIQQR	AIKQI	3		609.9849766	1826.93153	0.000451244	37	Y	51	67
Q91VC3	Parental	DVWAR	GLDVPQVSLIINYDLPNNR	ELYIH	2		1070.574007	2139.132415	0.000451244	22	N	339	358
Q91VC3	Parental	REEWK	FDTLCDLYDTLTITQAVIFCNTK	RKVDW	2	C5:+57.021,C20:+57.021	1376.664113	2751.312627	0.001229886	1	N	264	287
Q91VC3	Parental	REEWK	FDTLCDLYDTLTITQAVIFCNTK	RKVDW	3	C5:+57.021,C20:+57.021	918.1120089	2751.312627	0.000451244	14	N	264	287
Q91VC3	Parental	DVWAR	GLDVPQVSLIINYDLPNNRELY	IHRIG	2		1273.169	2544.322401	0.000870037	2	N	339	361
Q91VD9	Exosome	WKIIR	ALSEIAGITLPYDTLDQVR	NRLEE	2		1038.055116	2074.094632	0.000622848	1	N	624	643
Q91VD9	Exosome	SELAK	LVNQEVLADPLVPPQLTIK	DFYMT	2		1044.109694	2086.203789	0.001162105	2	N	673	692

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91VD9	Exosome	VRNEK	GLLTYTSWEDALSR	VAGML	2		806.4048166	1610.794033	0.002145581	1	N	311	325
Q91VD9	Parental	WKIIR	ALSEIAGITLPYDTLDQVR	NRLEE	2		1038.055116	2074.094632	0.000451244	21	N	624	643
Q91VD9	Parental	SELAK	LVNQEVLADPLVPPQLTIK	DFYMT	2		1044.109694	2086.203789	0.000451244	22	N	673	692
Q91VD9	Parental	PNLVR	YDDIEETNYFQQASELAK	LVNQE	2		1082.490003	2162.964406	0.001352548	2	N	655	673
Q91VE0	Parental	TELRK	EGFDPSVVKDPLFYLDAR	KGCYV	3		690.0182346	2067.031304	0.000451244	1	N	603	621
Q91VE0	Parental	RHPDK	TALIFEGTDTHWTFR	QLDEY	3		598.9656935	1793.873681	0.001162105	1	N	90	105
Q91VE0	Parental	HWTFR	QLDEYSSSVANFLQAR	GLASG	2		914.4477441	1826.879888	0.000451244	3	N	105	121
Q91VH2	Exosome	QKIGK	ALQSLAAVFSSSGYQGETDLNDAITEAGK	TYEEI	3		981.8126411	2942.414523	0.000451244	6	N	440	469
Q91VH2	Exosome	NHEYK	GFLGCFPDIIGAHK	GAIEK	3	C5:+57.021	511.2627511	1530.764853	0.002727428	1	N	497	511
Q91VH6	Exosome	RVVCR	EASHAGSWYTASGPQLNAQLEGWLSQVQSTK	RPARA	3		1111.204644	3330.590531	0.000451244	13	N	8	39
Q91VH6	Exosome	GQRFR	YSYYDESQGEIYR	SIEHL	2		836.8604389	1671.705278	0.000451244	9	N	198	211
Q91VH6	Exosome	TICGR	HPIGVLLNAITELQK	NGMNM	3		549.3265627	1644.956288	0.000451244	12	N	246	261
Q91VH6	Exosome	KLFSK	YLADPSNLFVVSSDFCHWGQR	FRYSY	3	C16:+57.021	833.390471	2497.148013	0.002981883	1	N	175	196
Q91VI7	Exosome	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	C1:+39.994	1078.554501	2155.093401	0.001654178	1	N	39	59
Q91VI7	Exosome	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	C1:+57.021	1087.068001	2172.120401	0.000451244	5	N	39	59
Q91VI7	Exosome	LTEVR	CKDISSAVQANPALTELSLR	TNELG	3	C1:+57.021	725.0479338	2172.120401	0.002296037	1	N	39	59
Q91VI7	Exosome	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	[0:-17.027,C1:+57.021	1078.554501	2155.093401	0.000451244	14	N	39	59
Q91VI7	Exosome	SLWIK	TCSLTAASCPYFCSVLTK	SRSLL	2	C2:+57.021,C9:+57.021,C13:+57.021	1033.473039	2064.930478	0.000451244	33	N	316	334
Q91VI7	Exosome	ELSLR	TNELGDGGVGLVLQGLQNPTCK	IQKLS	2	C21:+57.021	1135.57619	2269.13678	0.000451244	34	N	59	81
Q91VI7	Exosome	ELSLR	TNELGDGGVGLVLQGLQNPTCK	IQKLS	3	C21:+57.021	757.3867266	2269.13678	0.000451244	8	N	59	81
Q91VI7	Exosome	LSSNK	LGNAGIAALCPGLLLPSCK	LRTLW	2	C10:+57.021,C18:+57.021	963.0210478	1924.026496	0.000451244	22	N	233	252
Q91VI7	Exosome	CRLEK	LQLEYCNLTATSCEPLASVLR	VKADF	2	C6:+57.021,C13:+57.021	1219.606401	2437.197203	0.000451244	40	N	141	162
Q91VI7	Exosome	CRLEK	LQLEYCNLTATSCEPLASVLR	VKADF	3	C6:+57.021,C13:+57.021	813.4068676	2437.197203	0.000451244	22	N	141	162
Q91VI7	Exosome	DTVLR	ELWLGDCDVTNSGCSSLANVLLANR	SLREL	2	C7:+57.021,C14:+57.021	1382.655143	2763.294685	0.000451244	26	N	368	393
Q91VI7	Exosome	DTVLR	ELWLGDCDVTNSGCSSLANVLLANR	SLREL	3	C7:+57.021,C14:+57.021	922.1060284	2763.294685	0.000451244	7	N	368	393
Q91VI7	Exosome	LSDAR	WTELLPLIQQYEVVR	LDDCG	2		944.0228907	1886.030181	0.000622848	9	N	14	29
Q91VI7	Exosome	LSDAR	WTELLPLIQQYEVVR	LDDCG	3		629.6845271	1886.030181	0.000451244	2	N	14	29
Q91VI7	Exosome	DEGAR	LLCESLLEPGCQLESLWIK	TCSLT	2	C3:+57.021,C11:+57.021	1144.586949	2287.158298	0.000451244	23	N	297	316
Q91VI7	Exosome	DEGAR	LLCESLLEPGCQLESLWIK	TCSLT	3	C3:+57.021,C11:+57.021	763.3938993	2287.158298	0.000451244	11	N	297	316
Q91VI7	Exosome	KQSLK	ELSLASNELKDEGAR	LLCES	2		816.4159126	1630.816225	0.000451244	9	N	282	297
Q91VI7	Exosome	CKIQK	LSLQNCGLTEAGCGILPGMLR	SLSTL	2	C6:+57.021,C13:+57.021	1130.566026	2259.116451	0.000451244	4	N	84	105
Q91VI7	Exosome	EVRCK	DISSAVQANPALTELSLR	TNELG	2		943.0054263	1883.995253	0.000451244	21	N	41	59
Q91VI7	Exosome	DAGLK	LLCEGLQDPQCR	LEKLQ	2	C3:+57.021,C11:+57.021	744.850377	1487.685154	0.001463592	3	N	126	138
Q91VI7	Exosome	CQGLK	DSACQLESLKLENCGITAANCK	DLCDV	2	C4:+57.021,C14:+57.021,C21:+57.021	1241.572001	2481.128403	0.000451244	4	N	190	212
Q91VI7	Exosome	CQGLK	DSACQLESLKLENCGITAANCK	DLCDV	3	C4:+57.021,C14:+57.021,C21:+57.021	828.0506009	2481.128403	0.000451244	13	N	190	212
Q91VI7	Exosome	LESLK	QPSCTLQQLVLYDIYWTNEVEEQLR	ALEEE	3	C4:+57.021	1042.513495	3124.517086	0.000698008	4	N	418	443
Q91VI7	Exosome	KADFK	ELVLSNNDLHEPGVR	ILCQG	2		846.4397221	1690.863844	0.000451244	15	N	168	183
Q91VI7	Exosome	VVASK	ASLQELDLSSNK	LGNAG	2		652.8387781	1303.661956	0.000451244	16	N	221	233
Q91VI7	Exosome	SCKLR	TLWLWECDITAEGCKDLCR	VLRAK	3	C7:+57.021,C14:+57.021,C18:+57.021	809.3694937	2425.085081	0.000451244	6	N	254	273
Q91VI7	Exosome	LTKSR	SLLELQMSSNPLGDEGVQELCK	ALSQP	2	C21:+57.021	1224.093556	2446.171511	0.000662267	1	N	336	358
Q91VI7	Exosome	LTKSR	SLLELQMSSNPLGDEGVQELCK	ALSQP	2	M7:+15.995,C21:+57.021	1232.091056	2462.166511	0.000622848	4	N	336	358
Q91VI7	Parental	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	C1:+39.994	1078.554501	2155.093401	0.000979378	1	N	39	59
Q91VI7	Parental	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	C1:+57.021	1087.068001	2172.120401	0.000451244	24	N	39	59
Q91VI7	Parental	LTEVR	CKDISSAVQANPALTELSLR	TNELG	3	C1:+57.021	725.0479338	2172.120401	0.000622848	2	N	39	59
Q91VI7	Parental	LTEVR	CKDISSAVQANPALTELSLR	TNELG	2	[0:-17.027,C1:+57.021	1078.554501	2155.093401	0.000451244	26	N	39	59
Q91VI7	Parental	SLWIK	TCSLTAASCPYFCSVLTK	SRSLL	2	C2:+57.021,C9:+57.021,C13:+57.021	1033.473039	2064.930478	0.000451244	36	N	316	334
Q91VI7	Parental	ELSLR	TNELGDGGVGLVLQGLQNPTCK	IQKLS	2	C21:+57.021	1135.57619	2269.13678	0.000451244	45	N	59	81
Q91VI7	Parental	ELSLR	TNELGDGGVGLVLQGLQNPTCK	IQKLS	3	C21:+57.021	757.3867266	2269.13678	0.000451244	5	N	59	81
Q91VI7	Parental	LSSNK	LGNAGIAALCPGLLLPSCK	LRTLW	2	C10:+57.021,C18:+57.021	963.0210478	1924.026496	0.000451244	18	N	233	252
Q91VI7	Parental	CRLEK	LQLEYCNLTATSCEPLASVLR	VKADF	2	C6:+57.021,C13:+57.021	1219.606401	2437.197203	0.000451244	49	N	141	162
Q91VI7	Parental	CRLEK	LQLEYCNLTATSCEPLASVLR	VKADF	3	C6:+57.021,C13:+57.021	813.4068676	2437.197203	0.000451244	12	N	141	162
Q91VI7	Parental	VVASK	ASLQELDLSSNKLGNAGIAALCPGLLLPSCK	LRTLW	3	C22:+57.021,C30:+57.021	1070.900431	3209.677892	0.000451244	12	N	221	252
Q91VI7	Parental	DTVLR	ELWLGDCDVTNSGCSSLANVLLANR	SLREL	2	C7:+57.021,C14:+57.021	1382.655143	2763.294685	0.000451244	32	N	368	393
Q91VI7	Parental	DTVLR	ELWLGDCDVTNSGCSSLANVLLANR	SLREL	3	C7:+57.021,C14:+57.021	922.1060284	2763.294685	0.000451244	16	N	368	393
Q91VI7	Parental	LSDAR	WTELLPLIQQYEVVR	LDDCG	2		944.0228907	1886.030181	0.000451244	21	N	14	29
Q91VI7	Parental	LSDAR	WTELLPLIQQYEVVR	LDDCG	3		629.6845271	1886.030181	0.000622848	3	N	14	29
Q91VI7	Parental	DEGAR	LLCESLLEPGCQLESLWIK	TCSLT	2	C3:+57.021,C11:+57.021	1144.586949	2287.158298	0.000451244	23	N	297	316
Q91VI7	Parental	DEGAR	LLCESLLEPGCQLESLWIK	TCSLT	3	C3:+57.021,C11:+57.021	763.3938993	2287.158298	0.000451244	12	N	297	316
Q91VI7	Parental	KQSLK	ELSLASNELKDEGAR	LLCES	2		816.4159126	1630.816225	0.000451244	10	N	282	297
Q91VI7	Parental	CKIQK	LSLQNCGLTEAGCGILPGMLR	SLSTL	2	C6:+57.021,C13:+57.021	1130.566026	2259.116451	0.001162105	3	N	84	105

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91VI7	Parental	EVRCK	DISSAVQANPALTELSLR	TNELG	2		943.0054263	1883.995253	0.000451244	20	N	41	59
Q91VI7	Parental	DAGLK	LLCEGLQDPQCR	LEKLQ	2	C3:+57.021,C11:+57.021	744.850377	1487.685154	0.000451244	18	N	126	138
Q91VI7	Parental	CQGLK	DSACQLESLKLENCGITAANCK	DLCDV	2	C4:+57.021,C14:+57.021,C21:+57.021	1241.572001	2481.128403	0.000451244	6	N	190	212
Q91VI7	Parental	LESLK	QPSCTLQQLVLYDIYWTNEVEEQLR	ALEEE	3	C4:+57.021	1042.513495	3124.517086	0.000451244	13	N	418	443
Q91VI7	Parental	LESLK	QPSCTLQQLVLYDIYWTNEVEEQLR	ALEEE	3	Q1:-17.027,C4:+57.021	1036.837829	3107.490086	0.001352548	2	N	418	443
Q91VI7	Parental	KADFK	ELVLSNNDLHEPGVR	ILCQG	2		846.4397221	1690.863844	0.000451244	13	N	168	183
Q91VI7	Parental	KADFK	ELVLSNNDLHEPGVR	ILCQG	3		564.6290814	1690.863844	0.001654178	1	N	168	183
Q91VI7	Parental	VVASK	ASLQELDLSSNK	LGNAG	2		652.8387781	1303.661956	0.000451244	8	N	221	233
Q91VI7	Parental	SCKLR	TLWLWECDITAEGCKDLCR	VLRAK	2	C7:+57.021,C14:+57.021,C18:+57.021	1213.550341	2425.085081	0.000451244	5	N	254	273
Q91VI7	Parental	SCKLR	TLWLWECDITAEGCKDLCR	VLRAK	3	C7:+57.021,C14:+57.021,C18:+57.021	809.3694937	2425.085081	0.000637154	3	N	254	273
Q91VI7	Parental	DEGAR	LLCESLLEPGCQLESLWIKTCSLTAASCPYFCSVLTK	SRSLL	3	C3:+57.021,C11:+57.021,C21:+57.021,C28:+57.021,C32:+57.021	1445.700539	4334.078216	0.000451244	3	N	297	334
Q91VI7	Parental	SCKLR	TLWLWECDITAEGCK	DLCRV	2	C7:+57.021,C14:+57.021	941.4291886	1880.842777	0.000451244	6	N	254	269
Q91VI7	Parental	QELCK	ALSQPDTVLR	ELWLG	2		550.3094595	1098.603319	0.002296037	1	N	358	368
Q91VJ4	Exosome	SIEIK	SIDDTSNFDEFPESDILKPTVTTSSHPETDYK	NKDWV	3		1205.888604	3614.642411	0.000451244	6	N	402	434
Q91VJ4	Exosome	SIEIK	SIDDTSNFDEFPESDILKPTVTTSSHPETDYK	NKDWV	4		904.6684028	3614.642411	0.000451244	5	N	402	434
Q91VJ4	Exosome	LKRTR	LGLEDFESLK	VIGRG	2		575.8036756	1149.591751	0.00091018	4	N	83	93
Q91VJ4	Exosome	EWEHR	IGAPGVEEIKNNLFFEGVDWEHIR	ERPAA	3		923.8052039	2768.392212	0.000451244	4	N	367	391
Q91VJ4	Parental	SIEIK	SIDDTSNFDEFPESDILKPTVTTSSHPETDYK	NKDWV	3		1205.888604	3614.642411	0.000622848	3	N	402	434
Q91VJ4	Parental	SIEIK	SIDDTSNFDEFPESDILKPTVTTSSHPETDYK	NKDWV	4		904.6684028	3614.642411	0.002212458	1	N	402	434
Q91VJ5	Parental	RGILK	HLEPEPEEEIIAEDYDDDPVDYEATRIEGLPPSWYK	VFDPS	4		1065.742365	4258.938259	0.000451244	5	N	18	54
Q91VJ5	Parental	PSWYK	VFDPSCGLPYYWNVETDLVSWLSPHDPNFVVTK	SAKKV	3	C6:+57.021	1294.622545	3880.844234	0.000622848	9	N	54	87
Q91VJ5	Parental	PSWYK	VFDPSCGLPYYWNVETDLVSWLSPHDPNFVVTK	SAKKV	4	C6:+57.021	971.2188586	3880.844234	0.000451244	3	N	54	87
Q91VJ5	Parental	RNEAK	TGADTTAAGPLFQQRPYPSPGAVLR	ANAEA	3		857.7825107	2570.324132	0.001463592	1	N	226	251
Q91VJ5	Parental	RGILK	HLEPEPEEEIIAEDYDDDPVDYEATR	IEGLP	3		1030.451438	3088.330913	0.000451244	15	N	18	44
Q91VJ5	Parental	CGLPY	YWNVETDLVSWLSPHDPNFVVTK	SAKKV	3		916.1224215	2745.343865	0.002296037	2	N	64	87
Q91VR2	Parental	FNRTR	QAVITKELIEIISGAAALD	-	3		652.3740183	1954.098655	0.001463592	1	N	279	298
Q91VR2	Parental	KDVGR	KPPTFGDASVIALELLNSGYEFDEGSIIFNQFK	SVISY	3		1216.28256	3645.824279	0.000451244	39	N	158	191
Q91VR2	Parental	KDVGR	KPPTFGDASVIALELLNSGYEFDEGSIIFNQFK	SVISY	4		912.4638697	3645.824279	0.000451244	2	N	158	191
Q91VR5	Exosome	LSQVR	FLVLDEADGLLSQGYSDFINR	MHNQI	2		1186.592594	2371.169588	0.000451244	11	N	365	386
Q91VR5	Exosome	LSQVR	FLVLDEADGLLSQGYSDFINR	MHNQI	3		791.3976628	2371.169588	0.000451244	11	N	365	386
Q91VR5	Exosome	NPYDR	GSAFAIGSDGLCCQSR	EVKEW	2	C12:+57.021,C13:+57.021	843.3722049	1684.72881	0.000823681	1	N	98	114
Q91VR5	Parental	LSQVR	FLVLDEADGLLSQGYSDFINR	MHNQI	2		1186.592594	2371.169588	0.000451244	15	N	365	386
Q91VR5	Parental	LSQVR	FLVLDEADGLLSQGYSDFINR	MHNQI	3		791.3976628	2371.169588	0.000451244	14	N	365	386
Q91VR5	Parental	GVAAR	DQLSVLDNGVDIVVGTPGR	LDDLV	2		977.5161581	1953.016716	0.000851441	2	N	330	349
Q91VW3	Exosome	AGNPK	ATPPQIVNGNHYCGDYELFVEAVEQDTLQEFLK	LA-	3	C13:+57.021	1275.608964	3823.803492	0.000451244	34	N	58	91
Q91VW3	Parental	LDGKR	IQYQLVDISQDNALRDEMR	TLAGN	3		769.7186308	2306.132492	0.000451244	6	N	32	51
Q91VW3	Parental	DYELF	VEAVEQDTLQEFLK	LA-	2		824.9255819	1647.835564	0.000451244	21	N	77	91
Q91VW3	Parental	AGNPK	ATPPQIVNGNHYCGDYELFVEAVEQDTLQEFLK	LA-	3	C13:+57.021	1275.608964	3823.803492	0.000451244	64	N	58	91
Q91VW3	Parental	AGNPK	ATPPQIVNGNHYCGDYELFVEAVEQDTLQEFLK	LA-	4	C13:+57.021	956.9586729	3823.803492	0.000451244	1	N	58	91
Q91VW3	Parental	AGNPK	ATPPQIVNGNHYCGDYELFVEAVEQDTLQEFLKLA	-	3	C13:+57.021	1336.98269	4007.92467	0.000451244	7	N	58	93
Q91VW3	Parental	AGNPK	ATPPQIVNGNHYCGDYELFVEAVEQDTLQEFLKLA	-	4	C13:+57.021	1002.988967	4007.92467	0.001162105	1	N	58	93
Q91VW3	Parental	DYELF	VEAVEQDTLQEFLKLA	-	2		916.9861708	1831.956742	0.001463592	4	N	77	93
Q91VW3	Parental	NGNHY	CGDYELFVEAVEQDTLQEFLK	LA-	2	C1:+57.021	1267.094078	2532.172556	0.000622848	2	N	70	91
Q91VW3	Parental	AGNPK	ATPPQIVNGNHYCGDYELF	VEAVE	2	C13:+57.021	1097.997044	2193.978488	0.00307782	1	N	58	77
Q91W50	Parental	DKLER	ATNIEVLSNTFQFTNEAR	EMGVI	2		1028.01124	2054.00688	0.000451244	9	N	330	348
Q91W50	Parental	GVIEK	LLTSYGFIQCSER	QARLF	2	C10:+57.021	787.3878809	1572.760162	0.001162105	1	N	32	45
Q91W89	Exosome	NLRGR	LFGDSCSVTLSSFLTPER	LPYEK	2	C6:+57.021	1008.491063	2014.966526	0.001395409	1	N	34	52
Q91W89	Exosome	KKGNR	ECEQILHDVEVLSSLALAR	SAQFL	3	C2:+57.021	728.0443007	2181.109502	0.000451244	3	N	533	552
Q91W89	Exosome	LPYEK	AVQQNFSPAQVGDSFGPTWWTCWFR	VELVI	3	C22:+57.021	991.4576556	2971.349567	0.000823681	1	N	57	82
Q91W90	Parental	ALTEK	SFEDTIAQGITFVK	FYAPW	2		778.4042853	1554.792971	0.000998612	3	N	315	329
Q91W90	Parental	ELSKK	EFPGLSDVTIAEVDCTAER	NVCSK	2	C15:+57.021	1054.994167	2107.972734	0.001463592	1	N	351	370
Q91W90	Parental	VYVAK	VDCTADSDVCSAQGVR	GYPTL	2	C3:+57.021,C10:+57.021	870.3698592	1738.724118	0.000451244	7	N	104	120
Q91W90	Parental	KYSVR	GYPTLLLFR	GGEKV	2		540.3165562	1078.617512	0.002813207	1	N	379	388
Q91WJ8	Parental	QIAAK	IGGDAGTSLNSNDYGYGGQKRPLEDGDQPDAK	KVPPQ	3		1099.175301	3294.502504	0.000451244	4	N	40	72
Q91WJ8	Parental	QIAAK	IGGDAGTSLNSNDYGYGGQK	RPLED	2		987.4459298	1972.87626	0.000451244	10	N	40	60
Q91WK0	Parental	FKLSK	AEQDIATLEQSISRLEGQVLR	YKTAA	3		786.0875998	2355.239399	0.000451244	4	N	333	354
Q91WK0	Parental	PVKDR	FSAEDEALSNIAR	EAEAR	2		711.8471345	1421.678669	0.000451244	1	N	16	29
Q91WK0	Parental	FKLSK	AEQDIATLEQSISR	LEGQV	2		780.8973557	1559.779111	0.000451244	3	N	333	347
Q91WK2	Exosome	ELEKK	SAVADKHELLSLASSNHLGK	SLQLL	3		693.0399212	2076.096364	0.001763695	1	N	221	241
Q91WK2	Parental	ELEKK	SAVADKHELLSLASSNHLGK	SLQLL	3		693.0399212	2076.096364	0.000998612	6	N	221	241
Q91WK2	Parental	SFVTR	ALLDSQFSYQHAIEESVVLIYDPIKTAQGSLSLK	AYRLT	4		941.7508015	3762.972006	0.000451244	6	N	131	165

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91WK2	Parental	LKIIK	HYQEEGQGTEVVQGVLLGLVVEDR	LEITN	3		885.4527188	2653.334756	0.000662267	2	N	51	75
Q91WN1	Exosome	DKEQK	AVYDEQGTVDEDSAGLNQDRDWDAYWR	LLFKK	3		1058.794421	3173.359862	0.002813207	1	N	75	102
Q91WN1	Parental	DKEQK	AVYDEQGTVDEDSAGLNQDRDWDAYWR	LLFKK	3		1058.794421	3173.359862	0.000451244	27	N	75	102
Q91WN1	Parental	-M	GLLELCEQVFGTADLYQVLGVRR	EASDG	3	C6:+57.021	879.4673805	2635.378742	0.001162105	4	N	1	24
Q91WN1	Parental	-M	GLLELCEQVFGTADLYQVLGVR	REASD	2	C6:+57.021	1240.646615	2479.27763	0.001871652	1	N	1	23
Q91WN1	Parental	-M	GLLELCEQVFGTADLYQVLGVR	REASD	3	C6:+57.021	827.4336768	2479.27763	0.000622848	1	N	1	23
Q91WN1	Parental	LLFKK	ISLEDIQAFEK	TYKGS	2		646.8407895	1291.665979	0.001699387	2	N	107	118
Q91WQ3	Exosome	AEVVK	QVEHPLLSGLLYPGLQALDEEYLK	VDAQF	3		909.1536102	2724.437431	0.000451244	17	N	154	178
Q91WQ3	Exosome	KKLKK	AFCEPGNVENNGVLSFIK	HVLFP	2	C3:+57.021	997.9859479	1993.956296	0.000451244	9	N	247	265
Q91WQ3	Exosome	EGVSR	QVEPLDPPAGSAPGER	VFVQG	2		810.4053479	1618.795096	0.000622848	5	N	450	466
Q91WQ3	Exosome	WGGNK	TYTVYLELEKDFAAEVVHPGDLK	NSVEV	3		879.7869274	2636.337382	0.000823681	1	N	287	310
Q91WQ3	Parental	AEVVK	QVEHPLLSGLLYPGLQALDEEYLK	VDAQF	3		909.1536102	2724.437431	0.000451244	4	N	154	178
Q91WQ3	Parental	AEVVK	QVEHPLLSGLLYPGLQALDEEYLKVDAQFGGVDQR	KIFTF	4		975.2565167	3896.994867	0.000451244	1	N	154	189
Q91WU5	Exosome	LKNSR	FAPDFLFTPVDASLPAPQGR	SELET	2		1073.552544	2145.089487	0.000451244	13	N	315	335
Q91WU5	Parental	LKNSR	FAPDFLFTPVDASLPAPQGR	SELET	2		1073.552544	2145.089487	0.000451244	20	N	315	335
Q91WU5	Parental	FCPPR	LVTADIITVENKELEGVLGDCR	FVSAT	3	C21:+57.021	815.4285914	2443.262374	0.000637154	3	N	230	252
Q91WV0	Exosome	KSEKK	TISPEHVIQALESLGFGSYISEVK	EVLQE	3		868.7905604	2603.348281	0.000451244	4	N	64	88
Q91WV0	Exosome	ANDAR	ELVVNCCTEFIHLISSEANEICNK	SEKKT	3	C6:+57.021,C7:+57.021,C22:+57.021	960.4506531	2878.328559	0.000451244	24	N	36	60
Q91WV0	Exosome	KASSR	LENLGIPEEELLR	QQQEL	2		762.9175598	1523.81952	0.0025889	1	N	107	120
Q91WV0	Parental	ANDAR	ELVVNCCTEFIHLISSEANEICNK	SEKKT	3	C6:+57.021,C7:+57.021,C22:+57.021	960.4506531	2878.328559	0.000451244	19	N	36	60
Q91WV0	Parental	KSEKK	TISPEHVIQALESLGFGSYISEVKEVLQECK	TVALK	3	C30:+57.021	1164.264357	3489.769672	0.001352548	1	N	64	95
Q91X72	Exosome	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDKLNAAK	SLPQP	3	C7:+57.021,C24:+57.021	1279.273544	3834.797232	0.000451244	9	N	409	444
Q91X72	Exosome	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDKLNAAK	SLPQP	4	C7:+57.021,C24:+57.021	959.707108	3834.797232	0.000451244	15	N	409	444
Q91X72	Exosome	KRLEK	ELGSPPGISLETIDAAFSCPGSSR	LYVSS	2	C19:+57.021	1224.589494	2447.163388	0.000451244	40	N	345	369
Q91X72	Exosome	KRLEK	ELGSPPGISLETIDAAFSCPGSSR	LYVSS	3	C19:+57.021	816.7289295	2447.163388	0.000451244	28	N	345	369
Q91X72	Exosome	PMHSR	CSPDPGLTALLSDHR	GATYA	2	C1:+57.021	819.8991441	1637.782688	0.000451244	3	N	254	269
Q91X72	Exosome	PMHSR	CSPDPGLTALLSDHR	GATYA	3	C1:+57.021	546.9353628	1637.782688	0.000451244	17	N	254	269
Q91X72	Exosome	PMHSR	CSPDPGLTALLSDHR	GATYA	2	[0:-17.027,C1:+57.021	811.3856441	1620.755688	0.000735798	8	N	254	269
Q91X72	Exosome	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDK	LNAAK	3	C7:+57.021,C24:+57.021	1113.50815	3337.50105	0.000451244	43	N	409	439
Q91X72	Exosome	NGYPK	LFQEEFPGIPYPPDAAVECHR	GECQS	2	C19:+57.021	1236.586558	2471.157515	0.000451244	8	N	129	150
Q91X72	Exosome	NGYPK	LFQEEFPGIPYPPDAAVECHR	GECQS	3	C19:+57.021	824.7269717	2471.157515	0.000451244	19	N	129	150
Q91X72	Exosome	WLDLK	SGAQATWTEVSWPHEK	VDGAL	2		907.4293544	1812.843109	0.000451244	6	N	384	400
Q91X72	Exosome	WLDLK	SGAQATWTEVSWPHEK	VDGAL	3		605.2888362	1812.843109	0.002212458	1	N	384	400
Q91X72	Exosome	VECHR	GECQSEGVLFFQGNR	KWFWD	2	C3:+57.021	864.3942259	1726.772852	0.001162105	1	N	150	165
Q91X72	Exosome	LISAR	WKNPITSVDAAFR	GPDSV	2		752.8995044	1503.783409	0.001162105	2	N	89	102
Q91X72	Exosome	LISAR	WKNPITSVDAAFR	GPDSV	3		502.2689363	1503.783409	0.000451244	3	N	89	102
Q91X72	Exosome	RWLER	YYCFQGNKFLR	FNPVT	2	C3:+57.021	748.3614691	1494.707338	0.001162105	8	N	196	207
Q91X72	Exosome	NGYPK	LFQEEFPGIPYPPDAAVECHRGECQSEGVLFFQGNR	KWFWD	4	C19:+57.021,C24:+57.021	1045.987752	4179.919807	0.000622848	2	N	129	165
Q91X72	Exosome	VECHR	GECQSEGVLFFQGNRK	WFWDF	2	C3:+57.021	928.4417075	1854.867815	0.000451244	1	N	150	166
Q91X72	Exosome	WLDLK	SGAQATWTEVSWPHEKVDGALCLDK	SLGPN	3	C22:+57.021	929.1135545	2784.317264	0.000622848	6	N	384	409
Q91X72	Parental	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDKLNAAK	SLPQP	3	C7:+57.021,C24:+57.021	1279.273544	3834.797232	0.000451244	7	N	409	444
Q91X72	Parental	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDKLNAAK	SLPQP	4	C7:+57.021,C24:+57.021	959.707108	3834.797232	0.002019181	5	N	409	444
Q91X72	Parental	KRLEK	ELGSPPGISLETIDAAFSCPGSSR	LYVSS	2	C19:+57.021	1224.589494	2447.163388	0.000451244	39	N	345	369
Q91X72	Parental	KRLEK	ELGSPPGISLETIDAAFSCPGSSR	LYVSS	3	C19:+57.021	816.7289295	2447.163388	0.000662267	7	N	345	369
Q91X72	Parental	PMHSR	CSPDPGLTALLSDHR	GATYA	3	C1:+57.021	546.9353628	1637.782688	0.000451244	18	N	254	269
Q91X72	Parental	PMHSR	CSPDPGLTALLSDHR	GATYA	2	[0:-17.027,C1:+57.021	811.3856441	1620.755688	0.000998612	2	N	254	269
Q91X72	Parental	LCLDK	SLGPNTCSSNGSSLYFIHGPNLYCYSSIDK	LNAAK	3	C7:+57.021,C24:+57.021	1113.50815	3337.50105	0.000451244	42	N	409	439
Q91X72	Parental	NGYPK	LFQEEFPGIPYPPDAAVECHR	GECQS	3	C19:+57.021	824.7269717	2471.157515	0.000451244	23	N	129	150
Q91X72	Parental	WLDLK	SGAQATWTEVSWPHEK	VDGAL	2		907.4293544	1812.843109	0.000451244	4	N	384	400
Q91X72	Parental	WLDLK	SGAQATWTEVSWPHEK	VDGAL	3		605.2888362	1812.843109	0.000451244	3	N	384	400
Q91X72	Parental	VECHR	GECQSEGVLFFQGNR	KWFWD	2	C3:+57.021	864.3942259	1726.772852	0.001839721	1	N	150	165
Q91X72	Parental	LISAR	WKNPITSVDAAFR	GPDSV	3		502.2689363	1503.783409	0.000451244	3	N	89	102
Q91X72	Parental	VECHR	GECQSEGVLFFQGNRK	WFWDF	2	C3:+57.021	928.4417075	1854.867815	0.000451244	1	N	150	166
Q91X72	Parental	LFQEE	FPGIPYPPDAAVECHR	GECQS	3	C14:+57.021	609.294891	1824.861273	0.000451244	36	N	134	150
Q91X72	Parental	LNAAK	SLPQPQKVNSILGCSQ	-	2	C14:+57.021	878.4568263	1754.898053	0.0025889	1	N	444	460
Q91XL1	Exosome	LSSNR	LQALSPELLAPVPR	LRALD	2		752.4488302	1502.88206	0.000451244	29	N	96	110
Q91XL1	Exosome	GALHT	LDLGYNLLESLPEGLLR	GPRRL	2		958.0309127	1914.046225	0.002212458	1	N	185	202
Q91XL1	Exosome	NRLQR	LEDSLLAPQPFLR	VLFLN	2		749.9173628	1497.819126	0.000451244	21	N	219	232
Q91XL1	Exosome	ALHTL	DLGYNLLESLPEGLLR	GPRRL	2		901.4888807	1800.962161	0.000451244	6	N	186	202
Q91XL1	Exosome	QPFLR	VLFLNDNQLVGVATGSFQGL	QHLDM	2		1046.557826	2091.100052	0.001943752	3	N	232	252
Q91XL1	Parental	LSSNR	LQALSPELLAPVPR	LRALD	2		752.4488302	1502.88206	0.000451244	42	N	96	110
Q91XL1	Parental	LSSNR	LQALSPELLAPVPR	LRALD	3		501.9684868	1502.88206	0.000451244	19	N	96	110
Q91XL1	Parental	GALHT	LDLGYNLLESLPEGLLRGPR	RLQRL	3		742.4149881	2224.221564	0.000735798	4	N	185	205

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91XL1	Parental	GALHT	LDLGYNLLESLPEGLLR	GPRRL	2		958.0309127	1914.046225	0.000451244	11	N	185	202
Q91XL1	Parental	GALHT	LDLGYNLLESLPEGLLR	GPRRL	3		639.0232085	1914.046225	0.001699387	2	N	185	202
Q91XL1	Parental	ENQLR	EVSAQWLQGLDALGHLDLAENQLSSLPSGLLA	SLGAL	3		1115.916211	3344.725233	0.000451244	6	N	146	178
Q91XL1	Parental	NRLQR	LEDSLLAPQPFLR	VLFLN	2		749.9173628	1497.819126	0.000451244	30	N	219	232
Q91XL1	Parental	NRLQR	LEDSLLAPQPFLR	VLFLN	3		500.2808419	1497.819126	0.000698008	13	N	219	232
Q91XL1	Parental	SGLLA	SLGALHTLDLGYNLLESLPEGLLRGPR	RLQRL	4		726.9045223	2903.586889	0.001839721	2	N	178	205
Q91XL1	Parental	ENQLR	EVSAQWLQGLDALGHLDLAENQLSSLPSGLLASLGALHT	LDLGY	3		1342.371319	4024.090558	0.000451244	7	N	146	185
Q91XL1	Parental	SGLLA	SLGALHTLDLGYNLLESLPEGLLR	GPRRL	3		865.4783167	2593.41155	0.000823681	1	N	178	202
Q91XL1	Parental	MKGQR	LLDVAELGSL	-	2		515.2954864	1028.575373	0.002813207	1	N	332	342
Q91YI4	Exosome	TAQYK	CPVAQLEQDDQVSPSSTFCK	VYTIT	2	C1:+57.021,C19:+57.021	1148.514709	2295.013819	0.000451244	21	N	252	272
Q91YI4	Exosome	LIIRK	VQFAPETPGPQPSAETTR	HFLMS	2		956.9741261	1911.932652	0.000451244	6	N	171	189
Q91YI4	Exosome	RLIIR	KVQFAPETPGPQPSAETTR	HFLMS	2		1021.021608	2040.027615	0.002212458	1	N	170	189
Q91YI4	Exosome	RLIIR	KVQFAPETPGPQPSAETTR	HFLMS	3		681.0170051	2040.027615	0.000823681	5	N	170	189
Q91YI4	Exosome	YLGKR	DFVDHLDKVDPVDGVVLVDPDYLK	DRKVF	3		904.7976036	2711.369411	0.000451244	7	N	26	50
Q91YI4	Exosome	HAHPF	FFTIPQNLPCSVTLQPGPEDTGK	ACGVD	2	C10:+57.021	1273.633705	2545.25181	0.000451244	5	N	116	139
Q91YI4	Exosome	HAHPF	FFTIPQNLPCSVTLQPGPEDTGK	ACGVD	3	C10:+57.021	849.4250699	2545.25181	0.000451244	6	N	116	139
Q91YI4	Exosome	TCAFR	YGREDLDVLGLSFR	KDLFI	3		547.2866556	1638.836567	0.001839721	2	N	63	77
Q91YI4	Exosome	QSAPR	ETDVPVDTNLIEFD	TNYAT	2		803.8782973	1605.740995	0.000823681	3	N	364	378
Q91YI4	Parental	TAQYK	CPVAQLEQDDQVSPSSTFCK	VYTIT	2	C1:+39.994,C19:+57.021	1140.001209	2277.986819	0.001871652	1	N	252	272
Q91YI4	Parental	TAQYK	CPVAQLEQDDQVSPSSTFCK	VYTIT	2	C1:+57.021,C19:+57.021	1148.514709	2295.013819	0.000451244	51	N	252	272
Q91YI4	Parental	HAHPF	FFTIPQNLPCSVTLQPGPEDTGKACGVDFEIR	AFCAK	3	C10:+57.021,C25:+57.021	1198.585171	3592.732112	0.000451244	10	N	116	148
Q91YI4	Parental	LIIRK	VQFAPETPGPQPSAETTR	HFLMS	2		956.9741261	1911.932652	0.000451244	24	N	171	189
Q91YI4	Parental	RLIIR	KVQFAPETPGPQPSAETTR	HFLMS	2		1021.021608	2040.027615	0.000451244	8	N	170	189
Q91YI4	Parental	RLIIR	KVQFAPETPGPQPSAETTR	HFLMS	3		681.0170051	2040.027615	0.00091018	2	N	170	189
Q91YI4	Parental	NREKR	GLALDGQLKHEDTNLASSTIVK	EGANK	3		770.7486955	2309.222687	0.000451244	6	N	287	309
Q91YI4	Parental	YLGKR	DFVDHLDKVDPVDGVVLVDPDYLK	DRKVF	3		904.7976036	2711.369411	0.000451244	16	N	26	50
Q91YI4	Parental	YLGKR	DFVDHLDKVDPVDGVVLVDPDYLK	DRKVF	4		678.8501527	2711.369411	0.00091018	3	N	26	50
Q91YI4	Parental	HAHPF	FFTIPQNLPCSVTLQPGPEDTGK	ACGVD	2	C10:+57.021	1273.633705	2545.25181	0.000451244	14	N	116	139
Q91YI4	Parental	HAHPF	FFTIPQNLPCSVTLQPGPEDTGK	ACGVD	3	C10:+57.021	849.4250699	2545.25181	0.000451244	7	N	116	139
Q91YI4	Parental	IIRKV	QFAPETPGPQPSAETTR	HFLMS	2		907.4399191	1812.864238	0.000622848	2	N	172	189
Q91YI4	Parental	TCAFR	YGREDLDVLGLSFR	KDLFI	3		547.2866556	1638.836567	0.001463592	1	N	63	77
Q91YP3	Exosome	AWLLK	AVTFIDLTTLSGDDTFSNVQR	LCYKA	2		1150.574401	2299.133203	0.000451244	7	N	49	70
Q91YP3	Exosome	PDLFR	IGASSLLSDIER	QIYHH	2		630.8438635	1259.672127	0.00091018	8	N	287	299
Q91YP3	Exosome	LEEIR	LAVEDGATEIDVVINR	TLVLT	2		857.4550378	1712.894476	0.000451244	4	N	144	160
Q91YP3	Exosome	IRTAK	ESLAWLSLVKEELGDEWLTPDLFR	IGASS	2		1423.734705	2845.453809	0.000823681	1	N	263	287
Q91YP3	Exosome	IRTAK	ESLAWLSLVKEELGDEWLTPDLFR	IGASS	3		949.492403	2845.453809	0.000698008	4	N	263	287
Q91YP3	Exosome	AAHCR	GTELDLSWISK	VQVNH	2		624.8276821	1247.639764	0.000451244	7	N	6	17
Q91YP3	Exosome	EAHLK	TILATGELGSLTNVYK	ASLVA	2		840.4648742	1678.914148	0.000870037	1	N	188	204
Q91YQ5	Exosome	GSTSR	ASSFVLALEPELESR	LAHLG	2		824.4335741	1646.851548	0.000451244	2	N	66	81
Q91YQ5	Parental	SHLAK	VTAEVVLVHPGGGSTSR	ASSFV	2		833.4500898	1664.88458	0.000637154	27	N	49	66
Q91YQ5	Parental	SHLAK	VTAEVVLVHPGGGSTSR	ASSFV	3		555.9693265	1664.88458	0.001395409	1	N	49	66
Q91YQ5	Parental	ALKMR	FVDHVFDEQVIDSLTVK	IILPE	2		996.0101773	1990.004755	0.000451244	8	N	355	372
Q91YQ5	Parental	ALKMR	FVDHVFDEQVIDSLTVK	IILPE	3		664.3427182	1990.004755	0.000870037	1	N	355	372
Q91YQ5	Parental	GSTSR	ASSFVLALEPELESR	LAHLG	2		824.4335741	1646.851548	0.000451244	23	N	66	81
Q91YQ5	Parental	FGGWK	THYIVGYNLPSYEYLYNLGDQYALK	MRFVD	3		999.8276743	2996.459623	0.000451244	24	N	328	353
Q91YQ5	Parental	TQSEK	QFVVFEGNHYFYSPYPTK	TQTMR	2	[0:-17.027	1103.517944	2205.020288	0.002296037	1	N	152	170
Q91YQ5	Parental	YIVGY	NLPSYEYLYNLGDQYALK	MRFVD	2		1082.534017	2163.052433	0.000451244	14	N	335	353
Q91YQ5	Parental	GPFSR	YDYQRQPDSGISSIR	SFKTI	3		595.6241075	1783.848922	0.000451244	3	N	264	279
Q91YQ5	Parental	VETVY	THVLHPYPTQITQSEK	QFVVF	3		626.9956528	1877.963558	0.001463592	1	N	136	152
Q91YQ5	Parental	PEGAK	NIQVDSPYDISR	APDEL	2		703.8496771	1405.683754	0.000451244	2	N	380	392
Q91YR9	Exosome	SQYNR	TGPCPQGPAPEVVIYQQLR	MEGFI	2	C4:+57.021	1055.541422	2109.067243	0.000451244	47	N	247	266
Q91YR9	Exosome	SQYNR	TGPCPQGPAPEVVIYQQLR	MEGFI	3	C4:+57.021	704.0302145	2109.067243	0.000735798	4	N	247	266
Q91YR9	Exosome	KTFGR	IAICGAISQYNR	TGPCP	2	C4:+57.021	683.3511014	1364.686603	0.000451244	22	N	235	247
Q91YR9	Exosome	SAFPK	GTIVAALLGWTSHSISDGNGLTK	LPVEW	2		1149.608579	2297.201557	0.000451244	22	N	81	104
Q91YR9	Exosome	SAFPK	GTIVAALLGWTSHSISDGNGLTK	LPVEW	3		766.7416524	2297.201557	0.000451244	34	N	81	104
Q91YR9	Exosome	WTLKK	HFEGFPTDGNFELK	TTELP	2		819.3838842	1636.752168	0.000451244	6	N	11	25
Q91YR9	Exosome	AYLKK	LGFDVAFNYK	TVKSL	2		587.3011031	1172.586606	0.000451244	9	N	184	194
Q91YR9	Exosome	NFELK	TTELPPLNNGEVLLEALFLSVDPYMR	VAAKK	3		977.8444483	2930.509945	0.002080925	1	N	25	51
Q91YR9	Exosome	NFELK	TTELPPLNNGEVLLEAL	FLSVD	2		911.9939959	1821.972392	0.002374549	1	N	25	42
Q91YR9	Parental	SQYNR	TGPCPQGPAPEVVIYQQLR	MEGFI	2	C4:+57.021	1055.541422	2109.067243	0.000451244	30	N	247	266
Q91YR9	Parental	KTFGR	IAICGAISQYNR	TGPCP	2	C4:+57.021	683.3511014	1364.686603	0.001162105	2	N	235	247
Q91YR9	Parental	SAFPK	GTIVAALLGWTSHSISDGNGLTK	LPVEW	2		1149.608579	2297.201557	0.000451244	7	N	81	104
Q91YR9	Parental	SAFPK	GTIVAALLGWTSHSISDGNGLTK	LPVEW	3		766.7416524	2297.201557	0.000451244	22	N	81	104
Q91YR9	Parental	WTLKK	HFEGFPTDGNFELK	TTELP	2		819.3838842	1636.752168	0.000451244	8	N	11	25
Q91YR9	Parental	NFELK	TTELPPLNNGEVLLEALFLSVDPYMR	VAAKK	3		977.8444483	2930.509945	0.000451244	1	N	25	51

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91YR9	Parental	NFELK	TTELPPLNNGEVLLEALFLSVDPY	MRVAA	3		882.1305827	2643.368348	0.001463592	1	N	25	49
Q91YT0	Exosome	VFVVR	GAGAYICGEETALIESIEGK	QGKPR	2	C7:+57.021	1034.499085	2066.98257	0.000451244	1	N	199	219
Q91YT0	Exosome	ELIEK	HAGGVTGGWDNLLAVIPGGSSTPLIPK	SVCET	3		872.1382945	2613.391483	0.000622848	5	N	302	329
Q91YT0	Parental	VFVVR	GAGAYICGEETALIESIEGK	QGKPR	2	C7:+57.021	1034.499085	2066.98257	0.000451244	9	N	199	219
Q91YT0	Parental	ELIEK	HAGGVTGGWDNLLAVIPGGSSTPLIPK	SVCET	3		872.1382945	2613.391483	0.000823681	2	N	302	329
Q91YT0	Parental	QGKPR	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	RGGTW	3	C14:+57.021,C31:+57.021	1133.919714	3398.735741	0.000622848	6	N	224	256
Q91YT0	Parental	GLIGK	NACGSDYDFDVFVVR	GAGAY	2	C3:+57.021	882.3886093	1762.761619	0.002374549	1	N	184	199
Q91YW3	Exosome	ELGKK	LLAAGQLADALSQFHAAVDGDPDNYIAYYR	RATVF	3		1080.19883	3237.57309	0.000451244	15	N	46	76
Q91YW3	Parental	ELGKK	LLAAGQLADALSQFHAAVDGDPDNYIAYYR	RATVF	3		1080.19883	3237.57309	0.000451244	34	N	46	76
Q91YW3	Parental	KKLLA	AGQLADALSQFHAAVDGDPDNYIAYYR	RATVF	3		981.1304159	2940.367848	0.000451244	4	N	49	76
Q91YW3	Parental	KKVLK	SNPSEQEEKEAESQLVK	ADEMQ	2		966.4637882	1930.911976	0.001162105	1	N	133	150
Q91YX0	Exosome	VQLQK	VVCEYPETGQTLELNPNFTGLFSPLTSLR	SYRTL	3	C3:+57.021	1094.883588	3281.627365	0.000451244	4	N	59	88
Q91YX0	Exosome	FKPLR	LSEVLAGGGPFPLTTEILEVPEGPPVFLSPWVSFLR	KGQRL	3		1284.361033	3850.059699	0.00091018	1	N	247	283
Q91YX0	Parental	EIPPR	WLDLTVVEAEGQPAQVARPLSIAPVEELSEAFYY	SLRKL	3		1264.312519	3789.914157	0.000870037	6	N	504	538
Q91YX0	Parental	VQLQK	VVCEYPETGQTLELNPNFTGLFSPLTSLR	SYRTL	3	C3:+57.021	1094.883588	3281.627365	0.000451244	12	N	59	88
Q91YX0	Parental	EIPPR	WLDLTVVEAEGQPAQVARPLSIAPVEELSEAF	YYSLR	3		1155.603633	3463.787499	0.00091018	1	N	504	536
Q91YX0	Parental	KPLRL	SEVLAGGGPFPLTTEILEVPEGPPVFLSPWVSFLR	KGQRL	3		1246.666345	3736.975635	0.000979378	1	N	248	283
Q91YX0	Parental	EIPPR	WLDLTVVEAEGQPAQVAR	PLSIA	2		991.5212435	1981.026887	0.002374549	1	N	504	522
Q91Z50	Exosome	NWLHK	EAQQLFLEPEVLDPESVELKWSEPNEEELVK	FMCGE	3		1218.609001	3652.803603	0.000622848	8	N	277	308
Q91Z50	Exosome	FHLSR	VLQELGLNQEQFVDLCILLGSDYCESIR	GIGPK	3	C16:+57.021,C24:+57.021	1104.547946	3310.620437	0.001162105	1	N	211	239
Q91Z50	Exosome	HGLAK	LIADVAPSAIRENDIK	SYFGR	3		575.6567485	1723.946846	0.001229886	3	N	8	24
Q91Z50	Exosome	NWLHK	EAQQLFLEPEVLDPESVELK	WSEPN	2		1157.097178	2312.178756	0.000451244	42	N	277	297
Q91Z50	Exosome	NWLHK	EAQQLFLEPEVLDPESVELK	WSEPN	3		771.734052	2312.178756	0.000622848	4	N	277	297
Q91Z50	Parental	MGIPY	LDAPSEAEASCAALAK	AGKVY	2	C11:+57.021	802.3855352	1602.75547	0.000451244	18	N	152	168
Q91Z50	Parental	NWLHK	EAQQLFLEPEVLDPESVELKWSEPNEEELVK	FMCGE	3		1218.609001	3652.803603	0.000823681	6	N	277	308
Q91Z50	Parental	FHLSR	VLQELGLNQEQFVDLCILLGSDYCESIR	GIGPK	3	C16:+57.021,C24:+57.021	1104.547946	3310.620437	0.000451244	5	N	211	239
Q91Z50	Parental	HGLAK	LIADVAPSAIRENDIK	SYFGR	2		862.9812228	1723.946846	0.001329271	1	N	8	24
Q91Z50	Parental	HGLAK	LIADVAPSAIRENDIK	SYFGR	3		575.6567485	1723.946846	0.001763695	1	N	8	24
Q91Z50	Parental	NWLHK	EAQQLFLEPEVLDPESVELK	WSEPN	2		1157.097178	2312.178756	0.000451244	31	N	277	297
Q91Z50	Parental	NWLHK	EAQQLFLEPEVLDPESVELK	WSEPN	3		771.734052	2312.178756	0.000451244	2	N	277	297
Q91ZJ5	Exosome	LIGVR	NENTFLDLTVQQIEHLNK	TYNTD	2		1078.553272	2155.090944	0.000451244	26	N	133	151
Q91ZJ5	Exosome	LIGVR	NENTFLDLTVQQIEHLNK	TYNTD	3		719.371448	2155.090944	0.000451244	23	N	133	151
Q91ZJ5	Exosome	IVNPK	TLDGGLNVIQLETAVGAAIK	SFENS	2		992.0602015	1982.104803	0.000451244	23	N	357	377
Q91ZJ5	Exosome	IVNPK	TLDGGLNVIQLETAVGAAIK	SFENS	3		661.709401	1982.104803	0.000451244	25	N	357	377
Q91ZJ5	Exosome	VSKFK	IFNTNNLWISLGAVK	RLQEQ	2		845.4702939	1688.924988	0.000451244	10	N	325	340
Q91ZJ5	Exosome	VDWGK	IQRPPEDSIQPYEK	IKARG	2		850.4366481	1698.857696	0.002080925	1	N	77	91
Q91ZJ5	Exosome	VDWGK	IQRPPEDSIQPYEK	IKARG	3		567.2936987	1698.857696	0.002374549	1	N	77	91
Q91ZJ5	Exosome	GAAIK	SFENSLGINVPR	SRFLP	2		666.8494801	1331.68336	0.001463592	1	N	377	389
Q91ZJ5	Exosome	GASQF	QEVILQELELSVK	KELEK	2	Q1:-17.027	755.9220854	1509.828571	0.002019181	1	N	20	33
Q91ZJ5	Parental	LIGVR	NENTFLDLTVQQIEHLNK	TYNTD	2		1078.553272	2155.090944	0.000451244	2	N	133	151
Q91ZJ5	Parental	LIGVR	NENTFLDLTVQQIEHLNK	TYNTD	3		719.371448	2155.090944	0.000622848	5	N	133	151
Q91ZJ5	Parental	IVNPK	TLDGGLNVIQLETAVGAAIK	SFENS	2		992.0602015	1982.104803	0.000451244	7	N	357	377
Q91ZJ5	Parental	IVNPK	TLDGGLNVIQLETAVGAAIK	SFENS	3		661.709401	1982.104803	0.000622848	1	N	357	377
Q91ZJ5	Parental	IVNPK	TLDGGLNVIQLETAVGAAIKSFENSLGINVPR	SRFLP	3		1099.600334	3295.777603	0.001264573	2	N	357	389
Q91ZR1	Exosome	DITSR	ETYNSLAAWLTDAR	TLASP	2		805.894616	1609.773632	0.000451244	3	N	93	107
Q91ZR1	Exosome	CGNKK	DLDPEREVTFLEASR	FAQEN	3		592.9641297	1775.868989	0.001162105	1	N	123	138
Q91ZR1	Exosome	RSYYR	GAAGALLVYDITSR	ETYNS	2		703.8860627	1405.756525	0.000451244	1	N	79	93
Q91ZR1	Parental	GKTVK	LQIWDTAGQER	FRSVT	2		658.8338301	1315.65206	0.001591523	2	Y	58	69
Q91ZR1	Parental	DITSR	ETYNSLAAWLTDAR	TLASP	2		805.894616	1609.773632	0.000622848	3	N	93	107
Q91ZU6	Exosome	AMPGK	DVPELSQHMQESTAKFLEHR	KDLEA	3	M9:+15.995	800.0539305	2397.138391	0.000823681	5	N	4228	4248
Q91ZU6	Parental	AMPGK	DVPELSQHMQESTAKFLEHR	KDLEA	3	M9:+15.995	800.0539305	2397.138391	0.001839721	3	N	4228	4248
Q91ZU6	Parental	FPTSR	LEMSAVADIFDR	DGDGY	2	M3:+15.995	691.8352244	1381.654849	0.002212458	1	N	7057	7069
Q91ZW3	Exosome	PGKQK	EIQEPDPTYEEK	MQTDR	2		739.3388079	1476.662016	0.000823681	3	N	70	82
Q91ZW3	Exosome	YRHRR	TEQEEDEELLTESSK	ATNVC	2		883.8948727	1765.774145	0.000451244	8	N	144	159
Q91ZW3	Parental	FFPPR	LFELLEKEILYYR	KTIGY	3		576.9910686	1727.949806	0.00091018	4	N	779	792
Q91ZW3	Parental	KANEK	WGRDDIENIAR	EVEGK	3		448.8938694	1343.658208	0.001943752	4	N	858	869
Q91ZW3	Parental	PGKQK	EIQEPDPTYEEK	MQTDR	2		739.3388079	1476.662016	0.000622848	5	N	70	82
Q91ZW3	Parental	VFASK	ESEITDEDIDGILER	GAKKT	2		867.4079503	1732.800301	0.000451244	3	N	664	679
Q91ZX7	Exosome	GESCR	SLDPFKPFIIFSNR	HEIRR	3		560.9756414	1679.903524	0.002212458	4	N	1263	1277
Q91ZX7	Exosome	PHSCK	AVTDEEPFLIFANR	YYLRK	2		811.4151843	1620.814769	0.000823681	8	N	3023	3037
Q91ZX7	Exosome	VMHMK	VYDESIQLEHEGTNPCSVNNGDCSQLCLPTSETTR	SCMCT	3	C16:+57.021,C23:+57.021,C27:+57.021	1337.586145	4009.735034	0.000451244	1	N	1835	1870
Q91ZX7	Exosome	QVLHR	TGLSNPDGLAVDWVGGNLYWCDK	GRDTI	2	C21:+57.021	1269.092204	2536.168808	0.000451244	3	N	3099	3122
Q91ZX7	Exosome	QPCER	TSLCYAPSWVCDGANDCGDYSDERDCPGVK	RPRCP	3	C4:+57.021,C11:+57.021,C17:+57.021,C26:+57.021	1152.128596	3453.362387	0.000451244	2	N	2663	2693

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q91ZX7	Exosome	SKGWR	CDGERDCPDGSDEAPEICPQSK	AQRCP	3	C1:+57.021,C7:+57.021,C18:+57.021	841.3337251	2520.977775	0.00091018	1	N	47	69
Q91ZX7	Exosome	SCKAK	NEPVDRPPVLLIANSQNILATYLSGAQVSTITPTSTR	QTTAM	3		1313.039681	3936.095644	0.001591523	1	N	192	229
Q91ZX7	Parental	ALDPR	DGILFWTDWDASLPR	IEAAS	2		896.4391908	1790.862782	0.002453667	1	N	1398	1413
Q920B9	Exosome	TYALF	IGDTVLVDEDGPATILTSVK	KKVKN	2		1022.046957	2042.078314	0.000622848	9	N	402	422
Q920B9	Exosome	EEKTY	ALFIGDTVLVDEDGPATILTSVK	KKVKN	2		1187.641753	2373.267906	0.000662267	2	N	399	422
Q920B9	Parental	GAPYR	STCLLQPTSSALVNATEWPPFVVTLDEVELIHFER	VQFHL	3	C3:+57.021	1333.67883	3998.013091	0.000451244	12	N	812	847
Q920B9	Parental	TYALF	IGDTVLVDEDGPATILTSVK	KKVKN	2		1022.046957	2042.078314	0.000451244	17	N	402	422
Q920B9	Parental	GIFLK	NEDDEEEEEEKDEAEDLLGR	GSRAA	3		798.3302597	2391.967379	0.000662267	5	N	433	453
Q920B9	Parental	SALGR	NEGNIFPNPEATFVK	EITYR	2		838.9180912	1675.820582	0.001699387	1	N	581	596
Q920E5	Exosome	SLTRR	GQICWYQKPGIGLDAINDALLLEASIYR	LLKFY	3	C4:+57.021	1059.885263	3176.63239	0.000451244	30	N	113	141
Q920E5	Exosome	GKYNR	GLTVVQAFQELVEPK	KQDAE	2		829.4621346	1656.908669	0.000451244	51	N	60	75
Q920E5	Exosome	GKYNR	GLTVVQAFQELVEPK	KQDAE	3		553.3106897	1656.908669	0.000451244	4	N	60	75
Q920E5	Exosome	VARVK	ALYEALDLQSAFFK	YEEDS	2		808.422478	1614.829356	0.000451244	30	N	302	316
Q920E5	Exosome	VARVK	ALYEALDLQSAFFK	YEEDS	3		539.284252	1614.829356	0.000451244	7	N	302	316
Q920E5	Exosome	IQDNK	CSWLVVQCLLR	ASPQQ	2	C1:+39.994,C8:+57.021	708.8597909	1415.703982	0.0025889	2	N	266	277
Q920E5	Exosome	IQDNK	CSWLVVQCLLR	ASPQQ	2	C1:+57.021,C8:+57.021	717.3732909	1432.730982	0.000451244	24	N	266	277
Q920E5	Exosome	IQDNK	CSWLVVQCLLR	ASPQQ	2	[0:-17.027,C1:+57.021,C8:+57.021	708.8597909	1415.703982	0.001839721	6	N	266	277
Q920E5	Exosome	YNQEK	QNFIQHFSQIVK	VLTEK	2	[0:-17.027	736.3885471	1470.761494	0.000622848	15	N	14	26
Q920E5	Exosome	DAIAR	LKEVLEYNALGGK	YNRGL	2		717.4040883	1432.792577	0.000622848	10	N	44	57
Q920E5	Exosome	SQIVK	VLTEKELGHPEIGDAIAR	LKEVL	3		650.021979	1947.042537	0.000451244	8	N	26	44
Q920E5	Exosome	VARVK	ALYEALDLQSAFFKYEEDSYNR	LKSLI	3		891.4225367	2671.24421	0.000451244	14	N	302	324
Q920E5	Exosome	SPQQR	QILEENYGQKDPEK	VARVK	2	[0:-17.027	837.4047882	1672.793976	0.000823681	2	N	283	297
Q920E5	Parental	SLTRR	GQICWYQKPGIGLDAINDALLLEASIYR	LLKFY	3	C4:+57.021	1059.885263	3176.63239	0.000451244	15	N	113	141
Q920E5	Parental	GKYNR	GLTVVQAFQELVEPK	KQDAE	2		829.4621346	1656.908669	0.000451244	14	N	60	75
Q920E5	Parental	SVTGK	VGTDIQDNKCSWLVVQCLLR	ASPQQ	2	C10:+57.021,C17:+57.021	1202.609278	2403.202957	0.000451244	1	N	257	277
Q920E5	Parental	SVTGK	VGTDIQDNKCSWLVVQCLLR	ASPQQ	3	C10:+57.021,C17:+57.021	802.0754523	2403.202957	0.000622848	1	N	257	277
Q920E5	Parental	VARVK	ALYEALDLQSAFFK	YEEDS	2		808.422478	1614.829356	0.000451244	25	N	302	316
Q920E5	Parental	VARVK	ALYEALDLQSAFFK	YEEDS	3		539.284252	1614.829356	0.000451244	1	N	302	316
Q920E5	Parental	IQDNK	CSWLVVQCLLR	ASPQQ	2	C1:+39.994,C8:+57.021	708.8597909	1415.703982	0.0025889	1	N	266	277
Q920E5	Parental	IQDNK	CSWLVVQCLLR	ASPQQ	2	C1:+57.021,C8:+57.021	717.3732909	1432.730982	0.000451244	14	N	266	277
Q920E5	Parental	IQDNK	CSWLVVQCLLR	ASPQQ	2	[0:-17.027,C1:+57.021,C8:+57.021	708.8597909	1415.703982	0.001162105	5	N	266	277
Q920E5	Parental	DAIAR	LKEVLEYNALGGK	YNRGL	2		717.4040883	1432.792577	0.000451244	3	N	44	57
Q920E5	Parental	SQIVK	VLTEKELGHPEIGDAIAR	LKEVL	2		974.5290685	1947.042537	0.000451244	8	N	26	44
Q920E5	Parental	SQIVK	VLTEKELGHPEIGDAIAR	LKEVL	3		650.021979	1947.042537	0.000451244	5	N	26	44
Q920E5	Parental	SQIVK	VLTEKELGHPEIGDAIAR	LKEVL	4		487.7684343	1947.042537	0.000451244	7	N	26	44
Q920E5	Parental	EKVAR	VKALYEALDLQSAFFK	YEEDS	3		615.0053777	1841.992733	0.000451244	4	N	300	316
Q920E5	Parental	VARVK	ALYEALDLQSAFFKYEEDSYNR	LKSLI	2		1336.629905	2671.24421	0.000451244	3	N	302	324
Q920E5	Parental	SPQQR	QILEENYGQKDPEK	VARVK	2		845.9182882	1689.820976	0.000622848	1	N	283	297
Q920E5	Parental	SPQQR	QILEENYGQKDPEK	VARVK	3		564.2814588	1689.820976	0.001871652	3	N	283	297
Q921F2	Exosome	RAVQK	TSDLIVLGLPWK	TTEQD	2		671.3929922	1340.770384	0.000451244	10	N	102	114
Q921F2	Exosome	MRGVR	LVEGILHAPDAGWGNLVYVVNYPK	DNKRK	3		875.467752	2623.379856	0.000451244	30	N	55	79
Q921F2	Exosome	PKPFR	AFAFVTFADDKVAQSLCGEDLIIK	GISVH	3	C17:+57.021	886.7880082	2657.340625	0.000451244	43	N	227	251
Q921F2	Exosome	SEYIR	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR	YRNPV	3	C33:+57.021	1292.27772	3873.809759	0.000451244	13	N	6	42
Q921F2	Exosome	VFVGR	CTEDMTAEELQQFFCQYGEVVDVFIPKPFR	AFAFV	3	[0:-17.027,C1:+57.021,M5:+15.995,C15:+57.021	1228.2229	3681.645301	0.002019181	1	N	197	227
Q921F2	Exosome	ERSGR	FGGNPGGFGNQGGFGNSR	GGGAG	2		863.888188	1725.760776	0.000451244	1	N	275	293
Q921F2	Exosome	AFVTF	ADDKVAQSLCGEDLIIK	GISVH	2	C10:+57.021	937.9803312	1873.945062	0.000979378	1	N	234	251
Q921F2	Exosome	GLPWK	TTEQDLKDYFSTF	GEVLM	2		797.8677326	1593.719865	0.002080925	2	N	114	127
Q921F2	Parental	RAVQK	TSDLIVLGLPWK	TTEQD	2		671.3929922	1340.770384	0.000451244	29	N	102	114
Q921F2	Parental	MRGVR	LVEGILHAPDAGWGNLVYVVNYPK	DNKRK	2		1312.697728	2623.379856	0.002453667	1	N	55	79
Q921F2	Parental	MRGVR	LVEGILHAPDAGWGNLVYVVNYPK	DNKRK	3		875.467752	2623.379856	0.000451244	32	N	55	79
Q921F2	Parental	PKPFR	AFAFVTFADDKVAQSLCGEDLIIK	GISVH	3	C17:+57.021	886.7880082	2657.340625	0.000451244	28	N	227	251
Q921F2	Parental	SEYIR	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR	YRNPV	3	C33:+57.021	1292.27772	3873.809759	0.000451244	29	N	6	42
Q921F2	Parental	SEYIR	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR	YRNPV	4	C33:+57.021	969.4602398	3873.809759	0.000622848	3	N	6	42
Q921F2	Parental	VFVGR	CTEDMTAEELQQFFCQYGEVVDVFIPKPFR	AFAFV	3	C1:+39.994,C15:+57.021	1222.891234	3665.650301	0.001162105	1	N	197	227
Q921F2	Parental	VFVGR	CTEDMTAEELQQFFCQYGEVVDVFIPKPFR	AFAFV	3	C1:+57.021,C15:+57.021	1228.5669	3682.677301	0.001162105	2	N	197	227
Q921F2	Parental	VFVGR	CTEDMTAEELQQFFCQYGEVVDVFIPKPFR	AFAFV	3	[0:-	1222.891234	3665.650301	0.000451244	9	N	197	227
Q921F2	Parental	ERSGR	FGGNPGGFGNQGGFGNSR	GGGAG	2		863.888188	1725.760776	0.000451244	55	N	275	293
Q921F2	Parental	AFVTF	ADDKVAQSLCGEDLIIK	GISVH	2	C10:+57.021	937.9803312	1873.945062	0.000451244	5	N	234	251
Q921F2	Parental	GLPWK	TTEQDLKDYFSTF	GEVLM	2		797.8677326	1593.719865	0.001654178	1	N	114	127
Q921F2	Parental	MRGVR	LVEGILHAPDAGWGNLVYVVNYPKDNK	RKMDE	3		994.5226966	2980.54469	0.000823681	1	N	55	82
Q921F2	Parental	MRGVR	LVEGILHAPDAGWGNLVY	VVNYP	2		962.5023224	1922.989045	0.002727428	1	N	55	73
Q921F4	Exosome	VVHVR	GLCESVVEADLVEALEK	FGTIC	2	C3:+57.021	930.9668895	1859.918179	0.000451244	15	N	130	147

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q921F4	Exosome	VVHVR	GLCESVVEADLVEALEK	FGTIC	3	C3:+57.021	620.9805263	1859.918179	0.000451244	9	N	130	147
Q921F4	Exosome	GQASK	NIIQPPSCVLHYYNVPLCVTEETFTK	LCNDH	3	C8:+57.021,C18:+57.021	1041.515917	3121.524351	0.000622848	1	N	495	521
Q921F4	Exosome	MNCSR	VFNLFCLYGNIEK	VKFMK	2	C6:+57.021	808.9109919	1615.806384	0.000451244	4	N	400	413
Q921F4	Exosome	AQKAK	AALNGADIYAGCCTLK	IEYAR	2	C12:+57.021,C13:+57.021	849.4029738	1696.790348	0.000451244	3	N	271	287
Q921F4	Exosome	VCVSK	QHSVVPSQIFELEDGTSSY	KDFAM	2		1062.000538	2121.985476	0.000698008	2	N	457	476
Q921F4	Exosome	EWKCK	TDAVEALTALNHYQIR	VPNGS	3		605.6518861	1813.932258	0.000451244	2	N	555	571
Q921F4	Parental	VVHVR	GLCESVVEADLVEALEK	FGTIC	2	C3:+57.021	930.9668895	1859.918179	0.000451244	7	N	130	147
Q921F4	Parental	VVHVR	GLCESVVEADLVEALEK	FGTIC	3	C3:+57.021	620.9805263	1859.918179	0.000451244	26	N	130	147
Q921F4	Parental	GQASK	NIIQPPSCVLHYYNVPLCVTEETFTK	LCNDH	3	C8:+57.021,C18:+57.021	1041.515917	3121.524351	0.000622848	7	N	495	521
Q921F4	Parental	VCVSK	QHSVVPSQIFELEDGTSSY	KDFAM	2		1062.000538	2121.985476	0.000451244	7	N	457	476
Q921F4	Parental	ECVTF	AADVPVYIAGQQAFFNYSTSK	RITRP	2		1139.063473	2276.111345	0.001162105	1	N	179	200
Q921G6	Exosome	LGSLR	QLDVSSNELQSLPVELCSLR	SLRDL	2	C17:+57.021	1144.083848	2286.152095	0.000451244	12	N	162	182
Q921G6	Exosome	ADLSR	NRFPEVPEAACQLVSLEGLSLYHNCLK	CLNPA	4	C11:+57.021,C25:+57.021	786.8958743	3143.552297	0.001839721	1	N	77	104
Q921G6	Parental	LGSLR	QLDVSSNELQSLPVELCSLR	SLRDL	2	C17:+57.021	1144.083848	2286.152095	0.000451244	19	N	162	182
Q921G6	Parental	HNCLK	CLNPALGNLTALTYLNLSR	NQLSS	2	C1:+57.021	1052.564897	2103.114194	0.000451244	21	N	104	123
Q921G6	Parental	VLESR	LQQPLPEDLAEALANGVLLCQLANQLRPR	SVPFI	3	C20:+57.021	1080.9226	3239.744401	0.000451244	10	N	548	577
Q921G6	Parental	ADLSR	NRFPEVPEAACQLVSLEGLSLY	HNCLK	2	C11:+57.021	1246.628422	2491.241245	0.001654178	3	N	77	99
Q921G6	Parental	EAGRR	GAALGDLVPSRPPSFSPCPAEDLFPGR	RYDGG	3	C18:+57.021	937.4695612	2809.385284	0.000622848	3	N	265	292
Q921G6	Parental	LNVRR	NQLSTLPDELGDLPLVR	LDFSC	2		940.5103444	1879.005089	0.000622848	7	N	191	208
Q921G7	Parental	GPEQR	FCPAGVYEFVPLEQGDGFR	LQINA	2	C2:+57.021	1094.51233	2187.00906	0.000662267	3	N	558	577
Q921G7	Parental	KFDLR	ASCDAQTYGIGLKELWIIDEK	KWKPG	2	C3:+57.021	1205.601873	2409.188147	0.000637154	1	N	262	283
Q921H8	Exosome	RGGFK	NTTPDELLSAVLTAVLQDVR	LKPEQ	2		1078.084405	2154.15321	0.000451244	7	N	57	77
Q921H8	Exosome	RGGFK	NTTPDELLSAVLTAVLQDVR	LKPEQ	3		719.05887	2154.15321	0.000451244	6	N	57	77
Q921H8	Exosome	KPAFK	DGGSTTAGNSSQVSDGAAAVLLAR	RSKAE	2		1103.041257	2204.066914	0.000451244	5	N	265	289
Q921H8	Exosome	AVMAR	IAQFLSGIPETVPLSTVNR	QCSSG	2		1021.568194	2041.120787	0.000451244	13	N	102	121
Q921H8	Exosome	LLARR	SKAEELGLPILGVLR	SYAVV	3		532.3229297	1593.945389	0.001871652	3	N	290	305
Q921H8	Exosome	ARRSK	AEELGLPILGVLR	SYAVV	2		690.4169987	1378.818397	0.002663018	1	N	292	305
Q921H8	Parental	GRASR	GGFKNTTPDELLSAVLTAVLQDVR	LKPEQ	3		848.7943049	2543.359515	0.000622848	6	N	53	77
Q921H8	Parental	RGGFK	NTTPDELLSAVLTAVLQDVR	LKPEQ	2		1078.084405	2154.15321	0.000451244	16	N	57	77
Q921H8	Parental	RGGFK	NTTPDELLSAVLTAVLQDVR	LKPEQ	3		719.05887	2154.15321	0.000451244	19	N	57	77
Q921H8	Parental	KPAFK	DGGSTTAGNSSQVSDGAAAVLLAR	RSKAE	2		1103.041257	2204.066914	0.000451244	8	N	265	289
Q921H8	Parental	AVMAR	IAQFLSGIPETVPLSTVNR	QCSSG	2		1021.568194	2041.120787	0.000451244	12	N	102	121
Q921H8	Parental	PCSAR	FPQASASDVVVVHGR	RTPIG	3		523.6113621	1567.810686	0.0007646	1	N	29	44
Q921H8	Parental	LLARR	SKAEELGLPILGVLR	SYAVV	3		532.3229297	1593.945389	0.000823681	4	N	290	305
Q921I1	Exosome	VTAIR	NQQEGVCPEGSIDNSPVK	WCALS	2	C7:+57.021	979.4499266	1956.884253	0.000451244	77	N	343	361
Q921I1	Exosome	TGAFR	CLVEKGDVAFVK	HQTVL	2	C1:+57.021	682.866053	1363.716506	0.000451244	141	N	542	554
Q921I1	Exosome	TGAFR	CLVEKGDVAFVK	HQTVL	3	C1:+57.021	455.5799687	1363.716506	0.000451244	166	N	542	554
Q921I1	Exosome	TGAFR	CLVEKGDVAFVK	HQTVL	2	[0:-17.027,C1:+57.021	674.352553	1346.689506	0.000451244	85	N	542	554
Q921I1	Exosome	SPLEK	AVSSFFSGSCVPCADPVAFPK	LCQLC	2	C10:+57.021,C13:+57.021	1115.519066	2229.022533	0.000451244	29	N	167	188
Q921I1	Exosome	SPLEK	AVSSFFSGSCVPCADPVAFPK	LCQLC	3	C10:+57.021,C13:+57.021	744.0153109	2229.022533	0.000451244	9	N	167	188
Q921I1	Exosome	VAFPK	LCQLCPGCGCSSTQPFFGYVGAFK	CLKDG	2	C2:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	1371.102183	2740.188766	0.000451244	27	N	188	212
Q921I1	Exosome	VAFPK	LCQLCPGCGCSSTQPFFGYVGAFK	CLKDG	3	C2:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	914.4040554	2740.188766	0.000451244	30	N	188	212
Q921I1	Exosome	SPLGK	DLLFKDSAFGLLR	VPPRM	2		747.9199055	1493.824211	0.002663018	1	N	310	323
Q921I1	Exosome	SPLGK	DLLFKDSAFGLLR	VPPRM	3		498.9492037	1493.824211	0.000451244	17	N	310	323
Q921I1	Exosome	AARVK	AVLTSQETLFGGSDCTGNFCLFK	STTKD	2	C15:+57.021,C20:+57.021	1276.593491	2551.171382	0.000451244	44	N	618	641
Q921I1	Exosome	AARVK	AVLTSQETLFGGSDCTGNFCLFK	STTKD	3	C15:+57.021,C20:+57.021	851.3982607	2551.171382	0.000451244	36	N	618	641
Q921I1	Exosome	TGLGR	SAGWVIPIGLLFCK	LSEPR	2	C13:+57.021	780.93427	1559.85294	0.000622848	25	N	143	157
Q921I1	Exosome	VAFVK	HQTVLDNTEGKNPAEWAK	NLKQE	2		1019.503582	2036.991564	0.000451244	16	N	554	572
Q921I1	Exosome	VAFVK	HQTVLDNTEGKNPAEWAK	NLKQE	3		680.004988	2036.991564	0.000451244	46	N	554	572
Q921I1	Exosome	IGPLK	CAPNNKEEYNGYTGAFR	CLVEK	2	C1:+57.021	995.939529	1989.863458	0.000451244	12	N	525	542
Q921I1	Exosome	IGPLK	CAPNNKEEYNGYTGAFR	CLVEK	3	C1:+57.021	664.2956193	1989.863458	0.000735798	1	N	525	542
Q921I1	Exosome	IGPLK	CAPNNKEEYNGYTGAFR	CLVEK	2	[0:-17.027,C1:+57.021	987.426029	1972.836458	0.000451244	15	N	525	542
Q921I1	Exosome	LDNTR	KPVDQYEDCYLAR	IPSHA	2	C9:+57.021	828.8882451	1655.76089	0.000451244	19	N	251	264
Q921I1	Exosome	LDNTR	KPVDQYEDCYLAR	IPSHA	3	C9:+57.021	552.9280967	1655.76089	0.000451244	3	N	251	264
Q921I1	Exosome	VLPEK	ADRDQYELLCLDNTR	KPVDQ	2	C10:+57.021	941.4419045	1880.868209	0.000451244	235	N	236	251
Q921I1	Exosome	VLPEK	ADRDQYELLCLDNTR	KPVDQ	3	C10:+57.021	627.9638697	1880.868209	0.000451244	514	N	236	251
Q921I1	Exosome	AEWAK	NLKQEDFELLCPDGTR	KPVKD	2	C11:+57.021	967.9677551	1933.91991	0.000451244	40	N	572	588
Q921I1	Exosome	AEWAK	NLKQEDFELLCPDGTR	KPVKD	3	C11:+57.021	645.6477701	1933.91991	0.000451244	14	N	572	588
Q921I1	Exosome	INHCK	FDEFFSQGCAPGYEK	NSTLC	2	C9:+57.021	891.3777102	1780.73982	0.000451244	16	N	497	512
Q921I1	Exosome	EKADR	DQYELLCLDNTR	KPVDQ	2	C7:+57.021	770.3593204	1538.703041	0.000451244	132	N	239	251
Q921I1	Exosome	EKADR	DQYELLCLDNTR	KPVDQ	3	C7:+57.021	513.9088136	1538.703041	0.000451244	17	N	239	251
Q921I1	Exosome	ISEGK	IECESAETTEDCIEK	IVNGE	2	C3:+57.021,C12:+57.021	907.3770156	1812.738431	0.000451244	28	N	383	398
Q921I1	Exosome	GIFPK	GYYAVAVVK	ASDTS	2		485.274357	968.5331139	0.002080925	3	N	446	455

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q921I1	Exosome	KGKSK	DFQLFSSPLGK	DLLFK	2		619.8249424	1237.634285	0.000823681	3	N	299	310
Q921I1	Exosome	PDGTR	KPVKDFASCHLAQAPNHVVVSR	KEKAA	3	C9:+57.021	820.7695052	2459.285116	0.000451244	18	N	588	610
Q921I1	Exosome	PDGTR	KPVKDFASCHLAQAPNHVVVSR	KEKAA	4	C9:+57.021	615.8290789	2459.285116	0.000451244	12	N	588	610
Q921I1	Exosome	FGKGK	SKDFQLFSSPLGK	DLLFK	2		727.3884382	1452.761276	0.000451244	11	N	297	310
Q921I1	Exosome	FGKGK	SKDFQLFSSPLGK	DLLFK	3		485.2615588	1452.761276	0.002981883	1	N	297	310
Q921I1	Exosome	SHLER	TKCDEWSIISEGK	IECES	2	C3:+57.021	776.869521	1551.723442	0.000451244	3	N	370	383
Q921I1	Exosome	RMDYR	LYLGHNYVTAIR	NQQEG	2		710.3913152	1418.76703	0.000451244	3	N	331	343
Q921I1	Exosome	RMDYR	LYLGHNYVTAIR	NQQEG	3		473.9301435	1418.76703	0.000451244	6	N	331	343
Q921I1	Exosome	VVARK	NNGKEDLIWEILK	VAQEH	3		524.6196347	1570.835504	0.000451244	5	N	274	287
Q921I1	Exosome	RKPVK	DFASCHLAQAPNHVVVSR	KEKAA	2	C5:+57.021	1004.494806	2006.974012	0.000451244	6	N	592	610
Q921I1	Exosome	RKPVK	DFASCHLAQAPNHVVVSR	KEKAA	3	C5:+57.021	669.9991372	2006.974012	0.000451244	5	N	592	610
Q921I1	Exosome	RKPVK	DFASCHLAQAPNHVVVSR	KEKAA	4	C5:+57.021	502.7513029	2006.974012	0.000851441	1	N	592	610
Q921I1	Exosome	LERTK	CDEWSIISEGKIECESAETTEDCIEK	IVNGE	3	C1:+57.021,C14:+57.021,C23:+57.021	1040.110691	3117.308672	0.000451244	4	N	372	398
Q921I1	Exosome	EKADR	DQYELLCLDNTRKPVDQYE	DCYLA	2	C7:+57.021	1200.063112	2398.110625	0.001352548	2	N	239	258
Q921I1	Exosome	EKADR	DQYELLCLDNTRKPVDQYE	DCYLA	3	C7:+57.021	800.3780082	2398.110625	0.000698008	1	N	239	258
Q921I1	Exosome	RDDTK	CFVKLPEGTTPEK	YLGAE	3	C1:+57.021	502.5941664	1504.759099	0.000451244	2	N	654	667
Q921I1	Exosome	AARVK	AVLTSQETLFGGSDCTGNFCLF	KSTTK	2	C15:+57.021,C20:+57.021	1212.546009	2423.076419	0.001162105	2	N	618	640
Q921I1	Parental	VGAFK	CLKDGGGDVAFVK	HTTIF	2	[0:-17.027,C1:+57.021	674.8319847	1347.648369	0.0007646	1	N	212	225
Q921I1	Parental	VGAFK	CLKDGGGDVAFVK	HTTIF	3	[0:-17.027,C1:+57.021	450.2239231	1347.648369	0.000451244	35	N	212	225
Q921I1	Parental	VTAIR	NQQEGVCPEGSIDNSPVK	WCALS	2	C7:+57.021	979.4499266	1956.884253	0.000451244	68	N	343	361
Q921I1	Parental	TGAFR	CLVEKGDVAFVK	HQTVL	2	C1:+57.021	682.866053	1363.716506	0.001699387	3	N	542	554
Q921I1	Parental	TGAFR	CLVEKGDVAFVK	HQTVL	3	C1:+57.021	455.5799687	1363.716506	0.000451244	10	N	542	554
Q921I1	Parental	TGAFR	CLVEKGDVAFVK	HQTVL	2	[0:-17.027,C1:+57.021	674.352553	1346.689506	0.000451244	2	N	542	554
Q921I1	Parental	VTAIR	NQQEGVCPEGSIDNSPVKWCALSHLER	TKCDE	3	C7:+57.021,C20:+57.021	1037.48568	3109.433639	0.000451244	16	N	343	370
Q921I1	Parental	VTAIR	NQQEGVCPEGSIDNSPVKWCALSHLER	TKCDE	4	C7:+57.021,C20:+57.021	778.3662097	3109.433639	0.001329271	1	N	343	370
Q921I1	Parental	SPLEK	AVSSFFSGSCVPCADPVAFPK	LCQLC	2	C10:+57.021,C13:+57.021	1115.519066	2229.022533	0.000451244	35	N	167	188
Q921I1	Parental	SPLEK	AVSSFFSGSCVPCADPVAFPK	LCQLC	3	C10:+57.021,C13:+57.021	744.0153109	2229.022533	0.001763695	1	N	167	188
Q921I1	Parental	VAFPK	LCQLCPGCGCSSTQPFFGYVGAFK	CLKDG	2	C2:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	1371.102183	2740.188766	0.000451244	36	N	188	212
Q921I1	Parental	VAFPK	LCQLCPGCGCSSTQPFFGYVGAFK	CLKDG	3	C2:+57.021,C5:+57.021,C8:+57.021,C10:+57.021	914.4040554	2740.188766	0.000451244	19	N	188	212
Q921I1	Parental	SPLGK	DLLFKDSAFGLLR	VPPRM	3		498.9492037	1493.824211	0.000622848	10	N	310	323
Q921I1	Parental	AARVK	AVLTSQETLFGGSDCTGNFCLFK	STTKD	2	C15:+57.021,C20:+57.021	1276.593491	2551.171382	0.000451244	37	N	618	641
Q921I1	Parental	AARVK	AVLTSQETLFGGSDCTGNFCLFK	STTKD	3	C15:+57.021,C20:+57.021	851.3982607	2551.171382	0.000451244	18	N	618	641
Q921I1	Parental	TGLGR	SAGWVIPIGLLFCK	LSEPR	2	C13:+57.021	780.93427	1559.85294	0.000622848	19	N	143	157
Q921I1	Parental	VAFVK	HQTVLDNTEGKNPAEWAK	NLKQE	2		1019.503582	2036.991564	0.000451244	3	N	554	572
Q921I1	Parental	VAFVK	HQTVLDNTEGKNPAEWAK	NLKQE	3		680.004988	2036.991564	0.000451244	15	N	554	572
Q921I1	Parental	IGPLK	CAPNNKEEYNGYTGAFR	CLVEK	2	C1:+57.021	995.939529	1989.863458	0.000451244	6	N	525	542
Q921I1	Parental	IGPLK	CAPNNKEEYNGYTGAFR	CLVEK	2	[0:-17.027,C1:+57.021	987.426029	1972.836458	0.000451244	15	N	525	542
Q921I1	Parental	LDNTR	KPVDQYEDCYLAR	IPSHA	2	C9:+57.021	828.8882451	1655.76089	0.000451244	14	N	251	264
Q921I1	Parental	VLPEK	ADRDQYELLCLDNTR	KPVDQ	2	C10:+57.021	941.4419045	1880.868209	0.000451244	1	N	236	251
Q921I1	Parental	AEWAK	NLKQEDFELLCPDGTR	KPVKD	2	C11:+57.021	967.9677551	1933.91991	0.000451244	19	N	572	588
Q921I1	Parental	AEWAK	NLKQEDFELLCPDGTR	KPVKD	3	C11:+57.021	645.6477701	1933.91991	0.001871652	2	N	572	588
Q921I1	Parental	INHCK	FDEFFSQGCAPGYEK	NSTLC	2	C9:+57.021	891.3777102	1780.73982	0.000698008	3	N	497	512
Q921I1	Parental	EKADR	DQYELLCLDNTR	KPVDQ	2	C7:+57.021	770.3593204	1538.703041	0.000451244	3	N	239	251
Q921I1	Parental	ISEGK	IECESAETTEDCIEK	IVNGE	2	C3:+57.021,C12:+57.021	907.3770156	1812.738431	0.000451244	28	N	383	398
Q921I1	Parental	KGKSK	DFQLFSSPLGK	DLLFK	2		619.8249424	1237.634285	0.0007646	1	N	299	310
Q921I1	Parental	SHLER	TKCDEWSIISEGK	IECES	2	C3:+57.021	776.869521	1551.723442	0.000451244	1	N	370	383
Q921I1	Parental	RMDYR	LYLGHNYVTAIR	NQQEG	2		710.3913152	1418.76703	0.000622848	6	N	331	343
Q921I1	Parental	VAVVK	ASDTSITWNNLK	GKKSC	2		675.3389453	1348.662291	0.000622848	2	N	455	467
Q921I1	Parental	AARVK	AVLTSQETLFGGSDCTGNFCLF	KSTTK	2	C15:+57.021,C20:+57.021	1212.546009	2423.076419	0.0025889	1	N	618	640
Q921M3	Exosome	VAVCR	FSNTGEDWYVLVGVAK	DLILS	2		892.9468486	1783.878097	0.000451244	16	N	895	911
Q921M3	Exosome	LALEK	LGAVFNQVAFPLQYTPR	KFVIH	2		961.0206823	1920.025765	0.000451244	34	N	769	786
Q921M3	Exosome	LALEK	LGAVFNQVAFPLQYTPR	KFVIH	3		641.0163882	1920.025765	0.001162105	2	N	769	786
Q921M3	Exosome	DTYPR	WVTTASLLDYDTVAGADKFGNICVVR	LPPNT	3	C23:+57.021	957.816738	2870.426814	0.000451244	25	N	1031	1057
Q921M3	Exosome	SYQSR	FHLTPLSYETLEFASGFASEQCPEGIVAISTNTLR	ILALE	3	C22:+57.021	1295.972014	3884.892641	0.000451244	40	N	728	763
Q921M3	Exosome	SYQSR	FHLTPLSYETLEFASGFASEQCPEGIVAISTNTLR	ILALE	4	C22:+57.021	972.2309603	3884.892641	0.000451244	16	N	728	763
Q921M3	Exosome	PRPLK	NLVLVDELDSLSPILFCQIADLANEDTPQLYVACGR	GPRSS	3	C17:+57.021,C34:+57.021	1354.678347	4061.011642	0.000451244	24	N	393	429
Q921M3	Exosome	PRPLK	NLVLVDELDSLSPILFCQIADLANEDTPQLYVACGR	GPRSS	4	C17:+57.021,C34:+57.021	1016.26071	4061.011642	0.000451244	2	N	393	429
Q921M3	Exosome	GVLLR	TVLDPVTGDLSDTR	TRYLG	2		744.8811743	1487.746749	0.000451244	1	N	676	690
Q921M3	Exosome	TIGHR	VIVSDVQESFIWVR	YKRNE	2		838.9544767	1675.893353	0.000451244	17	N	999	1013
Q921M3	Exosome	ICVVR	LPPNTNDEVDEDPTGNK	ALWDR	2		927.9217562	1853.827912	0.000451244	13	N	1057	1074
Q921M3	Exosome	EFLHK	TPVEEVPAAIAPFQGR	VLIGV	2		841.4495585	1680.883517	0.000451244	23	N	942	958
Q921M3	Exosome	DTYPR	WVTTASLLDYDTVAGADK	FGNIC	2		963.47871	1924.94182	0.000451244	4	N	1031	1049

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q921M3	Exosome	EQRSR	FLAVGLVDNTVR	IISLD	2		652.3725911	1302.729582	0.000622848	2	N	603	615
Q921M3	Exosome	QYTPR	KFVIHPESNNLIIIETDHNAYTEATK	AQRKQ	4		750.1388871	2996.524348	0.000451244	16	N	786	812
Q921M3	Exosome	KCENK	HIANYISGIQTIGHR	VIVSD	3		560.6379112	1678.890334	0.000451244	3	N	984	999
Q921M3	Exosome	PRPLK	NLVLVDELDSLSPILFC	QIADL	2	C17:+57.021	974.0111001	1946.0066	0.000622848	3	N	393	410
Q921M3	Exosome	THKTK	SMFFFLAQTEQGDIFK	ITLET	2	M2:+15.995	962.9616847	1923.907769	0.000451244	5	N	296	312
Q921M3	Parental	VAVCR	FSNTGEDWYVLVGVAK	DLILS	2		892.9468486	1783.878097	0.000451244	7	N	895	911
Q921M3	Parental	LALEK	LGAVFNQVAFPLQYTPR	KFVIH	2		961.0206823	1920.025765	0.000451244	28	N	769	786
Q921M3	Parental	DTYPR	WVTTASLLDYDTVAGADKFGNICVVR	LPPNT	2	C23:+57.021	1436.221207	2870.426814	0.000823681	1	N	1031	1057
Q921M3	Parental	DTYPR	WVTTASLLDYDTVAGADKFGNICVVR	LPPNT	3	C23:+57.021	957.816738	2870.426814	0.000451244	18	N	1031	1057
Q921M3	Parental	SYQSR	FHLTPLSYETLEFASGFASEQCPEGIVAISTNTLR	ILALE	3	C22:+57.021	1295.972014	3884.892641	0.000451244	25	N	728	763
Q921M3	Parental	SYQSR	FHLTPLSYETLEFASGFASEQCPEGIVAISTNTLR	ILALE	4	C22:+57.021	972.2309603	3884.892641	0.001162105	2	N	728	763
Q921M3	Parental	PNKQK	NVSEELDRTPPEVSK	KLEDI	2		850.42902	1698.84244	0.000622848	8	N	1191	1206
Q921M3	Parental	PRPLK	NLVLVDELDSLSPILFCQIADLANEDTPQLYVACGR	GPRSS	3	C17:+57.021,C34:+57.021	1354.678347	4061.011642	0.000451244	33	N	393	429
Q921M3	Parental	PRPLK	NLVLVDELDSLSPILFCQIADLANEDTPQLYVACGR	GPRSS	4	C17:+57.021,C34:+57.021	1016.26071	4061.011642	0.000451244	2	N	393	429
Q921M3	Parental	GVLLR	TVLDPVTGDLSDTR	TRYLG	2		744.8811743	1487.746749	0.002727428	1	N	676	690
Q921M3	Parental	ICVVR	LPPNTNDEVDEDPTGNK	ALWDR	2		927.9217562	1853.827912	0.000451244	3	N	1057	1074
Q921M3	Parental	DTYPR	WVTTASLLDYDTVAGADK	FGNIC	2		963.47871	1924.94182	0.000451244	9	N	1031	1049
Q921M3	Parental	EQRSR	FLAVGLVDNTVR	IISLD	2		652.3725911	1302.729582	0.000823681	3	N	603	615
Q921M3	Parental	QYTPR	KFVIHPESNNLIIIETDHNAYTEATK	AQRKQ	4		750.1388871	2996.524348	0.000823681	5	N	786	812
Q921M3	Parental	PRPLK	NLVLVDELDSLSPILF	CQIAD	2		893.9960072	1785.976414	0.001162105	4	N	393	409
Q921M3	Parental	SPILF	CQIADLANEDTPQLYVACGR	GPRSS	2	C1:+57.021,C18:+57.021	1147.530694	2293.045787	0.001839721	1	N	409	429
Q921M7	Exosome	LSRMR	INNVPAEGENEVNNELANR	MSLFY	2		1048.50431	2094.993021	0.000451244	30	N	167	186
Q921M7	Exosome	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEKEIYNQVNVVLK	DAEGI	3	C4:+57.021	1477.056695	4428.146684	0.000451244	45	N	6	44
Q921M7	Exosome	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEKEIYNQVNVVLK	DAEGI	4	C4:+57.021	1108.044471	4428.146684	0.000451244	27	N	6	44
Q921M7	Exosome	KLQEK	AWGAVVPLVGK	LKKFY	2		548.8298307	1095.644061	0.000451244	6	N	78	89
Q921M7	Exosome	EAALR	GLLGALTSTPYSPTQHLER	EQALA	3		681.0291336	2040.064001	0.000451244	2	N	105	124
Q921M7	Exosome	NVVLK	DAEGILEDLQSYR	GAGHE	2		754.8655242	1507.715448	0.000451244	18	N	44	57
Q921M7	Exosome	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEK	EIYNQ	3	C4:+57.021	1043.817132	3128.427996	0.001871652	1	N	6	33
Q921M7	Exosome	KGCIK	VLKDQPPNSVEGLLNALR	YTTKH	3		655.0377405	1962.089822	0.000451244	14	N	286	304
Q921M7	Exosome	QALAK	QFAEILHFTLR	FDELK	2		687.8805833	1373.745567	0.002884417	1	N	130	141
Q921M7	Parental	LSRMR	INNVPAEGENEVNNELANR	MSLFY	2		1048.50431	2094.993021	0.000451244	61	N	167	186
Q921M7	Parental	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEKEIYNQVNVVLK	DAEGI	3	C4:+57.021	1477.056695	4428.146684	0.000451244	29	N	6	44
Q921M7	Parental	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEKEIYNQVNVVLK	DAEGI	4	C4:+57.021	1108.044471	4428.146684	0.000451244	21	N	6	44
Q921M7	Parental	KLQEK	AWGAVVPLVGK	LKKFY	2		548.8298307	1095.644061	0.000622848	1	N	78	89
Q921M7	Parental	EAALR	GLLGALTSTPYSPTQHLER	EQALA	2		1021.0398	2040.064001	0.000662267	2	N	105	124
Q921M7	Parental	EAALR	GLLGALTSTPYSPTQHLER	EQALA	3		681.0291336	2040.064001	0.001264573	1	N	105	124
Q921M7	Parental	NVVLK	DAEGILEDLQSYR	GAGHE	2		754.8655242	1507.715448	0.000451244	13	N	44	57
Q921M7	Parental	GNLLK	VLTCTDLEQGPNFFLDFENAQPTESEK	EIYNQ	3	C4:+57.021	1043.817132	3128.427996	0.000823681	1	N	6	33
Q921M7	Parental	KGCIK	VLKDQPPNSVEGLLNALR	YTTKH	2		982.0527108	1962.089822	0.000451244	5	N	286	304
Q921M7	Parental	KGCIK	VLKDQPPNSVEGLLNALR	YTTKH	3		655.0377405	1962.089822	0.000451244	7	N	286	304
Q921W4	Exosome	LEVGR	KVTFFQPDDEVVGILPLDSEDPGLCEVIR	VHEHY	3	C25:+57.021	1096.55536	3286.642681	0.000451244	8	N	75	104
Q921W4	Exosome	DVMEK	LSAGVFRPLLDEPIPLYEAK	VSMEV	3		743.4162176	2227.225253	0.000451244	5	N	309	329
Q921W4	Exosome	CLFLK	GATVAFLNDEVWNLSNAQQGK	YLCIL	2		1131.561628	2261.107657	0.000451244	3	N	277	298
Q921W4	Parental	LEVGR	KVTFFQPDDEVVGILPLDSEDPGLCEVIR	VHEHY	3	C25:+57.021	1096.55536	3286.642681	0.000451244	11	N	75	104
Q921Z5	Exosome	KMVSK	SIATTLIDDTSSEVLDELYR	VTKEY	2		1121.060793	2240.105985	0.000451244	11	N	36	56
Q921Z5	Exosome	KMVSK	SIATTLIDDTSSEVLDELYR	VTKEY	3		747.709795	2240.105985	0.000451244	17	N	36	56
Q921Z5	Exosome	KSHGR	VNNVFDHFSDCDFLAALYNPFGK	FKPHL	3	C11:+57.021	897.4166858	2689.226657	0.000451244	2	N	154	177
Q921Z5	Parental	KMVSK	SIATTLIDDTSSEVLDELYR	VTKEY	2		1121.060793	2240.105985	0.000451244	18	N	36	56
Q921Z5	Parental	KMVSK	SIATTLIDDTSSEVLDELYR	VTKEY	3		747.709795	2240.105985	0.000451244	8	N	36	56
Q921Z5	Parental	KSHGR	VNNVFDHFSDCDFLAALYNPFGK	FKPHL	2	C11:+57.021	1345.621129	2689.226657	0.000823681	2	N	154	177
Q922B2	Exosome	IQTPK	IISAASEGGANVFTVSYFK	NNAYL	2		981.0048949	1959.99419	0.000823681	4	N	222	241
Q922B2	Exosome	VSYFK	NNAYLAQSPQLYK	QMCIC	2		755.3889695	1508.762339	0.000451244	4	N	241	254
Q922B2	Exosome	KVNQK	IGSCTQQDVELHVQK	IYVIS	3	C4:+57.021	581.2898056	1740.846017	0.000451244	8	N	126	141
Q922B2	Exosome	FLVLR	QQQFNVQALVAVGDHASK	QMVKF	3		647.33819	1938.99117	0.000637154	5	N	81	99
Q922B2	Exosome	ANINK	ESIIDVEGVVR	KVNQK	2		608.3331316	1214.650663	0.002519933	1	N	110	121
Q922B2	Parental	VSYFK	NNAYLAQSPQLYK	QMCIC	2		755.3889695	1508.762339	0.002019181	4	N	241	254
Q922B2	Parental	KVNQK	IGSCTQQDVELHVQK	IYVIS	3	C4:+57.021	581.2898056	1740.846017	0.000451244	5	N	126	141
Q922D4	Exosome	ATLEK	QEIIEQLLSNIFHK	EKNES	3		571.3179557	1710.930467	0.000451244	15	N	244	258
Q922D4	Exosome	SLLMK	LYSFLLNESPLNPLLASFFSK	VLSIL	2		1200.646641	2399.277682	0.000451244	1	N	105	126
Q922D4	Exosome	PPQPR	QDVLNWLNEER	IIQRL	2		708.3498443	1414.684089	0.000622848	1	N	179	190
Q922D4	Parental	ATLEK	QEIIEQLLSNIFHK	EKNES	3		571.3179557	1710.930467	0.000451244	13	N	244	258
Q922D4	Parental	SLLMK	LYSFLLNESPLNPLLASFFSK	VLSIL	2		1200.646641	2399.277682	0.000823681	3	N	105	126
Q922D4	Parental	SEEEK	LSTSQDAACKDAEETPEPAEAK	CTAPL	3	C9:+57.021	783.3571613	2347.048084	0.000451244	4	N	792	814
Q922D4	Parental	NIFHK	EKNESAIVSAIQILLTLLETR	RPTFE	3		781.1166078	2340.326423	0.001943752	1	N	258	279
Q922D4	Parental	FHKEK	NESAIVSAIQILLTLLETR	RPTFE	3		695.4040891	2083.188867	0.000451244	1	N	260	279

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q922D8	Exosome	IIAQR	IYGADDIELLPEAQNK	AEIYT	2		894.9548707	1787.894141	0.000622848	4	N	832	848
Q922D8	Exosome	NRFAR	LDIDPETITWQR	VLDTN	2		743.8809773	1485.746355	0.001654178	1	N	520	532
Q922D8	Exosome	GNLAR	EIGLLTEEVELYGETK	AKVLL	2		911.9701864	1821.924773	0.000622848	1	N	336	352
Q922D8	Exosome	FDAVK	CTHWAEGGQGALALAQAVQR	ASQAP	2	[0:-17.027,C1:+57.021	1054.010595	2106.005589	0.000451244	3	N	784	804
Q922D8	Exosome	VNVFK	TDTDAELDLVSR	LSREH	2		667.8258677	1333.636135	0.001591523	1	N	760	772
Q922D8	Parental	NRFAR	LDIDPETITWQR	VLDTN	2		743.8809773	1485.746355	0.00307782	1	N	520	532
Q922F4	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	ECEHC	2		1044.04254	2086.06948	0.000451244	4	Y	103	122
Q922F4	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	ECEHC	3		696.3642934	2086.06948	0.000451244	41	Y	103	122
Q922F4	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	ECEHC	4		522.5251701	2086.06948	0.000451244	6	Y	103	122
Q922F4	Exosome	AIQNK	NSSYFVEWIPNNVK	VAVCD	2		848.9206338	1695.825668	0.000451244	24	Y	336	350
Q922F4	Exosome	AIQNK	NSSYFVEWIPNNVK	VAVCD	3		566.2830226	1695.825668	0.000451244	1	Y	336	350
Q922F4	Exosome	PRGLK	MASTFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.000451244	2	N	362	380
Q922F4	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KECEH	2		979.9950585	1957.974517	0.000451244	26	Y	103	121
Q922F4	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KECEH	3		653.6659724	1957.974517	0.000451244	38	Y	103	121
Q922F4	Exosome	PRGLK	MASTFIGNSTAIQELFK	RISEQ	2		929.4749166	1856.934233	0.000451244	4	N	362	379
Q922F4	Exosome	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	28	Y	183	213
Q922F4	Exosome	SQQYR	ALTVPELTQQMFDAK	NMMAA	2		846.4378027	1690.860005	0.00091018	1	Y	282	297
Q922F4	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	ECEHC	2		1044.04254	2086.06948	0.000451244	30	Y	103	122
Q922F4	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	ECEHC	3		696.3642934	2086.06948	0.000451244	68	Y	103	122
Q922F4	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	ECEHC	4		522.5251701	2086.06948	0.000451244	45	Y	103	122
Q922F4	Parental	AIQNK	NSSYFVEWIPNNVK	VAVCD	2		848.9206338	1695.825668	0.000451244	38	Y	336	350
Q922F4	Parental	AIQNK	NSSYFVEWIPNNVK	VAVCD	3		566.2830226	1695.825668	0.000451244	19	Y	336	350
Q922F4	Parental	PRGLK	MASTFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.000622848	3	N	362	380
Q922F4	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KECEH	2		979.9950585	1957.974517	0.000451244	36	Y	103	121
Q922F4	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KECEH	3		653.6659724	1957.974517	0.000451244	49	Y	103	121
Q922F4	Parental	PRGLK	MASTFIGNSTAIQELFK	RISEQ	2		929.4749166	1856.934233	0.000451244	7	N	362	379
Q922F4	Parental	MPSPK	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	4	C27:+57.021,C37:+57.021	1149.032553	4592.099013	0.001162105	8	Y	174	213
Q922F4	Parental	EPYNA	TLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C16:+57.021,C26:+57.021	1140.190598	3417.548394	0.000823681	4	Y	185	213
Q922F4	Parental	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	125	Y	183	213
Q922F4	Parental	TTSLR	FPGQLNADLRK	LAVNM	3		420.2354554	1257.682966	0.001162105	3	Y	241	252
Q922F4	Parental	TTSLR	FPGQLNADLR	KLAVN	2		565.8018016	1129.588003	0.000451244	5	Y	241	251
Q922F4	Parental	GNNWA	KGHYTEGAELVDSVLDVVR	KECEH	2		1044.04254	2086.06948	0.000451244	3	Y	102	121
Q922P9	Exosome	ARLGR	TPAEVVSTCDITFACVSDPK	AAKDL	2	C9:+57.021,C15:+57.021	1099.011271	2196.006942	0.001162105	4	N	308	328
Q922P9	Parental	ARLGR	TPAEVVSTCDITFACVSDPK	AAKDL	2	C9:+57.021,C15:+57.021	1099.011271	2196.006942	0.000451244	27	N	308	328
Q922P9	Parental	NKGKR	FQQAVDAVEEFLR	RAKGK	2		776.3942519	1550.772904	0.000451244	3	N	78	91
Q922P9	Parental	PKAAK	DLVLGPSGVLQGIRPGK	CYVDM	3		569.3373503	1704.988651	0.001395409	2	N	331	348
Q922P9	Parental	FLDQK	CQNILQGNFKPDFYLK	YIQKD	3	C1:+57.021	662.3368673	1983.987202	0.001699387	1	N	478	494
Q922Q8	Exosome	LLNNR	LVTLPVSFAQLK	NLKWL	2		658.4033599	1314.79112	0.001162105	1	N	96	108
Q922Q8	Parental	ADFGR	LVNLQHLDLLNNR	LVTLP	3		521.299007	1560.873621	0.000451244	8	N	83	96
Q922Q8	Parental	LKNLK	WLDLKDNPLDPVLAK	VAGDC	3		579.6580894	1735.950868	0.00091018	5	N	111	126
Q922Q8	Parental	NLRDK	LDGNELDLSLSDLNEVPVK	ELAAL	2		1035.534214	2069.052827	0.001162105	2	N	14	33
Q922Q8	Parental	GGNLR	DKLDGNELDLSLSDLNEVPVK	ELAAL	2		1157.095167	2312.174733	0.000451244	15	N	12	33
Q922Q8	Parental	GGNLR	DKLDGNELDLSLSDLNEVPVK	ELAAL	3		771.7327111	2312.174733	0.000451244	8	N	12	33
Q922Q8	Parental	LLNNR	LVTLPVSFAQLK	NLKWL	2		658.4033599	1314.79112	0.002080925	1	N	96	108
Q922R8	Exosome	FPTIK	IFQKGESPVDYDGGR	TRSDI	2		834.4053479	1666.795096	0.001591523	2	N	241	256
Q922R8	Exosome	FPTIK	IFQKGESPVDYDGGR	TRSDI	3		556.6061653	1666.795096	0.000451244	5	N	241	256
Q922R8	Exosome	KDVVK	VGAVNADKHQSLGGQYGVQGFPTIK	IFGAN	3		857.7825107	2570.324132	0.000622848	3	N	77	102
Q922R8	Exosome	LSFGR	GSTAPVGGGSFPTITPR	EPWDG	2		801.4182583	1600.820917	0.000451244	8	N	392	409
Q922R8	Exosome	LAVSG	LYSSSDDVIELTPSNFNR	EVIQS	2		1028.995256	2055.974911	0.000451244	23	N	19	37
Q922R8	Exosome	GAAGR	NSYLEVLLK	LADKY	2		539.8113036	1077.607007	0.000451244	29	N	313	322
Q922R8	Exosome	YQGGR	TGEAIVDAALSALR	QLVKD	2		693.88352	1385.75144	0.000451244	44	N	118	132
Q922R8	Exosome	DIVSR	ALDLFSDNAPPPELLEIINEDIAKK	TCEEH	3		922.4922916	2764.453475	0.000451244	14	N	264	289
Q922R8	Exosome	DIVSR	ALDLFSDNAPPPELLEIINEDIAK	KTCEE	3		879.7939706	2636.358512	0.000451244	31	N	264	288
Q922R8	Exosome	KGKVK	LAAVDATVNQVLASR	YGIKG	2		764.428626	1526.841652	0.000451244	24	N	216	231
Q922R8	Exosome	FALLK	GSFSEQGINEFLR	ELSFG	2		742.3629517	1482.710303	0.000451244	18	N	373	386
Q922R8	Exosome	FLAVS	GLYSSSDDVIELTPSNFNR	EVIQS	2		1057.505987	2112.996375	0.000979378	2	N	18	37
Q922R8	Parental	FPTIK	IFQKGESPVDYDGGR	TRSDI	2		834.4053479	1666.795096	0.000451244	25	N	241	256
Q922R8	Parental	FPTIK	IFQKGESPVDYDGGR	TRSDI	3		556.6061653	1666.795096	0.000823681	9	N	241	256
Q922R8	Parental	KDVVK	VGAVNADKHQSLGGQYGVQGFPTIK	IFGAN	2		1286.169866	2570.324132	0.000451244	9	N	77	102
Q922R8	Parental	KDVVK	VGAVNADKHQSLGGQYGVQGFPTIK	IFGAN	3		857.7825107	2570.324132	0.000451244	19	N	77	102
Q922R8	Parental	LSFGR	GSTAPVGGGSFPTITPR	EPWDG	2		801.4182583	1600.820917	0.000451244	24	N	392	409
Q922R8	Parental	CGHCK	NLEPEWAAAATEVKEQTK	GKVKL	2		1008.008166	2014.000732	0.000451244	12	N	194	212
Q922R8	Parental	LAVSG	LYSSSDDVIELTPSNFNR	EVIQS	2		1028.995256	2055.974911	0.000451244	46	N	19	37
Q922R8	Parental	GAAGR	NSYLEVLLK	LADKY	2		539.8113036	1077.607007	0.000451244	34	N	313	322
Q922R8	Parental	YQGGR	TGEAIVDAALSALR	QLVKD	2		693.88352	1385.75144	0.000451244	41	N	118	132

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q922R8	Parental	YQGGR	TGEAIVDAALSALR	QLVKD	3		462.9249467	1385.75144	0.000451244	25	N	118	132
Q922R8	Parental	SNFNR	EVIQSDGLWLVEFYAPWCGHCQR	LTPEW	3	C18:+57.021,C21:+57.021	950.775954	2849.304462	0.000451244	7	N	37	60
Q922R8	Parental	DIVSR	ALDLFSDNAPPPELLEIINEDIAKK	TCEEH	3		922.4922916	2764.453475	0.000451244	60	N	264	289
Q922R8	Parental	DIVSR	ALDLFSDNAPPPELLEIINEDIAK	KTCEE	2		1319.187056	2636.358512	0.000451244	30	N	264	288
Q922R8	Parental	DIVSR	ALDLFSDNAPPPELLEIINEDIAK	KTCEE	3		879.7939706	2636.358512	0.000451244	23	N	264	288
Q922R8	Parental	KGKVK	LAAVDATVNQVLASR	YGIKG	2		764.428626	1526.841652	0.000451244	32	N	216	231
Q922R8	Parental	KGKVK	LAAVDATVNQVLASR	YGIKG	3		509.9550174	1526.841652	0.002296037	1	N	216	231
Q922R8	Parental	QTKGK	VKLAAVDATVNQVLASR	YGIKG	2		878.0103146	1754.005029	0.000662267	1	N	214	231
Q922R8	Parental	QTKGK	VKLAAVDATVNQVLASR	YGIKG	3		585.6761431	1754.005029	0.001329271	1	N	214	231
Q922R8	Parental	FALLK	GSFSEQGINEFLR	ELSFG	2		742.3629517	1482.710303	0.000451244	8	N	373	386
Q922R8	Parental	FLAVS	GLYSSSDDVIELTPSNFNR	EVIQS	2		1057.505987	2112.996375	0.000451244	16	N	18	37
Q922R8	Parental	ALDLF	SDNAPPPELLEIINEDIAK	KTCEE	2		1039.536756	2077.057912	0.000622848	2	N	269	288
Q922R8	Parental	PWDGK	DGELPVEDDIDLSDVELDDLEKDEL	-	2		1415.648551	2829.281503	0.000998612	3	N	415	440
Q922R8	Parental	PWDGK	DGELPVEDDIDLSDVELDDLEKDEL	-	3		944.1016343	2829.281503	0.001763695	1	N	415	440
Q922R8	Parental	VNADK	HQSLGGQYGVQGFPTIK	IFGAN	2		908.9711894	1815.926779	0.000451244	1	N	85	102
Q922R8	Parental	DIAKK	TCEEHQLCVVAVLPHILDTGAAGR	NSYLE	3	C2:+57.021,C8:+57.021	882.775954	2645.304462	0.000451244	3	N	289	313
Q922R8	Parental	DIAKK	TCEEHQLCVVAVLPHILDTGAAGR	NSYLE	4	C2:+57.021,C8:+57.021	662.3339155	2645.304462	0.000662267	3	N	289	313
Q922S4	Exosome	LQVAK	NLFTHLDDVSVLLQEIITEAR	NLSNA	3		809.436229	2425.285287	0.000451244	3	N	377	398
Q922S4	Exosome	ITEAR	NLSNAEICSVFLLDQNELVAK	VFDGG	2	C8:+57.021	1189.107323	2376.199046	0.000451244	9	N	398	419
Q922S4	Exosome	SLQLK	VLQYLQQETQATHCCLLLVSEDNLQLSCK	VIGDK	3	C14:+57.021,C15:+57.021,C28:+57.021	1164.57049	3490.68807	0.000451244	7	N	223	252
Q922S4	Exosome	DEYTK	LLHDGIQPVAAIDSNFANFTYTPR	SLPED	3		887.4542826	2659.339448	0.000451244	16	N	560	584
Q922S4	Exosome	ELVAK	VFDGGVVDDESYEIR	IPADQ	2		850.3946459	1698.773692	0.000662267	3	N	419	434
Q922S4	Exosome	SYEIR	IPADQGIAGHVATTGQILNIPDAYAHPLFYR	GVDDS	4		830.6865358	3318.714943	0.001591523	4	N	434	465
Q922S4	Parental	LQVAK	NLFTHLDDVSVLLQEIITEAR	NLSNA	3		809.436229	2425.285287	0.000451244	15	N	377	398
Q922S4	Parental	ITEAR	NLSNAEICSVFLLDQNELVAK	VFDGG	2	C8:+57.021	1189.107323	2376.199046	0.000451244	33	N	398	419
Q922S4	Parental	ISQKR	LSCNGLGPSDLLGKPLAR	LVAPL	3	C3:+57.021	623.3405003	1866.998101	0.00091018	2	N	95	113
Q922S4	Parental	SLQLK	VLQYLQQETQATHCCLLLVSEDNLQLSCK	VIGDK	3	C14:+57.021,C15:+57.021,C28:+57.021	1164.57049	3490.68807	0.000451244	6	N	223	252
Q922S4	Parental	DEYTK	LLHDGIQPVAAIDSNFANFTYTPR	SLPED	3		887.4542826	2659.339448	0.001654178	1	N	560	584
Q922S4	Parental	ELVAK	VFDGGVVDDESYEIR	IPADQ	2		850.3946459	1698.773692	0.000823681	1	N	419	434
Q922S4	Parental	SYEIR	IPADQGIAGHVATTGQILNIPDAYAHPLFYR	GVDDS	3		1107.246114	3318.714943	0.001871652	1	N	434	465
Q922S4	Parental	MYHMK	VSDDEYTKLLHDGIQPVAAIDSNFANFTYTPR	SLPED	3		1199.921913	3596.74234	0.002374549	1	N	552	584
Q922S4	Parental	GFRTR	NILCFPIKNENQEVIGVAELVNK	INGPW	3	C4:+57.021	881.1391524	2640.394057	0.000451244	15	N	476	499
Q922S4	Parental	KFTIR	GLPSNNSLDFLDEEYEVPDLDGTR	APVNG	2		1348.122641	2694.229682	0.001699387	1	N	881	905
Q922S4	Parental	PWFSK	FDEDLATAFSIYCGISIAHSLLYK	KVNEA	3	C13:+57.021	912.1196465	2733.335539	0.000451244	5	N	507	531
Q923B6	Exosome	AHVVK	AFNTISAWALQSGTLDASR	QVFVC	2		1005.0085	2008.001401	0.000451244	4	N	132	151
Q923B6	Exosome	LAMHR	EHYDSLTELVDYLK	GKVLV	3		575.6179595	1723.830478	0.000451244	2	N	83	97
Q923B6	Parental	-MEK	AHADEFPLTTDSSEKQGVVCIFGTGDFGK	SLGLK	3	C20:+57.021	1038.489238	3112.444315	0.000451244	2	N	3	32
Q923B6	Parental	LAMHR	EHYDSLTELVDYLKGK	VLVDV	3		637.3234351	1908.946905	0.000451244	2	N	83	99
Q923B6	Parental	AHVVK	AFNTISAWALQSGTLDASR	QVFVC	2		1005.0085	2008.001401	0.000451244	11	N	132	151
Q923B6	Parental	DSSEK	QGVVCIFGTGDFGK	SLGLK	2	C5:+57.021	742.8640416	1483.712483	0.000622848	6	N	18	32
Q923B6	Parental	FVQSK	LGYLTLVLCTAHTLVYGGK	RFLSP	3	C9:+57.021	693.7154558	2078.122967	0.002727428	1	N	385	404
Q923B6	Parental	SNNRK	INQYPESNAEYLAQLEPGAHVVK	AFNTI	3		857.4348881	2569.281264	0.000451244	4	N	109	132
Q923B6	Parental	LAMHR	EHYDSLTELVDYLK	GKVLV	2		862.9230392	1723.830478	0.000451244	4	N	83	97
Q923B6	Parental	LAMHR	EHYDSLTELVDYLK	GKVLV	3		575.6179595	1723.830478	0.000451244	20	N	83	97
Q923L7	Exosome	RYQTK	GSVEYYTVACEPR	VAWDC	2	C10:+57.021	765.8485886	1529.681577	0.000451244	66	N	123	136
Q923L7	Exosome	ACEPR	VAWDCPIYPVVPVHLDGTF	-	2	C5:+57.021	1093.043266	2184.070932	0.000622848	12	N	136	155
Q923L7	Exosome	ACEPR	VAWDCPIYPVVPVHLDGTF	-	3	C5:+57.021	729.0314439	2184.070932	0.000622848	6	N	136	155
Q923L7	Parental	RYQTK	GSVEYYTVACEPR	VAWDC	2	C10:+57.021	765.8485886	1529.681577	0.000451244	19	N	123	136
Q923L7	Parental	ACEPR	VAWDCPIYPVVPVHLDGTF	-	2	C5:+57.021	1093.043266	2184.070932	0.000622848	6	N	136	155
Q93092	Exosome	EEQIK	NAIDKLFVLFGAEILK	KIPGR	2		896.024902	1790.034204	0.000451244	7	N	81	97
Q93092	Exosome	EEQIK	NAIDKLFVLFGAEILK	KIPGR	3		597.685868	1790.034204	0.000451244	35	N	81	97
Q93092	Exosome	NAIDK	LFVLFGAEILK	KIPGR	2		625.3818962	1248.748192	0.000451244	19	N	86	97
Q93092	Exosome	TGEIK	ALAGCDFLTISPK	LLGEL	2	C5:+57.021	696.8635103	1391.711421	0.000451244	23	N	245	258
Q93092	Exosome	TISPK	LLGELLKDNSK	LAPAL	2		615.3591494	1228.702699	0.000451244	12	N	258	269
Q93092	Parental	EEQIK	NAIDKLFVLFGAEILK	KIPGR	2		896.024902	1790.034204	0.000823681	4	N	81	97
Q93092	Parental	EEQIK	NAIDKLFVLFGAEILK	KIPGR	3		597.685868	1790.034204	0.000451244	32	N	81	97
Q93092	Parental	NAIDK	LFVLFGAEILK	KIPGR	2		625.3818962	1248.748192	0.000451244	5	N	86	97
Q93092	Parental	TISPK	LLGELLKDNSK	LAPAL	2		615.3591494	1228.702699	0.001591523	2	N	258	269
Q99J09	Exosome	QGVTR	LVFSPHSVPLLTSLSEDCSLAVLDSSLSEVFR	SRAHR	3	C18:+57.021	1168.936241	3503.785322	0.000451244	16	N	260	292
Q99J09	Exosome	LNSYR	AHAGQVTCVAASPHKDSVFLSCSEDSR	ILLWD	4	C8:+57.021,C22:+57.021	729.8398277	2915.328111	0.000451244	6	N	164	191
Q99J09	Exosome	LVDTK	NASCTLSSAVHSQGVTR	LVFSP	3	C4:+57.021	592.2885762	1773.842329	0.000823681	7	N	243	260
Q99J09	Parental	QGVTR	LVFSPHSVPLLTSLSEDCSLAVLDSSLSEVFR	SRAHR	3	C18:+57.021	1168.936241	3503.785322	0.000451244	20	N	260	292
Q99J09	Parental	LNSYR	AHAGQVTCVAASPHKDSVFLSCSEDSR	ILLWD	4	C8:+57.021,C22:+57.021	729.8398277	2915.328111	0.000451244	1	N	164	191

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99J45	Exosome	RPTAR	ELLFHPALFEVPSLK	LLAAH	3		580.6630634	1738.96579	0.00091018	11	N	319	334
Q99J45	Exosome	AGPGR	EPVQTLYSQSPALELDKFLEDVR	NGIYP	3		893.1293532	2676.36466	0.000451244	1	N	375	398
Q99J45	Parental	RPTAR	ELLFHPALFEVPSLK	LLAAH	3		580.6630634	1738.96579	0.001395409	5	N	319	334
Q99J45	Parental	AGPGR	EPVQTLYSQSPALELDKFLEDVR	NGIYP	3		893.1293532	2676.36466	0.00091018	1	N	375	398
Q99J62	Parental	AVLRK	SLEGADLPNLLFYGPPGTGK	TSTIL	2		1023.531277	2045.046954	0.000637154	1	N	64	84
Q99J62	Parental	LTGGK	EVSEDVITDIAGVIPAATIDGIFTACHSGSFDKLEAVVK	NLIDE	4	C26:+57.021	1019.520366	4074.050264	0.001871652	1	N	255	294
Q99J77	Exosome	MDTMK	QVYQIVKPLNPNFCFLQCTSAYPLQPEDANLR	VISEY	3	C14:+57.021,C18:+57.021	1275.302886	3822.885259	0.000451244	33	N	166	198
Q99J77	Exosome	MDTMK	QVYQIVKPLNPNFCFLQCTSAYPLQPEDANLR	VISEY	4	C14:+57.021,C18:+57.021	956.7291148	3822.885259	0.000823681	1	N	166	198
Q99J77	Exosome	MDTMK	QVYQIVKPLNPNFCFLQCTSAYPLQPEDANLR	VISEY	3	Q1:-17.027,C14:+57.021,C18:+57.021	1269.62722	3805.858259	0.000451244	5	N	166	198
Q99J77	Exosome	MDTMK	QVYQIVKPLNPNFCFLQCTSAYPLQPEDANLR	VISEY	3	[0:-17.027,C14:+57.021,C18:+57.021	1269.62722	3805.858259	0.000451244	7	N	166	198
Q99J77	Exosome	SEYQK	LFPDIPIGYSGHETGIAISVAAVALGAK	VLERH	3		923.1730048	2766.495614	0.000451244	17	N	205	233
Q99J77	Exosome	DKTWK	GSDHSASLEPGELAELVR	SVRLV	2		933.9637584	1865.911917	0.000451244	13	N	246	264
Q99J77	Exosome	DKTWK	GSDHSASLEPGELAELVR	SVRLV	3		622.9784389	1865.911917	0.000451244	5	N	246	264
Q99J77	Exosome	SVVAK	VKIPAGTTLTLDMLTVK	VGEPK	3		601.0221518	1800.043055	0.001264573	1	N	298	315
Q99J77	Exosome	WVGGK	HPCFIIAEIGQNHQGDIDVAKR	MIRTA	4	C3:+57.021	630.3213524	2517.25421	0.000451244	11	N	16	38
Q99J77	Exosome	VPFFK	VGSGDTNNFPYLEK	TAKKG	2		770.8680669	1539.720534	0.000451244	6	N	131	145
Q99J77	Exosome	-M	PLELELCPGR	WVGGK	2	C7:+57.021	592.3109136	1182.606227	0.000622848	1	N	1	11
Q99J77	Exosome	WVGGK	HPCFIIAEIGQNHQGDIDVAK	RMIRT	3	C3:+57.021	788.0588328	2361.153098	0.000622848	1	N	16	37
Q99J77	Parental	MDTMK	QVYQIVKPLNPNFCFLQCTSAYPLQPEDANLR	VISEY	3	C14:+57.021,C18:+57.021	1275.302886	3822.885259	0.000451244	18	N	166	198
Q99J77	Parental	SEYQK	LFPDIPIGYSGHETGIAISVAAVALGAK	VLERH	3		923.1730048	2766.495614	0.000451244	4	N	205	233
Q99J99	Exosome	LFKEK	KVDLSKPLVATCGSGVTACHVVLGAFLCGK	SDVPV	3	C12:+57.021,C19:+57.021,C28:+57.021	1048.883792	3143.627976	0.000451244	6	N	236	266
Q99J99	Exosome	LFKEK	KVDLSKPLVATCGSGVTACHVVLGAFLCGK	SDVPV	4	C12:+57.021,C19:+57.021,C28:+57.021	786.9147941	3143.627976	0.000451244	12	N	236	266
Q99J99	Exosome	PQLFR	ALVSAQWVAEALK	APRSS	2		693.3935235	1384.771447	0.000451244	26	N	8	21
Q99J99	Exosome	SQPLK	LLDASWYLPK	LGRDA	2		603.3324032	1204.649206	0.000451244	18	N	30	40
Q99J99	Exosome	WWMFR	AFGHHSVSLLDGGFR	HWLNQ	3		533.9395902	1598.79537	0.000451244	8	N	118	133
Q99J99	Exosome	EFEER	HIPGAAFFDIDR	CSDHT	3		453.5670936	1357.677881	0.000451244	10	N	52	64
Q99J99	Exosome	DGGFR	HWLNQNLPISSGK	SHSEP	2		747.3971289	1492.778658	0.002453667	1	N	133	146
Q99J99	Exosome	PSFIK	THEDILENLDAR	RFQVV	2		713.352584	1424.689568	0.000451244	7	N	164	176
Q99J99	Exosome	FKEKK	VDLSKPLVATCGSGVTACHVVLGAFLCGK	SDVPV	4	C11:+57.021,C18:+57.021,C27:+57.021	754.8910533	3015.533013	0.00307782	1	N	237	266
Q99J99	Exosome	APQLF	RALVSAQWVAEALK	APRSS	3		514.6319861	1540.872558	0.002019181	1	N	7	21
Q99JB2	Parental	AEAIR	ILAGALTQHNGDAAASLTVAEQYVSAFSK	LAKDS	3		978.5054828	2932.493048	0.000622848	6	N	259	288
Q99JB2	Parental	VFRER	ESLNANIVDAINQAADCWGIR	CLRYE	2	C17:+57.021	1165.563614	2329.111628	0.000451244	9	N	150	171
Q99JB2	Parental	VFRER	ESLNANIVDAINQAADCWGIR	CLRYE	3	C17:+57.021	777.3783425	2329.111628	0.000622848	2	N	150	171
Q99JB2	Parental	SGLPR	NTVILFVPQQEAWVVER	MGRFH	2		1014.549804	2027.084008	0.000451244	5	N	34	51
Q99JB2	Parental	SEAEK	AEQINQAAGEASAVLAK	AKAKA	2		835.9395549	1669.86351	0.000622848	1	N	233	250
Q99JI4	Exosome	-M	PLENLEEEGLPKNPDLR	IAQLR	3		655.0097391	1962.005817	0.000451244	8	N	1	18
Q99JI4	Exosome	RLHCK	IDKVNEIVETNRPDSK	NWQYQ	3		619.6624508	1855.963952	0.000451244	10	N	346	362
Q99JI4	Exosome	AMMAK	AEYLCQIGDKEGALTAFR	KTYDK	3	C5:+57.021	681.3389366	2040.99341	0.000451244	2	N	107	125
Q99JI4	Exosome	EKVIK	GAEILEVLHSLPAVR	QYLFS	3		535.3109126	1602.909338	0.000451244	12	N	242	257
Q99JI4	Parental	-M	PLENLEEEGLPKNPDLR	IAQLR	2		982.0107086	1962.005817	0.000451244	5	N	1	18
Q99JI4	Parental	-M	PLENLEEEGLPKNPDLR	IAQLR	3		655.0097391	1962.005817	0.000451244	9	N	1	18
Q99JI4	Parental	RLHCK	IDKVNEIVETNRPDSK	NWQYQ	4		464.9987881	1855.963952	0.000622848	3	N	346	362
Q99JI4	Parental	EKVIK	GAEILEVLHSLPAVR	QYLFS	3		535.3109126	1602.909338	0.000451244	5	N	242	257
Q99JR1	Parental	VHDYR	QGIVPAGLTENELWR	AKYAY	2		841.947183	1681.878766	0.000823681	4	N	55	70
Q99JR1	Parental	NYTNR	SGDAPLTVNELGTAYVSATTGAVATALGLNALTK	RVSPL	3		1083.240583	3246.69835	0.000451244	18	N	136	170
Q99JR1	Parental	NYTNR	SGDAPLTVNELGTAYVSATTGAVATALGLNALTKR	VSPLI	3		1135.274287	3402.799461	0.000451244	8	N	136	171
Q99JR1	Parental	VTDPR	NILLTNEQLENAR	KVVHD	2		764.4104333	1526.805267	0.000451244	19	N	35	48
Q99JR1	Parental	LWRAK	YAYDSAFHPDTGEK	MTLIG	2		800.8498741	1599.684148	0.001329271	1	N	72	86
Q99JR1	Parental	PAVLF	WQWINQSFNAVVNYTNR	SGDAP	2		1070.522109	2139.028618	0.000870037	2	N	119	136
Q99JT2	Exosome	EELEK	SIAVAETACPGITDK	MVKKL	2	C9:+57.021	766.8851711	1531.754742	0.000622848	1	N	383	398
Q99JT2	Exosome	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSSYVTK	YYGSY	3	C24:+57.021	1204.905112	3611.691935	0.000451244	7	N	53	84
Q99JT2	Exosome	AYDSK	ADIWSLGITAIELAK	GEPPN	2		800.9514027	1599.887205	0.000451244	15	Y	199	214
Q99JT2	Parental	EELEK	SIAVAETACPGITDK	MVKKL	2	C9:+57.021	766.8851711	1531.754742	0.000451244	12	N	383	398
Q99JT2	Parental	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSSYVTK	YYGSY	3	C24:+57.021	1204.905112	3611.691935	0.000451244	36	N	53	84
Q99JT2	Parental	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSSYVTK	YYGSY	4	C24:+57.021	903.9307838	3611.691935	0.000451244	7	N	53	84
Q99JT2	Parental	QGDVK	LADFGVAGQLTDTQIKR	NTFVG	2		916.9974042	1831.979208	0.000622848	2	Y	159	176
Q99JT2	Parental	QGDVK	LADFGVAGQLTDTQIKR	NTFVG	3		611.6675361	1831.979208	0.000622848	7	Y	159	176
Q99JT2	Parental	AYDSK	ADIWSLGITAIELAK	GEPPN	2		800.9514027	1599.887205	0.000451244	26	Y	199	214
Q99JT2	Parental	AYDSK	ADIWSLGITAIELAK	GEPPN	3		534.3035351	1599.887205	0.000451244	3	Y	199	214
Q99JW2	Exosome	RQYLR	ICTVQPNPDYGGAITFLEER	ARQLG	2	C2:+57.021	1140.552183	2279.088767	0.000451244	10	N	21	41

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99JW2	Exosome	FQALR	AGFALDEGLANPTDAFTVFYSER	SPWWV	2		1246.092958	2490.170317	0.000451244	9	N	168	191
Q99JW2	Parental	RQYLR	ICTVQPNPDYGGAITFLEER	ARQLG	2	C2:+57.021	1140.552183	2279.088767	0.000451244	1	N	21	41
Q99JW4	Exosome	PECFR	CDLCQEVLADIGFVK	NAGRH	2	C1:+57.021,C4:+57.021	883.9262817	1765.836963	0.000451244	26	N	96	111
Q99JW4	Exosome	PECFR	CDLCQEVLADIGFVK	NAGRH	3	C1:+57.021,C4:+57.021	589.6201211	1765.836963	0.000451244	10	N	96	111
Q99JW4	Exosome	APAEK	IVNSNGELYHEQCFVCAQCFQQFPEGLFYEFEGR	KYCEH	3	C13:+57.021,C16:+57.021,C19:+57.021	1401.620572	4201.838317	0.001463592	1	N	22	56
Q99JW4	Exosome	SALNK	AWCVSCFACSTCNTK	LTLKN	2	C3:+57.021,C6:+57.021,C9:+57.021,C12:+57.021	926.3672881	1850.718976	0.000451244	3	N	269	284
Q99JW4	Parental	PECFR	CDLCQEVLADIGFVK	NAGRH	2	C1:+39.994,C4:+57.021	875.4127817	1748.809963	0.000451244	4	N	96	111
Q99JW4	Parental	PECFR	CDLCQEVLADIGFVK	NAGRH	2	C1:+57.021,C4:+57.021	883.9262817	1765.836963	0.000451244	27	N	96	111
Q99JW4	Parental	PECFR	CDLCQEVLADIGFVK	NAGRH	3	C1:+57.021,C4:+57.021	589.6201211	1765.836963	0.000451244	30	N	96	111
Q99JW4	Parental	PECFR	CDLCQEVLADIGFVK	NAGRH	2	[0:-17.027,C1:+57.021,C4:+57.021	875.4127817	1748.809963	0.000451244	3	N	96	111
Q99JW4	Parental	APAEK	IVNSNGELYHEQCFVCAQCFQQFPEGLFYEFEGR	KYCEH	3	C13:+57.021,C16:+57.021,C19:+57.021	1401.620572	4201.838317	0.000451244	25	N	22	56
Q99JW4	Parental	SALNK	AWCVSCFACSTCNTK	LTLKN	2	C3:+57.021,C6:+57.021,C9:+57.021,C12:+57.021	926.3672881	1850.718976	0.000451244	6	N	269	284
Q99JW4	Parental	YICQK	CHAIIDEQPLIFKNDPYHPDHFNCANCGK	ELTAD	3	C1:+57.021,C24:+57.021,C27:+57.021	1170.864119	3509.568958	0.000698008	1	N	137	166
Q99JW4	Parental	TADAR	ELKGELYCLPCHDK	MGVPI	4	C8:+57.021,C11:+57.021	441.2132119	1760.821648	0.000823681	1	N	173	187
Q99JX3	Parental	TLELR	EASVTPSNLWGGQGLLGVSIR	FCSFD	2		1071.071632	2140.127664	0.000451244	25	N	80	101
Q99JX3	Parental	SPGHR	AGLEPFFDFIVSINGSR	LNKDN	2		934.9812228	1867.946846	0.000451244	8	N	30	47
Q99JX3	Parental	SPGHR	AGLEPFFDFIVSINGSR	LNKDN	3		623.6567485	1867.946846	0.000451244	4	N	30	47
Q99JX3	Parental	MTTAK	ADASSLTVDVTSPASKVPTTVEDR	VSDCT	2		1223.619537	2445.223475	0.001352548	1	N	406	430
Q99JX3	Parental	TVEDR	VSDCTPAVEKPVSDADASEPS	-	2	C4:+57.021	1080.983996	2159.952392	0.002374549	3	N	430	451
Q99JX3	Parental	MTTAK	ADASSLTVDVTSPASK	VPTTV	2		774.891739	1547.767878	0.001162105	1	N	406	422
Q99JX3	Parental	TDNCR	EVIITPNSAWGGEGSLGCGIGYGYLHR	IPTRP	3	C18:+57.021	955.1329491	2862.375447	0.001264573	4	N	174	201
Q99JX3	Parental	AKPLK	LYVYNTDTDNCR	EVIIT	2	C11:+57.021	767.3358453	1532.656091	0.000451244	1	N	162	174
Q99JX4	Exosome	RTFGK	QQWQQLYDTLNAWK	QNLNK	2		911.4500898	1820.88458	0.000622848	4	N	344	358
Q99JX4	Exosome	RTFGK	QQWQQLYDTLNAWK	QNLNK	3		607.9693265	1820.88458	0.002296037	1	N	344	358
Q99JX4	Exosome	LKPVK	FLEGELIHDLLTIFVSAK	LASYV	3		682.3826253	2044.124476	0.000622848	2	N	230	248
Q99JX4	Exosome	CSLIK	VAASCGAIQYIPTELDQVR	KWISD	2	C5:+57.021	1046.030887	2090.046174	0.001329271	1	N	129	148
Q99JX4	Exosome	RCIVR	ALKDPNAFLFDHLLTLKPVK	FLEGE	4		570.8338429	2279.304172	0.000451244	13	N	210	230
Q99JX4	Exosome	DAASK	VMVELLGSYTEDNASQAR	VDAHR	3		661.6549678	1981.941504	0.002884417	1	N	183	201
Q99JX4	Parental	LKPVK	FLEGELIHDLLTIFVSAK	LASYV	3		682.3826253	2044.124476	0.000451244	4	N	230	248
Q99JX4	Parental	CSLIK	VAASCGAIQYIPTELDQVR	KWISD	2	C5:+57.021	1046.030887	2090.046174	0.001162105	3	N	129	148
Q99JX4	Parental	RCIVR	ALKDPNAFLFDHLLTLKPVK	FLEGE	4		570.8338429	2279.304172	0.000451244	4	N	210	230
Q99JX4	Parental	CSLIK	VAASCGAIQYIPTELDQVRK	WISDW	3	C5:+57.021	740.3881789	2218.141137	0.001329271	2	N	129	149
Q99JX7	Exosome	RAFTR	TFIAVPASNSGLCIVNDELFVR	NASPE	2	C13:+57.021	1211.625683	2421.235766	0.000451244	6	N	514	536
Q99JX7	Exosome	LKHTR	LNVVAFLNELPK	TQHDV	2		678.8984417	1355.781283	0.000823681	3	N	458	470
Q99JX7	Parental	RAFTR	TFIAVPASNSGLCIVNDELFVR	NASPE	2	C13:+57.021	1211.625683	2421.235766	0.000451244	13	N	514	536
Q99JX7	Parental	RAFTR	TFIAVPASNSGLCIVNDELFVR	NASPE	3	C13:+57.021	808.0863885	2421.235766	0.001329271	1	N	514	536
Q99JX7	Parental	RENRR	ISIIINASAPPYTVQNELKPEQIEQLK	LIMSK	3		1012.892567	3035.6543	0.001763695	1	N	185	212
Q99JY0	Exosome	TNIPK	DVVDYIIFGTVIQEVK	TSNVA	2		919.5014568	1836.987314	0.000637154	1	N	96	112
Q99JY0	Parental	GLLHR	TNIPKDVVDYIIFGTVIQEVK	TSNVA	3		797.7777036	2390.309711	0.000451244	8	N	91	112
Q99JY0	Parental	KAYLR	DFIYVSQDPKDQLLLGPTYATPK	VLEKA	2		1305.179034	2608.342468	0.001395409	1	N	339	362
Q99JY0	Parental	TNIPK	DVVDYIIFGTVIQEVK	TSNVA	2		919.5014568	1836.987314	0.000823681	3	N	96	112
Q99JY0	Parental	TNIPK	DVVDYIIFGTVIQEVK	TSNVA	3		613.3369045	1836.987314	0.000451244	2	N	96	112
Q99JY9	Exosome	QQLLR	DREVGIPPEQSLETAK	AVKER	2		884.9579447	1767.900289	0.000451244	106	N	209	225
Q99JY9	Exosome	QQLLR	DREVGIPPEQSLETAK	AVKER	3		590.3078965	1767.900289	0.000622848	4	N	209	225
Q99JY9	Exosome	AISKK	EFSIDVGYER	FLGPE	2		607.7885569	1213.561514	0.000451244	57	N	265	275
Q99JY9	Exosome	QVIFK	YLRAEPEDHYFLLTEPPLNTPENR	EYTAE	3		972.1510399	2913.42972	0.000451244	15	N	99	123
Q99JY9	Exosome	RRVMK	GVDDLDFFIGDEAIEKPTYATK	WPIRH	2		1222.597542	2443.179484	0.000451244	51	N	53	75
Q99JY9	Exosome	RRVMK	GVDDLDFFIGDEAIEKPTYATK	WPIRH	3		815.4009615	2443.179484	0.000451244	60	N	53	75
Q99JY9	Exosome	TGYTK	LGYAGNTEPQFIIPSCIAIK	ESAKV	2	C16:+57.021	1096.57493	2191.13426	0.000451244	61	N	18	38
Q99JY9	Exosome	TGYTK	LGYAGNTEPQFIIPSCIAIK	ESAKV	3	C16:+57.021	731.3858868	2191.13426	0.000451244	30	N	18	38
Q99JY9	Exosome	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	HIPIA	3	C28:+57.021	1020.197396	3057.568787	0.000451244	144	N	161	191
Q99JY9	Exosome	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	HIPIA	4	C28:+57.021	765.3999968	3057.568787	0.000451244	30	N	161	191
Q99JY9	Exosome	PIAGR	DITYFIQQLLR	DREVG	2		705.3935235	1408.771447	0.000451244	85	N	198	209
Q99JY9	Exosome	PIAGR	DITYFIQQLLR	DREVG	3		470.5982824	1408.771447	0.000451244	19	N	198	209
Q99JY9	Exosome	VGYER	FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C32:+57.021	1439.372177	4315.093132	0.000451244	95	N	275	312
Q99JY9	Exosome	VGYER	FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	4	C32:+57.021	1079.781083	4315.093132	0.000451244	51	N	275	312
Q99JY9	Exosome	-MAGR	LPACVVDCGTGYTK	LGYAG	2	C4:+57.021,C8:+57.021	770.8604104	1539.705221	0.000451244	125	N	4	18
Q99JY9	Exosome	NAISK	KEFSIDVGYER	FLGPE	3		448.2266256	1341.656477	0.000451244	22	N	264	275
Q99JY9	Exosome	CHTKK	DYEEIGPSICR	HNPVF	2	C10:+57.021	669.8036497	1337.591699	0.000451244	41	N	398	409
Q99JY9	Exosome	AGRDI	TYFIQQLLR	DREVG	2		591.3380199	1180.66044	0.001229886	3	N	200	209

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99JY9	Exosome	FKYLR	AEPEDHYFLLTEPPLNTPENR	EYTAE	2		1241.598408	2481.181216	0.000451244	55	N	102	123
Q99JY9	Exosome	FKYLR	AEPEDHYFLLTEPPLNTPENR	EYTAE	3		828.0682052	2481.181216	0.000451244	35	N	102	123
Q99JY9	Exosome	VCHTK	KDYEEIGPSICR	HNPVF	2	C11:+57.021	733.8511312	1465.686662	0.000451244	19	N	397	409
Q99JY9	Exosome	VCHTK	KDYEEIGPSICR	HNPVF	3	C11:+57.021	489.5700208	1465.686662	0.000451244	46	N	397	409
Q99JY9	Exosome	GPEIF	FHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C25:+57.021	1171.564918	3511.671355	0.000451244	16	N	282	312
Q99JY9	Exosome	RRVMK	GVDDLDFFIGDEAIEKPTY	ATKWP	2		1072.507664	2142.999729	0.000622848	4	N	53	72
Q99JY9	Exosome	HHMQR	YAVWFGGSMLASTPEFYQVCHTK	KDYEE	3	C20:+57.021	893.7509004	2678.229301	0.002981883	1	N	374	397
Q99JY9	Exosome	HHMQR	YAVWFGGSMLASTPEFYQVCHTK	KDYEE	3	M9:+15.995,C20:+57.021	899.082567	2694.224301	0.000451244	10	N	374	397
Q99JY9	Exosome	TPENR	EYTAEIMFESFNVPGLYIAVQAVLALAASWTSR	QVGER	3		1216.620519	3646.838156	0.000451244	5	N	123	156
Q99JY9	Exosome	KWPIR	HGIVEDWDLMER	FMEQV	2		750.3515303	1498.687461	0.000637154	5	N	79	91
Q99JY9	Exosome	FTQPI	SEVVDEVIQNCPIDVR	RPLYK	2	C11:+57.021	936.4623056	1870.909011	0.000451244	9	N	296	312
Q99JY9	Exosome	RRVMK	GVDDLDFFIGDEAIEKPTYA	TKWPI	2		1108.026221	2214.036843	0.000451244	9	N	53	73
Q99JY9	Exosome	QAQRR	VMKGVDDLDFFIGDEAIEKPTYATK	WPIRH	4	M2:+15.995	705.3523868	2817.378347	0.000451244	12	N	50	75
Q99JY9	Exosome	RPLYK	NIVLSGGSTMFR	DFGRR	2	M10:+15.995	649.3326519	1296.649704	0.000622848	3	N	317	329
Q99JY9	Exosome	AKAVK	ERYSYVCPDLVK	EFNKY	2	C7:+57.021	764.877149	1527.738698	0.001463592	2	N	228	240
Q99JY9	Exosome	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGS	CIKHI	2		1329.187587	2656.359574	0.00307782	1	N	161	188
Q99JY9	Exosome	LSGGR	LKPKPIDVQVITHHMQR	YAVWF	4	M15:+15.995	514.793108	2055.141232	0.002296037	1	N	357	374
Q99JY9	Parental	QQLLR	DREVGIPPEQSLETAK	AVKER	2		884.9579447	1767.900289	0.000451244	9	N	209	225
Q99JY9	Parental	AISKK	EFSIDVGYER	FLGPE	2		607.7885569	1213.561514	0.000451244	9	N	265	275
Q99JY9	Parental	QVIFK	YLRAEPEDHYFLLTEPPLNTPENR	EYTAE	3		972.1510399	2913.42972	0.000451244	8	N	99	123
Q99JY9	Parental	RRVMK	GVDDLDFFIGDEAIEKPTYATK	WPIRH	2		1222.597542	2443.179484	0.000451244	46	N	53	75
Q99JY9	Parental	RRVMK	GVDDLDFFIGDEAIEKPTYATK	WPIRH	3		815.4009615	2443.179484	0.000451244	49	N	53	75
Q99JY9	Parental	TGYTK	LGYAGNTEPQFIIPSCIAIK	ESAKV	2	C16:+57.021	1096.57493	2191.13426	0.000451244	41	N	18	38
Q99JY9	Parental	TGYTK	LGYAGNTEPQFIIPSCIAIK	ESAKV	3	C16:+57.021	731.3858868	2191.13426	0.000451244	24	N	18	38
Q99JY9	Parental	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	HIPIA	3	C28:+57.021	1020.197396	3057.568787	0.000451244	139	N	161	191
Q99JY9	Parental	QVGER	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	HIPIA	4	C28:+57.021	765.3999968	3057.568787	0.000451244	23	N	161	191
Q99JY9	Parental	PIAGR	DITYFIQQLLR	DREVG	2		705.3935235	1408.771447	0.000451244	28	N	198	209
Q99JY9	Parental	PIAGR	DITYFIQQLLR	DREVG	3		470.5982824	1408.771447	0.000451244	10	N	198	209
Q99JY9	Parental	VGYER	FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C32:+57.021	1439.372177	4315.093132	0.000451244	66	N	275	312
Q99JY9	Parental	VGYER	FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	4	C32:+57.021	1079.781083	4315.093132	0.000451244	60	N	275	312
Q99JY9	Parental	-MAGR	LPACVVDCGTGYTK	LGYAG	2	C4:+57.021,C8:+57.021	770.8604104	1539.705221	0.000451244	61	N	4	18
Q99JY9	Parental	TGYTK	LGYAGNTEPQFIIPSCIAIKESAK	VGDQA	3	C16:+57.021	869.7881197	2606.340959	0.0007646	4	N	18	42
Q99JY9	Parental	NAISK	KEFSIDVGYER	FLGPE	3		448.2266256	1341.656477	0.000622848	2	N	264	275
Q99JY9	Parental	CHTKK	DYEEIGPSICR	HNPVF	2	C10:+57.021	669.8036497	1337.591699	0.000451244	20	N	398	409
Q99JY9	Parental	AGRDI	TYFIQQLLR	DREVG	2		591.3380199	1180.66044	0.001229886	4	N	200	209
Q99JY9	Parental	FKYLR	AEPEDHYFLLTEPPLNTPENR	EYTAE	2		1241.598408	2481.181216	0.000451244	46	N	102	123
Q99JY9	Parental	FKYLR	AEPEDHYFLLTEPPLNTPENR	EYTAE	3		828.0682052	2481.181216	0.000451244	13	N	102	123
Q99JY9	Parental	VCHTK	KDYEEIGPSICR	HNPVF	2	C11:+57.021	733.8511312	1465.686662	0.000451244	4	N	397	409
Q99JY9	Parental	VCHTK	KDYEEIGPSICR	HNPVF	3	C11:+57.021	489.5700208	1465.686662	0.000451244	31	N	397	409
Q99JY9	Parental	GPEIF	FHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C25:+57.021	1171.564918	3511.671355	0.000451244	4	N	282	312
Q99JY9	Parental	RRVMK	GVDDLDFFIGDEAIEKPTY	ATKWP	2		1072.507664	2142.999729	0.000451244	9	N	53	72
Q99JY9	Parental	RRVMK	GVDDLDFFIGDEAIEKPTYATKWPIR	HGIVE	3		999.5067122	2995.496737	0.000451244	3	N	53	79
Q99JY9	Parental	TPENR	EYTAEIMFESFNVPGLYIAVQAVLALAASWTSR	QVGER	3		1216.620519	3646.838156	0.000823681	3	N	123	156
Q99JY9	Parental	AVKER	YSYVCPDLVK	EFNKY	2	C5:+57.021	622.3052969	1242.594994	0.000622848	1	N	230	240
Q99JY9	Parental	GYERF	LGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	RPLYK	3	C31:+57.021	1390.349373	4168.024718	0.001839721	1	N	276	312
Q99K01	Parental	GEQLK	QLVPQCGLTVIDLEVDGTCVR	FSPLM	2	C6:+57.021,C19:+57.021	1186.601119	2371.186638	0.00307782	1	N	437	458
Q99K01	Parental	DLTAR	QTEALQNQAQHQEDDHSQVEELER	LR-	3		954.7682058	2861.281218	0.001463592	1	N	761	785
Q99K01	Parental	ADKLR	ALPLWLSLQYLGLDGIVER	IKHAC	2		1078.609862	2155.204123	0.001162105	2	N	337	356
Q99K41	Exosome	EERFR	GLEEGQAQAGQCPSLEGR	LGRLE	2	C12:+57.021	943.9369863	1885.858373	0.000451244	15	N	709	727
Q99K41	Exosome	VPFDR	VLLNDGGYYDPETGVFTAPLAGR	YLLSA	2		1213.105869	2424.196137	0.000451244	26	N	892	915
Q99K41	Exosome	LLQAR	GDEGCGACGGVQEELGR	LRDGV	2	C5:+57.021,C8:+57.021	875.8596587	1749.703717	0.000451244	5	N	578	595
Q99K41	Exosome	DSEGR	LQLVGSGLHEAEAAGEAQQAVLEGLQGLLSR	LRERM	3		1048.893629	3143.657488	0.000451244	8	N	511	542
Q99K41	Exosome	RQLER	QLQESCSVCLTGLDGFR	QQQQE	2	C6:+57.021,C9:+57.021	985.4590087	1968.902417	0.000451244	3	N	297	314
Q99K41	Exosome	ESEER	FRGLEEGQAQAGQCPSLEGR	LGRLE	3	C14:+57.021	730.6837659	2189.027898	0.000451244	1	N	707	727
Q99K41	Exosome	VLSGR	RGSELGGAAGQGGHPPGYTSLASR	LSRLE	4		571.5366004	2282.115202	0.002374549	1	N	383	407
Q99K41	Parental	EERFR	GLEEGQAQAGQCPSLEGR	LGRLE	2	C12:+57.021	943.9369863	1885.858373	0.000451244	1	N	709	727
Q99K41	Parental	VPFDR	VLLNDGGYYDPETGVFTAPLAGR	YLLSA	2		1213.105869	2424.196137	0.000451244	6	N	892	915
Q99K41	Parental	LLQAR	GDEGCGACGGVQEELGR	LRDGV	2	C5:+57.021,C8:+57.021	875.8596587	1749.703717	0.000622848	8	N	578	595
Q99K41	Parental	DSEGR	LQLVGSGLHEAEAAGEAQQAVLEGLQGLLSR	LRERM	3		1048.893629	3143.657488	0.000451244	11	N	511	542
Q99K48	Exosome	SLTVR	NLPQYVSNELLEEAFSVFGQVER	AVVIV	2		1334.666822	2667.318044	0.000451244	30	N	155	178
Q99K48	Exosome	SLTVR	NLPQYVSNELLEEAFSVFGQVER	AVVIV	3		890.1138146	2667.318044	0.000451244	23	N	155	178
Q99K48	Exosome	KALDR	CSEGSFLLTTFPRPVTVEPMDQLDDEEGLPEK	LVIKN	3	C1:+57.021,M20:+15.995	1218.239689	3651.695667	0.000451244	9	N	209	241
Q99K48	Exosome	KALDR	CSEGSFLLTTFPRPVTVEPMDQLDDEEGLPEK	LVIKN	3	[0:-	1212.564022	3634.668667	0.000622848	1	N	209	241
Q99K48	Parental	SLTVR	NLPQYVSNELLEEAFSVFGQVER	AVVIV	2		1334.666822	2667.318044	0.000451244	40	N	155	178
Q99K48	Parental	SLTVR	NLPQYVSNELLEEAFSVFGQVER	AVVIV	3		890.1138146	2667.318044	0.000451244	31	N	155	178

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99K48	Parental	SLTVR	NLPQYVSNELLEEAFSVF	GQVER	2		1050.020742	2098.025884	0.001763695	1	N	155	173
Q99K85	Exosome	VGGIR	ASLYNAVTTEDVEK	LAAFM	2		770.3810071	1538.746414	0.000451244	20	N	342	356
Q99K85	Exosome	PNNYK	VIFVQGGGSGQFSAVPLNLIGLK	AGRSA	2		1151.152425	2300.28925	0.000451244	16	N	71	94
Q99K85	Exosome	PNNYK	VIFVQGGGSGQFSAVPLNLIGLK	AGRSA	3		767.7708833	2300.28925	0.000979378	3	N	71	94
Q99K85	Exosome	LKAGR	SADYVVTGAWSAK	AAEEA	2		677.8360384	1353.656477	0.001329271	1	N	97	110
Q99K85	Parental	VGGIR	ASLYNAVTTEDVEK	LAAFM	2		770.3810071	1538.746414	0.000451244	1	N	342	356
Q99K85	Parental	GSYTK	IPDPSTWNLNPDASYVYFCANETVHGVEFDFVPDVK	GAVLV	3	C19:+57.021	1381.642445	4141.903934	0.00307782	1	N	133	169
Q99KE1	Exosome	LEAAK	ALTTQLTDAELAQGR	LYPSL	2		794.420998	1586.826396	0.000451244	18	N	496	511
Q99KE1	Exosome	LVKGR	TASIDSNQEPYAHAAPESIPATFEDAVNK	LKPSV	3		1025.151545	3072.431236	0.000451244	40	N	354	383
Q99KE1	Exosome	LAQGR	LYPSLANIQEVSANIAIK	LAEYL	2		972.5441873	1943.072775	0.000451244	27	N	511	529
Q99KE1	Exosome	ERIWR	SNYVSLLPDVYDWPESSLTPPQITEEKLPH	-	3		1152.240472	3453.698016	0.000622848	6	N	559	589
Q99KE1	Exosome	LQDGR	VFTPGQGNNAYIFPGVALAVILCEAR	HISDT	2	C23:+57.021	1389.226095	2776.436591	0.000451244	13	N	458	484
Q99KE1	Exosome	LQDGR	VFTPGQGNNAYIFPGVALAVILCEAR	HISDT	3	C23:+57.021	926.4866636	2776.436591	0.000451244	28	N	458	484
Q99KE1	Exosome	KYQQK	YCTFNDDIQGTAAVALSGLLAAQR	VINKP	2	C2:+57.021	1278.131861	2554.248121	0.000451244	11	N	272	296
Q99KE1	Exosome	KYQQK	YCTFNDDIQGTAAVALSGLLAAQR	VINKP	3	C2:+57.021	852.4238404	2554.248121	0.000451244	25	N	272	296
Q99KE1	Exosome	IPVGK	LCLYTACAGIQPEK	CLPVC	2	C2:+57.021,C7:+57.021	812.3971601	1622.77872	0.000451244	13	N	183	197
Q99KE1	Exosome	LTEGR	CLFASGSPFEPVKLQDGR	VFTPG	3	C1:+57.021	670.0037768	2006.98793	0.000823681	1	N	440	458
Q99KE1	Exosome	DAVNK	LKPSVIIGVAGAGPLFTHGVIK	AMASI	3		725.4406975	2173.298692	0.000451244	1	N	383	405
Q99KE1	Exosome	DAVNK	LKPSVIIGVAGAGPLFTHGVIK	AMASI	4		544.3324731	2173.298692	0.000451244	16	N	383	405
Q99KE1	Exosome	LTEGR	CLFASGSPFEPVK	LQDGR	2	C1:+57.021	719.8556853	1437.695771	0.002981883	1	N	440	453
Q99KE1	Exosome	LTEGR	CLFASGSPFEPVK	LQDGR	2	[0:-17.027,C1:+57.021	711.3421853	1420.668771	0.000662267	4	N	440	453
Q99KE1	Exosome	RPIIF	ALSNPTAQAECTAEDAYTLTEGR	CLFAS	2	C11:+57.021	1235.063841	2468.112081	0.000451244	13	N	417	440
Q99KE1	Exosome	KLFYR	ILQDDIESLMPIVYTPTVGLACCQYGHIFR	RPKGL	3	C22:+57.021,C23:+57.021	1170.580593	3508.718378	0.002981883	1	N	98	128
Q99KE1	Exosome	ERIWR	SNYVSLLPDVYDWPE	SSLTP	2		898.9230392	1795.830478	0.001654178	1	N	559	574
Q99KE1	Exosome	ERIWR	SNYVSLLPDVYDWPESSLTPPQITEEK	LPH-	3		1036.508559	3106.502276	0.001463592	1	N	559	586
Q99KE1	Exosome	NIAIK	LAEYLYANK	MAFRY	2		542.7878285	1083.560057	0.001162105	1	N	529	538
Q99KE1	Parental	LEAAK	ALTTQLTDAELAQGR	LYPSL	2		794.420998	1586.826396	0.000451244	10	N	496	511
Q99KE1	Parental	LVKGR	TASIDSNQEPYAHAAPESIPATFEDAVNK	LKPSV	3		1025.151545	3072.431236	0.000451244	29	N	354	383
Q99KE1	Parental	LAQGR	LYPSLANIQEVSANIAIK	LAEYL	2		972.5441873	1943.072775	0.000451244	15	N	511	529
Q99KE1	Parental	ERIWR	SNYVSLLPDVYDWPESSLTPPQITEEKLPH	-	3		1152.240472	3453.698016	0.000451244	16	N	559	589
Q99KE1	Parental	LQDGR	VFTPGQGNNAYIFPGVALAVILCEAR	HISDT	2	C23:+57.021	1389.226095	2776.436591	0.000451244	6	N	458	484
Q99KE1	Parental	LQDGR	VFTPGQGNNAYIFPGVALAVILCEAR	HISDT	3	C23:+57.021	926.4866636	2776.436591	0.000451244	26	N	458	484
Q99KE1	Parental	KYQQK	YCTFNDDIQGTAAVALSGLLAAQR	VINKP	2	C2:+57.021	1278.131861	2554.248121	0.000451244	1	N	272	296
Q99KE1	Parental	KYQQK	YCTFNDDIQGTAAVALSGLLAAQR	VINKP	3	C2:+57.021	852.4238404	2554.248121	0.000451244	6	N	272	296
Q99KE1	Parental	IPVGK	LCLYTACAGIQPEK	CLPVC	2	C2:+57.021,C7:+57.021	812.3971601	1622.77872	0.000451244	1	N	183	197
Q99KE1	Parental	LTEGR	CLFASGSPFEPVKLQDGR	VFTPG	2	C1:+57.021	1004.501765	2006.98793	0.000451244	1	N	440	458
Q99KH8	Exosome	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTK	YYGSY	3	C24:+57.021	1208.245357	3621.712671	0.000451244	14	N	53	84
Q99KH8	Exosome	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTK	YYGSY	4	C24:+57.021	906.4359676	3621.712671	0.002813207	1	N	53	84
Q99KH8	Exosome	AYDSK	ADIWSLGITAIELAK	GEPPH	2		800.9514027	1599.887205	0.000451244	15	Y	199	214
Q99KH8	Exosome	KDIPK	RPFSQCLSTIISPLFAELK	EKSQA	3	C6:+57.021	736.4016483	2206.181545	0.000622848	2	N	357	376
Q99KH8	Exosome	ELKEK	SQACGGNLGSIEELR	GAIYL	2	C4:+57.021	795.8809514	1589.746303	0.000622848	3	N	378	393
Q99KH8	Parental	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTK	YYGSY	3	C24:+57.021	1208.245357	3621.712671	0.000451244	35	N	53	84
Q99KH8	Parental	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTK	YYGSY	4	C24:+57.021	906.4359676	3621.712671	0.000451244	7	N	53	84
Q99KH8	Parental	HGEVK	LADFGVAGQLTDTQIKR	NTFVG	2		916.9974042	1831.979208	0.000622848	2	Y	159	176
Q99KH8	Parental	HGEVK	LADFGVAGQLTDTQIKR	NTFVG	3		611.6675361	1831.979208	0.000622848	7	Y	159	176
Q99KH8	Parental	AYDSK	ADIWSLGITAIELAK	GEPPH	2		800.9514027	1599.887205	0.000451244	26	Y	199	214
Q99KH8	Parental	AYDSK	ADIWSLGITAIELAK	GEPPH	3		534.3035351	1599.887205	0.000451244	3	Y	199	214
Q99KH8	Parental	KDIPK	RPFSQCLSTIISPLFAELK	EKSQA	3	C6:+57.021	736.4016483	2206.181545	0.000451244	8	N	357	376
Q99KH8	Parental	ELKEK	SQACGGNLGSIEELR	GAIYL	2	C4:+57.021	795.8809514	1589.746303	0.000451244	3	N	378	393
Q99KH8	Parental	VVAIK	IIDLEEAEDEIEDIQQEITVLSQCDSPYVTKY	YGSYL	3	C24:+57.021	1262.5998	3784.775999	0.001463592	1	N	53	85
Q99KI0	Exosome	TLSEK	IVYGHLDDPANQEIER	GKTYL	2		934.9610187	1867.906437	0.000622848	6	N	68	84
Q99KI0	Exosome	TLSEK	IVYGHLDDPANQEIER	GKTYL	3		623.6432791	1867.906437	0.000451244	7	N	68	84
Q99KI0	Exosome	ANSVR	NAVTQEFGPVPDTAR	YYKKH	2		801.4000656	1600.784531	0.000451244	10	N	633	648
Q99KI0	Exosome	NFTGR	NDANPETHAFVTSPEIVTALAIAGTLK	FNPET	2		1390.727411	2779.439222	0.001699387	1	N	479	506
Q99KI0	Exosome	NFTGR	NDANPETHAFVTSPEIVTALAIAGTLK	FNPET	3		927.4875406	2779.439222	0.000451244	17	N	479	506
Q99KI0	Exosome	LRRAK	DINQEVYNFLATAGAK	YGVGF	2		877.4419304	1752.868261	0.000451244	14	N	144	160
Q99KI0	Exosome	LRRAK	DINQEVYNFLATAGAK	YGVGF	3		585.2972203	1752.868261	0.000451244	4	N	144	160
Q99KI0	Exosome	AQILR	DVGGIVLANACGPCIGQWDR	KDIKK	2	C11:+57.021,C14:+57.021	1079.512107	2157.008614	0.000451244	12	N	437	457
Q99KI0	Exosome	GLKCK	SQFTITPGSEQIR	ATIER	2		732.3786018	1462.741604	0.000451244	9	N	411	424
Q99KI0	Exosome	KDLRR	AKDINQEVYNFLATAGAK	YGVGF	3		651.6745793	1952.000338	0.000451244	9	N	142	160
Q99KI0	Exosome	WLKFR	GHLDNISNNLLIGAINIENGK	ANSVR	3		740.3979971	2218.170591	0.000622848	9	N	607	628
Q99KI0	Exosome	VIGVK	LTGSLSGWTSPK	DVILK	2		617.3278492	1232.640098	0.001463592	3	N	233	245
Q99KI0	Exosome	DELPR	SDFDPGQDTYQHPPKDSSGQR	VDVSP	3		788.0163925	2361.025778	0.001871652	1	N	534	555
Q99KI0	Exosome	AQILR	DVGGIVLANACGPCIGQWDRK	DIKKG	2	C11:+57.021,C14:+57.021	1143.559589	2285.103577	0.000622848	2	N	437	458
Q99KI0	Exosome	AQILR	DVGGIVLANACGPCIGQWDRK	DIKKG	3	C11:+57.021,C14:+57.021	762.7089923	2285.103577	0.000451244	3	N	437	458

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99KI0	Exosome	SKTGR	TDIANLAEEF	KDHLV	2		561.7698328	1121.524066	0.002080925	1	N	312	322
Q99KI0	Parental	TLSEK	IVYGHLDDPANQEIER	GKTYL	2		934.9610187	1867.906437	0.000451244	7	N	68	84
Q99KI0	Parental	TLSEK	IVYGHLDDPANQEIER	GKTYL	3		623.6432791	1867.906437	0.000451244	12	N	68	84
Q99KI0	Parental	ANSVR	NAVTQEFGPVPDTAR	YYKKH	2		801.4000656	1600.784531	0.000451244	5	N	633	648
Q99KI0	Parental	NFTGR	NDANPETHAFVTSPEIVTALAIAGTLK	FNPET	3		927.4875406	2779.439222	0.000451244	20	N	479	506
Q99KI0	Parental	LRRAK	DINQEVYNFLATAGAK	YGVGF	2		877.4419304	1752.868261	0.000451244	5	N	144	160
Q99KI0	Parental	AQILR	DVGGIVLANACGPCIGQWDR	KDIKK	2	C11:+57.021,C14:+57.021	1079.512107	2157.008614	0.000622848	2	N	437	457
Q99KI0	Parental	GLKCK	SQFTITPGSEQIR	ATIER	2		732.3786018	1462.741604	0.000662267	2	N	411	424
Q99KI0	Parental	KHGIR	WVVIGDENYGEGSSR	EHAAL	2		834.3871552	1666.75871	0.000451244	1	N	656	671
Q99KJ8	Exosome	SHLEK	LLGPDAAINLADPDGALAK	RLLLQ	2		917.9996126	1833.983625	0.001162105	3	N	156	175
Q99KJ8	Exosome	LLQAK	VSALDLAVLDQVEAR	LQSVL	2		799.9415663	1597.867533	0.000451244	10	N	268	283
Q99KJ8	Exosome	LLQAK	VSALDLAVLDQVEAR	LQSVL	3		533.6303109	1597.867533	0.001591523	1	N	268	283
Q99KJ8	Exosome	ETIQR	WSPVASTLPELVQR	LVTIK	2		791.9335442	1581.851488	0.001352548	3	N	319	333
Q99KJ8	Exosome	QTTMR	ENLATVEGNFASIDAR	MKRLG	2		853.9213622	1705.827124	0.000451244	8	N	380	396
Q99KJ8	Parental	SHLEK	LLGPDAAINLADPDGALAKR	LLLQL	3		664.3693788	1990.084736	0.000451244	1	N	156	176
Q99KJ8	Parental	SHLEK	LLGPDAAINLADPDGALAK	RLLLQ	2		917.9996126	1833.983625	0.000451244	12	N	156	175
Q99KJ8	Parental	LLQAK	VSALDLAVLDQVEAR	LQSVL	2		799.9415663	1597.867533	0.000451244	37	N	268	283
Q99KJ8	Parental	LLQAK	VSALDLAVLDQVEAR	LQSVL	3		533.6303109	1597.867533	0.000451244	4	N	268	283
Q99KJ8	Parental	ETIQR	WSPVASTLPELVQR	LVTIK	2		791.9335442	1581.851488	0.000622848	11	N	319	333
Q99KJ8	Parental	QKYQR	LLHEVQELTTEVEK	IKTTV	2		834.4466815	1666.877763	0.000451244	3	N	105	119
Q99KJ8	Parental	QTTMR	ENLATVEGNFASIDAR	MKRLG	2		853.9213622	1705.827124	0.000451244	11	N	380	396
Q99KK2	Exosome	GWVLR	AALDAGVFQSVWVSTDHDEIENVAK	QFGAQ	3		901.1088407	2700.303122	0.00091018	4	N	75	100
Q99KK2	Exosome	RGAIR	EFAEHIFLLIEK	VNNSC	3		496.9419376	1487.802413	0.000698008	1	N	413	425
Q99KK2	Exosome	GLCWK	EVAYLGNEVSDEECLKR	VGLSA	2	C14:+57.021	1005.975777	2009.935954	0.000451244	1	N	364	381
Q99KK2	Exosome	GLCWK	EVAYLGNEVSDEECLKR	VGLSA	3	C14:+57.021	670.9864515	2009.935954	0.001395409	1	N	364	381
Q99KK2	Parental	RGAIR	EFAEHIFLLIEK	VNNSC	3		496.9419376	1487.802413	0.001943752	1	N	413	425
Q99KK2	Parental	GLCWK	EVAYLGNEVSDEECLKR	VGLSA	2	C14:+57.021	1005.975777	2009.935954	0.000622848	1	N	364	381
Q99KK7	Exosome	AGLIR	SFCERFPEDGPELEEVLIQLAAADAR	FWRNQ	3	C3:+57.021	988.1469239	2961.417372	0.000451244	13	N	698	724
Q99KK7	Exosome	HYEVR	LASVLNTDPALDSELTSK	LKRYE	2		937.4918174	1872.968035	0.000451244	34	N	215	233
Q99KK7	Exosome	MEDAK	LAQDFLDSQNLSAYNTR	LFKVV	2		978.4770329	1954.938466	0.000451244	24	N	182	199
Q99KK7	Exosome	TEGFK	NVSLGNVLAVAYAAK	REKLT	2		745.4228124	1488.830025	0.000451244	15	N	405	420
Q99KK7	Exosome	VVAGR	ALYEGYAAVTDAPPECFLTLR	DTVLL	2	C16:+57.021	1179.078034	2356.140468	0.000451244	36	N	638	659
Q99KK7	Exosome	QPNTR	LEGSEVQLVEYEASAAGLIR	SFCER	2		1067.55548	2133.095361	0.000451244	36	N	678	698
Q99KK7	Exosome	QPNTR	LEGSEVQLVEYEASAAGLIR	SFCER	3		712.0395869	2133.095361	0.000451244	21	N	678	698
Q99KK7	Exosome	FVILR	VLLEAGEGLVTVTPTTGSDGRPDAR	VRLDR	3		837.7736809	2510.297643	0.000451244	13	N	577	602
Q99KK7	Exosome	VQDEK	GAFNFDKETVINPETGEQIQSWYR	SGETW	2		1415.178085	2828.34057	0.000622848	3	N	466	490
Q99KK7	Exosome	VQDEK	GAFNFDKETVINPETGEQIQSWYR	SGETW	3		943.7879901	2828.34057	0.000451244	33	N	466	490
Q99KK7	Exosome	LNMVR	AGLLALEFYTPEAANWR	QAHMQ	2		961.4944974	1920.973395	0.000451244	23	N	548	565
Q99KK7	Exosome	SFCER	FPEDGPELEEVLIQLAAADAR	FWRNQ	2		1142.07932	2282.143039	0.000451244	5	N	703	724
Q99KK7	Exosome	SFCER	FPEDGPELEEVLIQLAAADAR	FWRNQ	3		761.7221464	2282.143039	0.000451244	27	N	703	724
Q99KK7	Exosome	WIQDK	GPIVESYIGFIESYRDPFGSR	GEFEG	3		797.066136	2388.175008	0.000451244	13	N	304	325
Q99KK7	Exosome	LAFEK	DKFLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1228.293347	3681.856642	0.0007646	5	N	365	399
Q99KK7	Exosome	FEKDK	FLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1147.252712	3438.734735	0.000451244	8	N	367	399
Q99KK7	Exosome	HHLSR	AAWYGGLAVLLQTSPEAPYIYALLSR	LFRAQ	3		941.8413666	2822.5007	0.000451244	6	N	39	65
Q99KK7	Exosome	DLYIR	WKGPSFDVQVGLHELLGHGSGK	LFVQD	4		587.8096278	2347.207311	0.001839721	1	N	437	459
Q99KK7	Parental	AGLIR	SFCERFPEDGPELEEVLIQLAAADAR	FWRNQ	3	C3:+57.021	988.1469239	2961.417372	0.000451244	23	N	698	724
Q99KK7	Parental	HYEVR	LASVLNTDPALDSELTSK	LKRYE	2		937.4918174	1872.968035	0.000451244	8	N	215	233
Q99KK7	Parental	MEDAK	LAQDFLDSQNLSAYNTR	LFKVV	2		978.4770329	1954.938466	0.000451244	3	N	182	199
Q99KK7	Parental	TEGFK	NVSLGNVLAVAYAAK	REKLT	2		745.4228124	1488.830025	0.000451244	3	N	405	420
Q99KK7	Parental	VVAGR	ALYEGYAAVTDAPPECFLTLR	DTVLL	2	C16:+57.021	1179.078034	2356.140468	0.002813207	1	N	638	659
Q99KK7	Parental	QPNTR	LEGSEVQLVEYEASAAGLIR	SFCER	2		1067.55548	2133.095361	0.000451244	14	N	678	698
Q99KK7	Parental	VQDEK	GAFNFDKETVINPETGEQIQSWYR	SGETW	2		1415.178085	2828.34057	0.000451244	1	N	466	490
Q99KK7	Parental	VQDEK	GAFNFDKETVINPETGEQIQSWYR	SGETW	3		943.7879901	2828.34057	0.000451244	21	N	466	490
Q99KK7	Parental	LNMVR	AGLLALEFYTPEAANWR	QAHMQ	2		961.4944974	1920.973395	0.000451244	14	N	548	565
Q99KK7	Parental	SFCER	FPEDGPELEEVLIQLAAADAR	FWRNQ	2		1142.07932	2282.143039	0.000622848	1	N	703	724
Q99KK7	Parental	SFCER	FPEDGPELEEVLIQLAAADAR	FWRNQ	3		761.7221464	2282.143039	0.000823681	2	N	703	724
Q99KK7	Parental	LAFEK	DKFLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1228.293347	3681.856642	0.001264573	3	N	365	399
Q99KK7	Parental	FEKDK	FLTPDFTSLDVLTFAGSGIPAGINIPNYDDLR	QTEGF	3		1147.252712	3438.734735	0.000451244	8	N	367	399
Q99KK7	Parental	LIRSF	CERFPEDGPELEEVLIQLAAADAR	FWRNQ	3	C1:+39.994	904.4377764	2710.289929	0.000451244	3	N	700	724
Q99KK7	Parental	TWDSK	FSTIASSYEECR	AESVG	2	C11:+57.021	725.3196639	1448.623728	0.001463592	2	N	498	510
Q99KK7	Parental	HHLSR	AAWYGGLAVLLQTSPEAPYIYALLSR	LFRAQ	3		941.8413666	2822.5007	0.000622848	2	N	39	65
Q99KN1	Exosome	PCPGR	ESSPGTLSLVVPSAPPQEEAEAVASGPHFSDPVSLSTK	SHSQQ	3		1268.965847	3803.874142	0.000851441	8	N	297	335
Q99KN1	Exosome	SLADK	GSLPAGEHNFPFQFLLPATAPTSFEGPFGK	IVHQV	3		1054.52974	3160.565819	0.000622848	8	N	76	106
Q99KN1	Exosome	SKDHK	CSLVFYILSPLNLNSIPDIEQPNVASTTKK	FSYKL	3	C1:+57.021	1121.262288	3360.763464	0.000451244	4	N	125	155
Q99KN1	Exosome	SKDHK	CSLVFYILSPLNLNSIPDIEQPNVASTTK	KFSYK	3	C1:+57.021	1078.563967	3232.668501	0.000451244	2	N	125	154

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99KN1	Exosome	QVSMK	APEATVTLPLFVGNIAVNQTPLSPCPGR	ESSPG	3	C25:+57.021	973.8517827	2918.531948	0.000451244	2	N	269	297
Q99KP6	Exosome	RLIEK	YIAENGTDPINNQPLSEEQLIDIK	VAHPI	2		1357.680126	2713.344653	0.000451244	45	N	32	56
Q99KP6	Exosome	RLIEK	YIAENGTDPINNQPLSEEQLIDIK	VAHPI	3		905.4560175	2713.344653	0.002019181	1	N	32	56
Q99KP6	Exosome	LSKYR	QVASHVGLHSASIPGILALDLCPSDTNK	ILTGG	3	C22:+57.021	967.503042	2899.485726	0.001162105	3	N	208	236
Q99KP6	Exosome	RVLTK	VTDETSGCSLTCAQFHPDGLIFGTGTMDSQIK	IWDLK	3	C8:+57.021,C12:+57.021,M27:+15.995	1163.85866	3488.55258	0.000451244	7	N	343	375
Q99KP6	Exosome	DATIR	IWSVPNTSCVQVVR	AHESA	2	C9:+57.021	822.9302473	1643.844895	0.001463592	3	N	289	303
Q99KP6	Exosome	KKRGK	TVPEELVKPEELSK	YRQVA	2		799.4383251	1596.86105	0.001264573	1	N	192	206
Q99KP6	Exosome	TSIAF	SENGYYLATAADDSSVK	LWDLR	2		895.9081174	1789.800635	0.002296037	1	N	400	417
Q99KP6	Exosome	KGHTK	KVTSVVFHPSQELVFSASPDATIR	IWSVP	3		872.4662997	2614.375499	0.000451244	2	N	265	289
Q99KP6	Parental	RLIEK	YIAENGTDPINNQPLSEEQLIDIK	VAHPI	2		1357.680126	2713.344653	0.000451244	68	N	32	56
Q99KP6	Parental	RLIEK	YIAENGTDPINNQPLSEEQLIDIK	VAHPI	3		905.4560175	2713.344653	0.000823681	2	N	32	56
Q99KP6	Parental	LSKYR	QVASHVGLHSASIPGILALDLCPSDTNK	ILTGG	3	C22:+57.021	967.503042	2899.485726	0.000662267	7	N	208	236
Q99KP6	Parental	DLKER	TNVANFPGHSGPITSIAFSENGYYLATAADDSSVK	LWDLR	3		1201.241423	3600.700869	0.002296037	1	N	382	417
Q99KP6	Parental	TSIAF	SENGYYLATAADDSSVK	LWDLR	2		895.9081174	1789.800635	0.000979378	1	N	400	417
Q99KQ4	Exosome	LIVSR	STEAPLIIRPDSGNPLDTVLK	VLDIL	2		1118.61333	2235.211059	0.000662267	7	N	302	323
Q99KQ4	Exosome	LIVSR	STEAPLIIRPDSGNPLDTVLK	VLDIL	3		746.0781531	2235.211059	0.000451244	5	N	302	323
Q99KQ4	Exosome	KILAK	YLLETSGNLDGLEYK	LHDFG	2		857.9308642	1713.846128	0.000451244	6	N	174	189
Q99KQ4	Exosome	LSLHR	TPAGNFVTLEEGKGDLEEYGHDLLHTVFK	NGKVT	4		804.9021766	3215.577506	0.000451244	11	N	434	463
Q99KQ4	Exosome	DEVRK	NAQLNIEQDVAPH	-	2		724.8605762	1447.705552	0.000735798	2	N	478	491
Q99KV1	Exosome	QAQEK	FQDLGAAYEVLSDSEK	RKQYD	2		886.4234034	1770.831207	0.000451244	5	N	66	82
Q99KV1	Exosome	LGPGR	FQMTQEVVCDECPNVK	LVNEE	2	M3:+15.995,C9:+57.021,C12:+57.021	1000.431646	1998.847691	0.001162105	3	N	184	200
Q99KY4	Parental	PSQTK	SQNLDPFADLSDLSSSLQGLPAGLPAGGFVGAPAPTQK	SNSPW	3		1241.967523	3722.879168	0.000451244	15	N	1075	1113
Q99KY4	Parental	SGPSR	AQPPCGGTVNSSGVLALAEYDQPYGGFLDILR	GGTER	3	C5:+57.021	1122.554242	3364.639327	0.000451244	6	N	345	377
Q99L04	Exosome	NTTNK	SFWEVPASIWDDINNVGLR	GHYLC	2		1109.550532	2217.085465	0.000451244	5	N	106	125
Q99L04	Exosome	SLGGR	CVPVVCDSSQESEVK	SLFEQ	2	C1:+57.021,C6:+57.021	861.8873535	1721.759107	0.000662267	1	N	57	72
Q99L04	Exosome	DREQK	GRLDVLVNNAYAGVQAILNTTNK	SFWEV	3		815.4472395	2443.318318	0.000451244	5	N	83	106
Q99L04	Parental	NTTNK	SFWEVPASIWDDINNVGLR	GHYLC	2		1109.550532	2217.085465	0.000451244	11	N	106	125
Q99L04	Parental	SLGGR	CVPVVCDSSQESEVK	SLFEQ	2	C1:+57.021,C6:+57.021	861.8873535	1721.759107	0.000451244	9	N	57	72
Q99L04	Parental	DREQK	GRLDVLVNNAYAGVQAILNTTNK	SFWEV	3		815.4472395	2443.318318	0.000451244	13	N	83	106
Q99L04	Parental	EMSGK	CVVALATDPNILNLSGK	VLPSC	2	C1:+39.994	884.4691769	1766.922754	0.001463592	1	N	234	251
Q99L13	Exosome	GYSKK	DFSSVFQYLREEEPF	-	2		946.9392206	1891.862841	0.001329271	4	N	320	335
Q99L13	Exosome	CKEFK	EAGEQVASSPAEVAEK	ADRII	2		801.3868208	1600.758042	0.001871652	1	N	78	94
Q99L45	Exosome	DEDSK	KDDGISFSSQTAWAGSER	DYTYE	4		486.2294076	1940.88643	0.000823681	1	N	152	170
Q99L45	Parental	KKTKK	IFDIDEAEEAIKDVK	IESDA	3		578.9652478	1733.872343	0.000451244	12	N	87	102
Q99L45	Parental	DSRKK	DASDDLDDLNFFNQK	KKKKK	2		878.887185	1755.75877	0.000451244	1	N	64	79
Q99L45	Parental	PSETK	EVEPEPTEEKDVDADEEDSR	KKDAS	3		773.331712	2316.971736	0.000451244	1	N	42	62
Q99LB4	Exosome	ISRMR	YSPNTQVEILPQGR	ESPIF	2		801.4182583	1600.820917	0.000451244	34	N	322	336
Q99LB4	Exosome	MNLTK	VADSSPFASELLIPDDCFVLDNGLCGK	IYIWK	2	C17:+57.021,C25:+57.021	1470.193766	2938.371933	0.000451244	16	N	266	293
Q99LB4	Exosome	MNLTK	VADSSPFASELLIPDDCFVLDNGLCGK	IYIWK	3	C17:+57.021,C25:+57.021	980.4651109	2938.371933	0.000451244	20	N	266	293
Q99LB4	Exosome	RATER	ALSWDSFNTGDCFILDLGQNIFAWCGGK	SNILE	3	C12:+57.021,C25:+57.021	1064.823521	3191.447163	0.000451244	21	N	154	182
Q99LB4	Exosome	NEKER	QAALQVADGFISR	MRYSP	2		688.3705798	1374.72556	0.000698008	1	N	307	320
Q99LB4	Exosome	NEKER	QAALQVADGFISR	MRYSP	2	Q1:-17.027	679.8570798	1357.69856	0.002374549	1	N	307	320
Q99LB4	Exosome	NEKER	QAALQVADGFISR	MRYSP	2	[0:-17.027	679.8570798	1357.69856	0.000451244	14	N	307	320
Q99LB4	Exosome	KPALK	EGNPEEDITADQTNAQAAALYK	VSDAT	2		1175.046205	2348.07681	0.000451244	36	N	232	254
Q99LB4	Exosome	QQSSR	DEQGACAVLAVHLNTLLGERPVQHR	EVQGN	3	C6:+57.021	928.4842047	2782.429214	0.000451244	2	N	71	96
Q99LB4	Exosome	QQSSR	DEQGACAVLAVHLNTLLGERPVQHR	EVQGN	4	C6:+57.021	696.6151035	2782.429214	0.002663018	1	N	71	96
Q99LB4	Exosome	DSSPF	ASELLIPDDCFVLDNGLCGK	IYIWK	2	C10:+57.021,C18:+57.021	1118.534913	2235.054227	0.000823681	6	N	273	293
Q99LB4	Exosome	TGDCF	ILDLGQNIFAWCGGK	SNILE	2	C12:+57.021	846.4326228	1690.849646	0.000451244	3	N	167	182
Q99LB4	Exosome	KPALK	EGNPEEDITADQTNAQAAALY	KVSDA	2		1110.998724	2219.981847	0.001463592	2	N	232	253
Q99LB4	Exosome	PVQHR	EVQGNESDLFMSYFPR	GLKYR	2		959.9361555	1917.856711	0.001329271	1	N	96	112
Q99LB4	Parental	ISRMR	YSPNTQVEILPQGR	ESPIF	2		801.4182583	1600.820917	0.000451244	39	N	322	336
Q99LB4	Parental	MNLTK	VADSSPFASELLIPDDCFVLDNGLCGK	IYIWK	2	C17:+57.021,C25:+57.021	1470.193766	2938.371933	0.000451244	10	N	266	293
Q99LB4	Parental	MNLTK	VADSSPFASELLIPDDCFVLDNGLCGK	IYIWK	3	C17:+57.021,C25:+57.021	980.4651109	2938.371933	0.000451244	14	N	266	293
Q99LB4	Parental	RATER	ALSWDSFNTGDCFILDLGQNIFAWCGGK	SNILE	3	C12:+57.021,C25:+57.021	1064.823521	3191.447163	0.000451244	31	N	154	182
Q99LB4	Parental	NEKER	QAALQVADGFISR	MRYSP	2	[0:-17.027	679.8570798	1357.69856	0.00091018	1	N	307	320
Q99LB4	Parental	KPALK	EGNPEEDITADQTNAQAAALYK	VSDAT	2		1175.046205	2348.07681	0.000451244	34	N	232	254
Q99LB4	Parental	DSSPF	ASELLIPDDCFVLDNGLCGK	IYIWK	2	C10:+57.021,C18:+57.021	1118.534913	2235.054227	0.000622848	6	N	273	293
Q99LB4	Parental	TGDCF	ILDLGQNIFAWCGGK	SNILE	2	C12:+57.021	846.4326228	1690.849646	0.000451244	12	N	167	182
Q99LB4	Parental	RATER	ALSWDSFNTGDCF	ILDLG	2	C12:+57.021	760.3118389	1518.608078	0.001839721	1	N	154	167
Q99LB4	Parental	KPALK	EGNPEEDITADQTNAQAAALY	KVSDA	2		1110.998724	2219.981847	0.000451244	11	N	232	253
Q99LB4	Parental	HGIFF	SGDSYLVLHNGPEEASHLHLWIGQQSSR	DEQGA	3		1039.843269	3116.506407	0.001162105	1	N	43	71
Q99LC3	Parental	LYASR	LLQYADALEHLLSTGQGVVLER	SIYSD	3		809.1082238	2424.301271	0.000451244	19	N	139	161
Q99LC3	Parental	HCKLR	YGLLAAILGDK	TTKKL	2		567.3324032	1132.649206	0.000451244	10	N	37	48

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99LC5	Exosome	GENFK	LLYDLADQLHAAVGASR	AAVDA	2		906.9842968	1811.952994	0.000451244	9	N	232	249
Q99LC5	Exosome	GENFK	LLYDLADQLHAAVGASR	AAVDA	3		604.9921312	1811.952994	0.000451244	16	N	232	249
Q99LC5	Exosome	MKDSK	TIVAINKDPEAPIFQVADYGIVADLFK	VVPEM	3		983.1992196	2946.574259	0.000451244	24	N	294	321
Q99LC5	Exosome	HDAYK	GLLPEELTPLILETQK	QFSYT	2		897.5171068	1793.018614	0.000451244	18	N	85	101
Q99LC5	Exosome	HDAYK	GLLPEELTPLILETQK	QFSYT	3		598.6806712	1793.018614	0.00091018	6	N	85	101
Q99LC5	Exosome	SLLRF	QSTLVIAEHANDSLAPITLNTITAAGR	LGGEV	2	Q1:-17.027	1380.730259	2759.444919	0.000451244	1	N	19	46
Q99LC5	Exosome	SLLRF	QSTLVIAEHANDSLAPITLNTITAAGR	LGGEV	2	[0:-17.027	1380.730259	2759.444919	0.000622848	7	N	19	46
Q99LC5	Exosome	TAAGR	LGGEVSCLVAGTK	CDKVV	2	C7:+57.021	645.8400352	1289.66447	0.000451244	7	N	46	59
Q99LC5	Exosome	ASSEK	APSSSSVGISEWLDQK	LTKSD	2		845.9182882	1689.820976	0.000451244	4	N	187	203
Q99LC5	Exosome	DTFVR	TIYAGNALCTVK	CDEKV	2	C9:+57.021	655.8425779	1309.669556	0.000451244	4	N	146	158
Q99LC5	Exosome	PIFQV	ADYGIVADLFK	VVPEM	2		606.3194928	1210.623386	0.001162105	4	N	310	321
Q99LC5	Exosome	RVAAK	LNVAPVSDIIEIK	SPDTF	2		705.9142888	1409.812978	0.000451244	5	N	126	139
Q99LC5	Exosome	VAINK	DPEAPIFQVADYGIVADLFK	VVPEM	2		1104.565317	2207.115033	0.001329271	1	N	301	321
Q99LC5	Parental	GENFK	LLYDLADQLHAAVGASR	AAVDA	3		604.9921312	1811.952994	0.000451244	23	N	232	249
Q99LC5	Parental	MKDSK	TIVAINKDPEAPIFQVADYGIVADLFK	VVPEM	3		983.1992196	2946.574259	0.000451244	38	N	294	321
Q99LC5	Parental	AGVAK	VLVAQHDAYKGLLPEELTPLILETQK	QFSYT	3		973.5466193	2917.616458	0.001352548	1	N	75	101
Q99LC5	Parental	HDAYK	GLLPEELTPLILETQK	QFSYT	2		897.5171068	1793.018614	0.000451244	18	N	85	101
Q99LC5	Parental	SLLRF	QSTLVIAEHANDSLAPITLNTITAAGR	LGGEV	3		926.4984396	2776.471919	0.0025889	1	N	19	46
Q99LC5	Parental	SLLRF	QSTLVIAEHANDSLAPITLNTITAAGR	LGGEV	2	Q1:-17.027	1380.730259	2759.444919	0.000622848	5	N	19	46
Q99LC5	Parental	SLLRF	QSTLVIAEHANDSLAPITLNTITAAGR	LGGEV	2	[0:-17.027	1380.730259	2759.444919	0.000622848	5	N	19	46
Q99LC5	Parental	VFSVR	GTSFEAAATSGGSASSEKAPSSSSVGISEWLDQK	LTKSD	3		1106.187095	3315.537886	0.000451244	7	N	169	203
Q99LC5	Parental	TAAGR	LGGEVSCLVAGTK	CDKVV	2	C7:+57.021	645.8400352	1289.66447	0.000451244	2	N	46	59
Q99LC5	Parental	ASSEK	APSSSSVGISEWLDQK	LTKSD	2		845.9182882	1689.820976	0.000451244	3	N	187	203
Q99LC5	Parental	VAINK	DPEAPIFQVADYGIVADLFK	VVPEM	2		1104.565317	2207.115033	0.000823681	2	N	301	321
Q99LD4	Exosome	KQAAK	CFLLASFDHCDFPELLSPSNVAVYGGLCALATFDR	QELQR	3	C1:+57.021,C10:+57.021,C28:+57.021	1321.623254	3961.846362	0.002813207	1	N	248	283
Q99LD4	Exosome	SEATR	ELQNAPDAIPESGVEPPPLDTAWVEATR	KKALL	3		1001.496764	3001.466893	0.000451244	14	N	87	115
Q99LD4	Parental	SEATR	ELQNAPDAIPESGVEPPPLDTAWVEATR	KKALL	3		1001.496764	3001.466893	0.002080925	2	N	87	115
Q99LF4	Exosome	LPAMK	QIGNVAALPGIVHR	SIGLP	3		482.2848092	1443.831028	0.000451244	10	N	67	81
Q99LF4	Exosome	RAKKR	GLPQLGTLGAGNHYAEIQVVDEIFNEYAAK	KMGID	3		1073.210847	3216.609141	0.000451244	1	N	214	244
Q99LF4	Exosome	QAFAK	VFNTTPDDLDLHVIYDVSHNIAK	VEQHV	4		657.3346698	2625.307479	0.000451244	2	N	334	357
Q99LF4	Parental	LPAMK	QIGNVAALPGIVHR	SIGLP	3		482.2848092	1443.831028	0.000451244	12	N	67	81
Q99LF4	Parental	AKSRR	NLDFQDVLDKLADMGIAIR	VASPK	3		716.3775459	2146.109238	0.000451244	2	N	441	460
Q99LF4	Parental	RAKKR	GLPQLGTLGAGNHYAEIQVVDEIFNEYAAK	KMGID	3		1073.210847	3216.609141	0.000451244	6	N	214	244
Q99LL3	Exosome	SAGLK	VSFANFIQYLLDPHTEK	LAPFN	3		674.6830748	2021.025824	0.000451244	24	N	302	319
Q99LL3	Exosome	RQVYR	LCHPCQIDYDFVGKLETLDEDAAQLLR	FLKVD	4	C2:+57.021,C5:+57.021	805.6419767	3218.536707	0.000823681	1	N	332	359
Q99LL3	Exosome	SYRNR	TASSWEEDWFANIPLAWR	QQLYK	2		1090.016325	2178.017051	0.000622848	6	N	376	394
Q99LL3	Exosome	QQLYK	LYEADFVLFGYPKPENLLRD	-	3		800.4147652	2398.220896	0.002080925	1	N	399	419
Q99LL3	Parental	SAGLK	VSFANFIQYLLDPHTEK	LAPFN	3		674.6830748	2021.025824	0.000451244	12	N	302	319
Q99LL3	Parental	RQVYR	LCHPCQIDYDFVGKLETLDEDAAQLLR	FLKVD	3	C2:+57.021,C5:+57.021	1073.853369	3218.536707	0.000979378	3	N	332	359
Q99LL3	Parental	RQVYR	LCHPCQIDYDFVGKLETLDEDAAQLLR	FLKVD	4	C2:+57.021,C5:+57.021	805.6419767	3218.536707	0.000622848	4	N	332	359
Q99LL3	Parental	SYRNR	TASSWEEDWFANIPLAWR	QQLYK	2		1090.016325	2178.017051	0.000451244	17	N	376	394
Q99LL3	Parental	PTKDR	SFDDIPNYELNHLIVDDR	HGVIY	3		725.6838031	2174.028009	0.000451244	2	N	149	167
Q99LP6	Exosome	QGFCK	DLLEVADILEK	ATQSV	2		629.35099	1256.68638	0.002080925	6	N	109	120
Q99LP6	Parental	QGFCK	DLLEVADILEK	ATQSV	2		629.35099	1256.68638	0.000823681	11	N	109	120
Q99LP6	Parental	VEEAK	LYGIQGFCKDLLEVADILEK	ATQSV	3	C8:+57.021	775.4121016	2323.212905	0.000451244	10	N	100	120
Q99LT0	Exosome	AVLAK	ERPPNPIEFLASYLLK	NKAQF	3		629.6845271	1886.030181	0.000451244	27	N	74	90
Q99LT0	Exosome	SLPTR	AYLDQTVVPILLQGLAVLAK	ERPPN	2		1063.135712	2124.255825	0.000451244	11	N	54	74
Q99LT0	Exosome	SLPTR	AYLDQTVVPILLQGLAVLAK	ERPPN	3		709.0930748	2124.255825	0.000451244	19	N	54	74
Q99LT0	Parental	AVLAK	ERPPNPIEFLASYLLK	NKAQF	2		944.0228907	1886.030181	0.001591523	2	N	74	90
Q99LT0	Parental	AVLAK	ERPPNPIEFLASYLLK	NKAQF	3		629.6845271	1886.030181	0.000451244	32	N	74	90
Q99LT0	Parental	SLPTR	AYLDQTVVPILLQGLAVLAK	ERPPN	2		1063.135712	2124.255825	0.000451244	24	N	54	74
Q99LT0	Parental	SLPTR	AYLDQTVVPILLQGLAVLAK	ERPPN	3		709.0930748	2124.255825	0.000451244	36	N	54	74
Q99LT0	Parental	PTRAY	LDQTVVPILLQGLAVLAK	ERPPN	3		631.059594	1890.155382	0.000451244	4	N	56	74
Q99LX0	Exosome	RAGIK	VTVAGLAGKDPVQCSR	DVMIC	2	C14:+57.021	829.4384365	1656.861273	0.000451244	7	N	32	48
Q99LX0	Exosome	RAGIK	VTVAGLAGKDPVQCSR	DVMIC	3	C14:+57.021	553.294891	1656.861273	0.000451244	24	N	32	48
Q99LX0	Exosome	EQESR	KGLIAAICAGPTALLAHEVGFGCK	VTTHP	3	C8:+57.021,C23:+57.021	818.7715927	2453.291378	0.000451244	12	N	98	122
Q99LX0	Exosome	EQESR	KGLIAAICAGPTALLAHEVGFGCK	VTTHP	4	C8:+57.021,C23:+57.021	614.3306445	2453.291378	0.000451244	7	N	98	122
Q99LX0	Exosome	ILTSR	GPGTSFEFALAIVEALVGK	DMANQ	2		953.5201808	1905.024762	0.000451244	8	N	156	175
Q99LX0	Exosome	ILTSR	GPGTSFEFALAIVEALVGK	DMANQ	3		636.0160539	1905.024762	0.000451244	28	N	156	175
Q99LX0	Exosome	HPLAK	DKMMNGSHYSYSESR	VEKDG	3	M3:+15.995,M4:+15.995	608.5828722	1822.725217	0.002453667	3	N	130	145
Q99LX0	Parental	RAGIK	VTVAGLAGKDPVQCSR	DVMIC	2	C14:+57.021	829.4384365	1656.861273	0.000451244	29	N	32	48
Q99LX0	Parental	RAGIK	VTVAGLAGKDPVQCSR	DVMIC	3	C14:+57.021	553.294891	1656.861273	0.000451244	12	N	32	48
Q99LX0	Parental	EQESR	KGLIAAICAGPTALLAHEVGFGCK	VTTHP	2	C8:+57.021,C23:+57.021	1227.653489	2453.291378	0.000451244	2	N	98	122
Q99LX0	Parental	EQESR	KGLIAAICAGPTALLAHEVGFGCK	VTTHP	3	C8:+57.021,C23:+57.021	818.7715927	2453.291378	0.000451244	13	N	98	122

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99LX0	Parental	EQESR	KGLIAAICAGPTALLAHEVGFGCK	VTTHP	4	C8:+57.021,C23:+57.021	614.3306445	2453.291378	0.000451244	24	N	98	122
Q99LX0	Parental	ILTSR	GPGTSFEFALAIVEALVGK	DMANQ	2		953.5201808	1905.024762	0.000451244	21	N	156	175
Q99LX0	Parental	ILTSR	GPGTSFEFALAIVEALVGK	DMANQ	3		636.0160539	1905.024762	0.000451244	33	N	156	175
Q99LX0	Parental	QESRK	GLIAAICAGPTALLAHEVGFGCK	VTTHP	3	C7:+57.021,C22:+57.021	776.0732716	2325.196415	0.000823681	5	N	99	122
Q99LX0	Parental	TSFEF	ALAIVEALVGK	DMANQ	2		542.342771	1082.669942	0.002374549	1	N	164	175
Q99M15	Exosome	EQVRK	SLETCSIEKDIQYFVNQR	KTGQT	3	C5:+57.021	744.0321722	2229.073117	0.000451244	6	N	254	272
Q99M15	Exosome	SEHIK	ACEVFEAQECER	INFFR	2	C2:+57.021,C10:+57.021	764.3138243	1526.612049	0.000622848	1	N	211	223
Q99M15	Parental	EQVRK	SLETCSIEKDIQYFVNQR	KTGQT	3	C5:+57.021	744.0321722	2229.073117	0.000451244	6	N	254	272
Q99M15	Parental	SEHIK	ACEVFEAQECER	INFFR	2	C2:+57.021,C10:+57.021	764.3138243	1526.612049	0.000451244	9	N	211	223
Q99M31	Exosome	SGMYR	VLSTNTSDNIGGAHFTDTLAQYLASEFQR	LFKHD	3		1052.846456	3155.515969	0.000451244	4	N	216	245
Q99M31	Parental	SGMYR	VLSTNTSDNIGGAHFTDTLAQYLASEFQR	LFKHD	3		1052.846456	3155.515969	0.000451244	15	N	216	245
Q99M31	Parental	AEVAK	HSLSTLGSANCFVDSLYEGQDFDCNVSR	ARFEL	3	C11:+57.021,C24:+57.021	1060.133083	3177.375849	0.000451244	3	N	269	297
Q99M46	Exosome	KEHAK	WNPTAGVAFEYDPDNALR	HTVYP	2		1018.479576	2034.943551	0.000823681	1	N	175	193
Q99M46	Parental	KEHAK	WNPTAGVAFEYDPDNALR	HTVYP	2		1018.479576	2034.943551	0.000451244	13	N	175	193
Q99M46	Parental	GKPER	FYYNVESCGSLRPETIVLSALSGLK	KKLSD	3	C8:+57.021	935.1497172	2802.425751	0.000451244	4	N	228	253
Q99MD9	Parental	LLGKK	YGETANECGEAFFFYGK	SLLEL	2	C8:+57.021	995.4201064	1988.824613	0.001162105	3	N	76	93
Q99MD9	Parental	QAHLK	LGEVSVESENYIQAVEEFQACLSLQEQYLEAHDR	LLAET	3	C21:+57.021	1328.625342	3982.852627	0.000451244	27	N	533	567
Q99MD9	Parental	QAHLK	LGEVSVESENYIQAVEEFQACLSLQEQYLEAHDR	LLAET	4	C21:+57.021	996.7209567	3982.852627	0.000451244	15	N	533	567
Q99MD9	Parental	EAHDR	LLAETHYQLGLAYGYNSQYDEAVAQFGK	SIDVI	3		1050.512526	3148.514178	0.002884417	1	N	567	595
Q99MK8	Exosome	TISER	WQQEVAETVFDTINAETDRLEAR	KKAKN	3		907.7758616	2720.304185	0.000451244	7	N	516	539
Q99MK8	Exosome	SPELR	SLLEGLLQR	DVNRR	2		514.8090953	1027.602591	0.001162105	6	N	422	431
Q99MK8	Exosome	IRGGK	QFVLQCDSDPELVQWK	KELRD	2	C6:+57.021	996.4804984	1990.945397	0.000451244	7	N	628	644
Q99MK8	Exosome	YLLFR	DFCLNHLEEAKPLVEFYEEIKK	YEKLE	4	C3:+57.021	688.5983221	2750.362089	0.001654178	1	N	69	91
Q99MK8	Exosome	HLVKK	QVPPDLFQPYIEEICQNLR	GDVFQ	2	C15:+57.021	1180.091476	2358.167352	0.001329271	1	N	139	158
Q99MK8	Exosome	HLVKK	QVPPDLFQPYIEEICQNLR	GDVFQ	3	C15:+57.021	787.0635838	2358.167352	0.000451244	3	N	139	158
Q99MK8	Parental	TISER	WQQEVAETVFDTINAETDRLEAR	KKAKN	3		907.7758616	2720.304185	0.000451244	9	N	516	539
Q99MK8	Parental	IRGGK	QFVLQCDSDPELVQWK	KELRD	2	C6:+57.021	996.4804984	1990.945397	0.000823681	4	N	628	644
Q99MK8	Parental	LIPPR	GEVNAADAFDIGSFDEEDTK	GIKLL	2		1065.461443	2128.907285	0.000451244	3	N	474	494
Q99MN1	Exosome	ELSEK	QLNQTASAPNHTADNGVGAEEETLDPNQYYK	IRSQA	3		1125.850706	3374.528718	0.000451244	26	N	45	76
Q99MN1	Exosome	RYRQR	YLDLILNDFVR	QKFIV	2		690.880249	1379.744898	0.000451244	10	N	228	239
Q99MN1	Exosome	FVMKK	EICNAYTELNDPVR	QRQLF	2	C3:+57.021	847.3964343	1692.777269	0.000451244	3	N	491	505
Q99MN1	Parental	ELSEK	QLNQTASAPNHTADNGVGAEEETLDPNQYYK	IRSQA	3		1125.850706	3374.528718	0.000451244	47	N	45	76
Q99MN1	Parental	FVMKK	EICNAYTELNDPVR	QRQLF	2	C3:+57.021	847.3964343	1692.777269	0.000451244	4	N	491	505
Q99MR6	Parental	RGDPR	AIVEYRDLDAPDDVDFF	-	2		1000.468342	1998.921084	0.0025889	1	N	858	875
Q99MR6	Parental	VTFDR	SVNIKEICWNLQNIR	LRECE	3	C8:+57.021	629.6687284	1885.982785	0.000998612	1	N	470	485
Q99N15	Exosome	PFPSR	LGDPAEYAHLVQTIIENPFLNGEVIR	LDGAI	2		1454.764328	2907.513055	0.000451244	1	N	226	252
Q99N15	Exosome	PFPSR	LGDPAEYAHLVQTIIENPFLNGEVIR	LDGAI	3		970.1788185	2907.513055	0.000451244	29	N	226	252
Q99N15	Exosome	PFPSR	LGDPAEYAHLVQTIIENPFLNGEVIR	LDGAI	4		727.8860638	2907.513055	0.000451244	3	N	226	252
Q99N15	Exosome	PTGIR	VVTIAPGLFATPLLTTLPEK	VRNFL	2		1041.116988	2080.218376	0.000451244	14	N	192	212
Q99N15	Exosome	PTGIR	VVTIAPGLFATPLLTTLPEK	VRNFL	3		694.4139254	2080.218376	0.000622848	8	N	192	212
Q99N15	Exosome	ATAKR	LVGQGATAVLLDVPDSEGEAQAK	KLGES	2		1134.590052	2267.164503	0.000451244	14	N	29	52
Q99N15	Exosome	QGGQR	GVIINTASVAAFEGQVGQAAYSASK	GGIVG	2		1220.129875	2438.24415	0.000451244	10	N	147	172
Q99N15	Exosome	QGGQR	GVIINTASVAAFEGQVGQAAYSASK	GGIVG	3		813.7558501	2438.24415	0.000622848	2	N	147	172
Q99N15	Exosome	LATAK	RLVGQGATAVLLDVPDSEGEAQAK	KLGES	3		808.7630047	2423.265614	0.000622848	3	N	28	52
Q99N15	Exosome	VRSVK	GLVAVVTGGASGLGLATAK	RLVGQ	2		821.4808586	1640.946117	0.000451244	8	N	9	28
Q99N15	Exosome	VRSVK	GLVAVVTGGASGLGLATAK	RLVGQ	3		547.9898391	1640.946117	0.000735798	2	N	9	28
Q99N15	Exosome	EDFQR	VINVNLIGTFNVIR	LVAGE	2		786.4675542	1570.919508	0.000451244	1	N	116	130
Q99N15	Parental	PFPSR	LGDPAEYAHLVQTIIENPFLNGEVIR	LDGAI	3		970.1788185	2907.513055	0.000451244	29	N	226	252
Q99N15	Parental	PFPSR	LGDPAEYAHLVQTIIENPFLNGEVIR	LDGAI	4		727.8860638	2907.513055	0.000451244	3	N	226	252
Q99N15	Parental	ATAKR	LVGQGATAVLLDVPDSEGEAQAK	KLGES	2		1134.590052	2267.164503	0.000451244	8	N	29	52
Q99N15	Parental	QGGQR	GVIINTASVAAFEGQVGQAAYSASK	GGIVG	2		1220.129875	2438.24415	0.000451244	5	N	147	172
Q99N16	Parental	KAKAK	TLDFIDVLLLSKDEHGK	ALSDE	4		486.518085	1942.04114	0.000823681	1	N	294	311
Q99N16	Parental	KAKAK	TLDFIDVLLLSK	DEHGK	2		688.9059325	1375.796265	0.001763695	2	N	294	306
Q99N80	Parental	AAPER	STETQGPDLSSPYVPSK	ASEGQ	2		896.9341352	1791.85267	0.000451244	10	N	149	166
Q99N80	Parental	KATSK	ILENGEEAPGLGPSLDR	MLSSS	2		883.9501196	1765.884639	0.002727428	2	N	221	238
Q99NB9	Exosome	NTTAR	AFAVVASALGIPSLLPFLK	AVCKS	2		957.5773018	1913.139004	0.000451244	16	N	630	649
Q99NB9	Exosome	NTTAR	AFAVVASALGIPSLLPFLK	AVCKS	3		638.7208012	1913.139004	0.000451244	6	N	630	649
Q99NB9	Exosome	QQKVR	TISALAIAALAEAATPYGIESFDSVLKPLWK	GIRQH	3		1082.927388	3245.758765	0.000451244	22	N	702	733
Q99NB9	Exosome	DRTMK	SVNDQPSGNLPFLKPDDIQY	FDKLL	2		1124.050562	2246.085524	0.00091018	6	N	454	474
Q99NB9	Exosome	REWMR	ICFELLELLK	AHKKA	2	C2:+57.021	639.3626148	1276.70963	0.000451244	2	N	1057	1067
Q99NB9	Exosome	PYVHK	ILVVIEPLLIDEDYYAR	VEGRE	2		1017.562046	2033.108491	0.000451244	6	N	573	590
Q99NB9	Exosome	GYIAK	AIGPHDVLATLLNNLK	VQERQ	3		563.6618339	1687.962102	0.000451244	16	N	1086	1102
Q99NB9	Exosome	LKVVK	QCCGTDGVEANYIK	TEILP	2	C2:+57.021,C3:+57.021	807.8480313	1613.680463	0.000451244	3	N	793	807
Q99NB9	Exosome	LPHLR	SLVEIIEHGLVDEQQK	VRTIS	3		612.9954299	1835.96289	0.000451244	9	N	684	700
Q99NB9	Exosome	QQKVR	TISALAIAALAEAATPY	GIESF	2		823.9541423	1645.892685	0.000823681	3	N	702	719

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99NB9	Exosome	QQKVR	TISALAIAALAEAATPY	GIESF	3		549.6386949	1645.892685	0.000451244	3	N	702	719
Q99NB9	Exosome	TDKAR	EFGAGPLFNQILPLLMSPTLEDQER	HLLVK	3	M16:+15.995	944.4815384	2830.421215	0.000622848	1	N	524	549
Q99NB9	Exosome	NRHEK	VQENCIDLVGR	IADRG	2	C5:+57.021	651.8274591	1301.639318	0.000451244	2	N	1030	1041
Q99NB9	Parental	EIQGK	KAALDEAQGVGLDSTGYYDQEIYGGSDSR	FAGYV	3		1022.471055	3064.389765	0.000451244	5	N	21	50
Q99NB9	Parental	GSDSR	FAGYVTSIAATELEDDDDDYSSSTSLLGQK	KPGYH	3		1066.821531	3197.441192	0.000451244	35	N	50	80
Q99NB9	Parental	NTTAR	AFAVVASALGIPSLLPFLK	AVCKS	2		957.5773018	1913.139004	0.000451244	13	N	630	649
Q99NB9	Parental	NTTAR	AFAVVASALGIPSLLPFLK	AVCKS	3		638.7208012	1913.139004	0.001162105	1	N	630	649
Q99NB9	Parental	QQKVR	TISALAIAALAEAATPYGIESFDSVLKPLWK	GIRQH	3		1082.927388	3245.758765	0.000451244	27	N	702	733
Q99NB9	Parental	DRTMK	SVNDQPSGNLPFLKPDDIQY	FDKLL	2		1124.050562	2246.085524	0.000451244	29	N	454	474
Q99NB9	Parental	REWMR	ICFELLELLK	AHKKA	2	C2:+57.021	639.3626148	1276.70963	0.001839721	8	N	1057	1067
Q99NB9	Parental	PYVHK	ILVVIEPLLIDEDYYAR	VEGRE	2		1017.562046	2033.108491	0.000451244	8	N	573	590
Q99NB9	Parental	GYIAK	AIGPHDVLATLLNNLK	VQERQ	3		563.6618339	1687.962102	0.000451244	12	N	1086	1102
Q99NB9	Parental	GATPK	KLSSWDQAETPGHTPSLR	WDETP	3		670.6733498	2008.996649	0.001329271	1	N	213	231
Q99NB9	Parental	QYFDK	LLVDVDESTLSPEEQKER	KIMKL	2		1044.029295	2086.042991	0.000451244	2	N	477	495
Q99NB9	Parental	LKVVK	QCCGTDGVEANYIK	TEILP	2	C2:+57.021,C3:+57.021	807.8480313	1613.680463	0.000451244	4	N	793	807
Q99NB9	Parental	LPHLR	SLVEIIEHGLVDEQQK	VRTIS	3		612.9954299	1835.96289	0.000451244	2	N	684	700
Q99P88	Parental	KEYQK	ISNQVDLPSVCAQYR	QVRFY	2	C11:+57.021	875.4333511	1748.851102	0.000662267	2	N	906	921
Q99P88	Parental	DLVIR	DKEVTGALIASLINCYIR	DNAAV	3	C15:+57.021	679.3667151	2035.076745	0.000451244	14	N	829	847
Q99P88	Parental	KSSNR	EITAIESSVPVQLLESVLQELK	GLQEF	2		1213.17596	2424.33632	0.000451244	4	N	693	715
Q99P88	Parental	KSSNR	EITAIESSVPVQLLESVLQELK	GLQEF	3		809.1199065	2424.33632	0.000451244	3	N	693	715
Q99P88	Parental	EFLDR	NSQFSGGPLGNPNTTAR	VQQRL	2		859.4167783	1716.817957	0.000451244	7	N	723	740
Q99P88	Parental	VDQLR	HLLVSNVGGDGEEIER	FFKLH	2		862.4346367	1722.853673	0.00091018	1	N	521	537
Q99P88	Parental	NCYIR	DNAAVDGISLHLQDTCPLLYSTDDAVCSK	ANELL	3	C16:+57.021,C27:+57.021	1060.160639	3177.458516	0.000451244	16	N	847	876
Q99P88	Parental	WNRVK	SPLHLLDCIHVLLTR	YVENP	3	C8:+57.021	596.3384311	1785.991893	0.000622848	3	N	1318	1333
Q99PL5	Parental	DIVLK	LREAEETQNSLQAECDQYR	TILAE	3	C15:+57.021	780.6892453	2339.044336	0.000451244	9	N	1312	1331
Q99PL5	Parental	VLKLR	EAEETQNSLQAECDQYR	TILAE	2	C13:+57.021	1035.93738	2069.859161	0.000451244	28	N	1314	1331
Q99PL5	Parental	TERIR	SIEALLEAGQAQDTQASHAEANQQQTR	LKELE	2		1448.195526	2894.375452	0.0007646	2	N	1161	1188
Q99PL5	Parental	TERIR	SIEALLEAGQAQDTQASHAEANQQQTR	LKELE	3		965.7996174	2894.375452	0.000451244	30	N	1161	1188
Q99PL5	Parental	EAQTK	ETLLALLPGLSISAHQNYAEWLQEFKEK	GSELL	3		1076.903354	3227.686663	0.000662267	5	N	1264	1292
Q99PL5	Parental	EAQTK	ETLLALLPGLSISAHQNYAEWLQEFKEK	GSELL	4		807.9294657	3227.686663	0.000451244	7	N	1264	1292
Q99PL5	Parental	EAQTK	ETLLALLPGLSISAHQNYAEWLQEFK	EKGSE	3		991.1908355	2970.549107	0.000451244	15	N	1264	1290
Q99PL5	Parental	NSILR	DALNQATSQVESK	QNTEL	2		695.8445918	1389.673584	0.000451244	5	N	1009	1022
Q99PL5	Parental	VAGLR	QLLLESQSQLDEAKSEAQK	QSDEL	3		715.7064963	2144.096089	0.000451244	2	N	1426	1445
Q99PT1	Exosome	PPAQK	SIQEIQELDKDDESLR	KYKEA	2		959.4741559	1916.932712	0.000451244	6	N	33	49
Q99PT1	Exosome	ALLGR	VAVSADPNVPNVIVTR	LTLVC	2		825.962833	1649.910066	0.000451244	44	N	58	74
Q99PT1	Exosome	VIVTR	LTLVCSTAPGPLELDLTGDLESFKK	QSFVL	2	C5:+57.021	1352.70961	2703.403619	0.000451244	11	N	74	99
Q99PT1	Exosome	VIVTR	LTLVCSTAPGPLELDLTGDLESFKK	QSFVL	3	C5:+57.021	902.1423397	2703.403619	0.000451244	43	N	74	99
Q99PT1	Exosome	VIVTR	LTLVCSTAPGPLELDLTGDLESFK	KQSFV	3	C5:+57.021	859.4440186	2575.308656	0.000451244	3	N	74	98
Q99PT1	Parental	PPAQK	SIQEIQELDKDDESLR	KYKEA	2		959.4741559	1916.932712	0.000451244	49	N	33	49
Q99PT1	Parental	PPAQK	SIQEIQELDKDDESLR	KYKEA	3		639.9853706	1916.932712	0.000451244	5	N	33	49
Q99PT1	Parental	ALLGR	VAVSADPNVPNVIVTR	LTLVC	2		825.962833	1649.910066	0.000451244	46	N	58	74
Q99PT1	Parental	VIVTR	LTLVCSTAPGPLELDLTGDLESFKK	QSFVL	2	C5:+57.021	1352.70961	2703.403619	0.000451244	22	N	74	99
Q99PT1	Parental	VIVTR	LTLVCSTAPGPLELDLTGDLESFKK	QSFVL	3	C5:+57.021	902.1423397	2703.403619	0.000451244	57	N	74	99
Q99PT1	Parental	VIVTR	LTLVCSTAPGPLELDLTGDLESFKK	QSFVL	4	C5:+57.021	676.8587048	2703.403619	0.001162105	1	N	74	99
Q99PT1	Parental	VIVTR	LTLVCSTAPGPLELDLTGDLESFK	KQSFV	2	C5:+57.021	1288.662128	2575.308656	0.000622848	5	N	74	98
Q99PT1	Parental	VIVTR	LTLVCSTAPGPLELDLTGDLESFK	KQSFV	3	C5:+57.021	859.4440186	2575.308656	0.000451244	3	N	74	98
Q99PV0	Exosome	MTYFR	EAVVNTQELLDLLVK	CENKI	2		842.4805243	1682.945449	0.000451244	15	N	1275	1290
Q99PV0	Exosome	STLYR	LANQLLTDLVDDNYFYLFDLK	AFFTS	2		1267.147202	2532.278805	0.000451244	7	N	240	261
Q99PV0	Exosome	STLYR	LANQLLTDLVDDNYFYLFDLK	AFFTS	3		845.1007349	2532.278805	0.000823681	3	N	240	261
Q99PV0	Exosome	RHSVK	SQEPLPDDDEEFELPEFVEPFLK	DTPLY	3		917.0976073	2748.269422	0.000451244	7	N	366	389
Q99PV0	Exosome	EPLVR	DINLQDEDWNEFNDINK	IIIRQ	2		1061.472145	2120.928689	0.000451244	5	N	284	301
Q99PV0	Exosome	AQNRR	LTLEDLEDSWDR	GIPRI	2		746.3522497	1490.688899	0.000662267	1	N	1402	1414
Q99PV0	Exosome	NRLLR	LIVDHNIADYMTAKNNVVIN	YKDMN	3		753.0602169	2256.157251	0.002813207	1	N	998	1018
Q99PV0	Exosome	EHTLF	KGTYFPTWEGLFWEK	ASGFE	3		630.3143227	1887.919568	0.001763695	1	N	1490	1505
Q99PV0	Exosome	HLWQK	IHESIVMDLCQVFDQELDALEIETVQK	ETIHP	3	M7:+15.995,C10:+57.021	1073.525101	3217.551903	0.002884417	1	N	1584	1611
Q99PV0	Parental	MTYFR	EAVVNTQELLDLLVK	CENKI	2		842.4805243	1682.945449	0.00091018	1	N	1275	1290
Q99PV0	Parental	STLYR	LANQLLTDLVDDNYFYLFDLK	AFFTS	2		1267.147202	2532.278805	0.000451244	3	N	240	261
Q99PV0	Parental	STLYR	LANQLLTDLVDDNYFYLFDLK	AFFTS	3		845.1007349	2532.278805	0.000622848	3	N	240	261
Q99PV0	Parental	RHSVK	SQEPLPDDDEEFELPEFVEPFLK	DTPLY	2		1375.142511	2748.269422	0.00091018	8	N	366	389
Q99PV0	Parental	RHSVK	SQEPLPDDDEEFELPEFVEPFLK	DTPLY	3		917.0976073	2748.269422	0.000451244	13	N	366	389
Q99PV0	Parental	EPLVR	DINLQDEDWNEFNDINK	IIIRQ	2		1061.472145	2120.928689	0.000451244	3	N	284	301
Q99PV0	Parental	PPLDY	ADNILDVEPLEAIQLELDPEEDAPVLDWFYDHQPLR	DSRKY	3		1406.690495	4217.048084	0.001699387	1	N	178	214
Q99PV0	Parental	RHSVK	SQEPLPDDDEEFELPEFVEPFLKDTPLY	TDNTA	3		1113.522533	3337.5442	0.000622848	1	N	366	394
Q99PV0	Parental	ISDLR	AQIAGYLYGVSPPDNPQVK	EIRCI	2		1009.023619	2016.031638	0.000622848	4	N	2121	2140
Q99PV0	Parental	EPFLK	DTPLYTDNTANGIALLWAPRPF	NLRSG	2		1223.624229	2445.232857	0.000451244	2	N	389	411

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q99PV0	Parental	RTVNK	HGDEIITSTTSNYETQTFSSK	TEWRV	3		782.6964371	2345.065911	0.000823681	2	N	2049	2070
Q9CPR4	Exosome	NAELK	GLDVDSLVIEHIQVNK	APKMR	3		593.6602701	1777.95741	0.001264573	1	N	105	121
Q9CPR4	Parental	NAELK	GLDVDSLVIEHIQVNKAPK	MRRRT	3		692.3885504	2074.142251	0.001763695	1	N	105	124
Q9CPR4	Parental	NAELK	GLDVDSLVIEHIQVNKAPK	MRRRT	4		519.5433628	2074.142251	0.001763695	2	N	105	124
Q9CPR4	Parental	IEMIL	TEKEQIVPKPEEEVAQK	KKISQ	2		991.5261915	1981.036783	0.002145581	1	N	150	167
Q9CPR4	Parental	IEMIL	TEKEQIVPKPEEEVAQK	KKISQ	3		661.3533944	1981.036783	0.000451244	11	N	150	167
Q9CPR4	Parental	NAELK	GLDVDSLVIEHIQVNK	APKMR	2		889.9865052	1777.95741	0.000451244	4	N	105	121
Q9CPR4	Parental	NAELK	GLDVDSLVIEHIQVNK	APKMR	3		593.6602701	1777.95741	0.000451244	8	N	105	121
Q9CPR4	Parental	ILTEK	EQIVPKPEEEVAQK	KKISQ	2		812.4335741	1622.851548	0.0025889	1	N	153	167
Q9CPR4	Parental	ILTEK	EQIVPKPEEEVAQKK	KISQK	4		438.7444278	1750.946511	0.002813207	1	N	153	168
Q9CPV4	Exosome	WPLSK	VAEGIFETEAPGGYK	FYLQD	2		784.3860925	1566.756585	0.001591523	1	N	109	124
Q9CPV4	Parental	EEKQR	ALLGYADNQCKLELQGIQGAVDHAAAFGR	IAFSC	4	C10:+57.021	772.3927717	3085.539887	0.000451244	7	N	172	201
Q9CPV4	Parental	WPLSK	VAEGIFETEAPGGYKFYLQDR	SPSQS	2		1195.587312	2389.159024	0.00091018	1	N	109	130
Q9CPV4	Parental	WPLSK	VAEGIFETEAPGGYK	FYLQD	2		784.3860925	1566.756585	0.000451244	4	N	109	124
Q9CPW4	Exosome	QWHEK	ALAAGGVGSIVR	VLTAR	2		535.8199943	1069.624389	0.000451244	61	N	131	143
Q9CPW4	Exosome	KYIYK	GFESPSDNSSAVLLQWHEK	ALAAG	2		1066.008697	2130.001795	0.000451244	56	N	112	131
Q9CPW4	Exosome	KYIYK	GFESPSDNSSAVLLQWHEK	ALAAG	3		711.0083982	2130.001795	0.000451244	19	N	112	131
Q9CPW4	Exosome	ARFRK	VDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C32:+57.021	1253.850506	3758.528117	0.000451244	83	N	13	47
Q9CPW4	Exosome	VDEED	GGDGQAGPDEGEVDSCLR	QGNMT	2	C16:+57.021	909.8818767	1817.748153	0.000451244	44	N	29	47
Q9CPW4	Exosome	RFRKV	DVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C31:+57.021	1220.827701	3659.459703	0.000451244	16	N	14	47
Q9CPW4	Exosome	DENKF	VDEEDGGDGQAGPDEGEVDSCLR	QGNMT	2	C21:+57.021	1203.48562	2404.95564	0.000451244	3	N	24	47
Q9CPW4	Exosome	YDENK	FVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	2	C22:+57.021	1277.019827	2552.024054	0.000451244	2	N	23	47
Q9CPW4	Exosome	FRKVD	VDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C30:+57.021	1182.485387	3544.43276	0.000451244	3	N	15	47
Q9CPW4	Exosome	ENKFV	DEEDGGDGQAGPDEGEVDSCLR	QGNMT	2	C20:+57.021	1153.951413	2305.887226	0.000698008	1	N	25	47
Q9CPW4	Exosome	DVDEY	DENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C26:+57.021	1013.751627	3038.231481	0.000451244	3	N	19	47
Q9CPW4	Parental	QWHEK	ALAAGGVGSIVR	VLTAR	2		535.8199943	1069.624389	0.000451244	20	N	131	143
Q9CPW4	Parental	KYIYK	GFESPSDNSSAVLLQWHEK	ALAAG	2		1066.008697	2130.001795	0.000451244	41	N	112	131
Q9CPW4	Parental	ARFRK	VDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR	QGNMT	3	C32:+57.021	1253.850506	3758.528117	0.000451244	72	N	13	47
Q9CPW4	Parental	DLLMK	YIYKGFESPSDNSSAVLLQWHEK	ALAAG	3		900.110293	2697.307479	0.000451244	7	N	108	131
Q9CPW4	Parental	DLLMK	YIYKGFESPSDNSSAVLLQWHEK	ALAAG	4		675.3346698	2697.307479	0.000622848	9	N	108	131
Q9CPX6	Exosome	LIFLK	FVQAVIPTIEYDYTR	HFTM-	2		907.9703238	1813.925048	0.000451244	15	N	295	310
Q9CPX6	Exosome	ACKAK	ADAGGEDAILQTR	TYDLY	2		658.826202	1315.636804	0.001162105	4	N	185	198
Q9CPX6	Parental	TVKGK	ALEVAEYLTPVLK	ESKFK	2		723.4166643	1444.817729	0.000451244	3	N	11	24
Q9CPX6	Parental	LIFLK	FVQAVIPTIEYDYTR	HFTM-	2		907.9703238	1813.925048	0.000998612	2	N	295	310
Q9CPX6	Parental	ACKAK	ADAGGEDAILQTR	TYDLY	2		658.826202	1315.636804	0.000622848	1	N	185	198
Q9CPY7	Exosome	AAGCR	QVQDLELPSVEVDPCGDAQAAAEGAVLGLYEYDDLKQK	KKVAV	3	C15:+57.021	1378.667207	4132.978222	0.000451244	14	N	130	168
Q9CPY7	Exosome	AAGCR	QVQDLELPSVEVDPCGDAQAAAEGAVLGLYEYDDLK	QKKKV	3	C15:+57.021	1293.282694	3876.824681	0.000698008	1	N	130	166
Q9CPY7	Parental	AAGCR	QVQDLELPSVEVDPCGDAQAAAEGAVLGLYEYDDLKQK	KKVAV	3	C15:+57.021	1378.667207	4132.978222	0.000451244	6	N	130	168
Q9CPY7	Parental	VTHTK	WAHLDIAGVMTNK	DEIPY	3	M10:+15.995	491.2508056	1470.729017	0.00091018	7	N	476	489
Q9CQ19	Exosome	MFGEK	LNGTDPEDVIR	NAFAC	2		614.8125633	1227.609527	0.000451244	52	Y	93	104
Q9CQ19	Exosome	EDVIR	NAFACFDEEASGFIHEDHLR	ELLTT	2	C5:+57.021	1183.019039	2364.022478	0.000451244	3	N	104	124
Q9CQ19	Exosome	EDVIR	NAFACFDEEASGFIHEDHLR	ELLTT	3	C5:+57.021	789.0152927	2364.022478	0.001162105	4	N	104	124
Q9CQ19	Exosome	PQRAT	SNVFAMFDQSQIQEFK	EAFNM	2	M6:+15.995	967.9518483	1933.888097	0.000451244	6	Y	19	35
Q9CQ19	Exosome	KRPQR	ATSNVFAMFDQSQIQEFK	EAFNM	2	M8:+15.995	1053.994245	2105.972889	0.000451244	21	Y	17	35
Q9CQ19	Exosome	KRPQR	ATSNVFAMFDQSQIQEF	KEAFN	2	M8:+15.995	989.9467629	1977.877926	0.000451244	13	Y	17	34
Q9CQ19	Exosome	IDQNR	DGFIDKEDLHDMLASLGK	NPTDE	3		668.6634633	2002.96699	0.000451244	6	Y	45	63
Q9CQ19	Parental	MFGEK	LNGTDPEDVIR	NAFAC	2		614.8125633	1227.609527	0.000451244	58	Y	93	104
Q9CQ19	Parental	PIDKK	GNFNYVEFTR	ILKHG	2		623.7967162	1245.577832	0.000622848	12	N	151	161
Q9CQ19	Parental	EDVIR	NAFACFDEEASGFIHEDHLR	ELLTT	2	C5:+57.021	1183.019039	2364.022478	0.000451244	9	N	104	124
Q9CQ19	Parental	EDVIR	NAFACFDEEASGFIHEDHLR	ELLTT	3	C5:+57.021	789.0152927	2364.022478	0.000451244	3	N	104	124
Q9CQ19	Parental	EDVIR	NAFACFDEEASGFIHEDHLR	ELLTT	4	C5:+57.021	592.0134195	2364.022478	0.000451244	13	N	104	124
Q9CQ19	Parental	FLTMF	GEKLNGTDPEDVIR	NAFAC	2		771.8920734	1541.768547	0.000451244	4	Y	90	104
Q9CQ19	Parental	IDQNR	DGFIDKEDLHDMLASLGK	NPTDE	3		668.6634633	2002.96699	0.000451244	8	Y	45	63
Q9CQ60	Exosome	LVQPR	TGALCWFLDEAAAR	LLSVP	2	C5:+57.021	790.8802231	1579.744846	0.000451244	20	N	231	245
Q9CQ60	Exosome	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	4	C25:+57.021	1007.020602	4024.051208	0.000451244	11	N	131	168
Q9CQ60	Exosome	PPPQR	VTLTLPVLNAAQSIIFVATGEGK	AAVLK	2		1171.670648	2341.325695	0.000870037	4	N	185	208
Q9CQ60	Exosome	PPPQR	VTLTLPVLNAAQSIIFVATGEGK	AAVLK	3		781.4496984	2341.325695	0.000451244	3	N	185	208
Q9CQ60	Exosome	HLLSK	LPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	2		1404.227244	2806.438887	0.000451244	10	N	102	128
Q9CQ60	Exosome	HLLSK	LPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	3		936.4874291	2806.438887	0.000451244	12	N	102	128
Q9CQ60	Parental	LVQPR	TGALCWFLDEAAAR	LLSVP	2	C5:+57.021	790.8802231	1579.744846	0.000451244	29	N	231	245
Q9CQ60	Parental	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	3	C25:+57.021	1342.358203	4024.051208	0.000451244	11	N	131	168
Q9CQ60	Parental	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	4	C25:+57.021	1007.020602	4024.051208	0.000451244	33	N	131	168
Q9CQ60	Parental	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	3	Q1:-17.027,C25:+57.021	1336.682536	4007.024208	0.000662267	9	N	131	168
Q9CQ60	Parental	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	3	[0:-17.027,C25:+57.021	1336.682536	4007.024208	0.000451244	14	N	131	168
Q9CQ60	Parental	ARKLR	QALQGDAVPVFDLLILGVGPDGHTCSLFPDHPLLQER	EKIVA	4	[0:-17.027,C25:+57.021	1002.763852	4007.024208	0.000451244	1	N	131	168

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CQ60	Parental	PPPQR	VTLTLPVLNAAQSIIFVATGEGK	AAVLK	2		1171.670648	2341.325695	0.000451244	15	N	185	208
Q9CQ60	Parental	PPPQR	VTLTLPVLNAAQSIIFVATGEGK	AAVLK	3		781.4496984	2341.325695	0.000451244	40	N	185	208
Q9CQ60	Parental	-MAA	PAPSLISVFSSPQELGASLAQLVAQR	AASCL	3		889.4891044	2665.443913	0.000622848	4	N	3	29
Q9CQ60	Parental	HLLSK	LPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	2		1404.227244	2806.438887	0.000451244	22	N	102	128
Q9CQ60	Parental	HLLSK	LPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	3		936.4874291	2806.438887	0.000451244	19	N	102	128
Q9CQ60	Parental	AVLKR	ILEDKEGTLPAALVQPR	TGALC	2		925.5232548	1849.03091	0.000451244	14	N	214	231
Q9CQ60	Parental	YGLYR	THLLSKLPIPDSQVLTINPALPVEDAAEDYAR	KLRQA	3		1162.954666	3485.840598	0.001352548	1	N	96	128
Q9CQ60	Parental	SMLAR	DLPAAAAPAGPASFAR	WTLGF	2		741.8891367	1481.762673	0.000698008	3	N	56	72
Q9CQ80	Exosome	QWVSR	SGQNNSVFTLYELTSGEDTEDEEFHGLDEATLLR	ALQAL	3		1272.917333	3815.7286	0.000451244	15	N	117	151
Q9CQ80	Exosome	VKLQR	KLPVESIQIVLEELR	KKGNL	3		589.3527775	1765.034932	0.000451244	1	N	67	82
Q9CQ80	Parental	QWVSR	SGQNNSVFTLYELTSGEDTEDEEFHGLDEATLLR	ALQAL	3		1272.917333	3815.7286	0.000451244	18	N	117	151
Q9CQ92	Parental	EDIRR	GIVLLEELLPK	GSKEE	2		612.3846358	1222.753672	0.001463592	8	N	53	64
Q9CQ92	Parental	MALGV	AGLAGLIGLAVSK	SKS-	2		585.3667774	1168.717955	0.001591523	2	N	136	149
Q9CQC6	Exosome	KRDEK	ERFDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	3	C11:+57.021	1061.515565	3181.523294	0.000622848	2	N	24	52
Q9CQC6	Exosome	DEKER	FDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	2	C9:+57.021	1449.197595	2896.379589	0.000451244	18	N	26	52
Q9CQC6	Exosome	DEKER	FDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	3	C9:+57.021	966.4676631	2896.379589	0.000451244	13	N	26	52
Q9CQC6	Exosome	DPTQF	QDCIIQGLTETGTDLEAVAK	FLDAS	2	C3:+57.021	1081.536199	2161.056798	0.000451244	1	N	32	52
Q9CQC6	Parental	KRDEK	ERFDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	3	C11:+57.021	1061.515565	3181.523294	0.000451244	3	N	24	52
Q9CQC6	Parental	DEKER	FDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	2	C9:+57.021	1449.197595	2896.379589	0.000451244	6	N	26	52
Q9CQC6	Parental	DEKER	FDPTQFQDCIIQGLTETGTDLEAVAK	FLDAS	3	C9:+57.021	966.4676631	2896.379589	0.000451244	5	N	26	52
Q9CQC6	Parental	DEKER	FDPTQFQDCIIQGLTETGTDLEAVAKF	LDASG	3	C9:+57.021	1015.490468	3043.448003	0.001871652	1	N	26	53
Q9CQC6	Parental	EHFTK	YFTEAGLKELSEYVR	NQQTI	3		602.3092374	1803.904312	0.001699387	1	N	231	246
Q9CQC6	Parental	DPTQF	QDCIIQGLTETGTDLEAVAK	FLDAS	2	C3:+57.021	1081.536199	2161.056798	0.000451244	10	N	32	52
Q9CQC6	Parental	IKHLK	QYSPLLAAFTTQGQSELTLLLK	IQEYC	2		1211.665562	2421.315524	0.000451244	2	N	322	344
Q9CQE1	Exosome	VAAVR	ESVSYLESQQNTFLIPTSFSPLK	-	2		1308.166123	2614.316647	0.000451244	35	N	224	247
Q9CQE1	Exosome	VAAVR	ESVSYLESQQNTFLIPTSFSPLK	-	3		872.4466823	2614.316647	0.000451244	13	N	224	247
Q9CQE1	Exosome	NAFKR	AVNAHVELGYSTLVGVFHTEYGALNR	VHVLW	3		939.8159915	2816.424575	0.000451244	8	N	167	193
Q9CQE1	Exosome	NAFKR	AVNAHVELGYSTLVGVFHTEYGALNR	VHVLW	4		705.1139437	2816.424575	0.001463592	3	N	167	193
Q9CQE1	Exosome	EWQER	FLIPNLAFIDKQEVEITYLVPWCK	IGTPP	3	C23:+57.021	979.5262364	2935.555309	0.000622848	9	N	112	136
Q9CQE1	Exosome	LKPSK	TNEFLENFK	NSVHL	2		571.2803676	1140.545135	0.001352548	1	N	48	57
Q9CQE1	Parental	VAAVR	ESVSYLESQQNTFLIPTSFSPLK	-	2		1308.166123	2614.316647	0.000451244	14	N	224	247
Q9CQE8	Exosome	ELQTK	INEAIVAVQAIIADPK	TDHRL	3		555.6580894	1663.950868	0.000451244	9	N	218	234
Q9CQE8	Exosome	VALEK	HILGFDTGDAVLNEAAQILR	LLHIE	3		718.3836879	2152.127664	0.000451244	24	N	185	205
Q9CQE8	Exosome	NCPFK	IQDRQEAIDWLLGLAVR	LEYGD	3		666.037852	1995.090156	0.000451244	1	N	72	89
Q9CQE8	Exosome	KIQDR	QEAIDWLLGLAVR	LEYGD	2		742.41753	1482.81946	0.000451244	1	N	76	89
Q9CQE8	Parental	ELQTK	INEAIVAVQAIIADPK	TDHRL	2		832.9832342	1663.950868	0.000451244	14	N	218	234
Q9CQE8	Parental	ELQTK	INEAIVAVQAIIADPK	TDHRL	3		555.6580894	1663.950868	0.000451244	25	N	218	234
Q9CQE8	Parental	VALEK	HILGFDTGDAVLNEAAQILR	LLHIE	2		1077.071632	2152.127664	0.000451244	5	N	185	205
Q9CQE8	Parental	VALEK	HILGFDTGDAVLNEAAQILR	LLHIE	3		718.3836879	2152.127664	0.000451244	34	N	185	205
Q9CQE8	Parental	NCPFK	IQDRQEAIDWLLGLAVR	LEYGD	3		666.037852	1995.090156	0.000998612	2	N	72	89
Q9CQE8	Parental	KIQDR	QEAIDWLLGLAVR	LEYGD	2		742.41753	1482.81946	0.000823681	2	N	76	89
Q9CQE8	Parental	DNAAK	NAEPLINLDVNNPDFK	AGVMA	2		906.9604874	1811.905375	0.002813207	1	N	115	131
Q9CQF3	Exosome	PKNYK	LVAAPLFELYDNAPGYGPIISSLPQLLSR	FNFIY	3		1038.901174	3113.680121	0.000451244	7	N	192	221
Q9CQF3	Parental	PKNYK	LVAAPLFELYDNAPGYGPIISSLPQLLSR	FNFIY	3		1038.901174	3113.680121	0.000451244	17	N	192	221
Q9CQF3	Parental	TTFFK	LPGGELNPGEDEVEGLKR	LMTEI	3		636.994089	1907.958867	0.000823681	1	N	105	123
Q9CQF3	Parental	VAAPL	FELYDNAPGYGPIISSLPQLLSR	FNFIY	2		1275.666094	2549.316587	0.000451244	4	N	198	221
Q9CQF3	Parental	VAAPL	FELYDNAPGYGPIISSLPQLLSR	FNFIY	3		850.7799957	2549.316587	0.00307782	1	N	198	221
Q9CQF9	Parental	KRFVK	ELGLSSVPASGGLVGVYNGK	SLVFE	2		952.5103444	1903.005089	0.000451244	4	N	104	124
Q9CQF9	Parental	NITFR	NFDPPIEEFNDPYQQLVTTFIK	GELNS	2		1328.153016	2654.290432	0.000451244	6	N	327	349
Q9CQF9	Parental	NITFR	NFDPPIEEFNDPYQQLVTTFIK	GELNS	3		885.7712773	2654.290432	0.000451244	12	N	327	349
Q9CQI6	Exosome	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVR	LFAFV	3	C22:+57.021	1023.793321	3068.356562	0.000451244	41	N	30	57
Q9CQI6	Exosome	AMSKR	SKFALITWIGEDVSGLQR	AKTGT	2		1010.547261	2019.078923	0.000451244	13	N	73	91
Q9CQI6	Exosome	AMSKR	SKFALITWIGEDVSGLQR	AKTGT	3		674.0341075	2019.078923	0.000451244	9	N	73	91
Q9CQI6	Exosome	SKRSK	FALITWIGEDVSGLQR	AKTGT	2		902.9837655	1803.951931	0.000451244	25	N	75	91
Q9CQI6	Exosome	SKRSK	FALITWIGEDVSGLQR	AKTGT	3		602.3251103	1803.951931	0.000451244	23	N	75	91
Q9CQI6	Exosome	YNLVR	DDGSAVIWVTFR	YDGAT	2		683.3440306	1364.672461	0.000622848	6	N	18	30
Q9CQI6	Parental	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVR	LFAFV	3	C22:+57.021	1023.793321	3068.356562	0.000451244	64	N	30	57
Q9CQI6	Parental	AMSKR	SKFALITWIGEDVSGLQR	AKTGT	2		1010.547261	2019.078923	0.000451244	10	N	73	91
Q9CQI6	Parental	AMSKR	SKFALITWIGEDVSGLQR	AKTGT	3		674.0341075	2019.078923	0.000451244	9	N	73	91
Q9CQI6	Parental	SKRSK	FALITWIGEDVSGLQR	AKTGT	2		902.9837655	1803.951931	0.000451244	21	N	75	91
Q9CQI6	Parental	SKRSK	FALITWIGEDVSGLQR	AKTGT	3		602.3251103	1803.951931	0.000451244	15	N	75	91
Q9CQI6	Parental	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVRLFAFVR	FTTGD	3	C22:+57.021	1268.269165	3801.784094	0.000451244	2	N	30	63
Q9CQI6	Parental	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVRLFAFVR	FTTGD	4	C22:+57.021	951.4538234	3801.784094	0.000823681	9	N	30	63
Q9CQI6	Parental	YNLVR	DDGSAVIWVTFR	YDGAT	2		683.3440306	1364.672461	0.000451244	30	N	18	30
Q9CQI6	Parental	TGTDK	TLVKEVVQNFAK	EFVIS	2		688.4013486	1374.787097	0.002145581	2	N	98	110

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CQI6	Parental	WVTFR	YDGATIVPGDQGADYQHFIQQCTDDVRLF	AFVRF	3	C22:+57.021	1110.510814	3328.509041	0.000451244	7	N	30	59
Q9CQI6	Parental	IWVTF	RYDGATIVPGDQGADYQHFIQQCTDDVR	LFAFV	3	C23:+57.021	1075.827025	3224.457674	0.000451244	7	N	29	57
Q9CQI6	Parental	IWVTF	RYDGATIVPGDQGADYQHFIQQCTDDVR	LFAFV	4	C23:+57.021	807.1222184	3224.457674	0.000998612	2	N	29	57
Q9CQI7	Parental	FKEVR	LVPGRHDIAFVEFENDGQAGAAR	DALQG	3		823.747689	2468.219667	0.000622848	2	N	181	204
Q9CQI7	Parental	LVPGR	HDIAFVEFENDGQAGAAR	DALQG	2		973.953725	1945.89185	0.0007646	1	N	186	204
Q9CQK7	Parental	QTTLK	FTYSEKYPDETPLYEIFSQENLEDNDVSDILK	LLALQ	3		1281.267192	3840.778176	0.000622848	4	N	53	85
Q9CQK7	Parental	EAEKK	LFHGTPVTIENFLSWK	AKFDA	3		630.3372388	1887.988316	0.000637154	6	N	139	155
Q9CQM9	Exosome	VSFVK	LEAEAVPEVSEKYEISSVPTFLFFK	NSQKV	3		953.8287923	2858.462977	0.000451244	7	N	69	94
Q9CQM9	Parental	CGFSK	QILEILNSTGVEYETFDILEDEEVRQGLK	TFSNW	3		1127.575632	3379.703495	0.000451244	25	N	267	296
Q9CQM9	Parental	RQGLK	TYSNWPTYPQLYVSGELIGGLDIIKELEASEELDTICPK	APKLE	4	C37:+57.021	1111.305859	4441.192237	0.001162105	1	N	194	233
Q9CQM9	Parental	VSFVK	LEAEAVPEVSEKYEISSVPTFLFFK	NSQKV	3		953.8287923	2858.462977	0.000451244	13	N	69	94
Q9CQM9	Parental	EVSEK	YEISSVPTFLFFK	NSQKV	2		789.4166643	1576.817729	0.002374549	1	N	81	94
Q9CQM9	Parental	LDIIK	ELEASEELDTICPK	APKLE	2	C12:+57.021	817.3852009	1632.754802	0.000823681	3	N	219	233
Q9CQM9	Parental	QLYVR	GDLVGGLDIVK	ELKDN	2		543.3142105	1084.612821	0.002374549	1	N	310	321
Q9CQM9	Parental	EILHK	HNIQFSSFDIFSDEEVR	QGLKT	2		1035.482315	2068.949031	0.000823681	5	N	173	190
Q9CQR6	Exosome	NDLKR	LCDYVCDLLLEESNVQPVSTPVTVCGDIHGQFYDLCELFR	TGGQV	4	C2:+57.021,C6:+57.021,C25:+57.021,C36:+57.021	1191.055009	4760.188834	0.002813207	1	N	26	66
Q9CQR6	Exosome	EIPHK	GAFCDLVWSDPEDVDTWAISPR	GAGWL	2	C4:+57.021	1268.576387	2535.137174	0.000451244	25	N	188	210
Q9CQR6	Exosome	EIPHK	GAFCDLVWSDPEDVDTWAISPR	GAGWL	3	C4:+57.021	846.0535246	2535.137174	0.000451244	16	N	188	210
Q9CQR6	Exosome	MFDEK	LVTVWSAPNYCYR	CGNIA	2	C11:+57.021	814.8984158	1627.781232	0.000735798	8	N	251	264
Q9CQR6	Exosome	-M	APLDLDKYVEIAR	QCKYL	3		501.6124801	1501.81404	0.000451244	6	N	1	14
Q9CQR6	Exosome	HKGAF	CDLVWSDPEDVDTWAISPR	GAGWL	2	C1:+57.021	1131.012891	2260.010182	0.000637154	1	N	191	210
Q9CQR6	Parental	NDLKR	LCDYVCDLLLEESNVQPVSTPVTVCGDIHGQFYDLCELFR	TGGQV	4	C2:+57.021,C6:+57.021,C25:+57.021,C36:+57.021	1191.055009	4760.188834	0.000622848	5	N	26	66
Q9CQR6	Parental	EIPHK	GAFCDLVWSDPEDVDTWAISPR	GAGWL	2	C4:+57.021	1268.576387	2535.137174	0.000451244	28	N	188	210
Q9CQR6	Parental	EIPHK	GAFCDLVWSDPEDVDTWAISPR	GAGWL	3	C4:+57.021	846.0535246	2535.137174	0.000451244	3	N	188	210
Q9CQR6	Parental	-M	APLDLDKYVEIAR	QCKYL	3		501.6124801	1501.81404	0.002019181	2	N	1	14
Q9CQV8	Exosome	SGENK	QTTVSNSQQAYQEAFEISKK	EMQPT	2		1144.064201	2286.112802	0.000698008	4	N	140	160
Q9CQV8	Exosome	SGENK	QTTVSNSQQAYQEAFEISKK	EMQPT	3		763.0454006	2286.112802	0.000451244	26	N	140	160
Q9CQV8	Exosome	SGENK	QTTVSNSQQAYQEAFEISK	KEMQP	2		1080.016719	2158.017839	0.000451244	43	N	140	159
Q9CQV8	Exosome	GDYFR	YLSEVASGENKQTTVSNSQQAYQEAFEISK	KEMQP	3		1112.867586	3335.579357	0.000451244	13	N	129	159
Q9CQV8	Exosome	MQLLR	DNLTLWTSENQGDEGDAGEGEN	-	2		1175.981259	2349.946918	0.000451244	6	N	224	246
Q9CQV8	Exosome	CSLAK	TAFDEAIAELDTLNEESYK	DSTLI	2		1080.005486	2157.995372	0.000451244	31	N	195	214
Q9CQV8	Exosome	CSLAK	TAFDEAIAELDTLNEESYK	DSTLI	3		720.3395906	2157.995372	0.000451244	11	N	195	214
Q9CQV8	Exosome	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	2		1159.109891	2316.204183	0.000451244	40	Y	169	189
Q9CQV8	Exosome	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	3		773.075861	2316.204183	0.000451244	22	Y	169	189
Q9CQV8	Exosome	CSLAK	TAFDEAIAELDTLNEESYKDSTLIMQLLR	DNLTL	3		1110.553951	3328.638453	0.000451244	23	N	195	224
Q9CQV8	Exosome	CSLAK	TAFDEAIAELDTLNEESYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1115.885618	3344.633453	0.000451244	18	N	195	224
Q9CQV8	Exosome	EYREK	IEAELQDICNDVLELLDKYLILNATQAESK	VFYLK	3	C9:+57.021	1154.595884	3460.764252	0.000451244	13	N	87	117
Q9CQV8	Exosome	EYREK	IEAELQDICNDVLELLDK	YLILN	2	C9:+57.021	1065.535668	2129.055735	0.000451244	30	N	87	105
Q9CQV8	Exosome	IMQLL	RDNLTLWTSENQGDEGDAGEGEN	-	2		1254.031815	2506.048029	0.000698008	4	N	223	246
Q9CQV8	Exosome	ELLDK	YLILNATQAESK	VFYLK	2		675.8673386	1349.719077	0.000451244	13	N	105	117
Q9CQV8	Exosome	GKEYR	EKIEAELQDICNDVLELLDK	YLILN	3	C11:+57.021	796.4055639	2386.193292	0.000451244	6	N	85	105
Q9CQV8	Exosome	CSLAK	TAFDEAIAELDTLNEESY	KDSTL	2		1015.958004	2029.900409	0.000451244	7	N	195	213
Q9CQV8	Exosome	THPIR	LGLALNFSVF	YYEIL	2		540.808564	1079.601528	0.002453667	1	Y	169	179
Q9CQV8	Parental	SGENK	QTTVSNSQQAYQEAFEISKK	EMQPT	2		1144.064201	2286.112802	0.000451244	3	N	140	160
Q9CQV8	Parental	SGENK	QTTVSNSQQAYQEAFEISKK	EMQPT	3		763.0454006	2286.112802	0.000451244	25	N	140	160
Q9CQV8	Parental	SGENK	QTTVSNSQQAYQEAFEISK	KEMQP	2		1080.016719	2158.017839	0.000451244	63	N	140	159
Q9CQV8	Parental	GDYFR	YLSEVASGENKQTTVSNSQQAYQEAFEISK	KEMQP	3		1112.867586	3335.579357	0.000451244	11	N	129	159
Q9CQV8	Parental	MQLLR	DNLTLWTSENQGDEGDAGEGEN	-	2		1175.981259	2349.946918	0.000451244	36	N	224	246
Q9CQV8	Parental	CSLAK	TAFDEAIAELDTLNEESYK	DSTLI	2		1080.005486	2157.995372	0.000451244	28	N	195	214
Q9CQV8	Parental	CSLAK	TAFDEAIAELDTLNEESYK	DSTLI	3		720.3395906	2157.995372	0.000451244	6	N	195	214
Q9CQV8	Parental	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	2		1159.109891	2316.204183	0.000622848	12	Y	169	189
Q9CQV8	Parental	THPIR	LGLALNFSVFYYEILNSPEK	ACSLA	3		773.075861	2316.204183	0.000451244	5	Y	169	189
Q9CQV8	Parental	CSLAK	TAFDEAIAELDTLNEESYKDSTLIMQLLR	DNLTL	3		1110.553951	3328.638453	0.000451244	30	N	195	224
Q9CQV8	Parental	CSLAK	TAFDEAIAELDTLNEESYKDSTLIMQLLR	DNLTL	3	M25:+15.995	1115.885618	3344.633453	0.000451244	9	N	195	224
Q9CQV8	Parental	EYREK	IEAELQDICNDVLELLDKYLILNATQAESK	VFYLK	3	C9:+57.021	1154.595884	3460.764252	0.000451244	15	N	87	117
Q9CQV8	Parental	EYREK	IEAELQDICNDVLELLDK	YLILN	2	C9:+57.021	1065.535668	2129.055735	0.000451244	21	N	87	105
Q9CQV8	Parental	EYREK	IEAELQDICNDVLELLDK	YLILN	3	C9:+57.021	710.6930451	2129.055735	0.002453667	1	N	87	105
Q9CQV8	Parental	AAAMK	AVTEQGHELSNEERNLLSVAYK	NVVGA	3		829.7545092	2486.240128	0.000622848	2	N	29	51
Q9CQV8	Parental	IMQLL	RDNLTLWTSENQGDEGDAGEGEN	-	2		1254.031815	2506.048029	0.000451244	37	N	223	246
Q9CQV8	Parental	IMQLL	RDNLTLWTSENQGDEGDAGEGEN	-	3		836.3571431	2506.048029	0.001763695	1	N	223	246
Q9CQV8	Parental	GKEYR	EKIEAELQDICNDVLELLDK	YLILN	2	C11:+57.021	1194.104446	2386.193292	0.000451244	4	N	85	105
Q9CQV8	Parental	GKEYR	EKIEAELQDICNDVLELLDK	YLILN	3	C11:+57.021	796.4055639	2386.193292	0.000451244	9	N	85	105
Q9CQV8	Parental	GDYFR	YLSEVASGENKQTTVSNSQQAY	QEAFE	2		1202.567305	2403.119009	0.000451244	4	N	129	151

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CQV8	Parental	CSLAK	TAFDEAIAELDTLNEESY	KDSTL	2		1015.958004	2029.900409	0.000451244	18	N	195	213
Q9CQV8	Parental	CSLAK	TAFDEAIAELDTLNEESY	KDSTL	3		677.6412696	2029.900409	0.000823681	1	N	195	213
Q9CQV8	Parental	THPIR	LGLALNFSVFY	YEILN	2		622.3402283	1242.664857	0.001352548	2	Y	169	180
Q9CQV8	Parental	FSVFY	YEILNSPEKACSLAK	TAFDE	2	C11:+57.021	861.9404777	1721.865355	0.000451244	3	Y	180	195
Q9CQV8	Parental	AAAMK	AVTEQGHELSNEERNLLSVAY	KNVVG	2		1180.080382	2358.145165	0.001264573	3	N	29	50
Q9CQV8	Parental	EYREK	IEAELQDICNDVLEL	LDKYL	2	C9:+57.021	887.4326825	1772.849765	0.001654178	1	N	87	102
Q9CR16	Exosome	ERVGR	IVLELFADIVPK	TAENF	2		678.9110178	1355.806436	0.000451244	25	N	31	43
Q9CR16	Parental	EKPAK	LCVIAECGELKEGDDWGIFPK	DGSGD	2	C2:+57.021,C7:+57.021	1218.582395	2435.14919	0.000870037	2	N	174	195
Q9CR16	Parental	EKPAK	LCVIAECGELKEGDDWGIFPK	DGSGD	3	C2:+57.021,C7:+57.021	812.7241967	2435.14919	0.000451244	13	N	174	195
Q9CR16	Parental	ERVGR	IVLELFADIVPK	TAENF	2		678.9110178	1355.806436	0.000451244	6	N	31	43
Q9CR68	Parental	HRTKK	EIDQEAAVEVSQLRDPQHDLDR	VKKPE	3		855.0848065	2562.23102	0.000451244	2	N	182	204
Q9CR68	Parental	HRTKK	EIDQEAAVEVSQLRDPQHDLDR	VKKPE	4		641.5655549	2562.23102	0.00091018	2	N	182	204
Q9CR68	Parental	SATSR	GVAGALRPLLQGAVPAASEPPVLDVK	RPFLC	3		842.4870351	2524.437705	0.000637154	4	N	20	46
Q9CR86	Parental	KCFCR	SKGHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTYK	MCSIP	3		1358.992285	4073.953456	0.000451244	1	N	73	111
Q9CR86	Parental	KCFCR	SKGHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTYK	MCSIP	4		1019.496164	4073.953456	0.002981883	1	N	73	111
Q9CR86	Parental	FCRSK	GHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTY	KMCSI	3		1244.584967	3730.731501	0.001162105	2	N	75	110
Q9CR86	Parental	FCRSK	GHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTYK	MCSIP	3		1287.283288	3858.826464	0.000622848	2	N	75	111
Q9CRA5	Exosome	VECLK	ANTNEVLWAVVAAFTK	-	2		867.4652086	1732.914817	0.000451244	3	N	282	298
Q9CRA5	Exosome	VECLK	ANTNEVLWAVVAAFTK	-	3		578.6460724	1732.914817	0.000451244	26	N	282	298
Q9CRA5	Exosome	LKHVK	ETQPPETVQNWIELLSGETWNPLK	LHYQL	2		1405.206311	2808.397022	0.000451244	7	N	141	165
Q9CRA5	Exosome	LKHVK	ETQPPETVQNWIELLSGETWNPLK	LHYQL	3		937.1401408	2808.397022	0.000451244	7	N	141	165
Q9CRA5	Exosome	TKRVR	QLLDLDPEVECLK	ANTNE	2	C11:+57.021	786.4031967	1570.790793	0.001329271	1	N	269	282
Q9CRA5	Parental	VECLK	ANTNEVLWAVVAAFTK	-	3		578.6460724	1732.914817	0.000451244	20	N	282	298
Q9CRA5	Parental	TKRVR	QLLDLDPEVECLKANTNEVLWAVVAAFTK	-	3	C11:+57.021	1096.239483	3285.69505	0.000823681	1	N	269	298
Q9CRA5	Parental	LKHVK	ETQPPETVQNWIELLSGETWNPLK	LHYQL	2		1405.206311	2808.397022	0.00091018	1	N	141	165
Q9CRA5	Parental	LKHVK	ETQPPETVQNWIELLSGETWNPLK	LHYQL	3		937.1401408	2808.397022	0.000823681	2	N	141	165
Q9CRA8	Exosome	EKEAR	AILTFALDSAEQK	LLMST	2		703.880446	1405.745292	0.002453667	1	N	178	191
Q9CRA8	Exosome	MSTTK	GLYSDAELQQCLAAAQAASQHIFR	FYRES	3	C11:+57.021	883.4347395	2647.280818	0.000622848	3	N	198	222
Q9CRA8	Exosome	GVPMR	ALFCGVTCALDSDGNLVLDPTTK	QEKEA	2	C4:+57.021,C8:+57.021	1234.095867	2466.176133	0.000622848	2	N	149	172
Q9CRB2	Parental	MTKVK	AAPEESEAQAEGCSEERTY	KELLV	2	C13:+57.021	1057.43467	2112.853741	0.000451244	11	N	5	24
Q9CRB2	Parental	PIEVY	CHLPVLCEDQNLPYVYIPSK	TDLGA	3	C1:+57.021,C7:+57.021	815.7364366	2444.18591	0.000851441	5	N	91	111
Q9CRC8	Exosome	LSSNR	LATVPADFALLSSLLR	LNLSS	2		843.9936019	1685.971604	0.000622848	1	N	185	201
Q9CRC8	Exosome	LSSNR	LATVPADFALLSSLLR	LNLSS	3		562.9983346	1685.971604	0.000698008	2	N	185	201
Q9CRC8	Exosome	EVLYR	ISTLEAVLISNNQVGSVDPQK	MKLME	2		1106.595137	2211.174674	0.002374549	2	N	516	537
Q9CSU0	Exosome	PEFTR	EFESVLVDAFSHVAR	EADEG	3		569.2901771	1704.847131	0.000622848	5	N	79	94
Q9CSU0	Exosome	RKELK	SHIQSLPDLSLLPNVTGGLAPLPSAGDLFSTD	-	3		1078.229907	3231.666321	0.000451244	5	N	294	326
Q9CSU0	Parental	EELIK	ALQDLENAASGDATVR	QKIAS	2		815.9057121	1629.795824	0.000451244	21	N	182	198
Q9CSU0	Parental	PEFTR	EFESVLVDAFSHVAR	EADEG	3		569.2901771	1704.847131	0.000451244	13	N	79	94
Q9CSU0	Parental	RKELK	SHIQSLPDLSLLPNVTGGLAPLPSAGDLFSTD	-	3		1078.229907	3231.666321	0.000451244	32	N	294	326
Q9CSU0	Parental	ERLSK	TVDEACLLLAEYNGR	LAAEL	2	C6:+57.021	862.4199094	1722.824219	0.000451244	2	N	228	243
Q9CU62	Exosome	CVISK	VLTFDLTKYPDANPNPNEQ	-	2		1088.532005	2175.04841	0.000662267	19	N	1214	1233
Q9CU62	Exosome	KALSR	NSSAQAFLGPENPEEPYLDGINYNCVAPGKR	FRPMD	3	C25:+57.021	1136.537251	3406.588354	0.000451244	11	N	1090	1121
Q9CU62	Exosome	EFYTK	AESLIGVYPEQGDCVISK	VLTFD	2	C14:+57.021	982.9856136	1963.955627	0.000451244	9	N	1196	1214
Q9CU62	Exosome	ERFDR	FNACFESVATNIDEIYK	ALSRN	2	C4:+57.021	1010.969964	2019.924327	0.000451244	2	N	1069	1086
Q9CU62	Parental	CVISK	VLTFDLTKYPDANPNPNEQ	-	2		1088.532005	2175.04841	0.000451244	40	N	1214	1233
Q9CU62	Parental	KALSR	NSSAQAFLGPENPEEPYLDGINYNCVAPGKR	FRPMD	3	C25:+57.021	1136.537251	3406.588354	0.000451244	6	N	1090	1121
Q9CU62	Parental	EFYTK	AESLIGVYPEQGDCVISK	VLTFD	2	C14:+57.021	982.9856136	1963.955627	0.000451244	11	N	1196	1214
Q9CU62	Parental	PHIKK	ALQYACGNALVCDNVEDARR	IAFGG	3	C6:+57.021,C12:+57.021	765.6918899	2294.05227	0.000698008	2	N	607	627
Q9CU62	Parental	ERFDR	FNACFESVATNIDEIYK	ALSRN	2	C4:+57.021	1010.969964	2019.924327	0.000451244	6	N	1069	1086
Q9CVB6	Exosome	SVFEK	YFQFQEEGKEGENR	AVIHY	2		880.897887	1759.780174	0.000451244	55	N	127	141
Q9CVB6	Exosome	SVFEK	YFQFQEEGKEGENR	AVIHY	3		587.6011914	1759.780174	0.000451244	42	N	127	141
Q9CVB6	Exosome	NATAR	DNTINLIHTF	RDYLH	2		594.3069168	1186.598234	0.000451244	8	N	237	247
Q9CVB6	Exosome	DELLK	RVYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1085.563109	3253.665927	0.000451244	40	N	77	106
Q9CVB6	Exosome	LFSHR	EPPLELKDTDAAVGDNIGYITFVLFPR	HTNAT	3		997.5223623	2989.543687	0.000451244	60	N	203	230
Q9CVB6	Exosome	LFSHR	EPPLELKDTDAAVGDNIGYITFVLFPR	HTNAT	4		748.3937217	2989.543687	0.000451244	14	N	203	230
Q9CVB6	Exosome	ELLKR	VYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1033.529405	3097.564816	0.000451244	62	N	78	106
Q9CVB6	Exosome	ELLKR	VYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	4		775.3990041	3097.564816	0.000622848	3	N	78	106
Q9CVB6	Exosome	PLELK	DTDAAVGDNIGYITFVLFPR	HTNAT	2		1092.552741	2183.089881	0.000451244	92	N	210	230
Q9CVB6	Exosome	PLELK	DTDAAVGDNIGYITFVLFPR	HTNAT	3		728.7044271	2183.089881	0.000451244	86	N	210	230
Q9CVB6	Exosome	VTVVF	STVFKDDDDVVIGK	VFMQE	2		769.3913749	1536.76715	0.000622848	3	N	165	179
Q9CVB6	Exosome	KEGRR	ASHTAPQVLFSHR	EPPLE	3		484.2570306	1449.747692	0.000698008	4	N	190	203
Q9CVB6	Exosome	LKFYK	ELQAHGADELLKR	VYGSF	2		740.3998686	1478.784137	0.000698008	3	N	65	78
Q9CVB6	Exosome	LKFYK	ELQAHGADELLKR	VYGSF	3		493.9358457	1478.784137	0.000451244	36	N	65	78
Q9CVB6	Exosome	NATAR	DNTINLIHTFR	DYLHY	2		672.3574724	1342.699345	0.000451244	7	N	237	248
Q9CVB6	Exosome	NATAR	DNTINLIHTFR	DYLHY	3		448.5742482	1342.699345	0.000451244	27	N	237	248

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CVB6	Exosome	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTK	VMVSI	3		1289.294298	3864.859495	0.000451244	17	N	18	54
Q9CVB6	Exosome	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTK	VMVSI	4		967.2226739	3864.859495	0.000451244	30	N	18	54
Q9CVB6	Exosome	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK	TKVMV	3		1212.913418	3635.716854	0.000451244	25	N	18	52
Q9CVB6	Exosome	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK	TKVMV	4		909.9370134	3635.716854	0.000451244	50	N	18	52
Q9CVB6	Exosome	SKKDR	VTVVFSTVFKDDDDVVIGK	VFMQE	2		1042.052042	2082.088484	0.000451244	2	N	160	179
Q9CVB6	Exosome	SKKDR	VTVVFSTVFKDDDDVVIGK	VFMQE	3		695.0372948	2082.088484	0.000451244	507	N	160	179
Q9CVB6	Exosome	ELLKR	VYGSFLVNPEPGYNVSLL	YDLEN	2		984.5098131	1967.004026	0.000870037	1	N	78	96
Q9CVB6	Exosome	GMLKR	NCFASVFEK	YFQFQ	2	C2:+57.021	551.2556069	1100.495614	0.000622848	7	N	118	127
Q9CVB6	Exosome	PPLEL	KDTDAAVGDNIGYITFVLFPR	HTNAT	3		771.4027481	2311.184844	0.001329271	5	N	209	230
Q9CVB6	Exosome	KEGRR	ASHTAPQVLFSHREPPLELK	DTDAA	3		753.0749658	2256.201498	0.000451244	7	N	190	210
Q9CVB6	Exosome	NATAR	DNTINLIHTFRDYLHYHIK	CSKAY	4		604.0662651	2412.23386	0.002663018	2	N	237	256
Q9CVB6	Exosome	RVYGS	FLVNPEPGYNVSLLYDLENLPASK	DSIVH	2		1346.697591	2691.379581	0.001329271	2	N	82	106
Q9CVB6	Exosome	SISLK	FYKELQAHGADELLK	RVYGS	3		587.9777106	1760.909732	0.000622848	4	N	62	77
Q9CVB6	Exosome	PLELK	DTDAAVGDNIGYITF	VLFPR	2		786.3653571	1570.715114	0.001329271	4	N	210	225
Q9CVB6	Exosome	LFSHR	EPPLELKDTDAAVGDNIGYITF	VLFPR	2		1189.59226	2377.16892	0.000662267	2	N	203	225
Q9CVB6	Parental	SVFEK	YFQFQEEGKEGENR	AVIHY	2		880.897887	1759.780174	0.000451244	52	N	127	141
Q9CVB6	Parental	SVFEK	YFQFQEEGKEGENR	AVIHY	3		587.6011914	1759.780174	0.000451244	39	N	127	141
Q9CVB6	Parental	NATAR	DNTINLIHTF	RDYLH	2		594.3069168	1186.598234	0.000451244	22	N	237	247
Q9CVB6	Parental	DELLK	RVYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1085.563109	3253.665927	0.000451244	41	N	77	106
Q9CVB6	Parental	LFSHR	EPPLELKDTDAAVGDNIGYITFVLFPR	HTNAT	3		997.5223623	2989.543687	0.000451244	37	N	203	230
Q9CVB6	Parental	ELLKR	VYGSFLVNPEPGYNVSLLYDLENLPASK	DSIVH	3		1033.529405	3097.564816	0.000451244	30	N	78	106
Q9CVB6	Parental	PLELK	DTDAAVGDNIGYITFVLFPR	HTNAT	2		1092.552741	2183.089881	0.000451244	29	N	210	230
Q9CVB6	Parental	PLELK	DTDAAVGDNIGYITFVLFPR	HTNAT	3		728.7044271	2183.089881	0.000451244	44	N	210	230
Q9CVB6	Parental	VTVVF	STVFKDDDDVVIGK	VFMQE	2		769.3913749	1536.76715	0.000451244	11	N	165	179
Q9CVB6	Parental	LKFYK	ELQAHGADELLKR	VYGSF	2		740.3998686	1478.784137	0.000870037	2	N	65	78
Q9CVB6	Parental	LKFYK	ELQAHGADELLKR	VYGSF	3		493.9358457	1478.784137	0.000823681	1	N	65	78
Q9CVB6	Parental	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTK	VMVSI	3		1289.294298	3864.859495	0.000451244	4	N	18	54
Q9CVB6	Parental	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTK	VMVSI	4		967.2226739	3864.859495	0.000451244	6	N	18	54
Q9CVB6	Parental	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK	TKVMV	3		1212.913418	3635.716854	0.000451244	9	N	18	52
Q9CVB6	Parental	TLALK	FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK	TKVMV	4		909.9370134	3635.716854	0.000451244	28	N	18	52
Q9CVB6	Parental	ELLKR	VYGSFLVNPEPGYNVSLL	YDLEN	2		984.5098131	1967.004026	0.002145581	4	N	78	96
Q9CVB6	Parental	GMLKR	NCFASVFEK	YFQFQ	2	C2:+57.021	551.2556069	1100.495614	0.002453667	2	N	118	127
Q9CVB6	Parental	PGYNV	SLLYDLENLPASK	DSIVH	2		731.8935534	1461.771507	0.000735798	3	N	93	106
Q9CVB6	Parental	TLALK	FENAAAGNKPEAVEVTFADFDGVLY	HISNP	2		1337.63773	2673.25986	0.000451244	7	N	18	43
Q9CW03	Parental	FAIQK	CDPAPFYLFDEIDQALDAQHR	KAVSD	3	C1:+57.021	841.053636	2520.137508	0.000451244	5	N	1133	1154
Q9CW03	Parental	YIEER	LHTLEEEKEELAQYQK	WDKMR	2		994.5027164	1986.989833	0.001463592	2	N	199	215
Q9CW03	Parental	GESER	GSGSQSSVPSVDQFTGVGIR	VSFTG	2		982.9877648	1963.95993	0.001162105	3	N	1079	1099
Q9CWF2	Exosome	-M	REIVHIQAGQCGNQIGAK	FWEVI	3	C11:+57.021	660.3465369	1978.016211	0.000637154	2	Y	1	19
Q9CWF2	Exosome	-	MREIVHIQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000622848	4	Y	0	19
Q9CWF2	Exosome	-	MREIVHIQAGQCGNQIGAK	FWEVI	3	M1:+15.995,C12:+57.021	709.3583655	2125.051697	0.001229886	2	Y	0	19
Q9CWF2	Exosome	-MR	EIVHIQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	7	Y	2	19
Q9CWF2	Exosome	-MR	EIVHIQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	6	Y	2	19
Q9CWF2	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000662267	3	Y	81	103
Q9CWF2	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	9	Y	81	103
Q9CWF2	Exosome	QIGAK	FWEVISDEHGIDPTGSYHGDSDLQLER	INVYY	3		1034.80789	3101.40027	0.000451244	12	N	19	46
Q9CWF2	Exosome	QIGAK	FWEVISDEHGIDPTGSYHGDSDLQLER	INVYY	4		776.3578675	3101.40027	0.000451244	5	N	19	46
Q9CWF2	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	ESESC	2		1044.04254	2086.06948	0.000451244	4	Y	103	122
Q9CWF2	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	ESESC	3		696.3642934	2086.06948	0.000451244	41	Y	103	122
Q9CWF2	Exosome	NNWAK	GHYTEGAELVDSVLDVVRK	ESESC	4		522.5251701	2086.06948	0.000451244	6	Y	103	122
Q9CWF2	Exosome	NVQNK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	24	Y	336	350
Q9CWF2	Exosome	NVQNK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	1	Y	336	350
Q9CWF2	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KESES	2		979.9950585	1957.974517	0.000451244	26	Y	103	121
Q9CWF2	Exosome	NNWAK	GHYTEGAELVDSVLDVVR	KESES	3		653.6659724	1957.974517	0.000451244	38	Y	103	121
Q9CWF2	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	17	Y	77	103
Q9CWF2	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	66	Y	77	103
Q9CWF2	Exosome	PRGLK	MSATFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.000451244	8	Y	362	380
Q9CWF2	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.001162105	2	Y	216	241
Q9CWF2	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	M17:+15.995,C23:+57.021	908.7829573	2723.325472	0.001699387	1	Y	216	241
Q9CWF2	Exosome	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	28	Y	183	213
Q9CWF2	Exosome	PRGLK	MSATFIGNSTAIQELFK	RISEQ	2		929.4749166	1856.934233	0.000622848	2	Y	362	379
Q9CWF2	Exosome	DVVRK	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	E1:-18.011,C5:+57.021,C7:+57.021	1103.8444	3308.5098	0.000451244	2	N	122	154
Q9CWF2	Exosome	DVVRK	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	E1:-18.011,C5:+57.021,C7:+57.021,M25:+15.995	1109.176067	3324.5048	0.000622848	2	N	122	154
Q9CWF2	Parental	-M	REIVHIQAGQCGNQIGAK	FWEVI	3	C11:+57.021	660.3465369	1978.016211	0.002453667	1	Y	1	19

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CWF2	Parental	-	MREIVHIQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000451244	2	Y	0	19
Q9CWF2	Parental	-MR	EIVHIQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	30	Y	2	19
Q9CWF2	Parental	-MR	EIVHIQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	33	Y	2	19
Q9CWF2	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000451244	30	Y	81	103
Q9CWF2	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	20	Y	81	103
Q9CWF2	Parental	QIGAK	FWEVISDEHGIDPTGSYHGDSDLQLER	INVYY	3		1034.80789	3101.40027	0.000451244	44	N	19	46
Q9CWF2	Parental	QIGAK	FWEVISDEHGIDPTGSYHGDSDLQLER	INVYY	4		776.3578675	3101.40027	0.000451244	15	N	19	46
Q9CWF2	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	ESESC	2		1044.04254	2086.06948	0.000451244	30	Y	103	122
Q9CWF2	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	ESESC	3		696.3642934	2086.06948	0.000451244	68	Y	103	122
Q9CWF2	Parental	NNWAK	GHYTEGAELVDSVLDVVRK	ESESC	4		522.5251701	2086.06948	0.000451244	45	Y	103	122
Q9CWF2	Parental	NVQNK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	38	Y	336	350
Q9CWF2	Parental	NVQNK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	19	Y	336	350
Q9CWF2	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KESES	2		979.9950585	1957.974517	0.000451244	36	Y	103	121
Q9CWF2	Parental	NNWAK	GHYTEGAELVDSVLDVVR	KESES	3		653.6659724	1957.974517	0.000451244	49	Y	103	121
Q9CWF2	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	50	Y	77	103
Q9CWF2	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	220	Y	77	103
Q9CWF2	Parental	MPSPK	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	4	C27:+57.021,C37:+57.021	1149.032553	4592.099013	0.001162105	8	Y	174	213
Q9CWF2	Parental	PRGLK	MSATFIGNSTAIQELFKR	ISEQF	3		672.0195814	2013.035344	0.000622848	7	Y	362	380
Q9CWF2	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.000451244	22	Y	216	241
Q9CWF2	Parental	EPYNA	TLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C16:+57.021,C26:+57.021	1140.190598	3417.548394	0.000823681	4	Y	185	213
Q9CWF2	Parental	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	125	Y	183	213
Q9CWF2	Parental	PRGLK	MSATFIGNSTAIQELFK	RISEQ	2		929.4749166	1856.934233	0.000451244	4	Y	362	379
Q9CWF2	Parental	IGAKF	WEVISDEHGIDPTGSYHGDSDLQLER	INVYY	3		985.7850854	2954.331856	0.000451244	7	N	20	46
Q9CWF2	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	KLAVN	4	C23:+57.021	955.7347788	3818.907915	0.001654178	2	Y	216	251
Q9CWF2	Parental	TTCLR	FPGQLNADLRK	LAVNM	3		420.2354554	1257.682966	0.001162105	3	Y	241	252
Q9CWF2	Parental	TTCLR	FPGQLNADLR	KLAVN	2		565.8018016	1129.588003	0.000451244	5	Y	241	251
Q9CWF2	Parental	DVVRK	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	E1:-18.011,C5:+57.021,C7:+57.021	1103.8444	3308.5098	0.000698008	1	N	122	154
Q9CWF2	Parental	DVVRK	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	E1:-18.011,C5:+57.021,C7:+57.021,M25:+15.995	1109.176067	3324.5048	0.000451244	1	N	122	154
Q9CWF2	Parental	DVVRK	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEY	3	[0:-18.011,C5:+57.021,C7:+57.021	1103.8444	3308.5098	0.001162105	1	N	122	154
Q9CWF2	Parental	GNNWA	KGHYTEGAELVDSVLDVVR	KESES	2		1044.04254	2086.06948	0.000451244	3	Y	102	121
Q9CWF2	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAKG	HYTEG	3		952.4603192	2854.357558	0.000823681	4	Y	77	104
Q9CWF2	Parental	KYVPR	AILVDLEPGTMDSVR	SGPFG	2		808.4221527	1614.828705	0.000662267	1	Y	62	77
Q9CWJ9	Exosome	DRAKR	SGVAYIVAPSGSTADKVVIEACDELGIVLAHTDLR	LFHH-	3	C22:+57.021	1209.629699	3625.865698	0.000451244	5	N	553	588
Q9CWJ9	Exosome	DRAKR	SGVAYIVAPSGSTADKVVIEACDELGIVLAHTDLR	LFHH-	4	C22:+57.021	907.4742245	3625.865698	0.000979378	4	N	553	588
Q9CWJ9	Exosome	TLKPK	LPITVLNGAPGFINLCDALNAWQLVTELR	GAVDI	3	C16:+57.021	1070.244792	3207.710975	0.000451244	22	N	225	254
Q9CWJ9	Exosome	KIISR	EVSDGIVAPGYEEEALK	ILSKK	2		903.4443358	1804.873072	0.000451244	22	N	335	352
Q9CWJ9	Exosome	EWVDK	LSGVSVSSDAFFPFR	DNVDR	2		808.409902	1614.804204	0.000451244	7	N	530	545
Q9CWJ9	Exosome	EDLVK	WEALFEEVPELLTEAEKK	EWVDK	3		721.0408163	2160.099049	0.000451244	24	N	507	525
Q9CWJ9	Exosome	KAGVK	RAEISNAIDQYVTGTIGEGEDLVK	WEALF	3		860.1052077	2577.292223	0.000451244	4	N	483	507
Q9CWJ9	Exosome	YPFVK	TVASPDVTVEAAVEQIDIGGVTLLR	AAAKN	2		1277.192673	2552.369745	0.000637154	1	N	108	133
Q9CWJ9	Exosome	YPFVK	TVASPDVTVEAAVEQIDIGGVTLLR	AAAKN	3		851.797715	2552.369745	0.000451244	14	N	108	133
Q9CWJ9	Exosome	AASFK	HVSPAGAAVGVPLSEDEAR	VCMVY	2		931.4742933	1860.932987	0.001264573	1	N	266	285
Q9CWJ9	Exosome	AASFK	HVSPAGAAVGVPLSEDEAR	VCMVY	3		621.3187955	1860.932987	0.000451244	4	N	266	285
Q9CWJ9	Exosome	EAEKK	EWVDKLSGVSVSSDAFFPFR	DNVDR	3		758.3799435	2272.11643	0.000662267	3	N	525	545
Q9CWJ9	Exosome	AGVKR	AEISNAIDQYVTGTIGEGEDLVK	WEALF	2		1211.603356	2421.191112	0.000451244	4	N	484	507
Q9CWJ9	Exosome	EAEKK	EWVDKLSGVSVSSDAFFPF	RDNVD	2		1059.01546	2116.015319	0.000622848	4	N	525	544
Q9CWJ9	Exosome	-M	APSQLALFSVSDKTGLVEFAR	SLASL	3		746.0711099	2235.18993	0.000451244	3	N	1	22
Q9CWJ9	Exosome	VCYAK	DGQVIGIGAGQQSR	IHCTR	2		693.3607434	1384.705887	0.000451244	6	N	437	451
Q9CWJ9	Exosome	FNLVR	VVVCNLYPFVK	TVASP	2	C4:+57.021	669.3682315	1336.720863	0.001162105	1	N	97	108
Q9CWJ9	Parental	DRAKR	SGVAYIVAPSGSTADKVVIEACDELGIVLAHTDLR	LFHH-	4	C22:+57.021	907.4742245	3625.865698	0.000451244	7	N	553	588
Q9CWJ9	Parental	TLKPK	LPITVLNGAPGFINLCDALNAWQLVTELR	GAVDI	3	C16:+57.021	1070.244792	3207.710975	0.000451244	26	N	225	254
Q9CWJ9	Parental	KIISR	EVSDGIVAPGYEEEALK	ILSKK	2		903.4443358	1804.873072	0.000451244	12	N	335	352
Q9CWJ9	Parental	RGADR	MSSFGDFVALSDICDVPTAK	IISRE	2	C14:+57.021	1080.503314	2158.991028	0.001839721	1	N	311	331
Q9CWJ9	Parental	EDLVK	WEALFEEVPELLTEAEKK	EWVDK	3		721.0408163	2160.099049	0.000451244	3	N	507	525
Q9CWJ9	Parental	AASFK	HVSPAGAAVGVPLSEDEAR	VCMVY	2		931.4742933	1860.932987	0.000451244	5	N	266	285
Q9CWJ9	Parental	VEFAR	SLASLGLSLVASGGTAK	AIRDA	3		511.2950396	1530.861719	0.00091018	3	N	22	39
Q9CWJ9	Parental	AGVKR	AEISNAIDQYVTGTIGEGEDLVK	WEALF	2		1211.603356	2421.191112	0.000451244	2	N	484	507
Q9CWK3	Parental	DAQIR	DSWLDNIDWVR	IKERP	2		709.8391124	1417.662625	0.000451244	4	N	115	126
Q9CWK3	Parental	MPKRK	VTFQGVGDEDGEDEISVPK	KKLVD	2		1010.971446	2019.927292	0.001162105	3	N	5	24
Q9CWK8	Parental	DSPER	ELILSSEPSPAVTPVTPTTLIAPR	IESKS	2		1245.197227	2488.378853	0.000451244	3	N	88	112
Q9CWK8	Parental	TALSR	ALSQLAEVEEK	IDQLH	2		608.8251394	1215.634679	0.002663018	1	N	362	373
Q9CWZ3	Exosome	GSRAR	MREDYDSVEQDGDEPGPQR	SVEGW	3	M1:+15.995	746.9788673	2237.913202	0.000451244	4	N	49	68
Q9CWZ3	Parental	GSRAR	MREDYDSVEQDGDEPGPQR	SVEGW	3		741.6472007	2221.918202	0.000451244	6	N	49	68

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CWZ3	Parental	GWILF	VTGVHEEATEEDIHDKFAEYGEIK	NIHLN	3		916.1001223	2745.276967	0.000451244	1	N	76	100
Q9CWZ7	Parental	ERAGK	LIENVDPEKAVQLYQQTANVFENEER	LRQAV	3		1026.179435	3075.514906	0.000451244	2	N	123	149
Q9CWZ7	Parental	VDPEK	AVQLYQQTANVFENEER	LRQAV	2		1019.99559	2037.97558	0.000451244	9	N	132	149
Q9CX34	Exosome	EELTK	ALEQNPDDAQYYCQR	AYCHI	2	C13:+57.021	935.9051548	1869.79471	0.000451244	9	N	36	51
Q9CX34	Exosome	ASSQR	LFQSFSDALIDGDPQAALEELTK	ALEQN	3		836.7555158	2507.243147	0.000451244	4	N	13	36
Q9CX34	Parental	EELTK	ALEQNPDDAQYYCQR	AYCHI	2	C13:+57.021	935.9051548	1869.79471	0.000451244	25	N	36	51
Q9CX34	Parental	ASSQR	LFQSFSDALIDGDPQAALEELTK	ALEQN	2		1254.629374	2507.243147	0.000451244	15	N	13	36
Q9CX34	Parental	ASSQR	LFQSFSDALIDGDPQAALEELTK	ALEQN	3		836.7555158	2507.243147	0.000451244	7	N	13	36
Q9CX34	Parental	ASSQR	LFQSFSDALIDGDPQAALEELTKALEQNPDDAQYYCQR	AYCHI	3	C36:+57.021	1454.016899	4359.027297	0.000451244	12	N	13	51
Q9CX56	Exosome	YAKKR	GWVLGPNNYYSFASQQQKPEDSTIPSTELAK	QVIEY	3		1152.563837	3454.668112	0.000451244	7	N	309	340
Q9CX56	Parental	YAKKR	GWVLGPNNYYSFASQQQKPEDSTIPSTELAK	QVIEY	3		1152.563837	3454.668112	0.000451244	24	N	309	340
Q9CX56	Parental	SYTFF	IDILLDTIRDEIAGCIEK	AYEKI	3	C15:+57.021	696.3736468	2086.097541	0.000451244	9	N	262	280
Q9CX56	Parental	VFLAK	GNIPAESYTFFIDILLDTIRDEIAGCIEK	AYEKI	3	C26:+57.021	1105.227244	3312.658331	0.000622848	1	N	251	280
Q9CX86	Exosome	SQLCK	LFIGGLNVQTSESGLR	GHFEA	2		845.9602904	1689.904981	0.000451244	1	N	8	24
Q9CX86	Exosome	VGGLK	GDVAEGDLIEHFSQFGAVEK	AEIIA	3		716.6801701	2147.01711	0.001463592	2	N	106	126
Q9CX86	Parental	AKVKK	LFVGGLKGDVAEGDLIEHFSQFGAVEK	AEIIA	3		954.8277857	2861.459957	0.000451244	7	N	99	126
Q9CX86	Parental	AKVKK	LFVGGLKGDVAEGDLIEHFSQFGAVEK	AEIIA	4		716.3727893	2861.459957	0.000451244	8	N	99	126
Q9CX86	Parental	SQLCK	LFIGGLNVQTSESGLR	GHFEA	2		845.9602904	1689.904981	0.000451244	18	N	8	24
Q9CX86	Parental	VGGLK	GDVAEGDLIEHFSQFGAVEK	AEIIA	2		1074.516355	2147.01711	0.000451244	13	N	106	126
Q9CX86	Parental	VGGLK	GDVAEGDLIEHFSQFGAVEK	AEIIA	3		716.6801701	2147.01711	0.000451244	23	N	106	126
Q9CXF4	Exosome	IPGLK	INQQEEPGFEVITR	IDLGE	2		830.420998	1658.826396	0.001162105	5	N	271	285
Q9CXF4	Exosome	SSCGK	ANDQDSLISGILR	VLEKD	2		701.3707768	1400.725954	0.000451244	1	N	26	39
Q9CXF4	Parental	NCQNK	SLSQSFENLLDEPAYGLIQK	IKKDP	2		1126.576413	2251.137226	0.000622848	9	N	200	220
Q9CXF4	Parental	IPGLK	INQQEEPGFEVITR	IDLGE	2		830.420998	1658.826396	0.002663018	2	N	271	285
Q9CXI5	Exosome	GKENR	LCYYIGATDDAATK	IINEV	2	C2:+57.021	781.3640715	1560.712543	0.000622848	8	N	70	84
Q9CXI5	Exosome	YQDLK	DRDVTFSPATIEEELIK	FCREA	3		655.0059946	1961.994584	0.000451244	19	N	42	59
Q9CXI5	Exosome	DAATK	IINEVSKPLAHHIPVEK	ICEKL	4		481.7813447	1923.094179	0.000451244	6	N	84	101
Q9CXI5	Exosome	DLKDR	DVTFSPATIEEELIK	FCREA	2		846.4410648	1690.86653	0.000451244	5	N	44	59
Q9CXI5	Parental	GKENR	LCYYIGATDDAATK	IINEV	2	C2:+57.021	781.3640715	1560.712543	0.000451244	19	N	70	84
Q9CXI5	Parental	YQDLK	DRDVTFSPATIEEELIK	FCREA	3		655.0059946	1961.994584	0.000451244	8	N	42	59
Q9CXI5	Parental	DAATK	IINEVSKPLAHHIPVEK	ICEKL	3		642.0391929	1923.094179	0.000622848	4	N	84	101
Q9CXI5	Parental	PDSRA	LRPGDCEVCISYLGR	FYQDL	2	C6:+57.021,C9:+57.021	897.9349724	1793.854345	0.000451244	4	N	21	36
Q9CXI5	Parental	DLKDR	DVTFSPATIEEELIK	FCREA	2		846.4410648	1690.86653	0.000451244	11	N	44	59
Q9CXR1	Parental	KHALR	GFFNALHSELGQYPGITFCNVYPGPVQSDIVK	NAFTE	3	C19:+57.021	1185.585654	3553.733561	0.000622848	4	N	211	243
Q9CXR1	Parental	IQNFK	NNLDPDLPYK	FLKAK	2		594.7989246	1187.582249	0.001329271	1	N	321	331
Q9CXT8	Exosome	RDLPR	AVEILADIIQNSTLGEAEIERER	GVILR	3		857.1209692	2568.339508	0.000622848	2	N	152	175
Q9CXT8	Exosome	GDRLR	STQAAPQVVLNVPETQVTCLENGLR	VASEN	3	C19:+57.021	908.804721	2723.390763	0.001463592	2	N	43	68
Q9CXT8	Parental	RDLPR	AVEILADIIQNSTLGEAEIERER	GVILR	3		857.1209692	2568.339508	0.002727428	2	N	152	175
Q9CXW4	Exosome	TRAAK	VLEQLTGQTPVFSK	ARYTV	2		773.9279275	1545.840255	0.000451244	10	N	38	52
Q9CXW4	Parental	TRAAK	VLEQLTGQTPVFSK	ARYTV	2		773.9279275	1545.840255	0.000622848	27	N	38	52
Q9CXW4	Parental	ELRIR	KLCLNICVGESGDR	LTRAA	2	C3:+57.021,C7:+57.021	810.8953159	1619.775032	0.001591523	1	N	18	32
Q9CXW4	Parental	RAAKV	LEQLTGQTPVFSK	ARYTV	2		724.3937205	1446.771841	0.000622848	3	N	39	52
Q9CXY6	Exosome	GGFRK	ILGQEGDASYLASEISTWDGVIVTPSEK	AYEKP	3		989.1612703	2964.460411	0.0025889	1	N	328	356
Q9CXY6	Exosome	SLVTK	INNVIDNLIVAPGTFEVQIEEVR	QVGSY	2		1291.695382	2581.375165	0.000451244	4	N	80	103
Q9CXY6	Exosome	SLVTK	INNVIDNLIVAPGTFEVQIEEVR	QVGSY	3		861.4661882	2581.375165	0.000622848	6	N	80	103
Q9CXY6	Exosome	ALLKR	NQDLAPNSAEQASILSLVTK	INNVI	2		1050.053105	2098.09061	0.000451244	23	N	60	80
Q9CXY6	Exosome	VVILK	ILPTLEAVAALGNK	VVESL	2		705.422281	1408.828962	0.000451244	13	N	127	141
Q9CXY6	Exosome	VAYRR	CLQILAAGLFLPGSVGITDPCESGNFR	VHTVM	3	C1:+57.021,C21:+57.021	964.8178189	2891.430057	0.000823681	2	N	270	297
Q9CXY6	Parental	GGFRK	ILGQEGDASYLASEISTWDGVIVTPSEK	AYEKP	3		989.1612703	2964.460411	0.000451244	2	N	328	356
Q9CXY6	Parental	SLVTK	INNVIDNLIVAPGTFEVQIEEVR	QVGSY	2		1291.695382	2581.375165	0.000451244	3	N	80	103
Q9CXY6	Parental	SLVTK	INNVIDNLIVAPGTFEVQIEEVR	QVGSY	3		861.4661882	2581.375165	0.000622848	9	N	80	103
Q9CXY6	Parental	ALLKR	NQDLAPNSAEQASILSLVTK	INNVI	2		1050.053105	2098.09061	0.000451244	16	N	60	80
Q9CY50	Exosome	GFTNK	GTEDFIVESLDASFR	YPQDY	2		843.4050136	1684.794427	0.000451244	7	N	110	125
Q9CY50	Exosome	GFTNK	GTEDFIVESLDASFR	YPQDY	3		562.6059424	1684.794427	0.000451244	4	N	110	125
Q9CY50	Exosome	DEDDE	AEVEEDEPTDLAEDKEEEDVSSEPEASPSADTTILFVK	GEDFP	3		1384.296093	4149.864879	0.000735798	5	N	53	91
Q9CY50	Parental	GFTNK	GTEDFIVESLDASFR	YPQDY	2		843.4050136	1684.794427	0.000451244	20	N	110	125
Q9CY50	Parental	GFTNK	GTEDFIVESLDASFR	YPQDY	3		562.6059424	1684.794427	0.000451244	11	N	110	125
Q9CY50	Parental	DEDDE	AEVEEDEPTDLAEDKEEEDVSSEPEASPSADTTILFVK	GEDFP	3		1384.296093	4149.864879	0.000451244	31	N	53	91
Q9CY50	Parental	ILFVK	GEDFPANNIVK	FLVGF	2		602.3043741	1202.593148	0.001162105	1	N	91	102
Q9CY58	Exosome	VTNRF	DQLFDDESDPFEVLK	AAENK	2		898.9154111	1795.815222	0.001463592	1	N	17	32
Q9CY58	Exosome	VVTNR	FDQLFDDESDPFEVLK	AAENK	2		972.4496182	1942.883636	0.000451244	10	N	16	32
Q9CY58	Parental	VTNRF	DQLFDDESDPFEVLK	AAENK	2		898.9154111	1795.815222	0.000451244	4	N	17	32
Q9CY58	Parental	-M	PGHLQEGFGCVVTNRFDQLFDDESDPFEVLK	AAENK	3	C10:+57.021	1199.231828	3594.672083	0.000451244	6	N	1	32
Q9CY58	Parental	NRGSR	TDKSSASAPDVDDPEAFPALA	-	2		1052.490003	2102.964406	0.001329271	3	N	386	407
Q9CY58	Parental	FDQLF	DDESDPFEVLK	AAENK	2		647.2964117	1292.577223	0.001352548	4	N	21	32

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CY64	Exosome	KGSLR	FTASPLEEEKFGFPAFSGISR	LTWLV	3		773.0553484	2316.142645	0.000451244	6	N	150	171
Q9CY64	Exosome	IFIQK	LLGQVSAEDLAAEK	KRILH	2		722.3886352	1442.76167	0.000451244	4	N	260	274
Q9CY64	Exosome	SIHFK	SGSLEEVPNVGVNK	NIFLK	2		714.8706096	1427.725619	0.000451244	6	N	233	247
Q9CYA0	Parental	AGYTK	ESGQCTDIDECSLEEK	ACKRK	2	C5:+57.021,C11:+57.021	950.3828293	1898.750059	0.000451244	48	N	281	297
Q9CYA0	Parental	VHTLK	ACCLPGTYGPDCQECQGGSERPCSGNGYCSGDGSR	QGDGS	3	C2:+57.021,C3:+57.021,C12:+57.021,C15:+57.021,C23:+57.021,C29:+57.021	1286.156694	3855.446681	0.000451244	44	N	123	158
Q9CYA0	Parental	DESCK	TCSGPSNKDCIQCEVGWAR	VEDAC	2	C2:+57.021,C10:+57.021,C13:+57.021	1112.980082	2223.944565	0.000823681	1	N	202	221
Q9CYA0	Parental	DESCK	TCSGPSNKDCIQCEVGWAR	VEDAC	3	C2:+57.021,C10:+57.021,C13:+57.021	742.3226549	2223.944565	0.000451244	1	N	202	221
Q9CYA0	Parental	QTLKK	EHPNLFEWFCVHTLK	ACCLP	3	C10:+57.021	652.9860575	1955.934772	0.000823681	4	N	108	123
Q9CYA0	Parental	HTGYK	GPLCIDCTDGFFSLQR	NETHS	2	C4:+57.021,C7:+57.021	943.4322626	1884.848925	0.000451244	17	N	171	187
Q9CYA6	Exosome	FCLDK	LGQPLLNENPQLTEGWEIPK	YQQVF	2		1138.600222	2275.184844	0.000851441	1	N	185	205
Q9CYA6	Parental	FCLDK	LGQPLLNENPQLTEGWEIPK	YQQVF	2		1138.600222	2275.184844	0.000451244	15	N	185	205
Q9CYA6	Parental	NAISK	QYHQEIEEFVSNLVK	RFEEQ	3		621.6481416	1861.921025	0.000451244	1	N	109	124
Q9CYA6	Parental	PGWLK	EAELENSGLALYDGNDDADGETETGEIQNK	NVTYD	3		1066.467927	3196.380382	0.001162105	1	N	327	357
Q9CYG7	Exosome	YVDYK	TVLQIDNSVASALEGINR	ITRAL	2		950.5108758	1899.006152	0.001162105	1	N	109	127
Q9CYG7	Parental	LKDYK	SSLSDISSLLQIEPR	NGPAQ	2		822.944306	1643.873012	0.000451244	6	N	278	293
Q9CYG7	Parental	LKDYK	SSLSDISSLLQIEPR	NGPAQ	3		548.9654706	1643.873012	0.000451244	7	N	278	293
Q9CYG7	Parental	YVDYK	TVLQIDNSVASALEGINR	ITRAL	2		950.5108758	1899.006152	0.000735798	1	N	109	127
Q9CYG7	Parental	YVDYK	TVLQIDNSVASALEGINR	ITRAL	3		634.0098505	1899.006152	0.000637154	4	N	109	127
Q9CYL5	Exosome	FVVAR	YFPAGNIVNQGFFEENVPPPKK	-	3		831.4256643	2491.253593	0.000451244	17	N	132	154
Q9CYL5	Exosome	PESSR	GQCGENLAWASYDQTGKDVADR	WYSEI	3	C3:+57.021	814.3647617	2440.070885	0.000451244	8	N	60	82
Q9CYL5	Exosome	PESSR	GQCGENLAWASYDQTGK	DVADR	2	C3:+57.021	942.9129799	1883.81036	0.000451244	2	N	60	77
Q9CYL5	Exosome	IGVGK	ASASDGSSFVVAR	YFPAG	2		627.3101878	1252.604776	0.000451244	3	N	119	132
Q9CYL5	Exosome	KKLNR	EAQQYSEALASTR	ILKHS	2		727.3500413	1452.684483	0.000451244	2	N	37	50
Q9CYL5	Parental	FVVAR	YFPAGNIVNQGFFEENVPPPKK	-	2		1246.634596	2491.253593	0.000451244	5	N	132	154
Q9CYL5	Parental	FVVAR	YFPAGNIVNQGFFEENVPPPKK	-	3		831.4256643	2491.253593	0.000451244	14	N	132	154
Q9CYL5	Parental	PESSR	GQCGENLAWASYDQTGKDVADR	WYSEI	3	C3:+57.021	814.3647617	2440.070885	0.000451244	5	N	60	82
Q9CYL5	Parental	PESSR	GQCGENLAWASYDQTGK	DVADR	2	C3:+57.021	942.9129799	1883.81036	0.000451244	20	N	60	77
Q9CYL5	Parental	YSEIK	SYNFQQPGFTSGTGHFTA	MVWKN	2		973.9375436	1945.859487	0.002145581	1	N	88	106
Q9CZ04	Exosome	LRNVR	QLEDLVIEAVYADVLR	GSLDQ	2		923.5019881	1844.988376	0.000451244	3	N	126	142
Q9CZ04	Exosome	LRNVR	QLEDLVIEAVYADVLR	GSLDQ	3		616.0039254	1844.988376	0.000451244	17	N	126	142
Q9CZ04	Exosome	LRNVR	QLEDLVIEAVYADVLR	GSLDQ	2	[0:-17.027	914.9884881	1827.961376	0.002145581	1	N	126	142
Q9CZ04	Exosome	RDIQR	QDLSAIAQTLQEWCVGCEVVLSGIEEQVSR	ANQHK	3	C14:+57.021,C17:+57.021	1135.553759	3403.637878	0.000451244	24	N	164	194
Q9CZ04	Exosome	ASTFR	LLTVFAYGTYADYLAEAR	NLPPL	2		1019.020545	2036.02549	0.001763695	1	N	65	83
Q9CZ04	Exosome	AAKVK	CIPYAVLLEALALR	NVRQL	2	C1:+57.021	801.4581093	1600.900619	0.001654178	1	N	109	123
Q9CZ04	Parental	LRNVR	QLEDLVIEAVYADVLR	GSLDQ	3		616.0039254	1844.988376	0.000451244	2	N	126	142
Q9CZ04	Parental	RDIQR	QDLSAIAQTLQEWCVGCEVVLSGIEEQVSR	ANQHK	3	C14:+57.021,C17:+57.021	1135.553759	3403.637878	0.000451244	17	N	164	194
Q9CZ13	Exosome	KNILR	NALVSHLDGTTPVCEDIGR	SLLTY	2	C14:+57.021	1027.502493	2052.989387	0.000998612	1	N	396	415
Q9CZ13	Exosome	FKGTK	NRPGNALEKEVESIGAHLNAYSTR	EHTAY	4		657.3392808	2625.325923	0.000622848	1	N	102	126
Q9CZ13	Exosome	DICSK	YFYDQCPAVAGYGPIEQLPDYNR	IRSGM	2	C6:+57.021	1368.623868	2735.232137	0.000451244	2	N	447	470
Q9CZ13	Exosome	KDLPK	VVELLADIVQNSSLEDSQIEKER	DVILR	3		872.1243793	2613.349738	0.000451244	13	N	142	165
Q9CZ13	Exosome	SSVSR	VYEEDAVPGLTPCR	FTGSE	2	C13:+57.021	803.3827956	1604.749991	0.002519933	1	N	255	269
Q9CZ13	Parental	KNILR	NALVSHLDGTTPVCEDIGR	SLLTY	2	C14:+57.021	1027.502493	2052.989387	0.000451244	28	N	396	415
Q9CZ13	Parental	KNILR	NALVSHLDGTTPVCEDIGR	SLLTY	3	C14:+57.021	685.3375957	2052.989387	0.000451244	9	N	396	415
Q9CZ13	Parental	FKGTK	NRPGNALEKEVESIGAHLNAYSTR	EHTAY	3		876.116441	2625.325923	0.002727428	2	N	102	126
Q9CZ13	Parental	FKGTK	NRPGNALEKEVESIGAHLNAYSTR	EHTAY	4		657.3392808	2625.325923	0.000823681	4	N	102	126
Q9CZ13	Parental	DICSK	YFYDQCPAVAGYGPIEQLPDYNR	IRSGM	2	C6:+57.021	1368.623868	2735.232137	0.000451244	41	N	447	470
Q9CZ13	Parental	DICSK	YFYDQCPAVAGYGPIEQLPDYNR	IRSGM	3	C6:+57.021	912.7518456	2735.232137	0.000451244	20	N	447	470
Q9CZ13	Parental	KDLPK	VVELLADIVQNSSLEDSQIEKER	DVILR	2		1307.682669	2613.349738	0.002145581	2	N	142	165
Q9CZ13	Parental	KDLPK	VVELLADIVQNSSLEDSQIEKER	DVILR	3		872.1243793	2613.349738	0.000451244	28	N	142	165
Q9CZ13	Parental	PALRG	TATFAQALQSVPETQVSILDNGLR	VASEQ	2		1280.174814	2558.334028	0.000451244	28	N	34	58
Q9CZ13	Parental	PALRG	TATFAQALQSVPETQVSILDNGLR	VASEQ	3		853.7858094	2558.334028	0.000451244	18	N	34	58
Q9CZ13	Parental	SSVSR	VYEEDAVPGLTPCR	FTGSE	2	C13:+57.021	803.3827956	1604.749991	0.000637154	2	N	255	269
Q9CZ13	Parental	DICSK	YFYDQCPAVAGYGPIEQLPDYNRIR	SGMFW	3	C6:+57.021	1002.480237	3004.417312	0.001162105	1	N	447	472
Q9CZ13	Parental	NALEK	EVESIGAHLNAYSTR	EHTAY	2		823.9107974	1645.805995	0.000451244	1	N	111	126
Q9CZ13	Parental	NALEK	EVESIGAHLNAYSTR	EHTAY	3		549.6097983	1645.805995	0.000622848	3	N	111	126
Q9CZ13	Parental	KDLPK	VVELLADIVQNSSLEDSQIEK	ERDVI	2		1165.110817	2328.206034	0.000451244	18	N	142	163
Q9CZ30	Exosome	KPASK	IPAFLNVVDIAGLVK	GAHNG	2		784.9746808	1567.933762	0.000451244	33	N	83	98
Q9CZ30	Exosome	KPASK	IPAFLNVVDIAGLVK	GAHNG	3		523.6523872	1567.933762	0.000622848	3	N	83	98
Q9CZ30	Exosome	PNVGK	STFFNVLTNSQASAENFPFCTIDPNESR	VPVPD	3	C20:+57.021	1065.156259	3192.445378	0.000451244	33	N	35	63
Q9CZ30	Exosome	PKIIK	AGFAALQLEYFFTAGPDEVR	AWTIR	2		1101.547458	2201.079317	0.000451244	9	N	297	317
Q9CZ30	Exosome	RQQGR	NYIVEDGDIIFFK	FNTPQ	2		786.9013784	1571.787157	0.000451244	5	N	373	386

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CZ30	Exosome	PNVGK	STFFNVLTNSQASAENFPFCTIDPNESRVPVPDER	FDFLC	3	C20:+57.021	1329.293927	3984.858381	0.002663018	1	N	35	70
Q9CZ30	Parental	KPASK	IPAFLNVVDIAGLVK	GAHNG	2		784.9746808	1567.933762	0.000451244	10	N	83	98
Q9CZ30	Parental	KPASK	IPAFLNVVDIAGLVK	GAHNG	3		523.6523872	1567.933762	0.000451244	3	N	83	98
Q9CZ30	Parental	KSTFF	NVLTNSQASAENFPFCTIDPNESR	VPVPD	2	C16:+57.021	1356.122221	2710.228842	0.001162105	1	N	39	63
Q9CZ42	Exosome	GQDGR	IGIVGGCQEYTGAPYFAGISALK	VGADL	2	C7:+57.021	1186.601676	2371.187753	0.000451244	8	N	71	94
Q9CZ42	Exosome	APVIK	SYSPELIVHPVLDSSNAVEEVEK	WLPRL	3		847.7626704	2540.264611	0.001162105	6	N	113	136
Q9CZ42	Exosome	STKAR	DIPVVIDADGLWLVAQQPALIHSYHK	AILTP	4		725.3937904	2897.543962	0.000451244	8	N	170	196
Q9CZ42	Exosome	GSTLK	LSQALGNITVVQKGEQDLISNGQQVLVCNQEGSSR	RCGGQ	3	C28:+57.021	1257.3098	3768.906	0.000451244	4	N	229	264
Q9CZ42	Exosome	KWLPR	LHALVVGPGLGRDDLLLNNVR	GILES	4		561.0766328	2240.275331	0.000451244	1	N	140	161
Q9CZ42	Exosome	TVVQK	GEQDLISNGQQVLVCNQEGSSR	RCGGQ	2	C15:+57.021	1209.569624	2417.123649	0.002145581	1	N	242	264
Q9CZ42	Parental	GQDGR	IGIVGGCQEYTGAPYFAGISALK	VGADL	2	C7:+57.021	1186.601676	2371.187753	0.000451244	1	N	71	94
Q9CZ44	Exosome	GGGYR	LGAAPEEESAYVAGER	RRHSG	2		824.894813	1647.774026	0.000451244	18	N	156	172
Q9CZ44	Exosome	GEGQK	LGSTAPQVLNTSSPAQQAENEAK	ASSSI	2		1171.085665	2340.155729	0.000451244	29	N	259	282
Q9CZ44	Exosome	ENEAK	ASSSILINEAEPTTNIQIR	LADGG	2		1029.047822	2056.080045	0.000451244	30	N	282	301
Q9CZ44	Exosome	NQTLK	EANLLNAVIVQR	LT-	2		670.3887725	1338.761945	0.000979378	7	N	356	368
Q9CZ44	Exosome	NGDLR	SYQDPSNAQFLESIR	RGEVP	2		877.9213622	1753.827124	0.000451244	10	N	199	214
Q9CZ44	Exosome	PPRKK	SPNELVDDLFK	GAKEH	2		638.8251394	1275.634679	0.000451244	10	N	113	124
Q9CZ44	Parental	GGGYR	LGAAPEEESAYVAGER	RRHSG	2		824.894813	1647.774026	0.000451244	23	N	156	172
Q9CZ44	Parental	GEGQK	LGSTAPQVLNTSSPAQQAENEAK	ASSSI	2		1171.085665	2340.155729	0.000451244	44	N	259	282
Q9CZ44	Parental	ENEAK	ASSSILINEAEPTTNIQIR	LADGG	2		1029.047822	2056.080045	0.000451244	28	N	282	301
Q9CZ44	Parental	NGDLR	SYQDPSNAQFLESIR	RGEVP	2		877.9213622	1753.827124	0.000451244	12	N	199	214
Q9CZ44	Parental	RVTSF	RDLIHDQDEEEEEEEGQR	FYAGG	3		752.6602744	2254.957423	0.001162105	1	N	75	93
Q9CZD3	Exosome	ARKMR	LGDAVEQGVINNSVLGYFIGR	IYLYL	2		1111.084739	2220.153879	0.000451244	18	N	381	402
Q9CZD3	Exosome	ARKMR	LGDAVEQGVINNSVLGYFIGR	IYLYL	3		741.0590929	2220.153879	0.000451244	1	N	381	402
Q9CZD3	Exosome	KRFQK	TLHVEEVVPSVIEPSFGLGR	IMYTI	2		1083.084208	2164.152816	0.001162105	3	N	553	573
Q9CZD3	Exosome	KRFQK	TLHVEEVVPSVIEPSFGLGR	IMYTI	3		722.392072	2164.152816	0.000622848	5	N	553	573
Q9CZD3	Exosome	GDEQR	TFFSFPAVVAPFK	CSVLP	2		729.3955349	1456.77547	0.000451244	18	N	592	605
Q9CZD3	Exosome	DAESK	TSYGWIEIVGCADR	SCYDL	2	C11:+57.021	813.8829627	1625.750325	0.000662267	8	N	440	454
Q9CZD3	Parental	ARKMR	LGDAVEQGVINNSVLGYFIGR	IYLYL	2		1111.084739	2220.153879	0.000451244	2	N	381	402
Q9CZD3	Parental	ARKMR	LGDAVEQGVINNSVLGYFIGR	IYLYL	3		741.0590929	2220.153879	0.000451244	9	N	381	402
Q9CZD3	Parental	KRFQK	TLHVEEVVPSVIEPSFGLGR	IMYTI	2		1083.084208	2164.152816	0.00091018	1	N	553	573
Q9CZD3	Parental	GDEQR	TFFSFPAVVAPFK	CSVLP	2		729.3955349	1456.77547	0.000622848	11	N	592	605
Q9CZD3	Parental	DAESK	TSYGWIEIVGCADR	SCYDL	2	C11:+57.021	813.8829627	1625.750325	0.000870037	2	N	440	454
Q9CZE3	Exosome	-M	AGEGLGQQGASATAAPETR	EHLFK	2		886.4326254	1770.849651	0.000451244	9	N	1	20
Q9CZE3	Exosome	DLDSK	VHLPNGSPIPAVLLANK	CDQKK	3		580.6775954	1739.009386	0.002519933	1	N	125	142
Q9CZE3	Parental	-M	AGEGLGQQGASATAAPETR	EHLFK	2		886.4326254	1770.849651	0.000451244	5	N	1	20
Q9CZM2	Exosome	STYKF	FEVILIDPFHK	AIRRN	2		679.3798848	1356.74417	0.00091018	3	N	129	140
Q9CZM2	Exosome	STYKF	FEVILIDPFHK	AIRRN	3		453.2558565	1356.74417	0.000451244	13	N	129	140
Q9CZM2	Exosome	CGALR	VLNSYWVGEDSTYK	FFEVI	2		830.8968244	1659.778049	0.00091018	3	N	114	128
Q9CZM2	Exosome	DSTYK	FFEVILIDPFHK	AIRRN	2		752.9140918	1503.812584	0.002019181	1	N	128	140
Q9CZM2	Exosome	DSTYK	FFEVILIDPFHK	AIRRN	3		502.2786612	1503.812584	0.000451244	3	N	128	140
Q9CZM2	Parental	STYKF	FEVILIDPFHK	AIRRN	3		453.2558565	1356.74417	0.000823681	2	N	129	140
Q9CZN7	Exosome	LCQRR	ALEAFDLDPAQWGVNVQPYSGSPANLAAYTALLQPHDR	IMGLD	3		1366.012014	4095.012642	0.000451244	34	N	122	160
Q9CZN7	Exosome	LCQRR	ALEAFDLDPAQWGVNVQPYSGSPANLAAYTALLQPHDR	IMGLD	4		1024.760961	4095.012642	0.000451244	14	N	122	160
Q9CZN7	Exosome	YPGKR	YYGGAEVVDEIELLCQR	RALEA	2	C15:+57.021	1007.483238	2012.950876	0.000451244	27	N	104	121
Q9CZN7	Exosome	LCQRR	ALEAFDLDPAQWGVNVQPY	SGSPA	2		1067.018534	2132.021467	0.000451244	9	N	122	141
Q9CZN7	Exosome	SMPYK	LNPQTGLIDYDQLALTAR	LFRPR	2		1001.534351	2001.053102	0.000451244	15	N	196	214
Q9CZN7	Exosome	SMPYK	LNPQTGLIDYDQLALTAR	LFRPR	3		668.0255006	2001.053102	0.000451244	1	N	196	214
Q9CZN7	Exosome	NFCSR	AALEALGSCLNNK	YSEGY	2	C9:+57.021	680.8483916	1359.681183	0.000451244	6	N	82	95
Q9CZN7	Exosome	ARAER	VLELVSITANK	NTCPG	2		593.8562425	1185.696885	0.001162105	7	N	398	409
Q9CZN7	Exosome	LLCQR	RALEAFDLDPAQWGVNVQPY	SGSPA	2		1145.069089	2288.122578	0.001654178	6	N	121	141
Q9CZN7	Exosome	DRQCR	GLELIASENFCSR	AALEA	2	C11:+57.021	748.3644058	1494.713212	0.000451244	2	N	69	82
Q9CZN7	Exosome	LCQRR	ALEAFDLDPAQWGVNVQPYSGSPANLAAY	TALLQ	3		1022.161605	3063.461414	0.001162105	1	N	122	151
Q9CZN7	Parental	LCQRR	ALEAFDLDPAQWGVNVQPYSGSPANLAAYTALLQPHDR	IMGLD	3		1366.012014	4095.012642	0.000451244	25	N	122	160
Q9CZN7	Parental	LCQRR	ALEAFDLDPAQWGVNVQPYSGSPANLAAYTALLQPHDR	IMGLD	4		1024.760961	4095.012642	0.000451244	14	N	122	160
Q9CZN7	Parental	LLCQR	RALEAFDLDPAQWGVNVQPYSGSPANLAAYTALLQPHDR	IMGLD	4		1063.786238	4251.113753	0.001229886	2	N	121	160
Q9CZN7	Parental	YPGKR	YYGGAEVVDEIELLCQR	RALEA	2	C15:+57.021	1007.483238	2012.950876	0.000451244	23	N	104	121
Q9CZN7	Parental	LCQRR	ALEAFDLDPAQWGVNVQPY	SGSPA	2		1067.018534	2132.021467	0.000451244	12	N	122	141
Q9CZN7	Parental	SMPYK	LNPQTGLIDYDQLALTAR	LFRPR	2		1001.534351	2001.053102	0.000451244	10	N	196	214
Q9CZN7	Parental	NFCSR	AALEALGSCLNNK	YSEGY	2	C9:+57.021	680.8483916	1359.681183	0.000451244	1	N	82	95
Q9CZN7	Parental	ARAER	VLELVSITANKNTCPGDR	SAITP	2	C14:+57.021	994.0177794	1986.019959	0.000451244	1	N	398	416
Q9CZN7	Parental	ARAER	VLELVSITANK	NTCPG	2		593.8562425	1185.696885	0.000451244	3	N	398	409
Q9CZN7	Parental	LLCQR	RALEAFDLDPAQWGVNVQPY	SGSPA	2		1145.069089	2288.122578	0.002296037	1	N	121	141
Q9CZU3	Exosome	DAFQR	EAIQCVDNNQSVLVSAHTSAGK	TVCAE	3	C5:+57.021	776.7135023	2327.117107	0.000451244	1	N	143	165
Q9CZU3	Exosome	GKAAK	EYPFILDAFQR	EAIQC	2		699.8567739	1397.697948	0.001162105	1	N	132	143

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9CZU3	Parental	DAFQR	EAIQCVDNNQSVLVSAHTSAGK	TVCAE	3	C5:+57.021	776.7135023	2327.117107	0.000622848	4	N	143	165
Q9CZU6	Exosome	MRGMK	GLVYETSVLDPDEGIR	FRGYS	2		881.9470456	1761.878491	0.000451244	42	N	76	92
Q9CZU6	Exosome	LPKAK	GGEEPLPEGLFWLLVTGQMPTEEQVSWLSR	EWAKR	3		1129.231143	3384.670028	0.001162105	3	N	109	139
Q9CZU6	Exosome	FGVSR	ALGVLAQLIWSR	ALGFP	2		663.8987761	1325.781952	0.000451244	30	N	428	440
Q9CZU6	Exosome	STNLK	DVLSNLIPK	EQARI	2		499.7981962	997.5807925	0.001395409	3	N	34	43
Q9CZU6	Exosome	DEKLR	DYIWNTLNSGR	VVPGY	2		669.826005	1337.63641	0.000735798	4	N	329	340
Q9CZU6	Exosome	LAARH	ASASSTNLKDVLSNLIPK	EQARI	3		620.014713	1857.020739	0.000451244	17	N	25	43
Q9CZU6	Exosome	MRGMK	GLVYETSVLDPDEGIRF	RGYSI	2		955.4812526	1908.946905	0.000451244	6	N	76	93
Q9CZU6	Exosome	AQLYK	IVPNILLEQGK	AKNPW	2		612.3720598	1222.72852	0.0007646	2	N	382	393
Q9CZU6	Parental	MRGMK	GLVYETSVLDPDEGIR	FRGYS	2		881.9470456	1761.878491	0.000451244	9	N	76	92
Q9CZU6	Parental	MRGMK	GLVYETSVLDPDEGIRFR	GYSIP	2		1033.531808	2065.048016	0.001699387	1	N	76	94
Q9CZU6	Parental	MRGMK	GLVYETSVLDPDEGIRFR	GYSIP	3		689.3571388	2065.048016	0.000451244	6	N	76	94
Q9CZU6	Parental	LPKAK	GGEEPLPEGLFWLLVTGQMPTEEQVSWLSR	EWAKR	3		1129.231143	3384.670028	0.00091018	4	N	109	139
Q9CZU6	Parental	FGVSR	ALGVLAQLIWSR	ALGFP	2		663.8987761	1325.781952	0.000451244	6	N	428	440
Q9CZX8	Parental	-M	PGVTVKDVNQQEFVR	ALAAF	2		858.4579148	1714.90023	0.000451244	12	N	1	16
Q9CZX8	Parental	KKSGK	LKVPEWVDTVK	LAKHK	3		438.5874948	1312.739084	0.000451244	6	N	27	38
Q9D020	Exosome	NFFGK	LQQHGIPVFIFSAGIGDVLEEVIR	QAGVY	3		879.8186733	2636.43262	0.000451244	18	N	186	210
Q9D020	Exosome	LLQLK	EQYYAIEVDPVLTVEEK	FPYMV	2		1013.0073	2023.999001	0.000451244	8	N	123	140
Q9D020	Exosome	DGALK	NTDYFSQLKDNSNIILLGDSQGDLR	MADGV	2		1413.699382	2825.383163	0.000451244	2	N	253	278
Q9D020	Exosome	DGALK	NTDYFSQLKDNSNIILLGDSQGDLR	MADGV	3		942.8021878	2825.383163	0.000451244	12	N	253	278
Q9D020	Exosome	LLEKY	MDSYDIVLVKEESLEVVNSILQK	TL-	3		884.4669779	2650.377534	0.000823681	1	N	306	329
Q9D020	Exosome	EHILK	IGYLNDRVDELLEK	YMDSY	3		559.6338324	1675.878097	0.000451244	5	N	291	305
Q9D020	Exosome	FSQLK	DNSNIILLGDSQGDLR	MADGV	2		865.4399191	1728.864238	0.000451244	9	N	262	278
Q9D020	Exosome	PVFIF	SAGIGDVLEEVIR	QAGVY	2		679.3702454	1356.724891	0.001329271	2	N	197	210
Q9D020	Exosome	IVLVK	EESLEVVNSILQK	TL-	2		744.4017426	1486.787885	0.000622848	2	N	316	329
Q9D020	Exosome	KNPTR	VEEIICGLIK	GGAAK	2	C6:+57.021	587.3313147	1172.647029	0.002663018	1	N	62	72
Q9D020	Parental	NFFGK	LQQHGIPVFIFSAGIGDVLEEVIR	QAGVY	3		879.8186733	2636.43262	0.000451244	6	N	186	210
Q9D020	Parental	LLQLK	EQYYAIEVDPVLTVEEK	FPYMV	2		1013.0073	2023.999001	0.000451244	4	N	123	140
Q9D020	Parental	DGALK	NTDYFSQLKDNSNIILLGDSQGDLR	MADGV	2		1413.699382	2825.383163	0.000451244	3	N	253	278
Q9D020	Parental	DGALK	NTDYFSQLKDNSNIILLGDSQGDLR	MADGV	3		942.8021878	2825.383163	0.000451244	10	N	253	278
Q9D020	Parental	LLEKY	MDSYDIVLVKEESLEVVNSILQK	TL-	3		884.4669779	2650.377534	0.000662267	2	N	306	329
Q9D071	Exosome	AADVK	SGGYTVLQVVEALGSSLENAEPR	TRARG	3		792.7400886	2375.196866	0.000451244	2	N	41	64
Q9D071	Exosome	CSVLR	ADAEDLLGSFLSNILQDCR	HHLCE	2	C18:+57.021	1069.015434	2136.015267	0.000451244	2	N	339	358
Q9D071	Parental	AADVK	SGGYTVLQVVEALGSSLENAEPR	TRARG	3		792.7400886	2375.196866	0.000634081	2	N	41	64
Q9D0E1	Exosome	IEMER	GNFGGSFAGSFGGAGGHAPGVAR	KACQI	3		678.9896723	2033.945617	0.001162105	4	N	626	649
Q9D0E1	Parental	NGKSK	GCGVVKFESPEVAER	ACRMM	2	C2:+57.021	832.4093447	1662.803089	0.000451244	4	N	691	706
Q9D0E1	Parental	NGKSK	GCGVVKFESPEVAER	ACRMM	3	C2:+57.021	555.2754965	1662.803089	0.000979378	3	N	691	706
Q9D0E1	Parental	IEMER	GNFGGSFAGSFGGAGGHAPGVAR	KACQI	2		1017.980608	2033.945617	0.000451244	15	N	626	649
Q9D0E1	Parental	IEMER	GNFGGSFAGSFGGAGGHAPGVAR	KACQI	3		678.9896723	2033.945617	0.000622848	10	N	626	649
Q9D0E1	Parental	TKRYR	AFITNIPFDVK	WQSLK	2		632.8509602	1263.68632	0.001162105	4	N	71	82
Q9D0E1	Parental	MNMGR	INEILSNALK	RGEII	2		557.8274851	1113.63937	0.001871652	2	N	370	380
Q9D0F3	Exosome	NDGKK	NNPAIVVIGNNGQINYDHQNDGATQALASCQR	DFRNK	3	C30:+57.021	1151.550554	3451.628261	0.000870037	2	N	168	200
Q9D0F3	Parental	NDGKK	NNPAIVVIGNNGQINYDHQNDGATQALASCQR	DFRNK	3	C30:+57.021	1151.550554	3451.628261	0.000451244	21	N	168	200
Q9D0F3	Parental	SETVR	LVSGIQHPGSAGVYETTQHF	MDIKE	2		1064.527057	2127.038514	0.000622848	2	N	423	443
Q9D0F9	Exosome	ATMLR	NIFDFNALKELLSGPNR	LKIRI	3		650.0149359	1947.021408	0.0025889	2	N	200	217
Q9D0F9	Exosome	MILGK	HGFFVNPSDSVAVIAANIFSIPYFQQTGVR	GFARS	3		1094.563443	3280.66693	0.000451244	17	N	299	329
Q9D0F9	Exosome	RKRVK	VFQSNANYAENFIQSIVSTVEPALR	QEATL	2		1399.211928	2796.408256	0.000451244	8	N	27	52
Q9D0F9	Exosome	RKRVK	VFQSNANYAENFIQSIVSTVEPALR	QEATL	3		933.1438853	2796.408256	0.000451244	14	N	27	52
Q9D0F9	Exosome	YTVEK	ADNFEYSDPVDGSISK	NQGLR	2		872.3895605	1742.763521	0.000823681	8	N	470	486
Q9D0F9	Exosome	RKRVK	VFQSNANYAENFIQSIVSTVEPALRQEATLVVGGDGR	FYMTE	3		1327.343652	3979.007557	0.000451244	6	N	27	64
Q9D0F9	Parental	ATMLR	NIFDFNALKELLSGPNR	LKIRI	3		650.0149359	1947.021408	0.001395409	4	N	200	217
Q9D0F9	Parental	MILGK	HGFFVNPSDSVAVIAANIFSIPYFQQTGVR	GFARS	3		1094.563443	3280.66693	0.000622848	7	N	299	329
Q9D0F9	Parental	YTVEK	ADNFEYSDPVDGSISK	NQGLR	2		872.3895605	1742.763521	0.000735798	3	N	470	486
Q9D0F9	Parental	SNANY	AENFIQSIVSTVEPALRQEATLVVGGDGR	FYMTE	3		1019.539075	3055.593825	0.000451244	6	N	35	64
Q9D0F9	Parental	SNANY	AENFIQSIVSTVEPALR	QEATL	2		937.5050621	1872.994524	0.000451244	1	N	35	52
Q9D0F9	Parental	FQISK	TIEEYAICPDLK	VDLGV	2	C8:+57.021	726.3582578	1450.700916	0.001463592	1	N	152	164
Q9D0I9	Exosome	VHLRK	DFVSEQLTSLLVNGVQLPVLGDKEK	VIVDF	3		910.1642864	2727.469459	0.002212458	1	N	168	193
Q9D0I9	Exosome	VHLRK	DFVSEQLTSLLVNGVQLPVLGDKEK	VIVDF	4		682.8751648	2727.469459	0.000622848	1	N	168	193
Q9D0I9	Exosome	GCAIR	AAYPDLENPPLIVTPSQQPK	FGDYQ	2		1089.576216	2177.136832	0.000451244	23	N	89	109
Q9D0I9	Exosome	DDGRK	IVFVPGCSVPLTIVK	SDGGY	2	C7:+57.021	814.9761349	1627.93667	0.000451244	3	N	362	377
Q9D0I9	Exosome	MLDDR	GNTAAYLLYAFTR	IRSIA	2		730.8807803	1459.745961	0.000622848	5	N	527	540
Q9D0I9	Exosome	AVMAK	GFDILGIKPVQR	M-	3		448.2667556	1341.776867	0.000451244	2	N	647	659
Q9D0I9	Exosome	LTIVK	SDGGYTYDTSDLAAIK	QRLFE	2		838.8866537	1675.757707	0.001871652	1	N	377	393
Q9D0I9	Parental	VHLRK	DFVSEQLTSLLVNGVQLPVLGDKEK	VIVDF	3		910.1642864	2727.469459	0.000451244	20	N	168	193
Q9D0I9	Parental	GCAIR	AAYPDLENPPLIVTPSQQPK	FGDYQ	2		1089.576216	2177.136832	0.000451244	23	N	89	109

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D0I9	Parental	DDGRK	IVFVPGCSVPLTIVK	SDGGY	2	C7:+57.021	814.9761349	1627.93667	0.000662267	6	N	362	377
Q9D0K2	Exosome	GALLK	TGVKDLTAVSNNAGVDNFGLGLLLR	SKQIK	3		848.7980493	2543.370748	0.000979378	2	N	79	104
Q9D0K2	Exosome	AERIR	AGGAGVPAFYTSTGYGTLVQEGGSPIK	YNKDG	2		1293.148265	2584.28093	0.000451244	20	N	146	173
Q9D0K2	Exosome	KTGVK	DLTAVSNNAGVDNFGLGLLLR	SKQIK	2		1080.076914	2158.138229	0.000451244	23	N	83	104
Q9D0K2	Exosome	KTGVK	DLTAVSNNAGVDNFGLGLLLR	SKQIK	3		720.3872095	2158.138229	0.000451244	2	N	83	104
Q9D0K2	Exosome	VEAVK	DIPNGATLLVGGFGLCGIPENLIGALLK	TGVKD	3	C16:+57.021	941.5213739	2821.540722	0.000451244	3	N	51	79
Q9D0K2	Exosome	AEFER	QFLSGELEVELTPQGTLAER	IRAGG	2		1109.074037	2216.132475	0.000451244	6	N	124	144
Q9D0K2	Parental	GALLK	TGVKDLTAVSNNAGVDNFGLGLLLR	SKQIK	3		848.7980493	2543.370748	0.000451244	6	N	79	104
Q9D0K2	Parental	AERIR	AGGAGVPAFYTSTGYGTLVQEGGSPIK	YNKDG	2		1293.148265	2584.28093	0.000823681	3	N	146	173
Q9D0K2	Parental	KTGVK	DLTAVSNNAGVDNFGLGLLLR	SKQIK	2		1080.076914	2158.138229	0.000451244	20	N	83	104
Q9D0K2	Parental	VEAVK	DIPNGATLLVGGFGLCGIPENLIGALLK	TGVKD	3	C16:+57.021	941.5213739	2821.540722	0.000451244	2	N	51	79
Q9D0K2	Parental	HTKFY	TDPVEAVKDIPNGATLLVGGFGLCGIPENLIGALLK	TGVKD	3	C24:+57.021	1221.334335	3660.979606	0.002519933	1	N	43	79
Q9D0L8	Exosome	NACGR	LNPGGYFIGTTPNSFELIR	RLEAS	2		1048.544719	2095.073837	0.000451244	12	N	296	315
Q9D0L8	Parental	NACGR	LNPGGYFIGTTPNSFELIR	RLEAS	2		1048.544719	2095.073837	0.000451244	6	N	296	315
Q9D0L8	Parental	ASGQR	LPENTPPCQQVDQPK	MQKEF	2	C8:+57.021	875.9253589	1749.835118	0.000622848	8	N	29	44
Q9D0L8	Parental	PKMQK	EFGEDLVEQNSSYVQDSPSK	KRKLD	2		1129.508924	2257.002248	0.000998612	1	N	47	67
Q9D0L8	Parental	EGSAK	ASVASDPESPPGGNEPAAASGQR	LPENT	2		1076.499225	2150.98285	0.000622848	3	N	6	29
Q9D0M1	Parental	DVGGR	IAIIVDDIIDDVESFVAAAEILKER	GAYKI	3		919.8360583	2756.484775	0.001162105	1	N	250	275
Q9D0M1	Parental	DVGGR	IAIIVDDIIDDVESFVAAAEILK	ERGAY	3		824.7881569	2471.341071	0.001463592	1	N	250	273
Q9D0M3	Parental	MRPGK	LSDYFPKPYPNPEAAR	AANNG	3		622.3129818	1863.915545	0.000451244	35	N	170	186
Q9D0M3	Parental	IVRAR	HGGEDYVFSLLTGYCEPPTGVSLREGLY	FNPYF	3	C15:+57.021	1039.494212	3115.459237	0.001162105	1	N	204	232
Q9D0M3	Parental	IVRAR	HGGEDYVFSLLTGYCEPPTGVSLR	EGLYF	2	C15:+57.021	1327.631693	2653.247787	0.000451244	19	N	204	228
Q9D0M3	Parental	IVRAR	HGGEDYVFSLLTGYCEPPTGVSLR	EGLYF	3	C15:+57.021	885.423729	2653.247787	0.000451244	25	N	204	228
Q9D0M3	Parental	IVRAR	HGGEDYVFSLLTGYCEPPTGV	SLREG	2	C15:+57.021	1149.523092	2297.030583	0.000622848	5	N	204	225
Q9D0M3	Parental	PEAAR	AANNGALPPDLSYIVR	ARHGG	2		835.947183	1669.878766	0.00307782	1	N	186	202
Q9D0R2	Exosome	AESWK	TTPYQIACGISQGLADNTVVAK	VNKVV	2	C8:+57.021	1154.08639	2306.157181	0.000451244	16	N	98	120
Q9D0R2	Exosome	RKIGR	DQELYFFHELSPGSCFFLPK	GAYIY	2	C15:+57.021	1231.080577	2460.145553	0.002727428	1	N	327	347
Q9D0R2	Exosome	RKIGR	DQELYFFHELSPGSCFFLPK	GAYIY	3	C15:+57.021	821.0563178	2460.145553	0.000451244	23	N	327	347
Q9D0R2	Exosome	EYRKR	GFQEVVTPNIFNSR	LWMTS	2		804.412976	1606.810352	0.001943752	1	N	366	380
Q9D0R2	Exosome	TRPEK	FLGDIEIWNQAEK	QLENS	2		781.8966274	1561.777655	0.000622848	2	N	503	516
Q9D0R2	Exosome	NQAEK	QLENSLNEFGEKWELNPGDGAFYGPK	IDIQI	3		980.4669166	2938.37735	0.000451244	11	N	516	542
Q9D0R2	Exosome	ETLQR	IYGISFPDPK	LLKEW	2		568.8034786	1135.591357	0.001763695	6	N	295	305
Q9D0R2	Exosome	LDFLR	TVYSVFGFSFK	LNLST	2		641.3298606	1280.644121	0.000622848	1	N	483	494
Q9D0R2	Parental	RKIGR	DQELYFFHELSPGSCFFLPK	GAYIY	3	C15:+57.021	821.0563178	2460.145553	0.002374549	1	N	327	347
Q9D0T1	Parental	HLTKK	LLDLVQQSCNYK	QLRKG	2	C9:+57.021	740.877149	1479.738698	0.000451244	1	N	21	33
Q9D0T1	Parental	GSQLK	QQIQSIQQSIER	LLV-	2		729.3895008	1456.763402	0.000451244	5	N	113	125
Q9D154	Exosome	AQLSK	TFHFDSVEDIHSR	FQSLN	2		795.3713081	1588.727016	0.000451244	33	N	56	69
Q9D154	Exosome	AQLSK	TFHFDSVEDIHSR	FQSLN	3		530.5834721	1588.727016	0.000451244	5	N	56	69
Q9D154	Exosome	LYGEK	TYNFLPEYLASTQK	MYGAD	2		837.9228422	1673.830084	0.000451244	17	N	96	110
Q9D154	Exosome	ASTQK	MYGADLAPVDFLHASEDAR	KEINQ	2		1039.486544	2076.957488	0.000451244	7	N	110	129
Q9D154	Exosome	ASTQK	MYGADLAPVDFLHASEDAR	KEINQ	3		693.3269626	2076.957488	0.000451244	26	N	110	129
Q9D154	Exosome	ASTQK	MYGADLAPVDFLHASEDAR	KEINQ	3	M1:+15.995	698.6586293	2092.952488	0.000451244	12	N	110	129
Q9D154	Exosome	IFFIR	HNPTSNVLFLGR	VCSP-	2		677.8654646	1353.715329	0.000451244	10	N	363	375
Q9D154	Exosome	IFFIR	HNPTSNVLFLGR	VCSP-	3		452.246243	1353.715329	0.001839721	2	N	363	375
Q9D154	Exosome	VKLPR	FKIEESYTLNSNLGR	LGVQD	2		885.955205	1769.89481	0.000451244	26	N	275	290
Q9D154	Exosome	VKLPR	FKIEESYTLNSNLGR	LGVQD	3		590.9727367	1769.89481	0.000622848	1	N	275	290
Q9D154	Exosome	ASTQK	MYGADLAPVDFLHASEDARK	EINQW	3		736.0252837	2205.052451	0.000451244	10	N	110	130
Q9D154	Exosome	ASTQK	MYGADLAPVDFLHASEDARK	EINQW	4		552.2709128	2205.052451	0.000870037	11	N	110	130
Q9D154	Exosome	SNLGR	LGVQDLFSSSK	ADLSG	2		590.8145747	1179.613549	0.000662267	18	N	290	301
Q9D154	Exosome	DSMTK	LVLVNAIYFK	GMWEE	2		590.3609637	1178.706327	0.000823681	11	N	158	168
Q9D154	Exosome	QTEGK	IPELLSVGVVDSMTK	LVLVN	2	M13:+15.995	802.4347714	1602.853943	0.000451244	39	N	143	158
Q9D154	Exosome	LPRFK	IEESYTLNSNLGR	LGVQD	2		748.3735164	1494.731433	0.000451244	2	N	277	290
Q9D154	Parental	AQLSK	TFHFDSVEDIHSR	FQSLN	2		795.3713081	1588.727016	0.000451244	38	N	56	69
Q9D154	Parental	AQLSK	TFHFDSVEDIHSR	FQSLN	3		530.5834721	1588.727016	0.000451244	15	N	56	69
Q9D154	Parental	EWTKR	ENLEFIDVHVKLPR	FKIEE	2		854.9732008	1707.930802	0.001763695	1	N	261	275
Q9D154	Parental	EWTKR	ENLEFIDVHVKLPR	FKIEE	3		570.3180672	1707.930802	0.000451244	1	N	261	275
Q9D154	Parental	EWTKR	ENLEFIDVHVKLPR	FKIEE	4		427.9905004	1707.930802	0.000451244	10	N	261	275
Q9D154	Parental	LYGEK	TYNFLPEYLASTQK	MYGAD	2		837.9228422	1673.830084	0.000451244	22	N	96	110
Q9D154	Parental	ASTQK	MYGADLAPVDFLHASEDAR	KEINQ	2		1039.486544	2076.957488	0.000451244	4	N	110	129
Q9D154	Parental	ASTQK	MYGADLAPVDFLHASEDAR	KEINQ	3		693.3269626	2076.957488	0.000451244	33	N	110	129
Q9D154	Parental	IFFIR	HNPTSNVLFLGR	VCSP-	2		677.8654646	1353.715329	0.001395409	4	N	363	375
Q9D154	Parental	IFFIR	HNPTSNVLFLGR	VCSP-	3		452.246243	1353.715329	0.001654178	4	N	363	375
Q9D154	Parental	VKLPR	FKIEESYTLNSNLGR	LGVQD	2		885.955205	1769.89481	0.000451244	43	N	275	290
Q9D154	Parental	VKLPR	FKIEESYTLNSNLGR	LGVQD	3		590.9727367	1769.89481	0.000451244	9	N	275	290
Q9D154	Parental	ASTQK	MYGADLAPVDFLHASEDARK	EINQW	2		1103.534026	2205.052451	0.000823681	1	N	110	130

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D154	Parental	ASTQK	MYGADLAPVDFLHASEDARK	EINQW	3		736.0252837	2205.052451	0.000823681	1	N	110	130
Q9D154	Parental	ASTQK	MYGADLAPVDFLHASEDARK	EINQW	4		552.2709128	2205.052451	0.000823681	8	N	110	130
Q9D154	Parental	SNLGR	LGVQDLFSSSK	ADLSG	2		590.8145747	1179.613549	0.000451244	22	N	290	301
Q9D154	Parental	DSMTK	LVLVNAIYFK	GMWEE	2		590.3609637	1178.706327	0.001463592	4	N	158	168
Q9D154	Parental	LPRFK	IEESYTLNSNLGR	LGVQD	2		748.3735164	1494.731433	0.000451244	3	N	277	290
Q9D154	Parental	FFSPF	SISSALAMVILGAK	GSTAA	2		680.897585	1359.77957	0.001463592	1	N	33	47
Q9D154	Parental	KIVHK	SFVEVNEEGTEAAAATGGIATF	CMLLP	2		1086.011103	2170.006605	0.000451244	77	N	321	343
Q9D154	Parental	GIATF	CMLLPEEEFTVDHPFIFFIR	HNPTS	2	C1:+39.994	1262.108055	2522.20051	0.002813207	1	N	343	363
Q9D154	Parental	FALEL	FQTLNESSPTGNIFFSPFSISSALAMVILGAK	GSTAA	3		1125.583405	3373.726814	0.000622848	3	N	15	47
Q9D154	Parental	ANTLF	ALELFQTLNESSPTGNIFFSPFSISSALAMVILGAK	GSTAA	3		1267.666017	3799.97465	0.000823681	6	N	11	47
Q9D154	Parental	NQWVK	GQTEGKIPELLSVGVVDSMTK	LVLVN	2		1094.580641	2187.145683	0.000622848	1	N	137	158
Q9D154	Parental	EWTKR	ENLEFIDVHVK	LPRFK	3		448.2387541	1341.692862	0.000622848	4	N	261	272
Q9D1A2	Exosome	DPQKK	TVCIYGHLDVQPAALEDGWDSEPFTLVER	EGKLY	3	C3:+57.021	1106.531326	3316.570578	0.000451244	16	N	92	121
Q9D1A2	Exosome	DKFFK	DVDYVCISDNYWLGK	NKPCI	2	C6:+57.021	923.9197423	1845.823885	0.000451244	8	N	186	201
Q9D1A2	Exosome	ADVQR	LGGSVELVDIGK	QKLPD	2		593.8380498	1185.6605	0.001162105	5	N	54	66
Q9D1A2	Exosome	VDIGK	QKLPDGSEIPLPPILLGK	LGSDP	3		639.0474655	1914.118996	0.000622848	13	N	66	84
Q9D1A2	Exosome	MSALK	AVFQYIDENQDR	YVKKL	2		749.352584	1496.689568	0.000451244	4	N	5	17
Q9D1A2	Exosome	RYVKK	LAEWVAIQSVSAWPEK	RGEIR	2		907.478316	1812.941032	0.000622848	2	N	21	37
Q9D1A2	Exosome	ILMHR	WRYPSLSLHGIEGAFSGSGAK	TVIPR	4		555.785887	2219.112348	0.002519933	1	N	308	329
Q9D1A2	Exosome	RYVKK	LAEWVAIQSVSAWPEKR	GEIRR	3		657.355181	1969.042143	0.002727428	1	N	21	38
Q9D1A2	Parental	DPQKK	TVCIYGHLDVQPAALEDGWDSEPFTLVER	EGKLY	3	C3:+57.021	1106.531326	3316.570578	0.000451244	22	N	92	121
Q9D1A2	Parental	VDIGK	QKLPDGSEIPLPPILLGK	LGSDP	3		639.0474655	1914.118996	0.000622848	7	N	66	84
Q9D1G1	Exosome	CLLLR	FADDTYTESYISTIGVDFK	IRTIE	2		1086.505122	2170.994644	0.000451244	32	N	27	46
Q9D1G1	Exosome	NTTAK	EFADSLGVPFLETSAK	NATNV	2		855.9334069	1709.851214	0.000451244	2	N	137	153
Q9D1G1	Exosome	YANVK	QWLQEIDRYASENVNK	LLVGN	3		664.9978335	1991.9701	0.000870037	1	N	100	116
Q9D1G1	Exosome	DYLFK	LLLIGDSGVGK	SCLLL	2		536.3245782	1070.633556	0.002212458	2	N	10	21
Q9D1G1	Exosome	LDGKT	IKLQIWDTAGQER	FRTIT	3		519.9514958	1556.831087	0.000735798	1	Y	56	69
Q9D1G1	Parental	CLLLR	FADDTYTESYISTIGVDFK	IRTIE	2		1086.505122	2170.994644	0.000451244	24	N	27	46
Q9D1G1	Parental	LTTKK	VVDNTTAKEFADSLGVPFLETSAK	NATNV	3		847.1029155	2538.285347	0.001699387	1	N	129	153
Q9D1G1	Parental	GKTIK	LQIWDTAGQER	FRTIT	2		658.8338301	1315.65206	0.001591523	2	Y	58	69
Q9D1G1	Parental	NTTAK	EFADSLGVPFLETSAK	NATNV	2		855.9334069	1709.851214	0.000698008	8	N	137	153
Q9D1K2	Exosome	AGRGK	LIAVIGDEDTVTGFLLGGIGELNK	NRHPN	2		1222.668302	2443.321004	0.000451244	28	N	6	30
Q9D1K2	Exosome	AGRGK	LIAVIGDEDTVTGFLLGGIGELNK	NRHPN	3		815.4481346	2443.321004	0.000451244	14	N	6	30
Q9D1K2	Exosome	LVVEK	DTTINEIEDTFR	QFLNR	2		727.3444246	1452.673249	0.000451244	2	N	41	53
Q9D1K2	Parental	AGRGK	LIAVIGDEDTVTGFLLGGIGELNK	NRHPN	2		1222.668302	2443.321004	0.000451244	29	N	6	30
Q9D1K2	Parental	AGRGK	LIAVIGDEDTVTGFLLGGIGELNK	NRHPN	3		815.4481346	2443.321004	0.000622848	6	N	6	30
Q9D1K2	Parental	-MAGR	GKLIAVIGDEDTVTGFLLGGIGELNK	NRHPN	3		877.1536102	2628.437431	0.001699387	2	N	4	30
Q9D1L9	Parental	NLGCR	GTLSDEHAGVISVLAQQAAR	LTSDP	2		1012.032507	2022.049413	0.000451244	14	N	34	54
Q9D1L9	Parental	NLGCR	GTLSDEHAGVISVLAQQAAR	LTSDP	3		675.0242711	2022.049413	0.000451244	6	N	34	54
Q9D1L9	Parental	EDTMK	NPSIVGVLCTDSQGLNLGCR	GTLSD	2	C9:+57.021,C19:+57.021	1080.530497	2159.045393	0.000451244	2	N	14	34
Q9D1M0	Exosome	SDWVR	DVAWAPSIGLPTSTIASCSQDGR	VFIWT	2	C18:+57.021	1195.076554	2388.137508	0.000451244	19	N	216	239
Q9D1M0	Exosome	SQDGR	VFIWTCDDASGNMWSPK	LLHKF	2	C6:+57.021,M13:+15.995	1015.443102	2028.870604	0.001162105	5	N	239	256
Q9D1M0	Parental	SDWVR	DVAWAPSIGLPTSTIASCSQDGR	VFIWT	2	C18:+57.021	1195.076554	2388.137508	0.000451244	5	N	216	239
Q9D1M0	Parental	VTLWK	ESVDGQWVCISDVNK	GQGSV	2	C9:+57.021	868.4017167	1734.787833	0.001162105	4	N	290	305
Q9D1P4	Exosome	CCKRR	TTDFSDFLSIVGCTK	GRHNS	2	C13:+57.021	845.9035608	1689.791522	0.000622848	1	N	46	61
Q9D1P4	Parental	CCKRR	TTDFSDFLSIVGCTK	GRHNS	2	C13:+57.021	845.9035608	1689.791522	0.000451244	12	N	46	61
Q9D1P4	Parental	CCRRK	TSDFNTFLAQEGCTR	GKHVW	2	C13:+57.021	873.8915161	1745.767432	0.000451244	4	N	198	213
Q9D1Q6	Exosome	LHIQK	TPADCPVIAIDSFR	HMYVF	2	C5:+57.021	781.3878809	1560.760162	0.000451244	9	N	313	327
Q9D1Q6	Exosome	RVFER	VASILHDDCAFLSAFGDLSKPER	YNGDN	3	C9:+57.021	850.0885692	2547.242308	0.000451244	22	N	180	203
Q9D1Q6	Exosome	RVFER	VASILHDDCAFLSAFGDLSKPER	YNGDN	4	C9:+57.021	637.8183769	2547.242308	0.000451244	20	N	180	203
Q9D1Q6	Exosome	IRQQK	SNPVHEIQSLDEVTNLDR	SKRNI	2		1033.511604	2065.007608	0.000451244	17	N	140	158
Q9D1Q6	Exosome	TPITA	EIASLDSENIDEILNNADVALVNFYADWCR	FSQML	3	C29:+57.021	1157.212433	3468.6139	0.000823681	4	N	29	59
Q9D1Q6	Parental	LHSGK	LHREFHHGPDPTDTAPGEQDQDVASSPPESSFQK	LAPSE	3		1248.570602	3742.688407	0.001699387	4	N	355	389
Q9D1Q6	Parental	LHIQK	TPADCPVIAIDSFR	HMYVF	2	C5:+57.021	781.3878809	1560.760162	0.000451244	1	N	313	327
Q9D1Q6	Parental	RVFER	VASILHDDCAFLSAFGDLSKPER	YNGDN	3	C9:+57.021	850.0885692	2547.242308	0.000451244	5	N	180	203
Q9D1Q6	Parental	RVFER	VASILHDDCAFLSAFGDLSKPER	YNGDN	4	C9:+57.021	637.8183769	2547.242308	0.000451244	21	N	180	203
Q9D1Q6	Parental	IRQQK	SNPVHEIQSLDEVTNLDR	SKRNI	2		1033.511604	2065.007608	0.000451244	37	N	140	158
Q9D1Q6	Parental	IRQQK	SNPVHEIQSLDEVTNLDR	SKRNI	3		689.3436694	2065.007608	0.000451244	1	N	140	158
Q9D1Q6	Parental	TPITA	EIASLDSENIDEILNNADVALVNFYADWCR	FSQML	3	C29:+57.021	1157.212433	3468.6139	0.000451244	6	N	29	59
Q9D1Q6	Parental	LISEK	GTINFLHADCDKFR	HPLLH	3	C10:+57.021	565.2757193	1692.803758	0.000451244	1	N	291	305
Q9D2C2	Exosome	NDTWR	LLFDLVCHEFCQPDDPPVILQEQK	TVLAS	3	C7:+57.021,C11:+57.021	980.8140744	2939.418823	0.000451244	1	N	296	320
Q9D2C2	Parental	LQEQK	TVLASVFSVLSAISASR	AEQEH	3		569.9933607	1706.956682	0.000451244	7	N	320	337
Q9D2C2	Parental	NDTWR	LLFDLVCHEFCQPDDPPVILQEQK	TVLAS	3	C7:+57.021,C11:+57.021	980.8140744	2939.418823	0.000622848	3	N	296	320
Q9D2C2	Parental	MKILK	DISCEFLSNIFQVLTK	EKVAQ	2	C4:+57.021	957.4877921	1912.959984	0.000451244	9	N	397	413
Q9D2G2	Exosome	SAFVK	ASAFALQEQPVVNAVIDDATK	EVVYR	2		1094.068755	2186.12191	0.000451244	2	N	287	308

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D2G2	Parental	TAVCK	NDVITVQTPAFAESVTEGDVRWEK	AVGDA	2		1346.167186	2690.318772	0.000451244	1	N	68	92
Q9D2G2	Parental	AFVKA	SAFALQEQPVVNAVIDDATK	EVVYR	2		1058.550198	2115.084796	0.001264573	1	N	288	308
Q9D2V7	Exosome	VYEPR	SSPLPLQEGPGPEGGR	GARIV	2		789.4000656	1576.784531	0.000451244	14	N	664	680
Q9D2V7	Exosome	AMVAK	LGNREDPLPQDSFEGVDEDEWD	-	2		1281.549309	2561.083018	0.000622848	5	N	900	922
Q9D2V7	Exosome	GRGAR	IVWVCDGGCLLVSGFDSR	SERQL	2	C5:+57.021,C9:+57.021	1020.487569	2038.959538	0.000451244	33	N	683	701
Q9D2V7	Exosome	GRGAR	IVWVCDGGCLLVSGFDSR	SERQL	3	C5:+57.021,C9:+57.021	680.6609794	2038.959538	0.001229886	7	N	683	701
Q9D2V7	Exosome	PRVRK	EFFQDDVFPDTAVTWEPALSAK	AWFEG	2		1257.097709	2512.179819	0.000451244	44	N	817	839
Q9D2V7	Exosome	PRVRK	EFFQDDVFPDTAVTWEPALSAK	AWFEG	3		838.4010729	2512.179819	0.000451244	23	N	817	839
Q9D2V7	Exosome	EENKR	HVTYLGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	3	C7:+57.021	1190.88795	3569.640449	0.000451244	19	N	68	100
Q9D2V7	Exosome	EENKR	HVTYLGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	4	C7:+57.021	893.4179122	3569.640449	0.000451244	13	N	68	100
Q9D2V7	Exosome	ITNLK	GLNLTTPGESDGFCANR	LRVAV	2	C14:+57.021	904.9155225	1807.815445	0.000451244	18	N	488	505
Q9D2V7	Exosome	VLLPK	TECDIQDVEFAR	CLRLR	2	C3:+57.021	741.8303958	1481.645192	0.000451244	20	N	784	796
Q9D2V7	Exosome	VLAGK	GENQLYCYEVTPQQPALSPVTQCILENVLR	GAALV	3	C7:+57.021,C23:+57.021	1173.913287	3518.716462	0.000451244	32	N	280	310
Q9D2V7	Exosome	LPRVR	KEFFQDDVFPDTAVTWEPALSAK	AWFEG	3		881.099394	2640.274782	0.000622848	5	N	816	839
Q9D2V7	Exosome	IRLWR	VPPGGLENVLTTPETVLTGHTEK	IYSLR	3		797.0923508	2388.253652	0.000622848	3	N	570	593
Q9D2V7	Exosome	LWDTR	LFSSALASVTLDTSPGPLIPLLDPDSGLLVLAGK	GENQL	3		1126.632641	3376.874524	0.000451244	18	N	246	280
Q9D2V7	Exosome	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHK	GFVLL	3	C16:+57.021	1028.500527	3082.478181	0.000451244	32	N	751	777
Q9D2V7	Exosome	GNHIK	SSCSLIAFNSDRPGVLGVISLEGHEENKR	HVTYL	3	C3:+57.021	1057.866932	3170.577395	0.000451244	4	N	39	68
Q9D2V7	Exosome	GNHIK	SSCSLIAFNSDRPGVLGVISLEGHEENKR	HVTYL	4	C3:+57.021	793.6521487	3170.577395	0.000823681	5	N	39	68
Q9D2V7	Exosome	DTRLF	SSALASVTLDTSPGPLIPLLDPDSGLLVLAGK	GENQL	3		1039.915148	3116.722045	0.002145581	1	N	248	280
Q9D2V7	Exosome	IYSLR	FHPLAADVLASSSYDLTVR	IWDLQ	2		1031.534351	2061.053102	0.000823681	2	N	598	617
Q9D2V7	Exosome	IYSLR	FHPLAADVLASSSYDLTVR	IWDLQ	3		688.0255006	2061.053102	0.000622848	8	N	598	617
Q9D2V7	Exosome	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHKGFVLLPK	TECDI	3	C16:+57.021	1279.991909	3836.952328	0.001591523	4	N	751	784
Q9D2V7	Exosome	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHKGFVLLPK	TECDI	4	C16:+57.021	960.245882	3836.952328	0.000622848	5	N	751	784
Q9D2V7	Exosome	RHVTY	LGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	3	C3:+57.021	1024.141839	3069.402116	0.000451244	4	N	72	100
Q9D2V7	Exosome	QLQLY	IADALAQGPSALLGLDVAPSTLLPSYDPDTGLVLLTGK	GDTRV	3		1255.019224	3762.034272	0.000823681	3	N	709	747
Q9D2V7	Exosome	IKLWR	LSGTGEALPSVPGVVLGPEELPVEVL	QFHPT	2		1279.702342	2557.389083	0.002813207	1	N	106	132
Q9D2V7	Exosome	AERLK	LQGHQDQIFSLAWSPDGK	QLATV	2		1014.003218	2025.990836	0.000823681	1	N	629	647
Q9D2V7	Exosome	WDVAK	QQPLTELEAHKDLVQSAVWSR	DGAIV	3	[0:-17.027	806.7522897	2417.233469	0.001162105	4	N	157	178
Q9D2V7	Exosome	IKLWR	LSGTGEALPSVPGVVLGPEELPVEVLQFHPT	VDGVL	3		1056.89961	3167.67543	0.000823681	1	N	106	137
Q9D2V7	Exosome	QKPGR	LPDTALPTLQNGTAVMDLVWDPFDPHR	LAVAG	3		1007.171447	3018.490941	0.000451244	2	N	529	556
Q9D2V7	Exosome	ALSAK	AWFEGANGQPR	LLSLQ	2		616.7945079	1231.573416	0.000823681	3	N	839	850
Q9D2V7	Exosome	ENQLY	CYEVTPQQPALSPVTQCILENVLR	GAALV	2	C1:+57.021,C17:+57.021	1408.209554	2814.403508	0.00091018	2	N	286	310
Q9D2V7	Exosome	ENQLY	CYEVTPQQPALSPVTQCILENVLR	GAALV	3	C1:+57.021,C17:+57.021	939.1423025	2814.403508	0.000451244	3	N	286	310
Q9D2V7	Exosome	DLTVR	IWDLQTGAER	LKLQG	2		594.8045413	1187.593483	0.001699387	1	N	617	627
Q9D2V7	Exosome	PSSLM	SPSTPSSLGPSLSSTSGIGTSPSQR	SLQSL	2		1188.088404	2374.161209	0.002145581	1	N	433	458
Q9D2V7	Parental	VYEPR	SSPLPLQEGPGPEGGR	GARIV	2		789.4000656	1576.784531	0.000622848	13	N	664	680
Q9D2V7	Parental	AMVAK	LGNREDPLPQDSFEGVDEDEWD	-	2		1281.549309	2561.083018	0.000451244	43	N	900	922
Q9D2V7	Parental	GRGAR	IVWVCDGGCLLVSGFDSR	SERQL	2	C5:+57.021,C9:+57.021	1020.487569	2038.959538	0.000451244	23	N	683	701
Q9D2V7	Parental	PRVRK	EFFQDDVFPDTAVTWEPALSAK	AWFEG	2		1257.097709	2512.179819	0.000451244	36	N	817	839
Q9D2V7	Parental	PRVRK	EFFQDDVFPDTAVTWEPALSAK	AWFEG	3		838.4010729	2512.179819	0.000451244	3	N	817	839
Q9D2V7	Parental	EENKR	HVTYLGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	3	C7:+57.021	1190.88795	3569.640449	0.000622848	2	N	68	100
Q9D2V7	Parental	EENKR	HVTYLGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	4	C7:+57.021	893.4179122	3569.640449	0.002374549	1	N	68	100
Q9D2V7	Parental	ITNLK	GLNLTTPGESDGFCANR	LRVAV	2	C14:+57.021	904.9155225	1807.815445	0.000451244	28	N	488	505
Q9D2V7	Parental	VLLPK	TECDIQDVEFAR	CLRLR	2	C3:+57.021	741.8303958	1481.645192	0.000451244	28	N	784	796
Q9D2V7	Parental	VLAGK	GENQLYCYEVTPQQPALSPVTQCILENVLR	GAALV	3	C7:+57.021,C23:+57.021	1173.913287	3518.716462	0.000451244	32	N	280	310
Q9D2V7	Parental	LPRVR	KEFFQDDVFPDTAVTWEPALSAK	AWFEG	2		1321.145191	2640.274782	0.001162105	1	N	816	839
Q9D2V7	Parental	LPRVR	KEFFQDDVFPDTAVTWEPALSAK	AWFEG	3		881.099394	2640.274782	0.000622848	3	N	816	839
Q9D2V7	Parental	IRLWR	VPPGGLENVLTTPETVLTGHTEK	IYSLR	3		797.0923508	2388.253652	0.001699387	1	N	570	593
Q9D2V7	Parental	LWDTR	LFSSALASVTLDTSPGPLIPLLDPDSGLLVLAGK	GENQL	3		1126.632641	3376.874524	0.000622848	12	N	246	280
Q9D2V7	Parental	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHK	GFVLL	3	C16:+57.021	1028.500527	3082.478181	0.000451244	12	N	751	777
Q9D2V7	Parental	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHKGFVLLPK	TECDI	3	C16:+57.021	1279.991909	3836.952328	0.000823681	2	N	751	784
Q9D2V7	Parental	KGDTR	VFLYEVLPEAPFFLECNSFTSPDPHKGFVLLPK	TECDI	4	C16:+57.021	960.245882	3836.952328	0.002663018	1	N	751	784
Q9D2V7	Parental	RHVTY	LGCHSDLVTDLDFSPFDDFLLASGSADR	TIKLW	3	C3:+57.021	1024.141839	3069.402116	0.000451244	11	N	72	100
Q9D2V7	Parental	QLQLY	IADALAQGPSALLGLDVAPSTLLPSYDPDTGLVLLTGK	GDTRV	3		1255.019224	3762.034272	0.001162105	4	N	709	747
Q9D2V7	Parental	IKLWR	LSGTGEALPSVPGVVLGPEELPVEVLQFHPTVDGVLV	STAGK	3		1251.012181	3750.013143	0.001395409	1	N	106	143
Q9D2V7	Parental	RKEFF	QDDVFPDTAVTWEPALSAK	AWFEG	2		1045.507999	2089.000398	0.000622848	2	N	820	839
Q9D3D9	Parental	SANVK	QVDVPTLTGAFGILASHVPTLQVLRPGLVVVHTEDGTTTK	YFVSS	3		1389.765781	4166.273942	0.000451244	8	N	56	96
Q9D3D9	Parental	SANVK	QVDVPTLTGAFGILASHVPTLQVLRPGLVVVHTEDGTTTK	YFVSS	4		1042.576286	4166.273942	0.002145581	1	N	56	96
Q9D3D9	Parental	ANLEK	AQSELSGAADEAARAEIQIR	IEANE	3		696.0228188	2085.045056	0.000451244	3	N	136	156
Q9D4D4	Exosome	HPTPR	LSFVDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021	1266.117365	2530.21913	0.000451244	17	N	116	142
Q9D4D4	Exosome	HPTPR	LSFVDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021,M21:+15.995	1274.114865	2546.21413	0.000451244	2	N	116	142
Q9D4D4	Exosome	HPTPR	LSFVDVATGSLGQGLGAACGMAYTGKYFDK	ASYRV	4	C19:+57.021,M21:+15.995	775.8747448	3099.467779	0.001763695	1	N	116	146
Q9D4D4	Parental	HPTPR	LSFVDVATGSLGQGLGAACGMAYTGK	YFDKA	2	C19:+57.021	1266.117365	2530.21913	0.000451244	3	N	116	142
Q9D554	Exosome	LLKAR	ENPSEEAQNLVEFTDEEGYGR	YLDLH	2		1207.02547	2412.035339	0.000451244	5	N	117	138

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D554	Exosome	KASEK	LDYITYLSIFDQLFDIPK	ERKNA	2		1102.580435	2203.145271	0.000979378	1	N	157	175
Q9D554	Exosome	KASER	WQPDTEEEYEDSSGNVVNKK	TYEDL	3		785.3526703	2353.034611	0.000451244	1	N	470	490
Q9D554	Exosome	DYITY	LSIFDQLFDIPK	ERKNA	2		718.3957319	1434.775864	0.001654178	2	N	163	175
Q9D554	Parental	STKGK	SLESLDTSLFAK	NPKSK	2		655.8460718	1309.676544	0.001463592	1	N	291	303
Q9D554	Parental	LLKAR	ENPSEEAQNLVEFTDEEGYGR	YLDLH	2		1207.02547	2412.035339	0.000451244	27	N	117	138
Q9D554	Parental	PGWPK	ETSSALTHAGAHLDLSAFSSWEELASLGLDRLK	SALLA	4		878.9473811	3511.758325	0.001162105	4	N	231	264
Q9D554	Parental	AHGMR	CLGIPNTAHFANVTQIEDAVSLWAK	LKLQK	3	[0:-17.027,C1:+57.021	913.4586233	2737.35247	0.002374549	1	N	436	461
Q9D554	Parental	KASEK	LDYITYLSIFDQLFDIPK	ERKNA	2		1102.580435	2203.145271	0.000622848	2	N	157	175
Q9D554	Parental	KASER	WQPDTEEEYEDSSGNVVNKK	TYEDL	2		1177.525106	2353.034611	0.001654178	1	N	470	490
Q9D554	Parental	KASER	WQPDTEEEYEDSSGNVVNKK	TYEDL	3		785.3526703	2353.034611	0.000698008	5	N	470	490
Q9D554	Parental	DGLRK	EELNAISGPNEFAEFYNR	LKQIK	2		1050.487598	2098.959595	0.000451244	9	N	69	87
Q9D554	Parental	DYITY	LSIFDQLFDIPK	ERKNA	2		718.3957319	1434.775864	0.002212458	3	N	163	175
Q9D5T0	Parental	SLAIK	LQPSIIFIDEIDSFLR	NRSSS	2		953.5201808	1905.024762	0.002374549	1	N	183	199
Q9D5T0	Parental	LLCVR	EYVNSTSEESHDEDEIRPVQQQDLHR	AIEKM	3		1047.477092	3139.407875	0.001463592	1	N	312	338
Q9D5V6	Parental	ISLIK	QSAQLTALAAQQQASGKEEK	SSNRD	3		696.3629525	2086.065457	0.001463592	2	N	224	244
Q9D5V6	Parental	RDGDK	LSAGAAPSEESPERPVEPTEEQQQQPPTEDPQFLHQAK	GLGNY	4		1046.502243	4181.977773	0.000622848	10	N	31	69
Q9D5V6	Parental	KSQLK	SQEDEEEISTSPGVSEFVSDAFDTCSLNQEDLRK	EMEQL	3	C25:+57.021	1283.569451	3847.684952	0.000451244	7	N	272	306
Q9D662	Exosome	SLNVK	GPCVSENELGVGGTSQWK	ICGLD	2	C3:+57.021	952.94428	1903.87296	0.000622848	3	N	431	449
Q9D662	Exosome	YENFK	HLLQAPLDDAQEILQAR	FPMPR	2		966.0214107	1930.027221	0.000622848	1	N	684	701
Q9D662	Parental	SLNVK	GPCVSENELGVGGTSQWK	ICGLD	2	C3:+57.021	952.94428	1903.87296	0.002813207	1	N	431	449
Q9D6F9	Exosome	-MR	EIVHLQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	3	Y	2	19
Q9D6F9	Exosome	-MR	EIVHLQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	21	Y	2	19
Q9D6F9	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000662267	3	Y	81	103
Q9D6F9	Exosome	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	9	Y	81	103
Q9D6F9	Exosome	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		1039.479773	3115.41592	0.000451244	41	Y	19	46
Q9D6F9	Exosome	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	4		779.8617801	3115.41592	0.000451244	14	Y	19	46
Q9D6F9	Exosome	SVQSK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	24	Y	336	350
Q9D6F9	Exosome	SVQSK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	1	Y	336	350
Q9D6F9	Exosome	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEF	3	C5:+57.021,C7:+57.021	1104.516428	3310.525885	0.000451244	17	Y	122	154
Q9D6F9	Exosome	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEF	3	C5:+57.021,C7:+57.021,M25:+15.995	1109.848095	3326.520885	0.000451244	8	Y	122	154
Q9D6F9	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	17	Y	77	103
Q9D6F9	Exosome	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	66	Y	77	103
Q9D6F9	Exosome	PRGLK	MAATFIGNSTAIQELFK	RISEQ	2	M1:+15.995	929.4749593	1856.934319	0.000451244	14	N	362	379
Q9D6F9	Exosome	-	MREIVHLQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000622848	1	Y	0	19
Q9D6F9	Exosome	-	MREIVHLQAGQCGNQIGAK	FWEVI	3	M1:+15.995,C12:+57.021	709.3583655	2125.051697	0.000451244	2	Y	0	19
Q9D6F9	Exosome	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		990.4569687	2968.347506	0.000451244	10	Y	20	46
Q9D6F9	Exosome	PRHGR	YLTVAAVFR	GRMSM	2		520.3009061	1038.586212	0.000622848	18	Y	309	318
Q9D6F9	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.001162105	2	Y	216	241
Q9D6F9	Exosome	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	M17:+15.995,C23:+57.021	908.7829573	2723.325472	0.001699387	1	Y	216	241
Q9D6F9	Exosome	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	28	Y	183	213
Q9D6F9	Exosome	PRGLK	MAATFIGNSTAIQELFKR	ISEQF	3	M1:+15.995	672.0196099	2013.03543	0.000451244	1	N	362	380
Q9D6F9	Exosome	NYVPR	AVLVDLEPGTMDSVR	SGPFG	2	M11:+15.995	809.4118276	1616.808055	0.000698008	4	Y	62	77
Q9D6F9	Exosome	SQQYR	ALTVPELTQQMFDAK	NMMAA	2		846.4378027	1690.860005	0.00091018	1	Y	282	297
Q9D6F9	Exosome	-M	REIVHLQAGQCGNQIGAK	FWEVI	3	C11:+57.021	660.3465369	1978.016211	0.002981883	1	Y	1	19
Q9D6F9	Parental	-MR	EIVHLQAGQCGNQIGAK	FWEVI	2	C10:+57.021	911.9653498	1821.9151	0.000451244	41	Y	2	19
Q9D6F9	Parental	-MR	EIVHLQAGQCGNQIGAK	FWEVI	3	C10:+57.021	608.3128332	1821.9151	0.000451244	28	Y	2	19
Q9D6F9	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1205.588512	2409.161424	0.000451244	30	Y	81	103
Q9D6F9	Parental	RSGPF	GQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		804.0616079	2409.161424	0.000451244	20	Y	81	103
Q9D6F9	Parental	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		1039.479773	3115.41592	0.000451244	80	Y	19	46
Q9D6F9	Parental	QIGAK	FWEVISDEHGIDPTGTYHGDSDLQLER	INVYY	4		779.8617801	3115.41592	0.000451244	30	Y	19	46
Q9D6F9	Parental	SVQSK	NSSYFVEWIPNNVK	TAVCD	2		848.9206338	1695.825668	0.000451244	38	Y	336	350
Q9D6F9	Parental	SVQSK	NSSYFVEWIPNNVK	TAVCD	3		566.2830226	1695.825668	0.000451244	19	Y	336	350
Q9D6F9	Parental	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEF	3	C5:+57.021,C7:+57.021	1104.516428	3310.525885	0.000451244	27	Y	122	154
Q9D6F9	Parental	DVVRK	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	IREEF	3	C5:+57.021,C7:+57.021,M25:+15.995	1109.848095	3326.520885	0.000451244	16	Y	122	154
Q9D6F9	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	2		1399.675847	2797.336094	0.000451244	50	Y	77	103
Q9D6F9	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAK	GHYTE	3		933.4531646	2797.336094	0.000451244	220	Y	77	103
Q9D6F9	Parental	PRGLK	MAATFIGNSTAIQELFK	RISEQ	2	M1:+15.995	929.4749593	1856.934319	0.000451244	18	N	362	379
Q9D6F9	Parental	VPSPK	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	4	C27:+57.021,C37:+57.021	1149.032553	4592.099013	0.001162105	8	Y	174	213
Q9D6F9	Parental	-	MREIVHLQAGQCGNQIGAK	FWEVI	3	C12:+57.021	704.0266989	2109.056697	0.000622848	5	Y	0	19
Q9D6F9	Parental	EFPDR	IMNTFSVVPSPK	VSDTV	2		660.355553	1318.695506	0.001763695	2	Y	162	174
Q9D6F9	Parental	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLER	INVYY	3		990.4569687	2968.347506	0.000451244	33	Y	20	46
Q9D6F9	Parental	IGAKF	WEVISDEHGIDPTGTYHGDSDLQLER	INVYY	4		743.0946766	2968.347506	0.00091018	1	Y	20	46
Q9D6F9	Parental	PRHGR	YLTVAAVFR	GRMSM	2		520.3009061	1038.586212	0.000622848	23	Y	309	318

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D6F9	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLR	FPGQL	3	C23:+57.021	903.4512906	2707.330472	0.000451244	22	Y	216	241
Q9D6F9	Parental	EPYNA	TLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C16:+57.021,C26:+57.021	1140.190598	3417.548394	0.000823681	4	Y	185	213
Q9D6F9	Parental	VVEPY	NATLSVHQLVENTDETYCIDNEALYDICFR	TLKLT	3	C18:+57.021,C28:+57.021	1201.883945	3602.628435	0.000451244	125	Y	183	213
Q9D6F9	Parental	FRTLK	LTTPTYGDLNHLVSATMSGVTTCLRFPGQLNADLR	KLAVN	4	C23:+57.021	955.7347788	3818.907915	0.001654178	2	Y	216	251
Q9D6F9	Parental	TTCLR	FPGQLNADLRK	LAVNM	3		420.2354554	1257.682966	0.001162105	3	Y	241	252
Q9D6F9	Parental	TTCLR	FPGQLNADLR	KLAVN	2		565.8018016	1129.588003	0.000451244	5	Y	241	251
Q9D6F9	Parental	PRGLK	MAATFIGNSTAIQELFKR	ISEQF	3	M1:+15.995	672.0196099	2013.03543	0.000870037	1	N	362	380
Q9D6F9	Parental	MDSVR	SGPFGQIFRPDNFVFGQSGAGNNWAKG	HYTEG	3		952.4603192	2854.357558	0.000823681	4	Y	77	104
Q9D6F9	Parental	QIGAK	FWEVISDEHGIDPTGTY	HGDSD	2		983.4474098	1964.87922	0.000823681	1	Y	19	36
Q9D6J6	Exosome	DLTPK	DIEEIIDELK	AGKVP	2		608.8195227	1215.623445	0.001839721	3	N	198	208
Q9D6J6	Parental	EAIVK	NYPEGHQAAAVLPVLDLAQR	QNGWL	2		1081.571799	2161.127998	0.001463592	2	N	67	87
Q9D6J6	Parental	EAIVK	NYPEGHQAAAVLPVLDLAQR	QNGWL	3		721.3837994	2161.127998	0.001229886	3	N	67	87
Q9D6J6	Parental	PRSGR	FCCEPAGGLTSLTEPPKGPGFGVQAGL	-	2	C2:+57.021,C3:+57.021	1374.162072	2746.308544	0.000451244	8	N	221	248
Q9D6J6	Parental	PRSGR	FCCEPAGGLTSLTEPPKGPGFGVQAGL	-	3	C2:+57.021,C3:+57.021	916.4439815	2746.308544	0.001654178	1	N	221	248
Q9D6J6	Parental	DLTPK	DIEEIIDELK	AGKVP	2		608.8195227	1215.623445	0.000735798	9	N	198	208
Q9D6J6	Parental	LFVHR	DTPENNPDTPFDFTPENYKR	IEAIV	2		1199.03564	2396.055681	0.002813207	1	N	41	61
Q9D6J6	Parental	LFVHR	DTPENNPDTPFDFTPENYK	RIEAI	2		1120.985085	2239.95457	0.001162105	3	N	41	60
Q9D6R2	Exosome	IVTIR	ENTEGEYSGIEHVIVDGVVQSIK	LITEE	2		1251.62208	2501.22856	0.000451244	8	N	146	169
Q9D6R2	Exosome	IVTIR	ENTEGEYSGIEHVIVDGVVQSIK	LITEE	3		834.7506533	2501.22856	0.000451244	9	N	146	169
Q9D6R2	Exosome	IEGYK	TPYTDVNIVTIR	ENTEG	2		696.3806131	1390.745626	0.000451244	1	N	134	146
Q9D6R2	Exosome	NLLLR	KTFDLYANVRPCVSIEGYK	TPYTD	3	C12:+57.021	754.0529077	2259.135323	0.001654178	1	N	115	134
Q9D6R2	Exosome	LLLRK	TFDLYANVRPCVSIEGYK	TPYTD	3	C11:+57.021	711.3545866	2131.04036	0.002663018	1	N	116	134
Q9D6R2	Parental	IEGYK	TPYTDVNIVTIRENTEGEYSGIEHVIVDGVVQSIK	LITEE	4		969.4987066	3873.963626	0.000622848	3	N	134	169
Q9D6R2	Parental	IVTIR	ENTEGEYSGIEHVIVDGVVQSIK	LITEE	2		1251.62208	2501.22856	0.000622848	5	N	146	169
Q9D6R2	Parental	IVTIR	ENTEGEYSGIEHVIVDGVVQSIK	LITEE	3		834.7506533	2501.22856	0.000451244	6	N	146	169
Q9D6R2	Parental	IEGYK	TPYTDVNIVTIR	ENTEG	2		696.3806131	1390.745626	0.002519933	1	N	134	146
Q9D6R2	Parental	EASKR	IAEFAFEYAR	NNHRS	2		608.8040099	1215.59242	0.002884417	1	N	178	188
Q9D6Y7	Parental	AEVVR	VVYRPEHISFEELLK	VFWEN	4		465.5075203	1857.998881	0.000451244	4	N	118	133
Q9D6Y7	Parental	DSASK	VISAEEALPGRTEPIPVTAK	HHVSG	2		1039.578758	2077.141917	0.000451244	9	N	27	47
Q9D6Y7	Parental	KVLSK	HNFGPITTDIR	EGQVF	2		635.8310904	1269.646581	0.001264573	1	N	183	194
Q9D6Y7	Parental	TTDIR	EGQVFYYAEDYHQQYLSK	NPDGY	2		1134.516355	2267.01711	0.000823681	3	N	194	212
Q9D6Y9	Exosome	PELAR	LLEIDPYLKPFAADFQR	RYKKF	3		679.3670866	2035.07786	0.000451244	15	N	30	47
Q9D6Y9	Exosome	ITFER	AGLLFIFNFHPSK	SYTDY	3		497.6105223	1489.808167	0.002019181	5	N	618	631
Q9D6Y9	Parental	PELAR	LLEIDPYLKPFAADFQR	RYKKF	3		679.3670866	2035.07786	0.000451244	9	N	30	47
Q9D6Y9	Parental	GIYCK	EWAPGAEGVFLTGEFSGWNPF	SHPYK	2		1149.529266	2297.042931	0.001699387	3	N	89	110
Q9D6Z1	Exosome	HNVVR	LVAFCPFSSSQVALENANAVSEGVVHEDLR	LLLET	3	C5:+57.021	1082.535071	3244.581812	0.000451244	11	N	47	77
Q9D6Z1	Exosome	VGDPK	IGAAIQEELGYNCQTGGVIAEILR	GVRLH	2	C13:+57.021	1288.163161	2574.310722	0.001871652	1	N	99	123
Q9D6Z1	Parental	HNVVR	LVAFCPFSSSQVALENANAVSEGVVHEDLR	LLLET	3	C5:+57.021	1082.535071	3244.581812	0.000451244	27	N	47	77
Q9D6Z1	Parental	HAVGY	ALLALKEVEEISLLLPQVEECVLNLGK	FHNVV	3	C21:+57.021	1007.570282	3019.687446	0.001463592	1	N	14	41
Q9D6Z1	Parental	LLALK	EVEEISLLLPQVEECVLNLGK	FHNVV	2	C15:+57.021	1206.140831	2410.266063	0.002296037	1	N	20	41
Q9D6Z1	Parental	LLALK	EVEEISLLLPQVEECVLNLGK	FHNVV	3	C15:+57.021	804.4298209	2410.266063	0.001763695	1	N	20	41
Q9D7G0	Exosome	AGATR	VYAILTHGIFSGPAISR	INNAC	3		601.3373503	1800.988651	0.000451244	7	N	243	260
Q9D7G0	Exosome	HCSKI	QVIDISMILAEAIR	RTHNG	3	Q1:-17.027,M7:+15.995	524.2888872	1569.843262	0.002019181	1	N	287	301
Q9D7G0	Exosome	PAISR	INNACFEAVVVTNTIPQEDK	MKHCS	2	C5:+57.021	1131.557466	2261.099332	0.000451244	2	N	260	280
Q9D7G0	Parental	AGATR	VYAILTHGIFSGPAISR	INNAC	2		901.5021254	1800.988651	0.001352548	1	N	243	260
Q9D7M8	Parental	GSDPR	AGDVEEDASQLIFPK	EFETA	2		809.9021067	1617.788613	0.000451244	2	N	9	24
Q9D7M8	Parental	SLEGR	FEDEELQQILDDIQTK	RSFQY	2		982.478907	1962.942214	0.001763695	1	N	121	137
Q9D7S9	Exosome	PTDTK	NKDGVLVDEFGLPQIPAS	-	2		949.9970699	1897.97854	0.001329271	1	N	201	219
Q9D7S9	Parental	KAKPK	APPPSLTDCIGTVDSR	AESID	2	C9:+57.021	843.4120844	1684.808569	0.002813207	1	N	11	27
Q9D7S9	Parental	PTDTK	NKDGVLVDEFGLPQIPAS	-	2		949.9970699	1897.97854	0.00091018	4	N	201	219
Q9D819	Exosome	GHSDK	HTGCCGDNDPIDVCEIGSK	VCARG	3	C4:+57.021,C5:+57.021,C14:+57.021	711.9593822	2132.854747	0.000451244	2	N	109	128
Q9D819	Exosome	LFPYK	GYIWNYGAIPQTWEDPGHSDKHTGCCGDNDPIDVCEIGSK	VCARG	4	C25:+57.021,C26:+57.021,C35:+57.021	1137.994489	4547.946758	0.000451244	7	N	88	128
Q9D819	Exosome	ETDWK	VIAINVDDPDAANYK	DISDV	2		809.410099	1616.804598	0.000637154	2	N	155	170
Q9D819	Exosome	SDVER	LKPGYLEATVDWFR	RYKVP	3		565.6353962	1693.882789	0.002212458	1	N	177	191
Q9D819	Parental	GHSDK	HTGCCGDNDPIDVCEIGSK	VCARG	3	C4:+57.021,C5:+57.021,C14:+57.021	711.9593822	2132.854747	0.001839721	1	N	109	128
Q9D824	Parental	GEVER	LVELSGGTGGDEEEEWLYGGPWDVHVHSDLAK	DLDEN	4		871.1605479	3480.610992	0.001871652	1	N	8	40
Q9D824	Parental	SDLAK	DLDENEVERPEEENASANPPSGIEEEAAENGVAKPK	VTETE	4		966.6982229	3862.761692	0.000451244	11	N	40	76
Q9D824	Parental	GTKVK	GVDLDAPGSINGVPLLEVDLDSFEDKPWR	KPGAD	3		1051.863336	3152.566607	0.000451244	11	N	136	165
Q9D855	Parental	LGLMR	DDTLHETEDVKEAIR	RLPED	3		590.9555228	1769.843168	0.00091018	8	N	34	49
Q9D855	Parental	DQWTK	YEEDKFYLEPYLK	EVIRE	3		579.6193004	1735.834501	0.000698008	4	N	83	96
Q9D883	Exosome	DLNNR	WFNGQPIHAELSPVTDFR	EACCR	3		705.3538401	2113.03812	0.000451244	3	N	133	151
Q9D883	Parental	DLNNR	WFNGQPIHAELSPVTDFR	EACCR	3		705.3538401	2113.03812	0.000451244	15	N	133	151

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D883	Parental	QTIAL	LNIYRNPQNSSQSADGLR	CAVSD	3		678.3440037	2032.008611	0.000698008	2	N	48	66
Q9D883	Parental	DLNNR	WFNGQPIHAELSPVTDF	REACC	2		979.4763046	1956.937009	0.000870037	7	N	133	150
Q9D892	Exosome	REAAR	QVQGPVLVEDTCLCFNALGGLPGPYIK	WFLQK	3	C12:+57.021,C14:+57.021	982.5017193	2944.481758	0.000451244	7	N	62	89
Q9D892	Exosome	GFEDK	SAYALCTFALSTGDPSQPVLLFR	GQTSG	2	C6:+57.021	1257.63879	2513.26198	0.000451244	22	N	110	133
Q9D892	Exosome	GFEDK	SAYALCTFALSTGDPSQPVLLFR	GQTSG	3	C6:+57.021	838.7617934	2513.26198	0.000451244	9	N	110	133
Q9D892	Parental	REAAR	QVQGPVLVEDTCLCFNALGGLPGPYIK	WFLQK	3	C12:+57.021,C14:+57.021	982.5017193	2944.481758	0.000451244	14	N	62	89
Q9D892	Parental	GFEDK	SAYALCTFALSTGDPSQPVLLFR	GQTSG	2	C6:+57.021	1257.63879	2513.26198	0.000622848	8	N	110	133
Q9D8B3	Exosome	KRYEK	QLAQIDGTLSTIEFQR	EALEN	2		910.481587	1818.947574	0.000451244	20	N	77	93
Q9D8B3	Exosome	KRYEK	QLAQIDGTLSTIEFQR	EALEN	3		607.323658	1818.947574	0.000823681	1	N	77	93
Q9D8B3	Exosome	KRYEK	QLAQIDGTLSTIEFQR	EALEN	2	[0:-17.027	901.968087	1801.920574	0.002519933	1	N	77	93
Q9D8B3	Exosome	IEFQR	EALENANTNTEVLK	NMGYA	2		773.3919062	1544.768212	0.000823681	6	N	93	107
Q9D8B3	Parental	KRYEK	QLAQIDGTLSTIEFQR	EALEN	2		910.481587	1818.947574	0.000451244	12	N	77	93
Q9D8B3	Parental	KRYEK	QLAQIDGTLSTIEFQR	EALEN	3		607.323658	1818.947574	0.000451244	3	N	77	93
Q9D8B3	Parental	IEFQR	EALENANTNTEVLK	NMGYA	2		773.3919062	1544.768212	0.000823681	6	N	93	107
Q9D8E6	Exosome	SKGHR	IEEVPELPLVVEDKVEGY	KKTKE	2		1029.0386	2056.061601	0.001839721	2	N	143	161
Q9D8E6	Exosome	TTQKR	YAICSALAASALPALVMSK	GHRIE	2	C4:+57.021,M17:+15.995	977.013163	1952.010726	0.000451244	4	N	121	140
Q9D8E6	Exosome	GHVGR	FCIWTESAFR	KLDEL	2	C2:+57.021	658.808538	1315.601476	0.000451244	3	N	248	258
Q9D8E6	Parental	TNLRK	NNRQPYAVSELAGHQTSAESWGTGR	AVARI	3		906.09945	2715.27495	0.000451244	12	N	46	71
Q9D8E6	Parental	NRQPY	AVSELAGHQTSAESWGTGR	AVARI	2		972.4644569	1942.913314	0.000451244	9	N	52	71
Q9D8E6	Parental	NRQPY	AVSELAGHQTSAESWGTGR	AVARI	3		648.6455712	1942.913314	0.0007646	5	N	52	71
Q9D8E6	Parental	RKNNR	QPYAVSELAGHQTSAESWGTGR	AVARI	2		1166.551792	2331.087984	0.000451244	1	N	49	71
Q9D8E6	Parental	RKNNR	QPYAVSELAGHQTSAESWGTGR	AVARI	3		778.037128	2331.087984	0.000451244	15	N	49	71
Q9D8E6	Parental	SKGHR	IEEVPELPLVVEDKVEGY	KKTKE	2		1029.0386	2056.061601	0.000451244	7	N	143	161
Q9D8E6	Parental	GHVGR	FCIWTESAFR	KLDEL	2	C2:+57.021	658.808538	1315.601476	0.000979378	2	N	248	258
Q9D8N0	Exosome	QTLVR	EYFSWEGTFQHVGK	AVNQG	2		857.8971587	1713.778717	0.000823681	4	N	414	428
Q9D8N0	Exosome	QTLVR	EYFSWEGTFQHVGK	AVNQG	3		572.2673725	1713.778717	0.001162105	8	N	414	428
Q9D8N0	Exosome	PNTNR	WFLTCINQPQFR	AILGE	2	C5:+57.021	805.4011257	1608.786651	0.000451244	26	N	189	201
Q9D8N0	Exosome	FPAGK	VPAFEGDDGFCVFESNAIAYYVSNEELR	GSTPE	3	C11:+57.021	1066.817243	3197.42833	0.000451244	35	N	57	85
Q9D8N0	Exosome	LVGER	VTLADITVVCTLLWLYK	QVLEP	2	C10:+57.021	1004.563303	2007.111006	0.000451244	6	N	156	173
Q9D8N0	Exosome	SYTWR	KLDPGSEETQTLVR	EYFSW	2		786.9155485	1571.815497	0.000451244	5	N	400	414
Q9D8N0	Exosome	SYTWR	KLDPGSEETQTLVR	EYFSW	3		524.946299	1571.815497	0.000451244	29	N	400	414
Q9D8N0	Exosome	WRAFK	ALIAAQYSGAQVR	VLSAP	2		674.3731224	1346.730645	0.000451244	10	N	17	30
Q9D8N0	Exosome	EEVKR	ILGLLDTHLK	TRTFL	2		561.8482205	1121.680841	0.000979378	4	N	137	147
Q9D8N0	Exosome	VWVFR	GQELAFPLSPDWQVDYESYTWR	KLDPG	2		1344.12479	2686.23398	0.000451244	36	N	378	400
Q9D8N0	Exosome	VWVFR	GQELAFPLSPDWQVDYESYTWR	KLDPG	3		896.4191266	2686.23398	0.000870037	3	N	378	400
Q9D8N0	Exosome	RKEEK	KAAAPAPEEEMDECEQALAAEPK	AKDPF	3	M11:+15.995,C14:+57.021	834.3775968	2500.109391	0.000451244	28	N	252	275
Q9D8N0	Exosome	NEELR	GSTPEAAAQVVQWVSF	ADSDI	2		838.9180912	1675.820582	0.000451244	8	N	85	101
Q9D8N0	Exosome	SVILF	GTNNSSSISGVWVFR	GQELA	2		805.9002327	1609.784865	0.000451244	2	N	363	378
Q9D8N0	Exosome	YTWRK	LDPGSEETQTLVR	EYFSW	2		722.8680669	1443.720534	0.000823681	1	N	401	414
Q9D8N0	Parental	QTLVR	EYFSWEGTFQHVGK	AVNQG	3		572.2673725	1713.778717	0.000622848	10	N	414	428
Q9D8N0	Parental	PNTNR	WFLTCINQPQFR	AILGE	2	C5:+57.021	805.4011257	1608.786651	0.000451244	27	N	189	201
Q9D8N0	Parental	FPAGK	VPAFEGDDGFCVFESNAIAYYVSNEELR	GSTPE	3	C11:+57.021	1066.817243	3197.42833	0.000451244	41	N	57	85
Q9D8N0	Parental	LVGER	VTLADITVVCTLLWLYK	QVLEP	2	C10:+57.021	1004.563303	2007.111006	0.000451244	15	N	156	173
Q9D8N0	Parental	LVGER	VTLADITVVCTLLWLYK	QVLEP	3	C10:+57.021	670.0448019	2007.111006	0.001162105	1	N	156	173
Q9D8N0	Parental	SYTWR	KLDPGSEETQTLVR	EYFSW	2		786.9155485	1571.815497	0.000851441	1	N	400	414
Q9D8N0	Parental	SYTWR	KLDPGSEETQTLVR	EYFSW	3		524.946299	1571.815497	0.000451244	12	N	400	414
Q9D8N0	Parental	WRAFK	ALIAAQYSGAQVR	VLSAP	2		674.3731224	1346.730645	0.000451244	5	N	17	30
Q9D8N0	Parental	EEVKR	ILGLLDTHLK	TRTFL	2		561.8482205	1121.680841	0.000979378	2	N	137	147
Q9D8N0	Parental	VWVFR	GQELAFPLSPDWQVDYESYTWR	KLDPG	2		1344.12479	2686.23398	0.000451244	19	N	378	400
Q9D8N0	Parental	VWVFR	GQELAFPLSPDWQVDYESYTWR	KLDPG	3		896.4191266	2686.23398	0.000451244	8	N	378	400
Q9D8N0	Parental	NEELR	GSTPEAAAQVVQWVSF	ADSDI	2		838.9180912	1675.820582	0.000451244	7	N	85	101
Q9D8N0	Parental	SVILF	GTNNSSSISGVWVFR	GQELA	2		805.9002327	1609.784865	0.001463592	1	N	363	378
Q9D8N2	Exosome	GKLHK	EIGQLIVQSAEDPEKSDSQVIQDIALK	TKEIF	3		985.1841864	2952.529159	0.000451244	7	N	277	304
Q9D8N2	Exosome	GLIEK	DSNGEALWVWCYPSTTASLR	NLLLR	2	C11:+57.021	1157.034158	2312.052716	0.001763695	1	N	20	40
Q9D8N2	Parental	GKLHK	EIGQLIVQSAEDPEKSDSQVIQDIALK	TKEIF	3		985.1841864	2952.529159	0.000451244	1	N	277	304
Q9D8T2	Parental	CSIGK	QLSLLSDGIDEEELIEAADFQGLYAEVK	ACSSE	3		1032.515602	3094.523405	0.000451244	5	N	269	297
Q9D8T2	Parental	FWKPR	YSCVNLSIKDILEPSAPEPEPECFGSFK	VSDVV	3	C3:+57.021,C23:+57.021	1071.842358	3212.503675	0.000637154	1	N	54	82
Q9D8T2	Parental	NLSIK	DILEPSAPEPEPECFGSFK	VSDVV	2	C14:+57.021	1074.993636	2147.971671	0.000662267	1	N	63	82
Q9D8W5	Exosome	AKEGR	LQEVIETLLSLEK	QTRTA	2		757.9379609	1513.860322	0.000451244	22	N	39	52
Q9D8W5	Exosome	QQALK	SVVLYVILAPFDNEQSDLVHR	ISSDK	3		805.4291858	2413.264158	0.000451244	13	N	268	289
Q9D8W5	Exosome	CKHYR	AIYDTPCIQAESDKWQQALK	SVVLY	3	C7:+57.021	789.0549769	2364.141531	0.000451244	1	N	248	268
Q9D8W5	Parental	AKEGR	LQEVIETLLSLEK	QTRTA	2		757.9379609	1513.860322	0.000451244	17	N	39	52
Q9D8W5	Parental	QQALK	SVVLYVILAPFDNEQSDLVHR	ISSDK	3		805.4291858	2413.264158	0.000451244	2	N	268	289
Q9D8Y0	Parental	KLLRR	ADLNQGIGEPQSPSR	RVFNP	2		784.8873223	1567.759045	0.000451244	19	N	62	77
Q9D8Y0	Parental	AKLLR	RADLNQGIGEPQSPSR	RVFNP	2		862.9378779	1723.860156	0.002663018	1	N	61	77

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9D8Y7	Exosome	LVECR	DILLELVEHHLTPK	SHDRI	3		552.9826845	1655.924654	0.000823681	8	N	124	138
Q9D8Y7	Exosome	HDRIR	HVFDHYSDPDLLAALYGPDFTQHLGK	ICDGL	4		739.8625887	2955.419155	0.000451244	7	N	144	170
Q9D8Y7	Exosome	KMAGR	SVAHLFIDETSSEVLDELYR	VSKEY	3		775.0537846	2322.137954	0.000451244	5	N	24	44
Q9D8Y7	Parental	LVECR	DILLELVEHHLTPK	SHDRI	3		552.9826845	1655.924654	0.001395409	5	N	124	138
Q9D8Y7	Parental	HDRIR	HVFDHYSDPDLLAALYGPDFTQHLGK	ICDGL	3		986.1475183	2955.419155	0.000823681	2	N	144	170
Q9D906	Exosome	LKKPK	QQGAGDLCPSHLVAPADLGSSLFANIPGYK	LGCYF	3	C8:+57.021	1028.513718	3082.517755	0.000451244	13	N	512	542
Q9D906	Exosome	IPGYK	LGCYFCNDVVAPGDSTR	DRTLD	2	C3:+57.021,C6:+57.021	965.9248017	1929.834003	0.000637154	4	N	542	559
Q9D906	Exosome	DDLCR	AEGVTALPYFLFK	YDDDT	2		728.3982746	1454.780949	0.000735798	9	N	185	198
Q9D906	Exosome	GQRTK	ITVGVYDPCNLAQYPGWPLR	NFLVL	2	C9:+57.021	1160.083454	2318.151307	0.000451244	4	N	222	242
Q9D906	Exosome	GFLSR	FDNVLPVSLAFDK	CTACS	2		732.8908137	1463.766027	0.000451244	1	N	627	640
Q9D906	Exosome	TADKK	LLLEQSANEIWEAIK	SGAAL	2		878.9781488	1755.940698	0.000451244	3	N	98	113
Q9D906	Parental	LKKPK	QQGAGDLCPSHLVAPADLGSSLFANIPGYK	LGCYF	3	C8:+57.021	1028.513718	3082.517755	0.000451244	12	N	512	542
Q9D906	Parental	IPGYK	LGCYFCNDVVAPGDSTR	DRTLD	2	C3:+57.021,C6:+57.021	965.9248017	1929.834003	0.001463592	1	N	542	559
Q9D906	Parental	GQRTK	ITVGVYDPCNLAQYPGWPLR	NFLVL	2	C9:+57.021	1160.083454	2318.151307	0.000451244	5	N	222	242
Q9D906	Parental	GFLSR	FDNVLPVSLAFDK	CTACS	2		732.8908137	1463.766027	0.001763695	1	N	627	640
Q9D906	Parental	PGLAK	LQFAPFNSALDVGFWHELTQK	KLNEY	3		816.7502593	2447.227378	0.002519933	1	N	8	29
Q9D964	Exosome	HPLPK	DCPVSSYNEWDPLEEVIVGR	AENAC	2	C2:+57.021	1182.544555	2363.073511	0.000451244	11	N	62	82
Q9D964	Exosome	KVNIR	NANSLGGGFHCWTCDVR	RRGTL	2	C11:+57.021,C14:+57.021	975.920385	1949.82517	0.000823681	1	N	396	413
Q9D964	Exosome	AAQGK	FVTTEFEPCFDAADFIR	AGRDI	2	C9:+57.021	1032.972506	2063.929412	0.002374549	1	N	243	260
Q9D964	Parental	HPLPK	DCPVSSYNEWDPLEEVIVGR	AENAC	2	C2:+57.021	1182.544555	2363.073511	0.000451244	15	N	62	82
Q9D964	Parental	KVNIR	NANSLGGGFHCWTCDVR	RRGTL	2	C11:+57.021,C14:+57.021	975.920385	1949.82517	0.000698008	1	N	396	413
Q9DAR7	Exosome	AEADR	IVFENPDPSDGFVLIPDLK	WNQQQ	2		1058.054585	2114.09357	0.000451244	6	N	187	206
Q9DAR7	Exosome	TFALR	TDDPLLQLLQK	AQQER	2		642.3644317	1282.713263	0.000451244	2	N	321	332
Q9DAR7	Exosome	VILEK	TPFQVEHVAQLLTGSPELK	LQFSN	2		1047.565651	2093.115702	0.000451244	1	N	85	104
Q9DAR7	Exosome	VILEK	TPFQVEHVAQLLTGSPELK	LQFSN	3		698.713034	2093.115702	0.000451244	5	N	85	104
Q9DAR7	Exosome	SGVER	AHLLAQVIENLECDPK	HYQQR	3	C13:+57.021	617.3211058	1848.939917	0.000451244	7	N	293	309
Q9DAR7	Parental	AEADR	IVFENPDPSDGFVLIPDLK	WNQQQ	2		1058.054585	2114.09357	0.000451244	3	N	187	206
Q9DAR7	Parental	TFALR	TDDPLLQLLQK	AQQER	2		642.3644317	1282.713263	0.000637154	10	N	321	332
Q9DAR7	Parental	VILEK	TPFQVEHVAQLLTGSPELK	LQFSN	2		1047.565651	2093.115702	0.000451244	4	N	85	104
Q9DAR7	Parental	VILEK	TPFQVEHVAQLLTGSPELK	LQFSN	3		698.713034	2093.115702	0.000823681	2	N	85	104
Q9DAR7	Parental	IPDLK	WNQQQLDDLYLIAICHR	RGIRS	3	C15:+57.021	729.3655971	2185.073391	0.000823681	5	N	206	223
Q9DAU1	Parental	SKQRK	ELGGLGEDANAEEEEGVQK	ASPLP	2		987.4508778	1972.886156	0.000451244	14	N	245	264
Q9DAU1	Parental	EDWYR	NHQEEDLTEFLCANHVLK	GKDTS	3	C12:+57.021	733.0166336	2196.026501	0.000823681	1	N	182	200
Q9DB05	Exosome	VDVEK	AIAHYEQSADYYKGEESNSSANK	CLLKV	3		854.7180123	2561.130637	0.000451244	10	N	140	163
Q9DB05	Exosome	VDVEK	AIAHYEQSADYYKGEESNSSANK	CLLKV	4		641.2904592	2561.130637	0.000451244	8	N	140	163
Q9DB05	Exosome	ERKVK	NSQSFFSGLFGGSSK	IEEAC	2		775.3682341	1548.720868	0.000451244	4	N	22	37
Q9DB05	Exosome	KLMKK	LLEAHEEQNVDSYTEAVKEYDSISR	LDQWL	3		975.796991	2924.367573	0.000823681	1	N	246	271
Q9DB05	Exosome	KCLLK	VAGYAAQLEQYQK	AIDIY	2		734.8756949	1467.73579	0.001229886	3	N	167	180
Q9DB05	Exosome	QLQSK	HDAATCFVDAGNAFK	KADPQ	2	C6:+57.021	812.3649371	1622.714274	0.000451244	2	N	78	93
Q9DB05	Parental	VDVEK	AIAHYEQSADYYKGEESNSSANK	CLLKV	3		854.7180123	2561.130637	0.000451244	12	N	140	163
Q9DB05	Parental	VDVEK	AIAHYEQSADYYKGEESNSSANK	CLLKV	4		641.2904592	2561.130637	0.000451244	18	N	140	163
Q9DB05	Parental	ERKVK	NSQSFFSGLFGGSSK	IEEAC	2		775.3682341	1548.720868	0.000451244	9	N	22	37
Q9DB05	Parental	KLMKK	LLEAHEEQNVDSYTEAVKEYDSISR	LDQWL	3		975.796991	2924.367573	0.000622848	4	N	246	271
Q9DB05	Parental	KLMKK	LLEAHEEQNVDSYTEAVKEYDSISR	LDQWL	4		732.0996932	2924.367573	0.000823681	1	N	246	271
Q9DB05	Parental	LAVQK	YEELFPAFSDSR	ECKLM	2		730.8387781	1459.661956	0.000823681	10	N	227	239
Q9DB15	Parental	EYPPK	IQQLVQDIASLTLLEISDLNELLKK	TLKIQ	3		946.5465079	2836.616124	0.000451244	16	N	64	89
Q9DB15	Parental	EYPPK	IQQLVQDIASLTLLEISDLNELLK	KTLKI	3		903.8481868	2708.52116	0.000451244	8	N	64	88
Q9DB20	Exosome	MSVHR	GEVPCTVTTASPLDDAVLSELK	TVLKS	2	C5:+57.021	1151.578064	2301.140528	0.000451244	8	N	136	158
Q9DB20	Parental	MSVHR	GEVPCTVTTASPLDDAVLSELKTVLK	SFLSP	3	C5:+57.021	915.1530158	2742.435648	0.000451244	7	N	136	162
Q9DB20	Parental	MSVHR	GEVPCTVTTASPLDDAVLSELK	TVLKS	2	C5:+57.021	1151.578064	2301.140528	0.000451244	37	N	136	158
Q9DB20	Parental	MSVHR	GEVPCTVTTASPLDDAVLSELK	TVLKS	3	C5:+57.021	768.0546426	2301.140528	0.000451244	6	N	136	158
Q9DB77	Parental	APKVK	TSAAPGGVPLQPQDLEFTKLPNGLVIASLENYAPLSR	IGLFV	3		1288.690101	3863.046902	0.000622848	8	N	23	60
Q9DB77	Parental	DVSAF	NASYSDSGLFGIYTISQAAAAGEVINAAYNQVK	AVAQG	3		1131.891954	3392.652462	0.000451244	14	N	326	359
Q9DB77	Parental	FNASY	SDSGLFGIYTISQAAAAGEVINAAYNQVK	AVAQG	3		986.833488	2957.477064	0.000698008	10	N	330	359
Q9DB77	Parental	KAGSR	YEDSNNLGTSHLLR	LASSL	3		540.2660316	1617.774695	0.001871652	1	N	70	84
Q9DB77	Parental	YNQVK	AVAQGNLSSADVQAAK	NKLKA	2		765.4000656	1528.784531	0.000622848	35	N	359	375
Q9DBC7	Exosome	EDGQK	IVVQGEPGDEFFIILEGTAAVLQR	RSENE	2		1301.200301	2600.385001	0.000451244	8	N	281	305
Q9DBC7	Exosome	DKWER	LTVADALEPVQFEDGQK	IVVQG	2		930.4734276	1858.931255	0.0025889	1	N	264	281
Q9DBC7	Parental	EDGQK	IVVQGEPGDEFFIILEGTAAVLQR	RSENE	2		1301.200301	2600.385001	0.000451244	3	N	281	305
Q9DBC7	Parental	EDGQK	IVVQGEPGDEFFIILEGTAAVLQR	RSENE	3		867.8028004	2600.385001	0.000823681	3	N	281	305
Q9DBC7	Parental	DKWER	LTVADALEPVQFEDGQK	IVVQG	2		930.4734276	1858.931255	0.000451244	4	N	264	281
Q9DBC7	Parental	EFLSK	VSILESLDKWER	LTVAD	3		492.2687134	1473.78274	0.000637154	1	N	252	264
Q9DBG3	Exosome	DIMIR	LASQANIAQVLAELKEYATEVDVDFVR	KAVRA	3		998.1929048	2991.555314	0.000451244	40	Y	344	371
Q9DBG3	Exosome	EYAER	IDNADELLESFLEGFHDESTQVQLTLLTAIVK	LFLKK	3		1196.949358	3587.824673	0.000451244	15	N	458	490
Q9DBG3	Exosome	EYAER	IDNADELLESFLEGFHDESTQVQLTLLTAIVK	LFLKK	4		897.9639682	3587.824673	0.000451244	3	N	458	490

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DBG3	Exosome	MLLKK	LAPPLVTLLSGEPEVQYVALR	NINLI	2		1133.146808	2264.278017	0.000451244	41	N	283	304
Q9DBG3	Exosome	MLLKK	LAPPLVTLLSGEPEVQYVALR	NINLI	3		755.7671389	2264.278017	0.000451244	29	N	283	304
Q9DBG3	Exosome	LIQTK	VNYVVQEAIVVIR	DIFRK	2		751.4410051	1500.86641	0.000451244	6	N	402	415
Q9DBG3	Exosome	DIMIR	LASQANIAQVLAELK	EYATE	2		784.9544767	1567.893353	0.000451244	33	Y	344	359
Q9DBG3	Exosome	DIMIR	LASQANIAQVLAELK	EYATE	3		523.6389178	1567.893353	0.000662267	6	Y	344	359
Q9DBG3	Exosome	QNINK	LLTALNECTEWGQIFILDCLSNYNPK	DDREA	3	C8:+57.021,C19:+57.021	1038.175672	3111.503616	0.000451244	20	N	206	232
Q9DBG3	Exosome	QSAER	CVSTLLDLIQTK	VNYVV	2	C1:+39.994	687.3709428	1372.726286	0.000851441	3	Y	390	402
Q9DBG3	Exosome	QSAER	CVSTLLDLIQTK	VNYVV	2	C1:+57.021	695.8844428	1389.753286	0.000451244	28	Y	390	402
Q9DBG3	Exosome	QSAER	CVSTLLDLIQTK	VNYVV	2	[0:-17.027,C1:+57.021	687.3709428	1372.726286	0.00091018	21	Y	390	402
Q9DBG3	Exosome	DIFRK	YPNKYESIIATLCENLDSLDEPDAR	AAMIW	3	C13:+57.021	976.1310509	2925.369753	0.000451244	11	N	420	445
Q9DBG3	Exosome	NSFVK	DCEDPNPLIR	ALAVR	2	C2:+57.021	614.7852599	1227.55492	0.000622848	2	Y	93	103
Q9DBG3	Exosome	SLKCR	APEVSQYIYQVYDSILKN	-	2		1065.541842	2129.068083	0.000622848	2	N	919	937
Q9DBG3	Exosome	KLFLK	KPSETQELVQQVLSLATQDSDNPDLRDR	GYIYW	4		796.4040778	3181.585111	0.000451244	8	N	494	522
Q9DBG3	Exosome	NMLLK	KLAPPLVTLLSGEPEVQYVALR	NINLI	3		798.4654599	2392.37298	0.000451244	9	N	282	304
Q9DBG3	Exosome	KLFLK	KPSETQELVQQVLSLATQDSDNPDLR	DRGYI	3		971.1601523	2910.457057	0.002374549	1	N	494	520
Q9DBG3	Exosome	YQSLK	LTNGIWILAELR	IQPGN	2		699.9093408	1397.803082	0.000979378	5	N	892	904
Q9DBG3	Exosome	QNINK	LLTALNECTEWGQIFILDCLSNYNPKDDR	EAQSI	3	C8:+57.021,C19:+57.021	1166.894004	3497.658613	0.001229886	2	N	206	235
Q9DBG3	Exosome	NPMVV	ANAVAALSEISESHPNSNLLDLNPQNINK	LLTAL	3		1025.190334	3072.547603	0.001229886	3	N	177	206
Q9DBG3	Exosome	LAELK	EYATEVDVDFVR	KAVRA	2		721.8440605	1441.672521	0.001329271	1	Y	359	371
Q9DBG3	Parental	GKMER	QVFLATWKDIPNENELQFQIK	ECHLN	3		854.4519905	2560.332572	0.0025889	1	N	834	855
Q9DBG3	Parental	DIMIR	LASQANIAQVLAELKEYATEVDVDFVR	KAVRA	3		998.1929048	2991.555314	0.000451244	39	Y	344	371
Q9DBG3	Parental	EYAER	IDNADELLESFLEGFHDESTQVQLTLLTAIVK	LFLKK	3		1196.949358	3587.824673	0.000451244	21	N	458	490
Q9DBG3	Parental	EYAER	IDNADELLESFLEGFHDESTQVQLTLLTAIVK	LFLKK	4		897.9639682	3587.824673	0.000451244	5	N	458	490
Q9DBG3	Parental	MLLKK	LAPPLVTLLSGEPEVQYVALR	NINLI	2		1133.146808	2264.278017	0.000451244	18	N	283	304
Q9DBG3	Parental	MLLKK	LAPPLVTLLSGEPEVQYVALR	NINLI	3		755.7671389	2264.278017	0.000451244	13	N	283	304
Q9DBG3	Parental	DIMIR	LASQANIAQVLAELK	EYATE	2		784.9544767	1567.893353	0.000451244	5	Y	344	359
Q9DBG3	Parental	QNINK	LLTALNECTEWGQIFILDCLSNYNPK	DDREA	3	C8:+57.021,C19:+57.021	1038.175672	3111.503616	0.000451244	10	N	206	232
Q9DBG3	Parental	QSAER	CVSTLLDLIQTK	VNYVV	2	C1:+57.021	695.8844428	1389.753286	0.000451244	13	Y	390	402
Q9DBG3	Parental	QSAER	CVSTLLDLIQTK	VNYVV	2	[0:-17.027,C1:+57.021	687.3709428	1372.726286	0.000735798	12	Y	390	402
Q9DBG3	Parental	DIFRK	YPNKYESIIATLCENLDSLDEPDAR	AAMIW	3	C13:+57.021	976.1310509	2925.369753	0.000451244	3	N	420	445
Q9DBG3	Parental	SLKCR	APEVSQYIYQVYDSILKN	-	3		710.6971611	2129.068083	0.001463592	1	N	919	937
Q9DBG3	Parental	KLFLK	KPSETQELVQQVLSLATQDSDNPDLRDR	GYIYW	4		796.4040778	3181.585111	0.000451244	1	N	494	522
Q9DBG3	Parental	KLFLK	KPSETQELVQQVLSLATQDSDNPDLR	DRGYI	3		971.1601523	2910.457057	0.000851441	3	N	494	520
Q9DBG3	Parental	YQSLK	LTNGIWILAELR	IQPGN	2		699.9093408	1397.803082	0.000823681	9	N	892	904
Q9DBG3	Parental	QVAVK	NNIDVFYFSCLIPLNVLFVEDGK	MERQV	3	C10:+57.021	906.1282534	2715.36136	0.002884417	1	N	808	831
Q9DBG5	Exosome	AQQAR	SQVNDLQATFSGIHSFQDLSAGVLAQTR	ERIAR	3		997.5042533	2989.48936	0.000451244	4	N	367	395
Q9DBG5	Parental	AQQAR	SQVNDLQATFSGIHSFQDLSAGVLAQTR	ERIAR	3		997.5042533	2989.48936	0.000451244	25	N	367	395
Q9DBG5	Parental	LSMFR	DITQQLQSMCVALGASIQGLPSHVR	EQAQQ	3	C10:+57.021	903.7989133	2708.37334	0.000451244	8	N	335	360
Q9DBG5	Parental	EKGVK	TLTTAAVSTAQPILSK	LEPQI	2		801.4595919	1600.903584	0.000451244	22	N	68	84
Q9DBG5	Parental	TVATR	VTGAVDVTLGAVQNSVDKTK	SAMTS	3		668.0325437	2001.074231	0.000823681	4	N	150	170
Q9DBG5	Parental	EKGVK	TLTTAAVSTAQPILSKLEPQIATASEYAHR	GLDRL	3		1056.902013	3167.68264	0.000451244	3	N	68	98
Q9DBG5	Parental	EKGVK	TLTTAAVSTAQPILSKLEPQIATASEYAHR	GLDRL	4		792.9284601	3167.68264	0.001943752	1	N	68	98
Q9DBG5	Parental	RGLDR	LQESLPILQQPTEK	VLADT	2		812.4517668	1622.887934	0.000823681	3	N	102	116
Q9DBG5	Parental	IARAR	EALDNTVEYVAQNTPAMWLVGPFAPGITEKTPEGK	-	3		1258.629742	3772.865827	0.002884417	1	N	402	437
Q9DBG5	Parental	PILSK	LEPQIATASEYAHR	GLDRL	2		793.4026082	1584.789616	0.000823681	3	N	84	98
Q9DBG6	Exosome	IFSKK	NFESLSEAFSVASAAAALSQNR	YHVPV	2		1135.556543	2269.097486	0.000451244	1	N	244	266
Q9DBG6	Exosome	IFSKK	NFESLSEAFSVASAAAALSQNR	YHVPV	3		757.3736287	2269.097486	0.000823681	1	N	244	266
Q9DBG6	Exosome	TVLQK	TPFSLVGNVFELNFK	NVKLS	2		856.4568522	1710.898104	0.000662267	2	N	322	337
Q9DBG6	Exosome	VERLK	ASLDRPFTDLESAFYSIVGLSSLGVQVPDVKK	ACTFI	4		860.4598587	3437.808235	0.000451244	3	N	38	70
Q9DBG6	Exosome	ALTAR	LGKEETVLATVQALQTASHLSQQADLR	NIVEE	3		969.8565155	2906.546147	0.001352548	2	N	151	178
Q9DBG6	Exosome	LSQNR	YHVPVVVVPEGSTSDTQEQAILR	LQVSN	3		842.1067714	2523.296914	0.000451244	2	N	266	289
Q9DBG6	Exosome	TIFSK	KNFESLSEAFSVASAAAALSQNR	YHVPV	3		800.0719497	2397.192449	0.000622848	5	N	243	266
Q9DBG6	Exosome	QADLR	NIVEEIEDLVAR	LDELG	2		700.3755278	1398.735456	0.002884417	1	N	178	190
Q9DBG6	Parental	IFSKK	NFESLSEAFSVASAAAALSQNR	YHVPV	2		1135.556543	2269.097486	0.000451244	36	N	244	266
Q9DBG6	Parental	IFSKK	NFESLSEAFSVASAAAALSQNR	YHVPV	3		757.3736287	2269.097486	0.000451244	23	N	244	266
Q9DBG6	Parental	TVLQK	TPFSLVGNVFELNFK	NVKLS	2		856.4568522	1710.898104	0.000451244	21	N	322	337
Q9DBG6	Parental	VERLK	ASLDRPFTDLESAFYSIVGLSSLGVQVPDVKK	ACTFI	3		1146.943878	3437.808235	0.000451244	8	N	38	70
Q9DBG6	Parental	VERLK	ASLDRPFTDLESAFYSIVGLSSLGVQVPDVKK	ACTFI	4		860.4598587	3437.808235	0.000451244	20	N	38	70
Q9DBG6	Parental	ALTAR	LGKEETVLATVQALQTASHLSQQADLR	NIVEE	3		969.8565155	2906.546147	0.000451244	31	N	151	178
Q9DBG6	Parental	ALTAR	LGKEETVLATVQALQTASHLSQQADLR	NIVEE	4		727.6443366	2906.546147	0.000451244	10	N	151	178
Q9DBG6	Parental	LSQNR	YHVPVVVVPEGSTSDTQEQAILR	LQVSN	2		1262.656257	2523.296914	0.001463592	3	N	266	289
Q9DBG6	Parental	NFALF	FQLVDVNTGAELTPHQTFVR	LHNQK	2		1136.590189	2271.164778	0.000451244	2	N	417	437
Q9DBG6	Parental	VERLK	ASLDRPFTDLESAFYSIVGLSSLGVQVPDVK	KACTF	3		1104.245557	3309.713272	0.000622848	15	N	38	69
Q9DBG6	Parental	QAILR	LQVSNVLSQPLAQAAVK	LEHAK	2		883.5126901	1765.00978	0.000451244	6	N	289	306
Q9DBG6	Parental	TIFSK	KNFESLSEAFSVASAAAALSQNR	YHVPV	3		800.0719497	2397.192449	0.000451244	8	N	243	266

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DBG6	Parental	QADLR	NIVEEIEDLVAR	LDELG	2		700.3755278	1398.735456	0.000451244	24	N	178	190
Q9DBG6	Parental	LHNQK	TGQEVVFVAEPDNK	NVYKF	2		766.883717	1531.751834	0.000451244	15	N	442	456
Q9DBG6	Parental	ELRVK	ISTEVGITNVDLSTVDKDQSIAPK	TTRVT	2		1265.666488	2529.317375	0.000451244	2	N	368	392
Q9DBG6	Parental	DLVAR	LDELGGVYLQFEEGLELTALFVAATYK	LMDHV	3		997.1868682	2988.537205	0.000451244	5	N	190	217
Q9DBG6	Parental	SNETK	ELLLAAVSEDSPIAQIY	HAVAA	2		916.4885464	1830.961493	0.002374549	1	N	109	126
Q9DBJ1	Exosome	SKDRR	YADLTEDQLPSCESLKDTIAR	ALPFW	2	C12:+57.021	1213.081502	2424.147404	0.000451244	42	N	141	162
Q9DBJ1	Exosome	SKDRR	YADLTEDQLPSCESLKDTIAR	ALPFW	3	C12:+57.021	809.0569347	2424.147404	0.000451244	2	N	141	162
Q9DBJ1	Exosome	DTIAR	ALPFWNEEIVPQIK	EGKRV	2		842.4593949	1682.90319	0.000451244	37	N	162	176
Q9DBJ1	Exosome	DTIAR	ALPFWNEEIVPQIK	EGKRV	3		561.9755299	1682.90319	0.001264573	1	N	162	176
Q9DBJ1	Exosome	RLNER	HYGGLTGLNKAETAAK	HGEAQ	3		544.2902886	1629.847466	0.000451244	3	N	90	106
Q9DBJ1	Exosome	NLENR	FSGWYDADLSPAGHEEAK	RGGQA	2		990.4426588	1978.869718	0.001162105	3	N	21	39
Q9DBJ1	Exosome	NLENR	FSGWYDADLSPAGHEEAK	RGGQA	3		660.6310392	1978.869718	0.000451244	12	N	21	39
Q9DBJ1	Exosome	GQALR	DAGYEFDICFTSVQKR	AIRTL	3	C9:+57.021	645.9687321	1934.882796	0.001654178	4	N	46	62
Q9DBJ1	Exosome	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	2		1068.493214	2134.970829	0.000451244	14	N	21	40
Q9DBJ1	Exosome	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	3		712.6647429	2134.970829	0.000451244	10	N	21	40
Q9DBJ1	Exosome	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	4		534.7505072	2134.970829	0.000451244	32	N	21	40
Q9DBJ1	Exosome	IARAL	PFWNEEIVPQIK	EGKRV	2		750.3988059	1498.782012	0.000451244	4	N	164	176
Q9DBJ1	Exosome	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	2		1078.58279	2155.14998	0.000451244	8	N	65	83
Q9DBJ1	Exosome	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	3		719.3911267	2155.14998	0.000622848	3	N	65	83
Q9DBJ1	Exosome	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	2	M12:+15.995	1086.58029	2171.14498	0.000451244	8	N	65	83
Q9DBJ1	Exosome	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	3	M12:+15.995	724.7227934	2171.14498	0.001162105	3	N	65	83
Q9DBJ1	Exosome	GQALR	DAGYEFDICFTSVQK	RAIRT	2	C9:+57.021	890.3986426	1778.781685	0.000451244	31	N	46	61
Q9DBJ1	Exosome	SKDRR	YADLTEDQLPSCESLK	DTIAR	2	C12:+57.021	934.9330467	1867.850493	0.000451244	13	N	141	157
Q9DBJ1	Parental	SKDRR	YADLTEDQLPSCESLKDTIAR	ALPFW	2	C12:+57.021	1213.081502	2424.147404	0.000451244	37	N	141	162
Q9DBJ1	Parental	SKDRR	YADLTEDQLPSCESLKDTIAR	ALPFW	3	C12:+57.021	809.0569347	2424.147404	0.000451244	11	N	141	162
Q9DBJ1	Parental	DTIAR	ALPFWNEEIVPQIK	EGKRV	2		842.4593949	1682.90319	0.000451244	14	N	162	176
Q9DBJ1	Parental	DTIAR	ALPFWNEEIVPQIK	EGKRV	3		561.9755299	1682.90319	0.000451244	2	N	162	176
Q9DBJ1	Parental	RLNER	HYGGLTGLNKAETAAK	HGEAQ	3		544.2902886	1629.847466	0.000451244	4	N	90	106
Q9DBJ1	Parental	NLENR	FSGWYDADLSPAGHEEAK	RGGQA	2		990.4426588	1978.869718	0.000451244	7	N	21	39
Q9DBJ1	Parental	NLENR	FSGWYDADLSPAGHEEAK	RGGQA	3		660.6310392	1978.869718	0.000451244	15	N	21	39
Q9DBJ1	Parental	GQALR	DAGYEFDICFTSVQKR	AIRTL	2	C9:+57.021	968.4491982	1934.882796	0.000451244	4	N	46	62
Q9DBJ1	Parental	GQALR	DAGYEFDICFTSVQKR	AIRTL	3	C9:+57.021	645.9687321	1934.882796	0.000622848	7	N	46	62
Q9DBJ1	Parental	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	2		1068.493214	2134.970829	0.000451244	2	N	21	40
Q9DBJ1	Parental	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	3		712.6647429	2134.970829	0.000451244	5	N	21	40
Q9DBJ1	Parental	NLENR	FSGWYDADLSPAGHEEAKR	GGQAL	4		534.7505072	2134.970829	0.000451244	16	N	21	40
Q9DBJ1	Parental	IARAL	PFWNEEIVPQIK	EGKRV	2		750.3988059	1498.782012	0.000451244	11	N	164	176
Q9DBJ1	Parental	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	2		1078.58279	2155.14998	0.000451244	7	N	65	83
Q9DBJ1	Parental	KRAIR	TLWTVLDAIDQMWLPVVR	TWRLN	3		719.3911267	2155.14998	0.000451244	6	N	65	83
Q9DBJ1	Parental	GQALR	DAGYEFDICFTSVQK	RAIRT	2	C9:+57.021	890.3986426	1778.781685	0.000451244	6	N	46	61
Q9DBJ1	Parental	SKDRR	YADLTEDQLPSCESLK	DTIAR	2	C12:+57.021	934.9330467	1867.850493	0.001943752	5	N	141	157
Q9DBK7	Exosome	QLHGR	LPKPWDPDDAETVVELAQDLEPLKGTEEESLDEALLR	TIALS	3		1387.697426	4160.068879	0.000451244	1	N	297	334
Q9DBK7	Exosome	QLHGR	LPKPWDPDDAETVVELAQDLEPLKGTEEESLDEALLR	TIALS	4		1041.02502	4160.068879	0.000451244	18	N	297	334
Q9DBK7	Exosome	PRNCR	YDGQIAVFGTDLQEK	LSDQH	2		842.4153813	1682.815163	0.000622848	1	N	401	416
Q9DBK7	Exosome	NPDLR	ATPYTCPLDPTTEDIYDDSFFSR	VNGVV	2	C6:+57.021	1356.094806	2710.174013	0.001162105	11	N	495	518
Q9DBK7	Exosome	IQEAK	VLLCGLQGLGAEVAK	NLVLT	2	C4:+57.021	764.4320915	1526.848583	0.000451244	3	N	25	40
Q9DBK7	Parental	QLHGR	LPKPWDPDDAETVVELAQDLEPLKGTEEESLDEALLR	TIALS	4		1041.02502	4160.068879	0.000451244	2	N	297	334
Q9DBL1	Exosome	FRDAK	IGTIYEGASNIQLNTIAK	HIDAE	2		953.5181695	1905.020739	0.000451244	2	N	408	426
Q9DBL1	Exosome	QFGKR	IFDFQGLQHQVAQVATQLEATR	LLTYN	3		834.1034728	2499.287018	0.000451244	8	N	325	347
Q9DBL1	Exosome	EELAK	VDASVALLCDIQNTIINNLFR	KHASE	2	C9:+57.021	1195.131132	2388.246665	0.000451244	8	N	130	151
Q9DBL1	Parental	FRDAK	IGTIYEGASNIQLNTIAK	HIDAE	2		953.5181695	1905.020739	0.000451244	3	N	408	426
Q9DBL1	Parental	QFGKR	IFDFQGLQHQVAQVATQLEATR	LLTYN	3		834.1034728	2499.287018	0.000662267	2	N	325	347
Q9DBL1	Parental	EELAK	VDASVALLCDIQNTIINNLFR	KHASE	2	C9:+57.021	1195.131132	2388.246665	0.000451244	4	N	130	151
Q9DBL9	Exosome	PMLQR	IGGLHPDIPVSVIFGAR	SCIDG	3		583.3338287	1746.978086	0.001162105	1	N	282	299
Q9DBL9	Parental	SSRPR	FDSDAEEVENQFVESIEEWR	CALRL	2		1229.538213	2457.060826	0.000451244	9	N	121	141
Q9DBL9	Parental	PMLQR	IGGLHPDIPVSVIFGAR	SCIDG	3		583.3338287	1746.978086	0.00091018	1	N	282	299
Q9DBR0	Parental	PHTEK	LLEEQTCEAASETR	SIEDK	2	C7:+57.021	818.8780744	1635.740549	0.000451244	12	N	619	633
Q9DBR0	Parental	TAAVK	AVEGEGEPAAAHSDVLTEVEGPVDTAEASSDPHTEK	LLEEQ	4		908.6689341	3630.644536	0.000451244	3	N	583	619
Q9DBR1	Exosome	VPMLR	DLTQNTAVSINFKDPQFAEDYVFK	AAMLP	3		930.7927411	2789.354823	0.000451244	16	N	743	767
Q9DBR1	Exosome	LNGKK	YAWQGVALLPFVDER	RLRAA	2		882.4599262	1762.904252	0.000870037	2	N	641	656
Q9DBR1	Parental	VPMLR	DLTQNTAVSINFKDPQFAEDYVFK	AAMLP	3		930.7927411	2789.354823	0.001699387	1	N	743	767
Q9DBR1	Parental	LNGKK	YAWQGVALLPFVDER	RLRAA	2		882.4599262	1762.904252	0.000451244	9	N	641	656
Q9DBR7	Exosome	ETVNK	VGQTAFDVADEDILGYLEELQKK	QTLLH	3		861.1064371	2580.295911	0.000451244	5	N	263	286
Q9DBR7	Exosome	KTKVK	FDDGAVFLAACSSGDTDEVLK	LLHRG	2	C11:+57.021	1109.004732	2215.993863	0.000622848	2	N	37	58
Q9DBR7	Exosome	ETVNK	VGQTAFDVADEDILGYLEELQK	KQTLL	3		818.4081161	2452.200948	0.000451244	5	N	263	285
Q9DBR7	Parental	ETVNK	VGQTAFDVADEDILGYLEELQKK	QTLLH	3		861.1064371	2580.295911	0.000451244	16	N	263	286

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DBR7	Parental	ETVNK	VGQTAFDVADEDILGYLEELQK	KQTLL	2		1227.108274	2452.200948	0.000451244	3	N	263	285
Q9DBR7	Parental	ETVNK	VGQTAFDVADEDILGYLEELQK	KQTLL	3		818.4081161	2452.200948	0.000662267	2	N	263	285
Q9DBR7	Parental	DGAVF	LAACSSGDTDEVLK	LLHRG	2	C4:+57.021	733.3458787	1464.676157	0.000851441	1	N	44	58
Q9DBR7	Parental	ETYTR	YRPVSTSSSSAPSSSSLSTLGSTLY	ASSQL	2		1261.616995	2521.218389	0.000823681	3	N	766	791
Q9DBS1	Exosome	VGDVR	VSFSYAGLSSDDPDLGPAHVVTVIAR	QRGDQ	3		891.789331	2672.344593	0.000451244	2	N	240	266
Q9DBS1	Parental	VGDVR	VSFSYAGLSSDDPDLGPAHVVTVIAR	QRGDQ	3		891.789331	2672.344593	0.000451244	16	N	240	266
Q9DBS1	Parental	VQIGR	FFLSAGLIDKIDNFK	ALSLA	3		576.6509348	1726.929405	0.000979378	3	N	189	204
Q9DBT5	Exosome	ESELR	SAPYEFPEESPIEQLEER	RQRLE	2		1075.500371	2148.985141	0.000622848	12	N	60	78
Q9DBT5	Parental	ESELR	SAPYEFPEESPIEQLEER	RQRLE	2		1075.500371	2148.985141	0.000451244	19	N	60	78
Q9DBT5	Parental	HVYTR	RDPDEHCPEVELPYPDLQEFVADVNVL	MALII	3	C7:+57.021	1065.836527	3194.48618	0.002453667	1	N	255	282
Q9DBZ5	Exosome	LAVLK	LYQFNPAFFQTTVTAQILLK	ALTNL	2		1172.141526	2342.267452	0.000622848	2	N	52	72
Q9DBZ5	Exosome	VWMSK	YGWSADESGQVFICSQEESIKPK	NIVEK	3	C14:+57.021	882.411489	2644.211067	0.001654178	1	N	176	199
Q9DBZ5	Exosome	ETQAK	ENAYDLEANLAVLK	LYQFN	2		781.9071921	1561.798784	0.000662267	3	N	38	52
Q9DBZ5	Exosome	KGIDR	YNPENLATLER	YVETQ	2		660.3336629	1318.651726	0.000451244	2	N	20	31
Q9DBZ5	Parental	LAVLK	LYQFNPAFFQTTVTAQILLK	ALTNL	2		1172.141526	2342.267452	0.001463592	2	N	52	72
Q9DBZ5	Parental	VWMSK	YGWSADESGQVFICSQEESIKPK	NIVEK	3	C14:+57.021	882.411489	2644.211067	0.000637154	2	N	176	199
Q9DBZ5	Parental	KGIDR	YNPENLATLER	YVETQ	2		660.3336629	1318.651726	0.001463592	1	N	20	31
Q9DBZ5	Parental	GKLLK	GIDRYNPENLATLER	YVETQ	2		880.950454	1759.885308	0.001352548	2	N	16	31
Q9DC23	Exosome	IQVGR	FDCSSAPGICSDLYVFQPCLAVFK	GQGTK	3	C3:+57.021,C10:+57.021,C19:+57.021	927.7622799	2780.26344	0.001352548	2	N	400	424
Q9DC23	Exosome	AYSLR	SWGLGFLPQASIDLTPQTFNEK	VLQGK	2		1225.124062	2448.232523	0.001229886	2	N	661	683
Q9DC23	Exosome	HHGKK	ILYDILAFAK	ESVNS	2		583.8451465	1165.674693	0.001162105	1	N	438	448
Q9DC50	Exosome	LLIAK	EEGLPVPELFEDPLFSR	SGGGG	2		987.4969027	1972.978205	0.000451244	8	N	515	532
Q9DC50	Exosome	LCRGR	AFVFDVLHEGCLITPPELLR	QLTYI	3	C11:+57.021	776.0806863	2325.218659	0.000451244	16	N	199	219
Q9DC50	Exosome	SVEER	TFQYQDSLPSLPVPALEESLKK	YLESV	3		830.7762512	2489.305354	0.000451244	8	N	12	34
Q9DC51	Exosome	ICNNK	WFTDTSIILFLNKK	DLFEE	3		575.99118	1724.95014	0.002145581	5	Y	257	271
Q9DC51	Exosome	ATDTK	NVQFVFDAVTDVIIK	NNLKE	2		854.4699596	1706.924319	0.000451244	11	Y	330	345
Q9DC51	Exosome	ATDTK	NVQFVFDAVTDVIIK	NNLKE	3		569.9825731	1706.924319	0.000622848	2	Y	330	345
Q9DC51	Exosome	EKIKR	SPLTICYPEYTGSNTYEEAAAYIQCQFEDLNR	RKDTK	3	C6:+57.021,C25:+57.021	1268.566393	3802.67578	0.000451244	2	N	280	312
Q9DC51	Exosome	EKIKR	SPLTICYPEYTGSNTYEEAAAY	IQCQF	2	C6:+57.021	1250.546961	2499.078321	0.001463592	1	N	280	302
Q9DC51	Parental	NDLDR	ISQTNYIPTQQDVLR	TRVKT	2		888.4684796	1774.921359	0.001162105	3	N	161	176
Q9DC51	Parental	ICNNK	WFTDTSIILFLNKK	DLFEE	2		863.48287	1724.95014	0.000451244	7	Y	257	271
Q9DC51	Parental	ICNNK	WFTDTSIILFLNKK	DLFEE	3		575.99118	1724.95014	0.002145581	10	Y	257	271
Q9DC51	Parental	ATDTK	NVQFVFDAVTDVIIK	NNLKE	2		854.4699596	1706.924319	0.000451244	461	Y	330	345
Q9DC51	Parental	ATDTK	NVQFVFDAVTDVIIK	NNLKE	3		569.9825731	1706.924319	0.000451244	161	Y	330	345
Q9DC51	Parental	AKEVK	LLLLGAGESGK	STIVK	2		529.3167532	1056.617906	0.001329271	2	Y	35	46
Q9DC51	Parental	EEKIK	RSPLTICYPEYTGSNTYEEAAAYIQCQFEDLNR	RKDTK	3	C7:+57.021,C26:+57.021	1320.600097	3958.776891	0.000451244	2	N	279	312
Q9DC51	Parental	FSRSR	EYQLNDSASYYLNDLDR	ISQTN	2		1039.969238	2077.922875	0.000451244	7	N	144	161
Q9DC51	Parental	ICNNK	WFTDTSIILFLNK	KDLFE	2		799.4353884	1596.855177	0.000451244	14	Y	257	270
Q9DC51	Parental	EKIKR	SPLTICYPEYTGSNTYEEAAAYIQCQFEDLNR	RKDTK	3	C6:+57.021,C25:+57.021	1268.566393	3802.67578	0.000451244	23	N	280	312
Q9DC51	Parental	RTRVK	TTGIVETHFTF	KELYF	2		626.8145747	1251.613549	0.000622848	10	Y	180	191
Q9DC51	Parental	HESMK	LFDSICNNK	WFTDT	2	C6:+57.021	555.7663388	1109.517078	0.000622848	4	Y	248	257
Q9DC61	Exosome	SADSK	GLDTVVDLLADVVLHPR	LTDEE	2		916.5179725	1831.020345	0.000622848	3	N	157	174
Q9DC61	Exosome	SADSK	GLDTVVDLLADVVLHPR	LTDEE	3		611.347915	1831.020345	0.000451244	17	N	157	174
Q9DC61	Exosome	SSTAR	FDSKDEILLTLEK	HGGIC	3		517.6157788	1549.823936	0.000451244	2	N	121	134
Q9DC61	Exosome	SKMLR	GKPAVAALGDLTDLPTYEHIQAALSSR	NGHLP	4		699.3743263	2793.466105	0.000698008	2	N	485	512
Q9DC61	Parental	SADSK	GLDTVVDLLADVVLHPR	LTDEE	3		611.347915	1831.020345	0.000451244	12	N	157	174
Q9DCC5	Exosome	NGKSK	KVEEAEPEEFVVEK	VLDRR	2		831.4175897	1660.819579	0.000451244	13	N	20	34
Q9DCC5	Exosome	NGKSK	KVEEAEPEEFVVEK	VLDRR	3		554.6143264	1660.819579	0.000451244	2	N	20	34
Q9DCC5	Exosome	MFLMK	WKDSDEADLVLAK	EANMK	2		745.3808101	1488.74602	0.000451244	10	N	141	154
Q9DCC5	Exosome	EANMK	CPQIVIAFYEER	LTWHS	2	C1:+39.994	754.3661917	1506.716783	0.001352548	4	N	159	171
Q9DCC5	Exosome	EANMK	CPQIVIAFYEER	LTWHS	2	C1:+57.021	762.8796917	1523.743783	0.000451244	20	N	159	171
Q9DCC5	Exosome	EANMK	CPQIVIAFYEER	LTWHS	2	[0:-17.027,C1:+57.021	754.3661917	1506.716783	0.000451244	7	N	159	171
Q9DCC5	Exosome	EYFLK	WKGFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C19:+57.021	1232.898514	3695.672143	0.000451244	32	N	50	81
Q9DCC5	Exosome	FLKWK	GFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C17:+57.021	1128.173756	3381.497867	0.000451244	34	N	52	81
Q9DCC5	Parental	NGKSK	KVEEAEPEEFVVEK	VLDRR	2		831.4175897	1660.819579	0.000451244	77	N	20	34
Q9DCC5	Parental	NGKSK	KVEEAEPEEFVVEK	VLDRR	3		554.6143264	1660.819579	0.000451244	20	N	20	34
Q9DCC5	Parental	MFLMK	WKDSDEADLVLAK	EANMK	2		745.3808101	1488.74602	0.000451244	35	N	141	154
Q9DCC5	Parental	MFLMK	WKDSDEADLVLAK	EANMK	3		497.2564734	1488.74602	0.000451244	33	N	141	154
Q9DCC5	Parental	EANMK	CPQIVIAFYEER	LTWHS	2	C1:+57.021	762.8796917	1523.743783	0.000451244	19	N	159	171
Q9DCC5	Parental	EANMK	CPQIVIAFYEER	LTWHS	3	C1:+57.021	508.9223945	1523.743783	0.002884417	1	N	159	171
Q9DCC5	Parental	EANMK	CPQIVIAFYEER	LTWHS	2	[0:-17.027,C1:+57.021	754.3661917	1506.716783	0.000451244	10	N	159	171
Q9DCC5	Parental	EYFLK	WKGFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C19:+57.021	1232.898514	3695.672143	0.000451244	47	N	50	81
Q9DCC5	Parental	EYFLK	WKGFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	4	C19:+57.021	924.9258357	3695.672143	0.000451244	3	N	50	81
Q9DCC5	Parental	FLKWK	GFTDADNTWEPEENLDCPELIEAFLNSQK	AGKEK	3	C17:+57.021	1128.173756	3381.497867	0.000451244	64	N	52	81

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DCC5	Parental	FLKWK	GFTDADNTWEPEENLDCPELIEAF	LNSQK	2	C17:+57.021	1406.600453	2811.185306	0.000451244	10	N	52	76
Q9DCC5	Parental	GKSKK	VEEAEPEEFVVEK	VLDRR	2		767.3701081	1532.724616	0.000451244	10	N	21	34
Q9DCC5	Parental	FYEER	LTWHSCPEDEAQ	-	2	C6:+57.021	736.8094634	1471.603327	0.000735798	5	N	171	183
Q9DCD0	Exosome	CAFNR	TVSKVDDFLANEAK	GTKVV	2		768.8993671	1535.783134	0.000451244	92	N	34	48
Q9DCD0	Exosome	CAFNR	TVSKVDDFLANEAK	GTKVV	3		512.9355114	1535.783134	0.000451244	9	N	34	48
Q9DCD0	Exosome	ILLVK	AGQAVDDFIEK	LVPLL	2		596.7963819	1191.577164	0.000451244	79	N	76	87
Q9DCD0	Exosome	CRDLK	AKGILFVGSGVSGGEEGAR	YGPSL	2		895.9739291	1789.932258	0.000451244	4	N	117	136
Q9DCD0	Exosome	CRDLK	AKGILFVGSGVSGGEEGAR	YGPSL	3		597.6518861	1789.932258	0.000451244	1	N	117	136
Q9DCD0	Exosome	AIAAK	VGTGEPCCDWVGDEGAGHFVK	MVHNG	2	C7:+57.021,C8:+57.021	1138.988662	2275.961723	0.000451244	40	N	163	184
Q9DCD0	Exosome	AIAAK	VGTGEPCCDWVGDEGAGHFVK	MVHNG	3	C7:+57.021,C8:+57.021	759.6617078	2275.961723	0.000451244	54	N	163	184
Q9DCD0	Exosome	DLKAK	GILFVGSGVSGGEEGAR	YGPSL	2		796.4078906	1590.800181	0.000451244	150	N	119	136
Q9DCD0	Exosome	IQAQR	DYFGAHTYELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		1310.938515	3929.792144	0.000451244	34	N	447	483
Q9DCD0	Exosome	DFIEK	LVPLLDTGDIIIDGGNSEYR	DTTRR	2		1080.563305	2159.111011	0.000451244	140	N	87	107
Q9DCD0	Exosome	DFIEK	LVPLLDTGDIIIDGGNSEYR	DTTRR	3		720.7114703	2159.111011	0.000451244	38	N	87	107
Q9DCD0	Exosome	LGKIK	DAFERNPELQNLLLDDFFK	SAVDN	2		1162.582029	2323.148459	0.000451244	33	N	377	396
Q9DCD0	Exosome	LGKIK	DAFERNPELQNLLLDDFFK	SAVDN	3		775.3906196	2323.148459	0.000451244	48	N	377	396
Q9DCD0	Exosome	DAFER	NPELQNLLLDDFFK	SAVDN	2		853.4439418	1704.872284	0.000451244	84	N	382	396
Q9DCD0	Exosome	DAFER	NPELQNLLLDDFFK	SAVDN	3		569.2985612	1704.872284	0.000451244	13	N	382	396
Q9DCD0	Exosome	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	2		1248.154308	2494.293016	0.000451244	29	N	265	288
Q9DCD0	Exosome	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	3		832.4388053	2494.293016	0.000451244	22	N	265	288
Q9DCD0	Exosome	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	2	M11:+15.995	1256.151808	2510.288016	0.000451244	13	N	265	288
Q9DCD0	Exosome	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	3	M11:+15.995	837.770472	2510.288016	0.000451244	10	N	265	288
Q9DCD0	Exosome	DFIEK	LVPLLDTGDIIIDGGNSEY	RDTTR	2		1002.51275	2003.0099	0.00091018	7	N	87	106
Q9DCD0	Exosome	WPHIK	AIFQAIAAK	VGTGE	2		466.7823492	931.5490983	0.000698008	30	N	154	163
Q9DCD0	Exosome	DFIEK	LVPLLDTGDIIIDGGNSEYRDTTR	RCRDL	2		1317.175011	2632.334422	0.000451244	4	N	87	111
Q9DCD0	Exosome	DFIEK	LVPLLDTGDIIIDGGNSEYRDTTR	RCRDL	3		878.4526074	2632.334422	0.000451244	32	N	87	111
Q9DCD0	Exosome	RTVSK	VDDFLANEAK	GTKVV	2		561.277825	1120.54005	0.000451244	30	N	38	48
Q9DCD0	Exosome	IPMPC	FTTALSFYDGYR	HEMLP	2		720.8438635	1439.672127	0.000622848	3	N	422	434
Q9DCD0	Exosome	IEKLV	PLLDTGDIIIDGGNSEYR	DTTRR	2		974.4870663	1946.958533	0.000622848	5	N	89	107
Q9DCD0	Exosome	IEKLV	PLLDTGDIIIDGGNSEYR	DTTRR	3		649.9939776	1946.958533	0.000622848	1	N	89	107
Q9DCD0	Exosome	EEWNK	TELDSFLIEITANILK	YRDTD	2		910.5067391	1818.997878	0.000451244	25	N	225	241
Q9DCD0	Exosome	EEWNK	TELDSFLIEITANILK	YRDTD	3		607.3404261	1818.997878	0.000451244	28	N	225	241
Q9DCD0	Exosome	IEKLV	PLLDTGDIIIDGGNSEYRDTTR	RCRDL	3		807.7351147	2420.181944	0.000451244	5	N	89	111
Q9DCD0	Exosome	YDGYR	HEMLPANLIQAQR	DYFGA	2	M3:+15.995	768.9017644	1535.787929	0.002453667	1	N	434	447
Q9DCD0	Exosome	GAHTY	ELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		992.8094538	2975.404961	0.000662267	10	N	455	483
Q9DCD0	Exosome	LYASK	IISYAQGFMLLR	QAATE	2		706.3924698	1410.76934	0.000451244	13	N	331	343
Q9DCD0	Exosome	IQAQR	DYFGAHTYELLTKPGEF	IHTNW	3		663.3199135	1986.936341	0.001871652	2	N	447	464
Q9DCD0	Exosome	WTAIS	ALEYGMPVTLIGEAVFAR	CLSSL	2		969.0142089	1936.012818	0.001463592	1	N	270	288
Q9DCD0	Exosome	KLVPL	LDTGDIIIDGGNSEYR	DTTRR	2		869.4186523	1736.821705	0.000698008	2	N	91	107
Q9DCD0	Exosome	AFERN	PELQNLLLDDFFK	SAVDN	2		796.422478	1590.829356	0.000622848	1	N	383	396
Q9DCD0	Parental	CAFNR	TVSKVDDFLANEAK	GTKVV	2		768.8993671	1535.783134	0.000451244	66	N	34	48
Q9DCD0	Parental	CAFNR	TVSKVDDFLANEAK	GTKVV	3		512.9355114	1535.783134	0.000451244	3	N	34	48
Q9DCD0	Parental	ILLVK	AGQAVDDFIEK	LVPLL	2		596.7963819	1191.577164	0.000451244	28	N	76	87
Q9DCD0	Parental	CRDLK	AKGILFVGSGVSGGEEGAR	YGPSL	2		895.9739291	1789.932258	0.000451244	12	N	117	136
Q9DCD0	Parental	CRDLK	AKGILFVGSGVSGGEEGAR	YGPSL	3		597.6518861	1789.932258	0.000451244	6	N	117	136
Q9DCD0	Parental	AIAAK	VGTGEPCCDWVGDEGAGHFVK	MVHNG	2	C7:+57.021,C8:+57.021	1138.988662	2275.961723	0.000451244	62	N	163	184
Q9DCD0	Parental	AIAAK	VGTGEPCCDWVGDEGAGHFVK	MVHNG	3	C7:+57.021,C8:+57.021	759.6617078	2275.961723	0.000451244	20	N	163	184
Q9DCD0	Parental	DLKAK	GILFVGSGVSGGEEGAR	YGPSL	2		796.4078906	1590.800181	0.000451244	59	N	119	136
Q9DCD0	Parental	IQAQR	DYFGAHTYELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		1310.938515	3929.792144	0.000451244	25	N	447	483
Q9DCD0	Parental	DFIEK	LVPLLDTGDIIIDGGNSEYR	DTTRR	2		1080.563305	2159.111011	0.000451244	40	N	87	107
Q9DCD0	Parental	DFIEK	LVPLLDTGDIIIDGGNSEYR	DTTRR	3		720.7114703	2159.111011	0.000451244	8	N	87	107
Q9DCD0	Parental	LGKIK	DAFERNPELQNLLLDDFFK	SAVDN	2		1162.582029	2323.148459	0.001264573	3	N	377	396
Q9DCD0	Parental	LGKIK	DAFERNPELQNLLLDDFFK	SAVDN	3		775.3906196	2323.148459	0.000451244	29	N	377	396
Q9DCD0	Parental	DAFER	NPELQNLLLDDFFK	SAVDN	2		853.4439418	1704.872284	0.000451244	50	N	382	396
Q9DCD0	Parental	DAFER	NPELQNLLLDDFFK	SAVDN	3		569.2985612	1704.872284	0.000823681	3	N	382	396
Q9DCD0	Parental	ILLVK	AGQAVDDFIEKLVPLLDTGDIIIDGGNSEYR	DTTRR	3		1111.900338	3332.677615	0.000451244	12	N	76	107
Q9DCD0	Parental	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	2		1248.154308	2494.293016	0.000451244	3	N	265	288
Q9DCD0	Parental	KGTGK	WTAISALEYGMPVTLIGEAVFAR	CLSSL	3		832.4388053	2494.293016	0.000451244	8	N	265	288
Q9DCD0	Parental	DFIEK	LVPLLDTGDIIIDGGNSEY	RDTTR	2		1002.51275	2003.0099	0.000451244	21	N	87	106
Q9DCD0	Parental	WPHIK	AIFQAIAAK	VGTGE	2		466.7823492	931.5490983	0.000698008	15	N	154	163
Q9DCD0	Parental	DFIEK	LVPLLDTGDIIIDGGNSEYRDTTR	RCRDL	3		878.4526074	2632.334422	0.000451244	8	N	87	111
Q9DCD0	Parental	EEWNK	TELDSFLIEITANILK	YRDTD	2		910.5067391	1818.997878	0.000451244	9	N	225	241
Q9DCD0	Parental	EEWNK	TELDSFLIEITANILK	YRDTD	3		607.3404261	1818.997878	0.000451244	15	N	225	241
Q9DCD0	Parental	IEKLV	PLLDTGDIIIDGGNSEYRDTTR	RCRDL	3		807.7351147	2420.181944	0.000622848	2	N	89	111
Q9DCD0	Parental	KLVPL	LDTGDIIIDGGNSEYRDTTR	RCRDL	2		1106.030358	2210.045116	0.002727428	2	N	91	111

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9DCD0	Parental	KLVPL	LDTGDIIIDGGNSEYRDTTR	RCRDL	3		737.6895054	2210.045116	0.000823681	2	N	91	111
Q9DCD0	Parental	ILLVK	AGQAVDDFIEKLVPLLDTGDIIIDGGNSEY	RDTTR	3		1059.866634	3176.576503	0.000451244	3	N	76	106
Q9DCD0	Parental	GAHTY	ELLTKPGEFIHTNWTGHGGSVSSSSYNA	-	3		992.8094538	2975.404961	0.000662267	4	N	455	483
Q9DCD0	Parental	KLVPL	LDTGDIIIDGGNSEYR	DTTRR	2		869.4186523	1736.821705	0.000451244	3	N	91	107
Q9DCH4	Exosome	GASAR	IQDALSTVLQYAEDVLSGK	VSADN	2		1025.539299	2049.062998	0.000451244	38	N	282	301
Q9DCH4	Exosome	GASAR	IQDALSTVLQYAEDVLSGK	VSADN	3		684.0287993	2049.062998	0.000451244	12	N	282	301
Q9DCH4	Exosome	FSPNR	VIGLSSDLQQVGGASAR	IQDAL	2		829.4475471	1656.879494	0.000451244	17	N	265	282
Q9DCH4	Exosome	GRVVR	LHPVILASIVDSYER	RNEGA	3		571.3179557	1710.930467	0.000662267	9	N	97	112
Q9DCH4	Parental	GASAR	IQDALSTVLQYAEDVLSGKVSADNTVGR	FLMSL	3		983.8441641	2948.509092	0.000451244	11	N	282	310
Q9DCH4	Parental	GASAR	IQDALSTVLQYAEDVLSGK	VSADN	2		1025.539299	2049.062998	0.000451244	29	N	282	301
Q9DCH4	Parental	GASAR	IQDALSTVLQYAEDVLSGK	VSADN	3		684.0287993	2049.062998	0.000451244	23	N	282	301
Q9DCH4	Parental	FSPNR	VIGLSSDLQQVGGASAR	IQDAL	2		829.4475471	1656.879494	0.000451244	11	N	265	282
Q9DCJ5	Parental	QQQAK	FDQCVLDKLGWVRPDLGQLSK	VTKVK	4	C4:+57.021	619.3273748	2473.278299	0.002145581	1	N	106	127
Q9DCJ5	Parental	-M	PGIVELPTLEELKVEEVK	VSSAV	3		674.7176736	2021.129621	0.000622848	8	N	1	19
Q9DCL9	Exosome	AISNK	ITSCIFQLLQEAGIK	TAFTK	2	C4:+57.021	860.9690382	1719.922476	0.000451244	24	N	59	74
Q9DCL9	Exosome	DVTTK	EIVLADVIDNDSWR	LWPSG	2		822.9155485	1643.815497	0.000451244	10	N	201	215
Q9DCL9	Exosome	WSSLR	LPSGIGCSTILSPEGSAQFAAQIFGLNNHLVWAK	LRASI	3	C7:+57.021	1195.284086	3582.828859	0.000451244	18	N	367	401
Q9DCL9	Parental	AISNK	ITSCIFQLLQEAGIK	TAFTK	2	C4:+57.021	860.9690382	1719.922476	0.000451244	8	N	59	74
Q9DCL9	Parental	DVTTK	EIVLADVIDNDSWR	LWPSG	2		822.9155485	1643.815497	0.00091018	2	N	201	215
Q9DCL9	Parental	WSSLR	LPSGIGCSTILSPEGSAQFAAQIFGLNNHLVWAK	LRASI	3	C7:+57.021	1195.284086	3582.828859	0.000451244	14	N	367	401
Q9DCL9	Parental	QMVKK	NFEWVADRVELLLK	SDSQC	3		577.9863175	1730.935553	0.000823681	2	N	247	261
Q9DCM0	Exosome	ELGLK	LLYAVNTHCHADHITGTGVLR	SLLPG	3	C9:+57.021	783.4028224	2347.185067	0.001329271	1	N	71	92
Q9DCM0	Exosome	SVHEK	IFTLPGNCLIYPAHDYHGLTVSTVEEER	TLNPR	4	C8:+57.021	808.650346	3230.570184	0.000451244	4	N	181	209
Q9DCM0	Parental	ELGLK	LLYAVNTHCHADHITGTGVLR	SLLPG	3	C9:+57.021	783.4028224	2347.185067	0.000451244	4	N	71	92
Q9DCM0	Parental	ELGLK	LLYAVNTHCHADHITGTGVLR	SLLPG	4	C9:+57.021	587.8040668	2347.185067	0.001463592	1	N	71	92
Q9DCM0	Parental	SVHEK	IFTLPGNCLIYPAHDYHGLTVSTVEEER	TLNPR	3	C8:+57.021	1077.864528	3230.570184	0.000451244	22	N	181	209
Q9DCM0	Parental	SVHEK	IFTLPGNCLIYPAHDYHGLTVSTVEEER	TLNPR	4	C8:+57.021	808.650346	3230.570184	0.000622848	15	N	181	209
Q9DCM0	Parental	SVISR	LSGAQADLHIGEGDSIR	FGRFA	2		869.9400863	1737.864573	0.000451244	2	N	104	121
Q9DCM0	Parental	DRESR	EAVLIDPVLETAHR	DAQLI	3		521.6232677	1561.846403	0.000622848	1	N	46	60
Q9DCR2	Exosome	PRLSK	FYQPYSEDTQQQIIR	ETFHL	2		958.4633942	1914.911188	0.001329271	2	N	18	33
Q9DCR2	Parental	PRLSK	FYQPYSEDTQQQIIR	ETFHL	2		958.4633942	1914.911188	0.000451244	19	N	18	33
Q9DCR2	Parental	PEIPR	NINIGDISIKVPNLPSFK	-	3		657.042603	1968.104409	0.002981883	1	N	175	193
Q9DCS2	Exosome	AVNGK	ISPQSNVDFDLTLR	CRNPE	2		802.9180912	1603.820582	0.000735798	2	N	147	161
Q9DCS2	Exosome	EWGLR	DTVLLEELGQASGLVLER	MVDMP	3		648.0217561	1941.041868	0.000451244	8	N	170	188
Q9DCS2	Exosome	QRCVR	VLEVASGSGQHAAHFAQAFPNAEWQPSDVDQR	CLDSI	3		1150.547292	3448.618477	0.000622848	2	N	30	62
Q9DCS3	Exosome	GLLPK	LPAVGGNEGVGQVIAVGSSVSALKPGDWVIPANAGLGTWR	TEAVF	3		1300.69759	3899.069369	0.000622848	4	N	99	139
Q9DCS3	Exosome	IGIPK	DIPLQSAATLGVNPCTAYR	MLVDF	2	C15:+57.021	1024.017779	2046.019959	0.000451244	3	N	154	173
Q9DCS3	Exosome	SQWKK	NHSPDEFKELILTLCNLIR	QGRLT	3	C15:+57.021	771.407462	2311.198986	0.001654178	1	N	317	336
Q9DCS9	Parental	-M	PDSWDKDVYPEPPSR	TPAPS	2		894.4159126	1786.816225	0.002145581	1	N	1	16
Q9DCS9	Parental	TYLTK	AYDLVVDWPVTLVR	EFIER	2		823.4515698	1644.88754	0.000622848	4	N	35	49
Q9DCS9	Parental	LTKAY	DLVVDWPVTLVR	EFIER	2		706.4013486	1410.787097	0.001943752	5	N	37	49
Q9DCW4	Exosome	KKLVK	EIIAVSCGPSQCQETIR	TALAM	2	C7:+57.021,C12:+57.021	974.4668337	1946.918067	0.000451244	24	N	59	76
Q9DCW4	Exosome	MGADR	GIHVEIPGAQAESLGPLQVAR	VLAKL	2		1071.587449	2141.159298	0.000662267	2	N	85	106
Q9DCW4	Exosome	MGADR	GIHVEIPGAQAESLGPLQVAR	VLAKL	3		714.7275661	2141.159298	0.000451244	3	N	85	106
Q9DCW4	Exosome	DLTSK	VSVISVEEPPQR	SAGVK	2		670.3649631	1338.714326	0.000622848	3	N	221	233
Q9DCW4	Parental	KKLVK	EIIAVSCGPSQCQETIR	TALAM	2	C7:+57.021,C12:+57.021	974.4668337	1946.918067	0.000451244	35	N	59	76
Q9DCW4	Parental	LETLR	LKLPAVVTADLR	LNEPR	3		432.6068893	1294.797268	0.000622848	10	N	174	186
Q9DCW4	Parental	MGADR	GIHVEIPGAQAESLGPLQVAR	VLAKL	2		1071.587449	2141.159298	0.000451244	4	N	85	106
Q9DCW4	Parental	DLTSK	VSVISVEEPPQR	SAGVK	2		670.3649631	1338.714326	0.001329271	1	N	221	233
Q9DCZ1	Exosome	ASEGK	TVEVPYKGDVENTILDILGGLR	STCTY	3		801.1044793	2400.290038	0.000451244	3	N	291	313
Q9DCZ1	Exosome	VEVPY	KGDVENTILDILGGLR	STCTY	3		571.6567485	1711.946846	0.00307782	1	N	297	313
Q9DCZ1	Parental	ASEGK	TVEVPYKGDVENTILDILGGLR	STCTY	3		801.1044793	2400.290038	0.001654178	2	N	291	313
Q9EPB4	Exosome	MGRAR	DAILDALENLSGDELKK	FKMKL	2		922.486535	1842.95747	0.000451244	17	N	5	22
Q9EPB4	Exosome	MGRAR	DAILDALENLSGDELKK	FKMKL	3		615.3269567	1842.95747	0.001395409	2	N	5	22
Q9EPB4	Exosome	ALIAR	VTEVDGVLDALHGSVLTEGQYQAVR	AETTS	3		886.1246022	2655.350407	0.000451244	6	N	123	148
Q9EPB4	Parental	MGRAR	DAILDALENLSGDELKK	FKMKL	2		922.486535	1842.95747	0.000451244	16	N	5	22
Q9EPB4	Parental	MGRAR	DAILDALENLSGDELKK	FKMKL	3		615.3269567	1842.95747	0.002981883	1	N	5	22
Q9EPB4	Parental	ALIAR	VTEVDGVLDALHGSVLTEGQYQAVR	AETTS	2		1328.683003	2655.350407	0.001352548	2	N	123	148
Q9EPB4	Parental	LQTTK	EESGAVAAAASVPAQSTAR	TGHFV	2		886.9428259	1771.870052	0.000451244	13	N	89	108
Q9EPB4	Parental	MGRAR	DAILDALENLSGDELK	KFKMK	2		858.4390534	1714.862507	0.000451244	3	N	5	21
Q9EPJ9	Parental	FTAHR	ASGQPQSAAASGDKAFEDWLNDDLGSYQGAQENR	YVGFG	3		1195.20392	3582.588359	0.000451244	13	N	148	182
Q9EPJ9	Parental	LAEGK	EWSLESSPAQNWTPPQPK	TLQFT	2		1041.500508	2080.985416	0.000451244	10	N	122	140
Q9EPK2	Exosome	STNIK	FGCFQWYYPELAAQFK	DAGLS	2	C3:+57.021	1027.977395	2053.939189	0.000622848	5	N	141	157
Q9EPK2	Exosome	VFQEK	ASDFLLLLNK	GPVIA	2		567.3324032	1132.649206	0.000662267	6	N	281	291
Q9EPK2	Parental	STNIK	FGCFQWYYPELAAQFK	DAGLS	2	C3:+57.021	1027.977395	2053.939189	0.000451244	6	N	141	157

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9EPK2	Parental	VFQEK	ASDFLLLLNK	GPVIA	2		567.3324032	1132.649206	0.000662267	3	N	281	291
Q9EPK7	Exosome	TDVTR	FLQDSVEYCIIGVTILSQLTNEINQADTTHPLTK	HRKIA	3	C9:+57.021	1287.991185	3860.950156	0.000622848	2	N	139	173
Q9EPK7	Exosome	ASSFR	DSSLFDIFTLSCNLLK	QASGK	2	C12:+57.021	936.9745175	1871.933435	0.000451244	6	N	182	198
Q9EPK7	Parental	ASSFR	DSSLFDIFTLSCNLLK	QASGK	2	C12:+57.021	936.9745175	1871.933435	0.000451244	5	N	182	198
Q9EPL4	Parental	KKKYR	VLGINEWQNTGFQYDVISCLNLLDRCDQPLTLLK	DIRSV	3	C19:+57.021,C26:+57.021	1346.015294	4035.022481	0.001395409	4	N	189	223
Q9EPL4	Parental	EVFRK	AGFVVEAFTR	LPYLC	2		548.7934452	1095.57129	0.002080925	3	N	282	292
Q9EPL8	Exosome	RHCIR	ENIVEAIIHSPELIR	VQLTT	3		578.3251103	1731.951931	0.000451244	22	N	92	107
Q9EPL8	Exosome	DDAEE	TALEGYSTIIDDEDNPVDEYQIFK	AIFQT	2		1388.148325	2774.281049	0.000451244	4	N	939	963
Q9EPL8	Exosome	QCKGR	GIDQCIPLFVEAALER	LTREV	2	C5:+57.021	915.9748519	1829.934104	0.000622848	10	N	752	768
Q9EPL8	Exosome	QCKGR	GIDQCIPLFVEAALER	LTREV	3	C5:+57.021	610.9858346	1829.934104	0.000451244	3	N	752	768
Q9EPL8	Exosome	TIQNR	NPVWYQALTHGLNEEQR	KQLQD	2		1028.006292	2053.996984	0.001395409	1	N	972	989
Q9EPL8	Exosome	DPRKK	DGALHMIGSLAEILLK	KKIYK	3		560.9838085	1679.928025	0.000823681	1	N	429	445
Q9EPL8	Exosome	YEYIR	MKFDVFEDFISPTTAAQTLLFTACSK	RKEVL	3	M1:+15.995,C24:+57.021	995.4859179	2983.434354	0.001463592	1	N	377	403
Q9EPL8	Parental	RHCIR	ENIVEAIIHSPELIR	VQLTT	3		578.3251103	1731.951931	0.000451244	7	N	92	107
Q9EPL8	Parental	QCKGR	GIDQCIPLFVEAALER	LTREV	3	C5:+57.021	610.9858346	1829.934104	0.000823681	6	N	752	768
Q9EPL8	Parental	ALEGY	STIIDDEDNPVDEYQIFK	AIFQT	2		1071.000204	2139.984807	0.000451244	2	N	945	963
Q9EPU0	Exosome	NCGCR	NVFLLGFIPAK	ADSVV	2		609.8664133	1217.717227	0.000851441	11	N	184	195
Q9EPU0	Exosome	YHLAR	QGNGPVLVCAPSNIAVDQLTEK	IHQTG	2	C9:+57.021	1155.59184	2309.16808	0.000823681	2	N	517	539
Q9EPU0	Exosome	QSSLK	DINWDSSQWQPLIQDR	CFLSW	2		1000.9772	1999.9388	0.0007646	3	N	215	231
Q9EPU0	Exosome	HVLLR	YEDAYQYQNIFGPLVK	LEADY	2		974.478513	1946.941426	0.000451244	1	N	290	306
Q9EPU0	Parental	NCGCR	NVFLLGFIPAKADSVVVLLCR	QPCAS	3	C20:+57.021	777.7804597	2330.317979	0.000451244	5	N	184	205
Q9EPU0	Parental	NCGCR	NVFLLGFIPAK	ADSVV	2		609.8664133	1217.717227	0.001264573	10	N	184	195
Q9EPU0	Parental	YHLAR	QGNGPVLVCAPSNIAVDQLTEK	IHQTG	2	C9:+57.021	1155.59184	2309.16808	0.000622848	1	N	517	539
Q9EPU0	Parental	QSSLK	DINWDSSQWQPLIQDR	CFLSW	2		1000.9772	1999.9388	0.001162105	2	N	215	231
Q9EQ06	Exosome	VGFHR	ALTDELAALGR	TGVRT	2		565.3147418	1128.613884	0.002296037	1	N	197	208
Q9EQ06	Parental	VGFHR	ALTDELAALGR	TGVRT	2		565.3147418	1128.613884	0.000823681	18	N	197	208
Q9EQ06	Parental	PQIEK	TFEVNVLAHFWTTK	AFLPV	3		564.9635129	1691.867139	0.000735798	11	N	139	153
Q9EQ06	Parental	AGVVY	TADLFATQDPQIEK	TFEVN	2		788.8968244	1575.778049	0.000451244	9	N	125	139
Q9EQ32	Parental	KLDEK	VSTEAEFSPEDSPSIR	VEGTL	2		875.9106601	1749.80572	0.000622848	9	N	206	222
Q9EQ32	Parental	KYGLK	NLTALLLTCPGALQAYSVANK	HGHYP	2	C9:+57.021	1109.598937	2217.182273	0.000451244	19	N	350	371
Q9EQ32	Parental	SGWGR	GCDILIFYSPDAEEWCQYLQDLFVSCR	QVRSQ	3	C2:+57.021,C16:+57.021,C26:+57.021	1128.838577	3383.49233	0.000451244	2	N	8	35
Q9EQG9	Exosome	DELQR	DKVVEDDEDDFPTTR	SDGDF	2		890.8977497	1779.779899	0.000662267	3	N	196	211
Q9EQG9	Exosome	NILCK	ITYVANVNPGGWAPASVLR	AVAKR	2		993.0343211	1984.053042	0.000451244	16	N	576	595
Q9EQG9	Exosome	FDECR	FDISVNDSVWYLR	AQDPE	2		807.4020769	1612.788554	0.002374549	1	N	85	98
Q9EQG9	Exosome	LSAIR	KIPALTENDPETWIVCNFSVDHDSAPLNNR	CVRAK	4	C16:+57.021	863.9193507	3451.646203	0.000451244	3	N	513	543
Q9EQG9	Exosome	PASQR	DVLYLSAIR	KIPAL	2		525.3036458	1048.591692	0.00091018	1	N	504	513
Q9EQG9	Parental	DELQR	DKVVEDDEDDFPTTR	SDGDF	2		890.8977497	1779.779899	0.000451244	20	N	196	211
Q9EQG9	Parental	FDECR	FDISVNDSVWYLR	AQDPE	2		807.4020769	1612.788554	0.000662267	2	N	85	98
Q9EQG9	Parental	LSAIR	KIPALTENDPETWIVCNFSVDHDSAPLNNR	CVRAK	3	C16:+57.021	1151.556534	3451.646203	0.000451244	4	N	513	543
Q9EQG9	Parental	DTLQK	YFDVCADAVSKDELQR	DKVVE	2	C5:+57.021	958.4466555	1914.877711	0.000451244	1	N	180	196
Q9EQG9	Parental	LSAIR	KIPALTENDPETWIVCNF	SVDHD	2	C16:+57.021	1074.027813	2146.040026	0.000998612	1	N	513	531
Q9EQG9	Parental	WVVLK	NNTLSYYKSEDETEYGCR	GSICL	2	C17:+57.021	1114.973963	2227.932326	0.000451244	1	N	48	66
Q9EQG9	Parental	KKKPR	FGGPDYEEGPNSLINEEEFFDAVEAALDR	QDKIE	3		1077.486594	3229.436381	0.000451244	10	N	303	332
Q9EQH2	Exosome	SSNDR	ASLINNAFQLVSIEK	LSIEK	2		823.959759	1645.903918	0.000698008	5	N	625	640
Q9EQH2	Exosome	GEIIK	TQEFPHILTLIGR	NPVGY	3		508.9564697	1523.846009	0.000451244	19	N	817	830
Q9EQH2	Parental	SSNDR	ASLINNAFQLVSIEK	LSIEK	2		823.959759	1645.903918	0.000622848	2	N	625	640
Q9EQH2	Parental	GEIIK	TQEFPHILTLIGR	NPVGY	3		508.9564697	1523.846009	0.000451244	4	N	817	830
Q9EQH3	Exosome	IHLLR	SDDPDQQYLILNTAR	KHFGA	2		874.9266445	1747.837689	0.000451244	27	N	499	514
Q9EQH3	Exosome	-M	PTTQQSPQDEQEKLLDEAIQAVK	VQSFQ	3		866.1087292	2595.302788	0.000451244	22	N	1	24
Q9EQH3	Exosome	GGNQR	IRFTLPPLVFAAYQLAFR	YKENS	3		708.4108496	2122.209149	0.00307782	1	N	524	542
Q9EQH3	Exosome	PAEIK	LFDIFSQQVATVIQSR	QDMPS	2		926.5023224	1850.989045	0.000451244	28	N	323	339
Q9EQH3	Exosome	PAEIK	LFDIFSQQVATVIQSR	QDMPS	3		618.0041483	1850.989045	0.000451244	19	N	323	339
Q9EQH3	Exosome	VERYK	QIVLTGILEQVVNCR	DALAQ	2	C14:+57.021	871.4853867	1740.955173	0.000451244	2	N	239	254
Q9EQH3	Exosome	VERYK	QIVLTGILEQVVNCR	DALAQ	3	C14:+57.021	581.3261912	1740.955173	0.000451244	15	N	239	254
Q9EQH3	Exosome	AKGRK	VADLYELVQYAGNIIPR	LYLLI	3		645.3514366	1933.03091	0.000451244	18	N	90	107
Q9EQH3	Exosome	NVNVK	NIIIALIDR	LALFA	2		520.8272881	1039.638976	0.002663018	6	N	296	305
Q9EQH3	Exosome	ISDSK	AQLAAITLIIGTFER	MKCFS	2		808.9726694	1615.929739	0.000622848	1	N	622	637
Q9EQH3	Exosome	ISDSK	AQLAAITLIIGTFER	MKCFS	3		539.6510463	1615.929739	0.001162105	5	N	622	637
Q9EQH3	Exosome	NQRIR	FTLPPLVFAAYQLAFR	YKENS	2		927.5197868	1853.023974	0.001329271	1	N	526	542
Q9EQH3	Exosome	NQRIR	FTLPPLVFAAYQLAFR	YKENS	3		618.6824579	1853.023974	0.000451244	5	N	526	542
Q9EQH3	Exosome	QLIQK	IREDLPNLESSEETEQINK	HFHNT	2		1122.553666	2243.091732	0.000451244	5	N	749	768
Q9EQH3	Exosome	QLIQK	IREDLPNLESSEETEQINK	HFHNT	3		748.705044	2243.091732	0.000451244	5	N	749	768
Q9EQH3	Exosome	EIFNK	LNLEHIATSSAVSK	ELTRL	2		735.4020769	1468.788554	0.001162105	2	N	382	396
Q9EQH3	Exosome	VNVER	YKQIVLTGILEQVVNCR	DALAQ	3	C16:+57.021	678.3789551	2032.113465	0.000451244	5	N	237	254

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9EQH3	Exosome	KELTR	LLKIPVDTYNNILTVLK	LKHFH	3		653.0631156	1956.165947	0.000622848	3	N	400	417
Q9EQH3	Exosome	VVNCR	DALAQEYLMECIIQVFPDEFHLQTLNPFLR	ACAEL	3	C11:+57.021	1217.605949	3649.794448	0.000622848	1	N	254	284
Q9EQH3	Exosome	FAKGR	KVADLYELVQYAGNIIPR	LYLLI	3		688.0497576	2061.125873	0.000735798	1	N	89	107
Q9EQH3	Parental	IHLLR	SDDPDQQYLILNTAR	KHFGA	2		874.9266445	1747.837689	0.000451244	21	N	499	514
Q9EQH3	Parental	-M	PTTQQSPQDEQEKLLDEAIQAVK	VQSFQ	3		866.1087292	2595.302788	0.000451244	7	N	1	24
Q9EQH3	Parental	GGNQR	IRFTLPPLVFAAYQLAFR	YKENS	3		708.4108496	2122.209149	0.001943752	1	N	524	542
Q9EQH3	Parental	PAEIK	LFDIFSQQVATVIQSR	QDMPS	2		926.5023224	1850.989045	0.000451244	12	N	323	339
Q9EQH3	Parental	PAEIK	LFDIFSQQVATVIQSR	QDMPS	3		618.0041483	1850.989045	0.000451244	17	N	323	339
Q9EQH3	Parental	VERYK	QIVLTGILEQVVNCR	DALAQ	3	C14:+57.021	581.3261912	1740.955173	0.000451244	12	N	239	254
Q9EQH3	Parental	AKGRK	VADLYELVQYAGNIIPR	LYLLI	3		645.3514366	1933.03091	0.000451244	6	N	90	107
Q9EQH3	Parental	NVNVK	NIIIALIDR	LALFA	2		520.8272881	1039.638976	0.002212458	2	N	296	305
Q9EQH3	Parental	ISDSK	AQLAAITLIIGTFER	MKCFS	3		539.6510463	1615.929739	0.000698008	5	N	622	637
Q9EQH3	Parental	NQRIR	FTLPPLVFAAYQLAFR	YKENS	3		618.6824579	1853.023974	0.000451244	5	N	526	542
Q9EQH3	Parental	QLIQK	IREDLPNLESSEETEQINK	HFHNT	2		1122.553666	2243.091732	0.000451244	12	N	749	768
Q9EQH3	Parental	QLIQK	IREDLPNLESSEETEQINK	HFHNT	3		748.705044	2243.091732	0.000451244	14	N	749	768
Q9EQH3	Parental	EIFNK	LNLEHIATSSAVSK	ELTRL	2		735.4020769	1468.788554	0.000451244	2	N	382	396
Q9EQI5	Exosome	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	3	C1:+39.994,C25:+57.021	1276.653546	3826.937238	0.000823681	5	N	53	88
Q9EQI5	Exosome	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	3	C1:+57.021,C25:+57.021	1282.329213	3843.964238	0.000451244	14	N	53	88
Q9EQI5	Exosome	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	4	C1:+57.021,C25:+57.021	961.9988595	3843.964238	0.000451244	8	N	53	88
Q9EQI5	Exosome	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	3	[0:-	1276.653546	3826.937238	0.002884417	1	N	53	88
Q9EQI5	Exosome	KNGQK	TCLDPNAPGVK	RIVMK	2	C2:+57.021	586.2927208	1170.569842	0.001264573	1	N	92	103
Q9EQI5	Exosome	ELRCR	CTNTISGIPFNSISLVNVYR	PGVHC	2	C1:+57.021	1128.078368	2254.141137	0.000451244	10	N	53	73
Q9EQI5	Parental	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	3	C1:+39.994,C25:+57.021	1276.653546	3826.937238	0.001763695	2	N	53	88
Q9EQI5	Parental	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	3	C1:+57.021,C25:+57.021	1282.329213	3843.964238	0.000451244	9	N	53	88
Q9EQI5	Parental	ELRCR	CTNTISGIPFNSISLVNVYRPGVHCADVEVIATLK	NGQKT	4	C1:+57.021,C25:+57.021	961.9988595	3843.964238	0.000823681	2	N	53	88
Q9EQI5	Parental	SGIPF	NSISLVNVYRPGVHCADVEVIATLK	NGQKT	2	C15:+57.021	1377.734285	2753.452969	0.001763695	1	N	63	88
Q9EQK5	Exosome	VVEER	QAIPLDQNEGIYVQDVK	TGKVR	2		965.4999767	1928.984353	0.000451244	27	N	377	394
Q9EQK5	Exosome	VVEER	QAIPLDQNEGIYVQDVK	TGKVR	2	[0:-17.027	956.9864767	1911.957353	0.000823681	1	N	377	394
Q9EQK5	Exosome	ERLER	GIQDVYVLSEQQGLLLK	ALQPL	2		952.0309127	1902.046225	0.000451244	37	N	318	335
Q9EQK5	Exosome	ERLER	GIQDVYVLSEQQGLLLK	ALQPL	3		635.0232085	1902.046225	0.000451244	23	N	318	335
Q9EQK5	Exosome	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGRPK	RPHAR	3		972.1907241	2913.548772	0.000451244	38	N	479	506
Q9EQK5	Exosome	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGRPK	RPHAR	4		729.3949931	2913.548772	0.000451244	4	N	479	506
Q9EQK5	Exosome	DQEIR	LAQDPFPLYPGELLEKDITPLQVVLPNTALHLK	ALLDF	3		1228.35399	3682.038569	0.000451244	8	N	91	124
Q9EQK5	Exosome	DQEIR	LAQDPFPLYPGELLEKDITPLQVVLPNTALHLK	ALLDF	4		921.5174423	3682.038569	0.000451244	26	N	91	124
Q9EQK5	Exosome	GVAHR	TGEEWLVTVQDTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	3		1283.658466	3847.951999	0.000451244	27	N	244	279
Q9EQK5	Exosome	GVAHR	TGEEWLVTVQDTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	4		962.9957997	3847.951999	0.000451244	6	N	244	279
Q9EQK5	Exosome	SLGLK	STLITDGSSPINLFNTAFGLLGLGSDGQPPVQK	-	3		1115.584461	3343.729984	0.000451244	38	N	828	861
Q9EQK5	Exosome	EWLVR	SVGAYLPAVFEEVLDLVDAVILTEK	TALHL	2		1345.731099	2689.446598	0.000451244	7	N	199	224
Q9EQK5	Exosome	EWLVR	SVGAYLPAVFEEVLDLVDAVILTEK	TALHL	3		897.4899995	2689.446598	0.000451244	18	N	199	224
Q9EQK5	Exosome	TVPPR	HYCIVANPVSR	DAQSS	2	C3:+57.021	658.3327116	1314.649823	0.000451244	15	N	56	67
Q9EQK5	Exosome	RARDR	AVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	2		1285.166989	2568.318378	0.000451244	19	N	625	649
Q9EQK5	Exosome	RARDR	AVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	3		857.113926	2568.318378	0.000451244	10	N	625	649
Q9EQK5	Exosome	EETAK	LFSVPDFVGDACK	AIASR	2	C12:+57.021	727.8531426	1453.690685	0.000451244	14	N	560	573
Q9EQK5	Exosome	ELLEK	DITPLQVVLPNTALHLK	ALLDF	2		936.5518153	1871.088031	0.000451244	19	N	107	124
Q9EQK5	Exosome	ELLEK	DITPLQVVLPNTALHLK	ALLDF	3		624.7038102	1871.088031	0.000451244	19	N	107	124
Q9EQK5	Exosome	DQEIR	LAQDPFPLYPGELLEK	DITPL	2		915.4883494	1828.961099	0.000451244	21	N	91	107
Q9EQK5	Exosome	YIPQK	EVEVVEIIQATVIK	QNQAL	2		785.4590605	1568.902521	0.000451244	6	N	155	169
Q9EQK5	Exosome	YIPQK	EVEVVEIIQATVIK	QNQAL	3		523.975307	1568.902521	0.000451244	7	N	155	169
Q9EQK5	Exosome	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGR	PKRPH	2		1345.208323	2688.401045	0.000662267	3	N	479	504
Q9EQK5	Exosome	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGR	PKRPH	3		897.1414817	2688.401045	0.000451244	3	N	479	504
Q9EQK5	Exosome	PHARR	ALCLLLGPDFFTDVITIETADHAR	LQLQL	3	C3:+57.021	896.7952743	2687.362423	0.000451244	6	N	512	536
Q9EQK5	Exosome	VVSYR	VPHNAAVQVYDYR	AKRAR	2		766.3867612	1530.757922	0.000451244	1	N	461	474
Q9EQK5	Exosome	DALQR	SVQLAIEITTNSQEAAAK	HEAQR	2		937.497434	1872.979268	0.000451244	9	N	656	674
Q9EQK5	Exosome	NPVSR	DAQSSVLFDVTGQVR	LRHAD	2		811.413173	1620.810746	0.000451244	4	N	67	82
Q9EQK5	Exosome	NPVSR	DAQSSVLFDVTGQVR	LRHAD	3		541.2780486	1620.810746	0.000451244	15	N	67	82
Q9EQK5	Exosome	VLWEK	ELPSGVEELLNLGHDPLADR	GQKGT	2		1087.558554	2173.101509	0.000451244	19	N	417	437
Q9EQK5	Exosome	VLWEK	ELPSGVEELLNLGHDPLADR	GQKGT	3		725.3749696	2173.101509	0.000451244	18	N	417	437
Q9EQK5	Exosome	AEAAR	IEGEGSVLQAK	LKAQA	2		565.8067496	1129.597899	0.002019181	1	N	734	745
Q9EQK5	Exosome	QAKLK	AQALAIETEAELER	VKKVR	2		772.4022739	1542.788948	0.000451244	1	N	747	761
Q9EQK5	Exosome	ARIIR	MAVFGFEMSEDAGPDGALLPR	ARDRA	2	M1:+15.995,M8:+15.995	1121.511987	2241.008375	0.000451244	3	N	600	621
Q9EQK5	Exosome	EAIIR	IPPYHYIHVLDQNSNVSR	VEVGP	2		1076.550867	2151.086133	0.000451244	5	N	9	27
Q9EQK5	Exosome	AKRAR	VVFGPELVSLDPEEQFTVL	SLSAG	2		1059.554418	2117.093235	0.002212458	1	N	479	498
Q9EQK5	Exosome	GLLLK	ALQPLEEGEGEEKVAHQAGDR	WLIRG	3		755.0370165	2262.08765	0.001463592	2	N	335	356
Q9EQK5	Exosome	VLQAK	LKAQALAIETEAELER	VKKVR	3		595.6637917	1783.967975	0.000698008	1	N	745	761
Q9EQK5	Exosome	LPRAR	DRAVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	3		947.4899441	2839.446432	0.000451244	11	N	623	649

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9EQK5	Exosome	LVTVQ	DTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	3		902.8048696	2705.391209	0.002981883	1	N	254	279
Q9EQK5	Parental	VVEER	QAIPLDQNEGIYVQDVK	TGKVR	2		965.4999767	1928.984353	0.000451244	25	N	377	394
Q9EQK5	Parental	ERLER	GIQDVYVLSEQQGLLLK	ALQPL	2		952.0309127	1902.046225	0.000451244	31	N	318	335
Q9EQK5	Parental	AKRAR	VVFGPELVSLDPEEQFTVLSLSAGRPK	RPHAR	3		972.1907241	2913.548772	0.000451244	24	N	479	506
Q9EQK5	Parental	DQEIR	LAQDPFPLYPGELLEKDITPLQVVLPNTALHLK	ALLDF	3		1228.35399	3682.038569	0.000451244	7	N	91	124
Q9EQK5	Parental	DQEIR	LAQDPFPLYPGELLEKDITPLQVVLPNTALHLK	ALLDF	4		921.5174423	3682.038569	0.000451244	10	N	91	124
Q9EQK5	Parental	GVAHR	TGEEWLVTVQDTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	3		1283.658466	3847.951999	0.000451244	16	N	244	279
Q9EQK5	Parental	GVAHR	TGEEWLVTVQDTEAHVPDVYEEVLGVVPITTLGPR	HYCVI	4		962.9957997	3847.951999	0.000451244	8	N	244	279
Q9EQK5	Parental	SLGLK	STLITDGSSPINLFNTAFGLLGLGSDGQPPVQK	-	3		1115.584461	3343.729984	0.000451244	17	N	828	861
Q9EQK5	Parental	LGLKS	TLITDGSSPINLFNTAFGLLGLGSDGQPPVQK	-	3		1086.573785	3256.697956	0.000451244	3	N	829	861
Q9EQK5	Parental	EWLVR	SVGAYLPAVFEEVLDLVDAVILTEK	TALHL	2		1345.731099	2689.446598	0.000622848	4	N	199	224
Q9EQK5	Parental	EWLVR	SVGAYLPAVFEEVLDLVDAVILTEK	TALHL	3		897.4899995	2689.446598	0.000451244	11	N	199	224
Q9EQK5	Parental	RARDR	AVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	2		1285.166989	2568.318378	0.000451244	18	N	625	649
Q9EQK5	Parental	RARDR	AVFPQNGLVVSSVDVQSVEPVDQR	TRDAL	3		857.113926	2568.318378	0.000622848	1	N	625	649
Q9EQK5	Parental	EETAK	LFSVPDFVGDACK	AIASR	2	C12:+57.021	727.8531426	1453.690685	0.0025889	1	N	560	573
Q9EQK5	Parental	ELLEK	DITPLQVVLPNTALHLK	ALLDF	3		624.7038102	1871.088031	0.000622848	3	N	107	124
Q9EQK5	Parental	DQEIR	LAQDPFPLYPGELLEK	DITPL	2		915.4883494	1828.961099	0.001591523	4	N	91	107
Q9EQK5	Parental	NPVSR	DAQSSVLFDVTGQVR	LRHAD	3		541.2780486	1620.810746	0.001654178	1	N	67	82
Q9EQK5	Parental	VLWEK	ELPSGVEELLNLGHDPLADR	GQKGT	2		1087.558554	2173.101509	0.000451244	21	N	417	437
Q9EQK5	Parental	VLWEK	ELPSGVEELLNLGHDPLADR	GQKGT	3		725.3749696	2173.101509	0.001871652	4	N	417	437
Q9EQK5	Parental	EAIIR	IPPYHYIHVLDQNSNVSR	VEVGP	2		1076.550867	2151.086133	0.000622848	3	N	9	27
Q9EQK5	Parental	AKRAR	VVFGPELVSLDPEEQFTVL	SLSAG	2		1059.554418	2117.093235	0.001463592	5	N	479	498
Q9EQK5	Parental	GLLLK	ALQPLEEGEGEEKVAHQAGDR	WLIRG	2		1132.051625	2262.08765	0.000979378	1	N	335	356
Q9EQK5	Parental	GLLLK	ALQPLEEGEGEEKVAHQAGDR	WLIRG	3		755.0370165	2262.08765	0.002981883	1	N	335	356
Q9EQK5	Parental	DALQR	SVQLAIEITTNSQEAAAKHEAQR	LEQEA	3		832.4336586	2494.277576	0.000735798	2	N	656	679
Q9EQK5	Parental	VLQAK	LKAQALAIETEAELER	VKKVR	2		892.9917875	1783.967975	0.000451244	4	N	745	761
Q9EQP2	Exosome	QRISR	GYDFCQVLQWFAER	VDRII	2	C5:+57.021	909.9173369	1817.819074	0.000451244	7	N	170	184
Q9EQP2	Exosome	TDNRR	LFEAEAQDLFR	DIQSL	2		669.8385811	1337.661562	0.000451244	2	N	272	283
Q9EQU5	Exosome	WVTTF	VNHPQVSALLGEEDEEALHYLTR	VEVTE	3		874.1054305	2619.292892	0.000870037	6	N	98	121
Q9EQU5	Exosome	WVTTF	VNHPQVSALLGEEDEEALHYLTR	VEVTE	4		655.8310229	2619.292892	0.000823681	10	N	98	121
Q9EQU5	Exosome	FEDIK	SGYRIDFYFDENPYFENK	VLSKE	3		768.6801701	2303.01711	0.001162105	1	N	131	149
Q9EQU5	Exosome	KSGYR	IDFYFDENPYFENK	VLSKE	2		920.9073891	1839.799178	0.000451244	27	N	135	149
Q9EQU5	Exosome	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR	VEVTE	3		1242.62532	3724.852559	0.000451244	8	N	89	121
Q9EQU5	Exosome	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR	VEVTE	4		932.2209398	3724.852559	0.000451244	43	N	89	121
Q9EQU5	Exosome	PKGEK	EQQEAIEHIDEVQNEIDRLNEQASEEILK	VEQKY	3		1150.560933	3448.659398	0.001839721	2	N	38	67
Q9EQU5	Exosome	NFWVT	TFVNHPQVSALLGEEDEEALHYLTR	VEVTE	4		717.860046	2867.408984	0.002813207	1	N	96	121
Q9EQU5	Parental	WVTTF	VNHPQVSALLGEEDEEALHYLTR	VEVTE	2		1310.654246	2619.292892	0.000451244	2	N	98	121
Q9EQU5	Parental	WVTTF	VNHPQVSALLGEEDEEALHYLTR	VEVTE	3		874.1054305	2619.292892	0.000451244	26	N	98	121
Q9EQU5	Parental	WVTTF	VNHPQVSALLGEEDEEALHYLTR	VEVTE	4		655.8310229	2619.292892	0.000823681	14	N	98	121
Q9EQU5	Parental	FEDIK	SGYRIDFYFDENPYFENK	VLSKE	2		1152.516355	2303.01711	0.000451244	4	N	131	149
Q9EQU5	Parental	FEDIK	SGYRIDFYFDENPYFENK	VLSKE	3		768.6801701	2303.01711	0.000622848	4	N	131	149
Q9EQU5	Parental	KSGYR	IDFYFDENPYFENK	VLSKE	2		920.9073891	1839.799178	0.000451244	27	N	135	149
Q9EQU5	Parental	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHY	LTRVE	3		1119.214369	3354.619706	0.000823681	4	N	89	118
Q9EQU5	Parental	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR	VEVTE	3		1242.62532	3724.852559	0.000451244	11	N	89	121
Q9EQU5	Parental	ELIAK	IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR	VEVTE	4		932.2209398	3724.852559	0.000451244	22	N	89	121
Q9EQU5	Parental	HYLTR	VEVTEFEDIKSGYR	IDFYF	2		836.4153813	1670.815163	0.000451244	2	N	121	135
Q9EQU5	Parental	PKGEK	EQQEAIEHIDEVQNEIDRLNEQASEEILK	VEQKY	3		1150.560933	3448.659398	0.001162105	3	N	38	67
Q9EQU5	Parental	NEIDR	LNEQASEEILKVEQK	YNKLR	3		586.6480302	1756.92069	0.000451244	1	N	56	71
Q9ER72	Exosome	EVDSK	VQVLLEEAKDLLSDWLDSTGGSEVTDNSIFSK	LPKFW	3		1165.917946	3494.730438	0.000451244	23	N	265	297
Q9ER72	Exosome	LEEAK	DLLSDWLDSTGGSEVTDNSIFSK	LPKFW	2		1243.58262	2485.149641	0.000451244	11	N	274	297
Q9ER72	Exosome	AREKK	VLEVLQLSDALRDDILPELGVR	FEDHE	3		821.7992788	2462.374436	0.000451244	23	N	689	711
Q9ER72	Exosome	DVLTR	VSEYVPEIVNFVQK	IVDNG	2		825.9410349	1649.86647	0.001591523	1	N	323	337
Q9ER72	Parental	EVDSK	VQVLLEEAKDLLSDWLDSTGGSEVTDNSIFSK	LPKFW	3		1165.917946	3494.730438	0.000451244	17	N	265	297
Q9ER72	Parental	LEEAK	DLLSDWLDSTGGSEVTDNSIFSK	LPKFW	2		1243.58262	2485.149641	0.000451244	3	N	274	297
Q9ERB0	Parental	PNLRR	LQDAELDSVPKEPSSTVNTEVYPK	NSTLR	3		882.7768681	2645.307204	0.000451244	35	N	169	193
Q9ERB0	Parental	SIKSV	FGGFINYFK	SKPVE	2		546.7798065	1091.544013	0.0007646	6	N	115	124
Q9ERB0	Parental	INSIK	SVFGGFINYFK	SKPVE	2		639.8300277	1277.644455	0.000451244	5	N	113	124
Q9ERB0	Parental	INYFK	SKPVEPPPEQNGSIVSQPNSR	LKEAI	3		749.7175068	2246.12912	0.000622848	7	N	124	145
Q9ERB0	Parental	TYHQK	IDSNLDELSVGLGHLK	DIALG	3		570.640987	1708.899561	0.000451244	8	N	203	219
Q9ERD8	Exosome	TIFNK	DLLATLHLLVALAK	RFQPD	2		745.9693984	1489.923197	0.000622848	5	N	134	148
Q9ERD8	Parental	TIFNK	DLLATLHLLVALAK	RFQPD	3		497.6488656	1489.923197	0.001352548	1	N	134	148
Q9ERD8	Parental	-	MELEFLYDLLQLPK	EVAQP	2	M1:+15.995	884.4660716	1766.916543	0.001591523	2	N	0	14
Q9ERD8	Parental	LQLPK	EVAQPTEEELPR	GGKKK	2		699.34951	1396.68342	0.000823681	1	N	14	26
Q9ERD8	Parental	SQRHK	LGVILEAVNQNLQVEEK	QAKWS	2		948.5259945	1895.036389	0.000451244	6	N	105	122
Q9ERF3	Exosome	SPDGK	YLASGAIDGIINIFDIATGK	LLHTL	2		1026.554752	2051.093904	0.000451244	16	N	161	181

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9ERF3	Exosome	SPDGK	YLASGAIDGIINIFDIATGK	LLHTL	3		684.705768	2051.093904	0.000622848	2	N	161	181
Q9ERF3	Exosome	AMPIR	SLTFSPDSQLLVTASDDGYIK	IYDVQ	2		1129.065878	2256.116156	0.000451244	25	N	194	215
Q9ERF3	Exosome	GNGSK	IVSVGDDQEIHVYDCPI	-	2	C15:+57.021	979.9621385	1957.908677	0.001352548	3	N	288	305
Q9ERF3	Exosome	ETNKK	ENIETVVTGSLDDLVK	VWKWR	2		866.4547035	1730.893807	0.000662267	1	N	29	45
Q9ERF3	Exosome	ETNKK	ENIETVVTGSLDDLVK	VWKWR	3		577.9724023	1730.893807	0.000451244	3	N	29	45
Q9ERF3	Parental	SPDGK	YLASGAIDGIINIFDIATGK	LLHTL	3		684.705768	2051.093904	0.000823681	2	N	161	181
Q9ERF3	Parental	AMPIR	SLTFSPDSQLLVTASDDGYIK	IYDVQ	2		1129.065878	2256.116156	0.000451244	22	N	194	215
Q9ERI2	Parental	DAMGF	LLLFDLTNEQSFLNVR	NWISQ	2		961.5232548	1921.03091	0.000451244	11	N	95	111
Q9ERI2	Parental	GRGQR	IHLQLWDTAGQER	FRSLT	2		783.9053181	1565.795036	0.0025889	1	N	67	80
Q9ERI2	Parental	GRGQR	IHLQLWDTAGQER	FRSLT	3		522.9394787	1565.795036	0.001871652	1	N	67	80
Q9ERK4	Exosome	RPAEK	FLESVEGNQNYPLLLLTLLEK	SQDNV	2		1217.167938	2432.320275	0.000451244	27	N	31	52
Q9ERK4	Exosome	RPAEK	FLESVEGNQNYPLLLLTLLEK	SQDNV	3		811.7812252	2432.320275	0.000451244	22	N	31	52
Q9ERK4	Exosome	TLDNK	LLQTDDEEEAGLLELLK	SQICD	2		965.0073003	1927.999001	0.000451244	17	N	251	268
Q9ERK4	Exosome	LYCIK	YGALALQEIFDGIQPK	MFGMV	2		881.9728664	1761.930133	0.000451244	9	N	800	816
Q9ERK4	Exosome	AFLER	GSSTIATAAADKIPGLLGVFQK	LIASK	3		715.7358387	2144.184116	0.000451244	19	N	714	736
Q9ERK4	Exosome	GREVK	YDLLVSNAIQFLASVCERPHYK	NLFED	4	C16:+57.021	656.5892944	2622.325978	0.001943752	2	N	309	331
Q9ERK4	Exosome	WTEIK	LVLDAFALPLTNLFK	ATIEL	2		837.9956132	1673.975626	0.000451244	12	N	174	189
Q9ERK4	Exosome	RPHYK	NLFEDQNTLTSICEK	VIVPN	2	C13:+57.021	906.4279315	1810.840263	0.000451244	18	N	331	346
Q9ERK4	Exosome	AQTQK	HGITQANELVNLTEFF	VNHIL	2		916.96303	1831.91046	0.000622848	3	N	445	461
Q9ERK4	Exosome	RYLPR	FVTAIWNLLVTTGR	EVKYD	2		795.9542797	1589.892959	0.000622848	6	N	292	306
Q9ERK4	Exosome	NMEFR	AADEEAFEDNSEEYIRR	DLEGS	3		681.9683796	2042.881739	0.001162105	2	N	355	372
Q9ERK4	Exosome	PAEKF	LESVEGNQNYPLLLLTLLEK	SQDNV	2		1143.633731	2285.251861	0.000451244	7	N	32	52
Q9ERK4	Exosome	PAEKF	LESVEGNQNYPLLLLTLLEK	SQDNV	3		762.7584205	2285.251861	0.000451244	2	N	32	52
Q9ERK4	Exosome	AQTQK	HGITQANELVNLTEFFVNHILPDLK	SNNVN	4		716.384694	2861.507576	0.000451244	2	N	445	470
Q9ERK4	Exosome	KAIMR	SFSLLQEAIIPYIPTLITQLTQK	LLAVS	2		1309.246719	2616.477839	0.000823681	1	N	578	601
Q9ERK4	Parental	RPAEK	FLESVEGNQNYPLLLLTLLEK	SQDNV	2		1217.167938	2432.320275	0.000451244	26	N	31	52
Q9ERK4	Parental	RPAEK	FLESVEGNQNYPLLLLTLLEK	SQDNV	3		811.7812252	2432.320275	0.000451244	14	N	31	52
Q9ERK4	Parental	RPHYK	NLFEDQNTLTSICEK	VIVPN	2	C13:+57.021	906.4279315	1810.840263	0.001463592	2	N	331	346
Q9ERK4	Parental	AQTQK	HGITQANELVNLTEFFVNHILPDLK	SNNVN	3		954.8436587	2861.507576	0.002884417	2	N	445	470
Q9ERK4	Parental	AQTQK	HGITQANELVNLTEFFVNHILPDLK	SNNVN	4		716.384694	2861.507576	0.000451244	2	N	445	470
Q9ERK4	Parental	KAIMR	SFSLLQEAIIPYIPTLITQLTQK	LLAVS	3		873.1670796	2616.477839	0.000823681	3	N	578	601
Q9ERL7	Exosome	VFEIR	TTDDLTETWLKEK	LAFFR	2		790.3966572	1578.777714	0.0007646	2	N	124	137
Q9ERL7	Exosome	VDKDR	QMVVLEDELQNISPEELKLELPER	QPRFV	3	M2:+15.995	956.4956247	2866.463474	0.000451244	10	N	40	64
Q9ERL7	Exosome	VFEIR	TTDDLTETWLK	EKLAF	2		661.8278791	1321.640158	0.000622848	1	N	124	135
Q9ERL7	Parental	VFEIR	TTDDLTETWLKEK	LAFFR	2		790.3966572	1578.777714	0.000451244	8	N	124	137
Q9ERL7	Parental	VFEIR	TTDDLTETWLKEK	LAFFR	3		527.2670381	1578.777714	0.000662267	2	N	124	137
Q9ERL7	Parental	VFEIR	TTDDLTETWLK	EKLAF	2		661.8278791	1321.640158	0.000451244	11	N	124	135
Q9ERR7	Exosome	DPVLK	LLDDNGNIAEELSILK	WNTDS	2		878.9705208	1755.925442	0.000451244	22	N	129	145
Q9ERR7	Exosome	SEACR	ELGFSSNLLCSSCDLLGQFNLLPLDPVCR	GCCQE	3	C10:+57.021,C13:+57.021,C28:+57.021	1108.873621	3323.597464	0.000451244	24	N	39	68
Q9ERR7	Exosome	LSILK	WNTDSVEEFLSEKLER	I-	3		661.3220942	1980.942883	0.000451244	9	N	145	161
Q9ERR7	Parental	DPVLK	LLDDNGNIAEELSILK	WNTDS	2		878.9705208	1755.925442	0.000451244	19	N	129	145
Q9ERR7	Parental	SEACR	ELGFSSNLLCSSCDLLGQFNLLPLDPVCR	GCCQE	3	C10:+57.021,C13:+57.021,C28:+57.021	1108.873621	3323.597464	0.000451244	25	N	39	68
Q9ERR7	Parental	LSILK	WNTDSVEEFLSEKLER	I-	3		661.3220942	1980.942883	0.000451244	5	N	145	161
Q9ERR7	Parental	LSILK	WNTDSVEEFLSEK	LERI-	2		792.3653571	1582.715114	0.001329271	1	N	145	158
Q9ERU9	Exosome	SSKER	SFLGNDDIGNLDGQVPDPDDLAR	YDTGA	2		1222.072754	2442.129908	0.000451244	5	N	398	421
Q9ERU9	Parental	FSSEK	SKPFAFGNSSATGSLFGFSFNAPLK	NSNSE	3		860.4363404	2578.285621	0.000823681	3	N	2367	2392
Q9ERU9	Parental	EETTR	ERTDLTQGDEVIDTTSEAGETSSTSETTPK	AVVSP	3		1062.487099	3184.437897	0.000823681	3	N	2314	2344
Q9ERU9	Parental	KIEVK	TGEEDEEEFFCNR	AKLFR	2	C11:+57.021	831.3231319	1660.630664	0.000451244	4	N	1179	1192
Q9ERU9	Parental	SSKER	SFLGNDDIGNLDGQVPDPDDLAR	YDTGA	2		1222.072754	2442.129908	0.002080925	2	N	398	421
Q9ES46	Exosome	KELVK	VLLDWINDVLAEER	IIVKQ	2		842.9493913	1683.883183	0.000451244	26	N	92	106
Q9ES46	Exosome	GRFER	DAFDTLFDHAPDKLNLVK	KSLIT	4		515.5183507	2058.042203	0.000451244	1	N	240	258
Q9ES46	Exosome	RIIVK	QLEEDLYDGQVLQK	LLEKL	2		839.4206637	1676.825727	0.000622848	1	N	110	124
Q9ES46	Parental	KELVK	VLLDWINDVLAEER	IIVKQ	2		842.9493913	1683.883183	0.000451244	10	N	92	106
Q9ES52	Exosome	EEHLK	AIQDYLSTQLLLDSDFLK	TGSSN	2		1042.052042	2082.088484	0.000451244	36	N	185	203
Q9ES52	Exosome	EEHLK	AIQDYLSTQLLLDSDFLK	TGSSN	3		695.0372948	2082.088484	0.000451244	6	N	185	203
Q9ES52	Exosome	TMVAK	LSQLTSLLSSIEDK	VKSLL	2		767.422675	1532.82975	0.000451244	8	N	267	281
Q9ES52	Exosome	TMVAK	LSQLTSLLSSIEDKVK	SLLHE	3		587.6721757	1759.993127	0.000998612	3	N	267	283
Q9ES52	Exosome	LISIK	SSDSDESYGEGCIALR	LETTE	2	C12:+57.021	873.3680708	1744.720542	0.000451244	5	N	810	826
Q9ES52	Exosome	ESFVK	SQEGENEEGSEGELVVR	FGETL	2		924.416838	1846.818076	0.000451244	4	N	765	782
Q9ES52	Parental	EEHLK	AIQDYLSTQLLLDSDFLK	TGSSN	2		1042.052042	2082.088484	0.000451244	23	N	185	203
Q9ES52	Parental	EEHLK	AIQDYLSTQLLLDSDFLK	TGSSN	3		695.0372948	2082.088484	0.000451244	5	N	185	203
Q9ES52	Parental	TMVAK	LSQLTSLLSSIEDKVK	SLLHE	3		587.6721757	1759.993127	0.001352548	2	N	267	283
Q9ES52	Parental	LISIK	SSDSDESYGEGCIALR	LETTE	2	C12:+57.021	873.3680708	1744.720542	0.000451244	10	N	810	826

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9ES52	Parental	ESFVK	SQEGENEEGSEGELVVR	FGETL	2		924.416838	1846.818076	0.000451244	13	N	765	782
Q9ES52	Parental	ETLPK	LKPIISDPEYLLDQHILISIK	SSDSD	3		816.8091152	2447.403946	0.001229886	1	N	789	810
Q9ESP1	Exosome	SHDIK	YGSGSGQQSVTGVEESDDANSYWR	IRGGS	2		1290.050007	2578.084415	0.000451244	27	N	59	83
Q9ESP1	Exosome	VLTGK	NLHTHHFPSPLSNNQEVSAFGEDGEGDDLDLWTVR	CSGQH	3		1311.940807	3932.79902	0.002019181	2	N	113	148
Q9ESP1	Exosome	EASVR	FQHVGTSVFLSVTGEQYGNPIR	GQHEV	3		812.7489184	2435.223355	0.000662267	8	N	161	183
Q9ESP1	Parental	SHDIK	YGSGSGQQSVTGVEESDDANSYWR	IRGGS	2		1290.050007	2578.084415	0.000451244	42	N	59	83
Q9ESP1	Parental	VLTGK	NLHTHHFPSPLSNNQEVSAFGEDGEGDDLDLWTVR	CSGQH	3		1311.940807	3932.79902	0.000451244	7	N	113	148
Q9ESP1	Parental	EASVR	FQHVGTSVFLSVTGEQYGNPIR	GQHEV	3		812.7489184	2435.223355	0.000451244	3	N	161	183
Q9EST5	Exosome	LDCLK	SLDLFGCEVTNR	SDYRE	2	C7:+57.021	705.8380238	1409.660448	0.000451244	29	N	116	128
Q9EST5	Exosome	GGLDR	LAEELPSLTHLNLSGNNLK	DISTL	2		1032.060733	2062.105866	0.000451244	6	N	82	101
Q9EST5	Exosome	GGLDR	LAEELPSLTHLNLSGNNLK	DISTL	3		688.3764219	2062.105866	0.000451244	16	N	82	101
Q9EST5	Parental	GEEEE	FGHDGEVDEDEEDEDEDEDEEEEESGKGEK	RKRET	3		1152.759941	3455.256423	0.000451244	50	N	230	260
Q9EST5	Parental	GEEEE	FGHDGEVDEDEEDEDEDEDEEEEESGKGEK	RKRET	4		864.8219058	3455.256423	0.000451244	59	N	230	260
Q9EST5	Parental	LDCLK	SLDLFGCEVTNR	SDYRE	2	C7:+57.021	705.8380238	1409.660448	0.000451244	27	N	116	128
Q9EST5	Parental	GGLDR	LAEELPSLTHLNLSGNNLKDISTLEPLK	RLDCL	3		1020.559476	3058.655028	0.000451244	7	N	82	110
Q9EST5	Parental	GGLDR	LAEELPSLTHLNLSGNNLKDISTLEPLK	RLDCL	4		765.6715571	3058.655028	0.001162105	4	N	82	110
Q9EST5	Parental	GGLDR	LAEELPSLTHLNLSGNNLK	DISTL	2		1032.060733	2062.105866	0.000451244	13	N	82	101
Q9EST5	Parental	GGLDR	LAEELPSLTHLNLSGNNLK	DISTL	3		688.3764219	2062.105866	0.000451244	25	N	82	101
Q9EST5	Parental	GHDGE	VDEDEEDEDEDEDEEEEESGKGEK	RKRET	3		938.6800112	2813.016634	0.000451244	4	N	236	260
Q9EST5	Parental	AMDGK	IEGLTDEFVNLEFLSLISVGLFSVSDLPK	LPKLK	3		1061.235999	3180.684597	0.000451244	8	N	33	62
Q9ESU7	Exosome	LIQVK	NEVSLNPLPLATEEGNPLLK	QYQGP	2		1074.581498	2147.147396	0.001329271	1	N	516	536
Q9ESU7	Exosome	DPCAR	SAPTKEVLDSFLDLVR	NIFPS	3		597.3285205	1788.962161	0.000451244	3	N	176	192
Q9ESU7	Parental	CTVLN	VEGDAFGAGLLQSYVDR	TKMPS	3		599.6324915	1795.874075	0.000451244	1	N	485	502
Q9ESX5	Exosome	KPESK	VAQLDTSQWPLLLK	NFDKL	2		806.4593949	1610.90319	0.000451244	11	N	43	57
Q9ESX5	Exosome	KLNVR	TAHYTPLPCGSNPLKR	EIGDY	3	C9:+57.021	604.6459238	1810.914371	0.001871652	1	N	65	81
Q9ESX5	Parental	SDSGK	NTLVTEAVQAPQLAAEAVNVIK	RKRDS	2		1140.134429	2278.253258	0.000451244	1	N	424	446
Q9ESX5	Parental	SDSGK	NTLVTEAVQAPQLAAEAVNVIK	RKRDS	3		760.4255528	2278.253258	0.000662267	4	N	424	446
Q9ET01	Exosome	SQLTK	LHSFVSDDIFLR	EIAKV	2		724.8807803	1447.745961	0.000451244	15	N	521	533
Q9ET01	Exosome	SQLTK	LHSFVSDDIFLR	EIAKV	3		483.5897869	1447.745961	0.000451244	193	N	521	533
Q9ET01	Exosome	IFNQK	IREGWQVEEADDWLR	HGNPW	2		951.4611859	1900.906772	0.000451244	29	N	170	185
Q9ET01	Exosome	IFNQK	IREGWQVEEADDWLR	HGNPW	3		634.6433906	1900.906772	0.000451244	27	N	170	185
Q9ET01	Exosome	SQLTK	LHSFVSDDIFLREIAK	VKQEN	3		630.6760316	1889.004695	0.000451244	6	N	521	537
Q9ET01	Exosome	GITPR	RWLLLCNPGLADLIAEK	IGEDY	2	C6:+57.021	991.5485184	1981.081437	0.000451244	32	N	490	507
Q9ET01	Exosome	GITPR	RWLLLCNPGLADLIAEK	IGEDY	3	C6:+57.021	661.3682789	1981.081437	0.000451244	49	N	490	507
Q9ET01	Exosome	ITPRR	WLLLCNPGLADLIAEK	IGEDY	2	C5:+57.021	913.4979628	1824.980326	0.000451244	55	N	491	507
Q9ET01	Exosome	ITPRR	WLLLCNPGLADLIAEK	IGEDY	3	C5:+57.021	609.3345752	1824.980326	0.000451244	31	N	491	507
Q9ET01	Exosome	LWSAR	APNDFNLQDFNVGDYIQAVLDRNLAENISR	VLYPN	3		1141.231081	3420.669844	0.000451244	16	N	248	278
Q9ET01	Exosome	LWSAR	APNDFNLQDFNVGDYIQAVLDR	NLAEN	2		1262.609307	2523.203014	0.000451244	126	N	248	270
Q9ET01	Exosome	LWSAR	APNDFNLQDFNVGDYIQAVLDR	NLAEN	3		842.0754713	2523.203014	0.000451244	71	N	248	270
Q9ET01	Exosome	LIAEK	IGEDYVKDLSQLTK	LHSFV	2		804.9281245	1607.840649	0.000451244	24	N	507	521
Q9ET01	Exosome	LIAEK	IGEDYVKDLSQLTK	LHSFV	3		536.954683	1607.840649	0.000451244	22	N	507	521
Q9ET01	Exosome	LPELK	LVIDQIDNGFFSPNQPDLF	KDIIN	2		1090.039466	2178.063332	0.000451244	25	N	740	759
Q9ET01	Exosome	KLLPR	HLEIIYEINQK	HLDRI	2		700.3831558	1398.750712	0.000451244	92	N	399	410
Q9ET01	Exosome	KLLPR	HLEIIYEINQK	HLDRI	3		467.2580372	1398.750712	0.000451244	12	N	399	410
Q9ET01	Exosome	NQKIR	EGWQVEEADDWLR	HGNPW	2		816.8685982	1631.721596	0.000451244	33	N	172	185
Q9ET01	Exosome	PSDLK	ISLSNESSNGVSANGK	-	2		782.3846125	1562.753625	0.000451244	22	N	834	850
Q9ET01	Exosome	QISIR	GIVGVENVAELK	KGFNR	2		614.3513243	1226.687049	0.000622848	5	N	17	29
Q9ET01	Exosome	EITKK	TFAYTNHTVLPEALER	WPVEL	2		931.4763046	1860.937009	0.000451244	44	N	371	387
Q9ET01	Exosome	EITKK	TFAYTNHTVLPEALER	WPVEL	3		621.3201364	1860.937009	0.000451244	19	N	371	387
Q9ET01	Exosome	HDRFK	VFADYEAYVK	CQEKV	2		602.7983932	1203.581186	0.000451244	44	N	773	783
Q9ET01	Exosome	KMIIK	LITSVAEVVNNDPMVGSK	LKVIF	2		936.9909308	1871.966262	0.000451244	20	N	622	640
Q9ET01	Exosome	KMIIK	LITSVAEVVNNDPMVGSK	LKVIF	2	M14:+15.995	944.9884308	1887.961262	0.000451244	44	N	622	640
Q9ET01	Exosome	KMIIK	LITSVAEVVNNDPMVGSK	LKVIF	3	M14:+15.995	630.3282205	1887.961262	0.000979378	2	N	622	640
Q9ET01	Exosome	ENISR	VLYPNDNFFEGK	ELRLK	2		721.8516885	1441.687777	0.000451244	21	Y	278	290
Q9ET01	Exosome	GKELR	LKQEYFVVAATLQDVIR	RFKAS	2		997.0600045	1992.104409	0.000451244	35	N	293	310
Q9ET01	Exosome	GKELR	LKQEYFVVAATLQDVIR	RFKAS	3		665.042603	1992.104409	0.000451244	38	N	293	310
Q9ET01	Exosome	LLLCN	PGLADLIAEK	IGEDY	2		513.7956536	1025.575707	0.000735798	5	N	497	507
Q9ET01	Exosome	ELRLK	QEYFVVAATLQDVIR	RFKAS	2		876.4704909	1750.925382	0.000451244	21	N	295	310
Q9ET01	Exosome	ELRLK	QEYFVVAATLQDVIR	RFKAS	3		584.6495939	1750.925382	0.001264573	5	N	295	310
Q9ET01	Exosome	LPELK	LVIDQIDNGFFSPNQPDLFK	DIINM	2		1154.086948	2306.158295	0.000451244	68	N	740	760
Q9ET01	Exosome	LPELK	LVIDQIDNGFFSPNQPDLFK	DIINM	3		769.7272318	2306.158295	0.000451244	40	N	740	760
Q9ET01	Exosome	LWSAR	APNDFNLQDFNVGDYIQAV	LDRNL	2		1070.503248	2138.990895	0.000451244	27	N	248	267
Q9ET01	Exosome	GGLGR	LAACFLDSMATLGLAAYGYGIR	YEYGI	2	C4:+57.021	1167.584973	2333.154345	0.000451244	23	Y	139	161
Q9ET01	Exosome	GGLGR	LAACFLDSMATLGLAAYGYGIR	YEYGI	3	C4:+57.021	778.725915	2333.154345	0.000451244	32	Y	139	161
Q9ET01	Exosome	GGLGR	LAACFLDSMATLGLAAYGYGIR	YEYGI	2	C4:+57.021,M9:+15.995	1175.582473	2349.149345	0.001162105	1	Y	139	161

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9ET01	Exosome	QISIR	GIVGVENVAELKK	GFNRH	2		678.3988059	1354.782012	0.000451244	6	N	17	30
Q9ET01	Exosome	QISIR	GIVGVENVAELKK	GFNRH	3		452.6018039	1354.782012	0.001264573	2	N	17	30
Q9ET01	Exosome	GYGIR	YEYGIFNQK	IREGW	2		581.2829103	1160.550221	0.000979378	34	N	161	170
Q9ET01	Exosome	TQVFK	DFSELEPDKFQNK	TNGIT	2		798.8811743	1595.746749	0.000451244	13	N	470	483
Q9ET01	Exosome	TQVFK	DFSELEPDKFQNK	TNGIT	3		532.9233829	1595.746749	0.002019181	1	N	470	483
Q9ET01	Exosome	VATPR	DYYFALAHTVR	DHLVG	2		678.3412909	1354.666982	0.000451244	48	N	50	61
Q9ET01	Exosome	VATPR	DYYFALAHTVR	DHLVG	3		452.5634606	1354.666982	0.000451244	18	N	50	61
Q9ET01	Exosome	GYEAK	EYYEALPELK	LVIDQ	2		627.816783	1253.617966	0.001463592	5	N	730	740
Q9ET01	Exosome	PELMR	IFVDIEKLPWAK	AWEIT	2		729.9219169	1457.828234	0.000451244	33	N	352	364
Q9ET01	Exosome	PELMR	IFVDIEKLPWAK	AWEIT	3		486.9505446	1457.828234	0.000451244	20	N	352	364
Q9ET01	Exosome	MVGSK	LKVIFLENYR	VSLAE	3		432.255968	1293.744504	0.000451244	19	N	640	650
Q9ET01	Exosome	FYHDR	FKVFADYEAYVK	CQEKV	3		493.9226545	1478.744564	0.000451244	1	N	771	783
Q9ET01	Exosome	LPELK	LVIDQIDNGFFSPNQPDLFKDIINMLFYHDR	FKVFA	3		1242.287651	3723.839553	0.000451244	8	N	740	771
Q9ET01	Exosome	LPELK	LVIDQIDNGFFSPNQPDLFKDIINMLFYHDR	FKVFA	4		931.9676882	3723.839553	0.000622848	3	N	740	771
Q9ET01	Exosome	LPELK	LVIDQIDNGFFSPNQPDLFKDIINMLFYHDR	FKVFA	4	M25:+15.995	935.9664382	3739.834553	0.000823681	1	N	740	771
Q9ET01	Exosome	SIRGI	VGVENVAELKK	GFNRH	2		593.346042	1184.676484	0.001264573	1	N	19	30
Q9ET01	Exosome	LQDFN	VGDYIQAVLDR	NLAEN	2		624.8332987	1247.650997	0.000451244	2	N	259	270
Q9ET01	Exosome	VATPR	DYYFALAHTVRDHLVGR	WIRTQ	3		678.35043	2032.02789	0.000735798	9	N	50	67
Q9ET01	Exosome	VATPR	DYYFALAHTVRDHLVGR	WIRTQ	4		509.0147725	2032.02789	0.000622848	7	N	50	67
Q9ET01	Exosome	EITKK	TFAYTNHTVLPEALERWPVELVEK	LLPRH	3		948.1645093	2841.470128	0.000451244	10	N	371	395
Q9ET01	Exosome	EITKK	TFAYTNHTVLPEALERWPVELVEK	LLPRH	4		711.375332	2841.470128	0.000637154	2	N	371	395
Q9ET01	Exosome	NPWEK	ARPEFMLPVHFYGR	VEHTQ	3		573.9649712	1718.871513	0.000451244	7	N	192	206
Q9ET01	Exosome	NPWEK	ARPEFMLPVHFYGR	VEHTQ	4		430.7256784	1718.871513	0.000451244	5	N	192	206
Q9ET01	Exosome	HEYKR	QLLNCLHVITMYNR	IKKDP	2	C5:+57.021	887.9584824	1773.901365	0.002981883	1	N	576	590
Q9ET01	Exosome	SLAEK	VIPATDLSEQISTAGTEASGTGNMK	FMLNG	2		1239.605573	2477.195546	0.000451244	10	N	656	681
Q9ET01	Exosome	SLAEK	VIPATDLSEQISTAGTEASGTGNMK	FMLNG	3		826.7396488	2477.195546	0.000451244	1	N	656	681
Q9ET01	Exosome	KEYAK	DIWNMEPSDLK	ISLSN	2		674.3166248	1346.61765	0.000451244	4	N	823	834
Q9ET01	Exosome	PDLFK	DIINMLFYHDR	FKVFA	3		479.5717392	1435.691818	0.001699387	3	N	760	771
Q9ET01	Exosome	AIYQL	GLDMEELEEIEEDAGLGNGGLGR	LAACF	2		1202.053173	2402.090747	0.000451244	1	N	116	139
Q9ET01	Exosome	ITPRR	WLLLCNPGLADLIAEKIGEDYVK	DLSQL	3	C5:+57.021	877.4684985	2629.382096	0.001162105	1	N	491	514
Q9ET01	Exosome	DFNLQ	DFNVGDYIQAVLDR	NLAEN	2		812.9024411	1623.789282	0.000823681	2	N	256	270
Q9ET01	Exosome	ENKLK	FSQFLEKEYK	VKINP	2		659.8380498	1317.6605	0.002519933	1	N	545	555
Q9ET01	Exosome	ELMRI	FVDIEKLPWAK	AWEIT	2		673.3798848	1344.74417	0.000979378	1	N	353	364
Q9ET01	Exosome	QTGTK	WVDTQVVLALPY	DTPVP	2		702.3826245	1402.749649	0.001352548	2	N	215	227
Q9ET01	Exosome	GKELR	LKQEYFVVAATL	QDVIR	2		691.3904495	1380.765299	0.002813207	1	Y	293	305
Q9ET01	Parental	SQLTK	LHSFVSDDIFLR	EIAKV	3		483.5897869	1447.745961	0.000451244	36	N	521	533
Q9ET01	Parental	IFNQK	IREGWQVEEADDWLR	HGNPW	2		951.4611859	1900.906772	0.000451244	8	N	170	185
Q9ET01	Parental	IFNQK	IREGWQVEEADDWLR	HGNPW	3		634.6433906	1900.906772	0.001329271	1	N	170	185
Q9ET01	Parental	SQLTK	LHSFVSDDIFLREIAK	VKQEN	3		630.6760316	1889.004695	0.000622848	7	N	521	537
Q9ET01	Parental	SQLTK	LHSFVSDDIFLREIAK	VKQEN	4		473.2589737	1889.004695	0.001352548	1	N	521	537
Q9ET01	Parental	GITPR	RWLLLCNPGLADLIAEK	IGEDY	2	C6:+57.021	991.5485184	1981.081437	0.000451244	14	N	490	507
Q9ET01	Parental	GITPR	RWLLLCNPGLADLIAEK	IGEDY	3	C6:+57.021	661.3682789	1981.081437	0.000451244	35	N	490	507
Q9ET01	Parental	ITPRR	WLLLCNPGLADLIAEK	IGEDY	2	C5:+57.021	913.4979628	1824.980326	0.000451244	21	N	491	507
Q9ET01	Parental	ITPRR	WLLLCNPGLADLIAEK	IGEDY	3	C5:+57.021	609.3345752	1824.980326	0.00091018	3	N	491	507
Q9ET01	Parental	LWSAR	APNDFNLQDFNVGDYIQAVLDRNLAENISR	VLYPN	3		1141.231081	3420.669844	0.000451244	12	N	248	278
Q9ET01	Parental	LWSAR	APNDFNLQDFNVGDYIQAVLDR	NLAEN	2		1262.609307	2523.203014	0.000451244	32	N	248	270
Q9ET01	Parental	LWSAR	APNDFNLQDFNVGDYIQAVLDR	NLAEN	3		842.0754713	2523.203014	0.000451244	21	N	248	270
Q9ET01	Parental	LIAEK	IGEDYVKDLSQLTK	LHSFV	2		804.9281245	1607.840649	0.000451244	2	N	507	521
Q9ET01	Parental	LIAEK	IGEDYVKDLSQLTK	LHSFV	3		536.954683	1607.840649	0.000451244	10	N	507	521
Q9ET01	Parental	LPELK	LVIDQIDNGFFSPNQPDLF	KDIIN	2		1090.039466	2178.063332	0.000451244	32	N	740	759
Q9ET01	Parental	LPELK	LVIDQIDNGFFSPNQPDLF	KDIIN	3		727.0289107	2178.063332	0.0007646	7	N	740	759
Q9ET01	Parental	KLLPR	HLEIIYEINQK	HLDRI	2		700.3831558	1398.750712	0.000451244	12	N	399	410
Q9ET01	Parental	KLLPR	HLEIIYEINQK	HLDRI	3		467.2580372	1398.750712	0.002663018	1	N	399	410
Q9ET01	Parental	ALDKK	GYEAKEYYEALPELK	LVIDQ	2		901.9465143	1801.877429	0.000451244	4	N	725	740
Q9ET01	Parental	ALDKK	GYEAKEYYEALPELK	LVIDQ	3		601.6336095	1801.877429	0.000622848	2	N	725	740
Q9ET01	Parental	NQKIR	EGWQVEEADDWLR	HGNPW	2		816.8685982	1631.721596	0.000451244	21	N	172	185
Q9ET01	Parental	PSDLK	ISLSNESSNGVSANGK	-	2		782.3846125	1562.753625	0.000451244	5	N	834	850
Q9ET01	Parental	EITKK	TFAYTNHTVLPEALER	WPVEL	2		931.4763046	1860.937009	0.000451244	5	N	371	387
Q9ET01	Parental	EITKK	TFAYTNHTVLPEALER	WPVEL	3		621.3201364	1860.937009	0.000451244	12	N	371	387
Q9ET01	Parental	ENISR	VLYPNDNFFEGK	ELRLK	2		721.8516885	1441.687777	0.001871652	1	Y	278	290
Q9ET01	Parental	LPELK	LVIDQIDNGFFSPNQPDLFK	DIINM	2		1154.086948	2306.158295	0.000451244	6	N	740	760
Q9ET01	Parental	LPELK	LVIDQIDNGFFSPNQPDLFK	DIINM	3		769.7272318	2306.158295	0.000622848	1	N	740	760
Q9ET01	Parental	GYGIR	YEYGIFNQK	IREGW	2		581.2829103	1160.550221	0.002212458	8	N	161	170
Q9ET01	Parental	VATPR	DYYFALAHTVR	DHLVG	2		678.3412909	1354.666982	0.000451244	8	N	50	61
Q9ET01	Parental	VATPR	DYYFALAHTVR	DHLVG	3		452.5634606	1354.666982	0.001162105	3	N	50	61

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9ET01	Parental	PELMR	IFVDIEKLPWAK	AWEIT	2		729.9219169	1457.828234	0.001463592	2	N	352	364
Q9ET01	Parental	MVGSK	LKVIFLENYR	VSLAE	3		432.255968	1293.744504	0.00091018	3	N	640	650
Q9ET01	Parental	ENISR	VLYPNDNFFEGKELR	LKQEY	3		614.3129818	1839.915545	0.000637154	3	Y	278	293
Q9ET01	Parental	VATPR	DYYFALAHTVRDHLVGR	WIRTQ	3		678.35043	2032.02789	0.002981883	1	N	50	67
Q9ET01	Parental	VATPR	DYYFALAHTVRDHLVGR	WIRTQ	4		509.0147725	2032.02789	0.002663018	1	N	50	67
Q9ET01	Parental	EITKK	TFAYTNHTVLPEALERWPVELVEK	LLPRH	3		948.1645093	2841.470128	0.000451244	2	N	371	395
Q9ET01	Parental	EITKK	TFAYTNHTVLPEALERWPVEL	VEKLL	2		1243.639879	2485.264158	0.001162105	1	N	371	392
Q9ET01	Parental	DEAIY	QLGLDMEELEEIEEDAGLGNGGLGR	LAACF	2		1322.624494	2643.233389	0.000823681	1	N	114	139
Q9ET66	Exosome	MLQMR	WDDELAAFAK	AYAQK	2		583.2803676	1164.545135	0.001329271	6	N	51	61
Q9ET66	Exosome	SKTER	IGCGSHFCETLQGVEEANIHLLVCNYEPPGNVK	GRKPY	4	C3:+57.021,C8:+57.021,C24:+57.021	936.1920865	3740.737146	0.000637154	3	N	132	165
Q9ET66	Parental	MLQMR	WDDELAAFAK	AYAQK	2		583.2803676	1164.545135	0.001329271	13	N	51	61
Q9ET66	Parental	SKTER	IGCGSHFCETLQGVEEANIHLLVCNYEPPGNVK	GRKPY	3	C3:+57.021,C8:+57.021,C24:+57.021	1247.920182	3740.737146	0.000451244	23	N	132	165
Q9ET66	Parental	SKTER	IGCGSHFCETLQGVEEANIHLLVCNYEPPGNVK	GRKPY	4	C3:+57.021,C8:+57.021,C24:+57.021	936.1920865	3740.737146	0.000451244	9	N	132	165
Q9ET66	Parental	AESPK	AESPEAEAESPLSSEALVPVLPAQER	GGQKA	2		1353.677584	2705.339567	0.001463592	1	N	385	411
Q9JHF5	Exosome	GSMFR	SEEVALVQLLLPTGSAYNCVSQLGELGLVEFR	DLNES	3	C19:+57.021	1164.608236	3490.801307	0.001871652	1	N	6	38
Q9JHF5	Parental	EARFR	TLQQLQQQSQELQEVLGETDRFLSQVLGR	VQQLL	3		1124.590498	3370.748094	0.000622848	4	N	256	285
Q9JHF5	Parental	GSMFR	SEEVALVQLLLPTGSAYNCVSQLGELGLVEFR	DLNES	3	C19:+57.021	1164.608236	3490.801307	0.000451244	25	N	6	38
Q9JHF5	Parental	RDLLR	IQEETDRLAQELR	DVRGN	2		800.9186225	1599.821645	0.00091018	1	N	96	109
Q9JHF5	Parental	EARFR	TLQQLQQQSQELQEVLGETDR	FLSQV	2		1236.122778	2470.229957	0.000451244	1	N	256	277
Q9JHF5	Parental	EVALV	QLLLPTGSAYNCVSQLGELGLVEFR	DLNES	2	C12:+57.021	1382.720843	2763.426086	0.001264573	2	N	13	38
Q9JHF5	Parental	LVEFR	DLNESVSAFQR	RFVVD	2		633.3101878	1264.604776	0.002727428	1	N	38	49
Q9JHF5	Parental	IRTNR	FTSSFQGIVDAYGVGR	YREVN	2		852.4235407	1702.831481	0.002212458	1	N	367	383
Q9JHI5	Exosome	LNGNK	FWITNGPDADILVVYAK	TDLTA	2		961.5070734	1920.998547	0.002981883	1	N	194	211
Q9JHI5	Exosome	KLGMR	GSNTCELVFEDCKVPAANVLSQESK	GVYVL	3	C5:+57.021,C12:+57.021	928.1058055	2781.294017	0.000451244	5	N	247	272
Q9JHJ0	Exosome	ESELK	QLETVLDDLDPENALLPAGFR	QKNQT	2		1163.600419	2325.185238	0.000451244	37	N	30	51
Q9JHJ0	Exosome	ESELK	QLETVLDDLDPENALLPAGFR	QKNQT	3		776.0695461	2325.185238	0.000622848	8	N	30	51
Q9JHJ0	Parental	VKGEK	ILPVFDEPPNPTNVEESLKR	IREND	2		1147.605505	2293.195409	0.000451244	8	N	172	192
Q9JHJ0	Parental	VKGEK	ILPVFDEPPNPTNVEESLKR	IREND	3		765.4062697	2293.195409	0.002080925	1	N	172	192
Q9JHJ0	Parental	ESELK	QLETVLDDLDPENALLPAGFR	QKNQT	2		1163.600419	2325.185238	0.000451244	39	N	30	51
Q9JHJ0	Parental	ESELK	QLETVLDDLDPENALLPAGFR	QKNQT	3		776.0695461	2325.185238	0.000451244	30	N	30	51
Q9JHJ0	Parental	ESELK	QLETVLDDLDPENALLPAGFR	QKNQT	2	Q1:-17.027	1155.086919	2308.158238	0.000451244	15	N	30	51
Q9JHJ0	Parental	ESELK	QLETVLDDLDPENALLPAGFR	QKNQT	2	[0:-17.027	1155.086919	2308.158238	0.000823681	1	N	30	51
Q9JHJ0	Parental	ELLGK	LSESELKQLETVLDDLDPENALLPAGFR	QKNQT	3		1038.206991	3111.597573	0.000451244	12	N	23	51
Q9JHJ0	Parental	ENDAR	LVEVNLNNIK	NIPIP	2		578.3407596	1154.665919	0.000451244	11	N	199	209
Q9JHJ0	Parental	LPFRK	DLGDYKDLDEDELLGK	LSESE	2		919.4392504	1836.862901	0.000622848	1	N	7	23
Q9JHJ0	Parental	LPFRK	DLGDYKDLDEDELLGK	LSESE	3		613.2954336	1836.862901	0.000451244	14	N	7	23
Q9JHJ0	Parental	VKGEK	ILPVFDEPPNPTNVEESLK	RIREN	2		1069.554949	2137.094298	0.001395409	3	N	172	191
Q9JHK4	Exosome	NVLLR	ELELVQNAFFTDPNDQSAWFYHR	WLLGR	3		943.1090636	2826.303791	0.000451244	8	N	210	233
Q9JHK4	Exosome	LAALR	CLEVLQASDNVLENLDGVANLPR	LRELL	2	C1:+57.021	1270.144968	2538.274336	0.000451244	1	N	486	509
Q9JHK4	Exosome	WDYRR	FVAAQAAVAPAEELAFTDSLITR	NFSNY	3		797.757191	2390.248173	0.001591523	1	N	150	173
Q9JHK4	Parental	VFQKR	EAGELDESVLELTSQILGANPDFATLWNCRR	EVLQQ	3	C29:+57.021	1168.907344	3503.698632	0.000622848	3	N	39	70
Q9JHK5	Exosome	EKDKK	VFNHCLTGSGVIDWLVSNK	LVRNR	2	C5:+57.021	1073.541422	2145.067243	0.000451244	29	N	150	169
Q9JHK5	Exosome	EKDKK	VFNHCLTGSGVIDWLVSNK	LVRNR	3	C5:+57.021	716.0302145	2145.067243	0.000451244	29	N	150	169
Q9JHK5	Exosome	SHDVK	KSDEENLFEIITADEVHYYLQAATSK	ERTEW	3		1005.49302	3013.45566	0.000451244	23	N	307	333
Q9JHK5	Exosome	HDVKK	SDEENLFEIITADEVHYYLQAATSK	ERTEW	3		962.7946989	2885.360697	0.000451244	28	N	308	333
Q9JHK5	Exosome	ITTTK	QQDHFFQAAFLEER	DAWVR	2		883.4187896	1764.821979	0.002212458	1	N	75	89
Q9JHK5	Exosome	ITTTK	QQDHFFQAAFLEER	DAWVR	3		589.2817931	1764.821979	0.000451244	15	N	75	89
Q9JHK5	Exosome	ITTTK	QQDHFFQAAFLEER	DAWVR	2	[0:-17.027	874.9052896	1747.794979	0.000451244	26	N	75	89
Q9JHK5	Exosome	KFILR	EDPAYLHYYDPAGGEDPLGAVHLR	GCVVT	2		1328.127864	2654.240128	0.000451244	2	N	269	293
Q9JHK5	Exosome	KFILR	EDPAYLHYYDPAGGEDPLGAVHLR	GCVVT	3		885.7545092	2654.240128	0.000451244	11	N	269	293
Q9JHK5	Exosome	KFILR	EDPAYLHYYDPAGGEDPLGAVHLR	GCVVT	4		664.5678319	2654.240128	0.000451244	24	N	269	293
Q9JHK5	Parental	EKDKK	VFNHCLTGSGVIDWLVSNK	LVRNR	2	C5:+57.021	1073.541422	2145.067243	0.000451244	35	N	150	169
Q9JHK5	Parental	EKDKK	VFNHCLTGSGVIDWLVSNK	LVRNR	3	C5:+57.021	716.0302145	2145.067243	0.000451244	40	N	150	169
Q9JHK5	Parental	SHDVK	KSDEENLFEIITADEVHYYLQAATSK	ERTEW	3		1005.49302	3013.45566	0.000451244	28	N	307	333
Q9JHK5	Parental	SHDVK	KSDEENLFEIITADEVHYYLQAATSK	ERTEW	4		754.3717149	3013.45566	0.000451244	16	N	307	333
Q9JHK5	Parental	HDVKK	SDEENLFEIITADEVHYYLQAATSK	ERTEW	3		962.7946989	2885.360697	0.000451244	21	N	308	333
Q9JHK5	Parental	ITTTK	QQDHFFQAAFLEER	DAWVR	2	[0:-17.027	874.9052896	1747.794979	0.000451244	2	N	75	89
Q9JHK5	Parental	KVRKF	ILREDPAYLHYYDPAGGEDPLGAVHLR	GCVVT	3		1013.177589	3036.509367	0.002727428	1	N	266	293
Q9JHK5	Parental	SHDVK	KSDEENLFEIITADEVHYY	LQAAT	2		1158.03986	2314.06412	0.001699387	3	N	307	326
Q9JHK5	Parental	SHDVK	KSDEENLFEIITADEVHYY	LQAAT	3		772.3625067	2314.06412	0.0025889	1	N	307	326
Q9JHK5	Parental	GDLSK	NAADGIAENPFLDSPDAF	YYFPD	2		932.4239347	1862.832269	0.001463592	2	N	198	216
Q9JHS3	Exosome	MLRPK	ALTQVLSQANTGGVQSTLLLNNEGSLLAYSGYGDTDAR	VTAAI	3		1299.987534	3896.939202	0.000979378	2	N	5	43

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JHS3	Parental	MLRPK	ALTQVLSQANTGGVQSTLLLNNEGSLLAYSGYGDTDAR	VTAAI	3		1299.987534	3896.939202	0.000451244	30	N	5	43
Q9JHS3	Parental	GMLKA	KAQALVQYLEEPLTQVAAS	-	2		1030.057659	2058.099718	0.001162105	2	N	106	125
Q9JHU4	Exosome	ESALR	FGNPLLVQDVESYDPVLNPVLNR	EVRRT	2		1299.682275	2597.34895	0.000451244	11	N	3626	3649
Q9JHU4	Exosome	ESALR	FGNPLLVQDVESYDPVLNPVLNR	EVRRT	3		866.7907833	2597.34895	0.000451244	11	N	3626	3649
Q9JHU4	Exosome	KHLRK	LVPLLLEDGGDAPAALEAALEEK	SALEQ	3		778.7533351	2333.236605	0.000622848	3	N	34	57
Q9JHU4	Exosome	PAAVK	LALESICLLLGESTTDWK	QIRSI	3	C7:+57.021	683.6909759	2048.049528	0.000451244	3	N	3316	3334
Q9JHU4	Exosome	ELQKR	QWIVFDGDVDPEWVENLNSVLDDNKLLTLPNGER	LSLPP	3		1313.985353	3938.93266	0.000451244	2	N	2296	2330
Q9JHU4	Exosome	SSQLR	VLTLSEDSPYETLHSFISNAVAPFFK	SYIRE	3		971.4959246	2911.464374	0.000451244	3	N	134	160
Q9JHU4	Exosome	TMVPK	LVAEDIPLLFSLLSDVFPGVQYHR	GEMTA	3		910.1623286	2727.463586	0.000637154	2	N	2146	2170
Q9JHU4	Exosome	SIIMR	ENFIPTIVNFSAEEISDAIR	EKMKK	2		1133.074037	2264.132475	0.000823681	10	N	3342	3362
Q9JHU4	Exosome	SIIMR	ENFIPTIVNFSAEEISDAIR	EKMKK	3		755.7186248	2264.132475	0.000698008	4	N	3342	3362
Q9JHU4	Exosome	ELQKR	QWIVFDGDVDPEWVENLNSVLDDNK	LLTLP	3		982.7984433	2945.37193	0.000979378	1	N	2296	2321
Q9JHU4	Exosome	PDGIR	REEFVQWVELLPDAQTPSWLGLPNNAER	VLLTT	3		1098.890108	3293.646923	0.000451244	4	N	4299	4327
Q9JHU4	Exosome	EVKGR	ILDDDTIITTLENLKR	EAAEV	3		625.0146015	1872.020405	0.002145581	3	N	3757	3773
Q9JHU4	Exosome	DGIRR	EEFVQWVELLPDAQTPSWLGLPNNAER	VLLTT	3		1046.856404	3137.545812	0.000823681	3	N	4300	4327
Q9JHU4	Exosome	GEKPK	VTDFGDKVEDPTFLNQLQSGVNR	WIREI	3		860.4299142	2578.266342	0.000451244	9	N	226	249
Q9JHU4	Exosome	LKQIR	EVWNTYELDLVNYQNK	CRLIR	2		1014.489609	2026.963618	0.000451244	4	N	1465	1481
Q9JHU4	Exosome	DLIAK	VQADEQFGIWLDSSSPEQTVPYLWSEETPTTPIGQAIHR	LLLIQ	3		1471.715703	4412.123709	0.000451244	2	N	3948	3987
Q9JHU4	Exosome	SSFPR	FYFVGDEDLLEIIGNSK	NVAKL	2		979.9914532	1957.967306	0.000451244	7	N	1626	1643
Q9JHU4	Exosome	QKVTK	LDRDPASGTALQEISFWLNLER	ALYRI	3		844.4349995	2530.281599	0.000823681	2	N	259	281
Q9JHU4	Exosome	NIYNR	LGEDLNKWQALLVQIR	KARGT	3		632.6954262	1895.062879	0.002080925	1	N	1069	1085
Q9JHU4	Exosome	PQDMK	VAEVLFDAADANAIEEVNLAYENVK	EVDGL	2		1354.177219	2706.338839	0.000451244	2	N	504	529
Q9JHU4	Exosome	SIITK	DLFQVAFNR	VARGM	2		555.2910697	1108.566539	0.000451244	2	N	3859	3868
Q9JHU4	Exosome	PQDMK	VAEVLFDAADANAIEEVNLAYENVKEVDGLDVSK	EGTEA	3		1217.276022	3648.804666	0.002145581	1	N	504	538
Q9JHU4	Parental	QKHLR	KLVPLLLEDGGDAPAALEAALEEK	SALEQ	2		1231.673584	2461.331569	0.000451244	4	N	33	57
Q9JHU4	Parental	QKHLR	KLVPLLLEDGGDAPAALEAALEEK	SALEQ	3		821.4516562	2461.331569	0.000451244	30	N	33	57
Q9JHU4	Parental	GSEER	VQVALEELQDLKGVWSELSK	VWEQI	3		757.7464034	2270.21581	0.000823681	2	N	1316	1336
Q9JHU4	Parental	ESALR	FGNPLLVQDVESYDPVLNPVLNR	EVRRT	2		1299.682275	2597.34895	0.000451244	16	N	3626	3649
Q9JHU4	Parental	ESALR	FGNPLLVQDVESYDPVLNPVLNR	EVRRT	3		866.7907833	2597.34895	0.000451244	4	N	3626	3649
Q9JHU4	Parental	KHLRK	LVPLLLEDGGDAPAALEAALEEK	SALEQ	2		1167.626103	2333.236605	0.000451244	8	N	34	57
Q9JHU4	Parental	KHLRK	LVPLLLEDGGDAPAALEAALEEK	SALEQ	3		778.7533351	2333.236605	0.000451244	16	N	34	57
Q9JHU4	Parental	PAAVK	LALESICLLLGESTTDWK	QIRSI	2	C7:+57.021	1025.032564	2048.049528	0.000451244	6	N	3316	3334
Q9JHU4	Parental	PAAVK	LALESICLLLGESTTDWK	QIRSI	3	C7:+57.021	683.6909759	2048.049528	0.000451244	10	N	3316	3334
Q9JHU4	Parental	ALFNR	CVLNWFGDWSTEALYQVGKEFTSK	MDLEK	3	C1:+57.021	955.7903004	2864.347501	0.000622848	3	N	3086	3110
Q9JHU4	Parental	ELQKR	QWIVFDGDVDPEWVENLNSVLDDNKLLTLPNGER	LSLPP	3		1313.985353	3938.93266	0.000451244	17	N	2296	2330
Q9JHU4	Parental	SSQLR	VLTLSEDSPYETLHSFISNAVAPFFK	SYIRE	3		971.4959246	2911.464374	0.000451244	29	N	134	160
Q9JHU4	Parental	SIIMR	ENFIPTIVNFSAEEISDAIREK	MKKNY	3		841.4311436	2521.270031	0.001352548	3	N	3342	3364
Q9JHU4	Parental	TMVPK	LVAEDIPLLFSLLSDVFPGVQYHR	GEMTA	3		910.1623286	2727.463586	0.002080925	1	N	2146	2170
Q9JHU4	Parental	SIIMR	ENFIPTIVNFSAEEISDAIR	EKMKK	2		1133.074037	2264.132475	0.000451244	11	N	3342	3362
Q9JHU4	Parental	SIIMR	ENFIPTIVNFSAEEISDAIR	EKMKK	3		755.7186248	2264.132475	0.001162105	3	N	3342	3362
Q9JHU4	Parental	PDGIR	REEFVQWVELLPDAQTPSWLGLPNNAER	VLLTT	3		1098.890108	3293.646923	0.000451244	8	N	4299	4327
Q9JHU4	Parental	DGIRR	EEFVQWVELLPDAQTPSWLGLPNNAER	VLLTT	3		1046.856404	3137.545812	0.000622848	8	N	4300	4327
Q9JHU4	Parental	GEKPK	VTDFGDKVEDPTFLNQLQSGVNR	WIREI	3		860.4299142	2578.266342	0.002374549	1	N	226	249
Q9JHU4	Parental	LKQIR	EVWNTYELDLVNYQNK	CRLIR	2		1014.489609	2026.963618	0.000451244	4	N	1465	1481
Q9JHU4	Parental	DLIAK	VQADEQFGIWLDSSSPEQTVPYLWSEETPTTPIGQAIHR	LLLIQ	3		1471.715703	4412.123709	0.000451244	8	N	3948	3987
Q9JHU4	Parental	SSFPR	FYFVGDEDLLEIIGNSK	NVAKL	2		979.9914532	1957.967306	0.000451244	2	N	1626	1643
Q9JHU4	Parental	QKVTK	LDRDPASGTALQEISFWLNLER	ALYRI	3		844.4349995	2530.281599	0.000451244	7	N	259	281
Q9JHU4	Parental	AGLKK	EVQALIAEGIALVWESYK	LDPYV	3		673.6986134	2018.07244	0.000451244	3	N	808	826
Q9JHU4	Parental	NIYNR	LGEDLNKWQALLVQIR	KARGT	3		632.6954262	1895.062879	0.001763695	1	N	1069	1085
Q9JHU4	Parental	ALFNR	CVLNWFGDWSTEALYQVGK	EFTSK	2	C1:+57.021	1137.038712	2272.061824	0.001162105	1	N	3086	3105
Q9JHU9	Exosome	QTKVK	SVLVDFLIGSGLK	TMSIV	2		674.3982746	1346.780949	0.000451244	24	N	312	325
Q9JHU9	Exosome	ELCQR	VSFCTDSDPEPQGFHTVLSLLSFLFK	APLVP	3	C4:+57.021	991.1567603	2970.446881	0.000451244	15	N	439	465
Q9JHU9	Exosome	SLRPR	PSVYIPEFIAANQTAR	ADNLI	2		888.9681154	1775.920631	0.000823681	1	N	175	191
Q9JHU9	Parental	ELCQR	VSFCTDSDPEPQGFHTVLSLLSFLFK	APLVP	3	C4:+57.021	991.1567603	2970.446881	0.000451244	1	N	439	465
Q9JHW4	Exosome	VKKVK	SMQMFHTPVTSAMQGDRLGICVTQFDPK	LLERG	3	M2:+15.995,M4:+15.995,C21:+57.021	1072.164885	3213.471255	0.00307782	1	N	254	282
Q9JHW4	Exosome	TVMGR	TLFFSPAPDSFDLEPVLDSFDLSR	EYLFQ	2		1358.163581	2714.311561	0.000451244	2	N	333	357
Q9JHW4	Exosome	TVMGR	TLFFSPAPDSFDLEPVLDSFDLSR	EYLFQ	3		905.7783205	2714.311561	0.000622848	1	N	333	357
Q9JIF0	Exosome	VLHAR	DKWLAPDGLIFPDR	ATLYV	3		548.2916295	1641.851488	0.000451244	6	N	181	195
Q9JIF0	Exosome	DLDFK	GQLCELSCSTDYR	MR-	2	C4:+57.021,C8:+57.021	794.8402063	1587.664813	0.000451244	9	N	356	369
Q9JIF0	Exosome	IYTVK	VEDLTFTSPFCLQVK	RNDYV	2	C11:+57.021	892.4506782	1782.885756	0.000698008	4	N	261	276
Q9JIF0	Parental	VLHAR	DKWLAPDGLIFPDR	ATLYV	3		548.2916295	1641.851488	0.000451244	1	N	181	195
Q9JIF0	Parental	DLDFK	GQLCELSCSTDYR	MR-	2	C4:+57.021,C8:+57.021	794.8402063	1587.664813	0.000451244	1	N	356	369
Q9JIF0	Parental	RCHKR	TGFSTSPESPYTHWK	QTVFY	2		862.8998984	1723.784197	0.002374549	1	N	298	313
Q9JIF7	Exosome	YTIYR	NFEHLIPDAPELIHDFLVNEK	DASCK	3		830.760824	2489.259072	0.000451244	2	N	164	185

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JIF7	Exosome	YTIYR	NFEHLIPDAPELIHDFLVNEK	DASCK	4		623.322568	2489.259072	0.000451244	6	N	164	185
Q9JIF7	Exosome	KANVK	VASTENGIIFGNIVYDVSGAASDR	NCVVL	2		1228.10914	2454.20268	0.000451244	2	N	790	814
Q9JIF7	Exosome	KANVK	VASTENGIIFGNIVYDVSGAASDR	NCVVL	3		819.0753598	2454.20268	0.002212458	1	N	790	814
Q9JIF7	Exosome	EVRKK	TLQLALDLVSSR	NVEEL	2		658.3831558	1314.750712	0.001352548	2	N	339	351
Q9JIF7	Exosome	PAHER	VLQDLVMDILR	VLSTP	2		657.8766526	1313.737705	0.000823681	1	N	316	327
Q9JIF7	Parental	NLYAR	SIFGEDALANVSIEKPVHQGPDAAVTGHIR	IRAKS	3		1043.542819	3127.605058	0.000451244	10	N	898	928
Q9JIF7	Parental	LGDLK	LVEKPSPLTLAPHDFANIK	ANVKV	3		697.3935243	2089.157173	0.002019181	1	N	767	786
Q9JIF7	Parental	LGDLK	LVEKPSPLTLAPHDFANIK	ANVKV	4		523.2970932	2089.157173	0.000451244	13	N	767	786
Q9JIF7	Parental	YTIYR	NFEHLIPDAPELIHDFLVNEK	DASCK	3		830.760824	2489.259072	0.000451244	4	N	164	185
Q9JIF7	Parental	YTIYR	NFEHLIPDAPELIHDFLVNEK	DASCK	4		623.322568	2489.259072	0.000451244	2	N	164	185
Q9JIF7	Parental	KANVK	VASTENGIIFGNIVYDVSGAASDR	NCVVL	2		1228.10914	2454.20268	0.000451244	23	N	790	814
Q9JIF7	Parental	KANVK	VASTENGIIFGNIVYDVSGAASDR	NCVVL	3		819.0753598	2454.20268	0.001871652	2	N	790	814
Q9JIF7	Parental	SEIKK	EAGELKPEEEITVGPVQK	LVTEM	2		977.012917	1952.010234	0.000622848	6	N	495	513
Q9JIF7	Parental	ADQDR	ALDYLSTCIDQVQTFGDILQLVIVELIYK	VCHAN	3	C8:+57.021	1124.267039	3369.777718	0.000451244	13	N	204	233
Q9JIF7	Parental	SYVRR	NAVLAIYTIYR	NFEHL	2		648.8696843	1295.723769	0.001162105	2	N	153	164
Q9JIX8	Exosome	TTDTK	AESPAGRVSDESVLPLAQK	SSLPE	3		652.0133721	1953.016716	0.002519933	1	N	488	507
Q9JIX8	Exosome	FRKTK	AAPCIYWLPLTESQIVQK	EAEQA	2	C4:+57.021	1059.058916	2116.102232	0.001162105	1	N	1218	1236
Q9JIX8	Parental	PGVSR	DSNTSYTETKDPSCGQEAAAPSGPQLQVLEPK	EKAPT	3	C14:+57.021	1135.863581	3404.567343	0.000451244	40	N	662	694
Q9JIX8	Parental	ELLGR	TGTLVEEAFWIDKIK	SHCFV	3		583.9860946	1748.934884	0.000451244	17	N	1033	1048
Q9JIX8	Parental	SHLAR	QQQEKETQIVSLPQEENEVK	SSQSL	2		1192.601148	2383.186695	0.002145581	1	N	358	378
Q9JIX8	Parental	SHLAR	QQQEKETQIVSLPQEENEVK	SSQSL	3		795.403365	2383.186695	0.002813207	2	N	358	378
Q9JIX8	Parental	ELLGR	TGTLVEEAFWIDK	IKSHC	2		754.8857283	1507.755857	0.000823681	3	N	1033	1046
Q9JIX8	Parental	QQQEK	ETQIVSLPQEENEVK	SSQSL	2		871.944503	1741.873406	0.000622848	3	N	363	378
Q9JIX8	Parental	EDLEK	APVVLQPEQIVSEEETPPPLLTK	EASSP	2		1257.689234	2513.362869	0.000451244	1	N	401	424
Q9JIY5	Exosome	PTSPR	SQYNFIADVVEK	TAPAV	2		706.8569709	1411.698342	0.00091018	4	N	144	156
Q9JIY5	Parental	PTSPR	SQYNFIADVVEK	TAPAV	2		706.8569709	1411.698342	0.001763695	2	N	144	156
Q9JIY5	Parental	AIGEK	LAQNAEDVYEAVR	TQSQL	2		739.3682341	1476.720868	0.000451244	2	N	419	432
Q9JIZ9	Exosome	MYELR	SGTGQQLGQAAEESNCCAR	LCCGA	2	C16:+57.021,C17:+57.021	1012.431511	2022.847422	0.000451244	15	N	110	129
Q9JIZ9	Exosome	GGLLR	EALTDADDFGLQFPVDLDVK	VKAVL	2		1104.539496	2207.063392	0.000451244	14	N	246	266
Q9JIZ9	Exosome	QPVLR	VVGPCWTCGCGTDTNFEVK	TKDES	2	C5:+57.021,C8:+57.021,C10:+57.021	1093.968652	2185.921704	0.000451244	7	N	207	226
Q9JIZ9	Parental	GGLLR	EALTDADDFGLQFPVDLDVK	VKAVL	2		1104.539496	2207.063392	0.001943752	1	N	246	266
Q9JJ00	Exosome	SGFVR	EAFTDADNFGIQFPLDLDVK	MKAVM	2		1128.047488	2254.079376	0.000451244	11	N	277	297
Q9JJ00	Exosome	SGFVR	EAFTDADNFGIQFPLDLDVK	MKAVM	3		752.3675921	2254.079376	0.002019181	1	N	277	297
Q9JJ00	Exosome	ERPLR	CSSCCFPCCLQEIEIQAPPGVPVGYVTQTWHPCLPK	FTLQN	4	C1:+57.021,C4:+57.021,C5:+57.021,C8:+57.021,C9:+57.021,C33:+57.021	1069.736565	4274.915061	0.0025889	1	N	189	225
Q9JJ00	Parental	SGFVR	EAFTDADNFGIQFPLDLDVK	MKAVM	2		1128.047488	2254.079376	0.000451244	20	N	277	297
Q9JJ00	Parental	SGFVR	EAFTDADNFGIQFPLDLDVK	MKAVM	3		752.3675921	2254.079376	0.001162105	1	N	277	297
Q9JJ00	Parental	SLGQR	VYFAVEDTDCCTR	NCCGA	2	C10:+57.021,C11:+57.021	818.3425818	1634.669564	0.000823681	1	N	147	160
Q9JJ00	Parental	ERPLR	CSSCCFPCCLQEIEIQAPPGVPVGYVTQTWHPCLPK	FTLQN	3	C1:+57.021,C4:+57.021,C5:+57.021,C8:+57.021,C9:+57.021,C33:+57.021	1425.979487	4274.915061	0.001654178	2	N	189	225
Q9JJ00	Parental	ERPLR	CSSCCFPCCLQEIEIQAPPGVPVGYVTQTWHPCLPK	FTLQN	4	C1:+57.021,C4:+57.021,C5:+57.021,C8:+57.021,C9:+57.021,C33:+57.021	1069.736565	4274.915061	0.002884417	1	N	189	225
Q9JJ28	Exosome	TDQMK	ADLTALFLPR	QPPMP	2		558.8247454	1115.633891	0.001329271	9	N	874	884
Q9JJ28	Exosome	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTRVPECLYTLPSLR	RLNLS	3	C22:+57.021,C31:+57.021	1460.056435	4377.145904	0.000979378	1	N	210	249
Q9JJ28	Exosome	CFILK	VPFESEDNQGIVYAWVGR	ASDPD	2		1033.503051	2064.990501	0.000451244	19	N	1091	1109
Q9JJ28	Exosome	LNKNR	LVTLPEAIHFLTEIQVLDVR	ENPSL	3		769.4426552	2305.304566	0.000698008	7	N	351	371
Q9JJ28	Exosome	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTR	VPECL	2	C22:+57.021	1475.209222	2948.402844	0.001591523	1	N	210	237
Q9JJ28	Exosome	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTR	VPECL	3	C22:+57.021	983.808748	2948.402844	0.000451244	3	N	210	237
Q9JJ28	Exosome	ANSLK	NSGVPDDIFKLDDLSVLDLSHNQLTECPR	ELENA	3	C27:+57.021	1099.873752	3296.597856	0.000451244	3	N	92	121
Q9JJ28	Exosome	KPADR	TAEWYNIDFSLQNQLR	LAGAS	2		999.4899433	1996.964287	0.000622848	1	N	385	401
Q9JJ28	Exosome	PKLYK	VGLGLGYLELPQINYK	LSVEH	2		888.9988842	1775.982168	0.000451244	5	N	730	746
Q9JJ28	Exosome	TKLKK	LYLNSNKLDFDGLPSGIGK	LTSLE	3		684.3656343	2050.073503	0.001943752	2	N	296	315
Q9JJ28	Exosome	NDLTR	VPECLYTLPSLR	RLNLS	2	C4:+57.021	724.3846099	1446.75362	0.002080925	1	N	237	249
Q9JJ28	Parental	VFKAK	FKNWDDVLTVDYTR	NAEAV	3		591.2936987	1770.857696	0.002519933	1	N	834	848
Q9JJ28	Parental	TDQMK	ADLTALFLPR	QPPMP	2		558.8247454	1115.633891	0.000823681	13	N	874	884
Q9JJ28	Parental	SAEAR	EGEEAAAEAEEKQPEEDFQCIVYFWQGR	EASNM	3	C20:+57.021	1115.826579	3344.456336	0.000451244	33	N	964	992
Q9JJ28	Parental	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTRVPECLYTLPSLR	RLNLS	3	C22:+57.021,C31:+57.021	1460.056435	4377.145904	0.000451244	7	N	210	249
Q9JJ28	Parental	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTRVPECLYTLPSLR	RLNLS	4	C22:+57.021,C31:+57.021	1095.294276	4377.145904	0.000823681	1	N	210	249
Q9JJ28	Parental	CFILK	VPFESEDNQGIVYAWVGR	ASDPD	2		1033.503051	2064.990501	0.000451244	19	N	1091	1109
Q9JJ28	Parental	YSEFF	TEDVGQLPGLTIWQIENFVPVLVEEAFHGK	FYEAD	3		1122.585914	3364.734341	0.000451244	9	N	491	521
Q9JJ28	Parental	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTR	VPECL	2	C22:+57.021	1475.209222	2948.402844	0.000451244	7	N	210	237

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JJ28	Parental	RNTQR	TQSNLPTSLEGLSNLSDVDLSCNDLTR	VPECL	3	C22:+57.021	983.808748	2948.402844	0.000451244	2	N	210	237
Q9JJ28	Parental	ANSLK	NSGVPDDIFKLDDLSVLDLSHNQLTECPR	ELENA	3	C27:+57.021	1099.873752	3296.597856	0.000451244	5	N	92	121
Q9JJ28	Parental	VDYTR	NAEAVLQGQGLSGK	VKRDT	2		686.3654944	1370.715389	0.000451244	7	N	848	862
Q9JJ28	Parental	KPADR	TAEWYNIDFSLQNQLR	LAGAS	2		999.4899433	1996.964287	0.002727428	1	N	385	401
Q9JJ28	Parental	PSLRR	LNLSSNQIAELSLCIDQWVHLETLNLSR	NQLTS	3	C14:+57.021	1089.566482	3265.676046	0.000451244	7	N	250	278
Q9JJ28	Parental	LKLNR	TGLCYLPEELAALQK	LEHLS	2	C4:+57.021	853.4453959	1704.875192	0.002519933	1	N	42	57
Q9JJ28	Parental	SAEAR	EGEEAAAEAEAEEKQPEEDFQCIVY	FWQGR	2	C20:+57.021	1336.071528	2670.127457	0.002453667	1	N	964	987
Q9JJK2	Exosome	LQMHR	TIVCQESELPDELLYGR	AGYLY	2	C4:+57.021	1011.496345	2020.977091	0.000451244	4	N	183	200
Q9JJK2	Exosome	EMEER	SFPNPFPDYEAAASAAGLAAGSAEETGR	VCPLP	2		1377.63625	2753.2569	0.000451244	3	N	21	49
Q9JJK2	Exosome	EMEER	SFPNPFPDYEAAASAAGLAAGSAEETGR	VCPLP	3		918.7601	2753.2569	0.000451244	2	N	21	49
Q9JJK2	Exosome	LSGRR	VTFLCGDAGPLAVGAVIYHK	LKSEC	3	C5:+57.021	696.7034387	2087.086916	0.002080925	1	N	144	164
Q9JJK2	Parental	LQMHR	TIVCQESELPDELLYGR	AGYLY	2	C4:+57.021	1011.496345	2020.977091	0.001162105	1	N	183	200
Q9JJU8	Exosome	FFEAR	ENNAVYAFLGLTAPPGSK	EAEAQ	2		924.9786801	1847.94176	0.000451244	7	N	86	104
Q9JJU8	Exosome	RKWMR	ENVPEDSRPSTGYPLPPQIFNECQYR	GDYDA	3	C23:+57.021	1031.817578	3092.429333	0.001395409	1	N	50	76
Q9JJU8	Parental	FFEAR	ENNAVYAFLGLTAPPGSK	EAEAQ	2		924.9786801	1847.94176	0.000451244	4	N	86	104
Q9JJU8	Parental	FFEAR	ENNAVYAFLGLTAPPGSK	EAEAQ	3		616.9883867	1847.94176	0.00091018	2	N	86	104
Q9JJU8	Parental	RKWMR	ENVPEDSRPSTGYPLPPQIFNECQYR	GDYDA	3	C23:+57.021	1031.817578	3092.429333	0.000662267	17	N	50	76
Q9JJU8	Parental	ECQYR	GDYDAFFEAR	ENNAV	2		595.7597994	1189.503999	0.000823681	4	N	76	86
Q9JKC8	Exosome	EKHWK	SVVSQSVCDYFFEAQEK	AADVE	2	C8:+57.021	1011.959596	2021.903592	0.000451244	10	N	21	38
Q9JKC8	Exosome	NNEAY	FDVVEEIDAIIDK	SGSTV	2		753.3908435	1504.766087	0.000979378	1	N	180	193
Q9JKC8	Parental	EKHWK	SVVSQSVCDYFFEAQEK	AADVE	2	C8:+57.021	1011.959596	2021.903592	0.000451244	8	N	21	38
Q9JKC8	Parental	PTILR	SVVNSITGSSNVGDTLPTGQLSNIPWRR	AGVKY	3		985.8481315	2954.520994	0.000870037	3	N	141	169
Q9JKC8	Parental	RAGVK	YTNNEAYFDVVEEIDAIIDK	SGSTV	2		1181.060793	2360.105985	0.000451244	6	N	173	193
Q9JKC8	Parental	NNEAY	FDVVEEIDAIIDK	SGSTV	2		753.3908435	1504.766087	0.001162105	1	N	180	193
Q9JKC8	Parental	PTILR	SVVNSITGSSNVGDTLPTGQLSNIPWR	RAGVK	3		933.8144277	2798.419883	0.000870037	1	N	141	168
Q9JKF1	Exosome	PGETL	TEILETPATNEQEAEHQR	AMQRR	2		1048.498694	2094.981787	0.000451244	2	N	1404	1422
Q9JKF1	Exosome	PGETL	TEILETPATNEQEAEHQR	AMQRR	3		699.3350625	2094.981787	0.000451244	4	N	1404	1422
Q9JKF1	Exosome	TTVWK	QLSSSVTGLTNIEEENCQR	YLDEL	2	C17:+57.021	1083.01088	2164.006159	0.000451244	50	N	477	496
Q9JKF1	Exosome	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	C9:+57.021	674.9952813	2021.962444	0.000451244	10	N	36	52
Q9JKF1	Exosome	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	Q1:-17.027,C9:+57.021	669.3196146	2004.935444	0.002981883	1	N	36	52
Q9JKF1	Exosome	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	[0:-17.027,C9:+57.021	669.3196146	2004.935444	0.000451244	17	N	36	52
Q9JKF1	Exosome	LQQKR	QSGQTDPLQKEEVQAGVDAANSAAQQYQR	RLAAV	3		1039.833098	3116.475895	0.000451244	56	N	358	387
Q9JKF1	Exosome	LQQKR	QSGQTDPLQKEEVQAGVDAANSAAQQYQR	RLAAV	3	[0:-17.027	1034.157432	3099.448895	0.001352548	1	N	358	387
Q9JKF1	Exosome	EIKSK	VDQIQEIVTGNPTVIK	MVVSF	2		877.4888807	1752.962161	0.000451244	26	N	1037	1053
Q9JKF1	Exosome	AAYNR	EQLWLANEGLITK	LQACC	2		757.9148201	1513.81404	0.000451244	31	N	738	751
Q9JKF1	Exosome	QANQF	KNVIFEIGPTEEVGDFEVK	AKFMG	2		1075.554949	2149.094298	0.000451244	5	N	1585	1604
Q9JKF1	Exosome	VDVIR	FQPGETLTEILETPATNEQEAEHQR	AMQRR	2		1434.686471	2867.357343	0.000451244	11	N	1397	1422
Q9JKF1	Exosome	VDVIR	FQPGETLTEILETPATNEQEAEHQR	AMQRR	3		956.7935809	2867.357343	0.000451244	34	N	1397	1422
Q9JKF1	Exosome	VDVIR	FQPGETLTEILETPATNEQEAEHQR	AMQRR	4		717.8471356	2867.357343	0.002019181	1	N	1397	1422
Q9JKF1	Exosome	LSALR	SPDVGLYGVIPECGETYQSDLAEAK	KKRLA	2	C13:+57.021	1349.631556	2697.247512	0.000451244	29	N	647	672
Q9JKF1	Exosome	LSALR	SPDVGLYGVIPECGETYQSDLAEAK	KKRLA	3	C13:+57.021	900.0903041	2697.247512	0.000451244	25	N	647	672
Q9JKF1	Exosome	QEAQR	FALGISAINEAVDSGDVGR	TLSAL	2		945.9819511	1889.948302	0.000451244	33	N	622	641
Q9JKF1	Exosome	QEAQR	FALGISAINEAVDSGDVGR	TLSAL	3		630.9905674	1889.948302	0.002374549	1	N	622	641
Q9JKF1	Exosome	IPAAK	LEGVLAEVAQHYQDTLIR	AKREK	3		685.701017	2054.079651	0.000451244	45	N	567	585
Q9JKF1	Exosome	RLHEK	GVLLEIEDLQANQFK	NVIFE	2		858.9624987	1715.909397	0.000451244	9	N	1571	1586
Q9JKF1	Exosome	KNMPR	CIYCIHALSLYLFK	LGLAP	2	C1:+57.021,C4:+57.021	900.9624702	1799.90934	0.00091018	1	N	147	161
Q9JKF1	Exosome	KNMPR	CIYCIHALSLYLFK	LGLAP	3	C1:+57.021,C4:+57.021	600.9775802	1799.90934	0.000451244	4	N	147	161
Q9JKF1	Exosome	ANQFK	NVIFEIGPTEEVGDFEVK	AKFMG	2		1011.507467	2020.999335	0.000451244	34	N	1586	1604
Q9JKF1	Exosome	ANQFK	NVIFEIGPTEEVGDFEVK	AKFMG	3		674.674245	2020.999335	0.00307782	1	N	1586	1604
Q9JKF1	Exosome	AASNK	MFLGDNAHLSIINEYLSQSYQK	FRRFF	2		1286.131561	2570.247522	0.000622848	1	N	1239	1261
Q9JKF1	Exosome	AASNK	MFLGDNAHLSIINEYLSQSYQK	FRRFF	3		857.7569741	2570.247522	0.000451244	12	N	1239	1261
Q9JKF1	Exosome	AASNK	MFLGDNAHLSIINEYLSQSYQK	FRRFF	3	M1:+15.995	863.0886408	2586.242522	0.000451244	15	N	1239	1261
Q9JKF1	Exosome	EEHER	ILAIGLINEALDEGDAQK	TLQAL	2		942.0101773	1882.004755	0.000451244	42	N	538	556
Q9JKF1	Exosome	EEHER	ILAIGLINEALDEGDAQK	TLQAL	3		628.3427182	1882.004755	0.000451244	36	N	538	556
Q9JKF1	Exosome	AKREK	AQETQDESAVLWLDEIQGGIWQSNKDTQEAQR	FALGI	3		1225.25087	3672.729209	0.000451244	33	N	590	622
Q9JKF1	Exosome	AKREK	AQETQDESAVLWLDEIQGGIWQSNKDTQEAQR	FALGI	4		919.1901024	3672.729209	0.001162105	1	N	590	622
Q9JKF1	Exosome	GLHFR	HTDNVIQWLNAMDEIGLPK	IFYPE	3		732.0374122	2193.088837	0.002981883	1	N	111	130
Q9JKF1	Exosome	RLHEK	GVLLEIEDLQANQF	KNVIF	2		794.9150171	1587.814434	0.000451244	11	N	1571	1585
Q9JKF1	Exosome	EEHER	ILAIGLINEALDEGDAQKTLQALQIPAAK	LEGVL	3		1006.568083	3016.680849	0.000451244	19	N	538	567
Q9JKF1	Exosome	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDRR	VAADT	3		1038.902236	3113.683309	0.000451244	8	N	201	231
Q9JKF1	Exosome	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDRR	VAADT	4		779.4286272	3113.683309	0.000451244	26	N	201	231
Q9JKF1	Exosome	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDR	RVAAD	3		986.8685326	2957.582198	0.000451244	3	N	201	230
Q9JKF1	Exosome	TGLKK	LTELGTVDPK	NRYQE	2		536.7983932	1071.581186	0.002019181	1	N	1465	1475
Q9JKF1	Exosome	VTLLK	ALQSLALGLR	GLQTQ	2		521.3249125	1040.634225	0.000451244	10	N	326	336
Q9JKF1	Exosome	IRAKR	EKAQETQDESAVLWLDEIQGGIWQSNK	DTQEA	3		1034.83919	3101.494171	0.000451244	14	N	588	615

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JKF1	Exosome	IGLPK	IFYPETTDIYDRK	NMPRC	2		830.9150171	1659.814434	0.000998612	1	N	130	143
Q9JKF1	Exosome	IGLPK	IFYPETTDIYDRK	NMPRC	3		554.2792781	1659.814434	0.002519933	1	N	130	143
Q9JKF1	Exosome	YLLLR	LFQTALQEEIK	SKVDQ	2		660.3644317	1318.713263	0.000451244	21	N	1024	1035
Q9JKF1	Exosome	QEEIK	SKVDQIQEIVTGNPTVIK	MVVSF	2		985.0523765	1968.089153	0.000451244	24	N	1035	1053
Q9JKF1	Exosome	QEEIK	SKVDQIQEIVTGNPTVIK	MVVSF	3		657.0375177	1968.089153	0.000451244	7	N	1035	1053
Q9JKF1	Exosome	GDAQK	TLQALQIPAAK	LEGVL	2		577.3511273	1152.686655	0.000451244	15	N	556	567
Q9JKF1	Exosome	EAQRF	ALGISAINEAVDSGDVGR	TLSAL	2		872.4477441	1742.879888	0.000451244	5	N	623	641
Q9JKF1	Exosome	VQLSR	EEIQSSISGVTAAYNR	EQLWL	2		862.9266445	1723.837689	0.000451244	46	N	722	738
Q9JKF1	Exosome	KHWVK	GGYHYYHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	3		1174.215543	3519.623228	0.000451244	36	N	691	722
Q9JKF1	Exosome	KHWVK	GGYHYYHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	4		880.913607	3519.623228	0.000451244	19	N	691	722
Q9JKF1	Exosome	GNVNK	VNTSSALANISLALEQGCAVTLLK	ALQSL	2	C18:+57.021	1237.170454	2472.325309	0.000451244	32	N	302	326
Q9JKF1	Exosome	GNVNK	VNTSSALANISLALEQGCAVTLLK	ALQSL	3	C18:+57.021	825.1162363	2472.325309	0.000451244	7	N	302	326
Q9JKF1	Exosome	FDRAK	VNVNLLIFLLNK	KFYGK	2		700.4377341	1398.859868	0.001162105	2	N	1640	1652
Q9JKF1	Exosome	AIDRR	VAADTFTALKNPNAMLVNLEEGLAPTYQDVLYQAK	QDKMT	3	M15:+15.995	1275.652576	3823.934327	0.000451244	26	N	231	266
Q9JKF1	Exosome	AEEVD	GLGVVRPHYGSVLDNER	LTAEE	3		623.3311469	1866.970041	0.000451244	7	N	8	25
Q9JKF1	Exosome	DPLQK	EEVQAGVDAANSAAQQYQR	RLAAV	2		1017.977928	2033.940257	0.000451244	6	N	368	387
Q9JKF1	Exosome	LYLFK	LGLAPQIQDLYGK	VDFTE	2		708.3988059	1414.782012	0.000622848	2	N	161	174
Q9JKF1	Exosome	ENSDR	ERDVYEELLTQAEIQGNVNK	VNTSS	2		1174.590583	2347.165566	0.000451244	4	N	282	302
Q9JKF1	Exosome	SKEKR	EKLEAYQHLFYLLQTNPTYLAK	LIFQM	3		895.1430455	2682.405737	0.000451244	8	N	966	988
Q9JKF1	Exosome	SKEKR	EKLEAYQHLFYLLQTNPTYLAK	LIFQM	4		671.6092341	2682.405737	0.000451244	1	N	966	988
Q9JKF1	Exosome	SDRER	DVYEELLTQAEIQGNVNK	VNTSS	2		1032.018731	2062.021861	0.000622848	1	N	284	302
Q9JKF1	Exosome	AKREK	AQETQDESAVLWLDEIQGGIWQSNK	DTQEA	2		1423.186107	2844.356614	0.000451244	4	N	590	615
Q9JKF1	Exosome	AKVLK	DSLHEKFPDAGEDELLK	IIGNL	2		971.9737918	1941.931984	0.000662267	1	N	1168	1185
Q9JKF1	Exosome	DELLK	IIGNLLYYR	YMNPA	2		562.8272881	1123.638976	0.001162105	12	N	1185	1194
Q9JKF1	Exosome	FDRAK	VNVNLLIFLLNKK	FYGK-	3		509.9927438	1526.954831	0.002981883	1	N	1640	1653
Q9JKF1	Exosome	EKREK	LEAYQHLFYLLQTNPTYLAK	LIFQM	3		809.4305267	2425.26818	0.002813207	2	N	968	988
Q9JKF1	Exosome	GLLVK	NKITLQDVVSHSK	KLTKK	3		490.2759794	1467.804538	0.000735798	4	N	922	935
Q9JKF1	Exosome	LLYYR	YMNPAIVAPDAFDIIDLSAGGQLTTDQR	RNLGS	3	M2:+15.995	1003.494395	3007.459786	0.000622848	2	N	1194	1222
Q9JKF1	Parental	PGETL	TEILETPATNEQEAEHQR	AMQRR	2		1048.498694	2094.981787	0.000451244	45	N	1404	1422
Q9JKF1	Parental	PGETL	TEILETPATNEQEAEHQR	AMQRR	3		699.3350625	2094.981787	0.000451244	36	N	1404	1422
Q9JKF1	Parental	TTVWK	QLSSSVTGLTNIEEENCQR	YLDEL	2	C17:+57.021	1083.01088	2164.006159	0.000451244	49	N	477	496
Q9JKF1	Parental	TTVWK	QLSSSVTGLTNIEEENCQR	YLDEL	2	[0:-17.027,C17:+57.021	1074.49738	2146.979159	0.002519933	1	N	477	496
Q9JKF1	Parental	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	C9:+57.021	674.9952813	2021.962444	0.000451244	17	N	36	52
Q9JKF1	Parental	DERRR	QNVAYEYLCHLEEAKR	WMEAC	4	C9:+57.021	506.498411	2021.962444	0.000451244	29	N	36	52
Q9JKF1	Parental	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	Q1:-17.027,C9:+57.021	669.3196146	2004.935444	0.001395409	1	N	36	52
Q9JKF1	Parental	DERRR	QNVAYEYLCHLEEAKR	WMEAC	3	[0:-17.027,C9:+57.021	669.3196146	2004.935444	0.000451244	24	N	36	52
Q9JKF1	Parental	LQQKR	QSGQTDPLQKEEVQAGVDAANSAAQQYQR	RLAAV	3		1039.833098	3116.475895	0.000451244	57	N	358	387
Q9JKF1	Parental	LQQKR	QSGQTDPLQKEEVQAGVDAANSAAQQYQR	RLAAV	3	[0:-17.027	1034.157432	3099.448895	0.000823681	2	N	358	387
Q9JKF1	Parental	EIKSK	VDQIQEIVTGNPTVIK	MVVSF	2		877.4888807	1752.962161	0.000451244	22	N	1037	1053
Q9JKF1	Parental	EIKSK	VDQIQEIVTGNPTVIK	MVVSF	3		585.3285205	1752.962161	0.000662267	1	N	1037	1053
Q9JKF1	Parental	AAYNR	EQLWLANEGLITK	LQACC	2		757.9148201	1513.81404	0.000451244	20	N	738	751
Q9JKF1	Parental	QANQF	KNVIFEIGPTEEVGDFEVK	AKFMG	2		1075.554949	2149.094298	0.000451244	45	N	1585	1604
Q9JKF1	Parental	QANQF	KNVIFEIGPTEEVGDFEVK	AKFMG	3		717.372566	2149.094298	0.000451244	37	N	1585	1604
Q9JKF1	Parental	VDVIR	FQPGETLTEILETPATNEQEAEHQR	AMQRR	2		1434.686471	2867.357343	0.001463592	1	N	1397	1422
Q9JKF1	Parental	VDVIR	FQPGETLTEILETPATNEQEAEHQR	AMQRR	3		956.7935809	2867.357343	0.000451244	17	N	1397	1422
Q9JKF1	Parental	GDVGR	TLSALRSPDVGLYGVIPECGETYQSDLAEAK	KKRLA	3	C19:+57.021	1113.885657	3338.633572	0.000451244	6	N	641	672
Q9JKF1	Parental	LSALR	SPDVGLYGVIPECGETYQSDLAEAK	KKRLA	2	C13:+57.021	1349.631556	2697.247512	0.000451244	24	N	647	672
Q9JKF1	Parental	LSALR	SPDVGLYGVIPECGETYQSDLAEAK	KKRLA	3	C13:+57.021	900.0903041	2697.247512	0.000451244	10	N	647	672
Q9JKF1	Parental	QEAQR	FALGISAINEAVDSGDVGR	TLSAL	2		945.9819511	1889.948302	0.000451244	18	N	622	641
Q9JKF1	Parental	QEAQR	FALGISAINEAVDSGDVGR	TLSAL	3		630.9905674	1889.948302	0.000451244	12	N	622	641
Q9JKF1	Parental	IPAAK	LEGVLAEVAQHYQDTLIR	AKREK	3		685.701017	2054.079651	0.000451244	52	N	567	585
Q9JKF1	Parental	RLHEK	GVLLEIEDLQANQFK	NVIFE	2		858.9624987	1715.909397	0.000451244	20	N	1571	1586
Q9JKF1	Parental	KNMPR	CIYCIHALSLYLFK	LGLAP	2	C1:+57.021,C4:+57.021	900.9624702	1799.90934	0.000451244	8	N	147	161
Q9JKF1	Parental	KNMPR	CIYCIHALSLYLFK	LGLAP	3	C1:+57.021,C4:+57.021	600.9775802	1799.90934	0.000637154	2	N	147	161
Q9JKF1	Parental	KNMPR	CIYCIHALSLYLFK	LGLAP	2	[0:-17.027,C1:+57.021,C4:+57.021	892.4489702	1782.88234	0.002981883	3	N	147	161
Q9JKF1	Parental	ANQFK	NVIFEIGPTEEVGDFEVK	AKFMG	2		1011.507467	2020.999335	0.000451244	26	N	1586	1604
Q9JKF1	Parental	AASNK	MFLGDNAHLSIINEYLSQSYQK	FRRFF	2		1286.131561	2570.247522	0.000451244	10	N	1239	1261
Q9JKF1	Parental	AASNK	MFLGDNAHLSIINEYLSQSYQK	FRRFF	3		857.7569741	2570.247522	0.000451244	25	N	1239	1261
Q9JKF1	Parental	VQLSR	EEIQSSISGVTAAYNREQLWLANEGLITK	LQACC	3		1074.221523	3219.641169	0.000451244	14	N	722	751
Q9JKF1	Parental	EEHER	ILAIGLINEALDEGDAQK	TLQAL	2		942.0101773	1882.004755	0.000451244	46	N	538	556
Q9JKF1	Parental	EEHER	ILAIGLINEALDEGDAQK	TLQAL	3		628.3427182	1882.004755	0.000451244	22	N	538	556
Q9JKF1	Parental	AKREK	AQETQDESAVLWLDEIQGGIWQSNKDTQEAQR	FALGI	3		1225.25087	3672.729209	0.000451244	36	N	590	622
Q9JKF1	Parental	AKREK	AQETQDESAVLWLDEIQGGIWQSNKDTQEAQR	FALGI	4		919.1901024	3672.729209	0.001352548	1	N	590	622
Q9JKF1	Parental	GLHFR	HTDNVIQWLNAMDEIGLPK	IFYPE	3		732.0374122	2193.088837	0.000637154	5	N	111	130
Q9JKF1	Parental	RLHEK	GVLLEIEDLQANQF	KNVIF	2		794.9150171	1587.814434	0.000451244	33	N	1571	1585

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JKF1	Parental	EEHER	ILAIGLINEALDEGDAQKTLQALQIPAAK	LEGVL	3		1006.568083	3016.680849	0.000451244	21	N	538	567
Q9JKF1	Parental	EEHER	ILAIGLINEALDEGDAQKTLQALQIPAAK	LEGVL	4		755.1780123	3016.680849	0.000622848	10	N	538	567
Q9JKF1	Parental	GDAQK	TLQALQIPAAKLEGVLAEVAQHYQDTLIR	AKREK	3		1063.926382	3188.755746	0.000451244	4	N	556	585
Q9JKF1	Parental	GDAQK	TLQALQIPAAKLEGVLAEVAQHYQDTLIR	AKREK	4		798.1967364	3188.755746	0.000451244	6	N	556	585
Q9JKF1	Parental	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDRR	VAADT	3		1038.902236	3113.683309	0.000451244	23	N	201	231
Q9JKF1	Parental	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDRR	VAADT	4		779.4286272	3113.683309	0.000451244	40	N	201	231
Q9JKF1	Parental	PAFSK	IGGILANELSVDEAALHAAVIAINEAIDR	RVAAD	3		986.8685326	2957.582198	0.000451244	8	N	201	230
Q9JKF1	Parental	TGLKK	LTELGTVDPK	NRYQE	2		536.7983932	1071.581186	0.000451244	25	N	1465	1475
Q9JKF1	Parental	VTLLK	ALQSLALGLR	GLQTQ	2		521.3249125	1040.634225	0.000622848	21	N	326	336
Q9JKF1	Parental	IRAKR	EKAQETQDESAVLWLDEIQGGIWQSNK	DTQEA	3		1034.83919	3101.494171	0.000451244	17	N	588	615
Q9JKF1	Parental	IGLPK	IFYPETTDIYDRK	NMPRC	2		830.9150171	1659.814434	0.000622848	18	N	130	143
Q9JKF1	Parental	IGLPK	IFYPETTDIYDRK	NMPRC	3		554.2792781	1659.814434	0.0007646	6	N	130	143
Q9JKF1	Parental	YLLLR	LFQTALQEEIK	SKVDQ	2		660.3644317	1318.713263	0.000451244	18	N	1024	1035
Q9JKF1	Parental	QEEIK	SKVDQIQEIVTGNPTVIK	MVVSF	2		985.0523765	1968.089153	0.000451244	38	N	1035	1053
Q9JKF1	Parental	QEEIK	SKVDQIQEIVTGNPTVIK	MVVSF	3		657.0375177	1968.089153	0.000451244	5	N	1035	1053
Q9JKF1	Parental	GDAQK	TLQALQIPAAK	LEGVL	2		577.3511273	1152.686655	0.000451244	35	N	556	567
Q9JKF1	Parental	EAQRF	ALGISAINEAVDSGDVGR	TLSAL	2		872.4477441	1742.879888	0.000451244	21	N	623	641
Q9JKF1	Parental	KHWVK	GGYHYYHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	3		1174.215543	3519.623228	0.000451244	15	N	691	722
Q9JKF1	Parental	KHWVK	GGYHYYHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	4		880.913607	3519.623228	0.000698008	1	N	691	722
Q9JKF1	Parental	GNVNK	VNTSSALANISLALEQGCAVTLLK	ALQSL	3	C18:+57.021	825.1162363	2472.325309	0.000451244	22	N	302	326
Q9JKF1	Parental	AIDRR	VAADTFTALKNPNAMLVNLEEGLAPTYQDVLYQAK	QDKMT	3	M15:+15.995	1275.652576	3823.934327	0.000622848	10	N	231	266
Q9JKF1	Parental	DPLQK	EEVQAGVDAANSAAQQYQR	RLAAV	2		1017.977928	2033.940257	0.000451244	11	N	368	387
Q9JKF1	Parental	LYLFK	LGLAPQIQDLYGK	VDFTE	2		708.3988059	1414.782012	0.000622848	6	N	161	174
Q9JKF1	Parental	ENSDR	ERDVYEELLTQAEIQGNVNK	VNTSS	2		1174.590583	2347.165566	0.00091018	1	N	282	302
Q9JKF1	Parental	ENSDR	ERDVYEELLTQAEIQGNVNK	VNTSS	3		783.3963219	2347.165566	0.000622848	3	N	282	302
Q9JKF1	Parental	SDRER	DVYEELLTQAEIQGNVNK	VNTSS	2		1032.018731	2062.021861	0.000451244	19	N	284	302
Q9JKF1	Parental	AKREK	AQETQDESAVLWLDEIQGGIWQSNK	DTQEA	2		1423.186107	2844.356614	0.000451244	18	N	590	615
Q9JKF1	Parental	AKREK	AQETQDESAVLWLDEIQGGIWQSNK	DTQEA	3		949.1266714	2844.356614	0.000451244	22	N	590	615
Q9JKF1	Parental	SAVLW	LDEIQGGIWQSNKDTQEAQR	FALGI	2		1158.564899	2315.114199	0.000451244	5	N	602	622
Q9JKF1	Parental	SAVLW	LDEIQGGIWQSNKDTQEAQR	FALGI	3		772.7125329	2315.114199	0.000451244	7	N	602	622
Q9JKF1	Parental	GYHYY	HNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	2		1390.673501	2779.331402	0.000451244	4	N	697	722
Q9JKF1	Parental	GYHYY	HNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	3		927.4516008	2779.331402	0.000451244	18	N	697	722
Q9JKF1	Parental	GGYHY	YHNLETQAGGWAEPPDFVQNSVQLSR	EEIQS	3		981.8060437	2942.394731	0.000451244	14	N	696	722
Q9JKF1	Parental	GDVGR	TLSALRSPDVGLYGVIPECGETY	QSDLA	2	C19:+57.021	1249.117888	2496.220175	0.0007646	1	N	641	664
Q9JKF1	Parental	AKVLK	DSLHEKFPDAGEDELLK	IIGNL	2		971.9737918	1941.931984	0.000451244	9	N	1168	1185
Q9JKF1	Parental	AKVLK	DSLHEKFPDAGEDELLK	IIGNL	3		648.3184612	1941.931984	0.000451244	14	N	1168	1185
Q9JKF1	Parental	NFLKK	QIPAITCIQSQWR	GYKQK	2	C7:+57.021	800.9171399	1599.81868	0.002884417	1	N	774	787
Q9JKF1	Parental	GEASK	LPYDVTPEQALSHEEVK	TRLDN	3		652.3305897	1953.968369	0.000451244	1	N	1111	1128
Q9JKF1	Parental	QYQRR	LAAVAAINAAIQK	GIAEK	2		627.3829588	1252.750318	0.002453667	1	N	388	401
Q9JKF1	Parental	DELLK	IIGNLLYYR	YMNPA	2		562.8272881	1123.638976	0.000851441	10	N	1185	1194
Q9JKF1	Parental	DERRR	QNVAYEYLCHLEEAK	RWMEA	3	C9:+57.021	622.9615776	1865.861333	0.000662267	5	N	36	51
Q9JKF1	Parental	QFKNV	IFEIGPTEEVGDFEVK	AKFMG	2		904.9517967	1807.887993	0.000823681	2	N	1588	1604
Q9JKF1	Parental	LSALR	SPDVGLYGVIPECGETY	QSDLA	2	C13:+57.021	928.4248574	1854.834115	0.002019181	2	N	647	664
Q9JKR6	Exosome	MAGLK	VLQLINDNTATALSYGVFR	RKDIN	2		1048.063276	2094.110951	0.000451244	36	N	198	217
Q9JKR6	Exosome	LNYSR	SLAEDFAEQPIKDAVITVPAFFNQAER	RAVLQ	3		1002.845616	3005.513449	0.002453667	2	N	158	185
Q9JKR6	Exosome	PFVVR	DAVIYPILVEFTR	EVEEE	2		768.4275634	1534.839527	0.000451244	14	N	438	451
Q9JKR6	Exosome	SKGIK	AHFNLDESGVLSLDRVESVFETLVEDSPEEESTLTK	LGNTI	3		1341.318727	4020.93278	0.000823681	1	N	540	576
Q9JKR6	Exosome	SKGIK	AHFNLDESGVLSLDRVESVFETLVEDSPEEESTLTK	LGNTI	4		1006.240995	4020.93278	0.002884417	1	N	540	576
Q9JKR6	Exosome	QEREK	AANSLEAFIFETQDK	LYQPE	2		842.4153813	1682.815163	0.000451244	15	N	738	753
Q9JKR6	Exosome	QEREK	AANSLEAFIFETQDK	LYQPE	3		561.9461875	1682.815163	0.000451244	4	N	738	753
Q9JKR6	Exosome	LDRVE	SVFETLVEDSPEEESTLTK	LGNTI	2		1070.513144	2139.010688	0.000622848	8	N	557	576
Q9JKR6	Parental	ITFNR	YSHDFNFHINYGDLGFLGPEDLR	VFGSQ	3		909.426504	2725.256112	0.000451244	1	N	486	509
Q9JKR6	Parental	ITFNR	YSHDFNFHINYGDLGFLGPEDLR	VFGSQ	4		682.321828	2725.256112	0.000622848	2	N	486	509
Q9JKR6	Parental	MAGLK	VLQLINDNTATALSYGVFR	RKDIN	2		1048.063276	2094.110951	0.000451244	34	N	198	217
Q9JKR6	Parental	MAGLK	VLQLINDNTATALSYGVFR	RKDIN	3		699.0447837	2094.110951	0.000451244	10	N	198	217
Q9JKR6	Parental	LNYSR	SLAEDFAEQPIKDAVITVPAFFNQAER	RAVLQ	3		1002.845616	3005.513449	0.000451244	17	N	158	185
Q9JKR6	Parental	PFVVR	DAVIYPILVEFTR	EVEEE	2		768.4275634	1534.839527	0.000622848	11	N	438	451
Q9JKR6	Parental	PFVVR	DAVIYPILVEFTR	EVEEE	3		512.6209756	1534.839527	0.000622848	8	N	438	451
Q9JKR6	Parental	SKGIK	AHFNLDESGVLSLDRVESVFETLVEDSPEEESTLTK	LGNTI	3		1341.318727	4020.93278	0.000451244	25	N	540	576
Q9JKR6	Parental	SKGIK	AHFNLDESGVLSLDRVESVFETLVEDSPEEESTLTK	LGNTI	4		1006.240995	4020.93278	0.000451244	18	N	540	576
Q9JKR6	Parental	PFVVR	DAVIYPILVEFTREVEEEPGLR	SLKHN	3		858.7870388	2573.337717	0.000637154	1	N	438	460
Q9JKR6	Parental	QEREK	AANSLEAFIFETQDK	LYQPE	2		842.4153813	1682.815163	0.000451244	12	N	738	753
Q9JKR6	Parental	QEREK	AANSLEAFIFETQDK	LYQPE	3		561.9461875	1682.815163	0.000622848	6	N	738	753
Q9JKR6	Parental	PFVVR	DAVIYPILVEF	TREVE	2		639.8531685	1277.690737	0.002145581	1	N	438	449
Q9JKR6	Parental	ETQDK	LYQPEYQEVSTEEQR	EEISG	2		949.9424916	1897.869383	0.001463592	1	N	753	768

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JKR6	Parental	LSLDR	VESVFETLVEDSPEEESTLTK	LGNTI	2		1184.568647	2367.121695	0.000451244	15	N	555	576
Q9JKR6	Parental	LSLDR	VESVFETLVEDSPEEESTLTK	LGNTI	3		790.0483649	2367.121695	0.000622848	3	N	555	576
Q9JKV1	Exosome	CWKDR	TSGTVEDDLIIFPDDCEFKR	VPQCP	3	C16:+57.021	786.3707422	2356.088826	0.000451244	1	N	64	84
Q9JKV1	Parental	CWKDR	TSGTVEDDLIIFPDDCEFK	RVPQC	2	C16:+57.021	1101.001658	2199.987715	0.00091018	11	N	64	83
Q9JKV1	Parental	CWKDR	TSGTVEDDLIIFPDDCEFKR	VPQCP	2	C16:+57.021	1179.052213	2356.088826	0.000451244	1	N	64	84
Q9JKV1	Parental	CWKDR	TSGTVEDDLIIFPDDCEFKR	VPQCP	3	C16:+57.021	786.3707422	2356.088826	0.000451244	8	N	64	84
Q9JKY5	Parental	LAVLR	SAAAEAEAILQDAVSKLDDPLHLR	CTSSP	4		634.0873945	2532.318378	0.000451244	6	N	625	649
Q9JKY5	Parental	YLVSR	AQAALDSVSGLEQGHTQYLASSEDASALVAALTR	FSHLA	3		1144.241535	3429.701204	0.000451244	8	N	660	694
Q9JL26	Exosome	HFLDK	AGSVSLDSVLGDVR	SLQRG	2		687.8653272	1373.715054	0.000451244	5	N	901	915
Q9JL26	Exosome	KGLIR	ILRGPGDVVSIEILPGAAATPSGDDAQAPR	VSTDS	3		981.8565155	2942.546147	0.000979378	3	N	489	519
Q9JL26	Exosome	LADSK	TAQEAYESVVEYFGENPK	TTSPS	2		1030.976531	2059.937463	0.000451244	7	N	956	974
Q9JL26	Exosome	RKQQK	EPLIYESDRDGAIEDIITDLR	NQPYI	3		811.7434987	2432.207096	0.001839721	2	N	1042	1063
Q9JL26	Exosome	LGADR	ICQAIETYDLQTLSLDFLELLTR	FLPTD	2	C2:+57.021	1378.215059	2754.414518	0.001943752	1	N	726	749
Q9JL26	Exosome	LGADR	ICQAIETYDLQTLSLDFLELLTR	FLPTD	3	C2:+57.021	919.1459727	2754.414518	0.000622848	1	N	726	749
Q9JL26	Exosome	QIQAY	LDNVFDVGTLLEETETK	NAVLE	2		961.9838252	1921.95205	0.000451244	8	N	376	393
Q9JL26	Exosome	IRILR	GPGDVVSIEILPGAAATPSGDDAQAPR	VSTDS	2		1281.146254	2560.276907	0.001162105	1	N	492	519
Q9JL26	Exosome	VCLVR	GGHDIILAAFDNFK	EVCGE	3		506.5969415	1516.767424	0.000823681	1	N	282	296
Q9JL26	Parental	HFLDK	AGSVSLDSVLGDVR	SLQRG	2		687.8653272	1373.715054	0.000451244	7	N	901	915
Q9JL26	Parental	KGLIR	ILRGPGDVVSIEILPGAAATPSGDDAQAPR	VSTDS	3		981.8565155	2942.546147	0.000451244	22	N	489	519
Q9JL26	Parental	LADSK	TAQEAYESVVEYFGENPK	TTSPS	2		1030.976531	2059.937463	0.000451244	43	N	956	974
Q9JL26	Parental	RKQQK	EPLIYESDRDGAIEDIITDLR	NQPYI	3		811.7434987	2432.207096	0.000451244	4	N	1042	1063
Q9JL26	Parental	LGADR	ICQAIETYDLQTLSLDFLELLTR	FLPTD	2	C2:+57.021	1378.215059	2754.414518	0.000451244	9	N	726	749
Q9JL26	Parental	LGADR	ICQAIETYDLQTLSLDFLELLTR	FLPTD	3	C2:+57.021	919.1459727	2754.414518	0.000451244	19	N	726	749
Q9JL26	Parental	QIQAY	LDNVFDVGTLLEETETK	NAVLE	2		961.9838252	1921.95205	0.000451244	21	N	376	393
Q9JL26	Parental	QIQAY	LDNVFDVGTLLEETETK	NAVLE	3		641.6584834	1921.95205	0.000622848	4	N	376	393
Q9JL26	Parental	ITLRK	GNLGADRICQAIETYDLQTLSLDFLELLTR	FLPTD	3	C9:+57.021	1146.924335	3437.749605	0.002663018	1	N	719	749
Q9JL26	Parental	AIETY	DLQTLSLDFLELLTR	FLPTD	2		888.9912562	1775.966912	0.000451244	5	N	734	749
Q9JL26	Parental	IRILR	GPGDVVSIEILPGAAATPSGDDAQAPR	VSTDS	2		1281.146254	2560.276907	0.000451244	32	N	492	519
Q9JL26	Parental	EPLIY	ESDRDGAIEDIITDLR	NQPYI	3		606.6345608	1816.880282	0.000451244	9	N	1047	1063
Q9JL62	Exosome	LPADR	QIETGPFLEAVAHLPPFFDCLGSPVFTPIK	ADISG	3	C20:+57.021	1109.909298	3326.704493	0.000451244	5	N	16	46
Q9JL62	Parental	LPADR	QIETGPFLEAVAHLPPFFDCLGSPVFTPIK	ADISG	3	C20:+57.021	1109.909298	3326.704493	0.000451244	8	N	16	46
Q9JL62	Parental	LPADR	QIETGPFLEAVAHLPPFFDCLGSPVFTPIKADISGNITK	IKAVY	4	C20:+57.021	1057.551735	4226.17574	0.00091018	5	N	16	55
Q9JLF6	Exosome	DCWMK	RPDLPSGFDGWQVVDATPQETSSGIFCCGPCSVESVK	NGLVY	3	C27:+57.021,C28:+57.021,C31:+57.021	1357.283737	4068.827812	0.000451244	4	N	443	480
Q9JLF6	Parental	RPGPR	QLIASLDSPQLSQVHGVIQVDVAPASGGSGFSDAGGDSR	SGENI	3		1274.968474	3821.882022	0.000451244	7	N	763	802
Q9JLF6	Parental	DCWMK	RPDLPSGFDGWQVVDATPQETSSGIFCCGPCSVESVK	NGLVY	3	C27:+57.021,C28:+57.021,C31:+57.021	1357.283737	4068.827812	0.000622848	9	N	443	480
Q9JLF6	Parental	GDYSR	GTNPSAWVGSVEILLSYLR	TGYSV	2		1031.552544	2061.089487	0.000451244	10	N	347	366
Q9JLJ2	Exosome	FGYTR	REPLGVCVGIGAWNYPFQIACWK	SAPAL	3	C7:+57.021,C21:+57.021	907.7860133	2720.33464	0.000622848	12	N	143	166
Q9JLJ2	Exosome	QRAHR	VAAELQAGTCYINNYNVSPVELPFGGYKK	SGFGR	3	C10:+57.021	1068.20114	3201.580021	0.000451244	15	N	433	462
Q9JLJ2	Exosome	VKLAK	EQGATVLCGGEVYVPEDPKLK	HGYYM	3	C8:+57.021	763.7195942	2288.135383	0.000451244	9	N	347	368
Q9JLJ2	Exosome	EVLER	ANDTTFGLAAGVFTR	DIQRA	2		770.8918764	1539.768153	0.000662267	5	N	411	426
Q9JLJ2	Exosome	VKLAK	EQGATVLCGGEVYVPEDPK	LKHGY	2	C8:+57.021	1024.485978	2046.956355	0.000451244	9	N	347	366
Q9JLJ2	Exosome	VFVQK	EIADKFINEVVK	QTQKI	3		468.9298091	1403.766027	0.000823681	3	N	298	310
Q9JLJ2	Exosome	IFEAR	LDVDTCWQCLEYYAGLAASMAGEHIQLPGGSFGYTR	REPLG	3	C6:+57.021,C9:+57.021	1346.281823	4035.822068	0.000451244	1	N	107	143
Q9JLJ2	Exosome	REVAK	ISFTGSVPTGVK	IMEMS	2		596.8327674	1191.649935	0.002212458	2	N	227	239
Q9JLJ2	Exosome	AGTCY	INNYNVSPVELPFGGYK	KSGFG	2		955.9865052	1909.95741	0.001162105	2	N	444	461
Q9JLJ2	Parental	FGYTR	REPLGVCVGIGAWNYPFQIACWK	SAPAL	3	C7:+57.021,C21:+57.021	907.7860133	2720.33464	0.000622848	9	N	143	166
Q9JLJ2	Parental	VKLAK	EQGATVLCGGEVYVPEDPKLK	HGYYM	3	C8:+57.021	763.7195942	2288.135383	0.001871652	1	N	347	368
Q9JLJ2	Parental	VKLAK	EQGATVLCGGEVYVPEDPK	LKHGY	2	C8:+57.021	1024.485978	2046.956355	0.001329271	2	N	347	366
Q9JLQ2	Exosome	QKLAR	FNAHEFATLVIDILSDAK	RRQQG	3		668.6865964	2003.036389	0.000451244	26	N	335	353
Q9JLQ2	Exosome	SECRK	ALPGDSSLPTDVQLVTQQVIQCAYDIAK	AAKQL	3	C22:+57.021	1010.853629	3029.537487	0.002080925	1	N	665	693
Q9JLQ2	Exosome	SKRLR	SSDVCADCNGPDPSWASVNR	GTFIC	2	C5:+57.021,C8:+57.021	1097.449901	2192.884201	0.000451244	8	N	6	26
Q9JLQ2	Exosome	HVASK	AGQILQAELLAVYGADPGTQDSSGK	TPVDY	2		1245.130072	2488.244544	0.000451244	5	N	176	201
Q9JLQ2	Exosome	HVASK	AGQILQAELLAVYGADPGTQDSSGKTPVDYAR	QGGHH	3		1097.888433	3290.641898	0.000451244	7	N	176	208
Q9JLQ2	Exosome	EVDRR	ETDAVWLATQNHSTLVTETTVVPFLPVNPEYSSTR	NQGRQ	3		1301.653604	3901.937411	0.001162105	2	N	291	326
Q9JLQ2	Parental	QKLAR	FNAHEFATLVIDILSDAK	RRQQG	3		668.6865964	2003.036389	0.000451244	36	N	335	353
Q9JLQ2	Parental	SECRK	ALPGDSSLPTDVQLVTQQVIQCAYDIAK	AAKQL	3	C22:+57.021	1010.853629	3029.537487	0.000451244	29	N	665	693
Q9JLQ2	Parental	SKRLR	SSDVCADCNGPDPSWASVNR	GTFIC	2	C5:+57.021,C8:+57.021	1097.449901	2192.884201	0.000451244	18	N	6	26
Q9JLQ2	Parental	QSECR	KALPGDSSLPTDVQLVTQQVIQCAYDIAK	AAKQL	3	C23:+57.021	1053.55195	3157.63245	0.000735798	3	N	664	693
Q9JLQ2	Parental	EVDRR	ETDAVWLATQNHSTLVTETTVVPFLPVNPEYSSTR	NQGRQ	3		1301.653604	3901.937411	0.001699387	1	N	291	326
Q9JLT4-2	Exosome	QLGKK	VAVADYVEPSPR	GTKWG	2		651.8385811	1301.661562	0.000851441	1	N	31	43
Q9JLT4-2	Exosome	PRGTK	WGLGGTCVNVGCIPK	KLMHQ	2	C7:+57.021,C12:+57.021	809.3974944	1616.779389	0.000451244	2	Y	46	61
Q9JLT4-2	Exosome	PKNQK	IIVDAQEATSVPHIYAIGDVAEGRPELTPTAIK	AGKLL	3		1158.954666	3473.840598	0.000998612	2	N	307	340
Q9JLT4-2	Exosome	MVCMR	EPPQLVLGLHFLGPNAGEVTQGFALGIK	CGASY	3		968.1995539	2901.575262	0.000451244	4	N	421	449

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JLT4-2	Parental	QLGKK	VAVADYVEPSPR	GTKWG	2		651.8385811	1301.661562	0.002374549	1	N	31	43
Q9JLT4-2	Parental	-	MEGQQSFDLLVIGGGSGGLACAKEAAQLGK	KVAVA	4	C21:+57.021	748.8775318	2991.478927	0.002296037	1	N	0	30
Q9JLV6	Exosome	QLGSR	GRLWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	3		977.2069314	2928.597394	0.000451244	7	N	7	35
Q9JLV6	Exosome	GSRGR	LWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	2		1358.74521	2715.474819	0.000451244	16	N	9	35
Q9JLV6	Exosome	GSRGR	LWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	3		906.1660731	2715.474819	0.000451244	36	N	9	35
Q9JLV6	Exosome	MFSYR	KQFEPPTLAEGFLEILEIPFR	LQEHL	3		825.4496984	2473.325695	0.000622848	2	N	482	503
Q9JLV6	Exosome	SCADR	LFALNVGLPFATPEEFFLK	WPAAR	2		1077.088231	2152.160861	0.000451244	28	N	310	329
Q9JLV6	Exosome	SCADR	LFALNVGLPFATPEEFFLK	WPAAR	3		718.3947538	2152.160861	0.000451244	5	N	310	329
Q9JLV6	Exosome	FSYRK	QFEPPTLAEGFLEILEIPFR	LQEHL	2		1173.623166	2345.230732	0.000451244	14	N	483	503
Q9JLV6	Exosome	FSYRK	QFEPPTLAEGFLEILEIPFR	LQEHL	3		782.7513773	2345.230732	0.000451244	4	N	483	503
Q9JLV6	Exosome	EIPFR	LQEHLDPALQR	LYRQF	3		440.5742482	1318.699345	0.001352548	1	N	503	514
Q9JLV6	Exosome	KPQGK	VAAFDLDGTLITTR	SGKVF	2		746.9044524	1491.793305	0.000451244	24	N	165	179
Q9JLV6	Exosome	WPAAR	FELPAFDPR	TISSA	2		546.2801706	1090.544741	0.001162105	6	N	334	343
Q9JLV6	Exosome	PLTLR	WEELSTSGSQPDAPPDTPGDPEEGEDTEPQKK	RVRKS	3		1151.841653	3452.50156	0.000451244	50	N	105	137
Q9JLV6	Exosome	AVLEK	LGVPFQVLVATHAGLNR	KPVSG	3		598.0129781	1791.015534	0.000979378	5	N	241	258
Q9JLV6	Exosome	SCADR	LFALNVGLPFATPEEF	FLKWP	2		882.9645101	1763.91342	0.000662267	7	N	310	326
Q9JLV6	Exosome	PLTLR	WEELSTSGSQPDAPPDTPGDPEEGEDTEPQK	KRVRK	3		1109.143332	3324.406597	0.000622848	3	N	105	136
Q9JLV6	Exosome	LRWEE	LSTSGSQPDAPPDTPGDPEEGEDTEPQKK	RVRKS	3		1003.78682	3008.337061	0.000622848	1	N	108	137
Q9JLV6	Exosome	PGAGK	STFIQEHLVSAGYVHVNR	DTLGS	3		686.3574731	2056.049019	0.000451244	9	N	377	395
Q9JLV6	Exosome	FSYRK	QFEPPTLAEGFLEILEIPF	RLQEH	2		1095.57261	2189.129621	0.002727428	1	N	483	502
Q9JLV6	Exosome	ADRLF	ALNVGLPFATPEEFFLK	WPAAR	2		947.0119916	1892.008383	0.000451244	4	N	312	329
Q9JLV6	Exosome	AFDPR	TISSAGPLYLPESSSLLSPNPEVV	VAVGF	2		1229.142117	2456.268634	0.001463592	1	N	343	367
Q9JLV6	Parental	RKCSR	NQVELIADPESR	TVAVK	2		685.8496771	1369.683754	0.000451244	9	N	48	60
Q9JLV6	Parental	QLGSR	GRLWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	3		977.2069314	2928.597394	0.000451244	10	N	7	35
Q9JLV6	Parental	AFDPR	TISSAGPLYLPESSSLLSPNPEVVVAVGFPGAGK	STFIQ	3		1114.261207	3339.760222	0.000451244	18	N	343	377
Q9JLV6	Parental	GSRGR	LWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	2		1358.74521	2715.474819	0.000451244	27	N	9	35
Q9JLV6	Parental	GSRGR	LWLQSPTGGPPPIFLPSDGQALVLGR	GPLTQ	3		906.1660731	2715.474819	0.000451244	40	N	9	35
Q9JLV6	Parental	MFSYR	KQFEPPTLAEGFLEILEIPFR	LQEHL	3		825.4496984	2473.325695	0.001352548	1	N	482	503
Q9JLV6	Parental	GRKKK	DFSCADRLFALNVGLPFATPEEFFLK	WPAAR	3	C4:+57.021	1002.169	3003.483601	0.002813207	1	N	303	329
Q9JLV6	Parental	SCADR	LFALNVGLPFATPEEFFLK	WPAAR	2		1077.088231	2152.160861	0.001463592	5	N	310	329
Q9JLV6	Parental	KPQGK	VAAFDLDGTLITTR	SGKVF	2		746.9044524	1491.793305	0.000451244	18	N	165	179
Q9JLV6	Parental	PLTLR	WEELSTSGSQPDAPPDTPGDPEEGEDTEPQKK	RVRKS	3		1151.841653	3452.50156	0.000451244	13	N	105	137
Q9JLV6	Parental	GRKKK	DFSCADRLFALNVGLPFATPEEF	FLKWP	2	C4:+57.021	1308.62588	2615.23616	0.000451244	4	N	303	326
Q9JLV6	Parental	SCADR	LFALNVGLPFATPEEF	FLKWP	2		882.9645101	1763.91342	0.000698008	5	N	310	326
Q9JLV6	Parental	PLTLR	WEELSTSGSQPDAPPDTPGDPEEGEDTEPQK	KRVRK	3		1109.143332	3324.406597	0.000451244	9	N	105	136
Q9JLV6	Parental	PPIFL	PSDGQALVLGR	GPLTQ	2		556.8070839	1111.598568	0.001871652	1	N	24	35
Q9JM14	Exosome	DLAEK	VASVYESPGFFLNLEPIPGALDALR	EMNDM	2		1338.208126	2674.400651	0.000451244	9	N	62	87
Q9JM14	Exosome	DLAEK	VASVYESPGFFLNLEPIPGALDALR	EMNDM	3		892.4746837	2674.400651	0.000451244	9	N	62	87
Q9JM14	Exosome	LEQRR	GFLANEQYGALRPDLAEK	VASVY	3		664.6782123	1991.011237	0.000451244	9	N	44	62
Q9JM14	Exosome	GEKYR	WVEQNLGPEFVER	IILTR	2		801.8997014	1601.783803	0.000622848	7	N	116	129
Q9JM14	Parental	DLAEK	VASVYESPGFFLNLEPIPGALDALR	EMNDM	2		1338.208126	2674.400651	0.000451244	12	N	62	87
Q9JM14	Parental	DLAEK	VASVYESPGFFLNLEPIPGALDALR	EMNDM	3		892.4746837	2674.400651	0.000451244	6	N	62	87
Q9JM14	Parental	KRPVR	VLVDMDGVLADFESGLLQGFR	RRFPE	2		1141.080809	2280.146017	0.000451244	1	N	8	29
Q9JM76	Exosome	RLCEK	VFDPQSDKPSKWWTCFVK	RQFMN	4	C15:+57.021	564.5297111	2254.087644	0.000998612	8	N	147	165
Q9JM76	Exosome	DPDTK	LIGNMALLPLR	SQFKG	2		605.8711732	1209.726746	0.000823681	7	N	14	25
Q9JM76	Exosome	GPAPR	ETKDTDIVDEAIYYFK	ANVFF	2		975.4730933	1948.930587	0.000451244	37	N	34	50
Q9JM76	Exosome	GPAPR	ETKDTDIVDEAIYYFK	ANVFF	3		650.6513288	1948.930587	0.000451244	37	N	34	50
Q9JM76	Exosome	PRETK	DTDIVDEAIYYFK	ANVFF	2		796.3804758	1590.745352	0.000451244	51	N	37	50
Q9JM76	Exosome	PRETK	DTDIVDEAIYYFK	ANVFF	3		531.2562505	1590.745352	0.000451244	9	N	37	50
Q9JM76	Exosome	EKEMY	TLGITNFPIPGEPGFPLNAIYAKPASK	QEDEM	3		938.5132499	2812.51635	0.000823681	1	N	96	123
Q9JM76	Exosome	KCNSK	SQGEKEMYTLGITNFPIPGEPGFPLNAIYAK	PASKQ	3		1128.239638	3381.695514	0.000451244	8	N	88	119
Q9JM76	Exosome	KCNSK	SQGEKEMYTLGITNFPIPGEPGFPLNAIYAK	PASKQ	3	M7:+15.995	1133.571305	3397.690514	0.000622848	5	N	88	119
Q9JM76	Exosome	SQGEK	EMYTLGITNFPIPGEPGFPLNAIYAK	PASKQ	3		951.823096	2852.445888	0.002453667	1	N	93	119
Q9JM76	Exosome	SQGEK	EMYTLGITNFPIPGEPGFPLNAIYAKPASK	QEDEM	3		1079.562052	3235.662757	0.002145581	1	N	93	123
Q9JM76	Parental	RLCEK	VFDPQSDKPSKWWTCFVK	RQFMN	4	C15:+57.021	564.5297111	2254.087644	0.000998612	6	N	147	165
Q9JM76	Parental	DPDTK	LIGNMALLPLR	SQFKG	2		605.8711732	1209.726746	0.001699387	1	N	14	25
Q9JM76	Parental	GPAPR	ETKDTDIVDEAIYYFK	ANVFF	2		975.4730933	1948.930587	0.000451244	29	N	34	50
Q9JM76	Parental	GPAPR	ETKDTDIVDEAIYYFK	ANVFF	3		650.6513288	1948.930587	0.000451244	29	N	34	50
Q9JM76	Parental	PRETK	DTDIVDEAIYYFK	ANVFF	2		796.3804758	1590.745352	0.000451244	34	N	37	50
Q9JM76	Parental	PRETK	DTDIVDEAIYYFK	ANVFF	3		531.2562505	1590.745352	0.000622848	1	N	37	50
Q9JM76	Parental	EKEMY	TLGITNFPIPGEPGFPLNAIYAKPASK	QEDEM	3		938.5132499	2812.51635	0.000451244	8	N	96	123
Q9JM76	Parental	PRETK	DTDIVDEAIYYF	KANVF	2		732.3329942	1462.650388	0.000823681	5	N	37	49
Q9JMA1	Exosome	VLQQK	LEAIEDDSGRETDSSSAPAVTPSK	KKSLI	2		1231.580609	2461.145618	0.000622848	1	N	214	238
Q9JMA1	Exosome	VLQQK	LEAIEDDSGRETDSSSAPAVTPSK	KKSLI	3		821.3896727	2461.145618	0.000451244	47	N	214	238
Q9JMA1	Exosome	PKEIK	YEPFSFADDIGSNNCGYYDLQAVLTHQGR	SSSSG	3	C15:+57.021	1113.167047	3336.47774	0.000451244	37	N	399	428

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9JMA1	Exosome	EDILR	LSGGGDWHIAYVLLYGPR	RVEIM	3		658.6797761	1973.015928	0.001591523	3	N	464	482
Q9JMA1	Exosome	DEWIK	FDDDKVSIVTPEDILR	LSGGG	3		621.3234351	1860.946905	0.000451244	9	N	448	464
Q9JMA1	Exosome	PMVFK	AQLFALTGVQPAR	QKVMV	2		686.3913152	1370.76703	0.001264573	1	N	30	43
Q9JMA1	Exosome	NSPPK	EIKYEPFSFADDIGSNNCGYYDLQAVLTHQGR	SSSSG	4	C18:+57.021	927.6826402	3706.699361	0.000451244	3	N	396	428
Q9JMA1	Exosome	KYEPF	SFADDIGSNNCGYYDLQAVLTHQGR	SSSSG	3	C11:+57.021	934.4246802	2800.250641	0.001352548	1	N	403	428
Q9JMA1	Exosome	VTKGK	ENQLQLSCFINQEVK	YLFTG	2	C8:+57.021	925.4595659	1848.903532	0.001162105	1	N	269	284
Q9JMA1	Parental	VLQQK	LEAIEDDSGRETDSSSAPAVTPSK	KKSLI	2		1231.580609	2461.145618	0.000451244	4	N	214	238
Q9JMA1	Parental	VLQQK	LEAIEDDSGRETDSSSAPAVTPSK	KKSLI	3		821.3896727	2461.145618	0.000451244	39	N	214	238
Q9JMA1	Parental	PKEIK	YEPFSFADDIGSNNCGYYDLQAVLTHQGR	SSSSG	3	C15:+57.021	1113.167047	3336.47774	0.000451244	22	N	399	428
Q9JMA1	Parental	EDILR	LSGGGDWHIAYVLLYGPR	RVEIM	3		658.6797761	1973.015928	0.001699387	1	N	464	482
Q9JMH6	Exosome	KDDER	VVGFHVLGPNAGEVTQGFAAALK	CGLTK	2		1141.618749	2281.221899	0.000451244	16	N	548	571
Q9JMH6	Exosome	KDDER	VVGFHVLGPNAGEVTQGFAAALK	CGLTK	3		761.4150995	2281.221899	0.000451244	39	N	548	571
Q9JMH6	Exosome	CGLTK	QQLDSTIGIHPVCAEIFTTLSVTK	RSGGD	3	C13:+57.021	886.7987959	2657.372988	0.000451244	19	N	576	600
Q9JMH6	Exosome	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	2	C1:+39.994,C18:+57.021,C19:+57.021	1469.11641	2936.217221	0.002663018	1	N	478	503
Q9JMH6	Exosome	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	3	C1:+39.994,C18:+57.021,C19:+57.021	979.7468735	2936.217221	0.001395409	1	N	478	503
Q9JMH6	Exosome	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	2	C1:+57.021,C18:+57.021,C19:+57.021	1477.62991	2953.244221	0.000451244	36	N	478	503
Q9JMH6	Exosome	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	3	C1:+57.021,C18:+57.021,C19:+57.021	985.4225402	2953.244221	0.000451244	17	N	478	503
Q9JMH6	Exosome	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	2	[0:-17.027,C1:+57.021,C18:+57.021,C19:+57.021	1469.11641	2936.217221	0.000451244	5	N	478	503
Q9JMH6	Exosome	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	3	[0:-17.027,C1:+57.021,C18:+57.021,C19:+57.021	979.7468735	2936.217221	0.000823681	3	N	478	503
Q9JMH6	Exosome	GERPR	YLGIPGDKEYCISSDDLFSLPYCPGK	TLVVG	3	C11:+57.021,C23:+57.021	998.801723	2993.381769	0.000451244	27	N	280	306
Q9JMH6	Exosome	PGRLR	VTAQSTNSEETIEGEFNTVLLAVGR	DSCTR	2		1333.169926	2664.324251	0.000451244	40	N	382	407
Q9JMH6	Exosome	PGRLR	VTAQSTNSEETIEGEFNTVLLAVGR	DSCTR	3		889.1158838	2664.324251	0.000451244	38	N	382	407
Q9JMH6	Exosome	KAVEK	FGEENIEVYHSFFWPLEWTVPSR	DNNKC	3		957.1260545	2868.354764	0.000451244	41	N	507	530
Q9JMH6	Exosome	EKTGK	IPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGR	LLAQR	3		1309.365283	3925.072449	0.000451244	39	N	429	465
Q9JMH6	Exosome	EKTGK	IPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGR	LLAQR	4		982.2759121	3925.072449	0.000451244	10	N	429	465
Q9JMH6	Exosome	KFDKK	VLVLDFVTPTPLGTR	WGLGG	2		814.475045	1626.93449	0.000451244	29	N	151	166
Q9JMH6	Exosome	PLGTR	WGLGGTCVNVGCIPK	KLMHQ	2	C7:+57.021,C12:+57.021	809.3974944	1616.779389	0.000451244	2	Y	166	181
Q9JMH6	Exosome	IPGDK	EYCISSDDLFSLPYCPGK	TLVVG	2	C3:+57.021,C15:+57.021	1075.974157	2149.932715	0.000451244	2	N	288	306
Q9JMH6	Exosome	EKTGK	IPVTDEEQTNVPYIYAIGDILEGK	LELTP	2		1339.184513	2676.353426	0.000451244	6	N	429	453
Q9JMH6	Exosome	CGLTK	QQLDSTIGIHPVCAEIFTTLSVTKR	SGGDI	3	C13:+57.021	938.8324996	2813.474099	0.000735798	3	N	576	601
Q9JMH6	Exosome	CGLTK	QQLDSTIGIHPVCAEIFTTLSVTKR	SGGDI	4	C13:+57.021	704.3763247	2813.474099	0.001162105	1	N	576	601
Q9JMH6	Exosome	KINEK	TGKIPVTDEEQTNVPYIYAIGDILEGK	LELTP	3		988.5136439	2962.517532	0.000451244	14	N	426	453
Q9JMH6	Exosome	IKFIR	QFVPTKIEQIEAGTPGR	LRVTA	3		624.3394195	1869.994859	0.0007646	2	N	363	380
Q9JMH6	Exosome	ILEGK	LELTPVAIQAGR	LLAQR	2		634.3725911	1266.729582	0.001162105	2	N	453	465
Q9JMH6	Parental	KDDER	VVGFHVLGPNAGEVTQGFAAALK	CGLTK	3		761.4150995	2281.221899	0.000451244	3	N	548	571
Q9JMH6	Parental	GSNVK	CDYDNVPTTVFTPLEYGCCGLSEEK	AVEKF	2	C1:+57.021,C18:+57.021,C19:+57.021	1477.62991	2953.244221	0.000451244	1	N	478	503
Q9JMH6	Parental	PGRLR	VTAQSTNSEETIEGEFNTVLLAVGR	DSCTR	2		1333.169926	2664.324251	0.000451244	8	N	382	407
Q9JMH6	Parental	PGRLR	VTAQSTNSEETIEGEFNTVLLAVGR	DSCTR	3		889.1158838	2664.324251	0.000451244	4	N	382	407
Q9JMH6	Parental	KAVEK	FGEENIEVYHSFFWPLEWTVPSR	DNNKC	3		957.1260545	2868.354764	0.000451244	12	N	507	530
Q9JMH6	Parental	EKTGK	IPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGR	LLAQR	3		1309.365283	3925.072449	0.000451244	13	N	429	465
Q9JMH6	Parental	KFDKK	VLVLDFVTPTPLGTR	WGLGG	2		814.475045	1626.93449	0.000451244	5	N	151	166
Q9JMH9	Exosome	RLETR	ISELTSELTDERNTGESASQLLDAETAER	LRTEK	3		1055.839696	3164.495687	0.001839721	1	N	1286	1315
Q9JMH9	Exosome	GFTQK	VVSLEAELQDISSQESKDEASLAK	VKKQL	3		859.436623	2575.286469	0.000622848	1	N	1511	1535
Q9JMH9	Exosome	IAQLK	NQLEESEFTCAAAVK	ARKAM	2	C10:+57.021	848.8962671	1695.776934	0.000622848	1	N	1685	1700
Q9JMH9	Exosome	EWAQK	AAYLLGCSLEELSSAIFK	HQLKG	2	C7:+57.021	986.5087245	1971.001849	0.000451244	4	N	697	715
Q9JMH9	Parental	RLETR	ISELTSELTDERNTGESASQLLDAETAER	LRTEK	3		1055.839696	3164.495687	0.000451244	33	N	1286	1315
Q9JMH9	Parental	GFTQK	VVSLEAELQDISSQESKDEASLAK	VKKQL	3		859.436623	2575.286469	0.000451244	8	N	1511	1535
Q9JMH9	Parental	IAQLK	NQLEESEFTCAAAVK	ARKAM	2	C10:+57.021	848.8962671	1695.776934	0.000451244	17	N	1685	1700
Q9JMH9	Parental	ARLIR	AAEINGEVDDDDAGGEWR	LKYER	2		959.9066374	1917.797675	0.000451244	14	N	1350	1368
Q9JMH9	Parental	EWAQK	AAYLLGCSLEELSSAIFK	HQLKG	2	C7:+57.021	986.5087245	1971.001849	0.002727428	1	N	697	715
Q9JMH9	Parental	EKKQR	RFDSELSQAHEETQR	EKLQR	3		611.6227666	1831.8449	0.000823681	12	N	1457	1472
Q9JMH9	Parental	LTDER	NTGESASQLLDAETAER	LRTEK	2		896.4219233	1790.828247	0.000451244	4	N	1298	1315
Q9JMH9	Parental	VDEKR	AVEELLESLDLEK	SSCCL	2		744.3961259	1486.776652	0.002663018	1	N	1143	1156
Q9QUG9	Exosome	PDTIK	LWEGLTELVTATGNYSNYR	RRLAA	2		1094.039997	2186.064395	0.000662267	1	N	271	290
Q9QUG9	Parental	CHLVR	YWISAFPAEFDLNPELAEQIKELK	ALLDQ	3		951.1571318	2850.447995	0.000451244	4	N	80	104
Q9QUG9	Parental	CHLVR	YWISAFPAEFDLNPELAEQIK	ELKAL	2		1241.120988	2480.226375	0.001162105	1	N	80	101

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QUH0	Exosome	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3		1060.877756	3179.609869	0.000451244	31	N	39	68
Q9QUH0	Exosome	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3	Q1:-17.027	1055.20209	3162.582869	0.000451244	13	N	39	68
Q9QUH0	Exosome	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3	[0:-17.027	1055.20209	3162.582869	0.000451244	8	N	39	68
Q9QUH0	Exosome	SQLPF	KQGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3		1103.576077	3307.704832	0.000451244	3	N	38	68
Q9QUH0	Exosome	IQSGK	VVVFIKPTCPY	CRKTQ	2	C9:+57.021	661.862782	1321.709964	0.001591523	1	N	14	25
Q9QUH0	Parental	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3		1060.877756	3179.609869	0.000451244	61	N	39	68
Q9QUH0	Parental	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3	Q1:-17.027	1055.20209	3162.582869	0.000451244	20	N	39	68
Q9QUH0	Parental	QLPFK	QGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3	[0:-17.027	1055.20209	3162.582869	0.000451244	16	N	39	68
Q9QUH0	Parental	CPYCR	KTQEILSQLPFK	QGLLE	2		716.414456	1430.813312	0.000451244	10	N	27	39
Q9QUH0	Parental	PYCRK	TQEILSQLPFK	QGLLE	2		652.3669744	1302.718349	0.000698008	4	N	28	39
Q9QUH0	Parental	GLLEF	VDITATNNTSAIQDYLQQLTGAR	TVPRV	2		1247.133146	2492.250692	0.000451244	6	N	45	68
Q9QUH0	Parental	SQLPF	KQGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	3		1103.576077	3307.704832	0.000451244	12	N	38	68
Q9QUH0	Parental	PYCRK	TQEILSQLPFKQGLLEFVDITATNNTSAIQDYLQQLTGAR	TVPRV	4		1117.087215	4464.317658	0.000451244	4	N	28	68
Q9QUH0	Parental	IQSGK	VVVFIKPTCPY	CRKTQ	2	C9:+57.021	661.862782	1321.709964	0.001763695	1	N	14	25
Q9QUI0	Exosome	TPEVK	HFCPNVPIILVGNKK	DLRND	2	C3:+57.021	868.4877324	1734.959865	0.000451244	9	N	104	119
Q9QUI0	Exosome	TPEVK	HFCPNVPIILVGNKK	DLRND	3	C3:+57.021	579.3277549	1734.959865	0.000451244	32	N	104	119
Q9QUI0	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2		1004.966498	2007.917396	0.000451244	25	Y	51	68
Q9QUI0	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	3		670.3135987	2007.917396	0.002813207	2	Y	51	68
Q9QUI0	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	Q1:-17.027	996.4529981	1990.890396	0.000622848	3	Y	51	68
Q9QUI0	Exosome	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	[0:-17.027	996.4529981	1990.890396	0.000823681	4	Y	51	68
Q9QUI0	Exosome	DVILM	CFSIDSPDSLENIPEKWTPEVK	HFCPN	2	C1:+39.994	1287.607127	2573.198654	0.00091018	1	N	82	104
Q9QUI0	Exosome	DVILM	CFSIDSPDSLENIPEKWTPEVK	HFCPN	2	C1:+57.021	1296.120627	2590.225654	0.001352548	1	N	82	104
Q9QUI0	Exosome	DVILM	CFSIDSPDSLENIPEKWTPEVK	HFCPN	3	C1:+57.021	864.4163515	2590.225654	0.000451244	5	N	82	104
Q9QUI0	Exosome	IVFSK	DQFPEVYVPTVFENYVADIEVDGK	QVELA	2		1387.16632	2772.317041	0.000451244	27	N	27	51
Q9QUI0	Exosome	IVFSK	DQFPEVYVPTVFENYVADIEVDGK	QVELA	3		925.1134803	2772.317041	0.000451244	24	N	27	51
Q9QUI0	Exosome	GACGK	TCLLIVFSK	DQFPE	2	C2:+57.021	540.8100181	1079.604436	0.0007646	23	Y	18	27
Q9QUI0	Exosome	TPEVK	HFCPNVPIILVGNK	KDLRN	2	C3:+57.021	804.4402509	1606.864902	0.000451244	5	N	104	118
Q9QUI0	Exosome	TPEVK	HFCPNVPIILVGNK	KDLRN	3	C3:+57.021	536.6294339	1606.864902	0.000451244	3	N	104	118
Q9QUI0	Exosome	EDYDR	LRPLSYPDTDVILMCFSIDSPDSLENIPEKWTPEVK	HFCPN	4	C15:+57.021	1052.026393	4204.074372	0.000622848	6	N	68	104
Q9QUI0	Exosome	IVFSK	DQFPEVYVPTVF	ENYVA	2		720.8564395	1439.697279	0.002727428	1	N	27	39
Q9QUI0	Exosome	AIRKK	LVIVGDGACGK	TCLLI	2	C9:+57.021	544.7923566	1087.569113	0.000870037	3	N	7	18
Q9QUI0	Exosome	LLIVF	SKDQFPEVYVPTVFENYVADIEVDGK	QVELA	3		996.8224775	2987.444032	0.002813207	1	N	25	51
Q9QUI0	Parental	TPEVK	HFCPNVPIILVGNKK	DLRND	3	C3:+57.021	579.3277549	1734.959865	0.000451244	27	N	104	119
Q9QUI0	Parental	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2		1004.966498	2007.917396	0.000451244	33	Y	51	68
Q9QUI0	Parental	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	Q1:-17.027	996.4529981	1990.890396	0.000622848	3	Y	51	68
Q9QUI0	Parental	EVDGK	QVELALWDTAGQEDYDR	LRPLS	2	[0:-17.027	996.4529981	1990.890396	0.000823681	7	Y	51	68
Q9QUI0	Parental	DVILM	CFSIDSPDSLENIPEKWTPEVK	HFCPN	2	C1:+39.994	1287.607127	2573.198654	0.000662267	5	N	82	104
Q9QUI0	Parental	DVILM	CFSIDSPDSLENIPEKWTPEVK	HFCPN	2	C1:+57.021	1296.120627	2590.225654	0.000451244	6	N	82	104
Q9QUI0	Parental	DVILM	CFSIDSPDSLENIPEKWTPEVK	HFCPN	3	C1:+57.021	864.4163515	2590.225654	0.000451244	23	N	82	104
Q9QUI0	Parental	VPTVF	ENYVADIEVDGKQVELALWDTAGQEDYDR	LRPLS	3		1114.520186	3340.537158	0.000451244	3	Y	39	68
Q9QUI0	Parental	GACGK	TCLLIVFSKDQFPEVYVPTVF	ENYVA	2	C2:+57.021	1251.653378	2501.291155	0.000451244	2	N	18	39
Q9QUI0	Parental	GACGK	TCLLIVFSKDQFPEVYVPTVFENYVADIEVDGK	QVELA	3	C2:+57.021	1278.978106	3833.910917	0.000622848	4	N	18	51
Q9QUI0	Parental	IVFSK	DQFPEVYVPTVFENYVADIEVDGK	QVELA	2		1387.16632	2772.317041	0.000451244	23	N	27	51
Q9QUI0	Parental	IVFSK	DQFPEVYVPTVFENYVADIEVDGK	QVELA	3		925.1134803	2772.317041	0.000451244	27	N	27	51
Q9QUI0	Parental	GACGK	TCLLIVFSK	DQFPE	2	C2:+57.021	540.8100181	1079.604436	0.000823681	10	Y	18	27
Q9QUI0	Parental	DVILM	CFSIDSPDSLENIPEK	WTPEV	2	C1:+57.021	925.9277643	1849.839929	0.000622848	2	N	82	98
Q9QUI0	Parental	TPEVK	HFCPNVPIILVGNK	KDLRN	2	C3:+57.021	804.4402509	1606.864902	0.000622848	1	N	104	118
Q9QUM0	Exosome	RRQAF	LQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	C16:+57.021,C22:+57.021,C27:+57.021	1096.188269	3285.541406	0.000451244	67	N	889	919
Q9QUM0	Exosome	ANGGK	CNPLLFDLRDETR	NLGFQ	3	C1:+57.021	550.2756079	1647.803424	0.000451244	4	N	95	108
Q9QUM0	Exosome	VSNQR	FTYDNSNPVFFDGYR	GYSVA	2		921.4106303	1840.805661	0.000451244	37	N	250	265
Q9QUM0	Exosome	QEQTR	IILDCGEDDLCVPQLR	LTATA	2	C5:+57.021,C11:+57.021	958.4663024	1914.917005	0.000451244	31	N	627	643
Q9QUM0	Exosome	RDETR	NLGFQIFQTFK	TGQGL	2		671.8618592	1341.708118	0.000451244	28	N	108	119
Q9QUM0	Exosome	VPQLR	LTATAGDSPLLIGADNVLELK	IEAAN	2		1056.083874	2110.152147	0.000451244	40	N	643	664
Q9QUM0	Exosome	VPQLR	LTATAGDSPLLIGADNVLELK	IEAAN	3		704.3918491	2110.152147	0.000451244	15	N	643	664
Q9QUM0	Exosome	FQTFK	TGQGLGASVVSWNDVIVACAPWQHWNVLEK	RDEAE	3	C19:+57.021	1107.887667	3320.639601	0.000451244	27	N	119	149
Q9QUM0	Exosome	VNGLR	LLIHIPGQSQPSDLLYILDVQPQGGLLCSTQPSPK	VDWKL	3	C28:+57.021	1271.680394	3812.017782	0.000451244	42	N	828	863
Q9QUM0	Exosome	VNGLR	LLIHIPGQSQPSDLLYILDVQPQGGLLCSTQPSPK	VDWKL	4	C28:+57.021	954.0122455	3812.017782	0.000451244	19	N	828	863
Q9QUM0	Exosome	GFSLR	GAVDIDDNGYPDLIVGAYGASK	VAVYR	2		1105.534745	2209.05389	0.000451244	21	N	452	474
Q9QUM0	Exosome	FLQPK	GPQALSTPTLLLTGTQLYGR	FGSAI	2		1044.078926	2086.142251	0.000451244	32	N	365	385
Q9QUM0	Exosome	FLQPK	GPQALSTPTLLLTGTQLYGR	FGSAI	3		696.3885504	2086.142251	0.000451244	11	N	365	385
Q9QUM0	Exosome	ANGGK	CNPLLFDLR	DETRN	2	C1:+57.021	574.3003488	1146.585098	0.000622848	13	N	95	104
Q9QUM0	Exosome	ANGGK	CNPLLFDLR	DETRN	2	[0:-17.027,C1:+57.021	565.7868488	1129.558098	0.002813207	1	N	95	104
Q9QUM0	Exosome	GLLAR	VPIENIISSYRPGTLLWHVSNQR	FTYDN	3		893.8175553	2678.429266	0.000451244	17	N	227	250
Q9QUM0	Exosome	GLLAR	VPIENIISSYRPGTLLWHVSNQR	FTYDN	4		670.6151165	2678.429266	0.000622848	7	N	227	250

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QUM0	Exosome	GLSPR	PSQVLDSPFPTGSGFGFSLR	GAVDI	2		1048.526526	2095.037452	0.000451244	36	N	432	452
Q9QUM0	Exosome	GDLNR	DGYNDIAVAAPYGGPSGQGQVLIFLGQSEGLSPR	PSQVL	3		1145.239465	3432.694996	0.000622848	18	N	398	432
Q9QUM0	Exosome	VLEKR	DEAEKTPVGGCFLAQLQSGGR	AEYSP	2	C11:+57.021	1110.539607	2219.063615	0.000451244	13	N	150	171
Q9QUM0	Exosome	VLEKR	DEAEKTPVGGCFLAQLQSGGR	AEYSP	3	C11:+57.021	740.6956716	2219.063615	0.000451244	6	N	150	171
Q9QUM0	Exosome	VDFHK	DKHGSVSIVVGAPR	ALNAS	3		474.6006859	1420.778658	0.002727428	1	N	58	72
Q9QUM0	Exosome	DEAEK	TPVGGCFLAQLQSGGR	AEYSP	2	C6:+57.021	824.4175041	1646.819408	0.000622848	1	N	155	171
Q9QUM0	Exosome	RWVSR	LEHTYELHNIGPGTVNGLR	LLIHI	2		1060.548324	2119.081048	0.000451244	4	N	809	828
Q9QUM0	Exosome	SDLLY	ILDVQPQGGLLCSTQPSPK	VDWKL	2	C12:+57.021	1019.535805	2037.05601	0.0025889	1	N	844	863
Q9QUM0	Exosome	QRERR	QAFLQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	Q1:-17.027,C19:+57.021,C25:+57.021,C30:+57.021	1205.900637	3614.678511	0.000823681	1	N	886	919
Q9QUM0	Exosome	QRERR	QAFLQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	[0:-17.027,C19:+57.021,C25:+57.021,C30:+57.021	1205.900637	3614.678511	0.002453667	1	N	886	919
Q9QUM0	Parental	RRQAF	LQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	C16:+57.021,C22:+57.021,C27:+57.021	1096.188269	3285.541406	0.000451244	42	N	889	919
Q9QUM0	Parental	ANGGK	CNPLLFDLRDETR	NLGFQ	2	C1:+57.021	824.9095119	1647.803424	0.001654178	1	N	95	108
Q9QUM0	Parental	ANGGK	CNPLLFDLRDETR	NLGFQ	3	C1:+57.021	550.2756079	1647.803424	0.000451244	12	N	95	108
Q9QUM0	Parental	VSNQR	FTYDNSNPVFFDGYR	GYSVA	2		921.4106303	1840.805661	0.000451244	22	N	250	265
Q9QUM0	Parental	QEQTR	IILDCGEDDLCVPQLR	LTATA	2	C5:+57.021,C11:+57.021	958.4663024	1914.917005	0.000451244	22	N	627	643
Q9QUM0	Parental	QEQTR	IILDCGEDDLCVPQLR	LTATA	3	C5:+57.021,C11:+57.021	639.3134683	1914.917005	0.001162105	3	N	627	643
Q9QUM0	Parental	RDETR	NLGFQIFQTFK	TGQGL	2		671.8618592	1341.708118	0.000451244	13	N	108	119
Q9QUM0	Parental	VPQLR	LTATAGDSPLLIGADNVLELK	IEAAN	2		1056.083874	2110.152147	0.000451244	28	N	643	664
Q9QUM0	Parental	VPQLR	LTATAGDSPLLIGADNVLELK	IEAAN	3		704.3918491	2110.152147	0.000622848	2	N	643	664
Q9QUM0	Parental	FQTFK	TGQGLGASVVSWNDVIVACAPWQHWNVLEK	RDEAE	3	C19:+57.021	1107.887667	3320.639601	0.000451244	17	N	119	149
Q9QUM0	Parental	VNGLR	LLIHIPGQSQPSDLLYILDVQPQGGLLCSTQPSPK	VDWKL	3	C28:+57.021	1271.680394	3812.017782	0.000451244	35	N	828	863
Q9QUM0	Parental	VNGLR	LLIHIPGQSQPSDLLYILDVQPQGGLLCSTQPSPK	VDWKL	4	C28:+57.021	954.0122455	3812.017782	0.000451244	19	N	828	863
Q9QUM0	Parental	GFSLR	GAVDIDDNGYPDLIVGAYGASK	VAVYR	2		1105.534745	2209.05389	0.000451244	22	N	452	474
Q9QUM0	Parental	FLQPK	GPQALSTPTLLLTGTQLYGR	FGSAI	2		1044.078926	2086.142251	0.000451244	9	N	365	385
Q9QUM0	Parental	FLQPK	GPQALSTPTLLLTGTQLYGR	FGSAI	3		696.3885504	2086.142251	0.000451244	3	N	365	385
Q9QUM0	Parental	FQTFK	TGQGLGASVVSWNDVIVACAPWQHWNVLEKR	DEAEK	4	C19:+57.021	870.1929781	3476.740712	0.000451244	7	N	119	150
Q9QUM0	Parental	GLLAR	VPIENIISSYRPGTLLWHVSNQR	FTYDN	3		893.8175553	2678.429266	0.000451244	5	N	227	250
Q9QUM0	Parental	GLLAR	VPIENIISSYRPGTLLWHVSNQR	FTYDN	4		670.6151165	2678.429266	0.002663018	1	N	227	250
Q9QUM0	Parental	GLSPR	PSQVLDSPFPTGSGFGFSLR	GAVDI	2		1048.526526	2095.037452	0.000451244	13	N	432	452
Q9QUM0	Parental	GLSPR	PSQVLDSPFPTGSGFGFSLR	GAVDI	3		699.3536172	2095.037452	0.001591523	1	N	432	452
Q9QUM0	Parental	GDLNR	DGYNDIAVAAPYGGPSGQGQVLIFLGQSEGLSPR	PSQVL	3		1145.239465	3432.694996	0.000622848	7	N	398	432
Q9QUM0	Parental	VLEKR	DEAEKTPVGGCFLAQLQSGGR	AEYSP	2	C11:+57.021	1110.539607	2219.063615	0.000451244	8	N	150	171
Q9QUM0	Parental	VLEKR	DEAEKTPVGGCFLAQLQSGGR	AEYSP	3	C11:+57.021	740.6956716	2219.063615	0.000451244	7	N	150	171
Q9QUM0	Parental	RWVSR	LEHTYELHNIGPGTVNGLR	LLIHI	2		1060.548324	2119.081048	0.000451244	8	N	809	828
Q9QUM0	Parental	RWVSR	LEHTYELHNIGPGTVNGLR	LLIHI	3		707.3681493	2119.081048	0.000451244	9	N	809	828
Q9QUM0	Parental	SDLLY	ILDVQPQGGLLCSTQPSPK	VDWKL	2	C12:+57.021	1019.535805	2037.05601	0.000451244	9	N	844	863
Q9QUM0	Parental	VNGLR	LLIHIPGQSQPSDLLY	ILDVQ	2		897.493966	1792.972332	0.001264573	2	N	828	844
Q9QUM0	Parental	QRERR	QAFLQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	C19:+57.021,C25:+57.021,C30:+57.021	1211.576304	3631.705511	0.001463592	4	N	886	919
Q9QUM0	Parental	QRERR	QAFLQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	Q1:-17.027,C19:+57.021,C25:+57.021,C30:+57.021	1205.900637	3614.678511	0.0007646	5	N	886	919
Q9QUM0	Parental	QRERR	QAFLQGPKPGQQDPVLVSCDGSASCTVVECELR	EMVRG	3	[0:-17.027,C19:+57.021,C25:+57.021,C30:+57.021	1205.900637	3614.678511	0.000451244	11	N	886	919
Q9QUM0	Parental	QVLIF	LGQSEGLSPRPSQVLDSPFPTGSGFGFSLR	GAVDI	3		1040.86367	3119.56761	0.002296037	1	N	422	452
Q9QUM0	Parental	AHYMR	ALSNIEGFER	LVCTQ	2		568.2912667	1134.566933	0.000451244	1	N	691	701
Q9QUM0	Parental	QLYGR	FGSAIAPLGDLNR	DGYND	2		665.8598479	1329.704096	0.00307782	1	N	385	398
Q9QUM9	Exosome	AGFDR	HITIFSPEGR	LYQVE	2		578.8096266	1155.603653	0.000451244	15	N	11	21
Q9QUM9	Exosome	KVPDK	LLDSSTVTHLFK	ITESI	2		680.8777063	1359.739813	0.000451244	12	N	59	71
Q9QUM9	Exosome	KVPDK	LLDSSTVTHLFK	ITESI	3		454.2544042	1359.739813	0.001162105	6	N	59	71
Q9QUM9	Exosome	NPKFR	ILTEAEIDAHLVALAERD	-	2		990.0263587	1978.037117	0.000451244	28	N	228	246
Q9QUM9	Exosome	NPKFR	ILTEAEIDAHLVALAERD	-	3		660.3535058	1978.037117	0.000451244	47	N	228	246
Q9QUM9	Exosome	SPEGR	LYQVEYAFK	AINQG	2		580.8034786	1159.591357	0.000735798	12	N	21	30
Q9QUM9	Exosome	EYAFK	AINQGGLTSVAVR	GKDCA	2		643.3652974	1284.714995	0.000451244	20	N	30	43
Q9QUM9	Exosome	PQVYK	CDPAGYYCGFK	ATAAG	2	C1:+57.021,C8:+57.021	669.2681571	1336.520714	0.000451244	1	N	153	164
Q9QUM9	Exosome	PQVYK	CDPAGYYCGFK	ATAAG	2	[0:-17.027,C1:+57.021,C8:+57.021	660.7546571	1319.493714	0.001162105	2	N	153	164
Q9QUM9	Parental	KVPDK	LLDSSTVTHLFK	ITESI	3		454.2544042	1359.739813	0.002296037	2	N	59	71
Q9QUM9	Parental	NPKFR	ILTEAEIDAHLVALAERD	-	3		660.3535058	1978.037117	0.000823681	5	N	228	246
Q9QUN7	Exosome	IRVVK	TCIPQTLEVLDVSNNNLDSFSLFLPR	LQELY	3	C2:+57.021	998.1747025	2991.500708	0.000451244	1	N	452	478

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QUN7	Parental	IRVVK	TCIPQTLEVLDVSNNNLDSFSLFLPR	LQELY	3	C2:+57.021	998.1747025	2991.500708	0.000451244	1	N	452	478
Q9QUN7	Parental	FSHFR	LFDENNDAAILVLLEPIER	KAIPQ	2		1092.581498	2183.147396	0.000451244	1	N	723	742
Q9QUN7	Parental	FVPGK	WIIDNIIDSIEK	SHKTV	2		729.8960961	1457.776592	0.001871652	1	N	683	695
Q9QUR6	Exosome	EGEAR	VFLDPNTLSDDGTVALR	GYAFS	2		916.9735948	1831.93159	0.000451244	26	N	111	128
Q9QUR6	Exosome	ILANK	QNCFDDFQCAAEYLIK	EGYTS	2	C3:+57.021,C9:+57.021	1011.440285	2020.864969	0.000451244	33	N	523	539
Q9QUR6	Exosome	ILANK	QNCFDDFQCAAEYLIK	EGYTS	3	C3:+57.021,C9:+57.021	674.6294564	2020.864969	0.000451244	1	N	523	539
Q9QUR6	Exosome	ILANK	QNCFDDFQCAAEYLIK	EGYTS	2	[0:-17.027,C3:+57.021,C9:+57.021	1002.926785	2003.837969	0.000870037	1	N	523	539
Q9QUR6	Exosome	LKWVK	LIDNFEGEYDYVTNEGTVFTFK	TNRNS	2		1301.105731	2600.195863	0.000451244	26	N	281	303
Q9QUR6	Exosome	YHGHK	ICDPYSWLEDPDSEQTK	AFVEA	2	C2:+57.021	1041.951968	2081.888335	0.000451244	32	N	23	40
Q9QUR6	Exosome	VACVR	SNFLVLCYLHDVK	NILQL	2	C7:+57.021	804.4164414	1606.817283	0.00307782	1	N	345	358
Q9QUR6	Exosome	VACVR	SNFLVLCYLHDVK	NILQL	3	C7:+57.021	536.6135609	1606.817283	0.002519933	1	N	345	358
Q9QUR6	Exosome	ESKWK	VLVPEHEKDVLEWVACVR	SNFLV	3	C16:+57.021	726.7177479	2177.129844	0.000451244	12	N	327	345
Q9QUR6	Exosome	ESKWK	VLVPEHEKDVLEWVACVR	SNFLV	4	C16:+57.021	545.2902609	2177.129844	0.001463592	1	N	327	345
Q9QUR6	Exosome	KKGKR	YFYFYNTGLQNQR	VLYVQ	2		857.4051509	1712.794702	0.000451244	2	N	85	98
Q9QUR6	Exosome	SPNYR	LINIDFTDPDESKWK	VLVPE	2		910.9574134	1819.899227	0.000451244	2	N	312	327
Q9QUR6	Exosome	SPNYR	LINIDFTDPDESKWK	VLVPE	3		607.6408756	1819.899227	0.000451244	11	N	312	327
Q9QUR6	Exosome	LHSLK	FIATLQYIVGR	SRKQS	2		640.8722269	1279.728854	0.000823681	7	N	651	662
Q9QUR6	Exosome	NLHQK	LCYHVLGTDQSEDILCAEFPDEPK	WMGGA	3	C2:+57.021,C16:+57.021	946.0985395	2835.272219	0.000451244	25	N	209	233
Q9QUR6	Exosome	LHDVK	NILQLHDLTTGALLK	TFPLD	3		550.6582009	1648.951203	0.000451244	7	N	358	373
Q9QUR6	Exosome	LQNQR	VLYVQDSLEGEAR	VFLDP	2		739.8784346	1477.741269	0.000451244	21	N	98	111
Q9QUR6	Exosome	LKFHK	FTIGHAWTTDYGCSDTK	QHFEW	2	C13:+57.021	980.4310055	1958.846411	0.001329271	1	N	588	605
Q9QUR6	Exosome	EAQNK	ITVPFLEQCPIR	GLYKE	2	C9:+57.021	736.9004272	1471.785254	0.001162105	2	N	48	60
Q9QUR6	Exosome	EVTVK	GIDAADYQTIQIFYPSK	DGTKI	2		965.4837953	1928.951991	0.000451244	16	N	428	445
Q9QUR6	Exosome	GALLK	TFPLDVGSVVGYSGR	KKDSE	2		777.4020769	1552.788554	0.002813207	3	N	373	388
Q9QUR6	Exosome	SDDGR	YVLLSIWEGCDPVNR	LWYCD	2	C10:+57.021	910.9539194	1819.892239	0.000451244	1	N	245	260
Q9QUR6	Parental	EGEAR	VFLDPNTLSDDGTVALR	GYAFS	2		916.9735948	1831.93159	0.001162105	1	N	111	128
Q9QUR6	Parental	ILANK	QNCFDDFQCAAEYLIK	EGYTS	2	C3:+57.021,C9:+57.021	1011.440285	2020.864969	0.001162105	4	N	523	539
Q9QUR6	Parental	LKWVK	LIDNFEGEYDYVTNEGTVFTFK	TNRNS	2		1301.105731	2600.195863	0.000451244	14	N	281	303
Q9QUR6	Parental	YHGHK	ICDPYSWLEDPDSEQTK	AFVEA	2	C2:+57.021	1041.951968	2081.888335	0.000451244	13	N	23	40
Q9QUR6	Parental	EVTVK	GIDAADYQTIQIFYPSK	DGTKI	2		965.4837953	1928.951991	0.000451244	2	N	428	445
Q9QWK4	Exosome	EVLHK	GSWGSVCDDNWGEKEDQVVCK	QLGCG	2	C7:+57.021,C20:+57.021	1228.018147	2454.020695	0.000451244	1	N	264	285
Q9QWK4	Exosome	EVLHK	GSWGSVCDDNWGEKEDQVVCK	QLGCG	3	C7:+57.021,C20:+57.021	819.0146983	2454.020695	0.000451244	13	N	264	285
Q9QWK4	Exosome	PGAGR	IWLDDVNCSGKEQSLEFCR	HRLWG	2	C8:+57.021,C18:+57.021	1178.538519	2355.061437	0.000622848	1	N	309	328
Q9QWK4	Exosome	PGAGR	IWLDDVNCSGKEQSLEFCR	HRLWG	3	C8:+57.021,C18:+57.021	786.0282792	2355.061437	0.000451244	6	N	309	328
Q9QWK4	Exosome	AVVCR	ELNCGAVIQTPR	GASYQ	2	C4:+57.021	679.3485587	1356.681517	0.000451244	4	N	66	78
Q9QWK4	Exosome	HCQGR	VEVLHQSQWSTVCK	AGWNL	2	C13:+57.021	850.9251619	1699.834724	0.001591523	1	N	153	167
Q9QWR8	Exosome	IPDPK	RFPHGIAFLADYAHSLGLK	LGIYE	4		529.039519	2112.126876	0.000637154	5	N	96	115
Q9QWR8	Exosome	QDSWK	SVLSILDWFVR	HQDVL	2		667.8775093	1333.739419	0.000451244	10	N	223	234
Q9QWR8	Parental	IPDPK	RFPHGIAFLADYAHSLGLK	LGIYE	4		529.039519	2112.126876	0.000637154	6	N	96	115
Q9QWR8	Parental	QDSWK	SVLSILDWFVR	HQDVL	2		667.8775093	1333.739419	0.002296037	3	N	223	234
Q9QWR8	Parental	EVFKR	YLSNQASALVFFSR	RTDMP	2		801.9178942	1601.820188	0.000451244	1	N	329	343
Q9QWR8	Parental	WERFR	CNIDCVEDPKNCISER	LFMEM	2	C1:+57.021,C5:+57.021,C12:+57.021	1004.929527	2007.843454	0.002727428	1	N	37	53
Q9QX47	Parental	ADIGR	SLSSQLALELDTVGTSK	GFEFV	2		874.9679781	1747.920356	0.000451244	1	N	1620	1637
Q9QX47	Parental	AASAR	SLPNEEIVQKIEEVLSGVLDTELR	YKPDL	3		904.1556795	2709.443638	0.000451244	8	N	54	78
Q9QX47	Parental	ALSPK	ESSEDTEVPLPNKEIVPESGYSASIDEINEADLVRPLLPK	DMERL	4		1095.805496	4379.190786	0.000451244	15	N	1725	1765
Q9QX47	Parental	HLIVK	DAEHNTVCATTVGPVGEASEEK	ILPIS	2	C8:+57.021	1151.018902	2300.022203	0.000622848	3	N	1572	1594
Q9QX47	Parental	LTSLR	AGIEGPLLASEVER	DKSAA	2		720.8888023	1439.762005	0.000622848	2	N	1774	1788
Q9QXD6	Exosome	SSAVR	QAGIAQLYGIAGSTNVTGDQVK	KLDIL	2		1096.071829	2190.128058	0.000451244	8	N	50	72
Q9QXD6	Exosome	EKRGK	YVVCFDPLDGSSNIDCLVSIGTIFGIYR	KKSTD	3	C4:+57.021,C16:+57.021	1060.851077	3179.52983	0.002212458	1	N	113	141
Q9QXG4	Exosome	TKHSR	ASLQVLGTVGEPINPEAWLWYHR	VVGSQ	3		879.459368	2635.354704	0.000451244	3	N	429	452
Q9QXG4	Exosome	TEWMK	GATTNICYNVLDR	NVHEK	2	C7:+57.021	748.8620303	1495.708461	0.001763695	1	N	97	110
Q9QXK3	Exosome	GPLFK	SSEPVQLTEAETEYFVR	CVKHM	2		992.9790741	1983.942548	0.000451244	8	N	629	646
Q9QXK3	Exosome	TDSNR	SIATLAITTLLK	TGSES	2		622.8953677	1243.775135	0.000851441	19	Y	338	350
Q9QXK3	Exosome	NCTAR	ELAPAVSVLQLFCSSPK	PALRY	2	C13:+57.021	923.4928775	1844.970155	0.000451244	6	Y	283	300
Q9QXK3	Exosome	NCTAR	ELAPAVSVLQLFCSSPK	PALRY	3	C13:+57.021	615.9978516	1844.970155	0.001943752	1	Y	283	300
Q9QXK3	Exosome	DHIQK	ILKPNFAAAWEEVGDAFEKEETFALSSTK	TLEEA	4		807.9084646	3227.602659	0.000451244	4	N	763	792
Q9QXK3	Exosome	SALAK	FGAQNESLLPSILVLLQR	CMMDT	2		999.5732791	1997.130958	0.000451244	10	N	497	515
Q9QXK3	Exosome	SALAK	FGAQNESLLPSILVLLQR	CMMDT	3		666.7181194	1997.130958	0.001162105	6	N	497	515
Q9QXK3	Exosome	FEYKK	AIVDCIISIVEENPESK	EAGLA	2	C5:+57.021	958.4879891	1914.960378	0.000451244	5	N	415	432
Q9QXK3	Exosome	FEYKK	AIVDCIISIVEENPESK	EAGLA	3	C5:+57.021	639.3279261	1914.960378	0.000451244	4	N	415	432
Q9QXK3	Exosome	NCTAR	ELAPAVSVLQLF	CSSPK	2		643.8718926	1285.728185	0.001699387	1	Y	283	295
Q9QXK3	Parental	GPLFK	SSEPVQLTEAETEYFVR	CVKHM	2		992.9790741	1983.942548	0.000451244	23	N	629	646
Q9QXK3	Parental	TDSNR	SIATLAITTLLK	TGSES	2		622.8953677	1243.775135	0.000622848	22	Y	338	350
Q9QXK3	Parental	NCTAR	ELAPAVSVLQLFCSSPK	PALRY	2	C13:+57.021	923.4928775	1844.970155	0.000451244	17	Y	283	300

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QXK3	Parental	DHIQK	ILKPNFAAAWEEVGDAFEKEETFALSSTK	TLEEA	3		1076.875353	3227.602659	0.000451244	2	N	763	792
Q9QXK3	Parental	DHIQK	ILKPNFAAAWEEVGDAFEKEETFALSSTK	TLEEA	4		807.9084646	3227.602659	0.000451244	31	N	763	792
Q9QXK3	Parental	SALAK	FGAQNESLLPSILVLLQR	CMMDT	2		999.5732791	1997.130958	0.000451244	26	N	497	515
Q9QXK3	Parental	SALAK	FGAQNESLLPSILVLLQR	CMMDT	3		666.7181194	1997.130958	0.000698008	15	N	497	515
Q9QXK3	Parental	KFTVR	DCDPNTGVPDEDGYDDEYVLEDLEVTVSDHIQK	ILKPN	3	C2:+57.021	1261.211263	3780.61039	0.000451244	7	N	730	763
Q9QXK3	Parental	DHIQK	ILKPNFAAAWEEVGDAFEKEETF	ALSST	3		881.099394	2640.274782	0.001654178	1	N	763	786
Q9QXK3	Parental	FEYKK	AIVDCIISIVEENPESK	EAGLA	2	C5:+57.021	958.4879891	1914.960378	0.000451244	4	N	415	432
Q9QXK3	Parental	FEYKK	AIVDCIISIVEENPESK	EAGLA	3	C5:+57.021	639.3279261	1914.960378	0.000451244	8	N	415	432
Q9QXK3	Parental	NPESK	EAGLAHLCEFIEDCEHTVLATK	ILHLL	3	C8:+57.021,C14:+57.021	848.4018937	2542.182281	0.000451244	1	N	432	454
Q9QXS1	Exosome	EEAER	LKQSAEEQAQAQAQAQAAAEK	LRKEA	3		733.7053783	2198.092735	0.000451244	13	N	2261	2282
Q9QXS1	Exosome	RDDAR	VYHDPSTQEPVTYSQLQQR	CRSDQ	3		759.3701071	2275.086921	0.000451244	1	N	3323	3342
Q9QXS1	Exosome	EEALR	LLDAQLATGGIVDPR	LGFHL	2		769.9310016	1537.846403	0.001591523	1	N	3942	3957
Q9QXS1	Exosome	EEALR	LLDAQLATGGIVDPR	LGFHL	3		513.6232677	1537.846403	0.00307782	1	N	3942	3957
Q9QXS1	Exosome	ITGQR	LLEAQACTGGIIDPSTGERFPVTEAVNK	GLVDK	3	C7:+57.021	991.8380904	2972.490871	0.000451244	11	N	4454	4482
Q9QXS1	Exosome	IVDPR	LGFHLPLEVAYQR	GYLNK	3		514.9529481	1541.835444	0.000451244	5	N	3957	3970
Q9QXS1	Exosome	ESAWR	YLYGTGAVAGVYLPGSR	QTLTI	2		872.4573835	1742.899167	0.000451244	4	N	3828	3845
Q9QXS1	Exosome	PSHWK	VLSGSSSEAAVPSVCFLVPPPNQEAQEAVAR	LEAQH	3	C15:+57.021	1066.203321	3195.586563	0.000735798	3	N	985	1016
Q9QXS1	Exosome	SAGPR	TQLASWSDPTEETGPVAGILDTETLEK	VSITE	2		1444.706538	2887.397476	0.000451244	3	N	4408	4435
Q9QXS1	Exosome	SAGPR	TQLASWSDPTEETGPVAGILDTETLEK	VSITE	3		963.4736254	2887.397476	0.000451244	10	N	4408	4435
Q9QXS1	Exosome	EAGQR	FLEVQYLTGGLIEPDTPGR	VSLDE	2		1053.049834	2104.084068	0.000451244	22	N	4530	4549
Q9QXS1	Exosome	EALKK	DLLQPEVAVALLEAQAGTGHIIDPATSAR	LTVDE	3		986.1966492	2955.566548	0.000451244	37	N	3190	3219
Q9QXS1	Exosome	TALQR	QLLSPGTALILLEAQAASGFLLDPVR	NRRLT	3		898.5132499	2692.51635	0.000451244	25	N	2862	2888
Q9QXS1	Exosome	FEGLR	ALVPAAELLDSGVISHELYQQLQR	GERSV	3		884.1453376	2649.412613	0.000451244	8	N	3122	3146
Q9QXS1	Exosome	LGVTR	LLDPEDVDVPQPDEK	SIITY	2		854.9179538	1707.820308	0.001763695	1	N	382	397
Q9QXS1	Exosome	NKVYR	QTNLENLDQAFSVAER	DLGVT	2		917.950651	1833.885702	0.000622848	1	N	360	376
Q9QXS1	Exosome	SDDTK	GFFDPNTHENLTYLQLLER	CVEDP	2		1154.074372	2306.133143	0.002981883	1	N	2995	3014
Q9QXS1	Exosome	SDDTK	GFFDPNTHENLTYLQLLER	CVEDP	3		769.7188477	2306.133143	0.000451244	12	N	2995	3014
Q9QXS1	Exosome	KNLQK	FLEGTSCIAGVFVDATK	ERLSV	2	C7:+57.021	907.9535851	1813.89157	0.000451244	12	N	4071	4088
Q9QXS1	Exosome	WQEYR	ELVLLLLQWIR	HHTAA	2		698.4402768	1394.864954	0.001162105	1	N	433	444
Q9QXS1	Exosome	LRYYR	ESADPLSAWLQDAK	RRQEQ	2		765.8758919	1529.736184	0.001329271	3	N	1358	1372
Q9QXS1	Exosome	YEDLR	DGHNLISLLEVLSGDSLPR	EKGRM	3		679.0326552	2034.074566	0.000451244	6	N	219	238
Q9QXS1	Exosome	EAMRR	GLLRPSTATLLLEAQAATGFLVDPVR	NQRLY	3		903.8486326	2708.522498	0.000823681	2	N	3521	3547
Q9QXS1	Exosome	QAMKK	GIIRPGTAFELLEAQAATGYVIDPIK	GLKLT	3		915.1730048	2742.495614	0.000451244	5	N	4099	4125
Q9QXS1	Parental	EEAER	LKQSAEEQAQAQAQAQAAAEK	LRKEA	2		1100.054167	2198.092735	0.000622848	3	N	2261	2282
Q9QXS1	Parental	EEAER	LKQSAEEQAQAQAQAQAAAEK	LRKEA	3		733.7053783	2198.092735	0.000451244	45	N	2261	2282
Q9QXS1	Parental	RDDAR	VYHDPSTQEPVTYSQLQQR	CRSDQ	2		1138.551261	2275.086921	0.000451244	4	N	3323	3342
Q9QXS1	Parental	RDDAR	VYHDPSTQEPVTYSQLQQR	CRSDQ	3		759.3701071	2275.086921	0.000451244	6	N	3323	3342
Q9QXS1	Parental	EEALR	LLDAQLATGGIVDPR	LGFHL	2		769.9310016	1537.846403	0.000451244	8	N	3942	3957
Q9QXS1	Parental	EEALR	LLDAQLATGGIVDPR	LGFHL	3		513.6232677	1537.846403	0.000823681	1	N	3942	3957
Q9QXS1	Parental	ITGQR	LLEAQACTGGIIDPSTGERFPVTEAVNK	GLVDK	3	C7:+57.021	991.8380904	2972.490871	0.000451244	14	N	4454	4482
Q9QXS1	Parental	IVDPR	LGFHLPLEVAYQR	GYLNK	3		514.9529481	1541.835444	0.000451244	18	N	3957	3970
Q9QXS1	Parental	ESAWR	YLYGTGAVAGVYLPGSR	QTLTI	2		872.4573835	1742.899167	0.000451244	4	N	3828	3845
Q9QXS1	Parental	PSHWK	VLSGSSSEAAVPSVCFLVPPPNQEAQEAVAR	LEAQH	3	C15:+57.021	1066.203321	3195.586563	0.000451244	23	N	985	1016
Q9QXS1	Parental	EEMNR	VLADPSDDTKGFFDPNTHENLTYLQLLER	CVEDP	3		1116.8848	3347.630999	0.000662267	6	N	3644	3673
Q9QXS1	Parental	EEMNR	ILSDPSDDTKGFFDPNTHENLTYLQLLER	CVEDP	3		1126.888321	3377.641563	0.000451244	8	N	2985	3014
Q9QXS1	Parental	EEMNR	ILSDPSDDTKGFFDPNTHENLTYLQLLER	CVEDP	4		845.4181908	3377.641563	0.000451244	4	N	2985	3014
Q9QXS1	Parental	SAGPR	TQLASWSDPTEETGPVAGILDTETLEK	VSITE	2		1444.706538	2887.397476	0.000451244	11	N	4408	4435
Q9QXS1	Parental	SAGPR	TQLASWSDPTEETGPVAGILDTETLEK	VSITE	3		963.4736254	2887.397476	0.000451244	17	N	4408	4435
Q9QXS1	Parental	EAGQR	FLEVQYLTGGLIEPDTPGR	VSLDE	2		1053.049834	2104.084068	0.000451244	31	N	4530	4549
Q9QXS1	Parental	EAGQR	FLEVQYLTGGLIEPDTPGR	VSLDE	3		702.3691559	2104.084068	0.000451244	3	N	4530	4549
Q9QXS1	Parental	QAMKK	GIIRPGTAFELLEAQAATGYVIDPIKGLK	LTVEE	4		761.1818263	3040.696105	0.000622848	5	N	4099	4128
Q9QXS1	Parental	LRALV	PAAELLDSGVISHELYQQLQR	GERSV	3		789.748807	2366.223021	0.000823681	5	N	3125	3146
Q9QXS1	Parental	DSTLR	YLQDLLAWVEENQR	RIDSA	2		888.9499226	1775.884245	0.000451244	17	N	668	682
Q9QXS1	Parental	DSTLR	YLQDLLAWVEENQR	RIDSA	3		592.9692151	1775.884245	0.000451244	27	N	668	682
Q9QXS1	Parental	EALKK	DLLQPEVAVALLEAQAGTGHIIDPATSAR	LTVDE	3		986.1966492	2955.566548	0.000451244	29	N	3190	3219
Q9QXS1	Parental	EALKK	DLLQPEVAVALLEAQAGTGHIIDPATSAR	LTVDE	4		739.8994369	2955.566548	0.000451244	5	N	3190	3219
Q9QXS1	Parental	TALQR	QLLSPGTALILLEAQAASGFLLDPVR	NRRLT	2		1347.265975	2692.51635	0.000451244	9	N	2862	2888
Q9QXS1	Parental	TALQR	QLLSPGTALILLEAQAASGFLLDPVR	NRRLT	3		898.5132499	2692.51635	0.000451244	42	N	2862	2888
Q9QXS1	Parental	TALQR	QLLSPGTALILLEAQAASGFLLDPVR	NRRLT	2	Q1:-17.027	1338.752475	2675.48935	0.00091018	1	N	2862	2888
Q9QXS1	Parental	TALQR	QLLSPGTALILLEAQAASGFLLDPVR	NRRLT	2	[0:-17.027	1338.752475	2675.48935	0.000622848	4	N	2862	2888
Q9QXS1	Parental	LPNGR	DAPDGPSVEAEPEYTFEGLR	QKVPA	2		1089.995453	2177.975305	0.000451244	25	N	2774	2794
Q9QXS1	Parental	AEVAR	LLLEAQAATGFLLDPVKGER	LTVDE	3		714.4042005	2140.189201	0.000823681	3	N	3865	3885
Q9QXS1	Parental	FEGLR	ALVPAAELLDSGVISHELYQQLQR	GERSV	2		1325.714106	2649.412613	0.000451244	1	N	3122	3146
Q9QXS1	Parental	FEGLR	ALVPAAELLDSGVISHELYQQLQR	GERSV	3		884.1453376	2649.412613	0.000451244	9	N	3122	3146
Q9QXS1	Parental	QAMKK	ELIPAEEALRLLDAQLATGGIVDPR	LGFHL	3		887.4926259	2659.454478	0.000823681	2	N	3932	3957

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QXS1	Parental	IEQEK	AKLEQLFQDEVAK	AKQLR	2		759.9122775	1517.808955	0.000622848	3	N	2658	2671
Q9QXS1	Parental	FEGLR	QKVPAQQLQEAGILSQEELQR	LAQGH	2		1197.143317	2392.271034	0.000823681	1	N	2794	2815
Q9QXS1	Parental	FEGLR	QKVPAQQLQEAGILSQEELQR	LAQGH	3		798.4314779	2392.271034	0.000451244	5	N	2794	2815
Q9QXS1	Parental	AARQR	SQVEEELFSVR	VQMEE	2		661.8334957	1321.651391	0.000451244	7	N	2368	2379
Q9QXS1	Parental	EAMRR	GLLRPSTATLLLEAQAATGFLVDPVRNQR	LYVHE	4		777.6890785	3106.725114	0.000622848	3	N	3521	3550
Q9QXS1	Parental	AEAQR	HISDLYEDLRDGHNLISLLEVLSGDSLPR	EKGRM	3		1092.900673	3275.678618	0.000662267	1	N	209	238
Q9QXS1	Parental	LGVTR	LLDPEDVDVPQPDEK	SIITY	2		854.9179538	1707.820308	0.000451244	9	N	382	397
Q9QXS1	Parental	NKVYR	QTNLENLDQAFSVAER	DLGVT	2		917.950651	1833.885702	0.000451244	12	N	360	376
Q9QXS1	Parental	SDDTK	GFFDPNTHENLTYLQLLER	CVEDP	3		769.7188477	2306.133143	0.000622848	1	N	2995	3014
Q9QXS1	Parental	KNLQK	FLEGTSCIAGVFVDATK	ERLSV	2	C7:+57.021	907.9535851	1813.89157	0.000451244	21	N	4071	4088
Q9QXS1	Parental	VAYQR	GYLNKDTHDQLSEPSEVR	SYVDP	3		696.671786	2086.991958	0.002884417	1	N	3970	3988
Q9QXS1	Parental	AERLK	QSAEEQAQAQAQAQAAAEK	LRKEA	2		979.4646539	1956.913708	0.000451244	16	N	2263	2282
Q9QXS1	Parental	DAKRR	QEQIQAVPIANCQAAR	EQLRQ	2	C12:+57.021	898.9575248	1795.89945	0.000451244	3	N	1374	1390
Q9QXS1	Parental	TLRQK	AQVEQELTTLR	LQLEE	2		644.349313	1286.683026	0.000451244	5	N	2326	2337
Q9QXS1	Parental	ENQRR	IDSAEWGVDLPSVEAQLGSHR	GMHQS	3		756.0419904	2265.102571	0.000662267	8	N	683	704
Q9QXS1	Parental	QLMER	CITDPQTGLCLLPLK	EKKRE	2	C1:+57.021,C10:+57.021	864.9548422	1727.894084	0.000451244	12	N	4251	4266
Q9QXS1	Parental	LRYYR	ESADPLSAWLQDAK	RRQEQ	2		765.8758919	1529.736184	0.000451244	5	N	1358	1372
Q9QXS1	Parental	KFQGR	TVTIWEIINSEYFTAEQR	RDLLQ	2		1100.550198	2199.084796	0.000451244	8	N	3064	3082
Q9QXS1	Parental	YEDLR	DGHNLISLLEVLSGDSLPR	EKGRM	2		1018.045083	2034.074566	0.001162105	1	N	219	238
Q9QXS1	Parental	YEDLR	DGHNLISLLEVLSGDSLPR	EKGRM	3		679.0326552	2034.074566	0.000622848	3	N	219	238
Q9QXS1	Parental	GFRSR	SSSVGSSSSYPISSAGPR	TQLAS	2		856.9084518	1711.801304	0.000451244	5	N	4390	4408
Q9QXS1	Parental	QALQK	SFLSEKDSLLQR	ERFIE	2		711.88352	1421.75144	0.001943752	1	N	2638	2650
Q9QXS1	Parental	YVRRR	LTAEDLYEAR	IISLE	2		590.7963819	1179.577164	0.002453667	1	N	3790	3800
Q9QXS1	Parental	ITGQR	LLEAQACTGGIIDPSTGER	FPVTE	2	C7:+57.021	994.4915944	1986.967589	0.000622848	6	N	4454	4473
Q9QXS1	Parental	DHGVR	LLEAQIATGGIIDPVHSHR	VPVDV	3		676.3731232	2026.09597	0.002519933	1	N	2948	2967
Q9QXS1	Parental	GSCSR	HYQQLLQSLEQGEQEESR	CQRCI	3		734.6860952	2201.034886	0.000637154	1	N	1108	1126
Q9QXS1	Parental	EQGLR	LLDAQLSTGGIVDPSK	SHRVP	2		807.4413991	1612.867198	0.000622848	2	N	3276	3292
Q9QXS1	Parental	RQALR	GTNVIAGVWLEEAGQK	LSIYE	2		836.4391908	1670.862782	0.000637154	7	N	3165	3181
Q9QXS1	Parental	VTGYR	DPYSGQSVSLFQALK	KGLIP	2		820.4204667	1638.825333	0.000622848	1	N	3250	3265
Q9QXS1	Parental	EAMRR	GLLRPSTATLLLEAQAATGFLVDPVR	NQRLY	3		903.8486326	2708.522498	0.000451244	7	N	3521	3547
Q9QXS1	Parental	AGQRF	LEVQYLTGGLIEPDTPGR	VSLDE	2		979.5156268	1957.015654	0.000451244	9	N	4531	4549
Q9QXS1	Parental	QAMKK	GIIRPGTAFELLEAQAATGYVIDPIK	GLKLT	3		915.1730048	2742.495614	0.000451244	15	N	4099	4125
Q9QXS1	Parental	LYEAR	IISLETYNLFR	EGTKN	2		684.880249	1367.744898	0.001591523	1	N	3800	3811
Q9QXS1	Parental	ITVTR	LEDLLQDAQDEKEQLNEYK	GHLSG	3		774.3768159	2320.107048	0.00091018	1	N	904	923
Q9QXS1	Parental	QQRCR	SDQLTGLSLLPLSEK	AVRAR	2		800.9437746	1599.871949	0.002813207	1	N	3344	3359
Q9QXS1	Parental	VGSVR	TLLQGSGCLAGIYLEDSKEK	VTIYE	3	C8:+57.021	728.0405563	2181.098269	0.001591523	1	N	3492	3512
Q9QXT0	Parental	CGACR	ALVDELEWEIAR	VDPKK	2		722.3780705	1442.740541	0.000451244	4	N	32	44
Q9QXT0	Parental	SGTLK	FACESIVEEYEDELIEFFSR	EADNV	2	C3:+57.021	1256.565153	2511.114707	0.000637154	3	N	134	154
Q9QXT0	Parental	SGTLK	FACESIVEEYEDELIEFFSR	EADNV	3	C3:+57.021	838.0460356	2511.114707	0.000622848	3	N	134	154
Q9QXT0	Parental	MGSFR	INPDGSQSVVEVPYAR	SEAHL	2		865.9395549	1729.86351	0.001162105	2	N	57	73
Q9QXZ0	Exosome	YRKLK	ALNDAATAAEEGEALQWIVGTEVDVINQQLADFK	LFQKD	3		1210.604361	3628.789684	0.001329271	3	N	5202	5236
Q9QXZ0	Parental	VMEHR	LVLDTVNEVSHALLELVPWR	AREGL	3		768.4306382	2302.268515	0.000451244	1	N	5575	5595
Q9QXZ0	Parental	YRKLK	ALNDAATAAEEGEALQWIVGTEVDVINQQLADFK	LFQKD	3		1210.604361	3628.789684	0.000451244	11	N	5202	5236
Q9QXZ0	Parental	AEKRR	SLLEILNSAADILINSSEIDEDEIRDEK	AGLNQ	3		1048.865182	3143.572146	0.000451244	10	N	4920	4948
Q9QXZ0	Parental	LHCGK	FQDALEPLLSWLTDTEELIANQKPPSAEYK	VVKAQ	3		1149.584239	3445.729316	0.000823681	1	N	5307	5337
Q9QXZ0	Parental	VLQEK	TECLIQQYEAVSLLNSER	YARLE	2	C3:+57.021	1077.031084	2152.046568	0.002884417	1	N	5712	5730
Q9QXZ0	Parental	EKLQK	AAHDLLDIEGEPALDCRPIQETTDSISSR	FQNLS	3	C16:+57.021	1070.517857	3208.53017	0.000823681	1	N	4025	4054
Q9QY06	Parental	RLVER	GLLPRPQADFDDLCNLPELTEANLLQNLK	LRFMQ	3	C14:+57.021	1103.238254	3306.691362	0.000451244	10	N	138	167
Q9QY06	Parental	VTATK	DSTTSDVIQDVVASLHLDGSK	HYVLV	3		729.6978894	2186.070268	0.002981883	1	N	40	61
Q9QYB5	Exosome	ASLYR	LADLFGWAHLANTYISVR	ISKEQ	3		683.0306974	2046.068692	0.000451244	16	N	146	164
Q9QYB5	Exosome	VSSMK	CGILPISQESLILGDVAYYDYQGSLDEEEERIELQK	VLGPS	3	C1:+57.021	1391.679224	4172.014273	0.000622848	6	N	244	280
Q9QYB5	Exosome	STLVK	VNIIGEVVDQGSTDLK	IDHTG	2		843.9495883	1685.883577	0.000451244	3	N	191	207
Q9QYB5	Parental	REKPR	HKSDVEIPATVTAFSFEDDSAPLSPLK	FMAQR	4		726.1188917	2900.444367	0.000451244	1	N	399	426
Q9QYB5	Parental	ASLYR	LADLFGWAHLANTYISVR	ISKEQ	2		1024.042146	2046.068692	0.002019181	1	N	146	164
Q9QYB5	Parental	ASLYR	LADLFGWAHLANTYISVR	ISKEQ	3		683.0306974	2046.068692	0.000823681	4	N	146	164
Q9QYB5	Parental	VSSMK	CGILPISQESLILGDVAYYDYQGSLDEEEERIELQK	VLGPS	3	C1:+57.021	1391.679224	4172.014273	0.000998612	3	N	244	280
Q9QYB5	Parental	EDSSK	VSSGTPIKIEDPNQFVPLNTNPTEVLEK	RNKIR	3		1022.871831	3065.592094	0.002663018	1	N	476	504
Q9QYC0	Exosome	EDGHR	TSTSAVPNLFVPLNTNPK	EVQEM	2		950.5128871	1899.010174	0.000451244	12	N	479	497
Q9QYC0	Exosome	HITTR	VNSEQEHFLIVPFGLLYSEVTASSLVK	VNLQG	3		1002.866129	3005.574987	0.000451244	19	N	172	199
Q9QYC0	Exosome	VSAMK	CGLLPISPEALSLGDVAYHDYHGILVDEEEK	ILIQK	4	C1:+57.021	860.6740182	3438.664873	0.000451244	10	N	252	283
Q9QYC0	Exosome	VSAMK	CGLLPISPEALSLGDVAYHDYHGILVDEEEK	ILIQK	3	[0:-17.027,C1:+57.021	1141.553758	3421.637873	0.000451244	1	N	252	283
Q9QYC0	Exosome	ERSKK	YSDVEVPASVTGHSFASDGDSGTCSPLR	HSFQK	3	C24:+57.021	966.7667717	2897.276915	0.000451244	17	N	406	434
Q9QYC0	Exosome	AAFYR	LADLFGWSQLIYNHITTR	VNSEQ	2		1074.565985	2147.116371	0.002981883	1	N	154	172
Q9QYC0	Exosome	AAFYR	LADLFGWSQLIYNHITTR	VNSEQ	3		716.7132569	2147.116371	0.000451244	15	N	154	172
Q9QYC0	Parental	EDGHR	TSTSAVPNLFVPLNTNPK	EVQEM	2		950.5128871	1899.010174	0.000451244	16	N	479	497

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QYC0	Parental	HITTR	VNSEQEHFLIVPFGLLYSEVTASSLVK	VNLQG	3		1002.866129	3005.574987	0.000451244	20	N	172	199
Q9QYC0	Parental	VSAMK	CGLLPISPEALSLGDVAYHDYHGILVDEEEK	ILIQK	4	C1:+57.021	860.6740182	3438.664873	0.000451244	2	N	252	283
Q9QYC0	Parental	VSAMK	CGLLPISPEALSLGDVAYHDYHGILVDEEEK	ILIQK	3	[0:-17.027,C1:+57.021	1141.553758	3421.637873	0.002019181	1	N	252	283
Q9QYC0	Parental	AAFYR	LADLFGWSQLIYNHITTR	VNSEQ	3		716.7132569	2147.116371	0.000451244	11	N	154	172
Q9QYC0	Parental	PHKER	YFDRVDENNPEYLR	ERNMA	2		915.4268117	1828.838023	0.001264573	1	N	23	37
Q9QYC0	Parental	EQKEK	SPPDQSAVPNTPPSTPVKLEEDLPQEPTSR	DDSDA	3		1071.869038	3212.583714	0.000451244	18	N	599	629
Q9QYC0	Parental	AIIEK	EYQPHVIVSTTGPNPFNTLTDR	ELEEY	3		829.4157164	2485.223749	0.000451244	1	N	548	570
Q9QYJ0	Exosome	KHGQR	ITFTGEADQAPGVEPGDIVLLLQEKEHEVFQR	DGNDL	4		892.2103065	3564.810026	0.000735798	3	N	230	262
Q9QYJ0	Exosome	HMTYK	IGLVEALCGFQFTFK	HLDAR	2	C8:+57.021	865.4530239	1728.890448	0.000451244	8	N	272	287
Q9QYJ0	Parental	KHGQR	ITFTGEADQAPGVEPGDIVLLLQEKEHEVFQR	DGNDL	3		1189.277809	3564.810026	0.002019181	2	N	230	262
Q9QYJ0	Parental	KHGQR	ITFTGEADQAPGVEPGDIVLLLQEKEHEVFQR	DGNDL	4		892.2103065	3564.810026	0.000451244	4	N	230	262
Q9QYJ0	Parental	HMTYK	IGLVEALCGFQFTFK	HLDAR	2	C8:+57.021	865.4530239	1728.890448	0.000451244	3	N	272	287
Q9QYJ0	Parental	KHGQR	ITFTGEADQAPGVEPGDIVLLLQEK	EHEVF	3		880.7976036	2639.369411	0.001162105	1	N	230	255
Q9QZ06	Exosome	VSTQR	GPVYIGELPQDFLR	ITPTQ	2		802.4280947	1602.840589	0.002663018	3	N	9	23
Q9QZ06	Parental	PRWNK	VIQCTVPPGVDSFYLEIFDER	AFSMD	3	C4:+57.021	828.7423989	2483.203797	0.002374549	1	N	102	123
Q9QZ06	Parental	SMDDR	IAWTHITIPESLK	QGQVE	3		503.621087	1507.839861	0.000662267	6	N	130	143
Q9QZ06	Parental	QDFLR	ITPTQQQQQIQLDAQAAQQLQYGGTVGTVGR	LSITV	3		1109.574959	3325.701478	0.000823681	1	N	23	54
Q9QZ06	Parental	PESLK	QGQVEDEWYSLSGR	QGDDK	2		827.3793301	1652.74306	0.000622848	3	N	143	157
Q9QZ88	Exosome	VHIVR	GDFDENLNYPEQK	VVTVG	2		784.8473315	1567.679063	0.000451244	9	N	60	73
Q9QZ88	Exosome	-	MLVLVLGDLHIPHR	CNSLP	3		538.3172334	1611.9283	0.000735798	3	N	0	14
Q9QZD9	Exosome	CNDSK	ITSAVWGPLGECVIAGHESGELNQYSAK	SGEVL	3	C12:+57.021	991.8189187	2972.433356	0.000451244	13	N	148	176
Q9QZD9	Exosome	KFEAR	FFHLAFEEEFGR	VKGHF	3		510.2460202	1527.71466	0.000622848	23	N	268	280
Q9QZD9	Exosome	IKYNR	EGDLLFTVAKDPIVNVWYSVNGER	LGTYM	3		907.8014595	2720.380978	0.000451244	18	N	20	44
Q9QZD9	Exosome	DGYVR	IHYFDPQYFEFEFEA	-	2		991.4363138	1980.857028	0.00307782	1	N	310	325
Q9QZD9	Parental	CNDSK	ITSAVWGPLGECVIAGHESGELNQYSAK	SGEVL	3	C12:+57.021	991.8189187	2972.433356	0.000451244	30	N	148	176
Q9QZD9	Parental	KFEAR	FFHLAFEEEFGR	VKGHF	3		510.2460202	1527.71466	0.000622848	6	N	268	280
Q9QZD9	Parental	IKYNR	EGDLLFTVAKDPIVNVWYSVNGER	LGTYM	3		907.8014595	2720.380978	0.000451244	13	N	20	44
Q9QZD9	Parental	DGYVR	IHYFDPQYFEFEFEA	-	2		991.4363138	1980.857028	0.000622848	10	N	310	325
Q9QZE5	Exosome	GPLFK	SSPEPVALTESETEYVIR	CTKHT	2		1004.000007	2005.984413	0.000451244	10	N	631	649
Q9QZE5	Exosome	TDSNR	SIATLAITTLLK	TGSES	2		622.8953677	1243.775135	0.000851441	19	Y	338	350
Q9QZE5	Exosome	GCSAK	ELAPAVSVLQLFCSSPK	AALRY	2	C13:+57.021	923.4928775	1844.970155	0.000451244	6	Y	283	300
Q9QZE5	Exosome	GCSAK	ELAPAVSVLQLFCSSPK	AALRY	3	C13:+57.021	615.9978516	1844.970155	0.001943752	1	Y	283	300
Q9QZE5	Exosome	RVASK	QLEEEDGSRDSPLFDFIESCLR	NKHEM	3	C20:+57.021	881.4065151	2641.196145	0.000622848	4	N	238	260
Q9QZE5	Exosome	QKVMK	VNFEAAWDEVGDEFEKEETFTLSTIK	TLEEA	3		1012.145509	3033.413126	0.000451244	11	N	769	795
Q9QZE5	Exosome	QVTAR	SSEELPVDIILASVG	-	2		764.9094005	1527.803201	0.001463592	2	N	859	874
Q9QZE5	Exosome	KFTVK	DCDPNTGEIDEEGYEDEYVLEDLEVTVADHIQK	VMKVN	3	C2:+57.021	1280.558552	3838.652255	0.000451244	16	N	733	766
Q9QZE5	Exosome	FEYKR	AIVDCIISIIEENSESK	ETGLS	3	C5:+57.021	640.6595643	1918.955293	0.000451244	3	N	415	432
Q9QZE5	Exosome	GCSAK	ELAPAVSVLQLF	CSSPK	2		643.8718926	1285.728185	0.001699387	1	Y	283	295
Q9QZE5	Parental	GPLFK	SSPEPVALTESETEYVIR	CTKHT	2		1004.000007	2005.984413	0.000451244	33	N	631	649
Q9QZE5	Parental	TDSNR	SIATLAITTLLK	TGSES	2		622.8953677	1243.775135	0.000622848	22	Y	338	350
Q9QZE5	Parental	KQPEK	VAATRQEIFQEQLAAVPEFQGLGPLFK	SSPEP	3		996.5383467	2986.59164	0.002453667	1	N	604	631
Q9QZE5	Parental	GCSAK	ELAPAVSVLQLFCSSPK	AALRY	2	C13:+57.021	923.4928775	1844.970155	0.000451244	17	Y	283	300
Q9QZE5	Parental	SCVMK	FTVKDCDPNTGEIDEEGYEDEYVLEDLEVTVADHIQK	VMKVN	4	C6:+57.021	1079.490731	4313.931725	0.000451244	12	N	729	766
Q9QZE5	Parental	RVASK	QLEEEDGSRDSPLFDFIESCLR	NKHEM	3	C20:+57.021	881.4065151	2641.196145	0.000622848	4	N	238	260
Q9QZE5	Parental	VAATR	QEIFQEQLAAVPEFQGLGPLFK	SSPEP	2		1245.157904	2488.300209	0.000451244	25	N	609	631
Q9QZE5	Parental	VAATR	QEIFQEQLAAVPEFQGLGPLFK	SSPEP	3		830.4412029	2488.300209	0.000451244	20	N	609	631
Q9QZE5	Parental	PGLEK	ALQQYTLEPSEKPFDLK	SVPLA	2		1004.025827	2006.036055	0.000451244	3	N	560	577
Q9QZE5	Parental	PGLEK	ALQQYTLEPSEKPFDLK	SVPLA	3		669.6864849	2006.036055	0.000451244	10	N	560	577
Q9QZE5	Parental	EQKQK	ALNAGYILNGLTVSIPGLEK	ALQQY	2		1022.078394	2042.141189	0.000451244	10	N	540	560
Q9QZE5	Parental	QKVMK	VNFEAAWDEVGDEFEKEETFTLSTIK	TLEEA	3		1012.145509	3033.413126	0.000451244	30	N	769	795
Q9QZE5	Parental	QVTAR	SSEELPVDIILASVG	-	2		764.9094005	1527.803201	0.000451244	2	N	859	874
Q9QZE5	Parental	KFTVK	DCDPNTGEIDEEGYEDEYVLEDLEVTVADHIQK	VMKVN	3	C2:+57.021	1280.558552	3838.652255	0.000451244	35	N	733	766
Q9QZE5	Parental	QKVMK	VNFEAAWDEVGDEFEKEETF	TLSTI	2		1196.019125	2390.022649	0.000451244	5	N	769	789
Q9QZE5	Parental	NSESK	ETGLSHLCEFIEDCEFTVLATR	ILHLL	3	C8:+57.021,C14:+57.021	876.4089368	2626.203411	0.000637154	1	N	432	454
Q9QZE5	Parental	FEYKR	AIVDCIISIIEENSESK	ETGLS	3	C5:+57.021	640.6595643	1918.955293	0.000451244	9	N	415	432
Q9QZE5	Parental	DVVKR	WVNEAQEAASSDNIMVQYHALGLLYHVR	KNDRL	3		1072.196655	3213.566566	0.000823681	1	N	176	204
Q9QZF2	Exosome	KAQLR	DIQDFWISLPGTLCSEK	MAMSP	2	C14:+57.021	1004.988156	2007.960713	0.000622848	12	N	386	403
Q9QZF2	Exosome	RLYYR	GANLHLEETLAEFWAR	LLERL	3		619.6483645	1855.921693	0.002212458	1	N	153	169
Q9QZF2	Parental	KAQLR	DIQDFWISLPGTLCSEK	MAMSP	2	C14:+57.021	1004.988156	2007.960713	0.000622848	2	N	386	403
Q9QZK7	Exosome	RRVIR	LADCVSVLPADGESCPR	DTGAF	2	C4:+57.021,C15:+57.021	923.4271772	1844.838754	0.000451244	14	N	73	90
Q9QZK7	Exosome	FSSPR	APDICGVVAAAIAR	QRERL	2	C5:+57.021	692.3745765	1382.733553	0.000451244	18	N	239	253
Q9QZK7	Exosome	LPTPR	KLPLTDPGPQSLPLLLSPTQEGPASGLYASVCK	QTSKH	3	C32:+57.021	1145.613209	3433.816228	0.000622848	15	N	297	330
Q9QZK7	Exosome	AAQHR	QSWVDPICQLAFPGTGECSSGSGQAESPKR	GFVPM	3	C8:+57.021,C18:+57.021	1079.496244	3235.465333	0.000622848	10	N	111	141
Q9QZK7	Exosome	ESCPR	DTGAFLITTTER	SHLLA	2		662.8413208	1323.667042	0.001264573	1	N	90	102
Q9QZK7	Exosome	EAGRR	CDSGEGLFAFSSPR	APDIC	2	C1:+57.021	765.338388	1528.661176	0.000451244	2	N	225	239

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QZK7	Exosome	PPGGR	SPLGSPIYHNTEDLSWPGSAQDSNLEAQYR	RLLEL	3		1111.52052	3331.538161	0.001264573	5	N	370	400
Q9QZK7	Exosome	AAQHR	QSWVDPICQLAFPGTGECSSGSGQAESPK	RGFVP	3	C8:+57.021,C18:+57.021	1027.462541	3079.364222	0.00091018	1	N	111	140
Q9QZK7	Parental	RRVIR	LADCVSVLPADGESCPR	DTGAF	2	C4:+57.021,C15:+57.021	923.4271772	1844.838754	0.000622848	21	N	73	90
Q9QZK7	Parental	FSSPR	APDICGVVAAAIAR	QRERL	2	C5:+57.021	692.3745765	1382.733553	0.000451244	17	N	239	253
Q9QZK7	Parental	EATSR	CQLKGPYLLVLGQDDIQLR	ETSKP	3	C1:+57.021	743.7405526	2228.198258	0.001162105	1	N	173	192
Q9QZK7	Parental	EATSR	CQLKGPYLLVLGQDDIQLR	ETSKP	2	[0:-17.027,C1:+57.021	1106.593429	2211.171258	0.002727428	1	N	173	192
Q9QZK7	Parental	LPTPR	KLPLTDPGPQSLPLLLSPTQEGPASGLYASVCK	QTSKH	3	C32:+57.021	1145.613209	3433.816228	0.000451244	8	N	297	330
Q9QZK7	Parental	AAQHR	QSWVDPICQLAFPGTGECSSGSGQAESPKR	GFVPM	3	C8:+57.021,C18:+57.021	1079.496244	3235.465333	0.000451244	18	N	111	141
Q9QZK7	Parental	ESCPR	DTGAFLITTTER	SHLLA	2		662.8413208	1323.667042	0.000637154	7	N	90	102
Q9QZK7	Parental	EAGRR	CDSGEGLFAFSSPR	APDIC	2	C1:+57.021	765.338388	1528.661176	0.000622848	2	N	225	239
Q9QZK7	Parental	ENSIY	SSWQEVTEFPVIVQR	TEATS	2		902.9655727	1803.915545	0.000451244	2	N	152	167
Q9QZQ8	Exosome	LEYLT	AEILELAGNAAR	DNKKG	2		614.3387483	1226.661897	0.000451244	66	Y	57	69
Q9QZQ8	Exosome	LEYLT	AEILELAGNAAR	DNKKG	3		409.8950988	1226.661897	0.001463592	3	Y	57	69
Q9QZQ8	Exosome	GLPAK	FVIHCNSPVWGADKCEELLEK	TVKNC	3	C5:+57.021,C15:+57.021	844.4069791	2530.197537	0.000451244	50	N	271	292
Q9QZQ8	Exosome	GLPAK	FVIHCNSPVWGADKCEELLEK	TVKNC	4	C5:+57.021,C15:+57.021	633.5571843	2530.197537	0.000451244	61	N	271	292
Q9QZQ8	Exosome	VLEYL	TAEILELAGNAAR	DNKKG	2		664.8625875	1327.709575	0.000451244	73	Y	56	69
Q9QZQ8	Exosome	NQLLK	GVTIASGGVLPNIHPELLAK	KRGSK	2		993.5732791	1985.130958	0.000451244	40	N	96	116
Q9QZQ8	Exosome	NQLLK	GVTIASGGVLPNIHPELLAK	KRGSK	3		662.7181194	1985.130958	0.000451244	50	N	96	116
Q9QZQ8	Exosome	AVLEY	LTAEILELAGNAAR	DNKKG	2		721.4046196	1440.793639	0.000451244	693	Y	55	69
Q9QZQ8	Exosome	AVLEY	LTAEILELAGNAAR	DNKKG	3		481.2723464	1440.793639	0.000451244	322	Y	55	69
Q9QZQ8	Exosome	TLEKK	GGKEFVEAVLELR	KKNGP	2		723.9017127	1445.787825	0.000622848	1	N	236	249
Q9QZQ8	Exosome	TLEKK	GGKEFVEAVLELR	KKNGP	3		482.9370752	1445.787825	0.000451244	22	N	236	249
Q9QZQ8	Exosome	RVTPR	HILLAVANDEELNQLLK	GVTIA	2		967.0418118	1932.068024	0.000451244	50	Y	79	96
Q9QZQ8	Exosome	RVTPR	HILLAVANDEELNQLLK	GVTIA	3		645.0304745	1932.068024	0.000451244	67	Y	79	96
Q9QZQ8	Exosome	KKGGK	EFVEAVLELR	KKNGP	2		602.8327674	1203.649935	0.000622848	19	N	239	249
Q9QZQ8	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKG	2		867.4575805	1732.899561	0.000451244	127	Y	53	69
Q9QZQ8	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKG	3		578.640987	1732.899561	0.000451244	83	Y	53	69
Q9QZQ8	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKG	2	E1:-18.011	858.4520805	1714.888561	0.000451244	13	Y	53	69
Q9QZQ8	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKG	3	E1:-18.011	572.6373203	1714.888561	0.000451244	14	Y	53	69
Q9QZQ8	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKG	2	[0:-18.011	858.4520805	1714.888561	0.000998612	4	Y	53	69
Q9QZQ8	Exosome	MAAVL	EYLTAEILELAGNAAR	DNKKG	3	[0:-18.011	572.6373203	1714.888561	0.001329271	6	Y	53	69
Q9QZQ8	Exosome	YMAAV	LEYLTAEILELAGNAAR	DNKKG	2		923.9996126	1845.983625	0.000451244	1105	Y	52	69
Q9QZQ8	Exosome	YMAAV	LEYLTAEILELAGNAAR	DNKKG	3		616.335675	1845.983625	0.000451244	1302	Y	52	69
Q9QZQ8	Exosome	FLGQK	LNLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	3		1417.067854	4248.180161	0.000823681	1	N	196	235
Q9QZQ8	Exosome	FLGQK	LNLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	4		1063.05284	4248.180161	0.000451244	15	N	196	235
Q9QZQ8	Exosome	VYMAA	VLEYLTAEILELAGNAAR	DNKKG	2		973.5338196	1945.052039	0.000451244	625	Y	51	69
Q9QZQ8	Exosome	VYMAA	VLEYLTAEILELAGNAAR	DNKKG	3		649.3584797	1945.052039	0.000451244	910	Y	51	69
Q9QZQ8	Exosome	YLTAE	ILELAGNAAR	DNKKG	2		514.2988947	1026.582189	0.000622848	2	Y	59	69
Q9QZQ8	Exosome	PVYMA	AVLEYLTAEILELAGNAAR	DNKKG	2		1009.052376	2016.089153	0.000451244	342	Y	50	69
Q9QZQ8	Exosome	PVYMA	AVLEYLTAEILELAGNAAR	DNKKG	3		673.0375177	2016.089153	0.000451244	299	Y	50	69
Q9QZQ8	Exosome	APVYM	AAVLEYLTAEILELAGNAAR	DNKKG	2		1044.570933	2087.126267	0.000451244	349	Y	49	69
Q9QZQ8	Exosome	APVYM	AAVLEYLTAEILELAGNAAR	DNKKG	3		696.7165556	2087.126267	0.000451244	563	Y	49	69
Q9QZQ8	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	2		1110.091176	2218.166753	0.000451244	78	Y	48	69
Q9QZQ8	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	3		740.3967175	2218.166753	0.000451244	63	Y	48	69
Q9QZQ8	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	2	M1:+15.995	1118.088676	2234.161753	0.000451244	21	Y	48	69
Q9QZQ8	Exosome	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	3	M1:+15.995	745.7283842	2234.161753	0.000451244	39	Y	48	69
Q9QZQ8	Exosome	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	2		1488.299689	2974.583779	0.000451244	41	N	40	69
Q9QZQ8	Exosome	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	3		992.5357262	2974.583779	0.000451244	86	N	40	69
Q9QZQ8	Exosome	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	4		744.6537447	2974.583779	0.000451244	32	N	40	69
Q9QZQ8	Exosome	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	2	M9:+15.995	1496.297189	2990.578779	0.000451244	28	N	40	69
Q9QZQ8	Exosome	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	3	M9:+15.995	997.8673929	2990.578779	0.000451244	174	N	40	69
Q9QZQ8	Exosome	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	4	M9:+15.995	748.6524947	2990.578779	0.000451244	16	N	40	69
Q9QZQ8	Exosome	GEVSK	AASADSTTEGTPTDGFTVLSTK	SLFLG	2		1079.013842	2156.012085	0.000451244	78	N	167	189
Q9QZQ8	Exosome	GEVSK	AASADSTTEGTPTDGFTVLSTK	SLFLG	3		719.6784949	2156.012085	0.001463592	2	N	167	189
Q9QZQ8	Exosome	DRKLK	SIAFPSIGSGR	NGFPK	2		546.2963521	1090.577104	0.000451244	8	N	307	318
Q9QZQ8	Exosome	GEVSK	AASADSTTEGTPTDGFTVL	STKSL	2		920.9265072	1839.837414	0.000451244	17	N	167	186
Q9QZQ8	Exosome	KRGSK	GKLEAIITPPPAK	KAKSP	2		667.9062668	1333.796934	0.000622848	6	N	121	134
Q9QZQ8	Exosome	GSKGK	LEAIITPPPAK	KAKSP	2		575.3480533	1148.680507	0.000622848	2	N	123	134
Q9QZQ8	Exosome	EYLTA	EILELAGNAAR	DNKKG	2		578.8201913	1155.624783	0.000451244	37	Y	58	69
Q9QZQ8	Exosome	ELRKK	NGPLEVAGAAISAGHGLPAK	FVIHC	2		915.4975714	1828.979543	0.000451244	5	N	251	271
Q9QZQ8	Exosome	ELRKK	NGPLEVAGAAISAGHGLPAK	FVIHC	3		610.6676476	1828.979543	0.000451244	30	N	251	271
Q9QZQ8	Exosome	NQLLK	GVTIASGGVLPNIHPELL	AKKRG	2		894.0072406	1785.998881	0.000451244	21	N	96	114
Q9QZQ8	Exosome	AAVLE	YLTAEILELAGNAAR	DNKKG	2		802.9362839	1603.856968	0.000451244	70	Y	54	69
Q9QZQ8	Exosome	QLILK	AISSYFVSTMSSSIK	TVYFM	2	M10:+15.995	812.4009286	1622.786257	0.000451244	23	N	332	347
Q9QZQ8	Exosome	IGVGA	PVYMAAVLEYLTAEILELAGNAAR	DNKKG	2		1289.68343	2577.351259	0.000451244	2	Y	45	69

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QZQ8	Exosome	LPAKF	VIHCNSPVWGADKCEELLEK	TVKNC	3	C4:+57.021,C14:+57.021	795.3841744	2383.129123	0.002453667	1	N	272	292
Q9QZQ8	Exosome	RVTPR	HILLAVANDEELNQLLKGVTIASGGVLPNIHPELLAK	KRGSK	4		975.8049054	3899.188422	0.000823681	5	N	79	116
Q9QZQ8	Exosome	NQLLK	GVTIASGGVLPNIHPEL	LAKKR	2		837.4652086	1672.914817	0.000451244	7	N	96	113
Q9QZQ8	Parental	LEYLT	AEILELAGNAAR	DNKKG	2		614.3387483	1226.661897	0.000451244	149	Y	57	69
Q9QZQ8	Parental	LEYLT	AEILELAGNAAR	DNKKG	3		409.8950988	1226.661897	0.000662267	10	Y	57	69
Q9QZQ8	Parental	GLPAK	FVIHCNSPVWGADKCEELLEK	TVKNC	2	C5:+57.021,C15:+57.021	1266.106569	2530.197537	0.000451244	16	N	271	292
Q9QZQ8	Parental	GLPAK	FVIHCNSPVWGADKCEELLEK	TVKNC	3	C5:+57.021,C15:+57.021	844.4069791	2530.197537	0.000451244	44	N	271	292
Q9QZQ8	Parental	GLPAK	FVIHCNSPVWGADKCEELLEK	TVKNC	4	C5:+57.021,C15:+57.021	633.5571843	2530.197537	0.000451244	32	N	271	292
Q9QZQ8	Parental	VLEYL	TAEILELAGNAAR	DNKKG	2		664.8625875	1327.709575	0.000451244	59	Y	56	69
Q9QZQ8	Parental	NQLLK	GVTIASGGVLPNIHPELLAK	KRGSK	2		993.5732791	1985.130958	0.000451244	32	N	96	116
Q9QZQ8	Parental	NQLLK	GVTIASGGVLPNIHPELLAK	KRGSK	3		662.7181194	1985.130958	0.000451244	24	N	96	116
Q9QZQ8	Parental	AVLEY	LTAEILELAGNAAR	DNKKG	2		721.4046196	1440.793639	0.000451244	1756	Y	55	69
Q9QZQ8	Parental	AVLEY	LTAEILELAGNAAR	DNKKG	3		481.2723464	1440.793639	0.000451244	1299	Y	55	69
Q9QZQ8	Parental	TLEKK	GGKEFVEAVLELR	KKNGP	3		482.9370752	1445.787825	0.000451244	8	N	236	249
Q9QZQ8	Parental	RVTPR	HILLAVANDEELNQLLK	GVTIA	2		967.0418118	1932.068024	0.000451244	16	Y	79	96
Q9QZQ8	Parental	RVTPR	HILLAVANDEELNQLLK	GVTIA	3		645.0304745	1932.068024	0.000451244	10	Y	79	96
Q9QZQ8	Parental	KKGGK	EFVEAVLELR	KKNGP	2		602.8327674	1203.649935	0.000451244	28	N	239	249
Q9QZQ8	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKG	2		867.4575805	1732.899561	0.000451244	60	Y	53	69
Q9QZQ8	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKG	3		578.640987	1732.899561	0.000451244	106	Y	53	69
Q9QZQ8	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKG	3	E1:-18.011	572.6373203	1714.888561	0.000451244	29	Y	53	69
Q9QZQ8	Parental	MAAVL	EYLTAEILELAGNAAR	DNKKG	3	[0:-18.011	572.6373203	1714.888561	0.000870037	6	Y	53	69
Q9QZQ8	Parental	YMAAV	LEYLTAEILELAGNAAR	DNKKG	2		923.9996126	1845.983625	0.000451244	127	Y	52	69
Q9QZQ8	Parental	YMAAV	LEYLTAEILELAGNAAR	DNKKG	3		616.335675	1845.983625	0.000451244	230	Y	52	69
Q9QZQ8	Parental	LGQKL	NLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	3		1379.373166	4135.096097	0.002212458	1	N	197	235
Q9QZQ8	Parental	LGQKL	NLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	4		1034.781824	4135.096097	0.000622848	8	N	197	235
Q9QZQ8	Parental	FLGQK	LNLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	3		1417.067854	4248.180161	0.000634081	2	N	196	235
Q9QZQ8	Parental	FLGQK	LNLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	KGGKE	4		1063.05284	4248.180161	0.000622848	26	N	196	235
Q9QZQ8	Parental	VYMAA	VLEYLTAEILELAGNAAR	DNKKG	2		973.5338196	1945.052039	0.000451244	63	Y	51	69
Q9QZQ8	Parental	VYMAA	VLEYLTAEILELAGNAAR	DNKKG	3		649.3584797	1945.052039	0.000451244	120	Y	51	69
Q9QZQ8	Parental	YLTAE	ILELAGNAAR	DNKKG	2		514.2988947	1026.582189	0.000622848	1	Y	59	69
Q9QZQ8	Parental	PVYMA	AVLEYLTAEILELAGNAAR	DNKKG	2		1009.052376	2016.089153	0.000451244	52	Y	50	69
Q9QZQ8	Parental	PVYMA	AVLEYLTAEILELAGNAAR	DNKKG	3		673.0375177	2016.089153	0.000451244	71	Y	50	69
Q9QZQ8	Parental	APVYM	AAVLEYLTAEILELAGNAAR	DNKKG	2		1044.570933	2087.126267	0.000451244	817	Y	49	69
Q9QZQ8	Parental	APVYM	AAVLEYLTAEILELAGNAAR	DNKKG	3		696.7165556	2087.126267	0.000451244	954	Y	49	69
Q9QZQ8	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	2		1110.091176	2218.166753	0.000451244	93	Y	48	69
Q9QZQ8	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	3		740.3967175	2218.166753	0.000451244	96	Y	48	69
Q9QZQ8	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	2	M1:+15.995	1118.088676	2234.161753	0.000451244	29	Y	48	69
Q9QZQ8	Parental	GAPVY	MAAVLEYLTAEILELAGNAAR	DNKKG	3	M1:+15.995	745.7283842	2234.161753	0.000451244	43	Y	48	69
Q9QZQ8	Parental	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	2		1488.299689	2974.583779	0.001763695	2	N	40	69
Q9QZQ8	Parental	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	3		992.5357262	2974.583779	0.001943752	2	N	40	69
Q9QZQ8	Parental	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	4		744.6537447	2974.583779	0.001763695	2	N	40	69
Q9QZQ8	Parental	HPKYR	IGVGAPVYMAAVLEYLTAEILELAGNAAR	DNKKG	3	M9:+15.995	997.8673929	2990.578779	0.000451244	18	N	40	69
Q9QZQ8	Parental	GEVSK	AASADSTTEGTPTDGFTVLSTK	SLFLG	2		1079.013842	2156.012085	0.000823681	5	N	167	189
Q9QZQ8	Parental	DRKLK	SIAFPSIGSGR	NGFPK	2		546.2963521	1090.577104	0.000998612	3	N	307	318
Q9QZQ8	Parental	GEVSK	AASADSTTEGTPTDGFTVL	STKSL	2		920.9265072	1839.837414	0.000622848	6	N	167	186
Q9QZQ8	Parental	EYLTA	EILELAGNAAR	DNKKG	2		578.8201913	1155.624783	0.000451244	6	Y	58	69
Q9QZQ8	Parental	ELRKK	NGPLEVAGAAISAGHGLPAK	FVIHC	3		610.6676476	1828.979543	0.000823681	7	N	251	271
Q9QZQ8	Parental	AAVLE	YLTAEILELAGNAAR	DNKKG	2		802.9362839	1603.856968	0.001395409	1	Y	54	69
Q9QZQ8	Parental	LPAKF	VIHCNSPVWGADKCEELLEK	TVKNC	2	C4:+57.021,C14:+57.021	1192.572362	2383.129123	0.000451244	2	N	272	292
Q9QZQ8	Parental	LPAKF	VIHCNSPVWGADKCEELLEK	TVKNC	3	C4:+57.021,C14:+57.021	795.3841744	2383.129123	0.00091018	1	N	272	292
Q9QZQ8	Parental	LPAKF	VIHCNSPVWGADKCEELLEK	TVKNC	4	C4:+57.021,C14:+57.021	596.7900808	2383.129123	0.000451244	3	N	272	292
Q9QZQ8	Parental	IINPT	NADIDLKDDLGNTLEK	KGGKE	2		887.4474098	1772.87922	0.000451244	1	N	219	235
Q9QZQ8	Parental	HILLA	VANDEELNQLLK	GVTIA	2		693.3677027	1384.719805	0.000622848	1	Y	84	96
Q9QZQ8	Parental	ELRKK	NGPLEVAGAAISAGHGLPAKF	VIHCN	3		659.6904523	1976.047957	0.0025889	1	N	251	272
Q9QZQ8	Parental	RHILL	AVANDEELNQLLK	GVTIA	2		728.8862597	1455.756919	0.001463592	1	Y	83	96
Q9QZS3	Parental	ASGNR	HAEVPPGTCPVDPFEAQWAALESK	SKQRT	3	C9:+57.021	879.4202074	2635.237222	0.000451244	1	N	604	628
Q9QZS3	Parental	KSKQR	TNPSPTNPFSSDLQK	TFEIE	2		816.8973557	1631.779111	0.002727428	1	N	632	647
Q9QZU3	Exosome	GPEPR	ASLSFWELLQGDPWCPDPR	SLPLD	2	C15:+57.021	1137.536336	2273.057073	0.000451244	19	N	457	476
Q9QZU3	Exosome	GPEPR	ASLSFWELLQGDPWCPDPR	SLPLD	3	C15:+57.021	758.6934909	2273.057073	0.000451244	6	N	457	476
Q9QZU3	Exosome	VKLEK	LLLYSNQLTSVDSGLLSNLGALTELR	LERNH	2		1395.766536	2789.517472	0.000451244	21	N	198	224
Q9QZU3	Exosome	VKLEK	LLLYSNQLTSVDSGLLSNLGALTELR	LERNH	3		930.8469574	2789.517472	0.000451244	25	N	198	224
Q9QZU3	Exosome	FQQLR	NLQELGLNQNQLSFLPANLFSSLR	ELKLL	2		1358.725005	2715.434411	0.000451244	9	N	146	170
Q9QZU3	Exosome	AILDK	MVLLEQLFLDHNALR	DLDQN	2		906.4959863	1810.976373	0.002019181	3	N	120	135
Q9QZU3	Exosome	AILDK	MVLLEQLFLDHNALR	DLDQN	3		604.6665909	1810.976373	0.001839721	2	N	120	135
Q9QZU3	Exosome	VKLEK	LLLYSNQLTSVDSGLLSNLGALTELRLER	NHLRS	3		1063.589547	3187.745241	0.000451244	3	N	198	227

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9QZU3	Exosome	SSVSR	LTLFENPLEELPDVLFGEMAGLR	ELWLN	2		1302.175437	2602.335275	0.000451244	5	N	270	293
Q9QZU3	Exosome	HNALR	DLDQNLFQQLR	NLQEL	2		695.360212	1388.704824	0.000698008	3	N	135	146
Q9QZU3	Exosome	LRELR	VLALHTNALAELRDDALR	GLGHL	4		498.5317924	1990.09597	0.000698008	2	N	342	360
Q9QZU3	Parental	GPEPR	ASLSFWELLQGDPWCPDPR	SLPLD	2	C15:+57.021	1137.536336	2273.057073	0.000451244	4	N	457	476
Q9QZU3	Parental	FQQLR	NLQELGLNQNQLSFLPANLFSSLR	ELKLL	2		1358.725005	2715.434411	0.000622848	2	N	146	170
Q9QZU3	Parental	KLLLY	SNQLTSVDSGLLSNLGALTELRLER	NHLRS	3		896.1510399	2685.42972	0.000451244	3	N	202	227
Q9QZU3	Parental	FQQLR	NLQELGLNQNQLSFLPANLF	SSLRE	2		1137.100389	2272.185179	0.000851441	2	N	146	166
Q9R059	Parental	LYGRK	YIQTDSGPYCVPCYDNTFANTCAECQQLIGHDSR	ELFYE	3	C10:+57.021,C13:+57.021,C22:+57.021,C25:+57.021	1347.569506	4039.685118	0.000451244	32	N	18	52
Q9R059	Parental	CTGCK	TPLAGQQFTSRDDDPYCVACFGELFAPK	CSSCK	3	C17:+57.021,C20:+57.021	1064.158681	3189.452643	0.000823681	1	N	192	220
Q9R059	Parental	MPGSR	KLEYGGQTWHEHCFLCSGCEQPLGSR	SFVPD	3	C13:+57.021,C16:+57.021,C19:+57.021	1046.132317	3135.373552	0.000823681	1	N	113	139
Q9R059	Parental	QFTSR	DDDPYCVACFGELFAPK	CSSCK	2	C6:+57.021,C9:+57.021	1002.429386	2002.843171	0.000451244	13	N	203	220
Q9R062	Exosome	NPQTK	SVNCDSQDPTVSHPEFLNLWWDTFTTNVLPLLQHHGLVK	DASSY	4	C4:+57.021	1137.063264	4544.221855	0.000451244	20	N	229	268
Q9R062	Exosome	DAYAK	GALVLGSSLK	QHRTT	2		472.7929139	943.5702278	0.001654178	4	N	17	27
Q9R062	Exosome	HGLVK	DASSYLMMEHVSGALSDLSFGEAPAAPQPSMSSEER	KERWE	3	M7:+15.995,M8:+15.995,M31:+15.995	1278.226214	3831.655243	0.000451244	32	N	268	304
Q9R062	Exosome	SIETY	NQLLHLASEQGSFDGGDQGLLNTYFSGWATTDITK	HLPFV	3		1262.275015	3783.801646	0.000451244	12	N	146	181
Q9R062	Exosome	HFLGR	TKPWNYTYNPQTK	SVNCD	2		820.9075264	1639.799453	0.000622848	21	N	216	229
Q9R062	Exosome	HFLGR	TKPWNYTYNPQTK	SVNCD	3		547.6076176	1639.799453	0.000735798	9	N	216	229
Q9R062	Exosome	ERKER	WEQGQADYMGADSFDNIKR	KLDTY	2	M9:+15.995	1123.992764	2245.969929	0.000451244	8	N	307	326
Q9R062	Exosome	ERKER	WEQGQADYMGADSFDNIKR	KLDTY	3	M9:+15.995	749.664443	2245.969929	0.000451244	12	N	307	326
Q9R062	Exosome	ITLTK	LHCWSLTQYSK	CVFMD	2	C3:+57.021	711.8456519	1421.675704	0.001162105	12	N	86	97
Q9R062	Exosome	ITLTK	LHCWSLTQYSK	CVFMD	3	C3:+57.021	474.8997013	1421.675704	0.002080925	1	N	86	97
Q9R062	Exosome	NPQTK	SVNCDSQDPTVSHPEFLNLWWDTFTTN	VLPLL	3	C4:+57.021	1070.808859	3209.403178	0.000622848	8	N	229	256
Q9R062	Exosome	MMEHV	SGALSDLSFGEAPAAPQPSMSSEER	KERWE	2	M20:+15.995	1269.077223	2536.138845	0.001654178	1	N	279	304
Q9R062	Exosome	ERKER	WEQGQADYMGADSFDNIK	RKLDT	2	M9:+15.995	1045.942209	2089.868818	0.000451244	4	N	307	325
Q9R062	Exosome	TYNQL	LHLASEQGSFDGGDQGLLNTYFSGWATTDITK	HLPFV	3		1143.879826	3428.616077	0.001591523	1	N	149	181
Q9R062	Parental	NPQTK	SVNCDSQDPTVSHPEFLNLWWDTFTTNVLPLLQHHGLVK	DASSY	4	C4:+57.021	1137.063264	4544.221855	0.000823681	6	N	229	268
Q9R062	Parental	SIETY	NQLLHLASEQGSFDGGDQGLLNTYFSGWATTDITK	HLPFV	3		1262.275015	3783.801646	0.000451244	13	N	146	181
Q9R062	Parental	ITLTK	LHCWSLTQYSK	CVFMD	2	C3:+57.021	711.8456519	1421.675704	0.001162105	4	N	86	97
Q9R078	Exosome	LPLTR	SQNNFVAILDLPEGEHQYK	FFVDG	3		734.6995646	2201.075294	0.001943752	1	N	107	126
Q9R078	Parental	EHQYK	FFVDGQWTHDPSEPIVTSQLGTVNNIIQVK	KTDFE	3		1123.909168	3368.704104	0.000451244	30	N	126	156
Q9R078	Parental	LPLTR	SQNNFVAILDLPEGEHQYK	FFVDG	3		734.6995646	2201.075294	0.000622848	3	N	107	126
Q9R0C8	Exosome	APLKR	FLTAAEFDSVFINIPDLVK	VHRSL	2		1070.072778	2138.129955	0.000451244	6	N	224	243
Q9R0C8	Exosome	TFGMR	KSELFEAFDLFDVR	DFGKV	3		572.6266778	1714.856634	0.000451244	10	N	89	103
Q9R0C8	Exosome	PPNHR	VTWDSAQVFDLAQTLR	DGVLL	2		925.4763046	1848.937009	0.000622848	2	N	22	38
Q9R0C8	Exosome	LREIK	QFQLSIENLNQPVLLFGRPQGDGEIR	ITTLD	3		990.1933505	2967.556652	0.001352548	3	N	382	408
Q9R0C8	Parental	APLKR	FLTAAEFDSVFINIPDLVK	VHRSL	2		1070.072778	2138.129955	0.000622848	3	N	224	243
Q9R0E1	Exosome	GMGKR	FLNSGGFIGFAPTIHQIVR	QWNYK	3		692.0464589	2073.115977	0.000662267	2	N	165	184
Q9R0E1	Exosome	QPPPR	VLLAVFVEQPTPFLPR	FLQRL	2		913.5328942	1825.050188	0.002453667	3	N	300	316
Q9R0E1	Exosome	HQIVR	QWNYKDDDDDQLFYTQLYLDPGLR	EKLKL	3		1007.802076	3020.382829	0.002813207	2	N	184	208
Q9R0E1	Exosome	DHKSR	IFQNLNGALDEVILK	FDQNR	2		843.9754091	1685.935218	0.002145581	1	N	220	235
Q9R0E1	Parental	SRHGK	LWSNFWGALSPNEYYAR	SEDYV	2		1037.495029	2072.974457	0.00307782	1	N	426	443
Q9R0N0	Exosome	QVCQR	AEHSFAGVPCGIMDQLIALLGQK	GYALL	3	C10:+57.021	819.0876239	2454.239472	0.000451244	12	N	172	195
Q9R0N0	Exosome	DEPQR	LQFPLPSAQWSLEPGIPQWANYVK	GVIQH	2		1385.22411	2768.43262	0.000451244	7	N	87	111
Q9R0N0	Exosome	DEPQR	LQFPLPSAQWSLEPGIPQWANYVK	GVIQH	3		923.8186733	2768.43262	0.000451244	8	N	87	111
Q9R0N0	Exosome	LLGQK	GYALLIDCR	SLETS	2	C8:+57.021	540.7792492	1079.542898	0.000698008	5	N	195	204
Q9R0N0	Exosome	LIDCR	SLETSLVPLSDPK	LAVLI	2		693.3802788	1384.744958	0.000451244	6	N	204	217
Q9R0N0	Exosome	VGSPR	TDGLVSLLTTSKDADEPQR	LQFPL	2		1023.521637	2045.027675	0.000451244	1	N	68	87
Q9R0N0	Exosome	EVATY	TFIQQLCPDSGAIAAR	AQVCQ	2	C7:+57.021	874.4437189	1746.871838	0.002019181	1	N	150	166
Q9R0N0	Exosome	VGSPR	TDGLVSLLTTSK	DADEP	2		617.8486145	1233.681629	0.000823681	1	N	68	80
Q9R0P3	Exosome	PGKYR	SVSAFAPICNPVLCSWGK	KAFSG	2	C9:+57.021,C14:+57.021	996.987205	1991.95881	0.000451244	28	N	167	185
Q9R0P3	Exosome	TCLVK	AYSGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	3	C34:+57.021	1362.660164	4084.957092	0.000622848	51	N	209	246
Q9R0P3	Exosome	TCLVK	AYSGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	4	C34:+57.021	1022.247073	4084.957092	0.000662267	6	N	209	246
Q9R0P3	Exosome	NFISK	SGYQQAASEHGLVVIAPDTSPR	GCNIK	2		1142.07236	2282.12912	0.000451244	25	N	64	86
Q9R0P3	Exosome	NFISK	SGYQQAASEHGLVVIAPDTSPR	GCNIK	3		761.7175068	2282.12912	0.000451244	56	N	64	86
Q9R0P3	Exosome	PVVFR	LQEGYDHSYYFIATFIADHIR	HHAKY	3		853.748807	2558.223021	0.000451244	11	N	253	274
Q9R0P3	Exosome	PVVFR	LQEGYDHSYYFIATFIADHIR	HHAKY	4		640.5635552	2558.223021	0.000622848	7	N	253	274
Q9R0P3	Exosome	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	C1:+39.994,C12:+57.021	1186.05833	2370.101061	0.000451244	9	N	44	64
Q9R0P3	Exosome	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	C1:+57.021,C12:+57.021	1194.57183	2387.128061	0.000451244	30	N	44	64
Q9R0P3	Exosome	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	3	C1:+57.021,C12:+57.021	796.7171535	2387.128061	0.000451244	30	N	44	64
Q9R0P3	Exosome	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	[0:-	1186.05833	2370.101061	0.001352548	9	N	44	64
Q9R0P3	Exosome	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	3	[0:-	791.0414868	2370.101061	0.002453667	1	N	44	64
Q9R0P3	Exosome	NYRMY	SYVTEELPQLINANFPVDPQR	MSIFG	2		1215.619143	2429.222687	0.000451244	17	N	121	142

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9R0P3	Exosome	NYRMY	SYVTEELPQLINANFPVDPQR	MSIFG	3		810.7486955	2429.222687	0.000451244	5	N	121	142
Q9R0P3	Exosome	DTSPR	GCNIKGEDDSWDFGTGAGFYVNATEDPWK	ANYRM	3	C2:+57.021	1079.468614	3235.382443	0.000451244	27	N	86	115
Q9R0P3	Exosome	LVKAY	SGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	3	C32:+57.021	1284.626683	3850.85665	0.000451244	4	N	211	246
Q9R0P3	Exosome	KANYR	MYSYVTEELPQLINANFPVDPQR	MSIFG	2		1362.671051	2723.326501	0.000451244	9	N	119	142
Q9R0P3	Exosome	KANYR	MYSYVTEELPQLINANFPVDPQR	MSIFG	3		908.7833004	2723.326501	0.000451244	9	N	119	142
Q9R0P3	Exosome	KANYR	MYSYVTEELPQLINANFPVDPQR	MSIFG	3	M1:+15.995	914.114967	2739.321501	0.000451244	4	N	119	142
Q9R0P3	Exosome	DTSPR	GCNIKGEDDSWDFGTGAGFY	VNATE	2	C2:+57.021	1098.452666	2194.889732	0.000662267	8	N	86	106
Q9R0P3	Exosome	GCNIK	GEDDSWDFGTGAGFYVNATEDPWK	ANYRM	2		1332.562219	2663.108839	0.000451244	8	N	91	115
Q9R0P3	Exosome	PGKYR	SVSAFAPICNPVLCSWGKK	AFSGY	2	C9:+57.021,C14:+57.021	1061.034687	2120.053773	0.000637154	1	N	167	186
Q9R0P3	Exosome	SWGKK	AFSGYLGPDESK	WKAYD	2		635.8016643	1269.587729	0.000451244	1	N	186	198
Q9R0P3	Exosome	CPALY	WLSGLTCTEQNFISK	SGYQQ	2	C7:+57.021	892.4381022	1782.860604	0.000451244	1	N	49	64
Q9R0P3	Parental	PGKYR	SVSAFAPICNPVLCSWGK	KAFSG	2	C9:+57.021,C14:+57.021	996.987205	1991.95881	0.000451244	14	N	167	185
Q9R0P3	Parental	TCLVK	AYSGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	3	C34:+57.021	1362.660164	4084.957092	0.000451244	26	N	209	246
Q9R0P3	Parental	TCLVK	AYSGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	4	C34:+57.021	1022.247073	4084.957092	0.001395409	2	N	209	246
Q9R0P3	Parental	NFISK	SGYQQAASEHGLVVIAPDTSPR	GCNIK	2		1142.07236	2282.12912	0.000451244	20	N	64	86
Q9R0P3	Parental	NFISK	SGYQQAASEHGLVVIAPDTSPR	GCNIK	3		761.7175068	2282.12912	0.000451244	11	N	64	86
Q9R0P3	Parental	PVVFR	LQEGYDHSYYFIATFIADHIR	HHAKY	4		640.5635552	2558.223021	0.000451244	4	N	253	274
Q9R0P3	Parental	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	C1:+39.994,C12:+57.021	1186.05833	2370.101061	0.000451244	9	N	44	64
Q9R0P3	Parental	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	C1:+57.021,C12:+57.021	1194.57183	2387.128061	0.000451244	10	N	44	64
Q9R0P3	Parental	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	3	C1:+57.021,C12:+57.021	796.7171535	2387.128061	0.000451244	8	N	44	64
Q9R0P3	Parental	AESGK	CPALYWLSGLTCTEQNFISK	SGYQQ	2	[0:-	1186.05833	2370.101061	0.002374549	1	N	44	64
Q9R0P3	Parental	NYRMY	SYVTEELPQLINANFPVDPQR	MSIFG	2		1215.619143	2429.222687	0.000451244	11	N	121	142
Q9R0P3	Parental	LVKAY	SGSQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	KIPVV	3	C32:+57.021	1284.626683	3850.85665	0.000451244	8	N	211	246
Q9R0P3	Parental	KANYR	MYSYVTEELPQLINANFPVDPQR	MSIFG	3		908.7833004	2723.326501	0.001654178	3	N	119	142
Q9R0P3	Parental	KCKMR	FAVYLPPQAESGKCPALYWLSGLTCTEQNFISK	SGYQQ	3	C14:+57.021,C25:+57.021	1259.288354	3774.841663	0.000698008	3	N	31	64
Q9R0P5	Exosome	KKRKK	AVIFCLSADKK	CIVVE	2	C5:+57.021	626.3422137	1250.668827	0.000451244	6	N	34	45
Q9R0P5	Exosome	EKDCR	YALYDASFETK	ESRKE	2		654.3118648	1306.60813	0.000451244	17	N	81	92
Q9R0P5	Exosome	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	C1:+39.994	1286.664445	2571.31329	0.000451244	13	N	45	69
Q9R0P5	Exosome	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	3	C1:+39.994	858.1122301	2571.31329	0.000451244	31	N	45	69
Q9R0P5	Exosome	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	C1:+57.021	1295.177945	2588.34029	0.000451244	17	N	45	69
Q9R0P5	Exosome	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	3	C1:+57.021	863.7878968	2588.34029	0.000451244	261	N	45	69
Q9R0P5	Exosome	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	[0:-17.027,C1:+57.021	1286.664445	2571.31329	0.000451244	7	N	45	69
Q9R0P5	Exosome	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	3	[0:-17.027,C1:+57.021	858.1122301	2571.31329	0.000451244	14	N	45	69
Q9R0P5	Exosome	CIAEK	LGGSLIVAFEGSPV	-	2		673.3722568	1344.728914	0.000451244	68	N	151	165
Q9R0P5	Exosome	VEEGK	EILVGDVGATITDPFK	HFVGM	2		837.9515997	1673.887599	0.000451244	7	N	53	69
Q9R0P5	Exosome	AIKKK	FPGIKHEYQANGPEDLNR	TCIAE	3		695.6769828	2084.007549	0.000451244	9	N	127	145
Q9R0P5	Exosome	TKESR	KEELMFFLWAPEQAPLK	SKMIY	3		693.0329394	2076.075418	0.000622848	8	N	95	112
Q9R0P5	Parental	KKRKK	AVIFCLSADKK	CIVVE	2	C5:+57.021	626.3422137	1250.668827	0.000451244	1	N	34	45
Q9R0P5	Parental	EKDCR	YALYDASFETK	ESRKE	2		654.3118648	1306.60813	0.000451244	28	N	81	92
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	C1:+39.994	1286.664445	2571.31329	0.000451244	10	N	45	69
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	3	C1:+39.994	858.1122301	2571.31329	0.000451244	17	N	45	69
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	C1:+57.021	1295.177945	2588.34029	0.000451244	4	N	45	69
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	3	C1:+57.021	863.7878968	2588.34029	0.000451244	275	N	45	69
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	2	[0:-17.027,C1:+57.021	1286.664445	2571.31329	0.000662267	2	N	45	69
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPFK	HFVGM	3	[0:-17.027,C1:+57.021	858.1122301	2571.31329	0.000823681	5	N	45	69
Q9R0P5	Parental	CIAEK	LGGSLIVAFEGSPV	-	2		673.3722568	1344.728914	0.000451244	32	N	151	165
Q9R0P5	Parental	AIKKK	FPGIKHEYQANGPEDLNR	TCIAE	2		1043.011574	2084.007549	0.000451244	4	N	127	145
Q9R0P5	Parental	AIKKK	FPGIKHEYQANGPEDLNR	TCIAE	3		695.6769828	2084.007549	0.000823681	2	N	127	145
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPF	KHFVG	3	C1:+39.994	815.4139091	2443.218327	0.001329271	1	N	45	68
Q9R0P5	Parental	SADKK	CIVVEEGKEILVGDVGATITDPF	KHFVG	2	C1:+57.021	1231.130464	2460.245327	0.000979378	3	N	45	68
Q9R0Q7	Exosome	FEKSK	LTFSCLGGSDNFK	HLNEI	2	C5:+57.021	723.3403994	1444.665199	0.000451244	15	N	35	48
Q9R0Q7	Exosome	SDNFK	HLNEIDLFHCIDPNDSK	HKRTD	2	C10:+57.021	1033.983937	2065.952273	0.000451244	3	N	48	65
Q9R0Q7	Exosome	SDNFK	HLNEIDLFHCIDPNDSK	HKRTD	3	C10:+57.021	689.6585577	2065.952273	0.000451244	13	N	48	65
Q9R0Q7	Exosome	VNFEK	SKLTFSCLGGSDNFK	HLNEI	2	C7:+57.021	830.9038952	1659.79219	0.001162105	1	N	33	48
Q9R0Q7	Exosome	KERAK	LNWLSVDFNNWK	DWEDD	2		768.3862298	1534.75686	0.000451244	8	N	95	107
Q9R0Q7	Parental	FEKSK	LTFSCLGGSDNFK	HLNEI	2	C5:+57.021	723.3403994	1444.665199	0.000451244	10	N	35	48
Q9R0Q7	Parental	SDNFK	HLNEIDLFHCIDPNDSK	HKRTD	2	C10:+57.021	1033.983937	2065.952273	0.000451244	9	N	48	65
Q9R0Q7	Parental	SDNFK	HLNEIDLFHCIDPNDSK	HKRTD	3	C10:+57.021	689.6585577	2065.952273	0.000451244	13	N	48	65
Q9R0Q7	Parental	VNFEK	SKLTFSCLGGSDNFK	HLNEI	2	C7:+57.021	830.9038952	1659.79219	0.000451244	7	N	33	48
Q9R0Q7	Parental	VNFEK	SKLTFSCLGGSDNFK	HLNEI	3	C7:+57.021	554.2718634	1659.79219	0.000451244	2	N	33	48
Q9R0Q7	Parental	FEKSK	LTFSCLGGSDNFKHLNEIDLFHCIDPNDSK	HKRTD	3	C5:+57.021,C23:+57.021	1165.210104	3492.606912	0.000451244	3	N	35	65
Q9R0Q7	Parental	KERAK	LNWLSVDFNNWK	DWEDD	2		768.3862298	1534.75686	0.000451244	7	N	95	107
Q9R0U0	Exosome	REFGR	YGPIVDVYVPLDFYTR	RPRGF	2		958.9937989	1915.971998	0.000451244	2	N	32	48
Q9R0U0	Parental	REFGR	YGPIVDVYVPLDFYTR	RPRGF	2		958.9937989	1915.971998	0.000451244	24	N	32	48
Q9R0U0	Parental	WICGR	QIEIQFAQGDR	KTPNQ	2		652.8338301	1303.65206	0.000451244	1	N	79	90

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9R0X4	Exosome	PRKMR	DSYIEVLLPLGTDPELR	DKYVT	2		965.5125528	1929.009506	0.000622848	5	N	83	100
Q9R0X4	Exosome	SSEER	NIIHELFLTTLDPK	TISFQ	3		551.9790515	1652.913754	0.001162105	1	N	258	272
Q9R111	Exosome	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	2		1256.127864	2510.240128	0.000451244	8	N	231	252
Q9R111	Exosome	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	3		837.7545092	2510.240128	0.000451244	34	N	231	252
Q9R111	Exosome	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	4		628.5678319	2510.240128	0.000451244	22	N	231	252
Q9R111	Exosome	MCAAR	TPPLALVFR	GTFVH	2		507.3112738	1012.606948	0.002374549	1	N	5	14
Q9R111	Exosome	AVIQK	FLYLGDDRNIEEVYVGGK	QVVPF	2		1044.026359	2086.037117	0.000451244	30	N	427	445
Q9R111	Exosome	AVIQK	FLYLGDDRNIEEVYVGGK	QVVPF	3		696.3535058	2086.037117	0.000451244	17	N	427	445
Q9R111	Exosome	LINPR	ASDSPIDLFYGDFVGDISEAVIQK	FLYLG	2		1293.634656	2585.253712	0.000451244	68	N	403	427
Q9R111	Exosome	LINPR	ASDSPIDLFYGDFVGDISEAVIQK	FLYLG	3		862.7590374	2585.253712	0.000451244	52	N	403	427
Q9R111	Exosome	RRTLK	NGTTTACYFGTIHTDSSLILAEITDKFGQR	AFVGK	3	C7:+57.021	1106.542114	3316.602941	0.000451244	10	N	133	163
Q9R111	Exosome	RRTLK	NGTTTACYFGTIHTDSSLILAEITDKFGQR	AFVGK	4	C7:+57.021	830.1585352	3316.602941	0.000451244	6	N	133	163
Q9R111	Exosome	IFSER	GASIAHCPNSNLSLSSGLLNVLEVLK	HKVKI	2	C7:+57.021	1347.218467	2692.421335	0.000451244	14	N	294	320
Q9R111	Exosome	IFSER	GASIAHCPNSNLSLSSGLLNVLEVLK	HKVKI	3	C7:+57.021	898.4815783	2692.421335	0.000451244	28	N	294	320
Q9R111	Exosome	KEVFR	LATLGGSQALGLDSEIGNFEVGKEFDALLINPR	ASDSP	3		1148.939016	3443.793647	0.000451244	89	N	370	403
Q9R111	Exosome	KEVFR	LATLGGSQALGLDSEIGNFEVGKEFDALLINPR	ASDSP	4		861.9562119	3443.793647	0.000451244	26	N	370	403
Q9R111	Exosome	YPSYK	NYTDVYDKNNLLTNK	TVMAH	2		907.9501196	1813.884639	0.000451244	30	N	259	274
Q9R111	Exosome	YPSYK	NYTDVYDKNNLLTNK	TVMAH	3		605.6360131	1813.884639	0.000662267	9	N	259	274
Q9R111	Exosome	EQRFR	STDVAEEVYTR	VVRRT	2		635.3020284	1268.588457	0.000451244	41	N	115	126
Q9R111	Exosome	SDSGK	IVFLEESSQQEK	LAKEW	2		718.8675356	1435.719471	0.000451244	68	N	41	53
Q9R111	Exosome	FEVGK	EFDALLINPR	ASDSP	2		594.3251095	1186.634619	0.000735798	9	N	393	403
Q9R111	Exosome	KEVFR	LATLGGSQALGLDSEIGNFEVGK	EFDAL	2		1138.592594	2275.169588	0.000451244	24	N	370	393
Q9R111	Exosome	KEVFR	LATLGGSQALGLDSEIGNFEVGK	EFDAL	3		759.3976628	2275.169588	0.000451244	11	N	370	393
Q9R111	Exosome	RRTLK	NGTTTACYFGTIHTDSSLILAEITDK	FGQRA	2	C7:+57.021	1415.184487	2828.353374	0.000451244	3	N	133	159
Q9R111	Exosome	RRTLK	NGTTTACYFGTIHTDSSLILAEITDK	FGQRA	3	C7:+57.021	943.7922581	2828.353374	0.000451244	46	N	133	159
Q9R111	Exosome	IVTPR	FTLSCTETLMSELGNIAK	THDLY	2	C5:+57.021	1007.995125	2013.974649	0.000451244	21	N	213	231
Q9R111	Exosome	IVTPR	FTLSCTETLMSELGNIAK	THDLY	3	C5:+57.021	672.3326831	2013.974649	0.000622848	3	N	213	231
Q9R111	Exosome	KHKVK	IGLGTDVAGGYSYSMLDAIR	RAVMV	2		1030.012395	2058.009189	0.000451244	7	N	324	344
Q9R111	Exosome	PIDLF	YGDFVGDISEAVIQK	FLYLG	2		820.9124745	1639.809349	0.000451244	8	N	412	427
Q9R111	Exosome	GSQAL	GLDSEIGNFEVGKEFDALLINPR	ASDSP	3		845.1031384	2532.286015	0.001162105	1	N	380	403
Q9R111	Parental	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	2		1256.127864	2510.240128	0.000451244	4	N	231	252
Q9R111	Parental	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	3		837.7545092	2510.240128	0.000823681	2	N	231	252
Q9R111	Parental	GNIAK	THDLYIQSHISENREEIEAVK	SLYPS	4		628.5678319	2510.240128	0.000451244	12	N	231	252
Q9R111	Parental	MCAAR	TPPLALVFR	GTFVH	2		507.3112738	1012.606948	0.002813207	1	N	5	14
Q9R111	Parental	AVIQK	FLYLGDDRNIEEVYVGGK	QVVPF	2		1044.026359	2086.037117	0.000451244	25	N	427	445
Q9R111	Parental	AVIQK	FLYLGDDRNIEEVYVGGK	QVVPF	3		696.3535058	2086.037117	0.000451244	8	N	427	445
Q9R111	Parental	LINPR	ASDSPIDLFYGDFVGDISEAVIQK	FLYLG	2		1293.634656	2585.253712	0.000451244	43	N	403	427
Q9R111	Parental	LINPR	ASDSPIDLFYGDFVGDISEAVIQK	FLYLG	3		862.7590374	2585.253712	0.000451244	31	N	403	427
Q9R111	Parental	RRTLK	NGTTTACYFGTIHTDSSLILAEITDKFGQR	AFVGK	3	C7:+57.021	1106.542114	3316.602941	0.000451244	10	N	133	163
Q9R111	Parental	IFSER	GASIAHCPNSNLSLSSGLLNVLEVLK	HKVKI	3	C7:+57.021	898.4815783	2692.421335	0.000451244	26	N	294	320
Q9R111	Parental	KEVFR	LATLGGSQALGLDSEIGNFEVGKEFDALLINPR	ASDSP	3		1148.939016	3443.793647	0.000451244	70	N	370	403
Q9R111	Parental	KEVFR	LATLGGSQALGLDSEIGNFEVGKEFDALLINPR	ASDSP	4		861.9562119	3443.793647	0.000451244	8	N	370	403
Q9R111	Parental	YPSYK	NYTDVYDKNNLLTNK	TVMAH	3		605.6360131	1813.884639	0.000698008	4	N	259	274
Q9R111	Parental	VFRLA	TLGGSQALGLDSEIGNFEVGKEFDALLINPR	ASDSP	3		1087.56529	3259.67247	0.000451244	11	N	372	403
Q9R111	Parental	SDSGK	IVFLEESSQQEK	LAKEW	2		718.8675356	1435.719471	0.000451244	26	N	41	53
Q9R111	Parental	KEVFR	LATLGGSQALGLDSEIGNFEVGK	EFDAL	2		1138.592594	2275.169588	0.002296037	1	N	370	393
Q9R111	Parental	RRTLK	NGTTTACYFGTIHTDSSLILAEITDK	FGQRA	3	C7:+57.021	943.7922581	2828.353374	0.000451244	24	N	133	159
Q9R111	Parental	IVTPR	FTLSCTETLMSELGNIAK	THDLY	2	C5:+57.021	1007.995125	2013.974649	0.000451244	2	N	213	231
Q9R111	Parental	IVTPR	FTLSCTETLMSELGNIAK	THDLY	3	C5:+57.021	672.3326831	2013.974649	0.000622848	1	N	213	231
Q9R111	Parental	PIDLF	YGDFVGDISEAVIQK	FLYLG	2		820.9124745	1639.809349	0.000451244	9	N	412	427
Q9R112	Parental	SLSVR	STLSVIPSGVQWIQDR	VAELN	2		893.4788473	1784.942095	0.001229886	4	N	101	117
Q9R112	Parental	TGYNR	VILAEFDYTAQPLETPFDQSKER	ITMYL	3		948.8083912	2843.401774	0.000451244	11	N	387	411
Q9R112	Parental	TGYNR	VILAEFDYTAQPLETFPFDQSK	ERITM	2		1280.136835	2558.258069	0.000451244	25	N	387	409
Q9R112	Parental	TGYNR	VILAEFDYTAQPLETFPFDQSK	ERITM	3		853.7604897	2558.258069	0.001162105	2	N	387	409
Q9R112	Parental	LPTSK	TAAAVAAQSGILDR	TMCLI	2		672.3680371	1342.720474	0.000451244	4	N	344	358
Q9R112	Parental	RMKRR	VGAENVAIVEPSER	HFYQP	2		735.3838842	1468.752168	0.000823681	8	N	65	79
Q9R112	Parental	RPIKK	YDGYTSCPLVTGYNR	VILAE	2	C7:+57.021	883.3964343	1764.777269	0.001352548	1	N	372	387
Q9R112	Parental	GYNRV	ILAEFDYTAQPLETFPFDQSK	ERITM	2		1230.602628	2459.189655	0.000823681	2	N	388	409
Q9R190	Exosome	ANMYR	VGDYVYFENSSSNPYLVR	RIEEL	2		1055.000341	2107.985082	0.000451244	9	N	7	25
Q9R190	Parental	ANMYR	VGDYVYFENSSSNPYLVR	RIEEL	2		1055.000341	2107.985082	0.000451244	34	N	7	25
Q9R190	Parental	KMEMK	VWDPDNPLTDRQIDQFLVVAR	AVGTF	3		833.0998397	2496.276119	0.001839721	1	N	177	198
Q9R190	Parental	HIRGK	CSVTLLNETDILNQYLDKEDCFFYSLVFDPVQK	TLLAD	3	C1:+57.021,C21:+57.021	1338.644644	4012.910531	0.000451244	3	N	105	138
Q9R190	Parental	EKYGK	DFNDIRQDFLPWK	SLASI	3		565.283134	1692.826002	0.000622848	10	N	285	298
Q9R1C7	Exosome	KSMLK	QATPPIELDAVWEDIRER	FVKEP	3		713.3679264	2137.080379	0.001162105	1	N	751	769
Q9R1C7	Parental	WAKPK	ELEDLEGYQNTIVAGGLITK	SNLHA	2		1082.063138	2162.110676	0.000451244	19	N	213	233

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9R1C7	Parental	KSMLK	QATPPIELDAVWEDIRER	FVKEP	3		713.3679264	2137.080379	0.000637154	6	N	751	769
Q9R1C7	Parental	NTETK	QSTWEKPDDLKTPAEQLLSK	CPWKE	3		772.0695461	2313.185238	0.001264573	1	N	164	184
Q9R1C7	Parental	DIRER	FVKEPAFEDITLESER	KRIFK	3		637.3234351	1908.946905	0.000451244	13	N	769	785
Q9R1C7	Parental	DGERR	LSGSNLCSSSWVSADGFLR	RRPSM	2	C7:+57.021	1021.983937	2041.952273	0.000637154	1	N	32	51
Q9R1P0	Exosome	LIAQR	YLLQYQEPIPCEQLVTALCDIK	QAYTQ	2	C11:+57.021,C19:+57.021	1347.679566	2693.343533	0.000451244	43	N	96	118
Q9R1P0	Exosome	LIAQR	YLLQYQEPIPCEQLVTALCDIK	QAYTQ	3	C11:+57.021,C19:+57.021	898.7889776	2693.343533	0.000451244	46	N	96	118
Q9R1P0	Exosome	RNIHK	LLDEVFFSEK	IYKLN	2		613.8193257	1225.623051	0.000735798	29	N	54	64
Q9R1P0	Exosome	QFGGK	RPFGVSLLYIGWDK	HYGFQ	2		825.9542797	1649.892959	0.000451244	10	N	127	141
Q9R1P0	Exosome	QFGGK	RPFGVSLLYIGWDK	HYGFQ	3		550.9721198	1649.892959	0.000451244	8	N	127	141
Q9R1P0	Exosome	SPEGR	LYQVEYAMEAIGHAGTCLGILANDGVLLAAER	RNIHK	3	C17:+57.021	1140.243011	3417.705633	0.00091018	2	N	17	49
Q9R1P0	Exosome	SPEGR	LYQVEYAMEAIGHAGTCLGILANDGVLLAAER	RNIHK	3	M8:+15.995,C17:+57.021	1145.574678	3433.700633	0.000451244	2	N	17	49
Q9R1P0	Exosome	IGWDK	HYGFQLYQSDPSGNYGGWK	ATCIG	2		1102.495757	2202.975914	0.000451244	10	N	141	160
Q9R1P0	Exosome	MDVSK	LSAEKVEIATLTR	ESGKT	2		715.9148201	1429.81404	0.000451244	7	N	205	218
Q9R1P0	Exosome	EKIYK	LNEDMACSVAGITSDANVLTNELR	LIAQR	2	C7:+57.021	1297.115551	2592.215502	0.000451244	9	N	67	91
Q9R1P0	Exosome	EKIYK	LNEDMACSVAGITSDANVLTNELR	LIAQR	3	C7:+57.021	865.0796339	2592.215502	0.001162105	2	N	67	91
Q9R1P0	Exosome	YGGWK	ATCIGNNSAAAVSMLK	QDYKE	2	C3:+57.021	804.3979233	1606.780247	0.000451244	2	N	160	176
Q9R1P0	Parental	LIAQR	YLLQYQEPIPCEQLVTALCDIK	QAYTQ	2	C11:+57.021,C19:+57.021	1347.679566	2693.343533	0.000451244	22	N	96	118
Q9R1P0	Parental	LIAQR	YLLQYQEPIPCEQLVTALCDIK	QAYTQ	3	C11:+57.021,C19:+57.021	898.7889776	2693.343533	0.000451244	27	N	96	118
Q9R1P0	Parental	RNIHK	LLDEVFFSEK	IYKLN	2		613.8193257	1225.623051	0.002080925	2	N	54	64
Q9R1P0	Parental	IGWDK	HYGFQLYQSDPSGNYGGWK	ATCIG	2		1102.495757	2202.975914	0.001699387	1	N	141	160
Q9R1P0	Parental	IAQRY	LLQYQEPIPCEQLVTALCDIK	QAYTQ	2	C10:+57.021,C18:+57.021	1266.147902	2530.280204	0.000451244	10	N	97	118
Q9R1P0	Parental	LIAQR	YLLQYQEPIPCEQLVTAL	CDIKQ	2	C11:+57.021	1089.561488	2177.107377	0.001352548	2	N	96	114
Q9R1P0	Parental	EKIYK	LNEDMACSVAGITSDANVLTNELR	LIAQR	2	C7:+57.021	1297.115551	2592.215502	0.000451244	1	N	67	91
Q9R1P1	Exosome	LYEKR	FGPYYTEPVIAGLDPK	TFKPF	2		883.9541423	1765.892685	0.000451244	31	N	99	115
Q9R1P1	Exosome	LYEKR	FGPYYTEPVIAGLDPK	TFKPF	3		589.6386949	1765.892685	0.000823681	2	N	99	115
Q9R1P1	Exosome	PMGDR	LYIGLAGLATDVQTVAQR	LKFRL	2		945.0287044	1888.041809	0.000451244	36	N	48	66
Q9R1P1	Exosome	PMGDR	LYIGLAGLATDVQTVAQR	LKFRL	3		630.3550696	1888.041809	0.000451244	38	N	48	66
Q9R1P1	Parental	LYEKR	FGPYYTEPVIAGLDPK	TFKPF	2		883.9541423	1765.892685	0.000451244	11	N	99	115
Q9R1P1	Parental	PMGDR	LYIGLAGLATDVQTVAQR	LKFRL	3		630.3550696	1888.041809	0.000451244	11	N	48	66
Q9R1P1	Parental	GDRLY	IGLAGLATDVQTVAQR	LKFRL	2		806.955008	1611.894416	0.000451244	4	N	50	66
Q9R1P3	Exosome	KMSEK	ILLLCVGEAGDTVQFAEYIQK	NVQLY	2	C5:+57.021	1184.117159	2366.218718	0.000451244	34	N	41	62
Q9R1P3	Exosome	KMSEK	ILLLCVGEAGDTVQFAEYIQK	NVQLY	3	C5:+57.021	789.7473728	2366.218718	0.000451244	14	N	41	62
Q9R1P3	Exosome	LYKMR	NGYELSPTAAANFTR	RNLAD	2		806.3922405	1610.768881	0.000451244	30	N	70	85
Q9R1P3	Exosome	AALAK	APFAAHGYGAFLTLSILDR	YYTPT	2		1010.536697	2019.057793	0.000451244	9	N	126	145
Q9R1P3	Exosome	AALAK	APFAAHGYGAFLTLSILDR	YYTPT	3		674.0270644	2019.057793	0.000451244	7	N	126	145
Q9R1P3	Exosome	TFSVR	VIDKDGIHNLENIAFPK	RDS-	2		962.0208793	1922.026159	0.000451244	22	N	181	198
Q9R1P3	Exosome	TFSVR	VIDKDGIHNLENIAFPK	RDS-	3		641.6831862	1922.026159	0.000451244	30	N	181	198
Q9R1P3	Exosome	TFSVR	VIDKDGIHNLENIAFPK	RDS-	4		481.5143397	1922.026159	0.000662267	7	N	181	198
Q9R1P3	Exosome	LAKAP	FAAHGYGAFLTLSILDR	YYTPT	3		617.9971051	1850.967915	0.002727428	1	N	128	145
Q9R1P3	Exosome	KMSEK	ILLLCVGEAGDTVQF	AEYIQ	2	C5:+57.021	817.926839	1633.838078	0.001329271	5	N	41	56
Q9R1P3	Exosome	ELQKR	FILNLPTFSVR	VIDKD	2		653.880052	1305.744504	0.000451244	10	N	170	181
Q9R1P3	Exosome	KILLL	CVGEAGDTVQFAEYIQK	NVQLY	2	C1:+57.021	957.9490311	1913.882462	0.000451244	3	N	45	62
Q9R1P3	Parental	KMSEK	ILLLCVGEAGDTVQFAEYIQK	NVQLY	2	C5:+57.021	1184.117159	2366.218718	0.000451244	2	N	41	62
Q9R1P3	Parental	LYKMR	NGYELSPTAAANFTR	RNLAD	2		806.3922405	1610.768881	0.000662267	1	N	70	85
Q9R1P3	Parental	KMSEK	ILLLCVGEAGDTVQF	AEYIQ	2	C5:+57.021	817.926839	1633.838078	0.000451244	7	N	41	56
Q9R1P3	Parental	-MEY	LIGIQGPDYVLVASDR	VAASN	2		858.4704909	1714.925382	0.000451244	6	N	3	19
Q9R1P4	Exosome	GIVGK	DLEFTIYDDDDVSPFLDGLEERPQRK	AQPSQ	3		1038.163562	3111.467287	0.000451244	33	N	217	243
Q9R1P4	Exosome	GIVGK	DLEFTIYDDDDVSPFLDGLEERPQRK	AQPSQ	4		778.8746218	3111.467287	0.000451244	28	N	217	243
Q9R1P4	Exosome	-MFR	NQYDNDVTVWSPQGR	IHQIE	2		889.9087861	1777.801972	0.000451244	49	N	3	18
Q9R1P4	Exosome	GIVGK	DLEFTIYDDDDVSPFLDGLEERPQR	KAQPS	3		995.4652413	2983.372324	0.000451244	18	N	217	242
Q9R1P4	Exosome	LRALR	ETLPAEQDLTTK	NVSIG	2		673.346436	1344.677272	0.000622848	3	N	196	208
Q9R1P4	Exosome	AHQKK	ILHVDNHIGISIAGLTADAR	LLCNF	2		1043.574342	2085.133084	0.002145581	1	N	62	82
Q9R1P4	Exosome	AHQKK	ILHVDNHIGISIAGLTADAR	LLCNF	3		696.0521612	2085.133084	0.000451244	4	N	62	82
Q9R1P4	Exosome	QRYGR	RPYGVGLLIAGYDDMGPHIFQTCPSANYFDCR	AMSIG	3	M15:+15.995,C23:+57.021,C31:+57.021	1236.234284	3705.679452	0.000451244	9	N	125	157
Q9R1P4	Exosome	CLDSR	FVFDRPLPVSR	LVSLI	3		444.9194673	1331.735002	0.000662267	4	N	96	107
Q9R1P4	Parental	GIVGK	DLEFTIYDDDDVSPFLDGLEERPQRK	AQPSQ	3		1038.163562	3111.467287	0.000451244	9	N	217	243
Q9R1P4	Parental	-MFR	NQYDNDVTVWSPQGR	IHQIE	2		889.9087861	1777.801972	0.000451244	26	N	3	18
Q9R1T2	Exosome	AALKR	TAPDYFLLQVLLK	FRTDK	2		760.9403066	1519.865013	0.000451244	11	N	239	252
Q9R1T2	Exosome	AALKR	TAPDYFLLQVLLK	FRTDK	3		507.6294711	1519.865013	0.002884417	1	N	239	252
Q9R1T2	Exosome	LLQIR	NDVFDSLGISPDLLPDDFVR	YCFSE	2		1117.552938	2233.090275	0.000451244	37	N	277	297
Q9R1T2	Exosome	LLQIR	NDVFDSLGISPDLLPDDFVR	YCFSE	3		745.3712251	2233.090275	0.000451244	2	N	277	297
Q9R1T2	Exosome	-M	VEKEEAGGGGGGGISEEEAAQYDR	QIRLW	3		799.0268458	2394.057137	0.000451244	13	N	1	25
Q9R1T2	Exosome	LKRTA	PDYFLLQVLLK	FRTDK	2		674.8979104	1347.780221	0.001763695	1	N	241	252
Q9R1T2	Parental	AALKR	TAPDYFLLQVLLK	FRTDK	2		760.9403066	1519.865013	0.002080925	2	N	239	252

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9R1T2	Parental	AALKR	TAPDYFLLQVLLK	FRTDK	3		507.6294711	1519.865013	0.000451244	9	N	239	252
Q9R1T2	Parental	LLQIR	NDVFDSLGISPDLLPDDFVR	YCFSE	2		1117.552938	2233.090275	0.000451244	29	N	277	297
Q9R1T2	Parental	-M	VEKEEAGGGGGGGISEEEAAQYDR	QIRLW	3		799.0268458	2394.057137	0.000451244	1	N	1	25
Q9R1T2	Parental	LKRTA	PDYFLLQVLLK	FRTDK	2		674.8979104	1347.780221	0.002145581	1	N	241	252
Q9R1T2	Parental	RNSIK	FFTGDVFGYHGYTFANLGEHEFVEEK	TKVAK	3		1014.131645	3039.371536	0.002884417	1	N	156	182
Q9R1T4	Exosome	QLVNK	SVSQGFCFNILCVGETGLGK	STLMD	2	C7:+57.021,C12:+57.021	1087.024516	2172.033432	0.000451244	11	N	35	55
Q9R1T4	Exosome	LFNTK	FEGEPATHTQPGVQLQSNTYDLQESNVGLK	LTIVS	3		1096.532537	3286.574212	0.000451244	2	N	66	96
Q9R1T4	Parental	QLVNK	SVSQGFCFNILCVGETGLGK	STLMD	2	C7:+57.021,C12:+57.021	1087.024516	2172.033432	0.000451244	8	N	35	55
Q9R1T4	Parental	LFNTK	FEGEPATHTQPGVQLQSNTYDLQESNVGLK	LTIVS	3		1096.532537	3286.574212	0.000451244	10	N	66	96
Q9R257	Exosome	LGMIR	NSLFGSVETWPWQVLSTGGKEDVSYEER	ACEGG	3		1067.511074	3199.509821	0.000451244	20	N	6	34
Q9R257	Exosome	CEGGK	FATVEVTDKPVDEALR	EAMPK	2		895.4706879	1788.925776	0.001699387	1	N	40	56
Q9R257	Exosome	CEGGK	FATVEVTDKPVDEALR	EAMPK	3		597.3163919	1788.925776	0.001162105	2	N	40	56
Q9R257	Exosome	LGMIR	NSLFGSVETWPWQVLSTGGK	EDVSY	2		1097.052908	2192.090216	0.002019181	1	N	6	26
Q9R257	Parental	LGMIR	NSLFGSVETWPWQVLSTGGKEDVSYEER	ACEGG	3		1067.511074	3199.509821	0.000451244	20	N	6	34
Q9WTI7	Parental	KIIAK	GEELLSPLNLEQAAYAR	DALAK	2		937.4868693	1872.958139	0.001229886	2	N	361	378
Q9WTI7	Parental	EEKFK	GIISILDEECLRPGEATDLTF	LEKLE	2	C10:+57.021	1175.086056	2348.156512	0.002296037	1	N	488	509
Q9WTL7	Exosome	SGAER	ETAAVIFLHGLGDTGHSWADALSTIR	LPHVK	3		913.4685918	2737.382375	0.000451244	3	N	22	48
Q9WTL7	Exosome	SGAER	ETAAVIFLHGLGDTGHSWADALSTIR	LPHVK	4		685.3533938	2737.382375	0.000451244	11	N	22	48
Q9WTL7	Exosome	ALSLY	TALTCPHPLAGIVALSCWLPLHR	NFPQA	4	C5:+57.021,C17:+57.021	646.5979152	2582.360461	0.000451244	1	N	130	153
Q9WTL7	Parental	SGAER	ETAAVIFLHGLGDTGHSWADALSTIR	LPHVK	4		685.3533938	2737.382375	0.000622848	1	N	22	48
Q9WTM5	Exosome	HSHIR	GLGLDDALEPR	QASQG	2		578.3043741	1154.593148	0.001229886	2	N	29	40
Q9WTM5	Exosome	VINSR	TQGFLALFSGDTGEIKSEVR	EQINA	3		719.0396983	2154.095695	0.000451244	1	N	253	273
Q9WTM5	Parental	HSHIR	GLGLDDALEPR	QASQG	2		578.3043741	1154.593148	0.001352548	1	N	29	40
Q9WTM5	Parental	GSQTK	FVQCPDGELQK	RKEVV	2	C4:+57.021	660.8165601	1319.61752	0.001352548	1	N	223	234
Q9WTP6	Exosome	YYRKR	GIHCAIDASQTPDIVFASILAAFSK	ATCKD	3	C4:+57.021	878.1198693	2631.336208	0.000451244	29	N	204	229
Q9WTP6	Exosome	ALKTR	LEAYHTQTTPLVEYYR	KRGIH	2		992.4946944	1982.973789	0.000979378	1	N	186	202
Q9WTP6	Parental	-M	APNVLASEPEIPK	GIRAV	2		682.8751636	1363.734727	0.000451244	10	N	1	14
Q9WTP6	Parental	YYRKR	GIHCAIDASQTPDIVFASILAAFSK	ATCKD	2	C4:+57.021	1316.675904	2631.336208	0.000451244	8	N	204	229
Q9WTP6	Parental	YYRKR	GIHCAIDASQTPDIVFASILAAFSK	ATCKD	3	C4:+57.021	878.1198693	2631.336208	0.000451244	31	N	204	229
Q9WTP6	Parental	EKALK	TRLEAYHTQTTPLVEYYR	KRGIH	3		747.7153262	2240.122578	0.000451244	1	N	184	202
Q9WTP6	Parental	EYYRK	RGIHCAIDASQTPDIVFASILAAFSK	ATCKD	4	C5:+57.021	697.8671298	2787.437319	0.001871652	1	N	203	229
Q9WTP6	Parental	ALKTR	LEAYHTQTTPLVEYYR	KRGIH	2		992.4946944	1982.973789	0.000451244	6	N	186	202
Q9WTP6	Parental	ALKTR	LEAYHTQTTPLVEYYR	KRGIH	3		661.9990629	1982.973789	0.000451244	8	N	186	202
Q9WTX5	Exosome	QEFLK	VDQGTLFELILAANYLDIK	GLLDV	2		1068.583509	2135.151419	0.000451244	32	N	94	113
Q9WTX5	Exosome	QEFLK	VDQGTLFELILAANYLDIK	GLLDV	3		712.7249397	2135.151419	0.000451244	8	N	94	113
Q9WTX5	Parental	QEFLK	VDQGTLFELILAANYLDIK	GLLDV	2		1068.583509	2135.151419	0.000451244	30	N	94	113
Q9WTX5	Parental	QEFLK	VDQGTLFELILAANYLDIK	GLLDV	3		712.7249397	2135.151419	0.000451244	21	N	94	113
Q9WTX5	Parental	NKEKR	TDDIPVWDQEFLKVDQGTLF	ELILA	2		1183.581695	2365.14779	0.000698008	3	N	81	101
Q9WTX6	Exosome	VLIEK	HLEIFHTEFQNLLDADKNEDLGR	MYNLV	4		689.3430261	2753.340905	0.000622848	1	N	298	321
Q9WTX6	Exosome	PHGLK	QIGLDQIWDDLR	AGIQQ	2		736.3811445	1470.746689	0.000622848	1	N	13	25
Q9WTX6	Parental	PHGLK	QIGLDQIWDDLRAGIQQVYTR	QSMAK	3		830.1034728	2487.287018	0.001591523	1	N	13	34
Q9WU28	Exosome	LEMLK	NQLDQEVEFLSTSIAQLK	VVQTK	2		1032.036923	2062.058247	0.000451244	26	N	19	37
Q9WU28	Exosome	LEMLK	NQLDQEVEFLSTSIAQLK	VVQTK	3		688.3605489	2062.058247	0.000451244	20	N	19	37
Q9WU28	Exosome	YVPGK	LHDVEHVLIDVGTGYYVEK	TAEDA	3		729.3763105	2185.105531	0.001763695	1	N	75	94
Q9WU28	Parental	MMSQK	IQQLTALGAAQATVKA	-	2		792.4599262	1582.904252	0.002813207	1	N	138	154
Q9WU28	Parental	LEMLK	NQLDQEVEFLSTSIAQLK	VVQTK	2		1032.036923	2062.058247	0.000451244	3	N	19	37
Q9WU28	Parental	LEMLK	NQLDQEVEFLSTSIAQLK	VVQTK	3		688.3605489	2062.058247	0.00091018	3	N	19	37
Q9WU78	Exosome	KPLVK	FIQQTYPSGGEEQAQYCR	AAEEL	2	C17:+57.021	1081.484301	2160.953001	0.000451244	46	N	23	41
Q9WU78	Exosome	KPLVK	FIQQTYPSGGEEQAQYCR	AAEEL	3	C17:+57.021	721.3254671	2160.953001	0.000451244	4	N	23	41
Q9WU78	Exosome	KEGTK	FYNELTEILVR	FQNKC	2		698.8777063	1395.739813	0.000451244	20	N	675	686
Q9WU78	Exosome	EEVLK	NLATAYDNFVELVANLK	EGTKF	2		947.9996126	1893.983625	0.000451244	32	N	654	671
Q9WU78	Exosome	EEVLK	NLATAYDNFVELVANLK	EGTKF	3		632.335675	1893.983625	0.000451244	8	N	654	671
Q9WU78	Exosome	IAQMR	EATTLANGVLASLNLPAAIEDVSGDTVPQSILTK	STSVV	3		1136.942315	3407.803544	0.000451244	32	N	386	420
Q9WU78	Exosome	SILTK	STSVVEQGGIQTVDQLIK	ELPEL	2		951.5130841	1901.010568	0.000451244	47	N	420	438
Q9WU78	Exosome	LGYEK	SCVLFNCAALASQIAAEQNLDNDEGLK	TAAKQ	2	C2:+57.021,C7:+57.021	1476.197372	2950.379143	0.000451244	1	N	120	147
Q9WU78	Exosome	LGYEK	SCVLFNCAALASQIAAEQNLDNDEGLK	TAAKQ	3	C2:+57.021,C7:+57.021	984.4675145	2950.379143	0.000451244	19	N	120	147
Q9WU78	Exosome	DMTSK	FLTALAQDGVINEEALSVTELDR	IYGGL	2		1252.648098	2503.280596	0.000451244	40	N	583	606
Q9WU78	Exosome	DMTSK	FLTALAQDGVINEEALSVTELDR	IYGGL	3		835.4346652	2503.280596	0.000451244	17	N	583	606
Q9WU78	Exosome	EESLR	LLDEEEATDNDLR	AKFKD	2		766.8578962	1531.700192	0.000451244	6	N	456	469
Q9WU78	Exosome	AIIAK	LANQAADYFGDAFK	QCQYK	2		765.8653272	1529.715054	0.000451244	13	N	215	229
Q9WU78	Exosome	YQSHR	DTIALLCKPEPELNAAIPSANPAK	TMQGS	2	C7:+57.021	1267.170454	2532.325309	0.000451244	18	N	517	541
Q9WU78	Exosome	YQSHR	DTIALLCKPEPELNAAIPSANPAK	TMQGS	3	C7:+57.021	845.1162363	2532.325309	0.000451244	32	N	517	541
Q9WU78	Exosome	FLTAL	AQDGVINEEALSVTELDR	IYGGL	2		979.9874305	1957.959261	0.000622848	1	N	588	606
Q9WU78	Exosome	DPIGK	ATLVKPTPVNVPVSQK	FTDLF	2		839.4990514	1676.982503	0.002813207	1	N	334	350
Q9WU78	Exosome	SKLRR	SALGRPLDKHEGALETLLR	YYDQI	4		519.7949834	2075.148734	0.001229886	1	N	51	70

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9WU78	Exosome	WVQLK	KTSEVDLAKPLVK	FIQQT	3		476.6209756	1426.839527	0.002374549	1	N	10	23
Q9WU78	Exosome	QSIAR	EPSAPSIPPPAYQSSPAAGHAAAPPTPAPR	TMPPA	3		964.1547843	2889.440953	0.001871652	1	N	715	745
Q9WU78	Exosome	VSVLK	SLLSNLDEIKK	ERESL	3		420.5788878	1258.713263	0.001871652	1	N	553	564
Q9WU78	Parental	KPLVK	FIQQTYPSGGEEQAQYCR	AAEEL	2	C17:+57.021	1081.484301	2160.953001	0.000451244	50	N	23	41
Q9WU78	Parental	KEGTK	FYNELTEILVR	FQNKC	2		698.8777063	1395.739813	0.000698008	15	N	675	686
Q9WU78	Parental	DMTSK	FLTALAQDGVINEEALSVTELDRIYGGLTSK	VQESL	3		1108.58435	3322.72965	0.000451244	10	N	583	614
Q9WU78	Parental	SILTK	STSVVEQGGIQTVDQLIKELPELLQR	NREIL	3		960.8612665	2879.5604	0.000451244	13	N	420	446
Q9WU78	Parental	EEVLK	NLATAYDNFVELVANLK	EGTKF	2		947.9996126	1893.983625	0.000451244	19	N	654	671
Q9WU78	Parental	EEVLK	NLATAYDNFVELVANLK	EGTKF	3		632.335675	1893.983625	0.000451244	2	N	654	671
Q9WU78	Parental	IAQMR	EATTLANGVLASLNLPAAIEDVSGDTVPQSILTK	STSVV	3		1136.942315	3407.803544	0.000451244	29	N	386	420
Q9WU78	Parental	SILTK	STSVVEQGGIQTVDQLIK	ELPEL	2		951.5130841	1901.010568	0.000451244	19	N	420	438
Q9WU78	Parental	ETLLR	YYDQICSIEPK	FPFSE	2	C6:+57.021	708.3295003	1414.643401	0.0025889	1	N	70	81
Q9WU78	Parental	DMTSK	FLTALAQDGVINEEALSVTELDR	IYGGL	2		1252.648098	2503.280596	0.000451244	12	N	583	606
Q9WU78	Parental	EESLR	LLDEEEATDNDLR	AKFKD	2		766.8578962	1531.700192	0.000451244	15	N	456	469
Q9WU78	Parental	YQSHR	DTIALLCKPEPELNAAIPSANPAK	TMQGS	2	C7:+57.021	1267.170454	2532.325309	0.000451244	6	N	517	541
Q9WU78	Parental	YQSHR	DTIALLCKPEPELNAAIPSANPAK	TMQGS	3	C7:+57.021	845.1162363	2532.325309	0.000451244	20	N	517	541
Q9WU78	Parental	EESLR	LLDEEEATDNDLRAK	FKDRW	2		866.4239347	1730.832269	0.000451244	2	N	456	471
Q9WU78	Parental	VSVLK	SLLSNLDEIKK	ERESL	3		420.5788878	1258.713263	0.002019181	1	N	553	564
Q9WUA2	Exosome	VYYNK	TPGFEIIHGLLDR	IMQLL	3		489.9371866	1466.78816	0.000451244	16	N	504	517
Q9WUA2	Exosome	VSVKR	DLLFQALGR	TYTDE	2		516.7959879	1031.576376	0.000451244	6	N	8	17
Q9WUA2	Exosome	VVLYK	IDVPANRYDLLCLEGLAR	GLQVF	3	C12:+57.021	696.7020978	2087.082893	0.001699387	2	N	64	82
Q9WUA2	Parental	VYYNK	TPGFEIIHGLLDR	IMQLL	3		489.9371866	1466.78816	0.000451244	8	N	504	517
Q9WUA2	Parental	VSVKR	DLLFQALGR	TYTDE	2		516.7959879	1031.576376	0.000451244	5	N	8	17
Q9WUA3	Exosome	YTGAK	VYFIYEGYQGLVDGGSNIVEAK	WDCVS	2		1211.102795	2420.189989	0.000451244	9	N	55	77
Q9WUA3	Exosome	IVEAK	WDCVSSILQVGGTIIGSAR	CKAFR	2	C3:+57.021	1010.020322	2018.025044	0.000451244	2	N	77	96
Q9WUA3	Exosome	IVEAK	WDCVSSILQVGGTIIGSAR	CKAFR	3	C3:+57.021	673.6828147	2018.025044	0.000451244	3	N	77	96
Q9WUA3	Exosome	CNLAR	LGITNLCVIGGDGSLTGANLFR	KEWSG	2	C7:+57.021	1124.591643	2247.167686	0.000451244	6	N	115	137
Q9WUA3	Exosome	CNLAR	LGITNLCVIGGDGSLTGANLFR	KEWSG	3	C7:+57.021	750.0636953	2247.167686	0.000979378	1	N	115	137
Q9WUA3	Exosome	NGQIK	EIGWADVGGWTGQGGSILGTK	RTLPG	2		1045.021608	2088.027615	0.001871652	1	N	458	479
Q9WUA3	Exosome	GLVLR	NESCSVNYTTDFIYQLYSEEGK	GVFDC	2	C4:+57.021	1324.079156	2646.142713	0.000451244	1	N	636	658
Q9WUA3	Parental	YTGAK	VYFIYEGYQGLVDGGSNIVEAK	WDCVS	2		1211.102795	2420.189989	0.000451244	6	N	55	77
Q9WUA3	Parental	IVEAK	WDCVSSILQVGGTIIGSAR	CKAFR	3	C3:+57.021	673.6828147	2018.025044	0.000622848	4	N	77	96
Q9WUA3	Parental	CNLAR	LGITNLCVIGGDGSLTGANLFR	KEWSG	2	C7:+57.021	1124.591643	2247.167686	0.000451244	8	N	115	137
Q9WUA3	Parental	NGQIK	EIGWADVGGWTGQGGSILGTK	RTLPG	2		1045.021608	2088.027615	0.002519933	1	N	458	479
Q9WUA3	Parental	GLVLR	NESCSVNYTTDFIYQLYSEEGK	GVFDC	2	C4:+57.021	1324.079156	2646.142713	0.001162105	1	N	636	658
Q9WUA3	Parental	GFEAY	LGLLELAAAR	EKHEA	2		513.819463	1025.623326	0.001591523	4	N	511	521
Q9WUA3	Parental	AVIAL	LEATPETPACVVSLR	GNQAV	2	C10:+57.021	821.9273703	1641.839141	0.001463592	1	N	332	347
Q9WUK2	Exosome	SRSQK	ELPTEPPYTAYVGNLPFNTVQGDIDAIFK	DLSIR	3		1070.540082	3208.596845	0.000451244	18	N	34	63
Q9WUK2	Parental	GHGSR	SQKELPTEPPYTAYVGNLPFNTVQGDIDAIFK	DLSIR	3		1184.935271	3551.782414	0.000451244	8	N	31	63
Q9WUK2	Parental	TDKFK	GFCYVEFDEVDSLKEALTYDGALLGDR	SLRVD	3	C3:+57.021	1028.150223	3081.427268	0.000451244	6	N	82	109
Q9WUK2	Parental	SRSQK	ELPTEPPYTAYVGNLPFNTVQGDIDAIFK	DLSIR	3		1070.540082	3208.596845	0.000451244	40	N	34	63
Q9WUK2	Parental	QLKPR	TVATPLNQVANPNSAIFGGARPR	EEVVQ	3		784.4246577	2350.250573	0.000979378	7	N	216	239
Q9WUK2	Parental	PYTAY	VGNLPFNTVQGDIDAIFKDLSIR	SVRLV	3		844.7872617	2531.338385	0.000823681	3	N	45	68
Q9WUK2	Parental	SRSQK	ELPTEPPYTAYVGNLPFNTVQGDIDAIFKDLSIR	SVRLV	3		1265.316152	3792.925056	0.000451244	6	N	34	68
Q9WUK2	Parental	PYTAY	VGNLPFNTVQGDIDAIFK	DLSIR	2		974.5128871	1947.010174	0.000451244	20	N	45	63
Q9WUK2	Parental	PYTAY	VGNLPFNTVQGDIDAIFK	DLSIR	3		650.0111914	1947.010174	0.001654178	1	N	45	63
Q9WUM3	Exosome	ASYSR	SGASTATAVTDVPSGNLAGAGEAGKLEEVMQELR	ALRML	3		1106.216221	3315.625263	0.000451244	18	N	422	456
Q9WUM3	Exosome	ASYSR	SGASTATAVTDVPSGNLAGAGEAGKLEEVMQELR	ALRML	3	M30:+15.995	1111.547888	3331.620263	0.000823681	2	N	422	456
Q9WUM3	Exosome	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	3		1420.692675	4259.054626	0.000451244	28	N	354	393
Q9WUM3	Exosome	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	4		1065.771457	4259.054626	0.000451244	6	N	354	393
Q9WUM3	Exosome	IRVSR	VTWDSTFCAVNPK	FLAVI	2	C8:+57.021	762.861499	1523.707398	0.000451244	14	N	33	46
Q9WUM3	Exosome	ASYSR	SGASTATAVTDVPSGNLAGAGEAGK	LEEVM	2		1095.038183	2188.060766	0.000451244	6	N	422	447
Q9WUM3	Exosome	TAGPE	AALEAEDWVSGQDANPILISLR	EAYVP	2		1184.611318	2367.207037	0.000451244	22	N	371	393
Q9WUM3	Exosome	DSSIR	YFEITDEPPYIHFLNTFTSK	EPQRG	3		821.4025253	2461.184176	0.000451244	26	N	293	313
Q9WUM3	Exosome	MTVPR	KSDLFQDDLYPDTAGPE	AALEA	2		955.9368749	1909.85815	0.000451244	4	Y	354	371
Q9WUM3	Exosome	HPTAR	NVLLSAGCDNVVLIWNVGTAEELYR	LDSLH	3	C8:+57.021	935.8132165	2804.416249	0.000622848	2	N	145	170
Q9WUM3	Exosome	EELYR	LDSLHPDLIYNVSWNHNGSLFCSACK	DKSVR	4	C22:+57.021,C25:+57.021	762.6092082	3046.405633	0.000622848	3	N	170	196
Q9WUM3	Parental	ASYSR	SGASTATAVTDVPSGNLAGAGEAGKLEEVMQELR	ALRML	3		1106.216221	3315.625263	0.000451244	11	N	422	456
Q9WUM3	Parental	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	3		1420.692675	4259.054626	0.000451244	21	N	354	393
Q9WUM3	Parental	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	4		1065.771457	4259.054626	0.000451244	10	N	354	393
Q9WUM3	Parental	IRVSR	VTWDSTFCAVNPK	FLAVI	2	C8:+57.021	762.861499	1523.707398	0.000451244	8	N	33	46
Q9WUM3	Parental	ARPMR	AIFLADGKVFTTGFSR	MSERQ	3		577.3144342	1728.919902	0.001162105	4	N	225	241
Q9WUM3	Parental	ASYSR	SGASTATAVTDVPSGNLAGAGEAGK	LEEVM	2		1095.038183	2188.060766	0.000451244	5	N	422	447
Q9WUM3	Parental	DSSIR	YFEITDEPPYIHFLNTFTSK	EPQRG	3		821.4025253	2461.184176	0.000662267	1	N	293	313
Q9WUM3	Parental	MTVPR	KSDLFQDDLYPDTAGPEAALEAEDWVSGQDANPILISL	REAYV	3		1368.658972	4102.953515	0.001162105	5	N	354	392

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9WUM3	Parental	KSDLF	QDDLYPDTAGPEAALEAEDWVSGQDANPILISLR	EAYVP	3		1223.923871	3668.748214	0.000451244	6	N	359	393
Q9WUM4	Exosome	IRVSR	VTWDSSFCAVNPR	FVAII	2	C8:+57.021	769.8567479	1537.697896	0.000451244	13	N	31	44
Q9WUM4	Exosome	ARPMR	AIFLADGNVFTTGFSR	MSERQ	2		858.4417334	1714.867867	0.000451244	28	N	223	239
Q9WUM4	Exosome	MTVPR	KSDLFQDDLYPDTAGPEAALEAEEWFEGK	NADPI	3		1091.170494	3270.488082	0.000451244	50	N	352	381
Q9WUM4	Exosome	DSSIR	YFEITDESPYVHYLNTFSSK	EPQRG	2		1220.571327	2439.127055	0.000998612	2	N	291	311
Q9WUM4	Exosome	DSSIR	YFEITDESPYVHYLNTFSSK	EPQRG	3		814.0501516	2439.127055	0.000451244	21	N	291	311
Q9WUM4	Exosome	WFEGK	NADPILISLK	HGYIP	2		542.3245782	1082.633556	0.000451244	15	N	381	391
Q9WUM4	Exosome	MTVPR	KSDLFQDDLYPDTAGPE	AALEA	2		955.9368749	1909.85815	0.000451244	4	Y	352	369
Q9WUM4	Parental	IRVSR	VTWDSSFCAVNPR	FVAII	2	C8:+57.021	769.8567479	1537.697896	0.000451244	6	N	31	44
Q9WUM4	Parental	ARPMR	AIFLADGNVFTTGFSR	MSERQ	2		858.4417334	1714.867867	0.000451244	10	N	223	239
Q9WUM4	Parental	MTVPR	KSDLFQDDLYPDTAGPEAALEAEEWFEGK	NADPI	3		1091.170494	3270.488082	0.000451244	7	N	352	381
Q9WUM4	Parental	KSDLF	QDDLYPDTAGPEAALEAEEWFEGKNADPILISLK	HGYIP	3		1249.276022	3744.804666	0.000451244	2	N	357	391
Q9WUM4	Parental	WFEGK	NADPILISLK	HGYIP	2		542.3245782	1082.633556	0.000451244	8	N	381	391
Q9WUM4	Parental	KSDLF	QDDLYPDTAGPEAALEAEEWFEGK	NADPI	2		1341.098635	2680.181669	0.000622848	1	N	357	381
Q9WUP7	Exosome	GFGCR	GAQVEEIWSLEPESFEK	LKPVH	2		989.4761673	1976.936735	0.000451244	10	N	28	45
Q9WUP7	Exosome	IFLFK	WQPGEEPAGSVVQDSR	LETIF	2		871.4111616	1740.806723	0.001329271	1	N	57	73
Q9WUP7	Parental	GFGCR	GAQVEEIWSLEPESFEK	LKPVH	2		989.4761673	1976.936735	0.000451244	22	N	28	45
Q9WUP7	Parental	IFLFK	WQPGEEPAGSVVQDSR	LETIF	2		871.4111616	1740.806723	0.000823681	1	N	57	73
Q9WUP7	Parental	LDGLR	EGPIDLGACNQDDWITAVRPVIEK	RIQKY	3	C9:+57.021	899.4501667	2695.3271	0.000451244	5	N	182	206
Q9WUP7	Parental	IFFAK	QVINNACATQAIVSVLLNCTHQDVHLGETLSEFK	EFSQS	4	C7:+57.021,C19:+57.021	953.229479	3808.886716	0.000622848	4	N	81	115
Q9WUP7	Parental	EFDTK	TPAKEEDAFHFVSYVPVNGR	LYELD	3		755.0434428	2262.106928	0.000451244	1	N	154	174
Q9WUU7	Exosome	NIKRK	GAWPSILLSVQNVIDCGNAGSCEGGNDLPVWEYAHK	HGIPD	3	C16:+57.021,C22:+57.021	1305.28081	3912.81903	0.000451244	2	N	112	148
Q9WUU7	Parental	INIKR	KGAWPSILLSVQNVIDCGNAGSCEGGNDLPVWEYAHK	HGIPD	4	C17:+57.021,C23:+57.021	1011.236298	4040.913993	0.000451244	27	N	111	148
Q9WUU7	Parental	NIKRK	GAWPSILLSVQNVIDCGNAGSCEGGNDLPVWEYAHK	HGIPD	3	C16:+57.021,C22:+57.021	1305.28081	3912.81903	0.000451244	32	N	112	148
Q9WUU7	Parental	NYQAK	DQDCDKFNQCGTCTEFK	ECHTI	2	C4:+57.021,C10:+57.021,C13:+57.021	1076.921899	2151.828197	0.000451244	10	N	162	179
Q9WUU7	Parental	NYQAK	DQDCDKFNQCGTCTEFK	ECHTI	3	C4:+57.021,C10:+57.021,C13:+57.021	718.2838658	2151.828197	0.000451244	7	N	162	179
Q9WUU7	Parental	TSTYK	GGTGDSYNLAIESACTFGDPIV	-	2	C15:+57.021	1122.510181	2243.004762	0.000451244	15	N	284	306
Q9WUU7	Parental	PSILL	SVQNVIDCGNAGSCEGGNDLPVWEYAHK	HGIPD	3	C8:+57.021,C14:+57.021	1026.122518	3075.344155	0.000622848	4	N	120	148
Q9WUU7	Parental	NYQAK	DQDCDKFNQCGTCTEF	KECHT	2	C4:+57.021,C10:+57.021,C13:+57.021	1012.874417	2023.733234	0.000451244	9	N	162	178
Q9WV02	Exosome	SLDGK	AIKVEQATKPSFESGR	RGLPP	3		583.3166148	1746.926444	0.002019181	2	N	77	93
Q9WV02	Exosome	DRPGK	LFIGGLNTETNEK	ALEAV	2		718.3755278	1434.735456	0.000637154	4	N	9	22
Q9WV02	Exosome	TNKSR	GFAFVTFESPADAK	DAARD	2		743.8647959	1485.713992	0.000451244	9	N	49	63
Q9WV02	Parental	SLDGK	AIKVEQATKPSFESGR	RGLPP	3		583.3166148	1746.926444	0.000823681	2	N	77	93
Q9WV02	Parental	SLDGK	AIKVEQATKPSFESGR	RGLPP	4		437.7394111	1746.926444	0.000622848	4	N	77	93
Q9WV02	Parental	DRPGK	LFIGGLNTETNEKALEAVFGK	YGRIV	2		1126.102598	2250.189595	0.001329271	3	N	9	30
Q9WV02	Parental	DRPGK	LFIGGLNTETNEKALEAVFGK	YGRIV	3		751.0709985	2250.189595	0.000451244	3	N	9	30
Q9WV02	Parental	DRPGK	LFIGGLNTETNEK	ALEAV	2		718.3755278	1434.735456	0.000451244	5	N	9	22
Q9WV32	Exosome	AKWNK	VHELKEHNGQVTGIDWAPESNR	IVTCG	2		1258.617998	2515.220395	0.000662267	2	N	44	66
Q9WV32	Exosome	AKWNK	VHELKEHNGQVTGIDWAPESNR	IVTCG	3		839.4145984	2515.220395	0.000451244	43	N	44	66
Q9WV32	Exosome	WNKDR	TQIAICPNNHEVHIYEK	SGAKW	2	C6:+57.021	1033.510122	2065.004643	0.000451244	31	N	20	37
Q9WV32	Exosome	WNKDR	TQIAICPNNHEVHIYEK	SGAKW	3	C6:+57.021	689.342681	2065.004643	0.000637154	14	N	20	37
Q9WV32	Exosome	WNKDR	TQIAICPNNHEVHIYEK	SGAKW	4	C6:+57.021	517.2589608	2065.004643	0.000451244	28	N	20	37
Q9WV32	Exosome	DSLHK	NSVSQISVLSGGK	AKCSQ	2		638.349313	1274.683026	0.000451244	26	N	326	339
Q9WV32	Exosome	KKPIR	STVLSLDWHPNNVLLAAGSCDFK	CRIFS	2	C20:+57.021	1272.631496	2543.247393	0.000451244	44	N	142	165
Q9WV32	Exosome	KKPIR	STVLSLDWHPNNVLLAAGSCDFK	CRIFS	3	C20:+57.021	848.756931	2543.247393	0.000451244	54	N	142	165
Q9WV32	Exosome	GSGSR	VISICYFEQENDWWVCK	HIKKP	2	C5:+57.021,C16:+57.021	1138.511241	2275.006883	0.000451244	33	N	118	135
Q9WV32	Exosome	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	2	C11:+57.021	1015.504505	2028.99341	0.000451244	33	N	216	234
Q9WV32	Exosome	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	3	C11:+57.021	677.3389366	2028.99341	0.000451244	58	N	216	234
Q9WV32	Exosome	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	4	C11:+57.021	508.2561524	2028.99341	0.000851441	2	N	216	234
Q9WV32	Exosome	QNLDK	KASSEGGAATGAGLDSLHK	NSVSQ	3		586.2995124	1755.875137	0.000451244	3	N	307	326
Q9WV32	Exosome	QNLDK	KASSEGGAATGAGLDSLHK	NSVSQ	4		439.9765843	1755.875137	0.000451244	1	N	307	326
Q9WV32	Exosome	NLDKK	ASSEGGAATGAGLDSLHK	NSVSQ	2		814.897887	1627.780174	0.000451244	6	N	308	326
Q9WV32	Exosome	NLDKK	ASSEGGAATGAGLDSLHK	NSVSQ	3		543.6011914	1627.780174	0.001699387	4	N	308	326
Q9WV32	Exosome	VHELK	EHNGQVTGIDWAPESNR	IVTCG	2		955.4435244	1908.871449	0.000451244	49	N	49	66
Q9WV32	Exosome	VHELK	EHNGQVTGIDWAPESNR	IVTCG	3		637.2982829	1908.871449	0.000451244	21	N	49	66
Q9WV32	Exosome	HAWNK	DRTQIAICPNNHEVHIYEK	SGAKW	3	C8:+57.021	779.7186991	2336.132697	0.000451244	1	N	18	37
Q9WV32	Exosome	HAWNK	DRTQIAICPNNHEVHIYEK	SGAKW	4	C8:+57.021	585.0409743	2336.132697	0.000451244	14	N	18	37
Q9WV32	Exosome	SAYIK	EVEERPAPTPWGSK	MPFGE	2		791.8971587	1581.778717	0.000451244	10	N	174	188
Q9WV32	Exosome	SAYIK	EVEERPAPTPWGSK	MPFGE	3		528.2673725	1581.778717	0.000451244	12	N	174	188
Q9WV32	Exosome	ARCVR	WAPNENKFAVGSGSR	VISIC	3		540.6028666	1618.7852	0.000451244	4	N	103	118
Q9WV32	Exosome	GGKAK	CSQFCTTGMDGGMSIWDVK	SLESA	2	C1:+57.021,C5:+57.021,M9:+15.995,M13:+15.995	1106.44447	2210.87334	0.000451244	3	N	341	360

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9WV32	Exosome	TVLSL	DWHPNNVLLAAGSCDFK	CRIFS	2	C14:+57.021	972.4573576	1942.899115	0.001264573	1	N	148	165
Q9WV32	Exosome	VISIC	YFEQENDWWVCK	HIKKP	2	C11:+57.021	852.3618631	1702.708126	0.000451244	4	N	123	135
Q9WV32	Parental	AKWNK	VHELKEHNGQVTGIDWAPESNR	IVTCG	2		1258.617998	2515.220395	0.000451244	3	N	44	66
Q9WV32	Parental	AKWNK	VHELKEHNGQVTGIDWAPESNR	IVTCG	3		839.4145984	2515.220395	0.000451244	12	N	44	66
Q9WV32	Parental	WNKDR	TQIAICPNNHEVHIYEK	SGAKW	2	C6:+57.021	1033.510122	2065.004643	0.000451244	27	N	20	37
Q9WV32	Parental	WNKDR	TQIAICPNNHEVHIYEK	SGAKW	3	C6:+57.021	689.342681	2065.004643	0.001591523	2	N	20	37
Q9WV32	Parental	DSLHK	NSVSQISVLSGGK	AKCSQ	2		638.349313	1274.683026	0.000451244	12	N	326	339
Q9WV32	Parental	NLDKK	ASSEGGAATGAGLDSLHKNSVSQISVLSGGK	AKCSQ	2		1443.23412	2884.45264	0.000622848	1	N	308	339
Q9WV32	Parental	NLDKK	ASSEGGAATGAGLDSLHKNSVSQISVLSGGK	AKCSQ	3		962.4920134	2884.45264	0.000451244	10	N	308	339
Q9WV32	Parental	KKPIR	STVLSLDWHPNNVLLAAGSCDFKCR	IFSAY	3	C20:+57.021,C24:+57.021	954.1340299	2859.37869	0.002296037	2	N	142	167
Q9WV32	Parental	KKPIR	STVLSLDWHPNNVLLAAGSCDFK	CRIFS	2	C20:+57.021	1272.631496	2543.247393	0.000451244	21	N	142	165
Q9WV32	Parental	KKPIR	STVLSLDWHPNNVLLAAGSCDFK	CRIFS	3	C20:+57.021	848.756931	2543.247393	0.000451244	33	N	142	165
Q9WV32	Parental	GSGSR	VISICYFEQENDWWVCK	HIKKP	2	C5:+57.021,C16:+57.021	1138.511241	2275.006883	0.000451244	26	N	118	135
Q9WV32	Parental	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	2	C11:+57.021	1015.504505	2028.99341	0.000451244	23	N	216	234
Q9WV32	Parental	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	3	C11:+57.021	677.3389366	2028.99341	0.000451244	29	N	216	234
Q9WV32	Parental	ASGSR	VAWVSHDSTVCLVDADKK	MAVAT	4	C11:+57.021	508.2561524	2028.99341	0.000451244	5	N	216	234
Q9WV32	Parental	NLDKK	ASSEGGAATGAGLDSLHK	NSVSQ	2		814.897887	1627.780174	0.000451244	13	N	308	326
Q9WV32	Parental	NLDKK	ASSEGGAATGAGLDSLHK	NSVSQ	3		543.6011914	1627.780174	0.001162105	13	N	308	326
Q9WV32	Parental	VHELK	EHNGQVTGIDWAPESNR	IVTCG	2		955.4435244	1908.871449	0.000451244	32	N	49	66
Q9WV32	Parental	VHELK	EHNGQVTGIDWAPESNR	IVTCG	3		637.2982829	1908.871449	0.000451244	10	N	49	66
Q9WV32	Parental	HAWNK	DRTQIAICPNNHEVHIYEK	SGAKW	4	C8:+57.021	585.0409743	2336.132697	0.000622848	2	N	18	37
Q9WV32	Parental	SAYIK	EVEERPAPTPWGSK	MPFGE	2		791.8971587	1581.778717	0.000451244	10	N	174	188
Q9WV32	Parental	SAYIK	EVEERPAPTPWGSK	MPFGE	3		528.2673725	1581.778717	0.000622848	2	N	174	188
Q9WV32	Parental	RSTVL	SLDWHPNNVLLAAGSCDFK	CRIFS	2	C16:+57.021	1072.515404	2143.015208	0.000451244	17	N	146	165
Q9WV32	Parental	ISICY	FEQENDWWVCK	HIKKP	2	C10:+57.021	770.8301988	1539.644798	0.000451244	10	N	124	135
Q9WV32	Parental	DADKK	MAVATLASETLPLLAVTF	ITENS	2		924.5135105	1847.011421	0.001463592	3	N	234	252
Q9WV32	Parental	ARCVR	WAPNENKFAVGSGSR	VISIC	3		540.6028666	1618.7852	0.002374549	1	N	103	118
Q9WV60	Exosome	KDGSK	VTTVVATPGQGPDRPQEVSYTDTK	VIGNG	3		849.4298027	2545.266008	0.000451244	8	N	36	60
Q9WV60	Exosome	LPNGR	DTPALFNFTTQELSSNPPLATILIPPHAR	IQAAA	3		1054.559699	3160.655697	0.000451244	2	N	354	383
Q9WV60	Parental	KDGSK	VTTVVATPGQGPDRPQEVSYTDTK	VIGNG	3		849.4298027	2545.266008	0.0007646	1	N	36	60
Q9WV60	Parental	PPHAR	IQAAASPPANATAASDTNAGDRGQTNNAASASASNST	-	3		1144.527174	3430.558121	0.000451244	6	N	383	420
Q9WV60	Parental	LPNGR	DTPALFNFTTQELSSNPPLATILIPPHAR	IQAAA	3		1054.559699	3160.655697	0.000451244	2	N	354	383
Q9WV98	Parental	GTYNK	LTETCFLDCVKDFTTR	EVKPE	3	C5:+57.021,C9:+57.021	669.3169898	2004.92757	0.000451244	8	N	23	39
Q9WV98	Parental	DFTTR	EVKPEEVTCSEHCLQK	YLKMT	3	C9:+57.021,C13:+57.021	658.3084943	1971.902083	0.000662267	3	N	39	55
Q9WVA3	Exosome	ISSVK	FSPNTSQFLLVSSWDTSVR	LYDVP	2		1086.04254	2170.06948	0.000451244	12	N	21	40
Q9WVA3	Exosome	SIEGR	VAVEYLDPSPEVQK	KKYAF	2		787.4095676	1572.803535	0.000451244	6	N	202	216
Q9WVA3	Exosome	SMRLK	YQHTGAVLDCAFYDPTHAWSGGLDHQLK	MHDLN	4	C10:+57.021	797.6231256	3186.461302	0.000451244	5	N	52	80
Q9WVA3	Parental	ISSVK	FSPNTSQFLLVSSWDTSVR	LYDVP	2		1086.04254	2170.06948	0.000451244	39	N	21	40
Q9WVA4	Exosome	LAVAR	DDGLFSGDPNWFPKK	SKENP	2		861.9102661	1721.804932	0.000823681	8	N	139	154
Q9WVA4	Exosome	LAVAR	DDGLFSGDPNWFPKK	SKENP	3		574.9427774	1721.804932	0.000451244	23	N	139	154
Q9WVA4	Exosome	QAAER	YGINTTDIFQTVDLWEGK	NMACV	2		1050.518366	2099.021133	0.000451244	51	N	102	120
Q9WVA4	Exosome	QAAER	YGINTTDIFQTVDLWEGK	NMACV	3		700.681511	2099.021133	0.001395409	2	N	102	120
Q9WVA4	Exosome	QKIEK	QYDADLEQILIQWITTQCREDVGQPQPGR	ENFQK	3	C18:+57.021	1153.232051	3456.672752	0.000451244	4	N	20	49
Q9WVA4	Exosome	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	C18:+57.021	1197.59184	2393.16808	0.000451244	18	N	20	39
Q9WVA4	Exosome	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	3	C18:+57.021	798.7304933	2393.16808	0.000451244	9	N	20	39
Q9WVA4	Exosome	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	Q1:-17.027,C18:+57.021	1189.07834	2376.14108	0.000622848	3	N	20	39
Q9WVA4	Exosome	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	[0:-17.027,C18:+57.021	1189.07834	2376.14108	0.000735798	1	N	20	39
Q9WVA4	Exosome	TVLCK	LINSLYPEGQAPVKK	IQASS	2		828.9701268	1655.924654	0.000451244	16	N	64	79
Q9WVA4	Exosome	LAVAR	DDGLFSGDPNWFPK	KSKEN	2		797.8627845	1593.709969	0.00091018	8	N	139	153
Q9WVA4	Parental	TVLCK	LINSLYPEGQAPVK	KIQAS	2		764.9226452	1527.82969	0.000823681	8	N	64	78
Q9WVA4	Parental	LAVAR	DDGLFSGDPNWFPKK	SKENP	2		861.9102661	1721.804932	0.000451244	16	N	139	154
Q9WVA4	Parental	LAVAR	DDGLFSGDPNWFPKK	SKENP	3		574.9427774	1721.804932	0.000451244	12	N	139	154
Q9WVA4	Parental	QAAER	YGINTTDIFQTVDLWEGK	NMACV	2		1050.518366	2099.021133	0.000451244	42	N	102	120
Q9WVA4	Parental	QAAER	YGINTTDIFQTVDLWEGK	NMACV	3		700.681511	2099.021133	0.000622848	4	N	102	120
Q9WVA4	Parental	EVQQK	IEKQYDADLEQILIQWITTQCR	EDVGQ	3	C21:+57.021	922.1377001	2763.3897	0.000451244	14	N	17	39
Q9WVA4	Parental	QKIEK	QYDADLEQILIQWITTQCREDVGQPQPGR	ENFQK	3	C18:+57.021	1153.232051	3456.672752	0.000451244	8	N	20	49
Q9WVA4	Parental	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	C18:+57.021	1197.59184	2393.16808	0.000451244	35	N	20	39
Q9WVA4	Parental	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	3	C18:+57.021	798.7304933	2393.16808	0.000451244	33	N	20	39
Q9WVA4	Parental	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	Q1:-17.027,C18:+57.021	1189.07834	2376.14108	0.000451244	17	N	20	39
Q9WVA4	Parental	QKIEK	QYDADLEQILIQWITTQCR	EDVGQ	2	[0:-17.027,C18:+57.021	1189.07834	2376.14108	0.000451244	8	N	20	39
Q9WVA4	Parental	TVLCK	LINSLYPEGQAPVKK	IQASS	2		828.9701268	1655.924654	0.000451244	17	N	64	79
Q9WVA4	Parental	LAVAR	DDGLFSGDPNWFPK	KSKEN	2		797.8627845	1593.709969	0.000823681	9	N	139	153
Q9WVA4	Parental	ACVQR	TLMNLGGLAVARDDGLFSGDPNWFPK	KSKEN	3		931.1344446	2790.379934	0.000622848	1	N	127	153
Q9WVE8	Parental	ELSFK	AGDELTKIEDEDEQGWCK	GRLDS	2	C17:+57.021	1061.965606	2121.915613	0.000451244	6	N	448	466
Q9WVE8	Parental	WCKGR	LDSGQVGLYPANYVEAIQ	-	2		968.9867022	1935.957804	0.002374549	1	N	468	486

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9WVG5	Exosome	AVHLF	VDSLVNQDKPSFAFQCTDSSR	FKRGI	2	C16:+57.021	1201.058361	2400.101123	0.00091018	1	N	281	302
Q9WVG5	Exosome	AFNIR	TSKDPEQEGCNLSLGDSK	LLENC	2	C10:+57.021	982.9472167	1963.878833	0.000451244	10	N	54	72
Q9WVG5	Exosome	AFNIR	TSKDPEQEGCNLSLGDSK	LLENC	3	C10:+57.021	655.6340778	1963.878833	0.000451244	24	N	54	72
Q9WVG5	Exosome	QPTLY	ITLYGSNADSQNLPLEIVEK	IELNA	2		1102.576413	2203.137226	0.000451244	17	N	369	389
Q9WVG5	Exosome	LLKMR	LTWEGVAHSWYNLWNEFR	NYLSQ	3		770.0365111	2307.086133	0.000451244	17	N	413	431
Q9WVG5	Exosome	CEHER	AVHLFVDSLVNQDKPSFAFQCTDSSR	FKRGI	3	C21:+57.021	990.1471468	2967.41804	0.000451244	12	N	276	302
Q9WVG5	Exosome	CEHER	AVHLFVDSLVNQDKPSFAFQCTDSSR	FKRGI	4	C21:+57.021	742.8623101	2967.41804	0.000451244	15	N	276	302
Q9WVG5	Exosome	GTVGR	ITGLDPAGPMFEGVDINRR	LSPDD	3	M10:+15.995	692.018269	2073.031407	0.001839721	2	N	188	207
Q9WVG5	Exosome	QMREK	DANVVVVDWLPLAHQLY	TDAVN	2		976.5179725	1951.020345	0.000622848	4	N	114	131
Q9WVG5	Exosome	GTVGR	ITGLDPAGPMFEGVDINR	RLSPD	2	M10:+15.995	959.4729479	1916.930296	0.000451244	3	N	188	206
Q9WVG5	Parental	AVHLF	VDSLVNQDKPSFAFQCTDSSR	FKRGI	2	C16:+57.021	1201.058361	2400.101123	0.000451244	8	N	281	302
Q9WVG5	Parental	AVHLF	VDSLVNQDKPSFAFQCTDSSR	FKRGI	3	C16:+57.021	801.0415075	2400.101123	0.000451244	10	N	281	302
Q9WVG5	Parental	AFNIR	TSKDPEQEGCNLSLGDSK	LLENC	2	C10:+57.021	982.9472167	1963.878833	0.000622848	7	N	54	72
Q9WVG5	Parental	AFNIR	TSKDPEQEGCNLSLGDSK	LLENC	3	C10:+57.021	655.6340778	1963.878833	0.000451244	6	N	54	72
Q9WVG5	Parental	QPTLY	ITLYGSNADSQNLPLEIVEK	IELNA	2		1102.576413	2203.137226	0.000451244	18	N	369	389
Q9WVG5	Parental	LLKMR	LTWEGVAHSWYNLWNEF	RNYLS	2		1076.500311	2150.985022	0.002080925	1	N	413	430
Q9WVJ2	Exosome	EFEHR	VNPLSLVEIILHVVR	QMTDP	2		851.0252364	1700.034873	0.000451244	1	N	70	85
Q9WVJ2	Exosome	EFEHR	VNPLSLVEIILHVVR	QMTDP	3		567.6860909	1700.034873	0.000451244	2	N	70	85
Q9WVJ2	Exosome	RDTDR	QWLIDTLYAFNSGAVDR	FQTLK	2		984.9948615	1967.974123	0.000451244	1	N	230	247
Q9WVJ2	Exosome	FQTLK	CAWGQQPDLAANEAQLLR	KIQLL	2	C1:+57.021	1020.999921	2039.984242	0.000451244	16	N	252	270
Q9WVJ2	Exosome	DGLIK	LYENFISEFEHR	VNPLS	3		528.5883345	1582.741604	0.001463592	2	N	58	70
Q9WVJ2	Parental	EFEHR	VNPLSLVEIILHVVR	QMTDP	3		567.6860909	1700.034873	0.000451244	1	N	70	85
Q9WVJ2	Parental	FQTLK	CAWGQQPDLAANEAQLLR	KIQLL	2	C1:+57.021	1020.999921	2039.984242	0.000451244	2	N	252	270
Q9WVJ2	Parental	LYTKK	LWHQLTLEVLDFVQDPCFAQGDGLIK	LYENF	3	C17:+57.021	1014.851671	3041.531614	0.000622848	2	N	32	58
Q9WVJ2	Parental	LESLR	DTDRQWLIDTLYAFNSGAVDR	FQTLK	3		819.4000663	2455.176799	0.002813207	1	N	226	247
Q9WVK4	Exosome	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	2		1277.655923	2553.296246	0.000451244	1	N	486	509
Q9WVK4	Exosome	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	3		852.1065486	2553.296246	0.000451244	23	N	486	509
Q9WVK4	Exosome	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	4		639.3318614	2553.296246	0.000451244	21	N	486	509
Q9WVK4	Exosome	PDNRK	LFEAEEQDLFKDIQSLPR	NAALR	2		1089.558023	2177.100446	0.000451244	5	N	269	287
Q9WVK4	Exosome	PDNRK	LFEAEEQDLFKDIQSLPR	NAALR	3		726.7079487	2177.100446	0.000451244	29	N	269	287
Q9WVK4	Exosome	QRISR	GYDFAAVLEWFAERVDR	IILLF	3		682.0028074	2042.985022	0.001839721	1	N	167	184
Q9WVK4	Exosome	WVVGK	DKPTYDEIFYTLSPVNGK	ITGAN	2		1044.020742	2086.025884	0.000451244	5	N	443	461
Q9WVK4	Exosome	WVVGK	DKPTYDEIFYTLSPVNGK	ITGAN	3		696.3497613	2086.025884	0.001264573	2	N	443	461
Q9WVK4	Exosome	QRISR	GYDFAAVLEWFAER	VDRII	2		837.4020769	1672.788554	0.000451244	3	N	167	181
Q9WVK4	Exosome	QRISR	GYDFAAVLEWFAER	VDRII	3		558.6039846	1672.788554	0.000451244	4	N	167	181
Q9WVK4	Exosome	HGYGE	GAGEGIDDVEWVVGK	DKPTY	2		765.8758919	1529.736184	0.000451244	6	N	428	443
Q9WVK4	Exosome	PEVVR	VYIGSFWSHPLLIPDNR	KLFEA	3		672.0235428	2013.047228	0.000451244	8	N	251	268
Q9WVK4	Exosome	ERVDR	IILLFDAHKLDISDEFSEVIK	ALKNH	3		815.7812252	2444.320275	0.001699387	2	N	184	205
Q9WVK4	Exosome	ERVDR	IILLFDAHKLDISDEFSEVIK	ALKNH	4		612.0878689	2444.320275	0.000637154	1	N	184	205
Q9WVK4	Exosome	ESKKK	ELVNNLGEIYQK	IEREH	2		710.3780705	1418.740541	0.000451244	6	N	329	341
Q9WVK4	Exosome	PDNRK	LFEAEEQDLFK	DIQSL	2		684.8382468	1367.660894	0.001871652	1	N	269	280
Q9WVK4	Exosome	ARRKK	EPELFQTVAEGLR	QLYAQ	2		744.8888023	1487.762005	0.001839721	1	N	13	26
Q9WVK4	Parental	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	2		1277.655923	2553.296246	0.000451244	1	N	486	509
Q9WVK4	Parental	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	3		852.1065486	2553.296246	0.000451244	26	N	486	509
Q9WVK4	Parental	GKIWK	LADVDKDGLLDDEEFALANHLIK	VKLEG	4		639.3318614	2553.296246	0.000451244	18	N	486	509
Q9WVK4	Parental	PDNRK	LFEAEEQDLFKDIQSLPR	NAALR	3		726.7079487	2177.100446	0.000451244	13	N	269	287
Q9WVK4	Parental	QRISR	GYDFAAVLEWFAERVDR	IILLF	3		682.0028074	2042.985022	0.001699387	2	N	167	184
Q9WVK4	Parental	WVVGK	DKPTYDEIFYTLSPVNGK	ITGAN	2		1044.020742	2086.025884	0.000451244	2	N	443	461
Q9WVK4	Parental	QRISR	GYDFAAVLEWFAER	VDRII	2		837.4020769	1672.788554	0.000451244	1	N	167	181
Q9WVK4	Parental	QRISR	GYDFAAVLEWFAER	VDRII	3		558.6039846	1672.788554	0.000451244	11	N	167	181
Q9Z0H3	Exosome	SWHQK	TYAFSENPLPTVEIAIR	NTGDA	2		961.0074376	1919.999275	0.000823681	1	N	324	341
Q9Z0H3	Exosome	TPEMF	SEILCDDLDLNPLTFVPAIASAIR	QQIES	2	C5:+57.021	1322.188844	2642.362089	0.000451244	1	N	218	242
Q9Z0H3	Exosome	ASAIR	QQIESYPTDSILEDQSDQR	VIIKL	2		1126.519823	2251.024046	0.001839721	1	N	242	261
Q9Z0H3	Parental	SWHQK	TYAFSENPLPTVEIAIR	NTGDA	2		961.0074376	1919.999275	0.000823681	3	N	324	341
Q9Z0H3	Parental	TPEMF	SEILCDDLDLNPLTFVPAIASAIR	QQIES	2	C5:+57.021	1322.188844	2642.362089	0.000451244	14	N	218	242
Q9Z0H3	Parental	TPEMF	SEILCDDLDLNPLTFVPAIASAIR	QQIES	3	C5:+57.021	881.7951628	2642.362089	0.000637154	5	N	218	242
Q9Z0H3	Parental	ASAIR	QQIESYPTDSILEDQSDQR	VIIKL	2		1126.519823	2251.024046	0.000451244	14	N	242	261
Q9Z0H4	Exosome	EKELK	ELFEPYGAVYQINVLR	DRSQN	2		956.0046979	1909.993796	0.000451244	10	N	57	73
Q9Z0H4	Exosome	PPQSK	GCCFVTFYTR	KAALE	2	C2:+57.021,C3:+57.021	655.786517	1309.557434	0.000622848	2	N	83	93
Q9Z0H4	Exosome	SWSEK	ELKELFEPYGAVYQINVLR	DRSQN	3		761.0796054	2280.215416	0.000622848	1	N	54	73
Q9Z0H4	Parental	EKELK	ELFEPYGAVYQINVLR	DRSQN	2		956.0046979	1909.993796	0.000451244	13	N	57	73
Q9Z0I7	Exosome	EILPR	TVSAFANTDGGYLFIGLDEK	KQEIV	2		1059.523649	2117.031698	0.000451244	13	N	217	237
Q9Z0I7	Exosome	RNITK	ALCALINSGEGK	VKAHI	2	C3:+57.021	616.8191028	1231.622606	0.000622848	8	N	42	54
Q9Z0I7	Exosome	SPSAR	PSDRPGDDTQEEGHIQELAAAFFK	QSKLT	3		886.7530569	2657.235771	0.00091018	2	N	155	179
Q9Z0I7	Exosome	SPSAR	PSDRPGDDTQEEGHIQELAAAFFK	QSKLT	4		665.3167427	2657.235771	0.000451244	4	N	155	179

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z0I7	Exosome	SEIEK	CIQQLPVTHFCEER	EKIKY	3	C1:+57.021,C11:+57.021	606.2873649	1815.838695	0.001839721	1	N	260	274
Q9Z0I7	Parental	EILPR	TVSAFANTDGGYLFIGLDEK	KQEIV	2		1059.523649	2117.031698	0.000851441	3	N	217	237
Q9Z0I7	Parental	RNITK	ALCALINSGEGK	VKAHI	2	C3:+57.021	616.8191028	1231.622606	0.000622848	1	N	42	54
Q9Z0I7	Parental	PLDFK	QYQSYFFICVEK	SQSPD	2	C9:+57.021	806.3795246	1610.743449	0.002145581	1	N	91	103
Q9Z0J0	Parental	VGVIK	EVNVSPCPTDPCQLHK	GQSYS	2	C7:+57.021,C12:+57.021	940.9351694	1879.854739	0.000451244	16	N	35	51
Q9Z0J0	Parental	VGVIK	EVNVSPCPTDPCQLHK	GQSYS	3	C7:+57.021,C12:+57.021	627.6260463	1879.854739	0.000622848	6	N	35	51
Q9Z0J0	Parental	DCGSK	VGVIKEVNVSPCPTDPCQLHK	GQSYS	3	C12:+57.021,C17:+57.021	793.0718193	2376.192058	0.000451244	9	N	30	51
Q9Z0J0	Parental	DCGSK	VGVIKEVNVSPCPTDPCQLHK	GQSYS	4	C12:+57.021,C17:+57.021	595.0558145	2376.192058	0.000451244	3	N	30	51
Q9Z0J0	Parental	LEGIR	VPFPIPEPDGCK	SGINC	2	C11:+57.021	678.3371284	1354.658657	0.000451244	6	N	82	94
Q9Z0J0	Parental	EDDKK	NNLFCWEIPVQITS	-	2	C5:+57.021	860.9220879	1719.828576	0.000622848	3	N	135	149
Q9Z0N1	Exosome	PIFSK	IVSLFAEHNDLQYAAPGGLIGVGTK	IDPTL	2		1285.684818	2569.354035	0.002212458	2	N	317	342
Q9Z0N1	Exosome	PIFSK	IVSLFAEHNDLQYAAPGGLIGVGTK	IDPTL	3		857.4591451	2569.354035	0.000451244	34	N	317	342
Q9Z0N1	Exosome	ESQAK	EQYEQILAFVQGTVAEGAPIIPISAQLK	YNIEV	3		1005.213529	3012.617186	0.000451244	26	N	201	229
Q9Z0N1	Exosome	SAQLK	YNIEVVCEYIVK	KIPVP	2	C7:+57.021	764.8897251	1527.76385	0.0025889	2	N	229	241
Q9Z0N1	Exosome	IDLVK	ESQAKEQYEQILAFVQGTVAEGAPIIPISAQLK	YNIEV	3		1186.301954	3555.882463	0.000451244	2	N	196	229
Q9Z0N1	Exosome	KGVLK	VGQEIEVRPGIVSK	DSEGK	3		504.2916295	1509.851488	0.000622848	3	N	289	303
Q9Z0N1	Exosome	LIVIR	SFDVNKPGCEVDDLKGGVAGGSILK	GVLKV	3	C9:+57.021	854.7674957	2561.279087	0.000451244	2	N	260	285
Q9Z0N1	Parental	PIFSK	IVSLFAEHNDLQYAAPGGLIGVGTK	IDPTL	3		857.4591451	2569.354035	0.000451244	28	N	317	342
Q9Z0N1	Parental	ESQAK	EQYEQILAFVQGTVAEGAPIIPISAQLK	YNIEV	3		1005.213529	3012.617186	0.000451244	21	N	201	229
Q9Z0N1	Parental	PECYR	SCGSSTPDEFPTDIPGTK	GNFKL	2	C2:+57.021	948.4203034	1894.825007	0.000451244	15	N	103	121
Q9Z0N1	Parental	IDLVK	ESQAKEQYEQILAFVQGTVAEGAPIIPISAQLK	YNIEV	3		1186.301954	3555.882463	0.000637154	4	N	196	229
Q9Z0P4	Parental	KEEQK	SETLVNAQQTPLGTPK	ENRTS	2		842.4497555	1682.883911	0.000622848	6	N	131	147
Q9Z0P4	Parental	TRLEK	EIDVLEFGESAPAASK	ENSAA	2		831.9152141	1661.814828	0.000823681	2	N	93	109
Q9Z0P5	Exosome	IRLIK	VIIEDEQLVLGASQEPVGR	WDQDY	2		1026.552741	2051.089881	0.000451244	44	N	29	48
Q9Z0P5	Exosome	IRLIK	VIIEDEQLVLGASQEPVGR	WDQDY	3		684.7044271	2051.089881	0.001943752	1	N	29	48
Q9Z0P5	Exosome	SCKSR	LLDSVEQDFQLEIAK	KIEIG	2		874.4597889	1746.903978	0.000451244	24	N	278	293
Q9Z0P5	Exosome	QDYDR	AVLPLLDAQEPCYLLFR	LDSQN	2	C12:+57.021	1009.542902	2017.070203	0.000451244	24	N	55	72
Q9Z0P5	Exosome	QDYDR	AVLPLLDAQEPCYLLFR	LDSQN	3	C12:+57.021	673.3645345	2017.070203	0.000451244	10	N	55	72
Q9Z0P5	Exosome	YLLFR	LDSQNAQGFEWLFLAWSPDNSPVR	LKMLY	2		1389.170063	2776.324526	0.000451244	8	N	72	96
Q9Z0P5	Exosome	YLLFR	LDSQNAQGFEWLFLAWSPDNSPVR	LKMLY	3		926.4493087	2776.324526	0.000451244	2	N	72	96
Q9Z0P5	Exosome	YIQLK	LDLERETIELVHTEPTNVAQLPSR	IPRDA	3		920.8229232	2759.44537	0.000451244	12	N	204	228
Q9Z0P5	Exosome	AGYQK	HLSSCAAPAPLTSAER	ELQQI	2	C5:+57.021	834.4124187	1666.809237	0.000451244	5	N	136	152
Q9Z0P5	Exosome	AGYQK	HLSSCAAPAPLTSAER	ELQQI	3	C5:+57.021	556.6108791	1666.809237	0.00307782	1	N	136	152
Q9Z0P5	Exosome	SVESK	HQTLQGLAFPLQPEAQR	ALQQL	2		967.5162955	1933.016991	0.000622848	2	N	171	188
Q9Z0P5	Exosome	SVESK	HQTLQGLAFPLQPEAQR	ALQQL	3		645.346797	1933.016991	0.000451244	3	N	171	188
Q9Z0P5	Exosome	LDLER	ETIELVHTEPTNVAQLPSR	IPRDA	3		712.0433313	2133.106594	0.000823681	2	N	209	228
Q9Z0P5	Parental	IRLIK	VIIEDEQLVLGASQEPVGR	WDQDY	2		1026.552741	2051.089881	0.000451244	44	N	29	48
Q9Z0P5	Parental	IRLIK	VIIEDEQLVLGASQEPVGR	WDQDY	3		684.7044271	2051.089881	0.001162105	2	N	29	48
Q9Z0P5	Parental	IRLIK	VIIEDEQLVLGASQEPVGRWDQDYDR	AVLPL	3		1010.832147	3029.473041	0.000451244	6	N	29	55
Q9Z0P5	Parental	SCKSR	LLDSVEQDFQLEIAK	KIEIG	2		874.4597889	1746.903978	0.000451244	30	N	278	293
Q9Z0P5	Parental	QDYDR	AVLPLLDAQEPCYLLFR	LDSQN	2	C12:+57.021	1009.542902	2017.070203	0.000451244	28	N	55	72
Q9Z0P5	Parental	QDYDR	AVLPLLDAQEPCYLLFR	LDSQN	3	C12:+57.021	673.3645345	2017.070203	0.000622848	2	N	55	72
Q9Z0P5	Parental	YLLFR	LDSQNAQGFEWLFLAWSPDNSPVR	LKMLY	2		1389.170063	2776.324526	0.000451244	23	N	72	96
Q9Z0P5	Parental	YLLFR	LDSQNAQGFEWLFLAWSPDNSPVR	LKMLY	3		926.4493087	2776.324526	0.000979378	3	N	72	96
Q9Z0P5	Parental	YIQLK	LDLERETIELVHTEPTNVAQLPSR	IPRDA	3		920.8229232	2759.44537	0.000451244	18	N	204	228
Q9Z0P5	Parental	EPVGR	WDQDYDRAVLPLLDAQEPCYLLFR	LDSQN	3	C19:+57.021	999.4922544	2995.453363	0.000451244	5	N	48	72
Q9Z0P5	Parental	AGYQK	HLSSCAAPAPLTSAER	ELQQI	2	C5:+57.021	834.4124187	1666.809237	0.000451244	2	N	136	152
Q9Z0P5	Parental	SVESK	HQTLQGLAFPLQPEAQR	ALQQL	2		967.5162955	1933.016991	0.000451244	8	N	171	188
Q9Z0P5	Parental	SVESK	HQTLQGLAFPLQPEAQR	ALQQL	3		645.346797	1933.016991	0.000451244	15	N	171	188
Q9Z0P5	Parental	QDYDR	AVLPLLDAQEPCYLLF	RLDSQ	2	C12:+57.021	931.4923461	1860.969092	0.000451244	8	N	55	71
Q9Z0P5	Parental	EPVGR	WDQDYDRAVLPLLDAQEPCYLLF	RLDSQ	2	C19:+57.021	1420.683926	2839.352252	0.002080925	1	N	48	71
Q9Z0P5	Parental	LEIAK	KIEIGDGAELTAEFLYDEVHPK	QHAFK	3		825.420356	2473.237668	0.001839721	1	N	293	315
Q9Z0P5	Parental	LEIAK	KIEIGDGAELTAEFLYDEVHPK	QHAFK	4		619.317217	2473.237668	0.000622848	3	N	293	315
Q9Z0P5	Parental	LDLER	ETIELVHTEPTNVAQLPSR	IPRDA	2		1067.561097	2133.106594	0.000451244	1	N	209	228
Q9Z0W3	Parental	GEVQK	ALECFCQAASEVGKEEFLDR	LIRSE	3	C4:+57.021,C6:+57.021	787.0281677	2358.061103	0.001871652	1	N	891	911
Q9Z0W3	Parental	HAPKR	GQFCVFQLVSTENNR	YSLDH	2	C4:+57.021	899.9309756	1797.846351	0.002212458	1	N	331	346
Q9Z0W3	Parental	FLICR	DLLILQQLLTR	LGDAV	2		663.4117163	1324.807833	0.000823681	4	N	698	709
Q9Z0X1	Parental	EKQRR	AIASATEGGSVPQIR	APSHV	3		486.2638509	1455.768153	0.002519933	1	N	111	126
Q9Z0X1	Parental	HQSMF	WSDLGPDVGYEAIGLVDSSLPTVGVFAK	ATAQD	2		1446.737444	2891.459288	0.000451244	5	N	481	509
Q9Z0X1	Parental	HQSMF	WSDLGPDVGYEAIGLVDSSLPTVGVFAK	ATAQD	3		964.8275628	2891.459288	0.000451244	1	N	481	509
Q9Z0X1	Parental	PPSFY	VSAQDLPNIENGGVAVLTGK	KVVHL	2		991.5318082	1981.048016	0.002374549	2	N	210	230
Q9Z126	Exosome	PAVVA	VTSAGPEESDGDLSCVCVK	TISSG	2	C15:+57.021,C17:+57.021	1005.443221	2008.870843	0.000451244	167	N	29	48
Q9Z126	Exosome	PAVVA	VTSAGPEESDGDLSCVCVK	TISSG	3	C15:+57.021,C17:+57.021	670.6314142	2008.870843	0.001229886	3	N	29	48
Q9Z126	Exosome	GIHLK	HITSLEVIK	AGRHC	2		520.3114708	1038.607342	0.000851441	11	N	57	66
Q9Z126	Exosome	AVVAV	TSAGPEESDGDLSCVCVK	TISSG	2	C14:+57.021,C16:+57.021	955.9090143	1909.802429	0.000451244	103	N	30	48

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z126	Exosome	IKAGR	HCAVPQLIATLK	NGRKI	2	C2:+57.021	675.8820374	1349.748475	0.000451244	120	N	69	81
Q9Z126	Exosome	IKAGR	HCAVPQLIATLK	NGRKI	3	C2:+57.021	450.9239583	1349.748475	0.000451244	60	N	69	81
Q9Z126	Exosome	VVAVT	SAGPEESDGDLSCVCVK	TISSG	2	C13:+57.021,C15:+57.021	905.385175	1808.75475	0.000451244	5	N	31	48
Q9Z126	Parental	PAVVA	VTSAGPEESDGDLSCVCVK	TISSG	2	C15:+57.021,C17:+57.021	1005.443221	2008.870843	0.000451244	78	N	29	48
Q9Z126	Parental	AVVAV	TSAGPEESDGDLSCVCVK	TISSG	2	C14:+57.021,C16:+57.021	955.9090143	1909.802429	0.001395409	3	N	30	48
Q9Z126	Parental	IKAGR	HCAVPQLIATLK	NGRKI	2	C2:+57.021	675.8820374	1349.748475	0.000451244	7	N	69	81
Q9Z126	Parental	IKAGR	HCAVPQLIATLK	NGRKI	3	C2:+57.021	450.9239583	1349.748475	0.000622848	9	N	69	81
Q9Z130	Parental	EYLSR	FGEVVDCTIK	TDPVT	2	C7:+57.021	584.2896468	1166.563694	0.000451244	25	Y	51	61
Q9Z130	Parental	EYLSR	FGEVVDCTIKTDPVTGR	SRGFG	2	C7:+57.021	947.4726733	1892.929747	0.000662267	1	N	51	68
Q9Z130	Parental	EPPKK	VFVGGLSPDTSEEQIKEY	FGAFG	2		999.4892747	1996.962949	0.000451244	4	N	115	133
Q9Z183	Exosome	YPLGR	ILIGNSGYSSSESR	DMHQA	2		735.3656914	1468.715783	0.000451244	10	N	427	441
Q9Z183	Exosome	SLLDK	SNPELPEALVFQDSVTFR	VAPWI	2		1025.018534	2048.021467	0.000451244	25	N	274	292
Q9Z183	Exosome	QQFSY	CLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C1:+57.021	971.785215	2912.332245	0.000622848	7	N	236	262
Q9Z183	Exosome	GPQQF	SYCLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C3:+57.021	1055.150334	3162.427602	0.000451244	10	N	234	262
Q9Z183	Exosome	AVLKR	ELGLAEGDIIDIPQLFK	LAGNS	2		936.0121886	1870.008777	0.000451244	21	N	554	571
Q9Z183	Exosome	YYGPK	TSPVQALIYITGVELSLSADVTR	TGRVK	2		1217.165926	2432.316253	0.000451244	11	N	100	123
Q9Z183	Exosome	YYGPK	TSPVQALIYITGVELSLSADVTR	TGRVK	3		811.7798843	2432.316253	0.000662267	3	N	100	123
Q9Z183	Exosome	-M	AQGAVIHVAPEQPTHAVCVVGTATPLDVR	GSAPK	3	C18:+57.021	998.5260696	2992.554809	0.002080925	1	N	1	30
Q9Z183	Exosome	LSSPR	ACYQLFQELQSQGHGEATLFEGLK	RKRQT	3	C2:+57.021	918.7782833	2753.31145	0.000451244	7	N	495	519
Q9Z183	Exosome	LSSPR	ACYQLFQELQSQGHGEATLFEGLKR	KRQTI	4	C2:+57.021	728.3609403	2909.412561	0.0025889	5	N	495	520
Q9Z183	Exosome	PSRYK	VALGPQQFSYCLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C11:+57.021	1335.30013	4002.876991	0.000451244	20	N	226	262
Q9Z183	Exosome	TRKLY	MSELTGLDAFGNLEVSPPVTVR	GKEYP	2	M1:+15.995	1174.594323	2347.173046	0.000451244	2	N	397	419
Q9Z183	Exosome	SSESR	DMHQALQDFLSAQQVQAPVR	LFSDW	3	M2:+15.995	766.7152491	2297.122347	0.000451244	12	N	441	461
Q9Z183	Parental	YPLGR	ILIGNSGYSSSESR	DMHQA	2		735.3656914	1468.715783	0.000451244	10	N	427	441
Q9Z183	Parental	SLLDK	SNPELPEALVFQDSVTFR	VAPWI	2		1025.018534	2048.021467	0.000451244	18	N	274	292
Q9Z183	Parental	QQFSY	CLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	2	C1:+39.994	1448.660423	2895.305245	0.000735798	1	N	236	262
Q9Z183	Parental	QQFSY	CLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C1:+57.021	971.785215	2912.332245	0.000451244	24	N	236	262
Q9Z183	Parental	GPQQF	SYCLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C3:+57.021	1055.150334	3162.427602	0.000451244	35	N	234	262
Q9Z183	Parental	AVLKR	ELGLAEGDIIDIPQLFK	LAGNS	2		936.0121886	1870.008777	0.000451244	32	N	554	571
Q9Z183	Parental	DADFK	GLIPLTISLLDKSNPELPEALVFQDSVTFR	VAPWI	3		1104.941698	3311.801693	0.000823681	4	N	262	292
Q9Z183	Parental	YYGPK	TSPVQALIYITGVELSLSADVTR	TGRVK	2		1217.165926	2432.316253	0.000451244	10	N	100	123
Q9Z183	Parental	YYGPK	TSPVQALIYITGVELSLSADVTR	TGRVK	3		811.7798843	2432.316253	0.000451244	12	N	100	123
Q9Z183	Parental	-M	AQGAVIHVAPEQPTHAVCVVGTATPLDVR	GSAPK	3	C18:+57.021	998.5260696	2992.554809	0.000451244	24	N	1	30
Q9Z183	Parental	LSSPR	ACYQLFQELQSQGHGEATLFEGLK	RKRQT	3	C2:+57.021	918.7782833	2753.31145	0.000735798	2	N	495	519
Q9Z183	Parental	LSNKK	LRDQNAYVESCIDWNR	AVLKR	2	C11:+57.021	1019.973903	2037.932206	0.000637154	2	N	533	549
Q9Z183	Parental	LSNKK	LRDQNAYVESCIDWNR	AVLKR	3	C11:+57.021	680.3185354	2037.932206	0.000451244	3	N	533	549
Q9Z183	Parental	LSSPR	ACYQLFQELQSQGHGEATLFEGLKR	KRQTI	4	C2:+57.021	728.3609403	2909.412561	0.000622848	3	N	495	520
Q9Z183	Parental	GPQQF	SYCLELPGGQHSTDFYVEGLAFPDADFKGLIPLTISLLDK	SNPEL	4	C3:+57.021	1107.559757	4426.207828	0.000451244	2	N	234	274
Q9Z183	Parental	DADFK	GLIPLTISLLDKSNPELPEALVF	QDSVT	2		1240.207063	2478.398526	0.000622848	2	N	262	285
Q9Z183	Parental	AVLKR	ELGLAEGDIIDIPQLF	KLAGN	2		871.9647071	1741.913814	0.001329271	3	N	554	570
Q9Z183	Parental	TRKLY	MSELTGLDAFGNLEVSPPVTVR	GKEYP	2		1166.596823	2331.178046	0.000451244	2	N	397	419
Q9Z183	Parental	SRYKV	ALGPQQFSYCLELPGGQHSTDFYVEGLAFPDADFK	GLIPL	3	C10:+57.021	1302.277326	3903.808577	0.000622848	4	N	227	262
Q9Z183	Parental	MGASK	WPLDPELEVTLQVK	AASSR	2		833.956685	1665.89777	0.002884417	1	N	67	81
Q9Z183	Parental	DADFK	GLIPLTISLLDK	SNPEL	2		641.9031928	1281.790786	0.000735798	2	N	262	274
Q9Z1B7	Exosome	KTLFK	GKDYLDQLTQILK	VTGVP	2		767.9279275	1533.840255	0.001162105	6	N	224	237
Q9Z1B7	Exosome	KTLFK	GKDYLDQLTQILK	VTGVP	3		512.287885	1533.840255	0.000870037	9	N	224	237
Q9Z1B7	Exosome	GIVHR	DLKPGNLAVNEDCELK	ILDFG	3	C13:+57.021	605.6369825	1813.887547	0.000451244	1	N	149	165
Q9Z1B7	Exosome	LFKGK	DYLDQLTQILK	VTGVP	2		675.3697141	1348.723828	0.001763695	2	N	226	237
Q9Z1D1	Exosome	SELLK	GIPLPTGDTSPEPELLPGDPLPPPKEVINGNIK	TVTEY	3		1134.612129	3400.812986	0.000451244	7	N	32	65
Q9Z1D1	Exosome	SEDTR	ETDLQELFRPFGSISR	IYLAK	3		632.327291	1893.958473	0.000451244	8	N	251	267
Q9Z1D1	Parental	SELLK	GIPLPTGDTSPEPELLPGDPLPPPKEVINGNIK	TVTEY	3		1134.612129	3400.812986	0.000622848	5	N	32	65
Q9Z1D1	Parental	SEDTR	ETDLQELFRPFGSISR	IYLAK	3		632.327291	1893.958473	0.000451244	15	N	251	267
Q9Z1D1	Parental	NATIR	VTNLSEDTRETDLQELFRPFGSISR	IYLAK	3		970.8251039	2909.451912	0.002884417	1	N	242	267
Q9Z1E4	Exosome	DRRFR	SLDDSCSQLTSFLYSFCQQSR	RQRII	2	C6:+57.021,C17:+57.021	1265.05473	2528.09386	0.000451244	30	N	558	579
Q9Z1E4	Exosome	DRRFR	SLDDSCSQLTSFLYSFCQQSR	RQRII	3	C6:+57.021,C17:+57.021	843.7057533	2528.09386	0.000451244	6	N	558	579
Q9Z1E4	Exosome	ADRVK	VIFHPEFLSSTSPLLPVDYEEFVR	GCHLG	2		1411.226515	2820.437431	0.000451244	1	N	474	498
Q9Z1E4	Exosome	ADRVK	VIFHPEFLSSTSPLLPVDYEEFVR	GCHLG	3		941.1536102	2820.437431	0.000451244	11	N	474	498
Q9Z1E4	Exosome	EFSNK	GADVFLEALAR	LNYLL	2		581.3172845	1160.618969	0.000451244	1	N	337	348
Q9Z1E4	Exosome	QTKAK	VTGDEWGDNYYLVGPYTEQGVR	TQVEL	2		1259.580215	2517.14483	0.000451244	8	N	52	74
Q9Z1E4	Exosome	MPLSR	SLSVSSLPGLEDWEDEFDPENAVLFEVAWEVANK	VGGIY	3		1274.60766	3820.79958	0.000823681	1	N	5	39
Q9Z1E4	Exosome	TLLGR	YLCAGAVDFYNNLENFNVDKEAGER	QIYHR	3	C3:+57.021	970.1121022	2907.312907	0.000451244	5	N	211	236
Q9Z1E4	Parental	DRRFR	SLDDSCSQLTSFLYSFCQQSR	RQRII	2	C6:+57.021,C17:+57.021	1265.05473	2528.09386	0.000451244	35	N	558	579
Q9Z1E4	Parental	ADRVK	VIFHPEFLSSTSPLLPVDYEEFVR	GCHLG	2		1411.226515	2820.437431	0.000823681	1	N	474	498
Q9Z1E4	Parental	ADRVK	VIFHPEFLSSTSPLLPVDYEEFVR	GCHLG	3		941.1536102	2820.437431	0.000451244	12	N	474	498
Q9Z1E4	Parental	QTKAK	VTGDEWGDNYYLVGPYTEQGVR	TQVEL	2		1259.580215	2517.14483	0.000451244	18	N	52	74

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z1E4	Parental	TLLGR	YLCAGAVDFYNNLENFNVDKEAGER	QIYHR	3	C3:+57.021	970.1121022	2907.312907	0.000622848	4	N	211	236
Q9Z1E4	Parental	VYFGR	WLIEGGPLVVLLDVGASAWALER	WKGEL	3		822.1253262	2463.352579	0.000451244	5	N	105	128
Q9Z1F9	Exosome	IVWAK	YLFNQLFGEEDADQEVSPDRADPEAAWEPTEAEAR	ARASN	3		1332.600116	3994.776948	0.000451244	18	N	190	225
Q9Z1F9	Exosome	RNGSR	LQADDFLQDYTLLINILHSEDLGKDVEFEVVGDSPEK	VGPKQ	4		1052.026291	4204.073965	0.001871652	1	N	514	551
Q9Z1F9	Exosome	LWRKR	KPPVPLDWAEVQSQGEANADQQNEPQLGLK	DQQVL	3		1096.216661	3285.626582	0.000870037	3	N	276	306
Q9Z1F9	Exosome	VSGGR	VLVVGAGGIGCELLK	NLVLT	2	C11:+57.021	742.9291846	1483.842769	0.000451244	11	N	19	34
Q9Z1F9	Exosome	DYTLL	INILHSEDLGKDVEFEVVGDSPEK	VGPKQ	3		890.4488629	2668.323189	0.000823681	1	N	527	551
Q9Z1F9	Exosome	NHVNR	MCLAADVPLIESGTAGYLGQVTTIKK	GVTEC	3	C2:+57.021	912.8155699	2735.42331	0.001162105	2	N	127	153
Q9Z1F9	Exosome	IVWAK	YLFNQLFGEEDADQEVSPDR	ADPEA	2		1186.538016	2371.060432	0.000851441	1	N	190	210
Q9Z1F9	Parental	IVWAK	YLFNQLFGEEDADQEVSPDRADPEAAWEPTEAEAR	ARASN	3		1332.600116	3994.776948	0.000451244	25	N	190	225
Q9Z1F9	Parental	RNGSR	LQADDFLQDYTLLINILHSEDLGKDVEFEVVGDSPEK	VGPKQ	4		1052.026291	4204.073965	0.001162105	4	N	514	551
Q9Z1F9	Parental	LWRKR	KPPVPLDWAEVQSQGEANADQQNEPQLGLK	DQQVL	3		1096.216661	3285.626582	0.000451244	2	N	276	306
Q9Z1F9	Parental	IVWAK	YLFNQLFGEEDADQEVSPDR	ADPEA	2		1186.538016	2371.060432	0.000451244	1	N	190	210
Q9Z1F9	Parental	CELLK	NLVLTGFSHIDLIDLDTIDVSNLNR	QFLFQ	3		933.1630569	2796.465771	0.000622848	4	N	34	59
Q9Z1F9	Parental	AKYLF	NQLFGEEDADQEVSPDRADPEAAWEPTEAEAR	ARASN	3		1191.52818	3571.561141	0.000451244	1	N	193	225
Q9Z1G3	Parental	IPDLK	VGTLDVLVGLSDELAKLDAFVEGVVK	KVAQY	3		896.1691489	2685.484047	0.001162105	1	N	44	70
Q9Z1G3	Parental	IPDLK	VGTLDVLVGLSDELAK	LDAFV	2		814.9594247	1627.903249	0.000735798	7	N	44	60
Q9Z1G3	Parental	IPDLK	VGTLDVLVGLSDELAK	LDAFV	3		543.6422165	1627.903249	0.001264573	2	N	44	60
Q9Z1N5	Exosome	RFGTK	GLAITFVSDENDAK	ILNDV	2		740.3704424	1478.725285	0.000451244	12	N	384	398
Q9Z1N5	Exosome	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	C1:+39.994	1130.617238	2259.218877	0.000451244	9	N	299	319
Q9Z1N5	Exosome	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	3	C1:+39.994	754.0807589	2259.218877	0.000451244	3	N	299	319
Q9Z1N5	Exosome	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	C1:+57.021	1139.130738	2276.245877	0.000451244	13	N	299	319
Q9Z1N5	Exosome	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	3	C1:+57.021	759.7564255	2276.245877	0.000451244	39	N	299	319
Q9Z1N5	Exosome	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	4	C1:+57.021	570.0692691	2276.245877	0.000823681	4	N	299	319
Q9Z1N5	Exosome	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	[0:-17.027,C1:+57.021	1130.617238	2259.218877	0.000451244	15	N	299	319
Q9Z1N5	Exosome	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	3	[0:-17.027,C1:+57.021	754.0807589	2259.218877	0.000451244	9	N	299	319
Q9Z1N5	Exosome	MPNVK	VAVFFGGLSIK	KDEEV	2		569.3374886	1136.659377	0.000823681	7	N	144	155
Q9Z1N5	Exosome	DFQRR	ILVATNLFGR	GMDIE	2		552.3327376	1102.649875	0.001654178	5	Y	339	349
Q9Z1N5	Exosome	-MAE	NDVDNELLDYEDDEVETAAGADGTEAPAKK	DVKGS	3		1065.476423	3193.405869	0.000451244	23	N	3	33
Q9Z1N5	Exosome	KKDVK	GSYVSIHSSGFR	DFLLK	2		648.8207227	1295.625845	0.001763695	1	Y	36	48
Q9Z1N5	Exosome	MDIER	VNIAFNYDMPEDSDTYLHR	VARAG	3		767.348315	2299.021545	0.000634081	1	N	355	374
Q9Z1N5	Parental	RFGTK	GLAITFVSDENDAK	ILNDV	2		740.3704424	1478.725285	0.000451244	11	N	384	398
Q9Z1N5	Parental	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	C1:+39.994	1130.617238	2259.218877	0.000451244	5	N	299	319
Q9Z1N5	Parental	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	3	C1:+39.994	754.0807589	2259.218877	0.000622848	5	N	299	319
Q9Z1N5	Parental	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	C1:+57.021	1139.130738	2276.245877	0.000870037	1	N	299	319
Q9Z1N5	Parental	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	3	C1:+57.021	759.7564255	2276.245877	0.000451244	41	N	299	319
Q9Z1N5	Parental	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	2	[0:-17.027,C1:+57.021	1130.617238	2259.218877	0.000451244	11	N	299	319
Q9Z1N5	Parental	KSVQR	CIALAQLLVEQNFPAIAIHR	GMPQE	3	[0:-17.027,C1:+57.021	754.0807589	2259.218877	0.000451244	15	N	299	319
Q9Z1N5	Parental	ENDAK	ILNDVQDRFEVNISELPDEIDISSYIEQTR	-	3		1184.256962	3549.747485	0.000451244	16	N	398	428
Q9Z1N5	Parental	NEKNR	KLFDLLDVLEFNQVVIFVK	SVQRC	3		760.4403631	2278.297689	0.001699387	1	Y	276	295
Q9Z1N5	Parental	EKNRK	LFDLLDVLEFNQVVIFVK	SVQRC	2		1076.109163	2150.202726	0.000451244	6	Y	277	295
Q9Z1N5	Parental	KKDVK	GSYVSIHSSGFRDFLLKPELLR	AIVDC	4		631.0950226	2520.34889	0.002296037	3	Y	36	58
Q9Z1N5	Parental	DFQRR	ILVATNLFGR	GMDIE	2		552.3327376	1102.649875	0.001395409	3	Y	339	349
Q9Z1N5	Parental	-MAE	NDVDNELLDYEDDEVETAAGADGTEAPAKK	DVKGS	3		1065.476423	3193.405869	0.000451244	2	N	3	33
Q9Z1N5	Parental	DVQDR	FEVNISELPDEIDISSYIEQTR	-	2		1299.13502	2596.25444	0.000451244	7	N	406	428
Q9Z1N5	Parental	DVQDR	FEVNISELPDEIDISSYIEQTR	-	3		866.4259468	2596.25444	0.00307782	1	N	406	428
Q9Z1Q5	Exosome	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQRK	FLDGN	3		1045.505765	3133.493896	0.000451244	11	N	138	166
Q9Z1Q5	Exosome	PRYPK	LAALNPESNTSGLDIFAK	FSAYI	2		930.9892448	1859.96289	0.000451244	29	N	95	113
Q9Z1Q5	Exosome	PRYPK	LAALNPESNTSGLDIFAK	FSAYI	3		620.9954299	1859.96289	0.000823681	2	N	95	113
Q9Z1Q5	Exosome	NAYAR	EEFASTCPDDEEIELAYEQVAR	ALK-	2	C7:+57.021	1301.068789	2600.121977	0.000451244	69	N	216	238
Q9Z1Q5	Exosome	NAYAR	EEFASTCPDDEEIELAYEQVAR	ALK-	3	C7:+57.021	867.7151258	2600.121977	0.000451244	33	N	216	238
Q9Z1Q5	Exosome	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQR	KFLDG	3		1002.807444	3005.398933	0.000451244	58	N	138	165
Q9Z1Q5	Exosome	ISQRK	FLDGNELTLADCNLLPK	LHIVQ	2	C12:+57.021	966.9906989	1931.965798	0.000451244	25	N	166	183
Q9Z1Q5	Exosome	ISQRK	FLDGNELTLADCNLLPK	LHIVQ	3	C12:+57.021	644.9963993	1931.965798	0.001162105	2	N	166	183
Q9Z1Q5	Exosome	VLWLK	GVTFNVTTVDTK	RRTET	2		641.3384139	1280.661228	0.000451244	22	N	37	49
Q9Z1Q5	Exosome	VLWLK	GVTFNVTTVDTKR	RTETV	2		719.3889695	1436.762339	0.000622848	7	N	37	50
Q9Z1Q5	Exosome	VLWLK	GVTFNVTTVDTKR	RTETV	3		479.9285797	1436.762339	0.000451244	9	N	37	50
Q9Z1Q5	Exosome	GISQR	KFLDGNELTLADCNLLPK	LHIVQ	2	C13:+57.021	1031.038181	2060.060761	0.000451244	15	N	165	183
Q9Z1Q5	Exosome	GISQR	KFLDGNELTLADCNLLPK	LHIVQ	3	C13:+57.021	687.6947203	2060.060761	0.000451244	10	N	165	183
Q9Z1Q5	Exosome	PRYPK	LAALNPESNTSGLDIFAKF	SAYIK	2		1004.523452	2007.031304	0.000451244	6	N	95	114
Q9Z1Q5	Exosome	LDNYL	TSPLPEEVDETSAEDEGISQR	KFLDG	2		1145.022396	2288.029191	0.000698008	3	N	144	165
Q9Z1Q5	Exosome	REEFA	STCPDDEEIELAYEQVAR	ALK-	2	C3:+57.021	1062.973432	2123.931263	0.000451244	10	N	220	238
Q9Z1Q5	Exosome	NAYAR	EEFASTCPDDEEIELAYEQVARAL	K-	3	C7:+57.021	929.0888517	2784.243155	0.000622848	4	N	216	240
Q9Z1Q5	Exosome	NAYAR	EEFASTCPDDEEIELAYEQV	ARALK	2	C7:+57.021	1187.499676	2372.983752	0.000637154	3	N	216	236
Q9Z1Q5	Exosome	NAYAR	EEFASTCPDDEEIELAYEQVA	RALK-	2	C7:+57.021	1223.018233	2444.020866	0.000622848	2	N	216	237

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z1Q5	Exosome	ETVQK	LCPGGQLPFLLY	GTEVH	2	C2:+57.021	689.3656888	1376.715778	0.001839721	1	N	57	69
Q9Z1Q5	Exosome	ETVQK	LCPGGQLPFLLYGTEVHTDTNKIEEFLEAMLCPPR	YPKLA	4	C2:+57.021,C32:+57.021	1012.25226	4044.97784	0.002727428	1	N	57	92
Q9Z1Q5	Parental	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQRK	FLDGN	3		1045.505765	3133.493896	0.000451244	22	N	138	166
Q9Z1Q5	Parental	PRYPK	LAALNPESNTSGLDIFAK	FSAYI	2		930.9892448	1859.96289	0.000451244	30	N	95	113
Q9Z1Q5	Parental	NAYAR	EEFASTCPDDEEIELAYEQVAR	ALK-	2	C7:+57.021	1301.068789	2600.121977	0.000451244	65	N	216	238
Q9Z1Q5	Parental	NAYAR	EEFASTCPDDEEIELAYEQVAR	ALK-	3	C7:+57.021	867.7151258	2600.121977	0.000451244	12	N	216	238
Q9Z1Q5	Parental	LKALK	VLDNYLTSPLPEEVDETSAEDEGISQR	KFLDG	3		1002.807444	3005.398933	0.000451244	37	N	138	165
Q9Z1Q5	Parental	ISQRK	FLDGNELTLADCNLLPK	LHIVQ	2	C12:+57.021	966.9906989	1931.965798	0.000451244	17	N	166	183
Q9Z1Q5	Parental	VLWLK	GVTFNVTTVDTK	RRTET	2		641.3384139	1280.661228	0.000451244	3	N	37	49
Q9Z1Q5	Parental	GISQR	KFLDGNELTLADCNLLPK	LHIVQ	2	C13:+57.021	1031.038181	2060.060761	0.000451244	14	N	165	183
Q9Z1Q5	Parental	PRYPK	LAALNPESNTSGLDIFAKF	SAYIK	2		1004.523452	2007.031304	0.000622848	2	N	95	114
Q9Z1Q9	Exosome	RRTPK	APASLCVTPYPEPSECSWKDPEAEAALELALSITR	AVRSL	3	C6:+57.021,C16:+57.021	1286.957222	3857.848265	0.000451244	5	N	1080	1115
Q9Z1Q9	Exosome	RKMSK	SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDPSEVEK	AKEGQ	3		1297.672775	3889.994926	0.000451244	37	N	864	900
Q9Z1Q9	Exosome	YSGAR	SVTQQPGSEVIAPQK	TPAQL	2		784.9180912	1567.820582	0.000451244	12	N	214	229
Q9Z1Q9	Exosome	SFAYK	VQGSDSDEEVVVATTR	IETML	2		846.4082846	1690.800969	0.000451244	11	N	520	536
Q9Z1Q9	Exosome	PGGSR	AAVLVQQWVSYADTELIPAACGATLPALGLR	GPGQD	3	C21:+57.021	1085.579952	3253.716455	0.000451244	9	N	91	122
Q9Z1Q9	Exosome	SYSAK	VPLEVQEADEAKLQQTEAELR	KVDEA	3		799.4154935	2395.223081	0.000451244	6	N	1229	1250
Q9Z1Q9	Exosome	FPPPR	LPALEQGPGGLWVWGAPAVAQLLWPAGLGGPGGSR	AAVLV	3		1145.949521	3434.825163	0.000622848	2	N	56	91
Q9Z1Q9	Exosome	EDWLR	LHTYLAGDAPTLADLAAVTALLLPFR	YVLDP	3		908.5097283	2722.505785	0.002519933	2	N	147	173
Q9Z1Q9	Exosome	WWGHR	IPAYFITVHDPAVPPGEDPDGR	YWVSG	3		788.3942527	2362.159358	0.000451244	4	N	729	751
Q9Z1Q9	Exosome	YRSTR	LVNWSCTLNSAISDIEVDKK	ELTGR	3	C6:+57.021	764.7232273	2291.146282	0.000451244	6	N	472	492
Q9Z1Q9	Exosome	LIAAR	YGEAGDGPGWGGPHPR	ICLQP	3		537.2434498	1608.706949	0.00091018	4	N	23	39
Q9Z1Q9	Exosome	HQLGR	EAFLEEVWK	WKAEK	2		575.7931109	1149.570622	0.001329271	1	N	408	417
Q9Z1Q9	Exosome	QWVSY	ADTELIPAACGATLPALGLR	GPGQD	2	C10:+57.021	1005.538348	2009.061095	0.000451244	5	N	102	122
Q9Z1Q9	Parental	RRTPK	APASLCVTPYPEPSECSWKDPEAEAALELALSITR	AVRSL	3	C6:+57.021,C16:+57.021	1286.957222	3857.848265	0.000451244	21	N	1080	1115
Q9Z1Q9	Parental	RKMSK	SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDPSEVEK	AKEGQ	3		1297.672775	3889.994926	0.000451244	24	N	864	900
Q9Z1Q9	Parental	RKMSK	SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDPSEVEK	AKEGQ	4		973.5065316	3889.994926	0.000451244	1	N	864	900
Q9Z1Q9	Parental	YSGAR	SVTQQPGSEVIAPQK	TPAQL	2		784.9180912	1567.820582	0.000622848	14	N	214	229
Q9Z1Q9	Parental	SFAYK	VQGSDSDEEVVVATTR	IETML	2		846.4082846	1690.800969	0.000451244	10	N	520	536
Q9Z1Q9	Parental	PGGSR	AAVLVQQWVSYADTELIPAACGATLPALGLR	GPGQD	3	C21:+57.021	1085.579952	3253.716455	0.002145581	1	N	91	122
Q9Z1Q9	Parental	SYSAK	VPLEVQEADEAKLQQTEAELR	KVDEA	3		799.4154935	2395.223081	0.000451244	11	N	1229	1250
Q9Z1Q9	Parental	YNLTR	TRPDCFLEVADEATGALASAVSGY	VQALA	2	C5:+57.021	1250.586952	2499.158303	0.001395409	2	N	1128	1152
Q9Z1Q9	Parental	FPPPR	LPALEQGPGGLWVWGAPAVAQLLWPAGLGGPGGSR	AAVLV	3		1145.949521	3434.825163	0.000622848	7	N	56	91
Q9Z1Q9	Parental	RKMSK	SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDPSEVEKAK	EGQKA	4		1023.289551	4089.127003	0.002145581	1	N	864	902
Q9Z1Q9	Parental	EDWLR	LHTYLAGDAPTLADLAAVTALLLPFR	YVLDP	3		908.5097283	2722.505785	0.00307782	1	N	147	173
Q9Z1Q9	Parental	WWGHR	IPAYFITVHDPAVPPGEDPDGR	YWVSG	3		788.3942527	2362.159358	0.001264573	2	N	729	751
Q9Z1Q9	Parental	YRSTR	LVNWSCTLNSAISDIEVDKK	ELTGR	3	C6:+57.021	764.7232273	2291.146282	0.000451244	2	N	472	492
Q9Z1R2	Exosome	HLVER	APPQTQLPSGASSGTGSASATHGGAPLPGTR	GPGAS	3		939.4694316	2815.384895	0.000451244	5	N	87	118
Q9Z1R2	Parental	HLVER	APPQTQLPSGASSGTGSASATHGGAPLPGTR	GPGAS	3		939.4694316	2815.384895	0.000451244	24	N	87	118
Q9Z1R2	Parental	PFLQR	YCEVLGAAATTDYNNNHEGREEDQR	LINLV	3	C2:+57.021	971.4218869	2911.242261	0.000451244	5	N	297	322
Q9Z1R2	Parental	VDIIR	TNLEFLQEQFNSIAAHVLHCTDSGFGAR	LLELC	4	C20:+57.021	791.382404	3161.498416	0.000823681	2	N	858	886
Q9Z1T1	Parental	MILQK	VVNVANLGAVPSSQDNVHR	FAART	3		659.3489776	1975.023533	0.000451244	14	N	1036	1055
Q9Z1T1	Parental	TLNIK	ASGYLELSNWPEVAPDPSVR	NVEVI	2		1094.039997	2186.064395	0.000451244	8	N	630	650
Q9Z1X4	Exosome	EEMEK	VLAGETLSVNDPPDVLDR	QKCLA	2		955.497434	1908.979268	0.000451244	12	N	182	200
Q9Z1X4	Parental	GGQQK	ASYSSGYQSHQGQQQPYNQSQYSSYGTPQGK	QKGYG	3		1147.838801	3440.493002	0.001463592	2	N	743	774
Q9Z1X4	Parental	GSGGR	SGGNSYGSSGSSSYNTGSHGGYGTGSGGSSSYQGK	QGGYS	3		1075.107616	3222.299447	0.000451244	25	N	817	852
Q9Z1X4	Parental	KFAAK	PHNPGFGMGGPMHNEVPPPPNIR	GRGRG	3	M8:+15.995,M12:+15.995	827.723779	2480.147937	0.001591523	1	N	617	640
Q9Z1Z0	Exosome	LADSR	EIIRNDGVLLLQALTR	SNGAI	3		608.6954262	1823.062879	0.000451244	1	N	179	195
Q9Z1Z0	Exosome	LQTDR	SDSEIIAYALDTLYNIISNDEEEELEENSTR	QSEDL	3		1192.55188	3574.63224	0.001839721	1	N	73	104
Q9Z1Z0	Exosome	LTALK	SQLCSQSLEITR	LQTEN	2	C4:+57.021	711.3565808	1420.697562	0.001763695	1	N	798	810
Q9Z1Z0	Parental	VSTLK	CQNEQLQTAVTQQASQIQQHKDQYNLLK	VQLGK	4	C1:+57.021	836.4182465	3341.641786	0.002884417	2	N	677	705
Q9Z1Z0	Parental	NAFER	LLDIITEEGNSDGGIVVEDCLILLQNLLK	TNNSN	3	C20:+57.021	1066.239261	3195.694382	0.000451244	9	N	212	241
Q9Z1Z0	Parental	LQLVR	VLVSPTNPPGATSSCQK	AMFQC	2	C15:+57.021	871.941009	1741.866418	0.000823681	7	N	288	305
Q9Z1Z0	Parental	LADSR	EIIRNDGVLLLQALTR	SNGAI	3		608.6954262	1823.062879	0.001229886	2	N	179	195
Q9Z1Z0	Parental	LQTDR	SDSEIIAYALDTLYNIISNDEEEELEENSTR	QSEDL	3		1192.55188	3574.63224	0.000622848	4	N	73	104
Q9Z1Z0	Parental	LTALK	SQLCSQSLEITR	LQTEN	2	C4:+57.021	711.3565808	1420.697562	0.000451244	3	N	798	810
Q9Z1Z0	Parental	VSTLK	CQNEQLQTAVTQQASQIQQHK	DQYNL	3	C1:+57.021	823.4034393	2467.186918	0.001162105	1	N	677	698
Q9Z1Z2	Exosome	KPMLR	QGDTGDWIGTFLGHK	GAVWG	3		544.5991221	1630.773966	0.000451244	26	N	44	59
Q9Z1Z2	Exosome	KHIVK	TVDFTQDSNYLLTGGQDK	LLRIY	2		1001.474156	2000.932712	0.000451244	27	N	104	122
Q9Z1Z2	Exosome	IHCVR	FSPDGELYASGSEDGTLR	LWQTV	2		950.9321239	1899.848648	0.000451244	11	N	272	290
Q9Z1Z2	Exosome	FKLYK	YDYNSGEELESYK	GHFGP	2		798.8391721	1595.662744	0.000451244	12	N	249	262
Q9Z1Z2	Parental	KPMLR	QGDTGDWIGTFLGHK	GAVWG	3		544.5991221	1630.773966	0.000451244	5	N	44	59
Q9Z1Z2	Parental	LAKPK	IGFPETAEEELEEIASENSDSIYSSTPEVKA	-	3		1124.523262	3370.546385	0.000451244	3	N	319	350
Q9Z1Z2	Parental	KHIVK	TVDFTQDSNYLLTGGQDK	LLRIY	2		1001.474156	2000.932712	0.000451244	15	N	104	122
Q9Z1Z2	Parental	IHCVR	FSPDGELYASGSEDGTLR	LWQTV	2		950.9321239	1899.848648	0.000823681	1	N	272	290

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z1Z2	Parental	FKLYK	YDYNSGEELESYK	GHFGP	2		798.8391721	1595.662744	0.000451244	6	N	249	262
Q9Z204-2	Exosome	CSVHK	GFAFVQYVNER	NARAA	2		665.3334659	1328.651332	0.001591523	3	N	50	61
Q9Z204-2	Parental	AAEMY	GSSFDLDYDFQR	DYYDR	2		725.3182098	1448.62082	0.000823681	6	N	105	117
Q9Z204-2	Parental	SMNSR	VFIGNLNTLVVK	KSDVE	2		658.9009844	1315.786369	0.000451244	1	N	17	29
Q9Z204-2	Parental	GEDGR	MIAGQVLDINLAAEPK	VNRGK	2		841.961445	1681.90729	0.001264573	2	N	73	89
Q9Z277	Parental	PLLGR	KPFPLVKPLPGEEPLFTIPHTQEAFR	TREEY	4		747.9146243	2987.627297	0.001352548	3	N	7	33
Q9Z277	Parental	QLTHK	EAWEEEQEVAELLKEEFPNWYEK	LVLEM	3		975.7875443	2924.339233	0.000823681	6	N	63	86
Q9Z2D3	Exosome	WQRPK	YQILSATLEDVLTEGHCLSPVVVESDFVK	YESKC	3	C17:+57.021	1083.551727	3247.631782	0.000451244	3	N	50	79
Q9Z2D3	Parental	WQRPK	YQILSATLEDVLTEGHCLSPVVVESDFVK	YESKC	3	C17:+57.021	1083.551727	3247.631782	0.000451244	16	N	50	79
Q9Z2D3	Parental	RNFLK	EVDAGGDLISVSHLNDSDKLQLLSLVTK	KKRYW	4		742.3979984	2965.560794	0.000662267	3	N	11	39
Q9Z2D3	Parental	ATILK	DSCIFPLILHITLSGLSTLSK	EHEEE	3	C3:+57.021	772.4278631	2314.260189	0.000735798	6	N	475	496
Q9Z2E1	Parental	MELPK	GLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEK	NPAVW	3		1240.641587	3718.90136	0.000451244	16	N	310	349
Q9Z2E1	Parental	QPLCK	AFIVTDEDIR	KQEER	2		589.8067496	1177.597899	0.000451244	4	N	363	373
Q9Z2G9	Exosome	EWLAR	KFFGSLPDSWASGYAVPVVTVVR	AMLNN	3		828.1096761	2481.305628	0.000979378	1	N	185	208
Q9Z2G9	Exosome	WLARK	FFGSLPDSWASGYAVPVVTVVR	AMLNN	2		1177.613133	2353.210665	0.000451244	2	N	186	208
Q9Z2I8	Exosome	HLFLK	IDATQVEVNPFGETPEGQVVCFDAK	INFDD	2	C21:+57.021	1375.652823	2749.290046	0.000823681	1	N	235	260
Q9Z2I8	Exosome	ILMDR	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	EQIDI	3		1011.856293	3032.545478	0.001329271	1	N	161	191
Q9Z2I8	Parental	YEAFK	LLTSDPKVEAILVNIFGGIVNCAIIANGITK	ACREL	3	C22:+57.021	1085.279502	3252.815106	0.000451244	5	N	348	379
Q9Z2I8	Parental	HLFLK	IDATQVEVNPFGETPEGQVVCF	DAKIN	2	C21:+57.021	1218.573313	2435.131026	0.000823681	3	N	235	257
Q9Z2I8	Parental	HLFLK	IDATQVEVNPFGETPEGQVVCFDAK	INFDD	2	C21:+57.021	1375.652823	2749.290046	0.000622848	1	N	235	260
Q9Z2I8	Parental	ILMDR	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	EQIDI	3		1011.856293	3032.545478	0.001162105	3	N	161	191
Q9Z2I8	Parental	PLVVR	LEGTNVQEAQNILK	SSGLP	2		778.9180912	1555.820582	0.000451244	3	N	393	407
Q9Z2L7	Exosome	DDLVR	EGEIAILGGIEEESDKLWNFTK	KASHI	3		826.7519942	2477.232583	0.000451244	26	N	111	133
Q9Z2L7	Exosome	LLDER	LVTLLQEVDTIEQETIKPLDDCQK	LIEHG	3	C22:+57.021	943.4918087	2827.452026	0.000451244	34	N	73	97
Q9Z2L7	Exosome	NFTKK	ASHIQLDSLPEVPLLVDVPCLSAQLDDSILNIVK	DHIFK	3	C20:+57.021	1238.001133	3710.98	0.000451244	22	N	134	168
Q9Z2L7	Exosome	NIALR	NDAESSGVLYSSAPTYFCGQTLTFR	VETVG	2	C18:+57.021	1386.134797	2770.253995	0.000451244	8	N	295	320
Q9Z2L7	Exosome	NIALR	NDAESSGVLYSSAPTYFCGQTLTFR	VETVG	3	C18:+57.021	924.4257982	2770.253995	0.000451244	6	N	295	320
Q9Z2L7	Exosome	RGDGR	QEWSPWSVPQTGHSTLVPHEWTTGFEGYSLSSR	RNIAL	4		944.1964591	3772.754636	0.0025889	1	N	256	289
Q9Z2L7	Parental	DDLVR	EGEIAILGGIEEESDKLWNFTK	KASHI	2		1239.624091	2477.232583	0.000451244	1	N	111	133
Q9Z2L7	Parental	DDLVR	EGEIAILGGIEEESDKLWNFTK	KASHI	3		826.7519942	2477.232583	0.000451244	22	N	111	133
Q9Z2L7	Parental	LLDER	LVTLLQEVDTIEQETIKPLDDCQK	LIEHG	3	C22:+57.021	943.4918087	2827.452026	0.000451244	36	N	73	97
Q9Z2L7	Parental	NFTKK	ASHIQLDSLPEVPLLVDVPCLSAQLDDSILNIVK	DHIFK	3	C20:+57.021	1238.001133	3710.98	0.000698008	9	N	134	168
Q9Z2L7	Parental	NIALR	NDAESSGVLYSSAPTYFCGQTLTFR	VETVG	2	C18:+57.021	1386.134797	2770.253995	0.000451244	1	N	295	320
Q9Z2L7	Parental	NIALR	NDAESSGVLYSSAPTYFCGQTLTFR	VETVG	3	C18:+57.021	924.4257982	2770.253995	0.000451244	3	N	295	320
Q9Z2L7	Parental	NFTKK	ASHIQLDSLPEVPLLVDVPCLSAQLDDSILNIVKDHIFK	HGTVA	4	C20:+57.021	1088.836124	4351.313296	0.000870037	1	N	134	173
Q9Z2L7	Parental	RGDGR	QEWSPWSVPQTGHSTLVPHEWTTGFEGYSLSSR	RNIAL	4		944.1964591	3772.754636	0.001352548	4	N	256	289
Q9Z2L7	Parental	DDCQK	LIEHGVNTADDLVR	EGEIA	2		776.4104333	1550.805267	0.000451244	2	N	97	111
Q9Z2L7	Parental	SSNNR	EVVFDWLLEQACGPLYFGCSFFYPGWK	VLVF-	3	C12:+57.021,C19:+57.021	1105.849008	3314.523623	0.000451244	4	N	411	438
Q9Z2M7	Exosome	KLLCK	QNIQGHLGEDVIQDLINYCLSYIANIK	LPKKR	3	C19:+57.021	1044.53289	3130.57527	0.000451244	11	N	80	107
Q9Z2M7	Parental	KLLCK	QNIQGHLGEDVIQDLINYCLSYIANIKLPK	KRGTF	4	C19:+57.021	868.2095652	3468.807061	0.000622848	1	N	80	110
Q9Z2M7	Parental	KLLCK	QNIQGHLGEDVIQDLINYCLSYIANIK	LPKKR	3	C19:+57.021	1044.53289	3130.57527	0.000451244	8	N	80	107
Q9Z2M7	Parental	KLLCK	QNIQGHLGEDVIQDLINY	CLSYI	2		1035.019065	2068.02253	0.002296037	1	N	80	98
Q9Z2R6	Exosome	NQLLK	SFDFHFGFCIPSSK	NTCEH	3	C9:+57.021	559.2576657	1674.749597	0.000451244	5	N	173	187
Q9Z2R6	Exosome	SEMIR	HPYETQSDSFYFVDDR	LVMHN	2		1003.432291	2004.848982	0.002296037	1	N	209	225
Q9Z2R6	Exosome	PLQGK	QPIGPEDVLGLQR	ITGDY	2		711.3915122	1420.767424	0.001352548	1	N	57	70
Q9Z2U0	Exosome	MSYDR	AITVFSPDGHLFQVEYAQEAVKK	GSTAV	2		1289.171543	2576.327486	0.000451244	9	N	5	28
Q9Z2U0	Exosome	MSYDR	AITVFSPDGHLFQVEYAQEAVKK	GSTAV	3		859.7836287	2576.327486	0.000451244	30	N	5	28
Q9Z2U0	Exosome	MSYDR	AITVFSPDGHLFQVEYAQEAVKK	GSTAV	4		645.0896715	2576.327486	0.001162105	18	N	5	28
Q9Z2U0	Exosome	AVGVR	GKDIVVLGVEK	KSVAK	2		578.8509602	1155.68632	0.00091018	3	N	36	47
Q9Z2U0	Exosome	EFLEK	NYTDDAIETDDLTIK	LVIKA	2		863.9050434	1725.794487	0.000451244	10	N	174	189
Q9Z2U0	Exosome	MSYDR	AITVFSPDGHLFQVEYAQEAVK	KGSTA	2		1225.124062	2448.232523	0.000451244	28	N	5	27
Q9Z2U0	Exosome	MSYDR	AITVFSPDGHLFQVEYAQEAVK	KGSTA	3		817.0853077	2448.232523	0.000451244	22	N	5	27
Q9Z2U0	Exosome	QSNGR	RPFGISALIVGFDFDGTPR	LYQTD	2		1033.047428	2064.079257	0.000451244	10	N	124	143
Q9Z2U0	Exosome	QSNGR	RPFGISALIVGFDFDGTPR	LYQTD	3		689.034219	2064.079257	0.000451244	32	N	124	143
Q9Z2U0	Exosome	KLVIK	ALLEVVQSGGK	NIELA	2		550.81966	1099.62372	0.000622848	14	N	193	204
Q9Z2U0	Exosome	DGTPR	LYQTDPSGTYHAWK	ANAIG	2		833.8971587	1665.778717	0.000451244	32	N	143	157
Q9Z2U0	Exosome	DGTPR	LYQTDPSGTYHAWK	ANAIG	3		556.2673725	1665.778717	0.00091018	10	N	143	157
Q9Z2U0	Exosome	CQSHR	LTVEDPVTVEYITR	YIASL	2		817.9359496	1633.856299	0.000451244	25	N	95	109
Q9Z2U0	Exosome	RTVRK	ICALDDNVCMAFAGLTADAR	IVINR	2	C2:+57.021,C9:+57.021	1092.497809	2182.980017	0.001329271	4	N	61	81
Q9Z2U0	Exosome	PFGIS	ALIVGFDFDGTPR	LYQTD	2		704.3675057	1406.719411	0.000451244	4	N	130	143
Q9Z2U0	Parental	MSYDR	AITVFSPDGHLFQVEYAQEAVKK	GSTAV	3		859.7836287	2576.327486	0.000451244	6	N	5	28
Q9Z2U0	Parental	MSYDR	AITVFSPDGHLFQVEYAQEAVKK	GSTAV	4		645.0896715	2576.327486	0.001162105	3	N	5	28
Q9Z2U0	Parental	QSNGR	RPFGISALIVGFDFDGTPR	LYQTD	3		689.034219	2064.079257	0.000823681	1	N	124	143
Q9Z2U0	Parental	DGTPR	LYQTDPSGTYHAWK	ANAIG	2		833.8971587	1665.778717	0.002884417	1	N	143	157
Q9Z2U1	Exosome	QCDAR	AIGSASEGAQSSLQEVYHK	SMTLK	2		981.4823153	1960.949031	0.000451244	41	N	168	187

Protein	Sample	Left Context	Peptide	Right Context	Charge	Mods	m/z	MW	Min FDR	Spectral Count	Shared	Start	End
Q9Z2U1	Exosome	QCDAR	AIGSASEGAQSSLQEVYHK	SMTLK	3		654.6574769	1960.949031	0.000451244	27	N	168	187
Q9Z2U1	Exosome	SPEGR	LFQVEYAIEAIK	LGSTA	2		712.3957319	1422.775864	0.000451244	36	N	20	32
Q9Z2U1	Exosome	SPEGR	LFQVEYAIEAIK	LGSTA	3		475.2664213	1422.775864	0.001871652	1	N	20	32
Q9Z2U1	Exosome	GAMSR	PFGVALLFGGVDEK	GPQLF	2		724.8933564	1447.771113	0.000451244	13	N	135	149
Q9Z2U1	Exosome	IEAIK	LGSTAIGIQTSEGVCLAVEK	RITSP	2	C15:+57.021	1017.033095	2032.05059	0.000451244	8	N	32	52
Q9Z2U1	Exosome	HMFTK	EELEEVIKDI	-	2		608.8195227	1215.623445	0.001329271	8	N	231	241
Q9Z2U1	Parental	QCDAR	AIGSASEGAQSSLQEVYHK	SMTLK	2		981.4823153	1960.949031	0.000451244	29	N	168	187
Q9Z2U1	Parental	SPEGR	LFQVEYAIEAIK	LGSTA	2		712.3957319	1422.775864	0.000451244	32	N	20	32
Q9Z2W0	Exosome	DLMVR	NDSPCGTTIGPILASR	LGLRV	2	C5:+57.021	829.9122515	1657.808903	0.000451244	17	N	406	422
Q9Z2W0	Exosome	MHSIR	ETACTTGVLQTLTLFK	GFFEL	2	C4:+57.021	891.9692352	1781.92287	0.000451244	31	N	441	457
Q9Z2W0	Exosome	LTLFK	GFFELFPSVSR	NLLVD	2		643.3329346	1284.650269	0.000451244	26	N	457	468
Q9Z2W0	Exosome	YFLTR	NSSSIIAFAVGGQYVPGNGFSLIGAHTDSPCLR	VKRKS	3	C31:+57.021	1131.56162	3391.661459	0.000451244	22	N	66	99
Q9Z2W0	Exosome	IHLQR	NINENFGPNTEIHLVPILATAVQEELEK	GTPEP	3		1044.879097	3131.613892	0.000451244	42	N	171	199
Q9Z2W0	Exosome	IFAPR	LDNLHSCFCALQALIDSCASPASLAR	DPHVR	3	C7:+57.021,C9:+57.021,C18:+57.021	964.1263924	2889.355777	0.000451244	32	N	260	286
Q9Z2W0	Exosome	DPHVR	MVTLYDNEEVGSESAQGAQSLLTELILR	RISAS	3		1022.848698	3065.522695	0.000451244	14	N	291	319
Q9Z2W0	Exosome	RKSRR	SQVGYHQVGVETYGGGIWSTWFDR	DLTLA	3		910.430137	2728.267011	0.002663018	1	N	106	130
Q9Z2W0	Exosome	RKSRR	SQVGYHQVGVETYGGGIWSTWFDRDLTLAGR	VIIKC	4		864.6751624	3454.66945	0.000662267	3	N	106	137
Q9Z2W0	Exosome	GVETY	GGGIWSTWFDRDLTLAGR	VIIKC	3		670.0065518	2006.996255	0.001395409	1	N	119	137
Q9Z2W0	Parental	IHLQR	NINENFGPNTEIHLVPILATAVQEELEK	GTPEP	3		1044.879097	3131.613892	0.000451244	16	N	171	199
Q9Z2W0	Parental	IFAPR	LDNLHSCFCALQALIDSCASPASLAR	DPHVR	3	C7:+57.021,C9:+57.021,C18:+57.021	964.1263924	2889.355777	0.000451244	2	N	260	286
Q9Z2X1	Exosome	DPEGK	ITGEAFVQFASQELAEK	ALGKH	2		934.4759703	1866.936341	0.000451244	34	N	150	167
Q9Z2X1	Exosome	DPEGK	ITGEAFVQFASQELAEK	ALGKH	3		623.3199135	1866.936341	0.000451244	3	N	150	167
Q9Z2X1	Exosome	EIVQF	FSGLEIVPNGITLPVDPEGK	ITGEA	2		1041.560034	2081.104469	0.000451244	7	N	130	150
Q9Z2X1	Exosome	GLPYK	ATENDIYNFFSPLNPVR	VHIEI	2		998.9923189	1995.969038	0.000451244	46	Y	299	316
Q9Z2X1	Exosome	GLPYK	ATENDIYNFFSPLNPVR	VHIEI	3		666.3308126	1995.969038	0.000451244	28	Y	299	316
Q9Z2X1	Exosome	LDRMR	SGAYSAGYGGYEEYSGLSDGYGFTTDLFGR	DLSYC	3		1049.788384	3146.341752	0.000451244	5	N	232	262
Q9Z2X1	Exosome	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	3	C6:+57.021,C18:+57.021	1265.262979	3792.765538	0.002663018	1	N	16	49
Q9Z2X1	Exosome	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	4	C6:+57.021,C18:+57.021	949.1991845	3792.765538	0.001162105	5	N	16	49
Q9Z2X1	Exosome	FGCTK	EEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	2		1414.242362	2826.469125	0.000451244	37	N	124	150
Q9Z2X1	Exosome	FGCTK	EEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	3		943.164175	2826.469125	0.000451244	16	N	124	150
Q9Z2X1	Exosome	FVRLR	GLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	3	C6:+57.021	1229.971174	3686.890122	0.000451244	16	N	116	150
Q9Z2X1	Exosome	TREGR	QSGEAFVELESEDDVK	LALKK	2		891.4079503	1780.800301	0.000622848	13	N	52	68
Q9Z2X1	Exosome	EYSGL	SDGYGFTTDLFGR	DLSYC	2		718.3285775	1434.641555	0.000451244	5	N	249	262
Q9Z2X1	Parental	DPEGK	ITGEAFVQFASQELAEK	ALGKH	2		934.4759703	1866.936341	0.000451244	30	N	150	167
Q9Z2X1	Parental	DPEGK	ITGEAFVQFASQELAEK	ALGKH	3		623.3199135	1866.936341	0.000451244	33	N	150	167
Q9Z2X1	Parental	CVHMR	GLPYKATENDIYNFFSPLNPVR	VHIEI	3		852.4363404	2554.285621	0.001329271	2	N	294	316
Q9Z2X1	Parental	EIVQF	FSGLEIVPNGITLPVDPEGK	ITGEA	2		1041.560034	2081.104469	0.000451244	42	N	130	150
Q9Z2X1	Parental	GLPYK	ATENDIYNFFSPLNPVR	VHIEI	2		998.9923189	1995.969038	0.000451244	68	Y	299	316
Q9Z2X1	Parental	GLPYK	ATENDIYNFFSPLNPVR	VHIEI	3		666.3308126	1995.969038	0.000451244	36	Y	299	316
Q9Z2X1	Parental	LDRMR	SGAYSAGYGGYEEYSGLSDGYGFTTDLFGR	DLSYC	3		1049.788384	3146.341752	0.000451244	45	N	232	262
Q9Z2X1	Parental	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	3	C6:+57.021,C18:+57.021	1265.262979	3792.765538	0.000451244	40	N	16	49
Q9Z2X1	Parental	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	4	C6:+57.021,C18:+57.021	949.1991845	3792.765538	0.000451244	16	N	16	49
Q9Z2X1	Parental	FGCTK	EEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	2		1414.242362	2826.469125	0.000451244	30	N	124	150
Q9Z2X1	Parental	FGCTK	EEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	3		943.164175	2826.469125	0.000451244	28	N	124	150
Q9Z2X1	Parental	FVRLR	GLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	3	C6:+57.021	1229.971174	3686.890122	0.000451244	33	N	116	150
Q9Z2X1	Parental	FVRLR	GLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK	ITGEA	4	C6:+57.021	922.7303304	3686.890122	0.000451244	7	N	116	150
Q9Z2X1	Parental	RGLPW	SCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	3	C2:+57.021,C14:+57.021	1114.183778	3339.527933	0.000451244	20	N	20	49
Q9Z2X1	Parental	RIGHR	YIEVFKSSQEEVR	SYSDP	2		807.4126416	1612.809683	0.001943752	1	N	179	192
Q9Z2X1	Parental	TREGR	QSGEAFVELESEDDVK	LALKK	2		891.4079503	1780.800301	0.000451244	18	N	52	68
Q9Z2X1	Parental	RSGAY	SAGYGGYEEYSGLSDGYGFTTDLFGR	DLSYC	2		1385.101709	2768.187817	0.000451244	28	N	236	262
Q9Z2X1	Parental	EYSGL	SDGYGFTTDLFGR	DLSYC	2		718.3285775	1434.641555	0.000451244	11	N	249	262
Q9Z2X1	Parental	KLRGL	PWSCSIEDVQNFLSDCTIHDGVAGVHFIYTR	EGRQS	4	C4:+57.021,C16:+57.021	906.6728025	3622.66001	0.001943752	2	N	18	49
Q9Z2X1	Parental	RGLPY	KATENDIYNFFSPLNPVR	VHIEI	2		1063.0398	2124.064001	0.002080925	2	N	298	316
Q9Z2X1	Parental	LNPVR	VHIEIGPDGR	VTGEA	2		546.7939765	1091.572353	0.001763695	4	Y	316	326
Q9Z2X1	Parental	GLPYK	ATENDIYNFFSPLNPVRV	HIEIG	2		1048.526526	2095.037452	0.000451244	5	Y	299	317
Q9Z2X1	Parental	MYDHR	YGDSEFTVQSTTGHCVH	MRGLP	2	C15:+57.021	962.9104372	1923.805274	0.000823681	1	N	275	292
Q9Z2X1	Parental	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHFIYT	REGRQ	3	C6:+57.021,C18:+57.021	1213.229276	3636.664427	0.000622848	4	N	16	48
Q9Z2X1	Parental	VVKLR	GLPWSCSIEDVQNFLSDCTIHDGVAGVHF	IYTRE	3	C6:+57.021,C18:+57.021	1087.497585	3259.469355	0.000823681	4	N	16	45
Q9Z315	Parental	LYSAR	DLQGLTVEHAIDSFREGETVVLTLK	DKGVL	3		924.1594239	2769.454872	0.000662267	2	N	252	277
Q9Z315	Parental	LGKIK	TLGEDDPWLDDTAAWIER	SRQLQ	2		1051.98743	2101.959261	0.000451244	4	N	188	206

Protein relative quantitation by Spectral counting

Proteins identified in the 3 comparisons: (1) exosomes (inflammatory vs. conventional), (2) MDSC (inflammatory vs. conventional) and (3) MDSC vs. exosomes obtained by performing global parsimony. Ratios from spectral counts (Rsc) were included for each comparison with their FDR. Statistically significant differences in abundance correspond to observed fold-change ≥ 2 (Rsc ≥ 1 or Rsc ≤ -1) and Fisher's Exact test FDR ≤ 5%.

Note: All proteins were identified with spectra FDR ≤ 0.31% achieving a protein FDR < 1% in all cases. Prot. Cov. % is the protein coverage. NA – not applicable

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
A0A075B5R8	Protein Ighv11-2 (Fragment)	36	-4.8	1.40E-08	NA	NA	NA	36	-4.5	5.80E-08
A0A075B5U4	Protein Ighv1-18	39	-0.8	1.00E+00	NA	NA	NA	39	-1.8	3.60E-01
A0A087WR50	Fibronectin	61	1	1.80E-72	30	2.4	1.30E-37	62	-3.2	#######
A0A087WSP5	Signal transducer and activator of transcription	8	1	1.70E-01	8	0.4	5.80E-01	8	0.8	5.00E-02
A0A0B4J1J5	Protein Ighv9-3 (Fragment)	27	3.2	2.40E-03	NA	NA	NA	33	-2.7	4.00E-03
A0A0D9SEG8	Protein Adgre5	16	0.4	2.80E-01	15	-1.2	9.30E-05	20	0.9	3.20E-05
A2AFG7	Neural cell adhesion molecule L1	6	-1.3	1.80E-01	12	-5	1.10E-10	12	0.6	1.30E-01
A2AIV8	Caspase recruitment domain-containing protein 9	5	0.9	3.90E-01	16	1	3.90E-02	16	2.5	3.00E-08
A2AN08	E3 ubiquitin-protein ligase UBR4	3	3.1	1.80E-04	5	1.2	3.10E-02	6	0.9	1.90E-02
A2AQ07	Tubulin beta-1 chain	21	-0.8	4.90E-02	42	-0.3	6.00E-01	44	0.3	1.20E-01
A2ASS6	Titin	0	-0.8	1.00E+00	NA	NA	NA	0	-0.9	8.20E-01
A2AUR7	Ras suppressor protein 1	46	-0.5	4.40E-01	63	1.1	4.10E-04	63	0.5	1.70E-02
A6H630	Protein-glutamate O-methyltransferase	16	2.3	4.70E-03	NA	NA	NA	16	-4.1	6.00E-06
A6X935	Inter alpha-trypsin inhibitor, heavy chain 4	12	-2.8	2.00E-11	4	-1.9	4.00E-01	12	-4.1	2.70E-17
A6ZI44	Fructose-bisphosphate aldolase	65	0	4.60E-01	51	1.2	5.60E-28	70	-1.7	#######
A6ZI46	Fructose-bisphosphate aldolase	35	-0.3	4.20E-03	NA	NA	NA	38	-1.3	2.70E-51
A8E0Y8	Immunoglobulin superfamily member 2	5	-2.1	5.20E-01	3	-1.5	6.90E-01	6	-0.4	#######
B1AZI6	THO complex subunit 2	2	1.8	1.90E-01	NA	NA	NA	4	-1.2	5.20E-01
B2RPV6	Multimerin-1	2	-0.9	8.70E-01	2	0.2	8.40E-01	2	0.6	2.40E-01
B2RQC6	CAD protein	6	3.7	1.80E-04	7	2	1.90E-03	8	0.8	7.80E-02
B2RV77	MCG130182, isoform CRA_a	44	1.3	1.70E-03	61	2.6	1.80E-29	61	1.8	6.90E-23
B2RXR6	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B	7	0.9	2.00E-01	16	0.1	8.90E-01	19	1.4	5.30E-05
B2RY50	Armadillo repeat-containing protein 4	4	0.2	8.30E-01	NA	NA	NA	4	-1.8	3.60E-01
B5THE2	Maltase-glucoamylase	11	0.4	1.80E-01	11	-1.6	3.70E-06	13	-0.3	1.80E-01
B9EJ54	MCG21756, isoform CRA_b	2	1.1	5.00E-01	3	1.9	2.30E-01	4	0.7	6.40E-01
D3YVV0	Protein Ttc13	5	1.1	5.00E-01	NA	NA	NA	5	-1.4	6.80E-01
D3Z6Q9	Bridging integrator 2	25	-0.7	1.10E-02	22	0.2	5.80E-01	26	0	#######
D4AFX7	Protein Dnajc13	1	2	1.20E-01	6	0.4	5.00E-01	6	2.6	2.10E-06
E9PUM5	Protein Gm4788	5	-2.6	1.40E-01	NA	NA	NA	5	-2.3	1.00E-01
E9PV24	Fibrinogen alpha chain	32	0.2	1.40E-01	30	-0.5	1.70E-01	33	-1.4	1.50E-27
E9PVA8	Protein Gcn1l1	2	1.5	3.10E-01	2	2.2	1.50E-02	3	2.1	3.90E-03
E9PX59	Sterile alpha motif domain-containing protein 9-like	4	1.5	3.10E-01	7	2.2	1.40E-01	10	0.6	6.70E-01
E9PYK3	Protein Parp4	4	-0.7	1.00E+00	NA	NA	NA	4	-1.5	3.20E-01
E9PZF0	Nucleoside diphosphate kinase	25	0.7	1.50E-01	19	1.8	2.50E-02	25	-1	3.00E-02
E9Q070	Uncharacterized protein	48	0.6	4.90E-02	59	0.5	2.70E-02	59	1.3	6.70E-17
E9Q0F0	Protein Krt78	1	-3.8	5.00E-04	NA	NA	NA	1	-3.5	6.10E-04
E9Q0K6	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	44	-0.2	6.60E-01	27	0.6	1.90E-02	45	-1	2.90E-12
E9Q0Y4	Signal-induced proliferation-associated protein 1	6	2.6	2.80E-02	15	0.1	8.70E-01	19	1.5	6.70E-03

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
E9Q397	Spectrin beta chain, erythrocytic	42	-2.8	2.80E-155	24	-6.8	5.40E-67	43	-2.2	#######
E9Q586	Dynactin subunit 1	8	1.3	5.40E-02	13	0	1.00E+00	14	0.5	2.90E-01
E9Q604	Integrin alpha-M	45	-0.8	4.00E-16	46	-1.1	1.10E-36	55	0.2	1.60E-02
E9Q6Q4	Protein Rap1gds1	10	1.8	1.90E-01	9	2.4	1.80E-02	18	1.4	6.00E-02
E9Q6U4	Prefoldin subunit 4	21	0.8	9.00E-02	21	0.3	7.80E-01	21	-1.4	7.50E-04
E9QL65	Conserved oligomeric Golgi complex subunit 3	6	2	1.20E-01	NA	NA	NA	6	0.7	4.20E-01
E9QNN1	ATP-dependent RNA helicase A	12	0.9	2.10E-03	16	0.4	1.80E-01	19	0.5	3.90E-03
E9QPU1	von Willebrand factor	32	-0.5	6.40E-06	17	0.5	3.10E-02	34	-2.3	#######
F6RPJ9	Insulin-degrading enzyme (Fragment)	6	-1.4	2.10E-01	NA	NA	NA	6	-3	3.70E-04
F6ZDS4	Nucleoprotein TPR	2	-1.5	6.80E-01	11	-0.5	1.40E-01	11	4.4	6.40E-32
F8VPN4	Protein Agl	3	1.1	1.90E-01	NA	NA	NA	4	-1.7	3.90E-02
F8WI35	Histone H3	31	-0.5	4.90E-07	32	-1.3	3.20E-31	32	-0.5	1.50E-11
G3UWD6	Glucose-6-phosphate 1-dehydrogenase	18	0.2	1.80E-01	NA	NA	NA	18	-0.9	5.30E-11
G3X8U3	MCG6895	22	2.6	9.20E-05	NA	NA	NA	22	-4.8	1.10E-09
G3X972	Protein Sec24c	6	1.5	1.00E-01	NA	NA	NA	6	-2	2.50E-02
G5E870	E3 ubiquitin-protein ligase TRIP12	2	2	1.20E-01	3	0.3	7.80E-01	3	1.4	5.10E-02
G5E8K5	Ankyrin-3	1	-1.2	1.00E+00	NA	NA	NA	1	-2.1	1.90E-01
O08528	Hexokinase-2	7	3.3	1.40E-03	10	0.2	8.40E-01	14	0.5	3.20E-01
O08553	Dihydropyrimidinase-related protein 2	10	1.6	3.90E-02	6	1.7	1.60E-01	13	-1.1	1.20E-01
O08582	GTP-binding protein 1	6	1.5	2.10E-02	13	-0.5	6.40E-01	13	0.3	4.50E-01
O08583	THO complex subunit 4	22	0.2	5.00E-01	38	-0.5	9.00E-02	38	1.4	3.50E-10
O08585	Clathrin light chain A	14	-0.1	9.20E-01	21	-0.8	5.50E-02	21	1.2	5.80E-05
O08663	Methionine aminopeptidase 2	26	1	2.20E-02	34	0.1	8.40E-01	36	-0.3	4.70E-01
O08691	Arginase-2, mitochondrial	15	1.7	9.60E-02	NA	NA	NA	15	-3	8.10E-03
O08692	Neutrophilic granule protein	57	0.3	1.40E-04	75	-0.8	2.10E-78	76	1.5	#######
O08709	Peroxiredoxin-6	50	-0.2	7.30E-01	54	-0.2	4.70E-01	54	0.2	1.30E-01
O08738	Caspase-6	20	3.3	2.80E-05	10	2.6	5.30E-02	20	-1.8	1.90E-03
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	29	0.3	1.80E-01	18	-0.7	8.00E-02	29	-0.7	1.50E-03
O08795	Glucosidase 2 subunit beta	12	0	8.40E-01	14	-1	9.20E-03	22	2	1.70E-09
O08808	Protein diaphanous homolog 1	13	-0.4	5.60E-01	10	0.3	3.30E-01	14	0.1	6.10E-01
O08810	116 kDa U5 small nuclear ribonucleoprotein component	24	1.2	1.50E-05	22	-0.3	4.30E-01	29	0.3	7.90E-02
O08917	Flotillin-1	7	1.8	1.90E-01	22	0	1.00E+00	22	4	1.30E-19
O08992	Syntenin-1	50	0.6	2.10E-03	14	-0.6	5.30E-01	50	-2.9	1.50E-41
O09043	Napsin-A	22	0.6	8.60E-02	22	0.5	2.40E-01	30	0	8.90E-01
O09061	Proteasome subunit beta type-1	49	-0.8	8.60E-05	34	1.5	2.00E-03	49	-2.1	1.50E-27
O09106	Histone deacetylase 1	16	1.4	5.40E-02	11	-0.7	2.60E-01	16	1.1	4.00E-03
O09110	Dual specificity mitogen-activated protein kinase kinase 3	12	2.4	4.50E-02	12	2.4	9.10E-04	12	1.8	1.40E-03
O09126	Semaphorin-4D	5	-1.1	4.60E-01	NA	NA	NA	5	-3.7	1.60E-04
O09131	Glutathione S-transferase omega-1	27	3.6	3.10E-04	12	2.2	1.40E-01	27	-1.5	3.10E-02
O09159	Lysosomal alpha-mannosidase	17	-0.5	7.60E-02	17	-1.7	6.70E-07	23	-1.1	5.60E-11
O09172	Glutamate--cysteine ligase regulatory subunit	28	0.1	6.40E-01	23	0.1	8.90E-01	28	-0.4	2.80E-01
O35218	Cleavage and polyadenylation specificity factor subunit 2	3	1.1	5.00E-01	8	-2.5	1.30E-01	8	0.9	4.40E-01
O35286	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	12	2.3	5.10E-05	10	1.2	9.10E-02	15	-0.8	6.10E-02
O35343	Importin subunit alpha-3	18	-0.1	9.20E-01	23	-0.5	2.50E-01	23	0	9.90E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
O35344	Importin subunit alpha-4	17	1.4	4.10E-02	21	-0.3	1.00E+00	27	0.1	8.90E-01
O35350	Calpain-1 catalytic subunit	39	-0.2	8.60E-01	36	0.1	7.20E-01	44	-0.6	5.90E-06
O35381	Acidic leucine-rich nuclear phosphoprotein 32 family member A	20	0.3	5.20E-01	47	0.7	9.00E-04	47	3.3	1.90E-50
O35459	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	11	0.6	3.10E-01	NA	NA	NA	11	-4.6	1.50E-08
O35598	Disintegrin and metalloproteinase domain-containing protein 10	14	-0.6	4.60E-01	NA	NA	NA	14	-5.5	7.30E-16
O35638	Cohesin subunit SA-2	7	1.4	2.90E-02	NA	NA	NA	7	-3.7	3.90E-07
O35639	Annexin A3	45	0.3	7.80E-02	49	0.7	2.40E-04	49	-0.1	8.70E-01
O35643	AP-1 complex subunit beta-1	30	-0.4	1.50E-01	23	0.1	6.50E-01	30	-0.7	2.50E-07
O35737	Heterogeneous nuclear ribonucleoprotein H	15	0.6	4.90E-02	35	0.2	3.20E-01	35	1.3	8.20E-18
O35744	Chitinase-like protein 3	65	0.4	5.10E-03	65	-0.1	5.60E-01	72	0.8	3.70E-20
O35841	Apoptosis inhibitor 5	27	0.5	1.80E-01	28	0.4	2.40E-01	28	0.5	3.10E-02
O35855	Branched-chain-amino-acid aminotransferase, mitochondrial	18	1.8	1.00E-02	NA	NA	NA	18	-3	1.70E-05
O35900	U6 snRNA-associated Sm-like protein LSm2	40	0.2	6.00E-01	40	0.8	1.90E-01	40	-0.1	#######
O35904	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform	6	1.5	3.10E-01	NA	NA	NA	6	-1.8	3.60E-01
O35930	Platelet glycoprotein Ib alpha chain	18	-1.7	3.20E-16	13	1.2	3.60E-02	18	-2.6	5.40E-36
O35955	Proteasome subunit beta type-10	18	0.1	6.60E-01	NA	NA	NA	18	-4.5	5.30E-13
O54774	AP-3 complex subunit delta-1	5	3	6.30E-03	5	-1.3	2.70E-01	7	0.3	6.40E-01
O54824	Pro-interleukin-16	3	-1.7	9.60E-01	6	-0.8	2.20E-01	10	3.9	1.10E-11
O54879	High mobility group protein B3	14	-2.5	4.20E-02	NA	NA	NA	14	-3.2	4.20E-03
O54890	Integrin beta-3	18	-0.3	6.60E-01	11	-0.4	1.00E+00	18	-3.2	2.70E-20
O54990	Prominin-1	4	1.5	3.10E-01	NA	NA	NA	4	-1.8	3.60E-01
O55029	Coatomer subunit beta'	13	2.4	8.70E-05	26	-0.1	9.30E-01	26	1.7	1.70E-11
O55106	Striatin	13	1.9	7.40E-05	16	-0.5	3.50E-01	21	0.1	6.60E-01
O55131	Septin-7	9	-1	4.10E-01	21	1.4	1.10E-02	21	0.8	4.50E-02
O55135	Eukaryotic translation initiation factor 6	47	2	8.70E-06	63	0.1	6.60E-01	63	1	4.20E-06
O55201	Transcription elongation factor SPT5	4	1.1	5.00E-01	12	0.6	3.90E-01	14	3.2	2.20E-06
O55222	Integrin-linked protein kinase	15	0.8	1.70E-01	14	1.2	1.40E-02	15	0.9	9.60E-03
O70138	Neutrophil collagenase	42	-0.1	9.70E-01	32	-0.3	4.20E-01	42	-0.9	1.60E-08
O70145	Neutrophil cytosol factor 2	36	0.7	8.60E-05	35	0.6	3.30E-03	43	-0.2	1.70E-01
O70165	Ficolin-1	13	3.1	4.00E-03	NA	NA	NA	13	-3.4	1.20E-03
O70194	Eukaryotic translation initiation factor 3 subunit D	13	3.4	1.20E-05	13	1.3	3.10E-02	13	0.2	6.50E-01
O70251	Elongation factor 1-beta	38	-0.1	8.90E-01	34	0.4	2.10E-01	51	0.6	2.00E-02
O70310	Glycylpeptide N-tetradecanoyltransferase 1	16	0.2	5.30E-01	11	1.3	3.60E-01	16	-2.8	7.50E-09
O70435	Proteasome subunit alpha type-3	29	-0.4	6.20E-01	9	2.2	1.40E-01	29	-4	2.90E-22
O70497	Ficolin-2	16	-0.3	1.00E+00	16	-0.9	3.60E-01	16	-1.4	6.20E-05
O88307	Sortilin-related receptor	26	0.4	4.70E-03	19	-1.9	1.60E-12	26	-2	5.20E-61
O88342	WD repeat-containing protein 1	61	-0.1	9.90E-01	54	0.7	2.40E-07	66	-0.7	1.20E-20
O88456	Calpain small subunit 1	29	0.7	5.10E-01	NA	NA	NA	29	1	1.50E-01
O88487	Cytoplasmic dynein 1 intermediate chain 2	11	-0.5	1.00E+00	NA	NA	NA	11	-0.5	7.00E-01
O88520	Leucine-rich repeat protein SHOC-2	15	2.4	1.20E-02	10	1.5	1.60E-01	15	-0.3	8.80E-01
O88544	COP9 signalosome complex subunit 4	27	0.4	2.40E-01	16	0	1.00E+00	30	-1.1	3.70E-04
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	47	0.2	3.40E-01	44	-0.1	5.60E-01	50	1.1	3.70E-26
O88593	Peptidoglycan recognition protein 1	50	-0.3	4.10E-02	63	-0.9	1.20E-51	63	2	#######
O88622	Poly(ADP-ribose) glycohydrolase	5	1.1	5.00E-01	NA	NA	NA	5	-1.4	6.80E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
O88685	26S protease regulatory subunit 6A	25	0	8.30E-01	25	0.4	3.20E-01	25	-0.4	1.20E-01
O88712	C-terminal-binding protein 1	12	1.7	2.70E-02	12	-0.1	1.00E+00	12	0.6	2.10E-01
O88783	Coagulation factor V	8	-1.8	1.40E-10	9	-1.4	5.90E-09	11	0.4	2.70E-02
O88842	FYVE, RhoGEF and PH domain-containing protein 3	7	2.2	7.20E-02	12	0.7	3.60E-01	12	1.9	9.10E-04
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	26	0.6	1.10E-01	14	3	6.60E-04	26	-1.8	4.50E-08
O88879	Apoptotic protease-activating factor 1	9	2.5	8.40E-04	7	2.6	1.50E-04	9	0.4	4.20E-01
O88947	Coagulation factor X	9	-1.1	1.00E-01	NA	NA	NA	9	-4.9	7.20E-11
O88958	Glucosamine-6-phosphate isomerase 1	27	-0.5	1.00E+00	NA	NA	NA	27	-4.3	4.10E-07
O88968	Transcobalamin-2	35	-0.9	9.80E-04	37	-1.4	1.70E-06	37	-0.3	2.10E-01
O89023	Tripeptidyl-peptidase 1	17	-0.1	8.80E-01	NA	NA	NA	17	1.1	1.50E-03
O89051	Integral membrane protein 2B	21	0.9	1.90E-01	NA	NA	NA	21	-2.3	4.60E-04
O89053	Coronin-1A	47	0.9	7.50E-14	39	1	3.20E-13	50	-0.5	1.50E-08
O89079	Coatomer subunit epsilon	17	1.4	3.40E-03	33	-0.6	2.40E-01	33	0.6	3.80E-02
O89086	RNA-binding protein 3	22	0.3	4.10E-01	22	0.8	2.70E-03	22	1.4	4.40E-11
P00375	Dihydrofolate reductase	18	2.2	7.20E-02	NA	NA	NA	18	-2.5	5.50E-02
P00493	Hypoxanthine-guanine phosphoribosyltransferase	44	0.2	4.30E-01	35	0.9	7.40E-02	47	-0.9	1.30E-03
P01027	Complement C3	51	-0.9	3.60E-31	39	-1.1	3.80E-20	54	-1.2	4.60E-69
P01029	Complement C4-B	21	2.6	4.00E-22	2	0.3	8.00E-01	21	-3.4	4.30E-37
P01326	Insulin-2	35	-0.2	7.10E-01	34	-4.3	2.70E-06	35	-3.1	6.10E-33
P01639	Ig kappa chain V-V region MOPC 41	28	2.6	4.90E-03	NA	NA	NA	28	-3.8	8.60E-05
P01723	Ig lambda-1 chain V region	48	0.6	6.00E-01	NA	NA	NA	48	-2.1	1.90E-01
P01786	Ig heavy chain V region MOPC 47A	21	-3.9	2.30E-04	NA	NA	NA	21	-3.6	3.20E-04
P01812	Ig heavy chain V region MOPC 173	21	1.7	9.60E-02	NA	NA	NA	21	-3	8.10E-03
P01837	Ig kappa chain C region	45	-0.1	9.40E-01	NA	NA	NA	45	-2.9	9.70E-13
P01868	Ig gamma-1 chain C region secreted form	25	0.1	7.10E-01	NA	NA	NA	25	-4.1	1.30E-09
P01872	Ig mu chain C region	53	-0.8	3.60E-07	NA	NA	NA	53	-6	#######
P01878	Ig alpha chain C region	11	-4	1.10E-04	NA	NA	NA	11	-3.7	1.60E-04
P01887	Beta-2-microglobulin	19	-0.4	1.00E+00	19	-0.7	1.50E-01	19	1.7	2.00E-07
P01900	H-2 class I histocompatibility antigen, D-D alpha chain	7	-0.5	1.00E+00	NA	NA	NA	10	-1.9	4.10E-02
P01921	H-2 class II histocompatibility antigen, A-D beta chain	14	1.8	1.90E-01	NA	NA	NA	14	-2.1	1.90E-01
P01942	Hemoglobin subunit alpha	80	-1.9	1.30E-95	79	-2.3	1.90E-35	80	-1.9	#######
P02088	Hemoglobin subunit beta-1	95	-1.7	2.90E-118	95	-3.6	7.80E-55	95	-2.6	#######
P02089	Hemoglobin subunit beta-2	86	-1.6	8.70E-84	85	-3.2	4.50E-37	86	-2.8	#######
P02535	Keratin, type I cytoskeletal 10	6	-2.5	4.20E-02	NA	NA	NA	6	-3.2	4.20E-03
P04104	Keratin, type II cytoskeletal 1	4	-0.4	1.00E+00	NA	NA	NA	4	-1.7	9.10E-05
P04202	Transforming growth factor beta-1	32	-0.6	1.10E-01	10	0	9.90E-01	32	-2.1	8.40E-14
P04228	H-2 class II histocompatibility antigen, A-D alpha chain	26	3	6.30E-03	NA	NA	NA	26	-2.4	1.30E-02
P04919	Band 3 anion transport protein	29	-2.8	7.50E-94	23	-3.6	2.70E-32	29	-1.9	1.10E-61
P05201	Aspartate aminotransferase, cytoplasmic	25	-0.5	2.70E-01	18	2.3	9.80E-06	25	-1.3	1.20E-07
P05202	Aspartate aminotransferase, mitochondrial	34	0.1	5.70E-01	26	-0.5	1.20E-01	40	-0.2	5.10E-01
P06151	L-lactate dehydrogenase A chain	56	-0.2	2.50E-01	55	1.2	1.20E-12	64	-1.2	8.60E-41
P06336	Ig epsilon chain C region	11	-1.4	2.10E-01	NA	NA	NA	11	-3.9	4.50E-05
P06745	Glucose-6-phosphate isomerase	61	-0.4	6.40E-06	43	1.4	1.20E-22	61	-1.5	5.90E-94
P06800	Receptor-type tyrosine-protein phosphatase C	13	0.4	2.00E-01	28	-1.3	1.60E-23	28	2.2	1.30E-68

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P06909	Complement factor H	15	-2.2	1.60E-06	NA	NA	NA	15	-5.5	1.90E-16
P07356	Annexin A2	51	0.1	4.60E-01	63	0	1.00E+00	63	0.6	1.90E-13
P07607	Thymidylate synthase	9	2.2	7.20E-02	NA	NA	NA	13	-1.7	1.90E-01
P07724	Serum albumin	59	-1.2	5.80E-53	55	-0.2	2.10E-02	65	0.5	1.60E-18
P07742	Ribonucleoside-diphosphate reductase large subunit	19	1.7	7.50E-06	11	1.3	1.40E-02	19	-1	4.00E-04
P07759	Serine protease inhibitor A3K	24	-1.7	1.00E-05	31	-2	1.70E-07	31	0.1	7.40E-01
P07901	Heat shock protein HSP 90-alpha	29	-0.3	5.60E-01	37	0.2	2.00E-01	42	1.3	4.10E-21
P08003	Protein disulfide-isomerase A4	22	-0.5	2.90E-01	25	-1.2	1.00E-02	27	-0.9	2.20E-04
P08030	Adenine phosphoribosyltransferase	83	1.2	9.60E-11	43	1.4	2.30E-03	83	-2.5	9.70E-49
P08032	Spectrin alpha chain, erythrocytic 1	57	-2.8	2.40E-307	31	-5.6	1.00E-105	58	-2.4	#######
P08071	Lactotransferrin	73	-0.9	1.30E-216	73	-1.4	0.00E+00	76	-0.7	#######
P08103	Tyrosine-protein kinase HCK	16	3.4	8.40E-04	14	-0.5	4.70E-01	16	1.6	7.60E-05
P08113	Endoplasmin	26	-0.5	2.90E-01	35	-0.7	2.60E-07	38	2.5	1.10E-73
P08226	Apolipoprotein E	23	0.2	5.60E-01	18	-1.1	4.60E-01	23	-2.8	5.90E-13
P08228	Superoxide dismutase [Cu-Zn]	36	-1.3	1.30E-02	36	1.1	2.10E-02	36	0.2	4.30E-01
P08249	Malate dehydrogenase, mitochondrial	39	-0.2	9.90E-01	42	0.1	7.20E-01	42	0.2	1.90E-01
P08556	GTPase NRas	22	2.2	7.20E-02	22	-0.4	6.40E-01	22	2.5	8.50E-07
P08607	C4b-binding protein	24	4.2	4.20E-41	8	1.9	2.30E-01	24	-5.4	4.30E-57
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	40	1.4	5.30E-04	54	-0.8	1.70E-17	54	3.7	#######
P08775	DNA-directed RNA polymerase II subunit RPB1	3	1.8	1.90E-01	3	-0.5	8.60E-01	4	1.5	3.90E-02
P08905	Lysozyme C-2	51	-0.4	3.20E-02	51	-2.4	2.60E-144	51	1.3	1.30E-73
P09055	Integrin beta-1	13	-1.3	1.90E-02	NA	NA	NA	13	-3.5	3.20E-10
P09103	Protein disulfide-isomerase	44	-0.1	1.00E+00	52	-0.5	2.50E-05	56	0.7	2.20E-15
P09405	Nucleolin	25	0.1	6.20E-01	22	-0.1	1.00E+00	28	0.2	2.00E-01
P09411	Phosphoglycerate kinase 1	50	0.3	1.40E-02	45	1.1	1.70E-14	51	-0.6	5.90E-13
P09528	Ferritin heavy chain	35	-1.2	3.30E-02	NA	NA	NA	35	-5.3	2.20E-14
P09581	Macrophage colony-stimulating factor 1 receptor	6	-1	1.40E-01	NA	NA	NA	6	-5	3.70E-11
P0C0S6	Histone H2A.Z	54	0.2	5.90E-03	56	-0.6	9.90E-09	56	-1.4	#######
P0CW02	Lymphocyte antigen 6C1	30	0.8	3.40E-01	46	-5.7	2.10E-17	46	2.2	6.80E-08
P10107	Annexin A1	63	0.3	1.90E-04	69	-0.1	2.90E-01	69	2.1	#######
P10126	Elongation factor 1-alpha 1	54	1.1	2.30E-18	43	1.6	1.90E-48	56	0.4	1.90E-08
P10518	Delta-aminolevulinic acid dehydratase	38	-1.1	1.30E-05	17	-1	5.10E-01	38	-3.7	4.30E-36
P10605	Cathepsin B	38	1.2	4.60E-04	49	-0.7	1.00E-03	52	1.4	1.20E-17
P10639	Thioredoxin	53	-1.5	6.40E-04	60	2.6	1.90E-74	60	3.4	#######
P10649	Glutathione S-transferase Mu 1	20	0.1	5.00E-01	22	2.4	3.20E-11	22	-0.5	8.60E-03
P10810	Monocyte differentiation antigen CD14	28	0	7.50E-01	30	-0.6	2.90E-01	33	0.1	7.70E-01
P10852	4F2 cell-surface antigen heavy chain	22	3.1	4.00E-03	31	0	1.00E+00	31	1.2	1.10E-02
P10853	Histone H2B type 1-F/J/L	26	-1	2.80E-06	25	1.1	1.00E-01	39	-2.9	9.70E-36
P11031	Activated RNA polymerase II transcriptional coactivator p15	26	0.2	5.10E-01	NA	NA	NA	26	-3.1	9.20E-11
P11152	Lipoprotein lipase	11	-3	3.40E-03	NA	NA	NA	11	-3.6	3.20E-04
P11247	Myeloperoxidase	42	0	7.00E-01	40	0.3	1.90E-03	45	0.1	1.80E-01
P11352	Glutathione peroxidase 1	65	0.4	1.10E-01	47	0.3	3.30E-01	66	-0.4	2.90E-02
P11499	Heat shock protein HSP 90-beta	29	0.1	5.00E-01	45	0	9.80E-01	45	2	2.70E-54
P11672	Neutrophil gelatinase-associated lipocalin	38	0.6	1.60E-03	49	-1.5	4.30E-136	49	3.3	#######

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P11680	Properdin	11	0.2	5.40E-01	6	-2.3	6.50E-05	12	-1	1.30E-03
P11835	Integrin beta-2	43	-0.8	3.30E-13	37	-1.5	5.40E-26	45	-0.9	2.60E-24
P11983	T-complex protein 1 subunit alpha	21	0.3	3.10E-01	19	0.5	2.00E-01	25	0.2	5.10E-01
P12023	Amyloid beta A4 protein	7	0.6	2.20E-01	12	-1	3.70E-02	12	0.3	3.30E-01
P12246	Serum amyloid P-component	21	-1.6	4.20E-04	NA	NA	NA	21	-5.6	1.30E-17
P12265	Beta-glucuronidase	18	-0.4	7.40E-01	NA	NA	NA	18	-5.6	6.60E-18
P12382	ATP-dependent 6-phosphofructokinase, liver type	6	3.2	2.40E-03	6	3	1.10E-02	6	-0.3	8.70E-01
P12815	Programmed cell death protein 6	48	1	4.90E-03	37	0.9	1.30E-01	48	-1.4	6.10E-07
P12970	60S ribosomal protein L7a	17	3.1	4.00E-03	14	1.7	5.50E-02	21	0.5	4.50E-01
P13020	Gelsolin	44	-0.8	9.20E-12	46	-0.6	9.80E-07	51	0.2	5.40E-02
P13439	Uridine 5'-monophosphate synthase	10	2	8.70E-03	10	2.8	1.70E-03	10	-0.3	8.20E-01
P13609	Serglycin	18	-1.7	9.60E-01	NA	NA	NA	29	1.7	7.80E-02
P13634	Carbonic anhydrase 1	18	-2.6	1.40E-01	NA	NA	NA	18	-2.3	1.00E-01
P13864	DNA (cytosine-5)-methyltransferase 1	2	1.1	5.00E-01	5	0	1.00E+00	6	3.5	1.80E-08
P14069	Protein S100-A6	65	0.1	4.80E-01	75	0.7	9.90E-05	75	0.2	1.70E-01
P14131	40S ribosomal protein S16	14	2.9	1.00E-02	NA	NA	NA	14	1.1	4.40E-02
P14152	Malate dehydrogenase, cytoplasmic	42	-0.8	1.30E-02	23	0.9	1.20E-01	42	-1.5	6.90E-09
P14206	40S ribosomal protein SA	35	0.6	5.30E-02	38	0.6	8.50E-02	38	-0.3	2.10E-01
P14211	Calreticulin	49	-0.2	3.30E-01	60	-0.6	2.70E-14	60	1.7	########
P14234	Tyrosine-protein kinase Fgr	23	3.8	9.60E-11	30	-0.7	1.40E-03	30	2	1.50E-24
P14685	26S proteasome non-ATPase regulatory subunit 3	24	-0.1	8.50E-01	16	2.3	6.30E-03	26	-1.8	1.80E-07
P14733	Lamin-B1	21	-0.5	2.50E-01	42	-0.7	5.00E-07	42	1.9	1.80E-54
P14824	Annexin A6	27	-0.8	1.70E-04	25	-1.9	9.30E-07	27	-1.5	4.20E-16
P15532	Nucleoside diphosphate kinase A	38	-0.2	1.00E+00	26	1.5	4.20E-03	38	-1.4	8.40E-09
P15864	Histone H1.2	27	0.3	3.80E-02	27	-0.4	2.00E-02	27	-0.3	1.80E-02
P16110	Galectin-3	27	-0.4	2.10E-01	19	-0.8	1.50E-03	27	-0.5	6.10E-04
P16125	L-lactate dehydrogenase B chain	20	-2.2	1.40E-01	NA	NA	NA	20	-2.9	1.50E-02
P16546	Spectrin alpha chain, non-erythrocytic 1	27	-0.8	1.80E-10	36	-0.6	2.10E-08	38	0.4	4.20E-08
P16675	Lysosomal protective protein	11	-0.2	9.80E-01	14	-1.5	1.10E-02	18	0.1	8.20E-01
P16858	Glyceraldehyde-3-phosphate dehydrogenase	64	1.7	4.50E-119	68	2.3	4.50E-192	75	0	8.00E-01
P16879	Tyrosine-protein kinase Fes/Fps	5	1.5	3.10E-01	8	3	1.10E-02	8	1.4	1.10E-01
P17182	Alpha-enolase	58	1.9	8.20E-210	69	2.3	1.70E-221	69	-0.4	5.90E-24
P17426	Isoform B of AP-2 complex subunit alpha-1	20	1.4	8.90E-06	18	2.8	2.60E-04	26	-2.1	8.40E-14
P17427	AP-2 complex subunit alpha-2	20	0.7	1.80E-02	17	0.2	7.50E-01	25	-1.2	4.50E-07
P17563	Selenium-binding protein 1	8	1.5	3.10E-01	NA	NA	NA	8	-1.8	3.60E-01
P17710	Hexokinase-1	12	0.1	5.90E-01	12	0	9.90E-01	16	-0.2	6.70E-01
P17742	Peptidyl-prolyl cis-trans isomerase A	50	0.1	3.10E-01	65	0.5	5.90E-03	65	0	########
P17751	Triosephosphate isomerase	41	0.3	6.90E-02	43	0.7	3.90E-04	43	-0.2	7.10E-02
P17918	Proliferating cell nuclear antigen	12	2.7	1.70E-02	30	0.8	8.70E-02	30	2.6	8.90E-10
P18242	Cathepsin D	20	0.5	2.20E-01	37	-0.1	1.00E+00	37	1.1	3.10E-07
P18337	L-selectin	7	0.1	7.70E-01	NA	NA	NA	7	-3.4	1.20E-03
P18572	Isoform 2 of Basigin	14	-1.7	5.80E-02	19	-3.9	1.80E-04	19	-0.4	6.80E-01
P18653	Ribosomal protein S6 kinase alpha-1	6	2.2	7.20E-02	6	3.7	2.80E-04	6	1.3	4.40E-02
P18760	Cofilin-1	57	0.2	1.50E-01	57	0.6	1.80E-12	57	1.6	########

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P19096	Fatty acid synthase	20	1.2	2.90E-07	15	2.5	1.10E-17	20	-0.5	4.20E-03
P19157	Glutathione S-transferase P 1	33	1.1	6.40E-02	32	1.1	5.30E-01	42	-2.4	3.80E-05
P19221	Prothrombin	8	-1.7	9.60E-01	9	-2.9	4.20E-13	15	4.7	3.40E-21
P19973	Lymphocyte-specific protein 1	38	-0.8	1.50E-01	50	-0.6	3.10E-07	50	3.2	#######
P20029	78 kDa glucose-regulated protein	47	-0.7	1.40E-10	50	-0.5	7.70E-11	52	0.9	3.70E-47
P20060	Beta-hexosaminidase subunit beta	26	-0.5	3.20E-01	26	-0.3	6.40E-01	26	-0.8	4.20E-04
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	32	-0.3	1.00E+00	27	-0.7	2.80E-01	34	0.7	3.40E-02
P20152	Vimentin	48	-0.2	6.70E-01	68	-0.1	5.30E-01	68	3.2	#######
P20918	Plasminogen	22	-4.7	1.40E-13	NA	NA	NA	22	-5.3	8.40E-14
P21107	Tropomyosin alpha-3 chain	22	-0.8	5.10E-02	26	-0.6	1.00E-05	26	1.2	1.60E-24
P21107	Tropomyosin alpha-3 chain	22	-0.8	5.10E-02	26	-0.6	1.00E-05	41	1.2	6.00E-12
P21107	Tropomyosin alpha-3 chain	22	-0.8	5.10E-02	36	-0.6	9.90E-03	26	1.2	1.60E-24
P21107	Tropomyosin alpha-3 chain	22	-0.8	5.10E-02	36	-0.6	9.90E-03	41	1.2	6.00E-12
P21107	Isoform 2 of Tropomyosin alpha-3 chain	38	-0.4	2.80E-01	26	-0.6	1.00E-05	26	1.2	1.60E-24
P21107	Isoform 2 of Tropomyosin alpha-3 chain	38	-0.4	2.80E-01	26	-0.6	1.00E-05	41	1.2	6.00E-12
P21107	Isoform 2 of Tropomyosin alpha-3 chain	38	-0.4	2.80E-01	36	-0.6	9.90E-03	26	1.2	1.60E-24
P21107	Isoform 2 of Tropomyosin alpha-3 chain	38	-0.4	2.80E-01	36	-0.6	9.90E-03	41	1.2	6.00E-12
P21614	Vitamin D-binding protein	16	-1.7	5.90E-04	20	-0.2	9.30E-01	25	-0.2	7.10E-01
P22366	Myeloid differentiation primary response protein MyD88	13	0.6	6.00E-01	NA	NA	NA	13	-1.2	5.20E-01
P22599	Alpha-1-antitrypsin 1-2	14	-2.8	7.30E-02	36	-3.8	6.30E-15	36	3.2	2.10E-13
P22892	AP-1 complex subunit gamma-1	7	0.1	7.40E-01	NA	NA	NA	7	-1.4	8.80E-03
P23116	Eukaryotic translation initiation factor 3 subunit A	7	0.6	1.00E-01	4	1.2	5.30E-02	7	-1.1	5.10E-04
P23249	Putative helicase MOV-10	7	0.8	3.10E-01	NA	NA	NA	7	-3.6	3.20E-04
P23492	Purine nucleoside phosphorylase	45	-0.3	4.40E-01	32	0.8	9.90E-02	45	-2	5.30E-23
P23591	GDP-L-fucose synthase	19	1.3	7.20E-02	11	2.9	1.80E-02	24	-1.2	5.30E-02
P23953	Carboxylesterase 1C	8	-1.3	1.80E-01	10	-1.7	2.00E-01	10	-1	8.40E-02
P24063	Integrin alpha-L	11	0.8	8.20E-02	20	-1.6	3.00E-10	22	1.8	7.10E-17
P24270	Catalase	45	-0.9	2.60E-08	9	-1.3	2.70E-01	45	-4.6	1.20E-88
P24369	Peptidyl-prolyl cis-trans isomerase B	25	-2.1	2.80E-03	20	2.2	1.40E-01	27	-2.1	4.80E-04
P24527	Leukotriene A-4 hydrolase	46	-0.2	5.00E-01	44	2.2	2.40E-23	49	-1.1	1.80E-24
P24549	Retinal dehydrogenase 1	10	-1.8	4.30E-01	NA	NA	NA	10	-0.5	9.50E-01
P25206	DNA replication licensing factor MCM3	6	2	1.20E-01	18	0.3	4.70E-01	20	4.1	1.10E-24
P25444	40S ribosomal protein S2	10	1.2	3.10E-01	9	-0.7	6.90E-01	14	1	1.80E-01
P25911	Tyrosine-protein kinase Lyn	26	1.5	2.50E-06	14	-0.6	4.40E-01	26	-1.6	1.00E-10
P26039	Talin-1	48	-0.3	1.70E-05	49	0.2	2.40E-02	54	0.3	4.80E-08
P26040	Ezrin	21	-0.2	7.50E-01	20	0.8	4.10E-04	23	-0.8	2.90E-10
P26041	Moesin	39	-0.1	9.70E-01	27	0.9	5.70E-07	39	-1.2	1.00E-39
P26043	Radixin	29	0	6.20E-01	18	1.1	6.00E-03	29	-2.1	8.80E-38
P26369	Splicing factor U2AF 65 kDa subunit	18	0.5	2.10E-01	18	-0.5	2.30E-01	18	1	5.30E-05
P26443	Glutamate dehydrogenase 1, mitochondrial	27	-0.1	9.20E-01	20	-0.4	4.30E-01	27	-0.9	3.10E-07
P26450	Phosphatidylinositol 3-kinase regulatory subunit alpha	13	1	8.10E-02	9	0.2	7.60E-01	13	0.2	5.80E-01
P26516	26S proteasome non-ATPase regulatory subunit 7	37	-0.2	1.00E+00	29	0.5	3.20E-01	37	-0.2	5.60E-01
P26638	Serine--tRNA ligase, cytoplasmic	14	2.4	5.30E-04	NA	NA	NA	14	-1	5.50E-02
P26645	Myristoylated alanine-rich C-kinase substrate	21	1.1	5.00E-01	NA	NA	NA	21	-1.4	6.80E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P27005	Protein S100-A8	81	-0.2	2.20E-01	85	2.1	0.00E+00	85	2.5	#######
P27601	Guanine nucleotide-binding protein subunit alpha-13	11	2	1.20E-01	14	-1.1	6.00E-01	14	0.4	7.10E-01
P27612	Phospholipase A-2-activating protein	28	1.9	8.90E-07	NA	NA	NA	28	-5.2	3.80E-23
P27661	Histone H2AX	55	0.4	1.50E-49	55	-0.7	2.00E-149	56	-0.3	1.00E-56
P27773	Protein disulfide-isomerase A3	53	-0.4	6.60E-03	53	-0.5	2.00E-05	56	0.3	2.10E-03
P27784	C-C motif chemokine 6	40	1.5	3.10E-01	NA	NA	NA	40	0	#######
P27870	Proto-oncogene vav	17	1.9	7.40E-05	13	0.6	1.20E-01	17	0.6	2.00E-02
P27931	Interleukin-1 receptor type 2	26	2.3	2.40E-07	12	3.3	2.30E-03	26	-2.3	6.10E-10
P28063	Proteasome subunit beta type-8	21	0.2	5.10E-01	NA	NA	NA	21	-5.3	8.40E-14
P28076	Proteasome subunit beta type-9	17	-0.2	9.50E-01	NA	NA	NA	17	-3.4	3.70E-09
P28271	Cytoplasmic aconitate hydratase	5	2.2	7.20E-02	NA	NA	NA	5	-2.5	5.50E-02
P28293	Cathepsin G	42	1.1	3.10E-05	47	-0.4	1.00E-01	50	0.9	4.30E-10
P28352	DNA-(apurinic or apyrimidinic site) lyase	29	0.2	4.00E-01	11	2.3	6.30E-03	29	-2.5	1.40E-17
P28474	Alcohol dehydrogenase class-3	23	2.6	8.90E-10	10	2.4	8.70E-02	23	-3.5	1.40E-17
P28650	Adenylosuccinate synthetase isozyme 1	35	0.2	3.50E-01	16	0.6	5.40E-01	35	-3.7	2.80E-49
P28656	Nucleosome assembly protein 1-like 1	15	0.9	1.10E-02	20	0.1	7.10E-01	20	0.3	2.50E-01
P28658	Ataxin-10	9	3.3	1.40E-03	10	2	1.10E-02	12	0.5	3.20E-01
P28665	Murinoglobulin-1	19	-1.2	2.10E-05	6	-3.2	3.70E-04	19	-2.9	2.10E-24
P28798	Granulins	31	1	8.00E-07	42	-0.7	1.20E-13	42	1.7	3.00E-81
P28867	Protein kinase C delta type	23	1.7	1.70E-05	15	0.9	1.90E-01	26	-1.5	1.60E-06
P29341	Polyadenylate-binding protein 1	15	-0.4	5.50E-01	18	-0.9	2.20E-02	21	-0.6	1.60E-02
P29351	Tyrosine-protein phosphatase non-receptor type 6	46	0.7	5.50E-07	44	0.7	3.50E-04	46	-0.8	2.10E-13
P29391	Ferritin light chain 1	52	-1.7	1.80E-08	NA	NA	NA	52	-6.6	9.00E-36
P29416	Beta-hexosaminidase subunit alpha	28	-1	7.60E-02	17	-1.1	3.00E-01	33	-1.7	1.10E-05
P29452	Caspase-1	8	2.6	2.80E-02	NA	NA	NA	8	-0.4	9.90E-01
P29621	Serine protease inhibitor A3C	7	-1.5	4.10E-02	7	-0.5	5.40E-01	7	0.5	2.40E-01
P29699	Alpha-2-HS-glycoprotein	26	-0.9	1.20E-02	28	-0.1	1.00E+00	28	-0.1	7.00E-01
P29758	Ornithine aminotransferase, mitochondrial	20	1.1	6.00E-02	8	-0.2	1.00E+00	20	-0.4	5.10E-01
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4	13	2.2	2.80E-02	13	2.2	1.50E-02	13	0.5	4.50E-01
P30681	High mobility group protein B2	40	0.1	5.00E-01	28	0.1	5.40E-01	40	-0.1	7.10E-01
P31725	Protein S100-A9	27	0.7	9.60E-11	63	0.9	8.00E-63	63	1.9	#######
P31750	RAC-alpha serine/threonine-protein kinase	7	0.9	1.50E-01	7	1.4	1.10E-01	7	-0.5	5.10E-01
P31938	Dual specificity mitogen-activated protein kinase kinase 1	12	2.7	3.40E-04	12	1.9	2.30E-01	12	-2.4	1.60E-04
P32067	Lupus La protein homolog	7	1	1.70E-01	13	-0.7	7.00E-01	17	-0.3	8.00E-01
P32921	Tryptophan--tRNA ligase, cytoplasmic	25	2.4	7.10E-09	NA	NA	NA	25	-3.3	1.70E-16
P34022	Ran-specific GTPase-activating protein	28	1.1	1.30E-01	40	0.7	8.80E-02	40	1.9	1.60E-08
P34152	Focal adhesion kinase 1	3	1.1	5.00E-01	NA	NA	NA	3	-1.4	6.80E-01
P34884	Macrophage migration inhibitory factor	44	1.5	6.20E-03	22	3.7	2.80E-04	44	-1.1	9.20E-03
P35123	Ubiquitin carboxyl-terminal hydrolase 4	8	2	1.20E-01	10	1.9	2.00E-03	12	2.5	3.50E-06
P35174	Isoform 2 of Stefin-2	64	1.1	6.30E-04	79	3.7	0.00E+00	79	4.1	#######
P35235	Tyrosine-protein phosphatase non-receptor type 11	9	2.2	7.20E-02	NA	NA	NA	9	-2.5	5.50E-02
P35276	Ras-related protein Rab-3D	21	2.4	4.50E-02	21	0	1.00E+00	21	1.4	1.70E-02
P35343	C-X-C chemokine receptor type 2	10	0.7	4.60E-01	NA	NA	NA	10	-1.8	6.70E-02
P35441	Thrombospondin-1	49	-1.3	9.40E-111	29	-0.2	5.00E-01	49	-3.5	#######

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P35461	Lymphocyte antigen 6G (Fragment)	24	-0.3	1.00E+00	24	-1.8	6.80E-06	24	-0.1	9.40E-01
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	17	2.9	1.00E-02	12	-0.7	4.20E-01	20	1.6	6.80E-04
P35505	Fumarylacetoacetase	21	0.1	6.70E-01	16	2.9	5.70E-05	21	-2	8.70E-13
P35564	Calnexin	14	1.7	1.40E-02	33	-0.9	4.10E-05	33	3.2	1.30E-41
P35585	AP-1 complex subunit mu-1	7	-0.5	1.00E+00	NA	NA	NA	7	-4.3	4.10E-07
P35700	Peroxiredoxin-1	48	-0.8	5.20E-02	50	1.1	1.00E-02	53	-0.4	1.60E-01
P35821	Tyrosine-protein phosphatase non-receptor type 1	8	2.9	1.00E-02	NA	NA	NA	8	-1.8	6.70E-02
P35979	60S ribosomal protein L12	49	1	1.30E-02	44	0	8.90E-01	53	0.9	2.10E-05
P35991	Tyrosine-protein kinase BTK	6	2.2	7.20E-02	NA	NA	NA	6	-2.5	5.50E-02
P36993	Protein phosphatase 1B	11	1.8	1.90E-01	NA	NA	NA	11	-2.1	1.90E-01
P37913	DNA ligase 1	6	1.1	5.00E-01	10	1.7	2.60E-02	10	2.8	7.20E-05
P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	13	2.9	8.00E-04	NA	NA	NA	13	-0.8	2.20E-01
P38647	Stress-70 protein, mitochondrial	9	2.3	4.70E-03	15	0.4	3.20E-01	15	2.2	5.80E-12
P39039	Mannose-binding protein A	32	-4.1	5.10E-05	NA	NA	NA	32	-3.8	8.60E-05
P39054	Dynamin-2	25	0.9	8.20E-03	21	1.1	4.40E-04	26	0.1	4.80E-01
P39654	Arachidonate 15-lipoxygenase	37	0	8.10E-01	35	0.1	6.90E-01	37	-0.5	6.40E-03
P39655	Arachidonate 12-lipoxygenase, 12S-type	32	-1.9	3.50E-14	16	2.3	3.10E-05	32	-1.9	4.50E-17
P40124	Adenylyl cyclase-associated protein 1	62	-0.4	1.30E-04	60	0.8	9.20E-19	67	0	5.80E-01
P40142	Transketolase	54	0.3	1.20E-05	46	1	1.60E-23	55	-1.5	#######
P40240	CD9 antigen	17	-0.1	9.00E-01	NA	NA	NA	17	-6.5	1.70E-32
P41241	Tyrosine-protein kinase CSK	18	1.1	2.10E-02	NA	NA	NA	18	-3.7	8.10E-12
P41245	Matrix metalloproteinase-9	42	-0.9	2.80E-37	48	-1.6	6.50E-92	48	-0.2	2.20E-06
P42208	Septin-2	14	-0.3	1.00E+00	16	1.7	1.60E-01	21	-1.3	3.00E-02
P42227	Signal transducer and activator of transcription 3	17	0.2	4.90E-01	26	1.3	1.20E-02	26	-0.3	5.20E-01
P42232	Signal transducer and activator of transcription 5B	7	2	1.20E-01	NA	NA	NA	7	-1.5	3.20E-01
P42567	Epidermal growth factor receptor substrate 15	4	-2.6	1.40E-01	19	0.2	7.10E-01	19	3.1	4.70E-10
P42669	Transcriptional activator protein Pur-alpha	24	-0.5	6.60E-01	18	-0.2	1.00E+00	35	-1.3	1.10E-03
P42932	T-complex protein 1 subunit theta	14	0.8	4.30E-02	16	0.8	1.60E-02	16	0.7	2.20E-03
P43274	Histone H1.4	26	0.4	2.30E-02	26	-0.5	3.10E-03	26	-0.2	3.90E-02
P43275	Histone H1.1	30	1	3.80E-03	29	-0.4	3.50E-01	30	0.4	7.30E-02
P43276	Histone H1.5	18	0.9	1.90E-03	18	-0.2	6.00E-01	18	0.6	3.70E-04
P43277	Histone H1.3	24	0.5	8.30E-04	26	-0.4	1.70E-02	26	-0.2	5.60E-02
P45376	Aldose reductase	26	1.9	2.80E-05	NA	NA	NA	26	-4.8	1.90E-16
P46467	Vacuolar protein sorting-associated protein 4B	28	1.2	3.60E-02	NA	NA	NA	28	-4.1	2.40E-09
P46471	26S protease regulatory subunit 7	21	-0.3	1.00E+00	18	0.3	7.10E-01	21	-0.6	1.00E-01
P46638	Ras-related protein Rab-11B	19	-0.3	1.00E+00	24	-0.8	2.70E-02	24	0.7	5.30E-03
P46664	Adenylosuccinate synthetase isozyme 2	18	1.1	2.30E-02	9	4	1.60E-05	18	-1	9.80E-03
P47738	Aldehyde dehydrogenase, mitochondrial	56	0.1	4.80E-01	61	-0.4	1.60E-02	64	-0.2	1.50E-02
P47754	F-actin-capping protein subunit alpha-2	53	-0.3	6.60E-01	54	0.2	5.30E-01	59	0.3	7.80E-02
P47757	F-actin-capping protein subunit beta	35	-0.3	5.20E-01	45	0.5	2.80E-02	47	0.3	6.00E-02
P47791	Glutathione reductase, mitochondrial	48	-0.4	5.90E-03	35	0	1.00E+00	51	-1.2	4.50E-31
P47809	Dual specificity mitogen-activated protein kinase kinase 4	17	1.1	1.90E-01	NA	NA	NA	17	-2.1	1.50E-02
P47811	Mitogen-activated protein kinase 14	34	0.5	9.20E-02	24	1.7	2.60E-04	34	-0.8	2.50E-03
P47911	60S ribosomal protein L6	11	1.5	4.70E-03	9	-1.9	4.00E-01	14	-3.4	2.10E-09

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P47941	Crk-like protein	9	1.5	3.10E-01	20	0.6	5.80E-01	29	1.6	4.40E-02
P47955	60S acidic ribosomal protein P1	48	0.6	1.90E-01	68	-0.2	7.60E-01	83	1.5	3.80E-09
P47962	60S ribosomal protein L5	28	2.5	2.10E-04	15	0.6	5.40E-01	28	-0.8	9.90E-02
P47968	Ribose-5-phosphate isomerase	11	-0.6	1.00E+00	11	2.4	8.70E-02	11	-1.1	1.80E-01
P48024	Eukaryotic translation initiation factor 1	37	1.8	1.90E-01	38	-0.1	1.00E+00	38	2.3	2.00E-04
P48025	Tyrosine-protein kinase SYK	9	0.5	3.20E-01	NA	NA	NA	9	-1.7	2.10E-04
P48036	Annexin A5	39	-0.3	5.70E-01	38	-0.5	1.40E-01	41	-0.3	5.30E-02
P48193	Protein 4.1	18	-3.4	1.00E-13	5	-2.7	7.20E-02	18	-3.2	2.30E-13
P48758	Carbonyl reductase [NADPH] 1	17	3	6.30E-03	NA	NA	NA	17	-3.3	2.20E-03
P48999	Arachidonate 5-lipoxygenase	5	1.8	1.90E-01	23	-0.1	8.80E-01	23	4.5	6.30E-30
P49138	MAP kinase-activated protein kinase 2	12	1.7	9.60E-02	NA	NA	NA	12	-3	8.10E-03
P49222	Erythrocyte membrane protein band 4.2	12	-3.3	2.20E-04	NA	NA	NA	12	-1.9	8.90E-03
P49290	Eosinophil peroxidase	7	1.3	4.10E-02	5	-2.8	5.10E-04	7	-0.3	6.40E-01
P49312	Heterogeneous nuclear ribonucleoprotein A1	17	0.2	4.20E-01	22	-0.7	7.10E-03	22	0.3	5.30E-02
P49710	Hematopoietic lineage cell-specific protein	7	1.1	2.90E-01	36	0	8.20E-01	36	4.9	3.30E-78
P49718	DNA replication licensing factor MCM5	3	1.5	3.10E-01	NA	NA	NA	5	-0.4	#######
P49722	Proteasome subunit alpha type-2	33	-0.5	3.00E-02	37	0.4	3.40E-01	45	-1.9	6.30E-33
P49813	Tropomodulin-1	10	-3.5	4.40E-03	NA	NA	NA	10	-3.2	4.20E-03
P50247	Adenosylhomocysteinase	20	1.4	7.30E-04	12	2	7.40E-02	20	-2.7	3.10E-12
P50396	Rab GDP dissociation inhibitor alpha	36	-0.4	1.20E-01	25	0.9	2.40E-03	36	-1.3	6.80E-21
P50429	Arylsulfatase B	11	-1	4.80E-01	12	-1.8	1.90E-05	16	1.9	1.10E-07
P50431	Serine hydroxymethyltransferase, cytosolic	18	2.3	1.80E-02	NA	NA	NA	18	-2.7	4.00E-03
P50446	Keratin, type II cytoskeletal 6A	4	-0.7	5.60E-01	NA	NA	NA	4	-3.9	1.60E-08
P50516	V-type proton ATPase catalytic subunit A	39	0.2	2.40E-01	32	1.7	1.90E-14	39	-0.1	6.90E-01
P50518	V-type proton ATPase subunit E 1	27	0.4	3.10E-01	27	1.8	8.30E-05	27	0.1	7.80E-01
P50543	Protein S100-A11	64	0.1	5.70E-01	81	-0.5	9.40E-16	81	3.7	#######
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	10	3	6.30E-03	NA	NA	NA	13	-1.5	9.60E-02
P50580	Proliferation-associated protein 2G4	25	0.5	1.20E-01	32	1.3	2.70E-02	32	-1.3	1.10E-06
P51125	Calpastatin	13	0.3	5.00E-01	21	-0.1	1.00E+00	21	1.6	1.20E-10
P51150	Ras-related protein Rab-7a	48	0.8	4.50E-02	33	0.1	8.10E-01	51	0.3	3.10E-01
P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	24	1.2	1.00E-02	13	2	3.50E-02	24	-1.7	1.90E-05
P51410	60S ribosomal protein L9	43	1.2	7.10E-02	58	1.6	1.20E-04	58	1.4	1.00E-05
P51437	Cathelin-related antimicrobial peptide	45	-0.1	9.00E-01	46	-1.3	4.40E-50	46	2.1	#######
P51807	Dynein light chain Tctex-type 1	30	3.2	2.40E-03	NA	NA	NA	30	0	#######
P51859	Hepatoma-derived growth factor	25	-1.8	3.70E-02	42	-0.2	9.60E-01	42	1.6	3.60E-06
P51863	V-type proton ATPase subunit d 1	10	3.3	1.40E-03	36	-0.7	7.50E-02	36	2.8	2.60E-17
P51881	ADP/ATP translocase 2	13	2.4	4.50E-02	21	0	9.90E-01	21	3	1.90E-12
P52480	Pyruvate kinase PKM	64	0.5	5.30E-09	59	1	1.10E-26	66	-0.5	1.80E-21
P52624	Uridine phosphorylase 1	34	1.4	6.60E-05	19	1.6	6.20E-03	34	-1.3	1.80E-06
P53994	Ras-related protein Rab-2A	13	2.7	1.70E-02	20	-0.2	1.00E+00	27	1.5	3.90E-03
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	24	1.5	8.90E-06	15	-0.8	1.70E-01	24	-1.2	6.20E-06
P54310	Hormone-sensitive lipase	8	1.8	1.90E-01	NA	NA	NA	8	-2.1	1.90E-01
P54775	26S protease regulatory subunit 6B	31	-0.4	4.00E-01	26	0.1	7.50E-01	32	0.1	5.30E-01
P54822	Adenylosuccinate lyase	22	-1.2	6.30E-02	12	2.4	1.80E-02	22	-1.4	3.10E-03

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P54823	Probable ATP-dependent RNA helicase DDX6	13	0	8.40E-01	12	1.7	7.70E-04	17	0.7	5.50E-02
P54923	[Protein ADP-ribosylarginine] hydrolase	9	0.6	6.00E-01	NA	NA	NA	9	-2.1	1.90E-01
P55264	Adenosine kinase	35	1.2	1.00E-02	NA	NA	NA	35	-5.3	2.20E-14
P56391	Cytochrome c oxidase subunit 6B1	29	0.1	8.40E-01	71	-1.2	8.50E-03	71	3.2	1.50E-11
P56399	Ubiquitin carboxyl-terminal hydrolase 5	32	0.6	1.60E-02	26	0.6	1.50E-02	33	0.3	9.50E-02
P56480	ATP synthase subunit beta, mitochondrial	38	0.1	5.80E-01	58	0.1	6.40E-01	58	2.2	#######
P56565	Protein S100-A1	27	3.4	8.40E-04	27	1.3	4.40E-02	27	1	2.50E-02
P56959	RNA-binding protein FUS	14	0.1	6.40E-01	14	-0.5	1.30E-01	14	1	1.60E-05
P57716	Nicastrin	7	-0.3	1.00E+00	8	-2	1.40E-01	11	0.8	3.90E-01
P57780	Alpha-actinin-4	51	-0.7	2.80E-10	45	-0.5	3.00E-05	54	-0.4	2.80E-08
P57784	U2 small nuclear ribonucleoprotein A'	36	1	5.50E-02	51	0.7	1.20E-01	54	0.7	1.70E-02
P58058	NAD kinase	21	-1.1	1.70E-01	13	-0.7	5.80E-01	21	-0.6	2.40E-01
P58252	Elongation factor 2	47	0.4	9.30E-05	40	1.1	3.40E-28	49	-0.3	1.20E-04
P58389	Serine/threonine-protein phosphatase 2A activator	28	0.1	6.90E-01	22	1.3	2.00E-02	28	-0.1	9.40E-01
P59108	Copine-2	9	0.2	5.80E-01	18	-2.9	1.60E-05	18	-0.4	4.70E-01
P59999	Actin-related protein 2/3 complex subunit 4	18	-0.6	3.50E-02	18	1.4	1.10E-02	18	-2	8.30E-19
P60122	RuvB-like 1	22	1.1	1.60E-02	18	-0.4	5.60E-01	26	0.2	5.50E-01
P60229	Eukaryotic translation initiation factor 3 subunit E	7	1	2.70E-01	18	2.8	2.60E-04	18	1	4.20E-02
P60335	Poly(rC)-binding protein 1	28	2	2.50E-05	37	0.3	2.40E-01	42	1.7	1.50E-16
P60670	Nuclear protein localization protein 4 homolog	17	1.3	5.40E-02	18	0.2	8.90E-01	21	-0.9	1.40E-01
P60710	Actin, cytoplasmic 1	82	0.9	6.90E-175	81	1.2	3.30E-171	85	-0.8	#######
P60766	Cell division control protein 42 homolog	58	1	1.70E-06	48	0.3	2.30E-01	59	-0.5	3.40E-04
P60843	Eukaryotic initiation factor 4A-I	48	1.1	3.70E-05	26	0.8	3.70E-03	49	-0.2	2.10E-01
P61022	Calcineurin B homologous protein 1	18	0.9	4.40E-01	18	-2.9	2.80E-04	18	1.9	2.40E-03
P61079	Ubiquitin-conjugating enzyme E2 D3	29	0.7	1.80E-01	29	1.2	7.70E-03	29	0.8	1.10E-02
P61089	Ubiquitin-conjugating enzyme E2 N	32	0.9	9.70E-02	51	0.8	8.00E-02	51	0.7	1.30E-02
P61161	Actin-related protein 2	45	-0.4	1.20E-03	41	0.5	4.20E-03	53	-1.4	3.10E-50
P61164	Alpha-centractin	32	-0.2	1.00E+00	28	-0.2	8.90E-01	32	-1.1	7.50E-06
P61202	COP9 signalosome complex subunit 2	10	0.1	8.40E-01	NA	NA	NA	10	1.3	7.60E-02
P61222	ATP-binding cassette sub-family E member 1	18	4	1.50E-05	8	2.4	8.70E-02	18	-1.7	5.00E-03
P61327	Protein mago nashi homolog	39	0	8.70E-01	NA	NA	NA	39	-1.7	1.10E-01
P61750	ADP-ribosylation factor 4	58	1.2	1.50E-07	57	0.6	6.30E-02	58	-0.9	1.60E-07
P61965	WD repeat-containing protein 5	14	0.7	5.10E-01	NA	NA	NA	20	-0.4	9.80E-01
P61979	Heterogeneous nuclear ribonucleoprotein K	33	0.6	6.10E-03	50	0.4	4.90E-03	50	1.4	1.90E-35
P61982	14-3-3 protein gamma	45	-0.5	1.10E-01	52	0.3	9.80E-02	52	0.4	1.10E-03
P62082	40S ribosomal protein S7	34	2.6	1.20E-05	41	0.3	3.20E-01	41	1.7	1.30E-12
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	37	0.6	2.00E-03	41	0.9	2.40E-03	41	-1	3.20E-11
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	38	0.4	2.70E-02	30	0.9	7.50E-03	39	-1.3	4.40E-16
P62192	26S protease regulatory subunit 4	6	1.5	3.10E-01	8	0.4	6.40E-01	11	2.5	1.70E-04
P62196	26S protease regulatory subunit 8	15	-0.6	5.60E-01	8	1	4.50E-01	18	-2.3	2.20E-06
P62204	Calmodulin	46	-0.3	1.90E-01	31	-0.4	8.10E-02	46	-0.1	3.20E-01
P62242	40S ribosomal protein S8	13	2.7	1.70E-02	28	-0.5	6.30E-01	28	1.7	7.50E-04
P62259	14-3-3 protein epsilon	47	-0.4	1.60E-01	38	0.4	9.60E-02	56	-0.1	8.00E-01
P62267	40S ribosomal protein S23	20	3	6.30E-03	20	0.6	2.60E-01	20	1.8	4.70E-05

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P62281	40S ribosomal protein S11	18	2.4	4.50E-02	12	-0.8	2.80E-01	18	2.1	5.30E-05
P62315	Small nuclear ribonucleoprotein Sm D1	37	0.6	8.60E-02	32	-0.4	1.00E+00	37	-3.1	1.40E-15
P62317	Small nuclear ribonucleoprotein Sm D2	16	0.2	5.00E-01	16	0.1	8.40E-01	16	-1	2.20E-03
P62320	Small nuclear ribonucleoprotein Sm D3	25	-0.1	9.80E-01	18	0.2	4.90E-01	26	0.1	5.80E-01
P62331	ADP-ribosylation factor 6	45	2.2	6.90E-04	16	1.5	5.40E-02	45	-0.6	1.90E-01
P62334	26S protease regulatory subunit 10B	7	0.4	4.00E-01	12	1.4	1.10E-01	12	-0.9	4.80E-02
P62482	Voltage-gated potassium channel subunit beta-2	17	0.7	4.00E-01	NA	NA	NA	17	-3.5	6.10E-04
P62702	40S ribosomal protein S4, X isoform	12	1.1	2.90E-01	NA	NA	NA	12	-0.7	5.90E-01
P62715	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	37	0.6	1.50E-01	37	-0.1	1.00E+00	37	-0.5	1.60E-01
P62774	Myotrophin	32	-0.1	9.00E-01	61	-0.4	3.90E-01	61	2.6	2.50E-15
P62806	Histone H4	60	-0.1	1.00E-02	56	-0.3	6.90E-03	60	-1.8	#######
P62814	V-type proton ATPase subunit B, brain isoform	28	0.5	2.70E-02	29	0	9.40E-01	31	-1.4	4.90E-16
P62827	GTP-binding nuclear protein Ran	58	1.3	1.80E-15	22	0.9	8.10E-02	58	-2.9	1.20E-67
P62830	60S ribosomal protein L23	15	2.9	1.00E-02	24	0.7	1.60E-01	24	2.2	1.70E-07
P62835	Ras-related protein Rap-1A	38	-0.4	4.80E-01	50	-0.1	1.00E+00	50	-0.1	8.30E-01
P62874	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	31	0.4	1.50E-01	31	-1.1	5.10E-04	31	0.1	7.30E-01
P62880	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	49	1.6	1.00E-05	56	-0.6	4.30E-03	65	1.5	1.70E-18
P62889	60S ribosomal protein L30	24	1.3	2.80E-02	41	-0.7	3.00E-01	41	0.2	5.30E-01
P62908	40S ribosomal protein S3	39	3.8	7.70E-08	33	0.1	7.60E-01	39	0.9	3.50E-03
P62960	Nuclease-sensitive element-binding protein 1	30	0.3	3.80E-01	30	-0.2	8.30E-01	30	0.5	4.70E-02
P62962	Profilin-1	41	0.5	7.50E-02	59	1.7	3.80E-16	59	0.8	2.00E-07
P62996	Transformer-2 protein homolog beta	19	0.5	2.40E-01	18	-0.6	9.30E-02	19	1.1	1.10E-05
P63001	Ras-related C3 botulinum toxin substrate 1	48	1.4	4.60E-06	NA	NA	NA	48	-1	5.90E-06
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	25	1	1.80E-02	9	1.8	1.20E-02	25	-1.5	1.00E-05
P63017	Heat shock cognate 71 kDa protein	59	0	9.20E-01	53	0.3	6.10E-03	62	0.3	1.10E-07
P63028	Translationally-controlled tumor protein	9	0.1	6.80E-01	25	0.3	6.20E-01	25	0.2	5.30E-01
P63073	Eukaryotic translation initiation factor 4E	21	2.1	1.00E-02	NA	NA	NA	21	-2.6	9.80E-04
P63085	Mitogen-activated protein kinase 1	30	2.3	5.10E-05	10	2.2	1.40E-01	30	-2.8	9.10E-08
P63094	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	9	3.6	3.10E-04	12	-0.3	1.00E+00	12	0.1	7.90E-01
P63101	14-3-3 protein zeta/delta	56	-0.4	3.80E-03	61	0.1	3.30E-01	61	0.2	4.20E-03
P63158	High mobility group protein B1	35	0.6	4.40E-02	NA	NA	NA	35	-0.9	1.10E-04
P63242	Eukaryotic translation initiation factor 5A-1	38	0.3	2.50E-01	47	0.3	2.00E-01	58	0.3	3.30E-02
P63325	40S ribosomal protein S10	24	0.9	2.00E-01	NA	NA	NA	24	-3.3	3.30E-05
P63328	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	10	0.3	6.00E-01	NA	NA	NA	10	-3.1	2.00E-04
P67778	Prohibitin	14	1.5	2.10E-02	72	0.2	2.50E-01	72	3.3	1.10E-53
P68033	Actin, alpha cardiac muscle 1	61	1.1	4.30E-118	55	1.3	2.30E-141	64	-0.1	7.80E-02
P68037	Ubiquitin-conjugating enzyme E2 L3	49	-0.3	1.00E+00	39	1.1	1.70E-02	49	0.8	8.20E-03
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	62	1	8.90E-09	50	0.8	1.30E-03	62	-0.9	4.50E-12
P68254	14-3-3 protein theta	46	-0.3	4.60E-01	55	-0.1	8.30E-01	55	0.1	4.40E-01
P68368	Tubulin alpha-4A chain	52	0.4	3.10E-03	67	0.1	2.20E-01	67	1.1	2.20E-44
P68369	Tubulin alpha-1A chain	53	0.5	2.80E-03	67	0	9.30E-01	67	1.3	9.70E-54
P68433	Histone H3.1	32	-0.2	4.20E-02	32	-1.2	2.80E-36	32	-1.2	#######
P68510	14-3-3 protein eta	56	-0.6	1.30E-02	56	0.2	3.40E-01	56	-0.2	2.30E-01
P70168	Importin subunit beta-1	30	0	6.30E-01	36	0.4	7.40E-02	40	-0.3	1.40E-02

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
P70195	Proteasome subunit beta type-7	54	-0.8	5.20E-03	NA	NA	NA	54	-7	6.80E-46
P70268	Serine/threonine-protein kinase N1	11	3.4	1.70E-05	15	2.1	6.70E-05	17	0.8	2.30E-02
P70290	55 kDa erythrocyte membrane protein	16	-1.2	1.00E-03	23	-0.2	9.00E-01	26	-0.8	3.30E-03
P70296	Phosphatidylethanolamine-binding protein 1	33	0.3	4.00E-01	49	1.2	1.30E-03	56	0.3	2.10E-01
P70315	Wiskott-Aldrich syndrome protein homolog	10	0.9	4.40E-01	19	1.8	3.80E-02	24	1.6	1.50E-02
P70335	Rho-associated protein kinase 1	5	0.3	6.40E-01	5	0.2	8.10E-01	5	1.1	1.90E-02
P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	24	0.7	1.80E-01	35	0.1	8.20E-01	35	0.6	5.00E-02
P70460	Vasodilator-stimulated phosphoprotein	10	1.1	5.60E-03	14	0.3	2.40E-01	14	1	5.00E-07
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	3	0.5	2.60E-01	2	0.1	7.50E-01	3	1.2	4.40E-06
P70677	Caspase-3	23	0.4	4.00E-01	NA	NA	NA	23	-1.2	1.30E-02
P70697	Uroporphyrinogen decarboxylase	16	4	9.80E-06	NA	NA	NA	16	-4.3	4.10E-07
P70698	CTP synthase 1	5	2.6	4.90E-03	6	1.9	2.30E-01	8	-1.7	2.20E-02
P80313	T-complex protein 1 subunit eta	27	0.6	3.20E-02	21	1.1	6.10E-06	27	0.4	1.60E-02
P80314	T-complex protein 1 subunit beta	32	0.5	2.70E-02	27	0.7	1.20E-02	36	-0.3	1.20E-01
P80315	T-complex protein 1 subunit delta	18	0.8	4.20E-02	19	1.2	1.00E-03	22	0.4	1.40E-01
P80316	T-complex protein 1 subunit epsilon	31	0.6	4.40E-02	27	0.3	3.10E-01	33	0.3	7.50E-02
P80317	T-complex protein 1 subunit zeta	22	0.2	4.20E-01	22	0.3	3.10E-01	25	0.5	4.40E-03
P80318	T-complex protein 1 subunit gamma	17	2.3	4.70E-03	11	2	3.50E-02	23	-0.4	6.80E-01
P82198	Transforming growth factor-beta-induced protein ig-h3	37	-0.6	1.90E-05	24	-0.3	2.80E-01	37	-1.6	9.50E-46
P83917	Chromobox protein homolog 1	17	1.6	7.20E-02	32	-0.9	1.20E-02	32	2.7	1.50E-14
P84078	ADP-ribosylation factor 1	70	1.1	1.20E-08	56	0.8	1.30E-03	70	-0.8	3.40E-08
P84084	ADP-ribosylation factor 5	58	1	1.70E-06	52	0.8	3.70E-03	58	-0.8	1.80E-07
P84091	AP-2 complex subunit mu	14	2	4.30E-02	10	1.3	3.60E-01	14	-0.8	4.70E-01
P84096	Rho-related GTP-binding protein RhoG	62	0.7	8.30E-04	48	0.1	7.90E-01	62	-1	3.10E-11
P84104	Serine/arginine-rich splicing factor 3	29	1.4	1.60E-02	29	-0.6	1.10E-01	29	1.5	5.50E-08
P84228	Histone H3.2	32	-0.5	2.70E-20	32	-1.1	3.00E-37	32	-1.6	#######
P84244	Histone H3.3	32	-0.4	6.50E-07	32	-1.1	9.80E-32	32	-0.9	9.00E-58
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	29	1.7	4.90E-02	29	1.5	1.10E-01	29	0.1	8.90E-01
P97310	DNA replication licensing factor MCM2	7	3.2	2.40E-03	6	0.8	3.40E-01	10	0.5	3.80E-01
P97311	DNA replication licensing factor MCM6	5	1.5	3.10E-01	14	0.7	1.10E-01	14	3.9	2.70E-14
P97315	Cysteine and glycine-rich protein 1	18	0.3	7.00E-01	46	0.3	5.10E-01	46	2.8	4.70E-11
P97351	40S ribosomal protein S3a	12	3.6	3.10E-04	7	-1.1	1.40E-01	12	0.8	9.30E-02
P97355	Spermine synthase	19	3.3	1.40E-03	NA	NA	NA	19	-2.2	8.60E-03
P97364	Selenide, water dikinase 2	8	0.2	8.30E-01	NA	NA	NA	8	-1.8	3.60E-01
P97369	Neutrophil cytosol factor 4	43	0.8	2.10E-04	44	0.3	8.10E-02	45	0.5	7.60E-05
P97371	Proteasome activator complex subunit 1	27	-0.1	9.30E-01	25	0.3	3.70E-01	31	0.5	1.60E-02
P97372	Proteasome activator complex subunit 2	42	0	8.50E-01	36	1.7	2.90E-07	42	0.1	6.00E-01
P97384	Annexin A11	28	0.4	4.20E-02	29	-1.4	2.70E-09	31	-0.8	2.80E-10
P97425	Eosinophil cationic protein 2	39	-2.3	4.10E-10	39	-1.5	7.10E-02	39	-2.1	1.80E-10
P97426	Eosinophil cationic protein 1	45	-2.5	4.10E-16	38	-1.9	6.50E-04	45	-1.6	2.10E-10
P97429	Annexin A4	20	1.6	3.90E-02	NA	NA	NA	20	-3.1	2.00E-04
P97484	Leukocyte immunoglobulin-like receptor subfamily B member 3	9	2.2	7.20E-02	NA	NA	NA	9	0.6	4.50E-01
P97807	Fumarate hydratase, mitochondrial	10	-0.6	1.10E-01	14	-0.6	1.90E-01	14	-0.6	9.50E-03
P97821	Dipeptidyl peptidase 1	18	-0.4	7.40E-01	18	-0.5	3.20E-01	18	0.3	2.80E-01

		Exosomes			MDSCs			Global		
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P97822	Acidic leucine-rich nuclear phosphoprotein 32 family member E	12	1.5	3.10E-01	28	1.3	2.70E-03	28	4	1.20E-15
P97823	Acyl-protein thioesterase 1	50	2.4	2.70E-09	21	1.6	8.00E-02	50	-2.4	1.70E-12
P97855	Ras GTPase-activating protein-binding protein 1	9	0.8	3.10E-01	17	0.4	4.80E-01	17	1.5	2.90E-04
P97864	Caspase-7	15	1.1	2.90E-01	15	1.5	2.40E-01	30	-0.3	#######
P99024	Tubulin beta-5 chain	51	1.1	4.90E-11	67	0.3	1.70E-03	67	1.6	1.90E-91
P99026	Proteasome subunit beta type-4	39	-2.5	1.40E-05	NA	NA	NA	39	-2.4	3.00E-06
P99027	60S acidic ribosomal protein P2	91	0	6.90E-01	80	0	8.40E-01	95	0.9	5.20E-12
P99029	Peroxiredoxin-5, mitochondrial	48	0.6	2.70E-02	65	0.5	3.30E-03	65	1.6	2.80E-33
Q00519	Xanthine dehydrogenase/oxidase	35	-0.5	2.00E-05	21	1.8	5.50E-09	36	-2.7	#######
Q00612	Glucose-6-phosphate 1-dehydrogenase X	43	0.4	2.00E-03	35	0.6	6.10E-04	47	-0.5	2.00E-07
Q00623	Apolipoprotein A-I	19	-0.1	9.00E-01	24	-2.8	5.40E-05	24	0.8	7.80E-02
Q00896	Alpha-1-antitrypsin 1-3	14	-3	3.70E-02	NA	NA	NA	34	2.7	4.90E-09
Q01102	P-selectin	9	-1.8	8.80E-03	7	-0.6	7.10E-01	12	-0.7	1.60E-01
Q01339	Beta-2-glycoprotein 1	30	-3.7	3.40E-06	NA	NA	NA	30	-4.3	4.10E-07
Q01514	Interferon-induced guanylate-binding protein 1	8	0.6	3.10E-01	NA	NA	NA	8	-2.3	4.60E-04
Q01853	Transitional endoplasmic reticulum ATPase	68	-0.5	1.10E-11	53	-0.3	8.00E-02	69	-1.2	7.90E-87
Q02053	Ubiquitin-like modifier-activating enzyme 1	48	0.5	2.00E-05	33	1.1	4.20E-13	50	-0.9	5.40E-27
Q02357	Ankyrin-1	20	-3.2	4.00E-40	7	-4.6	1.60E-07	20	-3.1	4.70E-39
Q02819	Nucleobindin-1	14	1.5	1.00E-01	23	-1	1.70E-03	23	3.2	8.10E-22
Q03265	ATP synthase subunit alpha, mitochondrial	15	0.9	4.90E-02	38	-0.2	2.90E-01	38	2.8	2.40E-59
Q04750	DNA topoisomerase 1	15	-0.2	8.00E-01	12	-0.4	3.40E-01	17	-1	2.90E-07
Q05144	Ras-related C3 botulinum toxin substrate 2	61	1.5	7.40E-15	56	0.6	5.00E-02	61	-1.3	9.50E-18
Q06890	Clusterin	19	-1.8	1.30E-05	8	-2.8	4.30E-03	19	-2.1	2.10E-08
Q07076	Annexin A7	16	0.2	4.30E-01	8	-0.2	1.00E+00	16	-1.6	7.10E-07
Q07797	Galectin-3-binding protein	31	-1	2.90E-05	7	-0.3	1.00E+00	31	-3.3	1.00E-33
Q08761	Vitamin K-dependent protein S	10	-2.7	2.00E-03	NA	NA	NA	10	-3.9	2.30E-05
Q08943	FACT complex subunit SSRP1	11	0.2	6.30E-01	12	-0.4	5.60E-01	16	1.5	6.00E-05
Q09014	Neutrophil cytosol factor 1	26	0.9	1.10E-04	27	0.3	2.40E-01	32	0	#######
Q09200	Beta-1,4 N-acetylgalactosaminyltransferase 1	7	1.9	6.50E-02	NA	NA	NA	7	-1.8	6.70E-02
Q09PK2	Retroviral-like aspartic protease 1	59	0.3	1.60E-02	60	2.8	4.10E-177	60	1.4	3.00E-85
Q11011	Puromycin-sensitive aminopeptidase	31	-0.4	1.20E-01	18	1.6	1.10E-03	33	-2.5	1.30E-43
Q11136	Xaa-Pro dipeptidase	12	-0.2	9.40E-01	NA	NA	NA	12	-2	2.10E-03
Q20BD0	Heterogeneous nuclear ribonucleoprotein A/B	11	0.2	5.70E-01	20	-0.1	1.00E+00	20	1.6	3.30E-17
Q2NL51	Glycogen synthase kinase-3 alpha	10	3.6	3.10E-04	NA	NA	NA	18	-1.3	6.00E-02
Q2VLH6	Scavenger receptor cysteine-rich type 1 protein M130	7	2.9	1.00E-02	NA	NA	NA	7	-3.2	4.20E-03
Q3TBD2	Minor histocompatibility protein HA-1	7	0.7	1.10E-01	11	0.5	1.70E-01	12	1.2	1.30E-06
Q3THK7	GMP synthase [glutamine-hydrolyzing]	21	1.5	2.10E-04	18	-0.3	8.60E-01	21	-1.1	3.90E-04
Q3TIU4	2',5'-phosphodiesterase 12	6	0.6	6.00E-01	NA	NA	NA	6	-1.2	5.20E-01
Q3TIX9	U4/U6.U5 tri-snRNP-associated protein 2	10	2.4	4.50E-02	12	1.5	2.40E-01	15	0	#######
Q3TRM8	Hexokinase-3	47	-0.1	1.00E+00	43	0.5	3.90E-05	48	-0.5	4.10E-11
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	18	0.4	2.30E-01	10	2.1	2.50E-03	23	-1.7	6.40E-09
Q3TXS7	26S proteasome non-ATPase regulatory subunit 1	21	1.1	1.70E-02	17	0.7	1.00E-01	24	0.3	2.40E-01
Q3U0V1	Far upstream element-binding protein 2	11	2.8	1.40E-04	32	0	9.50E-01	32	3	2.10E-38
Q3U0V2	Tumor necrosis factor receptor type 1-associated DEATH domain protein	10	2.2	7.20E-02	22	2.4	9.10E-04	26	2	5.70E-04

		Exosomes			MDSCs			Global		
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Q3U1J4	DNA damage-binding protein 1	15	-0.6	1.10E-01	12	-0.1	1.00E+00	17	-0.7	1.10E-03
Q3U2G2	Heat shock 70 kDa protein 4	35	-0.1	9.90E-01	26	0	9.20E-01	40	-0.3	9.70E-02
Q3U5Q7	UMP-CMP kinase 2, mitochondrial	15	1.3	4.10E-02	NA	NA	NA	15	-4.5	5.80E-08
Q3U7R1	Extended synaptotagmin-1	12	0.7	3.10E-02	24	-0.2	6.40E-01	24	1.2	8.30E-11
Q3UDE2	Tubulin--tyrosine ligase-like protein 12	6	2.6	3.10E-03	NA	NA	NA	7	-3	3.70E-04
Q3UHD6	Sorting nexin-27	11	3.4	8.40E-04	NA	NA	NA	11	-0.1	#######
Q3UJB9	Enhancer of mRNA-decapping protein 4	4	1.5	3.10E-01	9	-1.2	1.10E-01	13	2.7	3.20E-05
Q3UKJ7	WD40 repeat-containing protein SMU1	5	2.2	7.20E-02	NA	NA	NA	11	-1.7	1.90E-01
Q3ULJ0	Glycerol-3-phosphate dehydrogenase 1-like protein	24	4.3	7.00E-07	26	3.1	7.00E-06	33	0.2	6.50E-01
Q3UM45	Protein phosphatase 1 regulatory subunit 7	22	0.2	5.30E-01	16	1.8	7.60E-04	22	-0.1	#######
Q3UND0	Src kinase-associated phosphoprotein 2	47	1.8	4.40E-07	70	-0.1	8.40E-01	70	1.9	5.80E-35
Q3UP87	Neutrophil elastase	38	-0.5	6.80E-03	51	-0.5	1.70E-05	51	1.1	3.00E-40
Q3UPH1	Protein PRRC1	14	1.1	5.00E-01	25	1.3	8.10E-03	25	4.1	2.40E-13
Q3UPL0	Protein transport protein Sec31A	5	2	1.20E-01	NA	NA	NA	7	-0.9	6.20E-01
Q3UQ44	Ras GTPase-activating-like protein IQGAP2	5	1.2	3.10E-01	12	0.8	4.80E-02	13	3.4	2.90E-16
Q3UW53	Protein Niban	19	1	7.30E-03	19	0.2	5.70E-01	24	0.9	2.60E-05
Q3UYV9	Nuclear cap-binding protein subunit 1	15	2.4	2.00E-03	5	0.5	5.10E-01	15	0.4	4.00E-01
Q3UZ39	Leucine-rich repeat flightless-interacting protein 1	12	-1.1	2.20E-01	27	0.2	4.30E-01	27	2.5	1.00E-24
Q3UZA1	CapZ-interacting protein	22	-2.2	1.40E-01	32	-0.2	7.20E-01	32	4.5	3.20E-49
Q3UZZ4	Olfactomedin-4	37	0	6.90E-01	40	-1	7.50E-08	40	-0.4	2.20E-03
Q3V0K9	Plastin-1	12	-0.8	2.90E-01	NA	NA	NA	12	-2	1.00E-05
Q3V1G4	Olfactomedin-like protein 2B	15	-0.9	3.00E-02	22	-0.9	1.60E-04	22	1.3	3.00E-12
Q3V1L4	Cytosolic purine 5'-nucleotidase	41	0.2	4.40E-01	16	4.3	1.50E-06	41	-2.5	4.00E-23
Q3V3R1	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	8	2.2	2.80E-02	8	-1	5.10E-01	11	0	#######
Q4LDD4	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	3	1.5	3.10E-01	NA	NA	NA	3	0	#######
Q501J6	Probable ATP-dependent RNA helicase DDX17	7	4	1.50E-05	NA	NA	NA	9	-0.1	#######
Q571E4	N-acetylgalactosamine-6-sulfatase	16	-0.7	2.90E-01	18	-0.6	2.20E-01	18	0.4	1.50E-01
Q571I9	Aldehyde dehydrogenase family 16 member A1	18	0	8.30E-01	9	0.6	9.90E-02	18	-0.9	6.20E-06
Q5FWK3	Rho GTPase-activating protein 1	10	0.3	6.00E-01	18	0.8	1.30E-01	18	1.4	5.10E-04
Q5RKN9	Capping protein (Actin filament) muscle Z-line, alpha 1	52	0	7.30E-01	53	-0.2	7.20E-01	53	-0.3	1.20E-01
Q5SQX6	Cytoplasmic FMR1-interacting protein 2	3	-0.5	1.00E+00	NA	NA	NA	4	-1	3.80E-01
Q5SSL4	Active breakpoint cluster region-related protein	4	1.5	3.10E-01	NA	NA	NA	4	-1.8	3.60E-01
Q5SUA5	Unconventional myosin-Ig	4	1.8	1.90E-01	12	0.1	8.50E-01	13	2.8	5.20E-07
Q5SUR0	Phosphoribosylformylglycinamidine synthase	34	0.1	3.80E-01	22	1.1	7.60E-03	34	-2	1.30E-32
Q5SVD0	Filamin-interacting protein FAM101B	24	1.2	3.10E-01	30	-0.6	2.60E-01	30	3.2	1.30E-12
Q5XJF6	Ribosomal protein	13	0.6	1.40E-01	NA	NA	NA	13	-1.9	1.40E-06
Q5XJY5	Coatomer subunit delta	5	0.6	6.00E-01	10	0	1.00E+00	10	2.7	1.60E-06
Q60605	Isoform Smooth muscle of Myosin light polypeptide 6	70	0	6.50E-01	66	-0.8	1.10E-05	71	0.5	1.50E-05
Q60631	Growth factor receptor-bound protein 2	25	0.3	5.40E-01	31	-0.9	1.80E-01	31	0.1	7.50E-01
Q60668	Heterogeneous nuclear ribonucleoprotein D0	20	1.7	4.90E-02	14	0.6	8.80E-02	24	2.7	1.30E-16
Q60675	Laminin subunit alpha-2	1	-1.7	9.60E-01	NA	NA	NA	1	-1.4	6.80E-01
Q60676	Serine/threonine-protein phosphatase 5	6	0.3	5.80E-01	NA	NA	NA	6	-3.8	8.60E-05
Q60692	Proteasome subunit beta type-6	32	-0.5	2.50E-01	27	0.2	7.80E-01	32	-2.4	9.00E-19
Q60737	Casein kinase II subunit alpha	11	1.3	7.30E-02	15	-0.1	1.00E+00	15	0.5	3.10E-01

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Q60767	Lymphocyte antigen 75	7	0.2	5.10E-01	5	-0.5	7.20E-01	9	-1.4	1.10E-04
Q60864	Stress-induced-phosphoprotein 1	14	-0.1	9.60E-01	23	0.3	5.30E-01	23	0	#######
Q60865	Caprin-1	8	-1	4.80E-01	15	0.7	5.50E-02	15	2.2	9.70E-11
Q60960	Importin subunit alpha-5	9	1.5	3.10E-01	12	0.8	2.60E-01	12	2.6	5.60E-05
Q60963	Platelet-activating factor acetylhydrolase	13	0.3	5.20E-01	NA	NA	NA	13	-4.4	1.10E-07
Q60972	Histone-binding protein RBBP4	32	0.1	6.20E-01	28	-0.1	1.00E+00	32	0.7	8.00E-04
Q60973	Histone-binding protein RBBP7	46	2.6	2.10E-07	41	-0.7	2.50E-01	54	-0.4	2.10E-01
Q61024	Asparagine synthetase [glutamine-hydrolyzing]	7	1.6	7.20E-02	NA	NA	NA	7	-0.6	5.30E-01
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta	26	0.4	2.10E-01	34	-0.7	2.30E-05	36	2.4	6.50E-53
Q61035	Histidine--tRNA ligase, cytoplasmic	29	-0.2	8.50E-01	10	1.4	3.40E-02	29	-2.5	1.90E-24
Q61081	Hsp90 co-chaperone Cdc37	15	1.3	4.10E-02	16	0.5	1.40E-01	16	1.8	2.00E-10
Q61093	Cytochrome b-245 heavy chain	21	2.8	1.90E-06	33	-0.9	2.00E-06	33	2.7	7.10E-48
Q61096	Myeloblastin	56	-0.4	1.40E-01	64	-0.6	2.30E-11	64	1.9	#######
Q61147	Ceruloplasmin	17	-1.2	6.20E-04	NA	NA	NA	17	-6.3	6.40E-29
Q61166	Microtubule-associated protein RP/EB family member 1	12	0.6	3.10E-01	35	0.6	2.20E-01	36	1.1	1.20E-03
Q61171	Peroxiredoxin-2	82	-2.6	1.30E-54	80	-0.7	1.20E-01	82	-2.2	2.30E-46
Q61176	Arginase-1	27	3.7	1.10E-04	31	3	1.10E-02	46	-0.9	2.10E-01
Q61191	Host cell factor 1	3	0.6	3.10E-01	4	0	9.90E-01	5	0.1	8.00E-01
Q61207	Prosaposin	16	0.6	1.90E-01	17	-1.3	1.80E-04	20	1.1	2.40E-05
Q61210	Isoform 5 of Rho guanine nucleotide exchange factor 1	16	4	1.50E-05	23	0.3	2.90E-01	27	2.7	6.60E-25
Q61233	Plastin-2	73	0	1.00E+00	70	1	6.80E-53	75	-0.2	8.30E-07
Q61362	Chitinase-3-like protein 1	23	-0.9	8.90E-04	26	-1	3.40E-03	29	-0.5	1.80E-02
Q61508	Extracellular matrix protein 1	20	1.3	2.40E-03	8	0.4	9.90E-01	20	-3.9	5.50E-14
Q61543	Golgi apparatus protein 1	10	1.2	2.70E-02	7	-2.7	1.70E-03	10	-0.9	4.00E-02
Q61545	RNA-binding protein EWS	8	2.4	4.50E-02	10	0.1	7.90E-01	10	3	3.40E-12
Q61550	Double-strand-break repair protein rad21 homolog	6	-0.9	8.50E-01	15	-1.6	3.70E-02	15	1	5.10E-02
Q61578	NADPH:adrenodoxin oxidoreductase, mitochondrial	9	2	1.20E-01	NA	NA	NA	9	-2.3	1.00E-01
Q61598	Rab GDP dissociation inhibitor beta	52	-0.3	1.20E-01	28	0.6	3.70E-03	52	-1	5.60E-22
Q61599	Rho GDP-dissociation inhibitor 2	61	-0.2	9.60E-01	67	1.2	1.10E-23	67	1.4	1.60E-41
Q61635	GTP-binding protein	31	0.2	4.80E-01	18	2.7	3.10E-02	35	-2.8	2.90E-11
Q61646	Haptoglobin	59	-0.8	1.40E-27	54	-1	7.00E-26	59	-0.5	1.00E-20
Q61655	ATP-dependent RNA helicase DDX19A	9	3.9	4.10E-05	14	1.2	2.00E-01	14	-0.4	6.80E-01
Q61656	Probable ATP-dependent RNA helicase DDX5	17	3.2	7.30E-05	19	0.8	2.40E-02	27	2	2.30E-12
Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	6	-2.6	1.40E-01	6	-3.2	1.00E-02	6	0.7	4.20E-01
Q61739	Integrin alpha-6	7	-1.4	2.90E-01	NA	NA	NA	8	-2.2	8.60E-03
Q61749	Translation initiation factor eIF-2B subunit delta	8	1.2	3.10E-01	NA	NA	NA	13	0	#######
Q61753	D-3-phosphoglycerate dehydrogenase	22	2.5	7.50E-06	33	2.8	4.90E-10	35	0.6	4.30E-02
Q61768	Kinesin-1 heavy chain	9	2	5.90E-03	8	0.3	5.10E-01	12	1.6	1.30E-06
Q61838	Alpha-2-macroglobulin	28	-1.7	1.70E-10	NA	NA	NA	28	-6.9	8.30E-44
Q61878	Bone marrow proteoglycan	25	0.3	5.40E-01	26	-1.2	4.20E-04	30	1.8	2.90E-10
Q61881	DNA replication licensing factor MCM7	16	2.7	1.70E-02	16	1.8	1.10E-03	18	2.1	4.90E-06
Q61937	Nucleophosmin	22	-0.2	1.00E+00	24	-0.2	7.90E-01	34	0.1	5.40E-01
Q61990	Poly(rC)-binding protein 2	31	2	8.40E-04	22	0.7	1.10E-01	35	1.1	2.40E-04
Q62059	Versican core protein	3	2.3	1.80E-02	NA	NA	NA	3	-3.5	6.10E-04

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q62167	ATP-dependent RNA helicase DDX3X	16	2.7	5.30E-07	16	0	1.00E+00	22	0.7	4.80E-03
Q62178	Semaphorin-4A	15	0.5	1.30E-01	13	-1.2	1.30E-01	15	-1.7	2.30E-08
Q62193	Replication protein A 32 kDa subunit	17	2.4	1.20E-02	17	-1.1	3.70E-01	17	-0.1	#######
Q62261	Spectrin beta chain, non-erythrocytic 1	19	-0.5	1.70E-02	22	-0.5	1.10E-03	24	0.7	9.20E-11
Q62318	Transcription intermediary factor 1-beta	6	2.4	4.50E-02	26	0	1.00E+00	26	3.6	2.00E-20
Q62348	Translin	33	-1.4	9.10E-03	NA	NA	NA	33	-5.3	4.40E-14
Q62376	U1 small nuclear ribonucleoprotein 70 kDa	6	0.6	6.00E-01	7	-1.7	2.40E-02	10	2.3	2.00E-04
Q62393	Tumor protein D52	22	1	1.10E-01	15	0.2	6.20E-01	29	1.3	3.70E-05
Q62418	Drebrin-like protein	17	-0.1	8.50E-01	32	0.2	3.90E-01	32	1.6	4.80E-16
Q62419	Endophilin-A2	8	2.4	4.50E-02	8	-0.7	5.70E-01	8	1.2	5.30E-02
Q62422	Osteoclast-stimulating factor 1	32	0.4	1.30E-01	39	0.8	8.00E-03	39	0.3	1.10E-01
Q62465	Synaptic vesicle membrane protein VAT-1 homolog	24	0.9	4.10E-02	24	0.5	4.20E-01	24	-0.7	4.50E-02
Q62469	Integrin alpha-2	5	-0.3	1.00E+00	NA	NA	NA	8	-0.2	#######
Q62523	Zyxin	18	0.2	5.70E-01	27	0	1.00E+00	27	2.4	2.50E-22
Q63810	Calcineurin subunit B type 1	27	0	8.40E-01	27	0.3	6.90E-01	27	-0.8	1.50E-02
Q63844	Mitogen-activated protein kinase 3	34	3.3	1.50E-08	NA	NA	NA	34	-5.4	2.80E-15
Q640N3	Rho GTPase-activating protein 30	3	1.8	1.90E-01	NA	NA	NA	3	-2.1	1.90E-01
Q64324	Syntaxin-binding protein 2	31	1.4	2.90E-04	32	-0.1	1.00E+00	32	0.5	1.30E-02
Q64442	Sorbitol dehydrogenase	17	-1.7	5.40E-03	NA	NA	NA	17	-2.8	1.10E-06
Q64455	Receptor-type tyrosine-protein phosphatase eta	7	-1.3	5.80E-02	6	-0.9	1.50E-01	8	0.3	3.70E-01
Q64511	DNA topoisomerase 2-beta	4	3	6.30E-03	4	0.5	6.60E-01	6	0.5	4.40E-01
Q64514	Tripeptidyl-peptidase 2	18	-0.4	4.60E-01	11	1.5	5.80E-03	19	-1.3	9.90E-07
Q64516	Glycerol kinase	9	2	1.20E-01	NA	NA	NA	9	-2.3	1.00E-01
Q64523	Histone H2A type 2-C	63	0.4	9.20E-46	59	-0.7	6.90E-144	64	-0.3	9.20E-63
Q64674	Spermidine synthase	27	3.7	6.00E-07	NA	NA	NA	27	-2.1	4.40E-05
Q64727	Vinculin	33	-0.8	1.90E-08	25	1	1.30E-03	36	-2	1.30E-57
Q64737	Trifunctional purine biosynthetic protein adenosine-3	9	1.8	1.80E-02	6	0.6	4.70E-01	9	0	9.90E-01
Q68FD5	Clathrin heavy chain 1	36	0.4	5.90E-03	39	0.1	5.40E-01	41	0.6	2.20E-15
Q68FL6	Methionine--tRNA ligase, cytoplasmic	10	2.6	2.80E-02	11	1.5	1.10E-01	11	0.8	2.30E-01
Q69ZK0	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	4	2.4	4.50E-02	9	2	3.50E-02	10	1	1.50E-01
Q6A026	Sister chromatid cohesion protein PDS5 homolog A	2	1.5	3.10E-01	6	1.1	1.60E-01	7	2.4	2.90E-04
Q6A4J8	Ubiquitin carboxyl-terminal hydrolase 7	14	0.6	1.30E-01	10	0.3	6.80E-01	16	-0.8	1.30E-02
Q6DTY7	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	10	2	1.20E-01	17	1.2	2.20E-01	24	1.2	1.10E-01
Q6IRU2	Tropomyosin alpha-4 chain	39	-1.1	8.40E-06	39	-0.8	9.80E-04	39	0	9.30E-01
Q6NSR8	Probable aminopeptidase NPEPL1	16	-2.6	1.40E-01	NA	NA	NA	16	-2.3	1.00E-01
Q6NZJ6	Eukaryotic translation initiation factor 4 gamma 1	3	-0.1	9.00E-01	7	1.8	1.10E-03	8	1.6	1.40E-04
Q6P069	Isoform 2 of Sorcin	69	0.5	2.70E-02	51	-0.3	4.20E-01	70	-0.4	1.60E-02
Q6P1B1	Xaa-Pro aminopeptidase 1	32	0.4	2.00E-01	24	3	6.50E-08	32	-1	1.40E-04
Q6P1F6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	8	1.6	1.40E-01	12	2.4	8.70E-02	17	-0.4	9.90E-01
Q6P2B1	Transportin-3	7	0.9	3.90E-01	NA	NA	NA	7	0	#######
Q6P4S8	Integrator complex subunit 1	3	1.5	3.10E-01	NA	NA	NA	3	-1.8	3.60E-01
Q6P4T2	U5 small nuclear ribonucleoprotein 200 kDa helicase	14	0.5	1.10E-01	11	0.3	4.30E-01	16	0.2	3.20E-01
Q6P542	ATP-binding cassette sub-family F member 1	6	1.1	5.00E-01	13	0	1.00E+00	16	3.3	6.70E-07
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	27	-0.3	1.40E-01	16	-1.1	6.10E-06	29	-0.9	9.10E-12

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q6P5F9	Exportin-1	13	0.1	5.80E-01	11	1.1	4.50E-03	14	-1.1	2.40E-09
Q6P8X1	Sorting nexin-6	17	2.8	1.40E-04	13	1.6	8.70E-03	17	0.3	5.00E-01
Q6P9Q4	FH1/FH2 domain-containing protein 1	3	-0.9	8.70E-01	NA	NA	NA	3	-2.1	1.50E-02
Q6PAV2	Probable E3 ubiquitin-protein ligase HERC4	8	1.7	9.60E-02	NA	NA	NA	8	-3	8.10E-03
Q6PD03	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	13	3.1	4.00E-03	NA	NA	NA	13	-0.5	6.80E-01
Q6PDG5	SWI/SNF complex subunit SMARCC2	7	0.7	2.40E-01	10	-0.6	4.00E-01	10	0.8	1.80E-02
Q6PDI5	Proteasome-associated protein ECM29 homolog	7	3.7	1.10E-04	8	1.7	4.40E-03	10	0.9	3.90E-02
Q6PDM2	Serine/arginine-rich splicing factor 1	13	-0.2	9.80E-01	27	-1.8	1.10E-08	27	1.7	1.60E-10
Q6PE01	U5 small nuclear ribonucleoprotein 40 kDa protein	20	2.9	1.00E-02	NA	NA	NA	20	-0.3	#######
Q6PEB6	MOB-like protein phocein	25	1.1	9.20E-02	NA	NA	NA	25	0.3	5.50E-01
Q6PHU5	Sortilin	10	0.2	6.00E-01	11	-0.2	1.00E+00	12	0.2	5.00E-01
Q6PHZ2	Calcium/calmodulin-dependent protein kinase type II subunit delta	8	3	6.30E-03	8	0.5	3.90E-01	8	1.8	4.70E-05
Q6URW6	Myosin-14	4	-0.2	1.00E+00	4	-0.3	4.00E-01	5	0.8	1.90E-05
Q6WVG3	BTB/POZ domain-containing protein KCTD12	34	-0.5	5.50E-01	25	0.2	8.00E-01	36	-0.5	2.00E-01
Q6ZPJ3	E2/E3 hybrid ubiquitin-protein ligase UBE2O	4	-0.6	1.00E+00	NA	NA	NA	6	-1.9	1.10E-01
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	11	-0.1	8.70E-01	11	2.5	3.70E-04	14	-1.7	2.50E-09
Q6ZQA0	Neurobeachin-like protein 2	2	2.2	7.20E-02	7	1.7	3.10E-03	7	2.5	8.50E-07
Q6ZWM4	U6 snRNA-associated Sm-like protein LSm8	61	-0.2	9.60E-01	71	0.9	1.70E-01	71	0.1	7.30E-01
Q6ZWQ0	Nesprin-2	1	-0.8	1.00E+00	2	-0.8	3.90E-01	3	2.7	3.20E-05
Q6ZWQ9	MCG5400	46	-0.1	9.70E-01	37	-0.4	9.20E-03	48	1.1	3.30E-20
Q6ZWR6	Nesprin-1	4	0.8	1.60E-02	13	-0.6	2.40E-06	14	2.4	2.60E-73
Q6ZWV3	60S ribosomal protein L10	14	2.4	4.50E-02	NA	NA	NA	14	-2.7	2.90E-02
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	14	2.9	5.00E-04	21	0.2	7.40E-01	21	1	8.70E-03
Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	35	0.3	1.40E-01	33	0.3	1.30E-01	41	0	#######
Q78PY7	Staphylococcal nuclease domain-containing protein 1	27	1.9	9.60E-11	33	0.6	1.80E-02	36	0.1	4.80E-01
Q78ZA7	Nucleosome assembly protein 1-like 4	14	0.6	3.10E-01	NA	NA	NA	14	-3	3.10E-05
Q7M6Y3	Phosphatidylinositol-binding clathrin assembly protein	8	1	1.90E-01	20	1.9	3.50E-04	20	1.5	3.20E-04
Q7TMB8	Cytoplasmic FMR1-interacting protein 1	2	1.1	5.00E-01	NA	NA	NA	3	0	#######
Q7TMK9	Heterogeneous nuclear ribonucleoprotein Q	8	1.7	5.80E-03	17	0.7	9.30E-02	17	1.3	6.50E-06
Q7TNG5	Echinoderm microtubule-associated protein-like 2	15	0.3	3.70E-01	22	3.4	1.30E-03	26	-2.2	1.10E-09
Q7TPR4	Alpha-actinin-1	61	-0.8	1.60E-20	47	-0.4	4.80E-04	62	-0.7	2.60E-23
Q7TPV4	Myb-binding protein 1A	12	3.9	2.50E-05	8	1.5	6.00E-03	13	0.9	3.00E-02
Q7TQI3	Ubiquitin thioesterase OTUB1	22	0.9	2.40E-02	NA	NA	NA	22	-1.7	1.50E-06
Q7TSI3	Serine/threonine-protein phosphatase 6 regulatory subunit 1	6	0.7	2.70E-01	15	-0.2	9.60E-01	15	0.5	1.80E-01
Q7TSV4	Phosphoglucomutase-2	15	-0.3	9.60E-01	11	1.7	1.20E-02	19	-1.7	3.80E-08
Q80T06	Elongation factor 1-delta	19	0	7.50E-01	28	0.1	7.50E-01	28	1.2	3.40E-07
Q80UM3	N-alpha-acetyltransferase 15, NatA auxiliary subunit	8	2	4.30E-02	NA	NA	NA	8	-1.5	9.60E-02
Q80UP5	Ankyrin repeat domain-containing protein 13A	5	0.6	6.00E-01	NA	NA	NA	9	-0.7	8.80E-01
Q80UR4	Mast cell protease-11	18	1.6	1.40E-01	18	-0.7	1.00E+00	18	-1.1	3.30E-01
Q80VD1	Protein FAM98B	8	2.2	7.20E-02	17	-0.1	1.00E+00	20	3	1.30E-10
Q80WQ2	Protein VAC14 homolog	4	1.1	5.00E-01	6	1.2	6.20E-01	8	0	#######
Q80X41	Serine/threonine-protein kinase VRK1	24	1.1	2.50E-02	13	0.1	9.30E-01	24	-0.4	4.30E-01
Q80X90	Filamin-B	3	0	8.40E-01	10	-0.6	2.10E-01	10	0.9	1.50E-03
Q80ZJ2	Impa1 protein	25	-0.4	1.00E+00	21	0.8	3.90E-01	25	-1.4	1.40E-03

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q80ZX0	Protein Sec24b	3	2.6	2.80E-02	NA	NA	NA	3	-2.9	1.50E-02
Q810B6	Rabankyrin-5	4	1.5	2.90E-02	9	0.3	6.90E-01	9	0.1	8.00E-01
Q8BFR5	Elongation factor Tu, mitochondrial	7	2.4	4.50E-02	13	-0.4	7.20E-01	13	2	2.20E-04
Q8BFY6	Peflin	9	-0.3	1.00E+00	9	-2.6	1.40E-02	9	-0.7	3.20E-01
Q8BFY9	Transportin-1	16	0.4	2.20E-01	23	0.5	1.30E-01	28	0.4	6.00E-02
Q8BFZ3	Beta-actin-like protein 2	42	1.4	3.30E-148	39	1.4	1.30E-156	49	0.1	2.00E-02
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	21	1.2	1.20E-04	21	-0.4	2.10E-01	21	0.8	2.30E-06
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	14	0	8.40E-01	16	2.5	1.10E-02	22	-0.5	5.40E-01
Q8BGD9	Eukaryotic translation initiation factor 4B	9	0.1	6.70E-01	12	0.7	1.40E-01	12	0.2	4.40E-01
Q8BGE6	Cysteine protease ATG4B	9	3.4	8.40E-04	NA	NA	NA	9	-1	2.00E-01
Q8BGJ5	MCG13402, isoform CRA_a	27	1.1	3.30E-05	31	0.4	1.80E-01	31	0.2	1.60E-01
Q8BGQ7	Alanine--tRNA ligase, cytoplasmic	18	1	5.80E-03	23	2.4	2.10E-10	26	0	#######
Q8BH04	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	22	3.4	1.70E-05	9	-0.2	1.00E+00	25	-1.1	3.10E-02
Q8BH43	Wiskott-Aldrich syndrome protein family member 2	10	3.3	2.80E-05	9	-0.6	6.00E-01	13	-0.3	7.50E-01
Q8BH61	Coagulation factor XIII A chain	22	-0.8	1.40E-02	6	-0.5	1.00E+00	22	-4	6.60E-29
Q8BH69	Selenide, water dikinase 1	9	1.9	2.30E-02	NA	NA	NA	9	-2.4	2.90E-03
Q8BH95	Enoyl-CoA hydratase, mitochondrial	17	2.6	2.80E-02	20	0.2	7.60E-01	24	2	8.40E-05
Q8BHD7	Polypyrimidine tract-binding protein 3	22	2.5	1.40E-04	29	0.5	1.80E-01	29	1.4	6.10E-07
Q8BHG1	Nardilysin	18	-0.7	4.10E-02	8	2.8	1.20E-05	18	-1.9	4.10E-14
Q8BHJ5	F-box-like/WD repeat-containing protein TBL1XR1	9	1	1.70E-01	9	-0.7	3.20E-01	9	1.2	1.80E-03
Q8BHN3	Neutral alpha-glucosidase AB	21	-1.1	2.00E-03	19	0	9.90E-01	26	0.2	4.90E-01
Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	3	3.2	2.40E-03	NA	NA	NA	3	-1	2.50E-01
Q8BJ71	Nuclear pore complex protein Nup93	7	1.2	3.10E-01	9	-0.4	4.30E-01	9	3.5	4.90E-17
Q8BJS4	SUN domain-containing protein 2	10	1.6	3.90E-02	23	-0.4	3.50E-01	23	2.6	3.70E-17
Q8BJW6	Eukaryotic translation initiation factor 2A	7	1.1	5.00E-01	NA	NA	NA	10	-0.5	#######
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5	18	0.1	7.10E-01	15	1.7	1.10E-03	18	0	9.60E-01
Q8BK67	Protein RCC2	31	1.7	6.90E-08	11	1.5	2.40E-01	31	-4	1.90E-29
Q8BKC5	Importin-5	23	0.5	1.80E-02	11	2.1	2.50E-03	23	-3	4.70E-41
Q8BL97	Serine/arginine-rich splicing factor 7	14	0.2	5.10E-01	18	-1.1	5.20E-03	18	0.7	1.30E-02
Q8BMA6	Signal recognition particle subunit SRP68	6	1.5	3.10E-01	12	-0.6	6.00E-01	13	2.4	2.90E-04
Q8BMJ2	Leucine--tRNA ligase, cytoplasmic	4	1.9	2.30E-02	6	0.7	2.20E-01	7	1.4	9.90E-04
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	7	3.2	2.40E-03	21	-0.3	5.20E-01	21	3.4	3.00E-28
Q8BND5	Sulfhydryl oxidase 1	21	-0.4	4.50E-01	16	-0.6	1.50E-01	24	-0.3	2.40E-01
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	16	1.7	3.10E-03	27	3	6.50E-08	31	0.4	2.60E-01
Q8BP56	Acid trehalase-like protein 1	7	-0.3	9.90E-01	NA	NA	NA	7	-3.4	1.20E-03
Q8BPU7	Engulfment and cell motility protein 1	11	0.7	3.10E-01	14	-0.7	3.20E-01	14	1.2	3.40E-03
Q8BRF7	Sec1 family domain-containing protein 1	13	2.8	1.30E-03	12	0.8	5.30E-01	15	-0.9	2.10E-01
Q8BT60	Copine-3	33	0.3	1.30E-01	42	-0.4	3.50E-02	42	0.6	2.50E-06
Q8BTE6	Protein Wfdc21	52	1.5	1.10E-02	62	-0.7	1.00E-05	62	3.5	3.10E-77
Q8BTM8	Filamin-A	46	-0.3	3.20E-08	54	-0.4	7.40E-18	58	1	#######
Q8BTZ7	Mannose-1-phosphate guanyltransferase beta	20	1.5	4.10E-02	13	1.9	2.30E-01	20	-2.1	2.10E-03
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic	2	2	1.20E-01	6	2.4	8.70E-02	8	0.2	8.90E-01
Q8BUM3	Tyrosine-protein phosphatase non-receptor type 7	18	2	4.30E-02	NA	NA	NA	18	-3.3	2.20E-03
Q8BV13	COP9 signalosome complex subunit 7b	15	0.1	8.40E-01	NA	NA	NA	15	-2.3	1.00E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q8BVE3	V-type proton ATPase subunit H	9	-0.2	1.00E+00	9	0.2	8.00E-01	9	-0.1	#######
Q8BVG4	Dipeptidyl peptidase 9	6	1.4	6.20E-03	6	1.1	5.30E-01	6	-2.8	9.10E-08
Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	32	2.4	2.30E-05	22	0.2	7.90E-01	32	-0.2	8.50E-01
Q8BWY3	Eukaryotic peptide chain release factor subunit 1	16	2.2	1.80E-03	11	2.3	3.00E-02	16	-1	5.80E-02
Q8BX94	Oxysterol-binding protein-related protein 2	12	1.5	3.10E-01	NA	NA	NA	12	-0.9	8.20E-01
Q8BXK9	Chloride intracellular channel protein 5	7	0.6	6.00E-01	7	0.4	9.90E-01	7	-0.3	#######
Q8BY71	Histone acetyltransferase type B catalytic subunit	8	2.4	4.50E-02	16	3.1	6.50E-03	16	0.6	4.70E-01
Q8BYA0	Tubulin-specific chaperone D	5	1.5	3.10E-01	NA	NA	NA	8	-0.9	8.20E-01
Q8BZA9	Fructose-2,6-bisphosphatase TIGAR	19	2.9	1.00E-02	NA	NA	NA	19	-3.2	4.20E-03
Q8C0D5	Elongation factor Tu GTP-binding domain-containing protein 1	5	1.1	5.00E-01	NA	NA	NA	8	0	#######
Q8C0E2	Vacuolar protein sorting-associated protein 26B	14	0.7	5.10E-01	NA	NA	NA	14	-2.7	2.90E-02
Q8C0I1	Alkyldihydroxyacetonephosphate synthase, peroxisomal	6	2	1.20E-01	25	-0.4	5.60E-01	25	3.4	3.60E-14
Q8C147	Dedicator of cytokinesis protein 8	5	1.7	9.60E-02	9	0.9	5.30E-02	9	2.6	8.90E-10
Q8C166	Copine-1	20	0.5	2.90E-01	27	-0.2	7.80E-01	30	1.3	3.00E-07
Q8C1A5	Thimet oligopeptidase	11	3.4	8.40E-04	NA	NA	NA	11	-3.7	1.60E-04
Q8C1B7	Septin-11	14	0.2	5.90E-01	14	0.5	4.40E-01	14	0	9.70E-01
Q8C3J5	Dedicator of cytokinesis protein 2	3	2.9	1.00E-02	6	1.2	8.50E-02	6	1.3	1.10E-02
Q8C4Y3	Negative elongation factor B	6	1.1	5.00E-01	NA	NA	NA	6	-1.4	6.80E-01
Q8C570	mRNA export factor	21	3.4	8.40E-04	NA	NA	NA	21	-3.7	1.60E-04
Q8C5P5	5'-nucleotidase domain-containing protein 1	12	3.8	6.90E-05	NA	NA	NA	12	-0.8	2.20E-01
Q8C6G8	WD repeat-containing protein 26	6	1.1	5.00E-01	6	-0.8	3.80E-01	9	3	2.30E-05
Q8C708	Transmembrane protein C16orf54 homolog	14	0	8.40E-01	NA	NA	NA	14	-3.2	6.10E-05
Q8CBW3	Abl interactor 1	10	0.9	4.40E-01	13	0.5	7.90E-01	13	0.2	8.90E-01
Q8CC86	Nicotinate phosphoribosyltransferase	19	2.1	1.50E-05	9	1.5	1.60E-01	19	-2.2	8.10E-08
Q8CCK0	Core histone macro-H2A.2	12	-0.2	1.00E+00	NA	NA	NA	12	-0.3	7.30E-02
Q8CDN6	Thioredoxin-like protein 1	36	1.1	8.80E-03	36	0.4	3.90E-01	36	0.1	7.30E-01
Q8CFI7	DNA-directed RNA polymerase II subunit RPB2	5	1.1	5.00E-01	NA	NA	NA	5	1.3	1.90E-01
Q8CFQ3	Intron-binding protein aquarius	4	1.1	5.00E-01	NA	NA	NA	4	-1.4	6.80E-01
Q8CFV9	Riboflavin kinase	39	1.8	1.90E-01	NA	NA	NA	39	-2.1	1.90E-01
Q8CFX1	GDH/6PGL endoplasmic bifunctional protein	9	0.2	8.30E-01	NA	NA	NA	9	-1.8	3.60E-01
Q8CG03	cGMP-specific 3',5'-cyclic phosphodiesterase	19	-2.7	8.00E-14	5	0.3	8.60E-01	19	-3	2.00E-16
Q8CG19	Latent-transforming growth factor beta-binding protein 1	7	-2.4	2.30E-06	4	2.6	5.30E-02	9	-2.6	8.60E-08
Q8CG29	Myosin IF	6	0.7	1.20E-01	17	-0.7	7.90E-03	17	1.6	1.00E-12
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	11	1.8	1.60E-04	15	0.7	7.10E-02	18	0.4	1.10E-01
Q8CGP4	Histone H2A	58	0	1.00E+00	59	-0.6	6.60E-48	59	-0.4	9.00E-58
Q8CHP8	Phosphoglycolate phosphatase	24	0.2	5.20E-01	22	2.2	4.90E-03	24	-1.2	6.40E-04
Q8CI94	Glycogen phosphorylase, brain form	15	-0.5	3.50E-01	5	2.7	3.10E-02	16	-3.4	1.10E-19
Q8CIE6	Coatomer subunit alpha	13	2.1	5.70E-04	13	0.7	1.90E-01	18	0.5	1.50E-01
Q8CIH5	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	33	0.1	5.00E-01	16	0	9.20E-01	33	-0.8	4.20E-08
Q8CIM3	D-2-hydroxyglutarate dehydrogenase, mitochondrial	11	3	6.30E-03	NA	NA	NA	11	-3.3	2.20E-03
Q8CIN4	Serine/threonine-protein kinase PAK 2	20	1.6	1.70E-05	27	1.1	6.30E-05	28	0.9	4.80E-06
Q8CJG0	Protein argonaute-2	8	1.5	4.10E-02	NA	NA	NA	8	-4.2	3.00E-06
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B	25	0.8	4.30E-02	27	0.5	9.30E-02	36	1	1.20E-05
Q8JZV7	Putative N-acetylglucosamine-6-phosphate deacetylase	11	1.8	1.90E-01	NA	NA	NA	16	-0.7	8.80E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q8K0C9	GDP-mannose 4,6 dehydratase	19	3.5	5.30E-04	NA	NA	NA	19	-3.8	8.60E-05
Q8K0E8	Fibrinogen beta chain	43	1	2.70E-09	46	0.4	1.70E-01	50	-1.1	5.00E-19
Q8K183	Pyridoxal kinase	7	-0.7	1.00E+00	NA	NA	NA	7	-2.3	1.00E-01
Q8K1B8	Fermitin family homolog 3	47	0.4	7.00E-03	34	1.3	7.60E-06	49	-1.8	6.00E-46
Q8K1M6	Dynamin-1-like protein	11	1.1	4.20E-02	13	0.6	4.10E-01	15	-0.8	5.70E-02
Q8K1X4	NCK associated protein 1 like	6	2.4	4.50E-02	9	2.7	4.50E-03	9	1.1	1.10E-01
Q8K274	Ketosamine-3-kinase	14	1.1	5.00E-01	NA	NA	NA	14	-1.4	6.80E-01
Q8K296	Myotubularin-related protein 3	5	0.9	4.40E-01	6	-0.3	1.00E+00	9	2.1	5.70E-04
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	17	1.7	1.00E-02	10	-0.8	3.20E-01	17	0	8.90E-01
Q8K2H4	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1	7	1.5	3.10E-01	NA	NA	NA	9	-0.9	8.20E-01
Q8K2T1	NmrA-like family domain-containing protein 1	11	2.9	1.00E-02	NA	NA	NA	11	-3.2	4.20E-03
Q8K352	SAM and SH3 domain-containing protein 3	11	0.5	5.70E-01	47	0.4	3.60E-01	47	2.8	1.20E-11
Q8K354	Carbonyl reductase [NADPH] 3	25	3.6	3.10E-04	NA	NA	NA	25	-3	3.70E-04
Q8K411	Presequence protease, mitochondrial	11	1.2	5.00E-02	NA	NA	NA	11	-3.8	2.10E-07
Q8K426	Myeloid cysteine-rich protein	48	1.7	3.80E-06	58	-1.3	3.10E-12	58	1.6	2.10E-22
Q8K482	EMILIN-2	19	0.6	1.70E-02	9	-0.3	7.00E-01	19	-1.1	6.50E-09
Q8K4L3	Supervillin	4	1.3	5.20E-02	7	-0.6	9.80E-02	7	2	5.70E-13
Q8K4Z3	NAD(P)H-hydrate epimerase	29	0.4	6.10E-01	NA	NA	NA	29	-2.4	1.30E-02
Q8K558	Trem-like transcript 1 protein	23	0	8.30E-01	23	1.5	5.40E-02	23	-0.5	3.60E-01
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	18	3.9	4.10E-05	13	-1	2.00E-01	21	0.5	2.30E-01
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L	24	0.1	5.00E-01	22	1.4	4.10E-04	24	-0.9	4.10E-05
Q8QZY6	Tetraspanin-14	12	-0.2	1.00E+00	NA	NA	NA	12	-5.4	1.40E-15
Q8QZY9	Splicing factor 3B subunit 4	9	0.7	3.10E-01	18	-0.5	5.40E-01	18	0.9	2.90E-02
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	30	1.1	1.90E-01	NA	NA	NA	30	1.4	2.30E-03
Q8R016	Bleomycin hydrolase	32	-1	4.60E-05	11	1.5	1.10E-01	32	-3.6	1.50E-40
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	8	0.9	2.40E-01	12	0.5	4.40E-01	12	1	2.50E-02
Q8R081	Heterogeneous nuclear ribonucleoprotein L	27	1.3	4.30E-05	33	0.2	3.70E-01	33	1.3	2.40E-17
Q8R0J7	Vacuolar protein sorting-associated protein 37B	12	-0.1	8.80E-01	NA	NA	NA	12	-3.3	2.20E-03
Q8R146	Acylamino-acid-releasing enzyme	30	-1.2	1.10E-07	7	2.9	1.80E-02	30	-4.4	6.50E-52
Q8R180	ERO1-like protein alpha	32	-0.1	9.10E-01	25	-0.4	3.40E-01	32	0.3	2.10E-01
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	6	1.4	4.10E-02	9	1.4	5.10E-02	9	0.1	8.00E-01
Q8R1Q8	Cytoplasmic dynein 1 light intermediate chain 1	17	2.4	4.50E-02	31	0.1	9.30E-01	31	1.1	1.10E-01
Q8R2S8	CD177 antigen	40	0	8.80E-01	52	-1.3	1.90E-42	52	0.9	9.70E-33
Q8R3G1	Nuclear inhibitor of protein phosphatase 1	6	2.7	1.70E-02	NA	NA	NA	6	0.1	8.90E-01
Q8R550	SH3 domain-containing kinase-binding protein 1	5	1.7	9.60E-02	11	0	1.00E+00	13	2.6	1.50E-09
Q8R5A3	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	7	0.1	6.30E-01	7	-0.1	1.00E+00	7	0.5	9.30E-02
Q8R5H1	Ubiquitin carboxyl-terminal hydrolase 15	5	0.5	5.70E-01	5	0.5	4.20E-01	5	2.1	3.10E-06
Q8R5L1	Complement component 1 Q subcomponent-binding protein, mitochondrial	37	-0.1	9.60E-01	39	-0.7	9.30E-03	39	0.1	4.40E-01
Q8VBT9	Tether containing UBX domain for GLUT4	8	1.6	1.40E-01	NA	NA	NA	11	-0.4	9.90E-01
Q8VBV7	COP9 signalosome complex subunit 8	38	0.5	3.10E-01	24	4	2.80E-05	38	-1	1.20E-02
Q8VBW6	NEDD8-activating enzyme E1 regulatory subunit	12	2.5	7.60E-03	NA	NA	NA	12	-1.4	7.10E-02
Q8VC03	Echinoderm microtubule-associated protein-like 3	5	2.7	1.70E-02	NA	NA	NA	5	-3	8.10E-03
Q8VC30	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	12	0	8.70E-01	NA	NA	NA	12	-3	8.10E-03
Q8VC88	Grancalcin	30	0.6	1.00E-01	27	0.9	1.20E-01	30	-1.1	1.10E-04

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q8VCI0	Phospholipase B-like 1	24	-1.3	2.10E-07	22	-1.1	3.10E-05	24	-0.1	7.00E-01
Q8VCM7	Fibrinogen gamma chain	56	1.2	5.70E-17	43	-0.1	1.00E+00	58	-1.8	2.10E-48
Q8VCN9	Tubulin-specific chaperone C	18	2.6	2.80E-02	NA	NA	NA	18	-2.9	1.50E-02
Q8VCT3	Aminopeptidase B	39	0.8	1.70E-03	21	3.3	4.80E-10	39	-1.6	1.00E-15
Q8VDD5	Myosin-9	36	-0.3	6.00E-04	44	-0.1	2.70E-02	46	1.1	#######
Q8VDK1	Nitrilase homolog 1	27	0	8.30E-01	NA	NA	NA	27	-4.6	1.50E-08
Q8VDL4	ADP-dependent glucokinase	15	0.6	1.90E-01	55	-0.9	2.10E-06	55	2.7	8.70E-43
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	19	-0.1	8.70E-01	18	0.2	5.40E-01	20	-0.4	1.70E-02
Q8VDM6	Heterogeneous nuclear ribonucleoprotein U-like protein 1	20	3	2.80E-12	29	-0.4	3.40E-01	30	0.2	3.50E-01
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	6	1.5	7.30E-02	11	-1.3	3.20E-02	11	1.2	4.00E-03
Q8VDP3	Protein-methionine sulfoxide oxidase MICAL1	6	0.6	1.70E-01	7	0.3	7.20E-01	8	-1.4	1.70E-04
Q8VDP4	Cell cycle and apoptosis regulator protein 2	14	0.8	9.00E-02	22	0.2	5.90E-01	22	1.8	4.50E-15
Q8VDQ8	NAD-dependent protein deacetylase sirtuin-2	12	1.9	6.50E-02	13	2.5	1.10E-02	13	0.4	5.10E-01
Q8VDW0	ATP-dependent RNA helicase DDX39A	18	2.5	1.30E-03	25	-0.1	1.00E+00	32	0.1	8.00E-01
Q8VE11	Myotubularin-related protein 6	5	1.4	1.50E-01	NA	NA	NA	5	-3.3	2.20E-03
Q8VE37	Regulator of chromosome condensation	19	2.3	3.10E-03	11	-0.5	3.60E-01	19	1.5	1.70E-05
Q8VEE0	Ribulose-phosphate 3-epimerase	18	-0.1	9.00E-01	18	1.7	1.20E-02	18	-0.2	7.90E-01
Q8VEE4	Replication protein A 70 kDa DNA-binding subunit	7	1.8	1.90E-01	8	1.6	3.70E-01	11	-0.3	#######
Q8VEH3	ADP-ribosylation factor-like protein 8A	22	1.1	2.90E-01	NA	NA	NA	22	1	1.00E-01
Q8VEK3	Heterogeneous nuclear ribonucleoprotein U	28	0.9	1.40E-03	33	0.2	1.40E-01	35	1.7	1.50E-37
Q8VHM5	Heterogeneous nuclear ribonucleoprotein R	5	1.9	6.50E-02	6	1.7	8.00E-02	9	0.3	6.30E-01
Q8VHX6	Filamin-C	2	-0.4	1.00E+00	NA	NA	NA	2	0.1	7.00E-01
Q8VI36	Paxillin	10	0.5	3.30E-01	30	0.3	3.40E-01	30	1.5	8.20E-09
Q8VI93	2'-5'-oligoadenylate synthase 3	10	3.5	5.30E-04	NA	NA	NA	10	-3.8	8.60E-05
Q8VIJ6	Splicing factor, proline- and glutamine-rich	10	1.7	6.30E-04	11	-0.5	6.10E-02	11	2.1	6.60E-25
Q91UZ5	Inositol monophosphatase 2	16	1.7	9.60E-02	16	2.6	5.30E-02	16	-0.3	#######
Q91V12	Cytosolic acyl coenzyme A thioester hydrolase	6	0.3	6.40E-01	NA	NA	NA	6	-3.5	6.10E-04
Q91V41	Ras-related protein Rab-14	41	1	1.80E-02	33	0.3	6.80E-01	41	-0.7	5.30E-02
Q91V55	40S ribosomal protein S5	24	4	9.80E-06	29	0.5	1.10E-01	35	2.4	6.50E-18
Q91V92	ATP-citrate synthase	32	0	8.60E-01	19	2	1.70E-13	32	-0.9	7.90E-10
Q91VC3	Eukaryotic initiation factor 4A-III	18	1.1	1.30E-03	15	0.8	2.40E-02	18	0	9.40E-01
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	7	1.8	1.90E-01	8	-0.4	7.20E-01	10	3.1	3.10E-09
Q91VH2	Sorting nexin-9	7	2.4	4.50E-02	NA	NA	NA	7	-2.7	2.90E-02
Q91VH6	Protein MEMO1	27	4.6	2.70E-08	NA	NA	NA	27	-4.9	2.80E-10
Q91VI7	Ribonuclease inhibitor	71	0.9	2.00E-07	68	0.9	1.20E-09	73	0.3	2.60E-03
Q91VJ4	Serine/threonine-protein kinase 38	14	3.7	1.10E-04	NA	NA	NA	14	-2	5.50E-03
Q91VR5	ATP-dependent RNA helicase DDX1	5	2	5.90E-03	5	1	1.20E-01	8	0.4	3.50E-01
Q91W89	Alpha-mannosidase 2C1	6	-2.6	1.40E-01	NA	NA	NA	6	-2.3	1.00E-01
Q91WQ3	Tyrosine--tRNA ligase, cytoplasmic	15	1.6	8.00E-03	7	2.2	1.40E-01	17	-2.4	2.20E-05
Q91WV0	Protein Dr1	35	1.2	5.00E-02	31	-0.4	8.60E-01	39	-0.5	3.60E-01
Q91X72	Hemopexin	35	0.2	4.10E-01	34	-0.1	8.80E-01	38	-0.2	2.70E-01
Q91XL1	Leucine-rich HEV glycoprotein	19	-0.3	1.00E+00	28	-1.2	8.60E-06	34	1.2	9.60E-08
Q91YI4	Beta-arrestin-2	28	1.8	1.60E-04	32	0.9	1.30E-03	35	1.4	1.10E-09
Q91YP3	Deoxyribose-phosphate aldolase	31	0	7.50E-01	NA	NA	NA	31	-4.7	2.10E-09

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q91YR9	Prostaglandin reductase 1	32	-0.3	5.40E-01	29	1.9	8.00E-06	32	-1	1.20E-06
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	10	2.2	7.20E-02	20	0.4	6.90E-01	20	1.4	3.00E-02
Q91YX0	Protein THEMIS2	10	2	1.20E-01	15	1.3	9.90E-02	15	1.8	3.80E-03
Q91Z50	Flap endonuclease 1	20	0.5	2.30E-01	24	0	9.90E-01	24	0.1	6.10E-01
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	18	-0.6	1.60E-01	10	1.3	1.40E-01	18	-2.6	2.90E-17
Q91ZR1	Ras-related protein Rab-4B	20	2	1.20E-01	NA	NA	NA	25	0	#######
Q91ZW3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	3	3	6.30E-03	5	-0.5	8.60E-01	6	0.5	4.40E-01
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	4	1.4	5.40E-02	NA	NA	NA	4	-3.2	6.10E-05
Q920B9	FACT complex subunit SPT16	2	3	6.30E-03	9	0.9	1.50E-01	9	1.6	9.10E-04
Q920E5	Farnesyl pyrophosphate synthase	38	0.5	2.10E-02	37	3.5	2.00E-19	41	-0.9	7.30E-07
Q921F2	TAR DNA-binding protein 43	38	0.2	3.90E-01	39	-0.1	9.30E-01	39	1	9.30E-08
Q921F4	Heterogeneous nuclear ribonucleoprotein L-like	18	2.4	1.30E-04	14	0.8	1.30E-01	22	0.4	2.40E-01
Q921G6	Leucine-rich repeat and calponin homology domain-containing protein 4	7	0.3	6.40E-01	20	-0.7	2.10E-01	20	2.2	1.70E-08
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	18	1.3	2.10E-02	23	0.4	3.40E-01	23	0.9	4.00E-03
Q921I1	Serotransferrin	47	-1.1	5.60E-57	44	-0.7	1.40E-05	52	-2.1	#######
Q921M3	Splicing factor 3B subunit 3	21	-0.2	5.60E-01	18	-0.6	3.40E-02	23	-0.7	4.70E-06
Q921M7	Protein FAM49B	40	-0.2	1.00E+00	36	1.7	5.50E-09	40	0	#######
Q921W4	Quinone oxidoreductase-like protein 1	20	1.9	2.30E-02	NA	NA	NA	20	-0.5	6.10E-01
Q921Z5	Tumor necrosis factor alpha-induced protein 8	22	0.8	1.60E-01	22	0.8	2.40E-01	22	-0.1	#######
Q922B2	Aspartate--tRNA ligase, cytoplasmic	15	1.3	7.20E-02	6	1.2	3.30E-01	15	-1.2	5.30E-02
Q922D4	Serine/threonine-protein phosphatase 6 regulatory subunit 3	5	-0.4	1.00E+00	9	0.3	7.40E-01	11	0.3	5.00E-01
Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	8	2.9	1.00E-02	NA	NA	NA	8	-2.3	2.20E-02
Q922F4	Tubulin beta-6 chain	21	0.6	2.30E-02	23	0.7	2.40E-06	26	1.3	1.20E-26
Q922R8	Protein disulfide-isomerase A6	35	-0.4	2.20E-01	55	-0.7	4.70E-06	55	1.1	1.50E-19
Q922S4	cGMP-dependent 3',5'-cyclic phosphodiesterase	15	0	8.30E-01	26	0.7	6.90E-02	26	0.9	9.50E-04
Q923B6	Metalloreductase STEAP4	7	2.2	7.20E-02	23	-1.6	1.20E-03	23	2.8	3.80E-09
Q923L7	Ear6 protein	21	-1.3	7.50E-04	21	-2.3	1.80E-03	21	-1.7	4.60E-08
Q93092	Transaldolase	12	-0.5	4.20E-01	8	0.8	1.30E-01	12	-1.1	2.40E-05
Q99J09	Methylosome protein 50	22	2.8	8.90E-05	17	0.2	8.40E-01	22	-0.4	4.60E-01
Q99J45	Nuclear receptor-binding protein	7	0.5	5.00E-01	NA	NA	NA	7	-0.9	3.50E-01
Q99J77	N-acetylneuraminic acid synthase (Sialic acid synthase)	39	1.6	6.30E-06	17	3.1	2.50E-04	39	-2.1	1.50E-12
Q99J99	3-mercaptopyruvate sulfurtransferase	36	1.8	1.10E-06	NA	NA	NA	36	-6.2	1.60E-26
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	17	1.4	2.10E-02	12	2.1	7.50E-03	17	-0.5	3.20E-01
Q99JT2	Serine/threonine-protein kinase 26	15	4	1.50E-05	19	0.5	2.00E-01	19	2	1.60E-10
Q99JW2	Aminoacylase-1	11	-1	5.00E-01	NA	NA	NA	11	-3.2	1.10E-04
Q99JW4	LIM and senescent cell antigen-like-containing domain protein 1	20	-0.3	1.00E+00	33	0.3	3.70E-01	33	1.2	3.10E-06
Q99JX4	Eukaryotic translation initiation factor 3 subunit M	24	0.4	4.70E-01	16	1.7	8.00E-02	24	-0.7	2.60E-01
Q99JX7	Nuclear RNA export factor 1	6	1.1	2.90E-01	8	1.5	1.10E-01	10	0.7	3.20E-01
Q99JY9	Actin-related protein 3	74	-0.5	2.80E-09	59	0.4	3.90E-04	76	-0.8	8.10E-31
Q99K41	EMILIN-1	13	-1	4.30E-02	9	1.1	1.10E-01	13	-1.1	1.10E-03
Q99K48	Non-POU domain-containing octamer-binding protein	12	0.3	4.20E-01	5	-0.1	1.00E+00	12	0.2	4.80E-01
Q99K85	Phosphoserine aminotransferase	14	1.4	1.10E-02	14	1.2	6.20E-01	23	-3.7	1.80E-09
Q99KE1	NAD-dependent malic enzyme, mitochondrial	44	1.2	9.10E-08	30	-0.1	9.00E-01	44	-1	6.20E-09
Q99KH8	Serine/threonine-protein kinase 24	19	2	8.40E-04	23	0.5	1.70E-01	23	1.4	1.20E-06

		Exosomes			MDSCs			Global		
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Q99KI0	Aconitate hydratase, mitochondrial	22	2.9	4.20E-14	16	-0.4	6.40E-01	24	-1	7.40E-05
Q99KJ8	Dynactin subunit 2	16	-0.2	9.50E-01	20	-0.6	2.40E-01	20	1.6	3.10E-07
Q99KK2	N-acylneuraminate cytidylyltransferase	13	1.4	2.10E-01	NA	NA	NA	13	-1.3	2.70E-01
Q99KK7	Dipeptidyl peptidase 3	39	-0.5	1.20E-02	31	3.5	6.00E-19	40	-1.5	1.40E-23
Q99KN1	Arrestin domain-containing protein 1	29	3.1	1.10E-04	NA	NA	NA	29	-4.3	4.10E-07
Q99KP6	Pre-mRNA-processing factor 19	30	1.7	1.40E-04	17	0.5	2.00E-01	34	0.3	2.30E-01
Q99KQ4	Nicotinamide phosphoribosyltransferase	16	0.9	1.20E-01	NA	NA	NA	16	-4.7	4.00E-09
Q99KV1	DnaJ homolog subfamily B member 11	9	0.3	7.00E-01	NA	NA	NA	9	-2.9	1.50E-02
Q99L04	Dehydrogenase/reductase SDR family member 1	18	2	4.30E-02	24	2.8	3.30E-05	24	1.5	1.40E-03
Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial	9	2	1.20E-01	NA	NA	NA	9	-2.3	1.00E-01
Q99LB4	Capping protein (Actin filament), gelsolin-like	42	0.9	8.40E-04	38	0.1	7.00E-01	50	0	8.70E-01
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	42	2	9.60E-09	43	0.2	5.30E-01	51	0	9.80E-01
Q99LD4	COP9 signalosome complex subunit 1	13	-0.8	8.80E-01	NA	NA	NA	13	-2.3	5.00E-03
Q99LF4	tRNA-splicing ligase RtcB homolog	13	2.3	1.80E-02	12	2.4	4.10E-03	17	0.6	3.10E-01
Q99LL3	Carbohydrate sulfotransferase 12	20	0.4	4.40E-01	19	-1.2	4.60E-02	24	0.2	5.20E-01
Q99LT0	Protein dpy-30 homolog	36	0	8.40E-01	36	-0.1	1.00E+00	36	0.8	2.00E-03
Q99LX0	Protein deglycase DJ-1	39	-0.2	1.00E+00	31	0.6	5.30E-02	39	0.6	1.60E-03
Q99M15	Proline-serine-threonine phosphatase-interacting protein 2	9	2.4	4.50E-02	9	2.6	7.30E-03	9	1	1.50E-01
Q99MK8	Beta-adrenergic receptor kinase 1	13	3.2	7.30E-05	9	2.1	2.30E-02	16	-0.6	3.10E-01
Q99MN1	Lysine--tRNA ligase	9	0.6	2.00E-01	8	1.2	1.90E-02	9	0.4	2.60E-01
Q99N15	17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase	49	1.8	6.00E-07	28	-0.2	9.30E-01	49	-1.1	8.00E-05
Q99NB9	Splicing factor 3B subunit 1	14	1.6	1.50E-05	18	0.2	4.30E-01	21	0.6	1.70E-03
Q99PT1	Rho GDP-dissociation inhibitor 1	28	0.1	5.90E-01	28	1.2	4.20E-07	28	0.8	7.00E-06
Q99PV0	Pre-mRNA-processing-splicing factor 8	6	0.9	7.60E-02	7	1.3	1.50E-02	11	0	9.60E-01
Q9CPW4	Actin-related protein 2/3 complex subunit 5	43	0	8.70E-01	46	0.1	7.90E-01	46	-1	5.30E-11
Q9CPX6	Ubiquitin-like-conjugating enzyme ATG3	9	1	1.70E-01	13	-0.9	8.30E-01	13	-1.5	2.70E-02
Q9CPY7	Cytosol aminopeptidase	7	3.4	8.40E-04	NA	NA	NA	10	-0.2	#######
Q9CQ60	6-phosphogluconolactonase	39	0.5	2.40E-01	64	1.5	1.30E-10	64	1.8	1.10E-20
Q9CQ80	Vacuolar protein-sorting-associated protein 25	28	1.5	7.30E-02	NA	NA	NA	28	0.2	7.80E-01
Q9CQC6	Basic leucine zipper and W2 domain-containing protein 1	7	0.9	1.10E-01	16	-0.7	4.00E-01	16	-0.3	7.00E-01
Q9CQE1	Protein NipSnap homolog 3B	33	0.1	6.70E-01	NA	NA	NA	33	-2.2	2.90E-09
Q9CQE8	UPF0568 protein C14orf166 homolog	22	1.1	4.50E-02	28	-0.6	1.70E-01	28	1.2	2.60E-05
Q9CQI6	Coactosin-like protein	40	-0.3	7.00E-01	53	0.9	7.30E-04	53	0.6	8.20E-04
Q9CQR6	Serine/threonine-protein phosphatase 6 catalytic subunit	29	0	8.40E-01	25	1.2	3.60E-02	29	-0.6	1.00E-01
Q9CQV8	14-3-3 protein beta/alpha	54	-0.2	5.20E-01	66	0.1	5.80E-01	66	0.2	1.60E-01
Q9CRA5	Golgi phosphoprotein 3	18	1.7	1.20E-03	18	-0.2	1.00E+00	18	-0.8	3.70E-02
Q9CRA8	Exosome complex component RRP46	26	2.2	7.20E-02	NA	NA	NA	26	-2.5	5.50E-02
Q9CRC8	Leucine-rich repeat-containing protein 40	6	2	1.20E-01	NA	NA	NA	6	-2.3	1.00E-01
Q9CSU0	Regulation of nuclear pre-mRNA domain-containing protein 1B	14	2.9	1.00E-02	24	-0.5	3.70E-01	24	2.6	4.50E-11
Q9CU62	Structural maintenance of chromosomes protein 1A	7	-0.1	8.80E-01	9	-0.9	4.80E-02	9	0.6	3.30E-02
Q9CVB6	Actin-related protein 2/3 complex subunit 2	60	-0.4	1.40E-06	50	0.4	3.10E-02	60	-1.7	#######
Q9CWF2	Tubulin beta-2B chain	47	1	2.50E-08	55	0.5	6.40E-07	55	1.5	4.40E-68
Q9CWJ9	Bifunctional purine biosynthesis protein PURH	39	1.2	9.90E-05	30	1.7	2.60E-04	46	-1.1	1.10E-06
Q9CX34	Protein SGT1 homolog	11	0.3	6.40E-01	11	0.2	7.60E-01	11	2.1	1.20E-07

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0	12	1.5	3.10E-01	14	-0.5	3.10E-01	14	4	1.70E-16
Q9CXF4	TBC1 domain family member 15	4	2.2	7.20E-02	5	1.5	1.60E-01	7	0.8	3.40E-01
Q9CXI5	Mesencephalic astrocyte-derived neurotrophic factor	27	0.6	2.40E-01	35	-1	6.80E-02	35	0.3	4.40E-01
Q9CXT8	Mitochondrial-processing peptidase subunit beta	10	1.8	1.90E-01	NA	NA	NA	10	-0.7	8.80E-01
Q9CXY6	Interleukin enhancer-binding factor 2	29	0.6	2.00E-01	18	1.2	7.90E-02	29	-0.7	7.10E-02
Q9CY50	Translocon-associated protein subunit alpha	19	3.5	5.30E-04	22	-0.3	7.20E-01	22	1.9	2.80E-07
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein	4	0.4	6.10E-01	13	0.3	8.00E-01	13	0.6	3.50E-01
Q9CY64	Biliverdin reductase A	17	3.5	5.30E-04	NA	NA	NA	17	-3.8	8.60E-05
Q9CYL5	Golgi-associated plant pathogenesis-related protein 1	45	3	2.30E-05	40	-0.4	7.20E-01	57	0.5	1.90E-01
Q9CZ04	COP9 signalosome complex subunit 7a	28	-0.8	2.20E-01	17	0.8	3.40E-01	28	-1.3	1.70E-03
Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	21	1.2	1.00E-01	27	-0.4	1.10E-01	27	3.4	4.20E-40
Q9CZ30	Obg-like ATPase 1	21	0.1	6.00E-01	10	2.5	1.10E-02	21	-2.5	1.30E-12
Q9CZ42	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	37	4.3	1.20E-06	NA	NA	NA	37	-3.7	3.90E-07
Q9CZ44	NSFL1 cofactor p47	26	0.1	5.30E-01	25	0.1	6.90E-01	31	0.1	7.70E-01
Q9CZD3	Glycine--tRNA ligase	9	2	4.50E-05	9	2.7	4.00E-04	9	-1.1	4.30E-03
Q9CZE3	Ras-related protein Rab-32	16	1.9	6.50E-02	NA	NA	NA	16	-0.9	4.30E-01
Q9CZM2	60S ribosomal protein L15	13	4	1.50E-05	NA	NA	NA	13	-2.9	5.70E-05
Q9CZN7	Serine hydroxymethyltransferase	22	1	5.80E-04	21	0.6	8.20E-02	23	-0.4	7.80E-02
Q9CZU3	Superkiller viralicidic activity 2-like 2	3	1.1	5.00E-01	NA	NA	NA	3	0.7	6.40E-01
Q9CZU6	Citrate synthase, mitochondrial	21	0.9	5.00E-03	13	-2.3	1.10E-03	22	-2	3.70E-12
Q9D020	Cytosolic 5'-nucleotidase 3A	34	1.5	9.80E-04	27	4.2	2.70E-06	34	-1.2	4.70E-04
Q9D071	MMS19 nucleotide excision repair protein homolog	4	1.8	1.90E-01	NA	NA	NA	4	-0.7	8.80E-01
Q9D0F9	Phosphoglucomutase-1	18	-0.2	1.00E+00	19	2.1	7.50E-03	20	-1.3	5.40E-04
Q9D0I9	Arginine--tRNA ligase, cytoplasmic	15	0.5	3.30E-01	9	1.7	1.10E-03	15	0.4	2.10E-01
Q9D0K2	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	19	1.2	7.30E-03	17	0.2	8.20E-01	21	-0.8	2.60E-02
Q9D0R2	Threonine--tRNA ligase, cytoplasmic	16	1.1	8.80E-03	NA	NA	NA	16	-4.8	1.90E-16
Q9D154	Leukocyte elastase inhibitor A	29	-0.3	3.50E-01	55	2.2	8.70E-30	55	0.5	5.00E-04
Q9D1A2	Cytosolic non-specific dipeptidase	26	1.8	4.60E-04	10	0.9	1.90E-01	26	-0.8	4.30E-02
Q9D1G1	Ras-related protein Rab-1B	37	0.3	5.00E-01	27	-0.6	5.30E-01	41	-0.1	#######
Q9D1K2	V-type proton ATPase subunit F	30	-0.7	4.60E-01	22	0.5	4.20E-01	32	-0.2	6.80E-01
Q9D1M0	Protein SEC13 homolog	12	-0.1	8.70E-01	12	0.6	6.70E-01	17	-1.3	2.50E-02
Q9D1Q6	Endoplasmic reticulum resident protein 44	21	-0.4	8.20E-01	33	-1.1	7.20E-03	33	0.1	7.40E-01
Q9D2V7	Coronin-7	53	1.1	1.30E-09	36	0.2	2.70E-01	54	-0.4	2.00E-03
Q9D4D4	Transketolase-like protein 2	5	-0.3	1.00E+00	NA	NA	NA	5	-2.3	1.20E-03
Q9D554	Splicing factor 3A subunit 3	12	1.1	2.90E-01	29	-0.4	5.60E-01	29	2.4	3.40E-08
Q9D662	Protein transport protein Sec23B	5	0.6	6.00E-01	NA	NA	NA	5	-1.2	5.20E-01
Q9D6F9	Tubulin beta-4A chain	52	1.1	6.50E-09	52	0.4	3.10E-04	59	1.5	6.10E-59
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	15	3.8	6.90E-05	12	-1.1	3.00E-01	17	-0.3	8.10E-01
Q9D6Y9	1,4-alpha-glucan-branching enzyme	4	1.8	1.80E-02	5	2.3	3.00E-02	7	-0.7	3.20E-01
Q9D6Z1	Nucleolar protein 56	9	3.1	4.00E-03	10	-0.2	1.00E+00	14	1.2	1.10E-02
Q9D7G0	Ribose-phosphate pyrophosphokinase 1	16	1.9	6.50E-02	NA	NA	NA	16	-2.3	2.20E-02
Q9D819	Inorganic pyrophosphatase	24	3.1	4.00E-03	NA	NA	NA	24	-2.6	7.20E-03
Q9D892	Inosine triphosphate pyrophosphatase	25	1.7	3.10E-03	25	2.5	1.70E-03	25	-0.8	8.70E-02
Q9D8B3	Charged multivesicular body protein 4b	13	3.4	1.70E-05	13	-0.5	7.20E-01	13	-0.4	5.40E-01

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Q9D8E6	60S ribosomal protein L4	11	2.7	1.70E-02	13	-0.7	2.80E-01	17	2.3	9.60E-08
Q9D8N0	Elongation factor 1-gamma	42	0.7	3.50E-03	37	0.8	4.50E-03	42	-0.5	6.90E-03
Q9D8N2	Protein FAM45A	13	2.6	2.80E-02	NA	NA	NA	13	-2	6.70E-02
Q9D8W5	26S proteasome non-ATPase regulatory subunit 12	12	-0.6	6.90E-01	7	0.2	8.20E-01	12	-0.9	5.30E-02
Q9D8Y7	Tumor necrosis factor alpha-induced protein 8-like protein 2	33	2.3	4.70E-03	22	2.6	5.30E-02	33	-1.4	3.50E-02
Q9D906	Ubiquitin-like modifier-activating enzyme ATG7	15	1.7	4.10E-03	14	1.2	1.30E-01	18	-0.7	1.20E-01
Q9D964	Glycine amidinotransferase, mitochondrial	13	1.1	1.90E-01	9	-0.5	8.60E-01	13	0.3	6.60E-01
Q9DAR7	m7GpppX diphosphatase	19	-0.9	5.20E-01	20	4.2	4.90E-06	24	0.2	7.10E-01
Q9DB05	Alpha-soluble NSF attachment protein	31	2.3	8.00E-04	25	-1.5	1.80E-03	35	0.9	8.00E-03
Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit	11	0	8.70E-01	14	2.2	4.80E-02	14	0.3	7.50E-01
Q9DBG3	AP-2 complex subunit beta	27	0.1	4.50E-01	26	0.3	2.50E-01	32	-0.9	8.40E-10
Q9DBG6	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	21	0.8	2.90E-01	40	-0.4	1.30E-01	40	3.7	1.50E-47
Q9DBJ1	Phosphoglycerate mutase 1	41	0.2	2.40E-01	41	1.7	1.60E-10	41	-0.5	8.60E-04
Q9DBK7	MCG18845, isoform CRA_d	9	-0.3	1.00E+00	NA	NA	NA	9	-3.4	7.50E-08
Q9DBL1	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	14	2.1	1.00E-02	14	0.6	6.70E-01	14	-0.9	1.90E-01
Q9DBR1	5'-3' exoribonuclease 2	4	0.9	2.20E-01	4	3	1.10E-02	4	-0.8	2.70E-01
Q9DBR7	Protein phosphatase 1 regulatory subunit 12A	4	-0.3	9.90E-01	6	-0.1	1.00E+00	7	1	5.80E-02
Q9DBZ5	Eukaryotic translation initiation factor 3 subunit K	31	1.6	1.40E-01	27	1.5	2.40E-01	33	-0.2	#######
Q9DC23	DnaJ homolog subfamily C member 10	7	0.1	8.40E-01	NA	NA	NA	7	-2.3	1.00E-01
Q9DC50	Peroxisomal carnitine O-octanoyltransferase	10	0.2	5.90E-01	NA	NA	NA	10	-4.7	2.10E-09
Q9DC51	Guanine nucleotide-binding protein G(k) subunit alpha	17	0.9	2.00E-01	35	-0.9	2.90E-14	35	5	#######
Q9DC61	Mitochondrial-processing peptidase subunit alpha	11	1.1	9.20E-02	NA	NA	NA	11	-0.9	1.10E-01
Q9DCC5	Cbx3 protein	38	-0.3	6.20E-01	45	-1	2.90E-08	45	1.4	7.90E-23
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	47	0.1	2.30E-01	40	1.1	2.60E-16	47	-1.1	6.40E-46
Q9DCH4	Eukaryotic translation initiation factor 3 subunit F	14	-0.2	1.00E+00	12	0.2	6.40E-01	17	0	#######
Q9DCL9	Multifunctional protein ADE2	15	-0.1	8.70E-01	18	3.4	2.80E-05	18	-1	8.80E-03
Q9DCM0	Persulfide dioxygenase ETHE1, mitochondrial	19	2	1.20E-01	32	-1	8.90E-02	32	2.9	1.40E-08
Q9DCS2	UPF0585 protein C16orf13 homolog	31	3.1	4.00E-03	NA	NA	NA	31	-3.4	1.20E-03
Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial	21	2.6	2.80E-02	NA	NA	NA	21	-2.9	1.50E-02
Q9DCW4	Electron transfer flavoprotein subunit beta	20	1.2	4.80E-02	24	0	9.30E-01	24	0.6	7.30E-02
Q9DCZ1	GMP reductase 1	6	0.6	6.00E-01	NA	NA	NA	6	-0.7	8.80E-01
Q9EPB4	Apoptosis-associated speck-like protein containing a CARD	22	-0.4	1.00E+00	32	2.2	5.60E-04	32	0.5	2.60E-01
Q9EPK2	Protein XRP2	7	-1.4	3.90E-01	7	-3.2	1.00E-02	7	-0.3	#######
Q9EPK7	Exportin-7	5	0.3	7.00E-01	NA	NA	NA	5	-0.6	7.70E-01
Q9EPL8	Importin-7	11	0.1	6.80E-01	5	3.5	8.20E-04	11	-1.4	1.10E-03
Q9EPU0	Regulator of nonsense transcripts 1	6	2	1.60E-02	5	1	2.30E-01	7	0.1	8.90E-01
Q9EQG9	Collagen type IV alpha-3-binding protein	14	4	9.80E-06	19	1.6	4.40E-03	24	0.7	9.10E-02
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	3	0.6	3.10E-01	3	-2.7	7.20E-02	3	-1.8	3.20E-03
Q9EQH3	Vacuolar protein sorting-associated protein 35	27	0.5	4.80E-02	20	-0.2	8.30E-01	27	-0.6	2.50E-03
Q9EQI5	Chemokine (C-X-C motif) ligand 7, isoform CRA_b	41	-1.4	2.00E-02	31	1.4	1.50E-01	41	-1.4	1.90E-03
Q9EQK5	Major vault protein	50	-0.4	8.60E-03	39	0.5	2.50E-02	50	-1.1	3.20E-23
Q9EQP2	EH domain-containing protein 4	5	1.1	2.90E-01	NA	NA	NA	5	-3	8.10E-03
Q9EQU5	Protein SET	27	-0.1	9.40E-01	32	-0.8	8.40E-03	32	0.3	1.70E-01
Q9ER72	Cysteine--tRNA ligase, cytoplasmic	8	-0.5	6.50E-01	4	2.4	4.10E-03	8	-1.5	5.60E-05

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q9ERF3	WD repeat-containing protein 61	24	1.8	4.60E-04	13	0.5	5.40E-01	24	-1	7.10E-03
Q9ERK4	Exportin-2	21	1.6	2.10E-08	9	1.4	7.10E-03	21	-1.6	3.20E-12
Q9ERL7	Glia maturation factor gamma	26	0.7	4.00E-01	9	-0.5	7.20E-01	26	0.6	2.40E-01
Q9ERR7	15 kDa selenoprotein	38	0.5	2.50E-01	38	-0.7	2.30E-01	38	-0.1	8.80E-01
Q9ES46	Beta-parvin	13	-0.5	1.00E+00	NA	NA	NA	13	-1.4	1.00E-02
Q9ES52	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	6	0.5	1.80E-01	7	0.2	6.60E-01	7	-0.2	6.90E-01
Q9ESP1	Stromal cell-derived factor 2-like protein 1	37	0.2	5.60E-01	37	-0.2	1.00E+00	37	0.5	1.50E-01
Q9EST5	Acidic leucine-rich nuclear phosphoprotein 32 family member B	11	1.5	2.50E-03	36	0.8	1.40E-03	36	1.9	1.80E-20
Q9ESU7	Amino acid transporter	6	1.8	1.90E-01	NA	NA	NA	10	-1.2	5.20E-01
Q9ESX5	H/ACA ribonucleoprotein complex subunit 4	6	3.1	4.00E-03	NA	NA	NA	10	-1.1	2.20E-01
Q9ET01	Glycogen phosphorylase, liver form	53	-0.3	1.60E-04	31	1.2	3.70E-11	54	-2.3	#######
Q9ET66	Peptidase inhibitor 16	9	-0.5	1.00E+00	14	-1.3	1.40E-02	14	2.2	1.20E-06
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	10	2.2	7.20E-02	NA	NA	NA	10	-2.5	5.50E-02
Q9JHK4	Geranylgeranyl transferase type-2 subunit alpha	12	2.9	1.00E-02	NA	NA	NA	18	-1.4	1.50E-01
Q9JHK5	Pleckstrin	24	-0.1	9.20E-01	30	0.3	2.30E-01	30	-0.3	6.40E-02
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	8	1.5	6.60E-05	8	0.7	4.00E-03	10	1.2	6.10E-11
Q9JHU9	Inositol-3-phosphate synthase 1	10	-1.4	1.30E-02	NA	NA	NA	10	-4.2	1.80E-10
Q9JHW4	Selenocysteine-specific elongation factor	9	1.8	1.90E-01	NA	NA	NA	9	-2.1	1.90E-01
Q9JIF0	Protein arginine N-methyltransferase 1	11	1.3	7.30E-02	11	0.4	9.90E-01	15	-2.3	2.00E-03
Q9JIF7	Coatomer subunit beta	7	2.4	1.20E-02	16	0.3	4.10E-01	18	2.3	8.00E-11
Q9JIZ9	Phospholipid scramblase 3	20	1.4	1.60E-02	NA	NA	NA	20	-4.1	2.40E-09
Q9JJ00	Phospholipid scramblase 1	17	1.6	7.20E-02	21	-0.9	2.90E-01	21	0.9	8.60E-02
Q9JJ28	Protein flightless-1 homolog	13	0	7.50E-01	19	-0.1	1.00E+00	23	1.1	4.30E-06
Q9JJK2	LanC-like protein 2	14	2.9	1.00E-02	NA	NA	NA	14	-2.3	2.20E-02
Q9JKC8	AP-3 complex subunit mu-1	7	1.4	1.50E-01	16	2.9	1.10E-03	16	0.7	2.20E-01
Q9JKF1	Ras GTPase-activating-like protein IQGAP1	40	0.1	4.00E-01	37	-0.1	3.00E-01	43	0.5	7.40E-13
Q9JKR6	Hypoxia up-regulated protein 1	11	0.2	5.30E-01	16	-0.8	3.20E-03	16	1	2.80E-07
Q9JL26	Formin-like protein 1	13	3.4	1.20E-05	12	0.1	6.70E-01	13	2.5	8.70E-26
Q9JLJ2	4-trimethylaminobutyraldehyde dehydrogenase	30	1.4	1.80E-03	9	1.1	2.90E-01	30	-2.2	8.40E-08
Q9JLQ2	ARF GTPase-activating protein GIT2	19	1.7	6.30E-04	14	0.1	7.70E-01	19	0.8	2.30E-03
Q9JLT4	Isoform 2 of Thioredoxin reductase 2, mitochondrial	18	-1.1	8.20E-01	NA	NA	NA	24	-1.7	1.10E-01
Q9JLV6	Bifunctional polynucleotide phosphatase/kinase	37	0.9	9.90E-05	32	0.5	7.70E-02	43	-0.5	3.30E-03
Q9JM14	5'(3')-deoxyribonucleotidase, cytosolic type	28	3.6	9.60E-07	23	3.8	9.00E-05	39	-0.8	8.90E-02
Q9JM76	Actin-related protein 2/3 complex subunit 3	45	-0.3	6.60E-01	40	0.6	8.70E-02	45	-0.5	4.50E-03
Q9JMA1	Ubiquitin carboxyl-terminal hydrolase 14	24	0.1	5.70E-01	14	0.7	1.10E-01	24	-0.6	1.10E-02
Q9JMH6	Thioredoxin reductase 1, cytoplasmic	38	-0.2	6.20E-01	24	3.2	6.20E-08	38	-3.1	1.90E-68
Q9JMH9	Unconventional myosin-XVIIIa	4	2.4	4.50E-02	6	-2.1	4.00E-09	6	3.5	1.40E-18
Q9QUH0	Glutaredoxin-1	38	0.3	4.10E-01	49	2.3	1.50E-13	49	1.2	4.80E-08
Q9QUI0	Transforming protein RhoA	58	0.9	2.10E-04	45	0.1	8.20E-01	58	0	9.00E-01
Q9QUM0	Integrin alpha-IIb	34	-0.6	2.20E-05	35	-1.1	1.10E-11	36	-0.5	2.30E-06
Q9QUM9	Proteasome subunit alpha type-6	30	-0.8	1.30E-02	12	1.5	2.40E-01	30	-4.1	4.80E-33
Q9QUR6	Prolyl endopeptidase	38	0.2	2.40E-01	13	4.6	1.10E-08	38	-2.7	2.40E-36
Q9QWK4	CD5 antigen-like	19	-2.1	2.80E-03	NA	NA	NA	19	-4.4	1.10E-07
Q9QWR8	Alpha-N-acetylgalactosaminidase	7	-1.1	4.60E-01	14	-0.8	6.80E-01	14	-0.4	7.40E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q9QXD6	Fructose-1,6-bisphosphatase 1	15	-1.6	3.20E-01	NA	NA	NA	15	-3	8.10E-03
Q9QXG4	Acetyl-coenzyme A synthetase, cytoplasmic	5	1.8	1.90E-01	NA	NA	NA	5	-2.1	1.90E-01
Q9QXK3	Coatomer subunit gamma-2	13	1	1.60E-02	19	-0.3	5.10E-01	19	1.3	1.30E-09
Q9QXS1	Plectin	9	0.7	4.60E-03	19	-0.6	3.40E-06	19	1.6	4.50E-45
Q9QYB5	Gamma-adducin	10	-0.4	1.00E+00	15	0.3	8.60E-01	18	-1.2	3.10E-02
Q9QYC0	Alpha-adducin	17	-0.9	5.70E-02	22	-0.5	3.70E-01	26	-0.1	9.30E-01
Q9QYJ0	DnaJ homolog subfamily A member 2	11	1.4	1.50E-01	11	-0.2	1.00E+00	11	-0.1	#######
Q9QZ88	Vacuolar protein sorting-associated protein 29	15	3.1	4.00E-03	NA	NA	NA	15	-3.4	1.20E-03
Q9QZD9	Eukaryotic translation initiation factor 3 subunit I	24	0.6	1.70E-01	24	-1.3	4.10E-03	24	0.1	7.20E-01
Q9QZE5	Coatomer subunit gamma-1	18	0.8	4.20E-02	32	-0.2	4.80E-01	32	1.7	5.90E-21
Q9QZF2	Glypican-1	6	-1.3	4.30E-01	NA	NA	NA	6	-2.1	1.50E-02
Q9QZK7	Docking protein 3	34	1.8	5.00E-05	35	0.5	2.60E-01	41	0.2	4.10E-01
Q9QZQ8	Core histone macro-H2A.1	59	0.7	5.80E-98	52	-0.7	9.20E-85	59	-0.3	3.00E-45
Q9QZU3	Platelet glycoprotein V (Fragment)	25	-2.2	9.60E-11	12	3.1	6.50E-03	25	-3	9.60E-18
Q9R062	Glycogenin-1	49	-0.7	1.30E-02	26	2.2	4.90E-03	49	-2.6	6.00E-22
Q9R0C8	Guanine nucleotide exchange factor VAV3	9	3.9	4.10E-05	NA	NA	NA	9	-2.4	6.80E-04
Q9R0E1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	10	-0.3	9.90E-01	NA	NA	NA	12	-2	6.70E-02
Q9R0N0	Galactokinase	27	2.9	2.90E-06	NA	NA	NA	27	-5.1	4.80E-12
Q9R0P3	S-formylglutathione hydrolase	65	1.1	1.60E-10	55	2.8	2.90E-17	70	-1.5	1.30E-24
Q9R0P5	Destrin	58	1.7	5.80E-26	47	2.4	3.30E-40	58	-0.3	2.10E-02
Q9R0Q7	Prostaglandin E synthase 3	28	2.5	2.50E-05	28	2.5	1.90E-06	28	0.3	3.10E-01
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial	7	0.4	6.60E-01	NA	NA	NA	7	-2.5	5.50E-02
Q9R111	Guanine deaminase	52	-0.3	1.20E-02	45	0.8	2.80E-05	52	-1.1	7.50E-31
Q9R1P0	Proteasome subunit alpha type-4	57	-0.4	2.90E-01	29	1.2	7.70E-03	57	-1.4	2.50E-11
Q9R1P1	Proteasome subunit beta type-3	17	-0.2	1.00E+00	17	1.7	1.80E-02	17	-2	3.70E-12
Q9R1P3	Proteasome subunit beta type-2	41	-0.9	8.90E-04	26	1.6	8.00E-02	49	-3.3	3.70E-33
Q9R1P4	Proteasome subunit alpha type-1	44	-0.7	1.30E-02	16	-0.4	7.20E-01	44	-2.1	4.00E-17
Q9R1T2	SUMO-activating enzyme subunit 1	16	0.1	6.40E-01	24	0	9.90E-01	24	-0.6	7.20E-02
Q9R1T4	Septin-6	12	1.6	7.20E-02	12	0.4	6.90E-01	12	0.4	4.60E-01
Q9R257	Heme-binding protein 1	23	1.7	1.40E-02	NA	NA	NA	23	-0.3	8.40E-01
Q9WTL7	Acyl-protein thioesterase 2	21	0.6	4.50E-01	NA	NA	NA	21	-2.9	1.20E-03
Q9WTM5	RuvB-like 2	7	1.5	3.10E-01	NA	NA	NA	9	-0.4	#######
Q9WTP6	Adenylate kinase 2, mitochondrial	17	0.6	2.70E-01	24	-0.3	7.20E-01	24	1.1	7.50E-04
Q9WTX6	Cullin-1	5	1.1	5.00E-01	NA	NA	NA	6	-0.5	#######
Q9WU28	Prefoldin subunit 5	24	0.2	5.10E-01	NA	NA	NA	34	-2.6	8.60E-08
Q9WU78	Programmed cell death 6-interacting protein	33	0.3	1.00E-01	23	0.5	5.80E-02	36	-0.7	2.50E-07
Q9WUA2	Phenylalanine--tRNA ligase beta subunit	7	1.1	9.20E-02	4	3.3	2.30E-03	7	-0.8	1.60E-01
Q9WUA3	ATP-dependent 6-phosphofructokinase, platelet type	14	2.5	1.30E-03	17	4.2	2.70E-06	17	0.1	8.00E-01
Q9WUM3	Coronin-1B	32	0.8	4.80E-03	25	0.6	1.60E-01	36	-0.9	8.00E-05
Q9WUM4	Coronin-1C	19	0.2	4.00E-01	14	1	1.10E-01	19	-1.9	2.90E-14
Q9WUP7	Ubiquitin carboxyl-terminal hydrolase isozyme L5	10	3	6.30E-03	34	0.4	5.50E-01	34	1.5	2.00E-03
Q9WV02	RNA-binding motif protein, X chromosome	11	3.4	8.40E-04	9	-1.3	2.20E-01	13	0.2	7.80E-01
Q9WV32	Actin-related protein 2/3 complex subunit 1B	48	-0.2	6.30E-01	48	0.8	2.30E-05	53	-0.7	8.50E-10
Q9WV60	Glycogen synthase kinase-3 beta	13	1.9	6.50E-02	21	1.2	3.30E-01	21	-0.1	#######

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q9WVA3	Mitotic checkpoint protein BUB3	19	2.5	1.30E-03	NA	NA	NA	19	0.7	6.80E-02
Q9WVA4	Transgelin-2	39	0.2	4.50E-01	46	1	2.70E-06	46	0.6	5.90E-05
Q9WVG5	Endothelial lipase	24	1.1	6.30E-04	15	-0.8	1.40E-01	24	-1.1	3.40E-05
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	16	1.3	7.20E-02	21	1.3	3.60E-01	24	-1.7	7.80E-03
Q9WVK4	EH domain-containing protein 1	29	0.6	5.80E-02	14	0.4	3.00E-01	29	-0.7	3.20E-03
Q9Z0H3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	16	0.2	8.30E-01	16	2.2	3.70E-04	16	3.1	1.10E-07
Q9Z0H4	CUGBP Elav-like family member 2	6	3.2	2.40E-03	NA	NA	NA	6	0	#######
Q9Z0I7	Protein Slfn1	21	1.7	1.00E-02	13	1.1	5.30E-01	24	-2.2	1.80E-04
Q9Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	23	0.6	1.40E-01	16	0.7	1.20E-01	27	-0.1	#######
Q9Z0P5	Twinfilin-2	38	0	6.90E-01	46	0.5	4.50E-02	46	0.5	1.50E-03
Q9Z126	Platelet factor 4	38	-1.2	9.10E-18	30	0.1	7.00E-01	38	-2.3	3.00E-58
Q9Z183	Protein-arginine deiminase type-4	31	-0.1	9.00E-01	34	-0.6	1.50E-02	37	0.5	1.30E-03
Q9Z1B7	Mitogen-activated protein kinase 13	8	2.7	2.00E-03	NA	NA	NA	8	-3.9	2.30E-05
Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G	15	1.3	1.00E-01	18	-0.8	4.60E-01	18	0.5	4.10E-01
Q9Z1E4	Glycogen [starch] synthase, muscle	19	0.7	1.00E-01	16	1.1	4.50E-03	22	0.2	3.60E-01
Q9Z1F9	SUMO-activating enzyme subunit 2	22	1.4	1.10E-02	20	1.8	3.10E-03	26	0	9.70E-01
Q9Z1N5	Spliceosome RNA helicase Ddx39b	27	0.5	6.00E-02	34	-0.2	8.10E-01	41	-0.1	6.30E-01
Q9Z1Q5	Chloride intracellular channel protein 1	56	0.9	4.60E-07	41	0.9	9.90E-05	56	-0.7	5.50E-07
Q9Z1Q9	Valine--tRNA ligase	22	1.6	2.20E-06	22	1.7	1.40E-06	24	-0.1	8.60E-01
Q9Z1Z0	General vesicular transport factor p115	6	-0.8	1.00E+00	14	0.8	2.40E-01	14	2.8	1.10E-05
Q9Z1Z2	Serine-threonine kinase receptor-associated protein	18	1.2	1.60E-03	27	-0.5	6.30E-01	27	-1.3	2.70E-05
Q9Z2G9	Oxidoreductase HTATIP2	10	1.5	3.10E-01	NA	NA	NA	10	-1.8	3.60E-01
Q9Z2I8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	13	1.1	5.00E-01	23	0	1.00E+00	23	2.3	3.60E-03
Q9Z2L7	Cytokine receptor-like factor 3	31	-0.4	4.70E-01	42	0.1	8.60E-01	42	-0.2	4.70E-01
Q9Z2R6	Protein unc-119 homolog A	18	2.4	4.50E-02	NA	NA	NA	18	-2.7	2.90E-02
Q9Z2U0	Proteasome subunit alpha type-7	51	-0.9	6.00E-06	23	2.2	4.80E-02	51	-4.4	4.80E-59
Q9Z2U1	Proteasome subunit alpha type-5	31	-0.6	6.00E-02	13	-0.1	1.00E+00	31	-1.1	6.00E-07
Q9Z2W0	Aspartyl aminopeptidase	40	-0.5	1.00E-01	11	1.4	1.10E-01	40	-3.3	4.40E-36
Q9Z2X1	Heterogeneous nuclear ribonucleoprotein F	35	0.2	2.40E-01	46	0.2	1.10E-01	46	1.2	3.70E-27
A2A8Z1	Oxysterol-binding protein-related protein 9	NA	NA	NA	9	0.4	7.50E-01	9	2.7	2.90E-03
A2ADY9	Protein DDI1 homolog 2	NA	NA	NA	23	1.2	5.80E-02	23	2.6	8.10E-06
A2AJW4	Protein phosphatase 1 regulatory subunit	NA	NA	NA	17	2.2	1.40E-01	25	0.9	4.40E-01
A2AL36	Centriolin	NA	NA	NA	1	0.2	1.00E+00	1	2.3	7.50E-02
A3KGV1	Outer dense fiber protein 2	NA	NA	NA	3	-1.7	2.00E-01	3	3.2	3.00E-03
B1AUY2	Protein Arhgap4	NA	NA	NA	11	1.5	1.60E-01	11	1.9	2.90E-02
B1AVH7	TBC1 domain family member 2A	NA	NA	NA	6	2.2	1.40E-01	6	2.3	7.50E-02
B2RUP2	Protein unc-13 homolog D	NA	NA	NA	6	0	1.00E+00	6	3.9	3.20E-05
B2RY56	RNA-binding protein 25	NA	NA	NA	4	-1.6	3.50E-01	4	2.5	3.90E-02
D3YTQ8	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 5, isoform CRA_a	NA	NA	NA	53	0.7	7.40E-01	53	2.1	1.40E-01
D3YXK2	Scaffold attachment factor B1	NA	NA	NA	12	-0.8	1.30E-02	12	6.6	9.30E-35
D3YZZ5	Protein Tmed7	NA	NA	NA	11	-1.1	7.80E-01	11	2.1	1.40E-01
E9PVX6	Protein Mki67	NA	NA	NA	11	-0.9	4.90E-03	11	5.6	6.10E-31
E9PWG6	Protein Ncapg	NA	NA	NA	7	0.9	3.40E-01	7	3.6	2.30E-04
E9Q394	Protein Akap13	NA	NA	NA	3	-1.4	7.00E-02	3	4.4	1.80E-07

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
E9Q555	E3 ubiquitin-protein ligase RNF213	NA	NA	NA	1	-1.5	6.90E-01	2	0	#######
E9Q616	Protein Ahnak	NA	NA	NA	1	1.9	2.30E-01	1	1.2	3.80E-01
E9Q6E5	Protein Srsf11	NA	NA	NA	7	-3.2	1.00E-02	7	3	5.70E-03
E9Q7G0	Protein Numa1	NA	NA	NA	14	-0.8	1.20E-02	14	5.8	1.20E-35
E9Q8K8	Zinc finger CCCH domain-containing protein 4	NA	NA	NA	6	0.1	9.00E-01	6	4.6	1.30E-08
E9Q8L9	Rab11 family-interacting protein 1	NA	NA	NA	6	-1.6	4.60E-02	6	4.2	2.40E-06
F7BJB9	Protein Morc3	NA	NA	NA	5	-1.5	6.90E-01	5	1.4	4.80E-01
F8VQC1	Signal recognition particle subunit SRP72	NA	NA	NA	8	1.3	1.40E-01	8	3.9	3.20E-05
O08677	Kininogen-1	NA	NA	NA	9	-2.4	9.10E-03	9	0.7	2.40E-01
O08734	Bcl-2 homologous antagonist/killer	NA	NA	NA	23	-1.1	1.70E-01	23	4.5	4.80E-08
O08759	Ubiquitin-protein ligase E3A	NA	NA	NA	6	1.5	2.40E-01	9	1	3.50E-01
O08807	Peroxiredoxin-4	NA	NA	NA	13	-2.2	2.40E-01	13	0.3	8.90E-01
O08997	Copper transport protein ATOX1	NA	NA	NA	51	1.5	8.20E-03	51	3.7	1.60E-09
O09130	NFATC2-interacting protein	NA	NA	NA	11	0.5	7.90E-01	11	2.5	3.90E-02
O35129	Prohibitin-2	NA	NA	NA	17	-1.3	1.40E-02	17	5.2	1.50E-13
O35226	26S proteasome non-ATPase regulatory subunit 4	NA	NA	NA	26	0.5	4.20E-01	26	4.1	1.10E-09
O35326	Serine/arginine-rich splicing factor 5	NA	NA	NA	7	-2.2	2.40E-01	7	2.1	1.40E-01
O35704	Serine palmitoyltransferase 1	NA	NA	NA	7	-1.9	4.00E-01	7	1.8	2.60E-01
O35887	Calumenin	NA	NA	NA	12	-3.3	5.20E-03	12	3.2	3.00E-03
O35892	Nuclear autoantigen Sp-100	NA	NA	NA	8	-1.3	2.70E-01	8	3.6	2.30E-04
O54734	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	NA	NA	NA	14	-3	1.30E-03	14	3.8	6.20E-05
O54941	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	NA	NA	NA	7	-3.5	2.60E-03	7	1.9	2.90E-02
O54950	5'-AMP-activated protein kinase subunit gamma-1	NA	NA	NA	15	3.4	1.30E-03	15	1.3	7.60E-02
O54988	STE20-like serine/threonine-protein kinase	NA	NA	NA	11	1	8.00E-02	11	3.8	2.40E-10
O55098	Serine/threonine-protein kinase 10	NA	NA	NA	5	0.3	6.30E-01	5	2	1.30E-05
O70252	Heme oxygenase 2	NA	NA	NA	10	-0.2	1.00E+00	10	2.1	1.40E-01
O70400	PDZ and LIM domain protein 1	NA	NA	NA	22	3.1	6.50E-03	22	3.3	1.60E-03
O70492	Sorting nexin-3	NA	NA	NA	30	1.2	1.20E-01	30	4.3	6.50E-07
O70566	Protein diaphanous homolog 2	NA	NA	NA	4	1.2	6.20E-01	4	1.4	4.80E-01
O88379	Bromodomain adjacent to zinc finger domain protein 1A	NA	NA	NA	5	-0.9	6.40E-01	5	3	5.70E-03
O88536	Formyl peptide receptor 2	NA	NA	NA	11	-2.9	1.50E-04	11	4.3	6.50E-07
O88668	Protein CREG1	NA	NA	NA	13	-1.3	4.10E-01	13	1.1	2.40E-01
O88746	Target of Myb protein 1	NA	NA	NA	16	-0.5	4.10E-01	16	5.6	2.50E-17
P00405	Cytochrome c oxidase subunit 2	NA	NA	NA	9	0.1	8.40E-01	9	4.8	4.60E-10
P03958	Adenosine deaminase	NA	NA	NA	19	2.6	5.30E-02	19	2.7	2.10E-02
P10711	Transcription elongation factor A protein 1	NA	NA	NA	9	0.4	7.50E-01	9	0.3	6.30E-01
P12787	Cytochrome c oxidase subunit 5A, mitochondrial	NA	NA	NA	42	-0.6	1.60E-01	42	2.9	2.00E-17
P13595	Neural cell adhesion molecule 1	NA	NA	NA	4	-1.9	4.00E-01	4	0	#######
P14115	60S ribosomal protein L27a	NA	NA	NA	24	-0.7	7.00E-01	24	1.6	2.50E-02
P14148	60S ribosomal protein L7	NA	NA	NA	12	-2	7.50E-02	12	2.6	5.10E-03
P16045	Galectin-1	NA	NA	NA	53	-0.1	1.00E+00	53	5.2	3.20E-22
P17047	Lysosome-associated membrane glycoprotein 2	NA	NA	NA	13	-1.3	2.20E-01	13	1.8	1.00E-02
P17439	Glucosylceramidase	NA	NA	NA	12	-0.5	7.20E-01	12	2	5.70E-04
P19536	Cytochrome c oxidase subunit 5B, mitochondrial	NA	NA	NA	34	-0.9	3.10E-02	34	2.5	1.10E-12

		Exosomes			MDSCs			Global		
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P20491	High affinity immunoglobulin epsilon receptor subunit gamma	NA	NA	NA	34	-0.2	1.00E+00	34	1.4	1.10E-01
P21619	Lamin-B2	NA	NA	NA	16	-0.6	5.30E-01	16	3.1	2.00E-07
P22682	E3 ubiquitin-protein ligase CBL	NA	NA	NA	9	1.9	1.70E-02	9	4.1	4.60E-06
P24547	Inosine-5'-monophosphate dehydrogenase 2	NA	NA	NA	11	3.9	5.10E-05	11	1.4	2.50E-02
P26350	Prothymosin alpha	NA	NA	NA	62	1.8	5.60E-31	62	7.2	#######
P27659	60S ribosomal protein L3	NA	NA	NA	6	-0.5	8.60E-01	12	2.8	1.60E-03
P28667	MARCKS-related protein	NA	NA	NA	37	0.7	2.70E-01	54	4.1	1.10E-09
P29788	Vitronectin	NA	NA	NA	4	-3.1	2.50E-08	4	0.2	6.20E-01
P30355	Arachidonate 5-lipoxygenase-activating protein	NA	NA	NA	27	2.6	5.30E-02	27	2.7	2.10E-02
P31230	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	NA	NA	NA	24	-0.2	1.00E+00	24	2.1	1.40E-01
P31786	Acyl-CoA-binding protein	NA	NA	NA	23	1.6	3.70E-04	23	2.9	3.40E-11
P31809	Carcinoembryonic antigen-related cell adhesion molecule 1	NA	NA	NA	9	-3.2	1.00E-02	9	1.7	7.80E-02
P32020	Non-specific lipid-transfer protein	NA	NA	NA	14	-0.5	2.30E-01	14	5	6.50E-27
P35173	Stefin-3	NA	NA	NA	38	5.4	4.20E-15	38	5.6	4.80E-17
P35278	Ras-related protein Rab-5C	NA	NA	NA	15	-0.7	2.50E-01	15	0.6	1.10E-01
P35282	Ras-related protein Rab-21	NA	NA	NA	14	-0.5	7.20E-01	14	1	4.80E-02
P35550	rRNA 2'-O-methyltransferase fibrillarin	NA	NA	NA	28	0.7	3.60E-01	28	4.4	9.30E-08
P35831	Tyrosine-protein phosphatase non-receptor type 12	NA	NA	NA	9	0.3	8.60E-01	9	0.6	4.50E-01
P36371	Antigen peptide transporter 2	NA	NA	NA	8	-0.5	3.50E-01	8	5.6	1.30E-17
P37040	NADPH--cytochrome P450 reductase	NA	NA	NA	13	-0.7	8.90E-02	13	6.1	4.30E-24
P40223	Granulocyte colony-stimulating factor receptor	NA	NA	NA	5	-1.9	4.00E-01	5	1.8	2.60E-01
P41216	Long-chain-fatty-acid--CoA ligase 1	NA	NA	NA	5	-0.9	8.30E-01	5	2.5	3.90E-02
P43024	Cytochrome c oxidase subunit 6A1, mitochondrial	NA	NA	NA	26	0.9	2.40E-01	26	3.4	7.00E-06
P43430	Mast cell protease 8	NA	NA	NA	13	2.6	5.30E-02	13	-0.7	5.10E-01
P45878	Peptidyl-prolyl cis-trans isomerase FKBP2	NA	NA	NA	36	-1.8	3.50E-02	36	4	8.80E-06
P46061	Ran GTPase-activating protein 1	NA	NA	NA	16	0.3	5.60E-01	16	4	1.60E-12
P46414	Cyclin-dependent kinase inhibitor 1B	NA	NA	NA	12	1.5	1.10E-01	12	3.7	1.20E-04
P46460	Vesicle-fusing ATPase	NA	NA	NA	6	0.3	8.60E-01	6	1.8	4.80E-02
P46935	E3 ubiquitin-protein ligase NEDD4	NA	NA	NA	4	1.2	3.30E-01	4	3	5.70E-03
P47740	Fatty aldehyde dehydrogenase	NA	NA	NA	9	-0.5	6.40E-01	9	4.9	1.30E-10
P49717	DNA replication licensing factor MCM4	NA	NA	NA	4	2.4	8.70E-02	4	2.5	3.90E-02
P50637	Translocator protein	NA	NA	NA	15	1.2	6.20E-01	15	1.4	4.80E-01
P52503	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NA	NA	NA	21	-4.6	7.70E-08	21	4.4	9.30E-08
P52633	Signal transducer and transcription activator 6	NA	NA	NA	10	1.4	7.40E-02	10	2.1	9.00E-04
P53996	Isoform 2 of Cellular nucleic acid-binding protein	NA	NA	NA	22	2.3	2.10E-03	22	4.4	1.80E-07
P54103	DnaJ homolog subfamily C member 2	NA	NA	NA	8	0.5	7.20E-01	8	3.3	1.60E-03
P54728	UV excision repair protein RAD23 homolog B	NA	NA	NA	9	0.7	2.50E-01	9	2.3	1.10E-05
P54818	Galactocerebrosidase	NA	NA	NA	6	-1.5	6.90E-01	6	-1.8	6.70E-02
P55772	Ectonucleoside triphosphate diphosphohydrolase 1	NA	NA	NA	11	-3.7	7.20E-04	11	3.5	4.30E-04
P55937	Golgin subfamily A member 3	NA	NA	NA	2	-1.4	5.30E-01	2	2.3	7.50E-02
P56395	Cytochrome b5	NA	NA	NA	25	-1.5	6.90E-01	25	1.4	4.80E-01
P56546	C-terminal-binding protein 2	NA	NA	NA	13	2	3.50E-02	13	3.7	1.20E-04
P56812	Programmed cell death protein 5	NA	NA	NA	20	-0.2	1.00E+00	20	4.1	4.60E-06
P57746	V-type proton ATPase subunit D	NA	NA	NA	18	2.2	4.80E-02	18	1.2	1.40E-01

		Exosomes			MDSCs			Global		
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P57759	Endoplasmic reticulum resident protein 29	NA	NA	NA	11	-0.5	6.40E-01	11	0.8	4.60E-02
P58742	Aladin	NA	NA	NA	12	-0.9	5.30E-01	12	3.6	2.30E-04
P59325	Eukaryotic translation initiation factor 5	NA	NA	NA	7	0.6	6.70E-01	7	-0.1	#######
P59708	Splicing factor 3B subunit 6	NA	NA	NA	22	-0.2	1.00E+00	22	1.7	1.40E-01
P60867	40S ribosomal protein S20	NA	NA	NA	19	1.6	3.70E-01	19	0.4	8.90E-01
P60898	DNA-directed RNA polymerase II subunit RPB9	NA	NA	NA	32	-2.8	6.20E-06	32	4.9	2.40E-10
P61087	Ubiquitin-conjugating enzyme E2 K	NA	NA	NA	24	2.4	8.70E-02	24	0.8	4.80E-01
P61205	ADP-ribosylation factor 3	NA	NA	NA	56	0.9	2.00E-03	70	-0.8	3.10E-07
P61219	DNA-directed RNA polymerases I, II, and III subunit RPABC2	NA	NA	NA	20	2.2	1.40E-01	20	2.3	7.50E-02
P61290	Proteasome activator complex subunit 3	NA	NA	NA	20	1.2	6.20E-01	20	-0.4	#######
P61924	Coatomer subunit zeta-1	NA	NA	NA	40	0.4	7.50E-01	40	3.5	4.30E-04
P61961	Ubiquitin-fold modifier 1	NA	NA	NA	41	0.8	2.10E-01	41	2.2	8.30E-05
P62264	40S ribosomal protein S14	NA	NA	NA	39	0.3	5.80E-01	39	4.9	2.50E-17
P62492	Ras-related protein Rab-11A	NA	NA	NA	27	-0.6	2.70E-01	27	0.9	2.10E-03
P62746	Rho-related GTP-binding protein RhoB	NA	NA	NA	26	0.3	4.20E-01	26	0	9.40E-01
P62751	60S ribosomal protein L23a	NA	NA	NA	12	-0.3	8.60E-01	12	4.6	6.60E-09
P62754	40S ribosomal protein S6	NA	NA	NA	18	0.7	2.60E-01	18	3.3	6.70E-07
P62858	40S ribosomal protein S28	NA	NA	NA	28	0.7	4.30E-01	28	2.6	7.00E-04
P62869	Transcription elongation factor B polypeptide 2	NA	NA	NA	53	2.7	3.10E-02	53	2.9	1.10E-02
P62983	Ubiquitin-40S ribosomal protein S27a	NA	NA	NA	37	-0.1	8.80E-01	37	2.2	1.40E-18
P63024	Vesicle-associated membrane protein 3	NA	NA	NA	23	-2.2	2.40E-01	23	2.1	1.40E-01
P63038	60 kDa heat shock protein, mitochondrial	NA	NA	NA	37	-0.7	2.10E-03	37	7.3	1.10E-57
P63139	Nuclear transcription factor Y subunit beta	NA	NA	NA	12	-0.8	3.20E-01	12	4.6	1.30E-08
P63147	Ubiquitin-conjugating enzyme E2 B	NA	NA	NA	26	1.2	2.00E-01	26	2.9	4.90E-04
P63276	40S ribosomal protein S17	NA	NA	NA	45	-0.1	1.00E+00	45	4.6	2.40E-20
P63280	SUMO-conjugating enzyme UBC9	NA	NA	NA	20	3.1	3.10E-07	20	0.8	4.80E-02
P63321	Ras-related protein Ral-A	NA	NA	NA	22	-1.9	2.30E-01	22	2.7	2.10E-02
P67871	Casein kinase II subunit beta	NA	NA	NA	14	0.6	6.70E-01	14	2.2	2.80E-02
P67984	60S ribosomal protein L22	NA	NA	NA	42	0.8	3.40E-01	42	4	8.80E-06
P68372	Tubulin beta-4B chain	NA	NA	NA	65	0.4	9.50E-05	72	1.4	1.80E-70
P68404	Isoform Beta-II of Protein kinase C beta type	NA	NA	NA	10	-0.2	1.00E+00	10	4.1	4.60E-06
P70158	Acid sphingomyelinase-like phosphodiesterase 3a	NA	NA	NA	8	-3.9	1.80E-04	8	2.8	8.80E-04
P70333	Heterogeneous nuclear ribonucleoprotein H2	NA	NA	NA	17	0.7	1.10E-01	17	1.1	1.50E-04
P70349	Histidine triad nucleotide-binding protein 1	NA	NA	NA	33	2.4	1.20E-04	33	2.1	3.20E-05
P70372	ELAV-like protein 1	NA	NA	NA	12	0.5	6.20E-01	12	1.5	3.90E-02
P70388	DNA repair protein RAD50	NA	NA	NA	3	1.2	6.20E-01	3	1.4	4.80E-01
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	NA	NA	NA	5	4	2.80E-05	5	3.3	2.40E-05
P70444	BH3-interacting domain death agonist	NA	NA	NA	32	2.8	2.60E-04	32	3.1	7.10E-06
P70699	Lysosomal alpha-glucosidase	NA	NA	NA	4	-1.9	4.00E-01	6	0	#######
P81117	Nucleobindin-2	NA	NA	NA	20	-0.7	2.30E-01	20	1.6	3.10E-05
P83870	PHD finger-like domain-containing protein 5A	NA	NA	NA	33	-0.8	2.90E-01	33	1.3	4.00E-03
P84089	Enhancer of rudimentary homolog	NA	NA	NA	44	-0.4	7.20E-01	44	2.8	6.10E-06
P84099	60S ribosomal protein L19	NA	NA	NA	9	0.8	3.00E-01	9	0.9	9.40E-02
P97302	Transcription regulator protein BACH1	NA	NA	NA	7	-0.7	1.00E+00	7	1.8	2.60E-01

		Exosomes			MDSCs			Global		
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P97363	Serine palmitoyltransferase 2	NA	NA	NA	7	1.5	1.10E-01	7	3.7	1.20E-04
P97370	Sodium/potassium-transporting ATPase subunit beta-3	NA	NA	NA	11	-1.1	7.80E-01	11	1.2	3.80E-01
P97376	Protein FRG1	NA	NA	NA	7	-0.4	1.00E+00	7	3	5.70E-03
P97450	ATP synthase-coupling factor 6, mitochondrial	NA	NA	NA	34	-0.9	2.10E-03	34	3.5	6.20E-27
P97492	Regulator of G-protein signaling 14	NA	NA	NA	15	0.3	8.00E-01	15	3.9	3.20E-05
P97493	Thioredoxin, mitochondrial	NA	NA	NA	21	-1.6	3.50E-01	21	2.5	3.90E-02
P97496	SWI/SNF complex subunit SMARCC1	NA	NA	NA	4	2.4	8.70E-02	4	1.7	1.40E-01
P97797	Tyrosine-protein phosphatase non-receptor type substrate 1	NA	NA	NA	13	-3.5	2.60E-03	13	1.5	6.90E-02
P97814	Proline-serine-threonine phosphatase-interacting protein 1	NA	NA	NA	14	0.8	1.10E-01	14	5.3	2.00E-14
P97872	Dimethylaniline monooxygenase [N-oxide-forming] 5	NA	NA	NA	8	-0.4	1.00E+00	8	3	5.70E-03
P98083	SHC-transforming protein 1	NA	NA	NA	7	0.6	3.30E-01	7	2.2	2.00E-05
P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	NA	NA	NA	42	-0.1	1.00E+00	42	4.6	4.50E-20
Q00PI9	Heterogeneous nuclear ribonucleoprotein U-like protein 2	NA	NA	NA	18	-0.5	2.90E-01	18	2.8	5.40E-16
Q01320	DNA topoisomerase 2-alpha	NA	NA	NA	4	-0.4	5.60E-01	5	3.1	1.50E-10
Q04998	Inhibin beta A chain	NA	NA	NA	10	-2.9	2.40E-03	10	3.7	1.20E-04
Q08093	Calponin-2	NA	NA	NA	16	-0.3	6.40E-01	16	1.6	2.80E-06
Q1HFZ0	tRNA (cytosine(34)-C(5))-methyltransferase	NA	NA	NA	11	0.8	5.30E-01	11	2.3	1.60E-02
Q2YFS3	Paired immunoglobulin-like type 2 receptor alpha	NA	NA	NA	21	-0.7	1.00E+00	21	1.8	2.60E-01
Q3TDN2	FAS-associated factor 2	NA	NA	NA	11	-1.9	4.00E-01	11	1.8	2.60E-01
Q3TGF2	Protein FAM107B	NA	NA	NA	11	0.1	9.00E-01	11	4.6	1.30E-08
Q3THE2	Myosin regulatory light chain 12B	NA	NA	NA	48	-1.2	1.50E-38	58	2	#######
Q3THK3	General transcription factor IIF subunit 1	NA	NA	NA	5	2.7	3.10E-02	5	2.9	1.10E-02
Q3TJD7	PDZ and LIM domain protein 7	NA	NA	NA	15	-0.2	1.00E+00	15	2.1	1.40E-01
Q3TKT4	Transcription activator BRG1	NA	NA	NA	3	-2.2	2.40E-01	4	1.2	3.80E-01
Q3TLH4	Protein PRRC2C	NA	NA	NA	1	0.4	9.90E-01	1	1.8	2.60E-01
Q3TVI8	Pre-B-cell leukemia transcription factor-interacting protein 1	NA	NA	NA	7	-1.1	7.80E-01	7	1.2	3.80E-01
Q3TZZ7	Extended synaptotagmin-2	NA	NA	NA	5	-2.7	7.20E-02	5	2.5	3.90E-02
Q3U141	Inhibitor of nuclear factor kappa-B kinase subunit beta	NA	NA	NA	12	0.7	7.40E-01	12	2.1	1.40E-01
Q3U1F9	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1	NA	NA	NA	10	-0.3	9.80E-01	10	4.7	3.40E-09
Q3U1Z5	G-protein-signaling modulator 3	NA	NA	NA	52	-1.1	1.10E-03	52	6.4	6.80E-31
Q3U5V8	MCG49559	NA	NA	NA	20	-1.9	4.00E-01	20	1.8	2.60E-01
Q3U9G9	Lamin-B receptor	NA	NA	NA	20	0	1.00E+00	20	5.8	3.60E-34
Q3UEB3	Poly(U)-binding-splicing factor PUF60	NA	NA	NA	14	0.3	7.80E-01	14	3.7	1.20E-04
Q3UI43	BRISC and BRCA1-A complex member 1	NA	NA	NA	20	-0.4	5.60E-01	20	5.4	1.40E-15
Q3UJB0	Protein Sf3b2	NA	NA	NA	11	-2.8	5.40E-05	11	3.2	2.20E-06
Q497J0	MCG130175, isoform CRA_b	NA	NA	NA	34	5	9.70E-20	34	6.1	4.30E-24
Q4KML4	Costars family protein ABRACL	NA	NA	NA	52	0.6	2.20E-01	52	2.2	1.10E-07
Q4QRL3	Coiled-coil domain-containing protein 88B	NA	NA	NA	10	-0.4	8.60E-01	10	4.5	2.40E-08
Q52KI8	Serine/arginine repetitive matrix protein 1	NA	NA	NA	5	-0.4	5.60E-01	5	4.1	1.30E-13
Q569Z6	Thyroid hormone receptor-associated protein 3	NA	NA	NA	6	-0.1	1.00E+00	6	2.9	1.90E-11
Q5EG47	5'-AMP-activated protein kinase catalytic subunit alpha-1	NA	NA	NA	6	0.7	3.00E-01	6	1	4.80E-02
Q5SFM8	RNA-binding protein 27	NA	NA	NA	6	1	2.30E-01	6	3.9	1.70E-05
Q5SUH6	Clathrin interactor 1	NA	NA	NA	15	0.1	9.40E-01	18	3.1	1.50E-04
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	NA	NA	NA	5	2	7.40E-02	5	1.1	1.90E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q60634	Flotillin-2	NA	NA	NA	19	-1.1	9.60E-02	19	5	3.40E-11
Q60648	Ganglioside GM2 activator	NA	NA	NA	21	-0.3	8.30E-01	21	1.6	8.50E-05
Q60664	Lymphoid-restricted membrane protein	NA	NA	NA	8	-0.8	3.20E-01	8	4.6	1.30E-08
Q60739	BAG family molecular chaperone regulator 1	NA	NA	NA	15	1.3	1.40E-01	15	3	2.70E-04
Q60790	Ras GTPase-activating protein 3	NA	NA	NA	8	-0.9	4.40E-01	8	4	8.80E-06
Q60875	Rho guanine nucleotide exchange factor 2	NA	NA	NA	7	0.4	5.50E-01	9	3.9	1.40E-08
Q60902	Epidermal growth factor receptor substrate 15-like 1	NA	NA	NA	9	-0.9	2.70E-01	9	4.7	1.70E-09
Q60930	Voltage-dependent anion-selective channel protein 2	NA	NA	NA	31	-0.4	7.20E-01	31	4.1	1.10E-09
Q60931	Voltage-dependent anion-selective channel protein 3	NA	NA	NA	11	0.8	6.20E-01	11	1.9	8.30E-02
Q60932	Voltage-dependent anion-selective channel protein 1	NA	NA	NA	27	-0.6	2.50E-01	27	5.6	1.30E-17
Q60953	Protein PML	NA	NA	NA	13	-4.3	2.40E-10	13	4.2	3.00E-10
Q61029	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	NA	NA	NA	39	-0.7	1.50E-05	42	2.5	5.20E-54
Q61074	Protein phosphatase 1G	NA	NA	NA	14	0.3	4.30E-01	16	5	2.50E-19
Q61103	Zinc finger protein ubi-d4	NA	NA	NA	13	-0.4	8.60E-01	13	3.2	2.20E-06
Q61152	Tyrosine-protein phosphatase non-receptor type 18	NA	NA	NA	10	-0.2	9.20E-01	10	5.3	2.00E-14
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	NA	NA	NA	22	0.6	6.70E-01	22	-0.4	8.60E-01
Q61687	Transcriptional regulator ATRX	NA	NA	NA	1	2.6	5.30E-02	1	2.7	2.10E-02
Q61792	LIM and SH3 domain protein 1	NA	NA	NA	17	0.4	5.30E-01	17	2.9	2.00E-06
Q61805	Lipopolysaccharide-binding protein	NA	NA	NA	11	0.1	8.80E-01	11	0.8	2.40E-02
Q62086	Serum paraoxonase/arylesterase 2	NA	NA	NA	13	-1.1	2.40E-01	13	4	8.80E-06
Q62186	Translocon-associated protein subunit delta	NA	NA	NA	34	-1.5	7.10E-02	34	4.1	4.60E-06
Q62219	Transforming growth factor beta-1-induced transcript 1 protein	NA	NA	NA	8	2.6	5.30E-02	8	2.7	2.10E-02
Q62383	Transcription elongation factor SPT6	NA	NA	NA	2	-1.5	6.90E-01	2	1.4	4.80E-01
Q62431	AT-rich interactive domain-containing protein 3A	NA	NA	NA	10	0.4	7.50E-01	10	3.5	4.30E-04
Q62448	Eukaryotic translation initiation factor 4 gamma 2	NA	NA	NA	6	3	1.10E-02	6	3.2	3.00E-03
Q64012	RNA-binding protein Raly	NA	NA	NA	13	0.4	6.00E-01	13	4.5	2.40E-08
Q64152	Transcription factor BTF3	NA	NA	NA	24	1.1	1.10E-02	24	2.2	1.60E-08
Q64277	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2	NA	NA	NA	15	-3.9	1.80E-04	15	1	1.50E-01
Q64433	10 kDa heat shock protein, mitochondrial	NA	NA	NA	25	-0.7	2.00E-01	25	4.7	2.50E-15
Q64521	Glycerol-3-phosphate dehydrogenase, mitochondrial	NA	NA	NA	19	-1.3	9.10E-04	19	6	1.70E-23
Q65Z40	Wings apart-like protein homolog	NA	NA	NA	7	-1	4.00E-01	7	3.7	1.20E-04
Q66JX5	FGFR1 oncogene partner	NA	NA	NA	7	1.9	2.30E-01	14	1.2	3.80E-01
Q6A068	Cell division cycle 5-like protein	NA	NA	NA	15	-1.4	5.50E-02	15	4.5	2.40E-08
Q6BCL1	PML-RARA-regulated adapter molecule 1	NA	NA	NA	26	0.4	4.20E-01	26	5.4	1.40E-15
Q6DFW4	Nucleolar protein 58	NA	NA	NA	5	-0.2	1.00E+00	5	4.5	2.40E-08
Q6DFZ1	Golgi-specific brefeldin A-resistance factor 1	NA	NA	NA	4	0.5	7.90E-01	4	2.5	3.90E-02
Q6GQT9	Nodal modulator 1	NA	NA	NA	8	-1.1	2.00E-01	8	4.2	1.30E-06
Q6NVF9	Cleavage and polyadenylation specificity factor subunit 6	NA	NA	NA	10	0.5	2.10E-01	10	1.2	1.50E-04
Q6NZB0	DnaJ homolog subfamily C member 8	NA	NA	NA	25	-0.2	1.00E+00	25	1.6	5.40E-04
Q6NZC7	SEC23-interacting protein	NA	NA	NA	5	0.3	7.80E-01	5	2.3	3.60E-03
Q6P9Q6	FK506-binding protein 15	NA	NA	NA	8	-0.3	1.00E+00	8	4.2	2.40E-06
Q6PCP5	Mitochondrial fission factor	NA	NA	NA	20	-1.1	7.80E-01	20	2.1	1.40E-01
Q6PDQ2	Chromodomain-helicase-DNA-binding protein 4	NA	NA	NA	6	0.6	3.70E-01	6	3.9	1.40E-08
Q6PFD9	Nuclear pore complex protein Nup98-Nup96	NA	NA	NA	5	-1	3.50E-01	5	4.1	4.60E-06

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q6PFR5	Transformer-2 protein homolog alpha	NA	NA	NA	12	-2.2	2.90E-03	12	4.3	3.40E-07
Q6PGG2	GEM-interacting protein	NA	NA	NA	9	0	1.00E+00	9	3.3	1.60E-03
Q6SJQ7	CMRF35-like molecule 1	NA	NA	NA	13	-0.3	9.90E-01	13	4.6	1.30E-08
Q6ZQI3	Malectin	NA	NA	NA	12	-1.5	3.20E-03	12	5.2	3.00E-13
Q6ZQK5	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	NA	NA	NA	9	1.5	1.60E-01	9	2.4	9.20E-03
Q6ZWZ6	40S ribosomal protein S12	NA	NA	NA	57	1.2	5.30E-02	57	4.8	4.60E-10
Q7TMY8	E3 ubiquitin-protein ligase HUWE1	NA	NA	NA	2	2.9	1.80E-02	2	2.2	2.80E-02
Q7TNC4	Putative RNA-binding protein Luc7-like 2	NA	NA	NA	15	-0.2	1.00E+00	15	2.7	3.20E-05
Q7TNP2	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	NA	NA	NA	16	0.3	3.00E-01	19	0.4	3.80E-02
Q7TNV0	Protein DEK	NA	NA	NA	9	-1.4	2.00E-03	9	5.6	6.60E-18
Q7TPD0	Integrator complex subunit 3	NA	NA	NA	6	0.1	8.90E-01	6	3.6	6.00E-07
Q7TSS2	Ubiquitin-conjugating enzyme E2 Q1	NA	NA	NA	15	1.5	7.90E-02	15	4	8.80E-06
Q80TH2	Protein LAP2	NA	NA	NA	3	0.2	8.20E-01	3	1.5	2.00E-02
Q80TP3	E3 ubiquitin-protein ligase UBR5	NA	NA	NA	2	1.6	3.70E-01	2	1.8	2.60E-01
Q80TY0	Formin-binding protein 1	NA	NA	NA	9	0.7	2.70E-01	9	4.9	6.50E-11
Q80U16	Isoform 5 of Protein FAM65B	NA	NA	NA	16	0.3	4.20E-01	16	6.3	3.30E-28
Q80U93	Nuclear pore complex protein Nup214	NA	NA	NA	4	1.1	2.60E-01	4	2.8	8.80E-04
Q80VP1	Epsin-1	NA	NA	NA	10	1.7	8.00E-02	10	3.5	4.30E-04
Q80VQ0	Aldehyde dehydrogenase family 3 member B1	NA	NA	NA	12	-0.2	1.00E+00	12	2.2	2.40E-03
Q80WJ7	Protein LYRIC	NA	NA	NA	12	0.5	7.90E-01	12	2.5	3.90E-02
Q80X50	Ubiquitin-associated protein 2-like	NA	NA	NA	4	2	7.40E-02	4	3.2	3.00E-03
Q80XU3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NA	NA	NA	12	-1.5	6.90E-01	12	1.4	4.80E-01
Q80Y14	Glutaredoxin-related protein 5, mitochondrial	NA	NA	NA	22	-0.5	5.50E-01	22	5.1	1.20E-12
Q810A7	ATP-dependent RNA helicase DDX42	NA	NA	NA	5	-1.9	2.30E-01	5	1.3	1.90E-01
Q8BFQ8	Parkinson disease 7 domain-containing protein 1	NA	NA	NA	22	2.4	8.70E-02	22	2.5	3.90E-02
Q8BGG7	Ubiquitin-associated and SH3 domain-containing protein B	NA	NA	NA	7	2.4	8.70E-02	7	1.7	1.40E-01
Q8BGT7	Survival of motor neuron-related-splicing factor 30	NA	NA	NA	24	-1.7	2.40E-02	24	4.4	1.80E-07
Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1	NA	NA	NA	8	-2.2	2.60E-02	8	3.6	2.30E-04
Q8BH74	Nuclear pore complex protein Nup107	NA	NA	NA	8	-0.7	6.90E-01	12	2.7	2.90E-03
Q8BH78	Reticulon	NA	NA	NA	18	-2.5	1.00E-03	22	3.4	7.00E-06
Q8BIQ5	Cleavage stimulation factor subunit 2	NA	NA	NA	13	-1.4	3.70E-02	13	4.6	1.30E-08
Q8BIW1	Protein prune homolog	NA	NA	NA	7	0.4	9.90E-01	7	0.9	5.80E-01
Q8BJU0	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	NA	NA	NA	9	-2.2	2.40E-01	9	2.1	1.40E-01
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	NA	NA	NA	11	0	1.00E+00	11	-1.3	1.30E-02
Q8BMD8	Calcium-binding mitochondrial carrier protein SCaMC-1	NA	NA	NA	9	-0.7	6.90E-01	9	3.5	4.30E-04
Q8BMJ3	Eukaryotic translation initiation factor 1A, X-chromosomal	NA	NA	NA	31	1.2	2.20E-01	31	3.5	4.30E-04
Q8BMK4	Cytoskeleton-associated protein 4	NA	NA	NA	21	-0.6	1.50E-01	21	4.8	1.80E-23
Q8BML9	Glutaminyl-tRNA synthetase	NA	NA	NA	5	0.4	9.90E-01	5	1.8	2.60E-01
Q8BQ30	Phostensin	NA	NA	NA	10	-0.5	1.00E+00	10	2.7	2.10E-02
Q8BQ46	Protein Taf15	NA	NA	NA	13	-0.2	9.10E-01	13	1.3	5.40E-04
Q8BQ47	Protein canopy homolog 4	NA	NA	NA	17	-2	7.50E-02	17	3.4	8.30E-04
Q8BRN9	Coiled-coil and C2 domain-containing protein 1B	NA	NA	NA	6	-1.1	7.80E-01	6	2.1	1.40E-01
Q8BTI8	Serine/arginine repetitive matrix protein 2	NA	NA	NA	3	-2.9	3.70E-02	3	2.7	2.10E-02
Q8BTS4	Nuclear pore complex protein Nup54	NA	NA	NA	7	-1.1	7.80E-01	7	2.1	1.40E-01

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q8BUK6	Protein Hook homolog 3	NA	NA	NA	12	0.3	7.60E-01	12	4.3	3.40E-07
Q8BYC6	Serine/threonine-protein kinase TAO3	NA	NA	NA	6	1.6	3.70E-01	6	1.8	2.60E-01
Q8BYI6	Lysophosphatidylcholine acyltransferase 2	NA	NA	NA	10	-0.7	8.50E-01	10	1.5	1.30E-01
Q8BYW1	Rho GTPase-activating protein 25	NA	NA	NA	17	-1	4.00E-01	17	2.8	8.80E-04
Q8C079	Striatin-interacting protein 1	NA	NA	NA	9	1	4.50E-01	9	2.9	1.10E-02
Q8C0C7	Phenylalanine--tRNA ligase alpha subunit	NA	NA	NA	9	2.2	3.30E-03	9	-0.1	########
Q8C0G2	TRAF3-interacting JNK-activating modulator	NA	NA	NA	10	-1.4	1.50E-01	10	2.6	7.00E-04
Q8C0L0	Thioredoxin-related transmembrane protein 4	NA	NA	NA	16	0.1	9.60E-01	16	4.1	4.60E-06
Q8C2Q3	RNA-binding protein 14	NA	NA	NA	12	0.4	5.00E-01	12	4.9	1.30E-10
Q8CAQ8	MICOS complex subunit Mic60	NA	NA	NA	12	-0.9	2.10E-01	12	4.8	9.10E-10
Q8CB87	Ras-related protein Rab-44	NA	NA	NA	16	2.9	1.10E-03	19	3.2	8.00E-05
Q8CBY8	Dynactin subunit 4	NA	NA	NA	14	0.5	6.60E-01	14	2.9	4.90E-04
Q8CCF0	U4/U6 small nuclear ribonucleoprotein Prp31	NA	NA	NA	9	-1.3	4.10E-01	9	2	4.80E-02
Q8CCJ3	E3 UFM1-protein ligase 1	NA	NA	NA	5	1.9	2.30E-01	5	2.1	1.40E-01
Q8CCS6	Polyadenylate-binding protein 2	NA	NA	NA	21	-0.2	1.00E+00	21	3.2	3.00E-03
Q8CD10	Calcium uptake protein 2, mitochondrial	NA	NA	NA	10	1.2	6.20E-01	10	1.4	4.80E-01
Q8CEC0	Nuclear pore complex protein Nup88	NA	NA	NA	10	-0.5	8.60E-01	10	3.6	2.30E-04
Q8CEC6	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	NA	NA	NA	8	1.2	6.20E-01	8	-1.7	1.10E-01
Q8CH18	Cell division cycle and apoptosis regulator protein 1	NA	NA	NA	3	0.8	5.30E-01	3	3.2	3.00E-03
Q8CHC4	Synaptojanin-1	NA	NA	NA	2	1.9	2.30E-01	2	2.1	1.40E-01
Q8CHG3	GRIP and coiled-coil domain-containing protein 2	NA	NA	NA	2	0.1	1.00E+00	2	2.7	2.10E-02
Q8CHK3	Lysophospholipid acyltransferase 7	NA	NA	NA	11	1	4.50E-01	11	2.9	1.10E-02
Q8CI95	Oxysterol-binding protein-related protein 11	NA	NA	NA	12	-0.2	1.00E+00	12	2.5	3.90E-02
Q8CIS0	Caspase recruitment domain-containing protein 11	NA	NA	NA	2	-0.7	1.00E+00	2	1.8	2.60E-01
Q8K124	Pleckstrin homology domain-containing family O member 2	NA	NA	NA	27	0.5	1.40E-01	27	3.7	1.50E-22
Q8K1T1	Leucine-rich repeat-containing protein 25	NA	NA	NA	16	-4	6.60E-08	16	4.7	3.40E-09
Q8K2K6	Arf-GAP domain and FG repeat-containing protein 1	NA	NA	NA	11	1.5	1.10E-01	11	3.7	1.20E-04
Q8K2Z4	Condensin complex subunit 1	NA	NA	NA	3	1.5	1.10E-01	3	1.6	2.50E-02
Q8K310	Matrin-3	NA	NA	NA	8	-0.6	4.40E-01	8	2.2	7.40E-06
Q8K3K8	Optineurin	NA	NA	NA	6	0.1	1.00E+00	6	2.7	2.10E-02
Q8K4I3	Rho guanine nucleotide exchange factor 6	NA	NA	NA	14	-0.2	1.00E+00	14	1.7	3.40E-05
Q8K4Z5	Splicing factor 3A subunit 1	NA	NA	NA	12	-0.5	7.20E-01	12	2.6	5.60E-05
Q8QZW8	Protein Arhgap9	NA	NA	NA	16	2.1	8.60E-04	16	2.7	1.60E-06
Q8R0G9	Nuclear pore complex protein Nup133	NA	NA	NA	12	1.2	1.20E-01	12	3.4	7.00E-06
Q8R0H9	ADP-ribosylation factor-binding protein GGA1	NA	NA	NA	9	0.2	7.50E-01	9	5.2	1.50E-13
Q8R0T6	Probable G-protein coupled receptor 97	NA	NA	NA	6	-0.9	1.50E-01	6	1.7	1.60E-04
Q8R1G6	PDZ and LIM domain protein 2	NA	NA	NA	27	-2.4	1.80E-03	27	4.2	1.30E-06
Q8R2Y8	Peptidyl-tRNA hydrolase 2, mitochondrial	NA	NA	NA	20	1.5	2.40E-01	20	2.7	2.10E-02
Q8R307	Vacuolar protein sorting-associated protein 18 homolog	NA	NA	NA	4	1.2	6.20E-01	4	1.4	4.80E-01
Q8R326	Paraspeckle component 1	NA	NA	NA	11	1.7	1.60E-01	11	2.9	1.10E-02
Q8R460	Interleukin-36 gamma	NA	NA	NA	24	1.5	3.70E-02	24	3.5	3.90E-06
Q8R4R6	Nucleoporin NUP53	NA	NA	NA	12	0.6	5.40E-01	12	3.9	3.20E-05
Q8R574	Phosphoribosyl pyrophosphate synthase-associated protein 2	NA	NA	NA	7	0.2	1.00E+00	7	2.3	7.50E-02
Q8VBT6	Apolipoprotein B receptor	NA	NA	NA	31	0.2	3.00E-01	31	7.5	2.70E-67

		Exosomes			MDSCs			Global		
Protein Accession #	Description	Prot Cov. %	Rsc Exo Infl vs. Conv	FDR	ProtCov. %	Rsc MDSC Infl vs. Conv	FDR	Prot Cov. %	Rsc MDSC vs. Exo	FDR
Q8VCI5	Peroxisomal biogenesis factor 19	NA	NA	NA	13	-1.1	3.70E-01	13	3.5	4.30E-04
Q8VD04	GRIP1-associated protein 1	NA	NA	NA	9	-1.7	1.00E-01	9	3.6	2.30E-04
Q8VD58	Protein EVI2B	NA	NA	NA	6	-1.3	2.70E-01	6	3.6	2.30E-04
Q8VDJ3	Vigilin	NA	NA	NA	4	0.5	4.40E-01	4	4.7	1.70E-09
Q8VE47	Ubiquitin-like modifier-activating enzyme 5	NA	NA	NA	16	2.2	1.40E-01	16	-0.2	#######
Q8VEM8	Phosphate carrier protein, mitochondrial	NA	NA	NA	12	-1.2	9.00E-02	12	3.7	1.70E-07
Q8VH51	RNA-binding protein 39	NA	NA	NA	14	-0.5	3.30E-01	14	5.3	2.30E-23
Q91VE0	Long-chain fatty acid transport protein 4	NA	NA	NA	8	-1.4	5.30E-01	8	2.3	7.50E-02
Q91VJ5	Polyglutamine-binding protein 1	NA	NA	NA	36	-0.2	9.70E-01	36	4.9	2.40E-10
Q91VR2	ATP synthase subunit gamma, mitochondrial	NA	NA	NA	17	-1.1	5.70E-02	17	5.1	2.30E-12
Q91VW3	SH3 domain-binding glutamic acid-rich-like protein 3	NA	NA	NA	58	0.2	5.30E-01	58	1.6	2.10E-09
Q91W50	Cold shock domain-containing protein E1	NA	NA	NA	4	1.3	2.30E-01	4	3.2	3.00E-03
Q91W90	Thioredoxin domain-containing protein 5	NA	NA	NA	14	-2.6	1.40E-02	14	3.4	8.30E-04
Q91WJ8	Far upstream element-binding protein 1	NA	NA	NA	5	1.9	5.30E-02	5	3.6	2.30E-04
Q91WK0	Leucine-rich repeat flightless-interacting protein 2	NA	NA	NA	8	-3.1	1.90E-02	8	2.9	1.10E-02
Q91WK2	Eukaryotic translation initiation factor 3 subunit H	NA	NA	NA	22	1.9	5.30E-02	22	2.8	1.60E-03
Q91WN1	DnaJ homolog subfamily C member 9	NA	NA	NA	24	-1.2	5.80E-02	24	4	3.90E-09
Q91WU5	Arsenite methyltransferase	NA	NA	NA	11	0.4	6.40E-01	11	0.8	1.50E-01
Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	NA	NA	NA	22	-0.3	5.50E-01	22	5	9.10E-28
Q91YW3	DnaJ homolog subfamily C member 3	NA	NA	NA	9	0.3	6.20E-01	9	1.3	2.40E-03
Q91ZU6	Dystonin	NA	NA	NA	0	-2.2	2.40E-01	0	-0.3	#######
Q921G7	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	NA	NA	NA	6	-0.2	1.00E+00	6	2.1	1.40E-01
Q922P9	Putative oxidoreductase GLYR1	NA	NA	NA	12	-1.3	5.10E-02	12	2.7	2.80E-06
Q922Q8	Leucine-rich repeat-containing protein 59	NA	NA	NA	20	0.2	7.90E-01	20	4.2	3.00E-10
Q99J62	Replication factor C subunit 4	NA	NA	NA	16	1.2	6.20E-01	16	1.4	4.80E-01
Q99JB2	Stomatin-like protein 2, mitochondrial	NA	NA	NA	24	-0.3	1.00E+00	24	4.3	6.50E-07
Q99JR1	Sideroflexin-1	NA	NA	NA	29	-0.2	1.00E+00	29	5.4	2.60E-15
Q99JX3	Golgi reassembly-stacking protein 2	NA	NA	NA	27	-0.9	9.50E-02	27	5.3	7.90E-14
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	NA	NA	NA	9	-0.5	8.60E-01	9	2.8	1.60E-03
Q99K01	Pyridoxal-dependent decarboxylase domain-containing protein 1	NA	NA	NA	8	1.9	2.30E-01	8	2.1	1.40E-01
Q99KY4	Cyclin-G-associated kinase	NA	NA	NA	5	2	1.10E-02	5	4.2	2.40E-06
Q99L45	Eukaryotic translation initiation factor 2 subunit 2	NA	NA	NA	15	-1.3	2.70E-01	21	2.8	1.60E-03
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NA	NA	NA	9	1.1	1.00E-01	9	4.6	1.30E-08
Q99LP6	GrpE protein homolog 1, mitochondrial	NA	NA	NA	9	0	1.00E+00	9	1.6	8.60E-03
Q99M31	Heat shock 70 kDa protein 14	NA	NA	NA	11	-0.2	1.00E+00	11	1.9	6.40E-03
Q99M46	DNA-directed RNA polymerase II subunit RPB3	NA	NA	NA	16	-2	2.40E-02	16	3	2.70E-04
Q99MD9	Nuclear autoantigenic sperm protein	NA	NA	NA	10	0.2	7.50E-01	10	5.2	1.50E-13
Q99MR6	Serrate RNA effector molecule homolog	NA	NA	NA	4	-1.5	6.90E-01	4	1.4	4.80E-01
Q99N16	Leukotriene-B(4) omega-hydroxylase 2	NA	NA	NA	3	1.6	3.70E-01	3	1.8	2.60E-01
Q99N80	Synaptotagmin-like protein 1	NA	NA	NA	6	-1.4	2.40E-01	6	3.4	8.30E-04
Q99P88	Nuclear pore complex protein Nup155	NA	NA	NA	9	0.3	6.20E-01	9	5.4	1.00E-14
Q99PL5	Ribosome-binding protein 1	NA	NA	NA	7	-0.7	6.00E-02	7	6.4	2.70E-30
Q9CPR4	60S ribosomal protein L17	NA	NA	NA	20	-0.3	9.90E-01	20	3.7	1.70E-07
Q9CPV4	Glyoxalase domain-containing protein 4	NA	NA	NA	17	2.3	3.00E-02	17	2.6	5.10E-03

		Exosomes			MDSCs			Global		
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Q9CQ19	Myosin regulatory light polypeptide 9	NA	NA	NA	36	-0.5	2.00E-01	47	0	8.60E-01
Q9CQ92	Mitochondrial fission 1 protein	NA	NA	NA	16	-0.6	8.60E-01	16	3.2	3.00E-03
Q9CQF3	Cleavage and polyadenylation specificity factor subunit 5	NA	NA	NA	21	-0.1	1.00E+00	21	1.6	7.60E-03
Q9CQF9	Prenylcysteine oxidase	NA	NA	NA	8	-0.6	6.00E-01	8	4.2	1.30E-06
Q9CQI7	U2 small nuclear ribonucleoprotein B"	NA	NA	NA	10	-0.7	1.00E+00	10	1.8	2.60E-01
Q9CQK7	RWD domain-containing protein 1	NA	NA	NA	20	3	1.10E-02	20	3.2	3.00E-03
Q9CQM9	Glutaredoxin-3	NA	NA	NA	36	1.8	3.60E-04	36	2.6	2.40E-08
Q9CR16	Peptidyl-prolyl cis-trans isomerase D	NA	NA	NA	9	0	1.00E+00	9	-0.2	8.50E-01
Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochondrial	NA	NA	NA	18	-2	1.40E-01	18	2.9	1.10E-02
Q9CR86	Calcium-regulated heat stable protein 1	NA	NA	NA	26	1.3	3.60E-01	26	2.5	3.90E-02
Q9CRB2	H/ACA ribonucleoprotein complex subunit 2	NA	NA	NA	25	-1.9	4.00E-02	25	3.8	6.20E-05
Q9CW03	Structural maintenance of chromosomes protein 3	NA	NA	NA	5	-0.6	8.60E-01	5	3.2	3.00E-03
Q9CWK3	CD2 antigen cytoplasmic tail-binding protein 2	NA	NA	NA	9	-0.5	1.00E+00	9	2.7	2.10E-02
Q9CWK8	Sorting nexin-2	NA	NA	NA	7	-0.2	1.00E+00	7	2.1	1.40E-01
Q9CWZ3	RNA-binding protein 8A	NA	NA	NA	25	1.5	2.40E-01	25	0.6	5.20E-01
Q9CWZ7	Gamma-soluble NSF attachment protein	NA	NA	NA	8	-1.8	1.20E-01	8	3.3	1.60E-03
Q9CX56	26S proteasome non-ATPase regulatory subunit 8	NA	NA	NA	17	1.6	8.70E-03	17	2.1	5.30E-05
Q9CXR1	Dehydrogenase/reductase SDR family member 7	NA	NA	NA	12	-1.4	5.30E-01	12	2.3	7.50E-02
Q9CXW4	60S ribosomal protein L11	NA	NA	NA	16	-0.1	1.00E+00	16	1.5	2.30E-03
Q9CYA0	Cysteine-rich with EGF-like domain protein 2	NA	NA	NA	29	-0.8	1.60E-02	29	6.5	7.20E-34
Q9CYA6	Zinc finger CCHC domain-containing protein 8	NA	NA	NA	9	-1.3	2.20E-01	9	3	2.70E-04
Q9CYG7	Mitochondrial import receptor subunit TOM34	NA	NA	NA	11	2.8	1.70E-03	11	3.1	1.50E-04
Q9CZX8	40S ribosomal protein S19	NA	NA	NA	18	1	2.30E-01	18	3.9	1.70E-05
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	NA	NA	NA	8	-1.4	1.90E-02	8	2.9	1.70E-07
Q9D0F3	Protein ERGIC-53	NA	NA	NA	10	-1	2.80E-01	10	2.9	4.10E-05
Q9D0L8	mRNA cap guanine-N7 methyltransferase	NA	NA	NA	17	2.8	1.70E-03	17	0.5	3.70E-01
Q9D0M1	Phosphoribosyl pyrophosphate synthase-associated protein 1	NA	NA	NA	7	1.2	6.20E-01	7	1.4	4.80E-01
Q9D0M3	Cytochrome c1, heme protein, mitochondrial	NA	NA	NA	18	-0.4	3.80E-01	18	6.1	2.90E-25
Q9D0T1	NHP2-like protein 1	NA	NA	NA	19	2.4	8.70E-02	19	2.5	3.90E-02
Q9D1L9	Ragulator complex protein LAMTOR5	NA	NA	NA	44	-1.7	2.90E-02	44	4.2	1.30E-06
Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	NA	NA	NA	9	2.1	2.30E-02	9	2.9	4.90E-04
Q9D2C2	Protein SAAL1	NA	NA	NA	12	2.3	6.30E-03	12	3.2	8.00E-05
Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	NA	NA	NA	10	-1.5	6.90E-01	10	0	#######
Q9D3D9	ATP synthase subunit delta, mitochondrial	NA	NA	NA	36	0.2	8.90E-01	36	3.4	8.30E-04
Q9D5T0	ATPase family AAA domain-containing protein 1	NA	NA	NA	12	-1.5	6.90E-01	12	1.4	4.80E-01
Q9D5V6	Synapse-associated protein 1	NA	NA	NA	25	1.5	7.90E-02	25	4	8.80E-06
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NA	NA	NA	31	-0.5	7.20E-01	31	2.7	1.90E-05
Q9D6Y7	Mitochondrial peptide methionine sulfoxide reductase	NA	NA	NA	27	1.7	5.50E-02	27	3.9	3.20E-05
Q9D7M8	DNA-directed RNA polymerase II subunit RPB4	NA	NA	NA	22	-1.9	4.00E-01	22	1.8	2.60E-01
Q9D7S9	Charged multivesicular body protein 5	NA	NA	NA	16	0.2	1.00E+00	16	1.5	2.30E-01
Q9D824	Pre-mRNA 3'-end-processing factor FIP1	NA	NA	NA	17	-1	2.80E-01	17	4.3	6.50E-07
Q9D855	Cytochrome b-c1 complex subunit 7	NA	NA	NA	25	-2.6	1.40E-02	25	3.4	8.30E-04
Q9D883	Splicing factor U2AF 35 kDa subunit	NA	NA	NA	15	-1.3	9.90E-02	15	2.6	9.80E-05
Q9D8T2	Gasdermin-D	NA	NA	NA	12	1.5	2.40E-01	12	2.7	2.10E-02

		Exosomes			MDSCs			Global		
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Q9D8Y0	EF-hand domain-containing protein D2	NA	NA	NA	7	1.2	1.30E-01	7	4.1	4.60E-06
Q9DAU1	Protein canopy homolog 3	NA	NA	NA	13	-1.4	2.00E-01	13	3.7	1.20E-04
Q9DB15	39S ribosomal protein L12, mitochondrial	NA	NA	NA	12	1	1.90E-01	12	4.3	3.40E-07
Q9DB20	ATP synthase subunit O, mitochondrial	NA	NA	NA	12	0.4	4.70E-01	12	2.5	5.00E-08
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	NA	NA	NA	22	0.6	1.80E-01	22	5.8	5.60E-20
Q9DBG5	Perilipin-3	NA	NA	NA	35	0.7	8.60E-02	35	3.8	8.20E-16
Q9DBL9	1-acylglycerol-3-phosphate O-acyltransferase ABHD5	NA	NA	NA	11	3	1.10E-02	11	2.3	1.60E-02
Q9DBR0	A-kinase anchor protein 8	NA	NA	NA	7	-1	4.00E-01	7	3.7	1.20E-04
Q9DBS1	Transmembrane protein 43	NA	NA	NA	10	0.8	3.40E-01	10	2.6	4.00E-04
Q9DBT5	AMP deaminase 2	NA	NA	NA	6	0.6	4.70E-01	6	0.7	2.30E-01
Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NA	NA	NA	23	-0.9	6.40E-01	23	3	5.70E-03
Q9DCR2	AP-3 complex subunit sigma-1	NA	NA	NA	17	-0.4	8.60E-01	17	2.7	2.30E-04
Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NA	NA	NA	16	0.3	8.60E-01	16	3.2	3.00E-03
Q9EPJ9	ADP-ribosylation factor GTPase-activating protein 1	NA	NA	NA	13	0.4	6.40E-01	13	4.3	6.50E-07
Q9EPL4	Methyltransferase-like protein 9	NA	NA	NA	14	0.8	6.20E-01	14	2.7	2.10E-02
Q9EQ06	Estradiol 17-beta-dehydrogenase 11	NA	NA	NA	13	-0.6	4.40E-01	13	4.1	5.80E-10
Q9EQ32	Phosphoinositide 3-kinase adapter protein 1	NA	NA	NA	8	-0.3	8.60E-01	8	4.6	6.60E-09
Q9ERB0	Synaptosomal-associated protein 29	NA	NA	NA	28	-1.5	8.00E-04	28	5.6	6.60E-18
Q9ERD8	Gamma-parvin	NA	NA	NA	17	3	1.10E-02	17	0.8	3.10E-01
Q9ERI2	Ras-related protein Rab-27A	NA	NA	NA	13	0.4	7.50E-01	13	3.5	4.30E-04
Q9ERU9	E3 SUMO-protein ligase RanBP2	NA	NA	NA	3	-1	5.10E-01	3	1.1	1.60E-01
Q9JHF5	V-type proton ATPase subunit a	NA	NA	NA	12	-0.4	7.20E-01	12	4	3.90E-09
Q9JHJ0	Tropomodulin-3	NA	NA	NA	21	-0.4	2.20E-01	21	1.6	5.70E-11
Q9JHS3	Ragulator complex protein LAMTOR2	NA	NA	NA	46	-0.7	4.20E-01	46	3.4	2.00E-07
Q9JIX8	Apoptotic chromatin condensation inducer in the nucleus	NA	NA	NA	7	-1.3	3.00E-03	9	4.4	5.60E-17
Q9JIY5	Serine protease HTRA2, mitochondrial	NA	NA	NA	5	-1.1	7.80E-01	5	0	#######
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	NA	NA	NA	47	1.7	1.20E-02	47	1.6	3.00E-03
Q9JKV1	Proteasomal ubiquitin receptor ADRM1	NA	NA	NA	5	0.3	7.20E-01	5	3.2	4.40E-05
Q9JKY5	Huntingtin-interacting protein 1-related protein	NA	NA	NA	5	0.9	3.40E-01	5	3.6	2.30E-04
Q9JL62	Glycolipid transfer protein	NA	NA	NA	19	3.3	2.30E-03	19	1.2	1.10E-01
Q9JLF6	Protein-glutamine gamma-glutamyltransferase K	NA	NA	NA	12	-0.6	6.10E-01	12	2.4	1.20E-04
Q9QUG9	RAS guanyl-releasing protein 2	NA	NA	NA	4	2.2	1.40E-01	7	1.5	2.30E-01
Q9QUN7	Toll-like receptor 2	NA	NA	NA	7	-1.9	4.00E-01	7	0.9	5.80E-01
Q9QX47	Protein SON	NA	NA	NA	5	-0.8	3.20E-01	5	4.6	1.30E-08
Q9QXT0	Protein canopy homolog 2	NA	NA	NA	26	-3.6	1.40E-03	26	3.4	8.30E-04
Q9QXZ0	Microtubule-actin cross-linking factor 1	NA	NA	NA	2	-0.1	1.00E+00	2	2.6	5.60E-05
Q9QY06	Unconventional myosin-IXb	NA	NA	NA	2	0	1.00E+00	2	3.3	1.60E-03
Q9QZ06	Toll-interacting protein	NA	NA	NA	29	0	1.00E+00	34	1.5	6.90E-02
Q9QZS3	Protein numb homolog	NA	NA	NA	6	-1.5	6.90E-01	6	1.4	4.80E-01
Q9R059	Four and a half LIM domains protein 3	NA	NA	NA	30	-0.5	5.50E-01	30	5.3	7.90E-14
Q9R078	5'-AMP-activated protein kinase subunit beta-1	NA	NA	NA	18	-0.3	9.80E-01	18	3.9	1.40E-08
Q9R0U0	Serine/arginine-rich splicing factor 10	NA	NA	NA	10	-1.2	1.60E-01	10	3	1.30E-05
Q9R112	Sulfide:quinone oxidoreductase, mitochondrial	NA	NA	NA	18	-0.2	8.90E-01	18	5.5	9.20E-17
Q9R190	Metastasis-associated protein MTA2	NA	NA	NA	13	-0.9	1.30E-01	13	2.3	4.30E-07

		Exosomes			MDSCs			Global		
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Q9R1C7	Pre-mRNA-processing factor 40 homolog A	NA	NA	NA	10	-2	2.80E-04	10	4.2	1.60E-10
Q9WTI7	Unconventional myosin-Ic	NA	NA	NA	4	1.6	3.70E-01	4	1.8	2.60E-01
Q9WTX5	S-phase kinase-associated protein 1	NA	NA	NA	20	-0.2	1.00E+00	20	0.4	2.00E-01
Q9WUK2	Eukaryotic translation initiation factor 4H	NA	NA	NA	35	0	1.00E+00	35	2.3	3.20E-12
Q9WUU7	Cathepsin Z	NA	NA	NA	25	-0.3	6.10E-01	25	5	1.80E-27
Q9WV98	Mitochondrial import inner membrane translocase subunit Tim9	NA	NA	NA	36	-3.5	2.60E-03	36	3.3	1.60E-03
Q9WVE8	Protein kinase C and casein kinase substrate in neurons protein 2	NA	NA	NA	7	0.8	6.20E-01	7	2.7	2.10E-02
Q9Z0J0	Epididymal secretory protein E1	NA	NA	NA	32	-0.6	3.80E-01	32	5.1	1.20E-12
Q9Z0P4	Paralemmin-1	NA	NA	NA	8	-0.7	8.50E-01	8	2.9	1.10E-02
Q9Z0W3	Nuclear pore complex protein Nup160	NA	NA	NA	3	0.5	7.90E-01	3	2.5	3.90E-02
Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial	NA	NA	NA	10	1.2	3.30E-01	10	3	5.70E-03
Q9Z130	Heterogeneous nuclear ribonucleoprotein D-like	NA	NA	NA	12	0.6	4.20E-01	12	4.6	6.60E-09
Q9Z1G3	V-type proton ATPase subunit C 1	NA	NA	NA	7	3	1.10E-02	7	3.2	3.00E-03
Q9Z1R2	Large proline-rich protein BAG6	NA	NA	NA	7	1	1.20E-01	7	2.4	2.80E-05
Q9Z1T1	AP-3 complex subunit beta-1	NA	NA	NA	4	1.4	7.40E-02	4	4.2	1.30E-06
Q9Z1X4	Interleukin enhancer-binding factor 3	NA	NA	NA	10	-0.7	4.00E-01	12	1.1	2.20E-02
Q9Z204	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	NA	NA	NA	13	-1.5	2.90E-01	17	1.3	1.60E-01
Q9Z277	Tyrosine-protein kinase BAZ1B	NA	NA	NA	3	-2.2	8.10E-02	3	3	5.70E-03
Q9Z2D3	Non-syndromic hearing impairment protein 5 homolog	NA	NA	NA	15	0.8	2.60E-01	15	2.6	5.60E-05
Q9Z2E1	Methyl-CpG-binding domain protein 2	NA	NA	NA	12	-1	3.50E-01	12	4.1	4.60E-06
Q9Z2M7	Phosphomannomutase 2	NA	NA	NA	12	2	7.40E-02	12	-0.1	#######
Q9Z315	U4/U6.U5 tri-snRNP-associated protein 1	NA	NA	NA	5	-2.7	7.20E-02	5	2.5	3.90E-02